



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 06:07 am GMT

PDB ID : 1J5E
Title : Structure of the Thermus thermophilus 30S Ribosomal Subunit
Authors : Wimberly, B.T.; Brodersen, D.E.; Clemons Jr., W.M.; Morgan-Warren, R.;
Carter, A.P.; Vornrhein, C.; Hartsch, T.; Ramakrishnan, V.
Deposited on : 2002-04-08
Resolution : 3.05 Å(reported)

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

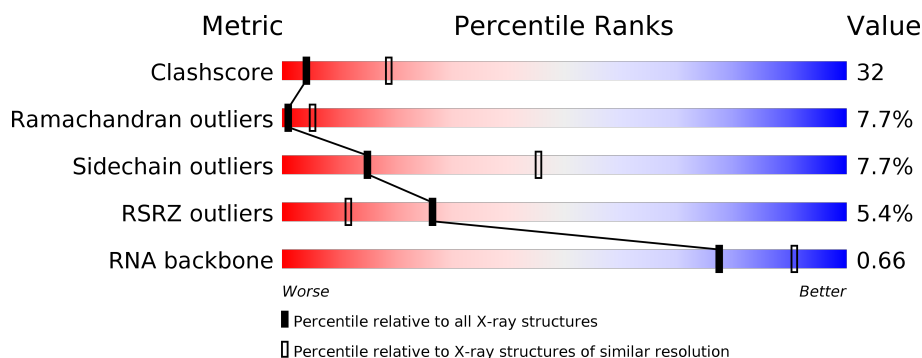
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	1462 (3.10-3.02)
Ramachandran outliers	110173	1410 (3.10-3.02)
Sidechain outliers	110143	1410 (3.10-3.02)
RSRZ outliers	101464	1355 (3.10-3.02)
RNA backbone	2435	1037 (3.42-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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>3%</div> <div>33% 53% 11% ..</div> </div>
2	B	256	<div> <div>3%</div> <div>25% 52% 13% • 9%</div> </div>
3	C	239	<div> <div>2%</div> <div>25% 45% 15% • 14%</div> </div>
4	D	208	<div> <div>3%</div> <div>43% 52% 5%</div> </div>
5	E	161	<div> <div>%</div> <div>37% 47% 8% • 7%</div> </div>
6	F	101	<div> <div></div> <div>43% 55% •</div> </div>

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Mol	Chain	Length	Quality of chain
7	G	155	
8	H	138	
9	I	128	
10	J	104	
11	K	129	
12	L	135	
13	M	126	
14	N	60	
15	O	88	
16	P	88	
17	Q	104	
18	R	88	
19	S	92	
20	T	106	
21	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	UNX	A	1562	-	-	-	X
23	UNX	A	1569	-	-	-	X
23	UNX	A	1571	-	-	-	X
23	UNX	A	1575	-	-	-	X
23	UNX	A	1592	-	-	-	X
23	UNX	A	1598	-	-	-	X
23	UNX	A	1604	-	-	-	X
23	UNX	A	1607	-	-	-	X
23	UNX	A	1608	-	-	-	X
23	UNX	A	1609	-	-	-	X
23	UNX	A	1611	-	-	-	X
23	UNX	A	1615	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	UNX	A	1621	-	-	-	X
23	UNX	A	1625	-	-	-	X
23	UNX	A	1627	-	-	-	X
23	UNX	A	1631	-	-	-	X
23	UNX	A	1633	-	-	-	X
23	UNX	A	1639	-	-	-	X
23	UNX	A	1648	-	-	-	X
23	UNX	A	1664	-	-	-	X
23	UNX	A	1668	-	-	-	X
23	UNX	A	1672	-	-	-	X
23	UNX	A	1680	-	-	-	X
23	UNX	A	1696	-	-	-	X
23	UNX	A	1697	-	-	-	X
23	UNX	A	1698	-	-	-	X
23	UNX	A	1699	-	-	-	X
23	UNX	A	1700	-	-	-	X
23	UNX	A	1701	-	-	-	X
23	UNX	A	1702	-	-	-	X
23	UNX	A	1703	-	-	-	X
23	UNX	A	1711	-	-	-	X
23	UNX	A	1716	-	-	-	X
23	UNX	A	1719	-	-	-	X
23	UNX	B	257	-	-	-	X

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 51933 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	1513	Total	C	N	O	P	66	0	0
			32514	14472	6016	10513	1513			

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

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

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

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

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

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

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S5.

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

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

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

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S7.

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

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

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

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

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

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

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

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

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

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

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

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14.

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

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

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

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

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

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

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

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

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

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

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

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	41	VAL	ILE	CONFLICT	EMBL 11125386

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

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

- Molecule 22 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

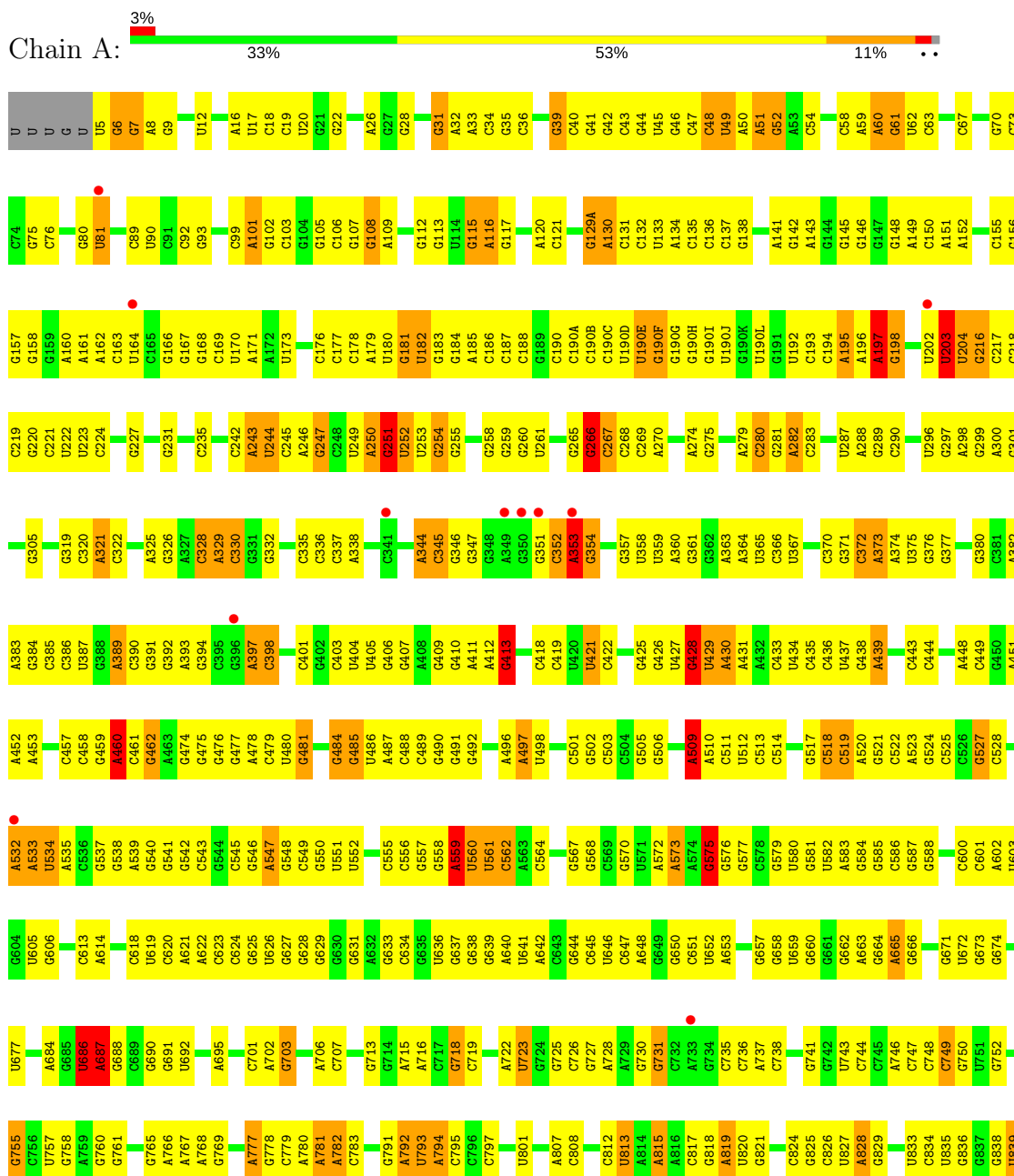
- Molecule 23 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

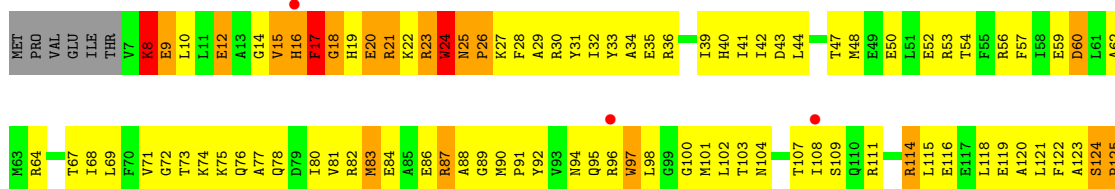
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	B	1	Total	X	0	0
			1	1		
23	A	186	Total	X	0	0
			186	186		
23	M	1	Total	X	0	0
			1	1		

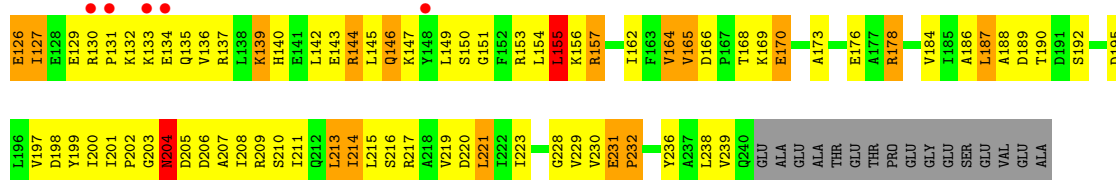
3 Residue-property plots

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.

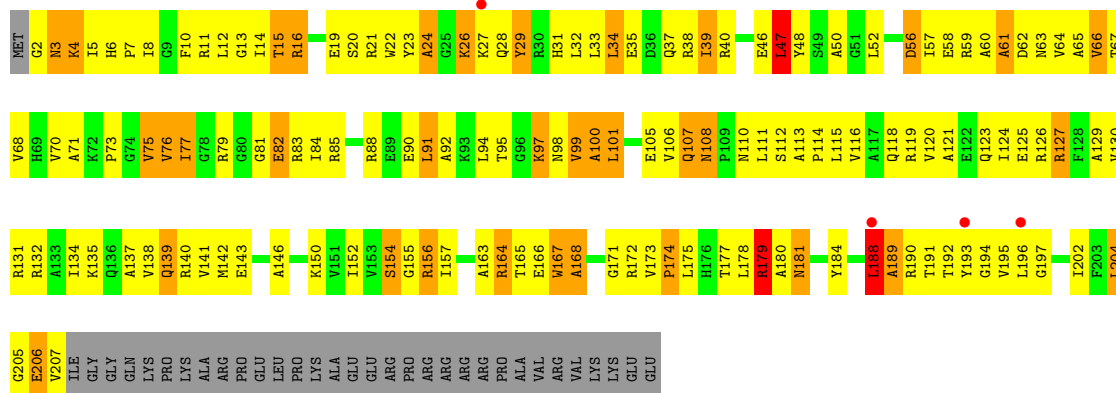
• Molecule 1: 16S ribosomal RNA



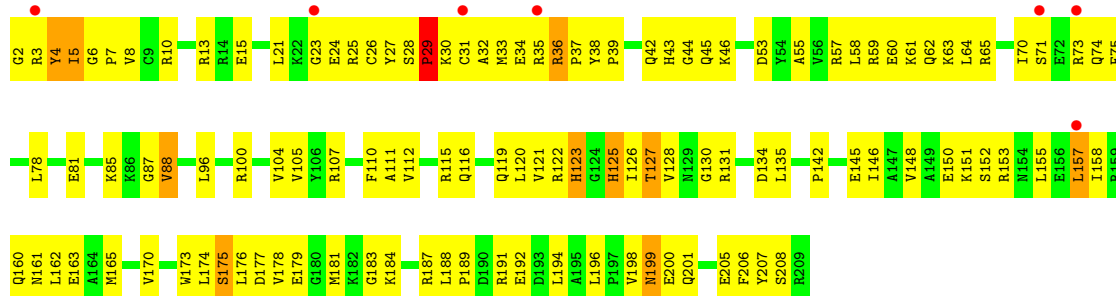
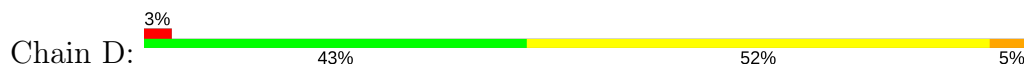




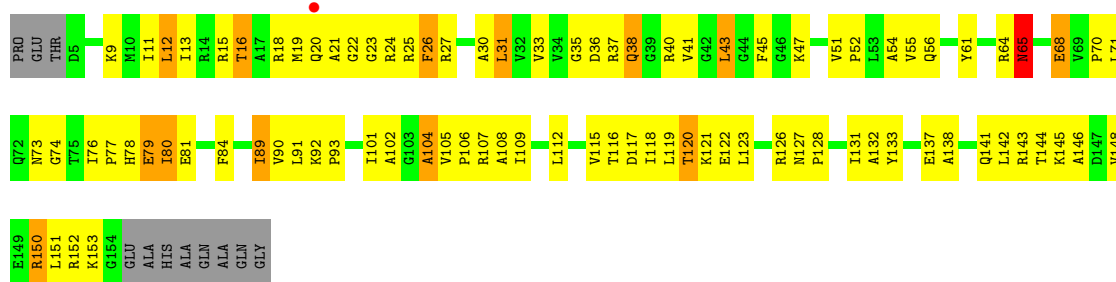
• Molecule 3: 30S RIBOSOMAL PROTEIN S3



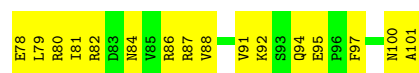
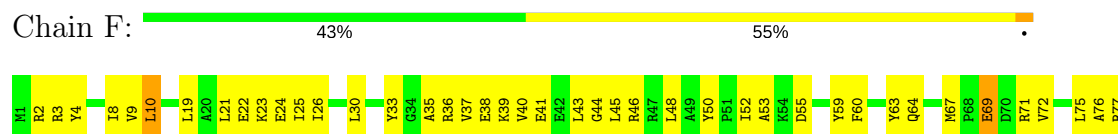
• Molecule 4: 30S RIBOSOMAL PROTEIN S4



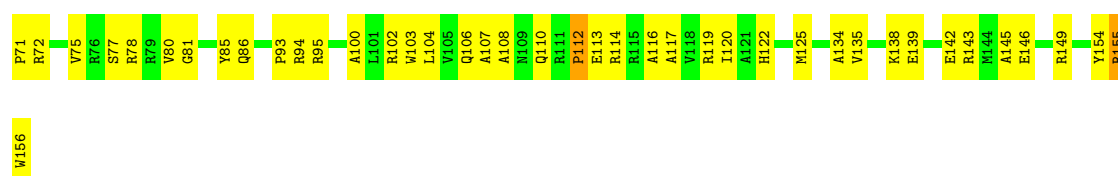
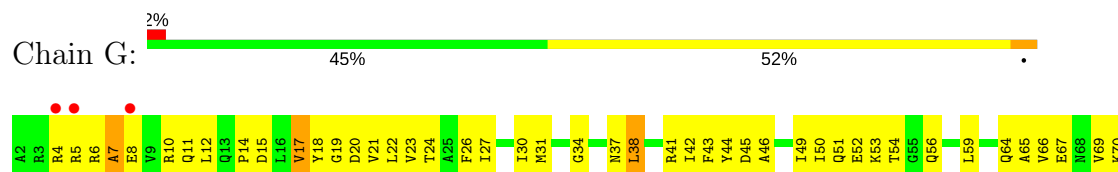
• Molecule 5: 30S RIBOSOMAL PROTEIN S5



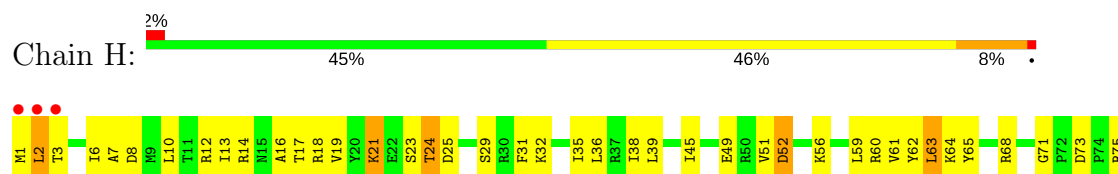
• Molecule 6: 30S RIBOSOMAL PROTEIN S6



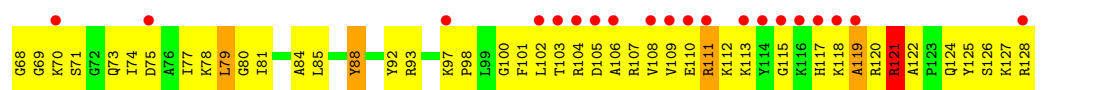
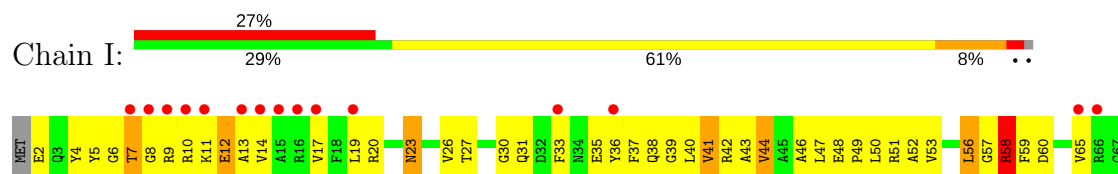
• Molecule 7: 30S RIBOSOMAL PROTEIN S7



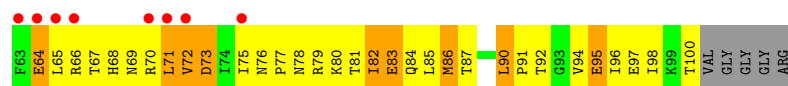
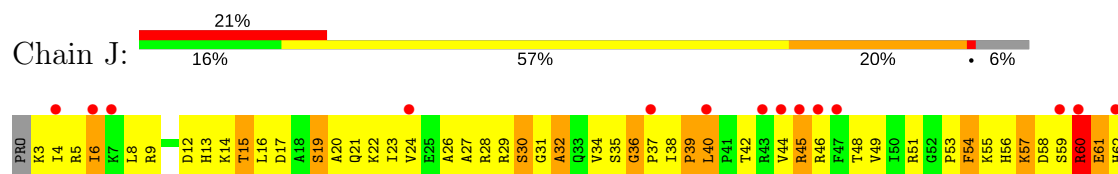
• Molecule 8: 30S RIBOSOMAL PROTEIN S8



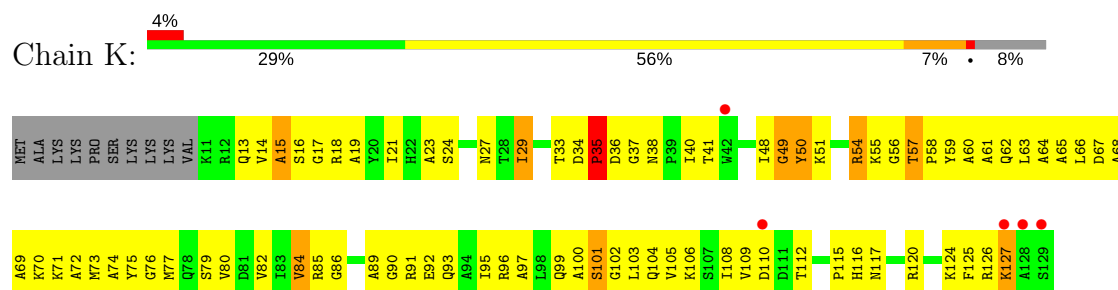
• Molecule 9: 30S RIBOSOMAL PROTEIN S9



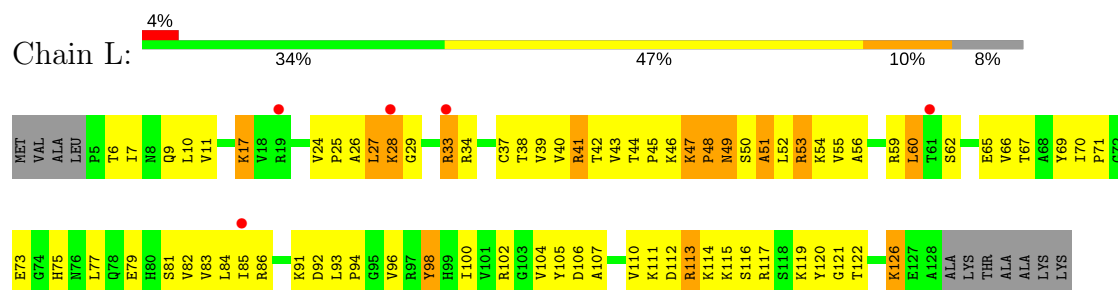
• Molecule 10: 30S RIBOSOMAL PROTEIN S10



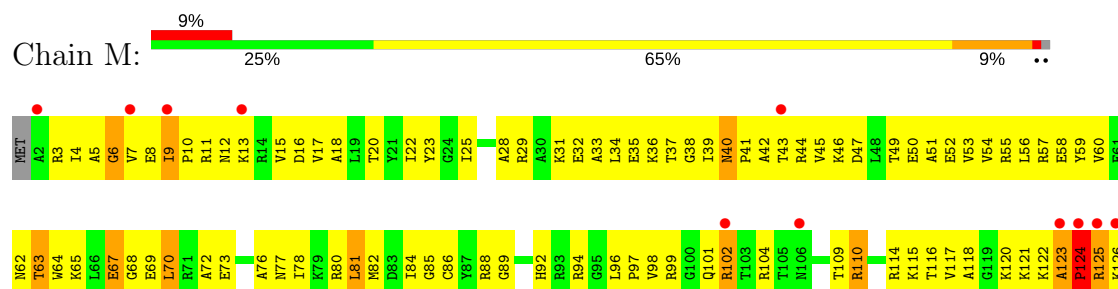
- Molecule 11: 30S RIBOSOMAL PROTEIN S11



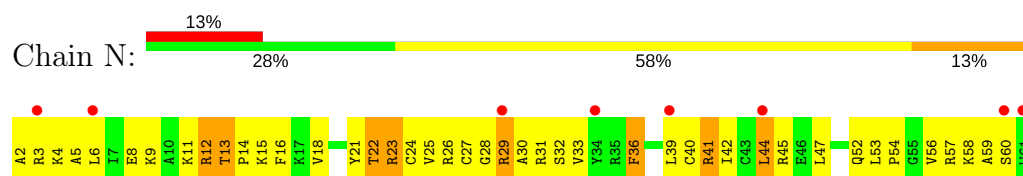
- Molecule 12: 30S RIBOSOMAL PROTEIN S12



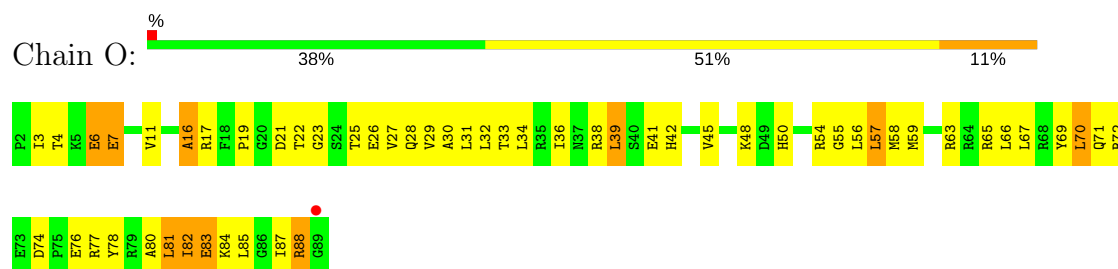
- Molecule 13: 30S RIBOSOMAL PROTEIN S13



- Molecule 14: 30S RIBOSOMAL PROTEIN S14



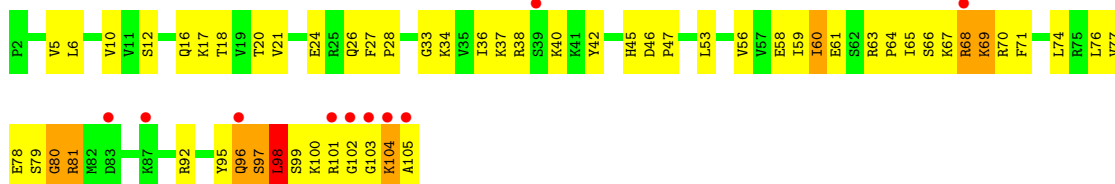
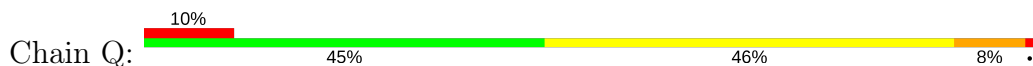
- Molecule 15: 30S RIBOSOMAL PROTEIN S15



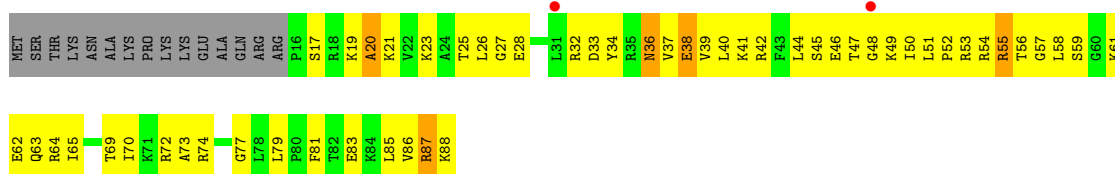
- Molecule 16: 30S RIBOSOMAL PROTEIN S16



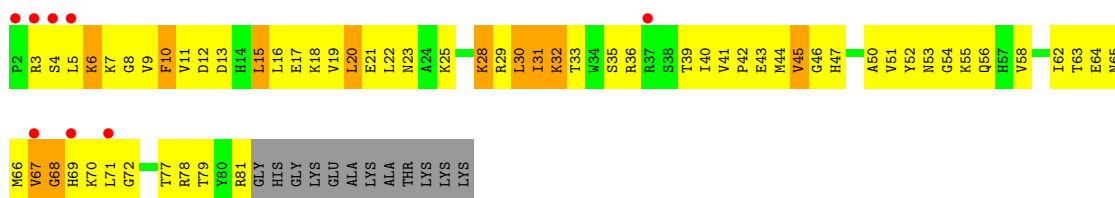
● Molecule 17: 30S RIBOSOMAL PROTEIN S17



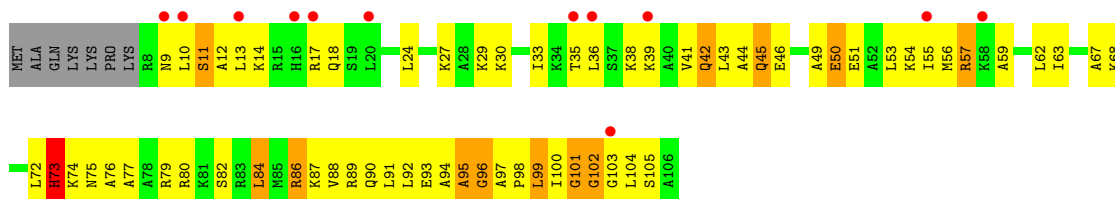
● Molecule 18: 30S RIBOSOMAL PROTEIN S18



• Molecule 19: 30S RIBOSOMAL PROTEIN S19



● Molecule 20: 30S RIBOSOMAL PROTEIN S20



- Molecule 21: 30S RIBOSOMAL PROTEIN THX





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	401.38Å 401.38Å 175.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.76 – 3.05 179.50 – 3.05	Depositor EDS
% Data completeness (in resolution range)	94.0 (59.76-3.05) 93.8 (179.50-3.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 3.07Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.208 , 0.252 (Not available) , (Not available)	Depositor DCC
R_{free} test set	NotAvailable	DCC
Wilson B-factor (Å ²)	68.0	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 76.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	51933	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.42% 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: UNX, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.48	0/36393	0.75	41/56797 (0.1%)
2	B	0.36	0/1935	0.67	1/2609 (0.0%)
3	C	0.37	0/1636	0.66	0/2205
4	D	0.37	0/1733	0.63	0/2318
5	E	0.48	0/1162	0.79	0/1564
6	F	0.33	0/856	0.62	0/1154
7	G	0.34	0/1276	0.61	0/1709
8	H	0.44	0/1136	0.74	0/1527
9	I	0.36	0/1029	0.62	0/1378
10	J	0.36	0/805	0.71	0/1082
11	K	0.39	0/900	0.70	0/1213
12	L	0.42	0/986	0.73	0/1320
13	M	0.35	0/1008	0.67	0/1347
14	N	0.40	0/501	0.78	0/664
15	O	0.36	0/745	0.63	1/992 (0.1%)
16	P	0.43	0/716	0.76	0/963
17	Q	0.44	0/870	0.75	0/1159
18	R	0.36	0/603	0.63	0/799
19	S	0.34	0/661	0.72	1/890 (0.1%)
20	T	0.39	0/764	0.73	0/1006
21	V	0.42	0/212	0.64	0/277
All	All	0.45	0/55927	0.73	44/82973 (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	2	40

There are no bond length outliers.

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1498	U	C2'-C3'-O3'	9.93	131.35	109.50
1	A	243	A	C2'-C3'-O3'	9.45	130.28	109.50
1	A	181	G	C2'-C3'-O3'	9.13	129.59	109.50
1	A	559	A	C2'-C3'-O3'	9.12	129.56	109.50
1	A	1299	A	N9-C1'-C2'	8.59	125.17	114.00
1	A	1528	U	C2'-C3'-O3'	8.05	127.22	109.50
1	A	366	C	C2'-C3'-O3'	7.86	126.79	109.50
1	A	197	A	N9-C1'-C2'	7.76	124.09	114.00
1	A	687	A	C2'-C3'-O3'	7.72	126.48	109.50
1	A	575	G	C2'-C3'-O3'	7.68	126.40	109.50
1	A	266	G	C2'-C3'-O3'	7.59	126.19	109.50
1	A	60	A	C2'-C3'-O3'	7.56	126.13	109.50
1	A	792	A	C2'-C3'-O3'	7.23	125.41	109.50
1	A	115	G	N9-C1'-C2'	6.94	123.02	114.00
1	A	1505	G	C2'-C3'-O3'	6.65	124.34	113.70
1	A	1067	A	C2'-C3'-O3'	6.59	124.25	113.70
1	A	1502	A	N9-C1'-C2'	6.55	122.52	114.00
1	A	115	G	C2'-C3'-O3'	6.46	124.03	113.70
1	A	372	C	C2'-C3'-O3'	6.37	123.89	113.70
1	A	7	G	C2'-C3'-O3'	6.35	123.85	113.70
1	A	509	A	C2'-C3'-O3'	6.32	123.81	113.70
1	A	1528	U	C4'-C3'-O3'	6.13	125.27	113.00
1	A	460	A	N9-C1'-C2'	6.12	121.96	114.00
19	S	54	GLY	N-CA-C	-6.05	97.97	113.10
1	A	428	G	C2'-C3'-O3'	5.85	123.06	113.70
1	A	63	C	C5'-C4'-C3'	-5.71	106.86	116.00
1	A	266	G	C5'-C4'-C3'	-5.64	106.97	116.00
1	A	1124	G	N9-C1'-C2'	5.63	121.32	114.00
1	A	203	U	N1-C1'-C2'	5.56	121.23	114.00
1	A	1380	U	C2'-C3'-O3'	5.52	122.53	113.70
1	A	353	A	C5'-C4'-O4'	-5.50	102.50	109.10
1	A	1065	U	C1'-O4'-C4'	-5.45	105.54	109.90
15	O	45	VAL	N-CA-C	-5.39	96.44	111.00
2	B	187	LEU	N-CA-C	-5.38	96.46	111.00
1	A	1085	U	N1-C1'-C2'	5.36	120.96	114.00
1	A	389	A	C5'-C4'-C3'	5.30	124.49	116.00
1	A	484	G	C2'-C3'-O3'	5.30	122.18	113.70
1	A	181	G	C4'-C3'-O3'	5.21	123.42	113.00
1	A	108	G	O4'-C1'-N9	5.18	112.34	108.20
1	A	686	U	C5'-C4'-C3'	-5.12	107.80	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	960	U	C2'-C3'-O3'	5.07	121.81	113.70
1	A	993	G	N9-C1'-C2'	5.04	120.55	114.00
1	A	976	G	C5'-C4'-O4'	5.04	115.15	109.10
1	A	49	U	C5'-C4'-C3'	-5.03	107.96	116.00

All (2) chirality outliers are listed below:

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

All (40) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1073	U	Sidechain
1	A	1079	G	Sidechain
1	A	1085	U	Sidechain
1	A	1092	A	Sidechain
1	A	1130	A	Sidechain
1	A	1139	G	Sidechain
1	A	12	U	Sidechain
1	A	1281	U	Sidechain
1	A	1289	A	Sidechain
1	A	1293	G	Sidechain
1	A	1299	A	Sidechain
1	A	1301	U	Sidechain
1	A	1305	G	Sidechain
1	A	1340	A	Sidechain
1	A	1360	A	Sidechain
1	A	1506	U	Sidechain
1	A	1525	G	Sidechain
1	A	197	A	Sidechain
1	A	203	U	Sidechain
1	A	231	G	Sidechain
1	A	249	U	Sidechain
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	254	G	Sidechain
1	A	266	G	Sidechain
1	A	274	A	Sidechain
1	A	290	C	Sidechain

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Mol	Chain	Res	Type	Group
1	A	297	G	Sidechain
1	A	305	G	Sidechain
1	A	380	G	Sidechain
1	A	413	G	Sidechain
1	A	481	G	Sidechain
1	A	573	A	Sidechain
1	A	575	G	Sidechain
1	A	603	U	Sidechain
1	A	727	G	Sidechain
1	A	879	C	Sidechain
1	A	898	G	Sidechain
1	A	982	U	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32514	0	16410	1113	0
2	B	1900	0	1951	217	1
3	C	1612	0	1677	226	0
4	D	1703	0	1764	146	0
5	E	1146	0	1207	104	0
6	F	843	0	857	72	0
7	G	1257	0	1296	93	0
8	H	1116	0	1177	67	0
9	I	1011	0	1043	113	0
10	J	792	0	835	130	0
11	K	885	0	904	85	0
12	L	970	0	1057	118	0
13	M	997	0	1072	121	0
14	N	492	0	529	74	0
15	O	734	0	771	55	0
16	P	700	0	720	56	0
17	Q	857	0	930	84	0
18	R	597	0	668	68	0
19	S	647	0	673	81	0
20	T	762	0	859	78	0
21	V	208	0	221	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	D	1	0	0	0	0
22	N	1	0	0	0	0
23	A	186	0	0	0	0
23	B	1	0	0	0	0
23	M	1	0	0	0	0
All	All	51933	0	36621	2836	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 32.

All (2836) 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)
12:L:41:ARG:HG2	12:L:42:THR:H	1.03	1.15
2:B:77:ALA:HB2	2:B:211:ILE:HD13	1.22	1.14
1:A:1443:G:H5''	1:A:1446:A:H5'	1.28	1.11
9:I:8:GLY:HA2	9:I:79:LEU:HD12	1.32	1.09
4:D:36:ARG:H	4:D:37:PRO:HD3	1.19	1.07
11:K:110:ASP:HB2	18:R:88:LYS:HD2	1.35	1.07
1:A:1489:G:H2'	1:A:1490:C:H5''	1.37	1.05
1:A:243:A:H4'	1:A:244:U:H5'	1.36	1.04
4:D:150:GLU:HG3	4:D:153:ARG:HH21	1.19	1.04
12:L:60:LEU:HD11	12:L:85:ILE:HD12	1.39	1.04
10:J:51:ARG:HB2	10:J:59:SER:HB3	1.34	1.03
20:T:39:LYS:HD2	20:T:55:ILE:HD13	1.41	1.02
13:M:49:THR:HG22	13:M:51:ALA:H	1.26	1.00
3:C:52:LEU:H	3:C:52:LEU:HD23	1.26	1.00
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.43	0.99
2:B:178:ARG:HG3	2:B:178:ARG:HH11	1.21	0.99
11:K:54:ARG:HH11	11:K:54:ARG:HB3	1.26	0.99
19:S:28:LYS:HG2	19:S:29:ARG:H	1.26	0.98
1:A:1116:C:H2'	1:A:1117:G:H5''	1.46	0.97
1:A:1057:G:H5''	3:C:154:SER:HB2	1.47	0.96
3:C:91:LEU:HD21	3:C:99:VAL:HG13	1.48	0.96
11:K:54:ARG:O	11:K:57:THR:HG22	1.66	0.95
1:A:1489:G:C2'	1:A:1490:C:H5''	1.96	0.94
10:J:31:GLY:HA2	10:J:78:ASN:HD22	1.32	0.94
3:C:14:ILE:HG22	3:C:15:THR:H	1.31	0.94
1:A:1190:G:OP1	3:C:4:LYS:HA	1.66	0.93
12:L:41:ARG:HG2	12:L:42:THR:N	1.83	0.93
6:F:94:GLN:HE21	18:R:32:ARG:HD3	1.32	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:31:ILE:HG22	19:S:32:LYS:H	1.34	0.93
1:A:1256:A:H4'	1:A:1257:U:H5'	1.50	0.93
2:B:124:SER:HB2	2:B:125:PRO:HD2	1.49	0.93
12:L:75:HIS:HD2	12:L:77:LEU:H	1.05	0.92
1:A:1086:U:H3	1:A:1099:G:H22	1.08	0.92
16:P:58:TYR:O	16:P:61:SER:HB3	1.68	0.92
1:A:1137:C:H4'	1:A:1138:G:C2	2.05	0.92
13:M:40:ASN:HD22	13:M:41:PRO:CD	1.82	0.92
1:A:664:G:H22	1:A:741:G:H1	1.16	0.91
3:C:131:ARG:HG2	3:C:135:LYS:HE3	1.50	0.91
1:A:1305:G:HO2'	1:A:1306:A:H8	0.92	0.91
1:A:838:G:H2'	1:A:839:U:H5''	1.52	0.91
3:C:195:VAL:O	3:C:196:LEU:HD23	1.68	0.91
1:A:1101:A:H4'	1:A:1102:A:O5'	1.65	0.90
5:E:81:GLU:HG2	5:E:90:VAL:HG22	1.52	0.90
9:I:70:LYS:O	9:I:74:ILE:HG13	1.72	0.90
1:A:1502:A:H2	1:A:1505:G:H1	1.20	0.90
3:C:58:GLU:HB3	10:J:92:THR:HG21	1.51	0.90
1:A:1497:G:O2'	1:A:1498:U:H5'	1.71	0.89
1:A:235:C:H5'	17:Q:70:ARG:HG2	1.51	0.89
2:B:91:PRO:HG2	2:B:155:LEU:HD23	1.54	0.89
10:J:8:LEU:HD21	10:J:96:ILE:HG12	1.54	0.88
17:Q:97:SER:HB2	17:Q:102:GLY:C	1.94	0.88
2:B:59:GLU:HG2	2:B:221:LEU:HD11	1.51	0.88
4:D:36:ARG:N	4:D:37:PRO:HD3	1.88	0.87
1:A:1125:U:H3	10:J:5:ARG:HH21	1.18	0.86
4:D:150:GLU:HG3	4:D:153:ARG:NH2	1.90	0.86
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.57	0.86
1:A:1435:G:H2'	1:A:1436:U:C6	2.10	0.86
2:B:116:GLU:HG2	2:B:153:ARG:HH12	1.39	0.86
3:C:70:VAL:HG21	3:C:76:VAL:HG21	1.58	0.86
5:E:51:VAL:HB	5:E:52:PRO:HD3	1.55	0.86
5:E:115:VAL:HG11	5:E:118:ILE:HG13	1.57	0.86
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.55	0.86
6:F:30:LEU:HD23	6:F:75:LEU:HD21	1.57	0.86
1:A:1305:G:O2'	1:A:1306:A:H8	1.58	0.85
3:C:110:ASN:HD21	3:C:140:ARG:HB3	1.41	0.85
3:C:52:LEU:HD21	3:C:118:GLN:HE22	1.40	0.85
10:J:22:LYS:HE2	10:J:90:LEU:HD12	1.57	0.85
2:B:102:LEU:HD21	2:B:162:ILE:HD11	1.57	0.85
3:C:190:ARG:HB3	3:C:190:ARG:NH1	1.92	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1131:G:H1	1:A:1143:G:H21	1.22	0.84
13:M:50:GLU:O	13:M:54:VAL:HG23	1.77	0.84
10:J:49:VAL:HG13	14:N:41:ARG:HB2	1.57	0.84
1:A:250:A:H4'	1:A:251:G:O5'	1.76	0.84
3:C:64:VAL:HB	3:C:99:VAL:HB	1.59	0.84
13:M:3:ARG:HG2	13:M:9:ILE:HG23	1.56	0.84
1:A:1497:G:C2'	1:A:1498:U:H5'	2.08	0.84
1:A:1064:G:H4'	1:A:1065:U:H5'	1.58	0.84
1:A:141:A:H1'	1:A:182:U:O2	1.78	0.84
17:Q:27:PHE:CZ	17:Q:36:ILE:HD11	2.12	0.84
9:I:8:GLY:HA2	9:I:79:LEU:CD1	2.07	0.84
3:C:190:ARG:HB3	3:C:190:ARG:HH11	1.43	0.84
4:D:104:VAL:HG11	4:D:146:ILE:HD12	1.58	0.83
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.60	0.83
19:S:55:LYS:HG2	19:S:56:GLN:HE21	1.41	0.83
6:F:36:ARG:HH12	6:F:38:GLU:HG2	1.44	0.83
4:D:61:LYS:HD2	4:D:207:TYR:OH	1.78	0.83
3:C:172:ARG:HH12	3:C:174:PRO:HG3	1.43	0.83
1:A:135:C:O2	16:P:1:MET:HB2	1.78	0.83
1:A:1281:U:H5'	1:A:1282:C:H5	1.44	0.82
1:A:1356:G:H2'	1:A:1357:A:C8	2.15	0.82
3:C:191:THR:HG22	3:C:193:TYR:H	1.44	0.82
7:G:75:VAL:CG1	7:G:86:GLN:HB3	2.10	0.82
3:C:91:LEU:HD23	3:C:92:ALA:N	1.94	0.82
12:L:25:PRO:C	12:L:27:LEU:H	1.79	0.82
19:S:29:ARG:O	19:S:30:LEU:HB2	1.80	0.82
13:M:22:ILE:HD12	13:M:25:ILE:HD12	1.61	0.82
15:O:78:TYR:CZ	15:O:82:ILE:HD11	2.15	0.81
4:D:150:GLU:HA	4:D:153:ARG:HE	1.44	0.81
20:T:43:LEU:HD13	20:T:51:GLU:HG3	1.62	0.81
3:C:8:ILE:HG23	3:C:16:ARG:HG2	1.60	0.81
13:M:78:ILE:HA	13:M:81:LEU:HD21	1.62	0.81
6:F:30:LEU:HB3	6:F:35:ALA:HB3	1.62	0.81
10:J:19:SER:HB2	10:J:91:PRO:HG3	1.60	0.81
1:A:1060:C:C5	3:C:2:GLY:HA3	2.14	0.81
2:B:101:MET:HA	2:B:108:ILE:HD12	1.63	0.81
12:L:41:ARG:CG	12:L:42:THR:H	1.88	0.80
12:L:70:ILE:HD13	12:L:77:LEU:HD12	1.63	0.80
2:B:27:LYS:HD3	2:B:195:ASP:OD2	1.82	0.80
18:R:55:ARG:HB3	18:R:55:ARG:NH1	1.95	0.80
1:A:1285:A:H4'	1:A:1286:A:O5'	1.82	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:95:GLU:H	6:F:95:GLU:CD	1.85	0.80
1:A:673:G:H2'	1:A:674:G:C8	2.17	0.80
7:G:75:VAL:HG11	7:G:86:GLN:HB3	1.63	0.79
12:L:126:LYS:HD2	12:L:126:LYS:H	1.47	0.79
5:E:118:ILE:HG22	5:E:119:LEU:N	1.95	0.79
10:J:8:LEU:CD2	10:J:96:ILE:HG12	2.11	0.79
11:K:54:ARG:NH1	11:K:54:ARG:HB3	1.97	0.79
1:A:80:G:H3'	1:A:81:U:H5''	1.63	0.79
12:L:67:THR:HG22	12:L:96:VAL:HG13	1.63	0.79
12:L:28:LYS:HD2	12:L:33:ARG:HH22	1.47	0.79
2:B:8:LYS:O	2:B:9:GLU:HB2	1.81	0.79
4:D:25:ARG:C	4:D:27:TYR:H	1.85	0.79
20:T:54:LYS:HG3	20:T:100:ILE:CD1	2.13	0.79
1:A:1116:C:C2'	1:A:1117:G:H5''	2.12	0.78
1:A:1490:C:H5'	1:A:1490:C:H6	1.47	0.78
1:A:255:G:H1'	17:Q:16:GLN:NE2	1.97	0.78
2:B:132:LYS:HA	2:B:135:GLN:HB3	1.63	0.78
12:L:120:TYR:O	12:L:122:THR:HG23	1.83	0.78
3:C:15:THR:O	3:C:16:ARG:HB2	1.82	0.78
1:A:838:G:C2'	1:A:839:U:H5''	2.14	0.78
2:B:84:GLU:OE1	2:B:216:SER:HA	1.83	0.78
5:E:43:LEU:HD11	5:E:132:ALA:HB1	1.64	0.78
19:S:31:ILE:HG22	19:S:32:LYS:N	1.99	0.78
16:P:21:VAL:HG21	16:P:59:TRP:CD1	2.19	0.78
5:E:64:ARG:O	5:E:65:ASN:HB3	1.84	0.77
2:B:197:VAL:HB	2:B:200:ILE:HG12	1.66	0.77
1:A:939:G:H5''	7:G:102:ARG:NH2	1.98	0.77
15:O:17:ARG:HH11	15:O:17:ARG:HG3	1.49	0.77
1:A:1226:C:H4'	1:A:1227:A:OP1	1.84	0.77
3:C:150:LYS:HE2	3:C:152:ILE:HD11	1.66	0.77
7:G:66:VAL:HG12	7:G:70:LYS:HE3	1.65	0.77
1:A:761:G:H1'	17:Q:104:LYS:O	1.85	0.77
1:A:130:A:OP2	1:A:190(E):U:H2'	1.84	0.77
6:F:100:ASN:HD22	18:R:23:LYS:HG2	1.49	0.77
1:A:1250:A:H4'	9:I:68:GLY:H	1.47	0.77
1:A:243:A:C4'	1:A:244:U:H5'	2.13	0.77
3:C:110:ASN:O	3:C:111:LEU:HD23	1.85	0.77
6:F:86:ARG:O	6:F:87:ARG:HG2	1.85	0.77
9:I:118:LYS:O	9:I:119:ALA:HB3	1.85	0.77
15:O:16:ALA:HB1	15:O:21:ASP:HB3	1.64	0.77
1:A:1366:C:H2'	1:A:1367:C:H6	1.48	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:839:U:H5'	1:A:840:C:H5	1.50	0.77
1:A:1152:A:H5''	10:J:13:HIS:CD2	2.19	0.77
20:T:54:LYS:HG3	20:T:100:ILE:HD13	1.66	0.77
1:A:1236:A:H4'	1:A:1304:G:H4'	1.67	0.76
4:D:150:GLU:CD	4:D:150:GLU:H	1.86	0.76
7:G:95:ARG:HG3	7:G:95:ARG:HH11	1.50	0.76
8:H:90:GLY:O	8:H:91:ARG:HB2	1.82	0.76
13:M:4:ILE:HG22	13:M:5:ALA:N	2.00	0.76
17:Q:95:TYR:C	17:Q:97:SER:H	1.89	0.76
1:A:1256:A:N6	1:A:1278:U:H1'	2.00	0.76
2:B:57:PHE:O	2:B:60:ASP:HB3	1.85	0.76
14:N:14:PRO:C	14:N:16:PHE:H	1.86	0.76
17:Q:97:SER:OG	17:Q:103:GLY:HA2	1.85	0.76
21:V:5:ASP:O	21:V:11:GLY:HA3	1.85	0.76
1:A:328:C:O2	1:A:328:C:H2'	1.85	0.76
3:C:19:GLU:HB3	3:C:40:ARG:HH21	1.50	0.76
2:B:139:LYS:O	2:B:143:GLU:HG2	1.86	0.76
20:T:14:LYS:O	20:T:18:GLN:HG3	1.86	0.76
3:C:107:GLN:H	3:C:107:GLN:CD	1.88	0.76
16:P:74:LEU:O	16:P:79:VAL:HG23	1.85	0.76
1:A:1025:U:H2'	1:A:1026:G:C8	2.21	0.76
2:B:36:ARG:HD2	2:B:41:ILE:HD12	1.68	0.75
10:J:82:ILE:O	10:J:86:MET:HB2	1.86	0.75
12:L:126:LYS:H	12:L:126:LYS:CD	1.96	0.75
3:C:50:ALA:HB1	3:C:70:VAL:HG11	1.68	0.75
19:S:16:LEU:O	19:S:19:VAL:HG12	1.87	0.75
3:C:116:VAL:HG21	3:C:202:ILE:HD11	1.68	0.75
10:J:96:ILE:HG22	10:J:97:GLU:H	1.52	0.75
12:L:48:PRO:HG2	12:L:49:ASN:H	1.52	0.75
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.51	0.75
1:A:351:G:H4'	1:A:352:C:OP1	1.85	0.75
1:A:80:G:H3'	1:A:81:U:C5'	2.16	0.75
1:A:839:U:H5'	1:A:840:C:C5	2.22	0.75
1:A:840:C:H5''	1:A:841:U:OP1	1.85	0.75
2:B:130:ARG:HH22	3:C:179:ARG:HH12	1.35	0.75
12:L:75:HIS:HD2	12:L:77:LEU:N	1.82	0.74
13:M:3:ARG:HA	13:M:8:GLU:O	1.86	0.74
1:A:1391:U:H2'	1:A:1392:G:C8	2.22	0.74
4:D:162:LEU:HD13	4:D:181:MET:HG2	1.67	0.74
13:M:88:ARG:HD2	19:S:3:ARG:HH21	1.50	0.74
1:A:1234:C:H5'	1:A:1365:G:OP1	1.86	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:72:GLY:HA3	2:B:81:VAL:HG21	1.69	0.74
19:S:40:ILE:HD13	19:S:62:ILE:HD13	1.68	0.74
1:A:1064:G:H4'	1:A:1065:U:C5'	2.18	0.74
15:O:33:THR:HG23	15:O:63:ARG:NH1	2.03	0.74
17:Q:95:TYR:O	17:Q:97:SER:N	2.19	0.74
19:S:17:GLU:O	19:S:21:GLU:HG3	1.87	0.74
1:A:579:G:H5'	1:A:728:A:H1'	1.69	0.74
2:B:16:HIS:NE2	2:B:214:ILE:HG12	2.02	0.74
2:B:77:ALA:HB2	2:B:211:ILE:CD1	2.10	0.74
3:C:52:LEU:HD23	3:C:52:LEU:N	2.02	0.74
2:B:178:ARG:NH1	2:B:178:ARG:HG3	1.92	0.74
1:A:1117:G:H4'	9:I:104:ARG:NH1	2.03	0.74
12:L:75:HIS:CD2	12:L:77:LEU:H	1.97	0.74
18:R:55:ARG:HB3	18:R:55:ARG:HH11	1.50	0.74
1:A:748:C:H1'	1:A:749:C:H5	1.53	0.74
6:F:69:GLU:HA	6:F:72:VAL:HG23	1.70	0.74
1:A:1125:U:H3	10:J:5:ARG:NH2	1.85	0.73
4:D:64:LEU:HD12	4:D:75:PHE:HZ	1.53	0.73
21:V:6:ARG:HD3	21:V:15:ARG:HH12	1.52	0.73
1:A:1279:A:H5''	1:A:1280:A:OP1	1.88	0.73
1:A:792:A:H4'	1:A:793:U:H5''	1.68	0.73
7:G:23:VAL:HG12	7:G:27:ILE:HD11	1.70	0.73
12:L:27:LEU:HG	12:L:28:LYS:H	1.53	0.73
2:B:23:ARG:NH1	2:B:24:TRP:N	2.35	0.73
9:I:44:VAL:HG13	9:I:51:ARG:HH22	1.52	0.73
3:C:52:LEU:H	3:C:52:LEU:CD2	2.00	0.73
12:L:27:LEU:O	12:L:29:GLY:N	2.21	0.73
1:A:1488:G:H2'	1:A:1489:G:C8	2.24	0.73
1:A:992:U:H4'	1:A:993:G:O5'	1.86	0.73
2:B:95:GLN:O	2:B:96:ARG:HD2	1.88	0.73
12:L:59:ARG:HD3	12:L:65:GLU:HG3	1.68	0.73
1:A:1412:C:H2'	1:A:1413:A:C8	2.24	0.73
2:B:91:PRO:HG3	2:B:154:LEU:HB2	1.69	0.73
3:C:13:GLY:HA3	14:N:57:ARG:HH21	1.54	0.73
6:F:26:ILE:HG21	6:F:63:TYR:HE2	1.54	0.73
2:B:23:ARG:HH11	2:B:24:TRP:N	1.86	0.72
2:B:116:GLU:HG2	2:B:153:ARG:NH1	2.04	0.72
8:H:1:MET:HG2	8:H:2:LEU:N	2.05	0.72
1:A:434:U:H2'	1:A:435:C:C6	2.24	0.72
18:R:26:LEU:HD12	18:R:27:GLY:H	1.53	0.72
1:A:197:A:H4'	1:A:198:G:O5'	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:A:H5'	1:A:353:A:H8	1.53	0.72
1:A:161:A:H2'	1:A:162:A:C8	2.23	0.72
4:D:158:ILE:HG22	4:D:181:MET:HE2	1.70	0.72
1:A:1152:A:H5''	10:J:13:HIS:HD2	1.53	0.72
10:J:39:PRO:O	10:J:40:LEU:HB2	1.89	0.72
11:K:77:MET:HE3	11:K:80:VAL:HG22	1.72	0.72
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.23	0.72
20:T:10:LEU:O	20:T:12:ALA:N	2.22	0.72
1:A:877:C:O2	8:H:3:THR:HG21	1.89	0.72
6:F:67:MET:HE1	6:F:72:VAL:HA	1.71	0.72
8:H:1:MET:HG2	8:H:2:LEU:H	1.54	0.72
1:A:1250:A:H4'	9:I:68:GLY:N	2.05	0.72
11:K:84:VAL:HG11	11:K:95:ILE:HD11	1.70	0.72
1:A:1148:U:H2'	1:A:1149:C:O4'	1.90	0.71
10:J:35:SER:HB2	10:J:72:VAL:O	1.90	0.71
17:Q:59:ILE:HG23	17:Q:71:PHE:HB3	1.70	0.71
1:A:501:C:H2'	1:A:502:G:H8	1.53	0.71
9:I:4:TYR:CE2	9:I:88:TYR:HA	2.24	0.71
1:A:974:A:OP1	14:N:31:ARG:HG2	1.89	0.71
18:R:33:ASP:OD2	18:R:36:ASN:HB2	1.90	0.71
1:A:1065:U:H4'	1:A:1066:C:O5'	1.89	0.71
1:A:1413:A:H2	1:A:1487:G:H22	1.39	0.71
1:A:977:A:H2'	1:A:978:A:H5''	1.72	0.71
10:J:45:ARG:HH22	14:N:36:PHE:HD2	1.36	0.71
1:A:344:A:H4'	1:A:345:C:OP2	1.91	0.71
9:I:111:ARG:HD3	9:I:112:LYS:N	2.06	0.71
1:A:1281:U:H5'	1:A:1282:C:C5	2.25	0.71
1:A:1343:G:H2'	1:A:1344:C:C6	2.26	0.71
9:I:65:VAL:HG21	9:I:73:GLN:HB3	1.72	0.71
1:A:954:G:H5''	13:M:120:LYS:HD3	1.73	0.71
8:H:108:GLY:HA3	8:H:138:TRP:HB3	1.70	0.71
19:S:15:LEU:HD12	19:S:16:LEU:N	2.06	0.71
19:S:70:LYS:O	19:S:72:GLY:N	2.24	0.71
1:A:1411:C:H2'	1:A:1412:C:C6	2.26	0.70
3:C:7:PRO:HG2	3:C:184:TYR:HB2	1.73	0.70
1:A:706:A:C1'	11:K:29:ILE:HD11	2.21	0.70
1:A:818:G:C3'	1:A:819:A:H5''	2.21	0.70
5:E:102:ALA:HB1	5:E:120:THR:HG21	1.73	0.70
13:M:40:ASN:HB3	13:M:43:THR:HG23	1.72	0.70
1:A:1351:U:H2'	1:A:1352:C:H6	1.55	0.70
6:F:10:LEU:HD11	6:F:59:TYR:HD2	1.54	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:32:ALA:HB2	10:J:76:ASN:HD22	1.57	0.70
1:A:706:A:O4'	11:K:29:ILE:HD11	1.91	0.70
1:A:537:G:OP1	12:L:113:ARG:NH2	2.24	0.70
14:N:22:THR:HB	14:N:33:VAL:HG21	1.73	0.70
1:A:107:G:C2'	1:A:108:G:H5'	2.21	0.70
1:A:1489:G:C3'	1:A:1490:C:H5''	2.21	0.70
1:A:496:A:H4'	1:A:497:A:OP1	1.92	0.70
1:A:761:G:H4'	17:Q:102:GLY:C	2.11	0.70
2:B:124:SER:HB2	2:B:125:PRO:CD	2.22	0.70
3:C:180:ALA:O	3:C:181:ASN:HB3	1.92	0.70
10:J:65:LEU:HD23	10:J:65:LEU:O	1.91	0.70
10:J:78:ASN:O	10:J:80:LYS:N	2.24	0.70
13:M:49:THR:HG22	13:M:51:ALA:N	2.02	0.70
13:M:6:GLY:O	13:M:7:VAL:HG22	1.92	0.70
1:A:1278:U:H5''	1:A:1279:A:C5'	2.21	0.70
4:D:36:ARG:H	4:D:37:PRO:CD	2.02	0.70
9:I:97:LYS:HG2	9:I:102:LEU:HD12	1.72	0.70
4:D:70:ILE:HD11	4:D:100:ARG:CZ	2.21	0.70
15:O:17:ARG:NH1	15:O:77:ARG:NH1	2.40	0.70
4:D:157:LEU:CD2	4:D:161:ASN:HD21	2.05	0.70
17:Q:45:HIS:HB2	17:Q:65:ILE:HD13	1.71	0.70
18:R:39:VAL:O	18:R:42:ARG:HB2	1.90	0.70
1:A:1168:A:H2'	1:A:1169:A:C8	2.27	0.70
4:D:28:SER:O	4:D:30:LYS:N	2.25	0.70
9:I:97:LYS:CG	9:I:102:LEU:HD12	2.22	0.70
10:J:30:SER:O	10:J:78:ASN:HB2	1.92	0.70
10:J:61:GLU:OE1	14:N:45:ARG:NH1	2.25	0.70
3:C:6:HIS:CD2	3:C:8:ILE:HB	2.27	0.69
13:M:81:LEU:O	13:M:86:CYS:HB3	1.92	0.69
1:A:438:G:H4'	1:A:439:A:OP1	1.90	0.69
4:D:150:GLU:CG	4:D:153:ARG:HH21	2.02	0.69
15:O:39:LEU:HD13	15:O:56:LEU:HB2	1.74	0.69
1:A:254:G:OP1	17:Q:67:LYS:O	2.10	0.69
1:A:954:G:C5'	13:M:120:LYS:HD3	2.23	0.69
13:M:40:ASN:HD22	13:M:41:PRO:HD2	1.56	0.69
3:C:52:LEU:HD21	3:C:118:GLN:NE2	2.07	0.69
13:M:81:LEU:H	13:M:81:LEU:HD23	1.56	0.69
19:S:62:ILE:HD12	19:S:66:MET:HG3	1.75	0.69
1:A:352:C:H4'	1:A:354:G:OP1	1.91	0.69
10:J:46:ARG:HH11	10:J:64:GLU:CB	2.05	0.69
12:L:55:VAL:HG12	12:L:56:ALA:H	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1137:C:H4'	1:A:1138:G:N2	2.06	0.69
1:A:1281:U:H4'	1:A:1282:C:OP2	1.92	0.69
3:C:52:LEU:CD2	3:C:118:GLN:HE22	2.05	0.69
4:D:199:ASN:ND2	4:D:201:GLN:HB2	2.08	0.69
13:M:11:ARG:HG2	13:M:12:ASN:N	2.07	0.69
1:A:17:U:H2'	1:A:18:C:C6	2.28	0.69
10:J:30:SER:HB2	10:J:80:LYS:HB3	1.75	0.69
11:K:108:ILE:HB	18:R:87:ARG:O	1.91	0.69
1:A:392:G:H2'	1:A:393:A:H8	1.55	0.69
16:P:34:GLU:OE2	16:P:55:ARG:HD3	1.93	0.69
17:Q:66:SER:O	17:Q:70:ARG:NH1	2.26	0.69
1:A:939:G:H5''	7:G:102:ARG:HH22	1.56	0.69
4:D:64:LEU:HD23	4:D:198:VAL:HG21	1.75	0.69
4:D:64:LEU:HD12	4:D:75:PHE:CZ	2.28	0.68
6:F:36:ARG:NH1	6:F:38:GLU:HG2	2.08	0.68
12:L:47:LYS:CB	12:L:48:PRO:CD	2.71	0.68
21:V:6:ARG:CD	21:V:15:ARG:HH12	2.06	0.68
1:A:477:G:H2'	1:A:478:A:H8	1.56	0.68
10:J:42:THR:HG23	10:J:67:THR:O	1.93	0.68
17:Q:24:GLU:OE2	17:Q:37:LYS:HD3	1.92	0.68
19:S:5:LEU:O	19:S:6:LYS:HB2	1.92	0.68
1:A:1443:G:C5'	1:A:1446:A:H5'	2.15	0.68
2:B:187:LEU:HD12	2:B:205:ASP:HA	1.74	0.68
19:S:41:VAL:HG23	19:S:43:GLU:HG2	1.75	0.68
1:A:1141:C:H2'	1:A:1142:G:H8	1.57	0.68
1:A:1412:C:H2'	1:A:1413:A:H8	1.59	0.68
1:A:731:G:OP1	1:A:766:A:H1'	1.94	0.68
2:B:22:LYS:HD2	2:B:35:GLU:OE1	1.93	0.68
5:E:51:VAL:O	5:E:55:VAL:HG23	1.93	0.68
9:I:93:ARG:HD3	9:I:97:LYS:HE3	1.75	0.68
1:A:701:C:H5'	1:A:703:G:O4'	1.93	0.68
3:C:38:ARG:HH11	3:C:38:ARG:HG3	1.58	0.68
1:A:99:C:H2'	1:A:101:A:C8	2.28	0.68
1:A:382:A:H2'	1:A:383:A:C8	2.28	0.68
6:F:75:LEU:O	6:F:79:LEU:HG	1.94	0.68
20:T:45:GLN:HA	20:T:91:LEU:HD22	1.75	0.68
2:B:25:ASN:C	2:B:25:ASN:HD22	1.96	0.68
4:D:151:LYS:N	4:D:151:LYS:HD2	2.08	0.68
9:I:26:VAL:HB	9:I:33:PHE:HB2	1.76	0.68
13:M:81:LEU:HD12	13:M:88:ARG:HD3	1.74	0.68
6:F:100:ASN:ND2	18:R:23:LYS:HG2	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:948:C:OP1	13:M:109:THR:HG22	1.94	0.68
4:D:3:ARG:HH22	4:D:74:GLN:CD	1.97	0.68
12:L:126:LYS:HD2	12:L:126:LYS:N	2.07	0.68
1:A:376:G:OP2	16:P:67:THR:HG21	1.94	0.68
1:A:1064:G:C4'	1:A:1065:U:H5'	2.23	0.68
1:A:939:G:H2'	1:A:940:C:C6	2.27	0.68
15:O:55:GLY:O	15:O:59:MET:HG3	1.94	0.68
1:A:1016:A:H2'	1:A:1017:G:O4'	1.93	0.67
1:A:173:U:H5'	1:A:197:A:O4'	1.95	0.67
12:L:47:LYS:HB2	12:L:48:PRO:CD	2.23	0.67
13:M:40:ASN:HD22	13:M:41:PRO:N	1.91	0.67
18:R:45:SER:OG	18:R:49:LYS:HB2	1.94	0.67
2:B:18:GLY:HA2	2:B:42:ILE:H	1.59	0.67
3:C:82:GLU:O	3:C:85:ARG:HB3	1.94	0.67
1:A:1366:C:H2'	1:A:1367:C:C6	2.30	0.67
16:P:20:VAL:HG11	16:P:32:TYR:HB3	1.74	0.67
1:A:105:G:H2'	1:A:106:C:C6	2.29	0.67
1:A:328:C:H4'	1:A:329:A:O5'	1.94	0.67
3:C:179:ARG:HD3	3:C:206:GLU:HG2	1.76	0.67
1:A:31:G:N1	1:A:48:C:H5'	2.09	0.67
1:A:1112:C:O2	3:C:179:ARG:HB3	1.95	0.67
3:C:190:ARG:HH11	3:C:190:ARG:CB	2.07	0.67
1:A:1368:G:O2'	1:A:1369:C:H5'	1.95	0.67
1:A:915:A:H2'	1:A:916:G:H5'	1.76	0.67
4:D:151:LYS:H	4:D:151:LYS:HD2	1.60	0.67
18:R:26:LEU:HD21	18:R:39:VAL:CG2	2.25	0.67
1:A:371:G:O2'	1:A:372:C:H5'	1.95	0.67
3:C:195:VAL:C	3:C:196:LEU:HD23	2.15	0.67
13:M:33:ALA:HA	13:M:59:TYR:HE2	1.60	0.67
1:A:1057:G:O2'	1:A:1058:G:H5'	1.95	0.67
1:A:1502:A:H2	1:A:1505:G:N1	1.90	0.67
4:D:187:ARG:HH21	4:D:188:LEU:HD12	1.60	0.67
1:A:186:C:O3'	20:T:82:SER:HB3	1.95	0.67
3:C:130:VAL:HG21	3:C:157:ILE:HG23	1.75	0.67
1:A:686:U:HO2'	1:A:687:A:H8	1.40	0.66
1:A:748:C:H1'	1:A:749:C:C5	2.30	0.66
3:C:26:LYS:H	3:C:26:LYS:HD3	1.58	0.66
1:A:967:C:H4'	9:I:128:ARG:HG3	1.75	0.66
10:J:94:VAL:HG12	10:J:95:GLU:N	2.10	0.66
4:D:30:LYS:C	4:D:32:ALA:H	1.97	0.66
5:E:12:LEU:HD13	5:E:31:LEU:HB2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:14:VAL:O	11:K:15:ALA:HB3	1.95	0.66
1:A:80:G:C3'	1:A:81:U:H5''	2.25	0.66
1:A:650:G:O2'	1:A:651:C:H5'	1.94	0.66
10:J:49:VAL:O	10:J:60:ARG:HA	1.95	0.66
11:K:66:LEU:HB3	11:K:70:LYS:HE3	1.78	0.66
15:O:33:THR:HG23	15:O:63:ARG:HH12	1.59	0.66
1:A:195:A:H4'	20:T:68:LYS:HE2	1.77	0.66
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.10	0.66
13:M:65:LYS:HG3	13:M:69:GLU:OE2	1.96	0.66
1:A:761:G:H5''	17:Q:102:GLY:HA3	1.78	0.66
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.59	0.66
1:A:662:G:H2'	1:A:663:A:C8	2.30	0.66
5:E:150:ARG:HH11	5:E:150:ARG:HG3	1.60	0.66
8:H:6:ILE:HD11	8:H:31:PHE:CD2	2.30	0.66
10:J:60:ARG:O	10:J:61:GLU:HB3	1.95	0.66
13:M:81:LEU:CD2	13:M:81:LEU:H	2.08	0.66
17:Q:97:SER:OG	17:Q:103:GLY:CA	2.44	0.66
18:R:45:SER:C	18:R:47:THR:H	1.97	0.66
20:T:56:MET:HE3	20:T:88:VAL:HG11	1.77	0.66
2:B:71:VAL:O	2:B:165:VAL:HG23	1.96	0.66
3:C:107:GLN:NE2	3:C:107:GLN:H	1.94	0.66
7:G:85:TYR:HD1	7:G:154:TYR:HE1	1.42	0.66
9:I:10:ARG:HG2	9:I:75:ASP:HB2	1.77	0.66
19:S:33:THR:HG22	19:S:35:SER:H	1.60	0.66
1:A:353:A:H5'	1:A:353:A:C8	2.31	0.66
12:L:33:ARG:HD3	12:L:62:SER:HB3	1.77	0.66
14:N:14:PRO:HB2	14:N:16:PHE:O	1.95	0.66
3:C:155:GLY:O	3:C:156:ARG:HB2	1.96	0.65
1:A:427:U:OP1	4:D:13:ARG:NH2	2.29	0.65
1:A:266:G:O3'	17:Q:67:LYS:HB2	1.95	0.65
1:A:1216:G:H5''	14:N:5:ALA:CB	2.27	0.65
1:A:443:C:H2'	1:A:444:C:H6	1.61	0.65
11:K:14:VAL:HG21	11:K:40:ILE:HD11	1.77	0.65
18:R:47:THR:HG23	18:R:83:GLU:H	1.61	0.65
1:A:524:G:H2'	1:A:525:C:C6	2.31	0.65
5:E:80:ILE:HD11	5:E:91:LEU:HD12	1.76	0.65
13:M:34:LEU:HD13	13:M:41:PRO:HA	1.77	0.65
1:A:1278:U:H5''	1:A:1279:A:H5'	1.76	0.65
1:A:1495:U:H2'	1:A:1496:C:C6	2.31	0.65
2:B:18:GLY:HA3	2:B:41:ILE:HA	1.79	0.65
2:B:15:VAL:CG2	2:B:209:ARG:HG3	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:38:ILE:CG1	10:J:71:LEU:HB3	2.26	0.65
21:V:6:ARG:HD3	21:V:15:ARG:NH1	2.12	0.65
3:C:188:LEU:O	3:C:189:ALA:HB2	1.96	0.65
13:M:36:LYS:HD2	13:M:59:TYR:CZ	2.32	0.65
1:A:1224:G:H2'	19:S:78:ARG:HH22	1.62	0.65
1:A:1402:C:H2'	1:A:1403:C:O4'	1.97	0.65
1:A:1475:G:H2'	1:A:1476:G:H8	1.62	0.65
2:B:74:LYS:HZ1	2:B:206:ASP:HA	1.60	0.65
3:C:172:ARG:HB3	3:C:172:ARG:HH11	1.61	0.65
10:J:96:ILE:HG22	10:J:97:GLU:N	2.10	0.65
11:K:18:ARG:HB2	11:K:33:THR:HG23	1.78	0.65
12:L:86:ARG:HG3	12:L:86:ARG:HH11	1.61	0.65
19:S:17:GLU:HA	19:S:20:LEU:HD11	1.78	0.65
1:A:1425:U:H2'	1:A:1426:C:C6	2.31	0.65
1:A:287:U:O2'	1:A:288:A:H5'	1.97	0.65
3:C:172:ARG:HB3	3:C:172:ARG:NH1	2.11	0.65
5:E:40:ARG:HG2	5:E:68:GLU:OE2	1.96	0.65
15:O:29:VAL:HG12	15:O:85:LEU:CD1	2.26	0.65
19:S:28:LYS:HG2	19:S:29:ARG:N	2.06	0.65
1:A:1522:U:O2'	1:A:1523:G:H5'	1.96	0.65
1:A:403:C:O2'	1:A:404:U:H5'	1.97	0.65
1:A:677:U:H3	1:A:713:G:H22	1.45	0.65
5:E:15:ARG:O	5:E:15:ARG:HD2	1.96	0.65
7:G:50:ILE:O	7:G:54:THR:HB	1.96	0.65
13:M:33:ALA:HA	13:M:59:TYR:CE2	2.32	0.65
14:N:22:THR:CB	14:N:33:VAL:HG21	2.27	0.65
4:D:187:ARG:NH2	4:D:188:LEU:HD12	2.10	0.65
6:F:100:ASN:HD22	18:R:23:LYS:CG	2.10	0.65
13:M:81:LEU:O	13:M:89:GLY:HA3	1.97	0.65
6:F:94:GLN:NE2	18:R:32:ARG:HD3	2.09	0.65
1:A:392:G:H2'	1:A:393:A:C8	2.32	0.64
20:T:87:LYS:O	20:T:91:LEU:HD12	1.96	0.64
1:A:168:G:O2'	1:A:169:C:H5'	1.97	0.64
1:A:738:C:OP2	6:F:92:LYS:HE3	1.97	0.64
20:T:50:GLU:HG2	20:T:100:ILE:HG13	1.79	0.64
1:A:281:G:O2'	1:A:282:A:OP2	2.12	0.64
9:I:118:LYS:O	9:I:119:ALA:CB	2.45	0.64
1:A:203:U:H5''	1:A:204:U:OP1	1.97	0.64
1:A:397:A:H5'	1:A:398:C:OP1	1.98	0.64
1:A:765:G:H1	1:A:812:C:H2'	1.62	0.64
5:E:115:VAL:CG1	5:E:118:ILE:HG13	2.25	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:90:LEU:H	10:J:91:PRO:HD2	1.61	0.64
11:K:18:ARG:HB2	11:K:33:THR:CG2	2.28	0.64
1:A:1040:U:H2'	1:A:1041:A:C8	2.33	0.64
1:A:393:A:O2'	1:A:394:G:H5'	1.98	0.64
3:C:112:SER:HB2	3:C:115:LEU:HD12	1.79	0.64
6:F:21:LEU:O	6:F:24:GLU:HB3	1.97	0.64
9:I:49:PRO:O	9:I:52:ALA:HB3	1.97	0.64
16:P:18:ARG:HD3	16:P:35:LYS:HE3	1.79	0.64
16:P:45:THR:HB	16:P:46:PRO:HD2	1.80	0.64
19:S:64:GLU:O	19:S:67:VAL:HG23	1.97	0.64
1:A:818:G:H3'	1:A:819:A:C5'	2.28	0.64
1:A:918:A:H2'	1:A:919:A:C8	2.32	0.64
5:E:79:GLU:HG3	5:E:93:PRO:HD2	1.79	0.64
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.33	0.64
19:S:40:ILE:HB	19:S:67:VAL:O	1.98	0.64
3:C:177:THR:CG2	3:C:180:ALA:HB2	2.28	0.64
11:K:40:ILE:HG22	11:K:41:THR:HG23	1.80	0.64
1:A:1142:G:H2'	1:A:1143:G:O4'	1.97	0.64
1:A:1347:G:O2'	1:A:1348:U:OP2	2.16	0.64
5:E:151:LEU:HD11	8:H:77:GLU:OE2	1.98	0.64
11:K:48:ILE:HG22	11:K:49:GLY:H	1.61	0.64
12:L:55:VAL:HG12	12:L:56:ALA:N	2.12	0.64
21:V:6:ARG:CD	21:V:15:ARG:NH1	2.61	0.64
1:A:922:G:H2'	1:A:923:A:C8	2.33	0.64
5:E:120:THR:CG2	5:E:121:LYS:N	2.61	0.64
2:B:215:LEU:O	2:B:219:VAL:HG23	1.97	0.64
3:C:64:VAL:HB	3:C:99:VAL:CB	2.27	0.64
17:Q:101:ARG:HE	17:Q:101:ARG:HA	1.62	0.64
19:S:44:MET:O	19:S:47:HIS:HB2	1.97	0.64
1:A:1153:C:H2'	1:A:1154:G:H8	1.62	0.63
1:A:1497:G:H2'	1:A:1498:U:H5'	1.78	0.63
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.78	0.63
9:I:48:GLU:N	9:I:49:PRO:HD2	2.13	0.63
12:L:110:VAL:O	12:L:122:THR:HG21	1.97	0.63
12:L:25:PRO:C	12:L:27:LEU:N	2.52	0.63
1:A:1020:U:H2'	1:A:1021:G:H8	1.63	0.63
1:A:1346:A:H2'	7:G:10:ARG:HH22	1.64	0.63
2:B:74:LYS:NZ	2:B:206:ASP:HA	2.13	0.63
2:B:95:GLN:OE1	2:B:95:GLN:HA	1.96	0.63
3:C:120:VAL:O	3:C:124:ILE:HG13	1.99	0.63
1:A:1442:G:H2'	1:A:1442:G:N3	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:70:ILE:HD11	4:D:100:ARG:NE	2.13	0.63
1:A:620:C:N1	4:D:135:LEU:HD13	2.12	0.63
4:D:152:SER:HB3	4:D:155:LEU:HD12	1.80	0.63
3:C:29:TYR:OH	14:N:54:PRO:HG2	1.98	0.63
1:A:1141:C:H2'	1:A:1142:G:C8	2.32	0.63
2:B:82:ARG:O	2:B:86:GLU:HG3	1.98	0.63
4:D:131:ARG:H	4:D:131:ARG:HD2	1.62	0.63
1:A:1131:G:H1	1:A:1143:G:N2	1.95	0.63
1:A:1316:G:H4'	14:N:18:VAL:CG1	2.29	0.63
1:A:243:A:H4'	1:A:244:U:C5'	2.22	0.63
2:B:130:ARG:NH2	3:C:207:VAL:HG22	2.14	0.63
3:C:155:GLY:O	3:C:196:LEU:HD22	1.98	0.63
1:A:1026:G:H2'	1:A:1027:C:H5'	1.80	0.63
1:A:1053:G:C3'	1:A:1054:C:H5'	2.29	0.63
3:C:64:VAL:CB	3:C:99:VAL:HB	2.27	0.63
5:E:102:ALA:CB	5:E:120:THR:HG21	2.29	0.63
7:G:114:ARG:HH11	7:G:114:ARG:HG2	1.64	0.63
7:G:42:ILE:HG22	7:G:120:ILE:HD12	1.80	0.63
2:B:132:LYS:HG2	2:B:135:GLN:OE1	1.99	0.63
2:B:20:GLU:HG2	2:B:189:ASP:OD2	1.99	0.63
7:G:71:PRO:HD3	7:G:103:TRP:CZ3	2.33	0.63
14:N:27:CYS:SG	14:N:29:ARG:HB2	2.37	0.63
19:S:39:THR:HA	19:S:70:LYS:HG2	1.81	0.63
1:A:405:U:H3'	1:A:406:G:H5'	1.80	0.63
3:C:50:ALA:O	3:C:70:VAL:HG12	1.99	0.63
5:E:150:ARG:NH1	5:E:150:ARG:HG3	2.14	0.63
16:P:8:ARG:HB2	16:P:28:ARG:NH1	2.14	0.63
19:S:43:GLU:H	19:S:43:GLU:CD	2.00	0.63
1:A:1132:C:H2'	1:A:1133:G:H8	1.64	0.63
1:A:1347:G:O2'	1:A:1348:U:P	2.57	0.63
1:A:1487:G:O2'	1:A:1488:G:H5'	1.99	0.63
1:A:448:A:H2'	1:A:449:C:H6	1.64	0.63
1:A:538:G:OP2	12:L:115:LYS:HG3	1.99	0.63
3:C:91:LEU:CD2	3:C:99:VAL:HG13	2.27	0.63
5:E:116:THR:HG23	5:E:117:ASP:OD2	1.98	0.63
1:A:1347:G:C4	9:I:107:ARG:NH1	2.67	0.63
1:A:1343:G:H1'	9:I:121:ARG:HH12	1.64	0.63
1:A:1238:A:H5'	1:A:1336:C:H41	1.64	0.62
1:A:556:C:O2'	1:A:557:G:H5'	1.99	0.62
2:B:73:THR:HB	2:B:170:GLU:OE2	1.99	0.62
15:O:17:ARG:CZ	15:O:77:ARG:HH11	2.11	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1132:C:H2'	1:A:1133:G:C8	2.35	0.62
1:A:1189:C:OP1	10:J:51:ARG:NH2	2.29	0.62
1:A:1229:A:OP2	13:M:114:ARG:HD3	1.99	0.62
2:B:184:VAL:N	2:B:198:ASP:OD2	2.32	0.62
4:D:61:LYS:HZ1	4:D:62:GLN:NE2	1.97	0.62
12:L:43:VAL:HG12	12:L:44:THR:N	2.14	0.62
13:M:84:ILE:O	13:M:86:CYS:N	2.33	0.62
1:A:1260:C:O5'	1:A:1284:C:H4'	1.99	0.62
1:A:475:G:H2'	1:A:476:G:H8	1.63	0.62
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.80	0.62
1:A:1148:U:H4'	9:I:14:VAL:HG11	1.81	0.62
1:A:1225:A:N3	1:A:1225:A:H2'	2.14	0.62
3:C:177:THR:HG23	3:C:180:ALA:HB2	1.81	0.62
3:C:60:ALA:O	3:C:61:ALA:HB2	2.00	0.62
1:A:976:G:OP1	14:N:32:SER:HA	1.98	0.62
1:A:501:C:H2'	1:A:502:G:C8	2.34	0.62
1:A:113:G:H1'	1:A:354:G:H5'	1.80	0.62
2:B:142:LEU:HD22	2:B:146:GLN:NE2	2.14	0.62
2:B:69:LEU:HD12	2:B:155:LEU:HD11	1.81	0.62
2:B:186:ALA:HB3	2:B:197:VAL:HG11	1.82	0.62
7:G:23:VAL:O	7:G:27:ILE:HG13	2.00	0.62
10:J:62:HIS:HB3	14:N:59:ALA:HB3	1.81	0.62
1:A:1307:U:H5'	13:M:109:THR:HG21	1.81	0.62
1:A:1392:G:O2'	1:A:1502:A:H5''	1.99	0.62
2:B:115:LEU:HG	2:B:153:ARG:NH2	2.14	0.62
1:A:542:G:OP1	4:D:10:ARG:NH2	2.33	0.62
1:A:216:G:H2'	1:A:217:C:C6	2.35	0.62
1:A:434:U:H2'	1:A:435:C:H6	1.64	0.62
4:D:148:VAL:CG1	4:D:158:ILE:HD13	2.30	0.62
5:E:120:THR:HG23	5:E:121:LYS:N	2.15	0.62
19:S:52:TYR:HA	19:S:56:GLN:O	1.99	0.62
20:T:43:LEU:HD12	20:T:55:ILE:HD12	1.81	0.62
1:A:1176:A:H2'	1:A:1177:G:C8	2.35	0.62
1:A:1425:U:H2'	1:A:1426:C:H6	1.65	0.62
1:A:476:G:O2'	1:A:477:G:H5'	2.00	0.62
1:A:706:A:H1'	11:K:29:ILE:HD11	1.81	0.62
3:C:129:ALA:HB3	3:C:132:ARG:HD2	1.82	0.62
2:B:130:ARG:NH2	3:C:179:ARG:HH12	1.97	0.62
9:I:19:LEU:O	9:I:20:ARG:HG3	1.99	0.62
1:A:959:A:H3'	1:A:960:U:H5''	1.82	0.62
5:E:80:ILE:CD1	5:E:91:LEU:HB2	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:139:GLU:O	7:G:143:ARG:HG3	2.00	0.62
7:G:155:ARG:O	7:G:156:TRP:HB3	1.99	0.62
9:I:93:ARG:NH1	9:I:97:LYS:HZ2	1.97	0.62
1:A:1440:C:H2'	1:A:1441:G:H5'	1.82	0.61
4:D:61:LYS:NZ	4:D:62:GLN:HE21	1.98	0.61
17:Q:76:LEU:HD23	17:Q:76:LEU:C	2.20	0.61
20:T:50:GLU:HG3	20:T:99:LEU:HD12	1.82	0.61
1:A:1370:G:O2'	1:A:1371:G:H5'	2.00	0.61
1:A:193:C:H2'	1:A:194:C:C6	2.35	0.61
1:A:539:A:OP1	12:L:114:LYS:HE2	2.00	0.61
1:A:812:C:O2'	1:A:813:U:OP2	2.17	0.61
3:C:191:THR:HG22	3:C:192:THR:N	2.15	0.61
4:D:25:ARG:O	4:D:27:TYR:N	2.33	0.61
10:J:30:SER:OG	10:J:81:THR:HA	1.99	0.61
14:N:53:LEU:HB3	14:N:56:VAL:HG21	1.81	0.61
2:B:80:ILE:HD11	2:B:208:ILE:HG23	1.81	0.61
5:E:115:VAL:HG11	5:E:118:ILE:CG1	2.28	0.61
7:G:78:ARG:HB2	7:G:156:TRP:CZ3	2.36	0.61
17:Q:21:VAL:HG21	17:Q:59:ILE:HD11	1.82	0.61
1:A:190(L):U:H3	20:T:105:SER:CB	2.12	0.61
1:A:954:G:H21	1:A:1227:A:H62	1.49	0.61
2:B:34:ALA:O	2:B:41:ILE:N	2.31	0.61
4:D:32:ALA:C	4:D:34:GLU:H	2.04	0.61
4:D:61:LYS:NZ	4:D:62:GLN:NE2	2.48	0.61
1:A:1147:C:H4'	9:I:5:TYR:HE1	1.64	0.61
11:K:84:VAL:CG1	11:K:95:ILE:HD11	2.31	0.61
12:L:27:LEU:C	12:L:29:GLY:H	2.04	0.61
12:L:33:ARG:CD	12:L:62:SER:HB3	2.29	0.61
19:S:31:ILE:CG2	19:S:32:LYS:H	2.10	0.61
1:A:187:C:O2	20:T:105:SER:HB3	2.00	0.61
1:A:1182:G:H4'	1:A:1183:A:O5'	1.99	0.61
4:D:23:GLY:HA3	4:D:112:VAL:CG1	2.30	0.61
4:D:191:ARG:HD2	4:D:191:ARG:O	2.00	0.61
1:A:1329:A:P	13:M:28:ALA:HB3	2.41	0.61
1:A:664:G:OP1	18:R:64:ARG:HD2	2.00	0.61
3:C:83:ARG:C	3:C:85:ARG:H	2.04	0.61
7:G:38:LEU:HD12	7:G:38:LEU:O	2.01	0.61
9:I:44:VAL:HG12	9:I:51:ARG:HH12	1.66	0.61
1:A:386:C:O2'	1:A:387:U:H5'	2.00	0.61
2:B:115:LEU:O	2:B:119:GLU:HG3	2.00	0.61
16:P:4:ILE:HG13	16:P:64:ALA:HB1	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1091:U:O2	1:A:1093:A:C8	2.54	0.61
1:A:1484:C:H2'	1:A:1485:U:H6	1.65	0.61
4:D:148:VAL:HG11	4:D:158:ILE:HG21	1.81	0.61
7:G:78:ARG:HB2	7:G:156:TRP:HZ3	1.65	0.61
12:L:40:VAL:O	12:L:40:VAL:HG12	1.99	0.61
17:Q:101:ARG:NE	17:Q:101:ARG:HA	2.16	0.61
1:A:1053:G:C4'	1:A:1054:C:H5'	2.31	0.61
1:A:551:U:H2'	1:A:552:U:H6	1.64	0.61
2:B:98:LEU:O	2:B:101:MET:HG3	2.01	0.61
3:C:191:THR:CG2	3:C:192:THR:N	2.64	0.61
9:I:4:TYR:CZ	9:I:88:TYR:HD1	2.17	0.61
16:P:67:THR:HG22	16:P:68:ASP:N	2.15	0.61
20:T:54:LYS:HE3	20:T:100:ILE:HD11	1.82	0.61
1:A:1003:G:H2'	1:A:1003(A):G:C8	2.36	0.61
1:A:1475:G:H2'	1:A:1476:G:C8	2.36	0.61
1:A:1226:C:N4	13:M:104:ARG:HD2	2.16	0.61
13:M:54:VAL:O	13:M:58:GLU:HG2	2.01	0.61
1:A:1316:G:H4'	14:N:18:VAL:HG11	1.83	0.61
3:C:13:GLY:HA3	14:N:57:ARG:NH2	2.14	0.61
1:A:107:G:H2'	1:A:108:G:H5'	1.83	0.60
2:B:143:GLU:O	2:B:147:LYS:HG3	2.00	0.60
5:E:80:ILE:HD11	5:E:91:LEU:HB2	1.83	0.60
11:K:48:ILE:HG22	11:K:49:GLY:N	2.16	0.60
17:Q:76:LEU:HD23	17:Q:77:VAL:N	2.15	0.60
1:A:1147:C:H4'	9:I:5:TYR:CE1	2.36	0.60
4:D:157:LEU:HD22	4:D:161:ASN:ND2	2.16	0.60
13:M:40:ASN:ND2	13:M:41:PRO:HD2	2.16	0.60
15:O:29:VAL:HG12	15:O:85:LEU:HD11	1.82	0.60
17:Q:104:LYS:O	17:Q:105:ALA:HB2	2.01	0.60
2:B:33:TYR:O	2:B:34:ALA:HB2	2.02	0.60
3:C:47:LEU:HD23	3:C:68:VAL:HG11	1.83	0.60
10:J:46:ARG:HH11	10:J:64:GLU:HB3	1.65	0.60
10:J:71:LEU:O	10:J:72:VAL:HB	2.00	0.60
18:R:52:PRO:O	18:R:56:THR:HG23	2.00	0.60
1:A:112:G:N2	1:A:354:G:H5'	2.16	0.60
1:A:390:C:H2'	1:A:391:G:H8	1.66	0.60
1:A:425:G:O2'	1:A:426:G:H5'	2.02	0.60
7:G:72:ARG:HG2	7:G:142:GLU:OE1	2.02	0.60
12:L:27:LEU:C	12:L:29:GLY:N	2.54	0.60
19:S:13:ASP:HA	19:S:16:LEU:HB3	1.83	0.60
1:A:686:U:O2'	1:A:687:A:H8	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:20:SER:HB3	3:C:22:TRP:HE1	1.67	0.60
8:H:64:LYS:HG2	8:H:79:VAL:HG21	1.84	0.60
20:T:96:GLY:O	20:T:97:ALA:HB3	2.00	0.60
1:A:112:G:H21	1:A:354:G:H5'	1.65	0.60
1:A:390:C:O3'	16:P:28:ARG:NH2	2.34	0.60
3:C:6:HIS:HD2	3:C:8:ILE:HB	1.66	0.60
5:E:76:ILE:HD13	5:E:142:LEU:HD11	1.84	0.60
7:G:42:ILE:HG23	7:G:117:ALA:HA	1.84	0.60
16:P:52:ASP:OD2	16:P:55:ARG:HG3	2.00	0.60
1:A:1305:G:H5'	21:V:4:GLY:HA3	1.84	0.60
2:B:122:PHE:HE2	2:B:139:LYS:HG2	1.65	0.60
3:C:26:LYS:N	3:C:26:LYS:HD3	2.17	0.60
10:J:30:SER:HB3	10:J:84:GLN:HE21	1.67	0.60
12:L:46:LYS:HG2	12:L:47:LYS:N	2.16	0.60
16:P:81:ARG:HG3	16:P:83:GLU:HG2	1.84	0.60
2:B:114:ARG:NH1	2:B:118:LEU:HD21	2.15	0.60
3:C:33:LEU:HD11	14:N:53:LEU:CD2	2.32	0.60
5:E:24:ARG:HH11	5:E:24:ARG:HG2	1.66	0.60
5:E:65:ASN:CG	5:E:65:ASN:O	2.40	0.60
2:B:178:ARG:O	8:H:71:GLY:HA2	2.02	0.60
11:K:19:ALA:HB2	11:K:80:VAL:HG11	1.82	0.60
1:A:435:C:H2'	1:A:436:C:H6	1.67	0.60
2:B:140:HIS:O	2:B:143:GLU:HB2	2.01	0.60
3:C:47:LEU:CD1	3:C:47:LEU:H	2.15	0.60
11:K:69:ALA:O	11:K:73:MET:HG2	2.02	0.60
1:A:1352:C:H2'	1:A:1353:G:C8	2.37	0.60
1:A:1381:U:O2'	1:A:1382:C:H5'	2.02	0.60
3:C:6:HIS:NE2	3:C:8:ILE:HD12	2.17	0.60
6:F:10:LEU:CD1	6:F:59:TYR:HB3	2.29	0.60
12:L:28:LYS:HD2	12:L:33:ARG:HH12	1.65	0.60
1:A:953:G:H1'	13:M:125:ARG:CB	2.31	0.60
13:M:10:PRO:O	13:M:45:VAL:HG11	2.01	0.60
1:A:1306:A:N6	1:A:1331:G:H1'	2.17	0.59
1:A:1470:G:O2'	1:A:1471:G:H5'	2.02	0.59
3:C:79:ARG:HE	3:C:82:GLU:HG2	1.66	0.59
8:H:91:ARG:HG3	12:L:7:ILE:HG13	1.84	0.59
11:K:110:ASP:HB2	18:R:88:LYS:CD	2.20	0.59
14:N:11:LYS:O	14:N:13:THR:N	2.35	0.59
1:A:449:C:O2	16:P:42:ARG:HD2	2.02	0.59
11:K:84:VAL:HG21	18:R:88:LYS:HD3	1.83	0.59
1:A:1231:G:H5''	9:I:126:SER:CB	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1376:U:H2'	1:A:1377:A:C8	2.36	0.59
1:A:505:G:H2'	1:A:506:G:C8	2.37	0.59
9:I:93:ARG:NH1	9:I:97:LYS:NZ	2.51	0.59
14:N:24:CYS:HB3	14:N:28:GLY:H	1.66	0.59
15:O:11:VAL:HG21	15:O:34:LEU:HD12	1.83	0.59
1:A:996:A:H2'	1:A:997:U:C6	2.37	0.59
3:C:46:GLU:O	3:C:48:TYR:N	2.33	0.59
9:I:5:TYR:CD2	9:I:6:GLY:N	2.70	0.59
1:A:1086:U:H3	1:A:1099:G:N2	1.91	0.59
1:A:1247:U:O2'	1:A:1248:A:H5'	2.02	0.59
1:A:457:C:H2'	1:A:458:C:H6	1.67	0.59
20:T:57:ARG:HH21	20:T:100:ILE:CG2	2.16	0.59
1:A:1130:A:OP2	1:A:1130:A:H3'	2.02	0.59
1:A:839:U:O2	1:A:839:U:H2'	2.01	0.59
2:B:101:MET:CA	2:B:108:ILE:HD12	2.33	0.59
4:D:33:MET:O	4:D:37:PRO:HG3	2.02	0.59
5:E:118:ILE:CG2	5:E:119:LEU:N	2.65	0.59
13:M:94:ARG:HH22	19:S:81:ARG:NH1	2.00	0.59
1:A:109:A:H2'	1:A:326:G:N2	2.17	0.59
1:A:502:G:H4'	1:A:550:G:H4'	1.83	0.59
1:A:972:C:OP1	10:J:57:LYS:NZ	2.28	0.59
4:D:151:LYS:H	4:D:151:LYS:CD	2.16	0.59
4:D:25:ARG:C	4:D:27:TYR:N	2.55	0.59
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.06	0.59
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.66	0.59
11:K:74:ALA:C	11:K:76:GLY:H	2.06	0.59
12:L:28:LYS:HD2	12:L:33:ARG:NH2	2.17	0.59
1:A:513:C:O2'	1:A:514:C:H5'	2.03	0.59
1:A:736:C:H2'	1:A:737:A:C8	2.38	0.59
7:G:95:ARG:HG3	7:G:95:ARG:NH1	2.17	0.59
8:H:83:ILE:O	8:H:83:ILE:HG23	2.03	0.59
1:A:457:C:H2'	1:A:458:C:C6	2.38	0.59
1:A:560:U:H4'	1:A:561:U:H5''	1.83	0.59
2:B:120:ALA:O	2:B:124:SER:HB3	2.02	0.59
2:B:130:ARG:HD2	2:B:131:PRO:HD2	1.85	0.59
10:J:46:ARG:NH1	10:J:64:GLU:HG2	2.18	0.59
10:J:3:LYS:N	10:J:77:PRO:HD3	2.18	0.59
12:L:55:VAL:CG1	12:L:67:THR:HG23	2.33	0.59
1:A:390:C:H2'	1:A:391:G:C8	2.38	0.59
3:C:3:ASN:C	3:C:4:LYS:HG2	2.23	0.59
7:G:122:HIS:HA	7:G:125:MET:HE3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1251:A:H4'	9:I:12:GLU:OE2	2.02	0.59
14:N:14:PRO:C	14:N:16:PHE:N	2.56	0.59
16:P:51:VAL:O	16:P:51:VAL:HG12	2.02	0.59
1:A:1490:C:C5'	1:A:1490:C:H6	2.13	0.58
3:C:14:ILE:O	3:C:16:ARG:N	2.35	0.58
7:G:51:GLN:HA	7:G:51:GLN:OE1	2.02	0.58
1:A:538:G:P	12:L:115:LYS:HG3	2.43	0.58
13:M:81:LEU:N	13:M:81:LEU:HD23	2.17	0.58
1:A:1441:G:H4'	1:A:1442:G:N7	2.18	0.58
1:A:1521:G:H2'	1:A:1522:U:C6	2.38	0.58
2:B:144:ARG:HG3	2:B:145:LEU:N	2.19	0.58
4:D:23:GLY:HA3	4:D:112:VAL:HG12	1.84	0.58
4:D:157:LEU:HD22	4:D:161:ASN:HD21	1.66	0.58
10:J:60:ARG:N	10:J:60:ARG:HD2	2.17	0.58
10:J:45:ARG:O	10:J:64:GLU:HA	2.03	0.58
14:N:8:GLU:O	14:N:11:LYS:HB2	2.02	0.58
1:A:1072:G:H2'	1:A:1073:U:C6	2.38	0.58
6:F:3:ARG:HH21	6:F:64:GLN:NE2	2.01	0.58
10:J:82:ILE:O	10:J:82:ILE:HG22	2.03	0.58
12:L:24:VAL:HG12	12:L:24:VAL:O	2.03	0.58
1:A:255:G:H1'	17:Q:16:GLN:HE22	1.69	0.58
18:R:86:VAL:O	18:R:87:ARG:HB2	2.03	0.58
1:A:1152:A:H5'	10:J:70:ARG:HH22	1.68	0.58
1:A:1316:G:N2	1:A:1318:A:H3'	2.18	0.58
1:A:39:G:O2'	1:A:40:C:H5'	2.03	0.58
1:A:60:A:H4'	1:A:61:G:O5'	2.03	0.58
1:A:991:U:O2'	1:A:992:U:H5'	2.02	0.58
2:B:10:LEU:HD23	2:B:48:MET:HG3	1.86	0.58
3:C:64:VAL:HB	3:C:99:VAL:CG2	2.33	0.58
9:I:11:LYS:O	9:I:11:LYS:HG2	2.03	0.58
9:I:79:LEU:HD23	9:I:101:PHE:O	2.02	0.58
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.39	0.58
1:A:1182:G:O2'	1:A:1183:A:OP2	2.20	0.58
1:A:976:G:OP2	1:A:1358:U:H1'	2.03	0.58
2:B:133:LYS:O	2:B:137:ARG:HG3	2.03	0.58
2:B:156:LYS:O	2:B:156:LYS:HD3	2.03	0.58
2:B:76:GLN:HG3	2:B:206:ASP:OD1	2.03	0.58
3:C:10:PHE:CZ	3:C:178:LEU:HD13	2.38	0.58
8:H:17:THR:HG22	8:H:63:LEU:HG	1.86	0.58
9:I:46:ALA:HB1	9:I:77:ILE:HG22	1.86	0.58
10:J:51:ARG:HB2	10:J:59:SER:CB	2.23	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:53:LEU:O	20:T:57:ARG:HD2	2.04	0.58
1:A:1054:C:OP1	1:A:1197:G:OP1	2.21	0.58
1:A:812:C:O2'	1:A:813:U:P	2.62	0.58
15:O:17:ARG:NH1	15:O:77:ARG:HH11	2.01	0.58
15:O:87:ILE:O	15:O:88:ARG:HB2	2.04	0.58
1:A:411:A:N9	1:A:413:G:H1'	2.19	0.58
1:A:518:C:H5''	1:A:519:C:C6	2.38	0.58
1:A:761:G:C1'	17:Q:103:GLY:O	2.51	0.58
9:I:5:TYR:O	9:I:84:ALA:HA	2.03	0.58
13:M:94:ARG:NH2	19:S:81:ARG:HD3	2.19	0.58
1:A:1117:G:H5'	1:A:1117:G:H8	1.66	0.58
1:A:376:G:P	16:P:67:THR:HG21	2.44	0.58
3:C:10:PHE:CE2	3:C:178:LEU:HD13	2.38	0.58
12:L:92:ASP:O	12:L:94:PRO:HD3	2.04	0.58
13:M:120:LYS:HE2	13:M:123:ALA:HB2	1.86	0.58
13:M:40:ASN:ND2	13:M:41:PRO:CD	2.62	0.58
14:N:12:ARG:O	14:N:14:PRO:N	2.36	0.58
1:A:723:U:O2	1:A:723:U:H2'	2.04	0.58
1:A:818:G:C2'	1:A:819:A:H5''	2.34	0.58
2:B:115:LEU:HG	2:B:153:ARG:HH21	1.69	0.58
3:C:191:THR:HG21	3:C:193:TYR:CZ	2.39	0.58
10:J:24:VAL:HG12	10:J:28:ARG:HE	1.68	0.58
10:J:15:THR:HG23	10:J:94:VAL:HG22	1.85	0.58
5:E:122:GLU:O	5:E:123:LEU:HD23	2.03	0.58
9:I:111:ARG:HD3	9:I:112:LYS:C	2.24	0.58
11:K:109:VAL:HG13	18:R:85:LEU:O	2.04	0.58
12:L:85:ILE:HG23	12:L:98:TYR:HB3	1.86	0.58
1:A:1228:C:OP1	13:M:115:LYS:HG3	2.03	0.57
1:A:1498:U:H4'	1:A:1519:A:H2	1.69	0.57
2:B:16:HIS:NE2	2:B:214:ILE:CG1	2.66	0.57
9:I:7:THR:HG21	9:I:9:ARG:NH1	2.19	0.57
13:M:84:ILE:CG2	19:S:65:ASN:HD22	2.17	0.57
19:S:40:ILE:HG21	19:S:62:ILE:CD1	2.33	0.57
1:A:657:G:H4'	15:O:28:GLN:HG2	1.87	0.57
6:F:97:PHE:HB2	18:R:32:ARG:CZ	2.34	0.57
7:G:15:ASP:OD1	7:G:17:VAL:N	2.37	0.57
11:K:40:ILE:HG23	11:K:75:TYR:CD2	2.39	0.57
12:L:26:ALA:O	12:L:27:LEU:O	2.22	0.57
13:M:13:LYS:O	13:M:45:VAL:HG23	2.04	0.57
1:A:375:U:H4'	16:P:17:TYR:CE2	2.39	0.57
17:Q:69:LYS:C	17:Q:70:ARG:HD2	2.24	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1095:U:H2'	1:A:1096:C:C6	2.39	0.57
9:I:17:VAL:HG21	9:I:80:GLY:HA3	1.86	0.57
13:M:84:ILE:C	13:M:86:CYS:H	2.08	0.57
16:P:17:TYR:HE1	16:P:41:PRO:HG2	1.69	0.57
20:T:10:LEU:HD12	20:T:12:ALA:HB3	1.85	0.57
1:A:346:G:C2'	1:A:347:G:H5'	2.34	0.57
13:M:31:LYS:O	13:M:35:GLU:HB2	2.05	0.57
14:N:24:CYS:HB3	14:N:28:GLY:N	2.20	0.57
1:A:1014:A:H2'	1:A:1015:A:C8	2.39	0.57
1:A:1015:A:H2'	1:A:1016:A:C8	2.40	0.57
1:A:757:U:H2'	1:A:758:G:O4'	2.03	0.57
1:A:860:A:H2'	1:A:861:G:O4'	2.03	0.57
2:B:23:ARG:NH1	2:B:23:ARG:C	2.58	0.57
3:C:121:ALA:O	3:C:125:GLU:HG3	2.04	0.57
4:D:30:LYS:C	4:D:32:ALA:N	2.58	0.57
4:D:7:PRO:HG2	4:D:10:ARG:HD2	1.87	0.57
1:A:1298:C:C4	7:G:114:ARG:HD3	2.40	0.57
8:H:29:SER:OG	8:H:32:LYS:HB2	2.04	0.57
8:H:91:ARG:HG2	12:L:7:ILE:HG21	1.87	0.57
9:I:9:ARG:HA	9:I:13:ALA:O	2.05	0.57
14:N:29:ARG:HH11	14:N:29:ARG:HG2	1.69	0.57
14:N:3:ARG:NH1	14:N:6:LEU:HD11	2.19	0.57
1:A:1241:G:H2'	1:A:1242:C:C6	2.39	0.57
1:A:1347:G:N2	1:A:1373:G:H2'	2.19	0.57
1:A:1504:G:H3'	1:A:1504:G:OP2	2.04	0.57
8:H:19:VAL:HG23	8:H:21:LYS:HD3	1.86	0.57
19:S:25:LYS:HD2	19:S:25:LYS:H	1.68	0.57
19:S:7:LYS:HG3	19:S:7:LYS:O	2.03	0.57
1:A:1414:U:O2'	1:A:1415:G:H5'	2.04	0.57
12:L:6:THR:OG1	12:L:9:GLN:HG3	2.05	0.57
18:R:47:THR:HG22	18:R:48:GLY:N	2.18	0.57
1:A:835:U:OP1	18:R:64:ARG:NH2	2.34	0.57
20:T:39:LYS:HD2	20:T:55:ILE:CD1	2.27	0.57
1:A:1044:A:C2'	1:A:1045:C:H5'	2.34	0.57
1:A:1305:G:N2	1:A:1331:G:O2'	2.38	0.57
1:A:192:U:O2'	1:A:193:C:H5'	2.05	0.57
2:B:12:GLU:C	2:B:14:GLY:H	2.07	0.57
2:B:223:ILE:HG21	2:B:230:VAL:CG2	2.35	0.57
4:D:35:ARG:O	4:D:36:ARG:HB2	2.04	0.57
8:H:103:VAL:HG21	8:H:110:ALA:HB2	1.87	0.57
12:L:82:VAL:N	12:L:106:ASP:OD1	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:49:THR:HB	13:M:52:GLU:HG3	1.86	0.57
1:A:1004:A:H5''	1:A:1025:U:C5	2.40	0.57
1:A:1152:A:H5'	10:J:70:ARG:NH2	2.19	0.57
1:A:1278:U:H5''	1:A:1279:A:O4'	2.04	0.57
3:C:91:LEU:HD11	3:C:99:VAL:HG13	1.87	0.57
5:E:80:ILE:HD12	5:E:80:ILE:O	2.05	0.57
12:L:47:LYS:CB	12:L:48:PRO:HD3	2.35	0.57
18:R:25:THR:O	18:R:26:LEU:HB2	2.04	0.57
1:A:1040:U:H2'	1:A:1041:A:H8	1.70	0.57
1:A:780:A:O2'	1:A:781:A:H5''	2.05	0.57
2:B:209:ARG:HE	2:B:239:VAL:HG11	1.68	0.57
6:F:80:ARG:NH1	6:F:88:VAL:HB	2.19	0.57
17:Q:5:VAL:HG22	17:Q:60:ILE:HG12	1.87	0.57
19:S:5:LEU:O	19:S:6:LYS:CB	2.51	0.57
1:A:1230:C:H1'	13:M:126:LYS:HA	1.86	0.56
1:A:1317:C:H2'	1:A:1318:A:O4'	2.04	0.56
1:A:1372:U:OP1	9:I:71:SER:HB3	2.04	0.56
1:A:946:A:H2'	1:A:947:G:C8	2.40	0.56
3:C:84:ILE:O	3:C:88:ARG:HB2	2.05	0.56
8:H:123:GLU:O	8:H:127:LEU:HD23	2.05	0.56
13:M:13:LYS:HD3	13:M:17:VAL:HG11	1.86	0.56
3:C:29:TYR:CZ	14:N:54:PRO:HG2	2.40	0.56
1:A:1223:C:OP1	1:A:1224:G:H3'	2.04	0.56
1:A:129(A):G:O2'	1:A:190(E):U:H2'	2.05	0.56
15:O:41:GLU:OE2	15:O:41:GLU:HA	2.05	0.56
15:O:3:ILE:HG22	15:O:7:GLU:HB3	1.86	0.56
17:Q:59:ILE:HG22	17:Q:71:PHE:CD1	2.39	0.56
19:S:28:LYS:CG	19:S:29:ARG:H	2.08	0.56
1:A:1195:C:H3'	1:A:1196:U:C5'	2.35	0.56
1:A:1499:A:H1'	1:A:1520:G:H5'	1.87	0.56
1:A:448:A:H2'	1:A:449:C:C6	2.40	0.56
1:A:915:A:C2'	1:A:916:G:H5'	2.35	0.56
2:B:126:GLU:HG2	2:B:129:GLU:OE1	2.05	0.56
2:B:88:ALA:C	2:B:90:MET:H	2.09	0.56
9:I:39:GLY:O	9:I:40:LEU:HD23	2.05	0.56
10:J:4:ILE:HA	10:J:100:THR:HA	1.88	0.56
13:M:17:VAL:O	13:M:20:THR:HB	2.06	0.56
14:N:36:PHE:O	14:N:36:PHE:CD1	2.58	0.56
20:T:67:ALA:HA	20:T:73:HIS:H	1.70	0.56
13:M:8:GLU:OE1	13:M:22:ILE:HG12	2.05	0.56
1:A:1443:G:H5''	1:A:1446:A:C5'	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:47:THR:HA	2:B:202:PRO:HG2	1.87	0.56
3:C:188:LEU:HD13	3:C:195:VAL:HG13	1.86	0.56
6:F:2:ARG:CD	6:F:69:GLU:HG2	2.35	0.56
7:G:146:GLU:HA	7:G:149:ARG:HB2	1.87	0.56
8:H:60:ARG:HG3	8:H:60:ARG:HH11	1.70	0.56
10:J:12:ASP:HB3	10:J:15:THR:HB	1.88	0.56
19:S:63:THR:HG22	19:S:64:GLU:H	1.71	0.56
1:A:1257:U:H4'	1:A:1258:G:O5'	2.06	0.56
1:A:1256:A:H61	1:A:1278:U:H1'	1.70	0.56
1:A:818:G:H3'	1:A:819:A:H5''	1.87	0.56
3:C:7:PRO:CG	3:C:184:TYR:HB2	2.35	0.56
13:M:15:VAL:HG23	13:M:43:THR:O	2.04	0.56
17:Q:26:GLN:HE21	17:Q:37:LYS:HE2	1.71	0.56
17:Q:59:ILE:CG2	17:Q:71:PHE:HB3	2.36	0.56
1:A:1028:C:H2'	1:A:1029:C:C6	2.40	0.56
1:A:1339:A:H2'	1:A:1340:A:O4'	2.06	0.56
1:A:1346:A:H4'	1:A:1347:G:O5'	2.06	0.56
1:A:477:G:H2'	1:A:478:A:C8	2.40	0.56
3:C:32:LEU:HD23	3:C:32:LEU:O	2.05	0.56
3:C:33:LEU:O	3:C:33:LEU:HD23	2.04	0.56
4:D:176:LEU:HA	4:D:183:GLY:HA2	1.87	0.56
4:D:6:GLY:O	4:D:8:VAL:HG23	2.06	0.56
20:T:86:ARG:O	20:T:90:GLN:HG3	2.05	0.56
1:A:1053:G:H4'	1:A:1054:C:H5'	1.88	0.56
4:D:199:ASN:HD21	4:D:201:GLN:HB2	1.71	0.56
8:H:105:ARG:HG3	8:H:105:ARG:HH11	1.71	0.56
10:J:81:THR:O	10:J:85:LEU:HG	2.06	0.56
17:Q:67:LYS:O	17:Q:68:ARG:HB3	2.05	0.56
19:S:10:PHE:CD2	19:S:11:VAL:N	2.73	0.56
1:A:1257:U:O2'	1:A:1258:G:OP2	2.21	0.56
1:A:411:A:C4	1:A:413:G:H1'	2.41	0.56
1:A:438:G:C4'	1:A:439:A:OP1	2.53	0.56
13:M:117:VAL:HG12	13:M:118:ALA:H	1.70	0.56
18:R:53:ARG:HD3	18:R:63:GLN:CB	2.36	0.56
3:C:3:ASN:ND2	3:C:4:LYS:HE2	2.21	0.56
4:D:57:ARG:HB3	4:D:206:PHE:HB2	1.88	0.56
4:D:24:GLU:HG2	4:D:25:ARG:N	2.21	0.56
5:E:118:ILE:HG22	5:E:119:LEU:H	1.67	0.56
1:A:1216:G:H5''	14:N:5:ALA:HB1	1.88	0.56
19:S:40:ILE:HG21	19:S:62:ILE:HD11	1.88	0.56
1:A:1044:A:H2'	1:A:1045:C:C5'	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:22:LYS:CE	10:J:90:LEU:HD12	2.33	0.56
13:M:40:ASN:ND2	13:M:42:ALA:H	2.04	0.56
15:O:36:ILE:HA	15:O:59:MET:HE3	1.87	0.56
17:Q:103:GLY:O	17:Q:104:LYS:O	2.24	0.56
1:A:1326:C:OP1	21:V:12:LYS:NZ	2.37	0.55
1:A:166:G:O2'	1:A:167:G:H5'	2.06	0.55
2:B:21:ARG:HG3	2:B:23:ARG:HD2	1.88	0.55
4:D:148:VAL:HG11	4:D:158:ILE:HD13	1.88	0.55
16:P:26:ARG:HD2	16:P:31:LYS:O	2.06	0.55
1:A:1042:G:O2'	1:A:1043:C:H5'	2.05	0.55
4:D:24:GLU:H	4:D:112:VAL:CG1	2.19	0.55
7:G:116:ALA:HA	7:G:119:ARG:NH2	2.21	0.55
12:L:50:SER:O	12:L:51:ALA:HB2	2.05	0.55
20:T:35:THR:O	20:T:39:LYS:HB2	2.06	0.55
20:T:94:ALA:O	20:T:95:ALA:HB3	2.06	0.55
1:A:1202:G:O2'	1:A:1203:C:H5'	2.06	0.55
1:A:518:C:O2'	12:L:50:SER:HB3	2.06	0.55
2:B:74:LYS:HZ1	2:B:206:ASP:CA	2.19	0.55
3:C:33:LEU:HD11	14:N:53:LEU:HD22	1.87	0.55
1:A:1251:A:H2'	1:A:1252:A:C8	2.41	0.55
1:A:505:G:H2'	1:A:506:G:H8	1.69	0.55
2:B:23:ARG:N	2:B:23:ARG:HD3	2.22	0.55
3:C:38:ARG:HB3	3:C:94:LEU:HD21	1.88	0.55
10:J:24:VAL:HG21	10:J:37:PRO:HD3	1.88	0.55
12:L:43:VAL:HG12	12:L:44:THR:H	1.72	0.55
13:M:65:LYS:HE3	13:M:69:GLU:OE2	2.07	0.55
1:A:1193:G:O2'	1:A:1194:U:H5'	2.07	0.55
1:A:1236:A:H2'	1:A:1237:C:C6	2.41	0.55
1:A:1268:A:H2'	1:A:1269:A:C8	2.41	0.55
2:B:15:VAL:HG22	2:B:209:ARG:HG3	1.88	0.55
2:B:67:THR:HG22	2:B:68:ILE:N	2.21	0.55
6:F:69:GLU:HA	6:F:72:VAL:CG2	2.37	0.55
12:L:47:LYS:HB2	12:L:48:PRO:HD2	1.88	0.55
16:P:81:ARG:CG	16:P:83:GLU:HG2	2.36	0.55
1:A:1006:C:H2'	1:A:1007:C:H6	1.72	0.55
1:A:490:G:H2'	1:A:491:G:H8	1.72	0.55
1:A:760:G:C2	17:Q:103:GLY:O	2.60	0.55
1:A:761:G:O4'	17:Q:103:GLY:O	2.25	0.55
4:D:107:ARG:HH21	4:D:194:LEU:HD12	1.70	0.55
13:M:37:THR:O	13:M:37:THR:HG22	2.07	0.55
18:R:86:VAL:O	18:R:87:ARG:CB	2.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1460:A:H2'	1:A:1461:G:O4'	2.07	0.55
1:A:620:C:H2'	1:A:621:A:O4'	2.07	0.55
1:A:818:G:C3'	1:A:819:A:C5'	2.83	0.55
4:D:177:ASP:OD1	4:D:179:GLU:HB2	2.07	0.55
6:F:46:ARG:HB2	6:F:60:PHE:HE1	1.71	0.55
6:F:76:ALA:O	6:F:80:ARG:HG3	2.06	0.55
10:J:49:VAL:HG11	14:N:41:ARG:O	2.07	0.55
1:A:437:U:O2'	4:D:123:HIS:CD2	2.60	0.55
1:A:954:G:H2'	1:A:955:U:C6	2.42	0.55
9:I:7:THR:HG22	9:I:8:GLY:N	2.22	0.55
1:A:1066:C:O2'	1:A:1067:A:H5'	2.07	0.55
1:A:1442:G:H21	1:A:1446:A:H5''	1.72	0.55
1:A:551:U:H2'	1:A:552:U:C6	2.41	0.55
1:A:227:G:O2'	16:P:62:VAL:HG11	2.05	0.55
17:Q:68:ARG:N	17:Q:70:ARG:NH1	2.55	0.55
20:T:67:ALA:HB2	20:T:77:ALA:HB2	1.88	0.55
20:T:82:SER:O	20:T:86:ARG:HB2	2.06	0.55
1:A:1333:A:H2'	1:A:1334:G:O4'	2.07	0.55
3:C:138:VAL:HG21	3:C:168:ALA:HB1	1.89	0.55
3:C:181:ASN:HD21	3:C:204:LEU:HD12	1.72	0.55
10:J:51:ARG:H	10:J:59:SER:HB2	1.72	0.55
15:O:87:ILE:O	15:O:88:ARG:CB	2.54	0.55
1:A:761:G:H1'	17:Q:103:GLY:O	2.06	0.55
1:A:193:C:H2'	1:A:194:C:H6	1.72	0.54
1:A:532:A:H2'	1:A:533:A:H5''	1.89	0.54
2:B:75:LYS:HD3	2:B:75:LYS:O	2.08	0.54
6:F:25:ILE:HD12	6:F:82:ARG:HD2	1.88	0.54
3:C:37:GLN:NE2	14:N:52:GLN:OE1	2.40	0.54
1:A:1319:A:H5'	1:A:1320:C:OP1	2.06	0.54
1:A:190(F):G:H4'	1:A:190(G):G:OP2	2.07	0.54
1:A:195:A:H4'	20:T:68:LYS:CE	2.38	0.54
1:A:26:A:N6	1:A:558:G:H1'	2.21	0.54
1:A:54:C:H2'	1:A:352:C:H41	1.71	0.54
1:A:939:G:H2'	1:A:940:C:H6	1.71	0.54
1:A:977:A:C2'	1:A:978:A:H5''	2.38	0.54
2:B:17:PHE:CD1	2:B:18:GLY:N	2.75	0.54
2:B:33:TYR:HB2	2:B:43:ASP:HB2	1.89	0.54
3:C:112:SER:CB	3:C:115:LEU:HD12	2.36	0.54
5:E:21:ALA:O	5:E:23:GLY:N	2.40	0.54
8:H:56:LYS:N	8:H:56:LYS:HD2	2.23	0.54
8:H:36:LEU:HD12	8:H:59:LEU:HD13	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:967:C:C4'	9:I:128:ARG:HG3	2.37	0.54
2:B:17:PHE:HD1	2:B:18:GLY:N	2.04	0.54
2:B:33:TYR:HB3	2:B:41:ILE:O	2.08	0.54
7:G:116:ALA:HA	7:G:119:ARG:CZ	2.37	0.54
13:M:125:ARG:C	13:M:125:ARG:HD2	2.27	0.54
15:O:32:LEU:O	15:O:36:ILE:HG13	2.06	0.54
1:A:130:A:C8	17:Q:63:ARG:HG3	2.42	0.54
17:Q:79:SER:O	17:Q:80:GLY:O	2.25	0.54
3:C:150:LYS:CE	3:C:152:ILE:HD11	2.38	0.54
5:E:137:GLU:O	5:E:141:GLN:HG3	2.07	0.54
5:E:15:ARG:O	5:E:27:ARG:O	2.25	0.54
7:G:69:VAL:HG12	7:G:100:ALA:HA	1.90	0.54
13:M:60:VAL:O	13:M:63:THR:HG22	2.07	0.54
1:A:1128:C:H2'	1:A:1129:C:H5''	1.90	0.54
1:A:743:U:H2'	1:A:744:C:C6	2.43	0.54
3:C:58:GLU:H	3:C:65:ALA:HB3	1.72	0.54
1:A:425:G:H4'	4:D:45:GLN:HE22	1.73	0.54
6:F:4:TYR:OH	6:F:69:GLU:HB3	2.07	0.54
7:G:113:GLU:HG2	7:G:119:ARG:HG2	1.90	0.54
13:M:29:ARG:HB3	13:M:64:TRP:CH2	2.42	0.54
15:O:27:VAL:O	15:O:31:LEU:HD13	2.07	0.54
16:P:21:VAL:O	16:P:33:ILE:HB	2.07	0.54
1:A:1320:C:N3	19:S:36:ARG:HG3	2.23	0.54
2:B:12:GLU:C	2:B:14:GLY:N	2.59	0.54
7:G:18:TYR:CE2	7:G:59:LEU:HB2	2.42	0.54
9:I:85:LEU:O	9:I:92:TYR:HD1	1.91	0.54
10:J:3:LYS:N	10:J:75:ILE:HA	2.22	0.54
17:Q:18:THR:HG23	17:Q:69:LYS:HE3	1.88	0.54
17:Q:67:LYS:CA	17:Q:70:ARG:HH12	2.21	0.54
1:A:960:U:O2	1:A:960:U:H5'	2.08	0.54
3:C:77:ILE:HG22	3:C:81:GLY:HA2	1.90	0.54
1:A:429:U:H2'	4:D:25:ARG:HH12	1.73	0.54
7:G:138:LYS:HE2	7:G:142:GLU:OE1	2.08	0.54
10:J:31:GLY:HA2	10:J:78:ASN:ND2	2.12	0.54
13:M:94:ARG:HH22	19:S:81:ARG:HH11	1.54	0.54
1:A:1030(A):G:N2	1:A:1030(C):G:H3'	2.23	0.54
1:A:190:C:H2'	1:A:190(A):C:C6	2.43	0.54
1:A:750:G:H1'	15:O:22:THR:OG1	2.08	0.54
2:B:187:LEU:HD23	2:B:214:ILE:HG21	1.90	0.54
4:D:160:GLN:O	4:D:163:GLU:HB3	2.08	0.54
6:F:26:ILE:HG21	6:F:63:TYR:CE2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:53:VAL:O	13:M:57:ARG:HB2	2.08	0.54
17:Q:95:TYR:C	17:Q:97:SER:N	2.58	0.54
20:T:72:LEU:HD21	20:T:80:ARG:CZ	2.38	0.54
1:A:1351:U:H2'	1:A:1352:C:C6	2.40	0.54
1:A:35:G:H2'	1:A:36:C:C6	2.43	0.54
1:A:983:A:H5'	1:A:984:C:OP2	2.07	0.54
2:B:142:LEU:HD22	2:B:146:GLN:HE22	1.73	0.54
1:A:429:U:H2'	4:D:25:ARG:NH1	2.22	0.54
9:I:81:ILE:O	9:I:85:LEU:HB2	2.08	0.54
1:A:1318:A:H4'	19:S:10:PHE:CE1	2.42	0.54
1:A:1494:G:O2'	1:A:1495:U:H5'	2.08	0.54
1:A:1516:G:H2'	1:A:1518:A:OP2	2.08	0.54
1:A:281:G:O2'	1:A:282:A:P	2.65	0.54
3:C:116:VAL:O	3:C:120:VAL:HG23	2.07	0.54
3:C:14:ILE:HG22	3:C:15:THR:N	2.12	0.54
1:A:1222:G:P	19:S:77:THR:HG21	2.48	0.54
1:A:299:G:H2'	1:A:300:A:C8	2.43	0.53
1:A:475:G:H2'	1:A:476:G:C8	2.43	0.53
2:B:10:LEU:C	2:B:12:GLU:H	2.12	0.53
2:B:134:GLU:C	2:B:136:VAL:H	2.12	0.53
3:C:33:LEU:HD23	3:C:33:LEU:C	2.29	0.53
4:D:126:ILE:HG22	4:D:127:THR:N	2.23	0.53
8:H:119:LEU:HD12	8:H:124:ALA:HA	1.90	0.53
14:N:9:LYS:HD3	14:N:9:LYS:C	2.28	0.53
16:P:43:LYS:HB3	16:P:48:TRP:CD1	2.43	0.53
1:A:1218:C:H2'	1:A:1219:U:C6	2.42	0.53
1:A:1347:G:C2'	1:A:1348:U:OP2	2.56	0.53
1:A:639:G:O2'	1:A:640:A:H5'	2.08	0.53
3:C:174:PRO:HB2	3:C:177:THR:HG22	1.89	0.53
5:E:101:ILE:O	5:E:120:THR:HB	2.08	0.53
7:G:44:TYR:HE1	9:I:41:VAL:HG11	1.72	0.53
9:I:97:LYS:O	9:I:100:GLY:N	2.36	0.53
11:K:14:VAL:O	11:K:15:ALA:CB	2.57	0.53
15:O:70:LEU:HD11	15:O:77:ARG:HB2	1.89	0.53
16:P:11:SER:OG	16:P:14:ASN:HB3	2.08	0.53
1:A:957:U:H4'	19:S:79:THR:HB	1.89	0.53
1:A:1003:G:C2	1:A:1003(A):G:C6	2.96	0.53
1:A:1300:G:HO2'	1:A:1301:U:H6	1.54	0.53
1:A:33:A:H2'	1:A:34:C:H6	1.73	0.53
2:B:18:GLY:CA	2:B:42:ILE:H	2.20	0.53
9:I:17:VAL:HG11	9:I:81:ILE:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:46:LYS:CG	12:L:47:LYS:N	2.71	0.53
19:S:51:VAL:HG12	19:S:52:TYR:N	2.23	0.53
1:A:1402:C:O2	1:A:1500:A:N1	2.41	0.53
3:C:113:ALA:HB3	3:C:114:PRO:HD3	1.90	0.53
1:A:1117:G:H4'	9:I:104:ARG:HH11	1.72	0.53
14:N:44:LEU:C	14:N:44:LEU:HD12	2.29	0.53
14:N:44:LEU:O	14:N:44:LEU:HD12	2.08	0.53
1:A:190(L):U:H3	20:T:105:SER:HG	1.56	0.53
1:A:101:A:O2'	1:A:102:G:H5'	2.07	0.53
1:A:33:A:H2'	1:A:34:C:C6	2.44	0.53
1:A:382:A:H2'	1:A:383:A:H8	1.70	0.53
1:A:386:C:C2'	1:A:387:U:H5'	2.39	0.53
1:A:979:C:H2'	1:A:980:C:H5'	1.91	0.53
7:G:71:PRO:HD3	7:G:103:TRP:HZ3	1.74	0.53
7:G:42:ILE:CG2	7:G:120:ILE:HD12	2.39	0.53
9:I:23:ASN:HD22	9:I:23:ASN:C	2.12	0.53
10:J:48:THR:HG1	10:J:62:HIS:CD2	2.26	0.53
1:A:1003:G:N2	1:A:1039:C:C2	2.77	0.53
1:A:1121:U:H2'	1:A:1122:U:H6	1.73	0.53
1:A:959:A:C2	1:A:1222:G:O4'	2.61	0.53
1:A:1305:G:O2'	1:A:1306:A:C8	2.44	0.53
1:A:300:A:H2'	1:A:301:G:O4'	2.08	0.53
8:H:80:ILE:O	8:H:80:ILE:HG22	2.08	0.53
9:I:48:GLU:OE1	9:I:51:ARG:HD2	2.09	0.53
10:J:38:ILE:HG13	10:J:71:LEU:HB3	1.90	0.53
13:M:8:GLU:OE1	13:M:22:ILE:HA	2.08	0.53
17:Q:27:PHE:CE1	17:Q:36:ILE:HD11	2.42	0.53
1:A:1157:A:H4'	1:A:1158:C:O5'	2.08	0.53
1:A:818:G:O2'	1:A:819:A:H5''	2.08	0.53
1:A:407:G:O2'	4:D:116:GLN:HG3	2.08	0.53
5:E:18:ARG:HG2	5:E:19:MET:N	2.23	0.53
5:E:76:ILE:O	5:E:93:PRO:HB3	2.07	0.53
8:H:8:ASP:O	8:H:12:ARG:HG3	2.08	0.53
13:M:102:ARG:NH1	13:M:102:ARG:HB2	2.24	0.53
16:P:19:ILE:HG22	16:P:36:ILE:HG13	1.90	0.53
18:R:61:LYS:O	18:R:65:ILE:HG13	2.08	0.53
19:S:42:PRO:O	19:S:45:VAL:HG23	2.09	0.53
21:V:9:ARG:NH1	21:V:22:ARG:HA	2.23	0.53
1:A:1068:G:H8	1:A:1068:G:OP2	1.91	0.53
2:B:23:ARG:O	2:B:24:TRP:O	2.27	0.53
3:C:130:VAL:O	3:C:134:ILE:HG13	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:91:LEU:HD21	3:C:99:VAL:CG1	2.30	0.53
12:L:53:ARG:HG2	12:L:69:TYR:HE1	1.73	0.53
12:L:55:VAL:HG11	12:L:67:THR:HG23	1.91	0.53
13:M:11:ARG:CG	13:M:12:ASN:N	2.72	0.53
1:A:187:C:C2	20:T:105:SER:HB3	2.43	0.53
20:T:76:ALA:O	20:T:80:ARG:HG2	2.09	0.53
1:A:1426:C:H2'	1:A:1427:U:C6	2.44	0.53
1:A:623:C:O2'	1:A:624:C:H5'	2.09	0.53
2:B:124:SER:O	2:B:127:ILE:HG13	2.08	0.53
2:B:166:ASP:OD2	2:B:169:LYS:HB2	2.09	0.53
3:C:32:LEU:HD21	3:C:59:ARG:HD2	1.91	0.53
4:D:32:ALA:C	4:D:34:GLU:N	2.60	0.53
9:I:31:GLN:HB3	9:I:35:GLU:HB3	1.91	0.53
10:J:44:VAL:HG22	10:J:66:ARG:HB3	1.91	0.53
20:T:93:GLU:OE2	20:T:93:GLU:HA	2.09	0.53
1:A:1305:G:OP1	21:V:2:GLY:N	2.42	0.53
1:A:101:A:H2'	1:A:102:G:H8	1.74	0.53
1:A:1184:G:H2'	1:A:1185:G:H8	1.73	0.53
1:A:148:G:H2'	1:A:149:A:H8	1.74	0.53
1:A:373:A:O2'	1:A:374:A:H5'	2.09	0.53
7:G:69:VAL:HG21	7:G:104:LEU:HD21	1.90	0.53
10:J:81:THR:C	10:J:83:GLU:H	2.10	0.53
1:A:528:C:H41	12:L:49:ASN:ND2	2.06	0.53
1:A:1006:C:H2'	1:A:1007:C:C6	2.44	0.52
1:A:188:C:H4'	20:T:89:ARG:NH1	2.25	0.52
1:A:370:C:O2'	1:A:371:G:H5'	2.09	0.52
1:A:1038:C:H2'	1:A:1039:C:C6	2.43	0.52
1:A:252:U:H2'	1:A:253:U:C6	2.44	0.52
1:A:246:A:N6	1:A:281:G:H1'	2.24	0.52
2:B:32:ILE:HD13	2:B:40:HIS:CD2	2.44	0.52
5:E:31:LEU:HD22	5:E:43:LEU:CD2	2.39	0.52
12:L:47:LYS:HB3	12:L:48:PRO:HD3	1.91	0.52
14:N:33:VAL:HA	14:N:40:CYS:HA	1.91	0.52
1:A:1423:G:O2'	1:A:1424:C:H5'	2.09	0.52
3:C:23:TYR:CD2	3:C:24:ALA:N	2.78	0.52
12:L:55:VAL:HG11	12:L:67:THR:CG2	2.39	0.52
13:M:102:ARG:HH11	13:M:102:ARG:HB2	1.75	0.52
1:A:761:G:C5'	17:Q:102:GLY:HA3	2.39	0.52
20:T:50:GLU:O	20:T:100:ILE:HD12	2.09	0.52
1:A:1128:C:H1'	1:A:1146:A:H61	1.75	0.52
1:A:621:A:H2'	1:A:622:A:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:684:A:H1'	11:K:38:ASN:HB3	1.91	0.52
1:A:922:G:N3	1:A:1398:A:H2	2.07	0.52
5:E:12:LEU:CD1	5:E:31:LEU:HB2	2.39	0.52
6:F:10:LEU:HD11	6:F:59:TYR:CD2	2.41	0.52
11:K:13:GLN:HA	11:K:75:TYR:O	2.08	0.52
13:M:86:CYS:SG	13:M:88:ARG:HB3	2.49	0.52
1:A:1038:C:H2'	1:A:1039:C:H6	1.74	0.52
1:A:1513:A:H2'	1:A:1514:C:C6	2.44	0.52
1:A:401:C:H1'	1:A:622:A:H1'	1.91	0.52
3:C:139:GLN:NE2	3:C:139:GLN:HA	2.25	0.52
3:C:22:TRP:CZ2	14:N:54:PRO:HG3	2.44	0.52
4:D:65:ARG:HB2	4:D:75:PHE:CE1	2.45	0.52
6:F:43:LEU:H	6:F:43:LEU:CD2	2.23	0.52
8:H:14:ARG:O	8:H:18:ARG:HD3	2.10	0.52
13:M:117:VAL:HG12	13:M:118:ALA:N	2.24	0.52
19:S:13:ASP:O	19:S:17:GLU:HG2	2.10	0.52
1:A:103:C:P	20:T:17:ARG:HH11	2.32	0.52
20:T:43:LEU:CD1	20:T:55:ILE:HD12	2.40	0.52
1:A:115:G:O2'	1:A:116:A:OP2	2.22	0.52
1:A:1397:C:H4'	1:A:1398:A:OP2	2.09	0.52
1:A:953:G:H2'	1:A:954:G:O4'	2.09	0.52
3:C:70:VAL:O	3:C:106:VAL:HG23	2.09	0.52
4:D:104:VAL:HG11	4:D:146:ILE:CD1	2.37	0.52
5:E:80:ILE:HD13	5:E:138:ALA:HB1	1.90	0.52
14:N:3:ARG:O	14:N:4:LYS:C	2.48	0.52
21:V:17:THR:O	21:V:22:ARG:HD3	2.10	0.52
21:V:24:ARG:O	21:V:25:LYS:HB2	2.10	0.52
1:A:1428:A:H2'	1:A:1429:C:C6	2.44	0.52
1:A:518:C:HO2'	12:L:50:SER:HB3	1.75	0.52
3:C:154:SER:O	3:C:165:THR:HA	2.09	0.52
5:E:74:GLY:HA3	5:E:116:THR:HG22	1.92	0.52
11:K:17:GLY:O	11:K:80:VAL:HA	2.09	0.52
18:R:19:LYS:O	18:R:20:ALA:HB2	2.10	0.52
18:R:73:ALA:HB3	18:R:79:LEU:HD12	1.91	0.52
19:S:50:ALA:HA	19:S:58:VAL:O	2.10	0.52
1:A:1202:G:H2'	1:A:1203:C:O4'	2.10	0.52
1:A:1424:C:O2'	1:A:1425:U:H5'	2.09	0.52
1:A:190(E):U:O2'	17:Q:63:ARG:NH2	2.43	0.52
1:A:142:G:O2'	1:A:196:A:N1	2.40	0.52
1:A:791:G:H2'	1:A:792:A:H5'	1.91	0.52
2:B:73:THR:HG23	2:B:95:GLN:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:12:LEU:C	5:E:12:LEU:HD22	2.30	0.52
6:F:3:ARG:NH2	6:F:64:GLN:NE2	2.57	0.52
8:H:25:ASP:OD1	8:H:60:ARG:HD3	2.09	0.52
9:I:9:ARG:HG2	9:I:14:VAL:HG22	1.92	0.52
20:T:41:VAL:O	20:T:45:GLN:HB2	2.10	0.52
1:A:115:G:H1'	1:A:116:A:N7	2.24	0.52
1:A:1167:A:H2'	1:A:1168:A:C8	2.45	0.52
1:A:1451:A:O2'	1:A:1452:C:OP1	2.26	0.52
1:A:1481:U:O2'	1:A:1482:G:H5'	2.09	0.52
1:A:605:U:O2'	1:A:606:G:H5'	2.10	0.52
3:C:130:VAL:HG12	3:C:134:ILE:HD11	1.91	0.52
3:C:83:ARG:C	3:C:85:ARG:N	2.63	0.52
4:D:170:VAL:CG1	4:D:174:LEU:HB2	2.39	0.52
16:P:20:VAL:CG1	16:P:32:TYR:HB3	2.40	0.52
1:A:1021:G:C2'	1:A:1022:G:H5'	2.40	0.52
1:A:148:G:H2'	1:A:149:A:C8	2.45	0.52
1:A:357:G:O2'	1:A:358:U:H5'	2.09	0.52
6:F:8:ILE:HD11	6:F:79:LEU:HD13	1.92	0.52
11:K:27:ASN:HA	11:K:56:GLY:HA2	1.92	0.52
11:K:62:GLN:HG3	11:K:97:ALA:HB2	1.92	0.52
13:M:73:GLU:O	13:M:76:ALA:HB3	2.09	0.52
13:M:78:ILE:HA	13:M:81:LEU:CD2	2.38	0.52
18:R:88:LYS:HG2	18:R:88:LYS:OXT	2.10	0.52
21:V:24:ARG:O	21:V:25:LYS:CB	2.58	0.52
1:A:1241:G:H2'	1:A:1242:C:H6	1.75	0.51
1:A:1511:G:H2'	1:A:1512:U:O4'	2.09	0.51
1:A:443:C:H2'	1:A:444:C:C6	2.43	0.51
3:C:20:SER:HB3	3:C:22:TRP:NE1	2.25	0.51
8:H:24:THR:HG23	8:H:61:VAL:HB	1.92	0.51
9:I:115:GLY:HA2	10:J:58:ASP:OD1	2.10	0.51
9:I:44:VAL:HG13	9:I:51:ARG:NH2	2.24	0.51
10:J:22:LYS:NZ	10:J:91:PRO:HD3	2.25	0.51
12:L:42:THR:HG21	12:L:52:LEU:HB3	1.91	0.51
13:M:88:ARG:HG3	13:M:98:VAL:CG1	2.40	0.51
1:A:1329:A:O2'	1:A:1330:U:H5'	2.11	0.51
1:A:452:A:H4'	16:P:72:ARG:NH2	2.25	0.51
2:B:130:ARG:HH22	3:C:179:ARG:NH1	2.05	0.51
3:C:134:ILE:HG21	3:C:167:TRP:O	2.11	0.51
1:A:738:C:P	6:F:92:LYS:HE3	2.50	0.51
18:R:46:GLU:CD	18:R:46:GLU:H	2.14	0.51
1:A:1525:G:P	11:K:120:ARG:HH22	2.32	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:C:O2'	1:A:164:U:H5'	2.10	0.51
1:A:794:A:H2'	1:A:795:C:C6	2.45	0.51
2:B:126:GLU:O	2:B:129:GLU:HB2	2.11	0.51
3:C:94:LEU:HD22	3:C:95:THR:HG23	1.92	0.51
3:C:97:LYS:O	3:C:98:ASN:HB3	2.10	0.51
5:E:15:ARG:O	5:E:16:THR:O	2.28	0.51
5:E:40:ARG:HH11	5:E:40:ARG:HG2	1.76	0.51
7:G:156:TRP:HD1	7:G:156:TRP:OXT	1.93	0.51
10:J:20:ALA:O	10:J:24:VAL:HG23	2.11	0.51
10:J:39:PRO:O	10:J:40:LEU:CB	2.57	0.51
11:K:126:ARG:O	11:K:127:LYS:C	2.48	0.51
1:A:1221:G:O3'	19:S:77:THR:HG21	2.10	0.51
1:A:1003(A):G:N1	1:A:1004:A:H1'	2.25	0.51
1:A:1094:G:H5''	1:A:1095:U:H5	1.75	0.51
1:A:1191:A:H2'	1:A:1192:C:C6	2.45	0.51
1:A:502:G:H1'	1:A:550:G:H5'	1.91	0.51
1:A:560:U:O2'	1:A:561:U:OP2	2.27	0.51
3:C:84:ILE:O	3:C:84:ILE:HG12	2.10	0.51
5:E:13:ILE:HG22	5:E:30:ALA:CB	2.40	0.51
6:F:69:GLU:N	6:F:69:GLU:OE1	2.44	0.51
12:L:119:LYS:O	12:L:120:TYR:HB2	2.11	0.51
14:N:21:TYR:HE2	14:N:23:ARG:NE	2.09	0.51
19:S:53:ASN:HB2	19:S:56:GLN:H	1.74	0.51
1:A:190(L):U:H3	20:T:105:SER:HB2	1.75	0.51
1:A:580:U:H2'	1:A:581:G:O4'	2.11	0.51
3:C:108:ASN:C	3:C:110:ASN:H	2.12	0.51
4:D:24:GLU:O	4:D:25:ARG:HB3	2.10	0.51
7:G:102:ARG:O	7:G:106:GLN:HG3	2.11	0.51
10:J:23:ILE:N	10:J:23:ILE:HD12	2.26	0.51
10:J:69:ASN:O	10:J:70:ARG:HD3	2.11	0.51
14:N:57:ARG:HG2	14:N:58:LYS:H	1.75	0.51
1:A:1059:C:O2'	1:A:1060:C:H5'	2.11	0.51
1:A:1277:C:HO2'	1:A:1279:A:H8	1.54	0.51
1:A:1468:A:H2'	1:A:1469:G:O4'	2.09	0.51
1:A:1518:A:H2'	1:A:1519:A:C8	2.45	0.51
1:A:828:A:H2'	1:A:829:G:O4'	2.10	0.51
3:C:137:ALA:HA	3:C:140:ARG:NH1	2.26	0.51
3:C:61:ALA:O	3:C:63:ASN:N	2.44	0.51
6:F:67:MET:HE2	6:F:72:VAL:HG22	1.91	0.51
1:A:1346:A:C4	7:G:10:ARG:NH2	2.78	0.51
9:I:125:TYR:N	9:I:125:TYR:CD2	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:127:LYS:N	9:I:127:LYS:HD2	2.25	0.51
17:Q:45:HIS:CB	17:Q:65:ILE:HD13	2.39	0.51
17:Q:45:HIS:HB2	17:Q:65:ILE:CD1	2.37	0.51
19:S:81:ARG:O	19:S:81:ARG:HG2	2.11	0.51
1:A:1021:G:H2'	1:A:1022:G:O4'	2.11	0.51
1:A:1126:U:OP2	1:A:1281:U:O2	2.29	0.51
1:A:478:A:O2'	1:A:479:C:H5'	2.11	0.51
1:A:791:G:H2'	1:A:792:A:C5'	2.40	0.51
1:A:808:C:OP1	15:O:48:LYS:HE3	2.11	0.51
1:A:922:G:H5'	5:E:19:MET:O	2.11	0.51
2:B:15:VAL:HG11	2:B:209:ARG:C	2.30	0.51
2:B:26:PRO:O	2:B:29:ALA:HB2	2.10	0.51
3:C:34:LEU:HD23	3:C:34:LEU:O	2.10	0.51
8:H:49:GLU:HG2	8:H:62:TYR:HE2	1.75	0.51
14:N:28:GLY:O	14:N:30:ALA:N	2.43	0.51
19:S:10:PHE:CD2	19:S:10:PHE:C	2.83	0.51
19:S:45:VAL:HG12	19:S:46:GLY:N	2.26	0.51
1:A:1085:U:O3'	1:A:1086:U:C6	2.64	0.51
1:A:992:U:O2'	1:A:993:G:OP2	2.26	0.51
2:B:144:ARG:O	2:B:147:LYS:N	2.42	0.51
3:C:139:GLN:HE21	3:C:139:GLN:CA	2.23	0.51
5:E:104:ALA:O	5:E:105:VAL:C	2.49	0.51
5:E:115:VAL:HG12	5:E:116:THR:N	2.24	0.51
1:A:760:G:N1	17:Q:104:LYS:O	2.43	0.51
18:R:45:SER:C	18:R:47:THR:N	2.65	0.51
1:A:1152:A:H2'	1:A:1153:C:C6	2.45	0.51
1:A:1262:C:H42	1:A:1273:G:H1	1.59	0.51
1:A:160:A:H1'	1:A:344:A:C5	2.46	0.51
1:A:7:G:H5'	1:A:298:A:O4'	2.11	0.51
2:B:17:PHE:CD1	2:B:17:PHE:C	2.85	0.51
2:B:19:HIS:NE2	2:B:206:ASP:HB3	2.26	0.51
2:B:53:ARG:HG2	2:B:53:ARG:NH1	2.26	0.51
2:B:96:ARG:O	2:B:98:LEU:HD23	2.11	0.51
5:E:92:LYS:HB3	5:E:119:LEU:HB2	1.93	0.51
5:E:61:TYR:O	5:E:64:ARG:O	2.29	0.51
5:E:89:ILE:HD13	5:E:90:VAL:H	1.75	0.51
9:I:27:THR:HG23	9:I:30:GLY:O	2.11	0.51
9:I:44:VAL:CG1	9:I:51:ARG:HH12	2.23	0.51
9:I:93:ARG:HH11	9:I:97:LYS:HZ2	1.58	0.51
12:L:28:LYS:CD	12:L:33:ARG:HH12	2.24	0.51
1:A:1162:C:H2'	1:A:1163:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:G:H21	1:A:354:G:C5'	2.24	0.51
2:B:97:TRP:CZ2	2:B:102:LEU:HD13	2.45	0.51
4:D:81:GLU:O	4:D:85:LYS:HG3	2.11	0.51
6:F:43:LEU:H	6:F:43:LEU:HD22	1.76	0.51
6:F:9:VAL:HG22	6:F:60:PHE:CE2	2.46	0.51
8:H:126:LYS:C	8:H:128:GLY:H	2.14	0.51
12:L:53:ARG:NH1	12:L:92:ASP:OD2	2.42	0.51
1:A:1097:C:H2'	1:A:1098:C:C6	2.45	0.50
1:A:1190:G:O2'	1:A:1191:A:P	2.69	0.50
1:A:1396:A:H4'	1:A:1397:C:H5''	1.93	0.50
1:A:149:A:O2'	1:A:150:C:H5'	2.11	0.50
1:A:650:G:C2'	1:A:651:C:H5'	2.40	0.50
3:C:188:LEU:CD1	3:C:195:VAL:HG13	2.41	0.50
21:V:6:ARG:HD2	21:V:15:ARG:NH1	2.25	0.50
1:A:1035:A:H2'	1:A:1036:G:H8	1.76	0.50
1:A:1440:C:C2'	1:A:1441:G:H5'	2.41	0.50
1:A:659:U:O2'	1:A:660:G:H5'	2.11	0.50
1:A:853:G:O2'	1:A:854:G:H5'	2.11	0.50
3:C:112:SER:O	3:C:116:VAL:HG23	2.11	0.50
3:C:58:GLU:O	3:C:59:ARG:HG2	2.11	0.50
5:E:11:ILE:HB	5:E:31:LEU:HB3	1.93	0.50
9:I:47:LEU:C	9:I:49:PRO:HD2	2.32	0.50
10:J:71:LEU:O	10:J:72:VAL:CB	2.60	0.50
10:J:27:ALA:HB1	10:J:81:THR:HG23	1.92	0.50
14:N:29:ARG:O	14:N:33:VAL:HG13	2.11	0.50
1:A:1418:A:H2'	1:A:1419:G:O4'	2.12	0.50
9:I:17:VAL:CG2	9:I:80:GLY:HA3	2.41	0.50
12:L:115:LYS:O	12:L:117:ARG:N	2.37	0.50
13:M:77:ASN:O	13:M:80:ARG:HB3	2.10	0.50
14:N:22:THR:OG1	14:N:33:VAL:HG21	2.11	0.50
1:A:1021:G:C2	1:A:1022:G:H1'	2.45	0.50
1:A:1283:G:O2'	1:A:1284:C:H5'	2.11	0.50
1:A:824:C:H2'	1:A:825:G:H8	1.76	0.50
2:B:121:LEU:O	2:B:127:ILE:HG12	2.11	0.50
2:B:221:LEU:O	2:B:221:LEU:HD13	2.11	0.50
2:B:53:ARG:HH11	2:B:53:ARG:HG2	1.76	0.50
2:B:88:ALA:O	2:B:90:MET:N	2.45	0.50
3:C:47:LEU:N	3:C:47:LEU:CD1	2.74	0.50
4:D:151:LYS:N	4:D:151:LYS:CD	2.75	0.50
7:G:69:VAL:O	7:G:69:VAL:HG12	2.12	0.50
1:A:1179:A:H2'	1:A:1180:A:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1278:U:C5'	1:A:1279:A:O4'	2.59	0.50
1:A:1310:G:O2'	1:A:1311:G:H5'	2.12	0.50
1:A:222:U:H2'	1:A:223:U:C6	2.47	0.50
1:A:325:A:H2'	1:A:326:G:O4'	2.12	0.50
1:A:839:U:C2'	1:A:839:U:O2	2.59	0.50
2:B:186:ALA:HB3	2:B:197:VAL:CG1	2.41	0.50
3:C:177:THR:O	3:C:177:THR:HG23	2.10	0.50
5:E:121:LYS:HE3	5:E:123:LEU:HD21	1.93	0.50
6:F:67:MET:CE	6:F:72:VAL:HA	2.40	0.50
9:I:46:ALA:HA	9:I:78:LYS:HB2	1.93	0.50
1:A:999:C:H2'	1:A:1000:U:C6	2.45	0.50
1:A:1136:U:H5''	1:A:1137:C:OP2	2.12	0.50
1:A:960:U:H1'	1:A:1223:C:H5'	1.93	0.50
1:A:1305:G:OP2	1:A:1305:G:C8	2.64	0.50
1:A:556:C:C2'	1:A:557:G:H5'	2.40	0.50
1:A:792:A:H4'	1:A:793:U:C5'	2.40	0.50
2:B:124:SER:CB	2:B:125:PRO:HD2	2.32	0.50
2:B:132:LYS:O	2:B:136:VAL:HG23	2.12	0.50
2:B:33:TYR:HB3	2:B:41:ILE:HG22	1.93	0.50
2:B:44:LEU:HA	2:B:47:THR:OG1	2.12	0.50
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.93	0.50
6:F:38:GLU:O	6:F:39:LYS:HB3	2.12	0.50
1:A:1025:U:H4'	1:A:1025:U:OP1	2.11	0.50
1:A:1044:A:H2'	1:A:1045:C:H5'	1.92	0.50
1:A:1096:C:H2'	1:A:1097:C:H6	1.77	0.50
1:A:217:C:O2'	1:A:218:C:H5'	2.12	0.50
1:A:746:A:O2'	1:A:747:C:H5'	2.11	0.50
3:C:178:LEU:O	3:C:179:ARG:CB	2.60	0.50
4:D:3:ARG:NH2	4:D:74:GLN:OE1	2.43	0.50
4:D:8:VAL:HG11	4:D:21:LEU:HB3	1.94	0.50
1:A:1249:C:O2'	9:I:73:GLN:NE2	2.45	0.50
9:I:10:ARG:HG2	9:I:75:ASP:CB	2.41	0.50
10:J:3:LYS:HA	10:J:75:ILE:HA	1.94	0.50
13:M:82:MET:HE2	13:M:92:HIS:HB3	1.93	0.50
17:Q:27:PHE:HB2	17:Q:28:PRO:HD2	1.94	0.50
17:Q:97:SER:HB2	17:Q:103:GLY:N	2.26	0.50
1:A:1305:G:C5'	21:V:4:GLY:HA3	2.41	0.50
1:A:1306:A:H2'	1:A:1307:U:O4'	2.12	0.50
1:A:1074:G:O3'	2:B:103:THR:HG22	2.12	0.50
3:C:79:ARG:HG2	3:C:82:GLU:HG2	1.92	0.50
4:D:8:VAL:HG13	4:D:21:LEU:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:46:LYS:HG2	12:L:47:LYS:HG3	1.93	0.50
17:Q:10:VAL:O	17:Q:53:LEU:HD12	2.12	0.50
17:Q:45:HIS:NE2	17:Q:47:PRO:HG3	2.27	0.50
1:A:136:C:H2'	1:A:137:C:H6	1.77	0.50
1:A:1498:U:H4'	1:A:1519:A:C2	2.45	0.50
1:A:1499:A:O2'	1:A:1500:A:H5'	2.12	0.50
1:A:179:A:H2'	1:A:180:U:C6	2.46	0.50
1:A:255:G:O6	1:A:266:G:O6	2.29	0.50
1:A:959:A:H2'	1:A:960:U:O4'	2.12	0.50
4:D:126:ILE:CG2	4:D:127:THR:N	2.75	0.50
7:G:38:LEU:O	7:G:42:ILE:HG13	2.12	0.50
8:H:38:ILE:N	8:H:38:ILE:HD12	2.27	0.50
11:K:82:VAL:HG23	11:K:105:VAL:HG13	1.93	0.50
11:K:23:ALA:CB	11:K:91:ARG:HB2	2.42	0.50
13:M:5:ALA:O	13:M:6:GLY:C	2.51	0.50
20:T:101:GLY:O	20:T:102:GLY:O	2.30	0.50
1:A:1165:C:O2'	1:A:1166:G:H5'	2.12	0.49
1:A:1181:G:O2'	1:A:1184:G:H5'	2.11	0.49
1:A:430:A:C2'	1:A:431:A:H5'	2.42	0.49
1:A:865:A:H5'	1:A:1078:U:O4	2.12	0.49
1:A:89:C:H2'	1:A:90:U:O4'	2.12	0.49
2:B:17:PHE:HD1	2:B:17:PHE:C	2.14	0.49
3:C:139:GLN:O	3:C:143:GLU:N	2.37	0.49
3:C:167:TRP:O	3:C:168:ALA:HB3	2.10	0.49
7:G:18:TYR:HD2	7:G:59:LEU:HD22	1.76	0.49
14:N:15:LYS:HB3	14:N:16:PHE:CD1	2.47	0.49
15:O:3:ILE:CG2	15:O:7:GLU:HB3	2.41	0.49
17:Q:26:GLN:O	17:Q:27:PHE:HB3	2.12	0.49
18:R:87:ARG:HG2	18:R:87:ARG:HH11	1.76	0.49
1:A:1323:G:H2'	1:A:1324:A:C8	2.47	0.49
2:B:30:ARG:HG3	2:B:31:TYR:CD2	2.48	0.49
3:C:172:ARG:HH12	3:C:174:PRO:CG	2.22	0.49
3:C:171:GLY:O	3:C:173:VAL:HG23	2.12	0.49
3:C:47:LEU:N	3:C:47:LEU:HD12	2.27	0.49
5:E:31:LEU:HD22	5:E:43:LEU:HD21	1.94	0.49
7:G:108:ALA:O	7:G:119:ARG:HB3	2.12	0.49
8:H:113:SER:HB2	8:H:134:ILE:CD1	2.29	0.49
10:J:60:ARG:O	10:J:61:GLU:CB	2.61	0.49
11:K:48:ILE:HD13	11:K:63:LEU:HB3	1.93	0.49
11:K:51:LYS:O	11:K:55:LYS:HE3	2.11	0.49
12:L:45:PRO:HD3	12:L:51:ALA:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1085:U:O3'	1:A:1086:U:H6	1.95	0.49
1:A:1102:A:H2'	1:A:1103:C:C6	2.46	0.49
1:A:129(A):G:O2'	1:A:130:A:OP2	2.28	0.49
1:A:1301:U:O2'	1:A:1302:U:OP1	2.30	0.49
1:A:1365:G:O2'	1:A:1366:C:H5'	2.12	0.49
1:A:204:U:H4'	1:A:216:G:O5'	2.12	0.49
1:A:489:C:H2'	1:A:490:G:H8	1.77	0.49
1:A:521:G:O2'	1:A:522:C:H5'	2.12	0.49
1:A:625:G:H2'	1:A:626:U:C6	2.47	0.49
4:D:127:THR:CG2	4:D:128:VAL:N	2.75	0.49
9:I:36:TYR:HD2	9:I:37:PHE:CE2	2.30	0.49
11:K:124:LYS:HD2	11:K:125:PHE:CE1	2.48	0.49
11:K:65:ALA:HB3	11:K:97:ALA:HB3	1.93	0.49
12:L:48:PRO:HG2	12:L:49:ASN:N	2.26	0.49
1:A:1057:G:H5''	3:C:154:SER:CB	2.30	0.49
1:A:1172:C:O2'	1:A:1173:G:H5'	2.11	0.49
1:A:1256:A:C4'	1:A:1257:U:H5'	2.35	0.49
1:A:1366:C:C2	1:A:1367:C:C5	3.00	0.49
1:A:218:C:H2'	1:A:219:C:C6	2.47	0.49
1:A:245:C:O2	1:A:283:C:N3	2.46	0.49
1:A:647:C:H2'	1:A:648:A:H8	1.78	0.49
1:A:834:C:H2'	1:A:835:U:C6	2.48	0.49
2:B:124:SER:CB	2:B:125:PRO:CD	2.90	0.49
2:B:206:ASP:O	2:B:207:ALA:HB3	2.11	0.49
3:C:38:ARG:NH1	3:C:38:ARG:HG3	2.26	0.49
4:D:7:PRO:CG	4:D:10:ARG:HD2	2.43	0.49
12:L:45:PRO:HB2	12:L:49:ASN:O	2.13	0.49
15:O:36:ILE:HA	15:O:59:MET:CE	2.42	0.49
15:O:4:THR:HB	15:O:6:GLU:HG2	1.93	0.49
1:A:218:C:H2'	1:A:219:C:H6	1.76	0.49
3:C:14:ILE:CG2	3:C:15:THR:H	2.11	0.49
4:D:38:TYR:CE1	4:D:45:GLN:HG3	2.48	0.49
4:D:78:LEU:HD22	4:D:96:LEU:HB3	1.94	0.49
5:E:13:ILE:O	5:E:13:ILE:HG13	2.11	0.49
15:O:17:ARG:HG3	15:O:17:ARG:NH1	2.23	0.49
1:A:190:C:H2'	1:A:190(A):C:H6	1.76	0.49
2:B:168:THR:OG1	2:B:192:SER:HB3	2.12	0.49
6:F:43:LEU:N	6:F:43:LEU:HD22	2.27	0.49
15:O:34:LEU:O	15:O:34:LEU:HD23	2.12	0.49
6:F:100:ASN:O	18:R:28:GLU:HG3	2.13	0.49
13:M:94:ARG:CZ	19:S:81:ARG:HD3	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:A:H2'	1:A:150:C:C6	2.48	0.49
1:A:265:G:O2'	1:A:266:G:H5'	2.13	0.49
1:A:491:G:H2'	1:A:492:G:H8	1.77	0.49
1:A:659:U:H2'	1:A:660:G:O4'	2.13	0.49
2:B:102:LEU:CD2	2:B:162:ILE:HD11	2.37	0.49
2:B:97:TRP:CH2	2:B:173:ALA:HA	2.47	0.49
2:B:35:GLU:HA	2:B:39:ILE:O	2.13	0.49
3:C:180:ALA:O	3:C:181:ASN:CB	2.61	0.49
3:C:191:THR:HG22	3:C:193:TYR:N	2.23	0.49
7:G:85:TYR:CD1	7:G:154:TYR:HE1	2.28	0.49
10:J:16:LEU:HD23	10:J:94:VAL:HG22	1.95	0.49
11:K:48:ILE:HD11	11:K:64:ALA:HA	1.95	0.49
11:K:85:ARG:HH11	11:K:85:ARG:HG3	1.77	0.49
16:P:42:ARG:O	16:P:43:LYS:C	2.51	0.49
17:Q:78:GLU:O	17:Q:78:GLU:HG3	2.12	0.49
18:R:41:LYS:O	18:R:41:LYS:HG2	2.13	0.49
1:A:1153:C:H2'	1:A:1154:G:C8	2.46	0.49
1:A:1181:G:H4'	1:A:1184:G:H5'	1.94	0.49
1:A:1305:G:H22	1:A:1331:G:H2'	1.77	0.49
1:A:1503:A:O2'	1:A:1504:G:OP1	2.29	0.49
1:A:346:G:H2'	1:A:347:G:H5'	1.94	0.49
1:A:586:C:O2'	1:A:587:G:H5'	2.12	0.49
2:B:144:ARG:HG3	2:B:145:LEU:H	1.77	0.49
3:C:3:ASN:HD22	3:C:4:LYS:HG2	1.78	0.49
4:D:157:LEU:CD2	4:D:161:ASN:ND2	2.74	0.49
8:H:65:TYR:HA	8:H:79:VAL:HG23	1.94	0.49
10:J:32:ALA:HB2	10:J:76:ASN:HB2	1.94	0.49
15:O:30:ALA:HA	15:O:85:LEU:HD21	1.94	0.49
18:R:34:TYR:HA	18:R:69:THR:HG23	1.93	0.49
20:T:89:ARG:HE	20:T:104:LEU:HD22	1.78	0.49
1:A:1162:C:H2'	1:A:1163:C:H6	1.78	0.49
1:A:1194:U:O2'	1:A:1195:C:H5'	2.12	0.49
1:A:1250:A:H2'	1:A:1251:A:C8	2.47	0.49
1:A:1346:A:H1'	1:A:1348:U:C5	2.47	0.49
1:A:1505:G:C8	1:A:1505:G:H3'	2.48	0.49
1:A:269:C:H2'	1:A:270:A:C8	2.48	0.49
1:A:393:A:C2	1:A:394:G:C8	3.00	0.49
3:C:116:VAL:O	3:C:119:ARG:HB3	2.13	0.49
5:E:36:ASP:O	5:E:37:ARG:HB2	2.13	0.49
5:E:84:PHE:CE2	5:E:133:TYR:HD1	2.31	0.49
7:G:85:TYR:HD1	7:G:154:TYR:CE1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:60:ARG:NH1	8:H:60:ARG:HG3	2.28	0.49
11:K:79:SER:OG	11:K:106:LYS:HG2	2.12	0.49
1:A:1121:U:H2'	1:A:1122:U:C6	2.48	0.49
1:A:1129:C:O2'	1:A:1130:A:OP2	2.24	0.49
1:A:1279:A:O2'	1:A:1282:C:N4	2.46	0.49
1:A:1238:A:N7	1:A:1303:C:H1'	2.28	0.49
1:A:1413:A:O2'	1:A:1414:U:H5'	2.12	0.49
8:H:13:ILE:O	8:H:17:THR:HG23	2.13	0.49
10:J:27:ALA:C	10:J:29:ARG:H	2.15	0.49
16:P:51:VAL:CG1	16:P:51:VAL:O	2.60	0.49
16:P:52:ASP:OD2	16:P:55:ARG:HB2	2.13	0.49
19:S:5:LEU:HD11	19:S:70:LYS:NZ	2.28	0.49
1:A:1070:U:O2'	1:A:1071:C:H5'	2.13	0.48
1:A:1230:C:O2'	1:A:1231:G:H5'	2.13	0.48
1:A:178:C:O2'	1:A:179:A:H5'	2.14	0.48
1:A:624:C:O2'	1:A:625:G:H5'	2.13	0.48
1:A:722:A:H4'	1:A:723:U:C5	2.48	0.48
2:B:97:TRP:CH2	2:B:176:GLU:CD	2.85	0.48
2:B:17:PHE:HA	2:B:44:LEU:HD21	1.95	0.48
7:G:156:TRP:OXT	7:G:156:TRP:CD1	2.66	0.48
12:L:27:LEU:HG	12:L:28:LYS:N	2.25	0.48
13:M:78:ILE:O	13:M:82:MET:HB2	2.12	0.48
1:A:1222:G:OP1	19:S:77:THR:HG21	2.13	0.48
1:A:1369:C:H2'	1:A:1370:G:C8	2.48	0.48
1:A:220:G:O2'	1:A:221:C:H5'	2.12	0.48
2:B:188:ALA:O	2:B:202:PRO:HA	2.13	0.48
2:B:204:ASN:ND2	2:B:206:ASP:H	2.11	0.48
1:A:407:G:H5''	4:D:115:ARG:HB3	1.96	0.48
8:H:103:VAL:CG2	8:H:110:ALA:HB2	2.43	0.48
10:J:38:ILE:HG13	10:J:71:LEU:CB	2.43	0.48
10:J:45:ARG:NH2	14:N:36:PHE:CD2	2.81	0.48
1:A:974:A:OP2	14:N:41:ARG:NH1	2.45	0.48
1:A:1102:A:H2'	1:A:1103:C:H6	1.77	0.48
1:A:1347:G:N7	9:I:10:ARG:NH2	2.61	0.48
1:A:960:U:O2'	1:A:1223:C:H4'	2.13	0.48
2:B:25:ASN:O	2:B:27:LYS:N	2.47	0.48
6:F:48:LEU:HD13	6:F:52:ILE:HG13	1.95	0.48
2:B:178:ARG:NH2	8:H:68:ARG:NH2	2.62	0.48
12:L:28:LYS:O	12:L:29:GLY:C	2.51	0.48
17:Q:12:SER:HB3	17:Q:20:THR:HB	1.95	0.48
1:A:279:A:H5''	1:A:280:C:H3'	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:173:VAL:N	3:C:174:PRO:CD	2.76	0.48
7:G:6:ARG:O	7:G:7:ALA:C	2.52	0.48
12:L:42:THR:CG2	12:L:52:LEU:HB3	2.44	0.48
12:L:83:VAL:HG22	12:L:84:LEU:N	2.28	0.48
17:Q:68:ARG:O	17:Q:69:LYS:HB2	2.13	0.48
18:R:36:ASN:HD22	18:R:38:GLU:HG2	1.79	0.48
18:R:36:ASN:CG	18:R:39:VAL:HG12	2.34	0.48
19:S:39:THR:HG22	19:S:40:ILE:N	2.28	0.48
1:A:1195:C:H2'	1:A:1197:G:H5'	1.96	0.48
1:A:538:G:O2'	1:A:539:A:H5'	2.13	0.48
1:A:954:G:H2'	1:A:955:U:H6	1.78	0.48
4:D:119:GLN:HG2	4:D:123:HIS:CD2	2.47	0.48
10:J:6:ILE:HG23	10:J:98:ILE:HG12	1.94	0.48
12:L:83:VAL:HG21	12:L:100:ILE:HD13	1.95	0.48
17:Q:56:VAL:HG12	17:Q:77:VAL:HB	1.95	0.48
20:T:38:LYS:O	20:T:39:LYS:C	2.51	0.48
1:A:261:U:OP2	20:T:79:ARG:NH2	2.46	0.48
1:A:61:G:H2'	1:A:62:U:O4'	2.13	0.48
1:A:942:G:O2'	1:A:943:U:H5'	2.12	0.48
3:C:138:VAL:O	3:C:142:MET:HB2	2.13	0.48
4:D:57:ARG:NH2	4:D:205:GLU:OE2	2.46	0.48
9:I:23:ASN:ND2	9:I:23:ASN:C	2.66	0.48
9:I:65:VAL:O	9:I:65:VAL:HG13	2.13	0.48
10:J:39:PRO:HA	10:J:70:ARG:HH11	1.78	0.48
10:J:65:LEU:CD2	10:J:65:LEU:O	2.59	0.48
11:K:86:GLY:H	11:K:112:THR:HG23	1.79	0.48
15:O:25:THR:HG21	15:O:70:LEU:HD23	1.94	0.48
1:A:1181:G:H4'	1:A:1184:G:C4'	2.43	0.48
1:A:1329:A:C2'	1:A:1330:U:H5'	2.43	0.48
1:A:337:C:H2'	1:A:338:A:C8	2.49	0.48
1:A:31:G:H1	1:A:48:C:H5''	1.77	0.48
2:B:111:ARG:HB3	2:B:149:LEU:HD11	1.95	0.48
2:B:12:GLU:HG2	2:B:213:LEU:HD11	1.95	0.48
3:C:23:TYR:O	3:C:24:ALA:HB2	2.14	0.48
4:D:6:GLY:O	4:D:7:PRO:C	2.50	0.48
5:E:51:VAL:O	5:E:54:ALA:HB3	2.13	0.48
6:F:46:ARG:HB2	6:F:60:PHE:CE1	2.48	0.48
1:A:1298:C:C5	7:G:114:ARG:HD3	2.48	0.48
1:A:600:C:OP1	8:H:97:VAL:HG12	2.13	0.48
12:L:119:LYS:O	12:L:120:TYR:CB	2.62	0.48
18:R:28:GLU:OE1	18:R:28:GLU:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:47:THR:HA	18:R:83:GLU:HB2	1.96	0.48
1:A:1047:G:H5''	14:N:4:LYS:HD2	1.96	0.48
1:A:1056:U:O2'	1:A:1057:G:H5'	2.14	0.48
1:A:1342:C:O2'	1:A:1343:G:H5'	2.13	0.48
1:A:184:G:H2'	1:A:185:A:H8	1.77	0.48
1:A:555:C:H2'	1:A:556:C:C6	2.48	0.48
1:A:559:A:P	5:E:126:ARG:HH22	2.36	0.48
1:A:780:A:C2	1:A:801:U:C5	3.02	0.48
4:D:111:ALA:HB2	4:D:120:LEU:HD12	1.96	0.48
4:D:36:ARG:N	4:D:37:PRO:CD	2.65	0.48
4:D:3:ARG:O	4:D:5:ILE:HG13	2.13	0.48
5:E:20:GLN:C	5:E:21:ALA:O	2.51	0.48
9:I:111:ARG:NH1	9:I:111:ARG:HG3	2.28	0.48
16:P:6:LEU:HB3	16:P:17:TYR:CD2	2.49	0.48
18:R:39:VAL:HG13	18:R:40:LEU:N	2.28	0.48
19:S:32:LYS:O	19:S:32:LYS:HG3	2.13	0.48
1:A:1127:G:N2	1:A:1147:C:N4	2.62	0.48
1:A:1347:G:H3'	9:I:108:VAL:O	2.14	0.48
1:A:421:U:H5'	1:A:422:C:C5	2.48	0.48
2:B:187:LEU:CD2	2:B:214:ILE:HG13	2.44	0.48
1:A:1256:A:H8	3:C:27:LYS:HZ1	1.60	0.48
3:C:92:ALA:C	3:C:94:LEU:H	2.17	0.48
5:E:148:VAL:O	5:E:152:ARG:HG3	2.14	0.48
6:F:75:LEU:HD13	6:F:75:LEU:C	2.34	0.48
7:G:64:GLN:O	7:G:67:GLU:HB3	2.14	0.48
10:J:94:VAL:HG12	10:J:95:GLU:H	1.76	0.48
17:Q:17:LYS:HA	17:Q:46:ASP:O	2.14	0.48
1:A:620:C:C2	4:D:135:LEU:HD13	2.49	0.48
1:A:731:G:H5'	1:A:766:A:H4'	1.94	0.48
1:A:825:G:H2'	1:A:826:C:H6	1.78	0.48
2:B:230:VAL:HG13	2:B:231:GLU:OE2	2.13	0.48
4:D:200:GLU:OE1	4:D:200:GLU:N	2.46	0.48
9:I:117:HIS:HB2	9:I:121:ARG:HD2	1.95	0.48
11:K:58:PRO:HB2	11:K:93:GLN:HG3	1.95	0.48
12:L:53:ARG:HG2	12:L:93:LEU:HD11	1.95	0.48
18:R:53:ARG:HD3	18:R:63:GLN:HB3	1.95	0.48
1:A:1394:A:C5	1:A:1501:C:H4'	2.49	0.47
1:A:155:C:H2'	1:A:156:G:H8	1.79	0.47
1:A:657:G:O2'	1:A:658:G:H5'	2.13	0.47
1:A:848:C:H2'	1:A:849:C:C6	2.49	0.47
2:B:213:LEU:C	2:B:213:LEU:CD2	2.83	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:174:LEU:O	4:D:175:SER:HB3	2.13	0.47
12:L:110:VAL:O	12:L:122:THR:CG2	2.62	0.47
12:L:53:ARG:HB3	12:L:93:LEU:HD11	1.94	0.47
1:A:1051:C:O2'	1:A:1052:U:H5'	2.13	0.47
1:A:1488:G:H2'	1:A:1489:G:H8	1.77	0.47
1:A:190(I):G:O2'	1:A:190(J):U:H5'	2.14	0.47
1:A:528:C:H5'	1:A:535:A:C6	2.49	0.47
1:A:613:C:O2'	1:A:614:A:H5'	2.14	0.47
1:A:625:G:H2'	1:A:626:U:H6	1.79	0.47
1:A:760:G:O6	17:Q:105:ALA:HB2	2.14	0.47
2:B:23:ARG:HH11	2:B:23:ARG:C	2.16	0.47
3:C:100:ALA:O	3:C:101:LEU:HB2	2.14	0.47
5:E:71:LEU:HD21	5:E:115:VAL:HG22	1.96	0.47
12:L:86:ARG:HG3	12:L:86:ARG:NH1	2.28	0.47
1:A:1057:G:C2'	1:A:1058:G:H5'	2.44	0.47
1:A:513:C:H2'	1:A:514:C:C6	2.49	0.47
3:C:8:ILE:O	3:C:11:ARG:N	2.47	0.47
4:D:43:HIS:CE1	4:D:46:LYS:HZ2	2.31	0.47
12:L:34:ARG:HG3	12:L:34:ARG:O	2.13	0.47
20:T:59:ALA:O	20:T:63:ILE:HG13	2.14	0.47
1:A:1190:G:HO2'	1:A:1191:A:P	2.38	0.47
1:A:1497:G:H2'	1:A:1498:U:C5'	2.42	0.47
1:A:41:G:H2'	1:A:42:G:C8	2.49	0.47
1:A:560:U:H6	1:A:560:U:O5'	1.98	0.47
1:A:666:G:H5'	1:A:726:C:H1'	1.96	0.47
2:B:15:VAL:HG12	2:B:210:SER:HB2	1.97	0.47
9:I:111:ARG:HG3	9:I:111:ARG:HH11	1.80	0.47
19:S:10:PHE:HE2	19:S:12:ASP:OD1	1.97	0.47
1:A:19:C:H2'	1:A:20:U:H6	1.80	0.47
1:A:51:A:H4'	1:A:52:G:C5'	2.45	0.47
2:B:108:ILE:HG22	2:B:108:ILE:O	2.13	0.47
2:B:115:LEU:HD12	2:B:115:LEU:O	2.13	0.47
3:C:35:GLU:O	3:C:38:ARG:N	2.47	0.47
6:F:53:ALA:C	6:F:55:ASP:H	2.18	0.47
7:G:77:SER:O	7:G:156:TRP:HZ3	1.98	0.47
7:G:21:VAL:HG23	7:G:22:LEU:N	2.29	0.47
13:M:39:ILE:CD1	13:M:56:LEU:HG	2.44	0.47
20:T:29:LYS:O	20:T:33:ILE:HG13	2.14	0.47
20:T:42:GLN:NE2	20:T:42:GLN:O	2.47	0.47
20:T:94:ALA:O	20:T:95:ALA:CB	2.63	0.47
1:A:51:A:H4'	1:A:52:G:O5'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:75:LYS:HE3	2:B:78:GLN:OE1	2.14	0.47
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.49	0.47
7:G:54:THR:HG22	7:G:56:GLN:H	1.80	0.47
7:G:75:VAL:CG1	7:G:86:GLN:HE21	2.27	0.47
10:J:27:ALA:HB2	10:J:85:LEU:HD21	1.96	0.47
14:N:12:ARG:O	14:N:13:THR:C	2.52	0.47
14:N:53:LEU:HB3	14:N:56:VAL:CG2	2.45	0.47
1:A:1286:A:H5''	21:V:25:LYS:NZ	2.29	0.47
1:A:435:C:O2'	1:A:436:C:H5'	2.15	0.47
1:A:768:A:H2'	1:A:769:G:O4'	2.14	0.47
1:A:913:A:O2'	1:A:914:A:P	2.73	0.47
1:A:998:G:O2'	1:A:999:C:H5'	2.15	0.47
2:B:53:ARG:NH1	2:B:199:TYR:CD2	2.82	0.47
3:C:131:ARG:HA	3:C:134:ILE:HD12	1.96	0.47
4:D:105:VAL:HG13	4:D:110:PHE:HB2	1.95	0.47
1:A:1292:U:P	7:G:41:ARG:HH22	2.36	0.47
10:J:30:SER:CB	10:J:80:LYS:HB3	2.45	0.47
11:K:72:ALA:HB1	11:K:77:MET:HG3	1.97	0.47
12:L:28:LYS:HD2	12:L:33:ARG:NH1	2.29	0.47
1:A:187:C:N3	20:T:105:SER:HB3	2.30	0.47
21:V:3:LYS:HB3	21:V:14:TRP:CD1	2.50	0.47
1:A:1202:G:O4'	14:N:29:ARG:HD3	2.14	0.47
2:B:16:HIS:CE1	2:B:210:SER:HG	2.33	0.47
2:B:178:ARG:HH22	8:H:68:ARG:NH2	2.12	0.47
3:C:139:GLN:NE2	3:C:139:GLN:CA	2.78	0.47
4:D:24:GLU:CG	4:D:25:ARG:N	2.77	0.47
5:E:127:ASN:O	5:E:128:PRO:C	2.53	0.47
5:E:68:GLU:O	5:E:70:PRO:HD3	2.15	0.47
7:G:46:ALA:O	7:G:50:ILE:HG13	2.15	0.47
1:A:1123:A:O3'	10:J:36:GLY:HA3	2.15	0.47
13:M:49:THR:CG2	13:M:51:ALA:H	2.13	0.47
16:P:43:LYS:HG2	16:P:48:TRP:CE2	2.50	0.47
19:S:15:LEU:O	19:S:19:VAL:N	2.48	0.47
1:A:1194:U:H2'	1:A:1195:C:C6	2.50	0.47
1:A:1286:A:H2'	1:A:1287:A:H4'	1.96	0.47
1:A:1515:C:H2'	1:A:1516:G:C8	2.50	0.47
1:A:180:U:H2'	1:A:181:G:H5'	1.96	0.47
1:A:606:G:H2'	1:A:631:G:N2	2.30	0.47
2:B:215:LEU:O	2:B:216:SER:C	2.52	0.47
3:C:167:TRP:O	3:C:168:ALA:CB	2.63	0.47
7:G:23:VAL:HG12	7:G:27:ILE:CD1	2.41	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:94:VAL:CG1	10:J:95:GLU:N	2.77	0.47
15:O:77:ARG:O	15:O:80:ALA:HB3	2.15	0.47
1:A:1001:A:H2'	1:A:1002:G:H8	1.79	0.47
1:A:1231:G:H4'	9:I:126:SER:OG	2.14	0.47
1:A:1240:U:P	7:G:116:ALA:HB2	2.55	0.47
1:A:1245:A:H2'	1:A:1246:C:C6	2.50	0.47
1:A:1510:U:H2'	1:A:1511:G:C8	2.50	0.47
1:A:190(H):G:O2'	1:A:190(I):G:H5'	2.14	0.47
2:B:18:GLY:CA	2:B:41:ILE:HA	2.44	0.47
3:C:79:ARG:HG2	3:C:82:GLU:CG	2.45	0.47
4:D:162:LEU:HD13	4:D:181:MET:CG	2.42	0.47
5:E:92:LYS:O	5:E:118:ILE:HG23	2.15	0.47
6:F:2:ARG:NE	6:F:69:GLU:HG2	2.29	0.47
9:I:48:GLU:N	9:I:49:PRO:CD	2.77	0.47
1:A:1367:C:H4'	10:J:48:THR:HG21	1.97	0.47
11:K:110:ASP:OD2	18:R:88:LYS:NZ	2.45	0.47
12:L:54:LYS:N	12:L:54:LYS:HD2	2.30	0.47
17:Q:96:GLN:O	17:Q:96:GLN:CD	2.54	0.47
20:T:50:GLU:HG3	20:T:99:LEU:CD1	2.45	0.47
1:A:1326:C:H5''	21:V:12:LYS:NZ	2.30	0.47
1:A:1051:C:H2'	1:A:1052:U:H6	1.80	0.47
1:A:1262:C:H2'	1:A:1263:C:H6	1.79	0.47
1:A:926:G:H2'	1:A:1505:G:N3	2.30	0.47
1:A:184:G:C4'	1:A:224:C:H4'	2.44	0.47
1:A:517:G:H5'	1:A:519:C:C2	2.50	0.47
1:A:633:G:H2'	1:A:634:C:C6	2.49	0.47
1:A:1232:U:H5''	9:I:124:GLN:O	2.14	0.47
10:J:22:LYS:HE2	10:J:90:LEU:HB2	1.97	0.47
11:K:80:VAL:HG21	11:K:103:LEU:HD13	1.97	0.47
13:M:82:MET:CE	13:M:92:HIS:HB3	2.44	0.47
19:S:15:LEU:HD12	19:S:16:LEU:H	1.77	0.47
1:A:1004:A:N6	1:A:1035:A:H62	2.13	0.46
1:A:321:A:O2'	1:A:322:C:H5'	2.15	0.46
2:B:50:GLU:HB3	2:B:200:ILE:O	2.15	0.46
3:C:64:VAL:CG2	3:C:99:VAL:HB	2.45	0.46
5:E:107:ARG:HG2	5:E:108:ALA:N	2.29	0.46
6:F:2:ARG:HD2	6:F:69:GLU:HG2	1.96	0.46
17:Q:66:SER:OG	17:Q:69:LYS:HB3	2.15	0.46
17:Q:97:SER:O	17:Q:98:LEU:C	2.54	0.46
1:A:1320:C:H2'	1:A:1321:C:O4'	2.16	0.46
1:A:1481:U:H2'	1:A:1482:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1392:G:H21	1:A:1502:A:H8	1.61	0.46
1:A:190(L):U:N3	20:T:105:SER:OG	2.45	0.46
1:A:542:G:H2'	1:A:543:C:H6	1.80	0.46
1:A:781:A:H2'	1:A:782:A:H5'	1.98	0.46
1:A:952:U:O2'	1:A:953:G:H5'	2.14	0.46
3:C:130:VAL:CG2	3:C:157:ILE:HG23	2.41	0.46
3:C:173:VAL:HG12	3:C:173:VAL:O	2.14	0.46
5:E:18:ARG:HG2	5:E:19:MET:H	1.81	0.46
12:L:82:VAL:O	12:L:106:ASP:HB2	2.15	0.46
13:M:97:PRO:HB2	13:M:101:GLN:OE1	2.14	0.46
15:O:66:LEU:O	15:O:69:TYR:HB3	2.15	0.46
6:F:50:TYR:CE1	18:R:77:GLY:HA2	2.49	0.46
1:A:1238:A:H5'	1:A:1336:C:N4	2.29	0.46
1:A:1442:G:N2	1:A:1446:A:C8	2.80	0.46
1:A:458:C:H2'	1:A:459:G:H8	1.80	0.46
1:A:5:U:O2'	1:A:6:G:P	2.73	0.46
2:B:15:VAL:CG1	2:B:209:ARG:HG3	2.46	0.46
3:C:154:SER:OG	3:C:155:GLY:N	2.48	0.46
3:C:167:TRP:HB3	3:C:168:ALA:H	1.32	0.46
4:D:111:ALA:HB1	4:D:116:GLN:HB3	1.96	0.46
4:D:87:GLY:O	4:D:88:VAL:C	2.53	0.46
5:E:144:THR:C	5:E:146:ALA:N	2.67	0.46
7:G:15:ASP:O	7:G:19:GLY:HA2	2.16	0.46
9:I:33:PHE:CE2	9:I:47:LEU:HD11	2.51	0.46
12:L:77:LEU:HD21	12:L:107:ALA:HB2	1.97	0.46
12:L:59:ARG:NH1	12:L:65:GLU:HG2	2.31	0.46
13:M:62:ASN:O	13:M:63:THR:HB	2.16	0.46
1:A:1367:C:H5'	10:J:60:ARG:NH1	2.31	0.46
1:A:1496:C:H2'	1:A:1497:G:O4'	2.16	0.46
1:A:41:G:H2'	1:A:42:G:H8	1.80	0.46
1:A:624:C:H2'	1:A:625:G:H8	1.81	0.46
1:A:934:C:C4	1:A:1345:U:C5	3.04	0.46
1:A:976:G:C8	1:A:1358:U:C2	3.04	0.46
2:B:129:GLU:O	2:B:130:ARG:HB2	2.15	0.46
2:B:42:ILE:HD12	2:B:203:GLY:HA2	1.97	0.46
4:D:39:PRO:HG2	4:D:44:GLY:HA2	1.97	0.46
11:K:34:ASP:O	11:K:36:ASP:N	2.48	0.46
11:K:50:TYR:HD1	11:K:60:ALA:HB2	1.80	0.46
12:L:37:CYS:O	12:L:79:GLU:O	2.34	0.46
13:M:46:LYS:HG3	13:M:47:ASP:N	2.30	0.46
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:36:ASN:ND2	18:R:38:GLU:HG2	2.29	0.46
2:B:83:MET:HG3	2:B:238:LEU:CD1	2.46	0.46
4:D:162:LEU:HD13	4:D:181:MET:CE	2.46	0.46
7:G:154:TYR:O	7:G:156:TRP:N	2.49	0.46
8:H:92:ARG:HG2	8:H:94:TYR:OH	2.16	0.46
10:J:24:VAL:CG1	10:J:28:ARG:HE	2.29	0.46
10:J:96:ILE:CG2	10:J:97:GLU:H	2.25	0.46
18:R:59:SER:OG	18:R:62:GLU:HG3	2.15	0.46
1:A:103:C:OP2	20:T:17:ARG:NH1	2.48	0.46
1:A:1277:C:C2'	1:A:1278:U:H5'	2.46	0.46
1:A:1301:U:O2'	1:A:1302:U:P	2.74	0.46
1:A:132:C:O2'	1:A:133:U:H5'	2.15	0.46
1:A:377:G:P	16:P:3:LYS:HZ2	2.39	0.46
1:A:390:C:O5'	1:A:390:C:H6	1.99	0.46
1:A:743:U:H2'	1:A:744:C:H6	1.79	0.46
1:A:834:C:H2'	1:A:835:U:H6	1.79	0.46
1:A:828:A:H5''	1:A:859:A:C2	2.51	0.46
1:A:951:G:O2'	1:A:952:U:H5'	2.15	0.46
3:C:164:ARG:HB3	3:C:164:ARG:HH11	1.80	0.46
3:C:21:ARG:NH2	3:C:56:ASP:OD2	2.48	0.46
5:E:33:VAL:HG11	5:E:109:ILE:HA	1.96	0.46
7:G:135:VAL:O	7:G:139:GLU:HG3	2.15	0.46
7:G:20:ASP:OD1	7:G:22:LEU:HB3	2.15	0.46
11:K:16:SER:O	11:K:35:PRO:HD3	2.16	0.46
11:K:59:TYR:O	11:K:62:GLN:HB3	2.15	0.46
1:A:707:C:OP1	11:K:85:ARG:NH1	2.49	0.46
12:L:38:THR:HG22	12:L:39:VAL:HG23	1.97	0.46
13:M:5:ALA:O	13:M:8:GLU:N	2.45	0.46
10:J:49:VAL:CG1	14:N:41:ARG:HB2	2.38	0.46
1:A:279:A:C6	17:Q:98:LEU:HD13	2.51	0.46
19:S:18:LYS:HG2	19:S:18:LYS:O	2.16	0.46
19:S:22:LEU:CD1	19:S:31:ILE:HD11	2.46	0.46
20:T:67:ALA:O	20:T:73:HIS:ND1	2.47	0.46
1:A:1044:A:O2'	1:A:1045:C:H5'	2.15	0.46
1:A:1152:A:O2'	1:A:1153:C:H5'	2.16	0.46
1:A:1171:G:H2'	1:A:1172:C:C6	2.51	0.46
1:A:1474:G:O2'	1:A:1475:G:H5'	2.15	0.46
1:A:1394:A:C6	1:A:1501:C:H4'	2.50	0.46
2:B:97:TRP:CH2	2:B:176:GLU:OE2	2.69	0.46
2:B:178:ARG:NH1	2:B:178:ARG:CG	2.67	0.46
2:B:32:ILE:HG21	2:B:40:HIS:HD2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:173:TRP:CD2	4:D:189:PRO:HB3	2.51	0.46
7:G:107:ALA:O	7:G:110:GLN:HB2	2.16	0.46
8:H:6:ILE:HD12	8:H:35:ILE:HD12	1.97	0.46
10:J:53:PRO:O	10:J:54:PHE:O	2.34	0.46
10:J:48:THR:OG1	10:J:62:HIS:CD2	2.69	0.46
11:K:84:VAL:HG23	11:K:109:VAL:O	2.16	0.46
11:K:54:ARG:H	11:K:54:ARG:HG2	1.47	0.46
12:L:46:LYS:O	12:L:47:LYS:C	2.54	0.46
12:L:60:LEU:HD21	12:L:66:VAL:HG22	1.97	0.46
16:P:20:VAL:CG1	16:P:21:VAL:N	2.76	0.46
21:V:2:GLY:O	21:V:4:GLY:N	2.49	0.46
1:A:1300:G:O2'	1:A:1301:U:P	2.73	0.46
1:A:1238:A:OP1	1:A:1336:C:H5	1.98	0.46
1:A:160:A:H1'	1:A:344:A:N7	2.31	0.46
1:A:129(A):G:O2'	1:A:190(E):U:H5''	2.16	0.46
1:A:92:C:O2'	1:A:93:G:H5'	2.15	0.46
3:C:129:ALA:HB3	3:C:132:ARG:CD	2.45	0.46
3:C:174:PRO:O	3:C:177:THR:HG22	2.15	0.46
3:C:23:TYR:CG	3:C:24:ALA:N	2.84	0.46
5:E:121:LYS:HE3	5:E:123:LEU:CD2	2.46	0.46
8:H:23:SER:OG	8:H:60:ARG:HD2	2.15	0.46
9:I:50:LEU:C	9:I:52:ALA:N	2.69	0.46
12:L:46:LYS:CG	12:L:47:LYS:H	2.29	0.46
14:N:12:ARG:O	14:N:14:PRO:HD3	2.16	0.46
10:J:62:HIS:CB	14:N:59:ALA:HB3	2.45	0.46
1:A:1049:U:H4'	1:A:1050:G:OP2	2.16	0.46
1:A:1049:U:H1'	1:A:1201:A:N7	2.31	0.46
1:A:1221:G:O2'	1:A:1222:G:H5'	2.15	0.46
1:A:1237:C:H2'	1:A:1336:C:C5	2.51	0.46
1:A:458:C:H2'	1:A:459:G:O4'	2.16	0.46
1:A:518:C:H5''	1:A:519:C:H6	1.78	0.46
1:A:70:G:H2'	1:A:73:C:C6	2.51	0.46
2:B:22:LYS:O	2:B:23:ARG:HG3	2.16	0.46
2:B:78:GLN:O	2:B:94:ASN:OD1	2.33	0.46
4:D:152:SER:HA	4:D:155:LEU:HG	1.97	0.46
6:F:44:GLY:HA2	6:F:59:TYR:CE1	2.51	0.46
9:I:97:LYS:HG3	9:I:102:LEU:HD12	1.96	0.46
10:J:22:LYS:HZ3	10:J:91:PRO:HD3	1.81	0.46
12:L:48:PRO:CG	12:L:49:ASN:H	2.25	0.46
12:L:71:PRO:O	12:L:102:ARG:HD2	2.16	0.46
13:M:37:THR:HG23	13:M:55:ARG:CB	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:63:ILE:HG23	20:T:72:LEU:CD1	2.46	0.46
21:V:2:GLY:C	21:V:4:GLY:N	2.69	0.46
1:A:1158:C:N3	1:A:1181:G:N2	2.61	0.46
1:A:1390:U:H2'	1:A:1391:U:C6	2.51	0.46
1:A:1461:G:O2'	1:A:1462:G:H5'	2.16	0.46
1:A:1515:C:H2'	1:A:1516:G:H8	1.81	0.46
1:A:151:A:H2'	1:A:152:A:O4'	2.15	0.46
1:A:690:G:H2'	1:A:691:G:O4'	2.15	0.46
1:A:947:G:H2'	1:A:948:C:O4'	2.15	0.46
4:D:29:PRO:C	4:D:30:LYS:HG3	2.35	0.46
6:F:19:LEU:HD23	6:F:19:LEU:C	2.36	0.46
8:H:116:LYS:NZ	8:H:127:LEU:HD12	2.31	0.46
9:I:48:GLU:OE1	9:I:48:GLU:HA	2.16	0.46
11:K:93:GLN:HE21	11:K:96:ARG:NH2	2.13	0.46
1:A:1039:C:O2'	1:A:1040:U:H5'	2.16	0.45
1:A:1225:A:H5'	1:A:1226:C:OP2	2.16	0.45
1:A:1230:C:H2'	1:A:1231:G:H8	1.81	0.45
1:A:1256:A:O2'	1:A:1257:U:P	2.74	0.45
1:A:1296:C:H4'	1:A:1302:U:C5	2.51	0.45
1:A:1515:C:O2'	1:A:1516:G:H5'	2.16	0.45
1:A:421:U:H5'	1:A:422:C:H5	1.80	0.45
1:A:877:C:H5''	8:H:88:LYS:HD3	1.97	0.45
2:B:52:GLU:O	2:B:56:ARG:HB2	2.17	0.45
3:C:131:ARG:O	3:C:135:LYS:HG3	2.16	0.45
4:D:145:GLU:HG2	4:D:184:LYS:HE2	1.96	0.45
5:E:15:ARG:NE	5:E:26:PHE:CD2	2.84	0.45
5:E:21:ALA:C	5:E:23:GLY:H	2.19	0.45
8:H:45:ILE:HG13	8:H:45:ILE:O	2.16	0.45
1:A:1230:C:O2'	13:M:126:LYS:HA	2.16	0.45
16:P:72:ARG:O	16:P:72:ARG:HG2	2.16	0.45
1:A:1131:G:H2'	1:A:1132:C:C6	2.51	0.45
1:A:1202:G:C2'	1:A:1203:C:H5'	2.46	0.45
1:A:1532:U:H6	1:A:1532:U:O5'	1.99	0.45
1:A:242:C:H2'	1:A:243:A:H5'	1.98	0.45
1:A:513:C:H2'	1:A:514:C:H6	1.80	0.45
1:A:58:C:O2'	1:A:59:A:H5'	2.16	0.45
1:A:909:A:H2'	1:A:910:C:O4'	2.16	0.45
3:C:157:ILE:HD11	3:C:166:GLU:HB2	1.97	0.45
7:G:75:VAL:HG12	7:G:86:GLN:HE21	1.82	0.45
9:I:112:LYS:HD3	9:I:112:LYS:C	2.37	0.45
1:A:1250:A:H4'	9:I:68:GLY:CA	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:59:TYR:O	13:M:63:THR:HB	2.16	0.45
14:N:21:TYR:HE2	14:N:23:ARG:HE	1.63	0.45
14:N:39:LEU:CD1	14:N:47:LEU:HD12	2.46	0.45
17:Q:80:GLY:O	17:Q:81:ARG:HB3	2.15	0.45
6:F:101:ALA:HB2	18:R:28:GLU:HB3	1.97	0.45
1:A:1196:U:H4'	1:A:1197:G:OP2	2.15	0.45
1:A:1305:G:N2	1:A:1331:G:C2'	2.79	0.45
1:A:652:U:O4	1:A:752:G:O2'	2.28	0.45
1:A:882:C:O2'	1:A:883:C:H5'	2.16	0.45
1:A:975:A:H4'	1:A:976:G:OP2	2.16	0.45
2:B:142:LEU:HB3	2:B:146:GLN:HE22	1.80	0.45
2:B:19:HIS:HD2	2:B:189:ASP:OD2	1.99	0.45
3:C:99:VAL:CG2	3:C:100:ALA:N	2.80	0.45
4:D:121:VAL:O	4:D:134:ASP:HA	2.16	0.45
5:E:15:ARG:CD	5:E:26:PHE:CD2	2.99	0.45
5:E:35:GLY:HA3	5:E:112:LEU:HB3	1.97	0.45
10:J:4:ILE:HG12	10:J:100:THR:CB	2.47	0.45
10:J:51:ARG:HG3	10:J:60:ARG:O	2.17	0.45
10:J:8:LEU:HD12	10:J:20:ALA:HB2	1.97	0.45
11:K:40:ILE:HG23	11:K:75:TYR:CE2	2.51	0.45
13:M:51:ALA:O	13:M:55:ARG:HG3	2.16	0.45
13:M:49:THR:O	13:M:53:VAL:HG23	2.16	0.45
14:N:26:ARG:NH1	14:N:47:LEU:HD21	2.32	0.45
1:A:1318:A:H4'	19:S:10:PHE:CD1	2.51	0.45
1:A:1216:G:H5''	14:N:5:ALA:HB2	1.99	0.45
1:A:1309:G:N7	13:M:99:ARG:NH2	2.61	0.45
1:A:1435:G:H2'	1:A:1436:U:H6	1.69	0.45
1:A:190(B):C:H2'	1:A:190(C):C:O4'	2.17	0.45
1:A:808:C:OP2	15:O:48:LYS:HE2	2.17	0.45
1:A:920:U:H2'	1:A:921:U:C6	2.51	0.45
1:A:975:A:H4'	1:A:976:G:H5'	1.97	0.45
4:D:4:TYR:O	4:D:5:ILE:HB	2.17	0.45
4:D:78:LEU:HA	4:D:78:LEU:HD23	1.78	0.45
5:E:115:VAL:HG11	5:E:118:ILE:CD1	2.46	0.45
5:E:102:ALA:HB2	5:E:120:THR:CB	2.46	0.45
9:I:120:ARG:O	9:I:121:ARG:C	2.54	0.45
9:I:85:LEU:O	9:I:92:TYR:CD1	2.69	0.45
19:S:63:THR:HG22	19:S:64:GLU:N	2.32	0.45
1:A:1044:A:H2'	1:A:1045:C:C4'	2.46	0.45
1:A:113:G:H1'	1:A:354:G:C5'	2.46	0.45
1:A:1501:C:OP2	1:A:1504:G:H2'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:G:O2'	1:A:261:U:H5'	2.16	0.45
1:A:686:U:O4	1:A:703:G:H1'	2.17	0.45
1:A:848:C:H2'	1:A:849:C:H6	1.80	0.45
2:B:223:ILE:HG21	2:B:230:VAL:HG23	1.99	0.45
6:F:33:TYR:HB2	6:F:75:LEU:HD23	1.98	0.45
7:G:77:SER:O	7:G:156:TRP:CZ3	2.69	0.45
9:I:19:LEU:C	9:I:20:ARG:HG3	2.37	0.45
10:J:54:PHE:O	10:J:55:LYS:HG2	2.17	0.45
13:M:84:ILE:C	13:M:86:CYS:N	2.70	0.45
18:R:74:ARG:HB3	18:R:81:PHE:CE1	2.51	0.45
19:S:20:LEU:O	19:S:23:ASN:HB2	2.15	0.45
1:A:1019:C:O2'	1:A:1020:U:H5'	2.17	0.45
1:A:1489:G:H2'	1:A:1490:C:C5'	2.27	0.45
1:A:255:G:H1'	17:Q:16:GLN:HE21	1.77	0.45
1:A:28:G:O2'	1:A:296:U:OP1	2.33	0.45
1:A:439:A:C4	1:A:497:A:C2	3.04	0.45
1:A:533:A:O2'	1:A:534:U:P	2.75	0.45
1:A:797:C:OP1	11:K:124:LYS:HG3	2.17	0.45
1:A:826:C:H2'	1:A:827:U:H6	1.82	0.45
2:B:137:ARG:O	2:B:140:HIS:HB2	2.16	0.45
2:B:23:ARG:CZ	2:B:23:ARG:HB2	2.47	0.45
2:B:69:LEU:C	2:B:69:LEU:HD23	2.36	0.45
2:B:71:VAL:HB	2:B:164:VAL:HG23	1.99	0.45
4:D:142:PRO:HG2	4:D:187:ARG:NH1	2.32	0.45
5:E:102:ALA:HB2	5:E:120:THR:HB	1.97	0.45
9:I:121:ARG:HH11	9:I:121:ARG:HG2	1.81	0.45
14:N:25:VAL:HG13	14:N:25:VAL:O	2.16	0.45
18:R:58:LEU:HD22	18:R:62:GLU:HB3	1.99	0.45
19:S:67:VAL:O	19:S:69:HIS:N	2.49	0.45
20:T:42:GLN:O	20:T:45:GLN:HB3	2.16	0.45
1:A:1044:A:H2'	1:A:1045:C:O4'	2.17	0.45
1:A:1331:G:O2'	1:A:1332:A:OP2	2.31	0.45
1:A:976:G:C8	1:A:1358:U:O2	2.70	0.45
1:A:319:G:O2'	1:A:320:C:H5'	2.16	0.45
1:A:474:G:O2'	1:A:475:G:H5'	2.16	0.45
1:A:627:G:O2'	1:A:628:G:H5'	2.17	0.45
1:A:820:U:H4'	1:A:821:G:OP2	2.15	0.45
3:C:108:ASN:OD1	3:C:110:ASN:HB2	2.16	0.45
7:G:38:LEU:HD11	7:G:42:ILE:HD11	1.99	0.45
9:I:36:TYR:CD2	9:I:37:PHE:CE2	3.04	0.45
12:L:117:ARG:HD2	12:L:122:THR:OG1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:12:ARG:O	14:N:14:PRO:CD	2.65	0.45
18:R:47:THR:HG22	18:R:48:GLY:H	1.79	0.45
1:A:1108:G:H4'	1:A:1191:A:O4'	2.17	0.45
1:A:1206:G:C6	1:A:1207:G:C5	3.05	0.45
1:A:1300:G:O2'	1:A:1301:U:H6	1.98	0.45
1:A:197:A:H1'	1:A:198:G:O4'	2.17	0.45
1:A:258:G:H2'	1:A:259:G:H8	1.82	0.45
1:A:645:C:O2'	1:A:646:U:H5'	2.16	0.45
1:A:75:G:O2'	1:A:76:C:H5'	2.17	0.45
1:A:22:G:H4'	1:A:885:G:C8	2.51	0.45
2:B:100:GLY:O	2:B:104:ASN:N	2.44	0.45
1:A:1060:C:C4	3:C:2:GLY:HA3	2.52	0.45
3:C:60:ALA:O	3:C:61:ALA:CB	2.63	0.45
4:D:3:ARG:NE	4:D:71:SER:HB3	2.31	0.45
5:E:45:PHE:CD2	5:E:47:LYS:HE3	2.52	0.45
7:G:18:TYR:CD2	7:G:59:LEU:HB2	2.52	0.45
9:I:40:LEU:O	9:I:42:ARG:N	2.50	0.45
13:M:9:ILE:N	13:M:9:ILE:HD12	2.32	0.45
17:Q:104:LYS:HB3	17:Q:105:ALA:H	1.48	0.45
1:A:1450:U:H2'	1:A:1452:C:C5	2.52	0.45
1:A:411:A:C6	1:A:429:U:C4	3.04	0.45
1:A:452:A:O2'	1:A:453:A:O4'	2.34	0.45
1:A:735:C:O2'	1:A:736:C:H5'	2.17	0.45
2:B:25:ASN:HD22	2:B:27:LYS:H	1.65	0.45
3:C:113:ALA:N	3:C:114:PRO:CD	2.80	0.45
7:G:12:LEU:N	7:G:12:LEU:HD12	2.32	0.45
2:B:178:ARG:NH2	8:H:68:ARG:HH22	2.14	0.45
10:J:27:ALA:CB	10:J:81:THR:HG23	2.47	0.45
10:J:30:SER:CB	10:J:84:GLN:HE21	2.29	0.45
12:L:85:ILE:HG23	12:L:98:TYR:CB	2.46	0.45
14:N:29:ARG:HB3	14:N:40:CYS:HB3	1.99	0.45
17:Q:18:THR:HG23	17:Q:69:LYS:CE	2.47	0.45
17:Q:81:ARG:O	17:Q:81:ARG:HG3	2.17	0.45
18:R:70:ILE:O	18:R:74:ARG:HG3	2.17	0.45
1:A:1254:C:OP1	10:J:45:ARG:HD3	2.17	0.45
1:A:1353:G:H2'	1:A:1354:C:H6	1.82	0.45
1:A:1484:C:H2'	1:A:1485:U:C6	2.49	0.45
1:A:173:U:H5''	1:A:197:A:H5'	1.99	0.45
1:A:403:C:H2'	1:A:404:U:H6	1.81	0.45
1:A:485:G:C2'	1:A:486:U:OP2	2.65	0.45
1:A:509:A:H5''	4:D:55:ALA:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:583:A:H2'	1:A:584:G:O4'	2.17	0.45
1:A:600:C:O2'	1:A:601:C:H5'	2.17	0.45
1:A:718:G:H4'	11:K:117:ASN:HD21	1.81	0.45
2:B:92:TYR:CE1	2:B:151:GLY:HA3	2.51	0.45
3:C:123:GLN:HE22	3:C:140:ARG:HH22	1.65	0.45
11:K:74:ALA:C	11:K:76:GLY:N	2.69	0.45
13:M:80:ARG:C	13:M:82:MET:H	2.20	0.45
15:O:48:LYS:O	15:O:50:HIS:N	2.50	0.45
1:A:188:C:C4'	20:T:89:ARG:NH1	2.80	0.45
1:A:1005:A:H2'	1:A:1006:C:O4'	2.17	0.44
1:A:1074:G:O3'	2:B:103:THR:CG2	2.65	0.44
1:A:1305:G:N2	1:A:1331:G:HO2'	2.15	0.44
1:A:1347:G:C5	9:I:107:ARG:NH1	2.85	0.44
1:A:45:U:H2'	1:A:46:G:C8	2.53	0.44
3:C:188:LEU:O	3:C:189:ALA:CB	2.59	0.44
5:E:13:ILE:HG22	5:E:30:ALA:HB2	1.99	0.44
11:K:23:ALA:HB2	11:K:91:ARG:HB2	1.99	0.44
13:M:110:ARG:HG2	13:M:110:ARG:HH11	1.82	0.44
16:P:20:VAL:CG1	16:P:32:TYR:CB	2.95	0.44
16:P:55:ARG:O	16:P:58:TYR:HB3	2.17	0.44
1:A:1266:G:N2	1:A:1269:A:OP2	2.49	0.44
1:A:1372:U:O2'	1:A:1373:G:H5'	2.18	0.44
1:A:1503:A:O2'	1:A:1504:G:P	2.75	0.44
1:A:384:G:H2'	1:A:385:C:C6	2.53	0.44
1:A:662:G:H2'	1:A:663:A:H8	1.79	0.44
3:C:28:GLN:O	3:C:31:HIS:N	2.46	0.44
4:D:8:VAL:HG21	4:D:115:ARG:CZ	2.46	0.44
5:E:80:ILE:CD1	5:E:91:LEU:HD12	2.46	0.44
7:G:143:ARG:O	7:G:145:ALA:O	2.34	0.44
10:J:68:HIS:CD2	10:J:68:HIS:N	2.85	0.44
13:M:84:ILE:HG13	13:M:86:CYS:HB2	2.00	0.44
1:A:981:U:H5'	14:N:21:TYR:CE1	2.53	0.44
14:N:23:ARG:HD3	14:N:30:ALA:HB2	1.99	0.44
15:O:87:ILE:CG2	15:O:88:ARG:N	2.80	0.44
13:M:84:ILE:HG21	19:S:65:ASN:HD22	1.81	0.44
1:A:1097:C:H2'	1:A:1098:C:H6	1.82	0.44
1:A:1263:C:H2'	1:A:1264:C:H6	1.83	0.44
1:A:792:A:H1'	1:A:794:A:N7	2.31	0.44
1:A:691:G:O2'	1:A:797:C:H4'	2.17	0.44
1:A:865:A:H2'	1:A:866:C:C6	2.53	0.44
1:A:950:U:H2'	1:A:951:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:11:ARG:NH1	3:C:177:THR:O	2.50	0.44
5:E:119:LEU:HD23	5:E:119:LEU:HA	1.84	0.44
6:F:40:VAL:CG2	6:F:41:GLU:N	2.80	0.44
9:I:103:THR:HG22	9:I:104:ARG:N	2.31	0.44
10:J:8:LEU:CD1	10:J:20:ALA:HB2	2.48	0.44
10:J:46:ARG:NH1	10:J:64:GLU:CG	2.80	0.44
10:J:85:LEU:O	10:J:87:THR:N	2.50	0.44
16:P:20:VAL:HG13	16:P:21:VAL:N	2.32	0.44
16:P:43:LYS:HA	16:P:48:TRP:HB3	2.00	0.44
20:T:24:LEU:O	20:T:24:LEU:HD12	2.17	0.44
1:A:1289:A:H2'	1:A:1290:G:H5'	2.00	0.44
1:A:1299:A:C8	1:A:1301:U:H1'	2.53	0.44
1:A:129(A):G:C2	1:A:190(E):U:H5'	2.52	0.44
1:A:644:G:O2'	1:A:645:C:H5'	2.17	0.44
1:A:807:A:H2'	1:A:808:C:C6	2.52	0.44
1:A:975:A:O5'	1:A:976:G:H5'	2.17	0.44
2:B:54:THR:O	2:B:57:PHE:HB3	2.18	0.44
3:C:107:GLN:N	3:C:107:GLN:CD	2.64	0.44
3:C:6:HIS:CD2	3:C:8:ILE:H	2.36	0.44
9:I:46:ALA:O	9:I:49:PRO:HD2	2.17	0.44
10:J:3:LYS:CA	10:J:75:ILE:HA	2.48	0.44
12:L:111:LYS:O	12:L:112:ASP:HB2	2.18	0.44
14:N:9:LYS:HG3	14:N:21:TYR:O	2.17	0.44
17:Q:104:LYS:O	17:Q:105:ALA:CB	2.65	0.44
17:Q:68:ARG:H	17:Q:70:ARG:NH1	2.15	0.44
19:S:31:ILE:CG2	19:S:32:LYS:N	2.70	0.44
20:T:100:ILE:O	20:T:102:GLY:N	2.50	0.44
20:T:30:LYS:O	20:T:33:ILE:HB	2.18	0.44
1:A:1319:A:H5''	19:S:5:LEU:HD21	1.98	0.44
1:A:389:A:H2'	1:A:390:C:C5'	2.48	0.44
1:A:393:A:C2'	1:A:394:G:H5'	2.47	0.44
1:A:460:A:N7	1:A:462:G:C6	2.85	0.44
1:A:663:A:H5''	18:R:61:LYS:HE3	1.99	0.44
3:C:179:ARG:C	3:C:179:ARG:HD2	2.37	0.44
4:D:24:GLU:CG	4:D:25:ARG:H	2.31	0.44
10:J:72:VAL:O	10:J:73:ASP:HB2	2.18	0.44
11:K:51:LYS:O	11:K:55:LYS:CE	2.65	0.44
13:M:34:LEU:HD13	13:M:41:PRO:CA	2.45	0.44
13:M:39:ILE:HD12	13:M:56:LEU:HG	1.98	0.44
20:T:42:GLN:HA	20:T:45:GLN:HB2	1.99	0.44
1:A:1279:A:O2'	1:A:1281:U:OP2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1391:U:H2'	1:A:1392:G:H8	1.74	0.44
1:A:321:A:H2'	1:A:322:C:C6	2.52	0.44
1:A:50:A:N6	1:A:361:G:H4'	2.33	0.44
1:A:532:A:H2'	1:A:533:A:C5'	2.48	0.44
1:A:962:C:H2'	1:A:963:G:O4'	2.18	0.44
2:B:213:LEU:HD23	2:B:213:LEU:C	2.37	0.44
3:C:12:LEU:HD23	3:C:12:LEU:HA	1.76	0.44
7:G:95:ARG:CG	7:G:95:ARG:NH1	2.80	0.44
10:J:6:ILE:O	10:J:71:LEU:O	2.35	0.44
10:J:30:SER:HB3	10:J:84:GLN:NE2	2.31	0.44
13:M:110:ARG:HH11	13:M:110:ARG:CG	2.31	0.44
18:R:25:THR:HG22	18:R:25:THR:O	2.17	0.44
1:A:1010:G:O2'	1:A:1011:G:H5'	2.18	0.44
1:A:1095:U:H2'	1:A:1096:C:H6	1.83	0.44
1:A:927:G:H4'	1:A:1503:A:N7	2.32	0.44
4:D:8:VAL:HG11	4:D:21:LEU:CB	2.47	0.44
1:A:1178:G:P	9:I:97:LYS:HZ2	2.40	0.44
11:K:95:ILE:HD13	11:K:108:ILE:HG21	1.99	0.44
13:M:120:LYS:HE2	13:M:123:ALA:CB	2.47	0.44
20:T:63:ILE:HD13	20:T:80:ARG:CB	2.48	0.44
1:A:1152:A:H2'	1:A:1153:C:H6	1.83	0.44
1:A:116:A:H2'	1:A:117:G:O4'	2.17	0.44
1:A:1440:C:H2'	1:A:1441:G:C5'	2.48	0.44
1:A:397:A:N3	1:A:397:A:H3'	2.32	0.44
1:A:540:G:H2'	1:A:541:G:O4'	2.18	0.44
1:A:755:G:OP2	15:O:65:ARG:HD2	2.17	0.44
4:D:196:LEU:C	4:D:198:VAL:H	2.21	0.44
5:E:36:ASP:OD2	5:E:40:ARG:HD3	2.18	0.44
8:H:103:VAL:HG21	8:H:109:ILE:O	2.18	0.44
8:H:73:ASP:OD2	8:H:75:ARG:HB2	2.18	0.44
8:H:7:ALA:HB2	8:H:85:ARG:HD2	1.99	0.44
9:I:93:ARG:CD	9:I:97:LYS:HE3	2.47	0.44
16:P:6:LEU:HB3	16:P:17:TYR:HD2	1.81	0.44
16:P:39:TYR:CZ	16:P:41:PRO:HA	2.52	0.44
20:T:72:LEU:O	20:T:73:HIS:O	2.35	0.44
1:A:1231:G:OP1	9:I:127:LYS:NZ	2.50	0.44
1:A:1314:C:OP2	19:S:6:LYS:CD	2.66	0.44
1:A:1288:A:O4'	1:A:1353:G:H4'	2.18	0.44
1:A:582:U:O4'	17:Q:105:ALA:HA	2.17	0.44
1:A:665:A:H2'	1:A:725:G:N2	2.33	0.44
1:A:953:G:H1'	13:M:125:ARG:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:188:LEU:HD22	3:C:188:LEU:HA	1.79	0.44
4:D:31:CYS:C	4:D:33:MET:H	2.21	0.44
5:E:78:HIS:HD2	8:H:107:LEU:HD12	1.83	0.44
6:F:22:GLU:OE2	6:F:84:ASN:HB2	2.18	0.44
10:J:75:ILE:HG22	10:J:76:ASN:N	2.32	0.44
12:L:70:ILE:CD1	12:L:77:LEU:HD12	2.42	0.44
15:O:29:VAL:HG11	15:O:67:LEU:HD21	2.00	0.44
1:A:1131:G:H2'	1:A:1132:C:H6	1.82	0.43
1:A:1229:A:H2'	1:A:1230:C:H6	1.83	0.43
1:A:1314:C:H2'	1:A:1315:U:C6	2.53	0.43
1:A:1533:C:O2	1:A:1533:C:H2'	2.17	0.43
1:A:677:U:O2	1:A:777:A:O2'	2.33	0.43
1:A:80:G:C2'	1:A:81:U:H5''	2.48	0.43
3:C:79:ARG:C	3:C:81:GLY:H	2.21	0.43
4:D:10:ARG:HG3	4:D:10:ARG:HH11	1.83	0.43
7:G:78:ARG:HG2	7:G:80:VAL:HG23	1.99	0.43
9:I:69:GLY:O	9:I:73:GLN:HG3	2.18	0.43
15:O:54:ARG:O	15:O:58:MET:HG3	2.17	0.43
21:V:15:ARG:O	21:V:17:THR:HG23	2.18	0.43
1:A:1051:C:H2'	1:A:1052:U:C6	2.53	0.43
1:A:1128:C:O2'	1:A:1130:A:C8	2.62	0.43
2:B:204:ASN:HD22	2:B:206:ASP:H	1.66	0.43
2:B:92:TYR:CD1	2:B:151:GLY:HA3	2.53	0.43
3:C:134:ILE:HG22	3:C:168:ALA:CB	2.48	0.43
3:C:99:VAL:HG22	3:C:100:ALA:O	2.18	0.43
4:D:178:VAL:O	4:D:178:VAL:HG12	2.18	0.43
4:D:198:VAL:HG12	4:D:199:ASN:N	2.33	0.43
1:A:409:G:OP1	4:D:24:GLU:O	2.36	0.43
4:D:55:ALA:O	4:D:59:ARG:HG2	2.19	0.43
5:E:118:ILE:CG2	5:E:119:LEU:H	2.27	0.43
7:G:108:ALA:O	7:G:119:ARG:HD2	2.18	0.43
11:K:50:TYR:CD2	11:K:50:TYR:N	2.84	0.43
16:P:20:VAL:HG13	16:P:32:TYR:HB2	2.00	0.43
18:R:37:VAL:O	18:R:41:LYS:HB3	2.18	0.43
1:A:192:U:H1'	20:T:103:GLY:HA2	1.99	0.43
1:A:1497:G:C2'	1:A:1498:U:C5'	2.87	0.43
1:A:253:U:H2'	1:A:254:G:C8	2.53	0.43
1:A:363:A:O2'	1:A:364:A:H5'	2.18	0.43
1:A:718:G:C8	11:K:116:HIS:HB3	2.53	0.43
1:A:838:G:C3'	1:A:839:U:H5''	2.48	0.43
2:B:119:GLU:OE1	2:B:153:ARG:NH2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:123:GLN:HE22	3:C:140:ARG:NH2	2.16	0.43
1:A:1113:C:H1'	3:C:178:LEU:HD21	1.99	0.43
3:C:19:GLU:HB3	3:C:40:ARG:NH2	2.25	0.43
4:D:24:GLU:HG2	4:D:25:ARG:H	1.82	0.43
7:G:138:LYS:HD3	7:G:138:LYS:C	2.39	0.43
7:G:24:THR:HA	7:G:27:ILE:HD12	2.00	0.43
8:H:16:ALA:O	8:H:21:LYS:HG2	2.18	0.43
11:K:100:ALA:O	11:K:102:GLY:N	2.51	0.43
11:K:85:ARG:NH1	11:K:85:ARG:HG3	2.33	0.43
1:A:564:C:H5'	12:L:10:LEU:HD13	2.01	0.43
16:P:67:THR:CG2	16:P:68:ASP:N	2.82	0.43
1:A:1286:A:H5''	21:V:25:LYS:HZ2	1.83	0.43
1:A:1053:G:O2'	1:A:1199:U:H5	2.01	0.43
1:A:267:C:H2'	1:A:268:C:C6	2.53	0.43
1:A:430:A:H2'	1:A:431:A:H5'	1.99	0.43
2:B:83:MET:HG3	2:B:238:LEU:HD11	2.00	0.43
3:C:188:LEU:HD13	3:C:189:ALA:H	1.83	0.43
5:E:143:ARG:HA	5:E:143:ARG:HD3	1.71	0.43
7:G:112:PRO:O	7:G:113:GLU:C	2.57	0.43
8:H:86:ILE:HD12	8:H:133:LEU:HD22	2.00	0.43
10:J:56:HIS:O	10:J:58:ASP:N	2.52	0.43
11:K:60:ALA:O	11:K:61:ALA:C	2.56	0.43
12:L:7:ILE:O	12:L:11:VAL:HG23	2.18	0.43
18:R:46:GLU:CD	18:R:46:GLU:N	2.72	0.43
1:A:1031:G:H2'	1:A:1032:G:H8	1.83	0.43
1:A:16:A:O2'	1:A:17:U:H5'	2.18	0.43
1:A:383:A:H2'	1:A:384:G:H5'	1.99	0.43
1:A:618:C:N3	1:A:622:A:N6	2.67	0.43
2:B:146:GLN:O	2:B:150:SER:HB3	2.18	0.43
2:B:17:PHE:H	2:B:44:LEU:HD21	1.83	0.43
1:A:1152:A:OP1	10:J:13:HIS:HB2	2.19	0.43
12:L:60:LEU:CD2	12:L:66:VAL:HG22	2.49	0.43
13:M:23:TYR:CE2	13:M:70:LEU:HD13	2.53	0.43
15:O:17:ARG:HH11	15:O:17:ARG:CG	2.26	0.43
16:P:52:ASP:O	16:P:52:ASP:CG	2.57	0.43
16:P:75:ARG:O	16:P:78:GLY:N	2.49	0.43
18:R:26:LEU:HD21	18:R:39:VAL:HG23	2.00	0.43
19:S:12:ASP:HB2	19:S:35:SER:OG	2.19	0.43
20:T:50:GLU:HG2	20:T:100:ILE:CG1	2.47	0.43
1:A:1286:A:H4'	21:V:25:LYS:HE3	2.01	0.43
1:A:1125:U:H5''	1:A:1126:U:H5	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:C:O2'	1:A:138:G:H5'	2.17	0.43
1:A:143:A:H2	1:A:220:G:H22	1.66	0.43
1:A:436:C:H2'	1:A:437:U:C6	2.53	0.43
1:A:437:U:O2'	4:D:123:HIS:HD2	2.02	0.43
1:A:502:G:C1'	1:A:550:G:H5'	2.49	0.43
1:A:640:A:C2'	1:A:641:U:H5'	2.48	0.43
1:A:765:G:N2	1:A:812:C:O2'	2.51	0.43
1:A:961:U:C2'	1:A:962:C:H5'	2.48	0.43
2:B:28:PHE:CD2	2:B:190:THR:HA	2.54	0.43
3:C:70:VAL:HG12	3:C:71:ALA:H	1.84	0.43
4:D:25:ARG:HH21	4:D:30:LYS:HD3	1.82	0.43
1:A:1346:A:C4	7:G:10:ARG:CZ	3.02	0.43
7:G:75:VAL:HG13	7:G:86:GLN:HB3	1.94	0.43
11:K:127:LYS:HA	11:K:127:LYS:HD3	1.78	0.43
15:O:41:GLU:O	15:O:42:HIS:C	2.57	0.43
1:A:1399:C:C2	1:A:1502:A:N6	2.86	0.43
1:A:433:C:O2'	1:A:434:U:H5'	2.18	0.43
1:A:448:A:C4	1:A:487:A:C2	3.07	0.43
1:A:628:G:H2'	1:A:629:G:H8	1.84	0.43
1:A:851:G:H2'	1:A:852:G:H8	1.84	0.43
2:B:41:ILE:O	2:B:41:ILE:HG22	2.19	0.43
2:B:90:MET:HA	2:B:91:PRO:HD3	1.70	0.43
3:C:116:VAL:HG11	3:C:141:VAL:HG21	2.01	0.43
3:C:191:THR:HB	3:C:194:GLY:O	2.18	0.43
3:C:193:TYR:HE1	3:C:196:LEU:HD11	1.83	0.43
2:B:130:ARG:HH22	3:C:207:VAL:HG22	1.82	0.43
4:D:127:THR:HG23	4:D:128:VAL:N	2.34	0.43
9:I:106:ALA:O	9:I:108:VAL:HG23	2.19	0.43
9:I:56:LEU:HB3	9:I:57:GLY:H	1.74	0.43
16:P:40:ASP:HB3	16:P:48:TRP:HB2	2.00	0.43
17:Q:97:SER:O	17:Q:98:LEU:HD12	2.19	0.43
20:T:63:ILE:HD13	20:T:80:ARG:HB3	2.01	0.43
1:A:1064:G:H1'	1:A:1190:G:H21	1.84	0.43
1:A:1135:U:H6	1:A:1135:U:O5'	2.01	0.43
1:A:1376:U:H2'	1:A:1377:A:H8	1.80	0.43
1:A:254:G:O2'	1:A:255:G:H5'	2.18	0.43
1:A:487:A:H2'	1:A:488:C:O4'	2.19	0.43
1:A:730:G:C5	1:A:731:G:H1'	2.54	0.43
1:A:652:U:H2'	1:A:752:G:N1	2.33	0.43
1:A:913:A:O2'	1:A:914:A:OP2	2.36	0.43
1:A:991:U:O2	1:A:993:G:H8	2.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:134:GLU:C	2:B:136:VAL:N	2.71	0.43
2:B:137:ARG:HA	2:B:140:HIS:HD2	1.84	0.43
4:D:120:LEU:HD23	4:D:125:HIS:CD2	2.54	0.43
4:D:158:ILE:CG2	4:D:181:MET:HE2	2.45	0.43
5:E:105:VAL:HB	5:E:106:PRO:CD	2.40	0.43
1:A:718:G:H1'	11:K:116:HIS:HA	2.00	0.43
1:A:552:U:H4'	12:L:86:ARG:O	2.19	0.43
14:N:14:PRO:O	14:N:16:PHE:N	2.44	0.43
15:O:78:TYR:CE2	15:O:82:ILE:HD11	2.53	0.43
19:S:3:ARG:O	19:S:4:SER:HB3	2.18	0.43
1:A:1004:A:H5''	1:A:1025:U:C4	2.53	0.43
1:A:1441:G:H4'	1:A:1442:G:C8	2.54	0.43
1:A:1504:G:OP1	1:A:1507:A:H4'	2.19	0.43
1:A:157:G:O2'	1:A:158:G:H5'	2.18	0.43
1:A:782:A:H2'	1:A:783:C:O4'	2.19	0.43
3:C:7:PRO:HG2	3:C:184:TYR:CB	2.45	0.43
6:F:77:ARG:O	6:F:81:ILE:HG13	2.18	0.43
10:J:46:ARG:HH11	10:J:64:GLU:CG	2.31	0.43
13:M:33:ALA:HB2	13:M:64:TRP:CH2	2.54	0.43
15:O:39:LEU:HD12	15:O:59:MET:CE	2.48	0.43
17:Q:60:ILE:HD13	17:Q:61:GLU:N	2.34	0.43
19:S:41:VAL:HG22	19:S:44:MET:CE	2.49	0.43
19:S:40:ILE:HG23	19:S:44:MET:SD	2.59	0.43
1:A:1126:U:H2'	1:A:1127:G:O4'	2.19	0.43
1:A:1262:C:H2'	1:A:1263:C:C6	2.54	0.43
1:A:1270:C:H4'	1:A:1313:U:O2'	2.19	0.43
1:A:1288:A:H1'	1:A:1353:G:O4'	2.18	0.43
1:A:1331:G:O2'	1:A:1332:A:P	2.76	0.43
1:A:1438:G:H2'	1:A:1439:C:C6	2.54	0.43
1:A:359:U:O2'	1:A:360:A:H5'	2.18	0.43
1:A:719:C:O2	18:R:50:ILE:HG13	2.19	0.43
1:A:858:G:O2'	1:A:859:A:H5'	2.18	0.43
1:A:960:U:O2	1:A:960:U:H2'	2.18	0.43
2:B:125:PRO:C	2:B:127:ILE:H	2.22	0.43
2:B:74:LYS:HD2	2:B:166:ASP:HB2	2.00	0.43
5:E:40:ARG:NH1	5:E:68:GLU:OE1	2.51	0.43
6:F:75:LEU:HD13	6:F:75:LEU:O	2.18	0.43
8:H:68:ARG:HH11	8:H:68:ARG:HG2	1.84	0.43
9:I:78:LYS:HD3	9:I:101:PHE:CD2	2.54	0.43
1:A:718:G:H4'	11:K:117:ASN:ND2	2.34	0.43
16:P:39:TYR:CD2	16:P:73:LEU:HD11	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:4:ILE:HG23	16:P:36:ILE:HD11	2.01	0.43
17:Q:45:HIS:CD2	17:Q:47:PRO:HG3	2.54	0.43
19:S:25:LYS:HD2	19:S:25:LYS:N	2.34	0.43
1:A:994:A:N7	1:A:1216:G:H4'	2.34	0.42
1:A:1217:C:O2'	1:A:1218:C:H5'	2.19	0.42
1:A:1305:G:H22	1:A:1331:G:C2'	2.32	0.42
1:A:1397:C:O2'	1:A:1398:A:P	2.77	0.42
1:A:176:C:H2'	1:A:177:C:H6	1.83	0.42
1:A:247:G:OP2	17:Q:100:LYS:HG3	2.19	0.42
1:A:370:C:C2'	1:A:371:G:H5'	2.48	0.42
1:A:636:U:H2'	1:A:637:G:C8	2.54	0.42
1:A:942:G:C2	1:A:943:U:C6	3.07	0.42
1:A:1104:G:OP1	2:B:111:ARG:HD2	2.18	0.42
2:B:59:GLU:O	2:B:60:ASP:C	2.57	0.42
3:C:11:ARG:O	3:C:14:ILE:O	2.36	0.42
3:C:134:ILE:HD13	3:C:166:GLU:HB3	2.01	0.42
3:C:191:THR:HG21	3:C:193:TYR:CE1	2.53	0.42
5:E:115:VAL:CG1	5:E:116:THR:N	2.82	0.42
5:E:16:THR:HG23	5:E:27:ARG:O	2.19	0.42
9:I:78:LYS:HE2	9:I:78:LYS:HB3	1.87	0.42
9:I:97:LYS:HB2	9:I:98:PRO:HD3	2.01	0.42
10:J:17:ASP:O	10:J:21:GLN:HB2	2.19	0.42
10:J:32:ALA:HB2	10:J:75:ILE:O	2.19	0.42
10:J:55:LYS:O	10:J:56:HIS:HB2	2.19	0.42
11:K:104:GLN:OE1	11:K:106:LYS:HE2	2.19	0.42
12:L:26:ALA:C	12:L:27:LEU:O	2.57	0.42
19:S:20:LEU:HD12	19:S:21:GLU:N	2.34	0.42
1:A:413:G:N2	1:A:428:G:H1'	2.34	0.42
1:A:451:A:N6	1:A:480:U:H2'	2.33	0.42
1:A:647:C:H2'	1:A:648:A:C8	2.54	0.42
4:D:8:VAL:CG1	4:D:21:LEU:HD13	2.49	0.42
5:E:24:ARG:HG2	5:E:24:ARG:NH1	2.32	0.42
5:E:80:ILE:HD12	5:E:80:ILE:H	1.84	0.42
7:G:65:ALA:O	7:G:66:VAL:C	2.58	0.42
11:K:21:ILE:HD12	11:K:95:ILE:HG12	2.00	0.42
1:A:1126:U:H2'	1:A:1127:G:H8	1.84	0.42
1:A:1157:A:O4'	1:A:1158:C:C2	2.72	0.42
1:A:243:A:N6	1:A:281:G:O2'	2.51	0.42
1:A:418:C:H2'	1:A:419:C:H6	1.84	0.42
1:A:512:U:H1'	4:D:42:GLN:OE1	2.19	0.42
1:A:522:C:O2'	1:A:523:A:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:545:C:O2'	1:A:549:C:OP1	2.37	0.42
1:A:640:A:O2'	1:A:641:U:H5'	2.20	0.42
1:A:80:G:H2'	1:A:81:U:H5''	2.01	0.42
3:C:50:ALA:O	3:C:70:VAL:CG1	2.67	0.42
7:G:31:MET:SD	7:G:34:GLY:HA2	2.60	0.42
12:L:33:ARG:HD2	12:L:62:SER:HB3	2.01	0.42
15:O:39:LEU:HD12	15:O:59:MET:HE2	2.01	0.42
17:Q:59:ILE:CG2	17:Q:71:PHE:CD1	3.02	0.42
1:A:160:A:H2'	1:A:161:A:O4'	2.18	0.42
1:A:162:A:H2'	1:A:163:C:O4'	2.20	0.42
1:A:182:U:O4	1:A:223:U:H1'	2.20	0.42
1:A:409:G:H2'	1:A:410:G:O4'	2.18	0.42
6:F:19:LEU:HD21	6:F:23:LYS:HD2	2.01	0.42
10:J:12:ASP:OD1	10:J:14:LYS:N	2.50	0.42
1:A:1230:C:H1'	13:M:125:ARG:O	2.19	0.42
13:M:7:VAL:HG23	13:M:7:VAL:O	2.18	0.42
1:A:1057:G:H4'	3:C:197:GLY:H	1.85	0.42
1:A:1060:C:O2'	1:A:1061:G:H5'	2.18	0.42
1:A:1129:C:O2'	1:A:1130:A:P	2.78	0.42
1:A:1346:A:C8	7:G:10:ARG:NH2	2.87	0.42
1:A:833:U:H2'	1:A:834:C:C6	2.55	0.42
1:A:839:U:C5'	1:A:840:C:H5	2.27	0.42
1:A:942:G:H2'	1:A:943:U:H6	1.84	0.42
4:D:163:GLU:C	4:D:165:MET:N	2.72	0.42
6:F:30:LEU:HB3	6:F:35:ALA:CB	2.41	0.42
11:K:33:THR:OG1	11:K:37:GLY:C	2.58	0.42
11:K:93:GLN:NE2	11:K:96:ARG:NH2	2.67	0.42
21:V:9:ARG:HH11	21:V:22:ARG:HA	1.85	0.42
1:A:1181:G:O2'	1:A:1182:G:H5'	2.19	0.42
1:A:1244:C:O2'	1:A:1245:A:H5'	2.19	0.42
1:A:1353:G:H2'	1:A:1354:C:C6	2.54	0.42
1:A:173:U:C5'	1:A:197:A:O4'	2.65	0.42
1:A:825:G:H2'	1:A:826:C:C6	2.53	0.42
1:A:977:A:H2'	1:A:978:A:C5'	2.45	0.42
2:B:17:PHE:CA	2:B:44:LEU:HD21	2.49	0.42
2:B:187:LEU:HD21	2:B:214:ILE:HG13	2.00	0.42
4:D:70:ILE:HD11	4:D:100:ARG:CD	2.49	0.42
6:F:40:VAL:HG22	6:F:41:GLU:N	2.34	0.42
7:G:15:ASP:OD2	7:G:23:VAL:HG11	2.19	0.42
8:H:114:THR:C	8:H:116:LYS:H	2.22	0.42
8:H:75:ARG:HA	8:H:76:PRO:HD3	1.70	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:32:ALA:CB	10:J:76:ASN:HD22	2.30	0.42
3:C:23:TYR:OH	10:J:9:ARG:HD3	2.20	0.42
11:K:57:THR:OG1	11:K:58:PRO:HD2	2.20	0.42
12:L:41:ARG:CB	12:L:41:ARG:NH1	2.82	0.42
12:L:41:ARG:HH11	12:L:41:ARG:HB3	1.84	0.42
1:A:523:A:C2	12:L:91:LYS:HB3	2.54	0.42
19:S:41:VAL:HB	19:S:43:GLU:OE2	2.20	0.42
1:A:1327:C:O2'	1:A:1328:C:H5'	2.19	0.42
1:A:169:C:O2'	1:A:170:U:H5'	2.19	0.42
1:A:397:A:H5'	1:A:398:C:P	2.60	0.42
1:A:562:C:O2'	12:L:17:LYS:HE3	2.20	0.42
1:A:974:A:P	14:N:41:ARG:HH12	2.42	0.42
3:C:64:VAL:HG12	3:C:65:ALA:H	1.84	0.42
6:F:100:ASN:ND2	18:R:23:LYS:O	2.52	0.42
7:G:38:LEU:HD12	7:G:42:ILE:HG13	2.00	0.42
8:H:126:LYS:C	8:H:128:GLY:N	2.73	0.42
9:I:110:GLU:HG2	9:I:113:LYS:NZ	2.35	0.42
13:M:80:ARG:C	13:M:82:MET:N	2.73	0.42
13:M:96:LEU:HB3	13:M:97:PRO:HD2	2.01	0.42
1:A:1202:G:C2	14:N:42:ILE:HG21	2.55	0.42
15:O:38:ARG:O	15:O:41:GLU:HB3	2.20	0.42
16:P:51:VAL:O	16:P:52:ASP:C	2.58	0.42
1:A:1271:G:H5'	1:A:1314:C:OP1	2.20	0.42
1:A:1277:C:H1'	1:A:1282:C:O2	2.20	0.42
1:A:1505:G:H8	1:A:1505:G:H3'	1.85	0.42
1:A:418:C:H2'	1:A:419:C:C6	2.54	0.42
1:A:502:G:H2'	1:A:503:C:H6	1.84	0.42
2:B:187:LEU:HA	2:B:201:ILE:HB	2.02	0.42
2:B:87:ARG:NH2	2:B:220:ASP:OD1	2.51	0.42
2:B:8:LYS:O	2:B:9:GLU:CB	2.60	0.42
4:D:25:ARG:HA	4:D:28:SER:OG	2.19	0.42
4:D:60:GLU:HA	4:D:60:GLU:OE1	2.19	0.42
18:R:48:GLY:O	18:R:74:ARG:NH2	2.41	0.42
20:T:11:SER:C	20:T:13:LEU:H	2.22	0.42
1:A:1056:U:H5'	3:C:163:ALA:HB2	2.02	0.42
1:A:1091:U:O2	1:A:1093:A:H8	2.03	0.42
1:A:1375:A:OP1	7:G:12:LEU:HD21	2.20	0.42
1:A:815:A:N6	1:A:1509:C:H1'	2.35	0.42
1:A:252:U:O2'	1:A:275:G:N2	2.53	0.42
1:A:413:G:H22	1:A:428:G:H1'	1.85	0.42
1:A:602:A:C2	1:A:637:G:C2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:825:G:O2'	1:A:826:C:H5'	2.20	0.42
1:A:930:C:O2'	1:A:931:C:H5'	2.20	0.42
1:A:951:G:C6	1:A:1231:G:C6	3.08	0.42
1:A:965:A:O2'	1:A:966:G:C5'	2.67	0.42
2:B:8:LYS:HB2	2:B:9:GLU:H	1.58	0.42
4:D:8:VAL:CG1	4:D:21:LEU:CD1	2.98	0.42
5:E:131:ILE:HD13	5:E:131:ILE:HA	1.93	0.42
5:E:80:ILE:HD12	5:E:91:LEU:HB2	2.00	0.42
6:F:45:LEU:O	6:F:46:ARG:HG2	2.20	0.42
11:K:86:GLY:H	11:K:112:THR:CG2	2.32	0.42
1:A:965:A:C2	13:M:124:PRO:HB2	2.55	0.42
18:R:17:SER:HB2	18:R:54:ARG:HH21	1.85	0.42
20:T:54:LYS:HA	20:T:57:ARG:HD3	2.02	0.42
1:A:1260:C:H4'	1:A:1284:C:H5'	2.01	0.42
1:A:145:G:O2'	1:A:146:G:H5'	2.20	0.42
1:A:1531:A:O5'	1:A:1531:A:H8	2.03	0.42
1:A:373:A:H2'	1:A:374:A:H8	1.85	0.42
1:A:584:G:H2'	1:A:585:G:C8	2.54	0.42
1:A:974:A:H8	1:A:974:A:OP1	2.03	0.42
3:C:134:ILE:HG22	3:C:168:ALA:HB3	2.01	0.42
5:E:24:ARG:O	5:E:25:ARG:HG2	2.20	0.42
9:I:56:LEU:O	9:I:58:ARG:N	2.49	0.42
1:A:521:G:OP1	12:L:73:GLU:O	2.38	0.42
1:A:1306:A:O2'	13:M:109:THR:HG21	2.19	0.42
17:Q:40:LYS:HD3	17:Q:42:TYR:OH	2.20	0.42
17:Q:95:TYR:N	17:Q:95:TYR:CD1	2.88	0.42
18:R:51:LEU:HA	18:R:52:PRO:HD3	1.80	0.42
20:T:42:GLN:O	20:T:46:GLU:HG3	2.19	0.42
20:T:53:LEU:HD13	20:T:101:GLY:N	2.35	0.42
21:V:7:ARG:O	21:V:7:ARG:HG3	2.19	0.42
1:A:1264:C:H2'	1:A:1265:G:C8	2.54	0.41
1:A:1407:C:H2'	1:A:1408:A:H8	1.85	0.41
1:A:490:G:H2'	1:A:491:G:C8	2.54	0.41
1:A:767:A:H2'	1:A:768:A:O4'	2.20	0.41
3:C:108:ASN:C	3:C:110:ASN:N	2.73	0.41
3:C:77:ILE:CG2	3:C:81:GLY:HA2	2.50	0.41
3:C:38:ARG:CB	3:C:94:LEU:HD21	2.50	0.41
4:D:205:GLU:O	4:D:208:SER:HB2	2.20	0.41
6:F:48:LEU:HD13	6:F:52:ILE:CG1	2.50	0.41
7:G:93:PRO:HG2	7:G:94:ARG:H	1.85	0.41
8:H:6:ILE:O	8:H:10:LEU:HG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:104:ARG:O	9:I:105:ASP:C	2.59	0.41
9:I:120:ARG:O	9:I:122:ALA:N	2.53	0.41
13:M:36:LYS:C	13:M:38:GLY:H	2.24	0.41
1:A:1060:C:OP1	14:N:45:ARG:NH2	2.53	0.41
1:A:761:G:O2'	17:Q:104:LYS:HA	2.20	0.41
20:T:80:ARG:O	20:T:84:LEU:HB2	2.20	0.41
1:A:1034:G:O2'	1:A:1035:A:H5'	2.20	0.41
1:A:1061:G:C2'	1:A:1062:U:H5'	2.50	0.41
1:A:1239:A:C4	1:A:1298:C:N4	2.88	0.41
1:A:1426:C:H2'	1:A:1427:U:H6	1.84	0.41
1:A:867:G:O2'	1:A:868:C:H5'	2.20	0.41
1:A:961:U:O2'	1:A:962:C:H5'	2.20	0.41
2:B:10:LEU:C	2:B:12:GLU:N	2.72	0.41
2:B:116:GLU:CG	2:B:153:ARG:NH1	2.80	0.41
2:B:25:ASN:ND2	2:B:25:ASN:C	2.68	0.41
3:C:112:SER:HB2	3:C:115:LEU:HB2	2.01	0.41
5:E:36:ASP:OD1	5:E:38:GLN:N	2.39	0.41
1:A:1346:A:C5	7:G:10:ARG:CZ	3.02	0.41
7:G:155:ARG:O	7:G:156:TRP:CB	2.64	0.41
9:I:59:PHE:HB3	9:I:60:ASP:H	1.56	0.41
12:L:104:VAL:HG12	12:L:105:TYR:CD1	2.55	0.41
13:M:40:ASN:ND2	13:M:41:PRO:N	2.64	0.41
13:M:67:GLU:HB3	13:M:68:GLY:H	1.58	0.41
19:S:41:VAL:HG22	19:S:44:MET:HE2	2.01	0.41
1:A:1137:C:H4'	1:A:1138:G:N1	2.33	0.41
1:A:1264:C:H2'	1:A:1265:G:H8	1.85	0.41
1:A:184:G:O4'	1:A:224:C:H4'	2.19	0.41
1:A:489:C:H2'	1:A:490:G:C8	2.54	0.41
1:A:550:G:O2'	1:A:551:U:H5'	2.20	0.41
1:A:628:G:O2'	1:A:629:G:H5'	2.20	0.41
1:A:818:G:HO2'	1:A:819:A:H5''	1.84	0.41
2:B:165:VAL:O	2:B:187:LEU:O	2.38	0.41
4:D:24:GLU:H	4:D:112:VAL:HG11	1.85	0.41
8:H:108:GLY:CA	8:H:138:TRP:HB3	2.46	0.41
8:H:51:VAL:CG1	8:H:52:ASP:N	2.82	0.41
10:J:80:LYS:HA	10:J:83:GLU:HB2	2.03	0.41
11:K:48:ILE:O	11:K:49:GLY:C	2.59	0.41
15:O:83:GLU:C	15:O:83:GLU:OE1	2.58	0.41
15:O:87:ILE:HG22	15:O:88:ARG:N	2.34	0.41
16:P:19:ILE:HG22	16:P:36:ILE:CG1	2.51	0.41
1:A:1077:G:N2	1:A:1080:A:OP2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1094:G:OP2	1:A:1095:U:C5	2.74	0.41
1:A:1127:G:N2	1:A:1144:G:N2	2.69	0.41
1:A:1213:A:N1	1:A:1215:G:H1'	2.35	0.41
1:A:1262:C:N4	1:A:1273:G:H1	2.18	0.41
1:A:1352:C:OP1	21:V:3:LYS:NZ	2.51	0.41
1:A:47:C:C6	1:A:365:U:H2'	2.56	0.41
1:A:547:A:H4'	1:A:548:G:O5'	2.19	0.41
1:A:778:G:O2'	1:A:779:C:H5'	2.19	0.41
3:C:70:VAL:O	3:C:106:VAL:N	2.51	0.41
1:A:619:U:N3	4:D:134:ASP:OD1	2.52	0.41
4:D:148:VAL:HG13	4:D:158:ILE:HD13	2.01	0.41
13:M:32:GLU:O	13:M:35:GLU:N	2.53	0.41
15:O:34:LEU:HD23	15:O:34:LEU:C	2.40	0.41
20:T:57:ARG:HE	20:T:100:ILE:HG21	1.84	0.41
1:A:1126:U:H6	1:A:1126:U:P	2.43	0.41
1:A:1311:G:H2'	1:A:1312:G:O4'	2.20	0.41
1:A:1322:C:OP1	19:S:78:ARG:NH2	2.54	0.41
1:A:1350:A:C6	1:A:1351:U:N3	2.89	0.41
1:A:1371:G:H2'	1:A:1372:U:H6	1.86	0.41
1:A:1393:U:O4'	1:A:1502:A:H5'	2.20	0.41
1:A:67:C:O2'	1:A:171:A:H1'	2.20	0.41
1:A:546:G:OP1	4:D:73:ARG:HB2	2.21	0.41
3:C:73:PRO:HD3	3:C:105:GLU:HG3	2.03	0.41
3:C:179:ARG:O	3:C:179:ARG:CG	2.69	0.41
4:D:23:GLY:HA3	4:D:112:VAL:HG13	2.02	0.41
7:G:69:VAL:O	7:G:69:VAL:CG1	2.68	0.41
8:H:126:LYS:O	8:H:128:GLY:N	2.54	0.41
10:J:3:LYS:CG	10:J:75:ILE:HG23	2.50	0.41
12:L:55:VAL:CG1	12:L:67:THR:CG2	2.97	0.41
18:R:44:LEU:HD23	18:R:44:LEU:HA	1.89	0.41
1:A:1145:C:O2'	1:A:1146:A:O5'	2.39	0.41
1:A:1195:C:H3'	1:A:1196:U:H5''	2.02	0.41
1:A:1228:C:H4'	13:M:116:THR:HA	2.02	0.41
1:A:1292:U:P	7:G:41:ARG:NH2	2.94	0.41
1:A:1453:G:H2'	1:A:1454:G:O4'	2.21	0.41
1:A:625:G:O2'	1:A:626:U:H5'	2.20	0.41
2:B:228:GLY:O	2:B:229:VAL:C	2.58	0.41
2:B:62:ALA:C	2:B:64:ARG:H	2.23	0.41
7:G:45:ASP:O	7:G:49:ILE:HG13	2.20	0.41
10:J:3:LYS:HG3	10:J:75:ILE:HG23	2.02	0.41
11:K:65:ALA:O	11:K:68:ALA:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:70:LEU:HD12	15:O:78:TYR:HB2	2.01	0.41
16:P:4:ILE:CG1	16:P:64:ALA:HB1	2.49	0.41
16:P:82:GLN:O	16:P:83:GLU:C	2.59	0.41
1:A:1030(A):G:H21	1:A:1030(C):G:H3'	1.84	0.41
1:A:769:G:H4'	1:A:1513:A:H4'	2.02	0.41
1:A:43:C:H2'	1:A:44:G:O4'	2.21	0.41
1:A:736:C:H2'	1:A:737:A:H8	1.83	0.41
1:A:976:G:OP1	14:N:31:ARG:O	2.39	0.41
5:E:144:THR:O	5:E:145:LYS:C	2.59	0.41
5:E:51:VAL:HB	5:E:52:PRO:CD	2.37	0.41
10:J:75:ILE:O	10:J:76:ASN:HB2	2.21	0.41
11:K:86:GLY:N	11:K:112:THR:HG23	2.35	0.41
11:K:99:GLN:HG2	11:K:105:VAL:HG21	2.02	0.41
12:L:60:LEU:HD21	12:L:66:VAL:CG2	2.50	0.41
12:L:83:VAL:HG22	12:L:84:LEU:H	1.86	0.41
17:Q:95:TYR:HD1	17:Q:95:TYR:N	2.18	0.41
1:A:1053:G:C3'	1:A:1054:C:C5'	2.99	0.41
1:A:107:G:O2'	1:A:108:G:H5'	2.19	0.41
1:A:1390:U:H2'	1:A:1391:U:H6	1.86	0.41
1:A:1431:C:H2'	1:A:1432:G:O4'	2.21	0.41
1:A:439:A:N6	1:A:497:A:H1'	2.35	0.41
1:A:519:C:H2'	1:A:520:A:C8	2.56	0.41
1:A:866:C:H2'	1:A:867:G:O4'	2.20	0.41
1:A:913:A:H1'	1:A:914:A:O4'	2.21	0.41
1:A:913:A:O2'	1:A:914:A:O4'	2.26	0.41
3:C:47:LEU:HD13	3:C:47:LEU:H	1.83	0.41
6:F:48:LEU:HD13	6:F:52:ILE:HD12	2.03	0.41
7:G:23:VAL:HG13	7:G:43:PHE:CE2	2.56	0.41
8:H:82:HIS:O	8:H:83:ILE:HB	2.21	0.41
10:J:53:PRO:HA	14:N:41:ARG:HH21	1.85	0.41
11:K:100:ALA:O	11:K:101:SER:C	2.58	0.41
13:M:4:ILE:HG22	13:M:5:ALA:H	1.84	0.41
1:A:1203:C:OP1	14:N:2:ALA:HB3	2.20	0.41
16:P:43:LYS:HA	16:P:48:TRP:CB	2.51	0.41
18:R:21:LYS:HG3	18:R:57:GLY:CA	2.51	0.41
1:A:1460:A:P	20:T:27:LYS:NZ	2.94	0.41
1:A:1057:G:H2'	1:A:1058:G:O4'	2.20	0.41
1:A:1231:G:H5''	9:I:126:SER:HB3	2.01	0.41
1:A:436:C:H2'	1:A:437:U:H6	1.86	0.41
1:A:692:U:O2	1:A:695:A:C8	2.73	0.41
2:B:15:VAL:HG11	2:B:210:SER:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:67:THR:O	3:C:67:THR:HG22	2.21	0.41
5:E:40:ARG:NH1	5:E:68:GLU:OE2	2.49	0.41
6:F:33:TYR:HA	6:F:71:ARG:NH2	2.36	0.41
9:I:108:VAL:HG12	9:I:109:VAL:N	2.36	0.41
10:J:29:ARG:C	10:J:84:GLN:HE22	2.25	0.41
11:K:67:ASP:OD2	11:K:71:LYS:HE3	2.21	0.41
12:L:46:LYS:NZ	12:L:47:LYS:HE3	2.36	0.41
12:L:55:VAL:CG1	12:L:56:ALA:N	2.83	0.41
12:L:53:ARG:CB	12:L:93:LEU:HD11	2.50	0.41
19:S:16:LEU:O	19:S:20:LEU:HG	2.21	0.41
1:A:1116:C:O2'	9:I:108:VAL:HG21	2.21	0.41
1:A:1118:C:H1'	1:A:1179:A:C4	2.56	0.41
1:A:1191:A:H2'	1:A:1192:C:H6	1.84	0.41
1:A:1286:A:H2'	1:A:1287:A:O5'	2.21	0.41
1:A:134:A:H1'	1:A:325:A:C5	2.56	0.41
1:A:1495:U:H2'	1:A:1496:C:H6	1.83	0.41
1:A:382:A:C2	1:A:383:A:C4	3.09	0.41
1:A:527:G:O2'	1:A:535:A:N1	2.33	0.41
1:A:570:G:H1'	1:A:820:U:C4	2.56	0.41
1:A:836:G:C6	1:A:851:G:C6	3.09	0.41
2:B:134:GLU:HG2	2:B:137:ARG:HH21	1.86	0.41
2:B:14:GLY:O	2:B:15:VAL:HG22	2.21	0.41
3:C:57:ILE:O	3:C:57:ILE:HG22	2.20	0.41
5:E:118:ILE:HG21	5:E:118:ILE:HD13	1.74	0.41
5:E:152:ARG:NH2	8:H:107:LEU:O	2.54	0.41
9:I:110:GLU:OE2	9:I:113:LYS:NZ	2.53	0.41
11:K:95:ILE:HG22	11:K:95:ILE:O	2.20	0.41
12:L:27:LEU:HB3	12:L:62:SER:HB2	2.03	0.41
12:L:28:LYS:CG	12:L:33:ARG:HH12	2.34	0.41
13:M:78:ILE:CA	13:M:81:LEU:HD21	2.43	0.41
19:S:5:LEU:HA	19:S:5:LEU:HD23	1.88	0.41
20:T:43:LEU:HD13	20:T:51:GLU:CG	2.43	0.41
20:T:44:ALA:HB2	20:T:88:VAL:HG13	2.02	0.41
1:A:1326:C:H5''	21:V:12:LYS:HZ1	1.85	0.41
1:A:1096:C:H2'	1:A:1097:C:C6	2.56	0.41
1:A:19:C:O2'	1:A:20:U:H5'	2.20	0.41
1:A:750:G:N3	15:O:23:GLY:HA3	2.36	0.41
1:A:883:C:O2'	1:A:884:U:H5'	2.21	0.41
1:A:919:A:O2'	1:A:920:U:H5'	2.22	0.41
2:B:125:PRO:HG2	2:B:126:GLU:H	1.86	0.41
2:B:130:ARG:HB3	2:B:134:GLU:OE1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:53:ARG:NH1	2:B:199:TYR:HD2	2.19	0.41
2:B:60:ASP:O	2:B:64:ARG:HB2	2.20	0.41
2:B:95:GLN:C	2:B:96:ARG:HD2	2.40	0.41
3:C:174:PRO:HB2	3:C:177:THR:CG2	2.50	0.41
3:C:191:THR:HG21	3:C:193:TYR:CE2	2.56	0.41
3:C:79:ARG:NE	3:C:82:GLU:HG2	2.34	0.41
4:D:63:LYS:O	4:D:64:LEU:C	2.58	0.41
4:D:62:GLN:HE22	4:D:65:ARG:NH1	2.18	0.41
5:E:9:LYS:HG3	5:E:112:LEU:HD11	2.03	0.41
6:F:78:GLU:HA	6:F:81:ILE:CD1	2.51	0.41
8:H:39:LEU:HA	8:H:39:LEU:HD13	1.86	0.41
10:J:15:THR:HG23	10:J:94:VAL:CG2	2.49	0.41
15:O:74:ASP:OD1	15:O:76:GLU:HB3	2.21	0.41
15:O:26:GLU:HG3	15:O:81:LEU:HG	2.02	0.41
17:Q:97:SER:O	17:Q:99:SER:N	2.53	0.41
18:R:44:LEU:HD22	18:R:48:GLY:O	2.21	0.41
6:F:91:VAL:HG13	18:R:72:ARG:NH2	2.36	0.41
1:A:1028:C:H2'	1:A:1029:C:H6	1.84	0.40
1:A:1110:A:H8	1:A:1110:A:O5'	2.04	0.40
1:A:1138:G:N1	1:A:1140:C:C2	2.89	0.40
1:A:1257:U:H4'	1:A:1258:G:C5'	2.50	0.40
1:A:1263:C:H2'	1:A:1264:C:C6	2.56	0.40
1:A:1372:U:H5''	9:I:71:SER:CB	2.51	0.40
1:A:1392:G:H2'	1:A:1393:U:H6	1.86	0.40
1:A:1402:C:H2'	1:A:1403:C:H6	1.85	0.40
1:A:1437:C:H2'	1:A:1438:G:H8	1.86	0.40
1:A:502:G:H2'	1:A:503:C:C6	2.56	0.40
1:A:637:G:O2'	1:A:638:G:H5'	2.21	0.40
1:A:948:C:O2'	1:A:949:A:H5'	2.21	0.40
1:A:952:U:H2'	1:A:953:G:H8	1.85	0.40
3:C:126:ARG:C	3:C:127:ARG:HG3	2.42	0.40
4:D:130:GLY:O	4:D:131:ARG:C	2.58	0.40
4:D:194:LEU:HD22	4:D:194:LEU:N	2.36	0.40
1:A:642:A:C2	8:H:113:SER:O	2.74	0.40
10:J:23:ILE:N	10:J:23:ILE:CD1	2.85	0.40
13:M:96:LEU:O	13:M:110:ARG:NH1	2.54	0.40
1:A:953:G:H1'	13:M:125:ARG:HA	2.03	0.40
15:O:71:GLN:O	15:O:72:ARG:C	2.59	0.40
15:O:81:LEU:HD22	15:O:85:LEU:HD12	2.03	0.40
16:P:34:GLU:HG2	16:P:35:LYS:N	2.36	0.40
18:R:26:LEU:CD1	18:R:27:GLY:H	2.29	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:36:LEU:HD12	20:T:62:LEU:HD12	2.03	0.40
20:T:68:LYS:HA	20:T:68:LYS:HD2	1.92	0.40
1:A:1112:C:N3	3:C:178:LEU:N	2.62	0.40
1:A:1355:G:O2'	1:A:1356:G:H5'	2.21	0.40
1:A:671:G:H2'	1:A:672:U:O4'	2.21	0.40
1:A:965:A:O2'	1:A:966:G:P	2.80	0.40
3:C:77:ILE:O	3:C:83:ARG:HB3	2.21	0.40
4:D:58:LEU:HD23	4:D:206:PHE:CE1	2.57	0.40
7:G:104:LEU:HD23	7:G:134:ALA:HB1	2.03	0.40
11:K:115:PRO:C	11:K:117:ASN:H	2.25	0.40
13:M:37:THR:HG23	13:M:55:ARG:HB2	2.03	0.40
15:O:57:LEU:HA	15:O:57:LEU:HD12	1.86	0.40
1:A:1428:A:H2'	1:A:1429:C:O4'	2.22	0.40
1:A:176:C:H2'	1:A:177:C:C6	2.56	0.40
1:A:335:C:H2'	1:A:336:C:H6	1.86	0.40
1:A:458:C:H2'	1:A:459:G:C8	2.57	0.40
2:B:107:THR:C	2:B:109:SER:N	2.75	0.40
2:B:130:ARG:NH2	3:C:207:VAL:CG2	2.82	0.40
2:B:14:GLY:O	2:B:15:VAL:CG2	2.69	0.40
2:B:21:ARG:HG2	2:B:21:ARG:H	1.72	0.40
3:C:65:ALA:O	3:C:66:VAL:HB	2.21	0.40
5:E:76:ILE:HG23	5:E:77:PRO:HD2	2.04	0.40
6:F:30:LEU:CB	6:F:35:ALA:HB3	2.41	0.40
8:H:19:VAL:CG2	8:H:21:LYS:HD3	2.52	0.40
8:H:89:PRO:HA	8:H:92:ARG:NH1	2.37	0.40
10:J:59:SER:O	10:J:60:ARG:HB2	2.21	0.40
10:J:65:LEU:HD12	14:N:56:VAL:HG22	2.04	0.40
14:N:39:LEU:HD11	14:N:47:LEU:HD12	2.02	0.40
17:Q:6:LEU:O	17:Q:58:GLU:HA	2.21	0.40
1:A:155:C:H2'	1:A:156:G:C8	2.57	0.40
1:A:359:U:H2'	1:A:360:A:C8	2.57	0.40
1:A:567:G:H2'	1:A:568:G:O4'	2.21	0.40
1:A:973:G:H8	1:A:973:G:O5'	2.05	0.40
3:C:13:GLY:O	3:C:14:ILE:HD13	2.22	0.40
3:C:39:ILE:HG22	3:C:40:ARG:N	2.37	0.40
1:A:1298:C:H2'	7:G:114:ARG:HH12	1.86	0.40
8:H:111:ILE:O	8:H:134:ILE:HB	2.20	0.40
1:A:1372:U:H5''	9:I:71:SER:HB2	2.04	0.40
10:J:44:VAL:HG11	10:J:46:ARG:NH1	2.37	0.40
13:M:63:THR:HG23	13:M:64:TRP:CD2	2.56	0.40
13:M:69:GLU:O	13:M:72:ALA:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1003(A):G:H2'	1:A:1004:A:H4'	2.03	0.40
1:A:103:C:P	20:T:17:ARG:NH1	2.95	0.40
1:A:1124:G:C8	1:A:1145:C:C5	3.09	0.40
1:A:1408:A:O2'	1:A:1409:C:H5'	2.21	0.40
1:A:16:A:C2'	1:A:17:U:H5'	2.52	0.40
1:A:182:U:OP2	1:A:183:G:C8	2.74	0.40
1:A:330:C:H5''	1:A:330:C:H6	1.86	0.40
1:A:715:A:H2'	1:A:716:A:C8	2.57	0.40
1:A:939:G:C6	1:A:940:C:N4	2.89	0.40
2:B:216:SER:OG	2:B:217:ARG:N	2.55	0.40
2:B:24:TRP:CG	2:B:25:ASN:N	2.89	0.40
3:C:126:ARG:O	3:C:127:ARG:HB2	2.22	0.40
3:C:204:LEU:O	3:C:205:GLY:C	2.59	0.40
1:A:547:A:OP2	4:D:2:GLY:N	2.54	0.40
5:E:118:ILE:HG22	5:E:119:LEU:O	2.21	0.40
6:F:48:LEU:HD13	6:F:52:ILE:CD1	2.51	0.40
14:N:29:ARG:CG	14:N:29:ARG:HH11	2.32	0.40
17:Q:92:ARG:O	17:Q:95:TYR:HB2	2.22	0.40
19:S:67:VAL:HG12	19:S:68:GLY:N	2.35	0.40
20:T:92:LEU:O	20:T:96:GLY:HA3	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)
2:B:157:ARG:NH1	2:B:157:ARG:NH1[7_555]	1.70	0.50

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	232/256 (91%)	174 (75%)	34 (15%)	24 (10%)	0 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	204/239 (85%)	135 (66%)	40 (20%)	29 (14%)	0	1
4	D	206/208 (99%)	166 (81%)	31 (15%)	9 (4%)	3	15
5	E	148/161 (92%)	130 (88%)	13 (9%)	5 (3%)	4	21
6	F	99/101 (98%)	79 (80%)	19 (19%)	1 (1%)	18	52
7	G	153/155 (99%)	127 (83%)	16 (10%)	10 (6%)	1	8
8	H	136/138 (99%)	125 (92%)	7 (5%)	4 (3%)	5	25
9	I	125/128 (98%)	88 (70%)	27 (22%)	10 (8%)	1	5
10	J	96/104 (92%)	59 (62%)	20 (21%)	17 (18%)	0	0
11	K	117/129 (91%)	88 (75%)	20 (17%)	9 (8%)	1	5
12	L	122/135 (90%)	98 (80%)	15 (12%)	9 (7%)	1	6
13	M	123/126 (98%)	88 (72%)	27 (22%)	8 (6%)	1	8
14	N	58/60 (97%)	40 (69%)	11 (19%)	7 (12%)	0	1
15	O	86/88 (98%)	70 (81%)	11 (13%)	5 (6%)	2	10
16	P	81/88 (92%)	65 (80%)	15 (18%)	1 (1%)	15	47
17	Q	102/104 (98%)	84 (82%)	10 (10%)	8 (8%)	1	5
18	R	71/88 (81%)	62 (87%)	7 (10%)	2 (3%)	6	26
19	S	78/92 (85%)	49 (63%)	18 (23%)	11 (14%)	0	1
20	T	97/106 (92%)	65 (67%)	20 (21%)	12 (12%)	0	1
21	V	22/26 (85%)	19 (86%)	2 (9%)	1 (4%)	3	15
All	All	2356/2532 (93%)	1811 (77%)	363 (15%)	182 (8%)	1	5

All (182) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	9	GLU
2	B	15	VAL
2	B	16	HIS
2	B	17	PHE
2	B	21	ARG
2	B	24	TRP
3	C	4	LYS
3	C	15	THR
3	C	16	ARG
3	C	26	LYS
3	C	47	LEU

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Mol	Chain	Res	Type
3	C	61	ALA
3	C	62	ASP
3	C	97	LYS
3	C	101	LEU
3	C	146	ALA
3	C	154	SER
3	C	179	ARG
3	C	189	ALA
4	D	29	PRO
4	D	36	ARG
5	E	16	THR
5	E	153	LYS
7	G	7	ALA
7	G	155	ARG
8	H	24	THR
8	H	83	ILE
8	H	91	ARG
9	I	88	TYR
10	J	32	ALA
10	J	39	PRO
10	J	54	PHE
10	J	57	LYS
10	J	79	ARG
10	J	86	MET
11	K	57	THR
11	K	127	LYS
12	L	27	LEU
12	L	28	LYS
12	L	47	LYS
13	M	63	THR
13	M	67	GLU
13	M	121	LYS
13	M	122	LYS
13	M	124	PRO
14	N	22	THR
14	N	29	ARG
15	O	88	ARG
17	Q	69	LYS
17	Q	80	GLY
17	Q	81	ARG
17	Q	96	GLN
17	Q	98	LEU

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Mol	Chain	Res	Type
17	Q	104	LYS
18	R	87	ARG
19	S	6	LYS
19	S	71	LEU
20	T	11	SER
20	T	73	HIS
2	B	8	LYS
2	B	18	GLY
2	B	20	GLU
2	B	97	TRP
2	B	123	ALA
2	B	232	PRO
3	C	29	TYR
3	C	156	ARG
3	C	168	ALA
3	C	181	ASN
3	C	206	GLU
4	D	4	TYR
4	D	26	CYS
4	D	88	VAL
4	D	125	HIS
5	E	22	GLY
5	E	104	ALA
6	F	37	VAL
7	G	52	GLU
9	I	41	VAL
9	I	58	ARG
10	J	30	SER
10	J	34	VAL
10	J	40	LEU
10	J	72	VAL
11	K	15	ALA
11	K	49	GLY
11	K	50	TYR
11	K	89	ALA
12	L	41	ARG
12	L	48	PRO
12	L	51	ALA
12	L	116	SER
12	L	121	GLY
13	M	6	GLY
13	M	85	GLY

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Mol	Chain	Res	Type
16	P	10	GLY
18	R	20	ALA
19	S	9	VAL
19	S	45	VAL
19	S	67	VAL
19	S	68	GLY
20	T	9	ASN
20	T	49	ALA
20	T	95	ALA
20	T	99	LEU
20	T	102	GLY
2	B	26	PRO
2	B	60	ASP
2	B	83	MET
2	B	89	GLY
2	B	204	ASN
4	D	175	SER
5	E	65	ASN
7	G	5	ARG
8	H	127	LEU
9	I	56	LEU
10	J	19	SER
10	J	60	ARG
10	J	61	GLU
10	J	90	LEU
11	K	35	PRO
11	K	101	SER
12	L	49	ASN
14	N	13	THR
14	N	23	ARG
17	Q	97	SER
19	S	28	LYS
19	S	30	LEU
19	S	32	LYS
20	T	74	LYS
2	B	126	GLU
2	B	165	VAL
3	C	39	ILE
3	C	100	ALA
3	C	188	LEU
7	G	4	ARG
7	G	81	GLY

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Mol	Chain	Res	Type
7	G	112	PRO
9	I	7	THR
9	I	12	GLU
9	I	119	ALA
13	M	123	ALA
14	N	12	ARG
14	N	60	SER
15	O	16	ALA
17	Q	33	GLY
20	T	50	GLU
21	V	3	LYS
2	B	155	LEU
3	C	24	ALA
3	C	66	VAL
3	C	127	ARG
4	D	123	HIS
7	G	53	LYS
9	I	121	ARG
14	N	36	PHE
15	O	84	LYS
19	S	31	ILE
2	B	127	ILE
3	C	108	ASN
3	C	174	PRO
4	D	5	ILE
9	I	43	ALA
10	J	26	ALA
2	B	124	SER
2	B	214	ILE
7	G	14	PRO
10	J	82	ILE
20	T	98	PRO
2	B	125	PRO
3	C	76	VAL
3	C	77	ILE
7	G	17	VAL
10	J	36	GLY
15	O	82	ILE
9	I	44	VAL
19	S	8	GLY
20	T	101	GLY
15	O	19	PRO

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Mol	Chain	Res	Type
20	T	96	GLY
3	C	75	VAL
11	K	90	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	202/220 (92%)	180 (89%)	22 (11%)	7	27
3	C	160/188 (85%)	142 (89%)	18 (11%)	7	25
4	D	180/180 (100%)	172 (96%)	8 (4%)	33	67
5	E	115/122 (94%)	100 (87%)	15 (13%)	5	19
6	F	90/90 (100%)	88 (98%)	2 (2%)	57	83
7	G	126/126 (100%)	122 (97%)	4 (3%)	44	77
8	H	119/119 (100%)	109 (92%)	10 (8%)	13	41
9	I	98/99 (99%)	90 (92%)	8 (8%)	13	42
10	J	87/91 (96%)	78 (90%)	9 (10%)	8	29
11	K	90/99 (91%)	84 (93%)	6 (7%)	19	51
12	L	104/111 (94%)	96 (92%)	8 (8%)	15	45
13	M	100/101 (99%)	90 (90%)	10 (10%)	9	30
14	N	49/49 (100%)	47 (96%)	2 (4%)	35	70
15	O	79/79 (100%)	72 (91%)	7 (9%)	11	37
16	P	72/74 (97%)	67 (93%)	5 (7%)	18	50
17	Q	96/96 (100%)	90 (94%)	6 (6%)	21	53
18	R	64/77 (83%)	61 (95%)	3 (5%)	30	65
19	S	71/79 (90%)	68 (96%)	3 (4%)	34	69
20	T	76/82 (93%)	69 (91%)	7 (9%)	11	35
21	V	19/21 (90%)	19 (100%)	0	100	100
All	All	1997/2103 (95%)	1844 (92%)	153 (8%)	15	45

All (153) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	8	LYS
2	B	12	GLU
2	B	17	PHE
2	B	23	ARG
2	B	24	TRP
2	B	25	ASN
2	B	87	ARG
2	B	114	ARG
2	B	139	LYS
2	B	144	ARG
2	B	146	GLN
2	B	155	LEU
2	B	157	ARG
2	B	164	VAL
2	B	170	GLU
2	B	178	ARG
2	B	204	ASN
2	B	213	LEU
2	B	221	LEU
2	B	231	GLU
2	B	232	PRO
2	B	236	TYR
3	C	3	ASN
3	C	5	ILE
3	C	34	LEU
3	C	47	LEU
3	C	56	ASP
3	C	75	VAL
3	C	82	GLU
3	C	90	GLU
3	C	91	LEU
3	C	99	VAL
3	C	107	GLN
3	C	139	GLN
3	C	164	ARG
3	C	167	TRP
3	C	175	LEU
3	C	179	ARG
3	C	188	LEU
3	C	204	LEU
4	D	15	GLU
4	D	29	PRO

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Mol	Chain	Res	Type
4	D	53	ASP
4	D	122	ARG
4	D	127	THR
4	D	157	LEU
4	D	192	GLU
4	D	199	ASN
5	E	12	LEU
5	E	26	PHE
5	E	31	LEU
5	E	38	GLN
5	E	41	VAL
5	E	43	LEU
5	E	56	GLN
5	E	65	ASN
5	E	68	GLU
5	E	73	ASN
5	E	79	GLU
5	E	80	ILE
5	E	89	ILE
5	E	120	THR
5	E	150	ARG
6	F	10	LEU
6	F	69	GLU
7	G	8	GLU
7	G	11	GLN
7	G	37	ASN
7	G	38	LEU
8	H	2	LEU
8	H	21	LYS
8	H	52	ASP
8	H	63	LEU
8	H	85	ARG
8	H	91	ARG
8	H	92	ARG
8	H	104	ARG
8	H	105	ARG
8	H	119	LEU
9	I	2	GLU
9	I	23	ASN
9	I	38	GLN
9	I	53	VAL
9	I	58	ARG

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Mol	Chain	Res	Type
9	I	79	LEU
9	I	111	ARG
9	I	121	ARG
10	J	6	ILE
10	J	15	THR
10	J	45	ARG
10	J	60	ARG
10	J	64	GLU
10	J	71	LEU
10	J	73	ASP
10	J	83	GLU
10	J	95	GLU
11	K	24	SER
11	K	29	ILE
11	K	35	PRO
11	K	54	ARG
11	K	84	VAL
11	K	92	GLU
12	L	17	LYS
12	L	33	ARG
12	L	53	ARG
12	L	60	LEU
12	L	81	SER
12	L	98	TYR
12	L	113	ARG
12	L	126	LYS
13	M	9	ILE
13	M	16	ASP
13	M	40	ASN
13	M	44	ARG
13	M	70	LEU
13	M	81	LEU
13	M	102	ARG
13	M	110	ARG
13	M	124	PRO
13	M	125	ARG
14	N	41	ARG
14	N	44	LEU
15	O	6	GLU
15	O	7	GLU
15	O	39	LEU
15	O	57	LEU

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Mol	Chain	Res	Type
15	O	70	LEU
15	O	81	LEU
15	O	83	GLU
16	P	2	VAL
16	P	8	ARG
16	P	28	ARG
16	P	53	VAL
16	P	62	VAL
17	Q	34	LYS
17	Q	38	ARG
17	Q	60	ILE
17	Q	68	ARG
17	Q	74	LEU
17	Q	98	LEU
18	R	36	ASN
18	R	38	GLU
18	R	55	ARG
19	S	10	PHE
19	S	15	LEU
19	S	20	LEU
20	T	42	GLN
20	T	45	GLN
20	T	57	ARG
20	T	73	HIS
20	T	75	ASN
20	T	84	LEU
20	T	86	ARG

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

Mol	Chain	Res	Type
2	B	19	HIS
2	B	25	ASN
2	B	40	HIS
2	B	146	GLN
2	B	204	ASN
3	C	3	ASN
3	C	6	HIS
3	C	31	HIS
3	C	69	HIS
3	C	110	ASN
3	C	118	GLN

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Mol	Chain	Res	Type
3	C	123	GLN
3	C	139	GLN
3	C	181	ASN
4	D	45	GLN
4	D	62	GLN
4	D	123	HIS
4	D	161	ASN
4	D	199	ASN
5	E	73	ASN
6	F	18	GLN
6	F	27	GLN
6	F	32	ASN
6	F	57	GLN
6	F	64	GLN
6	F	94	GLN
6	F	100	ASN
7	G	37	ASN
7	G	86	GLN
9	I	23	ASN
9	I	73	GLN
10	J	56	HIS
10	J	62	HIS
10	J	76	ASN
10	J	78	ASN
10	J	84	GLN
11	K	22	HIS
11	K	62	GLN
11	K	93	GLN
11	K	117	ASN
12	L	49	ASN
12	L	75	HIS
13	M	12	ASN
13	M	40	ASN
13	M	62	ASN
13	M	77	ASN
15	O	13	GLN
15	O	37	ASN
17	Q	16	GLN
17	Q	26	GLN
18	R	36	ASN
19	S	14	HIS
19	S	53	ASN

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Mol	Chain	Res	Type
19	S	56	GLN
20	T	42	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1511/1522 (99%)	220 (14%)	0

All (220) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	48	C
1	A	49	U
1	A	51	A
1	A	52	G
1	A	61	G
1	A	81	U
1	A	101	A
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	182	U
1	A	190(D)	U
1	A	190(E)	U
1	A	190(F)	G
1	A	195	A
1	A	197	A
1	A	198	G
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G

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Mol	Chain	Res	Type
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	282	A
1	A	289	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	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	428	G
1	A	429	U
1	A	430	A
1	A	439	A
1	A	460	A
1	A	461	C
1	A	462	G
1	A	481	G
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

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Mol	Chain	Res	Type
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
1	A	575	G
1	A	576	G
1	A	577	G
1	A	588	G
1	A	653	A
1	A	665	A
1	A	686	U
1	A	687	A
1	A	688	G
1	A	702	A
1	A	703	G
1	A	718	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	782	A
1	A	793	U
1	A	794	A
1	A	813	U
1	A	815	A
1	A	817	C
1	A	819	A
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	858	G

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Mol	Chain	Res	Type
1	A	902	G
1	A	913	A
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	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
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	1050	G
1	A	1053	G
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	1126	U
1	A	1129	C
1	A	1130	A

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Mol	Chain	Res	Type
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	1146	A
1	A	1152	A
1	A	1157	A
1	A	1159	U
1	A	1183	A
1	A	1184	G
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1201	A
1	A	1202	G
1	A	1211	U
1	A	1212	U
1	A	1215	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1238	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	1299	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1305	G
1	A	1320	C
1	A	1332	A
1	A	1347	G

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Mol	Chain	Res	Type
1	A	1348	U
1	A	1363	A
1	A	1364	U
1	A	1365	G
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	1447	G
1	A	1452	C
1	A	1490	C
1	A	1499	A
1	A	1502	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G

There are no RNA pucker outliers to report.

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 190 ligands modelled in this entry, 188 are unknown and 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2			OWAB(Å ²)	Q < 0.9
1	A	1510/1522 (99%)	0.57	49 (3%)	48	24	28, 59, 140, 201	0
2	B	234/256 (91%)	0.11	8 (3%)	46	23	31, 77, 150, 191	0
3	C	206/239 (86%)	0.02	4 (1%)	67	44	35, 77, 131, 153	0
4	D	208/208 (100%)	0.31	7 (3%)	46	23	32, 64, 114, 169	0
5	E	150/161 (93%)	0.06	1 (0%)	87	72	26, 48, 86, 139	0
6	F	101/101 (100%)	-0.27	0	100	100	47, 84, 120, 138	0
7	G	155/155 (100%)	-0.18	3 (1%)	67	44	38, 72, 122, 156	0
8	H	138/138 (100%)	0.16	3 (2%)	62	39	19, 45, 78, 131	0
9	I	127/128 (99%)	1.24	35 (27%)	1	0	36, 85, 129, 175	0
10	J	98/104 (94%)	0.87	22 (22%)	1	0	41, 106, 158, 190	0
11	K	119/129 (92%)	0.52	5 (4%)	37	18	34, 59, 105, 175	0
12	L	124/135 (91%)	0.35	5 (4%)	39	19	25, 60, 113, 162	0
13	M	125/126 (99%)	0.66	11 (8%)	11	4	46, 79, 138, 189	0
14	N	60/60 (100%)	1.03	8 (13%)	4	1	39, 72, 108, 148	0
15	O	88/88 (100%)	0.21	1 (1%)	80	61	31, 60, 114, 182	0
16	P	83/88 (94%)	0.45	2 (2%)	59	34	31, 53, 74, 138	0
17	Q	104/104 (100%)	1.03	10 (9%)	9	3	32, 55, 128, 201	0
18	R	73/88 (82%)	0.28	2 (2%)	55	29	37, 68, 137, 186	0
19	S	80/92 (86%)	0.52	8 (10%)	8	3	54, 95, 153, 187	0
20	T	99/106 (93%)	0.68	12 (12%)	5	2	29, 60, 115, 187	0
21	V	24/26 (92%)	2.45	14 (58%)	0	0	36, 66, 103, 129	0
All	All	3906/4054 (96%)	0.46	210 (5%)	26	12	19, 64, 135, 201	0

All (210) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
11	K	129	SER	17.2
17	Q	102	GLY	16.5
19	S	3	ARG	15.3
17	Q	104	LYS	13.5
13	M	123	ALA	11.8
17	Q	105	ALA	11.6
13	M	124	PRO	10.9
17	Q	103	GLY	9.3
9	I	8	GLY	8.2
11	K	128	ALA	7.3
13	M	125	ARG	7.3
21	V	6	ARG	7.2
9	I	7	THR	6.9
7	G	5	ARG	6.5
20	T	103	GLY	6.4
1	A	1129	C	6.4
2	B	133	LYS	6.3
8	H	1	MET	5.8
15	O	89	GLY	5.8
11	K	127	LYS	5.7
9	I	105	ASP	5.4
20	T	9	ASN	5.2
7	G	4	ARG	4.8
10	J	43	ARG	4.7
10	J	45	ARG	4.7
10	J	71	LEU	4.6
1	A	81	U	4.5
13	M	126	LYS	4.4
12	L	19	ARG	4.3
2	B	16	HIS	4.2
9	I	9	ARG	4.2
21	V	16	GLY	4.2
9	I	10	ARG	4.2
14	N	61	TRP	4.1
14	N	29	ARG	4.0
9	I	15	ALA	4.0
9	I	119	ALA	4.0
4	D	3	ARG	3.9
9	I	104	ARG	3.9
10	J	59	SER	3.9
9	I	75	ASP	3.9
9	I	106	ALA	3.8
9	I	128	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
21	V	24	ARG	3.7
19	S	4	SER	3.7
9	I	109	VAL	3.6
21	V	17	THR	3.6
1	A	1144	G	3.6
9	I	66	ARG	3.5
4	D	35	ARG	3.5
9	I	102	LEU	3.5
1	A	1540	U	3.4
19	S	37	ARG	3.4
21	V	25	LYS	3.4
1	A	1286	A	3.4
9	I	14	VAL	3.4
14	N	6	LEU	3.4
1	A	1126	U	3.4
8	H	2	LEU	3.3
10	J	65	LEU	3.3
9	I	115	GLY	3.3
1	A	1283	G	3.3
19	S	69	HIS	3.3
10	J	70	ARG	3.2
10	J	64	GLU	3.2
20	T	36	LEU	3.2
1	A	349	A	3.2
9	I	103	THR	3.2
21	V	18	TYR	3.1
4	D	73	ARG	3.1
9	I	17	VAL	3.1
12	L	33	ARG	3.1
10	J	46	ARG	3.0
10	J	7	LYS	3.0
12	L	28	LYS	3.0
10	J	72	VAL	3.0
1	A	1446	A	3.0
10	J	47	PHE	3.0
9	I	11	LYS	3.0
9	I	110	GLU	3.0
16	P	12	LYS	3.0
10	J	40	LEU	2.9
1	A	202	U	2.9
4	D	23	GLY	2.9
2	B	134	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
2	B	130	ARG	2.9
9	I	114	TYR	2.9
17	Q	68	ARG	2.8
1	A	1251	A	2.8
1	A	1182	G	2.8
10	J	6	ILE	2.8
1	A	1183	A	2.8
9	I	65	VAL	2.8
1	A	1300	G	2.8
10	J	44	VAL	2.8
10	J	60	ARG	2.8
1	A	1237	C	2.8
7	G	8	GLU	2.7
9	I	113	LYS	2.7
1	A	1124	G	2.7
10	J	66	ARG	2.7
20	T	16	HIS	2.7
21	V	22	ARG	2.7
1	A	1279	A	2.6
10	J	63	PHE	2.6
21	V	14	TRP	2.6
8	H	3	THR	2.6
9	I	33	PHE	2.6
1	A	1280	A	2.6
1	A	1259	C	2.6
1	A	1539	C	2.6
9	I	116	LYS	2.6
1	A	351	G	2.6
1	A	1260	C	2.6
20	T	17	ARG	2.6
9	I	108	VAL	2.6
10	J	37	PRO	2.6
19	S	5	LEU	2.6
9	I	19	LEU	2.6
1	A	982	U	2.5
1	A	350	G	2.5
21	V	5	ASP	2.5
17	Q	101	ARG	2.5
14	N	60	SER	2.5
21	V	15	ARG	2.5
1	A	1139	G	2.5
18	R	48	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
21	V	12	LYS	2.5
20	T	55	ILE	2.5
14	N	39	LEU	2.5
17	Q	96	GLN	2.5
1	A	532	A	2.5
1	A	341	C	2.4
9	I	97	LYS	2.4
1	A	1138	G	2.4
2	B	108	ILE	2.4
4	D	71	SER	2.4
11	K	110	ASP	2.4
19	S	71	LEU	2.4
2	B	148	TYR	2.4
13	M	2	ALA	2.4
20	T	13	LEU	2.4
10	J	24	VAL	2.4
1	A	1171	G	2.4
1	A	1544	U	2.4
20	T	20	LEU	2.4
21	V	10	ARG	2.3
20	T	35	THR	2.3
20	T	58	LYS	2.3
1	A	1347	G	2.3
1	A	1355	G	2.3
1	A	1190	G	2.3
14	N	44	LEU	2.3
13	M	106	ASN	2.3
9	I	16	ARG	2.3
3	C	27	LYS	2.3
17	Q	87	LYS	2.3
1	A	164	U	2.2
12	L	61	THR	2.2
10	J	4	ILE	2.2
14	N	34	TYR	2.2
1	A	353	A	2.2
1	A	1253	G	2.2
21	V	3	LYS	2.2
9	I	111	ARG	2.2
19	S	2	PRO	2.2
9	I	117	HIS	2.2
18	R	31	LEU	2.2
13	M	102	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1282	C	2.2
13	M	7	VAL	2.2
9	I	118	LYS	2.2
4	D	157	LEU	2.2
17	Q	39	SER	2.2
1	A	1127	G	2.2
9	I	36	TYR	2.2
9	I	70	LYS	2.2
2	B	131	PRO	2.2
13	M	9	ILE	2.2
13	M	13	LYS	2.2
14	N	3	ARG	2.2
5	E	20	GLN	2.2
10	J	75	ILE	2.2
1	A	1091	U	2.1
10	J	62	HIS	2.1
1	A	1361(A)	C	2.1
3	C	193	TYR	2.1
9	I	13	ALA	2.1
11	K	42	TRP	2.1
13	M	43	THR	2.1
19	S	67	VAL	2.1
3	C	188	LEU	2.1
1	A	396	G	2.1
21	V	9	ARG	2.1
20	T	10	LEU	2.1
1	A	733	A	2.1
1	A	1092	A	2.1
1	A	1370	G	2.1
1	A	924	C	2.1
17	Q	83	ASP	2.1
1	A	1387	G	2.0
12	L	85	ILE	2.0
20	T	39	LYS	2.0
1	A	1403	C	2.0
4	D	31	CYS	2.0
1	A	1543	C	2.0
16	P	41	PRO	2.0
2	B	96	ARG	2.0
1	A	1252	A	2.0
3	C	196	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å ²)	Q<0.9
23	UNX	A	1697	1/1	0.07	2.06	127.12	57,57,57,57	1
23	UNX	A	1625	1/1	0.49	1.11	73.33	57,57,57,57	1
23	UNX	A	1696	1/1	0.45	1.47	72.82	57,57,57,57	1
23	UNX	A	1698	1/1	0.39	1.00	56.08	57,57,57,57	1
23	UNX	A	1701	1/1	0.15	1.08	51.47	57,57,57,57	1
23	UNX	A	1615	1/1	0.48	0.87	43.49	57,57,57,57	1
23	UNX	A	1609	1/1	0.70	0.67	42.01	57,57,57,57	1
23	UNX	A	1571	1/1	0.60	0.99	41.22	57,57,57,57	1
23	UNX	A	1648	1/1	0.76	0.62	38.39	57,57,57,57	1
23	UNX	A	1604	1/1	0.56	0.78	36.16	57,57,57,57	1
23	UNX	A	1607	1/1	0.81	0.74	32.83	57,57,57,57	1
23	UNX	A	1716	1/1	0.57	0.71	32.34	57,57,57,57	1
23	UNX	A	1699	1/1	0.75	0.95	31.27	57,57,57,57	1
23	UNX	A	1633	1/1	0.82	0.77	25.89	57,57,57,57	1
23	UNX	A	1611	1/1	0.69	0.79	21.13	57,57,57,57	1
23	UNX	A	1639	1/1	0.57	0.63	20.62	57,57,57,57	1
23	UNX	A	1562	1/1	0.82	0.99	19.19	57,57,57,57	1
23	UNX	A	1575	1/1	0.57	0.73	17.68	57,57,57,57	1
23	UNX	A	1627	1/1	0.87	0.78	17.61	57,57,57,57	1
23	UNX	A	1631	1/1	0.90	0.91	17.06	57,57,57,57	1
23	UNX	A	1592	1/1	0.81	0.69	15.98	57,57,57,57	0
23	UNX	A	1598	1/1	0.40	0.55	12.77	57,57,57,57	1
23	UNX	A	1700	1/1	0.53	0.53	12.22	57,57,57,57	1
23	UNX	A	1664	1/1	0.30	0.79	12.07	57,57,57,57	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
23	UNX	A	1711	1/1	0.68	0.66	10.11	57,57,57,57	1
23	UNX	B	257	1/1	0.73	0.46	8.61	57,57,57,57	1
23	UNX	A	1668	1/1	0.70	0.59	8.30	57,57,57,57	1
23	UNX	A	1672	1/1	0.57	0.63	7.86	57,57,57,57	1
23	UNX	A	1702	1/1	0.70	0.64	7.67	57,57,57,57	1
23	UNX	A	1703	1/1	0.32	0.45	6.94	57,57,57,57	1
23	UNX	A	1680	1/1	0.20	0.64	6.91	57,57,57,57	1
23	UNX	A	1719	1/1	0.75	0.84	6.33	57,57,57,57	1
23	UNX	A	1569	1/1	0.70	0.71	4.68	57,57,57,57	1
23	UNX	A	1608	1/1	0.77	0.41	4.19	57,57,57,57	1
23	UNX	A	1621	1/1	0.40	0.63	2.05	57,57,57,57	1
23	UNX	A	1630	1/1	0.69	0.28	-0.40	57,57,57,57	1
23	UNX	M	143	1/1	0.79	0.29	-0.50	57,57,57,57	1
22	ZN	N	307	1/1	0.99	0.17	-0.71	67,67,67,67	0
23	UNX	A	1566	1/1	0.80	1.02	-	57,57,57,57	1
23	UNX	A	94	1/1	0.78	1.23	-	57,57,57,57	1
23	UNX	A	1554	1/1	0.96	0.81	-	57,57,57,57	0
23	UNX	A	100	1/1	0.71	0.70	-	57,57,57,57	1
23	UNX	A	1578	1/1	0.83	1.02	-	57,57,57,57	1
23	UNX	A	1689	1/1	0.55	1.47	-	57,57,57,57	1
23	UNX	A	1597	1/1	0.79	0.85	-	57,57,57,57	1
23	UNX	A	1594	1/1	0.92	0.81	-	57,57,57,57	1
23	UNX	A	1637	1/1	0.52	0.85	-	57,57,57,57	1
23	UNX	A	1646	1/1	0.68	0.51	-	57,57,57,57	1
23	UNX	A	1705	1/1	0.65	0.93	-	57,57,57,57	1
23	UNX	A	1644	1/1	0.68	2.26	-	57,57,57,57	1
23	UNX	A	1574	1/1	0.78	0.87	-	57,57,57,57	1
23	UNX	A	1584	1/1	0.82	0.46	-	57,57,57,57	1
23	UNX	A	1563	1/1	0.90	0.91	-	57,57,57,57	1
23	UNX	A	1675	1/1	0.06	1.03	-	57,57,57,57	1
23	UNX	A	1649	1/1	0.89	0.97	-	57,57,57,57	1
23	UNX	A	1650	1/1	0.71	0.76	-	57,57,57,57	1
23	UNX	A	1596	1/1	0.82	0.94	-	57,57,57,57	1
23	UNX	A	1616	1/1	0.94	0.85	-	57,57,57,57	1
23	UNX	A	1721	1/1	0.64	1.25	-	57,57,57,57	1
23	UNX	A	1634	1/1	0.67	0.60	-	57,57,57,57	1
23	UNX	A	1662	1/1	0.77	0.37	-	57,57,57,57	1
23	UNX	A	1579	1/1	0.33	1.21	-	57,57,57,57	1
23	UNX	A	86	1/1	0.61	0.78	-	57,57,57,57	1
23	UNX	A	1679	1/1	0.37	1.15	-	57,57,57,57	1
23	UNX	A	1636	1/1	0.35	0.74	-	57,57,57,57	1
23	UNX	A	1591	1/1	0.93	1.18	-	57,57,57,57	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
23	UNX	A	1688	1/1	0.94	0.96	-	57,57,57,57	1
23	UNX	A	1635	1/1	0.71	0.57	-	57,57,57,57	1
23	UNX	A	1695	1/1	0.62	0.76	-	57,57,57,57	1
23	UNX	A	1556	1/1	0.89	0.92	-	57,57,57,57	1
23	UNX	A	1713	1/1	0.84	1.24	-	57,57,57,57	1
23	UNX	A	1655	1/1	0.46	1.37	-	57,57,57,57	1
23	UNX	A	1678	1/1	0.94	0.99	-	57,57,57,57	1
23	UNX	A	1704	1/1	0.76	0.99	-	57,57,57,57	1
23	UNX	A	1706	1/1	0.91	1.07	-	57,57,57,57	1
23	UNX	A	1572	1/1	0.77	1.08	-	57,57,57,57	1
23	UNX	A	1665	1/1	0.54	0.72	-	57,57,57,57	1
23	UNX	A	1723	1/1	0.76	1.06	-	55,55,55,55	1
23	UNX	A	1669	1/1	0.77	0.45	-	57,57,57,57	1
23	UNX	A	1641	1/1	0.66	0.75	-	57,57,57,57	1
23	UNX	A	1658	1/1	0.78	1.61	-	57,57,57,57	1
23	UNX	A	1599	1/1	0.86	0.94	-	57,57,57,57	1
23	UNX	A	1684	1/1	0.63	0.94	-	57,57,57,57	1
23	UNX	A	1643	1/1	0.53	0.51	-	57,57,57,57	1
23	UNX	A	1647	1/1	0.54	1.04	-	57,57,57,57	1
23	UNX	A	1686	1/1	0.91	0.99	-	57,57,57,57	1
23	UNX	A	71	1/1	0.84	0.87	-	57,57,57,57	1
23	UNX	A	1694	1/1	0.31	0.76	-	57,57,57,57	1
23	UNX	A	1623	1/1	0.88	0.93	-	57,57,57,57	1
23	UNX	A	1545	1/1	0.79	0.78	-	57,57,57,57	0
23	UNX	A	1656	1/1	0.81	1.06	-	57,57,57,57	1
23	UNX	A	1708	1/1	0.83	1.16	-	57,57,57,57	1
23	UNX	A	1552	1/1	0.95	0.89	-	57,57,57,57	1
23	UNX	A	1652	1/1	0.78	0.65	-	57,57,57,57	1
23	UNX	A	1550	1/1	0.96	0.92	-	57,57,57,57	1
23	UNX	A	1561	1/1	0.46	0.93	-	57,57,57,57	1
23	UNX	A	1547	1/1	0.95	0.88	-	57,57,57,57	0
23	UNX	A	1676	1/1	0.49	0.84	-	57,57,57,57	1
23	UNX	A	1582	1/1	0.16	0.81	-	57,57,57,57	1
23	UNX	A	1682	1/1	0.94	0.86	-	57,57,57,57	1
23	UNX	A	1717	1/1	0.59	0.69	-	57,57,57,57	1
23	UNX	A	1576	1/1	0.74	1.24	-	57,57,57,57	1
23	UNX	A	1602	1/1	0.82	0.99	-	57,57,57,57	1
23	UNX	A	1707	1/1	0.92	0.60	-	57,57,57,57	1
23	UNX	A	1617	1/1	0.80	0.80	-	57,57,57,57	1
23	UNX	A	1693	1/1	0.91	0.86	-	57,57,57,57	1
23	UNX	A	1603	1/1	0.85	0.81	-	57,57,57,57	1
23	UNX	A	1715	1/1	0.00	1.39	-	57,57,57,57	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
23	UNX	A	1660	1/1	0.84	0.97	-	57,57,57,57	1
23	UNX	A	1681	1/1	0.96	0.74	-	57,57,57,57	1
23	UNX	A	1691	1/1	0.31	1.33	-	57,57,57,57	1
23	UNX	A	1595	1/1	0.41	0.76	-	57,57,57,57	1
23	UNX	A	1666	1/1	0.77	1.06	-	57,57,57,57	1
23	UNX	A	1546	1/1	0.69	0.73	-	57,57,57,57	0
23	UNX	A	1548	1/1	0.90	0.82	-	57,57,57,57	0
23	UNX	A	1624	1/1	0.87	1.07	-	57,57,57,57	1
23	UNX	A	1663	1/1	0.74	0.95	-	57,57,57,57	1
23	UNX	A	1589	1/1	0.71	0.81	-	57,57,57,57	1
23	UNX	A	1667	1/1	0.53	0.68	-	57,57,57,57	1
23	UNX	A	1586	1/1	0.94	0.92	-	57,57,57,57	1
23	UNX	A	1673	1/1	0.36	1.06	-	57,57,57,57	1
23	UNX	A	1692	1/1	0.93	1.05	-	57,57,57,57	1
23	UNX	A	1570	1/1	0.43	0.81	-	57,57,57,57	1
23	UNX	A	1601	1/1	0.67	1.36	-	57,57,57,57	1
23	UNX	A	1687	1/1	0.81	1.06	-	57,57,57,57	1
23	UNX	A	1549	1/1	0.81	1.00	-	57,57,57,57	1
23	UNX	A	1555	1/1	0.91	0.77	-	57,57,57,57	0
23	UNX	A	1657	1/1	0.92	0.94	-	57,57,57,57	1
23	UNX	A	1638	1/1	0.56	1.05	-	57,57,57,57	1
23	UNX	A	1558	1/1	0.82	0.93	-	57,57,57,57	1
23	UNX	A	1614	1/1	0.71	1.03	-	57,57,57,57	1
23	UNX	A	1557	1/1	0.78	1.04	-	57,57,57,57	1
23	UNX	A	1613	1/1	0.48	0.96	-	57,57,57,57	1
23	UNX	A	1553	1/1	0.93	0.92	-	57,57,57,57	1
23	UNX	A	1654	1/1	0.89	1.17	-	57,57,57,57	1
23	UNX	A	1585	1/1	0.67	1.08	-	57,57,57,57	1
23	UNX	A	1626	1/1	0.60	2.34	-	57,57,57,57	1
23	UNX	A	1593	1/1	0.57	0.67	-	57,57,57,57	1
23	UNX	A	87	1/1	0.82	1.25	-	57,57,57,57	1
23	UNX	A	1683	1/1	-0.20	2.60	-	57,57,57,57	1
23	UNX	A	1645	1/1	0.66	0.54	-	57,57,57,57	1
23	UNX	A	1720	1/1	0.62	0.57	-	57,57,57,57	1
23	UNX	A	1670	1/1	0.26	0.75	-	57,57,57,57	1
23	UNX	A	72	1/1	0.46	1.52	-	57,57,57,57	1
23	UNX	A	1674	1/1	0.57	0.61	-	57,57,57,57	1
23	UNX	A	1618	1/1	0.45	0.46	-	57,57,57,57	1
23	UNX	A	1651	1/1	0.79	0.97	-	57,57,57,57	1
23	UNX	A	1565	1/1	0.63	1.41	-	57,57,57,57	1
23	UNX	A	1605	1/1	0.90	0.91	-	57,57,57,57	1
23	UNX	A	1685	1/1	0.68	0.40	-	57,57,57,57	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
23	UNX	A	1690	1/1	0.50	0.96	-	57,57,57,57	1
23	UNX	A	1606	1/1	0.80	0.71	-	57,57,57,57	1
23	UNX	A	1628	1/1	0.73	1.35	-	57,57,57,57	1
23	UNX	A	1583	1/1	0.57	1.45	-	57,57,57,57	1
23	UNX	A	1722	1/1	0.51	0.82	-	55,55,55,55	1
23	UNX	A	1629	1/1	0.61	0.54	-	57,57,57,57	1
23	UNX	A	1588	1/1	-0.47	1.00	-	57,57,57,57	1
23	UNX	A	1661	1/1	0.42	0.85	-	57,57,57,57	1
23	UNX	A	1659	1/1	0.74	1.13	-	57,57,57,57	1
22	ZN	D	306	1/1	0.95	0.48	-	67,67,67,67	0
23	UNX	A	1610	1/1	0.67	1.21	-	57,57,57,57	1
23	UNX	A	1642	1/1	0.75	0.85	-	57,57,57,57	1
23	UNX	A	1577	1/1	0.94	0.91	-	57,57,57,57	1
23	UNX	A	1710	1/1	0.86	1.00	-	57,57,57,57	1
23	UNX	A	1573	1/1	0.79	1.17	-	57,57,57,57	1
23	UNX	A	1712	1/1	0.91	0.92	-	57,57,57,57	1
23	UNX	A	1718	1/1	0.65	0.69	-	57,57,57,57	1
23	UNX	A	1567	1/1	0.90	0.81	-	57,57,57,57	1
23	UNX	A	1612	1/1	0.60	0.73	-	57,57,57,57	1
23	UNX	A	1559	1/1	0.92	0.89	-	57,57,57,57	0
23	UNX	A	1677	1/1	0.50	0.68	-	57,57,57,57	1
23	UNX	A	1714	1/1	0.93	1.07	-	57,57,57,57	1
23	UNX	A	1671	1/1	0.78	1.11	-	57,57,57,57	1
23	UNX	A	1632	1/1	0.25	0.92	-	57,57,57,57	1
23	UNX	A	1581	1/1	0.83	1.14	-	57,57,57,57	1
23	UNX	A	1600	1/1	0.49	0.74	-	57,57,57,57	1
23	UNX	A	1580	1/1	0.87	0.79	-	57,57,57,57	1
23	UNX	A	1587	1/1	0.97	1.11	-	57,57,57,57	1
23	UNX	A	1709	1/1	0.89	0.99	-	57,57,57,57	1
23	UNX	A	85	1/1	0.94	0.99	-	57,57,57,57	1
23	UNX	A	1653	1/1	0.86	0.56	-	57,57,57,57	1
23	UNX	A	1640	1/1	-0.02	1.00	-	57,57,57,57	1
23	UNX	A	1568	1/1	0.74	0.69	-	57,57,57,57	1
23	UNX	A	1551	1/1	0.66	0.82	-	57,57,57,57	1
23	UNX	A	1619	1/1	0.78	0.94	-	57,57,57,57	1
23	UNX	A	1564	1/1	0.91	0.98	-	57,57,57,57	1
23	UNX	A	1590	1/1	0.80	1.04	-	57,57,57,57	1
23	UNX	A	1620	1/1	0.59	1.36	-	57,57,57,57	1
23	UNX	A	1560	1/1	0.92	1.13	-	57,57,57,57	1
23	UNX	A	1622	1/1	0.80	1.42	-	57,57,57,57	1

6.5 Other polymers ⓘ

There are no such residues in this entry.