



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:43 AM UTC

PDB ID : 1IBM / pdb_00001ibm
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
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 : 3.31 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

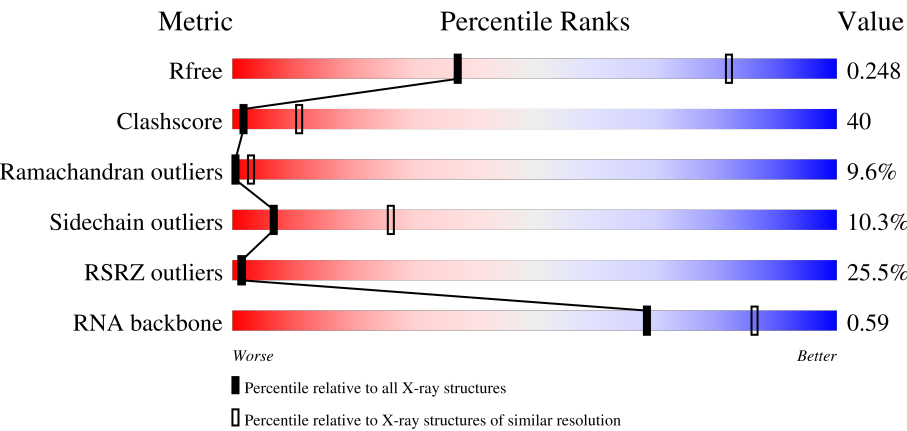
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.31 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}	180053	1153 (3.34-3.30)
Clashscore	190562	1193 (3.34-3.30)
Ramachandran outliers	187476	1172 (3.34-3.30)
Sidechain outliers	187428	1171 (3.34-3.30)
RSRZ outliers	180081	1153 (3.34-3.30)
RNA backbone	3983	1067 (3.64-3.00)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	20% 27% 59% 11% ..
2	X	6	50% 67% 33%
3	Y	15	33% 33% 27% 7% 7% 27%

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Mol	Chain	Length	Quality of chain
4	Z	4	
5	B	256	
6	C	239	
7	D	209	
8	E	162	
9	F	101	
10	G	156	
11	H	138	
12	I	128	
13	J	105	
14	K	129	
15	L	135	
16	M	126	
17	N	61	
18	O	89	
19	P	88	
20	Q	105	
21	R	88	
22	S	93	
23	T	106	
24	V	26	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1624	-	-	-	X
25	MG	A	1628	-	-	-	X

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 52160 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
1	A	1507	Total	C	N	O	P	0	0	0
			32391	14418	6002	10465	1506			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	Y	11	Total	C	N	O	P	0	0	0
			233	106	44	73	10			

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

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

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

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

- 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	GB 12056104
P	?	-	HIS	conflict	GB 12056104
P	?	-	TYR	conflict	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	S	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	87	Total	C	N	O	S	0	0	0
			697	444	130	121	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 MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	A	118	Total	Mg	0	0
			118	118		
25	D	1	Total	Mg	0	0
			1	1		

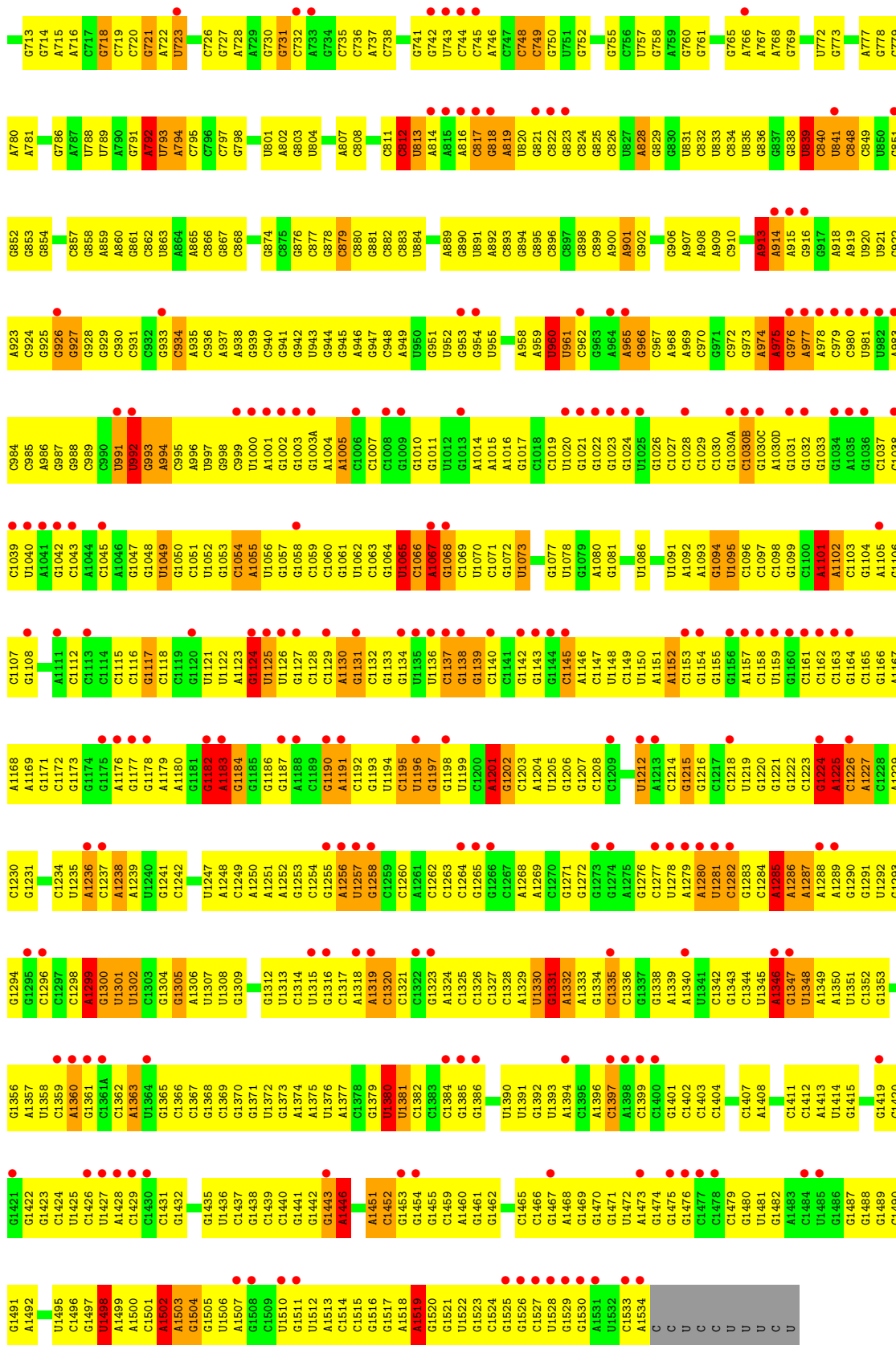
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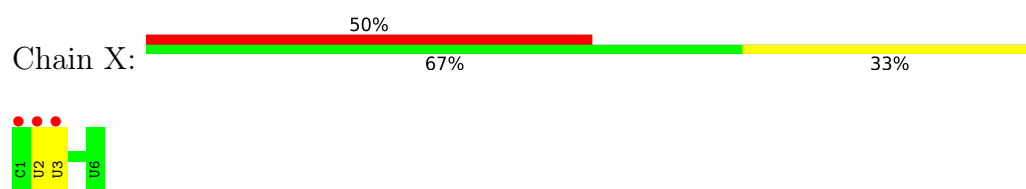
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	H	1	Total	Mg	0	0
			1	1		

- Molecule 26 is ZINC ION (CCD ID: ZN) (formula: Zn).

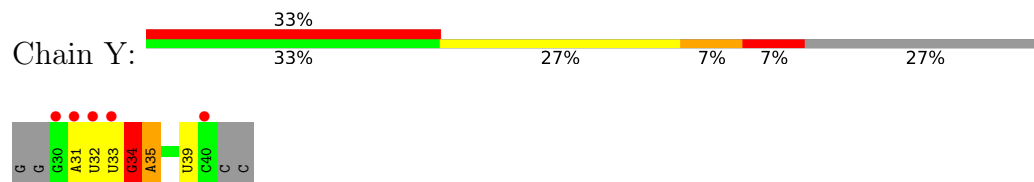
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	D	1	Total	Zn	0	0
			1	1		
26	N	1	Total	Zn	0	0
			1	1		



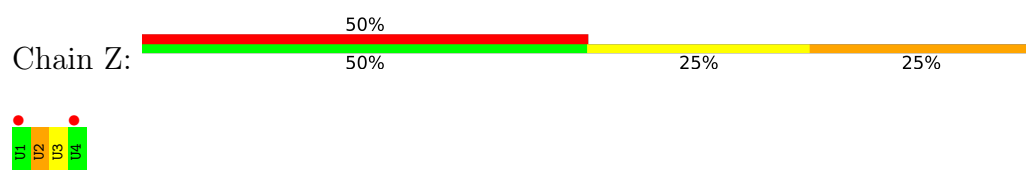
- Molecule 2: P-SITE MESSENGER RNA FRAGMENT



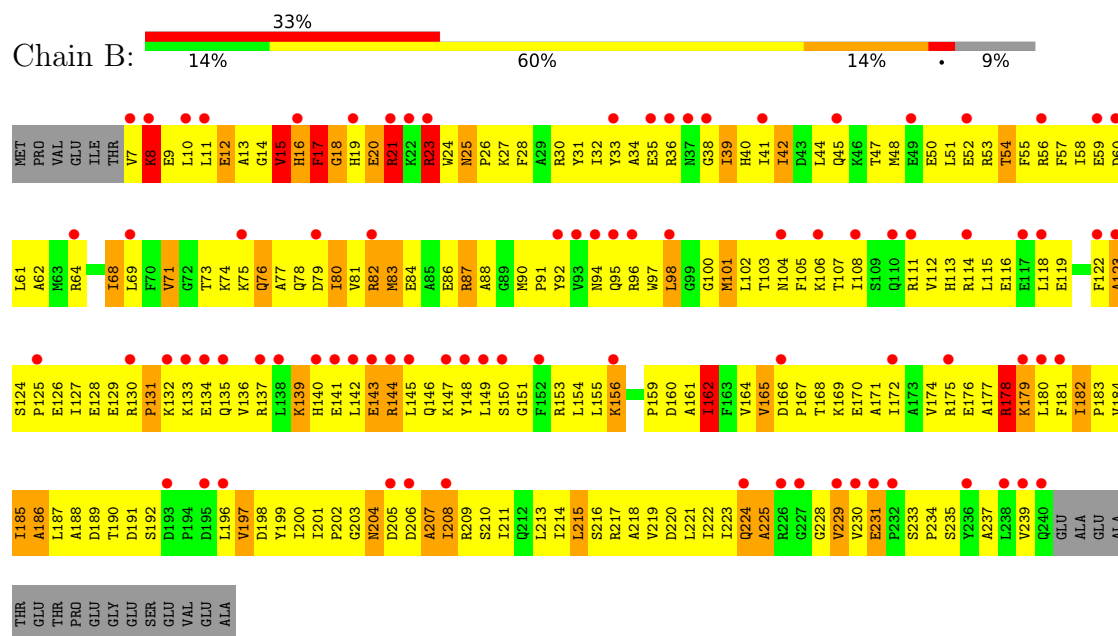
• Molecule 3: ANTICODON STEM-LOOP OF PHENYLALANINE TRANSFER RNA



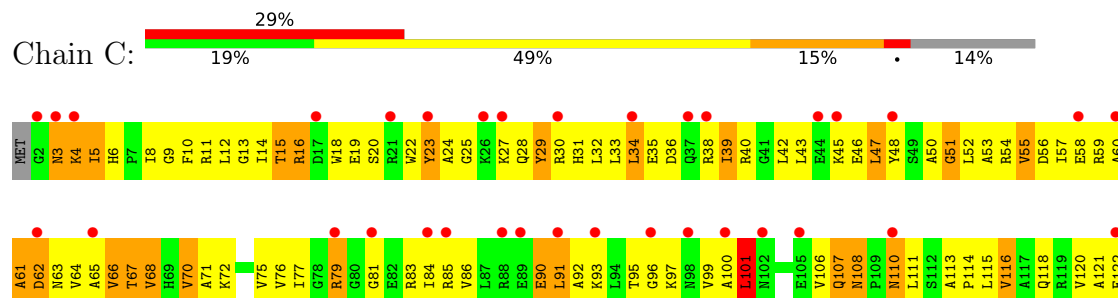
• Molecule 4: A-SITE MESSENGER RNA FRAGMENT

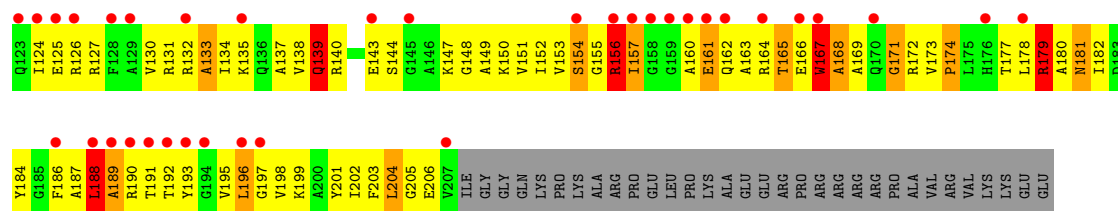


• Molecule 5: 30S RIBOSOMAL PROTEIN S2

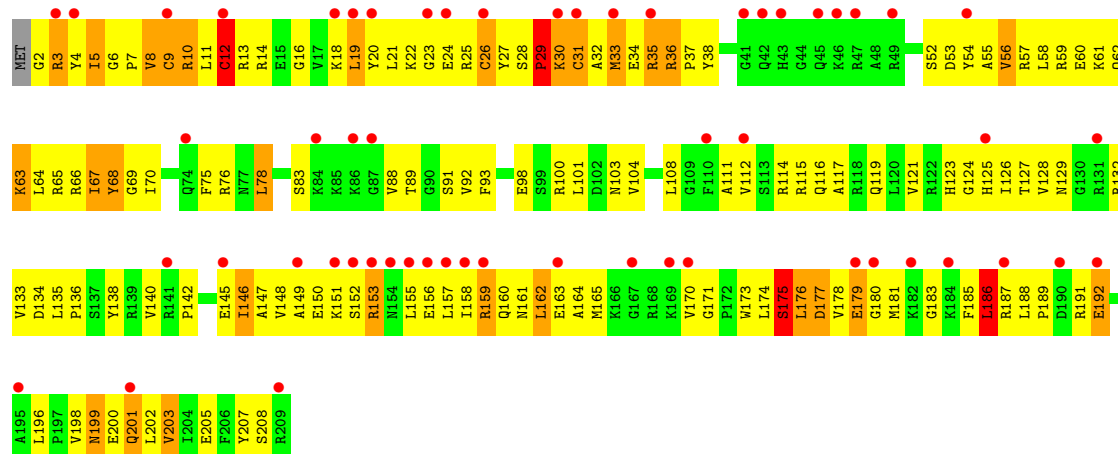


• Molecule 6: 30S RIBOSOMAL PROTEIN S3

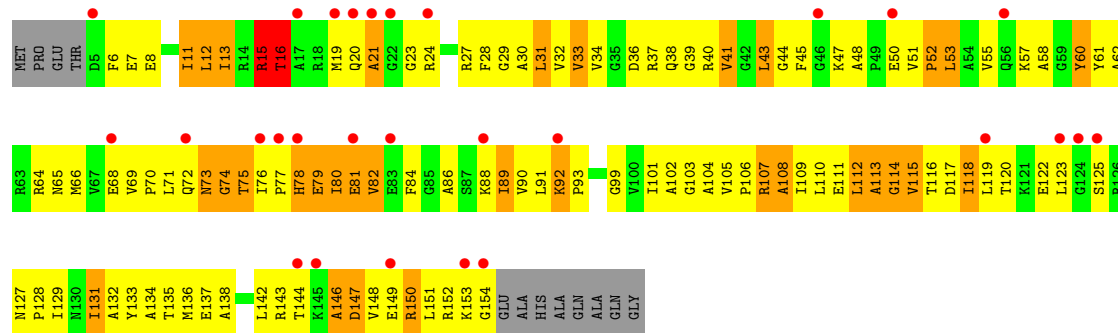




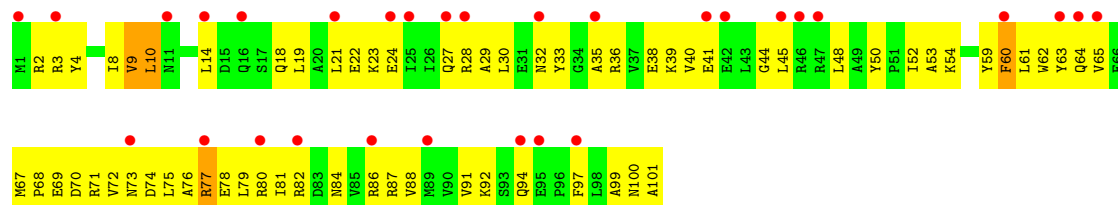
• Molecule 7: 30S RIBOSOMAL PROTEIN S4



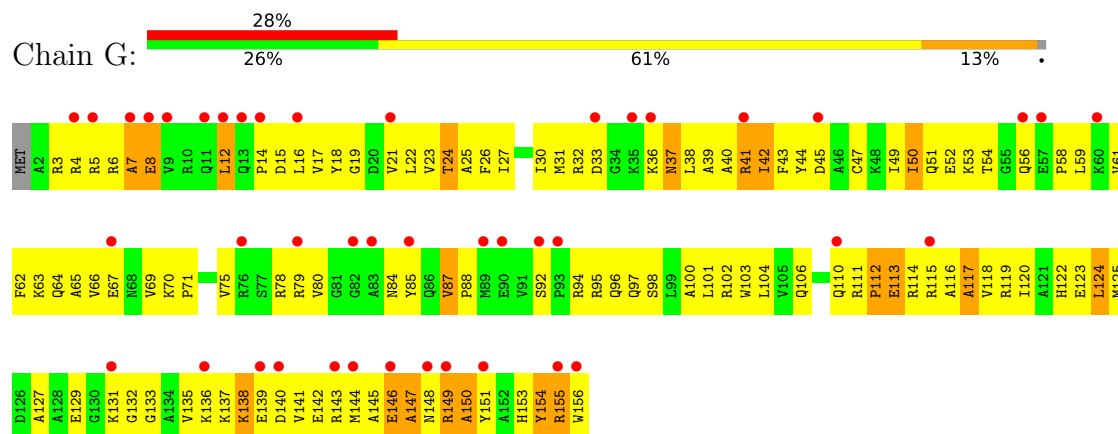
• Molecule 8: 30S RIBOSOMAL PROTEIN S5



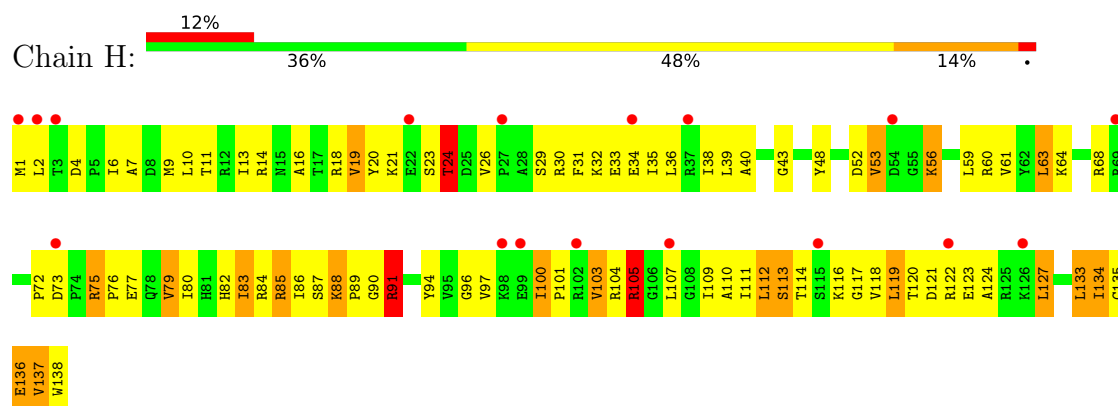
• Molecule 9: 30S RIBOSOMAL PROTEIN S6



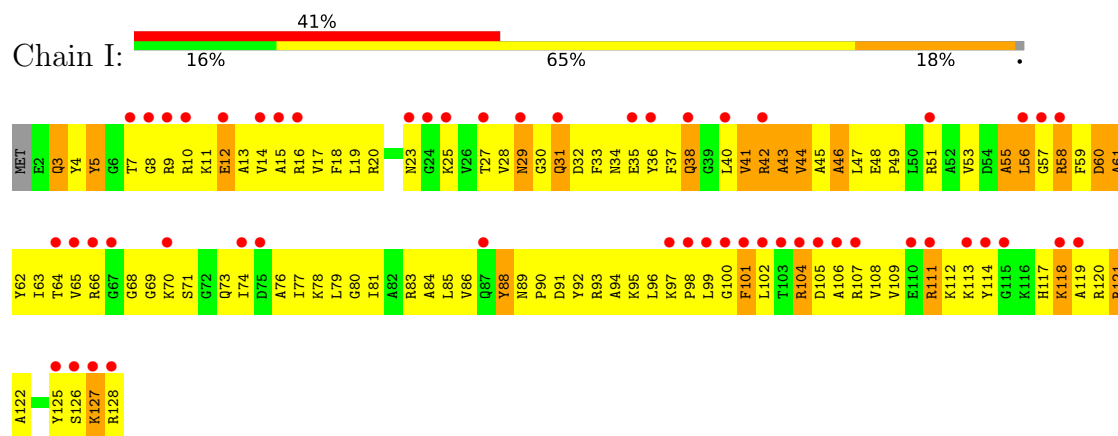
• Molecule 10: 30S RIBOSOMAL PROTEIN S7



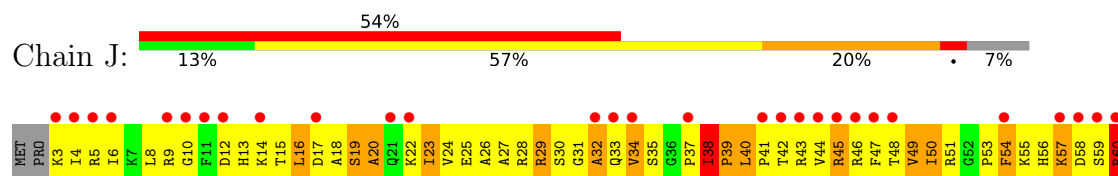
• Molecule 11: 30S RIBOSOMAL PROTEIN S8

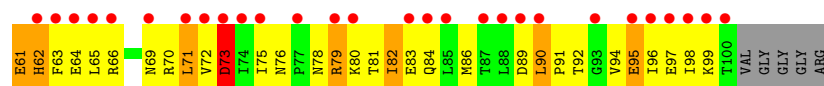


• Molecule 12: 30S RIBOSOMAL PROTEIN S9

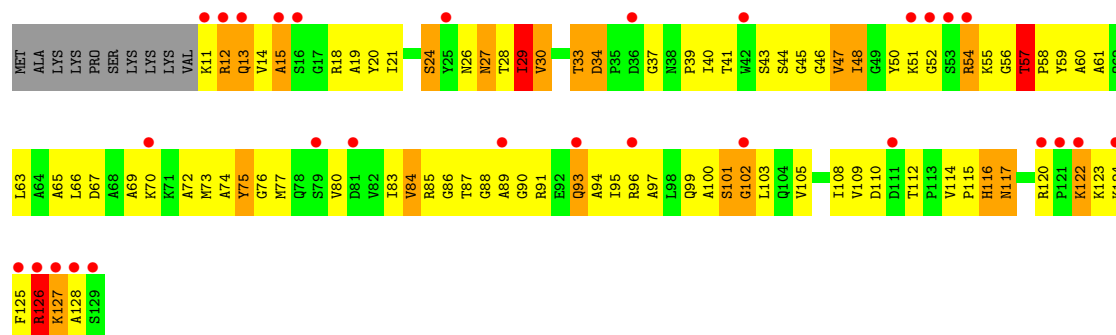


• Molecule 13: 30S RIBOSOMAL PROTEIN S10

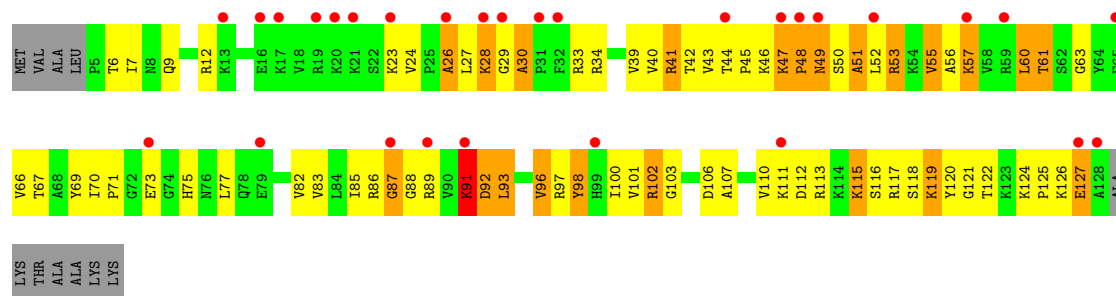




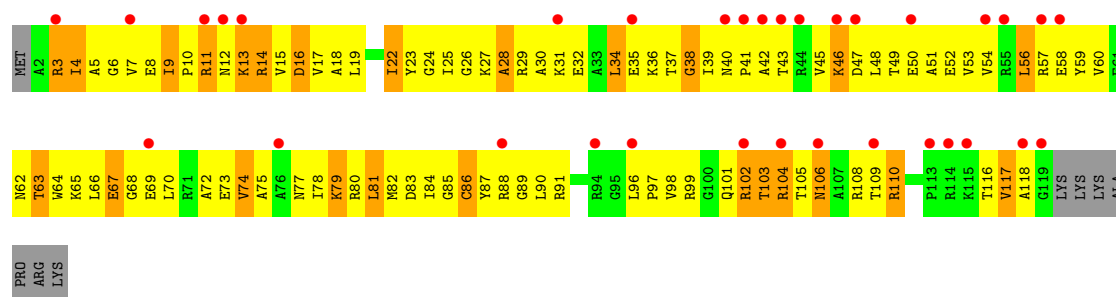
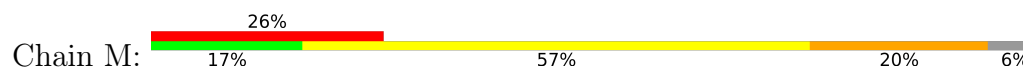
• Molecule 14: 30S RIBOSOMAL PROTEIN S11



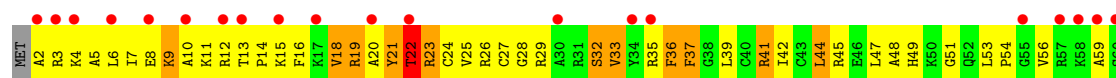
• Molecule 15: 30S RIBOSOMAL PROTEIN S12



• Molecule 16: 30S RIBOSOMAL PROTEIN S13



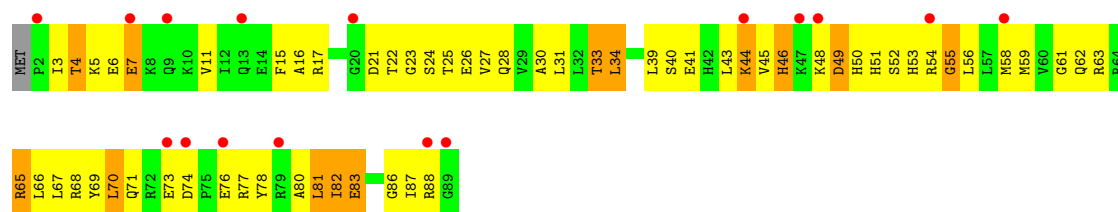
• Molecule 17: 30S RIBOSOMAL PROTEIN S14



W61

• Molecule 18: 30S RIBOSOMAL PROTEIN S15

Chain O: 18% 30% 54% 15%



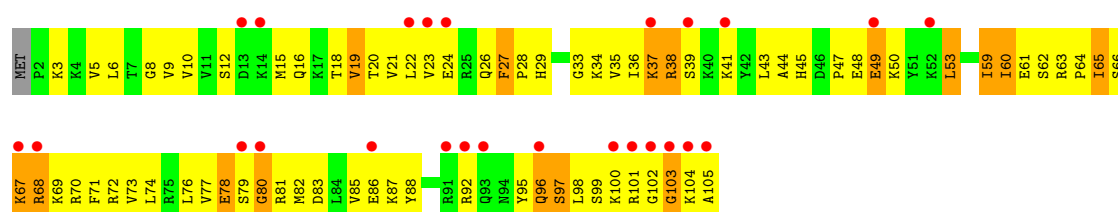
• Molecule 19: 30S RIBOSOMAL PROTEIN S16

Chain P: 15% 34% 50% 10% 6%



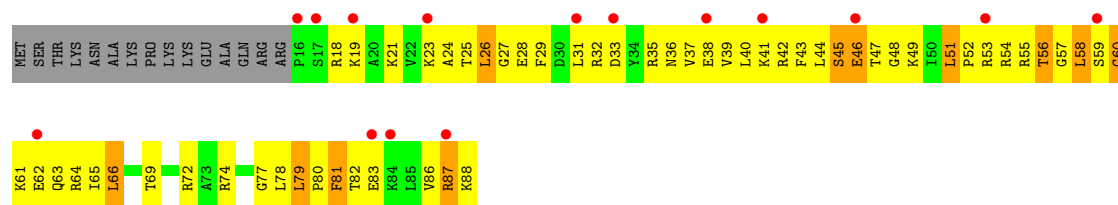
• Molecule 20: 30S RIBOSOMAL PROTEIN S17

Chain Q: 24% 27% 57% 15%



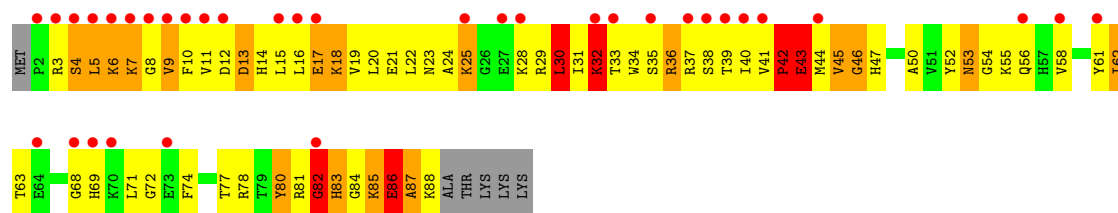
• Molecule 21: 30S RIBOSOMAL PROTEIN S18

Chain R: 17% 18% 52% 13% 17%

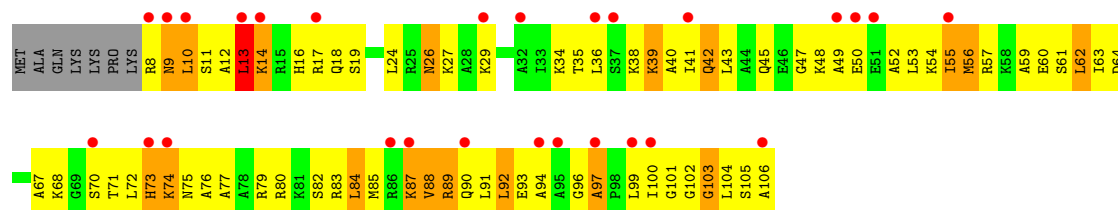


• Molecule 22: 30S RIBOSOMAL PROTEIN S19

Chain S: 38% 19% 48% 19% 6% 6%



● Molecule 23: 30S RIBOSOMAL PROTEIN S20



● Molecule 24: 30S RIBOSOMAL PROTEIN THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	401.57Å 401.57Å 176.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	316.23 – 3.31 283.96 – 3.31	Depositor EDS
% Data completeness (in resolution range)	90.6 (316.23-3.31) 90.6 (283.96-3.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.34 (at 3.33Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.231 , 0.286 0.204 , 0.248	Depositor DCC
R_{free} test set	9648 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	76.8	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 999.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	52160	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.54% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.46	0/36259	0.73	67/56593 (0.1%)
2	X	0.49	0/128	0.72	0/196
3	Y	0.41	0/261	0.77	1/405 (0.2%)
4	Z	0.43	0/84	0.83	0/128
5	B	0.41	0/1935	1.02	9/2609 (0.3%)
6	C	0.45	0/1636	0.96	5/2205 (0.2%)
7	D	0.51	2/1733 (0.1%)	1.02	8/2318 (0.3%)
8	E	0.61	0/1162	1.20	12/1564 (0.8%)
9	F	0.41	0/856	0.92	2/1154 (0.2%)
10	G	0.43	0/1276	0.99	6/1709 (0.4%)
11	H	0.60	0/1136	1.22	13/1527 (0.9%)
12	I	0.43	0/1029	1.01	4/1378 (0.3%)
13	J	0.43	0/805	1.07	7/1082 (0.6%)
14	K	0.54	0/900	0.98	2/1213 (0.2%)
15	L	0.51	0/986	1.10	5/1320 (0.4%)
16	M	0.46	0/947	1.01	5/1270 (0.4%)
17	N	0.45	0/501	1.19	5/664 (0.8%)
18	O	0.51	0/745	0.92	3/992 (0.3%)
19	P	0.59	0/716	1.16	4/963 (0.4%)
20	Q	0.60	0/870	1.18	8/1159 (0.7%)
21	R	0.44	0/603	1.05	8/799 (1.0%)
22	S	0.42	0/712	1.05	6/956 (0.6%)
23	T	0.54	0/765	1.11	6/1007 (0.6%)
24	V	0.52	0/212	0.93	0/277
All	All	0.47	2/56257 (0.0%)	0.84	186/83488 (0.2%)

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	1	29

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	201	GLN	C-N	-6.22	1.25	1.33
7	D	199	ASN	C-N	-5.82	1.26	1.33

All (186) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	181	G	C2'-C3'-O3'	13.64	129.96	109.50
1	A	559	A	C2'-C3'-O3'	13.19	129.29	109.50
1	A	575	G	C2'-C3'-O3'	13.17	129.25	109.50
1	A	366	C	C2'-C3'-O3'	13.10	129.15	109.50
1	A	243	A	C2'-C3'-O3'	12.04	127.56	109.50
1	A	1498	U	C2'-C3'-O3'	11.95	127.43	109.50
1	A	792	A	C2'-C3'-O3'	11.58	126.88	109.50
23	T	13	LEU	N-CA-C	-11.30	98.01	114.39
1	A	266	G	C2'-C3'-O3'	11.03	126.04	109.50
1	A	1346	A	C2'-C3'-O3'	10.69	125.54	109.50
1	A	60	A	C2'-C3'-O3'	10.69	125.53	109.50
7	D	11	LEU	N-CA-C	-10.68	100.38	113.41
15	L	26	ALA	N-CA-C	-10.58	100.40	113.20
19	P	21	VAL	N-CA-C	-10.55	94.79	109.45
7	D	12	CYS	N-CA-C	-10.41	98.74	111.33
1	A	687	A	C2'-C3'-O3'	10.20	124.80	109.50
1	A	115	G	C2'-C3'-O3'	9.86	124.29	109.50
1	A	812	C	C2'-C3'-O3'	9.59	123.89	109.50
1	A	965	A	C2'-C3'-O3'	9.57	123.86	109.50
5	B	13	ALA	N-CA-C	-9.51	101.69	113.20
1	A	533	A	C2'-C3'-O3'	9.49	123.74	109.50
1	A	197	A	C2'-C3'-O3'	9.17	123.25	109.50
17	N	9	LYS	N-CA-C	-9.11	101.94	113.23
10	G	154	TYR	N-CA-C	-9.06	103.36	112.97
1	A	1380	U	C2'-C3'-O3'	8.96	122.94	109.50
1	A	372	C	C2'-C3'-O3'	8.93	122.89	109.50
1	A	484	G	C2'-C3'-O3'	8.75	122.62	109.50
20	Q	39	SER	N-CA-C	8.56	119.94	108.38
7	D	31	CYS	N-CA-C	-8.41	103.18	113.19
1	A	366	C	C4'-C3'-O3'	8.36	121.94	109.40
16	M	11	ARG	N-CA-C	8.34	121.75	109.07
1	A	7	G	C2'-C3'-O3'	8.23	121.84	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1067	A	C2'-C3'-O3'	8.13	121.70	109.50
8	E	21	ALA	N-CA-C	-8.11	99.70	110.24
14	K	45	GLY	N-CA-C	-7.97	102.70	113.37
23	T	14	LYS	N-CA-C	-7.96	102.55	111.71
8	E	23	GLY	N-CA-C	7.85	121.87	110.80
1	A	560	U	C2'-C3'-O3'	7.80	125.41	113.70
1	A	181	G	C4'-C3'-O3'	7.77	121.06	109.40
23	T	92	LEU	N-CA-C	-7.76	103.70	113.01
1	A	1299	A	N9-C1'-C2'	7.76	123.64	112.00
1	A	1183	A	C2'-C3'-O3'	7.60	120.90	109.50
17	N	21	TYR	N-CA-C	7.52	120.81	107.80
11	H	103	VAL	N-CA-C	7.49	119.04	108.93
1	A	748	C	C2'-C3'-O3'	7.49	120.73	109.50
20	Q	65	ILE	N-CA-C	-7.48	106.20	113.53
22	S	36	ARG	N-CA-C	-7.46	104.31	113.19
1	A	1101	A	C2'-C3'-O3'	7.42	120.64	109.50
20	Q	37	LYS	N-CA-C	-7.30	99.71	110.52
1	A	1346	A	C4'-C3'-O3'	7.13	120.09	109.40
1	A	1285	A	C2'-C3'-O3'	7.11	120.16	109.50
23	T	49	ALA	N-CA-C	7.10	119.69	111.02
1	A	1182	G	C2'-C3'-O3'	7.08	120.12	109.50
18	O	5	LYS	N-CA-C	-7.07	102.62	111.11
5	B	23	ARG	N-CA-C	-7.03	101.92	112.54
1	A	250	A	C2'-C3'-O3'	7.03	120.04	109.50
15	L	61	THR	N-CA-C	-7.02	103.97	112.54
9	F	77	ARG	N-CA-C	-7.00	103.66	111.71
1	A	119	A	C2'-C3'-O3'	6.94	119.91	109.50
13	J	29	ARG	N-CA-C	-6.91	106.75	114.62
21	R	51	LEU	CA-C-N	6.81	128.35	119.84
21	R	51	LEU	C-N-CA	6.81	128.35	119.84
1	A	1331	G	C2'-C3'-O3'	6.81	119.71	109.50
13	J	38	ILE	CA-C-N	6.77	128.31	119.84
13	J	38	ILE	C-N-CA	6.77	128.31	119.84
8	E	92	LYS	CA-C-N	6.77	126.69	119.85
8	E	92	LYS	C-N-CA	6.77	126.69	119.85
11	H	56	LYS	CA-C-N	6.76	128.54	120.23
11	H	56	LYS	C-N-CA	6.76	128.54	120.23
1	A	1224	G	C2'-C3'-O3'	6.72	119.58	109.50
1	A	428	G	C2'-C3'-O3'	6.72	119.57	109.50
13	J	60	ARG	N-CA-C	6.60	124.86	110.80
15	L	119	LYS	N-CA-C	-6.58	98.90	109.96
11	H	137	VAL	N-CA-C	6.49	117.93	108.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	S	4	SER	N-CA-C	6.49	118.27	108.46
16	M	22	ILE	N-CA-C	-6.49	102.98	110.05
11	H	75	ARG	CA-C-N	6.46	127.92	119.84
11	H	75	ARG	C-N-CA	6.46	127.92	119.84
1	A	960	U	C2'-C3'-O3'	6.46	119.18	109.50
8	E	112	LEU	N-CA-C	-6.43	105.53	113.19
13	J	16	LEU	N-CA-C	-6.42	102.96	111.24
11	H	100	ILE	CA-C-N	6.41	126.79	119.93
11	H	100	ILE	C-N-CA	6.41	126.79	119.93
17	N	8	GLU	N-CA-C	-6.40	105.76	112.93
22	S	54	GLY	N-CA-C	-6.37	98.08	113.18
20	Q	29	HIS	CA-C-N	6.37	126.86	119.47
20	Q	29	HIS	C-N-CA	6.37	126.86	119.47
7	D	186	LEU	N-CA-C	6.34	118.27	111.36
20	Q	67	LYS	N-CA-C	-6.32	100.31	109.59
1	A	559	A	C4'-C3'-O3'	6.29	118.84	109.40
11	H	19	VAL	N-CA-C	-6.26	106.34	111.91
1	A	509	A	C2'-C3'-O3'	6.25	123.08	113.70
6	C	139	GLN	N-CA-C	-6.24	104.40	111.07
10	G	147	ALA	N-CA-C	-6.20	103.00	112.99
5	B	64	ARG	N-CA-C	-6.20	105.72	113.28
5	B	192	SER	N-CA-C	6.17	117.57	108.86
12	I	5	TYR	N-CA-C	6.17	118.45	109.07
17	N	18	VAL	N-CA-C	6.16	116.33	110.42
8	E	48	ALA	CA-C-N	6.15	127.53	119.84
8	E	48	ALA	C-N-CA	6.15	127.53	119.84
8	E	69	VAL	N-CA-C	6.14	113.15	107.56
10	G	50	ILE	N-CA-C	-6.14	104.96	112.76
5	B	182	ILE	N-CA-C	6.13	113.14	107.56
1	A	1065	U	C2'-C3'-O3'	6.07	118.60	109.50
16	M	108	ARG	N-CA-C	6.03	117.85	111.28
6	C	93	LYS	N-CA-C	-6.03	105.00	112.90
7	D	33	MET	N-CA-C	-6.03	105.05	113.37
1	A	389	A	C5'-C4'-C3'	6.02	125.04	116.00
1	A	1201	A	C2'-C3'-O3'	6.02	118.53	109.50
9	F	60	PHE	N-CA-C	6.02	119.31	110.59
13	J	62	HIS	N-CA-C	6.02	119.86	110.17
16	M	79	LYS	N-CA-C	-6.01	104.06	111.75
21	R	56	THR	N-CA-C	-5.97	104.12	111.40
8	E	113	ALA	N-CA-C	-5.96	105.27	112.54
8	E	114	GLY	N-CA-C	-5.93	106.98	115.64
21	R	60	GLY	N-CA-C	-5.92	105.39	113.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	129(A)	G	C2'-C3'-O3'	5.87	118.31	109.50
1	A	1124	G	N9-C1'-C2'	5.87	120.80	112.00
3	Y	34	G	C2'-C3'-O3'	5.76	122.35	113.70
16	M	104	ARG	N-CA-C	-5.74	105.16	111.82
6	C	70	VAL	N-CA-C	5.74	116.97	108.65
15	L	57	LYS	N-CA-C	-5.73	101.14	110.20
7	D	28	SER	CA-C-N	5.71	126.97	119.84
7	D	28	SER	C-N-CA	5.71	126.97	119.84
23	T	26	ASN	N-CA-C	-5.67	103.88	112.04
10	G	87	VAL	CA-C-N	5.67	126.11	119.99
10	G	87	VAL	C-N-CA	5.67	126.11	119.99
1	A	1195	C	N1-C1'-C2'	5.66	120.49	112.00
6	C	181	ASN	N-CA-C	-5.66	104.28	110.91
5	B	156	LYS	N-CA-C	-5.66	106.36	113.72
1	A	572	A	N9-C1'-C2'	5.64	120.46	112.00
18	O	44	LYS	N-CA-C	-5.62	104.53	111.33
12	I	29	ASN	N-CA-C	-5.59	106.04	112.86
19	P	40	ASP	CA-C-N	5.58	125.29	119.82
19	P	40	ASP	C-N-CA	5.58	125.29	119.82
11	H	113	SER	N-CA-C	-5.58	99.19	108.34
1	A	913	A	C2'-C3'-O3'	5.58	117.86	109.50
12	I	61	ALA	N-CA-C	5.55	117.71	108.99
1	A	1305	G	N9-C1'-C2'	5.55	120.32	112.00
7	D	208	SER	N-CA-C	-5.55	107.09	112.97
15	L	23	LYS	N-CA-C	-5.53	104.79	112.30
14	K	116	HIS	N-CA-C	-5.51	104.76	112.25
1	A	460	A	N9-C1'-C2'	5.50	120.26	112.00
1	A	1335	C	C4'-C3'-O3'	-5.50	104.76	113.00
1	A	413	G	C4'-C3'-O3'	-5.47	104.80	113.00
21	R	81	PHE	N-CA-C	-5.44	107.29	114.04
1	A	992	U	C2'-C3'-O3'	5.43	117.65	109.50
1	A	481	G	C5'-C4'-C3'	-5.43	107.06	115.20
13	J	50	ILE	N-CA-C	-5.38	101.82	109.51
11	H	137	VAL	CB-CA-C	-5.34	104.29	110.91
5	B	186	ALA	N-CA-C	5.32	117.05	108.32
1	A	48	C	C2'-C3'-O3'	5.30	117.45	109.50
19	P	67	THR	N-CA-C	-5.30	103.49	110.43
8	E	7	GLU	N-CA-C	-5.30	102.21	110.42
1	A	1195	C	C4'-C3'-O3'	-5.29	105.07	113.00
1	A	975	A	C2'-C3'-O3'	5.29	117.43	109.50
1	A	344	A	C2'-C3'-O3'	5.28	117.42	109.50
11	H	79	VAL	N-CA-C	-5.28	104.49	111.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	G	132	GLY	N-CA-C	5.28	118.64	111.72
21	R	46	GLU	N-CA-C	-5.24	104.27	111.81
6	C	167	TRP	N-CA-C	5.20	121.88	110.80
1	A	389	A	C2'-C3'-O3'	-5.19	105.91	113.70
1	A	413	G	N9-C1'-C2'	5.19	119.79	112.00
22	S	18	LYS	N-CA-C	-5.19	106.28	113.18
8	E	81	GLU	N-CA-C	-5.19	99.83	108.34
1	A	1225	A	C2'-C3'-O3'	-5.17	105.94	113.70
22	S	53	ASN	N-CA-C	-5.17	105.71	112.23
1	A	1236	A	C5'-C4'-C3'	5.16	123.74	116.00
17	N	10	ALA	N-CA-C	-5.15	106.09	112.38
1	A	1305	G	C4'-C3'-O3'	-5.15	105.28	113.00
1	A	839	U	N1-C1'-C2'	5.13	119.70	112.00
22	S	82	GLY	N-CA-C	5.11	125.29	113.18
18	O	55	GLY	N-CA-C	-5.11	106.60	112.83
20	Q	27	PHE	CA-C-N	5.10	124.86	119.76
20	Q	27	PHE	C-N-CA	5.10	124.86	119.76
23	T	56	MET	N-CA-C	-5.10	104.99	111.11
5	B	68	ILE	CB-CA-C	-5.10	106.08	111.23
1	A	563	A	C4'-C3'-O3'	-5.08	105.38	113.00
12	I	62	TYR	N-CA-C	-5.08	100.24	108.52
1	A	365	U	N1-C1'-C2'	5.08	119.62	112.00
1	A	1224	G	N9-C1'-C2'	5.06	121.59	114.00
1	A	1502	A	N9-C1'-C2'	5.03	121.54	114.00
21	R	79	LEU	CA-C-N	5.03	126.12	119.84
21	R	79	LEU	C-N-CA	5.03	126.12	119.84
11	H	96	GLY	N-CA-C	-5.01	103.56	112.54
5	B	71	VAL	N-CA-C	5.01	115.24	107.78

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	366	C	C3'

All (29) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1073	U	Sidechain
1	A	1299	A	Sidechain
1	A	1330	U	Sidechain
1	A	1360	A	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1396	A	Sidechain
1	A	1446	A	Sidechain
1	A	1502	A	Sidechain
1	A	1519	A	Sidechain
1	A	190(F)	G	Sidechain
1	A	197	A	Sidechain
1	A	24	U	Sidechain
1	A	249	U	Sidechain
1	A	251	G	Sidechain
1	A	253	U	Sidechain
1	A	254	G	Sidechain
1	A	37	U	Sidechain
1	A	380	G	Sidechain
1	A	404	U	Sidechain
1	A	490	G	Sidechain
1	A	528	C	Sidechain
1	A	561	U	Sidechain
1	A	575	G	Sidechain
1	A	641	U	Sidechain
1	A	664	G	Sidechain
1	A	727	G	Sidechain
1	A	879	C	Sidechain
1	A	898	G	Sidechain
1	A	901	A	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32391	0	16349	1276	0
2	X	117	0	64	3	0
3	Y	233	0	120	10	0
4	Z	77	0	42	4	0
5	B	1900	0	1951	304	0
6	C	1612	0	1677	256	0
7	D	1703	0	1764	175	0
8	E	1146	0	1207	133	0
9	F	843	0	857	89	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	G	1257	0	1296	139	0
11	H	1116	0	1177	114	0
12	I	1011	0	1043	170	0
13	J	792	0	835	148	0
14	K	885	0	904	94	0
15	L	970	0	1057	120	0
16	M	937	0	995	130	0
17	N	492	0	529	79	0
18	O	734	0	771	67	0
19	P	700	0	720	61	0
20	Q	857	0	930	104	0
21	R	597	0	668	85	0
22	S	697	0	723	125	0
23	T	763	0	861	96	0
24	V	208	0	221	14	0
25	A	118	0	0	0	0
25	D	1	0	0	0	0
25	H	1	0	0	0	0
26	D	1	0	0	0	0
26	N	1	0	0	0	0
All	All	52160	0	36761	3519	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 40.

All (3519) 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)
1:A:1397:C:OP2	8:E:24:ARG:NH2	1.62	1.27
5:B:84:GLU:HB3	5:B:219:VAL:HG21	1.25	1.18
6:C:14:ILE:HG22	6:C:15:THR:H	1.12	1.15
1:A:1443:G:H5''	1:A:1446:A:H5'	1.31	1.11
7:D:36:ARG:H	7:D:37:PRO:HD3	0.95	1.11
13:J:45:ARG:HB3	13:J:45:ARG:HH11	0.96	1.10
23:T:74:LYS:HG2	23:T:75:ASN:H	1.01	1.09
8:E:80:ILE:CD1	8:E:91:LEU:HB2	1.84	1.06
8:E:80:ILE:HD11	8:E:91:LEU:HB2	1.38	1.05
1:A:1116:C:H2'	1:A:1117:G:H5''	1.39	1.04
7:D:36:ARG:H	7:D:37:PRO:CD	1.70	1.04
19:P:22:THR:HA	19:P:33:ILE:HD13	1.37	1.04
10:G:5:ARG:HG3	10:G:6:ARG:H	1.21	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:N:24:CYS:HB3	17:N:28:GLY:H	1.20	1.04
12:I:65:VAL:HG11	12:I:73:GLN:HB3	1.37	1.04
15:L:41:ARG:HG2	15:L:42:THR:H	1.18	1.04
1:A:243:A:H4'	1:A:244:U:H5'	1.41	1.03
22:S:40:ILE:HD13	22:S:62:ILE:HD13	1.40	1.03
1:A:1004:A:H2'	1:A:1005:A:H5'	1.38	1.03
15:L:46:LYS:HG2	15:L:47:LYS:H	1.18	1.03
15:L:93:LEU:HD23	15:L:93:LEU:H	1.25	1.02
16:M:78:ILE:HA	16:M:81:LEU:HD21	1.42	1.02
12:I:93:ARG:HB3	12:I:97:LYS:HE3	1.39	1.02
13:J:45:ARG:HB3	13:J:45:ARG:NH1	1.74	1.01
14:K:54:ARG:HB3	14:K:54:ARG:HH11	1.23	1.01
16:M:49:THR:HG22	16:M:51:ALA:H	1.24	1.00
22:S:55:LYS:HG2	22:S:56:GLN:HE21	1.24	0.99
6:C:8:ILE:HG23	6:C:16:ARG:HG2	1.46	0.98
7:D:36:ARG:N	7:D:37:PRO:HD3	1.79	0.97
16:M:81:LEU:HD23	16:M:81:LEU:H	1.28	0.97
6:C:179:ARG:HD3	6:C:206:GLU:HB3	1.46	0.97
19:P:58:TYR:O	19:P:61:SER:HB3	1.63	0.96
13:J:90:LEU:H	13:J:91:PRO:HD2	1.29	0.96
16:M:10:PRO:HB2	16:M:18:ALA:HB1	1.48	0.95
18:O:70:LEU:HD12	18:O:78:TYR:HB2	1.48	0.95
5:B:16:HIS:NE2	5:B:214:ILE:HG12	1.81	0.95
1:A:1305:G:HO2'	1:A:1306:A:H8	1.10	0.95
20:Q:67:LYS:HA	20:Q:70:ARG:HH12	1.32	0.94
1:A:1443:G:H5''	1:A:1446:A:C5'	1.96	0.94
24:V:6:ARG:HB3	24:V:15:ARG:HH21	1.29	0.94
18:O:26:GLU:OE1	18:O:77:ARG:HD2	1.68	0.94
23:T:74:LYS:CG	23:T:75:ASN:H	1.80	0.94
7:D:151:LYS:H	7:D:151:LYS:HD2	1.31	0.93
1:A:1502:A:H2	1:A:1505:G:H1	1.12	0.93
23:T:74:LYS:HG2	23:T:75:ASN:N	1.84	0.93
7:D:7:PRO:HG2	7:D:10:ARG:HD2	1.49	0.93
6:C:179:ARG:O	6:C:179:ARG:HG2	1.68	0.93
5:B:75:LYS:HA	5:B:78:GLN:HG3	1.51	0.93
1:A:1139:G:H4'	1:A:1140:C:H5'	1.50	0.93
8:E:110:LEU:HD13	8:E:118:ILE:HD12	1.49	0.92
12:I:8:GLY:HA2	12:I:79:LEU:HD12	1.51	0.92
15:L:91:LYS:HA	15:L:91:LYS:HE3	1.52	0.92
3:Y:34:G:H2'	3:Y:35:A:H8	1.31	0.92
1:A:1305:G:O2'	1:A:1306:A:H8	1.51	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:40:ILE:HG22	14:K:41:THR:HG23	1.49	0.92
15:L:93:LEU:HD12	15:L:96:VAL:HG21	1.50	0.91
22:S:85:LYS:H	22:S:85:LYS:HE3	1.36	0.91
13:J:79:ARG:HH11	13:J:79:ARG:HA	1.33	0.91
1:A:939:G:H5''	10:G:102:ARG:HH22	1.36	0.91
6:C:188:LEU:HD13	6:C:189:ALA:H	1.36	0.91
11:H:113:SER:HB2	11:H:134:ILE:HD11	1.53	0.91
1:A:1116:C:C2'	1:A:1117:G:H5''	2.00	0.91
17:N:36:PHE:O	17:N:36:PHE:HD1	1.52	0.91
1:A:382:A:H2'	1:A:383:A:C8	2.06	0.91
1:A:1368:G:O2'	1:A:1369:C:H5'	1.71	0.91
23:T:73:HIS:C	23:T:74:LYS:HD3	1.95	0.90
9:F:44:GLY:HA2	9:F:59:TYR:CE1	2.06	0.90
7:D:175:SER:HB3	7:D:186:LEU:HD21	1.54	0.90
8:E:51:VAL:HB	8:E:52:PRO:HD3	1.50	0.90
22:S:41:VAL:HG22	22:S:44:MET:HE3	1.53	0.90
8:E:43:LEU:HD11	8:E:132:ALA:HB1	1.54	0.90
12:I:29:ASN:ND2	12:I:64:THR:HA	1.85	0.90
8:E:41:VAL:HG22	8:E:113:ALA:HA	1.53	0.89
1:A:967:C:H4'	12:I:128:ARG:HG3	1.54	0.89
23:T:57:ARG:HD2	23:T:102:GLY:HA3	1.53	0.89
7:D:29:PRO:O	7:D:30:LYS:HG3	1.73	0.89
18:O:16:ALA:HB1	18:O:21:ASP:HB3	1.51	0.89
3:Y:34:G:H2'	3:Y:35:A:C8	2.06	0.89
6:C:50:ALA:HB1	6:C:70:VAL:HG11	1.52	0.88
5:B:178:ARG:HH11	5:B:178:ARG:HG3	1.39	0.88
1:A:371:G:O2'	1:A:372:C:H5'	1.72	0.88
1:A:954:G:H21	1:A:1227:A:H62	1.21	0.88
13:J:32:ALA:HB2	13:J:76:ASN:HB2	1.56	0.88
12:I:17:VAL:HG21	12:I:80:GLY:HA3	1.56	0.87
1:A:438:G:H4'	1:A:439:A:OP1	1.74	0.87
5:B:80:ILE:HD11	5:B:208:ILE:HG12	1.53	0.87
1:A:1236:A:H4'	1:A:1304:G:H4'	1.57	0.87
1:A:1348:U:H2'	1:A:1349:A:H8	1.36	0.87
5:B:77:ALA:HB2	5:B:211:ILE:HD13	1.57	0.87
13:J:79:ARG:HA	13:J:79:ARG:NH1	1.89	0.87
3:Y:34:G:H1	4:Z:3:U:H3	1.22	0.86
1:A:1216:G:H5''	17:N:5:ALA:HB2	1.58	0.86
14:K:84:VAL:HG23	14:K:110:ASP:HA	1.57	0.86
16:M:4:ILE:HG22	16:M:5:ALA:N	1.89	0.86
1:A:1497:G:O2'	1:A:1498:U:H5'	1.76	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:31:ILE:HG22	22:S:32:LYS:H	1.40	0.86
7:D:19:LEU:HD21	7:D:67:ILE:HG12	1.56	0.86
7:D:149:ALA:HB3	7:D:152:SER:HB2	1.58	0.86
9:F:100:ASN:HD22	21:R:23:LYS:HG2	1.39	0.86
1:A:528:C:H41	15:L:49:ASN:HD21	1.22	0.85
1:A:946:A:H2'	1:A:947:G:C8	2.11	0.85
1:A:1054:C:O2	1:A:1054:C:H3'	1.76	0.85
1:A:977:A:H2'	1:A:978:A:H5''	1.58	0.85
22:S:42:PRO:O	22:S:45:VAL:HG23	1.76	0.85
8:E:115:VAL:HG11	8:E:118:ILE:HD11	1.57	0.85
13:J:23:ILE:HD12	13:J:23:ILE:H	1.40	0.85
1:A:243:A:C4'	1:A:244:U:H5'	2.06	0.84
1:A:1356:G:H2'	1:A:1357:A:C8	2.12	0.84
11:H:64:LYS:HG2	11:H:79:VAL:HG21	1.57	0.84
6:C:108:ASN:HD21	6:C:111:LEU:HG	1.42	0.84
1:A:1152:A:H5''	13:J:13:HIS:HD2	1.42	0.84
1:A:1298:C:H2'	10:G:114:ARG:HH12	1.41	0.84
6:C:32:LEU:HD21	6:C:59:ARG:HD2	1.58	0.83
5:B:197:VAL:HB	5:B:200:ILE:HG23	1.58	0.83
6:C:23:TYR:HD2	6:C:24:ALA:N	1.76	0.83
13:J:45:ARG:HH11	13:J:45:ARG:CB	1.86	0.83
1:A:1124:G:H3'	1:A:1145:C:H41	1.43	0.83
5:B:68:ILE:H	5:B:90:MET:HE3	1.43	0.83
1:A:1133:G:H2'	1:A:1134:G:H8	1.41	0.83
8:E:41:VAL:CG2	8:E:113:ALA:HA	2.08	0.83
10:G:69:VAL:HG21	10:G:104:LEU:HD21	1.59	0.83
6:C:150:LYS:HE2	6:C:152:ILE:HD11	1.61	0.83
17:N:3:ARG:NH1	17:N:6:LEU:HD11	1.94	0.82
7:D:32:ALA:C	7:D:34:GLU:H	1.85	0.82
12:I:89:ASN:HD21	12:I:91:ASP:HB2	1.43	0.82
1:A:1352:C:H2'	1:A:1353:G:C8	2.13	0.82
9:F:30:LEU:HD11	9:F:63:TYR:HD1	1.44	0.82
14:K:48:ILE:HD12	14:K:63:LEU:HB3	1.60	0.82
1:A:560:U:H5'	1:A:566:G:N2	1.94	0.82
6:C:14:ILE:HG22	6:C:15:THR:N	1.94	0.81
13:J:71:LEU:HD13	13:J:72:VAL:H	1.44	0.81
20:Q:76:LEU:HD23	20:Q:77:VAL:N	1.93	0.81
1:A:359:U:H2'	1:A:360:A:H8	1.44	0.81
1:A:939:G:H5''	10:G:102:ARG:NH2	1.95	0.81
1:A:1435:G:H2'	1:A:1436:U:C6	2.15	0.81
7:D:128:VAL:HG12	7:D:129:ASN:ND2	1.95	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:12:LEU:HD13	8:E:31:LEU:HB2	1.63	0.81
13:J:71:LEU:HD13	13:J:72:VAL:N	1.95	0.81
15:L:124:LYS:HD2	15:L:125:PRO:HD2	1.62	0.81
6:C:6:HIS:CD2	6:C:8:ILE:HB	2.16	0.81
1:A:1443:G:C5'	1:A:1446:A:H5'	2.11	0.81
6:C:157:ILE:HD11	6:C:166:GLU:HB2	1.62	0.81
12:I:127:LYS:H	12:I:127:LYS:HD2	1.45	0.81
11:H:119:LEU:HD12	11:H:124:ALA:HA	1.63	0.81
1:A:1115:C:H1'	17:N:61:TRP:O	1.81	0.81
1:A:579:G:H5'	1:A:728:A:H1'	1.62	0.81
1:A:1003(A):G:H2'	1:A:1004:A:H4'	1.62	0.81
1:A:1391:U:H2'	1:A:1392:G:C8	2.16	0.81
1:A:109:A:H2'	1:A:326:G:N2	1.95	0.80
7:D:35:ARG:O	7:D:36:ARG:HB2	1.79	0.80
1:A:1152:A:H5''	13:J:13:HIS:CD2	2.16	0.80
13:J:30:SER:HB3	13:J:84:GLN:HE21	1.46	0.80
11:H:80:ILE:O	11:H:80:ILE:HG22	1.82	0.80
1:A:1064:G:H4'	1:A:1065:U:C5'	2.12	0.80
1:A:235:C:H5'	20:Q:70:ARG:HG2	1.62	0.80
1:A:918:A:H2'	1:A:919:A:C8	2.16	0.80
7:D:150:GLU:HA	7:D:153:ARG:NE	1.97	0.80
8:E:11:ILE:HB	8:E:31:LEU:HB3	1.64	0.80
17:N:36:PHE:O	17:N:36:PHE:CD1	2.35	0.80
1:A:129(A):G:HO2'	1:A:190(E):U:H2'	1.44	0.80
1:A:1190:G:OP1	6:C:4:LYS:HA	1.82	0.80
15:L:27:LEU:C	15:L:29:GLY:H	1.90	0.80
16:M:86:CYS:SG	16:M:88:ARG:HG2	2.22	0.80
9:F:67:MET:HE2	9:F:72:VAL:HA	1.64	0.80
16:M:5:ALA:HB3	16:M:8:GLU:HG3	1.64	0.80
1:A:99:C:H2'	1:A:101:A:C8	2.17	0.79
5:B:25:ASN:HD22	5:B:25:ASN:C	1.90	0.79
6:C:24:ALA:HB2	6:C:32:LEU:HD13	1.65	0.79
1:A:501:C:H2'	1:A:502:G:H8	1.45	0.79
7:D:30:LYS:C	7:D:32:ALA:H	1.86	0.79
1:A:797:C:OP1	14:K:124:LYS:HE2	1.82	0.79
1:A:1356:G:H2'	1:A:1357:A:H8	1.47	0.79
16:M:91:ARG:HB2	16:M:98:VAL:HG13	1.65	0.79
7:D:83:SER:HA	7:D:89:THR:HG23	1.65	0.79
1:A:760:G:H1	20:Q:105:ALA:HA	1.48	0.79
14:K:66:LEU:HB3	14:K:70:LYS:HE3	1.65	0.79
1:A:351:G:H4'	1:A:352:C:OP1	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:14:ILE:CG2	6:C:15:THR:H	1.95	0.78
7:D:25:ARG:C	7:D:27:TYR:H	1.87	0.78
11:H:24:THR:HG22	11:H:63:LEU:HD21	1.64	0.78
7:D:142:PRO:HG2	7:D:187:ARG:HH21	1.48	0.78
1:A:254:G:OP1	20:Q:67:LYS:O	2.01	0.78
10:G:26:PHE:CE2	10:G:30:ILE:HD11	2.18	0.78
22:S:20:LEU:HA	22:S:23:ASN:HD22	1.47	0.78
22:S:16:LEU:O	22:S:19:VAL:HG12	1.84	0.78
23:T:73:HIS:O	23:T:74:LYS:HD3	1.83	0.78
1:A:1148:U:H4'	12:I:14:VAL:HG11	1.66	0.78
9:F:91:VAL:HG12	9:F:92:LYS:H	1.47	0.78
1:A:1064:G:H4'	1:A:1065:U:H5'	1.64	0.78
1:A:538:G:OP2	15:L:115:LYS:HG3	1.83	0.78
5:B:18:GLY:HA2	5:B:41:ILE:HA	1.63	0.78
5:B:84:GLU:HB3	5:B:219:VAL:CG2	2.11	0.78
6:C:58:GLU:HB3	13:J:92:THR:HG21	1.66	0.78
7:D:199:ASN:HD21	7:D:201:GLN:HB2	1.49	0.78
16:M:81:LEU:H	16:M:81:LEU:CD2	1.96	0.78
5:B:178:ARG:HH21	5:B:196:LEU:HA	1.49	0.78
12:I:53:VAL:HG21	12:I:85:LEU:HD21	1.66	0.78
6:C:191:THR:HG21	6:C:193:TYR:CZ	2.18	0.77
5:B:42:ILE:HD11	5:B:189:ASP:HB2	1.65	0.77
6:C:191:THR:HG22	6:C:192:THR:N	1.98	0.77
1:A:1168:A:H2'	1:A:1169:A:C8	2.19	0.77
1:A:1250:A:H4'	12:I:68:GLY:H	1.48	0.77
6:C:116:VAL:HG21	6:C:202:ILE:HD11	1.63	0.77
15:L:46:LYS:HG2	15:L:47:LYS:N	1.97	0.77
1:A:1226:C:H4'	1:A:1227:A:OP1	1.85	0.77
12:I:70:LYS:O	12:I:74:ILE:HG13	1.84	0.77
13:J:30:SER:OG	13:J:81:THR:HA	1.85	0.77
15:L:89:ARG:NH1	15:L:97:ARG:HG2	1.99	0.77
16:M:65:LYS:HG3	16:M:69:GLU:OE2	1.85	0.77
20:Q:15:MET:HE1	20:Q:43:LEU:HD22	1.65	0.77
1:A:1226:C:H1'	22:S:83:HIS:CE1	2.19	0.77
7:D:199:ASN:ND2	7:D:201:GLN:HB2	2.00	0.77
1:A:972:C:H4'	13:J:57:LYS:HD3	1.65	0.77
15:L:47:LYS:HB3	15:L:48:PRO:HD3	1.65	0.77
21:R:48:GLY:H	21:R:82:THR:HA	1.51	0.77
1:A:1366:C:H2'	1:A:1367:C:H6	1.47	0.76
6:C:195:VAL:O	6:C:196:LEU:HD23	1.85	0.76
1:A:17:U:H2'	1:A:18:C:C6	2.20	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:115:LEU:HD21	5:B:153:ARG:NH2	1.99	0.76
6:C:191:THR:HG22	6:C:193:TYR:H	1.50	0.76
9:F:10:LEU:H	9:F:10:LEU:HD12	1.49	0.76
20:Q:101:ARG:HA	20:Q:101:ARG:HE	1.50	0.76
1:A:983:A:H5'	1:A:984:C:OP2	1.86	0.76
1:A:1195:C:H3'	1:A:1196:U:H5''	1.66	0.76
5:B:200:ILE:HD13	5:B:202:PRO:HD3	1.67	0.76
12:I:29:ASN:HD21	12:I:64:THR:HA	1.47	0.76
14:K:54:ARG:O	14:K:57:THR:HG23	1.85	0.76
1:A:1236:A:H2'	1:A:1237:C:C6	2.21	0.76
5:B:44:LEU:HA	5:B:47:THR:OG1	1.85	0.76
5:B:53:ARG:O	5:B:56:ARG:HB3	1.85	0.76
7:D:2:GLY:N	7:D:3:ARG:HE	1.84	0.76
10:G:54:THR:HG22	10:G:56:GLN:H	1.50	0.76
1:A:180:U:H2'	1:A:181:G:H5'	1.67	0.76
7:D:146:ILE:N	7:D:146:ILE:HD12	2.01	0.76
5:B:188:ALA:O	5:B:202:PRO:HA	1.86	0.76
6:C:6:HIS:HD2	6:C:9:GLY:H	1.33	0.76
5:B:15:VAL:HG11	5:B:210:SER:N	2.01	0.75
5:B:178:ARG:HH21	5:B:196:LEU:C	1.94	0.75
16:M:3:ARG:HG2	16:M:9:ILE:HG23	1.67	0.75
19:P:22:THR:CA	19:P:33:ILE:HD13	2.16	0.75
1:A:266:G:H5''	1:A:268:C:H41	1.52	0.75
1:A:750:G:N3	18:O:23:GLY:HA3	2.01	0.75
6:C:5:ILE:HD13	6:C:10:PHE:HB2	1.69	0.75
17:N:24:CYS:HB3	17:N:28:GLY:N	2.00	0.75
3:Y:34:G:H8	3:Y:34:G:H5'	1.50	0.75
13:J:6:ILE:HA	13:J:98:ILE:HG12	1.69	0.75
1:A:818:G:O2'	1:A:819:A:H5''	1.87	0.75
6:C:23:TYR:CD2	6:C:24:ALA:N	2.54	0.75
11:H:63:LEU:HD22	11:H:63:LEU:H	1.52	0.75
1:A:250:A:H4'	1:A:251:G:O5'	1.86	0.75
1:A:447:G:H2'	1:A:485:G:N2	2.02	0.75
5:B:130:ARG:HB3	5:B:131:PRO:HD2	1.69	0.75
16:M:81:LEU:HD23	16:M:81:LEU:N	2.01	0.75
13:J:6:ILE:HG23	13:J:98:ILE:HD11	1.66	0.74
1:A:130:A:OP2	1:A:190(E):U:H2'	1.87	0.74
16:M:22:ILE:HB	16:M:25:ILE:HD12	1.69	0.74
9:F:36:ARG:HH12	9:F:38:GLU:HG2	1.52	0.74
13:J:61:GLU:OE1	17:N:45:ARG:HD2	1.88	0.74
11:H:90:GLY:O	11:H:91:ARG:HB2	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:106:ALA:O	12:I:108:VAL:HG23	1.87	0.74
15:L:77:LEU:HD21	15:L:107:ALA:HA	1.69	0.74
6:C:10:PHE:CE2	6:C:178:LEU:HD13	2.22	0.74
10:G:138:LYS:HD2	10:G:138:LYS:C	2.11	0.74
1:A:1145:C:HO2'	1:A:1146:A:H8	1.33	0.74
1:A:1281:U:H5'	1:A:1282:C:C5	2.23	0.74
1:A:1003(A):G:H2'	1:A:1004:A:C4'	2.17	0.74
10:G:23:VAL:O	10:G:27:ILE:HG13	1.87	0.74
1:A:129(A):G:O2'	1:A:190(E):U:H2'	1.87	0.73
15:L:93:LEU:HD23	15:L:93:LEU:N	2.02	0.73
18:O:70:LEU:HD12	18:O:78:TYR:CB	2.18	0.73
5:B:30:ARG:HG3	5:B:31:TYR:CD2	2.23	0.73
6:C:14:ILE:O	6:C:16:ARG:N	2.20	0.73
14:K:27:ASN:HA	14:K:56:GLY:HA2	1.68	0.73
20:Q:97:SER:HB2	20:Q:102:GLY:O	1.86	0.73
1:A:1435:G:H2'	1:A:1436:U:H6	1.51	0.73
6:C:134:ILE:HG23	6:C:151:VAL:HB	1.71	0.73
15:L:43:VAL:HG12	15:L:44:THR:N	2.03	0.73
5:B:124:SER:HB2	5:B:125:PRO:HD2	1.69	0.73
13:J:44:VAL:HG22	13:J:66:ARG:HG2	1.71	0.73
5:B:69:LEU:HB3	5:B:162:ILE:HG13	1.68	0.73
5:B:114:ARG:NH1	5:B:118:LEU:HD21	2.03	0.73
15:L:75:HIS:HD2	15:L:77:LEU:H	1.35	0.73
1:A:390:C:H2'	1:A:391:G:C8	2.24	0.73
19:P:74:LEU:O	19:P:79:VAL:HG23	1.88	0.73
1:A:474:G:H2'	1:A:475:G:H8	1.52	0.73
1:A:382:A:H2'	1:A:383:A:H8	1.54	0.72
15:L:86:ARG:HH11	15:L:86:ARG:HG3	1.52	0.72
1:A:1125:U:H5''	1:A:1126:U:H5	1.53	0.72
1:A:291:C:O2'	1:A:292:G:H5'	1.89	0.72
20:Q:67:LYS:O	20:Q:68:ARG:CB	2.37	0.72
1:A:817:C:H4'	1:A:818:G:OP1	1.88	0.72
9:F:99:ALA:HB2	21:R:31:LEU:HD11	1.71	0.72
13:J:8:LEU:HD23	13:J:96:ILE:HG12	1.72	0.72
13:J:39:PRO:O	13:J:40:LEU:HB2	1.89	0.72
1:A:1054:C:H2'	1:A:1055:A:H5''	1.71	0.72
1:A:1142:G:H2'	1:A:1143:G:O4'	1.89	0.72
6:C:137:ALA:HA	6:C:140:ARG:HH11	1.54	0.72
22:S:16:LEU:C	22:S:18:LYS:H	1.97	0.72
1:A:376:G:H5''	19:P:5:ARG:HD2	1.69	0.72
8:E:110:LEU:O	8:E:113:ALA:HB3	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Q:27:PHE:CZ	20:Q:36:ILE:HD11	2.24	0.72
6:C:25:GLY:H	6:C:28:GLN:HB2	1.53	0.72
6:C:107:GLN:H	6:C:107:GLN:CD	1.95	0.72
9:F:94:GLN:HB3	21:R:32:ARG:HD3	1.72	0.72
6:C:23:TYR:HD2	6:C:23:TYR:C	1.98	0.72
15:L:27:LEU:HD23	15:L:28:LYS:HB2	1.71	0.72
22:S:3:ARG:HH22	22:S:69:HIS:HE1	1.35	0.72
22:S:80:TYR:HD2	22:S:81:ARG:N	1.87	0.72
1:A:359:U:H2'	1:A:360:A:C8	2.25	0.72
1:A:524:G:H2'	1:A:525:C:C6	2.25	0.72
6:C:107:GLN:H	6:C:107:GLN:NE2	1.88	0.72
13:J:53:PRO:HA	17:N:41:ARG:HH21	1.53	0.72
5:B:15:VAL:CG2	5:B:209:ARG:HG3	2.20	0.71
7:D:126:ILE:HG22	7:D:127:THR:N	2.03	0.71
22:S:22:LEU:HD13	22:S:28:LYS:HB3	1.71	0.71
7:D:13:ARG:HD2	7:D:38:TYR:O	1.90	0.71
20:Q:45:HIS:NE2	20:Q:47:PRO:HG3	2.05	0.71
21:R:74:ARG:HB3	21:R:81:PHE:CE1	2.25	0.71
1:A:1137:C:H4'	1:A:1138:G:C2	2.25	0.71
6:C:195:VAL:C	6:C:196:LEU:HD23	2.15	0.71
12:I:114:TYR:HE1	13:J:59:SER:O	1.73	0.71
14:K:74:ALA:C	14:K:76:GLY:H	1.97	0.71
18:O:78:TYR:CZ	18:O:82:ILE:HD11	2.24	0.71
1:A:353:A:H5'	1:A:353:A:H8	1.54	0.71
1:A:447:G:H2'	1:A:485:G:H22	1.56	0.71
1:A:1112:C:O2	6:C:179:ARG:HB3	1.89	0.71
5:B:69:LEU:HD12	5:B:155:LEU:HD11	1.71	0.71
23:T:39:LYS:HD2	23:T:55:ILE:CD1	2.19	0.71
1:A:1277:C:H2'	1:A:1278:U:H5'	1.72	0.71
8:E:110:LEU:O	8:E:115:VAL:HB	1.90	0.71
1:A:900:A:H2'	1:A:901:A:C8	2.24	0.71
14:K:91:ARG:HD3	21:R:88:LYS:HE2	1.72	0.71
1:A:201:C:H42	1:A:216:G:H1	1.36	0.71
1:A:1095:U:H2'	1:A:1096:C:C6	2.25	0.71
6:C:131:ARG:HG2	6:C:135:LYS:HE3	1.71	0.71
12:I:111:ARG:CB	12:I:111:ARG:HH11	2.03	0.71
22:S:17:GLU:HA	22:S:20:LEU:HD11	1.71	0.71
5:B:25:ASN:ND2	5:B:27:LYS:H	1.88	0.71
7:D:32:ALA:C	7:D:34:GLU:N	2.48	0.71
10:G:116:ALA:HA	10:G:119:ARG:CZ	2.21	0.71
21:R:36:ASN:ND2	21:R:38:GLU:HG2	2.04	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:50:GLU:HG3	8:E:53:LEU:HB2	1.73	0.71
16:M:78:ILE:HA	16:M:81:LEU:CD2	2.16	0.71
19:P:8:ARG:HB2	19:P:28:ARG:NH1	2.05	0.71
1:A:1151:A:HO2'	1:A:1152:A:H8	1.39	0.71
5:B:15:VAL:HG21	5:B:209:ARG:HG3	1.72	0.71
6:C:191:THR:CG2	6:C:192:THR:N	2.53	0.71
17:N:4:LYS:HA	17:N:7:ILE:CD1	2.21	0.71
7:D:119:GLN:HG2	7:D:123:HIS:CD2	2.25	0.70
1:A:1152:A:H5'	13:J:70:ARG:HH21	1.56	0.70
1:A:1518:A:H2'	1:A:1519:A:C8	2.26	0.70
20:Q:12:SER:HB3	20:Q:20:THR:HB	1.73	0.70
24:V:6:ARG:HB3	24:V:15:ARG:NH2	2.04	0.70
1:A:1196:U:OP1	1:A:1197:G:H5'	1.91	0.70
1:A:1502:A:H2	1:A:1505:G:N1	1.87	0.70
5:B:185:ILE:N	5:B:185:ILE:HD12	2.06	0.70
12:I:9:ARG:HA	12:I:13:ALA:O	1.91	0.70
7:D:23:GLY:HA3	7:D:112:VAL:HG12	1.73	0.70
10:G:5:ARG:HG3	10:G:6:ARG:N	2.02	0.70
21:R:59:SER:OG	21:R:62:GLU:HG3	1.90	0.70
5:B:23:ARG:NH1	5:B:191:ASP:HA	2.05	0.70
6:C:100:ALA:O	6:C:101:LEU:HB2	1.89	0.70
1:A:370:C:O2'	1:A:371:G:H5'	1.91	0.70
15:L:41:ARG:HG2	15:L:42:THR:N	1.98	0.70
22:S:20:LEU:HD12	22:S:21:GLU:N	2.07	0.70
1:A:664:G:OP1	21:R:64:ARG:HD2	1.91	0.70
1:A:1402:C:H2'	1:A:1403:C:H6	1.56	0.70
23:T:53:LEU:HB2	23:T:100:ILE:HG21	1.72	0.70
16:M:3:ARG:HA	16:M:8:GLU:O	1.92	0.70
1:A:135:C:O2	19:P:1:MET:HB2	1.92	0.70
1:A:1133:G:H2'	1:A:1134:G:C8	2.27	0.70
1:A:1343:G:H2'	1:A:1344:C:C6	2.27	0.70
1:A:1475:G:H2'	1:A:1476:G:H8	1.56	0.70
11:H:119:LEU:HD12	11:H:124:ALA:CA	2.21	0.70
1:A:1298:C:H4'	1:A:1299:A:O4'	1.91	0.69
5:B:17:PHE:HB3	5:B:44:LEU:HD11	1.73	0.69
7:D:16:GLY:O	7:D:33:MET:HE2	1.91	0.69
16:M:88:ARG:NH1	22:S:3:ARG:HH21	1.90	0.69
19:P:42:ARG:O	19:P:43:LYS:C	2.34	0.69
1:A:269:C:H2'	1:A:270:A:C8	2.27	0.69
1:A:848:C:O2'	1:A:849:C:H5'	1.93	0.69
1:A:972:C:H4'	13:J:57:LYS:CD	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:188:LEU:CD1	6:C:189:ALA:H	2.02	0.69
7:D:151:LYS:H	7:D:151:LYS:CD	2.04	0.69
11:H:19:VAL:HG23	11:H:21:LYS:HG2	1.74	0.69
12:I:118:LYS:O	12:I:119:ALA:HB3	1.91	0.69
1:A:1064:G:C4'	1:A:1065:U:H5'	2.22	0.69
1:A:1313:U:O4	22:S:4:SER:HB3	1.91	0.69
15:L:75:HIS:CD2	15:L:77:LEU:H	2.10	0.69
1:A:939:G:H5''	10:G:102:ARG:HH12	1.56	0.69
7:D:25:ARG:NH2	7:D:30:LYS:HD3	2.07	0.69
11:H:31:PHE:O	11:H:34:GLU:HB2	1.92	0.69
1:A:1490:C:O2'	1:A:1491:G:H5'	1.91	0.69
6:C:52:LEU:HD23	6:C:52:LEU:H	1.58	0.69
1:A:478:A:O2'	1:A:479:C:H5'	1.92	0.69
10:G:138:LYS:HD2	10:G:138:LYS:O	1.92	0.69
14:K:54:ARG:HB3	14:K:54:ARG:NH1	2.05	0.69
18:O:65:ARG:NH1	18:O:65:ARG:HB2	2.08	0.69
5:B:91:PRO:HA	5:B:154:LEU:HD12	1.74	0.69
8:E:75:THR:HG23	8:E:76:ILE:N	2.08	0.69
9:F:19:LEU:C	9:F:19:LEU:HD23	2.18	0.69
10:G:61:VAL:O	10:G:64:GLN:HB3	1.91	0.69
1:A:731:G:OP1	1:A:766:A:H1'	1.93	0.69
1:A:959:A:H3'	1:A:960:U:H5''	1.75	0.69
1:A:1015:A:H2'	1:A:1016:A:C8	2.28	0.69
5:B:42:ILE:HD12	5:B:203:GLY:HA2	1.74	0.69
5:B:97:TRP:HZ2	5:B:102:LEU:HD13	1.58	0.69
5:B:132:LYS:O	5:B:136:VAL:HG23	1.92	0.69
6:C:62:ASP:HA	6:C:97:LYS:CG	2.23	0.69
7:D:65:ARG:HB2	7:D:75:PHE:CE1	2.28	0.69
7:D:103:ASN:OD1	7:D:114:ARG:NH2	2.26	0.69
7:D:156:GLU:O	7:D:159:ARG:HB2	1.93	0.69
9:F:64:GLN:O	9:F:64:GLN:HG2	1.93	0.69
13:J:94:VAL:HG12	13:J:95:GLU:N	2.06	0.69
16:M:4:ILE:HG22	16:M:5:ALA:H	1.57	0.69
22:S:40:ILE:HG21	22:S:62:ILE:HD13	1.73	0.69
23:T:53:LEU:HB2	23:T:100:ILE:CG2	2.23	0.69
13:J:60:ARG:HD2	13:J:60:ARG:N	2.06	0.69
5:B:156:LYS:O	5:B:156:LYS:HD3	1.93	0.69
9:F:30:LEU:HD11	9:F:63:TYR:CD1	2.27	0.69
12:I:89:ASN:ND2	12:I:91:ASP:HB2	2.07	0.69
1:A:393:A:O2'	1:A:394:G:H5'	1.91	0.68
6:C:23:TYR:CD2	6:C:23:TYR:C	2.71	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:87:GLY:HA2	15:L:98:TYR:HA	1.74	0.68
22:S:44:MET:O	22:S:47:HIS:HB2	1.94	0.68
1:A:975:A:O5'	1:A:976:G:H5'	1.93	0.68
1:A:1030(A):G:H1'	1:A:1031:G:H22	1.57	0.68
20:Q:68:ARG:H	20:Q:70:ARG:NH1	1.91	0.68
1:A:920:U:H2'	1:A:921:U:C6	2.28	0.68
1:A:1020:U:H2'	1:A:1021:G:C8	2.27	0.68
5:B:23:ARG:HH12	5:B:191:ASP:HA	1.58	0.68
7:D:142:PRO:HG2	7:D:187:ARG:NH2	2.07	0.68
13:J:10:GLY:N	13:J:16:LEU:HD21	2.08	0.68
1:A:425:G:O2'	1:A:426:G:H5'	1.94	0.68
1:A:977:A:C2'	1:A:978:A:H5''	2.24	0.68
1:A:1250:A:H5''	12:I:68:GLY:N	2.09	0.68
1:A:175:C:H2'	1:A:176:C:H6	1.59	0.68
1:A:1051:C:H2'	1:A:1052:U:H6	1.57	0.68
7:D:3:ARG:HB3	7:D:3:ARG:NH1	2.09	0.68
7:D:98:GLU:HG2	7:D:189:PRO:HG3	1.76	0.68
8:E:103:GLY:O	8:E:106:PRO:HD2	1.94	0.68
15:L:93:LEU:CD1	15:L:96:VAL:HG21	2.24	0.68
16:M:88:ARG:HH11	22:S:3:ARG:HH21	1.38	0.68
17:N:27:CYS:SG	17:N:29:ARG:HB2	2.32	0.68
22:S:20:LEU:HA	22:S:23:ASN:ND2	2.07	0.68
5:B:209:ARG:HE	5:B:239:VAL:HG11	1.58	0.68
15:L:27:LEU:C	15:L:29:GLY:N	2.48	0.68
21:R:53:ARG:HD2	21:R:58:LEU:O	1.93	0.68
1:A:528:C:H41	15:L:49:ASN:ND2	1.89	0.68
5:B:9:GLU:HG2	5:B:10:LEU:N	2.09	0.68
6:C:10:PHE:CZ	6:C:178:LEU:HD13	2.29	0.68
7:D:25:ARG:C	7:D:27:TYR:N	2.49	0.68
8:E:77:PRO:O	8:E:78:HIS:HB3	1.92	0.68
21:R:52:PRO:O	21:R:56:THR:HG23	1.93	0.68
23:T:56:MET:HE1	23:T:104:LEU:HG	1.75	0.68
1:A:1057:G:H5''	6:C:154:SER:HB2	1.76	0.68
16:M:117:VAL:HG12	16:M:118:ALA:H	1.59	0.68
18:O:39:LEU:HD23	18:O:39:LEU:C	2.19	0.68
22:S:80:TYR:CD2	22:S:81:ARG:N	2.62	0.68
1:A:75:G:O2'	1:A:76:C:H5'	1.95	0.67
1:A:731:G:O2'	1:A:732:C:H5'	1.94	0.67
1:A:620:C:N1	7:D:135:LEU:HD13	2.09	0.67
5:B:128:GLU:HA	5:B:135:GLN:NE2	2.10	0.67
7:D:3:ARG:HB3	7:D:3:ARG:HH11	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:16:ALA:CB	18:O:21:ASP:HB3	2.24	0.67
5:B:178:ARG:HH21	5:B:196:LEU:CA	2.06	0.67
8:E:144:THR:O	8:E:148:VAL:HG23	1.94	0.67
11:H:85:ARG:HD3	11:H:86:ILE:N	2.09	0.67
15:L:47:LYS:CB	15:L:48:PRO:CD	2.72	0.67
19:P:28:ARG:HG2	19:P:29:ASP:OD1	1.94	0.67
20:Q:97:SER:OG	20:Q:103:GLY:HA2	1.95	0.67
23:T:70:SER:HA	23:T:73:HIS:CD2	2.30	0.67
1:A:1226:C:H5'	16:M:103:THR:OG1	1.94	0.67
14:K:99:GLN:HA	14:K:105:VAL:HG21	1.76	0.67
19:P:10:GLY:HA3	19:P:14:ASN:O	1.94	0.67
12:I:128:ARG:HG2	12:I:128:ARG:OXT	1.95	0.67
15:L:110:VAL:O	15:L:122:THR:HG22	1.93	0.67
1:A:1003(A):G:C2'	1:A:1004:A:H4'	2.24	0.67
1:A:1016:A:H2'	1:A:1017:G:O4'	1.93	0.67
1:A:1319:A:H5'	1:A:1320:C:OP1	1.94	0.67
9:F:30:LEU:HB3	9:F:35:ALA:HB3	1.75	0.67
22:S:24:ALA:HB3	22:S:25:LYS:NZ	2.10	0.67
1:A:954:G:H2'	1:A:955:U:H6	1.60	0.67
1:A:1065:U:H4'	1:A:1066:C:O5'	1.94	0.67
1:A:1229:A:H2'	1:A:1230:C:H6	1.60	0.67
1:A:1329:A:O2'	1:A:1330:U:H5'	1.95	0.67
10:G:23:VAL:HG12	10:G:27:ILE:HD11	1.77	0.67
15:L:43:VAL:HG12	15:L:44:THR:H	1.59	0.67
23:T:39:LYS:HD2	23:T:55:ILE:HD12	1.76	0.67
1:A:452:A:O2'	1:A:453:A:H8	1.78	0.66
1:A:1480:G:H2'	1:A:1481:U:C6	2.30	0.66
7:D:23:GLY:O	7:D:27:TYR:HD1	1.78	0.66
1:A:1224:G:H2'	22:S:78:ARG:HH22	1.60	0.66
6:C:191:THR:HG21	6:C:193:TYR:CE2	2.29	0.66
9:F:91:VAL:HG12	9:F:92:LYS:N	2.10	0.66
20:Q:60:ILE:HD13	20:Q:61:GLU:N	2.10	0.66
23:T:90:GLN:O	23:T:93:GLU:HB2	1.94	0.66
24:V:12:LYS:HG3	24:V:17:THR:OG1	1.95	0.66
5:B:139:LYS:O	5:B:143:GLU:HG2	1.95	0.66
11:H:118:VAL:C	11:H:119:LEU:HD23	2.19	0.66
12:I:8:GLY:CA	12:I:79:LEU:HD12	2.23	0.66
13:J:15:THR:HG23	13:J:94:VAL:HG22	1.77	0.66
18:O:56:LEU:HA	18:O:59:MET:CE	2.26	0.66
1:A:1381:U:O2'	1:A:1382:C:H5'	1.94	0.66
12:I:47:LEU:C	12:I:49:PRO:HD2	2.20	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:30:LYS:C	7:D:32:ALA:N	2.49	0.66
13:J:10:GLY:H	13:J:16:LEU:HD11	1.60	0.66
14:K:87:THR:HG23	14:K:91:ARG:NH2	2.10	0.66
17:N:9:LYS:O	17:N:9:LYS:HD3	1.95	0.66
1:A:1086:U:H3	1:A:1099:G:H22	1.43	0.66
6:C:19:GLU:HB3	6:C:40:ARG:HH21	1.60	0.66
10:G:51:GLN:C	10:G:53:LYS:H	2.03	0.66
1:A:939:G:H5''	10:G:102:ARG:NH1	2.10	0.66
1:A:1057:G:O2'	1:A:1058:G:H5'	1.96	0.66
18:O:88:ARG:HH11	18:O:88:ARG:HA	1.60	0.66
21:R:26:LEU:HD23	21:R:29:PHE:CE2	2.31	0.66
22:S:85:LYS:HE3	22:S:85:LYS:N	2.09	0.66
5:B:223:ILE:C	5:B:225:ALA:H	2.03	0.66
16:M:19:LEU:HA	16:M:22:ILE:HD13	1.78	0.66
1:A:376:G:H2'	1:A:377:G:H8	1.61	0.66
5:B:102:LEU:HD21	5:B:162:ILE:CD1	2.26	0.66
11:H:10:LEU:HD22	11:H:83:ILE:HD11	1.78	0.66
12:I:111:ARG:HH11	12:I:111:ARG:HB3	1.60	0.66
15:L:117:ARG:NH2	15:L:124:LYS:HA	2.10	0.66
23:T:97:ALA:O	23:T:99:LEU:N	2.26	0.66
1:A:457:C:H2'	1:A:458:C:C6	2.31	0.65
1:A:1001:A:H2'	1:A:1002:G:C8	2.31	0.65
6:C:108:ASN:ND2	6:C:111:LEU:HG	2.10	0.65
7:D:162:LEU:HD13	7:D:181:MET:HE2	1.76	0.65
12:I:114:TYR:CE1	13:J:60:ARG:HB2	2.31	0.65
13:J:6:ILE:HB	13:J:72:VAL:HB	1.77	0.65
22:S:52:TYR:HA	22:S:56:GLN:O	1.94	0.65
12:I:5:TYR:O	12:I:84:ALA:HA	1.95	0.65
13:J:51:ARG:NH2	13:J:61:GLU:HB2	2.11	0.65
16:M:40:ASN:HB3	16:M:43:THR:HG23	1.78	0.65
18:O:39:LEU:HD22	18:O:56:LEU:HD13	1.78	0.65
19:P:69:THR:O	19:P:72:ARG:HB3	1.96	0.65
1:A:393:A:OP2	19:P:12:LYS:HE2	1.96	0.65
7:D:112:VAL:HG23	7:D:161:ASN:HD21	1.61	0.65
22:S:22:LEU:HD22	22:S:28:LYS:HD2	1.78	0.65
1:A:1369:C:H2'	1:A:1370:G:C8	2.31	0.65
16:M:102:ARG:NH1	16:M:102:ARG:HB2	2.11	0.65
18:O:77:ARG:O	18:O:80:ALA:HB3	1.95	0.65
23:T:13:LEU:HD12	23:T:14:LYS:N	2.11	0.65
1:A:1298:C:C4	10:G:114:ARG:HD3	2.31	0.65
7:D:10:ARG:HH11	7:D:10:ARG:HG3	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:72:GLN:O	8:E:73:ASN:HB3	1.95	0.65
1:A:129(A):G:O2'	1:A:130:A:OP2	2.14	0.65
1:A:1002:G:H2'	1:A:1003:G:C8	2.31	0.65
1:A:1178:G:N2	1:A:1180:A:H3'	2.12	0.65
1:A:1330:U:OP1	16:M:23:TYR:O	2.15	0.65
1:A:1426:C:H2'	1:A:1427:U:C6	2.31	0.65
5:B:134:GLU:C	5:B:136:VAL:H	2.04	0.65
13:J:16:LEU:CD2	13:J:94:VAL:HG13	2.26	0.65
15:L:46:LYS:HE3	15:L:47:LYS:HG3	1.78	0.65
1:A:992:U:H4'	1:A:993:G:O5'	1.96	0.65
1:A:1152:A:H2'	1:A:1153:C:C6	2.32	0.65
21:R:33:ASP:OD2	21:R:36:ASN:HB2	1.96	0.65
1:A:149:A:H2'	1:A:150:C:C6	2.30	0.65
1:A:338:A:H2'	1:A:339:C:C6	2.32	0.65
1:A:491:G:H2'	1:A:492:G:H8	1.62	0.65
1:A:1038:C:H2'	1:A:1039:C:C6	2.31	0.65
15:L:53:ARG:NH1	15:L:92:ASP:OD2	2.30	0.65
18:O:74:ASP:OD1	18:O:76:GLU:HB3	1.97	0.65
1:A:624:C:H2'	1:A:625:G:H8	1.62	0.65
1:A:1031:G:H2'	1:A:1032:G:H8	1.60	0.65
12:I:4:TYR:CG	12:I:88:TYR:HB2	2.31	0.65
1:A:860:A:H2'	1:A:861:G:O4'	1.97	0.65
1:A:1226:C:O2	22:S:83:HIS:CE1	2.50	0.65
11:H:104:ARG:NH2	11:H:138:TRP:CH2	2.65	0.65
12:I:93:ARG:HB3	12:I:97:LYS:CE	2.23	0.65
14:K:54:ARG:O	14:K:57:THR:CG2	2.45	0.65
20:Q:26:GLN:O	20:Q:27:PHE:HB3	1.97	0.65
1:A:405:U:H3'	1:A:406:G:H5'	1.79	0.64
1:A:1047:G:H5''	17:N:4:LYS:HG3	1.79	0.64
5:B:98:LEU:O	5:B:101:MET:HG3	1.97	0.64
6:C:55:VAL:O	6:C:55:VAL:HG12	1.96	0.64
1:A:1202:G:O2'	1:A:1203:C:H5'	1.97	0.64
10:G:15:ASP:HB3	10:G:19:GLY:H	1.61	0.64
10:G:70:LYS:HG2	10:G:100:ALA:HB2	1.79	0.64
1:A:141:A:H1'	1:A:182:U:O2	1.96	0.64
1:A:260:G:H2'	1:A:261:U:C6	2.32	0.64
1:A:458:C:H2'	1:A:459:G:H8	1.61	0.64
1:A:1010:G:H2'	1:A:1011:G:H8	1.63	0.64
1:A:1056:U:H5'	6:C:163:ALA:HB2	1.79	0.64
6:C:107:GLN:O	6:C:108:ASN:HB3	1.95	0.64
6:C:138:VAL:HG22	6:C:151:VAL:HG23	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:97:PHE:HB2	21:R:32:ARG:HH21	1.62	0.64
5:B:18:GLY:CA	5:B:41:ILE:HA	2.25	0.64
7:D:101:LEU:HD23	7:D:101:LEU:C	2.22	0.64
12:I:120:ARG:O	12:I:122:ALA:N	2.30	0.64
19:P:28:ARG:HG2	19:P:28:ARG:HH11	1.62	0.64
1:A:113:G:H1'	1:A:354:G:H5'	1.80	0.64
5:B:98:LEU:HG	5:B:101:MET:HE3	1.79	0.64
6:C:110:ASN:O	6:C:111:LEU:HD23	1.97	0.64
7:D:145:GLU:C	7:D:146:ILE:HD12	2.23	0.64
8:E:13:ILE:HG22	8:E:30:ALA:HB2	1.78	0.64
14:K:87:THR:HG22	14:K:88:GLY:H	1.61	0.64
16:M:37:THR:O	16:M:39:ILE:HG13	1.98	0.64
1:A:677:U:H3	1:A:713:G:H22	1.43	0.64
5:B:223:ILE:O	5:B:225:ALA:N	2.26	0.64
10:G:50:ILE:O	10:G:54:THR:HB	1.98	0.64
1:A:1001:A:H2'	1:A:1002:G:H8	1.62	0.64
1:A:1068:G:N7	1:A:1094:G:H2'	2.13	0.64
5:B:77:ALA:CB	5:B:211:ILE:HD13	2.27	0.64
15:L:45:PRO:HD3	15:L:51:ALA:O	1.98	0.64
6:C:110:ASN:HD21	6:C:140:ARG:HB3	1.62	0.64
10:G:67:GLU:HA	10:G:70:LYS:HE2	1.79	0.64
12:I:79:LEU:HD11	12:I:83:ARG:HD2	1.79	0.64
15:L:83:VAL:HG21	15:L:100:ILE:HD13	1.79	0.64
16:M:54:VAL:O	16:M:58:GLU:HG2	1.98	0.64
1:A:287:U:O2'	1:A:288:A:H5'	1.98	0.64
1:A:397:A:H5'	1:A:398:C:OP1	1.98	0.64
1:A:1145:C:O2'	1:A:1146:A:H8	1.79	0.64
6:C:64:VAL:HB	6:C:99:VAL:HG23	1.78	0.64
12:I:78:LYS:HD3	12:I:101:PHE:CD2	2.33	0.64
13:J:60:ARG:O	13:J:61:GLU:HB3	1.98	0.64
15:L:47:LYS:HB3	15:L:48:PRO:CD	2.28	0.64
1:A:147:G:O2'	1:A:148:G:H5'	1.98	0.64
6:C:189:ALA:HB3	6:C:196:LEU:O	1.98	0.64
18:O:33:THR:HG23	18:O:63:ARG:NH1	2.13	0.64
22:S:22:LEU:HD13	22:S:28:LYS:CB	2.27	0.64
1:A:328:C:H4'	1:A:329:A:O5'	1.97	0.63
1:A:853:G:O2'	1:A:854:G:H5'	1.98	0.63
1:A:1468:A:H2'	1:A:1469:G:O4'	1.97	0.63
6:C:188:LEU:O	6:C:189:ALA:HB2	1.97	0.63
7:D:150:GLU:H	7:D:150:GLU:CD	2.05	0.63
8:E:40:ARG:HG2	8:E:40:ARG:HH11	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:86:ILE:HD11	11:H:136:GLU:HB2	1.80	0.63
1:A:669:U:H2'	1:A:670:G:C8	2.33	0.63
1:A:1030:C:H2'	1:A:1030(A):G:H5'	1.80	0.63
1:A:1030(C):G:H2'	1:A:1030(D):A:H8	1.63	0.63
5:B:50:GLU:HG3	5:B:200:ILE:HD11	1.79	0.63
13:J:30:SER:HB3	13:J:84:GLN:NE2	2.14	0.63
16:M:36:LYS:HD2	16:M:59:TYR:OH	1.99	0.63
22:S:20:LEU:O	22:S:23:ASN:HB2	1.98	0.63
1:A:390:C:O3'	19:P:28:ARG:NH2	2.31	0.63
1:A:1054:C:O2	1:A:1054:C:C3'	2.45	0.63
6:C:62:ASP:HA	6:C:97:LYS:HG2	1.81	0.63
7:D:108:LEU:HD23	7:D:174:LEU:HD13	1.78	0.63
7:D:152:SER:O	7:D:158:ILE:HD12	1.99	0.63
11:H:31:PHE:O	11:H:35:ILE:HD12	1.98	0.63
12:I:112:LYS:HD3	12:I:112:LYS:C	2.23	0.63
6:C:134:ILE:HG22	6:C:168:ALA:HB3	1.81	0.63
8:E:93:PRO:HG2	11:H:105:ARG:NH2	2.13	0.63
10:G:87:VAL:HG13	10:G:88:PRO:HD2	1.80	0.63
14:K:84:VAL:HG21	21:R:88:LYS:HD3	1.80	0.63
23:T:10:LEU:HD12	23:T:12:ALA:HB3	1.80	0.63
1:A:1222:G:O2'	1:A:1223:C:H5'	1.99	0.63
1:A:1250:A:C4'	12:I:68:GLY:H	2.10	0.63
1:A:1333:A:H2'	1:A:1334:G:O4'	1.98	0.63
8:E:71:LEU:HD21	8:E:115:VAL:HG23	1.80	0.63
9:F:2:ARG:CZ	9:F:69:GLU:HG2	2.28	0.63
13:J:90:LEU:H	13:J:91:PRO:CD	2.06	0.63
1:A:452:A:HO2'	1:A:453:A:H8	1.45	0.63
1:A:1262:C:H2'	1:A:1263:C:H6	1.63	0.63
5:B:39:ILE:HG22	5:B:40:HIS:O	1.98	0.63
8:E:76:ILE:HG23	8:E:77:PRO:HD2	1.78	0.63
12:I:114:TYR:CD1	13:J:60:ARG:HB2	2.33	0.63
21:R:55:ARG:NH1	21:R:55:ARG:HB3	2.13	0.63
1:A:190(H):G:O2'	1:A:190(I):G:H5'	1.98	0.63
1:A:627:G:O2'	1:A:628:G:H5'	1.98	0.63
1:A:1347:G:O2'	1:A:1348:U:P	2.55	0.63
10:G:71:PRO:HD3	10:G:103:TRP:CZ3	2.33	0.63
6:C:15:THR:O	6:C:16:ARG:HB2	1.98	0.63
13:J:20:ALA:O	13:J:24:VAL:HG23	1.98	0.63
15:L:6:THR:OG1	15:L:9:GLN:HG3	1.99	0.63
1:A:353:A:H5'	1:A:353:A:C8	2.34	0.63
5:B:102:LEU:HD21	5:B:162:ILE:HD12	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:70:VAL:HG12	6:C:71:ALA:N	2.13	0.63
16:M:34:LEU:HD13	16:M:41:PRO:HA	1.79	0.63
20:Q:81:ARG:HG3	20:Q:81:ARG:O	1.97	0.63
1:A:1095:U:H2'	1:A:1096:C:H6	1.64	0.62
1:A:1370:G:O2'	1:A:1371:G:H5'	1.98	0.62
5:B:217:ARG:HA	5:B:220:ASP:OD2	1.98	0.62
6:C:77:ILE:HA	6:C:84:ILE:HB	1.80	0.62
7:D:126:ILE:HG22	7:D:127:THR:H	1.64	0.62
10:G:59:LEU:HD11	10:G:63:LYS:HE3	1.81	0.62
21:R:57:GLY:C	21:R:58:LEU:HD23	2.24	0.62
1:A:160:A:H1'	1:A:344:A:N7	2.14	0.62
1:A:186:C:O3'	23:T:82:SER:HB3	1.99	0.62
1:A:192:U:H1'	23:T:103:GLY:HA2	1.82	0.62
1:A:352:C:H4'	1:A:354:G:OP1	1.99	0.62
1:A:673:G:H2'	1:A:674:G:C8	2.34	0.62
1:A:1251:A:H4'	12:I:12:GLU:OE1	1.99	0.62
1:A:1306:A:N6	1:A:1331:G:H1'	2.14	0.62
5:B:102:LEU:HB3	5:B:180:LEU:HD12	1.81	0.62
13:J:81:THR:C	13:J:83:GLU:H	2.07	0.62
20:Q:63:ARG:HG2	20:Q:64:PRO:N	2.13	0.62
1:A:107:G:C2'	1:A:108:G:H5'	2.29	0.62
1:A:838:G:H2'	1:A:839:U:H5''	1.80	0.62
1:A:1250:A:H4'	12:I:68:GLY:N	2.14	0.62
15:L:115:LYS:O	15:L:117:ARG:N	2.32	0.62
17:N:3:ARG:CZ	17:N:6:LEU:HD11	2.29	0.62
1:A:258:G:H2'	1:A:259:G:H8	1.64	0.62
1:A:528:C:H5'	1:A:535:A:C6	2.34	0.62
1:A:960:U:O2	1:A:960:U:H2'	1.98	0.62
1:A:1513:A:H2'	1:A:1514:C:C6	2.34	0.62
6:C:47:LEU:H	6:C:47:LEU:CD1	2.13	0.62
12:I:25:LYS:HG2	12:I:60:ASP:OD2	1.99	0.62
12:I:100:GLY:O	12:I:102:LEU:N	2.30	0.62
14:K:80:VAL:HG21	14:K:103:LEU:HD13	1.81	0.62
17:N:14:PRO:O	17:N:15:LYS:HB3	1.99	0.62
1:A:1221:G:O3'	22:S:77:THR:HG21	1.98	0.62
1:A:1438:G:H2'	1:A:1439:C:C6	2.35	0.62
5:B:98:LEU:HD23	5:B:98:LEU:N	2.15	0.62
8:E:12:LEU:CD1	8:E:31:LEU:HB2	2.30	0.62
18:O:56:LEU:HA	18:O:59:MET:HE2	1.81	0.62
20:Q:68:ARG:H	20:Q:70:ARG:HH11	1.47	0.62
1:A:344:A:H4'	1:A:345:C:OP2	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:C:O2'	1:A:387:U:H5'	1.99	0.62
1:A:967:C:C4'	12:I:128:ARG:HG3	2.29	0.62
6:C:191:THR:CG2	6:C:192:THR:H	2.12	0.62
11:H:134:ILE:HG22	11:H:135:CYS:N	2.14	0.62
21:R:61:LYS:O	21:R:65:ILE:HG13	2.00	0.62
1:A:357:G:O2'	1:A:358:U:H5'	2.00	0.62
1:A:761:G:H5''	20:Q:102:GLY:HA3	1.79	0.62
1:A:1072:G:H2'	1:A:1073:U:C6	2.33	0.62
14:K:24:SER:C	14:K:26:ASN:H	2.08	0.62
23:T:96:GLY:O	23:T:97:ALA:CB	2.47	0.62
1:A:390:C:H2'	1:A:391:G:H8	1.63	0.62
5:B:124:SER:O	5:B:127:ILE:HG13	1.99	0.62
5:B:185:ILE:HD12	5:B:185:ILE:H	1.65	0.62
11:H:138:TRP:CE3	11:H:138:TRP:OXT	2.53	0.62
17:N:32:SER:HB2	17:N:41:ARG:HB3	1.81	0.62
1:A:192:U:C1'	23:T:103:GLY:HA2	2.30	0.62
1:A:371:G:C2'	1:A:372:C:H5'	2.30	0.62
5:B:84:GLU:OE1	5:B:216:SER:HA	1.99	0.62
15:L:24:VAL:O	15:L:26:ALA:N	2.31	0.62
1:A:190(F):G:H4'	1:A:190(G):G:OP2	1.99	0.61
8:E:36:ASP:O	8:E:37:ARG:HB2	1.99	0.61
13:J:51:ARG:CZ	13:J:61:GLU:HB2	2.30	0.61
15:L:57:LYS:HD3	15:L:67:THR:HB	1.82	0.61
16:M:49:THR:HG22	16:M:51:ALA:N	2.06	0.61
16:M:50:GLU:O	16:M:54:VAL:HG23	1.99	0.61
16:M:62:ASN:O	16:M:63:THR:HB	1.99	0.61
23:T:87:LYS:O	23:T:88:VAL:C	2.42	0.61
1:A:1152:A:H5'	13:J:70:ARG:NH2	2.15	0.61
1:A:1527:C:O2'	1:A:1528:U:H5'	1.99	0.61
7:D:176:LEU:HA	7:D:183:GLY:HA2	1.82	0.61
10:G:122:HIS:HA	10:G:125:MET:HE3	1.82	0.61
14:K:72:ALA:HB1	14:K:77:MET:HG3	1.81	0.61
1:A:1112:C:N3	6:C:178:LEU:N	2.47	0.61
1:A:1161:C:H2'	1:A:1162:C:C6	2.34	0.61
1:A:1226:C:C5	16:M:104:ARG:HA	2.35	0.61
2:X:2:U:H2'	2:X:3:U:H5'	1.82	0.61
12:I:49:PRO:HD3	12:I:78:LYS:HG2	1.82	0.61
15:L:34:ARG:O	15:L:61:THR:HG23	1.99	0.61
22:S:40:ILE:HG21	22:S:62:ILE:CD1	2.30	0.61
1:A:187:C:O2	23:T:105:SER:HB3	2.01	0.61
1:A:560:U:O2'	1:A:561:U:OP2	2.11	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:580:U:H2'	1:A:581:G:O4'	1.99	0.61
1:A:689:C:P	14:K:46:GLY:HA3	2.41	0.61
1:A:1148:U:H2'	1:A:1149:C:O4'	2.00	0.61
5:B:126:GLU:O	5:B:129:GLU:HB3	2.01	0.61
6:C:19:GLU:HG2	6:C:54:ARG:HE	1.65	0.61
8:E:33:VAL:HG11	8:E:109:ILE:HA	1.82	0.61
12:I:19:LEU:HD23	12:I:61:ALA:HB2	1.83	0.61
1:A:839:U:H5'	1:A:840:C:H5	1.65	0.61
1:A:840:C:H5''	1:A:841:U:OP1	2.00	0.61
1:A:1296:C:H4'	1:A:1302:U:C5	2.36	0.61
6:C:47:LEU:N	6:C:47:LEU:HD12	2.15	0.61
7:D:3:ARG:H	7:D:3:ARG:CZ	2.14	0.61
9:F:18:GLN:O	9:F:21:LEU:HB3	2.00	0.61
12:I:48:GLU:N	12:I:49:PRO:HD2	2.15	0.61
6:C:6:HIS:CD2	6:C:9:GLY:H	2.16	0.61
6:C:52:LEU:H	6:C:52:LEU:CD2	2.13	0.61
11:H:60:ARG:HH11	11:H:60:ARG:HG3	1.65	0.61
12:I:104:ARG:C	12:I:104:ARG:HD3	2.24	0.61
23:T:97:ALA:O	23:T:99:LEU:HG	2.01	0.61
1:A:501:C:H2'	1:A:502:G:C8	2.33	0.61
1:A:1202:G:C2'	1:A:1203:C:H5'	2.31	0.61
1:A:1325:C:O3'	24:V:17:THR:HG21	2.01	0.61
9:F:67:MET:CE	9:F:72:VAL:HA	2.30	0.61
9:F:99:ALA:HB2	21:R:31:LEU:CD1	2.31	0.61
10:G:51:GLN:O	10:G:53:LYS:N	2.34	0.61
18:O:7:GLU:O	18:O:11:VAL:HG23	2.00	0.61
20:Q:5:VAL:O	20:Q:6:LEU:HD23	2.00	0.61
22:S:87:ALA:O	22:S:88:LYS:HB3	2.00	0.61
1:A:386:C:C2'	1:A:387:U:H5'	2.30	0.61
1:A:496:A:H4'	1:A:497:A:OP1	1.98	0.61
1:A:958:A:C8	22:S:55:LYS:HD2	2.36	0.61
1:A:975:A:H5'	1:A:975:A:H8	1.65	0.61
1:A:1002:G:H2'	1:A:1003:G:H8	1.66	0.61
1:A:1250:A:H5''	12:I:68:GLY:H	1.63	0.61
1:A:545:C:O2'	1:A:546:G:H5'	2.01	0.61
1:A:939:G:H5''	10:G:102:ARG:CZ	2.31	0.61
1:A:1056:U:C5'	6:C:163:ALA:HB2	2.31	0.61
9:F:75:LEU:O	9:F:78:GLU:HB3	2.01	0.61
12:I:90:PRO:O	12:I:93:ARG:HG3	2.01	0.61
1:A:1339:A:H2'	1:A:1340:A:O4'	2.01	0.61
6:C:70:VAL:O	6:C:106:VAL:HG23	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:20:TYR:O	7:D:21:LEU:HD23	2.01	0.61
13:J:23:ILE:HD12	13:J:23:ILE:N	2.15	0.61
13:J:82:ILE:HG22	13:J:82:ILE:O	2.00	0.61
14:K:69:ALA:O	14:K:73:MET:HG2	2.00	0.61
15:L:92:ASP:HB2	15:L:93:LEU:HD23	1.83	0.61
15:L:119:LYS:O	15:L:120:TYR:HB2	2.01	0.61
22:S:45:VAL:HG12	22:S:46:GLY:N	2.16	0.61
23:T:87:LYS:O	23:T:91:LEU:HD12	2.01	0.61
1:A:411:A:N9	1:A:413:G:H1'	2.15	0.60
8:E:44:GLY:HA3	8:E:62:ALA:HB2	1.81	0.60
12:I:17:VAL:CG2	12:I:80:GLY:HA3	2.31	0.60
15:L:28:LYS:C	15:L:30:ALA:H	2.07	0.60
16:M:4:ILE:CG2	16:M:5:ALA:N	2.61	0.60
16:M:32:GLU:OE1	16:M:64:TRP:HZ2	1.83	0.60
21:R:53:ARG:NH1	21:R:60:GLY:N	2.49	0.60
1:A:924:C:H5'	1:A:1399:C:OP2	2.02	0.60
1:A:975:A:H5'	1:A:975:A:C8	2.36	0.60
1:A:1030(D):A:H2'	1:A:1031:G:H5'	1.83	0.60
5:B:8:LYS:N	5:B:8:LYS:HD2	2.16	0.60
5:B:136:VAL:HG12	5:B:140:HIS:NE2	2.17	0.60
11:H:101:PRO:HG3	11:H:133:LEU:HD11	1.81	0.60
12:I:81:ILE:O	12:I:85:LEU:HB2	2.01	0.60
13:J:6:ILE:HG23	13:J:98:ILE:CD1	2.30	0.60
16:M:97:PRO:HB2	16:M:101:GLN:OE1	2.01	0.60
1:A:560:U:H5'	1:A:566:G:C2	2.35	0.60
1:A:1004:A:H2'	1:A:1005:A:C5'	2.25	0.60
1:A:1053:G:C4'	1:A:1054:C:H5'	2.30	0.60
16:M:5:ALA:HB3	16:M:8:GLU:CG	2.31	0.60
23:T:67:ALA:HB2	23:T:77:ALA:HB2	1.83	0.60
1:A:1281:U:H4'	1:A:1282:C:OP2	2.02	0.60
1:A:1347:G:O2'	1:A:1348:U:OP2	2.18	0.60
6:C:27:LYS:HA	6:C:30:ARG:HH12	1.64	0.60
8:E:12:LEU:HD22	8:E:12:LEU:C	2.27	0.60
8:E:115:VAL:CG1	8:E:116:THR:N	2.65	0.60
11:H:91:ARG:HG3	15:L:7:ILE:HG13	1.84	0.60
13:J:23:ILE:H	13:J:23:ILE:CD1	2.12	0.60
16:M:102:ARG:HB2	16:M:102:ARG:HH11	1.66	0.60
22:S:30:LEU:O	22:S:31:ILE:HD13	2.02	0.60
22:S:53:ASN:HD22	22:S:53:ASN:N	1.99	0.60
1:A:858:G:O2'	1:A:859:A:H5'	2.02	0.60
1:A:954:G:H2'	1:A:955:U:C6	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1207:G:H2'	1:A:1208:C:H6	1.66	0.60
5:B:115:LEU:HD21	5:B:153:ARG:CZ	2.31	0.60
5:B:228:GLY:O	5:B:229:VAL:C	2.43	0.60
9:F:82:ARG:HA	9:F:82:ARG:HE	1.67	0.60
13:J:79:ARG:O	13:J:83:GLU:HB2	2.00	0.60
17:N:11:LYS:C	17:N:13:THR:H	2.10	0.60
1:A:420:U:H2'	1:A:422:C:C5	2.36	0.60
1:A:686:U:O4	1:A:703:G:H1'	2.01	0.60
1:A:1222:G:P	22:S:77:THR:HG21	2.42	0.60
6:C:19:GLU:O	6:C:40:ARG:NH2	2.35	0.60
6:C:29:TYR:OH	17:N:54:PRO:HG2	2.01	0.60
16:M:81:LEU:O	16:M:89:GLY:HA3	2.01	0.60
21:R:48:GLY:O	21:R:74:ARG:NH2	2.35	0.60
1:A:300:A:H2'	1:A:301:G:O4'	2.02	0.60
8:E:32:VAL:O	8:E:43:LEU:HD23	2.02	0.60
20:Q:104:LYS:O	20:Q:105:ALA:HB2	2.02	0.60
22:S:15:LEU:HD21	22:S:38:SER:CB	2.31	0.60
1:A:1358:U:H3'	1:A:1359:C:H6	1.65	0.60
1:A:1426:C:H2'	1:A:1427:U:H6	1.66	0.60
5:B:129:GLU:O	5:B:130:ARG:HB2	2.02	0.60
6:C:155:GLY:O	6:C:156:ARG:HB2	2.02	0.60
7:D:59:ARG:HH22	7:D:66:ARG:NH1	2.00	0.60
11:H:97:VAL:HA	11:H:100:ILE:HG13	1.83	0.60
14:K:99:GLN:HA	14:K:105:VAL:CG2	2.30	0.60
15:L:27:LEU:O	15:L:29:GLY:N	2.34	0.60
23:T:50:GLU:HA	23:T:100:ILE:HB	1.82	0.60
1:A:1004:A:H5'	1:A:1024:G:H1	1.66	0.60
1:A:1117:G:H5'	1:A:1117:G:H8	1.67	0.60
1:A:1251:A:H2'	1:A:1252:A:C8	2.37	0.60
5:B:218:ALA:O	5:B:222:ILE:HG13	2.01	0.60
7:D:162:LEU:O	7:D:162:LEU:HD23	2.02	0.60
8:E:81:GLU:HG2	8:E:90:VAL:HG13	1.81	0.60
8:E:92:LYS:O	8:E:118:ILE:HG22	2.02	0.60
11:H:48:TYR:CD1	11:H:48:TYR:C	2.78	0.60
16:M:19:LEU:O	16:M:22:ILE:HD13	2.02	0.60
22:S:28:LYS:HG2	22:S:29:ARG:H	1.67	0.60
23:T:71:THR:O	23:T:72:LEU:HD23	2.01	0.60
1:A:1128:C:O2'	1:A:1130:A:H8	1.84	0.60
1:A:1329:A:P	16:M:28:ALA:HB3	2.41	0.60
6:C:58:GLU:HB2	6:C:65:ALA:HB2	1.84	0.60
22:S:3:ARG:HH22	22:S:69:HIS:CE1	2.18	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:T:40:ALA:HB2	23:T:55:ILE:HG22	1.83	0.60
1:A:434:U:H2'	1:A:435:C:C6	2.37	0.59
1:A:1165:C:O2'	1:A:1166:G:H5'	2.01	0.59
1:A:1195:C:H3'	1:A:1196:U:C5'	2.32	0.59
1:A:1257:U:H5'	1:A:1258:G:OP1	2.02	0.59
5:B:42:ILE:CD1	5:B:203:GLY:HA2	2.32	0.59
5:B:87:ARG:NH1	5:B:233:SER:HA	2.15	0.59
5:B:167:PRO:HG2	5:B:168:THR:H	1.66	0.59
6:C:115:LEU:HD23	6:C:118:GLN:OE1	2.01	0.59
16:M:24:GLY:HA3	16:M:66:LEU:HD22	1.84	0.59
22:S:15:LEU:HD21	22:S:38:SER:HB3	1.84	0.59
9:F:3:ARG:HH21	9:F:64:GLN:NE2	2.00	0.59
15:L:47:LYS:CB	15:L:48:PRO:HD3	2.32	0.59
23:T:54:LYS:HA	23:T:57:ARG:HH11	1.67	0.59
1:A:179:A:H2'	1:A:180:U:C6	2.37	0.59
1:A:255:G:O6	1:A:266:G:O6	2.20	0.59
1:A:867:G:O2'	1:A:868:C:H5'	2.03	0.59
1:A:1182:G:O2'	1:A:1183:A:OP2	2.18	0.59
1:A:1470:G:O2'	1:A:1471:G:H5'	2.02	0.59
10:G:85:TYR:HD1	10:G:154:TYR:HE1	1.51	0.59
1:A:664:G:H22	1:A:741:G:H1	1.49	0.59
1:A:1495:U:H2'	1:A:1496:C:C6	2.37	0.59
6:C:36:ASP:HA	6:C:39:ILE:HD12	1.83	0.59
8:E:78:HIS:HD2	11:H:107:LEU:HD22	1.67	0.59
13:J:86:MET:HA	13:J:86:MET:HE3	1.84	0.59
13:J:96:ILE:HG22	13:J:97:GLU:N	2.17	0.59
16:M:74:VAL:O	16:M:77:ASN:HB3	2.03	0.59
17:N:21:TYR:HE2	17:N:23:ARG:NE	2.01	0.59
23:T:26:ASN:HB3	23:T:71:THR:HG23	1.83	0.59
15:L:97:ARG:HB2	15:L:98:TYR:CE1	2.38	0.59
1:A:1347:G:C2'	1:A:1348:U:OP2	2.51	0.59
1:A:1412:C:H2'	1:A:1413:A:C8	2.37	0.59
6:C:12:LEU:HD11	17:N:51:GLY:HA2	1.84	0.59
6:C:25:GLY:N	6:C:28:GLN:HB2	2.15	0.59
13:J:3:LYS:N	13:J:75:ILE:HA	2.18	0.59
1:A:1128:C:O2'	1:A:1130:A:C8	2.53	0.59
1:A:1329:A:OP1	16:M:28:ALA:HB3	2.02	0.59
1:A:1413:A:H2	1:A:1487:G:H22	1.47	0.59
6:C:3:ASN:ND2	6:C:3:ASN:H	1.99	0.59
7:D:104:VAL:HG21	7:D:140:VAL:HG21	1.84	0.59
10:G:58:PRO:HG2	10:G:59:LEU:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:47:PHE:HB2	13:J:63:PHE:HB2	1.84	0.59
15:L:28:LYS:C	15:L:30:ALA:N	2.59	0.59
1:A:666:G:H5'	1:A:726:C:H1'	1.83	0.59
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.37	0.59
1:A:1241:G:H2'	1:A:1242:C:C6	2.37	0.59
5:B:103:THR:O	5:B:103:THR:HG22	2.01	0.59
5:B:180:LEU:O	5:B:181:PHE:HB2	2.02	0.59
7:D:149:ALA:HB3	7:D:152:SER:CB	2.32	0.59
1:A:1367:C:H5'	13:J:60:ARG:NH1	2.17	0.59
5:B:114:ARG:HH12	5:B:118:LEU:HD21	1.66	0.59
5:B:187:LEU:HD23	5:B:214:ILE:HG21	1.83	0.59
6:C:147:LYS:HD2	6:C:203:PHE:HE2	1.68	0.59
20:Q:68:ARG:HG2	20:Q:68:ARG:HH11	1.68	0.59
20:Q:101:ARG:HA	20:Q:101:ARG:NE	2.18	0.59
22:S:33:THR:HG22	22:S:34:TRP:N	2.17	0.59
1:A:438:G:C4'	1:A:439:A:OP1	2.49	0.59
1:A:619:U:O2	7:D:133:VAL:HA	2.03	0.59
1:A:947:G:H2'	1:A:948:C:O4'	2.03	0.59
5:B:101:MET:HA	5:B:108:ILE:HG13	1.84	0.59
5:B:140:HIS:O	5:B:143:GLU:HB2	2.03	0.59
5:B:224:GLN:O	5:B:224:GLN:HG2	2.02	0.59
12:I:93:ARG:HE	12:I:97:LYS:HE3	1.68	0.59
16:M:40:ASN:HD22	16:M:41:PRO:CD	2.16	0.59
17:N:9:LYS:HD3	17:N:9:LYS:C	2.28	0.59
1:A:46:G:H2'	1:A:366:C:C5	2.38	0.58
1:A:149:A:O2'	1:A:150:C:H5'	2.02	0.58
1:A:160:A:H2'	1:A:161:A:O4'	2.02	0.58
1:A:1052:U:H2'	1:A:1055:A:OP1	2.03	0.58
1:A:1182:G:H4'	1:A:1183:A:H5''	1.84	0.58
1:A:1329:A:C2'	1:A:1330:U:H5'	2.33	0.58
5:B:118:LEU:HD11	5:B:141:GLU:OE2	2.03	0.58
5:B:184:VAL:N	5:B:198:ASP:OD2	2.33	0.58
5:B:200:ILE:HD12	5:B:200:ILE:O	2.02	0.58
7:D:57:ARG:NH2	7:D:205:GLU:OE2	2.36	0.58
13:J:12:ASP:HB3	13:J:15:THR:HB	1.85	0.58
1:A:899:C:H2'	1:A:900:A:C8	2.37	0.58
1:A:913:A:H1'	1:A:914:A:O4'	2.02	0.58
5:B:15:VAL:O	5:B:16:HIS:O	2.21	0.58
5:B:128:GLU:HA	5:B:135:GLN:HE21	1.68	0.58
12:I:79:LEU:HD13	12:I:79:LEU:C	2.28	0.58
20:Q:10:VAL:O	20:Q:53:LEU:HD13	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:7:LYS:O	22:S:7:LYS:HD3	2.02	0.58
22:S:62:ILE:HD12	22:S:63:THR:N	2.18	0.58
1:A:403:C:H2'	1:A:404:U:H6	1.67	0.58
1:A:1149:C:H2'	1:A:1150:U:C6	2.38	0.58
6:C:174:PRO:O	6:C:177:THR:HG22	2.04	0.58
7:D:3:ARG:CZ	7:D:3:ARG:N	2.66	0.58
7:D:61:LYS:HD2	7:D:207:TYR:OH	2.04	0.58
11:H:23:SER:C	11:H:24:THR:HG22	2.28	0.58
12:I:114:TYR:CE1	13:J:59:SER:O	2.56	0.58
1:A:652:U:O4	1:A:752:G:O2'	2.20	0.58
5:B:25:ASN:HD22	5:B:27:LYS:H	1.50	0.58
5:B:130:ARG:CB	5:B:131:PRO:HD2	2.33	0.58
5:B:178:ARG:HG3	5:B:178:ARG:NH1	2.11	0.58
6:C:47:LEU:HD23	6:C:68:VAL:HG11	1.85	0.58
6:C:131:ARG:O	6:C:135:LYS:HG3	2.04	0.58
12:I:78:LYS:HD3	12:I:101:PHE:HD2	1.68	0.58
18:O:41:GLU:HA	18:O:44:LYS:HG2	1.85	0.58
19:P:52:ASP:O	19:P:52:ASP:OD1	2.21	0.58
20:Q:69:LYS:O	20:Q:70:ARG:HD2	2.03	0.58
22:S:45:VAL:HA	22:S:62:ILE:HG13	1.85	0.58
1:A:481:G:O2'	1:A:483:C:N4	2.37	0.58
1:A:1226:C:O2	22:S:83:HIS:NE2	2.36	0.58
6:C:64:VAL:HG12	6:C:66:VAL:HG23	1.85	0.58
11:H:109:ILE:HG13	11:H:110:ALA:N	2.18	0.58
14:K:123:LYS:O	14:K:124:LYS:C	2.47	0.58
17:N:37:PHE:CE2	17:N:53:LEU:HD13	2.39	0.58
1:A:21:G:H2'	1:A:22:G:C8	2.39	0.58
1:A:613:C:O2'	1:A:614:A:H5'	2.02	0.58
1:A:691:G:O2'	1:A:797:C:H4'	2.03	0.58
1:A:1158:C:H5''	5:B:133:LYS:HE3	1.85	0.58
8:E:122:GLU:OE1	8:E:131:ILE:HG13	2.03	0.58
9:F:75:LEU:C	9:F:75:LEU:HD13	2.29	0.58
11:H:103:VAL:HG21	11:H:110:ALA:HB2	1.86	0.58
16:M:23:TYR:HB2	16:M:67:GLU:OE2	2.03	0.58
22:S:25:LYS:HD2	22:S:25:LYS:N	2.19	0.58
22:S:28:LYS:HG2	22:S:29:ARG:N	2.17	0.58
1:A:961:U:O2'	1:A:962:C:H5'	2.03	0.58
1:A:1091:U:O2	1:A:1093:A:C8	2.57	0.58
1:A:1138:G:C6	1:A:1140:C:H1'	2.38	0.58
9:F:10:LEU:HD11	9:F:59:TYR:HD2	1.69	0.58
10:G:23:VAL:CG1	10:G:27:ILE:HD11	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:79:LEU:CD1	12:I:83:ARG:HD2	2.34	0.58
13:J:31:GLY:HA2	13:J:78:ASN:ND2	2.19	0.58
15:L:88:GLY:H	15:L:98:TYR:HA	1.69	0.58
20:Q:66:SER:O	20:Q:70:ARG:NH1	2.37	0.58
1:A:254:G:O2'	1:A:255:G:H5'	2.04	0.58
1:A:256:U:H2'	1:A:257:G:C8	2.39	0.58
1:A:284:G:H2'	1:A:285:G:H8	1.69	0.58
1:A:403:C:O2'	1:A:404:U:H5'	2.04	0.58
1:A:915:A:H2'	1:A:916:G:H5'	1.84	0.58
1:A:939:G:H2'	1:A:940:C:C6	2.39	0.58
1:A:977:A:H2'	1:A:978:A:C5'	2.32	0.58
1:A:1320:C:N3	22:S:36:ARG:HG3	2.19	0.58
5:B:68:ILE:N	5:B:90:MET:HE3	2.16	0.58
6:C:29:TYR:CZ	17:N:54:PRO:HG2	2.39	0.58
1:A:882:C:O2'	1:A:883:C:H5'	2.03	0.58
1:A:1030(A):G:H1'	1:A:1031:G:N2	2.19	0.58
1:A:1053:G:C3'	1:A:1054:C:H5'	2.34	0.58
1:A:1366:C:H2'	1:A:1367:C:C6	2.34	0.58
1:A:1495:U:H2'	1:A:1496:C:H6	1.69	0.58
5:B:28:PHE:CE1	5:B:189:ASP:HA	2.39	0.58
7:D:132:ARG:O	7:D:133:VAL:HG23	2.04	0.58
13:J:51:ARG:HB3	13:J:59:SER:HB3	1.86	0.58
13:J:94:VAL:HG12	13:J:95:GLU:H	1.66	0.58
16:M:60:VAL:HG22	16:M:64:TRP:CZ3	2.39	0.58
16:M:81:LEU:O	16:M:86:CYS:HB3	2.03	0.58
19:P:67:THR:HG22	19:P:68:ASP:N	2.19	0.58
1:A:1423:G:O2'	1:A:1424:C:H5'	2.03	0.58
5:B:19:HIS:HB3	5:B:189:ASP:OD2	2.04	0.58
5:B:100:GLY:O	5:B:104:ASN:N	2.36	0.58
7:D:174:LEU:O	7:D:186:LEU:HD11	2.03	0.58
8:E:15:ARG:O	8:E:27:ARG:O	2.22	0.58
12:I:114:TYR:H	12:I:114:TYR:HD2	1.51	0.58
15:L:61:THR:C	15:L:63:GLY:H	2.12	0.58
18:O:50:HIS:O	18:O:53:HIS:N	2.37	0.58
18:O:87:ILE:O	18:O:88:ARG:HB2	2.04	0.58
5:B:142:LEU:HD22	5:B:146:GLN:HE22	1.68	0.57
7:D:8:VAL:O	7:D:10:ARG:N	2.37	0.57
7:D:146:ILE:N	7:D:146:ILE:CD1	2.67	0.57
9:F:101:ALA:HA	21:R:28:GLU:HG3	1.85	0.57
10:G:146:GLU:HA	10:G:149:ARG:HG2	1.85	0.57
11:H:1:MET:HG2	11:H:2:LEU:N	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:63:LEU:HD22	11:H:63:LEU:N	2.17	0.57
12:I:33:PHE:C	12:I:35:GLU:H	2.12	0.57
16:M:29:ARG:HB3	16:M:64:TRP:CH2	2.39	0.57
18:O:53:HIS:O	18:O:56:LEU:HB3	2.03	0.57
19:P:21:VAL:HG21	19:P:59:TRP:CD1	2.39	0.57
20:Q:67:LYS:O	20:Q:68:ARG:HB2	2.03	0.57
1:A:993:G:H4'	1:A:994:A:OP2	2.04	0.57
1:A:1132:C:H2'	1:A:1133:G:C8	2.38	0.57
1:A:1277:C:H2'	1:A:1278:U:C5'	2.33	0.57
1:A:1407:C:O2'	1:A:1408:A:H5'	2.04	0.57
7:D:191:ARG:O	7:D:191:ARG:HD2	2.03	0.57
10:G:21:VAL:HG23	10:G:22:LEU:N	2.19	0.57
18:O:70:LEU:HD12	18:O:78:TYR:CA	2.34	0.57
22:S:15:LEU:C	22:S:15:LEU:HD12	2.29	0.57
23:T:48:LYS:O	23:T:52:ALA:HB2	2.05	0.57
1:A:1154:G:H2'	1:A:1155:G:H8	1.69	0.57
1:A:1250:A:C5'	12:I:68:GLY:H	2.17	0.57
6:C:130:VAL:O	6:C:134:ILE:HG13	2.04	0.57
8:E:111:GLU:C	8:E:113:ALA:H	2.11	0.57
1:A:6:G:H4'	1:A:298:A:H4'	1.87	0.57
1:A:26:A:N6	1:A:558:G:H1'	2.20	0.57
1:A:457:C:H2'	1:A:458:C:H6	1.67	0.57
5:B:45:GLN:CD	5:B:45:GLN:H	2.12	0.57
8:E:144:THR:HG22	8:E:146:ALA:H	1.69	0.57
10:G:12:LEU:HD12	10:G:12:LEU:N	2.19	0.57
10:G:140:ASP:O	10:G:143:ARG:HB2	2.03	0.57
14:K:110:ASP:HB2	21:R:88:LYS:HD2	1.86	0.57
22:S:13:ASP:O	22:S:16:LEU:HB3	2.04	0.57
22:S:30:LEU:C	22:S:31:ILE:HD13	2.29	0.57
1:A:190(J):U:H2'	1:A:190(K):G:C8	2.40	0.57
1:A:1007:C:N4	1:A:1022:G:H1	2.02	0.57
1:A:1106:G:H5''	6:C:172:ARG:HG2	1.87	0.57
6:C:77:ILE:O	6:C:83:ARG:HB3	2.05	0.57
16:M:23:TYR:CB	16:M:67:GLU:HA	2.35	0.57
20:Q:97:SER:CB	20:Q:103:GLY:HA2	2.34	0.57
1:A:178:C:O2'	1:A:179:A:H5'	2.04	0.57
1:A:413:G:H22	1:A:428:G:H1'	1.70	0.57
1:A:1104:G:O5'	5:B:111:ARG:HD2	2.04	0.57
1:A:1277:C:O2'	1:A:1279:A:H1'	2.05	0.57
1:A:1522:U:O2'	1:A:1523:G:H5'	2.05	0.57
5:B:186:ALA:HB3	5:B:197:VAL:HG11	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:90:GLU:C	6:C:92:ALA:H	2.11	0.57
10:G:85:TYR:O	10:G:87:VAL:HG23	2.05	0.57
20:Q:8:GLY:HA3	20:Q:21:VAL:HG12	1.87	0.57
22:S:20:LEU:HD12	22:S:21:GLU:H	1.70	0.57
23:T:96:GLY:O	23:T:97:ALA:HB3	2.02	0.57
1:A:833:U:H2'	1:A:834:C:C6	2.38	0.57
1:A:839:U:H5'	1:A:840:C:C5	2.39	0.57
1:A:1097:C:H2'	1:A:1098:C:C6	2.39	0.57
1:A:1360:A:H2'	1:A:1361:G:O4'	2.05	0.57
6:C:70:VAL:HG12	6:C:71:ALA:H	1.67	0.57
7:D:128:VAL:HG12	7:D:129:ASN:HD21	1.69	0.57
12:I:29:ASN:HD21	12:I:64:THR:CA	2.15	0.57
13:J:49:VAL:O	13:J:60:ARG:HA	2.05	0.57
14:K:108:ILE:HB	21:R:87:ARG:O	2.05	0.57
1:A:337:C:H2'	1:A:338:A:H8	1.69	0.57
1:A:682:G:O2'	1:A:683:G:H5'	2.05	0.57
7:D:26:CYS:HA	7:D:31:CYS:HB2	1.86	0.57
11:H:10:LEU:CD2	11:H:83:ILE:HD11	2.35	0.57
12:I:23:ASN:HD22	12:I:23:ASN:C	2.12	0.57
13:J:63:PHE:CZ	17:N:45:ARG:HG3	2.40	0.57
15:L:98:TYR:N	15:L:98:TYR:CD1	2.72	0.57
16:M:60:VAL:HG22	16:M:64:TRP:HZ3	1.70	0.57
19:P:18:ARG:HE	19:P:35:LYS:NZ	2.03	0.57
1:A:1042:G:O2'	1:A:1043:C:H5'	2.04	0.57
5:B:178:ARG:O	5:B:181:PHE:N	2.28	0.57
6:C:46:GLU:O	6:C:48:TYR:N	2.36	0.57
6:C:59:ARG:HH11	6:C:97:LYS:HZ2	1.52	0.57
7:D:65:ARG:HB2	7:D:75:PHE:CD1	2.40	0.57
10:G:69:VAL:HG12	10:G:103:TRP:HE3	1.70	0.57
10:G:78:ARG:NH1	10:G:154:TYR:O	2.38	0.57
13:J:8:LEU:CD2	13:J:96:ILE:HG12	2.35	0.57
14:K:21:ILE:HG12	14:K:30:VAL:HG12	1.87	0.57
14:K:48:ILE:HD12	14:K:63:LEU:CB	2.34	0.57
21:R:36:ASN:O	21:R:39:VAL:HG12	2.05	0.57
1:A:227:G:O2'	19:P:62:VAL:HG11	2.05	0.57
1:A:1221:G:H4'	22:S:53:ASN:O	2.04	0.57
5:B:178:ARG:HH11	5:B:178:ARG:CG	2.14	0.57
8:E:51:VAL:HB	8:E:52:PRO:CD	2.28	0.57
10:G:139:GLU:O	10:G:143:ARG:HG3	2.05	0.57
12:I:36:TYR:CD2	12:I:37:PHE:CE2	2.93	0.57
13:J:12:ASP:HB3	13:J:15:THR:CG2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:86:ARG:HG3	15:L:86:ARG:NH1	2.18	0.57
1:A:1229:A:H2'	1:A:1230:C:C6	2.38	0.56
1:A:1277:C:H1'	1:A:1282:C:O2	2.05	0.56
6:C:47:LEU:H	6:C:47:LEU:HD12	1.70	0.56
8:E:77:PRO:O	8:E:78:HIS:CB	2.53	0.56
9:F:9:VAL:HG22	9:F:60:PHE:CD2	2.39	0.56
14:K:84:VAL:HG11	14:K:95:ILE:HD11	1.86	0.56
18:O:4:THR:OG1	18:O:7:GLU:HB2	2.04	0.56
21:R:46:GLU:CD	21:R:46:GLU:N	2.63	0.56
22:S:4:SER:O	22:S:5:LEU:HG	2.05	0.56
1:A:1064:G:H4'	1:A:1065:U:H5''	1.87	0.56
5:B:161:ALA:HB1	5:B:185:ILE:HD11	1.86	0.56
6:C:36:ASP:OD1	6:C:57:ILE:HD12	2.05	0.56
7:D:175:SER:CB	7:D:186:LEU:HD21	2.33	0.56
12:I:53:VAL:CG2	12:I:85:LEU:HD21	2.33	0.56
13:J:3:LYS:O	13:J:4:ILE:HD13	2.05	0.56
14:K:74:ALA:O	14:K:76:GLY:N	2.38	0.56
17:N:36:PHE:O	17:N:37:PHE:CG	2.58	0.56
23:T:13:LEU:HD12	23:T:13:LEU:C	2.31	0.56
1:A:394:G:H2'	1:A:395:C:C6	2.40	0.56
1:A:477:G:H2'	1:A:478:A:H8	1.70	0.56
1:A:538:G:H2'	1:A:539:A:C8	2.40	0.56
1:A:1054:C:H5	1:A:1196:U:C5	2.23	0.56
1:A:1351:U:O2'	1:A:1352:C:H5'	2.04	0.56
5:B:23:ARG:C	5:B:23:ARG:HD3	2.30	0.56
5:B:45:GLN:O	5:B:48:MET:HB2	2.04	0.56
6:C:132:ARG:O	6:C:133:ALA:C	2.48	0.56
8:E:74:GLY:HA3	8:E:116:THR:HG22	1.86	0.56
12:I:4:TYR:CD1	12:I:88:TYR:HB2	2.40	0.56
12:I:44:VAL:HG13	12:I:51:ARG:NH2	2.20	0.56
12:I:117:HIS:C	12:I:118:LYS:HG3	2.30	0.56
17:N:35:ARG:C	17:N:37:PHE:H	2.13	0.56
22:S:35:SER:C	22:S:37:ARG:H	2.13	0.56
23:T:57:ARG:HD2	23:T:102:GLY:CA	2.31	0.56
24:V:23:PRO:C	24:V:25:LYS:H	2.13	0.56
1:A:22:G:H2'	1:A:23:C:C6	2.39	0.56
1:A:878:G:H5'	11:H:89:PRO:HG2	1.87	0.56
1:A:949:A:N7	16:M:106:ASN:ND2	2.53	0.56
1:A:1216:G:H5''	17:N:5:ALA:CB	2.33	0.56
5:B:69:LEU:C	5:B:69:LEU:HD23	2.29	0.56
5:B:76:GLN:HG3	5:B:206:ASP:OD1	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:13:GLY:O	6:C:14:ILE:HD13	2.06	0.56
9:F:100:ASN:ND2	21:R:23:LYS:HG2	2.16	0.56
12:I:40:LEU:O	12:I:41:VAL:C	2.48	0.56
12:I:42:ARG:O	12:I:43:ALA:C	2.48	0.56
16:M:30:ALA:O	16:M:34:LEU:HB2	2.06	0.56
16:M:96:LEU:O	16:M:97:PRO:C	2.47	0.56
19:P:81:ARG:HG3	19:P:83:GLU:HG2	1.88	0.56
21:R:88:LYS:OXT	21:R:88:LYS:HG2	2.05	0.56
22:S:30:LEU:HD22	22:S:31:ILE:O	2.06	0.56
1:A:337:C:H2'	1:A:338:A:C8	2.40	0.56
1:A:1316:G:H4'	17:N:18:VAL:CG1	2.35	0.56
5:B:118:LEU:HD11	5:B:141:GLU:CD	2.31	0.56
6:C:54:ARG:HG3	6:C:55:VAL:H	1.71	0.56
7:D:121:VAL:O	7:D:134:ASP:HA	2.05	0.56
13:J:56:HIS:O	13:J:58:ASP:N	2.38	0.56
14:K:11:LYS:O	14:K:12:ARG:HB2	2.04	0.56
14:K:54:ARG:HH11	14:K:54:ARG:CB	2.07	0.56
18:O:26:GLU:HA	18:O:81:LEU:HD11	1.87	0.56
1:A:818:G:C2'	1:A:819:A:H5''	2.34	0.56
1:A:1091:U:O2	1:A:1093:A:H8	1.88	0.56
6:C:33:LEU:HD11	17:N:53:LEU:CD2	2.35	0.56
7:D:177:ASP:OD1	7:D:180:GLY:N	2.39	0.56
11:H:103:VAL:HG21	11:H:109:ILE:O	2.06	0.56
15:L:41:ARG:CG	15:L:42:THR:H	1.99	0.56
16:M:23:TYR:HB3	16:M:67:GLU:HA	1.86	0.56
16:M:110:ARG:HG2	16:M:110:ARG:HH11	1.71	0.56
22:S:16:LEU:O	22:S:18:LYS:N	2.38	0.56
1:A:109:A:H2'	1:A:326:G:H21	1.70	0.56
1:A:707:C:OP1	14:K:85:ARG:NH1	2.38	0.56
1:A:778:G:O2'	1:A:779:C:H5'	2.05	0.56
1:A:839:U:O2	1:A:839:U:H2'	2.05	0.56
1:A:1281:U:H5'	1:A:1282:C:H5	1.70	0.56
1:A:1510:U:H2'	1:A:1511:G:C8	2.40	0.56
6:C:171:GLY:O	6:C:173:VAL:HG23	2.06	0.56
8:E:144:THR:HB	8:E:147:ASP:OD2	2.05	0.56
14:K:77:MET:CE	14:K:80:VAL:HG22	2.36	0.56
20:Q:27:PHE:CE1	20:Q:36:ILE:HD11	2.40	0.56
1:A:56:U:H2'	1:A:57:G:C8	2.41	0.56
1:A:149:A:H2'	1:A:150:C:H6	1.71	0.56
1:A:991:U:O4	1:A:1212:U:H1'	2.05	0.56
1:A:997:U:O2'	1:A:998:G:H5'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1161:C:H2'	1:A:1162:C:H6	1.69	0.56
5:B:16:HIS:HE1	5:B:213:LEU:HD13	1.70	0.56
5:B:77:ALA:HB2	5:B:211:ILE:CD1	2.33	0.56
6:C:34:LEU:HD23	6:C:34:LEU:O	2.06	0.56
6:C:137:ALA:CA	6:C:140:ARG:HH11	2.17	0.56
6:C:154:SER:OG	6:C:155:GLY:N	2.39	0.56
8:E:115:VAL:HG11	8:E:118:ILE:CD1	2.33	0.56
8:E:147:ASP:OD2	8:E:147:ASP:N	2.39	0.56
17:N:4:LYS:HA	17:N:7:ILE:HD12	1.87	0.56
17:N:29:ARG:HG2	17:N:29:ARG:HH11	1.71	0.56
5:B:223:ILE:C	5:B:225:ALA:N	2.64	0.56
13:J:35:SER:HB3	13:J:72:VAL:O	2.06	0.56
16:M:6:GLY:O	16:M:8:GLU:N	2.39	0.56
16:M:31:LYS:O	16:M:35:GLU:HB2	2.05	0.56
1:A:833:U:H2'	1:A:834:C:H6	1.70	0.56
1:A:1230:C:H2'	1:A:1231:G:H8	1.71	0.56
10:G:23:VAL:HG12	10:G:27:ILE:CD1	2.35	0.56
12:I:93:ARG:C	12:I:95:LYS:H	2.13	0.56
12:I:125:TYR:HE1	12:I:128:ARG:HB3	1.71	0.56
14:K:40:ILE:HG23	14:K:75:TYR:CD2	2.41	0.56
20:Q:67:LYS:CA	20:Q:70:ARG:HH12	2.12	0.56
1:A:91:C:H2'	1:A:92:C:H6	1.71	0.55
1:A:258:G:O2'	1:A:259:G:H5'	2.05	0.55
1:A:760:G:N2	20:Q:104:LYS:H	2.04	0.55
1:A:959:A:C2	1:A:1222:G:O4'	2.59	0.55
21:R:43:PHE:C	21:R:51:LEU:HD12	2.31	0.55
1:A:401:C:H1'	1:A:622:A:H1'	1.88	0.55
1:A:791:G:H2'	1:A:792:A:H5''	1.88	0.55
1:A:1106:G:OP1	6:C:172:ARG:HD3	2.06	0.55
1:A:1437:C:H2'	1:A:1438:G:H8	1.70	0.55
1:A:1465:C:O2'	1:A:1466:C:H5'	2.06	0.55
5:B:10:LEU:HG	5:B:48:MET:HE2	1.88	0.55
6:C:24:ALA:HB1	6:C:28:GLN:HB3	1.86	0.55
6:C:177:THR:HG23	6:C:177:THR:O	2.06	0.55
12:I:59:PHE:HZ	12:I:88:TYR:CD2	2.25	0.55
12:I:117:HIS:HB2	12:I:121:ARG:O	2.07	0.55
13:J:24:VAL:O	13:J:28:ARG:HG3	2.06	0.55
23:T:38:LYS:O	23:T:39:LYS:C	2.49	0.55
1:A:889:A:H5'	1:A:891:U:H1'	1.89	0.55
1:A:1316:G:N2	1:A:1318:A:H3'	2.20	0.55
1:A:35:G:H2'	1:A:36:C:C6	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:G:H2'	1:A:539:A:H8	1.71	0.55
1:A:1358:U:H3'	1:A:1359:C:C6	2.41	0.55
5:B:111:ARG:NE	5:B:111:ARG:HA	2.22	0.55
7:D:6:GLY:H	7:D:115:ARG:HH22	1.54	0.55
11:H:107:LEU:N	11:H:107:LEU:CD1	2.70	0.55
12:I:93:ARG:NE	12:I:97:LYS:HE3	2.21	0.55
21:R:36:ASN:HD21	21:R:38:GLU:HG2	1.70	0.55
1:A:338:A:H2'	1:A:339:C:H6	1.71	0.55
1:A:547:A:H4'	1:A:548:G:O5'	2.06	0.55
1:A:818:G:H3'	1:A:819:A:C5'	2.37	0.55
1:A:974:A:H8	1:A:974:A:OP1	1.89	0.55
1:A:1367:C:C2	1:A:1368:G:C8	2.94	0.55
1:A:1454:G:H2'	1:A:1455:G:H8	1.72	0.55
6:C:134:ILE:CG2	6:C:168:ALA:HB3	2.37	0.55
9:F:48:LEU:HD21	9:F:60:PHE:CZ	2.41	0.55
11:H:14:ARG:HB3	11:H:14:ARG:HH11	1.72	0.55
20:Q:96:GLN:O	20:Q:97:SER:CB	2.54	0.55
1:A:266:G:H5'	1:A:266:G:C8	2.42	0.55
1:A:443:C:O2'	1:A:444:C:H5'	2.06	0.55
1:A:644:G:O2'	1:A:645:C:H5'	2.06	0.55
6:C:70:VAL:C	6:C:106:VAL:HG23	2.31	0.55
11:H:24:THR:HG23	11:H:61:VAL:HB	1.89	0.55
16:M:26:GLY:O	16:M:28:ALA:N	2.39	0.55
20:Q:67:LYS:HA	20:Q:70:ARG:NH1	2.13	0.55
1:A:838:G:C2'	1:A:839:U:H5''	2.37	0.55
1:A:1472:U:O2'	1:A:1473:A:H5'	2.06	0.55
1:A:1521:G:H2'	1:A:1522:U:C6	2.41	0.55
9:F:38:GLU:HB2	9:F:64:GLN:O	2.06	0.55
21:R:25:THR:HB	21:R:42:ARG:HH22	1.71	0.55
1:A:998:G:O2'	1:A:999:C:H5'	2.07	0.55
1:A:1223:C:OP1	1:A:1224:G:H3'	2.06	0.55
1:A:1264:C:H2'	1:A:1265:G:H8	1.72	0.55
1:A:1349:A:OP2	12:I:118:LYS:NZ	2.40	0.55
5:B:84:GLU:HA	5:B:87:ARG:HB2	1.88	0.55
7:D:64:LEU:HD12	7:D:75:PHE:HZ	1.72	0.55
13:J:5:ARG:HA	13:J:73:ASP:OD1	2.07	0.55
17:N:9:LYS:HG3	17:N:21:TYR:O	2.06	0.55
1:A:58:C:O2'	1:A:59:A:H5'	2.06	0.55
5:B:90:MET:N	5:B:90:MET:SD	2.80	0.55
7:D:18:LYS:HE2	7:D:20:TYR:HE2	1.71	0.55
9:F:10:LEU:HD12	9:F:59:TYR:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:36:LEU:CD1	11:H:59:LEU:HD13	2.37	0.55
13:J:45:ARG:NH2	17:N:36:PHE:CD2	2.75	0.55
19:P:55:ARG:O	19:P:56:ALA:C	2.47	0.55
21:R:48:GLY:N	21:R:82:THR:HA	2.22	0.55
22:S:12:ASP:O	22:S:15:LEU:HG	2.07	0.55
22:S:31:ILE:HG22	22:S:32:LYS:N	2.18	0.55
22:S:42:PRO:O	22:S:43:GLU:C	2.49	0.55
1:A:590:C:O2'	1:A:591:U:H5'	2.07	0.55
1:A:1226:C:H1'	22:S:83:HIS:HE1	1.68	0.55
1:A:1320:C:O2	22:S:36:ARG:NH1	2.40	0.55
5:B:91:PRO:HG3	5:B:154:LEU:HB2	1.88	0.55
8:E:6:PHE:HB3	8:E:34:VAL:CG1	2.37	0.55
22:S:10:PHE:CD2	22:S:11:VAL:N	2.75	0.55
1:A:165:C:H2'	1:A:166:G:H8	1.72	0.54
1:A:647:C:H2'	1:A:648:A:H8	1.72	0.54
1:A:975:A:O2'	17:N:32:SER:HA	2.07	0.54
1:A:1306:A:H2'	1:A:1307:U:O4'	2.06	0.54
6:C:91:LEU:HG	6:C:99:VAL:HG21	1.89	0.54
12:I:30:GLY:O	12:I:31:GLN:C	2.51	0.54
16:M:36:LYS:HD2	16:M:59:TYR:CZ	2.42	0.54
16:M:46:LYS:HE2	16:M:47:ASP:CG	2.31	0.54
1:A:255:G:H1'	20:Q:16:GLN:NE2	2.21	0.54
1:A:398:C:O2'	1:A:399:G:H5'	2.07	0.54
1:A:939:G:C5'	10:G:102:ARG:HH12	2.20	0.54
4:Z:2:U:H6	4:Z:2:U:H5'	1.73	0.54
5:B:223:ILE:HD13	5:B:230:VAL:HG21	1.89	0.54
7:D:67:ILE:C	7:D:69:GLY:H	2.15	0.54
11:H:4:ASP:OD2	11:H:85:ARG:NH1	2.40	0.54
12:I:8:GLY:HA2	12:I:79:LEU:CD1	2.32	0.54
12:I:43:ALA:O	12:I:44:VAL:C	2.50	0.54
12:I:86:VAL:HG13	12:I:90:PRO:HA	1.89	0.54
14:K:74:ALA:C	14:K:76:GLY:N	2.60	0.54
18:O:45:VAL:HB	18:O:46:HIS:ND1	2.22	0.54
1:A:499:A:H4'	1:A:500:G:H5'	1.88	0.54
1:A:797:C:O2'	1:A:798:G:H5'	2.06	0.54
1:A:951:G:O2'	1:A:952:U:H5'	2.06	0.54
1:A:1279:A:H5''	1:A:1280:A:OP1	2.07	0.54
1:A:1309:G:O3'	16:M:77:ASN:ND2	2.40	0.54
1:A:1402:C:O2	1:A:1500:A:N1	2.41	0.54
6:C:18:TRP:HE3	6:C:18:TRP:H	1.56	0.54
8:E:20:GLN:O	8:E:21:ALA:C	2.49	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:41:ARG:HB3	15:L:41:ARG:HH11	1.72	0.54
17:N:22:THR:OG1	17:N:33:VAL:HG21	2.07	0.54
1:A:110:C:H2'	1:A:111:G:O4'	2.06	0.54
1:A:644:G:C5	1:A:645:C:C5	2.96	0.54
1:A:818:G:C3'	1:A:819:A:H5''	2.37	0.54
1:A:942:G:H2'	1:A:943:U:H6	1.71	0.54
1:A:1291:G:H4'	12:I:38:GLN:O	2.08	0.54
5:B:28:PHE:CZ	5:B:189:ASP:HA	2.42	0.54
5:B:137:ARG:HA	5:B:140:HIS:HD2	1.73	0.54
15:L:83:VAL:HG22	15:L:100:ILE:HG23	1.89	0.54
21:R:40:LEU:O	21:R:42:ARG:N	2.41	0.54
22:S:22:LEU:CD2	22:S:28:LYS:HD2	2.38	0.54
1:A:437:U:H5''	7:D:155:LEU:HD22	1.89	0.54
1:A:528:C:H5'	1:A:535:A:N6	2.23	0.54
8:E:101:ILE:HD12	8:E:119:LEU:HD23	1.89	0.54
8:E:137:GLU:O	8:E:138:ALA:C	2.51	0.54
9:F:2:ARG:NE	9:F:69:GLU:HG2	2.22	0.54
16:M:40:ASN:HD22	16:M:41:PRO:HD2	1.73	0.54
22:S:15:LEU:CD2	22:S:33:THR:HG21	2.38	0.54
1:A:539:A:H2'	1:A:540:G:C8	2.43	0.54
1:A:1533:C:O2'	1:A:1534:A:H5'	2.08	0.54
5:B:10:LEU:O	5:B:10:LEU:HD23	2.08	0.54
5:B:97:TRP:HH2	5:B:176:GLU:CD	2.16	0.54
6:C:43:LEU:HD12	6:C:68:VAL:HG21	1.88	0.54
6:C:167:TRP:O	6:C:168:ALA:HB3	2.07	0.54
22:S:80:TYR:CD2	22:S:80:TYR:C	2.84	0.54
23:T:79:ARG:O	23:T:80:ARG:C	2.49	0.54
1:A:929:G:H5''	1:A:1533:C:N4	2.23	0.54
1:A:1255:G:O2'	1:A:1258:G:H1'	2.07	0.54
1:A:1293:G:O2'	1:A:1294:G:H5'	2.08	0.54
1:A:1381:U:H2'	1:A:1382:C:H6	1.72	0.54
5:B:73:THR:HG23	5:B:95:GLN:O	2.08	0.54
6:C:188:LEU:HD13	6:C:189:ALA:N	2.15	0.54
7:D:12:CYS:SG	7:D:19:LEU:O	2.66	0.54
19:P:34:GLU:OE2	19:P:55:ARG:HD3	2.08	0.54
21:R:47:THR:C	21:R:49:LYS:H	2.16	0.54
1:A:287:U:C2'	1:A:288:A:H5'	2.38	0.54
1:A:448:A:H2'	1:A:449:C:C6	2.43	0.54
1:A:920:U:H2'	1:A:921:U:H6	1.71	0.54
1:A:1342:C:O2'	1:A:1343:G:H5'	2.07	0.54
8:E:57:LYS:HG2	8:E:61:TYR:CE2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:145:ALA:O	10:G:147:ALA:N	2.41	0.54
12:I:118:LYS:O	12:I:119:ALA:CB	2.56	0.54
1:A:1366:C:C2	1:A:1367:C:C5	2.96	0.54
6:C:83:ARG:C	6:C:85:ARG:N	2.65	0.54
6:C:83:ARG:C	6:C:85:ARG:H	2.16	0.54
11:H:20:TYR:CE1	11:H:76:PRO:HD2	2.43	0.54
14:K:110:ASP:HB2	21:R:88:LYS:CD	2.38	0.54
19:P:12:LYS:O	19:P:13:HIS:HB2	2.07	0.54
20:Q:45:HIS:CD2	20:Q:47:PRO:HG3	2.42	0.54
1:A:513:C:H2'	1:A:514:C:C6	2.43	0.54
1:A:664:G:H2'	1:A:666:G:OP1	2.07	0.54
1:A:1258:G:H1	1:A:1277:C:N4	2.05	0.54
1:A:1428:A:H2'	1:A:1429:C:C6	2.43	0.54
5:B:166:ASP:OD2	5:B:169:LYS:HB2	2.08	0.54
7:D:76:ARG:HG2	7:D:76:ARG:HH11	1.73	0.54
7:D:126:ILE:CG2	7:D:127:THR:N	2.69	0.54
8:E:102:ALA:HB1	8:E:106:PRO:HB2	1.90	0.54
11:H:11:THR:HA	11:H:14:ARG:NH1	2.23	0.54
16:M:12:ASN:O	16:M:12:ASN:CG	2.51	0.54
20:Q:76:LEU:HD23	20:Q:76:LEU:C	2.33	0.54
23:T:91:LEU:C	23:T:93:GLU:N	2.65	0.54
23:T:100:ILE:O	23:T:100:ILE:HG12	2.08	0.54
1:A:281:G:O2'	1:A:282:A:OP2	2.22	0.53
1:A:502:G:H2'	1:A:503:C:H6	1.72	0.53
1:A:657:G:O2'	1:A:658:G:H5'	2.09	0.53
1:A:730:G:N2	1:A:765:G:H5''	2.23	0.53
1:A:750:G:C2	18:O:23:GLY:HA3	2.43	0.53
1:A:1461:G:O2'	1:A:1462:G:H5'	2.08	0.53
1:A:1497:G:C2'	1:A:1498:U:H5'	2.38	0.53
12:I:16:ARG:HB2	12:I:64:THR:HB	1.90	0.53
12:I:59:PHE:O	12:I:60:ASP:HB2	2.07	0.53
14:K:120:ARG:NH2	14:K:126:ARG:NH1	2.56	0.53
16:M:116:THR:HG22	16:M:117:VAL:N	2.23	0.53
20:Q:59:ILE:HG23	20:Q:71:PHE:CD1	2.43	0.53
20:Q:82:MET:O	20:Q:83:ASP:C	2.50	0.53
20:Q:95:TYR:O	20:Q:97:SER:N	2.42	0.53
21:R:86:VAL:O	21:R:87:ARG:HB2	2.08	0.53
1:A:16:A:C2'	1:A:17:U:H5'	2.39	0.53
1:A:722:A:H4'	1:A:723:U:C5	2.44	0.53
1:A:923:A:OP1	8:E:21:ALA:HB2	2.08	0.53
1:A:953:G:H2'	1:A:954:G:O4'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:18:ARG:C	21:R:19:LYS:HD2	2.33	0.53
22:S:33:THR:HG22	22:S:35:SER:H	1.73	0.53
1:A:254:G:H21	20:Q:16:GLN:NE2	2.07	0.53
1:A:1070:U:O2'	1:A:1071:C:H5'	2.07	0.53
1:A:1475:G:H2'	1:A:1476:G:C8	2.39	0.53
6:C:147:LYS:HD2	6:C:203:PHE:CE2	2.44	0.53
14:K:43:SER:HA	14:K:47:VAL:HG21	1.88	0.53
22:S:85:LYS:O	22:S:86:GLU:HG2	2.07	0.53
1:A:101:A:O2'	1:A:102:G:H5'	2.07	0.53
1:A:750:G:H1'	18:O:22:THR:OG1	2.08	0.53
1:A:1003(A):G:O2'	1:A:1004:A:H4'	2.08	0.53
13:J:12:ASP:OD1	13:J:14:LYS:N	2.39	0.53
15:L:43:VAL:CG1	15:L:44:THR:N	2.71	0.53
15:L:126:LYS:N	15:L:126:LYS:HD2	2.23	0.53
16:M:69:GLU:O	16:M:72:ALA:HB3	2.08	0.53
22:S:80:TYR:HD2	22:S:80:TYR:C	2.15	0.53
1:A:1264:C:H2'	1:A:1265:G:C8	2.43	0.53
1:A:1300:G:HO2'	1:A:1301:U:H6	1.55	0.53
5:B:9:GLU:OE1	5:B:12:GLU:HA	2.08	0.53
6:C:172:ARG:HB3	6:C:172:ARG:HH11	1.74	0.53
7:D:55:ALA:O	7:D:59:ARG:HG2	2.08	0.53
8:E:15:ARG:O	8:E:16:THR:CB	2.56	0.53
9:F:40:VAL:CG1	9:F:41:GLU:N	2.72	0.53
11:H:4:ASP:OD2	11:H:7:ALA:HB2	2.08	0.53
11:H:86:ILE:O	11:H:88:LYS:HG2	2.08	0.53
1:A:190(E):U:O2'	20:Q:63:ARG:NH2	2.41	0.53
1:A:513:C:H2'	1:A:514:C:H6	1.72	0.53
1:A:518:C:O2'	1:A:519:C:OP2	2.24	0.53
1:A:620:C:C6	7:D:135:LEU:HD13	2.44	0.53
1:A:743:U:H2'	1:A:744:C:C6	2.43	0.53
1:A:1511:G:H2'	1:A:1512:U:O4'	2.08	0.53
5:B:78:GLN:HA	5:B:94:ASN:OD1	2.07	0.53
5:B:142:LEU:O	5:B:143:GLU:C	2.52	0.53
6:C:70:VAL:HG12	6:C:72:LYS:H	1.74	0.53
8:E:80:ILE:N	8:E:80:ILE:HD12	2.23	0.53
8:E:105:VAL:HB	8:E:106:PRO:HD3	1.90	0.53
13:J:63:PHE:CE1	17:N:45:ARG:HG3	2.44	0.53
16:M:15:VAL:HG22	16:M:45:VAL:HG22	1.91	0.53
18:O:46:HIS:ND1	18:O:46:HIS:N	2.57	0.53
1:A:112:G:N2	1:A:354:G:H5'	2.23	0.53
1:A:692:U:OP1	14:K:124:LYS:HE3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1000:U:H2'	1:A:1001:A:O4'	2.08	0.53
1:A:1054:C:N4	3:Y:34:G:C8	2.72	0.53
1:A:1487:G:O2'	1:A:1488:G:H5'	2.08	0.53
5:B:12:GLU:C	5:B:14:GLY:H	2.17	0.53
5:B:15:VAL:HG11	5:B:209:ARG:HB3	1.90	0.53
5:B:137:ARG:NH1	5:B:137:ARG:HB3	2.24	0.53
5:B:178:ARG:O	5:B:180:LEU:N	2.41	0.53
6:C:62:ASP:HA	6:C:97:LYS:HG3	1.88	0.53
8:E:107:ARG:O	8:E:108:ALA:C	2.51	0.53
1:A:47:C:H5''	1:A:365:U:C6	2.44	0.53
1:A:80:G:H3'	1:A:81:U:H5''	1.91	0.53
1:A:277:C:H5''	20:Q:68:ARG:NH2	2.24	0.53
1:A:889:A:N1	1:A:907:A:H5''	2.24	0.53
1:A:915:A:C2'	1:A:916:G:H5'	2.39	0.53
1:A:1038:C:H2'	1:A:1039:C:C5	2.44	0.53
1:A:1313:U:OP2	22:S:6:LYS:HA	2.08	0.53
6:C:42:LEU:HA	6:C:45:LYS:HB2	1.91	0.53
6:C:118:GLN:O	6:C:122:GLU:HG3	2.09	0.53
7:D:34:GLU:HG3	7:D:35:ARG:NH2	2.24	0.53
1:A:105:G:H2'	1:A:106:C:C6	2.44	0.53
1:A:166:G:O2'	1:A:167:G:H5'	2.09	0.53
1:A:474:G:O2'	1:A:475:G:H5'	2.09	0.53
1:A:1167:A:H2'	1:A:1168:A:C8	2.43	0.53
1:A:1247:U:O2'	1:A:1248:A:H5'	2.09	0.53
6:C:95:THR:O	6:C:96:GLY:C	2.51	0.53
7:D:8:VAL:HG12	7:D:21:LEU:HD13	1.90	0.53
7:D:187:ARG:HE	7:D:188:LEU:H	1.56	0.53
8:E:111:GLU:C	8:E:113:ALA:N	2.64	0.53
9:F:22:GLU:OE2	9:F:84:ASN:HB2	2.08	0.53
11:H:14:ARG:O	11:H:18:ARG:HD3	2.09	0.53
15:L:75:HIS:HD2	15:L:77:LEU:N	2.05	0.53
19:P:1:MET:HE3	19:P:3:LYS:HD2	1.91	0.53
8:E:28:PHE:O	8:E:47:LYS:HA	2.09	0.53
11:H:86:ILE:HD11	11:H:136:GLU:CB	2.38	0.53
20:Q:12:SER:HB3	20:Q:20:THR:CB	2.38	0.53
23:T:63:ILE:HD13	23:T:80:ARG:HB3	1.91	0.53
1:A:180:U:C2'	1:A:181:G:H5'	2.37	0.52
1:A:490:G:H2'	1:A:491:G:H8	1.74	0.52
1:A:1348:U:H2'	1:A:1349:A:C8	2.28	0.52
1:A:1372:U:O2'	1:A:1373:G:H5'	2.09	0.52
6:C:57:ILE:CG2	6:C:58:GLU:N	2.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:52:SER:O	7:D:53:ASP:C	2.52	0.52
10:G:75:VAL:HA	10:G:87:VAL:O	2.08	0.52
10:G:116:ALA:HA	10:G:119:ARG:NH2	2.23	0.52
11:H:83:ILE:HG23	11:H:83:ILE:O	2.09	0.52
13:J:4:ILE:O	13:J:6:ILE:HG13	2.09	0.52
13:J:16:LEU:HD23	13:J:94:VAL:HG13	1.90	0.52
18:O:48:LYS:O	18:O:50:HIS:N	2.42	0.52
20:Q:33:GLY:O	20:Q:34:LYS:C	2.51	0.52
1:A:676:A:H1'	14:K:115:PRO:HB3	1.92	0.52
1:A:1124:G:C3'	1:A:1145:C:H41	2.19	0.52
1:A:1441:G:H4'	1:A:1442:G:C5	2.44	0.52
5:B:21:ARG:HH11	5:B:21:ARG:HG3	1.74	0.52
5:B:50:GLU:HG3	5:B:200:ILE:CD1	2.38	0.52
5:B:178:ARG:NH2	5:B:196:LEU:HA	2.21	0.52
5:B:230:VAL:HG12	5:B:231:GLU:N	2.24	0.52
9:F:91:VAL:HG13	21:R:72:ARG:NH2	2.23	0.52
10:G:15:ASP:OD1	10:G:44:TYR:OH	2.27	0.52
10:G:65:ALA:O	10:G:69:VAL:HG23	2.09	0.52
19:P:22:THR:HA	19:P:33:ILE:CD1	2.25	0.52
19:P:28:ARG:NH1	19:P:28:ARG:HG2	2.22	0.52
20:Q:68:ARG:N	20:Q:70:ARG:NH1	2.57	0.52
23:T:24:LEU:HD12	23:T:24:LEU:O	2.10	0.52
23:T:92:LEU:O	23:T:96:GLY:HA3	2.10	0.52
1:A:344:A:H5''	1:A:345:C:H5	1.74	0.52
1:A:760:G:H1	20:Q:105:ALA:CA	2.19	0.52
1:A:818:G:C3'	1:A:819:A:C5'	2.86	0.52
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.43	0.52
1:A:1222:G:OP1	22:S:77:THR:HG21	2.10	0.52
1:A:1241:G:H2'	1:A:1242:C:H6	1.75	0.52
5:B:159:PRO:HB2	5:B:161:ALA:O	2.09	0.52
6:C:139:GLN:O	6:C:143:GLU:N	2.41	0.52
8:E:6:PHE:CZ	8:E:66:MET:HE2	2.44	0.52
12:I:4:TYR:CE2	12:I:88:TYR:HA	2.45	0.52
15:L:102:ARG:NH2	15:L:110:VAL:HA	2.25	0.52
18:O:17:ARG:HG3	18:O:17:ARG:HH11	1.74	0.52
18:O:65:ARG:HB2	18:O:65:ARG:HH11	1.72	0.52
20:Q:60:ILE:HD13	20:Q:61:GLU:H	1.72	0.52
1:A:98:U:O2'	1:A:99:C:H5'	2.08	0.52
1:A:794:A:H2'	1:A:795:C:C6	2.44	0.52
1:A:927:G:H4'	1:A:1503:A:N7	2.25	0.52
1:A:1023:G:H2'	1:A:1023:G:N3	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1056:U:H5'	6:C:163:ALA:CB	2.39	0.52
1:A:1060:C:O2'	1:A:1061:G:H5'	2.09	0.52
1:A:1151:A:O2'	1:A:1152:A:H8	1.91	0.52
1:A:1286:A:C8	1:A:1287:A:H4'	2.44	0.52
7:D:142:PRO:CG	7:D:187:ARG:HH21	2.21	0.52
9:F:73:ASN:O	9:F:74:ASP:C	2.51	0.52
10:G:149:ARG:C	10:G:151:TYR:H	2.17	0.52
14:K:33:THR:HG21	14:K:37:GLY:HA2	1.90	0.52
15:L:50:SER:O	15:L:51:ALA:HB2	2.10	0.52
15:L:119:LYS:O	15:L:120:TYR:CB	2.57	0.52
21:R:74:ARG:HB3	21:R:81:PHE:CZ	2.44	0.52
1:A:538:G:O2'	1:A:539:A:H5'	2.10	0.52
1:A:1256:A:O2'	1:A:1257:U:H4'	2.10	0.52
6:C:40:ARG:HH11	6:C:40:ARG:HG3	1.75	0.52
7:D:100:ARG:O	7:D:103:ASN:HB3	2.08	0.52
7:D:111:ALA:HB3	7:D:117:ALA:HB2	1.90	0.52
7:D:151:LYS:HD2	7:D:151:LYS:N	2.11	0.52
8:E:80:ILE:HD12	8:E:80:ILE:H	1.75	0.52
8:E:82:VAL:O	8:E:88:LYS:HA	2.09	0.52
10:G:51:GLN:C	10:G:53:LYS:N	2.67	0.52
10:G:80:VAL:HG11	10:G:154:TYR:CE1	2.45	0.52
16:M:40:ASN:HD22	16:M:41:PRO:N	2.07	0.52
21:R:47:THR:HA	21:R:83:GLU:HB2	1.90	0.52
23:T:76:ALA:O	23:T:80:ARG:HG2	2.09	0.52
1:A:115:G:H1'	1:A:116:A:N7	2.25	0.52
1:A:625:G:H2'	1:A:626:U:C6	2.44	0.52
1:A:938:A:N6	1:A:939:G:C6	2.78	0.52
1:A:961:U:C2'	1:A:962:C:H5'	2.40	0.52
1:A:1049:U:H1'	1:A:1201:A:N7	2.24	0.52
6:C:33:LEU:HD11	17:N:53:LEU:HD22	1.90	0.52
6:C:174:PRO:HB2	6:C:177:THR:HG22	1.91	0.52
11:H:82:HIS:CG	11:H:83:ILE:H	2.27	0.52
20:Q:6:LEU:O	20:Q:59:ILE:N	2.37	0.52
21:R:86:VAL:HG12	21:R:87:ARG:HD2	1.90	0.52
1:A:229:U:O2'	1:A:230:G:H5'	2.10	0.52
1:A:417:C:O2'	1:A:418:C:H5'	2.10	0.52
1:A:521:G:O2'	1:A:522:C:H5'	2.10	0.52
1:A:836:G:C6	1:A:851:G:C6	2.98	0.52
1:A:980:C:H3'	1:A:981:U:C6	2.45	0.52
8:E:109:ILE:O	8:E:113:ALA:HB2	2.10	0.52
11:H:83:ILE:CB	11:H:137:VAL:HG22	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:27:THR:HG23	12:I:30:GLY:O	2.09	0.52
12:I:46:ALA:O	12:I:49:PRO:HD2	2.10	0.52
12:I:46:ALA:HA	12:I:78:LYS:HB2	1.92	0.52
21:R:60:GLY:O	21:R:64:ARG:HB2	2.09	0.52
1:A:718:G:C8	14:K:116:HIS:HB3	2.45	0.52
1:A:866:C:H2'	1:A:867:G:O4'	2.10	0.52
1:A:1453:G:H2'	1:A:1454:G:O4'	2.10	0.52
6:C:5:ILE:O	6:C:5:ILE:HD12	2.10	0.52
6:C:180:ALA:O	6:C:181:ASN:HB3	2.09	0.52
7:D:149:ALA:O	7:D:153:ARG:N	2.43	0.52
11:H:120:THR:HG23	11:H:123:GLU:OE2	2.09	0.52
12:I:4:TYR:HB2	12:I:19:LEU:HB2	1.91	0.52
13:J:30:SER:CB	13:J:81:THR:HA	2.40	0.52
13:J:49:VAL:O	13:J:60:ARG:O	2.27	0.52
16:M:24:GLY:CA	16:M:66:LEU:HD22	2.39	0.52
22:S:45:VAL:C	22:S:47:HIS:H	2.18	0.52
1:A:19:C:H2'	1:A:20:U:H6	1.75	0.52
1:A:186:C:H2'	1:A:187:C:C6	2.45	0.52
1:A:996:A:H2'	1:A:997:U:C6	2.45	0.52
1:A:1105:A:H2'	1:A:1106:G:H8	1.75	0.52
1:A:1238:A:OP1	1:A:1336:C:H5	1.92	0.52
1:A:1260:C:O5'	1:A:1284:C:H4'	2.10	0.52
1:A:1305:G:H5'	24:V:4:GLY:HA3	1.91	0.52
6:C:39:ILE:O	6:C:43:LEU:HD23	2.10	0.52
7:D:7:PRO:HG2	7:D:10:ARG:CD	2.31	0.52
15:L:70:ILE:HG12	15:L:100:ILE:HD12	1.92	0.52
1:A:424:G:O2'	1:A:425:G:H5'	2.10	0.52
5:B:44:LEU:O	5:B:45:GLN:C	2.52	0.52
5:B:83:MET:HE2	5:B:235:SER:HA	1.91	0.52
5:B:83:MET:HE3	5:B:234:PRO:HG2	1.91	0.52
6:C:153:VAL:O	6:C:154:SER:C	2.52	0.52
6:C:156:ARG:HH11	6:C:156:ARG:HG3	1.74	0.52
7:D:177:ASP:OD1	7:D:179:GLU:HB2	2.09	0.52
12:I:117:HIS:O	12:I:118:LYS:HG3	2.10	0.52
16:M:98:VAL:O	16:M:98:VAL:HG12	2.10	0.52
22:S:15:LEU:HD23	22:S:33:THR:HG21	1.92	0.52
22:S:24:ALA:HB3	22:S:25:LYS:HZ2	1.74	0.52
22:S:61:TYR:C	22:S:61:TYR:CD2	2.87	0.52
5:B:9:GLU:OE1	5:B:11:LEU:O	2.28	0.51
5:B:144:ARG:HG3	5:B:145:LEU:N	2.24	0.51
5:B:215:LEU:O	5:B:216:SER:C	2.51	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:108:LEU:CD2	7:D:174:LEU:HD13	2.41	0.51
8:E:135:THR:O	8:E:138:ALA:HB3	2.10	0.51
10:G:148:ASN:C	10:G:150:ALA:N	2.65	0.51
15:L:89:ARG:CZ	15:L:97:ARG:HG2	2.40	0.51
17:N:11:LYS:C	17:N:13:THR:N	2.68	0.51
18:O:33:THR:HG23	18:O:63:ARG:HH12	1.75	0.51
18:O:61:GLY:C	18:O:65:ARG:HH12	2.18	0.51
22:S:16:LEU:O	22:S:20:LEU:HG	2.10	0.51
1:A:334:C:H2'	1:A:335:C:C6	2.46	0.51
1:A:629:G:O2'	1:A:630:G:H5'	2.09	0.51
1:A:909:A:H2'	1:A:910:C:O4'	2.10	0.51
1:A:1060:C:H5''	13:J:51:ARG:HG2	1.92	0.51
1:A:1363:A:H1'	1:A:1365:G:N7	2.25	0.51
1:A:1366:C:HO2'	13:J:60:ARG:HH22	1.58	0.51
5:B:77:ALA:CB	5:B:80:ILE:HD12	2.39	0.51
7:D:160:GLN:O	7:D:163:GLU:HB3	2.10	0.51
7:D:187:ARG:HG3	7:D:188:LEU:N	2.26	0.51
8:E:68:GLU:O	8:E:70:PRO:HD3	2.11	0.51
11:H:83:ILE:HA	11:H:137:VAL:HG22	1.92	0.51
13:J:64:GLU:N	17:N:59:ALA:HB2	2.25	0.51
19:P:43:LYS:HB3	19:P:48:TRP:CD1	2.45	0.51
21:R:40:LEU:C	21:R:42:ARG:N	2.66	0.51
21:R:87:ARG:HG3	21:R:87:ARG:HH11	1.75	0.51
23:T:67:ALA:HA	23:T:73:HIS:H	1.74	0.51
1:A:107:G:H2'	1:A:108:G:H5'	1.92	0.51
1:A:1057:G:H2'	1:A:1058:G:O4'	2.10	0.51
1:A:1128:C:O2	1:A:1130:A:N7	2.43	0.51
5:B:207:ALA:O	5:B:210:SER:HB3	2.10	0.51
10:G:49:ILE:C	10:G:51:GLN:N	2.67	0.51
12:I:126:SER:O	12:I:128:ARG:N	2.43	0.51
15:L:124:LYS:HE2	15:L:127:GLU:OE2	2.10	0.51
22:S:11:VAL:HG22	22:S:39:THR:O	2.10	0.51
1:A:822:C:O2'	1:A:823:G:H5'	2.10	0.51
1:A:1077:G:N2	1:A:1080:A:OP2	2.41	0.51
1:A:1124:G:O2'	13:J:38:ILE:HD13	2.11	0.51
1:A:1153:C:H2'	1:A:1154:G:H8	1.76	0.51
1:A:1390:U:H2'	1:A:1391:U:H6	1.75	0.51
5:B:69:LEU:HD22	5:B:71:VAL:CG2	2.41	0.51
5:B:197:VAL:CB	5:B:200:ILE:HG23	2.37	0.51
6:C:34:LEU:CD1	17:N:25:VAL:HG21	2.40	0.51
7:D:192:GLU:N	7:D:192:GLU:OE1	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:48:GLU:HA	12:I:51:ARG:HH11	1.76	0.51
12:I:76:ALA:O	12:I:79:LEU:HB3	2.10	0.51
15:L:93:LEU:H	15:L:93:LEU:CD2	2.00	0.51
16:M:22:ILE:CB	16:M:25:ILE:HD12	2.41	0.51
18:O:70:LEU:O	18:O:71:GLN:C	2.52	0.51
1:A:189:G:H2'	1:A:190:C:C6	2.45	0.51
1:A:223:U:H5'	23:T:68:LYS:NZ	2.25	0.51
1:A:258:G:H2'	1:A:259:G:C8	2.44	0.51
1:A:761:G:H5'	20:Q:103:GLY:H	1.75	0.51
1:A:972:C:H4'	13:J:57:LYS:CG	2.40	0.51
1:A:1172:C:H2'	1:A:1173:G:H8	1.74	0.51
1:A:1176:A:H2'	1:A:1177:G:C8	2.45	0.51
1:A:1431:C:H2'	1:A:1432:G:H5'	1.92	0.51
5:B:33:TYR:O	5:B:34:ALA:HB2	2.10	0.51
5:B:126:GLU:HG2	5:B:129:GLU:OE1	2.11	0.51
6:C:120:VAL:O	6:C:124:ILE:HG13	2.10	0.51
6:C:126:ARG:O	6:C:127:ARG:HB2	2.09	0.51
6:C:134:ILE:HD11	6:C:153:VAL:CG2	2.41	0.51
7:D:21:LEU:O	7:D:22:LYS:HG3	2.10	0.51
7:D:62:GLN:O	7:D:66:ARG:HB2	2.09	0.51
7:D:111:ALA:CB	7:D:117:ALA:HB2	2.40	0.51
9:F:40:VAL:HG12	9:F:41:GLU:N	2.25	0.51
10:G:151:TYR:HA	10:G:153:HIS:CE1	2.45	0.51
15:L:101:VAL:O	15:L:103:GLY:N	2.43	0.51
16:M:11:ARG:CG	16:M:12:ASN:N	2.72	0.51
17:N:37:PHE:CZ	17:N:53:LEU:HD13	2.46	0.51
18:O:27:VAL:O	18:O:30:ALA:HB3	2.10	0.51
18:O:66:LEU:O	18:O:69:TYR:HB3	2.11	0.51
22:S:41:VAL:HG22	22:S:44:MET:CE	2.35	0.51
23:T:41:ILE:HD11	23:T:87:LYS:HZ1	1.74	0.51
1:A:625:G:O2'	1:A:626:U:H5'	2.10	0.51
1:A:811:C:H4'	1:A:900:A:N6	2.25	0.51
1:A:910:C:P	15:L:97:ARG:HH22	2.33	0.51
1:A:1268:A:H2'	1:A:1269:A:C8	2.45	0.51
1:A:1345:U:C2	1:A:1377:A:N1	2.79	0.51
5:B:132:LYS:HA	5:B:135:GLN:HB3	1.92	0.51
6:C:33:LEU:HD23	6:C:33:LEU:C	2.36	0.51
6:C:157:ILE:CD1	6:C:166:GLU:HB2	2.37	0.51
7:D:126:ILE:CG2	7:D:127:THR:H	2.24	0.51
9:F:53:ALA:O	9:F:54:LYS:HB2	2.09	0.51
10:G:22:LEU:HD11	10:G:101:LEU:HD21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:38:ILE:N	11:H:38:ILE:HD12	2.25	0.51
12:I:10:ARG:HD2	12:I:11:LYS:N	2.25	0.51
1:A:335:C:O2'	1:A:336:C:H5'	2.11	0.51
1:A:624:C:H2'	1:A:625:G:C8	2.44	0.51
1:A:1101:A:H4'	1:A:1102:A:O5'	2.11	0.51
1:A:1402:C:H2'	1:A:1403:C:C6	2.40	0.51
8:E:41:VAL:HG21	8:E:113:ALA:HA	1.91	0.51
10:G:145:ALA:C	10:G:147:ALA:N	2.69	0.51
11:H:31:PHE:O	11:H:35:ILE:CD1	2.58	0.51
11:H:135:CYS:SG	11:H:136:GLU:N	2.83	0.51
22:S:15:LEU:HD12	22:S:16:LEU:N	2.26	0.51
22:S:50:ALA:HA	22:S:58:VAL:O	2.11	0.51
23:T:8:ARG:O	23:T:9:ASN:HB2	2.11	0.51
1:A:16:A:H2'	1:A:17:U:H5'	1.92	0.51
1:A:308:C:H2'	1:A:309:G:H8	1.75	0.51
1:A:977:A:O2'	1:A:979:C:OP2	2.28	0.51
1:A:1054:C:C2'	1:A:1055:A:H5''	2.41	0.51
6:C:139:GLN:CA	6:C:139:GLN:HE21	2.24	0.51
9:F:10:LEU:CD1	9:F:59:TYR:HD2	2.24	0.51
10:G:144:MET:O	10:G:147:ALA:HB3	2.11	0.51
10:G:151:TYR:C	10:G:153:HIS:H	2.18	0.51
11:H:107:LEU:N	11:H:107:LEU:HD12	2.26	0.51
12:I:104:ARG:HD3	12:I:105:ASP:N	2.26	0.51
16:M:15:VAL:HG21	16:M:48:LEU:HD21	1.92	0.51
18:O:50:HIS:O	18:O:51:HIS:C	2.54	0.51
19:P:43:LYS:HB3	19:P:48:TRP:NE1	2.25	0.51
21:R:58:LEU:HD12	21:R:63:GLN:HA	1.93	0.51
22:S:10:PHE:CD2	22:S:10:PHE:C	2.88	0.51
1:A:39:G:O2'	1:A:40:C:H5'	2.11	0.51
1:A:243:A:C5'	1:A:244:U:H5'	2.41	0.51
1:A:657:G:H4'	18:O:28:GLN:HG2	1.91	0.51
1:A:890:G:O2'	1:A:906:G:O6	2.24	0.51
1:A:1010:G:H2'	1:A:1011:G:C8	2.44	0.51
1:A:1060:C:C2	1:A:1198:G:C2	2.99	0.51
1:A:1300:G:O2'	1:A:1301:U:H6	1.94	0.51
1:A:1347:G:N2	1:A:1373:G:H2'	2.26	0.51
3:Y:31:A:H2'	3:Y:32:U:O4'	2.11	0.51
5:B:127:ILE:C	5:B:129:GLU:H	2.19	0.51
5:B:213:LEU:HD23	5:B:213:LEU:C	2.36	0.51
6:C:134:ILE:HG22	6:C:168:ALA:CB	2.40	0.51
12:I:23:ASN:C	12:I:23:ASN:ND2	2.68	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:43:VAL:HG23	15:L:55:VAL:HG21	1.93	0.51
16:M:26:GLY:C	16:M:28:ALA:N	2.68	0.51
20:Q:48:GLU:O	20:Q:49:GLU:C	2.53	0.51
20:Q:63:ARG:HG2	20:Q:64:PRO:CD	2.41	0.51
22:S:38:SER:OG	22:S:71:LEU:HD12	2.11	0.51
22:S:41:VAL:HB	22:S:42:PRO:HD2	1.92	0.51
1:A:883:C:O2'	1:A:884:U:H5'	2.12	0.51
1:A:1030(B):C:H2'	1:A:1030(C):G:O4'	2.10	0.51
1:A:1053:G:C4	1:A:1199:U:C5	2.99	0.51
1:A:1206:G:C6	1:A:1207:G:C5	2.99	0.51
1:A:1431:C:C2'	1:A:1432:G:H5'	2.40	0.51
6:C:177:THR:CG2	6:C:180:ALA:HB2	2.41	0.51
7:D:117:ALA:O	7:D:121:VAL:HG23	2.11	0.51
11:H:103:VAL:CG2	11:H:110:ALA:HB2	2.40	0.51
13:J:94:VAL:CG1	13:J:95:GLU:N	2.74	0.51
14:K:58:PRO:O	14:K:61:ALA:HB3	2.10	0.51
16:M:86:CYS:SG	16:M:88:ARG:CG	2.97	0.51
1:A:130:A:H5'	20:Q:63:ARG:NH2	2.26	0.50
1:A:308:C:H2'	1:A:309:G:C8	2.46	0.50
1:A:491:G:H2'	1:A:492:G:C8	2.43	0.50
1:A:1466:C:H2'	1:A:1467:G:O4'	2.11	0.50
5:B:32:ILE:HG23	5:B:40:HIS:HB3	1.93	0.50
6:C:48:TYR:O	6:C:51:GLY:N	2.41	0.50
6:C:54:ARG:HG3	6:C:55:VAL:N	2.26	0.50
8:E:151:LEU:HD11	11:H:77:GLU:OE2	2.11	0.50
14:K:14:VAL:HG21	14:K:40:ILE:HD11	1.93	0.50
14:K:48:ILE:CD1	14:K:63:LEU:HB3	2.38	0.50
20:Q:78:GLU:HG3	20:Q:78:GLU:O	2.10	0.50
1:A:646:U:H2'	1:A:647:C:C6	2.46	0.50
1:A:954:G:H21	1:A:1227:A:N6	2.00	0.50
1:A:1221:G:C2'	1:A:1222:G:H5'	2.41	0.50
1:A:1313:U:O4	22:S:4:SER:CB	2.58	0.50
6:C:149:ALA:HA	6:C:201:TYR:O	2.11	0.50
6:C:172:ARG:HB3	6:C:172:ARG:NH1	2.26	0.50
13:J:75:ILE:HG22	13:J:76:ASN:N	2.24	0.50
1:A:356:A:H1'	1:A:368:U:O2'	2.11	0.50
1:A:384:G:O2'	1:A:385:C:H5'	2.11	0.50
2:X:2:U:OP2	2:X:3:U:H5	1.95	0.50
6:C:34:LEU:C	6:C:34:LEU:CD2	2.85	0.50
6:C:188:LEU:O	6:C:189:ALA:CB	2.60	0.50
8:E:74:GLY:CA	8:E:116:THR:HG22	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:4:TYR:CE2	9:F:72:VAL:HG22	2.47	0.50
9:F:60:PHE:CZ	21:R:78:LEU:HD21	2.46	0.50
12:I:5:TYR:C	12:I:84:ALA:HA	2.37	0.50
15:L:117:ARG:CZ	15:L:124:LYS:HA	2.41	0.50
16:M:8:GLU:C	16:M:9:ILE:HG13	2.37	0.50
16:M:110:ARG:HH11	16:M:110:ARG:CG	2.25	0.50
20:Q:18:THR:HG23	20:Q:69:LYS:HE3	1.92	0.50
1:A:189:G:H2'	1:A:190:C:H6	1.76	0.50
1:A:321:A:O2'	1:A:322:C:H5'	2.11	0.50
1:A:633:G:H2'	1:A:634:C:C6	2.46	0.50
1:A:1286:A:H2'	1:A:1287:A:H4'	1.93	0.50
1:A:1300:G:O2'	1:A:1301:U:P	2.70	0.50
1:A:1320:C:H41	22:S:37:ARG:HD3	1.76	0.50
5:B:149:LEU:O	5:B:153:ARG:HG3	2.11	0.50
9:F:101:ALA:HB2	21:R:28:GLU:HA	1.92	0.50
14:K:18:ARG:HD2	14:K:83:ILE:HD11	1.92	0.50
21:R:18:ARG:NH2	21:R:21:LYS:NZ	2.60	0.50
23:T:59:ALA:O	23:T:63:ILE:HG13	2.12	0.50
1:A:192:U:O4'	23:T:103:GLY:HA2	2.11	0.50
1:A:670:G:H2'	1:A:671:G:O4'	2.11	0.50
1:A:1202:G:H2'	1:A:1203:C:C5'	2.41	0.50
5:B:92:TYR:CE1	5:B:151:GLY:HA3	2.47	0.50
5:B:174:VAL:O	5:B:177:ALA:HB3	2.11	0.50
23:T:93:GLU:HA	23:T:93:GLU:OE2	2.11	0.50
1:A:281:G:O2'	1:A:282:A:P	2.68	0.50
1:A:373:A:O2'	1:A:374:A:H5'	2.12	0.50
1:A:741:G:H5'	18:O:39:LEU:HD12	1.94	0.50
1:A:818:G:H3'	1:A:819:A:H5'	1.94	0.50
1:A:940:C:H2'	1:A:941:G:H8	1.75	0.50
6:C:47:LEU:CD1	6:C:47:LEU:N	2.73	0.50
6:C:186:PHE:HE1	6:C:197:GLY:HA3	1.76	0.50
8:E:107:ARG:O	8:E:110:LEU:N	2.44	0.50
9:F:48:LEU:HD21	9:F:60:PHE:HZ	1.77	0.50
10:G:6:ARG:O	10:G:7:ALA:C	2.53	0.50
10:G:49:ILE:C	10:G:51:GLN:H	2.20	0.50
11:H:35:ILE:HG22	11:H:39:LEU:CD2	2.42	0.50
15:L:45:PRO:HB3	15:L:49:ASN:HB3	1.92	0.50
22:S:32:LYS:HG3	22:S:32:LYS:O	2.12	0.50
23:T:10:LEU:CD1	23:T:12:ALA:HB3	2.41	0.50
1:A:452:A:O2'	1:A:453:A:C8	2.62	0.50
1:A:620:C:H2'	1:A:621:A:O4'	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:722:A:H4'	1:A:723:U:C4	2.46	0.50
1:A:767:A:O2'	1:A:1524:C:O2	2.29	0.50
1:A:1102:A:H2'	1:A:1103:C:C6	2.46	0.50
1:A:1131:G:H1	1:A:1143:G:H21	1.60	0.50
3:Y:33:U:H5'	3:Y:34:G:OP2	2.12	0.50
5:B:54:THR:O	5:B:57:PHE:HB3	2.12	0.50
7:D:200:GLU:O	7:D:203:VAL:N	2.44	0.50
8:E:13:ILE:HA	8:E:29:GLY:O	2.12	0.50
12:I:59:PHE:HZ	12:I:88:TYR:CE2	2.30	0.50
14:K:13:GLN:HA	14:K:75:TYR:O	2.12	0.50
16:M:80:ARG:C	16:M:82:MET:H	2.19	0.50
1:A:415:A:H2'	1:A:416:G:C8	2.47	0.50
1:A:942:G:C2	1:A:943:U:C6	3.00	0.50
1:A:1096:C:O2'	1:A:1097:C:H5'	2.11	0.50
6:C:90:GLU:C	6:C:92:ALA:N	2.70	0.50
6:C:130:VAL:HG13	6:C:153:VAL:HG21	1.92	0.50
7:D:3:ARG:N	7:D:3:ARG:NE	2.59	0.50
8:E:40:ARG:HG2	8:E:40:ARG:NH1	2.27	0.50
11:H:138:TRP:OXT	11:H:138:TRP:HE3	1.94	0.50
12:I:111:ARG:O	12:I:119:ALA:HB2	2.12	0.50
14:K:100:ALA:O	14:K:102:GLY:N	2.45	0.50
19:P:55:ARG:O	19:P:58:TYR:N	2.45	0.50
1:A:115:G:O2'	1:A:116:A:OP2	2.25	0.50
1:A:518:C:O2'	15:L:50:SER:HB3	2.11	0.50
1:A:933:G:O6	10:G:3:ARG:NH2	2.45	0.50
1:A:1030(A):G:H21	1:A:1031:G:H1	1.58	0.50
1:A:1062:U:H2'	1:A:1063:C:C6	2.47	0.50
1:A:1092:A:H8	1:A:1092:A:O5'	1.95	0.50
1:A:1171:G:H2'	1:A:1172:C:C6	2.47	0.50
5:B:87:ARG:HB3	5:B:219:VAL:HG11	1.94	0.50
5:B:137:ARG:HB3	5:B:137:ARG:HH11	1.76	0.50
6:C:52:LEU:HD12	6:C:55:VAL:CG2	2.42	0.50
6:C:191:THR:HG21	6:C:193:TYR:CE1	2.46	0.50
9:F:62:TRP:C	9:F:63:TYR:HD2	2.20	0.50
15:L:60:LEU:HD23	15:L:66:VAL:HG22	1.93	0.50
15:L:126:LYS:O	15:L:127:GLU:C	2.54	0.50
16:M:40:ASN:HD22	16:M:40:ASN:C	2.19	0.50
1:A:36:C:H4'	15:L:122:THR:O	2.11	0.49
1:A:443:C:H2'	1:A:444:C:H6	1.76	0.49
1:A:458:C:H2'	1:A:459:G:C8	2.45	0.49
1:A:522:C:O2'	1:A:523:A:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:862:C:O2'	1:A:863:U:H5'	2.12	0.49
1:A:895:G:H2'	1:A:896:C:C6	2.48	0.49
1:A:1149:C:H2'	1:A:1150:U:H6	1.77	0.49
1:A:1280:A:O4'	13:J:41:PRO:HG3	2.12	0.49
5:B:59:GLU:O	5:B:62:ALA:HB3	2.12	0.49
5:B:91:PRO:CA	5:B:154:LEU:HD12	2.41	0.49
5:B:96:ARG:HD2	5:B:97:TRP:H	1.76	0.49
5:B:208:ILE:HA	5:B:211:ILE:HD12	1.94	0.49
11:H:112:LEU:HD22	11:H:112:LEU:N	2.27	0.49
13:J:19:SER:HB2	13:J:91:PRO:HG3	1.94	0.49
20:Q:20:THR:HG21	20:Q:41:LYS:HD2	1.95	0.49
21:R:18:ARG:HH22	21:R:21:LYS:NZ	2.09	0.49
21:R:86:VAL:HG12	21:R:87:ARG:N	2.27	0.49
23:T:42:GLN:O	23:T:43:LEU:C	2.55	0.49
23:T:87:LYS:O	23:T:89:ARG:N	2.45	0.49
23:T:105:SER:O	23:T:106:ALA:C	2.54	0.49
1:A:761:G:H4'	20:Q:103:GLY:N	2.28	0.49
1:A:1038:C:H2'	1:A:1039:C:H6	1.74	0.49
1:A:1306:A:O2'	16:M:109:THR:HG21	2.12	0.49
5:B:16:HIS:O	5:B:17:PHE:O	2.31	0.49
5:B:36:ARG:HD2	5:B:41:ILE:HD12	1.95	0.49
5:B:36:ARG:HD2	5:B:41:ILE:CD1	2.42	0.49
5:B:223:ILE:HG21	5:B:230:VAL:HG23	1.93	0.49
7:D:64:LEU:HD12	7:D:75:PHE:CZ	2.46	0.49
12:I:48:GLU:OE1	12:I:51:ARG:HD2	2.11	0.49
13:J:27:ALA:HB1	13:J:81:THR:HG23	1.94	0.49
13:J:62:HIS:HB3	17:N:59:ALA:HB3	1.93	0.49
17:N:44:LEU:C	17:N:44:LEU:HD12	2.38	0.49
18:O:39:LEU:CD2	18:O:56:LEU:HB2	2.42	0.49
1:A:363:A:OP1	15:L:33:ARG:HD2	2.12	0.49
1:A:394:G:H2'	1:A:395:C:H6	1.76	0.49
1:A:530:G:O6	4:Z:3:U:H1'	2.11	0.49
1:A:632:A:C2'	1:A:633:G:H5'	2.42	0.49
1:A:927:G:H2'	1:A:928:G:H8	1.77	0.49
1:A:1065:U:O2'	1:A:1066:C:OP2	2.28	0.49
6:C:160:ALA:O	6:C:162:GLN:N	2.45	0.49
7:D:59:ARG:NH2	7:D:66:ARG:NH1	2.60	0.49
8:E:24:ARG:HG2	8:E:24:ARG:HH11	1.77	0.49
8:E:76:ILE:HG23	8:E:142:LEU:HD13	1.95	0.49
8:E:79:GLU:OE2	11:H:105:ARG:HD3	2.12	0.49
8:E:91:LEU:CD2	8:E:120:THR:HG22	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:60:PHE:O	9:F:61:LEU:HD23	2.12	0.49
10:G:18:TYR:CD2	10:G:59:LEU:HB2	2.48	0.49
10:G:31:MET:CG	10:G:32:ARG:N	2.75	0.49
10:G:135:VAL:O	10:G:139:GLU:HG3	2.12	0.49
12:I:93:ARG:O	12:I:95:LYS:N	2.46	0.49
12:I:108:VAL:HG12	12:I:109:VAL:N	2.28	0.49
23:T:14:LYS:O	23:T:17:ARG:HB2	2.12	0.49
1:A:132:C:O2'	1:A:133:U:H5'	2.12	0.49
1:A:397:A:H5'	1:A:398:C:P	2.52	0.49
1:A:409:G:H2'	1:A:410:G:O4'	2.13	0.49
1:A:444:C:H2'	1:A:445:G:H8	1.77	0.49
1:A:879:C:O2'	1:A:880:C:H5'	2.12	0.49
1:A:1022:G:H2'	1:A:1023:G:H8	1.76	0.49
1:A:1347:G:C6	12:I:107:ARG:NH2	2.80	0.49
1:A:1474:G:O2'	1:A:1475:G:H5'	2.11	0.49
6:C:36:ASP:O	6:C:39:ILE:HB	2.12	0.49
6:C:61:ALA:O	6:C:62:ASP:C	2.55	0.49
6:C:156:ARG:HB3	6:C:196:LEU:HD22	1.95	0.49
9:F:19:LEU:HD23	9:F:19:LEU:O	2.12	0.49
14:K:101:SER:OG	14:K:102:GLY:N	2.45	0.49
15:L:111:LYS:O	15:L:112:ASP:HB2	2.12	0.49
17:N:35:ARG:O	17:N:37:PHE:N	2.40	0.49
1:A:622:A:C8	1:A:623:C:C6	3.00	0.49
1:A:633:G:H2'	1:A:634:C:H6	1.78	0.49
1:A:737:A:H2'	1:A:738:C:H6	1.77	0.49
1:A:803:G:H2'	1:A:804:U:O4'	2.12	0.49
1:A:939:G:C5'	10:G:102:ARG:HH22	2.17	0.49
1:A:981:U:H5'	17:N:21:TYR:CE1	2.48	0.49
1:A:1020:U:H2'	1:A:1021:G:H8	1.73	0.49
5:B:100:GLY:O	5:B:101:MET:C	2.55	0.49
6:C:18:TRP:O	6:C:54:ARG:NH2	2.44	0.49
16:M:15:VAL:HG23	16:M:43:THR:O	2.12	0.49
1:A:45:U:H2'	1:A:46:G:C8	2.48	0.49
1:A:404:U:O2'	1:A:405:U:H5'	2.11	0.49
1:A:691:G:O6	14:K:52:GLY:HA2	2.12	0.49
1:A:930:C:O2'	1:A:931:C:H5'	2.13	0.49
1:A:1218:C:H2'	1:A:1219:U:C6	2.47	0.49
1:A:1349:A:H2'	1:A:1350:A:H8	1.77	0.49
3:Y:39:U:O5'	3:Y:39:U:H6	1.94	0.49
5:B:12:GLU:C	5:B:12:GLU:CD	2.79	0.49
6:C:84:ILE:O	6:C:84:ILE:HG12	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:110:ASN:ND2	6:C:140:ARG:HB3	2.28	0.49
7:D:8:VAL:CG1	7:D:21:LEU:HD13	2.43	0.49
9:F:27:GLN:OE1	9:F:27:GLN:HA	2.13	0.49
10:G:85:TYR:CD1	10:G:154:TYR:HE1	2.30	0.49
11:H:59:LEU:O	11:H:61:VAL:HG23	2.13	0.49
13:J:89:ASP:CG	13:J:90:LEU:N	2.69	0.49
14:K:47:VAL:HG12	14:K:48:ILE:N	2.27	0.49
23:T:91:LEU:C	23:T:93:GLU:H	2.18	0.49
1:A:417:C:H2'	1:A:418:C:H6	1.77	0.49
1:A:674:G:O2'	1:A:675:A:H5'	2.13	0.49
1:A:1116:C:C3'	1:A:1117:G:H5''	2.43	0.49
5:B:71:VAL:O	5:B:165:VAL:HG23	2.12	0.49
6:C:8:ILE:O	6:C:12:LEU:N	2.45	0.49
11:H:53:VAL:O	11:H:53:VAL:HG12	2.13	0.49
13:J:9:ARG:C	13:J:16:LEU:HD21	2.37	0.49
18:O:39:LEU:HD21	18:O:56:LEU:HB2	1.94	0.49
18:O:56:LEU:HA	18:O:59:MET:HE3	1.94	0.49
20:Q:96:GLN:O	20:Q:97:SER:HB3	2.12	0.49
1:A:67:C:O2'	1:A:171:A:H1'	2.12	0.49
1:A:112:G:H4'	1:A:389:A:H5''	1.93	0.49
1:A:246:A:N6	1:A:281:G:H1'	2.28	0.49
1:A:338:A:H2	1:A:351:G:H22	1.60	0.49
1:A:647:C:H2'	1:A:648:A:C8	2.47	0.49
1:A:1399:C:C2	1:A:1401:G:C5	3.00	0.49
5:B:25:ASN:HD22	5:B:26:PRO:N	2.10	0.49
8:E:51:VAL:O	8:E:55:VAL:HG23	2.13	0.49
8:E:62:ALA:C	8:E:64:ARG:H	2.21	0.49
12:I:30:GLY:O	12:I:31:GLN:O	2.31	0.49
12:I:127:LYS:H	12:I:127:LYS:CD	2.20	0.49
15:L:43:VAL:CG1	15:L:44:THR:H	2.23	0.49
16:M:14:ARG:HB3	16:M:16:ASP:OD1	2.13	0.49
19:P:53:VAL:CG2	19:P:54:GLU:N	2.75	0.49
1:A:415:A:H2'	1:A:416:G:H8	1.78	0.49
1:A:716:A:N3	14:K:117:ASN:O	2.46	0.49
1:A:789:U:H4'	2:X:2:U:O2	2.13	0.49
1:A:812:C:H1'	1:A:813:U:OP2	2.13	0.49
1:A:934:C:N3	1:A:1345:U:C5	2.80	0.49
1:A:1205:U:H4'	6:C:195:VAL:CG2	2.43	0.49
1:A:1391:U:H2'	1:A:1392:G:H8	1.73	0.49
1:A:1425:U:H2'	1:A:1426:C:C6	2.47	0.49
5:B:141:GLU:O	5:B:142:LEU:C	2.55	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:200:ILE:CD1	5:B:202:PRO:HD3	2.41	0.49
6:C:50:ALA:HB2	6:C:75:VAL:HB	1.93	0.49
6:C:67:THR:O	6:C:67:THR:HG22	2.12	0.49
8:E:20:GLN:C	8:E:21:ALA:O	2.53	0.49
9:F:36:ARG:NH1	9:F:36:ARG:HG2	2.28	0.49
10:G:95:ARG:HG3	10:G:95:ARG:HH11	1.77	0.49
13:J:47:PHE:N	13:J:63:PHE:O	2.45	0.49
15:L:89:ARG:HH12	15:L:97:ARG:HE	1.61	0.49
17:N:14:PRO:O	17:N:15:LYS:CB	2.60	0.49
19:P:43:LYS:HB3	19:P:48:TRP:CE2	2.48	0.49
1:A:176:C:H2'	1:A:177:C:H6	1.78	0.49
1:A:255:G:H2'	1:A:256:U:C6	2.48	0.49
1:A:738:C:OP2	9:F:92:LYS:NZ	2.36	0.49
1:A:976:G:C8	1:A:1358:U:O2	2.66	0.49
1:A:1253:G:H2'	1:A:1254:C:C6	2.47	0.49
1:A:1481:U:O2'	1:A:1482:G:H5'	2.12	0.49
5:B:54:THR:O	5:B:57:PHE:N	2.46	0.49
5:B:162:ILE:O	5:B:162:ILE:CG2	2.61	0.49
6:C:34:LEU:HD22	6:C:38:ARG:NH1	2.28	0.49
6:C:203:PHE:O	6:C:204:LEU:HD23	2.13	0.49
7:D:162:LEU:HD13	7:D:181:MET:HG2	1.95	0.49
7:D:163:GLU:C	7:D:165:MET:H	2.21	0.49
9:F:14:LEU:HD13	9:F:19:LEU:HA	1.94	0.49
11:H:14:ARG:HB3	11:H:14:ARG:NH1	2.28	0.49
13:J:53:PRO:HA	17:N:41:ARG:NH2	2.24	0.49
15:L:124:LYS:CD	15:L:125:PRO:HD2	2.38	0.49
20:Q:69:LYS:C	20:Q:70:ARG:HD2	2.37	0.49
1:A:828:A:H2'	1:A:829:G:O4'	2.13	0.48
1:A:865:A:O2'	1:A:866:C:H5'	2.13	0.48
1:A:1194:U:H2'	1:A:1195:C:C6	2.48	0.48
1:A:1292:U:H5'	12:I:38:GLN:NE2	2.28	0.48
5:B:176:GLU:O	5:B:177:ALA:C	2.56	0.48
6:C:190:ARG:HB3	6:C:190:ARG:NH1	2.28	0.48
7:D:127:THR:HG23	7:D:147:ALA:HB3	1.95	0.48
9:F:33:TYR:C	9:F:71:ARG:NH2	2.70	0.48
11:H:123:GLU:O	11:H:127:LEU:HB2	2.12	0.48
19:P:43:LYS:HG2	19:P:48:TRP:CZ2	2.48	0.48
21:R:74:ARG:HA	21:R:79:LEU:O	2.13	0.48
23:T:14:LYS:O	23:T:18:GLN:HG3	2.13	0.48
1:A:201:C:N4	1:A:216:G:H1	2.08	0.48
1:A:728:A:H8	1:A:728:A:O5'	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1152:A:H2'	1:A:1153:C:H6	1.76	0.48
1:A:1488:G:H2'	1:A:1489:G:C8	2.48	0.48
6:C:3:ASN:ND2	6:C:4:LYS:HE2	2.28	0.48
10:G:148:ASN:O	10:G:150:ALA:N	2.46	0.48
12:I:93:ARG:C	12:I:95:LYS:N	2.71	0.48
13:J:30:SER:HB2	13:J:80:LYS:HG3	1.96	0.48
16:M:87:TYR:O	16:M:90:LEU:N	2.42	0.48
17:N:4:LYS:O	17:N:7:ILE:HG13	2.13	0.48
20:Q:97:SER:HB2	20:Q:103:GLY:CA	2.43	0.48
22:S:5:LEU:C	22:S:6:LYS:HG3	2.38	0.48
1:A:376:G:H2'	1:A:377:G:C8	2.47	0.48
1:A:749:C:P	1:A:749:C:H3'	2.54	0.48
1:A:814:A:N7	1:A:816:A:C4	2.81	0.48
1:A:1262:C:H2'	1:A:1263:C:C6	2.46	0.48
1:A:1392:G:H2'	1:A:1393:U:H6	1.78	0.48
5:B:88:ALA:HB3	5:B:90:MET:HG2	1.95	0.48
6:C:152:ILE:HB	6:C:199:LYS:HB2	1.96	0.48
7:D:127:THR:CG2	7:D:147:ALA:HB3	2.43	0.48
8:E:79:GLU:O	11:H:104:ARG:CZ	2.61	0.48
10:G:95:ARG:HG3	10:G:95:ARG:NH1	2.29	0.48
12:I:63:ILE:HG22	12:I:65:VAL:HG23	1.94	0.48
13:J:19:SER:O	13:J:20:ALA:C	2.56	0.48
19:P:4:ILE:HG13	19:P:64:ALA:HB1	1.95	0.48
21:R:52:PRO:HB2	21:R:54:ARG:HG3	1.93	0.48
22:S:32:LYS:HA	22:S:50:ALA:HB3	1.96	0.48
1:A:163:C:O2'	1:A:164:U:H5'	2.13	0.48
1:A:456:C:H2'	1:A:457:C:C6	2.48	0.48
1:A:1372:U:C2'	1:A:1373:G:H5'	2.44	0.48
1:A:1392:G:O2'	1:A:1393:U:H5'	2.13	0.48
3:Y:34:G:H5'	3:Y:34:G:C8	2.39	0.48
5:B:111:ARG:HB3	5:B:149:LEU:HD11	1.94	0.48
6:C:50:ALA:HB1	6:C:70:VAL:CG1	2.36	0.48
6:C:187:ALA:O	6:C:198:VAL:N	2.46	0.48
10:G:151:TYR:C	10:G:153:HIS:N	2.70	0.48
12:I:65:VAL:HG21	12:I:77:ILE:HD11	1.94	0.48
15:L:117:ARG:O	15:L:118:SER:C	2.55	0.48
19:P:1:MET:CE	19:P:3:LYS:HD2	2.44	0.48
22:S:35:SER:C	22:S:37:ARG:N	2.69	0.48
23:T:45:GLN:C	23:T:47:GLY:N	2.71	0.48
23:T:45:GLN:C	23:T:47:GLY:H	2.19	0.48
1:A:166:G:H2'	1:A:167:G:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:G:O2'	1:A:169:C:H5'	2.13	0.48
1:A:877:C:O2'	1:A:878:G:H5'	2.14	0.48
1:A:918:A:H2'	1:A:919:A:H8	1.74	0.48
1:A:1125:U:H3	13:J:5:ARG:HH21	1.61	0.48
9:F:8:ILE:HD11	9:F:79:LEU:HD13	1.94	0.48
10:G:153:HIS:C	10:G:155:ARG:H	2.22	0.48
13:J:45:ARG:O	13:J:64:GLU:HA	2.13	0.48
13:J:81:THR:C	13:J:83:GLU:N	2.70	0.48
14:K:116:HIS:O	14:K:117:ASN:HB2	2.14	0.48
15:L:69:TYR:HE2	15:L:71:PRO:HA	1.79	0.48
15:L:97:ARG:HB2	15:L:98:TYR:CD1	2.49	0.48
17:N:4:LYS:HA	17:N:7:ILE:HD11	1.95	0.48
20:Q:68:ARG:N	20:Q:70:ARG:HH11	2.08	0.48
23:T:10:LEU:O	23:T:12:ALA:N	2.46	0.48
1:A:112:G:H21	1:A:354:G:H5'	1.77	0.48
1:A:314:C:O2'	1:A:315:A:H5'	2.13	0.48
1:A:501:C:O2'	1:A:502:G:H5'	2.14	0.48
1:A:1030(C):G:H2'	1:A:1030(D):A:O4'	2.14	0.48
1:A:1097:C:H2'	1:A:1098:C:H6	1.78	0.48
1:A:1221:G:O2'	1:A:1222:G:H5'	2.12	0.48
1:A:1443:G:H5''	1:A:1446:A:H5''	1.89	0.48
5:B:87:ARG:HG3	5:B:87:ARG:HH11	1.77	0.48
5:B:116:GLU:HA	5:B:119:GLU:OE1	2.13	0.48
5:B:123:ALA:CA	5:B:127:ILE:HD11	2.43	0.48
5:B:203:GLY:O	5:B:204:ASN:C	2.56	0.48
9:F:69:GLU:O	9:F:72:VAL:HG23	2.14	0.48
17:N:37:PHE:C	17:N:39:LEU:H	2.20	0.48
22:S:53:ASN:N	22:S:53:ASN:ND2	2.61	0.48
23:T:18:GLN:O	23:T:19:SER:C	2.56	0.48
1:A:47:C:C6	1:A:365:U:H2'	2.48	0.48
1:A:103:C:P	23:T:17:ARG:NH1	2.87	0.48
1:A:344:A:O2'	1:A:345:C:OP1	2.30	0.48
1:A:959:A:H2'	1:A:960:U:O4'	2.14	0.48
1:A:966:G:H2'	1:A:967:C:C6	2.49	0.48
1:A:1305:G:H2'	1:A:1331:G:N2	2.28	0.48
1:A:1370:G:H2'	1:A:1371:G:H8	1.78	0.48
1:A:1394:A:C5	1:A:1501:C:H4'	2.49	0.48
1:A:1488:G:H2'	1:A:1489:G:H8	1.79	0.48
5:B:33:TYR:HB3	5:B:41:ILE:O	2.14	0.48
5:B:44:LEU:O	5:B:47:THR:N	2.47	0.48
6:C:43:LEU:CD1	6:C:68:VAL:HG21	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:170:VAL:HG22	7:D:171:GLY:H	1.79	0.48
7:D:173:TRP:HB2	7:D:187:ARG:O	2.14	0.48
8:E:99:GLY:O	8:E:117:ASP:HA	2.12	0.48
9:F:33:TYR:CD1	9:F:75:LEU:HA	2.49	0.48
9:F:33:TYR:HA	9:F:71:ARG:NH2	2.27	0.48
9:F:80:ARG:NH1	9:F:88:VAL:HB	2.29	0.48
10:G:62:PHE:HA	10:G:124:LEU:HD22	1.96	0.48
10:G:124:LEU:O	10:G:127:ALA:HB3	2.14	0.48
13:J:14:LYS:O	13:J:18:ALA:HB2	2.14	0.48
17:N:41:ARG:HG2	17:N:41:ARG:HH11	1.79	0.48
1:A:109:A:H4'	1:A:110:C:OP2	2.13	0.48
1:A:262:A:C6	1:A:263:A:C6	3.02	0.48
1:A:1345:U:C2	1:A:1377:A:C2	3.02	0.48
1:A:1346:A:H61	1:A:1374:A:H3'	1.79	0.48
1:A:1414:U:H2'	1:A:1415:G:H8	1.79	0.48
5:B:7:VAL:C	5:B:8:LYS:HG3	2.38	0.48
5:B:19:HIS:NE2	5:B:206:ASP:HB3	2.28	0.48
6:C:60:ALA:O	6:C:61:ALA:HB3	2.13	0.48
6:C:107:GLN:CD	6:C:107:GLN:N	2.69	0.48
8:E:15:ARG:O	8:E:16:THR:HB	2.13	0.48
8:E:78:HIS:C	8:E:78:HIS:HD1	2.21	0.48
8:E:86:ALA:C	8:E:125:SER:HB3	2.39	0.48
10:G:22:LEU:HD21	10:G:66:VAL:HG21	1.96	0.48
10:G:120:ILE:O	10:G:124:LEU:HD12	2.12	0.48
15:L:93:LEU:CG	15:L:96:VAL:HG21	2.43	0.48
17:N:21:TYR:CE2	17:N:23:ARG:NE	2.81	0.48
1:A:12:U:H4'	1:A:526:C:H4'	1.96	0.48
1:A:175:C:O2'	1:A:176:C:H5'	2.13	0.48
1:A:264:U:H2'	1:A:265:G:O4'	2.14	0.48
1:A:781:A:H2	1:A:1514:C:O4'	1.97	0.48
1:A:1014:A:H2'	1:A:1015:A:C8	2.48	0.48
5:B:35:GLU:HA	5:B:40:HIS:HA	1.95	0.48
5:B:141:GLU:O	5:B:145:LEU:HG	2.13	0.48
7:D:52:SER:C	7:D:54:TYR:N	2.72	0.48
10:G:38:LEU:O	10:G:42:ILE:HG13	2.14	0.48
12:I:88:TYR:CG	12:I:89:ASN:N	2.81	0.48
13:J:80:LYS:O	13:J:83:GLU:HB3	2.13	0.48
1:A:1183:A:O2'	1:A:1184:G:OP1	2.28	0.48
7:D:173:TRP:O	7:D:186:LEU:HG	2.14	0.48
8:E:127:ASN:O	8:E:128:PRO:C	2.56	0.48
9:F:72:VAL:O	9:F:75:LEU:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:15:ASP:HB3	10:G:19:GLY:N	2.27	0.48
12:I:4:TYR:CZ	12:I:88:TYR:CD1	3.02	0.48
12:I:66:ARG:CZ	12:I:66:ARG:HB2	2.43	0.48
12:I:97:LYS:HB2	12:I:98:PRO:HD3	1.96	0.48
15:L:101:VAL:O	15:L:102:ARG:C	2.56	0.48
21:R:47:THR:HG22	21:R:48:GLY:N	2.29	0.48
1:A:413:G:N2	1:A:428:G:H1'	2.29	0.47
1:A:669:U:H2'	1:A:670:G:H8	1.77	0.47
1:A:913:A:O2'	1:A:914:A:P	2.72	0.47
1:A:1288:A:H2'	1:A:1289:A:C8	2.49	0.47
1:A:1320:C:H2'	1:A:1321:C:O4'	2.14	0.47
1:A:1372:U:H2'	1:A:1373:G:C5'	2.44	0.47
5:B:87:ARG:HH12	5:B:233:SER:CB	2.27	0.47
6:C:32:LEU:HD23	6:C:32:LEU:O	2.14	0.47
6:C:54:ARG:O	6:C:55:VAL:HG23	2.14	0.47
6:C:57:ILE:HG22	6:C:58:GLU:N	2.28	0.47
6:C:139:GLN:HA	6:C:139:GLN:NE2	2.29	0.47
7:D:148:VAL:CG1	7:D:158:ILE:HD13	2.44	0.47
8:E:80:ILE:CD1	8:E:91:LEU:CB	2.76	0.47
8:E:82:VAL:HG12	8:E:89:ILE:HG22	1.96	0.47
14:K:46:GLY:O	14:K:47:VAL:C	2.56	0.47
20:Q:67:LYS:O	20:Q:68:ARG:HB3	2.14	0.47
21:R:86:VAL:CG1	21:R:87:ARG:N	2.77	0.47
22:S:41:VAL:O	22:S:42:PRO:C	2.57	0.47
1:A:222:U:H2'	1:A:223:U:C6	2.49	0.47
1:A:336:C:O2'	1:A:337:C:H5'	2.13	0.47
1:A:943:U:C2'	1:A:944:G:H5'	2.44	0.47
1:A:1276:G:O5'	1:A:1276:G:H8	1.97	0.47
6:C:59:ARG:HD3	6:C:97:LYS:NZ	2.29	0.47
7:D:163:GLU:C	7:D:165:MET:N	2.72	0.47
7:D:187:ARG:HE	7:D:187:ARG:HA	1.78	0.47
8:E:102:ALA:HB2	8:E:120:THR:OG1	2.13	0.47
10:G:62:PHE:HA	10:G:124:LEU:CD2	2.44	0.47
10:G:122:HIS:O	10:G:123:GLU:C	2.57	0.47
12:I:65:VAL:CG1	12:I:73:GLN:HB3	2.26	0.47
14:K:19:ALA:HB2	14:K:80:VAL:HG11	1.95	0.47
23:T:53:LEU:HD13	23:T:100:ILE:CG2	2.44	0.47
1:A:986:A:H2'	1:A:987:G:C8	2.49	0.47
1:A:1136:U:H5''	1:A:1137:C:OP2	2.13	0.47
5:B:12:GLU:OE1	5:B:15:VAL:N	2.46	0.47
5:B:102:LEU:N	5:B:102:LEU:HD12	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:142:LEU:HD22	5:B:146:GLN:NE2	2.28	0.47
5:B:162:ILE:C	5:B:185:ILE:HD13	2.39	0.47
6:C:47:LEU:CD2	6:C:68:VAL:HG11	2.43	0.47
7:D:19:LEU:HD23	7:D:20:TYR:H	1.78	0.47
7:D:63:LYS:O	7:D:64:LEU:C	2.57	0.47
8:E:86:ALA:O	8:E:125:SER:N	2.43	0.47
10:G:37:ASN:C	10:G:39:ALA:N	2.71	0.47
12:I:99:LEU:HD22	12:I:99:LEU:N	2.29	0.47
14:K:24:SER:C	14:K:26:ASN:N	2.72	0.47
14:K:29:ILE:O	14:K:29:ILE:HG12	2.14	0.47
14:K:33:THR:HG23	14:K:34:ASP:O	2.13	0.47
17:N:18:VAL:C	17:N:20:ALA:H	2.22	0.47
24:V:6:ARG:O	24:V:12:LYS:HD2	2.14	0.47
1:A:138:G:O2'	1:A:139:G:H5'	2.14	0.47
1:A:477:G:H2'	1:A:478:A:C8	2.48	0.47
1:A:509:A:N3	1:A:543:C:O2'	2.42	0.47
1:A:645:C:O2'	1:A:646:U:H5'	2.13	0.47
1:A:737:A:O2'	1:A:738:C:H5'	2.13	0.47
1:A:960:U:O2	1:A:960:U:C2'	2.63	0.47
1:A:992:U:O2'	1:A:993:G:OP2	2.24	0.47
1:A:1123:A:H4'	13:J:37:PRO:HD2	1.96	0.47
1:A:1460:A:H2'	1:A:1461:G:O4'	2.14	0.47
5:B:103:THR:O	5:B:103:THR:CG2	2.63	0.47
6:C:54:ARG:HG2	6:C:54:ARG:HH11	1.79	0.47
15:L:24:VAL:HG12	15:L:26:ALA:HB2	1.96	0.47
18:O:82:ILE:O	18:O:83:GLU:C	2.57	0.47
19:P:34:GLU:HG2	19:P:35:LYS:N	2.27	0.47
20:Q:62:SER:OG	20:Q:72:ARG:HG3	2.15	0.47
22:S:40:ILE:HA	22:S:44:MET:SD	2.54	0.47
1:A:26:A:H61	1:A:558:G:H1'	1.79	0.47
1:A:325:A:H2'	1:A:326:G:O4'	2.14	0.47
1:A:575:G:OP1	1:A:575:G:H4'	2.15	0.47
1:A:939:G:H2'	1:A:940:C:H6	1.80	0.47
1:A:1202:G:H2'	1:A:1203:C:H5'	1.96	0.47
1:A:1249:C:O2'	12:I:73:GLN:NE2	2.48	0.47
1:A:1309:G:N7	16:M:99:ARG:NH2	2.62	0.47
7:D:24:GLU:O	7:D:25:ARG:HB3	2.15	0.47
7:D:61:LYS:O	7:D:62:GLN:C	2.56	0.47
8:E:78:HIS:C	8:E:78:HIS:ND1	2.71	0.47
11:H:9:MET:O	11:H:10:LEU:C	2.57	0.47
12:I:97:LYS:N	12:I:98:PRO:CD	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:66:LEU:O	14:K:67:ASP:C	2.56	0.47
1:A:91:C:O2'	1:A:92:C:H5'	2.15	0.47
1:A:411:A:C6	1:A:429:U:C4	3.03	0.47
1:A:921:U:O2	8:E:19:MET:HB2	2.15	0.47
5:B:16:HIS:NE2	5:B:214:ILE:CG1	2.65	0.47
5:B:30:ARG:HG3	5:B:31:TYR:CE2	2.50	0.47
5:B:61:LEU:HD21	5:B:160:ASP:CB	2.44	0.47
5:B:134:GLU:C	5:B:136:VAL:N	2.71	0.47
6:C:202:ILE:HG22	6:C:204:LEU:HD21	1.96	0.47
11:H:9:MET:HE1	11:H:32:LYS:HA	1.96	0.47
12:I:48:GLU:HA	12:I:48:GLU:OE1	2.14	0.47
16:M:11:ARG:HG2	16:M:12:ASN:N	2.29	0.47
16:M:78:ILE:C	16:M:80:ARG:N	2.70	0.47
21:R:86:VAL:O	21:R:87:ARG:CB	2.62	0.47
1:A:16:A:O2'	1:A:17:U:H5'	2.15	0.47
1:A:270:A:H2'	1:A:271:C:C6	2.50	0.47
1:A:364:A:H2'	1:A:365:U:O2	2.13	0.47
1:A:539:A:H2'	1:A:540:G:H8	1.80	0.47
1:A:742:G:H5''	18:O:58:MET:CE	2.45	0.47
1:A:991:U:O2	1:A:993:G:H8	1.97	0.47
1:A:1057:G:C5'	6:C:154:SER:HB2	2.43	0.47
1:A:1315:U:H2'	1:A:1316:G:C8	2.50	0.47
1:A:1331:G:O2'	1:A:1332:A:OP2	2.31	0.47
1:A:1402:C:H2'	1:A:1403:C:O4'	2.15	0.47
5:B:17:PHE:HB3	5:B:44:LEU:HD21	1.95	0.47
5:B:96:ARG:O	5:B:98:LEU:HD23	2.15	0.47
6:C:83:ARG:O	6:C:86:VAL:N	2.47	0.47
6:C:139:GLN:O	6:C:140:ARG:C	2.58	0.47
6:C:156:ARG:O	6:C:156:ARG:CD	2.62	0.47
7:D:32:ALA:O	7:D:34:GLU:N	2.48	0.47
7:D:67:ILE:HG22	7:D:68:TYR:N	2.29	0.47
7:D:152:SER:HB3	7:D:155:LEU:HD12	1.97	0.47
8:E:15:ARG:O	8:E:16:THR:HG22	2.14	0.47
8:E:79:GLU:HA	8:E:91:LEU:O	2.14	0.47
8:E:122:GLU:O	8:E:123:LEU:HD23	2.14	0.47
9:F:19:LEU:C	9:F:19:LEU:CD2	2.87	0.47
11:H:11:THR:C	11:H:13:ILE:N	2.70	0.47
12:I:118:LYS:NZ	12:I:118:LYS:CB	2.77	0.47
14:K:69:ALA:C	14:K:73:MET:HG2	2.40	0.47
21:R:40:LEU:C	21:R:42:ARG:H	2.21	0.47
22:S:43:GLU:H	22:S:43:GLU:CD	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:T:59:ALA:O	23:T:60:GLU:C	2.57	0.47
23:T:91:LEU:HD12	23:T:91:LEU:H	1.79	0.47
1:A:393:A:C2'	1:A:394:G:H5'	2.45	0.47
1:A:502:G:H2'	1:A:503:C:C6	2.48	0.47
1:A:807:A:H2'	1:A:808:C:C6	2.49	0.47
1:A:991:U:C4	1:A:1212:U:H1'	2.50	0.47
1:A:1271:G:H2'	1:A:1272:G:C8	2.50	0.47
1:A:1327:C:O2'	1:A:1328:C:H5'	2.14	0.47
5:B:139:LYS:O	5:B:139:LYS:HD3	2.15	0.47
5:B:208:ILE:O	5:B:209:ARG:C	2.58	0.47
7:D:54:TYR:O	7:D:55:ALA:C	2.58	0.47
7:D:142:PRO:HA	7:D:185:PHE:HD2	1.79	0.47
10:G:41:ARG:O	10:G:42:ILE:C	2.57	0.47
13:J:46:ARG:HG2	13:J:46:ARG:HH11	1.80	0.47
14:K:33:THR:OG1	14:K:39:PRO:HA	2.15	0.47
15:L:43:VAL:CG2	15:L:55:VAL:HG21	2.44	0.47
18:O:21:ASP:OD1	18:O:24:SER:HB2	2.14	0.47
20:Q:53:LEU:HD12	20:Q:85:VAL:HG21	1.97	0.47
21:R:25:THR:O	21:R:26:LEU:HD13	2.13	0.47
22:S:13:ASP:O	22:S:16:LEU:N	2.48	0.47
23:T:41:ILE:HD13	23:T:87:LYS:HZ2	1.80	0.47
1:A:188:C:O4'	23:T:89:ARG:NH1	2.48	0.47
1:A:376:G:OP2	19:P:67:THR:HG21	2.15	0.47
1:A:857:C:H2'	1:A:858:G:O4'	2.14	0.47
1:A:1191:A:OP2	6:C:3:ASN:OD1	2.33	0.47
1:A:1238:A:OP2	1:A:1335:C:H1'	2.15	0.47
6:C:134:ILE:O	6:C:135:LYS:C	2.55	0.47
7:D:59:ARG:HH22	7:D:66:ARG:HH12	1.61	0.47
10:G:118:VAL:O	10:G:119:ARG:C	2.58	0.47
10:G:135:VAL:HG12	10:G:139:GLU:HG3	1.96	0.47
11:H:4:ASP:CG	11:H:85:ARG:HH12	2.23	0.47
13:J:9:ARG:HA	13:J:16:LEU:HD11	1.97	0.47
13:J:22:LYS:C	13:J:24:VAL:N	2.73	0.47
13:J:28:ARG:HG2	13:J:28:ARG:HH11	1.80	0.47
14:K:40:ILE:HG23	14:K:75:TYR:CE2	2.50	0.47
16:M:40:ASN:ND2	16:M:42:ALA:H	2.13	0.47
17:N:18:VAL:O	17:N:20:ALA:N	2.48	0.47
1:A:123:C:OP1	1:A:312:C:H5'	2.14	0.47
1:A:356:A:O2'	1:A:357:G:H5'	2.15	0.47
1:A:439:A:C4	1:A:497:A:C2	3.03	0.47
1:A:731:G:H5'	1:A:766:A:H4'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:737:A:H2'	1:A:738:C:C6	2.49	0.47
1:A:781:A:C5	1:A:802:A:C2	3.02	0.47
1:A:1004:A:N6	1:A:1037:C:H42	2.13	0.47
1:A:1235:U:O2'	1:A:1236:A:H5'	2.15	0.47
1:A:1271:G:H2'	1:A:1272:G:H8	1.80	0.47
1:A:1283:G:O2'	1:A:1284:C:H5'	2.15	0.47
1:A:1343:G:H4'	12:I:122:ALA:O	2.14	0.47
5:B:15:VAL:HG22	5:B:209:ARG:HG3	1.97	0.47
11:H:31:PHE:CE1	11:H:35:ILE:HD11	2.50	0.47
11:H:56:LYS:HD2	11:H:56:LYS:N	2.30	0.47
15:L:39:VAL:CG2	15:L:57:LYS:HG2	2.45	0.47
15:L:40:VAL:O	15:L:40:VAL:HG12	2.15	0.47
16:M:19:LEU:HA	16:M:22:ILE:CD1	2.45	0.47
19:P:39:TYR:CZ	19:P:41:PRO:HA	2.50	0.47
20:Q:79:SER:O	20:Q:80:GLY:C	2.58	0.47
21:R:39:VAL:HG13	21:R:40:LEU:N	2.30	0.47
22:S:10:PHE:HE2	22:S:12:ASP:OD1	1.98	0.47
1:A:488:C:H2'	1:A:489:C:C6	2.49	0.46
1:A:780:A:C2	1:A:801:U:C5	3.04	0.46
1:A:831:U:H2'	1:A:832:C:C6	2.50	0.46
1:A:1194:U:O2'	1:A:1195:C:H5'	2.14	0.46
1:A:1424:C:O2'	1:A:1425:U:H5'	2.16	0.46
1:A:1442:G:C6	1:A:1446:A:N6	2.83	0.46
7:D:10:ARG:HG3	7:D:10:ARG:NH1	2.28	0.46
7:D:53:ASP:O	7:D:57:ARG:HD3	2.15	0.46
9:F:36:ARG:HG2	9:F:36:ARG:HH11	1.80	0.46
12:I:111:ARG:HH11	12:I:111:ARG:CG	2.27	0.46
14:K:109:VAL:HG22	21:R:86:VAL:HA	1.97	0.46
18:O:87:ILE:HG22	18:O:88:ARG:N	2.29	0.46
19:P:18:ARG:HE	19:P:35:LYS:HZ2	1.63	0.46
1:A:690:G:H2'	1:A:691:G:C8	2.49	0.46
1:A:1121:U:H2'	1:A:1122:U:C6	2.50	0.46
1:A:1338:G:H2'	1:A:1339:A:C8	2.50	0.46
1:A:1411:C:O2'	1:A:1412:C:H5'	2.15	0.46
1:A:1513:A:H2'	1:A:1514:C:H6	1.79	0.46
5:B:15:VAL:CG1	5:B:209:ARG:HB3	2.45	0.46
5:B:20:GLU:O	5:B:39:ILE:HG23	2.16	0.46
7:D:25:ARG:CZ	7:D:30:LYS:HD3	2.45	0.46
11:H:4:ASP:CG	11:H:85:ARG:NH1	2.73	0.46
14:K:48:ILE:H	14:K:48:ILE:HG12	1.45	0.46
16:M:73:GLU:O	16:M:74:VAL:C	2.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:39:LEU:CD2	18:O:56:LEU:HD22	2.46	0.46
20:Q:27:PHE:CD1	20:Q:27:PHE:C	2.93	0.46
22:S:33:THR:HG22	22:S:35:SER:N	2.29	0.46
1:A:393:A:C2	1:A:394:G:C8	3.03	0.46
1:A:851:G:H2'	1:A:852:G:H8	1.80	0.46
1:A:988:G:H2'	1:A:989:C:O4'	2.16	0.46
1:A:1026:G:N7	1:A:1027:C:C2	2.83	0.46
1:A:1298:C:C5	10:G:114:ARG:HD3	2.49	0.46
1:A:1372:U:OP1	12:I:71:SER:HB3	2.15	0.46
5:B:187:LEU:HD12	5:B:205:ASP:HA	1.98	0.46
6:C:6:HIS:NE2	6:C:8:ILE:HD12	2.30	0.46
15:L:117:ARG:HD2	15:L:122:THR:OG1	2.15	0.46
18:O:31:LEU:O	18:O:34:LEU:HB3	2.14	0.46
19:P:75:ARG:O	19:P:78:GLY:N	2.47	0.46
21:R:47:THR:O	21:R:49:LYS:N	2.47	0.46
1:A:256:U:H2'	1:A:257:G:H8	1.81	0.46
1:A:583:A:H2'	1:A:584:G:O4'	2.14	0.46
1:A:960:U:O2	1:A:960:U:H5'	2.15	0.46
1:A:1055:A:C2	1:A:1056:U:H1'	2.50	0.46
1:A:1215:G:C2	1:A:1216:G:C8	3.03	0.46
1:A:1292:U:O2'	1:A:1293:G:H5'	2.15	0.46
1:A:1367:C:H5'	13:J:60:ARG:HH12	1.80	0.46
1:A:1394:A:C6	1:A:1501:C:H4'	2.50	0.46
5:B:167:PRO:O	5:B:171:ALA:N	2.49	0.46
5:B:178:ARG:NH1	5:B:178:ARG:CG	2.71	0.46
7:D:91:SER:O	7:D:92:VAL:C	2.57	0.46
12:I:96:LEU:HD12	12:I:96:LEU:N	2.31	0.46
13:J:4:ILE:O	13:J:73:ASP:HA	2.16	0.46
14:K:33:THR:HG23	14:K:34:ASP:N	2.29	0.46
15:L:93:LEU:HB2	15:L:96:VAL:HG21	1.97	0.46
17:N:9:LYS:C	17:N:11:LYS:N	2.71	0.46
18:O:54:ARG:O	18:O:55:GLY:C	2.58	0.46
1:A:370:C:H2'	1:A:371:G:H8	1.81	0.46
1:A:489:C:H2'	1:A:490:G:H8	1.81	0.46
1:A:579:G:H5'	1:A:728:A:C1'	2.37	0.46
1:A:767:A:H2'	1:A:768:A:O4'	2.15	0.46
1:A:908:A:H2'	1:A:909:A:C8	2.49	0.46
1:A:1250:A:H4'	12:I:68:GLY:CA	2.45	0.46
1:A:1349:A:P	12:I:118:LYS:NZ	2.88	0.46
1:A:1515:C:O2'	1:A:1516:G:H5'	2.16	0.46
5:B:78:GLN:HB3	5:B:94:ASN:HD21	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:50:TYR:CE1	21:R:77:GLY:HA2	2.51	0.46
9:F:71:ARG:HA	9:F:74:ASP:OD2	2.14	0.46
10:G:45:ASP:O	10:G:49:ILE:HG13	2.15	0.46
10:G:51:GLN:NE2	10:G:58:PRO:HD3	2.31	0.46
13:J:94:VAL:CG1	13:J:95:GLU:H	2.29	0.46
21:R:51:LEU:HA	21:R:52:PRO:HD3	1.71	0.46
21:R:53:ARG:C	21:R:55:ARG:H	2.21	0.46
1:A:57:G:H2'	1:A:58:C:C6	2.51	0.46
1:A:109:A:C6	1:A:327:A:C6	3.04	0.46
1:A:328:C:H4'	1:A:329:A:C5'	2.45	0.46
1:A:659:U:O2'	1:A:660:G:H5'	2.16	0.46
1:A:1229:A:C2	1:A:1230:C:C4	3.04	0.46
5:B:197:VAL:HB	5:B:200:ILE:CG2	2.35	0.46
6:C:34:LEU:HD23	6:C:34:LEU:C	2.41	0.46
7:D:155:LEU:O	7:D:159:ARG:HG2	2.15	0.46
12:I:5:TYR:HD2	12:I:18:PHE:CE2	2.34	0.46
19:P:45:THR:O	19:P:48:TRP:HD1	1.98	0.46
20:Q:48:GLU:C	20:Q:50:LYS:N	2.73	0.46
20:Q:63:ARG:O	20:Q:64:PRO:C	2.58	0.46
23:T:50:GLU:HA	23:T:100:ILE:CG2	2.45	0.46
1:A:406:G:H5''	7:D:5:ILE:CG2	2.45	0.46
1:A:730:G:H21	1:A:765:G:H5''	1.80	0.46
1:A:1004:A:C5'	1:A:1024:G:H1	2.27	0.46
1:A:1053:G:O3'	1:A:1054:C:H4'	2.15	0.46
1:A:1125:U:H5''	1:A:1126:U:C5	2.41	0.46
5:B:34:ALA:O	5:B:41:ILE:N	2.49	0.46
7:D:29:PRO:O	7:D:30:LYS:CG	2.54	0.46
9:F:9:VAL:HB	9:F:87:ARG:HB2	1.98	0.46
12:I:5:TYR:CD2	12:I:18:PHE:CE2	3.03	0.46
13:J:12:ASP:HB3	13:J:15:THR:CB	2.46	0.46
16:M:40:ASN:C	16:M:40:ASN:ND2	2.74	0.46
17:N:44:LEU:HD12	17:N:44:LEU:O	2.16	0.46
21:R:44:LEU:HD23	21:R:49:LYS:C	2.41	0.46
1:A:416:G:C5	1:A:417:C:C4	3.04	0.46
1:A:889:A:H61	1:A:907:A:H3'	1.81	0.46
1:A:948:C:OP1	16:M:109:THR:HG22	2.16	0.46
1:A:1367:C:H4'	13:J:48:THR:HG21	1.97	0.46
1:A:1427:U:H2'	1:A:1428:A:H8	1.81	0.46
5:B:7:VAL:HG23	5:B:7:VAL:O	2.15	0.46
5:B:105:PHE:O	5:B:106:LYS:C	2.59	0.46
9:F:80:ARG:HG2	9:F:80:ARG:HH11	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:84:GLN:C	13:J:86:MET:H	2.23	0.46
15:L:46:LYS:CG	15:L:47:LYS:N	2.67	0.46
15:L:55:VAL:HG12	15:L:56:ALA:H	1.81	0.46
18:O:3:ILE:HD13	18:O:34:LEU:HD22	1.98	0.46
23:T:53:LEU:HB2	23:T:100:ILE:HG23	1.98	0.46
1:A:254:G:H21	20:Q:16:GLN:HE22	1.63	0.46
1:A:269:C:H2'	1:A:270:A:H8	1.73	0.46
1:A:1053:G:C3'	1:A:1054:C:C5'	2.94	0.46
5:B:55:PHE:O	5:B:56:ARG:C	2.57	0.46
5:B:123:ALA:N	5:B:127:ILE:HD11	2.30	0.46
16:M:39:ILE:CD1	16:M:52:GLU:HB3	2.46	0.46
19:P:26:ARG:HD3	19:P:31:LYS:N	2.30	0.46
1:A:438:G:O2'	1:A:495:U:O4	2.30	0.46
1:A:1004:A:N1	1:A:1037:C:N4	2.64	0.46
1:A:1162:C:H2'	1:A:1163:C:C6	2.51	0.46
1:A:1373:G:H5''	10:G:36:LYS:CB	2.45	0.46
1:A:1423:G:H2'	1:A:1424:C:H6	1.80	0.46
5:B:59:GLU:O	5:B:62:ALA:N	2.49	0.46
5:B:74:LYS:HD3	5:B:76:GLN:HB3	1.97	0.46
5:B:137:ARG:O	5:B:140:HIS:HB2	2.16	0.46
5:B:178:ARG:O	5:B:179:LYS:C	2.59	0.46
5:B:235:SER:C	5:B:237:ALA:H	2.23	0.46
6:C:34:LEU:HD22	6:C:38:ARG:CZ	2.46	0.46
6:C:54:ARG:HG2	6:C:54:ARG:NH1	2.31	0.46
6:C:147:LYS:HB3	6:C:203:PHE:CD2	2.51	0.46
10:G:31:MET:HG2	10:G:32:ARG:N	2.32	0.46
12:I:112:LYS:C	12:I:112:LYS:CD	2.89	0.46
13:J:5:ARG:HB2	13:J:99:LYS:O	2.15	0.46
14:K:28:THR:C	14:K:29:ILE:HG22	2.41	0.46
23:T:10:LEU:O	23:T:13:LEU:HG	2.16	0.46
1:A:192:U:O2'	1:A:193:C:H5'	2.16	0.45
1:A:1227:A:H8	1:A:1227:A:H3'	1.80	0.45
1:A:1305:G:C8	1:A:1305:G:OP2	2.69	0.45
1:A:1360:A:O2'	1:A:1361:G:H5'	2.16	0.45
1:A:1451:A:O2'	1:A:1452:C:OP1	2.26	0.45
8:E:103:GLY:C	8:E:106:PRO:HD2	2.40	0.45
9:F:35:ALA:HA	9:F:67:MET:HB3	1.98	0.45
10:G:41:ARG:O	10:G:44:TYR:N	2.49	0.45
16:M:34:LEU:HD23	16:M:39:ILE:HB	1.98	0.45
16:M:65:LYS:HE3	16:M:69:GLU:HG2	1.98	0.45
18:O:6:GLU:O	18:O:7:GLU:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Q:104:LYS:O	20:Q:105:ALA:CB	2.63	0.45
1:A:476:G:O2'	1:A:477:G:H5'	2.16	0.45
1:A:599:C:O2'	1:A:600:C:H5'	2.16	0.45
1:A:660:G:C2	1:A:746:A:C2	3.04	0.45
1:A:1250:A:C5'	12:I:68:GLY:N	2.76	0.45
8:E:71:LEU:CD2	8:E:115:VAL:HG23	2.46	0.45
10:G:146:GLU:CD	10:G:149:ARG:HD3	2.41	0.45
11:H:119:LEU:CD1	11:H:124:ALA:HA	2.40	0.45
12:I:125:TYR:CD2	12:I:125:TYR:N	2.82	0.45
14:K:126:ARG:HB3	14:K:127:LYS:H	1.47	0.45
18:O:39:LEU:HD21	18:O:43:LEU:HD11	1.98	0.45
18:O:83:GLU:C	18:O:83:GLU:OE1	2.60	0.45
20:Q:83:ASP:O	20:Q:86:GLU:HB2	2.16	0.45
20:Q:88:TYR:OH	20:Q:92:ARG:NH2	2.49	0.45
21:R:29:PHE:HE1	21:R:31:LEU:HD23	1.80	0.45
1:A:255:G:H5'	20:Q:16:GLN:O	2.15	0.45
1:A:604:G:O2'	1:A:605:U:H5'	2.16	0.45
1:A:652:U:C5	1:A:752:G:C4	3.04	0.45
1:A:817:C:H1'	1:A:819:A:H5'	1.98	0.45
1:A:1184:G:OP1	1:A:1184:G:H3'	2.16	0.45
5:B:140:HIS:O	5:B:141:GLU:C	2.57	0.45
7:D:70:ILE:HD12	7:D:100:ARG:HD2	1.99	0.45
7:D:162:LEU:HD13	7:D:181:MET:CE	2.45	0.45
8:E:73:ASN:C	8:E:75:THR:H	2.23	0.45
10:G:62:PHE:HD1	10:G:124:LEU:HD21	1.81	0.45
12:I:118:LYS:C	12:I:120:ARG:H	2.25	0.45
13:J:25:GLU:O	13:J:28:ARG:HB2	2.16	0.45
18:O:25:THR:HG21	18:O:70:LEU:HD23	1.98	0.45
22:S:41:VAL:CG2	22:S:44:MET:HE3	2.36	0.45
23:T:83:ARG:O	23:T:87:LYS:HE2	2.16	0.45
1:A:124:G:C6	1:A:125:U:C4	3.04	0.45
1:A:589:C:O2'	1:A:590:C:H5'	2.16	0.45
1:A:639:G:O2'	1:A:640:A:H5'	2.16	0.45
1:A:766:A:C8	1:A:814:A:C6	3.04	0.45
1:A:788:U:O2'	1:A:789:U:H5'	2.16	0.45
1:A:915:A:H2'	1:A:916:G:C5'	2.46	0.45
1:A:922:G:H5'	8:E:19:MET:O	2.16	0.45
1:A:1234:C:O2'	1:A:1235:U:H5'	2.16	0.45
1:A:1288:A:H2'	1:A:1289:A:H8	1.81	0.45
1:A:1314:C:N3	1:A:1315:U:C4	2.85	0.45
1:A:1512:U:H2'	1:A:1513:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:74:LYS:HD3	5:B:206:ASP:OD1	2.16	0.45
5:B:187:LEU:HA	5:B:201:ILE:HB	1.99	0.45
6:C:130:VAL:CG1	6:C:153:VAL:HG21	2.47	0.45
6:C:134:ILE:O	6:C:138:VAL:HG23	2.17	0.45
8:E:89:ILE:HD13	8:E:90:VAL:H	1.81	0.45
12:I:32:ASP:O	12:I:35:GLU:HB3	2.17	0.45
12:I:92:TYR:O	12:I:96:LEU:HD13	2.16	0.45
15:L:39:VAL:HG22	15:L:57:LYS:CG	2.47	0.45
16:M:32:GLU:O	16:M:35:GLU:N	2.47	0.45
18:O:41:GLU:HA	18:O:44:LYS:CG	2.45	0.45
1:A:51:A:H4'	1:A:52:G:OP2	2.15	0.45
1:A:411:A:C4	1:A:413:G:H1'	2.52	0.45
1:A:1225:A:H2'	1:A:1225:A:N3	2.31	0.45
1:A:1234:C:H2'	1:A:1235:U:H6	1.81	0.45
1:A:1384:C:H2'	1:A:1385:G:C8	2.51	0.45
1:A:1390:U:H2'	1:A:1391:U:C6	2.52	0.45
5:B:69:LEU:C	5:B:69:LEU:CD2	2.90	0.45
5:B:81:VAL:O	5:B:82:ARG:C	2.58	0.45
6:C:154:SER:HB3	6:C:197:GLY:N	2.32	0.45
9:F:21:LEU:O	9:F:24:GLU:HB3	2.16	0.45
10:G:145:ALA:O	10:G:146:GLU:C	2.59	0.45
16:M:37:THR:O	16:M:38:GLY:C	2.60	0.45
16:M:78:ILE:O	16:M:81:LEU:HD23	2.17	0.45
18:O:39:LEU:HD21	18:O:56:LEU:HD22	1.98	0.45
21:R:38:GLU:OE1	21:R:38:GLU:N	2.34	0.45
21:R:45:SER:C	21:R:47:THR:H	2.25	0.45
23:T:56:MET:CE	23:T:88:VAL:HG11	2.46	0.45
1:A:116:A:H2'	1:A:117:G:C8	2.51	0.45
1:A:664:G:H1	1:A:741:G:H1	1.64	0.45
1:A:757:U:O2'	1:A:879:C:H1'	2.16	0.45
1:A:761:G:H5''	20:Q:102:GLY:CA	2.46	0.45
1:A:791:G:C2'	1:A:792:A:H5''	2.46	0.45
1:A:1051:C:C4	1:A:1052:U:C5	3.04	0.45
1:A:1345:U:C4	1:A:1377:A:C2	3.05	0.45
1:A:1479:C:O2'	1:A:1480:G:H5'	2.17	0.45
5:B:112:VAL:HG11	5:B:153:ARG:HA	1.98	0.45
6:C:160:ALA:C	6:C:162:GLN:N	2.73	0.45
6:C:167:TRP:HB3	6:C:168:ALA:H	1.32	0.45
8:E:43:LEU:HB2	8:E:136:MET:HE2	1.97	0.45
8:E:79:GLU:O	11:H:104:ARG:NH1	2.50	0.45
12:I:126:SER:O	12:I:127:LYS:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:N:35:ARG:C	17:N:37:PHE:N	2.73	0.45
20:Q:59:ILE:HA	20:Q:59:ILE:HD13	1.57	0.45
23:T:53:LEU:HD22	23:T:102:GLY:H	1.82	0.45
1:A:941:G:O2'	1:A:942:G:H5'	2.17	0.45
1:A:1124:G:C8	1:A:1145:C:C5	3.05	0.45
1:A:1368:G:HO2'	1:A:1369:C:H5'	1.74	0.45
5:B:12:GLU:C	5:B:14:GLY:N	2.74	0.45
6:C:22:TRP:CE3	6:C:32:LEU:HD22	2.51	0.45
14:K:58:PRO:HA	14:K:90:GLY:HA2	1.99	0.45
16:M:67:GLU:O	16:M:68:GLY:C	2.57	0.45
22:S:16:LEU:C	22:S:18:LYS:N	2.64	0.45
1:A:135:C:C2	19:P:1:MET:HB2	2.52	0.45
1:A:409:G:O2'	1:A:410:G:H5'	2.16	0.45
1:A:523:A:N6	15:L:92:ASP:OD2	2.48	0.45
1:A:555:C:H2'	1:A:556:C:C6	2.51	0.45
1:A:945:G:H2'	1:A:945:G:N3	2.31	0.45
1:A:1066:C:O2'	1:A:1067:A:H5'	2.16	0.45
5:B:103:THR:HA	5:B:180:LEU:HD11	1.99	0.45
7:D:5:ILE:HG22	7:D:5:ILE:O	2.15	0.45
7:D:158:ILE:HG22	7:D:181:MET:HE1	1.97	0.45
8:E:31:LEU:HD22	8:E:43:LEU:CD2	2.46	0.45
8:E:62:ALA:C	8:E:64:ARG:N	2.74	0.45
9:F:30:LEU:HD23	9:F:75:LEU:HD21	1.97	0.45
11:H:64:LYS:HE3	11:H:79:VAL:HG11	1.98	0.45
12:I:7:THR:O	12:I:15:ALA:O	2.35	0.45
12:I:10:ARG:HG2	12:I:10:ARG:NH1	2.31	0.45
14:K:100:ALA:O	14:K:101:SER:C	2.60	0.45
16:M:80:ARG:C	16:M:82:MET:N	2.74	0.45
17:N:45:ARG:HG2	17:N:49:HIS:CD2	2.52	0.45
1:A:299:G:H2'	1:A:300:A:C8	2.52	0.45
1:A:994:A:N7	1:A:1216:G:H4'	2.32	0.45
1:A:1053:G:O2'	1:A:1199:U:H5	2.00	0.45
1:A:1163:C:O2'	1:A:1164:G:H5'	2.17	0.45
1:A:1193:G:N2	1:A:1194:U:C2	2.85	0.45
7:D:138:TYR:C	7:D:138:TYR:CD2	2.95	0.45
9:F:23:LYS:O	9:F:24:GLU:C	2.58	0.45
10:G:23:VAL:HG13	10:G:43:PHE:CE2	2.51	0.45
11:H:60:ARG:HG3	11:H:60:ARG:NH1	2.32	0.45
14:K:14:VAL:O	14:K:15:ALA:HB3	2.16	0.45
15:L:89:ARG:HD3	15:L:97:ARG:HA	1.98	0.45
16:M:49:THR:O	16:M:53:VAL:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:76:GLU:O	18:O:77:ARG:C	2.60	0.45
20:Q:59:ILE:HD13	20:Q:73:VAL:HA	1.97	0.45
20:Q:65:ILE:HD11	20:Q:72:ARG:HG2	1.99	0.45
21:R:69:THR:O	21:R:72:ARG:HB2	2.17	0.45
1:A:285:G:O2'	1:A:286:G:H5'	2.17	0.45
1:A:1063:C:H3'	1:A:1064:G:H2'	1.99	0.45
1:A:1190:G:O2'	1:A:1191:A:P	2.74	0.45
1:A:1313:U:H2'	1:A:1314:C:H6	1.81	0.45
1:A:1317:C:H2'	1:A:1318:A:O4'	2.17	0.45
1:A:1323:G:H2'	1:A:1324:A:C8	2.52	0.45
5:B:144:ARG:O	5:B:147:LYS:HB2	2.16	0.45
6:C:11:ARG:HG3	6:C:178:LEU:HD12	2.00	0.45
7:D:25:ARG:O	7:D:27:TYR:N	2.49	0.45
7:D:149:ALA:O	7:D:150:GLU:C	2.60	0.45
10:G:16:LEU:H	10:G:16:LEU:HD22	1.82	0.45
11:H:85:ARG:CZ	11:H:87:SER:O	2.65	0.45
12:I:118:LYS:HB2	12:I:118:LYS:HZ2	1.82	0.45
13:J:91:PRO:HB2	13:J:94:VAL:HG23	1.99	0.45
14:K:73:MET:HE1	14:K:102:GLY:HA3	1.98	0.45
19:P:75:ARG:HA	19:P:80:PHE:HD1	1.82	0.45
23:T:26:ASN:O	23:T:27:LYS:C	2.60	0.45
1:A:514:C:O2'	1:A:515:G:H5'	2.17	0.44
1:A:551:U:H2'	1:A:552:U:C6	2.52	0.44
6:C:130:VAL:O	6:C:131:ARG:C	2.60	0.44
10:G:111:ARG:HB3	10:G:112:PRO:HD2	1.98	0.44
14:K:30:VAL:HG21	14:K:65:ALA:HA	1.98	0.44
1:A:280:C:O2	20:Q:38:ARG:HG3	2.17	0.44
1:A:722:A:H3'	1:A:722:A:N3	2.32	0.44
1:A:968:A:OP2	12:I:128:ARG:NH2	2.50	0.44
1:A:1038:C:C6	1:A:1039:C:H5	2.35	0.44
1:A:1098:C:H2'	1:A:1099:G:O4'	2.16	0.44
1:A:1179:A:H2'	1:A:1180:A:O4'	2.17	0.44
1:A:1284:C:H3'	1:A:1285:A:H8	1.82	0.44
1:A:1372:U:H2'	1:A:1373:G:O4'	2.17	0.44
5:B:44:LEU:HD23	5:B:47:THR:OG1	2.17	0.44
6:C:79:ARG:HG3	6:C:79:ARG:O	2.16	0.44
7:D:149:ALA:O	7:D:152:SER:N	2.50	0.44
8:E:84:PHE:CE2	8:E:133:TYR:HD1	2.35	0.44
8:E:91:LEU:HD23	8:E:120:THR:HG22	2.00	0.44
8:E:101:ILE:HD12	8:E:119:LEU:CD2	2.48	0.44
10:G:37:ASN:HD22	10:G:37:ASN:HA	1.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:82:HIS:CG	11:H:83:ILE:N	2.85	0.44
11:H:119:LEU:HD23	11:H:119:LEU:N	2.32	0.44
12:I:41:VAL:HG12	12:I:42:ARG:N	2.31	0.44
15:L:91:LYS:HA	15:L:91:LYS:CE	2.33	0.44
23:T:100:ILE:O	23:T:101:GLY:C	2.60	0.44
1:A:346:G:C2'	1:A:347:G:H5'	2.47	0.44
1:A:411:A:N3	1:A:413:G:O2'	2.51	0.44
1:A:433:C:O2'	1:A:434:U:H5'	2.18	0.44
1:A:892:A:C2	1:A:907:A:C4	3.06	0.44
1:A:922:G:H2'	1:A:923:A:C8	2.52	0.44
1:A:1130:A:H3'	1:A:1130:A:OP2	2.18	0.44
1:A:1186:G:N2	1:A:1187:G:H1'	2.33	0.44
1:A:1227:A:H3'	1:A:1227:A:C8	2.53	0.44
5:B:54:THR:O	5:B:55:PHE:C	2.61	0.44
6:C:35:GLU:OE2	6:C:59:ARG:NH1	2.50	0.44
6:C:95:THR:C	6:C:97:LYS:N	2.73	0.44
7:D:108:LEU:HD23	7:D:108:LEU:HA	1.80	0.44
9:F:48:LEU:HD13	9:F:52:ILE:HD12	1.99	0.44
9:F:75:LEU:HD11	9:F:79:LEU:HD11	1.98	0.44
10:G:18:TYR:N	10:G:18:TYR:CD1	2.85	0.44
12:I:57:GLY:O	12:I:58:ARG:HG2	2.16	0.44
13:J:32:ALA:HB2	13:J:76:ASN:HD22	1.82	0.44
13:J:37:PRO:HA	13:J:71:LEU:O	2.17	0.44
14:K:91:ARG:NH1	21:R:88:LYS:HE3	2.33	0.44
16:M:11:ARG:CG	16:M:12:ASN:H	2.31	0.44
22:S:8:GLY:O	22:S:9:VAL:C	2.60	0.44
1:A:191:G:H21	23:T:85:MET:HE1	1.82	0.44
1:A:487:A:H2'	1:A:488:C:O4'	2.18	0.44
1:A:745:C:OP1	1:A:851:G:O2'	2.35	0.44
1:A:881:G:OP2	15:L:12:ARG:NH2	2.51	0.44
1:A:942:G:N3	1:A:943:U:C6	2.86	0.44
1:A:1153:C:H2'	1:A:1154:G:C8	2.53	0.44
1:A:1182:G:H4'	1:A:1183:A:C5'	2.47	0.44
1:A:1203:C:OP1	17:N:2:ALA:HB3	2.18	0.44
1:A:1326:C:OP1	24:V:12:LYS:NZ	2.50	0.44
1:A:1422:G:O2'	1:A:1423:G:H5'	2.18	0.44
5:B:10:LEU:HD23	5:B:10:LEU:C	2.42	0.44
5:B:12:GLU:OE1	5:B:12:GLU:O	2.36	0.44
5:B:21:ARG:HG3	5:B:21:ARG:NH1	2.32	0.44
10:G:113:GLU:HG2	10:G:119:ARG:HG2	1.99	0.44
10:G:133:GLY:O	10:G:136:LYS:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:137:LYS:O	10:G:138:LYS:C	2.59	0.44
14:K:114:VAL:O	14:K:114:VAL:HG13	2.18	0.44
15:L:53:ARG:HG2	15:L:69:TYR:HE1	1.83	0.44
16:M:23:TYR:HE2	16:M:70:LEU:HB3	1.83	0.44
21:R:18:ARG:NH2	21:R:21:LYS:HZ2	2.16	0.44
23:T:13:LEU:C	23:T:13:LEU:CD1	2.90	0.44
24:V:3:LYS:HG2	24:V:14:TRP:CD1	2.53	0.44
1:A:974:A:P	17:N:29:ARG:HH22	2.41	0.44
1:A:1030:C:C2'	1:A:1030(A):G:H5'	2.45	0.44
1:A:1118:C:O5'	1:A:1118:C:H6	2.00	0.44
1:A:1118:C:H1'	1:A:1179:A:C4	2.52	0.44
5:B:80:ILE:H	5:B:80:ILE:HG13	1.66	0.44
5:B:87:ARG:NH1	5:B:87:ARG:HG3	2.33	0.44
5:B:174:VAL:O	5:B:175:ARG:C	2.60	0.44
6:C:110:ASN:HB3	6:C:144:SER:OG	2.17	0.44
7:D:56:VAL:O	7:D:57:ARG:C	2.60	0.44
7:D:150:GLU:HB3	7:D:153:ARG:NH2	2.32	0.44
9:F:28:ARG:NH1	9:F:28:ARG:HB2	2.33	0.44
10:G:115:ARG:HB2	10:G:118:VAL:HG23	1.99	0.44
16:M:60:VAL:O	16:M:63:THR:HG22	2.17	0.44
17:N:53:LEU:HB3	17:N:56:VAL:CG2	2.48	0.44
20:Q:63:ARG:HG2	20:Q:64:PRO:HD2	1.99	0.44
23:T:34:LYS:O	23:T:35:THR:C	2.60	0.44
1:A:116:A:H2'	1:A:117:G:H8	1.83	0.44
1:A:489:C:H2'	1:A:490:G:C8	2.52	0.44
1:A:625:G:H2'	1:A:626:U:H6	1.81	0.44
1:A:757:U:H2'	1:A:758:G:O4'	2.17	0.44
1:A:925:G:C2	1:A:927:G:C8	3.06	0.44
1:A:1138:G:N1	1:A:1140:C:C2	2.86	0.44
1:A:1288:A:O4'	1:A:1353:G:H4'	2.17	0.44
5:B:12:GLU:HA	5:B:12:GLU:OE2	2.18	0.44
5:B:133:LYS:O	5:B:137:ARG:HG3	2.17	0.44
8:E:11:ILE:HG22	8:E:12:LEU:N	2.31	0.44
8:E:36:ASP:CG	8:E:38:GLN:HB2	2.43	0.44
12:I:10:ARG:HG2	12:I:10:ARG:HH11	1.82	0.44
14:K:65:ALA:CB	14:K:97:ALA:HB3	2.47	0.44
16:M:77:ASN:O	16:M:81:LEU:CD2	2.65	0.44
18:O:26:GLU:O	18:O:27:VAL:C	2.60	0.44
19:P:11:SER:OG	19:P:14:ASN:HB3	2.17	0.44
19:P:75:ARG:O	19:P:76:GLN:C	2.59	0.44
22:S:5:LEU:O	22:S:6:LYS:CB	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:U:C2	1:A:361:G:N2	2.86	0.44
1:A:55:A:H2'	1:A:56:U:H6	1.83	0.44
1:A:92:C:O2'	1:A:93:G:H5'	2.17	0.44
1:A:1055:A:C6	1:A:1206:G:C5	3.06	0.44
1:A:1067:A:N3	1:A:1068:G:H1'	2.33	0.44
1:A:1439:C:H2'	1:A:1440:C:H6	1.82	0.44
5:B:7:VAL:N	5:B:8:LYS:HE3	2.33	0.44
5:B:162:ILE:H	5:B:185:ILE:CD1	2.31	0.44
5:B:221:LEU:HD22	5:B:224:GLN:OE1	2.17	0.44
6:C:8:ILE:CG2	6:C:16:ARG:HG2	2.34	0.44
8:E:30:ALA:O	8:E:45:PHE:HA	2.17	0.44
9:F:45:LEU:HD23	9:F:59:TYR:HD1	1.83	0.44
10:G:106:GLN:O	10:G:110:GLN:HG2	2.18	0.44
11:H:40:ALA:O	11:H:43:GLY:N	2.42	0.44
11:H:82:HIS:C	11:H:83:ILE:HG22	2.43	0.44
11:H:133:LEU:O	11:H:134:ILE:C	2.60	0.44
12:I:7:THR:O	12:I:80:GLY:HA3	2.17	0.44
12:I:93:ARG:NE	12:I:97:LYS:CE	2.81	0.44
12:I:120:ARG:O	12:I:121:ARG:C	2.61	0.44
15:L:28:LYS:O	15:L:30:ALA:N	2.51	0.44
22:S:45:VAL:CG1	22:S:46:GLY:N	2.80	0.44
1:A:386:C:H2'	1:A:387:U:H5'	1.99	0.44
1:A:1308:U:H2'	1:A:1309:G:C8	2.52	0.44
1:A:1455:G:O2'	1:A:1459:C:H5'	2.18	0.44
1:A:1521:G:H2'	1:A:1522:U:H6	1.81	0.44
5:B:32:ILE:HD13	5:B:40:HIS:CG	2.52	0.44
5:B:92:TYR:CD1	5:B:92:TYR:C	2.95	0.44
8:E:72:GLN:O	8:E:73:ASN:CB	2.63	0.44
8:E:103:GLY:O	8:E:104:ALA:C	2.61	0.44
8:E:153:LYS:HG2	8:E:154:GLY:N	2.33	0.44
10:G:8:GLU:OE1	10:G:8:GLU:O	2.36	0.44
11:H:85:ARG:HD3	11:H:85:ARG:C	2.40	0.44
11:H:89:PRO:O	11:H:90:GLY:C	2.59	0.44
12:I:105:ASP:OD1	12:I:107:ARG:HG3	2.18	0.44
13:J:22:LYS:O	13:J:24:VAL:N	2.51	0.44
14:K:44:SER:H	14:K:47:VAL:CG2	2.31	0.44
16:M:5:ALA:O	16:M:6:GLY:C	2.61	0.44
16:M:59:TYR:O	16:M:63:THR:HG22	2.18	0.44
19:P:56:ALA:O	19:P:57:ARG:C	2.61	0.44
20:Q:22:LEU:HD12	20:Q:23:VAL:N	2.32	0.44
22:S:24:ALA:HB3	22:S:25:LYS:HZ3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:43:GLU:CD	22:S:43:GLU:N	2.76	0.44
22:S:62:ILE:HD12	22:S:63:THR:H	1.81	0.44
22:S:74:PHE:CD1	22:S:74:PHE:N	2.86	0.44
23:T:61:SER:O	23:T:62:LEU:C	2.61	0.44
1:A:376:G:C5'	19:P:5:ARG:HD2	2.43	0.44
1:A:447:G:H1'	1:A:487:A:H61	1.82	0.44
1:A:540:G:H2'	1:A:541:G:O4'	2.18	0.44
1:A:811:C:O2'	1:A:901:A:N1	2.50	0.44
1:A:865:A:H5'	1:A:1078:U:O4	2.18	0.44
5:B:61:LEU:HD21	5:B:160:ASP:HB3	2.00	0.44
5:B:144:ARG:HD2	5:B:145:LEU:HD23	2.00	0.44
7:D:162:LEU:O	7:D:165:MET:HB2	2.17	0.44
7:D:202:LEU:O	7:D:203:VAL:C	2.61	0.44
8:E:8:GLU:HB3	8:E:34:VAL:HG22	2.00	0.44
8:E:44:GLY:CA	8:E:62:ALA:HB2	2.47	0.44
9:F:67:MET:HB2	9:F:68:PRO:CD	2.48	0.44
9:F:76:ALA:C	9:F:78:GLU:N	2.74	0.44
9:F:91:VAL:CG1	9:F:92:LYS:N	2.81	0.44
11:H:117:GLY:C	11:H:119:LEU:HD23	2.43	0.44
12:I:117:HIS:O	12:I:118:LYS:CG	2.66	0.44
13:J:98:ILE:HG22	13:J:99:LYS:N	2.33	0.44
14:K:122:LYS:O	14:K:123:LYS:C	2.61	0.44
1:A:22:G:H2'	1:A:23:C:H6	1.83	0.43
1:A:182:U:OP2	1:A:183:G:C8	2.70	0.43
1:A:376:G:C2	1:A:389:A:C2	3.06	0.43
1:A:390:C:H6	1:A:390:C:O5'	2.01	0.43
1:A:426:G:P	7:D:36:ARG:HH21	2.41	0.43
1:A:537:G:OP1	15:L:113:ARG:NH2	2.51	0.43
1:A:584:G:H2'	1:A:585:G:C8	2.52	0.43
1:A:1371:G:O3'	12:I:69:GLY:HA3	2.18	0.43
6:C:59:ARG:HD3	6:C:97:LYS:HZ3	1.83	0.43
6:C:134:ILE:CG2	6:C:151:VAL:HB	2.46	0.43
7:D:58:LEU:HD13	7:D:58:LEU:C	2.42	0.43
7:D:78:LEU:HB3	7:D:93:PHE:HE2	1.83	0.43
8:E:115:VAL:HG12	8:E:116:THR:N	2.33	0.43
11:H:29:SER:O	11:H:30:ARG:C	2.58	0.43
12:I:56:LEU:C	12:I:58:ARG:H	2.26	0.43
16:M:13:LYS:O	16:M:14:ARG:C	2.60	0.43
16:M:22:ILE:N	16:M:22:ILE:HD12	2.33	0.43
1:A:622:A:C8	1:A:623:C:C5	3.06	0.43
1:A:761:G:H1'	20:Q:104:LYS:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1124:G:H3'	1:A:1145:C:N4	2.22	0.43
1:A:1130:A:OP2	1:A:1131:G:OP2	2.36	0.43
1:A:1262:C:O2'	1:A:1263:C:H5'	2.18	0.43
1:A:1307:U:H2'	1:A:1308:U:C6	2.53	0.43
1:A:1490:C:C2'	1:A:1491:G:H5'	2.48	0.43
5:B:10:LEU:CG	5:B:48:MET:HE2	2.48	0.43
5:B:35:GLU:HG2	5:B:40:HIS:CD2	2.53	0.43
5:B:79:ASP:O	5:B:81:VAL:N	2.51	0.43
7:D:135:LEU:O	7:D:136:PRO:C	2.61	0.43
11:H:121:ASP:O	11:H:122:ARG:C	2.61	0.43
12:I:44:VAL:O	12:I:45:ALA:C	2.60	0.43
13:J:8:LEU:HD22	13:J:94:VAL:HG11	2.00	0.43
13:J:96:ILE:HG22	13:J:97:GLU:H	1.81	0.43
14:K:18:ARG:HB3	14:K:33:THR:HG22	2.01	0.43
14:K:58:PRO:HD3	14:K:89:ALA:HB1	2.00	0.43
1:A:179:A:O2'	1:A:180:U:H5'	2.19	0.43
1:A:259:G:O2'	1:A:260:G:H5'	2.17	0.43
1:A:346:G:H2'	1:A:347:G:O4'	2.18	0.43
1:A:397:A:H3'	1:A:397:A:N3	2.34	0.43
1:A:598:U:H4'	11:H:94:TYR:CG	2.54	0.43
1:A:803:G:N7	1:A:804:U:C5	2.86	0.43
1:A:1220:G:O2'	1:A:1221:G:H5'	2.18	0.43
1:A:1365:G:O2'	1:A:1366:C:H5'	2.18	0.43
5:B:172:ILE:O	5:B:172:ILE:HG22	2.17	0.43
10:G:85:TYR:HD1	10:G:154:TYR:CE1	2.32	0.43
12:I:55:ALA:O	12:I:56:LEU:HB3	2.18	0.43
13:J:53:PRO:O	13:J:54:PHE:O	2.36	0.43
16:M:3:ARG:CG	16:M:9:ILE:HG23	2.42	0.43
17:N:25:VAL:O	17:N:25:VAL:HG22	2.18	0.43
20:Q:68:ARG:HG2	20:Q:68:ARG:NH1	2.33	0.43
21:R:55:ARG:HB3	21:R:55:ARG:CZ	2.49	0.43
22:S:33:THR:CG2	22:S:34:TRP:N	2.80	0.43
23:T:16:HIS:O	23:T:17:ARG:C	2.60	0.43
23:T:41:ILE:CD1	23:T:87:LYS:NZ	2.81	0.43
1:A:294:U:H2'	1:A:295:C:H6	1.83	0.43
1:A:613:C:C2	1:A:628:G:N2	2.86	0.43
1:A:760:G:N2	20:Q:104:LYS:N	2.66	0.43
1:A:835:U:OP1	21:R:64:ARG:NH2	2.41	0.43
1:A:984:C:H2'	1:A:985:C:H6	1.83	0.43
1:A:1081:G:OP1	8:E:16:THR:HG23	2.19	0.43
1:A:1221:G:H2'	1:A:1222:G:H5'	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1288:A:H1'	1:A:1352:C:O2'	2.17	0.43
1:A:1305:G:H5''	24:V:4:GLY:C	2.44	0.43
1:A:1489:G:O2'	1:A:1490:C:H5'	2.18	0.43
5:B:19:HIS:O	5:B:39:ILE:HG23	2.18	0.43
5:B:105:PHE:O	5:B:107:THR:N	2.51	0.43
5:B:207:ALA:O	5:B:211:ILE:HG13	2.19	0.43
6:C:5:ILE:HD13	6:C:10:PHE:CB	2.44	0.43
6:C:130:VAL:C	6:C:132:ARG:N	2.75	0.43
6:C:155:GLY:O	6:C:156:ARG:CB	2.66	0.43
6:C:188:LEU:HD12	6:C:190:ARG:HG3	1.99	0.43
7:D:177:ASP:OD1	7:D:177:ASP:O	2.36	0.43
8:E:152:ARG:HB3	11:H:43:GLY:O	2.17	0.43
10:G:24:THR:O	10:G:25:ALA:C	2.61	0.43
10:G:144:MET:C	10:G:145:ALA:O	2.57	0.43
12:I:83:ARG:O	12:I:86:VAL:HB	2.19	0.43
12:I:84:ALA:C	12:I:86:VAL:N	2.76	0.43
12:I:99:LEU:HB2	12:I:101:PHE:CE1	2.54	0.43
14:K:93:GLN:O	14:K:96:ARG:HB2	2.18	0.43
22:S:61:TYR:C	22:S:61:TYR:HD2	2.26	0.43
22:S:85:LYS:C	22:S:86:GLU:HG2	2.43	0.43
23:T:36:LEU:HD23	23:T:36:LEU:HA	1.84	0.43
1:A:156:G:O2'	1:A:157:G:H5'	2.18	0.43
1:A:707:C:O2'	1:A:708:C:H5'	2.17	0.43
1:A:1053:G:C5'	1:A:1054:C:H5'	2.48	0.43
5:B:75:LYS:C	5:B:77:ALA:H	2.24	0.43
5:B:189:ASP:OD1	5:B:205:ASP:OD1	2.35	0.43
10:G:148:ASN:C	10:G:150:ALA:H	2.27	0.43
11:H:4:ASP:OD2	11:H:7:ALA:CB	2.66	0.43
11:H:35:ILE:O	11:H:39:LEU:HD23	2.18	0.43
15:L:61:THR:C	15:L:63:GLY:N	2.74	0.43
1:A:179:A:H2'	1:A:180:U:H6	1.81	0.43
1:A:276:G:O2'	1:A:277:C:H5'	2.18	0.43
1:A:382:A:C2	1:A:383:A:C4	3.07	0.43
1:A:429:U:H1'	1:A:430:A:H5''	2.00	0.43
1:A:772:U:O2'	1:A:773:G:H5'	2.18	0.43
1:A:789:U:O2	1:A:791:G:C8	2.72	0.43
1:A:926:G:H3'	1:A:1505:G:H21	1.84	0.43
1:A:943:U:H2'	1:A:944:G:H5'	2.00	0.43
1:A:974:A:OP2	17:N:29:ARG:NH2	2.52	0.43
1:A:1148:U:H4'	12:I:14:VAL:CG1	2.45	0.43
1:A:1183:A:O2'	1:A:1184:G:P	2.76	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1368:G:P	12:I:112:LYS:O	2.77	0.43
1:A:1440:C:H2'	1:A:1441:G:O4'	2.19	0.43
5:B:7:VAL:C	5:B:8:LYS:CG	2.92	0.43
6:C:113:ALA:N	6:C:114:PRO:CD	2.82	0.43
6:C:134:ILE:HD11	6:C:153:VAL:HG23	2.00	0.43
8:E:76:ILE:HG22	8:E:78:HIS:H	1.82	0.43
8:E:143:ARG:HA	8:E:143:ARG:HD3	1.82	0.43
9:F:63:TYR:N	9:F:63:TYR:CD2	2.85	0.43
10:G:101:LEU:O	10:G:102:ARG:C	2.62	0.43
10:G:156:TRP:O	10:G:156:TRP:CG	2.71	0.43
12:I:10:ARG:HD2	12:I:10:ARG:C	2.44	0.43
12:I:48:GLU:N	12:I:49:PRO:CD	2.81	0.43
12:I:111:ARG:O	12:I:113:LYS:HD2	2.19	0.43
13:J:81:THR:O	13:J:83:GLU:N	2.51	0.43
14:K:86:GLY:H	14:K:112:THR:HG23	1.83	0.43
16:M:110:ARG:CG	16:M:110:ARG:NH1	2.81	0.43
20:Q:48:GLU:O	20:Q:50:LYS:N	2.52	0.43
20:Q:92:ARG:O	20:Q:95:TYR:HB2	2.19	0.43
21:R:18:ARG:HH22	21:R:21:LYS:HZ1	1.65	0.43
1:A:113:G:H1'	1:A:354:G:C5'	2.47	0.43
1:A:720:C:H2'	1:A:721:G:C8	2.53	0.43
1:A:946:A:H2'	1:A:947:G:H8	1.75	0.43
1:A:953:G:N7	16:M:104:ARG:NH2	2.63	0.43
1:A:1030(D):A:C2'	1:A:1031:G:H5'	2.47	0.43
1:A:1068:G:N3	1:A:1191:A:C2	2.86	0.43
1:A:1192:C:H2'	1:A:1193:G:O4'	2.19	0.43
1:A:1234:C:H2'	1:A:1235:U:C6	2.53	0.43
1:A:1326:C:H5''	24:V:12:LYS:NZ	2.34	0.43
5:B:55:PHE:HA	5:B:58:ILE:HD12	2.00	0.43
7:D:36:ARG:N	7:D:37:PRO:CD	2.49	0.43
9:F:69:GLU:OE1	9:F:69:GLU:N	2.46	0.43
9:F:74:ASP:OD1	9:F:77:ARG:NH2	2.52	0.43
11:H:35:ILE:HD12	11:H:35:ILE:H	1.84	0.43
12:I:7:THR:HG22	12:I:8:GLY:N	2.33	0.43
15:L:71:PRO:HG2	15:L:102:ARG:HG2	2.01	0.43
16:M:26:GLY:C	16:M:28:ALA:H	2.27	0.43
21:R:24:ALA:O	21:R:26:LEU:N	2.50	0.43
21:R:36:ASN:CG	21:R:39:VAL:HG12	2.44	0.43
23:T:45:GLN:HA	23:T:91:LEU:HB3	2.00	0.43
23:T:53:LEU:HG	23:T:56:MET:HE3	2.01	0.43
24:V:8:THR:HG22	24:V:9:ARG:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:G:C5	1:A:58:C:C4	3.07	0.43
1:A:194:C:H2'	1:A:195:A:H5''	2.00	0.43
1:A:513:C:O2'	1:A:514:C:H5'	2.19	0.43
1:A:928:G:O2'	1:A:929:G:H5'	2.18	0.43
1:A:1329:A:HO2'	1:A:1330:U:H5'	1.84	0.43
1:A:1331:G:O2'	1:A:1332:A:P	2.77	0.43
5:B:82:ARG:O	5:B:86:GLU:HG3	2.18	0.43
5:B:215:LEU:O	5:B:218:ALA:N	2.51	0.43
6:C:33:LEU:O	6:C:34:LEU:C	2.60	0.43
10:G:5:ARG:CG	10:G:6:ARG:H	2.04	0.43
11:H:11:THR:HA	11:H:14:ARG:HH12	1.83	0.43
15:L:24:VAL:O	15:L:24:VAL:HG12	2.18	0.43
18:O:88:ARG:HH11	18:O:88:ARG:CA	2.29	0.43
19:P:1:MET:HE3	19:P:3:LYS:CG	2.48	0.43
1:A:913:A:H4'	1:A:914:A:O5'	2.19	0.43
1:A:942:G:H2'	1:A:943:U:C6	2.53	0.43
1:A:948:C:H2'	1:A:949:A:H8	1.84	0.43
1:A:1061:G:O4'	13:J:56:HIS:CE1	2.72	0.43
1:A:1190:G:C2'	1:A:1191:A:OP2	2.66	0.43
1:A:1309:G:C6	1:A:1329:A:C2	3.07	0.43
5:B:211:ILE:HG13	5:B:211:ILE:H	1.70	0.43
6:C:56:ASP:O	6:C:57:ILE:HG13	2.17	0.43
6:C:118:GLN:O	6:C:121:ALA:HB3	2.18	0.43
6:C:184:TYR:CD2	6:C:184:TYR:C	2.96	0.43
6:C:202:ILE:HG22	6:C:204:LEU:CD2	2.48	0.43
10:G:148:ASN:O	10:G:149:ARG:C	2.62	0.43
11:H:6:ILE:HD13	11:H:6:ILE:HA	1.90	0.43
12:I:69:GLY:O	12:I:70:LYS:C	2.62	0.43
14:K:54:ARG:H	14:K:54:ARG:HG2	1.54	0.43
18:O:39:LEU:O	18:O:40:SER:C	2.61	0.43
18:O:67:LEU:O	18:O:68:ARG:C	2.62	0.43
20:Q:59:ILE:CG2	20:Q:71:PHE:CD1	3.02	0.43
20:Q:97:SER:HB2	20:Q:103:GLY:HA2	2.01	0.43
1:A:934:C:C4	1:A:1345:U:C5	3.07	0.43
1:A:1070:U:H2'	1:A:1071:C:H6	1.84	0.43
1:A:1221:G:O3'	22:S:77:THR:CG2	2.67	0.43
1:A:1345:U:N3	1:A:1377:A:C2	2.87	0.43
5:B:9:GLU:HG2	5:B:10:LEU:H	1.81	0.43
5:B:10:LEU:O	5:B:12:GLU:N	2.46	0.43
5:B:16:HIS:CE1	5:B:213:LEU:HD13	2.53	0.43
6:C:20:SER:HB3	6:C:22:TRP:NE1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:97:LYS:HG2	6:C:97:LYS:O	2.19	0.43
6:C:150:LYS:HG3	6:C:169:ALA:HB2	2.01	0.43
7:D:67:ILE:C	7:D:69:GLY:N	2.77	0.43
7:D:68:TYR:HD1	7:D:68:TYR:H	1.67	0.43
7:D:163:GLU:O	7:D:165:MET:N	2.52	0.43
9:F:91:VAL:CG1	9:F:92:LYS:H	2.26	0.43
12:I:33:PHE:C	12:I:35:GLU:N	2.77	0.43
15:L:27:LEU:HD23	15:L:28:LYS:N	2.34	0.43
15:L:85:ILE:HG23	15:L:98:TYR:HB3	2.01	0.43
21:R:19:LYS:HD2	21:R:19:LYS:N	2.34	0.43
1:A:407:G:H2'	1:A:408:A:C8	2.54	0.42
1:A:943:U:O2'	1:A:944:G:H5'	2.19	0.42
1:A:1051:C:O2'	1:A:1052:U:H5'	2.18	0.42
1:A:1193:G:O2'	1:A:1194:U:H5'	2.19	0.42
1:A:1202:G:H2'	1:A:1203:C:O4'	2.19	0.42
1:A:1286:A:H2'	1:A:1287:A:O3'	2.19	0.42
1:A:1465:C:H2'	1:A:1466:C:O4'	2.19	0.42
5:B:122:PHE:HE2	5:B:139:LYS:HG2	1.83	0.42
8:E:55:VAL:O	8:E:58:ALA:HB3	2.19	0.42
11:H:111:ILE:O	11:H:134:ILE:HB	2.19	0.42
13:J:38:ILE:HA	13:J:39:PRO:HD2	1.73	0.42
13:J:46:ARG:HD3	17:N:61:TRP:CH2	2.54	0.42
18:O:70:LEU:CD1	18:O:78:TYR:HB2	2.33	0.42
20:Q:45:HIS:HB2	20:Q:69:LYS:HE2	2.01	0.42
22:S:87:ALA:O	22:S:88:LYS:CB	2.66	0.42
23:T:54:LYS:HA	23:T:57:ARG:NH1	2.32	0.42
1:A:56:U:H2'	1:A:57:G:H8	1.82	0.42
1:A:334:C:O2'	1:A:335:C:H5'	2.19	0.42
1:A:382:A:C2	1:A:383:A:C5	3.07	0.42
1:A:533:A:H2'	1:A:535:A:OP2	2.19	0.42
1:A:533:A:C2	1:A:536:C:C5	3.07	0.42
1:A:594:G:C2'	1:A:595:G:H5'	2.49	0.42
1:A:689:C:OP1	14:K:46:GLY:HA3	2.20	0.42
1:A:942:G:O2'	1:A:943:U:H5'	2.19	0.42
1:A:979:C:O2	17:N:19:ARG:HG2	2.19	0.42
1:A:1289:A:H2'	1:A:1290:G:H5'	2.01	0.42
5:B:25:ASN:C	5:B:25:ASN:ND2	2.62	0.42
5:B:61:LEU:HD13	5:B:61:LEU:O	2.19	0.42
5:B:143:GLU:O	5:B:147:LYS:HG3	2.18	0.42
8:E:115:VAL:HG13	8:E:116:THR:N	2.34	0.42
9:F:44:GLY:HA2	9:F:59:TYR:HE1	1.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:P:12:LYS:O	19:P:13:HIS:CB	2.66	0.42
1:A:245:C:O2	1:A:283:C:N3	2.52	0.42
1:A:959:A:C3'	1:A:960:U:H5''	2.47	0.42
1:A:1016:A:C2'	1:A:1017:G:H5'	2.49	0.42
1:A:1054:C:N3	3:Y:34:G:O4'	2.52	0.42
1:A:1069:C:H2'	1:A:1070:U:O5'	2.19	0.42
1:A:1207:G:C5	1:A:1208:C:C5	3.07	0.42
1:A:1345:U:OP1	12:I:120:ARG:NH1	2.52	0.42
5:B:112:VAL:O	5:B:115:LEU:HB3	2.19	0.42
5:B:178:ARG:NH2	5:B:196:LEU:C	2.72	0.42
7:D:5:ILE:HA	7:D:115:ARG:NH2	2.33	0.42
8:E:57:LYS:O	8:E:60:TYR:HB3	2.18	0.42
9:F:39:LYS:HG3	9:F:62:TRP:HZ3	1.84	0.42
9:F:78:GLU:HA	9:F:81:ILE:CD1	2.48	0.42
10:G:112:PRO:O	10:G:113:GLU:C	2.62	0.42
10:G:129:GLU:CB	10:G:131:LYS:HE2	2.49	0.42
11:H:72:PRO:O	11:H:73:ASP:HB3	2.20	0.42
11:H:83:ILE:HB	11:H:137:VAL:HG22	2.01	0.42
16:M:6:GLY:C	16:M:8:GLU:N	2.76	0.42
19:P:28:ARG:HG2	19:P:29:ASP:CG	2.43	0.42
19:P:51:VAL:O	19:P:52:ASP:HB3	2.19	0.42
22:S:5:LEU:O	22:S:6:LYS:HB2	2.20	0.42
24:V:5:ASP:O	24:V:11:GLY:HA3	2.19	0.42
1:A:33:A:H2'	1:A:34:C:C6	2.54	0.42
1:A:232:G:H1'	1:A:262:A:N1	2.34	0.42
1:A:419:C:O2'	1:A:420:U:H5'	2.18	0.42
1:A:1019:C:H2'	1:A:1020:U:O4'	2.20	0.42
1:A:1194:U:H2'	1:A:1195:C:H6	1.84	0.42
5:B:33:TYR:CB	5:B:41:ILE:O	2.67	0.42
5:B:34:ALA:O	5:B:40:HIS:HA	2.20	0.42
6:C:33:LEU:HD23	6:C:33:LEU:O	2.19	0.42
7:D:179:GLU:C	7:D:181:MET:H	2.28	0.42
11:H:35:ILE:HG22	11:H:39:LEU:HD21	2.01	0.42
12:I:55:ALA:O	12:I:56:LEU:CB	2.67	0.42
14:K:94:ALA:O	14:K:97:ALA:HB3	2.19	0.42
16:M:23:TYR:HB3	16:M:67:GLU:H	1.84	0.42
16:M:84:ILE:O	16:M:86:CYS:N	2.52	0.42
17:N:15:LYS:O	17:N:16:PHE:CG	2.73	0.42
19:P:53:VAL:HG23	19:P:54:GLU:N	2.33	0.42
20:Q:28:PRO:HA	20:Q:35:VAL:HA	2.02	0.42
21:R:27:GLY:O	21:R:29:PHE:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:G:H5'	1:A:298:A:O4'	2.19	0.42
1:A:55:A:H2'	1:A:56:U:C6	2.54	0.42
1:A:328:C:O2	1:A:328:C:H2'	2.20	0.42
1:A:406:G:H5''	7:D:5:ILE:HG21	2.00	0.42
1:A:573:A:O2'	1:A:574:A:H5'	2.19	0.42
1:A:652:U:O4'	1:A:653:A:H2	2.01	0.42
1:A:781:A:OP1	1:A:1523:G:H5'	2.20	0.42
1:A:973:G:H3'	1:A:974:A:H5''	2.02	0.42
1:A:974:A:OP2	17:N:41:ARG:NH1	2.51	0.42
1:A:1125:U:C5'	1:A:1126:U:H5	2.27	0.42
1:A:1379:G:O2'	1:A:1380:U:H5'	2.20	0.42
5:B:235:SER:C	5:B:237:ALA:N	2.77	0.42
7:D:187:ARG:NE	7:D:188:LEU:H	2.18	0.42
12:I:3:GLN:HG3	12:I:20:ARG:HG2	2.01	0.42
15:L:41:ARG:CB	15:L:41:ARG:NH1	2.82	0.42
15:L:110:VAL:O	15:L:122:THR:CG2	2.65	0.42
19:P:76:GLN:HE21	19:P:76:GLN:HB2	1.60	0.42
1:A:425:G:C2'	1:A:426:G:H5'	2.50	0.42
1:A:457:C:N3	1:A:476:G:C2	2.87	0.42
1:A:597:G:C4	1:A:644:G:C2	3.08	0.42
1:A:792:A:O2'	1:A:793:U:OP2	2.37	0.42
1:A:878:G:C5'	11:H:89:PRO:HG2	2.49	0.42
1:A:1252:A:H2'	1:A:1253:G:O4'	2.20	0.42
1:A:1258:G:H1	1:A:1277:C:H42	1.67	0.42
5:B:75:LYS:C	5:B:77:ALA:N	2.77	0.42
5:B:77:ALA:HA	5:B:80:ILE:HD12	2.02	0.42
6:C:11:ARG:O	6:C:14:ILE:O	2.37	0.42
16:M:65:LYS:O	16:M:66:LEU:HD23	2.19	0.42
17:N:3:ARG:O	17:N:7:ILE:HG13	2.20	0.42
17:N:41:ARG:HG3	17:N:42:ILE:N	2.35	0.42
20:Q:3:LYS:HB3	20:Q:60:ILE:CD1	2.49	0.42
22:S:25:LYS:HD2	22:S:25:LYS:H	1.85	0.42
1:A:75:G:H2'	1:A:76:C:H6	1.84	0.42
1:A:200:G:H1	1:A:217:C:H42	1.68	0.42
1:A:229:U:C2'	1:A:230:G:H5'	2.50	0.42
1:A:533:A:O2'	1:A:534:U:OP1	2.34	0.42
1:A:893:C:H2'	1:A:894:G:C8	2.54	0.42
1:A:1014:A:H5'	22:S:14:HIS:CD2	2.55	0.42
1:A:1150:U:O2	13:J:39:PRO:CG	2.67	0.42
5:B:21:ARG:NH1	5:B:23:ARG:HG2	2.35	0.42
5:B:92:TYR:CD1	5:B:151:GLY:HA3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:182:ILE:O	5:B:183:PRO:C	2.62	0.42
6:C:52:LEU:HD23	6:C:52:LEU:N	2.26	0.42
6:C:174:PRO:HB2	6:C:177:THR:CG2	2.48	0.42
7:D:24:GLU:HG2	7:D:25:ARG:N	2.33	0.42
8:E:65:ASN:O	8:E:65:ASN:CG	2.62	0.42
8:E:131:ILE:O	8:E:134:ALA:HB3	2.19	0.42
10:G:51:GLN:HE21	10:G:58:PRO:HD3	1.84	0.42
11:H:16:ALA:HB1	11:H:21:LYS:HB2	2.02	0.42
13:J:39:PRO:O	13:J:69:ASN:O	2.38	0.42
15:L:46:LYS:CG	15:L:47:LYS:H	1.95	0.42
18:O:61:GLY:O	18:O:62:GLN:C	2.63	0.42
1:A:28:G:O2'	1:A:296:U:OP1	2.32	0.42
1:A:277:C:O2'	1:A:278:G:H5'	2.19	0.42
1:A:408:A:O2'	1:A:409:G:H5'	2.19	0.42
1:A:519:C:H2'	1:A:520:A:O4'	2.19	0.42
1:A:632:A:H2'	1:A:633:G:H5'	2.00	0.42
1:A:644:G:C2'	1:A:645:C:H5'	2.50	0.42
1:A:938:A:C6	1:A:939:G:C5	3.08	0.42
1:A:980:C:H3'	1:A:981:U:H6	1.83	0.42
1:A:1288:A:C6	1:A:1289:A:C5	3.08	0.42
1:A:1347:G:H2'	1:A:1373:G:H1	1.83	0.42
1:A:1451:A:O3'	1:A:1452:C:H6	2.03	0.42
5:B:10:LEU:C	5:B:12:GLU:N	2.77	0.42
5:B:146:GLN:O	5:B:150:SER:HB3	2.20	0.42
6:C:177:THR:O	6:C:177:THR:CG2	2.67	0.42
7:D:25:ARG:HH21	7:D:30:LYS:HD3	1.79	0.42
9:F:2:ARG:CD	9:F:69:GLU:HG2	2.49	0.42
10:G:43:PHE:CZ	10:G:47:CYS:SG	3.13	0.42
10:G:79:ARG:HD3	10:G:84:ASN:OD1	2.20	0.42
10:G:145:ALA:C	10:G:147:ALA:H	2.28	0.42
10:G:155:ARG:O	10:G:156:TRP:HB3	2.19	0.42
13:J:28:ARG:HH12	13:J:33:GLN:HG2	1.84	0.42
13:J:49:VAL:O	13:J:50:ILE:C	2.61	0.42
13:J:96:ILE:CG2	13:J:97:GLU:N	2.83	0.42
14:K:52:GLY:N	14:K:55:LYS:HE3	2.34	0.42
20:Q:97:SER:O	20:Q:99:SER:N	2.51	0.42
21:R:39:VAL:O	21:R:42:ARG:HB2	2.19	0.42
23:T:97:ALA:C	23:T:99:LEU:N	2.78	0.42
1:A:9:G:C2	1:A:26:A:C2	3.08	0.42
1:A:107:G:O2'	1:A:108:G:H5'	2.20	0.42
1:A:191:G:N2	23:T:85:MET:HE1	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:G:P	19:P:3:LYS:HZ3	2.43	0.42
1:A:622:A:H2'	1:A:623:C:H5'	2.02	0.42
1:A:689:C:H2'	1:A:690:G:O4'	2.20	0.42
1:A:769:G:H4'	1:A:1513:A:H4'	2.01	0.42
1:A:977:A:H1'	1:A:1223:C:H42	1.85	0.42
1:A:995:C:O2	1:A:995:C:H2'	2.19	0.42
1:A:1298:C:N4	10:G:114:ARG:HD3	2.35	0.42
1:A:1328:C:O2'	1:A:1329:A:H5'	2.19	0.42
6:C:191:THR:HG23	6:C:192:THR:H	1.85	0.42
7:D:36:ARG:C	7:D:38:TYR:H	2.27	0.42
10:G:21:VAL:CG2	10:G:22:LEU:N	2.82	0.42
12:I:41:VAL:O	12:I:42:ARG:C	2.63	0.42
13:J:9:ARG:HG3	13:J:9:ARG:O	2.20	0.42
13:J:60:ARG:HD2	13:J:60:ARG:H	1.84	0.42
15:L:41:ARG:HH12	15:L:57:LYS:HE2	1.85	0.42
15:L:47:LYS:HB2	15:L:48:PRO:CD	2.48	0.42
20:Q:8:GLY:HA3	20:Q:21:VAL:CG1	2.50	0.42
1:A:22:G:C6	1:A:23:C:C4	3.08	0.42
1:A:45:U:H2'	1:A:46:G:H8	1.85	0.42
1:A:340:U:H2'	1:A:341:C:C6	2.55	0.42
1:A:407:G:O2'	7:D:116:GLN:HG3	2.20	0.42
1:A:444:C:O2'	1:A:445:G:H5'	2.20	0.42
1:A:582:U:H1'	20:Q:105:ALA:HA	2.01	0.42
1:A:1029:C:O5'	1:A:1029:C:H6	2.03	0.42
1:A:1121:U:H2'	1:A:1122:U:H6	1.84	0.42
1:A:1127:G:H21	1:A:1147:C:N4	2.18	0.42
1:A:1375:A:O2'	1:A:1376:U:H5'	2.20	0.42
5:B:53:ARG:CZ	5:B:53:ARG:HB3	2.50	0.42
5:B:154:LEU:O	5:B:155:LEU:C	2.63	0.42
5:B:178:ARG:C	5:B:180:LEU:N	2.78	0.42
6:C:66:VAL:O	6:C:66:VAL:HG12	2.19	0.42
6:C:148:GLY:HA3	6:C:172:ARG:O	2.20	0.42
6:C:165:THR:O	6:C:165:THR:HG22	2.19	0.42
7:D:59:ARG:O	7:D:60:GLU:C	2.63	0.42
8:E:143:ARG:HH12	11:H:77:GLU:CD	2.27	0.42
9:F:62:TRP:CD1	21:R:35:ARG:NH1	2.87	0.42
10:G:104:LEU:HD23	10:G:104:LEU:HA	1.83	0.42
10:G:135:VAL:O	10:G:136:LYS:C	2.63	0.42
13:J:30:SER:HB2	13:J:80:LYS:C	2.45	0.42
16:M:37:THR:O	16:M:37:THR:HG22	2.20	0.42
22:S:21:GLU:C	22:S:23:ASN:N	2.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:A:H2'	1:A:152:A:O4'	2.20	0.41
1:A:1027:C:H2'	1:A:1028:C:C6	2.55	0.41
1:A:1039:C:O2'	1:A:1040:U:H5'	2.20	0.41
1:A:1229:A:C2	1:A:1230:C:C5	3.08	0.41
1:A:1287:A:C6	1:A:1288:A:C6	3.07	0.41
1:A:1309:G:C6	1:A:1329:A:N1	2.88	0.41
4:Z:2:U:H2'	4:Z:3:U:H6	1.84	0.41
5:B:84:GLU:CB	5:B:219:VAL:HG21	2.18	0.41
5:B:200:ILE:HD12	5:B:200:ILE:C	2.44	0.41
6:C:40:ARG:HG3	6:C:40:ARG:NH1	2.35	0.41
6:C:125:GLU:OE2	6:C:189:ALA:HA	2.20	0.41
7:D:88:VAL:O	7:D:92:VAL:HG23	2.20	0.41
7:D:170:VAL:HG22	7:D:171:GLY:N	2.34	0.41
14:K:110:ASP:OD2	21:R:88:LYS:NZ	2.42	0.41
20:Q:24:GLU:OE2	20:Q:37:LYS:HD3	2.20	0.41
23:T:74:LYS:CG	23:T:75:ASN:N	2.55	0.41
1:A:101:A:H2'	1:A:102:G:H8	1.85	0.41
1:A:223:U:H5'	23:T:68:LYS:HZ1	1.84	0.41
1:A:821:G:O2'	1:A:822:C:H5'	2.20	0.41
1:A:961:U:H2'	1:A:962:C:H5'	2.02	0.41
1:A:1058:G:C6	1:A:1059:C:N3	2.89	0.41
1:A:1168:A:C6	1:A:1169:A:C6	3.08	0.41
1:A:1329:A:H2'	1:A:1330:U:H5'	2.02	0.41
5:B:17:PHE:O	5:B:17:PHE:CD2	2.73	0.41
6:C:155:GLY:HA3	6:C:164:ARG:O	2.21	0.41
8:E:31:LEU:HD23	8:E:31:LEU:HA	1.52	0.41
10:G:138:LYS:C	10:G:138:LYS:CD	2.90	0.41
13:J:34:VAL:HG12	13:J:35:SER:N	2.34	0.41
13:J:89:ASP:OD1	13:J:90:LEU:N	2.53	0.41
14:K:59:TYR:O	14:K:60:ALA:C	2.63	0.41
14:K:69:ALA:O	14:K:73:MET:N	2.53	0.41
15:L:43:VAL:HG23	15:L:55:VAL:CG2	2.50	0.41
16:M:8:GLU:HG3	16:M:22:ILE:HG13	2.02	0.41
18:O:15:PHE:O	18:O:16:ALA:C	2.62	0.41
19:P:67:THR:CG2	19:P:68:ASP:N	2.83	0.41
23:T:45:GLN:C	23:T:45:GLN:OE1	2.63	0.41
23:T:50:GLU:HA	23:T:100:ILE:CB	2.49	0.41
23:T:54:LYS:N	23:T:100:ILE:HD13	2.35	0.41
1:A:184:G:C4'	1:A:224:C:H4'	2.49	0.41
1:A:235:C:C5'	20:Q:70:ARG:HG2	2.40	0.41
1:A:429:U:H4'	1:A:430:A:O5'	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:502:G:OP1	15:L:118:SER:N	2.34	0.41
1:A:665:A:N3	1:A:732:C:H2'	2.36	0.41
1:A:939:G:C6	1:A:940:C:N4	2.87	0.41
1:A:959:A:H2	1:A:1221:G:N3	2.18	0.41
1:A:1032:G:H2'	1:A:1033:G:O4'	2.20	0.41
1:A:1057:G:C2'	1:A:1058:G:H5'	2.50	0.41
1:A:1107:C:H2'	1:A:1108:G:H5'	2.02	0.41
1:A:1152:A:O2'	1:A:1153:C:H5'	2.19	0.41
1:A:1419:G:H2'	1:A:1420:C:C6	2.55	0.41
1:A:1496:C:H2'	1:A:1497:G:O4'	2.20	0.41
5:B:7:VAL:O	5:B:8:LYS:HG3	2.20	0.41
5:B:16:HIS:O	5:B:17:PHE:HD2	2.03	0.41
5:B:96:ARG:HD2	5:B:97:TRP:N	2.33	0.41
5:B:148:TYR:N	5:B:148:TYR:CD2	2.87	0.41
6:C:160:ALA:O	6:C:161:GLU:C	2.63	0.41
9:F:30:LEU:C	9:F:35:ALA:HB3	2.45	0.41
11:H:7:ALA:HB2	11:H:85:ARG:HG3	2.02	0.41
13:J:47:PHE:CE2	17:N:37:PHE:HE1	2.37	0.41
13:J:51:ARG:CB	13:J:59:SER:HB3	2.50	0.41
13:J:60:ARG:O	13:J:61:GLU:CB	2.67	0.41
15:L:6:THR:O	15:L:7:ILE:C	2.63	0.41
16:M:8:GLU:CD	16:M:22:ILE:HA	2.46	0.41
16:M:19:LEU:CA	16:M:22:ILE:HD13	2.46	0.41
16:M:102:ARG:NH1	16:M:104:ARG:HB3	2.35	0.41
16:M:105:THR:O	16:M:106:ASN:C	2.63	0.41
19:P:45:THR:HB	19:P:46:PRO:HD2	2.01	0.41
1:A:164:U:H2'	1:A:165:C:C6	2.55	0.41
1:A:190:C:H2'	1:A:190(A):C:C6	2.55	0.41
1:A:474:G:H2'	1:A:475:G:C8	2.43	0.41
1:A:786:G:C2	1:A:797:C:C2	3.09	0.41
1:A:960:U:H1'	1:A:1223:C:H5'	2.02	0.41
1:A:1073:U:OP1	8:E:57:LYS:HE2	2.20	0.41
1:A:1220:G:H2'	1:A:1221:G:H8	1.85	0.41
1:A:1269:A:N1	1:A:1312:G:O2'	2.52	0.41
1:A:1319:A:OP1	22:S:5:LEU:HD21	2.21	0.41
1:A:1320:C:O2	22:S:72:GLY:HA3	2.21	0.41
1:A:1525:G:O2'	1:A:1526:G:H5'	2.20	0.41
5:B:122:PHE:O	5:B:123:ALA:HB2	2.19	0.41
5:B:169:LYS:C	5:B:169:LYS:HD3	2.45	0.41
6:C:6:HIS:HD2	6:C:8:ILE:HB	1.79	0.41
6:C:22:TRP:CZ3	6:C:32:LEU:HD22	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:111:LEU:HD11	6:C:144:SER:O	2.20	0.41
6:C:167:TRP:O	6:C:168:ALA:CB	2.68	0.41
10:G:43:PHE:CE2	10:G:47:CYS:SG	3.14	0.41
10:G:51:GLN:NE2	10:G:56:GLN:O	2.51	0.41
10:G:66:VAL:O	10:G:70:LYS:HG3	2.21	0.41
10:G:70:LYS:CG	10:G:100:ALA:HB2	2.47	0.41
12:I:114:TYR:CD2	12:I:114:TYR:N	2.86	0.41
13:J:19:SER:HA	13:J:22:LYS:HZ3	1.85	0.41
14:K:69:ALA:O	14:K:70:LYS:C	2.63	0.41
15:L:86:ARG:NH1	15:L:86:ARG:CG	2.79	0.41
17:N:12:ARG:O	17:N:14:PRO:HD3	2.20	0.41
20:Q:5:VAL:HG13	20:Q:59:ILE:O	2.20	0.41
20:Q:45:HIS:O	20:Q:47:PRO:HD3	2.20	0.41
1:A:37:U:O2'	1:A:38:G:H5'	2.20	0.41
1:A:825:G:O2'	1:A:826:C:H5'	2.21	0.41
1:A:1105:A:H2'	1:A:1106:G:C8	2.55	0.41
1:A:1130:A:P	1:A:1131:G:OP2	2.79	0.41
1:A:1521:G:O2'	1:A:1522:U:H5'	2.21	0.41
5:B:48:MET:O	5:B:51:LEU:HB2	2.21	0.41
5:B:59:GLU:O	5:B:60:ASP:C	2.64	0.41
5:B:79:ASP:O	5:B:80:ILE:C	2.63	0.41
6:C:70:VAL:CG1	6:C:71:ALA:N	2.82	0.41
6:C:121:ALA:O	6:C:125:GLU:HG3	2.20	0.41
6:C:180:ALA:CB	6:C:182:ILE:HG13	2.50	0.41
6:C:188:LEU:CD1	6:C:195:VAL:HG13	2.50	0.41
6:C:203:PHE:C	6:C:204:LEU:HD23	2.45	0.41
7:D:52:SER:O	7:D:54:TYR:N	2.53	0.41
7:D:112:VAL:HG23	7:D:161:ASN:ND2	2.33	0.41
7:D:162:LEU:HD23	7:D:178:VAL:HG13	2.01	0.41
9:F:9:VAL:HG22	9:F:60:PHE:HD2	1.83	0.41
10:G:116:ALA:O	10:G:117:ALA:C	2.64	0.41
22:S:39:THR:HG23	22:S:68:GLY:O	2.20	0.41
1:A:41:G:H2'	1:A:42:G:C8	2.56	0.41
1:A:186:C:H2'	1:A:187:C:H6	1.83	0.41
1:A:437:U:O2'	7:D:123:HIS:CD2	2.73	0.41
1:A:561:U:O2'	1:A:562:C:P	2.78	0.41
1:A:831:U:O2'	1:A:832:C:H5'	2.20	0.41
1:A:832:C:O2'	1:A:833:U:H5'	2.21	0.41
1:A:914:A:O2'	1:A:915:A:H5'	2.21	0.41
1:A:940:C:H2'	1:A:941:G:C8	2.53	0.41
1:A:970:C:OP1	13:J:57:LYS:HE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:977:A:C8	1:A:1223:C:N3	2.88	0.41
1:A:1057:G:C4'	6:C:154:SER:HB2	2.50	0.41
1:A:1108:G:H4'	1:A:1191:A:O4'	2.20	0.41
1:A:1237:C:H4'	1:A:1334:G:N2	2.35	0.41
1:A:1239:A:C4	1:A:1298:C:N4	2.88	0.41
5:B:10:LEU:C	5:B:12:GLU:H	2.27	0.41
5:B:23:ARG:NH1	5:B:23:ARG:O	2.54	0.41
5:B:185:ILE:HA	5:B:199:TYR:O	2.21	0.41
6:C:33:LEU:O	6:C:36:ASP:HB3	2.21	0.41
6:C:139:GLN:O	6:C:143:GLU:HG3	2.20	0.41
10:G:92:SER:C	10:G:94:ARG:N	2.76	0.41
13:J:71:LEU:HD22	13:J:71:LEU:HA	1.88	0.41
13:J:96:ILE:HG22	13:J:98:ILE:HG13	2.02	0.41
15:L:41:ARG:CG	15:L:42:THR:N	2.71	0.41
15:L:120:TYR:O	15:L:122:THR:HG23	2.21	0.41
1:A:75:G:HO2'	1:A:76:C:H5'	1.86	0.41
1:A:243:A:C2	1:A:246:A:C8	3.09	0.41
1:A:626:U:O2'	1:A:627:G:H5'	2.21	0.41
1:A:714:G:H2'	1:A:715:A:C8	2.56	0.41
1:A:1226:C:O2'	1:A:1227:A:H5'	2.21	0.41
5:B:16:HIS:O	5:B:17:PHE:CD2	2.74	0.41
6:C:31:HIS:C	6:C:33:LEU:H	2.28	0.41
8:E:107:ARG:O	8:E:109:ILE:N	2.53	0.41
10:G:78:ARG:O	10:G:84:ASN:HA	2.20	0.41
10:G:141:VAL:O	10:G:142:GLU:C	2.64	0.41
11:H:119:LEU:HD12	11:H:124:ALA:N	2.35	0.41
13:J:19:SER:HA	13:J:22:LYS:NZ	2.36	0.41
13:J:90:LEU:N	13:J:91:PRO:HD2	2.11	0.41
17:N:9:LYS:C	17:N:11:LYS:H	2.29	0.41
1:A:718:G:H5''	1:A:719:C:OP2	2.21	0.41
1:A:925:G:C6	1:A:927:G:N7	2.89	0.41
1:A:936:C:H2'	1:A:937:A:O4'	2.21	0.41
1:A:1015:A:H1'	1:A:1218:C:O2'	2.21	0.41
1:A:1055:A:N6	1:A:1206:G:C5	2.89	0.41
1:A:1057:G:C5	1:A:1204:A:C2	3.09	0.41
1:A:1165:C:C2'	1:A:1166:G:H5'	2.51	0.41
1:A:1250:A:H5'	12:I:68:GLY:O	2.20	0.41
1:A:1349:A:OP1	12:I:120:ARG:HB2	2.20	0.41
1:A:1438:G:H2'	1:A:1439:C:H6	1.83	0.41
1:A:1459:C:O2'	1:A:1460:A:H5'	2.20	0.41
5:B:105:PHE:C	5:B:107:THR:N	2.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:33:LEU:C	6:C:33:LEU:CD2	2.93	0.41
6:C:46:GLU:C	6:C:48:TYR:H	2.27	0.41
6:C:81:GLY:HA2	6:C:84:ILE:HG22	2.02	0.41
6:C:173:VAL:N	6:C:174:PRO:CD	2.83	0.41
6:C:191:THR:HG22	6:C:193:TYR:N	2.28	0.41
9:F:82:ARG:HA	9:F:82:ARG:NE	2.33	0.41
12:I:32:ASP:O	12:I:33:PHE:C	2.62	0.41
13:J:6:ILE:O	13:J:71:LEU:HD22	2.20	0.41
15:L:82:VAL:O	15:L:106:ASP:HB2	2.21	0.41
16:M:22:ILE:HG22	16:M:23:TYR:N	2.36	0.41
16:M:56:LEU:O	16:M:57:ARG:C	2.63	0.41
16:M:87:TYR:C	16:M:89:GLY:N	2.76	0.41
1:A:80:G:C3'	1:A:81:U:H5''	2.50	0.41
1:A:169:C:O2'	1:A:170:U:H5'	2.21	0.41
1:A:184:G:H2'	1:A:185:A:H8	1.86	0.41
1:A:247:G:OP2	20:Q:100:LYS:HG3	2.20	0.41
1:A:293:G:C6	1:A:294:U:C4	3.09	0.41
1:A:687:A:O2'	1:A:688:G:OP2	2.33	0.41
1:A:735:C:O2'	1:A:736:C:H5'	2.21	0.41
1:A:1028:C:N4	1:A:1033:G:N2	2.69	0.41
1:A:1061:G:O2'	1:A:1062:U:H5'	2.21	0.41
1:A:1104:G:P	5:B:111:ARG:HD2	2.60	0.41
1:A:1313:U:O2'	1:A:1314:C:H5'	2.21	0.41
1:A:1318:A:H4'	22:S:10:PHE:CD1	2.56	0.41
1:A:1372:U:H2'	1:A:1373:G:H5'	2.03	0.41
1:A:1373:G:H5''	10:G:36:LYS:HD3	2.03	0.41
5:B:90:MET:HA	5:B:91:PRO:HD3	1.78	0.41
5:B:124:SER:CB	5:B:125:PRO:HD2	2.44	0.41
5:B:135:GLN:O	5:B:135:GLN:HG2	2.21	0.41
7:D:14:ARG:O	7:D:14:ARG:HD3	2.21	0.41
8:E:39:GLY:O	8:E:68:GLU:HA	2.21	0.41
9:F:28:ARG:O	9:F:29:ALA:C	2.64	0.41
10:G:16:LEU:HD22	10:G:16:LEU:N	2.35	0.41
10:G:97:GLN:O	10:G:98:SER:C	2.63	0.41
11:H:33:GLU:HA	11:H:36:LEU:HD12	2.03	0.41
11:H:75:ARG:HA	11:H:76:PRO:HD3	1.68	0.41
11:H:103:VAL:HG21	11:H:109:ILE:C	2.46	0.41
11:H:104:ARG:HG3	11:H:138:TRP:CD2	2.56	0.41
12:I:48:GLU:HA	12:I:51:ARG:NH1	2.34	0.41
12:I:53:VAL:C	12:I:55:ALA:H	2.29	0.41
12:I:96:LEU:N	12:I:96:LEU:CD1	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:41:ARG:HB3	15:L:41:ARG:NH1	2.36	0.41
15:L:87:GLY:H	15:L:98:TYR:HB3	1.86	0.41
16:M:16:ASP:O	16:M:17:VAL:C	2.63	0.41
16:M:25:ILE:HG23	16:M:29:ARG:HB2	2.02	0.41
16:M:45:VAL:HG13	16:M:48:LEU:HD12	2.02	0.41
17:N:26:ARG:CD	17:N:47:LEU:HD11	2.51	0.41
19:P:53:VAL:O	19:P:54:GLU:C	2.61	0.41
19:P:67:THR:O	19:P:68:ASP:C	2.61	0.41
21:R:43:PHE:CD1	21:R:66:LEU:HD11	2.56	0.41
23:T:84:LEU:O	23:T:85:MET:C	2.64	0.41
1:A:296:U:H1'	1:A:556:C:H1'	2.03	0.41
1:A:393:A:OP2	19:P:12:LYS:CE	2.67	0.41
1:A:1031:G:H2'	1:A:1032:G:C8	2.48	0.41
1:A:1439:C:H2'	1:A:1440:C:C6	2.56	0.41
5:B:38:GLY:O	5:B:39:ILE:C	2.64	0.41
5:B:162:ILE:O	5:B:162:ILE:HG22	2.21	0.41
8:E:102:ALA:CB	8:E:120:THR:OG1	2.69	0.41
9:F:28:ARG:HG2	9:F:32:ASN:OD1	2.21	0.41
10:G:15:ASP:C	10:G:17:VAL:H	2.29	0.41
10:G:32:ARG:O	10:G:33:ASP:HB2	2.21	0.41
11:H:34:GLU:HA	11:H:34:GLU:OE1	2.21	0.41
11:H:68:ARG:HH11	11:H:68:ARG:HG2	1.85	0.41
12:I:44:VAL:CG1	12:I:51:ARG:NH2	2.83	0.41
12:I:45:ALA:O	12:I:46:ALA:C	2.64	0.41
13:J:24:VAL:HG12	13:J:28:ARG:HE	1.86	0.41
14:K:20:TYR:O	14:K:30:VAL:HA	2.21	0.41
14:K:56:GLY:O	14:K:57:THR:C	2.63	0.41
14:K:86:GLY:H	14:K:112:THR:CG2	2.34	0.41
16:M:59:TYR:O	16:M:63:THR:CG2	2.69	0.41
16:M:67:GLU:HB3	16:M:68:GLY:H	1.55	0.41
17:N:27:CYS:SG	17:N:29:ARG:CB	3.08	0.41
19:P:28:ARG:NH1	19:P:29:ASP:OD2	2.54	0.41
20:Q:76:LEU:HD23	20:Q:77:VAL:C	2.46	0.41
21:R:59:SER:O	21:R:60:GLY:C	2.61	0.41
22:S:42:PRO:O	22:S:44:MET:N	2.54	0.41
1:A:320:C:H2'	1:A:321:A:C8	2.56	0.40
1:A:328:C:HO2'	1:A:329:A:P	2.44	0.40
1:A:488:C:H2'	1:A:489:C:H6	1.86	0.40
1:A:517:G:H5'	1:A:519:C:C2	2.56	0.40
1:A:824:C:H2'	1:A:825:G:H8	1.86	0.40
1:A:1061:G:C4	1:A:1197:G:N2	2.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1318:A:H4'	22:S:10:PHE:CE1	2.56	0.40
1:A:1373:G:H5''	10:G:36:LYS:HB3	2.02	0.40
5:B:187:LEU:HA	5:B:201:ILE:O	2.20	0.40
7:D:67:ILE:O	7:D:69:GLY:N	2.54	0.40
7:D:174:LEU:HD23	7:D:174:LEU:HA	1.79	0.40
10:G:42:ILE:HG23	10:G:117:ALA:HA	2.02	0.40
10:G:62:PHE:C	10:G:64:GLN:N	2.78	0.40
11:H:39:LEU:N	11:H:39:LEU:HD22	2.36	0.40
12:I:17:VAL:HG21	12:I:80:GLY:CA	2.39	0.40
13:J:16:LEU:O	13:J:17:ASP:C	2.63	0.40
13:J:42:THR:HG22	13:J:43:ARG:N	2.36	0.40
15:L:7:ILE:HD13	15:L:7:ILE:HA	1.92	0.40
20:Q:97:SER:HB2	20:Q:103:GLY:C	2.46	0.40
1:A:148:G:O2'	1:A:149:A:H5'	2.21	0.40
1:A:300:A:H8	1:A:300:A:O5'	2.04	0.40
1:A:434:U:H2'	1:A:435:C:H6	1.85	0.40
1:A:445:G:O2'	1:A:446:G:H5'	2.21	0.40
1:A:448:A:C4	1:A:487:A:C2	3.09	0.40
1:A:488:C:O5'	1:A:488:C:H6	2.03	0.40
1:A:706:A:C5	1:A:707:C:C5	3.09	0.40
1:A:736:C:H2'	1:A:737:A:C8	2.57	0.40
1:A:761:G:H4'	20:Q:102:GLY:C	2.46	0.40
1:A:861:G:O2'	1:A:862:C:H5'	2.21	0.40
1:A:1327:C:OP1	24:V:20:LYS:HB3	2.21	0.40
1:A:1343:G:H2'	1:A:1344:C:H6	1.81	0.40
1:A:1403:C:O2'	1:A:1404:C:H5'	2.21	0.40
5:B:189:ASP:O	5:B:191:ASP:N	2.55	0.40
6:C:63:ASN:H	6:C:97:LYS:HE2	1.86	0.40
8:E:51:VAL:CB	8:E:52:PRO:HD3	2.35	0.40
11:H:80:ILE:HG23	11:H:82:HIS:O	2.22	0.40
11:H:114:THR:C	11:H:116:LYS:N	2.77	0.40
12:I:28:VAL:C	12:I:30:GLY:N	2.76	0.40
13:J:60:ARG:N	13:J:60:ARG:CD	2.79	0.40
14:K:28:THR:HG22	14:K:29:ILE:N	2.35	0.40
17:N:53:LEU:HA	17:N:54:PRO:HD2	1.96	0.40
22:S:16:LEU:HA	22:S:19:VAL:HG12	2.03	0.40
23:T:72:LEU:O	23:T:73:HIS:O	2.39	0.40
1:A:22:G:C5	1:A:23:C:C4	3.09	0.40
1:A:294:U:H2'	1:A:295:C:C6	2.56	0.40
1:A:376:G:O2'	1:A:377:G:H5'	2.21	0.40
1:A:422:C:H4'	1:A:423:G:C4	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:662:G:H2'	1:A:663:A:C8	2.56	0.40
1:A:1016:A:H2'	1:A:1017:G:C5'	2.51	0.40
1:A:1226:C:HO2'	1:A:1227:A:C5'	2.34	0.40
1:A:1504:G:OP1	1:A:1507:A:H4'	2.22	0.40
5:B:76:GLN:NE2	5:B:207:ALA:N	2.69	0.40
5:B:124:SER:HB2	5:B:125:PRO:CD	2.45	0.40
8:E:71:LEU:HD13	8:E:114:GLY:O	2.21	0.40
9:F:44:GLY:C	9:F:59:TYR:CD1	3.00	0.40
9:F:62:TRP:C	9:F:63:TYR:CD2	2.98	0.40
10:G:103:TRP:O	10:G:106:GLN:HB3	2.21	0.40
11:H:63:LEU:H	11:H:63:LEU:CD2	2.28	0.40
11:H:68:ARG:HG2	11:H:68:ARG:NH1	2.36	0.40
13:J:27:ALA:HA	13:J:30:SER:OG	2.22	0.40
13:J:55:LYS:O	13:J:56:HIS:HB2	2.20	0.40
15:L:42:THR:CG2	15:L:52:LEU:HB3	2.51	0.40
17:N:44:LEU:O	17:N:48:ALA:HB2	2.21	0.40
18:O:49:ASP:OD2	18:O:52:SER:HB2	2.21	0.40
21:R:74:ARG:HG2	21:R:80:PRO:O	2.21	0.40
21:R:82:THR:O	21:R:82:THR:HG23	2.20	0.40
1:A:411:A:C8	1:A:413:G:H1'	2.57	0.40
1:A:482:A:H2'	1:A:483:C:O4'	2.22	0.40
1:A:750:G:N2	18:O:23:GLY:HA3	2.36	0.40
1:A:1016:A:H8	1:A:1016:A:O5'	2.04	0.40
1:A:1068:G:N7	1:A:1094:G:C2'	2.83	0.40
1:A:1300:G:H1'	1:A:1301:U:H5	1.86	0.40
1:A:1346:A:N1	1:A:1374:A:H5''	2.36	0.40
5:B:126:GLU:HA	5:B:129:GLU:HB2	2.04	0.40
5:B:140:HIS:O	5:B:143:GLU:CB	2.69	0.40
6:C:76:VAL:O	6:C:83:ARG:HD3	2.22	0.40
8:E:146:ALA:O	8:E:149:GLU:HG2	2.22	0.40
11:H:60:ARG:NH1	11:H:60:ARG:CG	2.84	0.40
13:J:82:ILE:O	13:J:82:ILE:CG2	2.69	0.40
17:N:37:PHE:C	17:N:39:LEU:N	2.79	0.40
22:S:21:GLU:C	22:S:23:ASN:H	2.29	0.40
23:T:55:ILE:O	23:T:56:MET:C	2.64	0.40
1:A:252:U:H2'	1:A:253:U:C6	2.55	0.40
1:A:543:C:O2'	1:A:544:G:H5'	2.20	0.40
1:A:686:U:O2'	1:A:687:A:H8	2.03	0.40
1:A:958:A:C2	1:A:959:A:C2	3.10	0.40
1:A:1102:A:H2'	1:A:1103:C:H6	1.85	0.40
1:A:1362:C:H5'	1:A:1363:A:O5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1385:G:H2'	1:A:1386:G:O4'	2.22	0.40
1:A:1402:C:O2'	1:A:1403:C:H5'	2.21	0.40
5:B:187:LEU:HD22	5:B:201:ILE:O	2.21	0.40
7:D:196:LEU:C	7:D:198:VAL:H	2.30	0.40
8:E:50:GLU:O	8:E:51:VAL:C	2.65	0.40
8:E:128:PRO:O	8:E:129:ILE:C	2.63	0.40
8:E:150:ARG:O	8:E:150:ARG:HD3	2.20	0.40
10:G:37:ASN:O	10:G:40:ALA:N	2.55	0.40
14:K:70:LYS:O	14:K:73:MET:HB2	2.22	0.40
15:L:88:GLY:N	15:L:98:TYR:HA	2.35	0.40
16:M:79:LYS:HD3	16:M:83:ASP:OD2	2.22	0.40
17:N:22:THR:CB	17:N:33:VAL:HG21	2.52	0.40
17:N:29:ARG:HA	17:N:29:ARG:HD2	1.97	0.40
18:O:81:LEU:HA	18:O:81:LEU:HD23	1.88	0.40
19:P:21:VAL:O	19:P:22:THR:HB	2.20	0.40
20:Q:19:VAL:HG23	20:Q:44:ALA:HB3	2.03	0.40
20:Q:86:GLU:O	20:Q:87:LYS:C	2.64	0.40
21:R:66:LEU:O	21:R:69:THR:N	2.54	0.40
22:S:82:GLY:O	22:S:84:GLY:N	2.49	0.40
23:T:63:ILE:O	23:T:64:ASP:C	2.64	0.40
23:T:89:ARG:O	23:T:92:LEU:N	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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%)	143 (62%)	59 (25%)	30 (13%)	0	1
6	C	204/239 (85%)	125 (61%)	49 (24%)	30 (15%)	0	1
7	D	206/209 (99%)	139 (68%)	49 (24%)	18 (9%)	0	4
8	E	148/162 (91%)	114 (77%)	24 (16%)	10 (7%)	1	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	F	99/101 (98%)	81 (82%)	17 (17%)	1 (1%)	12	41
10	G	153/156 (98%)	104 (68%)	37 (24%)	12 (8%)	1	5
11	H	136/138 (99%)	112 (82%)	19 (14%)	5 (4%)	2	17
12	I	125/128 (98%)	85 (68%)	25 (20%)	15 (12%)	0	1
13	J	96/105 (91%)	58 (60%)	23 (24%)	15 (16%)	0	1
14	K	117/129 (91%)	84 (72%)	18 (15%)	15 (13%)	0	1
15	L	122/135 (90%)	84 (69%)	24 (20%)	14 (12%)	0	2
16	M	116/126 (92%)	74 (64%)	28 (24%)	14 (12%)	0	1
17	N	58/61 (95%)	38 (66%)	14 (24%)	6 (10%)	0	2
18	O	86/89 (97%)	58 (67%)	23 (27%)	5 (6%)	1	9
19	P	81/88 (92%)	59 (73%)	20 (25%)	2 (2%)	4	24
20	Q	102/105 (97%)	83 (81%)	12 (12%)	7 (7%)	1	7
21	R	71/88 (81%)	50 (70%)	17 (24%)	4 (6%)	1	10
22	S	85/93 (91%)	55 (65%)	17 (20%)	13 (15%)	0	1
23	T	97/106 (92%)	57 (59%)	30 (31%)	10 (10%)	0	2
24	V	22/26 (85%)	16 (73%)	6 (27%)	0	100	100
All	All	2356/2540 (93%)	1619 (69%)	511 (22%)	226 (10%)	0	3

All (226) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	B	16	HIS
5	B	17	PHE
5	B	20	GLU
5	B	21	ARG
5	B	24	TRP
5	B	39	ILE
5	B	123	ALA
5	B	190	THR
5	B	229	VAL
6	C	15	THR
6	C	16	ARG
6	C	47	LEU
6	C	55	VAL
6	C	79	ARG
6	C	101	LEU

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Mol	Chain	Res	Type
6	C	156	ARG
6	C	179	ARG
6	C	189	ALA
7	D	29	PRO
7	D	36	ARG
8	E	78	HIS
10	G	52	GLU
10	G	155	ARG
11	H	83	ILE
11	H	91	ARG
11	H	134	ILE
12	I	31	GLN
12	I	41	VAL
12	I	121	ARG
12	I	127	LYS
13	J	19	SER
13	J	34	VAL
13	J	54	PHE
13	J	57	LYS
13	J	90	LEU
14	K	50	TYR
14	K	57	THR
14	K	101	SER
14	K	126	ARG
15	L	47	LYS
15	L	73	GLU
15	L	116	SER
15	L	127	GLU
16	M	14	ARG
16	M	63	THR
16	M	67	GLU
16	M	86	CYS
17	N	19	ARG
17	N	22	THR
18	O	49	ASP
18	O	73	GLU
20	Q	68	ARG
20	Q	80	GLY
20	Q	96	GLN
20	Q	97	SER
21	R	87	ARG
22	S	42	PRO

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Mol	Chain	Res	Type
22	S	86	GLU
23	T	73	HIS
23	T	97	ALA
5	B	8	LYS
5	B	54	THR
5	B	83	MET
5	B	165	VAL
5	B	179	LYS
5	B	204	ASN
5	B	207	ALA
5	B	224	GLN
6	C	29	TYR
6	C	51	GLY
6	C	62	ASP
6	C	154	SER
6	C	161	GLU
6	C	171	GLY
6	C	188	LEU
6	C	205	GLY
7	D	10	ARG
7	D	63	LYS
7	D	68	TYR
7	D	124	GLY
7	D	175	SER
7	D	179	GLU
8	E	11	ILE
8	E	146	ALA
10	G	4	ARG
10	G	7	ALA
10	G	112	PRO
10	G	146	GLU
12	I	42	ARG
12	I	43	ALA
12	I	46	ALA
12	I	55	ALA
12	I	60	ASP
12	I	88	TYR
12	I	94	ALA
13	J	32	ALA
14	K	12	ARG
14	K	47	VAL
14	K	75	TYR

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Mol	Chain	Res	Type
14	K	127	LYS
15	L	41	ARG
15	L	92	ASP
15	L	102	ARG
16	M	4	ILE
16	M	27	LYS
16	M	38	GLY
16	M	106	ASN
17	N	36	PHE
20	Q	98	LEU
21	R	41	LYS
22	S	5	LEU
22	S	6	LYS
22	S	17	GLU
22	S	32	LYS
22	S	43	GLU
23	T	11	SER
23	T	87	LYS
23	T	88	VAL
23	T	94	ALA
5	B	15	VAL
5	B	52	GLU
5	B	101	MET
5	B	178	ARG
6	C	4	LYS
6	C	167	TRP
7	D	9	CYS
7	D	30	LYS
7	D	125	HIS
7	D	153	ARG
7	D	159	ARG
8	E	15	ARG
8	E	108	ALA
10	G	14	PRO
10	G	149	ARG
10	G	150	ALA
13	J	20	ALA
13	J	26	ALA
14	K	13	GLN
14	K	27	ASN
14	K	128	ALA
15	L	51	ALA

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Mol	Chain	Res	Type
15	L	87	GLY
15	L	115	LYS
16	M	85	GLY
17	N	37	PHE
18	O	86	GLY
19	P	43	LYS
20	Q	49	GLU
20	Q	103	GLY
22	S	30	LEU
22	S	82	GLY
22	S	87	ALA
5	B	80	ILE
5	B	215	LEU
5	B	225	ALA
6	C	53	ALA
6	C	68	VAL
6	C	133	ALA
6	C	168	ALA
7	D	4	TYR
8	E	16	THR
8	E	74	GLY
8	E	107	ARG
9	F	70	ASP
10	G	41	ARG
10	G	117	ALA
12	I	34	ASN
12	I	44	VAL
12	I	101	PHE
13	J	39	PRO
13	J	40	LEU
13	J	65	LEU
13	J	82	ILE
14	K	15	ALA
15	L	28	LYS
16	M	28	ALA
16	M	75	ALA
17	N	32	SER
18	O	82	ILE
19	P	10	GLY
23	T	103	GLY
5	B	131	PRO
5	B	143	GLU

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Mol	Chain	Res	Type
6	C	61	ALA
6	C	67	THR
7	D	164	ALA
8	E	60	TYR
8	E	73	ASN
11	H	24	THR
12	I	58	ARG
13	J	23	ILE
13	J	61	GLU
13	J	73	ASP
14	K	102	GLY
14	K	117	ASN
15	L	91	LYS
15	L	121	GLY
16	M	7	VAL
17	N	23	ARG
18	O	46	HIS
21	R	45	SER
22	S	46	GLY
23	T	9	ASN
23	T	74	LYS
5	B	208	ILE
10	G	42	ILE
11	H	105	ARG
15	L	30	ALA
16	M	3	ARG
16	M	74	VAL
23	T	89	ARG
6	C	108	ASN
21	R	37	VAL
22	S	45	VAL
6	C	157	ILE
6	C	174	PRO
7	D	5	ILE
7	D	56	VAL
22	S	9	VAL
5	B	42	ILE
5	B	162	ILE
14	K	29	ILE
6	C	66	VAL
7	D	67	ILE
5	B	18	GLY

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Mol	Chain	Res	Type
6	C	39	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	B	202/220 (92%)	181 (90%)	21 (10%)	7	25
6	C	160/188 (85%)	142 (89%)	18 (11%)	5	22
7	D	180/181 (99%)	162 (90%)	18 (10%)	7	27
8	E	115/123 (94%)	94 (82%)	21 (18%)	2	8
9	F	90/90 (100%)	86 (96%)	4 (4%)	25	54
10	G	126/127 (99%)	118 (94%)	8 (6%)	16	44
11	H	119/119 (100%)	104 (87%)	15 (13%)	4	19
12	I	98/99 (99%)	91 (93%)	7 (7%)	13	40
13	J	87/92 (95%)	78 (90%)	9 (10%)	7	26
14	K	90/99 (91%)	76 (84%)	14 (16%)	2	12
15	L	104/111 (94%)	95 (91%)	9 (9%)	9	33
16	M	94/101 (93%)	83 (88%)	11 (12%)	5	21
17	N	49/50 (98%)	45 (92%)	4 (8%)	10	36
18	O	79/80 (99%)	71 (90%)	8 (10%)	7	27
19	P	72/74 (97%)	66 (92%)	6 (8%)	10	35
20	Q	96/97 (99%)	88 (92%)	8 (8%)	10	35
21	R	64/77 (83%)	61 (95%)	3 (5%)	23	52
22	S	75/80 (94%)	63 (84%)	12 (16%)	2	12
23	T	76/82 (93%)	68 (90%)	8 (10%)	6	25
24	V	19/21 (90%)	18 (95%)	1 (5%)	20	49
All	All	1995/2111 (94%)	1790 (90%)	205 (10%)	7	26

All (205) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	8	LYS
5	B	12	GLU
5	B	15	VAL
5	B	17	PHE
5	B	21	ARG
5	B	23	ARG
5	B	25	ASN
5	B	76	GLN
5	B	82	ARG
5	B	87	ARG
5	B	98	LEU
5	B	113	HIS
5	B	139	LYS
5	B	144	ARG
5	B	162	ILE
5	B	164	VAL
5	B	170	GLU
5	B	178	ARG
5	B	185	ILE
5	B	197	VAL
5	B	231	GLU
6	C	3	ASN
6	C	5	ILE
6	C	23	TYR
6	C	34	LEU
6	C	90	GLU
6	C	91	LEU
6	C	101	LEU
6	C	107	GLN
6	C	110	ASN
6	C	116	VAL
6	C	139	GLN
6	C	156	ARG
6	C	165	THR
6	C	167	TRP
6	C	179	ARG
6	C	188	LEU
6	C	196	LEU
6	C	204	LEU
7	D	3	ARG
7	D	8	VAL
7	D	9	CYS
7	D	12	CYS

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Mol	Chain	Res	Type
7	D	19	LEU
7	D	26	CYS
7	D	29	PRO
7	D	35	ARG
7	D	78	LEU
7	D	146	ILE
7	D	157	LEU
7	D	162	LEU
7	D	175	SER
7	D	176	LEU
7	D	177	ASP
7	D	186	LEU
7	D	192	GLU
7	D	203	VAL
8	E	12	LEU
8	E	13	ILE
8	E	15	ARG
8	E	16	THR
8	E	31	LEU
8	E	33	VAL
8	E	41	VAL
8	E	43	LEU
8	E	52	PRO
8	E	53	LEU
8	E	75	THR
8	E	79	GLU
8	E	80	ILE
8	E	82	VAL
8	E	89	ILE
8	E	112	LEU
8	E	115	VAL
8	E	118	ILE
8	E	131	ILE
8	E	147	ASP
8	E	150	ARG
9	F	9	VAL
9	F	10	LEU
9	F	65	VAL
9	F	86	ARG
10	G	8	GLU
10	G	12	LEU
10	G	24	THR

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Mol	Chain	Res	Type
10	G	37	ASN
10	G	96	GLN
10	G	113	GLU
10	G	124	LEU
10	G	138	LYS
11	H	24	THR
11	H	26	VAL
11	H	52	ASP
11	H	53	VAL
11	H	63	LEU
11	H	84	ARG
11	H	85	ARG
11	H	88	LYS
11	H	91	ARG
11	H	105	ARG
11	H	112	LEU
11	H	119	LEU
11	H	127	LEU
11	H	133	LEU
11	H	136	GLU
12	I	3	GLN
12	I	12	GLU
12	I	38	GLN
12	I	56	LEU
12	I	104	ARG
12	I	111	ARG
12	I	118	LYS
13	J	29	ARG
13	J	38	ILE
13	J	45	ARG
13	J	49	VAL
13	J	60	ARG
13	J	71	LEU
13	J	73	ASP
13	J	79	ARG
13	J	95	GLU
14	K	24	SER
14	K	29	ILE
14	K	30	VAL
14	K	33	THR
14	K	34	ASP
14	K	48	ILE

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Mol	Chain	Res	Type
14	K	51	LYS
14	K	54	ARG
14	K	57	THR
14	K	84	VAL
14	K	93	GLN
14	K	122	LYS
14	K	125	PHE
14	K	126	ARG
15	L	48	PRO
15	L	49	ASN
15	L	53	ARG
15	L	55	VAL
15	L	60	LEU
15	L	91	LYS
15	L	93	LEU
15	L	96	VAL
15	L	98	TYR
16	M	9	ILE
16	M	13	LYS
16	M	16	ASP
16	M	34	LEU
16	M	46	LYS
16	M	56	LEU
16	M	81	LEU
16	M	102	ARG
16	M	103	THR
16	M	110	ARG
16	M	117	VAL
17	N	22	THR
17	N	33	VAL
17	N	41	ARG
17	N	44	LEU
18	O	4	THR
18	O	7	GLU
18	O	33	THR
18	O	34	LEU
18	O	65	ARG
18	O	70	LEU
18	O	81	LEU
18	O	83	GLU
19	P	2	VAL
19	P	8	ARG

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Mol	Chain	Res	Type
19	P	28	ARG
19	P	29	ASP
19	P	53	VAL
19	P	62	VAL
20	Q	9	VAL
20	Q	19	VAL
20	Q	38	ARG
20	Q	53	LEU
20	Q	59	ILE
20	Q	60	ILE
20	Q	74	LEU
20	Q	78	GLU
21	R	26	LEU
21	R	58	LEU
21	R	66	LEU
22	S	7	LYS
22	S	13	ASP
22	S	25	LYS
22	S	30	LEU
22	S	32	LYS
22	S	42	PRO
22	S	43	GLU
22	S	62	ILE
22	S	80	TYR
22	S	83	HIS
22	S	85	LYS
22	S	86	GLU
23	T	10	LEU
23	T	13	LEU
23	T	29	LYS
23	T	39	LYS
23	T	42	GLN
23	T	55	ILE
23	T	62	LEU
23	T	84	LEU
24	V	7	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
5	B	25	ASN
5	B	40	HIS

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Mol	Chain	Res	Type
5	B	110	GLN
5	B	240	GLN
6	C	3	ASN
6	C	6	HIS
6	C	63	ASN
6	C	98	ASN
6	C	107	GLN
6	C	108	ASN
6	C	110	ASN
6	C	136	GLN
6	C	139	GLN
6	C	162	GLN
7	D	62	GLN
7	D	74	GLN
7	D	123	HIS
7	D	129	ASN
7	D	199	ASN
8	E	73	ASN
9	F	13	ASN
9	F	18	GLN
9	F	57	GLN
9	F	64	GLN
9	F	94	GLN
9	F	100	ASN
10	G	51	GLN
10	G	96	GLN
11	H	82	HIS
12	I	23	ASN
12	I	29	ASN
12	I	73	GLN
12	I	89	ASN
13	J	13	HIS
13	J	76	ASN
13	J	84	GLN
14	K	22	HIS
14	K	38	ASN
14	K	62	GLN
14	K	78	GLN
14	K	117	ASN
15	L	49	ASN
15	L	75	HIS
16	M	40	ASN

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Mol	Chain	Res	Type
16	M	62	ASN
18	O	13	GLN
18	O	37	ASN
19	P	76	GLN
20	Q	16	GLN
21	R	36	ASN
22	S	14	HIS
22	S	23	ASN
22	S	53	ASN
22	S	56	GLN
22	S	69	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1522 (98%)	205 (13%)	70 (4%)
2	X	5/6 (83%)	0	0
3	Y	10/15 (66%)	2 (20%)	1 (10%)
4	Z	3/4 (75%)	1 (33%)	0
All	All	1524/1547 (98%)	208 (13%)	71 (4%)

All (208) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	52	G
1	A	60	A
1	A	61	G
1	A	81	U
1	A	82	U
1	A	116	A
1	A	120	A
1	A	121	C

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Mol	Chain	Res	Type
1	A	130	A
1	A	131	C
1	A	163	C
1	A	182	U
1	A	190(D)	U
1	A	190(E)	U
1	A	190(F)	G
1	A	195	A
1	A	197	A
1	A	198	G
1	A	201	C
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	301	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	330	C
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	423	G

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Mol	Chain	Res	Type
1	A	429	U
1	A	430	A
1	A	439	A
1	A	452	A
1	A	461	C
1	A	484	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	519	C
1	A	527	G
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	575	G
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	703	G
1	A	718	G
1	A	721	G
1	A	723	U
1	A	731	G
1	A	749	C
1	A	755	G
1	A	777	A
1	A	793	U
1	A	794	A
1	A	812	C

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Mol	Chain	Res	Type
1	A	813	U
1	A	817	C
1	A	818	G
1	A	819	A
1	A	820	U
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	874	G
1	A	876	G
1	A	902	G
1	A	913	A
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	993	G
1	A	994	A
1	A	1005	A
1	A	1030(B)	C
1	A	1045	C
1	A	1050	G
1	A	1054	C
1	A	1055	A
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1094	G
1	A	1095	U
1	A	1101	A

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Mol	Chain	Res	Type
1	A	1102	A
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1145	C
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	1201	A
1	A	1202	G
1	A	1212	U
1	A	1215	G
1	A	1224	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1238	A
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1320	C
1	A	1332	A

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Mol	Chain	Res	Type
1	A	1347	G
1	A	1348	U
1	A	1363	A
1	A	1381	U
1	A	1397	C
1	A	1443	G
1	A	1446	A
1	A	1452	C
1	A	1492	A
1	A	1498	U
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	1519	A
1	A	1520	G
1	A	1529	G
1	A	1530	G
3	Y	34	G
3	Y	35	A
4	Z	2	U

All (71) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	30	U
1	A	48	C
1	A	51	A
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	203	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G

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Mol	Chain	Res	Type
1	A	279	A
1	A	281	G
1	A	328	C
1	A	329	A
1	A	344	A
1	A	351	G
1	A	353	A
1	A	366	C
1	A	372	C
1	A	428	G
1	A	429	U
1	A	438	G
1	A	484	G
1	A	496	A
1	A	509	A
1	A	518	C
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A
1	A	748	C
1	A	792	A
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	976	G
1	A	992	U
1	A	993	G
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1101	A
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1196	U
1	A	1201	A
1	A	1214	C

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Mol	Chain	Res	Type
1	A	1224	G
1	A	1226	C
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1319	A
1	A	1331	G
1	A	1346	A
1	A	1347	G
1	A	1380	U
1	A	1451	A
1	A	1498	U
1	A	1502	A
3	Y	34	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 122 ligands modelled in this entry, 122 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1507/1522 (99%)	1.10	300 (19%) 3 3	16, 53, 140, 201	0
2	X	6/6 (100%)	3.95	3 (50%) 0 0	59, 71, 178, 201	0
3	Y	11/15 (73%)	1.65	5 (45%) 0 0	66, 90, 182, 190	0
4	Z	4/4 (100%)	1.45	2 (50%) 0 0	71, 77, 89, 119	0
5	B	234/256 (91%)	1.64	85 (36%) 1 1	19, 87, 173, 201	0
6	C	206/239 (86%)	1.61	69 (33%) 1 1	22, 80, 160, 201	0
7	D	208/209 (99%)	1.23	56 (26%) 1 1	17, 60, 145, 180	0
8	E	150/162 (92%)	1.02	28 (18%) 3 3	17, 48, 107, 201	0
9	F	101/101 (100%)	1.49	30 (29%) 1 1	35, 88, 148, 185	0
10	G	155/156 (99%)	1.22	43 (27%) 1 1	27, 70, 150, 201	0
11	H	138/138 (100%)	0.54	17 (12%) 8 7	5, 39, 108, 136	0
12	I	127/128 (99%)	1.89	53 (41%) 0 0	19, 82, 144, 184	0
13	J	98/105 (93%)	2.62	57 (58%) 0 0	30, 107, 188, 201	0
14	K	119/129 (92%)	1.75	29 (24%) 2 1	12, 54, 130, 201	0
15	L	124/135 (91%)	1.17	29 (23%) 2 2	16, 57, 144, 187	0
16	M	118/126 (93%)	1.29	33 (27%) 1 1	32, 70, 144, 170	0
17	N	60/61 (98%)	1.83	21 (35%) 1 1	39, 70, 140, 201	0
18	O	88/89 (98%)	1.07	16 (18%) 3 3	7, 56, 145, 201	0
19	P	83/88 (94%)	0.93	13 (15%) 5 4	10, 41, 101, 150	0
20	Q	104/105 (99%)	1.31	25 (24%) 2 1	10, 43, 157, 201	0
21	R	73/88 (82%)	1.19	15 (20%) 2 3	32, 66, 166, 201	0
22	S	87/93 (93%)	1.90	35 (40%) 0 0	54, 99, 176, 201	0
23	T	99/106 (93%)	1.35	27 (27%) 1 1	15, 50, 123, 156	0
24	V	24/26 (92%)	1.60	8 (33%) 1 1	26, 59, 128, 179	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3924/4087 (96%)	1.29	999 (25%) 1 1	5, 60, 152, 201	0

All (999) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
14	K	128	ALA	37.5
14	K	129	SER	33.2
18	O	89	GLY	12.8
23	T	9	ASN	12.7
10	G	13	GLN	11.4
14	K	127	LYS	10.4
6	C	161	GLU	10.3
15	L	19	ARG	10.1
8	E	154	GLY	9.9
14	K	126	ARG	9.9
20	Q	14	LYS	9.8
1	A	532	A	9.4
1	A	82	U	9.1
9	F	95	GLU	9.1
1	A	81	U	8.5
16	M	7	VAL	8.3
2	X	1	C	8.0
10	G	11	GLN	7.9
20	Q	13	ASP	7.9
1	A	202	U	7.7
12	I	128	ARG	7.6
22	S	3	ARG	7.6
2	X	2	U	7.5
1	A	88	A	7.4
24	V	25	LYS	7.4
1	A	1129	C	7.1
15	L	127	GLU	7.0
5	B	106	LYS	6.9
13	J	5	ARG	6.7
8	E	81	GLU	6.7
12	I	105	ASP	6.6
22	S	2	PRO	6.5
13	J	45	ARG	6.5
6	C	160	ALA	6.5
10	G	143	ARG	6.4
14	K	125	PHE	6.3
10	G	5	ARG	6.3

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Mol	Chain	Res	Type	RSRZ
13	J	64	GLU	6.3
5	B	148	TYR	6.2
1	A	1145	C	6.2
6	C	124	ILE	6.2
13	J	98	ILE	6.2
6	C	190	ARG	6.2
6	C	162	GLN	6.1
8	E	5	ASP	6.1
20	Q	52	LYS	6.1
1	A	1530	G	6.1
6	C	193	TYR	6.0
13	J	100	THR	6.0
1	A	1161	C	5.9
21	R	17	SER	5.9
10	G	8	GLU	5.9
13	J	85	LEU	5.9
20	Q	103	GLY	5.8
20	Q	105	ALA	5.8
7	D	209	ARG	5.8
6	C	159	GLY	5.8
12	I	114	TYR	5.7
5	B	134	GLU	5.7
10	G	79	ARG	5.6
20	Q	102	GLY	5.6
16	M	11	ARG	5.5
12	I	127	LYS	5.5
7	D	9	CYS	5.5
1	A	1138	G	5.5
1	A	1477	C	5.4
16	M	118	ALA	5.4
5	B	7	VAL	5.4
2	X	3	U	5.4
13	J	96	ILE	5.4
9	F	94	GLN	5.4
7	D	19	LEU	5.3
21	R	41	LYS	5.3
12	I	12	GLU	5.3
1	A	112	G	5.3
1	A	1384	C	5.3
10	G	33	ASP	5.3
7	D	187	ARG	5.2
1	A	163	C	5.2

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Mol	Chain	Res	Type	RSRZ
20	Q	101	ARG	5.2
22	S	4	SER	5.2
5	B	137	ARG	5.2
1	A	1397	C	5.1
15	L	59	ARG	5.1
16	M	40	ASN	5.1
1	A	83	U	5.1
5	B	133	LYS	5.1
6	C	158	GLY	5.1
12	I	106	ALA	5.0
11	H	22	GLU	5.0
6	C	125	GLU	5.0
1	A	733	A	4.9
1	A	723	U	4.9
1	A	1125	U	4.9
23	T	99	LEU	4.9
16	M	104	ARG	4.9
16	M	50	GLU	4.9
12	I	38	GLN	4.9
22	S	15	LEU	4.8
13	J	97	GLU	4.8
1	A	170	U	4.8
23	T	106	ALA	4.8
13	J	43	ARG	4.8
1	A	1127	G	4.8
13	J	90	LEU	4.7
12	I	31	GLN	4.7
15	L	29	GLY	4.7
14	K	122	LYS	4.7
14	K	124	LYS	4.7
1	A	42	G	4.7
1	A	981	U	4.7
12	I	99	LEU	4.7
16	M	12	ASN	4.7
7	D	131	ARG	4.7
19	P	50	LYS	4.7
5	B	98	LEU	4.7
10	G	146	GLU	4.7
1	A	1526	G	4.6
5	B	130	ARG	4.6
17	N	6	LEU	4.6
16	M	119	GLY	4.6

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Mol	Chain	Res	Type	RSRZ
5	B	141	GLU	4.6
15	L	28	LYS	4.6
5	B	10	LEU	4.6
13	J	93	GLY	4.6
15	L	128	ALA	4.6
1	A	390	C	4.6
12	I	66	ARG	4.6
21	R	38	GLU	4.6
13	J	88	LEU	4.6
5	B	156	LYS	4.5
1	A	461	C	4.5
13	J	47	PHE	4.5
12	I	113	LYS	4.5
7	D	49	ARG	4.5
1	A	84	U	4.5
1	A	394	G	4.5
19	P	54	GLU	4.5
13	J	14	LYS	4.5
23	T	95	ALA	4.5
6	C	188	LEU	4.5
17	N	4	LYS	4.5
7	D	23	GLY	4.4
1	A	1476	G	4.4
5	B	175	ARG	4.4
5	B	227	GLY	4.4
7	D	167	GLY	4.4
1	A	595	G	4.4
1	A	1529	G	4.4
1	A	915	A	4.4
1	A	1453	G	4.4
16	M	69	GLU	4.4
13	J	57	LYS	4.4
18	O	2	PRO	4.4
1	A	389	A	4.3
1	A	1296	C	4.3
1	A	204	U	4.3
3	Y	32	U	4.3
20	Q	49	GLU	4.3
7	D	46	LYS	4.3
7	D	152	SER	4.3
1	A	41	G	4.3
1	A	1190	G	4.3

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Mol	Chain	Res	Type	RSRZ
13	J	6	ILE	4.3
7	D	190	ASP	4.3
1	A	1001	A	4.2
23	T	36	LEU	4.2
13	J	73	ASP	4.2
6	C	126	ARG	4.2
1	A	169	C	4.2
1	A	1274	G	4.2
22	S	12	ASP	4.2
13	J	84	GLN	4.2
22	S	8	GLY	4.2
12	I	36	TYR	4.2
6	C	26	LYS	4.2
8	E	92	LYS	4.2
1	A	60	A	4.2
1	A	1160	G	4.2
8	E	153	LYS	4.2
5	B	95	GLN	4.2
5	B	96	ARG	4.1
7	D	47	ARG	4.1
1	A	597	G	4.1
14	K	89	ALA	4.1
10	G	136	LYS	4.1
1	A	1426	C	4.1
17	N	60	SER	4.1
17	N	61	TRP	4.1
1	A	1126	U	4.1
1	A	1281	U	4.1
12	I	119	ALA	4.1
11	H	3	THR	4.1
22	S	10	PHE	4.1
1	A	61	G	4.1
1	A	378	G	4.1
13	J	37	PRO	4.1
23	T	13	LEU	4.0
7	D	24	GLU	4.0
1	A	164	U	4.0
1	A	631	G	4.0
1	A	1002	G	4.0
9	F	41	GLU	4.0
5	B	180	LEU	4.0
12	I	97	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
7	D	158	ILE	4.0
12	I	103	THR	4.0
13	J	3	LYS	4.0
10	G	82	GLY	4.0
17	N	35	ARG	4.0
1	A	982	U	4.0
10	G	12	LEU	4.0
6	C	170	GLN	4.0
7	D	153	ARG	4.0
13	J	46	ARG	4.0
5	B	147	LYS	4.0
7	D	179	GLU	4.0
13	J	65	LEU	4.0
12	I	57	GLY	3.9
5	B	8	LYS	3.9
12	I	75	ASP	3.9
23	T	8	ARG	3.9
1	A	1427	U	3.9
7	D	149	ALA	3.9
13	J	58	ASP	3.9
22	S	35	SER	3.9
21	R	16	PRO	3.9
14	K	13	GLN	3.9
1	A	1428	A	3.9
1	A	1361(A)	C	3.9
5	B	229	VAL	3.9
20	Q	92	ARG	3.9
15	L	47	LYS	3.9
1	A	184	G	3.9
1	A	1003	G	3.9
5	B	195	ASP	3.9
17	N	17	LYS	3.9
6	C	178	LEU	3.9
1	A	732	C	3.8
24	V	5	ASP	3.8
8	E	119	LEU	3.8
22	S	9	VAL	3.8
5	B	132	LYS	3.8
7	D	192	GLU	3.8
14	K	51	LYS	3.8
15	L	13	LYS	3.8
13	J	63	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	965	A	3.8
12	I	87	GLN	3.8
6	C	176	HIS	3.8
7	D	151	LYS	3.8
1	A	1024	G	3.8
17	N	30	ALA	3.8
19	P	29	ASP	3.8
6	C	21	ARG	3.8
10	G	155	ARG	3.8
12	I	9	ARG	3.8
14	K	121	PRO	3.8
1	A	1025	U	3.8
1	A	1111	A	3.8
1	A	1531	A	3.8
1	A	596	C	3.7
10	G	56	GLN	3.7
6	C	110	ASN	3.7
9	F	65	VAL	3.7
6	C	167	TRP	3.7
1	A	413	G	3.7
10	G	85	TYR	3.7
22	S	39	THR	3.7
1	A	1528	U	3.7
17	N	55	GLY	3.7
1	A	1030(C)	G	3.7
1	A	1511	G	3.7
23	T	73	HIS	3.7
21	R	53	ARG	3.7
5	B	41	ILE	3.7
1	A	744	C	3.7
1	A	1162	C	3.7
12	I	111	ARG	3.7
13	J	66	ARG	3.7
1	A	1030(A)	G	3.7
11	H	34	GLU	3.7
16	M	58	GLU	3.7
1	A	1039	C	3.7
6	C	102	ASN	3.7
14	K	11	LYS	3.7
6	C	105	GLU	3.6
1	A	1003(A)	G	3.6
1	A	1028	C	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	641	U	3.6
6	C	27	LYS	3.6
3	Y	30	G	3.6
1	A	1176	A	3.6
1	A	1534	A	3.6
5	B	23	ARG	3.6
5	B	144	ARG	3.6
18	O	88	ARG	3.6
1	A	1478	C	3.6
6	C	189	ALA	3.6
22	S	16	LEU	3.6
9	F	27	GLN	3.6
6	C	96	GLY	3.6
12	I	126	SER	3.6
1	A	1163	C	3.6
16	M	47	ASP	3.6
15	L	89	ARG	3.6
6	C	207	VAL	3.6
5	B	118	LEU	3.6
5	B	143	GLU	3.6
7	D	31	CYS	3.6
1	A	815	A	3.5
1	A	818	G	3.5
1	A	1009	G	3.5
1	A	1224	G	3.5
1	A	1360	A	3.5
13	J	21	GLN	3.5
7	D	125	HIS	3.5
17	N	12	ARG	3.5
20	Q	68	ARG	3.5
15	L	31	PRO	3.5
18	O	76	GLU	3.5
24	V	9	ARG	3.5
20	Q	96	GLN	3.5
20	Q	104	LYS	3.5
1	A	663	A	3.5
1	A	1256	A	3.5
1	A	1280	A	3.5
1	A	1277	C	3.5
8	E	83	GLU	3.5
19	P	83	GLU	3.5
6	C	45	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
24	V	24	ARG	3.5
7	D	54	TYR	3.5
1	A	1158	C	3.5
6	C	62	ASP	3.5
9	F	35	ALA	3.5
11	H	102	ARG	3.5
1	A	1188	A	3.5
1	A	1124	G	3.5
1	A	1182	G	3.5
1	A	1508	G	3.5
23	T	17	ARG	3.5
20	Q	24	GLU	3.4
7	D	154	ASN	3.4
6	C	196	LEU	3.4
5	B	16	HIS	3.4
12	I	98	PRO	3.4
1	A	1030(B)	C	3.4
18	O	7	GLU	3.4
1	A	459	G	3.4
10	G	156	TRP	3.4
5	B	193	ASP	3.4
12	I	107	ARG	3.4
20	Q	80	GLY	3.4
1	A	147	G	3.4
7	D	12	CYS	3.4
13	J	44	VAL	3.4
1	A	1507	A	3.4
1	A	1527	C	3.4
1	A	1212	U	3.4
6	C	89	GLU	3.4
13	J	75	ILE	3.4
5	B	110	GLN	3.4
6	C	191	THR	3.4
17	N	13	THR	3.4
1	A	991	U	3.3
1	A	1006	C	3.3
10	G	16	LEU	3.3
10	G	139	GLU	3.3
13	J	62	HIS	3.3
1	A	146	G	3.3
24	V	6	ARG	3.3
1	A	1159	U	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	1038	C	3.3
6	C	192	THR	3.3
12	I	64	THR	3.3
12	I	70	LYS	3.3
13	J	80	LYS	3.3
17	N	58	LYS	3.3
21	R	23	LYS	3.3
1	A	1042	G	3.3
6	C	132	ARG	3.3
9	F	24	GLU	3.3
10	G	149	ARG	3.3
1	A	524	G	3.3
20	Q	93	GLN	3.3
20	Q	100	LYS	3.3
1	A	1196	U	3.3
14	K	52	GLY	3.3
11	H	37	ARG	3.2
13	J	79	ARG	3.2
14	K	12	ARG	3.2
14	K	36	ASP	3.2
1	A	157	G	3.2
1	A	331	G	3.2
1	A	1361	G	3.2
14	K	120	ARG	3.2
1	A	745	C	3.2
5	B	230	VAL	3.2
12	I	65	VAL	3.2
19	P	47	ASP	3.2
22	S	41	VAL	3.2
12	I	7	THR	3.2
23	T	97	ALA	3.2
22	S	17	GLU	3.2
1	A	1143	G	3.2
5	B	122	PHE	3.2
13	J	72	VAL	3.2
1	A	308	C	3.2
6	C	79	ARG	3.2
5	B	138	LEU	3.2
22	S	61	TYR	3.2
5	B	45	GLN	3.2
9	F	64	GLN	3.2
5	B	166	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
7	D	145	GLU	3.2
7	D	157	LEU	3.2
8	E	149	GLU	3.2
6	C	128	PHE	3.2
7	D	170	VAL	3.2
12	I	14	VAL	3.2
13	J	33	GLN	3.2
19	P	30	GLY	3.1
1	A	59	A	3.1
10	G	9	VAL	3.1
1	A	165	C	3.1
1	A	644	G	3.1
23	T	100	ILE	3.1
15	L	20	LYS	3.1
15	L	26	ALA	3.1
19	P	27	LYS	3.1
9	F	14	LEU	3.1
6	C	3	ASN	3.1
7	D	3	ARG	3.1
8	E	77	PRO	3.1
14	K	54	ARG	3.1
11	H	98	LYS	3.1
8	E	20	GLN	3.1
13	J	87	THR	3.1
23	T	10	LEU	3.1
13	J	17	ASP	3.1
5	B	35	GLU	3.1
16	M	3	ARG	3.1
16	M	88	ARG	3.1
13	J	41	PRO	3.1
1	A	992	U	3.1
5	B	75	LYS	3.1
1	A	1319	A	3.1
3	Y	31	A	3.1
6	C	194	GLY	3.1
1	A	395	C	3.1
5	B	117	GLU	3.1
7	D	112	VAL	3.1
13	J	99	LYS	3.1
1	A	1467	G	3.1
7	D	201	GLN	3.1
21	R	59	SER	3.1

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Mol	Chain	Res	Type	RSRZ
7	D	163	GLU	3.1
1	A	349	A	3.1
1	A	977	A	3.1
1	A	978	A	3.1
5	B	172	ILE	3.1
16	M	113	PRO	3.1
1	A	1144	G	3.0
1	A	1265	G	3.0
14	K	102	GLY	3.0
1	A	743	U	3.0
7	D	18	LYS	3.0
18	O	73	GLU	3.0
9	F	21	LEU	3.0
1	A	1400	C	3.0
6	C	154	SER	3.0
14	K	16	SER	3.0
1	A	396	G	3.0
20	Q	22	LEU	3.0
5	B	111	ARG	3.0
5	B	226	ARG	3.0
6	C	156	ARG	3.0
8	E	24	ARG	3.0
24	V	10	ARG	3.0
7	D	180	GLY	3.0
16	M	115	LYS	3.0
9	F	97	PHE	3.0
1	A	1533	C	3.0
12	I	74	ILE	3.0
5	B	56	ARG	3.0
14	K	96	ARG	3.0
1	A	1175	G	3.0
5	B	149	LEU	3.0
22	S	73	GLU	3.0
13	J	59	SER	3.0
1	A	999	C	3.0
3	Y	40	C	3.0
7	D	30	LYS	3.0
22	S	70	LYS	3.0
11	H	54	ASP	3.0
5	B	239	VAL	3.0
12	I	23	ASN	3.0
9	F	42	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
21	R	46	GLU	2.9
1	A	485	G	2.9
1	A	742	G	2.9
1	A	821	G	2.9
12	I	15	ALA	2.9
20	Q	37	LYS	2.9
1	A	412	A	2.9
21	R	33	ASP	2.9
22	S	68	GLY	2.9
1	A	1282	C	2.9
9	F	82	ARG	2.9
15	L	73	GLU	2.9
1	A	1385	G	2.9
1	A	1525	G	2.9
7	D	35	ARG	2.9
12	I	56	LEU	2.9
19	P	28	ARG	2.9
22	S	37	ARG	2.9
16	M	109	THR	2.9
1	A	979	C	2.9
7	D	41	GLY	2.9
23	T	70	SER	2.9
6	C	157	ILE	2.9
12	I	25	LYS	2.9
14	K	111	ASP	2.9
1	A	181	G	2.9
1	A	1295	G	2.9
5	B	123	ALA	2.9
6	C	143	GLU	2.9
1	A	460	A	2.9
1	A	1279	A	2.9
1	A	1289	A	2.9
1	A	1237	C	2.9
1	A	14	U	2.9
1	A	1020	U	2.9
6	C	85	ARG	2.9
17	N	57	ARG	2.9
22	S	5	LEU	2.9
16	M	43	THR	2.9
1	A	1288	A	2.9
1	A	1473	A	2.9
7	D	43	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
9	F	1	MET	2.9
11	H	1	MET	2.9
1	A	1040	U	2.8
4	Z	4	U	2.8
8	E	21	ALA	2.8
17	N	10	ALA	2.8
8	E	88	LYS	2.8
23	T	14	LYS	2.8
9	F	45	LEU	2.8
1	A	158	G	2.8
1	A	476	G	2.8
1	A	1022	G	2.8
1	A	1154	G	2.8
1	A	1156	G	2.8
1	A	1255	G	2.8
1	A	307	C	2.8
5	B	59	GLU	2.8
7	D	156	GLU	2.8
5	B	181	PHE	2.8
6	C	84	ILE	2.8
24	V	2	GLY	2.8
5	B	125	PRO	2.8
9	F	28	ARG	2.8
19	P	41	PRO	2.8
16	M	13	LYS	2.8
18	O	74	ASP	2.8
1	A	916	G	2.8
1	A	954	G	2.8
1	A	1187	G	2.8
6	C	129	ALA	2.8
12	I	16	ARG	2.8
13	J	60	ARG	2.8
18	O	48	LYS	2.8
10	G	89	MET	2.8
1	A	1157	A	2.8
1	A	458	C	2.8
1	A	643	C	2.8
17	N	20	ALA	2.8
7	D	86	LYS	2.8
1	A	183	G	2.8
1	A	251	G	2.8
5	B	11	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
7	D	155	LEU	2.8
23	T	37	SER	2.8
12	I	101	PHE	2.7
1	A	766	A	2.7
5	B	93	VAL	2.7
16	M	41	PRO	2.7
5	B	196	LEU	2.7
1	A	1226	C	2.7
6	C	186	PHE	2.7
15	L	87	GLY	2.7
1	A	156	G	2.7
12	I	10	ARG	2.7
18	O	54	ARG	2.7
8	E	145	LYS	2.7
5	B	135	GLN	2.7
8	E	56	GLN	2.7
7	D	33	MET	2.7
22	S	64	GLU	2.7
1	A	1041	A	2.7
1	A	176	C	2.7
1	A	314	C	2.7
1	A	822	C	2.7
17	N	2	ALA	2.7
1	A	326	G	2.7
1	A	1034	G	2.7
5	B	108	ILE	2.7
15	L	16	GLU	2.7
15	L	65	GLU	2.7
5	B	36	ARG	2.7
6	C	30	ARG	2.7
22	S	7	LYS	2.7
1	A	1136	U	2.7
12	I	102	LEU	2.7
1	A	1218	C	2.7
18	O	9	GLN	2.7
8	E	124	GLY	2.7
15	L	111	LYS	2.7
1	A	662	G	2.7
1	A	953	G	2.7
14	K	79	SER	2.7
12	I	40	LEU	2.7
13	J	89	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
5	B	232	PRO	2.6
5	B	152	PHE	2.6
9	F	89	MET	2.6
6	C	88	ARG	2.6
12	I	8	GLY	2.6
1	A	1137	C	2.6
22	S	33	THR	2.6
1	A	351	G	2.6
1	A	446	G	2.6
1	A	447	G	2.6
1	A	1131	G	2.6
1	A	1134	G	2.6
1	A	1000	U	2.6
5	B	37	ASN	2.6
9	F	73	ASN	2.6
13	J	22	LYS	2.6
16	M	31	LYS	2.6
8	E	22	GLY	2.6
17	N	22	THR	2.6
11	H	2	LEU	2.6
20	Q	39	SER	2.6
16	M	46	LYS	2.6
22	S	6	LYS	2.6
9	F	32	ASN	2.6
1	A	552	U	2.6
1	A	1278	U	2.6
1	A	1023	G	2.6
1	A	487	A	2.6
16	M	102	ARG	2.6
22	S	40	ILE	2.6
10	G	144	MET	2.6
18	O	58	MET	2.6
11	H	27	PRO	2.6
1	A	488	C	2.6
1	A	1043	C	2.6
1	A	1359	C	2.6
5	B	206	ASP	2.6
9	F	16	GLN	2.6
10	G	140	ASP	2.6
6	C	2	GLY	2.6
13	J	10	GLY	2.6
8	E	50	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	1177	G	2.6
1	A	1316	G	2.6
14	K	93	GLN	2.6
14	K	81	ASP	2.6
5	B	114	ARG	2.6
23	T	29	LYS	2.6
23	T	94	ALA	2.6
8	E	19	MET	2.5
9	F	60	PHE	2.5
1	A	406	G	2.5
1	A	1031	G	2.5
11	H	126	LYS	2.5
23	T	86	ARG	2.5
5	B	231	GLU	2.5
12	I	35	GLU	2.5
1	A	1430	C	2.5
15	L	99	HIS	2.5
16	M	44	ARG	2.5
18	O	79	ARG	2.5
13	J	34	VAL	2.5
10	G	45	ASP	2.5
16	M	106	ASN	2.5
22	S	44	MET	2.5
1	A	533	A	2.5
1	A	814	A	2.5
1	A	1213	A	2.5
1	A	1398	A	2.5
10	G	41	ARG	2.5
10	G	115	ARG	2.5
13	J	71	LEU	2.5
16	M	96	LEU	2.5
1	A	1429	C	2.5
8	E	72	GLN	2.5
6	C	100	ALA	2.5
1	A	841	U	2.5
11	H	73	ASP	2.5
8	E	144	THR	2.5
9	F	47	ARG	2.5
23	T	87	LYS	2.5
1	A	1318	A	2.5
1	A	1340	A	2.5
1	A	113	G	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	145	G	2.5
1	A	1142	G	2.5
1	A	680	C	2.5
13	J	83	GLU	2.5
12	I	27	THR	2.5
9	F	3	ARG	2.5
14	K	70	LYS	2.5
21	R	19	LYS	2.5
10	G	14	PRO	2.5
21	R	31	LEU	2.5
10	G	151	TYR	2.5
5	B	38	GLY	2.5
7	D	45	GLN	2.5
8	E	17	ALA	2.4
9	F	25	ILE	2.4
1	A	325	A	2.4
8	E	68	GLU	2.4
11	H	99	GLU	2.4
8	E	123	LEU	2.4
13	J	42	THR	2.4
14	K	42	TRP	2.4
1	A	1209	C	2.4
1	A	1335	C	2.4
1	A	1475	G	2.4
5	B	236	TYR	2.4
14	K	25	TYR	2.4
10	G	83	ALA	2.4
15	L	79	GLU	2.4
20	Q	91	ARG	2.4
21	R	87	ARG	2.4
6	C	48	TYR	2.4
8	E	46	GLY	2.4
12	I	125	TYR	2.4
6	C	60	ALA	2.4
1	A	1013	G	2.4
18	O	13	GLN	2.4
23	T	41	ILE	2.4
17	N	8	GLU	2.4
22	S	38	SER	2.4
6	C	98	ASN	2.4
13	J	12	ASP	2.4
12	I	100	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	914	A	2.4
1	A	983	A	2.4
1	A	1035	A	2.4
1	A	1346	A	2.4
10	G	4	ARG	2.4
13	J	9	ARG	2.4
15	L	91	LYS	2.4
20	Q	41	LYS	2.4
1	A	980	C	2.4
1	A	1140	C	2.4
1	A	1315	U	2.4
12	I	110	GLU	2.4
1	A	594	G	2.4
1	A	1178	G	2.4
15	L	44	THR	2.4
6	C	23	TYR	2.4
10	G	7	ALA	2.4
10	G	60	LYS	2.4
10	G	131	LYS	2.4
7	D	141	ARG	2.4
7	D	159	ARG	2.4
7	D	42	GLN	2.4
1	A	516	U	2.4
10	G	21	VAL	2.4
1	A	1153	C	2.3
1	A	1399	C	2.3
7	D	87	GLY	2.3
7	D	169	LYS	2.3
13	J	74	ILE	2.3
16	M	42	ALA	2.3
23	T	74	LYS	2.3
5	B	33	TYR	2.3
5	B	64	ARG	2.3
1	A	306	G	2.3
1	A	350	G	2.3
1	A	388	G	2.3
1	A	1347	G	2.3
22	S	56	GLN	2.3
6	C	44	GLU	2.3
21	R	62	GLU	2.3
13	J	77	PRO	2.3
15	L	48	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
5	B	179	LYS	2.3
12	I	118	LYS	2.3
7	D	26	CYS	2.3
8	E	78	HIS	2.3
19	P	68	ASP	2.3
1	A	1036	G	2.3
6	C	38	ARG	2.3
10	G	92	SER	2.3
12	I	67	GLY	2.3
11	H	107	LEU	2.3
1	A	964	A	2.3
1	A	495	U	2.3
16	M	35	GLU	2.3
1	A	962	C	2.3
1	A	1264	C	2.3
6	C	135	LYS	2.3
22	S	11	VAL	2.3
22	S	28	LYS	2.3
1	A	168	G	2.3
1	A	377	G	2.3
1	A	1443	G	2.3
5	B	52	GLU	2.3
16	M	114	ARG	2.3
19	P	81	ARG	2.3
21	R	83	GLU	2.3
1	A	182	U	2.3
1	A	1257	U	2.3
1	A	1364	U	2.3
1	A	89	C	2.3
12	I	29	ASN	2.3
15	L	23	LYS	2.3
5	B	21	ARG	2.3
12	I	104	ARG	2.3
6	C	122	GLU	2.2
22	S	27	GLU	2.2
1	A	650	G	2.2
6	C	81	GLY	2.2
1	A	30	U	2.2
1	A	640	A	2.2
1	A	1135	U	2.2
1	A	1191	A	2.2
5	B	69	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
5	B	238	LEU	2.2
5	B	22	LYS	2.2
7	D	84	LYS	2.2
10	G	36	LYS	2.2
20	Q	79	SER	2.2
1	A	1045	C	2.2
1	A	1322	C	2.2
16	M	55	ARG	2.2
16	M	94	ARG	2.2
5	B	104	ASN	2.2
5	B	60	ASP	2.2
5	B	145	LEU	2.2
14	K	15	ALA	2.2
17	N	59	ALA	2.2
23	T	32	ALA	2.2
1	A	1032	G	2.2
1	A	1323	G	2.2
1	A	1454	G	2.2
7	D	182	LYS	2.2
22	S	69	HIS	2.2
12	I	51	ARG	2.2
16	M	57	ARG	2.2
1	A	273	A	2.2
1	A	816	A	2.2
14	K	53	SER	2.2
5	B	224	GLN	2.2
10	G	110	GLN	2.2
23	T	90	GLN	2.2
10	G	90	GLU	2.2
13	J	4	ILE	2.2
23	T	50	GLU	2.2
15	L	52	LEU	2.2
20	Q	67	LYS	2.2
5	B	140	HIS	2.2
16	M	54	VAL	2.2
6	C	37	GLN	2.2
1	A	1058	G	2.2
1	A	1067	A	2.2
1	A	1068	G	2.2
1	A	1108	G	2.2
1	A	1198	G	2.2
1	A	1394	A	2.2

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Mol	Chain	Res	Type	RSRZ
13	J	95	GLU	2.2
6	C	145	GLY	2.2
7	D	195	ALA	2.2
18	O	20	GLY	2.2
23	T	49	ALA	2.2
22	S	32	LYS	2.2
10	G	76	ARG	2.2
13	J	11	PHE	2.2
15	L	32	PHE	2.2
1	A	40	C	2.2
1	A	1008	C	2.2
5	B	150	SER	2.2
6	C	91	LEU	2.2
9	F	11	ASN	2.2
10	G	57	GLU	2.2
21	R	84	LYS	2.2
9	F	86	ARG	2.2
17	N	3	ARG	2.2
7	D	110	PHE	2.2
1	A	1105	A	2.2
1	A	1183	A	2.2
1	A	332	G	2.2
1	A	333	G	2.2
1	A	1021	G	2.2
1	A	1120	G	2.2
1	A	1386	G	2.2
1	A	1421	G	2.2
5	B	92	TYR	2.1
7	D	4	TYR	2.1
7	D	20	TYR	2.1
9	F	63	TYR	2.1
17	N	34	TYR	2.1
1	A	679	C	2.1
1	A	1113	C	2.1
7	D	74	GLN	2.1
6	C	4	LYS	2.1
7	D	184	LYS	2.1
8	E	125	SER	2.1
15	L	21	LYS	2.1
6	C	58	GLU	2.1
1	A	1485	U	2.1
3	Y	33	U	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	26	A	2.1
1	A	926	G	2.1
1	A	933	G	2.1
1	A	1164	G	2.1
1	A	1258	G	2.1
9	F	80	ARG	2.1
16	M	76	ALA	2.1
11	H	115	SER	2.1
22	S	82	GLY	2.1
1	A	422	C	2.1
15	L	49	ASN	2.1
1	A	534	U	2.1
6	C	93	LYS	2.1
8	E	76	ILE	2.1
23	T	55	ILE	2.1
19	P	39	TYR	2.1
9	F	77	ARG	2.1
13	J	32	ALA	2.1
1	A	171	A	2.1
1	A	665	A	2.1
10	G	93	PRO	2.1
12	I	24	GLY	2.1
5	B	94	ASN	2.1
1	A	266	G	2.1
1	A	438	G	2.1
1	A	851	G	2.1
1	A	976	G	2.1
1	A	1273	G	2.1
1	A	1419	G	2.1
1	A	555	C	2.1
10	G	35	LYS	2.1
15	L	17	LYS	2.1
15	L	57	LYS	2.1
5	B	82	ARG	2.1
11	H	122	ARG	2.1
4	Z	1	U	2.1
12	I	115	GLY	2.1
5	B	49	GLU	2.1
20	Q	86	GLU	2.1
1	A	1236	A	2.1
10	G	148	ASN	2.1
18	O	47	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
19	P	12	LYS	2.1
22	S	25	LYS	2.1
6	C	34	LEU	2.1
6	C	164	ARG	2.1
5	B	79	ASP	2.1
6	C	17	ASP	2.1
1	A	1484	C	2.1
1	A	576	G	2.1
1	A	823	G	2.1
5	B	240	GLN	2.1
6	C	197	GLY	2.1
23	T	51	GLU	2.1
17	N	15	LYS	2.0
18	O	44	LYS	2.0
20	Q	23	VAL	2.0
5	B	205	ASP	2.0
6	C	65	ALA	2.0
13	J	48	THR	2.0
10	G	67	GLU	2.0
1	A	148	G	2.0
1	A	481	G	2.0
1	A	1266	G	2.0
5	B	142	LEU	2.0
12	I	42	ARG	2.0
12	I	58	ARG	2.0
5	B	208	ILE	2.0
1	A	1510	U	2.0
13	J	69	ASN	2.0
5	B	19	HIS	2.0
13	J	54	PHE	2.0
6	C	123	GLN	2.0
24	V	23	PRO	2.0
6	C	166	GLU	2.0
9	F	46	ARG	2.0
11	H	69	ARG	2.0
22	S	58	VAL	2.0
1	A	330	C	2.0
1	A	817	C	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSR	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1624	1/1	0.62	0.56	27,27,27,27	1
25	MG	A	1636	1/1	0.66	0.18	27,27,27,27	1
25	MG	A	1626	1/1	0.73	0.19	27,27,27,27	1
25	MG	A	1654	1/1	0.76	0.31	27,27,27,27	1
25	MG	A	1628	1/1	0.77	0.52	27,27,27,27	1
25	MG	A	1561	1/1	0.77	0.40	27,27,27,27	0
25	MG	A	1622	1/1	0.77	0.18	27,27,27,27	0
25	MG	A	1655	1/1	0.77	0.36	27,27,27,27	1
25	MG	A	1618	1/1	0.79	0.15	27,27,27,27	1
25	MG	A	1649	1/1	0.79	0.22	27,27,27,27	1
25	MG	A	1640	1/1	0.82	0.46	27,27,27,27	1
25	MG	A	1589	1/1	0.83	0.34	27,27,27,27	0
25	MG	A	210	1/1	0.83	0.20	27,27,27,27	1
25	MG	A	1565	1/1	0.83	0.34	27,27,27,27	0
25	MG	A	1574	1/1	0.83	0.33	27,27,27,27	0
25	MG	A	1641	1/1	0.85	0.39	27,27,27,27	1
25	MG	A	1548	1/1	0.85	0.30	27,27,27,27	1
25	MG	A	1606	1/1	0.86	0.20	27,27,27,27	1
25	MG	A	1560	1/1	0.87	0.37	27,27,27,27	0
25	MG	A	1597	1/1	0.87	0.25	27,27,27,27	0
25	MG	A	1579	1/1	0.87	0.16	27,27,27,27	1
25	MG	A	1627	1/1	0.88	0.16	27,27,27,27	0
25	MG	A	1545	1/1	0.88	0.26	27,27,27,27	0
25	MG	A	1613	1/1	0.88	0.29	27,27,27,27	0
25	MG	A	1562	1/1	0.88	0.20	27,27,27,27	1
25	MG	A	1656	1/1	0.88	0.14	27,27,27,27	0
25	MG	A	1621	1/1	0.89	0.25	27,27,27,27	0
25	MG	A	1591	1/1	0.89	0.32	27,27,27,27	0
25	MG	A	1652	1/1	0.89	0.10	27,27,27,27	0
25	MG	A	87	1/1	0.89	0.27	27,27,27,27	1
25	MG	A	1639	1/1	0.89	0.32	27,27,27,27	1
25	MG	A	1550	1/1	0.89	0.22	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1620	1/1	0.90	0.33	27,27,27,27	1
25	MG	A	1558	1/1	0.90	0.29	27,27,27,27	0
25	MG	A	1576	1/1	0.91	0.25	27,27,27,27	0
25	MG	A	1593	1/1	0.91	0.27	27,27,27,27	0
25	MG	A	1566	1/1	0.91	0.16	27,27,27,27	0
25	MG	A	1598	1/1	0.91	0.23	27,27,27,27	0
25	MG	A	1582	1/1	0.91	0.20	27,27,27,27	0
25	MG	A	1575	1/1	0.91	0.28	27,27,27,27	0
25	MG	A	214	1/1	0.92	0.12	27,27,27,27	1
25	MG	A	1547	1/1	0.92	0.22	27,27,27,27	0
25	MG	A	1581	1/1	0.92	0.08	27,27,27,27	0
25	MG	A	1637	1/1	0.92	0.17	27,27,27,27	1
25	MG	A	1615	1/1	0.92	0.23	27,27,27,27	0
25	MG	A	1594	1/1	0.92	0.40	27,27,27,27	0
25	MG	A	1625	1/1	0.93	0.09	27,27,27,27	0
25	MG	A	1604	1/1	0.93	0.07	27,27,27,27	0
25	MG	A	1569	1/1	0.93	0.24	27,27,27,27	0
25	MG	A	1607	1/1	0.93	0.24	27,27,27,27	1
25	MG	A	1609	1/1	0.93	0.13	27,27,27,27	0
25	MG	A	1611	1/1	0.93	0.15	27,27,27,27	0
25	MG	A	1638	1/1	0.93	0.24	27,27,27,27	0
25	MG	A	86	1/1	0.93	0.23	27,27,27,27	0
25	MG	A	1564	1/1	0.93	0.14	27,27,27,27	0
25	MG	A	1617	1/1	0.93	0.29	27,27,27,27	0
25	MG	A	1644	1/1	0.93	0.17	27,27,27,27	1
25	MG	A	1555	1/1	0.93	0.27	27,27,27,27	0
25	MG	A	1584	1/1	0.93	0.32	27,27,27,27	0
25	MG	A	1585	1/1	0.93	0.27	27,27,27,27	0
25	MG	A	1556	1/1	0.93	0.34	27,27,27,27	0
25	MG	A	1603	1/1	0.93	0.24	27,27,27,27	0
25	MG	A	1583	1/1	0.94	0.10	27,27,27,27	0
25	MG	A	1573	1/1	0.94	0.29	27,27,27,27	0
25	MG	A	1546	1/1	0.94	0.24	27,27,27,27	0
25	MG	A	1587	1/1	0.94	0.28	27,27,27,27	0
25	MG	A	1568	1/1	0.94	0.27	27,27,27,27	0
25	MG	A	71	1/1	0.94	0.26	27,27,27,27	0
25	MG	A	1552	1/1	0.94	0.34	27,27,27,27	0
25	MG	A	1645	1/1	0.94	0.08	27,27,27,27	0
25	MG	A	1646	1/1	0.94	0.34	27,27,27,27	0
25	MG	A	1580	1/1	0.94	0.21	27,27,27,27	0
25	MG	A	1557	1/1	0.94	0.21	27,27,27,27	0
25	MG	A	1572	1/1	0.94	0.09	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1629	1/1	0.94	0.17	27,27,27,27	0
25	MG	A	1630	1/1	0.94	0.32	27,27,27,27	0
25	MG	A	1602	1/1	0.95	0.13	27,27,27,27	0
25	MG	A	1578	1/1	0.95	0.25	27,27,27,27	0
25	MG	A	1590	1/1	0.95	0.13	27,27,27,27	0
25	MG	A	1571	1/1	0.95	0.18	27,27,27,27	0
25	MG	A	1619	1/1	0.95	0.29	27,27,27,27	0
25	MG	A	1648	1/1	0.95	0.09	27,27,27,27	0
25	MG	A	1592	1/1	0.95	0.17	27,27,27,27	0
25	MG	A	211	1/1	0.95	0.32	27,27,27,27	0
25	MG	A	1653	1/1	0.95	0.23	27,27,27,27	1
25	MG	A	1549	1/1	0.95	0.33	27,27,27,27	0
25	MG	A	1623	1/1	0.95	0.08	27,27,27,27	0
25	MG	A	1612	1/1	0.95	0.08	27,27,27,27	0
25	MG	D	215	1/1	0.95	0.11	27,27,27,27	0
25	MG	H	213	1/1	0.95	0.06	27,27,27,27	0
25	MG	A	1642	1/1	0.96	0.18	27,27,27,27	1
25	MG	A	1567	1/1	0.96	0.06	27,27,27,27	1
25	MG	A	1651	1/1	0.96	0.13	27,27,27,27	0
25	MG	A	1577	1/1	0.96	0.10	27,27,27,27	0
25	MG	A	1634	1/1	0.96	0.08	27,27,27,27	0
25	MG	A	1616	1/1	0.97	0.14	27,27,27,27	0
25	MG	A	1643	1/1	0.97	0.14	27,27,27,27	1
25	MG	A	1605	1/1	0.97	0.06	27,27,27,27	0
25	MG	A	1554	1/1	0.97	0.33	27,27,27,27	0
25	MG	A	1559	1/1	0.97	0.16	27,27,27,27	0
25	MG	A	1647	1/1	0.97	0.08	27,27,27,27	0
25	MG	A	1631	1/1	0.97	0.30	27,27,27,27	0
25	MG	A	1632	1/1	0.97	0.08	27,27,27,27	0
25	MG	A	1633	1/1	0.97	0.32	27,27,27,27	0
25	MG	A	1608	1/1	0.97	0.08	27,27,27,27	0
25	MG	A	1595	1/1	0.97	0.11	27,27,27,27	0
25	MG	A	1610	1/1	0.97	0.15	27,27,27,27	1
25	MG	A	1601	1/1	0.97	0.20	27,27,27,27	0
25	MG	A	1570	1/1	0.97	0.36	27,27,27,27	0
25	MG	A	1588	1/1	0.97	0.20	27,27,27,27	0
25	MG	A	1599	1/1	0.97	0.21	27,27,27,27	0
25	MG	A	1586	1/1	0.98	0.05	27,27,27,27	0
25	MG	A	1563	1/1	0.98	0.12	27,27,27,27	0
25	MG	A	1614	1/1	0.98	0.25	27,27,27,27	0
25	MG	A	1650	1/1	0.98	0.18	27,27,27,27	1
25	MG	A	1635	1/1	0.98	0.14	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1551	1/1	0.98	0.35	27,27,27,27	0
26	ZN	D	506	1/1	0.98	0.20	27,27,27,27	0
25	MG	A	1600	1/1	0.99	0.11	27,27,27,27	0
25	MG	A	1596	1/1	0.99	0.43	27,27,27,27	0
25	MG	A	1553	1/1	0.99	0.35	27,27,27,27	0
26	ZN	N	507	1/1	1.00	0.02	27,27,27,27	1

6.5 Other polymers [i](#)

There are no such residues in this entry.