Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 08:05 PM GMT

PDB ID	:	1IBL
Title	:	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH A MESSENGER RNA FRAGMENT AND COGNATE TRANSFER RNA ANTICODON STEM-LOOP BOUND AT THE A SITE AND WITH THE ANTIBIOTIC PAROMOMYCIN
Authors	:	Ogle, J.M.; Brodersen, D.E.; Clemons Jr., W.M.; Tarry, M.J.; Carter, A.P.; Ramakrishnan, V.
Deposited on	:	2001-03-28
Resolution	:	3.11 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

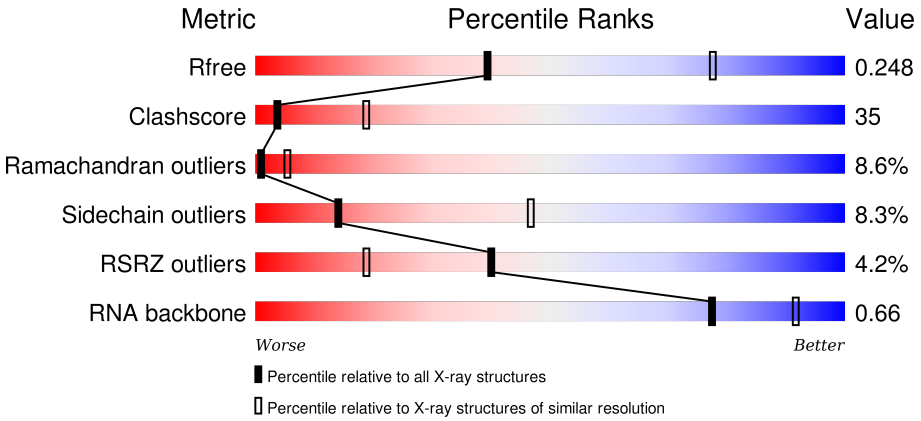
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 3.11 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}	91344	1112 (3.16-3.08)
Clashscore	102246	1218 (3.16-3.08)
Ramachandran outliers	100387	1175 (3.16-3.08)
Sidechain outliers	100360	1175 (3.16-3.08)
RSRZ outliers	91569	1114 (3.16-3.08)
RNA backbone	2183	1010 (3.54-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	% 31% 55% 11%
2	X	6	33% 100%
3	Y	15	40% 53% 7%
4	Z	4	25% 25% 50% 25%

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Mol	Chain	Length	Quality of chain
5	B	256	3% 20% 55% 13% 9%
6	C	239	% 24% 47% 15% 14%
7	D	209	4% 35% 57% 7%
8	E	162	% 36% 46% 11% 7%
9	F	101	% 40% 54% 6%
10	G	156	2% 33% 62%
11	H	138	% 43% 50%
12	I	128	9% 24% 63% 11%
13	J	105	27% 14% 55% 23% 7%
14	K	129	5% 35% 49% 9% 8%
15	L	135	5% 33% 46% 12% 8%
16	M	126	4% 23% 54% 16% 6%
17	N	61	25% 28% 49% 21%
18	O	89	% 44% 48% 7%
19	P	88	18% 33% 57% 5% 6%
20	Q	105	6% 43% 46% 9%
21	R	88	3% 31% 47% 6% 17%
22	S	93	13% 25% 51% 14% 10%
23	T	106	7% 33% 47% 12% 7%
24	V	26	8% 27% 62% 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	PAR	A	1545	-	-	-	X
26	MG	A	1561	-	-	-	X
26	MG	A	1562	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
26	MG	A	1564	-	-	-	X
26	MG	A	1589	-	-	-	X
26	MG	A	1601	-	-	-	X
26	MG	A	1608	-	-	-	X
26	MG	A	1623	-	-	-	X
26	MG	A	1633	-	-	-	X
26	MG	A	1646	-	-	-	X
26	MG	A	1648	-	-	-	X
26	MG	A	1651	-	-	-	X
26	MG	A	211	-	-	-	X

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 52270 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	1507	32391	14418	6002	10465	1506	0	0	0

- Molecule 2 is a RNA chain called P-SITE MESSENGER RNA FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	X	6	117	54	14	44	5	0	0	0

- Molecule 3 is a RNA chain called ANTICODON STEM-LOOP OF PHENYLALANINE TRANSFER RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	Y	15	319	144	60	101	14	0	0	0

- Molecule 4 is a RNA chain called A-SITE MESSENGER RNA FRAGMENT.

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

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S2.

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

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S3.

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

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S4.

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

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S5.

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

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S6.

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

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S7.

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

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S9.

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

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S10.

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

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S11.

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

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S12.

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

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S13.

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

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S14.

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

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S15.

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

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S16.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	?	-	PHE	CONFLICT/DELETION	GB 12056104
P	?	-	HIS	CONFLICT/DELETION	GB 12056104
P	?	-	TYR	CONFLICT/DELETION	GB 12056104

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S17.

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

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S18.

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

- Molecule 22 is a protein called 30S RIBOSOMAL PROTEIN S19.

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

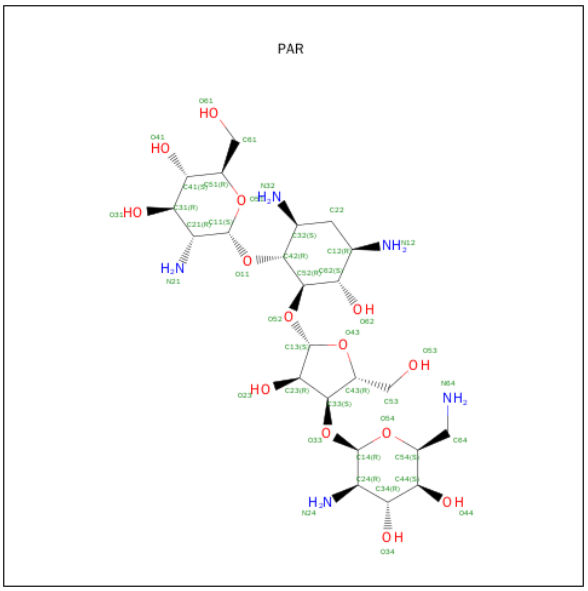
- Molecule 23 is a protein called 30S RIBOSOMAL PROTEIN S20.

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

- Molecule 24 is a protein called 30S RIBOSOMAL PROTEIN THX.

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

- Molecule 25 is PAROMOMYCIN (three-letter code: PAR) (formula: $C_{23}H_{45}N_5O_{14}$).



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

- Molecule 26 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	J	2	Total Mg 2 2	0	0
26	A	120	Total Mg 120 120	0	0
26	D	2	Total Mg 2 2	0	0
26	Y	1	Total Mg 1 1	0	0

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

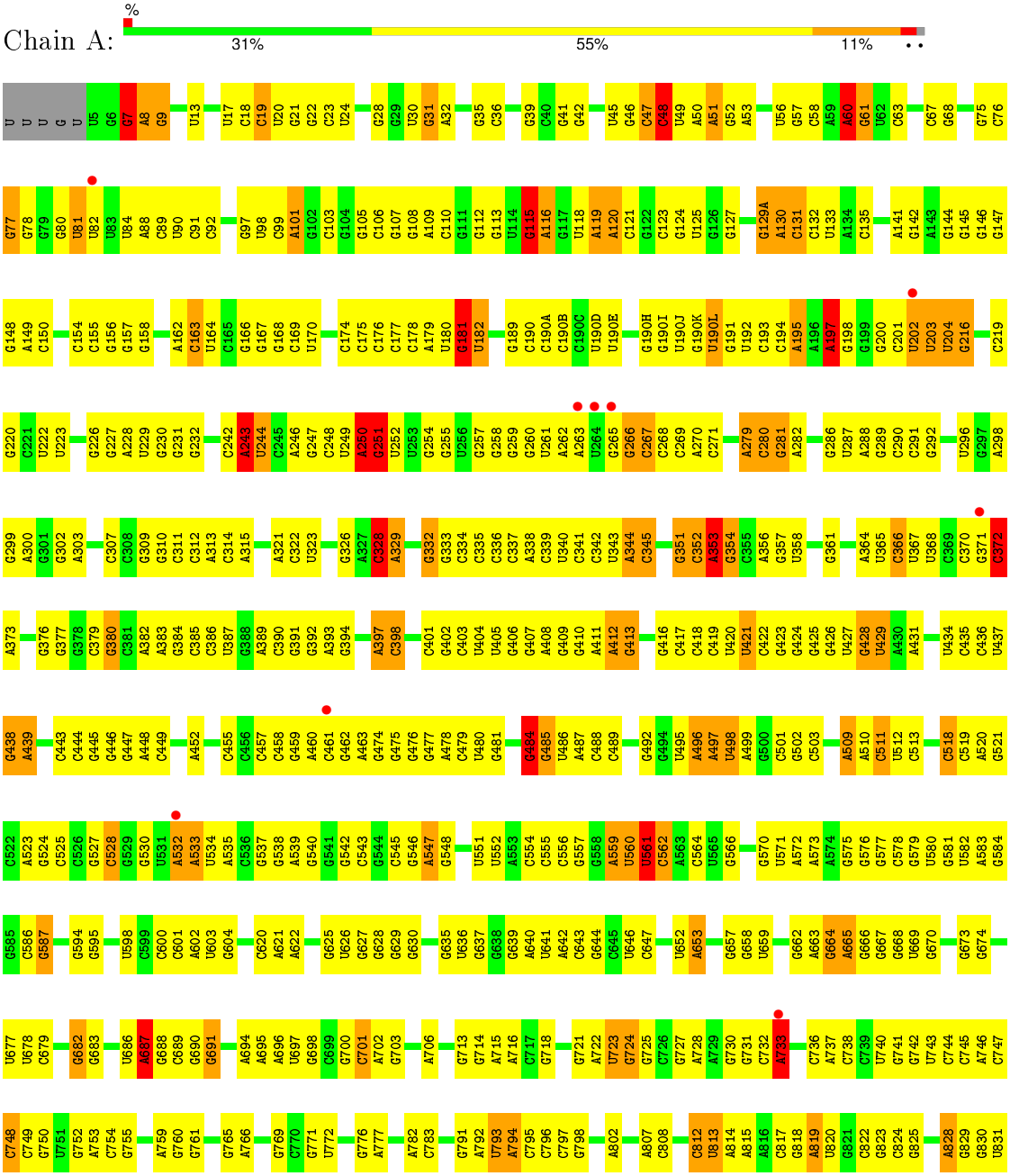
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
27	D	1	Total Zn 1 1	0	0
27	N	1	Total Zn 1 1	0	0

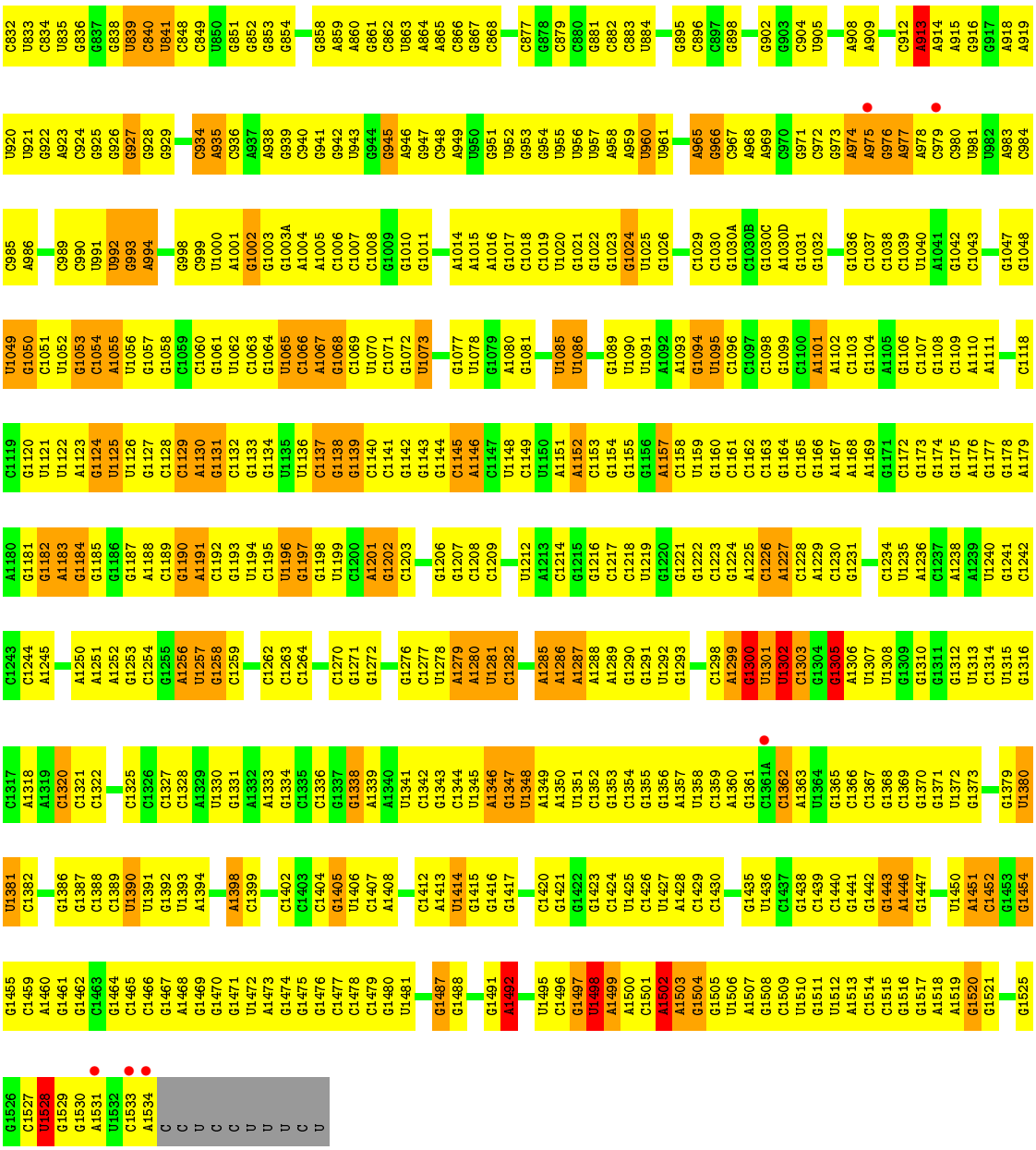
3 Residue-property plots (i)

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

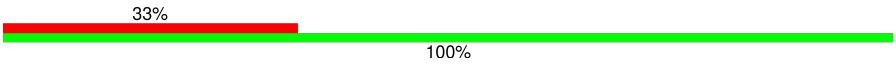
Chain A:





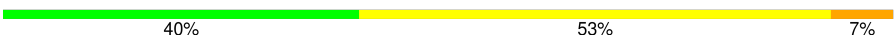
• Molecule 2: P-SITE MESSENGER RNA FRAGMENT

Chain X:



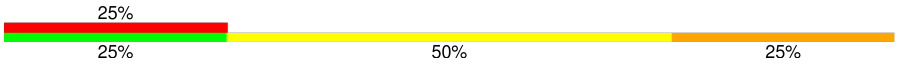
• Molecule 3: ANTICODON STEM-LOOP OF PHENYLALANINE TRANSFER RNA

Chain Y:



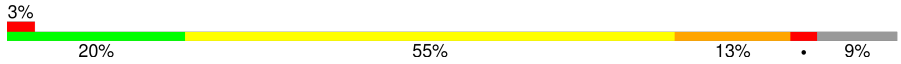
• Molecule 4: A-SITE MESSENGER RNA FRAGMENT

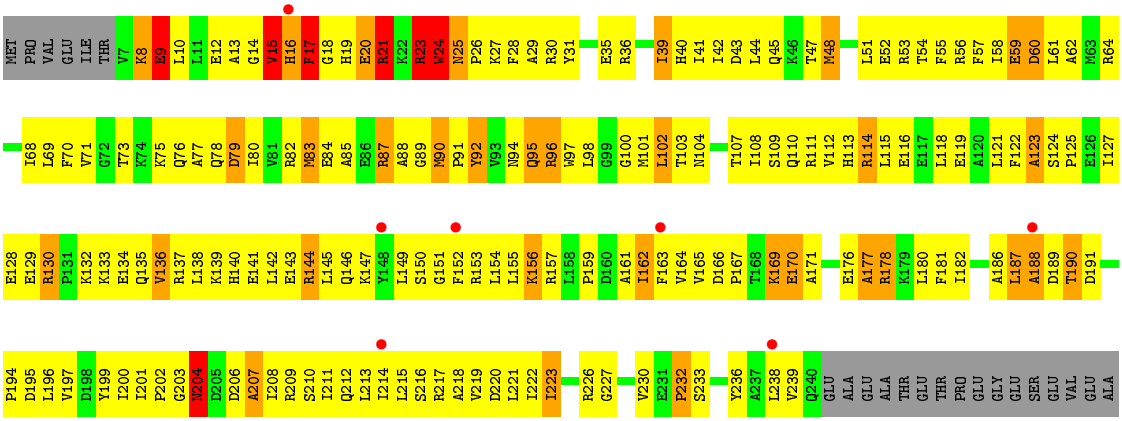
Chain Z:



- Molecule 5: 30S RIBOSOMAL PROTEIN S2

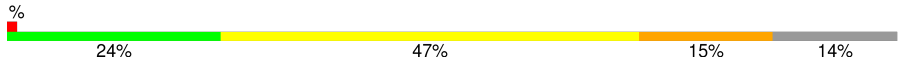
Chain B:

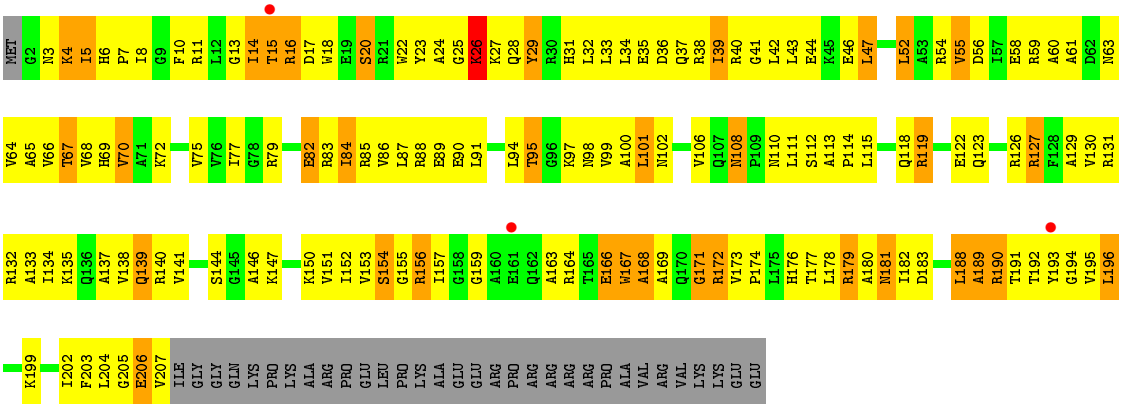




- Molecule 6: 30S RIBOSOMAL PROTEIN S3

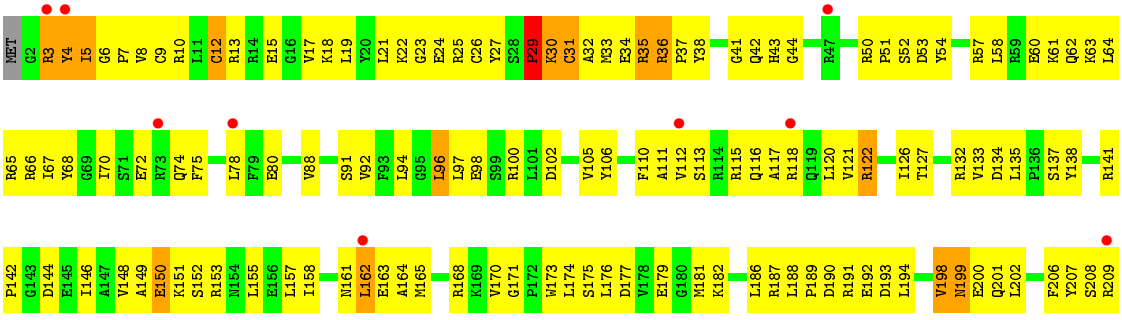
Chain C:





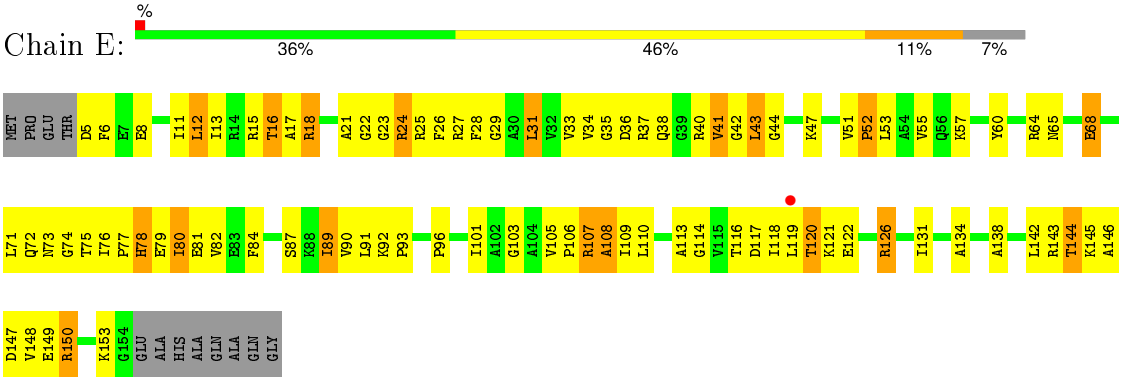
- Molecule 7: 30S RIBOSOMAL PROTEIN S4

Chain D:



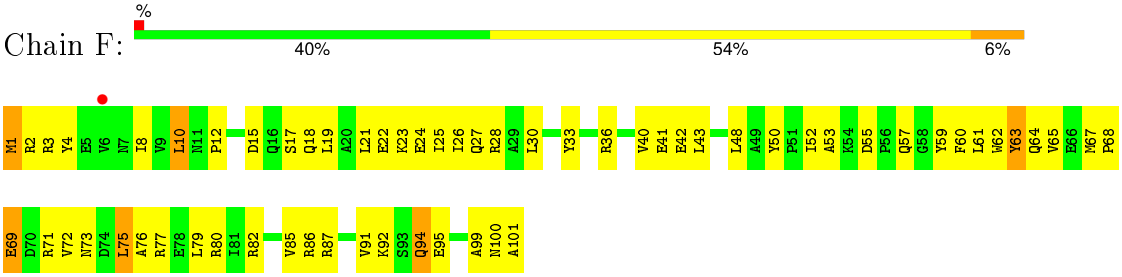
• Molecule 8: 30S RIBOSOMAL PROTEIN S5

Chain E:



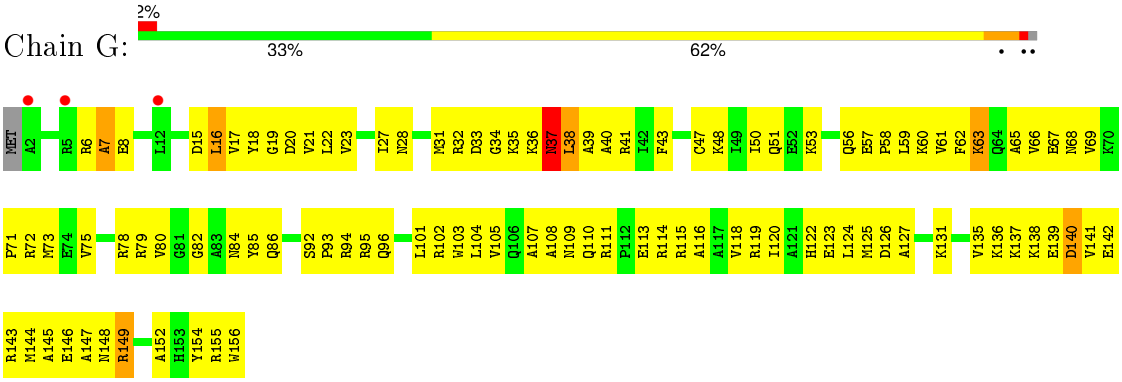
• Molecule 9: 30S RIBOSOMAL PROTEIN S6

Chain F:



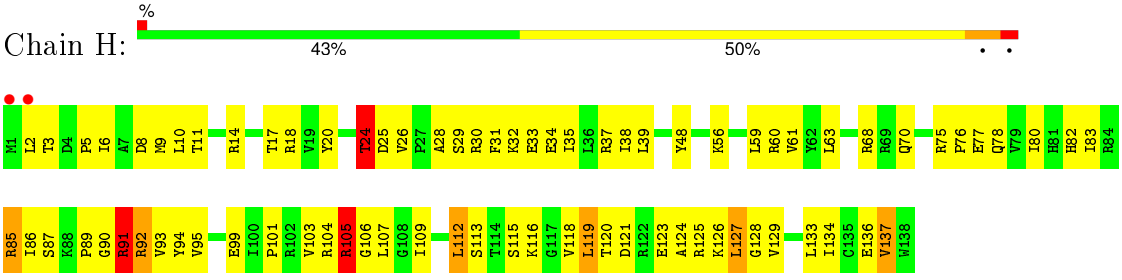
• Molecule 10: 30S RIBOSOMAL PROTEIN S7

Chain G:



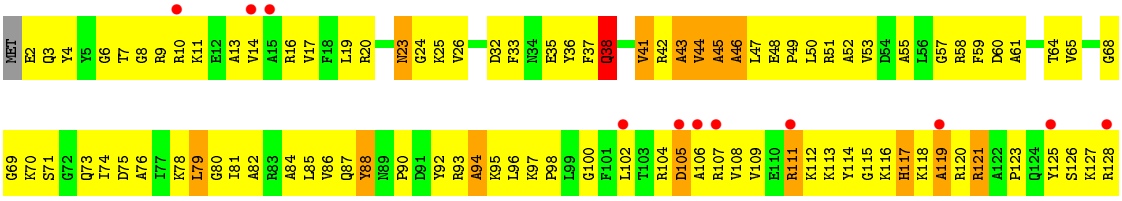
• Molecule 11: 30S RIBOSOMAL PROTEIN S8

Chain H:



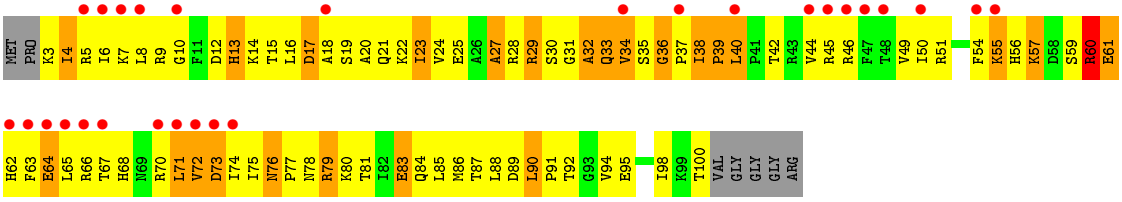
• Molecule 12: 30S RIBOSOMAL PROTEIN S9

Chain I:



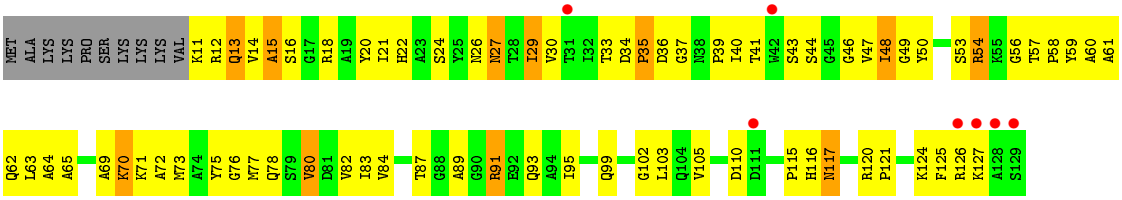
• Molecule 13: 30S RIBOSOMAL PROTEIN S10

Chain J:



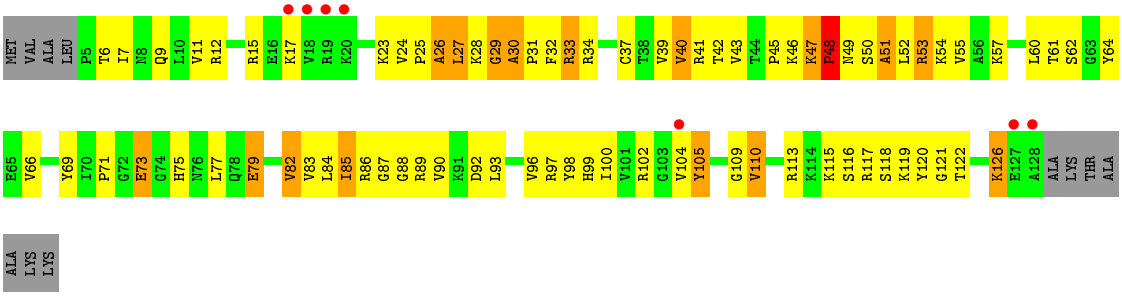
• Molecule 14: 30S RIBOSOMAL PROTEIN S11

Chain K:



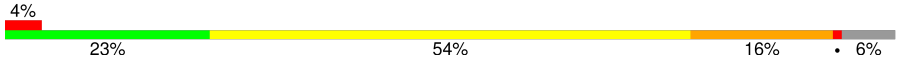
• Molecule 15: 30S RIBOSOMAL PROTEIN S12

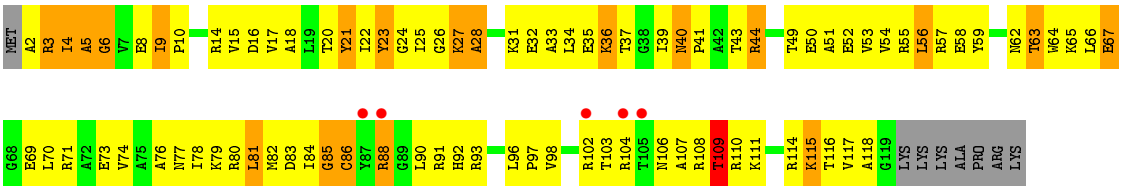
Chain L:



• Molecule 16: 30S RIBOSOMAL PROTEIN S13

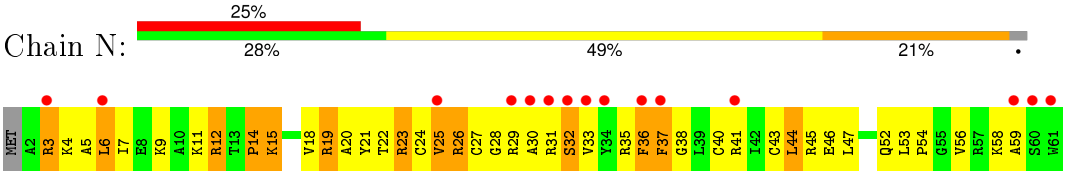
Chain M:





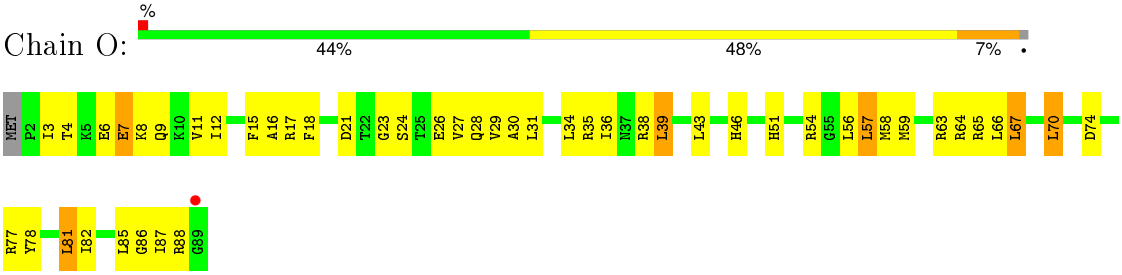
• Molecule 17: 30S RIBOSOMAL PROTEIN S14

Chain N:



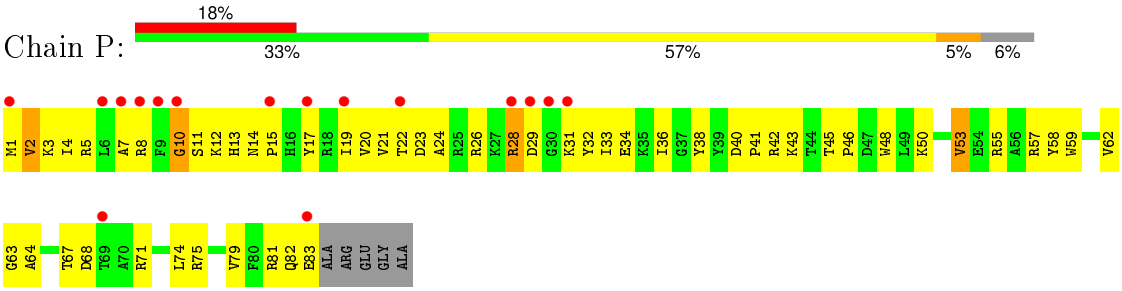
• Molecule 18: 30S RIBOSOMAL PROTEIN S15

Chain O:



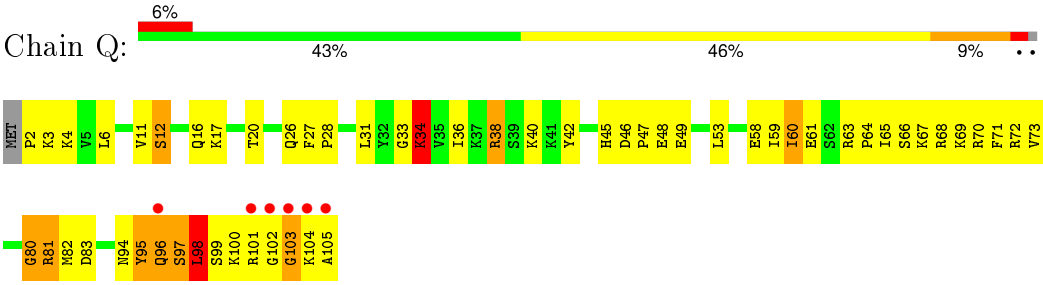
• Molecule 19: 30S RIBOSOMAL PROTEIN S16

Chain P:



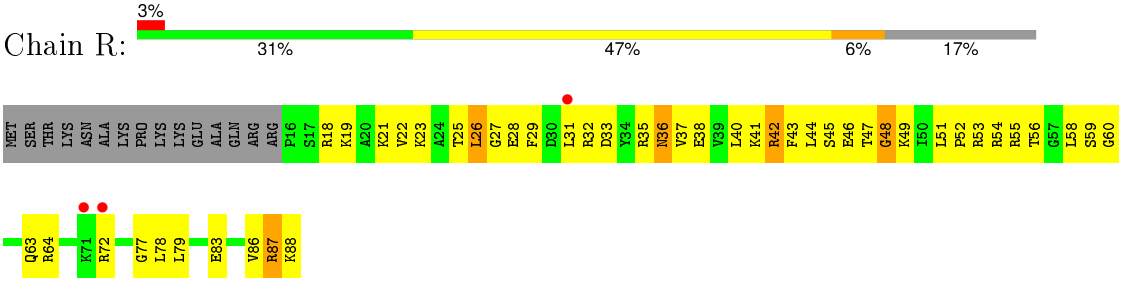
• Molecule 20: 30S RIBOSOMAL PROTEIN S17

Chain Q:



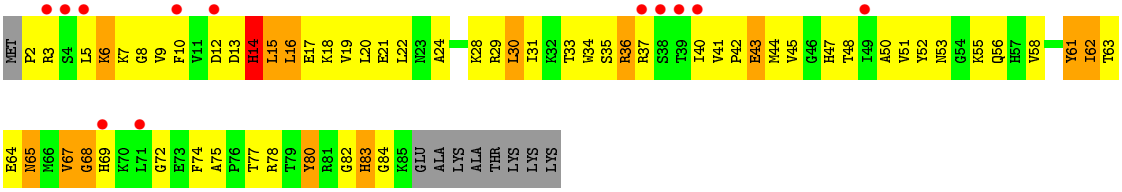
• Molecule 21: 30S RIBOSOMAL PROTEIN S18

Chain R:

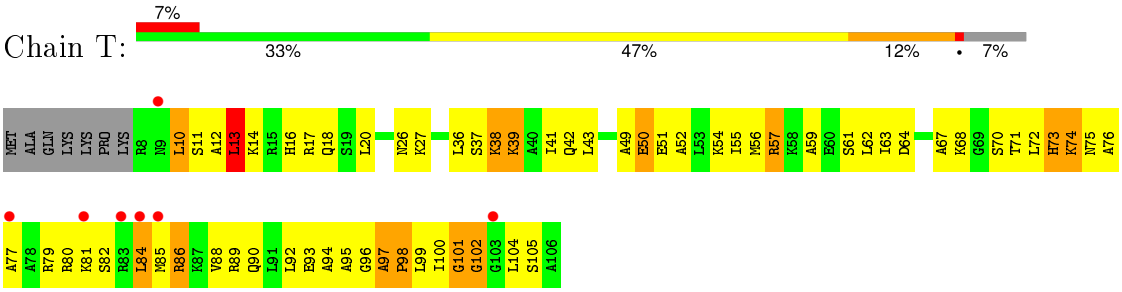


• Molecule 22: 30S RIBOSOMAL PROTEIN S19

Chain S:



- Molecule 23: 30S RIBOSOMAL PROTEIN S20



- Molecule 24: 30S RIBOSOMAL PROTEIN THX

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	400.80Å 400.80Å 175.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	316.23 – 3.11 200.40 – 3.11	Depositor EDS
% Data completeness (in resolution range)	89.9 (316.23-3.11) 89.8 (200.40-3.11)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	3.36 (at 3.13Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.232 , 0.275 0.212 , 0.248	Depositor DCC
R_{free} test set	11493 reflections (5.32%)	DCC
Wilson B-factor (Å^2)	72.7	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 83.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 227639 reflections	Xtriage
F_o,F_c correlation	0.84	EDS
Total number of atoms	52270	wwPDB-VP
Average B, all atoms (Å^2)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.48% 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, 0.375 respectively for untwinned datasets, and 0.333, 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

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	0.54	0/36259	0.74	34/56593 (0.1%)
2	X	0.45	0/128	0.64	0/196
3	Y	0.36	0/357	0.66	0/555
4	Z	0.42	0/84	0.81	0/128
5	B	0.33	0/1935	0.62	0/2609
6	C	0.36	0/1636	0.63	0/2205
7	D	0.47	2/1733 (0.1%)	0.65	1/2318 (0.0%)
8	E	0.47	0/1162	0.71	0/1564
9	F	0.31	0/856	0.62	0/1154
10	G	0.35	0/1276	0.59	0/1709
11	H	0.44	0/1136	0.77	0/1527
12	I	0.35	0/1029	0.64	0/1378
13	J	0.37	0/805	0.68	1/1082 (0.1%)
14	K	0.41	0/900	0.73	0/1213
15	L	0.47	0/986	0.80	2/1320 (0.2%)
16	M	0.34	0/947	0.64	0/1270
17	N	0.44	0/501	0.74	0/664
18	O	0.39	0/745	0.60	0/992
19	P	0.46	0/716	0.73	0/963
20	Q	0.48	0/870	0.74	0/1159
21	R	0.36	0/603	0.63	0/799
22	S	0.32	0/689	0.67	0/926
23	T	0.44	0/765	0.75	1/1007 (0.1%)
24	V	0.41	0/212	0.67	0/277
All	All	0.50	2/56330 (0.0%)	0.72	39/83608 (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	34

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	198	VAL	C-N	-8.29	1.15	1.34
7	D	200	GLU	C-N	5.60	1.47	1.34

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1498	U	C2'-C3'-O3'	10.07	131.65	109.50
1	A	243	A	C2'-C3'-O3'	9.49	130.37	109.50
1	A	281	G	C2'-C3'-O3'	9.34	130.05	109.50
1	A	484	G	C2'-C3'-O3'	8.78	128.82	109.50
1	A	1302	U	C2'-C3'-O3'	8.65	128.53	109.50
1	A	366	C	C2'-C3'-O3'	8.42	128.01	109.50
1	A	687	A	C2'-C3'-O3'	8.40	127.98	109.50
1	A	1528	U	C2'-C3'-O3'	8.08	127.28	109.50
1	A	965	A	C2'-C3'-O3'	7.49	125.97	109.50
1	A	181	G	C2'-C3'-O3'	7.46	125.91	109.50
1	A	328	C	C2'-C3'-O3'	7.37	125.71	109.50
1	A	372	C	C2'-C3'-O3'	7.29	125.55	109.50
1	A	1502	A	N9-C1'-C2'	7.17	123.32	114.00
1	A	1346	A	C2'-C3'-O3'	7.14	125.22	109.50
1	A	48	C	C2'-C3'-O3'	7.06	125.02	109.50
1	A	129(A)	G	C2'-C3'-O3'	6.73	124.47	113.70
1	A	353	A	C5'-C4'-O4'	-6.73	101.02	109.10
1	A	481	G	C5'-C4'-C3'	-6.71	105.26	116.00
1	A	60	A	C2'-C3'-O3'	6.58	124.23	113.70
1	A	197	A	C2'-C3'-O3'	6.48	124.07	113.70
1	A	1528	U	C4'-C3'-O3'	6.38	125.77	113.00
1	A	559	A	C2'-C3'-O3'	6.29	123.76	113.70
1	A	913	A	C2'-C3'-O3'	6.28	123.74	113.70
1	A	460	A	N9-C1'-C2'	6.21	122.07	114.00
1	A	1299	A	N9-C1'-C2'	6.09	121.92	114.00
1	A	1305	G	N9-C1'-C2'	5.88	121.65	114.00
7	D	12	CYS	CA-CB-SG	5.85	124.54	114.00
1	A	1225	A	N9-C1'-C2'	5.79	121.53	114.00
1	A	1380	U	C2'-C3'-O3'	5.57	122.61	113.70
1	A	63	C	C5'-C4'-C3'	-5.47	107.24	116.00
15	L	88	GLY	N-CA-C	-5.44	99.50	113.10
1	A	115	G	C2'-C3'-O3'	5.43	122.39	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	J	60	ARG	N-CA-C	5.41	125.60	111.00
15	L	26	ALA	N-CA-C	-5.40	96.42	111.00
23	T	13	LEU	N-CA-C	-5.14	97.12	111.00
1	A	115	G	N9-C1'-C2'	5.10	120.63	114.00
1	A	748	C	C2'-C3'-O3'	5.05	121.79	113.70
1	A	509	A	C2'-C3'-O3'	5.02	121.73	113.70
1	A	7	G	C2'-C3'-O3'	5.01	121.72	113.70

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	243	A	C3'
1	A	281	G	C3'
1	A	1528	U	C3'

All (34) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1073	U	Sidechain
1	A	1077	G	Sidechain
1	A	1185	G	Sidechain
1	A	1300	G	Sidechain
1	A	1341	U	Sidechain
1	A	1390	U	Sidechain
1	A	1405	G	Sidechain
1	A	1414	U	Sidechain
1	A	1454	G	Sidechain
1	A	1492	A	Sidechain
1	A	1519	A	Sidechain
1	A	19	C	Sidechain
1	A	190(L)	U	Sidechain
1	A	197	A	Sidechain
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	290	C	Sidechain
1	A	368	U	Sidechain
1	A	380	G	Sidechain
1	A	387	U	Sidechain
1	A	495	U	Sidechain
1	A	528	C	Sidechain
1	A	561	U	Sidechain
1	A	587	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	664	G	Sidechain
1	A	682	G	Sidechain
1	A	691	G	Sidechain
1	A	724	G	Sidechain
1	A	727	G	Sidechain
1	A	733	A	Sidechain
1	A	759	A	Sidechain
1	A	77	G	Sidechain
1	A	879	C	Sidechain
1	A	898	G	Sidechain

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32391	0	16349	1145	0
2	X	117	0	64	0	0
3	Y	319	0	164	12	0
4	Z	77	0	42	6	0
5	B	1900	0	1951	280	0
6	C	1612	0	1677	244	0
7	D	1703	0	1763	153	0
8	E	1146	0	1207	111	0
9	F	843	0	857	85	0
10	G	1257	0	1296	101	0
11	H	1116	0	1177	105	0
12	I	1011	0	1043	133	0
13	J	792	0	835	149	1
14	K	885	0	904	86	0
15	L	970	0	1057	126	0
16	M	937	0	995	130	0
17	N	492	0	529	79	0
18	O	734	0	771	53	0
19	P	700	0	720	57	0
20	Q	857	0	930	93	0
21	R	597	0	668	77	0
22	S	674	0	699	88	0
23	T	763	0	861	90	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	V	208	0	221	20	0
25	A	42	0	45	2	0
26	A	120	0	0	0	0
26	D	2	0	0	0	0
26	J	2	0	0	0	0
26	Y	1	0	0	0	0
27	D	1	0	0	0	0
27	N	1	0	0	0	0
All	All	52270	0	36825	3136	1

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 35.

All (3136) 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)
5:B:132:LYS:HA	5:B:135:GLN:HB3	1.20	1.14
7:D:36:ARG:H	7:D:37:PRO:HD3	1.09	1.13
1:A:975:A:H4'	1:A:976:G:H5"	1.25	1.12
1:A:1286:A:H3'	1:A:1287:A:H5"	1.28	1.12
8:E:80:ILE:HD11	8:E:91:LEU:HB2	1.31	1.11
5:B:84:GLU:HB3	5:B:219:VAL:HG21	1.24	1.11
1:A:1443:G:H5"	1:A:1446:A:H5'	1.20	1.10
8:E:80:ILE:CD1	8:E:91:LEU:HB2	1.81	1.09
14:K:48:ILE:HG22	14:K:49:GLY:H	0.99	1.08
6:C:33:LEU:HD11	17:N:53:LEU:HD22	1.33	1.08
17:N:26:ARG:HH12	17:N:47:LEU:HD21	1.15	1.06
5:B:21:ARG:HD3	5:B:21:ARG:H	1.17	1.05
22:S:33:THR:HG22	22:S:35:SER:H	1.18	1.04
15:L:47:LYS:HB3	15:L:48:PRO:HD3	1.37	1.04
7:D:151:LYS:H	7:D:151:LYS:HD2	1.16	1.04
5:B:77:ALA:HB2	5:B:211:ILE:HD13	1.40	1.04
1:A:1250:A:H4'	12:I:68:GLY:H	1.19	1.03
1:A:1286:A:C3'	1:A:1287:A:H5"	1.88	1.02
1:A:877:C:O2	11:H:3:THR:HG21	1.60	1.02
15:L:27:LEU:HD23	15:L:62:SER:HB2	1.43	1.00
22:S:28:LYS:HG2	22:S:29:ARG:H	1.22	1.00
1:A:1190:G:H3'	6:C:3:ASN:HD22	1.27	1.00
11:H:86:ILE:HD11	11:H:136:GLU:HG3	1.42	0.99
5:B:80:ILE:H	5:B:80:ILE:HD12	1.27	0.99
13:J:32:ALA:HB2	13:J:76:ASN:HD22	1.27	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:G:O2'	1:A:372:C:H5'	1.63	0.98
8:E:81:GLU:HG2	8:E:90:VAL:HG22	1.44	0.97
6:C:108:ASN:HD22	6:C:111:LEU:HG	1.30	0.96
10:G:50:ILE:HG21	10:G:61:VAL:HG21	1.47	0.96
1:A:1056:U:H5'	6:C:163:ALA:HB2	1.48	0.95
16:M:10:PRO:HB2	16:M:18:ALA:HB1	1.47	0.95
14:K:54:ARG:O	14:K:57:THR:HG22	1.65	0.95
10:G:75:VAL:HG21	10:G:86:GLN:HB3	1.45	0.95
1:A:243:A:H4'	1:A:244:U:H5'	1.48	0.95
6:C:14:ILE:HG22	6:C:15:THR:H	1.28	0.94
1:A:1086:U:H3	1:A:1099:G:H22	1.07	0.94
14:K:48:ILE:HG22	14:K:49:GLY:N	1.81	0.94
20:Q:67:LYS:HA	20:Q:70:ARG:HH12	1.31	0.94
1:A:737:A:H1'	9:F:73:ASN:HD21	1.31	0.94
1:A:1057:G:H5"	6:C:154:SER:HB2	1.52	0.92
9:F:100:ASN:HD22	21:R:23:LYS:HG2	1.35	0.92
1:A:1502:A:H2	1:A:1505:G:H1	1.03	0.91
1:A:1305:G:O2'	1:A:1306:A:H8	1.52	0.91
1:A:1190:G:H3'	6:C:3:ASN:ND2	1.85	0.91
8:E:11:ILE:HB	8:E:31:LEU:HB3	1.53	0.91
5:B:77:ALA:HA	5:B:80:ILE:HD13	1.52	0.90
1:A:975:A:H5'	1:A:975:A:H8	1.34	0.90
1:A:579:G:H5'	1:A:728:A:H1'	1.53	0.90
1:A:975:A:H4'	1:A:976:G:C5'	2.00	0.90
15:L:25:PRO:C	15:L:27:LEU:H	1.67	0.90
5:B:59:GLU:HG2	5:B:221:LEU:HD11	1.53	0.90
6:C:58:GLU:HB3	13:J:92:THR:HG21	1.52	0.90
10:G:16:LEU:H	10:G:16:LEU:HD22	1.36	0.89
15:L:28:LYS:C	15:L:30:ALA:H	1.76	0.89
8:E:76:ILE:HG13	8:E:77:PRO:HD2	1.55	0.89
18:O:70:LEU:HD13	18:O:78:TYR:HA	1.55	0.89
9:F:2:ARG:HE	9:F:69:GLU:HG2	1.38	0.89
1:A:1190:G:OP1	6:C:4:LYS:HA	1.71	0.89
6:C:174:PRO:HB2	6:C:177:THR:HG22	1.55	0.89
14:K:91:ARG:HH11	21:R:88:LYS:HZ1	1.21	0.88
18:O:16:ALA:HB1	18:O:21:ASP:HB3	1.52	0.88
1:A:390:C:H2'	1:A:391:G:H8	1.36	0.88
5:B:219:VAL:O	5:B:223:ILE:HG12	1.73	0.87
1:A:1504:G:OP1	1:A:1507:A:H4'	1.74	0.87
1:A:664:G:H22	1:A:741:G:H1	1.22	0.87
15:L:24:VAL:HG12	15:L:24:VAL:O	1.74	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:8:LEU:HD22	13:J:20:ALA:HB2	1.54	0.87
6:C:191:THR:HG21	6:C:193:TYR:CZ	2.10	0.87
1:A:390:C:H2'	1:A:391:G:C8	2.10	0.87
7:D:62:GLN:HE22	7:D:65:ARG:HH12	1.22	0.87
1:A:1250:A:H4'	12:I:68:GLY:N	1.90	0.87
5:B:71:VAL:HG23	5:B:164:VAL:HA	1.54	0.87
15:L:47:LYS:HB3	15:L:48:PRO:CD	2.04	0.86
9:F:28:ARG:NH1	9:F:28:ARG:HB2	1.91	0.86
14:K:48:ILE:CG2	14:K:49:GLY:H	1.85	0.85
17:N:27:CYS:SG	17:N:29:ARG:HB2	2.15	0.85
1:A:1256:A:H4'	1:A:1257:U:H5'	1.57	0.85
21:R:47:THR:HG23	21:R:83:GLU:H	1.40	0.85
15:L:60:LEU:HD21	15:L:66:VAL:HG22	1.58	0.85
6:C:26:LYS:H	6:C:26:LYS:HD3	1.40	0.85
5:B:69:LEU:HD23	5:B:70:PHE:N	1.91	0.85
14:K:40:ILE:HG22	14:K:41:THR:HG23	1.59	0.85
10:G:51:GLN:HE21	10:G:58:PRO:HD3	1.42	0.85
1:A:250:A:H4'	1:A:251:G:O5'	1.77	0.85
23:T:43:LEU:HD13	23:T:51:GLU:HG3	1.59	0.85
13:J:34:VAL:HA	13:J:74:ILE:HG22	1.59	0.84
6:C:119:ARG:HG2	6:C:140:ARG:NH1	1.92	0.84
7:D:36:ARG:N	7:D:37:PRO:HD3	1.88	0.84
8:E:76:ILE:HD11	8:E:142:LEU:HD13	1.59	0.84
1:A:1286:A:H3'	1:A:1287:A:C5'	2.06	0.84
17:N:6:LEU:HD22	17:N:23:ARG:NH2	1.92	0.84
8:E:79:GLU:HG3	8:E:93:PRO:HD2	1.59	0.84
13:J:23:ILE:H	13:J:23:ILE:HD12	1.43	0.84
14:K:91:ARG:HH11	21:R:88:LYS:NZ	1.76	0.84
5:B:144:ARG:HD2	5:B:145:LEU:HD23	1.60	0.84
15:L:28:LYS:O	15:L:30:ALA:N	2.09	0.84
15:L:47:LYS:CB	15:L:48:PRO:HD3	2.08	0.83
15:L:126:LYS:HD2	15:L:126:LYS:H	1.43	0.83
21:R:47:THR:HA	21:R:83:GLU:HB2	1.60	0.83
1:A:1226:C:H4'	1:A:1227:A:OP1	1.77	0.83
22:S:20:LEU:HD12	22:S:21:GLU:N	1.94	0.83
13:J:6:ILE:HG22	13:J:98:ILE:HG12	1.61	0.82
1:A:1015:A:H2'	1:A:1016:A:C8	2.14	0.82
5:B:80:ILE:HG12	5:B:208:ILE:HG23	1.60	0.82
1:A:254:G:H21	20:Q:16:GLN:HE21	1.24	0.82
1:A:1168:A:H2'	1:A:1169:A:C8	2.14	0.82
16:M:14:ARG:N	16:M:44:ARG:HH21	1.77	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:74:GLY:HA3	8:E:116:THR:HG22	1.62	0.82
5:B:139:LYS:O	5:B:143:GLU:HG2	1.80	0.82
6:C:34:LEU:HD23	6:C:34:LEU:C	2.00	0.82
1:A:1152:A:H2'	1:A:1153:C:C6	2.14	0.81
5:B:88:ALA:HB2	5:B:219:VAL:HG13	1.62	0.81
11:H:120:THR:OG1	11:H:123:GLU:HG3	1.80	0.81
10:G:15:ASP:HB3	10:G:19:GLY:N	1.95	0.81
16:M:14:ARG:H	16:M:44:ARG:HH21	1.28	0.81
15:L:25:PRO:C	15:L:27:LEU:N	2.32	0.80
13:J:49:VAL:O	13:J:60:ARG:HA	1.82	0.80
1:A:1502:A:H2	1:A:1505:G:N1	1.78	0.80
1:A:1279:A:H5"	1:A:1280:A:OP1	1.81	0.80
5:B:116:GLU:HG2	5:B:153:ARG:NH2	1.97	0.80
6:C:190:ARG:HB3	6:C:190:ARG:HH11	1.47	0.80
1:A:1250:A:C4'	12:I:68:GLY:H	1.93	0.80
9:F:33:TYR:HA	9:F:71:ARG:NH2	1.95	0.80
12:I:46:ALA:HB2	12:I:74:ILE:HG23	1.63	0.80
6:C:64:VAL:HB	6:C:99:VAL:HB	1.64	0.80
9:F:4:TYR:CZ	9:F:72:VAL:HG21	2.16	0.80
6:C:180:ALA:O	6:C:181:ASN:HB3	1.82	0.80
1:A:524:G:H2'	1:A:525:C:C6	2.17	0.80
5:B:71:VAL:HG21	5:B:164:VAL:HG22	1.64	0.80
14:K:18:ARG:HB2	14:K:33:THR:CG2	2.12	0.80
18:O:17:ARG:HH11	18:O:17:ARG:HG3	1.46	0.79
1:A:1443:G:H5"	1:A:1446:A:C5'	2.09	0.79
5:B:218:ALA:O	5:B:222:ILE:HG13	1.82	0.79
1:A:972:C:H4'	13:J:57:LYS:HG2	1.63	0.79
12:I:81:ILE:O	12:I:85:LEU:HB2	1.82	0.79
1:A:1003(A):G:H2'	1:A:1004:A:H4'	1.63	0.79
8:E:80:ILE:H	8:E:80:ILE:HD12	1.46	0.79
1:A:1151:A:HO2'	1:A:1152:A:H8	1.29	0.79
12:I:8:GLY:HA2	12:I:79:LEU:HD13	1.64	0.79
18:O:3:ILE:HD11	18:O:38:ARG:HG3	1.65	0.79
17:N:26:ARG:NH1	17:N:47:LEU:HD21	1.96	0.79
18:O:29:VAL:HG11	18:O:67:LEU:HD21	1.63	0.79
13:J:20:ALA:HA	13:J:23:ILE:HD13	1.63	0.79
16:M:78:ILE:HA	16:M:81:LEU:HD21	1.65	0.79
1:A:80:G:H3'	1:A:81:U:H5"	1.65	0.79
13:J:31:GLY:HA2	13:J:78:ASN:ND2	1.98	0.78
5:B:91:PRO:HB3	5:B:154:LEU:HB2	1.64	0.78
1:A:975:A:H5'	1:A:975:A:C8	2.17	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:118:LEU:HB3	5:B:142:LEU:HD12	1.64	0.78
6:C:14:ILE:O	6:C:16:ARG:N	2.16	0.78
12:I:26:VAL:HB	12:I:33:PHE:HB2	1.65	0.78
12:I:86:VAL:HG13	12:I:90:PRO:HA	1.66	0.78
12:I:106:ALA:O	12:I:108:VAL:HG23	1.83	0.78
5:B:57:PHE:CE2	5:B:61:LEU:HD11	2.17	0.78
16:M:4:ILE:HG22	16:M:5:ALA:N	1.99	0.78
1:A:1124:G:H5'	13:J:35:SER:O	1.83	0.78
1:A:853:G:O2'	1:A:854:G:H5'	1.83	0.78
1:A:1305:G:HO2'	1:A:1306:A:H8	1.19	0.78
9:F:28:ARG:HB2	9:F:28:ARG:HH11	1.49	0.78
23:T:56:MET:HE1	23:T:85:MET:HA	1.65	0.78
6:C:108:ASN:HD21	6:C:110:ASN:HB2	1.47	0.78
1:A:1226:C:H1'	22:S:83:HIS:HE1	1.49	0.78
5:B:57:PHE:O	5:B:61:LEU:HG	1.84	0.77
16:M:8:GLU:O	16:M:9:ILE:HG23	1.83	0.77
13:J:18:ALA:O	13:J:21:GLN:HB3	1.83	0.77
1:A:1201:A:H4'	1:A:1202:G:O5'	1.84	0.77
1:A:127:G:HO2'	20:Q:2:PRO:N	1.83	0.77
5:B:142:LEU:HD21	5:B:146:GLN:HE21	1.49	0.77
1:A:838:G:H2'	1:A:839:U:H5"	1.65	0.77
1:A:1238:A:H5'	1:A:1336:C:H41	1.48	0.77
15:L:34:ARG:O	15:L:61:THR:HG23	1.83	0.77
1:A:1369:C:H2'	1:A:1370:G:C8	2.19	0.77
1:A:1038:C:H2'	1:A:1039:C:C6	2.19	0.77
7:D:7:PRO:HB2	7:D:10:ARG:HD2	1.67	0.77
1:A:1196:U:H5"	1:A:1197:G:H5'	1.67	0.77
1:A:443:C:H2'	1:A:444:C:H6	1.50	0.77
16:M:62:ASN:O	16:M:63:THR:HB	1.82	0.77
1:A:1286:A:C2'	1:A:1287:A:H5"	2.14	0.77
13:J:8:LEU:HB2	13:J:70:ARG:HB2	1.67	0.77
13:J:31:GLY:HA2	13:J:78:ASN:HD22	1.50	0.77
1:A:1003(A):G:H2'	1:A:1004:A:C4'	2.15	0.76
23:T:13:LEU:HD12	23:T:13:LEU:H	1.51	0.76
9:F:2:ARG:HE	9:F:69:GLU:CG	1.98	0.76
1:A:328:C:O2	1:A:328:C:H2'	1.83	0.76
5:B:124:SER:HB2	5:B:125:PRO:HD2	1.66	0.76
5:B:123:ALA:N	5:B:127:ILE:HD11	2.01	0.76
1:A:371:G:C2'	1:A:372:C:H5'	2.14	0.76
1:A:1137:C:H4'	1:A:1138:G:C2	2.20	0.76
1:A:1443:G:C5'	1:A:1446:A:H5'	2.10	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:49:THR:HB	16:M:52:GLU:HG3	1.65	0.76
1:A:839:U:H5'	1:A:840:C:H5	1.49	0.76
8:E:51:VAL:HB	8:E:52:PRO:HD3	1.65	0.76
5:B:15:VAL:HG11	5:B:209:ARG:HB3	1.68	0.76
1:A:1278:U:H4'	1:A:1279:A:C5'	2.16	0.76
16:M:33:ALA:HA	16:M:59:TYR:CE2	2.20	0.76
1:A:8:A:H62	7:D:208:SER:HB2	1.51	0.76
20:Q:101:ARG:HE	20:Q:101:ARG:HA	1.51	0.76
18:O:39:LEU:HD13	18:O:56:LEU:HB2	1.68	0.76
16:M:108:ARG:HD3	16:M:114:ARG:NH1	2.00	0.76
11:H:24:THR:HG22	11:H:63:LEU:HD21	1.65	0.76
6:C:112:SER:HB3	6:C:115:LEU:HD12	1.69	0.75
1:A:1352:C:H2'	1:A:1353:G:C8	2.21	0.75
11:H:86:ILE:HG21	11:H:133:LEU:HD22	1.68	0.75
13:J:30:SER:HB3	13:J:84:GLN:NE2	2.00	0.75
1:A:1425:U:H2'	1:A:1426:C:C6	2.21	0.75
15:L:89:ARG:HG2	15:L:97:ARG:HA	1.67	0.75
1:A:254:G:OP1	20:Q:67:LYS:O	2.04	0.75
10:G:15:ASP:HB3	10:G:19:GLY:H	1.51	0.75
12:I:65:VAL:HG21	12:I:73:GLN:HB3	1.68	0.75
1:A:946:A:H2'	1:A:947:G:C8	2.22	0.75
5:B:21:ARG:HD3	5:B:21:ARG:N	2.00	0.75
5:B:25:ASN:ND2	5:B:27:LYS:H	1.83	0.75
6:C:191:THR:HG22	6:C:192:THR:N	2.01	0.75
6:C:15:THR:HB	6:C:181:ASN:HB2	1.69	0.75
7:D:111:ALA:HA	7:D:161:ASN:ND2	2.01	0.75
23:T:50:GLU:O	23:T:100:ILE:HD12	1.87	0.74
14:K:99:GLN:HG2	14:K:105:VAL:HG21	1.67	0.74
19:P:22:THR:HA	19:P:33:ILE:HG13	1.69	0.74
22:S:64:GLU:O	22:S:67:VAL:HG23	1.87	0.74
1:A:722:A:H4'	1:A:723:U:C5	2.21	0.74
16:M:33:ALA:HA	16:M:59:TYR:HE2	1.53	0.74
15:L:89:ARG:NH2	15:L:97:ARG:HE	1.85	0.74
1:A:1133:G:H2'	1:A:1134:G:H8	1.52	0.74
11:H:127:LEU:N	11:H:127:LEU:HD23	2.01	0.74
1:A:975:A:C4'	1:A:976:G:H5"	2.13	0.74
14:K:18:ARG:HB2	14:K:33:THR:HG22	1.69	0.74
1:A:112:G:H21	1:A:354:G:H5'	1.52	0.74
21:R:55:ARG:HB3	21:R:55:ARG:NH1	2.02	0.74
9:F:2:ARG:NE	9:F:69:GLU:HG2	2.02	0.74
5:B:197:VAL:HB	5:B:200:ILE:HG12	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:954:G:H2'	1:A:955:U:C6	2.23	0.74
1:A:1127:G:H21	1:A:1146:A:H62	1.33	0.74
8:E:105:VAL:HB	8:E:106:PRO:HD3	1.70	0.74
1:A:1355:G:H2'	1:A:1356:G:C8	2.23	0.74
11:H:103:VAL:HG21	11:H:109:ILE:O	1.88	0.74
1:A:761:G:H5"	20:Q:102:GLY:HA3	1.69	0.74
1:A:1191:A:P	6:C:3:ASN:HD21	2.10	0.74
5:B:16:HIS:HA	5:B:204:ASN:CB	2.18	0.74
18:O:78:TYR:CZ	18:O:82:ILE:HD11	2.22	0.74
1:A:1056:U:H5'	6:C:163:ALA:CB	2.17	0.73
1:A:1435:G:H2'	1:A:1436:U:C6	2.22	0.73
9:F:10:LEU:HD12	9:F:59:TYR:HB3	1.68	0.73
17:N:6:LEU:HD22	17:N:23:ARG:HH21	1.52	0.73
18:O:29:VAL:HG21	18:O:67:LEU:HD23	1.70	0.73
12:I:49:PRO:O	12:I:52:ALA:HB3	1.88	0.73
16:M:36:LYS:HD3	16:M:59:TYR:OH	1.89	0.73
22:S:45:VAL:HA	22:S:62:ILE:HG13	1.70	0.73
9:F:36:ARG:O	9:F:65:VAL:HB	1.88	0.73
5:B:84:GLU:OE1	5:B:216:SER:HA	1.87	0.73
1:A:1132:C:H2'	1:A:1133:G:H8	1.52	0.73
8:E:144:THR:HB	8:E:147:ASP:OD2	1.88	0.73
6:C:10:PHE:CE2	6:C:178:LEU:HD13	2.23	0.73
17:N:22:THR:HB	17:N:33:VAL:HG21	1.69	0.73
8:E:16:THR:HG22	8:E:27:ARG:HB3	1.70	0.73
20:Q:27:PHE:HB2	20:Q:28:PRO:HD2	1.69	0.73
8:E:11:ILE:HG22	8:E:12:LEU:HD12	1.70	0.72
1:A:750:G:N3	18:O:23:GLY:HA3	2.04	0.72
5:B:84:GLU:HB3	5:B:219:VAL:CG2	2.13	0.72
11:H:60:ARG:HG3	11:H:60:ARG:HH11	1.53	0.72
1:A:1125:U:H5"	1:A:1126:U:H5	1.53	0.72
1:A:840:C:H5"	1:A:841:U:OP1	1.89	0.72
5:B:92:TYR:CE2	5:B:151:GLY:HA3	2.24	0.72
1:A:677:U:H3	1:A:713:G:H22	1.37	0.72
11:H:82:HIS:HD2	11:H:83:ILE:N	1.88	0.72
1:A:1054:C:H3'	1:A:1054:C:O2	1.88	0.72
6:C:35:GLU:CD	6:C:59:ARG:HH22	1.93	0.72
21:R:86:VAL:HG12	21:R:87:ARG:H	1.54	0.72
5:B:71:VAL:O	5:B:165:VAL:HG23	1.89	0.72
1:A:438:G:H4'	1:A:439:A:OP1	1.88	0.72
5:B:141:GLU:O	5:B:145:LEU:HG	1.89	0.71
10:G:50:ILE:CG2	10:G:61:VAL:HG21	2.19	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:25:ASN:HD22	5:B:27:LYS:H	1.37	0.71
1:A:1086:U:H3	1:A:1099:G:N2	1.86	0.71
1:A:1355:G:H2'	1:A:1356:G:H8	1.54	0.71
1:A:35:G:H2'	1:A:36:C:C6	2.25	0.71
6:C:52:LEU:H	6:C:52:LEU:HD23	1.54	0.71
1:A:989:C:O2'	1:A:990:C:H5'	1.90	0.71
12:I:6:GLY:N	12:I:84:ALA:HB2	2.04	0.71
7:D:98:GLU:HG2	7:D:189:PRO:HG3	1.72	0.71
6:C:115:LEU:HD23	6:C:118:GLN:OE1	1.91	0.71
1:A:501:C:H2'	1:A:502:G:H8	1.55	0.71
16:M:34:LEU:HD13	16:M:41:PRO:HA	1.72	0.71
1:A:113:G:H1'	1:A:354:G:H5'	1.73	0.71
1:A:115:G:H1'	1:A:116:A:N7	2.05	0.71
7:D:36:ARG:H	7:D:37:PRO:CD	1.98	0.71
1:A:1190:G:C3'	6:C:3:ASN:ND2	2.53	0.71
1:A:1057:G:H5"	6:C:154:SER:CB	2.21	0.71
1:A:839:U:H5'	1:A:840:C:C5	2.26	0.71
1:A:1370:G:O2'	1:A:1371:G:H5'	1.91	0.71
14:K:54:ARG:H	14:K:54:ARG:HD3	1.54	0.71
6:C:171:GLY:O	6:C:173:VAL:HG23	1.91	0.71
7:D:62:GLN:HE22	7:D:65:ARG:NH1	1.89	0.71
19:P:58:TYR:O	19:P:62:VAL:HG23	1.90	0.71
7:D:57:ARG:HG3	7:D:57:ARG:HH11	1.55	0.71
1:A:1125:U:H3	13:J:5:ARG:HH21	1.38	0.71
6:C:6:HIS:HD2	6:C:8:ILE:H	1.36	0.71
1:A:1441:G:H4'	1:A:1442:G:C5	2.26	0.71
17:N:36:PHE:O	17:N:36:PHE:HD1	1.74	0.71
13:J:34:VAL:HG12	13:J:35:SER:H	1.56	0.71
17:N:27:CYS:SG	17:N:29:ARG:CB	2.79	0.71
5:B:69:LEU:HD12	5:B:155:LEU:HD11	1.73	0.71
1:A:1039:C:H2'	1:A:1040:U:C6	2.26	0.71
1:A:1139:G:H4'	1:A:1140:C:H5'	1.72	0.71
1:A:673:G:H2'	1:A:674:G:C8	2.26	0.71
1:A:265:G:H2'	1:A:267:C:H5	1.55	0.70
6:C:119:ARG:HG2	6:C:140:ARG:HH12	1.56	0.70
13:J:35:SER:HB2	13:J:72:VAL:O	1.90	0.70
12:I:93:ARG:HD3	12:I:97:LYS:NZ	2.06	0.70
1:A:1250:A:H5"	12:I:68:GLY:N	2.06	0.70
1:A:112:G:N2	1:A:354:G:H5'	2.07	0.70
22:S:28:LYS:HG2	22:S:29:ARG:N	2.03	0.70
8:E:76:ILE:HD11	8:E:142:LEU:CD1	2.22	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:118:LYS:HB2	12:I:118:LYS:HZ2	1.55	0.70
8:E:41:VAL:HG13	8:E:113:ALA:HA	1.73	0.70
5:B:95:GLN:O	5:B:96:ARG:HD2	1.90	0.70
1:A:1128:C:H4'	12:I:16:ARG:HH12	1.57	0.70
1:A:1300:G:HO2'	1:A:1301:U:H6	1.37	0.70
6:C:14:ILE:HG22	6:C:15:THR:N	2.07	0.70
1:A:328:C:H4'	1:A:329:A:H5'	1.74	0.70
5:B:133:LYS:O	5:B:137:ARG:HG3	1.92	0.70
5:B:82:ARG:HA	5:B:92:TYR:CD1	2.27	0.70
1:A:382:A:H2'	1:A:383:A:C8	2.26	0.70
5:B:55:PHE:HA	5:B:58:ILE:HD12	1.74	0.69
7:D:8:VAL:HG21	7:D:115:ARG:NH1	2.07	0.69
1:A:384:G:H2'	1:A:385:C:H6	1.56	0.69
1:A:420:U:H2'	1:A:422:C:C5	2.27	0.69
1:A:530:G:O6	4:Z:3:U:H1'	1.92	0.69
1:A:1038:C:H2'	1:A:1039:C:H6	1.57	0.69
1:A:912:C:O2'	1:A:913:A:H5'	1.92	0.69
1:A:202:U:H5"	1:A:203:U:OP2	1.92	0.69
1:A:1226:C:H1'	22:S:83:HIS:CE1	2.27	0.69
1:A:1372:U:O2'	1:A:1373:G:H5'	1.92	0.69
10:G:23:VAL:O	10:G:27:ILE:HG13	1.92	0.69
13:J:19:SER:HA	13:J:22:LYS:NZ	2.07	0.69
13:J:25:GLU:HA	13:J:28:ARG:HB2	1.74	0.69
6:C:6:HIS:CD2	6:C:8:ILE:H	2.08	0.69
1:A:1356:G:H2'	1:A:1357:A:C8	2.28	0.69
11:H:9:MET:HE2	11:H:32:LYS:HG2	1.74	0.69
8:E:80:ILE:N	8:E:80:ILE:HD12	2.07	0.69
23:T:54:LYS:HE3	23:T:100:ILE:CD1	2.21	0.69
16:M:50:GLU:O	16:M:54:VAL:HG23	1.92	0.69
1:A:706:A:O4'	14:K:29:ILE:HD11	1.92	0.69
5:B:219:VAL:HA	5:B:222:ILE:HD12	1.73	0.69
15:L:27:LEU:HD12	15:L:28:LYS:H	1.58	0.69
21:R:86:VAL:HG12	21:R:87:ARG:N	2.08	0.69
17:N:24:CYS:HB3	17:N:28:GLY:H	1.56	0.69
14:K:44:SER:H	14:K:47:VAL:HB	1.58	0.69
1:A:1222:G:OP1	22:S:77:THR:HG21	1.93	0.69
1:A:1287:A:H2'	1:A:1288:A:C8	2.28	0.69
14:K:48:ILE:HD13	14:K:63:LEU:HB3	1.74	0.69
1:A:1108:G:H5'	1:A:1191:A:H4'	1.75	0.69
1:A:1052:U:H2'	1:A:1055:A:OP1	1.93	0.69
14:K:84:VAL:HG11	14:K:91:ARG:HD3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1152:A:H5"	13:J:13:HIS:CD2	2.27	0.69
1:A:1330:U:OP1	16:M:23:TYR:O	2.11	0.69
21:R:37:VAL:O	21:R:41:LYS:HG3	1.93	0.69
1:A:434:U:H2'	1:A:435:C:C6	2.28	0.69
1:A:478:A:O2'	1:A:479:C:H5'	1.92	0.69
7:D:111:ALA:HB1	7:D:116:GLN:OE1	1.92	0.69
18:O:6:GLU:CD	18:O:6:GLU:H	1.95	0.69
1:A:1251:A:H2'	1:A:1252:A:C8	2.28	0.68
13:J:30:SER:OG	13:J:81:THR:HA	1.94	0.68
5:B:92:TYR:CD2	5:B:151:GLY:HA3	2.28	0.68
1:A:881:G:P	15:L:12:ARG:HH22	2.15	0.68
1:A:952:U:O4	16:M:104:ARG:HD3	1.94	0.68
21:R:55:ARG:HB3	21:R:55:ARG:HH11	1.58	0.68
5:B:114:ARG:HH11	5:B:118:LEU:HG	1.58	0.68
7:D:29:PRO:HA	7:D:34:GLU:HG2	1.73	0.68
6:C:20:SER:O	17:N:54:PRO:HB3	1.92	0.68
1:A:1343:G:H2'	1:A:1344:C:C6	2.29	0.68
1:A:1262:C:O2'	1:A:1263:C:H5'	1.94	0.68
1:A:967:C:H4'	12:I:128:ARG:HG3	1.73	0.68
11:H:90:GLY:O	11:H:91:ARG:HB2	1.92	0.68
1:A:794:A:H2'	1:A:795:C:C6	2.28	0.68
7:D:100:ARG:HB3	7:D:102:ASP:OD1	1.94	0.68
11:H:95:VAL:HB	11:H:99:GLU:HB2	1.75	0.68
1:A:384:G:H2'	1:A:385:C:C6	2.28	0.68
17:N:36:PHE:O	17:N:36:PHE:CD1	2.47	0.68
1:A:1257:U:H4'	1:A:1258:G:O5'	1.94	0.68
1:A:1259:C:H42	1:A:1276:G:H1	1.41	0.68
1:A:979:C:H2'	1:A:980:C:H5'	1.76	0.68
1:A:1333:A:H2'	1:A:1334:G:O4'	1.94	0.68
1:A:523:A:H61	15:L:92:ASP:HB2	1.57	0.68
1:A:539:A:H2'	1:A:540:G:C8	2.28	0.68
10:G:113:GLU:HG2	10:G:119:ARG:HG2	1.76	0.68
11:H:63:LEU:HD22	11:H:63:LEU:H	1.59	0.68
1:A:190(L):U:O2	23:T:105:SER:HB2	1.94	0.68
6:C:33:LEU:HD11	17:N:53:LEU:CD2	2.17	0.68
22:S:22:LEU:HD22	22:S:28:LYS:HD2	1.76	0.68
13:J:78:ASN:O	13:J:80:LYS:N	2.27	0.68
11:H:63:LEU:HD22	11:H:63:LEU:N	2.09	0.68
9:F:94:GLN:HB3	21:R:32:ARG:HH11	1.58	0.68
1:A:627:G:O2'	1:A:628:G:H5'	1.92	0.68
1:A:939:G:H5"	10:G:102:ARG:NH2	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:A:O2'	1:A:394:G:H5'	1.94	0.68
6:C:188:LEU:HD13	6:C:189:ALA:H	1.58	0.67
1:A:1305:G:O2'	1:A:1306:A:C8	2.39	0.67
1:A:195:A:H4'	23:T:68:LYS:HE2	1.76	0.67
5:B:25:ASN:C	5:B:25:ASN:HD22	1.96	0.67
16:M:14:ARG:HG3	16:M:44:ARG:NH2	2.09	0.67
16:M:54:VAL:O	16:M:58:GLU:HG2	1.94	0.67
8:E:126:ARG:HG3	8:E:126:ARG:NH1	2.09	0.67
5:B:137:ARG:O	5:B:141:GLU:HB2	1.95	0.67
13:J:3:LYS:HA	13:J:75:ILE:HG12	1.75	0.67
5:B:19:HIS:CD2	5:B:20:GLU:HG2	2.29	0.67
12:I:118:LYS:O	12:I:119:ALA:HB3	1.93	0.67
1:A:1127:G:N2	1:A:1146:A:H62	1.92	0.67
1:A:1320:C:N3	22:S:36:ARG:HG3	2.10	0.67
1:A:1095:U:H2'	1:A:1096:C:C6	2.29	0.67
6:C:195:VAL:HG12	6:C:196:LEU:N	2.10	0.67
8:E:76:ILE:CG1	8:E:77:PRO:HD2	2.24	0.67
1:A:357:G:O2'	1:A:358:U:H5'	1.94	0.67
1:A:974:A:C8	17:N:31:ARG:HD3	2.30	0.67
6:C:191:THR:HG21	6:C:193:TYR:CE1	2.29	0.67
6:C:47:LEU:HD12	6:C:47:LEU:H	1.59	0.67
1:A:351:G:H4'	1:A:352:C:OP1	1.93	0.67
1:A:984:C:H2'	1:A:985:C:H6	1.60	0.67
6:C:8:ILE:HG23	6:C:16:ARG:HG2	1.77	0.67
16:M:4:ILE:HD11	16:M:56:LEU:HD13	1.77	0.67
15:L:41:ARG:HG2	15:L:42:THR:H	1.59	0.67
1:A:180:U:H2'	1:A:181:G:H5'	1.76	0.67
6:C:33:LEU:CD1	17:N:53:LEU:HD22	2.16	0.67
1:A:1366:C:H2'	1:A:1367:C:C6	2.30	0.67
5:B:97:TRP:HZ2	5:B:102:LEU:HD13	1.59	0.67
1:A:1141:C:O2'	1:A:1142:G:H5'	1.95	0.67
1:A:954:G:H2'	1:A:955:U:H6	1.59	0.67
12:I:50:LEU:HA	12:I:55:ALA:HB3	1.75	0.67
11:H:80:ILE:HG22	11:H:80:ILE:O	1.94	0.67
11:H:91:ARG:HG3	15:L:7:ILE:HG13	1.76	0.66
10:G:145:ALA:O	10:G:147:ALA:N	2.25	0.66
13:J:22:LYS:HE2	13:J:90:LEU:HD12	1.77	0.66
1:A:838:G:C2'	1:A:839:U:H5"	2.24	0.66
7:D:70:ILE:HD11	7:D:100:ARG:CD	2.25	0.66
13:J:65:LEU:O	13:J:65:LEU:HD23	1.94	0.66
13:J:23:ILE:N	13:J:23:ILE:HD12	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:174:PRO:HB2	6:C:177:THR:CG2	2.24	0.66
24:V:5:ASP:O	24:V:11:GLY:HA3	1.95	0.66
17:N:33:VAL:HA	17:N:40:CYS:HA	1.78	0.66
11:H:89:PRO:HA	11:H:92:ARG:NH1	2.10	0.66
1:A:1196:U:H5"	1:A:1197:G:C5'	2.26	0.66
1:A:1128:C:O2'	1:A:1130:A:C8	2.47	0.66
1:A:761:G:H1'	20:Q:104:LYS:O	1.96	0.66
23:T:70:SER:HA	23:T:73:HIS:CD2	2.30	0.66
9:F:8:ILE:HD11	9:F:79:LEU:HD13	1.78	0.66
19:P:45:THR:HB	19:P:46:PRO:HD2	1.77	0.66
7:D:151:LYS:H	7:D:151:LYS:CD	1.94	0.66
23:T:51:GLU:HA	23:T:54:LYS:HB2	1.76	0.66
16:M:88:ARG:HH11	16:M:88:ARG:HG2	1.59	0.66
1:A:1241:G:H2'	1:A:1242:C:C6	2.30	0.66
1:A:1031:G:H2'	1:A:1032:G:H8	1.61	0.66
23:T:97:ALA:O	23:T:99:LEU:N	2.28	0.66
1:A:8:A:N6	7:D:209:ARG:H	1.94	0.66
23:T:10:LEU:HD12	23:T:12:ALA:HB3	1.78	0.66
14:K:121:PRO:HG2	14:K:126:ARG:HG2	1.78	0.66
12:I:33:PHE:CE1	12:I:47:LEU:HD21	2.30	0.66
16:M:4:ILE:CD1	16:M:56:LEU:HD13	2.25	0.66
15:L:41:ARG:HG2	15:L:42:THR:O	1.96	0.66
1:A:538:G:OP2	15:L:115:LYS:HG3	1.95	0.66
15:L:50:SER:O	15:L:51:ALA:HB2	1.95	0.66
22:S:5:LEU:O	22:S:6:LYS:HB2	1.94	0.66
10:G:75:VAL:CG2	10:G:86:GLN:HB3	2.25	0.66
6:C:64:VAL:HG12	6:C:65:ALA:N	2.11	0.66
11:H:105:ARG:HG3	11:H:105:ARG:HH11	1.61	0.66
5:B:118:LEU:HD13	5:B:142:LEU:HB2	1.76	0.66
1:A:1081:G:OP1	8:E:16:THR:HG23	1.96	0.66
7:D:64:LEU:HD12	7:D:75:PHE:CZ	2.31	0.66
5:B:101:MET:HA	5:B:108:ILE:HD12	1.78	0.66
7:D:165:MET:SD	7:D:168:ARG:HD3	2.35	0.66
1:A:1178:G:P	12:I:97:LYS:HZ2	2.18	0.65
13:J:94:VAL:HG12	13:J:95:GLU:N	2.10	0.65
12:I:47:LEU:C	12:I:49:PRO:HD2	2.16	0.65
20:Q:59:ILE:HG22	20:Q:71:PHE:CD1	2.31	0.65
1:A:443:C:H2'	1:A:444:C:C6	2.29	0.65
1:A:149:A:H2'	1:A:150:C:C6	2.32	0.65
17:N:18:VAL:HG23	17:N:19:ARG:H	1.60	0.65
1:A:353:A:H5'	1:A:353:A:H8	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:34:VAL:HG12	13:J:35:SER:N	2.11	0.65
1:A:243:A:C4'	1:A:244:U:H5'	2.23	0.65
15:L:75:HIS:HD2	15:L:77:LEU:H	1.45	0.65
1:A:689:C:P	14:K:46:GLY:HA3	2.36	0.65
1:A:1363:A:H1'	1:A:1365:G:N7	2.11	0.65
12:I:48:GLU:N	12:I:49:PRO:HD2	2.11	0.65
8:E:16:THR:CG2	8:E:27:ARG:HB3	2.26	0.65
7:D:177:ASP:OD1	7:D:179:GLU:HG2	1.97	0.65
7:D:175:SER:HB3	7:D:186:LEU:HD11	1.78	0.65
23:T:49:ALA:HB3	23:T:99:LEU:HG	1.78	0.65
13:J:22:LYS:C	13:J:24:VAL:H	2.00	0.65
14:K:91:ARG:NH1	21:R:88:LYS:NZ	2.44	0.65
15:L:24:VAL:CG1	15:L:24:VAL:O	2.42	0.65
8:E:144:THR:O	8:E:148:VAL:HG23	1.97	0.65
6:C:52:LEU:H	6:C:52:LEU:CD2	2.08	0.65
22:S:77:THR:HG22	22:S:78:ARG:N	2.11	0.65
1:A:992:U:H4'	1:A:993:G:O5'	1.96	0.65
1:A:168:G:O2'	1:A:169:C:H5'	1.96	0.65
17:N:24:CYS:HB3	17:N:28:GLY:N	2.11	0.65
11:H:133:LEU:HD23	11:H:133:LEU:C	2.16	0.65
1:A:1053:G:C4'	1:A:1054:C:H5'	2.27	0.65
12:I:69:GLY:O	12:I:73:GLN:HG3	1.97	0.65
1:A:1222:G:P	22:S:77:THR:HG21	2.37	0.65
5:B:16:HIS:HA	5:B:204:ASN:HB2	1.78	0.65
8:E:77:PRO:O	8:E:78:HIS:HB3	1.95	0.65
5:B:102:LEU:HD21	5:B:162:ILE:HD12	1.78	0.65
1:A:1053:G:C3'	1:A:1054:C:H5'	2.27	0.64
5:B:71:VAL:CG2	5:B:164:VAL:HG22	2.26	0.64
5:B:142:LEU:CD2	5:B:146:GLN:HE21	2.10	0.64
17:N:18:VAL:HG23	17:N:19:ARG:N	2.11	0.64
1:A:1281:U:H5'	1:A:1282:C:H5	1.61	0.64
1:A:424:G:O2'	1:A:425:G:H5'	1.97	0.64
5:B:12:GLU:C	5:B:14:GLY:H	1.99	0.64
16:M:26:GLY:O	16:M:28:ALA:N	2.31	0.64
1:A:807:A:H2'	1:A:808:C:C6	2.32	0.64
22:S:30:LEU:O	22:S:31:ILE:HD13	1.96	0.64
1:A:254:G:H21	20:Q:16:GLN:NE2	1.96	0.64
1:A:1305:G:N2	1:A:1331:G:O2'	2.30	0.64
5:B:16:HIS:O	5:B:18:GLY:N	2.30	0.64
1:A:1347:G:H2'	1:A:1373:G:H1	1.60	0.64
1:A:176:C:H2'	1:A:177:C:H6	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1292:U:P	10:G:41:ARG:HH22	2.20	0.64
5:B:135:GLN:HG2	5:B:139:LYS:HE2	1.79	0.64
1:A:1368:G:O2'	1:A:1369:C:H5'	1.96	0.64
13:J:16:LEU:O	13:J:19:SER:N	2.30	0.64
8:E:92:LYS:HB3	8:E:119:LEU:HB2	1.78	0.64
1:A:344:A:H4'	1:A:345:C:OP2	1.96	0.64
1:A:1176:A:H2'	1:A:1177:G:C8	2.32	0.64
18:O:24:SER:OG	18:O:27:VAL:HG23	1.98	0.64
6:C:34:LEU:HD23	6:C:34:LEU:O	1.96	0.64
1:A:1298:C:H4'	1:A:1299:A:O4'	1.97	0.64
10:G:135:VAL:O	10:G:139:GLU:HG3	1.98	0.64
13:J:49:VAL:O	13:J:60:ARG:O	2.15	0.64
11:H:101:PRO:HG3	11:H:133:LEU:HD11	1.78	0.64
1:A:1054:C:H42	3:Y:34:G:C1'	2.10	0.64
1:A:1004:A:H5"	1:A:1025:U:O4	1.98	0.64
15:L:87:GLY:HA2	15:L:98:TYR:HA	1.79	0.64
8:E:145:LYS:O	8:E:149:GLU:HG3	1.97	0.64
1:A:1194:U:H4'	8:E:22:GLY:CA	2.28	0.64
7:D:187:ARG:HG3	7:D:188:LEU:N	2.13	0.64
9:F:92:LYS:HB2	9:F:92:LYS:NZ	2.13	0.64
11:H:119:LEU:HB2	11:H:123:GLU:HB2	1.80	0.64
1:A:1194:U:H4'	8:E:22:GLY:HA3	1.78	0.64
1:A:1427:U:H2'	1:A:1428:A:C8	2.32	0.64
13:J:4:ILE:HB	13:J:74:ILE:HG13	1.80	0.64
1:A:662:G:H2'	1:A:663:A:C8	2.33	0.64
1:A:1454:G:H2'	1:A:1455:G:H8	1.63	0.64
7:D:29:PRO:O	7:D:30:LYS:HG3	1.98	0.64
5:B:178:ARG:HG3	5:B:178:ARG:HH11	1.62	0.64
13:J:30:SER:HB3	13:J:84:GLN:CD	2.18	0.63
14:K:91:ARG:NH1	21:R:88:LYS:HZ1	1.94	0.63
1:A:1241:G:H2'	1:A:1242:C:H6	1.63	0.63
7:D:3:ARG:NH1	7:D:118:ARG:HH12	1.96	0.63
14:K:126:ARG:NH1	14:K:126:ARG:HB3	2.13	0.63
17:N:35:ARG:C	17:N:37:PHE:H	2.01	0.63
18:O:21:ASP:OD2	18:O:24:SER:HB3	1.98	0.63
23:T:67:ALA:HA	23:T:73:HIS:H	1.63	0.63
1:A:1065:U:H4'	1:A:1066:C:O5'	1.98	0.63
9:F:22:GLU:OE1	9:F:22:GLU:HA	1.99	0.63
14:K:115:PRO:C	14:K:117:ASN:H	2.01	0.63
6:C:15:THR:O	6:C:16:ARG:HB2	1.97	0.63
6:C:43:LEU:HD13	6:C:68:VAL:HG23	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1351:U:H4'	10:G:33:ASP:OD2	1.98	0.63
1:A:760:G:N2	20:Q:104:LYS:H	1.95	0.63
1:A:620:C:N1	7:D:135:LEU:HD13	2.12	0.63
17:N:9:LYS:HD3	17:N:9:LYS:C	2.17	0.63
15:L:28:LYS:C	15:L:30:ALA:N	2.45	0.63
5:B:15:VAL:O	5:B:17:PHE:N	2.31	0.63
1:A:496:A:H4'	1:A:497:A:OP1	1.97	0.63
1:A:1125:U:H5"	1:A:1126:U:C5	2.34	0.63
21:R:47:THR:CG2	21:R:83:GLU:H	2.10	0.63
1:A:1152:A:H2'	1:A:1153:C:H6	1.61	0.63
9:F:10:LEU:CD1	9:F:59:TYR:HB3	2.27	0.63
10:G:146:GLU:HA	10:G:149:ARG:HG2	1.81	0.63
20:Q:67:LYS:CA	20:Q:70:ARG:HH12	2.07	0.63
1:A:1352:C:H2'	1:A:1353:G:H8	1.63	0.63
1:A:352:C:H4'	1:A:354:G:OP1	1.97	0.63
23:T:76:ALA:O	23:T:80:ARG:HG3	1.97	0.63
1:A:258:G:H2'	1:A:259:G:H8	1.62	0.63
6:C:13:GLY:O	6:C:14:ILE:HD13	1.99	0.63
5:B:17:PHE:CG	5:B:18:GLY:N	2.66	0.63
1:A:1258:G:H1	1:A:1277:C:H42	1.44	0.63
23:T:57:ARG:HH11	23:T:57:ARG:CB	2.11	0.63
1:A:112:G:H21	1:A:354:G:C5'	2.12	0.63
15:L:110:VAL:O	15:L:122:THR:HG21	1.98	0.63
5:B:206:ASP:O	5:B:207:ALA:HB3	1.99	0.63
5:B:17:PHE:HA	5:B:44:LEU:HD21	1.80	0.63
5:B:111:ARG:HB3	5:B:149:LEU:HD11	1.79	0.63
1:A:1510:U:H2'	1:A:1511:G:C8	2.34	0.63
18:O:70:LEU:HD13	18:O:78:TYR:CA	2.28	0.63
1:A:528:C:H5'	1:A:535:A:C6	2.34	0.63
15:L:41:ARG:HH12	15:L:57:LYS:HZ3	1.46	0.63
15:L:54:LYS:N	15:L:54:LYS:HD2	2.14	0.63
6:C:179:ARG:HD3	6:C:207:VAL:HA	1.80	0.62
1:A:328:C:O2	1:A:328:C:C2'	2.47	0.62
1:A:407:G:O2'	7:D:116:GLN:HG3	1.99	0.62
20:Q:97:SER:HB3	20:Q:103:GLY:C	2.19	0.62
1:A:713:G:H2'	1:A:714:G:C8	2.34	0.62
9:F:19:LEU:C	9:F:19:LEU:HD23	2.20	0.62
11:H:121:ASP:HB2	11:H:125:ARG:HH22	1.64	0.62
16:M:84:ILE:O	16:M:85:GLY:C	2.37	0.62
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.34	0.62
15:L:53:ARG:HG2	15:L:69:TYR:HE1	1.62	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:57:PHE:CZ	5:B:61:LEU:HD11	2.34	0.62
16:M:17:VAL:O	16:M:20:THR:HB	1.98	0.62
20:Q:101:ARG:NE	20:Q:101:ARG:HA	2.14	0.62
1:A:959:A:H3'	1:A:960:U:H5"	1.81	0.62
11:H:92:ARG:HH11	11:H:92:ARG:HG2	1.65	0.62
1:A:67:C:H2'	1:A:68:G:C8	2.35	0.62
15:L:28:LYS:HD3	15:L:33:ARG:HH22	1.63	0.62
1:A:1060:C:O2'	1:A:1061:G:H5'	1.99	0.62
1:A:31:G:N1	1:A:48:C:H5"	2.13	0.62
8:E:82:VAL:HG21	8:E:138:ALA:HA	1.81	0.62
22:S:16:LEU:O	22:S:19:VAL:HG12	2.00	0.62
1:A:1391:U:H2'	1:A:1392:G:C8	2.35	0.62
11:H:10:LEU:HD22	11:H:83:ILE:HD11	1.81	0.62
7:D:4:TYR:O	7:D:5:ILE:HB	1.99	0.62
13:J:32:ALA:HB2	13:J:76:ASN:ND2	2.07	0.62
23:T:50:GLU:H	23:T:99:LEU:HD12	1.64	0.62
1:A:1016:A:H2'	1:A:1017:G:O4'	1.99	0.62
1:A:941:G:O2'	1:A:942:G:H5'	1.99	0.62
1:A:1427:U:H2'	1:A:1428:A:H8	1.65	0.62
8:E:60:TYR:O	8:E:64:ARG:HG2	2.00	0.62
16:M:106:ASN:O	16:M:107:ALA:HB3	2.00	0.62
11:H:112:LEU:N	11:H:112:LEU:HD23	2.15	0.62
13:J:51:ARG:CZ	13:J:61:GLU:HB2	2.29	0.62
1:A:1305:G:C5'	24:V:4:GLY:HA3	2.30	0.62
9:F:33:TYR:HB2	9:F:75:LEU:HD23	1.82	0.62
1:A:1129:C:H1'	1:A:1132:C:H5	1.64	0.62
1:A:1314:C:C5	22:S:6:LYS:HE3	2.35	0.62
15:L:27:LEU:CD2	15:L:62:SER:HB2	2.26	0.62
1:A:254:G:OP1	20:Q:68:ARG:HB3	2.00	0.62
5:B:16:HIS:HA	5:B:204:ASN:HB3	1.82	0.62
24:V:3:LYS:HB3	24:V:14:TRP:CG	2.34	0.62
5:B:143:GLU:O	5:B:147:LYS:HG3	2.00	0.62
22:S:19:VAL:HG13	22:S:20:LEU:N	2.14	0.62
3:Y:36:A:H2'	3:Y:37:A:H8	1.64	0.62
6:C:64:VAL:HB	6:C:99:VAL:CB	2.29	0.62
17:N:12:ARG:O	17:N:14:PRO:HD3	2.00	0.62
10:G:38:LEU:HD12	10:G:38:LEU:O	2.00	0.62
1:A:1286:A:H2'	1:A:1287:A:H5"	1.81	0.61
6:C:191:THR:CG2	6:C:192:THR:N	2.63	0.61
1:A:851:G:H2'	1:A:852:G:H8	1.64	0.61
6:C:119:ARG:O	6:C:122:GLU:HB2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:82:ARG:HA	5:B:92:TYR:CE1	2.35	0.61
1:A:547:A:H4'	1:A:548:G:O5'	2.00	0.61
1:A:1347:G:O2'	1:A:1348:U:P	2.57	0.61
9:F:100:ASN:HD22	21:R:23:LYS:CG	2.12	0.61
23:T:54:LYS:HE3	23:T:100:ILE:HD13	1.81	0.61
1:A:382:A:H2'	1:A:383:A:H8	1.64	0.61
9:F:62:TRP:CH2	9:F:64:GLN:HB2	2.35	0.61
7:D:70:ILE:HD11	7:D:100:ARG:NE	2.14	0.61
15:L:120:TYR:O	15:L:122:THR:HG23	1.99	0.61
7:D:106:TYR:CE1	7:D:113:SER:HA	2.35	0.61
5:B:144:ARG:CD	5:B:145:LEU:HD23	2.30	0.61
5:B:23:ARG:HH11	5:B:24:TRP:HA	1.65	0.61
6:C:108:ASN:ND2	6:C:110:ASN:HB2	2.16	0.61
1:A:1004:A:H5"	1:A:1025:U:C4	2.35	0.61
1:A:984:C:H2'	1:A:985:C:C6	2.35	0.61
14:K:126:ARG:O	14:K:127:LYS:HB2	2.00	0.61
8:E:18:ARG:HG2	8:E:25:ARG:HB2	1.82	0.61
3:Y:29:G:H2'	3:Y:30:G:H8	1.65	0.61
22:S:15:LEU:O	22:S:19:VAL:N	2.31	0.61
13:J:49:VAL:HG13	17:N:41:ARG:HB2	1.83	0.61
5:B:68:ILE:O	5:B:90:MET:HB3	2.01	0.61
17:N:35:ARG:O	17:N:37:PHE:N	2.33	0.61
1:A:1132:C:H2'	1:A:1133:G:C8	2.34	0.61
11:H:86:ILE:HD12	11:H:133:LEU:HD21	1.82	0.61
1:A:580:U:H2'	1:A:581:G:O4'	2.01	0.61
5:B:59:GLU:CG	5:B:221:LEU:HD11	2.30	0.61
5:B:155:LEU:HD22	5:B:157:ARG:O	2.01	0.61
23:T:96:GLY:O	23:T:97:ALA:HB3	2.00	0.61
1:A:404:U:H2'	1:A:405:U:C6	2.35	0.61
8:E:144:THR:HG22	8:E:147:ASP:H	1.65	0.61
15:L:51:ALA:O	15:L:52:LEU:HD23	2.01	0.61
1:A:1193:G:O2'	1:A:1194:U:H5'	2.01	0.61
19:P:19:ILE:HG22	19:P:36:ILE:HG13	1.81	0.61
1:A:488:C:H2'	1:A:489:C:H6	1.64	0.61
13:J:38:ILE:HG13	13:J:71:LEU:HB3	1.82	0.61
13:J:87:THR:O	13:J:88:LEU:HD23	2.01	0.61
1:A:1198:G:H2'	1:A:1199:U:C6	2.36	0.61
1:A:265:G:H2'	1:A:267:C:C5	2.35	0.61
12:I:32:ASP:HB3	12:I:35:GLU:HB2	1.83	0.61
6:C:28:GLN:HA	6:C:31:HIS:HD2	1.64	0.61
1:A:1314:C:C6	22:S:6:LYS:HE3	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:83:ARG:C	6:C:85:ARG:H	2.04	0.61
18:O:36:ILE:HG12	18:O:59:MET:HE3	1.82	0.61
6:C:84:ILE:O	6:C:84:ILE:HG12	2.01	0.61
7:D:151:LYS:N	7:D:151:LYS:HD2	2.01	0.60
1:A:955:U:O2'	1:A:956:U:H5'	2.01	0.60
12:I:118:LYS:NZ	12:I:118:LYS:CB	2.63	0.60
11:H:31:PHE:O	11:H:35:ILE:HG13	2.01	0.60
12:I:44:VAL:HG13	12:I:51:ARG:NH2	2.16	0.60
1:A:1003:G:H2'	1:A:1003(A):G:C8	2.35	0.60
15:L:42:THR:O	15:L:43:VAL:HG23	2.01	0.60
11:H:11:THR:HA	11:H:14:ARG:NH1	2.16	0.60
1:A:639:G:O2'	1:A:640:A:H5'	2.02	0.60
9:F:50:TYR:CE1	21:R:77:GLY:HA2	2.36	0.60
7:D:150:GLU:HG3	7:D:153:ARG:NH2	2.16	0.60
5:B:16:HIS:NE2	5:B:214:ILE:HG12	2.15	0.60
5:B:48:MET:HA	5:B:51:LEU:HD12	1.84	0.60
12:I:113:LYS:H	12:I:119:ALA:HA	1.66	0.60
1:A:178:C:O2'	1:A:179:A:H5'	2.01	0.60
1:A:564:C:C2	20:Q:31:LEU:HD11	2.36	0.60
1:A:521:G:OP1	15:L:73:GLU:O	2.18	0.60
8:E:6:PHE:CE2	8:E:36:ASP:HB3	2.36	0.60
1:A:981:U:H5'	17:N:21:TYR:CE1	2.35	0.60
7:D:146:ILE:HD12	7:D:146:ILE:N	2.15	0.60
23:T:100:ILE:O	23:T:102:GLY:N	2.33	0.60
20:Q:98:LEU:H	20:Q:103:GLY:HA2	1.67	0.60
15:L:53:ARG:HG2	15:L:69:TYR:CE1	2.36	0.60
1:A:1285:A:H4'	1:A:1286:A:O5'	2.01	0.60
10:G:57:GLU:O	10:G:61:VAL:HG23	2.00	0.60
1:A:1104:G:OP1	5:B:111:ARG:HD2	2.00	0.60
16:M:15:VAL:HG23	16:M:43:THR:O	2.00	0.60
1:A:686:U:HO2'	1:A:687:A:H8	1.49	0.60
7:D:162:LEU:HD12	7:D:181:MET:HG2	1.83	0.60
12:I:70:LYS:O	12:I:74:ILE:HG13	2.01	0.60
11:H:127:LEU:H	11:H:127:LEU:HD23	1.65	0.60
1:A:1182:G:O2'	1:A:1183:A:OP2	2.14	0.60
1:A:1152:A:H5"	13:J:13:HIS:CG	2.36	0.60
16:M:63:THR:HG23	16:M:64:TRP:CD2	2.37	0.60
10:G:145:ALA:O	10:G:146:GLU:HB2	2.01	0.60
9:F:22:GLU:OE1	9:F:25:ILE:HD12	2.01	0.60
19:P:20:VAL:HG11	19:P:32:TYR:CB	2.31	0.60
6:C:155:GLY:O	6:C:156:ARG:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:51:ARG:HB2	13:J:59:SER:HB2	1.84	0.60
1:A:1208:C:H2'	1:A:1209:C:C6	2.37	0.60
5:B:187:LEU:HA	5:B:201:ILE:HB	1.82	0.60
17:N:29:ARG:HH11	17:N:29:ARG:HG2	1.67	0.60
15:L:41:ARG:NH1	15:L:57:LYS:NZ	2.49	0.60
1:A:1064:G:H4'	1:A:1065:U:H5"	1.84	0.60
6:C:72:LYS:O	6:C:75:VAL:HG23	2.01	0.60
14:K:34:ASP:O	14:K:36:ASP:N	2.34	0.60
1:A:657:G:H4'	18:O:28:GLN:HG2	1.84	0.60
14:K:57:THR:HG23	14:K:60:ALA:H	1.67	0.60
1:A:835:U:OP1	21:R:64:ARG:NH2	2.29	0.60
15:L:126:LYS:H	15:L:126:LYS:CD	2.10	0.60
19:P:34:GLU:OE2	19:P:55:ARG:HD3	2.01	0.60
20:Q:97:SER:HB2	20:Q:103:GLY:HA2	1.82	0.60
6:C:11:ARG:O	6:C:14:ILE:O	2.20	0.60
7:D:25:ARG:C	7:D:27:TYR:H	2.05	0.60
11:H:82:HIS:CD2	11:H:83:ILE:N	2.70	0.60
1:A:560:U:H5'	1:A:566:G:N2	2.17	0.60
9:F:3:ARG:HH11	9:F:3:ARG:HG3	1.66	0.60
20:Q:63:ARG:HG2	20:Q:64:PRO:HD2	1.83	0.59
1:A:353:A:H5'	1:A:353:A:C8	2.37	0.59
8:E:8:GLU:HG2	8:E:34:VAL:HG22	1.82	0.59
5:B:28:PHE:CD2	5:B:190:THR:HA	2.37	0.59
1:A:1108:G:H4'	1:A:1191:A:O4'	2.02	0.59
1:A:501:C:H2'	1:A:502:G:C8	2.37	0.59
8:E:89:ILE:HD13	8:E:90:VAL:H	1.66	0.59
17:N:14:PRO:O	17:N:15:LYS:HB2	2.02	0.59
6:C:35:GLU:CG	6:C:59:ARG:HH22	2.16	0.59
5:B:112:VAL:C	5:B:114:ARG:H	2.05	0.59
20:Q:58:GLU:O	20:Q:59:ILE:HD13	2.02	0.59
14:K:30:VAL:HG21	14:K:65:ALA:HA	1.84	0.59
1:A:1128:C:H4'	12:I:16:ARG:NH1	2.16	0.59
19:P:74:LEU:O	19:P:79:VAL:HG23	2.01	0.59
1:A:60:A:H4'	1:A:61:G:O5'	2.03	0.59
5:B:140:HIS:HA	5:B:143:GLU:HG2	1.84	0.59
5:B:102:LEU:CD1	5:B:102:LEU:N	2.65	0.59
5:B:79:ASP:HB3	5:B:238:LEU:HD13	1.83	0.59
18:O:17:ARG:HG3	18:O:17:ARG:NH1	2.17	0.59
16:M:88:ARG:HG2	16:M:88:ARG:NH1	2.18	0.59
7:D:7:PRO:CB	7:D:10:ARG:HD2	2.32	0.59
1:A:1121:U:H2'	1:A:1122:U:H6	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:39:VAL:HG12	15:L:40:VAL:N	2.17	0.59
1:A:818:G:C3'	1:A:819:A:H5"	2.33	0.59
15:L:82:VAL:HG12	15:L:105:TYR:HB3	1.84	0.59
8:E:72:GLN:C	8:E:74:GLY:H	2.04	0.59
20:Q:97:SER:HB3	20:Q:102:GLY:O	2.01	0.59
15:L:93:LEU:HB2	15:L:96:VAL:CG2	2.33	0.59
1:A:812:C:O2'	1:A:813:U:P	2.59	0.59
15:L:60:LEU:CD2	15:L:66:VAL:HG22	2.32	0.59
1:A:1154:G:H2'	1:A:1155:G:H8	1.68	0.59
1:A:1316:G:N2	1:A:1318:A:H3'	2.18	0.59
1:A:163:C:O2'	1:A:164:U:H5'	2.03	0.59
9:F:100:ASN:ND2	21:R:23:LYS:HG2	2.12	0.59
1:A:1231:G:H4'	12:I:126:SER:OG	2.03	0.59
22:S:82:GLY:O	22:S:83:HIS:HB2	2.03	0.59
1:A:1300:G:O2'	1:A:1301:U:H6	1.84	0.59
21:R:19:LYS:N	21:R:19:LYS:HD2	2.17	0.59
1:A:1366:C:H2'	1:A:1367:C:H6	1.67	0.59
13:J:4:ILE:HD12	13:J:74:ILE:HG13	1.84	0.59
5:B:201:ILE:HG21	5:B:214:ILE:HG21	1.84	0.59
5:B:102:LEU:HD12	5:B:102:LEU:N	2.17	0.59
11:H:119:LEU:HD12	11:H:124:ALA:HA	1.85	0.59
1:A:1425:U:H3	1:A:1475:G:H1	1.49	0.59
8:E:149:GLU:O	8:E:153:LYS:HG3	2.03	0.59
16:M:40:ASN:HD22	16:M:41:PRO:HD2	1.68	0.59
7:D:23:GLY:HA3	7:D:112:VAL:HG12	1.85	0.59
11:H:86:ILE:HD11	11:H:136:GLU:CG	2.27	0.59
20:Q:66:SER:O	20:Q:70:ARG:NH1	2.35	0.59
16:M:35:GLU:C	16:M:37:THR:H	2.07	0.59
20:Q:59:ILE:HG23	20:Q:71:PHE:HB3	1.85	0.59
1:A:404:U:O2'	1:A:405:U:H5'	2.03	0.59
1:A:130:A:C8	20:Q:63:ARG:HG3	2.38	0.59
1:A:861:G:O2'	1:A:862:C:H5'	2.03	0.59
1:A:1404:C:H2'	1:A:1405:G:C8	2.37	0.59
22:S:55:LYS:HG2	22:S:56:GLN:HE21	1.68	0.59
13:J:90:LEU:H	13:J:91:PRO:HD2	1.67	0.58
9:F:2:ARG:HH21	9:F:69:GLU:CB	2.16	0.58
10:G:51:GLN:NE2	10:G:56:GLN:O	2.36	0.58
23:T:86:ARG:HG3	23:T:90:GLN:NE2	2.18	0.58
19:P:81:ARG:HH11	19:P:81:ARG:HB2	1.68	0.58
1:A:1497:G:C2'	1:A:1498:U:H5'	2.33	0.58
21:R:45:SER:C	21:R:47:THR:N	2.56	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:43:SER:HA	14:K:47:VAL:HG21	1.83	0.58
9:F:92:LYS:HB2	9:F:92:LYS:HZ2	1.66	0.58
1:A:701:C:H5"	1:A:703:G:O4'	2.02	0.58
1:A:1091:U:O2	1:A:1093:A:C8	2.57	0.58
6:C:34:LEU:C	6:C:34:LEU:CD2	2.72	0.58
12:I:107:ARG:HH11	12:I:107:ARG:HB3	1.69	0.58
1:A:706:A:C4'	14:K:29:ILE:HD11	2.33	0.58
6:C:82:GLU:O	6:C:85:ARG:HB3	2.03	0.58
1:A:413:G:H2'	1:A:428:G:N2	2.18	0.58
1:A:1381:U:H2'	1:A:1382:C:H6	1.68	0.58
5:B:136:VAL:HA	5:B:139:LYS:HB2	1.84	0.58
1:A:1125:U:H3	13:J:5:ARG:NH2	2.01	0.58
12:I:8:GLY:HA3	12:I:79:LEU:HB3	1.83	0.58
15:L:41:ARG:HG2	15:L:42:THR:N	2.18	0.58
1:A:537:G:OP1	15:L:113:ARG:NH2	2.36	0.58
16:M:79:LYS:HG2	16:M:83:ASP:OD2	2.04	0.58
20:Q:76:LEU:HD23	20:Q:76:LEU:C	2.23	0.58
6:C:172:ARG:HB3	6:C:172:ARG:HH11	1.66	0.58
6:C:88:ARG:HA	6:C:101:LEU:HD12	1.85	0.58
5:B:35:GLU:HG2	5:B:40:HIS:HA	1.84	0.58
13:J:49:VAL:HG13	17:N:41:ARG:HD2	1.85	0.58
1:A:1125:U:H3	13:J:5:ARG:HE	1.50	0.58
1:A:948:C:OP1	16:M:109:THR:HG22	2.03	0.58
5:B:15:VAL:CG2	5:B:209:ARG:HG3	2.33	0.58
5:B:213:LEU:O	5:B:217:ARG:HG2	2.04	0.58
1:A:1278:U:H4'	1:A:1279:A:H5'	1.85	0.58
1:A:1372:U:OP1	12:I:71:SER:HB3	2.02	0.58
20:Q:104:LYS:O	20:Q:105:ALA:CB	2.50	0.58
12:I:95:LYS:C	12:I:98:PRO:HD2	2.23	0.58
10:G:78:ARG:HB2	10:G:156:TRP:HZ3	1.68	0.58
11:H:77:GLU:HG3	11:H:78:GLN:H	1.68	0.58
13:J:23:ILE:CD1	13:J:23:ILE:H	2.15	0.58
10:G:138:LYS:HE2	10:G:142:GLU:OE1	2.03	0.58
1:A:1195:C:H3'	1:A:1196:U:C5'	2.33	0.58
3:Y:34:G:H2'	3:Y:35:A:H8	1.69	0.58
5:B:55:PHE:O	5:B:58:ILE:HB	2.04	0.58
5:B:97:TRP:CZ2	5:B:102:LEU:HD13	2.37	0.58
1:A:1015:A:H2'	1:A:1016:A:H8	1.67	0.58
5:B:78:GLN:HG2	5:B:94:ASN:ND2	2.18	0.58
8:E:126:ARG:HH11	8:E:126:ARG:HG3	1.68	0.58
1:A:730:G:N2	1:A:765:G:H5"	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:G:H2'	1:A:428:G:H21	1.67	0.58
1:A:1412:C:H2'	1:A:1413:A:C8	2.38	0.58
1:A:1305:G:H5"	24:V:4:GLY:C	2.23	0.58
6:C:22:TRP:O	6:C:22:TRP:CE3	2.56	0.58
21:R:87:ARG:O	21:R:88:LYS:HB3	2.03	0.58
8:E:74:GLY:CA	8:E:116:THR:HG22	2.32	0.58
1:A:824:C:H2'	1:A:825:G:H8	1.68	0.58
23:T:39:LYS:HD2	23:T:55:ILE:CD1	2.33	0.58
7:D:152:SER:O	7:D:155:LEU:HD12	2.02	0.58
16:M:91:ARG:HB2	16:M:98:VAL:HG12	1.86	0.58
5:B:140:HIS:HA	5:B:143:GLU:CG	2.33	0.58
5:B:15:VAL:HG21	5:B:209:ARG:HG3	1.84	0.58
1:A:951:G:O2'	1:A:952:U:H5'	2.04	0.58
20:Q:60:ILE:HD13	20:Q:61:GLU:N	2.19	0.58
5:B:167:PRO:HG3	5:B:188:ALA:HB2	1.86	0.58
21:R:37:VAL:HG22	21:R:78:LEU:HB3	1.85	0.58
1:A:862:C:H2'	1:A:863:U:H6	1.68	0.58
7:D:63:LYS:HD2	7:D:198:VAL:HG22	1.84	0.58
6:C:113:ALA:HB3	6:C:114:PRO:HD3	1.86	0.58
5:B:77:ALA:HB2	5:B:211:ILE:CD1	2.26	0.58
22:S:30:LEU:HD23	22:S:31:ILE:N	2.19	0.58
1:A:1054:C:OP1	1:A:1197:G:OP1	2.20	0.58
8:E:12:LEU:HD13	8:E:31:LEU:HB2	1.84	0.58
5:B:98:LEU:O	5:B:101:MET:HG3	2.03	0.58
13:J:46:ARG:HH11	13:J:64:GLU:CB	2.17	0.58
1:A:948:C:O2'	1:A:949:A:H5'	2.04	0.57
16:M:4:ILE:HG22	16:M:5:ALA:H	1.69	0.57
6:C:134:ILE:O	6:C:138:VAL:HG23	2.04	0.57
5:B:23:ARG:HD3	5:B:24:TRP:N	2.19	0.57
13:J:19:SER:HA	13:J:22:LYS:HZ2	1.69	0.57
6:C:35:GLU:HB3	6:C:59:ARG:NH2	2.19	0.57
1:A:539:A:H2'	1:A:540:G:H8	1.68	0.57
7:D:60:GLU:HA	7:D:60:GLU:OE1	2.04	0.57
1:A:190:C:H2'	1:A:190(A):C:H6	1.69	0.57
6:C:55:VAL:HG12	6:C:55:VAL:O	2.04	0.57
3:Y:34:G:H2'	3:Y:35:A:C8	2.39	0.57
6:C:6:HIS:NE2	6:C:8:ILE:HD12	2.19	0.57
6:C:47:LEU:CD1	6:C:47:LEU:H	2.17	0.57
21:R:86:VAL:O	21:R:87:ARG:HB2	2.03	0.57
1:A:1347:G:N2	1:A:1373:G:H2'	2.18	0.57
12:I:93:ARG:HD3	12:I:97:LYS:HZ1	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:75:ASP:O	12:I:78:LYS:HB3	2.05	0.57
1:A:340:U:H2'	1:A:341:C:C6	2.39	0.57
1:A:1286:A:C3'	1:A:1287:A:C5'	2.73	0.57
13:J:32:ALA:CB	13:J:76:ASN:HD22	2.10	0.57
6:C:34:LEU:HD12	17:N:25:VAL:HG21	1.86	0.57
1:A:1349:A:H2'	1:A:1350:A:H8	1.69	0.57
9:F:10:LEU:HD11	9:F:59:TYR:HD2	1.69	0.57
19:P:4:ILE:HG23	19:P:36:ILE:HD11	1.86	0.57
1:A:927:G:H4'	1:A:1503:A:N7	2.19	0.57
1:A:1271:G:H2'	1:A:1272:G:C8	2.39	0.57
11:H:86:ILE:CG2	11:H:133:LEU:HD22	2.32	0.57
1:A:1314:C:OP2	22:S:6:LYS:HG2	2.03	0.57
14:K:116:HIS:O	14:K:117:ASN:HB2	2.04	0.57
10:G:16:LEU:HD22	10:G:16:LEU:N	2.15	0.57
19:P:28:ARG:HG3	19:P:29:ASP:OD2	2.03	0.57
11:H:119:LEU:HD23	11:H:119:LEU:N	2.20	0.57
1:A:1314:C:H3'	22:S:6:LYS:NZ	2.19	0.57
19:P:38:TYR:CE2	19:P:50:LYS:HD3	2.39	0.57
10:G:115:ARG:HB2	10:G:118:VAL:HG23	1.86	0.57
6:C:15:THR:HG21	6:C:179:ARG:O	2.04	0.57
17:N:24:CYS:SG	17:N:40:CYS:HB3	2.44	0.57
16:M:84:ILE:CG2	22:S:65:ASN:HD22	2.18	0.57
16:M:49:THR:HG22	16:M:51:ALA:H	1.68	0.57
11:H:10:LEU:CD2	11:H:83:ILE:HD11	2.34	0.57
1:A:76:C:O2'	1:A:77:G:H5'	2.04	0.57
13:J:51:ARG:NE	13:J:61:GLU:HB2	2.19	0.57
5:B:12:GLU:OE2	5:B:213:LEU:HD11	2.04	0.57
7:D:62:GLN:NE2	7:D:65:ARG:NH1	2.53	0.57
6:C:137:ALA:HA	6:C:140:ARG:HD2	1.86	0.57
1:A:109:A:H2'	1:A:326:G:N2	2.19	0.57
5:B:121:LEU:HD23	5:B:121:LEU:C	2.25	0.57
1:A:123:C:OP1	1:A:312:C:H5'	2.04	0.57
12:I:10:ARG:HD2	12:I:11:LYS:N	2.20	0.57
14:K:48:ILE:CG2	14:K:49:GLY:N	2.54	0.57
13:J:59:SER:O	13:J:60:ARG:HB2	2.05	0.57
13:J:38:ILE:HD12	13:J:71:LEU:HD12	1.87	0.57
1:A:1306:A:N6	1:A:1331:G:H1'	2.20	0.57
1:A:1306:A:O2'	16:M:109:THR:HG21	2.05	0.57
6:C:64:VAL:CG2	6:C:99:VAL:HG11	2.34	0.57
10:G:85:TYR:CD1	10:G:154:TYR:HE1	2.23	0.57
13:J:46:ARG:HH11	13:J:64:GLU:HB3	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:51:LEU:HB2	21:R:56:THR:HG22	1.87	0.57
5:B:159:PRO:HB2	5:B:161:ALA:O	2.05	0.57
16:M:90:LEU:O	16:M:93:ARG:HB2	2.04	0.57
1:A:1250:A:H2'	1:A:1251:A:C8	2.40	0.57
13:J:38:ILE:HG22	13:J:39:PRO:HD2	1.86	0.57
13:J:75:ILE:O	13:J:76:ASN:HB2	2.03	0.57
23:T:49:ALA:HB3	23:T:99:LEU:CD1	2.34	0.57
12:I:93:ARG:HB3	12:I:97:LYS:HE3	1.85	0.57
9:F:61:LEU:HB3	9:F:63:TYR:HE2	1.70	0.57
1:A:1061:G:O2'	1:A:1062:U:H5'	2.05	0.57
18:O:63:ARG:O	18:O:66:LEU:N	2.38	0.57
7:D:162:LEU:HG	7:D:181:MET:HE2	1.86	0.57
1:A:1148:U:H2'	1:A:1149:C:O4'	2.05	0.57
9:F:43:LEU:N	9:F:43:LEU:HD22	2.20	0.57
5:B:87:ARG:NH2	5:B:233:SER:HB2	2.20	0.56
22:S:18:LYS:O	22:S:22:LEU:HG	2.04	0.56
6:C:108:ASN:HD22	6:C:111:LEU:CG	2.13	0.56
20:Q:67:LYS:HA	20:Q:70:ARG:NH1	2.12	0.56
6:C:47:LEU:N	6:C:47:LEU:HD12	2.19	0.56
6:C:64:VAL:HG12	6:C:66:VAL:HG23	1.87	0.56
1:A:1454:G:O2'	1:A:1455:G:H5'	2.04	0.56
1:A:960:U:H1'	1:A:1223:C:H5'	1.86	0.56
1:A:939:G:H5"	10:G:102:ARG:CZ	2.35	0.56
15:L:41:ARG:HH12	15:L:57:LYS:NZ	2.03	0.56
1:A:812:C:O2'	1:A:813:U:OP2	2.23	0.56
23:T:14:LYS:O	23:T:18:GLN:HG3	2.05	0.56
15:L:29:GLY:O	15:L:30:ALA:O	2.23	0.56
6:C:181:ASN:C	6:C:182:ILE:HD12	2.26	0.56
11:H:118:VAL:C	11:H:119:LEU:HD23	2.25	0.56
1:A:972:C:OP1	13:J:57:LYS:HE2	2.05	0.56
1:A:967:C:O2'	12:I:128:ARG:HD3	2.05	0.56
16:M:107:ALA:O	16:M:111:LYS:HG3	2.05	0.56
1:A:1271:G:H2'	1:A:1272:G:H8	1.69	0.56
6:C:29:TYR:HE2	6:C:33:LEU:HD12	1.69	0.56
13:J:39:PRO:O	13:J:40:LEU:HB2	2.05	0.56
1:A:1054:C:C3'	1:A:1054:C:O2	2.53	0.56
5:B:204:ASN:ND2	5:B:206:ASP:H	2.03	0.56
5:B:213:LEU:HD23	5:B:213:LEU:C	2.26	0.56
5:B:162:ILE:HG23	5:B:164:VAL:HG23	1.86	0.56
12:I:17:VAL:HG11	12:I:81:ILE:HG12	1.87	0.56
18:O:26:GLU:OE1	18:O:77:ARG:HD2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:62:ASN:O	16:M:63:THR:CB	2.50	0.56
1:A:404:U:H2'	1:A:405:U:H6	1.69	0.56
7:D:100:ARG:HH12	7:D:137:SER:HB3	1.68	0.56
11:H:68:ARG:HH11	11:H:68:ARG:HG2	1.70	0.56
6:C:83:ARG:O	6:C:85:ARG:N	2.31	0.56
7:D:150:GLU:HG3	7:D:153:ARG:HH22	1.70	0.56
10:G:78:ARG:HB2	10:G:156:TRP:CZ3	2.40	0.56
13:J:45:ARG:O	13:J:64:GLU:HA	2.05	0.56
13:J:44:VAL:HG21	13:J:66:ARG:HH21	1.70	0.56
6:C:23:TYR:CD2	6:C:23:TYR:C	2.78	0.56
1:A:270:A:H2'	1:A:271:C:C6	2.40	0.56
1:A:1007:C:H42	1:A:1022:G:H1	1.53	0.56
1:A:248:C:O2'	1:A:249:U:H5'	2.06	0.56
1:A:1101:A:H4'	1:A:1102:A:O5'	2.04	0.56
5:B:21:ARG:HA	5:B:39:ILE:HA	1.87	0.56
22:S:28:LYS:HD3	22:S:31:ILE:HD11	1.86	0.56
13:J:30:SER:CB	13:J:81:THR:HA	2.34	0.56
1:A:1290:G:H21	12:I:70:LYS:HZ1	1.54	0.56
1:A:1347:G:C8	12:I:107:ARG:NH1	2.73	0.56
1:A:1347:G:H2'	1:A:1373:G:N1	2.21	0.56
1:A:1004:A:H5"	1:A:1025:U:C5	2.40	0.56
16:M:78:ILE:O	16:M:81:LEU:HD23	2.06	0.56
22:S:42:PRO:O	22:S:45:VAL:HG23	2.06	0.56
20:Q:95:TYR:O	20:Q:97:SER:N	2.37	0.56
16:M:40:ASN:HD22	16:M:41:PRO:CD	2.19	0.56
1:A:287:U:O2'	1:A:288:A:H5'	2.05	0.56
5:B:223:ILE:HD12	5:B:230:VAL:HG11	1.87	0.56
5:B:24:TRP:CG	5:B:25:ASN:N	2.70	0.56
15:L:23:LYS:O	15:L:24:VAL:HG23	2.06	0.56
1:A:1168:A:H2'	1:A:1169:A:H8	1.67	0.56
16:M:14:ARG:H	16:M:44:ARG:NH2	1.99	0.56
23:T:56:MET:HE1	23:T:104:LEU:HD21	1.88	0.56
1:A:8:A:H5'	8:E:101:ILE:HG22	1.86	0.56
10:G:114:ARG:HH11	10:G:114:ARG:HG2	1.71	0.56
10:G:146:GLU:C	10:G:148:ASN:H	2.07	0.56
7:D:110:PHE:CD1	7:D:162:LEU:HD21	2.41	0.56
19:P:20:VAL:CG1	19:P:32:TYR:HB2	2.34	0.56
14:K:77:MET:HE1	14:K:80:VAL:HG13	1.87	0.56
8:E:87:SER:HB3	8:E:131:ILE:HD13	1.87	0.56
15:L:31:PRO:HB2	15:L:32:PHE:CD2	2.41	0.56
11:H:104:ARG:O	11:H:106:GLY:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:T:11:SER:C	23:T:13:LEU:HD12	2.26	0.56
1:A:405:U:H3'	1:A:406:G:H5'	1.88	0.56
7:D:142:PRO:HG2	7:D:187:ARG:HH21	1.71	0.56
1:A:792:A:H4'	1:A:793:U:H5"	1.88	0.56
1:A:1094:G:OP2	1:A:1095:U:H5	1.89	0.56
1:A:586:C:O2'	1:A:587:G:H5'	2.05	0.56
15:L:62:SER:O	15:L:64:TYR:HD1	1.89	0.56
6:C:123:GLN:NE2	6:C:140:ARG:HH22	2.04	0.56
8:E:116:THR:HG23	8:E:117:ASP:OD2	2.06	0.56
1:A:714:G:H2'	1:A:715:A:C8	2.41	0.56
1:A:1343:G:H2'	1:A:1344:C:H6	1.69	0.56
19:P:67:THR:HG22	19:P:68:ASP:N	2.20	0.56
11:H:34:GLU:O	11:H:37:ARG:HB2	2.04	0.56
19:P:5:ARG:HH12	19:P:24:ALA:HA	1.71	0.56
13:J:10:GLY:N	13:J:16:LEU:HD11	2.21	0.56
1:A:455:C:H42	1:A:477:G:H1	1.53	0.56
1:A:1314:C:O5'	22:S:6:LYS:HE2	2.06	0.56
23:T:38:LYS:O	23:T:39:LYS:C	2.44	0.56
10:G:37:ASN:ND2	12:I:41:VAL:HG23	2.21	0.56
5:B:30:ARG:HG3	5:B:31:TYR:N	2.20	0.56
5:B:80:ILE:CD1	5:B:80:ILE:H	2.04	0.56
11:H:86:ILE:CD1	11:H:133:LEU:HD21	2.35	0.56
5:B:12:GLU:C	5:B:14:GLY:N	2.59	0.56
5:B:71:VAL:CG2	5:B:164:VAL:HA	2.30	0.56
1:A:416:G:H2'	1:A:417:C:C6	2.41	0.56
10:G:124:LEU:O	10:G:127:ALA:HB3	2.06	0.56
1:A:135:C:O2	19:P:1:MET:HB2	2.06	0.56
9:F:55:ASP:HB3	9:F:86:ARG:HH12	1.71	0.56
15:L:46:LYS:CG	15:L:47:LYS:N	2.69	0.56
17:N:31:ARG:O	17:N:32:SER:CB	2.53	0.56
5:B:217:ARG:HA	5:B:220:ASP:OD2	2.06	0.56
6:C:66:VAL:O	6:C:66:VAL:HG12	2.06	0.56
7:D:61:LYS:CE	7:D:62:GLN:HE21	2.18	0.56
12:I:33:PHE:HZ	12:I:46:ALA:HB3	1.71	0.56
1:A:1353:G:O2'	1:A:1354:C:H5'	2.06	0.56
1:A:967:C:C4'	12:I:128:ARG:HG3	2.35	0.56
1:A:851:G:H2'	1:A:852:G:C8	2.41	0.56
1:A:428:G:H4'	1:A:429:U:O5'	2.06	0.56
1:A:1515:C:O2'	1:A:1516:G:H5'	2.06	0.56
1:A:1468:A:H2'	1:A:1469:G:O4'	2.07	0.56
1:A:89:C:H2'	1:A:90:U:O4'	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:21:ALA:O	8:E:23:GLY:N	2.36	0.56
11:H:136:GLU:O	11:H:137:VAL:HG23	2.07	0.55
1:A:1133:G:H2'	1:A:1134:G:C8	2.39	0.55
21:R:46:GLU:CD	21:R:46:GLU:H	2.09	0.55
1:A:691:G:O2'	1:A:797:C:H4'	2.06	0.55
1:A:840:C:OP2	1:A:840:C:H3'	2.05	0.55
1:A:421:U:H5'	1:A:422:C:H5	1.70	0.55
1:A:528:C:H41	15:L:49:ASN:ND2	2.04	0.55
1:A:560:U:O2'	1:A:561:U:OP2	2.21	0.55
13:J:55:LYS:O	13:J:56:HIS:HB2	2.06	0.55
1:A:895:G:H2'	1:A:896:C:C6	2.41	0.55
1:A:174:C:H2'	1:A:175:C:H6	1.69	0.55
19:P:10:GLY:HA3	19:P:14:ASN:O	2.05	0.55
1:A:397:A:H5'	1:A:398:C:OP1	2.05	0.55
17:N:4:LYS:HA	17:N:7:ILE:HG12	1.88	0.55
19:P:21:VAL:HG21	19:P:59:TRP:CD1	2.41	0.55
1:A:1286:A:H8	1:A:1287:A:H5"	1.71	0.55
13:J:38:ILE:CG1	13:J:71:LEU:HB3	2.36	0.55
5:B:69:LEU:HD23	5:B:69:LEU:C	2.27	0.55
8:E:96:PRO:HA	8:E:117:ASP:OD2	2.06	0.55
12:I:50:LEU:CA	12:I:55:ALA:HB3	2.36	0.55
1:A:154:C:H2'	1:A:155:C:H6	1.72	0.55
11:H:87:SER:HA	11:H:93:VAL:HG23	1.86	0.55
5:B:24:TRP:HB3	5:B:40:HIS:CE1	2.42	0.55
15:L:46:LYS:HD2	15:L:47:LYS:H	1.70	0.55
12:I:84:ALA:O	12:I:87:GLN:HB2	2.07	0.55
19:P:11:SER:OG	19:P:14:ASN:HB3	2.06	0.55
20:Q:45:HIS:CD2	20:Q:47:PRO:HG3	2.40	0.55
1:A:448:A:OP2	1:A:485:G:N2	2.34	0.55
1:A:1051:C:H2'	1:A:1052:U:H6	1.70	0.55
1:A:1055:A:C2	1:A:1056:U:H1'	2.42	0.55
7:D:70:ILE:HD11	7:D:100:ARG:HD2	1.88	0.55
10:G:111:ARG:HB3	10:G:113:GLU:OE2	2.06	0.55
22:S:5:LEU:O	22:S:6:LYS:CB	2.54	0.55
10:G:115:ARG:HB2	10:G:118:VAL:CG2	2.37	0.55
10:G:107:ALA:O	10:G:110:GLN:HB2	2.06	0.55
17:N:26:ARG:NH1	17:N:47:LEU:HD11	2.22	0.55
13:J:4:ILE:HA	13:J:100:THR:CB	2.36	0.55
17:N:3:ARG:CZ	17:N:6:LEU:HD12	2.37	0.55
23:T:100:ILE:O	23:T:100:ILE:HG22	2.06	0.55
11:H:119:LEU:HD12	11:H:124:ALA:CA	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:T:85:MET:CE	23:T:104:LEU:HD23	2.37	0.55
19:P:19:ILE:N	19:P:19:ILE:HD12	2.21	0.55
8:E:6:PHE:HE2	8:E:36:ASP:HB3	1.71	0.55
6:C:54:ARG:HG2	6:C:55:VAL:H	1.71	0.55
9:F:55:ASP:CB	9:F:86:ARG:HH12	2.20	0.55
9:F:12:PRO:HG3	9:F:57:GLN:O	2.06	0.55
6:C:58:GLU:O	6:C:64:VAL:HA	2.07	0.55
11:H:24:THR:CG2	11:H:63:LEU:HD21	2.35	0.55
1:A:190(L):U:C2	23:T:105:SER:HB2	2.41	0.55
6:C:134:ILE:HG22	6:C:168:ALA:HB3	1.86	0.55
5:B:134:GLU:HG2	5:B:137:ARG:NH2	2.21	0.55
6:C:182:ILE:O	6:C:183:ASP:C	2.43	0.55
6:C:139:GLN:HE21	6:C:139:GLN:CA	2.18	0.55
22:S:82:GLY:O	22:S:83:HIS:CB	2.55	0.55
6:C:44:GLU:C	6:C:46:GLU:H	2.09	0.55
20:Q:104:LYS:O	20:Q:105:ALA:HB2	2.07	0.55
15:L:75:HIS:CD2	15:L:77:LEU:H	2.25	0.55
16:M:77:ASN:O	16:M:80:ARG:HB3	2.06	0.55
6:C:130:VAL:O	6:C:134:ILE:HG13	2.05	0.55
6:C:54:ARG:HG2	6:C:55:VAL:N	2.22	0.55
1:A:864:A:H2'	1:A:865:A:C8	2.42	0.55
13:J:80:LYS:HA	13:J:83:GLU:HB2	1.88	0.55
11:H:127:LEU:CD2	11:H:127:LEU:N	2.70	0.55
1:A:1121:U:H2'	1:A:1122:U:C6	2.41	0.55
13:J:27:ALA:HA	13:J:30:SER:OG	2.06	0.55
13:J:38:ILE:H	13:J:72:VAL:H	1.55	0.55
13:J:4:ILE:HD11	13:J:77:PRO:HB3	1.89	0.55
1:A:1053:G:H4'	1:A:1054:C:H4'	1.88	0.55
1:A:1278:U:H4'	1:A:1279:A:O4'	2.07	0.55
9:F:63:TYR:N	9:F:63:TYR:HD2	2.05	0.55
15:L:40:VAL:O	15:L:40:VAL:HG12	2.06	0.55
1:A:1118:C:O4'	1:A:1179:A:H1'	2.07	0.55
6:C:151:VAL:C	6:C:152:ILE:HD12	2.27	0.55
1:A:427:U:OP1	7:D:13:ARG:NH2	2.39	0.54
6:C:191:THR:HG21	6:C:193:TYR:CE2	2.41	0.54
11:H:120:THR:HG23	11:H:123:GLU:OE2	2.07	0.54
8:E:120:THR:HG23	8:E:121:LYS:N	2.21	0.54
12:I:93:ARG:O	12:I:95:LYS:N	2.39	0.54
7:D:100:ARG:NH1	7:D:137:SER:HA	2.22	0.54
1:A:1234:C:O2'	1:A:1235:U:H5'	2.07	0.54
1:A:458:C:H2'	1:A:459:G:H8	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:127:ILE:HB	5:B:128:GLU:OE2	2.07	0.54
1:A:1250:A:C5'	12:I:68:GLY:N	2.69	0.54
1:A:1250:A:C5'	12:I:68:GLY:H	2.20	0.54
1:A:1197:G:OP1	1:A:1197:G:H3'	2.07	0.54
1:A:947:G:O3'	16:M:109:THR:HB	2.07	0.54
12:I:117:HIS:CD2	12:I:123:PRO:HA	2.42	0.54
16:M:8:GLU:C	16:M:9:ILE:HG13	2.27	0.54
23:T:13:LEU:N	23:T:13:LEU:HD12	2.21	0.54
1:A:1128:C:H1'	1:A:1146:A:H61	1.71	0.54
9:F:91:VAL:HG12	9:F:92:LYS:O	2.06	0.54
15:L:53:ARG:CD	15:L:93:LEU:HD21	2.37	0.54
15:L:53:ARG:HD2	15:L:93:LEU:HD21	1.89	0.54
11:H:77:GLU:HG3	11:H:78:GLN:N	2.22	0.54
6:C:150:LYS:HE2	6:C:152:ILE:HD11	1.88	0.54
1:A:1347:G:C2'	1:A:1348:U:OP2	2.55	0.54
1:A:1137:C:H4'	1:A:1138:G:N1	2.22	0.54
8:E:51:VAL:O	8:E:55:VAL:HG23	2.07	0.54
1:A:408:A:O2'	1:A:409:G:H5'	2.07	0.54
9:F:87:ARG:HH11	9:F:87:ARG:HG2	1.71	0.54
13:J:55:LYS:HG3	13:J:56:HIS:N	2.22	0.54
7:D:190:ASP:HB3	7:D:193:ASP:OD2	2.08	0.54
18:O:87:ILE:HG22	18:O:88:ARG:HG2	1.88	0.54
20:Q:81:ARG:O	20:Q:81:ARG:HG3	2.07	0.54
1:A:56:U:H2'	1:A:57:G:C8	2.42	0.54
5:B:129:GLU:O	5:B:130:ARG:HB2	2.06	0.54
6:C:47:LEU:CD2	6:C:68:VAL:HG11	2.37	0.54
1:A:1423:G:O2'	1:A:1424:C:H5'	2.06	0.54
1:A:994:A:H2'	1:A:994:A:N3	2.22	0.54
21:R:18:ARG:C	21:R:19:LYS:HD2	2.27	0.54
18:O:87:ILE:HG22	18:O:88:ARG:N	2.21	0.54
1:A:1109:C:OP2	6:C:176:HIS:CD2	2.60	0.54
10:G:123:GLU:HA	10:G:123:GLU:OE2	2.08	0.54
1:A:243:A:H4'	1:A:244:U:C5'	2.29	0.54
22:S:67:VAL:HG12	22:S:68:GLY:N	2.23	0.54
1:A:1441:G:H4'	1:A:1442:G:C4	2.41	0.54
1:A:191:G:C4	23:T:105:SER:HB3	2.43	0.54
1:A:993:G:H4'	1:A:994:A:OP2	2.07	0.54
19:P:20:VAL:HG11	19:P:32:TYR:HB3	1.90	0.54
5:B:123:ALA:CA	5:B:127:ILE:HD11	2.37	0.54
15:L:46:LYS:HE3	15:L:47:LYS:HB2	1.88	0.54
1:A:1001:A:H2	1:A:1040:U:H3	1.54	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:52:LEU:HD23	6:C:52:LEU:N	2.21	0.54
1:A:1014:A:C2	1:A:1219:U:H1'	2.41	0.54
1:A:695:A:P	14:K:53:SER:HB2	2.47	0.54
1:A:1320:C:O2	22:S:72:GLY:HA3	2.08	0.54
15:L:41:ARG:HB3	15:L:41:ARG:HH11	1.73	0.54
1:A:1064:G:H4'	1:A:1065:U:C5'	2.37	0.54
1:A:1381:U:O2'	1:A:1382:C:H5'	2.07	0.54
20:Q:76:LEU:HD23	20:Q:77:VAL:N	2.22	0.54
19:P:21:VAL:HG21	19:P:59:TRP:CG	2.43	0.54
5:B:69:LEU:HD12	5:B:155:LEU:CD1	2.38	0.54
18:O:26:GLU:HA	18:O:81:LEU:HD11	1.88	0.54
1:A:229:U:O2'	1:A:230:G:H5'	2.08	0.54
1:A:1128:C:C4'	12:I:16:ARG:HH12	2.20	0.54
1:A:338:A:H2	1:A:351:G:H22	1.55	0.54
19:P:4:ILE:HG13	19:P:64:ALA:HB1	1.89	0.54
6:C:150:LYS:HB2	6:C:169:ALA:CB	2.38	0.54
1:A:977:A:H2'	1:A:978:A:H5"	1.90	0.54
9:F:101:ALA:HB2	21:R:28:GLU:CB	2.38	0.54
1:A:653:A:OP1	11:H:56:LYS:NZ	2.38	0.54
1:A:99:C:H2'	1:A:101:A:O4'	2.08	0.54
13:J:23:ILE:O	13:J:23:ILE:HG22	2.08	0.54
13:J:3:LYS:N	13:J:75:ILE:HG23	2.23	0.54
10:G:16:LEU:H	10:G:16:LEU:CD2	2.13	0.54
1:A:760:G:N2	20:Q:104:LYS:N	2.56	0.54
20:Q:97:SER:CB	20:Q:103:GLY:HA2	2.38	0.54
20:Q:27:PHE:CE1	20:Q:36:ILE:HD11	2.43	0.54
5:B:95:GLN:C	5:B:96:ARG:HD2	2.27	0.54
1:A:1066:C:C5	1:A:1067:A:N6	2.76	0.54
9:F:82:ARG:HB2	9:F:85:VAL:CG2	2.38	0.54
1:A:376:G:OP2	19:P:67:THR:HG21	2.08	0.54
15:L:83:VAL:CG2	15:L:100:ILE:HG23	2.37	0.54
13:J:38:ILE:CD1	13:J:71:LEU:HD12	2.38	0.54
6:C:95:THR:O	6:C:97:LYS:N	2.39	0.54
19:P:58:TYR:CZ	19:P:62:VAL:HG21	2.43	0.54
1:A:960:U:O2	1:A:960:U:H5'	2.08	0.54
12:I:125:TYR:CE1	12:I:128:ARG:HD2	2.42	0.54
10:G:116:ALA:HA	10:G:119:ARG:NH2	2.22	0.54
1:A:1320:C:C2	22:S:72:GLY:HA3	2.43	0.54
8:E:24:ARG:HH11	8:E:24:ARG:HG2	1.72	0.54
1:A:204:U:H5'	1:A:216:G:O5'	2.08	0.54
14:K:69:ALA:O	14:K:72:ALA:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:29:TYR:CE1	13:J:65:LEU:HD11	2.42	0.53
10:G:51:GLN:NE2	10:G:58:PRO:HD3	2.20	0.53
1:A:407:G:H2'	1:A:408:A:C8	2.44	0.53
8:E:103:GLY:O	8:E:106:PRO:HD2	2.07	0.53
7:D:189:PRO:HB2	7:D:194:LEU:HD21	1.89	0.53
1:A:940:C:H2'	1:A:941:G:H8	1.72	0.53
20:Q:45:HIS:NE2	20:Q:47:PRO:HG3	2.23	0.53
1:A:1499:A:O2'	1:A:1500:A:H5'	2.07	0.53
9:F:1:MET:HG2	9:F:68:PRO:HA	1.88	0.53
1:A:1005:A:H2'	1:A:1006:C:H5'	1.89	0.53
5:B:134:GLU:O	5:B:138:LEU:HG	2.07	0.53
1:A:975:A:O2'	1:A:976:G:OP2	2.25	0.53
1:A:1286:A:C2	24:V:18:TYR:OH	2.62	0.53
23:T:49:ALA:HB3	23:T:99:LEU:CG	2.39	0.53
11:H:60:ARG:CG	11:H:60:ARG:HH11	2.21	0.53
1:A:642:A:N7	11:H:115:SER:HA	2.23	0.53
5:B:189:ASP:HB3	5:B:203:GLY:O	2.07	0.53
5:B:204:ASN:HD22	5:B:206:ASP:H	1.56	0.53
19:P:81:ARG:HG3	19:P:83:GLU:HG2	1.90	0.53
1:A:1218:C:H2'	1:A:1219:U:C6	2.43	0.53
12:I:11:LYS:O	12:I:11:LYS:HG2	2.08	0.53
1:A:952:U:O2'	1:A:953:G:H5'	2.08	0.53
10:G:143:ARG:O	10:G:145:ALA:O	2.27	0.53
1:A:1031:G:H2'	1:A:1032:G:C8	2.43	0.53
6:C:28:GLN:O	6:C:31:HIS:N	2.37	0.53
7:D:150:GLU:CD	7:D:153:ARG:HH12	2.12	0.53
5:B:30:ARG:HD2	5:B:31:TYR:CE2	2.43	0.53
1:A:448:A:H2'	1:A:449:C:C6	2.43	0.53
1:A:1123:A:O3'	13:J:36:GLY:HA3	2.09	0.53
9:F:99:ALA:HB2	21:R:31:LEU:CD1	2.39	0.53
21:R:53:ARG:HD3	21:R:59:SER:HA	1.89	0.53
7:D:121:VAL:O	7:D:134:ASP:HA	2.09	0.53
8:E:37:ARG:HG2	8:E:37:ARG:HH11	1.74	0.53
10:G:92:SER:O	10:G:96:GLN:HG3	2.08	0.53
13:J:8:LEU:CD2	13:J:20:ALA:HB2	2.35	0.53
6:C:111:LEU:HD21	6:C:144:SER:O	2.08	0.53
1:A:1208:C:H2'	1:A:1209:C:H6	1.73	0.53
1:A:1002:G:O2'	1:A:1003:G:H5'	2.09	0.53
1:A:406:G:H2'	1:A:407:G:H8	1.74	0.53
15:L:93:LEU:HB2	15:L:96:VAL:HG21	1.89	0.53
1:A:458:C:H2'	1:A:459:G:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:18:GLN:O	9:F:21:LEU:HB3	2.08	0.53
1:A:1479:C:H2'	1:A:1480:G:C8	2.44	0.53
16:M:23:TYR:O	16:M:25:ILE:N	2.40	0.53
11:H:83:ILE:HG23	11:H:83:ILE:O	2.09	0.53
1:A:791:G:C6	1:A:792:A:N7	2.76	0.53
9:F:22:GLU:O	9:F:26:ILE:HG13	2.09	0.53
13:J:42:THR:HG23	13:J:68:HIS:HA	1.89	0.53
1:A:269:C:H2'	1:A:270:A:C8	2.43	0.53
1:A:695:A:OP2	14:K:53:SER:HB2	2.08	0.53
5:B:144:ARG:HG3	5:B:145:LEU:H	1.72	0.53
1:A:1196:U:H4'	1:A:1197:G:OP2	2.07	0.53
1:A:1349:A:H2'	1:A:1350:A:C8	2.43	0.53
16:M:22:ILE:HG21	16:M:25:ILE:HD12	1.91	0.53
9:F:63:TYR:CD2	9:F:63:TYR:N	2.76	0.53
1:A:1067:A:N3	1:A:1068:G:H1'	2.23	0.53
7:D:106:TYR:HE1	7:D:113:SER:HA	1.71	0.53
13:J:44:VAL:HG22	13:J:66:ARG:HB3	1.91	0.53
1:A:1118:C:H1'	1:A:1179:A:C4	2.44	0.53
14:K:73:MET:SD	14:K:102:GLY:HA3	2.49	0.53
1:A:190(D):U:O2'	1:A:190(E):U:H5'	2.09	0.53
1:A:919:A:O2'	1:A:920:U:H5'	2.09	0.53
1:A:1286:A:H8	1:A:1287:A:C5'	2.22	0.53
5:B:77:ALA:HA	5:B:80:ILE:CD1	2.34	0.53
15:L:33:ARG:HD2	15:L:62:SER:HB3	1.91	0.53
13:J:6:ILE:O	13:J:71:LEU:O	2.27	0.53
1:A:1373:G:H5"	10:G:36:LYS:HB2	1.90	0.53
16:M:78:ILE:HA	16:M:81:LEU:CD2	2.37	0.53
1:A:133:U:OP1	23:T:74:LYS:HE2	2.09	0.53
5:B:101:MET:CA	5:B:108:ILE:HD12	2.38	0.53
1:A:1163:C:O2'	1:A:1164:G:H5'	2.08	0.53
6:C:157:ILE:HG21	6:C:164:ARG:NH2	2.24	0.53
23:T:59:ALA:O	23:T:63:ILE:HG13	2.09	0.53
15:L:47:LYS:CB	15:L:48:PRO:CD	2.77	0.53
13:J:24:VAL:O	13:J:28:ARG:HG3	2.09	0.53
1:A:370:C:O2'	1:A:371:G:H5'	2.09	0.53
3:Y:36:A:H2'	3:Y:37:A:C8	2.43	0.53
5:B:68:ILE:HB	5:B:90:MET:HE2	1.91	0.53
1:A:105:G:H2'	1:A:106:C:C6	2.44	0.53
1:A:881:G:OP2	15:L:12:ARG:NH2	2.42	0.53
12:I:32:ASP:O	12:I:35:GLU:N	2.42	0.53
19:P:38:TYR:HE2	19:P:50:LYS:HD3	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:48:LEU:HD13	9:F:52:ILE:HG13	1.91	0.53
22:S:15:LEU:O	22:S:19:VAL:HG12	2.09	0.53
13:J:6:ILE:HG22	13:J:98:ILE:HG23	1.90	0.53
15:L:24:VAL:O	15:L:26:ALA:N	2.35	0.53
21:R:47:THR:O	21:R:49:LYS:N	2.43	0.53
1:A:1315:U:H2'	1:A:1316:G:O4'	2.08	0.53
17:N:14:PRO:O	17:N:15:LYS:CB	2.57	0.53
1:A:653:A:C8	11:H:56:LYS:HG2	2.44	0.53
1:A:598:U:H4'	11:H:94:TYR:CD1	2.44	0.53
24:V:12:LYS:HB3	24:V:22:ARG:HD2	1.91	0.53
5:B:87:ARG:C	5:B:87:ARG:HD2	2.29	0.52
13:J:12:ASP:HB3	13:J:15:THR:CG2	2.40	0.52
13:J:25:GLU:C	13:J:27:ALA:H	2.11	0.52
1:A:1053:G:C3'	1:A:1054:C:C5'	2.88	0.52
1:A:1228:C:H2'	1:A:1229:A:H8	1.74	0.52
1:A:80:G:H3'	1:A:81:U:C5'	2.37	0.52
1:A:542:G:H2'	1:A:543:C:H6	1.74	0.52
1:A:502:G:OP1	15:L:118:SER:CB	2.57	0.52
1:A:966:G:H2'	1:A:967:C:C6	2.44	0.52
10:G:111:ARG:NH2	10:G:122:HIS:HB3	2.23	0.52
22:S:36:ARG:NH2	22:S:75:ALA:O	2.38	0.52
1:A:262:A:H5'	23:T:74:LYS:HG3	1.91	0.52
7:D:17:VAL:HG12	7:D:18:LYS:N	2.24	0.52
8:E:89:ILE:HD13	8:E:90:VAL:N	2.24	0.52
6:C:191:THR:HG22	6:C:193:TYR:H	1.74	0.52
1:A:1048:G:H5"	17:N:3:ARG:HG2	1.92	0.52
1:A:1202:G:O2'	1:A:1203:C:H5'	2.09	0.52
7:D:6:GLY:O	7:D:8:VAL:HG23	2.08	0.52
1:A:498:U:O2'	1:A:499:A:H5'	2.09	0.52
1:A:421:U:H5'	1:A:422:C:C5	2.44	0.52
1:A:1095:U:H2'	1:A:1096:C:H6	1.74	0.52
8:E:107:ARG:O	8:E:109:ILE:N	2.43	0.52
14:K:59:TYR:O	14:K:62:GLN:N	2.43	0.52
19:P:26:ARG:HD2	19:P:31:LYS:O	2.08	0.52
5:B:10:LEU:O	5:B:12:GLU:N	2.39	0.52
16:M:37:THR:HG23	16:M:55:ARG:HB3	1.92	0.52
1:A:1129:C:O5'	1:A:1130:A:H5'	2.09	0.52
1:A:761:G:C5'	20:Q:102:GLY:HA3	2.38	0.52
8:E:110:LEU:HD13	8:E:118:ILE:HG21	1.92	0.52
1:A:730:G:H21	1:A:765:G:H5"	1.72	0.52
5:B:89:GLY:H	5:B:226:ARG:HH22	1.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:556:C:O2'	1:A:557:G:H5'	2.08	0.52
1:A:1250:A:H4'	12:I:68:GLY:CA	2.39	0.52
6:C:147:LYS:HE3	6:C:203:PHE:CE2	2.44	0.52
21:R:45:SER:C	21:R:47:THR:H	2.11	0.52
6:C:190:ARG:HH11	6:C:190:ARG:CB	2.19	0.52
12:I:118:LYS:HZ2	12:I:118:LYS:CB	2.20	0.52
16:M:8:GLU:HG3	16:M:22:ILE:HG12	1.91	0.52
8:E:101:ILE:O	8:E:120:THR:HB	2.10	0.52
22:S:44:MET:HA	22:S:47:HIS:HD2	1.74	0.52
9:F:60:PHE:CE2	21:R:78:LEU:HD21	2.45	0.52
7:D:64:LEU:HD12	7:D:75:PHE:CE1	2.43	0.52
23:T:79:ARG:O	23:T:82:SER:HB3	2.10	0.52
1:A:646:U:H2'	1:A:647:C:C6	2.43	0.52
20:Q:12:SER:HB3	20:Q:20:THR:HB	1.90	0.52
19:P:42:ARG:O	19:P:43:LYS:C	2.48	0.52
22:S:17:GLU:O	22:S:21:GLU:HG3	2.10	0.52
13:J:3:LYS:N	13:J:75:ILE:HA	2.24	0.52
19:P:28:ARG:HG3	19:P:29:ASP:N	2.24	0.52
23:T:85:MET:HE3	23:T:104:LEU:HD23	1.90	0.52
1:A:502:G:OP1	15:L:118:SER:HB2	2.08	0.52
5:B:178:ARG:NH1	5:B:178:ARG:HG3	2.23	0.52
14:K:15:ALA:O	14:K:77:MET:HA	2.09	0.52
10:G:120:ILE:O	10:G:124:LEU:HG	2.09	0.52
1:A:17:U:H2'	1:A:18:C:C6	2.44	0.52
1:A:668:G:O2'	18:O:46:HIS:HD2	1.93	0.52
1:A:242:C:H2'	1:A:243:A:H5'	1.91	0.52
5:B:97:TRP:HH2	5:B:176:GLU:CD	2.13	0.52
17:N:30:ALA:O	17:N:33:VAL:HG22	2.10	0.52
1:A:337:C:H2'	1:A:338:A:H8	1.75	0.52
10:G:23:VAL:HG13	10:G:43:PHE:CE2	2.43	0.52
1:A:795:C:H5"	1:A:796:C:OP2	2.09	0.52
6:C:157:ILE:HD13	6:C:166:GLU:OE1	2.10	0.52
1:A:1042:G:O2'	1:A:1043:C:H5'	2.09	0.52
1:A:1286:A:C8	1:A:1287:A:H5"	2.45	0.52
22:S:21:GLU:O	22:S:24:ALA:N	2.42	0.52
6:C:36:ASP:O	6:C:39:ILE:HB	2.09	0.52
5:B:102:LEU:HD21	5:B:162:ILE:CD1	2.38	0.52
18:O:74:ASP:CG	18:O:77:ARG:HG3	2.29	0.52
14:K:69:ALA:O	14:K:70:LYS:C	2.48	0.52
23:T:16:HIS:CE1	23:T:20:LEU:HD11	2.44	0.52
1:A:107:G:C2'	1:A:108:G:H5'	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:24:ARG:O	24:V:25:LYS:HB3	2.09	0.52
5:B:135:GLN:O	5:B:139:LYS:HE2	2.10	0.52
1:A:1207:G:O2'	1:A:1208:C:H5'	2.10	0.52
6:C:64:VAL:HG12	6:C:65:ALA:H	1.74	0.52
21:R:87:ARG:HH11	21:R:87:ARG:HG3	1.75	0.52
22:S:62:ILE:HD12	22:S:63:THR:N	2.25	0.52
1:A:760:G:H21	20:Q:104:LYS:H	1.58	0.52
5:B:78:GLN:HG3	5:B:94:ASN:O	2.10	0.52
1:A:1263:C:H2'	1:A:1264:C:C6	2.45	0.52
6:C:150:LYS:CE	6:C:152:ILE:HD11	2.40	0.52
1:A:21:G:H2'	1:A:22:G:C8	2.44	0.52
5:B:80:ILE:HG12	5:B:208:ILE:CG2	2.37	0.52
13:J:71:LEU:HD13	13:J:73:ASP:HB2	1.92	0.52
1:A:254:G:O2'	1:A:255:G:H5'	2.08	0.52
1:A:1057:G:O2'	1:A:1058:G:H5'	2.09	0.52
16:M:14:ARG:N	16:M:44:ARG:NH2	2.53	0.52
1:A:1351:U:O2'	1:A:1352:C:H5'	2.10	0.52
14:K:95:ILE:O	14:K:99:GLN:HG3	2.09	0.52
22:S:67:VAL:O	22:S:69:HIS:N	2.43	0.52
15:L:119:LYS:O	15:L:120:TYR:HB2	2.10	0.52
1:A:1049:U:H4'	1:A:1050:G:OP2	2.08	0.52
1:A:1394:A:C5	1:A:1501:C:H4'	2.44	0.52
13:J:19:SER:HA	13:J:22:LYS:HZ3	1.75	0.52
5:B:44:LEU:HA	5:B:47:THR:OG1	2.09	0.52
1:A:1228:C:H4'	16:M:116:THR:HA	1.92	0.52
14:K:18:ARG:CB	14:K:33:THR:HG22	2.39	0.52
16:M:8:GLU:OE2	16:M:8:GLU:HA	2.11	0.52
1:A:41:G:H2'	1:A:42:G:C8	2.45	0.52
1:A:1392:G:O2'	1:A:1502:A:H5"	2.10	0.51
6:C:43:LEU:HD13	6:C:68:VAL:CG2	2.39	0.51
23:T:57:ARG:HB3	23:T:57:ARG:HH11	1.73	0.51
16:M:63:THR:HG23	16:M:64:TRP:CG	2.44	0.51
1:A:761:G:H5'	20:Q:103:GLY:H	1.74	0.51
11:H:125:ARG:NH1	11:H:125:ARG:HB2	2.25	0.51
1:A:1161:C:H2'	1:A:1162:C:C6	2.44	0.51
1:A:47:C:H5"	1:A:365:U:C6	2.44	0.51
14:K:26:ASN:O	14:K:27:ASN:HB2	2.11	0.51
13:J:16:LEU:O	13:J:17:ASP:C	2.48	0.51
1:A:945:G:C2	1:A:946:A:C8	2.98	0.51
8:E:12:LEU:CD1	8:E:31:LEU:HB2	2.40	0.51
5:B:59:GLU:O	5:B:62:ALA:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1257:U:O2'	1:A:1258:G:OP2	2.25	0.51
14:K:40:ILE:HG23	14:K:75:TYR:CD2	2.46	0.51
8:E:110:LEU:O	8:E:113:ALA:HB3	2.10	0.51
8:E:126:ARG:CG	8:E:126:ARG:HH11	2.23	0.51
1:A:232:G:H1'	1:A:262:A:N1	2.25	0.51
6:C:61:ALA:C	6:C:63:ASN:H	2.12	0.51
23:T:94:ALA:O	23:T:95:ALA:HB3	2.09	0.51
1:A:1165:C:O2'	1:A:1166:G:H5'	2.10	0.51
1:A:377:G:OP1	19:P:3:LYS:NZ	2.43	0.51
12:I:114:TYR:CE1	13:J:59:SER:O	2.63	0.51
1:A:1195:C:H3'	1:A:1196:U:H5'	1.91	0.51
7:D:8:VAL:CG1	7:D:21:LEU:HD13	2.40	0.51
1:A:335:C:H2'	1:A:336:C:C6	2.45	0.51
1:A:190:C:H2'	1:A:190(A):C:C6	2.45	0.51
1:A:1056:U:C5'	6:C:163:ALA:HB2	2.32	0.51
6:C:195:VAL:CG1	6:C:196:LEU:N	2.73	0.51
12:I:116:LYS:O	12:I:118:LYS:N	2.43	0.51
1:A:1321:C:N4	22:S:37:ARG:HH12	2.08	0.51
7:D:64:LEU:HD13	7:D:64:LEU:C	2.31	0.51
9:F:91:VAL:HG13	21:R:72:ARG:NH2	2.25	0.51
1:A:1496:C:H2'	1:A:1497:G:O4'	2.10	0.51
5:B:166:ASP:OD2	5:B:169:LYS:HB2	2.10	0.51
20:Q:65:ILE:HD12	20:Q:65:ILE:N	2.25	0.51
22:S:15:LEU:HD12	22:S:16:LEU:H	1.74	0.51
14:K:87:THR:HG23	14:K:91:ARG:NH2	2.25	0.51
23:T:57:ARG:HB3	23:T:57:ARG:NH1	2.25	0.51
20:Q:104:LYS:CD	20:Q:105:ALA:H	2.24	0.51
1:A:1216:G:O2'	1:A:1217:C:H5'	2.10	0.51
1:A:1223:C:P	22:S:78:ARG:NH1	2.83	0.51
1:A:629:G:O2'	1:A:630:G:H5'	2.11	0.51
7:D:23:GLY:HA3	7:D:112:VAL:CG1	2.40	0.51
1:A:1029:C:H2'	1:A:1030:C:C6	2.45	0.51
21:R:42:ARG:HH11	21:R:42:ARG:HG3	1.74	0.51
1:A:1312:G:O2'	1:A:1313:U:H5'	2.11	0.51
17:N:37:PHE:CE2	17:N:53:LEU:HD13	2.46	0.51
22:S:28:LYS:CG	22:S:29:ARG:H	2.06	0.51
6:C:177:THR:O	6:C:177:THR:HG23	2.11	0.51
1:A:1392:G:O2'	1:A:1393:U:H5'	2.11	0.51
5:B:14:GLY:C	5:B:15:VAL:HG22	2.31	0.51
5:B:73:THR:HG23	5:B:95:GLN:O	2.11	0.51
1:A:190(L):U:O2'	1:A:191:G:H5'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:40:VAL:HG22	9:F:41:GLU:N	2.24	0.51
1:A:669:U:H2'	1:A:670:G:C8	2.45	0.51
1:A:364:A:N6	15:L:28:LYS:NZ	2.58	0.51
6:C:47:LEU:HD23	6:C:68:VAL:HG11	1.93	0.51
6:C:190:ARG:HB3	6:C:190:ARG:NH1	2.22	0.51
7:D:21:LEU:HD21	7:D:66:ARG:O	2.10	0.51
20:Q:104:LYS:HD2	20:Q:105:ALA:H	1.74	0.51
1:A:792:A:H4'	1:A:793:U:C5'	2.41	0.51
1:A:180:U:H2'	1:A:181:G:C5'	2.41	0.51
1:A:895:G:H2'	1:A:896:C:H6	1.75	0.51
21:R:25:THR:O	21:R:26:LEU:HB2	2.11	0.51
12:I:111:ARG:HD3	12:I:112:LYS:N	2.25	0.51
5:B:208:ILE:HG22	5:B:212:GLN:HB2	1.93	0.51
1:A:973:G:H3'	1:A:974:A:H5"	1.93	0.51
20:Q:60:ILE:HD13	20:Q:61:GLU:H	1.75	0.51
1:A:620:C:C1'	7:D:135:LEU:HD13	2.41	0.51
8:E:24:ARG:NH1	8:E:24:ARG:HG2	2.26	0.51
1:A:1469:G:O2'	1:A:1470:G:H5'	2.11	0.51
8:E:75:THR:HG23	8:E:76:ILE:N	2.24	0.51
23:T:43:LEU:HD12	23:T:52:ALA:HA	1.92	0.51
8:E:79:GLU:O	11:H:104:ARG:NH1	2.44	0.51
1:A:1227:A:H2'	1:A:1228:C:O5'	2.10	0.51
10:G:15:ASP:HB2	10:G:20:ASP:O	2.11	0.51
22:S:41:VAL:HB	22:S:42:PRO:HD2	1.93	0.51
1:A:722:A:H2'	1:A:724:G:H8	1.75	0.51
1:A:1129:C:H1'	1:A:1132:C:C5	2.45	0.51
5:B:101:MET:HB3	5:B:152:PHE:CZ	2.45	0.51
15:L:93:LEU:O	15:L:96:VAL:HG23	2.11	0.51
1:A:413:G:N2	1:A:428:G:O2'	2.44	0.51
23:T:39:LYS:HD2	23:T:55:ILE:HD13	1.93	0.51
23:T:38:LYS:O	23:T:41:ILE:N	2.43	0.51
13:J:33:GLN:O	13:J:33:GLN:HG2	2.11	0.51
5:B:156:LYS:NZ	5:B:156:LYS:HA	2.26	0.51
13:J:49:VAL:HG11	17:N:41:ARG:O	2.11	0.51
6:C:94:LEU:HD23	6:C:95:THR:N	2.25	0.51
5:B:146:GLN:O	5:B:150:SER:HB3	2.10	0.51
10:G:140:ASP:HA	10:G:143:ARG:HD2	1.91	0.51
13:J:94:VAL:CG1	13:J:95:GLU:N	2.73	0.51
6:C:77:ILE:O	6:C:83:ARG:N	2.44	0.51
1:A:411:A:N6	1:A:413:G:N2	2.59	0.51
1:A:1310:G:N7	22:S:2:PRO:HD3	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1148:U:H4'	12:I:14:VAL:HG11	1.93	0.51
19:P:5:ARG:NH1	19:P:24:ALA:HA	2.25	0.51
1:A:457:C:H2'	1:A:458:C:H6	1.76	0.51
5:B:144:ARG:HD2	5:B:145:LEU:CD2	2.38	0.50
1:A:740:U:O2'	1:A:741:G:H5'	2.11	0.50
7:D:179:GLU:OE1	7:D:179:GLU:N	2.33	0.50
1:A:1495:U:H2'	1:A:1496:C:H6	1.76	0.50
21:R:52:PRO:O	21:R:56:THR:HG23	2.10	0.50
1:A:1023:G:H2'	1:A:1024:G:H5'	1.92	0.50
5:B:87:ARG:HH22	5:B:233:SER:HB2	1.76	0.50
5:B:21:ARG:H	5:B:21:ARG:CD	2.02	0.50
1:A:877:C:H1'	11:H:3:THR:CG2	2.42	0.50
13:J:7:LYS:HE3	13:J:40:LEU:CD1	2.41	0.50
12:I:107:ARG:HH11	12:I:107:ARG:CB	2.25	0.50
1:A:1187:G:OP1	12:I:113:LYS:HE2	2.11	0.50
1:A:722:A:H2'	1:A:724:G:C8	2.46	0.50
1:A:393:A:C2'	1:A:394:G:H5'	2.41	0.50
23:T:67:ALA:O	23:T:73:HIS:ND1	2.44	0.50
19:P:20:VAL:CG1	19:P:32:TYR:CB	2.89	0.50
5:B:30:ARG:HD2	5:B:31:TYR:CZ	2.46	0.50
1:A:776:G:N2	1:A:802:A:OP2	2.41	0.50
17:N:36:PHE:O	17:N:37:PHE:CG	2.64	0.50
5:B:209:ARG:NH2	5:B:239:VAL:HG11	2.26	0.50
1:A:1277:C:HO2'	1:A:1279:A:C1'	2.24	0.50
1:A:954:G:H21	1:A:1227:A:H62	1.60	0.50
1:A:761:G:H5'	20:Q:103:GLY:N	2.26	0.50
1:A:1460:A:H2'	1:A:1461:G:O4'	2.11	0.50
1:A:1497:G:H2'	1:A:1498:U:H5'	1.93	0.50
21:R:22:VAL:HG13	21:R:42:ARG:HD2	1.92	0.50
1:A:157:G:O2'	1:A:158:G:H5'	2.11	0.50
1:A:1388:C:H2'	1:A:1389:C:C6	2.47	0.50
16:M:117:VAL:HG12	16:M:118:ALA:N	2.27	0.50
9:F:80:ARG:HH11	9:F:80:ARG:HG2	1.76	0.50
12:I:10:ARG:HD3	12:I:105:ASP:HB3	1.92	0.50
6:C:33:LEU:C	6:C:33:LEU:HD23	2.32	0.50
6:C:191:THR:HB	6:C:194:GLY:O	2.11	0.50
5:B:10:LEU:C	5:B:10:LEU:HD23	2.32	0.50
5:B:18:GLY:CA	5:B:41:ILE:HA	2.41	0.50
1:A:279:A:H4'	1:A:280:C:OP2	2.09	0.50
1:A:502:G:H2'	1:A:503:C:C6	2.47	0.50
1:A:1314:C:P	22:S:6:LYS:HE2	2.52	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:176:LEU:HG	7:D:177:ASP:N	2.27	0.50
8:E:40:ARG:HG2	8:E:68:GLU:OE2	2.12	0.50
1:A:694:A:H2'	1:A:695:A:O5'	2.11	0.50
1:A:1465:C:H2'	1:A:1466:C:O4'	2.12	0.50
1:A:667:G:H4'	18:O:51:HIS:ND1	2.27	0.50
6:C:37:GLN:NE2	17:N:52:GLN:OE1	2.45	0.50
5:B:151:GLY:C	5:B:153:ARG:H	2.14	0.50
12:I:53:VAL:CG2	12:I:85:LEU:HD21	2.41	0.50
1:A:9:G:H5'	8:E:122:GLU:OE2	2.11	0.50
12:I:128:ARG:O	12:I:128:ARG:HG2	2.11	0.50
1:A:519:C:H2'	1:A:520:A:C8	2.45	0.50
1:A:103:C:P	23:T:17:ARG:HH11	2.34	0.50
6:C:3:ASN:O	6:C:4:LYS:HB2	2.11	0.50
4:Z:2:U:H5'	4:Z:2:U:H6	1.77	0.50
6:C:182:ILE:N	6:C:182:ILE:HD12	2.26	0.50
1:A:1307:U:H5'	16:M:109:THR:HG21	1.94	0.50
6:C:64:VAL:CG1	6:C:66:VAL:HG23	2.41	0.50
1:A:392:G:H2'	1:A:393:A:C8	2.46	0.50
1:A:1193:G:C2'	1:A:1194:U:H5'	2.41	0.50
1:A:258:G:H2'	1:A:259:G:C8	2.44	0.50
1:A:818:G:O2'	1:A:819:A:H5"	2.12	0.50
13:J:62:HIS:HB3	17:N:59:ALA:HB3	1.93	0.50
5:B:89:GLY:N	5:B:226:ARG:HH22	2.10	0.50
20:Q:11:VAL:O	20:Q:12:SER:HB2	2.11	0.50
11:H:5:PRO:O	11:H:8:ASP:HB3	2.12	0.50
13:J:14:LYS:C	13:J:16:LEU:H	2.14	0.50
8:E:11:ILE:HG12	8:E:33:VAL:HG23	1.94	0.50
12:I:45:ALA:O	12:I:47:LEU:N	2.44	0.50
16:M:8:GLU:OE1	16:M:22:ILE:HA	2.10	0.50
20:Q:59:ILE:HD13	20:Q:73:VAL:HA	1.94	0.50
1:A:1298:C:C4	10:G:114:ARG:HD3	2.47	0.50
1:A:1491:G:C5	25:A:1545:PAR:H21	2.46	0.50
6:C:151:VAL:HA	6:C:199:LYS:O	2.11	0.50
19:P:26:ARG:HD3	19:P:31:LYS:N	2.27	0.50
12:I:25:LYS:HG2	12:I:60:ASP:OD2	2.11	0.50
15:L:71:PRO:HG2	15:L:102:ARG:HG3	1.93	0.50
5:B:43:ASP:OD1	5:B:45:GLN:HB2	2.12	0.50
12:I:23:ASN:HD22	12:I:23:ASN:C	2.14	0.50
1:A:1094:G:OP2	1:A:1095:U:C5	2.64	0.50
15:L:41:ARG:NH1	15:L:57:LYS:HZ1	2.10	0.50
6:C:75:VAL:O	6:C:83:ARG:HD3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:818:G:H3'	1:A:819:A:C5'	2.42	0.50
22:S:51:VAL:O	22:S:58:VAL:HG22	2.12	0.50
1:A:1473:A:H2'	1:A:1474:G:C8	2.47	0.50
1:A:731:G:OP1	1:A:766:A:H1'	2.12	0.50
6:C:108:ASN:ND2	6:C:111:LEU:HG	2.13	0.50
1:A:1278:U:H4'	1:A:1279:A:O5'	2.11	0.50
1:A:1201:A:O2'	1:A:1202:G:OP2	2.28	0.50
11:H:48:TYR:HB2	11:H:60:ARG:O	2.12	0.50
18:O:4:THR:OG1	18:O:7:GLU:HB2	2.12	0.50
7:D:163:GLU:O	7:D:165:MET:N	2.45	0.50
3:Y:29:G:H2'	3:Y:30:G:C8	2.46	0.50
1:A:1466:C:H2'	1:A:1467:G:O4'	2.12	0.50
6:C:126:ARG:O	6:C:127:ARG:HB2	2.12	0.50
13:J:89:ASP:O	13:J:90:LEU:HD23	2.12	0.49
1:A:1054:C:H5	1:A:1196:U:C6	2.29	0.49
6:C:173:VAL:O	6:C:173:VAL:HG12	2.11	0.49
7:D:61:LYS:HD2	7:D:207:TYR:OH	2.11	0.49
1:A:1278:U:C5'	1:A:1279:A:H5'	2.42	0.49
12:I:4:TYR:HB2	12:I:19:LEU:HB2	1.94	0.49
1:A:438:G:C4'	1:A:439:A:OP1	2.57	0.49
16:M:34:LEU:HD13	16:M:41:PRO:CA	2.41	0.49
9:F:94:GLN:CB	21:R:32:ARG:HH11	2.24	0.49
18:O:36:ILE:CG1	18:O:59:MET:HE3	2.42	0.49
1:A:640:A:O2'	1:A:641:U:H5'	2.12	0.49
1:A:818:G:C2'	1:A:819:A:H5"	2.42	0.49
1:A:918:A:H2'	1:A:919:A:O4'	2.12	0.49
5:B:130:ARG:HD2	5:B:134:GLU:OE1	2.12	0.49
1:A:1054:C:N3	3:Y:34:G:O4'	2.45	0.49
9:F:33:TYR:CD1	9:F:75:LEU:HD22	2.47	0.49
1:A:1372:U:C2'	1:A:1373:G:H5'	2.43	0.49
12:I:47:LEU:HB3	12:I:50:LEU:HD12	1.94	0.49
1:A:443:C:N3	1:A:492:G:C2	2.80	0.49
7:D:64:LEU:HD12	7:D:75:PHE:HZ	1.74	0.49
6:C:151:VAL:HG12	6:C:152:ILE:N	2.27	0.49
9:F:101:ALA:HB2	21:R:28:GLU:HB2	1.94	0.49
1:A:1477:C:O2'	1:A:1478:C:H5'	2.12	0.49
7:D:199:ASN:C	7:D:199:ASN:ND2	2.65	0.49
1:A:883:C:O2'	1:A:884:U:H5'	2.13	0.49
20:Q:53:LEU:N	20:Q:53:LEU:HD12	2.26	0.49
1:A:314:C:O2'	1:A:315:A:H5'	2.11	0.49
1:A:1369:C:H2'	1:A:1370:G:H8	1.73	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:19:VAL:HG13	22:S:20:LEU:H	1.76	0.49
1:A:1098:C:H2'	1:A:1099:G:O4'	2.12	0.49
1:A:737:A:H1'	9:F:73:ASN:ND2	2.14	0.49
17:N:29:ARG:O	17:N:33:VAL:HG13	2.13	0.49
6:C:137:ALA:O	6:C:141:VAL:HG23	2.12	0.49
17:N:25:VAL:HG13	17:N:25:VAL:O	2.12	0.49
12:I:7:THR:HG22	12:I:8:GLY:N	2.26	0.49
16:M:85:GLY:O	16:M:86:CYS:O	2.30	0.49
5:B:142:LEU:O	5:B:142:LEU:HD23	2.12	0.49
23:T:11:SER:HA	23:T:13:LEU:HD11	1.92	0.49
1:A:939:G:C6	1:A:940:C:N4	2.80	0.49
21:R:18:ARG:HE	21:R:18:ARG:HA	1.77	0.49
1:A:57:G:H2'	1:A:58:C:C6	2.47	0.49
6:C:67:THR:HG23	6:C:102:ASN:HB2	1.93	0.49
7:D:52:SER:O	7:D:53:ASP:C	2.51	0.49
22:S:33:THR:HG22	22:S:35:SER:N	2.03	0.49
1:A:1057:G:H2'	1:A:1058:G:O4'	2.12	0.49
6:C:139:GLN:NE2	6:C:139:GLN:HA	2.27	0.49
10:G:17:VAL:HG12	10:G:18:TYR:CD1	2.48	0.49
8:E:120:THR:CG2	8:E:121:LYS:N	2.76	0.49
1:A:403:C:O2'	1:A:404:U:H5'	2.12	0.49
14:K:21:ILE:HG12	14:K:30:VAL:HG12	1.93	0.49
1:A:942:G:H2'	1:A:943:U:H6	1.77	0.49
15:L:45:PRO:HD3	15:L:51:ALA:O	2.12	0.49
1:A:50:A:N6	1:A:361:G:H4'	2.27	0.49
1:A:484:G:H5'	1:A:486:U:O4'	2.12	0.49
5:B:144:ARG:HA	5:B:147:LYS:HD2	1.92	0.49
1:A:1288:A:N1	1:A:1371:G:H1'	2.27	0.49
22:S:15:LEU:HD12	22:S:16:LEU:N	2.28	0.49
11:H:136:GLU:O	11:H:137:VAL:CG2	2.60	0.49
1:A:242:C:C2'	1:A:243:A:H5'	2.43	0.49
1:A:1305:G:H5'	24:V:4:GLY:HA3	1.93	0.49
5:B:36:ARG:HG3	5:B:41:ILE:HD12	1.94	0.49
16:M:88:ARG:NH1	22:S:3:ARG:HH21	2.11	0.49
1:A:1216:G:H5"	17:N:5:ALA:CB	2.43	0.49
9:F:19:LEU:HD21	9:F:23:LYS:HD2	1.95	0.49
1:A:31:G:H1	1:A:48:C:H5"	1.76	0.49
1:A:686:U:O4	1:A:703:G:H1'	2.12	0.49
11:H:116:LYS:HD2	11:H:129:VAL:HG11	1.94	0.49
1:A:1174:G:O2'	1:A:1175:G:H5'	2.12	0.49
1:A:299:G:H2'	1:A:300:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:570:G:H2'	1:A:571:U:C6	2.48	0.49
10:G:95:ARG:HH11	10:G:95:ARG:HG3	1.76	0.49
5:B:124:SER:O	5:B:127:ILE:HG13	2.12	0.49
5:B:87:ARG:O	5:B:87:ARG:HD2	2.13	0.49
1:A:1367:C:H5'	13:J:60:ARG:NH1	2.28	0.49
6:C:180:ALA:HB1	6:C:203:PHE:CE1	2.47	0.49
23:T:54:LYS:HA	23:T:57:ARG:HD3	1.95	0.49
12:I:4:TYR:CE2	12:I:88:TYR:HA	2.47	0.49
20:Q:26:GLN:O	20:Q:27:PHE:HB3	2.12	0.49
1:A:750:G:H1'	18:O:23:GLY:H	1.78	0.49
1:A:957:U:H3	1:A:960:U:C5'	2.25	0.49
1:A:1172:C:H2'	1:A:1173:G:H8	1.78	0.49
19:P:7:ALA:O	19:P:17:TYR:HA	2.12	0.49
1:A:976:G:H5'	1:A:1358:U:O2'	2.13	0.49
1:A:1250:A:H5"	12:I:68:GLY:H	1.76	0.49
5:B:53:ARG:NH1	5:B:199:TYR:CD2	2.81	0.49
1:A:1048:G:H5"	17:N:3:ARG:CG	2.43	0.49
15:L:126:LYS:HD2	15:L:126:LYS:N	2.20	0.49
5:B:75:LYS:HA	5:B:78:GLN:HB2	1.94	0.49
1:A:382:A:C2	1:A:383:A:C4	3.00	0.49
1:A:1120:G:H2'	1:A:1121:U:C6	2.48	0.49
23:T:93:GLU:OE2	23:T:93:GLU:HA	2.12	0.49
20:Q:76:LEU:CD2	20:Q:76:LEU:C	2.81	0.49
1:A:1072:G:H2'	1:A:1073:U:C6	2.47	0.49
18:O:9:GLN:HA	18:O:9:GLN:OE1	2.11	0.49
22:S:30:LEU:HA	22:S:48:THR:O	2.13	0.49
13:J:27:ALA:HB2	13:J:85:LEU:HD21	1.94	0.49
16:M:109:THR:O	16:M:109:THR:HG23	2.13	0.49
18:O:78:TYR:CE1	18:O:82:ILE:HD11	2.48	0.49
7:D:58:LEU:HD23	7:D:206:PHE:CZ	2.48	0.49
21:R:47:THR:HG23	21:R:83:GLU:N	2.18	0.49
5:B:85:ALA:HB1	5:B:92:TYR:HB3	1.94	0.49
20:Q:2:PRO:O	20:Q:3:LYS:C	2.51	0.49
9:F:87:ARG:HH11	9:F:87:ARG:CG	2.24	0.49
1:A:169:C:O2'	1:A:170:U:H5'	2.13	0.49
5:B:194:PRO:O	5:B:196:LEU:N	2.46	0.49
1:A:302:G:H5"	15:L:17:LYS:NZ	2.27	0.49
7:D:36:ARG:N	7:D:37:PRO:CD	2.65	0.49
13:J:3:LYS:C	13:J:4:ILE:HG13	2.32	0.49
1:A:1054:C:H2'	1:A:1055:A:H5"	1.94	0.49
1:A:1053:G:C5'	1:A:1054:C:H5'	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1197:G:O2'	1:A:1198:G:H5'	2.12	0.49
1:A:578:C:O2'	1:A:728:A:N3	2.42	0.49
11:H:24:THR:HG23	11:H:61:VAL:HB	1.95	0.49
1:A:1424:C:O2'	1:A:1425:U:H5'	2.12	0.49
21:R:59:SER:O	21:R:60:GLY:C	2.51	0.49
1:A:19:C:H2'	1:A:20:U:H6	1.77	0.49
5:B:84:GLU:HA	5:B:87:ARG:HB3	1.95	0.49
10:G:62:PHE:O	10:G:65:ALA:HB3	2.12	0.49
1:A:1167:A:H2'	1:A:1168:A:C8	2.48	0.49
12:I:42:ARG:O	12:I:43:ALA:C	2.51	0.49
8:E:51:VAL:CB	8:E:52:PRO:HD3	2.38	0.49
1:A:112:G:O2'	1:A:113:G:H5'	2.12	0.49
1:A:337:C:H2'	1:A:338:A:C8	2.48	0.49
23:T:36:LEU:HD12	23:T:62:LEU:HD12	1.95	0.49
24:V:17:THR:O	24:V:22:ARG:NH1	2.41	0.49
23:T:26:ASN:OD1	23:T:71:THR:HG23	2.13	0.49
14:K:54:ARG:HH11	14:K:54:ARG:HG3	1.78	0.48
1:A:1038:C:H2'	1:A:1039:C:C5	2.48	0.48
1:A:1302:U:C5	16:M:17:VAL:HG21	2.47	0.48
19:P:22:THR:OG1	19:P:23:ASP:N	2.46	0.48
1:A:334:C:H2'	1:A:335:C:C6	2.49	0.48
1:A:1216:G:H5"	17:N:5:ALA:HB2	1.94	0.48
11:H:91:ARG:NH1	20:Q:33:GLY:HA3	2.28	0.48
15:L:104:VAL:O	15:L:105:TYR:HB2	2.12	0.48
1:A:411:A:C2	1:A:431:A:N6	2.81	0.48
23:T:36:LEU:O	23:T:37:SER:C	2.51	0.48
7:D:9:CYS:O	7:D:12:CYS:HB2	2.13	0.48
1:A:1429:C:H2'	1:A:1430:C:C6	2.48	0.48
10:G:6:ARG:O	10:G:7:ALA:C	2.51	0.48
6:C:112:SER:OG	6:C:115:LEU:HG	2.14	0.48
1:A:1348:U:O2'	1:A:1349:A:H5'	2.13	0.48
12:I:53:VAL:HG21	12:I:85:LEU:HD21	1.94	0.48
14:K:82:VAL:HG23	14:K:105:VAL:HG13	1.95	0.48
22:S:40:ILE:HB	22:S:67:VAL:O	2.13	0.48
1:A:1143:G:H2'	1:A:1144:G:C8	2.48	0.48
1:A:190(L):U:H3	23:T:105:SER:CB	2.26	0.48
1:A:1497:G:O2'	1:A:1498:U:H5'	2.13	0.48
7:D:190:ASP:O	7:D:193:ASP:HB2	2.13	0.48
22:S:13:ASP:O	22:S:14:HIS:C	2.51	0.48
1:A:1533:C:O2'	1:A:1534:A:H5'	2.14	0.48
1:A:753:A:H4'	1:A:754:C:H5"	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:144:ARG:HG3	5:B:145:LEU:N	2.27	0.48
17:N:35:ARG:C	17:N:37:PHE:N	2.66	0.48
6:C:188:LEU:O	6:C:189:ALA:HB2	2.13	0.48
16:M:81:LEU:HD23	16:M:81:LEU:N	2.29	0.48
20:Q:94:ASN:O	20:Q:97:SER:HB2	2.13	0.48
1:A:687:A:H2	1:A:700:G:N3	2.11	0.48
23:T:90:GLN:O	23:T:93:GLU:HB2	2.14	0.48
7:D:122:ARG:NH2	7:D:134:ASP:OD2	2.46	0.48
1:A:643:C:H2'	1:A:644:G:H8	1.78	0.48
15:L:60:LEU:HD11	15:L:85:ILE:HD12	1.94	0.48
1:A:1125:U:H3	13:J:5:ARG:NE	2.11	0.48
6:C:7:PRO:O	6:C:11:ARG:HD2	2.13	0.48
1:A:1048:G:OP1	17:N:3:ARG:HA	2.12	0.48
6:C:118:GLN:O	6:C:122:GLU:HG3	2.14	0.48
1:A:1229:A:H2'	1:A:1230:C:H6	1.79	0.48
12:I:43:ALA:O	12:I:44:VAL:C	2.52	0.48
20:Q:97:SER:O	20:Q:99:SER:N	2.47	0.48
1:A:502:G:H2'	1:A:503:C:H6	1.79	0.48
5:B:30:ARG:HG3	5:B:31:TYR:CD2	2.48	0.48
1:A:1451:A:O2'	1:A:1452:C:OP1	2.26	0.48
1:A:1053:G:H3'	1:A:1054:C:H5'	1.96	0.48
4:Z:1:U:H2'	4:Z:2:U:H5'	1.95	0.48
6:C:139:GLN:HE21	6:C:139:GLN:HA	1.78	0.48
5:B:92:TYR:HD2	5:B:92:TYR:H	1.60	0.48
1:A:1003(A):G:C2'	1:A:1004:A:H4'	2.39	0.48
16:M:88:ARG:HH11	22:S:3:ARG:HH21	1.62	0.48
8:E:52:PRO:O	8:E:53:LEU:C	2.52	0.48
11:H:92:ARG:HH11	11:H:92:ARG:CG	2.23	0.48
5:B:101:MET:HG2	5:B:108:ILE:HD13	1.95	0.48
1:A:860:A:H2'	1:A:861:G:O4'	2.13	0.48
14:K:15:ALA:HA	14:K:76:GLY:O	2.14	0.48
14:K:72:ALA:O	14:K:77:MET:HB2	2.14	0.48
1:A:88:A:H2'	1:A:89:C:O4'	2.14	0.48
21:R:29:PHE:HE1	21:R:31:LEU:HD23	1.79	0.48
9:F:76:ALA:O	9:F:77:ARG:C	2.50	0.48
1:A:1003(A):G:C4	1:A:1004:A:H1'	2.48	0.48
16:M:5:ALA:O	16:M:6:GLY:C	2.50	0.48
12:I:97:LYS:HB3	12:I:98:PRO:HD3	1.95	0.48
15:L:50:SER:O	15:L:51:ALA:CB	2.61	0.48
1:A:1060:C:H2'	1:A:1061:G:H8	1.78	0.48
13:J:46:ARG:HD3	13:J:64:GLU:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:867:G:O2'	1:A:868:C:H5'	2.13	0.48
5:B:156:LYS:HZ3	5:B:156:LYS:HA	1.78	0.48
1:A:562:C:H1'	15:L:15:ARG:HB3	1.95	0.48
1:A:545:C:O2'	1:A:546:G:H5'	2.13	0.48
1:A:423:G:H2'	1:A:424:G:O4'	2.13	0.48
22:S:17:GLU:HA	22:S:20:LEU:HD21	1.95	0.48
1:A:924:C:H5'	1:A:1399:C:OP2	2.13	0.48
5:B:18:GLY:HA2	5:B:41:ILE:HA	1.95	0.48
12:I:118:LYS:O	12:I:119:ALA:CB	2.59	0.48
8:E:144:THR:HG23	8:E:145:LYS:N	2.29	0.48
1:A:1062:U:H2'	1:A:1063:C:C6	2.49	0.48
20:Q:45:HIS:HB2	20:Q:69:LYS:HE2	1.95	0.48
1:A:920:U:H2'	1:A:921:U:C6	2.49	0.48
9:F:95:GLU:H	9:F:95:GLU:CD	2.17	0.48
15:L:46:LYS:CG	15:L:47:LYS:H	2.24	0.48
15:L:33:ARG:CD	15:L:62:SER:HB3	2.43	0.48
12:I:19:LEU:HB3	12:I:59:PHE:CD2	2.47	0.48
1:A:439:A:C4	1:A:497:A:C2	3.01	0.48
11:H:91:ARG:HH11	20:Q:33:GLY:HA3	1.79	0.48
1:A:167:G:H2'	1:A:168:G:H8	1.78	0.48
1:A:176:C:H2'	1:A:177:C:C6	2.45	0.48
1:A:258:G:O2'	1:A:259:G:H5'	2.13	0.48
16:M:74:VAL:HA	16:M:77:ASN:HD22	1.78	0.48
1:A:1160:G:O2'	1:A:1161:C:H5'	2.14	0.48
22:S:50:ALA:HA	22:S:58:VAL:O	2.14	0.48
6:C:69:HIS:O	6:C:70:VAL:HG13	2.14	0.48
7:D:191:ARG:O	7:D:191:ARG:HD2	2.14	0.48
12:I:111:ARG:HD3	12:I:112:LYS:O	2.13	0.48
15:L:60:LEU:N	15:L:64:TYR:O	2.47	0.48
6:C:188:LEU:HD13	6:C:195:VAL:HG13	1.94	0.48
8:E:77:PRO:O	8:E:78:HIS:CB	2.62	0.48
6:C:112:SER:CB	6:C:115:LEU:HD12	2.42	0.48
1:A:409:G:H2'	1:A:410:G:O4'	2.13	0.48
12:I:16:ARG:HB2	12:I:64:THR:HB	1.95	0.48
1:A:765:G:H1	1:A:812:C:H2'	1.78	0.48
20:Q:45:HIS:HB3	20:Q:72:ARG:HG2	1.94	0.48
1:A:1402:C:O2	1:A:1500:A:N1	2.47	0.48
5:B:42:ILE:HD12	5:B:203:GLY:HA2	1.95	0.48
9:F:40:VAL:CG2	9:F:41:GLU:N	2.76	0.48
5:B:23:ARG:HH12	5:B:191:ASP:HA	1.78	0.48
5:B:16:HIS:NE2	5:B:214:ILE:CG1	2.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:664:G:OP1	21:R:64:ARG:HD2	2.14	0.48
8:E:74:GLY:HA3	8:E:116:THR:CG2	2.38	0.48
6:C:34:LEU:CD2	6:C:38:ARG:HG2	2.44	0.48
14:K:99:GLN:CG	14:K:105:VAL:HG21	2.40	0.48
1:A:724:G:O2'	1:A:725:G:H5'	2.13	0.48
1:A:1128:C:H2'	1:A:1129:C:H5"	1.95	0.48
1:A:116:A:H61	1:A:313:A:H1'	1.79	0.48
1:A:411:A:N9	1:A:413:G:H1'	2.29	0.48
6:C:70:VAL:O	6:C:106:VAL:HG23	2.14	0.48
6:C:25:GLY:O	6:C:27:LYS:N	2.46	0.48
1:A:1291:G:H4'	12:I:38:GLN:O	2.13	0.48
6:C:191:THR:CG2	6:C:192:THR:H	2.26	0.47
24:V:2:GLY:O	24:V:4:GLY:N	2.47	0.47
8:E:72:GLN:C	8:E:74:GLY:N	2.67	0.47
6:C:38:ARG:O	6:C:42:LEU:HG	2.14	0.47
1:A:106:C:O2	1:A:379:C:H4'	2.14	0.47
7:D:30:LYS:C	7:D:32:ALA:H	2.18	0.47
19:P:63:GLY:O	19:P:64:ALA:C	2.51	0.47
1:A:730:G:N3	1:A:765:G:H4'	2.28	0.47
1:A:642:A:C8	11:H:115:SER:HA	2.49	0.47
1:A:22:G:H2'	1:A:23:C:C6	2.49	0.47
7:D:170:VAL:HG22	7:D:171:GLY:N	2.29	0.47
9:F:2:ARG:HH21	9:F:69:GLU:HB3	1.79	0.47
1:A:1081:G:OP1	8:E:16:THR:CG2	2.61	0.47
1:A:673:G:H5"	9:F:87:ARG:NH1	2.29	0.47
1:A:1223:C:P	22:S:78:ARG:HH12	2.37	0.47
23:T:72:LEU:O	23:T:73:HIS:C	2.52	0.47
1:A:1495:U:O2'	1:A:1496:C:H5'	2.14	0.47
10:G:85:TYR:HD1	10:G:154:TYR:CE1	2.31	0.47
20:Q:80:GLY:O	20:Q:81:ARG:HB3	2.15	0.47
1:A:1525:G:P	14:K:120:ARG:HH22	2.37	0.47
1:A:1010:G:O2'	1:A:1011:G:H5'	2.14	0.47
13:J:12:ASP:HB3	13:J:15:THR:HG22	1.96	0.47
6:C:159:GLY:HA2	6:C:193:TYR:CE2	2.49	0.47
24:V:2:GLY:C	24:V:4:GLY:N	2.65	0.47
6:C:43:LEU:HD11	6:C:66:VAL:CG1	2.44	0.47
1:A:662:G:O2'	1:A:836:G:H5'	2.14	0.47
5:B:68:ILE:O	5:B:91:PRO:HD2	2.13	0.47
16:M:14:ARG:NH1	16:M:16:ASP:OD1	2.47	0.47
16:M:23:TYR:HB2	16:M:67:GLU:OE2	2.13	0.47
11:H:10:LEU:HD12	11:H:85:ARG:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:7:GLU:O	18:O:11:VAL:HG23	2.14	0.47
15:L:41:ARG:CB	15:L:41:ARG:NH1	2.77	0.47
7:D:149:ALA:O	7:D:150:GLU:C	2.51	0.47
1:A:1089:G:O2'	1:A:1090:U:H5'	2.14	0.47
1:A:1470:G:O2'	1:A:1471:G:H5'	2.14	0.47
1:A:447:G:H2'	1:A:485:G:N2	2.29	0.47
24:V:24:ARG:O	24:V:25:LYS:CB	2.62	0.47
1:A:766:A:C8	1:A:814:A:C6	3.02	0.47
15:L:47:LYS:CG	15:L:48:PRO:HD3	2.44	0.47
13:J:30:SER:HB2	13:J:81:THR:HA	1.95	0.47
23:T:50:GLU:HA	23:T:100:ILE:HG13	1.95	0.47
1:A:1372:U:H2'	1:A:1373:G:O4'	2.14	0.47
12:I:108:VAL:HG12	12:I:109:VAL:N	2.29	0.47
1:A:840:C:H5'	1:A:848:C:O2	2.13	0.47
7:D:173:TRP:CD1	7:D:174:LEU:HG	2.49	0.47
7:D:57:ARG:NH1	7:D:57:ARG:HG3	2.25	0.47
6:C:79:ARG:N	6:C:82:GLU:HB3	2.29	0.47
1:A:537:G:H5"	15:L:113:ARG:NH2	2.28	0.47
6:C:167:TRP:O	6:C:168:ALA:HB3	2.13	0.47
1:A:41:G:H2'	1:A:42:G:H8	1.78	0.47
1:A:669:U:H2'	1:A:670:G:H8	1.79	0.47
15:L:71:PRO:O	15:L:102:ARG:HD2	2.14	0.47
7:D:199:ASN:HD21	7:D:201:GLN:HB3	1.80	0.47
1:A:771:G:H2'	1:A:772:U:C6	2.49	0.47
13:J:6:ILE:HG13	13:J:72:VAL:HB	1.97	0.47
13:J:37:PRO:HA	13:J:72:VAL:HA	1.96	0.47
6:C:8:ILE:O	6:C:11:ARG:N	2.42	0.47
10:G:47:CYS:SG	10:G:58:PRO:HB2	2.54	0.47
7:D:111:ALA:HB2	7:D:120:LEU:CD1	2.45	0.47
1:A:939:G:H2'	1:A:940:C:C6	2.50	0.47
10:G:146:GLU:C	10:G:148:ASN:N	2.67	0.47
23:T:76:ALA:HA	23:T:79:ARG:NH1	2.29	0.47
7:D:146:ILE:N	7:D:146:ILE:CD1	2.77	0.47
21:R:53:ARG:HG3	21:R:63:GLN:HB2	1.96	0.47
1:A:1327:C:O2'	1:A:1328:C:H5'	2.15	0.47
9:F:27:GLN:NE2	9:F:27:GLN:HA	2.30	0.47
5:B:181:PHE:HD2	11:H:70:GLN:HB3	1.78	0.47
1:A:1286:A:C8	1:A:1287:A:H4'	2.50	0.47
1:A:1107:C:H2'	1:A:1108:G:H5'	1.96	0.47
10:G:72:ARG:HG2	10:G:142:GLU:OE1	2.15	0.47
6:C:91:LEU:C	6:C:91:LEU:HD23	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:92:TYR:N	5:B:92:TYR:CD2	2.82	0.47
7:D:24:GLU:HG2	7:D:25:ARG:N	2.29	0.47
7:D:25:ARG:C	7:D:27:TYR:N	2.68	0.47
1:A:335:C:H2'	1:A:336:C:H6	1.79	0.47
1:A:392:G:H2'	1:A:393:A:H8	1.80	0.47
23:T:67:ALA:HB2	23:T:77:ALA:HB2	1.96	0.47
16:M:93:ARG:HG3	16:M:93:ARG:HH11	1.79	0.47
9:F:1:MET:N	9:F:1:MET:SD	2.80	0.47
19:P:71:ARG:HD3	19:P:75:ARG:HH21	1.79	0.47
11:H:29:SER:O	11:H:30:ARG:C	2.53	0.47
1:A:830:G:O2'	1:A:831:U:H5'	2.14	0.47
5:B:25:ASN:ND2	5:B:25:ASN:C	2.67	0.47
13:J:14:LYS:C	13:J:16:LEU:N	2.67	0.47
13:J:5:ARG:HA	13:J:73:ASP:OD1	2.14	0.47
1:A:1348:U:H2'	1:A:1349:A:H8	1.80	0.47
16:M:81:LEU:O	16:M:86:CYS:HB3	2.15	0.47
1:A:444:C:H2'	1:A:445:G:H8	1.79	0.47
1:A:401:C:O2'	1:A:402:G:H5'	2.15	0.47
1:A:406:G:H2'	1:A:407:G:C8	2.49	0.47
22:S:40:ILE:HG21	22:S:62:ILE:HD13	1.96	0.47
20:Q:97:SER:HB3	20:Q:103:GLY:CA	2.45	0.47
8:E:146:ALA:O	8:E:149:GLU:HB2	2.14	0.47
11:H:60:ARG:NH1	11:H:60:ARG:HG3	2.24	0.47
20:Q:33:GLY:O	20:Q:34:LYS:C	2.52	0.47
1:A:938:A:N6	1:A:939:G:C6	2.83	0.47
1:A:983:A:H2	1:A:984:C:C6	2.32	0.47
1:A:179:A:H2'	1:A:180:U:C6	2.50	0.47
5:B:177:ALA:O	5:B:180:LEU:N	2.44	0.47
1:A:1406:U:C2'	1:A:1407:C:H5'	2.44	0.47
1:A:18:C:O2'	1:A:19:C:H5'	2.14	0.47
7:D:68:TYR:CE2	7:D:97:LEU:HB3	2.49	0.47
1:A:636:U:H2'	1:A:637:G:H8	1.79	0.47
1:A:1157:A:H4'	1:A:1158:C:O5'	2.15	0.47
11:H:28:ALA:HB2	11:H:59:LEU:HG	1.96	0.47
1:A:1487:G:O2'	1:A:1488:G:H5'	2.15	0.47
22:S:80:TYR:C	22:S:80:TYR:CD2	2.88	0.47
1:A:426:G:H2'	1:A:427:U:C6	2.50	0.47
13:J:38:ILE:HB	13:J:71:LEU:CB	2.45	0.47
6:C:195:VAL:HG12	6:C:196:LEU:H	1.78	0.47
6:C:64:VAL:CG1	6:C:65:ALA:N	2.77	0.47
6:C:91:LEU:HD21	6:C:99:VAL:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:59:TYR:O	16:M:63:THR:CG2	2.62	0.47
5:B:78:GLN:HE22	5:B:96:ARG:NH1	2.12	0.47
1:A:1070:U:O2'	1:A:1071:C:H5'	2.14	0.47
18:O:36:ILE:HD12	18:O:63:ARG:NH1	2.30	0.47
19:P:81:ARG:NH1	19:P:81:ARG:HB2	2.30	0.47
1:A:75:G:O2'	1:A:76:C:H5'	2.15	0.47
1:A:154:C:H2'	1:A:155:C:C6	2.50	0.47
1:A:918:A:H2'	1:A:919:A:C8	2.50	0.47
7:D:18:LYS:HA	7:D:33:MET:HG3	1.97	0.47
8:E:15:ARG:HD3	8:E:26:PHE:CD2	2.50	0.47
6:C:129:ALA:HB3	6:C:132:ARG:HB3	1.96	0.47
7:D:78:LEU:HD22	7:D:96:LEU:HB3	1.97	0.47
1:A:291:C:O2'	1:A:292:G:H5'	2.15	0.47
1:A:222:U:H2'	1:A:223:U:C6	2.50	0.47
20:Q:67:LYS:CA	20:Q:70:ARG:NH1	2.74	0.47
18:O:27:VAL:O	18:O:30:ALA:HB3	2.15	0.47
1:A:445:G:O2'	1:A:446:G:H5'	2.15	0.47
1:A:1222:G:O2'	1:A:1223:C:H5'	2.15	0.47
23:T:64:ASP:OD2	23:T:81:LYS:NZ	2.44	0.47
1:A:1109:C:P	6:C:176:HIS:CD2	3.07	0.47
1:A:1005:A:C2'	1:A:1006:C:H5'	2.45	0.47
20:Q:82:MET:O	20:Q:83:ASP:C	2.51	0.47
10:G:79:ARG:HA	10:G:84:ASN:HA	1.96	0.47
15:L:32:PHE:HB3	15:L:85:ILE:O	2.14	0.47
15:L:60:LEU:HB2	15:L:64:TYR:HB2	1.97	0.47
13:J:75:ILE:O	13:J:76:ASN:CB	2.64	0.47
10:G:57:GLU:HB2	10:G:60:LYS:HB2	1.97	0.47
1:A:1206:G:H1'	6:C:193:TYR:O	2.14	0.47
6:C:206:GLU:O	6:C:207:VAL:O	2.33	0.47
1:A:1305:G:OP2	1:A:1305:G:C8	2.68	0.47
21:R:86:VAL:CG1	21:R:87:ARG:H	2.25	0.47
21:R:88:LYS:HG2	21:R:88:LYS:OXT	2.15	0.47
1:A:663:A:O2'	1:A:664:G:H5'	2.15	0.47
21:R:47:THR:C	21:R:49:LYS:H	2.18	0.47
12:I:44:VAL:O	12:I:45:ALA:C	2.53	0.47
1:A:407:G:H2'	1:A:408:A:H8	1.79	0.47
12:I:93:ARG:O	12:I:94:ALA:C	2.53	0.47
15:L:39:VAL:HG12	15:L:40:VAL:H	1.80	0.47
1:A:865:A:H5'	1:A:1078:U:O4	2.15	0.47
1:A:511:C:C2	1:A:512:U:C5	3.03	0.47
14:K:11:LYS:C	14:K:12:ARG:HG3	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:N:44:LEU:O	17:N:44:LEU:HD12	2.15	0.47
13:J:34:VAL:CA	13:J:74:ILE:HG22	2.38	0.46
6:C:173:VAL:N	6:C:174:PRO:CD	2.77	0.46
5:B:187:LEU:O	5:B:187:LEU:CD2	2.62	0.46
5:B:91:PRO:HA	5:B:154:LEU:HD12	1.96	0.46
1:A:402:G:O2'	1:A:403:C:H5'	2.16	0.46
20:Q:27:PHE:CZ	20:Q:36:ILE:HD11	2.50	0.46
12:I:84:ALA:O	12:I:87:GLN:N	2.49	0.46
1:A:1461:G:O2'	1:A:1462:G:H5'	2.15	0.46
1:A:1195:C:H2'	1:A:1197:G:H5'	1.98	0.46
1:A:664:G:N2	1:A:741:G:H1	2.03	0.46
11:H:104:ARG:O	11:H:105:ARG:C	2.54	0.46
5:B:112:VAL:C	5:B:114:ARG:N	2.68	0.46
22:S:63:THR:HG22	22:S:64:GLU:N	2.31	0.46
20:Q:98:LEU:O	20:Q:98:LEU:CD1	2.64	0.46
7:D:194:LEU:HD22	7:D:194:LEU:N	2.31	0.46
12:I:100:GLY:C	12:I:102:LEU:N	2.69	0.46
15:L:7:ILE:HG21	20:Q:34:LYS:HB3	1.96	0.46
8:E:60:TYR:CE1	8:E:64:ARG:CZ	2.98	0.46
22:S:52:TYR:HA	22:S:56:GLN:O	2.15	0.46
1:A:865:A:H2'	1:A:866:C:C6	2.50	0.46
8:E:43:LEU:HD22	8:E:44:GLY:N	2.31	0.46
7:D:126:ILE:HG22	7:D:127:THR:N	2.29	0.46
1:A:1189:C:OP1	13:J:51:ARG:NH2	2.38	0.46
10:G:28:ASN:OD1	10:G:36:LYS:NZ	2.49	0.46
15:L:89:ARG:NE	15:L:97:ARG:HG2	2.30	0.46
22:S:62:ILE:O	22:S:62:ILE:HG13	2.16	0.46
1:A:501:C:O3'	15:L:118:SER:HB2	2.16	0.46
1:A:792:A:H1'	1:A:794:A:N7	2.30	0.46
7:D:100:ARG:HH12	7:D:137:SER:CB	2.28	0.46
1:A:985:C:H2'	1:A:986:A:C8	2.51	0.46
15:L:41:ARG:HB3	15:L:41:ARG:NH1	2.30	0.46
16:M:91:ARG:CB	16:M:98:VAL:HG12	2.44	0.46
14:K:77:MET:HB3	14:K:103:LEU:HD21	1.96	0.46
10:G:37:ASN:HA	10:G:37:ASN:HD22	1.60	0.46
1:A:1019:C:O2'	1:A:1020:U:H5'	2.15	0.46
8:E:71:LEU:HD22	8:E:114:GLY:O	2.16	0.46
15:L:6:THR:OG1	15:L:9:GLN:HG3	2.16	0.46
1:A:427:U:OP2	7:D:36:ARG:NH2	2.47	0.46
15:L:46:LYS:HG3	15:L:47:LYS:N	2.30	0.46
5:B:13:ALA:C	5:B:15:VAL:N	2.67	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:51:GLN:C	10:G:53:LYS:H	2.19	0.46
10:G:18:TYR:CD2	10:G:59:LEU:HD13	2.50	0.46
12:I:55:ALA:C	12:I:57:GLY:H	2.19	0.46
16:M:58:GLU:OE2	16:M:58:GLU:HA	2.16	0.46
1:A:8:A:H62	7:D:209:ARG:H	1.62	0.46
1:A:665:A:N3	1:A:732:C:H2'	2.31	0.46
1:A:1021:G:H2'	1:A:1022:G:C8	2.50	0.46
1:A:46:G:O2'	1:A:365:U:H1'	2.16	0.46
1:A:915:A:H2'	1:A:916:G:H5'	1.98	0.46
1:A:689:C:OP2	14:K:46:GLY:HA3	2.14	0.46
1:A:877:C:H1'	11:H:3:THR:HG23	1.98	0.46
22:S:16:LEU:C	22:S:18:LYS:H	2.19	0.46
6:C:153:VAL:CG1	6:C:196:LEU:HD23	2.45	0.46
1:A:1227:A:C2'	1:A:1228:C:O5'	2.63	0.46
12:I:53:VAL:HG23	12:I:55:ALA:HB2	1.97	0.46
12:I:8:GLY:HA2	12:I:79:LEU:CD1	2.41	0.46
20:Q:3:LYS:HB3	20:Q:60:ILE:CD1	2.45	0.46
15:L:11:VAL:HG21	20:Q:34:LYS:HG2	1.96	0.46
10:G:139:GLU:O	10:G:143:ARG:HG3	2.16	0.46
1:A:1407:C:O2'	1:A:1408:A:H5'	2.16	0.46
20:Q:48:GLU:O	20:Q:49:GLU:C	2.54	0.46
1:A:743:U:H2'	1:A:744:C:C6	2.50	0.46
1:A:1531:A:H8	1:A:1531:A:O5'	1.99	0.46
1:A:1110:A:H8	1:A:1110:A:O5'	1.99	0.46
1:A:1051:C:H2'	1:A:1052:U:C6	2.49	0.46
5:B:206:ASP:O	5:B:207:ALA:CB	2.61	0.46
5:B:62:ALA:C	5:B:64:ARG:H	2.18	0.46
5:B:103:THR:OG1	5:B:176:GLU:HG2	2.16	0.46
17:N:23:ARG:NH1	17:N:30:ALA:HB2	2.30	0.46
17:N:25:VAL:O	17:N:25:VAL:HG22	2.16	0.46
16:M:39:ILE:HD13	16:M:52:GLU:HB3	1.97	0.46
7:D:24:GLU:O	7:D:25:ARG:HB3	2.16	0.46
20:Q:95:TYR:C	20:Q:97:SER:N	2.69	0.46
20:Q:95:TYR:O	20:Q:96:GLN:C	2.53	0.46
6:C:10:PHE:CD2	6:C:178:LEU:HD13	2.50	0.46
7:D:31:CYS:O	7:D:32:ALA:HB3	2.14	0.46
1:A:628:G:H2'	1:A:629:G:C8	2.51	0.46
1:A:927:G:H2'	1:A:928:G:H8	1.81	0.46
1:A:270:A:H2'	1:A:271:C:H6	1.80	0.46
5:B:89:GLY:HA3	5:B:226:ARG:HH12	1.81	0.46
1:A:600:C:H2'	1:A:601:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:134:GLU:C	5:B:136:VAL:H	2.18	0.46
1:A:1256:A:H4'	1:A:1257:U:C5'	2.39	0.46
23:T:49:ALA:HB3	23:T:99:LEU:HD12	1.98	0.46
1:A:1226:C:N4	16:M:104:ARG:HB2	2.30	0.46
5:B:92:TYR:HD2	5:B:92:TYR:N	2.13	0.46
1:A:1347:G:H2'	1:A:1348:U:OP2	2.16	0.46
23:T:56:MET:HE2	23:T:88:VAL:HB	1.97	0.46
1:A:113:G:C1'	1:A:354:G:H5'	2.45	0.46
1:A:1343:G:OP1	12:I:125:TYR:HE2	1.99	0.46
1:A:1070:U:OP1	8:E:25:ARG:NH1	2.49	0.46
6:C:23:TYR:CD2	6:C:24:ALA:N	2.84	0.46
5:B:169:LYS:C	5:B:169:LYS:HD2	2.35	0.46
15:L:86:ARG:NH2	15:L:99:HIS:CD2	2.84	0.46
1:A:689:C:H2'	1:A:690:G:O4'	2.16	0.46
17:N:53:LEU:HB3	17:N:56:VAL:HG21	1.97	0.46
22:S:28:LYS:HD3	22:S:31:ILE:CD1	2.45	0.46
5:B:79:ASP:HA	5:B:82:ARG:HG2	1.98	0.46
5:B:200:ILE:HG22	5:B:202:PRO:HD3	1.97	0.46
1:A:940:C:H2'	1:A:941:G:C8	2.51	0.46
1:A:1320:C:H41	22:S:37:ARG:CZ	2.28	0.46
11:H:6:ILE:HD11	11:H:31:PHE:CD2	2.50	0.46
1:A:818:G:C3'	1:A:819:A:C5'	2.94	0.46
19:P:82:GLN:O	19:P:83:GLU:C	2.53	0.46
13:J:64:GLU:HG2	17:N:59:ALA:HB2	1.97	0.46
1:A:925:G:C6	1:A:927:G:N7	2.84	0.46
1:A:1508:G:O2'	1:A:1509:C:H5'	2.16	0.46
1:A:828:A:H5"	1:A:859:A:C2	2.51	0.46
5:B:23:ARG:C	5:B:23:ARG:HD3	2.36	0.46
10:G:72:ARG:O	10:G:73:MET:HG2	2.16	0.46
1:A:1054:C:HO2'	1:A:1055:A:P	2.38	0.46
10:G:75:VAL:O	10:G:75:VAL:HG13	2.16	0.46
6:C:43:LEU:HA	6:C:47:LEU:HD13	1.98	0.46
12:I:115:GLY:O	12:I:116:LYS:HG3	2.16	0.46
1:A:409:G:OP1	7:D:24:GLU:O	2.33	0.46
22:S:41:VAL:HG22	22:S:44:MET:CE	2.46	0.46
1:A:665:A:C1'	1:A:733:A:H1'	2.45	0.46
1:A:1300:G:O2'	1:A:1301:U:P	2.73	0.46
7:D:70:ILE:HG23	7:D:74:GLN:HB2	1.98	0.46
1:A:1292:U:H2'	1:A:1293:G:C8	2.51	0.46
1:A:1183:A:O2'	1:A:1184:G:P	2.74	0.46
10:G:85:TYR:HD1	10:G:154:TYR:HE1	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:555:C:H2'	1:A:556:C:C6	2.51	0.46
5:B:208:ILE:CG2	5:B:212:GLN:HB2	2.46	0.46
10:G:65:ALA:O	10:G:69:VAL:HG23	2.15	0.46
1:A:1390:U:H2'	1:A:1391:U:C6	2.51	0.46
5:B:54:THR:HG23	5:B:199:TYR:HB3	1.97	0.46
8:E:79:GLU:N	8:E:79:GLU:OE1	2.44	0.46
14:K:44:SER:H	14:K:47:VAL:CB	2.26	0.46
21:R:35:ARG:O	21:R:37:VAL:HG23	2.16	0.46
1:A:200:G:H2'	1:A:201:C:O4'	2.16	0.46
11:H:126:LYS:C	11:H:128:GLY:H	2.19	0.46
1:A:1288:A:H2'	1:A:1289:A:C8	2.51	0.45
6:C:191:THR:HG22	6:C:192:THR:H	1.79	0.45
1:A:1392:G:N2	1:A:1502:A:C8	2.84	0.45
21:R:86:VAL:CG1	21:R:87:ARG:N	2.77	0.45
5:B:85:ALA:CB	5:B:92:TYR:HB3	2.46	0.45
16:M:23:TYR:CB	16:M:67:GLU:HA	2.46	0.45
1:A:112:G:H4'	1:A:389:A:C5'	2.46	0.45
14:K:126:ARG:HH11	14:K:126:ARG:HB3	1.78	0.45
1:A:824:C:H2'	1:A:825:G:C8	2.48	0.45
6:C:23:TYR:HE1	13:J:67:THR:HG23	1.81	0.45
1:A:753:A:H4'	1:A:754:C:C5'	2.46	0.45
1:A:782:A:H2'	1:A:783:C:O4'	2.16	0.45
1:A:975:A:C5'	1:A:975:A:H8	2.19	0.45
13:J:38:ILE:CG2	13:J:39:PRO:HD2	2.45	0.45
13:J:85:LEU:O	13:J:87:THR:N	2.50	0.45
10:G:69:VAL:O	10:G:138:LYS:HG3	2.15	0.45
1:A:1196:U:OP1	1:A:1197:G:H5'	2.17	0.45
1:A:1307:U:H2'	1:A:1308:U:C6	2.52	0.45
5:B:53:ARG:HA	5:B:56:ARG:HE	1.80	0.45
11:H:105:ARG:HH11	11:H:105:ARG:CG	2.28	0.45
17:N:25:VAL:HG12	17:N:38:GLY:O	2.16	0.45
12:I:19:LEU:HD23	12:I:61:ALA:HB2	1.98	0.45
16:M:4:ILE:CG2	16:M:5:ALA:N	2.68	0.45
14:K:44:SER:N	14:K:47:VAL:CG2	2.78	0.45
21:R:37:VAL:CG2	21:R:78:LEU:HB3	2.46	0.45
7:D:32:ALA:C	7:D:34:GLU:N	2.63	0.45
20:Q:63:ARG:HG2	20:Q:64:PRO:CD	2.46	0.45
6:C:72:LYS:HE2	6:C:75:VAL:HG21	1.96	0.45
1:A:1182:G:H4'	1:A:1183:A:H5"	1.97	0.45
16:M:80:ARG:O	16:M:83:ASP:N	2.48	0.45
8:E:143:ARG:NH1	11:H:77:GLU:OE2	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:882:C:O2'	1:A:883:C:H5'	2.16	0.45
6:C:86:VAL:O	6:C:90:GLU:HB2	2.16	0.45
19:P:12:LYS:O	19:P:13:HIS:HB2	2.15	0.45
1:A:742:G:P	18:O:35:ARG:HH22	2.38	0.45
1:A:1365:G:O2'	1:A:1366:C:H5'	2.16	0.45
1:A:265:G:O2'	1:A:266:G:H5'	2.17	0.45
18:O:12:ILE:HG23	18:O:27:VAL:CG1	2.46	0.45
1:A:1256:A:O2'	1:A:1257:U:P	2.75	0.45
1:A:1349:A:P	12:I:118:LYS:NZ	2.90	0.45
1:A:1139:G:N2	1:A:1143:G:C6	2.84	0.45
1:A:1223:C:OP2	1:A:1224:G:H2'	2.16	0.45
19:P:2:VAL:O	19:P:64:ALA:HA	2.15	0.45
6:C:83:ARG:C	6:C:85:ARG:N	2.69	0.45
18:O:63:ARG:O	18:O:64:ARG:C	2.55	0.45
1:A:109:A:H4'	1:A:110:C:OP2	2.16	0.45
1:A:286:G:O2'	1:A:287:U:H5'	2.17	0.45
20:Q:45:HIS:HA	20:Q:69:LYS:CE	2.47	0.45
1:A:302:G:N3	1:A:556:C:H4'	2.31	0.45
1:A:436:C:H2'	1:A:437:U:C6	2.52	0.45
22:S:74:PHE:N	22:S:74:PHE:CD1	2.83	0.45
11:H:20:TYR:HE2	11:H:75:ARG:HD2	1.81	0.45
5:B:23:ARG:NH1	5:B:24:TRP:HA	2.30	0.45
1:A:518:C:H2'	1:A:530:G:N3	2.31	0.45
5:B:12:GLU:O	5:B:14:GLY:N	2.50	0.45
1:A:1004:A:N7	1:A:1037:C:N3	2.64	0.45
16:M:81:LEU:HD12	16:M:88:ARG:HB3	1.98	0.45
16:M:4:ILE:HG23	16:M:57:ARG:HA	1.98	0.45
21:R:36:ASN:HD22	21:R:36:ASN:C	2.19	0.45
21:R:38:GLU:HA	21:R:41:LYS:HE2	1.97	0.45
15:L:90:VAL:HG11	15:L:93:LEU:CD1	2.47	0.45
19:P:43:LYS:HB3	19:P:48:TRP:CD1	2.51	0.45
11:H:30:ARG:O	11:H:33:GLU:HB3	2.16	0.45
22:S:33:THR:HG22	22:S:34:TRP:N	2.32	0.45
13:J:6:ILE:HD11	13:J:72:VAL:CG1	2.46	0.45
6:C:177:THR:CG2	6:C:180:ALA:HB2	2.46	0.45
6:C:177:THR:HG23	6:C:180:ALA:HB2	1.99	0.45
5:B:59:GLU:HG2	5:B:221:LEU:CD1	2.35	0.45
6:C:39:ILE:HG22	6:C:40:ARG:N	2.29	0.45
1:A:721:G:H4'	1:A:722:A:O4'	2.17	0.45
1:A:112:G:C2'	1:A:113:G:H5'	2.46	0.45
1:A:389:A:N3	1:A:389:A:H2'	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Q:98:LEU:O	20:Q:98:LEU:HD13	2.16	0.45
1:A:380:G:N2	1:A:384:G:C5	2.85	0.45
15:L:117:ARG:O	15:L:119:LYS:O	2.34	0.45
1:A:463:A:O4'	19:P:82:GLN:NE2	2.45	0.45
1:A:19:C:H2'	1:A:20:U:C6	2.50	0.45
1:A:91:C:H2'	1:A:92:C:H6	1.82	0.45
1:A:1108:G:C5'	1:A:1191:A:H4'	2.46	0.45
13:J:63:PHE:CE1	17:N:45:ARG:HG3	2.51	0.45
3:Y:37:A:C2	4:Z:1:U:N3	2.85	0.45
23:T:100:ILE:C	23:T:102:GLY:N	2.69	0.45
16:M:14:ARG:HH12	16:M:16:ASP:CG	2.18	0.45
7:D:8:VAL:C	7:D:10:ARG:N	2.70	0.45
1:A:665:A:H1'	1:A:733:A:H1'	1.99	0.45
15:L:49:ASN:OD1	15:L:92:ASP:OD2	2.35	0.45
11:H:125:ARG:CZ	11:H:125:ARG:HB2	2.46	0.45
8:E:35:GLY:HA2	8:E:40:ARG:O	2.16	0.45
22:S:53:ASN:HD21	22:S:56:GLN:HB2	1.82	0.45
1:A:474:G:H2'	1:A:475:G:H8	1.80	0.45
6:C:134:ILE:CG2	6:C:168:ALA:HB3	2.47	0.45
1:A:1478:C:O2'	1:A:1479:C:H5'	2.17	0.45
1:A:1165:C:C2'	1:A:1166:G:H5'	2.47	0.45
21:R:26:LEU:HD12	21:R:27:GLY:H	1.82	0.45
12:I:20:ARG:O	12:I:60:ASP:HB3	2.17	0.45
1:A:13:U:C5	1:A:916:G:O6	2.69	0.45
20:Q:40:LYS:HE2	20:Q:42:TYR:CZ	2.51	0.45
1:A:745:C:H2'	1:A:746:A:H8	1.81	0.45
1:A:226:G:O2'	1:A:227:G:H5'	2.16	0.45
5:B:80:ILE:HG21	5:B:212:GLN:HA	1.99	0.45
5:B:25:ASN:HD22	5:B:27:LYS:N	2.12	0.45
5:B:25:ASN:HD22	5:B:26:PRO:N	2.15	0.45
15:L:29:GLY:O	15:L:30:ALA:C	2.53	0.45
13:J:12:ASP:OD1	13:J:14:LYS:N	2.47	0.45
6:C:188:LEU:CD1	6:C:195:VAL:HG13	2.47	0.45
6:C:115:LEU:O	6:C:118:GLN:N	2.49	0.45
19:P:55:ARG:O	19:P:58:TYR:HB3	2.17	0.45
8:E:144:THR:H	8:E:147:ASP:HB2	1.82	0.45
1:A:434:U:H2'	1:A:435:C:H6	1.77	0.45
18:O:8:LYS:O	18:O:11:VAL:HB	2.16	0.45
1:A:1314:C:OP2	22:S:6:LYS:HE2	2.16	0.45
10:G:85:TYR:CD1	10:G:154:TYR:CE1	3.05	0.45
21:R:43:PHE:C	21:R:51:LEU:HD12	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:108:ALA:C	10:G:110:GLN:H	2.20	0.45
7:D:72:GLU:HA	7:D:72:GLU:OE2	2.16	0.45
1:A:1371:G:OP2	12:I:11:LYS:HE3	2.17	0.45
14:K:48:ILE:HD13	14:K:63:LEU:CB	2.45	0.45
1:A:1055:A:C8	1:A:1206:G:C2	3.05	0.45
1:A:1111:A:H61	6:C:177:THR:HA	1.81	0.45
21:R:21:LYS:C	21:R:23:LYS:N	2.70	0.45
6:C:87:LEU:O	6:C:91:LEU:N	2.50	0.45
6:C:66:VAL:HG11	6:C:91:LEU:HD11	1.97	0.45
21:R:47:THR:HG22	21:R:48:GLY:N	2.30	0.45
6:C:34:LEU:HD21	6:C:38:ARG:HG2	1.99	0.45
16:M:51:ALA:O	16:M:54:VAL:HB	2.17	0.45
9:F:26:ILE:O	9:F:30:LEU:HG	2.17	0.45
17:N:14:PRO:HG2	17:N:15:LYS:N	2.32	0.45
1:A:52:G:O2'	1:A:53:A:H5'	2.17	0.45
16:M:21:TYR:H	16:M:21:TYR:HD1	1.63	0.45
5:B:144:ARG:O	5:B:147:LYS:HB2	2.17	0.45
22:S:19:VAL:CG1	22:S:20:LEU:N	2.78	0.45
1:A:1191:A:OP1	6:C:4:LYS:HE3	2.17	0.45
1:A:1190:G:P	6:C:5:ILE:HG13	2.57	0.45
5:B:59:GLU:O	5:B:61:LEU:N	2.49	0.45
1:A:479:C:O2'	1:A:480:U:H5'	2.16	0.45
1:A:1342:C:O2'	1:A:1343:G:H5'	2.16	0.45
1:A:620:C:C2	7:D:135:LEU:HD13	2.52	0.45
11:H:77:GLU:CG	11:H:78:GLN:N	2.80	0.45
1:A:204:U:H4'	1:A:216:G:H5"	1.97	0.45
1:A:1072:G:O6	1:A:1102:A:N6	2.50	0.45
19:P:67:THR:CG2	19:P:68:ASP:N	2.79	0.45
1:A:107:G:O2'	1:A:108:G:H5'	2.17	0.45
8:E:28:PHE:O	8:E:47:LYS:HA	2.17	0.45
14:K:48:ILE:HD11	14:K:64:ALA:HA	1.98	0.45
5:B:27:LYS:C	5:B:29:ALA:H	2.20	0.45
1:A:1054:C:H5	1:A:1196:U:C5	2.34	0.45
1:A:1206:G:C6	1:A:1207:G:C5	3.04	0.45
12:I:85:LEU:O	12:I:92:TYR:HD1	2.00	0.45
1:A:1130:A:OP2	1:A:1131:G:OP2	2.34	0.45
12:I:97:LYS:O	12:I:100:GLY:N	2.42	0.45
1:A:942:G:H2'	1:A:943:U:C6	2.52	0.45
14:K:121:PRO:HG2	14:K:126:ARG:CG	2.44	0.45
14:K:115:PRO:C	14:K:117:ASN:N	2.70	0.45
23:T:89:ARG:O	23:T:93:GLU:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:A:P	15:L:17:LYS:HE2	2.57	0.45
1:A:322:C:O2'	1:A:323:U:H5'	2.17	0.45
10:G:21:VAL:HG23	10:G:22:LEU:N	2.31	0.45
14:K:54:ARG:NH1	14:K:54:ARG:HG3	2.33	0.44
1:A:255:G:O6	1:A:266:G:O6	2.34	0.44
5:B:204:ASN:HD22	5:B:204:ASN:C	2.19	0.44
21:R:44:LEU:HD22	21:R:48:GLY:O	2.17	0.44
10:G:48:LYS:O	10:G:51:GLN:HB2	2.17	0.44
12:I:107:ARG:CB	12:I:107:ARG:NH1	2.80	0.44
16:M:66:LEU:O	16:M:67:GLU:C	2.55	0.44
20:Q:59:ILE:CG2	20:Q:71:PHE:CD1	3.00	0.44
11:H:60:ARG:CG	11:H:60:ARG:NH1	2.75	0.44
9:F:87:ARG:NH1	9:F:87:ARG:CG	2.80	0.44
1:A:1333:A:O2'	1:A:1334:G:H5'	2.18	0.44
1:A:1176:A:H2'	1:A:1177:G:H8	1.82	0.44
9:F:3:ARG:NH1	9:F:3:ARG:HG3	2.31	0.44
6:C:167:TRP:HB3	6:C:168:ALA:H	1.30	0.44
1:A:77:G:O2'	1:A:78:G:H5'	2.17	0.44
1:A:1477:C:H2'	1:A:1478:C:C6	2.52	0.44
16:M:73:GLU:O	16:M:76:ALA:HB3	2.16	0.44
22:S:15:LEU:HA	22:S:18:LYS:HB3	1.98	0.44
1:A:1111:A:N6	6:C:177:THR:HA	2.31	0.44
1:A:947:G:H2'	1:A:948:C:O4'	2.18	0.44
6:C:89:GLU:C	6:C:91:LEU:H	2.20	0.44
21:R:45:SER:OG	21:R:49:LYS:HB2	2.18	0.44
10:G:36:LYS:O	10:G:39:ALA:HB3	2.18	0.44
20:Q:61:GLU:HA	20:Q:71:PHE:CE1	2.52	0.44
1:A:1145:C:O2'	1:A:1146:A:O5'	2.35	0.44
11:H:113:SER:HB2	11:H:134:ILE:HD11	1.98	0.44
7:D:150:GLU:HA	7:D:153:ARG:NH1	2.32	0.44
1:A:818:G:H3'	1:A:819:A:H5"	1.99	0.44
1:A:694:A:C2'	1:A:695:A:O5'	2.64	0.44
8:E:37:ARG:HG2	8:E:37:ARG:NH1	2.32	0.44
1:A:23:C:O2'	1:A:24:U:H5'	2.17	0.44
1:A:141:A:O2'	1:A:142:G:H5'	2.17	0.44
1:A:332:G:H2'	1:A:333:G:H8	1.82	0.44
5:B:77:ALA:HB1	5:B:211:ILE:HG21	1.99	0.44
15:L:46:LYS:O	15:L:47:LYS:C	2.55	0.44
20:Q:68:ARG:HH11	20:Q:68:ARG:HG2	1.82	0.44
1:A:1305:G:H2'	1:A:1331:G:N2	2.31	0.44
14:K:33:THR:HA	14:K:39:PRO:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:42:PRO:C	22:S:44:MET:H	2.20	0.44
1:A:1439:C:H2'	1:A:1440:C:C6	2.52	0.44
1:A:132:C:O3'	23:T:74:LYS:HE2	2.17	0.44
15:L:115:LYS:C	15:L:117:ARG:H	2.21	0.44
1:A:1091:U:O2	1:A:1093:A:H8	1.99	0.44
1:A:411:A:O2'	1:A:412:A:H5'	2.17	0.44
10:G:78:ARG:HG2	10:G:80:VAL:HG23	1.98	0.44
18:O:87:ILE:CG2	18:O:88:ARG:N	2.80	0.44
15:L:102:ARG:HB3	15:L:102:ARG:HE	1.62	0.44
1:A:822:C:O2'	1:A:823:G:H5'	2.18	0.44
7:D:182:LYS:HB3	7:D:182:LYS:NZ	2.33	0.44
5:B:87:ARG:CZ	5:B:233:SER:HB2	2.47	0.44
6:C:195:VAL:CG1	6:C:196:LEU:H	2.30	0.44
14:K:89:ALA:C	14:K:91:ARG:H	2.21	0.44
6:C:94:LEU:CD2	6:C:95:THR:N	2.81	0.44
12:I:71:SER:HA	12:I:74:ILE:HD12	1.99	0.44
1:A:280:C:O2	20:Q:38:ARG:HG3	2.17	0.44
12:I:125:TYR:CE1	12:I:128:ARG:HB3	2.52	0.44
8:E:18:ARG:NH2	8:E:25:ARG:HB3	2.33	0.44
1:A:162:A:H2'	1:A:163:C:O4'	2.17	0.44
11:H:17:THR:O	11:H:78:GLN:NE2	2.44	0.44
1:A:1270:C:O2'	1:A:1271:G:H5'	2.17	0.44
1:A:769:G:H4'	1:A:1513:A:H4'	2.00	0.44
1:A:1420:C:H2'	1:A:1421:G:H8	1.83	0.44
10:G:31:MET:SD	10:G:34:GLY:HA2	2.58	0.44
1:A:976:G:C8	1:A:1358:U:O2	2.70	0.44
1:A:1206:G:H2'	1:A:1207:G:H8	1.83	0.44
5:B:15:VAL:HB	5:B:210:SER:OG	2.17	0.44
8:E:76:ILE:HG23	8:E:78:HIS:H	1.83	0.44
21:R:87:ARG:O	21:R:88:LYS:CB	2.65	0.44
1:A:192:U:O2'	1:A:193:C:H5'	2.18	0.44
5:B:92:TYR:CE2	5:B:151:GLY:CA	2.99	0.44
16:M:81:LEU:CD2	16:M:81:LEU:H	2.30	0.44
16:M:84:ILE:HG21	22:S:65:ASN:HD22	1.82	0.44
8:E:121:LYS:HD2	8:E:122:GLU:N	2.32	0.44
21:R:36:ASN:HD21	21:R:38:GLU:HB2	1.81	0.44
19:P:19:ILE:N	19:P:19:ILE:CD1	2.80	0.44
7:D:105:VAL:HG13	7:D:110:PHE:HB2	2.00	0.44
1:A:397:A:H5'	1:A:398:C:P	2.58	0.44
1:A:447:G:H1'	1:A:487:A:N6	2.32	0.44
1:A:1476:G:O2'	1:A:1477:C:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1480:G:O2'	1:A:1481:U:H5'	2.17	0.44
6:C:60:ALA:O	6:C:61:ALA:HB3	2.17	0.44
1:A:1172:C:H2'	1:A:1173:G:C8	2.53	0.44
1:A:601:C:O2'	1:A:602:A:H5'	2.17	0.44
1:A:1240:U:O2'	10:G:32:ARG:HD2	2.18	0.44
13:J:19:SER:OG	13:J:91:PRO:HG3	2.18	0.44
9:F:4:TYR:OH	9:F:72:VAL:HG21	2.18	0.44
1:A:477:G:O2'	1:A:478:A:H5'	2.18	0.44
15:L:109:GLY:O	15:L:110:VAL:C	2.56	0.44
1:A:1061:G:C2'	1:A:1062:U:H5'	2.48	0.44
8:E:42:GLY:HA2	8:E:65:ASN:O	2.18	0.44
19:P:74:LEU:O	19:P:79:VAL:CG2	2.66	0.44
1:A:475:G:O2'	1:A:476:G:H5'	2.18	0.44
20:Q:45:HIS:HA	20:Q:69:LYS:HE3	1.99	0.44
1:A:695:A:H2'	1:A:696:A:C8	2.53	0.44
1:A:554:C:H2'	1:A:555:C:C6	2.53	0.44
1:A:668:G:O2'	18:O:46:HIS:CD2	2.71	0.44
1:A:1253:G:H2'	1:A:1254:C:C6	2.53	0.44
1:A:594:G:C2'	1:A:595:G:H5'	2.47	0.44
5:B:135:GLN:O	5:B:135:GLN:HG2	2.18	0.44
5:B:77:ALA:CB	5:B:211:ILE:HG21	2.47	0.44
5:B:87:ARG:NH1	5:B:233:SER:HB2	2.33	0.44
5:B:87:ARG:NH1	5:B:233:SER:CB	2.81	0.44
1:A:946:A:H2'	1:A:947:G:H8	1.76	0.44
10:G:51:GLN:C	10:G:53:LYS:N	2.71	0.44
11:H:119:LEU:HD12	11:H:124:ALA:N	2.32	0.44
16:M:86:CYS:SG	16:M:88:ARG:HB3	2.58	0.44
1:A:1238:A:C2	1:A:1241:G:N3	2.85	0.44
7:D:111:ALA:HB2	7:D:120:LEU:HD12	1.99	0.44
1:A:132:C:O2'	1:A:133:U:H5'	2.17	0.44
17:N:18:VAL:O	17:N:20:ALA:N	2.51	0.44
1:A:166:G:O2'	1:A:167:G:H5'	2.18	0.44
1:A:31:G:C6	1:A:48:C:H5"	2.53	0.44
6:C:134:ILE:HG22	6:C:168:ALA:CB	2.48	0.44
13:J:42:THR:HG23	13:J:67:THR:O	2.18	0.44
10:G:37:ASN:O	10:G:40:ALA:N	2.51	0.44
1:A:636:U:H2'	1:A:637:G:C8	2.52	0.44
1:A:908:A:H2'	1:A:909:A:C8	2.53	0.44
15:L:46:LYS:CD	15:L:47:LYS:H	2.31	0.44
1:A:1002:G:O6	1:A:1040:U:O2	2.35	0.44
1:A:1036:G:H2'	1:A:1037:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:34:ARG:HG2	15:L:61:THR:HG21	2.00	0.44
14:K:20:TYR:CZ	14:K:83:ILE:HD12	2.53	0.44
16:M:34:LEU:CD1	16:M:41:PRO:HA	2.43	0.44
1:A:1318:A:H4'	22:S:10:PHE:CE1	2.51	0.44
1:A:862:C:O2'	1:A:863:U:H5'	2.18	0.44
13:J:42:THR:HG23	13:J:67:THR:C	2.38	0.44
9:F:53:ALA:C	9:F:55:ASP:H	2.21	0.44
11:H:75:ARG:HA	11:H:76:PRO:HD3	1.77	0.44
13:J:34:VAL:HG22	13:J:74:ILE:CG2	2.48	0.44
6:C:179:ARG:HG3	6:C:179:ARG:HH11	1.82	0.44
21:R:21:LYS:C	21:R:23:LYS:H	2.21	0.44
5:B:9:GLU:OE2	5:B:12:GLU:HA	2.17	0.44
5:B:164:VAL:O	5:B:186:ALA:HA	2.17	0.44
6:C:112:SER:O	6:C:115:LEU:HB2	2.18	0.44
12:I:42:ARG:NH2	12:I:71:SER:OG	2.48	0.44
14:K:33:THR:OG1	14:K:37:GLY:C	2.56	0.44
23:T:11:SER:HA	23:T:13:LEU:CD1	2.48	0.44
23:T:11:SER:O	23:T:13:LEU:HD12	2.17	0.44
19:P:58:TYR:CE2	19:P:62:VAL:HG21	2.53	0.44
20:Q:98:LEU:HA	20:Q:102:GLY:HA2	2.00	0.44
23:T:70:SER:HA	23:T:73:HIS:HD2	1.82	0.44
1:A:1102:A:H2'	1:A:1103:C:C6	2.53	0.44
1:A:417:C:O2'	1:A:418:C:H5'	2.18	0.44
10:G:110:GLN:OE1	10:G:110:GLN:HA	2.18	0.44
19:P:26:ARG:CD	19:P:31:LYS:O	2.64	0.44
1:A:858:G:O2'	1:A:859:A:H5'	2.17	0.44
1:A:745:C:H2'	1:A:746:A:C8	2.52	0.44
1:A:603:U:H2'	1:A:604:G:H8	1.83	0.44
1:A:682:G:O2'	1:A:683:G:H5'	2.18	0.44
11:H:133:LEU:C	11:H:133:LEU:CD2	2.85	0.43
13:J:22:LYS:O	13:J:24:VAL:N	2.49	0.43
1:A:1054:C:O2'	1:A:1055:A:O5'	2.32	0.43
1:A:579:G:H2'	1:A:580:U:C6	2.53	0.43
6:C:22:TRP:HB3	6:C:59:ARG:H	1.84	0.43
18:O:15:PHE:O	18:O:16:ALA:C	2.56	0.43
1:A:1168:A:C6	1:A:1169:A:C6	3.05	0.43
16:M:37:THR:HG22	16:M:37:THR:O	2.18	0.43
8:E:101:ILE:HD12	8:E:119:LEU:HD23	1.99	0.43
1:A:583:A:H2'	1:A:584:G:O4'	2.18	0.43
5:B:108:ILE:O	5:B:111:ARG:HB2	2.17	0.43
1:A:1066:C:O2'	1:A:1067:A:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:C:H2'	1:A:458:C:C6	2.53	0.43
12:I:23:ASN:ND2	12:I:23:ASN:C	2.71	0.43
20:Q:4:LYS:HD2	20:Q:6:LEU:HD21	1.99	0.43
7:D:35:ARG:O	7:D:36:ARG:CB	2.66	0.43
12:I:10:ARG:O	12:I:11:LYS:C	2.55	0.43
13:J:6:ILE:O	13:J:6:ILE:HG13	2.18	0.43
1:A:243:A:C2	1:A:246:A:C8	3.06	0.43
1:A:1256:A:O2'	1:A:1257:U:O4'	2.34	0.43
1:A:192:U:H5'	23:T:102:GLY:O	2.17	0.43
5:B:82:ARG:HB2	5:B:92:TYR:HE1	1.83	0.43
1:A:1142:G:H2'	1:A:1143:G:O4'	2.18	0.43
7:D:187:ARG:HA	7:D:187:ARG:HE	1.83	0.43
9:F:62:TRP:O	9:F:62:TRP:HE3	2.01	0.43
7:D:31:CYS:SG	7:D:31:CYS:O	2.77	0.43
1:A:528:C:H5'	1:A:535:A:N6	2.33	0.43
15:L:119:LYS:O	15:L:120:TYR:CB	2.67	0.43
5:B:28:PHE:CD2	5:B:28:PHE:O	2.70	0.43
6:C:138:VAL:HG21	6:C:168:ALA:HB1	1.99	0.43
12:I:9:ARG:HG2	12:I:13:ALA:O	2.18	0.43
9:F:1:MET:SD	9:F:68:PRO:HG3	2.58	0.43
15:L:71:PRO:O	15:L:102:ARG:CD	2.66	0.43
7:D:199:ASN:C	7:D:199:ASN:HD22	2.20	0.43
17:N:44:LEU:C	17:N:44:LEU:HD12	2.37	0.43
14:K:14:VAL:O	14:K:16:SER:N	2.51	0.43
16:M:2:ALA:O	16:M:3:ARG:C	2.56	0.43
13:J:29:ARG:H	13:J:29:ARG:HD2	1.83	0.43
5:B:24:TRP:CD1	5:B:24:TRP:N	2.84	0.43
9:F:2:ARG:CZ	9:F:69:GLU:HG2	2.48	0.43
11:H:104:ARG:O	11:H:107:LEU:N	2.47	0.43
6:C:42:LEU:C	6:C:44:GLU:H	2.21	0.43
1:A:1153:C:C2	1:A:1154:G:C8	3.06	0.43
5:B:151:GLY:C	5:B:153:ARG:N	2.71	0.43
12:I:17:VAL:HG11	12:I:81:ILE:HA	2.01	0.43
16:M:81:LEU:HB2	16:M:86:CYS:SG	2.59	0.43
12:I:93:ARG:O	12:I:96:LEU:N	2.51	0.43
8:E:41:VAL:HG13	8:E:113:ALA:CA	2.46	0.43
1:A:958:A:C6	1:A:959:A:N1	2.86	0.43
1:A:1244:C:O2'	1:A:1245:A:H5'	2.18	0.43
1:A:1090:U:O2'	1:A:1091:U:H5'	2.18	0.43
1:A:428:G:O2'	1:A:429:U:P	2.76	0.43
21:R:22:VAL:CG1	21:R:42:ARG:HB3	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:20:ARG:O	12:I:60:ASP:N	2.51	0.43
1:A:1450:U:H2'	1:A:1452:C:C5	2.53	0.43
5:B:144:ARG:HA	5:B:147:LYS:CD	2.48	0.43
12:I:104:ARG:O	12:I:105:ASP:C	2.56	0.43
1:A:1206:G:H2'	1:A:1207:G:C8	2.54	0.43
6:C:154:SER:OG	6:C:196:LEU:HA	2.18	0.43
1:A:1167:A:C6	1:A:1168:A:C6	3.07	0.43
1:A:1003(A):G:H2'	1:A:1004:A:O4'	2.18	0.43
16:M:37:THR:O	16:M:39:ILE:HG13	2.17	0.43
1:A:8:A:C6	7:D:209:ARG:HA	2.54	0.43
1:A:1441:G:H1'	1:A:1460:A:H61	1.82	0.43
1:A:1455:G:O2'	1:A:1459:C:H5'	2.19	0.43
1:A:1459:C:O2'	1:A:1460:A:H5'	2.18	0.43
12:I:97:LYS:N	12:I:98:PRO:CD	2.81	0.43
9:F:94:GLN:H	9:F:94:GLN:NE2	2.16	0.43
7:D:162:LEU:HD22	7:D:162:LEU:HA	1.83	0.43
1:A:411:A:C6	1:A:429:U:C4	3.06	0.43
1:A:1030:C:H2'	1:A:1030(A):G:O4'	2.19	0.43
1:A:746:A:O2'	1:A:747:C:H5'	2.19	0.43
1:A:678:U:H2'	1:A:679:C:C6	2.54	0.43
5:B:135:GLN:O	5:B:136:VAL:HG23	2.19	0.43
5:B:212:GLN:NE2	5:B:216:SER:HB3	2.34	0.43
5:B:39:ILE:HG22	5:B:40:HIS:O	2.19	0.43
15:L:27:LEU:HD23	15:L:62:SER:CB	2.29	0.43
6:C:34:LEU:HD21	6:C:38:ARG:CG	2.48	0.43
12:I:88:TYR:O	12:I:90:PRO:HD3	2.18	0.43
1:A:1238:A:N7	1:A:1303:C:H1'	2.34	0.43
20:Q:99:SER:OG	20:Q:100:LYS:N	2.49	0.43
9:F:82:ARG:HB2	9:F:85:VAL:HG23	2.00	0.43
1:A:190(A):C:O2'	1:A:190(B):C:H5'	2.18	0.43
1:A:84:U:H2'	1:A:88:A:C8	2.54	0.43
8:E:15:ARG:C	8:E:15:ARG:HD2	2.38	0.43
19:P:57:ARG:HG2	19:P:57:ARG:HH11	1.83	0.43
6:C:204:LEU:O	6:C:205:GLY:C	2.57	0.43
10:G:66:VAL:O	10:G:68:ASN:N	2.51	0.43
6:C:15:THR:HB	6:C:181:ASN:CB	2.45	0.43
5:B:53:ARG:NH1	5:B:199:TYR:HD2	2.15	0.43
5:B:60:ASP:O	5:B:64:ARG:HB2	2.17	0.43
17:N:23:ARG:C	17:N:33:VAL:HG11	2.39	0.43
1:A:1277:C:H2'	1:A:1278:U:C2	2.54	0.43
8:E:53:LEU:O	8:E:57:LYS:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:G:O2'	8:E:120:THR:O	2.36	0.43
22:S:6:LYS:HB3	22:S:7:LYS:H	1.54	0.43
1:A:149:A:H2'	1:A:150:C:H6	1.80	0.43
8:E:60:TYR:HE1	8:E:64:ARG:NH2	2.17	0.43
1:A:560:U:H4'	1:A:561:U:H5"	2.01	0.43
1:A:1514:C:O2'	1:A:1515:C:H5'	2.19	0.43
1:A:1118:C:H1'	1:A:1179:A:N9	2.33	0.43
7:D:35:ARG:O	7:D:36:ARG:HB2	2.19	0.43
13:J:22:LYS:C	13:J:24:VAL:N	2.68	0.43
1:A:1085:U:O3'	1:A:1086:U:C6	2.72	0.43
6:C:39:ILE:C	6:C:41:GLY:H	2.22	0.43
1:A:1278:U:C4'	1:A:1279:A:H5'	2.47	0.43
11:H:104:ARG:C	11:H:106:GLY:N	2.70	0.43
1:A:1039:C:H2'	1:A:1040:U:H6	1.80	0.43
15:L:89:ARG:HG2	15:L:97:ARG:CA	2.42	0.43
1:A:1439:C:H2'	1:A:1440:C:H6	1.84	0.43
5:B:73:THR:HB	5:B:170:GLU:OE1	2.18	0.43
1:A:1298:C:H1'	1:A:1299:A:C2	2.53	0.43
9:F:62:TRP:CD1	21:R:35:ARG:CZ	3.02	0.43
21:R:33:ASP:OD2	21:R:36:ASN:HB2	2.18	0.43
10:G:111:ARG:HH21	10:G:122:HIS:HB3	1.84	0.43
11:H:68:ARG:NH1	11:H:68:ARG:HG2	2.34	0.43
17:N:14:PRO:HG2	17:N:15:LYS:H	1.83	0.43
11:H:31:PHE:HZ	11:H:134:ILE:CD1	2.32	0.43
23:T:62:LEU:HA	23:T:62:LEU:HD23	1.84	0.43
9:F:1:MET:HB2	9:F:67:MET:O	2.18	0.43
7:D:17:VAL:CG1	7:D:18:LYS:N	2.81	0.43
1:A:512:U:H2'	1:A:513:C:C6	2.54	0.43
1:A:190(J):U:H2'	1:A:190(K):G:C8	2.53	0.43
1:A:697:U:H2'	1:A:698:G:H5'	1.99	0.43
1:A:1251:A:H2'	1:A:1252:A:H8	1.80	0.43
6:C:39:ILE:C	6:C:41:GLY:N	2.72	0.43
23:T:96:GLY:O	23:T:97:ALA:CB	2.65	0.43
12:I:8:GLY:CA	12:I:79:LEU:HB3	2.47	0.43
16:M:35:GLU:O	16:M:37:THR:N	2.50	0.43
15:L:98:TYR:CD1	15:L:98:TYR:N	2.86	0.43
1:A:229:U:H5"	19:P:33:ILE:HD13	2.01	0.43
1:A:113:G:H1'	1:A:354:G:C5'	2.46	0.43
1:A:383:A:H2'	1:A:384:G:H5'	2.01	0.43
21:R:35:ARG:O	21:R:37:VAL:N	2.46	0.43
1:A:231:G:O2'	1:A:232:G:H5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:G:O2'	1:A:333:G:H5'	2.19	0.43
7:D:182:LYS:HZ3	7:D:182:LYS:HB3	1.84	0.43
1:A:935:A:C2	1:A:936:C:C2	3.07	0.43
1:A:1358:U:H2'	1:A:1359:C:O4'	2.18	0.43
1:A:1189:C:H5"	6:C:5:ILE:HG12	2.01	0.43
1:A:1190:G:C2'	1:A:1191:A:OP2	2.67	0.43
1:A:974:A:OP2	17:N:41:ARG:NH1	2.52	0.43
11:H:86:ILE:CD1	11:H:133:LEU:CD2	2.97	0.43
10:G:61:VAL:O	10:G:62:PHE:C	2.57	0.43
6:C:15:THR:HG21	6:C:179:ARG:C	2.39	0.43
5:B:10:LEU:HA	5:B:48:MET:HE1	2.00	0.43
6:C:43:LEU:HD22	6:C:68:VAL:HG21	2.01	0.43
1:A:662:G:H2'	1:A:663:A:H8	1.84	0.43
6:C:139:GLN:NE2	6:C:139:GLN:CA	2.82	0.43
16:M:25:ILE:HG22	16:M:26:GLY:N	2.33	0.43
1:A:279:A:C6	20:Q:98:LEU:HD13	2.54	0.43
9:F:62:TRP:C	9:F:63:TYR:HD2	2.22	0.43
1:A:262:A:C6	1:A:263:A:C6	3.06	0.43
5:B:178:ARG:NH2	11:H:68:ARG:HH22	2.17	0.43
1:A:1405:G:O2'	1:A:1406:U:H5'	2.19	0.43
1:A:1406:U:O2'	1:A:1407:C:H5'	2.19	0.43
1:A:118:U:O4	1:A:288:A:H2'	2.18	0.43
15:L:83:VAL:HG22	15:L:84:LEU:N	2.32	0.43
1:A:621:A:H2'	1:A:622:A:C8	2.54	0.43
6:C:17:ASP:OD1	6:C:18:TRP:N	2.52	0.43
7:D:19:LEU:HD22	7:D:67:ILE:HG12	2.01	0.43
5:B:128:GLU:HA	5:B:135:GLN:NE2	2.34	0.43
13:J:61:GLU:OE1	17:N:45:ARG:NH1	2.41	0.43
1:A:1392:G:H21	1:A:1502:A:H8	1.66	0.43
18:O:12:ILE:HG23	18:O:27:VAL:HG11	2.01	0.43
1:A:1229:A:C2	1:A:1230:C:C5	3.07	0.43
1:A:335:C:O2'	1:A:336:C:H5'	2.17	0.43
9:F:62:TRP:CE3	9:F:62:TRP:O	2.72	0.43
1:A:190(L):U:H3	23:T:105:SER:HB2	1.84	0.43
9:F:22:GLU:OE1	9:F:82:ARG:HD3	2.19	0.43
16:M:106:ASN:O	16:M:107:ALA:CB	2.65	0.43
21:R:22:VAL:HG13	21:R:42:ARG:HB3	2.01	0.43
14:K:124:LYS:HE2	14:K:125:PHE:CZ	2.53	0.43
1:A:975:A:C5'	1:A:975:A:C8	2.97	0.42
1:A:1286:A:C8	1:A:1287:A:C5'	3.02	0.42
13:J:81:THR:C	13:J:83:GLU:N	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:56:ARG:O	5:B:57:PHE:C	2.57	0.42
1:A:839:U:O2	1:A:839:U:H2'	2.19	0.42
1:A:228:A:H4'	19:P:62:VAL:HG11	2.01	0.42
1:A:761:G:H4'	20:Q:103:GLY:O	2.19	0.42
10:G:145:ALA:O	10:G:146:GLU:CB	2.66	0.42
23:T:10:LEU:CD1	23:T:12:ALA:H	2.32	0.42
8:E:5:ASP:CG	8:E:6:PHE:H	2.22	0.42
1:A:1091:U:C2	1:A:1093:A:OP2	2.71	0.42
16:M:80:ARG:C	16:M:82:MET:N	2.72	0.42
13:J:44:VAL:HG21	13:J:66:ARG:NH2	2.34	0.42
14:K:69:ALA:HA	14:K:103:LEU:HD11	2.01	0.42
24:V:22:ARG:N	24:V:23:PRO:HD3	2.34	0.42
21:R:22:VAL:O	21:R:22:VAL:HG12	2.18	0.42
1:A:97:G:H2'	1:A:98:U:O4'	2.19	0.42
7:D:50:ARG:NH1	7:D:51:PRO:O	2.52	0.42
1:A:1338:G:H2'	1:A:1339:A:C8	2.54	0.42
12:I:120:ARG:O	12:I:121:ARG:C	2.57	0.42
1:A:998:G:O2'	1:A:999:C:H5'	2.19	0.42
7:D:13:ARG:HD2	7:D:38:TYR:O	2.20	0.42
13:J:20:ALA:O	13:J:24:VAL:HG23	2.18	0.42
1:A:1229:A:H2'	1:A:1230:C:C6	2.54	0.42
6:C:94:LEU:HD23	6:C:94:LEU:C	2.39	0.42
1:A:1347:G:H1'	1:A:1348:U:H5	1.84	0.42
12:I:79:LEU:O	12:I:82:ALA:N	2.53	0.42
16:M:55:ARG:O	16:M:56:LEU:C	2.57	0.42
12:I:80:GLY:O	12:I:84:ALA:N	2.44	0.42
7:D:173:TRP:HB2	7:D:187:ARG:O	2.19	0.42
5:B:78:GLN:NE2	5:B:96:ARG:NH1	2.67	0.42
1:A:1299:A:C8	1:A:1301:U:H1'	2.54	0.42
1:A:380:G:C2	1:A:384:G:C6	3.07	0.42
1:A:960:U:H2'	1:A:960:U:O2	2.19	0.42
1:A:938:A:C6	1:A:939:G:C5	3.07	0.42
9:F:25:ILE:O	9:F:26:ILE:C	2.56	0.42
20:Q:81:ARG:HE	20:Q:81:ARG:HB2	1.27	0.42
1:A:635:G:O2'	1:A:636:U:H5'	2.19	0.42
1:A:219:C:H2'	1:A:220:G:O4'	2.19	0.42
7:D:141:ARG:N	7:D:144:ASP:OD2	2.52	0.42
11:H:25:ASP:OD1	11:H:25:ASP:N	2.52	0.42
1:A:530:G:O2'	3:Y:35:A:H4'	2.19	0.42
8:E:31:LEU:HA	8:E:31:LEU:HD23	1.76	0.42
5:B:209:ARG:O	5:B:213:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:35:GLU:O	6:C:36:ASP:C	2.58	0.42
5:B:69:LEU:C	5:B:69:LEU:CD2	2.87	0.42
12:I:76:ALA:O	12:I:79:LEU:N	2.52	0.42
8:E:101:ILE:HD12	8:E:119:LEU:CD2	2.49	0.42
1:A:1176:A:O2'	1:A:1177:G:H5'	2.20	0.42
7:D:150:GLU:CG	7:D:153:ARG:HH22	2.31	0.42
23:T:86:ARG:HG3	23:T:90:GLN:HE21	1.83	0.42
1:A:1072:G:H2'	1:A:1073:U:O4'	2.19	0.42
8:E:107:ARG:O	8:E:108:ALA:C	2.57	0.42
6:C:127:ARG:HG2	6:C:127:ARG:HH11	1.84	0.42
23:T:26:ASN:O	23:T:27:LYS:C	2.57	0.42
1:A:831:U:O2'	1:A:832:C:H5'	2.19	0.42
10:G:79:ARG:HH11	10:G:79:ARG:HG2	1.84	0.42
11:H:38:ILE:N	11:H:38:ILE:HD12	2.35	0.42
5:B:23:ARG:NH1	5:B:191:ASP:HA	2.34	0.42
5:B:76:GLN:HG3	5:B:206:ASP:OD1	2.19	0.42
1:A:1226:C:H6	16:M:103:THR:HG1	1.64	0.42
6:C:44:GLU:C	6:C:46:GLU:N	2.73	0.42
11:H:48:TYR:C	11:H:48:TYR:CD1	2.92	0.42
1:A:130:A:H1'	1:A:263:A:O2'	2.19	0.42
5:B:111:ARG:NE	5:B:111:ARG:HA	2.34	0.42
20:Q:45:HIS:CB	20:Q:69:LYS:HE2	2.49	0.42
16:M:21:TYR:N	16:M:21:TYR:CD1	2.87	0.42
1:A:28:G:O2'	1:A:296:U:OP1	2.37	0.42
12:I:36:TYR:CD2	12:I:37:PHE:CE2	3.08	0.42
1:A:1250:A:H5'	12:I:68:GLY:O	2.19	0.42
5:B:26:PRO:O	5:B:29:ALA:CB	2.67	0.42
15:L:28:LYS:HD3	15:L:33:ARG:NH2	2.33	0.42
1:A:1188:A:H2'	1:A:1189:C:O4'	2.19	0.42
3:Y:33:U:H5'	3:Y:34:G:OP2	2.19	0.42
4:Z:2:U:H2'	4:Z:3:U:C6	2.54	0.42
6:C:179:ARG:C	6:C:179:ARG:HD2	2.39	0.42
14:K:91:ARG:HH11	21:R:88:LYS:CE	2.31	0.42
5:B:100:GLY:O	5:B:104:ASN:N	2.47	0.42
18:O:39:LEU:O	18:O:43:LEU:HG	2.19	0.42
14:K:99:GLN:HG2	14:K:105:VAL:CG2	2.43	0.42
11:H:82:HIS:C	11:H:82:HIS:CD2	2.92	0.42
7:D:3:ARG:NH2	7:D:74:GLN:OE1	2.52	0.42
1:A:166:G:H2'	1:A:167:G:H8	1.84	0.42
9:F:23:LYS:NZ	9:F:42:GLU:OE2	2.50	0.42
24:V:24:ARG:HH11	24:V:24:ARG:HG3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:828:A:H2'	1:A:829:G:O4'	2.19	0.42
5:B:107:THR:C	5:B:109:SER:N	2.72	0.42
6:C:131:ARG:O	6:C:135:LYS:HG3	2.19	0.42
7:D:91:SER:O	7:D:94:LEU:N	2.53	0.42
17:N:43:CYS:HA	17:N:46:GLU:HG3	2.02	0.42
10:G:71:PRO:HG3	10:G:103:TRP:CH2	2.55	0.42
1:A:1492:A:H1'	4:Z:2:U:O2'	2.19	0.42
1:A:1392:G:N2	1:A:1502:A:H8	2.17	0.42
6:C:59:ARG:HG2	6:C:64:VAL:HG22	2.01	0.42
1:A:193:C:H2'	1:A:194:C:C6	2.55	0.42
6:C:139:GLN:O	6:C:140:ARG:C	2.56	0.42
1:A:1017:G:H2'	1:A:1018:C:C6	2.55	0.42
12:I:42:ARG:O	12:I:45:ALA:N	2.53	0.42
16:M:49:THR:HB	16:M:52:GLU:CG	2.43	0.42
7:D:6:GLY:O	7:D:7:PRO:C	2.57	0.42
16:M:96:LEU:HB3	16:M:97:PRO:HD2	2.01	0.42
11:H:63:LEU:CD2	11:H:63:LEU:N	2.82	0.42
20:Q:97:SER:CB	20:Q:103:GLY:C	2.87	0.42
8:E:144:THR:N	8:E:147:ASP:OD2	2.52	0.42
6:C:10:PHE:O	6:C:178:LEU:HD11	2.19	0.42
8:E:16:THR:HG23	8:E:17:ALA:N	2.33	0.42
1:A:379:C:O2'	1:A:380:G:H5'	2.20	0.42
1:A:385:C:O2'	1:A:386:C:H5'	2.19	0.42
1:A:1322:C:OP1	22:S:78:ARG:NH2	2.52	0.42
1:A:818:G:HO2'	1:A:820:U:H6	1.61	0.42
7:D:60:GLU:HG2	7:D:202:LEU:HB2	2.00	0.42
1:A:189:G:H2'	1:A:190:C:C6	2.54	0.42
1:A:448:A:C4	1:A:487:A:C2	3.07	0.42
21:R:53:ARG:HB2	21:R:63:GLN:HG2	2.02	0.42
1:A:1010:G:N2	1:A:1020:U:H1'	2.34	0.42
11:H:20:TYR:CE2	11:H:75:ARG:HD2	2.54	0.42
1:A:190(H):G:O2'	1:A:190(I):G:H5'	2.20	0.42
11:H:2:LEU:HD23	11:H:2:LEU:HA	1.87	0.42
13:J:49:VAL:HG12	13:J:50:ILE:N	2.34	0.42
5:B:19:HIS:CE1	5:B:206:ASP:HB3	2.54	0.42
5:B:221:LEU:O	5:B:221:LEU:HD13	2.20	0.42
5:B:100:GLY:N	5:B:176:GLU:OE2	2.53	0.42
17:N:29:ARG:NH1	17:N:29:ARG:HG2	2.34	0.42
5:B:68:ILE:N	5:B:90:MET:HE3	2.35	0.42
23:T:50:GLU:OE1	23:T:100:ILE:HD11	2.19	0.42
8:E:51:VAL:HB	8:E:52:PRO:CD	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:44:MET:O	22:S:45:VAL:C	2.56	0.42
1:A:791:G:C5	1:A:792:A:N7	2.88	0.42
5:B:111:ARG:HB3	5:B:149:LEU:CD1	2.46	0.42
1:A:687:A:C2	1:A:700:G:N3	2.87	0.42
1:A:1007:C:O2'	1:A:1008:C:H5'	2.19	0.42
10:G:22:LEU:HD12	10:G:101:LEU:HD11	2.01	0.42
19:P:53:VAL:O	19:P:57:ARG:HG3	2.20	0.42
1:A:999:C:H2'	1:A:1000:U:C6	2.54	0.42
1:A:1520:G:O2'	1:A:1521:G:H5'	2.19	0.42
8:E:84:PHE:HB2	8:E:134:ALA:HB2	2.01	0.42
5:B:80:ILE:N	5:B:80:ILE:HD12	2.11	0.42
13:J:12:ASP:O	13:J:15:THR:HG22	2.20	0.42
13:J:34:VAL:HG13	13:J:74:ILE:HG23	2.00	0.42
13:J:74:ILE:CD1	13:J:85:LEU:HD11	2.49	0.42
1:A:736:C:H2'	1:A:737:A:C8	2.54	0.42
5:B:51:LEU:O	5:B:55:PHE:HD1	2.03	0.42
17:N:24:CYS:CB	17:N:27:CYS:SG	3.07	0.42
6:C:119:ARG:CG	6:C:140:ARG:HH12	2.28	0.42
16:M:33:ALA:HA	16:M:59:TYR:CD2	2.53	0.42
7:D:163:GLU:C	7:D:165:MET:N	2.73	0.42
6:C:155:GLY:O	6:C:156:ARG:CB	2.68	0.42
1:A:418:C:H2'	1:A:419:C:H6	1.85	0.42
6:C:157:ILE:CG2	6:C:164:ARG:NH2	2.83	0.42
1:A:1533:C:H3'	1:A:1533:C:O2	2.20	0.42
21:R:40:LEU:HB3	21:R:79:LEU:HD11	2.02	0.42
13:J:9:ARG:O	13:J:9:ARG:HG3	2.19	0.42
10:G:126:ASP:HB3	10:G:131:LYS:HG3	2.02	0.42
1:A:1286:A:H2'	1:A:1287:A:C5'	2.50	0.42
5:B:211:ILE:O	5:B:215:LEU:HB2	2.19	0.42
22:S:22:LEU:HD22	22:S:28:LYS:CD	2.48	0.42
13:J:60:ARG:O	13:J:61:GLU:HB3	2.20	0.42
1:A:1207:G:H2'	1:A:1208:C:H6	1.85	0.42
6:C:14:ILE:O	6:C:15:THR:C	2.57	0.42
21:R:21:LYS:O	21:R:23:LYS:N	2.52	0.42
10:G:15:ASP:CG	10:G:18:TYR:H	2.23	0.42
16:M:31:LYS:O	16:M:35:GLU:HB2	2.20	0.42
23:T:56:MET:CE	23:T:104:LEU:HD21	2.49	0.42
16:M:108:ARG:C	16:M:110:ARG:H	2.24	0.42
22:S:61:TYR:HD2	22:S:62:ILE:N	2.17	0.42
1:A:582:U:C2	1:A:760:G:C6	3.07	0.42
18:O:6:GLU:O	18:O:7:GLU:C	2.58	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:144:MET:C	10:G:145:ALA:O	2.57	0.42
1:A:344:A:H5"	1:A:345:C:H5	1.85	0.42
18:O:63:ARG:O	18:O:65:ARG:N	2.53	0.42
1:A:268:C:H2'	1:A:269:C:H6	1.84	0.42
1:A:119:A:O2'	1:A:120:A:OP2	2.29	0.42
1:A:342:C:O2'	1:A:343:U:H5'	2.20	0.42
8:E:150:ARG:HH11	8:E:150:ARG:HG3	1.83	0.42
1:A:1288:A:H2'	1:A:1289:A:O4'	2.20	0.42
1:A:1370:G:C2	1:A:1371:G:N7	2.88	0.42
1:A:371:G:C2'	1:A:372:C:C5'	2.94	0.42
5:B:102:LEU:CD1	5:B:102:LEU:H	2.33	0.42
16:M:16:ASP:OD1	16:M:16:ASP:N	2.52	0.42
10:G:20:ASP:OD2	10:G:63:LYS:NZ	2.53	0.42
12:I:24:GLY:HA2	12:I:59:PHE:O	2.20	0.42
16:M:49:THR:O	16:M:50:GLU:C	2.58	0.42
1:A:542:G:OP1	7:D:10:ARG:NH2	2.53	0.42
7:D:8:VAL:C	7:D:10:ARG:H	2.22	0.42
1:A:502:G:P	15:L:118:SER:HB2	2.60	0.42
1:A:992:U:O2'	1:A:993:G:OP2	2.29	0.42
8:E:24:ARG:O	8:E:25:ARG:HD3	2.20	0.42
1:A:520:A:H2'	1:A:521:G:O4'	2.20	0.42
23:T:84:LEU:C	23:T:86:ARG:N	2.72	0.42
1:A:928:G:O2'	1:A:929:G:H5'	2.20	0.42
1:A:1047:G:H5"	17:N:4:LYS:HD2	2.01	0.42
1:A:642:A:C5	11:H:115:SER:HA	2.55	0.42
1:A:1328:C:H41	24:V:6:ARG:HH22	1.68	0.42
1:A:1157:A:H1'	1:A:1181:G:N2	2.35	0.42
1:A:145:G:O2'	1:A:146:G:H5'	2.20	0.42
14:K:58:PRO:O	14:K:61:ALA:HB3	2.20	0.42
7:D:133:VAL:HG11	7:D:138:TYR:CD1	2.54	0.42
1:A:652:U:O4	1:A:752:G:O2'	2.28	0.42
1:A:1386:G:H2'	1:A:1387:G:H8	1.85	0.42
7:D:192:GLU:OE1	7:D:192:GLU:HA	2.20	0.42
16:M:71:ARG:HG2	16:M:71:ARG:HH11	1.85	0.42
13:J:27:ALA:HA	13:J:30:SER:HG	1.84	0.41
5:B:103:THR:N	5:B:176:GLU:OE1	2.33	0.41
5:B:91:PRO:HG3	5:B:155:LEU:HG	2.01	0.41
6:C:38:ARG:HB3	6:C:94:LEU:HD11	2.02	0.41
18:O:17:ARG:NH1	18:O:77:ARG:NH1	2.68	0.41
5:B:112:VAL:O	5:B:114:ARG:N	2.53	0.41
14:K:20:TYR:CE1	14:K:83:ILE:HD12	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:163:GLU:HA	7:D:163:GLU:OE2	2.18	0.41
15:L:90:VAL:CG1	15:L:93:LEU:HG	2.50	0.41
16:M:82:MET:CE	16:M:92:HIS:HB3	2.50	0.41
10:G:78:ARG:NH1	10:G:154:TYR:HB3	2.35	0.41
6:C:113:ALA:N	6:C:114:PRO:CD	2.83	0.41
5:B:30:ARG:CG	5:B:31:TYR:N	2.84	0.41
1:A:1516:G:H2'	1:A:1518:A:OP2	2.20	0.41
1:A:1328:C:OP1	24:V:21:TYR:OH	2.35	0.41
6:C:132:ARG:O	6:C:133:ALA:C	2.58	0.41
1:A:310:G:H2'	1:A:311:C:H6	1.85	0.41
1:A:934:C:C4	1:A:1345:U:C5	3.08	0.41
1:A:1438:G:C2	1:A:1464:G:N3	2.88	0.41
15:L:27:LEU:C	15:L:29:GLY:N	2.74	0.41
13:J:38:ILE:CB	13:J:71:LEU:HB3	2.51	0.41
6:C:6:HIS:C	6:C:6:HIS:CD2	2.92	0.41
1:A:1399:C:C2	1:A:1502:A:N6	2.88	0.41
5:B:12:GLU:CD	5:B:213:LEU:HD11	2.40	0.41
5:B:52:GLU:O	5:B:56:ARG:HG3	2.20	0.41
6:C:89:GLU:C	6:C:91:LEU:N	2.73	0.41
23:T:50:GLU:CD	23:T:100:ILE:HD11	2.41	0.41
1:A:193:C:O3'	23:T:61:SER:HB2	2.20	0.41
1:A:1227:A:O3'	16:M:115:LYS:HE3	2.19	0.41
16:M:53:VAL:O	16:M:54:VAL:C	2.59	0.41
1:A:542:G:H5'	7:D:41:GLY:HA3	2.02	0.41
1:A:228:A:H2'	1:A:229:U:C6	2.55	0.41
1:A:628:G:H2'	1:A:629:G:H8	1.84	0.41
23:T:72:LEU:O	23:T:73:HIS:O	2.37	0.41
1:A:1315:U:OP2	22:S:6:LYS:NZ	2.53	0.41
5:B:101:MET:N	5:B:108:ILE:HD12	2.34	0.41
5:B:178:ARG:HH21	5:B:196:LEU:HA	1.85	0.41
11:H:112:LEU:H	11:H:112:LEU:HD23	1.83	0.41
1:A:640:A:C2'	1:A:641:U:H5'	2.50	0.41
1:A:686:U:O2'	1:A:687:A:H8	2.02	0.41
21:R:18:ARG:H	21:R:19:LYS:HD2	1.85	0.41
1:A:411:A:N3	1:A:413:G:O2'	2.54	0.41
21:R:52:PRO:HB2	21:R:54:ARG:HB2	2.02	0.41
1:A:1512:U:O2'	1:A:1513:A:H5'	2.19	0.41
1:A:425:G:O2'	1:A:426:G:H5'	2.20	0.41
1:A:1053:G:O3'	1:A:1054:C:H4'	2.20	0.41
24:V:2:GLY:C	24:V:4:GLY:H	2.24	0.41
5:B:16:HIS:O	5:B:17:PHE:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:16:ALA:CB	18:O:21:ASP:HB3	2.38	0.41
7:D:61:LYS:HD3	7:D:206:PHE:CD2	2.55	0.41
1:A:1153:C:O2'	1:A:1154:G:H5'	2.20	0.41
18:O:17:ARG:O	18:O:18:PHE:HB3	2.20	0.41
16:M:81:LEU:HD12	16:M:88:ARG:HG2	2.02	0.41
16:M:56:LEU:HA	16:M:56:LEU:HD23	1.87	0.41
16:M:20:THR:O	16:M:22:ILE:N	2.53	0.41
16:M:59:TYR:O	16:M:63:THR:HG21	2.20	0.41
16:M:96:LEU:O	16:M:110:ARG:NH1	2.54	0.41
15:L:7:ILE:O	15:L:11:VAL:HG23	2.20	0.41
5:B:177:ALA:O	5:B:178:ARG:C	2.59	0.41
18:O:36:ILE:HA	18:O:59:MET:HE1	2.01	0.41
8:E:34:VAL:O	8:E:42:GLY:N	2.51	0.41
1:A:1091:U:H2'	1:A:1093:A:OP2	2.19	0.41
16:M:82:MET:HE3	16:M:92:HIS:HB3	2.02	0.41
1:A:298:A:H2'	1:A:299:G:O4'	2.21	0.41
7:D:170:VAL:HG22	7:D:171:GLY:H	1.86	0.41
1:A:222:U:H2'	1:A:223:U:H6	1.85	0.41
14:K:14:VAL:O	14:K:14:VAL:HG12	2.19	0.41
1:A:147:G:O2'	1:A:148:G:H5'	2.20	0.41
10:G:93:PRO:HG2	10:G:94:ARG:H	1.85	0.41
1:A:1285:A:H8	1:A:1285:A:OP1	2.03	0.41
1:A:1362:C:H5'	1:A:1363:A:O5'	2.21	0.41
6:C:159:GLY:HA2	6:C:193:TYR:CD2	2.55	0.41
14:K:56:GLY:O	14:K:57:THR:C	2.59	0.41
5:B:19:HIS:CG	5:B:20:GLU:N	2.88	0.41
9:F:69:GLU:N	9:F:69:GLU:OE1	2.54	0.41
14:K:87:THR:HG23	14:K:91:ARG:HH21	1.85	0.41
1:A:336:C:H2'	1:A:337:C:H6	1.85	0.41
7:D:142:PRO:HG2	7:D:187:ARG:NH2	2.33	0.41
10:G:122:HIS:HD2	10:G:125:MET:CE	2.33	0.41
7:D:179:GLU:CD	7:D:179:GLU:H	2.17	0.41
1:A:1292:U:P	10:G:41:ARG:NH2	2.92	0.41
15:L:93:LEU:HB2	15:L:96:VAL:HG23	2.02	0.41
6:C:79:ARG:O	6:C:82:GLU:HB2	2.20	0.41
8:E:36:ASP:CG	8:E:40:ARG:HB2	2.41	0.41
8:E:36:ASP:OD2	8:E:40:ARG:HB2	2.21	0.41
1:A:339:C:H2'	1:A:340:U:C6	2.54	0.41
14:K:70:LYS:O	14:K:71:LYS:C	2.59	0.41
1:A:797:C:O2'	1:A:798:G:H5'	2.19	0.41
1:A:17:U:H1'	1:A:1080:A:N3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:27:GLN:HE21	9:F:27:GLN:CA	2.32	0.41
1:A:182:U:O4	1:A:223:U:H1'	2.19	0.41
1:A:1414:U:H2'	1:A:1415:G:H8	1.85	0.41
16:M:65:LYS:HD3	16:M:69:GLU:HG2	2.01	0.41
6:C:11:ARG:O	6:C:14:ILE:N	2.53	0.41
1:A:1236:A:OP1	24:V:2:GLY:HA3	2.19	0.41
6:C:64:VAL:CG1	6:C:65:ALA:H	2.34	0.41
23:T:49:ALA:HA	23:T:92:LEU:HD21	2.03	0.41
12:I:3:GLN:O	12:I:4:TYR:CG	2.74	0.41
16:M:49:THR:HG22	16:M:51:ALA:N	2.34	0.41
7:D:8:VAL:HG11	7:D:21:LEU:CB	2.51	0.41
1:A:257:G:O2'	1:A:258:G:H5'	2.20	0.41
9:F:19:LEU:C	9:F:19:LEU:CD2	2.89	0.41
1:A:519:C:O2'	1:A:520:A:H5'	2.21	0.41
1:A:519:C:H2'	1:A:520:A:H8	1.85	0.41
5:B:121:LEU:O	5:B:121:LEU:HD23	2.21	0.41
1:A:1472:U:H2'	1:A:1473:A:C8	2.56	0.41
7:D:52:SER:C	7:D:54:TYR:N	2.71	0.41
1:A:1429:C:H2'	1:A:1430:C:H6	1.85	0.41
5:B:107:THR:O	5:B:110:GLN:N	2.49	0.41
1:A:1416:G:H2'	1:A:1417:G:O4'	2.20	0.41
18:O:54:ARG:O	18:O:58:MET:HG3	2.21	0.41
22:S:43:GLU:CD	22:S:43:GLU:H	2.22	0.41
10:G:138:LYS:O	10:G:142:GLU:HG3	2.20	0.41
1:A:1054:C:C2'	1:A:1055:A:H5"	2.50	0.41
6:C:182:ILE:HG23	6:C:202:ILE:C	2.40	0.41
5:B:52:GLU:OE2	5:B:53:ARG:N	2.53	0.41
6:C:43:LEU:HD11	6:C:66:VAL:HG13	2.03	0.41
1:A:390:C:O2'	19:P:28:ARG:NH2	2.54	0.41
17:N:23:ARG:HA	17:N:30:ALA:HA	2.01	0.41
17:N:24:CYS:HB2	17:N:40:CYS:HB3	2.02	0.41
6:C:119:ARG:O	6:C:122:GLU:N	2.54	0.41
12:I:17:VAL:CG1	12:I:81:ILE:HG12	2.50	0.41
16:M:39:ILE:CD1	16:M:52:GLU:HB3	2.50	0.41
1:A:1145:C:HO2'	1:A:1146:A:H8	1.64	0.41
7:D:173:TRP:CD2	7:D:189:PRO:HB3	2.56	0.41
1:A:131:C:H2'	1:A:132:C:H6	1.86	0.41
14:K:126:ARG:HH11	14:K:126:ARG:CB	2.33	0.41
1:A:807:A:H2'	1:A:808:C:H6	1.82	0.41
1:A:738:C:OP1	9:F:92:LYS:HE3	2.20	0.41
10:G:152:ALA:C	10:G:154:TYR:H	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:9:ARG:HG2	12:I:14:VAL:HG22	2.02	0.41
1:A:866:C:H2'	1:A:867:G:O4'	2.21	0.41
14:K:26:ASN:O	14:K:27:ASN:CB	2.68	0.41
14:K:12:ARG:O	14:K:13:GLN:O	2.38	0.41
1:A:309:G:O2'	1:A:310:G:H5'	2.21	0.41
9:F:15:ASP:OD1	9:F:17:SER:HB2	2.21	0.41
1:A:1069:C:O2'	1:A:1192:C:H1'	2.21	0.41
1:A:625:G:H2'	1:A:626:U:C6	2.55	0.41
16:M:27:LYS:HA	16:M:27:LYS:HD3	1.91	0.41
19:P:40:ASP:HA	19:P:41:PRO:HD3	1.90	0.41
1:A:1368:G:OP2	12:I:112:LYS:HD2	2.20	0.41
5:B:55:PHE:HA	5:B:58:ILE:CD1	2.46	0.41
17:N:3:ARG:NH1	17:N:6:LEU:HD12	2.35	0.41
13:J:13:HIS:CD2	13:J:13:HIS:C	2.94	0.41
9:F:4:TYR:CE2	9:F:72:VAL:HG21	2.54	0.41
1:A:839:U:C2'	1:A:839:U:O2	2.68	0.41
7:D:7:PRO:HG2	7:D:10:ARG:HD2	2.02	0.41
20:Q:97:SER:CB	20:Q:103:GLY:CA	2.99	0.41
1:A:35:G:O2'	15:L:118:SER:O	2.35	0.41
1:A:356:A:O2'	1:A:357:G:H5'	2.20	0.41
1:A:1064:G:C8	1:A:1066:C:O2	2.74	0.41
23:T:37:SER:O	23:T:38:LYS:C	2.58	0.41
1:A:174:C:H2'	1:A:175:C:C6	2.51	0.41
7:D:190:ASP:O	7:D:193:ASP:N	2.46	0.41
7:D:12:CYS:HB3	7:D:33:MET:HG2	2.02	0.41
1:A:1527:C:O2'	1:A:1528:U:H5'	2.20	0.41
1:A:904:C:H2'	1:A:905:U:O4'	2.21	0.41
18:O:57:LEU:HA	18:O:57:LEU:HD12	1.87	0.41
6:C:5:ILE:O	6:C:5:ILE:HD12	2.21	0.41
13:J:50:ILE:HB	17:N:41:ARG:HE	1.86	0.41
1:A:1125:U:N3	13:J:5:ARG:NH2	2.66	0.41
1:A:1206:G:C6	1:A:1207:G:C6	3.09	0.41
1:A:532:A:N6	6:C:159:GLY:O	2.53	0.41
8:E:76:ILE:HG13	8:E:77:PRO:CD	2.38	0.41
23:T:100:ILE:O	23:T:101:GLY:C	2.59	0.41
23:T:50:GLU:N	23:T:99:LEU:HD12	2.34	0.41
5:B:82:ARG:HG3	5:B:83:MET:N	2.35	0.41
5:B:115:LEU:O	5:B:119:GLU:HG3	2.21	0.41
12:I:19:LEU:HB3	12:I:59:PHE:CE2	2.56	0.41
16:M:35:GLU:C	16:M:37:THR:N	2.73	0.41
7:D:7:PRO:CG	7:D:10:ARG:HD2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:32:GLU:OE1	16:M:64:TRP:HZ2	2.04	0.41
22:S:41:VAL:HB	22:S:42:PRO:CD	2.51	0.41
1:A:497:A:O2'	1:A:498:U:OP1	2.28	0.41
21:R:36:ASN:C	21:R:36:ASN:ND2	2.74	0.41
10:G:137:LYS:C	10:G:139:GLU:N	2.74	0.41
5:B:178:ARG:NH2	11:H:68:ARG:NH2	2.69	0.41
19:P:20:VAL:HG13	19:P:32:TYR:HB2	2.01	0.41
1:A:463:A:C8	1:A:474:G:C8	3.08	0.41
9:F:67:MET:HB2	9:F:68:PRO:CD	2.51	0.41
1:A:124:G:C6	1:A:125:U:C4	3.08	0.41
1:A:658:G:H2'	1:A:659:U:C6	2.55	0.41
6:C:29:TYR:HE1	13:J:65:LEU:HD11	1.85	0.41
17:N:31:ARG:O	17:N:32:SER:OG	2.34	0.41
13:J:4:ILE:HA	13:J:100:THR:HA	2.02	0.41
13:J:6:ILE:CG2	13:J:98:ILE:HG23	2.51	0.41
1:A:1053:G:H5'	1:A:1054:C:H5'	2.03	0.41
1:A:1054:C:C2'	1:A:1054:C:O2	2.69	0.41
1:A:926:G:H2'	1:A:1505:G:N3	2.36	0.41
5:B:55:PHE:O	5:B:56:ARG:C	2.60	0.41
1:A:1259:C:N4	1:A:1276:G:H1	2.15	0.41
11:H:119:LEU:CD1	11:H:124:ALA:HA	2.49	0.41
12:I:17:VAL:HG11	12:I:81:ILE:CG1	2.49	0.41
18:O:17:ARG:NH1	18:O:17:ARG:CG	2.79	0.41
1:A:1037:C:H2'	1:A:1038:C:O4'	2.20	0.41
23:T:56:MET:CE	23:T:88:VAL:HB	2.51	0.41
1:A:1302:U:H5	16:M:17:VAL:HG21	1.85	0.41
16:M:8:GLU:O	16:M:9:ILE:CG2	2.63	0.41
1:A:848:C:H2'	1:A:849:C:C6	2.56	0.41
1:A:848:C:O2'	1:A:849:C:H5'	2.21	0.41
14:K:21:ILE:HA	14:K:30:VAL:HG12	2.03	0.41
14:K:82:VAL:HG12	14:K:83:ILE:N	2.35	0.41
20:Q:98:LEU:N	20:Q:103:GLY:HA2	2.35	0.41
1:A:1440:C:O2'	1:A:1441:G:H5'	2.21	0.41
12:I:100:GLY:C	12:I:102:LEU:H	2.24	0.41
10:G:149:ARG:HH11	10:G:149:ARG:HG3	1.86	0.41
1:A:260:G:H2'	1:A:261:U:C6	2.56	0.41
23:T:73:HIS:HB3	23:T:74:LYS:H	1.58	0.41
17:N:9:LYS:HD3	17:N:9:LYS:O	2.20	0.41
7:D:148:VAL:HG23	7:D:181:MET:HB3	2.01	0.41
1:A:1106:G:OP1	6:C:172:ARG:HD3	2.21	0.41
19:P:14:ASN:N	19:P:15:PRO:CD	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:N:4:LYS:O	17:N:7:ILE:HG12	2.21	0.41
7:D:17:VAL:CA	7:D:33:MET:HE2	2.51	0.41
6:C:61:ALA:C	6:C:63:ASN:N	2.74	0.41
9:F:27:GLN:HE21	9:F:27:GLN:HA	1.86	0.41
15:L:37:CYS:O	15:L:79:GLU:O	2.39	0.41
5:B:122:PHE:HA	5:B:127:ILE:HG12	2.03	0.41
7:D:38:TYR:HB2	7:D:44:GLY:O	2.20	0.41
12:I:111:ARG:HD3	12:I:112:LYS:C	2.41	0.41
23:T:49:ALA:O	23:T:50:GLU:C	2.59	0.41
23:T:51:GLU:HA	23:T:54:LYS:HD2	2.03	0.41
18:O:17:ARG:HD3	18:O:26:GLU:CD	2.41	0.41
14:K:20:TYR:O	14:K:30:VAL:HA	2.21	0.41
1:A:1128:C:H42	1:A:1143:G:H1	1.68	0.41
15:L:7:ILE:HA	15:L:7:ILE:HD13	1.95	0.41
1:A:533:A:O2'	1:A:535:A:OP2	2.30	0.41
1:A:190(L):U:N3	23:T:105:SER:HB2	2.36	0.41
1:A:983:A:H5'	1:A:984:C:OP2	2.20	0.41
10:G:141:VAL:O	10:G:144:MET:N	2.53	0.41
7:D:158:ILE:HG22	7:D:181:MET:HE2	2.02	0.41
1:A:1406:U:OP2	25:A:1545:PAR:N24	2.54	0.41
1:A:556:C:C2'	1:A:557:G:H5'	2.51	0.41
1:A:22:G:O2'	1:A:23:C:H5'	2.21	0.41
1:A:91:C:H2'	1:A:92:C:C6	2.56	0.41
1:A:1052:U:C2'	1:A:1055:A:OP1	2.65	0.40
1:A:1258:G:O2'	1:A:1259:C:H5'	2.22	0.40
6:C:42:LEU:C	6:C:44:GLU:N	2.74	0.40
12:I:48:GLU:HA	12:I:51:ARG:HH11	1.85	0.40
5:B:118:LEU:O	5:B:119:GLU:C	2.59	0.40
7:D:8:VAL:HG13	7:D:21:LEU:HD13	2.03	0.40
7:D:116:GLN:O	7:D:117:ALA:C	2.59	0.40
1:A:582:U:H2'	1:A:583:A:C8	2.56	0.40
24:V:10:ARG:O	24:V:11:GLY:C	2.59	0.40
17:N:18:VAL:CG2	17:N:19:ARG:N	2.79	0.40
1:A:1193:G:N2	1:A:1194:U:C2	2.89	0.40
1:A:1066:C:H5	1:A:1067:A:N6	2.19	0.40
1:A:716:A:N3	14:K:117:ASN:O	2.54	0.40
5:B:159:PRO:HG2	5:B:182:ILE:HG21	2.03	0.40
1:A:155:C:O2'	1:A:156:G:H5'	2.21	0.40
1:A:1118:C:H6	1:A:1118:C:O5'	2.04	0.40
1:A:1325:C:O3'	24:V:17:THR:HG21	2.22	0.40
10:G:31:MET:HG3	10:G:35:LYS:H	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:121:ARG:C	12:I:121:ARG:CD	2.90	0.40
10:G:104:LEU:O	10:G:105:VAL:C	2.59	0.40
7:D:80:GLU:HA	7:D:80:GLU:OE2	2.21	0.40
6:C:32:LEU:HD12	6:C:32:LEU:N	2.36	0.40
13:J:38:ILE:O	13:J:71:LEU:N	2.54	0.40
1:A:1053:G:H4'	1:A:1054:C:C4'	2.52	0.40
1:A:664:G:H2'	1:A:666:G:OP1	2.21	0.40
1:A:1372:U:H2'	1:A:1373:G:C5'	2.51	0.40
16:M:81:LEU:H	16:M:81:LEU:HD23	1.85	0.40
16:M:53:VAL:CG1	16:M:57:ARG:HH21	2.34	0.40
7:D:41:GLY:O	7:D:43:HIS:N	2.54	0.40
20:Q:98:LEU:HA	20:Q:102:GLY:C	2.41	0.40
1:A:1221:G:O3'	22:S:77:THR:HG21	2.21	0.40
7:D:30:LYS:O	7:D:32:ALA:N	2.54	0.40
13:J:66:ARG:HB3	13:J:66:ARG:HE	1.71	0.40
3:Y:39:U:H2'	3:Y:40:C:C6	2.56	0.40
1:A:833:U:H2'	1:A:834:C:C6	2.56	0.40
13:J:38:ILE:HB	13:J:71:LEU:HB3	2.03	0.40
13:J:71:LEU:CD1	13:J:73:ASP:HB2	2.51	0.40
8:E:12:LEU:C	8:E:12:LEU:HD22	2.41	0.40
7:D:61:LYS:HE2	7:D:62:GLN:HE21	1.84	0.40
5:B:68:ILE:H	5:B:90:MET:HE3	1.86	0.40
10:G:51:GLN:O	10:G:53:LYS:N	2.54	0.40
1:A:1347:G:O2'	1:A:1348:U:C6	2.73	0.40
12:I:116:LYS:O	12:I:117:HIS:C	2.60	0.40
15:L:97:ARG:HB2	15:L:98:TYR:CE1	2.55	0.40
8:E:144:THR:CG2	8:E:145:LYS:N	2.84	0.40
14:K:22:HIS:HB3	14:K:29:ILE:HG12	2.03	0.40
1:A:794:A:H2'	1:A:795:C:H6	1.84	0.40
1:A:261:U:O2	1:A:263:A:C8	2.75	0.40
1:A:1310:G:OP1	16:M:80:ARG:NH2	2.54	0.40
6:C:101:LEU:CD2	6:C:101:LEU:O	2.70	0.40
1:A:1388:C:H2'	1:A:1389:C:H6	1.86	0.40
1:A:300:A:H8	1:A:300:A:O5'	2.04	0.40
11:H:126:LYS:C	11:H:128:GLY:N	2.75	0.40
20:Q:17:LYS:HA	20:Q:46:ASP:O	2.21	0.40
1:A:551:U:H2'	1:A:552:U:C6	2.56	0.40
1:A:45:U:OP1	1:A:307:C:O2'	2.40	0.40
1:A:922:G:N3	1:A:1398:A:H2	2.18	0.40
5:B:144:ARG:CG	5:B:145:LEU:N	2.84	0.40
1:A:1251:A:H1'	1:A:1369:C:HO2'	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:46:GLY:O	14:K:48:ILE:O	2.39	0.40
6:C:29:TYR:CZ	17:N:54:PRO:HG2	2.56	0.40
5:B:23:ARG:O	5:B:24:TRP:O	2.40	0.40
14:K:50:TYR:CD1	14:K:60:ALA:HB2	2.57	0.40
6:C:87:LEU:C	6:C:89:GLU:N	2.74	0.40
14:K:84:VAL:HB	14:K:110:ASP:HA	2.03	0.40
18:O:21:ASP:CG	18:O:24:SER:HB3	2.42	0.40
1:A:1278:U:H5"	1:A:1279:A:H5'	2.03	0.40
16:M:20:THR:C	16:M:22:ILE:H	2.24	0.40
20:Q:59:ILE:CD1	20:Q:73:VAL:HA	2.52	0.40
1:A:1314:C:N3	1:A:1315:U:C4	2.89	0.40
17:N:18:VAL:C	17:N:20:ALA:H	2.25	0.40
1:A:344:A:O2'	1:A:345:C:OP1	2.35	0.40
23:T:80:ARG:O	23:T:81:LYS:C	2.57	0.40
1:A:31:G:N2	1:A:48:C:OP1	2.42	0.40
18:O:36:ILE:HA	18:O:59:MET:CE	2.51	0.40
13:J:64:GLU:HG2	17:N:59:ALA:CB	2.51	0.40
1:A:109:A:H2'	1:A:326:G:H21	1.86	0.40
1:A:1513:A:H2'	1:A:1514:C:C6	2.56	0.40
1:A:1161:C:H2'	1:A:1162:C:H6	1.83	0.40
21:R:25:THR:O	21:R:26:LEU:CB	2.69	0.40
1:A:51:A:H4'	1:A:52:G:C5'	2.51	0.40
8:E:13:ILE:HA	8:E:29:GLY:O	2.20	0.40
13:J:6:ILE:HD11	13:J:72:VAL:HG11	2.03	0.40
8:E:11:ILE:HA	8:E:11:ILE:HD13	1.94	0.40
5:B:15:VAL:HB	5:B:16:HIS:H	1.51	0.40
1:A:1230:C:O2'	1:A:1231:G:H5'	2.22	0.40
5:B:153:ARG:HG2	5:B:153:ARG:HH11	1.85	0.40
15:L:39:VAL:CG1	15:L:40:VAL:N	2.84	0.40
5:B:167:PRO:O	5:B:171:ALA:CA	2.70	0.40
17:N:4:LYS:HA	17:N:7:ILE:CG1	2.51	0.40
1:A:977:A:C2'	1:A:978:A:H5"	2.52	0.40
15:L:83:VAL:HG21	15:L:100:ILE:HG23	2.03	0.40
1:A:554:C:H2'	1:A:555:C:H6	1.85	0.40
1:A:922:G:H2'	1:A:923:A:O4'	2.22	0.40
1:A:1360:A:O2'	1:A:1361:G:H5'	2.22	0.40

All (1) 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)
13:J:79:ARG:CD	13:J:79:ARG:CD[8_665]	2.14	0.06

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
5	B	232/256 (91%)	145 (62%)	59 (25%)	28 (12%)	0 2
6	C	204/239 (85%)	126 (62%)	51 (25%)	27 (13%)	0 1
7	D	206/209 (99%)	160 (78%)	32 (16%)	14 (7%)	1 9
8	E	148/162 (91%)	132 (89%)	13 (9%)	3 (2%)	9 39
9	F	99/101 (98%)	82 (83%)	17 (17%)	0	100 100
10	G	153/156 (98%)	118 (77%)	28 (18%)	7 (5%)	3 18
11	H	136/138 (99%)	112 (82%)	20 (15%)	4 (3%)	6 30
12	I	125/128 (98%)	94 (75%)	18 (14%)	13 (10%)	1 3
13	J	96/105 (91%)	59 (62%)	17 (18%)	20 (21%)	0 0
14	K	117/129 (91%)	88 (75%)	20 (17%)	9 (8%)	1 7
15	L	122/135 (90%)	96 (79%)	13 (11%)	13 (11%)	0 3
16	M	116/126 (92%)	77 (66%)	23 (20%)	16 (14%)	0 1
17	N	58/61 (95%)	37 (64%)	11 (19%)	10 (17%)	0 0
18	O	86/89 (97%)	67 (78%)	17 (20%)	2 (2%)	8 36
19	P	81/88 (92%)	71 (88%)	9 (11%)	1 (1%)	16 53
20	Q	102/105 (97%)	78 (76%)	15 (15%)	9 (9%)	1 5
21	R	71/88 (81%)	59 (83%)	8 (11%)	4 (6%)	2 13
22	S	82/93 (88%)	53 (65%)	18 (22%)	11 (13%)	0 1
23	T	97/106 (92%)	61 (63%)	26 (27%)	10 (10%)	1 3
24	V	22/26 (85%)	15 (68%)	5 (23%)	2 (9%)	1 5
All	All	2353/2540 (93%)	1730 (74%)	420 (18%)	203 (9%)	1 5

All (203) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	B	8	LYS
5	B	15	VAL
5	B	16	HIS
5	B	17	PHE
5	B	23	ARG
5	B	24	TRP
5	B	95	GLN
5	B	188	ALA
6	C	15	THR
6	C	26	LYS
6	C	82	GLU
6	C	84	ILE
6	C	98	ASN
6	C	100	ALA
6	C	179	ARG
7	D	29	PRO
7	D	36	ARG
7	D	88	VAL
11	H	91	ARG
12	I	41	VAL
12	I	88	TYR
12	I	94	ALA
12	I	117	HIS
13	J	32	ALA
13	J	34	VAL
13	J	54	PHE
13	J	86	MET
14	K	13	GLN
14	K	35	PRO
14	K	78	GLN
15	L	27	LEU
15	L	47	LYS
15	L	110	VAL
16	M	4	ILE
16	M	23	TYR
16	M	27	LYS
16	M	67	GLU
16	M	86	CYS
17	N	19	ARG
20	Q	80	GLY
20	Q	81	ARG
20	Q	98	LEU

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Mol	Chain	Res	Type
21	R	58	LEU
22	S	6	LYS
22	S	14	HIS
22	S	67	VAL
23	T	98	PRO
5	B	20	GLU
5	B	39	ILE
5	B	60	ASP
5	B	83	MET
5	B	123	ALA
5	B	190	THR
5	B	195	ASP
5	B	227	GLY
6	C	16	ARG
6	C	39	ILE
6	C	47	LEU
6	C	101	LEU
6	C	171	GLY
6	C	189	ALA
7	D	3	ARG
7	D	4	TYR
7	D	42	GLN
7	D	164	ALA
8	E	78	HIS
8	E	107	ARG
8	E	108	ALA
10	G	7	ALA
10	G	63	LYS
10	G	155	ARG
11	H	24	THR
11	H	105	ARG
12	I	38	GLN
12	I	46	ALA
12	I	58	ARG
12	I	127	LYS
13	J	23	ILE
13	J	33	GLN
13	J	36	GLY
13	J	60	ARG
13	J	72	VAL
13	J	79	ARG
14	K	15	ALA

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Mol	Chain	Res	Type
14	K	91	ARG
15	L	29	GLY
15	L	30	ALA
15	L	48	PRO
15	L	51	ALA
15	L	73	GLU
15	L	79	GLU
15	L	121	GLY
16	M	3	ARG
16	M	6	GLY
16	M	28	ALA
16	M	63	THR
16	M	85	GLY
17	N	15	LYS
17	N	32	SER
17	N	36	PHE
19	P	10	GLY
20	Q	96	GLN
20	Q	97	SER
21	R	26	LEU
21	R	48	GLY
22	S	8	GLY
22	S	43	GLU
22	S	68	GLY
22	S	83	HIS
22	S	84	GLY
23	T	50	GLU
23	T	73	HIS
23	T	74	LYS
23	T	86	ARG
23	T	101	GLY
23	T	102	GLY
24	V	9	ARG
5	B	9	GLU
5	B	21	ARG
5	B	136	VAL
5	B	204	ASN
6	C	20	SER
6	C	127	ARG
6	C	146	ALA
6	C	154	SER
6	C	156	ARG

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Mol	Chain	Res	Type
6	C	206	GLU
7	D	5	ILE
7	D	30	LYS
7	D	150	GLU
10	G	67	GLU
12	I	43	ALA
13	J	27	ALA
13	J	55	LYS
13	J	61	GLU
13	J	90	LEU
14	K	27	ASN
14	K	117	ASN
15	L	105	TYR
16	M	21	TYR
16	M	24	GLY
16	M	36	LYS
16	M	109	THR
17	N	11	LYS
17	N	14	PRO
17	N	23	ARG
17	N	37	PHE
21	R	87	ARG
22	S	9	VAL
23	T	39	LYS
5	B	113	HIS
5	B	177	ALA
6	C	67	THR
6	C	108	ASN
6	C	168	ALA
10	G	109	ASN
12	I	119	ALA
13	J	4	ILE
13	J	17	ASP
13	J	40	LEU
17	N	26	ARG
18	O	85	LEU
20	Q	12	SER
22	S	16	LEU
22	S	30	LEU
5	B	59	GLU
5	B	232	PRO
6	C	119	ARG

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Mol	Chain	Res	Type
6	C	181	ASN
7	D	22	LYS
7	D	31	CYS
7	D	35	ARG
10	G	37	ASN
12	I	45	ALA
12	I	105	ASP
13	J	73	ASP
16	M	5	ALA
18	O	86	GLY
20	Q	95	TYR
20	Q	103	GLY
23	T	38	LYS
5	B	48	MET
5	B	79	ASP
5	B	207	ALA
6	C	4	LYS
10	G	82	GLY
12	I	44	VAL
13	J	76	ASN
14	K	48	ILE
14	K	70	LYS
15	L	116	SER
16	M	9	ILE
20	Q	34	LYS
23	T	97	ALA
11	H	137	VAL
17	N	25	VAL
7	D	92	VAL
5	B	130	ARG
6	C	14	ILE
13	J	39	PRO
6	C	55	VAL
24	V	22	ARG
15	L	40	VAL

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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
5	B	202/220 (92%)	176 (87%)	26 (13%)	5 22
6	C	160/188 (85%)	146 (91%)	14 (9%)	12 43
7	D	180/181 (99%)	171 (95%)	9 (5%)	30 68
8	E	115/123 (94%)	98 (85%)	17 (15%)	4 16
9	F	90/90 (100%)	83 (92%)	7 (8%)	16 50
10	G	126/127 (99%)	119 (94%)	7 (6%)	26 63
11	H	119/119 (100%)	108 (91%)	11 (9%)	11 40
12	I	98/99 (99%)	92 (94%)	6 (6%)	23 60
13	J	87/92 (95%)	79 (91%)	8 (9%)	11 40
14	K	90/99 (91%)	84 (93%)	6 (7%)	20 56
15	L	104/111 (94%)	97 (93%)	7 (7%)	20 56
16	M	94/101 (93%)	85 (90%)	9 (10%)	10 37
17	N	49/50 (98%)	44 (90%)	5 (10%)	9 33
18	O	79/80 (99%)	71 (90%)	8 (10%)	9 34
19	P	72/74 (97%)	68 (94%)	4 (6%)	26 63
20	Q	96/97 (99%)	91 (95%)	5 (5%)	29 65
21	R	64/77 (83%)	62 (97%)	2 (3%)	47 80
22	S	73/80 (91%)	65 (89%)	8 (11%)	8 30
23	T	76/82 (93%)	69 (91%)	7 (9%)	11 40
24	V	19/21 (90%)	19 (100%)	0	100 100
All	All	1993/2111 (94%)	1827 (92%)	166 (8%)	14 47

All (166) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	8	LYS
5	B	9	GLU
5	B	15	VAL
5	B	17	PHE
5	B	21	ARG
5	B	23	ARG
5	B	24	TRP
5	B	25	ASN
5	B	87	ARG

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Mol	Chain	Res	Type
5	B	90	MET
5	B	92	TYR
5	B	96	ARG
5	B	102	LEU
5	B	114	ARG
5	B	144	ARG
5	B	156	LYS
5	B	162	ILE
5	B	163	PHE
5	B	169	LYS
5	B	170	GLU
5	B	178	ARG
5	B	187	LEU
5	B	204	ASN
5	B	223	ILE
5	B	232	PRO
5	B	236	TYR
6	C	5	ILE
6	C	26	LYS
6	C	29	TYR
6	C	52	LEU
6	C	56	ASP
6	C	70	VAL
6	C	95	THR
6	C	139	GLN
6	C	166	GLU
6	C	167	TRP
6	C	172	ARG
6	C	188	LEU
6	C	190	ARG
6	C	196	LEU
7	D	15	GLU
7	D	26	CYS
7	D	29	PRO
7	D	96	LEU
7	D	122	ARG
7	D	132	ARG
7	D	157	LEU
7	D	162	LEU
7	D	199	ASN
8	E	12	LEU
8	E	16	THR

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Mol	Chain	Res	Type
8	E	18	ARG
8	E	24	ARG
8	E	31	LEU
8	E	38	GLN
8	E	41	VAL
8	E	43	LEU
8	E	52	PRO
8	E	68	GLU
8	E	73	ASN
8	E	80	ILE
8	E	89	ILE
8	E	120	THR
8	E	126	ARG
8	E	144	THR
8	E	150	ARG
9	F	1	MET
9	F	10	LEU
9	F	24	GLU
9	F	63	TYR
9	F	69	GLU
9	F	75	LEU
9	F	94	GLN
10	G	8	GLU
10	G	16	LEU
10	G	37	ASN
10	G	38	LEU
10	G	136	LYS
10	G	140	ASP
10	G	149	ARG
11	H	18	ARG
11	H	24	THR
11	H	26	VAL
11	H	39	LEU
11	H	85	ARG
11	H	91	ARG
11	H	92	ARG
11	H	105	ARG
11	H	112	LEU
11	H	119	LEU
11	H	127	LEU
12	I	2	GLU
12	I	23	ASN

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Mol	Chain	Res	Type
12	I	38	GLN
12	I	79	LEU
12	I	111	ARG
12	I	121	ARG
13	J	13	HIS
13	J	29	ARG
13	J	38	ILE
13	J	57	LYS
13	J	60	ARG
13	J	64	GLU
13	J	71	LEU
13	J	83	GLU
14	K	24	SER
14	K	29	ILE
14	K	35	PRO
14	K	54	ARG
14	K	80	VAL
14	K	93	GLN
15	L	33	ARG
15	L	48	PRO
15	L	53	ARG
15	L	55	VAL
15	L	82	VAL
15	L	85	ILE
15	L	126	LYS
16	M	40	ASN
16	M	44	ARG
16	M	56	LEU
16	M	70	LEU
16	M	81	LEU
16	M	88	ARG
16	M	102	ARG
16	M	109	THR
16	M	115	LYS
17	N	3	ARG
17	N	6	LEU
17	N	12	ARG
17	N	44	LEU
17	N	58	LYS
18	O	7	GLU
18	O	31	LEU
18	O	34	LEU

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Mol	Chain	Res	Type
18	O	39	LEU
18	O	57	LEU
18	O	67	LEU
18	O	70	LEU
18	O	81	LEU
19	P	2	VAL
19	P	8	ARG
19	P	28	ARG
19	P	53	VAL
20	Q	34	LYS
20	Q	38	ARG
20	Q	60	ILE
20	Q	74	LEU
20	Q	98	LEU
21	R	36	ASN
21	R	42	ARG
22	S	12	ASP
22	S	14	HIS
22	S	15	LEU
22	S	36	ARG
22	S	61	TYR
22	S	62	ILE
22	S	65	ASN
22	S	80	TYR
23	T	10	LEU
23	T	13	LEU
23	T	42	GLN
23	T	57	ARG
23	T	75	ASN
23	T	84	LEU
23	T	98	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (56) such sidechains are listed below:

Mol	Chain	Res	Type
5	B	25	ASN
5	B	40	HIS
5	B	78	GLN
5	B	146	GLN
5	B	204	ASN
6	C	3	ASN
6	C	31	HIS

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Mol	Chain	Res	Type
6	C	37	GLN
6	C	108	ASN
6	C	110	ASN
6	C	123	GLN
6	C	136	GLN
6	C	139	GLN
6	C	176	HIS
7	D	42	GLN
7	D	62	GLN
7	D	119	GLN
7	D	123	HIS
7	D	161	ASN
7	D	199	ASN
8	E	20	GLN
8	E	73	ASN
9	F	18	GLN
9	F	27	GLN
9	F	32	ASN
9	F	73	ASN
9	F	94	GLN
9	F	100	ASN
10	G	37	ASN
10	G	51	GLN
10	G	106	GLN
10	G	122	HIS
12	I	23	ASN
12	I	73	GLN
13	J	56	HIS
13	J	76	ASN
13	J	78	ASN
14	K	38	ASN
14	K	117	ASN
15	L	49	ASN
15	L	75	HIS
16	M	12	ASN
16	M	40	ASN
16	M	77	ASN
17	N	52	GLN
18	O	13	GLN
18	O	37	ASN
18	O	46	HIS
19	P	76	GLN

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Mol	Chain	Res	Type
20	Q	16	GLN
21	R	36	ASN
22	S	23	ASN
22	S	47	HIS
22	S	56	GLN
22	S	83	HIS
23	T	90	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1522 (98%)	200 (13%)	67 (4%)
2	X	5/6 (83%)	0	0
3	Y	14/15 (93%)	1 (7%)	0
4	Z	3/4 (75%)	1 (33%)	0
All	All	1528/1547 (98%)	202 (13%)	67 (4%)

All (202) 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	51	A
1	A	61	G
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	129(A)	G
1	A	130	A
1	A	131	C
1	A	144	G
1	A	163	C

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Mol	Chain	Res	Type
1	A	181	G
1	A	182	U
1	A	195	A
1	A	197	A
1	A	198	G
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
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	282	A
1	A	289	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	344	A
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	428	G
1	A	429	U
1	A	439	A
1	A	452	A
1	A	461	C
1	A	462	G
1	A	484	G
1	A	485	G

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Mol	Chain	Res	Type
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	527	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
1	A	576	G
1	A	577	G
1	A	653	A
1	A	665	A
1	A	688	G
1	A	701	C
1	A	702	A
1	A	718	G
1	A	723	U
1	A	733	A
1	A	749	C
1	A	755	G
1	A	777	A
1	A	793	U
1	A	794	A
1	A	813	U
1	A	815	A
1	A	817	C
1	A	819	A
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	902	G
1	A	914	A

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Mol	Chain	Res	Type
1	A	927	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U
1	A	961	U
1	A	965	A
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
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1002	G
1	A	1024	G
1	A	1026	G
1	A	1050	G
1	A	1053	G
1	A	1054	C
1	A	1055	A
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1085	U
1	A	1086	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1124	G
1	A	1125	U
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1136	U
1	A	1137	C
1	A	1138	G

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Mol	Chain	Res	Type
1	A	1139	G
1	A	1146	A
1	A	1152	A
1	A	1157	A
1	A	1159	U
1	A	1183	A
1	A	1184	G
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1202	G
1	A	1212	U
1	A	1214	C
1	A	1226	C
1	A	1227	A
1	A	1257	U
1	A	1258	G
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1305	G
1	A	1320	C
1	A	1338	G
1	A	1347	G
1	A	1348	U
1	A	1362	C
1	A	1379	G
1	A	1381	U
1	A	1398	A
1	A	1443	G
1	A	1446	A
1	A	1447	G
1	A	1452	C
1	A	1487	G

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Mol	Chain	Res	Type
1	A	1492	A
1	A	1497	G
1	A	1499	A
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G
3	Y	34	G
4	Z	2	U

All (67) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	30	U
1	A	48	C
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	202	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	279	A
1	A	281	G
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	438	G
1	A	484	G
1	A	496	A

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Mol	Chain	Res	Type
1	A	497	A
1	A	509	A
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A
1	A	701	C
1	A	748	C
1	A	793	U
1	A	812	C
1	A	819	A
1	A	913	A
1	A	960	U
1	A	965	A
1	A	975	A
1	A	992	U
1	A	993	G
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1085	U
1	A	1145	C
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1196	U
1	A	1201	A
1	A	1226	C
1	A	1256	A
1	A	1257	U
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1346	A
1	A	1347	G
1	A	1380	U
1	A	1451	A
1	A	1498	U
1	A	1528	U

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 128 ligands modelled in this entry, 127 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	$\#\|Z\| > 2$
25	PAR	A	1545	-	45,45,45	1.35	7 (15%)	59,67,67	1.18	5 (8%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	PAR	A	1545	-	-	0/18/94/94	0/4/4/4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1545	PAR	O51-C11	2.20	1.47	1.41
25	A	1545	PAR	O33-C14	2.26	1.47	1.41
25	A	1545	PAR	C52-C42	2.33	1.57	1.52
25	A	1545	PAR	C31-C21	2.34	1.56	1.53
25	A	1545	PAR	C64-C54	2.48	1.58	1.52
25	A	1545	PAR	C11-C21	2.81	1.58	1.52
25	A	1545	PAR	O54-C14	3.12	1.49	1.41

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
25	A	1545	PAR	O11-C11-C21	2.85	113.24	107.96
25	A	1545	PAR	C14-O54-C54	2.89	119.35	113.75
25	A	1545	PAR	O33-C14-C24	2.93	113.39	107.96
25	A	1545	PAR	O52-C13-C23	3.00	114.00	107.75
25	A	1545	PAR	O54-C54-C64	3.51	112.96	106.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	A	1545	PAR	2	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

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	1507/1522 (99%)	0.37	15 (0%) 84 70	22, 56, 140, 201	0
2	X	6/6 (100%)	1.66	2 (33%) 0 0	47, 59, 141, 164	0
3	Y	15/15 (100%)	0.62	0 100 100	58, 100, 200, 201	0
4	Z	4/4 (100%)	1.31	1 (25%) 1 0	69, 71, 82, 141	0
5	B	234/256 (91%)	0.25	7 (2%) 54 30	30, 94, 172, 201	0
6	C	206/239 (86%)	0.03	3 (1%) 76 58	38, 81, 170, 192	0
7	D	208/209 (99%)	0.39	9 (4%) 39 18	25, 62, 145, 181	0
8	E	150/162 (92%)	0.03	1 (0%) 89 79	21, 47, 109, 164	0
9	F	101/101 (100%)	-0.10	1 (0%) 84 70	45, 90, 145, 176	0
10	G	155/156 (99%)	-0.12	3 (1%) 70 48	38, 73, 150, 191	0
11	H	138/138 (100%)	0.16	2 (1%) 78 61	17, 43, 103, 150	0
12	I	127/128 (99%)	0.52	11 (8%) 13 4	34, 89, 151, 180	0
13	J	98/105 (93%)	1.27	28 (28%) 1 0	36, 114, 185, 201	0
14	K	119/129 (92%)	0.59	7 (5%) 26 10	24, 60, 123, 201	0
15	L	124/135 (91%)	0.35	7 (5%) 28 11	16, 55, 125, 192	0
16	M	118/126 (93%)	0.11	5 (4%) 40 19	36, 74, 131, 165	0
17	N	60/61 (98%)	1.20	15 (25%) 1 0	44, 76, 139, 194	0
18	O	88/89 (98%)	0.04	1 (1%) 82 67	26, 56, 137, 199	0
19	P	83/88 (94%)	0.90	16 (19%) 2 1	22, 47, 77, 158	0
20	Q	104/105 (99%)	0.89	6 (5%) 26 11	13, 45, 137, 201	0
21	R	73/88 (82%)	0.42	3 (4%) 41 19	33, 71, 165, 201	0
22	S	84/93 (90%)	0.70	12 (14%) 4 2	54, 100, 165, 201	0
23	T	99/106 (93%)	0.68	7 (7%) 19 7	25, 57, 127, 198	0
24	V	24/26 (92%)	1.19	2 (8%) 14 5	42, 61, 113, 188	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
All	All	3925/4087 (96%)	0.38	164 (4%)	40	19	13, 63, 153, 201	0

All (164) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
14	K	129	SER	26.9
22	S	3	ARG	13.9
20	Q	103	GLY	12.6
14	K	128	ALA	11.5
20	Q	104	LYS	10.3
20	Q	105	ALA	10.0
20	Q	102	GLY	8.6
12	I	128	ARG	7.7
14	K	127	LYS	7.5
11	H	1	MET	6.6
13	J	65	LEU	6.2
13	J	72	VAL	6.1
13	J	47	PHE	5.4
13	J	64	GLU	5.4
13	J	6	ILE	5.3
15	L	128	ALA	4.7
13	J	7	LYS	4.5
12	I	105	ASP	4.5
13	J	70	ARG	4.4
23	T	84	LEU	4.4
11	H	2	LEU	4.4
15	L	19	ARG	4.2
17	N	6	LEU	4.2
1	A	532	A	4.1
18	O	89	GLY	4.0
7	D	3	ARG	3.9
13	J	8	LEU	3.9
22	S	37	ARG	3.8
12	I	119	ALA	3.8
13	J	46	ARG	3.8
16	M	102	ARG	3.8
24	V	6	ARG	3.7
13	J	18	ALA	3.7
13	J	62	HIS	3.7
13	J	73	ASP	3.6
13	J	10	GLY	3.6
4	Z	4	U	3.6

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Mol	Chain	Res	Type	RSRZ
17	N	59	ALA	3.5
13	J	45	ARG	3.5
1	A	1534	A	3.4
20	Q	101	ARG	3.4
7	D	209	ARG	3.4
13	J	54	PHE	3.4
22	S	10	PHE	3.4
22	S	4	SER	3.3
1	A	1531	A	3.3
14	K	126	ARG	3.3
2	X	2	U	3.3
10	G	5	ARG	3.3
23	T	83	ARG	3.3
17	N	29	ARG	3.2
17	N	60	SER	3.2
12	I	14	VAL	3.2
17	N	61	TRP	3.2
22	S	5	LEU	3.2
17	N	41	ARG	3.2
22	S	38	SER	3.2
20	Q	96	GLN	3.1
15	L	127	GLU	3.0
13	J	44	VAL	3.0
7	D	47	ARG	3.0
1	A	264	U	3.0
17	N	30	ALA	2.9
1	A	202	U	2.9
19	P	9	PHE	2.9
13	J	34	VAL	2.9
19	P	10	GLY	2.9
1	A	82	U	2.9
22	S	69	HIS	2.9
12	I	102	LEU	2.9
17	N	31	ARG	2.9
12	I	125	TYR	2.8
13	J	5	ARG	2.8
13	J	74	ILE	2.8
22	S	40	ILE	2.8
23	T	9	ASN	2.8
13	J	55	LYS	2.8
13	J	48	THR	2.8
13	J	67	THR	2.7

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Mol	Chain	Res	Type	RSRZ
7	D	4	TYR	2.7
16	M	105	THR	2.7
6	C	15	THR	2.7
10	G	12	LEU	2.7
16	M	88	ARG	2.7
17	N	34	TYR	2.7
7	D	78	LEU	2.7
13	J	37	PRO	2.7
19	P	1	MET	2.7
15	L	18	VAL	2.6
19	P	15	PRO	2.6
5	B	148	TYR	2.6
13	J	63	PHE	2.6
19	P	83	GLU	2.6
19	P	17	TYR	2.6
1	A	263	A	2.6
22	S	71	LEU	2.5
1	A	461	C	2.5
7	D	112	VAL	2.5
19	P	7	ALA	2.5
6	C	193	TYR	2.5
15	L	17	LYS	2.5
23	T	85	MET	2.5
7	D	118	ARG	2.5
12	I	15	ALA	2.4
7	D	73	ARG	2.4
1	A	1533	C	2.4
13	J	71	LEU	2.4
19	P	28	ARG	2.4
17	N	33	VAL	2.4
19	P	69	THR	2.4
14	K	31	THR	2.4
16	M	87	TYR	2.3
13	J	66	ARG	2.3
19	P	8	ARG	2.3
24	V	18	TYR	2.3
12	I	111	ARG	2.3
5	B	152	PHE	2.3
23	T	103	GLY	2.3
2	X	1	C	2.3
17	N	3	ARG	2.3
19	P	19	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
5	B	163	PHE	2.3
13	J	50	ILE	2.3
23	T	77	ALA	2.3
8	E	119	LEU	2.3
19	P	22	THR	2.3
22	S	49	ILE	2.3
15	L	20	LYS	2.3
12	I	106	ALA	2.2
5	B	16	HIS	2.2
16	M	104	ARG	2.2
19	P	29	ASP	2.2
19	P	31	LYS	2.2
14	K	42	TRP	2.2
7	D	162	LEU	2.2
1	A	265	G	2.2
6	C	161	GLU	2.2
17	N	25	VAL	2.2
13	J	40	LEU	2.1
17	N	37	PHE	2.1
1	A	733	A	2.1
21	R	72	ARG	2.1
5	B	188	ALA	2.1
15	L	104	VAL	2.1
22	S	12	ASP	2.1
1	A	975	A	2.1
12	I	107	ARG	2.1
10	G	2	ALA	2.1
14	K	111	ASP	2.1
19	P	30	GLY	2.1
17	N	36	PHE	2.1
21	R	71	LYS	2.1
1	A	1361(A)	C	2.0
19	P	6	LEU	2.0
12	I	10	ARG	2.0
17	N	32	SER	2.0
21	R	31	LEU	2.0
5	B	238	LEU	2.0
22	S	39	THR	2.0
23	T	81	LYS	2.0
1	A	371	G	2.0
9	F	6	VAL	2.0
5	B	214	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	979	C	2.0

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

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å^2)	Q<0.9
26	MG	A	1608	1/1	0.89	0.31	22.79	20,20,20,20	1
26	MG	A	1646	1/1	0.85	0.36	18.85	20,20,20,20	1
26	MG	A	1651	1/1	0.93	0.43	12.78	20,20,20,20	1
26	MG	A	1623	1/1	0.81	0.33	7.36	20,20,20,20	1
26	MG	A	1589	1/1	0.88	0.35	6.36	20,20,20,20	1
26	MG	A	1648	1/1	0.91	0.68	4.98	20,20,20,20	1
26	MG	A	211	1/1	0.75	0.32	4.82	20,20,20,20	1
26	MG	A	1601	1/1	0.92	0.25	4.13	20,20,20,20	1
26	MG	A	1561	1/1	0.98	0.26	3.82	20,20,20,20	0
26	MG	A	1564	1/1	0.96	0.37	3.08	20,20,20,20	0
25	PAR	A	1545	42/42	0.92	0.29	2.68	59,59,59,59	0
26	MG	A	1562	1/1	0.95	0.24	2.40	20,20,20,20	1
26	MG	A	441	1/1	0.40	0.21	1.92	20,20,20,20	1
26	MG	A	1596	1/1	0.97	0.28	1.88	20,20,20,20	0
26	MG	A	1597	1/1	0.89	0.23	1.85	20,20,20,20	1
26	MG	A	1642	1/1	0.79	0.20	1.62	20,20,20,20	1
26	MG	A	1653	1/1	0.79	0.23	1.60	20,20,20,20	1
26	MG	A	1622	1/1	0.62	0.23	1.59	20,20,20,20	1
26	MG	A	1633	1/1	0.49	0.41	1.07	20,20,20,20	1
26	MG	A	1573	1/1	0.98	0.26	1.03	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
26	MG	A	1552	1/1	0.95	0.28	0.87	20,20,20,20	0
26	MG	A	1572	1/1	0.96	0.36	0.81	20,20,20,20	1
26	MG	A	1579	1/1	0.98	0.25	0.64	20,20,20,20	0
26	MG	A	1600	1/1	0.95	0.25	0.29	20,20,20,20	0
26	MG	A	1592	1/1	0.98	0.21	0.04	20,20,20,20	0
26	MG	A	1598	1/1	0.88	0.24	-0.16	20,20,20,20	1
27	ZN	N	307	1/1	0.99	0.18	-0.53	20,20,20,20	1
26	MG	A	1644	1/1	0.83	0.20	-0.59	20,20,20,20	1
26	MG	A	1556	1/1	0.87	0.24	-0.70	20,20,20,20	0
26	MG	D	215	1/1	0.66	0.18	-0.84	20,20,20,20	1
26	MG	A	1546	1/1	0.99	0.20	-1.08	20,20,20,20	0
26	MG	J	422	1/1	0.98	0.20	-1.13	20,20,20,20	0
26	MG	J	449	1/1	0.96	0.25	-1.13	20,20,20,20	1
26	MG	A	210	1/1	0.75	0.17	-1.40	20,20,20,20	1
26	MG	A	1575	1/1	0.97	0.20	-1.40	20,20,20,20	1
26	MG	A	1593	1/1	0.99	0.20	-1.52	20,20,20,20	0
26	MG	A	1609	1/1	0.87	0.14	-1.63	20,20,20,20	1
26	MG	A	1599	1/1	0.94	0.18	-1.73	20,20,20,20	0
26	MG	A	1635	1/1	0.82	0.22	-1.81	20,20,20,20	1
26	MG	A	1588	1/1	0.95	0.20	-1.82	20,20,20,20	1
26	MG	A	1625	1/1	0.90	0.18	-2.27	20,20,20,20	1
26	MG	A	1604	1/1	0.92	0.16	-3.37	20,20,20,20	1
26	MG	A	1637	1/1	0.91	0.10	-3.50	20,20,20,20	0
26	MG	A	1559	1/1	0.95	0.17	-3.51	20,20,20,20	0
26	MG	A	1656	1/1	0.77	0.12	-3.57	20,20,20,20	1
26	MG	A	1634	1/1	0.93	0.11	-3.82	20,20,20,20	1
26	MG	A	1581	1/1	0.96	0.16	-4.40	20,20,20,20	0
26	MG	A	1605	1/1	0.87	0.15	-4.47	20,20,20,20	0
26	MG	A	1638	1/1	0.89	0.22	-5.01	20,20,20,20	1
26	MG	A	1614	1/1	0.94	0.09	-5.35	20,20,20,20	1
26	MG	A	1585	1/1	0.98	0.12	-6.35	20,20,20,20	0
26	MG	A	1594	1/1	0.94	0.08	-9.12	20,20,20,20	1
26	MG	A	1565	1/1	0.93	0.10	-11.19	20,20,20,20	0
26	MG	A	1616	1/1	0.90	0.44	-	20,20,20,20	1
26	MG	A	1568	1/1	0.94	0.25	-	20,20,20,20	0
26	MG	A	1570	1/1	0.94	0.29	-	20,20,20,20	1
26	MG	A	1583	1/1	0.90	0.32	-	20,20,20,20	1
26	MG	A	1586	1/1	0.98	0.21	-	20,20,20,20	0
26	MG	A	1610	1/1	0.91	0.40	-	20,20,20,20	1
26	MG	A	1617	1/1	0.82	0.37	-	20,20,20,20	1
26	MG	A	1652	1/1	0.95	0.45	-	20,20,20,20	1
26	MG	A	1603	1/1	0.94	0.21	-	20,20,20,20	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
26	MG	A	87	1/1	0.94	0.41	-	20,20,20,20	1
26	MG	A	1619	1/1	0.92	0.39	-	20,20,20,20	1
26	MG	A	1567	1/1	0.92	0.28	-	20,20,20,20	1
26	MG	A	1650	1/1	0.95	0.14	-	20,20,20,20	0
26	MG	A	1590	1/1	0.81	0.30	-	20,20,20,20	0
26	MG	A	1643	1/1	0.63	0.38	-	20,20,20,20	1
26	MG	A	1548	1/1	0.89	0.13	-	20,20,20,20	0
26	MG	A	1549	1/1	0.67	0.32	-	20,20,20,20	1
26	MG	A	1632	1/1	0.95	0.14	-	20,20,20,20	1
26	MG	A	1630	1/1	0.76	0.20	-	20,20,20,20	1
26	MG	A	1602	1/1	0.95	0.37	-	20,20,20,20	1
26	MG	A	1639	1/1	0.90	0.32	-	20,20,20,20	1
26	MG	A	1655	1/1	0.92	0.14	-	20,20,20,20	1
26	MG	A	1563	1/1	0.90	0.14	-	20,20,20,20	1
26	MG	A	1547	1/1	0.96	0.24	-	20,20,20,20	0
26	MG	A	1553	1/1	0.95	0.29	-	20,20,20,20	0
26	MG	A	1560	1/1	0.97	0.36	-	20,20,20,20	1
26	MG	A	1641	1/1	0.89	0.14	-	20,20,20,20	1
26	MG	A	1577	1/1	0.96	0.20	-	20,20,20,20	1
26	MG	A	1554	1/1	0.98	0.36	-	20,20,20,20	0
26	MG	A	1626	1/1	0.91	0.25	-	20,20,20,20	0
26	MG	A	1566	1/1	0.97	0.34	-	20,20,20,20	0
26	MG	A	1654	1/1	0.96	0.20	-	20,20,20,20	0
26	MG	A	1618	1/1	0.79	0.25	-	20,20,20,20	0
26	MG	A	1550	1/1	0.91	0.26	-	20,20,20,20	1
26	MG	D	210	1/1	0.96	0.33	-	20,20,20,20	1
26	MG	A	1606	1/1	0.91	0.19	-	20,20,20,20	1
26	MG	A	1645	1/1	0.70	0.43	-	20,20,20,20	1
26	MG	A	1615	1/1	0.76	0.37	-	20,20,20,20	1
26	MG	A	1613	1/1	0.94	0.08	-	20,20,20,20	0
26	MG	Y	456	1/1	0.25	0.33	-	20,20,20,20	1
26	MG	A	1582	1/1	0.98	0.32	-	20,20,20,20	1
26	MG	A	1591	1/1	0.93	0.40	-	20,20,20,20	1
26	MG	A	1578	1/1	0.89	0.36	-	20,20,20,20	1
27	ZN	D	306	1/1	0.97	0.35	-	20,20,20,20	1
26	MG	A	1584	1/1	0.91	0.26	-	20,20,20,20	1
26	MG	A	1629	1/1	0.87	0.20	-	20,20,20,20	1
26	MG	A	71	1/1	0.93	0.28	-	20,20,20,20	1
26	MG	A	1558	1/1	0.97	0.29	-	20,20,20,20	0
26	MG	A	1631	1/1	0.81	0.46	-	20,20,20,20	1
26	MG	A	1557	1/1	0.95	0.40	-	20,20,20,20	0
26	MG	A	1569	1/1	0.89	0.43	-	20,20,20,20	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
26	MG	A	1611	1/1	0.96	0.28	-	20,20,20,20	0
26	MG	A	1657	1/1	0.83	0.25	-	20,20,20,20	1
26	MG	A	1628	1/1	0.82	0.46	-	20,20,20,20	1
26	MG	A	1649	1/1	0.90	0.29	-	20,20,20,20	1
26	MG	A	86	1/1	0.97	0.28	-	20,20,20,20	1
26	MG	A	1647	1/1	0.86	0.34	-	20,20,20,20	1
26	MG	A	1607	1/1	0.97	0.21	-	20,20,20,20	1
26	MG	A	1624	1/1	0.92	0.27	-	20,20,20,20	1
26	MG	A	1555	1/1	0.79	0.22	-	20,20,20,20	0
26	MG	A	1627	1/1	0.90	0.29	-	20,20,20,20	1
26	MG	A	1640	1/1	0.69	0.21	-	20,20,20,20	1
26	MG	A	1580	1/1	0.92	0.17	-	20,20,20,20	0
26	MG	A	1571	1/1	0.96	0.14	-	20,20,20,20	1
26	MG	A	1636	1/1	0.91	0.27	-	20,20,20,20	1
26	MG	A	1595	1/1	0.94	0.31	-	20,20,20,20	0
26	MG	A	214	1/1	0.88	0.15	-	20,20,20,20	1
26	MG	A	1620	1/1	0.84	0.22	-	20,20,20,20	1
26	MG	A	1587	1/1	0.98	0.23	-	20,20,20,20	0
26	MG	A	1551	1/1	0.95	0.23	-	20,20,20,20	1
26	MG	A	1576	1/1	0.97	0.26	-	20,20,20,20	1
26	MG	A	1612	1/1	0.98	0.25	-	20,20,20,20	0
26	MG	A	213	1/1	0.97	0.26	-	20,20,20,20	1
26	MG	A	1621	1/1	0.88	0.29	-	20,20,20,20	1
26	MG	A	1574	1/1	0.90	0.24	-	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.