



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 11:09 am BST

PDB ID : 1HNZ
Title : STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL
SUBUNIT IN COMPLEX WITH HYGROMYCIN B
Authors : Brodersen, D.E.; Clemons Jr., W.M.; Carter, A.P.; Morgan-Warren, R.; Wim-
berly, B.T.; Ramakrishnan, V.
Deposited on : 2000-12-08
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

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

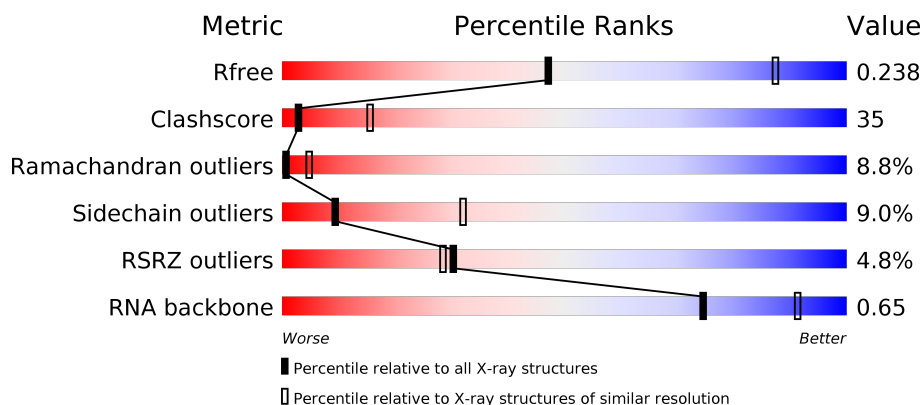
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)
RNA backbone	3102	1117 (3.70-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	<div> <div>5%</div> <div>28%</div> <div>56%</div> <div>13%</div> <div>..</div> </div>
2	X	6	<div> <div>50%</div> <div>100%</div> </div>
3	B	256	<div> <div>6%</div> <div>20%</div> <div>56%</div> <div>13%</div> <div>9%</div> </div>
4	C	239	<div> <div>%</div> <div>21%</div> <div>50%</div> <div>14%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
5	D	209	
6	E	162	
7	F	101	
8	G	156	
9	H	138	
10	I	128	
11	J	105	
12	K	129	
13	L	135	
14	M	126	
15	N	61	
16	O	89	
17	P	88	
18	Q	105	
19	R	88	
20	S	93	
21	T	106	
22	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
23	MG	A	1549	-	-	-	X
23	MG	A	1550	-	-	-	X
23	MG	A	1556	-	-	-	X
23	MG	A	1566	-	-	-	X
23	MG	A	1581	-	-	-	X
23	MG	A	1590	-	-	-	X
23	MG	A	1614	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	MG	A	1615	-	-	-	X
23	MG	A	1618	-	-	-	X
23	MG	A	1623	-	-	-	X
23	MG	A	1624	-	-	-	X
23	MG	A	1629	-	-	-	X
23	MG	A	211	-	-	-	X
23	MG	A	212	-	-	-	X
23	MG	H	213	-	-	-	X
24	HYG	A	1632	X	-	-	-

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 51906 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	22	0	0
			32391	14418	6002	10465	1506			

- Molecule 2 is a RNA chain called FRAGMENT OF MESSENGER RNA.

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 protein called 30S RIBOSOMAL PROTEIN S2.

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

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S3.

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

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S4.

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

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S5.

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

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S6.

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

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S7.

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

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S9.

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

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S10.

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

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S11.

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

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S12.

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

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	M	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S14.

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

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S15.

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

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	P	88	Total	C	N	O	S	0	0	0
			735	462	147	125	1			

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S17.

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

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S18.

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

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S19.

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

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	T	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			

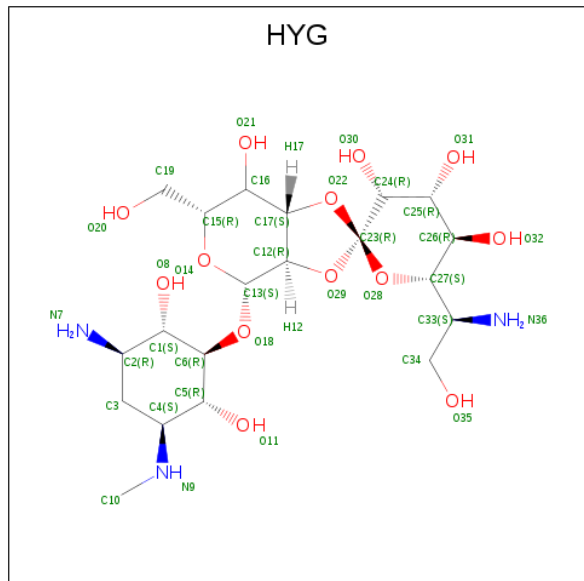
- Molecule 22 is a protein called 30S RIBOSOMAL PROTEIN THX.

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

- Molecule 23 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	H	1	Total	Mg	0	0
			1	1		
23	A	94	Total	Mg	0	0
			94	94		
23	D	1	Total	Mg	0	0
			1	1		

- Molecule 24 is HYGROMYCIN B (three-letter code: HYG) (formula: C₂₀H₃₇N₃O₁₃).



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

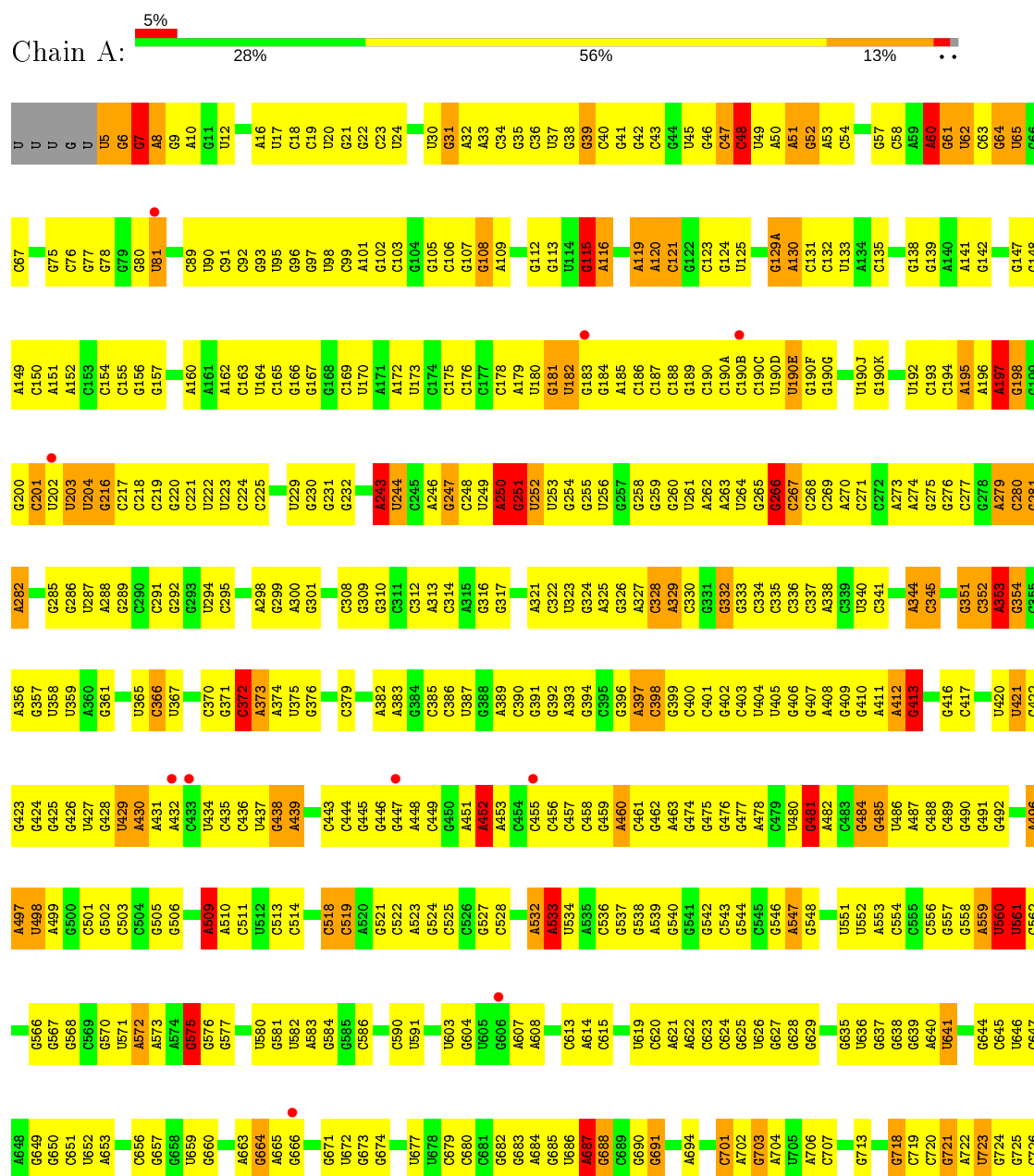
- Molecule 25 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

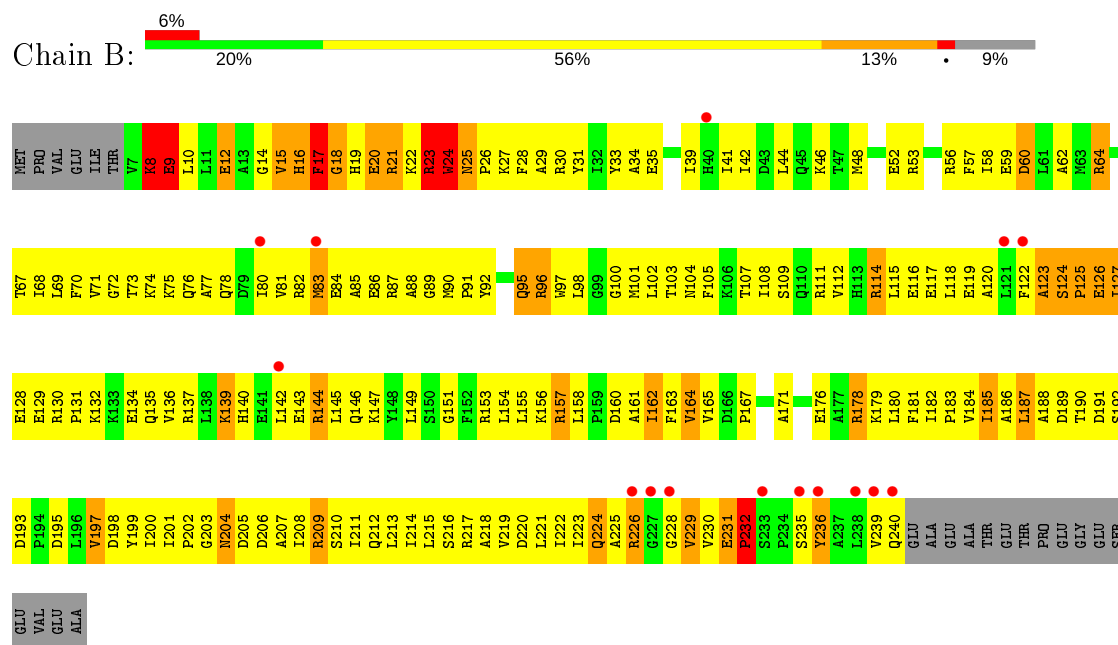
3 Residue-property plots

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

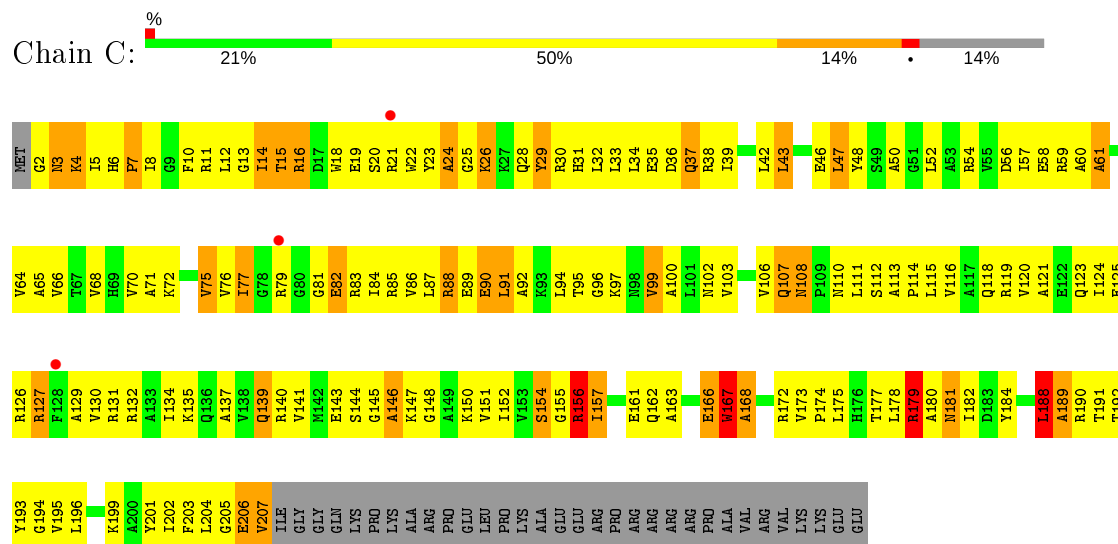
• Molecule 1: 16S RIBOSOMAL RNA



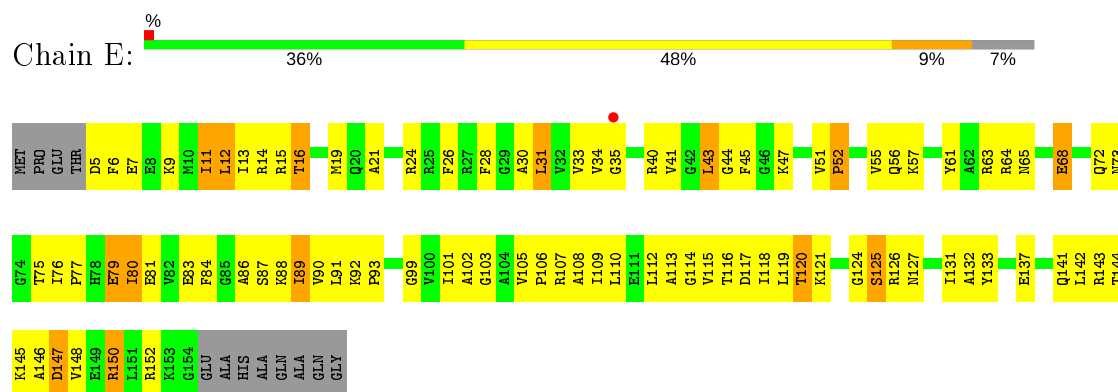
• Molecule 3: 30S RIBOSOMAL PROTEIN S2

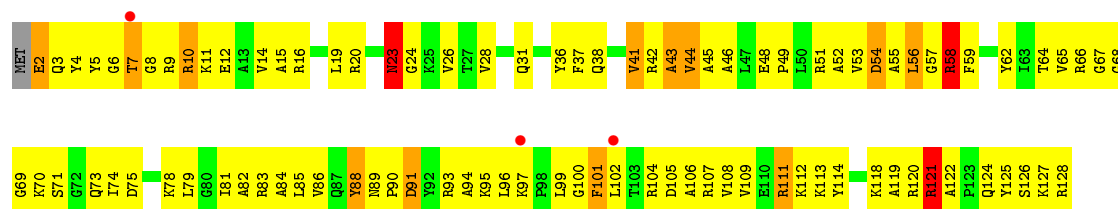


• Molecule 4: 30S RIBOSOMAL PROTEIN S3

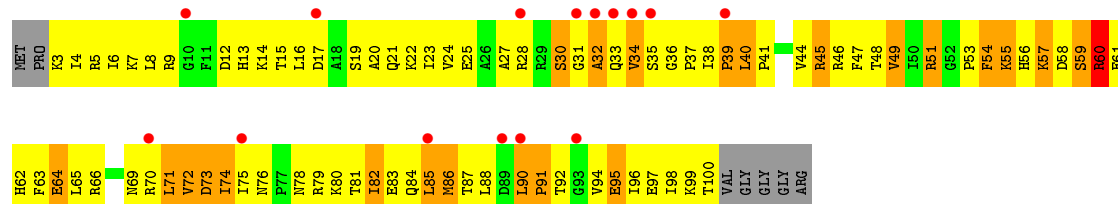
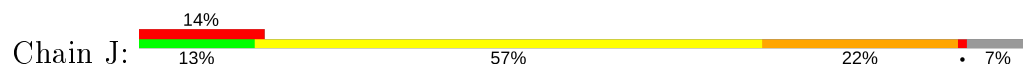


- Molecule 6: 30S RIBOSOMAL PROTEIN S5

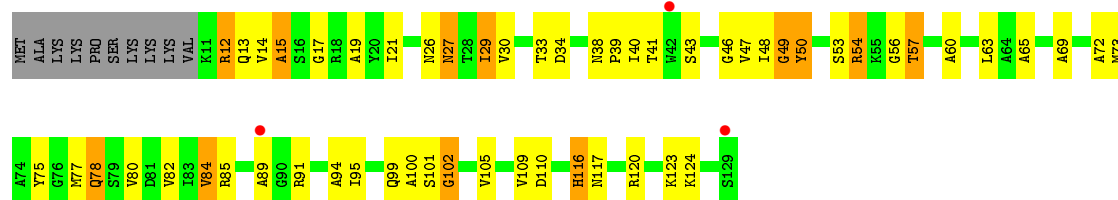




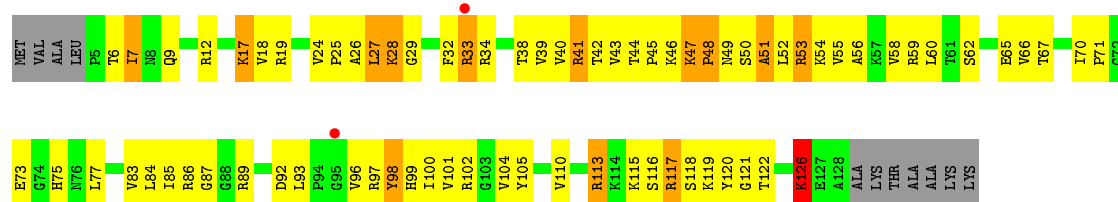
• Molecule 11: 30S RIBOSOMAL PROTEIN S10



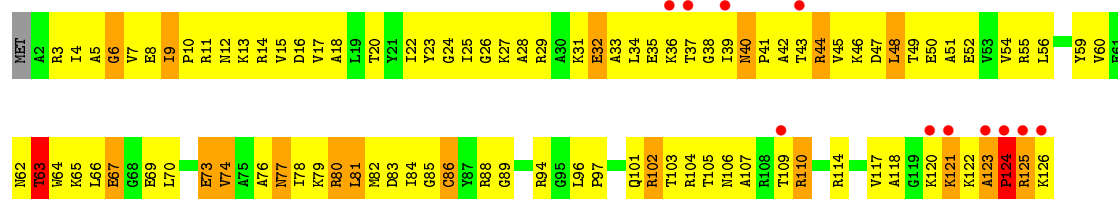
• Molecule 12: 30S RIBOSOMAL PROTEIN S11



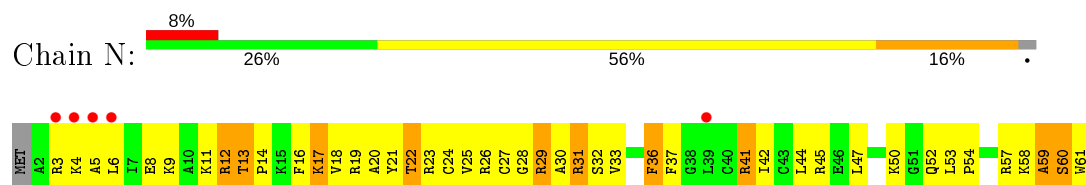
• Molecule 13: 30S RIBOSOMAL PROTEIN S12



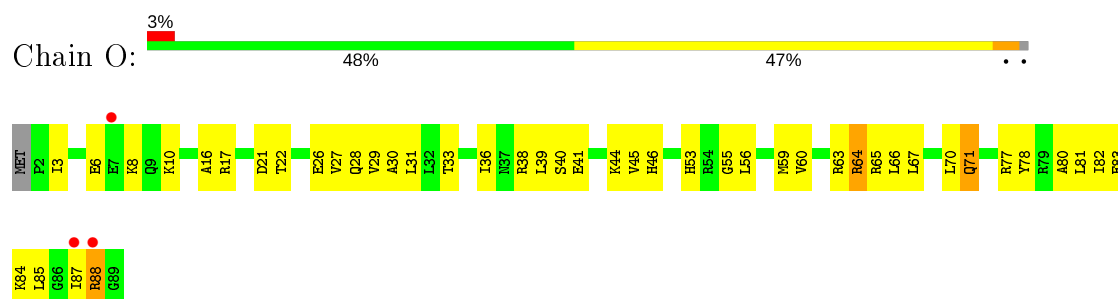
• Molecule 14: 30S RIBOSOMAL PROTEIN S13



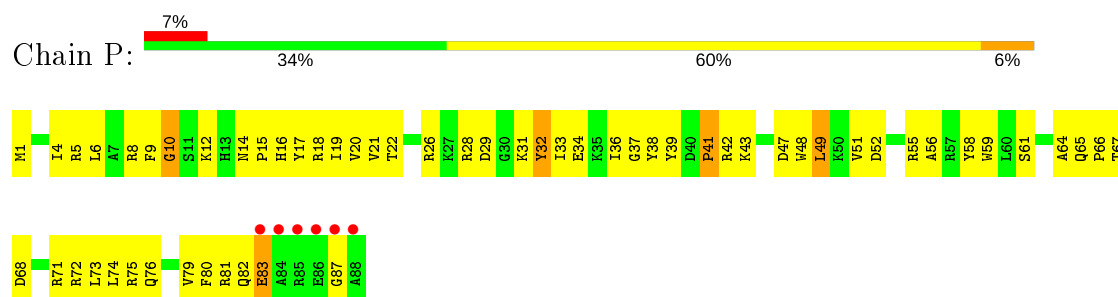
- Molecule 15: 30S RIBOSOMAL PROTEIN S14



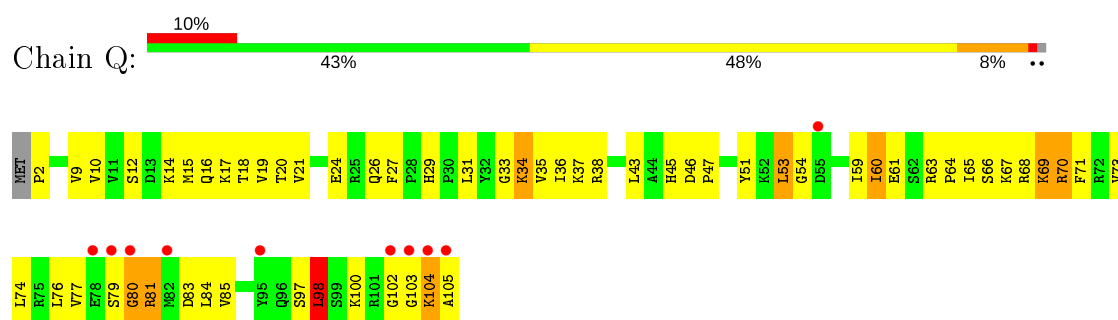
- Molecule 16: 30S RIBOSOMAL PROTEIN S15



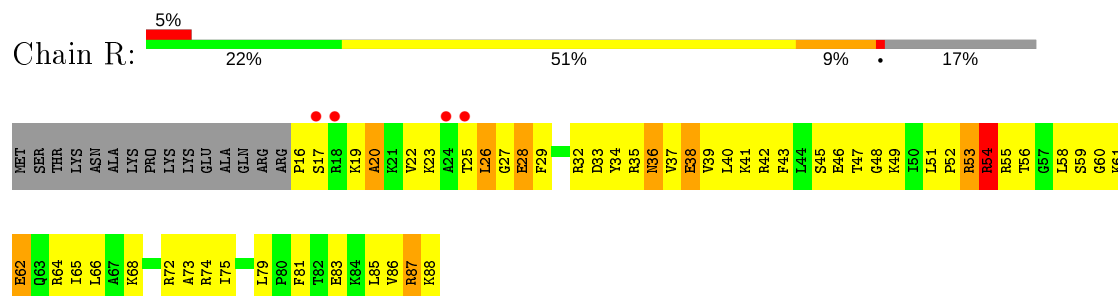
- Molecule 17: 30S RIBOSOMAL PROTEIN S16



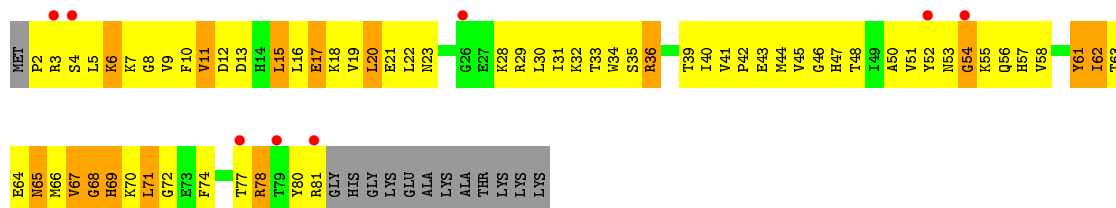
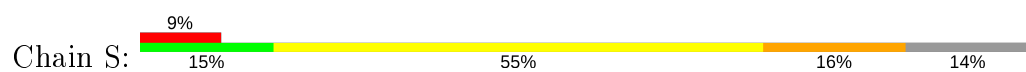
- Molecule 18: 30S RIBOSOMAL PROTEIN S17



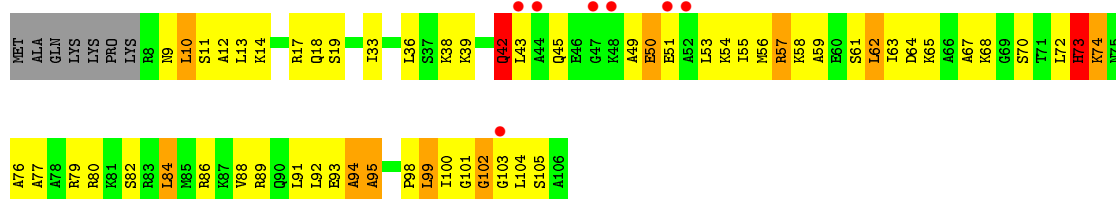
- Molecule 19: 30S RIBOSOMAL PROTEIN S18



- Molecule 20: 30S RIBOSOMAL PROTEIN S19



- Molecule 21: 30S RIBOSOMAL PROTEIN S20



- Molecule 22: 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	402.06 Å 402.06 Å 175.26 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.30 49.87 – 3.08	Depositor EDS
% Data completeness (in resolution range)	88.0 (50.00-3.30) 83.1 (49.87-3.08)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 3.07 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.218 , 0.261 0.201 , 0.238	Depositor DCC
R_{free} test set	10985 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	88.1	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 74.1	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	0.90	EDS
Total number of atoms	51906	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.46% 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: ZN, MG, HYG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.51	1/36259 (0.0%)	0.75	43/56593 (0.1%)
2	X	0.54	0/128	0.66	0/196
3	B	0.38	0/1935	0.68	0/2609
4	C	0.38	0/1636	0.68	0/2205
5	D	0.40	0/1733	0.68	1/2318 (0.0%)
6	E	0.47	0/1162	0.78	0/1564
7	F	0.34	0/856	0.64	0/1154
8	G	0.36	0/1276	0.61	0/1709
9	H	0.44	0/1136	0.76	0/1527
10	I	0.37	0/1029	0.67	0/1378
11	J	0.37	0/805	0.69	0/1082
12	K	0.38	0/900	0.71	0/1213
13	L	0.42	0/986	0.74	0/1320
14	M	0.36	0/1008	0.70	0/1347
15	N	0.42	0/501	0.79	0/664
16	O	0.36	0/745	0.62	0/992
17	P	0.43	0/751	0.76	0/1008
18	Q	0.46	0/870	0.77	0/1159
19	R	0.38	0/603	0.66	0/799
20	S	0.37	0/661	0.77	1/890 (0.1%)
21	T	0.39	0/764	0.74	0/1006
22	V	0.49	0/212	0.72	0/277
All	All	0.47	1/55956 (0.0%)	0.74	45/83010 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	3	39

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	H	0	1
All	All	3	40

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	121	C	N1-C2	5.29	1.45	1.40

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1498	U	C2'-C3'-O3'	10.50	132.60	109.50
1	A	559	A	C2'-C3'-O3'	9.09	129.51	109.50
1	A	181	G	C2'-C3'-O3'	8.86	128.99	109.50
1	A	1528	U	C2'-C3'-O3'	8.80	128.87	109.50
1	A	575	G	C2'-C3'-O3'	8.13	127.38	109.50
1	A	108	G	O4'-C1'-N9	8.08	114.66	108.20
1	A	60	A	C2'-C3'-O3'	8.08	127.27	109.50
1	A	366	C	C2'-C3'-O3'	7.92	126.94	109.50
1	A	792	A	C2'-C3'-O3'	7.90	126.88	109.50
1	A	7	G	C2'-C3'-O3'	7.66	126.35	109.50
1	A	197	A	N9-C1'-C2'	7.08	123.21	114.00
1	A	266	G	C2'-C3'-O3'	6.90	124.74	113.70
1	A	372	C	C2'-C3'-O3'	6.72	124.45	113.70
1	A	48	C	C2'-C3'-O3'	6.71	124.43	113.70
1	A	1299	A	N9-C1'-C2'	6.52	122.48	114.00
1	A	1504	G	C2'-C3'-O3'	6.51	124.12	113.70
1	A	1124	G	N9-C1'-C2'	6.42	122.34	114.00
1	A	509	A	C2'-C3'-O3'	6.26	123.72	113.70
1	A	243	A	C2'-C3'-O3'	6.05	123.38	113.70
5	D	12	CYS	CA-CB-SG	6.03	124.85	114.00
1	A	960	U	C2'-C3'-O3'	6.02	123.34	113.70
1	A	353	A	C5'-C4'-O4'	-6.01	101.88	109.10
1	A	115	G	C2'-C3'-O3'	5.92	123.18	113.70
1	A	993	G	N9-C1'-C2'	5.92	121.70	114.00
1	A	1502	A	N9-C1'-C2'	5.88	121.64	114.00
1	A	1065	U	C1'-O4'-C4'	-5.82	105.24	109.90
1	A	115	G	N9-C1'-C2'	5.76	121.49	114.00
1	A	533	A	C2'-C3'-O3'	5.74	122.88	113.70
1	A	687	A	C2'-C3'-O3'	5.66	122.76	113.70
1	A	266	G	O4'-C1'-N9	-5.63	103.70	108.20
1	A	484	G	C2'-C3'-O3'	5.59	122.64	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	S	54	GLY	N-CA-C	-5.57	99.18	113.10
1	A	1067	A	C2'-C3'-O3'	5.54	122.56	113.70
1	A	533	A	N9-C1'-C2'	5.44	121.07	114.00
1	A	243	A	N9-C1'-C2'	5.35	120.95	114.00
1	A	1528	U	C4'-C3'-O3'	5.33	123.67	113.00
1	A	1300	G	N9-C1'-C2'	5.32	120.91	114.00
1	A	1347	G	OP2-P-O3'	5.29	116.83	105.20
1	A	266	G	N9-C1'-C2'	5.28	120.87	114.00
1	A	1347	G	N9-C1'-C2'	5.24	120.81	114.00
1	A	452	A	N9-C1'-C2'	5.23	120.79	114.00
1	A	1181	G	N9-C1'-C2'	5.21	120.77	114.00
1	A	760	G	N9-C1'-C2'	-5.16	106.32	112.00
1	A	560	U	C2'-C3'-O3'	5.10	121.86	113.70
1	A	812	C	OP2-P-O3'	5.03	116.27	105.20

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	181	G	C3'
1	A	1498	U	C3'
1	A	1528	U	C3'

All (40) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1073	U	Sidechain
1	A	1077	G	Sidechain
1	A	1079	G	Sidechain
1	A	1085	U	Sidechain
1	A	1181	G	Sidechain
1	A	12	U	Sidechain
1	A	1281	U	Sidechain
1	A	1289	A	Sidechain
1	A	1299	A	Sidechain
1	A	1301	U	Sidechain
1	A	1330	U	Sidechain
1	A	1345	U	Sidechain
1	A	1358	U	Sidechain
1	A	1401	G	Sidechain
1	A	1434	A	Sidechain
1	A	1522	U	Sidechain
1	A	197	A	Sidechain

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Mol	Chain	Res	Type	Group
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	263	A	Sidechain
1	A	266	G	Sidechain
1	A	413	G	Sidechain
1	A	452	A	Sidechain
1	A	481	G	Sidechain
1	A	561	U	Sidechain
1	A	572	A	Sidechain
1	A	575	G	Sidechain
1	A	641	U	Sidechain
1	A	664	G	Sidechain
1	A	691	G	Sidechain
1	A	773	G	Sidechain
1	A	835	U	Sidechain
1	A	868	C	Sidechain
1	A	871	U	Sidechain
1	A	873	A	Sidechain
1	A	879	C	Sidechain
1	A	898	G	Sidechain
1	A	900	A	Sidechain
1	A	982	U	Sidechain
9	H	58	TYR	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32391	0	16349	1226	0
2	X	117	0	64	0	0
3	B	1900	0	1951	256	1
4	C	1612	0	1677	235	0
5	D	1703	0	1763	180	0
6	E	1146	0	1207	110	0
7	F	843	0	857	69	0
8	G	1257	0	1296	96	0
9	H	1116	0	1177	99	0
10	I	1011	0	1043	138	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	J	792	0	835	149	0
12	K	885	0	904	62	0
13	L	970	0	1057	114	0
14	M	997	0	1072	124	0
15	N	492	0	529	71	0
16	O	734	0	771	62	0
17	P	735	0	752	62	0
18	Q	857	0	930	76	0
19	R	597	0	668	82	0
20	S	647	0	673	82	0
21	T	762	0	859	61	0
22	V	208	0	221	22	0
23	A	94	0	0	0	0
23	D	1	0	0	0	0
23	H	1	0	0	0	0
24	A	36	0	36	8	0
25	D	1	0	0	0	0
25	N	1	0	0	0	0
All	All	51906	0	36691	3082	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 35.

All (3082) 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)
13:L:28:LYS:HD2	13:L:33:ARG:HH22	1.08	1.12
1:A:1443:G:H5''	1:A:1446:A:H5'	1.21	1.11
5:D:36:ARG:H	5:D:37:PRO:HD3	1.02	1.10
3:B:84:GLU:HB3	3:B:219:VAL:HG21	1.30	1.09
11:J:45:ARG:HH11	11:J:45:ARG:HB3	1.01	1.09
13:L:41:ARG:HG2	13:L:42:THR:H	1.10	1.09
1:A:80:G:H3'	1:A:81:U:H5''	1.33	1.08
3:B:77:ALA:HB2	3:B:211:ILE:HD13	1.15	1.08
4:C:25:GLY:HA2	4:C:29:TYR:HB2	1.32	1.07
12:K:110:ASP:HB2	19:R:88:LYS:HD2	1.33	1.07
10:I:8:GLY:HA2	10:I:79:LEU:HD12	1.34	1.06
11:J:51:ARG:HB2	11:J:59:SER:HB3	1.32	1.05
1:A:761:G:H4'	18:Q:103:GLY:H	1.21	1.04
20:S:33:THR:HG22	20:S:35:SER:H	1.15	1.04
9:H:119:LEU:HD12	9:H:124:ALA:HA	1.36	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:56:LEU:HA	16:O:59:MET:HE2	1.37	1.03
18:Q:104:LYS:HZ3	18:Q:104:LYS:H	1.05	1.02
1:A:1047:G:H5''	15:N:4:LYS:HD2	1.41	1.02
4:C:91:LEU:HD21	4:C:99:VAL:HG13	1.41	1.01
14:M:49:THR:HG22	14:M:51:ALA:H	1.24	1.01
1:A:1057:G:H5''	4:C:154:SER:HB2	1.41	1.01
11:J:45:ARG:NH1	11:J:45:ARG:HB3	1.75	1.01
4:C:94:LEU:HD23	4:C:95:THR:HG23	1.43	1.00
14:M:10:PRO:HB2	14:M:18:ALA:HB1	1.43	0.99
5:D:187:ARG:HE	5:D:188:LEU:H	1.02	0.99
13:L:60:LEU:HD11	13:L:85:ILE:HD12	1.40	0.99
21:T:39:LYS:HD2	21:T:55:ILE:HD13	1.43	0.99
6:E:51:VAL:HB	6:E:52:PRO:HD3	1.44	0.99
5:D:187:ARG:HH21	5:D:188:LEU:HG	1.29	0.98
13:L:33:ARG:HG2	13:L:60:LEU:HD12	1.46	0.98
1:A:1131:G:H1	1:A:1143:G:H21	1.03	0.97
1:A:761:G:H4'	18:Q:103:GLY:N	1.78	0.97
3:B:74:LYS:NZ	3:B:206:ASP:HA	1.81	0.96
1:A:64:G:H4'	1:A:65:U:O5'	1.65	0.96
3:B:74:LYS:HZ2	3:B:206:ASP:HA	1.30	0.95
5:D:140:VAL:HG11	5:D:146:ILE:HD11	1.46	0.95
5:D:36:ARG:N	5:D:37:PRO:HD3	1.82	0.95
12:K:54:ARG:HH11	12:K:54:ARG:HB3	1.31	0.94
1:A:1305:G:HO2'	1:A:1306:A:H8	0.96	0.94
1:A:1125:U:H3	11:J:5:ARG:HH21	1.08	0.94
4:C:3:ASN:N	4:C:3:ASN:HD22	1.65	0.93
1:A:1137:C:H4'	1:A:1138:G:C2	2.04	0.93
3:B:91:PRO:HG3	3:B:154:LEU:HB2	1.48	0.93
3:B:67:THR:HA	3:B:90:MET:HE1	1.50	0.93
7:F:8:ILE:HD11	7:F:79:LEU:HD13	1.47	0.93
1:A:1305:G:O2'	1:A:1306:A:H8	1.52	0.93
9:H:19:VAL:HG23	9:H:21:LYS:HD3	1.51	0.92
13:L:75:HIS:HD2	13:L:77:LEU:H	1.16	0.92
12:K:40:ILE:HG22	12:K:41:THR:HG23	1.49	0.92
13:L:24:VAL:HG13	13:L:98:TYR:HE2	1.34	0.91
1:A:1286:A:C3'	1:A:1287:A:H5''	2.00	0.91
1:A:1286:A:C2'	1:A:1287:A:H5''	2.02	0.90
18:Q:104:LYS:NZ	18:Q:104:LYS:H	1.69	0.90
1:A:1281:U:H5'	1:A:1282:C:H5	1.34	0.90
1:A:243:A:H4'	1:A:244:U:H5'	1.54	0.90
8:G:78:ARG:HB2	8:G:156:TRP:HZ3	1.35	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:686:U:HO2'	1:A:687:A:H8	0.90	0.90
19:R:36:ASN:ND2	19:R:38:GLU:HG2	1.87	0.90
1:A:1230:C:H1'	14:M:126:LYS:HA	1.52	0.90
1:A:7:G:H5'	1:A:298:A:O4'	1.72	0.90
1:A:351:G:H4'	1:A:352:C:OP1	1.71	0.89
1:A:1086:U:H3	1:A:1099:G:H22	0.93	0.89
5:D:25:ARG:NH1	5:D:30:LYS:HB3	1.88	0.89
1:A:1116:C:H2'	1:A:1117:G:H5''	1.52	0.89
3:B:77:ALA:HB2	3:B:211:ILE:CD1	2.03	0.89
4:C:3:ASN:HD22	4:C:3:ASN:H	1.19	0.88
1:A:1286:A:H2'	1:A:1287:A:H5''	1.54	0.88
4:C:195:VAL:O	4:C:196:LEU:HD23	1.74	0.87
1:A:1250:A:H4'	10:I:68:GLY:N	1.90	0.87
18:Q:97:SER:HB2	18:Q:103:GLY:N	1.90	0.87
5:D:199:ASN:HD21	5:D:201:GLN:HB3	1.40	0.86
1:A:1226:C:H4'	1:A:1227:A:OP1	1.72	0.86
4:C:108:ASN:ND2	4:C:111:LEU:HG	1.89	0.86
4:C:52:LEU:H	4:C:52:LEU:HD23	1.39	0.86
19:R:55:ARG:HB3	19:R:55:ARG:NH1	1.90	0.86
3:B:178:ARG:HG3	3:B:178:ARG:HH11	1.39	0.85
1:A:1152:A:H5''	11:J:13:HIS:HD2	1.40	0.85
5:D:187:ARG:HE	5:D:188:LEU:N	1.72	0.85
8:G:78:ARG:HB2	8:G:156:TRP:CZ3	2.12	0.85
11:J:62:HIS:HB3	15:N:59:ALA:HB3	1.57	0.85
1:A:954:G:H21	1:A:1227:A:H62	1.25	0.85
1:A:974:A:OP1	15:N:31:ARG:HG2	1.76	0.85
5:D:23:GLY:HA3	5:D:112:VAL:HG12	1.57	0.84
5:D:36:ARG:H	5:D:37:PRO:CD	1.85	0.84
6:E:80:ILE:CD1	6:E:91:LEU:HB2	2.08	0.84
1:A:438:G:H4'	1:A:439:A:OP1	1.75	0.84
1:A:664:G:H22	1:A:741:G:H1	1.20	0.84
3:B:124:SER:HB2	3:B:125:PRO:HD2	1.60	0.84
1:A:371:G:O2'	1:A:372:C:H5'	1.77	0.84
1:A:975:A:H5'	1:A:975:A:H8	1.40	0.84
4:C:131:ARG:HG2	4:C:135:LYS:HE3	1.59	0.84
9:H:1:MET:HG2	9:H:2:LEU:H	1.43	0.84
5:D:156:GLU:HG2	5:D:160:GLN:HE21	1.42	0.84
11:J:19:SER:HB2	11:J:91:PRO:HG3	1.58	0.84
7:F:10:LEU:HD12	7:F:59:TYR:HB3	1.60	0.84
1:A:1356:G:H2'	1:A:1357:A:C8	2.13	0.83
1:A:1286:A:H3'	1:A:1287:A:H5''	1.57	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:41:ARG:HG2	13:L:42:THR:N	1.93	0.83
3:B:130:ARG:HH22	4:C:207:VAL:HG23	1.43	0.83
5:D:150:GLU:CD	5:D:150:GLU:H	1.82	0.83
4:C:112:SER:HB2	4:C:115:LEU:HD12	1.59	0.83
12:K:91:ARG:NH1	19:R:88:LYS:HE2	1.94	0.83
11:J:39:PRO:HA	11:J:70:ARG:HH11	1.44	0.82
20:S:55:LYS:HG2	20:S:56:GLN:HE21	1.43	0.82
1:A:1443:G:C5'	1:A:1446:A:H5'	2.07	0.82
1:A:1117:G:H4'	10:I:104:ARG:NH1	1.93	0.82
13:L:70:ILE:HD13	13:L:77:LEU:HD12	1.59	0.82
1:A:1347:G:N2	1:A:1373:G:H2'	1.92	0.82
3:B:197:VAL:HB	3:B:200:ILE:HG12	1.59	0.82
13:L:28:LYS:HD2	13:L:33:ARG:NH2	1.91	0.82
4:C:58:GLU:HB3	11:J:92:THR:HG21	1.62	0.82
6:E:9:LYS:HD2	6:E:112:LEU:HD21	1.61	0.82
1:A:1060:C:C5	4:C:2:GLY:HA3	2.14	0.82
4:C:174:PRO:HB2	4:C:177:THR:HG22	1.60	0.81
1:A:80:G:H3'	1:A:81:U:C5'	2.09	0.81
1:A:1137:C:H4'	1:A:1138:G:N2	1.95	0.81
1:A:1065:U:H4'	1:A:1066:C:O5'	1.79	0.81
20:S:64:GLU:O	20:S:67:VAL:HG23	1.80	0.81
1:A:1412:C:H2'	1:A:1413:A:H8	1.44	0.81
1:A:686:U:O2'	1:A:687:A:H8	1.64	0.80
1:A:80:G:C3'	1:A:81:U:H5''	2.10	0.80
6:E:81:GLU:HG2	6:E:90:VAL:HG22	1.61	0.80
8:G:95:ARG:HG2	8:G:99:LEU:HD11	1.62	0.80
10:I:9:ARG:HG2	10:I:14:VAL:HG22	1.64	0.80
11:J:51:ARG:HH11	11:J:51:ARG:HG2	1.46	0.80
14:M:50:GLU:O	14:M:54:VAL:HG23	1.81	0.80
3:B:80:ILE:HD11	3:B:208:ILE:HG23	1.62	0.80
1:A:1025:U:H2'	1:A:1026:G:C8	2.16	0.80
1:A:1236:A:H4'	1:A:1304:G:H4'	1.62	0.80
1:A:1493:A:O2'	1:A:1494:G:H5'	1.82	0.80
20:S:33:THR:HG22	20:S:35:SER:N	1.95	0.80
1:A:1238:A:H5'	1:A:1336:C:H41	1.44	0.80
1:A:1190:G:OP1	4:C:4:LYS:HA	1.80	0.80
5:D:61:LYS:HD2	5:D:207:TYR:OH	1.81	0.80
1:A:1279:A:H5''	1:A:1280:A:OP1	1.82	0.80
1:A:839:U:H5'	1:A:840:C:C5	2.16	0.80
3:B:132:LYS:HA	3:B:135:GLN:HB3	1.63	0.80
1:A:1182:G:H4'	1:A:1183:A:O5'	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:199:ASN:ND2	5:D:201:GLN:HB3	1.96	0.79
1:A:953:G:H1'	14:M:125:ARG:CB	2.12	0.79
1:A:1006:C:H2'	1:A:1007:C:H6	1.46	0.79
1:A:328:C:O2	1:A:328:C:H2'	1.82	0.79
14:M:11:ARG:HG3	14:M:12:ASN:N	1.96	0.79
3:B:22:LYS:HD2	3:B:35:GLU:OE1	1.83	0.79
4:C:58:GLU:H	4:C:65:ALA:HB3	1.48	0.79
12:K:57:THR:HG23	12:K:60:ALA:H	1.48	0.79
13:L:27:LEU:HG	13:L:28:LYS:H	1.48	0.79
1:A:1132:C:H2'	1:A:1133:G:C8	2.18	0.79
1:A:1251:A:H2'	1:A:1252:A:C8	2.17	0.79
1:A:1366:C:H2'	1:A:1367:C:H6	1.47	0.79
3:B:16:HIS:NE2	3:B:214:ILE:HG12	1.97	0.79
13:L:24:VAL:HG13	13:L:98:TYR:CE2	2.18	0.79
14:M:52:GLU:HG2	14:M:55:ARG:HH21	1.48	0.79
1:A:1502:A:H2	1:A:1505:G:H1	1.31	0.79
6:E:110:LEU:HD13	6:E:118:ILE:HD12	1.65	0.79
15:N:26:ARG:NH1	15:N:47:LEU:HG	1.98	0.79
1:A:1475:G:H2'	1:A:1476:G:H8	1.46	0.78
9:H:138:TRP:OXT	9:H:138:TRP:HE3	1.65	0.78
11:J:37:PRO:HA	11:J:72:VAL:HG22	1.62	0.78
1:A:1488:G:H2'	1:A:1489:G:C8	2.19	0.78
1:A:435:C:H2'	1:A:436:C:H6	1.49	0.78
4:C:15:THR:O	4:C:16:ARG:HB2	1.80	0.78
16:O:29:VAL:HG12	16:O:85:LEU:CD1	2.13	0.78
1:A:620:C:C2	5:D:135:LEU:HD13	2.17	0.78
4:C:52:LEU:HD21	4:C:118:GLN:HE22	1.46	0.78
21:T:14:LYS:O	21:T:18:GLN:HG3	1.84	0.78
1:A:1343:G:H1'	10:I:121:ARG:HH12	1.49	0.78
1:A:1116:C:C2'	1:A:1117:G:H5''	2.13	0.78
1:A:975:A:H4'	1:A:976:G:H5'	1.66	0.78
8:G:79:ARG:HG2	8:G:84:ASN:OD1	1.81	0.78
13:L:41:ARG:CG	13:L:42:THR:H	1.93	0.78
16:O:16:ALA:HB1	16:O:21:ASP:HB3	1.65	0.78
20:S:17:GLU:HA	20:S:20:LEU:HD11	1.66	0.78
1:A:1487:G:O2'	1:A:1488:G:H5'	1.83	0.78
3:B:161:ALA:HB1	3:B:185:ILE:HD11	1.64	0.78
4:C:108:ASN:HD22	4:C:111:LEU:HG	1.46	0.78
5:D:104:VAL:HG11	5:D:146:ILE:HD13	1.66	0.78
1:A:393:A:O2'	1:A:394:G:H5'	1.84	0.77
1:A:1086:U:H3	1:A:1099:G:N2	1.76	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:G:OP2	13:L:115:LYS:HG3	1.84	0.77
1:A:706:A:H1'	12:K:29:ILE:HD11	1.65	0.77
6:E:93:PRO:HG2	9:H:105:ARG:HE	1.48	0.77
1:A:250:A:H4'	1:A:251:G:O5'	1.82	0.77
8:G:18:TYR:HB3	8:G:59:LEU:HD22	1.66	0.77
17:P:58:TYR:O	17:P:61:SER:HB3	1.85	0.77
10:I:86:VAL:HG13	10:I:90:PRO:HA	1.65	0.77
1:A:1443:G:H5''	1:A:1446:A:C5'	2.08	0.77
1:A:382:A:H2'	1:A:383:A:C8	2.19	0.77
3:B:142:LEU:HB3	3:B:146:GLN:HE21	1.50	0.77
5:D:70:ILE:HD11	5:D:100:ARG:CZ	2.15	0.77
13:L:27:LEU:O	13:L:29:GLY:N	2.18	0.76
7:F:33:TYR:HB2	7:F:75:LEU:HD23	1.67	0.76
1:A:1256:A:H4'	1:A:1257:U:H5'	1.67	0.76
1:A:1497:G:H2'	1:A:1498:U:H5'	1.68	0.76
1:A:1495:U:O4	24:A:1632:HYG:H2	1.86	0.76
9:H:51:VAL:HG21	9:H:60:ARG:HG2	1.66	0.76
13:L:33:ARG:CD	13:L:62:SER:HB3	2.15	0.76
17:P:21:VAL:HG21	17:P:59:TRP:CD1	2.21	0.76
1:A:939:G:H2'	1:A:940:C:C6	2.21	0.76
4:C:177:THR:HG23	4:C:180:ALA:HB2	1.68	0.76
1:A:141:A:H1'	1:A:182:U:O2	1.86	0.76
3:B:102:LEU:HD21	3:B:162:ILE:CD1	2.15	0.76
10:I:16:ARG:HB2	10:I:64:THR:HB	1.68	0.76
18:Q:24:GLU:OE2	18:Q:37:LYS:HD3	1.85	0.76
21:T:56:MET:HG3	21:T:88:VAL:HG21	1.68	0.76
12:K:77:MET:O	12:K:78:GLN:HG3	1.86	0.76
13:L:110:VAL:O	13:L:122:THR:HG21	1.85	0.76
1:A:1004:A:H5''	1:A:1025:U:C5	2.20	0.75
1:A:1278:U:H5''	1:A:1279:A:H5'	1.68	0.75
7:F:100:ASN:HD22	19:R:23:LYS:HG2	1.51	0.75
1:A:1064:G:H4'	1:A:1065:U:H5'	1.68	0.75
1:A:1391:U:H2'	1:A:1392:G:C8	2.21	0.75
10:I:10:ARG:HG2	10:I:75:ASP:HB2	1.68	0.75
1:A:1152:A:H5''	11:J:13:HIS:CD2	2.21	0.75
20:S:70:LYS:O	20:S:72:GLY:N	2.20	0.75
1:A:1281:U:H5'	1:A:1282:C:C5	2.20	0.75
1:A:501:C:H2'	1:A:502:G:H8	1.52	0.75
1:A:761:G:C2	18:Q:105:ALA:HB3	2.21	0.75
4:C:191:THR:HG22	4:C:192:THR:N	1.99	0.75
1:A:1497:G:C2'	1:A:1498:U:H5'	2.16	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:25:PRO:C	13:L:27:LEU:H	1.86	0.75
3:B:80:ILE:HD13	3:B:212:GLN:HB2	1.69	0.75
4:C:174:PRO:HB2	4:C:177:THR:CG2	2.17	0.75
10:I:48:GLU:HA	10:I:51:ARG:NH1	2.02	0.75
11:J:61:GLU:OE1	15:N:45:ARG:NH1	2.19	0.75
4:C:38:ARG:HH11	4:C:38:ARG:HG3	1.52	0.75
5:D:8:VAL:HG21	5:D:115:ARG:NH1	2.02	0.74
21:T:54:LYS:HG3	21:T:100:ILE:HD13	1.67	0.74
1:A:1064:G:H4'	1:A:1065:U:C5'	2.18	0.74
19:R:36:ASN:HD22	19:R:38:GLU:HG2	1.50	0.74
3:B:122:PHE:HE2	3:B:139:LYS:HG2	1.51	0.74
1:A:8:A:N6	5:D:209:ARG:HB2	2.03	0.74
15:N:14:PRO:C	15:N:16:PHE:H	1.88	0.74
18:Q:21:VAL:HG21	18:Q:59:ILE:HD11	1.70	0.74
1:A:839:U:O2	1:A:839:U:H2'	1.87	0.74
14:M:4:ILE:HG22	14:M:5:ALA:N	2.03	0.74
1:A:434:U:H2'	1:A:435:C:C6	2.23	0.74
5:D:191:ARG:O	5:D:191:ARG:HD2	1.87	0.74
10:I:70:LYS:O	10:I:74:ILE:HG13	1.88	0.74
14:M:88:ARG:HD2	20:S:3:ARG:HH21	1.52	0.74
1:A:1278:U:H5''	1:A:1279:A:C5'	2.18	0.74
1:A:129(A):G:O2'	1:A:190(E):U:H2'	1.88	0.74
7:F:101:ALA:HA	19:R:28:GLU:HB3	1.69	0.74
8:G:46:ALA:O	8:G:50:ILE:HG13	1.87	0.74
12:K:54:ARG:O	12:K:57:THR:HG22	1.86	0.74
1:A:1498:U:H4'	1:A:1519:A:H2	1.51	0.74
5:D:35:ARG:O	5:D:36:ARG:HB2	1.87	0.74
14:M:14:ARG:HG3	14:M:44:ARG:NH1	2.03	0.74
1:A:975:A:H5'	1:A:975:A:C8	2.23	0.74
7:F:26:ILE:HG21	7:F:63:TYR:HE2	1.53	0.74
4:C:107:GLN:NE2	4:C:107:GLN:H	1.86	0.73
6:E:93:PRO:CG	9:H:105:ARG:HE	2.01	0.73
1:A:1250:A:H4'	10:I:68:GLY:H	1.51	0.73
5:D:114:ARG:HG3	5:D:114:ARG:HH11	1.51	0.73
11:J:53:PRO:HA	15:N:41:ARG:HH21	1.53	0.73
1:A:1490:C:H2'	1:A:1491:G:H8	1.51	0.73
13:L:33:ARG:HD3	13:L:62:SER:HB3	1.70	0.73
4:C:110:ASN:HD21	4:C:140:ARG:HB3	1.53	0.73
11:J:30:SER:O	11:J:78:ASN:HB2	1.89	0.73
14:M:59:TYR:O	14:M:63:THR:HB	1.89	0.73
8:G:18:TYR:CD2	8:G:59:LEU:HB2	2.24	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:101:ALA:HB2	19:R:28:GLU:HB2	1.69	0.73
1:A:173:U:H5'	1:A:197:A:O4'	1.89	0.73
1:A:1298:C:C5	8:G:114:ARG:HD3	2.23	0.73
15:N:27:CYS:SG	15:N:29:ARG:HB2	2.29	0.73
18:Q:45:HIS:NE2	18:Q:47:PRO:HG3	2.02	0.73
20:S:22:LEU:HD22	20:S:28:LYS:HB2	1.69	0.73
1:A:1241:G:H2'	1:A:1242:C:C6	2.23	0.73
4:C:43:LEU:HD23	4:C:43:LEU:N	2.04	0.73
5:D:170:VAL:HG12	5:D:174:LEU:HB2	1.70	0.73
1:A:405:U:H3'	1:A:406:G:H5'	1.71	0.72
4:C:23:TYR:CD2	4:C:24:ALA:N	2.57	0.72
5:D:24:GLU:HG2	5:D:25:ARG:H	1.52	0.72
10:I:78:LYS:HD3	10:I:101:PHE:HD2	1.55	0.72
9:H:9:MET:SD	9:H:32:LYS:HG2	2.29	0.72
14:M:78:ILE:HA	14:M:81:LEU:HD21	1.71	0.72
5:D:25:ARG:HH12	5:D:30:LYS:HB3	1.54	0.72
16:O:45:VAL:HG12	16:O:46:HIS:H	1.53	0.72
1:A:1040:U:H2'	1:A:1041:A:C8	2.23	0.72
5:D:187:ARG:NE	5:D:188:LEU:H	1.84	0.72
5:D:32:ALA:C	5:D:34:GLU:H	1.93	0.72
12:K:84:VAL:HG21	19:R:88:LYS:HD3	1.71	0.72
1:A:1226:C:H5''	14:M:103:THR:OG1	1.89	0.72
12:K:110:ASP:HB2	19:R:88:LYS:CD	2.14	0.72
1:A:992:U:H4'	1:A:993:G:O5'	1.89	0.72
6:E:80:ILE:HD12	6:E:91:LEU:HB2	1.69	0.72
10:I:79:LEU:HD13	10:I:83:ARG:HD2	1.72	0.72
11:J:22:LYS:HE2	11:J:90:LEU:HB2	1.72	0.72
1:A:701:C:H5'	1:A:703:G:O4'	1.90	0.72
3:B:8:LYS:O	3:B:9:GLU:HB2	1.87	0.72
19:R:74:ARG:HB3	19:R:81:PHE:CE1	2.25	0.72
1:A:1355:G:O2'	1:A:1356:G:H5'	1.90	0.71
1:A:1372:U:OP1	10:I:71:SER:HB3	1.89	0.71
1:A:243:A:C4'	1:A:244:U:H5'	2.20	0.71
3:B:84:GLU:HB3	3:B:219:VAL:CG2	2.17	0.71
14:M:78:ILE:HG22	14:M:82:MET:HE3	1.72	0.71
17:P:28:ARG:HG3	17:P:29:ASP:OD2	1.90	0.71
1:A:1475:G:H2'	1:A:1476:G:C8	2.25	0.71
5:D:29:PRO:O	5:D:30:LYS:HG3	1.90	0.71
9:H:1:MET:HG2	9:H:2:LEU:N	2.05	0.71
1:A:1189:C:OP1	11:J:51:ARG:NH2	2.23	0.71
1:A:840:C:H5''	1:A:841:U:OP1	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:116:GLU:HG2	3:B:153:ARG:NH1	2.04	0.71
1:A:953:G:H1'	14:M:125:ARG:HB3	1.71	0.71
4:C:29:TYR:OH	15:N:54:PRO:HG2	1.91	0.71
1:A:195:A:H4'	21:T:68:LYS:HE2	1.71	0.71
4:C:188:LEU:CD1	4:C:189:ALA:H	2.04	0.71
20:S:15:LEU:HA	20:S:18:LYS:HB3	1.73	0.71
1:A:382:A:H2'	1:A:383:A:H8	1.55	0.71
1:A:448:A:OP2	1:A:485:G:N2	2.24	0.71
3:B:42:ILE:HD11	3:B:189:ASP:HB2	1.72	0.71
11:J:5:ARG:HA	11:J:73:ASP:OD1	1.91	0.71
4:C:188:LEU:HD13	4:C:189:ALA:H	1.56	0.71
1:A:923:A:OP1	6:E:21:ALA:HB2	1.90	0.71
13:L:83:VAL:HG22	13:L:84:LEU:H	1.55	0.71
1:A:135:C:O2	17:P:1:MET:HB2	1.90	0.71
1:A:791:G:H2'	1:A:792:A:H5'	1.73	0.71
4:C:3:ASN:N	4:C:3:ASN:ND2	2.32	0.71
11:J:39:PRO:O	11:J:40:LEU:HB2	1.89	0.71
21:T:57:ARG:HH21	21:T:100:ILE:CG2	2.03	0.71
1:A:254:G:O2'	1:A:255:G:H5'	1.91	0.70
11:J:32:ALA:HB2	11:J:75:ILE:O	1.91	0.70
16:O:39:LEU:HD22	16:O:56:LEU:HD13	1.71	0.70
18:Q:76:LEU:HD23	18:Q:77:VAL:N	2.06	0.70
1:A:1028:C:H2'	1:A:1029:C:C6	2.25	0.70
1:A:1006:C:H2'	1:A:1007:C:C6	2.26	0.70
1:A:760:G:O6	18:Q:105:ALA:HB2	1.91	0.70
7:F:86:ARG:O	7:F:87:ARG:HG2	1.92	0.70
12:K:27:ASN:HA	12:K:56:GLY:HA2	1.73	0.70
6:E:12:LEU:HD13	6:E:31:LEU:HB2	1.70	0.70
16:O:26:GLU:OE1	16:O:77:ARG:HD2	1.90	0.70
1:A:1141:C:H2'	1:A:1142:G:H8	1.57	0.70
19:R:86:VAL:O	19:R:87:ARG:HB2	1.90	0.70
1:A:1498:U:H4'	1:A:1519:A:C2	2.26	0.70
3:B:139:LYS:O	3:B:143:GLU:HG2	1.90	0.70
7:F:21:LEU:O	7:F:24:GLU:HB3	1.91	0.70
1:A:1148:U:H2'	1:A:1149:C:O4'	1.91	0.70
4:C:120:VAL:O	4:C:124:ILE:HG13	1.90	0.70
13:L:47:LYS:CB	13:L:48:PRO:HD3	2.22	0.70
12:K:77:MET:HE3	12:K:80:VAL:HG22	1.73	0.70
4:C:107:GLN:H	4:C:107:GLN:CD	1.95	0.70
4:C:6:HIS:CD2	4:C:8:ILE:HB	2.27	0.70
20:S:17:GLU:O	20:S:21:GLU:HG3	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:76:GLN:HG3	3:B:206:ASP:OD1	1.92	0.69
4:C:179:ARG:HD3	4:C:206:GLU:HG2	1.72	0.69
4:C:64:VAL:HB	4:C:99:VAL:CG2	2.22	0.69
10:I:108:VAL:HG12	10:I:109:VAL:N	2.07	0.69
1:A:1426:C:H2'	1:A:1427:U:C6	2.27	0.69
12:K:84:VAL:HG11	12:K:95:ILE:HD11	1.73	0.69
1:A:1132:C:H2'	1:A:1133:G:H8	1.54	0.69
1:A:1167:A:H2'	1:A:1168:A:C8	2.28	0.69
1:A:677:U:H3	1:A:713:G:H22	1.41	0.69
1:A:939:G:H5''	8:G:102:ARG:NH2	2.08	0.69
1:A:918:A:H2'	1:A:919:A:C8	2.28	0.69
4:C:180:ALA:O	4:C:181:ASN:HB3	1.91	0.69
4:C:35:GLU:HG3	4:C:95:THR:HG21	1.74	0.69
14:M:3:ARG:HA	14:M:8:GLU:O	1.92	0.69
7:F:80:ARG:NH1	7:F:88:VAL:HB	2.07	0.69
11:J:34:VAL:HG22	11:J:74:ILE:HG23	1.75	0.69
18:Q:53:LEU:HD11	18:Q:85:VAL:HG11	1.73	0.69
1:A:824:C:H2'	1:A:825:G:H8	1.58	0.69
14:M:65:LYS:HG3	14:M:69:GLU:OE2	1.93	0.69
10:I:2:GLU:OE1	10:I:3:GLN:HB2	1.92	0.69
1:A:401:C:H2'	1:A:402:G:H8	1.57	0.69
4:C:130:VAL:HG12	4:C:134:ILE:HD11	1.73	0.69
8:G:23:VAL:O	8:G:27:ILE:HG13	1.93	0.69
1:A:1250:A:H4'	10:I:68:GLY:CA	2.23	0.69
13:L:47:LYS:CB	13:L:48:PRO:CD	2.71	0.69
13:L:83:VAL:HG22	13:L:84:LEU:N	2.07	0.69
16:O:87:ILE:O	16:O:88:ARG:HB2	1.93	0.69
19:R:39:VAL:O	19:R:42:ARG:HB2	1.93	0.69
1:A:1415:G:H2'	1:A:1416:G:H8	1.58	0.69
1:A:149:A:H2'	1:A:150:C:C6	2.26	0.69
1:A:1113:C:H4'	4:C:14:ILE:HD11	1.74	0.69
14:M:49:THR:HG22	14:M:51:ALA:N	2.04	0.69
1:A:946:A:H2'	1:A:947:G:C8	2.27	0.69
1:A:948:C:OP1	14:M:109:THR:HG22	1.92	0.69
8:G:138:LYS:C	8:G:138:LYS:HD3	2.13	0.69
8:G:95:ARG:HG2	8:G:99:LEU:CD1	2.23	0.69
14:M:11:ARG:HG3	14:M:12:ASN:H	1.54	0.69
17:P:20:VAL:HG23	17:P:34:GLU:O	1.93	0.69
1:A:99:C:H2'	1:A:101:A:C8	2.27	0.69
4:C:52:LEU:HD23	4:C:52:LEU:N	2.07	0.69
6:E:51:VAL:O	6:E:55:VAL:HG23	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:43:SER:HA	12:K:47:VAL:HG21	1.74	0.68
1:A:1004:A:H5''	1:A:1025:U:C4	2.27	0.68
1:A:1241:G:H2'	1:A:1242:C:H6	1.58	0.68
1:A:1343:G:H2'	1:A:1344:C:C6	2.28	0.68
1:A:1412:C:H2'	1:A:1413:A:C8	2.27	0.68
1:A:243:A:H4'	1:A:244:U:C5'	2.22	0.68
1:A:113:G:H1'	1:A:354:G:H5'	1.75	0.68
1:A:476:G:H2'	1:A:477:G:H8	1.58	0.68
5:D:33:MET:HE3	5:D:37:PRO:HB3	1.74	0.68
10:I:48:GLU:HA	10:I:51:ARG:HH11	1.57	0.68
10:I:8:GLY:HA2	10:I:79:LEU:CD1	2.18	0.68
18:Q:63:ARG:HG2	18:Q:64:PRO:HD2	1.75	0.68
19:R:37:VAL:O	19:R:41:LYS:HB2	1.93	0.68
1:A:1163:C:H2'	1:A:1164:G:H8	1.58	0.68
1:A:1499:A:O2'	1:A:1500:A:H5'	1.94	0.68
4:C:50:ALA:HB1	4:C:70:VAL:HG11	1.75	0.68
7:F:38:GLU:O	7:F:39:LYS:HB3	1.92	0.68
19:R:43:PHE:C	19:R:51:LEU:HD12	2.14	0.68
1:A:1411:C:H2'	1:A:1412:C:C6	2.28	0.68
3:B:143:GLU:O	3:B:147:LYS:HG3	1.93	0.68
21:T:54:LYS:HG3	21:T:100:ILE:CD1	2.23	0.68
1:A:1256:A:N6	1:A:1278:U:H1'	2.09	0.68
3:B:25:ASN:C	3:B:25:ASN:HD22	1.96	0.68
5:D:24:GLU:HG2	5:D:25:ARG:N	2.08	0.68
13:L:126:LYS:HD2	13:L:126:LYS:N	2.06	0.68
1:A:1281:U:H4'	1:A:1282:C:OP2	1.93	0.68
1:A:285:G:O2'	1:A:286:G:H5'	1.93	0.68
11:J:51:ARG:CB	11:J:59:SER:HB3	2.17	0.68
11:J:49:VAL:HG11	15:N:41:ARG:O	1.92	0.68
19:R:45:SER:C	19:R:47:THR:H	1.96	0.68
1:A:1160:G:O2'	1:A:1161:C:H5'	1.94	0.68
20:S:62:ILE:HD12	20:S:66:MET:HG3	1.76	0.68
1:A:1053:G:C3'	1:A:1054:C:H5'	2.23	0.68
4:C:79:ARG:HG2	4:C:82:GLU:HG2	1.74	0.68
14:M:40:ASN:HD22	14:M:41:PRO:CD	2.07	0.68
13:L:45:PRO:HD3	13:L:51:ALA:O	1.94	0.68
1:A:1257:U:H4'	1:A:1258:G:C5'	2.24	0.67
19:R:53:ARG:HH21	19:R:60:GLY:N	1.91	0.67
1:A:1286:A:H2'	1:A:1287:A:C5'	2.23	0.67
9:H:7:ALA:HA	9:H:85:ARG:HG3	1.76	0.67
18:Q:59:ILE:HG23	18:Q:71:PHE:HB3	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:996:A:H2'	1:A:997:U:C6	2.30	0.67
1:A:1124:G:H5'	11:J:35:SER:O	1.95	0.67
11:J:54:PHE:O	11:J:55:LYS:HG2	1.94	0.67
17:P:67:THR:HG22	17:P:68:ASP:N	2.09	0.67
1:A:1262:C:H2'	1:A:1263:C:C6	2.29	0.67
1:A:1289:A:H2'	1:A:1290:G:H5'	1.77	0.67
1:A:1533:C:O2	1:A:1533:C:H2'	1.93	0.67
4:C:8:ILE:HG23	4:C:16:ARG:HG2	1.75	0.67
6:E:80:ILE:H	6:E:80:ILE:HD12	1.58	0.67
22:V:6:ARG:CD	22:V:15:ARG:NH1	2.57	0.67
1:A:255:G:H1'	18:Q:16:GLN:NE2	2.09	0.67
6:E:43:LEU:HD11	6:E:132:ALA:HB1	1.77	0.67
14:M:36:LYS:HD2	14:M:59:TYR:CZ	2.30	0.67
6:E:40:ARG:HG2	6:E:68:GLU:OE2	1.95	0.67
19:R:55:ARG:HB3	19:R:55:ARG:HH11	1.58	0.67
19:R:87:ARG:HG2	19:R:87:ARG:HH11	1.60	0.67
1:A:560:U:H5'	1:A:566:G:N2	2.10	0.67
3:B:15:VAL:HG11	3:B:209:ARG:C	2.15	0.67
11:J:45:ARG:NH2	15:N:36:PHE:CD2	2.62	0.67
12:K:19:ALA:HB2	12:K:80:VAL:HG11	1.75	0.67
14:M:40:ASN:HD22	14:M:41:PRO:HD2	1.60	0.67
16:O:17:ARG:NH1	16:O:77:ARG:NH1	2.43	0.67
20:S:42:PRO:O	20:S:45:VAL:HG23	1.94	0.67
1:A:1510:U:H2'	1:A:1511:G:C8	2.30	0.67
1:A:975:A:O2'	15:N:32:SER:HB2	1.94	0.67
12:K:69:ALA:O	12:K:73:MET:HG2	1.95	0.67
18:Q:59:ILE:HG22	18:Q:71:PHE:CD1	2.29	0.67
1:A:1502:A:H2	1:A:1505:G:N1	1.92	0.67
1:A:130:A:OP2	1:A:190(E):U:H2'	1.95	0.67
4:C:150:LYS:HE2	4:C:152:ILE:HD11	1.76	0.67
6:E:64:ARG:O	6:E:65:ASN:HB3	1.95	0.67
9:H:36:LEU:HD12	9:H:59:LEU:HD13	1.77	0.67
6:E:118:ILE:HG22	6:E:119:LEU:N	2.10	0.67
13:L:47:LYS:HB2	13:L:48:PRO:CD	2.25	0.67
1:A:1305:G:H5'	22:V:4:GLY:HA3	1.75	0.67
1:A:107:G:C2'	1:A:108:G:H5'	2.25	0.66
1:A:1285:A:H4'	1:A:1286:A:O5'	1.94	0.66
1:A:650:G:O2'	1:A:651:C:H5'	1.95	0.66
3:B:102:LEU:HD21	3:B:162:ILE:HD11	1.75	0.66
11:J:39:PRO:HA	11:J:70:ARG:NH1	2.10	0.66
22:V:6:ARG:HD3	22:V:15:ARG:NH1	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:972:C:P	11:J:57:LYS:HD3	2.35	0.66
3:B:84:GLU:OE1	3:B:216:SER:HA	1.95	0.66
1:A:1248:A:H1'	10:I:70:LYS:NZ	2.11	0.66
11:J:4:ILE:HG22	11:J:6:ILE:HG23	1.76	0.66
11:J:8:LEU:CD2	11:J:96:ILE:HG12	2.24	0.66
13:L:6:THR:OG1	13:L:9:GLN:HG3	1.96	0.66
3:B:124:SER:HB2	3:B:125:PRO:CD	2.26	0.66
5:D:162:LEU:HD12	5:D:181:MET:HE2	1.76	0.66
10:I:4:TYR:CE2	10:I:88:TYR:HA	2.30	0.66
1:A:1202:G:C2'	1:A:1203:C:H5'	2.26	0.66
1:A:1425:U:H2'	1:A:1426:C:C6	2.31	0.66
1:A:838:G:H2'	1:A:839:U:H5''	1.77	0.66
3:B:23:ARG:NH1	3:B:24:TRP:HA	2.11	0.66
16:O:29:VAL:HG11	16:O:67:LEU:HD21	1.78	0.66
1:A:1195:C:H3'	1:A:1196:U:H5''	1.76	0.66
1:A:1347:G:O2'	1:A:1348:U:OP2	2.13	0.66
1:A:723:U:O2	1:A:723:U:H2'	1.95	0.66
16:O:26:GLU:HA	16:O:81:LEU:HD11	1.76	0.66
17:P:39:TYR:CD2	17:P:73:LEU:HD11	2.30	0.66
1:A:1037:C:H2'	1:A:1038:C:C6	2.31	0.66
4:C:6:HIS:HD2	4:C:8:ILE:HB	1.60	0.66
9:H:31:PHE:O	9:H:35:ILE:HG13	1.96	0.66
17:P:34:GLU:OE2	17:P:55:ARG:HD3	1.95	0.66
22:V:5:ASP:O	22:V:11:GLY:HA3	1.96	0.66
1:A:1040:U:H2'	1:A:1041:A:H8	1.60	0.66
1:A:390:C:O3'	17:P:28:ARG:NH2	2.29	0.66
11:J:40:LEU:HD22	11:J:41:PRO:HD2	1.77	0.66
16:O:31:LEU:HD12	16:O:31:LEU:H	1.59	0.66
1:A:1142:G:H2'	1:A:1143:G:O4'	1.96	0.66
1:A:1145:C:O2'	1:A:1146:A:H8	1.79	0.66
4:C:113:ALA:HB3	4:C:114:PRO:HD3	1.77	0.66
9:H:60:ARG:HG3	9:H:60:ARG:HH11	1.59	0.66
1:A:130:A:C8	18:Q:63:ARG:HG3	2.31	0.66
1:A:1202:G:O2'	1:A:1203:C:H5'	1.96	0.65
1:A:1423:G:O2'	1:A:1424:C:H5'	1.97	0.65
1:A:197:A:H4'	1:A:198:G:O5'	1.96	0.65
6:E:115:VAL:HG11	6:E:118:ILE:CD1	2.25	0.65
13:L:75:HIS:CD2	13:L:77:LEU:H	2.06	0.65
20:S:52:TYR:HA	20:S:56:GLN:O	1.96	0.65
1:A:489:C:H2'	1:A:490:G:H8	1.60	0.65
1:A:953:G:O4'	14:M:125:ARG:HA	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:103:VAL:CG2	9:H:110:ALA:HB2	2.27	0.65
1:A:812:C:HO2'	1:A:813:U:P	2.20	0.65
11:J:8:LEU:HB3	11:J:16:LEU:HD22	1.78	0.65
13:L:59:ARG:HD3	13:L:65:GLU:HG3	1.77	0.65
3:B:23:ARG:HH11	3:B:24:TRP:HA	1.60	0.65
4:C:190:ARG:HB3	4:C:190:ARG:NH1	2.12	0.65
5:D:140:VAL:CG1	5:D:146:ILE:HD11	2.24	0.65
6:E:35:GLY:HA3	6:E:112:LEU:HB3	1.76	0.65
16:O:17:ARG:HH11	16:O:17:ARG:HG3	1.61	0.65
18:Q:18:THR:OG1	18:Q:69:LYS:HE3	1.96	0.65
22:V:6:ARG:HD3	22:V:15:ARG:HH12	1.60	0.65
1:A:1527:C:O2'	1:A:1528:U:H5'	1.97	0.65
3:B:97:TRP:HZ2	3:B:102:LEU:HD13	1.61	0.65
1:A:1195:C:H2'	1:A:1197:G:H5'	1.79	0.65
5:D:4:TYR:O	5:D:5:ILE:HB	1.95	0.65
1:A:1021:G:H2'	1:A:1022:G:O4'	1.97	0.65
1:A:1225:A:N3	1:A:1225:A:H2'	2.12	0.65
1:A:1348:U:H2'	1:A:1349:A:H8	1.60	0.65
1:A:1428:A:H2'	1:A:1429:C:C6	2.31	0.65
1:A:353:A:H5'	1:A:353:A:H8	1.62	0.65
5:D:121:VAL:O	5:D:134:ASP:HA	1.96	0.65
6:E:79:GLU:CD	6:E:79:GLU:H	2.00	0.65
18:Q:15:MET:HE3	18:Q:43:LEU:HD22	1.78	0.65
3:B:215:LEU:O	3:B:219:VAL:HG23	1.97	0.65
5:D:142:PRO:HG2	5:D:187:ARG:NH2	2.12	0.65
10:I:81:ILE:O	10:I:85:LEU:HB2	1.97	0.65
19:R:53:ARG:HH21	19:R:60:GLY:H	1.45	0.65
1:A:509:A:H5'	5:D:54:TYR:HD2	1.62	0.64
1:A:761:G:N3	18:Q:105:ALA:HB3	2.12	0.64
5:D:16:GLY:O	5:D:33:MET:HE2	1.97	0.64
10:I:78:LYS:HD3	10:I:101:PHE:CD2	2.32	0.64
1:A:1037:C:H2'	1:A:1038:C:H6	1.62	0.64
10:I:118:LYS:O	10:I:119:ALA:HB3	1.95	0.64
14:M:102:ARG:HH11	14:M:102:ARG:HB2	1.62	0.64
14:M:117:VAL:HG12	14:M:118:ALA:N	2.12	0.64
17:P:8:ARG:HB2	17:P:28:ARG:NH1	2.12	0.64
5:D:70:ILE:HD11	5:D:100:ARG:NE	2.12	0.64
13:L:120:TYR:O	13:L:122:THR:HG23	1.98	0.64
1:A:1323:G:H2'	1:A:1324:A:C8	2.32	0.64
1:A:1411:C:H2'	1:A:1412:C:H6	1.61	0.64
13:L:60:LEU:CD1	13:L:85:ILE:HD12	2.22	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:12:SER:HB3	18:Q:20:THR:HB	1.80	0.64
21:T:54:LYS:HE3	21:T:100:ILE:HD11	1.79	0.64
6:E:15:ARG:O	6:E:15:ARG:HD2	1.98	0.64
6:E:51:VAL:HB	6:E:52:PRO:CD	2.25	0.64
9:H:6:ILE:HD11	9:H:31:PHE:CD2	2.32	0.64
11:J:78:ASN:O	11:J:80:LYS:N	2.30	0.64
3:B:184:VAL:N	3:B:198:ASP:OD2	2.31	0.64
1:A:1251:A:H4'	10:I:12:GLU:OE2	1.98	0.64
21:T:67:ALA:HA	21:T:73:HIS:H	1.62	0.64
1:A:1368:G:O2'	1:A:1369:C:H5'	1.98	0.64
1:A:920:U:H2'	1:A:921:U:C6	2.33	0.64
1:A:939:G:H2'	1:A:940:C:H6	1.63	0.64
5:D:190:ASP:HB2	5:D:193:ASP:OD2	1.98	0.64
6:E:31:LEU:HD22	6:E:43:LEU:HD21	1.79	0.64
1:A:1117:G:H5'	1:A:1117:G:H8	1.62	0.64
1:A:735:C:O2'	1:A:736:C:H5'	1.98	0.64
17:P:59:TRP:HB3	17:P:64:ALA:HB2	1.80	0.64
1:A:1306:A:N6	1:A:1331:G:H1'	2.13	0.64
6:E:75:THR:HG23	6:E:76:ILE:N	2.12	0.64
6:E:86:ALA:HB3	6:E:125:SER:HB2	1.80	0.64
3:B:69:LEU:HD12	3:B:155:LEU:HD11	1.80	0.63
4:C:14:ILE:HG22	4:C:15:THR:H	1.62	0.63
4:C:26:LYS:N	4:C:26:LYS:HD3	2.13	0.63
4:C:95:THR:C	4:C:97:LYS:H	2.02	0.63
14:M:37:THR:O	14:M:37:THR:HG22	1.98	0.63
15:N:57:ARG:HG2	15:N:58:LYS:H	1.63	0.63
21:T:89:ARG:HE	21:T:104:LEU:HD22	1.63	0.63
5:D:55:ALA:O	5:D:59:ARG:HG2	1.98	0.63
1:A:328:C:H4'	1:A:329:A:O5'	1.98	0.63
3:B:95:GLN:O	3:B:96:ARG:HD2	1.98	0.63
4:C:155:GLY:O	4:C:156:ARG:HB2	1.97	0.63
1:A:1131:G:H1	1:A:1143:G:N2	1.86	0.63
1:A:1329:A:P	14:M:28:ALA:HB3	2.38	0.63
1:A:254:G:OP1	18:Q:67:LYS:O	2.14	0.63
1:A:411:A:N9	1:A:413:G:H1'	2.14	0.63
1:A:620:C:N1	5:D:135:LEU:HD13	2.13	0.63
5:D:25:ARG:C	5:D:27:TYR:H	2.01	0.63
8:G:71:PRO:HD3	8:G:103:TRP:HZ3	1.62	0.63
1:A:190(F):G:H4'	1:A:190(G):G:OP2	1.98	0.63
3:B:28:PHE:CZ	3:B:189:ASP:HA	2.34	0.63
5:D:104:VAL:HG11	5:D:146:ILE:CD1	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:100:GLY:O	10:I:102:LEU:N	2.31	0.63
1:A:31:G:N1	1:A:48:C:H5''	2.14	0.63
19:R:47:THR:HG23	19:R:83:GLU:H	1.64	0.63
1:A:1484:C:H2'	1:A:1485:U:H6	1.63	0.63
1:A:657:G:H4'	16:O:28:GLN:HG2	1.80	0.63
4:C:34:LEU:HD23	4:C:34:LEU:O	1.98	0.63
19:R:25:THR:O	19:R:26:LEU:HB2	1.98	0.63
1:A:1250:A:H2'	1:A:1251:A:C8	2.33	0.63
1:A:149:A:O2'	1:A:150:C:H5'	1.99	0.63
1:A:1520:G:O2'	1:A:1521:G:H5'	1.99	0.63
1:A:267:C:H2'	1:A:268:C:C6	2.34	0.63
6:E:115:VAL:HG11	6:E:118:ILE:HD11	1.80	0.63
7:F:30:LEU:HB3	7:F:35:ALA:HB3	1.80	0.63
11:J:35:SER:HB2	11:J:72:VAL:O	1.98	0.63
11:J:90:LEU:H	11:J:91:PRO:HD2	1.62	0.63
17:P:43:LYS:HG3	17:P:48:TRP:CD2	2.34	0.63
1:A:1216:G:H5''	15:N:5:ALA:CB	2.29	0.63
1:A:1257:U:H4'	1:A:1258:G:H5'	1.80	0.63
4:C:52:LEU:H	4:C:52:LEU:CD2	2.11	0.63
6:E:80:ILE:HD13	6:E:91:LEU:HD12	1.80	0.63
15:N:59:ALA:O	15:N:60:SER:CB	2.47	0.62
3:B:75:LYS:HE3	3:B:78:GLN:OE1	1.98	0.62
4:C:84:ILE:O	4:C:88:ARG:HB2	1.98	0.62
11:J:54:PHE:CD2	11:J:55:LYS:HD3	2.33	0.62
1:A:1413:A:O2'	1:A:1414:U:H5'	1.98	0.62
1:A:1425:U:H2'	1:A:1426:C:H6	1.63	0.62
1:A:476:G:H2'	1:A:477:G:C8	2.34	0.62
3:B:142:LEU:HB3	3:B:146:GLN:NE2	2.14	0.62
10:I:111:ARG:HD3	10:I:112:LYS:N	2.14	0.62
13:L:42:THR:CG2	13:L:52:LEU:HB3	2.29	0.62
20:S:16:LEU:O	20:S:19:VAL:HG12	1.99	0.62
1:A:175:C:H2'	1:A:176:C:H6	1.64	0.62
3:B:42:ILE:HD12	3:B:203:GLY:HA2	1.80	0.62
1:A:1298:C:H2'	8:G:114:ARG:HH12	1.65	0.62
18:Q:79:SER:O	18:Q:80:GLY:O	2.17	0.62
3:B:27:LYS:HD3	3:B:195:ASP:OD2	1.99	0.62
3:B:178:ARG:O	9:H:71:GLY:HA2	2.00	0.62
13:L:47:LYS:HB3	13:L:48:PRO:HD3	1.79	0.62
14:M:62:ASN:O	14:M:63:THR:HB	2.00	0.62
1:A:107:G:H2'	1:A:108:G:H5'	1.81	0.62
1:A:1347:G:H22	1:A:1373:G:H2'	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1632:HYG:H1	24:A:1632:HYG:O14	1.98	0.62
24:A:1632:HYG:O30	24:A:1632:HYG:H12	1.99	0.62
1:A:370:C:O2'	1:A:371:G:H5'	1.98	0.62
1:A:477:G:H2'	1:A:478:A:H8	1.65	0.62
6:E:120:THR:HG23	6:E:121:LYS:N	2.13	0.62
7:F:95:GLU:H	7:F:95:GLU:CD	2.03	0.62
14:M:45:VAL:O	14:M:48:LEU:HB2	1.99	0.62
20:S:29:ARG:O	20:S:30:LEU:HB2	2.00	0.62
1:A:664:G:OP1	19:R:64:ARG:HD2	2.00	0.62
4:C:11:ARG:HH11	4:C:11:ARG:HG2	1.65	0.62
14:M:77:ASN:O	14:M:80:ARG:HB3	1.98	0.62
1:A:1216:G:H5''	15:N:5:ALA:HB2	1.82	0.62
1:A:1314:C:H2'	1:A:1315:U:C6	2.34	0.62
1:A:1366:C:H2'	1:A:1367:C:C6	2.32	0.62
5:D:196:LEU:C	5:D:198:VAL:H	2.02	0.62
11:J:38:ILE:HG13	11:J:72:VAL:H	1.65	0.62
16:O:55:GLY:O	16:O:59:MET:HG3	1.99	0.62
1:A:1305:G:C5'	22:V:4:GLY:HA3	2.29	0.62
1:A:791:G:H2'	1:A:792:A:C5'	2.29	0.62
13:L:55:VAL:HG12	13:L:56:ALA:N	2.14	0.62
7:F:69:GLU:N	7:F:69:GLU:OE1	2.33	0.61
8:G:139:GLU:O	8:G:143:ARG:HG3	2.00	0.61
13:L:38:THR:HG22	13:L:39:VAL:HG23	1.81	0.61
14:M:117:VAL:HG12	14:M:118:ALA:H	1.65	0.61
14:M:14:ARG:HB3	14:M:16:ASP:OD1	2.00	0.61
1:A:835:U:OP1	19:R:64:ARG:NH2	2.33	0.61
19:R:72:ARG:O	19:R:75:ILE:HG22	2.00	0.61
1:A:614:A:H2'	1:A:615:C:C6	2.34	0.61
3:B:18:GLY:CA	3:B:41:ILE:HA	2.30	0.61
11:J:8:LEU:HB2	11:J:70:ARG:HB2	1.81	0.61
19:R:38:GLU:OE1	19:R:38:GLU:N	2.33	0.61
4:C:47:LEU:N	4:C:47:LEU:HD12	2.16	0.61
6:E:24:ARG:HH11	6:E:24:ARG:HG2	1.66	0.61
7:F:36:ARG:HH11	7:F:36:ARG:HG2	1.64	0.61
1:A:1346:A:N1	1:A:1374:A:H5''	2.15	0.61
1:A:1356:G:H2'	1:A:1357:A:H8	1.62	0.61
1:A:524:G:H2'	1:A:525:C:C6	2.35	0.61
5:D:173:TRP:HB2	5:D:187:ARG:O	2.00	0.61
15:N:11:LYS:O	15:N:13:THR:N	2.33	0.61
1:A:1397:C:H4'	1:A:1398:A:OP2	2.00	0.61
1:A:1425:U:O2'	1:A:1426:C:H5'	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:17:LYS:HE3	13:L:17:LYS:HA	1.80	0.61
17:P:22:THR:HA	17:P:33:ILE:HG13	1.81	0.61
17:P:52:ASP:OD2	17:P:55:ARG:HB2	2.01	0.61
19:R:16:PRO:O	19:R:17:SER:HB3	2.00	0.61
1:A:1352:C:H2'	1:A:1353:G:C8	2.36	0.61
1:A:373:A:O2'	1:A:374:A:H5'	2.00	0.61
3:B:53:ARG:NH1	3:B:199:TYR:CD2	2.69	0.61
1:A:1307:U:H5'	14:M:109:THR:HG21	1.83	0.61
14:M:11:ARG:CG	14:M:12:ASN:N	2.62	0.61
18:Q:74:LEU:C	18:Q:74:LEU:HD23	2.21	0.61
1:A:1016:A:H2'	1:A:1017:G:O4'	2.01	0.61
1:A:1057:G:H5''	4:C:154:SER:CB	2.23	0.61
1:A:1218:C:H2'	1:A:1219:U:C6	2.35	0.61
1:A:1489:G:H2'	1:A:1490:C:C6	2.35	0.61
1:A:1112:C:O2	4:C:179:ARG:HB3	1.99	0.61
1:A:953:G:C1'	14:M:125:ARG:HA	2.31	0.61
16:O:38:ARG:O	16:O:41:GLU:HB3	2.00	0.61
20:S:30:LEU:HD23	20:S:48:THR:O	2.00	0.61
22:V:6:ARG:CD	22:V:15:ARG:HH12	2.14	0.61
1:A:344:A:H4'	1:A:345:C:OP2	2.01	0.61
1:A:646:U:H2'	1:A:647:C:C6	2.36	0.61
4:C:46:GLU:O	4:C:48:TYR:N	2.32	0.61
8:G:12:LEU:H	8:G:12:LEU:HD12	1.65	0.61
13:L:33:ARG:HD2	13:L:62:SER:HB3	1.82	0.61
3:B:23:ARG:O	3:B:24:TRP:O	2.19	0.61
4:C:47:LEU:CD1	4:C:47:LEU:H	2.14	0.61
4:C:91:LEU:CD2	4:C:99:VAL:HG13	2.24	0.61
10:I:65:VAL:HG21	10:I:73:GLN:HB3	1.81	0.61
11:J:62:HIS:HB3	15:N:59:ALA:CB	2.30	0.61
1:A:1320:C:N3	20:S:36:ARG:HG3	2.16	0.61
1:A:1195:C:H3'	1:A:1196:U:C5'	2.30	0.61
1:A:35:G:H2'	1:A:36:C:C6	2.36	0.61
11:J:49:VAL:HG12	15:N:41:ARG:HD2	1.82	0.61
19:R:47:THR:HA	19:R:83:GLU:HB2	1.81	0.61
14:M:88:ARG:HD2	20:S:3:ARG:NH2	2.16	0.61
1:A:580:U:H2'	1:A:581:G:O4'	2.01	0.60
14:M:22:ILE:HD12	14:M:25:ILE:HD12	1.83	0.60
21:T:56:MET:HE3	21:T:88:VAL:HG11	1.81	0.60
1:A:1163:C:H2'	1:A:1164:G:C8	2.36	0.60
1:A:437:U:H5''	5:D:155:LEU:HD22	1.82	0.60
3:B:17:PHE:HB3	3:B:44:LEU:HD11	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:112:SER:CB	4:C:115:LEU:HD12	2.31	0.60
8:G:85:TYR:HD1	8:G:154:TYR:HE1	1.48	0.60
14:M:52:GLU:HG2	14:M:55:ARG:NH2	2.15	0.60
4:C:13:GLY:HA3	15:N:57:ARG:CZ	2.30	0.60
1:A:1066:C:O2'	1:A:1067:A:H5'	2.01	0.60
1:A:232:G:H1'	1:A:262:A:N1	2.16	0.60
1:A:765:G:H1	1:A:812:C:H2'	1.66	0.60
4:C:110:ASN:ND2	4:C:140:ARG:HB3	2.15	0.60
6:E:12:LEU:CD1	6:E:31:LEU:HB2	2.31	0.60
1:A:1223:C:P	20:S:78:ARG:HH12	2.24	0.60
5:D:209:ARG:HG2	5:D:209:ARG:HH11	1.66	0.60
5:D:30:LYS:C	5:D:32:ALA:H	2.03	0.60
9:H:138:TRP:OXT	9:H:138:TRP:CE3	2.51	0.60
11:J:31:GLY:HA2	11:J:78:ASN:HD22	1.66	0.60
11:J:82:ILE:O	11:J:86:MET:HB2	2.01	0.60
13:L:27:LEU:C	13:L:29:GLY:N	2.53	0.60
1:A:1111:A:H2'	1:A:1112:C:C6	2.35	0.60
1:A:474:G:H2'	1:A:475:G:H8	1.66	0.60
4:C:191:THR:CG2	4:C:192:THR:N	2.64	0.60
5:D:3:ARG:HE	5:D:71:SER:HB3	1.67	0.60
9:H:51:VAL:HG21	9:H:60:ARG:CG	2.31	0.60
17:P:21:VAL:HG21	17:P:59:TRP:CG	2.36	0.60
1:A:1053:G:C4'	1:A:1054:C:H5'	2.31	0.60
1:A:513:C:H2'	1:A:514:C:H6	1.66	0.60
3:B:18:GLY:HA3	3:B:41:ILE:HA	1.84	0.60
4:C:47:LEU:HD12	4:C:47:LEU:H	1.66	0.60
9:H:14:ARG:O	9:H:18:ARG:HD3	2.00	0.60
11:J:38:ILE:HB	11:J:71:LEU:HB3	1.83	0.60
1:A:1047:G:C5'	15:N:4:LYS:HD2	2.27	0.60
17:P:20:VAL:HG21	17:P:32:TYR:CG	2.37	0.60
1:A:761:G:H5''	18:Q:102:GLY:HA3	1.82	0.60
1:A:10:A:OP2	6:E:126:ARG:HG2	2.02	0.60
1:A:1409:C:H2'	1:A:1410:G:H8	1.67	0.60
5:D:176:LEU:HA	5:D:183:GLY:HA2	1.83	0.60
10:I:49:PRO:HD3	10:I:78:LYS:HG2	1.83	0.60
13:L:55:VAL:HG12	13:L:56:ALA:H	1.66	0.60
14:M:33:ALA:HA	14:M:59:TYR:HE2	1.66	0.60
1:A:1168:A:H2'	1:A:1169:A:C8	2.36	0.60
1:A:1522:U:O2'	1:A:1523:G:H5'	2.02	0.60
7:F:14:LEU:HA	7:F:18:GLN:NE2	2.16	0.60
10:I:24:GLY:HA2	10:I:59:PHE:O	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:69:ASN:O	11:J:70:ARG:HD3	2.02	0.60
1:A:969:A:N6	14:M:124:PRO:HB3	2.16	0.60
19:R:61:LYS:O	19:R:65:ILE:HG13	2.01	0.60
20:S:33:THR:HG22	20:S:34:TRP:N	2.17	0.60
1:A:765:G:N2	1:A:812:C:O2'	2.34	0.60
3:B:206:ASP:CG	3:B:207:ALA:H	2.04	0.60
5:D:150:GLU:HG3	5:D:153:ARG:NH2	2.16	0.60
5:D:13:ARG:HA	5:D:33:MET:SD	2.42	0.60
20:S:16:LEU:C	20:S:18:LYS:H	2.04	0.60
1:A:1521:G:H2'	1:A:1522:U:C6	2.37	0.60
8:G:71:PRO:HD3	8:G:103:TRP:CZ3	2.37	0.60
12:K:72:ALA:HB1	12:K:77:MET:HG3	1.84	0.60
13:L:46:LYS:NZ	13:L:47:LYS:HG3	2.17	0.60
1:A:1223:C:OP1	1:A:1224:G:H3'	2.02	0.59
1:A:1229:A:OP2	14:M:114:ARG:HD3	2.02	0.59
1:A:16:A:O2'	1:A:17:U:H5'	2.01	0.59
1:A:518:C:O2'	13:L:50:SER:HB3	2.02	0.59
14:M:14:ARG:HG3	14:M:44:ARG:HH12	1.65	0.59
14:M:60:VAL:HG12	14:M:66:LEU:HD11	1.83	0.59
20:S:44:MET:O	20:S:47:HIS:HB2	2.02	0.59
1:A:222:U:H2'	1:A:223:U:C6	2.37	0.59
1:A:532:A:H2'	1:A:533:A:C5'	2.32	0.59
1:A:673:G:H2'	1:A:674:G:C8	2.37	0.59
3:B:178:ARG:NH1	3:B:178:ARG:HG3	2.08	0.59
6:E:12:LEU:C	6:E:12:LEU:HD22	2.23	0.59
11:J:53:PRO:HA	15:N:41:ARG:NH2	2.17	0.59
1:A:164:U:H2'	1:A:165:C:H6	1.67	0.59
3:B:101:MET:N	3:B:108:ILE:HD12	2.17	0.59
4:C:179:ARG:CD	4:C:206:GLU:HG2	2.32	0.59
7:F:25:ILE:HD12	7:F:82:ARG:HD2	1.83	0.59
9:H:29:SER:OG	9:H:32:LYS:HB2	2.03	0.59
11:J:12:ASP:HB3	11:J:15:THR:CG2	2.32	0.59
21:T:82:SER:O	21:T:86:ARG:HB2	2.02	0.59
1:A:547:A:H4'	1:A:548:G:O5'	2.02	0.59
4:C:33:LEU:O	4:C:33:LEU:HD23	2.01	0.59
4:C:92:ALA:C	4:C:94:LEU:H	2.05	0.59
6:E:9:LYS:CD	6:E:112:LEU:HD21	2.31	0.59
16:O:29:VAL:HG12	16:O:85:LEU:HD12	1.84	0.59
21:T:76:ALA:O	21:T:80:ARG:HG2	2.02	0.59
1:A:1054:C:OP1	1:A:1197:G:OP1	2.21	0.59
1:A:22:G:O2'	1:A:23:C:H5'	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:56:LEU:HA	16:O:59:MET:CE	2.23	0.59
17:P:51:VAL:O	17:P:52:ASP:HB3	2.00	0.59
21:T:59:ALA:O	21:T:63:ILE:HG13	2.01	0.59
1:A:321:A:O2'	1:A:322:C:H5'	2.03	0.59
1:A:731:G:O2'	1:A:732:C:H5'	2.03	0.59
8:G:116:ALA:HA	8:G:119:ARG:CZ	2.32	0.59
18:Q:67:LYS:O	18:Q:68:ARG:HB3	2.01	0.59
1:A:1369:C:H2'	1:A:1370:G:C8	2.38	0.59
1:A:1392:G:H21	1:A:1502:A:H8	1.48	0.59
5:D:127:THR:HG23	5:D:128:VAL:N	2.18	0.59
16:O:41:GLU:OE2	16:O:41:GLU:HA	2.02	0.59
1:A:1283:G:O2'	1:A:1284:C:H5'	2.02	0.59
1:A:392:G:H2'	1:A:393:A:C8	2.37	0.59
1:A:627:G:O2'	1:A:628:G:H5'	2.02	0.59
4:C:42:LEU:O	4:C:46:GLU:HG2	2.03	0.59
1:A:427:U:OP1	5:D:13:ARG:NH2	2.35	0.59
5:D:3:ARG:HH22	5:D:74:GLN:CD	2.06	0.59
9:H:83:ILE:O	9:H:83:ILE:HG23	2.03	0.59
1:A:1226:C:N4	14:M:104:ARG:HD2	2.17	0.59
18:Q:97:SER:HB2	18:Q:102:GLY:C	2.23	0.59
1:A:187:C:O2	21:T:105:SER:HB3	2.01	0.59
1:A:1236:A:H2'	1:A:1237:C:C6	2.38	0.59
1:A:1305:G:N2	1:A:1331:G:O2'	2.35	0.59
3:B:230:VAL:HG13	3:B:231:GLU:OE2	2.02	0.59
8:G:38:LEU:HD12	8:G:38:LEU:O	2.03	0.59
9:H:119:LEU:HD12	9:H:124:ALA:CA	2.23	0.59
11:J:40:LEU:HD12	11:J:69:ASN:HB3	1.85	0.59
16:O:3:ILE:HD12	16:O:3:ILE:N	2.18	0.59
1:A:1064:G:C4'	1:A:1065:U:H5'	2.33	0.59
1:A:1172:C:H2'	1:A:1173:G:H8	1.65	0.59
5:D:32:ALA:C	5:D:34:GLU:N	2.54	0.59
10:I:125:TYR:CD1	10:I:128:ARG:HB2	2.38	0.59
1:A:266:G:C8	1:A:266:G:H5''	2.38	0.58
1:A:371:G:C2'	1:A:372:C:H5'	2.33	0.58
3:B:124:SER:CB	3:B:125:PRO:HD2	2.32	0.58
4:C:25:GLY:CA	4:C:29:TYR:HB2	2.21	0.58
10:I:49:PRO:O	10:I:52:ALA:HB3	2.02	0.58
10:I:4:TYR:CD2	10:I:88:TYR:HA	2.38	0.58
11:J:8:LEU:HD23	11:J:96:ILE:HG12	1.83	0.58
1:A:17:U:H2'	1:A:18:C:C6	2.38	0.58
3:B:97:TRP:HZ3	3:B:176:GLU:OE2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:49:VAL:O	11:J:60:ARG:HA	2.04	0.58
12:K:48:ILE:HD13	12:K:63:LEU:CB	2.33	0.58
14:M:102:ARG:NH1	14:M:102:ARG:HB2	2.17	0.58
1:A:1238:A:C8	1:A:1303:C:H1'	2.39	0.58
3:B:124:SER:O	3:B:127:ILE:HG13	2.03	0.58
4:C:64:VAL:HB	4:C:99:VAL:HG21	1.85	0.58
5:D:162:LEU:HD12	5:D:181:MET:CE	2.33	0.58
5:D:28:SER:O	5:D:30:LYS:N	2.36	0.58
12:K:95:ILE:O	12:K:99:GLN:HG3	2.03	0.58
17:P:6:LEU:HB3	17:P:17:TYR:CD2	2.38	0.58
18:Q:97:SER:OG	18:Q:98:LEU:N	2.35	0.58
1:A:37:U:O2'	1:A:38:G:H5'	2.03	0.58
1:A:683:G:H2'	1:A:684:A:C8	2.38	0.58
1:A:828:A:H2'	1:A:829:G:O4'	2.03	0.58
1:A:911:U:H2'	1:A:912:C:C6	2.39	0.58
1:A:977:A:H2'	1:A:978:A:H5''	1.84	0.58
3:B:114:ARG:NH1	3:B:118:LEU:HD21	2.17	0.58
11:J:38:ILE:HD12	11:J:71:LEU:HD12	1.85	0.58
1:A:1278:U:H5	11:J:99:LYS:NZ	2.01	0.58
1:A:1038:C:H2'	1:A:1039:C:C6	2.39	0.58
1:A:1333:A:H2'	1:A:1334:G:O4'	2.03	0.58
1:A:1343:G:H1'	10:I:121:ARG:NH1	2.18	0.58
1:A:178:C:O2'	1:A:179:A:H5'	2.03	0.58
1:A:255:G:H2'	1:A:256:U:C6	2.39	0.58
3:B:12:GLU:OE2	3:B:213:LEU:HD11	2.04	0.58
4:C:155:GLY:O	4:C:196:LEU:HD22	2.03	0.58
7:F:33:TYR:HA	7:F:71:ARG:NH2	2.17	0.58
11:J:46:ARG:NH1	11:J:64:GLU:HG2	2.18	0.58
18:Q:26:GLN:O	18:Q:27:PHE:HB3	2.03	0.58
4:C:177:THR:O	4:C:177:THR:HG23	2.03	0.58
10:I:48:GLU:N	10:I:49:PRO:HD2	2.18	0.58
17:P:19:ILE:HG22	17:P:36:ILE:HG13	1.86	0.58
1:A:403:C:O2'	1:A:404:U:H5'	2.03	0.58
3:B:52:GLU:O	3:B:56:ARG:HB2	2.03	0.58
7:F:19:LEU:C	7:F:19:LEU:HD23	2.24	0.58
8:G:113:GLU:HG2	8:G:119:ARG:HG2	1.85	0.58
1:A:761:G:C4'	18:Q:103:GLY:H	2.08	0.58
1:A:1039:C:O2'	1:A:1040:U:H5'	2.03	0.58
3:B:16:HIS:NE2	3:B:214:ILE:CG1	2.67	0.58
4:C:108:ASN:C	4:C:110:ASN:H	2.06	0.58
1:A:1113:C:H1'	4:C:178:LEU:HD21	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1262:C:H2'	1:A:1263:C:H6	1.68	0.58
1:A:1515:C:O2'	1:A:1516:G:H5'	2.04	0.58
1:A:243:A:C5'	1:A:244:U:H5'	2.34	0.58
3:B:88:ALA:C	3:B:90:MET:H	2.07	0.58
4:C:60:ALA:O	4:C:61:ALA:HB3	2.03	0.58
7:F:10:LEU:HD11	7:F:59:TYR:HD2	1.69	0.58
7:F:94:GLN:HE21	19:R:32:ARG:HD3	1.68	0.58
13:L:27:LEU:C	13:L:29:GLY:H	2.07	0.58
1:A:1239:A:H62	1:A:1299:A:H62	1.50	0.58
5:D:8:VAL:O	5:D:10:ARG:N	2.37	0.58
6:E:105:VAL:HB	6:E:106:PRO:HD3	1.86	0.58
3:B:179:LYS:HA	9:H:72:PRO:HD3	1.85	0.58
9:H:101:PRO:HG3	9:H:133:LEU:HD11	1.85	0.57
17:P:20:VAL:HG22	17:P:21:VAL:O	2.03	0.57
1:A:1286:A:C8	1:A:1287:A:H5''	2.39	0.57
3:B:116:GLU:HG2	3:B:153:ARG:HH12	1.70	0.57
10:I:11:LYS:O	10:I:11:LYS:HG2	2.03	0.57
1:A:542:G:O2'	1:A:543:C:H5'	2.04	0.57
1:A:959:A:H3'	1:A:960:U:H5''	1.84	0.57
1:A:1026:G:H2'	1:A:1027:C:H5'	1.85	0.57
1:A:105:G:H2'	1:A:106:C:C6	2.39	0.57
1:A:1101:A:H4'	1:A:1102:A:O5'	2.04	0.57
1:A:1347:G:O2'	1:A:1348:U:P	2.62	0.57
3:B:132:LYS:C	3:B:134:GLU:H	2.07	0.57
8:G:69:VAL:HG21	8:G:104:LEU:HD21	1.86	0.57
16:O:70:LEU:HD12	16:O:78:TYR:HB2	1.84	0.57
1:A:1310:G:O6	20:S:2:PRO:HB3	2.04	0.57
1:A:1153:C:H2'	1:A:1154:G:H8	1.69	0.57
1:A:129(A):G:O2'	1:A:130:A:OP2	2.23	0.57
1:A:203:U:H5''	1:A:204:U:OP1	2.04	0.57
1:A:5:U:H2'	1:A:5:U:O2	2.04	0.57
7:F:4:TYR:OH	7:F:69:GLU:HB3	2.04	0.57
13:L:46:LYS:HZ3	13:L:47:LYS:HG3	1.69	0.57
1:A:824:C:H2'	1:A:825:G:C8	2.38	0.57
1:A:930:C:O2'	1:A:931:C:H5'	2.04	0.57
3:B:97:TRP:CZ2	3:B:101:MET:HB2	2.39	0.57
1:A:376:G:H5''	17:P:5:ARG:HD2	1.86	0.57
22:V:24:ARG:O	22:V:25:LYS:HB2	2.05	0.57
1:A:993:G:H4'	1:A:994:A:OP2	2.03	0.57
3:B:221:LEU:O	3:B:221:LEU:HD13	2.05	0.57
4:C:157:ILE:HD11	4:C:166:GLU:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:195:VAL:C	4:C:196:LEU:HD23	2.24	0.57
5:D:142:PRO:HA	5:D:185:PHE:O	2.04	0.57
5:D:152:SER:O	5:D:158:ILE:HD12	2.04	0.57
6:E:116:THR:HG23	6:E:117:ASP:OD2	2.03	0.57
9:H:103:VAL:HG21	9:H:110:ALA:HB2	1.86	0.57
1:A:881:G:P	13:L:12:ARG:HH22	2.27	0.57
13:L:86:ARG:HB3	13:L:101:VAL:HG23	1.87	0.57
17:P:10:GLY:HA3	17:P:15:PRO:HA	1.86	0.57
1:A:1229:A:H2'	1:A:1230:C:H6	1.69	0.57
1:A:164:U:H2'	1:A:165:C:C6	2.39	0.57
1:A:736:C:H2'	1:A:737:A:C8	2.39	0.57
3:B:19:HIS:NE2	3:B:206:ASP:HB3	2.20	0.57
1:A:1117:G:H4'	10:I:104:ARG:HH12	1.66	0.57
10:I:97:LYS:HG2	10:I:102:LEU:HD12	1.87	0.57
1:A:1286:A:H3'	1:A:1287:A:C5'	2.32	0.57
1:A:448:A:O2'	1:A:449:C:H5'	2.05	0.57
3:B:132:LYS:HG2	3:B:135:GLN:OE1	2.05	0.57
3:B:213:LEU:HD23	3:B:213:LEU:C	2.26	0.57
20:S:63:THR:O	20:S:66:MET:HG2	2.05	0.57
14:M:94:ARG:HH12	20:S:81:ARG:HD3	1.70	0.57
1:A:826:C:H2'	1:A:827:U:H6	1.70	0.57
4:C:188:LEU:CD1	4:C:195:VAL:HG13	2.35	0.57
4:C:35:GLU:CG	4:C:95:THR:HG21	2.35	0.57
10:I:43:ALA:O	10:I:45:ALA:N	2.38	0.57
11:J:49:VAL:HG13	15:N:41:ARG:HB2	1.85	0.57
12:K:84:VAL:HG23	12:K:110:ASP:HA	1.86	0.57
1:A:974:A:OP2	15:N:41:ARG:NH1	2.38	0.57
1:A:1072:G:H2'	1:A:1073:U:C6	2.39	0.56
1:A:1182:G:O2'	1:A:1183:A:OP2	2.23	0.56
1:A:188:C:H4'	21:T:89:ARG:NH1	2.19	0.56
1:A:780:A:O2'	1:A:781:A:H5''	2.04	0.56
3:B:12:GLU:C	3:B:14:GLY:N	2.58	0.56
4:C:83:ARG:C	4:C:85:ARG:H	2.07	0.56
6:E:72:GLN:O	6:E:75:THR:HG22	2.05	0.56
7:F:22:GLU:OE2	7:F:84:ASN:HB2	2.04	0.56
16:O:36:ILE:HD11	16:O:60:VAL:HA	1.86	0.56
17:P:6:LEU:HB3	17:P:17:TYR:HD2	1.70	0.56
22:V:6:ARG:HD2	22:V:15:ARG:NH1	2.19	0.56
22:V:7:ARG:O	22:V:7:ARG:HG3	2.05	0.56
3:B:122:PHE:O	3:B:123:ALA:HB2	2.04	0.56
3:B:88:ALA:O	3:B:90:MET:N	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:41:VAL:HG13	6:E:113:ALA:HA	1.86	0.56
22:V:17:THR:O	22:V:22:ARG:HD3	2.05	0.56
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.41	0.56
1:A:149:A:H2'	1:A:150:C:H6	1.70	0.56
1:A:112:G:H4'	1:A:389:A:H5''	1.87	0.56
1:A:435:C:H2'	1:A:436:C:C6	2.36	0.56
3:B:101:MET:HA	3:B:108:ILE:HD12	1.88	0.56
3:B:73:THR:HG23	3:B:95:GLN:O	2.05	0.56
15:N:21:TYR:HE2	15:N:23:ARG:NE	2.03	0.56
20:S:41:VAL:HG23	20:S:43:GLU:HG2	1.86	0.56
1:A:1231:G:O3'	10:I:126:SER:HB3	2.05	0.56
1:A:393:A:HO2'	1:A:394:G:H5'	1.68	0.56
5:D:112:VAL:HG23	5:D:161:ASN:HD21	1.68	0.56
6:E:80:ILE:CD1	6:E:91:LEU:HD12	2.35	0.56
17:P:81:ARG:CG	17:P:83:GLU:HG2	2.34	0.56
1:A:1117:G:H21	1:A:1180:A:H1'	1.71	0.56
1:A:1245:A:H2'	1:A:1246:C:C6	2.40	0.56
1:A:477:G:H2'	1:A:478:A:C8	2.39	0.56
3:B:130:ARG:HH22	4:C:207:VAL:CG2	2.17	0.56
8:G:145:ALA:C	8:G:147:ALA:H	2.08	0.56
14:M:81:LEU:HD22	14:M:81:LEU:N	2.20	0.56
20:S:5:LEU:O	20:S:6:LYS:CB	2.52	0.56
1:A:1141:C:H2'	1:A:1142:G:C8	2.40	0.56
1:A:1263:C:H2'	1:A:1264:C:C6	2.40	0.56
1:A:765:G:H22	1:A:812:C:HO2'	1.53	0.56
1:A:838:G:C2'	1:A:839:U:H5''	2.34	0.56
3:B:111:ARG:HB3	3:B:149:LEU:HD11	1.88	0.56
4:C:137:ALA:O	4:C:141:VAL:HG23	2.06	0.56
4:C:154:SER:OG	4:C:155:GLY:N	2.39	0.56
4:C:177:THR:CG2	4:C:180:ALA:HB2	2.36	0.56
9:H:120:THR:H	9:H:123:GLU:HB2	1.71	0.56
9:H:123:GLU:O	9:H:127:LEU:HD23	2.05	0.56
10:I:93:ARG:HD3	10:I:97:LYS:HE3	1.88	0.56
13:L:50:SER:O	13:L:51:ALA:HB2	2.05	0.56
15:N:59:ALA:O	15:N:60:SER:HB2	2.04	0.56
1:A:882:C:O2'	1:A:883:C:H5'	2.05	0.56
6:E:150:ARG:HH11	6:E:150:ARG:HG3	1.71	0.56
8:G:26:PHE:CE2	8:G:30:ILE:HD11	2.41	0.56
12:K:48:ILE:HD13	12:K:63:LEU:HB3	1.86	0.56
13:L:25:PRO:C	13:L:27:LEU:N	2.58	0.56
18:Q:53:LEU:C	18:Q:53:LEU:HD12	2.26	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:15:LEU:O	20:S:19:VAL:N	2.38	0.56
20:S:20:LEU:HA	20:S:23:ASN:ND2	2.20	0.56
1:A:112:G:N2	1:A:354:G:H5'	2.21	0.56
1:A:151:A:H2'	1:A:152:A:O4'	2.06	0.56
1:A:390:C:H2'	1:A:391:G:C8	2.41	0.56
1:A:818:G:C3'	1:A:819:A:H5''	2.35	0.56
5:D:43:HIS:CE1	5:D:46:LYS:HZ2	2.22	0.56
9:H:118:VAL:C	9:H:119:LEU:HD23	2.26	0.56
21:T:43:LEU:HD13	21:T:51:GLU:HG3	1.88	0.56
1:A:1257:U:H4'	1:A:1258:G:O5'	2.06	0.56
1:A:193:C:H2'	1:A:194:C:C6	2.41	0.56
1:A:883:C:O2'	1:A:884:U:H5'	2.06	0.56
8:G:21:VAL:HG23	8:G:22:LEU:N	2.20	0.56
13:L:60:LEU:CD2	13:L:66:VAL:HG22	2.36	0.56
18:Q:80:GLY:O	18:Q:81:ARG:HB3	2.06	0.56
19:R:48:GLY:O	19:R:74:ARG:NH2	2.37	0.56
1:A:1268:A:H2'	1:A:1269:A:C8	2.41	0.56
1:A:353:A:H5'	1:A:353:A:C8	2.41	0.56
17:P:4:ILE:HG13	17:P:64:ALA:HB1	1.88	0.56
1:A:1316:G:N2	1:A:1318:A:H3'	2.21	0.56
1:A:407:G:H2'	1:A:408:A:H8	1.71	0.56
1:A:877:C:O2'	1:A:878:G:H5'	2.05	0.56
5:D:107:ARG:HD2	5:D:173:TRP:CZ2	2.41	0.56
6:E:11:ILE:HB	6:E:31:LEU:HB3	1.88	0.56
11:J:96:ILE:HG22	11:J:97:GLU:H	1.69	0.56
13:L:126:LYS:N	13:L:126:LYS:CD	2.69	0.56
19:R:22:VAL:HG23	19:R:55:ARG:O	2.05	0.56
1:A:1347:G:H3'	10:I:108:VAL:O	2.06	0.55
1:A:743:U:H2'	1:A:744:C:C6	2.42	0.55
3:B:15:VAL:CG2	3:B:209:ARG:HG3	2.35	0.55
19:R:33:ASP:OD2	19:R:36:ASN:HB2	2.06	0.55
1:A:1287:A:H2'	1:A:1288:A:C8	2.41	0.55
1:A:755:G:OP2	16:O:65:ARG:HD2	2.06	0.55
1:A:969:A:H61	14:M:124:PRO:HB3	1.70	0.55
16:O:53:HIS:O	16:O:56:LEU:HB3	2.06	0.55
19:R:86:VAL:O	19:R:87:ARG:CB	2.53	0.55
1:A:358:U:H2'	1:A:359:U:C6	2.42	0.55
3:B:223:ILE:HG21	3:B:230:VAL:CG2	2.37	0.55
4:C:130:VAL:O	4:C:134:ILE:HG13	2.06	0.55
9:H:19:VAL:CG2	9:H:21:LYS:HD3	2.32	0.55
10:I:53:VAL:O	10:I:54:ASP:HB2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:C:C2	21:T:105:SER:HB3	2.41	0.55
1:A:1003:G:N2	1:A:1039:C:C2	2.75	0.55
1:A:357:G:O2'	1:A:358:U:H5'	2.07	0.55
1:A:501:C:H2'	1:A:502:G:C8	2.37	0.55
1:A:513:C:H2'	1:A:514:C:C6	2.42	0.55
3:B:188:ALA:O	3:B:202:PRO:HA	2.06	0.55
5:D:111:ALA:HB3	5:D:117:ALA:HB2	1.88	0.55
5:D:19:LEU:HD22	5:D:67:ILE:HG12	1.88	0.55
7:F:8:ILE:CD1	7:F:79:LEU:HD13	2.29	0.55
9:H:7:ALA:HB2	9:H:85:ARG:HD2	1.88	0.55
15:N:24:CYS:HB3	15:N:28:GLY:H	1.71	0.55
18:Q:97:SER:HB2	18:Q:103:GLY:CA	2.36	0.55
19:R:53:ARG:HE	19:R:59:SER:C	2.10	0.55
1:A:1091:U:O2	1:A:1093:A:C8	2.60	0.55
1:A:1427:U:H2'	1:A:1428:A:C8	2.41	0.55
1:A:268:C:H2'	1:A:269:C:H6	1.71	0.55
1:A:730:G:N2	1:A:765:G:H5''	2.22	0.55
3:B:17:PHE:H	3:B:44:LEU:HD21	1.71	0.55
5:D:131:ARG:H	5:D:131:ARG:HD2	1.71	0.55
6:E:102:ALA:HB1	6:E:120:THR:HG21	1.88	0.55
10:I:65:VAL:CG2	10:I:73:GLN:HB3	2.35	0.55
11:J:46:ARG:HH11	11:J:64:GLU:HB3	1.71	0.55
1:A:1000:U:H2'	1:A:1001:A:C8	2.41	0.55
1:A:1130:A:OP2	1:A:1130:A:H3'	2.07	0.55
1:A:382:A:C2	1:A:383:A:C4	2.94	0.55
3:B:15:VAL:HG11	3:B:210:SER:N	2.21	0.55
3:B:160:ASP:O	3:B:183:PRO:HD2	2.06	0.55
4:C:191:THR:HG21	4:C:193:TYR:CZ	2.42	0.55
4:C:38:ARG:NH1	4:C:38:ARG:HG3	2.22	0.55
8:G:133:GLY:O	8:G:137:LYS:HG3	2.07	0.55
10:I:10:ARG:HG2	10:I:75:ASP:CB	2.35	0.55
11:J:51:ARG:H	11:J:59:SER:CB	2.20	0.55
16:O:71:GLN:HB2	16:O:78:TYR:CD1	2.41	0.55
1:A:101:A:O2'	1:A:102:G:H5'	2.06	0.55
1:A:1154:G:O2'	1:A:1155:G:H5'	2.07	0.55
1:A:532:A:H2'	1:A:533:A:H5'	1.87	0.55
3:B:77:ALA:CB	3:B:211:ILE:HD13	2.10	0.55
4:C:116:VAL:HG21	4:C:202:ILE:HD11	1.87	0.55
4:C:76:VAL:HG11	4:C:103:VAL:HG21	1.89	0.55
7:F:76:ALA:O	7:F:80:ARG:HG3	2.06	0.55
11:J:27:ALA:HB2	11:J:85:LEU:HD21	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:70:ILE:CD1	13:L:77:LEU:HD12	2.36	0.55
14:M:3:ARG:HG2	14:M:9:ILE:HG23	1.89	0.55
20:S:67:VAL:O	20:S:69:HIS:N	2.40	0.55
1:A:546:G:OP1	5:D:73:ARG:HB2	2.07	0.55
1:A:659:U:O2'	1:A:660:G:H5'	2.07	0.55
1:A:748:C:H1'	1:A:749:C:H5	1.72	0.55
3:B:101:MET:CA	3:B:108:ILE:HD12	2.37	0.55
5:D:17:VAL:HG12	5:D:18:LYS:N	2.22	0.55
5:D:25:ARG:C	5:D:27:TYR:N	2.60	0.55
7:F:36:ARG:NH1	7:F:36:ARG:HG2	2.21	0.55
10:I:97:LYS:CG	10:I:102:LEU:HD12	2.36	0.55
1:A:954:G:H5"	14:M:120:LYS:HD3	1.88	0.55
16:O:29:VAL:HG12	16:O:85:LEU:HD11	1.88	0.55
19:R:73:ALA:CB	19:R:79:LEU:HD12	2.37	0.55
22:V:7:ARG:HA	22:V:12:LYS:HE2	1.89	0.55
1:A:162:A:H8	1:A:162:A:O5'	1.90	0.55
3:B:209:ARG:HE	3:B:239:VAL:HG11	1.71	0.55
4:C:83:ARG:C	4:C:85:ARG:N	2.59	0.55
6:E:152:ARG:NH2	9:H:107:LEU:O	2.39	0.55
6:E:83:GLU:HG3	6:E:88:LYS:HG3	1.88	0.55
12:K:14:VAL:O	12:K:15:ALA:HB3	2.06	0.55
15:N:59:ALA:HB1	15:N:61:TRP:CZ3	2.42	0.55
16:O:28:GLN:OE1	16:O:66:LEU:HD11	2.07	0.55
20:S:7:LYS:HG3	20:S:7:LYS:O	2.07	0.55
1:A:1381:U:O2'	1:A:1382:C:H5'	2.07	0.55
1:A:972:C:O5'	11:J:57:LYS:HD3	2.07	0.55
5:D:36:ARG:N	5:D:37:PRO:CD	2.58	0.55
8:G:108:ALA:O	8:G:119:ARG:HD2	2.06	0.55
3:B:178:ARG:NH1	9:H:71:GLY:O	2.40	0.55
13:L:55:VAL:CG1	13:L:67:THR:HG23	2.36	0.55
1:A:192:U:H1'	21:T:103:GLY:HA2	1.88	0.55
1:A:1060:C:O2'	1:A:1061:G:H5'	2.07	0.54
1:A:204:U:H4'	1:A:216:G:O5'	2.05	0.54
1:A:972:C:OP1	11:J:57:LYS:NZ	2.37	0.54
6:E:15:ARG:HD3	6:E:26:PHE:CD2	2.41	0.54
6:E:84:PHE:CE2	6:E:133:TYR:HD1	2.25	0.54
8:G:53:LYS:O	8:G:54:THR:HG23	2.07	0.54
10:I:93:ARG:NH1	10:I:97:LYS:NZ	2.54	0.54
11:J:45:ARG:NH1	11:J:45:ARG:CB	2.63	0.54
13:L:126:LYS:H	13:L:126:LYS:CD	2.20	0.54
15:N:9:LYS:HD3	15:N:9:LYS:C	2.28	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:26:LEU:HD11	19:R:39:VAL:HG23	1.89	0.54
20:S:43:GLU:H	20:S:43:GLU:CD	2.09	0.54
1:A:1454:G:O2'	1:A:1455:G:H5'	2.06	0.54
5:D:145:GLU:HG3	5:D:184:LYS:HE2	1.88	0.54
5:D:16:GLY:O	5:D:33:MET:CE	2.56	0.54
6:E:87:SER:HB3	6:E:131:ILE:HD13	1.89	0.54
1:A:921:U:O2	6:E:19:MET:HB2	2.07	0.54
11:J:23:ILE:N	11:J:23:ILE:HD12	2.22	0.54
11:J:96:ILE:HG22	11:J:97:GLU:N	2.22	0.54
16:O:17:ARG:NH1	16:O:77:ARG:HH11	2.05	0.54
1:A:1202:G:H2'	1:A:1203:C:H5'	1.90	0.54
1:A:694:A:H5'	12:K:53:SER:HB2	1.89	0.54
1:A:794:A:H2'	1:A:795:C:C6	2.42	0.54
1:A:911:U:H2'	1:A:912:C:H6	1.72	0.54
5:D:173:TRP:CD2	5:D:189:PRO:HB3	2.42	0.54
11:J:36:GLY:O	11:J:72:VAL:HA	2.07	0.54
1:A:706:A:C1'	12:K:29:ILE:HD11	2.37	0.54
4:C:29:TYR:CZ	15:N:54:PRO:HG2	2.42	0.54
16:O:60:VAL:O	16:O:64:ARG:HG2	2.07	0.54
20:S:40:ILE:HG21	20:S:62:ILE:CD1	2.38	0.54
1:A:983:A:H5'	1:A:984:C:OP2	2.06	0.54
4:C:147:LYS:HE2	4:C:205:GLY:HA2	1.89	0.54
4:C:188:LEU:O	4:C:189:ALA:HB2	2.07	0.54
1:A:542:G:OP1	5:D:10:ARG:NH2	2.40	0.54
6:E:101:ILE:O	6:E:120:THR:HB	2.07	0.54
7:F:4:TYR:CZ	7:F:72:VAL:HG21	2.43	0.54
11:J:81:THR:C	11:J:83:GLU:H	2.11	0.54
1:A:965:A:C2	14:M:124:PRO:HB2	2.42	0.54
16:O:87:ILE:CG2	16:O:88:ARG:N	2.70	0.54
18:Q:15:MET:CE	18:Q:43:LEU:HD22	2.37	0.54
21:T:50:GLU:HG2	21:T:100:ILE:HG13	1.89	0.54
1:A:1308:U:H2'	1:A:1309:G:C8	2.42	0.54
1:A:189:G:H2'	1:A:190:C:C6	2.43	0.54
1:A:443:C:O2'	1:A:444:C:H5'	2.07	0.54
3:B:74:LYS:HZ3	3:B:76:GLN:HB2	1.71	0.54
4:C:191:THR:HG22	4:C:193:TYR:H	1.73	0.54
6:E:15:ARG:O	6:E:16:THR:O	2.25	0.54
8:G:15:ASP:OD1	8:G:17:VAL:HB	2.07	0.54
8:G:37:ASN:ND2	10:I:41:VAL:HG23	2.22	0.54
11:J:44:VAL:HG22	11:J:66:ARG:HB3	1.88	0.54
14:M:8:GLU:HG3	14:M:22:ILE:HG23	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:26:GLU:HA	16:O:81:LEU:CD1	2.37	0.54
16:O:39:LEU:HD22	16:O:56:LEU:HB2	1.89	0.54
4:C:48:TYR:HA	4:C:52:LEU:HD22	1.90	0.54
10:I:111:ARG:NH1	10:I:111:ARG:HG3	2.22	0.54
14:M:6:GLY:O	14:M:7:VAL:HG22	2.08	0.54
15:N:3:ARG:NH2	15:N:6:LEU:HG	2.22	0.54
18:Q:34:LYS:HD3	18:Q:35:VAL:O	2.08	0.54
18:Q:66:SER:O	18:Q:70:ARG:NH1	2.40	0.54
19:R:73:ALA:HB3	19:R:79:LEU:HD12	1.89	0.54
1:A:1425:U:H3	1:A:1475:G:H1	1.54	0.54
1:A:865:A:H5'	1:A:1078:U:O4	2.07	0.54
1:A:974:A:H8	1:A:974:A:OP1	1.91	0.54
3:B:144:ARG:HG3	3:B:145:LEU:H	1.72	0.54
9:H:103:VAL:HB	9:H:108:GLY:O	2.08	0.54
11:J:3:LYS:N	11:J:75:ILE:HA	2.23	0.54
11:J:84:GLN:O	11:J:88:LEU:HD12	2.08	0.54
13:L:75:HIS:HD2	13:L:77:LEU:N	1.97	0.54
14:M:81:LEU:HA	14:M:84:ILE:HG12	1.89	0.54
15:N:9:LYS:HD3	15:N:9:LYS:O	2.07	0.54
17:P:74:LEU:O	17:P:79:VAL:HG23	2.07	0.54
18:Q:68:ARG:O	18:Q:69:LYS:HB2	2.06	0.54
1:A:1014:A:H2'	1:A:1015:A:C8	2.43	0.54
1:A:106:C:O2	1:A:379:C:H4'	2.07	0.54
3:B:74:LYS:HZ1	3:B:206:ASP:HA	1.68	0.54
9:H:56:LYS:HD2	9:H:56:LYS:N	2.22	0.54
14:M:16:ASP:HB3	14:M:41:PRO:HB3	1.88	0.54
15:N:41:ARG:HG3	15:N:42:ILE:N	2.22	0.54
1:A:807:A:H2'	1:A:808:C:C6	2.42	0.54
1:A:818:G:C2'	1:A:819:A:H5''	2.37	0.54
3:B:92:TYR:CD1	3:B:151:GLY:HA3	2.43	0.54
6:E:112:LEU:N	6:E:112:LEU:HD23	2.22	0.54
8:G:83:ALA:HB3	8:G:85:TYR:CE2	2.42	0.54
10:I:108:VAL:CG1	10:I:109:VAL:N	2.70	0.54
16:O:78:TYR:CZ	16:O:82:ILE:HD11	2.42	0.54
18:Q:60:ILE:HD13	18:Q:61:GLU:N	2.23	0.54
1:A:336:C:O2'	1:A:337:C:H5'	2.07	0.54
3:B:134:GLU:C	3:B:136:VAL:H	2.11	0.54
4:C:32:LEU:HD21	4:C:59:ARG:HD2	1.90	0.54
9:H:18:ARG:N	9:H:18:ARG:HD2	2.23	0.54
9:H:23:SER:OG	9:H:60:ARG:HD2	2.08	0.54
11:J:16:LEU:HD13	11:J:70:ARG:HG2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:45:ARG:O	11:J:64:GLU:HA	2.08	0.54
1:A:1524:C:OP1	12:K:120:ARG:NH1	2.41	0.54
16:O:39:LEU:HD13	16:O:59:MET:CE	2.38	0.54
18:Q:76:LEU:HD23	18:Q:76:LEU:C	2.28	0.54
1:A:187:C:N3	21:T:105:SER:HB3	2.23	0.54
1:A:1004:A:H5''	1:A:1025:U:O4	2.08	0.53
1:A:1441:G:H4'	1:A:1442:G:C5	2.44	0.53
1:A:1417:G:H2'	1:A:1482:G:H22	1.72	0.53
1:A:148:G:H2'	1:A:149:A:C8	2.43	0.53
1:A:1521:G:H2'	1:A:1522:U:H6	1.73	0.53
1:A:613:C:O2'	1:A:614:A:H5'	2.08	0.53
3:B:228:GLY:O	3:B:229:VAL:C	2.47	0.53
5:D:187:ARG:NH2	5:D:188:LEU:HG	2.12	0.53
5:D:39:PRO:HG2	5:D:44:GLY:HA2	1.90	0.53
9:H:17:THR:HB	9:H:78:GLN:OE1	2.08	0.53
1:A:1232:U:H5''	10:I:124:GLN:O	2.08	0.53
12:K:15:ALA:HA	12:K:77:MET:HA	1.88	0.53
13:L:43:VAL:HG12	13:L:44:THR:N	2.23	0.53
19:R:55:ARG:HH11	19:R:55:ARG:CB	2.21	0.53
20:S:5:LEU:O	20:S:6:LYS:HB2	2.08	0.53
3:B:19:HIS:CE1	3:B:206:ASP:HB3	2.43	0.53
4:C:152:ILE:HB	4:C:199:LYS:HB2	1.90	0.53
6:E:89:ILE:HD13	6:E:90:VAL:N	2.23	0.53
8:G:122:HIS:HA	8:G:125:MET:HE3	1.89	0.53
11:J:24:VAL:HG12	11:J:28:ARG:HE	1.73	0.53
11:J:30:SER:OG	11:J:81:THR:HA	2.07	0.53
21:T:10:LEU:O	21:T:12:ALA:N	2.40	0.53
1:A:1102:A:H2'	1:A:1103:C:C6	2.43	0.53
1:A:200:G:H2'	1:A:201:C:O4'	2.08	0.53
1:A:505:G:H2'	1:A:506:G:C8	2.43	0.53
1:A:812:C:O2'	1:A:813:U:P	2.66	0.53
1:A:913:A:H1'	1:A:914:A:O4'	2.09	0.53
3:B:144:ARG:HG3	3:B:145:LEU:N	2.22	0.53
4:C:145:GLY:O	4:C:146:ALA:O	2.26	0.53
4:C:191:THR:HG22	4:C:192:THR:H	1.71	0.53
5:D:107:ARG:HD2	5:D:173:TRP:HZ2	1.72	0.53
11:J:47:PHE:CE2	15:N:37:PHE:HE1	2.26	0.53
13:L:48:PRO:HG2	13:L:49:ASN:H	1.73	0.53
18:Q:29:HIS:CE1	18:Q:31:LEU:H	2.27	0.53
1:A:959:A:C2	1:A:1222:G:O4'	2.62	0.53
1:A:556:C:O2'	1:A:557:G:H5'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:97:TRP:CZ3	3:B:176:GLU:OE2	2.61	0.53
3:B:162:ILE:O	3:B:185:ILE:HD12	2.09	0.53
4:C:180:ALA:HB1	4:C:203:PHE:CE1	2.43	0.53
6:E:102:ALA:CB	6:E:120:THR:HG21	2.38	0.53
1:A:490:G:H2'	1:A:491:G:H8	1.74	0.53
1:A:826:C:H2'	1:A:827:U:C6	2.44	0.53
3:B:25:ASN:HD22	3:B:27:LYS:H	1.56	0.53
4:C:106:VAL:HG11	4:C:115:LEU:CD1	2.38	0.53
5:D:127:THR:CG2	5:D:128:VAL:N	2.71	0.53
6:E:120:THR:CG2	6:E:121:LYS:N	2.72	0.53
1:A:954:G:C5'	14:M:120:LYS:HD3	2.39	0.53
16:O:39:LEU:CD2	16:O:56:LEU:HB2	2.38	0.53
16:O:30:ALA:HA	16:O:85:LEU:HD21	1.90	0.53
17:P:20:VAL:HG23	17:P:34:GLU:C	2.29	0.53
19:R:27:GLY:O	19:R:29:PHE:HD2	1.90	0.53
21:T:57:ARG:HH21	21:T:100:ILE:HG23	1.72	0.53
1:A:260:G:H2'	1:A:261:U:C6	2.44	0.53
1:A:614:A:H2'	1:A:615:C:H6	1.74	0.53
1:A:986:A:H1'	20:S:54:GLY:O	2.09	0.53
3:B:162:ILE:C	3:B:185:ILE:HD12	2.29	0.53
3:B:53:ARG:NH1	3:B:199:TYR:HD2	2.06	0.53
3:B:69:LEU:HD22	3:B:71:VAL:HG22	1.90	0.53
14:M:81:LEU:O	14:M:89:GLY:HA3	2.08	0.53
15:N:8:GLU:O	15:N:11:LYS:HB2	2.09	0.53
1:A:229:U:H5''	17:P:33:ILE:HD13	1.89	0.53
1:A:392:G:H2'	1:A:393:A:H8	1.72	0.53
1:A:797:C:O2'	1:A:798:G:H5'	2.09	0.53
1:A:818:G:O2'	1:A:819:A:H5''	2.08	0.53
3:B:137:ARG:HB3	3:B:137:ARG:NH1	2.24	0.53
5:D:64:LEU:HG	5:D:198:VAL:HG11	1.91	0.53
8:G:12:LEU:N	8:G:12:LEU:HD12	2.24	0.53
9:H:23:SER:O	9:H:24:THR:HB	2.09	0.53
16:O:81:LEU:O	16:O:81:LEU:HD23	2.08	0.53
17:P:81:ARG:HB2	17:P:81:ARG:NH1	2.23	0.53
1:A:1070:U:H2'	1:A:1071:C:H6	1.72	0.53
1:A:255:G:H2'	1:A:256:U:H6	1.72	0.53
1:A:258:G:O2'	1:A:259:G:H5'	2.09	0.53
1:A:268:C:H2'	1:A:269:C:C6	2.43	0.53
1:A:476:G:O2'	1:A:477:G:H5'	2.09	0.53
3:B:187:LEU:HD13	3:B:187:LEU:O	2.09	0.53
4:C:172:ARG:HH12	4:C:174:PRO:HG3	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:35:GLU:CD	4:C:95:THR:HG21	2.29	0.53
15:N:14:PRO:HB2	15:N:16:PHE:O	2.09	0.53
4:C:37:GLN:NE2	15:N:52:GLN:OE1	2.39	0.53
18:Q:18:THR:HG23	18:Q:69:LYS:HE2	1.91	0.53
20:S:51:VAL:O	20:S:57:HIS:HA	2.09	0.53
1:A:1044:A:H2'	1:A:1045:C:C4'	2.39	0.53
1:A:1288:A:H1'	1:A:1352:C:O2'	2.08	0.53
1:A:650:G:C2'	1:A:651:C:H5'	2.39	0.53
10:I:105:ASP:OD1	10:I:107:ARG:HG3	2.09	0.53
13:L:45:PRO:HB2	13:L:49:ASN:O	2.09	0.53
13:L:85:ILE:HG23	13:L:98:TYR:HB2	1.91	0.53
15:N:12:ARG:O	15:N:14:PRO:N	2.42	0.53
1:A:1053:G:H4'	1:A:1054:C:H5'	1.91	0.53
1:A:1498:U:O4	24:A:1632:HYG:H24	2.09	0.53
1:A:287:U:O2'	1:A:288:A:H5'	2.09	0.53
1:A:403:C:H2'	1:A:404:U:H6	1.73	0.53
1:A:420:U:H2'	1:A:422:C:C5	2.44	0.53
1:A:853:G:O2'	1:A:854:G:H5'	2.09	0.53
1:A:948:C:O2'	1:A:949:A:H5'	2.09	0.53
4:C:10:PHE:CZ	4:C:178:LEU:HD13	2.44	0.53
8:G:70:LYS:HB3	8:G:96:GLN:HG2	1.91	0.53
14:M:5:ALA:O	14:M:6:GLY:C	2.48	0.53
19:R:19:LYS:O	19:R:20:ALA:HB3	2.09	0.53
1:A:575:G:OP1	1:A:575:G:H4'	2.08	0.52
3:B:124:SER:CB	3:B:125:PRO:CD	2.87	0.52
7:F:44:GLY:HA2	7:F:59:TYR:CE1	2.44	0.52
11:J:7:LYS:NZ	11:J:40:LEU:HD11	2.24	0.52
11:J:46:ARG:HH11	11:J:64:GLU:CB	2.22	0.52
13:L:97:ARG:HB2	13:L:98:TYR:CE1	2.44	0.52
1:A:1319:A:H5'	1:A:1320:C:OP1	2.09	0.52
1:A:1438:G:H2'	1:A:1439:C:C6	2.43	0.52
1:A:217:C:O2'	1:A:218:C:H5'	2.08	0.52
3:B:19:HIS:HB2	3:B:204:ASN:OD1	2.09	0.52
9:H:9:MET:HB2	9:H:32:LYS:HD3	1.91	0.52
14:M:33:ALA:HB2	14:M:64:TRP:CH2	2.44	0.52
14:M:78:ILE:HG22	14:M:82:MET:CE	2.39	0.52
1:A:1370:G:O2'	1:A:1371:G:H5'	2.10	0.52
1:A:1453:G:H2'	1:A:1454:G:O4'	2.10	0.52
1:A:190(E):U:O2'	18:Q:63:ARG:NH2	2.42	0.52
1:A:393:A:C2'	1:A:394:G:H5'	2.39	0.52
5:D:190:ASP:O	5:D:194:LEU:HD23	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:85:TYR:HD1	8:G:154:TYR:CE1	2.27	0.52
11:J:6:ILE:HD11	11:J:72:VAL:CG1	2.39	0.52
7:F:100:ASN:ND2	19:R:23:LYS:HG2	2.22	0.52
22:V:7:ARG:O	22:V:8:THR:HG23	2.09	0.52
1:A:1126:U:H1'	1:A:1280:A:C6	2.44	0.52
1:A:1172:C:O2'	1:A:1173:G:H5'	2.09	0.52
1:A:1248:A:H1'	10:I:70:LYS:HZ2	1.73	0.52
1:A:757:U:H2'	1:A:758:G:O4'	2.09	0.52
7:F:18:GLN:O	7:F:21:LEU:HB3	2.10	0.52
14:M:84:ILE:HG22	20:S:65:ASN:HD22	1.74	0.52
16:O:27:VAL:O	16:O:30:ALA:HB3	2.09	0.52
16:O:87:ILE:O	16:O:88:ARG:CB	2.57	0.52
1:A:1136:U:H5''	1:A:1137:C:OP2	2.10	0.52
1:A:1414:U:H2'	1:A:1415:G:C8	2.44	0.52
3:B:126:GLU:O	3:B:129:GLU:HB2	2.09	0.52
3:B:15:VAL:HG21	3:B:209:ARG:HG3	1.90	0.52
4:C:110:ASN:O	4:C:111:LEU:HD23	2.10	0.52
8:G:15:ASP:HB3	8:G:19:GLY:N	2.24	0.52
11:J:60:ARG:N	11:J:60:ARG:HD2	2.24	0.52
1:A:103:C:P	21:T:17:ARG:HH11	2.33	0.52
1:A:567:G:H2'	1:A:568:G:O4'	2.10	0.52
1:A:663:A:O2'	1:A:664:G:H5'	2.10	0.52
3:B:72:GLY:HA3	3:B:81:VAL:HG21	1.91	0.52
6:E:144:THR:HG22	6:E:145:LYS:N	2.25	0.52
13:L:119:LYS:O	13:L:120:TYR:HB2	2.10	0.52
11:J:62:HIS:CB	15:N:59:ALA:HB3	2.35	0.52
17:P:67:THR:CG2	17:P:68:ASP:N	2.73	0.52
1:A:47:C:C6	1:A:365:U:H2'	2.44	0.52
1:A:690:G:H2'	1:A:691:G:O4'	2.10	0.52
1:A:989:C:O2'	1:A:990:C:H5'	2.10	0.52
3:B:71:VAL:O	3:B:165:VAL:HG23	2.09	0.52
3:B:19:HIS:HD2	3:B:205:ASP:OD1	1.92	0.52
4:C:151:VAL:HG12	4:C:152:ILE:N	2.24	0.52
8:G:48:LYS:O	8:G:51:GLN:HB2	2.10	0.52
18:Q:17:LYS:HA	18:Q:46:ASP:O	2.10	0.52
21:T:33:ILE:HD13	21:T:63:ILE:HG12	1.92	0.52
1:A:1460:A:H2'	1:A:1461:G:O4'	2.10	0.52
3:B:12:GLU:C	3:B:14:GLY:H	2.12	0.52
3:B:119:GLU:CD	3:B:153:ARG:HH22	2.13	0.52
4:C:107:GLN:O	4:C:108:ASN:CB	2.57	0.52
9:H:121:ASP:HB2	9:H:125:ARG:HH21	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:9:ARG:CG	10:I:14:VAL:HG22	2.37	0.52
13:L:85:ILE:HG23	13:L:98:TYR:CB	2.39	0.52
1:A:1306:A:H2'	1:A:1307:U:O4'	2.10	0.52
1:A:543:C:O2'	1:A:544:G:H5'	2.09	0.52
1:A:744:C:H2'	1:A:745:C:C6	2.45	0.52
5:D:70:ILE:HD11	5:D:100:ARG:HD2	1.92	0.52
15:N:14:PRO:C	15:N:16:PHE:N	2.59	0.52
4:C:13:GLY:HA3	15:N:57:ARG:NH2	2.24	0.52
1:A:1264:C:H2'	1:A:1265:G:H8	1.75	0.52
3:B:18:GLY:HA2	3:B:42:ILE:H	1.75	0.52
14:M:15:VAL:HG23	14:M:43:THR:O	2.10	0.52
18:Q:59:ILE:CG2	18:Q:71:PHE:CD1	2.93	0.52
1:A:1286:A:H8	1:A:1287:A:H5''	1.75	0.51
4:C:190:ARG:HH11	4:C:190:ARG:CB	2.22	0.51
4:C:23:TYR:O	4:C:24:ALA:HB2	2.09	0.51
5:D:70:ILE:HD11	5:D:100:ARG:CD	2.40	0.51
6:E:103:GLY:O	6:E:107:ARG:HB3	2.09	0.51
7:F:97:PHE:HB2	19:R:32:ARG:NH1	2.25	0.51
8:G:41:ARG:O	8:G:42:ILE:C	2.47	0.51
12:K:54:ARG:HH11	12:K:54:ARG:CB	2.15	0.51
13:L:60:LEU:HD21	13:L:66:VAL:HG22	1.92	0.51
18:Q:104:LYS:NZ	18:Q:104:LYS:N	2.50	0.51
1:A:1028:C:H2'	1:A:1029:C:H6	1.71	0.51
1:A:1491:G:N2	1:A:1492:A:H62	2.06	0.51
1:A:1405:G:O6	24:A:1632:HYG:N7	2.42	0.51
1:A:459:G:H3'	1:A:460:A:C5'	2.39	0.51
3:B:10:LEU:HD23	3:B:48:MET:HG3	1.92	0.51
1:A:1368:G:P	10:I:112:LYS:O	2.68	0.51
1:A:1250:A:H5''	10:I:68:GLY:N	2.25	0.51
14:M:5:ALA:O	14:M:7:VAL:N	2.43	0.51
19:R:39:VAL:HG13	19:R:40:LEU:N	2.25	0.51
20:S:22:LEU:HD21	20:S:28:LYS:HD2	1.92	0.51
1:A:1222:G:P	20:S:77:THR:HG21	2.49	0.51
1:A:316:G:H2'	1:A:317:G:H8	1.75	0.51
1:A:393:A:OP2	17:P:12:LYS:HE2	2.11	0.51
1:A:860:A:H2'	1:A:861:G:O4'	2.11	0.51
4:C:26:LYS:CD	4:C:26:LYS:N	2.73	0.51
1:A:738:C:OP1	7:F:92:LYS:HE3	2.10	0.51
9:H:119:LEU:CD1	9:H:124:ALA:HA	2.23	0.51
9:H:11:THR:HG22	9:H:15:ASN:ND2	2.26	0.51
10:I:36:TYR:CD2	10:I:37:PHE:CE2	2.98	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:22:THR:O	15:N:23:ARG:HB2	2.09	0.51
21:T:53:LEU:O	21:T:57:ARG:HD2	2.11	0.51
1:A:1038:C:H2'	1:A:1039:C:H6	1.76	0.51
1:A:1127:G:H5''	10:I:66:ARG:HH22	1.75	0.51
1:A:190(B):C:H2'	1:A:190(C):C:O4'	2.10	0.51
3:B:197:VAL:CB	3:B:200:ILE:HG12	2.38	0.51
6:E:47:LYS:HD2	6:E:47:LYS:N	2.25	0.51
13:L:54:LYS:N	13:L:54:LYS:HD2	2.25	0.51
1:A:761:G:H1'	18:Q:104:LYS:O	2.11	0.51
1:A:1036:G:H2'	1:A:1037:C:O4'	2.10	0.51
1:A:1348:U:H2'	1:A:1349:A:C8	2.45	0.51
1:A:308:C:H2'	1:A:309:G:H8	1.75	0.51
1:A:328:C:O2	1:A:328:C:C2'	2.56	0.51
1:A:736:C:H2'	1:A:737:A:H8	1.76	0.51
3:B:102:LEU:HD21	3:B:162:ILE:HD12	1.90	0.51
3:B:239:VAL:HG12	3:B:239:VAL:O	2.11	0.51
1:A:737:A:H1'	7:F:73:ASN:HD21	1.75	0.51
9:H:45:ILE:HG13	9:H:47:GLY:N	2.26	0.51
13:L:38:THR:HG22	13:L:39:VAL:CG2	2.39	0.51
14:M:78:ILE:O	14:M:81:LEU:CD2	2.58	0.51
18:Q:12:SER:HB3	18:Q:20:THR:CB	2.41	0.51
7:F:94:GLN:NE2	19:R:32:ARG:HD3	2.25	0.51
1:A:1415:G:H2'	1:A:1416:G:C8	2.43	0.51
1:A:407:G:H2'	1:A:408:A:C8	2.45	0.51
1:A:652:U:O4	1:A:752:G:O2'	2.23	0.51
3:B:137:ARG:HH11	3:B:137:ARG:HB3	1.76	0.51
14:M:37:THR:HG23	14:M:55:ARG:HB3	1.93	0.51
16:O:27:VAL:HG12	16:O:31:LEU:CD1	2.41	0.51
18:Q:63:ARG:HG2	18:Q:64:PRO:CD	2.41	0.51
4:C:52:LEU:CD2	4:C:118:GLN:HE22	2.21	0.51
4:C:20:SER:HB3	4:C:22:TRP:NE1	2.25	0.51
4:C:33:LEU:HD11	15:N:53:LEU:CD2	2.41	0.51
6:E:13:ILE:HG22	6:E:30:ALA:HA	1.92	0.51
9:H:104:ARG:HG2	9:H:104:ARG:HH11	1.76	0.51
1:A:1153:C:P	11:J:13:HIS:HE2	2.33	0.51
1:A:881:G:OP2	13:L:12:ARG:NH2	2.44	0.51
1:A:953:G:H1'	14:M:125:ARG:HA	1.92	0.51
16:O:56:LEU:O	16:O:60:VAL:HG23	2.11	0.51
20:S:45:VAL:HG12	20:S:46:GLY:N	2.26	0.51
1:A:1222:G:OP1	20:S:77:THR:HG21	2.11	0.51
1:A:1057:G:O2'	1:A:1058:G:H5'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:A:H5''	1:A:280:C:H3'	1.93	0.51
1:A:399:G:H2'	1:A:400:C:C6	2.45	0.51
1:A:848:C:H2'	1:A:849:C:C6	2.46	0.51
4:C:107:GLN:O	4:C:108:ASN:HB3	2.10	0.51
4:C:157:ILE:CD1	4:C:166:GLU:HB2	2.40	0.51
9:H:60:ARG:NH1	9:H:60:ARG:HG3	2.25	0.51
13:L:83:VAL:CG2	13:L:84:LEU:H	2.21	0.51
14:M:33:ALA:HA	14:M:59:TYR:CE2	2.45	0.51
14:M:78:ILE:HA	14:M:81:LEU:CD2	2.40	0.51
1:A:1003(A):G:H2'	1:A:1004:A:H4'	1.93	0.51
1:A:1153:C:H2'	1:A:1154:G:C8	2.46	0.51
1:A:1207:G:O2'	1:A:1208:C:H5'	2.11	0.51
1:A:332:G:O2'	1:A:333:G:H5'	2.10	0.51
4:C:106:VAL:HG11	4:C:115:LEU:HD11	1.93	0.51
5:D:3:ARG:HH22	5:D:74:GLN:CG	2.23	0.51
1:A:112:G:H21	1:A:354:G:H5'	1.76	0.51
1:A:1504:G:OP1	1:A:1507:A:H4'	2.11	0.51
1:A:411:A:C4	1:A:413:G:H1'	2.46	0.51
1:A:424:G:O2'	1:A:425:G:H5'	2.11	0.51
1:A:459:G:H3'	1:A:460:A:H5''	1.93	0.51
4:C:14:ILE:O	4:C:16:ARG:N	2.43	0.51
5:D:153:ARG:HG2	5:D:181:MET:SD	2.50	0.51
5:D:4:TYR:CG	5:D:5:ILE:N	2.79	0.51
6:E:144:THR:HB	6:E:147:ASP:OD2	2.11	0.51
6:E:92:LYS:O	6:E:118:ILE:HG23	2.11	0.51
7:F:14:LEU:HA	7:F:18:GLN:HE21	1.74	0.51
7:F:75:LEU:O	7:F:75:LEU:HD13	2.09	0.51
8:G:72:ARG:HG2	8:G:142:GLU:OE1	2.11	0.51
8:G:85:TYR:O	8:G:87:VAL:HG23	2.11	0.51
10:I:111:ARG:HD3	10:I:112:LYS:H	1.74	0.51
1:A:501:C:OP1	13:L:117:ARG:NH2	2.43	0.51
15:N:26:ARG:HH12	15:N:47:LEU:HG	1.72	0.51
21:T:50:GLU:HG3	21:T:99:LEU:HD12	1.93	0.51
1:A:731:G:H5'	1:A:766:A:H4'	1.93	0.50
4:C:11:ARG:HG2	4:C:11:ARG:NH1	2.27	0.50
8:G:143:ARG:O	8:G:145:ALA:O	2.29	0.50
11:J:20:ALA:O	11:J:24:VAL:HG23	2.10	0.50
16:O:31:LEU:N	16:O:31:LEU:HD12	2.25	0.50
1:A:1238:A:N7	1:A:1303:C:H1'	2.26	0.50
1:A:142:G:O2'	1:A:196:A:N1	2.32	0.50
5:D:165:MET:HE2	5:D:176:LEU:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:12:ASP:HB3	11:J:15:THR:HG22	1.93	0.50
11:J:45:ARG:HH11	11:J:45:ARG:CB	1.95	0.50
15:N:24:CYS:HB3	15:N:28:GLY:N	2.26	0.50
19:R:42:ARG:HG3	19:R:42:ARG:NH1	2.25	0.50
1:A:1477:C:H2'	1:A:1478:C:H6	1.76	0.50
1:A:437:U:O2'	5:D:123:HIS:CD2	2.64	0.50
1:A:861:G:O2'	1:A:862:C:H5'	2.11	0.50
3:B:17:PHE:CD1	3:B:17:PHE:C	2.85	0.50
3:B:17:PHE:HD1	3:B:17:PHE:C	2.15	0.50
4:C:34:LEU:HG	15:N:25:VAL:HG21	1.93	0.50
5:D:6:GLY:O	5:D:7:PRO:C	2.47	0.50
11:J:6:ILE:HG22	11:J:98:ILE:HG12	1.93	0.50
13:L:119:LYS:O	13:L:120:TYR:CB	2.60	0.50
19:R:42:ARG:HG3	19:R:42:ARG:HH11	1.77	0.50
1:A:1149:C:H2'	1:A:1150:U:C6	2.47	0.50
1:A:1176:A:H2'	1:A:1177:G:C8	2.46	0.50
1:A:1346:A:O2'	1:A:1347:G:OP2	2.27	0.50
1:A:337:C:H2'	1:A:338:A:H8	1.76	0.50
1:A:509:A:N3	1:A:543:C:O2'	2.36	0.50
1:A:551:U:H2'	1:A:552:U:C6	2.47	0.50
1:A:961:U:O2'	1:A:962:C:H5'	2.11	0.50
4:C:188:LEU:HD11	4:C:195:VAL:HG13	1.92	0.50
10:I:58:ARG:O	10:I:58:ARG:HD2	2.11	0.50
1:A:707:C:OP1	12:K:85:ARG:NH1	2.45	0.50
13:L:84:LEU:HD22	13:L:104:VAL:HG11	1.94	0.50
1:A:1326:C:OP1	22:V:12:LYS:NZ	2.44	0.50
3:B:98:LEU:O	3:B:101:MET:HG3	2.11	0.50
1:A:933:G:OP2	8:G:3:ARG:HB3	2.11	0.50
11:J:56:HIS:O	11:J:58:ASP:N	2.44	0.50
12:K:99:GLN:HG2	12:K:105:VAL:HG21	1.93	0.50
18:Q:27:PHE:CE1	18:Q:36:ILE:HD11	2.47	0.50
18:Q:81:ARG:O	18:Q:81:ARG:HG3	2.12	0.50
1:A:281:G:O2'	1:A:282:A:OP2	2.24	0.50
1:A:624:C:H2'	1:A:625:G:H8	1.76	0.50
1:A:918:A:H2'	1:A:919:A:H8	1.75	0.50
3:B:16:HIS:CD2	3:B:210:SER:HG	2.30	0.50
9:H:91:ARG:CG	13:L:7:ILE:HG13	2.41	0.50
13:L:26:ALA:O	13:L:27:LEU:O	2.30	0.50
21:T:94:ALA:O	21:T:95:ALA:HB3	2.10	0.50
1:A:505:G:H2'	1:A:506:G:H8	1.77	0.50
3:B:19:HIS:CD2	3:B:205:ASP:OD1	2.64	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:151:LYS:H	5:D:151:LYS:HD2	1.77	0.50
14:M:29:ARG:HB3	14:M:64:TRP:CH2	2.47	0.50
14:M:78:ILE:O	14:M:81:LEU:HD22	2.12	0.50
18:Q:59:ILE:CG2	18:Q:71:PHE:HB3	2.42	0.50
21:T:102:GLY:O	21:T:104:LEU:N	2.39	0.50
1:A:1113:C:H6	1:A:1113:C:O5'	1.95	0.50
1:A:1250:A:H5'	10:I:68:GLY:O	2.12	0.50
1:A:1392:G:H2'	1:A:1393:U:H6	1.77	0.50
1:A:190:C:H2'	1:A:190(A):C:C6	2.47	0.50
1:A:190(J):U:H2'	1:A:190(K):G:C8	2.47	0.50
1:A:276:G:C2'	1:A:277:C:H5'	2.42	0.50
1:A:522:C:H41	13:L:53:ARG:HH22	1.60	0.50
1:A:91:C:O2'	1:A:92:C:H5'	2.11	0.50
3:B:103:THR:HB	3:B:176:GLU:CD	2.32	0.50
3:B:187:LEU:HD23	3:B:201:ILE:HG22	1.92	0.50
4:C:87:LEU:C	4:C:89:GLU:N	2.65	0.50
6:E:148:VAL:O	6:E:152:ARG:HG3	2.12	0.50
1:A:965:A:H2	14:M:124:PRO:HB2	1.77	0.50
19:R:52:PRO:HB2	19:R:54:ARG:HD3	1.93	0.50
21:T:39:LYS:CD	21:T:55:ILE:HD13	2.31	0.50
1:A:1002:G:H2'	1:A:1003:G:O4'	2.12	0.50
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.47	0.50
1:A:1116:C:H2'	1:A:1117:G:C5'	2.34	0.50
1:A:1306:A:C2	1:A:1307:U:H1'	2.47	0.50
1:A:270:A:H2'	1:A:271:C:C6	2.47	0.50
1:A:298:A:H2'	1:A:299:G:O4'	2.12	0.50
1:A:628:G:O2'	1:A:629:G:H5'	2.11	0.50
4:C:167:TRP:O	4:C:168:ALA:HB3	2.12	0.50
8:G:135:VAL:O	8:G:139:GLU:HG3	2.12	0.50
9:H:20:TYR:CE1	9:H:76:PRO:HD2	2.47	0.50
11:J:24:VAL:CG1	11:J:28:ARG:HE	2.25	0.50
12:K:85:ARG:HH11	12:K:85:ARG:HG3	1.77	0.50
22:V:24:ARG:O	22:V:25:LYS:CB	2.60	0.50
1:A:1277:C:H2'	1:A:1278:U:H5'	1.94	0.49
1:A:1330:U:H2'	1:A:1331:G:H5'	1.94	0.49
1:A:666:G:H5'	1:A:726:C:H1'	1.92	0.49
3:B:137:ARG:O	3:B:140:HIS:HB2	2.12	0.49
7:F:36:ARG:HH12	7:F:38:GLU:HG2	1.77	0.49
3:B:181:PHE:CD2	9:H:70:GLN:HB3	2.47	0.49
1:A:1251:A:H4'	10:I:12:GLU:CD	2.32	0.49
10:I:93:ARG:NH1	10:I:97:LYS:HZ2	2.09	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:13:GLN:HA	12:K:75:TYR:O	2.11	0.49
1:A:521:G:OP1	13:L:73:GLU:O	2.29	0.49
19:R:58:LEU:HD22	19:R:62:GLU:HB3	1.93	0.49
1:A:1042:G:O2'	1:A:1043:C:H5'	2.12	0.49
1:A:109:A:H2'	1:A:326:G:N2	2.27	0.49
1:A:1139:G:O2'	1:A:1140:C:P	2.70	0.49
1:A:1420:C:H2'	1:A:1421:G:H8	1.76	0.49
1:A:5:U:HO2'	1:A:6:G:P	2.35	0.49
3:B:57:PHE:O	3:B:60:ASP:HB3	2.12	0.49
4:C:191:THR:CG2	4:C:192:THR:H	2.24	0.49
3:B:130:ARG:NH2	4:C:207:VAL:HG23	2.22	0.49
4:C:22:TRP:CZ3	4:C:32:LEU:HD22	2.46	0.49
5:D:63:LYS:O	5:D:64:LEU:C	2.51	0.49
9:H:104:ARG:NH2	9:H:138:TRP:CH2	2.80	0.49
19:R:51:LEU:HB2	19:R:56:THR:HG22	1.94	0.49
1:A:1498:U:C4'	1:A:1519:A:H2	2.24	0.49
1:A:444:C:O2'	1:A:445:G:H5'	2.12	0.49
1:A:625:G:H4'	17:P:16:HIS:CD2	2.48	0.49
1:A:818:G:H3'	1:A:819:A:C5'	2.42	0.49
3:B:164:VAL:HG12	3:B:186:ALA:CB	2.42	0.49
3:B:17:PHE:HD1	3:B:18:GLY:N	2.10	0.49
3:B:23:ARG:NH1	3:B:24:TRP:CA	2.75	0.49
11:J:34:VAL:CG2	11:J:74:ILE:HG23	2.43	0.49
12:K:19:ALA:HB2	12:K:80:VAL:CG1	2.43	0.49
20:S:45:VAL:C	20:S:47:HIS:H	2.15	0.49
1:A:1061:G:C2'	1:A:1062:U:H5'	2.43	0.49
1:A:1442:G:H2'	1:A:1442:G:N3	2.26	0.49
1:A:443:C:H2'	1:A:444:C:H6	1.78	0.49
1:A:448:A:H62	1:A:486:U:H3	1.59	0.49
7:F:75:LEU:HD13	7:F:75:LEU:C	2.33	0.49
8:G:110:GLN:OE1	8:G:110:GLN:HA	2.11	0.49
11:J:51:ARG:NH1	11:J:51:ARG:HG2	2.21	0.49
13:L:53:ARG:CB	13:L:93:LEU:HD11	2.43	0.49
21:T:53:LEU:HD13	21:T:101:GLY:N	2.27	0.49
1:A:141:A:H1'	1:A:182:U:C2	2.47	0.49
1:A:6:G:C4	6:E:119:LEU:HD11	2.47	0.49
1:A:77:G:O2'	1:A:78:G:H5'	2.13	0.49
3:B:16:HIS:CE1	3:B:214:ILE:HG12	2.47	0.49
4:C:131:ARG:O	4:C:135:LYS:HG3	2.12	0.49
10:I:111:ARG:HH11	10:I:111:ARG:HG3	1.77	0.49
10:I:89:ASN:ND2	10:I:91:ASP:HB2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:54:PHE:CE2	11:J:55:LYS:HD3	2.48	0.49
15:N:12:ARG:O	15:N:13:THR:C	2.51	0.49
1:A:1085:U:O3'	1:A:1086:U:H6	1.96	0.49
1:A:1256:A:H5'	1:A:1258:G:O4'	2.13	0.49
1:A:1413:A:H2	1:A:1487:G:H22	1.58	0.49
1:A:123:C:OP1	1:A:312:C:H5'	2.12	0.49
1:A:447:G:H2'	1:A:485:G:N2	2.27	0.49
1:A:687:A:H4'	1:A:688:G:O5'	2.11	0.49
3:B:103:THR:HB	3:B:176:GLU:OE1	2.12	0.49
3:B:109:SER:O	3:B:112:VAL:N	2.42	0.49
3:B:144:ARG:O	3:B:147:LYS:N	2.44	0.49
3:B:26:PRO:O	3:B:29:ALA:HB2	2.13	0.49
4:C:88:ARG:O	4:C:91:LEU:HD22	2.11	0.49
10:I:65:VAL:HG13	10:I:65:VAL:O	2.12	0.49
10:I:46:ALA:HA	10:I:78:LYS:HB2	1.95	0.49
11:J:51:ARG:N	11:J:59:SER:CB	2.76	0.49
11:J:71:LEU:O	11:J:72:VAL:HB	2.13	0.49
1:A:537:G:OP1	13:L:113:ARG:NH2	2.46	0.49
19:R:46:GLU:H	19:R:46:GLU:CD	2.16	0.49
20:S:62:ILE:CD1	20:S:66:MET:HG3	2.42	0.49
1:A:1023:G:N3	1:A:1023:G:H2'	2.26	0.49
1:A:1118:C:H1'	1:A:1179:A:C4	2.48	0.49
1:A:1053:G:O2'	1:A:1199:U:H5	1.96	0.49
1:A:1470:G:O2'	1:A:1471:G:H5'	2.13	0.49
1:A:1399:C:C2	1:A:1502:A:N6	2.80	0.49
1:A:485:G:C2'	1:A:486:U:OP2	2.61	0.49
1:A:929:G:O2'	1:A:930:C:H5'	2.12	0.49
4:C:20:SER:HB3	4:C:22:TRP:HE1	1.78	0.49
4:C:87:LEU:O	4:C:89:GLU:N	2.46	0.49
4:C:95:THR:O	4:C:97:LYS:N	2.44	0.49
5:D:158:ILE:HG22	5:D:181:MET:HE2	1.95	0.49
6:E:112:LEU:C	6:E:114:GLY:N	2.65	0.49
9:H:11:THR:HA	9:H:14:ARG:NH1	2.28	0.49
15:N:44:LEU:O	15:N:44:LEU:HD12	2.12	0.49
16:O:70:LEU:HD12	16:O:78:TYR:CB	2.43	0.49
1:A:1226:C:H5''	14:M:103:THR:HG1	1.75	0.49
1:A:1417:G:O2'	1:A:1483:A:N6	2.45	0.49
1:A:390:C:H2'	1:A:391:G:H8	1.77	0.49
1:A:646:U:H2'	1:A:647:C:H6	1.78	0.49
3:B:209:ARG:HH11	3:B:209:ARG:HG2	1.78	0.49
5:D:38:TYR:HB2	5:D:39:PRO:HD2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:92:VAL:O	5:D:96:LEU:HD13	2.12	0.49
8:G:72:ARG:HA	8:G:96:GLN:NE2	2.27	0.49
10:I:118:LYS:O	10:I:119:ALA:CB	2.61	0.49
11:J:80:LYS:O	11:J:84:GLN:HG3	2.12	0.49
21:T:42:GLN:CA	21:T:42:GLN:HE21	2.24	0.49
1:A:1128:C:O2'	1:A:1130:A:C8	2.65	0.49
1:A:913:A:O2'	1:A:914:A:OP2	2.28	0.49
3:B:182:ILE:O	3:B:183:PRO:C	2.50	0.49
5:D:3:ARG:NE	5:D:71:SER:H	2.11	0.49
7:F:19:LEU:HD23	7:F:20:ALA:N	2.28	0.49
1:A:552:U:H4'	13:L:86:ARG:O	2.12	0.49
14:M:31:LYS:O	14:M:35:GLU:HB2	2.12	0.49
14:M:97:PRO:HB2	14:M:101:GLN:OE1	2.12	0.49
15:N:29:ARG:HH11	15:N:29:ARG:HG2	1.77	0.49
20:S:51:VAL:HG12	20:S:52:TYR:N	2.28	0.49
21:T:79:ARG:O	21:T:80:ARG:C	2.51	0.49
1:A:1216:G:H2'	1:A:1217:C:H6	1.78	0.49
1:A:1238:A:H2	1:A:1241:G:N3	2.10	0.49
1:A:1487:G:H2'	1:A:1488:G:H8	1.77	0.49
1:A:246:A:N6	1:A:281:G:H1'	2.27	0.49
1:A:420:U:O2'	1:A:421:U:H5''	2.13	0.49
4:C:172:ARG:HB3	4:C:172:ARG:HH11	1.78	0.49
4:C:179:ARG:C	4:C:179:ARG:HD2	2.33	0.49
5:D:24:GLU:O	5:D:25:ARG:HB3	2.13	0.49
14:M:84:ILE:O	14:M:86:CYS:N	2.46	0.49
7:F:94:GLN:HB2	19:R:32:ARG:HD3	1.95	0.49
1:A:1075:C:H5'	3:B:103:THR:HG21	1.95	0.48
1:A:5:U:O2	1:A:5:U:C2'	2.61	0.48
3:B:119:GLU:CD	3:B:153:ARG:NH2	2.66	0.48
3:B:59:GLU:O	3:B:62:ALA:HB3	2.12	0.48
4:C:123:GLN:HE22	4:C:140:ARG:HH22	1.61	0.48
4:C:42:LEU:HD12	4:C:94:LEU:CD1	2.43	0.48
4:C:52:LEU:HG	4:C:52:LEU:O	2.13	0.48
4:C:58:GLU:HB2	4:C:65:ALA:HB2	1.95	0.48
5:D:68:TYR:CD2	5:D:97:LEU:HB3	2.48	0.48
5:D:68:TYR:CE2	5:D:97:LEU:HB3	2.48	0.48
6:E:107:ARG:HG2	6:E:108:ALA:N	2.27	0.48
1:A:1346:A:C4	8:G:10:ARG:NH2	2.81	0.48
8:G:15:ASP:O	8:G:19:GLY:HA2	2.12	0.48
11:J:4:ILE:HG23	11:J:98:ILE:HG21	1.95	0.48
16:O:27:VAL:HG12	16:O:31:LEU:HD11	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:36:ASN:HB3	19:R:39:VAL:HG12	1.94	0.48
20:S:74:PHE:N	20:S:74:PHE:CD1	2.80	0.48
20:S:80:TYR:CD2	20:S:81:ARG:N	2.80	0.48
21:T:53:LEU:HD21	21:T:104:LEU:HD12	1.95	0.48
1:A:1095:U:H2'	1:A:1096:C:C6	2.48	0.48
1:A:1202:G:H2'	1:A:1203:C:C5'	2.42	0.48
1:A:959:A:H2	1:A:1221:G:N3	2.11	0.48
1:A:1238:A:C2	1:A:1241:G:N3	2.81	0.48
1:A:1514:C:H2'	1:A:1515:C:C6	2.47	0.48
1:A:248:C:O2'	1:A:249:U:H5'	2.13	0.48
1:A:783:C:O2'	1:A:784:C:H5'	2.13	0.48
3:B:239:VAL:HB	3:B:240:GLN:NE2	2.28	0.48
4:C:18:TRP:HE3	4:C:18:TRP:H	1.59	0.48
5:D:24:GLU:CG	5:D:25:ARG:H	2.25	0.48
5:D:98:GLU:HA	5:D:103:ASN:ND2	2.28	0.48
6:E:43:LEU:CD2	6:E:44:GLY:N	2.76	0.48
7:F:53:ALA:C	7:F:55:ASP:H	2.16	0.48
14:M:36:LYS:HD2	14:M:59:TYR:OH	2.13	0.48
1:A:256:U:H5'	18:Q:17:LYS:HZ1	1.78	0.48
1:A:108:G:N2	1:A:109:A:N1	2.61	0.48
1:A:1172:C:H2'	1:A:1173:G:C8	2.47	0.48
1:A:1197:G:C2'	1:A:1198:G:H5'	2.44	0.48
1:A:1296:C:H4'	1:A:1302:U:C5	2.48	0.48
1:A:1472:U:O2'	1:A:1473:A:H5'	2.12	0.48
1:A:162:A:H2'	1:A:163:C:O4'	2.13	0.48
1:A:425:G:O2'	1:A:426:G:H5'	2.13	0.48
1:A:622:A:C8	1:A:623:C:C5	3.01	0.48
1:A:75:G:O2'	1:A:76:C:H5'	2.14	0.48
1:A:832:C:O2'	1:A:833:U:H5'	2.13	0.48
3:B:125:PRO:HG2	3:B:126:GLU:H	1.78	0.48
3:B:82:ARG:O	3:B:86:GLU:HG3	2.13	0.48
4:C:43:LEU:N	4:C:43:LEU:CD2	2.73	0.48
1:A:1020:U:H2'	1:A:1021:G:H8	1.78	0.48
1:A:1492:A:H2'	1:A:1493:A:C8	2.48	0.48
1:A:639:G:O2'	1:A:640:A:H5'	2.12	0.48
3:B:130:ARG:HB3	3:B:131:PRO:HD2	1.96	0.48
4:C:7:PRO:HG2	4:C:184:TYR:HB2	1.96	0.48
6:E:102:ALA:HB2	6:E:120:THR:HB	1.96	0.48
9:H:126:LYS:C	9:H:128:GLY:H	2.17	0.48
1:A:1231:G:H4'	10:I:126:SER:CB	2.44	0.48
10:I:93:ARG:CD	10:I:97:LYS:HE3	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:47:LYS:HB2	13:L:48:PRO:HD3	1.92	0.48
14:M:110:ARG:HG2	14:M:110:ARG:HH11	1.78	0.48
14:M:60:VAL:CG1	14:M:66:LEU:HD11	2.44	0.48
17:P:39:TYR:O	17:P:41:PRO:HD3	2.13	0.48
18:Q:59:ILE:HG22	18:Q:71:PHE:HD1	1.76	0.48
21:T:45:GLN:CB	21:T:91:LEU:HD22	2.42	0.48
1:A:1230:C:O2'	1:A:1231:G:H5'	2.14	0.48
1:A:1269:A:C2	1:A:1313:U:O4'	2.67	0.48
1:A:1402:C:O2	1:A:1500:A:N1	2.47	0.48
1:A:1531:A:O5'	1:A:1531:A:H8	1.96	0.48
1:A:1532:U:H6	1:A:1532:U:O5'	1.97	0.48
1:A:553:A:H2'	1:A:554:C:C6	2.48	0.48
3:B:17:PHE:CD1	3:B:18:GLY:N	2.81	0.48
3:B:230:VAL:CG1	3:B:231:GLU:N	2.77	0.48
3:B:33:TYR:O	3:B:34:ALA:HB2	2.13	0.48
4:C:5:ILE:O	4:C:5:ILE:HD12	2.14	0.48
6:E:57:LYS:HG2	6:E:61:TYR:CE2	2.48	0.48
1:A:1248:A:H1'	10:I:70:LYS:HZ1	1.78	0.48
11:J:46:ARG:HH11	11:J:64:GLU:HG2	1.78	0.48
11:J:51:ARG:HH11	11:J:51:ARG:CG	2.20	0.48
11:J:32:ALA:HB2	11:J:76:ASN:HD22	1.79	0.48
13:L:98:TYR:CD1	13:L:98:TYR:N	2.81	0.48
14:M:15:VAL:C	14:M:17:VAL:H	2.16	0.48
14:M:40:ASN:HD22	14:M:41:PRO:N	2.11	0.48
1:A:1488:G:H2'	1:A:1489:G:H8	1.73	0.48
1:A:218:C:H2'	1:A:219:C:C6	2.49	0.48
1:A:267:C:H2'	1:A:268:C:H6	1.78	0.48
1:A:33:A:H2'	1:A:34:C:C6	2.48	0.48
3:B:115:LEU:O	3:B:119:GLU:HG3	2.13	0.48
1:A:875:C:H1'	9:H:15:ASN:OD1	2.14	0.48
9:H:38:ILE:N	9:H:38:ILE:HD12	2.27	0.48
13:L:40:VAL:O	13:L:40:VAL:HG12	2.13	0.48
14:M:110:ARG:HH11	14:M:110:ARG:CG	2.27	0.48
1:A:1305:G:H2'	1:A:1331:G:N2	2.28	0.48
1:A:197:A:N1	1:A:220:G:O2'	2.45	0.48
1:A:244:U:O4	1:A:906:G:H1'	2.13	0.48
1:A:458:C:H2'	1:A:459:G:O4'	2.14	0.48
1:A:737:A:H1'	7:F:73:ASN:ND2	2.29	0.48
3:B:84:GLU:CB	3:B:219:VAL:HG21	2.22	0.48
3:B:8:LYS:O	3:B:9:GLU:CB	2.60	0.48
4:C:70:VAL:HG12	4:C:72:LYS:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:77:ILE:HG22	4:C:81:GLY:HA2	1.95	0.48
5:D:65:ARG:HA	5:D:75:PHE:CE1	2.48	0.48
6:E:144:THR:HG22	6:E:146:ALA:H	1.79	0.48
6:E:150:ARG:HG3	6:E:150:ARG:NH1	2.29	0.48
7:F:67:MET:HE1	7:F:72:VAL:HA	1.95	0.48
8:G:145:ALA:C	8:G:147:ALA:N	2.66	0.48
12:K:26:ASN:O	12:K:27:ASN:HB2	2.14	0.48
14:M:121:LYS:O	14:M:123:ALA:N	2.47	0.48
18:Q:104:LYS:O	18:Q:105:ALA:HB2	2.14	0.48
1:A:1420:C:H2'	1:A:1421:G:C8	2.49	0.48
1:A:41:G:H2'	1:A:42:G:H8	1.78	0.48
1:A:635:G:O2'	1:A:636:U:H5'	2.13	0.48
4:C:204:LEU:O	4:C:205:GLY:C	2.51	0.48
5:D:64:LEU:HD13	5:D:75:PHE:HZ	1.79	0.48
9:H:108:GLY:HA3	9:H:138:TRP:HB3	1.96	0.48
10:I:108:VAL:HG12	10:I:109:VAL:H	1.78	0.48
11:J:48:THR:OG1	11:J:62:HIS:CD2	2.66	0.48
14:M:79:LYS:O	14:M:83:ASP:OD2	2.32	0.48
15:N:23:ARG:HD3	15:N:30:ALA:HB2	1.96	0.48
21:T:72:LEU:HD23	21:T:72:LEU:HA	1.72	0.48
1:A:1096:C:O2'	1:A:1097:C:H5'	2.14	0.48
1:A:1256:A:H61	1:A:1278:U:H1'	1.75	0.48
1:A:1380:U:O2'	1:A:1381:U:OP2	2.31	0.48
1:A:1426:C:H2'	1:A:1427:U:H6	1.78	0.48
1:A:308:C:H2'	1:A:309:G:C8	2.48	0.48
1:A:39:G:O2'	1:A:40:C:H5'	2.13	0.48
1:A:736:C:OP2	19:R:68:LYS:HE2	2.14	0.48
1:A:760:G:O6	18:Q:105:ALA:CB	2.59	0.48
1:A:862:C:O2'	1:A:863:U:H5'	2.14	0.48
1:A:913:A:O2'	1:A:914:A:P	2.72	0.48
1:A:934:C:C4	1:A:1345:U:C5	3.02	0.48
1:A:959:A:H2'	1:A:960:U:O4'	2.14	0.48
4:C:32:LEU:O	4:C:32:LEU:HD23	2.14	0.48
4:C:95:THR:C	4:C:97:LYS:N	2.67	0.48
5:D:33:MET:HE3	5:D:37:PRO:CB	2.40	0.48
6:E:137:GLU:O	6:E:141:GLN:HG3	2.13	0.48
6:E:143:ARG:NH1	9:H:77:GLU:OE2	2.46	0.48
11:J:19:SER:O	11:J:23:ILE:HD13	2.14	0.48
11:J:51:ARG:N	11:J:59:SER:HB3	2.29	0.48
13:L:67:THR:HG22	13:L:96:VAL:HG13	1.96	0.48
1:A:523:A:H61	13:L:92:ASP:HB2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:96:LEU:O	14:M:110:ARG:NH1	2.47	0.48
20:S:5:LEU:O	20:S:6:LYS:HG3	2.14	0.48
1:A:1005:A:H2'	1:A:1006:C:H5'	1.94	0.48
1:A:1152:A:H2'	1:A:1153:C:C6	2.49	0.48
1:A:1392:G:H2'	1:A:1393:U:C6	2.49	0.48
1:A:197:A:H1'	1:A:198:G:O4'	2.14	0.48
5:D:162:LEU:HD23	5:D:165:MET:HG3	1.96	0.48
7:F:11:ASN:O	7:F:14:LEU:HG	2.13	0.48
8:G:124:LEU:O	8:G:127:ALA:HB3	2.14	0.48
1:A:1306:A:O2'	14:M:109:THR:HG21	2.13	0.48
19:R:46:GLU:CD	19:R:46:GLU:N	2.67	0.48
21:T:50:GLU:O	21:T:100:ILE:HD12	2.14	0.48
1:A:1277:C:C2'	1:A:1278:U:H5'	2.43	0.47
1:A:953:G:H1'	14:M:125:ARG:CA	2.44	0.47
3:B:208:ILE:O	3:B:210:SER:N	2.47	0.47
3:B:92:TYR:CE1	3:B:151:GLY:HA3	2.48	0.47
4:C:108:ASN:OD1	4:C:110:ASN:HB2	2.14	0.47
4:C:33:LEU:C	4:C:33:LEU:HD23	2.33	0.47
4:C:60:ALA:O	4:C:61:ALA:CB	2.61	0.47
12:K:56:GLY:O	12:K:57:THR:O	2.32	0.47
13:L:58:VAL:O	13:L:65:GLU:HA	2.14	0.47
16:O:87:ILE:HG22	16:O:88:ARG:N	2.29	0.47
1:A:1056:U:O2	1:A:1056:U:H2'	2.13	0.47
1:A:1064:G:H4'	1:A:1065:U:H5"	1.92	0.47
1:A:1065:U:H5"	1:A:1066:C:H5'	1.97	0.47
1:A:1516:G:H2'	1:A:1518:A:OP2	2.14	0.47
1:A:255:G:H1'	18:Q:16:GLN:HE22	1.79	0.47
1:A:498:U:O2'	1:A:499:A:H5'	2.14	0.47
1:A:920:U:H2'	1:A:921:U:H6	1.78	0.47
5:D:88:VAL:O	5:D:92:VAL:HG23	2.14	0.47
1:A:1298:C:C4	8:G:114:ARG:HD3	2.49	0.47
17:P:55:ARG:O	17:P:56:ALA:C	2.51	0.47
1:A:216:G:H2'	1:A:217:C:C6	2.49	0.47
1:A:409:G:H2'	1:A:410:G:O4'	2.13	0.47
1:A:518:C:H5"	1:A:519:C:C6	2.49	0.47
1:A:994:A:H8	1:A:994:A:OP1	1.97	0.47
4:C:190:ARG:NH1	4:C:190:ARG:CB	2.78	0.47
6:E:115:VAL:HG11	6:E:118:ILE:HG13	1.97	0.47
10:I:5:TYR:O	10:I:84:ALA:HA	2.14	0.47
20:S:63:THR:HG22	20:S:64:GLU:N	2.30	0.47
1:A:1286:A:C8	1:A:1287:A:C5'	2.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1513:A:H2'	1:A:1514:C:C6	2.49	0.47
1:A:792:A:H4'	1:A:793:U:H5''	1.97	0.47
4:C:188:LEU:HD13	4:C:189:ALA:N	2.27	0.47
4:C:42:LEU:HD12	4:C:94:LEU:HD12	1.97	0.47
5:D:53:ASP:O	5:D:57:ARG:HD3	2.14	0.47
7:F:91:VAL:HG12	7:F:92:LYS:O	2.14	0.47
8:G:114:ARG:HH11	8:G:114:ARG:HG2	1.79	0.47
14:M:32:GLU:O	14:M:35:GLU:HB3	2.15	0.47
1:A:160:A:H1'	1:A:344:A:N7	2.28	0.47
1:A:276:G:O2'	1:A:277:C:H5'	2.14	0.47
1:A:31:G:C2	1:A:48:C:H5''	2.50	0.47
1:A:356:A:O2'	1:A:357:G:H5'	2.15	0.47
1:A:438:G:C4'	1:A:439:A:OP1	2.55	0.47
1:A:60:A:H4'	1:A:61:G:O5'	2.14	0.47
1:A:582:U:C2	1:A:760:G:C6	3.02	0.47
1:A:802:A:H2'	1:A:803:G:O4'	2.15	0.47
4:C:46:GLU:C	4:C:48:TYR:H	2.16	0.47
4:C:79:ARG:CG	4:C:82:GLU:HG2	2.42	0.47
5:D:67:ILE:HG22	5:D:68:TYR:CD1	2.49	0.47
7:F:95:GLU:N	7:F:95:GLU:CD	2.68	0.47
1:A:1250:A:H5''	10:I:67:GLY:C	2.35	0.47
10:I:69:GLY:O	10:I:73:GLN:HG3	2.14	0.47
14:M:34:LEU:CD1	14:M:41:PRO:HA	2.45	0.47
17:P:26:ARG:HE	17:P:31:LYS:HB3	1.78	0.47
20:S:20:LEU:C	20:S:22:LEU:N	2.68	0.47
1:A:103:C:OP1	21:T:17:ARG:HD2	2.14	0.47
1:A:1327:C:O2'	1:A:1328:C:H5'	2.14	0.47
1:A:1367:C:H5'	11:J:60:ARG:NH1	2.29	0.47
1:A:488:C:O2'	1:A:489:C:H5'	2.15	0.47
1:A:67:C:H4'	1:A:172:A:O4'	2.14	0.47
1:A:730:G:H21	1:A:765:G:H5''	1.78	0.47
1:A:743:U:H2'	1:A:744:C:H6	1.78	0.47
1:A:836:G:C6	1:A:851:G:C6	3.02	0.47
3:B:195:ASP:O	9:H:74:PRO:HG3	2.14	0.47
4:C:110:ASN:HB3	4:C:144:SER:OG	2.13	0.47
4:C:205:GLY:O	4:C:206:GLU:HB2	2.13	0.47
4:C:47:LEU:N	4:C:47:LEU:CD1	2.76	0.47
4:C:77:ILE:CG2	4:C:81:GLY:HA2	2.45	0.47
5:D:160:GLN:O	5:D:163:GLU:HB3	2.14	0.47
6:E:24:ARG:NH1	6:E:24:ARG:HG2	2.27	0.47
9:H:103:VAL:HG23	9:H:110:ALA:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:51:VAL:HG12	9:H:52:ASP:N	2.29	0.47
10:I:120:ARG:O	10:I:122:ALA:N	2.47	0.47
21:T:56:MET:HE1	21:T:104:LEU:HG	1.97	0.47
1:A:1213:A:N1	1:A:1215:G:H1'	2.29	0.47
1:A:1238:A:H5'	1:A:1336:C:N4	2.21	0.47
1:A:1279:A:O2'	1:A:1282:C:N4	2.48	0.47
1:A:781:A:H2	1:A:1514:C:C4'	2.28	0.47
4:C:28:GLN:O	4:C:31:HIS:N	2.40	0.47
5:D:30:LYS:O	5:D:32:ALA:N	2.48	0.47
6:E:31:LEU:HD22	6:E:43:LEU:CD2	2.44	0.47
1:A:1298:C:H2'	8:G:114:ARG:NH1	2.29	0.47
8:G:18:TYR:HD2	8:G:59:LEU:HD22	1.80	0.47
8:G:59:LEU:O	8:G:63:LYS:HG3	2.15	0.47
1:A:1366:C:HO2'	11:J:60:ARG:HH22	1.61	0.47
13:L:33:ARG:HH11	13:L:62:SER:HB3	1.80	0.47
14:M:46:LYS:HE2	14:M:47:ASP:OD1	2.14	0.47
1:A:1303:C:H2'	1:A:1304:G:H5'	1.97	0.47
1:A:6:G:H4'	1:A:298:A:H4'	1.95	0.47
1:A:854:G:C6	1:A:855:G:N7	2.82	0.47
3:B:206:ASP:CG	3:B:207:ALA:N	2.68	0.47
3:B:23:ARG:HH12	3:B:191:ASP:HA	1.79	0.47
4:C:71:ALA:HA	4:C:106:VAL:HB	1.96	0.47
4:C:156:ARG:NH2	4:C:161:GLU:HA	2.29	0.47
5:D:196:LEU:C	5:D:198:VAL:N	2.68	0.47
5:D:78:LEU:CD1	5:D:97:LEU:HD23	2.44	0.47
6:E:33:VAL:HG11	6:E:109:ILE:HA	1.97	0.47
7:F:43:LEU:N	7:F:43:LEU:HD22	2.29	0.47
1:A:974:A:P	15:N:31:ARG:HG2	2.55	0.47
11:J:49:VAL:CG1	15:N:41:ARG:HB2	2.44	0.47
16:O:10:LYS:HD2	16:O:10:LYS:O	2.14	0.47
1:A:1523:G:OP1	12:K:123:LYS:HD2	2.15	0.47
1:A:649:G:O2'	1:A:650:G:H5'	2.14	0.47
3:B:119:GLU:OE1	3:B:153:ARG:NH2	2.37	0.47
3:B:151:GLY:C	3:B:153:ARG:H	2.17	0.47
4:C:70:VAL:HG21	4:C:76:VAL:HG21	1.96	0.47
7:F:12:PRO:HG3	7:F:55:ASP:OD1	2.15	0.47
9:H:84:ARG:HD2	9:H:85:ARG:O	2.14	0.47
12:K:46:GLY:O	12:K:47:VAL:C	2.52	0.47
7:F:62:TRP:CD1	19:R:35:ARG:NH1	2.83	0.47
1:A:1138:G:H2'	1:A:1140:C:H5'	1.97	0.47
1:A:115:G:H1'	1:A:116:A:N7	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:G:O2'	1:A:139:G:H5'	2.15	0.47
1:A:1440:C:H2'	1:A:1441:G:H5'	1.97	0.47
1:A:42:G:H2'	1:A:43:C:C6	2.50	0.47
1:A:953:G:N7	14:M:104:ARG:NH2	2.62	0.47
1:A:1060:C:C4	4:C:2:GLY:HA3	2.50	0.47
13:L:71:PRO:O	13:L:102:ARG:HD2	2.15	0.47
13:L:89:ARG:HG2	13:L:97:ARG:HA	1.95	0.47
17:P:9:PHE:CE2	17:P:18:ARG:HD2	2.50	0.47
19:R:45:SER:C	19:R:47:THR:N	2.66	0.47
19:R:53:ARG:C	19:R:55:ARG:H	2.18	0.47
1:A:148:G:H2'	1:A:149:A:H8	1.79	0.47
1:A:337:C:H2'	1:A:338:A:C8	2.50	0.47
1:A:760:G:H2'	1:A:761:G:H5'	1.97	0.47
3:B:95:GLN:OE1	3:B:95:GLN:HA	2.14	0.47
4:C:8:ILE:C	4:C:10:PHE:N	2.69	0.47
4:C:121:ALA:O	4:C:125:GLU:HG3	2.15	0.47
6:E:31:LEU:HA	6:E:31:LEU:HD23	1.66	0.47
6:E:76:ILE:O	6:E:93:PRO:HB3	2.15	0.47
1:A:1187:G:OP1	10:I:113:LYS:HE2	2.15	0.47
15:N:60:SER:H	15:N:61:TRP:HE3	1.63	0.47
18:Q:27:PHE:CZ	18:Q:36:ILE:HD11	2.50	0.47
1:A:1058:G:O2'	1:A:1059:C:H5'	2.15	0.46
1:A:1253:G:H2'	1:A:1254:C:C6	2.50	0.46
1:A:1347:G:HO2'	1:A:1373:G:H1	1.62	0.46
1:A:1480:G:O2'	1:A:1481:U:H5'	2.16	0.46
1:A:189:G:H2'	1:A:190:C:H6	1.80	0.46
1:A:965:A:H4'	1:A:966:G:O5'	2.15	0.46
3:B:59:GLU:HG2	3:B:221:LEU:HD11	1.96	0.46
4:C:182:ILE:HG12	4:C:203:PHE:HD1	1.80	0.46
5:D:109:GLY:HA3	5:D:165:MET:SD	2.55	0.46
12:K:109:VAL:HG13	19:R:85:LEU:O	2.15	0.46
14:M:9:ILE:N	14:M:9:ILE:HD12	2.30	0.46
1:A:264:U:O2'	18:Q:64:PRO:HB2	2.14	0.46
1:A:266:G:O3'	18:Q:67:LYS:HB2	2.14	0.46
1:A:1020:U:H2'	1:A:1021:G:C8	2.50	0.46
1:A:1123:A:H4'	11:J:37:PRO:HD2	1.96	0.46
1:A:163:C:O2'	1:A:164:U:H5'	2.16	0.46
1:A:243:A:H5''	1:A:244:U:H5'	1.97	0.46
1:A:373:A:H1'	1:A:481:G:H1'	1.96	0.46
1:A:426:G:O2'	1:A:427:U:H5'	2.15	0.46
1:A:590:C:O2'	1:A:591:U:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:774:G:O2'	1:A:775:G:H5'	2.16	0.46
1:A:781:A:H2'	1:A:782:A:H5'	1.96	0.46
1:A:812:C:O2'	1:A:813:U:OP2	2.23	0.46
1:A:814:A:N7	1:A:816:A:C4	2.83	0.46
1:A:93:G:O2'	1:A:95:U:H5'	2.15	0.46
5:D:58:LEU:HD23	5:D:206:PHE:CE1	2.50	0.46
6:E:79:GLU:N	6:E:79:GLU:OE1	2.47	0.46
9:H:75:ARG:HA	9:H:76:PRO:HD3	1.67	0.46
20:S:20:LEU:C	20:S:22:LEU:H	2.17	0.46
21:T:45:GLN:HB2	21:T:91:LEU:HD22	1.97	0.46
1:A:1138:G:H3'	1:A:1138:G:N3	2.31	0.46
1:A:1049:U:H1'	1:A:1201:A:N7	2.30	0.46
1:A:338:A:H2	1:A:351:G:H22	1.62	0.46
1:A:977:A:C2'	1:A:978:A:H5''	2.45	0.46
3:B:103:THR:HA	3:B:180:LEU:HD11	1.97	0.46
3:B:97:TRP:CH2	3:B:176:GLU:CD	2.89	0.46
3:B:236:TYR:HA	3:B:239:VAL:HG23	1.96	0.46
6:E:76:ILE:HG23	6:E:142:LEU:HD22	1.97	0.46
8:G:24:THR:HG22	8:G:28:ASN:HD21	1.80	0.46
9:H:114:THR:C	9:H:116:LYS:H	2.19	0.46
15:N:45:ARG:HH11	15:N:45:ARG:HG3	1.80	0.46
19:R:59:SER:OG	19:R:62:GLU:HG3	2.15	0.46
19:R:87:ARG:HG2	19:R:87:ARG:NH1	2.29	0.46
1:A:1005:A:C2'	1:A:1006:C:H5'	2.46	0.46
1:A:1068:G:N2	1:A:1191:A:N3	2.61	0.46
1:A:269:C:H2'	1:A:270:A:C8	2.49	0.46
1:A:750:G:H1'	16:O:22:THR:OG1	2.15	0.46
1:A:938:A:O5'	1:A:938:A:H8	1.98	0.46
1:A:954:G:H2'	1:A:955:U:C6	2.50	0.46
6:E:102:ALA:HA	6:E:120:THR:CG2	2.45	0.46
9:H:28:ALA:HB3	9:H:57:PRO:HB2	1.96	0.46
10:I:113:LYS:H	10:I:113:LYS:HD2	1.79	0.46
12:K:54:ARG:NH1	12:K:54:ARG:HB3	2.14	0.46
18:Q:74:LEU:C	18:Q:74:LEU:CD2	2.83	0.46
1:A:960:U:H1'	1:A:1223:C:H5'	1.98	0.46
1:A:1256:A:H4'	1:A:1257:U:C5'	2.40	0.46
1:A:247:G:OP2	18:Q:100:LYS:HG3	2.16	0.46
1:A:397:A:H5'	1:A:398:C:P	2.56	0.46
1:A:452:A:H2'	1:A:453:A:H8	1.81	0.46
1:A:722:A:H4'	1:A:723:U:C5	2.50	0.46
1:A:761:G:H2'	1:A:762:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:791:G:C2'	1:A:792:A:C5'	2.94	0.46
1:A:865:A:H2'	1:A:866:C:C6	2.51	0.46
1:A:89:C:O2'	1:A:90:U:H5'	2.15	0.46
4:C:108:ASN:C	4:C:110:ASN:N	2.69	0.46
4:C:83:ARG:HA	4:C:86:VAL:HG23	1.98	0.46
7:F:40:VAL:CG2	7:F:41:GLU:N	2.79	0.46
8:G:141:VAL:O	8:G:144:MET:HB2	2.16	0.46
10:I:111:ARG:O	10:I:119:ALA:HB2	2.16	0.46
10:I:44:VAL:O	10:I:44:VAL:HG12	2.16	0.46
11:J:54:PHE:HD2	11:J:55:LYS:HD3	1.77	0.46
13:L:28:LYS:HG3	13:L:33:ARG:HH12	1.79	0.46
18:Q:10:VAL:HG13	18:Q:19:VAL:HB	1.98	0.46
21:T:42:GLN:O	21:T:45:GLN:HB3	2.16	0.46
1:A:1003(A):G:N1	1:A:1004:A:H1'	2.30	0.46
1:A:1063:C:H2'	1:A:1064:G:C8	2.50	0.46
1:A:154:C:H2'	1:A:155:C:H6	1.81	0.46
1:A:16:A:N1	1:A:919:A:H2	2.12	0.46
1:A:51:A:H4'	1:A:52:G:C5'	2.46	0.46
1:A:619:U:N3	5:D:134:ASP:OD1	2.48	0.46
1:A:980:C:H2'	1:A:981:U:O4'	2.16	0.46
1:A:995:C:H2'	1:A:995:C:O2	2.14	0.46
4:C:141:VAL:O	4:C:146:ALA:HB3	2.16	0.46
4:C:173:VAL:N	4:C:174:PRO:CD	2.78	0.46
4:C:50:ALA:HB2	4:C:75:VAL:HB	1.96	0.46
5:D:130:GLY:O	5:D:131:ARG:C	2.53	0.46
13:L:27:LEU:HG	13:L:28:LYS:N	2.24	0.46
14:M:26:GLY:O	14:M:28:ALA:N	2.49	0.46
15:N:50:LYS:HD3	15:N:52:GLN:NE2	2.31	0.46
1:A:135:C:C2	17:P:1:MET:HB2	2.50	0.46
21:T:56:MET:HG2	21:T:84:LEU:HD11	1.98	0.46
1:A:1070:U:O2'	1:A:1071:C:H5'	2.16	0.46
1:A:1244:C:O2'	1:A:1245:A:H5'	2.16	0.46
1:A:1494:G:OP2	24:A:1632:HYG:O11	2.30	0.46
1:A:1525:G:P	12:K:120:ARG:HH22	2.39	0.46
1:A:815:A:H4'	1:A:817:C:C4	2.51	0.46
1:A:98:U:O2'	1:A:99:C:H5'	2.15	0.46
3:B:208:ILE:HG22	3:B:209:ARG:N	2.31	0.46
3:B:224:GLN:O	3:B:226:ARG:N	2.48	0.46
3:B:83:MET:HE3	3:B:235:SER:N	2.30	0.46
5:D:196:LEU:O	5:D:198:VAL:N	2.42	0.46
5:D:98:GLU:HG2	5:D:189:PRO:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:30:LEU:HA	7:F:75:LEU:HD21	1.96	0.46
18:Q:15:MET:HB2	18:Q:18:THR:HB	1.98	0.46
18:Q:81:ARG:NH2	18:Q:83:ASP:OD2	2.47	0.46
1:A:106:C:O2'	1:A:379:C:H5''	2.16	0.46
1:A:1085:U:O3'	1:A:1086:U:C6	2.69	0.46
1:A:1127:G:N2	1:A:1144:G:N2	2.64	0.46
1:A:193:C:H2'	1:A:194:C:H6	1.80	0.46
1:A:192:U:O2'	1:A:193:C:H5'	2.16	0.46
1:A:259:G:O2'	1:A:260:G:H5'	2.15	0.46
1:A:463:A:H2'	1:A:474:G:O4'	2.15	0.46
1:A:583:A:H2'	1:A:584:G:O4'	2.16	0.46
1:A:839:U:C2'	1:A:839:U:O2	2.60	0.46
3:B:197:VAL:HB	3:B:200:ILE:CG1	2.39	0.46
4:C:174:PRO:O	4:C:177:THR:HG22	2.16	0.46
6:E:76:ILE:HG23	6:E:77:PRO:HD2	1.97	0.46
13:L:46:LYS:O	13:L:47:LYS:C	2.54	0.46
13:L:86:ARG:HG3	13:L:86:ARG:HH11	1.80	0.46
14:M:120:LYS:HE2	14:M:123:ALA:HB2	1.98	0.46
17:P:17:TYR:CE1	17:P:41:PRO:HG2	2.51	0.46
19:R:53:ARG:HE	19:R:60:GLY:N	2.13	0.46
20:S:5:LEU:O	20:S:6:LYS:CG	2.64	0.46
21:T:38:LYS:O	21:T:42:GLN:HB2	2.15	0.46
1:A:1056:U:H5'	4:C:163:ALA:CB	2.46	0.46
1:A:1145:C:O2'	1:A:1146:A:C8	2.64	0.46
1:A:1285:A:H8	1:A:1285:A:OP1	1.99	0.46
3:B:105:PHE:HB2	3:B:158:LEU:HD21	1.97	0.46
3:B:97:TRP:HH2	3:B:176:GLU:CD	2.20	0.46
4:C:139:GLN:O	4:C:143:GLU:N	2.37	0.46
5:D:103:ASN:O	5:D:106:TYR:HB3	2.16	0.46
5:D:17:VAL:CG1	5:D:18:LYS:N	2.79	0.46
6:E:115:VAL:HG11	6:E:118:ILE:CG1	2.46	0.46
21:T:67:ALA:HB2	21:T:77:ALA:HB2	1.97	0.46
1:A:1004:A:C8	1:A:1037:C:O2	2.69	0.46
1:A:1044:A:H2'	1:A:1045:C:C5'	2.46	0.46
1:A:1118:C:H2'	1:A:1119:C:H6	1.80	0.46
1:A:1183:A:C2'	1:A:1184:G:OP1	2.64	0.46
1:A:21:G:H2'	1:A:22:G:C8	2.50	0.46
1:A:253:U:H2'	1:A:254:G:H8	1.79	0.46
1:A:581:G:HO2'	18:Q:105:ALA:C	2.18	0.46
1:A:960:U:O2'	1:A:1223:C:H4'	2.16	0.46
4:C:139:GLN:O	4:C:140:ARG:C	2.54	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:64:VAL:HB	4:C:99:VAL:HB	1.98	0.46
5:D:114:ARG:NH1	5:D:114:ARG:HG3	2.26	0.46
6:E:112:LEU:C	6:E:114:GLY:H	2.18	0.46
10:I:108:VAL:CG1	10:I:109:VAL:H	2.29	0.46
1:A:1343:G:C1'	10:I:121:ARG:HH12	2.25	0.46
13:L:6:THR:HG1	13:L:9:GLN:HG3	1.79	0.46
15:N:59:ALA:HB1	15:N:61:TRP:HZ3	1.79	0.46
14:M:94:ARG:HH12	20:S:81:ARG:CD	2.29	0.46
1:A:101:A:H2'	1:A:102:G:H8	1.81	0.45
1:A:1150:U:H6	1:A:1150:U:O5'	2.00	0.45
1:A:1220:G:H1'	20:S:52:TYR:HD2	1.82	0.45
1:A:248:C:C2'	1:A:249:U:H5'	2.46	0.45
1:A:406:G:H2'	1:A:407:G:H8	1.82	0.45
1:A:421:U:H5'	1:A:422:C:H5	1.80	0.45
1:A:767:A:H2'	1:A:768:A:C8	2.51	0.45
6:E:9:LYS:HG3	6:E:112:LEU:HD11	1.97	0.45
6:E:93:PRO:HG3	9:H:105:ARG:HE	1.79	0.45
11:J:40:LEU:HB3	11:J:69:ASN:HB2	1.98	0.45
19:R:39:VAL:CG1	19:R:40:LEU:N	2.78	0.45
1:A:1256:A:H2	1:A:1258:G:C2	2.33	0.45
1:A:1286:A:C3'	1:A:1287:A:C5'	2.85	0.45
1:A:1514:C:H2'	1:A:1515:C:H6	1.80	0.45
1:A:281:G:HO2'	1:A:282:A:P	2.39	0.45
1:A:437:U:C5'	5:D:155:LEU:HD22	2.45	0.45
4:C:156:ARG:HH21	4:C:161:GLU:HA	1.82	0.45
4:C:172:ARG:HB3	4:C:172:ARG:NH1	2.32	0.45
4:C:35:GLU:CG	4:C:59:ARG:HH22	2.29	0.45
5:D:145:GLU:CG	5:D:184:LYS:HE2	2.47	0.45
5:D:68:TYR:OH	5:D:196:LEU:HD11	2.16	0.45
6:E:102:ALA:HA	6:E:120:THR:HG22	1.98	0.45
6:E:65:ASN:CG	6:E:65:ASN:O	2.55	0.45
7:F:43:LEU:N	7:F:43:LEU:CD2	2.79	0.45
8:G:156:TRP:OXT	8:G:156:TRP:HD1	2.00	0.45
10:I:120:ARG:O	10:I:121:ARG:C	2.54	0.45
10:I:42:ARG:O	10:I:43:ALA:C	2.54	0.45
11:J:21:GLN:O	11:J:25:GLU:HG3	2.16	0.45
14:M:94:ARG:NH1	20:S:81:ARG:HD3	2.30	0.45
7:F:101:ALA:CA	19:R:28:GLU:HB3	2.42	0.45
20:S:61:TYR:HD2	20:S:61:TYR:C	2.19	0.45
21:T:73:HIS:C	21:T:74:LYS:HG2	2.37	0.45
22:V:15:ARG:O	22:V:17:THR:HG23	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1286:A:H8	1:A:1287:A:C5'	2.29	0.45
1:A:1308:U:H2'	1:A:1309:G:H8	1.81	0.45
1:A:1313:U:OP2	20:S:6:LYS:HA	2.16	0.45
1:A:1366:C:C2	1:A:1367:C:C5	3.04	0.45
3:B:134:GLU:C	3:B:136:VAL:N	2.69	0.45
3:B:224:GLN:C	3:B:226:ARG:H	2.20	0.45
4:C:7:PRO:O	4:C:11:ARG:HD2	2.15	0.45
4:C:91:LEU:HD23	4:C:92:ALA:N	2.31	0.45
6:E:28:PHE:O	6:E:47:LYS:HA	2.16	0.45
8:G:78:ARG:HD2	8:G:156:TRP:CE3	2.50	0.45
11:J:8:LEU:HD21	11:J:96:ILE:HG12	1.97	0.45
13:L:32:PHE:CE1	13:L:86:ARG:HB2	2.52	0.45
16:O:45:VAL:HB	16:O:46:HIS:ND1	2.31	0.45
16:O:71:GLN:HG3	16:O:78:TYR:CE2	2.52	0.45
1:A:1149:C:OP1	10:I:9:ARG:HD3	2.15	0.45
1:A:1229:A:H2'	1:A:1230:C:C6	2.50	0.45
1:A:334:C:H2'	1:A:335:C:C6	2.52	0.45
1:A:429:U:H4'	1:A:430:A:O5'	2.16	0.45
1:A:682:G:O2'	1:A:683:G:H5'	2.16	0.45
1:A:993:G:HO2'	1:A:994:A:P	2.40	0.45
3:B:208:ILE:C	3:B:210:SER:N	2.70	0.45
5:D:162:LEU:HD13	5:D:181:MET:HG2	1.98	0.45
5:D:24:GLU:CG	5:D:25:ARG:N	2.78	0.45
6:E:115:VAL:HG12	6:E:116:THR:N	2.31	0.45
7:F:35:ALA:HA	7:F:67:MET:HB3	1.97	0.45
7:F:45:LEU:HA	7:F:58:GLY:O	2.16	0.45
10:I:7:THR:HG22	10:I:8:GLY:N	2.31	0.45
10:I:97:LYS:O	10:I:100:GLY:N	2.39	0.45
20:S:61:TYR:CD2	20:S:61:TYR:C	2.89	0.45
1:A:1021:G:C2	1:A:1022:G:H1'	2.52	0.45
1:A:1051:C:O2'	1:A:1052:U:H5'	2.16	0.45
1:A:1063:C:H3'	1:A:1064:G:H2'	1.99	0.45
1:A:1486:G:H2'	1:A:1487:G:C8	2.52	0.45
1:A:291:C:O2'	1:A:292:G:H5'	2.17	0.45
1:A:818:G:C3'	1:A:819:A:C5'	2.94	0.45
1:A:96:G:O2'	1:A:97:G:H5'	2.17	0.45
5:D:165:MET:HE2	5:D:176:LEU:CD1	2.46	0.45
5:D:205:GLU:O	5:D:208:SER:HB2	2.16	0.45
5:D:3:ARG:NH2	5:D:74:GLN:HG3	2.31	0.45
10:I:118:LYS:CB	10:I:118:LYS:NZ	2.80	0.45
10:I:44:VAL:HG13	10:I:51:ARG:NH2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:42:THR:HG22	13:L:52:LEU:HB3	1.96	0.45
13:L:87:GLY:H	13:L:98:TYR:HB3	1.81	0.45
17:P:81:ARG:HB2	17:P:81:ARG:HH11	1.82	0.45
1:A:1070:U:H2'	1:A:1071:C:C6	2.51	0.45
1:A:1435:G:H2'	1:A:1436:U:C6	2.51	0.45
1:A:1392:G:N2	1:A:1502:A:H8	2.14	0.45
1:A:375:U:C2	1:A:376:G:C8	3.05	0.45
1:A:538:G:H2'	1:A:539:A:C8	2.52	0.45
1:A:975:A:C5'	1:A:975:A:C8	2.97	0.45
3:B:100:GLY:O	3:B:104:ASN:N	2.48	0.45
3:B:112:VAL:O	3:B:116:GLU:HG3	2.16	0.45
3:B:117:GLU:O	3:B:120:ALA:HB3	2.16	0.45
5:D:60:GLU:HA	5:D:60:GLU:OE1	2.17	0.45
7:F:48:LEU:HD13	7:F:52:ILE:HD12	1.99	0.45
8:G:26:PHE:O	8:G:30:ILE:HG13	2.16	0.45
10:I:19:LEU:CD1	10:I:85:LEU:HD12	2.47	0.45
16:O:70:LEU:HD12	16:O:78:TYR:CA	2.47	0.45
17:P:47:ASP:OD2	17:P:47:ASP:C	2.54	0.45
19:R:47:THR:HA	19:R:83:GLU:CB	2.47	0.45
1:A:1181:G:O2'	1:A:1182:G:O4'	2.34	0.45
1:A:1300:G:O2'	1:A:1301:U:H6	2.00	0.45
1:A:1533:C:O2	1:A:1533:C:C2'	2.64	0.45
1:A:113:G:C1'	1:A:354:G:H5'	2.45	0.45
1:A:45:U:H2'	1:A:46:G:C8	2.52	0.45
3:B:132:LYS:HE2	3:B:135:GLN:OE1	2.17	0.45
3:B:103:THR:N	3:B:176:GLU:OE1	2.44	0.45
4:C:12:LEU:HD23	4:C:12:LEU:HA	1.63	0.45
4:C:152:ILE:N	4:C:199:LYS:O	2.50	0.45
5:D:170:VAL:O	5:D:171:GLY:C	2.55	0.45
9:H:112:LEU:H	9:H:112:LEU:HD23	1.82	0.45
10:I:97:LYS:HE2	10:I:102:LEU:HD12	1.98	0.45
11:J:12:ASP:OD1	11:J:14:LYS:N	2.49	0.45
12:K:38:ASN:HA	12:K:39:PRO:HD2	1.78	0.45
12:K:49:GLY:O	12:K:50:TYR:C	2.54	0.45
13:L:27:LEU:O	13:L:28:LYS:C	2.55	0.45
16:O:40:SER:O	16:O:44:LYS:HG2	2.17	0.45
18:Q:9:VAL:HG21	18:Q:84:LEU:HD13	1.97	0.45
1:A:1003(A):G:C6	1:A:1004:A:H1'	2.52	0.45
1:A:1069:C:O2'	1:A:1192:C:H1'	2.17	0.45
1:A:1440:C:C2'	1:A:1441:G:H5'	2.47	0.45
1:A:147:G:O2'	1:A:148:G:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.31	0.45
1:A:231:G:O2'	1:A:232:G:H5'	2.17	0.45
1:A:300:A:H2'	1:A:301:G:O4'	2.17	0.45
1:A:640:A:O2'	1:A:641:U:H5'	2.17	0.45
1:A:792:A:H4'	1:A:793:U:C5'	2.47	0.45
1:A:838:G:N2	1:A:849:C:C2	2.85	0.45
1:A:893:C:H2'	1:A:894:G:C8	2.51	0.45
1:A:953:G:H2'	1:A:954:G:O4'	2.16	0.45
3:B:187:LEU:HA	3:B:201:ILE:O	2.17	0.45
3:B:25:ASN:ND2	3:B:27:LYS:H	2.14	0.45
4:C:129:ALA:HB3	4:C:132:ARG:HD2	1.99	0.45
4:C:87:LEU:C	4:C:89:GLU:H	2.20	0.45
5:D:151:LYS:N	5:D:151:LYS:HD2	2.32	0.45
5:D:189:PRO:HB2	5:D:194:LEU:HD21	1.98	0.45
7:F:67:MET:CE	7:F:72:VAL:HA	2.46	0.45
8:G:46:ALA:HB1	8:G:121:ALA:HB2	1.99	0.45
10:I:4:TYR:CZ	10:I:88:TYR:HD1	2.35	0.45
11:J:30:SER:HB3	11:J:80:LYS:CG	2.47	0.45
12:K:48:ILE:O	12:K:49:GLY:C	2.55	0.45
13:L:59:ARG:NH1	13:L:65:GLU:HG2	2.32	0.45
17:P:81:ARG:CB	17:P:81:ARG:HH11	2.30	0.45
20:S:13:ASP:HA	20:S:16:LEU:HB3	1.98	0.45
1:A:1221:G:O3'	20:S:77:THR:HG21	2.15	0.45
1:A:1217:C:O2'	1:A:1218:C:H5'	2.17	0.45
1:A:130:A:N7	18:Q:63:ARG:HG3	2.32	0.45
1:A:1409:C:H2'	1:A:1410:G:C8	2.50	0.45
1:A:1509:C:C2'	1:A:1510:U:H5'	2.46	0.45
1:A:385:C:H2'	1:A:386:C:C6	2.52	0.45
1:A:560:U:H4'	1:A:561:U:H5''	1.97	0.45
1:A:822:C:O2'	1:A:823:G:H5'	2.17	0.45
1:A:986:A:C2	1:A:1220:G:C2	3.05	0.45
3:B:167:PRO:O	3:B:171:ALA:N	2.50	0.45
3:B:75:LYS:HD3	3:B:75:LYS:O	2.17	0.45
5:D:33:MET:HE3	5:D:37:PRO:CA	2.47	0.45
9:H:91:ARG:HG2	13:L:7:ILE:HG13	1.98	0.45
10:I:46:ALA:O	10:I:49:PRO:HD2	2.17	0.45
11:J:34:VAL:HG12	11:J:36:GLY:N	2.31	0.45
11:J:51:ARG:H	11:J:59:SER:HB3	1.80	0.45
15:N:21:TYR:CD2	15:N:21:TYR:O	2.70	0.45
16:O:27:VAL:O	16:O:30:ALA:N	2.50	0.45
16:O:45:VAL:O	16:O:46:HIS:C	2.54	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1305:G:H5''	22:V:4:GLY:C	2.37	0.45
1:A:1129:C:O2'	1:A:1130:A:OP2	2.27	0.45
1:A:1176:A:H2'	1:A:1177:G:O4'	2.16	0.45
1:A:243:A:N6	1:A:281:G:O2'	2.50	0.45
1:A:456:C:H2'	1:A:457:C:C6	2.52	0.45
1:A:61:G:O2'	1:A:62:U:H5'	2.17	0.45
1:A:967:C:H2'	1:A:968:A:C8	2.52	0.45
4:C:180:ALA:O	4:C:181:ASN:CB	2.62	0.45
4:C:43:LEU:HD23	4:C:43:LEU:H	1.79	0.45
4:C:91:LEU:C	4:C:91:LEU:HD23	2.38	0.45
5:D:199:ASN:HD21	5:D:201:GLN:CB	2.19	0.45
10:I:79:LEU:CD1	10:I:83:ARG:HD2	2.45	0.45
11:J:94:VAL:HG12	11:J:95:GLU:N	2.32	0.45
13:L:53:ARG:HD2	13:L:53:ARG:N	2.32	0.45
21:T:10:LEU:O	21:T:13:LEU:HD12	2.17	0.45
1:A:1055:A:C6	1:A:1056:U:C6	3.04	0.44
1:A:1115:C:H1'	15:N:61:TRP:O	2.17	0.44
1:A:1305:G:N2	1:A:1331:G:HO2'	2.15	0.44
1:A:16:A:C2'	1:A:17:U:H5'	2.47	0.44
1:A:281:G:O2'	1:A:282:A:P	2.74	0.44
1:A:437:U:H5''	5:D:155:LEU:CD2	2.44	0.44
1:A:446:G:O2'	1:A:447:G:H5'	2.17	0.44
1:A:836:G:C6	1:A:851:G:C5	3.05	0.44
1:A:900:A:H2'	1:A:901:A:C8	2.52	0.44
1:A:922:G:N3	1:A:1398:A:H2	2.15	0.44
1:A:939:G:H5''	8:G:102:ARG:HH22	1.78	0.44
3:B:101:MET:HG2	3:B:108:ILE:HD13	1.97	0.44
3:B:108:ILE:O	3:B:108:ILE:CG2	2.65	0.44
4:C:82:GLU:O	4:C:85:ARG:HB3	2.17	0.44
11:J:34:VAL:HG12	11:J:36:GLY:H	1.82	0.44
11:J:38:ILE:O	11:J:70:ARG:HA	2.17	0.44
13:L:24:VAL:HG12	13:L:24:VAL:O	2.17	0.44
14:M:48:LEU:HD23	14:M:48:LEU:HA	1.85	0.44
19:R:43:PHE:HD1	19:R:66:LEU:HD11	1.81	0.44
21:T:53:LEU:HD21	21:T:104:LEU:CD1	2.46	0.44
1:A:1059:C:O2'	1:A:1060:C:H5'	2.17	0.44
1:A:1129:C:O2'	1:A:1130:A:P	2.75	0.44
1:A:1216:G:H2'	1:A:1217:C:C6	2.52	0.44
1:A:1477:C:H2'	1:A:1478:C:C6	2.51	0.44
1:A:19:C:OP1	6:E:125:SER:OG	2.24	0.44
1:A:491:G:H2'	1:A:492:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:156:LYS:O	3:B:156:LYS:HD3	2.17	0.44
4:C:70:VAL:C	4:C:106:VAL:HG23	2.37	0.44
5:D:25:ARG:HA	5:D:28:SER:OG	2.17	0.44
1:A:412:A:N1	5:D:35:ARG:HB3	2.32	0.44
6:E:118:ILE:CG2	6:E:119:LEU:N	2.79	0.44
8:G:20:ASP:OD1	8:G:21:VAL:N	2.50	0.44
9:H:112:LEU:HD23	9:H:112:LEU:N	2.33	0.44
15:N:18:VAL:C	15:N:20:ALA:H	2.20	0.44
1:A:1096:C:H2'	1:A:1097:C:H6	1.82	0.44
1:A:1162:C:H2'	1:A:1163:C:C6	2.52	0.44
1:A:1161:C:H2'	1:A:1162:C:H6	1.83	0.44
1:A:538:G:O2'	1:A:539:A:H5'	2.17	0.44
3:B:109:SER:C	3:B:111:ARG:H	2.20	0.44
4:C:30:ARG:HG2	4:C:30:ARG:HH11	1.83	0.44
5:D:150:GLU:HG3	5:D:153:ARG:HH21	1.83	0.44
5:D:162:LEU:HD23	5:D:162:LEU:HA	1.66	0.44
9:H:120:THR:O	9:H:121:ASP:C	2.55	0.44
9:H:39:LEU:HD11	9:H:137:VAL:HG21	2.00	0.44
10:I:43:ALA:C	10:I:45:ALA:H	2.20	0.44
1:A:1129:C:OP1	10:I:62:TYR:CE2	2.71	0.44
11:J:65:LEU:C	11:J:65:LEU:HD23	2.38	0.44
12:K:110:ASP:HB3	19:R:85:LEU:HB3	2.00	0.44
12:K:30:VAL:HG21	12:K:65:ALA:HA	1.98	0.44
14:M:80:ARG:C	14:M:82:MET:N	2.70	0.44
19:R:55:ARG:HB3	19:R:55:ARG:CZ	2.46	0.44
1:A:294:U:H2'	1:A:295:C:H6	1.83	0.44
1:A:337:C:O2'	1:A:338:A:H5'	2.18	0.44
1:A:452:A:H2'	1:A:453:A:C8	2.53	0.44
1:A:818:G:H3'	1:A:819:A:H5''	2.00	0.44
3:B:132:LYS:O	3:B:136:VAL:HG23	2.17	0.44
3:B:140:HIS:O	3:B:143:GLU:HB2	2.18	0.44
3:B:178:ARG:NH1	3:B:178:ARG:CG	2.76	0.44
3:B:80:ILE:CD1	3:B:212:GLN:HB2	2.43	0.44
3:B:231:GLU:OE1	3:B:232:PRO:O	2.35	0.44
3:B:10:LEU:CD2	3:B:48:MET:HG3	2.48	0.44
3:B:58:ILE:O	3:B:59:GLU:C	2.56	0.44
7:F:94:GLN:CB	19:R:32:ARG:HD3	2.46	0.44
1:A:1231:G:H4'	10:I:126:SER:HB3	1.98	0.44
12:K:17:GLY:O	12:K:80:VAL:HA	2.17	0.44
13:L:18:VAL:CG1	13:L:19:ARG:N	2.80	0.44
14:M:80:ARG:C	14:M:82:MET:H	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:50:ALA:HA	20:S:58:VAL:O	2.18	0.44
1:A:1127:G:H1'	1:A:1148:U:H3	1.81	0.44
1:A:1461:G:O2'	1:A:1462:G:H5'	2.17	0.44
1:A:179:A:H2'	1:A:180:U:C6	2.52	0.44
1:A:252:U:H2'	1:A:253:U:C6	2.53	0.44
1:A:313:A:H2'	1:A:314:C:C6	2.53	0.44
1:A:396:G:O2'	1:A:398:C:OP1	2.27	0.44
3:B:97:TRP:CZ2	3:B:102:LEU:HD13	2.48	0.44
3:B:122:PHE:CE2	3:B:139:LYS:HG2	2.41	0.44
3:B:10:LEU:HG	3:B:48:MET:HE1	1.99	0.44
5:D:151:LYS:CD	5:D:151:LYS:H	2.31	0.44
8:G:38:LEU:O	8:G:42:ILE:HG13	2.17	0.44
9:H:24:THR:HG22	9:H:61:VAL:O	2.18	0.44
12:K:12:ARG:O	12:K:13:GLN:HB2	2.18	0.44
14:M:24:GLY:HA3	14:M:66:LEU:HD22	1.99	0.44
17:P:71:ARG:HD3	17:P:75:ARG:HH21	1.83	0.44
20:S:28:LYS:HG2	20:S:29:ARG:N	2.32	0.44
20:S:30:LEU:O	20:S:31:ILE:HD13	2.18	0.44
1:A:1221:G:H1'	20:S:54:GLY:HA3	2.00	0.44
1:A:1190:G:C2'	1:A:1191:A:OP2	2.65	0.44
1:A:1427:U:H2'	1:A:1428:A:H8	1.81	0.44
24:A:1632:HYG:C1	24:A:1632:HYG:O14	2.65	0.44
1:A:166:G:O2'	1:A:167:G:H5'	2.18	0.44
1:A:224:C:H2'	1:A:225:C:H6	1.83	0.44
1:A:113:G:H1'	1:A:354:G:C5'	2.45	0.44
1:A:424:G:H2'	1:A:425:G:H8	1.83	0.44
1:A:518:C:H4'	1:A:519:C:O5'	2.18	0.44
1:A:942:G:C2	1:A:943:U:C6	3.05	0.44
1:A:952:U:O2'	1:A:953:G:H5'	2.17	0.44
3:B:125:PRO:C	3:B:127:ILE:H	2.20	0.44
3:B:132:LYS:C	3:B:134:GLU:N	2.70	0.44
3:B:24:TRP:CG	3:B:25:ASN:N	2.85	0.44
4:C:79:ARG:HG3	4:C:79:ARG:O	2.16	0.44
8:G:138:LYS:HE2	8:G:142:GLU:OE1	2.17	0.44
8:G:95:ARG:O	8:G:96:GLN:C	2.56	0.44
10:I:58:ARG:CG	10:I:58:ARG:HH11	2.31	0.44
11:J:30:SER:HB3	11:J:80:LYS:HG3	1.99	0.44
11:J:69:ASN:O	11:J:70:ARG:CD	2.66	0.44
12:K:69:ALA:O	12:K:73:MET:N	2.50	0.44
14:M:73:GLU:O	14:M:74:VAL:C	2.56	0.44
14:M:74:VAL:O	14:M:77:ASN:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:3:ARG:O	15:N:4:LYS:C	2.53	0.44
15:N:3:ARG:CZ	15:N:6:LEU:HG	2.48	0.44
1:A:636:U:C5'	18:Q:2:PRO:HG2	2.47	0.44
19:R:52:PRO:HB2	19:R:54:ARG:CD	2.47	0.44
1:A:1115:C:O2'	1:A:1116:C:H5'	2.17	0.44
1:A:1272:G:H2'	1:A:1273:G:H8	1.82	0.44
1:A:411:A:C8	1:A:413:G:H1'	2.53	0.44
1:A:52:G:H2'	1:A:53:A:H8	1.82	0.44
3:B:87:ARG:NH2	3:B:220:ASP:OD1	2.39	0.44
3:B:8:LYS:HD3	3:B:9:GLU:N	2.32	0.44
6:E:43:LEU:HD23	6:E:44:GLY:H	1.82	0.44
7:F:44:GLY:O	7:F:59:TYR:HA	2.17	0.44
3:B:181:PHE:HD2	9:H:70:GLN:HB3	1.81	0.44
16:O:71:GLN:HB2	16:O:78:TYR:CE1	2.52	0.44
1:A:375:U:H4'	17:P:17:TYR:CE2	2.51	0.44
17:P:82:GLN:O	17:P:83:GLU:C	2.56	0.44
1:A:1352:C:H2'	1:A:1353:G:O4'	2.17	0.44
1:A:781:A:H2	1:A:1514:C:H4'	1.82	0.44
1:A:409:G:O2'	1:A:410:G:H5'	2.18	0.44
1:A:458:C:O2'	1:A:459:G:H5'	2.18	0.44
3:B:109:SER:C	3:B:111:ARG:N	2.70	0.44
3:B:167:PRO:HG2	3:B:192:SER:OG	2.18	0.44
4:C:30:ARG:HG2	4:C:30:ARG:NH1	2.32	0.44
12:K:48:ILE:HD13	12:K:63:LEU:HB2	1.99	0.44
19:R:47:THR:C	19:R:49:LYS:H	2.21	0.44
19:R:52:PRO:O	19:R:56:THR:HG23	2.18	0.44
1:A:1347:G:C2'	1:A:1348:U:OP2	2.65	0.44
1:A:1417:G:N2	1:A:1484:C:N4	2.66	0.44
1:A:160:A:H1'	1:A:344:A:C5	2.52	0.44
1:A:186:C:H2'	1:A:187:C:H6	1.83	0.44
1:A:250:A:C2	1:A:274:A:C6	3.06	0.44
3:B:23:ARG:HH11	3:B:24:TRP:CA	2.30	0.44
3:B:53:ARG:HH11	3:B:53:ARG:HG2	1.83	0.44
5:D:68:TYR:N	5:D:68:TYR:CD1	2.85	0.44
8:G:18:TYR:N	8:G:18:TYR:CD1	2.85	0.44
9:H:119:LEU:HD23	9:H:119:LEU:N	2.33	0.44
9:H:4:ASP:HB3	9:H:7:ALA:HB3	2.00	0.44
10:I:49:PRO:CD	10:I:78:LYS:HG2	2.48	0.44
12:K:82:VAL:HG23	12:K:105:VAL:HG13	2.00	0.44
14:M:26:GLY:C	14:M:28:ALA:N	2.71	0.44
14:M:37:THR:CG2	14:M:37:THR:O	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:80:GLY:O	18:Q:81:ARG:CB	2.66	0.44
1:A:1202:G:O4'	15:N:29:ARG:HD3	2.18	0.43
1:A:1272:G:O2'	1:A:1273:G:H5'	2.18	0.43
1:A:1394:A:C5	1:A:1501:C:H4'	2.53	0.43
1:A:1490:C:O2'	1:A:1491:G:H5'	2.18	0.43
24:A:1632:HYG:H30	24:A:1632:HYG:H12	1.81	0.43
1:A:253:U:H2'	1:A:254:G:C8	2.53	0.43
1:A:489:C:H2'	1:A:490:G:C8	2.46	0.43
1:A:718:G:H5'	1:A:719:C:OP2	2.18	0.43
1:A:864:A:H2'	1:A:865:A:C8	2.53	0.43
6:E:11:ILE:HG23	6:E:105:VAL:HG22	2.00	0.43
1:A:1249:C:O2'	10:I:73:GLN:NE2	2.51	0.43
1:A:1054:C:O2'	1:A:1055:A:H5''	2.18	0.43
1:A:1157:A:H4'	1:A:1158:C:O5'	2.18	0.43
1:A:1223:C:P	20:S:78:ARG:NH1	2.90	0.43
1:A:1376:U:H2'	1:A:1377:A:C8	2.53	0.43
1:A:1519:A:H2'	1:A:1520:G:H5'	2.00	0.43
1:A:182:U:O4	1:A:223:U:H1'	2.18	0.43
1:A:521:G:O2'	1:A:522:C:H5'	2.18	0.43
3:B:84:GLU:HG3	3:B:215:LEU:HB3	2.00	0.43
4:C:5:ILE:C	4:C:5:ILE:HD12	2.38	0.43
5:D:162:LEU:CD1	5:D:181:MET:HG2	2.48	0.43
8:G:18:TYR:CD2	8:G:59:LEU:HD22	2.52	0.43
11:J:12:ASP:O	11:J:15:THR:HG22	2.18	0.43
1:A:1353:G:OP2	22:V:3:LYS:HE2	2.18	0.43
1:A:1301:U:O2'	1:A:1302:U:P	2.77	0.43
1:A:169:C:O2'	1:A:170:U:H5'	2.18	0.43
1:A:264:U:H4'	18:Q:63:ARG:HD3	1.99	0.43
1:A:352:C:H4'	1:A:354:G:OP1	2.18	0.43
1:A:586:C:O2'	1:A:878:G:H4'	2.18	0.43
1:A:992:U:O2'	1:A:993:G:OP2	2.31	0.43
3:B:88:ALA:C	3:B:90:MET:N	2.71	0.43
4:C:99:VAL:CG2	4:C:100:ALA:N	2.81	0.43
1:A:921:U:O2'	6:E:19:MET:O	2.28	0.43
7:F:36:ARG:NH1	7:F:38:GLU:HG2	2.34	0.43
8:G:151:TYR:N	8:G:151:TYR:CD1	2.85	0.43
11:J:12:ASP:HB3	11:J:15:THR:HB	2.00	0.43
11:J:90:LEU:N	11:J:91:PRO:HD2	2.29	0.43
13:L:34:ARG:HB3	13:L:105:TYR:HE1	1.83	0.43
21:T:54:LYS:HA	21:T:57:ARG:HD3	2.00	0.43
1:A:1003(A):G:H2'	1:A:1004:A:C4'	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1111:A:H2'	1:A:1112:C:H6	1.82	0.43
1:A:1117:G:N2	1:A:1180:A:H1'	2.33	0.43
1:A:1426:C:O2'	1:A:1427:U:H5'	2.19	0.43
1:A:926:G:H3'	1:A:1505:G:H21	1.83	0.43
1:A:186:C:H2'	1:A:187:C:C6	2.53	0.43
3:B:17:PHE:N	3:B:44:LEU:HD21	2.33	0.43
4:C:92:ALA:C	4:C:94:LEU:N	2.70	0.43
6:E:5:ASP:CG	6:E:6:PHE:H	2.22	0.43
8:G:129:GLU:CB	8:G:131:LYS:HE2	2.49	0.43
9:H:1:MET:CG	9:H:2:LEU:N	2.77	0.43
10:I:23:ASN:ND2	10:I:23:ASN:C	2.72	0.43
17:P:38:TYR:O	17:P:49:LEU:HD12	2.19	0.43
20:S:51:VAL:HG12	20:S:52:TYR:H	1.82	0.43
1:A:1417:G:N2	1:A:1484:C:H42	2.17	0.43
1:A:1509:C:O2'	1:A:1510:U:H5'	2.18	0.43
1:A:327:A:HO2'	1:A:328:C:H6	1.65	0.43
3:B:129:GLU:O	3:B:130:ARG:HB2	2.19	0.43
3:B:85:ALA:O	3:B:90:MET:O	2.37	0.43
4:C:147:LYS:HE2	4:C:205:GLY:CA	2.48	0.43
4:C:46:GLU:HB2	4:C:47:LEU:HD12	2.01	0.43
4:C:8:ILE:C	4:C:10:PHE:H	2.22	0.43
5:D:209:ARG:NH1	5:D:209:ARG:HG2	2.32	0.43
1:A:1298:C:N4	8:G:114:ARG:HB3	2.33	0.43
8:G:152:ALA:C	8:G:154:TYR:H	2.22	0.43
10:I:97:LYS:CE	10:I:102:LEU:HD12	2.49	0.43
11:J:15:THR:HG23	11:J:94:VAL:HG22	2.01	0.43
14:M:117:VAL:CG1	14:M:118:ALA:N	2.81	0.43
14:M:40:ASN:HD22	14:M:40:ASN:C	2.22	0.43
15:N:53:LEU:HA	15:N:54:PRO:HD2	1.85	0.43
17:P:36:ILE:O	17:P:51:VAL:O	2.36	0.43
20:S:3:ARG:O	20:S:4:SER:HB3	2.18	0.43
1:A:1014:A:C2	1:A:1219:U:H1'	2.53	0.43
1:A:1243:C:H2'	1:A:1244:C:C6	2.54	0.43
1:A:1329:A:O2'	1:A:1330:U:H5'	2.19	0.43
3:B:16:HIS:CD2	3:B:210:SER:OG	2.71	0.43
3:B:217:ARG:HA	3:B:220:ASP:OD2	2.19	0.43
5:D:174:LEU:C	5:D:186:LEU:HD12	2.39	0.43
5:D:174:LEU:O	5:D:186:LEU:HD12	2.18	0.43
5:D:189:PRO:HB2	5:D:194:LEU:CD2	2.48	0.43
8:G:80:VAL:O	8:G:82:GLY:N	2.51	0.43
1:A:755:G:H1'	9:H:1:MET:CE	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:39:LEU:HD13	9:H:39:LEU:HA	1.87	0.43
10:I:55:ALA:O	10:I:57:GLY:N	2.51	0.43
11:J:53:PRO:O	11:J:54:PHE:O	2.37	0.43
11:J:85:LEU:O	11:J:87:THR:N	2.52	0.43
19:R:39:VAL:HG13	19:R:40:LEU:HD23	2.00	0.43
20:S:16:LEU:C	20:S:18:LYS:N	2.68	0.43
1:A:1118:C:H2'	1:A:1119:C:C6	2.54	0.43
1:A:156:G:O2'	1:A:157:G:H5'	2.19	0.43
1:A:230:G:H2'	1:A:231:G:O4'	2.19	0.43
1:A:250:A:H2	1:A:274:A:C6	2.36	0.43
1:A:518:C:O2'	1:A:519:C:OP2	2.30	0.43
1:A:718:G:H4'	12:K:117:ASN:HD21	1.84	0.43
1:A:741:G:H5''	16:O:39:LEU:HD12	2.00	0.43
1:A:570:G:H1'	1:A:820:U:C4	2.53	0.43
4:C:114:PRO:O	4:C:118:GLN:HG3	2.18	0.43
4:C:188:LEU:HD22	4:C:188:LEU:HA	1.84	0.43
6:E:124:GLY:O	6:E:126:ARG:N	2.52	0.43
6:E:43:LEU:HD22	6:E:44:GLY:N	2.34	0.43
13:L:83:VAL:CG2	13:L:84:LEU:N	2.74	0.43
18:Q:24:GLU:CD	18:Q:37:LYS:HD3	2.38	0.43
20:S:40:ILE:HB	20:S:67:VAL:O	2.19	0.43
21:T:61:SER:O	21:T:65:LYS:HG3	2.18	0.43
1:A:1009:G:C6	1:A:1021:G:C6	3.07	0.43
1:A:1034:G:O2'	1:A:1035:A:H5'	2.19	0.43
1:A:1064:G:C2	1:A:1066:C:N4	2.87	0.43
1:A:1127:G:H21	1:A:1147:C:N4	2.17	0.43
1:A:1402:C:H2'	1:A:1403:C:O4'	2.18	0.43
1:A:1424:C:O2'	1:A:1425:U:H5'	2.19	0.43
1:A:386:C:C2'	1:A:387:U:H5'	2.49	0.43
1:A:448:A:O2'	1:A:449:C:C5'	2.66	0.43
1:A:542:G:H2'	1:A:543:C:H6	1.83	0.43
1:A:976:G:C8	1:A:1358:U:C2	3.07	0.43
3:B:208:ILE:O	3:B:209:ARG:C	2.57	0.43
5:D:156:GLU:HG2	5:D:160:GLN:NE2	2.21	0.43
5:D:163:GLU:OE2	5:D:166:LYS:HE3	2.19	0.43
9:H:60:ARG:CG	9:H:60:ARG:NH1	2.80	0.43
8:G:151:TYR:OH	12:K:54:ARG:NE	2.52	0.43
1:A:502:G:OP1	13:L:118:SER:CB	2.67	0.43
13:L:60:LEU:HD21	13:L:85:ILE:CD1	2.48	0.43
1:A:129(A):G:C2	1:A:190(E):U:H5'	2.54	0.43
1:A:421:U:H5'	1:A:422:C:C5	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:446:G:C2'	1:A:447:G:H5'	2.49	0.43
1:A:31:G:H1	1:A:48:C:H5''	1.83	0.43
3:B:120:ALA:O	3:B:124:SER:HB3	2.19	0.43
3:B:218:ALA:O	3:B:222:ILE:HG13	2.18	0.43
3:B:34:ALA:O	3:B:41:ILE:N	2.51	0.43
4:C:7:PRO:CG	4:C:184:TYR:HB2	2.49	0.43
5:D:114:ARG:CG	5:D:114:ARG:NH1	2.82	0.43
5:D:61:LYS:HA	5:D:203:VAL:HG22	2.00	0.43
10:I:58:ARG:HD2	10:I:58:ARG:C	2.39	0.43
10:I:5:TYR:CG	10:I:6:GLY:N	2.87	0.43
11:J:55:LYS:O	11:J:56:HIS:HB2	2.18	0.43
11:J:6:ILE:HG13	11:J:71:LEU:O	2.19	0.43
13:L:102:ARG:HB3	13:L:102:ARG:HE	1.69	0.43
20:S:20:LEU:HB3	20:S:23:ASN:HD22	1.84	0.43
21:T:72:LEU:O	21:T:73:HIS:O	2.36	0.43
1:A:1060:C:OP1	15:N:45:ARG:NH2	2.49	0.43
1:A:1097:C:H2'	1:A:1098:C:C6	2.52	0.43
1:A:1221:G:H4'	20:S:53:ASN:O	2.18	0.43
1:A:386:C:O2'	1:A:387:U:H5'	2.18	0.43
1:A:434:U:H2'	1:A:435:C:H6	1.78	0.43
1:A:452:A:O2'	1:A:453:A:O4'	2.24	0.43
1:A:620:C:H2'	1:A:621:A:O4'	2.18	0.43
1:A:688:G:N3	1:A:704:A:C2	2.87	0.43
1:A:761:G:H2'	1:A:762:C:H6	1.83	0.43
1:A:92:C:O2'	1:A:93:G:H5'	2.19	0.43
7:F:78:GLU:O	7:F:81:ILE:HG13	2.18	0.43
10:I:7:THR:O	10:I:15:ALA:O	2.37	0.43
10:I:36:TYR:HD2	10:I:37:PHE:CE2	2.37	0.43
10:I:44:VAL:CG1	10:I:51:ARG:NH2	2.82	0.43
11:J:3:LYS:HG3	11:J:75:ILE:HG23	2.01	0.43
11:J:51:ARG:H	11:J:59:SER:HB2	1.83	0.43
11:J:39:PRO:O	11:J:69:ASN:O	2.37	0.43
11:J:30:SER:HB2	11:J:80:LYS:HB3	2.00	0.43
14:M:123:ALA:O	14:M:125:ARG:N	2.51	0.43
14:M:37:THR:CG2	14:M:39:ILE:HD11	2.49	0.43
17:P:65:GLN:HA	17:P:66:PRO:HD2	1.85	0.43
12:K:84:VAL:CG2	19:R:88:LYS:HD3	2.44	0.43
21:T:92:LEU:HD23	21:T:92:LEU:HA	1.88	0.43
1:A:1262:C:O2'	1:A:1263:C:H5'	2.19	0.42
1:A:54:C:H2'	1:A:352:C:H41	1.84	0.42
1:A:720:C:H2'	1:A:721:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:849:C:O2'	1:A:850:U:H5'	2.19	0.42
3:B:46:LYS:C	3:B:48:MET:N	2.72	0.42
8:G:69:VAL:O	8:G:69:VAL:HG12	2.19	0.42
8:G:75:VAL:CG1	8:G:86:GLN:HB3	2.49	0.42
10:I:23:ASN:HD22	10:I:23:ASN:C	2.22	0.42
10:I:89:ASN:C	10:I:91:ASP:H	2.21	0.42
1:A:1280:A:O4'	11:J:41:PRO:HG3	2.19	0.42
14:M:13:LYS:O	14:M:14:ARG:C	2.57	0.42
16:O:8:LYS:HE3	16:O:31:LEU:HD23	2.01	0.42
17:P:21:VAL:HG12	17:P:22:THR:N	2.33	0.42
17:P:19:ILE:N	17:P:37:GLY:O	2.52	0.42
21:T:57:ARG:CG	21:T:57:ARG:HH11	2.32	0.42
1:A:1360:A:H2'	1:A:1361:G:O4'	2.18	0.42
1:A:1368:G:OP2	10:I:112:LYS:HD2	2.19	0.42
1:A:815:A:N6	1:A:1509:C:H1'	2.34	0.42
1:A:370:C:H2'	1:A:371:G:H8	1.83	0.42
1:A:923:A:O4'	1:A:1398:A:C2	2.72	0.42
4:C:7:PRO:HG2	4:C:184:TYR:CB	2.49	0.42
4:C:188:LEU:HD13	4:C:195:VAL:HG13	2.01	0.42
6:E:15:ARG:CD	6:E:26:PHE:CD2	3.01	0.42
8:G:145:ALA:O	8:G:147:ALA:N	2.52	0.42
1:A:1250:A:C4'	10:I:68:GLY:H	2.28	0.42
13:L:32:PHE:HE1	13:L:86:ARG:HB2	1.84	0.42
20:S:10:PHE:O	20:S:39:THR:HB	2.19	0.42
20:S:67:VAL:HG12	20:S:68:GLY:N	2.33	0.42
1:A:1222:G:O2'	1:A:1223:C:H5'	2.19	0.42
1:A:1279:A:O2'	1:A:1281:U:OP2	2.37	0.42
1:A:265:G:H2'	1:A:267:C:H5	1.85	0.42
1:A:748:C:H1'	1:A:749:C:C5	2.53	0.42
3:B:19:HIS:NE2	3:B:206:ASP:CB	2.82	0.42
4:C:151:VAL:C	4:C:152:ILE:HG13	2.40	0.42
4:C:175:LEU:HD11	4:C:201:TYR:CE2	2.54	0.42
4:C:3:ASN:C	4:C:4:LYS:HG2	2.40	0.42
5:D:163:GLU:C	5:D:165:MET:N	2.71	0.42
7:F:23:LYS:HE2	7:F:23:LYS:HB3	1.86	0.42
7:F:80:ARG:HH11	7:F:80:ARG:HG2	1.84	0.42
1:A:738:C:P	7:F:92:LYS:HE3	2.59	0.42
11:J:51:ARG:N	11:J:59:SER:HB2	2.34	0.42
1:A:656:C:O2'	16:O:28:GLN:OE1	2.30	0.42
17:P:17:TYR:HE1	17:P:41:PRO:HG2	1.83	0.42
18:Q:65:ILE:O	18:Q:65:ILE:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:71:LEU:O	20:S:74:PHE:N	2.39	0.42
21:T:58:LYS:O	21:T:62:LEU:HG	2.19	0.42
1:A:1010:G:H2'	1:A:1011:G:H8	1.84	0.42
1:A:1033:G:H2'	1:A:1034:G:C8	2.54	0.42
1:A:1061:G:H2'	1:A:1062:U:H5'	2.00	0.42
1:A:1501:C:OP2	1:A:1504:G:H2'	2.19	0.42
1:A:20:U:O2'	1:A:21:G:H5'	2.19	0.42
1:A:41:G:H2'	1:A:42:G:C8	2.54	0.42
1:A:496:A:H4'	1:A:497:A:OP1	2.19	0.42
1:A:925:G:C2	1:A:927:G:C8	3.07	0.42
3:B:164:VAL:HG12	3:B:186:ALA:HB1	2.01	0.42
3:B:208:ILE:HG21	3:B:239:VAL:HA	2.01	0.42
3:B:90:MET:HA	3:B:91:PRO:HD3	1.85	0.42
3:B:70:PHE:O	3:B:92:TYR:HA	2.19	0.42
4:C:86:VAL:O	4:C:90:GLU:HB2	2.20	0.42
5:D:152:SER:O	5:D:154:ASN:N	2.53	0.42
7:F:33:TYR:CB	7:F:75:LEU:HD23	2.45	0.42
8:G:75:VAL:HG11	8:G:86:GLN:HB3	2.01	0.42
10:I:99:LEU:HB3	10:I:101:PHE:CE1	2.54	0.42
11:J:46:ARG:HD3	11:J:64:GLU:HB3	2.01	0.42
15:N:27:CYS:SG	15:N:29:ARG:CB	3.04	0.42
17:P:52:ASP:OD2	17:P:55:ARG:HG3	2.19	0.42
17:P:71:ARG:HG3	17:P:80:PHE:CZ	2.54	0.42
19:R:87:ARG:CG	19:R:87:ARG:HH11	2.28	0.42
22:V:2:GLY:O	22:V:4:GLY:N	2.53	0.42
1:A:1240:U:P	8:G:116:ALA:HB2	2.59	0.42
1:A:1256:A:H5'	1:A:1258:G:C1'	2.49	0.42
1:A:1391:U:H2'	1:A:1392:G:H8	1.79	0.42
1:A:220:G:O2'	1:A:221:C:H5'	2.19	0.42
1:A:397:A:H3'	1:A:397:A:N3	2.34	0.42
1:A:401:C:O2'	1:A:402:G:H5'	2.19	0.42
1:A:42:G:H2'	1:A:43:C:H6	1.85	0.42
1:A:439:A:C4	1:A:497:A:C2	3.08	0.42
7:F:78:GLU:HA	7:F:81:ILE:CD1	2.49	0.42
12:K:40:ILE:HG23	12:K:75:TYR:CE2	2.55	0.42
13:L:89:ARG:O	13:L:99:HIS:HE1	2.02	0.42
17:P:42:ARG:O	17:P:43:LYS:C	2.58	0.42
17:P:48:TRP:O	17:P:49:LEU:HB2	2.20	0.42
1:A:376:G:OP2	17:P:67:THR:HG21	2.20	0.42
1:A:1113:C:H4'	4:C:14:ILE:CD1	2.46	0.42
1:A:1113:C:O2'	1:A:1114:C:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:A:H5''	1:A:345:C:H5	1.85	0.42
1:A:644:G:C5	1:A:645:C:C5	3.08	0.42
1:A:782:A:C6	1:A:801:U:C2	3.08	0.42
3:B:25:ASN:ND2	3:B:25:ASN:C	2.67	0.42
4:C:178:LEU:O	4:C:179:ARG:CB	2.66	0.42
4:C:84:ILE:O	4:C:84:ILE:HG12	2.19	0.42
5:D:150:GLU:O	5:D:152:SER:N	2.53	0.42
5:D:61:LYS:NZ	5:D:62:GLN:NE2	2.67	0.42
10:I:127:LYS:HD2	10:I:127:LYS:N	2.35	0.42
14:M:10:PRO:HB3	14:M:18:ALA:O	2.19	0.42
14:M:49:THR:HB	14:M:52:GLU:HG3	2.00	0.42
20:S:22:LEU:CD2	20:S:28:LYS:HD2	2.49	0.42
20:S:31:ILE:HG22	20:S:32:LYS:N	2.35	0.42
20:S:40:ILE:HG21	20:S:62:ILE:HD13	2.02	0.42
1:A:1031:G:H2'	1:A:1032:G:H8	1.85	0.42
1:A:1206:G:C6	1:A:1207:G:C5	3.08	0.42
1:A:1403:C:H1'	1:A:1500:A:N1	2.35	0.42
1:A:323:U:H2'	1:A:324:G:O4'	2.20	0.42
1:A:411:A:C2	1:A:431:A:N6	2.88	0.42
1:A:731:G:OP1	1:A:766:A:H1'	2.20	0.42
1:A:90:U:H2'	1:A:91:C:C6	2.55	0.42
4:C:134:ILE:HG23	4:C:151:VAL:HB	2.01	0.42
5:D:30:LYS:C	5:D:32:ALA:N	2.70	0.42
7:F:27:GLN:NE2	7:F:27:GLN:HA	2.34	0.42
8:G:116:ALA:HA	8:G:119:ARG:NH2	2.35	0.42
8:G:77:SER:O	8:G:78:ARG:HB2	2.19	0.42
9:H:45:ILE:HG13	9:H:47:GLY:H	1.85	0.42
10:I:93:ARG:O	10:I:95:LYS:N	2.53	0.42
11:J:8:LEU:CD1	11:J:20:ALA:HB2	2.49	0.42
1:A:449:C:O2	17:P:42:ARG:HD2	2.20	0.42
1:A:1041:A:H2'	1:A:1042:G:C8	2.55	0.42
1:A:1131:G:H2'	1:A:1132:C:C6	2.54	0.42
1:A:1231:G:OP1	10:I:127:LYS:NZ	2.53	0.42
1:A:1342:C:O2'	1:A:1343:G:H5'	2.20	0.42
1:A:275:G:H5'	18:Q:14:LYS:HD3	2.02	0.42
1:A:429:U:OP2	5:D:36:ARG:NH1	2.52	0.42
1:A:460:A:N7	1:A:462:G:C6	2.88	0.42
1:A:851:G:H2'	1:A:852:G:H8	1.85	0.42
1:A:862:C:O4'	1:A:874:G:H4'	2.20	0.42
3:B:107:THR:C	3:B:109:SER:N	2.73	0.42
3:B:68:ILE:H	3:B:90:MET:CE	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:85:ALA:CB	3:B:92:TYR:HB3	2.50	0.42
4:C:116:VAL:O	4:C:119:ARG:HB3	2.20	0.42
4:C:19:GLU:HG2	4:C:54:ARG:HE	1.85	0.42
4:C:64:VAL:HB	4:C:99:VAL:CB	2.49	0.42
5:D:126:ILE:HG22	5:D:127:THR:N	2.35	0.42
5:D:57:ARG:HB3	5:D:206:PHE:HB2	2.00	0.42
9:H:7:ALA:HB2	9:H:85:ARG:CD	2.50	0.42
10:I:114:TYR:CD1	11:J:60:ARG:HB2	2.55	0.42
10:I:26:VAL:HG12	10:I:28:VAL:HG23	2.01	0.42
10:I:48:GLU:N	10:I:49:PRO:CD	2.81	0.42
11:J:34:VAL:HG22	11:J:74:ILE:CG2	2.48	0.42
12:K:50:TYR:HD1	12:K:60:ALA:HB2	1.85	0.42
13:L:60:LEU:HD23	13:L:66:VAL:HG22	2.00	0.42
14:M:13:LYS:O	14:M:45:VAL:HG23	2.20	0.42
1:A:1006:C:O2'	1:A:1007:C:H5'	2.20	0.42
1:A:1015:A:H2'	1:A:1016:A:C8	2.55	0.42
1:A:1231:G:H5''	10:I:126:SER:CB	2.49	0.42
1:A:1508:G:O2'	1:A:1509:C:H5'	2.18	0.42
1:A:277:C:H5''	18:Q:68:ARG:NH2	2.35	0.42
1:A:321:A:H2'	1:A:322:C:C6	2.55	0.42
1:A:858:G:O2'	1:A:859:A:H5'	2.20	0.42
1:A:975:A:C4'	1:A:976:G:H5'	2.42	0.42
3:B:189:ASP:OD1	3:B:205:ASP:HB3	2.20	0.42
3:B:97:TRP:HH2	3:B:176:GLU:OE1	2.03	0.42
4:C:126:ARG:O	4:C:127:ARG:HB2	2.20	0.42
5:D:170:VAL:CG1	5:D:174:LEU:HB2	2.45	0.42
5:D:33:MET:HE3	5:D:37:PRO:HA	2.02	0.42
5:D:78:LEU:HA	5:D:78:LEU:HD23	1.73	0.42
6:E:80:ILE:N	6:E:80:ILE:HD12	2.29	0.42
10:I:82:ALA:O	10:I:96:LEU:HD21	2.19	0.42
11:J:47:PHE:N	11:J:63:PHE:O	2.48	0.42
14:M:73:GLU:O	14:M:76:ALA:N	2.52	0.42
17:P:10:GLY:HA3	17:P:14:ASN:O	2.19	0.42
20:S:7:LYS:CG	20:S:7:LYS:O	2.68	0.42
21:T:93:GLU:OE2	21:T:93:GLU:HA	2.19	0.42
1:A:557:G:C6	1:A:558:G:C6	3.08	0.42
1:A:724:G:O2'	1:A:725:G:H5'	2.20	0.42
1:A:930:C:C2'	1:A:931:C:H5'	2.50	0.42
1:A:965:A:C2	1:A:969:A:C2	3.08	0.42
1:A:992:U:O2'	1:A:993:G:P	2.78	0.42
4:C:191:THR:HG21	4:C:193:TYR:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:144:THR:N	6:E:147:ASP:OD2	2.48	0.42
6:E:7:GLU:O	6:E:34:VAL:HA	2.20	0.42
10:I:127:LYS:C	10:I:128:ARG:O	2.58	0.42
11:J:22:LYS:NZ	11:J:91:PRO:HD3	2.34	0.42
13:L:50:SER:O	13:L:51:ALA:CB	2.68	0.42
14:M:23:TYR:HB3	14:M:67:GLU:HA	2.02	0.42
1:A:1239:A:H62	1:A:1299:A:N6	2.18	0.41
1:A:431:A:O2'	1:A:432:A:H5'	2.20	0.41
1:A:50:A:N6	1:A:361:G:H4'	2.35	0.41
1:A:833:U:H2'	1:A:834:C:C6	2.55	0.41
6:E:110:LEU:O	6:E:113:ALA:HB3	2.20	0.41
13:L:73:GLU:OE2	13:L:73:GLU:HA	2.19	0.41
14:M:80:ARG:O	14:M:82:MET:N	2.53	0.41
21:T:62:LEU:N	21:T:62:LEU:HD23	2.35	0.41
1:A:124:G:C6	1:A:125:U:C4	3.08	0.41
1:A:182:U:H6	1:A:182:U:H5'	1.85	0.41
1:A:285:G:C2'	1:A:286:G:H5'	2.50	0.41
1:A:312:C:H2'	1:A:313:A:C8	2.55	0.41
1:A:401:C:H2'	1:A:402:G:C8	2.46	0.41
1:A:397:A:C6	1:A:548:G:N7	2.88	0.41
1:A:57:G:H2'	1:A:58:C:O4'	2.19	0.41
1:A:637:G:O2'	1:A:638:G:H5'	2.20	0.41
3:B:127:ILE:HB	3:B:128:GLU:OE1	2.19	0.41
3:B:69:LEU:HB3	3:B:162:ILE:HG12	2.02	0.41
4:C:47:LEU:CD2	4:C:68:VAL:HG11	2.51	0.41
5:D:54:TYR:O	5:D:55:ALA:C	2.59	0.41
8:G:14:PRO:HB2	8:G:19:GLY:O	2.19	0.41
17:P:26:ARG:HG2	17:P:26:ARG:HH11	1.85	0.41
20:S:33:THR:HG22	20:S:34:TRP:H	1.84	0.41
20:S:33:THR:CG2	20:S:34:TRP:N	2.81	0.41
1:A:1103:C:H2'	1:A:1104:G:O4'	2.21	0.41
1:A:1169:A:H2'	1:A:1171:G:O4'	2.20	0.41
1:A:1351:U:O2'	1:A:1352:C:H5'	2.19	0.41
1:A:224:C:H2'	1:A:225:C:C6	2.54	0.41
1:A:416:G:C5	1:A:417:C:C4	3.09	0.41
1:A:626:U:O2'	1:A:627:G:H5'	2.19	0.41
1:A:767:A:H2'	1:A:768:A:H8	1.85	0.41
1:A:820:U:H4'	1:A:821:G:OP2	2.20	0.41
3:B:109:SER:O	3:B:111:ARG:N	2.53	0.41
3:B:130:ARG:NH2	4:C:207:VAL:CG2	2.81	0.41
3:B:115:LEU:HG	3:B:153:ARG:NH2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:53:ARG:HG2	3:B:53:ARG:NH1	2.35	0.41
5:D:43:HIS:O	5:D:45:GLN:N	2.53	0.41
5:D:61:LYS:NZ	5:D:72:GLU:OE2	2.53	0.41
5:D:65:ARG:HB2	5:D:75:PHE:CE1	2.55	0.41
5:D:96:LEU:CD1	5:D:96:LEU:N	2.82	0.41
9:H:1:MET:CG	9:H:2:LEU:H	2.21	0.41
9:H:48:TYR:CD1	9:H:48:TYR:C	2.93	0.41
9:H:24:THR:HG23	9:H:61:VAL:HB	2.02	0.41
10:I:19:LEU:HB3	10:I:59:PHE:CE2	2.54	0.41
10:I:19:LEU:C	10:I:20:ARG:HG3	2.40	0.41
21:T:94:ALA:O	21:T:95:ALA:CB	2.68	0.41
1:A:1198:G:O2'	1:A:1199:U:H5'	2.21	0.41
1:A:1468:A:H2'	1:A:1469:G:O4'	2.20	0.41
1:A:255:G:O6	1:A:266:G:O6	2.38	0.41
1:A:309:G:O2'	1:A:310:G:H5'	2.19	0.41
1:A:448:A:C4	1:A:487:A:C2	3.08	0.41
1:A:926:G:H5'	1:A:927:G:O5'	2.20	0.41
5:D:114:ARG:CG	5:D:114:ARG:HH11	2.23	0.41
5:D:65:ARG:HE	5:D:72:GLU:N	2.17	0.41
7:F:101:ALA:HB2	19:R:28:GLU:CB	2.46	0.41
8:G:23:VAL:HG13	8:G:43:PHE:CE2	2.56	0.41
9:H:119:LEU:HB3	9:H:123:GLU:HB3	2.02	0.41
9:H:25:ASP:OD1	9:H:25:ASP:N	2.54	0.41
13:L:28:LYS:O	13:L:29:GLY:C	2.57	0.41
18:Q:51:TYR:CD1	18:Q:73:VAL:HG11	2.56	0.41
1:A:1221:G:O2'	1:A:1222:G:H5'	2.20	0.41
1:A:281:G:O2'	1:A:282:A:C8	2.73	0.41
1:A:393:A:C2	1:A:394:G:C8	3.08	0.41
1:A:451:A:C2	1:A:480:U:C4	3.08	0.41
1:A:607:A:O2'	1:A:608:A:H5'	2.21	0.41
1:A:622:A:C8	1:A:623:C:C6	3.09	0.41
3:B:180:LEU:HD23	3:B:180:LEU:HA	1.78	0.41
3:B:16:HIS:HE1	3:B:213:LEU:HB3	1.85	0.41
4:C:24:ALA:O	4:C:26:LYS:HE2	2.20	0.41
5:D:58:LEU:HD13	5:D:58:LEU:C	2.41	0.41
6:E:92:LYS:HB3	6:E:119:LEU:HB2	2.01	0.41
8:G:136:LYS:O	8:G:140:ASP:OD1	2.38	0.41
8:G:75:VAL:HG21	8:G:144:MET:HB3	2.02	0.41
9:H:73:ASP:OD2	9:H:75:ARG:HB2	2.21	0.41
11:J:85:LEU:O	11:J:86:MET:C	2.58	0.41
12:K:100:ALA:O	12:K:102:GLY:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:120:LYS:HE2	14:M:123:ALA:CB	2.50	0.41
14:M:22:ILE:HD12	14:M:25:ILE:CD1	2.49	0.41
1:A:393:A:OP2	17:P:12:LYS:CE	2.67	0.41
19:R:59:SER:O	19:R:60:GLY:C	2.59	0.41
1:A:325:A:OP2	21:T:70:SER:HB3	2.21	0.41
22:V:8:THR:O	22:V:9:ARG:C	2.58	0.41
1:A:1050:G:O2'	1:A:1051:C:H5'	2.20	0.41
1:A:458:C:C5	1:A:459:G:N7	2.89	0.41
1:A:560:U:O2'	1:A:561:U:OP2	2.28	0.41
1:A:603:U:O2'	1:A:604:G:H5'	2.20	0.41
1:A:401:C:H1'	1:A:622:A:H1'	2.01	0.41
1:A:899:C:H2'	1:A:900:A:C8	2.55	0.41
3:B:155:LEU:HA	3:B:155:LEU:HD23	1.90	0.41
3:B:23:ARG:HD3	3:B:23:ARG:C	2.41	0.41
5:D:159:ARG:O	5:D:163:GLU:N	2.54	0.41
5:D:3:ARG:HD3	5:D:3:ARG:HA	1.80	0.41
5:D:52:SER:O	5:D:53:ASP:C	2.59	0.41
6:E:143:ARG:HA	6:E:143:ARG:HD3	1.78	0.41
1:A:1079:G:O3'	6:E:14:ARG:NH2	2.53	0.41
9:H:24:THR:HG23	9:H:24:THR:O	2.21	0.41
9:H:61:VAL:O	9:H:63:LEU:HD13	2.20	0.41
12:K:85:ARG:NH1	12:K:85:ARG:HG3	2.34	0.41
16:O:33:THR:OG1	16:O:85:LEU:HD13	2.21	0.41
17:P:81:ARG:HD3	17:P:83:GLU:HG2	2.03	0.41
20:S:78:ARG:H	20:S:78:ARG:HG2	1.57	0.41
1:A:1145:C:O2'	1:A:1146:A:O5'	2.34	0.41
1:A:184:G:H2'	1:A:185:A:H8	1.86	0.41
1:A:463:A:O2'	1:A:474:G:H5'	2.21	0.41
1:A:685:G:C2	1:A:686:U:C4	3.08	0.41
1:A:963:G:HO2'	11:J:54:PHE:HZ	1.67	0.41
4:C:148:GLY:HA3	4:C:172:ARG:O	2.21	0.41
4:C:191:THR:HB	4:C:194:GLY:H	1.86	0.41
6:E:144:THR:CG2	6:E:145:LYS:N	2.84	0.41
8:G:152:ALA:C	8:G:154:TYR:N	2.74	0.41
8:G:18:TYR:HD1	8:G:18:TYR:H	1.67	0.41
9:H:6:ILE:O	9:H:10:LEU:HG	2.21	0.41
9:H:5:PRO:O	9:H:8:ASP:HB3	2.21	0.41
10:I:106:ALA:O	10:I:108:VAL:HG23	2.20	0.41
10:I:126:SER:OG	10:I:127:LYS:N	2.52	0.41
10:I:43:ALA:C	10:I:45:ALA:N	2.74	0.41
12:K:33:THR:OG1	12:K:34:ASP:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:84:VAL:CG1	12:K:95:ILE:HD11	2.46	0.41
12:K:99:GLN:HA	12:K:105:VAL:CG2	2.51	0.41
16:O:33:THR:HG23	16:O:63:ARG:HH12	1.86	0.41
16:O:77:ARG:O	16:O:80:ALA:HB3	2.20	0.41
18:Q:53:LEU:HD12	18:Q:54:GLY:N	2.36	0.41
20:S:10:PHE:CD2	20:S:11:VAL:N	2.88	0.41
1:A:141:A:O2'	1:A:142:G:H5'	2.21	0.41
1:A:324:G:N2	1:A:327:A:H8	2.19	0.41
1:A:370:C:C2'	1:A:371:G:H5'	2.50	0.41
1:A:452:A:O2'	17:P:72:ARG:HD2	2.20	0.41
1:A:502:G:H2'	1:A:503:C:H6	1.86	0.41
1:A:522:C:H2'	1:A:523:A:O4'	2.20	0.41
3:B:60:ASP:O	3:B:64:ARG:HB2	2.21	0.41
4:C:179:ARG:O	4:C:179:ARG:HD2	2.20	0.41
6:E:45:PHE:CE2	6:E:47:LYS:HE3	2.56	0.41
6:E:79:GLU:HA	6:E:91:LEU:O	2.21	0.41
8:G:71:PRO:HG3	8:G:103:TRP:CH2	2.56	0.41
8:G:51:GLN:HA	8:G:51:GLN:OE1	2.20	0.41
9:H:9:MET:HG3	9:H:26:VAL:HG21	2.02	0.41
14:M:40:ASN:ND2	14:M:40:ASN:C	2.74	0.41
15:N:36:PHE:O	15:N:36:PHE:CD1	2.74	0.41
1:A:982:U:H5''	15:N:6:LEU:CD1	2.51	0.41
21:T:56:MET:HG2	21:T:84:LEU:CD1	2.50	0.41
1:A:1080:A:C8	1:A:1081:G:H1'	2.56	0.41
1:A:1117:G:H4'	10:I:104:ARG:HH11	1.81	0.41
1:A:1126:U:H2'	1:A:1127:G:C8	2.56	0.41
1:A:1257:U:O2'	1:A:1258:G:OP2	2.28	0.41
1:A:5:U:O2'	1:A:6:G:P	2.79	0.41
1:A:62:U:H2'	1:A:63:C:C6	2.56	0.41
1:A:645:C:O2'	1:A:646:U:H5'	2.21	0.41
1:A:821:G:H2'	1:A:822:C:C6	2.55	0.41
1:A:961:U:C2'	1:A:962:C:H5'	2.51	0.41
3:B:122:PHE:O	3:B:123:ALA:CB	2.67	0.41
4:C:28:GLN:O	4:C:29:TYR:C	2.58	0.41
5:D:52:SER:C	5:D:54:TYR:N	2.73	0.41
9:H:51:VAL:CG1	9:H:52:ASP:N	2.84	0.41
10:I:42:ARG:O	10:I:44:VAL:N	2.53	0.41
10:I:48:GLU:CA	10:I:51:ARG:NH1	2.79	0.41
10:I:93:ARG:HH11	10:I:97:LYS:HZ2	1.69	0.41
11:J:4:ILE:HA	11:J:100:THR:HA	2.01	0.41
11:J:23:ILE:HG22	11:J:23:ILE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:26:ARG:HH11	15:N:47:LEU:HG	1.80	0.41
20:S:13:ASP:O	20:S:17:GLU:HG2	2.21	0.41
1:A:1196:U:HO2'	1:A:1197:G:P	2.43	0.41
1:A:1227:A:H2'	1:A:1228:C:O5'	2.21	0.41
1:A:1254:C:OP1	11:J:45:ARG:HD2	2.20	0.41
1:A:132:C:H2'	1:A:133:U:O4'	2.21	0.41
1:A:1442:G:C2'	1:A:1442:G:N3	2.84	0.41
1:A:273:A:N6	1:A:274:A:C6	2.89	0.41
1:A:652:U:H2'	1:A:752:G:N1	2.36	0.41
1:A:904:C:H2'	1:A:905:U:O4'	2.21	0.41
5:D:150:GLU:N	5:D:150:GLU:CD	2.61	0.41
9:H:126:LYS:C	9:H:128:GLY:N	2.74	0.41
9:H:136:GLU:HG2	9:H:136:GLU:O	2.19	0.41
10:I:99:LEU:CB	10:I:101:PHE:CE1	3.03	0.41
11:J:22:LYS:HE2	11:J:90:LEU:HD12	2.02	0.41
1:A:718:G:H1'	12:K:116:HIS:HA	2.03	0.41
14:M:15:VAL:C	14:M:17:VAL:N	2.75	0.41
14:M:22:ILE:HG21	14:M:66:LEU:HD13	2.02	0.41
1:A:1006:C:N3	1:A:1023:G:O6	2.53	0.41
1:A:1317:C:C6	15:N:16:PHE:CD2	3.09	0.41
1:A:1337:G:H5''	1:A:1338:G:OP1	2.21	0.41
1:A:1450:U:H2'	1:A:1452:C:C5	2.56	0.41
1:A:1499:A:H1'	1:A:1520:G:H5'	2.03	0.41
1:A:33:A:N3	13:L:32:PHE:HE2	2.18	0.41
1:A:922:G:H2'	1:A:923:A:C8	2.56	0.41
1:A:954:G:H2'	1:A:955:U:H6	1.85	0.41
1:A:994:A:C8	1:A:994:A:OP1	2.74	0.41
3:B:20:GLU:O	3:B:39:ILE:HG23	2.21	0.41
3:B:33:TYR:HB3	3:B:41:ILE:O	2.21	0.41
4:C:8:ILE:O	4:C:10:PHE:N	2.54	0.41
5:D:8:VAL:HG11	5:D:21:LEU:HB3	2.03	0.41
8:G:41:ARG:O	8:G:44:TYR:N	2.54	0.41
9:H:86:ILE:HD12	9:H:133:LEU:CD2	2.51	0.41
9:H:60:ARG:HA	9:H:60:ARG:HD3	1.93	0.41
1:A:586:C:O3'	9:H:89:PRO:HB2	2.20	0.41
11:J:84:GLN:O	11:J:88:LEU:HB2	2.21	0.41
12:K:15:ALA:CA	12:K:77:MET:HA	2.50	0.41
14:M:20:THR:C	14:M:22:ILE:H	2.24	0.41
16:O:39:LEU:HD13	16:O:59:MET:HE2	2.03	0.41
1:A:1033:G:H2'	1:A:1034:G:H8	1.86	0.40
1:A:1062:U:H2'	1:A:1063:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1158:C:C5	1:A:1160:G:C8	3.10	0.40
1:A:1256:A:O2'	1:A:1257:U:P	2.79	0.40
1:A:23:C:H2'	1:A:24:U:H6	1.86	0.40
1:A:474:G:OP2	17:P:75:ARG:NH1	2.53	0.40
1:A:7:G:H5''	1:A:298:A:H5'	2.03	0.40
1:A:893:C:H2'	1:A:894:G:H8	1.86	0.40
3:B:126:GLU:HG2	3:B:129:GLU:OE1	2.20	0.40
4:C:206:GLU:O	4:C:207:VAL:O	2.39	0.40
1:A:8:A:C6	5:D:209:ARG:HB2	2.55	0.40
6:E:127:ASN:O	6:E:131:ILE:HG12	2.20	0.40
8:G:104:LEU:HD23	8:G:134:ALA:CB	2.50	0.40
10:I:86:VAL:CG1	10:I:90:PRO:HA	2.44	0.40
11:J:13:HIS:O	11:J:17:ASP:OD2	2.39	0.40
11:J:82:ILE:O	11:J:82:ILE:HG22	2.20	0.40
13:L:110:VAL:O	13:L:122:THR:CG2	2.63	0.40
14:M:44:ARG:HA	14:M:44:ARG:HD2	1.88	0.40
19:R:51:LEU:HA	19:R:52:PRO:HD3	1.91	0.40
19:R:87:ARG:CG	19:R:87:ARG:NH1	2.83	0.40
1:A:1305:G:OP1	22:V:2:GLY:N	2.53	0.40
22:V:2:GLY:O	22:V:3:LYS:C	2.59	0.40
1:A:1152:A:H2'	1:A:1153:C:H6	1.86	0.40
1:A:1097:C:O2'	1:A:1168:A:N3	2.46	0.40
1:A:1288:A:H2'	1:A:1289:A:C8	2.56	0.40
1:A:1346:A:C5	8:G:10:ARG:NH2	2.89	0.40
1:A:322:C:O2'	1:A:323:U:H5'	2.20	0.40
1:A:340:U:H2'	1:A:341:C:C6	2.56	0.40
1:A:423:G:C2'	1:A:424:G:H5'	2.52	0.40
1:A:791:G:C2'	1:A:792:A:H5'	2.48	0.40
3:B:200:ILE:HG22	3:B:201:ILE:N	2.36	0.40
3:B:236:TYR:HA	3:B:239:VAL:CG2	2.51	0.40
3:B:96:ARG:O	3:B:98:LEU:HD23	2.21	0.40
4:C:155:GLY:O	4:C:156:ARG:CB	2.68	0.40
5:D:187:ARG:HH21	5:D:188:LEU:CG	2.15	0.40
6:E:115:VAL:CG1	6:E:116:THR:N	2.85	0.40
8:G:156:TRP:OXT	8:G:156:TRP:CD1	2.75	0.40
1:A:1291:G:H5''	8:G:41:ARG:NH2	2.37	0.40
10:I:78:LYS:CD	10:I:101:PHE:HD2	2.29	0.40
10:I:113:LYS:N	10:I:113:LYS:HD2	2.36	0.40
10:I:118:LYS:HB2	10:I:118:LYS:HZ2	1.86	0.40
14:M:110:ARG:CG	14:M:110:ARG:NH1	2.84	0.40
14:M:6:GLY:O	14:M:7:VAL:CG2	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:16:PRO:O	19:R:17:SER:CB	2.68	0.40
21:T:36:LEU:HA	21:T:39:LYS:HB2	2.03	0.40
1:A:1152:A:O2'	1:A:1153:C:H5'	2.21	0.40
1:A:1404:C:H2'	1:A:1405:G:C8	2.56	0.40
1:A:1451:A:H4'	1:A:1452:C:OP2	2.22	0.40
1:A:182:U:OP2	1:A:183:G:C8	2.74	0.40
1:A:294:U:H2'	1:A:295:C:C6	2.56	0.40
1:A:344:A:O2'	1:A:345:C:OP1	2.34	0.40
1:A:474:G:H2'	1:A:475:G:C8	2.50	0.40
1:A:536:C:H2'	1:A:537:G:C8	2.56	0.40
1:A:309:G:H1'	1:A:608:A:C2	2.57	0.40
1:A:671:G:H2'	1:A:672:U:O4'	2.22	0.40
1:A:679:C:H2'	1:A:680:C:C6	2.56	0.40
3:B:107:THR:C	3:B:109:SER:H	2.25	0.40
3:B:192:SER:OG	3:B:193:ASP:N	2.54	0.40
3:B:20:GLU:OE2	3:B:205:ASP:OD1	2.39	0.40
3:B:18:GLY:HA2	3:B:41:ILE:HA	2.03	0.40
5:D:108:LEU:HA	5:D:108:LEU:HD23	1.89	0.40
6:E:115:VAL:CG1	6:E:118:ILE:HG13	2.51	0.40
6:E:99:GLY:O	6:E:117:ASP:HA	2.21	0.40
8:G:21:VAL:CG2	8:G:22:LEU:N	2.84	0.40
9:H:84:ARG:HB3	9:H:84:ARG:HE	1.51	0.40
10:I:89:ASN:OD1	10:I:91:ASP:HB2	2.21	0.40
11:J:23:ILE:CD1	11:J:23:ILE:H	2.33	0.40
11:J:34:VAL:C	11:J:36:GLY:H	2.24	0.40
11:J:38:ILE:CG2	11:J:39:PRO:HD2	2.52	0.40
13:L:83:VAL:CG2	13:L:100:ILE:HG23	2.51	0.40
21:T:18:GLN:O	21:T:19:SER:C	2.58	0.40
21:T:42:GLN:CA	21:T:42:GLN:NE2	2.84	0.40
1:A:1068:G:OP2	1:A:1068:G:H8	2.05	0.40
1:A:1139:G:O2'	1:A:1140:C:OP2	2.36	0.40
1:A:119:A:H4'	1:A:120:A:O5'	2.21	0.40
1:A:1481:U:H2'	1:A:1482:G:C8	2.56	0.40
1:A:335:C:H2'	1:A:336:C:H6	1.86	0.40
1:A:455:C:O5'	1:A:455:C:H6	2.04	0.40
1:A:528:C:H41	13:L:49:ASN:CG	2.24	0.40
1:A:539:A:H2'	1:A:540:G:C8	2.57	0.40
1:A:760:G:H2'	1:A:761:G:C5'	2.51	0.40
1:A:981:U:H5'	15:N:21:TYR:CE1	2.55	0.40
3:B:10:LEU:C	3:B:12:GLU:H	2.24	0.40
3:B:30:ARG:HG3	3:B:31:TYR:CD2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:85:ALA:HB1	3:B:92:TYR:HB3	2.04	0.40
4:C:36:ASP:HA	4:C:39:ILE:HD12	2.03	0.40
5:D:70:ILE:HD11	5:D:100:ARG:NH1	2.36	0.40
7:F:22:GLU:O	7:F:26:ILE:HG13	2.22	0.40
8:G:18:TYR:HD2	8:G:59:LEU:HB2	1.77	0.40
8:G:62:PHE:O	8:G:65:ALA:HB3	2.20	0.40
9:H:56:LYS:CB	9:H:57:PRO:HD2	2.51	0.40
9:H:10:LEU:HD22	9:H:83:ILE:HD11	2.03	0.40
9:H:91:ARG:HG3	13:L:7:ILE:HG13	2.03	0.40
11:J:51:ARG:NH1	11:J:51:ARG:CG	2.80	0.40
13:L:47:LYS:HB2	13:L:48:PRO:HD2	2.02	0.40
15:N:8:GLU:HB2	15:N:11:LYS:HD2	2.04	0.40
1:A:1127:G:H1'	1:A:1148:U:N3	2.37	0.40
1:A:1282:C:O2'	1:A:1283:G:H5'	2.21	0.40
1:A:1423:G:HO2'	1:A:1424:C:H5'	1.85	0.40
1:A:1436:U:O2'	1:A:1437:C:H5'	2.22	0.40
1:A:179:A:H2'	1:A:180:U:H6	1.86	0.40
1:A:420:U:C2'	1:A:421:U:H5''	2.51	0.40
1:A:570:G:N2	1:A:571:U:C2	2.90	0.40
1:A:61:G:C2'	1:A:62:U:H5'	2.52	0.40
1:A:928:G:O2'	1:A:929:G:H5'	2.20	0.40
3:B:204:ASN:HD22	3:B:207:ALA:CB	2.35	0.40
3:B:8:LYS:CD	3:B:9:GLU:N	2.84	0.40
4:C:108:ASN:HD22	4:C:111:LEU:CG	2.27	0.40
4:C:126:ARG:C	4:C:127:ARG:HG3	2.42	0.40
5:D:78:LEU:HD13	5:D:97:LEU:HD23	2.02	0.40
1:A:1178:G:P	10:I:97:LYS:NZ	2.95	0.40
11:J:34:VAL:HA	11:J:74:ILE:HG23	2.03	0.40
12:K:21:ILE:HD13	12:K:94:ALA:HB3	2.03	0.40
16:O:17:ARG:HH11	16:O:17:ARG:CG	2.30	0.40
16:O:31:LEU:CD1	16:O:31:LEU:H	2.31	0.40
19:R:34:TYR:CD1	19:R:35:ARG:HG3	2.56	0.40
19:R:36:ASN:O	19:R:39:VAL:HG12	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:157:ARG:NH1	3:B:157:ARG:NH1[7_555]	1.94	0.26

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	232/256 (91%)	172 (74%)	34 (15%)	26 (11%)	0	2
4	C	204/239 (85%)	132 (65%)	44 (22%)	28 (14%)	0	1
5	D	206/209 (99%)	153 (74%)	37 (18%)	16 (8%)	1	6
6	E	148/162 (91%)	130 (88%)	15 (10%)	3 (2%)	7	32
7	F	99/101 (98%)	83 (84%)	13 (13%)	3 (3%)	4	24
8	G	153/156 (98%)	119 (78%)	23 (15%)	11 (7%)	1	7
9	H	136/138 (99%)	118 (87%)	15 (11%)	3 (2%)	6	30
10	I	125/128 (98%)	86 (69%)	26 (21%)	13 (10%)	0	3
11	J	96/105 (91%)	59 (62%)	19 (20%)	18 (19%)	0	1
12	K	117/129 (91%)	84 (72%)	23 (20%)	10 (8%)	1	5
13	L	122/135 (90%)	90 (74%)	22 (18%)	10 (8%)	1	5
14	M	123/126 (98%)	87 (71%)	20 (16%)	16 (13%)	0	1
15	N	58/61 (95%)	40 (69%)	9 (16%)	9 (16%)	0	1
16	O	86/89 (97%)	66 (77%)	18 (21%)	2 (2%)	6	29
17	P	86/88 (98%)	67 (78%)	14 (16%)	5 (6%)	1	11
18	Q	102/105 (97%)	83 (81%)	13 (13%)	6 (6%)	1	10
19	R	71/88 (81%)	51 (72%)	15 (21%)	5 (7%)	1	7
20	S	78/93 (84%)	56 (72%)	12 (15%)	10 (13%)	0	1
21	T	97/106 (92%)	66 (68%)	19 (20%)	12 (12%)	0	1
22	V	22/26 (85%)	17 (77%)	4 (18%)	1 (4%)	2	15
All	All	2361/2540 (93%)	1759 (74%)	395 (17%)	207 (9%)	1	5

All (207) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	8	LYS

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Mol	Chain	Res	Type
3	B	16	HIS
3	B	17	PHE
3	B	21	ARG
3	B	24	TRP
3	B	123	ALA
4	C	4	LYS
4	C	15	THR
4	C	16	ARG
4	C	24	ALA
4	C	29	TYR
4	C	47	LEU
4	C	108	ASN
4	C	146	ALA
4	C	154	SER
4	C	179	ARG
4	C	189	ALA
4	C	206	GLU
5	D	29	PRO
5	D	36	ARG
6	E	16	THR
9	H	24	THR
9	H	83	ILE
9	H	91	ARG
10	I	7	THR
10	I	43	ALA
10	I	44	VAL
10	I	101	PHE
11	J	30	SER
11	J	32	ALA
11	J	54	PHE
11	J	57	LYS
11	J	79	ARG
11	J	86	MET
12	K	57	THR
12	K	101	SER
13	L	27	LEU
13	L	28	LYS
13	L	47	LYS
14	M	63	THR
14	M	67	GLU
14	M	107	ALA
14	M	122	LYS

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Mol	Chain	Res	Type
14	M	124	PRO
15	N	22	THR
15	N	29	ARG
15	N	59	ALA
15	N	60	SER
16	O	88	ARG
17	P	83	GLU
18	Q	69	LYS
18	Q	80	GLY
18	Q	81	ARG
18	Q	98	LEU
18	Q	104	LYS
19	R	87	ARG
20	S	6	LYS
20	S	9	VAL
20	S	71	LEU
21	T	11	SER
21	T	73	HIS
21	T	99	LEU
3	B	9	GLU
3	B	18	GLY
3	B	20	GLU
3	B	23	ARG
3	B	126	GLU
3	B	127	ILE
3	B	190	THR
3	B	204	ASN
3	B	225	ALA
4	C	61	ALA
5	D	4	TYR
5	D	31	CYS
5	D	44	GLY
5	D	63	LYS
5	D	153	ARG
5	D	175	SER
6	E	11	ILE
6	E	125	SER
7	F	16	GLN
7	F	39	LYS
8	G	7	ALA
8	G	53	LYS
8	G	155	ARG

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Mol	Chain	Res	Type
10	I	23	ASN
10	I	41	VAL
10	I	94	ALA
11	J	33	GLN
11	J	34	VAL
11	J	59	SER
11	J	60	ARG
11	J	72	VAL
12	K	49	GLY
12	K	50	TYR
12	K	78	GLN
12	K	89	ALA
13	L	48	PRO
13	L	51	ALA
13	L	121	GLY
14	M	6	GLY
14	M	42	ALA
14	M	85	GLY
14	M	123	ALA
15	N	17	LYS
17	P	10	GLY
17	P	49	LEU
19	R	26	LEU
20	S	67	VAL
20	S	68	GLY
20	S	69	HIS
21	T	9	ASN
21	T	49	ALA
21	T	50	GLU
21	T	94	ALA
21	T	102	GLY
3	B	124	SER
3	B	232	PRO
4	C	26	LYS
4	C	88	ARG
4	C	167	TRP
4	C	168	ALA
5	D	10	ARG
5	D	151	LYS
5	D	179	GLU
8	G	77	SER
10	I	31	GLN

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Mol	Chain	Res	Type
10	I	54	ASP
10	I	56	LEU
10	I	58	ARG
10	I	121	ARG
11	J	39	PRO
11	J	90	LEU
12	K	15	ALA
13	L	117	ARG
14	M	27	LYS
14	M	38	GLY
14	M	80	ARG
15	N	12	ARG
15	N	13	THR
15	N	36	PHE
19	R	54	ARG
21	T	95	ALA
21	T	98	PRO
22	V	9	ARG
3	B	15	VAL
3	B	224	GLN
4	C	181	ASN
4	C	188	LEU
5	D	30	LYS
5	D	64	LEU
8	G	41	ARG
8	G	42	ILE
8	G	78	ARG
8	G	81	GLY
11	J	73	ASP
11	J	85	LEU
12	K	12	ARG
12	K	27	ASN
12	K	102	GLY
13	L	41	ARG
13	L	126	LYS
14	M	73	GLU
14	M	74	VAL
14	M	86	CYS
14	M	121	LYS
15	N	19	ARG
18	Q	33	GLY
21	T	42	GLN

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Mol	Chain	Res	Type
3	B	60	ASP
3	B	83	MET
3	B	95	GLN
3	B	125	PRO
4	C	127	ARG
4	C	156	ARG
5	D	5	ILE
5	D	32	ALA
7	F	32	ASN
10	I	88	TYR
16	O	84	LYS
19	R	20	ALA
19	R	62	GLU
20	S	65	ASN
21	T	74	LYS
3	B	209	ARG
4	C	96	GLY
4	C	157	ILE
8	G	83	ALA
13	L	116	SER
20	S	17	GLU
4	C	66	VAL
5	D	171	GLY
11	J	40	LEU
3	B	89	GLY
3	B	229	VAL
4	C	77	ILE
8	G	112	PRO
11	J	91	PRO
20	S	11	VAL
4	C	14	ILE
8	G	17	VAL
20	S	8	GLY
4	C	57	ILE
11	J	82	ILE
17	P	41	PRO
17	P	87	GLY
4	C	7	PRO

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	
3	B	202/220 (92%)	177 (88%)	25 (12%)	4	19
4	C	160/188 (85%)	140 (88%)	20 (12%)	4	19
5	D	180/181 (99%)	164 (91%)	16 (9%)	9	32
6	E	115/123 (94%)	101 (88%)	14 (12%)	5	20
7	F	90/90 (100%)	86 (96%)	4 (4%)	28	59
8	G	126/127 (99%)	122 (97%)	4 (3%)	39	67
9	H	119/119 (100%)	105 (88%)	14 (12%)	5	21
10	I	98/99 (99%)	89 (91%)	9 (9%)	9	31
11	J	87/92 (95%)	77 (88%)	10 (12%)	5	22
12	K	90/99 (91%)	85 (94%)	5 (6%)	21	52
13	L	104/111 (94%)	97 (93%)	7 (7%)	16	45
14	M	100/101 (99%)	84 (84%)	16 (16%)	2	11
15	N	49/50 (98%)	45 (92%)	4 (8%)	11	36
16	O	79/80 (99%)	75 (95%)	4 (5%)	24	54
17	P	74/74 (100%)	72 (97%)	2 (3%)	44	71
18	Q	96/97 (99%)	90 (94%)	6 (6%)	18	47
19	R	64/77 (83%)	59 (92%)	5 (8%)	12	38
20	S	71/80 (89%)	64 (90%)	7 (10%)	8	28
21	T	76/82 (93%)	69 (91%)	7 (9%)	9	31
22	V	19/21 (90%)	19 (100%)	0	100	100
All	All	1999/2111 (95%)	1820 (91%)	179 (9%)	9	32

All (179) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	8	LYS
3	B	9	GLU
3	B	12	GLU

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Mol	Chain	Res	Type
3	B	17	PHE
3	B	21	ARG
3	B	23	ARG
3	B	24	TRP
3	B	25	ASN
3	B	64	ARG
3	B	96	ARG
3	B	114	ARG
3	B	139	LYS
3	B	144	ARG
3	B	157	ARG
3	B	162	ILE
3	B	163	PHE
3	B	164	VAL
3	B	178	ARG
3	B	185	ILE
3	B	187	LEU
3	B	197	VAL
3	B	226	ARG
3	B	231	GLU
3	B	232	PRO
3	B	236	TYR
4	C	3	ASN
4	C	21	ARG
4	C	37	GLN
4	C	43	LEU
4	C	56	ASP
4	C	75	VAL
4	C	82	GLU
4	C	90	GLU
4	C	91	LEU
4	C	99	VAL
4	C	102	ASN
4	C	107	GLN
4	C	139	GLN
4	C	156	ARG
4	C	162	GLN
4	C	166	GLU
4	C	167	TRP
4	C	179	ARG
4	C	188	LEU
4	C	207	VAL

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Mol	Chain	Res	Type
5	D	9	CYS
5	D	10	ARG
5	D	12	CYS
5	D	15	GLU
5	D	29	PRO
5	D	34	GLU
5	D	59	ARG
5	D	64	LEU
5	D	68	TYR
5	D	78	LEU
5	D	122	ARG
5	D	127	THR
5	D	157	LEU
5	D	176	LEU
5	D	194	LEU
5	D	199	ASN
6	E	12	LEU
6	E	31	LEU
6	E	43	LEU
6	E	52	PRO
6	E	56	GLN
6	E	63	ARG
6	E	68	GLU
6	E	73	ASN
6	E	79	GLU
6	E	80	ILE
6	E	89	ILE
6	E	120	THR
6	E	147	ASP
6	E	150	ARG
7	F	10	LEU
7	F	40	VAL
7	F	69	GLU
7	F	86	ARG
8	G	8	GLU
8	G	12	LEU
8	G	96	GLN
8	G	149	ARG
9	H	2	LEU
9	H	21	LYS
9	H	26	VAL
9	H	52	ASP

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Mol	Chain	Res	Type
9	H	79	VAL
9	H	81	HIS
9	H	84	ARG
9	H	85	ARG
9	H	91	ARG
9	H	92	ARG
9	H	104	ARG
9	H	105	ARG
9	H	112	LEU
9	H	119	LEU
10	I	2	GLU
10	I	10	ARG
10	I	23	ASN
10	I	38	GLN
10	I	56	LEU
10	I	58	ARG
10	I	91	ASP
10	I	111	ARG
10	I	121	ARG
11	J	9	ARG
11	J	45	ARG
11	J	49	VAL
11	J	51	ARG
11	J	55	LYS
11	J	60	ARG
11	J	64	GLU
11	J	71	LEU
11	J	74	ILE
11	J	95	GLU
12	K	29	ILE
12	K	54	ARG
12	K	84	VAL
12	K	116	HIS
12	K	124	LYS
13	L	7	ILE
13	L	17	LYS
13	L	33	ARG
13	L	53	ARG
13	L	98	TYR
13	L	113	ARG
13	L	126	LYS
14	M	9	ILE

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Mol	Chain	Res	Type
14	M	32	GLU
14	M	40	ASN
14	M	44	ARG
14	M	48	LEU
14	M	56	LEU
14	M	63	THR
14	M	70	LEU
14	M	77	ASN
14	M	81	LEU
14	M	102	ARG
14	M	105	THR
14	M	106	ASN
14	M	110	ARG
14	M	124	PRO
14	M	125	ARG
15	N	17	LYS
15	N	31	ARG
15	N	33	VAL
15	N	41	ARG
16	O	6	GLU
16	O	64	ARG
16	O	71	GLN
16	O	83	GLU
17	P	32	TYR
17	P	76	GLN
18	Q	34	LYS
18	Q	38	ARG
18	Q	53	LEU
18	Q	60	ILE
18	Q	70	ARG
18	Q	98	LEU
19	R	28	GLU
19	R	36	ASN
19	R	38	GLU
19	R	53	ARG
19	R	54	ARG
20	S	12	ASP
20	S	15	LEU
20	S	20	LEU
20	S	36	ARG
20	S	61	TYR
20	S	62	ILE

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Mol	Chain	Res	Type
20	S	78	ARG
21	T	10	LEU
21	T	42	GLN
21	T	57	ARG
21	T	62	LEU
21	T	64	ASP
21	T	73	HIS
21	T	84	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	25	ASN
3	B	113	HIS
3	B	140	HIS
3	B	146	GLN
3	B	204	ASN
3	B	240	GLN
4	C	3	ASN
4	C	6	HIS
4	C	31	HIS
4	C	69	HIS
4	C	98	ASN
4	C	104	GLN
4	C	107	GLN
4	C	108	ASN
4	C	110	ASN
4	C	118	GLN
4	C	123	GLN
4	C	139	GLN
4	C	176	HIS
4	C	181	ASN
5	D	62	GLN
5	D	77	ASN
5	D	123	HIS
5	D	160	GLN
5	D	199	ASN
6	E	73	ASN
7	F	16	GLN
7	F	18	GLN
7	F	27	GLN
7	F	32	ASN

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Mol	Chain	Res	Type
7	F	57	GLN
7	F	94	GLN
7	F	100	ASN
8	G	37	ASN
8	G	86	GLN
8	G	106	GLN
10	I	23	ASN
10	I	73	GLN
10	I	117	HIS
11	J	56	HIS
11	J	62	HIS
11	J	76	ASN
11	J	78	ASN
11	J	84	GLN
12	K	117	ASN
13	L	75	HIS
14	M	12	ASN
14	M	40	ASN
14	M	62	ASN
16	O	13	GLN
16	O	37	ASN
17	P	16	HIS
18	Q	16	GLN
18	Q	26	GLN
19	R	36	ASN
20	S	23	ASN
20	S	53	ASN
20	S	56	GLN
21	T	42	GLN
21	T	90	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1507/1522 (99%)	215 (14%)	88 (5%)
2	X	5/6 (83%)	0	0
All	All	1512/1528 (98%)	215 (14%)	88 (5%)

All (215) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	51	A
1	A	52	G
1	A	61	G
1	A	62	U
1	A	65	U
1	A	81	U
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	182	U
1	A	190(D)	U
1	A	190(E)	U
1	A	195	A
1	A	197	A
1	A	198	G
1	A	201	C
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	282	A
1	A	289	G
1	A	328	C

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Mol	Chain	Res	Type
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	429	U
1	A	430	A
1	A	439	A
1	A	460	A
1	A	461	C
1	A	481	G
1	A	482	A
1	A	484	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	519	C
1	A	527	G
1	A	532	A
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A

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Mol	Chain	Res	Type
1	A	575	G
1	A	576	G
1	A	577	G
1	A	653	A
1	A	665	A
1	A	687	A
1	A	688	G
1	A	702	A
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	781	A
1	A	792	A
1	A	793	U
1	A	813	U
1	A	817	C
1	A	819	A
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	858	G
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G

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Mol	Chain	Res	Type
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1005	A
1	A	1023	G
1	A	1026	G
1	A	1045	C
1	A	1050	G
1	A	1053	G
1	A	1054	C
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1085	U
1	A	1086	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1128	C
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1145	C
1	A	1152	A
1	A	1159	U
1	A	1160	G
1	A	1183	A
1	A	1184	G
1	A	1191	A
1	A	1196	U
1	A	1197	G

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Mol	Chain	Res	Type
1	A	1201	A
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1215	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1257	U
1	A	1258	G
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1305	G
1	A	1320	C
1	A	1338	G
1	A	1347	G
1	A	1348	U
1	A	1353	G
1	A	1364	U
1	A	1381	U
1	A	1394	A
1	A	1398	A
1	A	1442	G
1	A	1443	G
1	A	1446	A
1	A	1452	C
1	A	1492	A
1	A	1497	G
1	A	1499	A
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U

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Mol	Chain	Res	Type
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G

All (88) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	7	G
1	A	30	U
1	A	48	C
1	A	51	A
1	A	60	A
1	A	64	G
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	202	U
1	A	204	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
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	497	A
1	A	509	A

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Mol	Chain	Res	Type
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	701	C
1	A	748	C
1	A	792	A
1	A	812	C
1	A	819	A
1	A	840	C
1	A	913	A
1	A	945	G
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	1085	U
1	A	1101	A
1	A	1117	G
1	A	1129	C
1	A	1139	G
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1196	U
1	A	1201	A
1	A	1212	U
1	A	1214	C
1	A	1224	G
1	A	1225	A
1	A	1226	C
1	A	1256	A
1	A	1257	U
1	A	1281	U
1	A	1285	A

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Mol	Chain	Res	Type
1	A	1300	G
1	A	1301	U
1	A	1319	A
1	A	1346	A
1	A	1347	G
1	A	1380	U
1	A	1397	C
1	A	1451	A
1	A	1498	U
1	A	1502	A
1	A	1504	G
1	A	1528	U

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 99 ligands modelled in this entry, 98 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
24	HYG	A	1632	-	35,39,39	2.67	16 (45%)	43,60,60	1.96	11 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	HYG	A	1632	-	1/1/16/17	10/12/87/87	0/4/4/4

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1632	HYG	O28-C23	7.73	1.49	1.40
24	A	1632	HYG	C27-C33	6.77	1.61	1.52
24	A	1632	HYG	O28-C27	4.45	1.51	1.44
24	A	1632	HYG	C26-C27	3.56	1.61	1.52
24	A	1632	HYG	O30-C24	3.33	1.49	1.42
24	A	1632	HYG	C1-C6	3.27	1.61	1.52
24	A	1632	HYG	C26-C25	3.10	1.60	1.52
24	A	1632	HYG	O29-C12	-3.01	1.38	1.43
24	A	1632	HYG	C3-C4	2.99	1.58	1.53
24	A	1632	HYG	C10-N9	2.54	1.53	1.46
24	A	1632	HYG	C25-C24	2.51	1.57	1.53
24	A	1632	HYG	C16-C15	2.24	1.57	1.53
24	A	1632	HYG	C19-C15	2.22	1.59	1.51
24	A	1632	HYG	O14-C13	2.10	1.47	1.41
24	A	1632	HYG	C34-C33	2.06	1.55	1.52
24	A	1632	HYG	O18-C13	2.00	1.47	1.41

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1632	HYG	O21-C16-C15	5.33	122.53	109.30
24	A	1632	HYG	O28-C27-C26	5.25	115.97	108.52
24	A	1632	HYG	O21-C16-C17	4.11	120.85	109.94
24	A	1632	HYG	C26-C25-C24	-3.50	106.48	111.30
24	A	1632	HYG	C23-O28-C27	3.45	118.57	112.00
24	A	1632	HYG	C16-C17-C12	-3.28	105.53	113.50
24	A	1632	HYG	C17-C16-C15	3.06	116.17	109.66
24	A	1632	HYG	O18-C6-C1	2.58	114.15	107.28
24	A	1632	HYG	O29-C12-C13	2.41	117.20	110.86
24	A	1632	HYG	O22-C17-C16	2.31	116.83	111.22
24	A	1632	HYG	C25-C26-C27	2.05	114.36	109.68

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
24	A	1632	HYG	C16

All (10) torsion outliers are listed below:

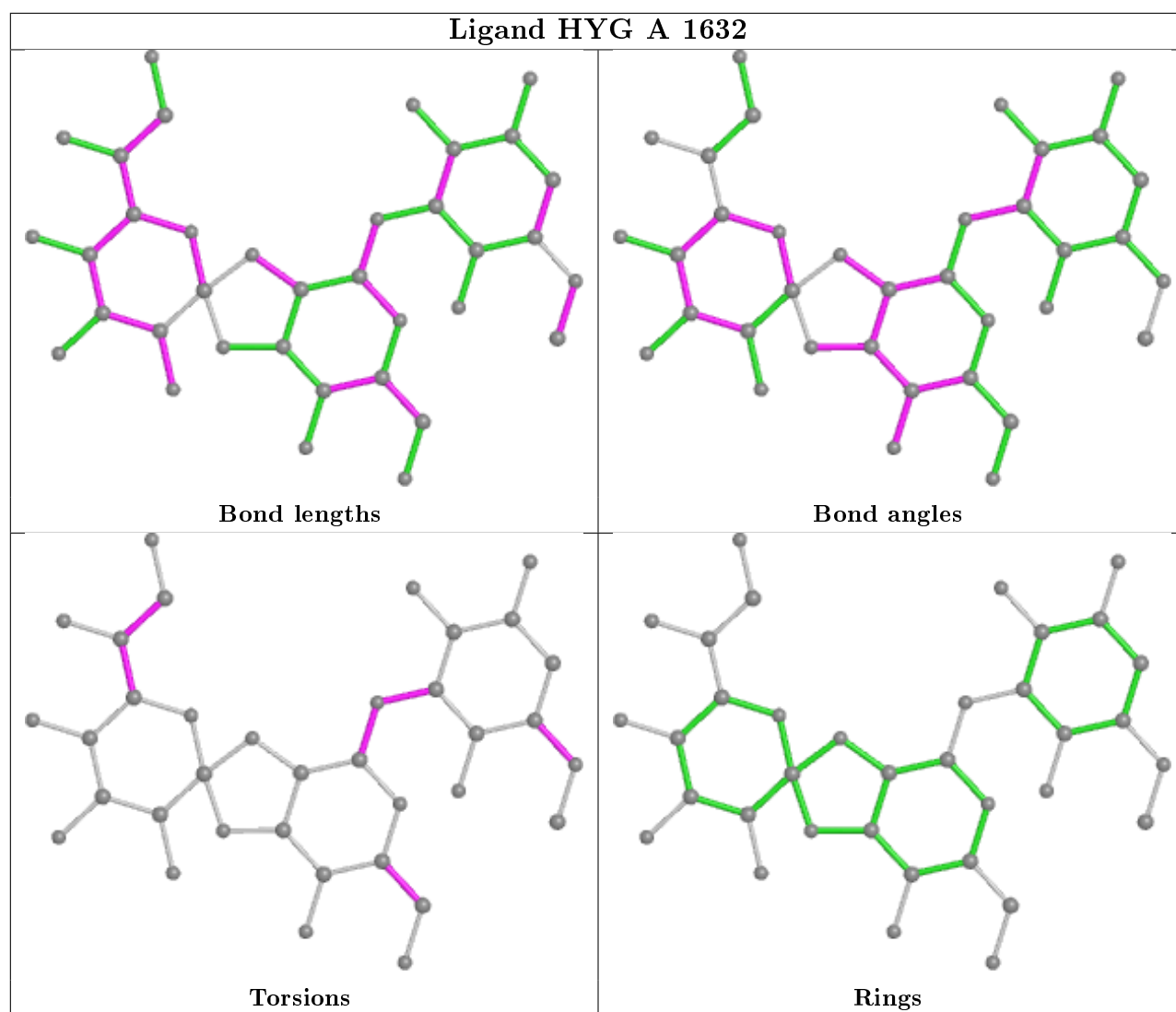
Mol	Chain	Res	Type	Atoms
24	A	1632	HYG	C5-C4-N9-C10
24	A	1632	HYG	C26-C27-C33-C34
24	A	1632	HYG	O28-C27-C33-C34
24	A	1632	HYG	N36-C33-C34-O35
24	A	1632	HYG	O14-C13-O18-C6
24	A	1632	HYG	C1-C6-O18-C13
24	A	1632	HYG	O14-C15-C19-O20
24	A	1632	HYG	C16-C15-C19-O20
24	A	1632	HYG	C27-C33-C34-O35
24	A	1632	HYG	C5-C6-O18-C13

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	1632	HYG	8	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	1506/1522 (98%)	0.46	76 (5%) 28 27	53, 82, 169, 199	0
2	X	6/6 (100%)	2.13	3 (50%) 0 0	78, 84, 140, 155	0
3	B	234/256 (91%)	0.10	15 (6%) 19 19	51, 102, 165, 199	0
4	C	206/239 (86%)	-0.18	3 (1%) 73 72	59, 103, 158, 177	0
5	D	208/209 (99%)	0.01	1 (0%) 91 91	55, 85, 131, 175	0
6	E	150/162 (92%)	-0.25	1 (0%) 87 88	50, 73, 114, 192	0
7	F	101/101 (100%)	0.02	6 (5%) 22 22	66, 109, 144, 174	0
8	G	155/156 (99%)	-0.02	3 (1%) 66 65	58, 100, 150, 177	0
9	H	138/138 (100%)	-0.21	1 (0%) 87 88	41, 70, 106, 153	0
10	I	127/128 (99%)	0.10	3 (2%) 59 56	62, 109, 150, 175	0
11	J	98/105 (93%)	0.78	15 (15%) 2 2	59, 128, 184, 199	0
12	K	119/129 (92%)	0.12	3 (2%) 57 54	57, 85, 140, 191	0
13	L	124/135 (91%)	0.05	2 (1%) 72 70	44, 83, 128, 182	0
14	M	125/126 (99%)	0.59	11 (8%) 10 10	61, 99, 158, 193	0
15	N	60/61 (98%)	0.25	5 (8%) 11 11	64, 96, 150, 162	0
16	O	88/89 (98%)	-0.07	3 (3%) 45 43	52, 83, 136, 185	0
17	P	88/88 (100%)	0.19	6 (6%) 17 17	53, 77, 158, 199	0
18	Q	104/105 (99%)	0.48	10 (9%) 8 8	55, 77, 140, 199	0
19	R	73/88 (82%)	0.10	4 (5%) 25 23	56, 87, 148, 191	0
20	S	80/93 (86%)	0.33	8 (10%) 7 7	84, 119, 170, 198	0
21	T	99/106 (93%)	0.41	7 (7%) 16 16	59, 86, 135, 199	0
22	V	24/26 (92%)	-0.01	0 100 100	60, 91, 127, 143	0
All	All	3913/4068 (96%)	0.25	186 (4%) 30 28	41, 88, 161, 199	0

All (186) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
14	M	124	PRO	20.2
18	Q	103	GLY	13.2
18	Q	105	ALA	12.1
11	J	33	GLN	9.2
14	M	123	ALA	9.1
12	K	129	SER	9.0
14	M	125	ARG	8.5
18	Q	104	LYS	8.3
17	P	87	GLY	8.2
21	T	103	GLY	7.8
1	A	1005	A	6.9
1	A	1036	G	6.7
1	A	1001	A	6.7
1	A	1027	C	6.5
11	J	89	ASP	6.2
1	A	1006	C	5.8
3	B	238	LEU	5.7
1	A	1002	G	5.5
21	T	51	GLU	5.4
1	A	1026	G	5.3
20	S	79	THR	5.2
1	A	1029	C	5.2
14	M	120	LYS	5.2
1	A	1124	G	5.1
14	M	126	LYS	5.1
18	Q	102	GLY	5.1
3	B	233	SER	5.1
1	A	1023	G	5.0
3	B	235	SER	5.0
21	T	48	LYS	5.0
17	P	85	ARG	4.9
11	J	34	VAL	4.8
1	A	81	U	4.8
3	B	239	VAL	4.4
1	A	1037	C	4.2
1	A	1274	G	4.1
21	T	47	GLY	4.1
3	B	227	GLY	4.1
17	P	88	ALA	4.1
1	A	1488	G	4.1
11	J	93	GLY	4.0
1	A	1129	C	4.0
1	A	1262	C	4.0

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Mol	Chain	Res	Type	RSRZ
18	Q	78	GLU	4.0
1	A	1139	G	4.0
5	D	33	MET	3.9
20	S	77	THR	3.8
11	J	31	GLY	3.8
1	A	1489	G	3.7
17	P	86	GLU	3.7
2	X	1	C	3.7
1	A	1024	G	3.7
18	Q	55	ASP	3.7
1	A	1144	G	3.6
1	A	1416	G	3.6
21	T	43	LEU	3.6
1	A	1123	A	3.6
1	A	1028	C	3.6
12	K	89	ALA	3.5
8	G	62	PHE	3.5
3	B	122	PHE	3.5
18	Q	80	GLY	3.5
2	X	4	U	3.4
21	T	44	ALA	3.4
1	A	1273	G	3.4
19	R	17	SER	3.3
10	I	97	LYS	3.3
1	A	1003	G	3.3
1	A	1022	G	3.2
11	J	90	LEU	3.2
11	J	17	ASP	3.2
19	R	18	ARG	3.2
11	J	10	GLY	3.2
1	A	1030(B)	C	3.2
20	S	81	ARG	3.2
1	A	1137	C	3.2
11	J	85	LEU	3.1
16	O	7	GLU	3.1
3	B	228	GLY	3.1
11	J	39	PRO	3.1
1	A	1030	C	3.1
1	A	958	A	3.1
20	S	54	GLY	3.0
1	A	1261	A	3.0
8	G	81	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
14	M	37	THR	3.0
10	I	102	LEU	3.0
1	A	1025	U	3.0
1	A	1275	A	3.0
20	S	3	ARG	2.9
11	J	75	ILE	2.9
11	J	28	ARG	2.9
1	A	1417	G	2.9
20	S	52	TYR	2.9
1	A	1035	A	2.9
14	M	36	LYS	2.9
18	Q	95	TYR	2.9
3	B	236	TYR	2.9
14	M	121	LYS	2.9
1	A	606	G	2.8
7	F	14	LEU	2.8
1	A	1283	G	2.8
3	B	240	GLN	2.8
1	A	991	U	2.8
16	O	88	ARG	2.7
1	A	1030(A)	G	2.7
18	Q	79	SER	2.7
20	S	4	SER	2.7
1	A	1220	G	2.7
1	A	432	A	2.7
14	M	43	THR	2.7
1	A	1426	C	2.7
3	B	80	ILE	2.7
11	J	70	ARG	2.6
1	A	190(B)	C	2.6
15	N	6	LEU	2.6
1	A	1420	C	2.6
7	F	4	TYR	2.6
21	T	52	ALA	2.6
3	B	83	MET	2.6
15	N	5	ALA	2.5
1	A	1428	A	2.5
1	A	455	C	2.5
1	A	989	C	2.5
11	J	35	SER	2.5
20	S	26	GLY	2.5
3	B	226	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
15	N	39	LEU	2.5
1	A	1007	C	2.5
1	A	433	C	2.5
1	A	1041	A	2.4
1	A	1126	U	2.4
1	A	1421	G	2.4
1	A	1427	U	2.4
19	R	25	THR	2.4
1	A	841	U	2.4
1	A	1145	C	2.4
16	O	87	ILE	2.4
1	A	666	G	2.4
1	A	1474	G	2.4
1	A	1260	C	2.3
15	N	3	ARG	2.3
6	E	35	GLY	2.3
1	A	1004	A	2.3
1	A	1018	C	2.3
13	L	33	ARG	2.3
3	B	121	LEU	2.3
1	A	993	G	2.3
12	K	42	TRP	2.3
1	A	1135	U	2.3
4	C	79	ARG	2.3
1	A	1259	C	2.2
3	B	40	HIS	2.2
1	A	1490	C	2.2
14	M	39	ILE	2.2
1	A	1418	A	2.2
1	A	1473	A	2.2
1	A	1531	A	2.2
7	F	3	ARG	2.2
17	P	84	ALA	2.2
4	C	21	ARG	2.2
11	J	32	ALA	2.2
1	A	1008	C	2.2
4	C	128	PHE	2.1
17	P	83	GLU	2.1
1	A	202	U	2.1
9	H	1	MET	2.1
7	F	66	GLU	2.1
1	A	447	G	2.1

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Mol	Chain	Res	Type	RSRZ
19	R	24	ALA	2.1
7	F	64	GLN	2.1
13	L	95	GLY	2.1
18	Q	82	MET	2.1
1	A	183	G	2.1
3	B	142	LEU	2.1
8	G	123	GLU	2.1
15	N	4	LYS	2.1
1	A	848	C	2.1
14	M	109	THR	2.0
1	A	1136	U	2.0
2	X	2	U	2.0
1	A	957	U	2.0
1	A	1176	A	2.0
7	F	38	GLU	2.0
1	A	1246	C	2.0
10	I	7	THR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1615	1/1	0.22	1.36	58,58,58,58	1
23	MG	A	1550	1/1	0.35	1.44	58,58,58,58	1
23	MG	A	1549	1/1	0.37	0.91	58,58,58,58	1
23	MG	A	1624	1/1	0.41	0.45	58,58,58,58	1
23	MG	A	211	1/1	0.58	0.73	58,58,58,58	0
23	MG	A	1618	1/1	0.61	0.41	58,58,58,58	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1566	1/1	0.63	0.44	58,58,58,58	0
23	MG	A	1581	1/1	0.64	0.53	58,58,58,58	1
23	MG	A	210	1/1	0.65	0.36	58,58,58,58	1
23	MG	A	1592	1/1	0.65	0.20	58,58,58,58	0
23	MG	D	215	1/1	0.66	0.24	58,58,58,58	1
23	MG	A	1619	1/1	0.67	0.28	58,58,58,58	0
23	MG	A	1585	1/1	0.69	0.25	58,58,58,58	1
23	MG	A	1623	1/1	0.70	1.37	58,58,58,58	1
23	MG	A	212	1/1	0.71	0.53	58,58,58,58	1
23	MG	H	213	1/1	0.71	1.41	58,58,58,58	1
23	MG	A	1548	1/1	0.72	0.36	58,58,58,58	0
23	MG	A	1629	1/1	0.74	0.45	58,58,58,58	1
23	MG	A	1564	1/1	0.75	0.17	58,58,58,58	0
23	MG	A	1614	1/1	0.76	0.65	58,58,58,58	1
23	MG	A	1556	1/1	0.76	1.02	58,58,58,58	1
23	MG	A	1590	1/1	0.77	0.45	58,58,58,58	0
23	MG	A	1620	1/1	0.78	0.38	58,58,58,58	0
23	MG	A	1609	1/1	0.83	0.43	58,58,58,58	0
23	MG	A	1560	1/1	0.83	0.23	58,58,58,58	0
23	MG	A	1595	1/1	0.83	0.30	58,58,58,58	0
23	MG	A	1604	1/1	0.83	0.29	58,58,58,58	0
23	MG	A	1596	1/1	0.83	0.65	58,58,58,58	1
23	MG	A	1611	1/1	0.83	0.15	58,58,58,58	1
23	MG	A	1612	1/1	0.84	0.41	58,58,58,58	1
23	MG	A	1563	1/1	0.84	0.17	58,58,58,58	0
23	MG	A	1594	1/1	0.84	0.24	58,58,58,58	0
23	MG	A	1558	1/1	0.85	0.47	58,58,58,58	0
23	MG	A	71	1/1	0.85	0.44	58,58,58,58	0
23	MG	A	1599	1/1	0.86	0.36	58,58,58,58	0
23	MG	A	1613	1/1	0.86	0.25	58,58,58,58	1
23	MG	A	1605	1/1	0.86	0.46	58,58,58,58	0
23	MG	A	1616	1/1	0.86	0.48	58,58,58,58	0
23	MG	A	1610	1/1	0.86	0.38	58,58,58,58	0
23	MG	A	1575	1/1	0.87	0.27	58,58,58,58	1
23	MG	A	1626	1/1	0.87	0.30	58,58,58,58	0
23	MG	A	1608	1/1	0.87	0.35	58,58,58,58	0
23	MG	A	1557	1/1	0.88	0.68	58,58,58,58	0
23	MG	A	1571	1/1	0.88	0.77	58,58,58,58	0
23	MG	A	1555	1/1	0.89	0.40	58,58,58,58	0
23	MG	A	1565	1/1	0.90	0.73	58,58,58,58	0
23	MG	A	1617	1/1	0.90	0.30	58,58,58,58	1
23	MG	A	1587	1/1	0.90	0.69	58,58,58,58	0

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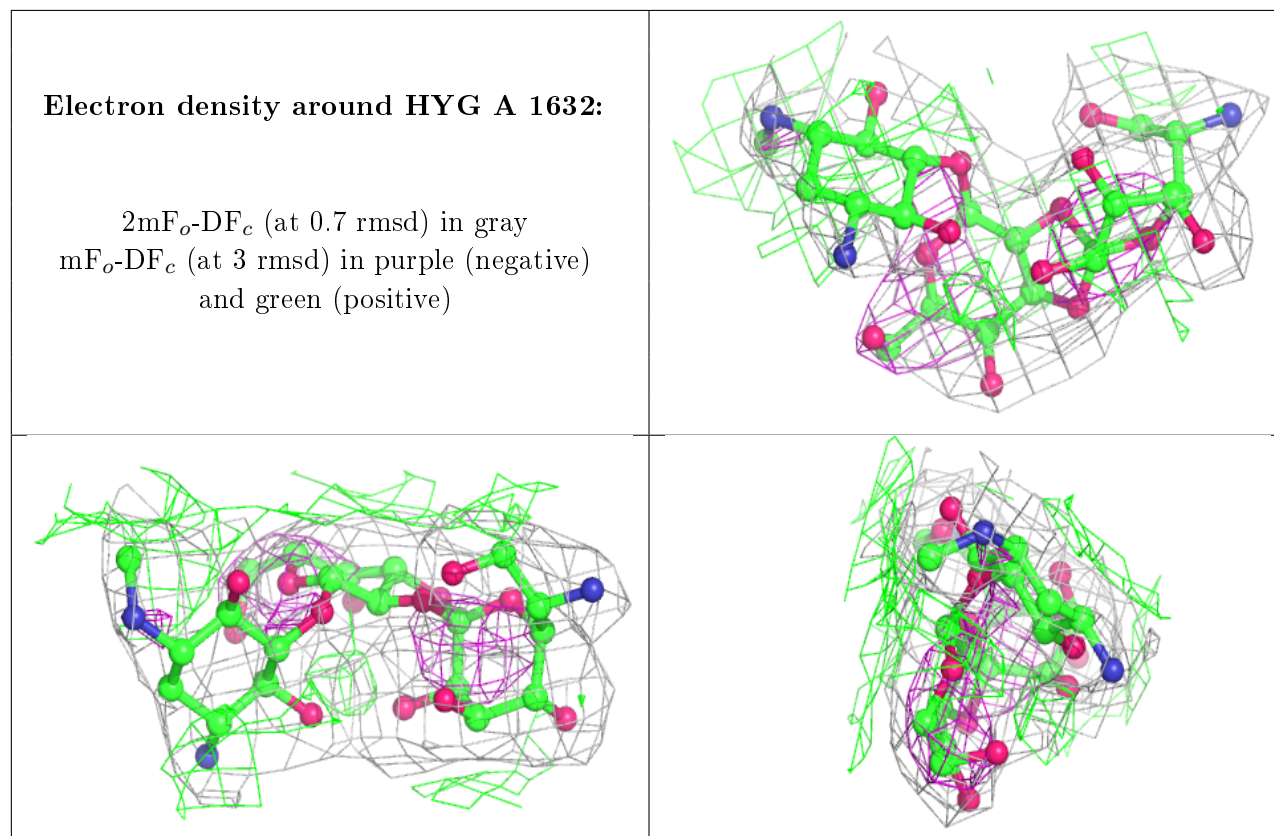
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1582	1/1	0.90	0.27	58,58,58,58	1
23	MG	A	1574	1/1	0.90	0.40	58,58,58,58	0
23	MG	A	1603	1/1	0.91	0.36	58,58,58,58	0
23	MG	A	1583	1/1	0.91	0.12	58,58,58,58	0
23	MG	A	1568	1/1	0.91	0.67	58,58,58,58	0
23	MG	A	87	1/1	0.91	0.45	58,58,58,58	1
23	MG	A	1579	1/1	0.91	0.25	58,58,58,58	0
23	MG	A	1545	1/1	0.91	0.17	58,58,58,58	1
23	MG	A	1562	1/1	0.92	0.57	58,58,58,58	0
24	HYG	A	1632	36/36	0.92	0.20	41,41,41,41	0
23	MG	A	1597	1/1	0.92	0.28	58,58,58,58	0
23	MG	A	1601	1/1	0.92	0.22	58,58,58,58	0
23	MG	A	214	1/1	0.92	0.72	58,58,58,58	0
23	MG	A	1577	1/1	0.92	0.30	58,58,58,58	0
23	MG	A	1567	1/1	0.92	0.57	58,58,58,58	0
23	MG	A	1576	1/1	0.93	1.01	58,58,58,58	0
23	MG	A	1586	1/1	0.93	0.55	58,58,58,58	0
23	MG	A	1561	1/1	0.93	0.64	58,58,58,58	0
23	MG	A	1553	1/1	0.93	0.51	58,58,58,58	0
23	MG	A	1559	1/1	0.94	0.38	58,58,58,58	0
23	MG	A	1546	1/1	0.94	0.39	58,58,58,58	0
23	MG	A	1554	1/1	0.94	0.62	58,58,58,58	0
23	MG	A	1589	1/1	0.94	0.35	58,58,58,58	0
23	MG	A	1547	1/1	0.94	0.64	58,58,58,58	0
23	MG	A	1578	1/1	0.94	0.30	58,58,58,58	0
23	MG	A	1588	1/1	0.95	0.19	58,58,58,58	0
23	MG	A	1606	1/1	0.95	0.37	58,58,58,58	0
23	MG	A	1631	1/1	0.95	0.36	58,58,58,58	1
23	MG	A	1580	1/1	0.95	0.43	58,58,58,58	0
23	MG	A	1569	1/1	0.95	0.46	58,58,58,58	1
23	MG	A	1572	1/1	0.95	0.62	58,58,58,58	0
23	MG	A	1607	1/1	0.96	0.72	58,58,58,58	0
23	MG	A	1593	1/1	0.96	0.31	58,58,58,58	0
23	MG	A	1600	1/1	0.96	0.55	58,58,58,58	0
23	MG	A	86	1/1	0.96	0.77	58,58,58,58	0
23	MG	A	1584	1/1	0.96	0.49	58,58,58,58	0
23	MG	A	1552	1/1	0.96	0.20	58,58,58,58	0
23	MG	A	1602	1/1	0.97	0.77	58,58,58,58	0
23	MG	A	1570	1/1	0.97	0.28	58,58,58,58	1
23	MG	A	1551	1/1	0.97	0.78	58,58,58,58	0
23	MG	A	1625	1/1	0.98	0.21	58,58,58,58	1
23	MG	A	1591	1/1	0.98	0.51	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1598	1/1	0.99	0.11	58,58,58,58	0
23	MG	A	1622	1/1	0.99	0.23	58,58,58,58	1
23	MG	A	1573	1/1	0.99	0.74	58,58,58,58	0
25	ZN	N	190	1/1	0.99	0.19	66,66,66,66	1
23	MG	A	1621	1/1	0.99	0.15	58,58,58,58	1
25	ZN	D	300	1/1	0.99	0.31	66,66,66,66	0
23	MG	A	1627	1/1	0.99	0.44	58,58,58,58	1
23	MG	A	1628	1/1	0.99	0.17	58,58,58,58	1
23	MG	A	1630	1/1	0.99	0.43	58,58,58,58	1

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



6.5 Other polymers ⓘ

There are no such residues in this entry.