Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 08:04 PM GMT

PDB ID	:	1IBM
Title	:	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH A MESSENGER RNA FRAGMENT AND COGNATE TRANSFER RNA ANTICODON STEM-LOOP BOUND AT THE A SITE
Authors	:	Ogle, J.M.; Brodersen, D.E.; Clemons Jr., W.M.; Tarry, M.J.; Carter, A.P.; Ramakrishnan, V.
Deposited on	:	2001-03-28
Resolution	:	3.31 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

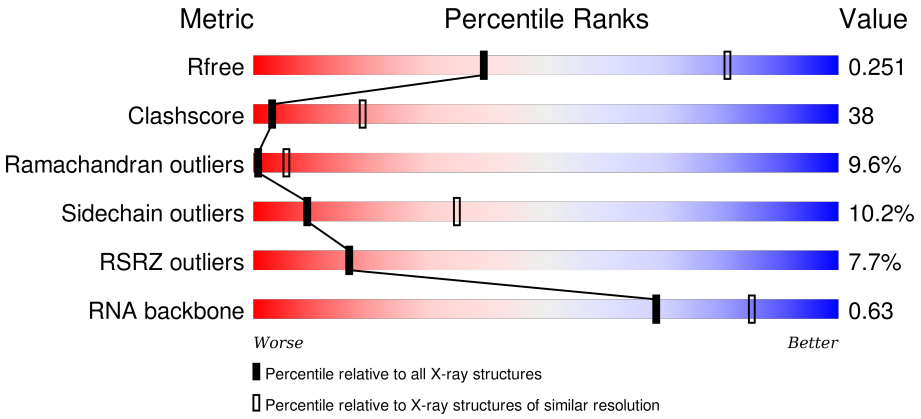
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.31 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1198 (3.40-3.24)
Clashscore	102246	1280 (3.40-3.24)
Ramachandran outliers	100387	1260 (3.40-3.24)
Sidechain outliers	100360	1259 (3.40-3.24)
RSRZ outliers	91569	1203 (3.40-3.24)
RNA backbone	2183	1002 (3.84-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1522	4%, 27%, 59%, 11%, • •
2	X	6	67%, 67%, 33%
3	Y	15	20%, 33%, 27%, 7%, 7%, 27%
4	Z	4	25%, 50%, 25%, 25%

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Mol	Chain	Length	Quality of chain
5	B	256	6% 18% 57% 14% 9%
6	C	239	3% 20% 50% 14% 14%
7	D	209	8% 36% 51% 11%
8	E	162	10% 28% 51% 12% 7%
9	F	101	2% 38% 61%
10	G	156	2% 32% 58% 9%
11	H	138	2% 42% 48% 8%
12	I	128	8% 18% 66% 15%
13	J	105	14% 15% 59% 17% 7%
14	K	129	7% 28% 48% 14% 8%
15	L	135	13% 36% 43% 13% 8%
16	M	126	7% 20% 58% 16% 6%
17	N	61	46% 26% 56% 15%
18	O	89	4% 36% 52% 10%
19	P	88	18% 38% 49% 8% 6%
20	Q	105	16% 32% 54% 12%
21	R	88	3% 18% 58% 7% 17%
22	S	93	20% 20% 51% 18% 6%
23	T	106	14% 31% 52% 9% 7%
24	V	26	35% 35% 58% 8%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1561	-	-	-	X
25	MG	A	1574	-	-	-	X
25	MG	A	1593	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1611	-	-	-	X
25	MG	A	1628	-	-	-	X
25	MG	A	1646	-	-	-	X

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 52160 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	1507	32391	14418	6002	10465	1506	0	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are 3 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	S	87	Total	C	N	O	S	0	0	0
			697	444	130	121	2			

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

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

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

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

- Molecule 25 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

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

- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

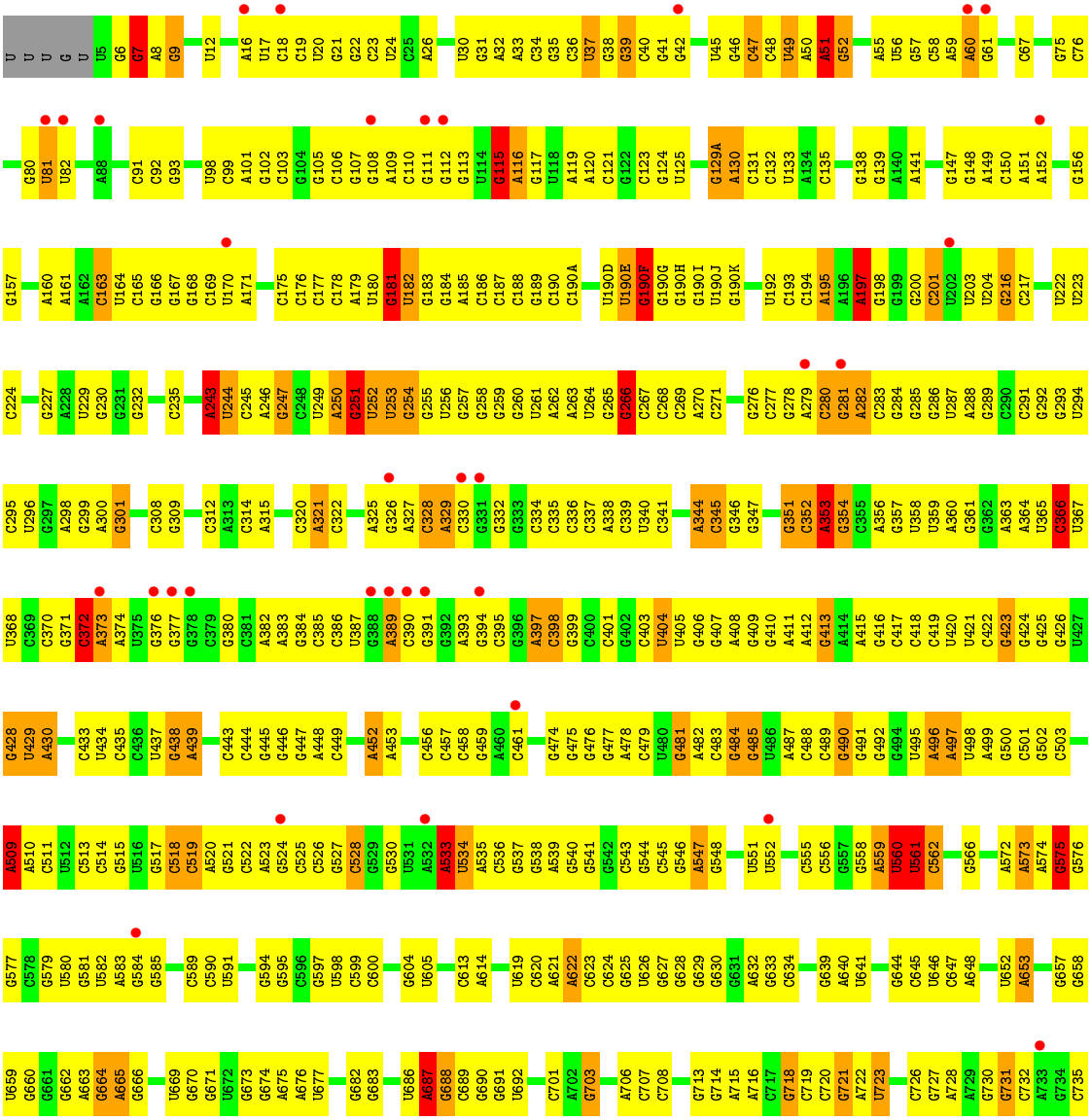
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	D	1	Total Zn 1 1	0	0
26	N	1	Total Zn 1 1	0	0

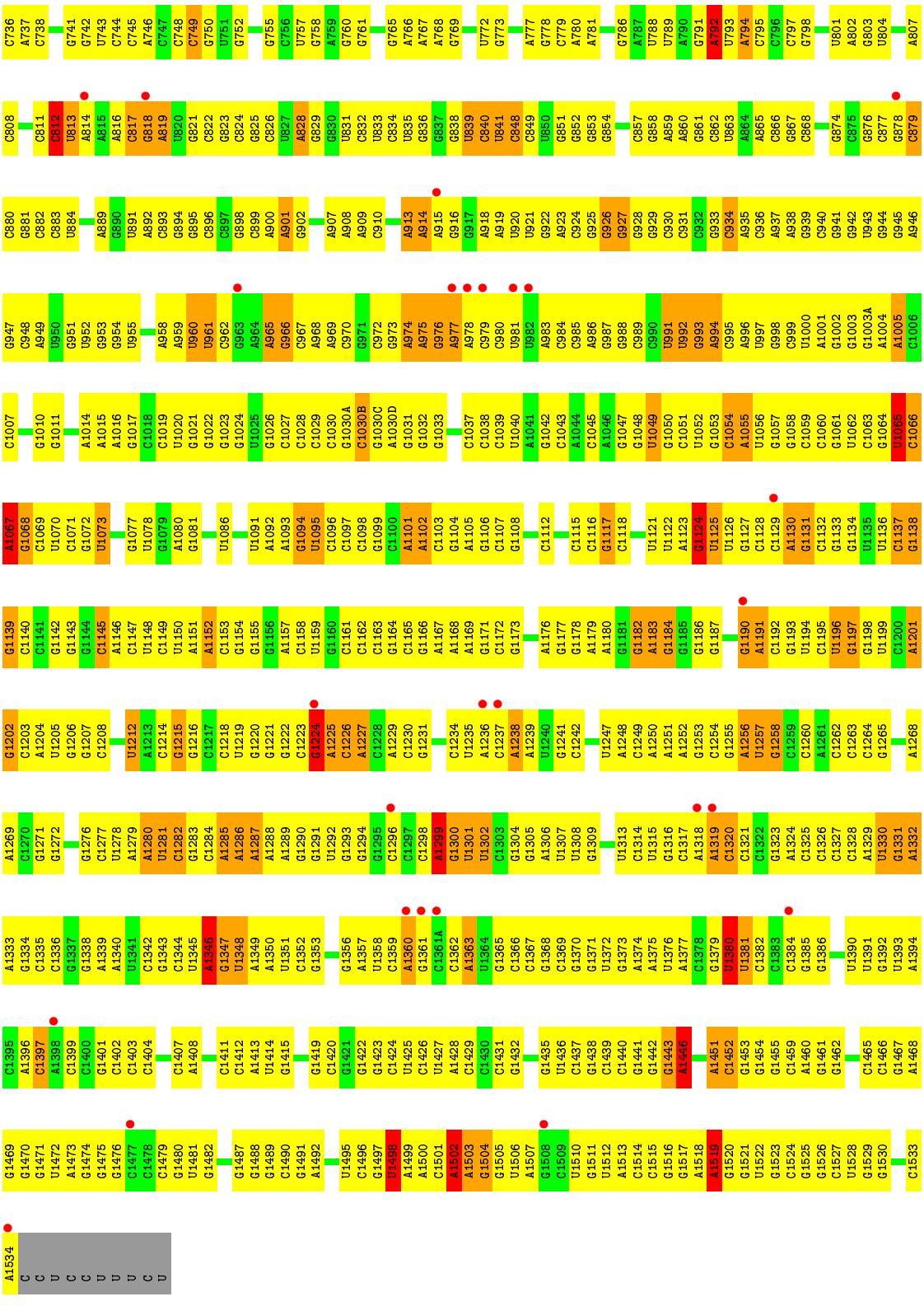
3 Residue-property plots (i)

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

- Molecule 1: 16S RIBOSOMAL RNA

Chain A: 



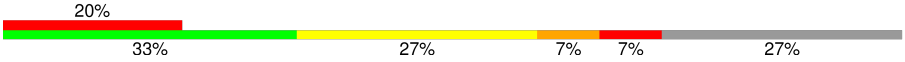


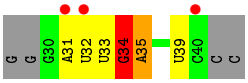
• Molecule 2: P-SITE MESSENGER RNA FRAGMENT

Chain X:

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

Chain Y:



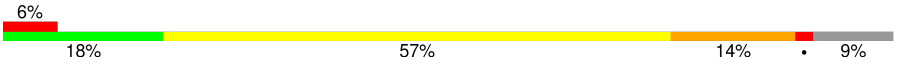


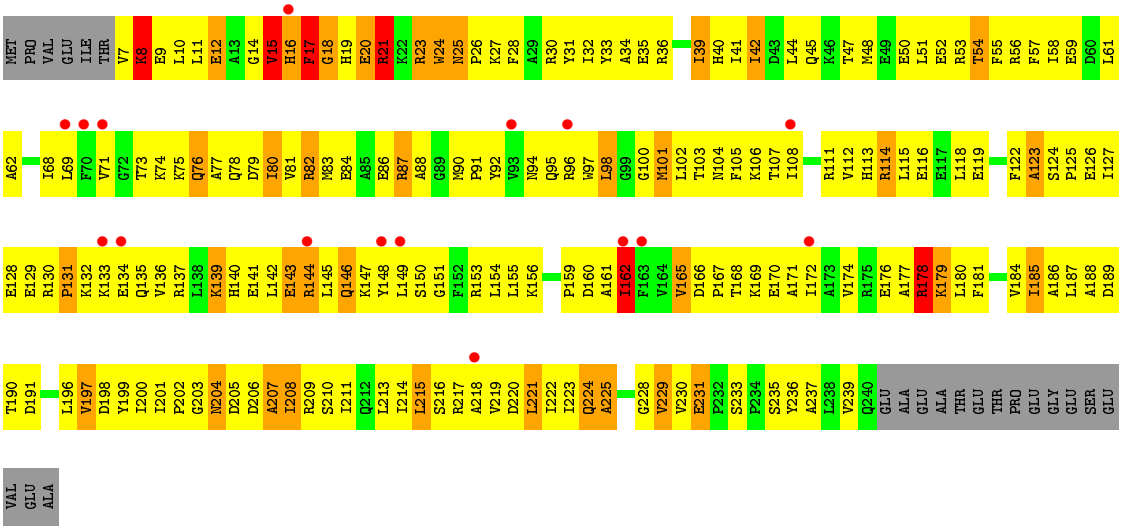
• Molecule 4: A-SITE MESSENGER RNA FRAGMENT

Chain Z:

• Molecule 5: 30S RIBOSOMAL PROTEIN S2

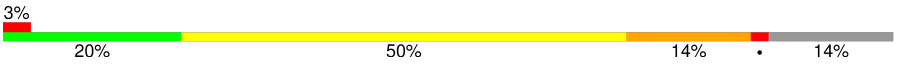
Chain B:

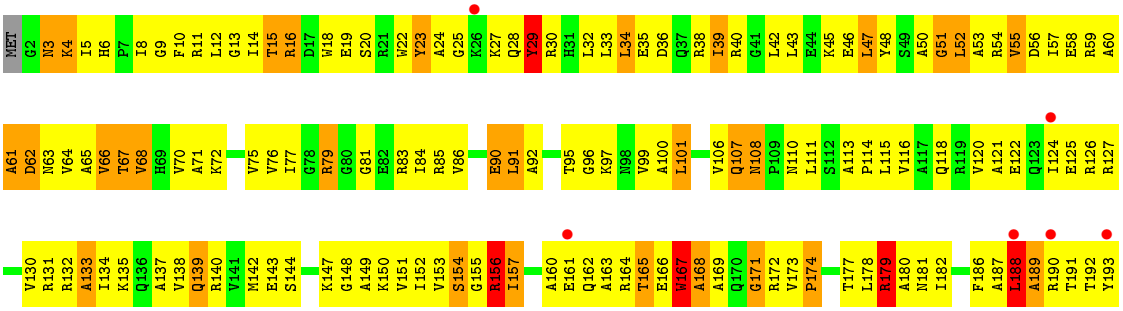


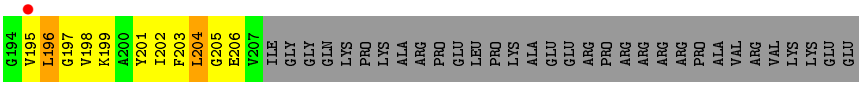


• Molecule 6: 30S RIBOSOMAL PROTEIN S3

Chain C:

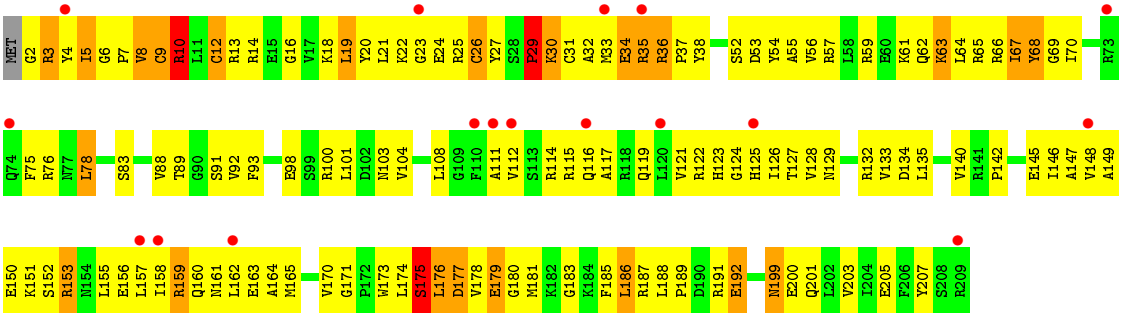






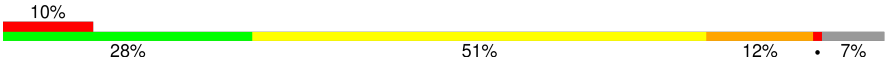
- Molecule 7: 30S RIBOSOMAL PROTEIN S4

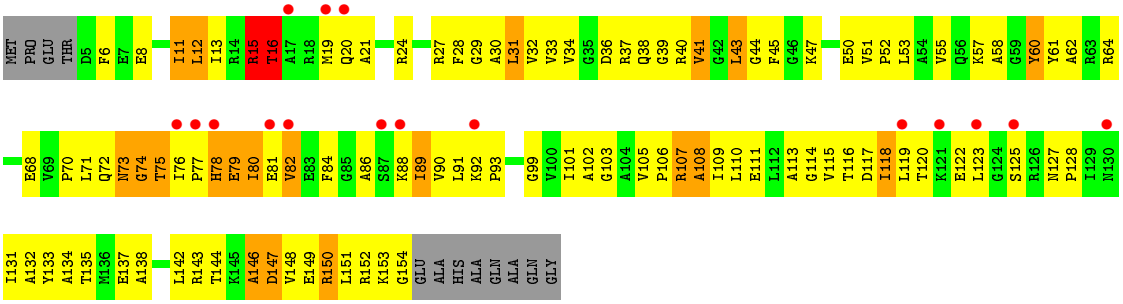
Chain D:



- Molecule 8: 30S RIBOSOMAL PROTEIN S5

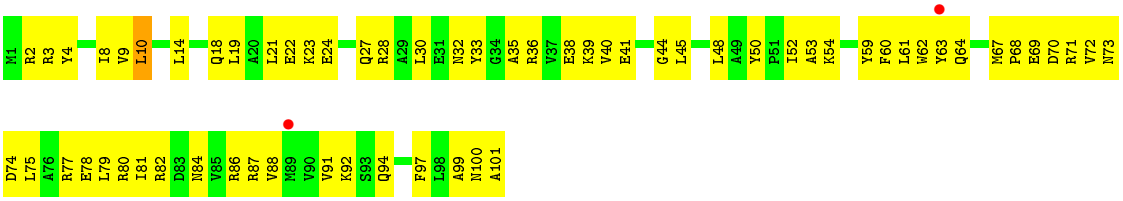
Chain E:





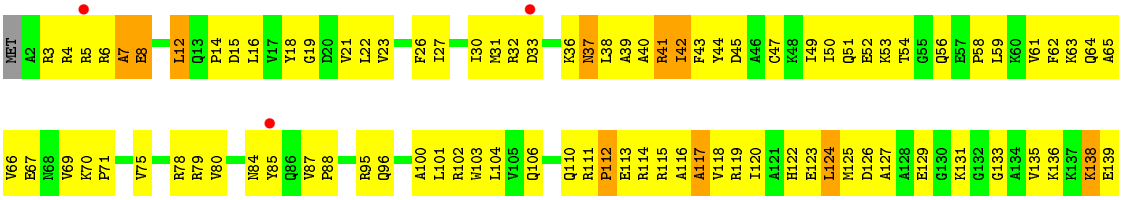
- Molecule 9: 30S RIBOSOMAL PROTEIN S6

Chain F:

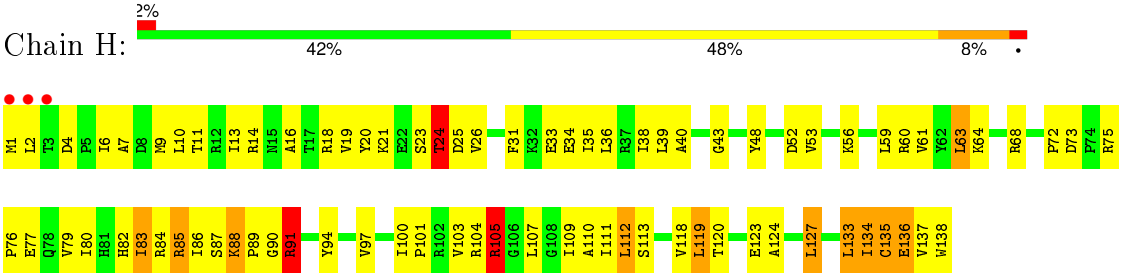


- Molecule 10: 30S RIBOSOMAL PROTEIN S7

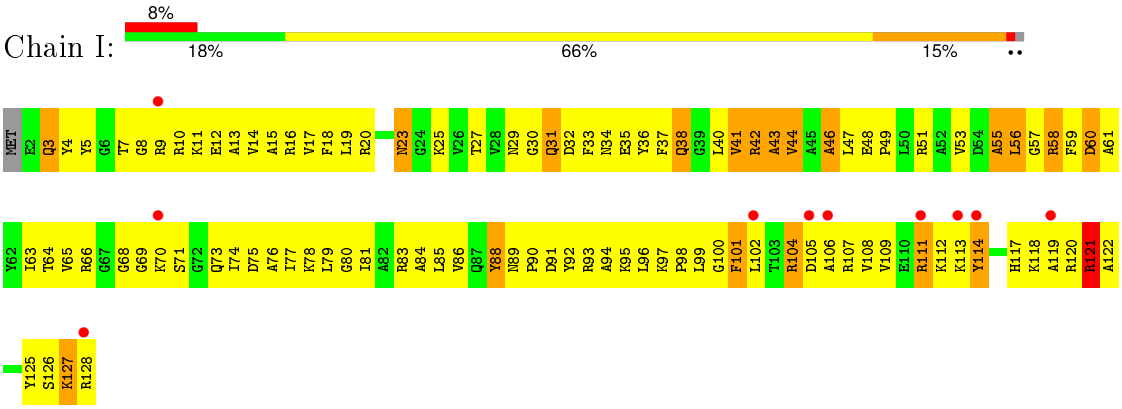
Chain G:



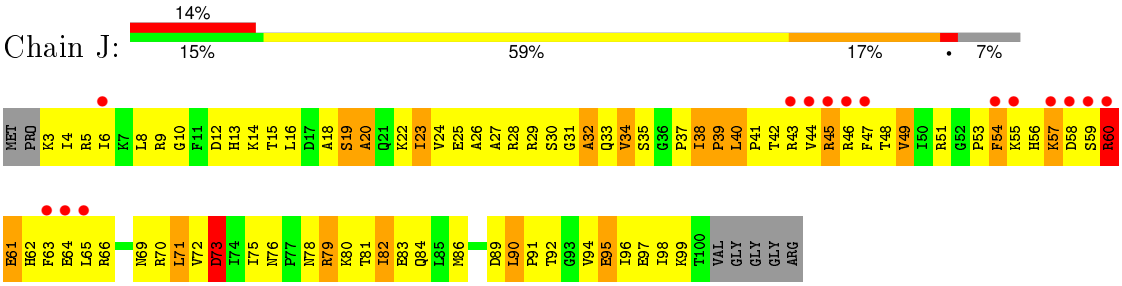
- Molecule 11: 30S RIBOSOMAL PROTEIN S8



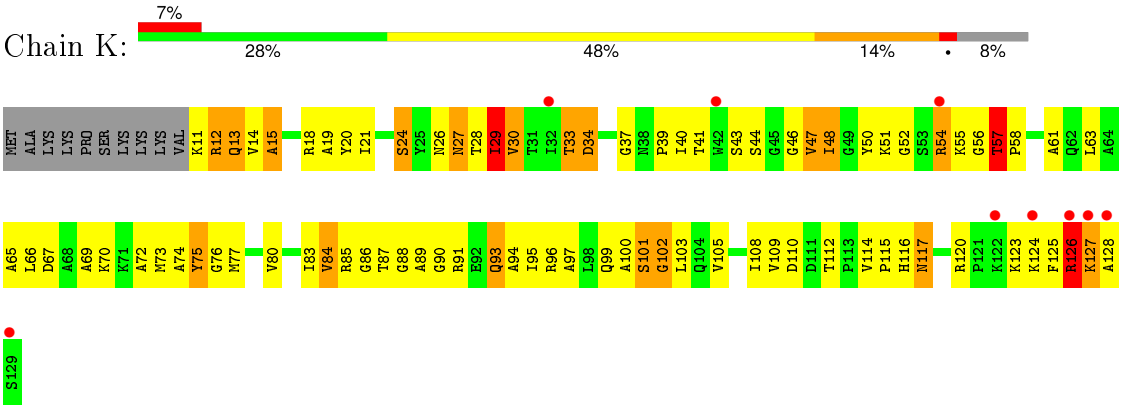
- Molecule 12: 30S RIBOSOMAL PROTEIN S9



- Molecule 13: 30S RIBOSOMAL PROTEIN S10

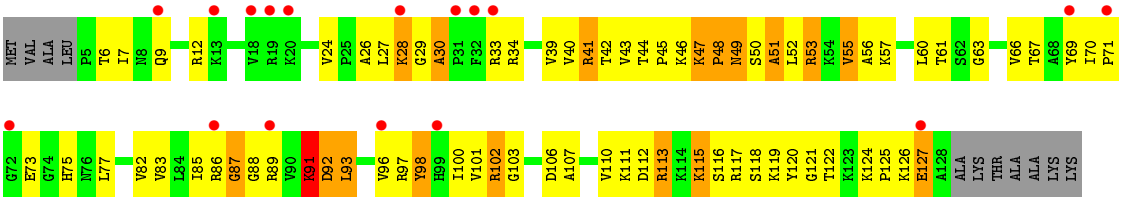


- Molecule 14: 30S RIBOSOMAL PROTEIN S11



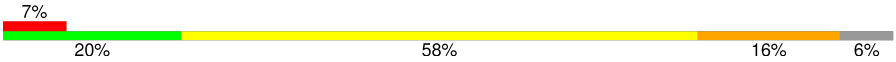
• Molecule 15: 30S RIBOSOMAL PROTEIN S12

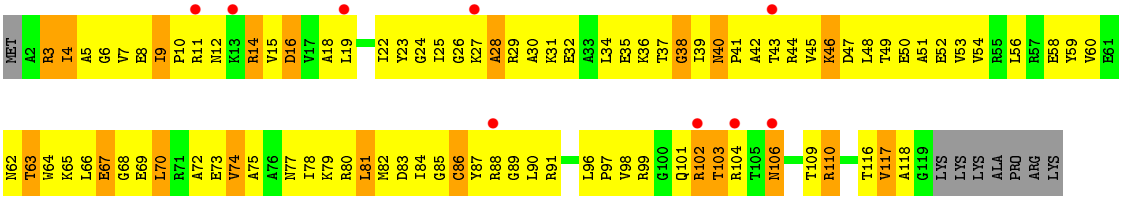
Chain L:



• Molecule 16: 30S RIBOSOMAL PROTEIN S13

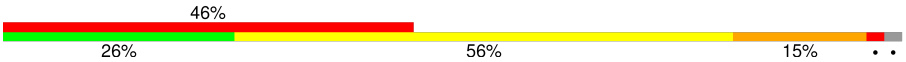
Chain M:

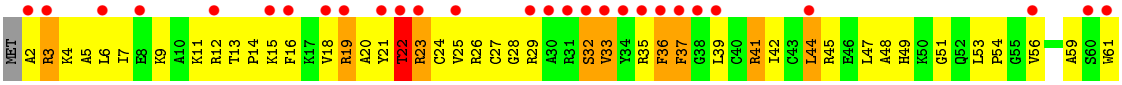




• Molecule 17: 30S RIBOSOMAL PROTEIN S14

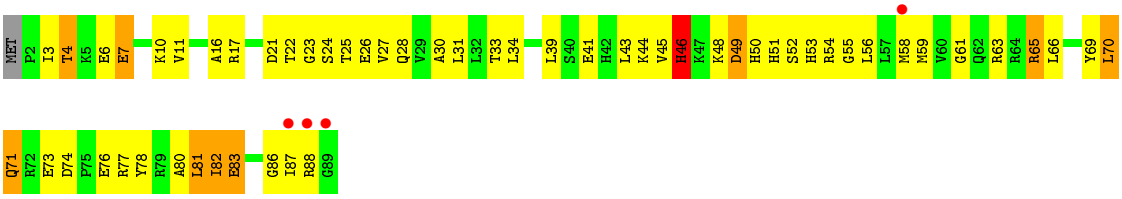
Chain N:





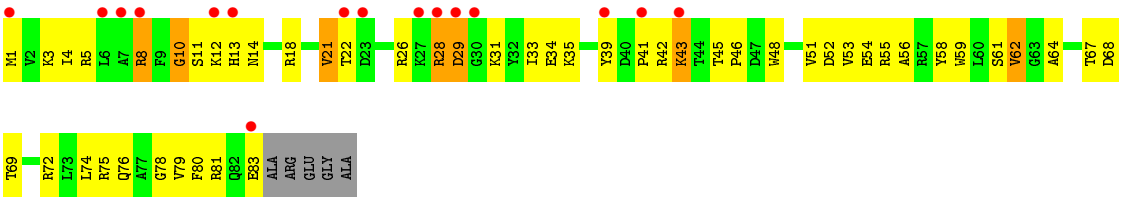
• Molecule 18: 30S RIBOSOMAL PROTEIN S15

Chain O:

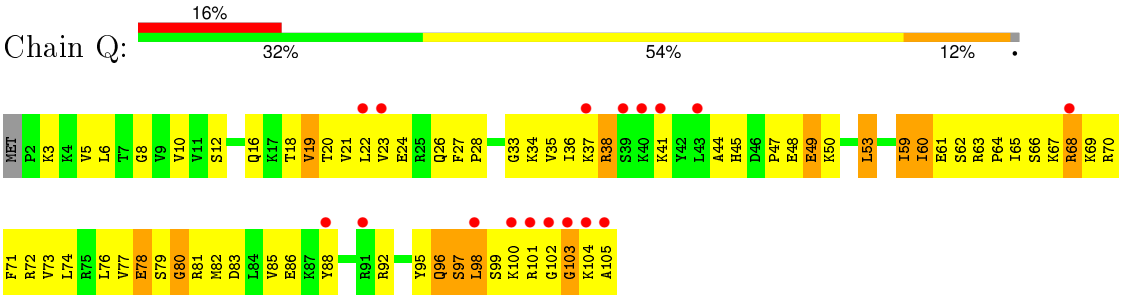


• Molecule 19: 30S RIBOSOMAL PROTEIN S16

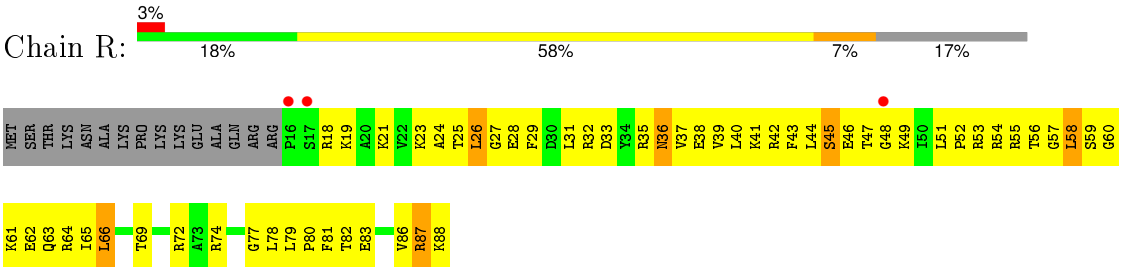
Chain P:



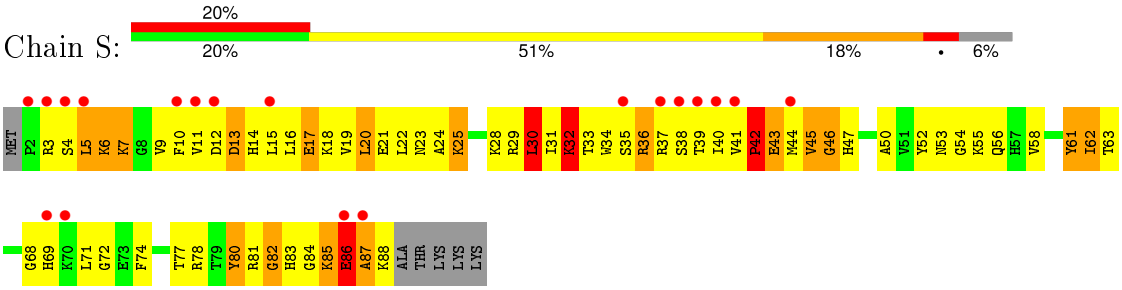
• Molecule 20: 30S RIBOSOMAL PROTEIN S17



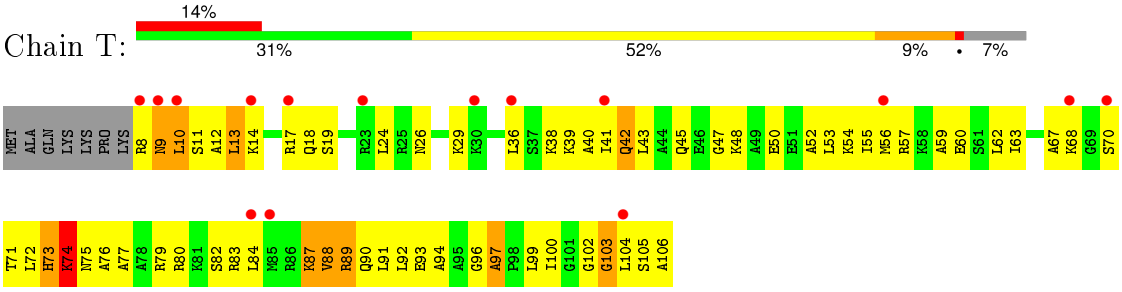
- Molecule 21: 30S RIBOSOMAL PROTEIN S18



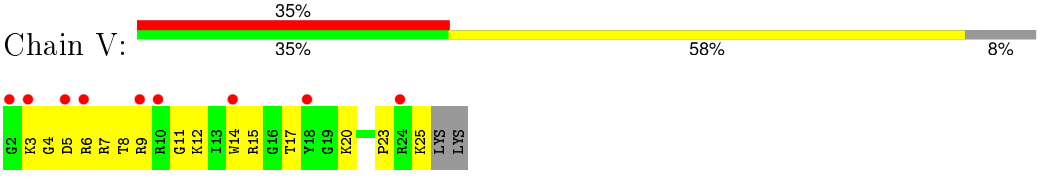
- Molecule 22: 30S RIBOSOMAL PROTEIN S19



- Molecule 23: 30S RIBOSOMAL PROTEIN S20



- Molecule 24: 30S RIBOSOMAL PROTEIN THX



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	401.57Å 401.57Å 176.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	316.23 – 3.31 200.79 – 3.31	Depositor EDS
% Data completeness (in resolution range)	90.6 (316.23-3.31) 90.6 (200.79-3.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	3.34 (at 3.33Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.231 , 0.286 0.209 , 0.251	Depositor DCC
R_{free} test set	9648 reflections (5.29%)	DCC
Wilson B-factor (Å^2)	76.8	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.25 , 83.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	1 of 191960 reflections (0.001%)	Xtriage
F_o,F_c correlation	0.73	EDS
Total number of atoms	52160	wwPDB-VP
Average B, all atoms (Å^2)	68.0	wwPDB-VP

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

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.57	0/36259	0.74	36/56593 (0.1%)
2	X	0.58	0/128	0.76	0/196
3	Y	0.33	0/261	0.76	1/405 (0.2%)
4	Z	0.46	0/84	0.81	0/128
5	B	0.34	0/1935	0.66	0/2609
6	C	0.36	0/1636	0.65	0/2205
7	D	0.39	0/1733	0.65	0/2318
8	E	0.46	0/1162	0.79	0/1564
9	F	0.32	0/856	0.61	0/1154
10	G	0.34	0/1276	0.61	0/1709
11	H	0.45	0/1136	0.75	0/1527
12	I	0.34	0/1029	0.67	0/1378
13	J	0.35	0/805	0.67	1/1082 (0.1%)
14	K	0.40	0/900	0.67	0/1213
15	L	0.43	0/986	0.74	0/1320
16	M	0.36	0/947	0.67	0/1270
17	N	0.41	0/501	0.76	0/664
18	O	0.39	0/745	0.62	0/992
19	P	0.46	0/716	0.77	1/963 (0.1%)
20	Q	0.48	0/870	0.76	0/1159
21	R	0.37	0/603	0.67	0/799
22	S	0.35	0/712	0.71	1/956 (0.1%)
23	T	0.39	0/765	0.71	0/1007
24	V	0.45	0/212	0.67	0/277
All	All	0.51	0/56257	0.73	40/83488 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	29

There are no bond length outliers.

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	181	G	C2'-C3'-O3'	9.30	129.96	109.50
1	A	559	A	C2'-C3'-O3'	8.99	129.29	109.50
1	A	575	G	C2'-C3'-O3'	8.98	129.25	109.50
1	A	366	C	C2'-C3'-O3'	8.93	129.15	109.50
1	A	243	A	C2'-C3'-O3'	8.21	127.56	109.50
1	A	1498	U	C2'-C3'-O3'	8.15	127.43	109.50
1	A	792	A	C2'-C3'-O3'	7.90	126.88	109.50
1	A	266	G	C2'-C3'-O3'	7.52	126.04	109.50
1	A	1299	A	N9-C1'-C2'	7.41	123.64	114.00
1	A	1346	A	C2'-C3'-O3'	7.29	125.54	109.50
1	A	60	A	C2'-C3'-O3'	7.29	125.53	109.50
1	A	560	U	C2'-C3'-O3'	7.23	125.41	109.50
1	A	687	A	C2'-C3'-O3'	6.94	124.80	113.70
1	A	115	G	C2'-C3'-O3'	6.62	124.29	113.70
1	A	812	C	C2'-C3'-O3'	6.37	123.89	113.70
1	A	965	A	C2'-C3'-O3'	6.35	123.86	113.70
1	A	533	A	C2'-C3'-O3'	6.27	123.74	113.70
22	S	54	GLY	N-CA-C	-6.01	98.08	113.10
19	P	21	VAL	N-CA-C	-6.00	94.79	111.00
1	A	197	A	C2'-C3'-O3'	5.97	123.25	113.70
1	A	509	A	C2'-C3'-O3'	5.86	123.08	113.70
1	A	1224	G	N9-C1'-C2'	5.84	121.59	114.00
1	A	1502	A	N9-C1'-C2'	5.80	121.54	114.00
1	A	1380	U	C2'-C3'-O3'	5.78	122.94	113.70
1	A	372	C	C2'-C3'-O3'	5.75	122.89	113.70
1	A	389	A	C5'-C4'-C3'	5.65	125.04	116.00
1	A	481	G	C5'-C4'-C3'	-5.59	107.06	116.00
1	A	484	G	C2'-C3'-O3'	5.58	122.62	113.70
1	A	533	A	N9-C1'-C2'	5.54	121.21	114.00
3	Y	34	G	C2'-C3'-O3'	5.41	122.35	113.70
1	A	353	A	C5'-C4'-O4'	-5.33	102.70	109.10
1	A	1124	G	N9-C1'-C2'	5.23	120.80	114.00
1	A	51	A	N9-C1'-C2'	5.19	120.75	114.00
13	J	60	ARG	N-CA-C	5.13	124.86	111.00
1	A	1380	U	N1-C1'-C2'	5.13	120.67	114.00
1	A	1065	U	C1'-O4'-C4'	-5.11	105.81	109.90
1	A	7	G	C2'-C3'-O3'	5.09	121.84	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	560	U	OP2-P-O3'	5.05	116.31	105.20
1	A	622	A	N9-C1'-C2'	-5.04	106.45	112.00
1	A	1067	A	C2'-C3'-O3'	5.00	121.70	113.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	366	C	C3'

All (29) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1073	U	Sidechain
1	A	1299	A	Sidechain
1	A	1330	U	Sidechain
1	A	1360	A	Sidechain
1	A	1396	A	Sidechain
1	A	1446	A	Sidechain
1	A	1502	A	Sidechain
1	A	1519	A	Sidechain
1	A	190(F)	G	Sidechain
1	A	197	A	Sidechain
1	A	24	U	Sidechain
1	A	249	U	Sidechain
1	A	251	G	Sidechain
1	A	253	U	Sidechain
1	A	254	G	Sidechain
1	A	37	U	Sidechain
1	A	380	G	Sidechain
1	A	404	U	Sidechain
1	A	490	G	Sidechain
1	A	528	C	Sidechain
1	A	561	U	Sidechain
1	A	575	G	Sidechain
1	A	641	U	Sidechain
1	A	664	G	Sidechain
1	A	727	G	Sidechain
1	A	879	C	Sidechain
1	A	898	G	Sidechain
1	A	901	A	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32391	0	16349	1272	0
2	X	117	0	64	3	0
3	Y	233	0	120	11	0
4	Z	77	0	42	4	0
5	B	1900	0	1951	279	0
6	C	1612	0	1677	245	0
7	D	1703	0	1764	163	0
8	E	1146	0	1207	124	0
9	F	843	0	857	84	0
10	G	1257	0	1296	124	0
11	H	1116	0	1177	103	0
12	I	1011	0	1043	158	0
13	J	792	0	835	145	0
14	K	885	0	904	88	0
15	L	970	0	1057	119	0
16	M	937	0	995	121	0
17	N	492	0	529	77	0
18	O	734	0	771	60	0
19	P	700	0	720	54	0
20	Q	857	0	930	99	0
21	R	597	0	668	81	0
22	S	697	0	723	120	0
23	T	763	0	861	82	0
24	V	208	0	221	13	0
25	A	118	0	0	0	0
25	D	1	0	0	0	0
25	H	1	0	0	0	0
26	D	1	0	0	0	0
26	N	1	0	0	0	0
All	All	52160	0	36761	3359	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 38.

All (3359) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1397:C:OP2	8:E:24:ARG:NH2	1.62	1.27
5:B:84:GLU:HB3	5:B:219:VAL:HG21	1.25	1.18
6:C:14:ILE:HG22	6:C:15:THR:H	1.12	1.15
1:A:1443:G:H5"	1:A:1446:A:H5'	1.31	1.11
7:D:36:ARG:H	7:D:37:PRO:HD3	0.95	1.11
13:J:45:ARG:HB3	13:J:45:ARG:HH11	0.96	1.10
23:T:74:LYS:HG2	23:T:75:ASN:H	1.01	1.09
8:E:80:ILE:CD1	8:E:91:LEU:HB2	1.84	1.06
8:E:80:ILE:HD11	8:E:91:LEU:HB2	1.38	1.05
7:D:36:ARG:H	7:D:37:PRO:CD	1.70	1.04
1:A:1116:C:H2'	1:A:1117:G:H5"	1.39	1.04
19:P:22:THR:HA	19:P:33:ILE:HD13	1.37	1.04
17:N:24:CYS:HB3	17:N:28:GLY:H	1.20	1.04
10:G:5:ARG:HG3	10:G:6:ARG:H	1.21	1.04
15:L:41:ARG:HG2	15:L:42:THR:H	1.18	1.04
12:I:65:VAL:HG11	12:I:73:GLN:HB3	1.37	1.04
22:S:40:ILE:HD13	22:S:62:ILE:HD13	1.40	1.03
1:A:243:A:H4'	1:A:244:U:H5'	1.41	1.03
15:L:46:LYS:HG2	15:L:47:LYS:H	1.18	1.03
1:A:1004:A:H2'	1:A:1005:A:H5'	1.38	1.03
15:L:93:LEU:HD23	15:L:93:LEU:H	1.25	1.02
16:M:78:ILE:HA	16:M:81:LEU:HD21	1.42	1.02
12:I:93:ARG:HB3	12:I:97:LYS:HE3	1.39	1.02
13:J:45:ARG:HB3	13:J:45:ARG:NH1	1.74	1.01
1:A:452:A:HO2'	1:A:453:A:H8	1.03	1.01
14:K:54:ARG:HB3	14:K:54:ARG:HH11	1.23	1.01
16:M:49:THR:HG22	16:M:51:ALA:H	1.24	1.00
22:S:55:LYS:HG2	22:S:56:GLN:HE21	1.24	0.99
6:C:8:ILE:HG23	6:C:16:ARG:HG2	1.46	0.98
7:D:36:ARG:N	7:D:37:PRO:HD3	1.79	0.97
16:M:81:LEU:HD23	16:M:81:LEU:H	1.28	0.97
6:C:179:ARG:HD3	6:C:206:GLU:HB3	1.46	0.97
19:P:58:TYR:O	19:P:61:SER:HB3	1.63	0.96
13:J:90:LEU:H	13:J:91:PRO:HD2	1.29	0.96
16:M:10:PRO:HB2	16:M:18:ALA:HB1	1.48	0.95
18:O:70:LEU:HD12	18:O:78:TYR:HB2	1.48	0.95
5:B:16:HIS:NE2	5:B:214:ILE:HG12	1.81	0.95
1:A:1305:G:HO2'	1:A:1306:A:H8	1.10	0.95
20:Q:67:LYS:HA	20:Q:70:ARG:HH12	1.32	0.94
1:A:1443:G:H5"	1:A:1446:A:C5'	1.96	0.94
24:V:6:ARG:HB3	24:V:15:ARG:HH21	1.29	0.94
18:O:26:GLU:OE1	18:O:77:ARG:HD2	1.68	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:T:74:LYS:CG	23:T:75:ASN:H	1.80	0.94
7:D:151:LYS:HD2	7:D:151:LYS:H	1.31	0.93
23:T:74:LYS:HG2	23:T:75:ASN:N	1.84	0.93
1:A:1502:A:H2	1:A:1505:G:H1	1.12	0.93
7:D:7:PRO:HG2	7:D:10:ARG:HD2	1.49	0.93
6:C:179:ARG:HG2	6:C:179:ARG:O	1.68	0.93
5:B:75:LYS:HA	5:B:78:GLN:HG3	1.51	0.93
1:A:1139:G:H4'	1:A:1140:C:H5'	1.50	0.93
8:E:110:LEU:HD13	8:E:118:ILE:HD12	1.49	0.92
12:I:8:GLY:HA2	12:I:79:LEU:HD12	1.51	0.92
15:L:91:LYS:HA	15:L:91:LYS:HE3	1.52	0.92
3:Y:34:G:H2'	3:Y:35:A:H8	1.31	0.92
1:A:1305:G:O2'	1:A:1306:A:H8	1.51	0.92
14:K:40:ILE:HG22	14:K:41:THR:HG23	1.49	0.92
15:L:93:LEU:HD12	15:L:96:VAL:HG21	1.50	0.91
22:S:85:LYS:HE3	22:S:85:LYS:H	1.36	0.91
13:J:79:ARG:HH11	13:J:79:ARG:HA	1.33	0.91
11:H:113:SER:HB2	11:H:134:ILE:HD11	1.53	0.91
6:C:188:LEU:HD13	6:C:189:ALA:H	1.36	0.91
1:A:939:G:H5"	10:G:102:ARG:HH22	1.36	0.91
1:A:1116:C:C2'	1:A:1117:G:H5"	2.00	0.91
17:N:36:PHE:O	17:N:36:PHE:HD1	1.52	0.91
1:A:1368:G:O2'	1:A:1369:C:H5'	1.71	0.91
1:A:382:A:H2'	1:A:383:A:C8	2.06	0.91
9:F:44:GLY:HA2	9:F:59:TYR:CE1	2.06	0.90
8:E:51:VAL:HB	8:E:52:PRO:HD3	1.50	0.90
7:D:175:SER:HB3	7:D:186:LEU:HD21	1.54	0.90
8:E:43:LEU:HD11	8:E:132:ALA:HB1	1.54	0.90
12:I:29:ASN:ND2	12:I:64:THR:HA	1.85	0.90
8:E:41:VAL:HG22	8:E:113:ALA:HA	1.53	0.89
1:A:967:C:H4'	12:I:128:ARG:HG3	1.54	0.89
23:T:57:ARG:HD2	23:T:102:GLY:HA3	1.53	0.89
7:D:29:PRO:O	7:D:30:LYS:HG3	1.73	0.89
18:O:16:ALA:HB1	18:O:21:ASP:HB3	1.51	0.89
3:Y:34:G:H2'	3:Y:35:A:C8	2.06	0.89
6:C:50:ALA:HB1	6:C:70:VAL:HG11	1.52	0.88
5:B:178:ARG:HH11	5:B:178:ARG:HG3	1.39	0.88
1:A:371:G:O2'	1:A:372:C:H5'	1.72	0.88
1:A:954:G:H21	1:A:1227:A:H62	1.21	0.88
13:J:32:ALA:HB2	13:J:76:ASN:HB2	1.56	0.88
12:I:17:VAL:HG21	12:I:80:GLY:HA3	1.56	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:G:H4'	1:A:439:A:OP1	1.74	0.87
5:B:80:ILE:HD11	5:B:208:ILE:HG12	1.53	0.87
1:A:1236:A:H4'	1:A:1304:G:H4'	1.57	0.87
5:B:77:ALA:HB2	5:B:211:ILE:HD13	1.57	0.87
1:A:1348:U:H2'	1:A:1349:A:H8	1.36	0.87
13:J:79:ARG:NH1	13:J:79:ARG:HA	1.89	0.87
3:Y:34:G:H1	4:Z:3:U:H3	1.22	0.86
1:A:1216:G:H5"	17:N:5:ALA:HB2	1.58	0.86
16:M:4:ILE:HG22	16:M:5:ALA:N	1.89	0.86
14:K:84:VAL:HG23	14:K:110:ASP:HA	1.57	0.86
22:S:31:ILE:HG22	22:S:32:LYS:H	1.40	0.86
1:A:1497:G:O2'	1:A:1498:U:H5'	1.76	0.86
7:D:19:LEU:HD21	7:D:67:ILE:HG12	1.56	0.86
9:F:100:ASN:HD22	21:R:23:LYS:HG2	1.39	0.86
7:D:149:ALA:HB3	7:D:152:SER:HB2	1.58	0.86
1:A:946:A:H2'	1:A:947:G:C8	2.11	0.85
1:A:528:C:H41	15:L:49:ASN:HD21	1.22	0.85
1:A:1054:C:H3'	1:A:1054:C:O2	1.76	0.85
23:T:73:HIS:C	23:T:74:LYS:HD3	1.95	0.85
22:S:42:PRO:O	22:S:45:VAL:HG23	1.76	0.85
1:A:977:A:H2'	1:A:978:A:H5"	1.58	0.85
8:E:115:VAL:HG11	8:E:118:ILE:HD11	1.57	0.85
13:J:23:ILE:H	13:J:23:ILE:HD12	1.40	0.85
1:A:243:A:C4'	1:A:244:U:H5'	2.06	0.84
1:A:1356:G:H2'	1:A:1357:A:C8	2.12	0.84
11:H:64:LYS:HG2	11:H:79:VAL:HG21	1.57	0.84
6:C:108:ASN:HD21	6:C:111:LEU:HG	1.42	0.84
1:A:1152:A:H5"	13:J:13:HIS:HD2	1.42	0.84
1:A:1298:C:H2'	10:G:114:ARG:HH12	1.41	0.84
6:C:32:LEU:HD21	6:C:59:ARG:HD2	1.58	0.83
6:C:23:TYR:HD2	6:C:24:ALA:N	1.76	0.83
5:B:197:VAL:HB	5:B:200:ILE:HG23	1.58	0.83
13:J:45:ARG:CB	13:J:45:ARG:HH11	1.86	0.83
1:A:1124:G:H3'	1:A:1145:C:H41	1.43	0.83
1:A:1133:G:H2'	1:A:1134:G:H8	1.41	0.83
8:E:41:VAL:CG2	8:E:113:ALA:HA	2.08	0.83
10:G:69:VAL:HG21	10:G:104:LEU:HD21	1.59	0.83
6:C:150:LYS:HE2	6:C:152:ILE:HD11	1.61	0.83
17:N:3:ARG:NH1	17:N:6:LEU:HD11	1.94	0.82
12:I:89:ASN:HD21	12:I:91:ASP:HB2	1.43	0.82
14:K:48:ILE:HD12	14:K:63:LEU:HB3	1.60	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1352:C:H2'	1:A:1353:G:C8	2.13	0.82
9:F:30:LEU:HD11	9:F:63:TYR:HD1	1.44	0.82
1:A:560:U:H5'	1:A:566:G:N2	1.94	0.82
6:C:14:ILE:HG22	6:C:15:THR:N	1.94	0.81
13:J:71:LEU:HD13	13:J:72:VAL:H	1.44	0.81
20:Q:76:LEU:HD23	20:Q:77:VAL:N	1.93	0.81
15:L:124:LYS:HD2	15:L:125:PRO:HD2	1.62	0.81
13:J:71:LEU:HD13	13:J:72:VAL:N	1.95	0.81
1:A:939:G:H5"	10:G:102:ARG:NH2	1.95	0.81
8:E:12:LEU:HD13	8:E:31:LEU:HB2	1.63	0.81
1:A:1435:G:H2'	1:A:1436:U:C6	2.15	0.81
7:D:128:VAL:HG12	7:D:129:ASN:ND2	1.95	0.81
1:A:359:U:H2'	1:A:360:A:H8	1.44	0.81
6:C:6:HIS:CD2	6:C:8:ILE:HB	2.16	0.81
1:A:1443:G:C5'	1:A:1446:A:H5'	2.11	0.81
12:I:127:LYS:HD2	12:I:127:LYS:H	1.45	0.81
6:C:157:ILE:HD11	6:C:166:GLU:HB2	1.62	0.81
11:H:119:LEU:HD12	11:H:124:ALA:HA	1.63	0.81
1:A:1115:C:H1'	17:N:61:TRP:O	1.81	0.81
1:A:1003(A):G:H2'	1:A:1004:A:H4'	1.62	0.81
1:A:1391:U:H2'	1:A:1392:G:C8	2.16	0.81
1:A:579:G:H5'	1:A:728:A:H1'	1.62	0.81
1:A:109:A:H2'	1:A:326:G:N2	1.95	0.80
7:D:35:ARG:O	7:D:36:ARG:HB2	1.79	0.80
13:J:30:SER:HB3	13:J:84:GLN:HE21	1.46	0.80
1:A:1152:A:H5"	13:J:13:HIS:CD2	2.16	0.80
11:H:80:ILE:O	11:H:80:ILE:HG22	1.82	0.80
1:A:1064:G:H4'	1:A:1065:U:C5'	2.12	0.80
1:A:235:C:H5'	20:Q:70:ARG:HG2	1.62	0.80
1:A:918:A:H2'	1:A:919:A:C8	2.16	0.80
17:N:36:PHE:O	17:N:36:PHE:CD1	2.35	0.80
8:E:11:ILE:HB	8:E:31:LEU:HB3	1.64	0.80
7:D:150:GLU:HA	7:D:153:ARG:NE	1.97	0.80
1:A:1190:G:OP1	6:C:4:LYS:HA	1.82	0.80
16:M:86:CYS:SG	16:M:88:ARG:HG2	2.22	0.80
1:A:129(A):G:HO2'	1:A:190(E):U:H2'	1.44	0.80
16:M:5:ALA:HB3	16:M:8:GLU:HG3	1.64	0.80
1:A:99:C:H2'	1:A:101:A:C8	2.17	0.79
6:C:24:ALA:HB2	6:C:32:LEU:HD13	1.65	0.79
1:A:501:C:H2'	1:A:502:G:H8	1.45	0.79
1:A:1356:G:H2'	1:A:1357:A:H8	1.47	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:797:C:OP1	14:K:124:LYS:HE2	1.82	0.79
16:M:91:ARG:HB2	16:M:98:VAL:HG13	1.65	0.79
7:D:83:SER:HA	7:D:89:THR:HG23	1.65	0.79
14:K:66:LEU:HB3	14:K:70:LYS:HE3	1.65	0.79
1:A:760:G:H1	20:Q:105:ALA:HA	1.48	0.79
1:A:351:G:H4'	1:A:352:C:OP1	1.81	0.79
6:C:14:ILE:CG2	6:C:15:THR:H	1.95	0.78
11:H:24:THR:HG22	11:H:63:LEU:HD21	1.64	0.78
7:D:142:PRO:HG2	7:D:187:ARG:HH21	1.48	0.78
1:A:254:G:OP1	20:Q:67:LYS:O	2.01	0.78
10:G:26:PHE:CE2	10:G:30:ILE:HD11	2.18	0.78
22:S:20:LEU:HA	22:S:23:ASN:HD22	1.47	0.78
7:D:32:ALA:C	7:D:34:GLU:H	1.85	0.78
23:T:73:HIS:O	23:T:74:LYS:HD3	1.83	0.78
22:S:16:LEU:O	22:S:19:VAL:HG12	1.84	0.78
1:A:1148:U:H4'	12:I:14:VAL:HG11	1.66	0.78
9:F:91:VAL:HG12	9:F:92:LYS:H	1.47	0.78
1:A:1064:G:H4'	1:A:1065:U:H5'	1.64	0.78
1:A:538:G:OP2	15:L:115:LYS:HG3	1.83	0.78
5:B:84:GLU:HB3	5:B:219:VAL:CG2	2.11	0.78
6:C:58:GLU:HB3	13:J:92:THR:HG21	1.66	0.78
16:M:81:LEU:CD2	16:M:81:LEU:H	1.96	0.78
5:B:18:GLY:HA2	5:B:41:ILE:HA	1.63	0.78
7:D:199:ASN:HD21	7:D:201:GLN:HB2	1.49	0.78
5:B:178:ARG:HH21	5:B:196:LEU:HA	1.49	0.78
12:I:53:VAL:HG21	12:I:85:LEU:HD21	1.66	0.78
6:C:191:THR:HG21	6:C:193:TYR:CZ	2.18	0.77
7:D:25:ARG:C	7:D:27:TYR:H	1.87	0.77
5:B:42:ILE:HD11	5:B:189:ASP:HB2	1.65	0.77
6:C:191:THR:HG22	6:C:192:THR:N	1.98	0.77
1:A:1168:A:H2'	1:A:1169:A:C8	2.19	0.77
6:C:116:VAL:HG21	6:C:202:ILE:HD11	1.63	0.77
1:A:1250:A:H4'	12:I:68:GLY:H	1.48	0.77
15:L:46:LYS:HG2	15:L:47:LYS:N	1.97	0.77
13:J:30:SER:OG	13:J:81:THR:HA	1.85	0.77
1:A:1226:C:H4'	1:A:1227:A:OP1	1.85	0.77
12:I:70:LYS:O	12:I:74:ILE:HG13	1.84	0.77
15:L:89:ARG:NH1	15:L:97:ARG:HG2	1.99	0.77
16:M:65:LYS:HG3	16:M:69:GLU:OE2	1.85	0.77
1:A:1226:C:H1'	22:S:83:HIS:CE1	2.19	0.77
7:D:199:ASN:ND2	7:D:201:GLN:HB2	2.00	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:47:LYS:HB3	15:L:48:PRO:HD3	1.65	0.77
1:A:972:C:H4'	13:J:57:LYS:HD3	1.65	0.77
21:R:48:GLY:H	21:R:82:THR:HA	1.51	0.77
1:A:1366:C:H2'	1:A:1367:C:H6	1.47	0.76
6:C:195:VAL:O	6:C:196:LEU:HD23	1.85	0.76
1:A:17:U:H2'	1:A:18:C:C6	2.20	0.76
9:F:10:LEU:HD12	9:F:10:LEU:H	1.49	0.76
6:C:191:THR:HG22	6:C:193:TYR:H	1.50	0.76
5:B:115:LEU:HD21	5:B:153:ARG:NH2	1.99	0.76
20:Q:101:ARG:HE	20:Q:101:ARG:HA	1.50	0.76
1:A:1195:C:H3'	1:A:1196:U:H5"	1.66	0.76
15:L:41:ARG:HG2	15:L:42:THR:N	1.98	0.76
12:I:29:ASN:HD21	12:I:64:THR:HA	1.47	0.76
5:B:200:ILE:HD13	5:B:202:PRO:HD3	1.67	0.76
1:A:983:A:H5'	1:A:984:C:OP2	1.86	0.76
14:K:54:ARG:O	14:K:57:THR:HG23	1.85	0.76
5:B:44:LEU:HA	5:B:47:THR:OG1	1.85	0.76
1:A:1236:A:H2'	1:A:1237:C:C6	2.21	0.76
7:D:2:GLY:N	7:D:3:ARG:HE	1.84	0.76
10:G:54:THR:HG22	10:G:56:GLN:H	1.50	0.76
5:B:53:ARG:O	5:B:56:ARG:HB3	1.85	0.76
1:A:180:U:H2'	1:A:181:G:H5'	1.67	0.76
7:D:146:ILE:N	7:D:146:ILE:HD12	2.01	0.76
6:C:6:HIS:HD2	6:C:9:GLY:H	1.33	0.76
5:B:188:ALA:O	5:B:202:PRO:HA	1.86	0.76
19:P:22:THR:CA	19:P:33:ILE:HD13	2.16	0.75
16:M:3:ARG:HG2	16:M:9:ILE:HG23	1.67	0.75
5:B:15:VAL:HG11	5:B:210:SER:N	2.01	0.75
7:D:30:LYS:C	7:D:32:ALA:H	1.86	0.75
1:A:266:G:H5"	1:A:268:C:H41	1.52	0.75
1:A:750:G:N3	18:O:23:GLY:HA3	2.01	0.75
6:C:5:ILE:HD13	6:C:10:PHE:HB2	1.69	0.75
17:N:24:CYS:HB3	17:N:28:GLY:N	2.00	0.75
3:Y:34:G:H8	3:Y:34:G:H5'	1.50	0.75
13:J:6:ILE:HA	13:J:98:ILE:HG12	1.69	0.75
6:C:23:TYR:CD2	6:C:24:ALA:N	2.54	0.75
11:H:63:LEU:H	11:H:63:LEU:HD22	1.52	0.75
1:A:818:G:O2'	1:A:819:A:H5"	1.87	0.75
1:A:250:A:H4'	1:A:251:G:O5'	1.86	0.75
16:M:81:LEU:HD23	16:M:81:LEU:N	2.01	0.75
5:B:130:ARG:HB3	5:B:131:PRO:HD2	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:G:H2'	1:A:485:G:N2	2.02	0.75
13:J:6:ILE:HG23	13:J:98:ILE:HD11	1.66	0.74
15:L:27:LEU:C	15:L:29:GLY:H	1.90	0.74
5:B:25:ASN:C	5:B:25:ASN:HD22	1.90	0.74
1:A:130:A:OP2	1:A:190(E):U:H2'	1.87	0.74
16:M:22:ILE:HB	16:M:25:ILE:HD12	1.69	0.74
13:J:61:GLU:OE1	17:N:45:ARG:HD2	1.88	0.74
9:F:36:ARG:HH12	9:F:38:GLU:HG2	1.52	0.74
12:I:106:ALA:O	12:I:108:VAL:HG23	1.87	0.74
11:H:90:GLY:O	11:H:91:ARG:HB2	1.87	0.74
15:L:77:LEU:HD21	15:L:107:ALA:HA	1.69	0.74
6:C:10:PHE:CE2	6:C:178:LEU:HD13	2.22	0.74
1:A:1281:U:H5'	1:A:1282:C:C5	2.23	0.74
1:A:1003(A):G:H2'	1:A:1004:A:C4'	2.17	0.74
10:G:23:VAL:O	10:G:27:ILE:HG13	1.87	0.74
15:L:93:LEU:HD23	15:L:93:LEU:N	2.02	0.73
18:O:70:LEU:HD12	18:O:78:TYR:CB	2.18	0.73
1:A:129(A):G:O2'	1:A:190(E):U:H2'	1.87	0.73
7:D:126:ILE:HG22	7:D:127:THR:N	2.03	0.73
6:C:14:ILE:O	6:C:16:ARG:N	2.20	0.73
14:K:27:ASN:HA	14:K:56:GLY:HA2	1.68	0.73
5:B:30:ARG:HG3	5:B:31:TYR:CD2	2.23	0.73
20:Q:97:SER:HB2	20:Q:102:GLY:O	1.86	0.73
6:C:134:ILE:HG23	6:C:151:VAL:HB	1.71	0.73
1:A:1145:C:HO2'	1:A:1146:A:H8	1.35	0.73
1:A:1435:G:H2'	1:A:1436:U:H6	1.51	0.73
15:L:43:VAL:HG12	15:L:44:THR:N	2.03	0.73
5:B:124:SER:HB2	5:B:125:PRO:HD2	1.69	0.73
13:J:44:VAL:HG22	13:J:66:ARG:HG2	1.71	0.73
5:B:69:LEU:HB3	5:B:162:ILE:HG13	1.68	0.73
5:B:114:ARG:NH1	5:B:118:LEU:HD21	2.03	0.73
15:L:75:HIS:HD2	15:L:77:LEU:H	1.35	0.73
19:P:74:LEU:O	19:P:79:VAL:HG23	1.88	0.73
1:A:390:C:H2'	1:A:391:G:C8	2.24	0.73
1:A:474:G:H2'	1:A:475:G:H8	1.52	0.73
1:A:382:A:H2'	1:A:383:A:H8	1.54	0.72
15:L:86:ARG:HG3	15:L:86:ARG:HH11	1.52	0.72
1:A:1125:U:H5"	1:A:1126:U:H5	1.53	0.72
20:Q:67:LYS:O	20:Q:68:ARG:CB	2.37	0.72
1:A:291:C:O2'	1:A:292:G:H5'	1.89	0.72
13:J:8:LEU:HD23	13:J:96:ILE:HG12	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:39:PRO:O	13:J:40:LEU:HB2	1.89	0.72
1:A:817:C:H4'	1:A:818:G:OP1	1.88	0.72
9:F:99:ALA:HB2	21:R:31:LEU:HD11	1.71	0.72
1:A:1054:C:H2'	1:A:1055:A:H5"	1.71	0.72
6:C:137:ALA:HA	6:C:140:ARG:HH11	1.54	0.72
1:A:1142:G:H2'	1:A:1143:G:O4'	1.89	0.72
8:E:110:LEU:O	8:E:113:ALA:HB3	1.89	0.72
1:A:376:G:H5"	19:P:5:ARG:HD2	1.69	0.72
20:Q:27:PHE:CZ	20:Q:36:ILE:HD11	2.24	0.72
6:C:25:GLY:H	6:C:28:GLN:HB2	1.53	0.72
9:F:94:GLN:HB3	21:R:32:ARG:HD3	1.72	0.72
15:L:27:LEU:HD23	15:L:28:LYS:HB2	1.71	0.72
22:S:3:ARG:HH22	22:S:69:HIS:HE1	1.35	0.72
22:S:80:TYR:HD2	22:S:81:ARG:N	1.87	0.72
6:C:107:GLN:H	6:C:107:GLN:NE2	1.88	0.72
1:A:359:U:H2'	1:A:360:A:C8	2.25	0.72
1:A:524:G:H2'	1:A:525:C:C6	2.25	0.72
13:J:53:PRO:HA	17:N:41:ARG:HH21	1.53	0.72
5:B:15:VAL:CG2	5:B:209:ARG:HG3	2.20	0.71
22:S:22:LEU:HD13	22:S:28:LYS:HB3	1.71	0.71
20:Q:45:HIS:NE2	20:Q:47:PRO:HG3	2.05	0.71
21:R:74:ARG:HB3	21:R:81:PHE:CE1	2.25	0.71
7:D:13:ARG:HD2	7:D:38:TYR:O	1.90	0.71
12:I:114:TYR:HE1	13:J:59:SER:O	1.73	0.71
18:O:78:TYR:CZ	18:O:82:ILE:HD11	2.24	0.71
1:A:1137:C:H4'	1:A:1138:G:C2	2.25	0.71
1:A:1112:C:O2	6:C:179:ARG:HB3	1.89	0.71
5:B:69:LEU:HD12	5:B:155:LEU:HD11	1.71	0.71
1:A:447:G:H2'	1:A:485:G:H22	1.56	0.71
23:T:39:LYS:HD2	23:T:55:ILE:CD1	2.19	0.71
1:A:353:A:H5'	1:A:353:A:H8	1.54	0.71
8:E:110:LEU:O	8:E:115:VAL:HB	1.90	0.71
1:A:1277:C:H2'	1:A:1278:U:H5'	1.72	0.71
14:K:91:ARG:HD3	21:R:88:LYS:HE2	1.72	0.71
1:A:900:A:H2'	1:A:901:A:C8	2.24	0.71
6:C:131:ARG:HG2	6:C:135:LYS:HE3	1.71	0.71
12:I:111:ARG:CB	12:I:111:ARG:HH11	2.03	0.71
22:S:17:GLU:HA	22:S:20:LEU:HD11	1.71	0.71
1:A:1095:U:H2'	1:A:1096:C:C6	2.25	0.71
1:A:201:C:H42	1:A:216:G:H1	1.36	0.71
5:B:25:ASN:ND2	5:B:27:LYS:H	1.88	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:36:ASN:ND2	21:R:38:GLU:HG2	2.04	0.71
10:G:116:ALA:HA	10:G:119:ARG:CZ	2.21	0.71
16:M:78:ILE:HA	16:M:81:LEU:CD2	2.16	0.71
5:B:178:ARG:HH21	5:B:196:LEU:C	1.94	0.71
19:P:8:ARG:HB2	19:P:28:ARG:NH1	2.05	0.71
8:E:50:GLU:HG3	8:E:53:LEU:HB2	1.73	0.71
5:B:15:VAL:HG21	5:B:209:ARG:HG3	1.72	0.71
1:A:1151:A:HO2'	1:A:1152:A:H8	1.39	0.71
17:N:4:LYS:HA	17:N:7:ILE:CD1	2.21	0.71
6:C:191:THR:CG2	6:C:192:THR:N	2.53	0.71
7:D:119:GLN:HG2	7:D:123:HIS:CD2	2.25	0.70
24:V:6:ARG:HB3	24:V:15:ARG:NH2	2.04	0.70
1:A:1152:A:H5'	13:J:70:ARG:HH21	1.56	0.70
1:A:1518:A:H2'	1:A:1519:A:C8	2.26	0.70
20:Q:12:SER:HB3	20:Q:20:THR:HB	1.73	0.70
1:A:1196:U:OP1	1:A:1197:G:H5'	1.91	0.70
1:A:1502:A:H2	1:A:1505:G:N1	1.87	0.70
5:B:185:ILE:N	5:B:185:ILE:HD12	2.06	0.70
10:G:138:LYS:C	10:G:138:LYS:HD2	2.11	0.70
12:I:9:ARG:HA	12:I:13:ALA:O	1.91	0.70
7:D:23:GLY:HA3	7:D:112:VAL:HG12	1.73	0.70
10:G:5:ARG:HG3	10:G:6:ARG:N	2.02	0.70
21:R:59:SER:OG	21:R:62:GLU:HG3	1.90	0.70
5:B:23:ARG:NH1	5:B:191:ASP:HA	2.05	0.70
6:C:100:ALA:O	6:C:101:LEU:HB2	1.89	0.70
1:A:370:C:O2'	1:A:371:G:H5'	1.91	0.70
22:S:20:LEU:HD12	22:S:21:GLU:N	2.07	0.70
23:T:53:LEU:HB2	23:T:100:ILE:HG21	1.72	0.70
1:A:1402:C:H2'	1:A:1403:C:H6	1.56	0.70
1:A:664:G:OP1	21:R:64:ARG:HD2	1.91	0.70
16:M:3:ARG:HA	16:M:8:GLU:O	1.92	0.70
1:A:1343:G:H2'	1:A:1344:C:C6	2.27	0.70
1:A:1133:G:H2'	1:A:1134:G:C8	2.27	0.70
11:H:119:LEU:HD12	11:H:124:ALA:CA	2.21	0.70
1:A:135:C:O2	19:P:1:MET:HB2	1.92	0.70
1:A:1475:G:H2'	1:A:1476:G:H8	1.56	0.70
16:M:88:ARG:NH1	22:S:3:ARG:HH21	1.90	0.69
5:B:17:PHE:HB3	5:B:44:LEU:HD11	1.73	0.69
1:A:1298:C:H4'	1:A:1299:A:O4'	1.91	0.69
7:D:151:LYS:CD	7:D:151:LYS:H	2.04	0.69
6:C:188:LEU:CD1	6:C:189:ALA:H	2.02	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:118:LYS:O	12:I:119:ALA:HB3	1.91	0.69
1:A:972:C:H4'	13:J:57:LYS:CD	2.22	0.69
1:A:269:C:H2'	1:A:270:A:C8	2.27	0.69
11:H:19:VAL:HG23	11:H:21:LYS:HG2	1.74	0.69
1:A:848:C:O2'	1:A:849:C:H5'	1.93	0.69
1:A:1064:G:C4'	1:A:1065:U:H5'	2.22	0.69
1:A:1313:U:O4	22:S:4:SER:HB3	1.91	0.69
15:L:75:HIS:CD2	15:L:77:LEU:H	2.10	0.69
7:D:25:ARG:NH2	7:D:30:LYS:HD3	2.07	0.69
1:A:1053:G:HO2'	1:A:1199:U:H5	1.39	0.69
1:A:939:G:H5"	10:G:102:ARG:HH12	1.56	0.69
11:H:31:PHE:O	11:H:34:GLU:HB2	1.92	0.69
1:A:1490:C:O2'	1:A:1491:G:H5'	1.91	0.69
6:C:52:LEU:H	6:C:52:LEU:HD23	1.58	0.69
14:K:54:ARG:HB3	14:K:54:ARG:NH1	2.05	0.69
10:G:138:LYS:O	10:G:138:LYS:HD2	1.92	0.69
18:O:65:ARG:NH1	18:O:65:ARG:HB2	2.08	0.69
1:A:478:A:O2'	1:A:479:C:H5'	1.92	0.69
5:B:91:PRO:HA	5:B:154:LEU:HD12	1.74	0.69
8:E:75:THR:HG23	8:E:76:ILE:N	2.08	0.69
10:G:61:VAL:O	10:G:64:GLN:HB3	1.91	0.69
22:S:40:ILE:HG21	22:S:62:ILE:HD13	1.73	0.69
16:M:4:ILE:HG22	16:M:5:ALA:H	1.57	0.69
1:A:959:A:H3'	1:A:960:U:H5"	1.75	0.69
13:J:94:VAL:HG12	13:J:95:GLU:N	2.06	0.69
5:B:42:ILE:HD12	5:B:203:GLY:HA2	1.74	0.69
23:T:53:LEU:HB2	23:T:100:ILE:CG2	2.23	0.69
5:B:97:TRP:HZ2	5:B:102:LEU:HD13	1.58	0.69
7:D:156:GLU:O	7:D:159:ARG:HB2	1.93	0.69
6:C:62:ASP:HA	6:C:97:LYS:CG	2.23	0.69
5:B:132:LYS:O	5:B:136:VAL:HG23	1.92	0.69
9:F:64:GLN:HG2	9:F:64:GLN:O	1.93	0.69
7:D:65:ARG:HB2	7:D:75:PHE:CE1	2.28	0.69
7:D:103:ASN:OD1	7:D:114:ARG:NH2	2.26	0.69
1:A:1015:A:H2'	1:A:1016:A:C8	2.28	0.69
1:A:731:G:OP1	1:A:766:A:H1'	1.93	0.69
13:J:60:ARG:HD2	13:J:60:ARG:N	2.06	0.69
12:I:89:ASN:ND2	12:I:91:ASP:HB2	2.07	0.69
9:F:30:LEU:HD11	9:F:63:TYR:CD1	2.27	0.69
5:B:156:LYS:O	5:B:156:LYS:HD3	1.93	0.69
22:S:44:MET:O	22:S:47:HIS:HB2	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:87:GLY:HA2	15:L:98:TYR:HA	1.74	0.68
1:A:393:A:O2'	1:A:394:G:H5'	1.91	0.68
20:Q:68:ARG:H	20:Q:70:ARG:NH1	1.91	0.68
1:A:975:A:O5'	1:A:976:G:H5'	1.93	0.68
1:A:1030(A):G:H1'	1:A:1031:G:H22	1.57	0.68
13:J:10:GLY:N	13:J:16:LEU:HD21	2.08	0.68
5:B:23:ARG:HH12	5:B:191:ASP:HA	1.58	0.68
7:D:142:PRO:HG2	7:D:187:ARG:NH2	2.07	0.68
6:C:107:GLN:H	6:C:107:GLN:CD	1.95	0.68
1:A:920:U:H2'	1:A:921:U:C6	2.28	0.68
1:A:1020:U:H2'	1:A:1021:G:C8	2.27	0.68
1:A:425:G:O2'	1:A:426:G:H5'	1.94	0.68
8:E:77:PRO:O	8:E:78:HIS:HB3	1.92	0.68
1:A:977:A:C2'	1:A:978:A:H5"	2.24	0.68
1:A:1250:A:H5"	12:I:68:GLY:N	2.09	0.68
1:A:1051:C:H2'	1:A:1052:U:H6	1.57	0.68
8:E:103:GLY:O	8:E:106:PRO:HD2	1.94	0.68
15:L:93:LEU:CD1	15:L:96:VAL:HG21	2.24	0.68
16:M:88:ARG:HH11	22:S:3:ARG:HH21	1.38	0.68
22:S:20:LEU:HA	22:S:23:ASN:ND2	2.07	0.68
7:D:3:ARG:NH1	7:D:3:ARG:HB3	2.09	0.68
17:N:27:CYS:SG	17:N:29:ARG:HB2	2.32	0.68
1:A:175:C:H2'	1:A:176:C:H6	1.59	0.68
7:D:98:GLU:HG2	7:D:189:PRO:HG3	1.76	0.68
5:B:209:ARG:HE	5:B:239:VAL:HG11	1.58	0.68
21:R:53:ARG:HD2	21:R:58:LEU:O	1.93	0.68
6:C:10:PHE:CZ	6:C:178:LEU:HD13	2.29	0.68
5:B:9:GLU:HG2	5:B:10:LEU:N	2.09	0.68
1:A:528:C:H41	15:L:49:ASN:ND2	1.89	0.68
21:R:52:PRO:O	21:R:56:THR:HG23	1.93	0.68
1:A:1057:G:H5"	6:C:154:SER:HB2	1.76	0.68
22:S:80:TYR:CD2	22:S:81:ARG:N	2.62	0.68
16:M:117:VAL:HG12	16:M:118:ALA:H	1.59	0.68
1:A:731:G:O2'	1:A:732:C:H5'	1.94	0.67
1:A:75:G:O2'	1:A:76:C:H5'	1.95	0.67
18:O:16:ALA:CB	18:O:21:ASP:HB3	2.24	0.67
7:D:3:ARG:HH11	7:D:3:ARG:HB3	1.58	0.67
5:B:128:GLU:HA	5:B:135:GLN:NE2	2.10	0.67
1:A:620:C:N1	7:D:135:LEU:HD13	2.09	0.67
23:T:70:SER:HA	23:T:73:HIS:CD2	2.30	0.67
15:L:47:LYS:CB	15:L:48:PRO:CD	2.72	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:85:ARG:HD3	11:H:86:ILE:N	2.09	0.67
5:B:178:ARG:HH21	5:B:196:LEU:CA	2.06	0.67
6:C:23:TYR:C	6:C:23:TYR:HD2	1.98	0.67
20:Q:97:SER:OG	20:Q:103:GLY:HA2	1.95	0.67
19:P:28:ARG:HG2	19:P:29:ASP:OD1	1.94	0.67
8:E:144:THR:O	8:E:148:VAL:HG23	1.94	0.67
1:A:1226:C:H5"	16:M:103:THR:OG1	1.94	0.67
14:K:99:GLN:HA	14:K:105:VAL:HG21	1.76	0.67
19:P:10:GLY:HA3	19:P:14:ASN:O	1.94	0.67
15:L:110:VAL:O	15:L:122:THR:HG22	1.93	0.67
12:I:128:ARG:OXT	12:I:128:ARG:HG2	1.95	0.67
7:D:32:ALA:C	7:D:34:GLU:N	2.48	0.67
1:A:1003(A):G:C2'	1:A:1004:A:H4'	2.24	0.67
9:F:30:LEU:HB3	9:F:35:ALA:HB3	1.75	0.67
1:A:1319:A:H5'	1:A:1320:C:OP1	1.94	0.67
1:A:1016:A:H2'	1:A:1017:G:O4'	1.93	0.67
22:S:24:ALA:HB3	22:S:25:LYS:NZ	2.10	0.67
14:K:74:ALA:C	14:K:76:GLY:H	1.97	0.67
7:D:30:LYS:C	7:D:32:ALA:N	2.49	0.67
1:A:1065:U:H4'	1:A:1066:C:O5'	1.94	0.67
1:A:954:G:H2'	1:A:955:U:H6	1.60	0.67
5:B:68:ILE:H	5:B:90:MET:HE3	1.60	0.67
1:A:1329:A:O2'	1:A:1330:U:H5'	1.95	0.67
10:G:23:VAL:HG12	10:G:27:ILE:HD11	1.77	0.67
15:L:43:VAL:HG12	15:L:44:THR:H	1.59	0.67
23:T:39:LYS:HD2	23:T:55:ILE:HD12	1.76	0.67
1:A:1229:A:H2'	1:A:1230:C:H6	1.60	0.67
7:D:23:GLY:O	7:D:27:TYR:HD1	1.78	0.66
1:A:1480:G:H2'	1:A:1481:U:C6	2.30	0.66
1:A:1224:G:H2'	22:S:78:ARG:HH22	1.60	0.66
24:V:12:LYS:HG3	24:V:17:THR:OG1	1.95	0.66
9:F:91:VAL:HG12	9:F:92:LYS:N	2.10	0.66
6:C:191:THR:HG21	6:C:193:TYR:CE2	2.29	0.66
23:T:90:GLN:O	23:T:93:GLU:HB2	1.94	0.66
20:Q:60:ILE:HD13	20:Q:61:GLU:N	2.10	0.66
12:I:8:GLY:CA	12:I:79:LEU:HD12	2.23	0.66
13:J:15:THR:HG23	13:J:94:VAL:HG22	1.77	0.66
5:B:139:LYS:O	5:B:143:GLU:HG2	1.95	0.66
18:O:56:LEU:HA	18:O:59:MET:CE	2.26	0.66
22:S:16:LEU:C	22:S:18:LYS:H	1.97	0.66
1:A:1381:U:O2'	1:A:1382:C:H5'	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:10:GLY:H	13:J:16:LEU:HD11	1.60	0.66
6:C:195:VAL:C	6:C:196:LEU:HD23	2.15	0.66
14:K:87:THR:HG23	14:K:91:ARG:NH2	2.10	0.66
17:N:9:LYS:HD3	17:N:9:LYS:O	1.95	0.66
1:A:1086:U:H3	1:A:1099:G:H22	1.43	0.66
6:C:19:GLU:HB3	6:C:40:ARG:HH21	1.60	0.66
1:A:1057:G:O2'	1:A:1058:G:H5'	1.96	0.66
1:A:939:G:H5"	10:G:102:ARG:NH1	2.10	0.66
22:S:85:LYS:HE3	22:S:85:LYS:N	2.09	0.66
21:R:26:LEU:HD23	21:R:29:PHE:CE2	2.31	0.66
18:O:88:ARG:HH11	18:O:88:ARG:HA	1.60	0.66
16:M:19:LEU:HA	16:M:22:ILE:HD13	1.78	0.66
15:L:117:ARG:NH2	15:L:124:LYS:HA	2.10	0.66
5:B:102:LEU:HD21	5:B:162:ILE:CD1	2.26	0.66
12:I:111:ARG:HH11	12:I:111:ARG:HB3	1.60	0.66
11:H:10:LEU:HD22	11:H:83:ILE:HD11	1.78	0.66
1:A:376:G:H2'	1:A:377:G:H8	1.61	0.66
23:T:97:ALA:O	23:T:99:LEU:N	2.26	0.66
12:I:114:TYR:CE1	13:J:60:ARG:HB2	2.31	0.65
22:S:52:TYR:HA	22:S:56:GLN:O	1.94	0.65
13:J:6:ILE:HB	13:J:72:VAL:HB	1.77	0.65
6:C:108:ASN:ND2	6:C:111:LEU:HG	2.10	0.65
1:A:457:C:H2'	1:A:458:C:C6	2.31	0.65
8:E:72:GLN:O	8:E:73:ASN:HB3	1.95	0.65
1:A:1001:A:H2'	1:A:1002:G:C8	2.31	0.65
13:J:51:ARG:NH2	13:J:61:GLU:HB2	2.11	0.65
18:O:39:LEU:HD22	18:O:56:LEU:HD13	1.78	0.65
12:I:5:TYR:O	12:I:84:ALA:HA	1.95	0.65
19:P:69:THR:O	19:P:72:ARG:HB3	1.96	0.65
16:M:40:ASN:HB3	16:M:43:THR:HG23	1.78	0.65
7:D:112:VAL:HG23	7:D:161:ASN:HD21	1.61	0.65
22:S:22:LEU:HD22	22:S:28:LYS:HD2	1.78	0.65
6:C:55:VAL:O	6:C:55:VAL:HG12	1.96	0.65
1:A:393:A:OP2	19:P:12:LYS:HE2	1.96	0.65
1:A:1369:C:H2'	1:A:1370:G:C8	2.31	0.65
18:O:77:ARG:O	18:O:80:ALA:HB3	1.95	0.65
16:M:102:ARG:NH1	16:M:102:ARG:HB2	2.11	0.65
23:T:13:LEU:HD12	23:T:14:LYS:N	2.11	0.65
1:A:452:A:O2'	1:A:453:A:H8	1.78	0.65
7:D:10:ARG:HG3	7:D:10:ARG:HH11	1.62	0.65
1:A:1298:C:C4	10:G:114:ARG:HD3	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:46:LYS:HE3	15:L:47:LYS:HG3	1.78	0.65
1:A:1330:U:OP1	16:M:23:TYR:O	2.15	0.65
13:J:16:LEU:CD2	13:J:94:VAL:HG13	2.26	0.65
1:A:129(A):G:O2'	1:A:130:A:OP2	2.14	0.65
1:A:1002:G:H2'	1:A:1003:G:C8	2.31	0.65
1:A:1426:C:H2'	1:A:1427:U:C6	2.31	0.65
1:A:1178:G:N2	1:A:1180:A:H3'	2.12	0.65
1:A:992:U:H4'	1:A:993:G:O5'	1.96	0.65
1:A:1152:A:H2'	1:A:1153:C:C6	2.32	0.65
21:R:33:ASP:OD2	21:R:36:ASN:HB2	1.96	0.65
19:P:42:ARG:O	19:P:43:LYS:C	2.34	0.65
15:L:53:ARG:NH1	15:L:92:ASP:OD2	2.30	0.65
1:A:338:A:H2'	1:A:339:C:C6	2.32	0.65
1:A:491:G:H2'	1:A:492:G:H8	1.62	0.65
1:A:149:A:H2'	1:A:150:C:C6	2.30	0.65
18:O:74:ASP:OD1	18:O:76:GLU:HB3	1.97	0.65
1:A:1038:C:H2'	1:A:1039:C:C6	2.31	0.65
12:I:4:TYR:CG	12:I:88:TYR:HB2	2.31	0.65
1:A:1031:G:H2'	1:A:1032:G:H8	1.60	0.65
1:A:624:C:H2'	1:A:625:G:H8	1.62	0.65
11:H:104:ARG:NH2	11:H:138:TRP:CH2	2.65	0.65
12:I:93:ARG:HB3	12:I:97:LYS:CE	2.23	0.65
14:K:54:ARG:O	14:K:57:THR:CG2	2.45	0.65
1:A:1226:C:O2	22:S:83:HIS:CE1	2.50	0.65
20:Q:26:GLN:O	20:Q:27:PHE:HB3	1.97	0.65
1:A:860:A:H2'	1:A:861:G:O4'	1.97	0.65
5:B:98:LEU:O	5:B:101:MET:HG3	1.97	0.64
1:A:1047:G:H5"	17:N:4:LYS:HG3	1.79	0.64
1:A:405:U:H3'	1:A:406:G:H5'	1.79	0.64
10:G:15:ASP:HB3	10:G:19:GLY:H	1.61	0.64
10:G:70:LYS:HG2	10:G:100:ALA:HB2	1.79	0.64
1:A:1202:G:O2'	1:A:1203:C:H5'	1.97	0.64
1:A:1056:U:H5'	6:C:163:ALA:HB2	1.79	0.64
6:C:138:VAL:HG22	6:C:151:VAL:HG23	1.79	0.64
6:C:107:GLN:O	6:C:108:ASN:HB3	1.95	0.64
9:F:97:PHE:HB2	21:R:32:ARG:HH21	1.62	0.64
1:A:458:C:H2'	1:A:459:G:H8	1.61	0.64
1:A:260:G:H2'	1:A:261:U:C6	2.32	0.64
1:A:141:A:H1'	1:A:182:U:O2	1.96	0.64
1:A:1010:G:H2'	1:A:1011:G:H8	1.63	0.64
5:B:18:GLY:CA	5:B:41:ILE:HA	2.25	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:120:ARG:O	12:I:122:ALA:N	2.30	0.64
19:P:28:ARG:HH11	19:P:28:ARG:HG2	1.62	0.64
9:F:19:LEU:HD23	9:F:19:LEU:C	2.18	0.64
20:Q:81:ARG:HG3	20:Q:81:ARG:O	1.97	0.64
14:K:87:THR:HG22	14:K:88:GLY:H	1.61	0.64
6:C:110:ASN:O	6:C:111:LEU:HD23	1.97	0.64
1:A:113:G:H1'	1:A:354:G:H5'	1.80	0.64
16:M:37:THR:O	16:M:39:ILE:HG13	1.98	0.64
8:E:13:ILE:HG22	8:E:30:ALA:HB2	1.78	0.64
10:G:50:ILE:O	10:G:54:THR:HB	1.98	0.64
5:B:223:ILE:O	5:B:225:ALA:N	2.26	0.64
1:A:677:U:H3	1:A:713:G:H22	1.43	0.64
1:A:1068:G:N7	1:A:1094:G:H2'	2.13	0.64
5:B:77:ALA:CB	5:B:211:ILE:HD13	2.27	0.64
15:L:45:PRO:HD3	15:L:51:ALA:O	1.98	0.64
6:C:23:TYR:C	6:C:23:TYR:CD2	2.71	0.64
1:A:1001:A:H2'	1:A:1002:G:H8	1.62	0.64
12:I:79:LEU:HD11	12:I:83:ARG:HD2	1.79	0.64
6:C:110:ASN:HD21	6:C:140:ARG:HB3	1.62	0.64
10:G:67:GLU:HA	10:G:70:LYS:HE2	1.79	0.64
15:L:83:VAL:HG21	15:L:100:ILE:HD13	1.79	0.64
16:M:54:VAL:O	16:M:58:GLU:HG2	1.98	0.64
13:J:60:ARG:O	13:J:61:GLU:HB3	1.98	0.64
15:L:47:LYS:HB3	15:L:48:PRO:CD	2.28	0.64
1:A:1145:C:O2'	1:A:1146:A:H8	1.79	0.64
6:C:64:VAL:HB	6:C:99:VAL:HG23	1.78	0.64
12:I:78:LYS:HD3	12:I:101:PHE:CD2	2.33	0.64
1:A:287:U:O2'	1:A:288:A:H5'	1.98	0.64
1:A:397:A:H5'	1:A:398:C:OP1	1.98	0.64
6:C:188:LEU:O	6:C:189:ALA:HB2	1.97	0.64
6:C:189:ALA:HB3	6:C:196:LEU:O	1.98	0.64
15:L:27:LEU:C	15:L:29:GLY:N	2.48	0.64
22:S:22:LEU:HD13	22:S:28:LYS:CB	2.27	0.64
1:A:147:G:O2'	1:A:148:G:H5'	1.98	0.64
18:O:33:THR:HG23	18:O:63:ARG:NH1	2.13	0.64
11:H:86:ILE:HD11	11:H:136:GLU:HB2	1.80	0.63
23:T:56:MET:HE3	23:T:88:VAL:HG11	1.78	0.63
1:A:328:C:H4'	1:A:329:A:O5'	1.97	0.63
1:A:1468:A:H2'	1:A:1469:G:O4'	1.97	0.63
1:A:853:G:O2'	1:A:854:G:H5'	1.98	0.63
8:E:40:ARG:HG2	8:E:40:ARG:HH11	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:36:LYS:HD2	16:M:59:TYR:OH	1.99	0.63
13:J:30:SER:HB3	13:J:84:GLN:NE2	2.14	0.63
5:B:50:GLU:HG3	5:B:200:ILE:HD11	1.79	0.63
22:S:20:LEU:O	22:S:23:ASN:HB2	1.98	0.63
1:A:1030:C:H2'	1:A:1030(A):G:H5'	1.80	0.63
1:A:1030(C):G:H2'	1:A:1030(D):A:H8	1.63	0.63
17:N:14:PRO:O	17:N:15:LYS:HB3	1.99	0.63
1:A:669:U:H2'	1:A:670:G:C8	2.33	0.63
1:A:1054:C:C3'	1:A:1054:C:O2	2.45	0.63
7:D:108:LEU:HD23	7:D:174:LEU:HD13	1.78	0.63
7:D:152:SER:O	7:D:158:ILE:HD12	1.99	0.63
6:C:62:ASP:HA	6:C:97:LYS:HG2	1.81	0.63
1:A:390:C:O3'	19:P:28:ARG:NH2	2.31	0.63
11:H:31:PHE:O	11:H:35:ILE:HD12	1.98	0.63
8:E:93:PRO:HG2	11:H:105:ARG:NH2	2.13	0.63
6:C:134:ILE:HG22	6:C:168:ALA:HB3	1.81	0.63
14:K:84:VAL:HG21	21:R:88:LYS:HD3	1.80	0.63
23:T:10:LEU:HD12	23:T:12:ALA:HB3	1.80	0.63
10:G:87:VAL:HG13	10:G:88:PRO:HD2	1.80	0.63
1:A:1222:G:O2'	1:A:1223:C:H5'	1.99	0.63
13:J:90:LEU:H	13:J:91:PRO:CD	2.06	0.63
8:E:71:LEU:HD21	8:E:115:VAL:HG23	1.80	0.63
1:A:1333:A:H2'	1:A:1334:G:O4'	1.98	0.63
9:F:2:ARG:CZ	9:F:69:GLU:HG2	2.28	0.63
1:A:1250:A:C4'	12:I:68:GLY:H	2.10	0.63
12:I:114:TYR:CD1	13:J:60:ARG:HB2	2.33	0.63
5:B:39:ILE:HG22	5:B:40:HIS:O	1.98	0.63
21:R:55:ARG:HB3	21:R:55:ARG:NH1	2.13	0.63
8:E:76:ILE:HG23	8:E:77:PRO:HD2	1.78	0.63
1:A:1262:C:H2'	1:A:1263:C:H6	1.63	0.63
1:A:1347:G:O2'	1:A:1348:U:P	2.55	0.63
10:G:71:PRO:HD3	10:G:103:TRP:CZ3	2.33	0.63
18:O:39:LEU:HD23	18:O:39:LEU:C	2.19	0.63
1:A:627:G:O2'	1:A:628:G:H5'	1.98	0.63
1:A:190(H):G:O2'	1:A:190(I):G:H5'	1.98	0.63
6:C:15:THR:O	6:C:16:ARG:HB2	1.98	0.63
13:J:20:ALA:O	13:J:24:VAL:HG23	1.98	0.63
15:L:6:THR:OG1	15:L:9:GLN:HG3	1.99	0.63
6:C:70:VAL:HG12	6:C:71:ALA:N	2.13	0.63
5:B:102:LEU:HD21	5:B:162:ILE:HD12	1.80	0.63
1:A:353:A:H5'	1:A:353:A:C8	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:34:LEU:HD13	16:M:41:PRO:HA	1.79	0.63
1:A:1370:G:O2'	1:A:1371:G:H5'	1.98	0.62
10:G:59:LEU:HD11	10:G:63:LYS:HE3	1.81	0.62
7:D:126:ILE:HG22	7:D:127:THR:H	1.64	0.62
1:A:1095:U:H2'	1:A:1096:C:H6	1.64	0.62
5:B:217:ARG:HA	5:B:220:ASP:OD2	1.98	0.62
6:C:77:ILE:HA	6:C:84:ILE:HB	1.80	0.62
1:A:1306:A:N6	1:A:1331:G:H1'	2.14	0.62
5:B:102:LEU:HB3	5:B:180:LEU:HD12	1.81	0.62
20:Q:63:ARG:HG2	20:Q:64:PRO:N	2.13	0.62
1:A:352:C:H4'	1:A:354:G:OP1	1.99	0.62
1:A:1251:A:H4'	12:I:12:GLU:OE1	1.99	0.62
1:A:160:A:H1'	1:A:344:A:N7	2.14	0.62
1:A:186:C:O3'	23:T:82:SER:HB3	1.99	0.62
1:A:192:U:H1'	23:T:103:GLY:HA2	1.82	0.62
1:A:673:G:H2'	1:A:674:G:C8	2.34	0.62
15:L:115:LYS:O	15:L:117:ARG:N	2.32	0.62
17:N:3:ARG:CZ	17:N:6:LEU:HD11	2.29	0.62
1:A:1250:A:H4'	12:I:68:GLY:N	2.14	0.62
1:A:838:G:H2'	1:A:839:U:H5"	1.80	0.62
1:A:107:G:C2'	1:A:108:G:H5'	2.29	0.62
6:C:47:LEU:CD1	6:C:47:LEU:H	2.13	0.62
16:M:62:ASN:O	16:M:63:THR:HB	1.99	0.62
1:A:960:U:H2'	1:A:960:U:O2	1.98	0.62
11:H:134:ILE:HG22	11:H:135:CYS:N	2.14	0.62
1:A:528:C:H5'	1:A:535:A:C6	2.34	0.62
12:I:25:LYS:HG2	12:I:60:ASP:OD2	1.99	0.62
1:A:258:G:H2'	1:A:259:G:H8	1.64	0.62
1:A:1513:A:H2'	1:A:1514:C:C6	2.34	0.62
14:K:80:VAL:HG21	14:K:103:LEU:HD13	1.81	0.62
12:I:100:GLY:O	12:I:102:LEU:N	2.30	0.62
1:A:1438:G:H2'	1:A:1439:C:C6	2.35	0.62
1:A:1221:G:O3'	22:S:77:THR:HG21	1.98	0.62
20:Q:68:ARG:H	20:Q:70:ARG:HH11	1.47	0.62
8:E:12:LEU:CD1	8:E:31:LEU:HB2	2.30	0.62
5:B:98:LEU:N	5:B:98:LEU:HD23	2.15	0.62
1:A:967:C:C4'	12:I:128:ARG:HG3	2.29	0.62
6:C:191:THR:CG2	6:C:192:THR:H	2.12	0.62
1:A:344:A:H4'	1:A:345:C:OP2	2.00	0.62
21:R:61:LYS:O	21:R:65:ILE:HG13	2.00	0.62
1:A:386:C:O2'	1:A:387:U:H5'	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:761:G:H5"	20:Q:102:GLY:HA3	1.79	0.62
23:T:96:GLY:O	23:T:97:ALA:CB	2.47	0.62
1:A:1072:G:H2'	1:A:1073:U:C6	2.33	0.62
1:A:357:G:O2'	1:A:358:U:H5'	2.00	0.62
11:H:138:TRP:OXT	11:H:138:TRP:CE3	2.53	0.62
5:B:185:ILE:H	5:B:185:ILE:HD12	1.65	0.62
5:B:124:SER:O	5:B:127:ILE:HG13	1.99	0.62
1:A:390:C:H2'	1:A:391:G:H8	1.63	0.62
17:N:32:SER:HB2	17:N:41:ARG:HB3	1.81	0.62
5:B:84:GLU:OE1	5:B:216:SER:HA	1.99	0.62
1:A:371:G:C2'	1:A:372:C:H5'	2.30	0.62
9:F:67:MET:CE	9:F:72:VAL:HA	2.30	0.62
12:I:47:LEU:C	12:I:49:PRO:HD2	2.20	0.62
1:A:192:U:C1'	23:T:103:GLY:HA2	2.30	0.62
15:L:24:VAL:O	15:L:26:ALA:N	2.31	0.62
13:J:51:ARG:CZ	13:J:61:GLU:HB2	2.30	0.61
15:L:57:LYS:HD3	15:L:67:THR:HB	1.82	0.61
16:M:49:THR:HG22	16:M:51:ALA:N	2.06	0.61
16:M:50:GLU:O	16:M:54:VAL:HG23	1.99	0.61
8:E:36:ASP:O	8:E:37:ARG:HB2	1.99	0.61
1:A:190(F):G:H4'	1:A:190(G):G:OP2	1.99	0.61
1:A:1152:A:H5'	13:J:70:ARG:NH2	2.15	0.61
9:F:67:MET:HE1	9:F:72:VAL:HA	1.82	0.61
14:K:72:ALA:HB1	14:K:77:MET:HG3	1.81	0.61
7:D:176:LEU:HA	7:D:183:GLY:HA2	1.82	0.61
1:A:1527:C:O2'	1:A:1528:U:H5'	1.99	0.61
22:S:87:ALA:O	22:S:88:LYS:HB3	2.00	0.61
1:A:1112:C:N3	6:C:178:LEU:N	2.47	0.61
22:S:40:ILE:HG21	22:S:62:ILE:CD1	2.30	0.61
1:A:1226:C:C5	16:M:104:ARG:HA	2.35	0.61
12:I:49:PRO:HD3	12:I:78:LYS:HG2	1.82	0.61
2:X:2:U:H2'	2:X:3:U:H5'	1.82	0.61
10:G:122:HIS:HA	10:G:125:MET:HE3	1.82	0.61
1:A:1161:C:H2'	1:A:1162:C:C6	2.34	0.61
15:L:34:ARG:O	15:L:61:THR:HG23	1.99	0.61
8:E:33:VAL:HG11	8:E:109:ILE:HA	1.82	0.61
1:A:1148:U:H2'	1:A:1149:C:O4'	2.00	0.61
12:I:19:LEU:HD23	12:I:61:ALA:HB2	1.83	0.61
1:A:689:C:P	14:K:46:GLY:HA3	2.41	0.61
1:A:560:U:O2'	1:A:561:U:OP2	2.11	0.61
10:G:51:GLN:C	10:G:53:LYS:H	2.03	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:126:GLU:O	5:B:129:GLU:HB3	2.01	0.61
6:C:19:GLU:HG2	6:C:54:ARG:HE	1.65	0.61
1:A:187:C:O2	23:T:105:SER:HB3	2.01	0.61
1:A:580:U:H2'	1:A:581:G:O4'	1.99	0.61
6:C:47:LEU:N	6:C:47:LEU:HD12	2.15	0.61
7:D:3:ARG:CZ	7:D:3:ARG:H	2.14	0.61
12:I:48:GLU:N	12:I:49:PRO:HD2	2.15	0.61
1:A:839:U:H5'	1:A:840:C:H5	1.65	0.61
1:A:840:C:H5"	1:A:841:U:OP1	2.00	0.61
9:F:18:GLN:O	9:F:21:LEU:HB3	2.00	0.61
1:A:1296:C:H4'	1:A:1302:U:C5	2.36	0.61
6:C:6:HIS:CD2	6:C:9:GLY:H	2.16	0.61
11:H:118:VAL:C	11:H:119:LEU:HD23	2.19	0.61
6:C:52:LEU:H	6:C:52:LEU:CD2	2.13	0.61
23:T:97:ALA:O	23:T:99:LEU:HG	2.01	0.61
11:H:60:ARG:HG3	11:H:60:ARG:HH11	1.65	0.61
1:A:501:C:H2'	1:A:502:G:C8	2.33	0.61
1:A:1325:C:O3'	24:V:17:THR:HG21	2.01	0.61
10:G:51:GLN:O	10:G:53:LYS:N	2.34	0.61
9:F:99:ALA:HB2	21:R:31:LEU:CD1	2.31	0.61
1:A:1202:G:C2'	1:A:1203:C:H5'	2.31	0.61
5:B:223:ILE:C	5:B:225:ALA:H	2.03	0.61
20:Q:5:VAL:O	20:Q:6:LEU:HD23	2.00	0.61
18:O:7:GLU:O	18:O:11:VAL:HG23	2.00	0.61
1:A:958:A:C8	22:S:55:LYS:HD2	2.36	0.61
1:A:496:A:H4'	1:A:497:A:OP1	1.98	0.61
1:A:1250:A:H5"	12:I:68:GLY:H	1.63	0.61
1:A:975:A:H8	1:A:975:A:H5'	1.65	0.61
1:A:1002:G:H2'	1:A:1003:G:H8	1.66	0.61
1:A:386:C:C2'	1:A:387:U:H5'	2.30	0.61
1:A:1056:U:C5'	6:C:163:ALA:HB2	2.31	0.61
12:I:90:PRO:O	12:I:93:ARG:HG3	2.01	0.61
1:A:939:G:H5"	10:G:102:ARG:CZ	2.31	0.61
9:F:75:LEU:O	9:F:78:GLU:HB3	2.01	0.61
1:A:545:C:O2'	1:A:546:G:H5'	2.01	0.61
22:S:45:VAL:HG12	22:S:46:GLY:N	2.16	0.61
15:L:119:LYS:O	15:L:120:TYR:HB2	2.01	0.61
15:L:92:ASP:HB2	15:L:93:LEU:HD23	1.83	0.61
7:D:20:TYR:O	7:D:21:LEU:HD23	2.01	0.61
6:C:70:VAL:O	6:C:106:VAL:HG23	2.00	0.61
13:J:23:ILE:N	13:J:23:ILE:HD12	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:69:ALA:O	14:K:73:MET:HG2	2.00	0.61
18:O:56:LEU:HA	18:O:59:MET:HE3	1.82	0.61
23:T:87:LYS:O	23:T:91:LEU:HD12	2.01	0.61
1:A:1339:A:H2'	1:A:1340:A:O4'	2.01	0.61
13:J:82:ILE:HG22	13:J:82:ILE:O	2.00	0.61
16:M:4:ILE:CG2	16:M:5:ALA:N	2.61	0.60
16:M:32:GLU:OE1	16:M:64:TRP:HZ2	1.83	0.60
12:I:17:VAL:CG2	12:I:80:GLY:HA3	2.31	0.60
21:R:53:ARG:NH1	21:R:60:GLY:N	2.49	0.60
1:A:411:A:N9	1:A:413:G:H1'	2.15	0.60
8:E:44:GLY:HA3	8:E:62:ALA:HB2	1.81	0.60
13:J:6:ILE:HG23	13:J:98:ILE:CD1	2.30	0.60
12:I:81:ILE:O	12:I:85:LEU:HB2	2.01	0.60
5:B:136:VAL:HG12	5:B:140:HIS:NE2	2.17	0.60
1:A:975:A:C8	1:A:975:A:H5'	2.36	0.60
1:A:1030(D):A:H2'	1:A:1031:G:H5'	1.83	0.60
11:H:101:PRO:HG3	11:H:133:LEU:HD11	1.81	0.60
1:A:924:C:H5'	1:A:1399:C:OP2	2.02	0.60
5:B:8:LYS:HD2	5:B:8:LYS:N	2.16	0.60
16:M:97:PRO:HB2	16:M:101:GLN:OE1	2.01	0.60
1:A:1053:G:C4'	1:A:1054:C:H5'	2.30	0.60
23:T:67:ALA:HB2	23:T:77:ALA:HB2	1.83	0.60
1:A:1004:A:H2'	1:A:1005:A:C5'	2.25	0.60
16:M:5:ALA:HB3	16:M:8:GLU:CG	2.31	0.60
1:A:560:U:H5'	1:A:566:G:C2	2.35	0.60
22:S:53:ASN:N	22:S:53:ASN:HD22	1.99	0.60
8:E:115:VAL:CG1	8:E:116:THR:N	2.65	0.60
16:M:102:ARG:HH11	16:M:102:ARG:HB2	1.66	0.60
1:A:1347:G:O2'	1:A:1348:U:OP2	2.18	0.60
22:S:30:LEU:O	22:S:31:ILE:HD13	2.02	0.60
13:J:23:ILE:H	13:J:23:ILE:CD1	2.12	0.60
5:B:134:GLU:C	5:B:136:VAL:H	2.04	0.60
11:H:91:ARG:HG3	15:L:7:ILE:HG13	1.84	0.60
1:A:1281:U:H4'	1:A:1282:C:OP2	2.02	0.60
6:C:27:LYS:HA	6:C:30:ARG:HH12	1.64	0.60
1:A:1207:G:H2'	1:A:1208:C:H6	1.66	0.60
13:J:79:ARG:O	13:J:83:GLU:HB2	2.00	0.60
1:A:954:G:H2'	1:A:955:U:C6	2.35	0.60
5:B:115:LEU:HD21	5:B:153:ARG:CZ	2.31	0.60
1:A:858:G:O2'	1:A:859:A:H5'	2.02	0.60
9:F:82:ARG:HE	9:F:82:ARG:HA	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:29:TYR:OH	17:N:54:PRO:HG2	2.01	0.60
16:M:81:LEU:O	16:M:89:GLY:HA3	2.01	0.60
1:A:1222:G:P	22:S:77:THR:HG21	2.42	0.60
21:R:48:GLY:O	21:R:74:ARG:NH2	2.35	0.60
6:C:19:GLU:O	6:C:40:ARG:NH2	2.35	0.60
1:A:420:U:H2'	1:A:422:C:C5	2.36	0.60
1:A:686:U:O4	1:A:703:G:H1'	2.01	0.60
8:E:32:VAL:O	8:E:43:LEU:HD23	2.02	0.60
20:Q:104:LYS:O	20:Q:105:ALA:HB2	2.02	0.60
22:S:15:LEU:HD21	22:S:38:SER:CB	2.31	0.60
1:A:300:A:H2'	1:A:301:G:O4'	2.02	0.60
6:C:155:GLY:O	6:C:156:ARG:HB2	2.02	0.60
23:T:50:GLU:HA	23:T:100:ILE:HB	1.82	0.60
5:B:129:GLU:O	5:B:130:ARG:HB2	2.02	0.60
15:L:27:LEU:O	15:L:29:GLY:N	2.34	0.60
1:A:1358:U:H3'	1:A:1359:C:H6	1.65	0.60
14:K:99:GLN:HA	14:K:105:VAL:CG2	2.30	0.60
1:A:1426:C:H2'	1:A:1427:U:H6	1.66	0.60
7:D:59:ARG:HH22	7:D:66:ARG:NH1	2.00	0.60
11:H:97:VAL:HA	11:H:100:ILE:HG13	1.83	0.60
5:B:218:ALA:O	5:B:222:ILE:HG13	2.01	0.60
23:T:71:THR:O	23:T:72:LEU:HD23	2.01	0.60
1:A:1117:G:H5'	1:A:1117:G:H8	1.67	0.60
1:A:1004:A:H5'	1:A:1024:G:H1	1.66	0.60
16:M:19:LEU:O	16:M:22:ILE:HD13	2.02	0.60
8:E:92:LYS:O	8:E:118:ILE:HG22	2.02	0.60
22:S:28:LYS:HG2	22:S:29:ARG:H	1.67	0.60
1:A:1251:A:H2'	1:A:1252:A:C8	2.37	0.60
8:E:81:GLU:HG2	8:E:90:VAL:HG13	1.81	0.60
7:D:162:LEU:O	7:D:162:LEU:HD23	2.02	0.60
6:C:58:GLU:HB2	6:C:65:ALA:HB2	1.84	0.60
1:A:1329:A:P	16:M:28:ALA:HB3	2.41	0.60
22:S:3:ARG:HH22	22:S:69:HIS:CE1	2.18	0.60
1:A:1128:C:O2'	1:A:1130:A:H8	1.84	0.60
23:T:40:ALA:HB2	23:T:55:ILE:HG22	1.83	0.60
5:B:87:ARG:NH1	5:B:233:SER:HA	2.15	0.59
7:D:25:ARG:C	7:D:27:TYR:N	2.49	0.59
1:A:1195:C:H3'	1:A:1196:U:C5'	2.32	0.59
5:B:42:ILE:CD1	5:B:203:GLY:HA2	2.32	0.59
6:C:115:LEU:HD23	6:C:118:GLN:OE1	2.01	0.59
22:S:15:LEU:HD21	22:S:38:SER:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:24:GLY:HA3	16:M:66:LEU:HD22	1.84	0.59
1:A:1257:U:H5'	1:A:1258:G:OP1	2.02	0.59
23:T:96:GLY:O	23:T:97:ALA:HB3	2.02	0.59
1:A:434:U:H2'	1:A:435:C:C6	2.37	0.59
1:A:1165:C:O2'	1:A:1166:G:H5'	2.01	0.59
5:B:167:PRO:HG2	5:B:168:THR:H	1.66	0.59
15:L:47:LYS:CB	15:L:48:PRO:HD3	2.32	0.59
23:T:54:LYS:HA	23:T:57:ARG:HH11	1.67	0.59
7:D:145:GLU:C	7:D:146:ILE:HD12	2.23	0.59
9:F:3:ARG:HH21	9:F:64:GLN:NE2	2.00	0.59
7:D:101:LEU:HD23	7:D:101:LEU:C	2.22	0.59
1:A:255:G:O6	1:A:266:G:O6	2.20	0.59
1:A:179:A:H2'	1:A:180:U:C6	2.37	0.59
10:G:85:TYR:HD1	10:G:154:TYR:HE1	1.51	0.59
1:A:867:G:O2'	1:A:868:C:H5'	2.03	0.59
1:A:1182:G:O2'	1:A:1183:A:OP2	2.18	0.59
1:A:1470:G:O2'	1:A:1471:G:H5'	2.02	0.59
6:C:36:ASP:HA	6:C:39:ILE:HD12	1.83	0.59
23:T:26:ASN:HB3	23:T:71:THR:HG23	1.83	0.59
16:M:74:VAL:O	16:M:77:ASN:HB3	2.03	0.59
13:J:96:ILE:HG22	13:J:97:GLU:N	2.17	0.59
1:A:1495:U:H2'	1:A:1496:C:C6	2.37	0.59
1:A:664:G:H22	1:A:741:G:H1	1.49	0.59
8:E:78:HIS:HD2	11:H:107:LEU:HD22	1.67	0.59
17:N:21:TYR:HE2	17:N:23:ARG:NE	2.01	0.59
12:I:112:LYS:HD3	12:I:112:LYS:C	2.23	0.59
15:L:97:ARG:HB2	15:L:98:TYR:CE1	2.38	0.59
6:C:12:LEU:HD11	17:N:51:GLY:HA2	1.84	0.59
13:J:3:LYS:N	13:J:75:ILE:HA	2.18	0.59
1:A:1347:G:C2'	1:A:1348:U:OP2	2.51	0.59
6:C:25:GLY:N	6:C:28:GLN:HB2	2.15	0.59
1:A:1412:C:H2'	1:A:1413:A:C8	2.37	0.59
6:C:3:ASN:H	6:C:3:ASN:ND2	1.99	0.59
13:J:47:PHE:HB2	13:J:63:PHE:HB2	1.84	0.59
1:A:1329:A:OP1	16:M:28:ALA:HB3	2.02	0.59
10:G:58:PRO:HG2	10:G:59:LEU:H	1.67	0.59
1:A:1128:C:O2'	1:A:1130:A:C8	2.53	0.59
1:A:1413:A:H2	1:A:1487:G:H22	1.47	0.59
7:D:104:VAL:HG21	7:D:140:VAL:HG21	1.84	0.59
5:B:103:THR:HG22	5:B:103:THR:O	2.01	0.59
5:B:180:LEU:O	5:B:181:PHE:HB2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:149:ALA:HB3	7:D:152:SER:CB	2.32	0.59
1:A:666:G:H5'	1:A:726:C:H1'	1.83	0.59
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.37	0.59
1:A:1241:G:H2'	1:A:1242:C:C6	2.37	0.59
1:A:1367:C:H5'	13:J:60:ARG:NH1	2.17	0.59
5:B:187:LEU:HD23	5:B:214:ILE:HG21	1.83	0.59
20:Q:68:ARG:HH11	20:Q:68:ARG:HG2	1.68	0.59
7:D:150:GLU:H	7:D:150:GLU:CD	2.05	0.59
22:S:33:THR:HG22	22:S:34:TRP:N	2.17	0.59
6:C:147:LYS:HD2	6:C:203:PHE:HE2	1.68	0.59
20:Q:101:ARG:NE	20:Q:101:ARG:HA	2.18	0.59
5:B:114:ARG:HH12	5:B:118:LEU:HD21	1.66	0.59
1:A:947:G:H2'	1:A:948:C:O4'	2.03	0.59
12:I:93:ARG:HE	12:I:97:LYS:HE3	1.68	0.59
5:B:101:MET:HA	5:B:108:ILE:HG13	1.84	0.59
1:A:438:G:C4'	1:A:439:A:OP1	2.49	0.59
5:B:140:HIS:O	5:B:143:GLU:HB2	2.03	0.59
16:M:40:ASN:HD22	16:M:41:PRO:CD	2.16	0.59
5:B:224:GLN:O	5:B:224:GLN:HG2	2.02	0.59
1:A:619:U:O2	7:D:133:VAL:HA	2.03	0.59
1:A:1052:U:H2'	1:A:1055:A:OP1	2.03	0.58
1:A:1329:A:C2'	1:A:1330:U:H5'	2.33	0.58
13:J:12:ASP:HB3	13:J:15:THR:HB	1.85	0.58
5:B:200:ILE:HD12	5:B:200:ILE:O	2.02	0.58
5:B:118:LEU:HD11	5:B:141:GLU:OE2	2.03	0.58
1:A:149:A:O2'	1:A:150:C:H5'	2.02	0.58
1:A:160:A:H2'	1:A:161:A:O4'	2.02	0.58
7:D:57:ARG:NH2	7:D:205:GLU:OE2	2.36	0.58
1:A:1182:G:H4'	1:A:1183:A:H5"	1.84	0.58
1:A:46:G:H2'	1:A:366:C:C5	2.38	0.58
5:B:184:VAL:N	5:B:198:ASP:OD2	2.33	0.58
22:S:62:ILE:HD12	22:S:63:THR:N	2.18	0.58
5:B:15:VAL:O	5:B:16:HIS:O	2.21	0.58
5:B:128:GLU:HA	5:B:135:GLN:HE21	1.68	0.58
1:A:899:C:H2'	1:A:900:A:C8	2.37	0.58
20:Q:10:VAL:O	20:Q:53:LEU:HD13	2.03	0.58
1:A:913:A:H1'	1:A:914:A:O4'	2.02	0.58
22:S:7:LYS:HD3	22:S:7:LYS:O	2.02	0.58
12:I:114:TYR:CE1	13:J:59:SER:O	2.56	0.58
1:A:1149:C:H2'	1:A:1150:U:C6	2.38	0.58
7:D:3:ARG:CZ	7:D:3:ARG:N	2.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:403:C:H2'	1:A:404:U:H6	1.67	0.58
7:D:61:LYS:HD2	7:D:207:TYR:OH	2.04	0.58
6:C:174:PRO:O	6:C:177:THR:HG22	2.04	0.58
6:C:47:LEU:HD23	6:C:68:VAL:HG11	1.85	0.58
22:S:45:VAL:HA	22:S:62:ILE:HG13	1.85	0.58
20:Q:69:LYS:O	20:Q:70:ARG:HD2	2.03	0.58
6:C:131:ARG:O	6:C:135:LYS:HG3	2.04	0.58
5:B:178:ARG:HG3	5:B:178:ARG:NH1	2.11	0.58
5:B:130:ARG:CB	5:B:131:PRO:HD2	2.33	0.58
5:B:25:ASN:HD22	5:B:27:LYS:H	1.50	0.58
12:I:78:LYS:HD3	12:I:101:PHE:HD2	1.68	0.58
19:P:52:ASP:O	19:P:52:ASP:OD1	2.21	0.58
18:O:41:GLU:HA	18:O:44:LYS:HG2	1.85	0.58
17:N:37:PHE:CE2	17:N:53:LEU:HD13	2.39	0.58
1:A:1226:C:O2	22:S:83:HIS:NE2	2.36	0.58
6:C:64:VAL:HG12	6:C:66:VAL:HG23	1.85	0.58
1:A:481:G:O2'	1:A:483:C:N4	2.37	0.58
11:H:109:ILE:HG13	11:H:110:ALA:N	2.18	0.58
16:M:23:TYR:HB2	16:M:67:GLU:OE2	2.03	0.58
1:A:691:G:O2'	1:A:797:C:H4'	2.03	0.58
1:A:1158:C:H5"	5:B:133:LYS:HE3	1.85	0.58
22:S:28:LYS:HG2	22:S:29:ARG:N	2.17	0.58
22:S:25:LYS:N	22:S:25:LYS:HD2	2.19	0.58
1:A:613:C:O2'	1:A:614:A:H5'	2.02	0.58
11:H:103:VAL:HG21	11:H:110:ALA:HB2	1.86	0.58
1:A:21:G:H2'	1:A:22:G:C8	2.39	0.58
8:E:122:GLU:OE1	8:E:131:ILE:HG13	2.03	0.58
12:I:79:LEU:CD1	12:I:83:ARG:HD2	2.34	0.58
20:Q:66:SER:O	20:Q:70:ARG:NH1	2.37	0.58
1:A:1138:G:C6	1:A:1140:C:H1'	2.38	0.58
9:F:10:LEU:HD11	9:F:59:TYR:HD2	1.69	0.58
15:L:88:GLY:H	15:L:98:TYR:HA	1.69	0.58
10:G:23:VAL:CG1	10:G:27:ILE:HD11	2.34	0.58
1:A:1091:U:O2	1:A:1093:A:C8	2.57	0.58
13:J:31:GLY:HA2	13:J:78:ASN:ND2	2.19	0.58
1:A:961:U:O2'	1:A:962:C:H5'	2.03	0.58
6:C:29:TYR:CZ	17:N:54:PRO:HG2	2.39	0.58
1:A:977:A:H2'	1:A:978:A:C5'	2.32	0.58
1:A:254:G:O2'	1:A:255:G:H5'	2.04	0.58
1:A:256:U:H2'	1:A:257:G:C8	2.39	0.58
1:A:939:G:H2'	1:A:940:C:C6	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1320:C:N3	22:S:36:ARG:HG3	2.19	0.58
21:R:57:GLY:C	21:R:58:LEU:HD23	2.24	0.58
1:A:403:C:O2'	1:A:404:U:H5'	2.04	0.58
1:A:915:A:H2'	1:A:916:G:H5'	1.84	0.58
1:A:284:G:H2'	1:A:285:G:H8	1.69	0.58
1:A:1053:G:C3'	1:A:1054:C:H5'	2.34	0.58
1:A:1366:C:H2'	1:A:1367:C:C6	2.34	0.58
13:J:51:ARG:HB3	13:J:59:SER:HB3	1.86	0.58
16:M:60:VAL:HG22	16:M:64:TRP:CZ3	2.39	0.58
16:M:81:LEU:O	16:M:86:CYS:HB3	2.03	0.58
13:J:94:VAL:HG12	13:J:95:GLU:H	1.66	0.58
5:B:28:PHE:CE1	5:B:189:ASP:HA	2.39	0.58
13:J:81:THR:C	13:J:83:GLU:H	2.07	0.58
1:A:1495:U:H2'	1:A:1496:C:H6	1.69	0.58
19:P:67:THR:HG22	19:P:68:ASP:N	2.19	0.58
1:A:1030(A):G:H1'	1:A:1031:G:N2	2.19	0.58
7:D:132:ARG:O	7:D:133:VAL:HG23	2.04	0.58
1:A:882:C:O2'	1:A:883:C:H5'	2.03	0.58
12:I:114:TYR:H	12:I:114:TYR:HD2	1.51	0.58
5:B:19:HIS:HB3	5:B:189:ASP:OD2	2.04	0.58
7:D:174:LEU:O	7:D:186:LEU:HD11	2.03	0.58
5:B:100:GLY:O	5:B:104:ASN:N	2.36	0.58
18:O:50:HIS:O	18:O:53:HIS:N	2.37	0.58
18:O:87:ILE:O	18:O:88:ARG:HB2	2.04	0.58
1:A:1423:G:O2'	1:A:1424:C:H5'	2.03	0.58
8:E:15:ARG:O	8:E:27:ARG:O	2.22	0.58
19:P:21:VAL:HG21	19:P:59:TRP:CD1	2.39	0.57
16:M:29:ARG:HB3	16:M:64:TRP:CH2	2.39	0.57
20:Q:67:LYS:O	20:Q:68:ARG:HB2	2.03	0.57
7:D:8:VAL:O	7:D:10:ARG:N	2.37	0.57
11:H:63:LEU:N	11:H:63:LEU:HD22	2.17	0.57
7:D:146:ILE:N	7:D:146:ILE:CD1	2.67	0.57
5:B:142:LEU:HD22	5:B:146:GLN:HE22	1.68	0.57
18:O:53:HIS:O	18:O:56:LEU:HB3	2.03	0.57
10:G:146:GLU:HA	10:G:149:ARG:HG2	1.85	0.57
9:F:101:ALA:HA	21:R:28:GLU:HG3	1.85	0.57
11:H:1:MET:HG2	11:H:2:LEU:N	2.19	0.57
18:O:70:LEU:HD12	18:O:78:TYR:CA	2.34	0.57
1:A:993:G:H4'	1:A:994:A:OP2	2.04	0.57
1:A:1132:C:H2'	1:A:1133:G:C8	2.38	0.57
1:A:1277:C:H2'	1:A:1278:U:C5'	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:21:VAL:HG23	10:G:22:LEU:N	2.19	0.57
23:T:48:LYS:O	23:T:52:ALA:HB2	2.05	0.57
7:D:191:ARG:HD2	7:D:191:ARG:O	2.03	0.57
1:A:1407:C:O2'	1:A:1408:A:H5'	2.04	0.57
6:C:130:VAL:O	6:C:134:ILE:HG13	2.04	0.57
1:A:1154:G:H2'	1:A:1155:G:H8	1.69	0.57
1:A:1250:A:C5'	12:I:68:GLY:H	2.17	0.57
14:K:110:ASP:HB2	21:R:88:LYS:HD2	1.86	0.57
22:S:13:ASP:O	22:S:16:LEU:HB3	2.04	0.57
1:A:457:C:H2'	1:A:458:C:H6	1.67	0.57
8:E:144:THR:HG22	8:E:146:ALA:H	1.69	0.57
10:G:140:ASP:O	10:G:143:ARG:HB2	2.03	0.57
1:A:6:G:H4'	1:A:298:A:H4'	1.87	0.57
1:A:26:A:N6	1:A:558:G:H1'	2.20	0.57
10:G:12:LEU:HD12	10:G:12:LEU:N	2.19	0.57
16:M:23:TYR:CB	16:M:67:GLU:HA	2.35	0.57
6:C:59:ARG:HH11	6:C:97:LYS:HZ2	1.52	0.57
20:Q:97:SER:CB	20:Q:103:GLY:HA2	2.34	0.57
6:C:77:ILE:O	6:C:83:ARG:HB3	2.05	0.57
1:A:190(J):U:H2'	1:A:190(K):G:C8	2.40	0.57
1:A:1106:G:H5"	6:C:172:ARG:HG2	1.87	0.57
1:A:1007:C:N4	1:A:1022:G:H1	2.02	0.57
5:B:186:ALA:HB3	5:B:197:VAL:HG11	1.85	0.57
22:S:20:LEU:HD12	22:S:21:GLU:H	1.70	0.57
1:A:1104:G:O5'	5:B:111:ARG:HD2	2.04	0.57
1:A:178:C:O2'	1:A:179:A:H5'	2.04	0.57
1:A:1277:C:O2'	1:A:1279:A:H1'	2.05	0.57
10:G:85:TYR:O	10:G:87:VAL:HG23	2.05	0.57
1:A:1522:U:O2'	1:A:1523:G:H5'	2.05	0.57
1:A:413:G:H22	1:A:428:G:H1'	1.70	0.57
20:Q:8:GLY:HA3	20:Q:21:VAL:HG12	1.87	0.57
13:J:49:VAL:O	13:J:60:ARG:HA	2.05	0.57
12:I:29:ASN:HD21	12:I:64:THR:CA	2.15	0.57
6:C:70:VAL:HG12	6:C:71:ALA:H	1.67	0.57
7:D:128:VAL:HG12	7:D:129:ASN:HD21	1.69	0.57
1:A:1097:C:H2'	1:A:1098:C:C6	2.39	0.57
1:A:839:U:H5'	1:A:840:C:C5	2.39	0.57
1:A:686:U:HO2'	1:A:687:A:H8	1.52	0.57
1:A:1360:A:H2'	1:A:1361:G:O4'	2.05	0.57
1:A:833:U:H2'	1:A:834:C:C6	2.38	0.57
14:K:108:ILE:HB	21:R:87:ARG:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:63:PHE:CZ	17:N:45:ARG:HG3	2.40	0.57
16:M:60:VAL:HG22	16:M:64:TRP:HZ3	1.70	0.57
19:P:18:ARG:HE	19:P:35:LYS:NZ	2.03	0.57
7:D:26:CYS:HA	7:D:31:CYS:HB2	1.86	0.57
11:H:10:LEU:CD2	11:H:83:ILE:HD11	2.35	0.57
1:A:337:C:H2'	1:A:338:A:H8	1.69	0.57
15:L:98:TYR:N	15:L:98:TYR:CD1	2.72	0.57
23:T:87:LYS:O	23:T:88:VAL:C	2.42	0.57
1:A:682:G:O2'	1:A:683:G:H5'	2.05	0.57
13:J:8:LEU:CD2	13:J:96:ILE:HG12	2.35	0.57
5:B:178:ARG:O	5:B:181:PHE:N	2.28	0.57
10:G:69:VAL:HG12	10:G:103:TRP:HE3	1.70	0.57
14:K:48:ILE:HD12	14:K:63:LEU:CB	2.34	0.57
21:R:36:ASN:O	21:R:39:VAL:HG12	2.05	0.57
7:D:65:ARG:HB2	7:D:75:PHE:CD1	2.40	0.57
10:G:78:ARG:NH1	10:G:154:TYR:O	2.38	0.57
6:C:46:GLU:O	6:C:48:TYR:N	2.36	0.57
14:K:21:ILE:HG12	14:K:30:VAL:HG12	1.87	0.57
1:A:1042:G:O2'	1:A:1043:C:H5'	2.04	0.57
1:A:1221:G:H4'	22:S:53:ASN:O	2.04	0.57
13:J:12:ASP:HB3	13:J:15:THR:CG2	2.35	0.57
8:E:51:VAL:HB	8:E:52:PRO:CD	2.28	0.57
5:B:178:ARG:HH11	5:B:178:ARG:CG	2.14	0.57
15:L:86:ARG:HG3	15:L:86:ARG:NH1	2.18	0.57
10:G:139:GLU:O	10:G:143:ARG:HG3	2.05	0.57
14:K:24:SER:C	14:K:26:ASN:H	2.08	0.57
1:A:227:G:O2'	19:P:62:VAL:HG11	2.05	0.57
12:I:36:TYR:CD2	12:I:37:PHE:CE2	2.93	0.57
6:C:47:LEU:H	6:C:47:LEU:HD12	1.70	0.56
14:K:84:VAL:HG11	14:K:95:ILE:HD11	1.86	0.56
22:S:4:SER:O	22:S:5:LEU:HG	2.05	0.56
1:A:1277:C:H1'	1:A:1282:C:O2	2.05	0.56
8:E:77:PRO:O	8:E:78:HIS:CB	2.53	0.56
1:A:1229:A:H2'	1:A:1230:C:C6	2.38	0.56
18:O:4:THR:OG1	18:O:7:GLU:HB2	2.04	0.56
9:F:9:VAL:HG22	9:F:60:PHE:CD2	2.39	0.56
1:A:1064:G:H4'	1:A:1065:U:H5"	1.87	0.56
6:C:36:ASP:OD1	6:C:57:ILE:HD12	2.05	0.56
17:N:36:PHE:O	17:N:37:PHE:CG	2.58	0.56
13:J:3:LYS:O	13:J:4:ILE:HD13	2.05	0.56
7:D:175:SER:CB	7:D:186:LEU:HD21	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:161:ALA:HB1	5:B:185:ILE:HD11	1.86	0.56
12:I:53:VAL:CG2	12:I:85:LEU:HD21	2.33	0.56
14:K:74:ALA:O	14:K:76:GLY:N	2.38	0.56
1:A:1054:C:H5	1:A:1196:U:C5	2.23	0.56
22:S:41:VAL:HG22	22:S:44:MET:CE	2.35	0.56
1:A:538:G:H2'	1:A:539:A:C8	2.40	0.56
5:B:45:GLN:O	5:B:48:MET:HB2	2.04	0.56
8:E:74:GLY:HA3	8:E:116:THR:HG22	1.86	0.56
23:T:57:ARG:HD2	23:T:102:GLY:CA	2.31	0.56
12:I:104:ARG:HD3	12:I:104:ARG:C	2.24	0.56
12:I:4:TYR:CD1	12:I:88:TYR:HB2	2.40	0.56
1:A:1351:U:O2'	1:A:1352:C:H5'	2.04	0.56
1:A:477:G:H2'	1:A:478:A:H8	1.70	0.56
1:A:394:G:H2'	1:A:395:C:C6	2.40	0.56
12:I:44:VAL:HG13	12:I:51:ARG:NH2	2.20	0.56
6:C:13:GLY:O	6:C:14:ILE:HD13	2.06	0.56
1:A:949:A:N7	16:M:106:ASN:ND2	2.53	0.56
5:B:76:GLN:HG3	5:B:206:ASP:OD1	2.06	0.56
1:A:1216:G:H5"	17:N:5:ALA:CB	2.33	0.56
21:R:88:LYS:HG2	21:R:88:LYS:OXT	2.05	0.56
22:S:30:LEU:HD22	22:S:31:ILE:O	2.06	0.56
9:F:100:ASN:ND2	21:R:23:LYS:HG2	2.16	0.56
16:M:30:ALA:O	16:M:34:LEU:HB2	2.06	0.56
1:A:22:G:H2'	1:A:23:C:C6	2.39	0.56
19:P:81:ARG:HG3	19:P:83:GLU:HG2	1.88	0.56
1:A:878:G:H5'	11:H:89:PRO:HG2	1.87	0.56
13:J:56:HIS:O	13:J:58:ASP:N	2.38	0.56
14:K:54:ARG:CB	14:K:54:ARG:HH11	2.07	0.56
18:O:26:GLU:HA	18:O:81:LEU:HD11	1.87	0.56
1:A:337:C:H2'	1:A:338:A:C8	2.40	0.56
1:A:1316:G:H4'	17:N:18:VAL:CG1	2.35	0.56
6:C:54:ARG:HG3	6:C:55:VAL:H	1.71	0.56
7:D:121:VAL:O	7:D:134:ASP:HA	2.05	0.56
14:K:11:LYS:O	14:K:12:ARG:HB2	2.04	0.56
6:C:33:LEU:HD11	17:N:53:LEU:CD2	2.35	0.56
15:L:41:ARG:CG	15:L:42:THR:H	1.99	0.56
16:M:23:TYR:HB3	16:M:67:GLU:HA	1.86	0.56
22:S:16:LEU:O	22:S:18:LYS:N	2.38	0.56
1:A:818:G:C2'	1:A:819:A:H5"	2.34	0.56
15:L:28:LYS:C	15:L:30:ALA:H	2.07	0.56
11:H:103:VAL:HG21	11:H:109:ILE:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1091:U:O2	1:A:1093:A:H8	1.88	0.56
7:D:177:ASP:OD1	7:D:180:GLY:N	2.39	0.56
16:M:110:ARG:HG2	16:M:110:ARG:HH11	1.71	0.56
7:D:16:GLY:O	7:D:33:MET:HE2	2.05	0.56
1:A:109:A:H2'	1:A:326:G:H21	1.70	0.56
1:A:1281:U:H5'	1:A:1282:C:H5	1.70	0.56
20:Q:27:PHE:CE1	20:Q:36:ILE:HD11	2.40	0.56
8:E:144:THR:HB	8:E:147:ASP:OD2	2.05	0.56
1:A:839:U:O2	1:A:839:U:H2'	2.05	0.56
1:A:1510:U:H2'	1:A:1511:G:C8	2.40	0.56
14:K:77:MET:CE	14:K:80:VAL:HG22	2.36	0.56
6:C:171:GLY:O	6:C:173:VAL:HG23	2.06	0.56
1:A:707:C:OP1	14:K:85:ARG:NH1	2.38	0.56
1:A:778:G:O2'	1:A:779:C:H5'	2.05	0.56
5:B:16:HIS:HE1	5:B:213:LEU:HD13	1.70	0.56
5:B:77:ALA:HB2	5:B:211:ILE:CD1	2.33	0.56
8:E:115:VAL:HG11	8:E:118:ILE:CD1	2.33	0.56
6:C:154:SER:OG	6:C:155:GLY:N	2.39	0.56
1:A:991:U:O4	1:A:1212:U:H1'	2.05	0.56
6:C:137:ALA:CA	6:C:140:ARG:HH11	2.17	0.56
17:N:4:LYS:HA	17:N:7:ILE:HD12	1.87	0.56
17:N:29:ARG:HH11	17:N:29:ARG:HG2	1.71	0.56
8:E:147:ASP:N	8:E:147:ASP:OD2	2.39	0.56
1:A:149:A:H2'	1:A:150:C:H6	1.71	0.56
1:A:1161:C:H2'	1:A:1162:C:H6	1.69	0.56
1:A:997:U:O2'	1:A:998:G:H5'	2.05	0.56
1:A:56:U:H2'	1:A:57:G:C8	2.41	0.56
6:C:34:LEU:O	6:C:34:LEU:HD23	2.06	0.56
16:M:31:LYS:O	16:M:35:GLU:HB2	2.05	0.56
16:M:6:GLY:O	16:M:8:GLU:N	2.39	0.56
13:J:35:SER:HB3	13:J:72:VAL:O	2.06	0.56
20:Q:67:LYS:CA	20:Q:70:ARG:HH12	2.12	0.56
14:K:40:ILE:HG23	14:K:75:TYR:CD2	2.41	0.56
8:E:12:LEU:C	8:E:12:LEU:HD22	2.27	0.56
12:I:125:TYR:HE1	12:I:128:ARG:HB3	1.71	0.56
10:G:23:VAL:HG12	10:G:27:ILE:CD1	2.35	0.56
1:A:1230:C:H2'	1:A:1231:G:H8	1.71	0.56
1:A:833:U:H2'	1:A:834:C:H6	1.70	0.56
1:A:959:A:C2	1:A:1222:G:O4'	2.59	0.55
1:A:760:G:N2	20:Q:104:LYS:H	2.04	0.55
17:N:11:LYS:C	17:N:13:THR:H	2.10	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:G:O2'	1:A:259:G:H5'	2.05	0.55
1:A:91:C:H2'	1:A:92:C:H6	1.71	0.55
1:A:1437:C:H2'	1:A:1438:G:H8	1.70	0.55
13:J:24:VAL:O	13:J:28:ARG:HG3	2.06	0.55
12:I:117:HIS:HB2	12:I:121:ARG:O	2.07	0.55
6:C:24:ALA:HB1	6:C:28:GLN:HB3	1.86	0.55
12:I:59:PHE:HZ	12:I:88:TYR:CD2	2.25	0.55
1:A:791:G:H2'	1:A:792:A:H5"	1.88	0.55
6:C:177:THR:O	6:C:177:THR:HG23	2.06	0.55
1:A:1106:G:OP1	6:C:172:ARG:HD3	2.06	0.55
5:B:228:GLY:O	5:B:229:VAL:C	2.43	0.55
1:A:401:C:H1'	1:A:622:A:H1'	1.88	0.55
1:A:1465:C:O2'	1:A:1466:C:H5'	2.06	0.55
1:A:1316:G:N2	1:A:1318:A:H3'	2.20	0.55
1:A:889:A:H5'	1:A:891:U:H1'	1.89	0.55
1:A:35:G:H2'	1:A:36:C:C6	2.41	0.55
1:A:538:G:H2'	1:A:539:A:H8	1.71	0.55
12:I:93:ARG:NE	12:I:97:LYS:HE3	2.21	0.55
5:B:111:ARG:HA	5:B:111:ARG:NE	2.22	0.55
21:R:36:ASN:HD21	21:R:38:GLU:HG2	1.70	0.55
1:A:1358:U:H3'	1:A:1359:C:C6	2.41	0.55
11:H:107:LEU:N	11:H:107:LEU:CD1	2.70	0.55
7:D:6:GLY:H	7:D:115:ARG:HH22	1.54	0.55
1:A:1367:C:C2	1:A:1368:G:C8	2.94	0.55
6:C:134:ILE:CG2	6:C:168:ALA:HB3	2.37	0.55
20:Q:96:GLN:O	20:Q:97:SER:CB	2.54	0.55
1:A:338:A:H2'	1:A:339:C:H6	1.71	0.55
1:A:818:G:H3'	1:A:819:A:C5'	2.37	0.55
1:A:974:A:H8	1:A:974:A:OP1	1.89	0.55
9:F:48:LEU:HD21	9:F:60:PHE:CZ	2.41	0.55
11:H:14:ARG:HH11	11:H:14:ARG:HB3	1.72	0.55
1:A:547:A:H4'	1:A:548:G:O5'	2.06	0.55
1:A:1454:G:H2'	1:A:1455:G:H8	1.72	0.55
11:H:48:TYR:CD1	11:H:48:TYR:C	2.78	0.55
16:M:26:GLY:O	16:M:28:ALA:N	2.39	0.55
1:A:266:G:H5'	1:A:266:G:C8	2.42	0.55
20:Q:67:LYS:HA	20:Q:70:ARG:NH1	2.13	0.55
11:H:24:THR:HG23	11:H:61:VAL:HB	1.89	0.55
1:A:443:C:O2'	1:A:444:C:H5'	2.06	0.55
1:A:644:G:O2'	1:A:645:C:H5'	2.06	0.55
9:F:38:GLU:HB2	9:F:64:GLN:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:25:THR:HB	21:R:42:ARG:HH22	1.71	0.55
1:A:838:G:C2'	1:A:839:U:H5"	2.37	0.55
1:A:1521:G:H2'	1:A:1522:U:C6	2.41	0.55
1:A:1472:U:O2'	1:A:1473:A:H5'	2.06	0.55
5:B:84:GLU:HA	5:B:87:ARG:HB2	1.88	0.55
1:A:1223:C:OP1	1:A:1224:G:H3'	2.06	0.55
13:J:5:ARG:HA	13:J:73:ASP:OD1	2.07	0.55
1:A:1349:A:OP2	12:I:118:LYS:NZ	2.40	0.55
7:D:64:LEU:HD12	7:D:75:PHE:HZ	1.72	0.55
19:P:12:LYS:O	19:P:13:HIS:HB2	2.07	0.55
17:N:9:LYS:HG3	17:N:21:TYR:O	2.06	0.55
1:A:998:G:O2'	1:A:999:C:H5'	2.07	0.55
1:A:1264:C:H2'	1:A:1265:G:H8	1.72	0.55
13:J:45:ARG:NH2	17:N:36:PHE:CD2	2.75	0.55
1:A:1326:C:H5"	24:V:12:LYS:HZ2	1.71	0.55
7:D:18:LYS:HE2	7:D:20:TYR:HE2	1.71	0.55
9:F:10:LEU:HD12	9:F:59:TYR:O	2.07	0.55
22:S:31:ILE:HG22	22:S:32:LYS:N	2.18	0.55
11:H:36:LEU:CD1	11:H:59:LEU:HD13	2.37	0.55
22:S:12:ASP:O	22:S:15:LEU:HG	2.07	0.55
21:R:48:GLY:N	21:R:82:THR:HA	2.22	0.55
5:B:90:MET:SD	5:B:90:MET:N	2.80	0.55
1:A:58:C:O2'	1:A:59:A:H5'	2.06	0.55
1:A:1226:C:H1'	22:S:83:HIS:HE1	1.68	0.55
22:S:10:PHE:CD2	22:S:11:VAL:N	2.75	0.55
1:A:1320:C:O2	22:S:36:ARG:NH1	2.40	0.55
5:B:91:PRO:HG3	5:B:154:LEU:HB2	1.88	0.55
8:E:6:PHE:HB3	8:E:34:VAL:CG1	2.37	0.55
1:A:590:C:O2'	1:A:591:U:H5'	2.07	0.55
1:A:1306:A:H2'	1:A:1307:U:O4'	2.06	0.54
16:M:36:LYS:HD2	16:M:59:TYR:CZ	2.42	0.54
5:B:74:LYS:HZ3	5:B:206:ASP:HB2	1.72	0.54
15:L:28:LYS:C	15:L:30:ALA:N	2.59	0.54
1:A:975:A:O2'	17:N:32:SER:HA	2.07	0.54
6:C:91:LEU:HG	6:C:99:VAL:HG21	1.89	0.54
1:A:647:C:H2'	1:A:648:A:H8	1.72	0.54
1:A:165:C:H2'	1:A:166:G:H8	1.72	0.54
4:Z:2:U:H5'	4:Z:2:U:H6	1.73	0.54
12:I:8:GLY:HA2	12:I:79:LEU:CD1	2.32	0.54
12:I:86:VAL:HG13	12:I:90:PRO:HA	1.89	0.54
1:A:255:G:H1'	20:Q:16:GLN:NE2	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:4:ASP:OD2	11:H:85:ARG:NH1	2.40	0.54
1:A:939:G:C5'	10:G:102:ARG:HH12	2.20	0.54
5:B:223:ILE:HD13	5:B:230:VAL:HG21	1.89	0.54
1:A:398:C:O2'	1:A:399:G:H5'	2.07	0.54
18:O:45:VAL:HB	18:O:46:HIS:ND1	2.22	0.54
15:L:41:ARG:HH11	15:L:41:ARG:HB3	1.72	0.54
1:A:1309:G:O3'	16:M:77:ASN:ND2	2.40	0.54
1:A:797:C:O2'	1:A:798:G:H5'	2.06	0.54
1:A:1279:A:H5"	1:A:1280:A:OP1	2.07	0.54
1:A:1402:C:O2	1:A:1500:A:N1	2.41	0.54
6:C:18:TRP:HE3	6:C:18:TRP:H	1.56	0.54
1:A:499:A:H4'	1:A:500:G:H5'	1.88	0.54
1:A:951:G:O2'	1:A:952:U:H5'	2.06	0.54
17:N:22:THR:OG1	17:N:33:VAL:HG21	2.07	0.54
5:B:28:PHE:CZ	5:B:189:ASP:HA	2.42	0.54
1:A:942:G:H2'	1:A:943:U:H6	1.71	0.54
1:A:110:C:H2'	1:A:111:G:O4'	2.06	0.54
1:A:818:G:C3'	1:A:819:A:H5"	2.37	0.54
5:B:137:ARG:HA	5:B:140:HIS:HD2	1.73	0.54
21:R:40:LEU:O	21:R:42:ARG:N	2.41	0.54
22:S:22:LEU:CD2	22:S:28:LYS:HD2	2.38	0.54
15:L:83:VAL:HG22	15:L:100:ILE:HG23	1.89	0.54
1:A:644:G:C5	1:A:645:C:C5	2.96	0.54
1:A:1291:G:H4'	12:I:38:GLN:O	2.08	0.54
1:A:437:U:H5"	7:D:155:LEU:HD22	1.89	0.54
1:A:528:C:H5'	1:A:535:A:N6	2.23	0.54
9:F:2:ARG:NE	9:F:69:GLU:HG2	2.22	0.54
22:S:15:LEU:CD2	22:S:33:THR:HG21	2.38	0.54
16:M:40:ASN:HD22	16:M:41:PRO:HD2	1.73	0.54
1:A:1300:G:HO2'	1:A:1301:U:H6	1.54	0.54
8:E:101:ILE:HD12	8:E:119:LEU:HD23	1.89	0.54
6:C:43:LEU:HD12	6:C:68:VAL:HG21	1.88	0.54
1:A:539:A:H2'	1:A:540:G:C8	2.43	0.54
5:B:10:LEU:HD23	5:B:10:LEU:O	2.08	0.54
6:C:167:TRP:O	6:C:168:ALA:HB3	2.07	0.54
17:N:9:LYS:C	17:N:9:LYS:HD3	2.28	0.54
1:A:1533:C:O2'	1:A:1534:A:H5'	2.08	0.54
19:P:34:GLU:OE2	19:P:55:ARG:HD3	2.08	0.54
7:D:12:CYS:SG	7:D:19:LEU:O	2.66	0.54
6:C:188:LEU:HD13	6:C:189:ALA:N	2.15	0.54
1:A:1255:G:O2'	1:A:1258:G:H1'	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1381:U:H2'	1:A:1382:C:H6	1.72	0.54
1:A:1293:G:O2'	1:A:1294:G:H5'	2.08	0.54
1:A:929:G:H5"	1:A:1533:C:N4	2.23	0.54
5:B:73:THR:HG23	5:B:95:GLN:O	2.08	0.54
12:I:79:LEU:HD13	12:I:79:LEU:C	2.28	0.54
1:A:1342:C:O2'	1:A:1343:G:H5'	2.07	0.54
12:I:118:LYS:O	12:I:119:ALA:CB	2.56	0.54
1:A:448:A:H2'	1:A:449:C:C6	2.43	0.54
1:A:920:U:H2'	1:A:921:U:H6	1.71	0.54
1:A:287:U:C2'	1:A:288:A:H5'	2.38	0.54
8:E:57:LYS:HG2	8:E:61:TYR:CE2	2.43	0.54
10:G:145:ALA:O	10:G:147:ALA:N	2.41	0.54
1:A:1366:C:C2	1:A:1367:C:C5	2.96	0.54
20:Q:45:HIS:CD2	20:Q:47:PRO:HG3	2.42	0.54
14:K:110:ASP:HB2	21:R:88:LYS:CD	2.38	0.54
11:H:20:TYR:CE1	11:H:76:PRO:HD2	2.43	0.54
8:E:102:ALA:HB1	8:E:106:PRO:HB2	1.90	0.54
23:T:100:ILE:O	23:T:100:ILE:HG12	2.08	0.54
1:A:1258:G:H1	1:A:1277:C:N4	2.05	0.54
7:D:126:ILE:CG2	7:D:127:THR:N	2.69	0.54
1:A:664:G:H2'	1:A:666:G:OP1	2.07	0.54
1:A:1428:A:H2'	1:A:1429:C:C6	2.43	0.54
11:H:11:THR:HA	11:H:14:ARG:NH1	2.23	0.54
1:A:513:C:H2'	1:A:514:C:C6	2.43	0.54
5:B:166:ASP:OD2	5:B:169:LYS:HB2	2.08	0.54
7:D:76:ARG:HH11	7:D:76:ARG:HG2	1.73	0.54
1:A:281:G:O2'	1:A:282:A:OP2	2.22	0.53
1:A:502:G:H2'	1:A:503:C:H6	1.72	0.53
12:I:16:ARG:HB2	12:I:64:THR:HB	1.90	0.53
1:A:1497:G:C2'	1:A:1498:U:H5'	2.38	0.53
12:I:59:PHE:O	12:I:60:ASP:HB2	2.07	0.53
14:K:123:LYS:O	14:K:124:LYS:C	2.47	0.53
20:Q:95:TYR:O	20:Q:97:SER:N	2.42	0.53
1:A:750:G:C2	18:O:23:GLY:HA3	2.43	0.53
16:M:116:THR:HG22	16:M:117:VAL:N	2.23	0.53
20:Q:59:ILE:HG23	20:Q:71:PHE:CD1	2.43	0.53
21:R:86:VAL:O	21:R:87:ARG:HB2	2.08	0.53
1:A:1461:G:O2'	1:A:1462:G:H5'	2.08	0.53
14:K:120:ARG:NH2	14:K:126:ARG:NH1	2.56	0.53
1:A:657:G:O2'	1:A:658:G:H5'	2.09	0.53
1:A:730:G:N2	1:A:765:G:H5"	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:33:MET:HE3	7:D:37:PRO:HB3	1.91	0.53
1:A:953:G:H2'	1:A:954:G:O4'	2.09	0.53
9:F:75:LEU:HD13	9:F:75:LEU:C	2.29	0.53
22:S:33:THR:HG22	22:S:35:SER:H	1.73	0.53
1:A:16:A:C2'	1:A:17:U:H5'	2.39	0.53
1:A:923:A:OP1	8:E:21:ALA:HB2	2.08	0.53
1:A:722:A:H4'	1:A:723:U:C5	2.44	0.53
1:A:254:G:H21	20:Q:16:GLN:NE2	2.07	0.53
22:S:85:LYS:O	22:S:86:GLU:HG2	2.07	0.53
14:K:43:SER:HA	14:K:47:VAL:HG21	1.88	0.53
6:C:147:LYS:HD2	6:C:203:PHE:CE2	2.44	0.53
1:A:1475:G:H2'	1:A:1476:G:C8	2.39	0.53
1:A:1070:U:O2'	1:A:1071:C:H5'	2.07	0.53
1:A:1003(A):G:O2'	1:A:1004:A:H4'	2.08	0.53
15:L:126:LYS:N	15:L:126:LYS:HD2	2.23	0.53
13:J:12:ASP:OD1	13:J:14:LYS:N	2.39	0.53
1:A:101:A:O2'	1:A:102:G:H5'	2.07	0.53
16:M:69:GLU:O	16:M:72:ALA:HB3	2.08	0.53
1:A:750:G:H1'	18:O:22:THR:OG1	2.08	0.53
15:L:43:VAL:CG1	15:L:44:THR:N	2.71	0.53
5:B:9:GLU:OE1	5:B:12:GLU:HA	2.08	0.53
11:H:4:ASP:OD2	11:H:7:ALA:HB2	2.08	0.53
11:H:86:ILE:O	11:H:88:LYS:HG2	2.08	0.53
7:D:55:ALA:O	7:D:59:ARG:HG2	2.08	0.53
8:E:15:ARG:O	8:E:16:THR:CB	2.56	0.53
6:C:172:ARG:HH11	6:C:172:ARG:HB3	1.74	0.53
1:A:1264:C:H2'	1:A:1265:G:C8	2.43	0.53
9:F:40:VAL:CG1	9:F:41:GLU:N	2.72	0.53
13:J:63:PHE:CE1	17:N:45:ARG:HG3	2.44	0.53
8:E:105:VAL:HB	8:E:106:PRO:HD3	1.90	0.53
8:E:80:ILE:N	8:E:80:ILE:HD12	2.23	0.53
5:B:78:GLN:HA	5:B:94:ASN:OD1	2.07	0.53
6:C:70:VAL:HG12	6:C:72:LYS:H	1.74	0.53
22:S:30:LEU:C	22:S:31:ILE:HD13	2.29	0.53
1:A:518:C:O2'	1:A:519:C:OP2	2.24	0.53
1:A:190(E):U:O2'	20:Q:63:ARG:NH2	2.41	0.53
1:A:620:C:C6	7:D:135:LEU:HD13	2.44	0.53
16:M:15:VAL:HG22	16:M:45:VAL:HG22	1.91	0.53
1:A:1511:G:H2'	1:A:1512:U:O4'	2.08	0.53
15:L:61:THR:C	15:L:63:GLY:H	2.12	0.53
18:O:46:HIS:N	18:O:46:HIS:ND1	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:513:C:H2'	1:A:514:C:H6	1.72	0.53
1:A:743:U:H2'	1:A:744:C:C6	2.43	0.53
1:A:1054:C:N4	3:Y:34:G:C8	2.72	0.53
5:B:15:VAL:HG11	5:B:209:ARG:HB3	1.90	0.53
5:B:178:ARG:O	5:B:180:LEU:N	2.41	0.53
6:C:62:ASP:HA	6:C:97:LYS:HG3	1.88	0.53
1:A:692:U:OP1	14:K:124:LYS:HE3	2.08	0.53
1:A:112:G:N2	1:A:354:G:H5'	2.23	0.53
11:H:23:SER:C	11:H:24:THR:HG22	2.28	0.53
22:S:15:LEU:HD12	22:S:15:LEU:C	2.29	0.53
5:B:137:ARG:HB3	5:B:137:ARG:NH1	2.24	0.53
1:A:1487:G:O2'	1:A:1488:G:H5'	2.08	0.53
1:A:75:G:HO2'	1:A:76:C:H5'	1.74	0.53
1:A:1000:U:H2'	1:A:1001:A:O4'	2.08	0.53
12:I:33:PHE:C	12:I:35:GLU:H	2.12	0.53
7:D:34:GLU:HG3	7:D:35:ARG:NH2	2.24	0.53
1:A:277:C:H5"	20:Q:68:ARG:NH2	2.24	0.53
8:E:111:GLU:C	8:E:113:ALA:H	2.11	0.53
6:C:118:GLN:O	6:C:122:GLU:HG3	2.09	0.53
1:A:1313:U:OP2	22:S:6:LYS:HA	2.08	0.53
1:A:1038:C:H2'	1:A:1039:C:C5	2.44	0.53
1:A:915:A:C2'	1:A:916:G:H5'	2.39	0.53
1:A:889:A:N1	1:A:907:A:H5"	2.24	0.53
6:C:42:LEU:HA	6:C:45:LYS:HB2	1.91	0.53
1:A:47:C:H5"	1:A:365:U:C6	2.44	0.53
1:A:80:G:H3'	1:A:81:U:H5"	1.91	0.53
5:B:45:GLN:CD	5:B:45:GLN:H	2.12	0.53
7:D:8:VAL:HG12	7:D:21:LEU:HD13	1.90	0.53
7:D:187:ARG:HE	7:D:188:LEU:H	1.56	0.53
1:A:1167:A:H2'	1:A:1168:A:C8	2.43	0.53
15:L:75:HIS:HD2	15:L:77:LEU:N	2.05	0.53
1:A:474:G:O2'	1:A:475:G:H5'	2.09	0.53
11:H:14:ARG:O	11:H:18:ARG:HD3	2.09	0.53
1:A:166:G:O2'	1:A:167:G:H5'	2.09	0.53
1:A:1247:U:O2'	1:A:1248:A:H5'	2.09	0.53
9:F:22:GLU:OE2	9:F:84:ASN:HB2	2.08	0.53
1:A:105:G:H2'	1:A:106:C:C6	2.44	0.53
11:H:86:ILE:HD11	11:H:136:GLU:CB	2.38	0.53
20:Q:12:SER:HB3	20:Q:20:THR:CB	2.38	0.53
23:T:56:MET:HE1	23:T:104:LEU:HG	1.91	0.53
23:T:63:ILE:HD13	23:T:80:ARG:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:28:PHE:O	8:E:47:LYS:HA	2.09	0.53
6:C:57:ILE:CG2	6:C:58:GLU:N	2.72	0.52
13:J:16:LEU:HD23	13:J:94:VAL:HG13	1.90	0.52
13:J:4:ILE:O	13:J:6:ILE:HG13	2.09	0.52
1:A:1348:U:H2'	1:A:1349:A:C8	2.28	0.52
1:A:1372:U:O2'	1:A:1373:G:H5'	2.09	0.52
11:H:83:ILE:O	11:H:83:ILE:HG23	2.09	0.52
1:A:180:U:C2'	1:A:181:G:H5'	2.37	0.52
1:A:490:G:H2'	1:A:491:G:H8	1.74	0.52
10:G:116:ALA:HA	10:G:119:ARG:NH2	2.23	0.52
18:O:48:LYS:O	18:O:50:HIS:N	2.42	0.52
10:G:75:VAL:HA	10:G:87:VAL:O	2.08	0.52
1:A:652:U:O4	1:A:752:G:O2'	2.20	0.52
1:A:1441:G:H4'	1:A:1442:G:C5	2.44	0.52
19:P:22:THR:HA	19:P:33:ILE:CD1	2.25	0.52
5:B:21:ARG:HH11	5:B:21:ARG:HG3	1.74	0.52
20:Q:68:ARG:N	20:Q:70:ARG:NH1	2.57	0.52
5:B:178:ARG:NH2	5:B:196:LEU:HA	2.21	0.52
5:B:50:GLU:HG3	5:B:200:ILE:CD1	2.38	0.52
1:A:1124:G:C3'	1:A:1145:C:H41	2.19	0.52
10:G:65:ALA:O	10:G:69:VAL:HG23	2.09	0.52
9:F:91:VAL:HG13	21:R:72:ARG:NH2	2.23	0.52
19:P:28:ARG:NH1	19:P:28:ARG:HG2	2.22	0.52
23:T:92:LEU:O	23:T:96:GLY:HA3	2.10	0.52
10:G:15:ASP:OD1	10:G:44:TYR:OH	2.27	0.52
5:B:230:VAL:HG12	5:B:231:GLU:N	2.24	0.52
1:A:676:A:H1'	14:K:115:PRO:HB3	1.92	0.52
23:T:24:LEU:O	23:T:24:LEU:HD12	2.10	0.52
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.43	0.52
15:L:102:ARG:NH2	15:L:110:VAL:HA	2.25	0.52
1:A:1222:G:OP1	22:S:77:THR:HG21	2.10	0.52
5:B:159:PRO:HB2	5:B:161:ALA:O	2.09	0.52
6:C:139:GLN:O	6:C:143:GLU:N	2.41	0.52
12:I:4:TYR:CE2	12:I:88:TYR:HA	2.45	0.52
1:A:760:G:H1	20:Q:105:ALA:CA	2.19	0.52
1:A:818:G:C3'	1:A:819:A:C5'	2.86	0.52
18:O:65:ARG:HH11	18:O:65:ARG:HB2	1.72	0.52
20:Q:60:ILE:HD13	20:Q:61:GLU:H	1.72	0.52
1:A:344:A:H5"	1:A:345:C:H5	1.74	0.52
1:A:1241:G:H2'	1:A:1242:C:H6	1.75	0.52
18:O:17:ARG:HH11	18:O:17:ARG:HG3	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1056:U:H5'	6:C:163:ALA:CB	2.39	0.52
1:A:1060:C:O2'	1:A:1061:G:H5'	2.09	0.52
15:L:119:LYS:O	15:L:120:TYR:CB	2.57	0.52
7:D:142:PRO:CG	7:D:187:ARG:HH21	2.21	0.52
15:L:50:SER:O	15:L:51:ALA:HB2	2.10	0.52
1:A:1151:A:O2'	1:A:1152:A:H8	1.91	0.52
1:A:1286:A:C8	1:A:1287:A:H4'	2.44	0.52
1:A:98:U:O2'	1:A:99:C:H5'	2.08	0.52
21:R:74:ARG:HB3	21:R:81:PHE:CZ	2.44	0.52
1:A:1023:G:H2'	1:A:1023:G:N3	2.24	0.52
1:A:927:G:H4'	1:A:1503:A:N7	2.25	0.52
1:A:794:A:H2'	1:A:795:C:C6	2.44	0.52
14:K:33:THR:HG21	14:K:37:GLY:HA2	1.90	0.52
12:I:23:ASN:C	12:I:23:ASN:HD22	2.12	0.52
8:E:80:ILE:H	8:E:80:ILE:HD12	1.75	0.52
1:A:538:G:O2'	1:A:539:A:H5'	2.10	0.52
7:D:151:LYS:N	7:D:151:LYS:HD2	2.11	0.52
21:R:47:THR:HA	21:R:83:GLU:HB2	1.90	0.52
1:A:1256:A:O2'	1:A:1257:U:H4'	2.10	0.52
6:C:40:ARG:HG3	6:C:40:ARG:HH11	1.75	0.52
7:D:100:ARG:O	7:D:103:ASN:HB3	2.08	0.52
16:M:40:ASN:HD22	16:M:41:PRO:N	2.07	0.52
10:G:80:VAL:HG11	10:G:154:TYR:CE1	2.45	0.52
8:E:82:VAL:O	8:E:88:LYS:HA	2.09	0.52
6:C:180:ALA:O	6:C:181:ASN:HB3	2.09	0.52
7:D:111:ALA:HB3	7:D:117:ALA:HB2	1.90	0.52
23:T:76:ALA:O	23:T:80:ARG:HG2	2.09	0.52
6:C:33:LEU:HD11	17:N:53:LEU:HD22	1.90	0.52
1:A:938:A:N6	1:A:939:G:C6	2.78	0.52
11:H:82:HIS:CG	11:H:83:ILE:H	2.27	0.52
1:A:625:G:H2'	1:A:626:U:C6	2.44	0.52
20:Q:6:LEU:O	20:Q:59:ILE:N	2.37	0.52
6:C:174:PRO:HB2	6:C:177:THR:HG22	1.91	0.52
1:A:961:U:C2'	1:A:962:C:H5'	2.40	0.52
21:R:86:VAL:HG12	21:R:87:ARG:HD2	1.90	0.52
1:A:115:G:H1'	1:A:116:A:N7	2.25	0.52
6:C:90:GLU:C	6:C:92:ALA:H	2.11	0.52
1:A:1049:U:H1'	1:A:1201:A:N7	2.24	0.52
1:A:521:G:O2'	1:A:522:C:H5'	2.10	0.52
8:E:109:ILE:O	8:E:113:ALA:HB2	2.10	0.52
11:H:83:ILE:CB	11:H:137:VAL:HG22	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:60:GLY:O	21:R:64:ARG:HB2	2.09	0.52
1:A:980:C:H3'	1:A:981:U:C6	2.45	0.52
12:I:46:ALA:HA	12:I:78:LYS:HB2	1.92	0.52
12:I:46:ALA:O	12:I:49:PRO:HD2	2.10	0.52
1:A:417:C:O2'	1:A:418:C:H5'	2.10	0.52
1:A:229:U:O2'	1:A:230:G:H5'	2.10	0.52
12:I:27:THR:HG23	12:I:30:GLY:O	2.09	0.52
1:A:836:G:C6	1:A:851:G:C6	2.98	0.52
6:C:5:ILE:HD12	6:C:5:ILE:O	2.10	0.52
13:J:49:VAL:O	13:J:60:ARG:O	2.27	0.52
13:J:30:SER:CB	13:J:81:THR:HA	2.40	0.52
7:D:149:ALA:O	7:D:153:ARG:N	2.43	0.52
12:I:4:TYR:HB2	12:I:19:LEU:HB2	1.91	0.52
16:M:24:GLY:CA	16:M:66:LEU:HD22	2.39	0.52
23:T:13:LEU:HD12	23:T:13:LEU:C	2.31	0.52
1:A:866:C:H2'	1:A:867:G:O4'	2.10	0.52
1:A:1453:G:H2'	1:A:1454:G:O4'	2.10	0.52
11:H:120:THR:HG23	11:H:123:GLU:OE2	2.09	0.52
1:A:718:G:C8	14:K:116:HIS:HB3	2.45	0.52
6:C:39:ILE:O	6:C:43:LEU:HD23	2.10	0.52
17:N:35:ARG:C	17:N:37:PHE:H	2.13	0.52
1:A:1305:G:H5'	24:V:4:GLY:HA3	1.91	0.52
5:B:23:ARG:C	5:B:23:ARG:HD3	2.30	0.52
7:D:7:PRO:HG2	7:D:10:ARG:CD	2.31	0.52
14:K:74:ALA:C	14:K:76:GLY:N	2.60	0.52
15:L:70:ILE:HG12	15:L:100:ILE:HD12	1.92	0.52
1:A:186:C:H2'	1:A:187:C:C6	2.45	0.52
1:A:1105:A:H2'	1:A:1106:G:H8	1.75	0.52
1:A:996:A:H2'	1:A:997:U:C6	2.45	0.52
1:A:1238:A:OP1	1:A:1336:C:H5	1.92	0.52
1:A:19:C:H2'	1:A:20:U:H6	1.75	0.52
1:A:1260:C:O5'	1:A:1284:C:H4'	2.10	0.52
24:V:23:PRO:C	24:V:25:LYS:H	2.13	0.52
21:R:46:GLU:N	21:R:46:GLU:CD	2.63	0.52
1:A:424:G:O2'	1:A:425:G:H5'	2.10	0.52
6:C:156:ARG:HG3	6:C:156:ARG:HH11	1.74	0.52
12:I:117:HIS:C	12:I:118:LYS:HG3	2.30	0.52
12:I:117:HIS:O	12:I:118:LYS:HG3	2.10	0.52
16:M:98:VAL:O	16:M:98:VAL:HG12	2.10	0.52
22:S:15:LEU:HD23	22:S:33:THR:HG21	1.92	0.52
22:S:35:SER:C	22:S:37:ARG:H	2.13	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:24:ALA:HB3	22:S:25:LYS:HZ2	1.74	0.52
7:D:177:ASP:OD1	7:D:179:GLU:HB2	2.09	0.52
6:C:132:ARG:O	6:C:133:ALA:C	2.48	0.52
5:B:9:GLU:OE1	5:B:11:LEU:O	2.28	0.51
7:D:108:LEU:CD2	7:D:174:LEU:HD13	2.41	0.51
22:S:16:LEU:O	22:S:20:LEU:HG	2.10	0.51
15:L:89:ARG:CZ	15:L:97:ARG:HG2	2.40	0.51
5:B:144:ARG:HG3	5:B:145:LEU:N	2.24	0.51
12:I:40:LEU:O	12:I:41:VAL:C	2.48	0.51
12:I:42:ARG:O	12:I:43:ALA:C	2.48	0.51
18:O:33:THR:HG23	18:O:63:ARG:HH12	1.75	0.51
16:M:96:LEU:O	16:M:97:PRO:C	2.47	0.51
8:E:135:THR:O	8:E:138:ALA:HB3	2.10	0.51
1:A:1060:C:H5"	13:J:51:ARG:HG2	1.92	0.51
1:A:1363:A:H1'	1:A:1365:G:N7	2.25	0.51
13:J:64:GLU:N	17:N:59:ALA:HB2	2.25	0.51
23:T:67:ALA:HA	23:T:73:HIS:H	1.74	0.51
5:B:77:ALA:CB	5:B:80:ILE:HD12	2.39	0.51
7:D:187:ARG:HG3	7:D:188:LEU:N	2.26	0.51
5:B:69:LEU:C	5:B:69:LEU:HD23	2.29	0.51
11:H:83:ILE:HA	11:H:137:VAL:HG22	1.92	0.51
1:A:334:C:H2'	1:A:335:C:C6	2.46	0.51
1:A:909:A:H2'	1:A:910:C:O4'	2.10	0.51
5:B:118:LEU:HD11	5:B:141:GLU:CD	2.31	0.51
19:P:43:LYS:HB3	19:P:48:TRP:CD1	2.45	0.51
7:D:160:GLN:O	7:D:163:GLU:HB3	2.10	0.51
21:R:87:ARG:HH11	21:R:87:ARG:HG3	1.75	0.51
8:E:68:GLU:O	8:E:70:PRO:HD3	2.11	0.51
1:A:629:G:O2'	1:A:630:G:H5'	2.09	0.51
15:L:124:LYS:HE2	15:L:127:GLU:OE2	2.10	0.51
5:B:207:ALA:O	5:B:210:SER:HB3	2.10	0.51
1:A:1057:G:H2'	1:A:1058:G:O4'	2.10	0.51
12:I:126:SER:O	12:I:128:ARG:N	2.43	0.51
22:S:11:VAL:HG22	22:S:39:THR:O	2.10	0.51
1:A:1128:C:O2	1:A:1130:A:N7	2.43	0.51
1:A:107:G:H2'	1:A:108:G:H5'	1.92	0.51
15:L:93:LEU:CD2	15:L:93:LEU:H	2.00	0.51
16:M:22:ILE:CB	16:M:25:ILE:HD12	2.41	0.51
12:I:76:ALA:O	12:I:79:LEU:HB3	2.10	0.51
5:B:69:LEU:HD22	5:B:71:VAL:CG2	2.41	0.51
1:A:1153:C:H2'	1:A:1154:G:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:197:VAL:CB	5:B:200:ILE:HG23	2.37	0.51
1:A:1124:G:O2'	13:J:38:ILE:HD13	2.11	0.51
1:A:1390:U:H2'	1:A:1391:U:H6	1.75	0.51
12:I:48:GLU:HA	12:I:51:ARG:HH11	1.76	0.51
6:C:34:LEU:CD1	17:N:25:VAL:HG21	2.40	0.51
16:M:11:ARG:CG	16:M:12:ASN:N	2.72	0.51
1:A:1077:G:N2	1:A:1080:A:OP2	2.41	0.51
1:A:822:C:O2'	1:A:823:G:H5'	2.10	0.51
7:D:192:GLU:OE1	7:D:192:GLU:N	2.44	0.51
17:N:37:PHE:CZ	17:N:53:LEU:HD13	2.46	0.51
15:L:101:VAL:O	15:L:103:GLY:N	2.43	0.51
12:I:93:ARG:C	12:I:95:LYS:H	2.13	0.51
5:B:33:TYR:O	5:B:34:ALA:HB2	2.10	0.51
7:D:21:LEU:O	7:D:22:LYS:HG3	2.10	0.51
8:E:111:GLU:C	8:E:113:ALA:N	2.64	0.51
6:C:134:ILE:HD11	6:C:153:VAL:CG2	2.41	0.51
1:A:761:G:H5'	20:Q:103:GLY:H	1.75	0.51
1:A:972:C:H4'	13:J:57:LYS:CG	2.40	0.51
5:B:126:GLU:HG2	5:B:129:GLU:OE1	2.11	0.51
23:T:41:ILE:HD11	23:T:87:LYS:HZ1	1.74	0.51
1:A:258:G:H2'	1:A:259:G:C8	2.44	0.51
7:D:62:GLN:O	7:D:66:ARG:HB2	2.09	0.51
10:G:151:TYR:HA	10:G:153:HIS:CE1	2.45	0.51
7:D:111:ALA:CB	7:D:117:ALA:HB2	2.40	0.51
9:F:40:VAL:HG12	9:F:41:GLU:N	2.25	0.51
18:O:66:LEU:O	18:O:69:TYR:HB3	2.11	0.51
6:C:120:VAL:O	6:C:124:ILE:HG13	2.10	0.51
6:C:126:ARG:O	6:C:127:ARG:HB2	2.09	0.51
1:A:1431:C:H2'	1:A:1432:G:H5'	1.92	0.51
1:A:1172:C:H2'	1:A:1173:G:H8	1.74	0.51
1:A:1176:A:H2'	1:A:1177:G:C8	2.45	0.51
1:A:189:G:H2'	1:A:190:C:C6	2.45	0.51
18:O:27:VAL:O	18:O:30:ALA:HB3	2.10	0.51
1:A:223:U:H5'	23:T:68:LYS:NZ	2.25	0.51
1:A:1345:U:C2	1:A:1377:A:N1	2.79	0.51
6:C:157:ILE:CD1	6:C:166:GLU:HB2	2.37	0.51
1:A:910:C:P	15:L:97:ARG:HH22	2.33	0.51
5:B:132:LYS:HA	5:B:135:GLN:HB3	1.92	0.51
7:D:126:ILE:CG2	7:D:127:THR:H	2.24	0.51
1:A:811:C:H4'	1:A:900:A:N6	2.25	0.51
1:A:625:G:O2'	1:A:626:U:H5'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:22:LEU:HD11	10:G:101:LEU:HD21	1.92	0.51
5:B:223:ILE:C	5:B:225:ALA:N	2.64	0.51
1:A:1268:A:H2'	1:A:1269:A:C8	2.45	0.51
9:F:53:ALA:O	9:F:54:LYS:HB2	2.09	0.51
12:I:10:ARG:HD2	12:I:11:LYS:N	2.25	0.51
11:H:38:ILE:N	11:H:38:ILE:HD12	2.25	0.51
8:E:41:VAL:HG21	8:E:113:ALA:HA	1.91	0.51
11:H:135:CYS:SG	11:H:136:GLU:N	2.83	0.51
22:S:50:ALA:HA	22:S:58:VAL:O	2.11	0.51
1:A:335:C:O2'	1:A:336:C:H5'	2.11	0.51
22:S:15:LEU:HD12	22:S:16:LEU:N	2.26	0.51
1:A:1402:C:H2'	1:A:1403:C:C6	2.40	0.51
11:H:31:PHE:O	11:H:35:ILE:CD1	2.58	0.51
1:A:624:C:H2'	1:A:625:G:C8	2.44	0.51
1:A:1101:A:H4'	1:A:1102:A:O5'	2.11	0.51
23:T:8:ARG:O	23:T:9:ASN:HB2	2.11	0.51
1:A:1054:C:C2'	1:A:1055:A:H5"	2.41	0.51
19:P:18:ARG:HE	19:P:35:LYS:HZ2	1.59	0.51
13:J:75:ILE:HG22	13:J:76:ASN:N	2.24	0.51
9:F:10:LEU:CD1	9:F:59:TYR:HD2	2.24	0.51
12:I:104:ARG:HD3	12:I:105:ASP:N	2.26	0.51
6:C:139:GLN:CA	6:C:139:GLN:HE21	2.24	0.51
21:R:43:PHE:C	21:R:51:LEU:HD12	2.31	0.51
1:A:16:A:H2'	1:A:17:U:H5'	1.92	0.51
21:R:58:LEU:HD12	21:R:63:GLN:HA	1.93	0.51
11:H:107:LEU:N	11:H:107:LEU:HD12	2.26	0.51
16:M:15:VAL:HG21	16:M:48:LEU:HD21	1.92	0.51
19:P:43:LYS:HB3	19:P:48:TRP:NE1	2.25	0.51
10:G:144:MET:O	10:G:147:ALA:HB3	2.11	0.51
1:A:308:C:H2'	1:A:309:G:H8	1.75	0.51
1:A:1060:C:C2	1:A:1198:G:C2	2.99	0.51
22:S:41:VAL:HB	22:S:42:PRO:HD2	1.92	0.51
1:A:243:A:C5'	1:A:244:U:H5'	2.41	0.51
6:C:134:ILE:HG22	6:C:168:ALA:CB	2.40	0.51
1:A:1347:G:N2	1:A:1373:G:H2'	2.26	0.51
20:Q:63:ARG:HG2	20:Q:64:PRO:CD	2.41	0.51
22:S:38:SER:OG	22:S:71:LEU:HD12	2.11	0.51
15:L:43:VAL:HG23	15:L:55:VAL:HG21	1.93	0.51
23:T:38:LYS:O	23:T:39:LYS:C	2.49	0.51
1:A:1010:G:H2'	1:A:1011:G:C8	2.44	0.51
1:A:1300:G:O2'	1:A:1301:U:H6	1.94	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:657:G:H4'	18:O:28:GLN:HG2	1.91	0.51
3:Y:31:A:H2'	3:Y:32:U:O4'	2.11	0.51
1:A:39:G:O2'	1:A:40:C:H5'	2.11	0.51
1:A:1053:G:C4	1:A:1199:U:C5	2.99	0.51
1:A:1206:G:C6	1:A:1207:G:C5	2.99	0.51
16:M:86:CYS:SG	16:M:88:ARG:CG	2.97	0.51
13:J:94:VAL:CG1	13:J:95:GLU:N	2.74	0.51
1:A:1030(B):C:H2'	1:A:1030(C):G:O4'	2.10	0.51
6:C:177:THR:CG2	6:C:180:ALA:HB2	2.41	0.51
11:H:103:VAL:CG2	11:H:110:ALA:HB2	2.40	0.51
1:A:883:C:O2'	1:A:884:U:H5'	2.12	0.51
7:D:117:ALA:O	7:D:121:VAL:HG23	2.11	0.51
1:A:1431:C:C2'	1:A:1432:G:H5'	2.40	0.51
14:K:58:PRO:O	14:K:61:ALA:HB3	2.10	0.51
5:B:32:ILE:HG23	5:B:40:HIS:HB3	1.93	0.50
14:K:14:VAL:HG21	14:K:40:ILE:HD11	1.93	0.50
14:K:48:ILE:CD1	14:K:63:LEU:HB3	2.38	0.50
1:A:130:A:H5'	20:Q:63:ARG:NH2	2.26	0.50
22:S:16:LEU:C	22:S:18:LYS:N	2.64	0.50
1:A:491:G:H2'	1:A:492:G:C8	2.43	0.50
6:C:54:ARG:HG3	6:C:55:VAL:N	2.26	0.50
6:C:48:TYR:O	6:C:51:GLY:N	2.41	0.50
1:A:1466:C:H2'	1:A:1467:G:O4'	2.11	0.50
1:A:308:C:H2'	1:A:309:G:C8	2.46	0.50
8:E:151:LEU:HD11	11:H:77:GLU:OE2	2.11	0.50
20:Q:78:GLU:HG3	20:Q:78:GLU:O	2.10	0.50
22:S:42:PRO:O	22:S:43:GLU:C	2.49	0.50
1:A:1221:G:C2'	1:A:1222:G:H5'	2.41	0.50
1:A:954:G:H21	1:A:1227:A:N6	2.00	0.50
1:A:1313:U:O4	22:S:4:SER:CB	2.58	0.50
6:C:172:ARG:HB3	6:C:172:ARG:NH1	2.26	0.50
1:A:646:U:H2'	1:A:647:C:C6	2.46	0.50
21:R:18:ARG:HH22	21:R:21:LYS:HZ1	1.58	0.50
6:C:149:ALA:HA	6:C:201:TYR:O	2.11	0.50
15:L:117:ARG:CZ	15:L:124:LYS:HA	2.41	0.50
20:Q:18:THR:HG23	20:Q:69:LYS:HE3	1.92	0.50
8:E:74:GLY:CA	8:E:116:THR:HG22	2.40	0.50
6:C:188:LEU:O	6:C:189:ALA:CB	2.60	0.50
6:C:70:VAL:C	6:C:106:VAL:HG23	2.31	0.50
9:F:4:TYR:CE2	9:F:72:VAL:HG22	2.47	0.50
1:A:356:A:H1'	1:A:368:U:O2'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:2:U:OP2	2:X:3:U:H5	1.95	0.50
9:F:60:PHE:CZ	21:R:78:LEU:HD21	2.46	0.50
16:M:110:ARG:HH11	16:M:110:ARG:CG	2.25	0.50
1:A:384:G:O2'	1:A:385:C:H5'	2.11	0.50
1:A:1286:A:H2'	1:A:1287:A:H4'	1.93	0.50
1:A:1320:C:H41	22:S:37:ARG:HD3	1.76	0.50
5:B:149:LEU:O	5:B:153:ARG:HG3	2.11	0.50
9:F:101:ALA:HB2	21:R:28:GLU:HA	1.92	0.50
1:A:1300:G:O2'	1:A:1301:U:P	2.70	0.50
23:T:59:ALA:O	23:T:63:ILE:HG13	2.12	0.50
14:K:18:ARG:HD2	14:K:83:ILE:HD11	1.92	0.50
1:A:189:G:H2'	1:A:190:C:H6	1.76	0.50
21:R:18:ARG:NH2	21:R:21:LYS:NZ	2.60	0.50
1:A:321:A:O2'	1:A:322:C:H5'	2.11	0.50
1:A:633:G:H2'	1:A:634:C:C6	2.46	0.50
5:B:174:VAL:O	5:B:177:ALA:HB3	2.11	0.50
23:T:93:GLU:OE2	23:T:93:GLU:HA	2.11	0.50
1:A:1202:G:H2'	1:A:1203:C:C5'	2.41	0.50
1:A:670:G:H2'	1:A:671:G:O4'	2.11	0.50
1:A:192:U:O4'	23:T:103:GLY:HA2	2.11	0.50
5:B:92:TYR:CE1	5:B:151:GLY:HA3	2.47	0.50
6:C:47:LEU:CD1	6:C:47:LEU:N	2.73	0.50
1:A:281:G:O2'	1:A:282:A:P	2.68	0.50
19:P:55:ARG:O	19:P:56:ALA:C	2.47	0.50
8:E:107:ARG:O	8:E:110:LEU:N	2.44	0.50
6:C:186:PHE:HE1	6:C:197:GLY:HA3	1.76	0.50
1:A:940:C:H2'	1:A:941:G:H8	1.75	0.50
22:S:32:LYS:O	22:S:32:LYS:HG3	2.12	0.50
15:L:45:PRO:HB3	15:L:49:ASN:HB3	1.92	0.50
1:A:818:G:H3'	1:A:819:A:H5'	1.94	0.50
1:A:741:G:H5'	18:O:39:LEU:HD12	1.94	0.50
11:H:35:ILE:HG22	11:H:39:LEU:CD2	2.42	0.50
23:T:10:LEU:CD1	23:T:12:ALA:HB3	2.41	0.50
9:F:48:LEU:HD21	9:F:60:PHE:HZ	1.77	0.50
10:G:148:ASN:C	10:G:150:ALA:N	2.65	0.50
1:A:373:A:O2'	1:A:374:A:H5'	2.12	0.50
3:Y:33:U:H5'	3:Y:34:G:OP2	2.12	0.50
14:K:13:GLN:HA	14:K:75:TYR:O	2.12	0.50
12:I:59:PHE:HZ	12:I:88:TYR:CE2	2.30	0.50
1:A:1131:G:H1	1:A:1143:G:H21	1.60	0.50
1:A:620:C:H2'	1:A:621:A:O4'	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:13:ILE:HA	8:E:29:GLY:O	2.12	0.50
1:A:722:A:H4'	1:A:723:U:C4	2.46	0.50
1:A:1102:A:H2'	1:A:1103:C:C6	2.46	0.50
7:D:200:GLU:O	7:D:203:VAL:N	2.44	0.50
1:A:767:A:O2'	1:A:1524:C:O2	2.29	0.50
5:B:54:THR:O	5:B:57:PHE:HB3	2.12	0.50
11:H:138:TRP:OXT	11:H:138:TRP:HE3	1.94	0.50
19:P:55:ARG:O	19:P:58:TYR:N	2.45	0.50
7:D:67:ILE:C	7:D:69:GLY:H	2.15	0.50
6:C:130:VAL:HG13	6:C:153:VAL:HG21	1.92	0.50
1:A:942:G:C2	1:A:943:U:C6	3.00	0.50
12:I:111:ARG:O	12:I:119:ALA:HB2	2.12	0.50
7:D:3:ARG:N	7:D:3:ARG:NE	2.59	0.50
1:A:1096:C:O2'	1:A:1097:C:H5'	2.11	0.50
8:E:40:ARG:HG2	8:E:40:ARG:NH1	2.27	0.50
1:A:415:A:H2'	1:A:416:G:C8	2.47	0.50
12:I:30:GLY:O	12:I:31:GLN:C	2.51	0.50
14:K:100:ALA:O	14:K:102:GLY:N	2.45	0.50
16:M:46:LYS:HE2	16:M:47:ASP:CG	2.31	0.50
5:B:87:ARG:HB3	5:B:219:VAL:HG11	1.94	0.50
1:A:1062:U:H2'	1:A:1063:C:C6	2.47	0.50
1:A:518:C:O2'	15:L:50:SER:HB3	2.11	0.50
6:C:191:THR:HG21	6:C:193:TYR:CE1	2.46	0.50
5:B:137:ARG:HB3	5:B:137:ARG:HH11	1.76	0.50
6:C:52:LEU:HD12	6:C:55:VAL:CG2	2.42	0.50
1:A:1030(A):G:H21	1:A:1031:G:H1	1.58	0.50
12:I:43:ALA:O	12:I:44:VAL:C	2.50	0.50
1:A:115:G:O2'	1:A:116:A:OP2	2.25	0.50
1:A:1171:G:H2'	1:A:1172:C:C6	2.47	0.50
15:L:60:LEU:HD23	15:L:66:VAL:HG22	1.93	0.50
1:A:933:G:O6	10:G:3:ARG:NH2	2.45	0.50
1:A:1092:A:H8	1:A:1092:A:O5'	1.95	0.50
1:A:522:C:O2'	1:A:523:A:H5'	2.12	0.49
1:A:36:C:H4'	15:L:122:THR:O	2.11	0.49
13:J:19:SER:HB2	13:J:91:PRO:HG3	1.94	0.49
5:B:208:ILE:HA	5:B:211:ILE:HD12	1.94	0.49
5:B:96:ARG:HD2	5:B:97:TRP:H	1.76	0.49
1:A:1149:C:H2'	1:A:1150:U:H6	1.77	0.49
1:A:1280:A:O4'	13:J:41:PRO:HG3	2.12	0.49
20:Q:20:THR:HG21	20:Q:41:LYS:HD2	1.95	0.49
18:O:56:LEU:HA	18:O:59:MET:HE2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:C:H2'	1:A:459:G:C8	2.45	0.49
5:B:91:PRO:CA	5:B:154:LEU:HD12	2.41	0.49
8:E:20:GLN:O	8:E:21:ALA:C	2.49	0.49
23:T:87:LYS:O	23:T:89:ARG:N	2.45	0.49
1:A:862:C:O2'	1:A:863:U:H5'	2.12	0.49
21:R:86:VAL:HG12	21:R:87:ARG:N	2.27	0.49
1:A:443:C:H2'	1:A:444:C:H6	1.76	0.49
21:R:18:ARG:HH22	21:R:21:LYS:NZ	2.09	0.49
1:A:895:G:H2'	1:A:896:C:C6	2.48	0.49
5:B:59:GLU:O	5:B:62:ALA:HB3	2.12	0.49
11:H:112:LEU:N	11:H:112:LEU:HD22	2.27	0.49
13:J:62:HIS:HB3	17:N:59:ALA:HB3	1.93	0.49
1:A:1306:A:O2'	16:M:109:THR:HG21	2.12	0.49
5:B:16:HIS:O	5:B:17:PHE:O	2.31	0.49
5:B:36:ARG:HD2	5:B:41:ILE:CD1	2.42	0.49
5:B:36:ARG:HD2	5:B:41:ILE:HD12	1.95	0.49
13:J:27:ALA:HB1	13:J:81:THR:HG23	1.94	0.49
1:A:761:G:H4'	20:Q:103:GLY:N	2.28	0.49
18:O:39:LEU:CD2	18:O:56:LEU:HB2	2.42	0.49
7:D:64:LEU:HD12	7:D:75:PHE:CZ	2.46	0.49
1:A:1038:C:H2'	1:A:1039:C:H6	1.74	0.49
5:B:223:ILE:HG21	5:B:230:VAL:HG23	1.93	0.49
12:I:48:GLU:OE1	12:I:51:ARG:HD2	2.11	0.49
8:E:24:ARG:HG2	8:E:24:ARG:HH11	1.77	0.49
1:A:1065:U:O2'	1:A:1066:C:OP2	2.28	0.49
1:A:530:G:O6	4:Z:3:U:H1'	2.11	0.49
8:E:91:LEU:CD2	8:E:120:THR:HG22	2.42	0.49
8:E:79:GLU:OE2	11:H:105:ARG:HD3	2.12	0.49
12:I:93:ARG:O	12:I:95:LYS:N	2.46	0.49
10:G:18:TYR:CD2	10:G:59:LEU:HB2	2.48	0.49
12:I:108:VAL:HG12	12:I:109:VAL:N	2.28	0.49
8:E:76:ILE:HG23	8:E:142:LEU:HD13	1.95	0.49
1:A:394:G:H2'	1:A:395:C:H6	1.76	0.49
23:T:14:LYS:O	23:T:17:ARG:HB2	2.12	0.49
7:D:59:ARG:NH2	7:D:66:ARG:NH1	2.60	0.49
10:G:135:VAL:O	10:G:139:GLU:HG3	2.12	0.49
9:F:60:PHE:O	9:F:61:LEU:HD23	2.12	0.49
1:A:927:G:H2'	1:A:928:G:H8	1.77	0.49
8:E:137:GLU:O	8:E:138:ALA:C	2.51	0.49
1:A:632:A:C2'	1:A:633:G:H5'	2.42	0.49
1:A:363:A:OP1	15:L:33:ARG:HD2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:31:MET:CG	10:G:32:ARG:N	2.75	0.49
6:C:160:ALA:O	6:C:162:GLN:N	2.45	0.49
6:C:36:ASP:O	6:C:39:ILE:HB	2.12	0.49
17:N:35:ARG:O	17:N:37:PHE:N	2.40	0.49
6:C:156:ARG:HB3	6:C:196:LEU:HD22	1.95	0.49
5:B:97:TRP:HH2	5:B:176:GLU:CD	2.16	0.49
1:A:1347:G:C6	12:I:107:ARG:NH2	2.80	0.49
22:S:80:TYR:C	22:S:80:TYR:CD2	2.84	0.49
1:A:1474:G:O2'	1:A:1475:G:H5'	2.11	0.49
9:F:19:LEU:HD23	9:F:19:LEU:O	2.12	0.49
1:A:397:A:H5'	1:A:398:C:P	2.52	0.49
1:A:1022:G:H2'	1:A:1023:G:H8	1.76	0.49
1:A:444:C:H2'	1:A:445:G:H8	1.77	0.49
23:T:79:ARG:O	23:T:80:ARG:C	2.49	0.49
14:K:101:SER:OG	14:K:102:GLY:N	2.45	0.49
15:L:111:LYS:O	15:L:112:ASP:HB2	2.12	0.49
1:A:879:C:O2'	1:A:880:C:H5'	2.12	0.49
1:A:409:G:H2'	1:A:410:G:O4'	2.13	0.49
1:A:132:C:O2'	1:A:133:U:H5'	2.12	0.49
1:A:939:G:C5'	10:G:102:ARG:HH22	2.17	0.49
1:A:737:A:H2'	1:A:738:C:H6	1.77	0.49
21:R:47:THR:C	21:R:49:LYS:H	2.16	0.49
6:C:18:TRP:O	6:C:54:ARG:NH2	2.44	0.49
5:B:68:ILE:N	5:B:90:MET:HE3	2.27	0.49
1:A:1020:U:H2'	1:A:1021:G:H8	1.73	0.49
1:A:981:U:H5'	17:N:21:TYR:CE1	2.48	0.49
16:M:15:VAL:HG23	16:M:43:THR:O	2.12	0.49
1:A:622:A:C8	1:A:623:C:C6	3.00	0.49
1:A:633:G:H2'	1:A:634:C:H6	1.78	0.49
1:A:803:G:H2'	1:A:804:U:O4'	2.12	0.49
7:D:8:VAL:CG1	7:D:21:LEU:HD13	2.43	0.49
1:A:1349:A:H2'	1:A:1350:A:H8	1.77	0.49
6:C:110:ASN:ND2	6:C:140:ARG:HB3	2.28	0.49
14:K:47:VAL:HG12	14:K:48:ILE:N	2.27	0.49
1:A:691:G:O6	14:K:52:GLY:HA2	2.12	0.49
11:H:59:LEU:O	11:H:61:VAL:HG23	2.13	0.49
1:A:1218:C:H2'	1:A:1219:U:C6	2.47	0.49
1:A:404:U:O2'	1:A:405:U:H5'	2.11	0.49
10:G:85:TYR:CD1	10:G:154:TYR:HE1	2.30	0.49
6:C:84:ILE:O	6:C:84:ILE:HG12	2.13	0.49
1:A:45:U:H2'	1:A:46:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:930:C:O2'	1:A:931:C:H5'	2.13	0.49
9:F:27:GLN:HA	9:F:27:GLN:OE1	2.13	0.49
3:Y:39:U:O5'	3:Y:39:U:H6	1.94	0.49
6:C:8:ILE:O	6:C:12:LEU:N	2.45	0.49
1:A:1116:C:C3'	1:A:1117:G:H5"	2.43	0.49
5:B:71:VAL:O	5:B:165:VAL:HG23	2.12	0.49
20:Q:96:GLN:O	20:Q:97:SER:HB3	2.12	0.49
18:O:39:LEU:HD21	18:O:56:LEU:HB2	1.94	0.49
23:T:91:LEU:C	23:T:93:GLU:N	2.65	0.49
6:C:83:ARG:C	6:C:85:ARG:N	2.65	0.49
1:A:674:G:O2'	1:A:675:A:H5'	2.13	0.49
1:A:1522:U:HO2'	1:A:1523:G:H5'	1.78	0.49
1:A:417:C:H2'	1:A:418:C:H6	1.77	0.49
11:H:53:VAL:HG12	11:H:53:VAL:O	2.13	0.49
1:A:246:A:N6	1:A:281:G:H1'	2.28	0.49
8:E:107:ARG:O	8:E:108:ALA:C	2.51	0.49
8:E:51:VAL:O	8:E:55:VAL:HG23	2.13	0.49
12:I:127:LYS:CD	12:I:127:LYS:H	2.20	0.49
1:A:338:A:H2	1:A:351:G:H22	1.60	0.49
1:A:112:G:H4'	1:A:389:A:H5"	1.93	0.49
5:B:25:ASN:HD22	5:B:26:PRO:N	2.10	0.49
15:L:43:VAL:CG1	15:L:44:THR:H	2.23	0.49
1:A:1399:C:C2	1:A:1401:G:C5	3.00	0.49
1:A:647:C:H2'	1:A:648:A:C8	2.47	0.49
12:I:30:GLY:O	12:I:31:GLN:O	2.31	0.49
16:M:12:ASN:CG	16:M:12:ASN:O	2.51	0.49
19:P:53:VAL:CG2	19:P:54:GLU:N	2.75	0.49
16:M:14:ARG:HB3	16:M:16:ASP:OD1	2.13	0.49
1:A:67:C:O2'	1:A:171:A:H1'	2.12	0.49
13:J:47:PHE:N	13:J:63:PHE:O	2.45	0.49
1:A:1205:U:H4'	6:C:195:VAL:CG2	2.43	0.49
6:C:50:ALA:HB2	6:C:75:VAL:HB	1.93	0.49
1:A:934:C:N3	1:A:1345:U:C5	2.80	0.49
5:B:200:ILE:CD1	5:B:202:PRO:HD3	2.41	0.49
20:Q:76:LEU:C	20:Q:76:LEU:HD23	2.33	0.49
1:A:1391:U:H2'	1:A:1392:G:H8	1.73	0.49
15:L:89:ARG:HH12	15:L:97:ARG:HE	1.61	0.49
9:F:36:ARG:NH1	9:F:36:ARG:HG2	2.28	0.49
1:A:1425:U:H2'	1:A:1426:C:C6	2.47	0.49
19:P:43:LYS:HB3	19:P:48:TRP:CE2	2.48	0.49
17:N:14:PRO:O	17:N:15:LYS:CB	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:789:U:H4'	2:X:2:U:O2	2.13	0.49
1:A:415:A:H2'	1:A:416:G:H8	1.78	0.49
1:A:716:A:N3	14:K:117:ASN:O	2.46	0.49
1:A:812:C:H1'	1:A:813:U:OP2	2.13	0.49
20:Q:82:MET:O	20:Q:83:ASP:C	2.50	0.49
10:G:95:ARG:HG3	10:G:95:ARG:HH11	1.77	0.49
6:C:67:THR:HG22	6:C:67:THR:O	2.12	0.49
15:L:124:LYS:CD	15:L:125:PRO:HD2	2.38	0.49
1:A:255:G:H2'	1:A:256:U:C6	2.48	0.49
5:B:162:ILE:O	5:B:162:ILE:CG2	2.61	0.49
1:A:738:C:OP2	9:F:92:LYS:NZ	2.36	0.49
6:C:203:PHE:O	6:C:204:LEU:HD23	2.13	0.49
5:B:25:ASN:ND2	5:B:25:ASN:C	2.62	0.49
1:A:976:G:C8	1:A:1358:U:O2	2.66	0.49
13:J:53:PRO:HA	17:N:41:ARG:NH2	2.24	0.49
1:A:176:C:H2'	1:A:177:C:H6	1.78	0.49
1:A:1481:U:O2'	1:A:1482:G:H5'	2.12	0.49
9:F:14:LEU:HD13	9:F:19:LEU:HA	1.94	0.49
1:A:1253:G:H2'	1:A:1254:C:C6	2.47	0.49
7:D:162:LEU:HD13	7:D:181:MET:HG2	1.95	0.49
6:C:34:LEU:HD22	6:C:38:ARG:NH1	2.28	0.49
11:H:14:ARG:NH1	11:H:14:ARG:HB3	2.28	0.49
21:R:18:ARG:C	21:R:19:LYS:HD2	2.33	0.49
5:B:54:THR:O	5:B:57:PHE:N	2.46	0.49
1:A:1194:U:H2'	1:A:1195:C:C6	2.48	0.48
6:C:190:ARG:NH1	6:C:190:ARG:HB3	2.28	0.48
21:R:74:ARG:HA	21:R:79:LEU:O	2.13	0.48
7:D:127:THR:HG23	7:D:147:ALA:HB3	1.95	0.48
23:T:14:LYS:O	23:T:18:GLN:HG3	2.13	0.48
19:P:43:LYS:HG2	19:P:48:TRP:CZ2	2.48	0.48
1:A:865:A:O2'	1:A:866:C:H5'	2.13	0.48
1:A:1292:U:H5'	12:I:38:GLN:NE2	2.28	0.48
11:H:123:GLU:O	11:H:127:LEU:HB2	2.12	0.48
1:A:828:A:H2'	1:A:829:G:O4'	2.13	0.48
6:C:3:ASN:ND2	6:C:4:LYS:HE2	2.28	0.48
13:J:30:SER:HB2	13:J:80:LYS:HG3	1.96	0.48
1:A:1152:A:H2'	1:A:1153:C:H6	1.76	0.48
17:N:4:LYS:O	17:N:7:ILE:HG13	2.13	0.48
1:A:728:A:H8	1:A:728:A:O5'	1.96	0.48
20:Q:97:SER:HB2	20:Q:103:GLY:CA	2.43	0.48
22:S:80:TYR:HD2	22:S:80:TYR:C	2.15	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:C:N4	1:A:216:G:H1	2.08	0.48
1:A:1488:G:H2'	1:A:1489:G:C8	2.48	0.48
6:C:83:ARG:C	6:C:85:ARG:H	2.16	0.48
10:G:148:ASN:O	10:G:150:ALA:N	2.46	0.48
16:M:87:TYR:O	16:M:90:LEU:N	2.42	0.48
8:E:79:GLU:O	11:H:104:ARG:CZ	2.61	0.48
12:I:63:ILE:HG22	12:I:65:VAL:HG23	1.94	0.48
22:S:32:LYS:HA	22:S:50:ALA:HB3	1.96	0.48
6:C:152:ILE:HB	6:C:199:LYS:HB2	1.96	0.48
1:A:1392:G:H2'	1:A:1393:U:H6	1.78	0.48
1:A:376:G:H2'	1:A:377:G:C8	2.47	0.48
21:R:52:PRO:HB2	21:R:54:ARG:HG3	1.93	0.48
7:D:127:THR:CG2	7:D:147:ALA:HB3	2.43	0.48
5:B:88:ALA:HB3	5:B:90:MET:HG2	1.95	0.48
1:A:814:A:N7	1:A:816:A:C4	2.81	0.48
1:A:1262:C:H2'	1:A:1263:C:C6	2.46	0.48
10:G:95:ARG:NH1	10:G:95:ARG:HG3	2.29	0.48
19:P:4:ILE:HG13	19:P:64:ALA:HB1	1.95	0.48
1:A:749:C:P	1:A:749:C:H3'	2.54	0.48
3:Y:34:G:C8	3:Y:34:G:H5'	2.39	0.48
12:I:65:VAL:HG21	12:I:77:ILE:HD11	1.94	0.48
6:C:50:ALA:HB1	6:C:70:VAL:CG1	2.36	0.48
1:A:1372:U:C2'	1:A:1373:G:H5'	2.44	0.48
1:A:1392:G:O2'	1:A:1393:U:H5'	2.13	0.48
19:P:1:MET:CE	19:P:3:LYS:HD2	2.44	0.48
5:B:111:ARG:HB3	5:B:149:LEU:HD11	1.94	0.48
5:B:142:LEU:O	5:B:143:GLU:C	2.52	0.48
1:A:456:C:H2'	1:A:457:C:C6	2.48	0.48
1:A:163:C:O2'	1:A:164:U:H5'	2.13	0.48
6:C:187:ALA:O	6:C:198:VAL:N	2.46	0.48
13:J:45:ARG:O	13:J:64:GLU:HA	2.13	0.48
15:L:69:TYR:HE2	15:L:71:PRO:HA	1.79	0.48
1:A:1125:U:H3	13:J:5:ARG:HH21	1.61	0.48
5:B:12:GLU:C	5:B:14:GLY:H	2.17	0.48
20:Q:68:ARG:N	20:Q:70:ARG:HH11	2.08	0.48
17:N:4:LYS:HA	17:N:7:ILE:HD11	1.95	0.48
9:F:8:ILE:HD11	9:F:79:LEU:HD13	1.94	0.48
1:A:918:A:H2'	1:A:919:A:H8	1.74	0.48
15:L:97:ARG:HB2	15:L:98:TYR:CD1	2.49	0.48
23:T:10:LEU:O	23:T:12:ALA:N	2.46	0.48
1:A:877:C:O2'	1:A:878:G:H5'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:G:H2'	1:A:167:G:H8	1.79	0.48
14:K:116:HIS:O	14:K:117:ASN:HB2	2.14	0.48
1:A:168:G:O2'	1:A:169:C:H5'	2.13	0.48
5:B:87:ARG:HH11	5:B:87:ARG:HG3	1.77	0.48
1:A:1443:G:H5"	1:A:1446:A:H5"	1.89	0.48
1:A:501:C:O2'	1:A:502:G:H5'	2.14	0.48
1:A:1221:G:O2'	1:A:1222:G:H5'	2.12	0.48
22:S:53:ASN:N	22:S:53:ASN:ND2	2.61	0.48
9:F:69:GLU:O	9:F:72:VAL:HG23	2.14	0.48
1:A:112:G:H21	1:A:354:G:H5'	1.77	0.48
5:B:123:ALA:CA	5:B:127:ILE:HD11	2.43	0.48
1:A:1097:C:H2'	1:A:1098:C:H6	1.78	0.48
1:A:1030(C):G:H2'	1:A:1030(D):A:O4'	2.14	0.48
5:B:116:GLU:HA	5:B:119:GLU:OE1	2.13	0.48
1:A:314:C:O2'	1:A:315:A:H5'	2.13	0.48
1:A:1370:G:H2'	1:A:1371:G:H8	1.78	0.48
6:C:43:LEU:CD1	6:C:68:VAL:HG21	2.44	0.48
1:A:1305:G:H2'	1:A:1331:G:N2	2.28	0.48
1:A:959:A:H2'	1:A:960:U:O4'	2.14	0.48
13:J:14:LYS:O	13:J:18:ALA:HB2	2.14	0.48
5:B:33:TYR:HB3	5:B:41:ILE:O	2.14	0.48
5:B:44:LEU:O	5:B:47:THR:N	2.47	0.48
7:D:173:TRP:HB2	7:D:187:ARG:O	2.14	0.48
1:A:966:G:H2'	1:A:967:C:C6	2.49	0.48
9:F:33:TYR:HA	9:F:71:ARG:NH2	2.27	0.48
9:F:33:TYR:CD1	9:F:75:LEU:HA	2.49	0.48
17:N:41:ARG:HG2	17:N:41:ARG:HH11	1.79	0.48
1:A:1488:G:H2'	1:A:1489:G:H8	1.79	0.48
1:A:103:C:P	23:T:17:ARG:NH1	2.87	0.48
1:A:344:A:O2'	1:A:345:C:OP1	2.30	0.48
10:G:149:ARG:C	10:G:151:TYR:H	2.17	0.48
1:A:47:C:C6	1:A:365:U:H2'	2.48	0.48
7:D:170:VAL:HG22	7:D:171:GLY:H	1.79	0.48
6:C:95:THR:O	6:C:96:GLY:C	2.51	0.48
8:E:99:GLY:O	8:E:117:ASP:HA	2.12	0.48
10:G:124:LEU:O	10:G:127:ALA:HB3	2.14	0.48
10:G:62:PHE:HA	10:G:124:LEU:HD22	1.96	0.48
1:A:1394:A:C5	1:A:1501:C:H4'	2.49	0.48
9:F:80:ARG:NH1	9:F:88:VAL:HB	2.29	0.48
15:L:93:LEU:CG	15:L:96:VAL:HG21	2.43	0.48
5:B:19:HIS:NE2	5:B:206:ASP:HB3	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1346:A:H61	1:A:1374:A:H3'	1.79	0.48
1:A:1345:U:C2	1:A:1377:A:C2	3.02	0.48
6:C:60:ALA:O	6:C:61:ALA:HB3	2.13	0.48
1:A:109:A:H4'	1:A:110:C:OP2	2.13	0.48
21:R:40:LEU:C	21:R:42:ARG:N	2.66	0.48
17:N:21:TYR:CE2	17:N:23:ARG:NE	2.81	0.48
10:G:22:LEU:HD21	10:G:66:VAL:HG21	1.96	0.48
8:E:15:ARG:O	8:E:16:THR:HB	2.13	0.48
10:G:120:ILE:O	10:G:124:LEU:HD12	2.12	0.48
1:A:1414:U:H2'	1:A:1415:G:H8	1.79	0.48
1:A:262:A:C6	1:A:263:A:C6	3.02	0.48
1:A:977:A:O2'	1:A:979:C:OP2	2.28	0.48
5:B:35:GLU:HA	5:B:40:HIS:HA	1.95	0.48
13:J:80:LYS:O	13:J:83:GLU:HB3	2.13	0.48
12:I:88:TYR:CG	12:I:89:ASN:N	2.81	0.48
5:B:141:GLU:O	5:B:145:LEU:HG	2.13	0.48
1:A:1014:A:H2'	1:A:1015:A:C8	2.48	0.48
1:A:175:C:O2'	1:A:176:C:H5'	2.13	0.48
10:G:38:LEU:O	10:G:42:ILE:HG13	2.14	0.48
1:A:781:A:H2	1:A:1514:C:O4'	1.97	0.48
7:D:52:SER:O	7:D:53:ASP:C	2.52	0.48
20:Q:33:GLY:O	20:Q:34:LYS:C	2.51	0.48
1:A:12:U:H4'	1:A:526:C:H4'	1.96	0.48
1:A:264:U:H2'	1:A:265:G:O4'	2.14	0.48
12:I:97:LYS:HB2	12:I:98:PRO:HD3	1.96	0.48
7:D:173:TRP:O	7:D:186:LEU:HG	2.14	0.48
12:I:4:TYR:CZ	12:I:88:TYR:CD1	3.02	0.48
9:F:72:VAL:O	9:F:75:LEU:HB3	2.14	0.48
21:R:47:THR:HG22	21:R:48:GLY:N	2.29	0.48
10:G:49:ILE:C	10:G:51:GLN:N	2.67	0.48
10:G:15:ASP:HB3	10:G:19:GLY:N	2.27	0.48
1:A:1183:A:O2'	1:A:1184:G:OP1	2.28	0.48
12:I:66:ARG:HB2	12:I:66:ARG:CZ	2.43	0.48
5:B:87:ARG:HH12	5:B:233:SER:CB	2.27	0.47
6:C:57:ILE:HG22	6:C:58:GLU:N	2.28	0.47
8:E:80:ILE:CD1	8:E:91:LEU:CB	2.76	0.47
20:Q:67:LYS:O	20:Q:68:ARG:HB3	2.14	0.47
1:A:1372:U:H2'	1:A:1373:G:C5'	2.44	0.47
7:D:148:VAL:CG1	7:D:158:ILE:HD13	2.44	0.47
6:C:139:GLN:HA	6:C:139:GLN:NE2	2.29	0.47
6:C:32:LEU:O	6:C:32:LEU:HD23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1288:A:H2'	1:A:1289:A:C8	2.49	0.47
1:A:1320:C:H2'	1:A:1321:C:O4'	2.14	0.47
6:C:54:ARG:O	6:C:55:VAL:HG23	2.14	0.47
1:A:669:U:H2'	1:A:670:G:H8	1.77	0.47
1:A:413:G:N2	1:A:428:G:H1'	2.29	0.47
8:E:82:VAL:HG12	8:E:89:ILE:HG22	1.96	0.47
1:A:913:A:O2'	1:A:914:A:P	2.72	0.47
21:R:86:VAL:CG1	21:R:87:ARG:N	2.77	0.47
8:E:102:ALA:HB2	8:E:120:THR:OG1	2.13	0.47
12:I:65:VAL:CG1	12:I:73:GLN:HB3	2.26	0.47
1:A:943:U:C2'	1:A:944:G:H5'	2.44	0.47
7:D:187:ARG:HA	7:D:187:ARG:HE	1.78	0.47
23:T:53:LEU:HD13	23:T:100:ILE:CG2	2.44	0.47
6:C:59:ARG:HD3	6:C:97:LYS:NZ	2.29	0.47
9:F:73:ASN:O	9:F:74:ASP:C	2.51	0.47
1:A:336:C:O2'	1:A:337:C:H5'	2.13	0.47
18:O:87:ILE:HG22	18:O:88:ARG:N	2.29	0.47
14:K:19:ALA:HB2	14:K:80:VAL:HG11	1.95	0.47
1:A:222:U:H2'	1:A:223:U:C6	2.49	0.47
10:G:62:PHE:HA	10:G:124:LEU:CD2	2.44	0.47
1:A:1276:G:H8	1:A:1276:G:O5'	1.97	0.47
22:S:61:TYR:C	22:S:61:TYR:CD2	2.87	0.47
6:C:47:LEU:CD2	6:C:68:VAL:HG11	2.43	0.47
5:B:12:GLU:OE1	5:B:15:VAL:N	2.46	0.47
24:V:6:ARG:O	24:V:12:LYS:HD2	2.14	0.47
7:D:19:LEU:HD23	7:D:20:TYR:H	1.78	0.47
1:A:1136:U:H5"	1:A:1137:C:OP2	2.13	0.47
5:B:102:LEU:HD12	5:B:102:LEU:N	2.29	0.47
10:G:51:GLN:C	10:G:53:LYS:N	2.67	0.47
5:B:142:LEU:HD22	5:B:146:GLN:NE2	2.28	0.47
12:I:99:LEU:N	12:I:99:LEU:HD22	2.29	0.47
14:K:33:THR:HG23	14:K:34:ASP:O	2.13	0.47
14:K:29:ILE:HG12	14:K:29:ILE:O	2.14	0.47
1:A:986:A:H2'	1:A:987:G:C8	2.49	0.47
8:E:86:ALA:O	8:E:125:SER:N	2.43	0.47
22:S:40:ILE:HA	22:S:44:MET:SD	2.54	0.47
1:A:960:U:C2'	1:A:960:U:O2	2.63	0.47
19:P:34:GLU:HG2	19:P:35:LYS:N	2.27	0.47
1:A:1123:A:H4'	13:J:37:PRO:HD2	1.96	0.47
5:B:103:THR:O	5:B:103:THR:CG2	2.63	0.47
1:A:992:U:O2'	1:A:993:G:OP2	2.24	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:737:A:O2'	1:A:738:C:H5'	2.13	0.47
6:C:54:ARG:HG2	6:C:54:ARG:HH11	1.79	0.47
1:A:477:G:H2'	1:A:478:A:C8	2.48	0.47
15:L:24:VAL:HG12	15:L:26:ALA:HB2	1.96	0.47
1:A:1460:A:H2'	1:A:1461:G:O4'	2.14	0.47
1:A:645:C:O2'	1:A:646:U:H5'	2.13	0.47
20:Q:62:SER:OG	20:Q:72:ARG:HG3	2.15	0.47
1:A:138:G:O2'	1:A:139:G:H5'	2.14	0.47
7:D:24:GLU:O	7:D:25:ARG:HB3	2.15	0.47
1:A:1249:C:O2'	12:I:73:GLN:NE2	2.48	0.47
22:S:45:VAL:C	22:S:47:HIS:H	2.18	0.47
1:A:1309:G:N7	16:M:99:ARG:NH2	2.62	0.47
12:I:97:LYS:N	12:I:98:PRO:CD	2.78	0.47
1:A:939:G:H2'	1:A:940:C:H6	1.80	0.47
1:A:325:A:H2'	1:A:326:G:O4'	2.14	0.47
1:A:1202:G:H2'	1:A:1203:C:H5'	1.96	0.47
1:A:26:A:H61	1:A:558:G:H1'	1.79	0.47
1:A:575:G:OP1	1:A:575:G:H4'	2.15	0.47
5:B:16:HIS:NE2	5:B:214:ILE:CG1	2.65	0.47
6:C:202:ILE:HG22	6:C:204:LEU:HD21	1.96	0.47
5:B:30:ARG:HG3	5:B:31:TYR:CE2	2.50	0.47
1:A:921:U:O2	8:E:19:MET:HB2	2.15	0.47
12:I:48:GLU:HA	12:I:48:GLU:OE1	2.14	0.47
1:A:411:A:C6	1:A:429:U:C4	3.03	0.47
21:R:86:VAL:O	21:R:87:ARG:CB	2.62	0.47
1:A:91:C:O2'	1:A:92:C:H5'	2.15	0.47
16:M:11:ARG:HG2	16:M:12:ASN:N	2.29	0.47
5:B:61:LEU:HD21	5:B:160:ASP:CB	2.44	0.47
7:D:32:ALA:O	7:D:34:GLU:N	2.48	0.47
8:E:79:GLU:HA	8:E:91:LEU:O	2.14	0.47
1:A:539:A:H2'	1:A:540:G:H8	1.80	0.47
1:A:1331:G:O2'	1:A:1332:A:OP2	2.31	0.47
5:B:17:PHE:HB3	5:B:44:LEU:HD21	1.95	0.47
5:B:44:LEU:O	5:B:45:GLN:C	2.52	0.47
7:D:67:ILE:HG22	7:D:68:TYR:N	2.29	0.47
6:C:156:ARG:CD	6:C:156:ARG:O	2.62	0.47
6:C:153:VAL:O	6:C:154:SER:C	2.52	0.47
1:A:1057:G:C5'	6:C:154:SER:HB2	2.43	0.47
5:B:96:ARG:O	5:B:98:LEU:HD23	2.15	0.47
12:I:118:LYS:NZ	12:I:118:LYS:CB	2.77	0.47
1:A:991:U:O2	1:A:993:G:H8	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:152:SER:HB3	7:D:155:LEU:HD12	1.97	0.47
1:A:1315:U:H2'	1:A:1316:G:C8	2.50	0.47
1:A:16:A:O2'	1:A:17:U:H5'	2.15	0.47
1:A:1402:C:H2'	1:A:1403:C:O4'	2.15	0.47
1:A:270:A:H2'	1:A:271:C:C6	2.50	0.47
23:T:91:LEU:HD12	23:T:91:LEU:H	1.79	0.47
6:C:83:ARG:O	6:C:86:VAL:N	2.47	0.47
8:E:122:GLU:O	8:E:123:LEU:HD23	2.14	0.47
8:E:15:ARG:O	8:E:16:THR:HG22	2.14	0.47
1:A:364:A:H2'	1:A:365:U:O2	2.13	0.47
1:A:742:G:H5"	18:O:58:MET:CE	2.45	0.47
5:B:215:LEU:O	5:B:216:SER:C	2.51	0.47
1:A:502:G:H2'	1:A:503:C:C6	2.48	0.47
1:A:1327:C:O2'	1:A:1328:C:H5'	2.14	0.47
7:D:142:PRO:HA	7:D:185:PHE:HD2	1.79	0.47
18:O:21:ASP:OD1	18:O:24:SER:HB2	2.14	0.47
1:A:991:U:C4	1:A:1212:U:H1'	2.50	0.47
13:J:46:ARG:HG2	13:J:46:ARG:HH11	1.80	0.47
22:S:13:ASP:O	22:S:16:LEU:N	2.48	0.47
5:B:139:LYS:HD3	5:B:139:LYS:O	2.15	0.47
15:L:43:VAL:CG2	15:L:55:VAL:HG21	2.44	0.47
21:R:25:THR:O	21:R:26:LEU:HD13	2.13	0.47
18:O:61:GLY:C	18:O:65:ARG:HH12	2.18	0.47
1:A:393:A:C2'	1:A:394:G:H5'	2.45	0.47
23:T:41:ILE:HD13	23:T:87:LYS:HZ2	1.80	0.47
17:N:11:LYS:C	17:N:13:THR:N	2.68	0.47
20:Q:53:LEU:HD12	20:Q:85:VAL:HG21	1.97	0.47
14:K:33:THR:OG1	14:K:39:PRO:HA	2.15	0.47
1:A:807:A:H2'	1:A:808:C:C6	2.49	0.47
1:A:1271:G:H2'	1:A:1272:G:C8	2.50	0.47
1:A:1191:A:OP2	6:C:3:ASN:OD1	2.33	0.47
13:J:9:ARG:HA	13:J:16:LEU:HD11	1.97	0.47
13:J:28:ARG:HH11	13:J:28:ARG:HG2	1.80	0.47
14:K:40:ILE:HG23	14:K:75:TYR:CE2	2.50	0.47
1:A:376:G:OP2	19:P:67:THR:HG21	2.15	0.47
17:N:18:VAL:O	17:N:20:ALA:N	2.48	0.47
1:A:188:C:O4'	23:T:89:ARG:NH1	2.48	0.47
16:M:40:ASN:ND2	16:M:42:ALA:H	2.13	0.47
1:A:857:C:H2'	1:A:858:G:O4'	2.14	0.47
7:D:59:ARG:HH22	7:D:66:ARG:HH12	1.61	0.47
10:G:135:VAL:HG12	10:G:139:GLU:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1238:A:OP2	1:A:1335:C:H1'	2.15	0.47
15:L:39:VAL:CG2	15:L:57:LYS:HG2	2.45	0.47
1:A:1004:A:N6	1:A:1037:C:H42	2.13	0.47
16:M:19:LEU:HA	16:M:22:ILE:CD1	2.45	0.47
5:B:15:VAL:HG22	5:B:209:ARG:HG3	1.97	0.47
1:A:439:A:C4	1:A:497:A:C2	3.03	0.47
1:A:1235:U:O2'	1:A:1236:A:H5'	2.15	0.47
1:A:1343:G:H4'	12:I:122:ALA:O	2.14	0.47
22:S:10:PHE:HE2	22:S:12:ASP:OD1	1.98	0.47
1:A:737:A:H2'	1:A:738:C:C6	2.49	0.47
21:R:39:VAL:HG13	21:R:40:LEU:N	2.30	0.47
11:H:31:PHE:CE1	11:H:35:ILE:HD11	2.50	0.47
1:A:731:G:H5'	1:A:766:A:H4'	1.96	0.47
1:A:781:A:C5	1:A:802:A:C2	3.02	0.47
1:A:356:A:O2'	1:A:357:G:H5'	2.15	0.47
1:A:1283:G:O2'	1:A:1284:C:H5'	2.15	0.47
1:A:1271:G:H2'	1:A:1272:G:H8	1.80	0.47
19:P:39:TYR:CZ	19:P:41:PRO:HA	2.50	0.47
15:L:40:VAL:O	15:L:40:VAL:HG12	2.15	0.47
11:H:56:LYS:N	11:H:56:LYS:HD2	2.30	0.47
1:A:123:C:OP1	1:A:312:C:H5'	2.14	0.47
1:A:1442:G:C6	1:A:1446:A:N6	2.83	0.46
1:A:1194:U:O2'	1:A:1195:C:H5'	2.14	0.46
13:J:89:ASP:CG	13:J:90:LEU:N	2.69	0.46
7:D:10:ARG:NH1	7:D:10:ARG:HG3	2.28	0.46
12:I:111:ARG:HH11	12:I:111:ARG:CG	2.27	0.46
1:A:488:C:H2'	1:A:489:C:C6	2.49	0.46
9:F:36:ARG:HH11	9:F:36:ARG:HG2	1.80	0.46
1:A:1424:C:O2'	1:A:1425:U:H5'	2.16	0.46
7:D:53:ASP:O	7:D:57:ARG:HD3	2.15	0.46
1:A:831:U:H2'	1:A:832:C:C6	2.50	0.46
14:K:109:VAL:HG22	21:R:86:VAL:HA	1.97	0.46
1:A:780:A:C2	1:A:801:U:C5	3.04	0.46
7:D:25:ARG:CZ	7:D:30:LYS:HD3	2.45	0.46
18:O:70:LEU:O	18:O:71:GLN:C	2.52	0.46
5:B:15:VAL:CG1	5:B:209:ARG:HB3	2.45	0.46
5:B:20:GLU:O	5:B:39:ILE:HG23	2.16	0.46
1:A:690:G:H2'	1:A:691:G:C8	2.49	0.46
14:K:48:ILE:HG12	14:K:48:ILE:H	1.45	0.46
22:S:33:THR:HG22	22:S:35:SER:N	2.29	0.46
18:O:39:LEU:CD2	18:O:56:LEU:HD22	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1411:C:O2'	1:A:1412:C:H5'	2.15	0.46
1:A:1513:A:H2'	1:A:1514:C:H6	1.79	0.46
1:A:1338:G:H2'	1:A:1339:A:C8	2.50	0.46
1:A:1121:U:H2'	1:A:1122:U:C6	2.50	0.46
6:C:6:HIS:NE2	6:C:8:ILE:HD12	2.30	0.46
6:C:33:LEU:HD23	6:C:33:LEU:C	2.36	0.46
15:L:117:ARG:HD2	15:L:122:THR:OG1	2.15	0.46
5:B:187:LEU:HD12	5:B:205:ASP:HA	1.98	0.46
1:A:1372:U:OP1	12:I:71:SER:HB3	2.15	0.46
1:A:1298:C:C5	10:G:114:ARG:HD3	2.49	0.46
21:R:47:THR:O	21:R:49:LYS:N	2.47	0.46
1:A:393:A:C2	1:A:394:G:C8	3.03	0.46
1:A:1026:G:N7	1:A:1027:C:C2	2.83	0.46
1:A:851:G:H2'	1:A:852:G:H8	1.80	0.46
1:A:988:G:H2'	1:A:989:C:O4'	2.16	0.46
19:P:75:ARG:O	19:P:78:GLY:N	2.47	0.46
18:O:31:LEU:O	18:O:34:LEU:HB3	2.14	0.46
1:A:1055:A:C2	1:A:1056:U:H1'	2.50	0.46
1:A:1367:C:H5'	13:J:60:ARG:HH12	1.80	0.46
15:L:93:LEU:HB2	15:L:96:VAL:HG21	1.97	0.46
1:A:960:U:H5'	1:A:960:U:O2	2.15	0.46
13:J:4:ILE:O	13:J:73:ASP:HA	2.16	0.46
1:A:256:U:H2'	1:A:257:G:H8	1.81	0.46
5:B:178:ARG:CG	5:B:178:ARG:NH1	2.71	0.46
1:A:1215:G:C2	1:A:1216:G:C8	3.03	0.46
5:B:167:PRO:O	5:B:171:ALA:N	2.49	0.46
1:A:1292:U:O2'	1:A:1293:G:H5'	2.15	0.46
14:K:33:THR:HG23	14:K:34:ASP:N	2.29	0.46
1:A:1394:A:C6	1:A:1501:C:H4'	2.50	0.46
12:I:96:LEU:N	12:I:96:LEU:HD12	2.31	0.46
1:A:583:A:H2'	1:A:584:G:O4'	2.14	0.46
16:M:26:GLY:C	16:M:28:ALA:N	2.68	0.46
13:J:94:VAL:CG1	13:J:95:GLU:H	2.29	0.46
5:B:78:GLN:HB3	5:B:94:ASN:HD21	1.80	0.46
1:A:370:C:H2'	1:A:371:G:H8	1.81	0.46
1:A:1349:A:P	12:I:118:LYS:NZ	2.88	0.46
9:F:71:ARG:HA	9:F:74:ASP:OD2	2.14	0.46
1:A:579:G:H5'	1:A:728:A:C1'	2.37	0.46
21:R:51:LEU:HA	21:R:52:PRO:HD3	1.71	0.46
1:A:1250:A:H4'	12:I:68:GLY:CA	2.45	0.46
1:A:908:A:H2'	1:A:909:A:C8	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:45:ASP:O	10:G:49:ILE:HG13	2.15	0.46
10:G:51:GLN:NE2	10:G:58:PRO:HD3	2.31	0.46
1:A:489:C:H2'	1:A:490:G:H8	1.81	0.46
18:O:50:HIS:O	18:O:51:HIS:C	2.54	0.46
23:T:91:LEU:C	23:T:93:GLU:H	2.18	0.46
7:D:162:LEU:HD13	7:D:181:MET:CE	2.45	0.46
1:A:767:A:H2'	1:A:768:A:O4'	2.15	0.46
1:A:1515:C:O2'	1:A:1516:G:H5'	2.16	0.46
9:F:50:TYR:CE1	21:R:77:GLY:HA2	2.51	0.46
23:T:50:GLU:HA	23:T:100:ILE:CG2	2.45	0.46
7:D:155:LEU:O	7:D:159:ARG:HG2	2.15	0.46
5:B:197:VAL:HB	5:B:200:ILE:CG2	2.35	0.46
1:A:109:A:C6	1:A:327:A:C6	3.04	0.46
5:B:127:ILE:C	5:B:129:GLU:H	2.19	0.46
1:A:1229:A:C2	1:A:1230:C:C4	3.04	0.46
12:I:5:TYR:HD2	12:I:18:PHE:CE2	2.34	0.46
19:P:45:THR:O	19:P:48:TRP:HD1	1.98	0.46
1:A:328:C:H4'	1:A:329:A:C5'	2.45	0.46
1:A:57:G:H2'	1:A:58:C:C6	2.51	0.46
12:I:23:ASN:ND2	12:I:23:ASN:C	2.68	0.46
20:Q:48:GLU:O	20:Q:49:GLU:C	2.53	0.46
1:A:659:U:O2'	1:A:660:G:H5'	2.16	0.46
7:D:29:PRO:O	7:D:30:LYS:CG	2.54	0.46
1:A:1053:G:O3'	1:A:1054:C:H4'	2.15	0.46
1:A:1004:A:C5'	1:A:1024:G:H1	2.27	0.46
1:A:1125:U:H5"	1:A:1126:U:C5	2.41	0.46
13:J:12:ASP:HB3	13:J:15:THR:CB	2.46	0.46
5:B:213:LEU:HD23	5:B:213:LEU:C	2.36	0.46
5:B:34:ALA:O	5:B:41:ILE:N	2.49	0.46
1:A:216:G:O2'	1:A:217:C:O4'	2.34	0.46
12:I:5:TYR:CD2	12:I:18:PHE:CE2	3.03	0.46
1:A:406:G:H5"	7:D:5:ILE:CG2	2.45	0.46
10:G:145:ALA:C	10:G:147:ALA:N	2.69	0.46
10:G:151:TYR:C	10:G:153:HIS:H	2.18	0.46
9:F:9:VAL:HB	9:F:87:ARG:HB2	1.98	0.46
1:A:730:G:H21	1:A:765:G:H5"	1.80	0.46
17:N:44:LEU:O	17:N:44:LEU:HD12	2.16	0.46
1:A:1367:C:H4'	13:J:48:THR:HG21	1.97	0.46
15:L:46:LYS:CG	15:L:47:LYS:N	2.67	0.46
1:A:948:C:OP1	16:M:109:THR:HG22	2.16	0.46
23:T:53:LEU:HB2	23:T:100:ILE:HG23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:55:VAL:HG12	15:L:56:ALA:H	1.81	0.46
1:A:1427:U:H2'	1:A:1428:A:H8	1.81	0.46
5:B:7:VAL:O	5:B:7:VAL:HG23	2.15	0.46
1:A:889:A:H61	1:A:907:A:H3'	1.81	0.46
1:A:416:G:C5	1:A:417:C:C4	3.04	0.46
9:F:80:ARG:HH11	9:F:80:ARG:HG2	1.81	0.46
18:O:3:ILE:HD13	18:O:34:LEU:HD22	1.98	0.46
1:A:1053:G:C3'	1:A:1054:C:C5'	2.94	0.46
10:G:6:ARG:O	10:G:7:ALA:C	2.53	0.46
1:A:254:G:H21	20:Q:16:GLN:HE22	1.63	0.46
5:B:123:ALA:N	5:B:127:ILE:HD11	2.30	0.46
1:A:269:C:H2'	1:A:270:A:H8	1.73	0.46
16:M:39:ILE:CD1	16:M:52:GLU:HB3	2.46	0.46
16:M:40:ASN:HD22	16:M:40:ASN:C	2.19	0.46
19:P:26:ARG:HD3	19:P:31:LYS:N	2.30	0.46
1:A:1004:A:N1	1:A:1037:C:N4	2.64	0.46
15:L:126:LYS:O	15:L:127:GLU:C	2.54	0.46
13:J:5:ARG:HB2	13:J:99:LYS:O	2.15	0.46
5:B:74:LYS:HD3	5:B:76:GLN:HB3	1.97	0.46
1:A:438:G:O2'	1:A:495:U:O4	2.30	0.46
1:A:1373:G:H5"	10:G:36:LYS:CB	2.45	0.46
6:C:147:LYS:HB3	6:C:203:PHE:CD2	2.51	0.46
5:B:137:ARG:O	5:B:140:HIS:HB2	2.16	0.46
6:C:54:ARG:NH1	6:C:54:ARG:HG2	2.31	0.46
12:I:5:TYR:C	12:I:84:ALA:HA	2.37	0.46
23:T:10:LEU:O	23:T:13:LEU:HG	2.16	0.46
1:A:1423:G:H2'	1:A:1424:C:H6	1.80	0.46
1:A:1162:C:H2'	1:A:1163:C:C6	2.51	0.46
6:C:34:LEU:HD22	6:C:38:ARG:CZ	2.46	0.46
5:B:59:GLU:O	5:B:62:ALA:N	2.49	0.46
10:G:31:MET:HG2	10:G:32:ARG:N	2.32	0.46
1:A:1305:G:OP2	1:A:1305:G:C8	2.69	0.45
1:A:1227:A:H3'	1:A:1227:A:H8	1.80	0.45
9:F:35:ALA:HA	9:F:67:MET:HB3	1.98	0.45
20:Q:104:LYS:O	20:Q:105:ALA:CB	2.63	0.45
16:M:65:LYS:HE3	16:M:69:GLU:HG2	1.98	0.45
16:M:34:LEU:HD23	16:M:39:ILE:HB	1.98	0.45
10:G:41:ARG:O	10:G:44:TYR:N	2.49	0.45
1:A:192:U:O2'	1:A:193:C:H5'	2.16	0.45
1:A:1360:A:O2'	1:A:1361:G:H5'	2.16	0.45
1:A:1451:A:O2'	1:A:1452:C:OP1	2.26	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1366:C:HO2'	13:J:60:ARG:HH22	1.63	0.45
8:E:71:LEU:CD2	8:E:115:VAL:HG23	2.46	0.45
12:I:125:TYR:CD2	12:I:125:TYR:N	2.82	0.45
11:H:119:LEU:CD1	11:H:124:ALA:HA	2.40	0.45
20:Q:88:TYR:OH	20:Q:92:ARG:NH2	2.49	0.45
22:S:10:PHE:CD2	22:S:10:PHE:C	2.88	0.45
1:A:1250:A:C5'	12:I:68:GLY:N	2.76	0.45
10:G:49:ILE:C	10:G:51:GLN:H	2.20	0.45
21:R:29:PHE:HE1	21:R:31:LEU:HD23	1.80	0.45
18:O:39:LEU:HD21	18:O:43:LEU:HD11	1.98	0.45
1:A:476:G:O2'	1:A:477:G:H5'	2.16	0.45
14:K:126:ARG:HB3	14:K:127:LYS:H	1.47	0.45
20:Q:83:ASP:O	20:Q:86:GLU:HB2	2.16	0.45
1:A:660:G:C2	1:A:746:A:C2	3.04	0.45
1:A:599:C:O2'	1:A:600:C:H5'	2.16	0.45
13:J:25:GLU:O	13:J:28:ARG:HB2	2.16	0.45
18:O:25:THR:HG21	18:O:70:LEU:HD23	1.98	0.45
1:A:255:G:H5'	20:Q:16:GLN:O	2.15	0.45
1:A:817:C:H1'	1:A:819:A:H5'	1.98	0.45
7:D:70:ILE:HD12	7:D:100:ARG:HD2	1.99	0.45
23:T:83:ARG:O	23:T:87:LYS:HE2	2.16	0.45
1:A:1184:G:OP1	1:A:1184:G:H3'	2.16	0.45
1:A:652:U:C5	1:A:752:G:C4	3.04	0.45
10:G:62:PHE:HD1	10:G:124:LEU:HD21	1.81	0.45
1:A:604:G:O2'	1:A:605:U:H5'	2.16	0.45
15:L:39:VAL:HG22	15:L:57:LYS:CG	2.47	0.45
16:M:32:GLU:O	16:M:35:GLU:N	2.47	0.45
16:M:80:ARG:C	16:M:82:MET:H	2.19	0.45
5:B:187:LEU:HA	5:B:201:ILE:HB	1.99	0.45
5:B:74:LYS:HD3	5:B:206:ASP:OD1	2.16	0.45
6:C:130:VAL:CG1	6:C:153:VAL:HG21	2.47	0.45
6:C:134:ILE:O	6:C:138:VAL:HG23	2.17	0.45
1:A:1234:C:O2'	1:A:1235:U:H5'	2.16	0.45
1:A:1288:A:H2'	1:A:1289:A:H8	1.81	0.45
1:A:1314:C:N3	1:A:1315:U:C4	2.85	0.45
1:A:766:A:C8	1:A:814:A:C6	3.04	0.45
1:A:922:G:H5'	8:E:19:MET:O	2.16	0.45
1:A:1512:U:H2'	1:A:1513:A:C8	2.52	0.45
1:A:788:U:O2'	1:A:789:U:H5'	2.16	0.45
8:E:89:ILE:HD13	8:E:90:VAL:H	1.81	0.45
1:A:915:A:H2'	1:A:916:G:C5'	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:41:GLU:HA	18:O:44:LYS:CG	2.45	0.45
10:G:151:TYR:C	10:G:153:HIS:N	2.70	0.45
1:A:589:C:O2'	1:A:590:C:H5'	2.16	0.45
12:I:32:ASP:O	12:I:35:GLU:HB3	2.17	0.45
12:I:92:TYR:O	12:I:96:LEU:HD13	2.16	0.45
1:A:124:G:C6	1:A:125:U:C4	3.04	0.45
1:A:639:G:O2'	1:A:640:A:H5'	2.16	0.45
16:M:78:ILE:O	16:M:81:LEU:HD23	2.17	0.45
6:C:154:SER:HB3	6:C:197:GLY:N	2.32	0.45
1:A:1234:C:H2'	1:A:1235:U:H6	1.81	0.45
9:F:62:TRP:C	9:F:63:TYR:HD2	2.20	0.45
1:A:1390:U:H2'	1:A:1391:U:C6	2.52	0.45
21:R:38:GLU:OE1	21:R:38:GLU:N	2.34	0.45
18:O:39:LEU:HD21	18:O:56:LEU:HD22	1.98	0.45
23:T:45:GLN:C	23:T:47:GLY:H	2.19	0.45
23:T:56:MET:CE	23:T:88:VAL:HG11	2.46	0.45
9:F:21:LEU:O	9:F:24:GLU:HB3	2.16	0.45
1:A:411:A:C4	1:A:413:G:H1'	2.52	0.45
6:C:34:LEU:CD2	6:C:34:LEU:C	2.85	0.45
1:A:1384:C:H2'	1:A:1385:G:C8	2.51	0.45
1:A:51:A:H4'	1:A:52:G:OP2	2.15	0.45
1:A:1225:A:H2'	1:A:1225:A:N3	2.31	0.45
1:A:1051:C:C4	1:A:1052:U:C5	3.04	0.45
8:E:79:GLU:O	11:H:104:ARG:NH1	2.50	0.45
6:C:167:TRP:HB3	6:C:168:ALA:H	1.32	0.45
23:T:53:LEU:HD22	23:T:102:GLY:H	1.82	0.45
1:A:1345:U:C4	1:A:1377:A:C2	3.05	0.45
1:A:761:G:H5"	20:Q:102:GLY:CA	2.46	0.45
5:B:112:VAL:HG11	5:B:153:ARG:HA	1.98	0.45
1:A:664:G:H1	1:A:741:G:H1	1.64	0.45
1:A:1479:C:O2'	1:A:1480:G:H5'	2.17	0.45
1:A:791:G:C2'	1:A:792:A:H5"	2.46	0.45
20:Q:59:ILE:HD13	20:Q:59:ILE:HA	1.57	0.45
1:A:116:A:H2'	1:A:117:G:C8	2.51	0.45
1:A:757:U:O2'	1:A:879:C:H1'	2.16	0.45
10:G:5:ARG:CG	10:G:6:ARG:N	2.73	0.45
1:A:941:G:O2'	1:A:942:G:H5'	2.17	0.45
6:C:22:TRP:CE3	6:C:32:LEU:HD22	2.51	0.45
1:A:1124:G:C8	1:A:1145:C:C5	3.05	0.45
23:T:105:SER:O	23:T:106:ALA:C	2.54	0.45
14:K:58:PRO:HA	14:K:90:GLY:HA2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:T:42:GLN:O	23:T:43:LEU:C	2.55	0.45
1:A:1066:C:O2'	1:A:1067:A:H5'	2.16	0.45
17:N:45:ARG:HG2	17:N:49:HIS:CD2	2.52	0.45
22:S:41:VAL:HG22	22:S:44:MET:HE1	1.99	0.45
1:A:523:A:N6	15:L:92:ASP:OD2	2.48	0.45
16:M:8:GLU:C	16:M:9:ILE:HG13	2.37	0.45
12:I:7:THR:O	12:I:15:ALA:O	2.35	0.45
8:E:31:LEU:HD22	8:E:43:LEU:CD2	2.46	0.45
5:B:103:THR:HA	5:B:180:LEU:HD11	1.99	0.45
11:H:64:LYS:HE3	11:H:79:VAL:HG11	1.98	0.45
9:F:30:LEU:HD23	9:F:75:LEU:HD21	1.97	0.45
1:A:135:C:C2	19:P:1:MET:HB2	2.52	0.45
7:D:5:ILE:O	7:D:5:ILE:HG22	2.15	0.45
6:C:90:GLU:C	6:C:92:ALA:N	2.70	0.45
12:I:10:ARG:NH1	12:I:10:ARG:HG2	2.31	0.45
1:A:409:G:O2'	1:A:410:G:H5'	2.16	0.45
1:A:555:C:H2'	1:A:556:C:C6	2.51	0.45
1:A:945:G:N3	1:A:945:G:H2'	2.31	0.45
1:A:1193:G:N2	1:A:1194:U:C2	2.85	0.45
16:M:49:THR:O	16:M:53:VAL:HG23	2.16	0.45
14:K:14:VAL:O	14:K:15:ALA:HB3	2.16	0.45
1:A:994:A:N7	1:A:1216:G:H4'	2.32	0.45
21:R:69:THR:O	21:R:72:ARG:HB2	2.17	0.45
15:L:89:ARG:HD3	15:L:97:ARG:HA	1.98	0.45
10:G:23:VAL:HG13	10:G:43:PHE:CE2	2.51	0.45
5:B:68:ILE:H	5:B:90:MET:CE	2.30	0.45
1:A:1163:C:O2'	1:A:1164:G:H5'	2.17	0.45
11:H:60:ARG:HG3	11:H:60:ARG:NH1	2.32	0.45
20:Q:59:ILE:HD13	20:Q:73:VAL:HA	1.97	0.45
1:A:299:G:H2'	1:A:300:A:C8	2.52	0.45
20:Q:65:ILE:HD11	20:Q:72:ARG:HG2	1.99	0.45
1:A:509:A:N3	1:A:543:C:O2'	2.42	0.45
6:C:11:ARG:HG3	6:C:178:LEU:HD12	2.00	0.45
7:D:25:ARG:O	7:D:27:TYR:N	2.49	0.45
1:A:1063:C:H3'	1:A:1064:G:H2'	1.99	0.45
1:A:1190:G:O2'	1:A:1191:A:P	2.74	0.45
13:J:91:PRO:HB2	13:J:94:VAL:HG23	1.99	0.45
11:H:85:ARG:CZ	11:H:87:SER:O	2.65	0.45
6:C:61:ALA:O	6:C:62:ASP:C	2.55	0.45
11:H:119:LEU:N	11:H:119:LEU:HD23	2.32	0.45
1:A:1313:U:H2'	1:A:1314:C:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1317:C:H2'	1:A:1318:A:O4'	2.17	0.45
5:B:144:ARG:O	5:B:147:LYS:HB2	2.16	0.45
1:A:285:G:O2'	1:A:286:G:H5'	2.17	0.45
19:P:75:ARG:HA	19:P:80:PHE:HD1	1.82	0.45
1:A:1323:G:H2'	1:A:1324:A:C8	2.52	0.45
10:G:16:LEU:HD22	10:G:16:LEU:H	1.82	0.45
5:B:100:GLY:O	5:B:101:MET:C	2.55	0.44
5:B:7:VAL:C	5:B:8:LYS:HG3	2.38	0.44
14:K:30:VAL:HG21	14:K:65:ALA:HA	1.98	0.44
1:A:514:C:O2'	1:A:515:G:H5'	2.17	0.44
1:A:551:U:H2'	1:A:552:U:C6	2.52	0.44
10:G:111:ARG:HB3	10:G:112:PRO:HD2	1.98	0.44
8:E:91:LEU:HD23	8:E:120:THR:HG22	2.00	0.44
5:B:44:LEU:HD23	5:B:47:THR:OG1	2.17	0.44
15:L:91:LYS:HA	15:L:91:LYS:CE	2.33	0.44
1:A:968:A:OP2	12:I:128:ARG:NH2	2.50	0.44
1:A:1372:U:H2'	1:A:1373:G:O4'	2.17	0.44
7:D:149:ALA:O	7:D:152:SER:N	2.50	0.44
11:H:82:HIS:CG	11:H:83:ILE:N	2.85	0.44
1:A:1098:C:H2'	1:A:1099:G:O4'	2.16	0.44
1:A:1179:A:H2'	1:A:1180:A:O4'	2.17	0.44
1:A:1038:C:C6	1:A:1039:C:H5	2.35	0.44
12:I:41:VAL:HG12	12:I:42:ARG:N	2.31	0.44
8:E:101:ILE:HD12	8:E:119:LEU:CD2	2.48	0.44
1:A:722:A:H3'	1:A:722:A:N3	2.32	0.44
1:A:1284:C:H3'	1:A:1285:A:H8	1.82	0.44
17:N:44:LEU:C	17:N:44:LEU:HD12	2.38	0.44
10:G:37:ASN:HA	10:G:37:ASN:HD22	1.60	0.44
1:A:280:C:O2	20:Q:38:ARG:HG3	2.17	0.44
8:E:84:PHE:CE2	8:E:133:TYR:HD1	2.35	0.44
6:C:79:ARG:O	6:C:79:ARG:HG3	2.16	0.44
13:J:32:ALA:HB2	13:J:76:ASN:HD22	1.82	0.44
13:J:37:PRO:HA	13:J:71:LEU:O	2.17	0.44
13:J:9:ARG:C	13:J:16:LEU:HD21	2.37	0.44
13:J:81:THR:C	13:J:83:GLU:N	2.70	0.44
7:D:108:LEU:HD23	7:D:108:LEU:HA	1.80	0.44
1:A:1227:A:H3'	1:A:1227:A:C8	2.53	0.44
14:K:91:ARG:NH1	21:R:88:LYS:HE3	2.33	0.44
6:C:35:GLU:OE2	6:C:59:ARG:NH1	2.50	0.44
9:F:75:LEU:HD11	9:F:79:LEU:HD11	1.98	0.44
10:G:18:TYR:CD1	10:G:18:TYR:N	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1130:A:OP2	1:A:1130:A:H3'	2.18	0.44
1:A:922:G:H2'	1:A:923:A:C8	2.52	0.44
23:T:45:GLN:C	23:T:47:GLY:N	2.71	0.44
1:A:411:A:N3	1:A:413:G:O2'	2.51	0.44
1:A:433:C:O2'	1:A:434:U:H5'	2.18	0.44
9:F:48:LEU:HD13	9:F:52:ILE:HD12	1.99	0.44
1:A:892:A:C2	1:A:907:A:C4	3.06	0.44
16:M:11:ARG:CG	16:M:12:ASN:H	2.31	0.44
1:A:346:G:C2'	1:A:347:G:H5'	2.47	0.44
1:A:1186:G:N2	1:A:1187:G:H1'	2.33	0.44
12:I:57:GLY:O	12:I:58:ARG:HG2	2.16	0.44
15:L:53:ARG:HG2	15:L:69:TYR:HE1	1.83	0.44
16:M:23:TYR:HE2	16:M:70:LEU:HB3	1.83	0.44
5:B:12:GLU:OE1	5:B:12:GLU:O	2.36	0.44
5:B:21:ARG:NH1	5:B:21:ARG:HG3	2.32	0.44
1:A:942:G:N3	1:A:943:U:C6	2.86	0.44
1:A:1153:C:H2'	1:A:1154:G:C8	2.53	0.44
1:A:487:A:H2'	1:A:488:C:O4'	2.18	0.44
10:G:113:GLU:HG2	10:G:119:ARG:HG2	1.99	0.44
1:A:1422:G:O2'	1:A:1423:G:H5'	2.18	0.44
1:A:1203:C:OP1	17:N:2:ALA:HB3	2.18	0.44
8:E:62:ALA:C	8:E:64:ARG:H	2.21	0.44
1:A:1182:G:H4'	1:A:1183:A:C5'	2.47	0.44
1:A:745:C:OP1	1:A:851:G:O2'	2.35	0.44
1:A:881:G:OP2	15:L:12:ARG:NH2	2.51	0.44
24:V:3:LYS:HG2	24:V:14:TRP:CD1	2.53	0.44
14:K:114:VAL:HG13	14:K:114:VAL:O	2.18	0.44
5:B:172:ILE:O	5:B:172:ILE:HG22	2.17	0.44
10:G:133:GLY:O	10:G:136:LYS:HB3	2.17	0.44
5:B:87:ARG:NH1	5:B:87:ARG:HG3	2.33	0.44
17:N:53:LEU:HB3	17:N:56:VAL:CG2	2.48	0.44
16:M:60:VAL:O	16:M:63:THR:HG22	2.17	0.44
5:B:80:ILE:H	5:B:80:ILE:HG13	1.66	0.44
7:D:150:GLU:HB3	7:D:153:ARG:NH2	2.32	0.44
6:C:110:ASN:HB3	6:C:144:SER:OG	2.17	0.44
20:Q:63:ARG:HG2	20:Q:64:PRO:HD2	1.99	0.44
5:B:141:GLU:O	5:B:142:LEU:C	2.55	0.44
1:A:974:A:P	17:N:29:ARG:HH22	2.41	0.44
10:G:115:ARG:HB2	10:G:118:VAL:HG23	1.99	0.44
1:A:1030:C:C2'	1:A:1030(A):G:H5'	2.45	0.44
8:E:20:GLN:C	8:E:21:ALA:O	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1118:C:H1'	1:A:1179:A:C4	2.52	0.44
1:A:1118:C:H6	1:A:1118:C:O5'	2.00	0.44
9:F:28:ARG:HB2	9:F:28:ARG:NH1	2.33	0.44
16:M:77:ASN:O	16:M:81:LEU:CD2	2.65	0.44
5:B:12:GLU:OE2	5:B:12:GLU:HA	2.18	0.44
20:Q:69:LYS:C	20:Q:70:ARG:HD2	2.37	0.44
1:A:1138:G:N1	1:A:1140:C:C2	2.86	0.44
8:E:11:ILE:HG22	8:E:12:LEU:N	2.31	0.44
1:A:1288:A:O4'	1:A:1353:G:H4'	2.17	0.44
22:S:5:LEU:O	22:S:6:LYS:CB	2.66	0.44
5:B:133:LYS:O	5:B:137:ARG:HG3	2.17	0.44
1:A:489:C:H2'	1:A:490:G:C8	2.52	0.44
19:P:11:SER:OG	19:P:14:ASN:HB3	2.17	0.44
1:A:625:G:H2'	1:A:626:U:H6	1.81	0.44
7:D:163:GLU:C	7:D:165:MET:H	2.21	0.44
14:K:65:ALA:CB	14:K:97:ALA:HB3	2.47	0.44
11:H:11:THR:C	11:H:13:ILE:N	2.70	0.44
1:A:925:G:C2	1:A:927:G:C8	3.06	0.44
1:A:116:A:H2'	1:A:117:G:H8	1.83	0.44
12:I:10:ARG:HH11	12:I:10:ARG:HG2	1.82	0.44
1:A:757:U:H2'	1:A:758:G:O4'	2.17	0.44
6:C:8:ILE:CG2	6:C:16:ARG:HG2	2.34	0.44
1:A:1439:C:H2'	1:A:1440:C:H6	1.82	0.44
1:A:1055:A:C6	1:A:1206:G:C5	3.06	0.44
1:A:1067:A:N3	1:A:1068:G:H1'	2.33	0.44
22:S:45:VAL:CG1	22:S:46:GLY:N	2.80	0.44
12:I:7:THR:O	12:I:80:GLY:HA3	2.17	0.44
12:I:93:ARG:NE	12:I:97:LYS:CE	2.81	0.44
9:F:45:LEU:HD23	9:F:59:TYR:HD1	1.83	0.44
5:B:162:ILE:H	5:B:185:ILE:CD1	2.31	0.44
5:B:176:GLU:O	5:B:177:ALA:C	2.56	0.44
10:G:106:GLN:O	10:G:110:GLN:HG2	2.18	0.44
15:L:28:LYS:O	15:L:30:ALA:N	2.51	0.44
8:E:30:ALA:O	8:E:45:PHE:HA	2.17	0.44
5:B:7:VAL:N	5:B:8:LYS:HE3	2.33	0.44
5:B:221:LEU:HD22	5:B:224:GLN:OE1	2.17	0.44
1:A:55:A:H2'	1:A:56:U:H6	1.83	0.44
1:A:92:C:O2'	1:A:93:G:H5'	2.17	0.44
1:A:49:U:C2	1:A:361:G:N2	2.86	0.44
11:H:40:ALA:O	11:H:43:GLY:N	2.42	0.44
22:S:62:ILE:HD12	22:S:63:THR:H	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1308:U:H2'	1:A:1309:G:C8	2.52	0.44
16:M:59:TYR:O	16:M:63:THR:HG22	2.18	0.44
12:I:93:ARG:C	12:I:95:LYS:N	2.71	0.44
13:J:22:LYS:O	13:J:24:VAL:N	2.51	0.44
5:B:32:ILE:HD13	5:B:40:HIS:CG	2.52	0.44
12:I:105:ASP:OD1	12:I:107:ARG:HG3	2.18	0.44
14:K:44:SER:H	14:K:47:VAL:CG2	2.31	0.44
9:F:33:TYR:C	9:F:71:ARG:NH2	2.70	0.44
22:S:35:SER:C	22:S:37:ARG:N	2.69	0.44
8:E:72:GLN:O	8:E:73:ASN:CB	2.63	0.44
22:S:24:ALA:HB3	22:S:25:LYS:HZ3	1.82	0.44
1:A:1521:G:H2'	1:A:1522:U:H6	1.81	0.44
1:A:386:C:H2'	1:A:387:U:H5'	1.99	0.44
1:A:1455:G:O2'	1:A:1459:C:H5'	2.18	0.44
8:E:153:LYS:HG2	8:E:154:GLY:N	2.33	0.44
10:G:8:GLU:OE1	10:G:8:GLU:O	2.36	0.44
22:S:74:PHE:N	22:S:74:PHE:CD1	2.86	0.44
20:Q:22:LEU:HD12	20:Q:23:VAL:N	2.32	0.44
1:A:540:G:H2'	1:A:541:G:O4'	2.18	0.44
13:J:19:SER:O	13:J:20:ALA:C	2.56	0.44
13:J:98:ILE:HG22	13:J:99:LYS:N	2.33	0.44
12:I:117:HIS:O	12:I:118:LYS:CG	2.66	0.44
9:F:67:MET:HB2	9:F:68:PRO:CD	2.48	0.44
1:A:376:G:C5'	19:P:5:ARG:HD2	2.43	0.44
22:S:5:LEU:C	22:S:6:LYS:HG3	2.38	0.44
9:F:91:VAL:CG1	9:F:92:LYS:N	2.81	0.44
5:B:144:ARG:HD2	5:B:145:LEU:HD23	2.00	0.44
1:A:447:G:H1'	1:A:487:A:H61	1.82	0.44
1:A:811:C:O2'	1:A:901:A:N1	2.50	0.44
8:E:44:GLY:CA	8:E:62:ALA:HB2	2.47	0.44
7:D:162:LEU:O	7:D:165:MET:HB2	2.17	0.44
1:A:865:A:H5'	1:A:1078:U:O4	2.18	0.44
8:E:8:GLU:HB3	8:E:34:VAL:HG22	2.00	0.44
5:B:61:LEU:HD21	5:B:160:ASP:HB3	2.00	0.44
1:A:426:G:P	7:D:36:ARG:HH21	2.41	0.43
1:A:1368:G:HO2'	1:A:1369:C:H5'	1.75	0.43
1:A:1371:G:O3'	12:I:69:GLY:HA3	2.18	0.43
16:M:22:ILE:N	16:M:22:ILE:HD12	2.33	0.43
8:E:115:VAL:HG12	8:E:116:THR:N	2.33	0.43
6:C:134:ILE:CG2	6:C:151:VAL:HB	2.46	0.43
1:A:376:G:C2	1:A:389:A:C2	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:C:O5'	1:A:390:C:H6	2.01	0.43
1:A:182:U:OP2	1:A:183:G:C8	2.70	0.43
1:A:22:G:H2'	1:A:23:C:H6	1.83	0.43
1:A:584:G:H2'	1:A:585:G:C8	2.52	0.43
7:D:78:LEU:HB3	7:D:93:PHE:HE2	1.83	0.43
1:A:537:G:OP1	15:L:113:ARG:NH2	2.51	0.43
15:L:117:ARG:O	15:L:118:SER:C	2.55	0.43
1:A:1307:U:H2'	1:A:1308:U:C6	2.53	0.43
13:J:8:LEU:HD22	13:J:94:VAL:HG11	2.00	0.43
13:J:96:ILE:HG22	13:J:97:GLU:H	1.81	0.43
5:B:35:GLU:HG2	5:B:40:HIS:CD2	2.53	0.43
12:I:118:LYS:HZ2	12:I:118:LYS:HB2	1.83	0.43
1:A:1124:G:H3'	1:A:1145:C:N4	2.22	0.43
1:A:761:G:H1'	20:Q:104:LYS:O	2.18	0.43
1:A:1130:A:OP2	1:A:1131:G:OP2	2.36	0.43
1:A:1490:C:C2'	1:A:1491:G:H5'	2.48	0.43
1:A:1262:C:O2'	1:A:1263:C:H5'	2.18	0.43
1:A:622:A:C8	1:A:623:C:C5	3.06	0.43
14:K:18:ARG:HB3	14:K:33:THR:HG22	2.01	0.43
14:K:58:PRO:HD3	14:K:89:ALA:HB1	2.00	0.43
5:B:79:ASP:O	5:B:81:VAL:N	2.51	0.43
1:A:1365:G:O2'	1:A:1366:C:H5'	2.18	0.43
16:M:3:ARG:CG	16:M:9:ILE:HG23	2.42	0.43
1:A:1220:G:O2'	1:A:1221:G:H5'	2.18	0.43
20:Q:68:ARG:NH1	20:Q:68:ARG:HG2	2.33	0.43
22:S:33:THR:CG2	22:S:34:TRP:N	2.80	0.43
1:A:179:A:O2'	1:A:180:U:H5'	2.19	0.43
13:J:53:PRO:O	13:J:54:PHE:O	2.36	0.43
21:R:55:ARG:HB3	21:R:55:ARG:CZ	2.49	0.43
23:T:41:ILE:CD1	23:T:87:LYS:NZ	2.81	0.43
23:T:18:GLN:O	23:T:19:SER:C	2.56	0.43
1:A:259:G:O2'	1:A:260:G:H5'	2.17	0.43
1:A:397:A:N3	1:A:397:A:H3'	2.34	0.43
10:G:85:TYR:HD1	10:G:154:TYR:CE1	2.32	0.43
17:N:25:VAL:O	17:N:25:VAL:HG22	2.18	0.43
1:A:803:G:N7	1:A:804:U:C5	2.86	0.43
1:A:346:G:H2'	1:A:347:G:O4'	2.18	0.43
1:A:598:U:H4'	11:H:94:TYR:CG	2.54	0.43
12:I:55:ALA:O	12:I:56:LEU:HB3	2.18	0.43
6:C:5:ILE:HD13	6:C:10:PHE:CB	2.44	0.43
12:I:83:ARG:O	12:I:86:VAL:HB	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1221:G:H2'	1:A:1222:G:H5'	2.01	0.43
5:B:203:GLY:O	5:B:204:ASN:C	2.56	0.43
5:B:207:ALA:O	5:B:211:ILE:HG13	2.19	0.43
5:B:19:HIS:O	5:B:39:ILE:HG23	2.18	0.43
6:C:155:GLY:O	6:C:156:ARG:CB	2.66	0.43
6:C:188:LEU:HD12	6:C:190:ARG:HG3	1.99	0.43
1:A:1288:A:H1'	1:A:1352:C:O2'	2.17	0.43
1:A:760:G:N2	20:Q:104:LYS:N	2.66	0.43
1:A:984:C:H2'	1:A:985:C:H6	1.83	0.43
1:A:835:U:OP1	21:R:64:ARG:NH2	2.41	0.43
1:A:1489:G:O2'	1:A:1490:C:H5'	2.18	0.43
1:A:613:C:C2	1:A:628:G:N2	2.86	0.43
12:I:99:LEU:HB2	12:I:101:PHE:CE1	2.54	0.43
1:A:1081:G:OP1	8:E:16:THR:HG23	2.19	0.43
7:D:177:ASP:OD1	7:D:177:ASP:O	2.36	0.43
8:E:152:ARG:HB3	11:H:43:GLY:O	2.17	0.43
5:B:105:PHE:O	5:B:107:THR:N	2.51	0.43
1:A:294:U:H2'	1:A:295:C:H6	1.83	0.43
14:K:93:GLN:O	14:K:96:ARG:HB2	2.18	0.43
23:T:36:LEU:HA	23:T:36:LEU:HD23	1.84	0.43
1:A:1053:G:C5'	1:A:1054:C:H5'	2.48	0.43
5:B:189:ASP:OD1	5:B:205:ASP:OD1	2.35	0.43
11:H:4:ASP:OD2	11:H:7:ALA:CB	2.66	0.43
11:H:35:ILE:O	11:H:39:LEU:HD23	2.18	0.43
1:A:707:C:O2'	1:A:708:C:H5'	2.17	0.43
8:E:86:ALA:C	8:E:125:SER:HB3	2.39	0.43
1:A:156:G:O2'	1:A:157:G:H5'	2.18	0.43
1:A:1440:C:H2'	1:A:1441:G:O4'	2.19	0.43
1:A:1368:G:P	12:I:112:LYS:O	2.77	0.43
1:A:276:G:O2'	1:A:277:C:H5'	2.18	0.43
1:A:926:G:H3'	1:A:1505:G:H21	1.84	0.43
13:J:81:THR:O	13:J:83:GLU:N	2.51	0.43
6:C:134:ILE:HD11	6:C:153:VAL:HG23	2.00	0.43
1:A:943:U:H2'	1:A:944:G:H5'	2.00	0.43
1:A:382:A:C2	1:A:383:A:C4	3.07	0.43
12:I:111:ARG:O	12:I:113:LYS:HD2	2.19	0.43
1:A:1148:U:H4'	12:I:14:VAL:CG1	2.45	0.43
9:F:63:TYR:N	9:F:63:TYR:CD2	2.85	0.43
20:Q:92:ARG:O	20:Q:95:TYR:HB2	2.19	0.43
1:A:179:A:H2'	1:A:180:U:H6	1.81	0.43
1:A:974:A:OP2	17:N:29:ARG:NH2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:76:ILE:HG22	8:E:78:HIS:H	1.82	0.43
12:I:48:GLU:N	12:I:49:PRO:CD	2.81	0.43
1:A:789:U:O2	1:A:791:G:C8	2.72	0.43
1:A:429:U:H1'	1:A:430:A:H5"	2.00	0.43
7:D:52:SER:C	7:D:54:TYR:N	2.72	0.43
1:A:1183:A:O2'	1:A:1184:G:P	2.76	0.43
10:G:156:TRP:CG	10:G:156:TRP:O	2.71	0.43
16:M:110:ARG:CG	16:M:110:ARG:NH1	2.81	0.43
20:Q:48:GLU:O	20:Q:50:LYS:N	2.52	0.43
6:C:113:ALA:N	6:C:114:PRO:CD	2.82	0.43
1:A:772:U:O2'	1:A:773:G:H5'	2.18	0.43
14:K:86:GLY:H	14:K:112:THR:HG23	1.83	0.43
8:E:143:ARG:HD3	8:E:143:ARG:HA	1.82	0.43
7:D:36:ARG:N	7:D:37:PRO:CD	2.49	0.43
1:A:1068:G:N3	1:A:1191:A:C2	2.86	0.43
1:A:1192:C:H2'	1:A:1193:G:O4'	2.19	0.43
17:N:37:PHE:C	17:N:39:LEU:H	2.20	0.43
3:Y:34:G:HO2'	3:Y:35:A:P	2.42	0.43
15:L:71:PRO:HG2	15:L:102:ARG:HG2	2.01	0.43
1:A:946:A:H2'	1:A:947:G:H8	1.75	0.43
12:I:7:THR:HG22	12:I:8:GLY:N	2.33	0.43
1:A:1326:C:H5"	24:V:12:LYS:NZ	2.34	0.43
5:B:162:ILE:C	5:B:185:ILE:HD13	2.39	0.43
1:A:953:G:N7	16:M:104:ARG:NH2	2.63	0.43
1:A:1234:C:H2'	1:A:1235:U:C6	2.53	0.43
9:F:69:GLU:N	9:F:69:GLU:OE1	2.46	0.43
9:F:74:ASP:OD1	9:F:77:ARG:NH2	2.52	0.43
1:A:113:G:H1'	1:A:354:G:C5'	2.47	0.43
5:B:55:PHE:HA	5:B:58:ILE:HD12	2.00	0.43
21:R:24:ALA:O	21:R:26:LEU:N	2.50	0.43
11:H:35:ILE:HD12	11:H:35:ILE:H	1.84	0.43
1:A:1030(D):A:C2'	1:A:1031:G:H5'	2.47	0.43
23:T:45:GLN:HA	23:T:91:LEU:HB3	2.00	0.43
24:V:8:THR:HG22	24:V:9:ARG:N	2.33	0.43
1:A:720:C:H2'	1:A:721:G:C8	2.53	0.43
8:E:127:ASN:O	8:E:128:PRO:C	2.56	0.43
5:B:215:LEU:O	5:B:218:ALA:N	2.51	0.43
10:G:5:ARG:CG	10:G:6:ARG:H	2.04	0.43
15:L:101:VAL:O	15:L:102:ARG:C	2.56	0.43
1:A:1331:G:O2'	1:A:1332:A:P	2.77	0.43
18:O:88:ARG:HH11	18:O:88:ARG:CA	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:24:VAL:HG12	15:L:24:VAL:O	2.18	0.43
1:A:57:G:C5	1:A:58:C:C4	3.07	0.43
11:H:11:THR:HA	11:H:14:ARG:HH12	1.83	0.43
1:A:928:G:O2'	1:A:929:G:H5'	2.18	0.43
1:A:513:C:O2'	1:A:514:C:H5'	2.19	0.43
10:G:37:ASN:C	10:G:39:ALA:N	2.71	0.43
5:B:82:ARG:O	5:B:86:GLU:HG3	2.18	0.43
1:A:194:C:H2'	1:A:195:A:H5"	2.00	0.43
1:A:1061:G:O4'	13:J:56:HIS:CE1	2.72	0.43
1:A:1190:G:C2'	1:A:1191:A:OP2	2.66	0.43
6:C:56:ASP:O	6:C:57:ILE:HG13	2.17	0.43
22:S:41:VAL:O	22:S:42:PRO:C	2.57	0.43
1:A:1309:G:C6	1:A:1329:A:C2	3.07	0.43
1:A:948:C:H2'	1:A:949:A:H8	1.84	0.43
16:M:67:GLU:O	16:M:68:GLY:C	2.57	0.43
14:K:54:ARG:HG2	14:K:54:ARG:H	1.54	0.43
5:B:211:ILE:H	5:B:211:ILE:HG13	1.70	0.43
6:C:118:GLN:O	6:C:121:ALA:HB3	2.18	0.43
1:A:942:G:H2'	1:A:943:U:C6	2.53	0.43
14:K:46:GLY:O	14:K:47:VAL:C	2.56	0.43
20:Q:97:SER:HB2	20:Q:103:GLY:HA2	2.01	0.43
6:C:202:ILE:HG22	6:C:204:LEU:CD2	2.48	0.43
20:Q:59:ILE:CG2	20:Q:71:PHE:CD1	3.02	0.43
7:D:163:GLU:C	7:D:165:MET:N	2.72	0.43
1:A:913:A:H4'	1:A:914:A:O5'	2.19	0.43
11:H:6:ILE:HD13	11:H:6:ILE:HA	1.90	0.43
1:A:1190:G:HO2'	1:A:1191:A:P	2.42	0.43
1:A:1221:G:O3'	22:S:77:THR:CG2	2.67	0.43
5:B:10:LEU:O	5:B:12:GLU:N	2.46	0.43
5:B:16:HIS:CE1	5:B:213:LEU:HD13	2.53	0.43
5:B:9:GLU:HG2	5:B:10:LEU:H	1.81	0.43
7:D:68:TYR:HD1	7:D:68:TYR:H	1.67	0.43
1:A:934:C:C4	1:A:1345:U:C5	3.07	0.43
1:A:1345:U:N3	1:A:1377:A:C2	2.87	0.43
6:C:20:SER:HB3	6:C:22:TRP:NE1	2.34	0.43
6:C:97:LYS:HG2	6:C:97:LYS:O	2.19	0.43
6:C:150:LYS:HG3	6:C:169:ALA:HB2	2.01	0.43
17:N:18:VAL:C	17:N:20:ALA:H	2.22	0.43
9:F:91:VAL:CG1	9:F:92:LYS:H	2.26	0.43
15:L:85:ILE:HG23	15:L:98:TYR:HB3	2.01	0.43
15:L:27:LEU:HD23	15:L:28:LYS:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:40:LEU:C	21:R:42:ARG:H	2.21	0.43
7:D:63:LYS:O	7:D:64:LEU:C	2.57	0.43
10:G:122:HIS:O	10:G:123:GLU:C	2.57	0.43
7:D:163:GLU:O	7:D:165:MET:N	2.52	0.43
1:A:1070:U:H2'	1:A:1071:C:H6	1.84	0.43
21:R:19:LYS:HD2	21:R:19:LYS:N	2.34	0.43
1:A:1051:C:O2'	1:A:1052:U:H5'	2.18	0.42
1:A:1193:G:O2'	1:A:1194:U:H5'	2.19	0.42
18:O:70:LEU:CD1	18:O:78:TYR:HB2	2.33	0.42
18:O:82:ILE:O	18:O:83:GLU:C	2.57	0.42
20:Q:45:HIS:HB2	20:Q:69:LYS:HE2	2.01	0.42
11:H:111:ILE:O	11:H:134:ILE:HB	2.19	0.42
1:A:943:U:O2'	1:A:944:G:H5'	2.19	0.42
8:E:55:VAL:O	8:E:58:ALA:HB3	2.19	0.42
23:T:54:LYS:HA	23:T:57:ARG:NH1	2.32	0.42
13:J:38:ILE:HA	13:J:39:PRO:HD2	1.73	0.42
1:A:1286:A:H2'	1:A:1287:A:O3'	2.19	0.42
13:J:46:ARG:HD3	17:N:61:TRP:CH2	2.54	0.42
5:B:122:PHE:HE2	5:B:139:LYS:HG2	1.83	0.42
1:A:1202:G:H2'	1:A:1203:C:O4'	2.19	0.42
22:S:87:ALA:O	22:S:88:LYS:CB	2.66	0.42
1:A:1465:C:H2'	1:A:1466:C:O4'	2.19	0.42
1:A:407:G:H2'	1:A:408:A:C8	2.54	0.42
1:A:979:C:O2	17:N:19:ARG:HG2	2.19	0.42
8:E:115:VAL:HG13	8:E:116:THR:N	2.34	0.42
1:A:942:G:O2'	1:A:943:U:H5'	2.19	0.42
1:A:382:A:C2	1:A:383:A:C5	3.07	0.42
9:F:44:GLY:HA2	9:F:59:TYR:HE1	1.77	0.42
1:A:533:A:C2	1:A:536:C:C5	3.07	0.42
1:A:533:A:H2'	1:A:535:A:OP2	2.19	0.42
1:A:689:C:OP1	14:K:46:GLY:HA3	2.20	0.42
1:A:1289:A:H2'	1:A:1290:G:H5'	2.01	0.42
11:H:9:MET:O	11:H:10:LEU:C	2.57	0.42
14:K:66:LEU:O	14:K:67:ASP:C	2.56	0.42
1:A:334:C:O2'	1:A:335:C:H5'	2.19	0.42
5:B:134:GLU:C	5:B:136:VAL:N	2.71	0.42
5:B:143:GLU:O	5:B:147:LYS:HG3	2.18	0.42
8:E:78:HIS:C	8:E:78:HIS:ND1	2.71	0.42
19:P:12:LYS:O	19:P:13:HIS:CB	2.66	0.42
7:D:61:LYS:O	7:D:62:GLN:C	2.56	0.42
10:G:153:HIS:C	10:G:155:ARG:H	2.22	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:U:H2'	1:A:57:G:H8	1.82	0.42
5:B:61:LEU:O	5:B:61:LEU:HD13	2.19	0.42
1:A:594:G:C2'	1:A:595:G:H5'	2.49	0.42
1:A:1054:C:N3	3:Y:34:G:O4'	2.52	0.42
1:A:1207:G:C5	1:A:1208:C:C5	3.07	0.42
16:M:78:ILE:C	16:M:80:ARG:N	2.70	0.42
1:A:959:A:C3'	1:A:960:U:H5"	2.47	0.42
1:A:1345:U:OP1	12:I:120:ARG:NH1	2.52	0.42
9:F:39:LYS:HG3	9:F:62:TRP:HZ3	1.84	0.42
9:F:78:GLU:HA	9:F:81:ILE:CD1	2.48	0.42
11:H:83:ILE:HB	11:H:137:VAL:HG22	2.01	0.42
22:S:5:LEU:O	22:S:6:LYS:HB2	2.20	0.42
5:B:112:VAL:O	5:B:115:LEU:HB3	2.19	0.42
1:A:1016:A:C2'	1:A:1017:G:H5'	2.49	0.42
7:D:5:ILE:HA	7:D:115:ARG:NH2	2.33	0.42
8:E:57:LYS:O	8:E:60:TYR:HB3	2.18	0.42
19:P:51:VAL:O	19:P:52:ASP:HB3	2.19	0.42
1:A:1069:C:H2'	1:A:1070:U:O5'	2.19	0.42
24:V:5:ASP:O	24:V:11:GLY:HA3	2.19	0.42
1:A:245:C:O2	1:A:283:C:N3	2.52	0.42
10:G:129:GLU:CB	10:G:131:LYS:HE2	2.49	0.42
11:H:72:PRO:O	11:H:73:ASP:HB3	2.20	0.42
1:A:1194:U:H2'	1:A:1195:C:H6	1.84	0.42
6:C:33:LEU:O	6:C:33:LEU:HD23	2.19	0.42
16:M:23:TYR:HB3	16:M:67:GLU:H	1.84	0.42
16:M:84:ILE:O	16:M:86:CYS:N	2.52	0.42
5:B:33:TYR:CB	5:B:41:ILE:O	2.67	0.42
5:B:34:ALA:O	5:B:40:HIS:HA	2.20	0.42
6:C:139:GLN:O	6:C:140:ARG:C	2.58	0.42
6:C:59:ARG:HD3	6:C:97:LYS:HZ3	1.85	0.42
21:R:27:GLY:O	21:R:29:PHE:HD2	2.02	0.42
11:H:35:ILE:HG22	11:H:39:LEU:HD21	2.01	0.42
1:A:1019:C:H2'	1:A:1020:U:O4'	2.20	0.42
9:F:19:LEU:C	9:F:19:LEU:CD2	2.87	0.42
17:N:15:LYS:O	17:N:16:PHE:CG	2.73	0.42
1:A:419:C:O2'	1:A:420:U:H5'	2.18	0.42
14:K:94:ALA:O	14:K:97:ALA:HB3	2.19	0.42
23:T:59:ALA:O	23:T:60:GLU:C	2.57	0.42
19:P:53:VAL:HG23	19:P:54:GLU:N	2.33	0.42
1:A:232:G:H1'	1:A:262:A:N1	2.34	0.42
12:I:55:ALA:O	12:I:56:LEU:CB	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:A:H2'	1:A:34:C:C6	2.54	0.42
20:Q:28:PRO:HA	20:Q:35:VAL:HA	2.02	0.42
15:L:41:ARG:NH1	15:L:41:ARG:CB	2.82	0.42
22:S:43:GLU:H	22:S:43:GLU:CD	2.22	0.42
15:L:110:VAL:O	15:L:122:THR:CG2	2.65	0.42
1:A:1125:U:C5'	1:A:1126:U:H5	2.27	0.42
7:D:187:ARG:NE	7:D:188:LEU:H	2.18	0.42
14:K:69:ALA:C	14:K:73:MET:HG2	2.40	0.42
1:A:973:G:H3'	1:A:974:A:H5"	2.02	0.42
1:A:974:A:OP2	17:N:41:ARG:NH1	2.51	0.42
1:A:406:G:H5"	7:D:5:ILE:HG21	2.00	0.42
10:G:41:ARG:O	10:G:42:ILE:C	2.57	0.42
1:A:328:C:H2'	1:A:328:C:O2	2.20	0.42
1:A:781:A:OP1	1:A:1523:G:H5'	2.20	0.42
1:A:7:G:H5'	1:A:298:A:O4'	2.19	0.42
1:A:55:A:H2'	1:A:56:U:C6	2.54	0.42
1:A:652:U:O4'	1:A:653:A:H2	2.01	0.42
1:A:1379:G:O2'	1:A:1380:U:H5'	2.20	0.42
12:I:3:GLN:HG3	12:I:20:ARG:HG2	2.01	0.42
1:A:573:A:O2'	1:A:574:A:H5'	2.19	0.42
19:P:76:GLN:HB2	19:P:76:GLN:HE21	1.60	0.42
6:C:11:ARG:O	6:C:14:ILE:O	2.37	0.42
1:A:425:G:C2'	1:A:426:G:H5'	2.50	0.42
5:B:208:ILE:O	5:B:209:ARG:C	2.58	0.42
5:B:77:ALA:HA	5:B:80:ILE:HD12	2.02	0.42
17:N:3:ARG:O	17:N:7:ILE:HG13	2.20	0.42
16:M:65:LYS:O	16:M:66:LEU:HD23	2.19	0.42
1:A:1258:G:H1	1:A:1277:C:H42	1.67	0.42
17:N:41:ARG:HG3	17:N:42:ILE:N	2.35	0.42
1:A:457:C:N3	1:A:476:G:C2	2.87	0.42
22:S:25:LYS:HD2	22:S:25:LYS:H	1.85	0.42
20:Q:3:LYS:HB3	20:Q:60:ILE:CD1	2.49	0.42
1:A:1252:A:H2'	1:A:1253:G:O4'	2.20	0.42
7:D:54:TYR:O	7:D:55:ALA:C	2.58	0.42
1:A:878:G:C5'	11:H:89:PRO:HG2	2.49	0.42
1:A:597:G:C4	1:A:644:G:C2	3.08	0.42
7:D:24:GLU:HG2	7:D:25:ARG:N	2.33	0.42
15:L:46:LYS:CG	15:L:47:LYS:H	1.95	0.42
5:B:21:ARG:NH1	5:B:23:ARG:HG2	2.35	0.42
11:H:4:ASP:CG	11:H:85:ARG:HH12	2.23	0.42
6:C:134:ILE:O	6:C:135:LYS:C	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:533:A:O2'	1:A:534:U:OP1	2.34	0.42
1:A:1150:U:O2	13:J:39:PRO:CG	2.67	0.42
13:J:39:PRO:O	13:J:69:ASN:O	2.38	0.42
10:G:51:GLN:HE21	10:G:58:PRO:HD3	1.84	0.42
1:A:200:G:H1	1:A:217:C:H42	1.68	0.42
10:G:118:VAL:O	10:G:119:ARG:C	2.58	0.42
11:H:16:ALA:HB1	11:H:21:LYS:HB2	2.02	0.42
6:C:52:LEU:HD23	6:C:52:LEU:N	2.26	0.42
1:A:1014:A:H5'	22:S:14:HIS:CD2	2.55	0.42
1:A:75:G:H2'	1:A:76:C:H6	1.84	0.42
6:C:174:PRO:HB2	6:C:177:THR:CG2	2.48	0.42
8:E:131:ILE:O	8:E:134:ALA:HB3	2.19	0.42
1:A:229:U:C2'	1:A:230:G:H5'	2.50	0.42
5:B:92:TYR:CD1	5:B:151:GLY:HA3	2.54	0.42
1:A:893:C:H2'	1:A:894:G:C8	2.54	0.42
7:D:25:ARG:HH21	7:D:30:LYS:HD3	1.79	0.42
13:J:28:ARG:HH12	13:J:33:GLN:HG2	1.84	0.42
13:J:96:ILE:CG2	13:J:97:GLU:N	2.83	0.42
1:A:277:C:O2'	1:A:278:G:H5'	2.19	0.42
1:A:938:A:C6	1:A:939:G:C5	3.08	0.42
1:A:1347:G:H2'	1:A:1373:G:H1	1.83	0.42
1:A:519:C:H2'	1:A:520:A:O4'	2.19	0.42
14:K:52:GLY:N	14:K:55:LYS:HE3	2.34	0.42
1:A:1288:A:C6	1:A:1289:A:C5	3.08	0.42
9:F:2:ARG:CD	9:F:69:GLU:HG2	2.49	0.42
20:Q:97:SER:O	20:Q:99:SER:N	2.51	0.42
5:B:146:GLN:O	5:B:150:SER:HB3	2.20	0.42
10:G:43:PHE:CZ	10:G:47:CYS:SG	3.13	0.42
21:R:39:VAL:O	21:R:42:ARG:HB2	2.19	0.42
1:A:980:C:H3'	1:A:981:U:H6	1.83	0.42
10:G:79:ARG:HD3	10:G:84:ASN:OD1	2.20	0.42
6:C:177:THR:CG2	6:C:177:THR:O	2.67	0.42
10:G:155:ARG:O	10:G:156:TRP:HB3	2.19	0.42
1:A:644:G:C2'	1:A:645:C:H5'	2.50	0.42
1:A:632:A:H2'	1:A:633:G:H5'	2.00	0.42
1:A:408:A:O2'	1:A:409:G:H5'	2.19	0.42
1:A:1451:A:O3'	1:A:1452:C:H6	2.03	0.42
20:Q:79:SER:O	20:Q:80:GLY:C	2.58	0.42
13:J:60:ARG:H	13:J:60:ARG:HD2	1.84	0.42
15:L:41:ARG:HH12	15:L:57:LYS:HE2	1.85	0.42
15:L:47:LYS:HB2	15:L:48:PRO:CD	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1328:C:O2'	1:A:1329:A:H5'	2.19	0.42
1:A:977:A:H1'	1:A:1223:C:H42	1.85	0.42
13:J:22:LYS:C	13:J:24:VAL:N	2.73	0.42
13:J:9:ARG:HG3	13:J:9:ARG:O	2.20	0.42
11:H:4:ASP:CG	11:H:85:ARG:NH1	2.73	0.42
1:A:1298:C:N4	10:G:114:ARG:HD3	2.35	0.42
1:A:689:C:H2'	1:A:690:G:O4'	2.20	0.42
1:A:377:G:P	19:P:3:LYS:HZ3	2.43	0.42
6:C:191:THR:HG23	6:C:192:THR:H	1.85	0.42
10:G:21:VAL:CG2	10:G:22:LEU:N	2.82	0.42
1:A:107:G:O2'	1:A:108:G:H5'	2.20	0.42
1:A:769:G:H4'	1:A:1513:A:H4'	2.01	0.42
1:A:9:G:C2	1:A:26:A:C2	3.08	0.42
20:Q:8:GLY:HA3	20:Q:21:VAL:CG1	2.50	0.42
1:A:622:A:H2'	1:A:623:C:H5'	2.02	0.42
1:A:995:C:H2'	1:A:995:C:O2	2.19	0.42
1:A:1053:G:O2'	1:A:1199:U:H5	2.00	0.42
16:M:73:GLU:O	16:M:74:VAL:C	2.57	0.42
1:A:1347:G:HO2'	1:A:1348:U:H5	1.64	0.42
10:G:104:LEU:HA	10:G:104:LEU:HD23	1.83	0.42
9:F:62:TRP:CD1	21:R:35:ARG:NH1	2.87	0.42
1:A:582:U:H1'	20:Q:105:ALA:HA	2.01	0.42
5:B:53:ARG:HB3	5:B:53:ARG:CZ	2.50	0.42
17:N:9:LYS:C	17:N:11:LYS:N	2.71	0.42
16:M:37:THR:O	16:M:37:THR:HG22	2.20	0.42
6:C:66:VAL:HG12	6:C:66:VAL:O	2.19	0.42
1:A:45:U:H2'	1:A:46:G:H8	1.85	0.42
1:A:22:G:C6	1:A:23:C:C4	3.08	0.42
6:C:148:GLY:HA3	6:C:172:ARG:O	2.20	0.42
1:A:444:C:O2'	1:A:445:G:H5'	2.20	0.42
1:A:407:G:O2'	7:D:116:GLN:HG3	2.20	0.42
1:A:1121:U:H2'	1:A:1122:U:H6	1.84	0.42
1:A:340:U:H2'	1:A:341:C:C6	2.55	0.42
1:A:1127:G:H21	1:A:1147:C:N4	2.18	0.42
1:A:1375:A:O2'	1:A:1376:U:H5'	2.20	0.42
6:C:165:THR:O	6:C:165:THR:HG22	2.19	0.42
1:A:1029:C:H6	1:A:1029:C:O5'	2.03	0.42
5:B:84:GLU:CB	5:B:219:VAL:HG21	2.18	0.41
4:Z:2:U:H2'	4:Z:3:U:H6	1.84	0.41
23:T:74:LYS:CG	23:T:75:ASN:N	2.55	0.41
1:A:1309:G:C6	1:A:1329:A:N1	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:125:GLU:OE2	6:C:189:ALA:HA	2.20	0.41
1:A:1287:A:C6	1:A:1288:A:C6	3.07	0.41
21:R:82:THR:O	21:R:82:THR:HG23	2.20	0.41
20:Q:27:PHE:CD1	20:Q:27:PHE:C	2.93	0.41
21:R:53:ARG:C	21:R:55:ARG:H	2.21	0.41
6:C:40:ARG:NH1	6:C:40:ARG:HG3	2.35	0.41
1:A:1027:C:H2'	1:A:1028:C:C6	2.55	0.41
1:A:1229:A:C2	1:A:1230:C:C5	3.08	0.41
1:A:1039:C:O2'	1:A:1040:U:H5'	2.20	0.41
7:D:170:VAL:HG22	7:D:171:GLY:N	2.34	0.41
1:A:151:A:H2'	1:A:152:A:O4'	2.20	0.41
7:D:88:VAL:O	7:D:92:VAL:HG23	2.20	0.41
20:Q:24:GLU:OE2	20:Q:37:LYS:HD3	2.20	0.41
1:A:1329:A:H2'	1:A:1330:U:H5'	2.02	0.41
16:M:8:GLU:HG3	16:M:22:ILE:HG13	2.02	0.41
13:J:34:VAL:HG12	13:J:35:SER:N	2.34	0.41
13:J:89:ASP:OD1	13:J:90:LEU:N	2.53	0.41
5:B:17:PHE:CD2	5:B:17:PHE:O	2.73	0.41
1:A:1058:G:C6	1:A:1059:C:N3	2.89	0.41
6:C:155:GLY:HA3	6:C:164:ARG:O	2.21	0.41
8:E:31:LEU:HA	8:E:31:LEU:HD23	1.52	0.41
23:T:54:LYS:N	23:T:100:ILE:HD13	2.35	0.41
23:T:50:GLU:HA	23:T:100:ILE:CB	2.49	0.41
1:A:101:A:H2'	1:A:102:G:H8	1.85	0.41
14:K:69:ALA:O	14:K:73:MET:N	2.53	0.41
19:P:67:THR:CG2	19:P:68:ASP:N	2.83	0.41
1:A:1168:A:C6	1:A:1169:A:C6	3.08	0.41
15:L:43:VAL:HG23	15:L:55:VAL:CG2	2.50	0.41
1:A:961:U:H2'	1:A:962:C:H5'	2.02	0.41
1:A:821:G:O2'	1:A:822:C:H5'	2.20	0.41
7:D:91:SER:O	7:D:92:VAL:C	2.57	0.41
1:A:1107:C:H2'	1:A:1108:G:H5'	2.02	0.41
13:J:47:PHE:CE2	17:N:37:PHE:HE1	2.37	0.41
13:J:51:ARG:CB	13:J:59:SER:HB3	2.50	0.41
13:J:60:ARG:O	13:J:61:GLU:CB	2.67	0.41
17:N:35:ARG:C	17:N:37:PHE:N	2.73	0.41
1:A:502:G:OP1	15:L:118:SER:N	2.34	0.41
16:M:19:LEU:CA	16:M:22:ILE:HD13	2.46	0.41
1:A:959:A:H2	1:A:1221:G:N3	2.18	0.41
5:B:16:HIS:O	5:B:17:PHE:HD2	2.03	0.41
1:A:235:C:C5'	20:Q:70:ARG:HG2	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:7:ALA:HB2	11:H:85:ARG:HG3	2.02	0.41
1:A:1057:G:C2'	1:A:1058:G:H5'	2.50	0.41
1:A:939:G:C6	1:A:940:C:N4	2.87	0.41
5:B:178:ARG:O	5:B:179:LYS:C	2.59	0.41
5:B:96:ARG:HD2	5:B:97:TRP:N	2.33	0.41
16:M:102:ARG:NH1	16:M:104:ARG:HB3	2.35	0.41
1:A:1496:C:H2'	1:A:1497:G:O4'	2.20	0.41
1:A:1152:A:O2'	1:A:1153:C:H5'	2.19	0.41
1:A:665:A:N3	1:A:732:C:H2'	2.36	0.41
1:A:1032:G:H2'	1:A:1033:G:O4'	2.20	0.41
19:P:45:THR:HB	19:P:46:PRO:HD2	2.01	0.41
1:A:429:U:H4'	1:A:430:A:O5'	2.19	0.41
5:B:7:VAL:O	5:B:8:LYS:HG3	2.20	0.41
1:A:1419:G:H2'	1:A:1420:C:C6	2.55	0.41
18:O:54:ARG:O	18:O:55:GLY:C	2.58	0.41
5:B:148:TYR:CD2	5:B:148:TYR:N	2.87	0.41
1:A:184:G:C4'	1:A:224:C:H4'	2.49	0.41
6:C:6:HIS:HD2	6:C:8:ILE:HB	1.79	0.41
12:I:114:TYR:CD2	12:I:114:TYR:N	2.86	0.41
22:S:41:VAL:HG22	22:S:44:MET:HE3	2.02	0.41
1:A:1220:G:H2'	1:A:1221:G:H8	1.85	0.41
1:A:960:U:H1'	1:A:1223:C:H5'	2.02	0.41
20:Q:45:HIS:O	20:Q:47:PRO:HD3	2.20	0.41
6:C:167:TRP:O	6:C:168:ALA:CB	2.68	0.41
1:A:1226:C:HO2'	1:A:1227:A:C5'	2.33	0.41
6:C:111:LEU:HD11	6:C:144:SER:O	2.20	0.41
6:C:22:TRP:CZ3	6:C:32:LEU:HD22	2.56	0.41
1:A:786:G:C2	1:A:797:C:C2	3.09	0.41
20:Q:63:ARG:O	20:Q:64:PRO:C	2.58	0.41
1:A:1319:A:OP1	22:S:5:LEU:HD21	2.21	0.41
1:A:1320:C:O2	22:S:72:GLY:HA3	2.21	0.41
10:G:51:GLN:NE2	10:G:56:GLN:O	2.51	0.41
5:B:122:PHE:O	5:B:123:ALA:HB2	2.19	0.41
10:G:43:PHE:CE2	10:G:47:CYS:SG	3.14	0.41
1:A:474:G:H2'	1:A:475:G:C8	2.43	0.41
15:L:86:ARG:CG	15:L:86:ARG:NH1	2.79	0.41
10:G:70:LYS:CG	10:G:100:ALA:HB2	2.47	0.41
10:G:66:VAL:O	10:G:70:LYS:HG3	2.21	0.41
17:N:12:ARG:O	17:N:14:PRO:HD3	2.20	0.41
1:A:1073:U:OP1	8:E:57:LYS:HE2	2.20	0.41
20:Q:5:VAL:HG13	20:Q:59:ILE:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:U:H2'	1:A:165:C:C6	2.55	0.41
1:A:190:C:H2'	1:A:190(A):C:C6	2.55	0.41
20:Q:48:GLU:C	20:Q:50:LYS:N	2.73	0.41
1:A:1525:G:O2'	1:A:1526:G:H5'	2.20	0.41
7:D:112:VAL:HG23	7:D:161:ASN:ND2	2.33	0.41
13:J:55:LYS:O	13:J:56:HIS:HB2	2.20	0.41
16:M:80:ARG:C	16:M:82:MET:N	2.74	0.41
5:B:48:MET:O	5:B:51:LEU:HB2	2.21	0.41
13:J:84:GLN:C	13:J:86:MET:H	2.23	0.41
6:C:121:ALA:O	6:C:125:GLU:HG3	2.20	0.41
6:C:188:LEU:CD1	6:C:195:VAL:HG13	2.50	0.41
6:C:70:VAL:CG1	6:C:71:ALA:N	2.82	0.41
22:S:39:THR:HG23	22:S:68:GLY:O	2.20	0.41
21:R:44:LEU:HD23	21:R:49:LYS:C	2.41	0.41
1:A:1130:A:P	1:A:1131:G:OP2	2.79	0.41
16:M:40:ASN:ND2	16:M:40:ASN:C	2.74	0.41
1:A:1521:G:O2'	1:A:1522:U:H5'	2.21	0.41
7:D:52:SER:O	7:D:54:TYR:N	2.53	0.41
7:D:162:LEU:HD23	7:D:178:VAL:HG13	2.01	0.41
6:C:180:ALA:CB	6:C:182:ILE:HG13	2.50	0.41
1:A:1105:A:H2'	1:A:1106:G:C8	2.55	0.41
9:F:9:VAL:HG22	9:F:60:PHE:HD2	1.83	0.41
1:A:37:U:O2'	1:A:38:G:H5'	2.20	0.41
1:A:825:G:O2'	1:A:826:C:H5'	2.21	0.41
1:A:1108:G:H4'	1:A:1191:A:O4'	2.20	0.41
6:C:33:LEU:O	6:C:36:ASP:HB3	2.21	0.41
19:P:21:VAL:O	19:P:22:THR:HB	2.20	0.41
15:L:41:ARG:CG	15:L:42:THR:N	2.71	0.41
15:L:120:TYR:O	15:L:122:THR:HG23	2.21	0.41
1:A:977:A:C8	1:A:1223:C:N3	2.88	0.41
13:J:71:LEU:HA	13:J:71:LEU:HD22	1.88	0.41
13:J:96:ILE:HG22	13:J:98:ILE:HG13	2.02	0.41
5:B:23:ARG:O	5:B:23:ARG:NH1	2.54	0.41
1:A:1057:G:C4'	6:C:154:SER:HB2	2.50	0.41
1:A:940:C:H2'	1:A:941:G:C8	2.53	0.41
5:B:185:ILE:HA	5:B:199:TYR:O	2.21	0.41
1:A:1237:C:H4'	1:A:1334:G:N2	2.35	0.41
1:A:437:U:O2'	7:D:123:HIS:CD2	2.73	0.41
6:C:139:GLN:O	6:C:143:GLU:HG3	2.20	0.41
1:A:1239:A:C4	1:A:1298:C:N4	2.88	0.41
1:A:561:U:O2'	1:A:562:C:P	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:970:C:OP1	13:J:57:LYS:HE2	2.20	0.41
1:A:186:C:H2'	1:A:187:C:H6	1.83	0.41
1:A:914:A:O2'	1:A:915:A:H5'	2.21	0.41
1:A:831:U:O2'	1:A:832:C:H5'	2.20	0.41
1:A:832:C:O2'	1:A:833:U:H5'	2.21	0.41
1:A:41:G:H2'	1:A:42:G:C8	2.56	0.41
12:I:112:LYS:C	12:I:112:LYS:CD	2.89	0.41
1:A:243:A:C2	1:A:246:A:C8	3.09	0.41
13:J:19:SER:HA	13:J:22:LYS:NZ	2.36	0.41
13:J:90:LEU:N	13:J:91:PRO:HD2	2.11	0.41
5:B:16:HIS:O	5:B:17:PHE:CD2	2.74	0.41
8:E:107:ARG:O	8:E:109:ILE:N	2.53	0.41
1:A:1226:C:O2'	1:A:1227:A:H5'	2.21	0.41
11:H:119:LEU:HD12	11:H:124:ALA:N	2.35	0.41
5:B:55:PHE:O	5:B:56:ARG:C	2.57	0.41
1:A:626:U:O2'	1:A:627:G:H5'	2.21	0.41
10:G:78:ARG:O	10:G:84:ASN:HA	2.20	0.41
5:B:105:PHE:O	5:B:106:LYS:C	2.59	0.41
1:A:714:G:H2'	1:A:715:A:C8	2.56	0.41
1:A:1438:G:H2'	1:A:1439:C:H6	1.83	0.41
1:A:1055:A:N6	1:A:1206:G:C5	2.89	0.41
16:M:22:ILE:HG22	16:M:23:TYR:N	2.36	0.41
13:J:6:ILE:O	13:J:71:LEU:HD22	2.20	0.41
1:A:1057:G:C5	1:A:1204:A:C2	3.09	0.41
1:A:1349:A:OP1	12:I:120:ARG:HB2	2.20	0.41
6:C:191:THR:HG22	6:C:193:TYR:N	2.28	0.41
1:A:1250:A:H5'	12:I:68:GLY:O	2.20	0.41
1:A:1015:A:H1'	1:A:1218:C:O2'	2.21	0.41
6:C:81:GLY:HA2	6:C:84:ILE:HG22	2.02	0.41
9:F:82:ARG:HA	9:F:82:ARG:NE	2.33	0.41
1:A:1165:C:C2'	1:A:1166:G:H5'	2.51	0.41
6:C:173:VAL:N	6:C:174:PRO:CD	2.83	0.41
1:A:1459:C:O2'	1:A:1460:A:H5'	2.20	0.41
1:A:925:G:C6	1:A:927:G:N7	2.89	0.41
1:A:718:G:H5"	1:A:719:C:OP2	2.21	0.41
14:K:28:THR:C	14:K:29:ILE:HG22	2.41	0.41
5:B:235:SER:C	5:B:237:ALA:H	2.23	0.41
1:A:936:C:H2'	1:A:937:A:O4'	2.21	0.41
15:L:82:VAL:O	15:L:106:ASP:HB2	2.21	0.41
1:A:1061:G:O2'	1:A:1062:U:H5'	2.21	0.41
11:H:104:ARG:HG3	11:H:138:TRP:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:41:ARG:HB3	15:L:41:ARG:NH1	2.36	0.41
16:M:25:ILE:HG23	16:M:29:ARG:HB2	2.02	0.41
1:A:1372:U:H2'	1:A:1373:G:H5'	2.03	0.41
1:A:1373:G:H5"	10:G:36:LYS:HD3	2.03	0.41
11:H:33:GLU:HA	11:H:36:LEU:HD12	2.03	0.41
1:A:1313:U:O2'	1:A:1314:C:H5'	2.21	0.41
1:A:1318:A:H4'	22:S:10:PHE:CD1	2.56	0.41
21:R:43:PHE:CD1	21:R:66:LEU:HD11	2.56	0.41
1:A:735:C:O2'	1:A:736:C:H5'	2.21	0.41
15:L:87:GLY:H	15:L:98:TYR:HB3	1.86	0.41
1:A:1104:G:P	5:B:111:ARG:HD2	2.60	0.41
5:B:124:SER:CB	5:B:125:PRO:HD2	2.44	0.41
5:B:135:GLN:O	5:B:135:GLN:HG2	2.21	0.41
5:B:90:MET:HA	5:B:91:PRO:HD3	1.78	0.41
1:A:1028:C:N4	1:A:1033:G:N2	2.69	0.41
16:M:45:VAL:HG13	16:M:48:LEU:HD12	2.02	0.41
12:I:48:GLU:HA	12:I:51:ARG:NH1	2.34	0.41
18:O:6:GLU:O	18:O:7:GLU:C	2.59	0.41
1:A:687:A:O2'	1:A:688:G:OP2	2.33	0.41
10:G:146:GLU:CD	10:G:149:ARG:HD3	2.41	0.41
11:H:75:ARG:HA	11:H:76:PRO:HD3	1.68	0.41
1:A:80:G:C3'	1:A:81:U:H5"	2.50	0.41
8:E:39:GLY:O	8:E:68:GLU:HA	2.21	0.41
1:A:169:C:O2'	1:A:170:U:H5'	2.21	0.41
12:I:96:LEU:CD1	12:I:96:LEU:N	2.84	0.41
10:G:16:LEU:HD22	10:G:16:LEU:N	2.35	0.41
1:A:293:G:C6	1:A:294:U:C4	3.09	0.41
1:A:184:G:H2'	1:A:185:A:H8	1.86	0.41
17:N:26:ARG:CD	17:N:47:LEU:HD11	2.51	0.41
7:D:14:ARG:HD3	7:D:14:ARG:O	2.21	0.41
1:A:247:G:OP2	20:Q:100:LYS:HG3	2.20	0.41
1:A:1439:C:H2'	1:A:1440:C:C6	2.56	0.41
8:E:102:ALA:CB	8:E:120:THR:OG1	2.69	0.41
22:S:42:PRO:O	22:S:44:MET:N	2.54	0.41
16:M:59:TYR:O	16:M:63:THR:CG2	2.69	0.41
16:M:67:GLU:HB3	16:M:68:GLY:H	1.55	0.41
13:J:24:VAL:HG12	13:J:28:ARG:HE	1.86	0.41
5:B:162:ILE:O	5:B:162:ILE:HG22	2.21	0.41
12:I:118:LYS:C	12:I:120:ARG:H	2.25	0.41
22:S:19:VAL:HG13	22:S:20:LEU:N	2.36	0.41
19:P:28:ARG:NH1	19:P:29:ASP:OD2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:N:27:CYS:SG	17:N:29:ARG:CB	3.08	0.41
1:A:216:G:HO2'	1:A:217:C:C5'	2.34	0.41
11:H:34:GLU:HA	11:H:34:GLU:OE1	2.21	0.41
8:E:73:ASN:C	8:E:75:THR:H	2.23	0.41
1:A:393:A:OP2	19:P:12:LYS:CE	2.67	0.41
1:A:1031:G:H2'	1:A:1032:G:C8	2.48	0.41
16:M:37:THR:O	16:M:38:GLY:C	2.60	0.41
12:I:44:VAL:CG1	12:I:51:ARG:NH2	2.83	0.41
14:K:20:TYR:O	14:K:30:VAL:HA	2.21	0.41
14:K:24:SER:C	14:K:26:ASN:N	2.72	0.41
10:G:32:ARG:O	10:G:33:ASP:HB2	2.21	0.41
1:A:296:U:H1'	1:A:556:C:H1'	2.03	0.41
9:F:28:ARG:HG2	9:F:32:ASN:OD1	2.21	0.41
14:K:86:GLY:H	14:K:112:THR:CG2	2.34	0.41
11:H:68:ARG:HG2	11:H:68:ARG:HH11	1.85	0.41
1:A:1061:G:C4	1:A:1197:G:N2	2.90	0.40
12:I:17:VAL:HG21	12:I:80:GLY:CA	2.39	0.40
5:B:187:LEU:HA	5:B:201:ILE:O	2.20	0.40
7:D:67:ILE:O	7:D:69:GLY:N	2.54	0.40
7:D:174:LEU:HA	7:D:174:LEU:HD23	1.79	0.40
1:A:1373:G:H5"	10:G:36:LYS:HB3	2.02	0.40
1:A:517:G:H5'	1:A:519:C:C2	2.56	0.40
1:A:1318:A:H4'	22:S:10:PHE:CE1	2.56	0.40
5:B:140:HIS:O	5:B:141:GLU:C	2.57	0.40
1:A:488:C:H2'	1:A:489:C:H6	1.86	0.40
15:L:7:ILE:HA	15:L:7:ILE:HD13	1.92	0.40
11:H:39:LEU:N	11:H:39:LEU:HD22	2.36	0.40
10:G:42:ILE:HG23	10:G:117:ALA:HA	2.02	0.40
1:A:328:C:HO2'	1:A:329:A:P	2.44	0.40
6:C:34:LEU:C	6:C:34:LEU:HD23	2.41	0.40
1:A:320:C:H2'	1:A:321:A:C8	2.56	0.40
1:A:824:C:H2'	1:A:825:G:H8	1.86	0.40
13:J:42:THR:HG22	13:J:43:ARG:N	2.36	0.40
13:J:60:ARG:CD	13:J:60:ARG:N	2.79	0.40
17:N:53:LEU:HA	17:N:54:PRO:HD2	1.96	0.40
23:T:72:LEU:O	23:T:73:HIS:O	2.39	0.40
1:A:1327:C:OP1	24:V:20:LYS:HB3	2.21	0.40
5:B:189:ASP:O	5:B:191:ASP:N	2.55	0.40
8:E:51:VAL:CB	8:E:52:PRO:HD3	2.35	0.40
5:B:69:LEU:C	5:B:69:LEU:CD2	2.90	0.40
1:A:1343:G:H2'	1:A:1344:C:H6	1.81	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:63:ASN:H	6:C:97:LYS:HE2	1.86	0.40
11:H:80:ILE:HG23	11:H:82:HIS:O	2.22	0.40
22:S:16:LEU:HA	22:S:19:VAL:HG12	2.03	0.40
1:A:736:C:H2'	1:A:737:A:C8	2.57	0.40
1:A:448:A:C4	1:A:487:A:C2	3.09	0.40
1:A:488:C:H6	1:A:488:C:O5'	2.03	0.40
1:A:1403:C:O2'	1:A:1404:C:H5'	2.21	0.40
1:A:148:G:O2'	1:A:149:A:H5'	2.21	0.40
1:A:861:G:O2'	1:A:862:C:H5'	2.21	0.40
9:F:23:LYS:O	9:F:24:GLU:C	2.58	0.40
1:A:300:A:H8	1:A:300:A:O5'	2.04	0.40
1:A:434:U:H2'	1:A:435:C:H6	1.85	0.40
10:G:145:ALA:O	10:G:146:GLU:C	2.59	0.40
1:A:706:A:C5	1:A:707:C:C5	3.09	0.40
1:A:445:G:O2'	1:A:446:G:H5'	2.21	0.40
14:K:28:THR:HG22	14:K:29:ILE:N	2.35	0.40
5:B:81:VAL:O	5:B:82:ARG:C	2.58	0.40
8:E:103:GLY:C	8:E:106:PRO:HD2	2.40	0.40
15:L:42:THR:CG2	15:L:52:LEU:HB3	2.51	0.40
5:B:76:GLN:NE2	5:B:207:ALA:N	2.69	0.40
8:E:71:LEU:HD13	8:E:114:GLY:O	2.21	0.40
13:J:27:ALA:HA	13:J:30:SER:OG	2.22	0.40
12:I:126:SER:O	12:I:127:LYS:C	2.60	0.40
10:G:103:TRP:O	10:G:106:GLN:HB3	2.21	0.40
1:A:376:G:O2'	1:A:377:G:H5'	2.21	0.40
11:H:63:LEU:H	11:H:63:LEU:CD2	2.28	0.40
21:R:45:SER:C	21:R:47:THR:H	2.25	0.40
21:R:74:ARG:HG2	21:R:80:PRO:O	2.21	0.40
5:B:124:SER:HB2	5:B:125:PRO:CD	2.45	0.40
1:A:1016:A:H2'	1:A:1017:G:C5'	2.51	0.40
1:A:422:C:H4'	1:A:423:G:C4	2.57	0.40
1:A:22:G:C5	1:A:23:C:C4	3.09	0.40
6:C:160:ALA:C	6:C:162:GLN:N	2.73	0.40
17:N:44:LEU:O	17:N:48:ALA:HB2	2.21	0.40
1:A:294:U:H2'	1:A:295:C:C6	2.56	0.40
11:H:68:ARG:NH1	11:H:68:ARG:HG2	2.36	0.40
1:A:1504:G:OP1	1:A:1507:A:H4'	2.22	0.40
1:A:662:G:H2'	1:A:663:A:C8	2.56	0.40
18:O:49:ASP:OD2	18:O:52:SER:HB2	2.21	0.40
1:A:1068:G:N7	1:A:1094:G:C2'	2.83	0.40
13:J:19:SER:HA	13:J:22:LYS:HZ3	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:30:SER:HG	13:J:81:THR:HA	1.83	0.40
1:A:1346:A:N1	1:A:1374:A:H5"	2.36	0.40
1:A:750:G:N2	18:O:23:GLY:HA3	2.36	0.40
5:B:126:GLU:HA	5:B:129:GLU:HB2	2.04	0.40
5:B:140:HIS:O	5:B:143:GLU:CB	2.69	0.40
1:A:1016:A:O5'	1:A:1016:A:H8	2.04	0.40
8:E:146:ALA:O	8:E:149:GLU:HG2	2.22	0.40
6:C:76:VAL:O	6:C:83:ARG:HD3	2.22	0.40
11:H:60:ARG:NH1	11:H:60:ARG:CG	2.84	0.40
13:J:82:ILE:O	13:J:82:ILE:CG2	2.69	0.40
1:A:411:A:C8	1:A:413:G:H1'	2.57	0.40
1:A:482:A:H2'	1:A:483:C:O4'	2.22	0.40
1:A:1300:G:H1'	1:A:1301:U:H5	1.86	0.40
1:A:1362:C:H5'	1:A:1363:A:O5'	2.21	0.40
1:A:958:A:C2	1:A:959:A:C2	3.10	0.40
5:B:187:LEU:HD22	5:B:201:ILE:O	2.21	0.40
18:O:81:LEU:HD23	18:O:81:LEU:HA	1.88	0.40
14:K:70:LYS:O	14:K:73:MET:HB2	2.22	0.40
21:R:66:LEU:O	21:R:69:THR:N	2.54	0.40
15:L:88:GLY:N	15:L:98:TYR:HA	2.35	0.40
17:N:29:ARG:HD2	17:N:29:ARG:HA	1.97	0.40
1:A:1402:C:O2'	1:A:1403:C:H5'	2.21	0.40
23:T:89:ARG:O	23:T:92:LEU:N	2.55	0.40
15:L:61:THR:C	15:L:63:GLY:N	2.74	0.40
8:E:62:ALA:C	8:E:64:ARG:N	2.74	0.40
1:A:686:U:O2'	1:A:687:A:H8	2.03	0.40
17:N:22:THR:CB	17:N:33:VAL:HG21	2.52	0.40
1:A:1102:A:H2'	1:A:1103:C:H6	1.85	0.40
14:K:100:ALA:O	14:K:101:SER:C	2.60	0.40
1:A:1385:G:H2'	1:A:1386:G:O4'	2.22	0.40
1:A:543:C:O2'	1:A:544:G:H5'	2.20	0.40
10:G:37:ASN:O	10:G:40:ALA:N	2.55	0.40
20:Q:19:VAL:HG23	20:Q:44:ALA:HB3	2.03	0.40
22:S:82:GLY:O	22:S:84:GLY:N	2.49	0.40
1:A:252:U:H2'	1:A:253:U:C6	2.55	0.40
16:M:79:LYS:HD3	16:M:83:ASP:OD2	2.22	0.40
8:E:150:ARG:O	8:E:150:ARG:HD3	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
5	B	232/256 (91%)	143 (62%)	59 (25%)	30 (13%)	0 2
6	C	204/239 (85%)	125 (61%)	49 (24%)	30 (15%)	0 1
7	D	206/209 (99%)	139 (68%)	49 (24%)	18 (9%)	1 7
8	E	148/162 (91%)	114 (77%)	24 (16%)	10 (7%)	1 12
9	F	99/101 (98%)	81 (82%)	17 (17%)	1 (1%)	19 59
10	G	153/156 (98%)	104 (68%)	37 (24%)	12 (8%)	1 9
11	H	136/138 (99%)	112 (82%)	19 (14%)	5 (4%)	4 28
12	I	125/128 (98%)	85 (68%)	25 (20%)	15 (12%)	0 3
13	J	96/105 (91%)	58 (60%)	23 (24%)	15 (16%)	0 1
14	K	117/129 (91%)	84 (72%)	18 (15%)	15 (13%)	0 2
15	L	122/135 (90%)	84 (69%)	24 (20%)	14 (12%)	0 3
16	M	116/126 (92%)	74 (64%)	28 (24%)	14 (12%)	0 2
17	N	58/61 (95%)	38 (66%)	14 (24%)	6 (10%)	1 4
18	O	86/89 (97%)	58 (67%)	23 (27%)	5 (6%)	2 16
19	P	81/88 (92%)	59 (73%)	20 (25%)	2 (2%)	7 38
20	Q	102/105 (97%)	83 (81%)	12 (12%)	7 (7%)	1 12
21	R	71/88 (81%)	50 (70%)	17 (24%)	4 (6%)	2 17
22	S	85/93 (91%)	55 (65%)	17 (20%)	13 (15%)	0 1
23	T	97/106 (92%)	57 (59%)	30 (31%)	10 (10%)	1 4
24	V	22/26 (85%)	16 (73%)	6 (27%)	0	100 100
All	All	2356/2540 (93%)	1619 (69%)	511 (22%)	226 (10%)	1 5

All (226) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	B	16	HIS

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Mol	Chain	Res	Type
5	B	17	PHE
5	B	20	GLU
5	B	21	ARG
5	B	24	TRP
5	B	39	ILE
5	B	123	ALA
5	B	190	THR
5	B	229	VAL
6	C	15	THR
6	C	16	ARG
6	C	47	LEU
6	C	55	VAL
6	C	79	ARG
6	C	101	LEU
6	C	156	ARG
6	C	179	ARG
6	C	189	ALA
7	D	29	PRO
7	D	36	ARG
8	E	78	HIS
10	G	52	GLU
10	G	155	ARG
11	H	83	ILE
11	H	91	ARG
11	H	134	ILE
12	I	31	GLN
12	I	41	VAL
12	I	121	ARG
12	I	127	LYS
13	J	19	SER
13	J	34	VAL
13	J	54	PHE
13	J	57	LYS
13	J	90	LEU
14	K	50	TYR
14	K	57	THR
14	K	101	SER
14	K	126	ARG
15	L	47	LYS
15	L	73	GLU
15	L	116	SER
15	L	127	GLU

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Mol	Chain	Res	Type
16	M	14	ARG
16	M	63	THR
16	M	67	GLU
16	M	86	CYS
17	N	19	ARG
17	N	22	THR
18	O	49	ASP
18	O	73	GLU
20	Q	68	ARG
20	Q	80	GLY
20	Q	96	GLN
20	Q	97	SER
21	R	87	ARG
22	S	42	PRO
22	S	86	GLU
23	T	73	HIS
23	T	97	ALA
5	B	8	LYS
5	B	54	THR
5	B	83	MET
5	B	165	VAL
5	B	179	LYS
5	B	204	ASN
5	B	207	ALA
5	B	224	GLN
6	C	29	TYR
6	C	51	GLY
6	C	62	ASP
6	C	154	SER
6	C	161	GLU
6	C	171	GLY
6	C	188	LEU
6	C	205	GLY
7	D	10	ARG
7	D	63	LYS
7	D	68	TYR
7	D	124	GLY
7	D	175	SER
7	D	179	GLU
8	E	11	ILE
8	E	146	ALA
10	G	4	ARG

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Mol	Chain	Res	Type
10	G	7	ALA
10	G	112	PRO
10	G	146	GLU
12	I	42	ARG
12	I	43	ALA
12	I	46	ALA
12	I	55	ALA
12	I	60	ASP
12	I	88	TYR
12	I	94	ALA
13	J	32	ALA
14	K	12	ARG
14	K	47	VAL
14	K	75	TYR
14	K	127	LYS
15	L	41	ARG
15	L	92	ASP
15	L	102	ARG
16	M	4	ILE
16	M	27	LYS
16	M	38	GLY
16	M	106	ASN
17	N	36	PHE
20	Q	98	LEU
21	R	41	LYS
22	S	5	LEU
22	S	6	LYS
22	S	17	GLU
22	S	32	LYS
22	S	43	GLU
23	T	11	SER
23	T	87	LYS
23	T	88	VAL
23	T	94	ALA
5	B	15	VAL
5	B	52	GLU
5	B	101	MET
5	B	178	ARG
6	C	4	LYS
6	C	167	TRP
7	D	9	CYS
7	D	30	LYS

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Mol	Chain	Res	Type
7	D	125	HIS
7	D	153	ARG
7	D	159	ARG
8	E	15	ARG
8	E	108	ALA
10	G	14	PRO
10	G	149	ARG
10	G	150	ALA
13	J	20	ALA
13	J	26	ALA
14	K	13	GLN
14	K	27	ASN
14	K	128	ALA
15	L	51	ALA
15	L	87	GLY
15	L	115	LYS
16	M	85	GLY
17	N	37	PHE
18	O	86	GLY
19	P	43	LYS
20	Q	49	GLU
20	Q	103	GLY
22	S	30	LEU
22	S	82	GLY
22	S	87	ALA
5	B	80	ILE
5	B	215	LEU
5	B	225	ALA
6	C	53	ALA
6	C	68	VAL
6	C	133	ALA
6	C	168	ALA
7	D	4	TYR
8	E	16	THR
8	E	74	GLY
8	E	107	ARG
9	F	70	ASP
10	G	41	ARG
10	G	117	ALA
12	I	34	ASN
12	I	44	VAL
12	I	101	PHE

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Mol	Chain	Res	Type
13	J	39	PRO
13	J	40	LEU
13	J	65	LEU
13	J	82	ILE
14	K	15	ALA
15	L	28	LYS
16	M	28	ALA
16	M	75	ALA
17	N	32	SER
18	O	82	ILE
19	P	10	GLY
23	T	103	GLY
5	B	131	PRO
5	B	143	GLU
6	C	61	ALA
6	C	67	THR
7	D	164	ALA
8	E	60	TYR
8	E	73	ASN
11	H	24	THR
12	I	58	ARG
13	J	23	ILE
13	J	61	GLU
13	J	73	ASP
14	K	102	GLY
14	K	117	ASN
15	L	91	LYS
15	L	121	GLY
16	M	7	VAL
17	N	23	ARG
18	O	46	HIS
21	R	45	SER
22	S	46	GLY
23	T	9	ASN
23	T	74	LYS
5	B	208	ILE
10	G	42	ILE
11	H	105	ARG
15	L	30	ALA
16	M	3	ARG
16	M	74	VAL
23	T	89	ARG

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Mol	Chain	Res	Type
6	C	108	ASN
21	R	37	VAL
22	S	45	VAL
6	C	157	ILE
6	C	174	PRO
7	D	5	ILE
7	D	56	VAL
22	S	9	VAL
5	B	42	ILE
5	B	162	ILE
14	K	29	ILE
6	C	66	VAL
7	D	67	ILE
5	B	18	GLY
6	C	39	ILE

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
5	B	202/220 (92%)	177 (88%)	25 (12%)	6 25
6	C	160/188 (85%)	143 (89%)	17 (11%)	8 32
7	D	180/181 (99%)	161 (89%)	19 (11%)	8 32
8	E	115/123 (94%)	100 (87%)	15 (13%)	5 22
9	F	90/90 (100%)	88 (98%)	2 (2%)	60 84
10	G	126/127 (99%)	119 (94%)	7 (6%)	26 65
11	H	119/119 (100%)	103 (87%)	16 (13%)	5 21
12	I	98/99 (99%)	89 (91%)	9 (9%)	11 40
13	J	87/92 (95%)	78 (90%)	9 (10%)	9 34
14	K	90/99 (91%)	77 (86%)	13 (14%)	4 18
15	L	104/111 (94%)	96 (92%)	8 (8%)	16 51
16	M	94/101 (93%)	82 (87%)	12 (13%)	5 23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
17	N	49/50 (98%)	44 (90%)	5 (10%)	9 35
18	O	79/80 (99%)	70 (89%)	9 (11%)	7 29
19	P	72/74 (97%)	68 (94%)	4 (6%)	26 65
20	Q	96/97 (99%)	88 (92%)	8 (8%)	14 47
21	R	64/77 (83%)	60 (94%)	4 (6%)	22 60
22	S	75/80 (94%)	62 (83%)	13 (17%)	2 11
23	T	76/82 (93%)	69 (91%)	7 (9%)	11 40
24	V	19/21 (90%)	18 (95%)	1 (5%)	28 66
All	All	1995/2111 (94%)	1792 (90%)	203 (10%)	9 35

All (203) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	8	LYS
5	B	12	GLU
5	B	15	VAL
5	B	17	PHE
5	B	21	ARG
5	B	23	ARG
5	B	24	TRP
5	B	25	ASN
5	B	76	GLN
5	B	82	ARG
5	B	87	ARG
5	B	98	LEU
5	B	113	HIS
5	B	114	ARG
5	B	139	LYS
5	B	144	ARG
5	B	146	GLN
5	B	162	ILE
5	B	170	GLU
5	B	178	ARG
5	B	185	ILE
5	B	197	VAL
5	B	221	LEU
5	B	231	GLU
5	B	236	TYR
6	C	3	ASN

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Mol	Chain	Res	Type
6	C	23	TYR
6	C	29	TYR
6	C	34	LEU
6	C	52	LEU
6	C	90	GLU
6	C	91	LEU
6	C	107	GLN
6	C	139	GLN
6	C	142	MET
6	C	156	ARG
6	C	165	THR
6	C	167	TRP
6	C	179	ARG
6	C	188	LEU
6	C	196	LEU
6	C	204	LEU
7	D	3	ARG
7	D	8	VAL
7	D	9	CYS
7	D	10	ARG
7	D	12	CYS
7	D	19	LEU
7	D	26	CYS
7	D	29	PRO
7	D	34	GLU
7	D	35	ARG
7	D	78	LEU
7	D	122	ARG
7	D	157	LEU
7	D	175	SER
7	D	176	LEU
7	D	177	ASP
7	D	186	LEU
7	D	192	GLU
7	D	199	ASN
8	E	12	LEU
8	E	15	ARG
8	E	16	THR
8	E	31	LEU
8	E	38	GLN
8	E	41	VAL
8	E	43	LEU

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Mol	Chain	Res	Type
8	E	75	THR
8	E	79	GLU
8	E	80	ILE
8	E	82	VAL
8	E	89	ILE
8	E	118	ILE
8	E	147	ASP
8	E	150	ARG
9	F	10	LEU
9	F	86	ARG
10	G	8	GLU
10	G	12	LEU
10	G	37	ASN
10	G	96	GLN
10	G	124	LEU
10	G	126	ASP
10	G	138	LYS
11	H	24	THR
11	H	25	ASP
11	H	26	VAL
11	H	52	ASP
11	H	63	LEU
11	H	84	ARG
11	H	85	ARG
11	H	88	LYS
11	H	91	ARG
11	H	105	ARG
11	H	112	LEU
11	H	119	LEU
11	H	127	LEU
11	H	133	LEU
11	H	135	CYS
11	H	136	GLU
12	I	3	GLN
12	I	23	ASN
12	I	38	GLN
12	I	56	LEU
12	I	75	ASP
12	I	104	ARG
12	I	111	ARG
12	I	114	TYR
12	I	121	ARG

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Mol	Chain	Res	Type
13	J	29	ARG
13	J	38	ILE
13	J	45	ARG
13	J	49	VAL
13	J	60	ARG
13	J	71	LEU
13	J	73	ASP
13	J	79	ARG
13	J	95	GLU
14	K	24	SER
14	K	29	ILE
14	K	30	VAL
14	K	33	THR
14	K	34	ASP
14	K	48	ILE
14	K	51	LYS
14	K	54	ARG
14	K	57	THR
14	K	84	VAL
14	K	93	GLN
14	K	125	PHE
14	K	126	ARG
15	L	48	PRO
15	L	49	ASN
15	L	53	ARG
15	L	55	VAL
15	L	91	LYS
15	L	93	LEU
15	L	98	TYR
15	L	113	ARG
16	M	9	ILE
16	M	16	ASP
16	M	40	ASN
16	M	44	ARG
16	M	46	LYS
16	M	56	LEU
16	M	70	LEU
16	M	81	LEU
16	M	102	ARG
16	M	103	THR
16	M	110	ARG
16	M	117	VAL

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Mol	Chain	Res	Type
17	N	3	ARG
17	N	22	THR
17	N	33	VAL
17	N	41	ARG
17	N	44	LEU
18	O	4	THR
18	O	7	GLU
18	O	10	LYS
18	O	46	HIS
18	O	65	ARG
18	O	70	LEU
18	O	71	GLN
18	O	81	LEU
18	O	83	GLU
19	P	8	ARG
19	P	28	ARG
19	P	29	ASP
19	P	62	VAL
20	Q	19	VAL
20	Q	38	ARG
20	Q	53	LEU
20	Q	59	ILE
20	Q	60	ILE
20	Q	74	LEU
20	Q	78	GLU
20	Q	98	LEU
21	R	26	LEU
21	R	36	ASN
21	R	58	LEU
21	R	66	LEU
22	S	7	LYS
22	S	13	ASP
22	S	20	LEU
22	S	25	LYS
22	S	30	LEU
22	S	32	LYS
22	S	36	ARG
22	S	42	PRO
22	S	61	TYR
22	S	62	ILE
22	S	80	TYR
22	S	85	LYS

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Mol	Chain	Res	Type
22	S	86	GLU
23	T	10	LEU
23	T	13	LEU
23	T	29	LYS
23	T	42	GLN
23	T	62	LEU
23	T	74	LYS
23	T	84	LEU
24	V	7	ARG

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

Mol	Chain	Res	Type
5	B	25	ASN
5	B	40	HIS
5	B	76	GLN
5	B	146	GLN
5	B	240	GLN
6	C	3	ASN
6	C	6	HIS
6	C	98	ASN
6	C	107	GLN
6	C	108	ASN
6	C	110	ASN
6	C	123	GLN
6	C	139	GLN
7	D	62	GLN
7	D	74	GLN
7	D	123	HIS
7	D	129	ASN
7	D	199	ASN
8	E	20	GLN
8	E	73	ASN
9	F	7	ASN
9	F	13	ASN
9	F	18	GLN
9	F	57	GLN
9	F	64	GLN
9	F	94	GLN
9	F	100	ASN
10	G	28	ASN
10	G	51	GLN

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Mol	Chain	Res	Type
10	G	96	GLN
10	G	106	GLN
11	H	82	HIS
12	I	23	ASN
12	I	29	ASN
12	I	73	GLN
12	I	89	ASN
13	J	76	ASN
13	J	84	GLN
14	K	22	HIS
14	K	38	ASN
14	K	78	GLN
14	K	117	ASN
15	L	49	ASN
15	L	75	HIS
16	M	40	ASN
16	M	62	ASN
18	O	13	GLN
18	O	37	ASN
19	P	76	GLN
20	Q	16	GLN
21	R	36	ASN
22	S	14	HIS
22	S	23	ASN
22	S	53	ASN
22	S	56	GLN
22	S	69	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1522 (98%)	201 (13%)	70 (4%)
2	X	5/6 (83%)	0	0
3	Y	10/15 (66%)	2 (20%)	1 (10%)
4	Z	3/4 (75%)	1 (33%)	0
All	All	1524/1547 (98%)	204 (13%)	71 (4%)

All (204) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A

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Mol	Chain	Res	Type
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	52	G
1	A	60	A
1	A	61	G
1	A	81	U
1	A	82	U
1	A	116	A
1	A	120	A
1	A	121	C
1	A	130	A
1	A	131	C
1	A	163	C
1	A	182	U
1	A	190(D)	U
1	A	190(E)	U
1	A	190(F)	G
1	A	195	A
1	A	197	A
1	A	198	G
1	A	201	C
1	A	203	U
1	A	204	U
1	A	216	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	282	A
1	A	289	G
1	A	301	G
1	A	321	A
1	A	328	C

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Mol	Chain	Res	Type
1	A	329	A
1	A	330	C
1	A	332	G
1	A	344	A
1	A	345	C
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	397	A
1	A	398	C
1	A	412	A
1	A	413	G
1	A	421	U
1	A	423	G
1	A	429	U
1	A	430	A
1	A	439	A
1	A	452	A
1	A	461	C
1	A	484	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	519	C
1	A	527	G
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G

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Mol	Chain	Res	Type
1	A	577	G
1	A	653	A
1	A	665	A
1	A	688	G
1	A	701	C
1	A	703	G
1	A	718	G
1	A	721	G
1	A	723	U
1	A	731	G
1	A	749	C
1	A	755	G
1	A	777	A
1	A	793	U
1	A	794	A
1	A	812	C
1	A	813	U
1	A	817	C
1	A	818	G
1	A	819	A
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	874	G
1	A	876	G
1	A	902	G
1	A	913	A
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A

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Mol	Chain	Res	Type
1	A	991	U
1	A	993	G
1	A	994	A
1	A	1005	A
1	A	1030(B)	C
1	A	1045	C
1	A	1050	G
1	A	1054	C
1	A	1055	A
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1145	C
1	A	1152	A
1	A	1157	A
1	A	1159	U
1	A	1183	A
1	A	1184	G
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1202	G
1	A	1212	U
1	A	1215	G
1	A	1224	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1238	A

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Mol	Chain	Res	Type
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1320	C
1	A	1332	A
1	A	1347	G
1	A	1348	U
1	A	1363	A
1	A	1381	U
1	A	1397	C
1	A	1443	G
1	A	1446	A
1	A	1452	C
1	A	1492	A
1	A	1499	A
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1506	U
1	A	1517	G
1	A	1519	A
1	A	1520	G
1	A	1529	G
1	A	1530	G
3	Y	34	G
3	Y	35	A
4	Z	2	U

All (71) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	30	U
1	A	48	C

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Mol	Chain	Res	Type
1	A	51	A
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	203	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	281	G
1	A	328	C
1	A	329	A
1	A	344	A
1	A	351	G
1	A	353	A
1	A	366	C
1	A	372	C
1	A	428	G
1	A	429	U
1	A	438	G
1	A	484	G
1	A	496	A
1	A	509	A
1	A	518	C
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A
1	A	748	C
1	A	792	A
1	A	812	C
1	A	819	A
1	A	913	A
1	A	960	U
1	A	965	A
1	A	975	A
1	A	976	G

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Mol	Chain	Res	Type
1	A	992	U
1	A	993	G
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1101	A
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1196	U
1	A	1201	A
1	A	1214	C
1	A	1224	G
1	A	1226	C
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1319	A
1	A	1331	G
1	A	1346	A
1	A	1347	G
1	A	1380	U
1	A	1451	A
1	A	1498	U
1	A	1502	A
3	Y	34	G

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	1507/1522 (99%)	0.58	60 (3%) 42 40	16, 53, 140, 201	0
2	X	6/6 (100%)	5.18	4 (66%) 0 0	59, 71, 178, 201	0
3	Y	11/15 (73%)	1.63	3 (27%) 1 1	66, 90, 182, 190	0
4	Z	4/4 (100%)	1.44	1 (25%) 1 1	71, 77, 89, 119	0
5	B	234/256 (91%)	0.30	16 (6%) 20 20	19, 87, 173, 201	0
6	C	206/239 (86%)	0.14	7 (3%) 49 48	22, 80, 160, 201	0
7	D	208/209 (99%)	0.53	17 (8%) 14 14	17, 60, 145, 180	0
8	E	150/162 (92%)	0.62	16 (10%) 8 7	17, 48, 107, 201	0
9	F	101/101 (100%)	0.08	2 (1%) 68 67	35, 88, 148, 185	0
10	G	155/156 (99%)	-0.03	3 (1%) 70 69	27, 70, 150, 201	0
11	H	138/138 (100%)	0.35	3 (2%) 65 65	5, 39, 108, 136	0
12	I	127/128 (99%)	0.47	10 (7%) 15 15	19, 82, 144, 184	0
13	J	98/105 (93%)	0.54	15 (15%) 3 3	30, 107, 188, 201	0
14	K	119/129 (92%)	0.59	9 (7%) 17 17	12, 54, 130, 201	0
15	L	124/135 (91%)	0.75	17 (13%) 4 4	16, 57, 144, 187	0
16	M	118/126 (93%)	0.59	9 (7%) 17 17	32, 70, 144, 170	0
17	N	60/61 (98%)	1.95	28 (46%) 0 0	39, 70, 140, 201	0
18	O	88/89 (98%)	0.43	4 (4%) 37 35	7, 56, 145, 201	0
19	P	83/88 (94%)	0.97	16 (19%) 2 2	10, 41, 101, 150	0
20	Q	104/105 (99%)	0.99	17 (16%) 2 2	10, 43, 157, 201	0
21	R	73/88 (82%)	0.52	3 (4%) 41 39	32, 66, 166, 201	0
22	S	87/93 (93%)	0.99	19 (21%) 1 1	54, 99, 176, 201	0
23	T	99/106 (93%)	0.94	15 (15%) 3 3	15, 50, 123, 156	0
24	V	24/26 (92%)	1.69	9 (37%) 0 1	26, 59, 128, 179	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
All	All	3924/4087 (96%)	0.57	303 (7%)	16	16	5, 60, 152, 201	0

All (303) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
14	K	129	SER	25.6
14	K	128	ALA	18.3
2	X	2	U	14.0
18	O	89	GLY	11.8
22	S	3	ARG	10.9
20	Q	102	GLY	10.4
21	R	17	SER	9.0
17	N	30	ALA	8.1
7	D	209	ARG	7.8
20	Q	103	GLY	7.0
2	X	1	C	6.7
20	Q	104	LYS	6.5
20	Q	105	ALA	6.1
24	V	2	GLY	6.1
17	N	6	LEU	6.0
23	T	9	ASN	5.9
20	Q	101	ARG	5.3
12	I	128	ARG	5.3
13	J	45	ARG	5.3
2	X	3	U	5.1
23	T	8	ARG	5.0
22	S	39	THR	5.0
3	Y	32	U	4.9
7	D	35	ARG	4.9
17	N	61	TRP	4.8
14	K	127	LYS	4.8
1	A	82	U	4.6
17	N	34	TYR	4.6
5	B	148	TYR	4.6
22	S	35	SER	4.5
24	V	6	ARG	4.5
22	S	86	GLU	4.4
17	N	29	ARG	4.4
11	H	1	MET	4.3
17	N	3	ARG	4.2
15	L	19	ARG	4.2
22	S	70	LYS	4.1

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Mol	Chain	Res	Type	RSRZ
18	O	88	ARG	4.1
22	S	38	SER	4.1
17	N	12	ARG	4.1
15	L	31	PRO	4.1
5	B	16	HIS	4.1
1	A	202	U	4.0
16	M	104	ARG	4.0
1	A	81	U	3.9
8	E	119	LEU	3.9
13	J	47	PHE	3.9
16	M	102	ARG	3.9
7	D	23	GLY	3.9
22	S	87	ALA	3.7
11	H	3	THR	3.7
16	M	106	ASN	3.7
12	I	114	TYR	3.7
1	A	978	A	3.6
6	C	161	GLU	3.6
12	I	106	ALA	3.6
12	I	70	LYS	3.6
17	N	60	SER	3.6
1	A	532	A	3.5
14	K	126	ARG	3.5
8	E	81	GLU	3.4
22	S	10	PHE	3.4
12	I	105	ASP	3.4
1	A	390	C	3.4
1	A	1534	A	3.4
1	A	1361(A)	C	3.4
23	T	14	LYS	3.4
22	S	37	ARG	3.4
1	A	378	G	3.3
23	T	70	SER	3.3
12	I	119	ALA	3.3
13	J	65	LEU	3.3
23	T	85	MET	3.3
23	T	10	LEU	3.3
1	A	61	G	3.3
6	C	26	LYS	3.3
23	T	56	MET	3.3
17	N	35	ARG	3.3
17	N	39	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	389	A	3.2
5	B	133	LYS	3.2
20	Q	68	ARG	3.2
3	Y	31	A	3.2
15	L	32	PHE	3.2
11	H	2	LEU	3.2
7	D	125	HIS	3.2
1	A	977	A	3.2
22	S	15	LEU	3.2
24	V	5	ASP	3.2
15	L	18	VAL	3.2
24	V	24	ARG	3.1
7	D	158	ILE	3.1
15	L	13	LYS	3.1
17	N	23	ARG	3.1
20	Q	39	SER	3.1
17	N	18	VAL	3.1
24	V	10	ARG	3.0
7	D	110	PHE	3.0
19	P	29	ASP	3.0
7	D	116	GLN	3.0
12	I	102	LEU	3.0
16	M	27	LYS	3.0
20	Q	23	VAL	3.0
1	A	112	G	3.0
6	C	124	ILE	3.0
7	D	112	VAL	3.0
24	V	3	LYS	3.0
7	D	74	GLN	3.0
19	P	8	ARG	3.0
1	A	982	U	2.9
13	J	59	SER	2.9
1	A	1129	C	2.9
17	N	37	PHE	2.9
1	A	524	G	2.9
17	N	33	VAL	2.9
19	P	41	PRO	2.9
1	A	878	G	2.9
17	N	44	LEU	2.9
5	B	93	VAL	2.9
19	P	83	GLU	2.9
1	A	981	U	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	60	A	2.9
1	A	979	C	2.9
20	Q	41	LYS	2.8
5	B	163	PHE	2.8
17	N	2	ALA	2.8
15	L	99	HIS	2.8
23	T	104	LEU	2.8
21	R	16	PRO	2.8
17	N	38	GLY	2.8
8	E	130	ASN	2.8
17	N	19	ARG	2.8
1	A	1296	C	2.8
19	P	30	GLY	2.8
12	I	111	ARG	2.8
20	Q	91	ARG	2.8
1	A	388	G	2.7
10	G	85	TYR	2.7
19	P	39	TYR	2.7
1	A	1237	C	2.7
5	B	69	LEU	2.7
1	A	733	A	2.7
1	A	1361	G	2.7
5	B	108	ILE	2.7
22	S	12	ASP	2.7
1	A	1224	G	2.7
20	Q	88	TYR	2.7
1	A	818	G	2.7
1	A	279	A	2.7
1	A	170	U	2.7
13	J	44	VAL	2.7
12	I	113	LYS	2.6
1	A	1318	A	2.6
13	J	54	PHE	2.6
3	Y	40	C	2.6
22	S	69	HIS	2.6
16	M	88	ARG	2.6
5	B	162	ILE	2.6
20	Q	22	LEU	2.6
15	L	28	LYS	2.6
17	N	25	VAL	2.6
17	N	8	GLU	2.6
1	A	376	G	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	1360	A	2.6
19	P	28	ARG	2.6
17	N	21	TYR	2.6
13	J	60	ARG	2.6
16	M	11	ARG	2.6
1	A	814	A	2.6
1	A	1236	A	2.6
8	E	125	SER	2.6
16	M	43	THR	2.6
2	X	6	U	2.6
13	J	43	ARG	2.5
7	D	120	LEU	2.5
15	L	127	GLU	2.5
19	P	27	LYS	2.5
9	F	89	MET	2.5
8	E	92	LYS	2.5
7	D	111	ALA	2.5
8	E	19	MET	2.5
6	C	195	VAL	2.5
15	L	33	ARG	2.5
1	A	331	G	2.4
10	G	33	ASP	2.4
15	L	86	ARG	2.4
22	S	4	SER	2.4
8	E	87	SER	2.4
19	P	1	MET	2.4
19	P	12	LYS	2.4
23	T	68	LYS	2.4
17	N	15	LYS	2.4
17	N	32	SER	2.4
15	L	71	PRO	2.4
15	L	72	GLY	2.4
13	J	63	PHE	2.4
1	A	152	A	2.4
15	L	89	ARG	2.4
19	P	7	ALA	2.4
1	A	326	G	2.4
22	S	11	VAL	2.4
12	I	9	ARG	2.4
5	B	149	LEU	2.4
16	M	13	LYS	2.4
20	Q	98	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
4	Z	4	U	2.4
1	A	1190	G	2.4
5	B	134	GLU	2.4
5	B	218	ALA	2.4
8	E	123	LEU	2.4
15	L	96	VAL	2.4
17	N	56	VAL	2.4
22	S	2	PRO	2.4
14	K	42	TRP	2.4
7	D	4	TYR	2.4
21	R	48	GLY	2.3
13	J	46	ARG	2.3
6	C	188	LEU	2.3
1	A	42	G	2.3
1	A	377	G	2.3
1	A	16	A	2.3
8	E	20	GLN	2.3
13	J	64	GLU	2.3
24	V	18	TYR	2.3
23	T	23	ARG	2.3
8	E	77	PRO	2.3
15	L	69	TYR	2.3
1	A	18	C	2.3
6	C	193	TYR	2.3
19	P	6	LEU	2.3
1	A	111	G	2.3
1	A	461	C	2.3
1	A	1398	A	2.3
23	T	17	ARG	2.2
1	A	1319	A	2.2
16	M	19	LEU	2.2
17	N	16	PHE	2.2
5	B	96	ARG	2.2
6	C	190	ARG	2.2
9	F	63	TYR	2.2
19	P	22	THR	2.2
22	S	5	LEU	2.2
1	A	88	A	2.2
7	D	162	LEU	2.2
20	Q	43	LEU	2.2
22	S	41	VAL	2.2
15	L	9	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
7	D	148	VAL	2.2
13	J	6	ILE	2.2
18	O	87	ILE	2.2
5	B	144	ARG	2.2
7	D	73	ARG	2.2
14	K	122	LYS	2.2
1	A	373	A	2.2
7	D	157	LEU	2.2
23	T	36	LEU	2.2
23	T	84	LEU	2.2
1	A	108	G	2.2
1	A	1477	C	2.2
14	K	32	ILE	2.2
1	A	915	A	2.2
20	Q	100	LYS	2.2
10	G	5	ARG	2.1
17	N	31	ARG	2.1
8	E	121	LYS	2.1
15	L	20	LYS	2.1
1	A	281	G	2.1
1	A	1508	G	2.1
17	N	36	PHE	2.1
8	E	76	ILE	2.1
22	S	40	ILE	2.1
17	N	22	THR	2.1
5	B	172	ILE	2.1
8	E	17	ALA	2.1
18	O	58	MET	2.1
14	K	54	ARG	2.1
7	D	33	MET	2.1
1	A	584	G	2.1
13	J	57	LYS	2.1
24	V	9	ARG	2.1
13	J	55	LYS	2.1
22	S	44	MET	2.1
5	B	70	PHE	2.1
19	P	13	HIS	2.0
1	A	1384	C	2.0
19	P	43	LYS	2.0
20	Q	40	LYS	2.0
24	V	14	TRP	2.0
1	A	963	G	2.0

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Mol	Chain	Res	Type	RSRZ
20	Q	37	LYS	2.0
1	A	552	U	2.0
8	E	88	LYS	2.0
14	K	124	LYS	2.0
23	T	30	LYS	2.0
1	A	391	G	2.0
8	E	82	VAL	2.0
13	J	58	ASP	2.0
23	T	41	ILE	2.0
1	A	330	C	2.0
8	E	78	HIS	2.0
5	B	71	VAL	2.0
19	P	23	ASP	2.0
1	A	394	G	2.0

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
25	MG	A	1628	1/1	0.72	0.56	19.64	27,27,27,27	1
25	MG	A	1646	1/1	0.93	0.75	12.45	27,27,27,27	0
25	MG	A	1561	1/1	0.88	0.28	7.52	27,27,27,27	0
25	MG	A	1574	1/1	0.94	0.28	4.17	27,27,27,27	0
25	MG	A	1611	1/1	0.96	0.16	2.56	27,27,27,27	0
25	MG	A	1593	1/1	0.95	0.23	2.38	27,27,27,27	0
26	ZN	D	506	1/1	0.98	0.34	1.15	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
25	MG	A	211	1/1	0.88	0.29	0.99	27,27,27,27	0
25	MG	A	1568	1/1	0.96	0.31	0.62	27,27,27,27	0
25	MG	A	1606	1/1	0.77	0.23	0.52	27,27,27,27	1
25	MG	A	1589	1/1	0.94	0.28	0.48	27,27,27,27	0
25	MG	A	1560	1/1	0.96	0.27	0.38	27,27,27,27	0
25	MG	A	1612	1/1	0.87	0.34	-0.11	27,27,27,27	0
25	MG	A	1551	1/1	0.95	0.28	-0.19	27,27,27,27	0
25	MG	A	1597	1/1	0.94	0.20	-0.52	27,27,27,27	0
25	MG	A	1567	1/1	0.94	0.21	-0.95	27,27,27,27	1
25	MG	A	1632	1/1	0.99	0.32	-0.97	27,27,27,27	0
25	MG	A	1601	1/1	0.97	0.21	-1.01	27,27,27,27	0
26	ZN	N	507	1/1	0.99	0.14	-1.04	27,27,27,27	1
25	MG	A	1599	1/1	0.94	0.19	-1.05	27,27,27,27	0
25	MG	A	1573	1/1	0.93	0.26	-1.09	27,27,27,27	0
25	MG	A	1617	1/1	0.96	0.22	-1.21	27,27,27,27	0
25	MG	A	1627	1/1	0.88	0.16	-1.22	27,27,27,27	0
25	MG	A	1594	1/1	0.90	0.22	-1.26	27,27,27,27	0
25	MG	A	1626	1/1	0.83	0.14	-1.32	27,27,27,27	1
25	MG	A	1645	1/1	0.90	0.18	-1.32	27,27,27,27	0
25	MG	A	1609	1/1	0.96	0.24	-1.53	27,27,27,27	0
25	MG	A	1656	1/1	0.76	0.17	-1.68	27,27,27,27	0
25	MG	A	1558	1/1	0.84	0.20	-1.82	27,27,27,27	0
25	MG	A	1555	1/1	0.98	0.26	-1.94	27,27,27,27	0
25	MG	A	1582	1/1	0.96	0.17	-1.98	27,27,27,27	0
25	MG	A	1587	1/1	0.94	0.19	-1.98	27,27,27,27	0
25	MG	A	1598	1/1	0.97	0.18	-2.22	27,27,27,27	0
25	MG	D	215	1/1	0.85	0.13	-2.53	27,27,27,27	0
25	MG	A	1576	1/1	0.95	0.16	-2.77	27,27,27,27	0
25	MG	A	1643	1/1	0.90	0.16	-2.82	27,27,27,27	1
25	MG	A	210	1/1	0.87	0.14	-3.57	27,27,27,27	1
25	MG	A	1564	1/1	0.93	0.13	-3.85	27,27,27,27	0
25	MG	A	1586	1/1	0.97	0.15	-3.93	27,27,27,27	0
25	MG	A	1629	1/1	0.92	0.13	-4.24	27,27,27,27	0
25	MG	A	1648	1/1	0.99	0.08	-4.44	27,27,27,27	0
25	MG	A	1605	1/1	0.88	0.12	-4.52	27,27,27,27	0
25	MG	A	1545	1/1	0.92	0.09	-4.56	27,27,27,27	0
25	MG	A	1654	1/1	0.85	0.06	-4.87	27,27,27,27	1
25	MG	A	1595	1/1	0.93	0.07	-6.81	27,27,27,27	0
25	MG	A	1563	1/1	0.94	0.20	-	27,27,27,27	0
25	MG	A	1569	1/1	0.91	0.34	-	27,27,27,27	0
25	MG	A	1600	1/1	0.98	0.06	-	27,27,27,27	0
25	MG	A	1603	1/1	0.91	0.24	-	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
25	MG	A	1590	1/1	0.89	0.20	-	27,27,27,27	0
25	MG	A	1584	1/1	0.85	0.24	-	27,27,27,27	0
25	MG	A	1625	1/1	0.87	0.21	-	27,27,27,27	0
25	MG	A	1610	1/1	0.92	0.27	-	27,27,27,27	1
25	MG	A	1591	1/1	0.97	0.33	-	27,27,27,27	0
25	MG	A	1548	1/1	0.89	0.30	-	27,27,27,27	1
25	MG	A	1546	1/1	0.98	0.32	-	27,27,27,27	0
25	MG	A	1634	1/1	0.91	0.15	-	27,27,27,27	0
25	MG	A	86	1/1	0.95	0.28	-	27,27,27,27	0
25	MG	A	1639	1/1	0.88	0.27	-	27,27,27,27	1
25	MG	A	214	1/1	0.83	0.19	-	27,27,27,27	1
25	MG	A	1614	1/1	0.97	0.20	-	27,27,27,27	0
25	MG	A	1613	1/1	0.93	0.34	-	27,27,27,27	0
25	MG	A	1575	1/1	0.92	0.32	-	27,27,27,27	0
25	MG	A	1607	1/1	0.69	0.24	-	27,27,27,27	1
25	MG	A	1604	1/1	0.95	0.10	-	27,27,27,27	0
25	MG	A	1559	1/1	0.94	0.26	-	27,27,27,27	0
25	MG	A	1649	1/1	0.89	0.14	-	27,27,27,27	1
25	MG	A	1572	1/1	0.97	0.11	-	27,27,27,27	0
25	MG	A	1647	1/1	0.88	0.15	-	27,27,27,27	0
25	MG	A	1655	1/1	0.56	0.26	-	27,27,27,27	1
25	MG	A	1550	1/1	0.97	0.34	-	27,27,27,27	0
25	MG	A	1631	1/1	0.94	0.31	-	27,27,27,27	0
25	MG	A	1596	1/1	0.95	0.40	-	27,27,27,27	0
25	MG	A	1642	1/1	0.95	0.24	-	27,27,27,27	1
25	MG	A	1552	1/1	0.96	0.34	-	27,27,27,27	0
25	MG	A	1651	1/1	0.60	0.12	-	27,27,27,27	0
25	MG	A	1641	1/1	0.66	0.28	-	27,27,27,27	1
25	MG	A	1602	1/1	0.94	0.17	-	27,27,27,27	0
25	MG	A	87	1/1	0.82	0.41	-	27,27,27,27	1
25	MG	A	1557	1/1	0.98	0.26	-	27,27,27,27	0
25	MG	A	1636	1/1	0.75	0.15	-	27,27,27,27	1
25	MG	A	1640	1/1	0.47	0.28	-	27,27,27,27	1
25	MG	A	1578	1/1	0.97	0.24	-	27,27,27,27	0
25	MG	A	1592	1/1	0.94	0.38	-	27,27,27,27	0
25	MG	A	1571	1/1	0.95	0.26	-	27,27,27,27	0
25	MG	A	1653	1/1	0.87	0.19	-	27,27,27,27	1
25	MG	A	1619	1/1	0.94	0.27	-	27,27,27,27	0
25	MG	A	1622	1/1	0.78	0.34	-	27,27,27,27	0
25	MG	A	1615	1/1	0.88	0.25	-	27,27,27,27	0
25	MG	A	1547	1/1	0.77	0.15	-	27,27,27,27	0
25	MG	A	1620	1/1	0.77	0.32	-	27,27,27,27	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
25	MG	A	1638	1/1	0.89	0.18	-	27,27,27,27	0
25	MG	A	1633	1/1	0.93	0.32	-	27,27,27,27	0
25	MG	A	1580	1/1	0.95	0.23	-	27,27,27,27	0
25	MG	A	1650	1/1	0.90	0.27	-	27,27,27,27	1
25	MG	A	1618	1/1	0.88	0.15	-	27,27,27,27	1
25	MG	A	1562	1/1	0.86	0.14	-	27,27,27,27	1
25	MG	A	1566	1/1	0.94	0.19	-	27,27,27,27	0
25	MG	A	1553	1/1	0.97	0.39	-	27,27,27,27	0
25	MG	A	1624	1/1	0.70	0.29	-	27,27,27,27	1
25	MG	A	1621	1/1	0.87	0.23	-	27,27,27,27	0
25	MG	A	1608	1/1	0.93	0.09	-	27,27,27,27	0
25	MG	A	1585	1/1	0.90	0.32	-	27,27,27,27	0
25	MG	A	1623	1/1	0.87	0.14	-	27,27,27,27	0
25	MG	A	71	1/1	0.96	0.37	-	27,27,27,27	0
25	MG	A	1556	1/1	0.86	0.43	-	27,27,27,27	0
25	MG	A	1565	1/1	0.95	0.36	-	27,27,27,27	0
25	MG	A	1616	1/1	0.89	0.10	-	27,27,27,27	0
25	MG	A	1652	1/1	0.89	0.10	-	27,27,27,27	0
25	MG	A	1644	1/1	0.89	0.25	-	27,27,27,27	1
25	MG	A	1554	1/1	0.98	0.23	-	27,27,27,27	0
25	MG	A	1549	1/1	0.97	0.33	-	27,27,27,27	0
25	MG	A	1583	1/1	0.97	0.16	-	27,27,27,27	0
25	MG	A	1588	1/1	0.94	0.17	-	27,27,27,27	0
25	MG	A	1637	1/1	0.77	0.12	-	27,27,27,27	1
25	MG	A	1581	1/1	0.95	0.16	-	27,27,27,27	0
25	MG	H	213	1/1	0.95	0.15	-	27,27,27,27	0
25	MG	A	1635	1/1	0.92	0.15	-	27,27,27,27	0
25	MG	A	1577	1/1	0.91	0.14	-	27,27,27,27	0
25	MG	A	1579	1/1	0.54	0.31	-	27,27,27,27	1
25	MG	A	1630	1/1	0.98	0.30	-	27,27,27,27	0
25	MG	A	1570	1/1	0.90	0.31	-	27,27,27,27	0

6.5 Other polymers (i)

There are no such residues in this entry.