Full wwPDB X-ray Structure Validation Report ⓘ

Sep 17, 2023 – 10:23 PM EDT

PDB ID	:	4YY3
Title	:	30S ribosomal subunit- HigB complex
Authors	:	Schureck, M.A.; Maehigashi, T.; Dunham, C.M.
Deposited on	:	2015-03-23
Resolution	:	3.60 Å(reported)

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

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

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

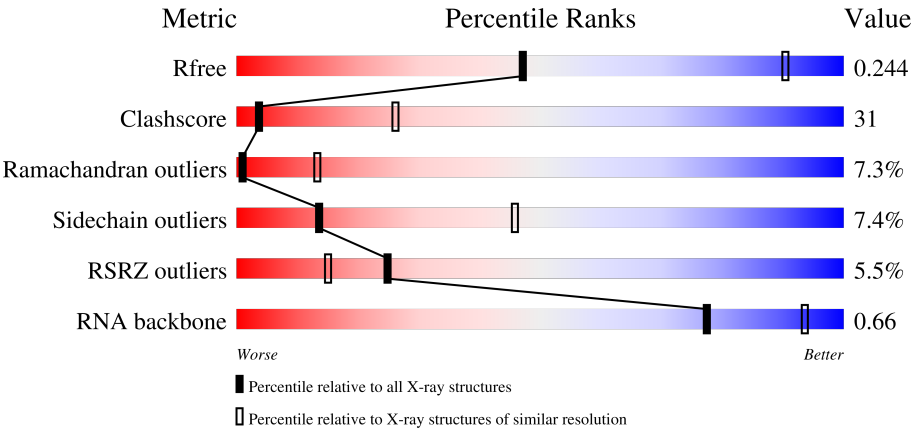
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)
RNA backbone	3102	1017 (4.20-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	6% 34% 51% 12% • •
2	B	256	3% 25% 52% 12% • 9%
3	C	239	5% 26% 46% 14% • 14%
4	D	209	5% 43% 51% 5%

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Mol	Chain	Length	Quality of chain
5	E	162	38% 46% 9% 7%
6	F	101	8% 45% 53%
7	G	156	2% 44% 53%
8	H	138	44% 47% 8%
9	I	128	8% 30% 61% 8%
10	J	105	9% 16% 56% 20% 7%
11	K	129	2% 30% 54% 7% 8%
12	L	132	% 35% 48% 11% 6%
13	M	126	8% 25% 60% 8% 6%
14	N	61	31% 51% 15%
15	O	89	3% 38% 49% 11%
16	P	88	36% 55% 6%
17	Q	105	% 49% 42% 5% 5%
18	R	88	3% 23% 55% 6% 17%
19	S	93	9% 22% 56% 12% 10%
20	T	106	8% 32% 49% 11% 7%
21	V	27	33% 52% 11%
22	Y	118	26% 53% 24% 22%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	MG	A	1603	-	-	-	X
23	MG	A	1604	-	-	-	X
23	MG	A	1605	-	-	-	X
23	MG	A	1614	-	-	-	X
23	MG	A	1616	-	-	-	X
23	MG	A	1622	-	-	-	X
23	MG	A	1623	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	MG	A	1624	-	-	-	X
23	MG	A	1628	-	-	-	X
23	MG	A	1629	-	-	-	X
23	MG	A	1632	-	-	-	X
23	MG	A	1634	-	-	-	X
23	MG	A	1635	-	-	-	X
23	MG	A	1637	-	-	-	X
23	MG	A	1639	-	-	-	X
23	MG	A	1642	-	-	-	X
23	MG	A	1643	-	-	-	X
23	MG	A	1665	-	-	-	X
23	MG	A	1671	-	-	-	X
23	MG	A	1677	-	-	-	X
23	MG	A	1689	-	-	-	X
23	MG	A	1696	-	-	-	X
23	MG	A	1699	-	-	-	X
23	MG	A	1701	-	-	-	X
23	MG	A	1705	-	-	-	X
23	MG	A	1713	-	-	-	X
23	MG	A	1714	-	-	-	X
23	MG	A	1718	-	-	-	X
23	MG	A	1730	-	-	-	X
23	MG	A	1734	-	-	-	X
23	MG	A	1735	-	-	-	X
23	MG	A	1742	-	-	-	X
23	MG	A	1743	-	-	-	X
23	MG	A	1747	-	-	-	X
23	MG	A	1748	-	-	-	X
23	MG	A	1760	-	-	-	X
23	MG	A	1761	-	-	-	X
23	MG	A	1762	-	-	-	X
23	MG	A	1763	-	-	-	X
23	MG	A	1764	-	-	-	X
23	MG	A	1767	-	-	-	X
23	MG	A	1769	-	-	-	X
23	MG	A	1774	-	-	-	X
23	MG	A	1775	-	-	-	X
23	MG	A	1776	-	-	-	X
23	MG	A	1777	-	-	-	X
23	MG	A	1779	-	-	-	X
23	MG	A	1782	-	-	-	X
23	MG	A	1784	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	MG	A	1785	-	-	-	X
23	MG	A	1789	-	-	-	X
23	MG	A	1790	-	-	-	X
23	MG	D	302	-	-	-	X

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 52640 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 rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	1513	32514	14472	6016	10513	1513	0	0	0

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

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

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

- 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	0	0	0
			1010	639	197	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	118	Total	C	N	O	S	0	0	0
			937	579	193	163	2			

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

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	100	Total	C	N	O	S	0	0	0
			834	534	155	143	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
			598	381	118	99			

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	84	Total	C	N	O	S	0	0	0
			674	430	126	116	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
			763	470	162	129	2			

- 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 a protein called Killer protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
22	Y	92	Total	C	N	O	0	0	0
			756	484	134	138			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	0	MET	-	initiating methionine	UNP Q7A225
Y	1	GLY	-	expression tag	UNP Q7A225
Y	93	LYS	-	expression tag	UNP Q7A225
Y	94	LEU	-	expression tag	UNP Q7A225
Y	95	GLY	-	expression tag	UNP Q7A225
Y	96	PRO	-	expression tag	UNP Q7A225
Y	97	GLU	-	expression tag	UNP Q7A225
Y	98	GLN	-	expression tag	UNP Q7A225
Y	99	LYS	-	expression tag	UNP Q7A225
Y	100	LEU	-	expression tag	UNP Q7A225
Y	101	ILE	-	expression tag	UNP Q7A225
Y	102	SER	-	expression tag	UNP Q7A225
Y	103	GLU	-	expression tag	UNP Q7A225
Y	104	GLU	-	expression tag	UNP Q7A225
Y	105	ASP	-	expression tag	UNP Q7A225
Y	106	LEU	-	expression tag	UNP Q7A225
Y	107	ASN	-	expression tag	UNP Q7A225
Y	108	SER	-	expression tag	UNP Q7A225
Y	109	ALA	-	expression tag	UNP Q7A225
Y	110	VAL	-	expression tag	UNP Q7A225
Y	111	ASP	-	expression tag	UNP Q7A225
Y	112	HIS	-	expression tag	UNP Q7A225
Y	113	HIS	-	expression tag	UNP Q7A225
Y	114	HIS	-	expression tag	UNP Q7A225
Y	115	HIS	-	expression tag	UNP Q7A225
Y	116	HIS	-	expression tag	UNP Q7A225
Y	117	HIS	-	expression tag	UNP Q7A225

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
23	A	191	Total Mg 191 191	0	0
23	B	1	Total Mg 1 1	0	0
23	D	1	Total Mg 1 1	0	0
23	E	1	Total Mg 1 1	0	0

- Molecule 24 is ZINC ION (three-letter code: ZN) (formula: Zn).

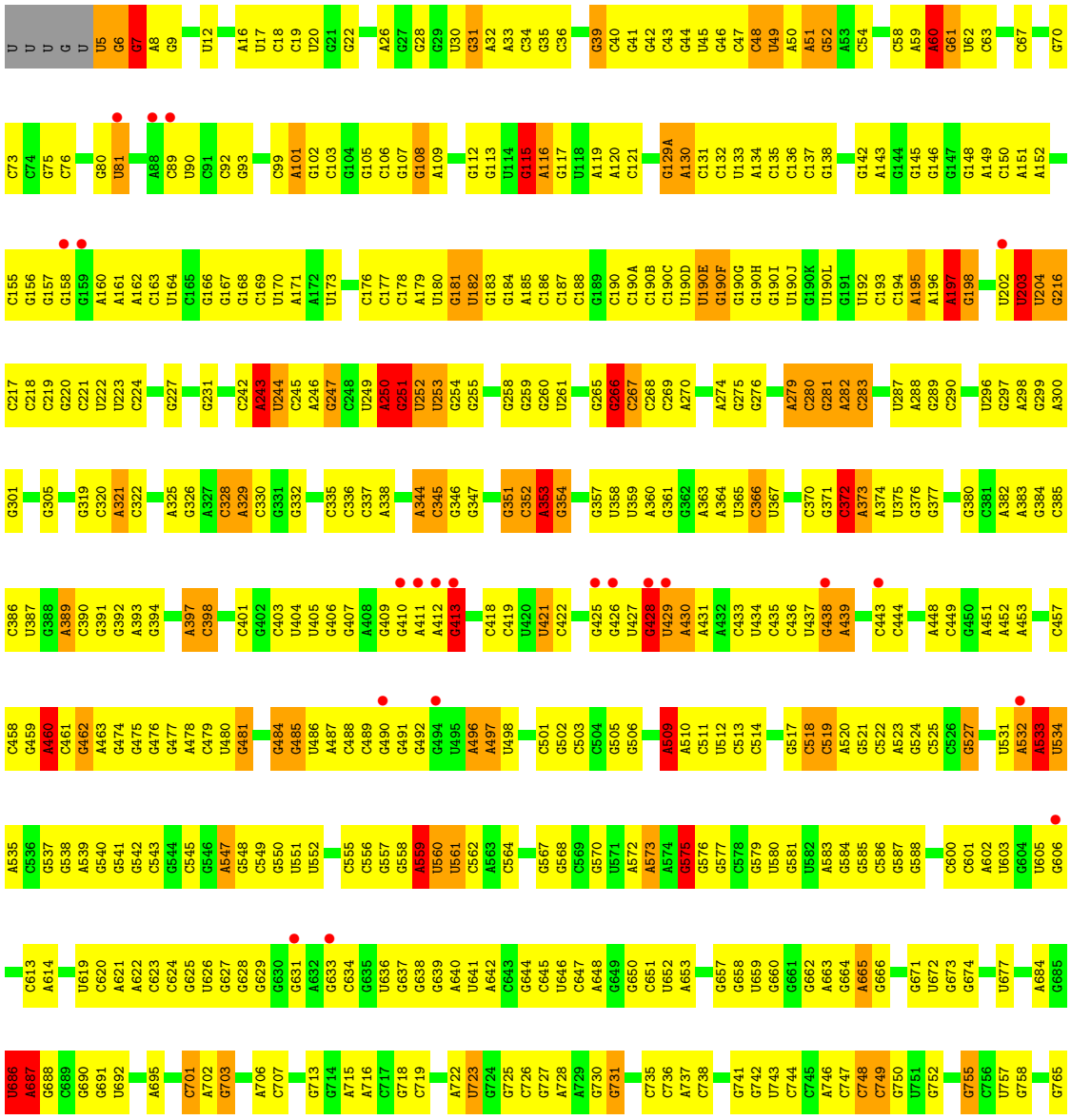
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
24	D	1	Total Zn 1 1	0	0
24	N	1	Total Zn 1 1	0	0

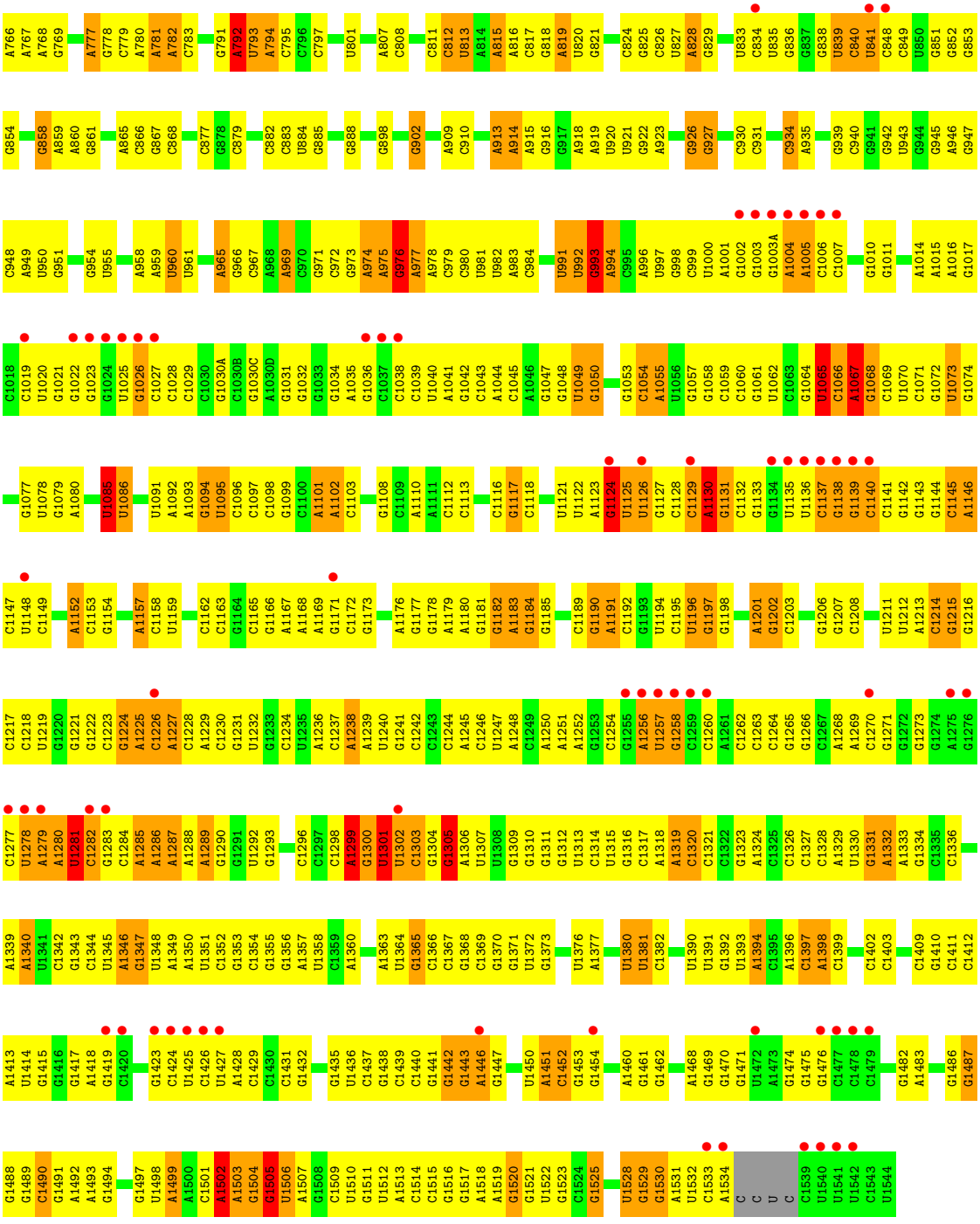
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 rRNA

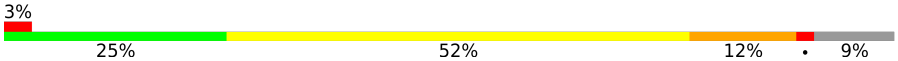
Chain A:

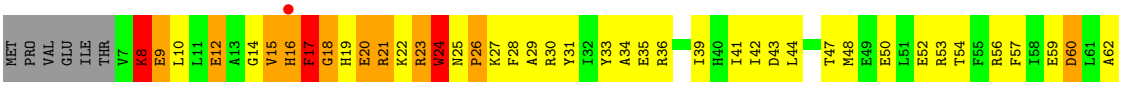


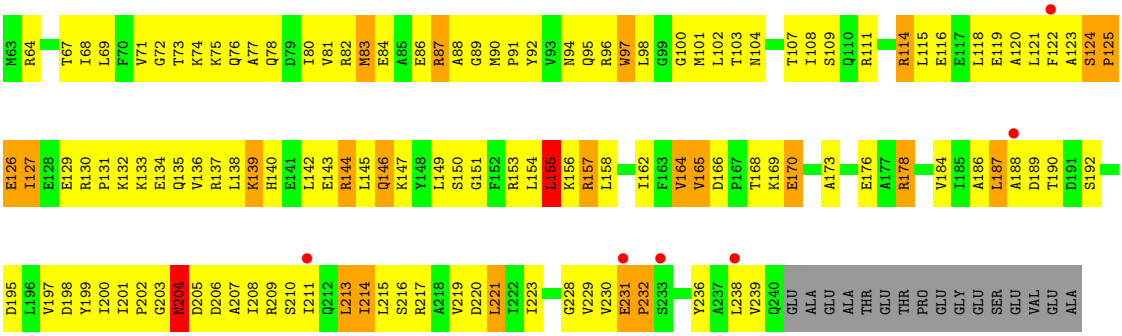


• Molecule 2: 30S ribosomal protein S2

Chain B:

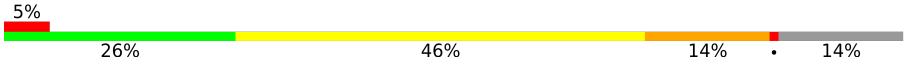


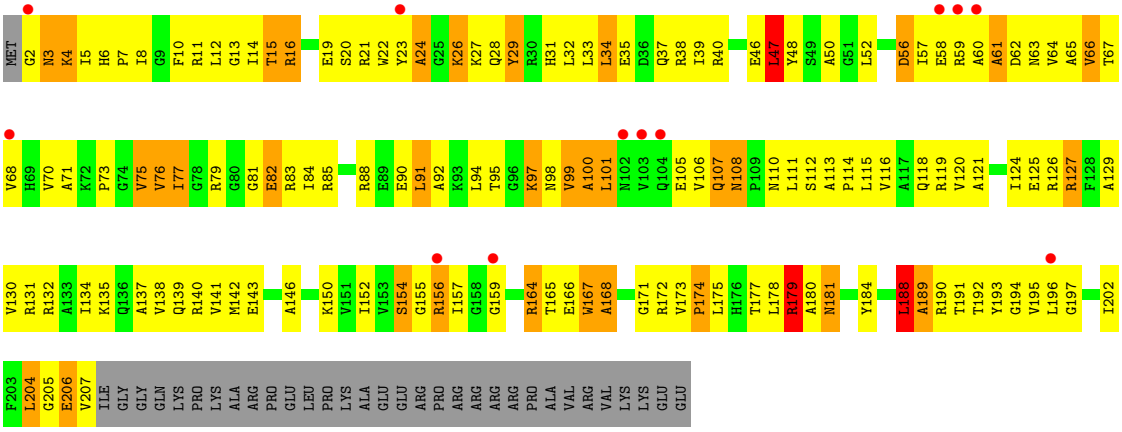




• Molecule 3: 30S ribosomal protein S3

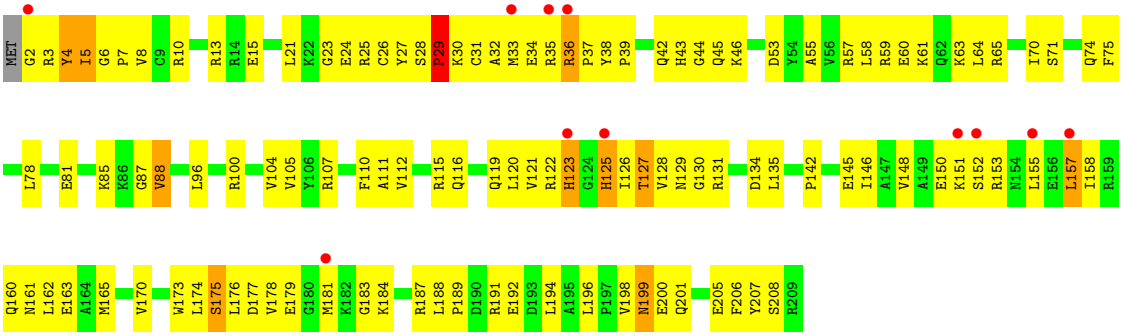
Chain C:





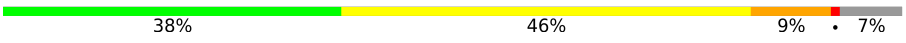
• Molecule 4: 30S ribosomal protein S4

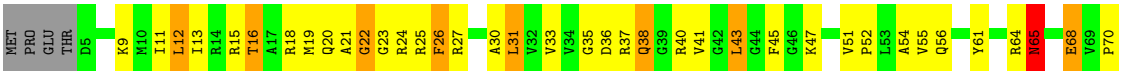
Chain D:

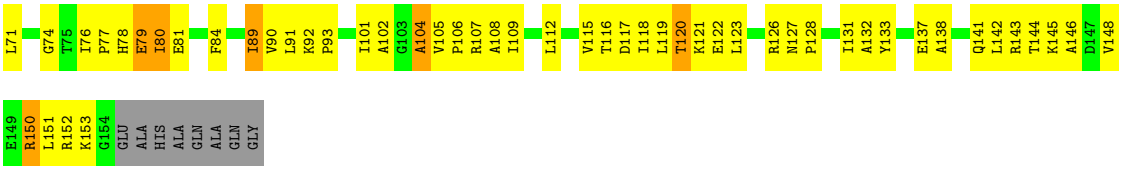


• Molecule 5: 30S ribosomal protein S5

Chain E:

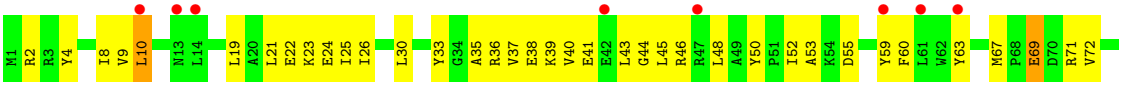


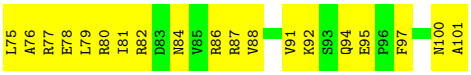




• Molecule 6: 30S ribosomal protein S6

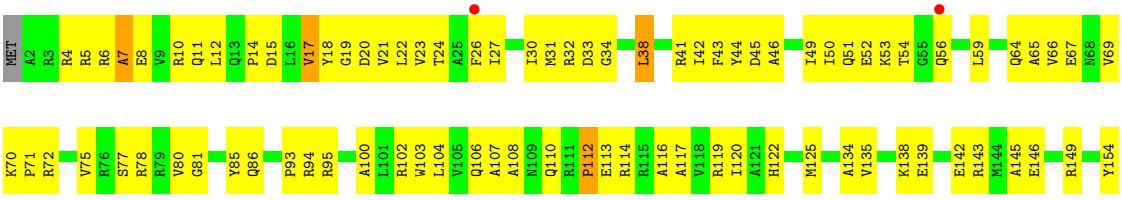
Chain F:





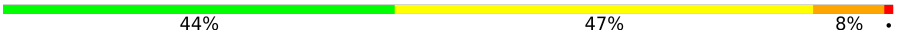
• Molecule 7: 30S ribosomal protein S7

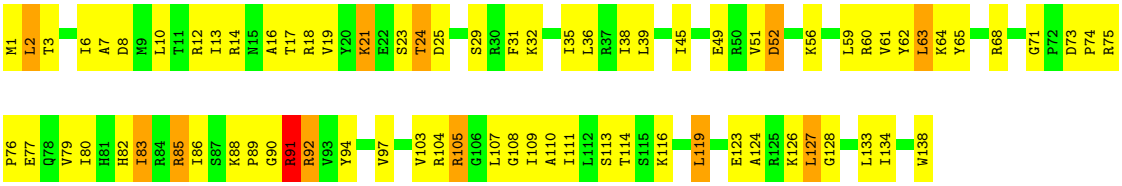
Chain G:



• Molecule 8: 30S ribosomal protein S8

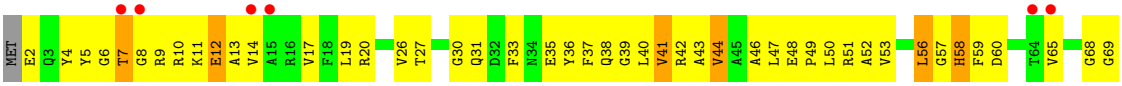
Chain H:

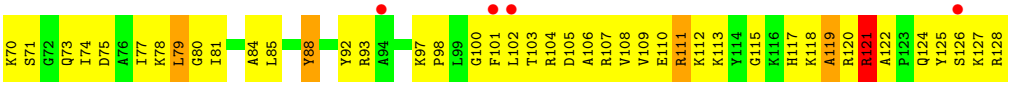




• Molecule 9: 30S ribosomal protein S9

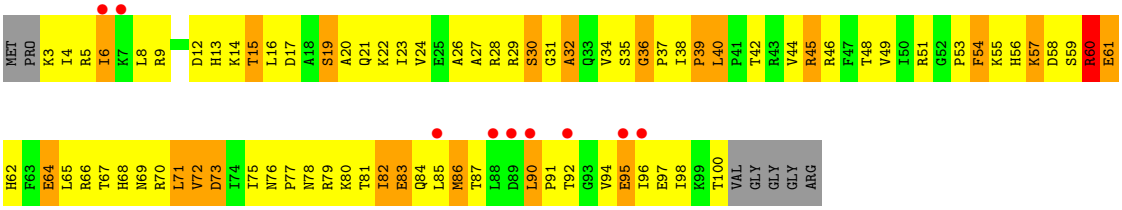
Chain I:





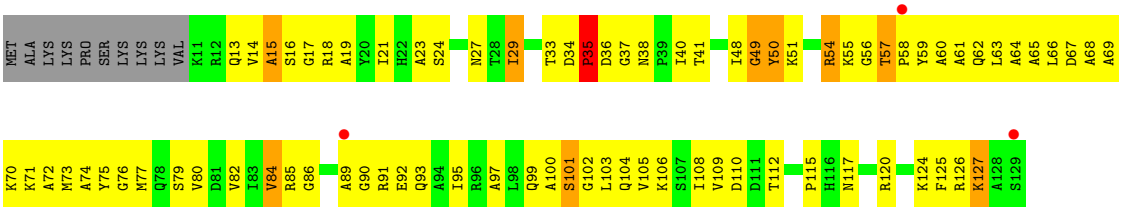
• Molecule 10: 30S ribosomal protein S10

Chain J:



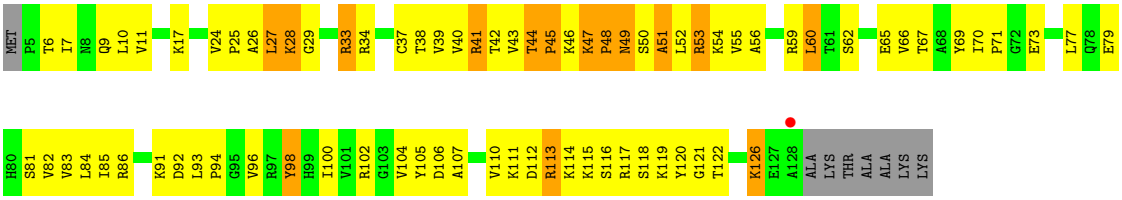
• Molecule 11: 30S ribosomal protein S11

Chain K:



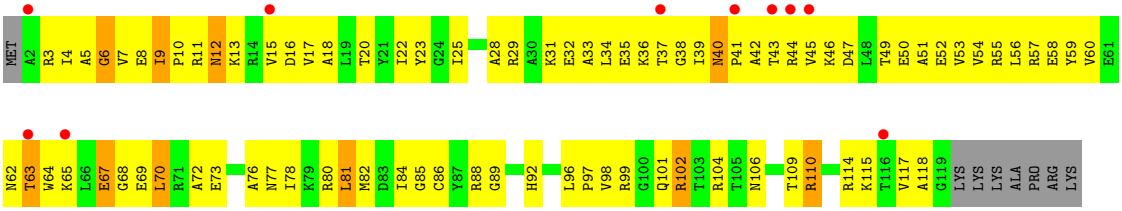
• Molecule 12: 30S ribosomal protein S12

Chain L:



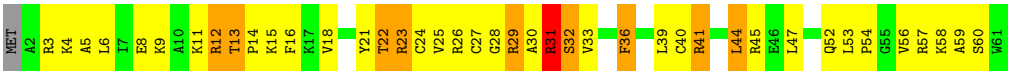
• Molecule 13: 30S ribosomal protein S13

Chain M:



• Molecule 14: 30S ribosomal protein S14 type Z

Chain N:

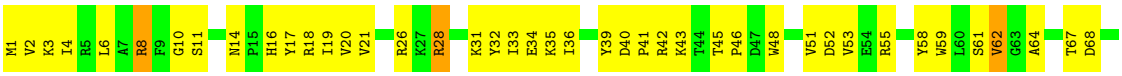


• Molecule 15: 30S ribosomal protein S15

Chain O:

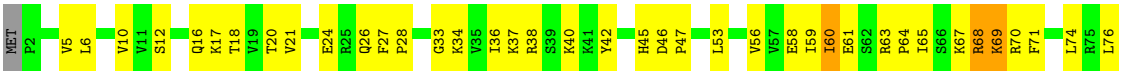
• Molecule 16: 30S ribosomal protein S16

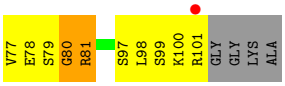
Chain P:



• Molecule 17: 30S ribosomal protein S17

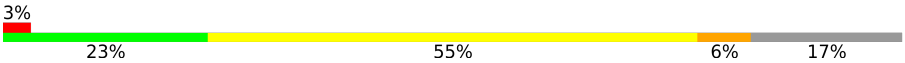
Chain Q:

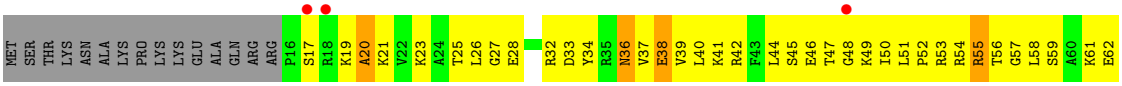


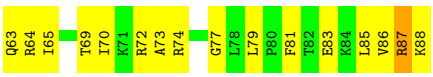


• Molecule 18: 30S ribosomal protein S18

Chain R:

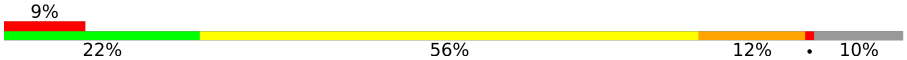


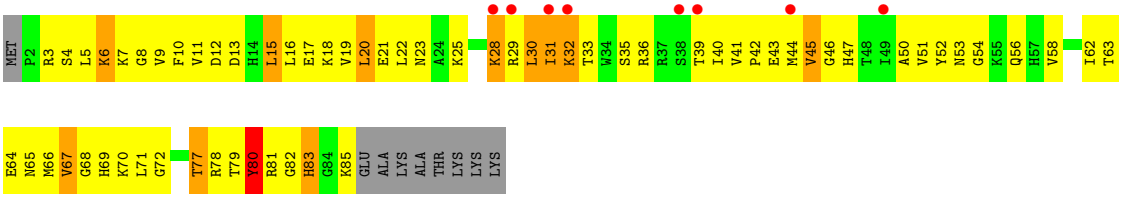




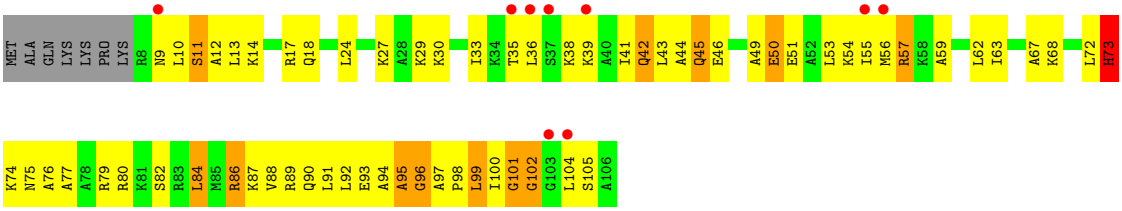
• Molecule 19: 30S ribosomal protein S19

Chain S:



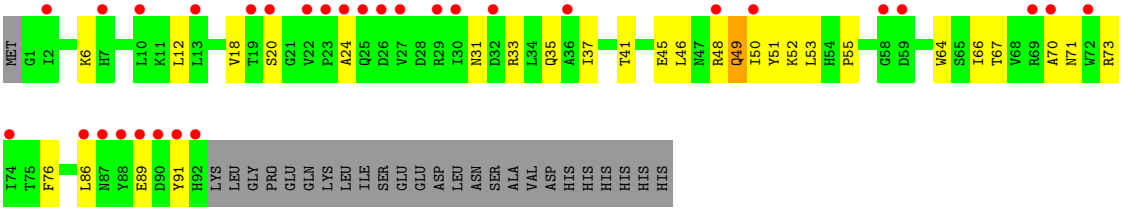


• Molecule 20: 30S ribosomal protein S20



• Molecule 21: 30S ribosomal protein Thx

• Molecule 22: Killer protein



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	402.59Å 402.59Å 176.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.16 – 3.60 49.91 – 3.60	Depositor EDS
% Data completeness (in resolution range)	98.5 (46.16-3.60) 98.6 (49.91-3.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.86 (at 3.57Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, R_{free}	0.214 , 0.239 0.218 , 0.244	Depositor DCC
R_{free} test set	7852 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å^2)	110.0	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 89.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	52640	wwPDB-VP
Average B, all atoms (Å^2)	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	38/56797 (0.1%)
2	B	0.36	0/1935	0.68	1/2609 (0.0%)
3	C	0.38	0/1636	0.66	0/2205
4	D	0.37	0/1733	0.63	0/2318
5	E	0.49	0/1162	0.79	0/1564
6	F	0.34	0/856	0.63	0/1154
7	G	0.35	0/1276	0.62	0/1709
8	H	0.44	0/1136	0.74	0/1527
9	I	0.36	0/1029	0.62	0/1379
10	J	0.35	0/805	0.70	0/1082
11	K	0.39	0/900	0.70	0/1213
12	L	0.46	1/986 (0.1%)	0.75	1/1320 (0.1%)
13	M	0.35	0/947	0.66	0/1270
14	N	0.41	0/501	0.77	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	0.45	0/847	0.73	0/1131
18	R	0.36	0/604	0.63	0/801
19	S	0.32	0/689	0.69	1/926 (0.1%)
20	T	0.39	0/765	0.73	0/1007
21	V	0.43	0/212	0.64	0/277
22	Y	0.33	0/773	0.46	0/1043
All	All	0.45	1/56646 (0.0%)	0.73	42/83951 (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	0	39

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	L	45	PRO	N-CD	5.02	1.54	1.47

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	243	A	C2'-C3'-O3'	9.49	130.38	109.50
1	A	559	A	C2'-C3'-O3'	9.13	129.59	109.50
1	A	1299	A	N9-C1'-C2'	8.60	125.18	114.00
1	A	366	C	C2'-C3'-O3'	7.85	126.77	109.50
1	A	687	A	C2'-C3'-O3'	7.74	126.54	109.50
1	A	197	A	N9-C1'-C2'	7.74	124.06	114.00
1	A	575	G	C2'-C3'-O3'	7.68	126.39	109.50
1	A	266	G	C2'-C3'-O3'	7.59	126.19	109.50
1	A	60	A	C2'-C3'-O3'	7.58	126.17	109.50
1	A	792	A	C2'-C3'-O3'	7.25	125.45	109.50
1	A	115	G	N9-C1'-C2'	6.99	123.09	114.00
1	A	1505	G	C2'-C3'-O3'	6.66	124.36	113.70
1	A	1067	A	C2'-C3'-O3'	6.57	124.22	113.70
1	A	1502	A	N9-C1'-C2'	6.56	122.52	114.00
1	A	115	G	C2'-C3'-O3'	6.42	123.97	113.70
1	A	372	C	C2'-C3'-O3'	6.38	123.91	113.70
1	A	7	G	C2'-C3'-O3'	6.34	123.85	113.70
1	A	509	A	C2'-C3'-O3'	6.31	123.80	113.70
1	A	460	A	N9-C1'-C2'	6.12	121.95	114.00
19	S	54	GLY	N-CA-C	-6.04	98.00	113.10
1	A	428	G	C2'-C3'-O3'	5.88	123.11	113.70
12	L	44	THR	C-N-CD	5.76	140.49	128.40
1	A	63	C	C5'-C4'-C3'	-5.75	106.79	116.00
1	A	266	G	C5'-C4'-C3'	-5.63	106.98	116.00
1	A	1124	G	N9-C1'-C2'	5.61	121.29	114.00
1	A	203	U	N1-C1'-C2'	5.57	121.24	114.00
1	A	1380	U	C2'-C3'-O3'	5.56	122.60	113.70
1	A	353	A	C5'-C4'-O4'	-5.50	102.50	109.10
15	O	45	VAL	N-CA-C	-5.43	96.34	111.00
1	A	1065	U	C1'-O4'-C4'	-5.42	105.56	109.90
1	A	533	A	P-O3'-C3'	5.40	126.18	119.70
2	B	187	LEU	N-CA-C	-5.36	96.53	111.00
1	A	1085	U	N1-C1'-C2'	5.36	120.96	114.00
1	A	389	A	C5'-C4'-C3'	5.33	124.53	116.00
1	A	484	G	C2'-C3'-O3'	5.32	122.21	113.70
1	A	108	G	O4'-C1'-N9	5.17	112.34	108.20
1	A	686	U	C5'-C4'-C3'	-5.11	107.82	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	960	U	P-O3'-C3'	5.10	125.82	119.70
1	A	49	U	C5'-C4'-C3'	-5.06	107.90	116.00
1	A	993	G	N9-C1'-C2'	5.05	120.56	114.00
1	A	413	G	N9-C1'-C2'	5.04	120.56	114.00
1	A	976	G	C5'-C4'-O4'	5.01	115.11	109.10

There are no chirality outliers.

All (39) 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	266	G	Sidechain
1	A	274	A	Sidechain
1	A	290	C	Sidechain
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

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Mol	Chain	Res	Type	Group
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 (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32514	0	16412	1110	0
2	B	1900	0	1951	211	0
3	C	1612	0	1677	220	0
4	D	1703	0	1765	140	0
5	E	1146	0	1207	106	0
6	F	843	0	857	72	0
7	G	1257	0	1296	93	0
8	H	1116	0	1177	66	0
9	I	1010	0	1037	114	0
10	J	792	0	835	137	0
11	K	885	0	904	80	0
12	L	970	0	1057	116	0
13	M	937	0	995	108	0
14	N	492	0	529	73	0
15	O	734	0	771	54	0
16	P	700	0	720	58	0
17	Q	834	0	904	61	0
18	R	598	0	670	70	0
19	S	674	0	699	85	0
20	T	763	0	861	78	0
21	V	208	0	221	23	0
22	Y	756	0	749	18	0
23	A	191	0	0	0	0
23	B	1	0	0	0	0
23	D	1	0	0	0	0
23	E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	D	1	0	0	0	0
24	N	1	0	0	0	0
All	All	52640	0	37294	2808	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 31.

All (2808) 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	1.14
2:B:77:ALA:HB2	2:B:211:ILE:HD13	1.22	1.14
1:A:1443:G:H5"	1:A:1446:A:H5'	1.29	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
1:A:182:U:H6	1:A:182:U:H5"	1.17	1.07
1:A:1528:U:O2'	1:A:1529:G:H3'	1.51	1.07
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	1.40	1.04
10:J:51:ARG:HB2	10:J:59:SER:HB3	1.34	1.03
1:A:182:U:C5	1:A:183:G:C8	2.46	1.03
1:A:182:U:C5	1:A:183:G:N9	2.28	1.02
20:T:39:LYS:HD2	20:T:55:ILE:HD13	1.41	1.02
1:A:1057:G:H5"	3:C:154:SER:HB2	1.43	1.00
13:M:49:THR:HG22	13:M:51:ALA:H	1.26	1.00
3:C:52:LEU:HD23	3:C:52:LEU:H	1.26	0.99
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.42	0.99
11:K:110:ASP:HB2	18:R:88:LYS:HD2	1.41	0.99
2:B:178:ARG:HH11	2:B:178:ARG:HG3	1.22	0.99
1:A:282:A:H5"	1:A:283:C:H5	1.22	0.99
11:K:54:ARG:HB3	11:K:54:ARG:HH11	1.26	0.99
1:A:182:U:H5	1:A:183:G:C8	1.78	0.98
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:1347:G:C6	9:I:107:ARG:NH2	2.32	0.97
1:A:1528:U:HO2'	1:A:1529:G:H3'	1.19	0.96
6:F:94:GLN:HE21	18:R:32:ARG:HD3	1.25	0.96
3:C:91:LEU:HD21	3:C:99:VAL:HG13	1.48	0.96
1:A:1226:C:H1'	19:S:83:HIS:CE1	2.00	0.96
11:K:54:ARG:O	11:K:57:THR:HG22	1.66	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
3:C:58:GLU:HB3	10:J:92:THR:HG21	1.50	0.94
12:L:41:ARG:HG2	12:L:42:THR:N	1.83	0.93
19:S:31:ILE:HG22	19:S:32:LYS:H	1.34	0.93
2:B:124:SER:HB2	2:B:125:PRO:HD2	1.49	0.93
1:A:1256:A:H4'	1:A:1257:U:H5'	1.51	0.92
1:A:1086:U:H3	1:A:1099:G:H22	1.08	0.92
1:A:1137:C:H4'	1:A:1138:G:C2	2.05	0.92
16:P:58:TYR:O	16:P:61:SER:HB3	1.68	0.92
1:A:1347:G:C5	9:I:107:ARG:NH1	2.37	0.92
13:M:40:ASN:HD22	13:M:41:PRO:CD	1.82	0.92
1:A:247:G:N3	1:A:282:A:C2	2.38	0.92
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:266:G:O3'	17:Q:67:LYS:HB2	1.70	0.91
1:A:664:G:H22	1:A:741:G:H1	1.16	0.91
1:A:1347:G:C4	9:I:107:ARG:NH1	2.38	0.91
1:A:838:G:H2'	1:A:839:U:H5"	1.52	0.91
1:A:1101:A:H4'	1:A:1102:A:O5'	1.65	0.90
3:C:195:VAL:O	3:C:196:LEU:HD23	1.69	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
10:J:49:VAL:HG13	14:N:41:ARG:HB2	1.52	0.90
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
1:A:182:U:H5"	1:A:182:U:C6	2.08	0.88
2:B:59:GLU:HG2	2:B:221:LEU:HD11	1.51	0.88
1:A:282:A:H5"	1:A:283:C:C5	2.08	0.87
4:D:36:ARG:N	4:D:37:PRO:HD3	1.88	0.87
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.57	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
4:D:150:GLU:HG3	4:D:153:ARG:NH2	1.90	0.86
1:A:1435:G:H2'	1:A:1436:U:C6	2.10	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
1:A:267:C:P	17:Q:67:LYS:HD2	2.16	0.86
1:A:255:G:H1'	17:Q:16:GLN:NE2	1.90	0.86
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.55	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:30:LEU:HD23	6:F:75:LEU:HD21	1.57	0.85
1:A:1305:G:O2'	1:A:1306:A:H8	1.58	0.85
3:C:110:ASN:HD21	3:C:140:ARG:HB3	1.40	0.85
3:C:52:LEU:HD21	3:C:118:GLN:HE22	1.40	0.85
3:C:190:ARG:HB3	3:C:190:ARG:NH1	1.91	0.85
2:B:102:LEU:HD21	2:B:162:ILE:HD11	1.57	0.85
10:J:22:LYS:HE2	10:J:90:LEU:HD12	1.57	0.85
1:A:972:C:O5'	10:J:57:LYS:HG3	1.75	0.84
1:A:182:U:C5	1:A:183:G:C4	2.66	0.84
1:A:1060:C:C5	3:C:2:GLY:HA3	2.11	0.84
13:M:50:GLU:O	13:M:54:VAL:HG23	1.77	0.84
1:A:279:A:C8	1:A:281:G:C2	2.64	0.84
1:A:1131:G:H1	1:A:1143:G:H21	1.22	0.84
1:A:135:C:O2	16:P:1:MET:HB2	1.76	0.84
13:M:3:ARG:HG2	13:M:9:ILE:HG23	1.56	0.84
1:A:250:A:H4'	1:A:251:G:O5'	1.76	0.84
1:A:1064:G:H4'	1:A:1065:U:H5'	1.58	0.84
3:C:64:VAL:HB	3:C:99:VAL:HB	1.59	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
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.60	0.84
4:D:104:VAL:HG11	4:D:146:ILE:HD12	1.58	0.83
1:A:1125:U:H3	10:J:5:ARG:HH21	1.22	0.83
3:C:172:ARG:HH12	3:C:174:PRO:HG3	1.43	0.83
4:D:61:LYS:HD2	4:D:207:TYR:OH	1.78	0.83
6:F:36:ARG:HH12	6:F:38:GLU:HG2	1.44	0.83
1:A:1281:U:H5'	1:A:1282:C:H5	1.44	0.82
3:C:91:LEU:HD23	3:C:92:ALA:N	1.94	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
19:S:29:ARG:O	19:S:30:LEU:HB2	1.80	0.82
1:A:1226:C:O2	19:S:83:HIS:HE1	1.62	0.82
15:O:78:TYR:CZ	15:O:82:ILE:HD11	2.15	0.82
10:J:19:SER:HB2	10:J:91:PRO:HG3	1.60	0.81
13:M:22:ILE:HD12	13:M:25:ILE:HD12	1.61	0.81
1:A:1152:A:H5"	10:J:13:HIS:CD2	2.14	0.81
4:D:150:GLU:HA	4:D:153:ARG:HE	1.44	0.81
12:L:25:PRO:C	12:L:27:LEU:H	1.79	0.81
20:T:43:LEU:HD13	20:T:51:GLU:HG3	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:101:MET:HA	2:B:108:ILE:HD12	1.63	0.81
1:A:811:C:H2'	1:A:812:C:H5"	1.61	0.81
12:L:70:ILE:HD13	12:L:77:LEU:HD12	1.63	0.81
1:A:247:G:N3	1:A:282:A:H2	1.79	0.80
12:L:41:ARG:CG	12:L:42:THR:H	1.88	0.80
18:R:55:ARG:NH1	18:R:55:ARG:HB3	1.94	0.80
2:B:27:LYS:HD3	2:B:195:ASP:OD2	1.82	0.80
1:A:1285:A:H4'	1:A:1286:A:O5'	1.82	0.80
1:A:673:G:H2'	1:A:674:G:C8	2.17	0.80
6:F:95:GLU:CD	6:F:95:GLU:H	1.85	0.80
1:A:182:U:H6	1:A:182:U:C5'	1.94	0.80
12:L:126:LYS:H	12:L:126:LYS:HD2	1.47	0.79
7:G:75:VAL:HG11	7:G:86:GLN:HB3	1.64	0.79
1:A:80:G:H3'	1:A:81:U:H5"	1.62	0.79
5:E:118:ILE:HG22	5:E:119:LEU:N	1.95	0.79
11:K:54:ARG:HB3	11:K:54:ARG:NH1	1.97	0.79
1:A:1152:A:H5"	10:J:13:HIS:HD2	1.47	0.79
10:J:8:LEU:CD2	10:J:96:ILE:HG12	2.11	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
12:L:67:THR:HG22	12:L:96:VAL:HG13	1.63	0.79
17:Q:69:LYS:C	17:Q:70:ARG:HD2	2.03	0.79
20:T:54:LYS:HG3	20:T:100:ILE:CD1	2.13	0.79
4:D:25:ARG:C	4:D:27:TYR:H	1.85	0.79
1:A:1116:C:C2'	1:A:1117:G:H5"	2.12	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
14:N:14:PRO:C	14:N:16:PHE:H	1.86	0.78
14:N:32:SER:O	14:N:40:CYS:HA	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
1:A:279:A:C8	1:A:281:G:N2	2.51	0.78
16:P:21:VAL:HG21	16:P:59:TRP:CD1	2.19	0.78
1:A:182:U:H5	1:A:183:G:C4	1.99	0.77
1:A:1226:C:H4'	1:A:1227:A:OP1	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:197:VAL:HB	2:B:200:ILE:HG12	1.66	0.77
5:E:64:ARG:O	5:E:65:ASN:HB3	1.84	0.77
15:O:17:ARG:HG3	15:O:17:ARG:HH11	1.49	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	1.66	0.77
1:A:130:A:OP2	1:A:190(E):U:H2'	1.84	0.77
1:A:1226:C:H1'	19:S:83:HIS:HE1	1.49	0.77
9:I:118:LYS:O	9:I:119:ALA:HB3	1.85	0.77
1:A:243:A:C4'	1:A:244:U:H5'	2.13	0.77
1:A:839:U:H5'	1:A:840:C:H5	1.50	0.77
1:A:1366:C:H2'	1:A:1367:C:H6	1.48	0.77
4:D:150:GLU:H	4:D:150:GLU:CD	1.86	0.77
15:O:16:ALA:HB1	15:O:21:ASP:HB3	1.64	0.77
20:T:54:LYS:HG3	20:T:100:ILE:HD13	1.65	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
7:G:95:ARG:HG3	7:G:95:ARG:HH11	1.50	0.77
8:H:90:GLY:O	8:H:91:ARG:HB2	1.82	0.77
1:A:1236:A:H4'	1:A:1304:G:H4'	1.67	0.76
13:M:4:ILE:HG22	13:M:5:ALA:N	2.00	0.76
2:B:57:PHE:O	2:B:60:ASP:HB3	1.84	0.76
6:F:100:ASN:HD22	18:R:23:LYS:HG2	1.49	0.76
21:V:5:ASP:O	21:V:11:GLY:HA3	1.85	0.76
1:A:1256:A:N6	1:A:1278:U:H1'	2.00	0.76
2:B:139:LYS:O	2:B:143:GLU:HG2	1.86	0.76
3:C:107:GLN:H	3:C:107:GLN:CD	1.88	0.76
17:Q:69:LYS:O	17:Q:70:ARG:HD2	1.85	0.76
1:A:328:C:O2	1:A:328:C:H2'	1.85	0.76
20:T:14:LYS:O	20:T:18:GLN:HG3	1.86	0.76
3:C:19:GLU:HB3	3:C:40:ARG:HH21	1.50	0.76
16:P:74:LEU:O	16:P:79:VAL:HG23	1.85	0.76
1:A:1190:G:OP1	3:C:4:LYS:HA	1.86	0.76
1:A:1025:U:H2'	1:A:1026:G:C8	2.21	0.75
10:J:45:ARG:HH22	14:N:36:PHE:HD2	1.31	0.75
10:J:82:ILE:O	10:J:86:MET:HB2	1.86	0.75
2:B:36:ARG:HD2	2:B:41:ILE:HD12	1.68	0.75
19:S:16:LEU:O	19:S:19:VAL:HG12	1.87	0.75
1:A:80:G:H3'	1:A:81:U:C5'	2.16	0.75
3:C:50:ALA:HB1	3:C:70:VAL:HG11	1.68	0.75
1:A:839:U:H5'	1:A:840:C:C5	2.22	0.75
12:L:48:PRO:HG2	12:L:49:ASN:H	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:126:LYS:H	12:L:126:LYS:CD	1.96	0.75
1:A:351:G:H4'	1:A:352:C:OP1	1.85	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:24:VAL:HG13	12:L:98:TYR:HE2	1.50	0.75
13:M:3:ARG:HA	13:M:8:GLU:O	1.86	0.75
1:A:840:C:H5"	1:A:841:U:OP1	1.85	0.75
4:D:162:LEU:HD13	4:D:181:MET:HG2	1.67	0.74
1:A:1234:C:H5'	1:A:1365:G:OP1	1.86	0.74
1:A:1391:U:H2'	1:A:1392:G:C8	2.22	0.74
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
18:R:55:ARG:HB3	18:R:55:ARG:HH11	1.49	0.74
19:S:17:GLU:O	19:S:21:GLU:HG3	1.87	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
2:B:16:HIS:NE2	2:B:214:ILE:HG12	2.01	0.74
2:B:77:ALA:HB2	2:B:211:ILE:CD1	2.10	0.74
1:A:579:G:H5'	1:A:728:A:H1'	1.69	0.74
2:B:178:ARG:HG3	2:B:178:ARG:NH1	1.92	0.74
1:A:1250:A:H4'	9:I:68:GLY:H	1.52	0.74
3:C:52:LEU:HD23	3:C:52:LEU:N	2.02	0.74
6:F:69:GLU:HA	6:F:72:VAL:HG23	1.70	0.74
21:V:6:ARG:HD3	21:V:15:ARG:HH12	1.52	0.74
1:A:748:C:H1'	1:A:749:C:H5	1.53	0.73
1:A:792:A:H4'	1:A:793:U:H5"	1.68	0.73
4:D:64:LEU:HD12	4:D:75:PHE:HZ	1.53	0.73
1:A:182:U:H5	1:A:183:G:N9	1.79	0.73
12:L:27:LEU:HG	12:L:28:LYS:H	1.53	0.73
1:A:1279:A:H5"	1:A:1280:A:OP1	1.88	0.73
7:G:23:VAL:HG12	7:G:27:ILE:HD11	1.70	0.73
1:A:195:A:H4'	20:T:68:LYS:HE2	1.68	0.73
2:B:23:ARG:NH1	2:B:24:TRP:N	2.35	0.73
1:A:992:U:H4'	1:A:993:G:O5'	1.86	0.73
12:L:59:ARG:HD3	12:L:65:GLU:HG3	1.68	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
2:B:95:GLN:O	2:B:96:ARG:HD2	1.88	0.73
9:I:44:VAL:HG13	9:I:51:ARG:HH22	1.53	0.73
12:L:43:VAL:HG12	12:L:44:THR:N	2.04	0.73
1:A:1412:C:H2'	1:A:1413:A:C8	2.24	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:26:ILE:HG21	6:F:63:TYR:HE2	1.54	0.73
1:A:1221:G:O3'	19:S:77:THR:HG21	1.88	0.72
2:B:23:ARG:HH11	2:B:24:TRP:N	1.86	0.72
2:B:91:PRO:HG3	2:B:154:LEU:HB2	1.69	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:353:A:H5'	1:A:353:A:H8	1.53	0.72
1:A:877:C:O2	8:H:3:THR:HG21	1.89	0.72
1:A:161:A:H2'	1:A:162:A:C8	2.23	0.72
1:A:434:U:H2'	1:A:435:C:C6	2.24	0.72
11:K:108:ILE:HB	18:R:87:ARG:O	1.89	0.72
1:A:197:A:H4'	1:A:198:G:O5'	1.90	0.72
4:D:158:ILE:HG22	4:D:181:MET:HE2	1.70	0.72
11:K:84:VAL:HG11	11:K:95:ILE:HD11	1.70	0.72
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.23	0.72
18:R:26:LEU:HD12	18:R:27:GLY:H	1.53	0.72
20:T:10:LEU:O	20:T:12:ALA:N	2.22	0.72
10:J:35:SER:HB2	10:J:72:VAL:O	1.90	0.72
17:Q:59:ILE:HG23	17:Q:71:PHE:HB3	1.69	0.72
6:F:67:MET:HE1	6:F:72:VAL:HA	1.71	0.72
10:J:39:PRO:O	10:J:40:LEU:HB2	1.89	0.72
8:H:1:MET:HG2	8:H:2:LEU:H	1.54	0.71
9:I:4:TYR:CE2	9:I:88:TYR:HA	2.24	0.71
1:A:1148:U:H2'	1:A:1149:C:O4'	1.90	0.71
1:A:501:C:H2'	1:A:502:G:H8	1.53	0.71
1:A:1065:U:H4'	1:A:1066:C:O5'	1.89	0.71
13:M:88:ARG:HD2	19:S:3:ARG:HH21	1.55	0.71
18:R:33:ASP:OD2	18:R:36:ASN:HB2	1.90	0.71
1:A:186:C:O3'	20:T:82:SER:HB3	1.91	0.71
1:A:977:A:H2'	1:A:978:A:H5"	1.72	0.71
6:F:94:GLN:NE2	18:R:32:ARG:HD3	2.03	0.71
10:J:61:GLU:OE1	14:N:45:ARG:NH1	2.22	0.71
1:A:1343:G:H2'	1:A:1344:C:C6	2.26	0.71
9:I:111:ARG:HD3	9:I:112:LYS:N	2.06	0.71
19:S:80:TYR:CE1	19:S:82:GLY:HA2	2.25	0.71
1:A:344:A:H4'	1:A:345:C:OP2	1.91	0.71
1:A:1281:U:H5'	1:A:1282:C:C5	2.25	0.71
9:I:65:VAL:HG21	9:I:73:GLN:HB3	1.72	0.71
1:A:279:A:C6	17:Q:98:LEU:CD1	2.74	0.71
1:A:279:A:H5"	1:A:280:C:H3'	1.72	0.71
8:H:108:GLY:HA3	8:H:138:TRP:HB3	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:G:H4'	1:A:182:U:O5'	1.91	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: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
12:L:43:VAL:HG12	12:L:44:THR:H	1.55	0.70
3:C:29:TYR:OH	14:N:54:PRO:HG2	1.91	0.70
13:M:40:ASN:HB3	13:M:43:THR:HG23	1.73	0.70
1:A:496:A:H4'	1:A:497:A:OP1	1.92	0.70
2:B:124:SER:HB2	2:B:125:PRO:CD	2.21	0.70
2:B:130:ARG:HH22	3:C:179:ARG:HH12	1.40	0.70
3:C:7:PRO:HG2	3:C:184:TYR:HB2	1.73	0.70
13:M:49:THR:HG22	13:M:51:ALA:N	2.02	0.70
1:A:107:G:C2'	1:A:108:G:H5'	2.21	0.70
1:A:1351:U:H2'	1:A:1352:C:H6	1.55	0.70
4:D:36:ARG:H	4:D:37:PRO:CD	2.02	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
1:A:1278:U:H5"	1:A:1279:A:C5'	2.21	0.70
3:C:180:ALA:O	3:C:181:ASN:HB3	1.92	0.70
4:D:70:ILE:HD11	4:D:100:ARG:CZ	2.21	0.70
14:N:22:THR:HB	14:N:33:VAL:HG21	1.73	0.70
18:R:39:VAL:O	18:R:42:ARG:HB2	1.90	0.70
9:I:97:LYS:HG2	9:I:102:LEU:HD12	1.72	0.70
15:O:17:ARG:NH1	15:O:77:ARG:NH1	2.40	0.70
1:A:1168:A:H2'	1:A:1169:A:C8	2.26	0.70
6:F:10:LEU:HD11	6:F:59:TYR:HD2	1.55	0.70
10:J:30:SER:O	10:J:78:ASN:HB2	1.92	0.70
13:M:6:GLY:O	13:M:7:VAL:HG22	1.92	0.70
17:Q:45:HIS:HB2	17:Q:65:ILE:HD13	1.71	0.70
4:D:28:SER:O	4:D:30:LYS:N	2.25	0.70
4:D:157:LEU:CD2	4:D:161:ASN:HD21	2.05	0.70
1:A:706:A:C1'	11:K:29:ILE:HD11	2.21	0.70
9:I:97:LYS:CG	9:I:102:LEU:HD12	2.22	0.70
1:A:1125:U:H3	10:J:5:ARG:NH2	1.89	0.70
13:M:81:LEU:O	13:M:86:CYS:HB3	1.92	0.70
3:C:6:HIS:CD2	3:C:8:ILE:HB	2.27	0.69
13:M:40:ASN:HD22	13:M:41:PRO:HD2	1.55	0.69
13:M:81:LEU:HD23	13:M:81:LEU:H	1.56	0.69
1:A:1316:G:H4'	14:N:18:VAL:CG1	2.21	0.69
3:C:52:LEU:HD21	3:C:118:GLN:NE2	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:39:LEU:HD13	15:O:56:LEU:HB2	1.74	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
1:A:352:C:H4'	1:A:354:G:OP1	1.91	0.69
19:S:62:ILE:HD12	19:S:66:MET:HG3	1.75	0.69
10:J:46:ARG:HH11	10:J:64:GLU:CB	2.05	0.69
1:A:620:C:N1	4:D:135:LEU:HD13	2.06	0.69
1:A:1137:C:H4'	1:A:1138:G:N2	2.06	0.69
3:C:52:LEU:CD2	3:C:118:GLN:HE22	2.05	0.69
1:A:811:C:H2'	1:A:812:C:C5'	2.21	0.69
10:J:30:SER:HB2	10:J:80:LYS:HB3	1.74	0.69
4:D:199:ASN:ND2	4:D:201:GLN:HB2	2.08	0.69
12:L:55:VAL:HG12	12:L:56:ALA:H	1.57	0.69
13:M:11:ARG:HG2	13:M:12:ASN:N	2.07	0.69
1:A:182:U:H5	1:A:183:G:C5	2.11	0.69
1:A:392:G:H2'	1:A:393:A:H8	1.55	0.69
1:A:1281:U:H4'	1:A:1282:C:OP2	1.92	0.69
10:J:42:THR:HG23	10:J:67:THR:O	1.92	0.69
21:V:6:ARG:CD	21:V:15:ARG:HH12	2.06	0.69
1:A:17:U:H2'	1:A:18:C:C6	2.28	0.69
1:A:946:A:H2'	1:A:947:G:C8	2.28	0.69
4:D:64:LEU:HD23	4:D:198:VAL:HG21	1.75	0.69
16:P:34:GLU:OE2	16:P:55:ARG:HD3	1.93	0.69
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:477:G:H2'	1:A:478:A:H8	1.56	0.68
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
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
12:L:47:LYS:CB	12:L:48:PRO:CD	2.71	0.68
19:S:41:VAL:HG23	19:S:43:GLU:HG2	1.75	0.68
9:I:93:ARG:HD3	9:I:97:LYS:HE3	1.75	0.68
19:S:80:TYR:CE1	19:S:82:GLY:CA	2.76	0.68
1:A:701:C:H5'	1:A:703:G:O4'	1.94	0.68
1:A:731:G:OP1	1:A:766:A:H1'	1.94	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
5:E:51:VAL:O	5:E:55:VAL:HG23	1.94	0.68
1:A:382:A:H2'	1:A:383:A:C8	2.28	0.68
2:B:22:LYS:HD2	2:B:35:GLU:OE1	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:151:LYS:N	4:D:151:LYS:HD2	2.08	0.68
6:F:75:LEU:O	6:F:79:LEU:HG	1.94	0.68
3:C:13:GLY:HA3	14:N:57:ARG:HH21	1.59	0.68
9:I:26:VAL:HB	9:I:33:PHE:HB2	1.76	0.68
1:A:99:C:H2'	1:A:101:A:C8	2.28	0.68
3:C:38:ARG:HH11	3:C:38:ARG:HG3	1.58	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
13:M:81:LEU:HD12	13:M:88:ARG:HD3	1.75	0.68
20:T:45:GLN:HA	20:T:91:LEU:HD22	1.75	0.68
1:A:173:U:H5'	1:A:197:A:O4'	1.94	0.68
1:A:1064:G:C4'	1:A:1065:U:H5'	2.23	0.68
18:R:45:SER:OG	18:R:49:LYS:HB2	1.94	0.68
1:A:939:G:H2'	1:A:940:C:C6	2.28	0.67
1:A:1016:A:H2'	1:A:1017:G:O4'	1.94	0.67
3:C:82:GLU:O	3:C:85:ARG:HB3	1.94	0.67
15:O:55:GLY:O	15:O:59:MET:HG3	1.95	0.67
1:A:1366:C:H2'	1:A:1367:C:C6	2.30	0.67
2:B:18:GLY:HA2	2:B:42:ILE:H	1.59	0.67
13:M:40:ASN:HD22	13:M:41:PRO:N	1.91	0.67
1:A:31:G:N1	1:A:48:C:H5"	2.09	0.67
1:A:328:C:H4'	1:A:329:A:O5'	1.94	0.67
3:C:190:ARG:HH11	3:C:190:ARG:CB	2.07	0.67
4:D:151:LYS:HD2	4:D:151:LYS:H	1.60	0.67
12:L:47:LYS:HB2	12:L:48:PRO:CD	2.23	0.67
1:A:105:G:H2'	1:A:106:C:C6	2.29	0.67
3:C:179:ARG:HD3	3:C:206:GLU:HG2	1.76	0.67
16:P:20:VAL:HG11	16:P:32:TYR:HB3	1.74	0.67
1:A:243:A:H62	1:A:281:G:H2'	1.60	0.67
1:A:686:U:HO2'	1:A:687:A:H8	1.40	0.67
1:A:915:A:H2'	1:A:916:G:H5'	1.76	0.67
1:A:1057:G:O2'	1:A:1058:G:H5'	1.95	0.67
1:A:1148:U:H4'	9:I:14:VAL:HG11	1.75	0.67
1:A:1368:G:O2'	1:A:1369:C:H5'	1.95	0.67
4:D:187:ARG:HH21	4:D:188:LEU:HD12	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
1:A:748:C:H1'	1:A:749:C:C5	2.30	0.67
1:A:1117:G:H4'	9:I:104:ARG:NH1	2.10	0.67
3:C:195:VAL:C	3:C:196:LEU:HD23	2.15	0.67
3:C:130:VAL:HG21	3:C:157:ILE:HG23	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:811:C:C2'	1:A:812:C:H5"	2.24	0.67
1:A:1413:A:H2	1:A:1487:G:H22	1.41	0.67
1:A:1502:A:H2	1:A:1505:G:N1	1.90	0.67
3:C:26:LYS:H	3:C:26:LYS:HD3	1.58	0.67
1:A:532:A:N6	3:C:159:GLY:O	2.27	0.66
13:M:33:ALA:HA	13:M:59:TYR:HE2	1.60	0.66
10:J:94:VAL:HG12	10:J:95:GLU:N	2.11	0.66
5:E:12:LEU:HD13	5:E:31:LEU:HB2	1.77	0.66
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:129(A):G:N3	1:A:190(E):U:H5'	2.10	0.66
1:A:813:U:H6	1:A:813:U:H5"	1.60	0.66
1:A:967:C:H4'	9:I:128:ARG:HG3	1.76	0.66
10:J:49:VAL:O	10:J:60:ARG:HA	1.95	0.66
1:A:650:G:O2'	1:A:651:C:H5'	1.94	0.66
11:K:66:LEU:HB3	11:K:70:LYS:HE3	1.78	0.66
13:M:81:LEU:H	13:M:81:LEU:CD2	2.07	0.66
4:D:30:LYS:C	4:D:32:ALA:H	1.98	0.66
6:F:100:ASN:ND2	18:R:23:LYS:HG2	2.09	0.66
8:H:6:ILE:HD11	8:H:31:PHE:CD2	2.30	0.66
12:L:33:ARG:HD3	12:L:62:SER:HB3	1.76	0.66
13:M:65:LYS:HG3	13:M:69:GLU:OE2	1.96	0.66
15:O:33:THR:HG23	15:O:63:ARG:HH12	1.60	0.66
19:S:81:ARG:HH11	19:S:81:ARG:HG3	1.60	0.66
20:T:56:MET:HE3	20:T:88:VAL:HG11	1.77	0.66
5:E:150:ARG:HG3	5:E:150:ARG:HH11	1.60	0.66
1:A:353:A:H5'	1:A:353:A:C8	2.31	0.66
1:A:662:G:H2'	1:A:663:A:C8	2.30	0.66
1:A:706:A:O4'	11:K:29:ILE:HD11	1.96	0.66
19:S:33:THR:HG22	19:S:35:SER:H	1.60	0.66
3:C:107:GLN:H	3:C:107:GLN:NE2	1.94	0.66
10:J:60:ARG:O	10:J:61:GLU:HB3	1.95	0.66
1:A:531:U:OP2	22:Y:70:ALA:HB2	1.96	0.66
2:B:71:VAL:O	2:B:165:VAL:HG23	1.96	0.66
3:C:155:GLY:O	3:C:156:ARG:HB2	1.96	0.66
7:G:85:TYR:HD2	7:G:154:TYR:HE2	1.42	0.66
9:I:10:ARG:HG2	9:I:75:ASP:HB2	1.76	0.66
11:K:14:VAL:HG21	11:K:40:ILE:HD11	1.77	0.65
14:N:14:PRO:HB2	14:N:16:PHE:O	1.95	0.65
18:R:45:SER:C	18:R:47:THR:H	1.97	0.65
18:R:47:THR:HG23	18:R:83:GLU:H	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:C:H2'	1:A:444:C:H6	1.61	0.65
1:A:939:G:H5"	7:G:102:ARG:NH2	2.10	0.65
1:A:524:G:H2'	1:A:525:C:C6	2.31	0.65
2:B:18:GLY:HA3	2:B:41:ILE:HA	1.79	0.65
5:E:80:ILE:HD11	5:E:91:LEU:HD12	1.76	0.65
10:J:38:ILE:CG1	10:J:71:LEU:HB3	2.26	0.65
13:M:34:LEU:HD13	13:M:41:PRO:HA	1.77	0.65
21:V:6:ARG:HD3	21:V:15:ARG:NH1	2.12	0.65
1:A:1278:U:H5"	1:A:1279:A:H5'	1.76	0.65
2:B:15:VAL:CG2	2:B:209:ARG:HG3	2.26	0.65
13:M:36:LYS:HD2	13:M:59:TYR:CZ	2.32	0.65
19:S:17:GLU:HA	19:S:20:LEU:HD11	1.78	0.65
1:A:376:G:OP2	16:P:67:THR:HG21	1.97	0.65
1:A:1425:U:H2'	1:A:1426:C:C6	2.31	0.65
15:O:29:VAL:HG12	15:O:85:LEU:CD1	2.26	0.65
1:A:1054:C:H41	22:Y:91:TYR:HE2	1.43	0.65
1:A:1112:C:O2	3:C:179:ARG:HB3	1.97	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
3:C:188:LEU:O	3:C:189:ALA:HB2	1.96	0.65
11:K:18:ARG:HB2	11:K:33:THR:HG23	1.79	0.65
3:C:172:ARG:HB3	3:C:172:ARG:HH11	1.61	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
7:G:50:ILE:O	7:G:54:THR:HB	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
1:A:1216:G:H5"	14:N:5:ALA:CB	2.27	0.65
1:A:1250:A:H4'	9:I:68:GLY:N	2.11	0.65
2:B:74:LYS:HZ1	2:B:206:ASP:HA	1.61	0.65
10:J:96:ILE:HG22	10:J:97:GLU:N	2.10	0.65
12:L:86:ARG:HH11	12:L:86:ARG:HG3	1.61	0.65
19:S:28:LYS:HG2	19:S:29:ARG:N	2.06	0.65
1:A:195:A:H4'	20:T:68:LYS:CE	2.27	0.65
1:A:287:U:O2'	1:A:288:A:H5'	1.97	0.65
1:A:1522:U:O2'	1:A:1523:G:H5'	1.96	0.65
5:E:151:LEU:HD11	8:H:77:GLU:OE2	1.97	0.65
4:D:187:ARG:NH2	4:D:188:LEU:HD12	2.10	0.65
5:E:15:ARG:HD2	5:E:15:ARG:O	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:81:LEU:O	13:M:89:GLY:HA3	1.97	0.64
1:A:392:G:H2'	1:A:393:A:C8	2.32	0.64
1:A:706:A:H1'	11:K:29:ILE:HD11	1.77	0.64
1:A:1226:C:O2	19:S:83:HIS:CE1	2.49	0.64
20:T:50:GLU:HG2	20:T:100:ILE:HG13	1.79	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'	1.98	0.64
1:A:203:U:H5"	1:A:204:U:OP1	1.97	0.64
5:E:115:VAL:CG1	5:E:118:ILE:HG13	2.25	0.64
9:I:118:LYS:O	9:I:119:ALA:CB	2.45	0.64
16:P:18:ARG:HD3	16:P:35:LYS:HE3	1.79	0.64
1:A:393:A:O2'	1:A:394:G:H5'	1.98	0.64
1:A:397:A:H5'	1:A:398:C:OP1	1.98	0.64
1:A:1346:A:C8	7:G:10:ARG:NH2	2.65	0.64
1:A:1346:A:C4	7:G:10:ARG:NH2	2.65	0.64
6:F:21:LEU:O	6:F:24:GLU:HB3	1.97	0.64
11:K:18:ARG:HB2	11:K:33:THR:CG2	2.28	0.64
1:A:246:A:N3	1:A:282:A:C6	2.66	0.64
1:A:1040:U:H2'	1:A:1041:A:C8	2.33	0.64
10:J:90:LEU:H	10:J:91:PRO:HD2	1.61	0.64
19:S:40:ILE:HB	19:S:67:VAL:O	1.98	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
3:C:29:TYR:CZ	14:N:54:PRO:HG2	2.33	0.64
3:C:177:THR:CG2	3:C:180:ALA:HB2	2.28	0.64
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.33	0.64
9:I:49:PRO:O	9:I:52:ALA:HB3	1.98	0.64
19:S:64:GLU:O	19:S:67:VAL:HG23	1.97	0.64
5:E:120:THR:CG2	5:E:121:LYS:N	2.60	0.64
11:K:40:ILE:HG22	11:K:41:THR:HG23	1.80	0.64
11:K:77:MET:HE3	11:K:80:VAL:HG22	1.80	0.64
16:P:45:THR:HB	16:P:46:PRO:HD2	1.80	0.64
1:A:922:G:H2'	1:A:923:A:C8	2.33	0.64
1:A:1142:G:H2'	1:A:1143:G:O4'	1.97	0.64
1:A:1347:G:C5	9:I:107:ARG:CZ	2.80	0.64
3:C:112:SER:HB2	3:C:115:LEU:HD12	1.79	0.64
5:E:79:GLU:HG3	5:E:93:PRO:HD2	1.79	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
19:S:44:MET:O	19:S:47:HIS:HB2	1.96	0.64
21:V:6:ARG:CD	21:V:15:ARG:NH1	2.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:101:ARG:HA	17:Q:101:ARG:HE	1.62	0.64
4:D:152:SER:HB3	4:D:155:LEU:HD12	1.80	0.64
9:I:48:GLU:N	9:I:49:PRO:HD2	2.13	0.64
1:A:1020:U:H2'	1:A:1021:G:H8	1.63	0.63
2:B:215:LEU:O	2:B:219:VAL:HG23	1.97	0.63
3:C:64:VAL:HB	3:C:99:VAL:CB	2.27	0.63
3:C:120:VAL:O	3:C:124:ILE:HG13	1.98	0.63
12:L:25:PRO:C	12:L:27:LEU:N	2.52	0.63
1:A:1153:C:H2'	1:A:1154:G:H8	1.62	0.63
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.78	0.63
4:D:131:ARG:H	4:D:131:ARG:HD2	1.62	0.63
1:A:255:G:H1'	17:Q:16:GLN:HE22	1.63	0.63
1:A:279:A:C6	17:Q:98:LEU:HD13	2.33	0.63
1:A:1442:G:N3	1:A:1442:G:H2'	2.12	0.63
8:H:91:ARG:HG3	12:L:7:ILE:HG13	1.80	0.63
12:L:110:VAL:O	12:L:122:THR:HG21	1.97	0.63
1:A:267:C:OP1	17:Q:67:LYS:HD2	1.96	0.63
1:A:1131:G:H1	1:A:1143:G:N2	1.95	0.63
2:B:74:LYS:NZ	2:B:206:ASP:HA	2.13	0.63
2:B:82:ARG:O	2:B:86:GLU:HG3	1.98	0.63
2:B:95:GLN:OE1	2:B:95:GLN:HA	1.97	0.63
4:D:70:ILE:HD11	4:D:100:ARG:NE	2.13	0.63
1:A:1141:C:H2'	1:A:1142:G:C8	2.33	0.63
3:C:155:GLY:O	3:C:196:LEU:HD22	1.98	0.63
1:A:243:A:H4'	1:A:244:U:C5'	2.22	0.63
1:A:1026:G:H2'	1:A:1027:C:H5'	1.80	0.63
3:C:64:VAL:CB	3:C:99:VAL:HB	2.28	0.63
5:E:102:ALA:CB	5:E:120:THR:HG21	2.29	0.63
7:G:71:PRO:HD3	7:G:103:TRP:CZ3	2.33	0.63
7:G:114:ARG:HG2	7:G:114:ARG:HH11	1.64	0.63
1:A:1238:A:H5'	1:A:1336:C:H41	1.63	0.63
2:B:20:GLU:HG2	2:B:189:ASP:OD2	1.99	0.63
2:B:132:LYS:HG2	2:B:135:GLN:OE1	1.99	0.63
3:C:50:ALA:O	3:C:70:VAL:HG12	1.99	0.63
7:G:42:ILE:HG22	7:G:120:ILE:HD12	1.80	0.63
14:N:27:CYS:SG	14:N:29:ARG:HB2	2.37	0.63
1:A:1132:C:H2'	1:A:1133:G:H8	1.64	0.63
16:P:8:ARG:HB2	16:P:28:ARG:NH1	2.14	0.63
19:S:39:THR:HA	19:S:70:LYS:HG2	1.81	0.63
1:A:448:A:H2'	1:A:449:C:H6	1.64	0.63
1:A:1226:C:N4	13:M:104:ARG:HD2	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
5:E:150:ARG:HG3	5:E:150:ARG:NH1	2.14	0.63
19:S:43:GLU:H	19:S:43:GLU:CD	2.00	0.63
1:A:279:A:H8	1:A:281:G:C2	2.13	0.62
1:A:405:U:H3'	1:A:406:G:H5'	1.80	0.62
1:A:556:C:O2'	1:A:557:G:H5'	1.99	0.62
1:A:1132:C:H2'	1:A:1133:G:C8	2.35	0.62
2:B:73:THR:HB	2:B:170:GLU:OE2	1.99	0.62
2:B:184:VAL:N	2:B:198:ASP:OD2	2.32	0.62
13:M:84:ILE:O	13:M:86:CYS:N	2.32	0.62
15:O:17:ARG:CZ	15:O:77:ARG:HH11	2.11	0.62
1:A:1260:C:O5'	1:A:1284:C:H4'	1.99	0.62
3:C:60:ALA:O	3:C:61:ALA:HB2	2.00	0.62
3:C:177:THR:HG23	3:C:180:ALA:HB2	1.81	0.62
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.80	0.62
1:A:475:G:H2'	1:A:476:G:H8	1.63	0.62
1:A:1225:A:H2'	1:A:1225:A:N3	2.14	0.62
7:G:23:VAL:O	7:G:27:ILE:HG13	2.00	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:69:LEU:HD12	2:B:155:LEU:HD11	1.81	0.62
2:B:142:LEU:HD22	2:B:146:GLN:NE2	2.15	0.62
2:B:186:ALA:HB3	2:B:197:VAL:HG11	1.82	0.62
3:C:129:ALA:HB3	3:C:132:ARG:HD2	1.82	0.62
5:E:120:THR:HG23	5:E:121:LYS:N	2.15	0.62
17:Q:64:PRO:HB3	17:Q:70:ARG:HE	1.63	0.62
1:A:216:G:H2'	1:A:217:C:C6	2.35	0.62
1:A:1176:A:H2'	1:A:1177:G:C8	2.35	0.62
1:A:1316:G:H4'	14:N:18:VAL:HG11	1.81	0.62
1:A:1347:G:C8	9:I:107:ARG:HB3	2.35	0.62
1:A:1392:G:O2'	1:A:1502:A:H5"	1.99	0.62
1:A:1425:U:H2'	1:A:1426:C:H6	1.65	0.62
7:G:155:ARG:O	7:G:156:TRP:HB3	1.98	0.62
9:I:19:LEU:O	9:I:20:ARG:HG3	1.99	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:476:G:O2'	1:A:477:G:H5'	2.00	0.62
2:B:115:LEU:HG	2:B:153:ARG:NH2	2.14	0.62
4:D:148:VAL:CG1	4:D:158:ILE:HD13	2.30	0.62
1:A:434:U:H2'	1:A:435:C:H6	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1231:G:H5”	9:I:126:SER:CB	2.30	0.62
7:G:139:GLU:O	7:G:143:ARG:HG3	2.00	0.62
14:N:53:LEU:HB3	14:N:56:VAL:HG21	1.81	0.62
20:T:50:GLU:HG3	20:T:99:LEU:HD12	1.81	0.62
5:E:80:ILE:CD1	5:E:91:LEU:HB2	2.30	0.61
7:G:78:ARG:HB2	7:G:156:TRP:CZ3	2.35	0.61
1:A:193:C:H2’	1:A:194:C:C6	2.35	0.61
1:A:1214:C:C4	22:Y:20:SER:HB3	2.34	0.61
1:A:1370:G:O2’	1:A:1371:G:H5’	2.00	0.61
1:A:1440:C:H2’	1:A:1441:G:H5’	1.83	0.61
2:B:80:ILE:HD11	2:B:208:ILE:HG23	1.81	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
5:E:115:VAL:HG11	5:E:118:ILE:CG1	2.28	0.61
4:D:32:ALA:C	4:D:34:GLU:H	2.04	0.61
10:J:30:SER:OG	10:J:81:THR:HA	1.99	0.61
12:L:33:ARG:CD	12:L:62:SER:HB3	2.29	0.61
17:Q:21:VAL:HG21	17:Q:59:ILE:HD11	1.82	0.61
2:B:34:ALA:O	2:B:41:ILE:N	2.31	0.61
2:B:130:ARG:NH2	3:C:207:VAL:HG22	2.16	0.61
4:D:23:GLY:HA3	4:D:112:VAL:CG1	2.30	0.61
11:K:84:VAL:CG1	11:K:95:ILE:HD11	2.31	0.61
17:Q:76:LEU:C	17:Q:76:LEU:HD23	2.21	0.61
19:S:31:ILE:CG2	19:S:32:LYS:H	2.10	0.61
1:A:1182:G:H4’	1:A:1183:A:O5’	1.99	0.61
12:L:40:VAL:O	12:L:40:VAL:HG12	1.99	0.61
1:A:267:C:OP2	17:Q:67:LYS:HD2	2.00	0.61
1:A:279:A:H4’	1:A:280:C:OP2	2.00	0.61
3:C:83:ARG:C	3:C:85:ARG:H	2.04	0.61
9:I:44:VAL:HG12	9:I:51:ARG:HH12	1.66	0.61
12:L:27:LEU:C	12:L:29:GLY:H	2.04	0.61
1:A:386:C:O2’	1:A:387:U:H5’	2.00	0.61
1:A:1305:G:H5’	21:V:4:GLY:HA3	1.83	0.61
2:B:115:LEU:O	2:B:119:GLU:HG3	2.00	0.61
4:D:191:ARG:O	4:D:191:ARG:HD2	2.00	0.61
7:G:78:ARG:HB2	7:G:156:TRP:HZ3	1.65	0.61
16:P:4:ILE:HG13	16:P:64:ALA:HB1	1.83	0.61
1:A:551:U:H2’	1:A:552:U:H6	1.64	0.61
1:A:1091:U:O2	1:A:1093:A:C8	2.54	0.61
3:C:191:THR:CG2	3:C:192:THR:N	2.64	0.61
4:D:148:VAL:HG11	4:D:158:ILE:HG21	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:38:LEU:HD12	7:G:38:LEU:O	2.01	0.61
16:P:67:THR:HG22	16:P:68:ASP:N	2.15	0.61
17:Q:101:ARG:HA	17:Q:101:ARG:NE	2.16	0.61
20:T:54:LYS:HE3	20:T:100:ILE:HD11	1.82	0.61
1:A:107:G:H2'	1:A:108:G:H5'	1.83	0.61
1:A:1346:A:C5	7:G:10:ARG:CZ	2.84	0.61
9:I:4:TYR:CZ	9:I:88:TYR:HD1	2.17	0.61
11:K:48:ILE:HG22	11:K:49:GLY:N	2.16	0.61
13:M:54:VAL:O	13:M:58:GLU:HG2	2.01	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
10:J:48:THR:OG1	10:J:62:HIS:CE1	2.54	0.61
1:A:939:G:H5"	7:G:102:ARG:HH22	1.65	0.60
2:B:143:GLU:O	2:B:147:LYS:HG3	2.00	0.60
15:O:29:VAL:HG12	15:O:85:LEU:HD11	1.82	0.60
1:A:190(E):U:O2'	17:Q:63:ARG:NH2	2.34	0.60
1:A:686:U:O2'	1:A:687:A:H8	1.84	0.60
2:B:33:TYR:O	2:B:34:ALA:HB2	2.01	0.60
2:B:98:LEU:O	2:B:101:MET:HG3	2.01	0.60
10:J:46:ARG:HH11	10:J:64:GLU:HB3	1.65	0.60
13:M:40:ASN:ND2	13:M:41:PRO:HD2	2.16	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:1346:A:H2'	7:G:10:ARG:HH22	1.66	0.60
3:C:47:LEU:HD23	3:C:68:VAL:HG11	1.83	0.60
4:D:157:LEU:HD22	4:D:161:ASN:ND2	2.16	0.60
5:E:80:ILE:HD11	5:E:91:LEU:HB2	1.84	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
1:A:1292:U:P	7:G:41:ARG:HH22	2.24	0.60
1:A:1343:G:H1'	9:I:121:ARG:HH12	1.66	0.60
12:L:27:LEU:C	12:L:29:GLY:N	2.54	0.60
17:Q:76:LEU:HD23	17:Q:77:VAL:N	2.15	0.60
1:A:112:G:H21	1:A:354:G:H5'	1.65	0.60
3:C:20:SER:HB3	3:C:22:TRP:HE1	1.67	0.60
7:G:72:ARG:HG2	7:G:142:GLU:OE1	2.02	0.60
8:H:64:LYS:HG2	8:H:79:VAL:HG21	1.84	0.60
11:K:84:VAL:HG21	18:R:88:LYS:HD3	1.82	0.60
19:S:13:ASP:HA	19:S:16:LEU:HB3	1.83	0.60
2:B:114:ARG:NH1	2:B:118:LEU:HD21	2.15	0.60
10:J:30:SER:HB3	10:J:84:GLN:HE21	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:71:LEU:O	10:J:72:VAL:HB	2.00	0.60
2:B:122:PHE:HE2	2:B:139:LYS:HG2	1.65	0.60
3:C:6:HIS:HD2	3:C:8:ILE:HB	1.66	0.60
5:E:65:ASN:CG	5:E:65:ASN:O	2.40	0.60
16:P:52:ASP:OD2	16:P:55:ARG:HG3	2.01	0.60
1:A:1381:U:O2'	1:A:1382:C:H5'	2.02	0.60
2:B:140:HIS:O	2:B:143:GLU:HB2	2.01	0.60
3:C:47:LEU:H	3:C:47:LEU:CD1	2.15	0.60
5:E:76:ILE:HD13	5:E:142:LEU:HD11	1.84	0.60
6:F:10:LEU:CD1	6:F:59:TYR:HB3	2.29	0.60
7:G:42:ILE:HG23	7:G:117:ALA:HA	1.84	0.60
11:K:19:ALA:HB2	11:K:80:VAL:HG11	1.82	0.60
16:P:81:ARG:HG3	16:P:83:GLU:HG2	1.84	0.60
20:T:96:GLY:O	20:T:97:ALA:HB3	2.00	0.60
1:A:190(L):U:H3	20:T:105:SER:CB	2.14	0.60
3:C:26:LYS:HD3	3:C:26:LYS:N	2.17	0.60
6:F:100:ASN:HD22	18:R:23:LYS:CG	2.12	0.60
12:L:46:LYS:HG2	12:L:47:LYS:N	2.16	0.60
13:M:10:PRO:O	13:M:45:VAL:HG11	2.01	0.60
1:A:375:U:H4'	16:P:17:TYR:CE2	2.37	0.60
1:A:1306:A:N6	1:A:1331:G:H1'	2.17	0.60
3:C:6:HIS:NE2	3:C:8:ILE:HD12	2.17	0.60
3:C:79:ARG:HE	3:C:82:GLU:HG2	1.66	0.60
11:K:69:ALA:O	11:K:73:MET:HG2	2.02	0.60
1:A:505:G:H2'	1:A:506:G:C8	2.37	0.59
1:A:1376:U:H2'	1:A:1377:A:C8	2.36	0.59
5:E:24:ARG:HG2	5:E:24:ARG:HH11	1.66	0.59
12:L:28:LYS:HD2	12:L:33:ARG:HH12	1.65	0.59
14:N:11:LYS:O	14:N:13:THR:N	2.35	0.59
1:A:435:C:H2'	1:A:436:C:H6	1.67	0.59
1:A:1352:C:H2'	1:A:1353:G:C8	2.37	0.59
1:A:1470:G:O2'	1:A:1471:G:H5'	2.02	0.59
9:I:93:ARG:NH1	9:I:97:LYS:NZ	2.51	0.59
15:O:11:VAL:HG21	15:O:34:LEU:HD12	1.83	0.59
1:A:457:C:H2'	1:A:458:C:H6	1.67	0.59
1:A:996:A:H2'	1:A:997:U:C6	2.38	0.59
3:C:46:GLU:O	3:C:48:TYR:N	2.33	0.59
14:N:24:CYS:HB3	14:N:28:GLY:H	1.66	0.59
1:A:1086:U:H3	1:A:1099:G:N2	1.91	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:151:LYS:H	4:D:151:LYS:CD	2.16	0.59
20:T:57:ARG:HH21	20:T:100:ILE:CG2	2.16	0.59
1:A:1130:A:H3'	1:A:1130:A:OP2	2.02	0.59
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.66	0.59
4:D:25:ARG:C	4:D:27:TYR:N	2.55	0.59
5:E:118:ILE:CG2	5:E:119:LEU:N	2.65	0.59
9:I:5:TYR:CD1	9:I:6:GLY:N	2.71	0.59
1:A:109:A:H2'	1:A:326:G:N2	2.17	0.59
1:A:513:C:O2'	1:A:514:C:H5'	2.02	0.59
1:A:839:U:O2	1:A:839:U:H2'	2.01	0.59
1:A:1247:U:O2'	1:A:1248:A:H5'	2.02	0.59
11:K:74:ALA:C	11:K:76:GLY:H	2.06	0.59
1:A:538:G:P	12:L:115:LYS:HG3	2.42	0.59
7:G:95:ARG:HG3	7:G:95:ARG:NH1	2.17	0.59
1:A:457:C:H2'	1:A:458:C:C6	2.37	0.59
1:A:502:G:H4'	1:A:550:G:H4'	1.83	0.59
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.06	0.59
2:B:120:ALA:O	2:B:124:SER:HB3	2.02	0.59
8:H:83:ILE:HG23	8:H:83:ILE:O	2.03	0.59
13:M:81:LEU:HD23	13:M:81:LEU:N	2.17	0.59
1:A:187:C:O2	20:T:105:SER:HB3	2.02	0.59
1:A:390:C:H2'	1:A:391:G:C8	2.38	0.59
1:A:427:U:OP1	4:D:13:ARG:NH2	2.36	0.59
1:A:560:U:H4'	1:A:561:U:H5"	1.83	0.59
1:A:736:C:H2'	1:A:737:A:C8	2.38	0.59
2:B:130:ARG:HD2	2:B:131:PRO:HD2	1.85	0.59
3:C:3:ASN:C	3:C:4:LYS:HG2	2.23	0.59
3:C:14:ILE:O	3:C:16:ARG:N	2.35	0.59
10:J:3:LYS:N	10:J:77:PRO:HD3	2.18	0.59
12:L:28:LYS:HD2	12:L:33:ARG:NH2	2.17	0.59
14:N:14:PRO:C	14:N:16:PHE:N	2.56	0.59
7:G:122:HIS:HA	7:G:125:MET:HE3	1.85	0.59
10:J:60:ARG:HD2	10:J:60:ARG:N	2.17	0.59
1:A:972:C:O3'	10:J:57:LYS:HG2	2.02	0.58
4:D:23:GLY:HA3	4:D:112:VAL:HG12	1.83	0.58
7:G:51:GLN:OE1	7:G:51:GLN:HA	2.02	0.58
8:H:91:ARG:HG2	12:L:7:ILE:HG21	1.85	0.58
10:J:46:ARG:NH1	10:J:64:GLU:HG2	2.18	0.58
12:L:55:VAL:CG1	12:L:67:THR:HG23	2.33	0.58
18:R:86:VAL:O	18:R:87:ARG:HB2	2.03	0.58
22:Y:12:LEU:HB3	22:Y:18:VAL:HB	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:537:G:OP1	12:L:113:ARG:NH2	2.36	0.58
1:A:991:U:O2'	1:A:992:U:H5'	2.02	0.58
1:A:1072:G:H2'	1:A:1073:U:C6	2.38	0.58
1:A:1182:G:O2'	1:A:1183:A:OP2	2.20	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	2.18	0.58
9:I:79:LEU:HD23	9:I:101:PHE:O	2.02	0.58
12:L:24:VAL:O	12:L:24:VAL:HG12	2.03	0.58
1:A:39:G:O2'	1:A:40:C:H5'	2.03	0.58
1:A:1316:G:N2	1:A:1318:A:H3'	2.18	0.58
1:A:1329:A:P	13:M:28:ALA:HB3	2.43	0.58
2:B:133:LYS:O	2:B:137:ARG:HG3	2.03	0.58
3:C:33:LEU:HD11	14:N:53:LEU:CD2	2.33	0.58
4:D:157:LEU:HD22	4:D:161:ASN:HD21	1.66	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
16:P:51:VAL:O	16:P:51:VAL:HG12	2.02	0.58
1:A:60:A:H4'	1:A:61:G:O5'	2.03	0.58
1:A:130:A:C8	17:Q:63:ARG:HG3	2.38	0.58
1:A:1178:G:P	9:I:97:LYS:HZ2	2.27	0.58
1:A:1347:G:O6	9:I:107:ARG:NH2	2.36	0.58
1:A:1441:G:H4'	1:A:1442:G:N7	2.19	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
10:J:51:ARG:HB2	10:J:59:SER:CB	2.23	0.58
15:O:17:ARG:NH1	15:O:77:ARG:HH11	2.01	0.58
1:A:103:C:P	20:T:17:ARG:HH11	2.26	0.58
1:A:976:G:OP2	1:A:1358:U:H1'	2.03	0.58
2:B:10:LEU:HD23	2:B:48:MET:HG3	1.86	0.58
2:B:76:GLN:HG3	2:B:206:ASP:OD1	2.04	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
10:J:82:ILE:O	10:J:82:ILE:HG22	2.03	0.58
20:T:53:LEU:O	20:T:57:ARG:HD2	2.04	0.58
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.39	0.58
1:A:1347:G:O6	9:I:10:ARG:NH2	2.34	0.58
9:I:5:TYR:O	9:I:84:ALA:HA	2.03	0.58
9:I:46:ALA:HB1	9:I:77:ILE:HG22	1.86	0.58
12:L:92:ASP:O	12:L:94:PRO:HD3	2.04	0.58
1:A:518:C:H5"	1:A:519:C:C6	2.38	0.58
2:B:156:LYS:O	2:B:156:LYS:HD3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:24:VAL:HG12	10:J:28:ARG:HE	1.68	0.58
13:M:40:ASN:ND2	13:M:41:PRO:CD	2.62	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:818:G:C2'	1:A:819:A:H5"	2.34	0.58
1:A:723:U:O2	1:A:723:U:H2'	2.04	0.58
1:A:1528:U:HO2'	1:A:1529:G:C3'	2.04	0.58
3:C:10:PHE:CE2	3:C:178:LEU:HD13	2.38	0.58
3:C:191:THR:HG21	3:C:193:TYR:CZ	2.39	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
10:J:15:THR:HG23	10:J:94:VAL:HG22	1.85	0.58
14:N:12:ARG:O	14:N:14:PRO:N	2.36	0.58
19:S:40:ILE:HG21	19:S:62:ILE:CD1	2.33	0.58
1:A:181:G:O2'	1:A:182:U:H5"	2.04	0.58
1:A:1117:G:H5'	1:A:1117:G:H8	1.66	0.58
1:A:1493:A:H2'	1:A:1494:G:C8	2.38	0.58
2:B:115:LEU:HG	2:B:153:ARG:HH21	1.69	0.58
1:A:346:G:C2'	1:A:347:G:H5'	2.34	0.57
1:A:538:G:OP2	12:L:115:LYS:HG3	2.04	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
11:K:40:ILE:HG23	11:K:75:TYR:CD2	2.38	0.57
20:T:10:LEU:HD12	20:T:12:ALA:HB3	1.85	0.57
1:A:1346:A:H4'	1:A:1347:G:O5'	2.03	0.57
9:I:17:VAL:HG21	9:I:80:GLY:HA3	1.86	0.57
10:J:48:THR:HG23	10:J:62:HIS:CE1	2.39	0.57
12:L:85:ILE:HG23	12:L:98:TYR:HB3	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
1:A:279:A:N6	17:Q:98:LEU:CD1	2.67	0.57
7:G:15:ASP:OD1	7:G:17:VAL:N	2.37	0.57
12:L:26:ALA:O	12:L:27:LEU:O	2.22	0.57
1:A:835:U:OP1	18:R:64:ARG:NH2	2.36	0.57
1:A:1014:A:H2'	1:A:1015:A:C8	2.39	0.57
1:A:1095:U:H2'	1:A:1096:C:C6	2.39	0.57
4:D:7:PRO:HG2	4:D:10:ARG:HD2	1.87	0.57
8:H:29:SER:OG	8:H:32:LYS:HB2	2.04	0.57
13:M:13:LYS:O	13:M:45:VAL:HG23	2.04	0.57
14:N:3:ARG:NH1	14:N:6:LEU:HD11	2.19	0.57
14:N:24:CYS:HB3	14:N:28:GLY:N	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:39:LYS:HD2	20:T:55:ILE:CD1	2.27	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
1:A:1015:A:H2'	1:A:1016:A:C8	2.40	0.57
1:A:1241:G:H2'	1:A:1242:C:C6	2.39	0.57
1:A:1414:U:O2'	1:A:1415:G:H5'	2.04	0.57
9:I:9:ARG:HA	9:I:13:ALA:O	2.05	0.57
14:N:29:ARG:HG2	14:N:29:ARG:HH11	1.69	0.57
1:A:1147:C:H4'	9:I:5:TYR:HE2	1.69	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
8:H:19:VAL:HG23	8:H:21:LYS:HD3	1.86	0.57
13:M:31:LYS:O	13:M:35:GLU:HB2	2.05	0.57
1:A:182:U:O4	1:A:183:G:N3	2.38	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:1504:G:H3'	1:A:1504:G:OP2	2.04	0.57
4:D:35:ARG:O	4:D:36:ARG:HB2	2.04	0.57
12:L:82:VAL:N	12:L:106:ASP:OD2	2.34	0.57
13:M:49:THR:HB	13:M:52:GLU:HG3	1.86	0.57
18:R:47:THR:HG22	18:R:48:GLY:N	2.18	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	2.20	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
3:C:84:ILE:O	3:C:88:ARG:HB2	2.05	0.57
8:H:103:VAL:HG21	8:H:110:ALA:HB2	1.87	0.57
12:L:6:THR:OG1	12:L:9:GLN:HG3	2.05	0.57
12:L:47:LYS:CB	12:L:48:PRO:HD3	2.35	0.57
19:S:7:LYS:HG3	19:S:7:LYS:O	2.03	0.57
19:S:25:LYS:H	19:S:25:LYS:HD2	1.68	0.57
1:A:192:U:O2'	1:A:193:C:H5'	2.05	0.57
1:A:243:A:N6	1:A:281:G:O2'	2.38	0.57
1:A:390:C:O3'	16:P:28:ARG:NH2	2.37	0.57
1:A:1040:U:H2'	1:A:1041:A:H8	1.70	0.57
1:A:1317:C:H2'	1:A:1318:A:O4'	2.04	0.57
2:B:209:ARG:HE	2:B:239:VAL:HG11	1.68	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
6:F:80:ARG:NH1	6:F:88:VAL:HB	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:25:THR:O	18:R:26:LEU:HB2	2.04	0.57
1:A:532:A:H2'	1:A:533:A:H5"	1.85	0.57
1:A:780:A:O2'	1:A:781:A:H5"	2.05	0.57
1:A:1278:U:H5"	1:A:1279:A:O4'	2.04	0.57
3:C:188:LEU:HD13	3:C:195:VAL:HG13	1.86	0.57
13:M:13:LYS:HD3	13:M:17:VAL:HG11	1.86	0.57
19:S:5:LEU:O	19:S:6:LYS:CB	2.51	0.57
1:A:1223:C:OP1	1:A:1224:G:H3'	2.04	0.56
1:A:1309:G:N7	13:M:99:ARG:NH2	2.50	0.56
2:B:130:ARG:NH2	3:C:179:ARG:HH12	2.02	0.56
17:Q:5:VAL:HG22	17:Q:60:ILE:HG12	1.87	0.56
1:A:129(A):G:O2'	1:A:190(E):U:H2'	2.05	0.56
1:A:1152:A:H5'	10:J:70:ARG:HH22	1.69	0.56
8:H:123:GLU:O	8:H:127:LEU:HD23	2.05	0.56
10:J:4:ILE:HA	10:J:100:THR:HA	1.87	0.56
15:O:3:ILE:HG22	15:O:7:GLU:HB3	1.86	0.56
15:O:41:GLU:OE2	15:O:41:GLU:HA	2.05	0.56
17:Q:59:ILE:HG22	17:Q:71:PHE:CD1	2.39	0.56
1:A:448:A:H2'	1:A:449:C:C6	2.40	0.56
1:A:449:C:O2	16:P:42:ARG:HD2	2.05	0.56
1:A:813:U:H5"	1:A:813:U:C6	2.40	0.56
1:A:818:G:H3'	1:A:819:A:H5"	1.87	0.56
1:A:915:A:C2'	1:A:916:G:H5'	2.35	0.56
1:A:1443:G:H5"	1:A:1446:A:C5'	2.19	0.56
2:B:88:ALA:C	2:B:90:MET:H	2.09	0.56
2:B:126:GLU:HG2	2:B:129:GLU:OE1	2.05	0.56
6:F:2:ARG:CD	6:F:69:GLU:HG2	2.35	0.56
9:I:39:GLY:O	9:I:40:LEU:HD23	2.06	0.56
9:I:93:ARG:NH1	9:I:97:LYS:HZ1	2.03	0.56
10:J:12:ASP:HB3	10:J:15:THR:HB	1.87	0.56
13:M:8:GLU:OE1	13:M:22:ILE:HG12	2.05	0.56
14:N:36:PHE:O	14:N:36:PHE:CD1	2.58	0.56
19:S:28:LYS:CG	19:S:29:ARG:H	2.09	0.56
19:S:63:THR:HG22	19:S:64:GLU:H	1.71	0.56
20:T:67:ALA:HA	20:T:73:HIS:H	1.70	0.56
1:A:1307:U:H5'	13:M:109:THR:HG21	1.88	0.56
2:B:47:THR:HA	2:B:202:PRO:HG2	1.87	0.56
3:C:32:LEU:HD23	3:C:32:LEU:O	2.05	0.56
4:D:199:ASN:HD21	4:D:201:GLN:HB2	1.71	0.56
17:Q:59:ILE:CG2	17:Q:71:PHE:HB3	2.36	0.56
1:A:477:G:H2'	1:A:478:A:C8	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:7:PRO:CG	3:C:184:TYR:HB2	2.35	0.56
3:C:33:LEU:HD23	3:C:33:LEU:O	2.04	0.56
7:G:146:GLU:HA	7:G:149:ARG:HB2	1.87	0.56
8:H:60:ARG:HH11	8:H:60:ARG:HG3	1.70	0.56
13:M:12:ASN:O	13:M:12:ASN:ND2	2.39	0.56
13:M:15:VAL:HG23	13:M:43:THR:O	2.04	0.56
13:M:17:VAL:O	13:M:20:THR:HB	2.06	0.56
1:A:246:A:N6	1:A:281:G:H1'	2.19	0.56
1:A:1028:C:H2'	1:A:1029:C:C6	2.40	0.56
1:A:1257:U:O2'	1:A:1258:G:OP2	2.21	0.56
1:A:1339:A:H2'	1:A:1340:A:O4'	2.06	0.56
1:A:1493:A:H2'	1:A:1494:G:H8	1.71	0.56
4:D:176:LEU:HA	4:D:183:GLY:HA2	1.87	0.56
19:S:10:PHE:CD1	19:S:11:VAL:N	2.73	0.56
20:T:86:ARG:O	20:T:90:GLN:HG3	2.05	0.56
1:A:411:A:C4	1:A:413:G:H1'	2.41	0.56
1:A:1256:A:H61	1:A:1278:U:H1'	1.70	0.56
4:D:6:GLY:O	4:D:8:VAL:HG23	2.06	0.56
10:J:81:THR:O	10:J:85:LEU:HG	2.06	0.56
13:M:117:VAL:HG12	13:M:118:ALA:H	1.70	0.56
19:S:40:ILE:HG21	19:S:62:ILE:HD11	1.88	0.56
1:A:247:G:N2	1:A:282:A:C2	2.73	0.56
1:A:254:G:OP1	17:Q:67:LYS:O	2.24	0.56
1:A:438:G:C4'	1:A:439:A:OP1	2.53	0.56
1:A:1251:A:H4'	9:I:12:GLU:OE2	2.06	0.56
1:A:1257:U:H4'	1:A:1258:G:O5'	2.06	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
10:J:22:LYS:CE	10:J:90:LEU:HD12	2.33	0.56
18:R:53:ARG:HD3	18:R:63:GLN:CB	2.36	0.56
1:A:1044:A:H2'	1:A:1045:C:C5'	2.36	0.56
15:O:36:ILE:HA	15:O:59:MET:HE3	1.87	0.56
20:T:94:ALA:O	20:T:95:ALA:HB3	2.06	0.56
1:A:505:G:H2'	1:A:506:G:H8	1.69	0.56
4:D:57:ARG:HB3	4:D:206:PHE:HB2	1.88	0.56
1:A:166:G:O2'	1:A:167:G:H5'	2.06	0.55
1:A:1042:G:O2'	1:A:1043:C:H5'	2.05	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
8:H:105:ARG:HG3	8:H:105:ARG:HH11	1.71	0.55
12:L:50:SER:O	12:L:51:ALA:HB2	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:26:ARG:HD2	16:P:31:LYS:O	2.06	0.55
1:A:1251:A:H2'	1:A:1252:A:C8	2.41	0.55
4:D:24:GLU:H	4:D:112:VAL:CG1	2.19	0.55
10:J:62:HIS:HB3	14:N:59:ALA:HB3	1.87	0.55
13:M:40:ASN:ND2	13:M:42:ALA:H	2.05	0.55
1:A:1202:G:O2'	1:A:1203:C:H5'	2.06	0.55
2:B:74:LYS:HZ1	2:B:206:ASP:CA	2.19	0.55
13:M:65:LYS:HE3	13:M:69:GLU:OE2	2.07	0.55
20:T:35:THR:O	20:T:39:LYS:HB2	2.06	0.55
1:A:252:U:H2'	1:A:253:U:C6	2.41	0.55
2:B:23:ARG:HD3	2:B:23:ARG:N	2.22	0.55
3:C:13:GLY:HA3	14:N:57:ARG:NH2	2.20	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
10:J:48:THR:CG2	10:J:62:HIS:HE1	2.20	0.55
12:L:47:LYS:HB2	12:L:48:PRO:HD2	1.88	0.55
1:A:182:U:C5	1:A:183:G:C1'	2.90	0.55
1:A:1367:C:H4'	10:J:48:THR:HG21	1.89	0.55
2:B:15:VAL:HG22	2:B:209:ARG:HG3	1.89	0.55
6:F:69:GLU:HA	6:F:72:VAL:CG2	2.37	0.55
13:M:37:THR:HG22	13:M:37:THR:O	2.07	0.55
16:P:81:ARG:CG	16:P:83:GLU:HG2	2.36	0.55
1:A:490:G:H2'	1:A:491:G:H8	1.72	0.55
1:A:620:C:H2'	1:A:621:A:O4'	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:67:THR:HG22	2:B:68:ILE:N	2.21	0.55
4:D:107:ARG:HH21	4:D:194:LEU:HD12	1.70	0.55
7:G:116:ALA:HA	7:G:119:ARG:NH2	2.21	0.55
11:K:110:ASP:HB2	18:R:88:LYS:CD	2.25	0.55
13:M:84:ILE:CG2	19:S:65:ASN:HD22	2.19	0.55
18:R:86:VAL:O	18:R:87:ARG:CB	2.55	0.55
1:A:818:G:C3'	1:A:819:A:C5'	2.83	0.55
1:A:1006:C:H2'	1:A:1007:C:H6	1.72	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:1460:A:H2'	1:A:1461:G:O4'	2.07	0.55
9:I:7:THR:HG22	9:I:8:GLY:N	2.22	0.55
3:C:37:GLN:NE2	14:N:52:GLN:OE1	2.40	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:HE2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:C:H2'	1:A:194:C:H6	1.71	0.55
1:A:551:U:H2'	1:A:552:U:C6	2.41	0.55
6:F:76:ALA:O	6:F:80:ARG:HG3	2.06	0.55
1:A:26:A:N6	1:A:558:G:H1'	2.21	0.55
1:A:600:C:OP1	8:H:97:VAL:HG12	2.07	0.55
1:A:939:G:H2'	1:A:940:C:H6	1.71	0.55
1:A:1410:G:H1	1:A:1490:C:H42	1.53	0.55
2:B:178:ARG:O	8:H:71:GLY:HA2	2.07	0.55
7:G:44:TYR:HE2	9:I:41:VAL:HG11	1.71	0.55
15:O:87:ILE:O	15:O:88:ARG:CB	2.54	0.55
20:T:82:SER:O	20:T:86:ARG:HB2	2.06	0.55
1:A:54:C:H2'	1:A:352:C:H41	1.71	0.54
1:A:190(F):G:H4'	1:A:190(G):G:OP2	2.07	0.54
1:A:429:U:H2'	4:D:25:ARG:HH12	1.71	0.54
1:A:977:A:C2'	1:A:978:A:H5"	2.37	0.54
1:A:1333:A:H2'	1:A:1334:G:O4'	2.07	0.54
6:F:25:ILE:HD12	6:F:82:ARG:HD2	1.88	0.54
10:J:51:ARG:H	10:J:59:SER:HB2	1.72	0.54
20:T:67:ALA:HB2	20:T:77:ALA:HB2	1.88	0.54
1:A:1319:A:H5'	1:A:1320:C:OP1	2.06	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
2:B:75:LYS:O	2:B:75:LYS:HD3	2.08	0.54
3:C:138:VAL:HG21	3:C:168:ALA:HB1	1.89	0.54
4:D:43:HIS:CE1	4:D:46:LYS:HZ2	2.25	0.54
8:H:36:LEU:HD12	8:H:59:LEU:HD13	1.88	0.54
2:B:17:PHE:HD1	2:B:18:GLY:N	2.04	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
7:G:69:VAL:HG12	7:G:100:ALA:HA	1.90	0.54
7:G:116:ALA:HA	7:G:119:ARG:CZ	2.37	0.54
8:H:56:LYS:HD2	8:H:56:LYS:N	2.23	0.54
15:O:32:LEU:O	15:O:36:ILE:HG13	2.06	0.54
1:A:247:G:C2	1:A:282:A:C2	2.95	0.54
1:A:765:G:N1	1:A:812:C:H1'	2.23	0.54
2:B:33:TYR:HB3	2:B:41:ILE:O	2.08	0.54
5:E:15:ARG:O	5:E:27:ARG:O	2.25	0.54
5:E:137:GLU:O	5:E:141:GLN:HG3	2.08	0.54
6:F:4:TYR:OH	6:F:69:GLU:HB3	2.07	0.54
7:G:18:TYR:CE2	7:G:59:LEU:HB2	2.42	0.54
7:G:113:GLU:HG2	7:G:119:ARG:HG2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:60:VAL:O	13:M:63:THR:HG22	2.07	0.54
17:Q:79:SER:O	17:Q:80:GLY:O	2.25	0.54
1:A:246:A:C2	1:A:282:A:C6	2.96	0.54
1:A:376:G:P	16:P:67:THR:HG21	2.48	0.54
1:A:921:U:O2'	5:E:19:MET:O	2.24	0.54
2:B:12:GLU:C	2:B:14:GLY:N	2.58	0.54
3:C:58:GLU:H	3:C:65:ALA:HB3	1.72	0.54
3:C:150:LYS:CE	3:C:152:ILE:HD11	2.38	0.54
7:G:138:LYS:HE2	7:G:142:GLU:OE1	2.08	0.54
10:J:3:LYS:N	10:J:75:ILE:HA	2.22	0.54
13:M:29:ARG:HB3	13:M:64:TRP:CH2	2.42	0.54
14:N:32:SER:O	14:N:40:CYS:CA	2.55	0.54
15:O:27:VAL:O	15:O:31:LEU:HD13	2.07	0.54
1:A:743:U:H2'	1:A:744:C:C6	2.43	0.54
1:A:1030(A):G:N2	1:A:1030(C):G:H3'	2.23	0.54
1:A:1128:C:H2'	1:A:1129:C:H5"	1.90	0.54
9:I:85:LEU:O	9:I:92:TYR:HD2	1.91	0.54
16:P:21:VAL:O	16:P:33:ILE:HB	2.07	0.54
17:Q:18:THR:HG23	17:Q:69:LYS:HE3	1.88	0.54
1:A:182:U:C6	1:A:183:G:C8	2.94	0.54
1:A:190:C:H2'	1:A:190(A):C:C6	2.43	0.54
1:A:765:G:O6	1:A:812:C:C6	2.61	0.54
1:A:922:G:H5'	5:E:19:MET:O	2.08	0.54
1:A:1318:A:H4'	19:S:10:PHE:CE2	2.42	0.54
1:A:1367:C:H5'	10:J:60:ARG:NH1	2.23	0.54
20:T:72:LEU:HD21	20:T:80:ARG:CZ	2.38	0.54
1:A:35:G:H2'	1:A:36:C:C6	2.43	0.54
1:A:246:A:C2	1:A:282:A:C5	2.95	0.54
1:A:247:G:OP2	17:Q:100:LYS:HG3	2.07	0.54
1:A:811:C:C2'	1:A:812:C:C5'	2.85	0.54
1:A:983:A:H5'	1:A:984:C:OP2	2.07	0.54
1:A:1231:G:OP1	9:I:127:LYS:NZ	2.40	0.54
3:C:77:ILE:HG22	3:C:81:GLY:HA2	1.90	0.54
4:D:160:GLN:O	4:D:163:GLU:HB3	2.08	0.54
1:A:1320:C:N3	19:S:36:ARG:HG3	2.22	0.54
2:B:142:LEU:HD22	2:B:146:GLN:HE22	1.73	0.54
2:B:187:LEU:HD23	2:B:214:ILE:HG21	1.90	0.54
9:I:81:ILE:O	9:I:85:LEU:HB2	2.08	0.54
13:M:53:VAL:O	13:M:57:ARG:HB2	2.08	0.54
1:A:246:A:C4	1:A:282:A:N6	2.76	0.54
1:A:299:G:H2'	1:A:300:A:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1346:A:C5	7:G:10:ARG:NH2	2.76	0.54
1:A:1351:U:H2'	1:A:1352:C:C6	2.40	0.54
3:C:14:ILE:HG22	3:C:15:THR:N	2.12	0.54
3:C:116:VAL:O	3:C:120:VAL:HG23	2.07	0.54
10:J:45:ARG:NH2	14:N:36:PHE:CD2	2.75	0.54
15:O:70:LEU:HD11	15:O:77:ARG:HB2	1.89	0.54
1:A:750:G:H1'	15:O:22:THR:OG1	2.08	0.53
1:A:1516:G:H2'	1:A:1518:A:OP2	2.08	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
6:F:26:ILE:HG21	6:F:63:TYR:CE2	2.40	0.53
9:I:97:LYS:O	9:I:100:GLY:N	2.36	0.53
1:A:33:A:H2'	1:A:34:C:H6	1.72	0.53
1:A:475:G:H2'	1:A:476:G:C8	2.43	0.53
1:A:639:G:O2'	1:A:640:A:H5'	2.08	0.53
1:A:1218:C:H2'	1:A:1219:U:C6	2.42	0.53
3:C:113:ALA:HB3	3:C:114:PRO:HD3	1.90	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
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:11:SER:OG	16:P:14:ASN:HB3	2.08	0.53
1:A:1003:G:C2	1:A:1003(A):G:C6	2.96	0.53
1:A:1057:G:H5"	3:C:154:SER:CB	2.26	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
10:J:31:GLY:HA2	10:J:78:ASN:ND2	2.13	0.53
12:L:46:LYS:CG	12:L:47:LYS:N	2.71	0.53
16:P:43:LYS:HB3	16:P:48:TRP:CD1	2.43	0.53
1:A:1499:A:H1'	1:A:1520:G:H5'	1.89	0.53
7:G:71:PRO:HD3	7:G:103:TRP:HZ3	1.73	0.53
8:H:8:ASP:O	8:H:12:ARG:HG3	2.07	0.53
11:K:14:VAL:O	11:K:15:ALA:CB	2.57	0.53
14:N:44:LEU:C	14:N:44:LEU:HD12	2.29	0.53
19:S:51:VAL:HG12	19:S:52:TYR:N	2.23	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:979:C:H2'	1:A:980:C:H5'	1.91	0.53
5:E:18:ARG:HG2	5:E:19:MET:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
10:J:49:VAL:HG11	14:N:41:ARG:O	2.08	0.53
13:M:8:GLU:OE1	13:M:22:ILE:HA	2.08	0.53
14:N:44:LEU:HD12	14:N:44:LEU:O	2.08	0.53
1:A:300:A:H2'	1:A:301:G:O4'	2.08	0.53
1:A:386:C:C2'	1:A:387:U:H5'	2.39	0.53
5:E:76:ILE:O	5:E:93:PRO:HB3	2.07	0.53
8:H:80:ILE:O	8:H:80:ILE:HG22	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
17:Q:27:PHE:CE1	17:Q:36:ILE:HD11	2.42	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:101:A:O2'	1:A:102:G:H5'	2.07	0.53
1:A:227:G:O2'	16:P:62:VAL:HG11	2.07	0.53
1:A:818:G:O2'	1:A:819:A:H5"	2.08	0.53
1:A:1003:G:N2	1:A:1039:C:C2	2.77	0.53
1:A:1157:A:H4'	1:A:1158:C:O5'	2.08	0.53
1:A:1305:G:O2'	1:A:1306:A:C8	2.44	0.53
1:A:1372:U:OP1	9:I:71:SER:HB3	2.09	0.53
7:G:42:ILE:CG2	7:G:120:ILE:HD12	2.39	0.53
12:L:53:ARG:HG2	12:L:69:TYR:HE1	1.73	0.53
20:T:76:ALA:O	20:T:80:ARG:HG2	2.09	0.53
1:A:182:U:C4	1:A:183:G:C4	2.96	0.53
1:A:452:A:H4'	16:P:72:ARG:NH2	2.24	0.53
1:A:657:G:H4'	15:O:28:GLN:HG2	1.91	0.53
1:A:797:C:OP1	11:K:124:LYS:HG3	2.09	0.53
1:A:1147:C:H4'	9:I:5:TYR:CE2	2.43	0.53
1:A:1426:C:H2'	1:A:1427:U:C6	2.44	0.53
2:B:23:ARG:O	2:B:24:TRP:O	2.27	0.53
3:C:91:LEU:HD21	3:C:99:VAL:CG1	2.30	0.53
10:J:81:THR:C	10:J:83:GLU:H	2.10	0.53
13:M:11:ARG:CG	13:M:12:ASN:N	2.72	0.53
20:T:93:GLU:HA	20:T:93:GLU:OE2	2.09	0.53
1:A:623:C:O2'	1:A:624:C:H5'	2.09	0.53
1:A:1068:G:OP2	1:A:1068:G:H8	1.91	0.53
1:A:1184:G:H2'	1:A:1185:G:H8	1.73	0.53
1:A:1231:G:H4'	9:I:126:SER:OG	2.09	0.53
1:A:1277:C:HO2'	1:A:1279:A:H8	1.52	0.53
3:C:32:LEU:HD21	3:C:59:ARG:HD2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:61:LYS:O	18:R:65:ILE:HG13	2.08	0.53
1:A:101:A:H2'	1:A:102:G:H8	1.74	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
1:A:1006:C:H2'	1:A:1007:C:C6	2.44	0.53
1:A:1121:U:H2'	1:A:1122:U:H6	1.73	0.53
1:A:1300:G:HO2'	1:A:1301:U:H6	1.55	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
4:D:32:ALA:C	4:D:34:GLU:N	2.60	0.53
5:E:31:LEU:HD22	5:E:43:LEU:CD2	2.39	0.53
7:G:69:VAL:HG21	7:G:104:LEU:HD21	1.89	0.53
9:I:31:GLN:HB3	9:I:35:GLU:HB3	1.91	0.53
12:L:55:VAL:HG11	12:L:67:THR:HG23	1.91	0.53
1:A:1128:C:H1'	1:A:1146:A:H61	1.75	0.52
3:C:130:VAL:O	3:C:134:ILE:HG13	2.07	0.52
10:J:44:VAL:HG22	10:J:66:ARG:HB3	1.91	0.52
1:A:370:C:O2'	1:A:371:G:H5'	2.10	0.52
1:A:1038:C:H2'	1:A:1039:C:C6	2.43	0.52
1:A:1196:U:OP1	1:A:1197:G:H5'	2.09	0.52
1:A:1423:G:O2'	1:A:1424:C:H5'	2.09	0.52
11:K:109:VAL:HG13	18:R:85:LEU:O	2.10	0.52
12:L:47:LYS:HB3	12:L:48:PRO:HD3	1.91	0.52
13:M:102:ARG:HB2	13:M:102:ARG:HH11	1.75	0.52
20:T:50:GLU:O	20:T:100:ILE:HD12	2.09	0.52
1:A:621:A:H2'	1:A:622:A:C8	2.44	0.52
1:A:1229:A:OP2	13:M:114:ARG:HD3	2.09	0.52
1:A:1528:U:O2'	1:A:1530:G:C5'	2.57	0.52
5:E:12:LEU:CD1	5:E:31:LEU:HB2	2.39	0.52
11:K:13:GLN:HA	11:K:75:TYR:O	2.08	0.52
14:N:33:VAL:HA	14:N:40:CYS:HA	1.91	0.52
1:A:115:G:O2'	1:A:116:A:OP2	2.22	0.52
1:A:401:C:H1'	1:A:622:A:H1'	1.91	0.52
1:A:1216:G:H5"	14:N:5:ALA:HB1	1.92	0.52
1:A:1513:A:H2'	1:A:1514:C:C6	2.44	0.52
3:C:23:TYR:CD2	3:C:24:ALA:N	2.78	0.52
4:D:65:ARG:HB2	4:D:75:PHE:CE2	2.45	0.52
6:F:10:LEU:HD11	6:F:59:TYR:CD2	2.41	0.52
6:F:43:LEU:H	6:F:43:LEU:CD2	2.23	0.52
13:M:86:CYS:SG	13:M:88:ARG:HB3	2.49	0.52
13:M:117:VAL:HG12	13:M:118:ALA:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:922:G:N3	1:A:1398:A:H2	2.07	0.52
1:A:1038:C:H2'	1:A:1039:C:H6	1.74	0.52
1:A:1397:C:H4'	1:A:1398:A:OP2	2.08	0.52
3:C:33:LEU:HD11	14:N:53:LEU:HD22	1.91	0.52
3:C:70:VAL:O	3:C:106:VAL:HG23	2.09	0.52
8:H:14:ARG:O	8:H:18:ARG:HD3	2.10	0.52
12:L:55:VAL:HG11	12:L:67:THR:CG2	2.39	0.52
19:S:13:ASP:O	19:S:17:GLU:HG2	2.10	0.52
19:S:50:ALA:HA	19:S:58:VAL:O	2.10	0.52
20:T:43:LEU:CD1	20:T:55:ILE:HD12	2.40	0.52
21:V:17:THR:O	21:V:22:ARG:HD3	2.10	0.52
1:A:1054:C:N4	22:Y:91:TYR:HE2	2.06	0.52
1:A:1305:G:C5'	21:V:4:GLY:HA3	2.38	0.52
1:A:1424:C:O2'	1:A:1425:U:H5'	2.09	0.52
2:B:73:THR:HG23	2:B:95:GLN:O	2.09	0.52
4:D:104:VAL:HG11	4:D:146:ILE:CD1	2.37	0.52
5:E:74:GLY:HA3	5:E:116:THR:HG22	1.92	0.52
14:N:3:ARG:O	14:N:4:LYS:C	2.48	0.52
18:R:73:ALA:HB3	18:R:79:LEU:HD12	1.91	0.52
1:A:813:U:H5'	1:A:816:A:N6	2.25	0.52
3:C:154:SER:O	3:C:165:THR:HA	2.09	0.52
4:D:170:VAL:CG1	4:D:174:LEU:HB2	2.39	0.52
5:E:80:ILE:HD13	5:E:138:ALA:HB1	1.90	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
1:A:791:G:H2'	1:A:792:A:H5'	1.91	0.52
1:A:1021:G:C2'	1:A:1022:G:H5'	2.40	0.52
1:A:1202:G:H2'	1:A:1203:C:O4'	2.10	0.52
1:A:1428:A:H2'	1:A:1429:C:C6	2.44	0.52
1:A:1511:G:H2'	1:A:1512:U:O4'	2.09	0.52
3:C:83:ARG:C	3:C:85:ARG:N	2.63	0.52
5:E:12:LEU:HD22	5:E:12:LEU:C	2.30	0.52
8:H:25:ASP:OD1	8:H:60:ARG:HD3	2.09	0.52
17:Q:97:SER:C	17:Q:98:LEU:HG	2.29	0.52
20:T:41:ILE:O	20:T:45:GLN:HB2	2.10	0.52
21:V:24:ARG:O	21:V:25:LYS:HB2	2.10	0.52
1:A:142:G:O2'	1:A:196:A:N1	2.40	0.52
1:A:148:G:H2'	1:A:149:A:C8	2.45	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
9:I:9:ARG:HG2	9:I:14:VAL:HG22	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:G:H1'	1:A:116:A:N7	2.24	0.52
1:A:357:G:O2'	1:A:358:U: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
6:F:8:ILE:HD11	6:F:79:LEU:HD13	1.92	0.52
10:J:22:LYS:NZ	10:J:91:PRO:HD3	2.25	0.52
13:M:88:ARG:HG3	13:M:98:VAL:CG1	2.40	0.52
1:A:163:C:O2'	1:A:164:U:H5'	2.10	0.51
1:A:443:C:H2'	1:A:444:C:C6	2.43	0.51
1:A:1241:G:H2'	1:A:1242:C:H6	1.75	0.51
1:A:1305:G:OP1	21:V:2:GLY:N	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
11:K:27:ASN:HA	11:K:56:GLY:HA2	1.92	0.51
11:K:62:GLN:HG3	11:K:97:ALA:HB2	1.92	0.51
11:K:126:ARG:O	11:K:127:LYS:C	2.48	0.51
13:M:73:GLU:O	13:M:76:ALA:HB3	2.09	0.51
16:P:20:VAL:CG1	16:P:32:TYR:HB3	2.40	0.51
18:R:46:GLU:H	18:R:46:GLU:CD	2.13	0.51
21:V:24:ARG:O	21:V:25:LYS:CB	2.58	0.51
1:A:794:A:H2'	1:A:795:C:C6	2.45	0.51
1:A:1208:C:O2'	22:Y:24:ALA:HB3	2.11	0.51
1:A:1256:A:H8	3:C:27:LYS:HZ1	1.56	0.51
1:A:1346:A:C4	7:G:10:ARG:CZ	2.93	0.51
3:C:108:ASN:C	3:C:110:ASN:H	2.12	0.51
9:I:44:VAL:HG13	9:I:51:ARG:NH2	2.24	0.51
12:L:42:THR:HG21	12:L:52:LEU:HB3	1.91	0.51
12:L:43:VAL:CG1	12:L:44:THR:H	2.23	0.51
12:L:119:LYS:O	12:L:120:TYR:HB2	2.10	0.51
13:M:82:MET:HE2	13:M:92:HIS:HB3	1.92	0.51
18:R:88:LYS:OXT	18:R:88:LYS:HG2	2.10	0.51
1:A:560:U:O2'	1:A:561:U:OP2	2.27	0.51
1:A:1094:G:H5"	1:A:1095:U:H5	1.75	0.51
1:A:1329:A:O2'	1:A:1330:U:H5'	2.11	0.51
2:B:126:GLU:O	2:B:129:GLU:HB2	2.11	0.51
3:C:134:ILE:HG21	3:C:167:TRP:O	2.11	0.51
5:E:13:ILE:HG22	5:E:30:ALA:CB	2.40	0.51
5:E:40:ARG:HG2	5:E:40:ARG:HH11	1.76	0.51
6:F:69:GLU:OE1	6:F:69:GLU:N	2.44	0.51
7:G:156:TRP:OXT	7:G:156:TRP:HD1	1.93	0.51
10:J:20:ALA:O	10:J:24:VAL:HG23	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:39:PRO:O	10:J:40:LEU:CB	2.58	0.51
19:S:53:ASN:HB2	19:S:56:GLN:H	1.73	0.51
1:A:518:C:O2'	12:L:50:SER:HB3	2.10	0.51
1:A:1003(A):G:N1	1:A:1004:A:H1'	2.25	0.51
3:C:61:ALA:O	3:C:63:ASN:N	2.44	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
7:G:102:ARG:O	7:G:106:GLN:HG3	2.10	0.51
10:J:23:ILE:N	10:J:23:ILE:HD12	2.26	0.51
1:A:181:G:O2'	1:A:183:G:N7	2.26	0.51
1:A:828:A:H2'	1:A:829:G:O4'	2.10	0.51
1:A:981:U:H5'	14:N:21:TYR:CE1	2.46	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
4:D:24:GLU:O	4:D:25:ARG:HB3	2.10	0.51
10:J:49:VAL:CG1	14:N:41:ARG:HB2	2.32	0.51
14:N:21:TYR:HE2	14:N:23:ARG:NE	2.09	0.51
14:N:57:ARG:HG2	14:N:58:LYS:H	1.75	0.51
1:A:182:U:H5	1:A:183:G:N7	2.04	0.51
1:A:246:A:H61	1:A:281:G:H1'	1.75	0.51
1:A:502:G:H1'	1:A:550:G:H5'	1.92	0.51
1:A:580:U:H2'	1:A:581:G:O4'	2.11	0.51
1:A:1059:C:O2'	1:A:1060:C:H5'	2.11	0.51
2:B:19:HIS:NE2	2:B:206:ASP:HB3	2.26	0.51
3:C:34:LEU:HD23	3:C:34:LEU:O	2.10	0.51
3:C:84:ILE:O	3:C:84:ILE:HG12	2.10	0.51
3:C:137:ALA:HA	3:C:140:ARG:NH1	2.26	0.51
10:J:69:ASN:O	10:J:70:ARG:HD3	2.11	0.51
17:Q:45:HIS:CB	17:Q:65:ILE:HD13	2.39	0.51
19:S:10:PHE:CD1	19:S:10:PHE:C	2.83	0.51
1:A:243:A:H62	1:A:281:G:C2'	2.24	0.51
1:A:791:G:H2'	1:A:792:A:C5'	2.40	0.51
1:A:1021:G:H2'	1:A:1022:G:O4'	2.11	0.51
1:A:1085:U:O3'	1:A:1086:U:C6	2.64	0.51
1:A:1126:U:OP2	1:A:1281:U:O2	2.29	0.51
1:A:1346:A:N9	7:G:10:ARG:NH2	2.58	0.51
2:B:144:ARG:O	2:B:147:LYS:N	2.42	0.51
5:E:89:ILE:HD13	5:E:90:VAL:H	1.75	0.51
5:E:115:VAL:HG12	5:E:116:THR:N	2.24	0.51
9:I:127:LYS:N	9:I:127:LYS:HD2	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:28:GLY:O	14:N:30:ALA:N	2.43	0.51
17:Q:45:HIS:HB2	17:Q:65:ILE:CD1	2.37	0.51
1:A:160:A:H1'	1:A:344:A:C5	2.46	0.51
1:A:478:A:O2'	1:A:479:C:H5'	2.11	0.51
1:A:954:G:H21	1:A:1227:A:H62	1.59	0.51
1:A:992:U:O2'	1:A:993:G:OP2	2.26	0.51
1:A:1162:C:H2'	1:A:1163:C:C6	2.46	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
2:B:53:ARG:NH1	2:B:53:ARG:HG2	2.26	0.51
2:B:96:ARG:O	2:B:98:LEU:HD23	2.11	0.51
3:C:188:LEU:CD1	3:C:195:VAL:HG13	2.41	0.51
5:E:104:ALA:O	5:E:105:VAL:C	2.49	0.51
6:F:43:LEU:H	6:F:43:LEU:HD22	1.76	0.51
6:F:67:MET:HE2	6:F:72:VAL:HG22	1.92	0.51
9:I:125:TYR:CD1	9:I:125:TYR:N	2.79	0.51
12:L:28:LYS:CD	12:L:33:ARG:HH12	2.24	0.51
1:A:429:U:H2'	4:D:25:ARG:NH1	2.26	0.51
1:A:650:G:C2'	1:A:651:C:H5'	2.40	0.51
1:A:1152:A:H2'	1:A:1153:C:C6	2.45	0.51
2:B:17:PHE:CD1	2:B:17:PHE:C	2.85	0.51
4:D:81:GLU:O	4:D:85:LYS:HG3	2.11	0.51
5:E:92:LYS:HB3	5:E:119:LEU:HB2	1.93	0.51
6:F:9:VAL:HG22	6:F:60:PHE:CE1	2.46	0.51
8:H:49:GLU:HG2	8:H:62:TYR:HE2	1.75	0.51
10:J:48:THR:CG2	10:J:62:HIS:CE1	2.94	0.51
12:L:115:LYS:O	12:L:117:ARG:N	2.37	0.51
18:R:45:SER:C	18:R:47:THR:N	2.65	0.51
19:S:45:VAL:HG12	19:S:46:GLY:N	2.26	0.51
1:A:7:G:H5'	1:A:298:A:O4'	2.11	0.51
1:A:103:C:OP2	20:T:17:ARG:NH1	2.44	0.51
1:A:112:G:H21	1:A:354:G:C5'	2.24	0.51
1:A:1097:C:H2'	1:A:1098:C:C6	2.45	0.51
1:A:1262:C:H42	1:A:1273:G:H1	1.59	0.51
1:A:1347:G:C6	9:I:107:ARG:CZ	2.94	0.51
1:A:1366:C:O2'	10:J:60:ARG:NH2	2.42	0.51
1:A:1396:A:H4'	1:A:1397:C:H5"	1.93	0.51
2:B:97:TRP:CZ2	2:B:102:LEU:HD13	2.45	0.51
5:E:61:TYR:O	5:E:64:ARG:O	2.29	0.51
9:I:27:THR:HG23	9:I:30:GLY:O	2.11	0.51
12:L:43:VAL:CG1	12:L:44:THR:N	2.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:G:H1'	17:Q:16:GLN:HE21	1.70	0.50
1:A:1108:G:H5'	1:A:1191:A:H4'	1.92	0.50
3:C:58:GLU:O	3:C:59:ARG:HG2	2.11	0.50
9:I:44:VAL:CG1	9:I:51:ARG:HH12	2.23	0.50
10:J:27:ALA:HB1	10:J:81:THR:HG23	1.92	0.50
12:L:53:ARG:NH1	12:L:92:ASP:OD2	2.42	0.50
1:A:149:A:O2'	1:A:150:C:H5'	2.12	0.50
1:A:190(L):U:H3	20:T:105:SER:HB2	1.76	0.50
1:A:1418:A:H2'	1:A:1419:G:O4'	2.12	0.50
2:B:53:ARG:HG2	2:B:53:ARG:HH11	1.75	0.50
7:G:69:VAL:HG12	7:G:69:VAL:O	2.12	0.50
8:H:126:LYS:C	8:H:128:GLY:H	2.14	0.50
14:N:22:THR:OG1	14:N:33:VAL:HG21	2.11	0.50
21:V:6:ARG:HD2	21:V:15:ARG:NH1	2.25	0.50
22:Y:41:THR:N	22:Y:45:GLU:OE1	2.41	0.50
22:Y:55:PRO:HD3	22:Y:64:TRP:CZ3	2.46	0.50
1:A:282:A:H3'	1:A:283:C:H6	1.76	0.50
1:A:853:G:O2'	1:A:854:G:H5'	2.11	0.50
1:A:1021:G:C2	1:A:1022:G:H1'	2.45	0.50
1:A:1035:A:H2'	1:A:1036:G:H8	1.76	0.50
1:A:1213:A:N1	1:A:1215:G:H1'	2.27	0.50
1:A:1326:C:OP1	21:V:12:LYS:NZ	2.41	0.50
2:B:88:ALA:O	2:B:90:MET:N	2.45	0.50
3:C:47:LEU:CD1	3:C:47:LEU:N	2.74	0.50
3:C:112:SER:O	3:C:116:VAL:HG23	2.11	0.50
4:D:151:LYS:N	4:D:151:LYS:CD	2.75	0.50
5:E:11:ILE:HB	5:E:31:LEU:HB3	1.93	0.50
6:F:67:MET:CE	6:F:72:VAL:HA	2.40	0.50
9:I:17:VAL:CG2	9:I:80:GLY:HA3	2.41	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
13:M:77:ASN:O	13:M:80:ARG:HB3	2.10	0.50
1:A:222:U:H2'	1:A:223:U:C6	2.47	0.50
1:A:539:A:OP1	12:L:114:LYS:HE2	2.11	0.50
1:A:659:U:O2'	1:A:660:G:H5'	2.11	0.50
1:A:1278:U:C5'	1:A:1279:A:O4'	2.59	0.50
1:A:1292:U:P	7:G:41:ARG:NH2	2.84	0.50
1:A:1440:C:C2'	1:A:1441:G:H5'	2.42	0.50
2:B:221:LEU:O	2:B:221:LEU:HD13	2.11	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:46:ALA:HA	9:I:78:LYS:HB2	1.93	0.50
14:N:29:ARG:O	14:N:33:VAL:HG13	2.11	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'	2.39	0.50
1:A:824:C:H2'	1:A:825:G:H8	1.77	0.50
1:A:839:U:O2	1:A:839:U:C2'	2.59	0.50
1:A:972:C:H4'	10:J:57:LYS:HG3	1.93	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:1179:A:H2'	1:A:1180:A:O4'	2.11	0.50
1:A:1283:G:O2'	1:A:1284:C:H5'	2.11	0.50
1:A:1310:G:O2'	1:A:1311:G:H5'	2.12	0.50
2:B:44:LEU:HA	2:B:47:THR:OG1	2.12	0.50
2:B:121:LEU:O	2:B:127:ILE:HG12	2.11	0.50
5:E:121:LYS:HE3	5:E:123:LEU:HD21	1.93	0.50
6:F:97:PHE:HB2	18:R:32:ARG:CZ	2.41	0.50
1:A:325:A:H2'	1:A:326:G:O4'	2.12	0.50
1:A:999:C:H2'	1:A:1000:U:C6	2.45	0.50
1:A:1152:A:OP1	10:J:13:HIS:HB2	2.11	0.50
2:B:33:TYR:HB3	2:B:41:ILE:HG22	1.93	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	2.11	0.50
2:B:186:ALA:HB3	2:B:197:VAL:CG1	2.41	0.50
3:C:79:ARG:HG2	3:C:82:GLU:HG2	1.92	0.50
3:C:177:THR:HG23	3:C:177:THR:O	2.10	0.50
4:D:8:VAL:HG11	4:D:21:LEU:HB3	1.94	0.50
13:M:78:ILE:HA	13:M:81:LEU:CD2	2.38	0.50
17:Q:27:PHE:HB2	17:Q:28:PRO:HD2	1.94	0.50
1:A:664:G:OP1	18:R:64:ARG:HD2	2.11	0.50
1:A:1025:U:OP1	1:A:1025:U:H4'	2.11	0.50
1:A:1136:U:H5"	1:A:1137:C:OP2	2.12	0.50
1:A:1305:G:C8	1:A:1305:G:OP2	2.64	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
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
11:K:23:ALA:CB	11:K:91:ARG:HB2	2.41	0.50
1:A:179:A:H2'	1:A:180:U:C6	2.46	0.50
1:A:217:C:O2'	1:A:218:C:H5'	2.12	0.50
1:A:755:G:OP2	15:O:65:ARG:HD2	2.11	0.50
1:A:1306:A:H2'	1:A:1307:U:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:113:SER:HB2	8:H:134:ILE:CD1	2.29	0.50
11:K:82:VAL:HG23	11:K:105:VAL:HG13	1.93	0.50
12:L:46:LYS:HG2	12:L:47:LYS:HG3	1.93	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:518:C:HO2'	12:L:50:SER:HB3	1.77	0.50
1:A:746:A:O2'	1:A:747:C:H5'	2.12	0.50
1:A:1085:U:O3'	1:A:1086:U:H6	1.95	0.50
1:A:1165:C:O2'	1:A:1166:G:H5'	2.12	0.50
1:A:1189:C:OP1	10:J:51:ARG:NH2	2.40	0.50
1:A:1347:G:C8	9:I:107:ARG:CB	2.95	0.50
2:B:17:PHE:HD1	2:B:17:PHE:C	2.14	0.50
4:D:126:ILE:CG2	4:D:127:THR:N	2.75	0.50
8:H:38:ILE:N	8:H:38:ILE:HD12	2.26	0.50
11:K:48:ILE:HD13	11:K:63:LEU:HB3	1.92	0.50
13:M:5:ALA:O	13:M:6:GLY:C	2.51	0.50
15:O:3:ILE:CG2	15:O:7:GLU:HB3	2.41	0.50
17:Q:10:VAL:O	17:Q:53:LEU:HD12	2.12	0.50
1:A:190(L):U:H3	20:T:105:SER:HG	1.60	0.49
1:A:255:G:O6	1:A:266:G:O6	2.29	0.49
1:A:1181:G:O2'	1:A:1184:G:H5'	2.11	0.49
2:B:30:ARG:HG3	2:B:31:TYR:CD1	2.47	0.49
3:C:47:LEU:N	3:C:47:LEU:HD12	2.27	0.49
3:C:172:ARG:HH12	3:C:174:PRO:CG	2.22	0.49
5:E:31:LEU:HD22	5:E:43:LEU:HD21	1.94	0.49
7:G:18:TYR:HD2	7:G:59:LEU:HD22	1.76	0.49
7:G:38:LEU:O	7:G:42:ILE:HG13	2.12	0.49
9:I:36:TYR:HD2	9:I:37:PHE:CE1	2.30	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	2.25	0.49
17:Q:26:GLN:O	17:Q:27:PHE:HB3	2.12	0.49
1:A:89:C:H2'	1:A:90:U:O4'	2.12	0.49
1:A:430:A:C2'	1:A:431:A:H5'	2.42	0.49
1:A:625:G:H2'	1:A:626:U:C6	2.47	0.49
1:A:865:A:H5'	1:A:1078:U:O4	2.12	0.49
3:C:171:GLY:O	3:C:173:VAL:HG23	2.12	0.49
4:D:8:VAL:HG13	4:D:21:LEU:HD13	1.93	0.49
7:G:108:ALA:O	7:G:119:ARG:HB3	2.12	0.49
9:I:36:TYR:HE2	9:I:73:GLN:NE2	2.10	0.49
11:K:124:LYS:HD2	11:K:125:PHE:CE1	2.47	0.49
18:R:87:ARG:HG2	18:R:87:ARG:HH11	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:101:GLY:O	20:T:102:GLY:O	2.30	0.49
1:A:129(A):G:O2'	1:A:130:A:OP2	2.28	0.49
1:A:245:C:O2	1:A:283:C:N3	2.46	0.49
1:A:267:C:P	17:Q:67:LYS:HB2	2.52	0.49
1:A:346:G:H2'	1:A:347:G:H5'	1.94	0.49
1:A:521:G:O2'	1:A:522:C:H5'	2.12	0.49
1:A:647:C:H2'	1:A:648:A:H8	1.77	0.49
1:A:1323:G:H2'	1:A:1324:A:C8	2.47	0.49
1:A:1366:C:C2	1:A:1367:C:C5	3.00	0.49
3:C:139:GLN:O	3:C:143:GLU:N	2.37	0.49
4:D:127:THR:CG2	4:D:128:VAL:N	2.75	0.49
10:J:60:ARG:O	10:J:61:GLU:CB	2.61	0.49
11:K:51:LYS:O	11:K:55:LYS:HE3	2.12	0.49
14:N:15:LYS:HB3	14:N:16:PHE:CD1	2.47	0.49
1:A:204:U:H4'	1:A:216:G:O5'	2.12	0.49
1:A:619:U:N3	4:D:134:ASP:OD1	2.44	0.49
1:A:738:C:OP2	6:F:92:LYS:HE3	2.11	0.49
1:A:834:C:H2'	1:A:835:U:C6	2.48	0.49
1:A:877:C:H5"	8:H:88:LYS:HD3	1.93	0.49
1:A:1102:A:H2'	1:A:1103:C:C6	2.46	0.49
1:A:1256:A:C4'	1:A:1257:U:H5'	2.35	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
2:B:124:SER:CB	2:B:125:PRO:CD	2.90	0.49
3:C:14:ILE:CG2	3:C:15:THR:H	2.11	0.49
3:C:167:TRP:O	3:C:168:ALA:HB3	2.11	0.49
4:D:78:LEU:HD22	4:D:96:LEU:HB3	1.94	0.49
4:D:119:GLN:CG	4:D:123:HIS:CE1	2.95	0.49
15:O:4:THR:HB	15:O:6:GLU:HG2	1.93	0.49
15:O:36:ILE:HA	15:O:59:MET:CE	2.42	0.49
1:A:190:C:H2'	1:A:190(A):C:H6	1.76	0.49
1:A:218:C:H2'	1:A:219:C:C6	2.47	0.49
1:A:1172:C:O2'	1:A:1173:G:H5'	2.11	0.49
2:B:206:ASP:O	2:B:207:ALA:HB3	2.11	0.49
3:C:38:ARG:HG3	3:C:38:ARG:NH1	2.26	0.49
4:D:7:PRO:CG	4:D:10:ARG:HD2	2.43	0.49
4:D:38:TYR:CE2	4:D:45:GLN:HG3	2.48	0.49
1:A:182:U:C6	1:A:182:U:C4'	2.96	0.49
1:A:489:C:H2'	1:A:490:G:H8	1.77	0.49
1:A:1413:A:O2'	1:A:1414:U:H5'	2.12	0.49
2:B:97:TRP:CH2	2:B:173:ALA:HA	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:191:THR:HG22	3:C:193:TYR:N	2.23	0.49
5:E:13:ILE:HG13	5:E:13:ILE:O	2.11	0.49
6:F:43:LEU:HD22	6:F:43:LEU:N	2.27	0.49
10:J:53:PRO:HA	14:N:41:ARG:HH21	1.78	0.49
15:O:34:LEU:O	15:O:34:LEU:HD23	2.12	0.49
1:A:149:A:H2'	1:A:150:C:C6	2.48	0.49
1:A:218:C:H2'	1:A:219:C:H6	1.77	0.49
1:A:659:U:H2'	1:A:660:G:O4'	2.13	0.49
1:A:1181:G:H4'	1:A:1184:G:H5'	1.94	0.49
2:B:144:ARG:HG3	2:B:145:LEU:H	1.77	0.49
2:B:168:THR:OG1	2:B:192:SER:HB3	2.12	0.49
5:E:36:ASP:O	5:E:37:ARG:HB2	2.13	0.49
6:F:100:ASN:O	18:R:28:GLU:HG3	2.13	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
11:K:48:ILE:HD11	11:K:64:ALA:HA	1.95	0.49
15:O:17:ARG:HG3	15:O:17:ARG:NH1	2.23	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:542:G:OP1	4:D:10:ARG:NH2	2.45	0.49
1:A:586:C:O2'	1:A:587:G:H5'	2.13	0.49
1:A:1153:C:H2'	1:A:1154:G:C8	2.46	0.49
1:A:1162:C:H2'	1:A:1163:C:H6	1.78	0.49
1:A:1195:C:H3'	1:A:1196:U:H5"	1.95	0.49
1:A:1503:A:O2'	1:A:1504:G:OP1	2.29	0.49
1:A:1505:G:C8	1:A:1505:G:H3'	2.48	0.49
2:B:102:LEU:CD2	2:B:162:ILE:HD11	2.37	0.49
3:C:180:ALA:O	3:C:181:ASN:CB	2.61	0.49
7:G:85:TYR:CD2	7:G:154:TYR:HE2	2.28	0.49
16:P:42:ARG:O	16:P:43:LYS:C	2.51	0.49
17:Q:78:GLU:HG3	17:Q:78:GLU:O	2.12	0.49
18:R:41:LYS:O	18:R:41:LYS:HG2	2.13	0.49
20:T:89:ARG:HE	20:T:104:LEU:HD22	1.78	0.49
1:A:624:C:O2'	1:A:625:G:H5'	2.13	0.49
1:A:1228:C:OP1	13:M:115:LYS:HG3	2.13	0.49
1:A:1250:A:H2'	1:A:1251:A:C8	2.47	0.49
1:A:1254:C:OP1	10:J:45:ARG:HD3	2.12	0.49
1:A:1305:G:H22	1:A:1331:G:H2'	1.77	0.49
4:D:157:LEU:CD2	4:D:161:ASN:ND2	2.74	0.49
7:G:85:TYR:HD2	7:G:154:TYR:CE2	2.27	0.49
10:J:16:LEU:HD23	10:J:94:VAL:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:79:SER:OG	11:K:106:LYS:HG2	2.12	0.49
12:L:27:LEU:HG	12:L:28:LYS:N	2.25	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
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
1:A:1070:U:O2'	1:A:1071:C:H5'	2.13	0.49
1:A:1238:A:N7	1:A:1303:C:H1'	2.28	0.49
1:A:1279:A:O2'	1:A:1282:C:N4	2.46	0.49
1:A:1347:G:N2	1:A:1373:G:H2'	2.28	0.49
2:B:35:GLU:HA	2:B:39:ILE:O	2.13	0.49
5:E:84:PHE:CE2	5:E:133:TYR:HD2	2.31	0.49
8:H:13:ILE:O	8:H:17:THR:HG23	2.13	0.49
8:H:60:ARG:HG3	8:H:60:ARG:NH1	2.28	0.49
11:K:85:ARG:HH11	11:K:85:ARG:HG3	1.77	0.49
19:S:5:LEU:HD11	19:S:70:LYS:NZ	2.28	0.49
1:A:220:G:O2'	1:A:221:C:H5'	2.12	0.48
1:A:722:A:H4'	1:A:723:U:C5	2.48	0.48
1:A:1129:C:O2'	1:A:1130:A:OP2	2.24	0.48
1:A:1230:C:O2'	1:A:1231:G:H5'	2.12	0.48
3:C:116:VAL:O	3:C:119:ARG:HB3	2.13	0.48
7:G:156:TRP:OXT	7:G:156:TRP:CD1	2.66	0.48
10:J:38:ILE:HG13	10:J:71:LEU:CB	2.42	0.48
10:J:48:THR:HG1	10:J:62:HIS:CE1	2.29	0.48
16:P:51:VAL:O	16:P:51:VAL:CG1	2.60	0.48
1:A:1369:C:H2'	1:A:1370:G:C8	2.48	0.48
2:B:17:PHE:HA	2:B:44:LEU:HD21	1.95	0.48
2:B:97:TRP:CH2	2:B:176:GLU:CD	2.85	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
8:H:103:VAL:CG2	8:H:110:ALA:HB2	2.43	0.48
10:J:27:ALA:C	10:J:29:ARG:H	2.15	0.48
12:L:28:LYS:O	12:L:29:GLY:C	2.51	0.48
13:M:78:ILE:O	13:M:82:MET:HB2	2.12	0.48
16:P:52:ASP:OD2	16:P:55:ARG:HB2	2.13	0.48
1:A:178:C:O2'	1:A:179:A:H5'	2.14	0.48
1:A:188:C:H4'	20:T:89:ARG:NH1	2.29	0.48
1:A:1121:U:H2'	1:A:1122:U:C6	2.48	0.48
1:A:1533:C:O2'	1:A:1534:A:H5'	2.13	0.48
2:B:25:ASN:O	2:B:27:LYS:N	2.47	0.48
18:R:36:ASN:HD22	18:R:38:GLU:HG2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:22:TRP:CZ2	14:N:54:PRO:HG3	2.48	0.48
3:C:173:VAL:N	3:C:174:PRO:CD	2.76	0.48
6:F:48:LEU:HD13	6:F:52:ILE:HG13	1.95	0.48
7:G:6:ARG:O	7:G:7:ALA:C	2.52	0.48
17:Q:12:SER:HB3	17:Q:20:THR:HB	1.95	0.48
18:R:36:ASN:CG	18:R:39:VAL:HG12	2.34	0.48
1:A:195:A:H4'	20:T:68:LYS:NZ	2.28	0.48
1:A:707:C:OP1	11:K:85:ARG:NH1	2.46	0.48
1:A:1102:A:H2'	1:A:1103:C:H6	1.77	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	2.13	0.48
9:I:65:VAL:HG13	9:I:65:VAL:O	2.13	0.48
10:J:65:LEU:O	10:J:65:LEU:CD2	2.59	0.48
12:L:42:THR:CG2	12:L:52:LEU:HB3	2.44	0.48
12:L:83:VAL:HG21	12:L:100:ILE:HD13	1.94	0.48
12:L:83:VAL:HG22	12:L:84:LEU:N	2.28	0.48
12:L:119:LYS:O	12:L:120:TYR:CB	2.61	0.48
19:S:39:THR:HG22	19:S:40:ILE:N	2.29	0.48
20:T:38:LYS:O	20:T:39:LYS:C	2.51	0.48
1:A:31:G:H1	1:A:48:C:H5"	1.77	0.48
1:A:61:G:H2'	1:A:62:U:O4'	2.13	0.48
1:A:184:G:H2'	1:A:185:A:H8	1.77	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
5:E:20:GLN:C	5:E:21:ALA:O	2.50	0.48
6:F:46:ARG:HB2	6:F:60:PHE:CE2	2.48	0.48
1:A:337:C:H2'	1:A:338:A:C8	2.49	0.48
1:A:538:G:O2'	1:A:539:A:H5'	2.13	0.48
1:A:684:A:H1'	11:K:38:ASN:HB3	1.95	0.48
1:A:742:G:H5"	15:O:58:MET:HE1	1.95	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:1491:G:C6	1:A:1492:A:C6	3.02	0.48
2:B:111:ARG:HB3	2:B:149:LEU:HD11	1.95	0.48
4:D:6:GLY:O	4:D:7:PRO:C	2.50	0.48
4:D:36:ARG:N	4:D:37:PRO:CD	2.65	0.48
4:D:111:ALA:HB2	4:D:120:LEU:HD12	1.95	0.48
10:J:6:ILE:HG23	10:J:98:ILE:HG12	1.94	0.48
15:O:25:THR:HG21	15:O:70:LEU:HD23	1.94	0.48
17:Q:17:LYS:HA	17:Q:46:ASP:O	2.14	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)
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
1:A:976:G:OP1	14:N:31:ARG:O	2.32	0.48
1:A:1342:C:O2'	1:A:1343:G:H5'	2.13	0.48
2:B:187:LEU:CD2	2:B:214:ILE:HG13	2.44	0.48
4:D:57:ARG:NH2	4:D:205:GLU:OE2	2.46	0.48
5:E:51:VAL:O	5:E:54:ALA:HB3	2.13	0.48
6:F:100:ASN:ND2	18:R:23:LYS:O	2.46	0.48
6:F:101:ALA:HB2	18:R:28:GLU:HB3	1.95	0.48
9:I:111:ARG:HG3	9:I:111:ARG:NH1	2.28	0.48
11:K:86:GLY:H	11:K:112:THR:HG23	1.79	0.48
12:L:53:ARG:HG2	12:L:93:LEU:HD11	1.95	0.48
17:Q:56:VAL:HG12	17:Q:77:VAL:HB	1.95	0.48
17:Q:97:SER:O	17:Q:98:LEU:HD12	2.14	0.48
18:R:39:VAL:HG13	18:R:40:LEU:N	2.28	0.48
18:R:47:THR:HA	18:R:83:GLU:HB2	1.96	0.48
18:R:53:ARG:HD3	18:R:63:GLN:HB3	1.95	0.48
1:A:421:U:H5'	1:A:422:C:C5	2.48	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
1:A:1127:G:N2	1:A:1147:C:N4	2.62	0.48
1:A:1216:G:H5"	14:N:5:ALA:HB2	1.96	0.48
4:D:3:ARG:O	4:D:5:ILE:HG13	2.13	0.48
5:E:148:VAL:O	5:E:152:ARG:HG3	2.14	0.48
6:F:75:LEU:C	6:F:75:LEU:HD13	2.34	0.48
19:S:32:LYS:HG3	19:S:32:LYS:O	2.13	0.48
1:A:625:G:H2'	1:A:626:U:H6	1.79	0.48
1:A:848:C:H2'	1:A:849:C:C6	2.49	0.48
2:B:230:VAL:HG13	2:B:231:GLU:OE2	2.13	0.48
3:C:92:ALA:C	3:C:94:LEU:H	2.17	0.48
4:D:200:GLU:OE1	4:D:200:GLU:N	2.46	0.48
5:E:71:LEU:HD21	5:E:115:VAL:HG22	1.96	0.48
7:G:64:GLN:O	7:G:67:GLU:HB3	2.14	0.48
10:J:39:PRO:HA	10:J:70:ARG:HH11	1.78	0.48
12:L:34:ARG:HG3	12:L:34:ARG:O	2.13	0.48
16:P:6:LEU:HB3	16:P:17:TYR:CD2	2.49	0.48
1:A:103:C:P	20:T:17:ARG:NH1	2.87	0.47
1:A:155:C:H2'	1:A:156:G:H8	1.79	0.47
1:A:190(I):G:O2'	1:A:190(J):U:H5'	2.14	0.47
1:A:974:A:OP2	14:N:41:ARG:NH1	2.47	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
9:I:117:HIS:HB2	9:I:121:ARG:HD2	1.95	0.47
10:J:94:VAL:HG12	10:J:95:GLU:H	1.76	0.47
12:L:110:VAL:O	12:L:122:THR:CG2	2.62	0.47
1:A:560:U:O5'	1:A:560:U:H6	1.98	0.47
1:A:657:G:O2'	1:A:658:G:H5'	2.13	0.47
1:A:1057:G:C2'	1:A:1058:G:H5'	2.44	0.47
1:A:1394:A:C5	1:A:1501:C:H4'	2.49	0.47
1:A:1411:C:H2'	1:A:1412:C:C6	2.49	0.47
2:B:23:ARG:HH11	2:B:23:ARG:C	2.16	0.47
2:B:213:LEU:C	2:B:213:LEU:CD2	2.83	0.47
11:K:58:PRO:HB2	11:K:93:GLN:HG3	1.95	0.47
12:L:53:ARG:HB3	12:L:93:LEU:HD11	1.95	0.47
1:A:513:C:H2'	1:A:514:C:C6	2.49	0.47
1:A:613:C:O2'	1:A:614:A:H5'	2.14	0.47
1:A:620:C:C6	4:D:135:LEU:HD13	2.49	0.47
1:A:666:G:H5'	1:A:726:C:H1'	1.96	0.47
1:A:1123:A:O3'	10:J:36:GLY:HA3	2.14	0.47
1:A:1489:G:H2'	1:A:1490:C:O4'	2.15	0.47
3:C:8:ILE:O	3:C:11:ARG:N	2.47	0.47
6:F:101:ALA:HB2	18:R:28:GLU:CG	2.44	0.47
9:I:111:ARG:HG3	9:I:111:ARG:HH11	1.80	0.47
12:L:86:ARG:HG3	12:L:86:ARG:NH1	2.28	0.47
1:A:41:G:H2'	1:A:42:G:C8	2.49	0.47
1:A:51:A:H4'	1:A:52:G:C5'	2.45	0.47
1:A:808:C:OP1	15:O:48:LYS:HE3	2.14	0.47
3:C:35:GLU:O	3:C:38:ARG:N	2.47	0.47
3:C:100:ALA:O	3:C:101:LEU:HB2	2.14	0.47
5:E:78:HIS:HD2	8:H:107:LEU:HD12	1.79	0.47
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.49	0.47
7:G:77:SER:O	7:G:156:TRP:HZ3	1.98	0.47
10:J:27:ALA:HB2	10:J:85:LEU:HD21	1.96	0.47
13:M:39:ILE:CD1	13:M:56:LEU:HG	2.44	0.47
19:S:10:PHE:HE1	19:S:12:ASP:OD1	1.97	0.47
21:V:3:LYS:HB3	21:V:14:TRP:CD1	2.50	0.47
1:A:19:C:H2'	1:A:20:U:H6	1.80	0.47
1:A:181:G:O2'	1:A:182:U:OP2	2.32	0.47
1:A:1305:G:N2	1:A:1331:G:HO2'	2.12	0.47
2:B:15:VAL:HG12	2:B:210:SER:HB2	1.97	0.47
2:B:115:LEU:O	2:B:115:LEU:HD12	2.13	0.47
7:G:21:VAL:HG23	7:G:22:LEU:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
16:P:43:LYS:HG2	16:P:48:TRP:CE2	2.49	0.47
20:T:42:GLN:NE2	20:T:42:GLN:O	2.47	0.47
20:T:59:ALA:O	20:T:63:ILE:HG13	2.14	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
2:B:108:ILE:O	2:B:108:ILE:HG22	2.14	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
7:G:54:THR:HG22	7:G:56:GLN:H	1.80	0.47
1:A:182:U:C6	1:A:182:U:C3'	2.98	0.47
1:A:182:U:C6	1:A:182:U:C5'	2.85	0.47
1:A:435:C:O2'	1:A:436:C:H5'	2.15	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:16:HIS:CE1	2:B:210:SER:HG	2.33	0.47
2:B:53:ARG:NH1	2:B:199:TYR:CD1	2.83	0.47
2:B:75:LYS:HE3	2:B:78:GLN:OE1	2.14	0.47
2:B:215:LEU:O	2:B:216:SER:C	2.52	0.47
3:C:79:ARG:HG2	3:C:82:GLU:CG	2.45	0.47
4:D:24:GLU:CG	4:D:25:ARG:N	2.77	0.47
4:D:162:LEU:HD13	4:D:181:MET:CG	2.42	0.47
5:E:68:GLU:O	5:E:70:PRO:HD3	2.15	0.47
5:E:127:ASN:O	5:E:128:PRO:C	2.53	0.47
6:F:53:ALA:C	6:F:55:ASP:H	2.18	0.47
10:J:30:SER:CB	10:J:80:LYS:HB3	2.45	0.47
13:M:49:THR:CG2	13:M:51:ALA:H	2.13	0.47
19:S:15:LEU:O	19:S:19:VAL:N	2.48	0.47
20:T:29:LYS:O	20:T:33:ILE:HG13	2.14	0.47
1:A:190(H):G:O2'	1:A:190(I):G:H5'	2.14	0.47
1:A:768:A:H2'	1:A:769:G:O4'	2.15	0.47
1:A:1001:A:H2'	1:A:1002:G:H8	1.79	0.47
1:A:1232:U:H5"	9:I:124:GLN:O	2.14	0.47
1:A:1488:G:H2'	1:A:1489:G:C8	2.49	0.47
6:F:50:TYR:CE1	18:R:77:GLY:HA2	2.49	0.47
7:G:23:VAL:HG12	7:G:27:ILE:CD1	2.41	0.47
7:G:46:ALA:O	7:G:50:ILE:HG13	2.15	0.47
11:K:80:VAL:HG21	11:K:103:LEU:HD13	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:80:TYR:CD1	19:S:80:TYR:C	2.88	0.47
1:A:606:G:H2'	1:A:631:G:N2	2.30	0.47
1:A:1060:C:C4	3:C:2:GLY:HA3	2.50	0.47
1:A:1245:A:H2'	1:A:1246: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
2:B:18:GLY:CA	2:B:41:ILE:HA	2.44	0.47
3:C:167:TRP:O	3:C:168:ALA:CB	2.63	0.47
6:F:2:ARG:HD2	6:F:69:GLU:HG2	1.96	0.47
6:F:2:ARG:NE	6:F:69:GLU:HG2	2.29	0.47
10:J:94:VAL:CG1	10:J:95:GLU:N	2.77	0.47
17:Q:97:SER:O	17:Q:98:LEU:HG	2.15	0.47
20:T:50:GLU:HG3	20:T:99:LEU:CD1	2.45	0.47
1:A:184:G:C4'	1:A:224:C:H4'	2.44	0.47
1:A:190(L):U:N3	20:T:105:SER:OG	2.46	0.47
1:A:633:G:H2'	1:A:634:C:C6	2.50	0.47
1:A:781:A:H2'	1:A:782:A:H5'	1.97	0.47
1:A:1348:U:H2'	1:A:1349:A:H8	1.80	0.47
1:A:1510:U:H2'	1:A:1511:G:C8	2.50	0.47
3:C:130:VAL:CG2	3:C:157:ILE:HG23	2.41	0.47
5:E:92:LYS:O	5:E:118:ILE:HG23	2.15	0.47
5:E:107:ARG:HG2	5:E:108:ALA:N	2.29	0.47
9:I:48:GLU:N	9:I:49:PRO:CD	2.77	0.47
10:J:22:LYS:HE2	10:J:90:LEU:HB2	1.97	0.47
12:L:54:LYS:N	12:L:54:LYS:HD2	2.30	0.47
15:O:77:ARG:O	15:O:80:ALA:HB3	2.15	0.47
19:S:15:LEU:HD12	19:S:16:LEU:H	1.77	0.47
1:A:321:A:O2'	1:A:322:C:H5'	2.15	0.46
1:A:458:C:H2'	1:A:459:G:H8	1.80	0.46
1:A:517:G:H5'	1:A:519:C:C2	2.51	0.46
1:A:926:G:H2'	1:A:1505:G:N3	2.30	0.46
1:A:1004:A:N6	1:A:1035:A:H62	2.13	0.46
1:A:1238:A:H5'	1:A:1336:C:N4	2.29	0.46
1:A:1262:C:H2'	1:A:1263:C:H6	1.79	0.46
1:A:1320:C:H2'	1:A:1321:C:O4'	2.15	0.46
3:C:64:VAL:CG2	3:C:99:VAL:HB	2.45	0.46
1:A:187:C:C2	20:T:105:SER:HB3	2.49	0.46
1:A:542:G:H2'	1:A:543:C:H6	1.80	0.46
1:A:1074:G:O3'	2:B:103:THR:HG22	2.14	0.46
2:B:15:VAL:CG1	2:B:209:ARG:HG3	2.46	0.46
2:B:50:GLU:HB3	2:B:200:ILE:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:129:GLU:O	2:B:130:ARG:HB2	2.15	0.46
4:D:87:GLY:O	4:D:88:VAL:C	2.53	0.46
5:E:18:ARG:HG2	5:E:19:MET:H	1.81	0.46
12:L:77:LEU:HD21	12:L:107:ALA:HB2	1.97	0.46
12:L:82:VAL:O	12:L:106:ASP:HB2	2.15	0.46
13:M:82:MET:CE	13:M:92:HIS:HB3	2.44	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
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	1.97	0.46
18:R:36:ASN:ND2	18:R:38:GLU:HG2	2.29	0.46
1:A:5:U:O2'	1:A:6:G:P	2.73	0.46
1:A:620:C:C2	4:D:135:LEU:HD13	2.50	0.46
1:A:976:G:C8	1:A:1358:U:C2	3.04	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
5:E:144:THR:C	5:E:146:ALA:N	2.67	0.46
7:G:154:TYR:O	7:G:156:TRP:N	2.49	0.46
9:I:33:PHE:CE2	9:I:47:LEU:HD11	2.50	0.46
10:J:96:ILE:CG2	10:J:97:GLU:H	2.25	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
13:M:62:ASN:O	13:M:63:THR:HB	2.16	0.46
1:A:41:G:H2'	1:A:42:G:H8	1.80	0.46
1:A:281:G:O2'	1:A:282:A:H8	1.98	0.46
1:A:624:C:H2'	1:A:625:G:H8	1.81	0.46
1:A:1306:A:O2'	13:M:109:THR:HG21	2.16	0.46
1:A:1392:G:H21	1:A:1502:A:H8	1.61	0.46
2:B:83:MET:HG3	2:B:238:LEU:CD1	2.46	0.46
3:C:154:SER:OG	3:C:155:GLY:N	2.48	0.46
3:C:173:VAL:O	3:C:173:VAL:HG12	2.15	0.46
7:G:15:ASP:O	7:G:19:GLY:HA2	2.16	0.46
11:K:50:TYR:HD2	11:K:60:ALA:HB2	1.80	0.46
12:L:59:ARG:NH1	12:L:65:GLU:HG2	2.31	0.46
18:R:59:SER:OG	18:R:62:GLU:HG3	2.15	0.46
1:A:182:U:O4	1:A:183:G:C4	2.68	0.46
1:A:390:C:H6	1:A:390:C:O5'	1.99	0.46
1:A:934:C:C4	1:A:1345:U:C5	3.04	0.46
1:A:1069:C:O2'	1:A:1192:C:H1'	2.14	0.46
1:A:1277:C:C2'	1:A:1278:U:H5'	2.46	0.46
4:D:162:LEU:HD13	4:D:181:MET:CE	2.46	0.46
5:E:33:VAL:HG11	5:E:109:ILE:HA	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:107:ALA:O	7:G:110:GLN:HB2	2.16	0.46
7:G:135:VAL:O	7:G:139:GLU:HG3	2.15	0.46
8:H:92:ARG:HG2	8:H:94:TYR:OH	2.15	0.46
10:J:24:VAL:CG1	10:J:28:ARG:HE	2.29	0.46
11:K:16:SER:O	11:K:35:PRO:HD3	2.16	0.46
11:K:34:ASP:O	11:K:36:ASP:N	2.48	0.46
19:S:18:LYS:HG2	19:S:18:LYS:O	2.15	0.46
19:S:53:ASN:ND2	19:S:56:GLN:HB2	2.31	0.46
1:A:132:C:O2'	1:A:133:U:H5'	2.15	0.46
1:A:160:A:H1'	1:A:344:A:N7	2.31	0.46
1:A:743:U:H2'	1:A:744:C:H6	1.79	0.46
1:A:1301:U:O2'	1:A:1302:U:P	2.74	0.46
2:B:42:ILE:HD12	2:B:203:GLY:HA2	1.98	0.46
2:B:97:TRP:CH2	2:B:176:GLU:OE2	2.69	0.46
3:C:23:TYR:OH	10:J:9:ARG:HD3	2.16	0.46
4:D:39:PRO:HG2	4:D:44:GLY:HA2	1.98	0.46
7:G:20:ASP:OD1	7:G:22:LEU:HB3	2.15	0.46
12:L:38:THR:HG22	12:L:39:VAL:HG23	1.97	0.46
16:P:20:VAL:CG1	16:P:21:VAL:N	2.76	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
21:V:2:GLY:O	21:V:4:GLY:N	2.49	0.46
1:A:1044:A:O2'	1:A:1045:C:H5'	2.15	0.46
1:A:1047:G:H5"	14:N:4:LYS:HD2	1.98	0.46
1:A:1171:G:H2'	1:A:1172:C:C6	2.51	0.46
1:A:1394:A:C6	1:A:1501:C:H4'	2.50	0.46
3:C:21:ARG:NH2	3:C:56:ASP:OD2	2.48	0.46
3:C:129:ALA:HB3	3:C:132:ARG:CD	2.45	0.46
4:D:173:TRP:CD2	4:D:189:PRO:HB3	2.51	0.46
11:K:59:TYR:O	11:K:62:GLN:HB3	2.15	0.46
11:K:84:VAL:HG23	11:K:109:VAL:O	2.16	0.46
13:M:5:ALA:O	13:M:8:GLU:N	2.45	0.46
14:N:12:ARG:O	14:N:14:PRO:HD3	2.16	0.46
1:A:92:C:O2'	1:A:93:G:H5'	2.15	0.46
1:A:518:C:H5"	1:A:519:C:H6	1.78	0.46
1:A:828:A:H5"	1:A:859:A:C2	2.51	0.46
1:A:834:C:H2'	1:A:835:U:H6	1.80	0.46
1:A:1049:U:H1'	1:A:1201:A:N7	2.31	0.46
1:A:1152:A:O2'	1:A:1153:C:H5'	2.16	0.46
1:A:1238:A:OP1	1:A:1336:C:H5	1.98	0.46
1:A:1474:G:O2'	1:A:1475:G:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:78:GLN:O	2:B:94:ASN:OD1	2.33	0.46
2:B:178:ARG:NH1	2:B:178:ARG:CG	2.67	0.46
3:C:164:ARG:HB3	3:C:164:ARG:HH11	1.81	0.46
5:E:121:LYS:HE3	5:E:123:LEU:CD2	2.46	0.46
6:F:44:GLY:HA2	6:F:59:TYR:CE1	2.51	0.46
8:H:6:ILE:HD12	8:H:35:ILE:HD12	1.97	0.46
9:I:48:GLU:OE1	9:I:48:GLU:HA	2.16	0.46
9:I:50:LEU:C	9:I:52:ALA:N	2.69	0.46
10:J:53:PRO:O	10:J:54:PHE:O	2.34	0.46
12:L:60:LEU:HD21	12:L:66:VAL:HG22	1.97	0.46
13:M:37:THR:HG23	13:M:55:ARG:CB	2.46	0.46
20:T:63:ILE:HG23	20:T:72:LEU:CD1	2.46	0.46
1:A:129(A):G:O2'	1:A:190(E):U:H5"	2.16	0.46
1:A:690:G:H2'	1:A:691:G:O4'	2.15	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:1300:G:O2'	1:A:1301:U:P	2.73	0.46
1:A:1390:U:H2'	1:A:1391:U:C6	2.51	0.46
2:B:22:LYS:O	2:B:23:ARG:HG3	2.16	0.46
3:C:23:TYR:CG	3:C:24:ALA:N	2.84	0.46
3:C:58:GLU:CB	10:J:92:THR:HG21	2.33	0.46
3:C:131:ARG:O	3:C:135:LYS:HG3	2.16	0.46
3:C:174:PRO:O	3:C:177:THR:HG22	2.15	0.46
4:D:145:GLU:HG2	4:D:184:LYS:HE2	1.96	0.46
8:H:23:SER:OG	8:H:60:ARG:HD2	2.15	0.46
8:H:116:LYS:NZ	8:H:127:LEU:HD12	2.31	0.46
10:J:22:LYS:HZ3	10:J:91:PRO:HD3	1.81	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:71:PRO:O	12:L:102:ARG:HD2	2.16	0.46
13:M:59:TYR:O	13:M:63:THR:HB	2.15	0.46
21:V:2:GLY:C	21:V:4:GLY:N	2.69	0.46
1:A:58:C:O2'	1:A:59:A:H5'	2.16	0.46
1:A:70:G:H2'	1:A:73:C:C6	2.51	0.46
1:A:458:C:H2'	1:A:459:G:O4'	2.16	0.46
1:A:527:G:O2'	1:A:535:A:N1	2.31	0.46
1:A:1039:C:O2'	1:A:1040:U:H5'	2.16	0.46
1:A:1049:U:H4'	1:A:1050:G:OP2	2.16	0.46
1:A:1113:C:H1'	3:C:178:LEU:HD21	1.97	0.46
2:B:52:GLU:O	2:B:56:ARG:HB2	2.17	0.46
12:L:46:LYS:CG	12:L:47:LYS:H	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:48:PRO:CG	12:L:49:ASN:H	2.25	0.46
16:P:72:ARG:O	16:P:72:ARG:HG2	2.16	0.46
1:A:151:A:H2'	1:A:152:A:O4'	2.15	0.45
1:A:513:C:H2'	1:A:514:C:H6	1.80	0.45
1:A:975:A:H4'	1:A:976:G:OP2	2.16	0.45
1:A:1057:G:H4'	3:C:197:GLY:H	1.81	0.45
1:A:1158:C:N3	1:A:1181:G:N2	2.61	0.45
1:A:1225:A:H5'	1:A:1226:C:OP2	2.16	0.45
1:A:1256:A:O2'	1:A:1257:U:P	2.74	0.45
1:A:1317:C:C6	14:N:16:PHE:CD2	3.03	0.45
1:A:1515:C:O2'	1:A:1516:G:H5'	2.16	0.45
4:D:29:PRO:C	4:D:30:LYS:HG3	2.35	0.45
4:D:152:SER:HA	4:D:155:LEU:HG	1.97	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
9:I:97:LYS:HG3	9:I:102:LEU:HD12	1.96	0.45
10:J:51:ARG:HG3	10:J:60:ARG:O	2.17	0.45
1:A:242:C:H2'	1:A:243:A:H5'	1.99	0.45
1:A:421:U:H5'	1:A:422:C:H5	1.80	0.45
1:A:882:C:O2'	1:A:883:C:H5'	2.16	0.45
1:A:909:A:H2'	1:A:910:C:O4'	2.16	0.45
1:A:955:U:O2'	19:S:83:HIS:CD2	2.70	0.45
1:A:975:A:H4'	1:A:976:G:H5'	1.97	0.45
1:A:1202:G:C2'	1:A:1203:C:H5'	2.46	0.45
1:A:1461:G:O2'	1:A:1462:G:H5'	2.16	0.45
3:C:99:VAL:CG2	3:C:100:ALA:N	2.79	0.45
3:C:157:ILE:HD11	3:C:166:GLU:HB2	1.97	0.45
4:D:121:VAL:O	4:D:134:ASP:HA	2.16	0.45
6:F:19:LEU:C	6:F:19:LEU:HD23	2.36	0.45
9:I:112:LYS:C	9:I:112:LYS:HD3	2.37	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
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
19:S:63:THR:HG22	19:S:64:GLU:N	2.31	0.45
1:A:1131:G:H2'	1:A:1132:C:C6	2.51	0.45
1:A:1230:C:H2'	1:A:1231:G:H8	1.82	0.45
1:A:1296:C:H4'	1:A:1302:U:C5	2.51	0.45
1:A:1515:C:H2'	1:A:1516:G:H8	1.81	0.45
1:A:1532:U:O5'	1:A:1532:U:H6	1.99	0.45
5:E:102:ALA:HB2	5:E:120:THR:CB	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:45:ILE:O	8:H:45:ILE:HG13	2.16	0.45
10:J:4:ILE:HG12	10:J:100:THR:CB	2.47	0.45
10:J:8:LEU:HD12	10:J:20:ALA:HB2	1.97	0.45
14:N:26:ARG:NH1	14:N:47:LEU:HD21	2.32	0.45
17:Q:80:GLY:O	17:Q:81:ARG:HB3	2.15	0.45
1:A:190(B):C:H2'	1:A:190(C):C:O4'	2.17	0.45
1:A:686:U:O4	1:A:703:G:H1'	2.17	0.45
1:A:1305:G:N2	1:A:1331:G:C2'	2.79	0.45
2:B:19:HIS:HD2	2:B:189:ASP:OD2	1.99	0.45
2:B:142:LEU:HB3	2:B:146:GLN:HE22	1.80	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
5:E:115:VAL:HG11	5:E:118:ILE:CD1	2.46	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
9:I:85:LEU:O	9:I:92:TYR:CD2	2.69	0.45
9:I:120:ARG:O	9:I:121:ARG:C	2.54	0.45
13:M:49:THR:O	13:M:53:VAL:HG23	2.16	0.45
18:R:47:THR:HG22	18:R:48:GLY:H	1.79	0.45
1:A:113:G:H1'	1:A:354:G:C5'	2.46	0.45
1:A:260:G:O2'	1:A:261:U:H5'	2.16	0.45
1:A:474:G:O2'	1:A:475:G:H5'	2.16	0.45
1:A:512:U:H1'	4:D:42:GLN:OE1	2.16	0.45
1:A:652:U:O4	1:A:752:G:O2'	2.28	0.45
1:A:826:C:H2'	1:A:827:U:H6	1.81	0.45
1:A:848:C:H2'	1:A:849:C:H6	1.80	0.45
1:A:920:U:H2'	1:A:921:U:C6	2.52	0.45
1:A:1019:C:O2'	1:A:1020:U:H5'	2.17	0.45
1:A:1435:G:H2'	1:A:1436:U:H6	1.69	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
12:L:117:ARG:HD2	12:L:122:THR:OG1	2.16	0.45
19:S:20:LEU:O	19:S:23:ASN:HB2	2.16	0.45
19:S:67:VAL:O	19:S:69:HIS:N	2.49	0.45
1:A:28:G:O2'	1:A:296:U:OP1	2.33	0.45
1:A:279:A:C6	17:Q:98:LEU:HD11	2.50	0.45
1:A:319:G:O2'	1:A:320:C:H5'	2.16	0.45
1:A:439:A:C4	1:A:497:A:C2	3.04	0.45
1:A:1044:A:H2'	1:A:1045:C:C4'	2.46	0.45
1:A:1240:U:P	7:G:116:ALA:HB2	2.56	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)
2:B:23:ARG:CZ	2:B:23:ARG:HB2	2.47	0.45
2:B:137:ARG:O	2:B:140:HIS:HB2	2.16	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
6:F:101:ALA:CB	18:R:28:GLU:HG2	2.46	0.45
7:G:18:TYR:CD2	7:G:59:LEU:HB2	2.52	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
14:N:25:VAL:O	14:N:25:VAL:HG13	2.16	0.45
18:R:74:ARG:HB3	18:R:81:PHE:CE1	2.51	0.45
22:Y:33:ARG:O	22:Y:37:ILE:HG13	2.16	0.45
1:A:820:U:H4'	1:A:821:G:OP2	2.15	0.45
1:A:1044:A:H2'	1:A:1045:C:O4'	2.17	0.45
1:A:1054:C:N3	22:Y:71:ASN:CG	2.70	0.45
1:A:1300:G:O2'	1:A:1301:U:H6	1.98	0.45
2:B:69:LEU:C	2:B:69:LEU:HD23	2.36	0.45
2:B:100:GLY:O	2:B:104:ASN:N	2.44	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
9:I:36:TYR:CD2	9:I:37:PHE:CE1	3.04	0.45
11:K:110:ASP:OD2	18:R:88:LYS:NZ	2.48	0.45
13:M:9:ILE:HD12	13:M:9:ILE:N	2.32	0.45
14:N:12:ARG:O	14:N:14:PRO:CD	2.65	0.45
19:S:80:TYR:CD1	19:S:82:GLY:N	2.83	0.45
20:T:42:GLN:O	20:T:45:GLN:HB3	2.16	0.45
1:A:22:G:H4'	1:A:885:G:C8	2.51	0.45
1:A:197:A:H1'	1:A:198:G:O4'	2.17	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:600:C:O2'	1:A:601:C:H5'	2.17	0.45
1:A:627:G:O2'	1:A:628:G:H5'	2.17	0.45
1:A:645:C:O2'	1:A:646:U:H5'	2.16	0.45
1:A:719:C:O2	18:R:50:ILE:HG13	2.16	0.45
1:A:976:G:C8	1:A:1358:U:O2	2.70	0.45
1:A:1206:G:C6	1:A:1207:G:C5	3.05	0.45
1:A:1331:G:O2'	1:A:1332:A:OP2	2.31	0.45
1:A:1353:G:H2'	1:A:1354:C:H6	1.82	0.45
1:A:1450:U:H2'	1:A:1452:C:C5	2.52	0.45
1:A:1528:U:H4'	1:A:1529:G:O5'	2.16	0.45
2:B:71:VAL:HB	2:B:164:VAL:HG23	1.99	0.45
3:C:60:ALA:O	3:C:61:ALA:CB	2.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:113:ALA:N	3:C:114:PRO:CD	2.80	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:38:LEU:HD11	7:G:42:ILE:HD11	1.99	0.45
9:I:40:LEU:O	9:I:42:ARG:N	2.50	0.45
9:I:121:ARG:HG2	9:I:121:ARG:HH11	1.81	0.45
10:J:27:ALA:CB	10:J:81:THR:HG23	2.47	0.45
17:Q:18:THR:HG23	17:Q:69:LYS:CE	2.47	0.45
18:R:58:LEU:HD22	18:R:62:GLU:HB3	1.99	0.45
22:Y:37:ILE:HD11	22:Y:66:ILE:HD11	1.99	0.45
1:A:258:G:H2'	1:A:259:G:H8	1.82	0.45
1:A:583:A:H2'	1:A:584:G:O4'	2.17	0.45
1:A:735:C:O2'	1:A:736:C:H5'	2.17	0.45
1:A:888:G:H4'	1:A:1489:G:H5'	1.98	0.45
1:A:1240:U:OP2	7:G:116:ALA:HB2	2.17	0.45
1:A:1346:A:H1'	1:A:1348:U:C5	2.51	0.45
2:B:92:TYR:CE1	2:B:151:GLY:HA3	2.51	0.45
3:C:188:LEU:O	3:C:189:ALA:CB	2.59	0.45
5:E:13:ILE:HG22	5:E:30:ALA:HB2	1.99	0.45
7:G:12:LEU:HD12	7:G:12:LEU:N	2.31	0.45
10:J:30:SER:CB	10:J:84:GLN:HE21	2.29	0.45
11:K:23:ALA:HB2	11:K:91:ARG:HB2	1.99	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
17:Q:81:ARG:HG3	17:Q:81:ARG:O	2.17	0.45
1:A:173:U:H5"	1:A:197:A:H5'	1.99	0.45
1:A:181:G:H1'	1:A:182:U:C5	2.52	0.45
1:A:403:C:H2'	1:A:404:U:H6	1.81	0.45
1:A:1347:G:HO2'	1:A:1373:G:H1	1.63	0.45
3:C:108:ASN:OD1	3:C:110:ASN:HB2	2.16	0.45
5:E:119:LEU:HD23	5:E:119:LEU:HA	1.84	0.45
14:N:23:ARG:HD3	14:N:30:ALA:HB2	1.99	0.45
1:A:75:G:O2'	1:A:76:C:H5'	2.17	0.44
1:A:485:G:C2'	1:A:486:U:OP2	2.65	0.44
1:A:1266:G:N2	1:A:1269:A:OP2	2.49	0.44
1:A:1298:C:C4	7:G:114:ARG:HD3	2.52	0.44
1:A:1312:G:N7	19:S:4:SER:HB3	2.32	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:N	10:J:68:HIS:CD2	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:85:ILE:HG23	12:L:98:TYR:CB	2.46	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
18:R:70:ILE:O	18:R:74:ARG:HG3	2.17	0.44
20:T:24:LEU:HD12	20:T:24:LEU:O	2.17	0.44
1:A:45:U:H2'	1:A:46:G:C8	2.53	0.44
1:A:129(A):G:C2	1:A:190(E):U:H5'	2.52	0.44
1:A:384:G:H2'	1:A:385:C:C6	2.53	0.44
1:A:393:A:C2'	1:A:394:G:H5'	2.46	0.44
1:A:691:G:O2'	1:A:797:C:H4'	2.17	0.44
1:A:1005:A:H2'	1:A:1006:C:O4'	2.17	0.44
1:A:1097:C:H2'	1:A:1098:C:H6	1.82	0.44
1:A:1314:C:OP2	19:S:6:LYS:CD	2.65	0.44
1:A:1329:A:OP1	13:M:28:ALA:HB3	2.16	0.44
1:A:1347:G:C5	9:I:107:ARG:NH2	2.84	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
10:J:3:LYS:CA	10:J:75:ILE:HA	2.48	0.44
10:J:8:LEU:CD1	10:J:20:ALA:HB2	2.48	0.44
14:N:29:ARG:HB3	14:N:40:CYS:HB3	1.99	0.44
15:O:87:ILE:CG2	15:O:88:ARG:N	2.80	0.44
1:A:644:G:O2'	1:A:645:C:H5'	2.17	0.44
1:A:662:G:H2'	1:A:663:A:H8	1.79	0.44
1:A:1289:A:H2'	1:A:1290:G:H5'	1.99	0.44
1:A:1299:A:C8	1:A:1301:U:H1'	2.53	0.44
1:A:1372:U:O2'	1:A:1373:G:H5'	2.18	0.44
1:A:1391:U:H2'	1:A:1392:G:H8	1.74	0.44
1:A:1503:A:O2'	1:A:1504:G:P	2.75	0.44
2:B:54:THR:O	2:B:57:PHE:HB3	2.18	0.44
3:C:11:ARG:NH1	3:C:177:THR:O	2.50	0.44
4:D:24:GLU:CG	4:D:25:ARG:H	2.30	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: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
20:T:30:LYS:O	20:T:33:ILE:HB	2.18	0.44
22:Y:50:ILE:HG13	22:Y:51:TYR:CD1	2.52	0.44
1:A:255:G:C1'	17:Q:16:GLN:HE21	2.30	0.44
1:A:792:A:H1'	1:A:794:A:N7	2.31	0.44
1:A:811:C:C3'	1:A:812:C:C5'	2.95	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:865:A:H2'	1:A:866:C:C6	2.53	0.44
1:A:975:A:O5'	1:A:976:G:H5'	2.17	0.44
1:A:1263:C:H2'	1:A:1264:C:H6	1.83	0.44
10:J:30:SER:HB3	10:J:84:GLN:NE2	2.31	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
13:M:84:ILE:HG13	13:M:86:CYS:HB2	2.00	0.44
14:N:9:LYS:HG3	14:N:21:TYR:O	2.17	0.44
14:N:29:ARG:HH21	14:N:31:ARG:HG2	1.82	0.44
16:P:43:LYS:HA	16:P:48:TRP:HB3	2.00	0.44
20:T:100:ILE:O	20:T:102:GLY:N	2.50	0.44
1:A:50:A:N6	1:A:361:G:H4'	2.33	0.44
1:A:389:A:H2'	1:A:390:C:C5'	2.48	0.44
1:A:807:A:H2'	1:A:808:C:C6	2.52	0.44
1:A:1117:G:H4'	9:I:104:ARG:HH11	1.81	0.44
1:A:1279:A:O2'	1:A:1281:U:OP2	2.33	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:46:ARG:NH1	10:J:64:GLU:CG	2.80	0.44
12:L:111:LYS:O	12:L:112:ASP:HB2	2.17	0.44
19:S:31:ILE:CG2	19:S:32:LYS:N	2.70	0.44
20:T:42:GLN:HA	20:T:45:GLN:HB2	1.99	0.44
1:A:181:G:O2'	1:A:182:U:C5'	2.64	0.44
1:A:181:G:O2'	1:A:182:U:P	2.76	0.44
1:A:321:A:H2'	1:A:322:C:C6	2.52	0.44
1:A:460:A:N7	1:A:462:G:C6	2.85	0.44
1:A:547:A:OP2	4:D:2:GLY:N	2.51	0.44
1:A:620:C:C1'	4:D:135:LEU:HD13	2.48	0.44
1:A:927:G:H4'	1:A:1503:A:N7	2.32	0.44
1:A:948:C:OP1	13:M:109:THR:HG22	2.17	0.44
2:B:195:ASP:O	8:H:74:PRO:HG3	2.17	0.44
3:C:12:LEU:HD23	3:C:12:LEU:HA	1.77	0.44
3:C:107:GLN:CD	3:C:107:GLN:N	2.64	0.44
3:C:179:ARG:HD2	3:C:179:ARG:C	2.37	0.44
5:E:143:ARG:NH1	8:H:77:GLU:CD	2.71	0.44
7:G:95:ARG:NH1	7:G:95:ARG:CG	2.80	0.44
8:H:73:ASP:OD1	8:H:75:ARG:HB2	2.18	0.44
10:J:65:LEU:HD12	14:N:56:VAL:HG22	2.00	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
11:K:95:ILE:HD13	11:K:108:ILE:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:A:N7	1:A:281:G:N2	2.64	0.44
1:A:281:G:O2'	1:A:282:A:C8	2.70	0.44
1:A:1010:G:O2'	1:A:1011:G:H5'	2.18	0.44
1:A:1152:A:H2'	1:A:1153:C:H6	1.83	0.44
2:B:157:ARG:O	2:B:158:LEU:C	2.56	0.44
4:D:8:VAL:HG11	4:D:21:LEU:CB	2.47	0.44
4:D:196:LEU:C	4:D:198:VAL:H	2.21	0.44
8:H:7:ALA:HB2	8:H:85:ARG:HD2	1.99	0.44
13:M:110:ARG:HH11	13:M:110:ARG:CG	2.31	0.44
17:Q:64:PRO:CB	17:Q:70:ARG:HE	2.31	0.44
18:R:25:THR:O	18:R:25:THR:HG22	2.17	0.44
20:T:63:ILE:HD13	20:T:80:ARG:CB	2.48	0.44
1:A:261:U:OP2	20:T:79:ARG:NH2	2.50	0.44
1:A:397:A:H3'	1:A:397:A:N3	2.32	0.44
1:A:540:G:H2'	1:A:541:G:O4'	2.18	0.44
1:A:1152:A:C5'	10:J:13:HIS:HD2	2.25	0.44
1:A:1288:A:O4'	1:A:1353:G:H4'	2.18	0.44
1:A:1482:G:HO2'	1:A:1483:A:H8	1.65	0.44
2:B:213:LEU:C	2:B:213:LEU:HD23	2.37	0.44
4:D:24:GLU:HG2	4:D:25:ARG:H	1.81	0.44
5:E:36:ASP:OD2	5:E:40:ARG:HD3	2.18	0.44
9:I:93:ARG:CD	9:I:97:LYS:HE3	2.47	0.44
10:J:6:ILE:O	10:J:71:LEU:O	2.35	0.44
15:O:54:ARG:O	15:O:58:MET:HG3	2.17	0.44
1:A:116:A:H2'	1:A:117:G:O4'	2.18	0.44
1:A:677:U:O2	1:A:777:A:O2'	2.33	0.44
1:A:1095:U:H2'	1:A:1096:C:H6	1.83	0.44
1:A:1440:C:H2'	1:A:1441:G:C5'	2.48	0.44
3:C:79:ARG:C	3:C:81:GLY:H	2.21	0.44
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
7:G:78:ARG:HG2	7:G:80:VAL:HG23	1.99	0.44
8:H:103:VAL:HG21	8:H:109:ILE:O	2.18	0.44
15:O:29:VAL:HG11	15:O:67:LEU:HD21	2.00	0.44
16:P:39:TYR:CZ	16:P:41:PRO:HA	2.52	0.44
1:A:80:G:C2'	1:A:81:U:H5"	2.48	0.43
1:A:665:A:H2'	1:A:725:G:N2	2.33	0.43
1:A:1128:C:O2'	1:A:1130:A:C8	2.62	0.43
1:A:1314:C:H2'	1:A:1315:U:C6	2.52	0.43
1:A:1533:C:O2	1:A:1533:C:H2'	2.17	0.43
2:B:92:TYR:CD1	2:B:151:GLY:HA3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:10:ARG:HH11	4:D:10:ARG:HG3	1.83	0.43
4:D:55:ALA:O	4:D:59:ARG:HG2	2.19	0.43
6:F:22:GLU:OE2	6:F:84:ASN:HB2	2.18	0.43
10:J:75:ILE:HG22	10:J:76:ASN:N	2.32	0.43
12:L:70:ILE:CD1	12:L:77:LEU:HD12	2.42	0.43
16:P:6:LEU:HB3	16:P:17:TYR:HD2	1.82	0.43
19:S:81:ARG:HG3	19:S:81:ARG:NH1	2.28	0.43
20:T:72:LEU:O	20:T:73:HIS:O	2.35	0.43
21:V:15:ARG:O	21:V:17:THR:HG23	2.18	0.43
1:A:1074:G:O3'	2:B:103:THR:CG2	2.67	0.43
2:B:83:MET:HG3	2:B:238:LEU:HD11	2.00	0.43
2:B:204:ASN:HD22	2:B:206:ASP:H	1.66	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
5:E:118:ILE:CG2	5:E:119:LEU:H	2.27	0.43
7:G:24:THR:HA	7:G:27:ILE:HD12	2.00	0.43
7:G:108:ALA:O	7:G:119:ARG:HD2	2.18	0.43
9:I:69:GLY:O	9:I:73:GLN:HG3	2.18	0.43
11:K:50:TYR:N	11:K:50:TYR:CD1	2.84	0.43
11:K:60:ALA:O	11:K:61:ALA:C	2.56	0.43
11:K:100:ALA:O	11:K:102:GLY:N	2.51	0.43
12:L:7:ILE:O	12:L:11:VAL:HG23	2.18	0.43
18:R:37:VAL:O	18:R:41:LYS:HB3	2.18	0.43
1:A:143:A:H2	1:A:220:G:H22	1.66	0.43
1:A:267:C:H2'	1:A:268:C:C6	2.53	0.43
1:A:363:A:O2'	1:A:364:A:H5'	2.18	0.43
1:A:838:G:C3'	1:A:839:U:H5"	2.48	0.43
1:A:1131:G:H2'	1:A:1132:C:H6	1.82	0.43
1:A:1229:A:H2'	1:A:1230:C:H6	1.84	0.43
2:B:119:GLU:OE1	2:B:153:ARG:NH2	2.51	0.43
4:D:198:VAL:HG12	4:D:199:ASN:N	2.33	0.43
7:G:138:LYS:HD3	7:G:138:LYS:C	2.39	0.43
8:H:86:ILE:HD12	8:H:133:LEU:HD22	2.00	0.43
11:K:85:ARG:HG3	11:K:85:ARG:NH1	2.34	0.43
16:P:20:VAL:HG13	16:P:32:TYR:HB2	2.00	0.43
16:P:67:THR:CG2	16:P:68:ASP:N	2.82	0.43
18:R:46:GLU:CD	18:R:46:GLU:N	2.72	0.43
22:Y:46:LEU:O	22:Y:53:LEU:HD22	2.18	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:407:G:O2'	4:D:116:GLN:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:A:O4'	16:P:82:GLN:NE2	2.30	0.43
1:A:1202:G:O4'	14:N:29:ARG:HD3	2.18	0.43
1:A:1409:C:H2'	1:A:1410:G:H8	1.83	0.43
3:C:134:ILE:HG22	3:C:168:ALA:CB	2.48	0.43
5:E:143:ARG:HD3	5:E:143:ARG:HA	1.71	0.43
7:G:112:PRO:O	7:G:113:GLU:C	2.57	0.43
10:J:56:HIS:O	10:J:58:ASP:N	2.52	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
1:A:35:G:O2'	12:L:118:SER:O	2.23	0.43
1:A:430:A:H2'	1:A:431:A:H5'	1.99	0.43
1:A:505:G:H5'	1:A:534:U:H2'	2.00	0.43
1:A:851:G:H2'	1:A:852:G:H8	1.84	0.43
1:A:1031:G:H2'	1:A:1032:G:H8	1.83	0.43
1:A:1125:U:H5"	1:A:1126:U:H5	1.83	0.43
1:A:1376:U:H2'	1:A:1377:A:H8	1.79	0.43
2:B:130:ARG:HH22	3:C:179:ARG:NH1	2.10	0.43
3:C:19:GLU:HB3	3:C:40:ARG:NH2	2.25	0.43
8:H:16:ALA:O	8:H:21:LYS:HG2	2.18	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	2.25	0.43
15:O:41:GLU:O	15:O:42:HIS:C	2.57	0.43
20:T:50:GLU:HG2	20:T:100:ILE:CG1	2.48	0.43
1:A:276:G:O3'	17:Q:68:ARG:NH1	2.47	0.43
1:A:436:C:H2'	1:A:437:U:C6	2.53	0.43
1:A:652:U:H2'	1:A:752:G:N1	2.33	0.43
1:A:730:G:C5	1:A:731:G:H1'	2.54	0.43
1:A:958:A:C6	1:A:959:A:N1	2.87	0.43
1:A:1399:C:C2	1:A:1502:A:N6	2.86	0.43
1:A:1525:G:P	11:K:120:ARG:HH22	2.41	0.43
2:B:17:PHE:H	2:B:44:LEU:HD21	1.83	0.43
2:B:28:PHE:CD2	2:B:190:THR:HA	2.54	0.43
2:B:146:GLN:O	2:B:150:SER:HB3	2.18	0.43
3:C:191:THR:HB	3:C:194:GLY:O	2.18	0.43
4:D:25:ARG:HH21	4:D:30:LYS:HD3	1.82	0.43
7:G:75:VAL:HG13	7:G:86:GLN:HB3	1.95	0.43
10:J:45:ARG:NH1	14:N:36:PHE:CD2	2.87	0.43
10:J:46:ARG:HH11	10:J:64:GLU:CG	2.31	0.43
16:P:39:TYR:CD2	16:P:73:LEU:HD11	2.54	0.43
19:S:12:ASP:HB2	19:S:35:SER:OG	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:79:THR:O	19:S:81:ARG:N	2.51	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:1231:G:O3'	9:I:126:SER:HB3	2.19	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	1.71	0.43
3:C:70:VAL:HG12	3:C:71:ALA:H	1.84	0.43
3:C:116:VAL:HG11	3:C:141:VAL:HG21	2.01	0.43
3:C:188:LEU:HD13	3:C:189:ALA:H	1.84	0.43
4:D:120:LEU:HD23	4:D:125:HIS:CD2	2.54	0.43
4:D:127:THR:HG23	4:D:128:VAL:N	2.34	0.43
5:E:105:VAL:HB	5:E:106:PRO:CD	2.40	0.43
9:I:56:LEU:HB3	9:I:57:GLY:H	1.74	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
1:A:137:C:O2'	1:A:138:G:H5'	2.18	0.43
1:A:433:C:O2'	1:A:434:U:H5'	2.19	0.43
1:A:448:A:C4	1:A:487:A:C2	3.07	0.43
1:A:965:A:H5'	1:A:969:A:O4'	2.19	0.43
1:A:991:U:O2	1:A:993:G:H8	2.02	0.43
1:A:1135:U:H6	1:A:1135:U:O5'	2.01	0.43
1:A:1262:C:H2'	1:A:1263:C:C6	2.54	0.43
1:A:1504:G:OP1	1:A:1507:A:H4'	2.19	0.43
2:B:134:GLU:C	2:B:136:VAL:N	2.71	0.43
6:F:101:ALA:HB2	18:R:28:GLU:HG2	2.01	0.43
9:I:106:ALA:O	9:I:108:VAL:HG23	2.19	0.43
10:J:55:LYS:O	10:J:56:HIS:HB2	2.19	0.43
12:L:60:LEU:CD2	12:L:66:VAL:HG22	2.49	0.43
16:P:4:ILE:HG23	16:P:36:ILE:HD11	2.01	0.43
16:P:40:ASP:HB3	16:P:48:TRP:HB2	2.00	0.43
19:S:41:VAL:HG22	19:S:44:MET:CE	2.48	0.43
20:T:63:ILE:HD13	20:T:80:ARG:HB3	2.01	0.43
22:Y:76:PHE:HB3	22:Y:86:LEU:HD13	1.99	0.43
1:A:247:G:OP2	17:Q:99:SER:HB2	2.17	0.43
1:A:487:A:H2'	1:A:488:C:O4'	2.19	0.43
1:A:782:A:H2'	1:A:783:C:O4'	2.19	0.43
1:A:913:A:O2'	1:A:914:A:OP2	2.36	0.43
1:A:1004:A:H5"	1:A:1025:U:C4	2.53	0.43
1:A:1126:U:H2'	1:A:1127:G:O4'	2.18	0.43
1:A:1270:C:H4'	1:A:1313:U:O2'	2.19	0.43
1:A:1410:G:H1	1:A:1490:C:N4	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1441:G:H4'	1:A:1442:G:C8	2.54	0.43
2:B:74:LYS:HD2	2:B:166:ASP:HB2	2.00	0.43
2:B:125:PRO:C	2:B:127:ILE:H	2.22	0.43
2:B:137:ARG:HA	2:B:140:HIS:HD2	1.84	0.43
3:C:7:PRO:HG2	3:C:184:TYR:CB	2.45	0.43
3:C:193:TYR:HE1	3:C:196:LEU:HD11	1.83	0.43
4:D:158:ILE:CG2	4:D:181:MET:HE2	2.45	0.43
8:H:68:ARG:HG2	8:H:68:ARG:HH11	1.84	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:3:ARG:O	19:S:4:SER:HB3	2.18	0.43
19:S:40:ILE:HG23	19:S:44:MET:SD	2.59	0.43
1:A:359:U:O2'	1:A:360:A:H5'	2.18	0.43
1:A:370:C:C2'	1:A:371:G:H5'	2.48	0.43
1:A:628:G:H2'	1:A:629:G:H8	1.84	0.43
1:A:647:C:H2'	1:A:648:A:C8	2.54	0.43
1:A:1438:G:H2'	1:A:1439:C:C6	2.54	0.43
2:B:59:GLU:O	2:B:60:ASP:C	2.57	0.43
6:F:75:LEU:O	6:F:75:LEU:HD13	2.18	0.43
6:F:77:ARG:O	6:F:81:ILE:HG13	2.19	0.43
9:I:78:LYS:HD3	9:I:101:PHE:CD1	2.54	0.43
10:J:32:ALA:HB2	10:J:75:ILE:O	2.19	0.43
12:L:26:ALA:C	12:L:27:LEU:O	2.57	0.43
17:Q:45:HIS:CD2	17:Q:47:PRO:HG3	2.54	0.43
1:A:157:G:O2'	1:A:158:G:H5'	2.19	0.42
1:A:176:C:H2'	1:A:177:C:H6	1.83	0.42
1:A:418:C:H2'	1:A:419:C:H6	1.84	0.42
1:A:858:G:O2'	1:A:859:A:H5'	2.18	0.42
1:A:942:G:C2	1:A:943:U:C6	3.07	0.42
1:A:1288:A:H1'	1:A:1353:G:O4'	2.18	0.42
1:A:1331:G:O2'	1:A:1332:A:P	2.77	0.42
2:B:130:ARG:NH2	3:C:207:VAL:CG2	2.82	0.42
3:C:11:ARG:O	3:C:14:ILE:O	2.36	0.42
5:E:40:ARG:NH1	5:E:68:GLU:OE1	2.51	0.42
5:E:80:ILE:HD12	5:E:80:ILE:H	1.84	0.42
5:E:115:VAL:CG1	5:E:116:THR:N	2.82	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
19:S:20:LEU:HD12	19:S:21:GLU:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:25:LYS:HD2	19:S:25:LYS:N	2.34	0.42
1:A:80:G:H2'	1:A:81:U:H5"	2.01	0.42
1:A:413:G:N2	1:A:428:G:H1'	2.34	0.42
1:A:522:C:O2'	1:A:523:A:H5'	2.19	0.42
1:A:636:U:H2'	1:A:637:G:C8	2.54	0.42
1:A:967:C:C4'	9:I:128:ARG:HG3	2.46	0.42
1:A:994:A:N7	1:A:1216:G:H4'	2.35	0.42
1:A:1206:G:H4'	3:C:192:THR:O	2.19	0.42
1:A:1305:G:C5'	21:V:4:GLY:C	2.87	0.42
1:A:1305:G:H22	1:A:1331:G:C2'	2.33	0.42
3:C:50:ALA:O	3:C:70:VAL:CG1	2.67	0.42
3:C:191:THR:HG21	3:C:193:TYR:CE1	2.53	0.42
6:F:91:VAL:HG13	18:R:72:ARG:NH2	2.33	0.42
7:G:65:ALA:O	7:G:66:VAL:C	2.58	0.42
17:Q:59:ILE:CG2	17:Q:71:PHE:CD1	3.02	0.42
1:A:451:A:N6	1:A:480:U:H2'	2.33	0.42
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:839:U:C5'	1:A:840:C:H5	2.27	0.42
1:A:974:A:P	14:N:41:ARG:HH12	2.42	0.42
1:A:1157:A:O4'	1:A:1158:C:C2	2.72	0.42
1:A:1217:C:O2'	1:A:1218:C:H5'	2.19	0.42
1:A:1397:C:O2'	1:A:1398:A:P	2.77	0.42
3:C:134:ILE:HD13	3:C:166:GLU:HB3	2.01	0.42
5:E:24:ARG:HG2	5:E:24:ARG:NH1	2.33	0.42
7:G:31:MET:SD	7:G:34:GLY:HA2	2.60	0.42
8:H:75:ARG:HA	8:H:76:PRO:HD3	1.70	0.42
11:K:104:GLN:OE1	11:K:106:LYS:HE2	2.19	0.42
1:A:1060:C:O2'	1:A:1061:G:H5'	2.18	0.42
1:A:1181:G:O2'	1:A:1182:G:H5'	2.19	0.42
1:A:1353:G:H2'	1:A:1354:C:C6	2.54	0.42
1:A:1412:C:O2	1:A:1489:G:N2	2.51	0.42
2:B:130:ARG:HH22	3:C:207:VAL:HG22	1.81	0.42
5:E:16:THR:HG23	5:E:27:ARG:O	2.19	0.42
11:K:21:ILE:HD12	11:K:95:ILE:HG12	2.00	0.42
12:L:41:ARG:CB	12:L:41:ARG:NH1	2.82	0.42
13:M:7:VAL:O	13:M:7:VAL:HG23	2.18	0.42
15:O:39:LEU:HD12	15:O:59:MET:HE2	2.01	0.42
19:S:80:TYR:HE1	19:S:83:HIS:N	2.17	0.42
1:A:160:A:H2'	1:A:161:A:O4'	2.18	0.42
1:A:825:G:H2'	1:A:826:C:C6	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:974:A:P	14:N:29:ARG:HH22	2.43	0.42
1:A:1129:C:O2'	1:A:1130:A:P	2.78	0.42
2:B:187:LEU:HD21	2:B:214:ILE:HG13	2.00	0.42
6:F:30:LEU:HB3	6:F:35:ALA:CB	2.41	0.42
10:J:12:ASP:OD1	10:J:14:LYS:N	2.50	0.42
11:K:33:THR:OG1	11:K:37:GLY:C	2.58	0.42
13:M:96:LEU:HB3	13:M:97:PRO:HD2	2.00	0.42
16:P:51:VAL:O	16:P:52:ASP:C	2.58	0.42
19:S:41:VAL:HB	19:S:43:GLU:OE2	2.20	0.42
21:V:9:ARG:HH11	21:V:22:ARG:HA	1.85	0.42
1:A:409:G:H2'	1:A:410:G:O4'	2.19	0.42
1:A:418:C:H2'	1:A:419:C:C6	2.54	0.42
1:A:521:G:OP1	12:L:73:GLU:O	2.37	0.42
1:A:833:U:H2'	1:A:834:C:C6	2.55	0.42
1:A:942:G:H2'	1:A:943:U:H6	1.85	0.42
1:A:1126:U:H2'	1:A:1127:G:H8	1.85	0.42
1:A:1505:G:H3'	1:A:1505:G:H8	1.84	0.42
4:D:8:VAL:CG1	4:D:21:LEU:HD13	2.49	0.42
4:D:163:GLU:C	4:D:165:MET:N	2.72	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
12:L:33:ARG:HD2	12:L:62:SER:HB3	2.01	0.42
12:L:41:ARG:HB3	12:L:41:ARG:HH11	1.84	0.42
1:A:162:A:H2'	1:A:163:C:O4'	2.20	0.42
1:A:169:C:O2'	1:A:170:U:H5'	2.19	0.42
1:A:173:U:C5'	1:A:197:A:O4'	2.65	0.42
1:A:252:U:O2'	1:A:275:G:N2	2.53	0.42
1:A:377:G:P	16:P:3:LYS:HZ2	2.43	0.42
1:A:825:G:O2'	1:A:826:C:H5'	2.20	0.42
1:A:977:A:H2'	1:A:978:A:C5'	2.46	0.42
1:A:1417:G:O2'	1:A:1483:A:N6	2.51	0.42
2:B:17:PHE:CA	2:B:44:LEU:HD21	2.49	0.42
2:B:87:ARG:NH2	2:B:220:ASP:OD1	2.51	0.42
3:C:64:VAL:HG12	3:C:65:ALA:H	1.84	0.42
5:E:131:ILE:HD13	5:E:131:ILE:HA	1.93	0.42
6:F:19:LEU:HD21	6:F:23:LYS:HD2	2.02	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
13:M:80:ARG:C	13:M:82:MET:N	2.73	0.42
15:O:38:ARG:O	15:O:41:GLU:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:11:SER:C	20:T:13:LEU:H	2.22	0.42
20:T:54:LYS:HA	20:T:57:ARG:HD3	2.02	0.42
1:A:397:A:H5'	1:A:398:C:P	2.60	0.42
1:A:413:G:H22	1:A:428:G:H1'	1.85	0.42
1:A:502:G:H2'	1:A:503:C:H6	1.84	0.42
1:A:815:A:N6	1:A:1509:C:H1'	2.35	0.42
1:A:974:A:H8	1:A:974:A:OP1	2.03	0.42
1:A:1244:C:O2'	1:A:1245:A:H5'	2.19	0.42
1:A:1271:G:H5'	1:A:1314:C:OP1	2.20	0.42
2:B:8:LYS:O	2:B:9:GLU:CB	2.60	0.42
2:B:8:LYS:HB2	2:B:9:GLU:H	1.58	0.42
4:D:70:ILE:HD11	4:D:100:ARG:CD	2.49	0.42
9:I:110:GLU:HG2	9:I:113:LYS:NZ	2.35	0.42
11:K:57:THR:OG1	11:K:58:PRO:HD2	2.20	0.42
20:T:80:ARG:O	20:T:84:LEU:HB2	2.20	0.42
1:A:602:A:C2	1:A:637:G:C2	3.08	0.42
1:A:930:C:O2'	1:A:931:C:H5'	2.20	0.42
1:A:1277:C:H1'	1:A:1282:C:O2	2.20	0.42
1:A:1327:C:O2'	1:A:1328:C:H5'	2.20	0.42
2:B:187:LEU:HA	2:B:201:ILE:HB	2.02	0.42
3:C:38:ARG:CB	3:C:94:LEU:HD21	2.49	0.42
3:C:108:ASN:C	3:C:110:ASN:N	2.73	0.42
4:D:25:ARG:HA	4:D:28:SER:OG	2.19	0.42
4:D:60:GLU:OE1	4:D:60:GLU:HA	2.20	0.42
4:D:205:GLU:O	4:D:208:SER:HB2	2.20	0.42
5:E:24:ARG:O	5:E:25:ARG:HG2	2.20	0.42
7:G:155:ARG:O	7:G:156:TRP:CB	2.63	0.42
20:T:53:LEU:HD13	20:T:101:GLY:N	2.35	0.42
1:A:145:G:O2'	1:A:146:G:H5'	2.20	0.42
1:A:490:G:H2'	1:A:491:G:C8	2.54	0.42
1:A:539:A:OP2	12:L:115:LYS:HE2	2.20	0.42
1:A:550:G:O2'	1:A:551:U:H5'	2.20	0.42
1:A:767:A:H2'	1:A:768:A:O4'	2.20	0.42
1:A:1091:U:O2	1:A:1093:A:H8	2.03	0.42
1:A:1260:C:H4'	1:A:1284:C:H5'	2.01	0.42
1:A:1264:C:H2'	1:A:1265:G:C8	2.54	0.42
5:E:36:ASP:OD1	5:E:38:GLN:N	2.39	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
7:G:93:PRO:HG2	7:G:94:ARG:H	1.85	0.42
11:K:86:GLY:H	11:K:112:THR:CG2	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:17:SER:HB2	18:R:54:ARG:HH21	1.85	0.42
18:R:51:LEU:HA	18:R:52:PRO:HD3	1.80	0.42
19:S:41:VAL:HG22	19:S:44:MET:HE2	2.01	0.42
20:T:42:GLN:O	20:T:46:GLU:HG3	2.19	0.42
22:Y:49:GLN:O	22:Y:52:LYS:HE3	2.20	0.42
1:A:373:A:H2'	1:A:374:A:H8	1.85	0.41
1:A:1034:G:O2'	1:A:1035:A:H5'	2.20	0.41
1:A:1326:C:H5"	21:V:12:LYS:NZ	2.35	0.41
1:A:1426:C:H2'	1:A:1427:U:H6	1.84	0.41
1:A:1531:A:O5'	1:A:1531:A:H8	2.03	0.41
3:C:134:ILE:HG22	3:C:168:ALA:HB3	2.01	0.41
4:D:8:VAL:CG1	4:D:21:LEU:CD1	2.98	0.41
6:F:48:LEU:HD13	6:F:52:ILE:CG1	2.50	0.41
9:I:59:PHE:HB3	9:I:60:ASP:H	1.56	0.41
9:I:104:ARG:O	9:I:105:ASP:C	2.59	0.41
13:M:36:LYS:C	13:M:38:GLY:H	2.24	0.41
17:Q:40:LYS:HD3	17:Q:42:TYR:OH	2.20	0.41
18:R:44:LEU:HD23	18:R:44:LEU:HA	1.89	0.41
18:R:48:GLY:O	18:R:74:ARG:NH2	2.41	0.41
21:V:7:ARG:O	21:V:7:ARG:HG3	2.19	0.41
1:A:547:A:H4'	1:A:548:G:O5'	2.19	0.41
1:A:584:G:H2'	1:A:585:G:C8	2.54	0.41
1:A:628:G:O2'	1:A:629:G:H5'	2.20	0.41
1:A:867:G:O2'	1:A:868:C:H5'	2.20	0.41
1:A:1239:A:C4	1:A:1298:C:N4	2.88	0.41
1:A:1250:A:H4'	9:I:68:GLY:CA	2.50	0.41
1:A:1264:C:H2'	1:A:1265:G:H8	1.85	0.41
2:B:10:LEU:C	2:B:12:GLU:N	2.72	0.41
3:C:77:ILE:CG2	3:C:81:GLY:HA2	2.50	0.41
8:H:6:ILE:O	8:H:10:LEU:HG	2.20	0.41
9:I:120:ARG:O	9:I:122:ALA:N	2.53	0.41
12:L:104:VAL:HG12	12:L:105:TYR:CD2	2.55	0.41
13:M:67:GLU:HB3	13:M:68:GLY:H	1.58	0.41
22:Y:31:ASN:O	22:Y:35:GLN:HG2	2.20	0.41
1:A:47:C:C6	1:A:365:U:H2'	2.56	0.41
1:A:818:G:HO2'	1:A:819:A:H5"	1.84	0.41
1:A:1061:G:C2'	1:A:1062:U:H5'	2.50	0.41
1:A:1137:C:H4'	1:A:1138:G:N1	2.33	0.41
1:A:1214:C:N3	22:Y:20:SER:HB3	2.36	0.41
1:A:1298:C:C5	7:G:114:ARG:HD3	2.55	0.41
1:A:1393:U:O4'	1:A:1502:A:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:116:GLU:CG	2:B:153:ARG:NH1	2.80	0.41
2:B:165:VAL:O	2:B:187:LEU:O	2.38	0.41
3:C:112:SER:HB2	3:C:115:LEU:HB2	2.01	0.41
4:D:24:GLU:H	4:D:112:VAL:HG11	1.85	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
13:M:32:GLU:O	13:M:35:GLU:N	2.53	0.41
15:O:83:GLU:C	15:O:83:GLU:OE1	2.58	0.41
16:P:19:ILE:HG22	16:P:36:ILE:CG1	2.51	0.41
22:Y:67:THR:HG23	22:Y:73:ARG:NH1	2.35	0.41
1:A:184:G:O4’	1:A:224:C:H4’	2.19	0.41
1:A:625:G:H4’	16:P:16:HIS:CD2	2.55	0.41
1:A:778:G:O2’	1:A:779:C:H5’	2.19	0.41
1:A:1055:A:C6	1:A:1206:G:C5	3.08	0.41
1:A:1077:G:N2	1:A:1080:A:OP2	2.50	0.41
1:A:1305:G:H5”	21:V:4:GLY:C	2.40	0.41
1:A:1366:C:HO2’	10:J:60:ARG:HH22	1.64	0.41
1:A:1371:G:H2’	1:A:1372:U:H6	1.86	0.41
3:C:70:VAL:O	3:C:106:VAL:N	2.51	0.41
7:G:69:VAL:O	7:G:69:VAL:CG1	2.68	0.41
9:I:115:GLY:HA2	10:J:58:ASP:OD1	2.20	0.41
13:M:40:ASN:ND2	13:M:41:PRO:N	2.64	0.41
15:O:34:LEU:HD23	15:O:34:LEU:C	2.40	0.41
16:P:4:ILE:CG1	16:P:64:ALA:HB1	2.48	0.41
20:T:57:ARG:HE	20:T:100:ILE:HG21	1.84	0.41
1:A:489:C:H2’	1:A:490:G:C8	2.54	0.41
1:A:1126:U:P	1:A:1126:U:H6	2.43	0.41
1:A:1127:G:N2	1:A:1144:G:N2	2.69	0.41
1:A:1145:C:O2’	1:A:1146:A:O5’	2.39	0.41
1:A:1262:C:N4	1:A:1273:G:H1	2.18	0.41
1:A:1311:G:H2’	1:A:1312:G:O4’	2.20	0.41
1:A:1410:G:C2	1:A:1491:G:C2	3.08	0.41
1:A:1460:A:P	20:T:27:LYS:NZ	2.94	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
4:D:148:VAL:HG13	4:D:158:ILE:HD13	2.01	0.41
7:G:45:ASP:O	7:G:49:ILE:HG13	2.20	0.41
8:H:82:HIS:O	8:H:83:ILE:HB	2.21	0.41
8:H:108:GLY:CA	8:H:138:TRP:HB3	2.46	0.41
9:I:56:LEU:O	9:I:58:HIS:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:83:VAL:HG22	12:L:84:LEU:H	1.85	0.41
16:P:82:GLN:O	16:P:83:GLU:C	2.59	0.41
1:A:43:C:H2'	1:A:44:G:O4'	2.21	0.41
1:A:564:C:H5'	12:L:10:LEU:HD13	2.03	0.41
1:A:642:A:C2	8:H:113:SER:O	2.74	0.41
1:A:913:A:H1'	1:A:914:A:O4'	2.21	0.41
1:A:949:A:N7	13:M:106:ASN:ND2	2.68	0.41
1:A:1094:G:OP2	1:A:1095:U:C5	2.74	0.41
1:A:1350:A:C6	1:A:1351:U:N3	2.89	0.41
1:A:1442:G:N2	1:A:1446:A:C8	2.80	0.41
1:A:1486:G:H2'	1:A:1487:G:O4'	2.19	0.41
2:B:62:ALA:C	2:B:64:ARG:H	2.23	0.41
3:C:73:PRO:HD3	3:C:105:GLU:HG3	2.03	0.41
5:E:51:VAL:HB	5:E:52:PRO:CD	2.37	0.41
5:E:144:THR:O	5:E:145:LYS:C	2.59	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	2.51	0.41
10:J:3:LYS:HG3	10:J:75:ILE:HG23	2.01	0.41
11:K:86:GLY:N	11:K:112:THR:HG23	2.35	0.41
11:K:100:ALA:O	11:K:101:SER:C	2.57	0.41
15:O:87:ILE:HG22	15:O:88:ARG:N	2.34	0.41
1:A:182:U:C4	1:A:183:G:H1'	2.56	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:736:C:H2'	1:A:737:A:H8	1.83	0.41
1:A:769:G:H4'	1:A:1513:A:H4'	2.02	0.41
1:A:913:A:O2'	1:A:914:A:O4'	2.26	0.41
1:A:1030(A):G:H21	1:A:1030(C):G:H3'	1.84	0.41
1:A:1453:G:H2'	1:A:1454:G:O4'	2.21	0.41
6:F:48:LEU:HD13	6:F:52:ILE:HD12	2.03	0.41
11:K:77:MET:CE	11:K:80:VAL:HG22	2.48	0.41
11:K:127:LYS:HD3	11:K:127:LYS:HA	1.78	0.41
12:L:55:VAL:CG1	12:L:67:THR:CG2	2.97	0.41
12:L:55:VAL:CG1	12:L:56:ALA:N	2.83	0.41
13:M:4:ILE:HG22	13:M:5:ALA:H	1.83	0.41
1:A:67:C:O2'	1:A:171:A:H1'	2.20	0.41
1:A:382:A:C2	1:A:383:A:C4	3.08	0.41
1:A:692:U:O2	1:A:695:A:C8	2.73	0.41
1:A:866:C:H2'	1:A:867:G:O4'	2.20	0.41
1:A:877:C:OP1	8:H:88:LYS:HE2	2.20	0.41
1:A:1057:G:H2'	1:A:1058:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1194:U:H4'	5:E:22:GLY:HA2	2.02	0.41
1:A:1286:A:H2'	1:A:1287:A:O5'	2.21	0.41
2:B:228:GLY:O	2:B:229:VAL:C	2.58	0.41
3:C:47:LEU:H	3:C:47:LEU:HD13	1.83	0.41
7:G:23:VAL:HG13	7:G:43:PHE:CE2	2.56	0.41
10:J:15:THR:HG23	10:J:94:VAL:CG2	2.48	0.41
10:J:75:ILE:O	10:J:76:ASN:HB2	2.21	0.41
11:K:65:ALA:O	11:K:68:ALA:HB3	2.20	0.41
11:K:99:GLN:HG2	11:K:105:VAL:HG21	2.02	0.41
15:O:70:LEU:HD12	15:O:78:TYR:HB2	2.02	0.41
1:A:19:C:O2'	1:A:20:U:H5'	2.20	0.41
1:A:107:G:O2'	1:A:108:G:H5'	2.20	0.41
1:A:280:C:H4'	1:A:281:G:OP2	2.20	0.41
1:A:436:C:H2'	1:A:437:U:H6	1.86	0.41
1:A:570:G:H1'	1:A:820:U:C4	2.56	0.41
1:A:625:G:O2'	1:A:626:U:H5'	2.21	0.41
1:A:1096:C:H2'	1:A:1097:C:C6	2.56	0.41
1:A:1118:C:H1'	1:A:1179:A:C4	2.56	0.41
1:A:1318:A:H4'	19:S:10:PHE:CD2	2.55	0.41
1:A:1355:G:O2'	1:A:1356:G:H5'	2.20	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
2:B:14:GLY:O	2:B:15:VAL:HG22	2.21	0.41
2:B:134:GLU:HG2	2:B:137:ARG:HH21	1.86	0.41
3:C:67:THR:O	3:C:67:THR:HG22	2.21	0.41
3:C:79:ARG:NE	3:C:82:GLU:HG2	2.34	0.41
3:C:191:THR:HG21	3:C:193:TYR:CE2	2.56	0.41
5:E:40:ARG:NH1	5:E:68:GLU:OE2	2.49	0.41
5:E:118:ILE:HD13	5:E:118:ILE:HG21	1.74	0.41
6:F:33:TYR:HA	6:F:71:ARG:NH2	2.36	0.41
6:F:78:GLU:HA	6:F:81:ILE:CD1	2.51	0.41
8:H:39:LEU:HD13	8:H:39:LEU:HA	1.86	0.41
9:I:108:VAL:HG12	9:I:109:VAL:N	2.36	0.41
9:I:110:GLU:OE2	9:I:113:LYS:NZ	2.53	0.41
10:J:29:ARG:C	10:J:84:GLN:HE22	2.24	0.41
11:K:67:ASP:OD1	11:K:71:LYS:HE3	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
12:L:46:LYS:NZ	12:L:47:LYS:HE3	2.36	0.41
12:L:53:ARG:CB	12:L:93:LEU:HD11	2.50	0.41
12:L:60:LEU:HD21	12:L:66:VAL:CG2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:22:ILE:HD12	13:M:25:ILE:CD1	2.41	0.41
13:M:78:ILE:CA	13:M:81:LEU:HD21	2.43	0.41
15:O:26:GLU:HG3	15:O:81:LEU:HG	2.02	0.41
15:O:57:LEU:HD12	15:O:57:LEU:HA	1.86	0.41
15:O:81:LEU:HD22	15:O:85:LEU:HD12	2.02	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
19:S:16:LEU:O	19:S:20:LEU:HG	2.21	0.41
19:S:80:TYR:CE1	19:S:82:GLY:C	2.94	0.41
20:T:44:ALA:HB2	20:T:88:VAL:HG13	2.02	0.41
20:T:68:LYS:HD2	20:T:68:LYS:HA	1.92	0.41
1:A:134:A:H1'	1:A:325:A:C5	2.56	0.41
1:A:509:A:H5"	4:D:55:ALA:HB2	2.03	0.41
1:A:812:C:OP1	1:A:902:G:N2	2.49	0.41
1:A:836:G:C6	1:A:851:G:C6	3.09	0.41
1:A:921:U:O2	5:E:19:MET:HB2	2.21	0.41
1:A:1110:A:O5'	1:A:1110:A:H8	2.04	0.41
1:A:1190:G:P	3:C:4:LYS:HA	2.60	0.41
1:A:1313:U:OP2	19:S:6:LYS:HA	2.21	0.41
2:B:15:VAL:HG11	2:B:210:SER:N	2.36	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
2:B:125:PRO:HG2	2:B:126:GLU:H	1.86	0.41
3:C:77:ILE:O	3:C:83:ARG:HB3	2.21	0.41
3:C:126:ARG:C	3:C:127:ARG:HG3	2.42	0.41
3:C:174:PRO:HB2	3:C:177:THR:CG2	2.50	0.41
4:D:63:LYS:O	4:D:64:LEU:C	2.58	0.41
5:E:9:LYS:HG3	5:E:112:LEU:HD11	2.03	0.41
10:J:23:ILE:N	10:J:23:ILE:CD1	2.84	0.41
20:T:36:LEU:HD12	20:T:62:LEU:HD12	2.03	0.41
20:T:43:LEU:HD13	20:T:51:GLU:CG	2.43	0.41
1:A:429:U:OP2	4:D:36:ARG:NH1	2.54	0.40
1:A:502:G:H2'	1:A:503:C:C6	2.56	0.40
1:A:883:C:O2'	1:A:884:U:H5'	2.21	0.40
1:A:919:A:O2'	1:A:920:U:H5'	2.22	0.40
1:A:1112:C:N3	3:C:178:LEU:N	2.63	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:1402:C:H2'	1:A:1403:C:H6	1.85	0.40
1:A:1428:A:H2'	1:A:1429:C:O4'	2.21	0.40
2:B:130:ARG:HB3	2:B:134:GLU:OE1	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:57:ILE:O	3:C:57:ILE:HG22	2.20	0.40
4:D:130:GLY:O	4:D:131:ARG:C	2.58	0.40
8:H:89:PRO:HA	8:H:92:ARG:NH1	2.37	0.40
11:K:95:ILE:O	11:K:95:ILE:HG22	2.20	0.40
13:M:96:LEU:O	13:M:110:ARG:NH1	2.54	0.40
15:O:71:GLN:O	15:O:72:ARG:C	2.59	0.40
15:O:74:ASP:OD1	15:O:76:GLU:HB3	2.21	0.40
19:S:5:LEU:HD23	19:S:5:LEU:HA	1.88	0.40
1:A:182:U:H6	1:A:182:U:C4'	2.30	0.40
1:A:335:C:H2'	1:A:336:C:H6	1.86	0.40
1:A:567:G:H2'	1:A:568:G:O4'	2.21	0.40
1:A:637:G:O2'	1:A:638:G:H5'	2.21	0.40
1:A:1028:C:H2'	1:A:1029:C:H6	1.85	0.40
2:B:53:ARG:NH1	2:B:199:TYR:HD1	2.19	0.40
3:C:65:ALA:O	3:C:66:VAL:HB	2.21	0.40
4:D:58:LEU:HD23	4:D:206:PHE:CE2	2.57	0.40
4:D:194:LEU:HD22	4:D:194:LEU:N	2.36	0.40
7:G:104:LEU:HD23	7:G:134:ALA:HB1	2.03	0.40
13:M:37:THR:HG23	13:M:55:ARG:HB2	2.03	0.40
13:M:63:THR:HG23	13:M:64:TRP:CD2	2.56	0.40
13:M:84:ILE:HG21	19:S:65:ASN:HD22	1.85	0.40
18:R:44:LEU:HD22	18:R:48:GLY:O	2.21	0.40
1:A:458:C:H2'	1:A:459:G:C8	2.56	0.40
1:A:950:U:H2'	1:A:951:G:C8	2.57	0.40
1:A:1124:G:C8	1:A:1145:C:C5	3.09	0.40
1:A:1138:G:N1	1:A:1140:C:C2	2.89	0.40
1:A:1392:G:H2'	1:A:1393:U:H6	1.86	0.40
1:A:1437:C:H2'	1:A:1438:G:H8	1.86	0.40
2:B:14:GLY:O	2:B:15:VAL:CG2	2.69	0.40
2:B:21:ARG:H	2:B:21:ARG:HG2	1.72	0.40
2:B:107:THR:C	2:B:109:SER:N	2.75	0.40
2:B:157:ARG:NH1	2:B:157:ARG:HG3	2.36	0.40
3:C:13:GLY:O	3:C:14:ILE:HD13	2.22	0.40
5:E:76:ILE:HG23	5:E:77:PRO:HD2	2.04	0.40
6:F:48:LEU:HD13	6:F:52:ILE:CD1	2.51	0.40
8:H:19:VAL:CG2	8:H:21:LYS:HD3	2.52	0.40
10:J:44:VAL:HG11	10:J:46:ARG:NH1	2.37	0.40
11:K:115:PRO:C	11:K:117:ASN:H	2.25	0.40
12:L:40:VAL:O	12:L:40:VAL:CG1	2.69	0.40
16:P:34:GLU:HG2	16:P:35:LYS:N	2.36	0.40
17:Q:6:LEU:O	17:Q:58:GLU:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:26:LEU:CD1	18:R:27:GLY:H	2.29	0.40
1:A:155:C:H2'	1:A:156:G:C8	2.57	0.40
1:A:176:C:H2'	1:A:177:C:C6	2.56	0.40
1:A:523:A:C2	12:L:91:LYS:HB3	2.57	0.40
1:A:671:G:H2'	1:A:672:U:O4'	2.21	0.40
1:A:715:A:H2'	1:A:716:A:C8	2.57	0.40
1:A:973:G:H8	1:A:973:G:O5'	2.05	0.40
1:A:1424:C:C2'	1:A:1425:U:H5'	2.52	0.40
2:B:134:GLU:O	2:B:138:LEU:HG	2.21	0.40
7:G:32:ARG:O	7:G:33:ASP:HB2	2.22	0.40
8:H:111:ILE:O	8:H:134:ILE:HB	2.20	0.40
10:J:59:SER:O	10:J:60:ARG:HB2	2.21	0.40
14:N:39:LEU:HD11	14:N:47:LEU:HD12	2.02	0.40
20:T:92:LEU:O	20:T:96:GLY:HA3	2.21	0.40
1:A:16:A:C2'	1:A:17:U:H5'	2.51	0.40
1:A:103:C:OP1	20:T:17:ARG:HD2	2.22	0.40
1:A:279:A:N6	17:Q:98:LEU:HD13	2.34	0.40
1:A:282:A:H5"	1:A:282:A:C8	2.55	0.40
1:A:865:A:H5'	1:A:1078:U:C4	2.57	0.40
1:A:939:G:C6	1:A:940:C:N4	2.89	0.40
1:A:1003(A):G:H2'	1:A:1004:A:H4'	2.03	0.40
1:A:1250:A:H5"	9:I:68:GLY:N	2.37	0.40
2:B:216:SER:OG	2:B:217:ARG:N	2.55	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
4:D:128:VAL:O	4:D:129:ASN:HB2	2.22	0.40
6:F:30:LEU:CB	6:F:35:ALA:HB3	2.41	0.40
12:L:52:LEU:O	12:L:54:LYS:HD2	2.22	0.40
13:M:69:GLU:O	13:M:72:ALA:HB3	2.21	0.40
20:T:90:GLN:O	20:T:93:GLU:HG2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	232/256 (91%)	174 (75%)	34 (15%)	24 (10%)	0 7
3	C	204/239 (85%)	135 (66%)	40 (20%)	29 (14%)	0 4
4	D	206/209 (99%)	166 (81%)	31 (15%)	9 (4%)	2 23
5	E	148/162 (91%)	130 (88%)	13 (9%)	5 (3%)	3 31
6	F	99/101 (98%)	79 (80%)	19 (19%)	1 (1%)	15 55
7	G	153/156 (98%)	127 (83%)	16 (10%)	10 (6%)	1 16
8	H	136/138 (99%)	125 (92%)	7 (5%)	4 (3%)	4 33
9	I	125/128 (98%)	88 (70%)	27 (22%)	10 (8%)	1 11
10	J	96/105 (91%)	59 (62%)	20 (21%)	17 (18%)	0 2
11	K	117/129 (91%)	88 (75%)	20 (17%)	9 (8%)	1 12
12	L	122/132 (92%)	98 (80%)	14 (12%)	10 (8%)	1 10
13	M	116/126 (92%)	85 (73%)	27 (23%)	4 (3%)	3 31
14	N	58/61 (95%)	39 (67%)	11 (19%)	8 (14%)	0 4
15	O	86/89 (97%)	70 (81%)	11 (13%)	5 (6%)	1 18
16	P	81/88 (92%)	65 (80%)	15 (18%)	1 (1%)	13 51
17	Q	98/105 (93%)	85 (87%)	9 (9%)	4 (4%)	3 26
18	R	71/88 (81%)	62 (87%)	7 (10%)	2 (3%)	5 34
19	S	82/93 (88%)	47 (57%)	22 (27%)	13 (16%)	0 3
20	T	97/106 (92%)	65 (67%)	20 (21%)	12 (12%)	0 5
21	V	22/27 (82%)	19 (86%)	2 (9%)	1 (4%)	2 23
22	Y	90/118 (76%)	82 (91%)	8 (9%)	0	100 100
All	All	2439/2656 (92%)	1888 (77%)	373 (15%)	178 (7%)	1 13

All (178) 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

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Mol	Chain	Res	Type
3	C	15	THR
3	C	16	ARG
3	C	26	LYS
3	C	47	LEU
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	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
14	N	22	THR
14	N	29	ARG
15	O	88	ARG
17	Q	80	GLY
17	Q	81	ARG
18	R	87	ARG
19	S	6	LYS
19	S	71	LEU

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Mol	Chain	Res	Type
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	HIS
10	J	30	SER
10	J	34	VAL
10	J	40	LEU
10	J	57	LYS
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
16	P	10	GLY
17	Q	69	LYS
18	R	20	ALA

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Mol	Chain	Res	Type
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	126	GLU
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
19	S	28	LYS
19	S	30	LEU
19	S	32	LYS
19	S	78	ARG
19	S	80	TYR
20	T	74	LYS
2	B	165	VAL
3	C	39	ILE
3	C	100	ALA
3	C	188	LEU
7	G	4	ARG
7	G	81	GLY
7	G	112	PRO

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Mol	Chain	Res	Type
9	I	7	THR
9	I	12	GLU
9	I	119	ALA
12	L	45	PRO
14	N	12	ARG
14	N	31	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
2	B	214	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
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 (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	202/220 (92%)	181 (90%)	21 (10%)	7 33
3	C	160/188 (85%)	143 (89%)	17 (11%)	6 32
4	D	180/181 (99%)	172 (96%)	8 (4%)	28 63
5	E	115/123 (94%)	101 (88%)	14 (12%)	5 26
6	F	90/90 (100%)	88 (98%)	2 (2%)	52 77
7	G	126/127 (99%)	123 (98%)	3 (2%)	49 75
8	H	119/119 (100%)	109 (92%)	10 (8%)	11 42
9	I	98/99 (99%)	92 (94%)	6 (6%)	18 53
10	J	87/92 (95%)	78 (90%)	9 (10%)	7 34
11	K	90/99 (91%)	84 (93%)	6 (7%)	16 50
12	L	104/109 (95%)	96 (92%)	8 (8%)	13 45
13	M	94/101 (93%)	85 (90%)	9 (10%)	8 37
14	N	49/50 (98%)	45 (92%)	4 (8%)	11 42
15	O	79/80 (99%)	72 (91%)	7 (9%)	9 40
16	P	72/74 (97%)	67 (93%)	5 (7%)	15 49
17	Q	95/97 (98%)	90 (95%)	5 (5%)	22 58
18	R	64/77 (83%)	61 (95%)	3 (5%)	26 61
19	S	73/80 (91%)	67 (92%)	6 (8%)	11 42
20	T	76/82 (93%)	69 (91%)	7 (9%)	9 39
21	V	19/22 (86%)	19 (100%)	0	100 100
22	Y	79/103 (77%)	75 (95%)	4 (5%)	24 58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2071/2213 (94%)	1917 (93%)	154 (7%)	13 46

All (154) 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	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	164	ARG
3	C	167	TRP
3	C	175	LEU
3	C	179	ARG
3	C	188	LEU

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Mol	Chain	Res	Type
3	C	204	LEU
4	D	15	GLU
4	D	29	PRO
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	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	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	38	GLN
9	I	53	VAL
9	I	79	LEU

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Mol	Chain	Res	Type
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	12	ASN
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
14	N	31	ARG
14	N	32	SER
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
18	R	36	ASN
18	R	38	GLU
18	R	55	ARG
19	S	15	LEU
19	S	20	LEU
19	S	77	THR
19	S	80	TYR
19	S	83	HIS
19	S	85	LYS
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
22	Y	6	LYS
22	Y	48	ARG
22	Y	49	GLN
22	Y	89	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	19	HIS
2	B	146	GLN
2	B	204	ASN
3	C	6	HIS
3	C	110	ASN

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Mol	Chain	Res	Type
3	C	118	GLN
4	D	161	ASN
4	D	199	ASN
6	F	94	GLN
6	F	100	ASN
10	J	62	HIS
10	J	78	ASN
10	J	84	GLN
13	M	40	ASN
17	Q	16	GLN
18	R	36	ASN
20	T	42	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1512/1522 (99%)	229 (15%)	90 (5%)

All (229) 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	181	G

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Mol	Chain	Res	Type
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
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	253	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	281	G
1	A	282	A
1	A	283	C
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	1054	C

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Mol	Chain	Res	Type
1	A	1055	A
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1085	U
1	A	1086	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	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
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	1198	G
1	A	1201	A
1	A	1202	G
1	A	1211	U
1	A	1212	U
1	A	1214	C
1	A	1215	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1238	A

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Mol	Chain	Res	Type
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
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	1487	G
1	A	1490	C
1	A	1497	G
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

All (90) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	7	G
1	A	30	U
1	A	48	C
1	A	51	A
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	202	U
1	A	203	U
1	A	204	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	281	G
1	A	282	A
1	A	328	C
1	A	329	A
1	A	344	A
1	A	351	G
1	A	353	A
1	A	366	C
1	A	372	C
1	A	428	G
1	A	429	U
1	A	438	G
1	A	484	G
1	A	496	A
1	A	497	A
1	A	509	A
1	A	518	C
1	A	532	A
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A
1	A	701	C

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Mol	Chain	Res	Type
1	A	748	C
1	A	792	A
1	A	812	C
1	A	813	U
1	A	840	C
1	A	913	A
1	A	960	U
1	A	965	A
1	A	975	A
1	A	976	G
1	A	992	U
1	A	993	G
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1085	U
1	A	1101	A
1	A	1129	C
1	A	1145	C
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1201	A
1	A	1214	C
1	A	1224	G
1	A	1226	C
1	A	1256	A
1	A	1257	U
1	A	1278	U
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1319	A
1	A	1331	G
1	A	1346	A
1	A	1347	G
1	A	1364	U
1	A	1380	U
1	A	1397	C
1	A	1451	A

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Mol	Chain	Res	Type
1	A	1498	U
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1528	U

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 196 ligands modelled in this entry, 196 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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	1513/1522 (99%)	0.57	90 (5%) 22 13	51, 88, 179, 307	0
2	B	234/256 (91%)	0.14	7 (2%) 50 34	64, 99, 175, 250	0
3	C	206/239 (86%)	0.07	12 (5%) 23 13	69, 115, 165, 205	0
4	D	208/209 (99%)	0.16	11 (5%) 26 16	61, 95, 141, 216	0
5	E	150/162 (92%)	0.06	0 100 100	40, 73, 120, 149	0
6	F	101/101 (100%)	0.23	8 (7%) 12 7	76, 116, 155, 175	0
7	G	155/156 (99%)	-0.10	3 (1%) 66 51	77, 110, 171, 198	0
8	H	138/138 (100%)	-0.33	0 100 100	45, 65, 97, 131	0
9	I	127/128 (99%)	0.13	10 (7%) 12 7	68, 119, 165, 185	0
10	J	98/105 (93%)	0.63	9 (9%) 9 5	74, 130, 216, 297	0
11	K	119/129 (92%)	0.05	3 (2%) 57 41	57, 93, 145, 228	0
12	L	124/132 (93%)	0.02	1 (0%) 86 75	49, 90, 128, 204	0
13	M	118/126 (93%)	0.54	10 (8%) 10 6	77, 116, 165, 200	0
14	N	60/61 (98%)	-0.07	0 100 100	77, 108, 155, 192	0
15	O	88/89 (98%)	-0.09	3 (3%) 45 30	56, 86, 143, 195	0
16	P	83/88 (94%)	-0.30	0 100 100	64, 84, 112, 165	0
17	Q	100/105 (95%)	0.17	1 (1%) 82 70	53, 81, 129, 186	0
18	R	73/88 (82%)	-0.04	3 (4%) 37 24	64, 97, 168, 223	0
19	S	84/93 (90%)	0.26	8 (9%) 8 4	97, 134, 168, 235	0
20	T	99/106 (93%)	0.35	9 (9%) 9 5	60, 96, 149, 227	0
21	V	24/27 (88%)	0.01	0 100 100	94, 117, 149, 157	0
22	Y	92/118 (77%)	1.52	31 (33%) 0 0	109, 178, 232, 276	0
All	All	3994/4178 (95%)	0.31	219 (5%) 25 15	40, 97, 175, 307	0

All (219) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1024	G	8.1
4	D	35	ARG	7.5
1	A	1129	C	7.3
1	A	1534	A	6.6
1	A	1006	C	6.3
1	A	1003(A)	G	5.8
1	A	1005	A	5.7
1	A	1036	G	5.7
22	Y	25	GLN	5.6
1	A	1025	U	5.6
1	A	412	A	5.3
1	A	1541	U	5.3
1	A	1540	U	5.2
1	A	1258	G	5.2
1	A	841	U	5.0
1	A	1260	C	5.0
22	Y	29	ARG	5.0
20	T	103	GLY	4.9
1	A	413	G	4.9
22	Y	26	ASP	4.8
1	A	1003	G	4.7
1	A	1477	C	4.6
1	A	1478	C	4.5
1	A	1023	G	4.5
1	A	1446	A	4.5
4	D	36	ARG	4.4
22	Y	19	THR	4.4
22	Y	58	GLY	4.3
22	Y	30	ILE	4.3
1	A	1259	C	4.3
1	A	81	U	4.2
22	Y	22	VAL	4.2
1	A	1026	G	4.1
1	A	1037	C	4.0
22	Y	69	ARG	3.9
22	Y	88	TYR	3.8
22	Y	24	ALA	3.8
1	A	1038	C	3.8
1	A	1426	C	3.8
4	D	152	SER	3.7
13	M	2	ALA	3.7
1	A	1004	A	3.7
17	Q	101	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	1539	C	3.6
1	A	1423	G	3.6
6	F	63	TYR	3.5
22	Y	7	HIS	3.5
4	D	125	HIS	3.5
1	A	1255	G	3.5
10	J	89	ASP	3.4
22	Y	86	LEU	3.4
1	A	848	C	3.4
1	A	1138	G	3.4
1	A	1139	G	3.3
1	A	426	G	3.3
1	A	88	A	3.3
1	A	1424	C	3.3
2	B	16	HIS	3.3
1	A	1476	G	3.2
3	C	58	GLU	3.2
11	K	89	ALA	3.2
1	A	1427	U	3.2
13	M	43	THR	3.2
1	A	1282	C	3.2
6	F	59	TYR	3.2
20	T	9	ASN	3.2
4	D	151	LYS	3.2
22	Y	87	ASN	3.2
13	M	63	THR	3.2
1	A	158	G	3.2
1	A	1136	U	3.2
1	A	1007	C	3.2
1	A	1126	U	3.1
6	F	61	LEU	3.1
1	A	1027	C	3.1
11	K	129	SER	3.1
3	C	23	TYR	3.1
20	T	37	SER	3.1
1	A	443	C	3.1
22	Y	20	SER	3.1
1	A	1479	C	3.1
4	D	123	HIS	3.1
20	T	56	MET	3.0
3	C	59	ARG	3.0
2	B	238	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	532	A	2.9
22	Y	23	PRO	2.9
18	R	17	SER	2.9
1	A	1425	U	2.9
1	A	1148	U	2.9
1	A	1002	G	2.9
13	M	41	PRO	2.9
1	A	1276	G	2.9
6	F	13	ASN	2.8
3	C	60	ALA	2.8
9	I	8	GLY	2.8
9	I	102	LEU	2.8
22	Y	59	ASP	2.8
1	A	159	G	2.8
22	Y	70	ALA	2.8
3	C	159	GLY	2.8
13	M	45	VAL	2.8
10	J	90	LEU	2.8
22	Y	32	ASP	2.8
22	Y	10	LEU	2.8
1	A	1135	U	2.7
1	A	1171	G	2.7
18	R	18	ARG	2.7
1	A	633	G	2.7
1	A	1137	C	2.7
1	A	428	G	2.7
1	A	429	U	2.7
9	I	15	ALA	2.7
9	I	126	SER	2.7
1	A	1278	U	2.7
22	Y	72	TRP	2.6
10	J	95	GLU	2.6
20	T	55	ILE	2.6
20	T	35	THR	2.6
1	A	425	G	2.6
3	C	102	ASN	2.6
1	A	606	G	2.6
22	Y	50	ILE	2.6
1	A	1533	C	2.6
2	B	233	SER	2.6
13	M	116	THR	2.5
1	A	1256	A	2.5

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Mol	Chain	Res	Type	RSRZ
10	J	6	ILE	2.5
3	C	103	VAL	2.5
19	S	29	ARG	2.5
10	J	85	LEU	2.5
19	S	31	ILE	2.5
1	A	202	U	2.5
4	D	2	GLY	2.5
2	B	231	GLU	2.5
19	S	39	THR	2.5
10	J	7	LYS	2.5
20	T	36	LEU	2.5
22	Y	2	ILE	2.5
22	Y	90	ASP	2.5
6	F	42	GLU	2.5
1	A	1140	C	2.5
3	C	68	VAL	2.4
22	Y	13	LEU	2.4
9	I	7	THR	2.4
9	I	65	VAL	2.4
20	T	104	LEU	2.4
1	A	1279	A	2.4
22	Y	36	ALA	2.4
19	S	28	LYS	2.4
1	A	1283	G	2.4
9	I	101	PHE	2.4
22	Y	74	ILE	2.4
1	A	1275	A	2.4
1	A	1542	U	2.4
3	C	196	LEU	2.4
12	L	128	ALA	2.4
1	A	1124	G	2.3
22	Y	89	GLU	2.3
22	Y	27	VAL	2.3
1	A	1257	U	2.3
10	J	96	ILE	2.3
6	F	10	LEU	2.3
1	A	1134	G	2.3
1	A	1277	C	2.3
2	B	122	PHE	2.3
3	C	2	GLY	2.3
7	G	56	GLN	2.3
1	A	1302	U	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	1226	C	2.3
10	J	92	THR	2.3
15	O	22	THR	2.3
22	Y	92	HIS	2.3
13	M	65	LYS	2.3
1	A	1022	G	2.2
1	A	1420	C	2.2
4	D	157	LEU	2.2
4	D	155	LEU	2.2
1	A	1270	C	2.2
2	B	188	ALA	2.2
9	I	94	ALA	2.2
3	C	104	GLN	2.2
13	M	15	VAL	2.2
1	A	411	A	2.2
9	I	64	THR	2.2
1	A	1472	U	2.2
20	T	39	LYS	2.2
15	O	89	GLY	2.2
1	A	494	G	2.2
7	G	155	ARG	2.1
13	M	37	THR	2.1
22	Y	91	TYR	2.1
19	S	44	MET	2.1
19	S	38	SER	2.1
1	A	834	C	2.1
4	D	33	MET	2.1
7	G	26	PHE	2.1
15	O	23	GLY	2.1
1	A	631	G	2.1
11	K	58	PRO	2.1
19	S	49	ILE	2.1
3	C	156	ARG	2.1
22	Y	48	ARG	2.1
10	J	88	LEU	2.1
1	A	438	G	2.1
1	A	1419	G	2.1
2	B	211	ILE	2.1
1	A	89	C	2.1
1	A	1019	C	2.1
6	F	47	ARG	2.1
9	I	14	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
13	M	44	ARG	2.0
19	S	32	LYS	2.0
18	R	48	GLY	2.0
1	A	410	G	2.0
4	D	181	MET	2.0
1	A	490	G	2.0
1	A	1454	G	2.0
6	F	14	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 monosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
23	MG	A	1624	1/1	0.15	0.41	102,102,102,102	0
23	MG	A	1748	1/1	0.28	0.86	80,80,80,80	0
23	MG	A	1779	1/1	0.37	0.90	71,71,71,71	0
23	MG	A	1605	1/1	0.44	0.79	79,79,79,79	0
23	MG	A	1790	1/1	0.45	0.61	81,81,81,81	0
23	MG	A	1742	1/1	0.46	0.42	49,49,49,49	0
23	MG	A	1614	1/1	0.46	0.53	97,97,97,97	0
23	MG	A	1603	1/1	0.48	0.47	68,68,68,68	0
23	MG	A	1701	1/1	0.48	0.55	92,92,92,92	0
23	MG	A	1702	1/1	0.49	0.34	96,96,96,96	0
23	MG	A	1713	1/1	0.51	1.00	84,84,84,84	0
23	MG	A	1629	1/1	0.52	0.84	80,80,80,80	0
23	MG	A	1693	1/1	0.53	0.32	117,117,117,117	0
23	MG	A	1752	1/1	0.54	0.27	76,76,76,76	0
23	MG	A	1639	1/1	0.55	0.69	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
23	MG	A	1734	1/1	0.56	1.11	68,68,68,68	0
23	MG	A	1710	1/1	0.58	0.39	46,46,46,46	0
23	MG	A	1628	1/1	0.58	0.48	60,60,60,60	0
23	MG	A	1699	1/1	0.59	1.40	78,78,78,78	0
23	MG	A	1650	1/1	0.60	0.37	70,70,70,70	0
23	MG	A	1665	1/1	0.60	0.51	60,60,60,60	0
23	MG	A	1696	1/1	0.61	0.47	67,67,67,67	0
23	MG	A	1619	1/1	0.61	0.35	75,75,75,75	0
23	MG	A	1747	1/1	0.62	0.42	44,44,44,44	0
23	MG	A	1642	1/1	0.64	0.44	74,74,74,74	0
23	MG	A	1751	1/1	0.64	0.36	89,89,89,89	0
23	MG	A	1739	1/1	0.64	0.24	94,94,94,94	0
23	MG	A	1776	1/1	0.64	0.50	91,91,91,91	0
23	MG	A	1680	1/1	0.64	0.17	73,73,73,73	0
23	MG	A	1654	1/1	0.64	0.17	63,63,63,63	0
23	MG	A	1714	1/1	0.65	0.69	65,65,65,65	0
23	MG	A	1730	1/1	0.65	0.42	69,69,69,69	0
23	MG	A	1623	1/1	0.65	1.39	96,96,96,96	0
23	MG	A	1777	1/1	0.66	0.72	79,79,79,79	0
23	MG	A	1604	1/1	0.67	0.62	69,69,69,69	0
23	MG	A	1689	1/1	0.67	1.12	50,50,50,50	0
23	MG	A	1622	1/1	0.68	1.59	89,89,89,89	0
23	MG	A	1694	1/1	0.68	0.24	87,87,87,87	0
23	MG	A	1616	1/1	0.68	0.69	70,70,70,70	0
23	MG	A	1621	1/1	0.69	0.33	69,69,69,69	0
23	MG	A	1669	1/1	0.69	0.29	63,63,63,63	0
23	MG	A	1638	1/1	0.69	0.19	83,83,83,83	0
23	MG	A	1764	1/1	0.69	0.60	80,80,80,80	0
23	MG	A	1753	1/1	0.70	0.27	77,77,77,77	0
23	MG	A	1775	1/1	0.70	0.41	74,74,74,74	0
23	MG	A	1649	1/1	0.71	0.32	56,56,56,56	0
23	MG	A	1670	1/1	0.71	0.26	43,43,43,43	0
23	MG	A	1634	1/1	0.71	0.51	60,60,60,60	0
23	MG	A	1666	1/1	0.71	0.24	8,8,8,8	0
23	MG	B	301	1/1	0.71	0.20	108,108,108,108	0
23	MG	D	302	1/1	0.71	1.31	94,94,94,94	0
23	MG	A	1768	1/1	0.72	0.26	66,66,66,66	0
23	MG	A	1632	1/1	0.73	1.73	79,79,79,79	0
23	MG	A	1643	1/1	0.73	0.52	69,69,69,69	0
23	MG	A	1610	1/1	0.74	0.26	61,61,61,61	0
23	MG	A	1774	1/1	0.74	0.79	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
23	MG	A	1743	1/1	0.74	0.66	38,38,38,38	0
23	MG	A	1785	1/1	0.75	0.67	90,90,90,90	0
23	MG	A	1769	1/1	0.75	1.07	106,106,106,106	0
23	MG	A	1761	1/1	0.75	1.39	69,69,69,69	0
23	MG	A	1762	1/1	0.75	0.59	66,66,66,66	0
23	MG	A	1735	1/1	0.76	0.97	87,87,87,87	0
23	MG	A	1756	1/1	0.76	0.37	48,48,48,48	0
23	MG	A	1718	1/1	0.76	0.72	85,85,85,85	0
23	MG	A	1784	1/1	0.76	0.71	63,63,63,63	0
23	MG	A	1763	1/1	0.77	0.61	55,55,55,55	0
23	MG	A	1758	1/1	0.78	0.17	44,44,44,44	0
23	MG	A	1677	1/1	0.78	0.58	52,52,52,52	0
23	MG	A	1716	1/1	0.78	0.27	62,62,62,62	0
23	MG	A	1705	1/1	0.78	0.55	51,51,51,51	0
23	MG	A	1782	1/1	0.78	0.44	58,58,58,58	0
23	MG	A	1635	1/1	0.79	0.49	104,104,104,104	0
23	MG	A	1703	1/1	0.80	0.52	72,72,72,72	0
23	MG	A	1682	1/1	0.80	0.72	66,66,66,66	0
23	MG	A	1767	1/1	0.80	0.61	42,42,42,42	0
23	MG	A	1726	1/1	0.80	0.62	40,40,40,40	0
23	MG	A	1671	1/1	0.80	0.46	33,33,33,33	0
23	MG	A	1789	1/1	0.80	0.68	50,50,50,50	0
23	MG	A	1760	1/1	0.80	0.70	72,72,72,72	0
23	MG	A	1637	1/1	0.80	1.21	48,48,48,48	0
23	MG	A	1609	1/1	0.80	0.39	45,45,45,45	0
23	MG	A	1725	1/1	0.81	0.37	83,83,83,83	0
23	MG	A	1772	1/1	0.81	0.34	94,94,94,94	0
23	MG	A	1746	1/1	0.81	0.52	44,44,44,44	0
23	MG	A	1754	1/1	0.81	0.80	41,41,41,41	0
23	MG	A	1681	1/1	0.81	0.19	74,74,74,74	0
23	MG	A	1602	1/1	0.81	0.12	74,74,74,74	0
23	MG	A	1733	1/1	0.81	0.34	56,56,56,56	0
23	MG	A	1745	1/1	0.82	0.27	61,61,61,61	0
23	MG	A	1783	1/1	0.82	0.38	61,61,61,61	0
23	MG	A	1679	1/1	0.82	0.64	37,37,37,37	0
23	MG	A	1740	1/1	0.82	0.46	66,66,66,66	0
23	MG	A	1607	1/1	0.83	0.39	68,68,68,68	0
23	MG	A	1712	1/1	0.83	0.74	37,37,37,37	0
23	MG	A	1620	1/1	0.83	0.74	62,62,62,62	0
23	MG	A	1630	1/1	0.83	1.00	85,85,85,85	0
23	MG	A	1744	1/1	0.83	0.55	36,36,36,36	0
23	MG	A	1781	1/1	0.83	0.75	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
23	MG	A	1738	1/1	0.83	0.85	62,62,62,62	0
23	MG	A	1686	1/1	0.84	0.77	68,68,68,68	0
23	MG	A	1641	1/1	0.85	0.95	33,33,33,33	0
23	MG	A	1645	1/1	0.85	1.12	54,54,54,54	0
23	MG	A	1608	1/1	0.85	0.64	94,94,94,94	0
23	MG	A	1684	1/1	0.85	0.34	49,49,49,49	0
23	MG	A	1721	1/1	0.85	0.41	38,38,38,38	0
24	ZN	D	301	1/1	0.85	0.37	72,72,72,72	0
23	MG	A	1786	1/1	0.86	0.39	56,56,56,56	0
23	MG	A	1640	1/1	0.86	0.43	59,59,59,59	0
23	MG	A	1709	1/1	0.86	0.49	32,32,32,32	0
23	MG	A	1674	1/1	0.86	1.15	56,56,56,56	0
23	MG	A	1695	1/1	0.86	0.39	67,67,67,67	0
23	MG	A	1690	1/1	0.86	0.38	81,81,81,81	0
23	MG	A	1719	1/1	0.87	1.02	76,76,76,76	0
23	MG	A	1655	1/1	0.87	0.52	57,57,57,57	0
23	MG	A	1771	1/1	0.87	0.40	51,51,51,51	0
23	MG	A	1731	1/1	0.87	0.20	76,76,76,76	0
23	MG	A	1613	1/1	0.87	0.40	95,95,95,95	0
23	MG	A	1749	1/1	0.88	0.47	41,41,41,41	0
23	MG	A	1659	1/1	0.88	0.70	32,32,32,32	0
23	MG	A	1765	1/1	0.88	0.35	48,48,48,48	0
23	MG	A	1631	1/1	0.89	0.33	57,57,57,57	0
23	MG	A	1778	1/1	0.89	0.38	64,64,64,64	0
23	MG	A	1678	1/1	0.89	0.98	40,40,40,40	0
23	MG	A	1606	1/1	0.89	0.72	49,49,49,49	0
23	MG	A	1700	1/1	0.89	0.15	70,70,70,70	0
23	MG	A	1737	1/1	0.89	0.23	60,60,60,60	0
23	MG	A	1653	1/1	0.89	0.46	24,24,24,24	0
23	MG	A	1723	1/1	0.90	0.33	37,37,37,37	0
23	MG	A	1667	1/1	0.90	0.90	54,54,54,54	0
23	MG	A	1773	1/1	0.90	0.34	31,31,31,31	0
23	MG	A	1715	1/1	0.90	0.46	37,37,37,37	0
23	MG	A	1697	1/1	0.90	0.25	83,83,83,83	0
23	MG	A	1711	1/1	0.90	0.29	31,31,31,31	0
23	MG	A	1676	1/1	0.90	0.70	25,25,25,25	0
23	MG	A	1720	1/1	0.90	0.61	40,40,40,40	0
23	MG	A	1618	1/1	0.90	0.62	59,59,59,59	0
23	MG	A	1736	1/1	0.90	0.18	39,39,39,39	0
23	MG	A	1770	1/1	0.91	0.42	52,52,52,52	0
23	MG	A	1759	1/1	0.91	0.42	53,53,53,53	0
23	MG	A	1636	1/1	0.91	0.52	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
23	MG	A	1766	1/1	0.91	0.32	44,44,44,44	0
23	MG	A	1617	1/1	0.91	0.69	67,67,67,67	0
23	MG	A	1706	1/1	0.91	0.21	77,77,77,77	0
23	MG	A	1729	1/1	0.91	0.35	71,71,71,71	0
23	MG	A	1601	1/1	0.92	0.12	67,67,67,67	0
23	MG	A	1633	1/1	0.92	0.20	74,74,74,74	0
23	MG	A	1675	1/1	0.92	1.01	58,58,58,58	0
23	MG	A	1750	1/1	0.92	0.25	51,51,51,51	0
23	MG	A	1626	1/1	0.92	0.45	98,98,98,98	0
23	MG	A	1691	1/1	0.92	0.26	36,36,36,36	0
23	MG	A	1615	1/1	0.92	0.47	24,24,24,24	0
23	MG	A	1657	1/1	0.93	0.32	36,36,36,36	0
23	MG	A	1698	1/1	0.93	0.34	33,33,33,33	0
23	MG	A	1612	1/1	0.93	0.68	35,35,35,35	0
23	MG	A	1780	1/1	0.93	0.24	48,48,48,48	0
23	MG	E	201	1/1	0.93	0.68	38,38,38,38	0
23	MG	A	1673	1/1	0.93	0.48	25,25,25,25	0
23	MG	A	1658	1/1	0.94	0.36	20,20,20,20	0
23	MG	A	1707	1/1	0.94	0.11	43,43,43,43	0
23	MG	A	1648	1/1	0.94	0.41	25,25,25,25	0
23	MG	A	1683	1/1	0.94	0.51	38,38,38,38	0
23	MG	A	1651	1/1	0.94	0.88	55,55,55,55	0
23	MG	A	1704	1/1	0.94	0.30	68,68,68,68	0
23	MG	A	1627	1/1	0.94	0.55	53,53,53,53	0
23	MG	A	1625	1/1	0.95	0.21	71,71,71,71	0
23	MG	A	1663	1/1	0.95	0.15	42,42,42,42	0
23	MG	A	1717	1/1	0.95	0.30	34,34,34,34	0
23	MG	A	1727	1/1	0.95	0.58	40,40,40,40	0
23	MG	A	1728	1/1	0.95	0.45	59,59,59,59	0
23	MG	A	1788	1/1	0.95	0.14	33,33,33,33	0
23	MG	A	1664	1/1	0.95	0.31	58,58,58,58	0
23	MG	A	1611	1/1	0.95	0.52	20,20,20,20	0
23	MG	A	1672	1/1	0.95	0.38	21,21,21,21	0
23	MG	A	1732	1/1	0.95	0.55	52,52,52,52	0
23	MG	A	1646	1/1	0.95	0.27	22,22,22,22	0
23	MG	A	1722	1/1	0.95	0.16	23,23,23,23	0
24	ZN	N	101	1/1	0.95	0.21	123,123,123,123	0
23	MG	A	1668	1/1	0.96	0.59	36,36,36,36	0
23	MG	A	1692	1/1	0.96	0.43	50,50,50,50	0
23	MG	A	1685	1/1	0.96	0.33	38,38,38,38	0
23	MG	A	1791	1/1	0.96	0.58	41,41,41,41	0
23	MG	A	1660	1/1	0.96	0.49	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
23	MG	A	1688	1/1	0.96	0.29	65,65,65,65	0
23	MG	A	1656	1/1	0.96	0.36	88,88,88,88	0
23	MG	A	1647	1/1	0.96	0.38	23,23,23,23	0
23	MG	A	1787	1/1	0.96	0.14	34,34,34,34	0
23	MG	A	1644	1/1	0.97	0.26	54,54,54,54	0
23	MG	A	1652	1/1	0.97	0.59	17,17,17,17	0
23	MG	A	1757	1/1	0.97	0.50	24,24,24,24	0
23	MG	A	1741	1/1	0.97	0.07	32,32,32,32	0
23	MG	A	1708	1/1	0.97	0.26	19,19,19,19	0
23	MG	A	1662	1/1	0.97	0.13	64,64,64,64	0
23	MG	A	1755	1/1	0.98	0.37	50,50,50,50	0
23	MG	A	1661	1/1	0.98	0.64	33,33,33,33	0
23	MG	A	1724	1/1	0.98	0.39	47,47,47,47	0
23	MG	A	1687	1/1	0.99	0.27	34,34,34,34	0

6.5 Other polymers (i)

There are no such residues in this entry.