



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:40 PM UTC

PDB ID : 1XNQ / pdb_00001xnq
Title : Structure of an Inosine-Adenine Wobble Base Pair Complex in the Context of the Decoding Center
Authors : Murphy, F.V.; Ramakrishnan, V.
Deposited on : 2004-10-05
Resolution : 3.05 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

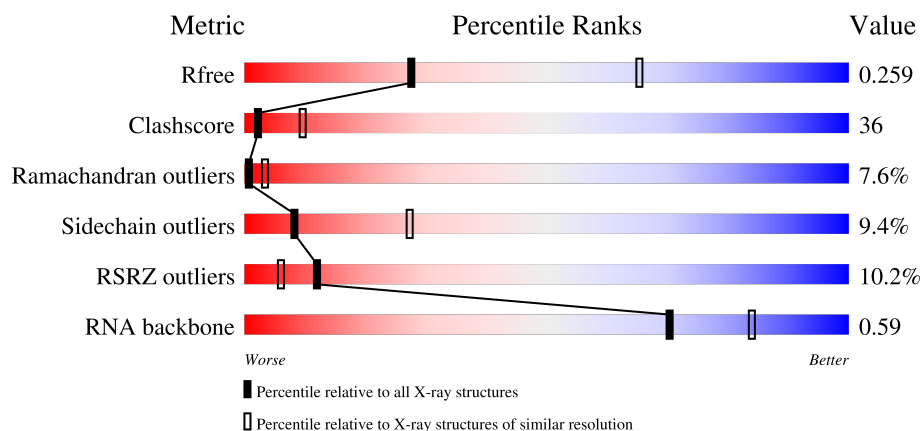
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)
RNA backbone	3983	1079 (3.30-2.82)

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

Mol	Chain	Length	Quality of chain
1	A	1522	11% 32% 53% 11% ••
2	X	11	45% 64% 36%
3	W	4	25% 50% 50%
4	B	256	11% 18% 54% 17% • 9%

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Mol	Chain	Length	Quality of chain
5	C	239	
6	D	209	
7	E	162	
8	F	101	
9	G	156	
10	H	138	
11	I	128	
12	J	105	
13	K	129	
14	L	135	
15	M	126	
16	N	61	
17	O	89	
18	P	88	
19	Q	105	
20	R	88	
21	S	93	
22	T	106	
23	V	27	

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	1546	-	-	-	X
25	MG	A	1547	-	-	-	X
25	MG	A	1551	-	-	-	X
25	MG	A	1552	-	-	-	X
25	MG	A	1557	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1558	-	-	-	X
25	MG	A	1560	-	-	-	X
25	MG	A	1564	-	-	-	X
25	MG	A	1565	-	-	-	X
25	MG	A	1568	-	-	-	X
25	MG	A	1570	-	-	-	X
25	MG	A	1571	-	-	-	X
25	MG	A	1572	-	-	-	X
25	MG	A	1573	-	-	-	X
25	MG	A	1574	-	-	-	X
25	MG	A	1576	-	-	-	X
25	MG	A	1578	-	-	-	X
25	MG	A	1579	-	-	-	X
25	MG	A	1582	-	-	-	X
25	MG	A	1583	-	-	-	X
25	MG	A	1584	-	-	-	X
25	MG	A	1586	-	-	-	X
25	MG	A	1587	-	-	-	X
25	MG	A	1588	-	-	-	X
25	MG	A	1590	-	-	-	X
25	MG	A	1591	-	-	-	X
25	MG	A	1592	-	-	-	X
25	MG	A	1598	-	-	-	X
25	MG	A	1600	-	-	-	X
25	MG	A	1605	-	-	-	X
25	MG	A	1611	-	-	-	X
25	MG	A	1612	-	-	-	X
25	MG	A	1617	-	-	-	X
25	MG	A	1618	-	-	-	X
25	MG	A	1621	-	-	-	X
25	MG	A	1629	-	-	-	X
25	MG	A	441	-	-	-	X
25	MG	A	71	-	-	-	X
25	MG	X	502	-	-	-	X

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 52076 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1507	Total	C	N	O	P	0	0	0
			32380	14414	5990	10470	1506			

- Molecule 2 is a RNA chain called Anticodon tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	X	11	Total	C	N	O	P	0	0	0
			232	105	43	74	10			

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	W	4	Total	C	N	O	P	0	0	0
			84	39	18	24	3			

- Molecule 4 is a protein called Ribosomal protein S2.

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

- Molecule 5 is a protein called Ribosomal protein S3.

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

- Molecule 6 is a protein called Ribosomal protein S4.

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

- Molecule 7 is a protein called Ribosomal protein S5.

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

- Molecule 8 is a protein called Ribosomal protein S6.

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

- Molecule 9 is a protein called Ribosomal protein S7.

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

- Molecule 10 is a protein called Ribosomal protein S8.

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

- Molecule 11 is a protein called Ribosomal protein S9.

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

- Molecule 12 is a protein called Ribosomal protein S10.

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

- Molecule 13 is a protein called Ribosomal protein S11.

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

- Molecule 14 is a protein called Ribosomal protein S12.

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

- Molecule 15 is a protein called Ribosomal protein S13.

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

- Molecule 16 is a protein called Ribosomal protein S14.

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

- Molecule 17 is a protein called Ribosomal protein S15.

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

- Molecule 18 is a protein called Ribosomal protein S16.

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

- Molecule 19 is a protein called Ribosomal protein S17.

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

- Molecule 20 is a protein called Ribosomal protein S18.

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

- Molecule 21 is a protein called Ribosomal protein S19.

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

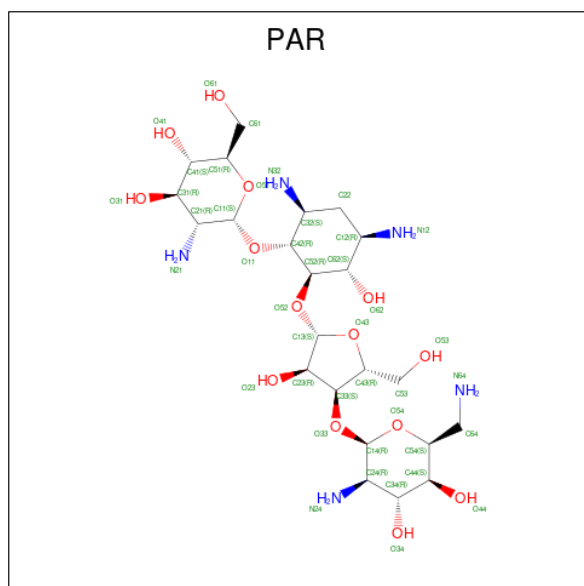
- Molecule 22 is a protein called Ribosomal protein S20.

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

- Molecule 23 is a protein called Ribosomal protein THX.

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

- Molecule 24 is PAROMOMYCIN (CCD ID: PAR) (formula: $C_{23}H_{45}N_5O_{14}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
24	A	1	Total	C	N	O	0	0
			42	23	5	14		

- Molecule 25 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	A	104	Total	Mg	0	0
			104	104		

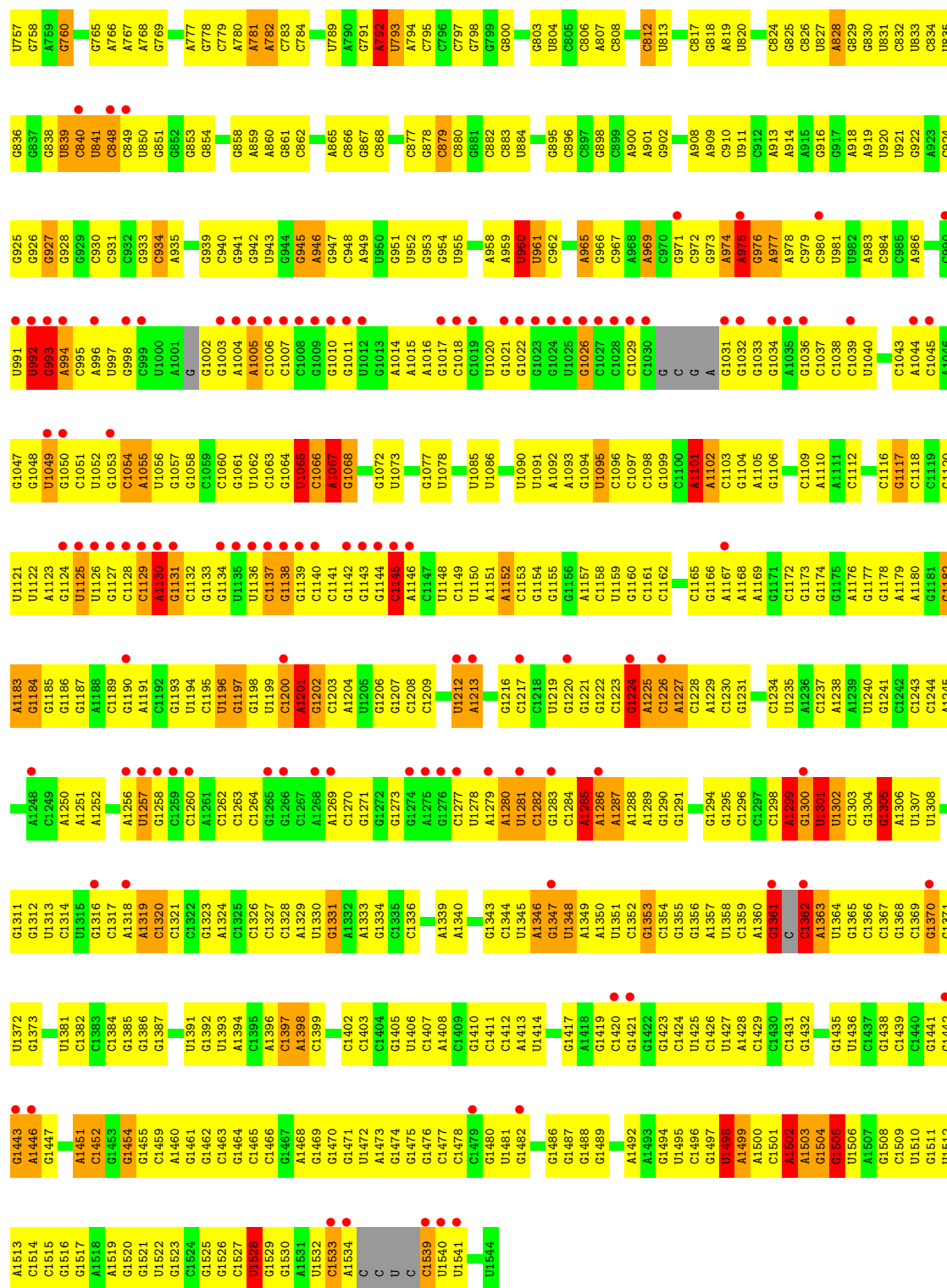
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	X	2	Total 2	Mg 2	0	0
25	J	1	Total 1	Mg 1	0	0

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

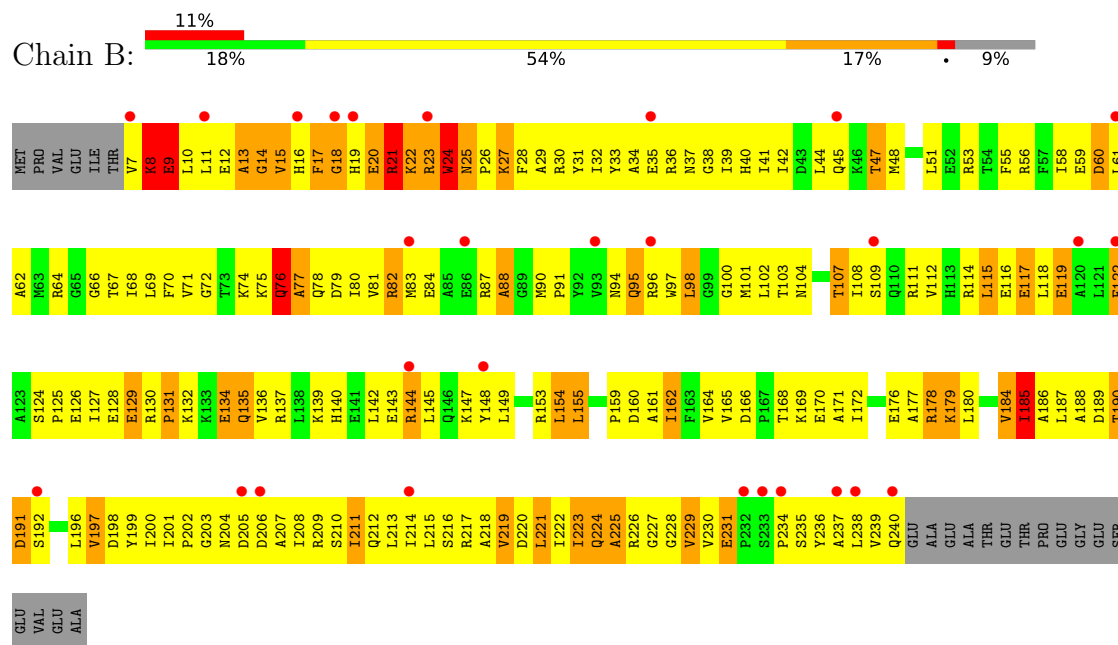
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	D	1	Total 1	Zn 1	0	0
26	N	1	Total 1	Zn 1	0	0



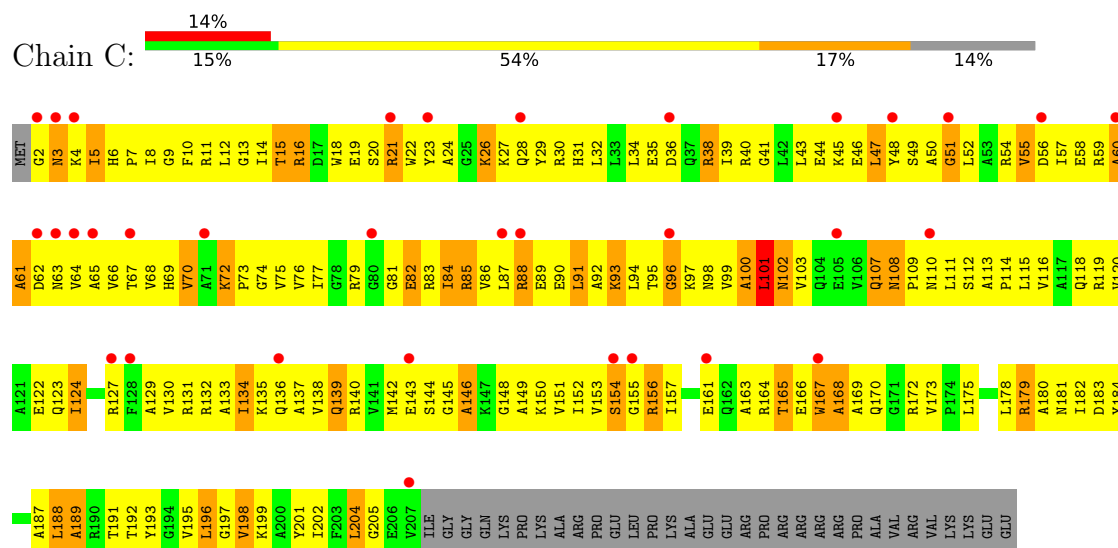
- Molecule 3: mRNA



- Molecule 4: Ribosomal protein S2

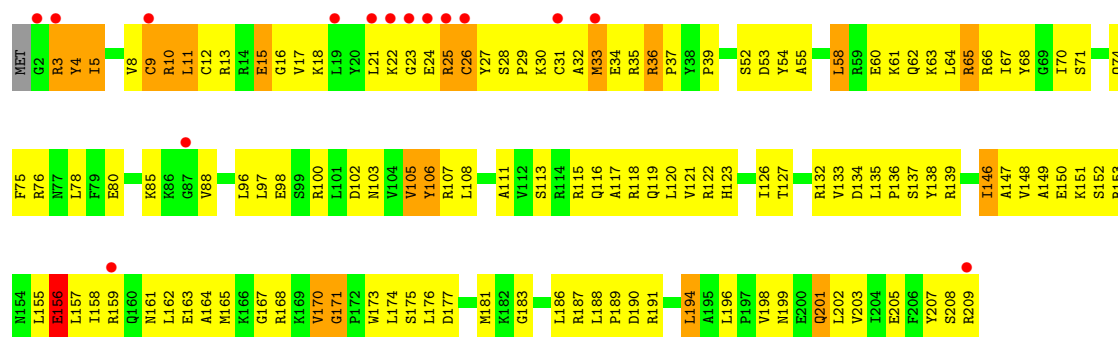


- Molecule 5: Ribosomal protein S3

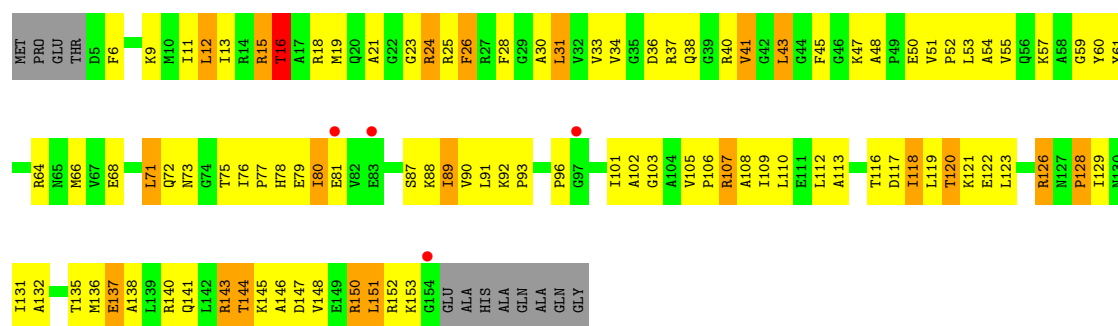


- Molecule 6: Ribosomal protein S4

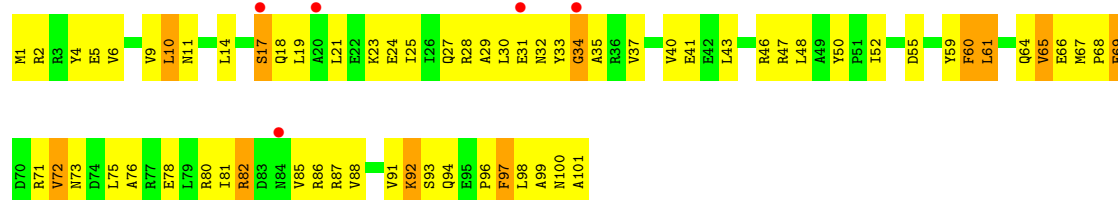




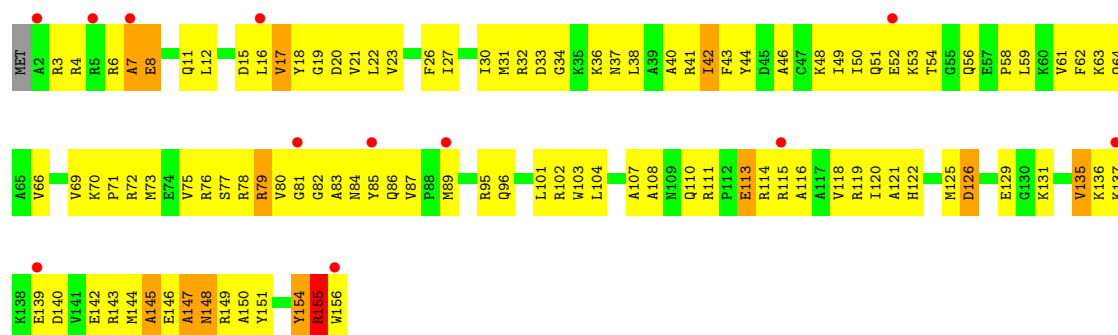
• Molecule 7: Ribosomal protein S5



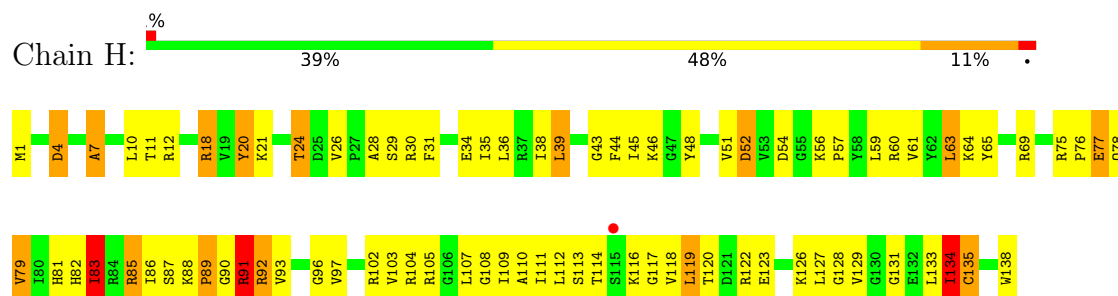
• Molecule 8: Ribosomal protein S6



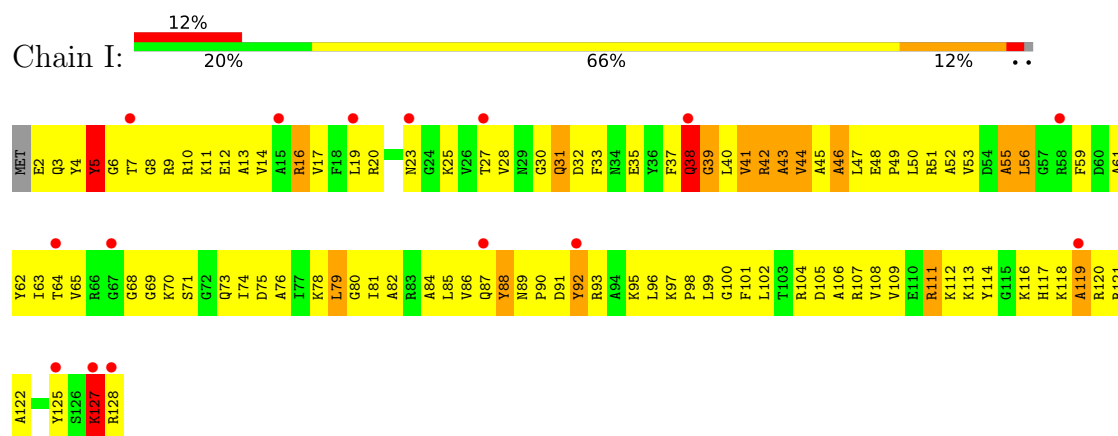
• Molecule 9: Ribosomal protein S7



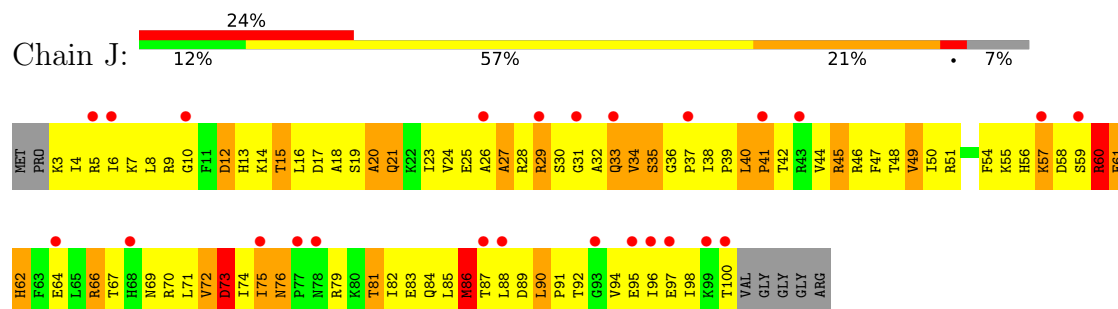
- Molecule 10: Ribosomal protein S8



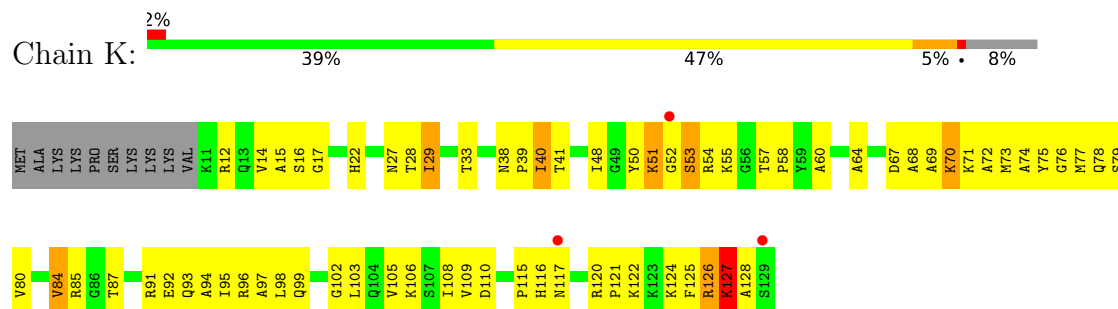
- Molecule 11: Ribosomal protein S9



- Molecule 12: Ribosomal protein S10

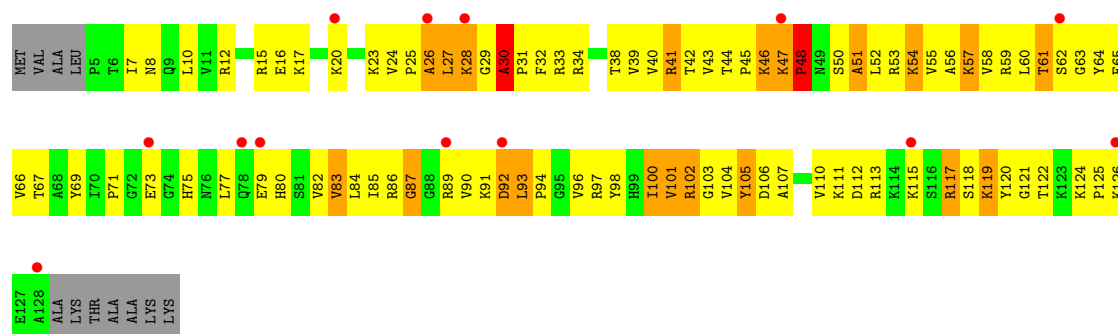


- Molecule 13: Ribosomal protein S11

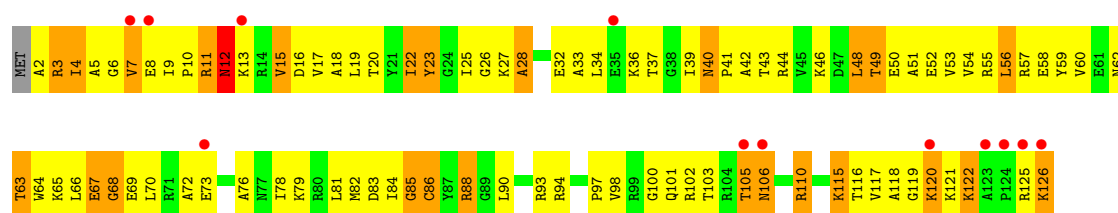


- Molecule 14: Ribosomal protein S12

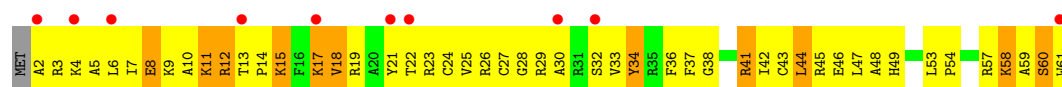




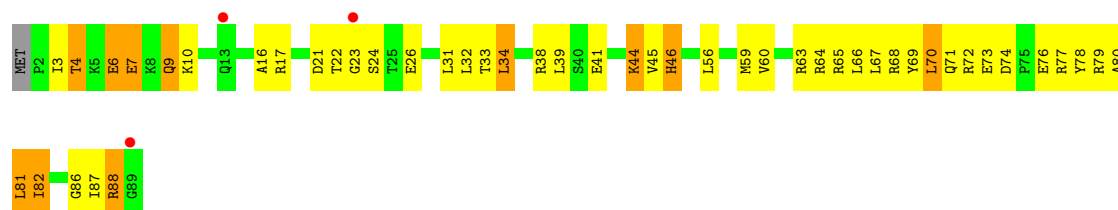
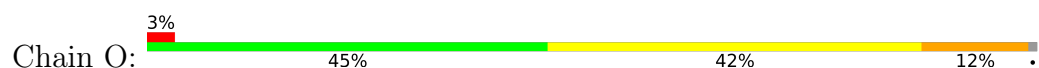
• Molecule 15: Ribosomal protein S13



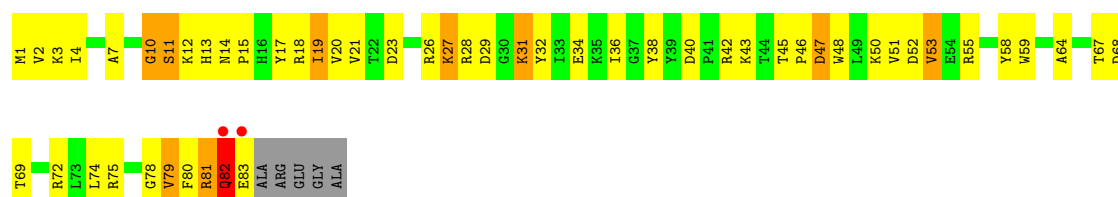
• Molecule 16: Ribosomal protein S14



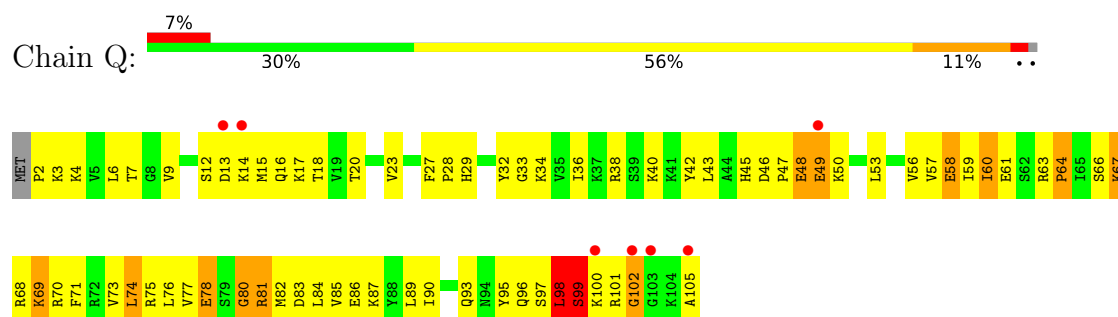
• Molecule 17: Ribosomal protein S15



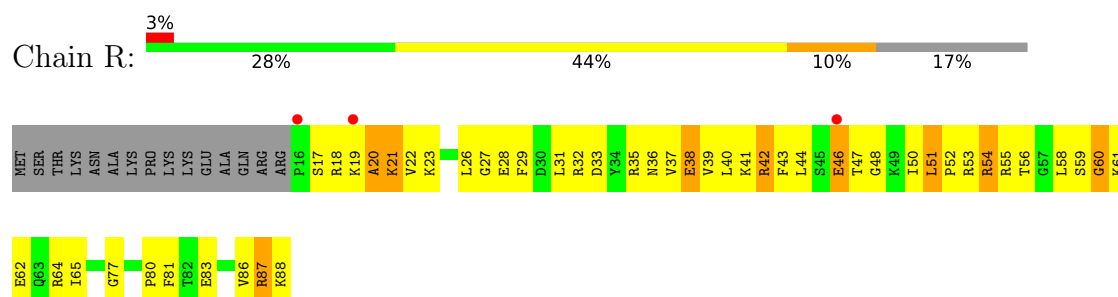
• Molecule 18: Ribosomal protein S16



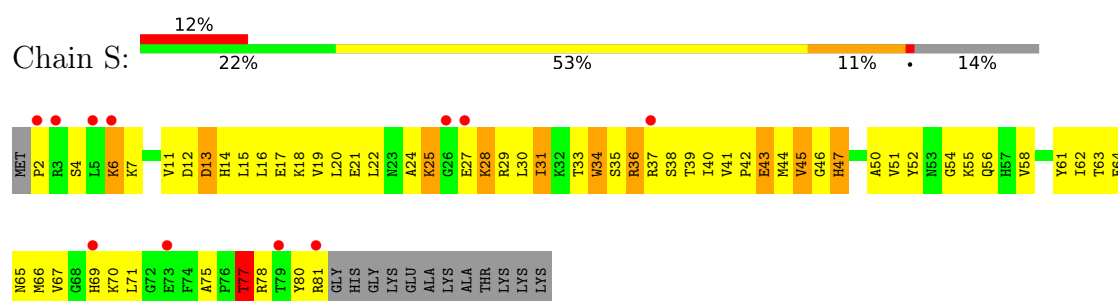
- Molecule 19: Ribosomal protein S17



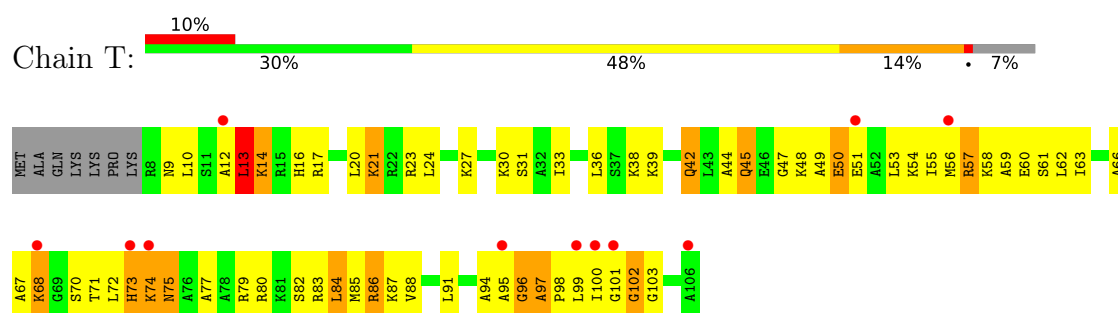
- Molecule 20: Ribosomal protein S18



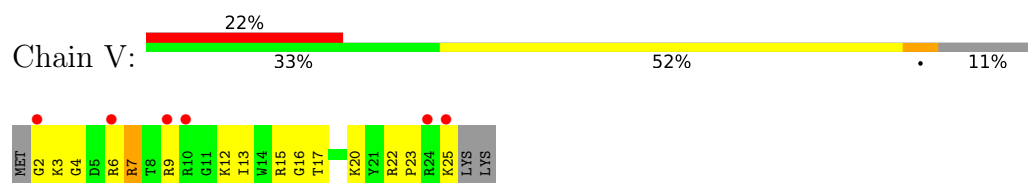
- Molecule 21: Ribosomal protein S19



- Molecule 22: Ribosomal protein S20



- Molecule 23: Ribosomal protein THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	401.13Å 401.13Å 175.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	99.00 – 3.05 99.00 – 3.05	Depositor EDS
% Data completeness (in resolution range)	89.6 (99.00-3.05) 90.4 (99.00-3.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.85 (at 2.96Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.228 , 0.270 0.219 , 0.259	Depositor DCC
R_{free} test set	13849 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	73.5	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 250.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	52076	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.45	3/36244 (0.0%)	0.72	67/56567 (0.1%)
2	X	0.60	0/258	0.83	0/398
3	W	0.40	0/94	0.81	1/145 (0.7%)
4	B	0.40	0/1935	1.01	12/2609 (0.5%)
5	C	0.44	0/1636	0.93	5/2205 (0.2%)
6	D	0.45	0/1733	0.97	5/2318 (0.2%)
7	E	0.55	0/1162	1.08	6/1564 (0.4%)
8	F	0.39	0/856	0.92	1/1154 (0.1%)
9	G	0.44	0/1276	0.97	5/1709 (0.3%)
10	H	0.57	0/1136	1.16	15/1527 (1.0%)
11	I	0.41	0/1029	0.97	4/1378 (0.3%)
12	J	0.43	0/805	1.05	8/1082 (0.7%)
13	K	0.52	0/900	0.94	4/1213 (0.3%)
14	L	0.52	0/986	1.24	16/1320 (1.2%)
15	M	0.43	0/1008	0.98	5/1347 (0.4%)
16	N	0.44	0/501	1.01	3/664 (0.5%)
17	O	0.46	0/745	0.84	1/992 (0.1%)
18	P	0.55	0/716	1.14	5/963 (0.5%)
19	Q	0.55	0/870	1.10	5/1159 (0.4%)
20	R	0.41	0/603	1.00	4/799 (0.5%)
21	S	0.38	0/661	0.97	4/890 (0.4%)
22	T	0.53	0/764	1.07	5/1006 (0.5%)
23	V	0.47	0/212	0.88	0/277
All	All	0.46	3/56130 (0.0%)	0.83	181/83286 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	3	42

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1361	G	O5'-C5'	6.13	1.51	1.42
1	A	1362	C	O5'-C5'	5.97	1.51	1.42
1	A	1361	G	C3'-O3'	5.18	1.50	1.42

All (181) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1498	U	C2'-C3'-O3'	14.96	131.94	109.50
1	A	115	G	C2'-C3'-O3'	14.20	130.79	109.50
1	A	243	A	C2'-C3'-O3'	13.57	129.85	109.50
1	A	559	A	C2'-C3'-O3'	13.13	129.20	109.50
1	A	575	G	C2'-C3'-O3'	12.89	128.84	109.50
1	A	366	C	C2'-C3'-O3'	12.52	128.28	109.50
1	A	181	G	C2'-C3'-O3'	12.36	128.03	109.50
1	A	1503	A	C2'-C3'-O3'	12.29	127.94	109.50
1	A	1528	U	C2'-C3'-O3'	12.29	127.93	109.50
1	A	965	A	C2'-C3'-O3'	11.49	126.73	109.50
1	A	533	A	C2'-C3'-O3'	11.06	126.10	109.50
1	A	792	A	C2'-C3'-O3'	11.05	126.08	109.50
1	A	60	A	C2'-C3'-O3'	10.97	125.95	109.50
22	T	14	LYS	N-CA-C	-10.40	99.76	111.82
14	L	26	ALA	N-CA-C	-10.33	102.02	112.97
1	A	1528	U	C4'-C3'-O3'	10.17	124.65	109.40
1	A	812	C	C2'-C3'-O3'	9.94	124.41	109.50
1	A	266	G	C2'-C3'-O3'	9.76	124.14	109.50
1	A	960	U	C2'-C3'-O3'	9.59	123.88	109.50
22	T	13	LEU	N-CA-C	-9.40	99.04	113.89
7	E	23	GLY	N-CA-C	9.14	123.70	110.63
1	A	243	A	C4'-C3'-O3'	9.06	123.00	109.40
1	A	372	C	C2'-C3'-O3'	9.05	123.08	109.50
18	P	19	ILE	N-CA-C	-9.04	98.00	109.30
1	A	328	C	C2'-C3'-O3'	8.95	122.92	109.50
1	A	1346	A	C2'-C3'-O3'	8.91	122.86	109.50
1	A	484	G	C2'-C3'-O3'	8.88	122.83	109.50
1	A	533	A	C4'-C3'-O3'	8.88	122.72	109.40
12	J	20	ALA	N-CA-C	-8.81	101.24	114.64
1	A	1101	A	C2'-C3'-O3'	8.79	122.69	109.50
1	A	1067	A	C2'-C3'-O3'	8.63	122.44	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	223	ILE	N-CA-C	-8.62	103.44	111.45
4	B	219	VAL	N-CA-C	-8.42	104.57	111.81
9	G	148	ASN	N-CA-C	-8.26	101.65	113.21
1	A	188	C	C2'-C3'-O3'	8.23	126.05	113.70
1	A	559	A	C4'-C3'-O3'	8.03	121.44	109.40
1	A	1505	G	C2'-C3'-O3'	7.91	125.57	113.70
9	G	147	ALA	N-CA-C	-7.91	93.95	110.80
9	G	145	ALA	N-CA-C	-7.85	98.70	110.24
1	A	181	G	C4'-C3'-O3'	7.81	121.12	109.40
1	A	366	C	C4'-C3'-O3'	7.80	121.10	109.40
5	C	156	ARG	N-CA-C	-7.78	103.74	113.23
14	L	46	LYS	N-CA-C	7.68	115.08	108.78
1	A	1301	U	C2'-C3'-O3'	7.65	120.98	109.50
20	R	51	LEU	CA-C-N	7.61	127.51	120.21
20	R	51	LEU	C-N-CA	7.61	127.51	120.21
18	P	11	SER	N-CA-C	-7.42	97.77	108.60
1	A	1299	A	N9-C1'-C2'	7.39	123.09	112.00
1	A	1503	A	C4'-C3'-O3'	7.33	120.40	109.40
1	A	687	A	C2'-C3'-O3'	7.25	120.38	109.50
20	R	46	GLU	N-CA-C	-7.18	103.45	111.28
14	L	61	THR	N-CA-C	-7.15	104.02	112.89
18	P	79	VAL	N-CA-C	-7.07	103.30	111.00
7	E	26	PHE	N-CA-C	7.01	120.02	110.55
1	A	1498	U	C4'-C3'-O3'	7.00	119.90	109.40
12	J	60	ARG	N-CA-C	6.96	125.63	110.80
14	L	117	ARG	N-CA-C	6.95	119.88	111.82
14	L	92	ASP	N-CA-C	6.92	118.61	111.14
6	D	10	ARG	N-CA-C	-6.91	106.74	114.62
12	J	66	ARG	N-CA-C	6.89	119.80	109.25
3	W	4	A	C2'-C3'-O3'	-6.87	99.19	109.50
10	H	56	LYS	CA-C-N	6.87	127.28	119.93
10	H	56	LYS	C-N-CA	6.87	127.28	119.93
14	L	119	LYS	N-CA-C	-6.85	99.43	110.32
1	A	992	U	C2'-C3'-O3'	6.84	119.76	109.50
1	A	115	G	C4'-C3'-O3'	6.82	119.63	109.40
6	D	11	LEU	N-CA-C	-6.76	103.98	111.82
1	A	1224	G	C2'-C3'-O3'	6.73	119.59	109.50
1	A	428	G	C2'-C3'-O3'	6.72	119.58	109.50
10	H	96	GLY	N-CA-C	-6.63	102.48	113.02
4	B	82	ARG	N-CA-C	-6.57	105.84	114.31
1	A	560	U	C2'-C3'-O3'	6.53	119.29	109.50
6	D	12	CYS	N-CA-C	-6.52	104.09	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1065	U	C2'-C3'-O3'	6.50	119.25	109.50
18	P	23	ASP	N-CA-C	-6.48	101.98	110.53
5	C	85	ARG	N-CA-C	-6.47	105.03	113.12
1	A	250	A	C2'-C3'-O3'	6.42	119.13	109.50
4	B	135	GLN	N-CA-C	-6.41	105.18	112.87
15	M	15	VAL	N-CA-C	6.41	116.89	110.23
6	D	26	CYS	N-CA-C	-6.40	104.53	113.37
1	A	1361	G	C4'-C3'-O3'	6.36	122.54	113.00
12	J	62	HIS	N-CA-C	6.35	120.17	109.76
8	F	60	PHE	N-CA-C	6.29	119.49	109.24
22	T	58	LYS	N-CA-C	-6.25	104.39	111.14
11	I	5	TYR	N-CA-C	6.25	118.57	108.32
1	A	190	C	C2'-C3'-O3'	6.21	118.82	109.50
10	H	7	ALA	N-CA-C	-6.16	104.68	111.82
16	N	38	GLY	N-CA-C	-6.15	107.28	115.40
14	L	118	SER	N-CA-C	-6.15	104.58	111.28
1	A	975	A	C2'-C3'-O3'	6.13	118.69	109.50
14	L	66	VAL	N-CA-C	6.11	119.03	108.90
4	B	122	PHE	N-CA-C	-6.05	105.07	112.88
21	S	36	ARG	N-CA-C	-6.05	105.16	112.54
20	R	81	PHE	N-CA-C	-6.03	106.05	113.41
13	K	53	SER	N-CA-C	6.02	117.53	110.97
1	A	407	G	C2'-C3'-O3'	6.01	118.51	109.50
11	I	87	GLN	N-CA-C	-6.00	104.74	111.28
12	J	21	GLN	N-CA-C	-5.99	105.93	113.18
1	A	1346	A	C4'-C3'-O3'	5.98	118.37	109.40
14	L	101	VAL	N-CA-C	5.96	112.59	106.21
16	N	18	VAL	N-CA-C	5.96	116.13	110.53
10	H	79	VAL	N-CA-C	-5.94	104.72	110.72
4	B	14	GLY	N-CA-C	-5.90	106.44	113.99
12	J	81	THR	N-CA-C	-5.90	104.44	111.69
13	K	116	HIS	N-CA-C	-5.89	103.33	111.81
19	Q	58	GLU	N-CA-C	-5.83	101.06	110.32
1	A	1305	G	N9-C1'-C2'	5.82	120.73	112.00
18	P	27	LYS	N-CA-C	-5.79	102.86	110.33
9	G	87	VAL	N-CA-C	5.79	114.88	108.05
1	A	1201	A	C2'-C3'-O3'	5.78	118.17	109.50
6	D	33	MET	N-CA-C	-5.77	104.37	111.75
14	L	100	ILE	N-CA-C	-5.76	100.02	109.12
7	E	118	ILE	N-CA-C	5.72	115.77	107.88
19	Q	57	VAL	N-CA-C	5.71	117.13	108.80
4	B	188	ALA	N-CA-C	5.70	118.20	108.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	189	G	N9-C1'-C2'	-5.70	103.46	112.00
11	I	61	ALA	N-CA-C	5.68	118.36	108.76
1	A	1285	A	C2'-C3'-O3'	5.68	118.02	109.50
1	A	344	A	C2'-C3'-O3'	5.68	118.01	109.50
15	M	65	LYS	N-CA-C	-5.67	99.94	108.96
15	M	11	ARG	N-CA-C	5.67	118.48	110.14
4	B	24	TRP	N-CA-C	5.66	122.84	110.80
5	C	124	ILE	N-CA-C	5.62	116.26	110.36
4	B	185	ILE	N-CA-C	-5.61	100.36	108.89
1	A	7	G	C2'-C3'-O3'	5.60	117.90	109.50
4	B	47	THR	N-CA-C	-5.59	105.18	111.28
1	A	748	C	N1-C1'-C2'	5.57	120.36	112.00
1	A	572	A	N9-C1'-C2'	5.57	120.35	112.00
5	C	88	ARG	N-CA-C	-5.56	106.34	113.01
11	I	62	TYR	N-CA-C	-5.54	100.22	109.24
1	A	701	C	C2'-C3'-O3'	5.51	117.76	109.50
1	A	63	C	C5'-C4'-C3'	-5.47	107.79	116.00
14	L	46	LYS	CA-C-O	5.47	121.11	117.94
21	S	77	THR	N-CA-C	5.47	117.05	111.14
7	E	21	ALA	N-CA-C	-5.46	103.27	110.43
17	O	44	LYS	N-CA-C	-5.45	105.44	111.71
1	A	389	A	C5'-C4'-C3'	5.44	124.17	116.00
16	N	10	ALA	N-CA-C	-5.44	106.34	112.87
14	L	87	GLY	N-CA-C	-5.43	106.36	112.33
1	A	119	A	C2'-C3'-O3'	5.40	117.61	109.50
15	M	23	TYR	N-CA-C	5.39	117.91	111.71
4	B	225	ALA	N-CA-C	-5.37	106.61	114.39
21	S	34	TRP	N-CA-C	-5.36	104.36	112.99
13	K	122	LYS	N-CA-C	-5.35	103.47	110.53
9	G	154	TYR	N-CA-C	-5.33	103.26	110.68
10	H	77	GLU	N-CA-C	-5.33	102.99	110.35
21	S	13	ASP	N-CA-C	5.32	117.50	111.02
13	K	40	ILE	N-CA-C	-5.31	106.63	111.67
1	A	1200	C	C2'-C3'-O3'	-5.29	105.76	113.70
1	A	686	U	N1-C1'-C2'	5.29	121.94	114.00
1	A	993	G	C2'-C3'-O3'	5.29	117.43	109.50
10	H	20	TYR	N-CA-C	5.28	118.86	111.74
7	E	151	LEU	N-CA-C	5.25	118.47	111.75
22	T	68	LYS	N-CA-C	-5.25	105.56	111.28
10	H	44	PHE	N-CA-C	-5.23	107.28	113.97
5	C	130	VAL	N-CA-C	5.22	115.66	110.23
4	B	13	ALA	N-CA-C	-5.18	106.65	112.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	E	48	ALA	N-CA-C	5.18	112.88	108.22
12	J	15	THR	N-CA-C	-5.18	106.80	113.01
22	T	44	ALA	N-CA-C	-5.16	105.83	111.82
10	H	134	ILE	N-CA-C	5.14	120.03	109.34
14	L	30	ALA	CA-C-N	5.13	124.63	119.19
14	L	30	ALA	C-N-CA	5.13	124.63	119.19
19	Q	29	HIS	CA-C-N	5.13	125.42	119.47
19	Q	29	HIS	C-N-CA	5.13	125.42	119.47
10	H	135	CYS	N-CA-C	5.12	115.30	108.38
1	A	353	A	C5'-C4'-O4'	-5.11	102.13	109.80
10	H	57	PRO	N-CA-C	5.10	119.58	111.26
1	A	1502	A	N9-C1'-C2'	5.08	121.62	114.00
10	H	4	ASP	CA-C-N	5.08	125.11	119.32
10	H	4	ASP	C-N-CA	5.08	125.11	119.32
15	M	22	ILE	N-CA-C	-5.08	102.55	109.55
10	H	93	VAL	N-CA-C	5.07	115.28	107.77
10	H	89	PRO	N-CA-C	-5.06	103.16	111.15
14	L	23	LYS	N-CA-C	-5.04	106.72	112.92
1	A	60	A	C4'-C3'-O3'	5.04	116.96	109.40
12	J	49	VAL	N-CA-C	5.04	115.28	107.78
19	Q	67	LYS	N-CA-C	-5.03	102.94	110.23
1	A	760	G	N9-C1'-C2'	-5.01	104.49	112.00
14	L	57	LYS	N-CA-C	-5.00	103.07	110.48
1	A	475	G	N9-C1'-C2'	5.00	119.50	112.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	243	A	C3'
1	A	1498	U	C3'
1	A	1528	U	C3'

All (42) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1077	G	Sidechain
1	A	108	G	Sidechain
1	A	1130	A	Sidechain
1	A	1145	C	Sidechain
1	A	1299	A	Sidechain
1	A	1331	G	Sidechain
1	A	1361	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1370	G	Sidechain
1	A	1414	U	Sidechain
1	A	1454	G	Sidechain
1	A	1498	U	Sidechain
1	A	1502	A	Sidechain
1	A	1519	A	Sidechain
1	A	189	G	Sidechain
1	A	197	A	Sidechain
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	299	G	Sidechain
1	A	323	U	Sidechain
1	A	37	U	Sidechain
1	A	380	G	Sidechain
1	A	387	U	Sidechain
1	A	404	U	Sidechain
1	A	460	A	Sidechain
1	A	490	G	Sidechain
1	A	528	C	Sidechain
1	A	554	C	Sidechain
1	A	561	U	Sidechain
1	A	571	U	Sidechain
1	A	572	A	Sidechain
1	A	573	A	Sidechain
1	A	575	G	Sidechain
1	A	580	U	Sidechain
1	A	587	G	Sidechain
1	A	639	G	Sidechain
1	A	727	G	Sidechain
1	A	741	G	Sidechain
1	A	743	U	Sidechain
1	A	77	G	Sidechain
1	A	879	C	Sidechain
1	A	880	C	Sidechain
1	A	898	G	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32380	0	16346	1158	0
2	X	232	0	120	4	0
3	W	84	0	46	1	0
4	B	1900	0	1951	294	0
5	C	1612	0	1677	278	0
6	D	1703	0	1764	166	0
7	E	1146	0	1207	125	0
8	F	843	0	857	72	0
9	G	1257	0	1296	119	0
10	H	1116	0	1177	118	0
11	I	1011	0	1043	130	0
12	J	792	0	835	157	1
13	K	885	0	904	84	0
14	L	970	0	1057	121	0
15	M	997	0	1072	128	0
16	N	492	0	529	68	0
17	O	734	0	771	60	0
18	P	700	0	720	70	0
19	Q	857	0	930	87	0
20	R	597	0	668	71	0
21	S	647	0	673	93	0
22	T	762	0	856	78	0
23	V	208	0	221	16	0
24	A	42	0	45	2	0
25	A	104	0	0	0	0
25	J	1	0	0	0	0
25	X	2	0	0	0	0
26	D	1	0	0	0	0
26	N	1	0	0	0	0
All	All	52076	0	36765	3235	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 36.

All (3235) 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:243:A:H4'	1:A:244:U:H5'	1.30	1.13
12:J:45:ARG:HB3	12:J:45:ARG:HH11	0.99	1.13
14:L:47:LYS:HB3	14:L:48:PRO:HD3	1.32	1.12
6:D:151:LYS:H	6:D:151:LYS:HD2	1.08	1.11
6:D:36:ARG:H	6:D:37:PRO:HD3	1.14	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:972:C:H4'	12:J:57:LYS:HG2	1.31	1.09
1:A:349:A:H2'	1:A:350:G:H5''	1.29	1.09
1:A:1053:G:H4'	1:A:1054:C:H5'	1.32	1.06
1:A:1250:A:H4'	11:I:68:GLY:H	1.15	1.06
14:L:126:LYS:H	14:L:126:LYS:HD2	1.16	1.06
12:J:4:ILE:HD11	12:J:74:ILE:HD12	1.38	1.06
1:A:462:G:N2	18:P:82:GLN:HB3	1.70	1.05
5:C:79:ARG:HG2	5:C:82:GLU:HB2	1.37	1.05
14:L:67:THR:HG22	14:L:96:VAL:HG13	1.37	1.04
4:B:91:PRO:HG3	4:B:154:LEU:HB2	1.40	1.03
1:A:1314:C:OP2	21:S:6:LYS:HG2	1.59	1.02
1:A:839:U:H5'	1:A:840:C:H5	1.20	1.02
13:K:106:LYS:HE2	13:K:106:LYS:HA	1.37	1.02
5:C:35:GLU:HA	5:C:38:ARG:HH12	1.24	1.02
4:B:84:GLU:HB3	4:B:219:VAL:HG21	1.42	1.01
7:E:126:ARG:HG3	7:E:126:ARG:HH11	1.20	1.01
21:S:33:THR:HG22	21:S:35:SER:H	1.26	1.01
5:C:19:GLU:HG2	5:C:54:ARG:HE	1.25	1.00
5:C:38:ARG:HH11	5:C:38:ARG:HB2	1.20	1.00
9:G:146:GLU:HG3	9:G:149:ARG:HH21	1.25	1.00
5:C:14:ILE:HG22	5:C:15:THR:H	1.28	0.99
1:A:478:A:O2'	1:A:479:C:H5'	1.62	0.99
1:A:189:G:H2'	1:A:190(K):G:N2	1.78	0.97
7:E:50:GLU:HB3	7:E:53:LEU:HD13	1.47	0.97
15:M:10:PRO:HB2	15:M:18:ALA:HB1	1.46	0.97
7:E:33:VAL:HG11	7:E:109:ILE:HG12	1.43	0.96
1:A:1057:G:H5''	5:C:154:SER:HB2	1.45	0.96
12:J:29:ARG:N	12:J:29:ARG:HH11	1.62	0.96
4:B:19:HIS:HE2	4:B:206:ASP:HB3	1.30	0.95
1:A:349:A:C2'	1:A:350:G:H5''	1.96	0.95
5:C:21:ARG:H	5:C:21:ARG:HD2	1.30	0.95
1:A:1116:C:H2'	1:A:1117:G:H5''	1.46	0.95
6:D:36:ARG:H	6:D:37:PRO:CD	1.80	0.95
1:A:664:G:H22	1:A:741:G:H1	1.11	0.95
5:C:188:LEU:HD13	5:C:189:ALA:H	1.31	0.95
15:M:37:THR:HG23	15:M:55:ARG:HD2	1.49	0.95
1:A:1305:G:HO2'	1:A:1306:A:H8	0.96	0.94
6:D:176:LEU:HA	6:D:183:GLY:HA2	1.48	0.94
12:J:45:ARG:HB3	12:J:45:ARG:NH1	1.82	0.94
1:A:839:U:H5'	1:A:840:C:C5	2.01	0.94
1:A:1054:C:C5	2:X:34:I:H1'	2.02	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:G:H2'	1:A:190:C:H5'	1.47	0.93
8:F:33:TYR:HA	8:F:71:ARG:HH21	1.33	0.93
1:A:188:C:H2'	1:A:189:G:H4'	1.50	0.93
6:D:22:LYS:HB2	6:D:26:CYS:SG	2.09	0.93
13:K:40:ILE:HG22	13:K:41:THR:HG23	1.48	0.93
15:M:82:MET:HE3	15:M:93:ARG:HG2	1.51	0.93
1:A:967:C:H4'	11:I:128:ARG:HH21	1.32	0.92
7:E:80:ILE:HD11	7:E:91:LEU:HB2	1.49	0.92
20:R:53:ARG:HH11	20:R:59:SER:HA	1.35	0.92
1:A:462:G:H21	18:P:82:GLN:NE2	1.66	0.92
4:B:132:LYS:HA	4:B:135:GLN:HB2	1.49	0.92
1:A:1086:U:H3	1:A:1099:G:H22	1.13	0.92
4:B:21:ARG:HH11	4:B:23:ARG:HD2	1.33	0.92
5:C:83:ARG:HH21	5:C:87:LEU:HD21	1.33	0.92
14:L:47:LYS:HB3	14:L:48:PRO:CD	2.00	0.92
11:I:16:ARG:HD3	11:I:64:THR:HB	1.53	0.91
1:A:408:A:H4'	1:A:429:U:O2	1.71	0.90
4:B:178:ARG:HH11	4:B:178:ARG:HG3	1.35	0.90
5:C:3:ASN:HD22	5:C:3:ASN:H	0.93	0.90
9:G:50:ILE:O	9:G:54:THR:HB	1.71	0.90
19:Q:68:ARG:HG3	19:Q:68:ARG:O	1.72	0.90
1:A:1356:G:H2'	1:A:1357:A:C8	2.06	0.90
11:I:43:ALA:HA	11:I:74:ILE:HD13	1.52	0.90
6:D:170:VAL:HG21	6:D:176:LEU:HD22	1.54	0.89
12:J:29:ARG:HH12	12:J:84:GLN:HE22	1.20	0.89
15:M:34:LEU:HD13	15:M:41:PRO:HA	1.51	0.89
15:M:117:VAL:HG12	15:M:118:ALA:H	1.37	0.89
1:A:1502:A:H2	1:A:1505:G:H1	1.16	0.89
13:K:84:VAL:HG23	13:K:110:ASP:HA	1.53	0.89
1:A:579:G:H5'	1:A:728:A:H1'	1.55	0.89
1:A:190:C:C5'	1:A:190(K):G:H21	1.85	0.88
1:A:1250:A:H4'	11:I:68:GLY:N	1.87	0.88
7:E:80:ILE:CD1	7:E:91:LEU:HB2	2.03	0.88
9:G:155:ARG:NH1	9:G:155:ARG:HA	1.88	0.88
12:J:10:GLY:H	12:J:16:LEU:HD11	1.39	0.88
12:J:29:ARG:H	12:J:29:ARG:NH1	1.71	0.88
21:S:28:LYS:HG2	21:S:29:ARG:H	1.36	0.88
12:J:29:ARG:HH11	12:J:29:ARG:H	0.93	0.88
19:Q:14:LYS:H	19:Q:14:LYS:HD2	1.38	0.87
1:A:838:G:H2'	1:A:839:U:H5''	1.55	0.87
7:E:50:GLU:HG3	7:E:52:PRO:HD2	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:A:H4'	1:A:251:G:O5'	1.72	0.87
6:D:36:ARG:N	6:D:37:PRO:HD3	1.89	0.87
21:S:63:THR:HB	21:S:66:MET:HE3	1.56	0.87
6:D:151:LYS:HD2	6:D:151:LYS:N	1.90	0.87
4:B:97:TRP:HZ2	4:B:102:LEU:HD13	1.39	0.87
4:B:61:LEU:HD23	4:B:64:ARG:HD2	1.54	0.86
1:A:266:G:H5''	1:A:268:C:H41	1.38	0.86
1:A:189:G:N2	1:A:190(J):U:H3	1.74	0.85
9:G:146:GLU:HG3	9:G:149:ARG:NH2	1.91	0.85
15:M:23:TYR:HB3	15:M:67:GLU:HA	1.58	0.85
7:E:15:ARG:HD3	7:E:26:PHE:CD2	2.10	0.85
19:Q:14:LYS:HD2	19:Q:14:LYS:N	1.92	0.85
5:C:64:VAL:HG12	5:C:66:VAL:HG23	1.56	0.85
1:A:969:A:H61	15:M:126:LYS:HG3	1.39	0.85
1:A:1116:C:C2'	1:A:1117:G:H5''	2.06	0.85
14:L:47:LYS:CB	14:L:48:PRO:HD3	2.07	0.85
1:A:1126:U:H3	1:A:1127:G:N2	1.74	0.84
1:A:1226:C:H4'	1:A:1227:A:OP1	1.77	0.84
5:C:3:ASN:H	5:C:3:ASN:ND2	1.71	0.84
4:B:15:VAL:HG12	4:B:16:HIS:H	1.42	0.84
17:O:56:LEU:HA	17:O:59:MET:HE2	1.57	0.84
11:I:6:GLY:N	11:I:84:ALA:HB2	1.92	0.84
4:B:139:LYS:O	4:B:139:LYS:HD3	1.78	0.84
5:C:191:THR:HG21	5:C:193:TYR:CZ	2.13	0.84
6:D:151:LYS:H	6:D:151:LYS:CD	1.90	0.84
7:E:51:VAL:HB	7:E:52:PRO:HD3	1.60	0.84
6:D:3:ARG:HD2	6:D:3:ARG:N	1.92	0.83
4:B:88:ALA:HB3	4:B:90:MET:HG2	1.58	0.83
4:B:25:ASN:HD22	4:B:25:ASN:C	1.86	0.83
4:B:101:MET:HA	4:B:108:ILE:HG13	1.61	0.83
7:E:81:GLU:HG2	7:E:90:VAL:HG22	1.58	0.83
1:A:1281:U:H5'	1:A:1282:C:H5	1.40	0.83
4:B:124:SER:HB2	4:B:125:PRO:HD2	1.59	0.83
7:E:53:LEU:H	7:E:53:LEU:HD12	1.44	0.83
5:C:6:HIS:HD2	5:C:8:ILE:HB	1.44	0.83
10:H:51:VAL:HG21	10:H:60:ARG:NH1	1.94	0.83
1:A:243:A:C4'	1:A:244:U:H5'	2.06	0.83
12:J:45:ARG:HH11	12:J:45:ARG:CB	1.88	0.83
14:L:126:LYS:HD2	14:L:126:LYS:N	1.94	0.83
20:R:47:THR:HG22	20:R:48:GLY:H	1.43	0.83
11:I:111:ARG:HB3	11:I:111:ARG:HH11	1.43	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:46:ARG:HG2	12:J:46:ARG:HH11	1.43	0.82
12:J:60:ARG:HD2	12:J:60:ARG:N	1.93	0.82
17:O:6:GLU:H	17:O:6:GLU:CD	1.86	0.82
1:A:406:G:H1	1:A:436:C:H42	1.28	0.82
5:C:91:LEU:HD23	5:C:92:ALA:N	1.95	0.82
4:B:69:LEU:HD12	4:B:155:LEU:HD11	1.62	0.82
1:A:1152:A:H5''	12:J:13:HIS:CD2	2.14	0.82
4:B:23:ARG:NH1	4:B:24:TRP:HA	1.95	0.82
5:C:3:ASN:HD22	5:C:3:ASN:N	1.70	0.82
17:O:87:ILE:HG22	17:O:88:ARG:HE	1.45	0.81
5:C:28:GLN:HA	5:C:31:HIS:HD2	1.45	0.81
4:B:18:GLY:H	4:B:42:ILE:H	1.29	0.81
1:A:1208:C:H2'	1:A:1209:C:C6	2.15	0.80
1:A:1006:C:H2'	1:A:1007:C:H6	1.47	0.80
13:K:33:THR:HG22	13:K:39:PRO:HA	1.63	0.80
1:A:302:G:H5''	14:L:17:LYS:NZ	1.96	0.80
1:A:1251:A:H2'	1:A:1252:A:C8	2.17	0.80
14:L:41:ARG:HG2	14:L:42:THR:H	1.47	0.80
21:S:55:LYS:HG2	21:S:56:GLN:HE21	1.47	0.80
1:A:190:C:O2	1:A:190:C:H2'	1.82	0.80
1:A:706:A:O2'	13:K:29:ILE:HD11	1.81	0.80
4:B:19:HIS:NE2	4:B:206:ASP:HB3	1.96	0.80
1:A:1053:G:C4'	1:A:1054:C:H5'	2.09	0.79
12:J:49:VAL:HG23	16:N:41:ARG:HB2	1.63	0.79
1:A:1305:G:O2'	1:A:1306:A:H8	1.65	0.79
21:S:22:LEU:HD21	21:S:28:LYS:HD2	1.64	0.79
1:A:1190:G:H3'	5:C:3:ASN:OD1	1.82	0.79
1:A:189:G:H22	1:A:190(J):U:H3	1.31	0.79
11:I:9:ARG:HG2	11:I:14:VAL:HG22	1.64	0.79
1:A:954:G:H21	1:A:1227:A:H62	1.27	0.79
1:A:1057:G:H5''	5:C:154:SER:CB	2.12	0.79
12:J:34:VAL:HG22	12:J:74:ILE:HG23	1.65	0.79
1:A:972:C:H4'	12:J:57:LYS:CG	2.12	0.79
19:Q:15:MET:HE1	19:Q:43:LEU:HD22	1.63	0.79
1:A:1208:C:H2'	1:A:1209:C:H6	1.47	0.78
1:A:189:G:H1	1:A:190(I):G:H1	0.82	0.78
4:B:18:GLY:HA2	4:B:41:ILE:HA	1.65	0.78
1:A:694:A:H3'	1:A:695:A:H5''	1.64	0.78
4:B:71:VAL:O	4:B:165:VAL:HG23	1.83	0.78
14:L:27:LEU:O	14:L:29:GLY:N	2.16	0.78
15:M:3:ARG:HH11	15:M:3:ARG:HB2	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1142:G:H2'	1:A:1143:G:O4'	1.83	0.78
7:E:79:GLU:HG3	7:E:93:PRO:HD2	1.64	0.78
12:J:32:ALA:HB2	12:J:75:ILE:HB	1.66	0.78
15:M:54:VAL:O	15:M:58:GLU:HG2	1.83	0.78
11:I:51:ARG:HG2	11:I:56:LEU:HD12	1.66	0.78
1:A:371:G:O2'	1:A:372:C:H5'	1.83	0.78
17:O:17:ARG:HG3	17:O:17:ARG:HH11	1.48	0.78
5:C:150:LYS:HG3	5:C:169:ALA:HB2	1.64	0.77
15:M:8:GLU:C	15:M:9:ILE:HD12	2.09	0.77
22:T:21:LYS:HB2	22:T:21:LYS:NZ	1.99	0.77
1:A:243:A:H4'	1:A:244:U:C5'	2.11	0.77
4:B:97:TRP:CZ2	4:B:102:LEU:HD13	2.18	0.77
4:B:178:ARG:HH21	4:B:196:LEU:HA	1.48	0.77
1:A:1223:C:P	21:S:78:ARG:HH12	2.07	0.77
4:B:80:ILE:HD11	4:B:208:ILE:HG23	1.65	0.77
10:H:92:ARG:HG2	10:H:92:ARG:HH11	1.49	0.77
1:A:412:A:H5'	1:A:417:C:C4	2.20	0.77
18:P:81:ARG:NE	18:P:81:ARG:HA	2.00	0.77
1:A:1216:G:H5''	16:N:5:ALA:HB2	1.67	0.77
5:C:75:VAL:O	5:C:83:ARG:HD3	1.84	0.77
12:J:75:ILE:H	12:J:75:ILE:HD12	1.48	0.77
14:L:59:ARG:HD3	14:L:65:GLU:HG3	1.65	0.77
4:B:197:VAL:HB	4:B:200:ILE:HG12	1.65	0.77
15:M:49:THR:HG22	15:M:51:ALA:H	1.48	0.77
21:S:6:LYS:HD2	21:S:6:LYS:N	2.00	0.77
1:A:328:C:O2	1:A:328:C:H2'	1.82	0.77
1:A:409:G:H5'	1:A:430:A:N6	2.00	0.76
1:A:1086:U:H3	1:A:1099:G:N2	1.83	0.76
5:C:191:THR:HG22	5:C:192:THR:N	2.00	0.76
18:P:1:MET:HE3	18:P:3:LYS:HD2	1.68	0.76
20:R:36:ASN:ND2	20:R:38:GLU:HG2	2.00	0.76
21:S:41:VAL:HG22	21:S:44:MET:HE3	1.66	0.76
1:A:133:U:OP1	22:T:74:LYS:HE2	1.85	0.76
1:A:462:G:N2	18:P:82:GLN:HE21	1.83	0.76
1:A:99:C:H2'	1:A:101:A:C8	2.21	0.76
1:A:738:C:H5''	8:F:69:GLU:HB3	1.67	0.76
1:A:430:A:H2'	1:A:431:A:H5''	1.67	0.76
5:C:21:ARG:HD2	5:C:21:ARG:N	2.00	0.76
5:C:64:VAL:HG23	5:C:99:VAL:HG11	1.67	0.76
15:M:12:ASN:HB2	15:M:46:LYS:HB3	1.67	0.76
6:D:3:ARG:HH11	6:D:3:ARG:H	1.32	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:78:LEU:HD22	6:D:96:LEU:HB3	1.68	0.76
9:G:26:PHE:CE2	9:G:30:ILE:HD11	2.21	0.76
13:K:29:ILE:C	13:K:29:ILE:HD12	2.12	0.75
1:A:112:G:H21	1:A:354:G:H5'	1.50	0.75
1:A:1425:U:H2'	1:A:1426:C:H6	1.50	0.75
4:B:88:ALA:CB	4:B:90:MET:HG2	2.16	0.75
21:S:41:VAL:H	21:S:44:MET:HE3	1.50	0.75
15:M:40:ASN:HD22	15:M:41:PRO:N	1.82	0.75
14:L:27:LEU:C	14:L:29:GLY:H	1.94	0.75
1:A:939:G:H5''	9:G:102:ARG:NH2	2.02	0.75
1:A:1201:A:H4'	1:A:1202:G:O5'	1.86	0.75
13:K:84:VAL:HG11	13:K:95:ILE:HD11	1.69	0.75
5:C:107:GLN:NE2	5:C:107:GLN:H	1.85	0.75
11:I:65:VAL:HG21	11:I:73:GLN:HB3	1.67	0.75
1:A:35:G:H2'	1:A:36:C:C6	2.20	0.75
8:F:10:LEU:CD1	8:F:59:TYR:HB3	2.16	0.74
5:C:38:ARG:HH11	5:C:38:ARG:CB	1.99	0.74
11:I:4:TYR:CD2	11:I:88:TYR:HA	2.22	0.74
16:N:9:LYS:HE3	16:N:21:TYR:O	1.87	0.74
1:A:190:C:H5''	1:A:190(K):G:H21	1.50	0.74
1:A:1391:U:H2'	1:A:1392:G:C8	2.22	0.74
1:A:556:C:O2'	1:A:557:G:H5'	1.87	0.74
9:G:23:VAL:O	9:G:27:ILE:HG13	1.87	0.74
1:A:189:G:H2'	1:A:190(K):G:H22	1.53	0.74
11:I:53:VAL:HG21	11:I:85:LEU:HD21	1.70	0.74
1:A:462:G:H22	18:P:82:GLN:HB3	1.52	0.74
1:A:1190:G:OP1	5:C:4:LYS:HA	1.87	0.74
6:D:146:ILE:N	6:D:146:ILE:HD12	2.02	0.74
12:J:84:GLN:O	12:J:88:LEU:HD12	1.86	0.74
13:K:57:THR:HG23	13:K:60:ALA:H	1.52	0.74
1:A:413:G:N3	1:A:416:G:H5'	2.03	0.74
5:C:34:LEU:HD22	5:C:38:ARG:CZ	2.18	0.74
7:E:126:ARG:HH11	7:E:126:ARG:CG	1.98	0.74
8:F:78:GLU:O	8:F:81:ILE:HG22	1.87	0.74
16:N:27:CYS:SG	16:N:29:ARG:HB2	2.28	0.73
5:C:58:GLU:HB3	12:J:92:THR:HG21	1.70	0.73
7:E:76:ILE:HG23	7:E:77:PRO:HD2	1.68	0.73
7:E:78:HIS:HD2	10:H:107:LEU:HD12	1.53	0.73
20:R:33:ASP:OD2	20:R:36:ASN:HB2	1.88	0.73
9:G:18:TYR:CD2	9:G:59:LEU:HB2	2.23	0.73
11:I:48:GLU:N	11:I:49:PRO:HD2	2.03	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:838:G:C2'	1:A:839:U:H5''	2.18	0.73
6:D:35:ARG:O	6:D:36:ARG:HB2	1.89	0.73
20:R:86:VAL:HG12	20:R:87:ARG:H	1.53	0.73
1:A:1224:G:H1	1:A:1362:C:H42	1.34	0.73
5:C:14:ILE:O	5:C:16:ARG:N	2.22	0.73
6:D:3:ARG:N	6:D:3:ARG:HH11	1.87	0.73
20:R:88:LYS:OXT	20:R:88:LYS:HG2	1.87	0.73
1:A:1168:A:H2'	1:A:1169:A:C8	2.22	0.73
12:J:38:ILE:HB	12:J:71:LEU:HB2	1.71	0.73
15:M:3:ARG:HA	15:M:8:GLU:O	1.89	0.73
1:A:190:C:H5'	1:A:190(K):G:H21	1.52	0.73
12:J:90:LEU:H	12:J:91:PRO:CD	2.02	0.73
1:A:928:G:H4'	1:A:1533:C:H5'	1.70	0.73
4:B:91:PRO:HG2	4:B:155:LEU:HG	1.70	0.73
6:D:25:ARG:C	6:D:27:TYR:H	1.96	0.73
7:E:24:ARG:HB3	7:E:24:ARG:HH11	1.54	0.73
16:N:26:ARG:NH1	16:N:47:LEU:HG	2.04	0.73
18:P:28:ARG:HG2	18:P:28:ARG:HH11	1.53	0.73
4:B:178:ARG:HH21	4:B:196:LEU:C	1.97	0.73
1:A:1057:G:O2'	1:A:1058:G:H5'	1.89	0.72
18:P:81:ARG:HA	18:P:81:ARG:HE	1.54	0.72
20:R:53:ARG:NH1	20:R:59:SER:HA	2.04	0.72
11:I:118:LYS:O	11:I:119:ALA:HB3	1.89	0.72
1:A:1032:G:H2'	1:A:1033:G:O4'	1.89	0.72
4:B:88:ALA:C	4:B:90:MET:H	1.97	0.72
1:A:839:U:C5'	1:A:840:C:H5	2.02	0.72
1:A:1250:A:C4'	11:I:68:GLY:H	1.97	0.72
4:B:95:GLN:O	4:B:96:ARG:HD2	1.88	0.72
22:T:57:ARG:HB2	22:T:57:ARG:HH11	1.54	0.72
1:A:1152:A:H2'	1:A:1153:C:C6	2.25	0.72
4:B:137:ARG:HA	4:B:140:HIS:HD2	1.53	0.72
5:C:123:GLN:HE22	5:C:140:ARG:HH22	1.36	0.72
19:Q:59:ILE:HG22	19:Q:71:PHE:CD1	2.24	0.72
1:A:112:G:N2	1:A:354:G:H5'	2.04	0.72
1:A:677:U:H3	1:A:713:G:H22	1.37	0.72
1:A:840:C:H5''	1:A:841:U:OP1	1.90	0.72
4:B:68:ILE:HB	4:B:90:MET:HE3	1.71	0.72
6:D:150:GLU:O	6:D:153:ARG:HG2	1.90	0.72
14:L:43:VAL:HG12	14:L:44:THR:H	1.55	0.72
1:A:462:G:N2	18:P:82:GLN:NE2	2.38	0.72
1:A:556:C:OP2	14:L:20:LYS:HE3	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:97:LYS:HB3	11:I:98:PRO:HD3	1.72	0.72
4:B:137:ARG:HA	4:B:140:HIS:CD2	2.25	0.71
1:A:1360:A:H2'	1:A:1361:G:C8	2.24	0.71
15:M:73:GLU:O	15:M:76:ALA:HB3	1.90	0.71
19:Q:12:SER:HA	19:Q:14:LYS:HZ3	1.54	0.71
5:C:64:VAL:CG2	5:C:99:VAL:HG11	2.20	0.71
9:G:113:GLU:HG2	9:G:119:ARG:HG2	1.71	0.71
20:R:86:VAL:HG12	20:R:87:ARG:N	2.05	0.71
5:C:123:GLN:NE2	5:C:140:ARG:HH22	1.88	0.71
5:C:156:ARG:H	5:C:163:ALA:HA	1.55	0.71
8:F:97:PHE:HB2	20:R:32:ARG:HH21	1.54	0.71
12:J:82:ILE:HG22	12:J:86:MET:SD	2.29	0.71
1:A:860:A:H2'	1:A:861:G:O4'	1.90	0.71
7:E:122:GLU:O	7:E:123:LEU:HD23	1.91	0.71
15:M:79:LYS:HG2	15:M:83:ASP:OD2	1.89	0.71
18:P:74:LEU:O	18:P:79:VAL:HG23	1.91	0.71
1:A:462:G:H21	18:P:82:GLN:HE21	1.37	0.71
1:A:1502:A:H2	1:A:1505:G:N1	1.88	0.71
9:G:79:ARG:HD3	9:G:80:VAL:N	2.04	0.71
14:L:45:PRO:HD3	14:L:51:ALA:O	1.91	0.71
17:O:78:TYR:CZ	17:O:82:ILE:HD11	2.25	0.71
18:P:34:GLU:OE2	18:P:55:ARG:HD3	1.90	0.71
1:A:413:G:H4'	1:A:416:G:H21	1.54	0.71
1:A:463:A:H4'	1:A:474:G:OP2	1.90	0.71
1:A:1369:C:H2'	1:A:1370:G:C8	2.25	0.71
7:E:24:ARG:HB3	7:E:24:ARG:NH1	2.05	0.71
21:S:20:LEU:HD12	21:S:21:GLU:N	2.06	0.71
1:A:977:A:H2'	1:A:978:A:H5''	1.72	0.71
1:A:1263:C:H2'	1:A:1264:C:C6	2.25	0.71
5:C:83:ARG:HA	5:C:86:VAL:HG23	1.73	0.71
7:E:137:GLU:O	7:E:141:GLN:HG3	1.90	0.71
11:I:111:ARG:HH11	11:I:111:ARG:CB	2.04	0.71
15:M:5:ALA:HB3	15:M:8:GLU:HG3	1.72	0.71
1:A:204:U:O2	1:A:204:U:H2'	1.90	0.70
1:A:1189:C:P	12:J:51:ARG:HH22	2.14	0.70
14:L:28:LYS:C	14:L:30:ALA:H	1.98	0.70
1:A:353:A:H5'	1:A:353:A:H8	1.56	0.70
1:A:1238:A:H5'	1:A:1336:C:H41	1.55	0.70
1:A:1285:A:H4'	1:A:1286:A:O5'	1.91	0.70
1:A:1343:G:H2'	1:A:1344:C:C6	2.25	0.70
1:A:1435:G:H2'	1:A:1436:U:C6	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:162:LEU:HD13	6:D:181:MET:SD	2.31	0.70
11:I:127:LYS:H	11:I:127:LYS:HE3	1.57	0.70
12:J:89:ASP:OD2	12:J:91:PRO:HD2	1.90	0.70
7:E:11:ILE:HG22	7:E:12:LEU:HD12	1.73	0.70
1:A:141:A:H1'	1:A:182:U:O2	1.92	0.70
7:E:11:ILE:HB	7:E:31:LEU:HB3	1.73	0.70
5:C:191:THR:HG21	5:C:193:TYR:CE2	2.25	0.70
12:J:8:LEU:HD22	12:J:20:ALA:HB2	1.72	0.70
19:Q:18:THR:HG23	19:Q:69:LYS:HE3	1.71	0.70
1:A:17:U:H2'	1:A:18:C:C6	2.25	0.70
1:A:1281:U:H5'	1:A:1282:C:C5	2.26	0.70
5:C:6:HIS:CD2	5:C:8:ILE:HB	2.26	0.70
6:D:126:ILE:HG22	6:D:127:THR:N	2.06	0.70
16:N:58:LYS:HZ2	16:N:58:LYS:HB3	1.57	0.70
5:C:70:VAL:HG21	5:C:76:VAL:HG21	1.73	0.70
6:D:153:ARG:NE	6:D:181:MET:HE3	2.06	0.70
12:J:10:GLY:N	12:J:16:LEU:HD11	2.06	0.70
1:A:524:G:H2'	1:A:525:C:C6	2.27	0.70
1:A:1366:C:H2'	1:A:1367:C:H6	1.57	0.70
5:C:102:ASN:N	5:C:102:ASN:HD22	1.88	0.70
10:H:91:ARG:HG3	14:L:7:ILE:HG13	1.74	0.70
13:K:50:TYR:HB3	13:K:54:ARG:HB2	1.74	0.70
1:A:135:C:O2	18:P:1:MET:HB2	1.92	0.69
5:C:5:ILE:O	5:C:5:ILE:HD12	1.92	0.69
12:J:31:GLY:HA2	12:J:76:ASN:HD21	1.55	0.69
14:L:55:VAL:HG12	14:L:56:ALA:N	2.07	0.69
21:S:17:GLU:HA	21:S:20:LEU:HG	1.74	0.69
4:B:98:LEU:HD23	4:B:98:LEU:H	1.56	0.69
12:J:50:ILE:HG12	12:J:60:ARG:HE	1.57	0.69
13:K:27:ASN:OD1	13:K:55:LYS:HB3	1.93	0.69
1:A:972:C:C4'	12:J:57:LYS:HG2	2.17	0.69
5:C:107:GLN:H	5:C:107:GLN:CD	1.99	0.69
6:D:173:TRP:HB2	6:D:187:ARG:O	1.92	0.69
10:H:46:LYS:H	10:H:64:LYS:HG3	1.57	0.69
15:M:49:THR:CG2	15:M:51:ALA:H	2.05	0.69
6:D:9:CYS:SG	6:D:22:LYS:HG3	2.32	0.69
5:C:49:SER:O	5:C:72:LYS:HD2	1.92	0.69
20:R:46:GLU:H	20:R:46:GLU:CD	1.99	0.69
21:S:33:THR:HG22	21:S:34:TRP:H	1.58	0.69
21:S:40:ILE:HG21	21:S:62:ILE:HD11	1.75	0.69
1:A:1392:G:H21	1:A:1502:A:H8	1.40	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:A:OP2	1:A:190(E):U:H2'	1.93	0.69
4:B:90:MET:HE2	4:B:222:ILE:HD13	1.73	0.69
5:C:204:LEU:HD12	5:C:204:LEU:O	1.93	0.69
7:E:15:ARG:HD3	7:E:26:PHE:HD2	1.55	0.69
13:K:124:LYS:HE3	13:K:125:PHE:CE1	2.28	0.69
14:L:55:VAL:HG11	14:L:67:THR:HG23	1.74	0.69
4:B:18:GLY:CA	4:B:41:ILE:HA	2.23	0.69
6:D:3:ARG:HH11	6:D:3:ARG:CA	2.05	0.69
12:J:49:VAL:O	12:J:60:ARG:O	2.11	0.69
19:Q:101:ARG:NE	19:Q:101:ARG:HA	2.07	0.69
1:A:1137:C:H4'	1:A:1138:G:C2	2.28	0.69
10:H:20:TYR:CE2	10:H:75:ARG:HD2	2.28	0.69
11:I:8:GLY:HA2	11:I:79:LEU:HD13	1.75	0.69
11:I:10:ARG:HG2	11:I:75:ASP:HB2	1.75	0.69
5:C:154:SER:OG	5:C:155:GLY:N	2.24	0.68
9:G:54:THR:HG22	9:G:56:GLN:H	1.57	0.68
14:L:27:LEU:C	14:L:29:GLY:N	2.50	0.68
20:R:22:VAL:HG13	20:R:42:ARG:HD2	1.74	0.68
1:A:853:G:O2'	1:A:854:G:H5'	1.93	0.68
12:J:75:ILE:HD12	12:J:75:ILE:N	2.08	0.68
15:M:40:ASN:HD22	15:M:41:PRO:CD	2.06	0.68
1:A:975:A:O5'	1:A:976:G:H5'	1.93	0.68
1:A:1123:A:H4'	12:J:37:PRO:HD2	1.76	0.68
5:C:64:VAL:HB	5:C:99:VAL:HB	1.75	0.68
1:A:687:A:H4'	1:A:688:G:O5'	1.94	0.68
5:C:38:ARG:HB2	5:C:38:ARG:NH1	2.02	0.68
6:D:62:GLN:HE22	6:D:65:ARG:HH12	1.39	0.68
7:E:36:ASP:OD2	7:E:40:ARG:HB2	1.94	0.68
1:A:406:G:H1	1:A:436:C:N4	1.91	0.68
1:A:1065:U:H4'	1:A:1066:C:O5'	1.93	0.68
1:A:1193:G:O2'	1:A:1194:U:H5'	1.93	0.68
4:B:35:GLU:HG2	4:B:40:HIS:HA	1.74	0.68
12:J:48:THR:HA	12:J:62:HIS:HD2	1.58	0.68
1:A:1128:C:O2'	1:A:1130:A:C8	2.47	0.68
4:B:178:ARG:HH21	4:B:196:LEU:CA	2.05	0.68
5:C:79:ARG:NH1	5:C:79:ARG:HB3	2.09	0.68
8:F:67:MET:HE2	8:F:72:VAL:H	1.59	0.68
20:R:36:ASN:HD21	20:R:38:GLU:HG2	1.56	0.68
1:A:1356:G:H2'	1:A:1357:A:H8	1.56	0.68
1:A:1425:U:H2'	1:A:1426:C:C6	2.28	0.68
11:I:23:ASN:HB3	11:I:25:LYS:HG3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:106:ALA:O	11:I:108:VAL:HG23	1.93	0.68
19:Q:97:SER:HB2	19:Q:98:LEU:HD12	1.75	0.68
1:A:195:A:H4'	22:T:68:LYS:HE2	1.75	0.68
1:A:353:A:H5'	1:A:353:A:C8	2.29	0.68
1:A:1367:C:H4'	12:J:48:THR:HG21	1.75	0.68
10:H:90:GLY:O	10:H:91:ARG:HB2	1.92	0.68
4:B:132:LYS:C	4:B:134:GLU:H	2.00	0.68
22:T:10:LEU:O	22:T:13:LEU:HG	1.94	0.68
1:A:1015:A:H2'	1:A:1016:A:C8	2.30	0.67
5:C:20:SER:HB3	5:C:22:TRP:NE1	2.09	0.67
5:C:35:GLU:HA	5:C:38:ARG:NH1	2.04	0.67
5:C:191:THR:HG22	5:C:193:TYR:H	1.60	0.67
8:F:2:ARG:CZ	8:F:69:GLU:HG2	2.24	0.67
9:G:22:LEU:HD11	9:G:101:LEU:HD21	1.74	0.67
15:M:94:ARG:HH11	15:M:94:ARG:HG3	1.57	0.67
1:A:895:G:H2'	1:A:896:C:C6	2.29	0.67
5:C:139:GLN:HA	5:C:139:GLN:HE21	1.58	0.67
17:O:70:LEU:HD12	17:O:78:TYR:HB2	1.76	0.67
21:S:13:ASP:HA	21:S:16:LEU:HB3	1.76	0.67
1:A:448:A:OP2	1:A:485:G:N2	2.28	0.67
5:C:13:GLY:HA3	16:N:57:ARG:NH2	2.08	0.67
18:P:81:ARG:C	18:P:83:GLU:H	2.01	0.67
1:A:113:G:H1'	1:A:354:G:H5'	1.76	0.67
1:A:1228:C:OP1	15:M:115:LYS:HE3	1.92	0.67
4:B:29:ALA:HA	4:B:32:ILE:HD12	1.75	0.67
6:D:70:ILE:HD11	6:D:100:ARG:HD2	1.76	0.67
12:J:6:ILE:HA	12:J:98:ILE:HG22	1.74	0.67
13:K:51:LYS:HE2	13:K:52:GLY:H	1.58	0.67
14:L:89:ARG:NH1	14:L:97:ARG:HG2	2.09	0.67
15:M:5:ALA:HB3	15:M:8:GLU:CG	2.25	0.67
1:A:109:A:H2'	1:A:326:G:N2	2.09	0.67
4:B:126:GLU:HA	4:B:129:GLU:OE2	1.94	0.67
5:C:23:TYR:CD2	5:C:24:ALA:N	2.62	0.67
1:A:287:U:O2'	1:A:288:A:H5'	1.93	0.67
1:A:1497:G:O2'	1:A:1498:U:H5'	1.94	0.67
1:A:423:G:H5''	1:A:424:G:N2	2.08	0.67
5:C:108:ASN:ND2	5:C:111:LEU:HG	2.09	0.67
12:J:60:ARG:O	12:J:61:GLU:O	2.13	0.67
14:L:38:THR:HG22	14:L:39:VAL:HG23	1.77	0.67
20:R:26:LEU:HD12	20:R:27:GLY:H	1.59	0.67
1:A:411:A:H1'	1:A:417:C:O2	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:939:G:H5''	9:G:102:ARG:HH22	1.58	0.67
4:B:25:ASN:C	4:B:25:ASN:ND2	2.53	0.67
10:H:116:LYS:HZ3	10:H:127:LEU:HB3	1.60	0.67
1:A:189:G:C6	1:A:190:C:H3'	2.29	0.67
15:M:17:VAL:O	15:M:20:THR:HB	1.95	0.67
18:P:11:SER:HB3	18:P:14:ASN:HB3	1.77	0.67
5:C:64:VAL:HB	5:C:99:VAL:CB	2.25	0.66
19:Q:12:SER:HB3	19:Q:20:THR:HB	1.77	0.66
7:E:150:ARG:HG3	7:E:150:ARG:HH11	1.59	0.66
11:I:127:LYS:HD3	15:M:126:LYS:HE2	1.77	0.66
13:K:54:ARG:O	13:K:57:THR:HG22	1.95	0.66
17:O:45:VAL:HG12	17:O:46:HIS:N	2.10	0.66
1:A:478:A:C2'	1:A:479:C:H5'	2.24	0.66
9:G:15:ASP:HB3	9:G:19:GLY:N	2.11	0.66
9:G:22:LEU:HG	9:G:62:PHE:HE2	1.59	0.66
10:H:77:GLU:HG2	10:H:78:GLN:H	1.60	0.66
22:T:36:LEU:HD12	22:T:62:LEU:HD12	1.76	0.66
1:A:147:G:O2'	1:A:148:G:H5'	1.96	0.66
1:A:370:C:O2'	1:A:371:G:H5'	1.95	0.66
1:A:1229:A:H2'	1:A:1230:C:H6	1.58	0.66
11:I:6:GLY:H	11:I:84:ALA:HB2	1.60	0.66
1:A:1372:U:OP1	11:I:71:SER:HB3	1.95	0.66
6:D:3:ARG:HH11	6:D:3:ARG:HA	1.60	0.66
8:F:10:LEU:H	8:F:10:LEU:HD12	1.59	0.66
9:G:155:ARG:HA	9:G:155:ARG:HH11	1.61	0.66
15:M:23:TYR:CB	15:M:67:GLU:HA	2.26	0.66
15:M:117:VAL:HG12	15:M:118:ALA:N	2.10	0.66
22:T:49:ALA:HB3	22:T:99:LEU:HG	1.77	0.66
1:A:403:C:O2'	1:A:404:U:H5'	1.95	0.66
1:A:1047:G:H5''	16:N:4:LYS:HD3	1.78	0.66
1:A:1118:C:H1'	1:A:1179:A:C4	2.31	0.66
5:C:115:LEU:HD23	5:C:118:GLN:OE1	1.95	0.66
7:E:76:ILE:HG22	7:E:78:HIS:H	1.60	0.66
8:F:33:TYR:HA	8:F:71:ARG:NH2	2.09	0.66
9:G:78:ARG:HB2	9:G:156:TRP:HZ3	1.60	0.66
12:J:46:ARG:HG2	12:J:46:ARG:NH1	2.10	0.66
1:A:344:A:H4'	1:A:345:C:OP2	1.95	0.66
1:A:946:A:H2'	1:A:947:G:C8	2.31	0.66
1:A:1428:A:H2'	1:A:1429:C:C6	2.31	0.66
4:B:36:ARG:HB2	4:B:41:ILE:HD11	1.77	0.66
6:D:3:ARG:H	6:D:3:ARG:NH1	1.93	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:100:GLY:O	11:I:102:LEU:N	2.27	0.66
20:R:38:GLU:H	20:R:38:GLU:CD	2.04	0.66
5:C:15:THR:O	5:C:16:ARG:HB2	1.94	0.66
10:H:51:VAL:HG11	10:H:60:ARG:NH2	2.11	0.66
18:P:81:ARG:HE	18:P:81:ARG:CA	2.09	0.66
1:A:390:C:H2'	1:A:391:G:C8	2.31	0.66
1:A:1132:C:H2'	1:A:1133:G:C8	2.30	0.66
18:P:80:PHE:O	18:P:82:GLN:N	2.29	0.66
1:A:1161:C:H2'	1:A:1162:C:H6	1.61	0.65
1:A:1278:U:H5''	1:A:1279:A:O4'	1.96	0.65
1:A:1352:C:H2'	1:A:1353:G:C8	2.31	0.65
1:A:1412:C:H2'	1:A:1413:A:C8	2.32	0.65
4:B:219:VAL:C	4:B:221:LEU:H	2.04	0.65
9:G:75:VAL:HG21	9:G:86:GLN:HB3	1.76	0.65
15:M:19:LEU:O	15:M:22:ILE:HD13	1.96	0.65
15:M:78:ILE:HA	15:M:81:LEU:HD12	1.78	0.65
21:S:41:VAL:HG23	21:S:43:GLU:HG2	1.78	0.65
1:A:673:G:H2'	1:A:674:G:C8	2.31	0.65
1:A:1154:G:H2'	1:A:1155:G:H8	1.61	0.65
5:C:86:VAL:O	5:C:89:GLU:HB3	1.96	0.65
5:C:139:GLN:HA	5:C:139:GLN:NE2	2.11	0.65
1:A:695:A:OP2	13:K:53:SER:HB2	1.97	0.65
1:A:1202:G:O2'	1:A:1203:C:H5'	1.96	0.65
9:G:115:ARG:HB2	9:G:118:VAL:HG23	1.79	0.65
20:R:36:ASN:O	20:R:39:VAL:HG12	1.96	0.65
1:A:1230:C:O2'	1:A:1231:G:H5'	1.95	0.65
13:K:15:ALA:HA	13:K:77:MET:HA	1.78	0.65
14:L:55:VAL:CG1	14:L:67:THR:HG23	2.27	0.65
17:O:77:ARG:O	17:O:80:ALA:HB3	1.96	0.65
19:Q:53:LEU:HG	19:Q:82:MET:HE1	1.77	0.65
21:S:33:THR:HG22	21:S:34:TRP:N	2.11	0.65
1:A:1234:C:O2'	1:A:1235:U:H5'	1.96	0.65
5:C:139:GLN:HE21	5:C:139:GLN:CA	2.10	0.65
14:L:43:VAL:HG12	14:L:44:THR:N	2.10	0.65
14:L:54:LYS:N	14:L:54:LYS:HE3	2.11	0.65
21:S:44:MET:O	21:S:62:ILE:HG21	1.96	0.65
23:V:23:PRO:C	23:V:25:LYS:H	2.03	0.65
1:A:406:G:H21	6:D:119:GLN:HE22	1.43	0.65
1:A:430:A:C2'	1:A:431:A:H5''	2.26	0.65
5:C:40:ARG:HB3	5:C:44:GLU:OE2	1.97	0.65
5:C:139:GLN:O	5:C:143:GLU:HG3	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:18:TYR:HB3	9:G:59:LEU:HD22	1.78	0.65
15:M:26:GLY:O	15:M:28:ALA:N	2.29	0.65
15:M:37:THR:CG2	15:M:55:ARG:HD2	2.26	0.65
15:M:49:THR:HG22	15:M:51:ALA:N	2.12	0.65
1:A:1229:A:H1'	15:M:125:ARG:HD3	1.78	0.65
13:K:126:ARG:C	13:K:128:ALA:H	2.04	0.65
1:A:1363:A:H1'	1:A:1365:G:N7	2.12	0.65
4:B:178:ARG:HH11	4:B:178:ARG:CG	2.07	0.65
5:C:83:ARG:C	5:C:85:ARG:H	2.04	0.65
6:D:8:VAL:C	6:D:10:ARG:H	2.05	0.65
5:C:3:ASN:O	5:C:4:LYS:HB2	1.97	0.65
7:E:126:ARG:HG3	7:E:126:ARG:NH1	2.00	0.65
14:L:54:LYS:HG2	14:L:75:HIS:CE1	2.32	0.65
15:M:37:THR:HG22	15:M:39:ILE:HG13	1.77	0.65
1:A:444:C:H2'	1:A:445:G:H8	1.62	0.65
1:A:691:G:O6	13:K:52:GLY:HA2	1.97	0.65
1:A:1223:C:P	21:S:78:ARG:NH1	2.70	0.65
8:F:97:PHE:HB2	20:R:32:ARG:NH2	2.12	0.65
12:J:45:ARG:O	12:J:64:GLU:HA	1.97	0.65
19:Q:9:VAL:HG21	19:Q:84:LEU:HD13	1.77	0.65
12:J:90:LEU:N	12:J:91:PRO:CD	2.60	0.64
1:A:76:C:O2'	1:A:77:G:H5'	1.98	0.64
1:A:129(A):G:O2'	1:A:190(E):U:H2'	1.97	0.64
1:A:392:G:H2'	1:A:393:A:C8	2.33	0.64
1:A:1151:A:HO2'	1:A:1152:A:H8	1.45	0.64
7:E:75:THR:HG23	7:E:76:ILE:N	2.12	0.64
7:E:101:ILE:HD12	7:E:119:LEU:CD2	2.27	0.64
13:K:14:VAL:HG21	13:K:40:ILE:HD11	1.77	0.64
1:A:1256:A:H5'	1:A:1258:G:H1'	1.78	0.64
4:B:72:GLY:HA3	4:B:81:VAL:HG21	1.79	0.64
1:A:314:C:O2'	1:A:315:A:H5'	1.97	0.64
1:A:350:G:H5'	1:A:350:G:H8	1.63	0.64
1:A:460:A:N6	1:A:463:A:C6	2.65	0.64
1:A:501:C:H2'	1:A:502:G:H8	1.62	0.64
1:A:939:G:H2'	1:A:940:C:C6	2.32	0.64
1:A:1148:U:H2'	1:A:1149:C:O4'	1.96	0.64
4:B:102:LEU:HD21	4:B:162:ILE:CD1	2.28	0.64
5:C:134:ILE:HD11	5:C:153:VAL:CG2	2.27	0.64
8:F:80:ARG:NH1	8:F:88:VAL:HB	2.12	0.64
15:M:4:ILE:HG22	15:M:5:ALA:N	2.13	0.64
16:N:9:LYS:C	16:N:11:LYS:H	2.05	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:590:C:O2'	1:A:591:U:H5'	1.98	0.64
1:A:1112:C:H1'	5:C:179:ARG:HH21	1.61	0.64
1:A:1477:C:H2'	1:A:1478:C:C6	2.33	0.64
4:B:30:ARG:HG3	4:B:31:TYR:N	2.12	0.64
5:C:14:ILE:HG22	5:C:15:THR:N	2.09	0.64
6:D:8:VAL:HB	6:D:21:LEU:HD12	1.79	0.64
10:H:92:ARG:HH11	10:H:92:ARG:CG	2.10	0.64
19:Q:97:SER:HA	19:Q:102:GLY:O	1.97	0.64
21:S:15:LEU:HD12	21:S:16:LEU:N	2.13	0.64
1:A:390:C:H2'	1:A:391:G:H8	1.62	0.64
12:J:29:ARG:N	12:J:29:ARG:HD3	2.12	0.64
15:M:88:ARG:HG3	15:M:98:VAL:HG11	1.79	0.64
5:C:79:ARG:HG2	5:C:82:GLU:CB	2.23	0.64
12:J:32:ALA:CB	12:J:75:ILE:HB	2.27	0.64
1:A:1182:G:O2'	1:A:1183:A:OP2	2.15	0.64
4:B:84:GLU:HB3	4:B:219:VAL:CG2	2.25	0.64
10:H:83:ILE:HG23	10:H:83:ILE:O	1.98	0.64
14:L:75:HIS:HD2	14:L:77:LEU:H	1.44	0.64
1:A:723:U:O2	1:A:723:U:H2'	1.98	0.64
1:A:1368:G:O2'	1:A:1369:C:H5'	1.97	0.64
4:B:139:LYS:HD3	4:B:139:LYS:C	2.22	0.64
12:J:39:PRO:O	12:J:40:LEU:HB2	1.98	0.64
4:B:223:ILE:C	4:B:225:ALA:H	2.05	0.64
5:C:191:THR:CG2	5:C:192:THR:N	2.60	0.64
1:A:1145:C:O2'	1:A:1146:A:H8	1.81	0.63
6:D:62:GLN:NE2	6:D:65:ARG:HH12	1.96	0.63
1:A:1320:C:N3	21:S:36:ARG:HD3	2.12	0.63
10:H:38:ILE:HD12	10:H:38:ILE:H	1.61	0.63
14:L:89:ARG:HA	14:L:97:ARG:HA	1.80	0.63
1:A:28:G:O2'	1:A:296:U:OP1	2.16	0.63
1:A:107:G:C2'	1:A:108:G:H5'	2.28	0.63
1:A:1161:C:H2'	1:A:1162:C:C6	2.34	0.63
4:B:77:ALA:HB2	4:B:211:ILE:HD13	1.80	0.63
11:I:70:LYS:O	11:I:74:ILE:HG13	1.98	0.63
12:J:86:MET:HA	12:J:86:MET:HE3	1.79	0.63
1:A:1064:G:H4'	1:A:1065:U:C5'	2.28	0.63
1:A:1133:G:H2'	1:A:1134:G:H8	1.63	0.63
1:A:1149:C:H2'	1:A:1150:U:C6	2.34	0.63
15:M:15:VAL:HG23	15:M:43:THR:O	1.99	0.63
1:A:748:C:HO2'	1:A:749:C:H6	1.41	0.63
4:B:178:ARG:HG3	4:B:178:ARG:NH1	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:101:VAL:O	14:L:101:VAL:HG12	1.96	0.63
1:A:895:G:H2'	1:A:896:C:H6	1.64	0.63
1:A:1330:U:H2'	1:A:1331:G:H5'	1.80	0.63
4:B:84:GLU:OE1	4:B:216:SER:HA	1.99	0.63
5:C:180:ALA:CB	5:C:182:ILE:HG13	2.29	0.63
9:G:78:ARG:HB2	9:G:156:TRP:CZ3	2.33	0.63
1:A:627:G:O2'	1:A:628:G:H5'	1.99	0.63
1:A:1095:U:H2'	1:A:1096:C:C6	2.34	0.63
1:A:1351:U:O2'	1:A:1352:C:H5'	1.99	0.63
1:A:1370:G:O2'	1:A:1371:G:H5'	1.99	0.63
4:B:19:HIS:HE2	4:B:206:ASP:CB	2.10	0.63
10:H:20:TYR:HE2	10:H:75:ARG:HD2	1.63	0.63
12:J:75:ILE:HG22	12:J:76:ASN:H	1.64	0.63
17:O:39:LEU:HD23	17:O:39:LEU:C	2.24	0.63
5:C:193:TYR:HE1	5:C:196:LEU:HD21	1.63	0.62
12:J:71:LEU:O	12:J:72:VAL:HB	1.98	0.62
1:A:753:A:C2	10:H:1:MET:HE2	2.34	0.62
4:B:95:GLN:C	4:B:96:ARG:HD2	2.24	0.62
9:G:59:LEU:O	9:G:63:LYS:HG2	2.00	0.62
10:H:38:ILE:HD12	10:H:38:ILE:N	2.14	0.62
12:J:36:GLY:O	12:J:72:VAL:HA	1.98	0.62
14:L:46:LYS:HG2	14:L:92:ASP:O	1.99	0.62
11:I:127:LYS:HE3	11:I:127:LYS:N	2.14	0.62
15:M:49:THR:HB	15:M:52:GLU:OE1	1.98	0.62
1:A:666:G:H5'	1:A:726:C:H1'	1.82	0.62
1:A:1010:G:H2'	1:A:1011:G:H8	1.65	0.62
5:C:47:LEU:CD2	5:C:68:VAL:HG11	2.29	0.62
5:C:58:GLU:HB3	12:J:92:THR:CG2	2.28	0.62
1:A:328:C:O2	1:A:328:C:C2'	2.48	0.62
1:A:392:G:H2'	1:A:393:A:H8	1.64	0.62
1:A:1144:G:N2	1:A:1146:A:H62	1.97	0.62
13:K:110:ASP:HB2	20:R:88:LYS:NZ	2.15	0.62
14:L:33:ARG:HG2	14:L:62:SER:HB3	1.81	0.62
1:A:190(L):U:O2'	1:A:191:G:H5'	1.99	0.62
5:C:148:GLY:HA3	5:C:172:ARG:O	1.99	0.62
12:J:31:GLY:CA	12:J:76:ASN:HD21	2.11	0.62
1:A:188:C:H6	1:A:188:C:H5''	1.64	0.62
1:A:639:G:O2'	1:A:640:A:H5'	1.99	0.62
1:A:1298:C:H2'	9:G:114:ARG:HH12	1.63	0.62
1:A:1495:U:H2'	1:A:1496:C:H6	1.64	0.62
1:A:528:C:H5'	1:A:535:A:C6	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:153:ARG:CZ	6:D:181:MET:HE3	2.30	0.62
11:I:93:ARG:NH1	11:I:93:ARG:HB3	2.14	0.62
14:L:25:PRO:C	14:L:27:LEU:H	2.07	0.62
21:S:63:THR:HG22	21:S:64:GLU:N	2.15	0.62
1:A:1488:G:O2'	1:A:1489:G:H5'	1.99	0.62
15:M:40:ASN:HD22	15:M:40:ASN:C	2.07	0.62
18:P:59:TRP:HB3	18:P:64:ALA:HB2	1.81	0.62
1:A:1152:A:H2'	1:A:1153:C:H6	1.64	0.62
8:F:23:LYS:O	8:F:27:GLN:HG2	2.00	0.62
1:A:107:G:H2'	1:A:108:G:H5'	1.82	0.61
1:A:1196:U:H4'	1:A:1197:G:OP2	1.99	0.61
6:D:153:ARG:HE	6:D:181:MET:HE3	1.64	0.61
10:H:116:LYS:NZ	10:H:127:LEU:HB3	2.16	0.61
13:K:121:PRO:HG2	13:K:126:ARG:HG2	1.82	0.61
15:M:3:ARG:HB2	15:M:3:ARG:NH1	2.14	0.61
21:S:71:LEU:H	21:S:71:LEU:HD12	1.65	0.61
1:A:409:G:OP2	1:A:431:A:H8	1.82	0.61
1:A:412:A:H5'	1:A:417:C:C5	2.35	0.61
1:A:437:U:C2'	1:A:438:G:H5'	2.30	0.61
1:A:919:A:O2'	1:A:920:U:H5'	1.99	0.61
1:A:975:A:H5'	1:A:975:A:H8	1.65	0.61
1:A:1003:G:N2	1:A:1004:A:H1'	2.16	0.61
1:A:1347:G:N2	1:A:1373:G:H2'	2.14	0.61
1:A:1521:G:H2'	1:A:1522:U:C6	2.35	0.61
20:R:47:THR:HG22	20:R:48:GLY:N	2.14	0.61
1:A:1104:G:OP1	4:B:111:ARG:HD2	2.00	0.61
4:B:124:SER:O	4:B:127:ILE:HG12	2.00	0.61
16:N:37:PHE:CE2	16:N:53:LEU:HD13	2.35	0.61
1:A:575:G:OP1	1:A:575:G:H4'	1.99	0.61
4:B:8:LYS:HD3	4:B:9:GLU:H	1.65	0.61
5:C:40:ARG:HG2	5:C:55:VAL:HG11	1.82	0.61
5:C:54:ARG:HG3	5:C:55:VAL:H	1.65	0.61
14:L:75:HIS:CD2	14:L:77:LEU:H	2.17	0.61
1:A:791:G:H2'	1:A:792:A:C5'	2.31	0.61
1:A:302:G:H5''	14:L:17:LYS:HZ1	1.66	0.61
1:A:1005:A:H1'	1:A:1026:G:H22	1.64	0.61
1:A:1068:G:OP2	1:A:1068:G:H8	1.82	0.61
4:B:231:GLU:H	4:B:231:GLU:CD	2.08	0.61
8:F:66:GLU:HG3	8:F:66:GLU:O	2.01	0.61
7:E:57:LYS:HG2	7:E:61:TYR:CE2	2.35	0.61
10:H:10:LEU:HD22	10:H:83:ILE:HD11	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:6:ARG:HG3	23:V:7:ARG:HD2	1.83	0.61
1:A:26:A:N6	1:A:558:G:H1'	2.16	0.61
9:G:51:GLN:C	9:G:53:LYS:H	2.09	0.61
17:O:33:THR:HG23	17:O:63:ARG:NH1	2.15	0.61
9:G:122:HIS:HD2	9:G:125:MET:HE3	1.66	0.61
21:S:40:ILE:HG21	21:S:62:ILE:CD1	2.31	0.61
1:A:996:A:H2'	1:A:997:U:C6	2.36	0.60
1:A:1124:G:H5'	12:J:35:SER:HB3	1.82	0.60
1:A:1391:U:H2'	1:A:1392:G:H8	1.64	0.60
4:B:38:GLY:C	4:B:39:ILE:HD12	2.26	0.60
4:B:178:ARG:NH2	4:B:196:LEU:HA	2.16	0.60
5:C:10:PHE:CE2	5:C:178:LEU:HD13	2.36	0.60
5:C:21:ARG:HD3	5:C:58:GLU:HG2	1.82	0.60
12:J:45:ARG:NH2	16:N:36:PHE:CD2	2.69	0.60
12:J:47:PHE:CE2	16:N:37:PHE:HE1	2.19	0.60
15:M:40:ASN:ND2	15:M:42:ALA:H	1.99	0.60
5:C:41:GLY:O	5:C:45:LYS:HG2	2.01	0.60
11:I:118:LYS:O	11:I:119:ALA:CB	2.49	0.60
12:J:51:ARG:H	12:J:59:SER:HB2	1.66	0.60
1:A:184:G:H2'	1:A:185:A:H8	1.66	0.60
1:A:409:G:H3'	1:A:431:A:N7	2.17	0.60
4:B:139:LYS:NZ	4:B:142:LEU:HD23	2.15	0.60
16:N:8:GLU:OE1	16:N:8:GLU:C	2.45	0.60
1:A:269:C:H2'	1:A:270:A:C8	2.36	0.60
1:A:352:C:H4'	1:A:354:G:OP1	2.01	0.60
1:A:413:G:H1'	1:A:416:G:OP1	2.02	0.60
1:A:794:A:H2'	1:A:795:C:C6	2.35	0.60
1:A:975:A:H5'	1:A:975:A:C8	2.36	0.60
5:C:89:GLU:O	5:C:93:LYS:HB2	2.00	0.60
15:M:97:PRO:HB2	15:M:101:GLN:OE1	2.00	0.60
22:T:21:LYS:HB2	22:T:21:LYS:HZ2	1.65	0.60
1:A:664:G:OP1	20:R:64:ARG:HD2	2.00	0.60
1:A:1443:G:H5''	1:A:1446:A:H5'	1.83	0.60
1:A:1527:C:O2'	1:A:1528:U:H5'	2.01	0.60
4:B:25:ASN:ND2	4:B:27:LYS:H	1.99	0.60
4:B:96:ARG:O	4:B:98:LEU:HD23	2.01	0.60
4:B:112:VAL:C	4:B:114:ARG:H	2.08	0.60
4:B:132:LYS:HD3	4:B:135:GLN:HB2	1.83	0.60
5:C:22:TRP:CH2	5:C:32:LEU:HB2	2.37	0.60
12:J:21:GLN:HE21	12:J:25:GLU:HG2	1.66	0.60
12:J:75:ILE:HG22	12:J:76:ASN:N	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:69:LYS:H	19:Q:70:ARG:HD2	1.67	0.60
1:A:1347:G:O2'	1:A:1348:U:P	2.59	0.60
4:B:111:ARG:HB3	4:B:149:LEU:HD11	1.83	0.60
12:J:49:VAL:CG2	16:N:41:ARG:HB2	2.30	0.60
21:S:6:LYS:H	21:S:6:LYS:CD	2.11	0.60
1:A:547:A:H4'	1:A:548:G:O5'	2.01	0.60
1:A:1152:A:H5'	12:J:70:ARG:HH22	1.67	0.60
5:C:47:LEU:H	5:C:47:LEU:HD12	1.67	0.60
6:D:153:ARG:NH2	6:D:181:MET:HE3	2.17	0.60
11:I:89:ASN:HD21	11:I:91:ASP:HB2	1.67	0.60
15:M:48:LEU:HD12	15:M:53:VAL:HG22	1.82	0.60
17:O:39:LEU:HD22	17:O:56:LEU:HB2	1.83	0.60
4:B:213:LEU:HD23	4:B:213:LEU:C	2.27	0.60
6:D:23:GLY:HA3	6:D:113:SER:HB3	1.84	0.60
9:G:37:ASN:O	9:G:41:ARG:HG3	2.01	0.60
12:J:3:LYS:N	12:J:3:LYS:HD2	2.17	0.60
17:O:76:GLU:HA	17:O:79:ARG:HH21	1.65	0.60
1:A:149:A:H2'	1:A:150:C:C6	2.37	0.60
1:A:189:G:C2'	1:A:190:C:H5'	2.25	0.60
1:A:190:C:H5'	1:A:190(K):G:N2	2.17	0.60
1:A:1128:C:O2'	1:A:1130:A:H8	1.84	0.60
1:A:1497:G:C2'	1:A:1498:U:H5'	2.31	0.60
14:L:26:ALA:O	14:L:27:LEU:O	2.20	0.60
14:L:58:VAL:O	14:L:65:GLU:HA	2.01	0.60
19:Q:76:LEU:HD23	19:Q:77:VAL:N	2.17	0.60
1:A:408:A:C4'	1:A:429:U:O2	2.48	0.60
1:A:453:A:H4'	18:P:72:ARG:HG3	1.84	0.60
1:A:620:C:N1	6:D:135:LEU:HD13	2.16	0.60
21:S:42:PRO:O	21:S:45:VAL:HG23	2.00	0.60
1:A:255:G:H1'	19:Q:16:GLN:OE1	2.02	0.59
4:B:74:LYS:HZ1	4:B:206:ASP:HB2	1.66	0.59
13:K:126:ARG:O	13:K:128:ALA:N	2.35	0.59
15:M:48:LEU:HD12	15:M:53:VAL:CG2	2.32	0.59
17:O:39:LEU:HD23	17:O:39:LEU:O	2.02	0.59
1:A:748:C:O2'	1:A:749:C:C6	2.54	0.59
1:A:1020:U:H2'	1:A:1021:G:C8	2.37	0.59
4:B:177:ALA:O	4:B:180:LEU:N	2.29	0.59
6:D:126:ILE:HG22	6:D:127:THR:H	1.66	0.59
8:F:19:LEU:C	8:F:19:LEU:HD23	2.27	0.59
8:F:25:ILE:HD12	8:F:82:ARG:HH11	1.67	0.59
13:K:14:VAL:HG12	13:K:16:SER:H	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:101:ARG:HA	19:Q:101:ARG:HE	1.65	0.59
1:A:502:G:H4'	1:A:550:G:H4'	1.84	0.59
1:A:750:G:N3	17:O:23:GLY:HA3	2.17	0.59
1:A:1062:U:H2'	1:A:1063:C:C6	2.36	0.59
4:B:185:ILE:N	4:B:185:ILE:HD12	2.16	0.59
5:C:18:TRP:HE3	5:C:18:TRP:H	1.49	0.59
10:H:112:LEU:C	10:H:112:LEU:HD12	2.27	0.59
11:I:86:VAL:HG13	11:I:90:PRO:HA	1.83	0.59
1:A:1121:U:O2'	1:A:1122:U:H5'	2.01	0.59
1:A:1251:A:H4'	11:I:12:GLU:OE2	2.03	0.59
1:A:1367:C:H5'	12:J:60:ARG:NH1	2.17	0.59
1:A:1510:U:H2'	1:A:1511:G:C8	2.36	0.59
4:B:166:ASP:OD2	4:B:169:LYS:HB2	2.02	0.59
12:J:4:ILE:HD11	12:J:74:ILE:CD1	2.25	0.59
16:N:26:ARG:HH11	16:N:43:CYS:HB3	1.66	0.59
19:Q:14:LYS:H	19:Q:14:LYS:CD	2.14	0.59
1:A:730:G:H21	1:A:765:G:H5''	1.67	0.59
4:B:17:PHE:HA	4:B:42:ILE:HB	1.84	0.59
4:B:178:ARG:CG	4:B:178:ARG:NH1	2.65	0.59
5:C:91:LEU:HD21	5:C:99:VAL:HG22	1.83	0.59
7:E:9:LYS:HB3	7:E:33:VAL:HG23	1.82	0.59
13:K:51:LYS:HE2	13:K:52:GLY:N	2.18	0.59
16:N:9:LYS:C	16:N:9:LYS:HD3	2.28	0.59
1:A:266:G:H5'	1:A:266:G:C8	2.37	0.59
1:A:960:U:O2	1:A:960:U:H2'	2.03	0.59
4:B:22:LYS:HG3	4:B:35:GLU:OE1	2.02	0.59
4:B:103:THR:HG23	4:B:176:GLU:OE1	2.02	0.59
7:E:33:VAL:CG1	7:E:109:ILE:HG12	2.25	0.59
7:E:36:ASP:OD1	7:E:38:GLN:N	2.31	0.59
13:K:22:HIS:HB3	13:K:29:ILE:HG13	1.85	0.59
14:L:39:VAL:H	14:L:57:LYS:HB2	1.67	0.59
16:N:9:LYS:C	16:N:11:LYS:N	2.60	0.59
5:C:55:VAL:O	5:C:55:VAL:HG12	2.01	0.59
7:E:53:LEU:H	7:E:53:LEU:CD1	2.15	0.59
9:G:115:ARG:HB2	9:G:118:VAL:CG2	2.33	0.59
18:P:67:THR:HG22	18:P:68:ASP:N	2.17	0.59
21:S:22:LEU:C	21:S:24:ALA:H	2.11	0.59
1:A:1091:U:O2	1:A:1093:A:C8	2.56	0.59
5:C:91:LEU:HD23	5:C:92:ALA:H	1.67	0.59
7:E:103:GLY:O	7:E:106:PRO:HD2	2.03	0.59
11:I:9:ARG:CG	11:I:14:VAL:HG22	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:882:C:O2'	1:A:883:C:H5'	2.02	0.59
6:D:187:ARG:HD2	6:D:188:LEU:H	1.67	0.59
7:E:9:LYS:HB3	7:E:33:VAL:CG2	2.33	0.59
9:G:76:ARG:HD2	9:G:89:MET:HE2	1.83	0.59
13:K:57:THR:OG1	13:K:58:PRO:HD2	2.03	0.59
18:P:81:ARG:HH21	18:P:82:GLN:HG2	1.66	0.59
1:A:1020:U:H2'	1:A:1021:G:H8	1.67	0.59
1:A:1117:G:H21	1:A:1180:A:H1'	1.68	0.59
1:A:1216:G:O2'	1:A:1217:C:H5'	2.03	0.59
7:E:37:ARG:HG2	7:E:37:ARG:HH11	1.68	0.59
10:H:69:ARG:NH1	10:H:75:ARG:O	2.35	0.59
12:J:5:ARG:HA	12:J:73:ASP:OD1	2.02	0.59
14:L:27:LEU:HG	14:L:28:LYS:H	1.68	0.59
15:M:9:ILE:HD12	15:M:9:ILE:N	2.17	0.59
20:R:39:VAL:O	20:R:42:ARG:HB2	2.03	0.59
1:A:254:G:OP1	19:Q:67:LYS:O	2.20	0.58
1:A:344:A:H5''	1:A:345:C:H5	1.67	0.58
1:A:662:G:H2'	1:A:663:A:C8	2.38	0.58
1:A:694:A:C3'	1:A:695:A:H5''	2.32	0.58
10:H:45:ILE:O	10:H:46:LYS:C	2.46	0.58
16:N:3:ARG:NH1	16:N:6:LEU:HD11	2.17	0.58
5:C:46:GLU:O	5:C:48:TYR:N	2.36	0.58
5:C:116:VAL:HG21	5:C:202:ILE:HD11	1.85	0.58
5:C:134:ILE:O	5:C:138:VAL:HG23	2.02	0.58
5:C:154:SER:O	5:C:165:THR:HA	2.02	0.58
10:H:51:VAL:HG12	10:H:52:ASP:N	2.18	0.58
10:H:63:LEU:HD22	10:H:63:LEU:H	1.68	0.58
10:H:77:GLU:HG2	10:H:78:GLN:N	2.19	0.58
22:T:54:LYS:HG3	22:T:100:ILE:HD12	1.85	0.58
1:A:977:A:C2'	1:A:978:A:H5''	2.33	0.58
4:B:8:LYS:CD	4:B:9:GLU:H	2.16	0.58
4:B:184:VAL:HG12	4:B:197:VAL:HG13	1.85	0.58
4:B:206:ASP:O	4:B:207:ALA:HB3	2.03	0.58
5:C:19:GLU:HB3	5:C:40:ARG:HH21	1.67	0.58
15:M:125:ARG:HD2	15:M:125:ARG:O	2.02	0.58
1:A:839:U:O2	1:A:839:U:H2'	2.02	0.58
5:C:34:LEU:HG	16:N:25:VAL:HG21	1.83	0.58
5:C:108:ASN:HD22	5:C:111:LEU:HG	1.68	0.58
9:G:135:VAL:O	9:G:139:GLU:HG3	2.02	0.58
20:R:42:ARG:HG3	20:R:42:ARG:HH11	1.69	0.58
21:S:15:LEU:O	21:S:19:VAL:HG12	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:A:HO2'	1:A:417:C:HO2'	1.51	0.58
1:A:459:G:H3'	1:A:460:A:H5''	1.84	0.58
1:A:792:A:H1'	1:A:794:A:N7	2.19	0.58
4:B:24:TRP:HB3	4:B:40:HIS:CE1	2.39	0.58
8:F:33:TYR:O	8:F:35:ALA:N	2.36	0.58
10:H:103:VAL:CG2	10:H:110:ALA:HB2	2.33	0.58
14:L:46:LYS:HE3	14:L:47:LYS:HB2	1.86	0.58
17:O:17:ARG:NH1	17:O:77:ARG:NH1	2.51	0.58
22:T:54:LYS:HE3	22:T:100:ILE:HD11	1.85	0.58
1:A:883:C:O2'	1:A:884:U:H5'	2.04	0.58
1:A:1117:G:H5'	1:A:1117:G:H8	1.68	0.58
1:A:1216:G:H5''	16:N:5:ALA:CB	2.34	0.58
6:D:36:ARG:HG2	6:D:36:ARG:HH11	1.68	0.58
22:T:24:LEU:HA	22:T:27:LYS:HE2	1.84	0.58
1:A:179:A:H2'	1:A:180:U:C6	2.38	0.58
1:A:413:G:OP2	1:A:417:C:H5''	2.03	0.58
1:A:560:U:H5'	1:A:566:G:N2	2.18	0.58
1:A:1225:A:H2'	1:A:1225:A:N3	2.18	0.58
1:A:1407:C:O2'	1:A:1408:A:H5'	2.03	0.58
5:C:34:LEU:HD23	5:C:34:LEU:O	2.02	0.58
14:L:50:SER:O	14:L:51:ALA:HB2	2.03	0.58
14:L:67:THR:HG21	14:L:96:VAL:HG22	1.84	0.58
5:C:47:LEU:HD12	5:C:47:LEU:N	2.19	0.58
7:E:152:ARG:HA	10:H:64:LYS:HZ1	1.68	0.58
9:G:121:ALA:O	9:G:125:MET:HG3	2.03	0.58
12:J:32:ALA:HB1	12:J:75:ILE:HD13	1.85	0.58
19:Q:45:HIS:CD2	19:Q:47:PRO:HG3	2.38	0.58
22:T:70:SER:HA	22:T:73:HIS:CD2	2.38	0.58
22:T:75:ASN:N	22:T:75:ASN:OD1	2.35	0.58
1:A:45:U:H2'	1:A:46:G:C8	2.39	0.58
1:A:748:C:OP2	1:A:748:C:H6	1.87	0.58
1:A:996:A:H2	1:A:1045:C:HO2'	1.51	0.58
1:A:1016:A:H2'	1:A:1017:G:O4'	2.04	0.58
1:A:1033:G:H2'	1:A:1034:G:H8	1.68	0.58
1:A:1072:G:H2'	1:A:1073:U:C6	2.39	0.58
4:B:25:ASN:ND2	4:B:27:LYS:N	2.51	0.58
12:J:29:ARG:HH12	12:J:84:GLN:NE2	1.95	0.58
15:M:32:GLU:OE1	15:M:64:TRP:HZ2	1.87	0.58
15:M:94:ARG:HG3	15:M:94:ARG:NH1	2.17	0.58
16:N:11:LYS:HB2	16:N:11:LYS:NZ	2.19	0.58
20:R:43:PHE:HA	20:R:51:LEU:HD12	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:731:G:OP1	1:A:766:A:H1'	2.04	0.58
1:A:1277:C:H2'	1:A:1278:U:H5'	1.86	0.58
1:A:1402:C:O2	1:A:1500:A:N1	2.37	0.58
4:B:75:LYS:HE2	4:B:96:ARG:HH12	1.69	0.58
4:B:98:LEU:HD23	4:B:98:LEU:N	2.19	0.58
4:B:98:LEU:O	4:B:101:MET:HG3	2.04	0.58
5:C:47:LEU:H	5:C:47:LEU:CD1	2.17	0.58
7:E:79:GLU:HG3	7:E:93:PRO:CD	2.33	0.58
14:L:46:LYS:CG	14:L:47:LYS:H	2.16	0.58
1:A:371:G:C2'	1:A:372:C:H5'	2.34	0.57
1:A:409:G:H5'	1:A:430:A:C6	2.38	0.57
1:A:865:A:H5'	1:A:1078:U:O4	2.04	0.57
1:A:1435:G:H2'	1:A:1436:U:H6	1.67	0.57
6:D:61:LYS:HD2	6:D:207:TYR:OH	2.03	0.57
7:E:76:ILE:HD12	7:E:118:ILE:HD12	1.85	0.57
10:H:60:ARG:HH11	10:H:60:ARG:HG3	1.69	0.57
13:K:70:LYS:O	13:K:73:MET:N	2.36	0.57
13:K:84:VAL:HG21	20:R:88:LYS:HD2	1.86	0.57
21:S:63:THR:HG22	21:S:65:ASN:H	1.69	0.57
1:A:427:U:OP1	6:D:13:ARG:NH2	2.36	0.57
1:A:1066:C:O2'	1:A:1067:A:H5'	2.04	0.57
5:C:60:ALA:O	5:C:61:ALA:HB2	2.04	0.57
6:D:158:ILE:HG23	6:D:162:LEU:HD12	1.86	0.57
8:F:86:ARG:O	8:F:87:ARG:HG2	2.04	0.57
9:G:15:ASP:HB3	9:G:19:GLY:H	1.67	0.57
22:T:96:GLY:O	22:T:97:ALA:HB3	2.03	0.57
7:E:79:GLU:OE1	7:E:79:GLU:N	2.37	0.57
8:F:93:SER:O	8:F:94:GLN:HG3	2.03	0.57
11:I:40:LEU:O	11:I:41:VAL:C	2.47	0.57
22:T:100:ILE:C	22:T:102:GLY:N	2.59	0.57
1:A:409:G:H22	1:A:432:A:C3'	2.17	0.57
1:A:423:G:C8	1:A:424:G:N3	2.72	0.57
1:A:556:C:C2'	1:A:557:G:H5'	2.33	0.57
4:B:122:PHE:C	4:B:127:ILE:HG21	2.30	0.57
7:E:144:THR:HB	7:E:147:ASP:OD1	2.05	0.57
21:S:30:LEU:O	21:S:31:ILE:HD13	2.04	0.57
1:A:376:G:OP2	18:P:67:THR:HG21	2.04	0.57
1:A:425:G:O2'	1:A:426:G:H5'	2.05	0.57
1:A:1195:C:H3'	1:A:1196:U:H5'	1.86	0.57
1:A:1330:U:C2'	1:A:1331:G:H5'	2.33	0.57
4:B:80:ILE:HD13	4:B:212:GLN:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:15:ARG:C	7:E:16:THR:HG23	2.29	0.57
9:G:144:MET:O	9:G:145:ALA:C	2.47	0.57
12:J:12:ASP:OD1	12:J:14:LYS:N	2.36	0.57
15:M:23:TYR:HB3	15:M:67:GLU:CA	2.34	0.57
21:S:28:LYS:CG	21:S:29:ARG:H	2.14	0.57
1:A:429:U:H2'	6:D:25:ARG:HH12	1.68	0.57
1:A:1121:U:H2'	1:A:1122:U:H6	1.69	0.57
1:A:1262:C:H2'	1:A:1263:C:H6	1.69	0.57
4:B:18:GLY:N	4:B:42:ILE:H	2.02	0.57
7:E:144:THR:HG22	7:E:146:ALA:N	2.18	0.57
9:G:78:ARG:NH1	9:G:154:TYR:HB3	2.19	0.57
18:P:81:ARG:NE	18:P:81:ARG:CA	2.65	0.57
1:A:617:G:H5'	18:P:45:THR:HG22	1.87	0.57
1:A:1006:C:H2'	1:A:1007:C:C6	2.33	0.57
19:Q:80:GLY:O	19:Q:81:ARG:HB3	2.04	0.57
21:S:51:VAL:O	21:S:58:VAL:N	2.37	0.57
21:S:51:VAL:HG21	21:S:71:LEU:HB3	1.86	0.57
1:A:474:G:H5'	1:A:475:G:C8	2.40	0.57
1:A:476:G:H21	1:A:478:A:H5''	1.68	0.57
4:B:35:GLU:HA	4:B:39:ILE:O	2.04	0.57
4:B:39:ILE:HD12	4:B:39:ILE:N	2.19	0.57
5:C:30:ARG:HG2	5:C:30:ARG:HH11	1.69	0.57
1:A:112:G:H4'	1:A:389:A:H5''	1.86	0.57
1:A:1016:A:H8	1:A:1016:A:O5'	1.87	0.57
1:A:1103:C:H5''	4:B:98:LEU:CD1	2.35	0.57
1:A:1279:A:H5''	1:A:1280:A:OP1	2.05	0.57
9:G:75:VAL:CG2	9:G:86:GLN:HB3	2.34	0.57
9:G:80:VAL:HG22	9:G:83:ALA:O	2.04	0.57
12:J:26:ALA:C	12:J:84:GLN:HE21	2.12	0.57
1:A:918:A:H2'	1:A:919:A:C8	2.39	0.57
1:A:1112:C:H1'	5:C:179:ARG:NH2	2.20	0.57
1:A:1280:A:O4'	12:J:41:PRO:HG3	2.04	0.57
4:B:15:VAL:HG13	4:B:209:ARG:HG3	1.87	0.57
4:B:30:ARG:HG3	4:B:31:TYR:H	1.69	0.57
5:C:79:ARG:CG	5:C:82:GLU:HB2	2.22	0.57
7:E:24:ARG:HH11	7:E:24:ARG:CB	2.18	0.57
8:F:71:ARG:O	8:F:73:ASN:N	2.38	0.57
9:G:23:VAL:HG13	9:G:43:PHE:CE2	2.40	0.57
10:H:46:LYS:N	10:H:64:LYS:HG3	2.20	0.57
14:L:24:VAL:O	14:L:24:VAL:HG12	2.03	0.57
15:M:8:GLU:OE1	15:M:22:ILE:HA	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:43:PHE:C	20:R:51:LEU:HD12	2.30	0.57
1:A:113:G:H1'	1:A:354:G:C5'	2.35	0.56
1:A:1329:A:P	15:M:28:ALA:HB3	2.45	0.56
4:B:224:GLN:O	4:B:224:GLN:HG2	2.05	0.56
10:H:120:THR:HG23	10:H:123:GLU:OE2	2.05	0.56
12:J:44:VAL:HG21	12:J:66:ARG:HH21	1.70	0.56
12:J:90:LEU:H	12:J:91:PRO:HD3	1.68	0.56
15:M:12:ASN:O	15:M:12:ASN:CG	2.48	0.56
17:O:74:ASP:OD1	17:O:76:GLU:HB3	2.04	0.56
1:A:188:C:H5''	1:A:188:C:C6	2.40	0.56
1:A:1244:C:O2'	1:A:1245:A:H5'	2.06	0.56
1:A:1286:A:C8	1:A:1287:A:H4'	2.41	0.56
6:D:62:GLN:HE22	6:D:65:ARG:NH1	2.01	0.56
10:H:97:VAL:HG21	10:H:128:GLY:HA2	1.86	0.56
11:I:3:GLN:HB2	11:I:20:ARG:HD3	1.87	0.56
12:J:4:ILE:HA	12:J:100:THR:CB	2.35	0.56
1:A:112:G:H21	1:A:354:G:C5'	2.15	0.56
1:A:1103:C:H5''	4:B:98:LEU:HD13	1.86	0.56
1:A:1229:A:H2'	1:A:1230:C:C6	2.40	0.56
1:A:1251:A:H2'	1:A:1252:A:H8	1.66	0.56
1:A:1405:G:O2'	1:A:1406:U:H5'	2.04	0.56
5:C:83:ARG:C	5:C:85:ARG:N	2.61	0.56
5:C:107:GLN:O	5:C:108:ASN:HB3	2.05	0.56
6:D:162:LEU:HD13	6:D:181:MET:CG	2.35	0.56
10:H:24:THR:HG23	10:H:61:VAL:HB	1.86	0.56
10:H:24:THR:HG22	10:H:63:LEU:HD21	1.86	0.56
10:H:63:LEU:HD22	10:H:63:LEU:N	2.21	0.56
11:I:10:ARG:HE	11:I:11:LYS:HB2	1.71	0.56
12:J:6:ILE:HD12	12:J:72:VAL:HG11	1.87	0.56
15:M:25:ILE:HG22	15:M:26:GLY:N	2.20	0.56
17:O:17:ARG:HG3	17:O:17:ARG:NH1	2.20	0.56
21:S:43:GLU:H	21:S:43:GLU:CD	2.12	0.56
1:A:168:G:O2'	1:A:169:C:H5'	2.04	0.56
1:A:421:U:H2'	1:A:423:G:OP1	2.04	0.56
1:A:953:G:H1'	15:M:125:ARG:CA	2.35	0.56
1:A:1117:G:N2	1:A:1180:A:H1'	2.19	0.56
4:B:18:GLY:H	4:B:42:ILE:N	2.02	0.56
4:B:228:GLY:O	4:B:229:VAL:C	2.47	0.56
5:C:10:PHE:CZ	5:C:178:LEU:HD13	2.41	0.56
5:C:90:GLU:O	5:C:94:LEU:HD13	2.05	0.56
6:D:64:LEU:HD12	6:D:75:PHE:CZ	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:36:LEU:CD1	10:H:59:LEU:HD13	2.36	0.56
15:M:50:GLU:O	15:M:54:VAL:HG23	2.06	0.56
1:A:376:G:H2'	1:A:377:G:H8	1.71	0.56
1:A:411:A:N6	1:A:426:G:H22	2.04	0.56
1:A:730:G:N2	1:A:765:G:H5''	2.20	0.56
1:A:1256:A:O3'	1:A:1257:U:H4'	2.06	0.56
1:A:1366:C:H2'	1:A:1367:C:C6	2.40	0.56
6:D:105:VAL:HG12	6:D:117:ALA:HB1	1.86	0.56
6:D:205:GLU:HA	6:D:208:SER:OG	2.06	0.56
9:G:149:ARG:O	9:G:149:ARG:HG2	2.06	0.56
1:A:972:C:H4'	12:J:57:LYS:HE2	1.87	0.56
1:A:1090:U:O2'	1:A:1091:U:H5'	2.06	0.56
1:A:1106:G:H5''	5:C:172:ARG:HG2	1.87	0.56
5:C:188:LEU:HD13	5:C:189:ALA:N	2.13	0.56
7:E:102:ALA:HB1	7:E:120:THR:HG21	1.88	0.56
15:M:34:LEU:HD13	15:M:41:PRO:CA	2.32	0.56
22:T:67:ALA:HA	22:T:73:HIS:H	1.69	0.56
1:A:41:G:H2'	1:A:42:G:C8	2.41	0.56
1:A:437:U:H2'	1:A:438:G:H5'	1.88	0.56
1:A:1014:A:C2	1:A:1219:U:H1'	2.40	0.56
1:A:1206:G:H1'	5:C:193:TYR:O	2.06	0.56
2:X:39:C:O5'	2:X:39:C:H6	1.89	0.56
5:C:195:VAL:C	5:C:196:LEU:HD23	2.30	0.56
6:D:15:GLU:HG2	6:D:63:LYS:HG3	1.88	0.56
10:H:48:TYR:HB2	10:H:60:ARG:O	2.06	0.56
12:J:19:SER:OG	12:J:91:PRO:HD3	2.06	0.56
15:M:121:LYS:O	15:M:122:LYS:HB2	2.05	0.56
18:P:81:ARG:O	18:P:83:GLU:N	2.28	0.56
22:T:79:ARG:O	22:T:83:ARG:HG3	2.05	0.56
1:A:397:A:H5'	1:A:398:C:OP1	2.05	0.56
1:A:463:A:N3	18:P:82:GLN:HB2	2.20	0.56
1:A:591:U:OP1	10:H:30:ARG:NE	2.36	0.56
1:A:1262:C:H2'	1:A:1263:C:C6	2.40	0.56
1:A:1475:G:H2'	1:A:1476:G:H8	1.69	0.56
4:B:12:GLU:C	4:B:14:GLY:N	2.63	0.56
5:C:54:ARG:HG3	5:C:55:VAL:N	2.21	0.56
6:D:11:LEU:HD22	6:D:66:ARG:CZ	2.36	0.56
6:D:163:GLU:C	6:D:165:MET:H	2.14	0.56
10:H:119:LEU:HD23	10:H:119:LEU:N	2.19	0.56
13:K:92:GLU:OE1	13:K:92:GLU:HA	2.06	0.56
16:N:14:PRO:O	16:N:15:LYS:CB	2.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:57:ARG:HB2	22:T:57:ARG:NH1	2.19	0.56
22:T:101:GLY:O	22:T:102:GLY:C	2.48	0.56
1:A:129:U:H5'	1:A:129(A):G:OP1	2.05	0.56
1:A:697:U:H2'	1:A:698:G:H5'	1.88	0.56
4:B:71:VAL:CG2	4:B:164:VAL:HA	2.36	0.56
6:D:29:PRO:C	6:D:30:LYS:HG2	2.29	0.56
8:F:27:GLN:O	8:F:31:GLU:HG3	2.06	0.56
10:H:31:PHE:HZ	10:H:134:ILE:HD11	1.69	0.56
12:J:24:VAL:O	12:J:28:ARG:HB2	2.05	0.56
18:P:11:SER:HB3	18:P:14:ASN:HD22	1.70	0.56
21:S:28:LYS:HD3	21:S:31:ILE:CD1	2.36	0.56
1:A:791:G:H2'	1:A:792:A:H5'	1.87	0.56
1:A:1381:U:O2'	1:A:1382:C:H5'	2.05	0.56
4:B:95:GLN:HG3	4:B:148:TYR:HD2	1.71	0.56
5:C:50:ALA:HA	5:C:72:LYS:HG3	1.87	0.56
1:A:834:C:H2'	1:A:835:U:H6	1.71	0.55
1:A:877:C:O2'	1:A:878:G:H5'	2.05	0.55
4:B:75:LYS:C	4:B:77:ALA:H	2.14	0.55
11:I:8:GLY:CA	11:I:79:LEU:HB3	2.37	0.55
21:S:6:LYS:N	21:S:6:LYS:CD	2.64	0.55
1:A:418:C:H2'	1:A:419:C:C2	2.41	0.55
7:E:152:ARG:HA	10:H:64:LYS:NZ	2.21	0.55
8:F:10:LEU:HD12	8:F:59:TYR:O	2.07	0.55
8:F:43:LEU:HD22	8:F:43:LEU:N	2.20	0.55
19:Q:66:SER:O	19:Q:70:ARG:NH1	2.39	0.55
21:S:45:VAL:HA	21:S:62:ILE:HG13	1.87	0.55
1:A:35:G:H2'	1:A:36:C:H6	1.69	0.55
1:A:163:C:O2'	1:A:164:U:H5'	2.07	0.55
1:A:197:A:N1	1:A:220:G:O2'	2.39	0.55
1:A:382:A:H2'	1:A:383:A:C8	2.40	0.55
1:A:1443:G:H5''	1:A:1446:A:C5'	2.37	0.55
1:A:1513:A:H2'	1:A:1514:C:C6	2.41	0.55
1:A:1515:C:O2'	1:A:1516:G:H5'	2.06	0.55
5:C:93:LYS:HB3	5:C:94:LEU:HD12	1.88	0.55
14:L:41:ARG:HH21	14:L:57:LYS:HE2	1.72	0.55
1:A:190(E):U:O2'	19:Q:63:ARG:NH2	2.38	0.55
7:E:109:ILE:O	7:E:109:ILE:HG22	2.06	0.55
11:I:28:VAL:HA	11:I:63:ILE:O	2.06	0.55
13:K:110:ASP:HB2	20:R:88:LYS:CE	2.37	0.55
18:P:4:ILE:HG13	18:P:64:ALA:HB1	1.88	0.55
22:T:24:LEU:HD12	22:T:24:LEU:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:A:O2'	1:A:781:A:H5''	2.07	0.55
1:A:975:A:O2'	16:N:32:SER:HA	2.06	0.55
1:A:1298:C:H4'	1:A:1299:A:O4'	2.06	0.55
4:B:144:ARG:O	4:B:147:LYS:N	2.39	0.55
4:B:207:ALA:O	4:B:210:SER:HB3	2.06	0.55
5:C:180:ALA:HB1	5:C:182:ILE:HG13	1.89	0.55
14:L:117:ARG:NH2	14:L:124:LYS:HA	2.22	0.55
20:R:37:VAL:HG12	20:R:41:LYS:HD3	1.89	0.55
5:C:154:SER:HB3	5:C:197:GLY:H	1.72	0.55
6:D:148:VAL:CG1	6:D:158:ILE:HD13	2.36	0.55
11:I:127:LYS:CD	15:M:126:LYS:HE2	2.36	0.55
12:J:29:ARG:NH1	12:J:84:GLN:HE22	1.98	0.55
1:A:975:A:H4'	1:A:976:G:O5'	2.07	0.55
1:A:1238:A:H5'	1:A:1336:C:N4	2.20	0.55
5:C:58:GLU:O	5:C:59:ARG:HG3	2.06	0.55
8:F:21:LEU:O	8:F:24:GLU:HB3	2.07	0.55
20:R:59:SER:OG	20:R:62:GLU:HG3	2.06	0.55
1:A:393:A:O2'	1:A:394:G:H5'	2.07	0.55
1:A:958:A:C8	21:S:55:LYS:HD2	2.42	0.55
1:A:1126:U:N3	1:A:1127:G:C2	2.75	0.55
1:A:1131:G:H2'	1:A:1132:C:C6	2.41	0.55
1:A:1167:A:H2'	1:A:1168:A:C8	2.42	0.55
4:B:77:ALA:CB	4:B:211:ILE:HD13	2.36	0.55
10:H:35:ILE:HG23	10:H:111:ILE:HG21	1.88	0.55
10:H:103:VAL:HG21	10:H:110:ALA:HB2	1.88	0.55
15:M:11:ARG:HG3	15:M:12:ASN:N	2.21	0.55
15:M:36:LYS:HD2	15:M:59:TYR:CZ	2.42	0.55
15:M:69:GLU:O	15:M:72:ALA:HB3	2.07	0.55
18:P:52:ASP:CG	18:P:55:ARG:HG3	2.31	0.55
1:A:349:A:C3'	1:A:350:G:H5''	2.36	0.55
1:A:353:A:H8	1:A:353:A:C5'	2.20	0.55
1:A:409:G:H5''	1:A:431:A:N7	2.20	0.55
1:A:463:A:H3'	1:A:475:G:O6	2.07	0.55
1:A:959:A:C2	1:A:1222:G:O4'	2.60	0.55
5:C:34:LEU:HD22	5:C:38:ARG:NH2	2.21	0.55
6:D:32:ALA:C	6:D:34:GLU:N	2.61	0.55
7:E:13:ILE:C	7:E:13:ILE:HD12	2.32	0.55
7:E:152:ARG:HB3	10:H:43:GLY:O	2.07	0.55
15:M:19:LEU:HA	15:M:22:ILE:HD13	1.89	0.55
15:M:62:ASN:O	15:M:63:THR:CB	2.55	0.55
1:A:1116:C:H2'	1:A:1117:G:C5'	2.28	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1125:U:H5''	1:A:1126:U:C5	2.42	0.55
1:A:1316:G:H4'	16:N:18:VAL:CG1	2.36	0.55
4:B:115:LEU:HG	4:B:116:GLU:N	2.22	0.55
5:C:64:VAL:HB	5:C:99:VAL:CG2	2.37	0.55
5:C:66:VAL:O	5:C:66:VAL:HG12	2.06	0.55
5:C:73:PRO:O	5:C:76:VAL:HB	2.07	0.55
5:C:84:ILE:O	5:C:88:ARG:HB2	2.06	0.55
15:M:3:ARG:HH11	15:M:3:ARG:CB	2.17	0.55
18:P:81:ARG:C	18:P:83:GLU:N	2.63	0.55
1:A:189:G:C2'	1:A:190(K):G:N2	2.62	0.54
1:A:427:U:OP2	6:D:36:ARG:NH2	2.40	0.54
1:A:760:G:H1	19:Q:105:ALA:HA	1.72	0.54
1:A:1289:A:H2'	1:A:1290:G:H5'	1.89	0.54
4:B:12:GLU:C	4:B:14:GLY:H	2.14	0.54
14:L:41:ARG:NH2	14:L:57:LYS:HE2	2.22	0.54
18:P:28:ARG:HG2	18:P:28:ARG:NH1	2.21	0.54
21:S:15:LEU:HD12	21:S:15:LEU:C	2.32	0.54
21:S:63:THR:HG21	21:S:65:ASN:ND2	2.22	0.54
1:A:457:C:N4	1:A:475:G:H22	2.05	0.54
1:A:959:A:H3'	1:A:960:U:H5''	1.89	0.54
1:A:1392:G:N2	1:A:1502:A:H8	2.04	0.54
4:B:21:ARG:N	4:B:21:ARG:HD2	2.22	0.54
4:B:69:LEU:C	4:B:69:LEU:HD23	2.32	0.54
4:B:184:VAL:N	4:B:198:ASP:OD2	2.40	0.54
11:I:7:THR:HG22	11:I:8:GLY:N	2.23	0.54
1:A:532:A:H5''	5:C:161:GLU:OE1	2.07	0.54
1:A:644:G:O2'	1:A:645:C:H5'	2.06	0.54
1:A:1305:G:H5''	23:V:4:GLY:C	2.32	0.54
4:B:81:VAL:O	4:B:81:VAL:HG12	2.05	0.54
4:B:88:ALA:C	4:B:90:MET:N	2.65	0.54
5:C:64:VAL:HB	5:C:99:VAL:HG21	1.90	0.54
7:E:40:ARG:HG2	7:E:68:GLU:OE1	2.07	0.54
7:E:96:PRO:HA	7:E:117:ASP:OD2	2.08	0.54
9:G:148:ASN:C	9:G:150:ALA:H	2.16	0.54
1:A:477:G:O2'	1:A:478:A:H5'	2.07	0.54
1:A:974:A:OP2	16:N:41:ARG:NH1	2.40	0.54
6:D:111:ALA:HB2	6:D:120:LEU:HD12	1.89	0.54
6:D:173:TRP:CD2	6:D:189:PRO:HB3	2.43	0.54
6:D:173:TRP:O	6:D:186:LEU:HB2	2.07	0.54
7:E:101:ILE:HD12	7:E:119:LEU:HD21	1.89	0.54
10:H:116:LYS:HD3	10:H:127:LEU:CD1	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:112:LYS:HD3	11:I:112:LYS:C	2.32	0.54
12:J:32:ALA:HB2	12:J:76:ASN:OD1	2.07	0.54
1:A:613:C:O2'	1:A:614:A:H5'	2.08	0.54
1:A:1532:U:O2'	1:A:1533:C:H4'	2.07	0.54
5:C:13:GLY:O	5:C:14:ILE:HD13	2.07	0.54
7:E:128:PRO:O	7:E:129:ILE:C	2.48	0.54
9:G:38:LEU:HD12	9:G:38:LEU:O	2.07	0.54
9:G:54:THR:HG22	9:G:56:GLN:N	2.22	0.54
11:I:10:ARG:HH21	11:I:11:LYS:HD2	1.73	0.54
11:I:28:VAL:HG12	11:I:63:ILE:HB	1.89	0.54
13:K:74:ALA:C	13:K:76:GLY:H	2.16	0.54
15:M:84:ILE:O	15:M:85:GLY:C	2.50	0.54
17:O:87:ILE:O	17:O:88:ARG:HB2	2.08	0.54
4:B:71:VAL:HG21	4:B:164:VAL:HG22	1.89	0.54
5:C:22:TRP:CZ3	5:C:32:LEU:HB2	2.42	0.54
6:D:102:ASP:OD2	6:D:103:ASN:N	2.41	0.54
9:G:79:ARG:HG2	9:G:79:ARG:HH11	1.71	0.54
9:G:146:GLU:HA	9:G:149:ARG:HB2	1.89	0.54
11:I:114:TYR:CE1	12:J:59:SER:O	2.61	0.54
14:L:10:LEU:HB3	19:Q:32:TYR:CE1	2.42	0.54
15:M:88:ARG:CB	15:M:88:ARG:HH11	2.20	0.54
1:A:1263:C:H2'	1:A:1264:C:H6	1.68	0.54
4:B:17:PHE:CD1	4:B:17:PHE:C	2.84	0.54
4:B:127:ILE:HG13	4:B:128:GLU:CD	2.31	0.54
7:E:87:SER:HB3	7:E:131:ILE:HD13	1.90	0.54
9:G:59:LEU:HD11	9:G:63:LYS:HE2	1.89	0.54
12:J:60:ARG:HD2	12:J:60:ARG:H	1.69	0.54
13:K:110:ASP:HB2	20:R:88:LYS:HE3	1.89	0.54
1:A:1427:U:O2'	1:A:1428:A:H5'	2.08	0.54
4:B:21:ARG:HD2	4:B:21:ARG:H	1.73	0.54
4:B:53:ARG:NH1	4:B:199:TYR:HD2	2.05	0.54
5:C:50:ALA:HB1	5:C:70:VAL:HG11	1.88	0.54
5:C:195:VAL:O	5:C:196:LEU:HD22	2.08	0.54
6:D:165:MET:SD	6:D:168:ARG:HD2	2.48	0.54
7:E:107:ARG:O	7:E:108:ALA:C	2.50	0.54
10:H:119:LEU:HB2	10:H:123:GLU:HB2	1.90	0.54
11:I:9:ARG:HA	11:I:13:ALA:O	2.08	0.54
11:I:11:LYS:O	11:I:11:LYS:HG2	2.08	0.54
18:P:20:VAL:HG11	18:P:32:TYR:HB3	1.90	0.54
19:Q:76:LEU:HD23	19:Q:76:LEU:C	2.33	0.54
1:A:189:G:C2'	1:A:190(K):G:H22	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:707:C:OP1	13:K:85:ARG:NH1	2.41	0.54
1:A:1037:C:H2'	1:A:1038:C:C6	2.43	0.54
5:C:83:ARG:O	5:C:86:VAL:N	2.41	0.54
5:C:187:ALA:O	5:C:198:VAL:HG23	2.08	0.54
6:D:70:ILE:HG22	6:D:71:SER:N	2.21	0.54
10:H:45:ILE:O	10:H:45:ILE:HG13	2.07	0.54
10:H:64:LYS:CB	10:H:79:VAL:HG21	2.38	0.54
12:J:30:SER:OG	12:J:81:THR:HA	2.08	0.54
12:J:34:VAL:C	12:J:36:GLY:H	2.16	0.54
14:L:113:ARG:HB2	14:L:122:THR:HG21	1.88	0.54
1:A:130:A:C8	19:Q:63:ARG:HG3	2.43	0.54
1:A:141:A:O2'	1:A:142:G:H5'	2.08	0.54
1:A:701:C:O2'	1:A:702:A:OP2	2.24	0.54
1:A:986:A:H1'	21:S:54:GLY:O	2.08	0.54
4:B:184:VAL:CG1	4:B:197:VAL:HG13	2.38	0.54
5:C:47:LEU:HD23	5:C:68:VAL:HG11	1.89	0.54
12:J:27:ALA:HB2	12:J:85:LEU:HD21	1.90	0.54
14:L:55:VAL:CG1	14:L:56:ALA:N	2.71	0.54
16:N:12:ARG:HA	16:N:12:ARG:HE	1.73	0.54
16:N:26:ARG:HD3	16:N:43:CYS:HB3	1.90	0.54
18:P:28:ARG:HG2	18:P:29:ASP:OD2	2.08	0.54
22:T:30:LYS:O	22:T:33:ILE:HB	2.08	0.54
1:A:580:U:H2'	1:A:581:G:O4'	2.08	0.53
1:A:1112:C:C1'	5:C:179:ARG:HH21	2.20	0.53
15:M:40:ASN:C	15:M:40:ASN:ND2	2.65	0.53
1:A:101:A:O2'	1:A:102:G:H5'	2.07	0.53
1:A:867:G:O2'	1:A:868:C:H5'	2.08	0.53
1:A:952:U:O2'	1:A:953:G:H5'	2.08	0.53
1:A:1347:G:C6	11:I:107:ARG:NH2	2.76	0.53
1:A:1505:G:H2'	1:A:1541:U:OP2	2.08	0.53
4:B:239:VAL:HB	4:B:240:GLN:HE22	1.73	0.53
5:C:155:GLY:O	5:C:156:ARG:HB2	2.07	0.53
5:C:180:ALA:O	5:C:181:ASN:C	2.52	0.53
6:D:23:GLY:CA	6:D:113:SER:HB3	2.38	0.53
6:D:194:LEU:HD22	6:D:194:LEU:H	1.73	0.53
9:G:110:GLN:OE1	9:G:110:GLN:HA	2.07	0.53
10:H:102:ARG:HG3	10:H:102:ARG:O	2.09	0.53
19:Q:82:MET:HA	19:Q:85:VAL:HG23	1.89	0.53
21:S:16:LEU:C	21:S:19:VAL:HG12	2.33	0.53
1:A:16:A:O2'	1:A:17:U:H5'	2.08	0.53
1:A:1095:U:H5''	1:A:1109:C:O2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1152:A:H5''	12:J:13:HIS:CG	2.42	0.53
1:A:1539:C:O2'	1:A:1540:U:H5'	2.07	0.53
4:B:139:LYS:O	4:B:143:GLU:HG2	2.08	0.53
6:D:15:GLU:CG	6:D:63:LYS:HG3	2.38	0.53
7:E:53:LEU:HD12	7:E:53:LEU:N	2.18	0.53
8:F:37:VAL:HA	8:F:65:VAL:HG12	1.89	0.53
11:I:8:GLY:HA2	11:I:79:LEU:HB3	1.90	0.53
12:J:29:ARG:NH1	12:J:29:ARG:HB2	2.24	0.53
12:J:96:ILE:HG22	12:J:97:GLU:N	2.24	0.53
13:K:106:LYS:HA	13:K:106:LYS:CE	2.25	0.53
13:K:126:ARG:C	13:K:128:ALA:N	2.65	0.53
15:M:22:ILE:HB	15:M:25:ILE:HD12	1.90	0.53
16:N:24:CYS:HB3	16:N:28:GLY:H	1.72	0.53
17:O:45:VAL:HG12	17:O:46:HIS:ND1	2.23	0.53
19:Q:81:ARG:HG3	19:Q:81:ARG:O	2.08	0.53
22:T:39:LYS:CD	22:T:55:ILE:HD13	2.38	0.53
1:A:338:A:H2'	1:A:339:C:C6	2.44	0.53
1:A:1243:C:H2'	1:A:1244:C:C6	2.43	0.53
5:C:156:ARG:NH2	5:C:161:GLU:HA	2.23	0.53
6:D:64:LEU:HD12	6:D:75:PHE:HZ	1.72	0.53
8:F:1:MET:HE3	8:F:66:GLU:OE1	2.08	0.53
8:F:60:PHE:C	8:F:61:LEU:HD23	2.34	0.53
11:I:117:HIS:C	11:I:118:LYS:HG3	2.33	0.53
17:O:66:LEU:O	17:O:69:TYR:HB3	2.09	0.53
17:O:87:ILE:HG22	17:O:88:ARG:N	2.23	0.53
1:A:404:U:H2'	1:A:405:U:H6	1.74	0.53
1:A:983:A:H5'	1:A:984:C:OP2	2.08	0.53
4:B:140:HIS:HA	4:B:143:GLU:HG3	1.90	0.53
5:C:30:ARG:HG2	5:C:30:ARG:NH1	2.24	0.53
5:C:178:LEU:O	5:C:179:ARG:CB	2.56	0.53
6:D:17:VAL:HG12	6:D:18:LYS:N	2.23	0.53
11:I:4:TYR:CZ	11:I:88:TYR:HD1	2.27	0.53
13:K:91:ARG:NH1	20:R:88:LYS:HZ3	2.05	0.53
22:T:54:LYS:HG3	22:T:100:ILE:CD1	2.38	0.53
1:A:1064:G:H4'	1:A:1065:U:H5'	1.89	0.53
1:A:1121:U:H2'	1:A:1122:U:C6	2.43	0.53
1:A:1190:G:C3'	5:C:3:ASN:OD1	2.56	0.53
4:B:128:GLU:C	4:B:129:GLU:OE1	2.52	0.53
7:E:126:ARG:CG	7:E:126:ARG:NH1	2.63	0.53
9:G:15:ASP:O	9:G:19:GLY:HA2	2.08	0.53
9:G:77:SER:HB2	9:G:86:GLN:HE22	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:51:VAL:HG21	10:H:60:ARG:HG3	1.91	0.53
17:O:16:ALA:HB1	17:O:21:ASP:HB3	1.89	0.53
1:A:9:G:H5'	7:E:122:GLU:OE2	2.08	0.53
1:A:404:U:O2'	1:A:405:U:H5'	2.09	0.53
1:A:1101:A:C8	4:B:172:ILE:HD13	2.43	0.53
1:A:1423:G:O2'	1:A:1424:C:H5'	2.08	0.53
6:D:8:VAL:C	6:D:10:ARG:N	2.67	0.53
7:E:80:ILE:HG23	10:H:104:ARG:NH2	2.23	0.53
12:J:85:LEU:O	12:J:87:THR:N	2.41	0.53
15:M:110:ARG:HG2	15:M:110:ARG:HH11	1.73	0.53
21:S:6:LYS:HD2	21:S:6:LYS:H	1.68	0.53
23:V:13:ILE:O	23:V:16:GLY:N	2.39	0.53
1:A:333:G:H4'	22:T:16:HIS:CE1	2.44	0.53
1:A:475:G:OP1	1:A:475:G:O4'	2.27	0.53
1:A:858:G:O2'	1:A:859:A:H5'	2.09	0.53
1:A:1043:C:O2'	1:A:1044:A:H5'	2.08	0.53
1:A:1095:U:H2'	1:A:1096:C:H6	1.72	0.53
4:B:20:GLU:OE2	4:B:20:GLU:HA	2.08	0.53
8:F:69:GLU:H	8:F:69:GLU:CD	2.15	0.53
10:H:28:ALA:HB2	10:H:59:LEU:HG	1.91	0.53
12:J:4:ILE:HG22	12:J:100:THR:CB	2.39	0.53
15:M:11:ARG:CD	15:M:12:ASN:H	2.21	0.53
21:S:17:GLU:O	21:S:20:LEU:HG	2.09	0.53
21:S:19:VAL:HG13	21:S:20:LEU:N	2.24	0.53
1:A:1124:G:H5'	12:J:35:SER:CB	2.38	0.53
1:A:1229:A:O2'	15:M:125:ARG:NE	2.41	0.53
6:D:31:CYS:O	6:D:31:CYS:SG	2.66	0.53
15:M:7:VAL:O	15:M:7:VAL:HG12	2.09	0.53
15:M:37:THR:HG23	15:M:55:ARG:CD	2.32	0.53
1:A:386:C:C2'	1:A:387:U:H5'	2.39	0.53
1:A:501:C:H2'	1:A:502:G:C8	2.43	0.53
1:A:523:A:H61	14:L:92:ASP:HB2	1.74	0.53
1:A:650:G:O2'	1:A:651:C:H5'	2.09	0.53
1:A:1392:G:H2'	1:A:1393:U:H6	1.74	0.53
1:A:1441:G:H4'	1:A:1442:G:C6	2.43	0.53
4:B:55:PHE:HD2	4:B:221:LEU:HG	1.74	0.53
6:D:61:LYS:HA	6:D:203:VAL:HG22	1.90	0.53
9:G:31:MET:SD	9:G:34:GLY:HA2	2.49	0.53
9:G:66:VAL:HG12	9:G:70:LYS:HE3	1.90	0.53
18:P:46:PRO:O	18:P:47:ASP:HB2	2.08	0.53
1:A:518:C:H4'	1:A:519:C:O5'	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:748:C:O2'	1:A:749:C:H6	1.90	0.52
1:A:1314:C:N4	21:S:4:SER:HB2	2.24	0.52
5:C:81:GLY:HA2	5:C:84:ILE:HG22	1.91	0.52
6:D:3:ARG:NH2	6:D:74:GLN:HE21	2.07	0.52
9:G:71:PRO:HD3	9:G:103:TRP:CZ3	2.44	0.52
1:A:190(A):C:H42	1:A:190(H):G:H1	1.56	0.52
1:A:340:U:H2'	1:A:341:C:C6	2.44	0.52
1:A:357:G:O2'	1:A:358:U:H5'	2.08	0.52
1:A:413:G:H4'	1:A:416:G:N2	2.22	0.52
1:A:740:U:O2'	1:A:741:G:H5'	2.10	0.52
1:A:1262:C:O2'	1:A:1263:C:H5'	2.09	0.52
1:A:1313:U:OP2	21:S:6:LYS:HA	2.09	0.52
1:A:1525:G:O2'	1:A:1526:G:H5'	2.09	0.52
4:B:77:ALA:HB2	4:B:211:ILE:CD1	2.39	0.52
4:B:137:ARG:HG2	4:B:137:ARG:HH11	1.74	0.52
4:B:219:VAL:C	4:B:221:LEU:N	2.66	0.52
6:D:76:ARG:HG2	6:D:76:ARG:HH11	1.75	0.52
8:F:4:TYR:O	8:F:5:GLU:HG3	2.09	0.52
15:M:16:ASP:N	15:M:16:ASP:OD1	2.40	0.52
16:N:34:TYR:HD1	16:N:34:TYR:H	1.55	0.52
19:Q:27:PHE:HB2	19:Q:28:PRO:HD2	1.91	0.52
20:R:61:LYS:O	20:R:65:ILE:HG13	2.09	0.52
1:A:189:G:C5	1:A:190:C:H3'	2.44	0.52
1:A:195:A:H4'	22:T:68:LYS:CE	2.40	0.52
1:A:460:A:H2'	1:A:461:C:H5''	1.92	0.52
4:B:19:HIS:CE1	4:B:204:ASN:HB3	2.45	0.52
4:B:44:LEU:HA	4:B:47:THR:OG1	2.09	0.52
4:B:107:THR:C	4:B:109:SER:N	2.66	0.52
5:C:123:GLN:HE22	5:C:140:ARG:NH2	2.06	0.52
5:C:191:THR:HG21	5:C:193:TYR:CE1	2.42	0.52
6:D:148:VAL:HG11	6:D:158:ILE:HD13	1.91	0.52
11:I:5:TYR:HE2	11:I:16:ARG:HB3	1.74	0.52
12:J:34:VAL:HG22	12:J:74:ILE:HG12	1.90	0.52
15:M:22:ILE:HG21	15:M:66:LEU:HD13	1.90	0.52
1:A:753:A:H2	10:H:1:MET:HE2	1.72	0.52
1:A:1196:U:OP1	1:A:1197:G:H5'	2.08	0.52
1:A:1317:C:H2'	1:A:1318:A:O4'	2.09	0.52
1:A:1539:C:H5	9:G:82:GLY:HA2	1.75	0.52
4:B:12:GLU:OE2	4:B:213:LEU:HD11	2.10	0.52
5:C:34:LEU:HG	16:N:25:VAL:CG2	2.39	0.52
7:E:41:VAL:HG22	7:E:113:ALA:HA	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:8:GLU:OE1	9:G:8:GLU:O	2.28	0.52
11:I:81:ILE:O	11:I:85:LEU:HB2	2.10	0.52
12:J:55:LYS:HG3	12:J:56:HIS:CD2	2.44	0.52
19:Q:48:GLU:O	19:Q:49:GLU:C	2.52	0.52
19:Q:66:SER:OG	19:Q:69:LYS:HB3	2.09	0.52
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.25	0.52
1:A:1347:G:C2'	1:A:1348:U:OP2	2.58	0.52
1:A:1522:U:O2'	1:A:1523:G:H5'	2.10	0.52
4:B:102:LEU:HD21	4:B:162:ILE:HD12	1.90	0.52
5:C:108:ASN:OD1	5:C:110:ASN:HB2	2.10	0.52
8:F:98:LEU:HD11	8:F:101:ALA:HA	1.92	0.52
18:P:26:ARG:NH2	18:P:31:LYS:NZ	2.57	0.52
1:A:258:G:O2'	1:A:259:G:H5'	2.09	0.52
1:A:308:C:H2'	1:A:309:G:H8	1.74	0.52
1:A:1260:C:O5'	1:A:1284:C:H4'	2.09	0.52
4:B:51:LEU:HD22	4:B:55:PHE:HE1	1.73	0.52
5:C:112:SER:HB3	5:C:115:LEU:HD12	1.90	0.52
5:C:134:ILE:HD11	5:C:153:VAL:HG23	1.91	0.52
7:E:144:THR:O	7:E:145:LYS:C	2.52	0.52
9:G:6:ARG:O	9:G:7:ALA:C	2.52	0.52
14:L:46:LYS:HG3	14:L:47:LYS:N	2.25	0.52
16:N:23:ARG:NH1	16:N:30:ALA:HB2	2.24	0.52
18:P:55:ARG:O	18:P:58:TYR:HB3	2.09	0.52
20:R:26:LEU:HD12	20:R:27:GLY:N	2.25	0.52
1:A:848:C:H2'	1:A:849:C:C6	2.45	0.52
1:A:1054:C:C6	2:X:34:I:H1'	2.45	0.52
1:A:1154:G:H2'	1:A:1155:G:C8	2.42	0.52
5:C:20:SER:HB3	5:C:22:TRP:CD1	2.44	0.52
8:F:2:ARG:NH1	8:F:69:GLU:HG2	2.25	0.52
11:I:46:ALA:O	11:I:49:PRO:HD2	2.10	0.52
19:Q:45:HIS:NE2	19:Q:47:PRO:HG3	2.24	0.52
1:A:346:G:H2'	1:A:347:G:O4'	2.09	0.52
1:A:502:G:H2'	1:A:503:C:C6	2.45	0.52
1:A:755:G:OP2	17:O:65:ARG:HD2	2.10	0.52
1:A:1031:G:H4'	1:A:1032:G:C8	2.45	0.52
1:A:1124:G:O2'	1:A:1145:C:N4	2.42	0.52
1:A:1141:C:H2'	1:A:1142:G:H8	1.74	0.52
1:A:1307:U:H2'	1:A:1308:U:C6	2.45	0.52
1:A:1495:U:H2'	1:A:1496:C:C6	2.44	0.52
4:B:17:PHE:HB3	4:B:44:LEU:HD11	1.91	0.52
4:B:18:GLY:HA2	4:B:40:HIS:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:80:ILE:HD11	4:B:208:ILE:CG2	2.37	0.52
5:C:54:ARG:O	5:C:55:VAL:HG23	2.10	0.52
8:F:32:ASN:O	8:F:71:ARG:NH2	2.42	0.52
8:F:47:ARG:N	8:F:47:ARG:HD3	2.24	0.52
9:G:79:ARG:HG2	9:G:79:ARG:NH1	2.25	0.52
10:H:116:LYS:HD3	10:H:127:LEU:HD13	1.92	0.52
11:I:96:LEU:HD12	11:I:96:LEU:N	2.25	0.52
12:J:38:ILE:HD12	12:J:71:LEU:CD1	2.40	0.52
15:M:53:VAL:CG1	15:M:57:ARG:HH21	2.23	0.52
21:S:41:VAL:HG22	21:S:44:MET:CE	2.37	0.52
1:A:831:U:H2'	1:A:832:C:C6	2.44	0.52
1:A:1117:G:H4'	11:I:104:ARG:NH1	2.25	0.52
1:A:1202:G:C2	16:N:42:ILE:HG21	2.45	0.52
1:A:1487:G:O2'	1:A:1488:G:H5'	2.10	0.52
4:B:7:VAL:HG12	4:B:221:LEU:HD23	1.91	0.52
5:C:133:ALA:O	5:C:136:GLN:N	2.43	0.52
6:D:150:GLU:OE1	6:D:150:GLU:HA	2.08	0.52
6:D:157:LEU:CD2	6:D:161:ASN:HD21	2.23	0.52
6:D:194:LEU:HD22	6:D:194:LEU:N	2.25	0.52
8:F:28:ARG:HH11	8:F:28:ARG:HG2	1.74	0.52
10:H:31:PHE:HZ	10:H:134:ILE:CD1	2.23	0.52
12:J:71:LEU:O	12:J:72:VAL:CB	2.57	0.52
13:K:84:VAL:CG1	13:K:95:ILE:HD11	2.39	0.52
18:P:38:TYR:CE2	18:P:50:LYS:HB3	2.44	0.52
22:T:100:ILE:C	22:T:102:GLY:H	2.17	0.52
1:A:382:A:C2	1:A:383:A:C4	2.98	0.52
1:A:939:G:H2'	1:A:940:C:H6	1.75	0.52
1:A:1270:C:O2'	1:A:1271:G:H5'	2.10	0.52
1:A:1354:C:H2'	1:A:1355:G:H8	1.74	0.52
4:B:9:GLU:OE2	4:B:12:GLU:HA	2.10	0.52
4:B:47:THR:O	4:B:51:LEU:HG	2.10	0.52
4:B:87:ARG:O	4:B:88:ALA:CB	2.57	0.52
4:B:236:TYR:O	4:B:236:TYR:HD2	1.92	0.52
6:D:8:VAL:O	6:D:10:ARG:N	2.37	0.52
15:M:63:THR:HG22	15:M:64:TRP:CD1	2.44	0.52
22:T:63:ILE:HD13	22:T:80:ARG:HB2	1.92	0.52
1:A:252:U:H2'	1:A:253:U:C6	2.44	0.51
1:A:478:A:C3'	1:A:479:C:H5'	2.41	0.51
1:A:628:G:H2'	1:A:629:G:C8	2.45	0.51
1:A:1317:C:OP1	16:N:17:LYS:HG2	2.09	0.51
5:C:29:TYR:CZ	16:N:54:PRO:HG2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:3:ARG:HG2	6:D:118:ARG:NE	2.25	0.51
8:F:81:ILE:HG23	8:F:82:ARG:N	2.25	0.51
15:M:82:MET:HE3	15:M:93:ARG:CG	2.32	0.51
19:Q:93:GLN:O	19:Q:96:GLN:HG3	2.10	0.51
1:A:15:G:H1'	7:E:24:ARG:HH12	1.75	0.51
1:A:127:G:HO2'	19:Q:2:PRO:N	2.09	0.51
1:A:839:U:O2	1:A:839:U:C2'	2.58	0.51
4:B:83:MET:HG3	4:B:238:LEU:HD12	1.92	0.51
4:B:220:ASP:HB3	4:B:230:VAL:HG11	1.92	0.51
5:C:107:GLN:O	5:C:108:ASN:CB	2.58	0.51
6:D:170:VAL:HG13	6:D:174:LEU:HB2	1.92	0.51
9:G:69:VAL:HG12	9:G:69:VAL:O	2.09	0.51
10:H:31:PHE:CZ	10:H:134:ILE:HD11	2.45	0.51
16:N:58:LYS:HB3	16:N:58:LYS:NZ	2.25	0.51
17:O:39:LEU:CD2	17:O:56:LEU:HB2	2.40	0.51
22:T:21:LYS:HB2	22:T:21:LYS:HZ3	1.76	0.51
1:A:408:A:O5'	1:A:431:A:OP2	2.27	0.51
1:A:818:G:O2'	1:A:819:A:H5'	2.11	0.51
1:A:841:U:H3'	1:A:848:C:O4'	2.10	0.51
1:A:1151:A:O2'	1:A:1152:A:H8	1.92	0.51
1:A:1402:C:H2'	1:A:1403:C:O4'	2.10	0.51
4:B:87:ARG:O	4:B:88:ALA:HB2	2.09	0.51
11:I:10:ARG:HG2	11:I:75:ASP:CB	2.40	0.51
14:L:86:ARG:NH1	14:L:87:GLY:O	2.43	0.51
19:Q:17:LYS:HA	19:Q:46:ASP:O	2.10	0.51
1:A:1366:C:C2	1:A:1367:C:C5	2.98	0.51
4:B:124:SER:HB2	4:B:125:PRO:CD	2.36	0.51
9:G:129:GLU:OE1	9:G:131:LYS:HE2	2.09	0.51
13:K:33:THR:HB	13:K:38:ASN:C	2.34	0.51
14:L:83:VAL:HG22	14:L:100:ILE:HG23	1.93	0.51
15:M:53:VAL:HG12	15:M:57:ARG:HH21	1.74	0.51
19:Q:97:SER:HB2	19:Q:98:LEU:CD1	2.39	0.51
20:R:53:ARG:HD2	20:R:58:LEU:O	2.10	0.51
1:A:418:C:H2'	1:A:419:C:O2	2.10	0.51
1:A:591:U:P	10:H:30:ARG:HE	2.32	0.51
1:A:1364:U:O2'	1:A:1365:G:H5'	2.09	0.51
5:C:112:SER:OG	5:C:115:LEU:HG	2.10	0.51
6:D:105:VAL:HG12	6:D:117:ALA:CB	2.41	0.51
8:F:96:PRO:O	8:F:98:LEU:N	2.43	0.51
15:M:36:LYS:HD2	15:M:59:TYR:OH	2.11	0.51
17:O:33:THR:HG23	17:O:63:ARG:HH12	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:42:ARG:HG3	20:R:42:ARG:NH1	2.26	0.51
20:R:86:VAL:CG1	20:R:87:ARG:H	2.23	0.51
21:S:47:HIS:O	21:S:62:ILE:HG22	2.10	0.51
1:A:409:G:H5''	1:A:431:A:C8	2.46	0.51
1:A:849:C:O2'	1:A:850:U:H5'	2.10	0.51
1:A:959:A:H2'	1:A:960:U:O4'	2.10	0.51
6:D:70:ILE:HD11	6:D:100:ARG:CD	2.40	0.51
8:F:10:LEU:HD12	8:F:59:TYR:HB3	1.92	0.51
8:F:25:ILE:CD1	8:F:82:ARG:HH11	2.23	0.51
8:F:67:MET:HE2	8:F:72:VAL:N	2.25	0.51
9:G:31:MET:HE2	9:G:36:LYS:HG3	1.91	0.51
10:H:35:ILE:HG22	10:H:39:LEU:CD2	2.41	0.51
10:H:92:ARG:CG	10:H:92:ARG:NH1	2.74	0.51
10:H:118:VAL:C	10:H:119:LEU:HD23	2.36	0.51
19:Q:75:ARG:HH11	19:Q:75:ARG:HG3	1.75	0.51
1:A:27:G:O2'	1:A:28:G:H5'	2.11	0.51
1:A:179:A:H2'	1:A:180:U:H6	1.75	0.51
1:A:865:A:O2'	1:A:866:C:H5'	2.11	0.51
1:A:972:C:C4'	12:J:57:LYS:HE2	2.41	0.51
7:E:110:LEU:O	7:E:113:ALA:HB3	2.11	0.51
8:F:35:ALA:HB1	8:F:65:VAL:HG21	1.92	0.51
14:L:86:ARG:HG3	14:L:87:GLY:O	2.10	0.51
20:R:59:SER:O	20:R:60:GLY:C	2.53	0.51
21:S:24:ALA:O	21:S:25:LYS:HB3	2.10	0.51
23:V:12:LYS:HB3	23:V:22:ARG:HD2	1.93	0.51
1:A:475:G:O4'	1:A:475:G:P	2.69	0.51
1:A:659:U:O2'	1:A:660:G:H5'	2.11	0.51
1:A:695:A:H2'	1:A:696:A:C8	2.46	0.51
1:A:1005:A:H1'	1:A:1026:G:N2	2.24	0.51
4:B:76:GLN:NE2	4:B:207:ALA:H	2.09	0.51
12:J:39:PRO:O	12:J:69:ASN:O	2.28	0.51
13:K:33:THR:HB	13:K:38:ASN:O	2.10	0.51
23:V:2:GLY:C	23:V:4:GLY:H	2.19	0.51
1:A:327:A:O2'	1:A:328:C:O4'	2.25	0.51
1:A:1250:A:H4'	11:I:68:GLY:CA	2.41	0.51
1:A:1354:C:O2'	1:A:1355:G:H5'	2.10	0.51
5:C:179:ARG:CG	5:C:179:ARG:O	2.58	0.51
6:D:64:LEU:HB2	6:D:198:VAL:HG11	1.93	0.51
10:H:82:HIS:O	10:H:83:ILE:HB	2.11	0.51
10:H:108:GLY:HA3	10:H:138:TRP:HB3	1.92	0.51
12:J:4:ILE:HG13	12:J:4:ILE:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:43:CYS:O	16:N:44:LEU:C	2.54	0.51
1:A:792:A:H4'	1:A:793:U:H5''	1.91	0.51
1:A:834:C:H2'	1:A:835:U:C6	2.46	0.51
1:A:1157:A:H4'	1:A:1158:C:O5'	2.12	0.51
1:A:1397:C:H4'	1:A:1398:A:OP2	2.11	0.51
5:C:191:THR:CG2	5:C:192:THR:H	2.22	0.51
7:E:91:LEU:HB3	7:E:118:ILE:HD11	1.93	0.51
13:K:69:ALA:O	13:K:73:MET:HG2	2.09	0.51
20:R:36:ASN:HA	20:R:38:GLU:OE2	2.11	0.51
1:A:459:G:H3'	1:A:460:A:C5'	2.41	0.50
1:A:1347:G:O2'	1:A:1348:U:OP2	2.29	0.50
5:C:167:TRP:O	5:C:168:ALA:HB3	2.11	0.50
10:H:117:GLY:O	10:H:119:LEU:HD23	2.11	0.50
11:I:5:TYR:C	11:I:5:TYR:CD1	2.88	0.50
1:A:16:A:C2'	1:A:17:U:H5'	2.41	0.50
1:A:184:G:C4'	1:A:224:C:H4'	2.41	0.50
1:A:189:G:H2'	1:A:190(K):G:H21	1.72	0.50
1:A:954:G:H2'	1:A:955:U:H6	1.76	0.50
1:A:1142:G:C2	1:A:1143:G:H1'	2.46	0.50
1:A:1149:C:O2'	1:A:1280:A:N1	2.39	0.50
5:C:7:PRO:HG2	5:C:184:TYR:HB2	1.92	0.50
6:D:35:ARG:O	6:D:36:ARG:CB	2.58	0.50
12:J:34:VAL:CG2	12:J:74:ILE:HG12	2.41	0.50
12:J:48:THR:HG23	12:J:62:HIS:NE2	2.26	0.50
14:L:93:LEU:HB2	14:L:96:VAL:HG21	1.92	0.50
19:Q:27:PHE:CE1	19:Q:36:ILE:HD11	2.46	0.50
19:Q:64:PRO:HB3	19:Q:70:ARG:NH1	2.26	0.50
21:S:33:THR:HG22	21:S:35:SER:N	2.09	0.50
23:V:6:ARG:HG3	23:V:7:ARG:N	2.27	0.50
1:A:828:A:H2'	1:A:829:G:O4'	2.11	0.50
1:A:1132:C:H2'	1:A:1133:G:H8	1.74	0.50
1:A:1367:C:C2	1:A:1368:G:C8	2.99	0.50
1:A:1474:G:O2'	1:A:1475:G:H5'	2.10	0.50
5:C:56:ASP:O	5:C:57:ILE:HG13	2.10	0.50
5:C:134:ILE:HG22	5:C:168:ALA:HB3	1.92	0.50
5:C:173:VAL:HG12	5:C:175:LEU:HD21	1.93	0.50
7:E:80:ILE:HD12	7:E:80:ILE:O	2.11	0.50
9:G:48:LYS:O	9:G:51:GLN:HB2	2.11	0.50
10:H:103:VAL:HG21	10:H:109:ILE:O	2.12	0.50
11:I:23:ASN:O	11:I:23:ASN:ND2	2.44	0.50
11:I:113:LYS:H	11:I:119:ALA:HA	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:2:ALA:O	15:M:4:ILE:HG13	2.11	0.50
15:M:6:GLY:O	15:M:7:VAL:HB	2.12	0.50
16:N:22:THR:OG1	16:N:33:VAL:HG21	2.11	0.50
18:P:1:MET:HE3	18:P:3:LYS:CD	2.37	0.50
19:Q:68:ARG:O	19:Q:68:ARG:CG	2.51	0.50
21:S:52:TYR:HA	21:S:56:GLN:O	2.12	0.50
1:A:192:U:H4'	22:T:57:ARG:HD2	1.94	0.50
1:A:263:A:OP2	22:T:79:ARG:NH1	2.44	0.50
1:A:1228:C:H4'	15:M:116:THR:HA	1.93	0.50
4:B:210:SER:O	4:B:211:ILE:C	2.54	0.50
5:C:129:ALA:O	5:C:132:ARG:HB3	2.12	0.50
6:D:126:ILE:CG2	6:D:127:THR:N	2.72	0.50
14:L:40:VAL:O	14:L:40:VAL:HG12	2.11	0.50
14:L:53:ARG:HG3	14:L:93:LEU:HD21	1.92	0.50
1:A:781:A:H2'	1:A:782:A:H5'	1.94	0.50
6:D:157:LEU:HD21	6:D:161:ASN:HD21	1.76	0.50
9:G:21:VAL:HG23	9:G:22:LEU:N	2.27	0.50
14:L:61:THR:C	14:L:63:GLY:H	2.18	0.50
15:M:11:ARG:CG	15:M:12:ASN:N	2.74	0.50
15:M:25:ILE:HG22	15:M:26:GLY:H	1.76	0.50
15:M:88:ARG:HG3	15:M:98:VAL:CG1	2.42	0.50
17:O:78:TYR:OH	17:O:82:ILE:HD11	2.11	0.50
18:P:1:MET:CE	18:P:3:LYS:HD2	2.40	0.50
19:Q:59:ILE:CG2	19:Q:71:PHE:CD1	2.95	0.50
21:S:39:THR:HG22	21:S:40:ILE:N	2.27	0.50
1:A:167:G:O2'	1:A:168:G:H5'	2.10	0.50
1:A:258:G:H2'	1:A:259:G:H8	1.76	0.50
1:A:628:G:H2'	1:A:629:G:H8	1.77	0.50
1:A:807:A:H2'	1:A:808:C:C6	2.47	0.50
1:A:1152:A:H5''	12:J:13:HIS:HD2	1.72	0.50
1:A:1195:C:H3'	1:A:1196:U:C5'	2.41	0.50
4:B:45:GLN:O	4:B:48:MET:HB2	2.11	0.50
4:B:69:LEU:HD12	4:B:155:LEU:CD1	2.40	0.50
5:C:29:TYR:C	5:C:29:TYR:CD2	2.90	0.50
5:C:115:LEU:O	5:C:116:VAL:C	2.55	0.50
6:D:62:GLN:NE2	6:D:65:ARG:NH1	2.58	0.50
7:E:76:ILE:HD12	7:E:118:ILE:CD1	2.42	0.50
9:G:69:VAL:HG21	9:G:104:LEU:HD21	1.93	0.50
14:L:27:LEU:HB3	14:L:62:SER:HB2	1.93	0.50
15:M:16:ASP:HB3	15:M:34:LEU:HD12	1.93	0.50
1:A:1064:G:H4'	1:A:1065:U:H5''	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1300:G:O2'	1:A:1301:U:P	2.70	0.50
5:C:76:VAL:HG11	5:C:103:VAL:HG21	1.93	0.50
7:E:51:VAL:O	7:E:54:ALA:HB3	2.12	0.50
7:E:76:ILE:HG23	7:E:77:PRO:CD	2.41	0.50
10:H:31:PHE:O	10:H:34:GLU:HB2	2.12	0.50
19:Q:58:GLU:HB2	19:Q:74:LEU:HB3	1.94	0.50
1:A:463:A:H1'	1:A:474:G:OP1	2.12	0.50
1:A:521:G:OP1	14:L:73:GLU:O	2.30	0.50
1:A:530:G:O6	3:W:3:A:H1'	2.12	0.50
1:A:953:G:H1'	15:M:125:ARG:HA	1.92	0.50
4:B:19:HIS:CE1	4:B:206:ASP:HB3	2.47	0.50
6:D:54:TYR:O	6:D:55:ALA:C	2.54	0.50
11:I:45:ALA:O	11:I:48:GLU:N	2.44	0.50
12:J:42:THR:HG23	12:J:67:THR:O	2.11	0.50
13:K:67:ASP:OD2	13:K:71:LYS:HE3	2.12	0.50
19:Q:59:ILE:HG23	19:Q:71:PHE:HB3	1.93	0.50
19:Q:60:ILE:HD13	19:Q:61:GLU:N	2.27	0.50
22:T:50:GLU:O	22:T:100:ILE:HD12	2.12	0.50
23:V:23:PRO:C	23:V:25:LYS:N	2.69	0.50
8:F:82:ARG:HB2	8:F:85:VAL:CG2	2.41	0.50
12:J:75:ILE:H	12:J:75:ILE:CD1	2.19	0.50
14:L:46:LYS:CG	14:L:47:LYS:N	2.75	0.50
14:L:101:VAL:O	14:L:103:GLY:N	2.45	0.50
17:O:60:VAL:O	17:O:64:ARG:HG2	2.12	0.50
21:S:12:ASP:H	21:S:38:SER:HB3	1.77	0.50
1:A:163:C:C2'	1:A:164:U:H5'	2.41	0.49
1:A:279:A:C4	19:Q:98:LEU:HD23	2.46	0.49
1:A:457:C:H42	1:A:475:G:H22	1.60	0.49
1:A:1223:C:OP1	1:A:1224:G:H3'	2.12	0.49
1:A:1316:G:H4'	16:N:18:VAL:HG11	1.93	0.49
1:A:1411:C:O2'	1:A:1412:C:H5'	2.12	0.49
1:A:1475:G:H2'	1:A:1476:G:C8	2.46	0.49
4:B:179:LYS:HB2	4:B:179:LYS:NZ	2.27	0.49
5:C:83:ARG:O	5:C:85:ARG:N	2.45	0.49
5:C:100:ALA:O	5:C:101:LEU:HB2	2.12	0.49
6:D:64:LEU:C	6:D:64:LEU:HD13	2.36	0.49
9:G:51:GLN:OE1	9:G:51:GLN:HA	2.12	0.49
9:G:78:ARG:NH1	9:G:154:TYR:O	2.45	0.49
11:I:48:GLU:N	11:I:49:PRO:CD	2.73	0.49
16:N:3:ARG:O	16:N:7:ILE:HG13	2.12	0.49
19:Q:12:SER:HA	19:Q:14:LYS:NZ	2.23	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:C:H6	1:A:188:C:C5'	2.25	0.49
1:A:1316:G:N2	1:A:1318:A:H3'	2.28	0.49
1:A:1333:A:H2'	1:A:1334:G:O4'	2.12	0.49
6:D:8:VAL:HG11	6:D:115:ARG:CZ	2.42	0.49
9:G:18:TYR:CE2	9:G:58:PRO:HG2	2.47	0.49
10:H:87:SER:OG	10:H:92:ARG:HD2	2.12	0.49
12:J:4:ILE:HG12	12:J:74:ILE:HB	1.94	0.49
14:L:8:ASN:O	14:L:12:ARG:HG3	2.11	0.49
14:L:34:ARG:O	14:L:61:THR:HG23	2.12	0.49
15:M:40:ASN:HD22	15:M:41:PRO:HD2	1.74	0.49
17:O:32:LEU:HD13	17:O:63:ARG:HB2	1.93	0.49
1:A:359:U:O2'	1:A:360:A:H5'	2.12	0.49
1:A:1091:U:O2	1:A:1093:A:H8	1.94	0.49
1:A:1305:G:H2'	1:A:1331:G:N2	2.28	0.49
4:B:118:LEU:O	4:B:119:GLU:C	2.55	0.49
5:C:195:VAL:HG12	5:C:196:LEU:N	2.28	0.49
7:E:28:PHE:O	7:E:47:LYS:HA	2.12	0.49
12:J:89:ASP:HB2	12:J:91:PRO:HD2	1.94	0.49
14:L:53:ARG:HG3	14:L:53:ARG:HH11	1.76	0.49
22:T:39:LYS:HE2	22:T:55:ILE:CD1	2.41	0.49
22:T:72:LEU:O	22:T:73:HIS:C	2.55	0.49
1:A:384:G:H2'	1:A:385:C:C6	2.47	0.49
5:C:5:ILE:HD12	5:C:5:ILE:C	2.36	0.49
5:C:150:LYS:CG	5:C:169:ALA:HB2	2.40	0.49
6:D:5:ILE:HG22	6:D:5:ILE:O	2.12	0.49
7:E:51:VAL:O	7:E:55:VAL:HG23	2.13	0.49
7:E:102:ALA:CB	7:E:120:THR:HG21	2.43	0.49
8:F:48:LEU:HD13	8:F:52:ILE:HD12	1.94	0.49
8:F:50:TYR:CE1	20:R:77:GLY:HA2	2.47	0.49
10:H:20:TYR:CE1	10:H:76:PRO:HD2	2.48	0.49
11:I:45:ALA:O	11:I:48:GLU:HB2	2.12	0.49
12:J:90:LEU:N	12:J:91:PRO:HD2	2.27	0.49
15:M:11:ARG:HD2	15:M:12:ASN:H	1.76	0.49
19:Q:12:SER:HB3	19:Q:20:THR:CB	2.42	0.49
20:R:37:VAL:O	20:R:41:LYS:HG3	2.12	0.49
1:A:476:G:N3	1:A:478:A:OP1	2.46	0.49
1:A:586:C:O3'	10:H:89:PRO:HB2	2.13	0.49
1:A:628:G:O2'	1:A:629:G:H5'	2.12	0.49
1:A:701:C:H5''	1:A:703:G:O4'	2.12	0.49
1:A:1368:G:OP2	11:I:112:LYS:HD3	2.13	0.49
5:C:110:ASN:HB3	5:C:144:SER:OG	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:13:ILE:HD12	7:E:13:ILE:O	2.12	0.49
7:E:109:ILE:O	7:E:113:ALA:HB2	2.12	0.49
13:K:38:ASN:HD22	13:K:38:ASN:N	2.09	0.49
14:L:60:LEU:N	14:L:64:TYR:O	2.45	0.49
15:M:125:ARG:HD2	15:M:125:ARG:C	2.38	0.49
1:A:269:C:H2'	1:A:270:A:H8	1.77	0.49
1:A:626:U:O2'	1:A:627:G:H5'	2.11	0.49
5:C:19:GLU:O	5:C:40:ARG:NH2	2.46	0.49
7:E:148:VAL:O	7:E:152:ARG:HG3	2.11	0.49
8:F:2:ARG:O	8:F:66:GLU:HA	2.12	0.49
9:G:85:TYR:HD1	9:G:154:TYR:HE1	1.59	0.49
11:I:8:GLY:HA2	11:I:79:LEU:CD1	2.41	0.49
12:J:21:GLN:O	12:J:25:GLU:HG2	2.13	0.49
12:J:69:ASN:O	12:J:70:ARG:HD3	2.11	0.49
1:A:235:C:H5'	19:Q:70:ARG:HG2	1.95	0.49
1:A:1104:G:P	4:B:111:ARG:HD2	2.52	0.49
1:A:1250:A:O2'	1:A:1251:A:H5'	2.13	0.49
1:A:1271:G:H5'	1:A:1314:C:OP1	2.12	0.49
5:C:20:SER:HB3	5:C:22:TRP:HE1	1.76	0.49
5:C:32:LEU:HD22	5:C:59:ARG:NH1	2.27	0.49
8:F:67:MET:HE1	8:F:75:LEU:HB2	1.93	0.49
9:G:18:TYR:OH	9:G:58:PRO:HG3	2.13	0.49
9:G:71:PRO:HG3	9:G:103:TRP:CH2	2.47	0.49
13:K:94:ALA:O	13:K:95:ILE:C	2.55	0.49
18:P:75:ARG:HH11	18:P:75:ARG:HG3	1.78	0.49
20:R:35:ARG:O	20:R:37:VAL:HG23	2.12	0.49
22:T:51:GLU:HA	22:T:54:LYS:HD2	1.95	0.49
1:A:103:C:P	22:T:17:ARG:NH1	2.85	0.49
1:A:412:A:H2'	1:A:413:G:H5'	1.94	0.49
1:A:830:G:O2'	1:A:831:U:H5'	2.12	0.49
1:A:1152:A:H5''	12:J:13:HIS:HB2	1.95	0.49
1:A:1178:G:N2	1:A:1180:A:H3'	2.27	0.49
1:A:1521:G:H2'	1:A:1522:U:H6	1.76	0.49
6:D:146:ILE:N	6:D:146:ILE:CD1	2.74	0.49
11:I:10:ARG:HD3	11:I:105:ASP:HB3	1.95	0.49
11:I:44:VAL:HG12	11:I:51:ARG:HH12	1.78	0.49
13:K:74:ALA:O	13:K:76:GLY:N	2.46	0.49
1:A:353:A:C8	1:A:353:A:C5'	2.96	0.49
1:A:995:C:O2	1:A:995:C:H2'	2.13	0.49
4:B:212:GLN:O	4:B:216:SER:HB3	2.13	0.49
5:C:84:ILE:O	5:C:84:ILE:HG12	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:195:VAL:C	5:C:196:LEU:CD2	2.86	0.49
11:I:43:ALA:O	11:I:44:VAL:C	2.56	0.49
17:O:26:GLU:HA	17:O:81:LEU:HD11	1.95	0.49
21:S:15:LEU:HD21	21:S:38:SER:OG	2.12	0.49
22:T:56:MET:O	22:T:59:ALA:HB3	2.12	0.49
1:A:409:G:N2	1:A:432:A:O2'	2.46	0.49
1:A:502:G:H2'	1:A:503:C:H6	1.78	0.49
1:A:736:C:H2'	1:A:737:A:C8	2.48	0.49
1:A:1269:A:N1	1:A:1312:G:O2'	2.43	0.49
4:B:115:LEU:C	4:B:115:LEU:HD12	2.36	0.49
7:E:144:THR:O	7:E:148:VAL:HG23	2.13	0.49
10:H:51:VAL:HG21	10:H:60:ARG:CG	2.43	0.49
12:J:6:ILE:HD12	12:J:72:VAL:CG1	2.42	0.49
13:K:29:ILE:C	13:K:29:ILE:CD1	2.81	0.49
15:M:90:LEU:O	15:M:93:ARG:HB2	2.12	0.49
22:T:56:MET:HE3	22:T:88:VAL:HG11	1.94	0.49
1:A:542:G:OP1	6:D:10:ARG:NH2	2.45	0.48
1:A:998:G:N2	1:A:1043:C:O2	2.46	0.48
1:A:1463:C:O2'	1:A:1464:G:H5'	2.13	0.48
4:B:48:MET:HE2	4:B:51:LEU:HD12	1.95	0.48
4:B:75:LYS:HE2	4:B:96:ARG:NH1	2.27	0.48
5:C:107:GLN:CD	5:C:107:GLN:N	2.68	0.48
6:D:16:GLY:C	6:D:33:MET:HE1	2.38	0.48
17:O:41:GLU:OE2	17:O:41:GLU:HA	2.12	0.48
20:R:86:VAL:CG1	20:R:87:ARG:N	2.75	0.48
21:S:50:ALA:HA	21:S:58:VAL:O	2.13	0.48
1:A:338:A:H2'	1:A:339:C:H6	1.77	0.48
1:A:1237:C:H4'	1:A:1334:G:N2	2.28	0.48
1:A:1283:G:O2'	1:A:1284:C:H5'	2.12	0.48
1:A:1323:G:H2'	1:A:1324:A:C8	2.48	0.48
1:A:1347:G:H2'	1:A:1373:G:H1	1.78	0.48
4:B:117:GLU:OE1	4:B:117:GLU:C	2.56	0.48
6:D:119:GLN:HG2	6:D:123:HIS:CD2	2.48	0.48
9:G:95:ARG:HG3	9:G:95:ARG:HH11	1.78	0.48
11:I:50:LEU:C	11:I:52:ALA:H	2.21	0.48
17:O:4:THR:OG1	17:O:7:GLU:HB2	2.13	0.48
18:P:67:THR:CG2	18:P:68:ASP:N	2.76	0.48
19:Q:78:GLU:O	19:Q:78:GLU:HG3	2.13	0.48
20:R:39:VAL:HG13	20:R:40:LEU:N	2.26	0.48
1:A:8:A:N6	6:D:205:GLU:O	2.46	0.48
1:A:359:U:H2'	1:A:360:A:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:434:U:H2'	1:A:435:C:C6	2.47	0.48
1:A:457:C:H2'	1:A:458:C:H6	1.77	0.48
1:A:1172:C:O2'	1:A:1173:G:H5'	2.13	0.48
1:A:1226:C:H5''	15:M:103:THR:OG1	2.13	0.48
6:D:199:ASN:HD21	6:D:201:GLN:HB2	1.79	0.48
7:E:71:LEU:O	7:E:72:GLN:HG3	2.13	0.48
9:G:22:LEU:HG	9:G:62:PHE:CE2	2.43	0.48
11:I:17:VAL:CG2	11:I:80:GLY:HA3	2.42	0.48
14:L:126:LYS:H	14:L:126:LYS:CD	2.00	0.48
22:T:16:HIS:O	22:T:17:ARG:C	2.56	0.48
22:T:54:LYS:HA	22:T:57:ARG:HH12	1.78	0.48
1:A:60:A:H4'	1:A:61:G:O5'	2.14	0.48
1:A:129(A):G:O2'	1:A:130:A:OP2	2.32	0.48
1:A:410:G:N1	1:A:411:A:N7	2.61	0.48
1:A:596:C:O2'	1:A:597:G:H5'	2.13	0.48
1:A:954:G:H2'	1:A:955:U:C6	2.49	0.48
1:A:1396:A:H2	7:E:19:MET:HG3	1.78	0.48
5:C:88:ARG:HG3	5:C:101:LEU:HD12	1.95	0.48
6:D:126:ILE:CG2	6:D:127:THR:H	2.27	0.48
7:E:37:ARG:HG2	7:E:37:ARG:NH1	2.27	0.48
11:I:16:ARG:NH1	11:I:16:ARG:HG2	2.28	0.48
11:I:127:LYS:HE3	11:I:127:LYS:CA	2.43	0.48
13:K:74:ALA:C	13:K:76:GLY:N	2.70	0.48
1:A:934:C:H5	1:A:1344:C:H2'	1.78	0.48
1:A:992:U:O2'	1:A:993:G:OP2	2.29	0.48
1:A:1165:C:O2'	1:A:1166:G:H5'	2.13	0.48
1:A:1243:C:H2'	1:A:1244:C:H6	1.78	0.48
1:A:1300:G:HO2'	1:A:1301:U:H6	1.58	0.48
4:B:55:PHE:HA	4:B:58:ILE:HD12	1.96	0.48
4:B:71:VAL:CG2	4:B:164:VAL:HG22	2.44	0.48
5:C:43:LEU:HD22	5:C:68:VAL:HG21	1.96	0.48
5:C:77:ILE:HA	5:C:84:ILE:HB	1.93	0.48
5:C:77:ILE:CD1	5:C:84:ILE:HD12	2.43	0.48
5:C:116:VAL:O	5:C:120:VAL:HG23	2.13	0.48
5:C:139:GLN:O	5:C:143:GLU:N	2.44	0.48
5:C:142:MET:HG3	5:C:170:GLN:HB2	1.95	0.48
9:G:59:LEU:CD1	9:G:63:LYS:HE2	2.43	0.48
10:H:48:TYR:CD1	10:H:48:TYR:C	2.89	0.48
13:K:57:THR:CG2	13:K:60:ALA:H	2.24	0.48
14:L:65:GLU:CD	14:L:65:GLU:N	2.71	0.48
14:L:69:TYR:HB2	14:L:90:VAL:HG21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:6:GLU:CD	17:O:6:GLU:N	2.65	0.48
20:R:37:VAL:O	20:R:41:LYS:HE2	2.14	0.48
1:A:337:C:H2'	1:A:338:A:H8	1.77	0.48
1:A:951:G:O2'	1:A:952:U:H5'	2.14	0.48
1:A:1191:A:OP1	5:C:3:ASN:ND2	2.47	0.48
1:A:1462:G:O2'	1:A:1463:C:H5'	2.13	0.48
4:B:112:VAL:C	4:B:114:ARG:N	2.71	0.48
5:C:180:ALA:C	5:C:182:ILE:N	2.70	0.48
6:D:24:GLU:O	6:D:25:ARG:CB	2.62	0.48
6:D:117:ALA:O	6:D:121:VAL:HG23	2.13	0.48
9:G:26:PHE:HB2	9:G:62:PHE:HZ	1.79	0.48
9:G:58:PRO:HG2	9:G:59:LEU:H	1.77	0.48
16:N:14:PRO:HG2	16:N:15:LYS:H	1.79	0.48
1:A:1060:C:O2'	1:A:1061:G:H5'	2.13	0.48
4:B:71:VAL:O	4:B:71:VAL:HG23	2.14	0.48
4:B:90:MET:HE2	4:B:222:ILE:HG21	1.95	0.48
4:B:100:GLY:O	4:B:104:ASN:N	2.47	0.48
4:B:201:ILE:O	4:B:203:GLY:N	2.47	0.48
5:C:8:ILE:O	5:C:9:GLY:C	2.57	0.48
5:C:14:ILE:CG2	5:C:15:THR:H	2.07	0.48
8:F:10:LEU:HD13	8:F:59:TYR:HB3	1.95	0.48
8:F:33:TYR:O	8:F:34:GLY:C	2.55	0.48
8:F:100:ASN:HB2	20:R:23:LYS:HZ2	1.78	0.48
9:G:148:ASN:C	9:G:150:ALA:N	2.72	0.48
10:H:31:PHE:O	10:H:35:ILE:HG13	2.14	0.48
1:A:19:C:H2'	1:A:20:U:H6	1.79	0.48
1:A:1064:G:C4'	1:A:1065:U:H5'	2.43	0.48
1:A:1182:G:H4'	1:A:1183:A:H5''	1.95	0.48
1:A:1240:U:OP2	9:G:116:ALA:HB2	2.13	0.48
1:A:1281:U:H3'	1:A:1281:U:H6	1.79	0.48
1:A:1499:A:O2'	1:A:1500:A:H5'	2.14	0.48
2:X:33:U:H2'	2:X:35:C:OP2	2.14	0.48
4:B:61:LEU:CD2	4:B:64:ARG:HD2	2.35	0.48
5:C:118:GLN:O	5:C:122:GLU:HG3	2.14	0.48
5:C:180:ALA:HB3	5:C:182:ILE:HG13	1.94	0.48
10:H:114:THR:HG21	10:H:129:VAL:HG23	1.96	0.48
11:I:95:LYS:O	11:I:98:PRO:HD2	2.13	0.48
18:P:7:ALA:O	18:P:17:TYR:HA	2.14	0.48
1:A:26:A:H61	1:A:558:G:H1'	1.79	0.48
1:A:189:G:N3	1:A:190(K):G:N2	2.59	0.48
1:A:1256:A:H5'	1:A:1258:G:Cl'	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1319:A:H5'	1:A:1320:C:OP1	2.14	0.48
1:A:1343:G:H2'	1:A:1344:C:H6	1.74	0.48
4:B:154:LEU:O	4:B:155:LEU:C	2.55	0.48
5:C:58:GLU:CB	12:J:92:THR:HG21	2.42	0.48
7:E:92:LYS:HB3	7:E:119:LEU:HB2	1.95	0.48
7:E:102:ALA:HB2	7:E:120:THR:HB	1.96	0.48
8:F:69:GLU:OE1	8:F:69:GLU:N	2.47	0.48
11:I:44:VAL:HG12	11:I:51:ARG:NH1	2.28	0.48
11:I:84:ALA:C	11:I:86:VAL:H	2.22	0.48
14:L:71:PRO:HG2	14:L:102:ARG:HG2	1.95	0.48
14:L:86:ARG:HG3	14:L:86:ARG:HH11	1.79	0.48
14:L:104:VAL:O	14:L:105:TYR:HB2	2.14	0.48
15:M:33:ALA:HA	15:M:59:TYR:CE2	2.49	0.48
15:M:81:LEU:O	15:M:86:CYS:HB3	2.14	0.48
1:A:922:G:N3	1:A:1398:A:H2	2.11	0.48
1:A:1014:A:H2'	1:A:1015:A:C8	2.48	0.48
1:A:1106:G:H5''	5:C:172:ARG:CG	2.43	0.48
1:A:1128:C:H5'	11:I:16:ARG:NH2	2.29	0.48
1:A:1305:G:O2'	1:A:1306:A:C8	2.50	0.48
4:B:76:GLN:O	4:B:208:ILE:HG13	2.14	0.48
5:C:22:TRP:NE1	5:C:36:ASP:OD1	2.45	0.48
6:D:70:ILE:CG2	6:D:71:SER:N	2.77	0.48
10:H:59:LEU:O	10:H:60:ARG:C	2.55	0.48
10:H:64:LYS:HB3	10:H:79:VAL:HG21	1.94	0.48
11:I:37:PHE:O	11:I:39:GLY:N	2.47	0.48
11:I:42:ARG:O	11:I:43:ALA:C	2.56	0.48
14:L:28:LYS:C	14:L:30:ALA:N	2.67	0.48
14:L:77:LEU:HD21	14:L:107:ALA:HA	1.95	0.48
14:L:92:ASP:O	14:L:94:PRO:HD3	2.14	0.48
16:N:11:LYS:C	16:N:13:THR:H	2.22	0.48
18:P:10:GLY:HA3	18:P:15:PRO:HA	1.96	0.48
21:S:61:TYR:CD1	21:S:61:TYR:C	2.92	0.48
21:S:71:LEU:HD12	21:S:71:LEU:N	2.29	0.48
1:A:404:U:OP2	6:D:3:ARG:HD3	2.13	0.47
1:A:462:G:N2	18:P:82:GLN:CB	2.61	0.47
1:A:866:C:H2'	1:A:867:G:O4'	2.14	0.47
1:A:942:G:H2'	1:A:943:U:H6	1.78	0.47
1:A:1160:G:O2'	1:A:1161:C:H5'	2.14	0.47
1:A:1311:G:O6	21:S:2:PRO:HB3	2.14	0.47
4:B:69:LEU:HD23	4:B:70:PHE:N	2.28	0.47
5:C:179:ARG:O	5:C:179:ARG:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:6:VAL:O	8:F:6:VAL:HG12	2.14	0.47
9:G:72:ARG:HA	9:G:96:GLN:NE2	2.28	0.47
10:H:134:ILE:HG22	10:H:135:CYS:N	2.28	0.47
11:I:82:ALA:HB1	11:I:96:LEU:HD23	1.96	0.47
14:L:117:ARG:NH2	14:L:124:LYS:CA	2.76	0.47
19:Q:69:LYS:C	19:Q:70:ARG:HD2	2.39	0.47
23:V:2:GLY:C	23:V:4:GLY:N	2.72	0.47
1:A:337:C:H2'	1:A:338:A:C8	2.48	0.47
1:A:462:G:H2'	1:A:463:A:H5''	1.96	0.47
1:A:832:C:O2'	1:A:833:U:H5'	2.13	0.47
5:C:145:GLY:O	5:C:146:ALA:HB3	2.14	0.47
5:C:187:ALA:HB3	5:C:198:VAL:HB	1.96	0.47
6:D:138:TYR:C	6:D:138:TYR:CD2	2.92	0.47
7:E:12:LEU:HD13	7:E:31:LEU:HB2	1.96	0.47
7:E:12:LEU:HD22	7:E:12:LEU:C	2.39	0.47
8:F:33:TYR:CA	8:F:71:ARG:HH21	2.15	0.47
11:I:84:ALA:C	11:I:86:VAL:N	2.72	0.47
11:I:120:ARG:O	11:I:122:ALA:N	2.47	0.47
12:J:9:ARG:HG3	12:J:9:ARG:O	2.14	0.47
13:K:79:SER:OG	13:K:106:LYS:HG2	2.14	0.47
1:A:1060:C:O2	1:A:1198:G:C2	2.67	0.47
1:A:1222:G:O2'	1:A:1223:C:H5'	2.15	0.47
1:A:1461:G:O2'	1:A:1462:G:H5'	2.14	0.47
4:B:114:ARG:O	4:B:117:GLU:HB3	2.15	0.47
5:C:3:ASN:ND2	5:C:3:ASN:N	2.39	0.47
6:D:17:VAL:CG1	6:D:18:LYS:N	2.77	0.47
6:D:155:LEU:O	6:D:156:GLU:C	2.57	0.47
6:D:163:GLU:C	6:D:165:MET:N	2.72	0.47
7:E:51:VAL:HB	7:E:52:PRO:CD	2.40	0.47
21:S:11:VAL:HA	21:S:38:SER:HB2	1.96	0.47
22:T:56:MET:CE	22:T:85:MET:HA	2.44	0.47
22:T:79:ARG:HG2	22:T:83:ARG:HE	1.79	0.47
1:A:434:U:H2'	1:A:435:C:H6	1.79	0.47
1:A:479:C:H5	1:A:480:U:C4	2.32	0.47
1:A:490:G:H2'	1:A:491:G:H8	1.78	0.47
1:A:1313:U:P	21:S:6:LYS:HB3	2.54	0.47
4:B:59:GLU:O	4:B:62:ALA:HB3	2.14	0.47
4:B:98:LEU:N	4:B:98:LEU:CD2	2.78	0.47
4:B:101:MET:CA	4:B:108:ILE:HG13	2.36	0.47
4:B:190:THR:O	4:B:190:THR:CG2	2.60	0.47
4:B:223:ILE:C	4:B:225:ALA:N	2.71	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:176:LEU:H	6:D:176:LEU:HD23	1.79	0.47
10:H:110:ALA:O	10:H:111:ILE:C	2.57	0.47
14:L:29:GLY:O	14:L:30:ALA:O	2.33	0.47
15:M:117:VAL:CG1	15:M:118:ALA:H	2.19	0.47
16:N:26:ARG:HH12	16:N:46:GLU:HB2	1.80	0.47
19:Q:80:GLY:O	19:Q:81:ARG:CB	2.62	0.47
21:S:28:LYS:HD3	21:S:31:ILE:HD11	1.97	0.47
21:S:63:THR:CG2	21:S:64:GLU:N	2.77	0.47
1:A:114:U:O2'	1:A:115:G:H5'	2.15	0.47
1:A:190(F):G:H4'	1:A:190(G):G:OP2	2.14	0.47
1:A:255:G:O6	1:A:266:G:O6	2.31	0.47
1:A:376:G:P	18:P:67:THR:HG21	2.54	0.47
1:A:406:G:H5'	6:D:5:ILE:HD13	1.96	0.47
1:A:1101:A:H4'	1:A:1102:A:O5'	2.15	0.47
1:A:1187:G:OP1	11:I:113:LYS:HE2	2.14	0.47
1:A:1326:C:H2'	1:A:1327:C:H6	1.79	0.47
4:B:88:ALA:CB	4:B:226:ARG:HH22	2.28	0.47
5:C:29:TYR:OH	16:N:54:PRO:HG2	2.15	0.47
6:D:175:SER:HB3	6:D:186:LEU:HD11	1.96	0.47
7:E:80:ILE:HD11	7:E:91:LEU:HD12	1.94	0.47
12:J:33:GLN:OE1	12:J:33:GLN:O	2.33	0.47
13:K:92:GLU:HB3	13:K:96:ARG:HH22	1.79	0.47
14:L:40:VAL:HG21	14:L:77:LEU:O	2.13	0.47
15:M:67:GLU:HB3	15:M:68:GLY:H	1.49	0.47
15:M:88:ARG:HH11	15:M:88:ARG:HB3	1.80	0.47
19:Q:9:VAL:HG22	19:Q:56:VAL:HG22	1.97	0.47
20:R:28:GLU:H	20:R:28:GLU:CD	2.23	0.47
1:A:180:U:H2'	1:A:181:G:H5'	1.96	0.47
1:A:245:C:O2	1:A:283:C:N3	2.47	0.47
1:A:411:A:H62	1:A:426:G:H22	1.62	0.47
1:A:537:G:OP1	14:L:113:ARG:NH2	2.47	0.47
1:A:543:C:O2'	1:A:544:G:H5'	2.14	0.47
1:A:620:C:C1'	6:D:135:LEU:HD13	2.45	0.47
1:A:1347:G:C2'	1:A:1373:G:H1	2.27	0.47
4:B:237:ALA:C	4:B:239:VAL:H	2.21	0.47
4:B:239:VAL:HB	4:B:240:GLN:NE2	2.29	0.47
5:C:113:ALA:N	5:C:114:PRO:CD	2.77	0.47
5:C:119:ARG:O	5:C:122:GLU:HB2	2.15	0.47
7:E:18:ARG:NH1	7:E:25:ARG:HB2	2.30	0.47
7:E:152:ARG:NH2	10:H:107:LEU:O	2.47	0.47
13:K:15:ALA:HA	13:K:77:MET:CA	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:119:LYS:O	14:L:120:TYR:HB2	2.15	0.47
19:Q:48:GLU:C	19:Q:50:LYS:N	2.71	0.47
1:A:112:G:H5'	1:A:389:A:H4'	1.96	0.47
1:A:1038:C:H2'	1:A:1039:C:C6	2.49	0.47
1:A:1047:G:O2'	1:A:1048:G:H5'	2.14	0.47
1:A:1288:A:H2'	1:A:1289:A:O4'	2.15	0.47
1:A:1290:G:H2'	1:A:1291:G:H8	1.80	0.47
1:A:1343:G:OP1	11:I:125:TYR:HE2	1.96	0.47
1:A:1451:A:O2'	1:A:1452:C:OP1	2.25	0.47
4:B:51:LEU:O	4:B:55:PHE:HD1	1.98	0.47
4:B:55:PHE:O	4:B:56:ARG:C	2.57	0.47
4:B:69:LEU:HD22	4:B:71:VAL:HG13	1.97	0.47
4:B:208:ILE:C	4:B:210:SER:N	2.71	0.47
5:C:36:ASP:HB3	5:C:40:ARG:HH12	1.80	0.47
7:E:43:LEU:HD11	7:E:132:ALA:HB1	1.97	0.47
8:F:76:ALA:O	8:F:80:ARG:HG3	2.14	0.47
10:H:24:THR:CG2	10:H:63:LEU:HD21	2.45	0.47
10:H:86:ILE:O	10:H:88:LYS:HG3	2.15	0.47
12:J:16:LEU:O	12:J:17:ASP:C	2.55	0.47
12:J:94:VAL:HG12	12:J:95:GLU:N	2.29	0.47
13:K:72:ALA:HB1	13:K:77:MET:HG3	1.96	0.47
13:K:92:GLU:OE1	13:K:95:ILE:HD12	2.15	0.47
14:L:28:LYS:O	14:L:28:LYS:HG2	2.15	0.47
14:L:82:VAL:N	14:L:106:ASP:OD1	2.46	0.47
16:N:8:GLU:OE1	16:N:9:LYS:N	2.48	0.47
17:O:39:LEU:HD22	17:O:56:LEU:HD22	1.96	0.47
21:S:45:VAL:HG12	21:S:46:GLY:N	2.30	0.47
1:A:390:C:O3'	18:P:28:ARG:NH2	2.48	0.47
1:A:425:G:C8	1:A:425:G:OP2	2.67	0.47
1:A:848:C:H2'	1:A:849:C:H6	1.80	0.47
1:A:1177:G:O5'	11:I:97:LYS:HE3	2.15	0.47
1:A:1298:C:C4	9:G:114:ARG:HD3	2.50	0.47
4:B:10:LEU:O	4:B:12:GLU:N	2.46	0.47
20:R:39:VAL:CG1	20:R:40:LEU:N	2.76	0.47
20:R:53:ARG:C	20:R:55:ARG:H	2.21	0.47
21:S:36:ARG:NH2	21:S:75:ALA:HB3	2.29	0.47
22:T:56:MET:HE3	22:T:88:VAL:CB	2.44	0.47
23:V:15:ARG:O	23:V:17:THR:HG23	2.15	0.47
1:A:222:U:H2'	1:A:223:U:C6	2.50	0.47
1:A:922:G:O2'	1:A:1398:A:N1	2.45	0.47
1:A:1223:C:H3'	1:A:1224:G:H5''	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1329:A:C2'	1:A:1330:U:H5'	2.44	0.47
1:A:1392:G:H2'	1:A:1393:U:C6	2.50	0.47
1:A:1412:C:H2'	1:A:1413:A:H8	1.78	0.47
1:A:1424:C:O2'	1:A:1425:U:H5'	2.15	0.47
1:A:1508:G:O2'	1:A:1509:C:H5'	2.15	0.47
4:B:30:ARG:HG3	4:B:31:TYR:CD2	2.50	0.47
4:B:102:LEU:HD21	4:B:162:ILE:HD11	1.96	0.47
4:B:134:GLU:C	4:B:136:VAL:N	2.72	0.47
4:B:168:THR:O	4:B:171:ALA:HB2	2.14	0.47
5:C:61:ALA:C	5:C:63:ASN:H	2.23	0.47
6:D:132:ARG:HH11	6:D:132:ARG:HG3	1.80	0.47
14:L:102:ARG:HH22	14:L:110:VAL:HA	1.80	0.47
15:M:22:ILE:CB	15:M:25:ILE:HD12	2.45	0.47
15:M:119:GLY:O	15:M:120:LYS:C	2.58	0.47
1:A:647:C:H2'	1:A:648:A:H8	1.80	0.47
1:A:1014:A:H2	1:A:1219:U:H1'	1.80	0.47
1:A:1054:C:N4	1:A:1196:U:H5	2.13	0.47
1:A:1129:C:O2'	1:A:1131:G:H3'	2.14	0.47
4:B:71:VAL:HG22	4:B:164:VAL:HA	1.97	0.47
5:C:76:VAL:O	5:C:83:ARG:HG3	2.15	0.47
5:C:92:ALA:O	5:C:96:GLY:HA2	2.15	0.47
6:D:78:LEU:CD2	6:D:96:LEU:HB3	2.42	0.47
9:G:136:LYS:O	9:G:139:GLU:N	2.48	0.47
13:K:120:ARG:NH2	13:K:126:ARG:NH1	2.63	0.47
14:L:55:VAL:HG12	14:L:56:ALA:H	1.76	0.47
16:N:24:CYS:HB3	16:N:28:GLY:N	2.30	0.47
17:O:87:ILE:HG22	17:O:88:ARG:NE	2.24	0.47
18:P:19:ILE:HG22	18:P:36:ILE:HG13	1.96	0.47
18:P:28:ARG:NH1	18:P:29:ASP:OD2	2.48	0.47
18:P:43:LYS:HG3	18:P:48:TRP:CD2	2.50	0.47
19:Q:82:MET:O	19:Q:83:ASP:C	2.58	0.47
1:A:437:U:O2'	1:A:438:G:H5'	2.15	0.46
1:A:782:A:H2'	1:A:783:C:O4'	2.15	0.46
1:A:791:G:H2'	1:A:792:A:H5''	1.95	0.46
1:A:861:G:O2'	1:A:862:C:H5'	2.15	0.46
1:A:1060:C:C5	5:C:2:GLY:N	2.83	0.46
1:A:1262:C:H42	1:A:1273:G:H1	1.63	0.46
1:A:1372:U:O2'	1:A:1373:G:H5'	2.15	0.46
1:A:1511:G:O2'	1:A:1512:U:H5'	2.15	0.46
4:B:77:ALA:O	4:B:81:VAL:HG23	2.15	0.46
5:C:129:ALA:HB3	5:C:132:ARG:NE	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:25:ARG:C	6:D:27:TYR:N	2.62	0.46
6:D:106:TYR:CD2	6:D:106:TYR:C	2.93	0.46
11:I:17:VAL:HG11	11:I:81:ILE:HA	1.96	0.46
13:K:87:THR:HG22	13:K:91:ARG:NH2	2.30	0.46
14:L:39:VAL:HG12	14:L:40:VAL:N	2.30	0.46
19:Q:3:LYS:HB3	19:Q:60:ILE:CD1	2.45	0.46
1:A:279:A:H5''	1:A:280:C:H3'	1.96	0.46
1:A:640:A:O2'	1:A:641:U:H5'	2.15	0.46
1:A:908:A:H2'	1:A:909:A:C8	2.49	0.46
1:A:973:G:H3'	1:A:974:A:H5''	1.98	0.46
1:A:1373:G:H5''	9:G:36:LYS:HB2	1.98	0.46
1:A:1486:G:H2'	1:A:1487:G:O4'	2.15	0.46
4:B:7:VAL:C	4:B:8:LYS:HG3	2.40	0.46
4:B:15:VAL:HG12	4:B:16:HIS:N	2.20	0.46
4:B:82:ARG:HB3	4:B:94:ASN:HD21	1.80	0.46
5:C:52:LEU:H	5:C:52:LEU:CD2	2.28	0.46
7:E:135:THR:O	7:E:138:ALA:HB3	2.15	0.46
9:G:16:LEU:HD22	9:G:16:LEU:N	2.30	0.46
11:I:99:LEU:HD22	11:I:99:LEU:N	2.30	0.46
18:P:34:GLU:OE1	18:P:55:ARG:NH1	2.48	0.46
21:S:17:GLU:HA	21:S:20:LEU:CG	2.43	0.46
22:T:39:LYS:HG2	22:T:55:ILE:HD13	1.98	0.46
1:A:1392:G:N2	1:A:1502:A:C8	2.83	0.46
1:A:1425:U:H3	1:A:1475:G:H1	1.63	0.46
1:A:1476:G:O2'	1:A:1477:C:H5'	2.14	0.46
4:B:22:LYS:HG2	4:B:22:LYS:O	2.15	0.46
9:G:51:GLN:C	9:G:53:LYS:N	2.73	0.46
10:H:21:LYS:O	10:H:65:TYR:OH	2.31	0.46
11:I:85:LEU:O	11:I:92:TYR:HD1	1.98	0.46
12:J:4:ILE:CG1	12:J:74:ILE:HB	2.44	0.46
12:J:28:ARG:C	12:J:29:ARG:HD3	2.40	0.46
12:J:32:ALA:CB	12:J:75:ILE:HD13	2.45	0.46
17:O:70:LEU:HD12	17:O:78:TYR:CB	2.45	0.46
17:O:78:TYR:C	17:O:80:ALA:N	2.70	0.46
19:Q:6:LEU:O	19:Q:59:ILE:N	2.44	0.46
19:Q:33:GLY:O	19:Q:34:LYS:C	2.57	0.46
19:Q:68:ARG:O	19:Q:69:LYS:HB2	2.15	0.46
1:A:166:G:O2'	1:A:167:G:H5'	2.15	0.46
1:A:456:C:O2'	1:A:457:C:H5'	2.15	0.46
1:A:1250:A:C5'	11:I:68:GLY:N	2.78	0.46
1:A:1294:G:O2'	1:A:1295:G:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1405:G:P	24:A:1545:PAR:O34	2.74	0.46
4:B:60:ASP:OD1	4:B:64:ARG:NH2	2.49	0.46
5:C:191:THR:HG22	5:C:192:THR:H	1.79	0.46
7:E:106:PRO:O	7:E:110:LEU:HG	2.15	0.46
7:E:144:THR:CG2	7:E:146:ALA:H	2.28	0.46
11:I:5:TYR:HA	11:I:17:VAL:O	2.16	0.46
12:J:48:THR:HA	12:J:62:HIS:CD2	2.45	0.46
1:A:22:G:O2'	1:A:23:C:H5'	2.15	0.46
1:A:192:U:O4'	22:T:103:GLY:HA2	2.14	0.46
1:A:386:C:O2'	1:A:387:U:H5'	2.16	0.46
1:A:640:A:C2'	1:A:641:U:H5'	2.46	0.46
1:A:706:A:H1'	13:K:29:ILE:CD1	2.45	0.46
1:A:797:C:O2'	1:A:798:G:H5'	2.16	0.46
1:A:1129:C:HO2'	1:A:1131:G:H8	1.54	0.46
1:A:1202:G:C2'	1:A:1203:C:H5'	2.45	0.46
1:A:1301:U:O2'	1:A:1302:U:P	2.74	0.46
1:A:1406:U:O2'	1:A:1407:C:H5'	2.16	0.46
4:B:159:PRO:HB2	4:B:161:ALA:O	2.16	0.46
10:H:82:HIS:CB	10:H:138:TRP:CE2	2.98	0.46
12:J:33:GLN:O	12:J:34:VAL:HB	2.14	0.46
14:L:111:LYS:O	14:L:112:ASP:HB2	2.16	0.46
22:T:39:LYS:HE2	22:T:55:ILE:HD11	1.96	0.46
1:A:298:A:H2'	1:A:299:G:O4'	2.15	0.46
1:A:539:A:H2'	1:A:540:G:C8	2.51	0.46
1:A:803:G:H2'	1:A:804:U:O4'	2.15	0.46
4:B:25:ASN:HD22	4:B:27:LYS:N	2.13	0.46
4:B:80:ILE:CD1	4:B:208:ILE:HG23	2.41	0.46
4:B:83:MET:HE3	4:B:235:SER:HA	1.98	0.46
6:D:31:CYS:O	6:D:32:ALA:HB3	2.15	0.46
7:E:107:ARG:O	7:E:110:LEU:N	2.32	0.46
11:I:93:ARG:CB	11:I:93:ARG:HH11	2.29	0.46
13:K:48:ILE:HD11	13:K:64:ALA:HA	1.98	0.46
18:P:81:ARG:HE	18:P:81:ARG:C	2.23	0.46
21:S:39:THR:O	21:S:44:MET:HE1	2.16	0.46
1:A:22:G:H2'	1:A:23:C:C6	2.51	0.46
1:A:1056:U:H5'	5:C:163:ALA:CB	2.46	0.46
1:A:1237:C:C4'	1:A:1334:G:N2	2.79	0.46
1:A:1296:C:H4'	1:A:1302:U:C5	2.51	0.46
4:B:88:ALA:O	4:B:90:MET:N	2.47	0.46
5:C:46:GLU:C	5:C:48:TYR:H	2.23	0.46
5:C:139:GLN:O	5:C:140:ARG:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:159:ARG:HD3	6:D:159:ARG:HA	1.83	0.46
8:F:43:LEU:N	8:F:43:LEU:CD2	2.79	0.46
10:H:51:VAL:CG1	10:H:52:ASP:N	2.79	0.46
14:L:52:LEU:O	14:L:54:LYS:NZ	2.39	0.46
15:M:78:ILE:O	15:M:81:LEU:HB2	2.16	0.46
19:Q:86:GLU:O	19:Q:87:LYS:C	2.59	0.46
1:A:7:G:H21	7:E:121:LYS:HG2	1.80	0.46
1:A:430:A:C3'	1:A:431:A:H5''	2.45	0.46
1:A:645:C:O2'	1:A:646:U:H5'	2.15	0.46
1:A:646:U:O2'	1:A:647:C:H5'	2.15	0.46
1:A:831:U:H2'	1:A:832:C:H6	1.80	0.46
4:B:95:GLN:OE1	4:B:95:GLN:HA	2.15	0.46
4:B:107:THR:C	4:B:109:SER:H	2.23	0.46
9:G:122:HIS:HD2	9:G:125:MET:CE	2.28	0.46
11:I:42:ARG:HG2	11:I:42:ARG:HH11	1.81	0.46
14:L:59:ARG:NH1	14:L:65:GLU:HG2	2.30	0.46
19:Q:48:GLU:O	19:Q:50:LYS:N	2.49	0.46
1:A:131:C:H2'	1:A:132:C:C6	2.51	0.46
1:A:624:C:O2'	1:A:625:G:H5'	2.16	0.46
1:A:961:U:O2'	1:A:962:C:H5'	2.16	0.46
1:A:992:U:O2'	1:A:993:G:P	2.73	0.46
1:A:1277:C:C2'	1:A:1278:U:H5'	2.46	0.46
4:B:134:GLU:HA	4:B:137:ARG:HB3	1.98	0.46
5:C:108:ASN:C	5:C:110:ASN:H	2.23	0.46
6:D:170:VAL:O	6:D:171:GLY:C	2.57	0.46
9:G:136:LYS:O	9:G:137:LYS:C	2.57	0.46
9:G:140:ASP:O	9:G:143:ARG:HB3	2.15	0.46
9:G:155:ARG:O	9:G:156:TRP:HB3	2.15	0.46
12:J:96:ILE:CG2	12:J:97:GLU:N	2.78	0.46
18:P:21:VAL:HG21	18:P:59:TRP:CD1	2.51	0.46
18:P:31:LYS:NZ	18:P:31:LYS:HB3	2.31	0.46
20:R:87:ARG:O	20:R:88:LYS:HB3	2.16	0.46
1:A:123:C:OP1	1:A:312:C:H5'	2.16	0.46
1:A:193:C:H2'	1:A:194:C:C6	2.51	0.46
1:A:744:C:H2'	1:A:745:C:C6	2.50	0.46
1:A:1010:G:N2	1:A:1020:U:H1'	2.31	0.46
1:A:1131:G:H2'	1:A:1132:C:H6	1.79	0.46
4:B:44:LEU:O	4:B:47:THR:N	2.49	0.46
5:C:32:LEU:HB3	5:C:59:ARG:NH1	2.31	0.46
6:D:4:TYR:O	6:D:5:ILE:HB	2.16	0.46
8:F:100:ASN:CB	20:R:23:LYS:HZ2	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:107:ALA:O	9:G:110:GLN:HB2	2.16	0.46
10:H:36:LEU:HD12	10:H:59:LEU:HD13	1.97	0.46
1:A:119:A:H4'	1:A:120:A:O5'	2.16	0.45
1:A:716:A:N3	13:K:117:ASN:O	2.49	0.45
1:A:925:G:C2	1:A:927:G:C8	3.04	0.45
1:A:1320:C:O2'	1:A:1321:C:H5'	2.15	0.45
1:A:1339:A:H2'	1:A:1340:A:O4'	2.16	0.45
1:A:1371:G:O3'	11:I:69:GLY:HA3	2.16	0.45
4:B:21:ARG:HB2	4:B:22:LYS:H	1.61	0.45
8:F:92:LYS:HB2	8:F:92:LYS:NZ	2.31	0.45
10:H:38:ILE:CG2	10:H:120:THR:HG22	2.46	0.45
1:A:178:C:O2'	1:A:179:A:H5'	2.17	0.45
1:A:757:U:H2'	1:A:758:G:O4'	2.16	0.45
1:A:819:A:H4'	1:A:820:U:OP2	2.14	0.45
1:A:826:C:H2'	1:A:827:U:H6	1.80	0.45
1:A:934:C:C4	1:A:1345:U:C5	3.04	0.45
5:C:7:PRO:CB	5:C:11:ARG:HH21	2.28	0.45
6:D:8:VAL:HB	6:D:21:LEU:CD1	2.44	0.45
7:E:80:ILE:CD1	7:E:91:LEU:HD12	2.46	0.45
10:H:85:ARG:C	10:H:85:ARG:HD3	2.41	0.45
10:H:104:ARG:O	10:H:105:ARG:C	2.59	0.45
11:I:27:THR:HG23	11:I:30:GLY:O	2.16	0.45
11:I:89:ASN:ND2	11:I:91:ASP:HB2	2.30	0.45
16:N:6:LEU:C	16:N:8:GLU:H	2.22	0.45
16:N:45:ARG:HG2	16:N:49:HIS:CD2	2.52	0.45
1:A:359:U:H2'	1:A:360:A:C8	2.51	0.45
1:A:1033:G:H2'	1:A:1034:G:C8	2.48	0.45
1:A:1110:A:H8	1:A:1110:A:O5'	1.98	0.45
1:A:1281:U:H4'	1:A:1282:C:OP2	2.17	0.45
4:B:25:ASN:HD21	4:B:27:LYS:HB2	1.81	0.45
4:B:66:GLY:HA2	4:B:160:ASP:OD2	2.16	0.45
4:B:75:LYS:C	4:B:77:ALA:N	2.74	0.45
4:B:79:ASP:O	4:B:82:ARG:HG2	2.16	0.45
7:E:11:ILE:CG2	7:E:12:LEU:HD12	2.45	0.45
7:E:43:LEU:HB2	7:E:136:MET:HE2	1.99	0.45
8:F:55:ASP:CB	8:F:86:ARG:HH12	2.29	0.45
11:I:44:VAL:CG1	11:I:51:ARG:HH12	2.30	0.45
13:K:97:ALA:O	13:K:98:LEU:C	2.59	0.45
15:M:110:ARG:HH11	15:M:110:ARG:CG	2.29	0.45
21:S:12:ASP:HB3	21:S:14:HIS:CE1	2.52	0.45
22:T:13:LEU:C	22:T:13:LEU:CD1	2.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:6:ARG:HE	23:V:7:ARG:HE	1.63	0.45
1:A:67:C:O2'	1:A:171:A:H1'	2.16	0.45
1:A:149:A:O2'	1:A:150:C:H5'	2.17	0.45
1:A:190(A):C:N4	1:A:190(H):G:H1	2.15	0.45
1:A:442:C:H2'	1:A:443:C:C6	2.52	0.45
1:A:602:A:O2'	1:A:603:U:H5'	2.16	0.45
1:A:1279:A:O2'	1:A:1282:C:N4	2.49	0.45
9:G:120:ILE:HD12	9:G:120:ILE:N	2.31	0.45
12:J:23:ILE:N	12:J:23:ILE:HD12	2.31	0.45
12:J:47:PHE:HD2	16:N:34:TYR:CD2	2.34	0.45
13:K:127:LYS:HA	13:K:127:LYS:HE3	1.98	0.45
15:M:2:ALA:O	15:M:3:ARG:C	2.57	0.45
16:N:59:ALA:O	16:N:60:SER:HB2	2.16	0.45
1:A:622:A:C8	1:A:623:C:C6	3.05	0.45
1:A:718:G:H5'	13:K:117:ASN:OD1	2.16	0.45
1:A:778:G:O2'	1:A:779:C:H5'	2.16	0.45
1:A:1222:G:O3'	21:S:78:ARG:NH1	2.49	0.45
1:A:1227:A:H2'	1:A:1228:C:O5'	2.17	0.45
1:A:1370:G:C2	1:A:1371:G:N7	2.84	0.45
4:B:74:LYS:NZ	4:B:206:ASP:HB2	2.31	0.45
6:D:58:LEU:CD2	6:D:62:GLN:HG2	2.46	0.45
6:D:107:ARG:HB3	6:D:174:LEU:CD1	2.47	0.45
6:D:118:ARG:HG3	6:D:136:PRO:HB3	1.98	0.45
6:D:208:SER:O	6:D:209:ARG:C	2.60	0.45
7:E:80:ILE:HD12	7:E:80:ILE:H	1.81	0.45
8:F:27:GLN:HA	8:F:27:GLN:NE2	2.31	0.45
14:L:38:THR:O	14:L:79:GLU:HB3	2.16	0.45
15:M:15:VAL:HG11	15:M:34:LEU:HD21	1.98	0.45
21:S:28:LYS:HG2	21:S:29:ARG:N	2.17	0.45
21:S:40:ILE:HG13	21:S:69:HIS:O	2.16	0.45
1:A:942:G:O2'	1:A:943:U:H5'	2.16	0.45
1:A:993:G:H4'	1:A:994:A:OP2	2.16	0.45
1:A:1206:G:C6	1:A:1207:G:C5	3.05	0.45
1:A:1256:A:H8	5:C:27:LYS:HZ1	1.63	0.45
1:A:1494:G:O2'	1:A:1495:U:H5'	2.17	0.45
5:C:73:PRO:O	5:C:74:GLY:C	2.60	0.45
5:C:133:ALA:O	5:C:134:ILE:C	2.60	0.45
6:D:173:TRP:CD1	6:D:174:LEU:HG	2.51	0.45
8:F:27:GLN:HA	8:F:27:GLN:HE21	1.82	0.45
12:J:6:ILE:HG23	12:J:98:ILE:CG2	2.46	0.45
12:J:7:LYS:HZ2	12:J:40:LEU:CD1	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:89:ASP:CG	12:J:91:PRO:HD2	2.41	0.45
13:K:17:GLY:O	13:K:80:VAL:HA	2.16	0.45
14:L:33:ARG:HD2	14:L:33:ARG:HA	1.66	0.45
14:L:83:VAL:CG2	14:L:100:ILE:HG23	2.47	0.45
15:M:44:ARG:HB3	15:M:46:LYS:HG2	1.98	0.45
15:M:66:LEU:O	15:M:67:GLU:C	2.59	0.45
16:N:14:PRO:O	16:N:15:LYS:HB2	2.16	0.45
22:T:53:LEU:O	22:T:54:LYS:C	2.59	0.45
23:V:9:ARG:NH1	23:V:22:ARG:HA	2.32	0.45
1:A:105:G:H2'	1:A:106:C:C6	2.51	0.45
1:A:109:A:H2'	1:A:326:G:H21	1.80	0.45
1:A:302:G:H5''	14:L:17:LYS:HZ2	1.80	0.45
1:A:425:G:H8	1:A:425:G:H5''	1.81	0.45
1:A:429:U:H4'	1:A:430:A:OP1	2.17	0.45
1:A:685:G:O2'	1:A:686:U:H5'	2.16	0.45
1:A:1136:U:H5''	1:A:1137:C:H5	1.81	0.45
1:A:1184:G:H2'	1:A:1185:G:H8	1.81	0.45
4:B:140:HIS:O	4:B:143:GLU:HB2	2.17	0.45
7:E:129:ILE:H	7:E:129:ILE:HD12	1.82	0.45
9:G:79:ARG:HD3	9:G:79:ARG:C	2.41	0.45
12:J:60:ARG:N	12:J:60:ARG:CD	2.74	0.45
14:L:117:ARG:CZ	14:L:124:LYS:HA	2.47	0.45
18:P:20:VAL:CG1	18:P:21:VAL:N	2.78	0.45
1:A:407:G:O2'	1:A:408:A:OP1	2.31	0.45
1:A:949:A:N7	15:M:106:ASN:ND2	2.65	0.45
1:A:1417:G:H2'	1:A:1482:G:H22	1.81	0.45
1:A:1438:G:H2'	1:A:1439:C:C6	2.52	0.45
6:D:153:ARG:HE	6:D:181:MET:CE	2.29	0.45
6:D:162:LEU:HD13	6:D:181:MET:HG2	1.97	0.45
7:E:51:VAL:CB	7:E:52:PRO:HD3	2.41	0.45
11:I:45:ALA:O	11:I:46:ALA:C	2.60	0.45
13:K:14:VAL:HG21	13:K:40:ILE:CD1	2.47	0.45
18:P:26:ARG:HG3	18:P:27:LYS:N	2.32	0.45
1:A:13:U:C5	1:A:916:G:O6	2.70	0.45
1:A:151:A:H2'	1:A:152:A:O4'	2.17	0.45
1:A:267:C:OP2	19:Q:67:LYS:HD2	2.16	0.45
1:A:423:G:H5''	1:A:424:G:H21	1.82	0.45
1:A:442:C:H2'	1:A:443:C:H6	1.81	0.45
1:A:601:C:O2'	1:A:602:A:H5'	2.17	0.45
1:A:624:C:H2'	1:A:625:G:H8	1.81	0.45
1:A:750:G:H1'	17:O:22:THR:OG1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:865:A:H2'	1:A:866:C:C6	2.52	0.45
1:A:1057:G:C5	1:A:1204:A:C2	3.04	0.45
1:A:1327:C:OP1	23:V:20:LYS:HB3	2.17	0.45
1:A:1370:G:C2	1:A:1371:G:C8	3.05	0.45
4:B:161:ALA:HB1	4:B:185:ILE:HD11	1.98	0.45
5:C:79:ARG:CB	5:C:79:ARG:HH11	2.30	0.45
7:E:89:ILE:HD13	7:E:90:VAL:H	1.81	0.45
14:L:27:LEU:HG	14:L:28:LYS:N	2.31	0.45
20:R:47:THR:HA	20:R:83:GLU:HB2	1.98	0.45
21:S:61:TYR:C	21:S:61:TYR:HD1	2.25	0.45
1:A:410:G:O4'	1:A:431:A:N6	2.46	0.45
1:A:562:C:H1'	14:L:15:ARG:HB3	1.98	0.45
1:A:629:G:O2'	1:A:630:G:H5'	2.17	0.45
1:A:783:C:O2'	1:A:784:C:H5'	2.17	0.45
1:A:1038:C:H2'	1:A:1039:C:H6	1.81	0.45
1:A:1194:U:O2'	1:A:1195:C:H5'	2.17	0.45
1:A:1509:C:H2'	1:A:1510:U:O4'	2.17	0.45
4:B:15:VAL:CG1	4:B:209:ARG:HG3	2.47	0.45
4:B:37:ASN:C	4:B:39:ILE:HD12	2.42	0.45
4:B:97:TRP:CE3	4:B:98:LEU:O	2.70	0.45
7:E:80:ILE:CG2	10:H:104:ARG:NH2	2.80	0.45
10:H:122:ARG:HH11	10:H:122:ARG:HG3	1.82	0.45
12:J:89:ASP:O	12:J:90:LEU:HD23	2.18	0.45
20:R:17:SER:HB2	20:R:54:ARG:CZ	2.47	0.45
22:T:56:MET:CE	22:T:88:VAL:HB	2.47	0.45
1:A:131:C:H2'	1:A:132:C:H6	1.82	0.44
1:A:769:G:H4'	1:A:1513:A:H4'	1.99	0.44
1:A:1118:C:C1'	1:A:1179:A:C4	3.00	0.44
1:A:1250:A:C5'	11:I:68:GLY:H	2.29	0.44
1:A:1329:A:O2'	1:A:1330:U:H5'	2.17	0.44
1:A:1371:G:OP2	11:I:11:LYS:HE2	2.18	0.44
1:A:1505:G:C8	1:A:1505:G:H3'	2.52	0.44
4:B:132:LYS:C	4:B:134:GLU:N	2.70	0.44
4:B:212:GLN:O	4:B:216:SER:CB	2.65	0.44
5:C:22:TRP:CZ3	5:C:32:LEU:HD12	2.52	0.44
12:J:29:ARG:HH11	12:J:29:ARG:CA	2.30	0.44
19:Q:59:ILE:HD13	19:Q:73:VAL:HA	1.99	0.44
1:A:254:G:O2'	1:A:255:G:H5'	2.16	0.44
1:A:532:A:C2'	1:A:533:A:OP1	2.65	0.44
1:A:1131:G:OP1	11:I:3:GLN:NE2	2.51	0.44
1:A:1328:C:O2'	1:A:1329:A:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1417:G:H2'	1:A:1482:G:N2	2.33	0.44
4:B:24:TRP:CG	4:B:25:ASN:N	2.80	0.44
4:B:132:LYS:HD3	4:B:135:GLN:CB	2.47	0.44
4:B:209:ARG:O	4:B:209:ARG:HD3	2.17	0.44
5:C:5:ILE:C	5:C:5:ILE:CD1	2.90	0.44
5:C:134:ILE:CG2	5:C:168:ALA:HB3	2.47	0.44
6:D:67:ILE:HG22	6:D:68:TYR:N	2.31	0.44
6:D:163:GLU:O	6:D:165:MET:N	2.50	0.44
14:L:47:LYS:CB	14:L:48:PRO:CD	2.76	0.44
21:S:33:THR:CG2	21:S:34:TRP:N	2.80	0.44
21:S:71:LEU:H	21:S:71:LEU:CD1	2.30	0.44
22:T:96:GLY:O	22:T:97:ALA:CB	2.64	0.44
1:A:948:C:O2'	1:A:949:A:H5'	2.17	0.44
1:A:1060:C:H2'	1:A:1061:G:H8	1.83	0.44
1:A:1306:A:H2'	1:A:1307:U:O4'	2.16	0.44
1:A:1406:U:OP2	24:A:1545:PAR:N24	2.50	0.44
1:A:1459:C:O2'	1:A:1460:A:H5'	2.17	0.44
1:A:1472:U:O2'	1:A:1473:A:H5'	2.17	0.44
4:B:9:GLU:C	4:B:9:GLU:OE1	2.61	0.44
4:B:115:LEU:HD21	4:B:153:ARG:NH1	2.32	0.44
6:D:190:ASP:O	6:D:191:ARG:C	2.59	0.44
15:M:37:THR:HG22	15:M:37:THR:O	2.17	0.44
15:M:67:GLU:O	15:M:68:GLY:C	2.59	0.44
16:N:29:ARG:HG2	16:N:29:ARG:HH11	1.81	0.44
23:V:2:GLY:O	23:V:4:GLY:N	2.50	0.44
1:A:52:G:O2'	1:A:53:A:H5'	2.16	0.44
1:A:109:A:H5'	1:A:110:C:C5	2.51	0.44
1:A:401:C:H1'	1:A:622:A:H1'	1.98	0.44
1:A:921:U:O2'	7:E:19:MET:O	2.34	0.44
1:A:924:C:H5'	1:A:1399:C:OP2	2.18	0.44
1:A:1060:C:N4	5:C:2:GLY:N	2.66	0.44
1:A:1133:G:H2'	1:A:1134:G:C8	2.50	0.44
1:A:1196:U:H5''	1:A:1197:G:H5'	2.00	0.44
1:A:1286:A:H2'	1:A:1287:A:O5'	2.17	0.44
4:B:58:ILE:O	4:B:62:ALA:HB2	2.17	0.44
5:C:39:ILE:C	5:C:41:GLY:N	2.73	0.44
5:C:136:GLN:O	5:C:139:GLN:HB2	2.17	0.44
11:I:111:ARG:O	11:I:113:LYS:HD2	2.16	0.44
12:J:4:ILE:HA	12:J:100:THR:HA	1.99	0.44
13:K:115:PRO:C	13:K:117:ASN:H	2.26	0.44
14:L:43:VAL:CG1	14:L:44:THR:N	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:34:LEU:HD23	15:M:34:LEU:HA	1.84	0.44
17:O:70:LEU:HD12	17:O:78:TYR:CA	2.47	0.44
18:P:20:VAL:HG13	18:P:32:TYR:HB2	1.99	0.44
22:T:97:ALA:O	22:T:99:LEU:N	2.51	0.44
1:A:188:C:N3	1:A:189:G:O2'	2.51	0.44
1:A:404:U:H2'	1:A:405:U:C6	2.52	0.44
1:A:448:A:H2'	1:A:449:C:C6	2.52	0.44
1:A:476:G:H21	1:A:478:A:C5'	2.31	0.44
1:A:652:U:O4	1:A:752:G:O2'	2.32	0.44
1:A:1112:C:O2	5:C:178:LEU:O	2.36	0.44
1:A:1148:U:O2'	1:A:1149:C:H5'	2.17	0.44
1:A:1413:A:H2	1:A:1487:G:H22	1.64	0.44
1:A:1427:U:H2'	1:A:1428:A:H8	1.82	0.44
4:B:187:LEU:HD13	4:B:214:ILE:HG21	1.99	0.44
5:C:43:LEU:CD2	5:C:68:VAL:HG21	2.47	0.44
5:C:167:TRP:HB3	5:C:168:ALA:H	1.48	0.44
6:D:150:GLU:HA	6:D:153:ARG:HG2	2.00	0.44
10:H:11:THR:O	10:H:12:ARG:C	2.59	0.44
13:K:33:THR:HG22	13:K:39:PRO:CA	2.41	0.44
15:M:60:VAL:CG1	15:M:66:LEU:HD11	2.48	0.44
17:O:56:LEU:HD12	17:O:56:LEU:O	2.18	0.44
18:P:18:ARG:NH1	18:P:32:TYR:OH	2.49	0.44
19:Q:75:ARG:HG3	19:Q:75:ARG:NH1	2.33	0.44
22:T:10:LEU:HD11	22:T:12:ALA:HB3	2.00	0.44
22:T:38:LYS:O	22:T:42:GLN:HB2	2.17	0.44
22:T:67:ALA:HB2	22:T:77:ALA:HB2	1.99	0.44
22:T:100:ILE:HG22	22:T:102:GLY:N	2.32	0.44
1:A:9:G:OP2	7:E:121:LYS:NZ	2.47	0.44
1:A:156:G:O2'	1:A:157:G:H5'	2.17	0.44
1:A:338:A:H2	1:A:351:G:H22	1.64	0.44
1:A:407:G:H2'	1:A:431:A:P	2.58	0.44
1:A:603:U:H2'	1:A:604:G:H8	1.83	0.44
1:A:690:G:H2'	1:A:691:G:O4'	2.17	0.44
1:A:806:C:O2'	1:A:807:A:H5'	2.17	0.44
1:A:1039:C:H2'	1:A:1040:U:H6	1.82	0.44
5:C:83:ARG:HA	5:C:86:VAL:CG2	2.46	0.44
7:E:101:ILE:HD12	7:E:119:LEU:HD23	1.98	0.44
9:G:50:ILE:CG2	9:G:61:VAL:HG21	2.47	0.44
11:I:114:TYR:C	11:I:116:LYS:H	2.26	0.44
12:J:32:ALA:O	12:J:34:VAL:HG23	2.17	0.44
12:J:66:ARG:HE	12:J:66:ARG:HB3	1.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:39:ILE:CD1	15:M:52:GLU:HB3	2.47	0.44
17:O:74:ASP:CG	17:O:77:ARG:HG3	2.43	0.44
20:R:27:GLY:O	20:R:29:PHE:HD2	2.00	0.44
1:A:50:A:N6	1:A:361:G:H4'	2.33	0.44
1:A:190:C:OP1	1:A:190(K):G:C2	2.71	0.44
1:A:920:U:H2'	1:A:921:U:C6	2.52	0.44
4:B:144:ARG:O	4:B:145:LEU:C	2.60	0.44
8:F:91:VAL:HG12	8:F:92:LYS:O	2.18	0.44
13:K:96:ARG:NH1	13:K:96:ARG:HB2	2.32	0.44
15:M:11:ARG:CG	15:M:12:ASN:H	2.31	0.44
16:N:34:TYR:N	16:N:34:TYR:CD1	2.85	0.44
20:R:52:PRO:O	20:R:56:THR:HG23	2.18	0.44
1:A:91:C:H2'	1:A:92:C:H6	1.83	0.44
1:A:488:C:O5'	1:A:488:C:H6	2.01	0.44
1:A:791:G:C2'	1:A:792:A:C5'	2.96	0.44
1:A:1182:G:H4'	1:A:1183:A:C5'	2.47	0.44
1:A:1221:G:O2'	1:A:1222:G:H5'	2.18	0.44
1:A:1431:C:C2'	1:A:1432:G:H5'	2.48	0.44
4:B:148:TYR:CD2	4:B:148:TYR:N	2.85	0.44
5:C:23:TYR:CG	5:C:24:ALA:N	2.86	0.44
9:G:18:TYR:HD2	9:G:59:LEU:HB2	1.79	0.44
12:J:24:VAL:O	12:J:24:VAL:HG12	2.18	0.44
12:J:26:ALA:HA	12:J:29:ARG:NH2	2.33	0.44
12:J:91:PRO:HB2	12:J:94:VAL:CG2	2.48	0.44
13:K:95:ILE:CG2	13:K:108:ILE:HD13	2.48	0.44
14:L:115:LYS:O	14:L:117:ARG:N	2.49	0.44
20:R:43:PHE:CA	20:R:51:LEU:HD12	2.48	0.44
1:A:17:U:H2'	1:A:18:C:H6	1.76	0.44
1:A:149:A:H2'	1:A:150:C:H6	1.82	0.44
1:A:160:A:H1'	1:A:344:A:N7	2.32	0.44
1:A:369:C:O2'	1:A:370:C:H5'	2.17	0.44
1:A:383:A:H2'	1:A:384:G:H5'	1.99	0.44
1:A:945:G:C2	1:A:946:A:C8	3.05	0.44
1:A:1137:C:C4'	1:A:1138:G:C2	2.99	0.44
4:B:91:PRO:HG3	4:B:154:LEU:CB	2.29	0.44
5:C:50:ALA:O	5:C:70:VAL:HG12	2.17	0.44
6:D:30:LYS:C	6:D:32:ALA:H	2.26	0.44
6:D:153:ARG:HH21	6:D:181:MET:HE3	1.80	0.44
7:E:60:TYR:O	7:E:64:ARG:HG2	2.18	0.44
8:F:14:LEU:HA	8:F:18:GLN:HE21	1.83	0.44
9:G:32:ARG:O	9:G:33:ASP:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:72:ARG:HG2	9:G:142:GLU:OE1	2.18	0.44
13:K:48:ILE:HG13	13:K:64:ALA:N	2.33	0.44
13:K:99:GLN:HA	13:K:105:VAL:CG2	2.48	0.44
14:L:73:GLU:OE2	14:L:73:GLU:HA	2.18	0.44
18:P:50:LYS:HG2	18:P:51:VAL:N	2.33	0.44
20:R:20:ALA:O	20:R:21:LYS:O	2.35	0.44
1:A:358:U:H2'	1:A:359:U:C6	2.53	0.43
1:A:978:A:C5	1:A:1319:A:C2	3.05	0.43
1:A:981:U:O5'	1:A:981:U:H6	2.00	0.43
1:A:1053:G:O2'	1:A:1199:U:H5	2.01	0.43
1:A:1060:C:H41	5:C:2:GLY:N	2.15	0.43
1:A:1349:A:H2'	1:A:1350:A:H8	1.83	0.43
1:A:1480:G:H2'	1:A:1481:U:C6	2.53	0.43
5:C:101:LEU:O	5:C:101:LEU:HD22	2.17	0.43
5:C:149:ALA:HA	5:C:201:TYR:O	2.18	0.43
6:D:111:ALA:HA	6:D:116:GLN:OE1	2.18	0.43
8:F:40:VAL:HG22	8:F:41:GLU:N	2.32	0.43
9:G:15:ASP:C	9:G:17:VAL:H	2.26	0.43
9:G:80:VAL:O	9:G:81:GLY:C	2.60	0.43
11:I:32:ASP:O	11:I:33:PHE:C	2.60	0.43
13:K:48:ILE:HD11	13:K:67:ASP:HB2	1.99	0.43
14:L:38:THR:HB	14:L:57:LYS:HB2	2.00	0.43
19:Q:13:ASP:H	19:Q:14:LYS:HD2	1.83	0.43
19:Q:95:TYR:O	19:Q:97:SER:O	2.36	0.43
1:A:200:G:H2'	1:A:201:C:O4'	2.18	0.43
1:A:538:G:OP2	14:L:115:LYS:HG3	2.17	0.43
1:A:756:C:H2'	1:A:757:U:O4'	2.17	0.43
1:A:826:C:H2'	1:A:827:U:C6	2.53	0.43
1:A:976:G:N7	1:A:1358:U:C2	2.86	0.43
1:A:1064:G:N2	1:A:1190:G:H2'	2.32	0.43
1:A:1397:C:O2'	1:A:1398:A:P	2.76	0.43
1:A:1426:C:H2'	1:A:1427:U:C6	2.53	0.43
1:A:1428:A:H2'	1:A:1429:C:H6	1.82	0.43
4:B:9:GLU:HB2	4:B:217:ARG:HH12	1.83	0.43
4:B:34:ALA:O	4:B:41:ILE:N	2.42	0.43
4:B:78:GLN:HG2	4:B:94:ASN:HB3	2.00	0.43
4:B:83:MET:HG3	4:B:238:LEU:CD1	2.49	0.43
5:C:79:ARG:NH1	5:C:79:ARG:CB	2.80	0.43
5:C:91:LEU:HD23	5:C:92:ALA:HB2	2.00	0.43
13:K:110:ASP:OD2	20:R:88:LYS:NZ	2.51	0.43
14:L:93:LEU:N	14:L:93:LEU:HD23	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:98:TYR:N	14:L:98:TYR:CD1	2.86	0.43
15:M:8:GLU:HG2	15:M:67:GLU:HG3	2.00	0.43
19:Q:13:ASP:O	19:Q:13:ASP:OD2	2.36	0.43
1:A:115:G:H1'	1:A:116:A:N7	2.34	0.43
1:A:619:U:O2	6:D:133:VAL:HA	2.18	0.43
1:A:833:U:H2'	1:A:834:C:C6	2.53	0.43
1:A:1481:U:O2'	1:A:1482:G:H5'	2.18	0.43
4:B:62:ALA:C	4:B:64:ARG:H	2.24	0.43
5:C:52:LEU:H	5:C:52:LEU:HD23	1.82	0.43
6:D:36:ARG:N	6:D:37:PRO:CD	2.51	0.43
6:D:187:ARG:NH1	6:D:188:LEU:HD12	2.33	0.43
10:H:61:VAL:O	10:H:63:LEU:HD22	2.18	0.43
12:J:55:LYS:O	12:J:56:HIS:C	2.61	0.43
13:K:108:ILE:HB	20:R:87:ARG:O	2.18	0.43
14:L:32:PHE:HB3	14:L:84:LEU:HD11	1.99	0.43
20:R:55:ARG:NH1	20:R:55:ARG:HB3	2.33	0.43
22:T:13:LEU:HD12	22:T:14:LYS:N	2.34	0.43
22:T:56:MET:HE2	22:T:85:MET:HA	1.99	0.43
22:T:61:SER:O	22:T:62:LEU:C	2.59	0.43
22:T:100:ILE:HG22	22:T:102:GLY:CA	2.48	0.43
1:A:158:G:O2'	1:A:159:G:H5'	2.19	0.43
1:A:251:G:H4'	1:A:252:U:O5'	2.18	0.43
1:A:444:C:H2'	1:A:445:G:C8	2.47	0.43
1:A:585:G:N3	1:A:879:C:H4'	2.34	0.43
1:A:751:U:H4'	17:O:24:SER:HA	1.99	0.43
1:A:789:U:N3	1:A:792:A:OP2	2.44	0.43
1:A:1151:A:H5''	12:J:42:THR:OG1	2.18	0.43
1:A:1207:G:H2'	1:A:1208:C:H6	1.84	0.43
4:B:15:VAL:HG11	4:B:210:SER:HA	1.99	0.43
4:B:236:TYR:CD2	4:B:239:VAL:HG21	2.53	0.43
5:C:39:ILE:HG22	5:C:40:ARG:N	2.33	0.43
5:C:58:GLU:HB2	5:C:65:ALA:HB2	1.99	0.43
5:C:193:TYR:CE1	5:C:196:LEU:HD21	2.49	0.43
8:F:46:ARG:HB2	8:F:60:PHE:CE1	2.54	0.43
12:J:12:ASP:OD1	12:J:14:LYS:HB2	2.18	0.43
17:O:3:ILE:HD13	17:O:34:LEU:HD13	2.00	0.43
19:Q:59:ILE:HD13	19:Q:59:ILE:HA	1.77	0.43
1:A:21:G:H2'	1:A:22:G:C8	2.54	0.43
1:A:731:G:H5'	1:A:766:A:H4'	2.00	0.43
1:A:1120:G:O2'	1:A:1121:U:H5'	2.18	0.43
1:A:1153:C:H2'	1:A:1154:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1240:U:H4'	1:A:1241:G:OP2	2.18	0.43
4:B:76:GLN:HG3	4:B:206:ASP:OD1	2.18	0.43
4:B:185:ILE:HD12	4:B:185:ILE:H	1.79	0.43
5:C:77:ILE:HD13	5:C:84:ILE:HD12	1.99	0.43
5:C:79:ARG:HG3	5:C:79:ARG:O	2.18	0.43
5:C:199:LYS:HB3	5:C:201:TYR:HE1	1.83	0.43
11:I:50:LEU:C	11:I:52:ALA:N	2.76	0.43
14:L:47:LYS:CG	14:L:48:PRO:HD3	2.49	0.43
15:M:105:THR:O	15:M:106:ASN:C	2.61	0.43
19:Q:60:ILE:HD13	19:Q:61:GLU:H	1.83	0.43
22:T:33:ILE:HD11	22:T:66:ALA:HB2	2.01	0.43
1:A:28:G:O2'	1:A:29:G:H5'	2.18	0.43
1:A:39:G:O2'	1:A:40:C:H5'	2.19	0.43
1:A:413:G:C4	1:A:416:G:H5'	2.53	0.43
1:A:539:A:OP2	14:L:115:LYS:HE3	2.18	0.43
1:A:1039:C:O2'	1:A:1040:U:H5'	2.19	0.43
1:A:1048:G:OP1	16:N:3:ARG:HA	2.18	0.43
1:A:1168:A:C6	1:A:1169:A:C6	3.06	0.43
1:A:1185:G:H2'	1:A:1186:G:H8	1.83	0.43
1:A:1281:U:H3'	1:A:1281:U:C6	2.53	0.43
1:A:1288:A:H1'	1:A:1352:C:O2'	2.18	0.43
1:A:1326:C:H2'	1:A:1327:C:C6	2.54	0.43
5:C:28:GLN:O	5:C:29:TYR:C	2.61	0.43
9:G:46:ALA:HA	9:G:49:ILE:HD12	2.00	0.43
10:H:59:LEU:O	10:H:61:VAL:HG23	2.19	0.43
11:I:8:GLY:HA3	11:I:79:LEU:HB3	2.01	0.43
12:J:3:LYS:HB3	12:J:74:ILE:O	2.18	0.43
15:M:105:THR:HB	15:M:106:ASN:H	1.63	0.43
19:Q:4:LYS:HD2	19:Q:6:LEU:HD21	2.01	0.43
19:Q:85:VAL:O	19:Q:89:LEU:HG	2.19	0.43
21:S:11:VAL:HG21	21:S:41:VAL:HG13	1.99	0.43
21:S:39:THR:HA	21:S:70:LYS:HD2	2.01	0.43
1:A:243:A:C5'	1:A:244:U:H5'	2.47	0.43
1:A:429:U:C2'	6:D:25:ARG:HH12	2.31	0.43
1:A:674:G:H2'	1:A:675:A:H8	1.84	0.43
1:A:1056:U:C5'	5:C:163:ALA:HB2	2.48	0.43
1:A:1141:C:O2'	1:A:1142:G:H5'	2.18	0.43
1:A:1167:A:C6	1:A:1168:A:C6	3.06	0.43
4:B:53:ARG:HH12	4:B:199:TYR:HD2	1.65	0.43
4:B:223:ILE:O	4:B:225:ALA:N	2.52	0.43
5:C:115:LEU:O	5:C:118:GLN:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:151:VAL:HG12	5:C:152:ILE:N	2.34	0.43
6:D:138:TYR:CD2	6:D:139:ARG:N	2.87	0.43
9:G:61:VAL:O	9:G:64:GLN:HB3	2.18	0.43
11:I:16:ARG:CD	11:I:64:THR:HB	2.36	0.43
15:M:11:ARG:O	15:M:12:ASN:C	2.62	0.43
19:Q:14:LYS:NZ	19:Q:53:LEU:HD22	2.34	0.43
19:Q:63:ARG:O	19:Q:64:PRO:C	2.62	0.43
20:R:86:VAL:O	20:R:87:ARG:HB2	2.19	0.43
21:S:64:GLU:HA	21:S:67:VAL:CG2	2.49	0.43
1:A:190(L):U:C2'	1:A:191:G:H5'	2.49	0.43
1:A:264:U:H4'	19:Q:63:ARG:HD3	2.00	0.43
1:A:409:G:H22	1:A:432:A:H3'	1.82	0.43
1:A:570:G:H2'	1:A:571:U:C6	2.54	0.43
1:A:910:C:P	14:L:97:ARG:HH22	2.42	0.43
1:A:934:C:N3	1:A:1345:U:C5	2.86	0.43
1:A:1288:A:N1	1:A:1371:G:H1'	2.33	0.43
1:A:1367:C:N3	1:A:1368:G:C8	2.87	0.43
6:D:121:VAL:HG12	6:D:134:ASP:HA	2.01	0.43
7:E:144:THR:HG22	7:E:146:ALA:HB3	2.00	0.43
8:F:18:GLN:O	8:F:21:LEU:HB3	2.18	0.43
9:G:111:ARG:NH2	9:G:126:ASP:CG	2.77	0.43
10:H:29:SER:O	10:H:30:ARG:C	2.61	0.43
11:I:112:LYS:HD3	11:I:112:LYS:O	2.18	0.43
13:K:27:ASN:ND2	13:K:28:THR:N	2.66	0.43
17:O:4:THR:HB	17:O:6:GLU:HG2	2.00	0.43
19:Q:86:GLU:O	19:Q:90:ILE:HG13	2.19	0.43
1:A:113:G:C2	1:A:315:A:C2	3.07	0.43
1:A:633:G:H2'	1:A:634:C:C6	2.54	0.43
1:A:1290:G:H2'	1:A:1291:G:C8	2.53	0.43
1:A:1291:G:H4'	11:I:38:GLN:O	2.18	0.43
1:A:1303:C:N4	1:A:1304:G:C6	2.87	0.43
4:B:127:ILE:HG13	4:B:128:GLU:OE2	2.19	0.43
6:D:58:LEU:CD2	6:D:58:LEU:C	2.91	0.43
9:G:116:ALA:HA	9:G:119:ARG:CZ	2.49	0.43
10:H:20:TYR:HA	10:H:65:TYR:CZ	2.53	0.43
11:I:16:ARG:HG2	11:I:16:ARG:HH11	1.84	0.43
13:K:99:GLN:HA	13:K:105:VAL:HG23	2.00	0.43
17:O:87:ILE:O	17:O:88:ARG:CB	2.66	0.43
18:P:40:ASP:HB3	18:P:48:TRP:HB2	2.01	0.43
20:R:44:LEU:HD23	20:R:50:ILE:HA	2.01	0.43
22:T:13:LEU:HD12	22:T:13:LEU:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:87:LYS:O	22:T:91:LEU:HG	2.19	0.43
1:A:253:U:H2'	1:A:254:G:C8	2.54	0.43
1:A:407:G:O2'	1:A:408:A:P	2.77	0.43
1:A:942:G:C2	1:A:943:U:C6	3.07	0.43
1:A:960:U:O2'	1:A:1223:C:H4'	2.18	0.43
1:A:967:C:OP1	1:A:969:A:H5'	2.19	0.43
1:A:1055:A:C6	1:A:1206:G:C5	3.07	0.43
1:A:1318:A:O2'	21:S:37:ARG:HD2	2.19	0.43
5:C:95:THR:O	5:C:97:LYS:HG2	2.19	0.43
6:D:108:LEU:CD2	6:D:174:LEU:HD13	2.49	0.43
7:E:15:ARG:HG3	7:E:15:ARG:NH1	2.34	0.43
8:F:29:ALA:O	8:F:30:LEU:C	2.62	0.43
13:K:102:GLY:O	13:K:103:LEU:C	2.62	0.43
14:L:24:VAL:HG13	14:L:98:TYR:HE2	1.84	0.43
20:R:46:GLU:CD	20:R:46:GLU:N	2.73	0.43
21:S:63:THR:HG21	21:S:65:ASN:HD22	1.83	0.43
22:T:82:SER:O	22:T:86:ARG:HB2	2.19	0.43
22:T:94:ALA:O	22:T:95:ALA:HB3	2.19	0.43
1:A:46:G:O2'	1:A:365:U:H1'	2.18	0.42
1:A:56:U:H2'	1:A:57:G:C8	2.54	0.42
1:A:160:A:H1'	1:A:344:A:C5	2.54	0.42
1:A:976:G:C8	1:A:1358:U:O2	2.72	0.42
1:A:1201:A:O2'	1:A:1202:G:OP2	2.32	0.42
1:A:1511:G:C2'	1:A:1512:U:H5'	2.49	0.42
1:A:1520:G:O2'	1:A:1521:G:H5'	2.19	0.42
4:B:14:GLY:C	4:B:15:VAL:CG2	2.92	0.42
4:B:130:ARG:HB3	4:B:131:PRO:HD2	2.01	0.42
4:B:189:ASP:CG	4:B:205:ASP:OD1	2.62	0.42
5:C:54:ARG:HG2	5:C:54:ARG:NH1	2.34	0.42
7:E:11:ILE:HG21	7:E:31:LEU:HD12	2.00	0.42
9:G:73:MET:HB3	9:G:145:ALA:HB1	2.01	0.42
9:G:78:ARG:HD2	9:G:156:TRP:CE3	2.53	0.42
11:I:23:ASN:ND2	11:I:23:ASN:C	2.76	0.42
11:I:42:ARG:NH2	11:I:71:SER:OG	2.49	0.42
15:M:4:ILE:HG22	15:M:5:ALA:H	1.84	0.42
15:M:48:LEU:HD13	15:M:52:GLU:HB2	2.00	0.42
20:R:38:GLU:HA	20:R:41:LYS:HE2	2.01	0.42
1:A:410:G:C2	1:A:411:A:C8	3.06	0.42
1:A:767:A:H2'	1:A:768:A:C8	2.54	0.42
1:A:1049:U:H1'	1:A:1201:A:N7	2.35	0.42
1:A:1057:G:C2'	1:A:1058:G:H5'	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1454:G:H2'	1:A:1455:G:H8	1.85	0.42
4:B:20:GLU:O	4:B:21:ARG:C	2.62	0.42
5:C:21:ARG:N	5:C:21:ARG:CD	2.72	0.42
6:D:26:CYS:HA	6:D:31:CYS:HB2	2.01	0.42
6:D:70:ILE:HD12	6:D:97:LEU:CD2	2.49	0.42
6:D:127:THR:HG23	6:D:147:ALA:HB3	2.02	0.42
8:F:17:SER:O	8:F:18:GLN:C	2.62	0.42
8:F:68:PRO:HB2	8:F:71:ARG:HG2	2.01	0.42
10:H:54:ASP:O	10:H:54:ASP:CG	2.62	0.42
11:I:32:ASP:O	11:I:35:GLU:N	2.52	0.42
13:K:127:LYS:HA	13:K:127:LYS:CE	2.49	0.42
15:M:4:ILE:O	15:M:5:ALA:C	2.61	0.42
18:P:4:ILE:CG1	18:P:64:ALA:HB1	2.48	0.42
18:P:12:LYS:O	18:P:13:HIS:HB2	2.18	0.42
20:R:53:ARG:NH1	20:R:60:GLY:H	2.16	0.42
21:S:30:LEU:C	21:S:31:ILE:HG12	2.44	0.42
1:A:110:C:H2'	1:A:111:G:O4'	2.19	0.42
1:A:620:C:H2'	1:A:621:A:O4'	2.19	0.42
1:A:687:A:H2'	1:A:701:C:H41	1.84	0.42
1:A:743:U:H2'	1:A:744:C:C6	2.53	0.42
1:A:767:A:H2'	1:A:768:A:O4'	2.20	0.42
1:A:979:C:O2	16:N:19:ARG:HG2	2.20	0.42
1:A:983:A:H2	1:A:984:C:C6	2.36	0.42
1:A:1097:C:H2'	1:A:1098:C:C6	2.53	0.42
1:A:1251:A:H1'	1:A:1369:C:O2'	2.19	0.42
1:A:1410:G:H2'	1:A:1411:C:H6	1.84	0.42
4:B:36:ARG:C	4:B:38:GLY:H	2.26	0.42
5:C:28:GLN:O	5:C:31:HIS:N	2.53	0.42
5:C:79:ARG:HB3	5:C:79:ARG:CZ	2.49	0.42
8:F:99:ALA:CB	20:R:31:LEU:HD12	2.49	0.42
10:H:60:ARG:NH1	10:H:60:ARG:HG3	2.34	0.42
11:I:27:THR:CG2	11:I:28:VAL:N	2.82	0.42
15:M:19:LEU:O	15:M:22:ILE:CD1	2.65	0.42
16:N:11:LYS:HG2	16:N:13:THR:H	1.82	0.42
18:P:51:VAL:O	18:P:53:VAL:N	2.51	0.42
19:Q:98:LEU:O	19:Q:99:SER:CB	2.65	0.42
23:V:6:ARG:CG	23:V:7:ARG:HD2	2.49	0.42
1:A:344:A:O2'	1:A:345:C:OP1	2.37	0.42
1:A:396:G:O2'	1:A:398:C:OP1	2.36	0.42
1:A:941:G:O2'	1:A:942:G:H5'	2.19	0.42
1:A:1085:U:H3'	1:A:1086:U:C5	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:130:ARG:HB3	4:B:134:GLU:OE1	2.18	0.42
4:B:137:ARG:HG2	4:B:137:ARG:NH1	2.34	0.42
6:D:121:VAL:O	6:D:134:ASP:HA	2.19	0.42
6:D:173:TRP:CE3	6:D:189:PRO:HB3	2.55	0.42
7:E:31:LEU:HD23	7:E:31:LEU:HA	1.90	0.42
7:E:150:ARG:HH11	7:E:150:ARG:CG	2.27	0.42
10:H:4:ASP:OD2	10:H:7:ALA:HB2	2.19	0.42
10:H:31:PHE:CZ	10:H:134:ILE:CD1	3.02	0.42
10:H:35:ILE:O	10:H:36:LEU:C	2.62	0.42
11:I:43:ALA:O	11:I:45:ALA:N	2.53	0.42
12:J:49:VAL:O	12:J:49:VAL:HG13	2.19	0.42
13:K:70:LYS:O	13:K:71:LYS:C	2.61	0.42
14:L:124:LYS:O	14:L:125:PRO:C	2.62	0.42
15:M:3:ARG:HB2	15:M:9:ILE:HG13	2.01	0.42
16:N:22:THR:O	16:N:23:ARG:HG3	2.19	0.42
16:N:36:PHE:C	16:N:36:PHE:CD1	2.97	0.42
16:N:59:ALA:HB1	16:N:61:TRP:HZ3	1.85	0.42
18:P:52:ASP:O	18:P:53:VAL:C	2.63	0.42
18:P:81:ARG:HD3	18:P:83:GLU:HB3	2.01	0.42
19:Q:76:LEU:C	19:Q:76:LEU:CD2	2.92	0.42
20:R:54:ARG:H	20:R:54:ARG:HG3	1.62	0.42
21:S:17:GLU:CA	21:S:20:LEU:HG	2.46	0.42
21:S:52:TYR:CD1	21:S:56:GLN:O	2.73	0.42
1:A:479:C:C5	1:A:480:U:C4	3.08	0.42
1:A:1193:G:N2	1:A:1194:U:C2	2.88	0.42
1:A:1321:C:O2'	21:S:77:THR:HG21	2.20	0.42
4:B:23:ARG:HH12	4:B:191:ASP:HA	1.84	0.42
4:B:169:LYS:C	4:B:169:LYS:HD3	2.44	0.42
5:C:150:LYS:HB2	5:C:169:ALA:HB1	2.01	0.42
6:D:52:SER:O	6:D:53:ASP:C	2.61	0.42
7:E:143:ARG:NH1	10:H:77:GLU:CD	2.78	0.42
10:H:39:LEU:HD13	10:H:39:LEU:HA	1.80	0.42
10:H:122:ARG:HG3	10:H:122:ARG:NH1	2.34	0.42
11:I:88:TYR:CD2	11:I:89:ASN:N	2.88	0.42
12:J:28:ARG:HG2	12:J:28:ARG:HH11	1.84	0.42
12:J:46:ARG:NH1	12:J:64:GLU:HB3	2.35	0.42
15:M:13:LYS:O	15:M:44:ARG:NE	2.52	0.42
15:M:126:LYS:HB2	15:M:126:LYS:NZ	2.35	0.42
17:O:67:LEU:O	17:O:68:ARG:C	2.63	0.42
17:O:88:ARG:NE	17:O:88:ARG:HA	2.34	0.42
18:P:67:THR:HG22	18:P:69:THR:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:75:ARG:O	18:P:78:GLY:N	2.50	0.42
21:S:7:LYS:O	21:S:7:LYS:CG	2.67	0.42
21:S:11:VAL:HG22	21:S:39:THR:O	2.19	0.42
1:A:300:A:H2'	1:A:301:G:O4'	2.19	0.42
1:A:356:A:O2'	1:A:357:G:H5'	2.18	0.42
1:A:1137:C:H5'	1:A:1138:G:C6	2.54	0.42
1:A:1153:C:C2	1:A:1154:G:C8	3.07	0.42
1:A:1399:C:C2	1:A:1502:A:N6	2.88	0.42
1:A:1465:C:O2'	1:A:1466:C:H5'	2.19	0.42
4:B:26:PRO:O	4:B:28:PHE:N	2.47	0.42
4:B:144:ARG:HG3	4:B:145:LEU:H	1.84	0.42
5:C:95:THR:O	5:C:96:GLY:C	2.62	0.42
5:C:178:LEU:O	5:C:179:ARG:HB2	2.19	0.42
6:D:196:LEU:C	6:D:198:VAL:H	2.28	0.42
9:G:15:ASP:OD2	9:G:44:TYR:OH	2.35	0.42
9:G:50:ILE:HG21	9:G:61:VAL:HG21	2.00	0.42
13:K:95:ILE:HG21	13:K:108:ILE:HD13	2.00	0.42
14:L:55:VAL:CG1	14:L:56:ALA:H	2.29	0.42
15:M:48:LEU:HD22	15:M:48:LEU:HA	1.89	0.42
22:T:36:LEU:HD12	22:T:62:LEU:CD1	2.47	0.42
22:T:71:THR:O	22:T:72:LEU:HD23	2.19	0.42
1:A:129(A):G:O2'	1:A:190(E):U:C6	2.71	0.42
1:A:409:G:C3'	1:A:431:A:N7	2.83	0.42
4:B:9:GLU:OE1	4:B:11:LEU:C	2.63	0.42
5:C:61:ALA:C	5:C:63:ASN:N	2.77	0.42
5:C:109:PRO:HA	5:C:115:LEU:HD12	2.02	0.42
8:F:11:ASN:O	8:F:14:LEU:HG	2.19	0.42
9:G:15:ASP:OD2	9:G:16:LEU:N	2.53	0.42
10:H:104:ARG:HD2	10:H:138:TRP:CD2	2.54	0.42
11:I:90:PRO:O	11:I:93:ARG:HG3	2.19	0.42
14:L:24:VAL:HG13	14:L:98:TYR:CE2	2.54	0.42
14:L:28:LYS:O	14:L:30:ALA:N	2.51	0.42
16:N:27:CYS:SG	16:N:29:ARG:CB	3.04	0.42
1:A:145:G:O2'	1:A:146:G:H5'	2.20	0.42
1:A:560:U:O2'	1:A:561:U:OP2	2.26	0.42
1:A:723:U:O2	1:A:723:U:C2'	2.67	0.42
1:A:741:G:H5''	17:O:39:LEU:HD12	2.00	0.42
1:A:1018:C:O5'	1:A:1018:C:H6	2.02	0.42
4:B:12:GLU:HA	4:B:12:GLU:OE1	2.19	0.42
4:B:16:HIS:NE2	4:B:214:ILE:CG1	2.83	0.42
4:B:60:ASP:C	4:B:62:ALA:N	2.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:87:ARG:HH11	4:B:234:PRO:HD2	1.84	0.42
4:B:136:VAL:HG12	4:B:140:HIS:CE1	2.55	0.42
4:B:206:ASP:O	4:B:207:ALA:CB	2.66	0.42
5:C:89:GLU:C	5:C:91:LEU:N	2.75	0.42
5:C:114:PRO:HD3	5:C:183:ASP:OD1	2.20	0.42
9:G:17:VAL:HG12	9:G:18:TYR:N	2.35	0.42
10:H:117:GLY:O	10:H:119:LEU:CD2	2.67	0.42
13:K:67:ASP:O	13:K:68:ALA:C	2.63	0.42
17:O:87:ILE:HG22	17:O:88:ARG:H	1.84	0.42
1:A:92:C:O2'	1:A:93:G:H5'	2.20	0.42
1:A:190(C):C:H1'	1:A:190(G):G:N2	2.34	0.42
1:A:707:C:O2'	1:A:708:C:H5'	2.20	0.42
1:A:838:G:H2'	1:A:839:U:C5'	2.39	0.42
1:A:930:C:C2'	1:A:931:C:H5'	2.50	0.42
1:A:1207:G:O2'	1:A:1208:C:H5'	2.20	0.42
1:A:1256:A:OP1	5:C:26:LYS:HE3	2.20	0.42
4:B:25:ASN:HD21	4:B:27:LYS:H	1.66	0.42
4:B:129:GLU:O	4:B:135:GLN:NE2	2.49	0.42
4:B:134:GLU:C	4:B:136:VAL:H	2.27	0.42
5:C:3:ASN:O	5:C:4:LYS:CB	2.67	0.42
5:C:120:VAL:O	5:C:124:ILE:HG13	2.20	0.42
5:C:131:ARG:HD3	5:C:166:GLU:OE2	2.20	0.42
9:G:151:TYR:OH	13:K:54:ARG:NE	2.53	0.42
12:J:9:ARG:HB2	12:J:9:ARG:HH11	1.84	0.42
21:S:45:VAL:HA	21:S:62:ILE:CG1	2.50	0.42
22:T:59:ALA:O	22:T:60:GLU:C	2.63	0.42
1:A:16:A:H2'	1:A:17:U:H5'	2.01	0.42
1:A:192:U:H1'	22:T:103:GLY:CA	2.50	0.42
1:A:267:C:P	19:Q:67:LYS:HB2	2.60	0.42
1:A:283:C:O2'	1:A:284:G:H5'	2.20	0.42
1:A:428:G:O4'	1:A:430:A:C8	2.72	0.42
1:A:789:U:O2	1:A:791:G:C8	2.72	0.42
1:A:994:A:N7	1:A:1216:G:H4'	2.35	0.42
1:A:1238:A:C2	1:A:1241:G:N3	2.88	0.42
4:B:23:ARG:HD3	4:B:23:ARG:H	1.85	0.42
5:C:101:LEU:O	5:C:101:LEU:CD2	2.68	0.42
6:D:187:ARG:HD2	6:D:188:LEU:N	2.33	0.42
9:G:18:TYR:HE2	9:G:58:PRO:HG2	1.85	0.42
12:J:89:ASP:CB	12:J:91:PRO:HD2	2.50	0.42
14:L:46:LYS:O	14:L:47:LYS:C	2.63	0.42
17:O:71:GLN:O	17:O:72:ARG:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:80:TYR:O	21:S:81:ARG:C	2.62	0.42
1:A:32:A:H2'	1:A:33:A:C8	2.55	0.41
1:A:109:A:H5'	1:A:110:C:H5	1.85	0.41
1:A:299:G:H2'	1:A:300:A:C8	2.55	0.41
1:A:459:G:C3'	1:A:460:A:H5''	2.50	0.41
1:A:478:A:HO2'	1:A:479:C:H5'	1.78	0.41
1:A:480:U:H5'	1:A:481:G:OP2	2.19	0.41
1:A:603:U:H2'	1:A:604:G:C8	2.55	0.41
1:A:747:C:H2'	1:A:748:C:H1'	2.02	0.41
1:A:974:A:H8	1:A:974:A:OP1	2.03	0.41
1:A:975:A:O2'	1:A:976:G:OP2	2.31	0.41
1:A:1203:C:OP1	16:N:2:ALA:HB3	2.20	0.41
1:A:1220:G:O2'	1:A:1221:G:H5'	2.19	0.41
1:A:1270:C:H4'	1:A:1314:C:H5'	2.02	0.41
1:A:1431:C:H2'	1:A:1432:G:H5'	2.01	0.41
1:A:1521:G:O2'	1:A:1522:U:H5'	2.20	0.41
4:B:118:LEU:O	4:B:122:PHE:N	2.53	0.41
5:C:22:TRP:HB2	5:C:59:ARG:HB2	2.02	0.41
6:D:32:ALA:O	6:D:33:MET:C	2.62	0.41
6:D:205:GLU:O	6:D:208:SER:HB2	2.19	0.41
10:H:18:ARG:HE	10:H:18:ARG:HA	1.85	0.41
10:H:113:SER:O	10:H:131:GLY:HA3	2.20	0.41
11:I:53:VAL:CG2	11:I:85:LEU:HD21	2.42	0.41
17:O:41:GLU:O	17:O:44:LYS:HB3	2.19	0.41
18:P:75:ARG:HG3	18:P:75:ARG:NH1	2.35	0.41
1:A:37:U:O2'	1:A:38:G:H5'	2.20	0.41
1:A:77:G:O2'	1:A:78:G:H5'	2.19	0.41
1:A:129(A):G:C2	1:A:190(E):U:H5'	2.56	0.41
1:A:562:C:N3	14:L:16:GLU:HG2	2.35	0.41
1:A:981:U:H5'	16:N:21:TYR:CE1	2.55	0.41
1:A:1021:G:O2'	1:A:1022:G:H5'	2.21	0.41
1:A:1152:A:O2'	1:A:1153:C:H5'	2.19	0.41
1:A:1176:A:H2'	1:A:1177:G:C8	2.55	0.41
1:A:1300:G:O2'	1:A:1301:U:H6	2.03	0.41
4:B:33:TYR:HB3	4:B:41:ILE:O	2.20	0.41
4:B:67:THR:N	4:B:160:ASP:OD2	2.52	0.41
4:B:112:VAL:HG22	4:B:149:LEU:HD13	2.02	0.41
8:F:99:ALA:HB2	20:R:31:LEU:HD12	2.01	0.41
8:F:99:ALA:O	8:F:100:ASN:HB3	2.20	0.41
9:G:40:ALA:O	9:G:41:ARG:C	2.63	0.41
12:J:89:ASP:HB2	12:J:91:PRO:CD	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:48:ILE:HD13	13:K:48:ILE:HA	1.91	0.41
13:K:76:GLY:O	13:K:78:GLN:HG3	2.19	0.41
16:N:47:LEU:O	16:N:48:ALA:C	2.64	0.41
17:O:9:GLN:O	17:O:10:LYS:C	2.63	0.41
18:P:42:ARG:O	18:P:43:LYS:C	2.63	0.41
19:Q:66:SER:OG	19:Q:69:LYS:CB	2.68	0.41
20:R:53:ARG:C	20:R:55:ARG:N	2.77	0.41
21:S:13:ASP:O	21:S:16:LEU:N	2.53	0.41
1:A:6:G:H4'	1:A:298:A:H4'	2.03	0.41
1:A:134:A:H1'	1:A:325:A:C5	2.55	0.41
1:A:190:C:OP1	1:A:190(K):G:N2	2.53	0.41
1:A:412:A:C2'	1:A:413:G:H5'	2.51	0.41
1:A:499:A:H4'	1:A:500:G:OP1	2.20	0.41
1:A:600:C:O2'	1:A:601:C:H5'	2.20	0.41
1:A:757:U:O2'	1:A:879:C:H1'	2.21	0.41
4:B:16:HIS:NE2	4:B:214:ILE:HG12	2.36	0.41
4:B:59:GLU:HA	4:B:62:ALA:HB3	2.01	0.41
5:C:12:LEU:HA	5:C:12:LEU:HD23	1.71	0.41
5:C:91:LEU:HD21	5:C:99:VAL:CG2	2.48	0.41
7:E:105:VAL:HB	7:E:106:PRO:HD3	2.01	0.41
7:E:143:ARG:NH1	10:H:77:GLU:OE2	2.53	0.41
7:E:150:ARG:HG3	7:E:150:ARG:NH1	2.31	0.41
7:E:150:ARG:CG	7:E:150:ARG:NH1	2.82	0.41
9:G:78:ARG:O	9:G:84:ASN:HA	2.20	0.41
12:J:27:ALA:HB2	12:J:85:LEU:CD2	2.50	0.41
12:J:54:PHE:C	12:J:55:LYS:HG2	2.45	0.41
15:M:19:LEU:CA	15:M:22:ILE:HD13	2.51	0.41
18:P:14:ASN:CG	18:P:14:ASN:O	2.61	0.41
21:S:12:ASP:HB2	21:S:35:SER:OG	2.21	0.41
1:A:182:U:OP2	1:A:183:G:C8	2.72	0.41
1:A:262:A:C6	1:A:263:A:C6	3.08	0.41
1:A:293:G:C6	1:A:294:U:C4	3.08	0.41
1:A:443:C:H2'	1:A:444:C:H6	1.85	0.41
1:A:501:C:O2'	1:A:502:G:H5'	2.19	0.41
1:A:824:C:H2'	1:A:825:G:H8	1.86	0.41
1:A:911:U:OP2	14:L:97:ARG:NH2	2.53	0.41
1:A:939:G:H5''	9:G:102:ARG:CZ	2.49	0.41
1:A:1051:C:O2'	1:A:1052:U:H5'	2.20	0.41
1:A:1196:U:H5''	1:A:1197:G:C5'	2.50	0.41
1:A:1372:U:H2'	1:A:1373:G:O4'	2.20	0.41
1:A:1504:G:H3'	1:A:1504:G:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:75:LYS:HA	4:B:78:GLN:HB2	2.03	0.41
4:B:239:VAL:O	4:B:239:VAL:HG12	2.20	0.41
5:C:155:GLY:CA	5:C:164:ARG:H	2.34	0.41
5:C:173:VAL:HG12	5:C:175:LEU:CD2	2.50	0.41
6:D:28:SER:C	6:D:30:LYS:H	2.28	0.41
6:D:152:SER:O	6:D:153:ARG:C	2.63	0.41
6:D:198:VAL:CG1	6:D:199:ASN:N	2.83	0.41
7:E:37:ARG:HG3	7:E:112:LEU:HA	2.02	0.41
7:E:80:ILE:CG2	10:H:104:ARG:HH22	2.33	0.41
8:F:101:ALA:C	20:R:28:GLU:HG3	2.46	0.41
9:G:20:ASP:OD2	9:G:63:LYS:NZ	2.49	0.41
9:G:95:ARG:HG3	9:G:95:ARG:NH1	2.35	0.41
9:G:108:ALA:C	9:G:110:GLN:H	2.28	0.41
9:G:115:ARG:CB	9:G:118:VAL:HG23	2.49	0.41
12:J:6:ILE:O	12:J:71:LEU:O	2.38	0.41
12:J:12:ASP:CG	12:J:13:HIS:N	2.78	0.41
17:O:17:ARG:NH1	17:O:17:ARG:CG	2.83	0.41
17:O:82:ILE:HD13	17:O:88:ARG:CG	2.50	0.41
17:O:88:ARG:NE	17:O:88:ARG:CA	2.83	0.41
19:Q:7:THR:O	19:Q:23:VAL:HG22	2.20	0.41
20:R:88:LYS:OXT	20:R:88:LYS:CG	2.64	0.41
22:T:39:LYS:HD3	22:T:55:ILE:HD13	2.01	0.41
22:T:56:MET:HG3	22:T:84:LEU:HD13	2.01	0.41
1:A:102:G:O2'	1:A:151:A:N3	2.43	0.41
1:A:103:C:OP2	22:T:17:ARG:NH1	2.52	0.41
1:A:242:C:H2'	1:A:243:A:H5'	2.02	0.41
1:A:555:C:H2'	1:A:556:C:C6	2.55	0.41
1:A:718:G:H5'	13:K:117:ASN:CG	2.45	0.41
1:A:737:A:H2'	1:A:738:C:C6	2.55	0.41
1:A:800:G:H8	1:A:800:G:O5'	2.03	0.41
1:A:900:A:H2'	1:A:901:A:C8	2.54	0.41
1:A:977:A:O2'	1:A:979:C:OP2	2.38	0.41
1:A:979:C:H2'	1:A:980:C:H5'	2.03	0.41
1:A:994:A:H2'	1:A:994:A:N3	2.34	0.41
1:A:996:A:H2	1:A:1045:C:O2'	2.03	0.41
1:A:1305:G:H2'	1:A:1331:G:H22	1.85	0.41
4:B:20:GLU:O	4:B:39:ILE:HG23	2.20	0.41
4:B:20:GLU:HG3	4:B:191:ASP:HB3	2.03	0.41
4:B:95:GLN:HG3	4:B:148:TYR:CD2	2.54	0.41
4:B:122:PHE:HA	4:B:127:ILE:HG21	2.03	0.41
7:E:6:PHE:CZ	7:E:66:MET:HE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:103:GLY:C	7:E:106:PRO:HD2	2.45	0.41
9:G:41:ARG:O	9:G:42:ILE:C	2.63	0.41
11:I:30:GLY:O	11:I:31:GLN:C	2.63	0.41
11:I:55:ALA:O	11:I:56:LEU:HB3	2.19	0.41
14:L:82:VAL:O	14:L:106:ASP:HB2	2.20	0.41
16:N:59:ALA:O	16:N:60:SER:CB	2.67	0.41
20:R:47:THR:HG23	20:R:83:GLU:O	2.20	0.41
22:T:68:LYS:HD2	22:T:68:LYS:HA	1.86	0.41
1:A:47:C:H5''	1:A:365:U:C6	2.56	0.41
1:A:328:C:H1'	1:A:329:A:OP2	2.20	0.41
1:A:397:A:H3'	1:A:397:A:N3	2.35	0.41
1:A:409:G:H22	1:A:432:A:C2'	2.32	0.41
1:A:1150:U:O3'	12:J:41:PRO:HA	2.20	0.41
1:A:1234:C:C2'	1:A:1235:U:H5'	2.51	0.41
1:A:1286:A:H2'	1:A:1287:A:H4'	2.01	0.41
1:A:1419:G:H2'	1:A:1420:C:C6	2.55	0.41
4:B:168:THR:OG1	4:B:192:SER:HB3	2.19	0.41
5:C:55:VAL:HG22	5:C:68:VAL:HG22	2.02	0.41
5:C:67:THR:O	5:C:69:HIS:CD2	2.73	0.41
5:C:137:ALA:HA	5:C:140:ARG:HE	1.86	0.41
5:C:180:ALA:O	5:C:182:ILE:N	2.53	0.41
7:E:59:GLY:O	7:E:60:TYR:C	2.64	0.41
10:H:34:GLU:OE2	10:H:34:GLU:HA	2.21	0.41
10:H:90:GLY:O	10:H:91:ARG:CB	2.65	0.41
13:K:69:ALA:O	13:K:70:LYS:C	2.62	0.41
17:O:76:GLU:CA	17:O:79:ARG:HH21	2.33	0.41
1:A:53:A:N6	1:A:54:C:C4	2.88	0.41
1:A:421:U:O2'	1:A:422:C:H5'	2.20	0.41
1:A:446:G:C2'	1:A:447:G:H5'	2.51	0.41
1:A:474:G:H5'	1:A:475:G:N7	2.35	0.41
1:A:933:G:OP2	9:G:3:ARG:HB3	2.19	0.41
1:A:1350:A:C2	1:A:1351:U:C2	3.09	0.41
1:A:1420:C:H2'	1:A:1421:G:H8	1.86	0.41
4:B:44:LEU:O	4:B:45:GLN:C	2.64	0.41
4:B:91:PRO:CG	4:B:155:LEU:HG	2.46	0.41
5:C:95:THR:O	5:C:97:LYS:N	2.53	0.41
6:D:167:GLY:O	6:D:168:ARG:C	2.64	0.41
7:E:30:ALA:O	7:E:45:PHE:HA	2.21	0.41
7:E:72:GLN:O	7:E:73:ASN:HB3	2.20	0.41
7:E:81:GLU:OE1	7:E:88:LYS:HE2	2.21	0.41
12:J:62:HIS:HB3	16:N:59:ALA:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:89:ARG:NH2	14:L:97:ARG:HD3	2.35	0.41
14:L:101:VAL:O	14:L:102:ARG:C	2.60	0.41
14:L:110:VAL:O	14:L:122:THR:HG22	2.20	0.41
15:M:49:THR:CG2	15:M:51:ALA:HB3	2.50	0.41
19:Q:67:LYS:O	19:Q:68:ARG:C	2.64	0.41
20:R:53:ARG:NH1	20:R:60:GLY:N	2.69	0.41
21:S:38:SER:OG	21:S:71:LEU:HD13	2.21	0.41
1:A:41:G:H2'	1:A:42:G:H8	1.83	0.41
1:A:103:C:P	22:T:17:ARG:HH11	2.44	0.41
1:A:1092:A:H5''	9:G:4:ARG:CZ	2.51	0.41
1:A:1144:G:H21	1:A:1146:A:H62	1.68	0.41
1:A:1145:C:O2'	1:A:1146:A:O5'	2.34	0.41
1:A:1368:G:OP2	11:I:112:LYS:CD	2.68	0.41
1:A:1381:U:C2'	1:A:1382:C:H5'	2.50	0.41
1:A:1392:G:O2'	1:A:1393:U:H5'	2.20	0.41
4:B:102:LEU:HB3	4:B:180:LEU:HD12	2.03	0.41
5:C:136:GLN:O	5:C:139:GLN:N	2.54	0.41
6:D:36:ARG:HG2	6:D:36:ARG:NH1	2.34	0.41
6:D:60:GLU:HG2	6:D:202:LEU:HB2	2.03	0.41
8:F:68:PRO:HB2	8:F:71:ARG:CG	2.50	0.41
10:H:82:HIS:O	10:H:83:ILE:CB	2.69	0.41
11:I:28:VAL:O	11:I:28:VAL:HG23	2.21	0.41
11:I:117:HIS:O	11:I:118:LYS:HG3	2.21	0.41
14:L:30:ALA:HA	14:L:31:PRO:HD3	1.88	0.41
22:T:23:ARG:HG2	22:T:23:ARG:NH1	2.36	0.41
22:T:49:ALA:CB	22:T:99:LEU:HG	2.47	0.41
1:A:192:U:H2'	1:A:193:C:O4'	2.21	0.41
1:A:253:U:H2'	1:A:254:G:H8	1.84	0.41
1:A:308:C:H2'	1:A:309:G:C8	2.55	0.41
1:A:356:A:H1'	1:A:368:U:O2'	2.21	0.41
1:A:358:U:H2'	1:A:359:U:H6	1.85	0.41
1:A:384:G:O2'	1:A:385:C:H5'	2.21	0.41
1:A:401:C:O2'	1:A:621:A:N3	2.50	0.41
1:A:411:A:C2	1:A:418:C:OP2	2.74	0.41
1:A:460:A:N6	1:A:463:A:C5	2.88	0.41
1:A:477:G:H2'	1:A:478:A:H4'	2.01	0.41
1:A:579:G:H2'	1:A:580:U:C6	2.55	0.41
1:A:622:A:C8	1:A:623:C:C5	3.09	0.41
1:A:668:G:O2'	17:O:46:HIS:CD2	2.74	0.41
1:A:972:C:H4'	12:J:57:LYS:CD	2.51	0.41
1:A:1060:C:H5''	12:J:51:ARG:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1298:C:C2'	9:G:114:ARG:HH12	2.33	0.41
1:A:1358:U:H3'	1:A:1359:C:C6	2.56	0.41
1:A:1384:C:H2'	1:A:1385:G:C8	2.56	0.41
1:A:1386:G:O2'	1:A:1387:G:H5'	2.21	0.41
1:A:1420:C:H2'	1:A:1421:G:C8	2.56	0.41
1:A:1468:A:H2'	1:A:1469:G:O4'	2.21	0.41
4:B:23:ARG:HH12	4:B:191:ASP:CB	2.33	0.41
4:B:79:ASP:C	4:B:81:VAL:N	2.77	0.41
4:B:213:LEU:C	4:B:213:LEU:CD2	2.93	0.41
4:B:216:SER:C	4:B:218:ALA:N	2.78	0.41
5:C:3:ASN:HB2	5:C:4:LYS:H	1.68	0.41
5:C:48:TYR:O	5:C:51:GLY:N	2.52	0.41
6:D:17:VAL:C	6:D:33:MET:HE2	2.46	0.41
6:D:80:GLU:HA	6:D:80:GLU:OE2	2.21	0.41
6:D:98:GLU:HG2	6:D:189:PRO:HG3	2.02	0.41
6:D:98:GLU:OE2	6:D:103:ASN:ND2	2.52	0.41
6:D:120:LEU:HD23	6:D:120:LEU:HA	1.91	0.41
6:D:135:LEU:C	6:D:137:SER:H	2.29	0.41
9:G:43:PHE:O	9:G:46:ALA:HB3	2.21	0.41
9:G:70:LYS:HB3	9:G:96:GLN:HG2	2.02	0.41
9:G:155:ARG:O	9:G:156:TRP:CB	2.68	0.41
10:H:64:LYS:HB3	10:H:64:LYS:HE2	1.87	0.41
11:I:76:ALA:O	11:I:79:LEU:N	2.48	0.41
11:I:108:VAL:HG12	11:I:109:VAL:N	2.35	0.41
17:O:70:LEU:HD11	17:O:77:ARG:HB2	2.03	0.41
19:Q:78:GLU:OE2	19:Q:81:ARG:NH1	2.50	0.41
21:S:47:HIS:C	21:S:62:ILE:HG22	2.46	0.41
22:T:20:LEU:HD23	22:T:20:LEU:HA	1.93	0.41
22:T:30:LYS:O	22:T:31:SER:C	2.63	0.41
22:T:62:LEU:HD23	22:T:62:LEU:HA	1.86	0.41
1:A:162:A:H2'	1:A:163:C:O4'	2.21	0.41
1:A:190(I):G:O2'	1:A:190(J):U:H5'	2.21	0.41
1:A:232:G:H1'	1:A:262:A:N1	2.35	0.41
1:A:953:G:H2'	1:A:954:G:O4'	2.20	0.41
1:A:1173:G:O2'	1:A:1174:G:H5'	2.21	0.41
1:A:1212:U:O2'	1:A:1213:A:P	2.78	0.41
1:A:1470:G:O2'	1:A:1471:G:H5'	2.20	0.41
1:A:1511:G:H2'	1:A:1512:U:O4'	2.21	0.41
4:B:122:PHE:HA	4:B:127:ILE:CG2	2.51	0.41
4:B:178:ARG:NE	4:B:196:LEU:O	2.54	0.41
4:B:209:ARG:NH2	4:B:239:VAL:HG11	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:72:LYS:HD3	5:C:75:VAL:CG2	2.51	0.41
5:C:157:ILE:HG21	5:C:164:ARG:NH2	2.36	0.41
6:D:3:ARG:N	6:D:3:ARG:CD	2.71	0.41
7:E:34:VAL:O	7:E:34:VAL:HG13	2.21	0.41
7:E:52:PRO:O	7:E:53:LEU:C	2.64	0.41
10:H:69:ARG:HG3	10:H:69:ARG:HH11	1.86	0.41
10:H:116:LYS:HD3	10:H:127:LEU:HD12	2.04	0.41
13:K:108:ILE:C	13:K:109:VAL:HG23	2.46	0.41
17:O:26:GLU:OE1	17:O:77:ARG:HD2	2.20	0.41
1:A:252:U:H2'	1:A:253:U:C5	2.56	0.40
1:A:363:A:OP1	14:L:33:ARG:HD2	2.22	0.40
1:A:676:A:H1'	13:K:115:PRO:HB3	2.03	0.40
1:A:709:G:O2'	1:A:710:G:H5'	2.21	0.40
4:B:13:ALA:C	4:B:15:VAL:N	2.77	0.40
4:B:51:LEU:HD22	4:B:55:PHE:CE1	2.55	0.40
4:B:115:LEU:O	4:B:116:GLU:C	2.62	0.40
4:B:122:PHE:CA	4:B:127:ILE:HG21	2.52	0.40
4:B:184:VAL:HG12	4:B:197:VAL:CG1	2.50	0.40
4:B:209:ARG:CZ	4:B:239:VAL:HG11	2.51	0.40
5:C:50:ALA:CB	5:C:70:VAL:HG11	2.51	0.40
5:C:151:VAL:HA	5:C:199:LYS:O	2.20	0.40
6:D:153:ARG:HG3	6:D:153:ARG:HH11	1.85	0.40
8:F:67:MET:CE	8:F:71:ARG:HB2	2.51	0.40
10:H:4:ASP:OD2	10:H:85:ARG:NH1	2.51	0.40
10:H:104:ARG:CZ	10:H:138:TRP:CH2	3.04	0.40
11:I:96:LEU:N	11:I:96:LEU:CD1	2.85	0.40
12:J:18:ALA:O	12:J:21:GLN:HB3	2.21	0.40
12:J:21:GLN:HE21	12:J:25:GLU:CG	2.34	0.40
12:J:56:HIS:C	12:J:58:ASP:H	2.29	0.40
12:J:71:LEU:HA	12:J:71:LEU:HD23	1.85	0.40
15:M:79:LYS:O	15:M:82:MET:N	2.51	0.40
1:A:113:G:C1'	1:A:354:G:C5'	2.99	0.40
1:A:116:A:H2'	1:A:117:G:H8	1.86	0.40
1:A:259:G:O2'	1:A:260:G:H5'	2.20	0.40
1:A:363:A:O2'	1:A:364:A:H5'	2.21	0.40
1:A:397:A:H5'	1:A:398:C:P	2.62	0.40
1:A:409:G:N1	1:A:433:C:OP1	2.50	0.40
1:A:425:G:H2'	1:A:426:G:O4'	2.21	0.40
1:A:443:C:H2'	1:A:444:C:C6	2.56	0.40
1:A:448:A:O2'	1:A:449:C:H5'	2.21	0.40
1:A:632:A:C2'	1:A:633:G:H5'	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:974:A:P	16:N:29:ARG:HH22	2.44	0.40
1:A:1036:G:O2'	1:A:1037:C:H5'	2.21	0.40
1:A:1104:G:O2'	1:A:1105:A:H5'	2.21	0.40
1:A:1225:A:H5'	1:A:1226:C:OP2	2.21	0.40
1:A:1394:A:C5	1:A:1501:C:H4'	2.56	0.40
4:B:69:LEU:C	4:B:69:LEU:CD2	2.94	0.40
4:B:187:LEU:HD12	4:B:201:ILE:O	2.21	0.40
5:C:110:ASN:ND2	5:C:140:ARG:HB3	2.37	0.40
6:D:149:ALA:O	6:D:150:GLU:C	2.64	0.40
7:E:78:HIS:CD2	10:H:107:LEU:HD12	2.44	0.40
10:H:126:LYS:C	10:H:128:GLY:H	2.29	0.40
11:I:19:LEU:HB3	11:I:59:PHE:CD2	2.56	0.40
12:J:16:LEU:HD23	12:J:94:VAL:HG22	2.02	0.40
12:J:38:ILE:HD12	12:J:71:LEU:HD13	2.03	0.40
14:L:50:SER:O	14:L:51:ALA:CB	2.68	0.40
19:Q:68:ARG:HE	19:Q:68:ARG:HB2	1.65	0.40
22:T:45:GLN:C	22:T:47:GLY:H	2.28	0.40
1:A:103:C:O2'	1:A:172:A:N1	2.47	0.40
1:A:273:A:N6	1:A:274:A:C6	2.89	0.40
1:A:485:G:O2'	1:A:486:U:C5	2.74	0.40
1:A:522:C:O2'	1:A:523:A:H5'	2.21	0.40
1:A:836:G:C6	1:A:851:G:C6	3.10	0.40
1:A:925:G:C6	1:A:927:G:N7	2.89	0.40
1:A:1152:A:H5''	12:J:13:HIS:CB	2.52	0.40
4:B:16:HIS:CE1	4:B:214:ILE:HG12	2.56	0.40
5:C:15:THR:O	5:C:16:ARG:CB	2.62	0.40
5:C:135:LYS:HD2	5:C:135:LYS:HA	1.87	0.40
10:H:38:ILE:N	10:H:38:ILE:CD1	2.84	0.40
10:H:86:ILE:HG22	10:H:87:SER:N	2.35	0.40
12:J:61:GLU:OE2	16:N:58:LYS:HE2	2.21	0.40
16:N:34:TYR:HD1	16:N:34:TYR:N	2.19	0.40
17:O:39:LEU:C	17:O:39:LEU:CD2	2.93	0.40
19:Q:40:LYS:HD3	19:Q:42:TYR:OH	2.21	0.40
1:A:419:C:C5	1:A:424:G:C4	3.10	0.40
1:A:426:G:O2'	1:A:427:U:H5'	2.21	0.40
1:A:435:C:O2	1:A:435:C:H2'	2.21	0.40
1:A:485:G:O2'	1:A:486:U:H5	2.04	0.40
1:A:620:C:C2	6:D:135:LEU:HD13	2.57	0.40
1:A:662:G:O2'	1:A:836:G:H5''	2.22	0.40
1:A:760:G:H1	19:Q:105:ALA:CB	2.34	0.40
1:A:961:U:O2	1:A:1201:A:N1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1063:C:H3'	1:A:1064:G:H2'	2.04	0.40
1:A:1250:A:H5''	11:I:68:GLY:N	2.35	0.40
1:A:1481:U:H2'	1:A:1482:G:O4'	2.21	0.40
4:B:36:ARG:HE	4:B:41:ILE:HD12	1.86	0.40
5:C:58:GLU:O	5:C:59:ARG:CG	2.69	0.40
11:I:19:LEU:HB3	11:I:59:PHE:HD2	1.86	0.40
15:M:56:LEU:O	15:M:56:LEU:HD23	2.22	0.40
20:R:18:ARG:NE	20:R:18:ARG:HA	2.37	0.40
21:S:28:LYS:CG	21:S:29:ARG:N	2.82	0.40
1:A:8:A:N6	6:D:209:ARG:HB2	2.36	0.40
1:A:142:G:O2'	1:A:196:A:N1	2.41	0.40
1:A:382:A:H2'	1:A:383:A:H8	1.84	0.40
1:A:742:G:H2'	1:A:743:U:O4'	2.22	0.40
1:A:828:A:H2'	1:A:829:G:O5'	2.22	0.40
1:A:1226:C:O2'	1:A:1227:A:O5'	2.36	0.40
1:A:1279:A:O2'	1:A:1281:U:OP2	2.28	0.40
4:B:115:LEU:CG	4:B:116:GLU:N	2.83	0.40
4:B:186:ALA:HB3	4:B:197:VAL:HG11	2.03	0.40
7:E:121:LYS:HD2	7:E:122:GLU:N	2.37	0.40
9:G:22:LEU:HD12	9:G:101:LEU:HD11	2.02	0.40
9:G:116:ALA:HA	9:G:119:ARG:NH2	2.36	0.40
10:H:38:ILE:H	10:H:38:ILE:CD1	2.30	0.40
11:I:43:ALA:C	11:I:45:ALA:N	2.78	0.40
11:I:69:GLY:O	11:I:73:GLN:HG3	2.22	0.40
12:J:15:THR:O	12:J:19:SER:HB3	2.20	0.40
16:N:26:ARG:CZ	16:N:47:LEU:HD21	2.51	0.40
17:O:38:ARG:HG3	17:O:38:ARG:NH1	2.37	0.40
18:P:67:THR:HG22	18:P:69:THR:N	2.36	0.40
19:Q:9:VAL:HG21	19:Q:84:LEU:CD1	2.47	0.40
19:Q:98:LEU:HD12	19:Q:98:LEU:N	2.37	0.40
21:S:33:THR:CG2	21:S:34:TRP:H	2.30	0.40
23:V:6:ARG:HG3	23:V:7:ARG:H	1.87	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:79:ARG:NE	12:J:79:ARG:NE[8_665]	2.15	0.05

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	232/256 (91%)	154 (66%)	52 (22%)	26 (11%)	0	1
5	C	204/239 (85%)	132 (65%)	48 (24%)	24 (12%)	0	1
6	D	206/209 (99%)	160 (78%)	37 (18%)	9 (4%)	2	9
7	E	148/162 (91%)	125 (84%)	17 (12%)	6 (4%)	2	10
8	F	99/101 (98%)	75 (76%)	19 (19%)	5 (5%)	1	8
9	G	153/156 (98%)	120 (78%)	27 (18%)	6 (4%)	2	11
10	H	136/138 (99%)	113 (83%)	18 (13%)	5 (4%)	2	12
11	I	125/128 (98%)	88 (70%)	23 (18%)	14 (11%)	0	1
12	J	96/105 (91%)	61 (64%)	23 (24%)	12 (12%)	0	1
13	K	117/129 (91%)	90 (77%)	22 (19%)	5 (4%)	2	10
14	L	122/135 (90%)	92 (75%)	18 (15%)	12 (10%)	0	2
15	M	123/126 (98%)	88 (72%)	21 (17%)	14 (11%)	0	1
16	N	58/61 (95%)	38 (66%)	17 (29%)	3 (5%)	1	8
17	O	86/89 (97%)	70 (81%)	11 (13%)	5 (6%)	1	6
18	P	81/88 (92%)	61 (75%)	16 (20%)	4 (5%)	1	8
19	Q	102/105 (97%)	80 (78%)	15 (15%)	7 (7%)	1	4
20	R	71/88 (81%)	53 (75%)	13 (18%)	5 (7%)	1	4
21	S	78/93 (84%)	50 (64%)	22 (28%)	6 (8%)	1	3
22	T	97/106 (92%)	71 (73%)	17 (18%)	9 (9%)	0	2
23	V	22/27 (82%)	16 (73%)	5 (23%)	1 (4%)	2	9
All	All	2356/2541 (93%)	1737 (74%)	441 (19%)	178 (8%)	1	3

All (178) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	8	LYS

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Mol	Chain	Res	Type
4	B	20	GLU
4	B	21	ARG
4	B	24	TRP
4	B	77	ALA
4	B	88	ALA
4	B	95	GLN
4	B	211	ILE
4	B	229	VAL
5	C	15	THR
5	C	16	ARG
5	C	47	LEU
5	C	55	VAL
5	C	61	ALA
5	C	96	GLY
5	C	100	ALA
5	C	101	LEU
5	C	179	ARG
6	D	36	ARG
8	F	34	GLY
8	F	72	VAL
9	G	7	ALA
9	G	147	ALA
10	H	83	ILE
10	H	91	ARG
11	I	38	GLN
11	I	41	VAL
11	I	127	LYS
12	J	27	ALA
12	J	61	GLU
12	J	72	VAL
13	K	127	LYS
14	L	27	LEU
14	L	28	LYS
14	L	30	ALA
14	L	41	ARG
14	L	47	LYS
14	L	48	PRO
14	L	80	HIS
15	M	7	VAL
15	M	27	LYS
15	M	67	GLU
15	M	86	CYS

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Mol	Chain	Res	Type
15	M	122	LYS
18	P	47	ASP
18	P	81	ARG
19	Q	69	LYS
19	Q	81	ARG
19	Q	99	SER
20	R	21	LYS
21	S	25	LYS
4	B	9	GLU
4	B	17	PHE
4	B	18	GLY
4	B	27	LYS
4	B	60	ASP
4	B	115	LEU
4	B	224	GLN
5	C	91	LEU
5	C	98	ASN
5	C	108	ASN
5	C	154	SER
6	D	25	ARG
7	E	140	ARG
7	E	153	LYS
9	G	17	VAL
10	H	134	ILE
11	I	39	GLY
11	I	55	ALA
11	I	88	TYR
11	I	121	ARG
12	J	34	VAL
12	J	57	LYS
13	K	12	ARG
13	K	126	ARG
14	L	91	LYS
14	L	102	ARG
15	M	12	ASN
15	M	28	ALA
15	M	63	THR
15	M	68	GLY
15	M	100	GLY
15	M	106	ASN
15	M	120	LYS
16	N	15	LYS

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Mol	Chain	Res	Type
16	N	60	SER
18	P	10	GLY
18	P	82	GLN
19	Q	49	GLU
19	Q	80	GLY
20	R	20	ALA
21	S	27	GLU
21	S	47	HIS
22	T	50	GLU
22	T	73	HIS
22	T	74	LYS
22	T	96	GLY
22	T	102	GLY
4	B	15	VAL
4	B	76	GLN
4	B	134	GLU
4	B	155	LEU
5	C	26	LYS
5	C	127	ARG
5	C	189	ALA
6	D	164	ALA
7	E	16	THR
7	E	71	LEU
8	F	64	GLN
9	G	52	GLU
9	G	155	ARG
10	H	81	HIS
11	I	31	GLN
11	I	43	ALA
11	I	46	ALA
11	I	56	LEU
11	I	119	ALA
12	J	73	ASP
12	J	86	MET
12	J	90	LEU
13	K	75	TYR
16	N	17	LYS
17	O	88	ARG
22	T	86	ARG
22	T	98	PRO
4	B	22	LYS
4	B	119	GLU

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Mol	Chain	Res	Type
4	B	154	LEU
5	C	60	ALA
5	C	62	ASP
6	D	4	TYR
12	J	35	SER
13	K	70	LYS
14	L	51	ALA
14	L	105	TYR
17	O	73	GLU
17	O	86	GLY
19	Q	98	LEU
20	R	19	LYS
22	T	9	ASN
22	T	97	ALA
23	V	3	LYS
4	B	227	GLY
5	C	51	GLY
5	C	146	ALA
5	C	168	ALA
6	D	156	GLU
7	E	107	ARG
8	F	17	SER
10	H	24	THR
12	J	40	LEU
20	R	87	ARG
21	S	28	LYS
4	B	202	PRO
5	C	134	ILE
5	C	205	GLY
6	D	5	ILE
6	D	171	GLY
7	E	128	PRO
8	F	97	PHE
11	I	101	PHE
12	J	41	PRO
15	M	85	GLY
17	O	46	HIS
5	C	84	ILE
15	M	4	ILE
4	B	131	PRO
11	I	44	VAL
21	S	31	ILE

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Mol	Chain	Res	Type
6	D	88	VAL
12	J	76	ASN
20	R	60	GLY
6	D	39	PRO
9	G	42	ILE
14	L	121	GLY
17	O	82	ILE
19	Q	102	GLY
21	S	45	VAL

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	
4	B	202/220 (92%)	179 (89%)	23 (11%)	5	20
5	C	160/188 (85%)	142 (89%)	18 (11%)	5	20
6	D	180/181 (99%)	165 (92%)	15 (8%)	10	32
7	E	115/123 (94%)	98 (85%)	17 (15%)	3	11
8	F	90/90 (100%)	83 (92%)	7 (8%)	11	34
9	G	126/127 (99%)	118 (94%)	8 (6%)	16	41
10	H	119/119 (100%)	108 (91%)	11 (9%)	8	28
11	I	98/99 (99%)	87 (89%)	11 (11%)	6	20
12	J	87/92 (95%)	78 (90%)	9 (10%)	7	24
13	K	90/99 (91%)	85 (94%)	5 (6%)	19	45
14	L	104/111 (94%)	99 (95%)	5 (5%)	23	50
15	M	100/101 (99%)	87 (87%)	13 (13%)	4	15
16	N	49/50 (98%)	42 (86%)	7 (14%)	3	12
17	O	79/80 (99%)	71 (90%)	8 (10%)	7	24
18	P	72/74 (97%)	68 (94%)	4 (6%)	19	45
19	Q	96/97 (99%)	87 (91%)	9 (9%)	8	27
20	R	64/77 (83%)	60 (94%)	4 (6%)	16	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	S	71/80 (89%)	67 (94%)	4 (6%)	19	45
22	T	75/82 (92%)	67 (89%)	8 (11%)	6	22
23	V	19/22 (86%)	18 (95%)	1 (5%)	20	47
All	All	1996/2112 (94%)	1809 (91%)	187 (9%)	8	27

All (187) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	8	LYS
4	B	9	GLU
4	B	21	ARG
4	B	23	ARG
4	B	25	ASN
4	B	76	GLN
4	B	98	LEU
4	B	107	THR
4	B	117	GLU
4	B	129	GLU
4	B	144	ARG
4	B	162	ILE
4	B	170	GLU
4	B	178	ARG
4	B	179	LYS
4	B	184	VAL
4	B	185	ILE
4	B	190	THR
4	B	191	ASP
4	B	197	VAL
4	B	215	LEU
4	B	221	LEU
4	B	231	GLU
5	C	3	ASN
5	C	5	ILE
5	C	21	ARG
5	C	38	ARG
5	C	70	VAL
5	C	72	LYS
5	C	82	GLU
5	C	93	LYS
5	C	101	LEU
5	C	102	ASN

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Mol	Chain	Res	Type
5	C	107	GLN
5	C	139	GLN
5	C	165	THR
5	C	167	TRP
5	C	188	LEU
5	C	196	LEU
5	C	198	VAL
5	C	204	LEU
6	D	3	ARG
6	D	9	CYS
6	D	15	GLU
6	D	58	LEU
6	D	65	ARG
6	D	85	LYS
6	D	105	VAL
6	D	106	TYR
6	D	122	ARG
6	D	146	ILE
6	D	156	GLU
6	D	170	VAL
6	D	177	ASP
6	D	194	LEU
6	D	201	GLN
7	E	12	LEU
7	E	15	ARG
7	E	16	THR
7	E	24	ARG
7	E	31	LEU
7	E	41	VAL
7	E	43	LEU
7	E	80	ILE
7	E	89	ILE
7	E	116	THR
7	E	120	THR
7	E	126	ARG
7	E	137	GLU
7	E	143	ARG
7	E	144	THR
7	E	150	ARG
7	E	151	LEU
8	F	9	VAL
8	F	10	LEU

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Mol	Chain	Res	Type
8	F	61	LEU
8	F	65	VAL
8	F	69	GLU
8	F	82	ARG
8	F	92	LYS
9	G	8	GLU
9	G	11	GLN
9	G	12	LEU
9	G	79	ARG
9	G	113	GLU
9	G	126	ASP
9	G	135	VAL
9	G	155	ARG
10	H	18	ARG
10	H	26	VAL
10	H	39	LEU
10	H	52	ASP
10	H	63	LEU
10	H	83	ILE
10	H	85	ARG
10	H	91	ARG
10	H	92	ARG
10	H	119	LEU
10	H	133	LEU
11	I	2	GLU
11	I	5	TYR
11	I	16	ARG
11	I	38	GLN
11	I	42	ARG
11	I	47	LEU
11	I	78	LYS
11	I	79	LEU
11	I	92	TYR
11	I	111	ARG
11	I	127	LYS
12	J	12	ASP
12	J	29	ARG
12	J	33	GLN
12	J	45	ARG
12	J	60	ARG
12	J	73	ASP
12	J	75	ILE

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Mol	Chain	Res	Type
12	J	83	GLU
12	J	86	MET
13	K	29	ILE
13	K	51	LYS
13	K	84	VAL
13	K	93	GLN
13	K	127	LYS
14	L	48	PRO
14	L	54	LYS
14	L	83	VAL
14	L	85	ILE
14	L	93	LEU
15	M	3	ARG
15	M	12	ASN
15	M	40	ASN
15	M	48	LEU
15	M	49	THR
15	M	56	LEU
15	M	70	LEU
15	M	88	ARG
15	M	102	ARG
15	M	105	THR
15	M	110	ARG
15	M	115	LYS
15	M	126	LYS
16	N	8	GLU
16	N	11	LYS
16	N	12	ARG
16	N	34	TYR
16	N	41	ARG
16	N	44	LEU
16	N	58	LYS
17	O	4	THR
17	O	6	GLU
17	O	7	GLU
17	O	9	GLN
17	O	31	LEU
17	O	34	LEU
17	O	70	LEU
17	O	81	LEU
18	P	2	VAL
18	P	31	LYS

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Mol	Chain	Res	Type
18	P	53	VAL
18	P	82	GLN
19	Q	38	ARG
19	Q	48	GLU
19	Q	60	ILE
19	Q	64	PRO
19	Q	74	LEU
19	Q	78	GLU
19	Q	98	LEU
19	Q	99	SER
19	Q	100	LYS
20	R	38	GLU
20	R	42	ARG
20	R	54	ARG
20	R	80	PRO
21	S	6	LYS
21	S	18	LYS
21	S	43	GLU
21	S	77	THR
22	T	13	LEU
22	T	21	LYS
22	T	42	GLN
22	T	45	GLN
22	T	48	LYS
22	T	57	ARG
22	T	75	ASN
22	T	84	LEU
23	V	7	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (67) such sidechains are listed below:

Mol	Chain	Res	Type
4	B	25	ASN
4	B	40	HIS
4	B	76	GLN
4	B	94	ASN
4	B	140	HIS
4	B	212	GLN
4	B	240	GLN
5	C	3	ASN
5	C	6	HIS
5	C	31	HIS

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Mol	Chain	Res	Type
5	C	37	GLN
5	C	63	ASN
5	C	102	ASN
5	C	107	GLN
5	C	123	GLN
5	C	139	GLN
5	C	170	GLN
5	C	176	HIS
5	C	181	ASN
6	D	42	GLN
6	D	45	GLN
6	D	62	GLN
6	D	74	GLN
6	D	119	GLN
6	D	123	HIS
6	D	161	ASN
6	D	199	ASN
7	E	56	GLN
7	E	73	ASN
7	E	78	HIS
8	F	11	ASN
8	F	13	ASN
8	F	18	GLN
8	F	27	GLN
8	F	100	ASN
9	G	28	ASN
9	G	37	ASN
9	G	84	ASN
9	G	86	GLN
9	G	96	GLN
9	G	106	GLN
11	I	23	ASN
11	I	73	GLN
12	J	21	GLN
12	J	33	GLN
12	J	84	GLN
13	K	13	GLN
13	K	22	HIS
13	K	38	ASN
13	K	116	HIS
13	K	117	ASN
14	L	49	ASN

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Mol	Chain	Res	Type
14	L	75	HIS
15	M	40	ASN
15	M	62	ASN
17	O	9	GLN
17	O	13	GLN
17	O	37	ASN
17	O	71	GLN
18	P	76	GLN
18	P	82	GLN
19	Q	94	ASN
20	R	36	ASN
21	S	14	HIS
21	S	23	ASN
21	S	56	GLN
21	S	65	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1522 (98%)	227 (15%)	73 (4%)
2	X	8/11 (72%)	0	0
3	W	3/4 (75%)	0	0
All	All	1517/1537 (98%)	227 (14%)	73 (4%)

All (227) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	51	A
1	A	61	G
1	A	101	A
1	A	116	A
1	A	120	A

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Mol	Chain	Res	Type
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	163	C
1	A	182	U
1	A	189	G
1	A	190	C
1	A	190(A)	C
1	A	190(D)	U
1	A	190(E)	U
1	A	195	A
1	A	197	A
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	289	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	345	C
1	A	350	G
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	406	G
1	A	407	G
1	A	408	A
1	A	409	G

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Mol	Chain	Res	Type
1	A	410	G
1	A	412	A
1	A	413	G
1	A	414	A
1	A	415	A
1	A	416	G
1	A	417	C
1	A	418	C
1	A	422	C
1	A	423	G
1	A	425	G
1	A	429	U
1	A	430	A
1	A	434	U
1	A	435	C
1	A	439	A
1	A	448	A
1	A	452	A
1	A	460	A
1	A	461	C
1	A	462	G
1	A	474	G
1	A	475	G
1	A	476	G
1	A	478	A
1	A	480	U
1	A	484	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	511	C
1	A	518	C
1	A	519	C
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U

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Mol	Chain	Res	Type
1	A	562	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	588	G
1	A	653	A
1	A	665	A
1	A	688	G
1	A	695	A
1	A	701	C
1	A	702	A
1	A	703	G
1	A	723	U
1	A	731	G
1	A	748	C
1	A	755	G
1	A	777	A
1	A	781	A
1	A	782	A
1	A	793	U
1	A	812	C
1	A	813	U
1	A	817	C
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	946	A
1	A	960	U
1	A	961	U
1	A	965	A
1	A	966	G

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Mol	Chain	Res	Type
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1002	G
1	A	1005	A
1	A	1026	G
1	A	1029	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	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	1140	C
1	A	1145	C
1	A	1152	A
1	A	1159	U
1	A	1183	A
1	A	1184	G
1	A	1196	U
1	A	1197	G
1	A	1200	C
1	A	1201	A

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Mol	Chain	Res	Type
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1224	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1257	U
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1305	G
1	A	1319	A
1	A	1320	C
1	A	1346	A
1	A	1347	G
1	A	1348	U
1	A	1353	G
1	A	1361	G
1	A	1362	C
1	A	1363	A
1	A	1398	A
1	A	1443	G
1	A	1446	A
1	A	1447	G
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	1505	G
1	A	1506	U
1	A	1517	G
1	A	1529	G
1	A	1530	G

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Mol	Chain	Res	Type
1	A	1533	C
1	A	1534	A
1	A	1539	C

All (73) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	30	U
1	A	48	C
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	188	C
1	A	190	C
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	328	C
1	A	344	A
1	A	350	G
1	A	353	A
1	A	366	C
1	A	372	C
1	A	407	G
1	A	428	G
1	A	429	U
1	A	434	U
1	A	463	A
1	A	484	G
1	A	496	A
1	A	518	C
1	A	532	A
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G

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Mol	Chain	Res	Type
1	A	687	A
1	A	701	C
1	A	792	A
1	A	812	C
1	A	840	C
1	A	913	A
1	A	945	G
1	A	960	U
1	A	965	A
1	A	975	A
1	A	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	1196	U
1	A	1201	A
1	A	1212	U
1	A	1224	G
1	A	1226	C
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1301	U
1	A	1319	A
1	A	1346	A
1	A	1347	G
1	A	1397	C
1	A	1451	A
1	A	1498	U
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1528	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 110 ligands modelled in this entry, 109 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	PAR	A	1545	-	44,45,45	1.39	6 (13%)	63,67,67	1.15	7 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	PAR	A	1545	-	-	4/18/94/94	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1545	PAR	O54-C14	3.59	1.51	1.41
24	A	1545	PAR	C11-C21	2.68	1.57	1.52
24	A	1545	PAR	O51-C11	2.59	1.48	1.41
24	A	1545	PAR	C31-C21	2.54	1.56	1.53
24	A	1545	PAR	C52-C42	2.33	1.57	1.52
24	A	1545	PAR	O33-C14	2.08	1.47	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1545	PAR	O33-C14-C24	3.63	114.02	108.08
24	A	1545	PAR	O54-C54-C64	3.38	112.56	106.07
24	A	1545	PAR	C14-O54-C54	2.93	119.44	113.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1545	PAR	O52-C13-O43	-2.35	108.97	111.37
24	A	1545	PAR	O11-C11-C21	2.24	111.74	108.08
24	A	1545	PAR	C11-O51-C51	2.09	117.80	113.72
24	A	1545	PAR	C22-C32-C42	2.05	114.54	109.50

There are no chirality outliers.

All (4) torsion outliers are listed below:

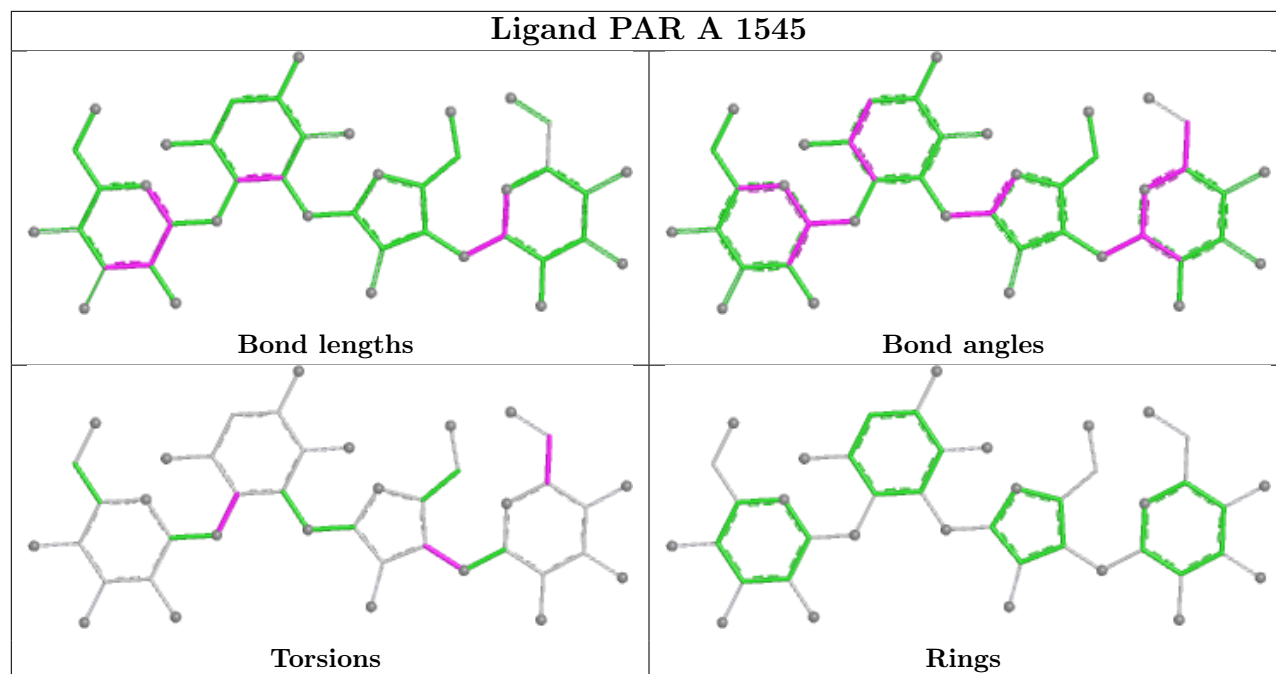
Mol	Chain	Res	Type	Atoms
24	A	1545	PAR	C44-C54-C64-N64
24	A	1545	PAR	O54-C54-C64-N64
24	A	1545	PAR	C52-C42-O11-C11
24	A	1545	PAR	C23-C33-O33-C14

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	1545	PAR	2	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1507/1522 (99%)	0.64	173 (11%) 9 5	31, 65, 156, 200	0
2	X	10/11 (90%)	2.05	5 (50%) 0 0	79, 120, 147, 149	0
3	W	4/4 (100%)	1.27	1 (25%) 2 1	63, 68, 79, 134	0
4	B	234/256 (91%)	0.96	28 (11%) 9 5	45, 102, 162, 200	0
5	C	206/239 (86%)	0.98	33 (16%) 5 2	44, 92, 150, 185	0
6	D	208/209 (99%)	0.53	15 (7%) 21 11	40, 73, 128, 164	0
7	E	150/162 (92%)	0.25	4 (2%) 56 33	35, 59, 110, 151	0
8	F	101/101 (100%)	0.63	5 (4%) 34 17	54, 95, 138, 162	0
9	G	155/156 (99%)	0.49	12 (7%) 19 10	46, 80, 138, 172	0
10	H	138/138 (100%)	0.13	1 (0%) 84 66	32, 57, 101, 130	0
11	I	127/128 (99%)	0.94	15 (11%) 9 5	45, 93, 141, 168	0
12	J	98/105 (93%)	1.44	25 (25%) 1 1	49, 116, 172, 189	0
13	K	119/129 (92%)	0.43	3 (2%) 58 35	38, 67, 123, 173	0
14	L	124/135 (91%)	0.51	13 (10%) 11 6	30, 69, 120, 189	0
15	M	125/126 (99%)	0.73	12 (9%) 13 7	51, 85, 149, 181	0
16	N	60/61 (98%)	1.12	10 (16%) 4 2	53, 81, 126, 188	0
17	O	88/89 (98%)	0.38	3 (3%) 48 27	39, 72, 131, 191	0
18	P	83/88 (94%)	0.20	2 (2%) 59 37	37, 54, 89, 146	0
19	Q	104/105 (99%)	0.26	7 (6%) 24 12	33, 57, 124, 200	0
20	R	73/88 (82%)	0.45	3 (4%) 41 22	48, 79, 153, 193	0
21	S	80/93 (86%)	1.06	11 (13%) 6 4	65, 110, 155, 178	0
22	T	99/106 (93%)	0.55	11 (11%) 10 5	35, 61, 118, 160	0
23	V	24/27 (88%)	1.06	6 (25%) 2 1	45, 70, 135, 147	0
All	All	3917/4078 (96%)	0.64	398 (10%) 12 6	30, 73, 150, 200	0

All (398) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	407	G	12.4
1	A	190	C	9.2
1	A	189	G	9.1
1	A	1129	C	8.3
1	A	463	A	8.1
1	A	423	G	7.9
1	A	1533	C	7.6
1	A	408	A	6.9
1	A	475	G	6.8
1	A	1540	U	6.7
1	A	424	G	6.6
1	A	410	G	6.4
1	A	1030	C	6.4
1	A	1361	G	6.4
1	A	631	G	6.2
1	A	409	G	6.2
1	A	1126	U	6.1
6	D	9	CYS	5.9
1	A	1031	G	5.9
19	Q	105	ALA	5.6
1	A	425	G	5.6
13	K	129	SER	5.6
1	A	462	G	5.5
21	S	2	PRO	5.4
1	A	1362	C	5.4
1	A	416	G	5.3
6	D	31	CYS	5.2
1	A	411	A	5.2
1	A	476	G	5.2
6	D	22	LYS	5.0
18	P	83	GLU	4.9
1	A	1018	C	4.9
1	A	1034	G	4.9
14	L	128	ALA	4.8
1	A	420	U	4.8
2	X	30	G	4.8
1	A	1442	G	4.8
1	A	415	A	4.7
16	N	30	ALA	4.7
4	B	16	HIS	4.7
21	S	37	ARG	4.6
1	A	460	A	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	422	C	4.5
4	B	86	GLU	4.5
15	M	126	LYS	4.5
14	L	73	GLU	4.4
1	A	1124	G	4.4
1	A	1212	U	4.4
19	Q	103	GLY	4.3
1	A	1027	C	4.3
9	G	16	LEU	4.3
22	T	100	ILE	4.2
4	B	19	HIS	4.1
1	A	993	G	4.1
1	A	417	C	4.0
1	A	1026	G	4.0
3	W	4	A	4.0
6	D	23	GLY	4.0
1	A	413	G	4.0
1	A	432	A	4.0
1	A	1025	U	4.0
1	A	412	A	4.0
6	D	24	GLU	3.9
1	A	1004	A	3.9
1	A	190(A)	C	3.9
1	A	1006	C	3.9
12	J	5	ARG	3.9
1	A	1135	U	3.9
1	A	1539	C	3.9
1	A	1130	A	3.8
1	A	1277	C	3.8
1	A	1127	G	3.8
23	V	25	LYS	3.8
1	A	1534	A	3.7
1	A	434	U	3.7
23	V	6	ARG	3.6
11	I	128	ARG	3.6
1	A	431	A	3.6
22	T	74	LYS	3.6
1	A	485	G	3.6
12	J	88	LEU	3.6
22	T	95	ALA	3.6
1	A	478	A	3.5
1	A	991	U	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	216	G	3.5
1	A	1131	G	3.5
2	X	40	C	3.5
14	L	79	GLU	3.5
12	J	77	PRO	3.5
5	C	110	ASN	3.5
13	K	117	ASN	3.5
1	A	1125	U	3.5
1	A	414	A	3.4
1	A	477	G	3.4
1	A	1024	G	3.4
1	A	996	A	3.4
5	C	3	ASN	3.4
1	A	1017	G	3.4
6	D	26	CYS	3.4
15	M	7	VAL	3.4
11	I	67	GLY	3.3
15	M	120	LYS	3.3
15	M	8	GLU	3.3
1	A	1541	U	3.3
21	S	81	ARG	3.3
1	A	433	C	3.3
1	A	1200	C	3.3
5	C	161	GLU	3.3
11	I	119	ALA	3.3
1	A	1146	A	3.3
6	D	33	MET	3.3
19	Q	102	GLY	3.2
1	A	1268	A	3.2
5	C	56	ASP	3.2
6	D	21	LEU	3.2
14	L	47	LYS	3.2
1	A	1036	G	3.2
4	B	240	GLN	3.2
1	A	418	C	3.2
9	G	5	ARG	3.2
1	A	1045	C	3.2
16	N	6	LEU	3.2
13	K	52	GLY	3.1
8	F	31	GLU	3.1
1	A	1140	C	3.1
1	A	1446	A	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	419	C	3.1
1	A	1003	G	3.1
12	J	99	LYS	3.1
7	E	154	GLY	3.1
4	B	122	PHE	3.1
1	A	1281	U	3.1
1	A	1035	A	3.1
1	A	344	A	3.0
11	I	23	ASN	3.0
11	I	87	GLN	3.0
5	C	21	ARG	3.0
1	A	1213	A	3.0
23	V	24	ARG	3.0
14	L	115	LYS	3.0
1	A	748	C	3.0
1	A	840	C	3.0
12	J	57	LYS	3.0
21	S	26	GLY	3.0
4	B	11	LEU	2.9
21	S	3	ARG	2.9
1	A	1443	G	2.9
22	T	106	ALA	2.9
1	A	1005	A	2.9
5	C	96	GLY	2.9
1	A	421	U	2.9
4	B	18	GLY	2.9
1	A	1145	C	2.9
5	C	71	ALA	2.9
15	M	123	ALA	2.9
1	A	1134	G	2.9
7	E	83	GLU	2.9
1	A	458	C	2.9
1	A	992	U	2.9
15	M	125	ARG	2.9
18	P	82	GLN	2.9
22	T	51	GLU	2.9
5	C	23	TYR	2.9
22	T	101	GLY	2.9
5	C	80	GLY	2.8
4	B	148	TYR	2.8
6	D	19	LEU	2.8
12	J	96	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
12	J	68	HIS	2.8
1	A	1279	A	2.8
1	A	1019	C	2.8
4	B	7	VAL	2.8
14	L	20	LYS	2.8
15	M	106	ASN	2.8
19	Q	100	LYS	2.8
1	A	202	U	2.8
12	J	10	GLY	2.8
1	A	1009	G	2.8
14	L	26	ALA	2.8
15	M	124	PRO	2.8
21	S	27	GLU	2.8
4	B	206	ASP	2.8
5	C	167	TRP	2.8
1	A	204	U	2.8
1	A	1143	G	2.8
1	A	1220	G	2.8
1	A	1370	G	2.8
12	J	41	PRO	2.8
5	C	154	SER	2.8
12	J	95	GLU	2.8
5	C	4	LYS	2.7
1	A	1256	A	2.7
11	I	38	GLN	2.7
11	I	64	THR	2.7
4	B	205	ASP	2.7
22	T	99	LEU	2.7
11	I	7	THR	2.7
1	A	980	C	2.7
14	L	78	GLN	2.7
14	L	28	LYS	2.7
11	I	92	TYR	2.7
5	C	155	GLY	2.7
17	O	89	GLY	2.7
2	X	39	C	2.6
4	B	61	LEU	2.6
1	A	459	G	2.6
4	B	96	ARG	2.6
5	C	128	PHE	2.6
12	J	78	ASN	2.6
12	J	31	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	1318	A	2.6
1	A	849	C	2.6
11	I	125	TYR	2.6
23	V	10	ARG	2.6
1	A	266	G	2.6
1	A	1266	G	2.6
22	T	12	ALA	2.6
20	R	16	PRO	2.6
1	A	848	C	2.6
1	A	999	C	2.6
23	V	2	GLY	2.6
9	G	2	ALA	2.6
16	N	13	THR	2.6
1	A	190(K)	G	2.6
1	A	1032	G	2.6
17	O	13	GLN	2.6
9	G	89	MET	2.5
4	B	234	PRO	2.5
9	G	81	GLY	2.5
1	A	1022	G	2.5
1	A	1139	G	2.5
1	A	1274	G	2.5
2	X	31	G	2.5
4	B	144	ARG	2.5
5	C	207	VAL	2.5
6	D	209	ARG	2.5
12	J	100	THR	2.5
1	A	1028	C	2.5
1	A	1029	C	2.5
5	C	48	TYR	2.5
6	D	87	GLY	2.5
4	B	35	GLU	2.5
5	C	67	THR	2.5
1	A	1283	G	2.5
16	N	21	TYR	2.5
4	B	238	LEU	2.5
6	D	3	ARG	2.5
12	J	43	ARG	2.5
1	A	5	U	2.5
19	Q	49	GLU	2.5
11	I	58	ARG	2.5
14	L	89	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
5	C	2	GLY	2.5
1	A	1011	G	2.5
5	C	65	ALA	2.5
15	M	35	GLU	2.5
1	A	975	A	2.4
9	G	52	GLU	2.4
9	G	139	GLU	2.4
1	A	630	G	2.4
1	A	1258	G	2.4
2	X	33	U	2.4
9	G	85	TYR	2.4
4	B	233	SER	2.4
5	C	105	GLU	2.4
6	D	25	ARG	2.4
19	Q	14	LYS	2.4
1	A	532	A	2.4
1	A	1137	C	2.4
1	A	1259	C	2.4
1	A	1260	C	2.4
4	B	120	ALA	2.4
1	A	723	U	2.4
1	A	1421	G	2.4
5	C	143	GLU	2.4
12	J	97	GLU	2.4
12	J	59	SER	2.4
19	Q	13	ASP	2.4
8	F	20	ALA	2.4
20	R	19	LYS	2.4
1	A	1039	C	2.4
21	S	5	LEU	2.4
1	A	1023	G	2.4
1	A	1138	G	2.4
1	A	1316	G	2.4
1	A	1167	A	2.4
1	A	1257	U	2.4
4	B	232	PRO	2.4
1	A	373	A	2.3
5	C	127	ARG	2.3
1	A	1217	C	2.3
1	A	1010	G	2.3
1	A	1300	G	2.3
6	D	2	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
12	J	87	THR	2.3
22	T	73	HIS	2.3
1	A	1479	C	2.3
8	F	34	GLY	2.3
1	A	998	G	2.3
1	A	1269	A	2.3
1	A	1012	U	2.3
1	A	436	C	2.3
1	A	1128	C	2.3
8	F	17	SER	2.3
4	B	45	GLN	2.3
22	T	68	LYS	2.3
9	G	115	ARG	2.3
15	M	105	THR	2.2
16	N	17	LYS	2.2
23	V	9	ARG	2.2
5	C	62	ASP	2.2
20	R	46	GLU	2.2
16	N	2	ALA	2.2
16	N	61	TRP	2.2
1	A	306	G	2.2
1	A	1050	G	2.2
1	A	1142	G	2.2
1	A	1265	G	2.2
11	I	27	THR	2.2
1	A	1044	A	2.2
10	H	115	SER	2.2
1	A	1008	C	2.2
4	B	83	MET	2.2
21	S	6	LYS	2.2
5	C	88	ARG	2.2
16	N	22	THR	2.2
5	C	64	VAL	2.2
4	B	109	SER	2.2
14	L	62	SER	2.2
1	A	429	U	2.2
1	A	1136	U	2.2
5	C	28	GLN	2.2
12	J	6	ILE	2.2
1	A	474	G	2.2
1	A	1021	G	2.2
1	A	1190	G	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1224	G	2.2
1	A	1482	G	2.2
21	S	73	GLU	2.2
12	J	93	GLY	2.2
5	C	36	ASP	2.2
14	L	92	ASP	2.2
1	A	479	C	2.2
4	B	93	VAL	2.2
11	I	19	LEU	2.2
5	C	45	LYS	2.2
4	B	214	ILE	2.1
8	F	84	ASN	2.1
16	N	4	LYS	2.1
1	A	971	G	2.1
9	G	7	ALA	2.1
12	J	37	PRO	2.1
16	N	32	SER	2.1
9	G	137	LYS	2.1
11	I	127	LYS	2.1
21	S	79	THR	2.1
12	J	29	ARG	2.1
5	C	60	ALA	2.1
12	J	33	GLN	2.1
1	A	1286	A	2.1
7	E	97	GLY	2.1
12	J	64	GLU	2.1
5	C	63	ASN	2.1
1	A	1053	G	2.1
1	A	1276	G	2.1
1	A	457	C	2.1
1	A	1420	C	2.1
15	M	13	LYS	2.1
4	B	23	ARG	2.1
22	T	56	MET	2.1
11	I	15	ALA	2.1
1	A	1049	U	2.1
5	C	136	GLN	2.1
14	L	126	LYS	2.1
6	D	159	ARG	2.1
9	G	156	TRP	2.1
21	S	69	HIS	2.1
1	A	435	C	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	990	C	2.1
1	A	157	G	2.1
1	A	1347	G	2.1
4	B	192	SER	2.0
1	A	733	A	2.0
1	A	1275	A	2.0
12	J	26	ALA	2.0
17	O	23	GLY	2.0
15	M	73	GLU	2.0
1	A	662	G	2.0
1	A	1144	G	2.0
5	C	87	LEU	2.0
12	J	75	ILE	2.0
4	B	237	ALA	2.0
5	C	51	GLY	2.0
1	A	994	A	2.0
1	A	1248	A	2.0
7	E	81	GLU	2.0
1	A	1007	C	2.0
1	A	1226	C	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1583	1/1	0.40	0.55	67,67,67,67	0
25	MG	A	1571	1/1	0.54	0.49	67,67,67,67	0
25	MG	A	1592	1/1	0.54	0.64	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1570	1/1	0.55	0.55	67,67,67,67	0
25	MG	A	1587	1/1	0.56	0.68	67,67,67,67	0
25	MG	A	1590	1/1	0.58	0.64	67,67,67,67	0
25	MG	A	1574	1/1	0.58	0.62	67,67,67,67	0
25	MG	A	1568	1/1	0.60	0.46	67,67,67,67	0
25	MG	A	1547	1/1	0.61	0.46	67,67,67,67	0
25	MG	A	1586	1/1	0.62	0.63	67,67,67,67	0
25	MG	A	1558	1/1	0.63	0.66	67,67,67,67	0
25	MG	A	1573	1/1	0.64	0.47	67,67,67,67	0
25	MG	A	1584	1/1	0.66	0.60	67,67,67,67	0
25	MG	A	1598	1/1	0.67	0.51	67,67,67,67	0
25	MG	A	1617	1/1	0.67	0.45	67,67,67,67	0
25	MG	A	1565	1/1	0.68	0.45	67,67,67,67	0
25	MG	A	1550	1/1	0.69	0.40	67,67,67,67	0
25	MG	A	1611	1/1	0.69	0.68	67,67,67,67	0
25	MG	A	210	1/1	0.69	0.32	67,67,67,67	0
25	MG	A	1594	1/1	0.70	0.25	67,67,67,67	1
25	MG	A	1605	1/1	0.70	0.46	67,67,67,67	0
25	MG	A	1618	1/1	0.70	0.54	67,67,67,67	0
25	MG	A	1576	1/1	0.71	0.61	67,67,67,67	0
25	MG	A	1551	1/1	0.72	0.96	67,67,67,67	0
25	MG	A	1557	1/1	0.72	0.52	67,67,67,67	0
25	MG	A	1546	1/1	0.72	0.53	67,67,67,67	0
25	MG	A	1564	1/1	0.72	0.65	67,67,67,67	0
25	MG	A	1588	1/1	0.73	0.79	67,67,67,67	0
25	MG	A	1633	1/1	0.73	0.28	67,67,67,67	0
25	MG	A	1629	1/1	0.74	0.54	67,67,67,67	0
25	MG	A	441	1/1	0.75	0.47	67,67,67,67	0
25	MG	A	1601	1/1	0.75	0.29	67,67,67,67	0
25	MG	A	1620	1/1	0.75	0.36	67,67,67,67	0
25	MG	A	1579	1/1	0.76	0.42	67,67,67,67	0
25	MG	A	1572	1/1	0.76	0.56	67,67,67,67	0
25	MG	A	71	1/1	0.77	0.47	67,67,67,67	0
25	MG	A	1560	1/1	0.78	0.70	67,67,67,67	0
25	MG	A	1621	1/1	0.78	0.51	67,67,67,67	0
25	MG	A	1626	1/1	0.78	0.29	67,67,67,67	0
25	MG	A	1591	1/1	0.78	0.58	67,67,67,67	0
25	MG	A	1630	1/1	0.78	0.39	67,67,67,67	0
25	MG	A	1600	1/1	0.78	0.41	67,67,67,67	0
25	MG	A	1582	1/1	0.79	0.47	67,67,67,67	0
25	MG	A	1578	1/1	0.79	0.43	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1612	1/1	0.79	0.64	67,67,67,67	0
25	MG	X	502	1/1	0.79	0.50	67,67,67,67	1
25	MG	A	469	1/1	0.80	0.33	67,67,67,67	1
25	MG	A	1561	1/1	0.80	0.34	67,67,67,67	0
25	MG	A	1552	1/1	0.80	0.56	67,67,67,67	0
25	MG	A	1608	1/1	0.81	0.68	67,67,67,67	0
25	MG	A	1625	1/1	0.81	0.57	67,67,67,67	0
25	MG	A	1624	1/1	0.82	0.46	67,67,67,67	0
25	MG	A	1555	1/1	0.82	0.70	67,67,67,67	0
25	MG	A	1599	1/1	0.82	0.33	67,67,67,67	0
25	MG	A	1619	1/1	0.82	0.18	67,67,67,67	0
25	MG	A	471	1/1	0.83	0.32	67,67,67,67	0
25	MG	A	214	1/1	0.83	0.39	67,67,67,67	0
25	MG	A	1623	1/1	0.83	0.73	67,67,67,67	0
25	MG	A	1614	1/1	0.84	0.35	67,67,67,67	0
25	MG	A	1610	1/1	0.85	0.37	67,67,67,67	1
25	MG	A	1585	1/1	0.85	0.52	67,67,67,67	0
25	MG	A	1548	1/1	0.86	0.30	67,67,67,67	0
25	MG	A	1602	1/1	0.86	0.52	67,67,67,67	0
25	MG	A	1616	1/1	0.87	0.15	67,67,67,67	0
25	MG	A	473	1/1	0.87	0.28	67,67,67,67	1
25	MG	A	86	1/1	0.88	0.42	67,67,67,67	0
25	MG	A	1575	1/1	0.88	0.61	67,67,67,67	1
25	MG	A	1569	1/1	0.88	0.61	67,67,67,67	0
25	MG	A	1577	1/1	0.88	0.44	67,67,67,67	0
25	MG	A	1606	1/1	0.89	0.23	67,67,67,67	0
25	MG	A	1562	1/1	0.89	0.50	67,67,67,67	0
25	MG	A	1556	1/1	0.90	0.65	67,67,67,67	0
25	MG	A	466	1/1	0.90	0.39	67,67,67,67	0
25	MG	A	467	1/1	0.90	0.20	67,67,67,67	0
25	MG	A	1595	1/1	0.90	0.30	67,67,67,67	0
25	MG	A	1607	1/1	0.90	0.23	67,67,67,67	1
25	MG	A	1597	1/1	0.90	0.18	67,67,67,67	0
25	MG	A	1628	1/1	0.90	0.62	67,67,67,67	0
24	PAR	A	1545	42/42	0.90	0.20	67,67,67,67	0
25	MG	A	1615	1/1	0.91	0.49	67,67,67,67	0
25	MG	A	493	1/1	0.91	0.16	67,67,67,67	1
25	MG	A	1635	1/1	0.91	0.43	67,67,67,67	1
25	MG	A	1609	1/1	0.91	0.64	67,67,67,67	0
25	MG	A	1567	1/1	0.92	0.79	67,67,67,67	0
25	MG	A	1559	1/1	0.92	0.60	67,67,67,67	0
25	MG	A	1604	1/1	0.92	0.42	67,67,67,67	0

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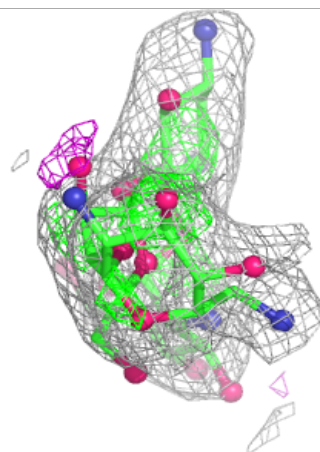
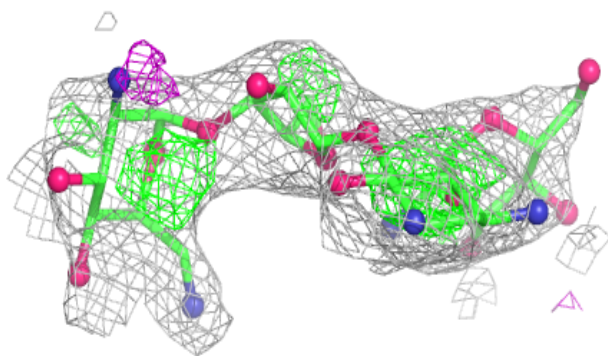
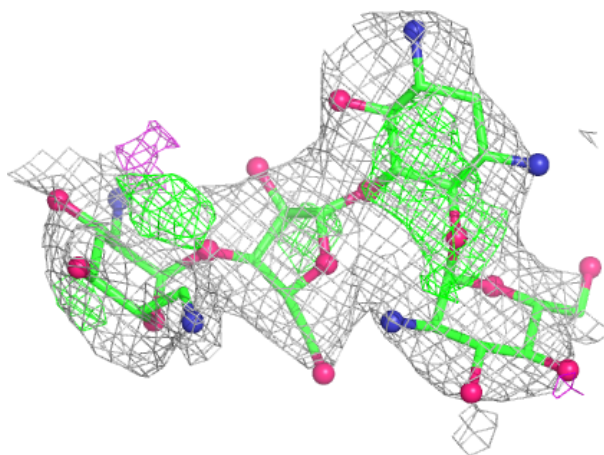
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1581	1/1	0.92	0.53	67,67,67,67	0
25	MG	A	1563	1/1	0.93	0.34	67,67,67,67	0
25	MG	A	1613	1/1	0.93	0.54	67,67,67,67	0
25	MG	A	1631	1/1	0.93	0.08	67,67,67,67	0
25	MG	A	1554	1/1	0.93	1.02	67,67,67,67	0
25	MG	A	1634	1/1	0.93	0.48	67,67,67,67	0
25	MG	A	1589	1/1	0.93	0.75	67,67,67,67	0
25	MG	A	87	1/1	0.93	0.38	67,67,67,67	0
25	MG	A	1627	1/1	0.93	0.39	67,67,67,67	0
25	MG	A	1580	1/1	0.94	0.87	67,67,67,67	0
25	MG	A	1596	1/1	0.94	0.37	67,67,67,67	0
25	MG	A	1632	1/1	0.94	0.15	67,67,67,67	0
25	MG	X	500	1/1	0.94	0.14	67,67,67,67	1
25	MG	A	1553	1/1	0.94	0.70	67,67,67,67	0
25	MG	J	449	1/1	0.94	0.27	67,67,67,67	0
26	ZN	D	306	1/1	0.94	0.28	67,67,67,67	0
25	MG	A	1622	1/1	0.95	0.56	67,67,67,67	0
25	MG	A	1549	1/1	0.95	0.57	67,67,67,67	0
25	MG	A	1603	1/1	0.95	0.55	67,67,67,67	0
25	MG	A	1566	1/1	0.95	0.41	67,67,67,67	0
25	MG	A	1593	1/1	0.96	0.58	67,67,67,67	0
25	MG	A	211	1/1	0.96	0.75	67,67,67,67	0
25	MG	A	470	1/1	0.98	0.50	67,67,67,67	0
26	ZN	N	307	1/1	0.99	0.03	67,67,67,67	0

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

Electron density around PAR A 1545:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.