Full wwPDB X-ray Structure Validation Report

May 25, 2020 – 06:13 pm BST

PDB ID	:	1N33
Title	:	Structure of the Thermus thermophilus 30S ribosomal subunit bound to codon and near-cognate transfer rna anticodon stem-loop mismatched at the second codon position at the a site with paromomycin
Authors	:	Ogle, J.M.; Murphy IV, F.V.; Tarry, M.J.; Ramakrishnan, V.
Deposited on	:	2002-10-25
Resolution	:	3.35 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

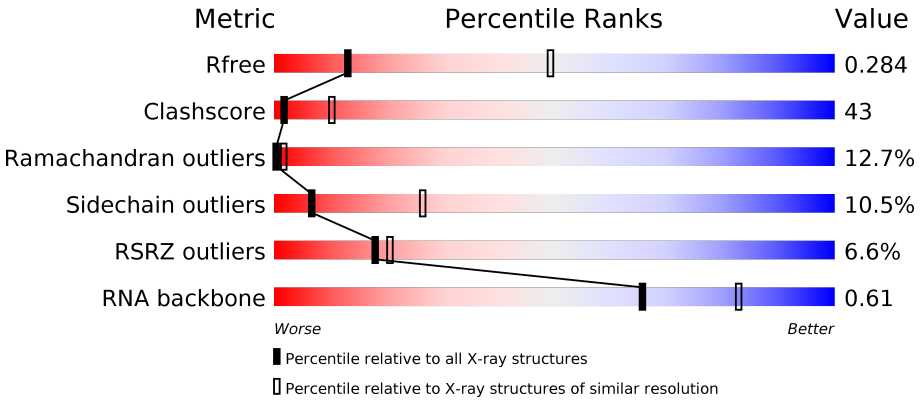
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.35 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1558 (3.42-3.30)
Clashscore	141614	1627 (3.42-3.30)
Ramachandran outliers	138981	1599 (3.42-3.30)
Sidechain outliers	138945	1598 (3.42-3.30)
RSRZ outliers	127900	1507 (3.42-3.30)
RNA backbone	3102	1023 (3.80-2.92)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1522	5% 25% 60% 13%
2	Y	17	18% 24% 24% 35%
3	Z	6	17% 50% 17% 33%
4	B	256	11% 16% 54% 18% 9%

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Mol	Chain	Length	Quality of chain
5	C	239	4% 18% 49% 18% 14%
6	D	208	10% 27% 59% 14%
7	E	161	31% 48% 12% 7%
8	F	101	14% 37% 51% 11%
9	G	155	3% 29% 58% 12%
10	H	138	% 25% 59% 14%
11	I	128	11% 19% 59% 20%
12	J	104	22% 11% 55% 27% 6%
13	K	129	5% 32% 51% 9% 8%
14	L	135	4% 25% 51% 16% 8%
15	M	126	6% 23% 56% 14% 6%
16	N	60	7% 17% 63% 18%
17	O	88	5% 33% 59% 8%
18	P	88	5% 18% 64% 11% 6%
19	Q	104	8% 16% 67% 14%
20	R	88	5% 13% 60% 9% 17%
21	S	92	17% 24% 47% 15% 13%
22	T	106	4% 18% 59% 15% 7%
23	V	26	8% 12% 69% 12% 8%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1548	-	-	-	X
25	MG	A	1585	-	-	-	X
25	MG	A	1597	-	-	-	X
25	MG	A	1606	-	-	-	X
25	MG	A	1607	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1618	-	-	-	X

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 52140 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	1513	32508	14472	6016	10509	1511	22	0	0

- Molecule 2 is a RNA chain called ANTICODON STEM-LOOP OF SER TRANSFER RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	Y	11	235	106	45	74	10	0	0	0

- Molecule 3 is a RNA chain called A-SITE MESSENGER RNA FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	Z	4	77	36	8	30	3	0	0	0

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S2.

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

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S3.

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

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S4.

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

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S5.

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

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S6.

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

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S7.

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

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	25	ASP	GLU	CONFLICT	UNP P24319
H	37	ARG	LYS	CONFLICT	UNP P24319
H	52	ASP	GLU	CONFLICT	UNP P24319
H	61	VAL	ILE	CONFLICT	UNP P24319
H	62	TYR	HIS	CONFLICT	UNP P24319
H	81	HIS	LYS	CONFLICT	UNP P24319
H	88	LYS	ARG	CONFLICT	UNP P24319
H	115	SER	PRO	CONFLICT	UNP P24319

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	I	127	Total	C	N	O	0	0	0
			1011	639	198	174			

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S10.

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

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S11.

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

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S12.

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

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S13.

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

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S14.

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

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S15.

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

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S16.

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

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	Q	104	Total	C	N	O	S	0	0	0
			857	547	161	147	2			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	50	LYS	ARG	CONFLICT	UNP P24321
Q	53	LEU	VAL	CONFLICT	UNP P24321
Q	62	SER	ALA	CONFLICT	UNP P24321
Q	79	SER	GLU	CONFLICT	UNP P24321
Q	82	MET	LEU	CONFLICT	UNP P24321
Q	90	ILE	VAL	CONFLICT	UNP P24321
Q	96	GLN	ALA	CONFLICT	UNP P24321

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
20	R	73	Total	C	N	O	0	0	0
			597	380	118	99			

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	S	80	Total	C	N	O	S	0	0	0
			647	414	119	112	2			

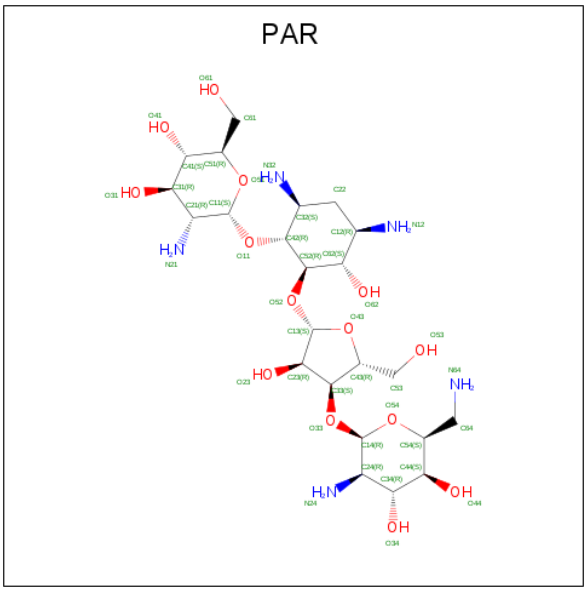
- Molecule 22 is a protein called 30S RIBOSOMAL PROTEIN S20.

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

- Molecule 23 is a protein called 30S RIBOSOMAL PROTEIN THX.

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

- Molecule 24 is PAROMOMYCIN (three-letter code: PAR) (formula: $C_{23}H_{45}N_5O_{14}$).



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

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
25	Z	2	Total Mg 2 2	0	0
25	A	103	Total Mg 103 103	0	0
25	Y	1	Total Mg 1 1	0	0

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

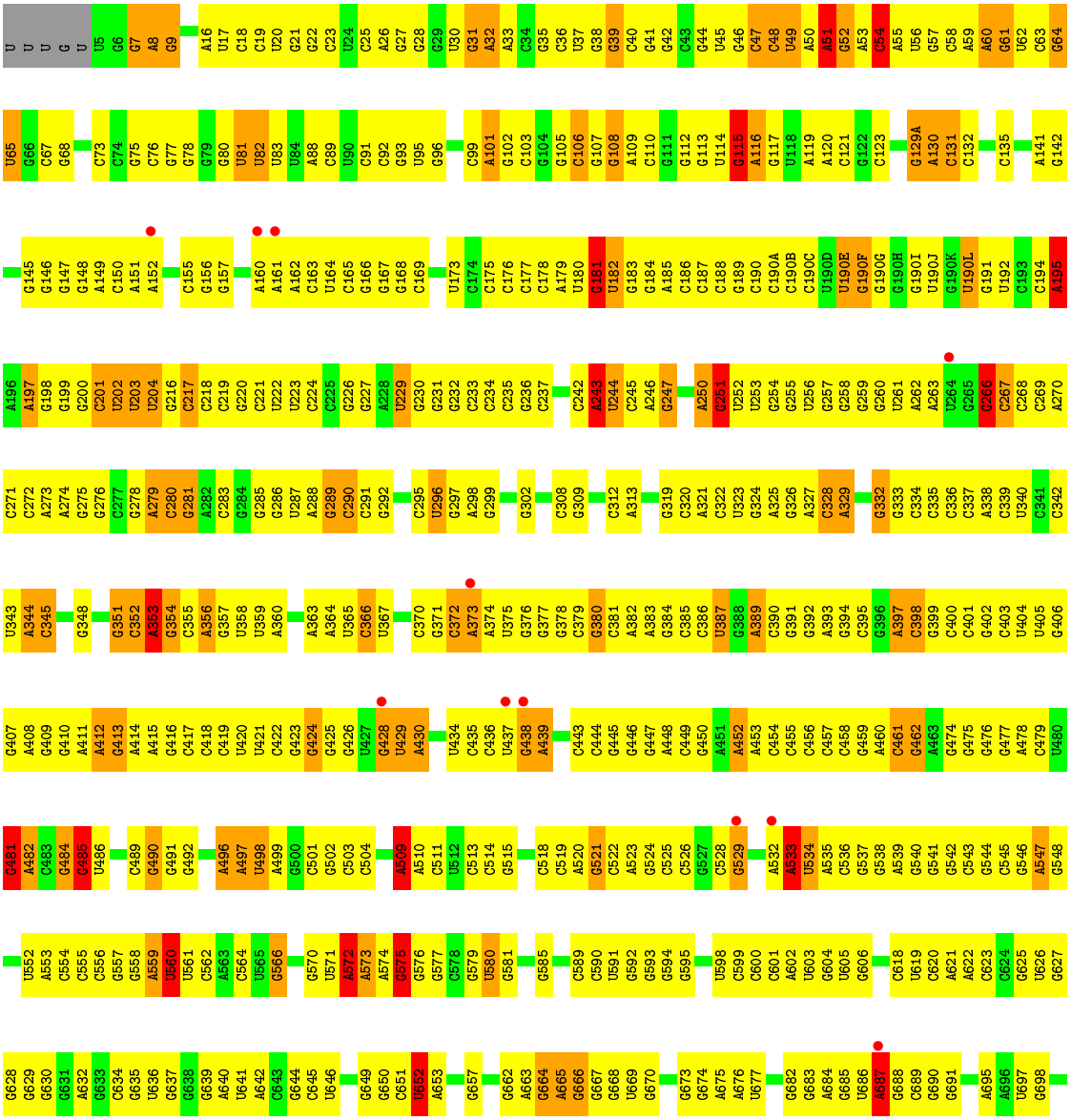
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	D	1	Total Zn 1 1	0	0
26	N	1	Total Zn 1 1	0	0

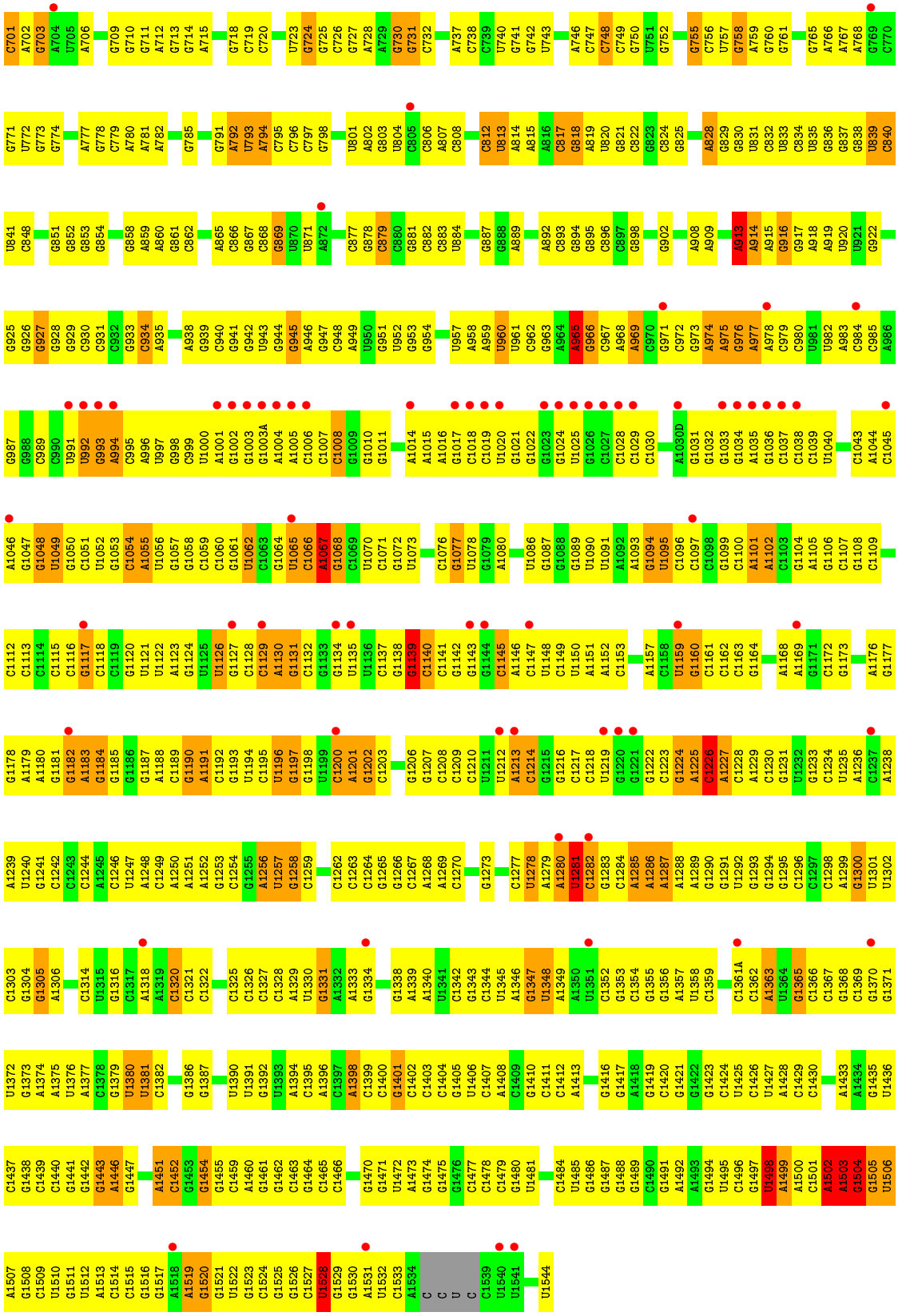
3 Residue-property plots (i)

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

- Molecule 1: 16S RIBOSOMAL RNA

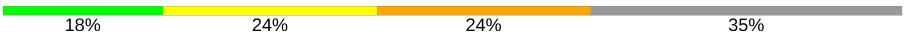
Chain A: 5% 25% 60% 13%

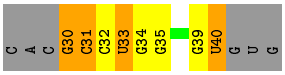




• Molecule 2: ANTICODON STEM-LOOP OF SER TRANSFER RNA

Chain Y:



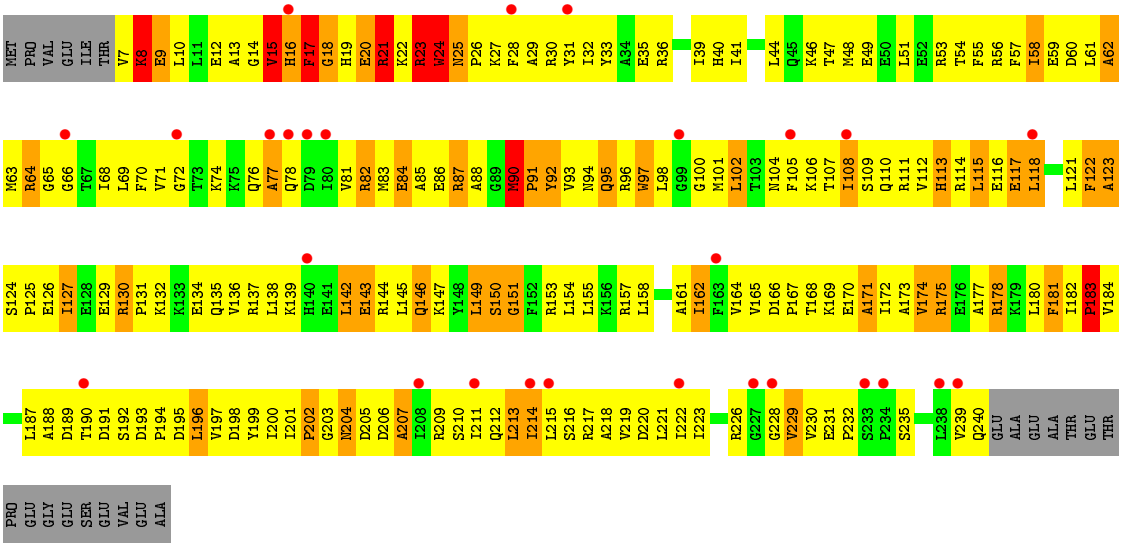


• Molecule 3: A-SITE MESSENGER RNA FRAGMENT

Chain Z:

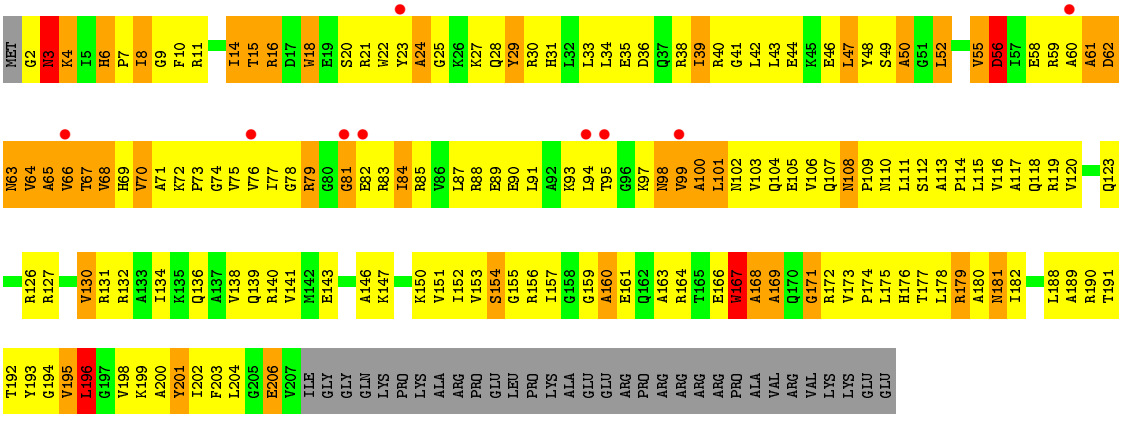
• Molecule 4: 30S RIBOSOMAL PROTEIN S2

Chain B:



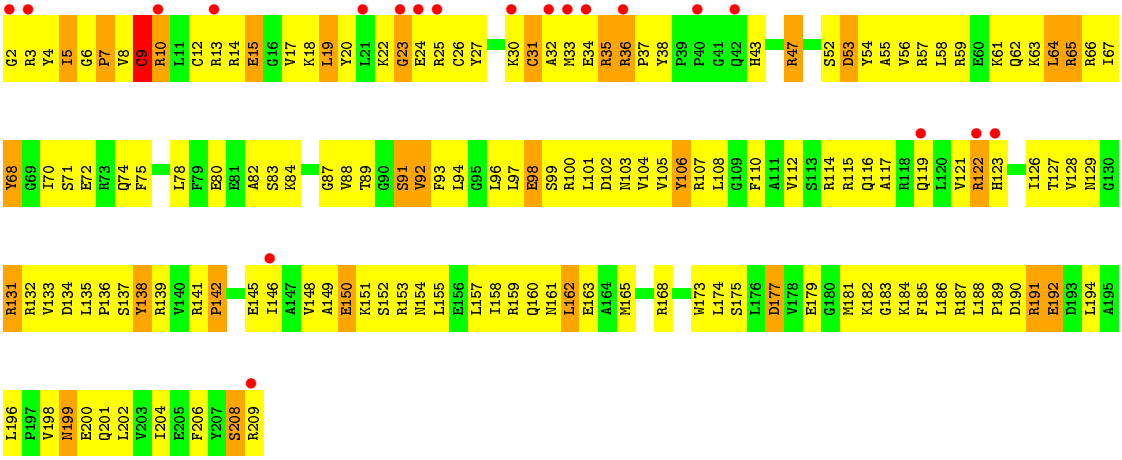
• Molecule 5: 30S RIBOSOMAL PROTEIN S3

Chain C:



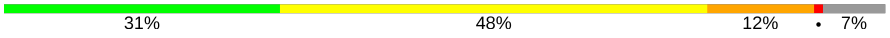
• Molecule 6: 30S RIBOSOMAL PROTEIN S4

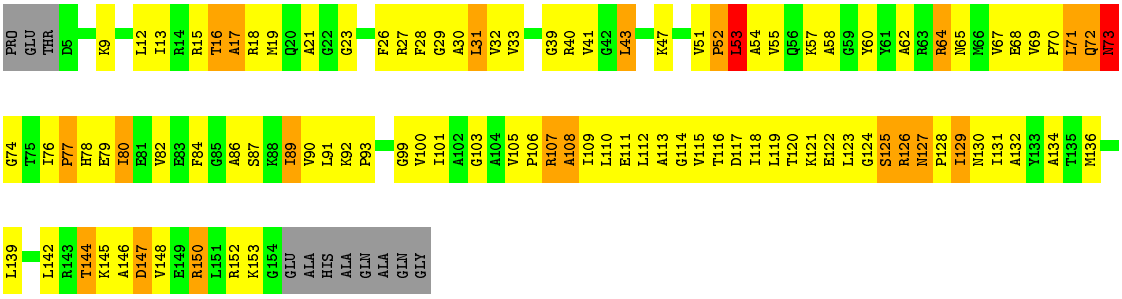
Chain D:



- Molecule 7: 30S RIBOSOMAL PROTEIN S5

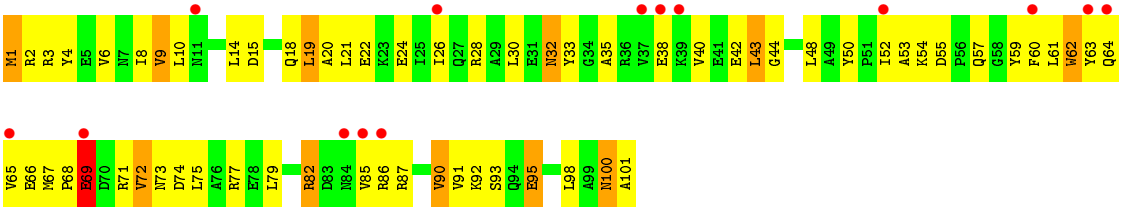
Chain E:





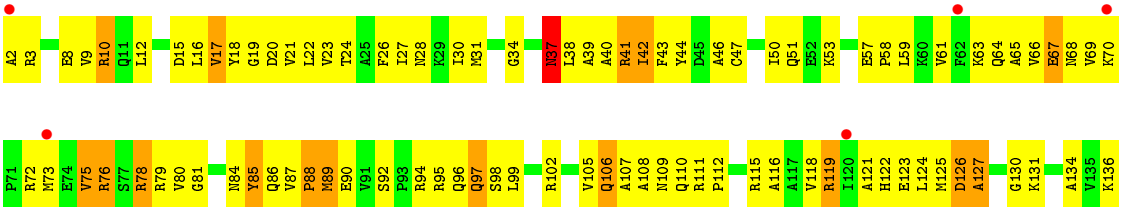
- Molecule 8: 30S RIBOSOMAL PROTEIN S6

Chain F:

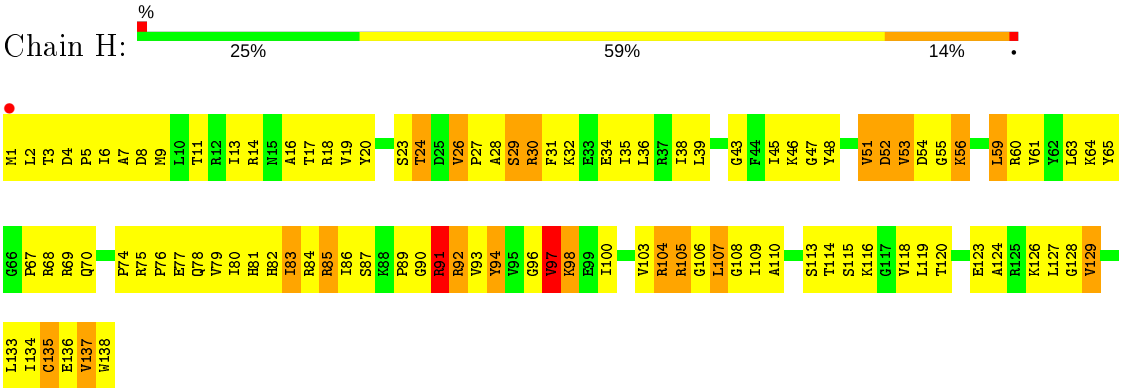


- Molecule 9: 30S RIBOSOMAL PROTEIN S7

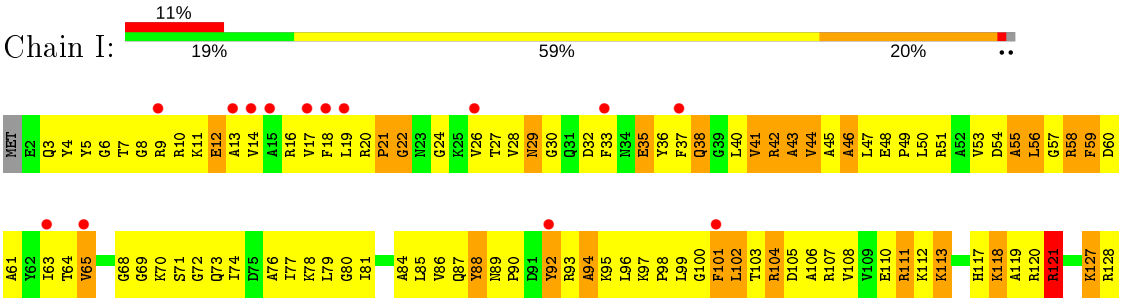
Chain G:



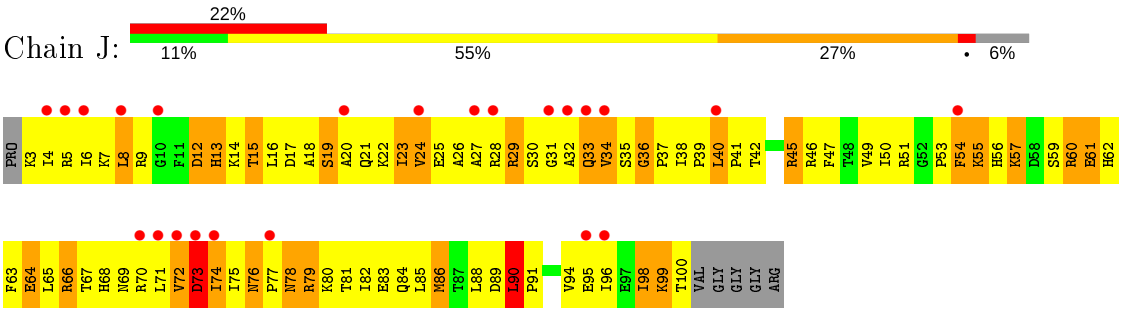
• Molecule 10: 30S RIBOSOMAL PROTEIN S8



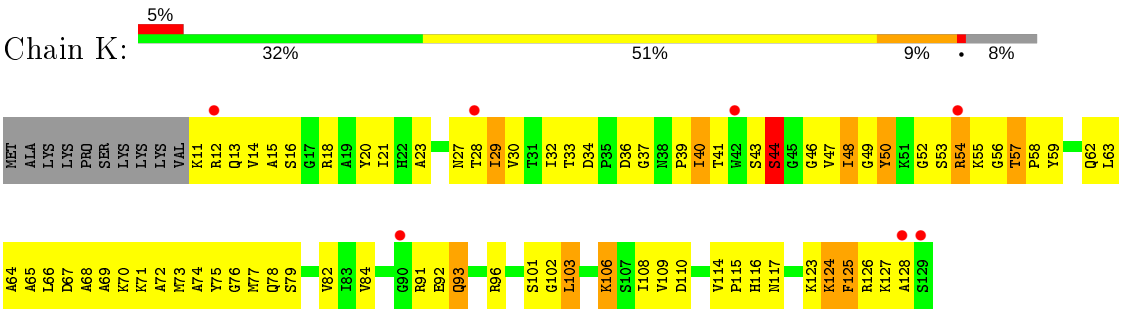
• Molecule 11: 30S RIBOSOMAL PROTEIN S9



• Molecule 12: 30S RIBOSOMAL PROTEIN S10

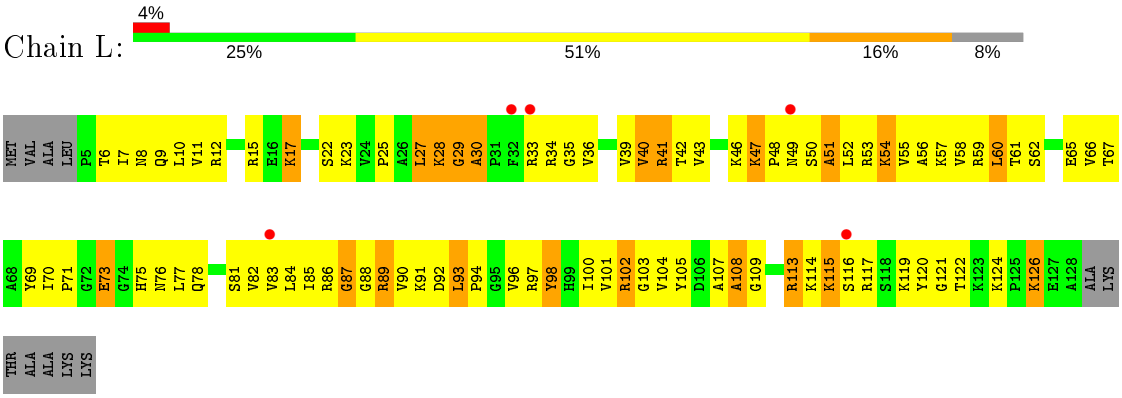


• Molecule 13: 30S RIBOSOMAL PROTEIN S11



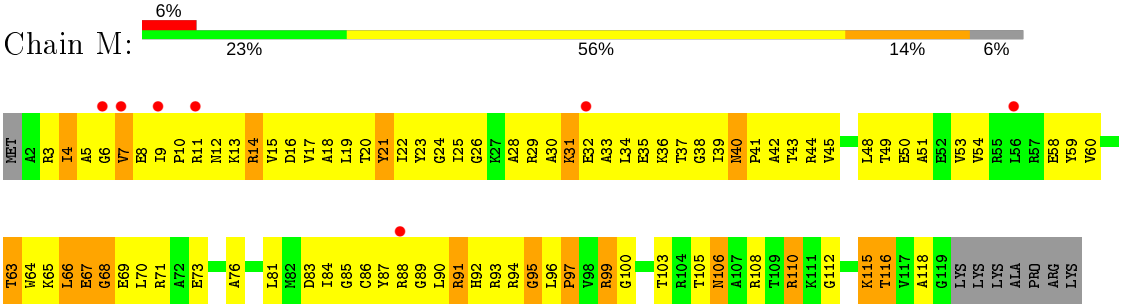
• Molecule 14: 30S RIBOSOMAL PROTEIN S12

Chain L:



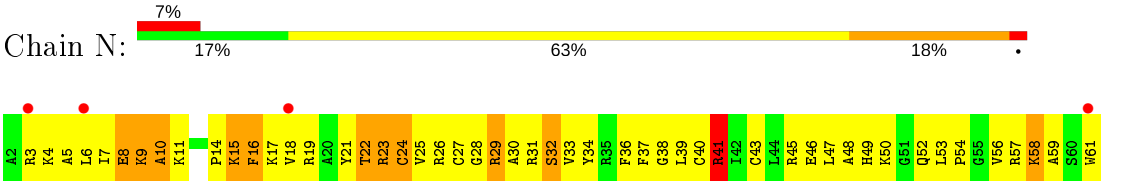
• Molecule 15: 30S RIBOSOMAL PROTEIN S13

Chain M:



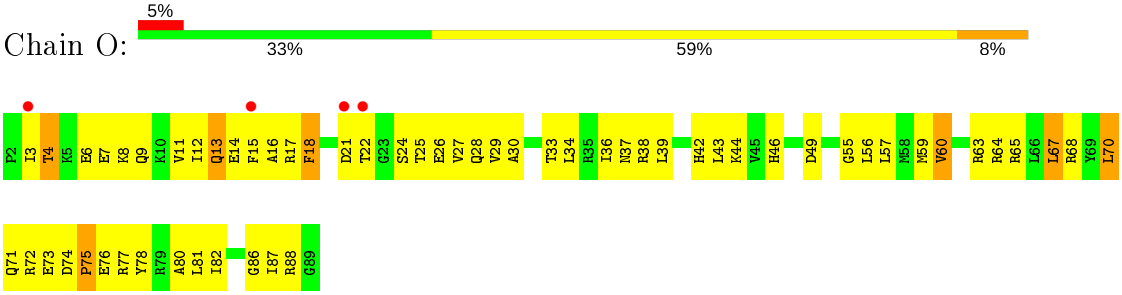
• Molecule 16: 30S RIBOSOMAL PROTEIN S14

Chain N:



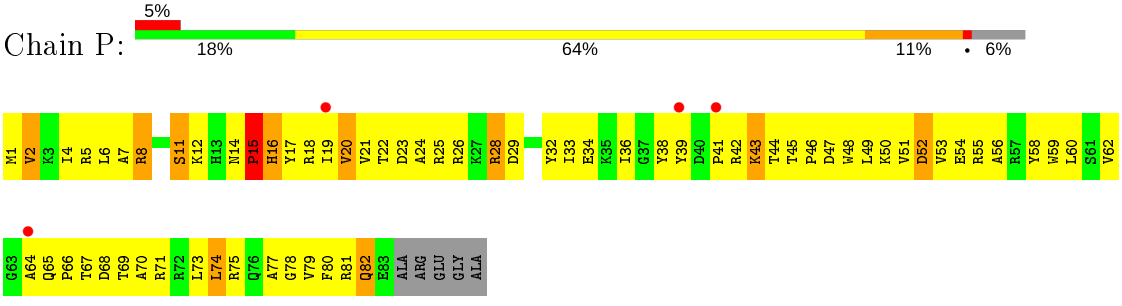
• Molecule 17: 30S RIBOSOMAL PROTEIN S15

Chain O:



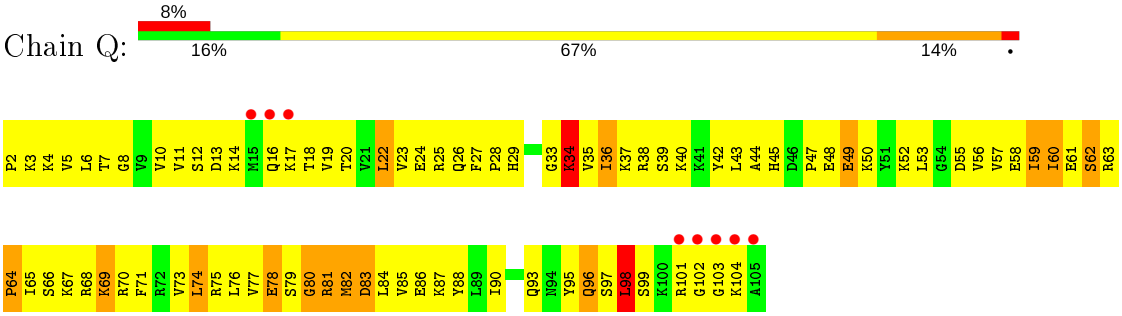
• Molecule 18: 30S RIBOSOMAL PROTEIN S16

Chain P:



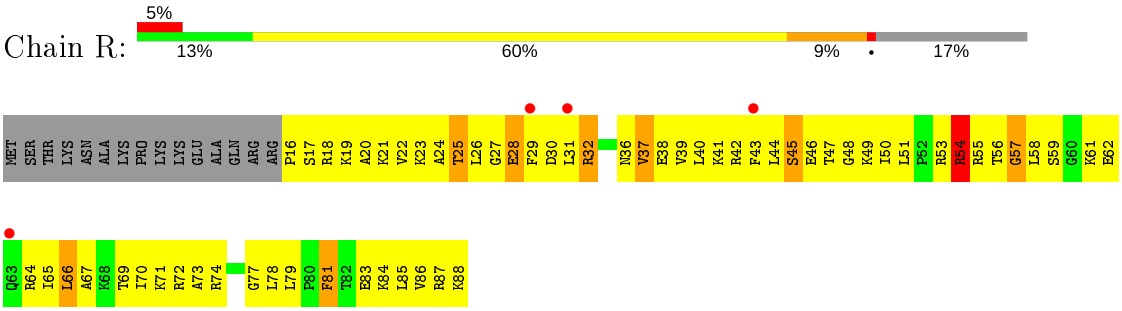
• Molecule 19: 30S RIBOSOMAL PROTEIN S17

Chain Q:



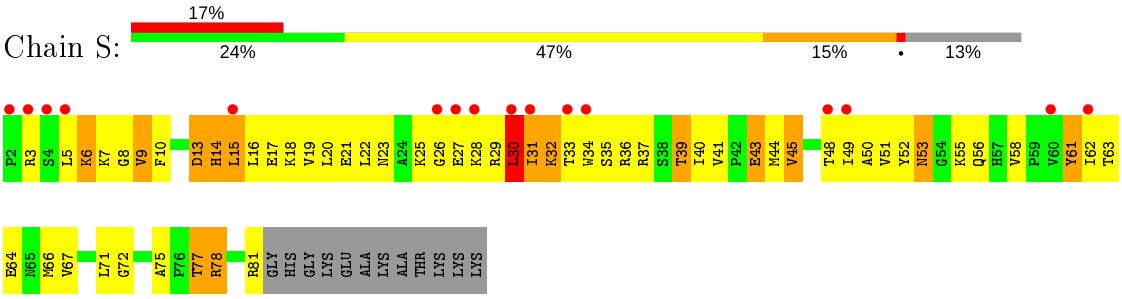
• Molecule 20: 30S RIBOSOMAL PROTEIN S18

Chain R:



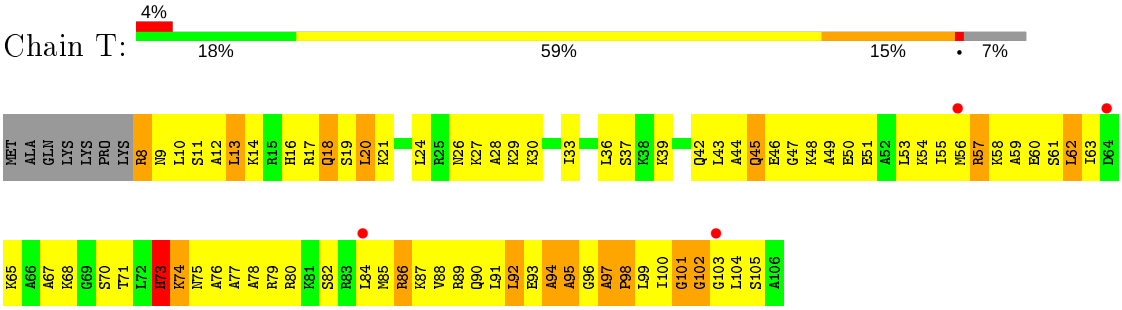
• Molecule 21: 30S RIBOSOMAL PROTEIN S19

Chain S:



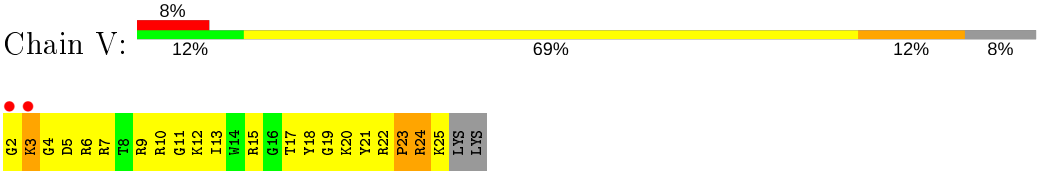
• Molecule 22: 30S RIBOSOMAL PROTEIN S20

Chain T:



• Molecule 23: 30S RIBOSOMAL PROTEIN THX

Chain V:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	401.60Å 401.60Å 176.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.54 – 3.35 74.58 – 3.35	Depositor EDS
% Data completeness (in resolution range)	88.6 (74.54-3.35) 88.6 (74.58-3.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$< I/\sigma(I) >$ [1]	2.31 (at 3.33Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.225 , 0.284 0.231 , 0.284	Depositor DCC
R_{free} test set	9128 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	104.3	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 136.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	52140	wwPDB-VP
Average B, all atoms (Å^2)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.56% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.58	1/36387 (0.0%)	0.76	33/56789 (0.1%)
2	Y	0.59	0/241	0.92	2/375 (0.5%)
3	Z	0.48	0/84	0.78	0/128
4	B	0.36	0/1935	0.66	0/2609
5	C	0.38	0/1636	0.65	0/2205
6	D	0.42	0/1733	0.68	0/2318
7	E	0.48	0/1162	0.77	0/1564
8	F	0.37	0/856	0.66	0/1154
9	G	0.35	0/1276	0.60	0/1709
10	H	0.53	0/1136	0.83	1/1527 (0.1%)
11	I	0.35	0/1029	0.64	0/1378
12	J	0.38	0/805	0.71	1/1082 (0.1%)
13	K	0.41	0/900	0.69	0/1213
14	L	0.44	0/986	0.79	0/1320
15	M	0.35	0/947	0.61	0/1270
16	N	0.39	0/501	0.66	0/664
17	O	0.41	0/745	0.63	0/992
18	P	0.53	0/716	0.84	0/963
19	Q	0.55	0/870	0.80	0/1159
20	R	0.39	0/603	0.68	0/799
21	S	0.35	0/661	0.68	0/890
22	T	0.45	0/765	0.81	2/1007 (0.2%)
23	V	0.37	0/212	0.59	0/277
All	All	0.53	1/56186 (0.0%)	0.74	39/83392 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	3	46
10	H	0	1
All	All	3	47

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	758	G	C5-C6	-5.26	1.37	1.42

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	243	A	C2'-C3'-O3'	10.26	132.07	109.50
1	A	366	C	C2'-C3'-O3'	8.95	129.19	109.50
1	A	1498	U	C2'-C3'-O3'	8.91	129.10	109.50
1	A	1528	U	C2'-C3'-O3'	8.77	128.80	109.50
1	A	181	G	C2'-C3'-O3'	8.66	128.56	109.50
1	A	1504	G	C2'-C3'-O3'	8.38	127.94	109.50
1	A	115	G	N9-C1'-C2'	7.93	124.31	114.00
1	A	575	G	C2'-C3'-O3'	7.73	126.50	109.50
1	A	559	A	C2'-C3'-O3'	7.61	126.23	109.50
1	A	115	G	C2'-C3'-O3'	7.25	125.44	109.50
1	A	266	G	C2'-C3'-O3'	7.22	125.39	109.50
1	A	1503	A	C2'-C3'-O3'	6.99	124.89	113.70
1	A	353	A	C5'-C4'-O4'	-6.71	101.05	109.10
1	A	748	C	C2'-C3'-O3'	6.43	123.99	113.70
2	Y	31	C	C1'-C2'-O2'	6.42	129.87	110.60
1	A	1502	A	N9-C1'-C2'	6.38	122.29	114.00
12	J	60	ARG	N-CA-C	6.16	127.64	111.00
1	A	389	A	C5'-C4'-C3'	5.95	125.51	116.00
1	A	818	G	N9-C1'-C2'	5.88	121.64	114.00
22	T	13	LEU	N-CA-C	-5.83	95.25	111.00
1	A	51	A	N9-C1'-C2'	5.83	121.57	114.00
1	A	1528	U	C4'-C3'-O3'	5.71	124.43	113.00
1	A	1380	U	C2'-C3'-O3'	5.71	122.83	113.70
1	A	108	G	N9-C1'-C2'	-5.60	105.84	112.00
1	A	266	G	O4'-C1'-N9	-5.48	103.82	108.20
1	A	533	A	C2'-C3'-O3'	5.40	122.34	113.70
1	A	509	A	C2'-C3'-O3'	5.39	122.33	113.70
1	A	965	A	C2'-C3'-O3'	5.35	122.27	113.70
1	A	1139	G	N9-C1'-C2'	5.35	120.96	114.00
1	A	687	A	C2'-C3'-O3'	5.34	122.24	113.70
22	T	24	LEU	CA-CB-CG	-5.29	103.13	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1504	G	C4'-C3'-O3'	5.25	123.50	113.00
1	A	1300	G	N9-C1'-C2'	5.19	120.75	114.00
1	A	1380	U	N1-C1'-C2'	5.19	120.74	114.00
10	H	137	VAL	CB-CA-C	-5.16	101.59	111.40
1	A	572	A	N9-C1'-C2'	5.11	120.64	114.00
2	Y	30	G	C1'-C2'-O2'	5.11	125.91	110.60
1	A	1067	A	C2'-C3'-O3'	5.07	121.81	113.70
1	A	485	G	N9-C1'-C2'	5.07	120.58	114.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	243	A	C3'
1	A	1504	G	C3'
1	A	1528	U	C3'

All (47) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1049	U	Sidechain
1	A	106	C	Sidechain
1	A	1062	U	Sidechain
1	A	1067	A	Sidechain
1	A	1077	G	Sidechain
1	A	115	G	Sidechain
1	A	1226	C	Sidechain
1	A	1281	U	Sidechain
1	A	1395	C	Sidechain
1	A	1396	A	Sidechain
1	A	1454	G	Sidechain
1	A	1498	U	Sidechain
1	A	1519	A	Sidechain
1	A	190(L)	U	Sidechain
1	A	195	A	Sidechain
1	A	229	U	Sidechain
1	A	251	G	Sidechain
1	A	274	A	Sidechain
1	A	281	G	Sidechain
1	A	290	C	Sidechain
1	A	296	U	Sidechain
1	A	297	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	356	A	Sidechain
1	A	380	G	Sidechain
1	A	387	U	Sidechain
1	A	481	G	Sidechain
1	A	490	G	Sidechain
1	A	51	A	Sidechain
1	A	529	G	Sidechain
1	A	54	C	Sidechain
1	A	560	U	Sidechain
1	A	566	G	Sidechain
1	A	575	G	Sidechain
1	A	580	U	Sidechain
1	A	634	C	Sidechain
1	A	652	U	Sidechain
1	A	664	G	Sidechain
1	A	687	A	Sidechain
1	A	727	G	Sidechain
1	A	730	G	Sidechain
1	A	879	C	Sidechain
1	A	887	G	Sidechain
1	A	898	G	Sidechain
1	A	913	A	Sidechain
1	A	916	G	Sidechain
10	H	94	TYR	Sidechain

5.2 Too-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 hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32508	0	16414	1353	0
2	Y	235	0	121	11	0
3	Z	77	0	42	1	0
4	B	1900	0	1951	303	0
5	C	1612	0	1677	285	0
6	D	1703	0	1764	212	0
7	E	1146	0	1207	129	0
8	F	843	0	857	94	0
9	G	1257	0	1296	132	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	H	1116	0	1177	143	0
11	I	1011	0	1043	177	0
12	J	792	0	835	169	2
13	K	885	0	904	103	0
14	L	970	0	1057	138	0
15	M	937	0	995	121	0
16	N	492	0	531	89	0
17	O	734	0	771	78	0
18	P	700	0	720	86	0
19	Q	857	0	930	130	0
20	R	597	0	668	93	0
21	S	647	0	673	94	0
22	T	763	0	861	96	0
23	V	208	0	221	37	0
24	A	42	0	45	4	0
25	A	103	0	0	0	0
25	Y	1	0	0	0	0
25	Z	2	0	0	0	0
26	D	1	0	0	0	0
26	N	1	0	0	0	0
All	All	52140	0	36760	3828	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 43.

All (3828) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:36:ARG:H	6:D:37:PRO:HD3	1.05	1.11
1:A:1443:G:H5"	1:A:1446:A:H5"	1.28	1.09
1:A:1356:G:H2'	1:A:1357:A:C8	1.90	1.06
6:D:63:LYS:HD2	6:D:198:VAL:HG23	1.34	1.06
1:A:1250:A:H4'	11:I:68:GLY:H	1.18	1.05
4:B:84:GLU:HB3	4:B:219:VAL:HG21	1.39	1.04
1:A:737:A:H1'	8:F:73:ASN:HD21	1.23	1.03
13:K:126:ARG:HG2	13:K:127:LYS:H	1.16	1.03
7:E:80:ILE:CD1	7:E:91:LEU:HB2	1.87	1.03
1:A:1305:G:H22	1:A:1331:G:H2'	1.16	1.02
5:C:91:LEU:HD11	5:C:99:VAL:HG13	1.42	1.01
1:A:112:G:H21	1:A:354:G:H5'	1.24	1.01
1:A:1286:A:H2'	1:A:1287:A:H4'	1.40	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:26:GLU:HA	17:O:81:LEU:HD11	1.41	0.99
13:K:54:ARG:HB3	13:K:54:ARG:HH11	1.28	0.98
19:Q:27:PHE:HB2	19:Q:28:PRO:HD2	1.43	0.98
4:B:21:ARG:HD3	4:B:21:ARG:H	1.27	0.98
5:C:35:GLU:HG2	5:C:59:ARG:HH22	1.25	0.98
1:A:411:A:H62	1:A:413:G:H21	1.04	0.98
1:A:975:A:H4'	1:A:976:G:H5"	1.43	0.97
5:C:67:THR:HG22	5:C:68:VAL:H	1.29	0.97
19:Q:63:ARG:HG2	19:Q:64:PRO:HD2	1.46	0.97
1:A:328:C:H4'	1:A:329:A:H5'	1.45	0.97
7:E:80:ILE:HD11	7:E:91:LEU:HB2	1.45	0.97
11:I:6:GLY:N	11:I:84:ALA:HB2	1.80	0.97
6:D:149:ALA:HB3	6:D:152:SER:HB3	1.42	0.97
1:A:1356:G:H2'	1:A:1357:A:H8	1.29	0.97
4:B:83:MET:HG2	4:B:235:SER:HB3	1.43	0.97
1:A:758:G:O5'	1:A:758:G:H8	1.48	0.96
1:A:1343:G:H2'	1:A:1344:C:H6	1.29	0.95
5:C:130:VAL:HG12	5:C:134:ILE:HD11	1.48	0.95
8:F:87:ARG:HG3	8:F:87:ARG:HH11	1.31	0.95
10:H:11:THR:HA	10:H:14:ARG:HH12	1.30	0.95
21:S:39:THR:HG22	21:S:40:ILE:H	1.31	0.95
20:R:21:LYS:HD3	20:R:57:GLY:HA3	1.48	0.95
20:R:47:THR:HG22	20:R:48:GLY:H	1.32	0.94
21:S:40:ILE:HG23	21:S:44:MET:HG3	1.49	0.94
11:I:28:VAL:HG12	11:I:29:ASN:H	1.31	0.94
1:A:371:G:O2'	1:A:372:C:H5'	1.68	0.94
1:A:390:C:H2'	1:A:391:G:H8	1.29	0.94
4:B:124:SER:O	4:B:127:ILE:HG13	1.66	0.94
2:Y:31:C:O2'	2:Y:32:C:H5'	1.66	0.94
1:A:458:C:H2'	1:A:459:G:H8	1.33	0.94
14:L:89:ARG:HB3	14:L:89:ARG:HH11	1.32	0.94
1:A:80:G:H3'	1:A:81:U:H5"	1.50	0.93
6:D:9:CYS:SG	6:D:22:LYS:HE3	2.06	0.93
1:A:1064:G:H4'	1:A:1065:U:H5'	1.48	0.93
11:I:46:ALA:HA	11:I:78:LYS:HB2	1.47	0.93
1:A:1116:C:H2'	1:A:1117:G:H5"	1.49	0.93
1:A:1250:A:H4'	11:I:68:GLY:N	1.81	0.93
5:C:50:ALA:HA	5:C:72:LYS:HB2	1.50	0.93
8:F:14:LEU:HD22	8:F:18:GLN:HB3	1.51	0.93
7:E:74:GLY:HA3	7:E:116:THR:HG22	1.51	0.93
12:J:15:THR:HG23	12:J:16:LEU:H	1.34	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:C:H2'	1:A:391:G:C8	2.04	0.92
1:A:1532:U:H2'	1:A:1533:C:H5"	1.51	0.92
10:H:29:SER:HB3	10:H:32:LYS:HE3	1.52	0.92
10:H:9:MET:SD	10:H:32:LYS:HG2	2.10	0.92
4:B:51:LEU:HD22	4:B:55:PHE:HE1	1.35	0.92
14:L:47:LYS:HB3	14:L:48:PRO:CD	2.00	0.92
21:S:28:LYS:HG2	21:S:29:ARG:H	1.35	0.92
22:T:57:ARG:HB3	22:T:57:ARG:NH1	1.85	0.91
12:J:8:LEU:HB3	12:J:16:LEU:HD21	1.51	0.91
1:A:1503:A:H5'	1:A:1531:A:H1'	1.52	0.91
1:A:1343:G:H2'	1:A:1344:C:C6	2.05	0.91
6:D:36:ARG:N	6:D:37:PRO:HD3	1.86	0.91
10:H:11:THR:HA	10:H:14:ARG:NH1	1.84	0.91
18:P:22:THR:HA	18:P:33:ILE:HD12	1.52	0.91
7:E:53:LEU:H	7:E:53:LEU:HD12	1.33	0.91
11:I:19:LEU:HB3	11:I:59:PHE:CZ	2.06	0.91
1:A:838:G:H2'	1:A:839:U:H5"	1.53	0.90
5:C:3:ASN:HD22	5:C:3:ASN:N	1.62	0.90
1:A:474:G:H4'	18:P:81:ARG:HH21	1.35	0.90
1:A:1147:C:H4'	11:I:5:TYR:HE1	1.37	0.90
11:I:64:THR:HG22	11:I:65:VAL:H	1.37	0.90
12:J:90:LEU:H	12:J:91:PRO:HD2	1.35	0.89
1:A:243:A:H4'	1:A:244:U:H5'	1.54	0.89
22:T:88:VAL:O	22:T:92:LEU:HB2	1.72	0.89
13:K:106:LYS:HA	13:K:106:LYS:HE2	1.54	0.89
22:T:57:ARG:HB3	22:T:57:ARG:HH11	1.36	0.89
15:M:10:PRO:HB2	15:M:18:ALA:HB1	1.54	0.89
5:C:64:VAL:HB	5:C:99:VAL:HB	1.52	0.89
22:T:53:LEU:O	22:T:57:ARG:HG3	1.73	0.89
13:K:54:ARG:O	13:K:57:THR:HG22	1.73	0.88
10:H:107:LEU:N	10:H:107:LEU:HD23	1.89	0.88
18:P:2:VAL:O	18:P:64:ALA:HA	1.74	0.88
19:Q:96:GLN:HB2	19:Q:103:GLY:HA2	1.55	0.88
5:C:18:TRP:HE3	5:C:18:TRP:H	1.21	0.87
1:A:1116:C:C2'	1:A:1117:G:H5"	2.04	0.87
1:A:1443:G:H5"	1:A:1446:A:C5'	2.05	0.86
7:E:41:VAL:CG1	7:E:113:ALA:HA	2.04	0.86
5:C:40:ARG:HB2	5:C:40:ARG:NH1	1.90	0.86
19:Q:98:LEU:HA	19:Q:102:GLY:HA2	1.55	0.86
20:R:66:LEU:HD23	20:R:67:ALA:N	1.90	0.86
5:C:27:LYS:HA	5:C:30:ARG:HH12	1.40	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:67:THR:O	5:C:68:VAL:HG23	1.74	0.86
12:J:34:VAL:HG12	12:J:35:SER:H	1.41	0.86
13:K:52:GLY:HA2	13:K:55:LYS:HE2	1.58	0.86
12:J:45:ARG:HB3	12:J:45:ARG:NH1	1.91	0.86
15:M:49:THR:HG22	15:M:51:ALA:H	1.40	0.86
1:A:524:G:H2'	1:A:525:C:C6	2.11	0.86
9:G:38:LEU:HD12	9:G:39:ALA:N	1.90	0.86
14:L:34:ARG:O	14:L:61:THR:HG23	1.74	0.85
15:M:105:THR:HG22	15:M:106:ASN:H	1.41	0.85
1:A:1057:G:H5"	5:C:154:SER:HB2	1.58	0.85
17:O:8:LYS:O	17:O:11:VAL:HG22	1.74	0.85
14:L:87:GLY:HA2	14:L:98:TYR:HA	1.58	0.85
17:O:39:LEU:HD22	17:O:56:LEU:HD12	1.56	0.85
19:Q:18:THR:HG23	19:Q:69:LYS:HE3	1.57	0.85
1:A:328:C:H4'	1:A:329:A:C5'	2.06	0.85
19:Q:56:VAL:HG12	19:Q:77:VAL:HB	1.57	0.85
19:Q:82:MET:O	19:Q:84:LEU:N	2.08	0.85
11:I:43:ALA:HA	11:I:74:ILE:HD12	1.57	0.85
14:L:54:LYS:HB3	14:L:70:ILE:HD12	1.58	0.85
4:B:137:ARG:HG3	4:B:138:LEU:N	1.92	0.84
1:A:337:C:H2'	1:A:338:A:H8	1.40	0.84
5:C:66:VAL:HG23	5:C:99:VAL:HG21	1.57	0.84
7:E:43:LEU:HD11	7:E:132:ALA:HB1	1.58	0.84
23:V:24:ARG:H	23:V:24:ARG:HD2	1.40	0.84
7:E:129:ILE:H	7:E:129:ILE:HD12	1.42	0.84
1:A:1065:U:H4'	1:A:1066:C:O5'	1.78	0.84
10:H:116:LYS:HD2	10:H:129:VAL:HG21	1.58	0.84
13:K:54:ARG:HB3	13:K:54:ARG:NH1	1.91	0.84
4:B:7:VAL:HG11	4:B:221:LEU:HD21	1.59	0.84
1:A:1189:C:P	12:J:51:ARG:HH22	1.99	0.84
1:A:1262:C:H42	1:A:1273:G:H1	1.24	0.84
1:A:625:G:H4'	18:P:16:HIS:CD2	2.12	0.83
1:A:1223:C:P	21:S:78:ARG:HH12	2.02	0.83
5:C:64:VAL:HG12	5:C:65:ALA:H	1.40	0.83
6:D:36:ARG:H	6:D:37:PRO:CD	1.91	0.83
5:C:131:ARG:HA	5:C:134:ILE:HD12	1.61	0.83
5:C:6:HIS:HD2	5:C:8:ILE:HD11	1.41	0.83
1:A:740:U:O2'	1:A:741:G:H5'	1.79	0.83
1:A:946:A:H2'	1:A:947:G:C8	2.14	0.83
11:I:8:GLY:HA2	11:I:79:LEU:HD12	1.59	0.83
5:C:35:GLU:HG2	5:C:59:ARG:NH2	1.94	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:131:ARG:H	6:D:131:ARG:HD3	1.43	0.82
7:E:15:ARG:HD3	7:E:26:PHE:HD2	1.44	0.82
1:A:984:C:H2'	1:A:985:C:H6	1.43	0.82
18:P:51:VAL:O	18:P:52:ASP:HB3	1.79	0.82
1:A:1007:C:H42	1:A:1022:G:H1	1.27	0.82
5:C:147:LYS:HD2	5:C:203:PHE:CE2	2.15	0.82
14:L:39:VAL:HG12	14:L:41:ARG:H	1.44	0.82
19:Q:36:ILE:H	19:Q:36:ILE:HD13	1.43	0.82
1:A:1366:C:H2'	1:A:1367:C:H6	1.44	0.82
4:B:223:ILE:HA	4:B:226:ARG:HB2	1.61	0.82
7:E:15:ARG:HD3	7:E:26:PHE:CD2	2.14	0.82
9:G:24:THR:HG22	9:G:28:ASN:HD21	1.45	0.82
1:A:1305:G:H22	1:A:1331:G:C2'	1.92	0.82
1:A:1362:C:H5'	1:A:1363:A:O5'	1.80	0.82
16:N:4:LYS:HD2	16:N:7:ILE:HD12	1.62	0.82
6:D:209:ARG:HH11	6:D:209:ARG:HB3	1.44	0.82
1:A:1368:G:OP2	11:I:112:LYS:HD2	1.80	0.82
5:C:157:ILE:HD11	5:C:166:GLU:HB2	1.62	0.82
11:I:42:ARG:O	11:I:44:VAL:N	2.13	0.82
7:E:51:VAL:HB	7:E:52:PRO:HD3	1.59	0.81
17:O:25:THR:HG21	17:O:70:LEU:HD23	1.62	0.81
8:F:50:TYR:HE1	20:R:77:GLY:HA2	1.45	0.81
1:A:1056:U:H5'	5:C:163:ALA:HB2	1.61	0.81
1:A:539:A:H2'	1:A:540:G:H8	1.46	0.81
4:B:77:ALA:HB2	4:B:211:ILE:HD13	1.62	0.81
7:E:82:VAL:HG12	7:E:89:ILE:HG22	1.61	0.81
10:H:65:TYR:HA	10:H:79:VAL:HG23	1.62	0.81
1:A:1225:A:H2'	1:A:1225:A:N3	1.93	0.81
11:I:65:VAL:HG21	11:I:73:GLN:HB3	1.61	0.81
20:R:22:VAL:HG13	20:R:42:ARG:HG2	1.60	0.81
1:A:1141:C:H2'	1:A:1142:G:H8	1.46	0.81
6:D:98:GLU:HG2	6:D:189:PRO:HG3	1.62	0.81
11:I:17:VAL:HA	11:I:63:ILE:HG22	1.62	0.81
1:A:560:U:H5'	1:A:566:G:N2	1.96	0.81
4:B:25:ASN:HD21	4:B:27:LYS:HG2	1.46	0.80
1:A:691:G:O2'	1:A:797:C:H4'	1.82	0.80
10:H:86:ILE:HD13	10:H:133:LEU:HD13	1.63	0.80
21:S:33:THR:HG21	21:S:71:LEU:HD13	1.63	0.80
13:K:78:GLN:O	13:K:103:LEU:HA	1.81	0.80
9:G:146:GLU:HG2	9:G:149:ARG:HH21	1.47	0.80
6:D:63:LYS:HD2	6:D:198:VAL:CG2	2.11	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:26:ARG:HH22	16:N:47:LEU:HD21	1.46	0.80
1:A:1031:G:H2'	1:A:1032:G:H8	1.47	0.80
17:O:17:ARG:HH11	17:O:17:ARG:HG3	1.47	0.80
1:A:1118:C:H1'	1:A:1179:A:C4	2.17	0.80
1:A:1148:U:H2'	1:A:1149:C:O4'	1.82	0.79
5:C:6:HIS:CD2	5:C:8:ILE:HD11	2.17	0.79
18:P:19:ILE:HG22	18:P:36:ILE:HG13	1.63	0.79
23:V:24:ARG:N	23:V:24:ARG:HD2	1.98	0.79
4:B:121:LEU:HD11	4:B:126:GLU:HB2	1.62	0.79
5:C:157:ILE:CD1	5:C:166:GLU:HB2	2.12	0.79
11:I:32:ASP:HB3	11:I:35:GLU:HB2	1.61	0.79
14:L:91:LYS:HA	14:L:91:LYS:HE3	1.63	0.79
16:N:16:PHE:HB2	16:N:18:VAL:HG22	1.64	0.79
1:A:242:C:H2'	1:A:243:A:H5'	1.62	0.79
4:B:109:SER:O	4:B:112:VAL:HG22	1.83	0.79
4:B:51:LEU:HD22	4:B:55:PHE:CE1	2.18	0.79
12:J:36:GLY:O	12:J:72:VAL:HA	1.82	0.79
1:A:250:A:H4'	1:A:251:G:O5'	1.80	0.79
12:J:82:ILE:H	12:J:82:ILE:HD12	1.47	0.79
22:T:10:LEU:O	22:T:12:ALA:N	2.14	0.79
1:A:791:G:H2'	1:A:792:A:H5'	1.65	0.79
11:I:28:VAL:HG12	11:I:29:ASN:N	1.96	0.79
6:D:187:ARG:HE	6:D:188:LEU:H	1.29	0.79
10:H:82:HIS:NE2	10:H:84:ARG:HD3	1.98	0.79
19:Q:67:LYS:HA	19:Q:70:ARG:HH12	1.47	0.79
22:T:50:GLU:H	22:T:99:LEU:HD12	1.47	0.79
5:C:25:GLY:HA2	5:C:29:TYR:HB2	1.64	0.79
1:A:1503:A:H5'	1:A:1531:A:C1'	2.12	0.78
4:B:32:ILE:HD13	4:B:40:HIS:HB3	1.63	0.78
10:H:85:ARG:HD3	10:H:86:ILE:N	1.98	0.78
1:A:1497:G:O2'	1:A:1498:U:H5'	1.84	0.78
1:A:975:A:H4'	1:A:976:G:C5'	2.13	0.78
9:G:92:SER:O	9:G:96:GLN:HG2	1.81	0.78
1:A:1251:A:H4'	11:I:12:GLU:OE1	1.82	0.78
5:C:114:PRO:O	5:C:118:GLN:HG3	1.83	0.78
7:E:51:VAL:O	7:E:54:ALA:HB3	1.84	0.78
23:V:24:ARG:N	23:V:24:ARG:HH11	1.81	0.78
1:A:411:A:H62	1:A:413:G:N2	1.79	0.78
12:J:8:LEU:HB2	12:J:70:ARG:HB2	1.63	0.78
1:A:877:C:H1'	10:H:3:THR:HG21	1.64	0.78
17:O:36:ILE:HG12	17:O:59:MET:HE3	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1168:A:H2'	1:A:1169:A:C8	2.19	0.78
4:B:12:GLU:OE2	4:B:12:GLU:HA	1.84	0.78
8:F:95:GLU:H	8:F:95:GLU:CD	1.85	0.78
1:A:644:G:H4'	10:H:92:ARG:HH12	1.47	0.78
21:S:5:LEU:O	21:S:6:LYS:HB2	1.83	0.78
1:A:393:A:O2'	1:A:394:G:H5'	1.85	0.77
12:J:32:ALA:CB	12:J:75:ILE:HB	2.13	0.77
13:K:91:ARG:NH1	20:R:88:LYS:HZ1	1.81	0.77
1:A:1195:C:H3'	1:A:1196:U:C5'	2.14	0.77
10:H:123:GLU:O	10:H:126:LYS:HB3	1.84	0.77
7:E:105:VAL:HB	7:E:106:PRO:HD3	1.65	0.77
14:L:54:LYS:N	14:L:54:LYS:HE3	1.99	0.77
21:S:6:LYS:HG2	21:S:7:LYS:H	1.49	0.77
1:A:405:U:H3'	1:A:406:G:H5'	1.67	0.77
12:J:49:VAL:HG13	16:N:41:ARG:HD2	1.67	0.77
1:A:1338:G:H2'	1:A:1339:A:C8	2.19	0.77
1:A:438:G:H4'	1:A:439:A:OP1	1.83	0.77
13:K:52:GLY:HA2	13:K:55:LYS:CE	2.14	0.77
1:A:1015:A:H2'	1:A:1016:A:C8	2.19	0.77
1:A:1491:G:C5	24:A:1545:PAR:H21	2.20	0.77
5:C:7:PRO:HB3	5:C:11:ARG:HH21	1.50	0.77
13:K:126:ARG:HG2	13:K:127:LYS:N	1.97	0.77
16:N:14:PRO:O	16:N:15:LYS:HB2	1.84	0.77
6:D:138:TYR:HD2	6:D:139:ARG:N	1.82	0.77
10:H:9:MET:HG3	10:H:26:VAL:HG21	1.66	0.77
20:R:53:ARG:HD3	20:R:58:LEU:O	1.85	0.76
21:S:55:LYS:HG2	21:S:56:GLN:HE21	1.48	0.76
1:A:1249:C:H2'	1:A:1250:A:H5'	1.67	0.76
9:G:75:VAL:HG12	9:G:76:ARG:H	1.48	0.76
1:A:1195:C:H3'	1:A:1196:U:H5"	1.66	0.76
1:A:1372:U:OP1	11:I:71:SER:HB3	1.84	0.76
5:C:91:LEU:CD1	5:C:99:VAL:HG13	2.16	0.76
11:I:89:ASN:O	11:I:92:TYR:HB2	1.85	0.76
16:N:9:LYS:C	16:N:9:LYS:HD3	2.05	0.76
1:A:1391:U:H2'	1:A:1392:G:C8	2.20	0.76
1:A:758:G:C8	1:A:758:G:O5'	2.38	0.76
1:A:975:A:H8	1:A:975:A:H5'	1.51	0.76
12:J:23:ILE:HG22	12:J:23:ILE:O	1.85	0.76
1:A:1416:G:H1	1:A:1484:C:H42	1.33	0.76
1:A:738:C:P	8:F:92:LYS:HE3	2.26	0.76
14:L:60:LEU:HD21	14:L:85:ILE:CD1	2.16	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:17:VAL:HG22	6:D:18:LYS:H	1.50	0.76
22:T:57:ARG:CB	22:T:57:ARG:HH11	1.99	0.76
4:B:57:PHE:CE2	4:B:61:LEU:HD21	2.21	0.75
5:C:101:LEU:O	5:C:101:LEU:HD23	1.86	0.75
8:F:19:LEU:HD23	8:F:20:ALA:N	2.01	0.75
11:I:113:LYS:N	11:I:113:LYS:HD2	2.01	0.75
1:A:1363:A:H1'	1:A:1365:G:N7	2.01	0.75
8:F:10:LEU:HD11	8:F:59:TYR:HD2	1.51	0.75
5:C:174:PRO:HB2	5:C:177:THR:HG22	1.66	0.75
8:F:3:ARG:HA	8:F:66:GLU:HA	1.68	0.75
1:A:1225:A:H5'	15:M:103:THR:OG1	1.85	0.75
1:A:581:G:N7	1:A:758:G:C6	2.54	0.75
7:E:15:ARG:O	7:E:16:THR:HG22	1.86	0.75
13:K:48:ILE:HG22	13:K:49:GLY:H	1.52	0.75
1:A:1116:C:H2'	1:A:1117:G:C5'	2.16	0.75
1:A:337:C:H2'	1:A:338:A:C8	2.22	0.75
4:B:26:PRO:HA	4:B:29:ALA:HB2	1.68	0.75
10:H:135:CYS:O	10:H:137:VAL:HG23	1.87	0.75
17:O:56:LEU:HA	17:O:59:MET:HE2	1.67	0.75
21:S:41:VAL:O	21:S:44:MET:HG2	1.86	0.75
2:Y:34:G:H2'	2:Y:35:G:C8	2.21	0.75
1:A:1061:G:O2'	1:A:1062:U:H5'	1.86	0.75
17:O:16:ALA:HB1	17:O:21:ASP:HB3	1.67	0.75
5:C:3:ASN:N	5:C:3:ASN:ND2	2.29	0.75
7:E:103:GLY:O	7:E:106:PRO:HD2	1.87	0.75
12:J:5:ARG:HB2	12:J:99:LYS:O	1.87	0.75
10:H:90:GLY:O	10:H:91:ARG:HB2	1.84	0.74
11:I:100:GLY:C	11:I:102:LEU:H	1.91	0.74
15:M:15:VAL:HG23	15:M:43:THR:O	1.87	0.74
1:A:738:C:OP2	8:F:92:LYS:HE3	1.87	0.74
9:G:111:ARG:HB3	9:G:112:PRO:HD2	1.68	0.74
1:A:1347:G:N2	1:A:1373:G:H2'	2.02	0.74
5:C:7:PRO:HA	5:C:10:PHE:HB3	1.67	0.74
18:P:8:ARG:HD3	18:P:17:TYR:CE2	2.21	0.74
1:A:1399:C:H4'	1:A:1400:C:H5"	1.69	0.74
4:B:166:ASP:OD2	4:B:169:LYS:HB2	1.87	0.74
12:J:35:SER:HB2	12:J:72:VAL:O	1.86	0.74
15:M:23:TYR:HB3	15:M:67:GLU:H	1.51	0.74
1:A:190(L):U:O2'	1:A:191:G:H5'	1.86	0.74
1:A:266:G:H5'	1:A:266:G:C8	2.22	0.74
1:A:1201:A:H4'	1:A:1202:G:O5'	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:C:H2'	1:A:336:C:H6	1.52	0.74
5:C:154:SER:OG	5:C:196:LEU:HB2	1.87	0.74
4:B:16:HIS:CE1	4:B:204:ASN:H	2.05	0.74
1:A:112:G:N2	1:A:354:G:H5'	2.01	0.74
1:A:560:U:H5'	1:A:566:G:C2	2.23	0.74
1:A:877:C:O2	10:H:3:THR:HG21	1.88	0.74
4:B:74:LYS:HD2	4:B:166:ASP:HB2	1.70	0.74
5:C:64:VAL:HB	5:C:99:VAL:CB	2.17	0.74
8:F:6:VAL:HG22	8:F:90:VAL:HG12	1.69	0.74
12:J:49:VAL:HG11	16:N:41:ARG:O	1.86	0.74
4:B:17:PHE:HD1	4:B:18:GLY:N	1.85	0.73
20:R:29:PHE:CE1	20:R:31:LEU:HD23	2.23	0.73
1:A:1178:G:N2	1:A:1180:A:H3'	2.03	0.73
1:A:291:C:O2'	1:A:292:G:H5'	1.87	0.73
6:D:107:ARG:HH21	6:D:194:LEU:HD12	1.53	0.73
11:I:46:ALA:HB1	11:I:77:ILE:HG22	1.69	0.73
6:D:149:ALA:HB3	6:D:152:SER:CB	2.17	0.73
10:H:80:ILE:O	10:H:80:ILE:HG22	1.87	0.73
11:I:8:GLY:CA	11:I:79:LEU:HD12	2.17	0.73
14:L:27:LEU:C	14:L:29:GLY:H	1.91	0.73
4:B:55:PHE:O	4:B:58:ILE:HG13	1.89	0.73
12:J:6:ILE:HD11	12:J:72:VAL:HB	1.70	0.73
5:C:40:ARG:HB2	5:C:40:ARG:HH11	1.52	0.73
7:E:41:VAL:HG11	7:E:113:ALA:HA	1.70	0.73
11:I:106:ALA:O	11:I:108:VAL:HG23	1.89	0.73
1:A:179:A:H2'	1:A:180:U:C6	2.24	0.73
1:A:579:G:H5'	1:A:728:A:H1'	1.69	0.73
9:G:26:PHE:CE2	9:G:30:ILE:HD11	2.24	0.73
9:G:67:GLU:HA	9:G:70:LYS:HE2	1.69	0.73
15:M:33:ALA:HA	15:M:59:TYR:HE2	1.54	0.73
1:A:824:C:H2'	1:A:825:G:H8	1.54	0.73
1:A:1301:U:H2'	1:A:1301:U:O2	1.88	0.73
1:A:332:G:O2'	1:A:333:G:H5'	1.88	0.73
6:D:64:LEU:HD13	6:D:65:ARG:N	2.04	0.73
22:T:26:ASN:OD1	22:T:71:THR:HG23	1.89	0.73
1:A:397:A:H5'	1:A:398:C:OP1	1.87	0.72
19:Q:27:PHE:O	19:Q:36:ILE:HD13	1.88	0.72
1:A:1121:U:H2'	1:A:1122:U:H6	1.54	0.72
6:D:145:GLU:C	6:D:146:ILE:HD12	2.09	0.72
23:V:24:ARG:NH1	23:V:24:ARG:HB3	2.04	0.72
1:A:287:U:O2'	1:A:288:A:H5'	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:C:O2'	1:A:323:U:H5'	1.88	0.72
4:B:16:HIS:CE1	4:B:210:SER:HB3	2.24	0.72
6:D:126:ILE:HG22	6:D:127:THR:N	2.04	0.72
1:A:1519:A:H2'	1:A:1520:G:H5'	1.71	0.72
1:A:352:C:H4'	1:A:354:G:OP1	1.88	0.72
1:A:539:A:H2'	1:A:540:G:C8	2.25	0.72
5:C:20:SER:HB3	5:C:22:TRP:HE1	1.53	0.72
10:H:105:ARG:O	10:H:105:ARG:HG3	1.89	0.72
11:I:46:ALA:HA	11:I:78:LYS:CB	2.19	0.72
19:Q:27:PHE:CE1	19:Q:36:ILE:HD11	2.23	0.72
5:C:150:LYS:HG3	5:C:169:ALA:HB2	1.71	0.72
7:E:52:PRO:O	7:E:54:ALA:N	2.22	0.72
10:H:53:VAL:C	10:H:55:GLY:H	1.92	0.72
10:H:51:VAL:HG21	10:H:60:ARG:CG	2.20	0.72
12:J:16:LEU:HD23	12:J:94:VAL:HG13	1.71	0.72
1:A:1149:C:H2'	1:A:1150:U:H6	1.54	0.72
1:A:882:C:O2'	1:A:883:C:H5'	1.88	0.72
12:J:49:VAL:O	12:J:60:ARG:O	2.06	0.72
13:K:109:VAL:HG11	20:R:84:LYS:HE2	1.70	0.72
10:H:51:VAL:HG21	10:H:60:ARG:HG2	1.70	0.72
4:B:180:LEU:O	4:B:182:ILE:HG13	1.90	0.72
8:F:33:TYR:HA	8:F:71:ARG:HH21	1.54	0.72
15:M:22:ILE:HB	15:M:25:ILE:HB	1.72	0.72
5:C:180:ALA:O	5:C:181:ASN:HB3	1.89	0.71
14:L:86:ARG:HG3	14:L:86:ARG:HH11	1.53	0.71
9:G:139:GLU:O	9:G:143:ARG:HG3	1.90	0.71
13:K:43:SER:OG	13:K:67:ASP:HB3	1.90	0.71
15:M:13:LYS:HA	15:M:44:ARG:HH21	1.54	0.71
9:G:65:ALA:O	9:G:69:VAL:HG23	1.89	0.71
11:I:4:TYR:HB2	11:I:19:LEU:HB2	1.70	0.71
12:J:64:GLU:OE1	12:J:66:ARG:HG2	1.91	0.71
19:Q:93:GLN:O	19:Q:96:GLN:HG2	1.90	0.71
1:A:80:G:H3'	1:A:81:U:C5'	2.19	0.71
1:A:865:A:O2'	1:A:866:C:H5'	1.89	0.71
10:H:60:ARG:HG3	10:H:60:ARG:HH11	1.54	0.71
12:J:38:ILE:HB	12:J:71:LEU:HB2	1.70	0.71
1:A:376:G:OP2	18:P:67:THR:HG21	1.91	0.71
8:F:50:TYR:CE1	20:R:77:GLY:HA2	2.24	0.71
1:A:1148:U:H4'	11:I:14:VAL:HG11	1.72	0.71
4:B:74:LYS:HB3	4:B:74:LYS:NZ	2.06	0.71
5:C:67:THR:HG22	5:C:68:VAL:N	2.04	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:46:ARG:NH1	12:J:64:GLU:HB3	2.06	0.71
20:R:59:SER:HB3	20:R:62:GLU:HG3	1.72	0.71
1:A:958:A:C8	21:S:55:LYS:HD2	2.26	0.71
1:A:992:U:H4'	1:A:993:G:O5'	1.90	0.71
4:B:68:ILE:HG12	4:B:161:ALA:HB3	1.71	0.71
20:R:26:LEU:HG	20:R:27:GLY:H	1.55	0.71
1:A:794:A:H2'	1:A:795:C:C6	2.26	0.71
4:B:87:ARG:O	4:B:87:ARG:HD3	1.90	0.71
6:D:153:ARG:CD	6:D:181:MET:HG3	2.21	0.71
7:E:16:THR:HG21	7:E:27:ARG:HB2	1.71	0.71
8:F:69:GLU:HA	8:F:72:VAL:CG2	2.20	0.71
12:J:18:ALA:O	12:J:21:GLN:HG2	1.91	0.71
1:A:474:G:H4'	18:P:81:ARG:NH2	2.06	0.71
4:B:124:SER:C	4:B:126:GLU:H	1.93	0.71
4:B:137:ARG:HG3	4:B:138:LEU:H	1.56	0.71
4:B:144:ARG:HG3	4:B:145:LEU:H	1.56	0.71
4:B:55:PHE:HA	4:B:58:ILE:HD11	1.73	0.71
1:A:685:G:H4'	13:K:40:ILE:O	1.91	0.71
1:A:1064:G:H4'	1:A:1065:U:C5'	2.21	0.70
5:C:130:VAL:O	5:C:134:ILE:HG13	1.91	0.70
7:E:92:LYS:HB3	7:E:119:LEU:HB2	1.73	0.70
21:S:41:VAL:HG23	21:S:43:GLU:HG2	1.73	0.70
1:A:1147:C:H4'	11:I:5:TYR:CE1	2.23	0.70
6:D:131:ARG:H	6:D:131:ARG:CD	2.04	0.70
6:D:209:ARG:NH1	6:D:209:ARG:HB3	2.04	0.70
17:O:87:ILE:HG22	17:O:88:ARG:H	1.55	0.70
1:A:556:C:C2'	1:A:557:G:H5'	2.20	0.70
5:C:64:VAL:HB	5:C:99:VAL:CG2	2.21	0.70
1:A:443:C:H2'	1:A:444:C:H6	1.55	0.70
1:A:556:C:O2'	1:A:557:G:H5'	1.91	0.70
6:D:165:MET:SD	6:D:168:ARG:HD3	2.31	0.70
7:E:74:GLY:CA	7:E:116:THR:HG22	2.21	0.70
10:H:103:VAL:HG21	10:H:110:ALA:HB2	1.72	0.70
12:J:62:HIS:HB3	16:N:59:ALA:HB3	1.73	0.70
14:L:47:LYS:HB3	14:L:48:PRO:HD3	1.72	0.70
1:A:173:U:H5'	1:A:197:A:O4'	1.92	0.70
1:A:443:C:H2'	1:A:444:C:C6	2.27	0.70
5:C:139:GLN:HA	5:C:139:GLN:NE2	2.06	0.70
6:D:25:ARG:C	6:D:27:TYR:H	1.93	0.70
10:H:69:ARG:HB2	10:H:69:ARG:NH1	2.07	0.70
1:A:1190:G:OP1	5:C:4:LYS:HA	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:201:GLN:HA	6:D:204:ILE:CD1	2.21	0.70
11:I:11:LYS:O	11:I:12:GLU:HB2	1.90	0.70
13:K:126:ARG:CG	13:K:127:LYS:H	1.96	0.70
18:P:55:ARG:O	18:P:58:TYR:N	2.25	0.70
19:Q:61:GLU:HA	19:Q:71:PHE:CE1	2.26	0.70
1:A:1105:A:H2'	1:A:1106:G:C8	2.26	0.70
1:A:394:G:H2'	1:A:395:C:H6	1.57	0.70
7:E:15:ARG:CD	7:E:26:PHE:HD2	2.03	0.70
7:E:43:LEU:HB2	7:E:136:MET:HE2	1.71	0.70
10:H:5:PRO:O	10:H:8:ASP:HB3	1.90	0.70
14:L:36:VAL:O	14:L:58:VAL:HG13	1.92	0.70
14:L:39:VAL:HG12	14:L:40:VAL:H	1.55	0.70
4:B:107:THR:C	4:B:109:SER:H	1.95	0.70
4:B:223:ILE:HD12	4:B:230:VAL:HG21	1.73	0.70
1:A:344:A:H4'	1:A:345:C:OP2	1.92	0.69
1:A:411:A:N7	1:A:413:G:N3	2.40	0.69
6:D:8:VAL:C	6:D:10:ARG:H	1.92	0.69
14:L:40:VAL:O	14:L:40:VAL:HG12	1.92	0.69
17:O:87:ILE:HG22	17:O:88:ARG:N	2.07	0.69
1:A:1240:U:P	9:G:116:ALA:HB2	2.32	0.69
1:A:406:G:H1	1:A:436:C:H42	1.40	0.69
7:E:129:ILE:H	7:E:129:ILE:CD1	2.06	0.69
8:F:3:ARG:HG3	8:F:93:SER:HB2	1.73	0.69
12:J:4:ILE:HD13	12:J:74:ILE:HB	1.74	0.69
16:N:26:ARG:HH22	16:N:47:LEU:CD2	2.04	0.69
2:Y:34:G:H2'	2:Y:35:G:H8	1.57	0.69
21:S:30:LEU:C	21:S:31:ILE:HD13	2.13	0.69
1:A:1435:G:H2'	1:A:1436:U:C6	2.28	0.69
6:D:64:LEU:C	6:D:64:LEU:HD13	2.12	0.69
9:G:40:ALA:HB3	11:I:41:VAL:HG21	1.74	0.69
12:J:94:VAL:HG12	12:J:95:GLU:N	2.07	0.69
6:D:30:LYS:C	6:D:32:ALA:H	1.95	0.69
10:H:103:VAL:HG12	10:H:108:GLY:HA3	1.73	0.69
1:A:1002:G:H22	1:A:1040:U:H1'	1.57	0.69
1:A:1104:G:OP1	4:B:111:ARG:HD2	1.92	0.69
6:D:105:VAL:CG1	6:D:117:ALA:HB1	2.23	0.69
7:E:9:LYS:HE2	7:E:112:LEU:HD11	1.73	0.69
14:L:25:PRO:C	14:L:27:LEU:H	1.96	0.69
1:A:235:C:H5'	19:Q:70:ARG:HG2	1.74	0.69
21:S:28:LYS:CG	21:S:29:ARG:H	2.00	0.69
1:A:285:G:O2'	1:A:286:G:H5'	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:47:THR:C	20:R:83:GLU:HG3	2.12	0.69
4:B:30:ARG:HG3	4:B:31:TYR:CD2	2.27	0.69
1:A:1056:U:C5'	5:C:163:ALA:HB2	2.23	0.69
7:E:9:LYS:HB3	7:E:33:VAL:CG2	2.21	0.69
1:A:149:A:H2'	1:A:150:C:C6	2.28	0.69
7:E:32:VAL:HG22	7:E:58:ALA:HB1	1.75	0.69
8:F:87:ARG:CG	8:F:87:ARG:HH11	2.05	0.69
20:R:42:ARG:HB2	20:R:42:ARG:NH1	2.07	0.69
1:A:1105:A:H2'	1:A:1106:G:H8	1.56	0.69
1:A:1107:C:H2'	1:A:1108:G:H5'	1.74	0.69
1:A:414:A:H2'	1:A:415:A:O4'	1.92	0.69
1:A:56:U:H2'	1:A:57:G:C8	2.28	0.69
5:C:43:LEU:O	5:C:43:LEU:HD23	1.92	0.69
17:O:26:GLU:OE1	17:O:77:ARG:HD2	1.91	0.69
1:A:1036:G:H2'	1:A:1037:C:C6	2.28	0.69
1:A:1161:C:H2'	1:A:1162:C:C6	2.28	0.69
1:A:939:G:H5"	9:G:102:ARG:NH2	2.07	0.69
17:O:39:LEU:HD22	17:O:56:LEU:CD1	2.22	0.69
1:A:149:A:H2'	1:A:150:C:H6	1.58	0.68
1:A:893:C:H2'	1:A:894:G:H8	1.58	0.68
9:G:46:ALA:HB1	9:G:121:ALA:HB2	1.75	0.68
1:A:645:C:H2'	1:A:646:U:H6	1.58	0.68
6:D:201:GLN:HA	6:D:204:ILE:HD12	1.75	0.68
1:A:538:G:H2'	1:A:539:A:C8	2.28	0.68
1:A:664:G:H22	1:A:741:G:H1	1.41	0.68
6:D:146:ILE:N	6:D:146:ILE:HD12	2.09	0.68
18:P:28:ARG:HG3	18:P:29:ASP:N	2.07	0.68
4:B:8:LYS:O	4:B:9:GLU:HB2	1.93	0.68
5:C:7:PRO:CB	5:C:11:ARG:HH21	2.05	0.68
5:C:64:VAL:HG12	5:C:65:ALA:N	2.08	0.68
8:F:14:LEU:CD2	8:F:18:GLN:HB3	2.23	0.68
9:G:26:PHE:HE2	9:G:30:ILE:HD11	1.58	0.68
21:S:53:ASN:N	21:S:53:ASN:HD22	1.91	0.68
1:A:1368:G:O2'	1:A:1369:C:H5'	1.94	0.68
1:A:456:C:H2'	1:A:457:C:C6	2.29	0.68
11:I:6:GLY:HA3	11:I:84:ALA:H	1.58	0.68
14:L:7:ILE:O	14:L:11:VAL:HG23	1.93	0.68
1:A:1160:G:O2'	1:A:1161:C:H5'	1.93	0.68
5:C:195:VAL:HG12	5:C:196:LEU:H	1.56	0.68
8:F:8:ILE:HD11	8:F:79:LEU:HD13	1.74	0.68
9:G:66:VAL:C	9:G:68:ASN:H	1.97	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:64:LYS:HG2	10:H:79:VAL:HG21	1.75	0.68
14:L:83:VAL:HG21	14:L:100:ILE:HG12	1.75	0.68
22:T:56:MET:HG3	22:T:88:VAL:HG21	1.75	0.68
1:A:1256:A:H5'	1:A:1258:G:H1'	1.75	0.68
1:A:19:C:H2'	1:A:20:U:H6	1.57	0.68
1:A:123:C:OP1	1:A:312:C:H5'	1.94	0.68
6:D:105:VAL:HG13	6:D:117:ALA:HB1	1.75	0.68
11:I:48:GLU:N	11:I:49:PRO:HD2	2.09	0.68
14:L:33:ARG:HA	14:L:33:ARG:HE	1.59	0.68
20:R:59:SER:HB3	20:R:62:GLU:CG	2.24	0.68
21:S:28:LYS:HG2	21:S:29:ARG:N	2.07	0.68
1:A:190(I):G:O2'	1:A:190(J):U:H5'	1.94	0.68
4:B:57:PHE:CE1	4:B:61:LEU:HD11	2.29	0.68
14:L:89:ARG:CB	14:L:89:ARG:HH11	2.05	0.68
19:Q:24:GLU:CD	19:Q:37:LYS:HD3	2.13	0.68
1:A:1329:A:P	15:M:28:ALA:HB3	2.34	0.68
1:A:353:A:H5'	1:A:353:A:C8	2.29	0.68
1:A:385:C:O2'	1:A:386:C:H5'	1.93	0.68
1:A:448:A:H2'	1:A:449:C:C6	2.29	0.68
1:A:80:G:C3'	1:A:81:U:H5"	2.23	0.68
4:B:91:PRO:HG3	4:B:154:LEU:HD12	1.76	0.68
5:C:156:ARG:HD2	5:C:160:ALA:O	1.93	0.68
1:A:1222:G:OP1	21:S:77:THR:HG21	1.94	0.68
22:T:21:LYS:HB3	22:T:21:LYS:NZ	2.09	0.68
1:A:1141:C:H2'	1:A:1142:G:C8	2.29	0.67
12:J:63:PHE:HE1	16:N:45:ARG:HG3	1.60	0.67
19:Q:60:ILE:HD13	19:Q:61:GLU:H	1.59	0.67
4:B:61:LEU:HD23	4:B:161:ALA:HB2	1.76	0.67
13:K:44:SER:HB3	13:K:47:VAL:HG23	1.76	0.67
13:K:72:ALA:HB1	13:K:77:MET:HG3	1.77	0.67
19:Q:81:ARG:HG3	19:Q:81:ARG:O	1.94	0.67
1:A:353:A:H5'	1:A:353:A:H8	1.59	0.67
1:A:794:A:H2'	1:A:795:C:H6	1.59	0.67
6:D:142:PRO:HA	6:D:185:PHE:HD2	1.59	0.67
1:A:835:U:OP1	20:R:64:ARG:NH2	2.27	0.67
1:A:242:C:C2'	1:A:243:A:H5'	2.24	0.67
5:C:174:PRO:HB2	5:C:177:THR:CG2	2.25	0.67
9:G:102:ARG:O	9:G:106:GLN:HB2	1.94	0.67
10:H:3:THR:HG23	10:H:4:ASP:H	1.59	0.67
1:A:1491:G:C6	24:A:1545:PAR:H21	2.30	0.67
4:B:108:ILE:HG22	4:B:108:ILE:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:71:VAL:HB	4:B:164:VAL:HG22	1.76	0.67
9:G:151:TYR:HA	9:G:153:HIS:CE1	2.29	0.67
1:A:1228:C:OP1	15:M:115:LYS:HD3	1.95	0.67
1:A:1031:G:H2'	1:A:1032:G:C8	2.29	0.67
1:A:1161:C:H2'	1:A:1162:C:H6	1.59	0.67
1:A:384:G:H2'	1:A:385:C:C6	2.30	0.67
1:A:833:U:H2'	1:A:834:C:C6	2.29	0.67
5:C:147:LYS:HD2	5:C:203:PHE:HE2	1.60	0.67
12:J:16:LEU:HD23	12:J:94:VAL:CG1	2.24	0.67
14:L:101:VAL:HG12	14:L:101:VAL:O	1.94	0.67
1:A:1021:G:O2'	1:A:1022:G:H5'	1.94	0.67
1:A:1053:G:N7	1:A:1200:C:H5"	2.08	0.67
5:C:64:VAL:CB	5:C:99:VAL:HB	2.25	0.67
9:G:137:LYS:O	9:G:141:VAL:HG23	1.95	0.67
19:Q:4:LYS:HG3	19:Q:5:VAL:N	2.10	0.67
1:A:867:G:O2'	1:A:868:C:H5'	1.94	0.67
1:A:957:U:H3	1:A:960:U:H5"	1.60	0.67
4:B:142:LEU:HD22	4:B:146:GLN:OE1	1.95	0.67
5:C:151:VAL:C	5:C:152:ILE:HD12	2.16	0.67
6:D:182:LYS:HG2	6:D:183:GLY:H	1.60	0.67
6:D:4:TYR:O	6:D:5:ILE:HB	1.94	0.67
11:I:93:ARG:HD3	11:I:97:LYS:NZ	2.10	0.67
19:Q:101:ARG:HE	19:Q:101:ARG:HA	1.58	0.67
8:F:28:ARG:O	8:F:32:ASN:HB2	1.94	0.67
17:O:4:THR:O	17:O:7:GLU:HB2	1.95	0.67
1:A:478:A:O2'	1:A:479:C:H5'	1.95	0.66
1:A:974:A:H8	1:A:974:A:OP1	1.78	0.66
5:C:14:ILE:HG22	5:C:15:THR:H	1.61	0.66
7:E:9:LYS:HB3	7:E:33:VAL:HG23	1.75	0.66
23:V:10:ARG:HA	23:V:13:ILE:HD12	1.77	0.66
1:A:1015:A:H2'	1:A:1016:A:H8	1.57	0.66
1:A:1305:G:N2	1:A:1331:G:H2'	2.00	0.66
4:B:69:LEU:HD21	4:B:93:VAL:HG23	1.76	0.66
7:E:147:ASP:N	7:E:147:ASP:OD2	2.28	0.66
7:E:18:ARG:HG2	7:E:19:MET:N	2.09	0.66
21:S:15:LEU:HD12	21:S:16:LEU:H	1.59	0.66
23:V:6:ARG:HD2	23:V:15:ARG:HH12	1.59	0.66
1:A:1129:C:H1'	1:A:1132:C:H5	1.61	0.66
1:A:1178:G:H22	1:A:1180:A:H3'	1.59	0.66
4:B:19:HIS:CD2	4:B:20:GLU:HG2	2.30	0.66
9:G:38:LEU:O	9:G:42:ILE:HG13	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:999:C:H2'	1:A:1000:U:C6	2.30	0.66
1:A:1060:C:O2'	1:A:1061:G:H5'	1.94	0.66
4:B:101:MET:N	4:B:108:ILE:HD12	2.09	0.66
6:D:162:LEU:HD22	6:D:181:MET:SD	2.36	0.66
6:D:108:LEU:CD2	6:D:174:LEU:HD13	2.26	0.66
9:G:156:TRP:CE3	9:G:156:TRP:HA	2.29	0.66
21:S:53:ASN:HD21	21:S:58:VAL:HG13	1.59	0.66
1:A:1095:U:H2'	1:A:1096:C:C6	2.31	0.66
1:A:737:A:H1'	8:F:73:ASN:ND2	2.03	0.66
12:J:4:ILE:HA	12:J:100:THR:HA	1.78	0.66
16:N:5:ALA:O	16:N:8:GLU:HG3	1.94	0.66
1:A:1353:G:O2'	1:A:1354:C:H5'	1.96	0.66
1:A:984:C:H2'	1:A:985:C:C6	2.28	0.66
6:D:173:TRP:CD2	6:D:189:PRO:HB3	2.30	0.66
16:N:26:ARG:NH2	16:N:47:LEU:HD11	2.09	0.66
18:P:43:LYS:HD2	18:P:43:LYS:N	2.11	0.66
19:Q:98:LEU:O	19:Q:98:LEU:HD13	1.95	0.66
1:A:1038:C:H2'	1:A:1039:C:H6	1.60	0.66
1:A:1101:A:H4'	1:A:1102:A:O5'	1.95	0.66
1:A:258:G:H2'	1:A:259:G:H8	1.60	0.66
10:H:3:THR:HG23	10:H:4:ASP:N	2.10	0.66
10:H:65:TYR:CA	10:H:79:VAL:HG23	2.25	0.66
19:Q:76:LEU:C	19:Q:76:LEU:HD23	2.15	0.66
1:A:1425:U:H2'	1:A:1426:C:C6	2.31	0.66
1:A:192:U:O4'	22:T:103:GLY:HA2	1.96	0.66
1:A:19:C:H5"	7:E:86:ALA:CB	2.26	0.66
4:B:20:GLU:O	4:B:39:ILE:HG23	1.96	0.66
12:J:8:LEU:HD22	12:J:20:ALA:HB2	1.77	0.66
12:J:30:SER:HB3	12:J:84:GLN:NE2	2.11	0.66
1:A:853:G:O2'	1:A:854:G:H5'	1.96	0.66
5:C:52:LEU:HD23	5:C:52:LEU:N	2.11	0.66
1:A:8:A:H62	6:D:208:SER:HB2	1.60	0.66
1:A:673:G:H2'	1:A:674:G:C8	2.31	0.65
6:D:92:VAL:O	6:D:96:LEU:HD22	1.96	0.65
14:L:115:LYS:O	14:L:117:ARG:HG3	1.96	0.65
22:T:70:SER:HA	22:T:73:HIS:CD2	2.30	0.65
1:A:41:G:H2'	1:A:42:G:C8	2.31	0.65
4:B:178:ARG:HH21	4:B:196:LEU:C	1.98	0.65
4:B:84:GLU:HB3	4:B:219:VAL:CG2	2.22	0.65
11:I:28:VAL:CG1	11:I:29:ASN:H	2.06	0.65
20:R:47:THR:HG22	20:R:48:GLY:N	2.08	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1123:A:H4'	12:J:37:PRO:HD2	1.77	0.65
1:A:954:G:H21	1:A:1227:A:H62	1.43	0.65
1:A:445:G:H2'	1:A:446:G:H8	1.61	0.65
1:A:730:G:H21	1:A:765:G:H5"	1.61	0.65
4:B:84:GLU:CB	4:B:219:VAL:HG21	2.22	0.65
19:Q:12:SER:HB3	19:Q:20:THR:OG1	1.96	0.65
1:A:1500:A:O2'	1:A:1501:C:H5'	1.96	0.65
1:A:682:G:O2'	1:A:683:G:H5'	1.96	0.65
5:C:191:THR:HG22	5:C:193:TYR:H	1.59	0.65
15:M:33:ALA:HA	15:M:59:TYR:CE2	2.31	0.65
17:O:3:ILE:HD11	17:O:38:ARG:HG3	1.77	0.65
13:K:91:ARG:NH1	20:R:88:LYS:NZ	2.44	0.65
1:A:413:G:H2'	1:A:428:G:N2	2.11	0.65
9:G:88:PRO:O	9:G:89:MET:HB3	1.95	0.65
12:J:32:ALA:HB2	12:J:75:ILE:HB	1.78	0.65
16:N:31:ARG:O	16:N:33:VAL:N	2.30	0.65
19:Q:83:ASP:CG	19:Q:84:LEU:H	2.00	0.65
1:A:1427:U:H2'	1:A:1428:A:C8	2.31	0.65
1:A:1479:C:H2'	1:A:1480:G:C8	2.30	0.65
1:A:385:C:H2'	1:A:386:C:C6	2.32	0.65
19:Q:24:GLU:OE2	19:Q:37:LYS:HD3	1.96	0.65
1:A:1208:C:H2'	1:A:1209:C:C6	2.32	0.65
1:A:1226:C:H4'	1:A:1227:A:OP1	1.95	0.65
4:B:121:LEU:HD12	4:B:124:SER:HB3	1.77	0.65
4:B:57:PHE:O	4:B:61:LEU:HD13	1.96	0.65
6:D:68:TYR:HD1	6:D:68:TYR:H	1.44	0.65
7:E:87:SER:OG	7:E:125:SER:HB3	1.96	0.65
10:H:69:ARG:HH22	10:H:77:GLU:N	1.95	0.65
12:J:82:ILE:O	12:J:86:MET:HB2	1.97	0.65
1:A:1208:C:H2'	1:A:1209:C:H6	1.62	0.65
1:A:197:A:N1	1:A:220:G:O2'	2.30	0.65
4:B:217:ARG:HA	4:B:220:ASP:OD2	1.96	0.65
6:D:173:TRP:CD1	6:D:189:PRO:HD3	2.32	0.65
8:F:2:ARG:HD2	8:F:69:GLU:HB3	1.77	0.65
14:L:75:HIS:HD2	14:L:77:LEU:N	1.94	0.65
18:P:43:LYS:HA	18:P:48:TRP:HB3	1.79	0.65
19:Q:101:ARG:NE	19:Q:101:ARG:HA	2.11	0.65
19:Q:96:GLN:HG3	19:Q:104:LYS:HG2	1.77	0.65
1:A:1065:U:H5"	1:A:1066:C:H5'	1.79	0.65
1:A:1366:C:H2'	1:A:1367:C:C6	2.31	0.65
1:A:701:C:H5'	1:A:703:G:O4'	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:32:ILE:HD11	4:B:190:THR:OG1	1.96	0.65
5:C:3:ASN:O	5:C:4:LYS:HB2	1.96	0.65
23:V:24:ARG:HG2	23:V:25:LYS:H	1.61	0.65
4:B:197:VAL:HB	4:B:200:ILE:HG23	1.79	0.65
7:E:64:ARG:HG2	7:E:64:ARG:HH11	1.62	0.65
12:J:32:ALA:C	12:J:34:VAL:H	2.00	0.65
23:V:2:GLY:C	23:V:4:GLY:H	2.00	0.65
1:A:575:G:OP1	1:A:575:G:H4'	1.97	0.64
4:B:28:PHE:HB2	4:B:194:PRO:HD3	1.79	0.64
7:E:53:LEU:N	7:E:53:LEU:HD12	2.10	0.64
12:J:34:VAL:HG13	12:J:74:ILE:HG23	1.79	0.64
14:L:83:VAL:HG22	14:L:84:LEU:N	2.12	0.64
4:B:149:LEU:O	4:B:153:ARG:HB2	1.97	0.64
4:B:71:VAL:HG12	4:B:164:VAL:HG13	1.78	0.64
4:B:92:TYR:CE1	4:B:151:GLY:HA3	2.32	0.64
5:C:23:TYR:O	5:C:24:ALA:HB2	1.97	0.64
12:J:46:ARG:HH12	12:J:64:GLU:HB3	1.62	0.64
21:S:18:LYS:O	21:S:22:LEU:HG	1.97	0.64
1:A:1057:G:C5'	5:C:154:SER:HB2	2.27	0.64
4:B:26:PRO:O	4:B:29:ALA:HB3	1.97	0.64
5:C:195:VAL:HG12	5:C:196:LEU:N	2.12	0.64
10:H:103:VAL:CG2	10:H:110:ALA:HB2	2.27	0.64
14:L:41:ARG:HG2	14:L:42:THR:H	1.62	0.64
15:M:3:ARG:HG3	15:M:8:GLU:H	1.61	0.64
1:A:1003(A):G:H2'	1:A:1004:A:O4'	1.98	0.64
1:A:1056:U:H5'	5:C:163:ALA:CB	2.27	0.64
1:A:1264:C:H2'	1:A:1265:G:H8	1.63	0.64
1:A:448:A:H2'	1:A:449:C:H6	1.63	0.64
4:B:102:LEU:HD12	4:B:102:LEU:N	2.11	0.64
11:I:8:GLY:HA3	11:I:79:LEU:HB3	1.79	0.64
14:L:41:ARG:HG2	14:L:42:THR:N	2.11	0.64
1:A:243:A:C4'	1:A:244:U:H5'	2.27	0.64
5:C:139:GLN:HE21	5:C:139:GLN:HA	1.61	0.64
5:C:191:THR:HG21	5:C:193:TYR:CZ	2.31	0.64
9:G:66:VAL:O	9:G:68:ASN:N	2.30	0.64
1:A:1495:U:O2'	1:A:1496:C:H5'	1.97	0.64
1:A:129(A):G:O2'	1:A:190(E):U:H2'	1.97	0.64
1:A:26:A:N6	1:A:558:G:H1'	2.12	0.64
1:A:778:G:O2'	1:A:779:C:H5'	1.98	0.64
4:B:144:ARG:HG3	4:B:145:LEU:N	2.12	0.64
4:B:60:ASP:O	4:B:64:ARG:HB2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:82:ARG:HA	4:B:92:TYR:CD2	2.33	0.64
5:C:78:GLY:HA3	5:C:83:ARG:HB2	1.80	0.64
10:H:59:LEU:O	10:H:61:VAL:HG23	1.98	0.64
12:J:45:ARG:HB3	12:J:45:ARG:HH11	1.62	0.64
13:K:32:ILE:HG22	13:K:40:ILE:HD12	1.80	0.64
17:O:82:ILE:HG23	17:O:87:ILE:H	1.63	0.64
23:V:5:ASP:O	23:V:11:GLY:HA3	1.96	0.64
1:A:868:C:C2'	1:A:869:G:H5'	2.27	0.64
4:B:101:MET:HA	4:B:108:ILE:HD12	1.80	0.64
10:H:45:ILE:C	10:H:47:GLY:H	2.01	0.64
16:N:26:ARG:HH12	16:N:47:LEU:HD21	1.62	0.64
1:A:1128:C:H2'	1:A:1139:G:O6	1.97	0.64
1:A:1338:G:H2'	1:A:1339:A:H8	1.63	0.64
1:A:618:C:H3'	1:A:619:U:H5"	1.80	0.64
11:I:120:ARG:O	11:I:121:ARG:C	2.35	0.64
12:J:82:ILE:H	12:J:82:ILE:CD1	2.11	0.64
19:Q:36:ILE:CD1	19:Q:36:ILE:H	2.11	0.64
1:A:1259:C:H1'	1:A:1283:G:H21	1.62	0.64
1:A:1365:G:O2'	1:A:1366:C:H5'	1.98	0.64
5:C:177:THR:HG23	5:C:180:ALA:HB2	1.79	0.64
7:E:107:ARG:HG3	7:E:107:ARG:HH11	1.63	0.64
7:E:129:ILE:N	7:E:129:ILE:HD12	2.12	0.64
1:A:881:G:P	14:L:12:ARG:HH22	2.21	0.64
14:L:43:VAL:HG21	14:L:55:VAL:HG21	1.79	0.64
1:A:836:G:C6	1:A:851:G:C6	2.85	0.64
1:A:892:A:H2'	1:A:893:C:C6	2.33	0.64
4:B:25:ASN:C	4:B:25:ASN:HD22	2.01	0.64
11:I:9:ARG:HA	11:I:13:ALA:O	1.97	0.64
17:O:70:LEU:HD12	17:O:78:TYR:HB2	1.78	0.64
23:V:6:ARG:NH1	23:V:15:ARG:HH22	1.96	0.64
1:A:357:G:O2'	1:A:358:U:H5'	1.99	0.63
4:B:129:GLU:O	4:B:130:ARG:HB2	1.96	0.63
4:B:162:ILE:HG22	4:B:184:VAL:HA	1.79	0.63
4:B:95:GLN:O	4:B:96:ARG:HD2	1.98	0.63
6:D:61:LYS:NZ	6:D:72:GLU:OE1	2.30	0.63
8:F:10:LEU:HD11	8:F:59:TYR:CD2	2.33	0.63
12:J:15:THR:HG23	12:J:16:LEU:N	2.12	0.63
1:A:247:G:OP2	19:Q:99:SER:HB2	1.98	0.63
20:R:56:THR:HB	20:R:58:LEU:HD22	1.80	0.63
1:A:650:G:O2'	1:A:651:C:H5'	1.98	0.63
1:A:407:G:O2'	6:D:116:GLN:HG3	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:C:N1	6:D:135:LEU:HD13	2.12	0.63
10:H:6:ILE:HD12	10:H:35:ILE:CD1	2.28	0.63
4:B:198:ASP:HA	10:H:68:ARG:NH1	2.14	0.63
19:Q:63:ARG:HG2	19:Q:64:PRO:CD	2.27	0.63
1:A:179:A:H2'	1:A:180:U:H6	1.62	0.63
1:A:8:A:N6	6:D:209:ARG:H	1.96	0.63
4:B:102:LEU:CD1	4:B:102:LEU:N	2.61	0.63
4:B:84:GLU:HA	4:B:87:ARG:HB3	1.80	0.63
9:G:156:TRP:HA	9:G:156:TRP:HE3	1.63	0.63
15:M:90:LEU:O	15:M:93:ARG:N	2.32	0.63
16:N:29:ARG:HB3	16:N:40:CYS:HB3	1.80	0.63
17:O:56:LEU:C	17:O:56:LEU:HD23	2.19	0.63
19:Q:27:PHE:HB2	19:Q:28:PRO:CD	2.26	0.63
20:R:44:LEU:CD1	20:R:79:LEU:HD22	2.28	0.63
21:S:52:TYR:HA	21:S:56:GLN:O	1.97	0.63
1:A:1285:A:H4'	1:A:1286:A:O5'	1.99	0.63
1:A:342:C:H2'	1:A:343:U:H5'	1.79	0.63
1:A:731:G:OP1	1:A:766:A:H1'	1.99	0.63
5:C:40:ARG:CB	5:C:40:ARG:HH11	2.11	0.63
6:D:70:ILE:HG22	6:D:71:SER:N	2.14	0.63
9:G:47:CYS:O	9:G:50:ILE:HG22	1.99	0.63
16:N:8:GLU:O	16:N:11:LYS:HB2	1.99	0.63
21:S:39:THR:HG22	21:S:40:ILE:N	2.10	0.63
22:T:50:GLU:O	22:T:54:LYS:HG2	1.98	0.63
6:D:35:ARG:O	6:D:36:ARG:HB2	1.99	0.63
7:E:13:ILE:HG22	7:E:30:ALA:HA	1.78	0.63
11:I:4:TYR:O	11:I:18:PHE:HA	1.98	0.63
23:V:6:ARG:HB3	23:V:15:ARG:HH11	1.63	0.63
22:T:20:LEU:N	22:T:20:LEU:HD23	2.13	0.63
1:A:1327:C:O2'	1:A:1328:C:H5'	1.99	0.63
1:A:746:A:O2'	1:A:747:C:H5'	1.98	0.63
4:B:178:ARG:HH11	4:B:178:ARG:HG3	1.64	0.63
4:B:95:GLN:C	4:B:96:ARG:HD2	2.19	0.63
5:C:14:ILE:O	5:C:16:ARG:N	2.32	0.63
12:J:84:GLN:O	12:J:88:LEU:HD12	1.98	0.63
17:O:70:LEU:HD12	17:O:78:TYR:CA	2.28	0.63
22:T:16:HIS:CD2	22:T:20:LEU:HD21	2.33	0.63
1:A:1298:C:H4'	1:A:1299:A:O4'	1.99	0.63
1:A:1391:U:H2'	1:A:1392:G:H8	1.63	0.63
1:A:544:G:H2'	1:A:545:C:H6	1.62	0.63
5:C:20:SER:HB3	5:C:22:TRP:NE1	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:49:VAL:HG13	16:N:41:ARG:HB2	1.81	0.63
1:A:1230:C:O2'	1:A:1231:G:H5'	1.98	0.63
1:A:1372:U:H2'	1:A:1373:G:O4'	1.99	0.63
1:A:175:C:O2'	1:A:176:C:H5'	1.99	0.63
4:B:17:PHE:CD1	4:B:18:GLY:N	2.66	0.63
6:D:23:GLY:HA3	6:D:112:VAL:HG12	1.80	0.63
1:A:1249:C:O2'	11:I:73:GLN:NE2	2.31	0.63
15:M:49:THR:HG22	15:M:51:ALA:HB3	1.81	0.63
18:P:59:TRP:O	18:P:62:VAL:O	2.17	0.63
1:A:1406:U:C2'	1:A:1407:C:H5'	2.29	0.62
1:A:627:G:O2'	1:A:628:G:H5'	1.99	0.62
1:A:64:G:H4'	1:A:65:U:O5'	1.98	0.62
4:B:204:ASN:C	4:B:204:ASN:HD22	1.99	0.62
6:D:187:ARG:NE	6:D:188:LEU:H	1.96	0.62
12:J:82:ILE:N	12:J:82:ILE:HD12	2.14	0.62
14:L:50:SER:O	14:L:51:ALA:HB2	1.98	0.62
15:M:45:VAL:HG13	15:M:48:LEU:HD12	1.81	0.62
19:Q:36:ILE:HD13	19:Q:36:ILE:N	2.13	0.62
19:Q:85:VAL:O	19:Q:88:TYR:HB3	1.98	0.62
1:A:1278:U:H5"	1:A:1279:A:O4'	1.99	0.62
1:A:385:C:H2'	1:A:386:C:H6	1.61	0.62
1:A:41:G:H2'	1:A:42:G:H8	1.63	0.62
1:A:838:G:C2'	1:A:839:U:H5"	2.29	0.62
6:D:8:VAL:C	6:D:10:ARG:N	2.52	0.62
11:I:64:THR:HG22	11:I:65:VAL:N	2.12	0.62
1:A:695:A:OP2	13:K:53:SER:HB2	1.99	0.62
1:A:1046:A:H2'	1:A:1047:G:H5'	1.80	0.62
1:A:229:U:O2'	1:A:230:G:H5'	2.00	0.62
4:B:146:GLN:O	4:B:150:SER:HB3	1.98	0.62
5:C:83:ARG:C	5:C:85:ARG:H	2.01	0.62
9:G:95:ARG:O	9:G:99:LEU:HB2	2.00	0.62
11:I:71:SER:O	11:I:74:ILE:N	2.32	0.62
12:J:90:LEU:H	12:J:91:PRO:CD	2.09	0.62
13:K:115:PRO:C	13:K:117:ASN:H	2.01	0.62
15:M:35:GLU:C	15:M:37:THR:H	2.02	0.62
20:R:56:THR:O	20:R:58:LEU:HD22	2.00	0.62
21:S:77:THR:HG22	21:S:78:ARG:N	2.13	0.62
22:T:96:GLY:O	22:T:97:ALA:HB3	1.97	0.62
1:A:1149:C:H2'	1:A:1150:U:C6	2.35	0.62
1:A:1193:G:O2'	1:A:1194:U:H5'	1.99	0.62
4:B:167:PRO:O	4:B:171:ALA:N	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:35:GLU:CG	5:C:59:ARG:HH22	2.07	0.62
6:D:8:VAL:O	6:D:10:ARG:N	2.32	0.62
6:D:126:ILE:HG22	6:D:127:THR:H	1.63	0.62
9:G:124:LEU:O	9:G:127:ALA:HB3	1.99	0.62
12:J:42:THR:HG23	12:J:67:THR:O	1.98	0.62
1:A:1424:C:O2'	1:A:1425:U:H5'	2.00	0.62
1:A:1496:C:H2'	1:A:1497:G:C8	2.34	0.62
1:A:35:G:H2'	1:A:36:C:C6	2.34	0.62
6:D:128:VAL:HG12	6:D:129:ASN:ND2	2.14	0.62
6:D:150:GLU:HA	6:D:153:ARG:CZ	2.29	0.62
6:D:57:ARG:HH11	6:D:57:ARG:HG3	1.64	0.62
8:F:48:LEU:HD13	8:F:52:ILE:HD12	1.80	0.62
10:H:83:ILE:O	10:H:83:ILE:HG23	1.99	0.62
19:Q:68:ARG:HH11	19:Q:68:ARG:HG2	1.65	0.62
1:A:555:C:H2'	1:A:556:C:C6	2.34	0.62
4:B:106:LYS:O	4:B:109:SER:HB2	1.99	0.62
4:B:168:THR:CG2	4:B:192:SER:HA	2.29	0.62
10:H:107:LEU:HD23	10:H:107:LEU:H	1.64	0.62
10:H:51:VAL:HG12	10:H:52:ASP:H	1.64	0.62
10:H:69:ARG:NH2	10:H:77:GLU:HB2	2.14	0.62
15:M:36:LYS:NZ	15:M:36:LYS:HB3	2.14	0.62
23:V:23:PRO:C	23:V:24:ARG:HH11	2.03	0.62
1:A:454:C:H2'	1:A:455:C:H5'	1.82	0.62
1:A:524:G:H2'	1:A:525:C:H6	1.63	0.62
1:A:76:C:O2'	1:A:77:G:H5'	2.00	0.62
1:A:974:A:P	16:N:41:ARG:HH12	2.22	0.62
4:B:168:THR:HG23	4:B:192:SER:HA	1.81	0.62
1:A:644:G:H4'	10:H:92:ARG:NH1	2.15	0.62
11:I:51:ARG:HG2	11:I:56:LEU:HD12	1.82	0.62
11:I:59:PHE:HD2	11:I:60:ASP:N	1.98	0.62
1:A:116:A:H2'	1:A:117:G:H8	1.63	0.62
1:A:639:G:O2'	1:A:640:A:H5'	1.99	0.62
5:C:171:GLY:O	5:C:173:VAL:HG23	2.00	0.62
5:C:178:LEU:C	5:C:180:ALA:H	2.03	0.62
7:E:15:ARG:O	7:E:27:ARG:O	2.18	0.62
14:L:55:VAL:HG12	14:L:56:ALA:N	2.15	0.62
14:L:60:LEU:CD2	14:L:66:VAL:HG22	2.30	0.62
1:A:1090:U:H2'	1:A:1091:U:H6	1.64	0.62
1:A:112:G:O2'	1:A:113:G:H5'	1.99	0.62
1:A:376:G:H2'	1:A:377:G:H8	1.65	0.62
4:B:35:GLU:HA	4:B:39:ILE:O	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:6:ILE:HG13	12:J:71:LEU:O	2.00	0.62
20:R:37:VAL:HG12	20:R:41:LYS:HE3	1.80	0.62
1:A:1451:A:O2'	1:A:1452:C:OP1	2.16	0.62
1:A:1532:U:H2'	1:A:1533:C:C5'	2.28	0.62
1:A:254:G:OP1	19:Q:67:LYS:O	2.17	0.62
1:A:319:G:O2'	1:A:320:C:H5'	1.99	0.62
6:D:12:CYS:HA	6:D:19:LEU:CD1	2.30	0.62
6:D:65:ARG:HH11	6:D:65:ARG:HG2	1.64	0.62
21:S:81:ARG:O	21:S:81:ARG:HD3	2.00	0.62
1:A:372:C:H4'	1:A:373:A:O5'	2.00	0.61
5:C:81:GLY:HA2	5:C:84:ILE:HG22	1.82	0.61
15:M:49:THR:CG2	15:M:51:ALA:HB3	2.30	0.61
1:A:1002:G:H2'	1:A:1003:G:C8	2.35	0.61
1:A:1256:A:H4'	1:A:1257:U:H5'	1.81	0.61
1:A:31:G:N1	1:A:48:C:H5"	2.15	0.61
4:B:77:ALA:O	4:B:81:VAL:HG23	2.01	0.61
6:D:183:GLY:O	6:D:184:LYS:HB2	1.99	0.61
6:D:12:CYS:HA	6:D:19:LEU:HD13	1.82	0.61
7:E:80:ILE:HD12	7:E:91:LEU:HB2	1.80	0.61
12:J:34:VAL:HG12	12:J:35:SER:N	2.14	0.61
12:J:98:ILE:H	12:J:98:ILE:HD12	1.63	0.61
14:L:60:LEU:HD21	14:L:85:ILE:HD12	1.82	0.61
18:P:75:ARG:O	18:P:78:GLY:N	2.32	0.61
1:A:1223:C:OP1	21:S:78:ARG:NH1	2.33	0.61
1:A:674:G:H2'	1:A:675:A:H8	1.65	0.61
5:C:173:VAL:O	5:C:173:VAL:HG12	1.99	0.61
12:J:51:ARG:HG3	12:J:59:SER:HB2	1.82	0.61
19:Q:35:VAL:O	19:Q:35:VAL:HG23	2.01	0.61
1:A:1352:C:N4	1:A:1370:G:H1	1.98	0.61
4:B:59:GLU:O	4:B:62:ALA:HB3	2.00	0.61
6:D:20:TYR:HA	6:D:26:CYS:SG	2.40	0.61
6:D:91:SER:OG	6:D:92:VAL:N	2.32	0.61
1:A:1352:C:H42	1:A:1370:G:H1	1.49	0.61
1:A:767:A:H2'	1:A:768:A:C8	2.35	0.61
21:S:5:LEU:O	21:S:6:LYS:CB	2.47	0.61
21:S:6:LYS:HG2	21:S:7:LYS:HG2	1.81	0.61
22:T:29:LYS:O	22:T:33:ILE:HG13	2.01	0.61
1:A:1059:C:H2'	1:A:1060:C:C6	2.36	0.61
1:A:1068:G:N7	1:A:1094:G:H2'	2.16	0.61
1:A:1506:U:O2'	1:A:1507:A:H5'	2.01	0.61
1:A:335:C:H2'	1:A:336:C:C6	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:U:H2'	1:A:57:G:H8	1.65	0.61
1:A:67:C:H2'	1:A:68:G:C8	2.35	0.61
12:J:4:ILE:HD12	12:J:4:ILE:N	2.16	0.61
14:L:39:VAL:HG12	14:L:41:ARG:N	2.16	0.61
1:A:908:A:H2'	1:A:909:A:H8	1.66	0.61
5:C:139:GLN:HE21	5:C:139:GLN:CA	2.12	0.61
5:C:67:THR:CG2	5:C:68:VAL:H	2.10	0.61
6:D:13:ARG:HD2	6:D:38:TYR:O	2.00	0.61
7:E:84:PHE:HB3	7:E:134:ALA:HB2	1.83	0.61
13:K:52:GLY:HA2	13:K:55:LYS:NZ	2.16	0.61
1:A:974:A:OP2	16:N:41:ARG:NH1	2.33	0.61
21:S:6:LYS:HG2	21:S:7:LYS:N	2.15	0.61
1:A:1358:U:H3'	1:A:1359:C:H6	1.66	0.61
4:B:151:GLY:O	4:B:154:LEU:HG	2.01	0.61
6:D:6:GLY:O	6:D:8:VAL:HG13	2.01	0.61
14:L:86:ARG:HG3	14:L:86:ARG:NH1	2.14	0.61
21:S:32:LYS:HA	21:S:50:ALA:O	2.01	0.61
1:A:1406:U:O2'	1:A:1407:C:H5'	2.01	0.61
1:A:1427:U:H2'	1:A:1428:A:H8	1.65	0.61
1:A:854:G:H3'	1:A:871:U:O4	2.01	0.61
6:D:153:ARG:HD3	6:D:181:MET:HG3	1.81	0.61
9:G:41:ARG:O	9:G:44:TYR:N	2.33	0.61
11:I:110:GLU:OE2	11:I:119:ALA:HB1	2.00	0.61
16:N:58:LYS:HB3	16:N:58:LYS:NZ	2.16	0.61
4:B:101:MET:CA	4:B:108:ILE:HD12	2.31	0.61
5:C:79:ARG:HB3	5:C:82:GLU:HB3	1.82	0.61
8:F:100:ASN:OD1	20:R:23:LYS:HE2	1.99	0.61
9:G:144:MET:O	9:G:147:ALA:HB3	2.01	0.61
14:L:27:LEU:C	14:L:29:GLY:N	2.54	0.61
15:M:23:TYR:HB2	15:M:67:GLU:OE2	2.00	0.61
21:S:26:GLY:O	21:S:27:GLU:HG2	2.00	0.61
1:A:1061:G:C6	1:A:1062:U:N3	2.69	0.60
1:A:19:C:O2'	1:A:20:U:H5'	2.01	0.60
1:A:547:A:H4'	1:A:548:G:O5'	2.00	0.60
4:B:124:SER:OG	4:B:125:PRO:HD2	2.01	0.60
4:B:28:PHE:CE2	4:B:190:THR:HA	2.35	0.60
10:H:31:PHE:O	10:H:35:ILE:HG13	2.00	0.60
14:L:46:LYS:HG3	14:L:47:LYS:N	2.14	0.60
18:P:39:TYR:HB2	18:P:73:LEU:HD13	1.83	0.60
22:T:61:SER:O	22:T:65:LYS:HG2	2.00	0.60
1:A:1182:G:O2'	1:A:1183:A:OP2	2.18	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:G:H4'	1:A:389:A:H5"	1.83	0.60
4:B:97:TRP:HZ2	4:B:102:LEU:HD13	1.66	0.60
5:C:69:HIS:HB3	5:C:106:VAL:CG2	2.31	0.60
7:E:72:GLN:O	7:E:73:ASN:HB3	2.01	0.60
15:M:8:GLU:OE1	15:M:22:ILE:HG12	2.00	0.60
18:P:20:VAL:HG21	18:P:32:TYR:CB	2.30	0.60
18:P:2:VAL:HG13	18:P:64:ALA:H	1.64	0.60
21:S:20:LEU:HA	21:S:23:ASN:ND2	2.15	0.60
1:A:791:G:C2'	1:A:792:A:H5'	2.30	0.60
5:C:100:ALA:O	5:C:101:LEU:HB2	2.01	0.60
1:A:1250:A:C4'	11:I:68:GLY:H	2.05	0.60
20:R:53:ARG:C	20:R:55:ARG:H	2.04	0.60
2:Y:39:G:H2'	2:Y:40:PSU:C4'	2.31	0.60
1:A:101:A:O2'	1:A:102:G:H5'	2.02	0.60
1:A:959:A:C2	1:A:1222:G:O4'	2.54	0.60
1:A:1257:U:O2'	1:A:1258:G:OP2	2.18	0.60
1:A:946:A:H2'	1:A:947:G:H8	1.65	0.60
9:G:145:ALA:C	9:G:147:ALA:H	2.03	0.60
13:K:44:SER:O	13:K:47:VAL:HB	2.01	0.60
18:P:15:PRO:O	18:P:16:HIS:ND1	2.35	0.60
18:P:52:ASP:OD1	18:P:52:ASP:C	2.39	0.60
22:T:90:GLN:O	22:T:93:GLU:N	2.32	0.60
1:A:279:A:H5"	1:A:280:C:H2'	1.83	0.60
1:A:403:C:O2'	1:A:404:U:H5'	2.02	0.60
1:A:31:G:H1	1:A:48:C:H5"	1.66	0.60
1:A:812:C:O2'	1:A:813:U:OP2	2.20	0.60
6:D:32:ALA:C	6:D:34:GLU:N	2.51	0.60
1:A:412:A:N1	6:D:35:ARG:HB3	2.15	0.60
9:G:79:ARG:HA	9:G:84:ASN:HA	1.83	0.60
11:I:90:PRO:C	11:I:92:TYR:H	2.02	0.60
15:M:8:GLU:O	15:M:9:ILE:HG23	2.01	0.60
1:A:1059:C:H2'	1:A:1060:C:H6	1.66	0.60
1:A:418:C:H2'	1:A:419:C:C6	2.36	0.60
1:A:458:C:H2'	1:A:459:G:C8	2.25	0.60
1:A:927:G:H2'	1:A:928:G:H8	1.67	0.60
4:B:15:VAL:HG11	4:B:209:ARG:HG2	1.83	0.60
1:A:1123:A:O3'	12:J:36:GLY:HA3	2.00	0.60
12:J:94:VAL:HG12	12:J:95:GLU:H	1.66	0.60
18:P:22:THR:CA	18:P:33:ILE:HD12	2.27	0.60
1:A:190(L):U:O2	22:T:105:SER:HB2	2.02	0.60
1:A:1201:A:O2'	1:A:1202:G:OP2	2.19	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1370:G:O2'	1:A:1371:G:H5'	2.01	0.60
5:C:164:ARG:HH11	5:C:164:ARG:HB3	1.67	0.60
10:H:28:ALA:HA	10:H:59:LEU:HD12	1.82	0.60
11:I:48:GLU:HB2	11:I:51:ARG:NH2	2.16	0.60
12:J:6:ILE:CD1	12:J:72:VAL:HB	2.31	0.60
5:C:23:TYR:OH	12:J:9:ARG:HD3	2.01	0.60
17:O:64:ARG:HH12	17:O:68:ARG:NH2	2.00	0.60
21:S:15:LEU:HD12	21:S:16:LEU:N	2.16	0.60
21:S:30:LEU:HD23	21:S:31:ILE:H	1.67	0.60
1:A:1279:A:H5"	1:A:1280:A:OP1	2.01	0.60
1:A:1411:C:O2'	1:A:1412:C:H5'	2.02	0.60
1:A:1461:G:O2'	1:A:1462:G:H5'	2.02	0.60
6:D:6:GLY:H	6:D:115:ARG:HH22	1.50	0.60
7:E:110:LEU:O	7:E:113:ALA:HB3	2.01	0.60
11:I:81:ILE:O	11:I:85:LEU:HB2	2.01	0.60
14:L:47:LYS:CB	14:L:48:PRO:HD3	2.29	0.60
19:Q:60:ILE:O	19:Q:71:PHE:HD1	1.85	0.60
1:A:1399:C:C2	1:A:1502:A:N6	2.70	0.60
1:A:973:G:H3'	1:A:974:A:H5"	1.83	0.60
4:B:174:VAL:O	4:B:177:ALA:N	2.35	0.60
1:A:1346:A:C6	9:G:10:ARG:NH1	2.69	0.60
1:A:109:A:H2'	1:A:326:G:N2	2.16	0.60
1:A:1121:U:H2'	1:A:1122:U:C6	2.35	0.60
1:A:1256:A:H5'	1:A:1258:G:C1'	2.32	0.60
1:A:1477:C:O2'	1:A:1478:C:H5'	2.02	0.60
1:A:767:A:H2'	1:A:768:A:H8	1.66	0.60
5:C:14:ILE:HG22	5:C:15:THR:N	2.17	0.60
6:D:152:SER:O	6:D:158:ILE:HD12	2.01	0.60
10:H:87:SER:OG	10:H:92:ARG:HA	2.01	0.60
15:M:13:LYS:HA	15:M:44:ARG:NH2	2.16	0.60
18:P:45:THR:C	18:P:47:ASP:H	2.06	0.60
20:R:44:LEU:HD12	20:R:79:LEU:HD22	1.81	0.60
1:A:1108:G:H4'	1:A:1191:A:O4'	2.02	0.59
1:A:1347:G:H22	1:A:1373:G:H2'	1.66	0.59
1:A:1381:U:O2'	1:A:1382:C:H5'	2.02	0.59
1:A:190(F):G:H4'	1:A:190(G):G:OP2	2.02	0.59
1:A:544:G:H2'	1:A:545:C:C6	2.37	0.59
5:C:52:LEU:HD23	5:C:52:LEU:H	1.67	0.59
6:D:59:ARG:HH22	6:D:66:ARG:NH1	2.00	0.59
12:J:76:ASN:O	12:J:78:ASN:N	2.35	0.59
1:A:706:A:O4'	13:K:29:ILE:HD11	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:55:VAL:CG1	14:L:56:ALA:N	2.64	0.59
1:A:1086:U:O5'	1:A:1086:U:H6	1.85	0.59
1:A:1349:A:P	11:I:118:LYS:HZ3	2.24	0.59
1:A:1522:U:O2'	1:A:1523:G:H5'	2.03	0.59
1:A:697:U:H2'	1:A:698:G:H5'	1.83	0.59
4:B:47:THR:HA	4:B:202:PRO:HG2	1.83	0.59
14:L:27:LEU:O	14:L:29:GLY:N	2.36	0.59
17:O:9:GLN:HG2	17:O:13:GLN:HE22	1.67	0.59
1:A:1057:G:H2'	1:A:1058:G:O4'	2.01	0.59
1:A:1277:C:H2'	1:A:1278:U:H5'	1.82	0.59
1:A:456:C:H2'	1:A:457:C:H6	1.66	0.59
1:A:818:G:O2'	1:A:819:A:H5'	2.02	0.59
1:A:8:A:C6	6:D:209:ARG:HA	2.37	0.59
4:B:23:ARG:NH1	4:B:191:ASP:HB3	2.17	0.59
4:B:64:ARG:HE	4:B:64:ARG:HA	1.66	0.59
5:C:72:LYS:HB3	5:C:75:VAL:CG2	2.32	0.59
6:D:107:ARG:HE	6:D:173:TRP:HH2	1.50	0.59
7:E:125:SER:O	7:E:126:ARG:HG2	2.02	0.59
11:I:10:ARG:HD3	11:I:105:ASP:HB3	1.84	0.59
12:J:39:PRO:O	12:J:40:LEU:HB3	2.02	0.59
13:K:58:PRO:HB2	13:K:93:GLN:HG3	1.83	0.59
19:Q:16:GLN:O	19:Q:17:LYS:HB2	2.01	0.59
1:A:1251:A:H2'	1:A:1252:A:C8	2.36	0.59
1:A:1298:C:H1'	1:A:1299:A:C2	2.37	0.59
1:A:675:A:H1'	13:K:116:HIS:CD2	2.37	0.59
5:C:110:ASN:ND2	5:C:140:ARG:HB3	2.17	0.59
5:C:130:VAL:HG12	5:C:134:ILE:CD1	2.29	0.59
5:C:191:THR:CG2	5:C:192:THR:N	2.65	0.59
5:C:195:VAL:O	5:C:196:LEU:HB3	2.01	0.59
6:D:138:TYR:CD2	6:D:139:ARG:N	2.70	0.59
6:D:87:GLY:O	6:D:89:THR:N	2.34	0.59
7:E:80:ILE:H	7:E:80:ILE:HD12	1.68	0.59
9:G:50:ILE:HG12	9:G:61:VAL:HG21	1.83	0.59
12:J:40:LEU:HD22	12:J:69:ASN:ND2	2.17	0.59
13:K:74:ALA:C	13:K:76:GLY:H	2.06	0.59
14:L:76:ASN:OD1	14:L:108:ALA:HB3	2.02	0.59
19:Q:66:SER:O	19:Q:70:ARG:NH1	2.35	0.59
1:A:194:C:H2'	1:A:195:A:H5"	1.83	0.59
1:A:203:U:H5"	1:A:204:U:OP1	2.02	0.59
4:B:87:ARG:HD2	4:B:219:VAL:HG11	1.85	0.59
5:C:182:ILE:HG23	5:C:203:PHE:N	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:43:LEU:H	8:F:43:LEU:HD22	1.68	0.59
9:G:41:ARG:O	9:G:42:ILE:C	2.40	0.59
9:G:40:ALA:CB	11:I:41:VAL:HG21	2.32	0.59
19:Q:97:SER:O	19:Q:99:SER:N	2.34	0.59
1:A:1004:A:H5"	1:A:1025:U:O4	2.02	0.59
1:A:258:G:H2'	1:A:259:G:C8	2.38	0.59
1:A:513:C:H2'	1:A:514:C:H6	1.67	0.59
4:B:132:LYS:O	4:B:136:VAL:HG23	2.02	0.59
4:B:204:ASN:HD22	4:B:205:ASP:N	1.99	0.59
13:K:102:GLY:C	13:K:103:LEU:HD23	2.22	0.59
16:N:26:ARG:NH2	16:N:47:LEU:HD21	2.15	0.59
20:R:42:ARG:HH11	20:R:42:ARG:HB2	1.66	0.59
1:A:1002:G:N2	1:A:1040:U:H1'	2.18	0.59
1:A:162:A:H2'	1:A:163:C:O4'	2.03	0.59
7:E:125:SER:OG	7:E:126:ARG:N	2.36	0.59
8:F:21:LEU:O	8:F:24:GLU:HB3	2.02	0.59
19:Q:22:LEU:HD13	19:Q:23:VAL:N	2.18	0.59
1:A:1289:A:H2'	1:A:1290:G:H5'	1.85	0.59
1:A:370:C:H2'	1:A:371:G:H8	1.68	0.59
1:A:384:G:H2'	1:A:385:C:H6	1.67	0.59
1:A:766:A:C2'	1:A:767:A:H5'	2.32	0.59
5:C:139:GLN:NE2	5:C:143:GLU:HB2	2.18	0.59
5:C:55:VAL:O	5:C:55:VAL:HG12	2.02	0.59
12:J:3:LYS:N	12:J:76:ASN:H	2.00	0.59
1:A:1006:C:H2'	1:A:1007:C:H6	1.68	0.59
1:A:1333:A:H2'	1:A:1334:G:O4'	2.03	0.59
1:A:351:G:H4'	1:A:352:C:OP1	2.01	0.59
1:A:60:A:H4'	1:A:61:G:O5'	2.02	0.59
16:N:57:ARG:HG2	16:N:58:LYS:H	1.68	0.59
1:A:376:G:H5"	18:P:5:ARG:HD2	1.84	0.59
1:A:107:G:C2'	1:A:108:G:H5'	2.33	0.59
1:A:1095:U:OP1	1:A:1108:G:N2	2.33	0.59
1:A:1527:C:O2'	1:A:1528:U:H5'	2.01	0.59
4:B:57:PHE:CZ	4:B:61:LEU:HD21	2.38	0.59
11:I:46:ALA:O	11:I:78:LYS:HA	2.03	0.59
1:A:112:G:H21	1:A:354:G:C5'	2.07	0.58
1:A:1223:C:OP1	1:A:1224:G:H3'	2.02	0.58
1:A:390:C:O2'	18:P:28:ARG:NH2	2.35	0.58
1:A:501:C:H2'	1:A:502:G:H8	1.67	0.58
5:C:36:ASP:HA	5:C:39:ILE:HD12	1.84	0.58
8:F:1:MET:HB3	8:F:68:PRO:HA	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:148:ASN:C	9:G:150:ALA:H	2.04	0.58
11:I:57:GLY:O	11:I:58:ARG:HB2	2.02	0.58
13:K:29:ILE:HG12	13:K:29:ILE:O	2.01	0.58
15:M:13:LYS:CA	15:M:44:ARG:HH21	2.15	0.58
16:N:23:ARG:HH11	16:N:23:ARG:HG3	1.68	0.58
18:P:45:THR:HB	18:P:46:PRO:HD2	1.85	0.58
1:A:1010:G:H2'	1:A:1011:G:H8	1.66	0.58
1:A:1342:C:O2'	1:A:1343:G:H5'	2.03	0.58
1:A:165:C:H2'	1:A:166:G:H8	1.68	0.58
1:A:186:C:H2'	1:A:187:C:C6	2.39	0.58
1:A:389:A:H2'	1:A:390:C:O4'	2.04	0.58
6:D:19:LEU:HD12	6:D:19:LEU:N	2.17	0.58
1:A:19:C:H5"	7:E:86:ALA:HB2	1.85	0.58
8:F:3:ARG:HG3	8:F:93:SER:CB	2.32	0.58
9:G:75:VAL:HG12	9:G:76:ARG:N	2.18	0.58
11:I:97:LYS:HA	11:I:102:LEU:HD11	1.85	0.58
13:K:70:LYS:O	13:K:73:MET:N	2.36	0.58
16:N:9:LYS:C	16:N:11:LYS:H	2.05	0.58
20:R:55:ARG:HH11	20:R:55:ARG:HA	1.68	0.58
21:S:44:MET:CB	21:S:62:ILE:HG12	2.33	0.58
1:A:1054:C:O2'	1:A:1055:A:H5'	2.03	0.58
1:A:1131:G:H1	1:A:1143:G:H21	1.51	0.58
7:E:41:VAL:HG13	7:E:113:ALA:HA	1.83	0.58
9:G:115:ARG:HB2	9:G:115:ARG:HH11	1.68	0.58
19:Q:60:ILE:HD13	19:Q:61:GLU:N	2.18	0.58
1:A:1066:C:O2'	1:A:1067:A:H5'	2.03	0.58
4:B:91:PRO:HB3	4:B:151:GLY:O	2.03	0.58
4:B:18:GLY:HA2	4:B:41:ILE:HA	1.85	0.58
4:B:92:TYR:CD1	4:B:151:GLY:HA3	2.38	0.58
6:D:132:ARG:HG2	6:D:133:VAL:N	2.19	0.58
9:G:41:ARG:O	9:G:43:PHE:N	2.37	0.58
1:A:1118:C:H5'	11:I:104:ARG:HG3	1.85	0.58
13:K:110:ASP:HB2	20:R:88:LYS:HD2	1.84	0.58
13:K:69:ALA:O	13:K:73:MET:HG2	2.03	0.58
21:S:53:ASN:N	21:S:53:ASN:ND2	2.50	0.58
1:A:22:G:H2'	1:A:23:C:C6	2.38	0.58
1:A:425:G:O2'	1:A:426:G:H5'	2.03	0.58
4:B:25:ASN:ND2	4:B:27:LYS:H	2.01	0.58
7:E:71:LEU:HD11	7:E:114:GLY:HA3	1.85	0.58
11:I:49:PRO:O	11:I:53:VAL:HG23	2.04	0.58
14:L:119:LYS:O	14:L:120:TYR:HB2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1191:A:OP2	5:C:3:ASN:OD1	2.21	0.58
1:A:669:U:H2'	1:A:670:G:H8	1.69	0.58
10:H:107:LEU:N	10:H:107:LEU:CD2	2.60	0.58
10:H:69:ARG:CZ	10:H:69:ARG:HB2	2.34	0.58
16:N:29:ARG:HH11	16:N:29:ARG:HG2	1.69	0.58
1:A:1223:C:P	21:S:78:ARG:NH1	2.75	0.58
1:A:1267:C:O2	23:V:20:LYS:HD3	2.04	0.58
1:A:976:G:C8	1:A:1358:U:O2	2.56	0.58
1:A:1416:G:H1	1:A:1484:C:N4	2.01	0.58
8:F:6:VAL:O	8:F:62:TRP:HA	2.03	0.58
9:G:86:GLN:NE2	9:G:86:GLN:HA	2.19	0.58
10:H:120:THR:OG1	10:H:123:GLU:HB2	2.04	0.58
12:J:5:ARG:HA	12:J:73:ASP:OD1	2.03	0.58
15:M:3:ARG:CG	15:M:7:VAL:HA	2.33	0.58
18:P:51:VAL:HG12	18:P:52:ASP:O	2.04	0.58
22:T:89:ARG:O	22:T:93:GLU:HG2	2.03	0.58
1:A:342:C:C2'	1:A:343:U:H5'	2.34	0.58
4:B:91:PRO:HG2	4:B:155:LEU:HB2	1.85	0.58
5:C:47:LEU:H	5:C:47:LEU:HD12	1.67	0.58
11:I:17:VAL:HG11	11:I:81:ILE:HA	1.86	0.58
11:I:5:TYR:C	11:I:84:ALA:HB2	2.23	0.58
12:J:3:LYS:HA	12:J:74:ILE:O	2.04	0.58
21:S:20:LEU:HD12	21:S:21:GLU:N	2.19	0.58
1:A:1283:G:O2'	1:A:1284:C:H5'	2.04	0.58
1:A:359:U:O2'	1:A:360:A:H5'	2.04	0.58
4:B:172:ILE:O	4:B:173:ALA:C	2.42	0.58
6:D:117:ALA:O	6:D:121:VAL:HG23	2.02	0.58
9:G:23:VAL:O	9:G:27:ILE:HG13	2.04	0.58
14:L:107:ALA:O	14:L:108:ALA:C	2.42	0.58
15:M:20:THR:C	15:M:22:ILE:H	2.07	0.58
16:N:43:CYS:HA	16:N:46:GLU:HG3	1.86	0.58
20:R:86:VAL:HG12	20:R:87:ARG:N	2.18	0.58
1:A:1070:U:O2'	1:A:1071:C:H5'	2.03	0.58
1:A:1355:G:O2'	1:A:1356:G:H5'	2.04	0.58
1:A:268:C:O2'	1:A:269:C:H5'	2.04	0.58
5:C:178:LEU:H	5:C:178:LEU:HD22	1.68	0.58
9:G:111:ARG:HH12	9:G:122:HIS:HB3	1.69	0.58
12:J:46:ARG:HG2	12:J:46:ARG:HH11	1.69	0.58
12:J:63:PHE:CE1	16:N:45:ARG:HG3	2.38	0.58
1:A:1044:A:H2'	1:A:1045:C:H5'	1.86	0.57
1:A:802:A:H2'	1:A:803:G:H5'	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:831:U:O2'	1:A:832:C:H5'	2.04	0.57
1:A:940:C:H2'	1:A:941:G:H8	1.68	0.57
4:B:134:GLU:O	4:B:136:VAL:N	2.37	0.57
4:B:68:ILE:O	4:B:90:MET:HB3	2.03	0.57
4:B:70:PHE:CE1	4:B:90:MET:HG3	2.39	0.57
6:D:22:LYS:HE2	6:D:26:CYS:HB2	1.86	0.57
10:H:48:TYR:C	10:H:48:TYR:CD1	2.77	0.57
14:L:39:VAL:HG12	14:L:40:VAL:N	2.18	0.57
19:Q:48:GLU:O	19:Q:50:LYS:N	2.37	0.57
20:R:25:THR:O	20:R:25:THR:HG22	2.03	0.57
1:A:1126:U:H2'	1:A:1127:G:C8	2.39	0.57
1:A:1349:A:P	11:I:118:LYS:NZ	2.77	0.57
1:A:254:G:O2'	1:A:255:G:H5'	2.04	0.57
1:A:88:A:H2'	1:A:89:C:O4'	2.04	0.57
4:B:101:MET:O	4:B:105:PHE:HA	2.04	0.57
6:D:78:LEU:HB3	6:D:93:PHE:HE2	1.69	0.57
12:J:78:ASN:C	12:J:80:LYS:H	2.07	0.57
19:Q:80:GLY:O	19:Q:81:ARG:HB3	2.04	0.57
1:A:1064:G:C4'	1:A:1065:U:H5'	2.27	0.57
1:A:1420:C:H2'	1:A:1421:G:H8	1.69	0.57
4:B:107:THR:C	4:B:109:SER:N	2.55	0.57
5:C:99:VAL:CG2	5:C:100:ALA:N	2.67	0.57
9:G:18:TYR:CE2	9:G:59:LEU:HB2	2.39	0.57
10:H:134:ILE:O	10:H:135:CYS:HB3	2.04	0.57
14:L:75:HIS:HD2	14:L:77:LEU:H	1.50	0.57
16:N:14:PRO:O	16:N:15:LYS:CB	2.52	0.57
21:S:15:LEU:O	21:S:19:VAL:N	2.33	0.57
23:V:24:ARG:CA	23:V:24:ARG:HH11	2.17	0.57
1:A:1152:A:O2'	1:A:1153:C:H5'	2.05	0.57
1:A:552:U:O2'	1:A:553:A:H5'	2.03	0.57
1:A:662:G:H2'	1:A:663:A:C8	2.39	0.57
1:A:975:A:C8	1:A:975:A:H5'	2.37	0.57
5:C:115:LEU:O	5:C:118:GLN:N	2.37	0.57
9:G:111:ARG:NH1	9:G:122:HIS:HB3	2.18	0.57
1:A:1329:A:O2'	1:A:1330:U:H5'	2.05	0.57
1:A:1352:C:H2'	1:A:1353:G:C8	2.39	0.57
1:A:1392:G:H21	1:A:1502:A:H8	1.52	0.57
1:A:666:G:H5'	1:A:726:C:H1'	1.87	0.57
4:B:92:TYR:C	4:B:92:TYR:HD1	2.07	0.57
6:D:108:LEU:HD21	6:D:174:LEU:HD13	1.84	0.57
10:H:53:VAL:C	10:H:55:GLY:N	2.57	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:71:LEU:O	12:J:72:VAL:HB	2.03	0.57
18:P:67:THR:HG22	18:P:68:ASP:N	2.19	0.57
18:P:74:LEU:O	18:P:79:VAL:CG2	2.53	0.57
19:Q:33:GLY:O	19:Q:34:LYS:C	2.42	0.57
22:T:84:LEU:O	22:T:88:VAL:HG23	2.04	0.57
1:A:1043:C:H2'	1:A:1044:A:H8	1.68	0.57
1:A:1096:C:H2'	1:A:1097:C:H6	1.69	0.57
1:A:428:G:H4'	1:A:429:U:O5'	2.05	0.57
1:A:636:U:H2'	1:A:637:G:H8	1.70	0.57
4:B:72:GLY:HA3	4:B:81:VAL:HG21	1.85	0.57
4:B:92:TYR:CD1	4:B:92:TYR:C	2.78	0.57
7:E:72:GLN:O	7:E:73:ASN:CB	2.52	0.57
8:F:10:LEU:HD12	8:F:59:TYR:HB3	1.86	0.57
9:G:138:LYS:C	9:G:140:ASP:H	2.07	0.57
1:A:130:A:C8	19:Q:63:ARG:HG3	2.40	0.57
1:A:192:U:C1'	22:T:103:GLY:HA2	2.35	0.57
2:Y:31:C:HO2'	2:Y:32:C:H5'	1.64	0.57
1:A:1089:G:H2'	1:A:1090:U:H5'	1.87	0.57
1:A:116:A:H2'	1:A:117:G:C8	2.40	0.57
1:A:820:U:H4'	1:A:821:G:OP2	2.04	0.57
4:B:204:ASN:ND2	4:B:206:ASP:H	2.02	0.57
4:B:44:LEU:HA	4:B:47:THR:OG1	2.05	0.57
5:C:191:THR:HG22	5:C:192:THR:N	2.18	0.57
12:J:9:ARG:HB2	12:J:9:ARG:HH11	1.69	0.57
1:A:695:A:P	13:K:53:SER:HB2	2.44	0.57
14:L:100:ILE:HG22	14:L:101:VAL:N	2.19	0.57
1:A:1010:G:H2'	1:A:1011:G:C8	2.39	0.57
1:A:99:C:H2'	1:A:101:A:C8	2.39	0.57
1:A:1305:G:OP2	1:A:1305:G:H8	1.88	0.57
4:B:90:MET:SD	4:B:222:ILE:HG21	2.44	0.57
5:C:107:GLN:H	5:C:107:GLN:CD	2.08	0.57
5:C:3:ASN:H	5:C:3:ASN:ND2	2.02	0.57
11:I:40:LEU:O	11:I:42:ARG:N	2.38	0.57
16:N:36:PHE:O	16:N:36:PHE:CD1	2.57	0.57
18:P:43:LYS:HG3	18:P:48:TRP:CD2	2.39	0.57
19:Q:48:GLU:C	19:Q:50:LYS:N	2.57	0.57
20:R:45:SER:HA	20:R:51:LEU:HD21	1.87	0.57
22:T:10:LEU:O	22:T:13:LEU:HD12	2.05	0.57
1:A:1072:G:H2'	1:A:1073:U:O4'	2.04	0.57
1:A:1320:C:O2'	1:A:1321:C:H5'	2.05	0.57
1:A:1392:G:N2	1:A:1502:A:H8	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1509:C:O2'	1:A:1510:U:H5'	2.04	0.57
1:A:677:U:H3	1:A:713:G:H22	1.51	0.57
1:A:893:C:H2'	1:A:894:G:C8	2.38	0.57
5:C:34:LEU:C	5:C:34:LEU:HD23	2.25	0.57
6:D:102:ASP:O	6:D:105:VAL:HG12	2.04	0.57
22:T:42:GLN:OE1	22:T:42:GLN:HA	2.05	0.57
22:T:8:ARG:N	22:T:8:ARG:HD2	2.20	0.57
1:A:773:G:O2'	1:A:774:G:H5'	2.04	0.57
6:D:59:ARG:HH22	6:D:66:ARG:HH12	1.53	0.57
11:I:33:PHE:CE2	11:I:47:LEU:HD11	2.40	0.57
19:Q:60:ILE:C	19:Q:71:PHE:HD1	2.08	0.57
1:A:253:U:OP1	19:Q:67:LYS:HE3	2.05	0.56
4:B:87:ARG:HG2	4:B:87:ARG:HH11	1.70	0.56
5:C:155:GLY:O	5:C:156:ARG:HB2	2.04	0.56
9:G:123:GLU:OE2	9:G:123:GLU:HA	2.05	0.56
1:A:521:G:OP1	14:L:73:GLU:O	2.23	0.56
14:L:93:LEU:HD12	14:L:96:VAL:HG21	1.87	0.56
2:Y:39:G:H2'	2:Y:40:PSU:O4'	2.04	0.56
1:A:1051:C:O2'	1:A:1052:U:H5'	2.04	0.56
1:A:1168:A:H2'	1:A:1169:A:H8	1.66	0.56
1:A:1286:A:H8	1:A:1287:A:H4'	1.68	0.56
1:A:1358:U:H3'	1:A:1359:C:C6	2.40	0.56
1:A:382:A:H2'	1:A:383:A:H8	1.70	0.56
1:A:37:U:H2'	1:A:38:G:O4'	2.05	0.56
1:A:603:U:O2'	1:A:604:G:H5'	2.04	0.56
1:A:7:G:H21	7:E:121:LYS:HG2	1.69	0.56
4:B:28:PHE:CD2	4:B:190:THR:HA	2.39	0.56
6:D:175:SER:OG	6:D:186:LEU:HD21	2.05	0.56
11:I:47:LEU:C	11:I:49:PRO:HD2	2.26	0.56
8:F:100:ASN:HD21	20:R:23:LYS:HD2	1.71	0.56
21:S:30:LEU:HD23	21:S:48:THR:O	2.04	0.56
1:A:1454:G:H2'	1:A:1455:G:H8	1.70	0.56
1:A:812:C:O2'	1:A:813:U:P	2.62	0.56
8:F:4:TYR:HD1	8:F:92:LYS:HA	1.70	0.56
11:I:97:LYS:HD3	11:I:102:LEU:CD1	2.35	0.56
11:I:113:LYS:N	11:I:113:LYS:CD	2.67	0.56
15:M:65:LYS:HE3	15:M:69:GLU:OE1	2.05	0.56
19:Q:6:LEU:O	19:Q:59:ILE:N	2.34	0.56
23:V:2:GLY:O	23:V:4:GLY:N	2.37	0.56
5:C:191:THR:HB	5:C:194:GLY:O	2.06	0.56
5:C:39:ILE:O	5:C:43:LEU:HB2	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:107:ARG:HH12	6:D:114:ARG:NH2	2.04	0.56
6:D:201:GLN:HG2	6:D:201:GLN:O	2.06	0.56
7:E:89:ILE:HD13	7:E:90:VAL:H	1.71	0.56
9:G:15:ASP:OD1	9:G:17:VAL:N	2.39	0.56
9:G:38:LEU:O	9:G:41:ARG:HB2	2.05	0.56
9:G:67:GLU:O	9:G:67:GLU:HG3	2.06	0.56
11:I:78:LYS:HD3	11:I:101:PHE:HD2	1.70	0.56
14:L:100:ILE:CG2	14:L:101:VAL:N	2.68	0.56
17:O:44:LYS:NZ	17:O:44:LYS:HB2	2.19	0.56
21:S:30:LEU:HD22	21:S:31:ILE:O	2.05	0.56
23:V:24:ARG:CB	23:V:24:ARG:HH11	2.17	0.56
1:A:1152:A:OP1	12:J:68:HIS:ND1	2.38	0.56
1:A:1229:A:C2	1:A:1230:C:C4	2.94	0.56
1:A:1287:A:H2	1:A:1353:G:H1'	1.69	0.56
1:A:64:G:O2'	1:A:65:U:OP2	2.23	0.56
1:A:840:C:OP2	1:A:840:C:H2'	2.06	0.56
9:G:107:ALA:O	9:G:110:GLN:HB2	2.06	0.56
12:J:15:THR:CG2	12:J:16:LEU:H	2.15	0.56
18:P:70:ALA:O	18:P:74:LEU:HB2	2.06	0.56
1:A:1163:C:O2'	1:A:1164:G:H5'	2.05	0.56
1:A:908:A:H2'	1:A:909:A:C8	2.40	0.56
5:C:191:THR:HG21	5:C:193:TYR:CE1	2.40	0.56
5:C:178:LEU:N	5:C:178:LEU:HD22	2.21	0.56
7:E:144:THR:HG22	7:E:146:ALA:N	2.20	0.56
1:A:165:C:H2'	1:A:166:G:C8	2.41	0.56
1:A:498:U:O2'	1:A:499:A:H5'	2.06	0.56
1:A:669:U:H2'	1:A:670:G:C8	2.40	0.56
4:B:21:ARG:HD3	4:B:21:ARG:N	2.11	0.56
5:C:194:GLY:O	5:C:196:LEU:HD23	2.06	0.56
6:D:68:TYR:OH	6:D:196:LEU:HD21	2.06	0.56
11:I:36:TYR:CD2	11:I:37:PHE:CE2	2.94	0.56
16:N:24:CYS:O	16:N:28:GLY:HA2	2.05	0.56
1:A:1249:C:H6	1:A:1249:C:H5"	1.71	0.56
6:D:119:GLN:HG2	6:D:123:HIS:CD2	2.40	0.56
11:I:70:LYS:O	11:I:74:ILE:HG12	2.05	0.56
23:V:6:ARG:HB3	23:V:15:ARG:NH1	2.21	0.56
1:A:1055:A:H2'	1:A:1055:A:N3	2.19	0.56
1:A:178:C:O2'	1:A:179:A:H5'	2.06	0.56
5:C:103:VAL:HG12	5:C:104:GLN:N	2.20	0.56
5:C:7:PRO:O	5:C:11:ARG:HB2	2.06	0.56
7:E:32:VAL:O	7:E:43:LEU:HD23	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:39:TYR:CE2	18:P:41:PRO:HG3	2.41	0.56
19:Q:18:THR:CG2	19:Q:69:LYS:HE3	2.34	0.56
22:T:91:LEU:HD12	22:T:91:LEU:H	1.71	0.56
1:A:1112:C:N3	5:C:178:LEU:HD23	2.20	0.56
1:A:359:U:H2'	1:A:360:A:H8	1.72	0.56
1:A:408:A:O2'	1:A:409:G:H5'	2.05	0.56
1:A:420:U:H1'	1:A:424:G:N2	2.21	0.56
1:A:51:A:H4'	1:A:52:G:C5'	2.36	0.56
4:B:25:ASN:HD21	4:B:27:LYS:CG	2.18	0.56
5:C:110:ASN:O	5:C:111:LEU:HD12	2.05	0.56
7:E:43:LEU:HD11	7:E:132:ALA:CB	2.34	0.56
8:F:22:GLU:O	8:F:26:ILE:HG13	2.06	0.56
10:H:86:ILE:HD11	10:H:136:GLU:H	1.71	0.56
11:I:44:VAL:HG12	11:I:51:ARG:CZ	2.36	0.56
14:L:82:VAL:HG23	14:L:105:TYR:HB3	1.88	0.56
21:S:50:ALA:HA	21:S:58:VAL:O	2.05	0.56
1:A:1316:G:N2	1:A:1318:A:H3'	2.21	0.55
1:A:1423:G:H2'	1:A:1424:C:C6	2.41	0.55
1:A:338:A:C2	1:A:339:C:C2	2.95	0.55
1:A:379:C:O2'	1:A:380:G:H5'	2.06	0.55
4:B:15:VAL:HG11	4:B:209:ARG:CG	2.36	0.55
12:J:80:LYS:O	12:J:83:GLU:HG2	2.06	0.55
1:A:537:G:OP1	14:L:113:ARG:NH2	2.39	0.55
16:N:37:PHE:HE2	16:N:53:LEU:HD13	1.72	0.55
21:S:62:ILE:HG13	21:S:63:THR:N	2.21	0.55
1:A:135:C:O2	18:P:1:MET:HB2	2.05	0.55
4:B:157:ARG:O	4:B:158:LEU:C	2.45	0.55
4:B:184:VAL:HG12	4:B:197:VAL:HG13	1.88	0.55
6:D:58:LEU:HD23	6:D:206:PHE:CE1	2.40	0.55
9:G:75:VAL:HG21	9:G:144:MET:HG2	1.88	0.55
14:L:103:GLY:H	14:L:107:ALA:HB3	1.71	0.55
19:Q:76:LEU:HD23	19:Q:77:VAL:N	2.21	0.55
1:A:975:A:C4'	1:A:976:G:H5"	2.27	0.55
7:E:15:ARG:HD2	7:E:16:THR:O	2.07	0.55
10:H:14:ARG:HH11	10:H:14:ARG:HB3	1.71	0.55
15:M:50:GLU:O	15:M:54:VAL:HG23	2.06	0.55
17:O:17:ARG:NH1	17:O:17:ARG:HG3	2.17	0.55
22:T:67:ALA:HB2	22:T:77:ALA:HB2	1.87	0.55
1:A:202:U:H4'	1:A:203:U:OP2	2.06	0.55
4:B:223:ILE:CA	4:B:226:ARG:HB2	2.36	0.55
10:H:105:ARG:HG3	10:H:105:ARG:HH11	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:42:THR:HG23	12:J:67:THR:C	2.26	0.55
15:M:49:THR:HG22	15:M:51:ALA:N	2.18	0.55
17:O:56:LEU:O	17:O:60:VAL:HG23	2.07	0.55
19:Q:12:SER:HB3	19:Q:20:THR:CB	2.36	0.55
1:A:916:G:H2'	1:A:917:G:H8	1.72	0.55
5:C:46:GLU:O	5:C:48:TYR:N	2.40	0.55
5:C:91:LEU:HD21	5:C:99:VAL:H	1.72	0.55
15:M:5:ALA:O	15:M:8:GLU:HG2	2.07	0.55
17:O:29:VAL:HG11	17:O:67:LEU:HD21	1.87	0.55
17:O:56:LEU:HD23	17:O:57:LEU:N	2.21	0.55
1:A:146:G:H2'	1:A:147:G:H8	1.71	0.55
1:A:766:A:H2'	1:A:767:A:H5'	1.88	0.55
4:B:142:LEU:HD22	4:B:146:GLN:CD	2.27	0.55
5:C:95:THR:CG2	5:C:97:LYS:HB3	2.37	0.55
6:D:5:ILE:O	6:D:5:ILE:HG22	2.07	0.55
12:J:37:PRO:HB3	12:J:72:VAL:HG22	1.89	0.55
15:M:94:ARG:O	15:M:96:LEU:N	2.40	0.55
1:A:1038:C:H2'	1:A:1039:C:C6	2.40	0.55
1:A:649:G:O2'	1:A:650:G:H5'	2.07	0.55
1:A:730:G:N3	1:A:765:G:H4'	2.22	0.55
4:B:18:GLY:CA	4:B:41:ILE:HA	2.36	0.55
4:B:215:LEU:HD13	4:B:215:LEU:C	2.27	0.55
5:C:83:ARG:C	5:C:85:ARG:N	2.60	0.55
6:D:102:ASP:HB3	6:D:136:PRO:HB3	1.88	0.55
8:F:75:LEU:HD13	8:F:75:LEU:C	2.27	0.55
1:A:1376:U:OP1	9:G:98:SER:HB3	2.06	0.55
10:H:28:ALA:HA	10:H:59:LEU:CD1	2.36	0.55
1:A:972:C:OP1	12:J:57:LYS:HE2	2.07	0.55
14:L:28:LYS:C	14:L:30:ALA:H	2.09	0.55
1:A:949:A:H62	15:M:106:ASN:HD21	1.54	0.55
15:M:14:ARG:NH2	15:M:42:ALA:HB2	2.21	0.55
1:A:1002:G:H2'	1:A:1003:G:H8	1.71	0.55
1:A:186:C:O3'	22:T:82:SER:HB3	2.07	0.55
4:B:74:LYS:HE3	4:B:206:ASP:HB2	1.89	0.55
7:E:16:THR:CG2	7:E:27:ARG:HB2	2.35	0.55
12:J:6:ILE:HG22	12:J:98:ILE:CG2	2.37	0.55
14:L:25:PRO:C	14:L:27:LEU:N	2.59	0.55
1:A:1286:A:H2'	1:A:1287:A:C4'	2.25	0.55
4:B:112:VAL:CG1	4:B:153:ARG:HG2	2.36	0.55
6:D:126:ILE:CG2	6:D:127:THR:N	2.69	0.55
9:G:115:ARG:HB3	9:G:118:VAL:HG23	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:111:ARG:HD3	11:I:113:LYS:HD2	1.88	0.55
11:I:8:GLY:O	11:I:76:ALA:HB1	2.07	0.55
13:K:30:VAL:HG21	13:K:65:ALA:HA	1.89	0.55
13:K:49:GLY:O	13:K:50:TYR:HB2	2.07	0.55
15:M:73:GLU:O	15:M:76:ALA:HB3	2.07	0.55
1:A:1499:A:O2'	1:A:1500:A:H5'	2.05	0.55
1:A:275:G:O2'	1:A:276:G:H5'	2.07	0.55
1:A:533:A:C5	1:A:536:C:C4	2.96	0.55
4:B:16:HIS:NE2	4:B:210:SER:HB3	2.22	0.55
5:C:167:TRP:O	5:C:168:ALA:HB3	2.07	0.55
8:F:15:ASP:OD2	8:F:18:GLN:HG3	2.07	0.55
8:F:87:ARG:NH1	8:F:87:ARG:HG3	2.12	0.55
11:I:19:LEU:HB3	11:I:59:PHE:HZ	1.69	0.55
11:I:95:LYS:C	11:I:98:PRO:HD2	2.28	0.55
18:P:26:ARG:HG2	18:P:26:ARG:HH11	1.72	0.55
1:A:107:G:H2'	1:A:108:G:H5'	1.89	0.54
4:B:90:MET:SD	4:B:90:MET:N	2.79	0.54
5:C:73:PRO:C	5:C:75:VAL:H	2.10	0.54
6:D:96:LEU:H	6:D:96:LEU:HD22	1.72	0.54
7:E:39:GLY:O	7:E:69:VAL:N	2.40	0.54
8:F:26:ILE:O	8:F:30:LEU:HG	2.07	0.54
9:G:16:LEU:HD22	9:G:16:LEU:H	1.71	0.54
10:H:69:ARG:HH21	10:H:77:GLU:HB2	1.72	0.54
14:L:102:ARG:HA	14:L:107:ALA:HB1	1.88	0.54
15:M:4:ILE:HG22	15:M:5:ALA:N	2.22	0.54
20:R:44:LEU:HD22	20:R:48:GLY:O	2.07	0.54
1:A:1234:C:O2'	1:A:1235:U:H5'	2.06	0.54
1:A:502:G:H2'	1:A:503:C:H6	1.72	0.54
1:A:7:G:N2	7:E:121:LYS:HG2	2.22	0.54
16:N:9:LYS:HD3	16:N:10:ALA:N	2.21	0.54
1:A:1486:G:H2'	1:A:1487:G:O4'	2.08	0.54
1:A:19:C:H2'	1:A:20:U:C6	2.42	0.54
8:F:1:MET:SD	8:F:66:GLU:HG2	2.47	0.54
11:I:28:VAL:O	11:I:30:GLY:N	2.41	0.54
13:K:74:ALA:O	13:K:76:GLY:N	2.39	0.54
15:M:28:ALA:C	15:M:30:ALA:H	2.11	0.54
1:A:1029:C:H2'	1:A:1030:C:C6	2.42	0.54
1:A:1347:G:O2'	1:A:1348:U:P	2.65	0.54
1:A:168:G:O2'	1:A:169:C:H5'	2.08	0.54
1:A:942:G:H2'	1:A:943:U:H6	1.71	0.54
4:B:115:LEU:HD23	4:B:153:ARG:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:47:THR:HG23	4:B:202:PRO:HG2	1.90	0.54
5:C:69:HIS:O	5:C:70:VAL:HG13	2.07	0.54
6:D:182:LYS:HG2	6:D:183:GLY:N	2.22	0.54
6:D:30:LYS:O	6:D:32:ALA:N	2.40	0.54
13:K:14:VAL:HG21	13:K:40:ILE:HD11	1.89	0.54
17:O:71:GLN:O	17:O:73:GLU:N	2.41	0.54
19:Q:56:VAL:HG12	19:Q:77:VAL:CB	2.33	0.54
20:R:26:LEU:CG	20:R:27:GLY:H	2.21	0.54
1:A:1008:C:H42	1:A:1021:G:H1	1.56	0.54
1:A:1423:G:H2'	1:A:1424:C:H6	1.72	0.54
1:A:833:U:H2'	1:A:834:C:C5	2.43	0.54
1:A:925:G:C6	1:A:927:G:N7	2.76	0.54
4:B:76:GLN:HB2	4:B:206:ASP:OD1	2.07	0.54
5:C:47:LEU:N	5:C:47:LEU:HD12	2.23	0.54
7:E:60:TYR:CE1	7:E:64:ARG:CZ	2.91	0.54
11:I:9:ARG:HG2	11:I:14:VAL:HG22	1.88	0.54
12:J:26:ALA:HB1	12:J:84:GLN:HB3	1.90	0.54
14:L:71:PRO:HG2	14:L:102:ARG:HG3	1.88	0.54
16:N:29:ARG:HB3	16:N:40:CYS:CB	2.37	0.54
16:N:32:SER:HB2	16:N:41:ARG:HB3	1.89	0.54
20:R:74:ARG:HB3	20:R:81:PHE:CE1	2.43	0.54
21:S:17:GLU:O	21:S:20:LEU:HG	2.07	0.54
21:S:6:LYS:CG	21:S:7:LYS:H	2.11	0.54
1:A:1406:U:H2'	1:A:1407:C:H5'	1.89	0.54
1:A:491:G:H2'	1:A:492:G:H8	1.72	0.54
4:B:20:GLU:HB2	4:B:190:THR:CG2	2.38	0.54
9:G:138:LYS:O	9:G:140:ASP:N	2.41	0.54
1:A:689:C:P	13:K:46:GLY:HA3	2.48	0.54
13:K:91:ARG:C	13:K:93:GLN:N	2.59	0.54
14:L:83:VAL:HG22	14:L:84:LEU:H	1.71	0.54
14:L:98:TYR:N	14:L:98:TYR:CD1	2.73	0.54
15:M:66:LEU:HD12	15:M:66:LEU:H	1.73	0.54
19:Q:34:LYS:HG3	19:Q:34:LYS:O	2.07	0.54
1:A:1244:C:OP1	23:V:9:ARG:HB2	2.08	0.54
1:A:147:G:O2'	1:A:148:G:H5'	2.08	0.54
1:A:1480:G:O2'	1:A:1481:U:H5'	2.07	0.54
1:A:180:U:H2'	1:A:181:G:H5'	1.90	0.54
1:A:477:G:H2'	1:A:478:A:H8	1.72	0.54
1:A:543:C:O2'	1:A:544:G:H5'	2.08	0.54
1:A:625:G:H2'	1:A:626:U:H6	1.73	0.54
1:A:1060:C:C5	5:C:2:GLY:N	2.76	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:148:VAL:HG11	6:D:158:ILE:HD13	1.90	0.54
6:D:17:VAL:HG13	6:D:18:LYS:N	2.22	0.54
7:E:13:ILE:HA	7:E:29:GLY:O	2.06	0.54
10:H:11:THR:CA	10:H:14:ARG:HH12	2.11	0.54
11:I:11:LYS:H	11:I:104:ARG:HH12	1.56	0.54
13:K:14:VAL:HG21	13:K:40:ILE:CD1	2.37	0.54
16:N:26:ARG:HG2	16:N:27:CYS:N	2.21	0.54
19:Q:25:ARG:HG2	19:Q:26:GLN:N	2.23	0.54
19:Q:45:HIS:HB2	19:Q:69:LYS:HE2	1.88	0.54
1:A:1055:A:N7	1:A:1206:G:C2	2.76	0.54
1:A:145:G:O2'	1:A:146:G:H5'	2.08	0.54
1:A:674:G:H2'	1:A:675:A:C8	2.42	0.54
1:A:16:A:C2	1:A:920:U:O2	2.60	0.54
1:A:930:C:C2'	1:A:931:C:H5'	2.38	0.54
4:B:82:ARG:HA	4:B:92:TYR:CE2	2.42	0.54
5:C:188:LEU:HD22	5:C:189:ALA:H	1.72	0.54
7:E:28:PHE:O	7:E:47:LYS:HA	2.08	0.54
12:J:8:LEU:HG	12:J:96:ILE:HG12	1.90	0.54
12:J:90:LEU:N	12:J:91:PRO:HD2	2.16	0.54
13:K:18:ARG:HG2	13:K:20:TYR:CE1	2.42	0.54
13:K:91:ARG:C	13:K:93:GLN:H	2.12	0.54
14:L:89:ARG:HD2	14:L:90:VAL:H	1.73	0.54
16:N:37:PHE:CE2	16:N:53:LEU:HD13	2.43	0.54
16:N:58:LYS:HZ2	16:N:58:LYS:HB3	1.73	0.54
19:Q:82:MET:O	19:Q:83:ASP:C	2.45	0.54
1:A:1076:C:C4	1:A:1077:G:N7	2.75	0.54
1:A:1281:U:H5'	1:A:1282:C:C5	2.43	0.54
1:A:606:G:H1'	1:A:632:A:N6	2.22	0.54
4:B:112:VAL:C	4:B:114:ARG:H	2.10	0.54
7:E:127:ASN:O	7:E:128:PRO:C	2.44	0.54
9:G:115:ARG:NH1	9:G:115:ARG:HB2	2.23	0.54
13:K:82:VAL:HG12	13:K:108:ILE:HG23	1.89	0.54
19:Q:65:ILE:N	19:Q:65:ILE:HD12	2.22	0.54
20:R:44:LEU:HD11	20:R:79:LEU:HD13	1.90	0.54
21:S:44:MET:HB2	21:S:62:ILE:HG12	1.89	0.54
1:A:1288:A:H1'	1:A:1352:C:O2'	2.07	0.54
1:A:635:G:O2'	1:A:636:U:H5'	2.08	0.54
1:A:883:C:O2'	1:A:884:U:H5'	2.08	0.54
4:B:47:THR:HA	4:B:202:PRO:CG	2.37	0.54
5:C:132:ARG:HH22	6:D:47:ARG:HH22	1.55	0.54
14:L:93:LEU:HB2	14:L:96:VAL:HG23	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:70:LEU:HD12	17:O:78:TYR:CB	2.38	0.54
18:P:53:VAL:HG23	18:P:54:GLU:N	2.23	0.54
22:T:62:LEU:O	22:T:65:LYS:HB2	2.08	0.54
1:A:1287:A:H2'	1:A:1288:A:C8	2.43	0.53
1:A:1314:C:OP2	21:S:6:LYS:HD3	2.08	0.53
1:A:1316:G:H2'	1:A:1318:A:OP2	2.08	0.53
1:A:513:C:H2'	1:A:514:C:C6	2.43	0.53
1:A:877:C:H1'	10:H:3:THR:CG2	2.36	0.53
1:A:914:A:H2'	1:A:915:A:H8	1.72	0.53
5:C:49:SER:HB3	5:C:72:LYS:HZ1	1.72	0.53
5:C:78:GLY:HA3	5:C:83:ARG:CB	2.37	0.53
6:D:31:CYS:SG	6:D:31:CYS:O	2.67	0.53
8:F:61:LEU:O	8:F:62:TRP:HB2	2.08	0.53
13:K:52:GLY:H	13:K:55:LYS:HG3	1.72	0.53
18:P:28:ARG:HG3	18:P:29:ASP:OD2	2.07	0.53
18:P:52:ASP:OD1	18:P:55:ARG:HB2	2.07	0.53
18:P:67:THR:HG22	18:P:69:THR:H	1.71	0.53
22:T:21:LYS:HB3	22:T:21:LYS:HZ2	1.72	0.53
1:A:1329:A:C2'	1:A:1330:U:H5'	2.37	0.53
1:A:399:G:H2'	1:A:400:C:C6	2.43	0.53
5:C:40:ARG:O	5:C:44:GLU:HG3	2.08	0.53
6:D:58:LEU:C	6:D:58:LEU:HD13	2.29	0.53
1:A:1292:U:H5'	11:I:38:GLN:NE2	2.24	0.53
11:I:78:LYS:HD2	11:I:78:LYS:O	2.08	0.53
12:J:94:VAL:HG11	12:J:96:ILE:HD11	1.90	0.53
13:K:109:VAL:HG12	13:K:109:VAL:O	2.09	0.53
13:K:43:SER:OG	13:K:44:SER:N	2.42	0.53
1:A:1003(A):G:N3	1:A:1004:A:H1'	2.23	0.53
1:A:1034:G:HO2'	1:A:1035:A:H8	1.54	0.53
1:A:370:C:H2'	1:A:371:G:C8	2.42	0.53
1:A:580:U:H2'	1:A:581:G:O4'	2.08	0.53
4:B:26:PRO:HA	4:B:29:ALA:CB	2.37	0.53
5:C:83:ARG:O	5:C:85:ARG:N	2.41	0.53
6:D:126:ILE:CG2	6:D:127:THR:H	2.22	0.53
6:D:187:ARG:HE	6:D:188:LEU:N	2.03	0.53
6:D:3:ARG:NH1	6:D:71:SER:H	2.07	0.53
7:E:128:PRO:O	7:E:129:ILE:C	2.45	0.53
9:G:145:ALA:C	9:G:147:ALA:N	2.59	0.53
9:G:31:MET:HE1	9:G:34:GLY:HA2	1.90	0.53
1:A:598:U:H4'	10:H:94:TYR:CD1	2.44	0.53
12:J:25:GLU:C	12:J:27:ALA:H	2.12	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:37:PHE:O	16:N:39:LEU:HG	2.09	0.53
1:A:1320:C:C2	21:S:72:GLY:HA3	2.43	0.53
23:V:24:ARG:HB3	23:V:24:ARG:HH11	1.73	0.53
1:A:328:C:O2'	1:A:329:A:P	2.67	0.53
4:B:124:SER:C	4:B:126:GLU:N	2.61	0.53
4:B:74:LYS:HB3	4:B:74:LYS:HZ3	1.73	0.53
5:C:15:THR:O	5:C:16:ARG:HB2	2.07	0.53
5:C:84:ILE:HG12	5:C:88:ARG:HH22	1.72	0.53
5:C:95:THR:HG23	5:C:97:LYS:HB3	1.89	0.53
7:E:64:ARG:HD2	7:E:64:ARG:N	2.23	0.53
11:I:64:THR:O	11:I:65:VAL:HB	2.09	0.53
14:L:102:ARG:NH2	14:L:108:ALA:O	2.41	0.53
14:L:126:LYS:O	14:L:126:LYS:HD2	2.08	0.53
19:Q:75:ARG:HH11	19:Q:75:ARG:HG3	1.74	0.53
1:A:1247:U:O2'	1:A:1248:A:H5'	2.07	0.53
1:A:1286:A:C8	1:A:1287:A:H4'	2.43	0.53
1:A:16:A:C2'	1:A:17:U:H5'	2.38	0.53
1:A:58:C:O2'	1:A:59:A:H5'	2.08	0.53
1:A:997:U:H2'	1:A:998:G:C8	2.44	0.53
4:B:17:PHE:HB3	4:B:44:LEU:HD11	1.90	0.53
9:G:146:GLU:CG	9:G:149:ARG:HH21	2.19	0.53
10:H:123:GLU:O	10:H:127:LEU:HD22	2.08	0.53
11:I:113:LYS:HD3	11:I:119:ALA:HA	1.89	0.53
15:M:15:VAL:C	15:M:17:VAL:H	2.12	0.53
16:N:18:VAL:HG23	16:N:19:ARG:N	2.23	0.53
1:A:1407:C:O2'	1:A:1408:A:H5'	2.09	0.53
1:A:1455:G:O2'	1:A:1459:C:H5'	2.08	0.53
1:A:386:C:O2'	1:A:387:U:H5'	2.08	0.53
1:A:484:G:H4'	1:A:485:G:O5'	2.09	0.53
4:B:121:LEU:CD1	4:B:126:GLU:HB2	2.37	0.53
10:H:98:LYS:HD2	10:H:98:LYS:H	1.73	0.53
11:I:50:LEU:HB3	11:I:56:LEU:H	1.73	0.53
14:L:51:ALA:O	14:L:52:LEU:HD23	2.09	0.53
14:L:90:VAL:CG1	14:L:93:LEU:HG	2.39	0.53
18:P:20:VAL:HG21	18:P:32:TYR:CG	2.44	0.53
19:Q:58:GLU:O	19:Q:59:ILE:HD13	2.09	0.53
22:T:100:ILE:O	22:T:102:GLY:N	2.42	0.53
23:V:23:PRO:C	23:V:24:ARG:NH1	2.62	0.53
1:A:1345:U:C2	1:A:1377:A:N1	2.77	0.53
6:D:25:ARG:C	6:D:27:TYR:N	2.59	0.53
13:K:124:LYS:HG2	13:K:125:PHE:CE1	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:46:LYS:O	14:L:47:LYS:C	2.46	0.53
15:M:58:GLU:OE2	15:M:58:GLU:HA	2.09	0.53
17:O:63:ARG:C	17:O:65:ARG:N	2.59	0.53
1:A:1225:A:H5'	15:M:103:THR:HG1	1.73	0.53
1:A:1474:G:H2'	1:A:1475:G:H8	1.73	0.53
1:A:184:G:C4'	1:A:224:C:H4'	2.39	0.53
1:A:269:C:H2'	1:A:270:A:C8	2.44	0.53
4:B:112:VAL:HG23	4:B:113:HIS:N	2.23	0.53
6:D:8:VAL:HG23	6:D:9:CYS:H	1.74	0.53
7:E:76:ILE:HB	7:E:77:PRO:HD2	1.90	0.53
8:F:82:ARG:HB2	8:F:85:VAL:CG2	2.39	0.53
11:I:6:GLY:HA3	11:I:84:ALA:N	2.23	0.53
14:L:41:ARG:HG2	14:L:42:THR:O	2.08	0.53
17:O:7:GLU:O	17:O:11:VAL:HG13	2.09	0.53
17:O:25:THR:CG2	17:O:70:LEU:HD23	2.36	0.53
19:Q:76:LEU:HD23	19:Q:77:VAL:C	2.29	0.53
22:T:56:MET:HG2	22:T:84:LEU:CD1	2.39	0.53
22:T:56:MET:HG2	22:T:84:LEU:HD11	1.91	0.53
1:A:22:G:O2'	1:A:23:C:H5'	2.09	0.53
1:A:625:G:H2'	1:A:626:U:C6	2.44	0.53
1:A:949:A:N7	15:M:106:ASN:ND2	2.56	0.53
4:B:96:ARG:O	4:B:98:LEU:HD23	2.09	0.53
5:C:21:ARG:HG3	5:C:58:GLU:HG2	1.89	0.53
6:D:63:LYS:O	6:D:67:ILE:HG13	2.09	0.53
7:E:15:ARG:CD	7:E:26:PHE:CD2	2.85	0.53
10:H:29:SER:O	10:H:30:ARG:C	2.47	0.53
12:J:98:ILE:N	12:J:98:ILE:HD12	2.24	0.53
15:M:88:ARG:NE	21:S:3:ARG:HH21	2.07	0.53
18:P:74:LEU:O	18:P:79:VAL:HG23	2.09	0.53
22:T:96:GLY:O	22:T:97:ALA:CB	2.56	0.53
1:A:1128:C:O2'	1:A:1130:A:N7	2.42	0.53
1:A:533:A:H2'	1:A:535:A:OP2	2.08	0.53
1:A:934:C:C4	1:A:1345:U:C5	2.96	0.53
4:B:122:PHE:HZ	4:B:139:LYS:HD3	1.72	0.53
8:F:72:VAL:O	8:F:75:LEU:HB3	2.08	0.53
10:H:104:ARG:O	10:H:106:GLY:N	2.42	0.53
12:J:12:ASP:OD1	12:J:15:THR:HG22	2.08	0.53
14:L:85:ILE:HG23	14:L:98:TYR:HB3	1.90	0.53
1:A:1179:A:O3'	11:I:103:THR:HG23	2.09	0.52
1:A:290:C:O2'	1:A:291:C:H5'	2.09	0.52
1:A:781:A:H2'	1:A:782:A:H5'	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:792:A:N3	1:A:794:A:C5	2.77	0.52
1:A:892:A:H2'	1:A:893:C:H6	1.74	0.52
1:A:91:C:H2'	1:A:92:C:H6	1.73	0.52
4:B:118:LEU:HB3	4:B:142:LEU:HG	1.91	0.52
4:B:12:GLU:C	4:B:14:GLY:H	2.11	0.52
4:B:149:LEU:N	4:B:149:LEU:HD23	2.25	0.52
4:B:17:PHE:CA	4:B:44:LEU:HD21	2.39	0.52
6:D:121:VAL:O	6:D:134:ASP:HA	2.10	0.52
6:D:91:SER:O	6:D:94:LEU:N	2.42	0.52
13:K:28:THR:C	13:K:29:ILE:HG22	2.29	0.52
14:L:75:HIS:CD2	14:L:77:LEU:H	2.27	0.52
15:M:23:TYR:HB3	15:M:67:GLU:N	2.23	0.52
12:J:49:VAL:CG1	16:N:41:ARG:HB2	2.39	0.52
19:Q:44:ALA:HB1	19:Q:73:VAL:HG22	1.91	0.52
21:S:30:LEU:O	21:S:31:ILE:HD13	2.09	0.52
22:T:87:LYS:O	22:T:91:LEU:HD12	2.09	0.52
1:A:475:G:O2'	1:A:476:G:H5'	2.09	0.52
1:A:652:U:O4	1:A:752:G:O2'	2.16	0.52
1:A:19:C:O2	1:A:917:G:C2	2.62	0.52
1:A:930:C:O2'	1:A:931:C:H5'	2.10	0.52
4:B:112:VAL:HG12	4:B:153:ARG:HG2	1.90	0.52
4:B:167:PRO:HG2	4:B:192:SER:CB	2.39	0.52
6:D:146:ILE:N	6:D:146:ILE:CD1	2.71	0.52
9:G:57:GLU:CG	9:G:58:PRO:HD2	2.39	0.52
10:H:85:ARG:HD3	10:H:86:ILE:H	1.71	0.52
11:I:33:PHE:C	11:I:35:GLU:H	2.11	0.52
11:I:99:LEU:N	11:I:99:LEU:HD22	2.24	0.52
12:J:27:ALA:HA	12:J:81:THR:HG23	1.90	0.52
13:K:48:ILE:HD13	13:K:63:LEU:HB3	1.91	0.52
15:M:90:LEU:O	15:M:92:HIS:N	2.42	0.52
1:A:192:U:H4'	22:T:57:ARG:NH2	2.23	0.52
1:A:1236:A:O2'	1:A:1304:G:H4'	2.09	0.52
1:A:503:C:O2'	1:A:504:C:H5'	2.08	0.52
1:A:663:A:O2'	1:A:664:G:H5'	2.10	0.52
4:B:209:ARG:HD2	4:B:239:VAL:CG1	2.40	0.52
4:B:10:LEU:HD23	4:B:48:MET:CE	2.39	0.52
4:B:69:LEU:HD22	4:B:71:VAL:HG23	1.90	0.52
5:C:22:TRP:O	5:C:22:TRP:CE3	2.63	0.52
9:G:116:ALA:HA	9:G:119:ARG:CZ	2.39	0.52
9:G:23:VAL:HG13	9:G:43:PHE:CE2	2.44	0.52
14:L:39:VAL:HG11	14:L:41:ARG:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:A:O2'	1:A:142:G:H5'	2.09	0.52
1:A:1488:G:H2'	1:A:1489:G:C8	2.43	0.52
1:A:333:G:H4'	22:T:16:HIS:CE1	2.44	0.52
1:A:1206:G:H4'	5:C:192:THR:O	2.09	0.52
9:G:122:HIS:HA	9:G:125:MET:HE3	1.91	0.52
21:S:13:ASP:HA	21:S:16:LEU:HB3	1.91	0.52
21:S:7:LYS:HG3	21:S:7:LYS:O	2.09	0.52
22:T:94:ALA:O	22:T:95:ALA:CB	2.57	0.52
1:A:1116:C:O2'	1:A:1117:G:H5"	2.10	0.52
1:A:1190:G:C2'	1:A:1191:A:OP2	2.56	0.52
1:A:1305:G:N2	1:A:1331:G:C2'	2.66	0.52
24:A:1545:PAR:H322	24:A:1545:PAR:H51	1.75	0.52
1:A:161:A:H2'	1:A:162:A:C8	2.44	0.52
1:A:750:G:H1'	17:O:22:THR:OG1	2.10	0.52
1:A:757:U:O2'	1:A:758:G:H5'	2.09	0.52
1:A:938:A:N6	1:A:939:G:C6	2.78	0.52
5:C:168:ALA:O	5:C:169:ALA:HB2	2.10	0.52
5:C:178:LEU:H	5:C:178:LEU:CD2	2.23	0.52
6:D:64:LEU:O	6:D:64:LEU:HD22	2.09	0.52
8:F:4:TYR:HE2	8:F:72:VAL:HG22	1.75	0.52
9:G:66:VAL:C	9:G:68:ASN:N	2.63	0.52
21:S:17:GLU:HA	21:S:20:LEU:HG	1.92	0.52
23:V:9:ARG:NH1	23:V:22:ARG:HA	2.25	0.52
1:A:1150:U:H2'	1:A:1151:A:H5'	1.92	0.52
1:A:1241:G:H2'	1:A:1242:C:C6	2.45	0.52
1:A:1301:U:C2'	1:A:1301:U:O2	2.56	0.52
1:A:1403:C:O2'	1:A:1404:C:H5'	2.09	0.52
1:A:321:A:O2'	1:A:322:C:H5'	2.09	0.52
1:A:411:A:C4	1:A:413:G:H1'	2.45	0.52
1:A:45:U:H2'	1:A:46:G:C8	2.45	0.52
5:C:62:ASP:CA	5:C:97:LYS:HE2	2.40	0.52
6:D:68:TYR:CD1	6:D:68:TYR:N	2.76	0.52
10:H:60:ARG:HG3	10:H:60:ARG:NH1	2.23	0.52
1:A:401:C:H2'	1:A:402:G:H8	1.75	0.52
1:A:952:U:O2'	1:A:953:G:H5'	2.08	0.52
4:B:100:GLY:O	4:B:104:ASN:N	2.39	0.52
4:B:97:TRP:CE3	4:B:98:LEU:O	2.63	0.52
7:E:26:PHE:CD1	7:E:26:PHE:N	2.77	0.52
9:G:70:LYS:HD2	9:G:96:GLN:HB3	1.92	0.52
12:J:13:HIS:C	12:J:13:HIS:CD2	2.83	0.52
12:J:31:GLY:HA3	12:J:78:ASN:ND2	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:119:LYS:O	14:L:120:TYR:CB	2.57	0.52
14:L:90:VAL:HG11	14:L:93:LEU:HG	1.90	0.52
15:M:23:TYR:CZ	15:M:71:ARG:HG2	2.45	0.52
16:N:3:ARG:O	16:N:7:ILE:HD11	2.09	0.52
1:A:1440:C:H2'	1:A:1441:G:H5'	1.91	0.52
1:A:620:C:C2	6:D:135:LEU:HD13	2.45	0.52
1:A:834:C:H2'	1:A:835:U:C6	2.44	0.52
4:B:98:LEU:O	4:B:101:MET:HG3	2.09	0.52
1:A:619:U:N3	6:D:134:ASP:OD2	2.42	0.52
7:E:107:ARG:O	7:E:108:ALA:C	2.47	0.52
11:I:55:ALA:O	11:I:57:GLY:N	2.43	0.52
11:I:71:SER:O	11:I:74:ILE:HB	2.09	0.52
13:K:23:ALA:CB	13:K:91:ARG:HB2	2.39	0.52
14:L:82:VAL:O	14:L:105:TYR:HB3	2.09	0.52
16:N:36:PHE:O	16:N:36:PHE:HD1	1.93	0.52
18:P:55:ARG:O	18:P:56:ALA:C	2.48	0.52
1:A:255:G:O3'	19:Q:17:LYS:HD2	2.10	0.52
1:A:1044:A:C2'	1:A:1045:C:H5'	2.40	0.52
1:A:1128:C:H5"	11:I:16:ARG:HH12	1.75	0.52
1:A:247:G:C5	1:A:278:G:C2	2.98	0.52
1:A:791:G:C6	1:A:792:A:N7	2.77	0.52
6:D:35:ARG:O	6:D:36:ARG:CB	2.58	0.52
9:G:148:ASN:C	9:G:150:ALA:N	2.62	0.52
12:J:16:LEU:HD13	12:J:17:ASP:N	2.24	0.52
12:J:71:LEU:O	12:J:72:VAL:CB	2.58	0.52
12:J:37:PRO:HA	12:J:72:VAL:HA	1.92	0.52
18:P:80:PHE:O	18:P:82:GLN:HG3	2.09	0.52
22:T:87:LYS:HA	22:T:90:GLN:HB2	1.90	0.52
1:A:1053:G:N7	1:A:1200:C:C5'	2.73	0.52
12:J:49:VAL:HG13	16:N:41:ARG:CD	2.36	0.52
19:Q:40:LYS:HD3	19:Q:42:TYR:CZ	2.45	0.52
1:A:1176:A:O2'	1:A:1177:G:H5'	2.10	0.51
1:A:35:G:H2'	1:A:36:C:H6	1.75	0.51
1:A:376:G:O2'	1:A:377:G:H5'	2.11	0.51
1:A:382:A:H2'	1:A:383:A:C8	2.45	0.51
1:A:881:G:OP2	14:L:12:ARG:NH2	2.44	0.51
18:P:6:LEU:N	18:P:6:LEU:HD12	2.25	0.51
1:A:192:U:O3'	22:T:57:ARG:NH2	2.41	0.51
1:A:438:G:C4'	1:A:439:A:OP1	2.54	0.51
1:A:606:G:H1'	1:A:632:A:H61	1.75	0.51
1:A:760:G:H2'	1:A:761:G:H5'	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:3:ASN:O	5:C:4:LYS:CB	2.58	0.51
6:D:57:ARG:NH1	6:D:57:ARG:HG3	2.24	0.51
11:I:78:LYS:HD3	11:I:101:PHE:CD2	2.45	0.51
17:O:39:LEU:CD1	17:O:56:LEU:HB2	2.40	0.51
20:R:24:ALA:C	20:R:26:LEU:H	2.14	0.51
1:A:1016:A:H2'	1:A:1017:G:O4'	2.10	0.51
1:A:1006:C:N4	1:A:1024:G:H21	2.08	0.51
1:A:1128:C:H2'	1:A:1139:G:C6	2.45	0.51
1:A:1264:C:H2'	1:A:1265:G:C8	2.44	0.51
1:A:1368:G:H5"	11:I:112:LYS:HB3	1.91	0.51
1:A:1345:U:C2	1:A:1377:A:C2	2.98	0.51
1:A:406:G:H2'	1:A:407:G:H8	1.74	0.51
1:A:718:G:C8	13:K:116:HIS:HB3	2.45	0.51
4:B:9:GLU:HB3	4:B:12:GLU:HB2	1.91	0.51
4:B:134:GLU:O	4:B:138:LEU:N	2.43	0.51
7:E:107:ARG:HG3	7:E:107:ARG:NH1	2.24	0.51
11:I:100:GLY:O	11:I:102:LEU:N	2.43	0.51
11:I:112:LYS:HG2	11:I:118:LYS:HA	1.91	0.51
12:J:22:LYS:O	12:J:24:VAL:N	2.37	0.51
12:J:4:ILE:HD13	12:J:74:ILE:CB	2.40	0.51
15:M:35:GLU:C	15:M:37:THR:N	2.63	0.51
19:Q:61:GLU:HA	19:Q:71:PHE:CD1	2.46	0.51
23:V:10:ARG:HA	23:V:13:ILE:CD1	2.41	0.51
1:A:17:U:H1'	1:A:1080:A:N3	2.25	0.51
1:A:1192:C:H2'	1:A:1193:G:O4'	2.11	0.51
1:A:378:G:O2'	1:A:379:C:H5'	2.10	0.51
1:A:765:G:H5"	1:A:766:A:OP1	2.11	0.51
7:E:87:SER:HB3	7:E:131:ILE:HD13	1.92	0.51
9:G:69:VAL:O	9:G:69:VAL:HG12	2.10	0.51
10:H:45:ILE:O	10:H:47:GLY:N	2.43	0.51
11:I:44:VAL:HG12	11:I:51:ARG:NH1	2.26	0.51
14:L:42:THR:CG2	14:L:52:LEU:HB3	2.39	0.51
14:L:54:LYS:HE3	14:L:54:LYS:CA	2.40	0.51
15:M:36:LYS:HG3	15:M:59:TYR:OH	2.11	0.51
8:F:74:ASP:O	8:F:77:ARG:HB3	2.10	0.51
10:H:109:ILE:HD11	10:H:137:VAL:HB	1.92	0.51
12:J:9:ARG:HG3	12:J:9:ARG:O	2.10	0.51
14:L:53:ARG:HH12	14:L:92:ASP:CG	2.14	0.51
20:R:44:LEU:HD23	20:R:50:ILE:HA	1.92	0.51
23:V:2:GLY:C	23:V:4:GLY:N	2.64	0.51
1:A:1201:A:HO2'	1:A:1202:G:P	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:830:G:O2'	1:A:831:U:H5'	2.10	0.51
1:A:942:G:H2'	1:A:943:U:C6	2.45	0.51
1:A:977:A:H2'	1:A:978:A:H5"	1.91	0.51
4:B:223:ILE:O	4:B:226:ARG:N	2.44	0.51
4:B:7:VAL:HG11	4:B:221:LEU:CD2	2.36	0.51
5:C:11:ARG:NH1	5:C:177:THR:O	2.43	0.51
5:C:23:TYR:CG	5:C:24:ALA:N	2.78	0.51
9:G:18:TYR:CD2	9:G:59:LEU:HD13	2.46	0.51
21:S:31:ILE:O	21:S:32:LYS:HB3	2.11	0.51
1:A:1006:C:O2'	1:A:1007:C:H5'	2.10	0.51
1:A:411:A:H2'	1:A:412:A:H4'	1.93	0.51
1:A:428:G:O4'	1:A:430:A:C8	2.64	0.51
1:A:860:A:H2'	1:A:861:G:O4'	2.10	0.51
4:B:15:VAL:CG1	4:B:209:ARG:HG2	2.41	0.51
4:B:12:GLU:OE1	4:B:213:LEU:HD11	2.11	0.51
6:D:107:ARG:NH2	6:D:194:LEU:HD12	2.21	0.51
8:F:4:TYR:OH	8:F:72:VAL:HG21	2.10	0.51
1:A:738:C:OP1	8:F:92:LYS:HE3	2.10	0.51
9:G:18:TYR:HD1	9:G:18:TYR:H	1.58	0.51
15:M:3:ARG:HG3	15:M:8:GLU:N	2.23	0.51
15:M:49:THR:C	15:M:51:ALA:N	2.64	0.51
16:N:16:PHE:O	16:N:18:VAL:N	2.43	0.51
16:N:23:ARG:NH1	16:N:23:ARG:HG3	2.25	0.51
20:R:26:LEU:HG	20:R:27:GLY:N	2.22	0.51
1:A:1091:U:O2	1:A:1093:A:C8	2.64	0.51
1:A:1091:U:O2	1:A:1093:A:H8	1.94	0.51
1:A:1202:G:O2'	1:A:1203:C:H5'	2.11	0.51
1:A:1229:A:H2'	1:A:1230:C:H6	1.76	0.51
1:A:600:C:O2'	1:A:601:C:H5'	2.11	0.51
1:A:868:C:H2'	1:A:869:G:O4'	2.11	0.51
4:B:86:GLU:C	4:B:88:ALA:H	2.11	0.51
5:C:34:LEU:O	5:C:34:LEU:HD23	2.11	0.51
1:A:939:G:P	9:G:95:ARG:HH22	2.34	0.51
12:J:45:ARG:HB3	12:J:45:ARG:CZ	2.39	0.51
13:K:48:ILE:HD13	13:K:63:LEU:CB	2.41	0.51
14:L:58:VAL:O	14:L:65:GLU:HA	2.11	0.51
15:M:49:THR:HG22	15:M:51:ALA:CB	2.40	0.51
1:A:501:C:O2'	1:A:502:G:H5'	2.11	0.51
4:B:10:LEU:HD23	4:B:48:MET:HE2	1.93	0.51
4:B:83:MET:HG2	4:B:235:SER:CB	2.30	0.51
5:C:123:GLN:NE2	5:C:140:ARG:HH22	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:23:TYR:CD2	5:C:24:ALA:N	2.79	0.51
5:C:31:HIS:C	5:C:33:LEU:H	2.14	0.51
7:E:68:GLU:O	7:E:70:PRO:HD3	2.11	0.51
8:F:4:TYR:CE1	8:F:92:LYS:HG2	2.46	0.51
17:O:39:LEU:HD13	17:O:56:LEU:HB2	1.92	0.51
18:P:34:GLU:OE2	18:P:55:ARG:HD3	2.10	0.51
19:Q:67:LYS:O	19:Q:68:ARG:HB3	2.10	0.51
1:A:1104:G:C6	1:A:1105:A:C5	2.99	0.51
1:A:1223:C:H3'	1:A:1224:G:H5"	1.93	0.51
1:A:113:G:H1'	1:A:354:G:H5'	1.92	0.51
1:A:760:G:C2'	1:A:761:G:H5'	2.41	0.51
1:A:792:A:H4'	1:A:793:U:O5'	2.11	0.51
4:B:114:ARG:O	4:B:118:LEU:HB2	2.11	0.51
4:B:189:ASP:HA	4:B:203:GLY:O	2.11	0.51
5:C:139:GLN:HE21	5:C:143:GLU:HB2	1.76	0.51
8:F:100:ASN:O	8:F:101:ALA:HB2	2.11	0.51
8:F:44:GLY:O	8:F:60:PHE:N	2.44	0.51
10:H:113:SER:HB2	10:H:134:ILE:HD11	1.93	0.51
12:J:12:ASP:OD1	12:J:14:LYS:N	2.38	0.51
12:J:55:LYS:HG3	12:J:56:HIS:CD2	2.46	0.51
20:R:88:LYS:HG2	20:R:88:LYS:OXT	2.09	0.51
1:A:1406:U:H2'	1:A:1407:C:C5'	2.41	0.50
4:B:167:PRO:HG2	4:B:192:SER:HB3	1.91	0.50
5:C:182:ILE:HG23	5:C:202:ILE:C	2.32	0.50
6:D:10:ARG:O	6:D:13:ARG:HB2	2.11	0.50
11:I:111:ARG:HD3	11:I:112:LYS:N	2.25	0.50
15:M:20:THR:O	15:M:22:ILE:N	2.43	0.50
5:C:9:GLY:HA3	16:N:49:HIS:HA	1.93	0.50
17:O:87:ILE:CG2	17:O:88:ARG:H	2.23	0.50
19:Q:79:SER:O	19:Q:80:GLY:O	2.29	0.50
1:A:1288:A:H2'	1:A:1289:A:H8	1.77	0.50
1:A:1502:A:H2	1:A:1505:G:N1	2.10	0.50
1:A:39:G:O2'	1:A:40:C:H5'	2.12	0.50
1:A:644:G:C5	1:A:645:C:C5	2.99	0.50
1:A:938:A:C6	1:A:939:G:C5	2.99	0.50
1:A:977:A:C2'	1:A:978:A:H5"	2.42	0.50
4:B:97:TRP:CZ2	4:B:102:LEU:HD13	2.46	0.50
6:D:155:LEU:HB2	6:D:158:ILE:HD12	1.92	0.50
7:E:13:ILE:HG13	7:E:13:ILE:O	2.11	0.50
7:E:52:PRO:O	7:E:53:LEU:C	2.49	0.50
8:F:33:TYR:HB2	8:F:75:LEU:HD23	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:4:TYR:HE1	8:F:92:LYS:HG2	1.76	0.50
11:I:46:ALA:HB1	11:I:77:ILE:CG2	2.41	0.50
15:M:49:THR:C	15:M:51:ALA:H	2.14	0.50
18:P:7:ALA:O	18:P:17:TYR:HA	2.10	0.50
21:S:64:GLU:HA	21:S:67:VAL:HG23	1.93	0.50
1:A:1106:G:H5"	5:C:172:ARG:HG2	1.93	0.50
1:A:112:G:C2	1:A:113:G:C8	2.99	0.50
1:A:1405:G:O4'	1:A:1519:A:H4'	2.11	0.50
1:A:166:G:H2'	1:A:167:G:H8	1.75	0.50
1:A:714:G:H2'	1:A:715:A:C8	2.47	0.50
5:C:103:VAL:CG1	5:C:104:GLN:N	2.73	0.50
9:G:105:VAL:HG12	9:G:105:VAL:O	2.12	0.50
9:G:31:MET:SD	9:G:34:GLY:HA2	2.52	0.50
17:O:17:ARG:N	17:O:21:ASP:OD1	2.39	0.50
18:P:22:THR:OG1	18:P:23:ASP:N	2.44	0.50
1:A:1222:G:P	21:S:77:THR:HG21	2.51	0.50
1:A:109:A:H4'	1:A:110:C:OP2	2.10	0.50
1:A:261:U:O2	1:A:263:A:C8	2.65	0.50
1:A:407:G:H2'	1:A:408:A:H8	1.77	0.50
1:A:445:G:H2'	1:A:446:G:C8	2.45	0.50
1:A:943:U:O2'	1:A:944:G:H5'	2.12	0.50
1:A:993:G:HO2'	1:A:994:A:P	2.34	0.50
4:B:105:PHE:O	4:B:106:LYS:C	2.49	0.50
4:B:134:GLU:C	4:B:136:VAL:H	2.14	0.50
5:C:136:GLN:O	5:C:139:GLN:N	2.44	0.50
5:C:150:LYS:HD3	5:C:152:ILE:HD11	1.93	0.50
6:D:53:ASP:O	6:D:57:ARG:HG2	2.12	0.50
9:G:21:VAL:HG23	9:G:22:LEU:N	2.27	0.50
10:H:104:ARG:CZ	10:H:138:TRP:CH2	2.94	0.50
11:I:17:VAL:HG11	11:I:81:ILE:CA	2.41	0.50
11:I:19:LEU:HB3	11:I:59:PHE:CE2	2.44	0.50
11:I:84:ALA:HA	11:I:87:GLN:CB	2.41	0.50
12:J:45:ARG:CB	12:J:45:ARG:HH11	2.25	0.50
18:P:8:ARG:HD3	18:P:17:TYR:HE2	1.73	0.50
19:Q:20:THR:HA	19:Q:43:LEU:HD23	1.92	0.50
20:R:16:PRO:O	20:R:17:SER:HB2	2.10	0.50
21:S:9:VAL:HG12	21:S:10:PHE:N	2.26	0.50
21:S:51:VAL:O	21:S:58:VAL:HG22	2.11	0.50
1:A:1066:C:C5	1:A:1067:A:N6	2.79	0.50
1:A:1329:A:OP1	15:M:28:ALA:HB3	2.12	0.50
1:A:525:C:H2'	1:A:526:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:807:A:H2'	1:A:808:C:C6	2.47	0.50
5:C:21:ARG:CG	5:C:58:GLU:HG2	2.42	0.50
6:D:141:ARG:O	6:D:185:PHE:CD2	2.65	0.50
7:E:32:VAL:HG22	7:E:58:ALA:CB	2.40	0.50
1:A:755:G:H1'	10:H:1:MET:CE	2.41	0.50
16:N:47:LEU:O	16:N:50:LYS:N	2.45	0.50
19:Q:11:VAL:HB	19:Q:88:TYR:CD2	2.46	0.50
21:S:9:VAL:CG1	21:S:10:PHE:N	2.75	0.50
24:A:1545:PAR:H11	24:A:1545:PAR:O53	2.11	0.50
1:A:965:A:H1'	1:A:966:G:OP2	2.12	0.50
4:B:102:LEU:CD1	4:B:102:LEU:H	2.25	0.50
4:B:23:ARG:O	4:B:23:ARG:NH1	2.45	0.50
5:C:89:GLU:O	5:C:93:LYS:HE3	2.11	0.50
6:D:151:LYS:N	6:D:151:LYS:HD2	2.27	0.50
7:E:144:THR:HB	7:E:147:ASP:OD2	2.11	0.50
7:E:18:ARG:HG2	7:E:19:MET:H	1.75	0.50
8:F:100:ASN:CG	20:R:23:LYS:HE2	2.32	0.50
9:G:24:THR:HG22	9:G:28:ASN:ND2	2.20	0.50
13:K:43:SER:O	13:K:44:SER:CB	2.60	0.50
13:K:15:ALA:O	13:K:77:MET:HA	2.12	0.50
20:R:26:LEU:HD21	20:R:39:VAL:CG2	2.41	0.50
22:T:56:MET:HE1	22:T:104:LEU:HG	1.94	0.50
22:T:44:ALA:O	22:T:45:GLN:C	2.49	0.50
1:A:1246:C:O2'	1:A:1247:U:H5'	2.12	0.50
1:A:706:A:C1'	13:K:29:ILE:HD11	2.42	0.50
4:B:47:THR:HG23	4:B:202:PRO:O	2.11	0.50
4:B:25:ASN:ND2	4:B:25:ASN:C	2.63	0.50
4:B:95:GLN:HA	4:B:95:GLN:OE1	2.12	0.50
7:E:64:ARG:O	7:E:65:ASN:HB3	2.11	0.50
10:H:113:SER:CB	10:H:134:ILE:HD11	2.42	0.50
11:I:90:PRO:C	11:I:92:TYR:N	2.65	0.50
17:O:6:GLU:OE2	17:O:6:GLU:N	2.45	0.50
18:P:21:VAL:HG11	18:P:59:TRP:CD2	2.47	0.50
19:Q:40:LYS:HD3	19:Q:42:TYR:OH	2.11	0.50
19:Q:64:PRO:C	19:Q:65:ILE:HD12	2.32	0.50
1:A:1124:G:H4'	12:J:38:ILE:HD11	1.94	0.50
1:A:1225:A:N3	1:A:1225:A:C2'	2.69	0.50
1:A:394:G:H2'	1:A:395:C:C6	2.41	0.50
1:A:477:G:H2'	1:A:478:A:C8	2.46	0.50
1:A:533:A:C6	1:A:536:C:C4	3.00	0.50
1:A:77:G:O2'	1:A:78:G:H5'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:35:GLU:HB3	4:B:40:HIS:HD2	1.77	0.50
4:B:91:PRO:HG3	4:B:154:LEU:CD1	2.42	0.50
5:C:190:ARG:HG2	5:C:191:THR:N	2.26	0.50
5:C:49:SER:O	5:C:50:ALA:HB2	2.12	0.50
6:D:108:LEU:HB3	6:D:110:PHE:HE1	1.77	0.50
7:E:144:THR:CG2	7:E:145:LYS:N	2.74	0.50
8:F:95:GLU:N	8:F:95:GLU:CD	2.62	0.50
9:G:111:ARG:HH22	9:G:126:ASP:CG	2.15	0.50
12:J:4:ILE:HA	12:J:100:THR:CB	2.40	0.50
15:M:48:LEU:HD13	15:M:53:VAL:HG22	1.94	0.50
21:S:43:GLU:H	21:S:43:GLU:CD	2.15	0.50
21:S:53:ASN:HD21	21:S:58:VAL:CG1	2.25	0.50
1:A:449:C:H2'	1:A:450:G:O4'	2.12	0.50
1:A:477:G:O2'	1:A:478:A:H5'	2.12	0.50
1:A:524:G:H2'	1:A:525:C:C5	2.47	0.50
1:A:77:G:H2'	1:A:78:G:H8	1.77	0.50
1:A:792:A:H1'	1:A:794:A:N7	2.26	0.50
4:B:154:LEU:HD12	4:B:154:LEU:O	2.11	0.50
5:C:84:ILE:O	5:C:84:ILE:HG12	2.12	0.50
7:E:89:ILE:HD13	7:E:90:VAL:N	2.27	0.50
9:G:57:GLU:HG2	9:G:58:PRO:HD2	1.94	0.50
9:G:86:GLN:HE21	9:G:86:GLN:HA	1.75	0.50
11:I:100:GLY:C	11:I:102:LEU:N	2.60	0.50
12:J:24:VAL:O	12:J:28:ARG:HG3	2.11	0.50
16:N:26:ARG:NH1	16:N:47:LEU:HD21	2.26	0.50
1:A:1028:C:H42	1:A:1034:G:H21	1.60	0.49
1:A:1339:A:H2'	1:A:1340:A:O4'	2.12	0.49
1:A:1347:G:C2'	1:A:1348:U:OP2	2.59	0.49
1:A:1392:G:O2'	1:A:1502:A:H5"	2.11	0.49
1:A:381:C:H2'	1:A:382:A:O4'	2.11	0.49
1:A:411:A:C5	1:A:413:G:N3	2.79	0.49
1:A:489:C:H2'	1:A:490:G:H8	1.77	0.49
1:A:644:G:O2'	1:A:645:C:H5'	2.12	0.49
1:A:652:U:C4	1:A:752:G:N3	2.80	0.49
5:C:47:LEU:O	5:C:52:LEU:HD22	2.11	0.49
1:A:1080:A:O3'	7:E:16:THR:OG1	2.30	0.49
9:G:150:ALA:O	9:G:151:TYR:CD2	2.65	0.49
11:I:27:THR:HG22	11:I:28:VAL:N	2.26	0.49
11:I:29:ASN:O	11:I:30:GLY:C	2.49	0.49
15:M:31:LYS:O	15:M:35:GLU:HB2	2.12	0.49
15:M:3:ARG:HG3	15:M:7:VAL:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:40:ASN:HD22	15:M:40:ASN:C	2.14	0.49
18:P:71:ARG:O	18:P:75:ARG:N	2.45	0.49
20:R:61:LYS:O	20:R:62:GLU:C	2.51	0.49
2:Y:30:G:O2'	2:Y:31:C:H5'	2.12	0.49
1:A:1054:C:N3	2:Y:34:G:O4'	2.45	0.49
1:A:1104:G:H2'	1:A:1105:A:O4'	2.11	0.49
1:A:17:U:H4'	1:A:1080:A:O4'	2.12	0.49
1:A:945:G:C2	1:A:946:A:C8	2.99	0.49
4:B:78:GLN:HG3	4:B:94:ASN:OD1	2.12	0.49
5:C:119:ARG:HD2	5:C:140:ARG:HH11	1.77	0.49
5:C:47:LEU:CD1	5:C:47:LEU:H	2.24	0.49
18:P:4:ILE:HG12	18:P:21:VAL:HG22	1.93	0.49
18:P:53:VAL:O	18:P:54:GLU:C	2.49	0.49
19:Q:83:ASP:CG	19:Q:84:LEU:N	2.65	0.49
20:R:53:ARG:O	20:R:55:ARG:N	2.45	0.49
21:S:36:ARG:NH2	21:S:75:ALA:HB3	2.26	0.49
22:T:30:LYS:O	22:T:33:ILE:N	2.45	0.49
1:A:1268:A:H2'	1:A:1269:A:C8	2.47	0.49
1:A:1429:C:O2'	1:A:1430:C:H5'	2.13	0.49
1:A:554:C:H2'	1:A:555:C:C6	2.48	0.49
1:A:724:G:O2'	1:A:725:G:H5'	2.12	0.49
1:A:940:C:H2'	1:A:941:G:C8	2.47	0.49
4:B:107:THR:O	4:B:109:SER:N	2.44	0.49
4:B:54:THR:O	4:B:57:PHE:HB3	2.13	0.49
4:B:68:ILE:HB	4:B:90:MET:CE	2.42	0.49
5:C:6:HIS:HB3	5:C:8:ILE:HG13	1.94	0.49
6:D:102:ASP:OD1	6:D:103:ASN:N	2.44	0.49
6:D:162:LEU:HD21	6:D:181:MET:HA	1.93	0.49
6:D:62:GLN:O	6:D:63:LYS:C	2.50	0.49
9:G:108:ALA:C	9:G:110:GLN:H	2.15	0.49
14:L:40:VAL:CG1	14:L:40:VAL:O	2.58	0.49
15:M:110:ARG:HH11	15:M:110:ARG:CG	2.24	0.49
15:M:15:VAL:HG22	15:M:45:VAL:HG22	1.94	0.49
20:R:45:SER:C	20:R:47:THR:N	2.65	0.49
21:S:15:LEU:HD22	21:S:49:ILE:HD13	1.93	0.49
22:T:56:MET:HE1	22:T:104:LEU:HD21	1.94	0.49
1:A:189:G:H1	1:A:190(J):U:H3	1.60	0.49
1:A:332:G:H2'	1:A:333:G:H8	1.77	0.49
1:A:851:G:H2'	1:A:852:G:H8	1.77	0.49
4:B:139:LYS:HE2	4:B:143:GLU:HG2	1.95	0.49
4:B:16:HIS:CD2	4:B:210:SER:HB3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:7:PRO:HB2	5:C:11:ARG:HE	1.76	0.49
5:C:8:ILE:HG13	5:C:9:GLY:H	1.77	0.49
1:A:642:A:C4	10:H:114:THR:O	2.66	0.49
1:A:1001:A:H2	1:A:1040:U:H3	1.61	0.49
1:A:1089:G:C2'	1:A:1090:U:H5'	2.42	0.49
1:A:1238:A:C2	1:A:1241:G:N3	2.80	0.49
1:A:1441:G:H4'	1:A:1442:G:C6	2.47	0.49
1:A:573:A:O2'	1:A:574:A:H5'	2.12	0.49
1:A:806:C:O2'	1:A:807:A:H5'	2.12	0.49
1:A:824:C:H2'	1:A:825:G:C8	2.41	0.49
4:B:167:PRO:HG2	4:B:192:SER:OG	2.13	0.49
5:C:157:ILE:HG21	5:C:164:ARG:NH2	2.28	0.49
9:G:146:GLU:HA	9:G:149:ARG:HB2	1.93	0.49
9:G:16:LEU:HD22	9:G:16:LEU:N	2.28	0.49
9:G:88:PRO:O	9:G:89:MET:CB	2.59	0.49
10:H:104:ARG:NH2	10:H:138:TRP:CH2	2.80	0.49
11:I:111:ARG:HG2	11:I:112:LYS:H	1.77	0.49
11:I:48:GLU:N	11:I:51:ARG:HH21	2.11	0.49
13:K:115:PRO:C	13:K:117:ASN:N	2.66	0.49
14:L:103:GLY:H	14:L:107:ALA:CB	2.26	0.49
15:M:30:ALA:O	15:M:33:ALA:N	2.46	0.49
15:M:59:TYR:O	15:M:63:THR:HG22	2.12	0.49
16:N:24:CYS:HB3	16:N:29:ARG:N	2.27	0.49
21:S:22:LEU:HB3	21:S:28:LYS:HB2	1.94	0.49
22:T:98:PRO:HB3	22:T:101:GLY:HA2	1.94	0.49
1:A:599:C:O2'	1:A:600:C:H5'	2.12	0.49
1:A:629:G:O2'	1:A:630:G:H5'	2.11	0.49
4:B:108:ILE:O	4:B:108:ILE:CG2	2.59	0.49
5:C:115:LEU:O	5:C:116:VAL:C	2.51	0.49
10:H:96:GLY:O	10:H:97:VAL:C	2.51	0.49
13:K:123:LYS:O	13:K:125:PHE:N	2.45	0.49
14:L:83:VAL:HG21	14:L:100:ILE:CG1	2.42	0.49
15:M:110:ARG:HG2	15:M:110:ARG:HH11	1.77	0.49
15:M:5:ALA:HB3	15:M:8:GLU:CG	2.43	0.49
18:P:20:VAL:CG2	18:P:21:VAL:N	2.75	0.49
21:S:44:MET:HB3	21:S:62:ILE:HG12	1.93	0.49
22:T:60:GLU:O	22:T:63:ILE:HB	2.12	0.49
1:A:457:C:H2'	1:A:458:C:C6	2.48	0.49
1:A:604:G:C5	1:A:605:U:C5	3.00	0.49
1:A:642:A:C5	10:H:115:SER:HA	2.48	0.49
4:B:184:VAL:N	4:B:198:ASP:OD2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:85:ALA:C	4:B:87:ARG:H	2.15	0.49
12:J:66:ARG:HB3	12:J:66:ARG:CZ	2.43	0.49
18:P:67:THR:O	18:P:70:ALA:HB3	2.12	0.49
1:A:1330:U:OP1	15:M:23:TYR:O	2.30	0.49
1:A:1525:G:O2'	1:A:1526:G:H5'	2.12	0.49
1:A:570:G:H2'	1:A:571:U:C6	2.47	0.49
1:A:645:C:O2'	1:A:646:U:H5'	2.11	0.49
8:F:1:MET:O	8:F:1:MET:HE3	2.12	0.49
9:G:138:LYS:C	9:G:140:ASP:N	2.64	0.49
1:A:1291:G:H5"	9:G:41:ARG:NH2	2.28	0.49
13:K:12:ARG:O	13:K:13:GLN:HB2	2.13	0.49
19:Q:60:ILE:CD1	19:Q:61:GLU:N	2.76	0.49
1:A:1061:G:C2'	1:A:1062:U:H5'	2.42	0.49
1:A:106:C:O2	1:A:379:C:H4'	2.12	0.49
1:A:1157:A:H1'	1:A:1181:G:N2	2.27	0.49
1:A:1189:C:OP1	12:J:51:ARG:NH2	2.35	0.49
1:A:1470:G:O2'	1:A:1471:G:H5'	2.12	0.49
1:A:1508:G:O2'	1:A:1509:C:H5'	2.13	0.49
1:A:1510:U:H2'	1:A:1511:G:C8	2.48	0.49
1:A:386:C:C2'	1:A:387:U:H5'	2.43	0.49
1:A:481:G:O2'	1:A:482:A:C8	2.60	0.49
4:B:189:ASP:N	4:B:189:ASP:OD1	2.45	0.49
4:B:97:TRP:CZ3	4:B:98:LEU:O	2.66	0.49
5:C:112:SER:O	5:C:116:VAL:HG23	2.13	0.49
5:C:164:ARG:NH1	5:C:164:ARG:HB3	2.28	0.49
5:C:173:VAL:N	5:C:174:PRO:CD	2.76	0.49
1:A:878:G:C5'	10:H:89:PRO:HG2	2.43	0.49
18:P:4:ILE:HG13	18:P:64:ALA:HB1	1.93	0.49
18:P:82:GLN:H	18:P:82:GLN:HE21	1.60	0.49
19:Q:93:GLN:O	19:Q:96:GLN:N	2.33	0.49
20:R:45:SER:HB2	20:R:46:GLU:OE1	2.12	0.49
1:A:233:C:H2'	1:A:234:C:H6	1.77	0.49
1:A:892:A:O2'	1:A:893:C:H5'	2.13	0.49
1:A:967:C:H4'	11:I:128:ARG:NE	2.27	0.49
4:B:17:PHE:HA	4:B:44:LEU:HD21	1.95	0.49
5:C:36:ASP:O	5:C:39:ILE:HB	2.13	0.49
5:C:58:GLU:HB2	5:C:65:ALA:HB3	1.93	0.49
5:C:64:VAL:CG2	5:C:99:VAL:HB	2.43	0.49
6:D:36:ARG:HG3	6:D:38:TYR:CZ	2.48	0.49
11:I:53:VAL:HG11	11:I:92:TYR:CZ	2.48	0.49
12:J:32:ALA:O	12:J:34:VAL:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:22:VAL:O	20:R:22:VAL:HG12	2.13	0.49
21:S:33:THR:HG21	21:S:71:LEU:CD1	2.39	0.49
1:A:1277:C:C2'	1:A:1278:U:H5'	2.41	0.48
1:A:392:G:H2'	1:A:393:A:H8	1.78	0.48
1:A:731:G:O2'	1:A:732:C:H5'	2.13	0.48
1:A:913:A:O2'	1:A:914:A:P	2.71	0.48
1:A:928:G:C2	1:A:1390:U:O2	2.66	0.48
1:A:951:G:O2'	1:A:952:U:H5'	2.13	0.48
5:C:123:GLN:HE22	5:C:140:ARG:NH2	2.11	0.48
5:C:50:ALA:HB1	5:C:70:VAL:HG11	1.95	0.48
6:D:149:ALA:C	6:D:151:LYS:N	2.67	0.48
7:E:107:ARG:O	7:E:110:LEU:N	2.46	0.48
1:A:644:G:C4'	10:H:92:ARG:HH12	2.22	0.48
11:I:24:GLY:HA2	11:I:60:ASP:HA	1.95	0.48
12:J:4:ILE:HA	12:J:100:THR:CA	2.42	0.48
12:J:64:GLU:HG2	16:N:59:ALA:HA	1.95	0.48
14:L:60:LEU:HD21	14:L:85:ILE:HD11	1.92	0.48
15:M:81:LEU:O	15:M:89:GLY:HA3	2.13	0.48
17:O:17:ARG:O	17:O:18:PHE:HB3	2.13	0.48
20:R:36:ASN:O	20:R:39:VAL:HG12	2.13	0.48
1:A:1095:U:H2'	1:A:1096:C:H6	1.75	0.48
1:A:1226:C:O2'	1:A:1227:A:P	2.71	0.48
1:A:1503:A:HO2'	1:A:1504:G:P	2.36	0.48
1:A:1514:C:O2'	1:A:1515:C:H5'	2.13	0.48
1:A:1503:A:C5'	1:A:1531:A:H1'	2.36	0.48
5:C:108:ASN:CG	5:C:111:LEU:HD13	2.33	0.48
9:G:151:TYR:HD2	9:G:153:HIS:HE1	1.61	0.48
10:H:113:SER:HA	10:H:118:VAL:HA	1.95	0.48
10:H:48:TYR:HB2	10:H:60:ARG:O	2.13	0.48
11:I:48:GLU:HA	11:I:51:ARG:NE	2.28	0.48
17:O:39:LEU:HD23	17:O:39:LEU:O	2.12	0.48
23:V:3:LYS:O	23:V:3:LYS:HG2	2.12	0.48
1:A:1544:U:H4'	3:Z:1:U:H5'	1.94	0.48
1:A:1355:G:H2'	1:A:1356:G:H8	1.79	0.48
1:A:1527:C:O5'	1:A:1527:C:H6	1.96	0.48
1:A:916:G:H2'	1:A:917:G:C8	2.48	0.48
1:A:939:G:H2'	1:A:940:C:C6	2.49	0.48
4:B:71:VAL:CG1	4:B:170:GLU:HG2	2.43	0.48
4:B:83:MET:HA	4:B:83:MET:CE	2.42	0.48
5:C:179:ARG:HD3	5:C:206:GLU:HG2	1.94	0.48
5:C:181:ASN:ND2	5:C:204:LEU:HD12	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:150:ARG:HH11	7:E:150:ARG:HG3	1.77	0.48
7:E:40:ARG:HA	7:E:67:VAL:O	2.14	0.48
10:H:109:ILE:C	10:H:109:ILE:HD12	2.34	0.48
11:I:59:PHE:HD2	11:I:60:ASP:H	1.61	0.48
12:J:9:ARG:CB	12:J:9:ARG:NH1	2.76	0.48
14:L:83:VAL:CG2	14:L:100:ILE:HG23	2.43	0.48
15:M:108:ARG:NE	15:M:108:ARG:HA	2.28	0.48
17:O:87:ILE:CG2	17:O:88:ARG:N	2.76	0.48
22:T:85:MET:CE	22:T:104:LEU:HD23	2.43	0.48
1:A:1019:C:C2'	1:A:1020:U:H5'	2.43	0.48
1:A:1121:U:O2'	1:A:1122:U:H5'	2.12	0.48
1:A:1177:G:H2'	1:A:1178:G:O4'	2.14	0.48
1:A:16:A:H2'	1:A:17:U:H5'	1.95	0.48
1:A:364:A:H2'	1:A:365:U:O2	2.13	0.48
7:E:51:VAL:O	7:E:55:VAL:HG23	2.13	0.48
10:H:39:LEU:H	10:H:39:LEU:HD22	1.77	0.48
12:J:54:PHE:O	12:J:55:LYS:HG2	2.13	0.48
17:O:63:ARG:C	17:O:65:ARG:H	2.16	0.48
19:Q:68:ARG:HH11	19:Q:68:ARG:CG	2.25	0.48
1:A:1090:U:O2'	1:A:1091:U:H5'	2.13	0.48
1:A:1238:A:O2'	1:A:1239:A:H5'	2.14	0.48
1:A:1520:G:O2'	1:A:1521:G:H5'	2.14	0.48
1:A:63:C:H5'	1:A:64:G:OP2	2.14	0.48
4:B:189:ASP:OD2	4:B:191:ASP:OD1	2.31	0.48
4:B:219:VAL:HA	4:B:222:ILE:HD12	1.94	0.48
6:D:22:LYS:HE2	6:D:26:CYS:CB	2.44	0.48
6:D:30:LYS:C	6:D:32:ALA:N	2.64	0.48
9:G:18:TYR:CD2	9:G:59:LEU:HB2	2.47	0.48
10:H:51:VAL:HG21	10:H:60:ARG:HG3	1.94	0.48
11:I:69:GLY:O	11:I:73:GLN:HG3	2.13	0.48
12:J:18:ALA:C	12:J:20:ALA:H	2.17	0.48
12:J:32:ALA:C	12:J:34:VAL:N	2.66	0.48
12:J:94:VAL:CG1	12:J:95:GLU:N	2.76	0.48
15:M:30:ALA:O	15:M:31:LYS:C	2.51	0.48
16:N:23:ARG:HA	16:N:30:ALA:HA	1.96	0.48
17:O:39:LEU:HD23	17:O:43:LEU:HG	1.96	0.48
1:A:103:C:P	22:T:17:ARG:HH11	2.36	0.48
23:V:24:ARG:CB	23:V:24:ARG:NH1	2.74	0.48
1:A:1089:G:H2'	1:A:1090:U:C5'	2.43	0.48
1:A:188:C:H6	1:A:188:C:O5'	1.97	0.48
4:B:83:MET:C	4:B:85:ALA:H	2.17	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:91:PRO:O	4:B:92:TYR:HB3	2.14	0.48
6:D:192:GLU:OE1	6:D:192:GLU:HA	2.12	0.48
10:H:63:LEU:N	10:H:63:LEU:HD12	2.28	0.48
11:I:53:VAL:C	11:I:55:ALA:H	2.14	0.48
14:L:39:VAL:CG1	14:L:41:ARG:HB2	2.44	0.48
1:A:398:C:O2'	1:A:399:G:H5'	2.12	0.48
1:A:411:A:N6	1:A:413:G:H21	1.89	0.48
1:A:948:C:O2'	1:A:949:A:H5'	2.13	0.48
5:C:52:LEU:CD2	5:C:52:LEU:H	2.27	0.48
5:C:91:LEU:HD21	5:C:98:ASN:HA	1.96	0.48
6:D:108:LEU:HD23	6:D:174:LEU:HD13	1.94	0.48
6:D:61:LYS:HD3	6:D:206:PHE:CD2	2.48	0.48
6:D:52:SER:O	6:D:55:ALA:HB3	2.13	0.48
9:G:145:ALA:O	9:G:147:ALA:N	2.46	0.48
9:G:78:ARG:HD2	9:G:156:TRP:HZ3	1.78	0.48
11:I:107:ARG:HH11	11:I:107:ARG:HB3	1.79	0.48
12:J:26:ALA:O	12:J:85:LEU:HD21	2.14	0.48
23:V:7:ARG:O	23:V:7:ARG:HG3	2.14	0.48
1:A:1408:A:C6	1:A:1494:G:C6	3.02	0.48
1:A:542:G:O2'	1:A:543:C:H5'	2.13	0.48
1:A:914:A:C4	1:A:915:A:C8	3.02	0.48
1:A:922:G:N3	1:A:1398:A:H2	2.12	0.48
4:B:68:ILE:HB	4:B:90:MET:HE3	1.95	0.48
5:C:143:GLU:O	5:C:143:GLU:HG2	2.13	0.48
5:C:177:THR:O	5:C:177:THR:HG23	2.13	0.48
7:E:122:GLU:O	7:E:123:LEU:HD23	2.13	0.48
9:G:72:ARG:C	9:G:73:MET:HG2	2.33	0.48
10:H:3:THR:CG2	10:H:4:ASP:H	2.26	0.48
4:B:181:PHE:HD2	10:H:70:GLN:HB3	1.79	0.48
12:J:39:PRO:HA	12:J:70:ARG:HD3	1.96	0.48
13:K:44:SER:CB	13:K:47:VAL:HG23	2.43	0.48
18:P:53:VAL:CG2	18:P:54:GLU:N	2.77	0.48
20:R:18:ARG:C	20:R:19:LYS:HG3	2.34	0.48
21:S:35:SER:C	21:S:37:ARG:N	2.65	0.48
22:T:94:ALA:O	22:T:95:ALA:HB3	2.13	0.48
1:A:1014:A:H2'	1:A:1015:A:C8	2.48	0.48
1:A:339:C:H2'	1:A:340:U:H6	1.79	0.48
1:A:411:A:C6	1:A:429:U:C4	3.02	0.48
1:A:474:G:O2'	1:A:475:G:H5'	2.14	0.48
1:A:628:G:H2'	1:A:629:G:C8	2.48	0.48
1:A:913:A:O2'	1:A:914:A:OP2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:962:C:H2'	1:A:963:G:O4'	2.14	0.48
4:B:206:ASP:O	4:B:207:ALA:HB2	2.14	0.48
5:C:14:ILE:CG2	5:C:15:THR:H	2.23	0.48
5:C:84:ILE:O	5:C:88:ARG:NH1	2.46	0.48
6:D:112:VAL:CG2	6:D:161:ASN:HD21	2.26	0.48
6:D:59:ARG:HA	6:D:59:ARG:NE	2.29	0.48
8:F:9:VAL:HG13	8:F:60:PHE:CD2	2.49	0.48
9:G:136:LYS:O	9:G:140:ASP:HB2	2.13	0.48
18:P:45:THR:C	18:P:47:ASP:N	2.66	0.48
21:S:15:LEU:O	21:S:19:VAL:HG12	2.14	0.48
21:S:51:VAL:HG22	21:S:71:LEU:HD22	1.96	0.48
1:A:1306:A:N6	1:A:1331:G:H1'	2.29	0.48
1:A:1372:U:O2'	1:A:1373:G:H5'	2.14	0.48
1:A:620:C:H2'	1:A:621:A:O4'	2.13	0.48
1:A:662:G:H2'	1:A:663:A:H8	1.78	0.48
4:B:70:PHE:CE2	4:B:215:LEU:HD21	2.48	0.48
5:C:195:VAL:O	5:C:196:LEU:HD23	2.14	0.48
5:C:73:PRO:C	5:C:75:VAL:N	2.68	0.48
8:F:79:LEU:O	8:F:85:VAL:HG11	2.14	0.48
13:K:57:THR:OG1	13:K:58:PRO:HD2	2.13	0.48
12:J:47:PHE:CZ	16:N:37:PHE:HE1	2.32	0.48
19:Q:83:ASP:O	19:Q:86:GLU:HB2	2.14	0.48
21:S:41:VAL:HB	21:S:43:GLU:OE2	2.13	0.48
22:T:13:LEU:HD12	22:T:13:LEU:N	2.29	0.48
22:T:54:LYS:HA	22:T:57:ARG:CD	2.44	0.48
1:A:28:G:O2'	1:A:296:U:OP1	2.31	0.47
1:A:533:A:O2'	1:A:534:U:OP1	2.31	0.47
1:A:689:C:C2'	1:A:690:G:H5'	2.44	0.47
4:B:109:SER:C	4:B:111:ARG:N	2.67	0.47
6:D:108:LEU:HB2	6:D:110:PHE:CE1	2.49	0.47
10:H:45:ILE:C	10:H:47:GLY:N	2.66	0.47
10:H:6:ILE:HD12	10:H:35:ILE:HD11	1.94	0.47
11:I:48:GLU:H	11:I:51:ARG:HH21	1.62	0.47
11:I:93:ARG:O	11:I:96:LEU:N	2.34	0.47
18:P:39:TYR:CZ	18:P:41:PRO:HA	2.48	0.47
19:Q:61:GLU:CA	19:Q:71:PHE:CE1	2.97	0.47
20:R:70:ILE:O	20:R:72:ARG:N	2.47	0.47
21:S:13:ASP:O	21:S:14:HIS:C	2.52	0.47
1:A:1019:C:O2'	1:A:1020:U:H5'	2.13	0.47
1:A:1394:A:OP1	1:A:1394:A:H8	1.97	0.47
1:A:1412:C:H2'	1:A:1413:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1460:A:H2'	1:A:1461:G:O4'	2.13	0.47
1:A:519:C:H2'	1:A:520:A:C8	2.49	0.47
1:A:755:G:H1'	10:H:1:MET:HE1	1.96	0.47
1:A:780:A:C2	1:A:801:U:C5	3.02	0.47
4:B:144:ARG:HG3	4:B:145:LEU:HD23	1.96	0.47
4:B:216:SER:O	4:B:219:VAL:HG23	2.14	0.47
4:B:85:ALA:CB	4:B:92:TYR:HD2	2.27	0.47
6:D:24:GLU:OE1	6:D:24:GLU:HA	2.14	0.47
10:H:6:ILE:HD12	10:H:35:ILE:HD12	1.96	0.47
1:A:538:G:H5"	14:L:114:LYS:HG2	1.97	0.47
17:O:27:VAL:O	17:O:28:GLN:C	2.52	0.47
1:A:1007:C:N4	1:A:1022:G:H1	2.03	0.47
1:A:1077:G:N2	1:A:1080:A:OP2	2.40	0.47
1:A:1096:C:H2'	1:A:1097:C:C6	2.48	0.47
1:A:1104:G:C4	1:A:1105:A:C8	3.02	0.47
1:A:25:C:O2'	1:A:26:A:H5'	2.14	0.47
1:A:409:G:H2'	1:A:410:G:O4'	2.14	0.47
1:A:865:A:H5'	1:A:1078:U:O4	2.14	0.47
1:A:927:G:C5	1:A:928:G:N7	2.82	0.47
1:A:93:G:H2'	1:A:95:U:C6	2.49	0.47
4:B:124:SER:O	4:B:126:GLU:N	2.48	0.47
4:B:218:ALA:O	4:B:222:ILE:HG13	2.15	0.47
5:C:38:ARG:C	5:C:94:LEU:HD11	2.35	0.47
7:E:60:TYR:HE1	7:E:64:ARG:NH2	2.11	0.47
9:G:24:THR:O	9:G:28:ASN:ND2	2.47	0.47
10:H:91:ARG:HG3	14:L:7:ILE:HG13	1.95	0.47
12:J:9:ARG:HB2	12:J:9:ARG:NH1	2.28	0.47
15:M:96:LEU:O	15:M:97:PRO:C	2.51	0.47
17:O:82:ILE:O	17:O:86:GLY:N	2.45	0.47
19:Q:95:TYR:O	19:Q:96:GLN:C	2.52	0.47
21:S:17:GLU:HA	21:S:20:LEU:CD2	2.45	0.47
1:A:192:U:H5'	22:T:102:GLY:O	2.14	0.47
1:A:1216:G:H2'	1:A:1217:C:H6	1.78	0.47
1:A:1362:C:H5'	1:A:1363:A:C5'	2.43	0.47
1:A:1495:U:H2'	1:A:1496:C:C6	2.50	0.47
1:A:502:G:H2'	1:A:503:C:C6	2.50	0.47
1:A:556:C:H2'	1:A:557:G:H5'	1.94	0.47
1:A:942:G:N3	1:A:943:U:C6	2.82	0.47
8:F:10:LEU:CD1	8:F:59:TYR:HD2	2.23	0.47
9:G:38:LEU:HD13	9:G:42:ILE:HD11	1.97	0.47
12:J:80:LYS:C	12:J:83:GLU:HG2	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:90:LEU:O	15:M:91:ARG:C	2.52	0.47
1:A:1191:A:P	5:C:3:ASN:OD1	2.72	0.47
1:A:1229:A:H2'	1:A:1230:C:C6	2.49	0.47
1:A:1249:C:C2'	1:A:1250:A:H5'	2.40	0.47
1:A:1402:C:C5	1:A:1403:C:N3	2.82	0.47
1:A:545:C:O2'	1:A:546:G:H5'	2.14	0.47
1:A:941:G:O2'	1:A:942:G:H5'	2.13	0.47
1:A:942:G:O2'	1:A:943:U:H5'	2.15	0.47
1:A:965:A:H5'	1:A:969:A:O4'	2.14	0.47
5:C:81:GLY:HA2	5:C:84:ILE:CG2	2.42	0.47
6:D:200:GLU:C	6:D:202:LEU:H	2.16	0.47
6:D:24:GLU:HG3	6:D:25:ARG:H	1.79	0.47
13:K:91:ARG:HG2	13:K:92:GLU:N	2.28	0.47
14:L:87:GLY:HA2	14:L:98:TYR:CA	2.39	0.47
15:M:23:TYR:CB	15:M:67:GLU:HA	2.44	0.47
17:O:21:ASP:OD2	17:O:24:SER:HB3	2.15	0.47
1:A:1126:U:H6	1:A:1126:U:O5'	1.98	0.47
1:A:359:U:H2'	1:A:360:A:C8	2.50	0.47
1:A:622:A:C8	1:A:623:C:C5	3.03	0.47
1:A:868:C:H2'	1:A:869:G:H5'	1.95	0.47
5:C:4:LYS:NZ	5:C:175:LEU:HD12	2.30	0.47
6:D:138:TYR:HD2	6:D:138:TYR:C	2.17	0.47
6:D:190:ASP:O	6:D:191:ARG:C	2.53	0.47
12:J:75:ILE:HG22	12:J:76:ASN:ND2	2.28	0.47
14:L:60:LEU:HD11	14:L:85:ILE:HD12	1.96	0.47
1:A:1424:C:C2'	1:A:1425:U:H5'	2.44	0.47
1:A:353:A:H8	1:A:353:A:C5'	2.27	0.47
1:A:372:C:O2'	1:A:373:A:OP2	2.30	0.47
1:A:496:A:H4'	1:A:497:A:OP1	2.12	0.47
1:A:686:U:O2'	1:A:687:A:H8	1.97	0.47
1:A:889:A:H8	1:A:889:A:OP1	1.98	0.47
1:A:946:A:C6	1:A:947:G:C6	3.03	0.47
5:C:110:ASN:ND2	5:C:140:ARG:CB	2.78	0.47
10:H:63:LEU:N	10:H:63:LEU:CD1	2.78	0.47
14:L:6:THR:OG1	14:L:9:GLN:HG3	2.14	0.47
20:R:42:ARG:HH11	20:R:42:ARG:CB	2.27	0.47
20:R:58:LEU:HD23	20:R:58:LEU:H	1.79	0.47
21:S:63:THR:O	21:S:66:MET:HG2	2.14	0.47
22:T:16:HIS:O	22:T:19:SER:N	2.48	0.47
1:A:1126:U:H2'	1:A:1127:G:H8	1.78	0.47
1:A:1488:G:H2'	1:A:1489:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:G:N3	1:A:348:G:H2'	2.29	0.47
1:A:581:G:N7	1:A:758:G:C5	2.83	0.47
1:A:803:G:H2'	1:A:804:U:C6	2.49	0.47
1:A:983:A:H5'	1:A:984:C:OP2	2.14	0.47
4:B:145:LEU:O	4:B:147:LYS:N	2.48	0.47
4:B:209:ARG:HD2	4:B:239:VAL:HG13	1.97	0.47
5:C:61:ALA:O	5:C:63:ASN:N	2.48	0.47
6:D:62:GLN:O	6:D:66:ARG:HB2	2.15	0.47
7:E:127:ASN:O	7:E:130:ASN:N	2.47	0.47
1:A:1240:U:OP2	9:G:116:ALA:HB2	2.14	0.47
11:I:21:PRO:O	11:I:22:GLY:O	2.32	0.47
13:K:11:LYS:HD2	13:K:11:LYS:N	2.29	0.47
13:K:34:ASP:OD1	13:K:36:ASP:HB3	2.15	0.47
15:M:5:ALA:O	15:M:6:GLY:C	2.52	0.47
16:N:39:LEU:HB3	16:N:43:CYS:SG	2.55	0.47
17:O:74:ASP:C	17:O:76:GLU:H	2.18	0.47
1:A:585:G:O3'	19:Q:34:LYS:NZ	2.47	0.47
19:Q:24:GLU:HA	19:Q:39:SER:HB3	1.97	0.47
21:S:33:THR:HG23	21:S:51:VAL:HG13	1.95	0.47
22:T:67:ALA:HB2	22:T:77:ALA:CB	2.45	0.47
1:A:1145:C:O2'	1:A:1146:A:O5'	2.33	0.47
1:A:1229:A:N1	1:A:1230:C:C4	2.83	0.47
1:A:1320:C:H2'	1:A:1321:C:O4'	2.14	0.47
1:A:529:G:H4'	1:A:533:A:C2	2.50	0.47
1:A:833:U:H2'	1:A:834:C:H6	1.75	0.47
1:A:925:G:N1	1:A:927:G:C5	2.83	0.47
1:A:941:G:C2	1:A:942:G:C8	3.02	0.47
4:B:113:HIS:HA	4:B:116:GLU:OE2	2.14	0.47
5:C:23:TYR:O	5:C:24:ALA:CB	2.62	0.47
6:D:108:LEU:CB	6:D:110:PHE:CE1	2.98	0.47
6:D:112:VAL:HG23	6:D:161:ASN:HD21	1.79	0.47
9:G:111:ARG:HB3	9:G:112:PRO:CD	2.38	0.47
10:H:4:ASP:OD2	10:H:85:ARG:NH1	2.46	0.47
15:M:15:VAL:C	15:M:17:VAL:N	2.68	0.47
15:M:24:GLY:HA3	15:M:66:LEU:HB3	1.97	0.47
17:O:63:ARG:O	17:O:65:ARG:N	2.47	0.47
18:P:38:TYR:CE2	18:P:50:LYS:HB3	2.49	0.47
19:Q:103:GLY:O	19:Q:104:LYS:HD3	2.15	0.47
20:R:22:VAL:HG13	20:R:42:ARG:CG	2.39	0.47
20:R:37:VAL:HG22	20:R:78:LEU:HB3	1.95	0.47
22:T:43:LEU:N	22:T:43:LEU:HD23	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:61:SER:O	22:T:62:LEU:C	2.53	0.47
22:T:82:SER:O	22:T:86:ARG:HB2	2.15	0.47
1:A:1126:U:H6	1:A:1126:U:P	2.38	0.47
1:A:1159:U:O4'	1:A:1159:U:O2	2.33	0.47
1:A:1172:C:H2'	1:A:1173:G:C8	2.50	0.47
1:A:156:G:O2'	1:A:157:G:H5'	2.15	0.47
1:A:334:C:H2'	1:A:335:C:C6	2.50	0.47
1:A:47:C:H4'	1:A:365:U:C5	2.49	0.47
1:A:861:G:O2'	1:A:862:C:H5'	2.15	0.47
1:A:916:G:C2	1:A:917:G:C5	3.03	0.47
1:A:995:C:O2'	1:A:996:A:H5'	2.15	0.47
4:B:215:LEU:O	4:B:219:VAL:HG23	2.14	0.47
4:B:24:TRP:CZ2	4:B:26:PRO:HG3	2.50	0.47
6:D:122:ARG:HA	6:D:122:ARG:HE	1.79	0.47
7:E:31:LEU:HA	7:E:31:LEU:HD23	1.80	0.47
9:G:111:ARG:CB	9:G:112:PRO:HD2	2.42	0.47
9:G:15:ASP:O	9:G:19:GLY:HA2	2.14	0.47
11:I:111:ARG:HH11	11:I:111:ARG:HG3	1.80	0.47
11:I:45:ALA:O	11:I:48:GLU:N	2.38	0.47
19:Q:60:ILE:O	19:Q:71:PHE:CD1	2.68	0.47
20:R:43:PHE:HA	20:R:51:LEU:HD12	1.97	0.47
21:S:28:LYS:CG	21:S:29:ARG:N	2.71	0.47
23:V:24:ARG:N	23:V:24:ARG:CD	2.73	0.47
1:A:1488:G:O2'	1:A:1489:G:H5'	2.15	0.47
1:A:93:G:H2'	1:A:95:U:H6	1.80	0.47
5:C:156:ARG:NH1	5:C:161:GLU:HA	2.30	0.47
5:C:72:LYS:HB3	5:C:75:VAL:HG21	1.97	0.47
6:D:128:VAL:HA	6:D:145:GLU:O	2.15	0.47
6:D:199:ASN:HD21	6:D:201:GLN:HB3	1.80	0.47
6:D:32:ALA:C	6:D:34:GLU:H	2.17	0.47
6:D:15:GLU:CD	6:D:59:ARG:HH21	2.17	0.47
8:F:14:LEU:HD22	8:F:18:GLN:CB	2.33	0.47
13:K:71:LYS:O	13:K:74:ALA:HB3	2.15	0.47
18:P:20:VAL:CG2	18:P:32:TYR:CB	2.94	0.47
19:Q:11:VAL:HB	19:Q:88:TYR:CE2	2.50	0.47
20:R:26:LEU:HD21	20:R:39:VAL:HG23	1.97	0.47
1:A:1229:A:C2	1:A:1230:C:C5	3.04	0.46
1:A:1419:G:H2'	1:A:1420:C:C6	2.50	0.46
1:A:190(L):U:C2'	1:A:191:G:H5'	2.45	0.46
1:A:27:G:H2'	1:A:28:G:H8	1.80	0.46
4:B:204:ASN:C	4:B:204:ASN:ND2	2.67	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:85:LEU:O	11:I:92:TYR:HD1	1.98	0.46
11:I:93:ARG:O	11:I:94:ALA:C	2.53	0.46
14:L:27:LEU:HD23	14:L:62:SER:HB2	1.97	0.46
15:M:105:THR:HG22	15:M:106:ASN:N	2.21	0.46
5:C:18:TRP:CD1	16:N:54:PRO:HA	2.51	0.46
1:A:1056:U:O2'	1:A:1057:G:H5'	2.14	0.46
1:A:1472:U:O2'	1:A:1473:A:H5'	2.16	0.46
1:A:18:C:P	7:E:127:ASN:HD21	2.37	0.46
1:A:434:U:H2'	1:A:435:C:C6	2.50	0.46
1:A:760:G:H2'	1:A:761:G:C5'	2.46	0.46
1:A:829:G:O2'	1:A:830:G:H5'	2.15	0.46
1:A:993:G:O2'	1:A:994:A:P	2.73	0.46
4:B:207:ALA:H	4:B:211:ILE:HD11	1.79	0.46
5:C:116:VAL:O	5:C:120:VAL:HG23	2.15	0.46
5:C:46:GLU:C	5:C:48:TYR:H	2.17	0.46
6:D:187:ARG:HG3	6:D:188:LEU:N	2.30	0.46
7:E:115:VAL:CG1	7:E:116:THR:N	2.77	0.46
7:E:77:PRO:HG2	7:E:142:LEU:HD22	1.98	0.46
10:H:3:THR:CG2	10:H:4:ASP:N	2.78	0.46
11:I:11:LYS:O	11:I:12:GLU:CB	2.59	0.46
11:I:97:LYS:N	11:I:98:PRO:CD	2.79	0.46
14:L:33:ARG:HG2	14:L:60:LEU:HG	1.97	0.46
14:L:86:ARG:O	14:L:87:GLY:O	2.33	0.46
15:M:20:THR:C	15:M:22:ILE:N	2.68	0.46
17:O:70:LEU:HD12	17:O:78:TYR:HA	1.97	0.46
19:Q:86:GLU:O	19:Q:87:LYS:C	2.54	0.46
22:T:17:ARG:O	22:T:21:LYS:HG3	2.16	0.46
22:T:76:ALA:O	22:T:80:ARG:HG2	2.15	0.46
23:V:12:LYS:HG3	23:V:17:THR:OG1	2.15	0.46
2:Y:30:G:N3	2:Y:30:G:H2'	2.29	0.46
2:Y:32:C:O2'	2:Y:33:U:C6	2.65	0.46
1:A:1288:A:H2'	1:A:1289:A:C8	2.50	0.46
1:A:425:G:C2'	1:A:426:G:H5'	2.46	0.46
1:A:765:G:H1	1:A:812:C:H2'	1.80	0.46
4:B:230:VAL:HG12	4:B:231:GLU:N	2.30	0.46
8:F:43:LEU:H	8:F:43:LEU:CD2	2.28	0.46
12:J:63:PHE:HA	16:N:59:ALA:H	1.81	0.46
14:L:27:LEU:HG	14:L:28:LYS:H	1.80	0.46
12:J:49:VAL:HG22	16:N:41:ARG:HB2	1.96	0.46
19:Q:14:LYS:HD2	19:Q:14:LYS:N	2.31	0.46
1:A:1061:G:C5	1:A:1062:U:N3	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1112:C:C4	5:C:178:LEU:HD23	2.50	0.46
1:A:1187:G:H2'	1:A:1188:A:C8	2.51	0.46
1:A:1347:G:C5	11:I:107:ARG:NH1	2.82	0.46
1:A:1520:G:H2'	1:A:1521:G:C8	2.50	0.46
1:A:259:G:H1	1:A:267:C:H42	1.64	0.46
1:A:272:C:O2'	1:A:273:A:H5'	2.15	0.46
1:A:771:G:H2'	1:A:772:U:C6	2.51	0.46
1:A:840:C:H6	1:A:840:C:P	2.38	0.46
1:A:997:U:H2'	1:A:998:G:H8	1.79	0.46
4:B:162:ILE:O	4:B:162:ILE:CG2	2.63	0.46
4:B:36:ARG:HB2	4:B:41:ILE:HD11	1.96	0.46
4:B:55:PHE:HA	4:B:58:ILE:CD1	2.43	0.46
5:C:182:ILE:HG23	5:C:203:PHE:CA	2.46	0.46
5:C:33:LEU:C	5:C:35:GLU:N	2.68	0.46
6:D:149:ALA:O	6:D:151:LYS:N	2.48	0.46
12:J:23:ILE:O	12:J:23:ILE:CG2	2.57	0.46
12:J:60:ARG:O	12:J:61:GLU:O	2.34	0.46
19:Q:12:SER:HB3	19:Q:20:THR:HB	1.96	0.46
22:T:14:LYS:HG2	22:T:18:GLN:OE1	2.16	0.46
1:A:1128:C:C5	1:A:1139:G:H2'	2.51	0.46
1:A:1145:C:O2'	1:A:1146:A:C8	2.64	0.46
1:A:1454:G:C2	1:A:1455:G:C8	3.04	0.46
1:A:1463:C:O2'	1:A:1464:G:H5'	2.15	0.46
1:A:1410:G:N2	1:A:1491:G:H1'	2.30	0.46
1:A:710:G:O2'	1:A:711:G:H5'	2.16	0.46
4:B:74:LYS:HB3	4:B:74:LYS:HZ2	1.80	0.46
4:B:9:GLU:HG2	4:B:217:ARG:NH1	2.30	0.46
5:C:119:ARG:HD2	5:C:140:ARG:NH1	2.29	0.46
6:D:24:GLU:H	6:D:112:VAL:CG1	2.28	0.46
6:D:52:SER:O	6:D:53:ASP:C	2.53	0.46
12:J:38:ILE:O	12:J:71:LEU:N	2.49	0.46
12:J:82:ILE:O	12:J:86:MET:N	2.48	0.46
17:O:12:ILE:O	17:O:15:PHE:N	2.48	0.46
19:Q:98:LEU:HA	19:Q:102:GLY:CA	2.37	0.46
21:S:64:GLU:O	21:S:67:VAL:HG23	2.15	0.46
1:A:1061:G:C2	1:A:1062:U:O2	2.68	0.46
1:A:1386:G:O2'	1:A:1387:G:H5'	2.16	0.46
1:A:1495:U:H2'	1:A:1496:C:H6	1.80	0.46
1:A:148:G:H2'	1:A:149:A:H8	1.79	0.46
1:A:266:G:H5"	1:A:268:C:H41	1.79	0.46
1:A:342:C:H2'	1:A:343:U:C5'	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:24:TRP:N	4:B:24:TRP:CD1	2.79	0.46
5:C:126:ARG:O	5:C:127:ARG:HB2	2.16	0.46
5:C:95:THR:C	5:C:97:LYS:H	2.19	0.46
6:D:138:TYR:C	6:D:138:TYR:CD2	2.89	0.46
7:E:80:ILE:HD11	7:E:91:LEU:CB	2.33	0.46
1:A:711:G:P	8:F:54:LYS:HZ2	2.39	0.46
9:G:149:ARG:O	9:G:149:ARG:HG2	2.16	0.46
9:G:87:VAL:CG1	9:G:88:PRO:HD2	2.45	0.46
10:H:51:VAL:HG11	10:H:60:ARG:NH1	2.30	0.46
11:I:88:TYR:C	11:I:88:TYR:CD2	2.87	0.46
12:J:30:SER:OG	12:J:81:THR:HA	2.15	0.46
13:K:70:LYS:O	13:K:71:LYS:C	2.53	0.46
19:Q:96:GLN:HB2	19:Q:103:GLY:CA	2.38	0.46
1:A:1055:A:N6	1:A:1206:G:C5	2.83	0.46
1:A:1216:G:H5"	16:N:5:ALA:HB2	1.98	0.46
1:A:1218:C:H2'	1:A:1219:U:C6	2.51	0.46
1:A:1281:U:H5'	1:A:1282:C:H5	1.80	0.46
1:A:497:A:O2'	1:A:498:U:OP1	2.25	0.46
1:A:730:G:N2	1:A:765:G:C5'	2.78	0.46
1:A:740:U:H4'	17:O:42:HIS:CD2	2.51	0.46
1:A:858:G:O6	1:A:869:G:C8	2.69	0.46
4:B:116:GLU:HB3	4:B:153:ARG:NH1	2.30	0.46
5:C:95:THR:C	5:C:97:LYS:N	2.67	0.46
7:E:107:ARG:O	7:E:109:ILE:N	2.48	0.46
11:I:14:VAL:O	11:I:65:VAL:HA	2.16	0.46
12:J:49:VAL:O	12:J:60:ARG:HA	2.15	0.46
13:K:102:GLY:O	13:K:103:LEU:HD23	2.16	0.46
15:M:17:VAL:O	15:M:20:THR:HB	2.15	0.46
15:M:30:ALA:O	15:M:32:GLU:N	2.49	0.46
1:A:1325:C:O2'	1:A:1326:C:H5'	2.16	0.46
1:A:1425:U:H3	1:A:1475:G:H1	1.62	0.46
1:A:339:C:H2'	1:A:340:U:C6	2.51	0.46
1:A:384:G:C4	1:A:385:C:C5	3.04	0.46
1:A:406:G:H1	1:A:436:C:N4	2.09	0.46
1:A:601:C:O2'	1:A:602:A:H5'	2.16	0.46
1:A:642:A:N7	10:H:115:SER:HA	2.30	0.46
1:A:755:G:OP2	17:O:65:ARG:HD2	2.15	0.46
4:B:85:ALA:C	4:B:87:ARG:N	2.69	0.46
5:C:150:LYS:HG3	5:C:169:ALA:CB	2.44	0.46
5:C:52:LEU:CD2	5:C:52:LEU:N	2.79	0.46
9:G:9:VAL:HG13	9:G:94:ARG:HE	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:127:LEU:H	10:H:127:LEU:HD22	1.81	0.46
11:I:86:VAL:C	11:I:88:TYR:N	2.68	0.46
12:J:16:LEU:HD11	12:J:70:ARG:CG	2.45	0.46
13:K:46:GLY:O	13:K:48:ILE:O	2.34	0.46
14:L:55:VAL:CG1	14:L:56:ALA:H	2.28	0.46
15:M:84:ILE:O	15:M:86:CYS:N	2.43	0.46
16:N:27:CYS:SG	16:N:29:ARG:HB2	2.56	0.46
18:P:52:ASP:OD1	18:P:53:VAL:N	2.49	0.46
19:Q:45:HIS:NE2	19:Q:47:PRO:HG3	2.31	0.46
1:A:1454:G:O2'	1:A:1455:G:H5'	2.16	0.46
1:A:82:U:O2	1:A:82:U:H2'	2.16	0.46
4:B:195:ASP:O	10:H:74:PRO:HG3	2.16	0.46
5:C:73:PRO:HG3	5:C:105:GLU:OE2	2.16	0.46
5:C:130:VAL:CG1	5:C:134:ILE:HD11	2.34	0.46
5:C:178:LEU:O	5:C:180:ALA:N	2.49	0.46
6:D:14:ARG:HD3	6:D:14:ARG:O	2.16	0.46
7:E:99:GLY:O	7:E:117:ASP:HA	2.15	0.46
1:A:564:C:H5'	14:L:10:LEU:HD13	1.98	0.46
15:M:60:VAL:HG13	15:M:66:LEU:HD21	1.98	0.46
12:J:47:PHE:HD2	16:N:34:TYR:CE1	2.34	0.46
17:O:4:THR:OG1	17:O:7:GLU:HG3	2.16	0.46
1:A:227:G:H21	18:P:62:VAL:HG12	1.81	0.46
19:Q:3:LYS:HB3	19:Q:60:ILE:HD11	1.98	0.46
23:V:6:ARG:CD	23:V:15:ARG:HH12	2.28	0.46
1:A:109:A:H2'	1:A:326:G:H21	1.79	0.46
1:A:1361(A):C:H2'	1:A:1362:C:H5"	1.97	0.46
1:A:1375:A:C6	1:A:1376:U:N3	2.83	0.46
1:A:1484:C:C2'	1:A:1485:U:H5'	2.45	0.46
1:A:1511:G:H2'	1:A:1512:U:O4'	2.15	0.46
4:B:200:ILE:HD12	4:B:200:ILE:O	2.14	0.46
5:C:157:ILE:HD13	5:C:166:GLU:HB2	1.97	0.46
5:C:62:ASP:HA	5:C:97:LYS:HE2	1.97	0.46
6:D:163:GLU:C	6:D:165:MET:H	2.19	0.46
7:E:144:THR:HG23	7:E:145:LYS:N	2.30	0.46
14:L:83:VAL:CG2	14:L:84:LEU:N	2.79	0.46
17:O:27:VAL:O	17:O:30:ALA:N	2.47	0.46
20:R:55:ARG:CA	20:R:55:ARG:HH11	2.28	0.46
21:S:15:LEU:HD23	21:S:33:THR:HB	1.97	0.46
22:T:14:LYS:O	22:T:17:ARG:HB3	2.16	0.46
1:A:1064:G:N2	1:A:1190:G:H2'	2.32	0.45
1:A:1347:G:C6	11:I:107:ARG:NH2	2.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:G:O2'	1:A:167:G:H5'	2.16	0.45
1:A:21:G:H2'	1:A:22:G:C8	2.51	0.45
8:F:63:TYR:O	8:F:65:VAL:HG13	2.16	0.45
12:J:62:HIS:CD2	16:N:61:TRP:HH2	2.34	0.45
13:K:110:ASP:OD2	20:R:88:LYS:NZ	2.49	0.45
15:M:28:ALA:C	15:M:30:ALA:N	2.70	0.45
19:Q:58:GLU:HB2	19:Q:74:LEU:HB3	1.98	0.45
23:V:22:ARG:N	23:V:23:PRO:HD3	2.30	0.45
1:A:161:A:H2'	1:A:162:A:H8	1.82	0.45
1:A:393:A:C2'	1:A:394:G:H5'	2.46	0.45
1:A:452:A:HO2'	1:A:453:A:H8	1.58	0.45
1:A:514:C:O2'	1:A:515:G:H5'	2.16	0.45
4:B:142:LEU:CD2	4:B:146:GLN:HG3	2.47	0.45
4:B:53:ARG:NH1	4:B:199:TYR:HD2	2.13	0.45
9:G:136:LYS:C	9:G:136:LYS:HD3	2.37	0.45
9:G:95:ARG:HG2	9:G:99:LEU:HD12	1.98	0.45
11:I:69:GLY:O	11:I:70:LYS:C	2.53	0.45
1:A:972:C:P	12:J:57:LYS:HE2	2.56	0.45
13:K:18:ARG:HB3	13:K:33:THR:CG2	2.46	0.45
16:N:54:PRO:C	16:N:56:VAL:H	2.19	0.45
19:Q:10:VAL:HG13	19:Q:19:VAL:HB	1.97	0.45
19:Q:36:ILE:O	19:Q:36:ILE:HG12	2.15	0.45
19:Q:66:SER:OG	19:Q:69:LYS:HB3	2.15	0.45
20:R:27:GLY:O	20:R:28:GLU:C	2.55	0.45
21:S:44:MET:O	21:S:45:VAL:C	2.54	0.45
1:A:1091:U:C2	1:A:1093:A:OP2	2.70	0.45
1:A:1474:G:H2'	1:A:1475:G:C8	2.51	0.45
1:A:1479:C:H2'	1:A:1480:G:H8	1.75	0.45
1:A:858:G:O2'	1:A:859:A:H5'	2.16	0.45
4:B:12:GLU:C	4:B:14:GLY:N	2.68	0.45
4:B:182:ILE:O	4:B:183:PRO:C	2.55	0.45
5:C:153:VAL:HG22	5:C:198:VAL:HG22	1.98	0.45
7:E:74:GLY:O	7:E:115:VAL:HG13	2.16	0.45
10:H:87:SER:HA	10:H:93:VAL:HG23	1.97	0.45
14:L:93:LEU:HD23	14:L:93:LEU:N	2.31	0.45
14:L:88:GLY:H	14:L:98:TYR:HA	1.81	0.45
15:M:22:ILE:HG22	15:M:23:TYR:N	2.32	0.45
17:O:12:ILE:C	17:O:14:GLU:N	2.69	0.45
17:O:29:VAL:HG21	17:O:67:LEU:CD2	2.47	0.45
17:O:73:GLU:O	17:O:75:PRO:HD3	2.16	0.45
1:A:719:C:O2'	20:R:49:LYS:HB3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:91:VAL:HG11	20:R:72:ARG:NH1	2.31	0.45
1:A:1287:A:C6	1:A:1288:A:C6	3.04	0.45
1:A:259:G:C6	1:A:260:G:C5	3.04	0.45
1:A:26:A:H61	1:A:558:G:H1'	1.79	0.45
1:A:730:G:H21	1:A:765:G:C5'	2.27	0.45
4:B:174:VAL:HG11	4:B:196:LEU:HD13	1.98	0.45
4:B:83:MET:O	4:B:87:ARG:HB2	2.16	0.45
5:C:167:TRP:O	5:C:168:ALA:CB	2.64	0.45
6:D:127:THR:O	6:D:146:ILE:HA	2.16	0.45
8:F:1:MET:H2	8:F:1:MET:CE	2.30	0.45
10:H:23:SER:OG	10:H:24:THR:N	2.49	0.45
18:P:25:ARG:HG3	18:P:25:ARG:HH11	1.80	0.45
19:Q:82:MET:O	19:Q:85:VAL:N	2.46	0.45
22:T:100:ILE:HG23	22:T:100:ILE:O	2.17	0.45
1:A:1207:G:O2'	1:A:1208:C:H5'	2.16	0.45
1:A:392:G:H2'	1:A:393:A:C8	2.51	0.45
1:A:689:C:O2'	1:A:690:G:H5'	2.16	0.45
1:A:989:C:N4	1:A:1216:G:H1	2.13	0.45
4:B:13:ALA:C	4:B:15:VAL:N	2.69	0.45
4:B:178:ARG:HG3	4:B:178:ARG:NH1	2.30	0.45
4:B:228:GLY:O	4:B:229:VAL:O	2.35	0.45
5:C:159:GLY:HA2	5:C:193:TYR:CZ	2.52	0.45
6:D:132:ARG:HG2	6:D:133:VAL:H	1.81	0.45
8:F:69:GLU:C	8:F:72:VAL:HG23	2.36	0.45
11:I:112:LYS:HD3	11:I:113:LYS:O	2.16	0.45
11:I:118:LYS:O	11:I:119:ALA:HB3	2.17	0.45
11:I:43:ALA:HA	11:I:74:ILE:HG23	1.98	0.45
11:I:84:ALA:HA	11:I:87:GLN:HB2	1.98	0.45
14:L:83:VAL:HG23	14:L:100:ILE:CG2	2.46	0.45
15:M:45:VAL:HA	15:M:48:LEU:HG	1.98	0.45
15:M:60:VAL:HG22	15:M:64:TRP:HZ3	1.81	0.45
17:O:25:THR:O	17:O:26:GLU:C	2.54	0.45
22:T:56:MET:HE1	22:T:104:LEU:CG	2.46	0.45
1:A:1256:A:O2'	1:A:1257:U:P	2.74	0.45
1:A:163:C:O2'	1:A:164:U:H5'	2.17	0.45
1:A:167:G:O2'	1:A:168:G:H5'	2.16	0.45
1:A:231:G:O2'	1:A:232:G:H5'	2.16	0.45
1:A:528:C:H5'	1:A:535:A:C6	2.52	0.45
1:A:913:A:H1'	1:A:914:A:O4'	2.17	0.45
1:A:1101:A:C8	4:B:172:ILE:HD13	2.52	0.45
5:C:113:ALA:HB3	5:C:114:PRO:HD3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:19:LEU:HD23	8:F:19:LEU:C	2.37	0.45
10:H:85:ARG:HH11	10:H:85:ARG:HG3	1.81	0.45
14:L:53:ARG:NH1	14:L:92:ASP:OD2	2.47	0.45
12:J:61:GLU:OE1	16:N:45:ARG:HD2	2.16	0.45
19:Q:25:ARG:CG	19:Q:26:GLN:N	2.79	0.45
19:Q:76:LEU:C	19:Q:76:LEU:CD2	2.84	0.45
20:R:58:LEU:HD23	20:R:58:LEU:N	2.31	0.45
21:S:36:ARG:HH21	21:S:75:ALA:HB3	1.82	0.45
21:S:30:LEU:HD21	21:S:50:ALA:HB2	1.98	0.45
1:A:146:G:H2'	1:A:147:G:C8	2.51	0.45
1:A:485:G:O2'	1:A:486:U:P	2.74	0.45
1:A:858:G:H8	1:A:858:G:O5'	2.00	0.45
1:A:938:A:H8	1:A:938:A:O5'	1.99	0.45
4:B:51:LEU:HD21	4:B:201:ILE:HG23	1.97	0.45
4:B:58:ILE:HG22	4:B:68:ILE:HD11	1.97	0.45
5:C:159:GLY:O	5:C:160:ALA:C	2.55	0.45
1:A:1190:G:H3'	5:C:3:ASN:HB2	1.98	0.45
7:E:65:ASN:O	7:E:65:ASN:CG	2.54	0.45
9:G:146:GLU:O	9:G:146:GLU:CD	2.55	0.45
10:H:124:ALA:O	10:H:128:GLY:N	2.50	0.45
11:I:60:ASP:OD2	11:I:61:ALA:N	2.49	0.45
11:I:7:THR:O	11:I:80:GLY:HA3	2.16	0.45
12:J:19:SER:CB	12:J:91:PRO:HG3	2.47	0.45
13:K:56:GLY:O	13:K:57:THR:C	2.55	0.45
14:L:50:SER:O	14:L:51:ALA:CB	2.64	0.45
15:M:26:GLY:C	15:M:28:ALA:H	2.20	0.45
15:M:81:LEU:HD21	15:M:88:ARG:NH1	2.30	0.45
17:O:39:LEU:HD23	17:O:39:LEU:C	2.37	0.45
18:P:5:ARG:C	18:P:6:LEU:HD12	2.37	0.45
19:Q:28:PRO:HA	19:Q:35:VAL:HA	1.99	0.45
1:A:1089:G:O6	1:A:1090:U:C4	2.70	0.45
1:A:1116:C:C2'	1:A:1117:G:C5'	2.84	0.45
1:A:1263:C:O2'	1:A:1264:C:H5'	2.17	0.45
1:A:1513:A:N1	1:A:1523:G:C6	2.85	0.45
1:A:156:G:C2	1:A:157:G:C8	3.04	0.45
1:A:203:U:H4'	1:A:204:U:O5'	2.17	0.45
5:C:174:PRO:O	5:C:182:ILE:HD11	2.16	0.45
5:C:87:LEU:C	5:C:89:GLU:H	2.20	0.45
6:D:13:ARG:HD3	6:D:36:ARG:O	2.16	0.45
6:D:157:LEU:O	6:D:157:LEU:HD23	2.17	0.45
7:E:51:VAL:HB	7:E:52:PRO:CD	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:55:ASP:HB3	8:F:86:ARG:HH12	1.82	0.45
1:A:737:A:C1'	8:F:73:ASN:HD21	2.10	0.45
9:G:20:ASP:OD1	9:G:63:LYS:NZ	2.45	0.45
9:G:64:GLN:O	9:G:68:ASN:HB2	2.16	0.45
15:M:115:LYS:HD3	15:M:115:LYS:N	2.32	0.45
22:T:79:ARG:O	22:T:80:ARG:C	2.55	0.45
22:T:49:ALA:HB3	22:T:99:LEU:CD1	2.46	0.45
1:A:131:C:H2'	1:A:132:C:C6	2.52	0.45
1:A:186:C:H2'	1:A:187:C:H6	1.78	0.45
1:A:424:G:H2'	1:A:425:G:H8	1.82	0.45
1:A:489:C:H2'	1:A:490:G:C8	2.52	0.45
1:A:781:A:C5	1:A:802:A:C2	3.05	0.45
1:A:953:G:H2'	1:A:954:G:O4'	2.17	0.45
7:E:64:ARG:HG2	7:E:64:ARG:NH1	2.31	0.45
9:G:15:ASP:C	9:G:17:VAL:H	2.20	0.45
10:H:14:ARG:NH1	10:H:14:ARG:HB3	2.32	0.45
10:H:23:SER:OG	10:H:60:ARG:HD3	2.17	0.45
11:I:117:HIS:C	11:I:118:LYS:HG2	2.36	0.45
11:I:117:HIS:O	11:I:118:LYS:HB3	2.17	0.45
11:I:64:THR:CG2	11:I:65:VAL:H	2.18	0.45
13:K:125:PHE:CD1	13:K:125:PHE:N	2.85	0.45
14:L:7:ILE:O	14:L:10:LEU:N	2.50	0.45
15:M:36:LYS:HB3	15:M:36:LYS:HZ3	1.80	0.45
15:M:54:VAL:O	15:M:58:GLU:HG2	2.17	0.45
16:N:21:TYR:HE2	16:N:23:ARG:NE	2.15	0.45
19:Q:8:GLY:HA3	19:Q:22:LEU:O	2.17	0.45
1:A:1067:A:O5'	1:A:1067:A:H8	1.99	0.45
1:A:184:G:H4'	1:A:224:C:H4'	1.99	0.45
1:A:285:G:C2'	1:A:286:G:H5'	2.47	0.45
1:A:942:G:C2	1:A:943:U:C6	3.05	0.45
4:B:122:PHE:O	4:B:123:ALA:HB2	2.17	0.45
4:B:134:GLU:C	4:B:136:VAL:N	2.70	0.45
4:B:23:ARG:CZ	4:B:23:ARG:O	2.65	0.45
5:C:134:ILE:O	5:C:138:VAL:HG23	2.16	0.45
5:C:27:LYS:CA	5:C:30:ARG:HH12	2.22	0.45
5:C:21:ARG:NH2	5:C:56:ASP:OD2	2.50	0.45
5:C:73:PRO:HA	5:C:76:VAL:HG23	1.99	0.45
12:J:5:ARG:H	12:J:100:THR:HA	1.82	0.45
15:M:14:ARG:HG2	15:M:14:ARG:HH11	1.81	0.45
15:M:37:THR:O	15:M:37:THR:HG22	2.17	0.45
5:C:34:LEU:HD12	16:N:25:VAL:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:34:LYS:HB2	19:Q:34:LYS:HE2	1.70	0.45
22:T:101:GLY:O	22:T:102:GLY:O	2.34	0.45
1:A:106:C:O2'	1:A:107:G:H5'	2.17	0.44
1:A:1296:C:H4'	1:A:1302:U:C5	2.52	0.44
1:A:1363:A:C4	1:A:1365:G:C6	3.05	0.44
1:A:176:C:H2'	1:A:177:C:C6	2.53	0.44
1:A:190(E):U:O4	19:Q:62:SER:HB3	2.16	0.44
1:A:22:G:H2'	1:A:23:C:H6	1.80	0.44
1:A:328:C:C2'	1:A:328:C:O2	2.63	0.44
4:B:178:ARG:NH2	4:B:196:LEU:O	2.48	0.44
5:C:157:ILE:HG21	5:C:164:ARG:HH21	1.81	0.44
5:C:39:ILE:C	5:C:41:GLY:H	2.19	0.44
5:C:35:GLU:CG	5:C:59:ARG:NH2	2.73	0.44
5:C:94:LEU:HD23	5:C:95:THR:N	2.31	0.44
6:D:151:LYS:HD2	6:D:151:LYS:H	1.81	0.44
15:M:29:ARG:HB3	15:M:64:TRP:CH2	2.52	0.44
17:O:17:ARG:NH1	17:O:77:ARG:NH1	2.65	0.44
23:V:24:ARG:HG2	23:V:25:LYS:N	2.28	0.44
1:A:1320:C:N3	21:S:36:ARG:NH1	2.66	0.44
1:A:250:A:H5"	1:A:251:G:OP1	2.18	0.44
1:A:383:A:H2'	1:A:384:G:H5'	1.98	0.44
1:A:401:C:H2'	1:A:402:G:C8	2.53	0.44
1:A:657:G:H4'	17:O:28:GLN:HG2	2.00	0.44
1:A:668:G:O2'	17:O:46:HIS:HD2	2.01	0.44
1:A:895:G:H2'	1:A:896:C:C6	2.51	0.44
4:B:112:VAL:O	4:B:116:GLU:HG2	2.17	0.44
4:B:17:PHE:CD1	4:B:17:PHE:C	2.91	0.44
4:B:189:ASP:HB3	4:B:205:ASP:H	1.82	0.44
5:C:113:ALA:O	5:C:115:LEU:N	2.50	0.44
6:D:70:ILE:CG2	6:D:71:SER:N	2.78	0.44
7:E:150:ARG:NH1	7:E:150:ARG:HG3	2.32	0.44
10:H:14:ARG:CB	10:H:14:ARG:NH1	2.81	0.44
11:I:45:ALA:HA	11:I:51:ARG:HH22	1.82	0.44
12:J:66:ARG:HG2	12:J:66:ARG:HH11	1.82	0.44
13:K:59:TYR:O	13:K:62:GLN:HB3	2.17	0.44
15:M:67:GLU:HB3	15:M:68:GLY:H	1.66	0.44
19:Q:5:VAL:O	19:Q:6:LEU:HD23	2.17	0.44
20:R:37:VAL:HG12	20:R:41:LYS:HG3	1.99	0.44
1:A:129(A):G:O2'	1:A:130:A:P	2.75	0.44
1:A:978:A:O2'	1:A:1322:C:N3	2.45	0.44
1:A:1502:A:C2	1:A:1504:G:C2	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1515:C:O2'	1:A:1516:G:H5'	2.17	0.44
1:A:589:C:O2'	1:A:590:C:H5'	2.18	0.44
1:A:650:G:C2'	1:A:651:C:H5'	2.47	0.44
1:A:709:G:O2'	1:A:710:G:H5'	2.17	0.44
1:A:972:C:O2'	12:J:55:LYS:HA	2.17	0.44
4:B:145:LEU:C	4:B:147:LYS:H	2.21	0.44
5:C:105:GLU:HG2	5:C:106:VAL:N	2.32	0.44
5:C:110:ASN:O	5:C:141:VAL:HG22	2.17	0.44
5:C:190:ARG:HG2	5:C:191:THR:H	1.83	0.44
8:F:9:VAL:HG13	8:F:60:PHE:CG	2.52	0.44
9:G:151:TYR:HA	9:G:153:HIS:ND1	2.32	0.44
10:H:53:VAL:O	10:H:54:ASP:HB3	2.18	0.44
1:A:878:G:H5"	10:H:89:PRO:HG2	1.99	0.44
13:K:43:SER:HB3	13:K:68:ALA:HB2	2.00	0.44
16:N:47:LEU:O	16:N:48:ALA:C	2.56	0.44
1:A:223:U:H5"	22:T:68:LYS:HZ2	1.83	0.44
1:A:1257:U:H4'	1:A:1258:G:O5'	2.17	0.44
1:A:1509:C:C2'	1:A:1510:U:H5'	2.47	0.44
1:A:218:C:H2'	1:A:219:C:C6	2.51	0.44
1:A:256:U:H2'	1:A:257:G:C8	2.53	0.44
1:A:324:G:N2	1:A:327:A:C8	2.85	0.44
1:A:418:C:H2'	1:A:419:C:H6	1.80	0.44
1:A:591:U:H2'	1:A:592:G:H8	1.81	0.44
1:A:918:A:H2'	1:A:919:A:C8	2.53	0.44
4:B:13:ALA:O	4:B:15:VAL:N	2.51	0.44
5:C:10:PHE:CE2	5:C:178:LEU:HD13	2.51	0.44
8:F:71:ARG:O	8:F:72:VAL:C	2.55	0.44
12:J:46:ARG:HG2	12:J:46:ARG:NH1	2.28	0.44
18:P:74:LEU:HD13	18:P:79:VAL:HG21	1.97	0.44
18:P:75:ARG:C	18:P:77:ALA:N	2.71	0.44
22:T:93:GLU:O	22:T:94:ALA:HB2	2.18	0.44
1:A:1280:A:H5"	12:J:40:LEU:HD21	1.98	0.44
1:A:1413:A:N1	1:A:1488:G:C2	2.86	0.44
1:A:197:A:N6	1:A:221:C:H5'	2.33	0.44
1:A:57:G:H2'	1:A:58:C:C6	2.53	0.44
1:A:645:C:H2'	1:A:646:U:C6	2.46	0.44
1:A:868:C:O2'	1:A:869:G:H5'	2.16	0.44
1:A:925:G:C2	1:A:927:G:C8	3.05	0.44
7:E:53:LEU:O	7:E:57:LYS:HB2	2.17	0.44
8:F:71:ARG:O	8:F:74:ASP:N	2.50	0.44
11:I:53:VAL:C	11:I:55:ALA:N	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:34:LEU:HD13	15:M:41:PRO:HA	2.00	0.44
17:O:6:GLU:CD	17:O:7:GLU:H	2.20	0.44
18:P:53:VAL:C	18:P:55:ARG:N	2.68	0.44
18:P:60:LEU:O	18:P:62:VAL:N	2.51	0.44
19:Q:52:LYS:O	19:Q:55:ASP:OD2	2.35	0.44
19:Q:3:LYS:HB3	19:Q:60:ILE:CD1	2.48	0.44
20:R:86:VAL:CG1	20:R:87:ARG:N	2.80	0.44
1:A:1028:C:N4	1:A:1034:G:H21	2.15	0.44
1:A:1086:U:H3	1:A:1099:G:H22	1.66	0.44
1:A:1109:C:P	5:C:176:HIS:CD2	3.11	0.44
1:A:1399:C:H4'	1:A:1400:C:C5'	2.44	0.44
1:A:1497:G:C2'	1:A:1498:U:H5'	2.47	0.44
1:A:454:C:C2'	1:A:455:C:H5'	2.47	0.44
1:A:529:G:C4'	1:A:533:A:C2	3.01	0.44
1:A:686:U:C2	1:A:687:A:N7	2.85	0.44
4:B:23:ARG:O	4:B:24:TRP:O	2.35	0.44
4:B:90:MET:HA	4:B:91:PRO:HD3	1.65	0.44
5:C:178:LEU:C	5:C:180:ALA:N	2.69	0.44
5:C:58:GLU:C	5:C:59:ARG:HG3	2.38	0.44
7:E:79:GLU:HG3	7:E:93:PRO:CD	2.47	0.44
8:F:38:GLU:HB2	8:F:64:GLN:O	2.18	0.44
8:F:42:GLU:O	8:F:43:LEU:C	2.56	0.44
14:L:83:VAL:CG2	14:L:100:ILE:CG2	2.96	0.44
15:M:21:TYR:N	15:M:21:TYR:CD1	2.86	0.44
1:A:1327:C:OP1	23:V:20:LYS:N	2.50	0.44
1:A:1066:C:C2'	1:A:1067:A:H5'	2.48	0.44
1:A:1262:C:N4	1:A:1273:G:H1	2.05	0.44
1:A:1292:U:O2'	1:A:1293:G:H5'	2.17	0.44
1:A:190:C:H2'	1:A:190(A):C:H6	1.82	0.44
1:A:542:G:H2'	1:A:543:C:H6	1.82	0.44
1:A:302:G:N3	1:A:556:C:H4'	2.33	0.44
1:A:73:C:O5'	1:A:73:C:H6	2.00	0.44
4:B:109:SER:O	4:B:111:ARG:N	2.51	0.44
5:C:110:ASN:C	5:C:111:LEU:HD12	2.38	0.44
6:D:100:ARG:O	6:D:103:ASN:HB3	2.17	0.44
6:D:78:LEU:HA	6:D:78:LEU:HD23	1.83	0.44
7:E:124:GLY:O	7:E:125:SER:O	2.36	0.44
7:E:64:ARG:H	7:E:64:ARG:HD2	1.83	0.44
9:G:30:ILE:HA	9:G:105:VAL:HG11	2.00	0.44
11:I:128:ARG:OXT	11:I:128:ARG:HG2	2.18	0.44
15:M:115:LYS:O	15:M:116:THR:C	2.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:87:TYR:O	15:M:90:LEU:HB2	2.17	0.44
18:P:20:VAL:CG2	18:P:32:TYR:HB2	2.47	0.44
20:R:66:LEU:C	20:R:66:LEU:HD23	2.38	0.44
1:A:1108:G:H2'	1:A:1109:C:C5'	2.47	0.44
1:A:1172:C:H2'	1:A:1173:G:H8	1.83	0.44
1:A:1320:C:C2'	1:A:1321:C:H5'	2.47	0.44
1:A:1417:G:N2	1:A:1484:C:N4	2.65	0.44
1:A:155:C:H2'	1:A:156:G:H8	1.83	0.44
1:A:242:C:C2'	1:A:243:A:C5'	2.92	0.44
1:A:45:U:H6	1:A:45:U:O5'	2.01	0.44
1:A:460:A:H2'	1:A:461:C:C5'	2.48	0.44
1:A:47:C:O2	1:A:49:U:C5	2.71	0.44
1:A:757:U:C2'	1:A:758:G:H5'	2.48	0.44
1:A:949:A:C4	1:A:1233:G:N2	2.86	0.44
4:B:16:HIS:HB3	4:B:17:PHE:H	1.43	0.44
5:C:150:LYS:CG	5:C:169:ALA:HB2	2.45	0.44
5:C:28:GLN:O	5:C:31:HIS:HB2	2.17	0.44
5:C:50:ALA:CA	5:C:72:LYS:HD3	2.47	0.44
7:E:110:LEU:HD13	7:E:118:ILE:HG21	1.98	0.44
9:G:85:TYR:CD1	9:G:85:TYR:N	2.85	0.44
10:H:24:THR:CG2	10:H:63:LEU:HD11	2.48	0.44
10:H:20:TYR:CE2	10:H:75:ARG:HD2	2.52	0.44
12:J:16:LEU:HD11	12:J:70:ARG:HG3	2.00	0.44
12:J:25:GLU:O	12:J:29:ARG:HD2	2.17	0.44
13:K:102:GLY:O	13:K:103:LEU:C	2.56	0.44
13:K:109:VAL:HA	20:R:85:LEU:O	2.18	0.44
13:K:43:SER:HB3	13:K:64:ALA:O	2.18	0.44
13:K:48:ILE:HG22	13:K:49:GLY:N	2.26	0.44
18:P:53:VAL:O	18:P:55:ARG:N	2.51	0.44
19:Q:80:GLY:O	19:Q:81:ARG:CB	2.65	0.44
1:A:664:G:OP1	20:R:64:ARG:NH1	2.51	0.44
1:A:1465:C:H2'	1:A:1466:C:C6	2.53	0.44
1:A:1521:G:C2	1:A:1522:U:C2	3.06	0.44
1:A:821:G:H2'	1:A:822:C:H6	1.83	0.44
1:A:895:G:H2'	1:A:896:C:H6	1.83	0.44
4:B:61:LEU:CD2	4:B:161:ALA:HB2	2.45	0.44
5:C:150:LYS:HB2	5:C:169:ALA:HB1	1.99	0.44
5:C:31:HIS:C	5:C:33:LEU:N	2.70	0.44
6:D:24:GLU:O	6:D:25:ARG:HB3	2.18	0.44
6:D:24:GLU:O	6:D:26:CYS:N	2.45	0.44
7:E:92:LYS:O	7:E:118:ILE:HG13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:69:VAL:CG2	7:E:139:LEU:HD13	2.48	0.44
11:I:49:PRO:HD3	11:I:78:LYS:HG2	1.99	0.44
13:K:66:LEU:O	13:K:69:ALA:N	2.51	0.44
13:K:70:LYS:O	13:K:73:MET:HB2	2.18	0.44
15:M:108:ARG:O	15:M:112:GLY:N	2.39	0.44
20:R:32:ARG:HE	20:R:32:ARG:HB2	1.55	0.44
22:T:16:HIS:O	22:T:17:ARG:C	2.56	0.44
1:A:259:G:H2'	1:A:260:G:O4'	2.17	0.43
1:A:325:A:H2'	1:A:326:G:O4'	2.18	0.43
1:A:393:A:HO2'	1:A:394:G:H5'	1.83	0.43
1:A:540:G:H2'	1:A:541:G:O4'	2.17	0.43
1:A:930:C:H2'	1:A:931:C:H5'	2.00	0.43
1:A:9:G:H1	1:A:25:C:H42	1.65	0.43
5:C:199:LYS:HB3	5:C:201:TYR:HE1	1.82	0.43
5:C:40:ARG:HA	5:C:43:LEU:HB3	1.99	0.43
9:G:75:VAL:O	9:G:76:ARG:HG3	2.18	0.43
10:H:20:TYR:HE2	10:H:75:ARG:HD2	1.83	0.43
1:A:600:C:OP1	10:H:97:VAL:HG12	2.17	0.43
11:I:93:ARG:HD3	11:I:97:LYS:HZ1	1.81	0.43
12:J:28:ARG:HH11	12:J:28:ARG:HG2	1.82	0.43
17:O:77:ARG:O	17:O:80:ALA:HB3	2.18	0.43
22:T:56:MET:HE1	22:T:104:LEU:CD2	2.48	0.43
22:T:89:ARG:NH2	22:T:104:LEU:HB3	2.32	0.43
1:A:112:G:C2'	1:A:113:G:H5'	2.48	0.43
1:A:416:G:C6	1:A:417:C:C4	3.06	0.43
1:A:423:G:H2'	1:A:424:G:C4'	2.49	0.43
1:A:428:G:O2'	1:A:429:U:P	2.75	0.43
1:A:756:C:C4	1:A:757:U:C4	3.05	0.43
1:A:730:G:N2	1:A:765:G:H5"	2.30	0.43
5:C:139:GLN:C	5:C:141:VAL:N	2.71	0.43
6:D:122:ARG:HH21	6:D:134:ASP:CG	2.22	0.43
6:D:152:SER:OG	6:D:155:LEU:HD12	2.18	0.43
1:A:405:U:C5	6:D:2:GLY:HA3	2.53	0.43
9:G:116:ALA:HA	9:G:119:ARG:NH2	2.33	0.43
7:E:152:ARG:HB3	10:H:43:GLY:O	2.18	0.43
11:I:26:VAL:HA	11:I:61:ALA:O	2.18	0.43
13:K:18:ARG:HG2	13:K:20:TYR:HE1	1.82	0.43
13:K:40:ILE:HG22	13:K:41:THR:HG23	2.00	0.43
14:L:46:LYS:HD3	14:L:94:PRO:CG	2.48	0.43
16:N:18:VAL:HG23	16:N:19:ARG:CG	2.48	0.43
19:Q:23:VAL:HG12	19:Q:23:VAL:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:48:GLU:C	19:Q:50:LYS:H	2.21	0.43
21:S:20:LEU:C	21:S:20:LEU:HD12	2.38	0.43
1:A:1372:U:C2'	1:A:1373:G:H5'	2.48	0.43
1:A:1440:C:H2'	1:A:1441:G:C5'	2.48	0.43
1:A:371:G:C2'	1:A:372:C:H5'	2.47	0.43
1:A:46:G:H1	1:A:395:C:H42	1.65	0.43
1:A:522:C:O2'	1:A:523:A:H5'	2.19	0.43
4:B:212:GLN:O	4:B:213:LEU:C	2.56	0.43
4:B:223:ILE:HD12	4:B:230:VAL:CG2	2.43	0.43
5:C:99:VAL:HG23	5:C:100:ALA:N	2.34	0.43
7:E:79:GLU:CG	7:E:93:PRO:HD2	2.48	0.43
9:G:51:GLN:C	9:G:53:LYS:N	2.72	0.43
10:H:13:ILE:O	10:H:14:ARG:C	2.54	0.43
10:H:24:THR:HG21	10:H:63:LEU:HD11	2.00	0.43
10:H:17:THR:HB	10:H:78:GLN:OE1	2.18	0.43
12:J:24:VAL:HG12	12:J:28:ARG:HG3	2.00	0.43
14:L:10:LEU:HD21	14:L:15:ARG:NE	2.33	0.43
14:L:60:LEU:HD11	14:L:85:ILE:CD1	2.49	0.43
16:N:18:VAL:HG23	16:N:19:ARG:HG3	2.00	0.43
16:N:25:VAL:HG12	16:N:39:LEU:HD23	2.00	0.43
18:P:11:SER:N	18:P:14:ASN:O	2.48	0.43
20:R:61:LYS:HG2	20:R:65:ILE:HD11	2.00	0.43
1:A:1006:C:N4	1:A:1024:G:N2	2.66	0.43
1:A:112:G:H5'	1:A:389:A:H4'	1.99	0.43
1:A:1503:A:H5'	1:A:1531:A:O4'	2.19	0.43
1:A:226:G:O2'	1:A:227:G:H5'	2.18	0.43
1:A:509:A:N3	1:A:543:C:O2'	2.46	0.43
1:A:676:A:H1'	13:K:115:PRO:HB3	2.00	0.43
4:B:28:PHE:CD2	4:B:28:PHE:O	2.71	0.43
5:C:71:ALA:CB	5:C:109:PRO:HB3	2.48	0.43
6:D:3:ARG:CZ	6:D:71:SER:HB3	2.48	0.43
10:H:24:THR:HG23	10:H:24:THR:O	2.18	0.43
11:I:40:LEU:O	11:I:41:VAL:C	2.56	0.43
11:I:48:GLU:HB2	11:I:51:ARG:HH21	1.84	0.43
11:I:84:ALA:HA	11:I:87:GLN:HB3	2.01	0.43
15:M:59:TYR:O	15:M:63:THR:CG2	2.66	0.43
18:P:51:VAL:O	18:P:52:ASP:CB	2.54	0.43
19:Q:10:VAL:O	19:Q:53:LEU:HD12	2.19	0.43
19:Q:6:LEU:HD13	19:Q:42:TYR:HE1	1.84	0.43
21:S:52:TYR:CD1	21:S:56:GLN:O	2.71	0.43
22:T:58:LYS:O	22:T:59:ALA:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1086:U:O2'	1:A:1087:G:H5'	2.18	0.43
1:A:674:G:O2'	1:A:675:A:H5'	2.19	0.43
1:A:684:A:N6	1:A:685:G:C6	2.86	0.43
1:A:992:U:O2'	1:A:993:G:P	2.77	0.43
5:C:180:ALA:O	5:C:181:ASN:CB	2.62	0.43
5:C:73:PRO:O	5:C:75:VAL:N	2.51	0.43
6:D:33:MET:O	6:D:37:PRO:HG3	2.19	0.43
7:E:105:VAL:HB	7:E:106:PRO:CD	2.42	0.43
7:E:52:PRO:C	7:E:54:ALA:N	2.71	0.43
11:I:7:THR:O	11:I:80:GLY:CA	2.67	0.43
14:L:39:VAL:O	14:L:40:VAL:HG23	2.18	0.43
16:N:29:ARG:HH11	16:N:29:ARG:CG	2.32	0.43
22:T:85:MET:HE1	22:T:104:LEU:HD23	2.00	0.43
1:A:1172:C:O2'	1:A:1173:G:H5'	2.19	0.43
1:A:1421:G:H1	1:A:1479:C:H42	1.67	0.43
1:A:1465:C:O2'	1:A:1466:C:H5'	2.17	0.43
1:A:32:A:H2'	1:A:33:A:C8	2.53	0.43
4:B:126:GLU:HA	4:B:129:GLU:OE2	2.17	0.43
5:C:6:HIS:O	5:C:9:GLY:N	2.51	0.43
1:A:620:C:C1'	6:D:135:LEU:HD13	2.49	0.43
6:D:6:GLY:O	6:D:7:PRO:C	2.56	0.43
6:D:68:TYR:CE2	6:D:97:LEU:HB3	2.53	0.43
9:G:15:ASP:HB3	9:G:19:GLY:N	2.33	0.43
10:H:4:ASP:CG	10:H:85:ARG:HH12	2.21	0.43
12:J:22:LYS:C	12:J:24:VAL:H	2.19	0.43
12:J:90:LEU:N	12:J:91:PRO:CD	2.77	0.43
14:L:42:THR:HG21	14:L:52:LEU:HB3	2.00	0.43
16:N:16:PHE:C	16:N:18:VAL:H	2.20	0.43
19:Q:10:VAL:O	19:Q:10:VAL:HG12	2.18	0.43
19:Q:13:ASP:OD2	19:Q:13:ASP:O	2.36	0.43
19:Q:2:PRO:O	19:Q:3:LYS:C	2.56	0.43
20:R:69:THR:O	20:R:72:ARG:HB2	2.18	0.43
20:R:73:ALA:HB3	20:R:79:LEU:HD12	1.99	0.43
22:T:56:MET:CE	22:T:104:LEU:HD21	2.49	0.43
1:A:1202:G:C2'	1:A:1203:C:H5'	2.49	0.43
1:A:221:C:O2'	1:A:222:U:H5'	2.19	0.43
1:A:36:C:C4	1:A:37:U:C5	3.07	0.43
1:A:538:G:OP1	14:L:114:LYS:N	2.43	0.43
1:A:686:U:O2'	1:A:687:A:C8	2.67	0.43
1:A:766:A:C8	1:A:814:A:C6	3.06	0.43
5:C:150:LYS:HG2	5:C:152:ILE:CD1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:173:TRP:HB2	6:D:187:ARG:O	2.19	0.43
6:D:162:LEU:CD2	6:D:181:MET:SD	3.05	0.43
6:D:36:ARG:N	6:D:37:PRO:CD	2.61	0.43
7:E:52:PRO:HB2	7:E:53:LEU:HD12	2.01	0.43
12:J:62:HIS:C	16:N:59:ALA:HB3	2.38	0.43
12:J:62:HIS:HD2	16:N:61:TRP:HH2	1.67	0.43
20:R:37:VAL:CG2	20:R:78:LEU:HB3	2.49	0.43
23:V:10:ARG:HA	23:V:13:ILE:CG1	2.49	0.43
1:A:1352:C:N3	1:A:1370:G:N2	2.67	0.43
1:A:295:C:H2'	1:A:296:U:O4'	2.19	0.43
1:A:644:G:C2'	1:A:645:C:H5'	2.49	0.43
1:A:652:U:C5	1:A:752:G:C4	3.06	0.43
1:A:77:G:C6	1:A:93:G:C6	3.07	0.43
4:B:17:PHE:HB3	4:B:44:LEU:HD21	2.00	0.43
4:B:86:GLU:C	4:B:88:ALA:N	2.72	0.43
5:C:87:LEU:C	5:C:89:GLU:N	2.72	0.43
6:D:148:VAL:CG2	6:D:181:MET:HB3	2.48	0.43
8:F:44:GLY:O	8:F:59:TYR:HA	2.19	0.43
8:F:69:GLU:N	8:F:69:GLU:OE1	2.52	0.43
11:I:111:ARG:O	11:I:119:ALA:HB2	2.18	0.43
11:I:78:LYS:HD2	11:I:78:LYS:C	2.38	0.43
17:O:39:LEU:HD13	17:O:59:MET:CE	2.49	0.43
21:S:30:LEU:HD23	21:S:31:ILE:N	2.33	0.43
21:S:64:GLU:HA	21:S:67:VAL:CG2	2.49	0.43
22:T:100:ILE:O	22:T:101:GLY:C	2.55	0.43
1:A:1048:G:N2	1:A:1210:C:C2	2.87	0.43
1:A:1196:U:OP1	1:A:1197:G:H5'	2.19	0.43
1:A:1497:G:HO2'	1:A:1498:U:H5'	1.81	0.43
1:A:335:C:C2	1:A:336:C:C5	3.07	0.43
1:A:335:C:O2	1:A:1433:A:H2	2.02	0.43
1:A:338:A:C6	1:A:339:C:C4	3.07	0.43
1:A:53:A:H2'	1:A:54:C:O4'	2.19	0.43
1:A:640:A:C2'	1:A:641:U:H5'	2.49	0.43
1:A:771:G:H2'	1:A:772:U:H6	1.84	0.43
1:A:91:C:H2'	1:A:92:C:C6	2.53	0.43
1:A:965:A:C2'	1:A:966:G:OP2	2.66	0.43
4:B:189:ASP:OD1	4:B:205:ASP:HB3	2.19	0.43
4:B:33:TYR:HB3	4:B:41:ILE:O	2.19	0.43
4:B:56:ARG:O	4:B:59:GLU:HB3	2.18	0.43
5:C:62:ASP:N	5:C:97:LYS:HE2	2.34	0.43
6:D:99:SER:HB2	6:D:139:ARG:HG3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:117:HIS:O	11:I:118:LYS:CB	2.66	0.43
12:J:81:THR:C	12:J:83:GLU:N	2.72	0.43
17:O:6:GLU:CD	17:O:7:GLU:N	2.72	0.43
18:P:26:ARG:NH1	18:P:26:ARG:HG2	2.33	0.43
19:Q:96:GLN:OE1	19:Q:96:GLN:HA	2.18	0.43
22:T:57:ARG:O	22:T:60:GLU:HB3	2.19	0.43
22:T:70:SER:HA	22:T:73:HIS:HD2	1.82	0.43
23:V:18:TYR:HE2	23:V:22:ARG:CZ	2.32	0.43
1:A:1057:G:O2'	1:A:1058:G:H5'	2.19	0.43
1:A:1065:U:C5	1:A:1190:G:N3	2.87	0.43
1:A:1227:A:O2'	15:M:115:LYS:HB2	2.19	0.43
1:A:1238:A:C6	1:A:1303:C:H4'	2.53	0.43
1:A:1363:A:H1'	1:A:1365:G:C8	2.54	0.43
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.34	0.43
1:A:502:G:C2	1:A:503:C:C2	3.07	0.43
4:B:22:LYS:HE2	4:B:22:LYS:HB3	1.86	0.43
4:B:78:GLN:O	4:B:94:ASN:OD1	2.36	0.43
5:C:43:LEU:HD13	5:C:55:VAL:HG11	2.01	0.43
5:C:47:LEU:O	5:C:48:TYR:C	2.56	0.43
6:D:104:VAL:HA	6:D:107:ARG:HB2	2.01	0.43
6:D:25:ARG:HH11	6:D:25:ARG:HG2	1.84	0.43
8:F:3:ARG:HH11	8:F:3:ARG:HB3	1.84	0.43
8:F:48:LEU:HD13	8:F:52:ILE:CD1	2.48	0.43
9:G:115:ARG:HB3	9:G:118:VAL:CG2	2.49	0.43
9:G:96:GLN:O	9:G:97:GLN:C	2.58	0.43
10:H:6:ILE:HG13	10:H:31:PHE:HE2	1.83	0.43
13:K:123:LYS:C	13:K:125:PHE:N	2.72	0.43
13:K:74:ALA:C	13:K:76:GLY:N	2.71	0.43
14:L:104:VAL:O	14:L:105:TYR:HB2	2.18	0.43
17:O:24:SER:OG	17:O:27:VAL:HG23	2.19	0.43
17:O:33:THR:O	17:O:33:THR:HG22	2.19	0.43
1:A:254:G:N2	19:Q:16:GLN:OE1	2.52	0.43
19:Q:68:ARG:NH1	19:Q:68:ARG:CG	2.80	0.43
20:R:47:THR:HA	20:R:83:GLU:HB2	2.01	0.43
21:S:39:THR:CG2	21:S:40:ILE:N	2.78	0.43
22:T:51:GLU:OE1	22:T:51:GLU:HA	2.19	0.43
22:T:73:HIS:O	22:T:74:LYS:HB2	2.19	0.43
1:A:1126:U:H2'	1:A:1127:G:O4'	2.19	0.42
1:A:1256:A:O2'	1:A:1257:U:O4'	2.31	0.42
1:A:1502:A:C2	1:A:1505:G:N1	2.81	0.42
1:A:195:A:H2	1:A:222:U:O2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:G:H2'	1:A:400:C:H6	1.83	0.42
1:A:458:C:C4	1:A:459:G:N7	2.87	0.42
1:A:720:C:H6	1:A:720:C:O5'	2.02	0.42
1:A:806:C:C2'	1:A:807:A:H5'	2.49	0.42
1:A:81:U:C6	1:A:83:U:OP2	2.72	0.42
1:A:828:A:H2'	1:A:829:G:O4'	2.19	0.42
1:A:939:G:H5"	9:G:102:ARG:CZ	2.49	0.42
1:A:979:C:H2'	1:A:980:C:H5'	2.01	0.42
6:D:110:PHE:HA	6:D:162:LEU:HD12	2.01	0.42
6:D:32:ALA:O	6:D:34:GLU:N	2.52	0.42
6:D:80:GLU:O	6:D:84:LYS:HG3	2.19	0.42
7:E:111:GLU:C	7:E:113:ALA:H	2.22	0.42
9:G:50:ILE:CD1	9:G:61:VAL:HG11	2.49	0.42
11:I:53:VAL:O	11:I:53:VAL:HG12	2.19	0.42
12:J:23:ILE:O	12:J:24:VAL:HG23	2.19	0.42
12:J:50:ILE:HG12	12:J:60:ARG:HE	1.84	0.42
13:K:106:LYS:CE	13:K:106:LYS:HA	2.37	0.42
13:K:27:ASN:CG	13:K:28:THR:N	2.73	0.42
13:K:27:ASN:ND2	13:K:29:ILE:HG22	2.34	0.42
13:K:48:ILE:CD1	13:K:63:LEU:HB2	2.49	0.42
14:L:34:ARG:HG2	14:L:35:GLY:N	2.33	0.42
15:M:40:ASN:ND2	15:M:40:ASN:C	2.72	0.42
21:S:35:SER:C	21:S:37:ARG:H	2.21	0.42
1:A:1281:U:H4'	1:A:1282:C:OP2	2.19	0.42
1:A:151:A:H2'	1:A:152:A:O4'	2.19	0.42
1:A:374:A:C6	1:A:375:U:C4	3.08	0.42
1:A:490:G:O2'	1:A:491:G:H5'	2.19	0.42
1:A:519:C:O2'	1:A:520:A:H5'	2.19	0.42
1:A:742:G:H2'	1:A:743:U:O4'	2.18	0.42
1:A:75:G:O2'	1:A:76:C:H5'	2.19	0.42
1:A:836:G:H2'	1:A:837:G:H8	1.83	0.42
1:A:572:A:H5"	1:A:917:G:H4'	2.00	0.42
1:A:9:G:H5'	7:E:122:GLU:OE2	2.19	0.42
4:B:46:LYS:HA	4:B:49:GLU:HB2	2.00	0.42
5:C:72:LYS:HE2	5:C:75:VAL:HG21	2.00	0.42
11:I:111:ARG:HD3	11:I:112:LYS:C	2.40	0.42
11:I:28:VAL:O	11:I:29:ASN:C	2.58	0.42
11:I:79:LEU:HD22	11:I:101:PHE:O	2.19	0.42
11:I:81:ILE:O	11:I:81:ILE:HG22	2.18	0.42
12:J:12:ASP:HB3	12:J:15:THR:HG22	2.00	0.42
12:J:49:VAL:CG2	16:N:41:ARG:HB2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:96:ILE:H	12:J:96:ILE:HD12	1.84	0.42
13:K:21:ILE:HG12	13:K:30:VAL:HG13	2.00	0.42
14:L:107:ALA:O	14:L:108:ALA:O	2.37	0.42
14:L:117:ARG:NH2	14:L:124:LYS:HA	2.34	0.42
17:O:37:ASN:HD22	17:O:37:ASN:HA	1.59	0.42
22:T:39:LYS:HD3	22:T:55:ILE:HD13	2.01	0.42
1:A:1095:U:H5"	1:A:1109:C:O2	2.19	0.42
1:A:114:U:H2'	1:A:115:G:C8	2.53	0.42
1:A:1343:G:C5	1:A:1344:C:C5	3.06	0.42
1:A:223:U:H5"	22:T:68:LYS:NZ	2.34	0.42
1:A:621:A:H2'	1:A:622:A:C8	2.54	0.42
1:A:686:U:O2	1:A:687:A:C8	2.73	0.42
1:A:859:A:O2'	1:A:860:A:H5'	2.19	0.42
1:A:929:G:O2'	1:A:930:C:H5'	2.19	0.42
4:B:107:THR:HG23	4:B:110:GLN:OE1	2.20	0.42
4:B:213:LEU:HD23	4:B:213:LEU:C	2.39	0.42
8:F:35:ALA:HA	8:F:67:MET:HB3	2.00	0.42
11:I:33:PHE:C	11:I:35:GLU:N	2.72	0.42
11:I:98:PRO:HB2	11:I:99:LEU:HD22	2.01	0.42
12:J:26:ALA:HA	12:J:29:ARG:NH1	2.34	0.42
13:K:110:ASP:HB2	20:R:88:LYS:CD	2.49	0.42
14:L:39:VAL:HG23	14:L:57:LYS:HD2	2.01	0.42
15:M:14:ARG:HG2	15:M:16:ASP:OD1	2.19	0.42
16:N:21:TYR:O	16:N:22:THR:C	2.57	0.42
18:P:38:TYR:O	18:P:49:LEU:HD12	2.18	0.42
22:T:50:GLU:HG3	22:T:100:ILE:HB	2.02	0.42
22:T:26:ASN:O	22:T:27:LYS:C	2.58	0.42
1:A:263:A:OP2	22:T:79:ARG:NH1	2.53	0.42
1:A:17:U:H2'	1:A:18:C:C6	2.53	0.42
1:A:190:C:H2'	1:A:190(A):C:C6	2.53	0.42
1:A:217:C:H2'	1:A:218:C:C6	2.55	0.42
1:A:308:C:H2'	1:A:309:G:H8	1.83	0.42
1:A:397:A:N3	1:A:397:A:H3'	2.34	0.42
1:A:417:C:O2'	1:A:418:C:H5'	2.20	0.42
1:A:302:G:O2'	1:A:556:C:H5"	2.18	0.42
1:A:712:A:H2'	1:A:713:G:O4'	2.19	0.42
1:A:998:G:O2'	1:A:999:C:H5'	2.18	0.42
4:B:168:THR:HG21	4:B:192:SER:HA	1.99	0.42
5:C:38:ARG:HH11	5:C:38:ARG:HG3	1.83	0.42
5:C:64:VAL:O	5:C:65:ALA:HB2	2.19	0.42
6:D:62:GLN:HE22	6:D:65:ARG:HH12	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:87:ARG:NH1	8:F:87:ARG:CG	2.70	0.42
8:F:8:ILE:HD11	8:F:79:LEU:CD1	2.47	0.42
9:G:78:ARG:O	9:G:80:VAL:HG23	2.20	0.42
10:H:26:VAL:HG13	10:H:59:LEU:HB2	2.01	0.42
11:I:27:THR:CG2	11:I:28:VAL:N	2.82	0.42
11:I:45:ALA:HA	11:I:51:ARG:NH2	2.35	0.42
11:I:48:GLU:N	11:I:49:PRO:CD	2.80	0.42
12:J:78:ASN:O	12:J:80:LYS:N	2.48	0.42
14:L:69:TYR:O	14:L:100:ILE:CD1	2.67	0.42
14:L:98:TYR:N	14:L:98:TYR:HD1	2.16	0.42
12:J:49:VAL:CG1	16:N:41:ARG:HD2	2.44	0.42
17:O:36:ILE:CG1	17:O:59:MET:HE3	2.44	0.42
18:P:18:ARG:O	18:P:20:VAL:HG12	2.19	0.42
18:P:60:LEU:C	18:P:62:VAL:N	2.69	0.42
1:A:191:G:N2	22:T:103:GLY:O	2.46	0.42
1:A:1108:G:H2'	1:A:1109:C:O5'	2.19	0.42
1:A:1216:G:O2'	1:A:1217:C:H5'	2.19	0.42
1:A:1294:G:O2'	1:A:1295:G:H5'	2.19	0.42
1:A:1346:A:H61	1:A:1374:A:H3'	1.84	0.42
1:A:1438:G:H2'	1:A:1439:C:C6	2.55	0.42
1:A:1514:C:H2'	1:A:1515:C:H6	1.83	0.42
1:A:1520:G:C2	1:A:1521:G:C5	3.08	0.42
1:A:881:G:P	14:L:12:ARG:NH2	2.91	0.42
1:A:930:C:H2'	1:A:931:C:C5'	2.49	0.42
4:B:68:ILE:O	4:B:90:MET:CB	2.67	0.42
5:C:156:ARG:HH21	5:C:193:TYR:HB2	1.84	0.42
6:D:65:ARG:HG2	6:D:65:ARG:NH1	2.30	0.42
9:G:24:THR:HA	9:G:27:ILE:HD12	2.02	0.42
10:H:35:ILE:O	10:H:36:LEU:C	2.58	0.42
10:H:48:TYR:CE1	10:H:59:LEU:HD23	2.55	0.42
10:H:83:ILE:O	10:H:83:ILE:HG12	2.19	0.42
11:I:3:GLN:HE22	11:I:20:ARG:HH21	1.66	0.42
11:I:36:TYR:HD2	11:I:37:PHE:CE2	2.36	0.42
17:O:39:LEU:CD2	17:O:56:LEU:HB2	2.50	0.42
19:Q:78:GLU:CD	19:Q:81:ARG:HD2	2.40	0.42
1:A:289:G:C6	1:A:290:C:N4	2.87	0.42
1:A:298:A:H2'	1:A:299:G:C8	2.55	0.42
4:B:25:ASN:ND2	4:B:27:LYS:HG2	2.24	0.42
5:C:2:GLY:C	5:C:3:ASN:HD22	2.20	0.42
5:C:66:VAL:O	5:C:66:VAL:HG12	2.19	0.42
5:C:91:LEU:HD11	5:C:99:VAL:CG1	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:71:SER:OG	6:D:74:GLN:HB2	2.20	0.42
7:E:9:LYS:HB2	7:E:112:LEU:HD11	2.02	0.42
8:F:79:LEU:HD23	8:F:79:LEU:HA	1.85	0.42
9:G:50:ILE:HG23	9:G:51:GLN:N	2.34	0.42
10:H:97:VAL:HA	10:H:100:ILE:HG13	2.02	0.42
10:H:75:ARG:HA	10:H:76:PRO:HD3	1.83	0.42
12:J:33:GLN:C	12:J:34:VAL:HG23	2.40	0.42
12:J:6:ILE:HD11	12:J:72:VAL:CB	2.44	0.42
12:J:5:ARG:O	12:J:98:ILE:HG22	2.20	0.42
14:L:11:VAL:HG13	19:Q:29:HIS:CD2	2.55	0.42
14:L:46:LYS:O	14:L:47:LYS:O	2.38	0.42
18:P:45:THR:O	18:P:47:ASP:N	2.53	0.42
19:Q:48:GLU:O	19:Q:49:GLU:C	2.57	0.42
19:Q:74:LEU:HD23	19:Q:74:LEU:O	2.19	0.42
1:A:1117:G:H21	1:A:1180:A:H1'	1.84	0.42
1:A:1129:C:H1'	1:A:1132:C:C5	2.48	0.42
1:A:176:C:H2'	1:A:177:C:H6	1.84	0.42
1:A:199:G:O2'	1:A:200:G:H5'	2.19	0.42
1:A:354:G:C2	1:A:355:C:C5	3.07	0.42
1:A:879:C:C3'	1:A:879:C:C6	3.03	0.42
1:A:879:C:H3'	1:A:879:C:C6	2.55	0.42
4:B:100:GLY:C	4:B:108:ILE:HD12	2.40	0.42
4:B:117:GLU:OE1	4:B:117:GLU:C	2.58	0.42
4:B:190:THR:O	4:B:190:THR:HG23	2.19	0.42
4:B:55:PHE:HA	4:B:58:ILE:CG1	2.50	0.42
4:B:63:MET:HE2	4:B:64:ARG:NH1	2.35	0.42
5:C:123:GLN:NE2	5:C:140:ARG:NH2	2.67	0.42
6:D:188:LEU:O	6:D:189:PRO:C	2.58	0.42
6:D:56:VAL:O	6:D:57:ARG:C	2.57	0.42
10:H:91:ARG:CG	14:L:7:ILE:HG13	2.49	0.42
12:J:39:PRO:O	12:J:40:LEU:CB	2.67	0.42
13:K:52:GLY:N	13:K:55:LYS:HG3	2.34	0.42
14:L:34:ARG:O	14:L:60:LEU:HD12	2.20	0.42
15:M:22:ILE:HB	15:M:25:ILE:CB	2.45	0.42
15:M:90:LEU:C	15:M:92:HIS:N	2.71	0.42
17:O:16:ALA:CB	17:O:21:ASP:HB3	2.44	0.42
19:Q:56:VAL:CG1	19:Q:77:VAL:HB	2.37	0.42
1:A:115:G:H1'	1:A:116:A:N7	2.35	0.42
1:A:1180:A:H2'	1:A:1181:G:H5'	2.02	0.42
1:A:1346:A:C4	1:A:1348:U:C4	3.08	0.42
1:A:1361(A):C:O2	1:A:1362:C:H5	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:U:OP2	1:A:183:G:C8	2.73	0.42
1:A:130:A:OP2	1:A:190(E):U:H2'	2.19	0.42
1:A:236:G:C6	1:A:237:C:C4	3.07	0.42
1:A:279:A:H4'	1:A:280:C:O5'	2.19	0.42
1:A:491:G:O2'	1:A:492:G:H5'	2.19	0.42
4:B:123:ALA:HA	4:B:127:ILE:HD11	2.01	0.42
5:C:109:PRO:HB2	5:C:115:LEU:HD13	2.02	0.42
5:C:77:ILE:O	5:C:83:ARG:HB3	2.19	0.42
6:D:107:ARG:HH12	6:D:114:ARG:HH22	1.65	0.42
6:D:185:PHE:HZ	6:D:188:LEU:HD23	1.85	0.42
7:E:118:ILE:HG12	7:E:119:LEU:N	2.35	0.42
7:E:144:THR:O	7:E:148:VAL:HG23	2.20	0.42
7:E:16:THR:HG23	7:E:17:ALA:N	2.34	0.42
10:H:105:ARG:HH11	10:H:105:ARG:CG	2.33	0.42
1:A:1061:G:O4'	12:J:56:HIS:CE1	2.72	0.42
14:L:104:VAL:H	14:L:107:ALA:HB3	1.84	0.42
14:L:22:SER:OG	14:L:23:LYS:N	2.53	0.42
15:M:14:ARG:HG2	15:M:14:ARG:NH1	2.34	0.42
15:M:49:THR:O	15:M:51:ALA:N	2.52	0.42
16:N:21:TYR:CD2	16:N:21:TYR:O	2.73	0.42
16:N:40:CYS:N	16:N:43:CYS:SG	2.92	0.42
20:R:39:VAL:HG13	20:R:40:LEU:HD23	2.01	0.42
5:C:139:GLN:O	5:C:140:ARG:C	2.57	0.42
6:D:101:LEU:O	6:D:102:ASP:C	2.57	0.42
6:D:159:ARG:O	6:D:160:GLN:C	2.57	0.42
7:E:118:ILE:CG1	7:E:119:LEU:N	2.82	0.42
8:F:53:ALA:C	8:F:55:ASP:H	2.23	0.42
9:G:51:GLN:O	9:G:53:LYS:N	2.53	0.42
7:E:78:HIS:CG	10:H:104:ARG:HD2	2.55	0.42
11:I:20:ARG:O	11:I:22:GLY:N	2.52	0.42
12:J:69:ASN:O	12:J:70:ARG:HG2	2.19	0.42
12:J:78:ASN:ND2	12:J:81:THR:OG1	2.53	0.42
12:J:90:LEU:N	12:J:90:LEU:HD23	2.34	0.42
12:J:8:LEU:CG	12:J:96:ILE:HG12	2.48	0.42
18:P:43:LYS:N	18:P:43:LYS:CD	2.79	0.42
20:R:21:LYS:CD	20:R:57:GLY:HA3	2.35	0.42
21:S:15:LEU:O	21:S:16:LEU:C	2.58	0.42
22:T:42:GLN:O	22:T:46:GLU:HG3	2.20	0.42
1:A:1032:G:H2'	1:A:1033:G:O4'	2.19	0.42
1:A:1134:G:H2'	1:A:1135:U:H5'	2.02	0.42
1:A:1060:C:C2	1:A:1198:G:C2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1314:C:OP2	21:S:6:LYS:CD	2.67	0.42
1:A:1478:C:O2'	1:A:1479:C:H5'	2.19	0.42
4:B:222:ILE:O	4:B:226:ARG:HD2	2.20	0.42
5:C:119:ARG:CD	5:C:140:ARG:NH1	2.82	0.42
5:C:39:ILE:C	5:C:41:GLY:N	2.73	0.42
5:C:22:TRP:CG	5:C:59:ARG:HD2	2.55	0.42
5:C:90:GLU:HA	5:C:93:LYS:CG	2.50	0.42
6:D:58:LEU:HD23	6:D:206:PHE:CZ	2.55	0.42
6:D:82:ALA:O	6:D:83:SER:C	2.57	0.42
6:D:92:VAL:O	6:D:96:LEU:CD2	2.67	0.42
8:F:55:ASP:OD1	8:F:57:GLN:N	2.53	0.42
8:F:69:GLU:HA	8:F:72:VAL:HG23	1.96	0.42
10:H:16:ALA:O	10:H:19:VAL:HG22	2.20	0.42
10:H:39:LEU:HA	10:H:39:LEU:HD13	1.80	0.42
11:I:79:LEU:HD21	11:I:102:LEU:HA	2.01	0.42
12:J:35:SER:O	12:J:36:GLY:O	2.38	0.42
1:A:1150:U:O2'	12:J:41:PRO:N	2.53	0.42
12:J:94:VAL:CG1	12:J:95:GLU:H	2.29	0.42
13:K:28:THR:C	13:K:29:ILE:CG2	2.87	0.42
13:K:18:ARG:HH21	13:K:37:GLY:HA2	1.84	0.42
13:K:50:TYR:CG	13:K:54:ARG:HB2	2.55	0.42
13:K:58:PRO:O	13:K:59:TYR:C	2.58	0.42
13:K:43:SER:CB	13:K:68:ALA:HB2	2.49	0.42
14:L:101:VAL:O	14:L:103:GLY:N	2.52	0.42
14:L:115:LYS:O	14:L:117:ARG:N	2.53	0.42
15:M:23:TYR:C	15:M:25:ILE:H	2.22	0.42
16:N:9:LYS:C	16:N:11:LYS:N	2.71	0.42
20:R:55:ARG:HB3	20:R:55:ARG:NH1	2.35	0.42
20:R:53:ARG:O	20:R:57:GLY:N	2.53	0.42
20:R:59:SER:HB3	20:R:62:GLU:CB	2.50	0.42
21:S:17:GLU:HA	21:S:20:LEU:CG	2.49	0.42
1:A:1191:A:H8	1:A:1191:A:O5'	2.02	0.41
1:A:1195:C:C3'	1:A:1196:U:H5"	2.42	0.41
1:A:22:G:C6	1:A:23:C:C4	3.07	0.41
1:A:262:A:C6	1:A:263:A:C6	3.07	0.41
1:A:287:U:C2'	1:A:288:A:H5'	2.50	0.41
1:A:436:C:H2'	1:A:437:U:C6	2.54	0.41
1:A:803:G:H2'	1:A:804:U:H6	1.84	0.41
1:A:938:A:N6	1:A:939:G:C5	2.88	0.41
1:A:982:U:OP1	1:A:982:U:H6	2.03	0.41
4:B:240:GLN:H	4:B:240:GLN:CD	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:62:ASP:HA	5:C:97:LYS:HG2	2.02	0.41
6:D:107:ARG:HB3	6:D:174:LEU:CD1	2.50	0.41
6:D:119:GLN:HG2	6:D:123:HIS:HD2	1.84	0.41
8:F:3:ARG:NH2	8:F:64:GLN:NE2	2.68	0.41
10:H:60:ARG:NH1	10:H:60:ARG:CG	2.79	0.41
12:J:7:LYS:C	12:J:96:ILE:HG23	2.39	0.41
21:S:61:TYR:C	21:S:61:TYR:CD2	2.94	0.41
22:T:78:ALA:O	22:T:79:ARG:C	2.58	0.41
1:A:1266:G:N2	1:A:1270:C:N3	2.68	0.41
1:A:269:C:H2'	1:A:270:A:H8	1.85	0.41
1:A:344:A:H5"	1:A:345:C:H5	1.84	0.41
1:A:382:A:C2	1:A:383:A:C4	3.08	0.41
1:A:415:A:H2'	1:A:416:G:C8	2.55	0.41
1:A:416:G:H2'	1:A:417:C:C6	2.55	0.41
1:A:424:G:O2'	1:A:425:G:H5'	2.20	0.41
1:A:44:G:OP2	18:P:12:LYS:HB2	2.20	0.41
4:B:19:HIS:CG	4:B:20:GLU:N	2.89	0.41
4:B:213:LEU:CD2	4:B:214:ILE:N	2.83	0.41
5:C:132:ARG:O	5:C:136:GLN:HG3	2.20	0.41
6:D:100:ARG:NH1	6:D:137:SER:HA	2.35	0.41
11:I:113:LYS:CD	11:I:113:LYS:H	2.31	0.41
11:I:42:ARG:NH2	11:I:71:SER:OG	2.53	0.41
11:I:43:ALA:O	11:I:44:VAL:C	2.58	0.41
12:J:85:LEU:O	12:J:88:LEU:HG	2.20	0.41
14:L:27:LEU:HG	14:L:28:LYS:N	2.35	0.41
18:P:42:ARG:O	18:P:44:THR:N	2.53	0.41
20:R:66:LEU:O	20:R:69:THR:HB	2.20	0.41
22:T:63:ILE:HD13	22:T:80:ARG:HB3	2.01	0.41
1:A:1251:A:H1'	1:A:1369:C:HO2'	1.85	0.41
1:A:1402:C:O2'	1:A:1403:C:H5'	2.19	0.41
1:A:377:G:O2'	1:A:378:G:H5'	2.20	0.41
1:A:782:A:C6	1:A:801:U:C2	3.08	0.41
1:A:927:G:C4	1:A:928:G:C8	3.09	0.41
4:B:118:LEU:HD12	4:B:142:LEU:HB2	2.01	0.41
4:B:231:GLU:HB3	4:B:232:PRO:HD2	2.03	0.41
5:C:42:LEU:HD23	5:C:42:LEU:O	2.21	0.41
5:C:72:LYS:HB3	5:C:75:VAL:HG23	2.01	0.41
6:D:17:VAL:HG22	6:D:18:LYS:N	2.27	0.41
7:E:21:ALA:O	7:E:23:GLY:N	2.50	0.41
9:G:50:ILE:CD1	9:G:125:MET:HG2	2.50	0.41
9:G:75:VAL:CG2	9:G:144:MET:HG2	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:5:TYR:CD2	11:I:5:TYR:C	2.91	0.41
14:L:46:LYS:HE3	14:L:47:LYS:HG3	2.01	0.41
14:L:93:LEU:HB2	14:L:96:VAL:CG2	2.51	0.41
14:L:85:ILE:CG2	14:L:98:TYR:HB3	2.50	0.41
15:M:11:ARG:O	15:M:12:ASN:HB3	2.20	0.41
15:M:73:GLU:O	15:M:76:ALA:N	2.53	0.41
19:Q:5:VAL:HA	19:Q:59:ILE:O	2.19	0.41
20:R:29:PHE:HE1	20:R:31:LEU:HD23	1.78	0.41
21:S:64:GLU:CA	21:S:67:VAL:HG23	2.50	0.41
1:A:105:G:H2'	1:A:106:C:C6	2.56	0.41
1:A:1287:A:C2	1:A:1353:G:H1'	2.51	0.41
1:A:1484:C:H2'	1:A:1485:U:H5'	2.02	0.41
1:A:9:G:OP1	7:E:122:GLU:HB2	2.20	0.41
4:B:84:GLU:HG3	4:B:215:LEU:HD12	2.01	0.41
5:C:195:VAL:O	5:C:196:LEU:CB	2.65	0.41
5:C:58:GLU:O	5:C:59:ARG:HG3	2.20	0.41
5:C:64:VAL:CG1	5:C:65:ALA:H	2.14	0.41
5:C:79:ARG:HB3	5:C:82:GLU:CB	2.50	0.41
6:D:54:TYR:O	6:D:55:ALA:C	2.58	0.41
8:F:33:TYR:CG	8:F:75:LEU:HD23	2.56	0.41
11:I:86:VAL:HG11	11:I:93:ARG:CG	2.51	0.41
13:K:18:ARG:HB3	13:K:33:THR:HG23	2.01	0.41
14:L:33:ARG:HA	14:L:33:ARG:NE	2.31	0.41
14:L:47:LYS:CB	14:L:48:PRO:CD	2.78	0.41
14:L:97:ARG:C	14:L:98:TYR:CD1	2.93	0.41
15:M:19:LEU:O	15:M:22:ILE:HG13	2.20	0.41
15:M:23:TYR:HB2	15:M:67:GLU:HA	2.03	0.41
15:M:60:VAL:HA	15:M:63:THR:CG2	2.51	0.41
15:M:99:ARG:HH11	15:M:99:ARG:HG2	1.86	0.41
19:Q:68:ARG:HG3	19:Q:68:ARG:O	2.20	0.41
20:R:70:ILE:C	20:R:72:ARG:N	2.74	0.41
21:S:30:LEU:CD2	21:S:31:ILE:N	2.83	0.41
21:S:36:ARG:NH2	21:S:75:ALA:O	2.54	0.41
22:T:8:ARG:N	22:T:8:ARG:CD	2.81	0.41
1:A:1037:C:O5'	1:A:1037:C:H6	2.03	0.41
1:A:106:C:H2'	1:A:107:G:H8	1.86	0.41
1:A:1227:A:C2'	1:A:1228:C:O5'	2.69	0.41
1:A:922:G:O2'	1:A:1398:A:N1	2.43	0.41
1:A:160:A:O2'	1:A:161:A:H5'	2.19	0.41
1:A:184:G:H5'	1:A:224:C:O2'	2.20	0.41
1:A:381:C:O2'	1:A:382:A:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:G:C6	1:A:385:C:N4	2.88	0.41
1:A:502:G:N2	1:A:503:C:H1'	2.36	0.41
1:A:62:U:H2'	1:A:63:C:C6	2.55	0.41
1:A:766:A:N7	1:A:814:A:C6	2.89	0.41
1:A:851:G:O2'	1:A:852:G:H5'	2.20	0.41
1:A:869:G:H8	1:A:869:G:OP2	2.02	0.41
1:A:914:A:H2'	1:A:915:A:C8	2.53	0.41
4:B:126:GLU:HA	4:B:129:GLU:HG3	2.02	0.41
4:B:122:PHE:CZ	4:B:139:LYS:HD3	2.54	0.41
6:D:103:ASN:O	6:D:106:TYR:HB3	2.20	0.41
6:D:64:LEU:CD1	6:D:75:PHE:CZ	3.03	0.41
7:E:58:ALA:O	7:E:62:ALA:N	2.48	0.41
8:F:44:GLY:HA2	8:F:59:TYR:CE1	2.56	0.41
1:A:933:G:OP2	9:G:3:ARG:HB3	2.20	0.41
10:H:97:VAL:O	10:H:100:ILE:HG13	2.20	0.41
14:L:43:VAL:CG2	14:L:55:VAL:HG21	2.49	0.41
17:O:71:GLN:C	17:O:73:GLU:N	2.74	0.41
18:P:67:THR:CG2	18:P:68:ASP:N	2.82	0.41
19:Q:25:ARG:HG2	19:Q:26:GLN:H	1.86	0.41
22:T:36:LEU:O	22:T:37:SER:C	2.59	0.41
1:A:1086:U:H2'	1:A:1087:G:O4'	2.20	0.41
1:A:1228:C:H4'	15:M:116:THR:HA	2.03	0.41
1:A:1399:C:N3	1:A:1401:G:C2	2.89	0.41
1:A:1496:C:H2'	1:A:1497:G:H8	1.82	0.41
1:A:767:A:O2'	1:A:1524:C:O2	2.37	0.41
1:A:220:G:O2'	1:A:221:C:H5'	2.21	0.41
1:A:381:C:C2	1:A:382:A:C8	3.08	0.41
1:A:392:G:C2	1:A:393:A:C5	3.08	0.41
1:A:55:A:H2'	1:A:56:U:C6	2.55	0.41
1:A:570:G:N2	1:A:571:U:C2	2.89	0.41
1:A:766:A:H2'	1:A:767:A:C5'	2.50	0.41
1:A:767:A:H2'	1:A:768:A:O4'	2.20	0.41
1:A:77:G:H2'	1:A:78:G:C8	2.56	0.41
6:D:200:GLU:C	6:D:202:LEU:N	2.73	0.41
6:D:64:LEU:CD1	6:D:64:LEU:C	2.85	0.41
10:H:133:LEU:HD23	10:H:133:LEU:HA	1.68	0.41
10:H:29:SER:O	10:H:32:LYS:N	2.54	0.41
10:H:34:GLU:HA	10:H:34:GLU:OE1	2.21	0.41
11:I:97:LYS:HD3	11:I:102:LEU:HD11	2.02	0.41
13:K:34:ASP:OD1	13:K:36:ASP:N	2.54	0.41
14:L:25:PRO:HD2	14:L:97:ARG:NH2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:71:ARG:HG2	15:M:71:ARG:NH1	2.35	0.41
16:N:50:LYS:HD3	16:N:52:GLN:NE2	2.36	0.41
17:O:65:ARG:O	17:O:68:ARG:HB3	2.20	0.41
17:O:87:ILE:O	17:O:88:ARG:HB2	2.20	0.41
19:Q:26:GLN:O	19:Q:27:PHE:HB3	2.20	0.41
20:R:37:VAL:O	20:R:39:VAL:N	2.54	0.41
1:A:1139:G:O2'	1:A:1140:C:P	2.79	0.41
1:A:1375:A:H2'	1:A:1376:U:O4'	2.19	0.41
1:A:1465:C:H2'	1:A:1466:C:O4'	2.20	0.41
1:A:460:A:N6	1:A:462:G:C6	2.89	0.41
1:A:622:A:C8	1:A:623:C:C6	3.09	0.41
1:A:815:A:H4'	1:A:817:C:C4	2.55	0.41
4:B:174:VAL:O	4:B:175:ARG:C	2.59	0.41
4:B:223:ILE:C	4:B:226:ARG:H	2.23	0.41
4:B:70:PHE:CD2	4:B:215:LEU:HD21	2.56	0.41
11:I:111:ARG:CG	11:I:112:LYS:N	2.83	0.41
12:J:14:LYS:O	12:J:15:THR:C	2.59	0.41
20:R:45:SER:O	20:R:47:THR:O	2.38	0.41
22:T:59:ALA:O	22:T:60:GLU:C	2.58	0.41
1:A:1018:C:O5'	1:A:1018:C:H6	2.04	0.41
1:A:1039:C:H2'	1:A:1039:C:O2	2.21	0.41
1:A:1150:U:C2'	1:A:1151:A:H5'	2.51	0.41
1:A:1238:A:H2	1:A:1241:G:N3	2.19	0.41
1:A:1279:A:O2'	1:A:1282:C:N4	2.53	0.41
1:A:155:C:H2'	1:A:156:G:C8	2.55	0.41
1:A:312:C:H2'	1:A:313:A:C8	2.56	0.41
1:A:949:A:C2	1:A:1233:G:C2	3.09	0.41
4:B:21:ARG:H	4:B:21:ARG:CD	2.05	0.41
5:C:139:GLN:O	5:C:143:GLU:CB	2.69	0.41
7:E:129:ILE:N	7:E:129:ILE:CD1	2.76	0.41
8:F:4:TYR:OH	8:F:69:GLU:HB3	2.21	0.41
8:F:6:VAL:HG22	8:F:90:VAL:CG1	2.44	0.41
10:H:6:ILE:O	10:H:7:ALA:C	2.58	0.41
11:I:3:GLN:HE22	11:I:20:ARG:NH2	2.18	0.41
13:K:33:THR:HA	13:K:39:PRO:HA	2.02	0.41
18:P:42:ARG:C	18:P:43:LYS:HD2	2.41	0.41
20:R:53:ARG:C	20:R:55:ARG:N	2.70	0.41
20:R:54:ARG:CZ	20:R:55:ARG:HD3	2.51	0.41
1:A:1046:A:C2'	1:A:1047:G:H5'	2.48	0.41
1:A:1184:G:H2'	1:A:1185:G:H8	1.86	0.41
1:A:1402:C:C4	1:A:1403:C:O2	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:G:C6	1:A:403:C:C5	3.09	0.41
1:A:556:C:H2'	1:A:557:G:C5'	2.50	0.41
1:A:581:G:O6	1:A:758:G:C8	2.74	0.41
1:A:95:U:O2'	1:A:96:G:H5'	2.21	0.41
1:A:961:U:O2'	1:A:962:C:H5'	2.20	0.41
6:D:119:GLN:C	6:D:121:VAL:H	2.23	0.41
9:G:18:TYR:CD1	9:G:18:TYR:N	2.88	0.41
10:H:6:ILE:HD11	10:H:31:PHE:CD2	2.56	0.41
10:H:39:LEU:N	10:H:39:LEU:HD22	2.36	0.41
10:H:82:HIS:CE1	10:H:84:ARG:HD3	2.55	0.41
11:I:45:ALA:O	11:I:47:LEU:N	2.54	0.41
14:L:92:ASP:O	14:L:94:PRO:HD3	2.20	0.41
17:O:22:THR:O	17:O:27:VAL:HG11	2.20	0.41
17:O:39:LEU:HD22	17:O:56:LEU:HB2	2.03	0.41
18:P:45:THR:OG1	18:P:47:ASP:O	2.38	0.41
18:P:50:LYS:HG2	18:P:51:VAL:N	2.36	0.41
19:Q:59:ILE:HD13	19:Q:59:ILE:HA	1.54	0.41
19:Q:60:ILE:C	19:Q:71:PHE:CD1	2.90	0.41
20:R:36:ASN:C	20:R:36:ASN:ND2	2.73	0.41
21:S:51:VAL:CG2	21:S:71:LEU:HD22	2.51	0.41
1:A:1054:C:O2	1:A:1054:C:C2'	2.69	0.41
1:A:1068:G:N7	1:A:1094:G:C2'	2.83	0.41
1:A:1195:C:C3'	1:A:1196:U:C5'	2.94	0.41
1:A:949:A:C2	1:A:1233:G:N3	2.89	0.41
1:A:190(B):C:H2'	1:A:190(C):C:O4'	2.20	0.41
1:A:200:G:N2	1:A:217:C:O2	2.41	0.41
1:A:246:A:O2'	19:Q:99:SER:HB3	2.21	0.41
1:A:455:C:O2'	1:A:456:C:H5'	2.20	0.41
4:B:130:ARG:HB3	4:B:134:GLU:HG3	2.02	0.41
4:B:31:TYR:CD1	4:B:202:PRO:HB3	2.56	0.41
5:C:67:THR:O	5:C:68:VAL:CG2	2.59	0.41
5:C:85:ARG:HG3	5:C:85:ARG:HH11	1.85	0.41
7:E:41:VAL:HG23	7:E:67:VAL:HB	2.02	0.41
7:E:76:ILE:CB	7:E:77:PRO:HD2	2.49	0.41
8:F:2:ARG:HD2	8:F:69:GLU:CB	2.49	0.41
8:F:55:ASP:CB	8:F:86:ARG:HH12	2.34	0.41
9:G:110:GLN:OE1	9:G:110:GLN:HA	2.20	0.41
10:H:109:ILE:CD1	10:H:137:VAL:HB	2.51	0.41
11:I:10:ARG:HE	11:I:11:LYS:HB2	1.86	0.41
13:K:70:LYS:HA	13:K:73:MET:HG3	2.03	0.41
15:M:34:LEU:HD22	15:M:39:ILE:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:67:GLU:O	15:M:68:GLY:C	2.59	0.41
19:Q:90:ILE:O	19:Q:93:GLN:HB3	2.21	0.41
1:A:1213:A:O2'	1:A:1214:C:H5"	2.21	0.41
1:A:1305:G:OP2	1:A:1305:G:C8	2.71	0.41
1:A:1437:C:O2'	1:A:1438:G:H5'	2.21	0.41
1:A:1394:A:C6	1:A:1501:C:H4'	2.56	0.41
1:A:184:G:H2'	1:A:185:A:H8	1.85	0.41
1:A:173:U:H6	1:A:198:G:HO2'	1.65	0.41
1:A:245:C:O2	1:A:283:C:N3	2.53	0.41
1:A:363:A:O2'	1:A:364:A:H5'	2.21	0.41
1:A:391:G:C6	1:A:392:G:N7	2.88	0.41
1:A:392:G:N2	1:A:393:A:C4	2.88	0.41
1:A:987:G:H1	1:A:1218:C:H42	1.68	0.41
4:B:53:ARG:HH12	4:B:199:TYR:HA	1.86	0.41
4:B:19:HIS:NE2	4:B:205:ASP:OD1	2.54	0.41
4:B:55:PHE:O	4:B:56:ARG:C	2.59	0.41
4:B:61:LEU:N	4:B:61:LEU:HD12	2.36	0.41
6:D:155:LEU:HB2	6:D:158:ILE:CD1	2.51	0.41
6:D:177:ASP:OD1	6:D:177:ASP:O	2.38	0.41
7:E:101:ILE:O	7:E:120:THR:HB	2.21	0.41
12:J:25:GLU:HB3	12:J:29:ARG:NH2	2.36	0.41
12:J:32:ALA:HB3	12:J:75:ILE:HB	1.97	0.41
13:K:59:TYR:O	13:K:62:GLN:N	2.54	0.41
16:N:25:VAL:HG12	16:N:38:GLY:O	2.20	0.41
16:N:52:GLN:O	16:N:53:LEU:HD23	2.21	0.41
18:P:39:TYR:CD2	18:P:73:LEU:HD11	2.56	0.41
1:A:192:U:H1'	22:T:103:GLY:HA2	2.03	0.41
22:T:44:ALA:O	22:T:47:GLY:N	2.54	0.41
1:A:1113:C:H6	1:A:1113:C:O5'	2.03	0.40
1:A:946:A:C2	1:A:1236:A:C2	3.09	0.40
1:A:1253:G:C2	1:A:1254:C:C2	3.09	0.40
1:A:1303:C:N4	1:A:1304:G:C6	2.89	0.40
1:A:1345:U:N3	1:A:1377:A:C2	2.89	0.40
1:A:16:A:O2'	1:A:17:U:H5'	2.22	0.40
1:A:203:U:C5'	1:A:204:U:OP1	2.68	0.40
1:A:183:G:O2'	1:A:224:C:H1'	2.21	0.40
1:A:409:G:O2'	1:A:410:G:H5'	2.21	0.40
1:A:618:C:H3'	1:A:619:U:C5'	2.48	0.40
1:A:701:C:O2	1:A:703:G:C6	2.74	0.40
1:A:943:U:H2'	1:A:944:G:H8	1.86	0.40
1:A:975:A:O2'	1:A:976:G:OP2	2.32	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:115:LEU:HG	4:B:116:GLU:N	2.36	0.40
4:B:162:ILE:O	4:B:162:ILE:HG23	2.20	0.40
4:B:178:ARG:NE	4:B:196:LEU:O	2.48	0.40
4:B:63:MET:O	4:B:64:ARG:C	2.58	0.40
5:C:195:VAL:HG23	5:C:195:VAL:H	1.65	0.40
8:F:69:GLU:HA	8:F:72:VAL:HG21	2.00	0.40
8:F:69:GLU:O	8:F:72:VAL:HG23	2.21	0.40
1:A:1377:A:O2'	9:G:2:ALA:HB3	2.21	0.40
9:G:31:MET:CE	9:G:34:GLY:HA2	2.50	0.40
10:H:55:GLY:O	10:H:56:LYS:HE3	2.22	0.40
11:I:71:SER:O	11:I:72:GLY:C	2.58	0.40
15:M:84:ILE:C	15:M:86:CYS:H	2.22	0.40
15:M:86:CYS:O	15:M:90:LEU:HG	2.21	0.40
1:A:1217:C:OP1	16:N:5:ALA:HB1	2.21	0.40
1:A:667:G:N2	17:O:49:ASP:OD2	2.42	0.40
19:Q:7:THR:HA	19:Q:57:VAL:O	2.22	0.40
8:F:98:LEU:HA	20:R:30:ASP:HA	2.02	0.40
20:R:66:LEU:HD23	20:R:67:ALA:CA	2.50	0.40
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.56	0.40
1:A:1057:G:H5"	5:C:154:SER:CB	2.41	0.40
1:A:1192:C:C2'	1:A:1193:G:O5'	2.69	0.40
1:A:1357:A:H5"	1:A:1358:U:OP2	2.21	0.40
1:A:1440:C:C2'	1:A:1441:G:H5'	2.50	0.40
1:A:1451:A:OP2	1:A:1452:C:H5	2.03	0.40
1:A:1501:C:C5	1:A:1504:G:C4	3.10	0.40
1:A:1520:G:H2'	1:A:1521:G:H8	1.86	0.40
1:A:21:G:C2	1:A:22:G:C6	3.10	0.40
1:A:352:C:N3	1:A:356:A:N6	2.68	0.40
1:A:538:G:H5"	14:L:114:LYS:CG	2.51	0.40
1:A:592:G:O2'	1:A:593:G:H5'	2.22	0.40
1:A:785:G:N2	1:A:798:G:C4	2.89	0.40
1:A:795:C:H5"	1:A:796:C:OP2	2.21	0.40
4:B:8:LYS:O	4:B:9:GLU:CB	2.66	0.40
5:C:134:ILE:C	5:C:136:GLN:N	2.74	0.40
5:C:7:PRO:O	5:C:11:ARG:N	2.54	0.40
1:A:410:G:OP2	6:D:25:ARG:HG3	2.21	0.40
7:E:69:VAL:HG22	7:E:139:LEU:HD13	2.03	0.40
7:E:60:TYR:CE1	7:E:64:ARG:NH2	2.89	0.40
9:G:37:ASN:O	9:G:38:LEU:C	2.58	0.40
12:J:38:ILE:HA	12:J:39:PRO:HD2	1.90	0.40
13:K:114:VAL:O	13:K:114:VAL:HG13	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:16:SER:HA	13:K:79:SER:O	2.21	0.40
16:N:26:ARG:HH22	16:N:47:LEU:CD1	2.34	0.40
1:A:741:G:O2'	17:O:55:GLY:HA3	2.21	0.40
18:P:39:TYR:OH	18:P:41:PRO:HA	2.22	0.40
18:P:74:LEU:CD1	18:P:79:VAL:HG21	2.51	0.40
2:Y:39:G:O2'	2:Y:40:PSU:H4'	2.22	0.40
1:A:1115:C:H2'	1:A:1116:C:H6	1.86	0.40
1:A:129(A):G:O2'	1:A:130:A:OP2	2.39	0.40
1:A:533:A:O2'	1:A:534:U:P	2.80	0.40
1:A:585:G:H4'	14:L:8:ASN:OD1	2.21	0.40
1:A:665:A:C2	1:A:732:C:C2	3.09	0.40
1:A:759:A:H2'	1:A:760:G:H5'	2.02	0.40
1:A:834:C:H2'	1:A:835:U:H6	1.86	0.40
4:B:30:ARG:HG3	4:B:31:TYR:CE2	2.57	0.40
4:B:85:ALA:HB2	4:B:92:TYR:HD2	1.85	0.40
5:C:181:ASN:C	5:C:182:ILE:HG13	2.42	0.40
7:E:39:GLY:O	7:E:68:GLU:HA	2.22	0.40
1:A:673:G:H5"	8:F:87:ARG:NH1	2.37	0.40
9:G:15:ASP:HB3	9:G:20:ASP:H	1.86	0.40
9:G:24:THR:C	9:G:28:ASN:HD22	2.25	0.40
10:H:26:VAL:HG23	10:H:27:PRO:HD2	2.02	0.40
11:I:26:VAL:O	11:I:26:VAL:HG23	2.21	0.40
1:A:538:G:O3'	14:L:114:LYS:HG3	2.21	0.40
14:L:60:LEU:HD13	14:L:60:LEU:HA	1.87	0.40
14:L:84:LEU:HD12	14:L:84:LEU:HA	1.87	0.40
15:M:49:THR:HG21	15:M:51:ALA:HB3	2.02	0.40
15:M:94:ARG:O	15:M:95:GLY:C	2.60	0.40
16:N:59:ALA:HB1	16:N:61:TRP:HZ3	1.86	0.40
1:A:668:G:O2'	17:O:46:HIS:CD2	2.75	0.40
19:Q:84:LEU:HA	19:Q:84:LEU:HD23	1.73	0.40
23:V:9:ARG:HG3	23:V:13:ILE:HD11	2.04	0.40
1:A:1100:C:C2	1:A:1102:A:H5'	2.57	0.40
1:A:1120:G:H2'	1:A:1121:U:C6	2.56	0.40
1:A:1139:G:H1'	1:A:1140:C:C5	2.57	0.40
1:A:1249:C:H6	1:A:1249:C:C5'	2.35	0.40
1:A:1304:G:C5	1:A:1305:G:C6	3.10	0.40
1:A:200:G:H2'	1:A:201:C:C6	2.56	0.40
1:A:270:A:H2'	1:A:271:C:H6	1.87	0.40
1:A:270:A:H2'	1:A:271:C:C6	2.56	0.40
1:A:353:A:C8	1:A:353:A:C5'	3.00	0.40
1:A:392:G:C2	1:A:393:A:C4	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:450:G:N7	1:A:481:G:C6	2.90	0.40
4:B:193:ASP:HA	4:B:194:PRO:HD2	1.90	0.40
5:C:117:ALA:HB2	5:C:200:ALA:HB2	2.03	0.40
5:C:188:LEU:HD13	5:C:189:ALA:N	2.37	0.40
9:G:37:ASN:O	9:G:40:ALA:N	2.53	0.40
10:H:126:LYS:C	10:H:128:GLY:H	2.25	0.40
1:A:967:C:O2'	11:I:128:ARG:HD3	2.21	0.40
12:J:90:LEU:HG	12:J:91:PRO:HD3	2.03	0.40
15:M:88:ARG:C	15:M:90:LEU:N	2.74	0.40
16:N:4:LYS:HA	16:N:7:ILE:CD1	2.52	0.40
16:N:47:LEU:HA	16:N:50:LYS:HB2	2.03	0.40
8:F:100:ASN:O	20:R:28:GLU:HG2	2.20	0.40
22:T:13:LEU:O	22:T:16:HIS:N	2.55	0.40
23:V:19:GLY:C	23:V:21:TYR:N	2.75	0.40
1:A:1399:C:O2	1:A:1401:G:C6	2.75	0.40
1:A:401:C:H3'	1:A:401:C:C6	2.56	0.40
1:A:436:C:O2'	1:A:437:U:H5'	2.22	0.40
1:A:447:G:O2'	1:A:448:A:H5'	2.21	0.40
1:A:594:G:H2'	1:A:595:G:H5'	2.03	0.40
1:A:779:C:H2'	1:A:780:A:C8	2.57	0.40
4:B:198:ASP:HA	10:H:68:ARG:HH12	1.83	0.40
5:C:155:GLY:HA2	5:C:164:ARG:O	2.22	0.40
5:C:28:GLN:O	5:C:31:HIS:N	2.47	0.40
5:C:59:ARG:HG2	5:C:64:VAL:HG13	2.02	0.40
6:D:148:VAL:HG12	6:D:149:ALA:N	2.37	0.40
6:D:174:LEU:HA	6:D:174:LEU:HD23	1.90	0.40
6:D:58:LEU:O	6:D:58:LEU:HD13	2.21	0.40
6:D:61:LYS:NZ	6:D:62:GLN:NE2	2.69	0.40
6:D:80:GLU:HA	6:D:80:GLU:OE2	2.21	0.40
1:A:1375:A:OP1	9:G:12:LEU:HD11	2.21	0.40
10:H:38:ILE:O	10:H:39:LEU:C	2.59	0.40
11:I:24:GLY:H	11:I:60:ASP:HB2	1.86	0.40
11:I:48:GLU:HA	11:I:51:ARG:HE	1.85	0.40
12:J:53:PRO:O	12:J:54:PHE:O	2.40	0.40
12:J:16:LEU:CD1	12:J:70:ARG:HG3	2.51	0.40
16:N:15:LYS:HD2	16:N:16:PHE:CE1	2.57	0.40
16:N:5:ALA:O	16:N:7:ILE:N	2.50	0.40
16:N:5:ALA:C	16:N:7:ILE:H	2.24	0.40
20:R:45:SER:HA	20:R:51:LEU:CD2	2.50	0.40
20:R:54:ARG:NH2	20:R:55:ARG:HD3	2.36	0.40
21:S:17:GLU:CA	21:S:20:LEU:HG	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:54:LYS:HA	22:T:57:ARG:HD3	2.03	0.40
23:V:18:TYR:CD2	23:V:22:ARG:HD3	2.56	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:79:ARG:NH1	12:J:79:ARG:NH1[8_665]	1.67	0.53
12:J:80:LYS:NZ	12:J:80:LYS:NZ[8_665]	1.96	0.24

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	B	232/256 (91%)	132 (57%)	57 (25%)	43 (18%)	0 0
5	C	204/239 (85%)	115 (56%)	46 (22%)	43 (21%)	0 0
6	D	206/208 (99%)	145 (70%)	46 (22%)	15 (7%)	1 7
7	E	148/161 (92%)	115 (78%)	20 (14%)	13 (9%)	1 5
8	F	99/101 (98%)	73 (74%)	21 (21%)	5 (5%)	2 15
9	G	153/155 (99%)	93 (61%)	39 (26%)	21 (14%)	0 1
10	H	136/138 (99%)	102 (75%)	24 (18%)	10 (7%)	1 7
11	I	125/128 (98%)	70 (56%)	37 (30%)	18 (14%)	0 1
12	J	96/104 (92%)	54 (56%)	22 (23%)	20 (21%)	0 0
13	K	117/129 (91%)	77 (66%)	29 (25%)	11 (9%)	0 4
14	L	122/135 (90%)	81 (66%)	23 (19%)	18 (15%)	0 1
15	M	116/126 (92%)	63 (54%)	35 (30%)	18 (16%)	0 1
16	N	58/60 (97%)	34 (59%)	14 (24%)	10 (17%)	0 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
17	O	86/88 (98%)	57 (66%)	26 (30%)	3 (4%)	3 23
18	P	81/88 (92%)	52 (64%)	24 (30%)	5 (6%)	1 11
19	Q	102/104 (98%)	81 (79%)	11 (11%)	10 (10%)	0 4
20	R	71/88 (81%)	47 (66%)	14 (20%)	10 (14%)	0 1
21	S	78/92 (85%)	46 (59%)	21 (27%)	11 (14%)	0 1
22	T	97/106 (92%)	51 (53%)	33 (34%)	13 (13%)	0 1
23	V	22/26 (85%)	16 (73%)	4 (18%)	2 (9%)	1 4
All	All	2349/2532 (93%)	1504 (64%)	546 (23%)	299 (13%)	0 2

All (299) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	8	LYS
4	B	9	GLU
4	B	15	VAL
4	B	16	HIS
4	B	21	ARG
4	B	24	TRP
4	B	77	ALA
4	B	90	MET
4	B	95	GLN
4	B	97	TRP
4	B	123	ALA
4	B	127	ILE
4	B	188	ALA
4	B	207	ALA
4	B	213	LEU
4	B	229	VAL
5	C	3	ASN
5	C	15	THR
5	C	24	ALA
5	C	47	LEU
5	C	50	ALA
5	C	64	VAL
5	C	65	ALA
5	C	68	VAL
5	C	98	ASN
5	C	100	ALA
5	C	101	LEU
5	C	130	VAL

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Mol	Chain	Res	Type
5	C	146	ALA
5	C	154	SER
5	C	196	LEU
6	D	36	ARG
6	D	88	VAL
7	E	52	PRO
7	E	53	LEU
7	E	73	ASN
7	E	125	SER
7	E	153	LYS
8	F	72	VAL
9	G	41	ARG
9	G	42	ILE
9	G	67	GLU
9	G	89	MET
9	G	155	ARG
10	H	83	ILE
10	H	91	ARG
11	I	22	GLY
11	I	29	ASN
11	I	41	VAL
11	I	42	ARG
11	I	43	ALA
11	I	55	ALA
11	I	58	ARG
11	I	65	VAL
11	I	94	ALA
11	I	118	LYS
12	J	34	VAL
12	J	55	LYS
12	J	61	GLU
12	J	72	VAL
12	J	90	LEU
12	J	99	LYS
13	K	75	TYR
14	L	47	LYS
14	L	73	GLU
14	L	78	GLN
14	L	115	LYS
15	M	4	ILE
15	M	38	GLY
15	M	95	GLY

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Mol	Chain	Res	Type
16	N	32	SER
18	P	43	LYS
19	Q	80	GLY
19	Q	81	ARG
19	Q	82	MET
19	Q	83	ASP
19	Q	96	GLN
21	S	6	LYS
21	S	32	LYS
21	S	39	THR
22	T	11	SER
22	T	73	HIS
22	T	94	ALA
22	T	95	ALA
23	V	3	LYS
4	B	18	GLY
4	B	20	GLU
4	B	23	ARG
4	B	66	GLY
4	B	84	GLU
4	B	135	GLN
4	B	165	VAL
4	B	214	ILE
5	C	16	ARG
5	C	52	LEU
5	C	56	ASP
5	C	60	ALA
5	C	79	ARG
5	C	102	ASN
5	C	171	GLY
5	C	179	ARG
5	C	206	GLU
6	D	9	CYS
6	D	31	CYS
6	D	191	ARG
7	E	107	ARG
9	G	17	VAL
9	G	37	ASN
9	G	76	ARG
9	G	134	ALA
10	H	24	THR
10	H	97	VAL

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Mol	Chain	Res	Type
10	H	105	ARG
11	I	12	GLU
12	J	23	ILE
12	J	24	VAL
12	J	33	GLN
12	J	54	PHE
12	J	65	LEU
12	J	73	ASP
12	J	78	ASN
12	J	86	MET
13	K	101	SER
13	K	103	LEU
14	L	28	LYS
14	L	41	ARG
14	L	51	ALA
14	L	87	GLY
14	L	102	ARG
14	L	108	ALA
14	L	109	GLY
14	L	116	SER
14	L	121	GLY
15	M	7	VAL
15	M	21	TYR
15	M	68	GLY
15	M	106	ASN
16	N	15	LYS
16	N	17	LYS
16	N	22	THR
17	O	72	ARG
18	P	16	HIS
18	P	24	ALA
19	Q	49	GLU
19	Q	98	LEU
20	R	28	GLU
20	R	32	ARG
20	R	38	GLU
20	R	54	ARG
20	R	57	GLY
21	S	9	VAL
21	S	43	GLU
21	S	45	VAL
22	T	9	ASN

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Mol	Chain	Res	Type
22	T	48	LYS
22	T	74	LYS
22	T	86	ARG
22	T	98	PRO
22	T	101	GLY
22	T	102	GLY
4	B	17	PHE
4	B	62	ALA
4	B	113	HIS
4	B	143	GLU
4	B	146	GLN
4	B	151	GLY
4	B	171	ALA
4	B	183	PRO
5	C	4	LYS
5	C	61	ALA
5	C	62	ASP
5	C	63	ASN
5	C	66	VAL
5	C	67	THR
5	C	84	ILE
5	C	168	ALA
6	D	7	PRO
6	D	43	HIS
6	D	154	ASN
6	D	179	GLU
7	E	71	LEU
7	E	77	PRO
7	E	108	ALA
7	E	126	ARG
8	F	43	LEU
9	G	10	ARG
9	G	97	GLN
9	G	139	GLU
10	H	46	LYS
10	H	81	HIS
11	I	21	PRO
11	I	46	ALA
11	I	56	LEU
11	I	101	PHE
11	I	127	LYS
13	K	44	SER

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Mol	Chain	Res	Type
13	K	106	LYS
13	K	124	LYS
14	L	17	LYS
14	L	27	LEU
15	M	91	ARG
15	M	99	ARG
15	M	100	GLY
16	N	6	LEU
16	N	10	ALA
16	N	24	CYS
16	N	41	ARG
19	Q	34	LYS
20	R	71	LYS
21	S	8	GLY
23	V	23	PRO
4	B	91	PRO
4	B	150	SER
4	B	181	PHE
5	C	167	TRP
6	D	150	GLU
8	F	62	TRP
8	F	69	GLU
9	G	90	GLU
9	G	119	ARG
9	G	127	ALA
10	H	30	ARG
10	H	135	CYS
11	I	121	ARG
12	J	76	ASN
13	K	40	ILE
13	K	48	ILE
13	K	128	ALA
14	L	40	VAL
15	M	31	LYS
15	M	67	GLU
15	M	83	ASP
15	M	116	THR
15	M	118	ALA
16	N	23	ARG
17	O	18	PHE
19	Q	69	LYS
20	R	25	THR

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Mol	Chain	Res	Type
21	S	14	HIS
21	S	77	THR
22	T	28	ALA
22	T	97	ALA
4	B	131	PRO
4	B	162	ILE
5	C	14	ILE
5	C	39	ILE
5	C	160	ALA
5	C	181	ASN
6	D	5	ILE
6	D	92	VAL
6	D	208	SER
7	E	17	ALA
8	F	100	ASN
9	G	78	ARG
9	G	109	ASN
9	G	130	GLY
10	H	67	PRO
12	J	19	SER
12	J	40	LEU
12	J	77	PRO
12	J	89	ASP
13	K	50	TYR
14	L	30	ALA
16	N	29	ARG
18	P	66	PRO
20	R	20	ALA
21	S	30	LEU
4	B	65	GLY
4	B	175	ARG
5	C	55	VAL
5	C	108	ASN
5	C	169	ALA
5	C	195	VAL
9	G	88	PRO
15	M	63	THR
15	M	85	GLY
20	R	45	SER
4	B	130	ARG
5	C	81	GLY
6	D	142	PRO

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Mol	Chain	Res	Type
9	G	75	VAL
11	I	44	VAL
13	K	57	THR
17	O	75	PRO
18	P	15	PRO
19	Q	64	PRO
4	B	202	PRO
6	D	23	GLY
7	E	127	ASN
12	J	36	GLY
15	M	97	PRO
20	R	37	VAL
21	S	31	ILE
5	C	74	GLY
9	G	81	GLY
4	B	174	VAL
4	B	108	ILE
7	E	129	ILE
14	L	29	GLY

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	B	202/220 (92%)	177 (88%)	25 (12%)	4 19
5	C	160/188 (85%)	149 (93%)	11 (7%)	15 46
6	D	180/180 (100%)	160 (89%)	20 (11%)	6 24
7	E	115/122 (94%)	101 (88%)	14 (12%)	5 19
8	F	90/90 (100%)	81 (90%)	9 (10%)	7 29
9	G	126/126 (100%)	118 (94%)	8 (6%)	18 49
10	H	119/119 (100%)	101 (85%)	18 (15%)	3 12
11	I	98/99 (99%)	86 (88%)	12 (12%)	5 19
12	J	87/91 (96%)	73 (84%)	14 (16%)	2 10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
13	K	90/99 (91%)	83 (92%)	7 (8%)	12 40
14	L	104/111 (94%)	91 (88%)	13 (12%)	4 18
15	M	94/101 (93%)	88 (94%)	6 (6%)	17 48
16	N	49/49 (100%)	44 (90%)	5 (10%)	7 28
17	O	79/79 (100%)	73 (92%)	6 (8%)	13 41
18	P	72/74 (97%)	62 (86%)	10 (14%)	3 15
19	Q	96/96 (100%)	86 (90%)	10 (10%)	7 27
20	R	64/77 (83%)	61 (95%)	3 (5%)	26 58
21	S	71/79 (90%)	63 (89%)	8 (11%)	6 23
22	T	76/82 (93%)	67 (88%)	9 (12%)	5 21
23	V	19/21 (90%)	18 (95%)	1 (5%)	22 54
All	All	1991/2103 (95%)	1782 (90%)	209 (10%)	7 26

All (209) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	8	LYS
4	B	15	VAL
4	B	17	PHE
4	B	21	ARG
4	B	23	ARG
4	B	24	TRP
4	B	25	ASN
4	B	58	ILE
4	B	64	ARG
4	B	82	ARG
4	B	87	ARG
4	B	90	MET
4	B	92	TYR
4	B	102	LEU
4	B	115	LEU
4	B	117	GLU
4	B	118	LEU
4	B	122	PHE
4	B	142	LEU
4	B	149	LEU
4	B	178	ARG
4	B	183	PRO

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Mol	Chain	Res	Type
4	B	187	LEU
4	B	196	LEU
4	B	204	ASN
5	C	3	ASN
5	C	6	HIS
5	C	8	ILE
5	C	18	TRP
5	C	29	TYR
5	C	56	ASP
5	C	70	VAL
5	C	99	VAL
5	C	167	TRP
5	C	196	LEU
5	C	201	TYR
6	D	9	CYS
6	D	10	ARG
6	D	15	GLU
6	D	19	LEU
6	D	35	ARG
6	D	47	ARG
6	D	53	ASP
6	D	64	LEU
6	D	65	ARG
6	D	68	TYR
6	D	91	SER
6	D	98	GLU
6	D	106	TYR
6	D	122	ARG
6	D	131	ARG
6	D	138	TYR
6	D	162	LEU
6	D	177	ASP
6	D	192	GLU
6	D	199	ASN
7	E	12	LEU
7	E	16	THR
7	E	31	LEU
7	E	43	LEU
7	E	53	LEU
7	E	64	ARG
7	E	72	GLN
7	E	73	ASN

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Mol	Chain	Res	Type
7	E	80	ILE
7	E	89	ILE
7	E	100	VAL
7	E	144	THR
7	E	147	ASP
7	E	150	ARG
8	F	1	MET
8	F	9	VAL
8	F	19	LEU
8	F	32	ASN
8	F	40	VAL
8	F	69	GLU
8	F	82	ARG
8	F	90	VAL
8	F	95	GLU
9	G	8	GLU
9	G	37	ASN
9	G	85	TYR
9	G	106	GLN
9	G	126	ASP
9	G	131	LYS
9	G	144	MET
9	G	156	TRP
10	H	2	LEU
10	H	18	ARG
10	H	26	VAL
10	H	29	SER
10	H	51	VAL
10	H	52	ASP
10	H	53	VAL
10	H	56	LYS
10	H	59	LEU
10	H	85	ARG
10	H	91	ARG
10	H	92	ARG
10	H	97	VAL
10	H	98	LYS
10	H	104	ARG
10	H	107	LEU
10	H	119	LEU
10	H	129	VAL
11	I	35	GLU

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Mol	Chain	Res	Type
11	I	38	GLN
11	I	54	ASP
11	I	59	PHE
11	I	88	TYR
11	I	92	TYR
11	I	102	LEU
11	I	104	ARG
11	I	111	ARG
11	I	113	LYS
11	I	121	ARG
11	I	127	LYS
12	J	8	LEU
12	J	12	ASP
12	J	13	HIS
12	J	15	THR
12	J	29	ARG
12	J	45	ARG
12	J	57	LYS
12	J	64	GLU
12	J	66	ARG
12	J	73	ASP
12	J	74	ILE
12	J	79	ARG
12	J	90	LEU
12	J	98	ILE
13	K	29	ILE
13	K	44	SER
13	K	54	ARG
13	K	84	VAL
13	K	93	GLN
13	K	96	ARG
13	K	125	PHE
14	L	17	LYS
14	L	49	ASN
14	L	54	LYS
14	L	59	ARG
14	L	60	LEU
14	L	67	THR
14	L	81	SER
14	L	89	ARG
14	L	93	LEU
14	L	98	TYR

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Mol	Chain	Res	Type
14	L	113	ARG
14	L	122	THR
14	L	126	LYS
15	M	14	ARG
15	M	40	ASN
15	M	66	LEU
15	M	70	LEU
15	M	110	ARG
15	M	115	LYS
16	N	8	GLU
16	N	9	LYS
16	N	16	PHE
16	N	41	ARG
16	N	58	LYS
17	O	4	THR
17	O	13	GLN
17	O	34	LEU
17	O	60	VAL
17	O	67	LEU
17	O	70	LEU
18	P	2	VAL
18	P	8	ARG
18	P	11	SER
18	P	15	PRO
18	P	20	VAL
18	P	28	ARG
18	P	52	ASP
18	P	65	GLN
18	P	74	LEU
18	P	82	GLN
19	Q	22	LEU
19	Q	34	LYS
19	Q	36	ILE
19	Q	38	ARG
19	Q	59	ILE
19	Q	60	ILE
19	Q	62	SER
19	Q	74	LEU
19	Q	78	GLU
19	Q	98	LEU
20	R	54	ARG
20	R	66	LEU

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Mol	Chain	Res	Type
20	R	81	PHE
21	S	13	ASP
21	S	15	LEU
21	S	25	LYS
21	S	30	LEU
21	S	34	TRP
21	S	53	ASN
21	S	61	TYR
21	S	78	ARG
22	T	8	ARG
22	T	18	GLN
22	T	20	LEU
22	T	45	GLN
22	T	57	ARG
22	T	62	LEU
22	T	73	HIS
22	T	75	ASN
22	T	92	LEU
23	V	24	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
4	B	25	ASN
4	B	37	ASN
4	B	40	HIS
4	B	204	ASN
5	C	3	ASN
5	C	6	HIS
5	C	31	HIS
5	C	98	ASN
5	C	118	GLN
5	C	123	GLN
5	C	139	GLN
5	C	162	GLN
5	C	181	ASN
6	D	45	GLN
6	D	62	GLN
6	D	123	HIS
6	D	129	ASN
6	D	161	ASN
6	D	199	ASN

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Mol	Chain	Res	Type
7	E	73	ASN
8	F	27	GLN
8	F	32	ASN
8	F	73	ASN
8	F	100	ASN
9	G	28	ASN
9	G	37	ASN
9	G	64	GLN
9	G	86	GLN
9	G	106	GLN
9	G	122	HIS
11	I	73	GLN
12	J	33	GLN
12	J	76	ASN
12	J	78	ASN
13	K	116	HIS
14	L	75	HIS
14	L	80	HIS
15	M	12	ASN
15	M	40	ASN
15	M	62	ASN
15	M	106	ASN
16	N	52	GLN
17	O	9	GLN
17	O	37	ASN
17	O	46	HIS
20	R	36	ASN
21	S	14	HIS
21	S	23	ASN
21	S	53	ASN
21	S	56	GLN
22	T	16	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1511/1522 (99%)	206 (13%)	66 (4%)
2	Y	10/17 (58%)	2 (20%)	0
3	Z	3/6 (50%)	0	0
All	All	1524/1545 (98%)	208 (13%)	66 (4%)

All (208) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	52	G
1	A	54	C
1	A	61	G
1	A	65	U
1	A	81	U
1	A	82	U
1	A	101	A
1	A	116	A
1	A	120	A
1	A	121	C
1	A	130	A
1	A	131	C
1	A	182	U
1	A	190(E)	U
1	A	190(F)	G
1	A	195	A
1	A	197	A
1	A	201	C
1	A	203	U
1	A	204	U
1	A	216	G
1	A	217	C
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	281	G
1	A	289	G
1	A	328	C
1	A	329	A

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Mol	Chain	Res	Type
1	A	332	G
1	A	345	C
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	397	A
1	A	398	C
1	A	412	A
1	A	413	G
1	A	421	U
1	A	422	C
1	A	424	G
1	A	428	G
1	A	429	U
1	A	430	A
1	A	439	A
1	A	452	A
1	A	461	C
1	A	462	G
1	A	481	G
1	A	482	A
1	A	484	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	521	G
1	A	532	A
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A

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Mol	Chain	Res	Type
1	A	575	G
1	A	576	G
1	A	577	G
1	A	652	U
1	A	653	A
1	A	665	A
1	A	666	G
1	A	688	G
1	A	702	A
1	A	703	G
1	A	723	U
1	A	724	G
1	A	731	G
1	A	749	C
1	A	755	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	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	869	G
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	945	G
1	A	960	U
1	A	966	G
1	A	968	A
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G

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Mol	Chain	Res	Type
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1005	A
1	A	1008	C
1	A	1050	G
1	A	1054	C
1	A	1055	A
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1117	G
1	A	1126	U
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1145	C
1	A	1159	U
1	A	1160	G
1	A	1183	A
1	A	1184	G
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1224	G
1	A	1225	A

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Mol	Chain	Res	Type
1	A	1226	C
1	A	1227	A
1	A	1257	U
1	A	1258	G
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1305	G
1	A	1320	C
1	A	1331	G
1	A	1348	U
1	A	1363	A
1	A	1365	G
1	A	1379	G
1	A	1381	U
1	A	1398	A
1	A	1401	G
1	A	1443	G
1	A	1446	A
1	A	1447	G
1	A	1451	A
1	A	1452	C
1	A	1492	A
1	A	1499	A
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G
2	Y	33	U
2	Y	40	PSU

All (66) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	30	U
1	A	48	C
1	A	51	A
1	A	60	A
1	A	64	G
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	202	U
1	A	203	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	328	C
1	A	344	A
1	A	351	G
1	A	353	A
1	A	366	C
1	A	372	C
1	A	428	G
1	A	429	U
1	A	438	G
1	A	484	G
1	A	496	A
1	A	497	A
1	A	509	A
1	A	533	A
1	A	559	A
1	A	575	G
1	A	687	A
1	A	701	C
1	A	748	C
1	A	812	C
1	A	913	A
1	A	945	G
1	A	965	A
1	A	975	A
1	A	992	U
1	A	993	G

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Mol	Chain	Res	Type
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1101	A
1	A	1139	G
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1201	A
1	A	1224	G
1	A	1226	C
1	A	1256	A
1	A	1257	U
1	A	1278	U
1	A	1281	U
1	A	1285	A
1	A	1347	G
1	A	1380	U
1	A	1451	A
1	A	1498	U
1	A	1503	A
1	A	1504	G
1	A	1528	U

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

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	$\#\|Z\| > 2$
2	PSU	Y	40	2	17,21,22	2.28	6 (35%)	20,30,33	5.41	6 (30%)

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
2	PSU	Y	40	2	-	5/7/25/26	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Y	40	PSU	C4-N3	5.55	1.42	1.33
2	Y	40	PSU	O3'-C3'	3.64	1.51	1.43
2	Y	40	PSU	C4-C5	3.38	1.48	1.41
2	Y	40	PSU	O4'-C1'	-2.91	1.40	1.44
2	Y	40	PSU	C6-N1	2.78	1.40	1.34
2	Y	40	PSU	C2-N1	2.60	1.43	1.38

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	Y	40	PSU	N1-C2-N3	-16.72	115.14	128.43
2	Y	40	PSU	C4-N3-C2	13.95	126.92	115.14
2	Y	40	PSU	C5-C4-N3	-8.67	114.19	125.36
2	Y	40	PSU	C6-N1-C2	3.35	120.88	115.36
2	Y	40	PSU	C4'-O4'-C1'	-2.54	106.29	109.42
2	Y	40	PSU	O4'-C4'-C3'	-2.09	100.98	105.11

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	Y	40	PSU	C2'-C1'-C5-C6
2	Y	40	PSU	O4'-C4'-C5'-O5'
2	Y	40	PSU	C3'-C4'-C5'-O5'
2	Y	40	PSU	C4'-C5'-O5'-P
2	Y	40	PSU	C2'-C1'-C5-C4

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Y	40	PSU	3	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 109 ligands modelled in this entry, 108 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	$\#\|Z\| > 2$
24	PAR	A	1545	-	45,45,45	2.15	14 (31%)	64,67,67	1.02	2 (3%)

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	PAR	A	1545	-	-	2/18/94/94	0/4/4/4

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1545	PAR	C31-C21	6.48	1.61	1.53
24	A	1545	PAR	C64-C54	4.73	1.58	1.52
24	A	1545	PAR	C34-C24	4.47	1.59	1.53
24	A	1545	PAR	O43-C13	4.17	1.49	1.41
24	A	1545	PAR	O54-C14	3.59	1.51	1.41
24	A	1545	PAR	C44-C54	3.23	1.59	1.53
24	A	1545	PAR	C24-N24	2.68	1.51	1.47
24	A	1545	PAR	O33-C14	2.66	1.49	1.41
24	A	1545	PAR	C11-C21	2.60	1.57	1.52
24	A	1545	PAR	C23-C33	2.46	1.58	1.52
24	A	1545	PAR	O51-C51	2.36	1.50	1.44
24	A	1545	PAR	C21-N21	2.13	1.50	1.47
24	A	1545	PAR	C14-C24	2.12	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1545	PAR	C44-C34	2.06	1.57	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	A	1545	PAR	O11-C11-C21	2.61	112.71	108.22
24	A	1545	PAR	O54-C54-C64	2.55	110.77	106.01

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A	1545	PAR	C24-C14-O33-C33
24	A	1545	PAR	C23-C13-O52-C52

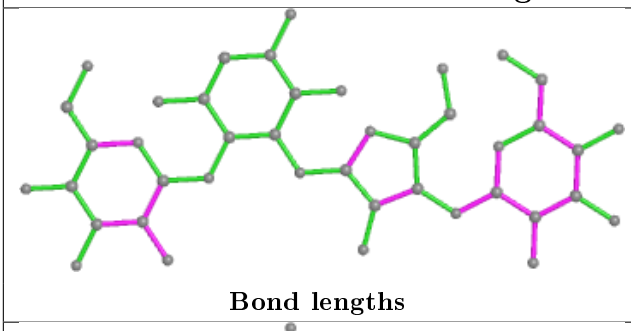
There are no ring outliers.

1 monomer is involved in 4 short contacts:

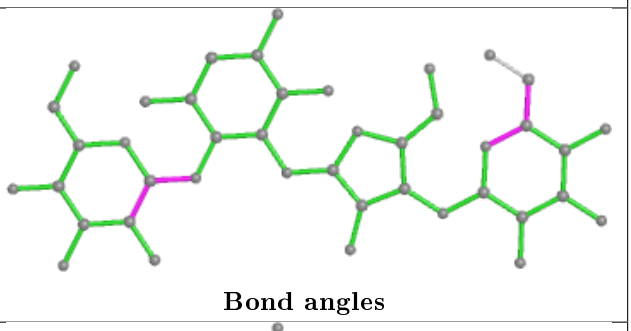
Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	1545	PAR	4	0

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

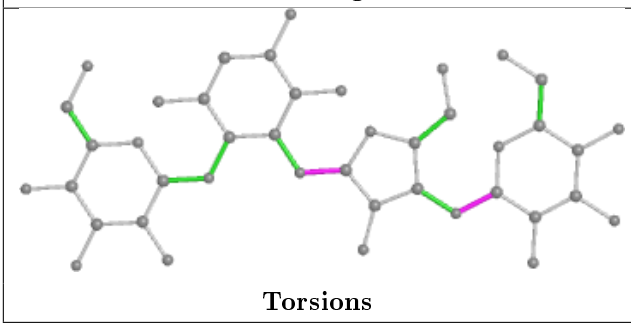
Ligand PAR A 1545



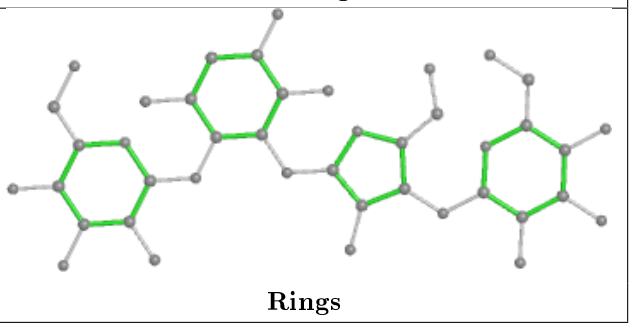
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	1512/1522 (99%)	0.59	81 (5%) 25 28	25, 86, 178, 198	0
2	Y	10/17 (58%)	0.39	0 100 100	91, 117, 190, 194	0
3	Z	4/6 (66%)	0.57	1 (25%) 0 0	87, 92, 96, 197	0
4	B	234/256 (91%)	0.47	27 (11%) 4 5	22, 132, 191, 198	0
5	C	206/239 (86%)	0.20	9 (4%) 34 37	55, 126, 183, 198	0
6	D	208/208 (100%)	0.35	20 (9%) 8 10	16, 91, 157, 197	0
7	E	150/161 (93%)	-0.09	0 100 100	31, 83, 138, 198	0
8	F	101/101 (100%)	0.62	14 (13%) 2 3	56, 117, 174, 194	0
9	G	155/155 (100%)	0.20	5 (3%) 47 50	64, 127, 175, 198	0
10	H	138/138 (100%)	-0.14	1 (0%) 87 91	4, 65, 145, 197	0
11	I	127/128 (99%)	0.59	14 (11%) 5 6	57, 140, 187, 198	0
12	J	98/104 (94%)	1.13	23 (23%) 0 0	51, 146, 197, 198	0
13	K	119/129 (92%)	0.36	7 (5%) 22 25	48, 99, 169, 198	0
14	L	124/135 (91%)	0.29	5 (4%) 38 40	37, 88, 157, 181	0
15	M	118/126 (93%)	0.33	7 (5%) 22 25	60, 120, 175, 196	0
16	N	60/60 (100%)	0.52	4 (6%) 17 20	60, 117, 174, 198	0
17	O	88/88 (100%)	0.19	4 (4%) 33 36	21, 83, 147, 198	0
18	P	83/88 (94%)	0.09	4 (4%) 30 33	10, 62, 121, 172	0
19	Q	104/104 (100%)	0.30	8 (7%) 13 15	14, 75, 157, 198	0
20	R	73/88 (82%)	0.46	4 (5%) 25 27	46, 99, 178, 194	0
21	S	80/92 (86%)	1.02	16 (20%) 1 1	74, 138, 191, 198	0
22	T	99/106 (93%)	0.02	4 (4%) 38 40	24, 70, 136, 186	0
23	V	24/26 (92%)	0.80	2 (8%) 11 13	44, 122, 183, 198	0
All	All	3915/4077 (96%)	0.44	260 (6%) 18 21	4, 98, 179, 198	0

All (260) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
12	J	10	GLY	9.0
21	S	3	ARG	8.7
6	D	23	GLY	7.8
21	S	2	PRO	6.5
16	N	3	ARG	6.4
4	B	66	GLY	6.3
9	G	2	ALA	6.3
1	A	1027	C	6.3
1	A	1034	G	5.5
6	D	25	ARG	5.4
13	K	129	SER	5.3
19	Q	105	ALA	5.1
6	D	2	GLY	5.1
10	H	1	MET	5.0
19	Q	102	GLY	5.0
4	B	79	ASP	5.0
1	A	1019	C	4.9
11	I	15	ALA	4.9
1	A	1005	A	4.9
21	S	28	LYS	4.8
21	S	49	ILE	4.5
1	A	993	G	4.5
17	O	22	THR	4.5
4	B	208	ILE	4.4
11	I	65	VAL	4.4
1	A	1129	C	4.4
1	A	1036	G	4.4
14	L	33	ARG	4.3
1	A	1026	G	4.3
12	J	72	VAL	4.3
12	J	33	GLN	4.2
4	B	238	LEU	4.1
1	A	1144	G	4.1
1	A	1540	U	4.1
1	A	1029	C	4.0
19	Q	104	LYS	4.0
21	S	31	ILE	4.0
19	Q	103	GLY	3.9
15	M	9	ILE	3.9
15	M	88	ARG	3.9
6	D	33	MET	3.8
6	D	122	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
8	F	86	ARG	3.8
4	B	233	SER	3.8
19	Q	101	ARG	3.7
22	T	56	MET	3.7
1	A	1006	C	3.7
5	C	23	TYR	3.7
12	J	74	ILE	3.7
1	A	992	U	3.6
4	B	80	ILE	3.6
1	A	529	G	3.6
12	J	6	ILE	3.6
20	R	31	LEU	3.6
11	I	14	VAL	3.6
6	D	21	LEU	3.6
11	I	19	LEU	3.5
12	J	24	VAL	3.5
16	N	6	LEU	3.4
8	F	64	GLN	3.4
12	J	5	ARG	3.4
1	A	1143	G	3.4
21	S	33	THR	3.4
21	S	27	GLU	3.4
9	G	73	MET	3.4
4	B	234	PRO	3.3
4	B	99	GLY	3.3
6	D	42	GLN	3.3
12	J	95	GLU	3.3
1	A	1220	G	3.2
6	D	36	ARG	3.2
6	D	123	HIS	3.2
19	Q	16	GLN	3.2
4	B	77	ALA	3.2
6	D	3	ARG	3.2
12	J	31	GLY	3.2
1	A	1035	A	3.2
14	L	49	ASN	3.1
4	B	31	TYR	3.1
1	A	1045	C	3.1
4	B	211	ILE	3.1
15	M	7	VAL	3.1
21	S	15	LEU	3.1
21	S	26	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
12	J	73	ASP	3.1
21	S	5	LEU	3.1
21	S	60	VAL	3.1
12	J	8	LEU	3.1
22	T	103	GLY	3.0
17	O	3	ILE	3.0
4	B	190	THR	3.0
1	A	1541	U	2.9
9	G	70	LYS	2.9
1	A	1518	A	2.9
11	I	92	TYR	2.9
16	N	18	VAL	2.9
4	B	228	GLY	2.9
12	J	54	PHE	2.9
19	Q	15	MET	2.9
9	G	120	ILE	2.9
1	A	1219	U	2.9
1	A	1213	A	2.9
1	A	1024	G	2.8
22	T	84	LEU	2.8
1	A	1127	G	2.8
1	A	1025	U	2.8
1	A	1159	U	2.8
1	A	532	A	2.8
1	A	991	U	2.8
12	J	34	VAL	2.8
8	F	84	ASN	2.8
1	A	1212	U	2.8
12	J	70	ARG	2.8
1	A	704	A	2.7
6	D	32	ALA	2.7
4	B	72	GLY	2.7
1	A	1147	C	2.7
17	O	21	ASP	2.7
11	I	17	VAL	2.7
18	P	64	ALA	2.7
8	F	52	ILE	2.7
13	K	12	ARG	2.7
14	L	32	PHE	2.7
18	P	39	TYR	2.7
8	F	26	ILE	2.7
21	S	4	SER	2.6

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Mol	Chain	Res	Type	RSRZ
20	R	43	PHE	2.6
1	A	1004	A	2.6
14	L	116	SER	2.6
1	A	1003(A)	G	2.6
1	A	373	A	2.6
5	C	95	THR	2.6
13	K	90	GLY	2.6
20	R	63	GLN	2.6
4	B	163	PHE	2.6
11	I	18	PHE	2.6
12	J	4	ILE	2.6
5	C	66	VAL	2.6
18	P	41	PRO	2.6
1	A	1280	A	2.5
12	J	28	ARG	2.5
4	B	214	ILE	2.5
8	F	39	LYS	2.5
19	Q	17	LYS	2.5
11	I	101	PHE	2.5
1	A	1038	C	2.5
12	J	96	ILE	2.5
4	B	239	VAL	2.5
1	A	687	A	2.5
1	A	1046	A	2.5
11	I	63	ILE	2.5
1	A	1020	U	2.4
12	J	20	ALA	2.4
1	A	769	G	2.4
8	F	60	PHE	2.4
1	A	1065	U	2.4
1	A	1135	U	2.4
5	C	76	VAL	2.4
1	A	1117	G	2.4
1	A	1237	C	2.4
6	D	30	LYS	2.4
1	A	1030(D)	A	2.4
1	A	438	G	2.4
6	D	146	ILE	2.4
21	S	62	ILE	2.4
1	A	971	G	2.4
20	R	29	PHE	2.4
4	B	140	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
12	J	32	ALA	2.4
15	M	6	GLY	2.4
5	C	81	GLY	2.4
1	A	1037	C	2.3
16	N	61	TRP	2.3
4	B	28	PHE	2.3
1	A	1097	C	2.3
13	K	128	ALA	2.3
15	M	11	ARG	2.3
4	B	108	ILE	2.3
1	A	428	G	2.3
1	A	1334	G	2.3
18	P	19	ILE	2.3
6	D	209	ARG	2.3
13	K	28	THR	2.3
4	B	105	PHE	2.3
6	D	10	ARG	2.3
23	V	2	GLY	2.3
1	A	161	A	2.3
1	A	1169	A	2.3
6	D	24	GLU	2.3
13	K	42	TRP	2.3
22	T	64	ASP	2.2
6	D	119	GLN	2.2
1	A	1001	A	2.2
13	K	54	ARG	2.2
12	J	71	LEU	2.2
11	I	33	PHE	2.2
1	A	1014	A	2.2
15	M	32	GLU	2.2
21	S	30	LEU	2.2
8	F	69	GLU	2.2
11	I	13	ALA	2.2
1	A	160	A	2.2
1	A	1002	G	2.2
1	A	1023	G	2.2
4	B	227	GLY	2.2
6	D	13	ARG	2.2
1	A	978	A	2.2
1	A	984	C	2.2
1	A	1182	G	2.2
4	B	222	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
8	F	85	VAL	2.2
1	A	152	A	2.2
11	I	9	ARG	2.2
4	B	118	LEU	2.2
12	J	27	ALA	2.2
9	G	62	PHE	2.2
5	C	82	GLU	2.2
1	A	1028	C	2.2
6	D	40	PRO	2.2
11	I	37	PHE	2.2
1	A	805	C	2.1
1	A	1200	C	2.1
1	A	994	A	2.1
4	B	215	LEU	2.1
1	A	1018	C	2.1
6	D	34	GLU	2.1
8	F	38	GLU	2.1
21	S	34	TRP	2.1
1	A	1221	G	2.1
1	A	1318	A	2.1
15	M	56	LEU	2.1
5	C	94	LEU	2.1
3	Z	4	U	2.1
1	A	1361(A)	C	2.1
14	L	83	VAL	2.1
1	A	437	U	2.1
1	A	1282	C	2.1
1	A	1370	G	2.1
1	A	1351	U	2.1
21	S	48	THR	2.1
1	A	1033	G	2.1
4	B	16	HIS	2.1
17	O	15	PHE	2.1
1	A	872	A	2.1
1	A	1531	A	2.1
5	C	60	ALA	2.0
1	A	264	U	2.0
5	C	99	VAL	2.0
8	F	63	TYR	2.0
12	J	40	LEU	2.0
1	A	1003	G	2.0
1	A	1134	G	2.0

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Mol	Chain	Res	Type	RSRZ
8	F	11	ASN	2.0
4	B	78	GLN	2.0
8	F	65	VAL	2.0
11	I	26	VAL	2.0
23	V	3	LYS	2.0
1	A	1017	G	2.0
12	J	77	PRO	2.0
8	F	37	VAL	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	PSU	Y	40	20/21	0.95	0.32	25,25,25,25	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	MG	A	1606	1/1	0.60	0.45	34,34,34,34	1
25	MG	A	1548	1/1	0.60	1.36	34,34,34,34	1
25	MG	A	1618	1/1	0.61	0.65	34,34,34,34	1
25	MG	A	1597	1/1	0.63	0.47	25,25,25,25	1
25	MG	A	1575	1/1	0.67	0.35	34,34,34,34	1
25	MG	A	1585	1/1	0.70	0.55	34,34,34,34	1
25	MG	A	1607	1/1	0.72	1.22	34,34,34,34	1
25	MG	A	441	1/1	0.72	0.31	34,34,34,34	1
25	MG	A	1595	1/1	0.76	0.37	34,34,34,34	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	MG	A	1609	1/1	0.77	0.31	34,34,34,34	1
25	MG	A	1594	1/1	0.78	0.20	34,34,34,34	0
25	MG	A	210	1/1	0.79	0.27	34,34,34,34	1
25	MG	A	87	1/1	0.81	0.31	34,34,34,34	0
25	MG	A	71	1/1	0.81	0.30	34,34,34,34	0
25	MG	A	1580	1/1	0.81	0.66	34,34,34,34	0
25	MG	A	1620	1/1	0.82	0.30	34,34,34,34	1
25	MG	A	1612	1/1	0.82	0.39	34,34,34,34	0
25	MG	A	1562	1/1	0.82	0.42	34,34,34,34	0
25	MG	A	1550	1/1	0.83	0.17	34,34,34,34	1
25	MG	A	1601	1/1	0.83	0.15	34,34,34,34	1
25	MG	A	1622	1/1	0.83	0.61	34,34,34,34	1
25	MG	A	466	1/1	0.85	0.26	34,34,34,34	1
25	MG	A	211	1/1	0.85	0.87	34,34,34,34	1
25	MG	A	1610	1/1	0.85	0.20	34,34,34,34	0
25	MG	A	1624	1/1	0.85	0.45	34,34,34,34	0
25	MG	A	1632	1/1	0.86	0.29	34,34,34,34	1
25	MG	A	1626	1/1	0.86	0.35	34,34,34,34	1
25	MG	A	1621	1/1	0.87	0.47	34,34,34,34	1
25	MG	A	1604	1/1	0.87	0.77	34,34,34,34	0
25	MG	A	1599	1/1	0.88	0.20	34,34,34,34	0
25	MG	A	1565	1/1	0.88	0.62	34,34,34,34	1
25	MG	A	1549	1/1	0.89	0.39	34,34,34,34	0
25	MG	A	1616	1/1	0.89	0.23	34,34,34,34	1
25	MG	A	1572	1/1	0.89	0.25	34,34,34,34	0
25	MG	A	1556	1/1	0.89	0.53	34,34,34,34	0
25	MG	A	1598	1/1	0.90	0.15	34,34,34,34	0
25	MG	A	1608	1/1	0.90	0.50	34,34,34,34	0
25	MG	A	1614	1/1	0.91	0.30	34,34,34,34	1
25	MG	A	1589	1/1	0.91	0.42	34,34,34,34	0
25	MG	A	1564	1/1	0.91	0.44	34,34,34,34	0
25	MG	A	1627	1/1	0.91	0.24	34,34,34,34	1
25	MG	A	1615	1/1	0.91	0.28	34,34,34,34	1
25	MG	A	1619	1/1	0.91	0.12	34,34,34,34	1
25	MG	A	1623	1/1	0.92	0.30	34,34,34,34	1
25	MG	A	1566	1/1	0.92	0.54	34,34,34,34	0
25	MG	A	1633	1/1	0.92	0.82	34,34,34,34	1
25	MG	A	1605	1/1	0.92	0.27	34,34,34,34	0
25	MG	A	1613	1/1	0.92	0.35	34,34,34,34	0
25	MG	A	470	1/1	0.92	0.55	34,34,34,34	0
25	MG	A	1592	1/1	0.93	0.30	34,34,34,34	0
24	PAR	A	1545	42/42	0.93	0.25	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	MG	A	214	1/1	0.93	0.23	34,34,34,34	1
25	MG	A	1567	1/1	0.93	0.34	34,34,34,34	0
25	MG	A	1581	1/1	0.93	0.75	34,34,34,34	0
25	MG	A	1634	1/1	0.93	0.59	34,34,34,34	1
25	MG	A	1603	1/1	0.93	0.52	34,34,34,34	1
25	MG	A	1577	1/1	0.94	0.23	34,34,34,34	1
25	MG	A	1561	1/1	0.94	0.14	34,34,34,34	1
25	MG	A	1591	1/1	0.94	0.21	34,34,34,34	0
25	MG	A	1571	1/1	0.94	0.25	34,34,34,34	0
25	MG	A	471	1/1	0.94	0.59	34,34,34,34	1
25	MG	A	469	1/1	0.94	0.19	34,34,34,34	1
25	MG	A	1588	1/1	0.94	0.54	34,34,34,34	0
25	MG	A	1573	1/1	0.94	0.30	34,34,34,34	0
25	MG	A	1628	1/1	0.94	0.35	34,34,34,34	0
25	MG	A	1557	1/1	0.94	0.38	34,34,34,34	0
25	MG	A	1584	1/1	0.94	0.31	34,34,34,34	0
25	MG	A	1593	1/1	0.94	0.21	34,34,34,34	0
25	MG	A	1586	1/1	0.94	0.17	34,34,34,34	0
25	MG	A	1617	1/1	0.94	0.49	34,34,34,34	0
25	MG	A	1576	1/1	0.95	0.42	34,34,34,34	1
25	MG	A	473	1/1	0.95	0.37	34,34,34,34	1
25	MG	A	493	1/1	0.95	0.26	34,34,34,34	1
25	MG	A	1559	1/1	0.95	0.76	34,34,34,34	0
25	MG	A	1611	1/1	0.95	0.32	34,34,34,34	0
25	MG	A	1602	1/1	0.95	0.16	34,34,34,34	1
25	MG	A	1583	1/1	0.95	0.24	34,34,34,34	0
25	MG	A	1546	1/1	0.96	0.39	34,34,34,34	0
25	MG	A	1569	1/1	0.96	0.38	34,34,34,34	0
25	MG	A	1630	1/1	0.96	0.81	34,34,34,34	0
25	MG	A	1579	1/1	0.96	0.26	34,34,34,34	0
25	MG	Y	500	1/1	0.96	0.28	25,25,25,25	1
25	MG	A	1558	1/1	0.96	0.46	34,34,34,34	0
25	MG	A	1568	1/1	0.96	0.26	34,34,34,34	0
25	MG	A	1596	1/1	0.97	0.20	34,34,34,34	1
25	MG	A	1552	1/1	0.97	0.42	34,34,34,34	0
25	MG	A	1587	1/1	0.97	0.41	34,34,34,34	0
25	MG	A	1560	1/1	0.97	0.54	34,34,34,34	0
25	MG	Z	400	1/1	0.97	0.10	34,34,34,34	1
25	MG	A	1563	1/1	0.97	0.63	34,34,34,34	0
25	MG	Z	501	1/1	0.97	0.25	34,34,34,34	1
25	MG	A	1547	1/1	0.97	0.57	34,34,34,34	0
25	MG	A	1551	1/1	0.97	0.42	34,34,34,34	0

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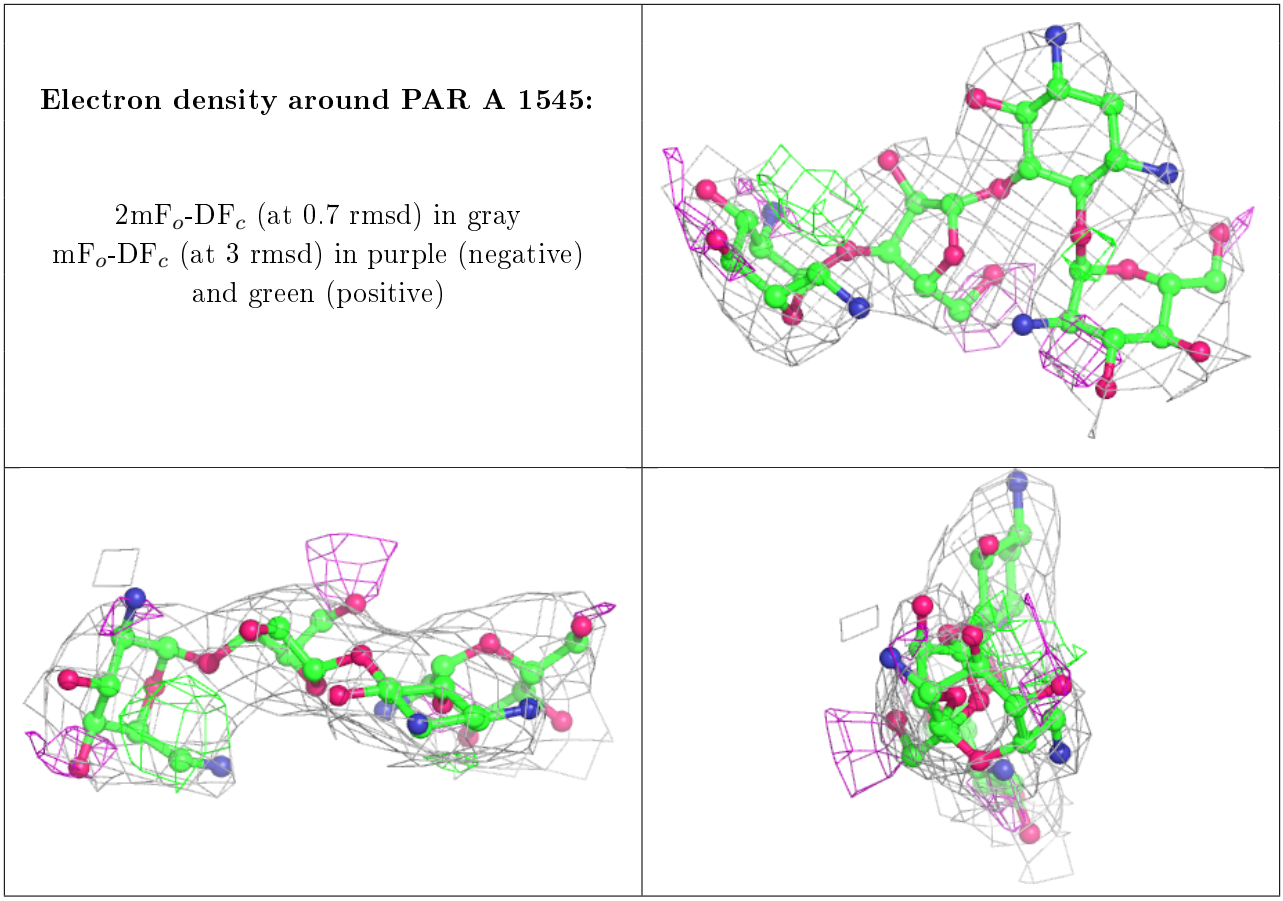
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	MG	A	1553	1/1	0.97	0.28	34,34,34,34	0
25	MG	A	1590	1/1	0.97	0.21	34,34,34,34	0
25	MG	A	1555	1/1	0.97	0.55	34,34,34,34	0
25	MG	A	1629	1/1	0.97	0.49	34,34,34,34	0
25	MG	A	1631	1/1	0.98	0.13	34,34,34,34	1
25	MG	A	1625	1/1	0.98	0.26	34,34,34,34	0
25	MG	A	1582	1/1	0.98	0.28	34,34,34,34	0
26	ZN	D	306	1/1	0.98	0.23	34,34,34,34	0
25	MG	A	86	1/1	0.98	0.32	34,34,34,34	0
25	MG	A	1570	1/1	0.98	0.24	34,34,34,34	0
25	MG	A	467	1/1	0.98	0.14	34,34,34,34	0
25	MG	A	1554	1/1	0.98	0.24	34,34,34,34	0
25	MG	A	1600	1/1	0.98	0.19	34,34,34,34	1
25	MG	A	1578	1/1	0.98	0.26	34,34,34,34	0
26	ZN	N	307	1/1	0.99	0.19	34,34,34,34	1
25	MG	A	1574	1/1	0.99	0.40	34,34,34,34	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around PAR A 1545:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers

There are no such residues in this entry.