



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:04 PM UTC

PDB ID : 1IBK / pdb_00001ibk
Title : STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL
SUBUNIT IN COMPLEX WITH THE ANTIBIOTIC PAROMOMYCIN
Authors : Ogle, J.M.; Brodersen, D.E.; Clemons Jr., W.M.; Tarry, M.J.; Carter, A.P.;
Ramakrishnan, V.
Deposited on : 2001-03-28
Resolution : 3.31 Å(reported)

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

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

A user guide is available at

<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

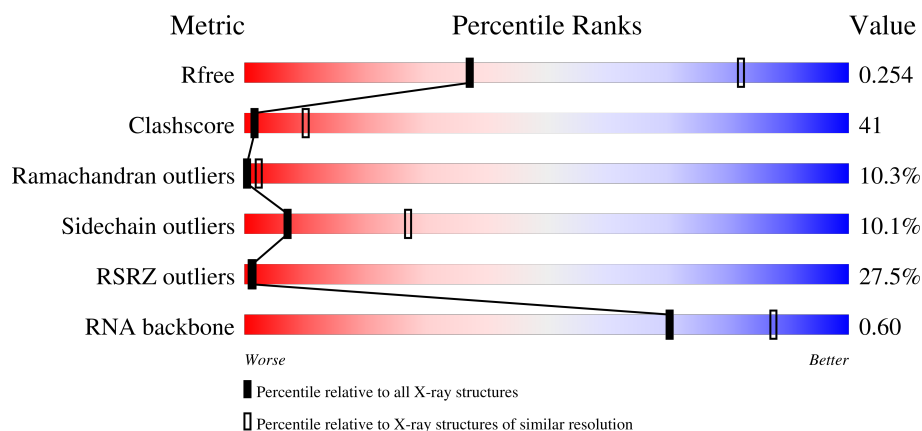
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.31 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1153 (3.34-3.30)
Clashscore	190562	1193 (3.34-3.30)
Ramachandran outliers	187476	1172 (3.34-3.30)
Sidechain outliers	187428	1171 (3.34-3.30)
RSRZ outliers	180081	1153 (3.34-3.30)
RNA backbone	3983	1067 (3.64-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	21% 26% 58% 12% . .
2	X	6	50% 67% 33%
3	B	256	37% 14% 56% 19% . 9%

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Mol	Chain	Length	Quality of chain
4	C	239	
5	D	209	
6	E	162	
7	F	101	
8	G	156	
9	H	138	
10	I	128	
11	J	105	
12	K	129	
13	L	135	
14	M	126	
15	N	61	
16	O	89	
17	P	88	
18	Q	105	
19	R	88	
20	S	93	
21	T	106	
22	V	26	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	MG	A	1647	-	-	-	X

2 Entry composition [i](#)

There are 25 unique types of molecules in this entry. The entry contains 51872 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	1506	Total	C	N	O	P	0	0	0
			32369	14408	5997	10459	1505			

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

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

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S2.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	?	-	PHE	conflict	GB 12056104
P	?	-	HIS	conflict	GB 12056104
P	?	-	TYR	conflict	GB 12056104

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	S	80	Total	C	N	O	S	0	0	0
			646	413	119	112	2			

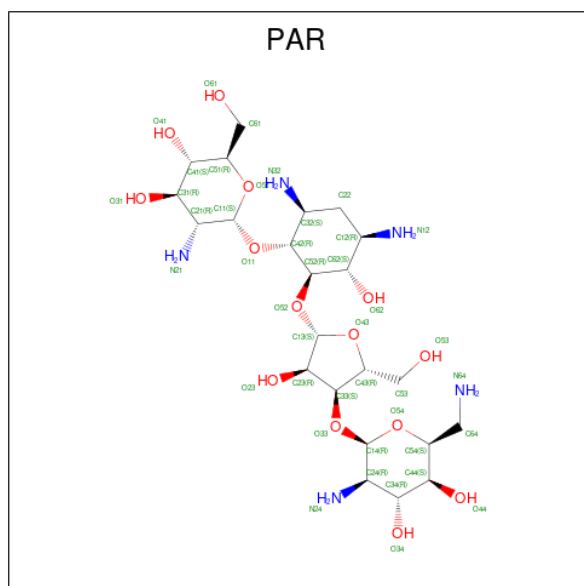
- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S20.

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

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

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

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



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

- Molecule 24 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	111	Total	Mg	0	0
			111	111		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	D	1	Total 1	Mg 1	0	0
24	L	1	Total 1	Mg 1	0	0

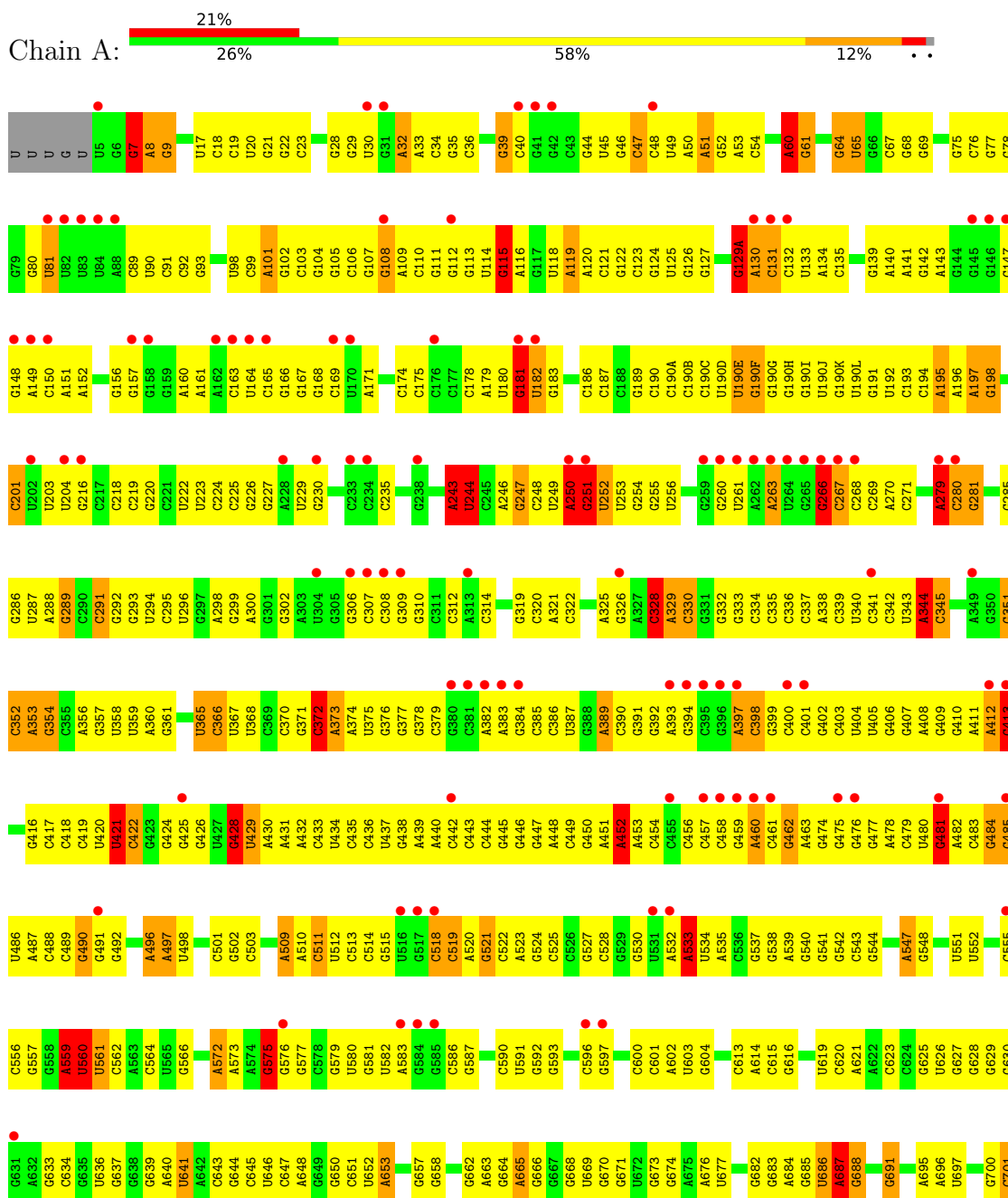
- Molecule 25 is ZINC ION (CCD ID: ZN) (formula: Zn).

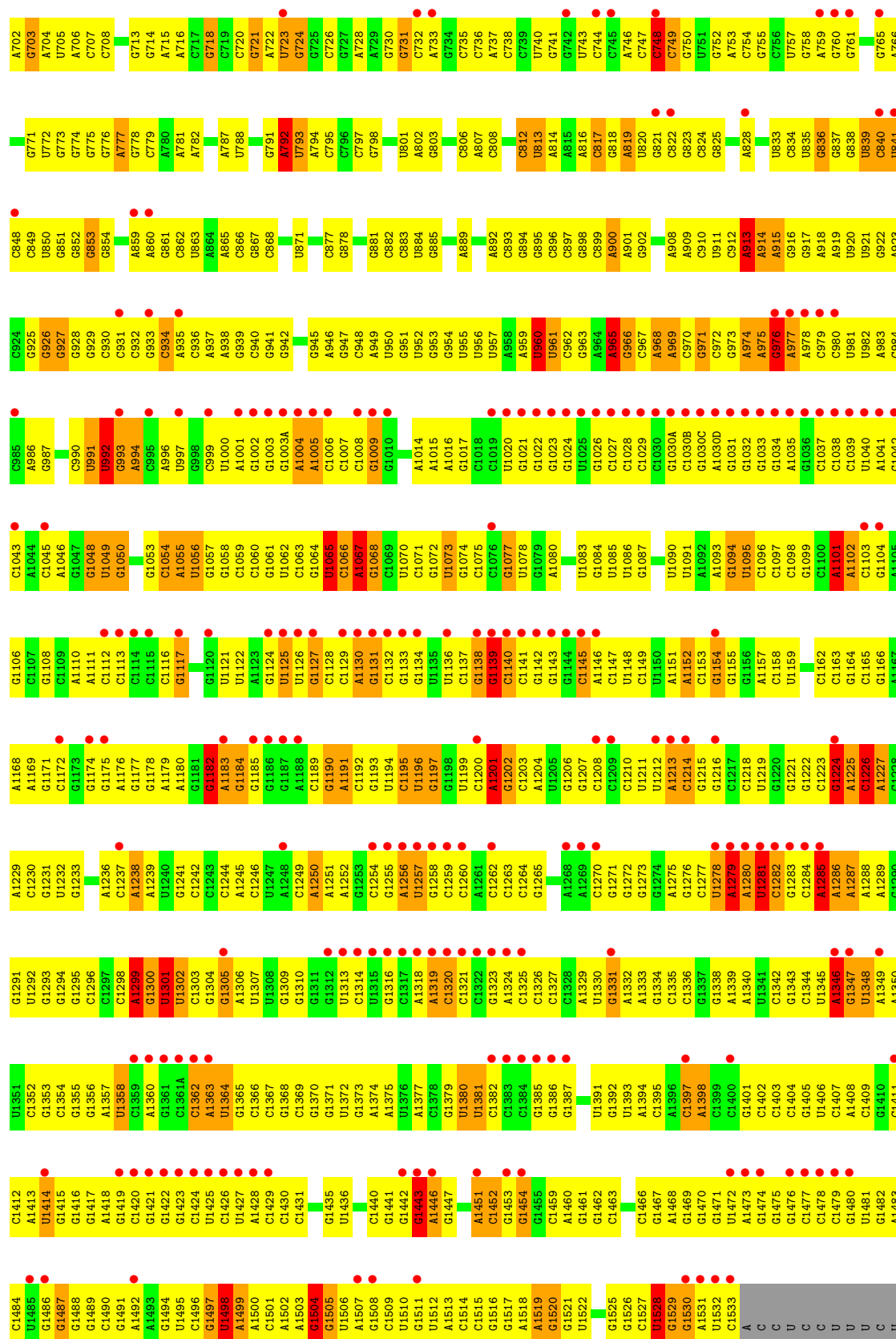
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	D	1	Total 1	Zn 1	0	0
25	N	1	Total 1	Zn 1	0	0

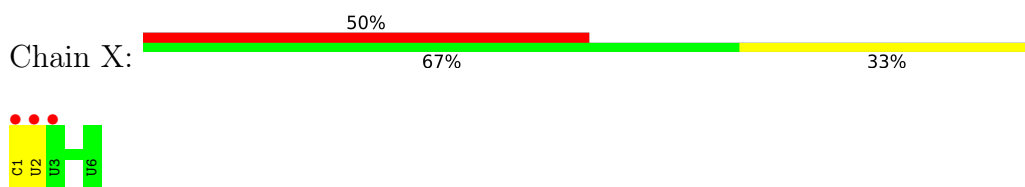
3 Residue-property plots

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

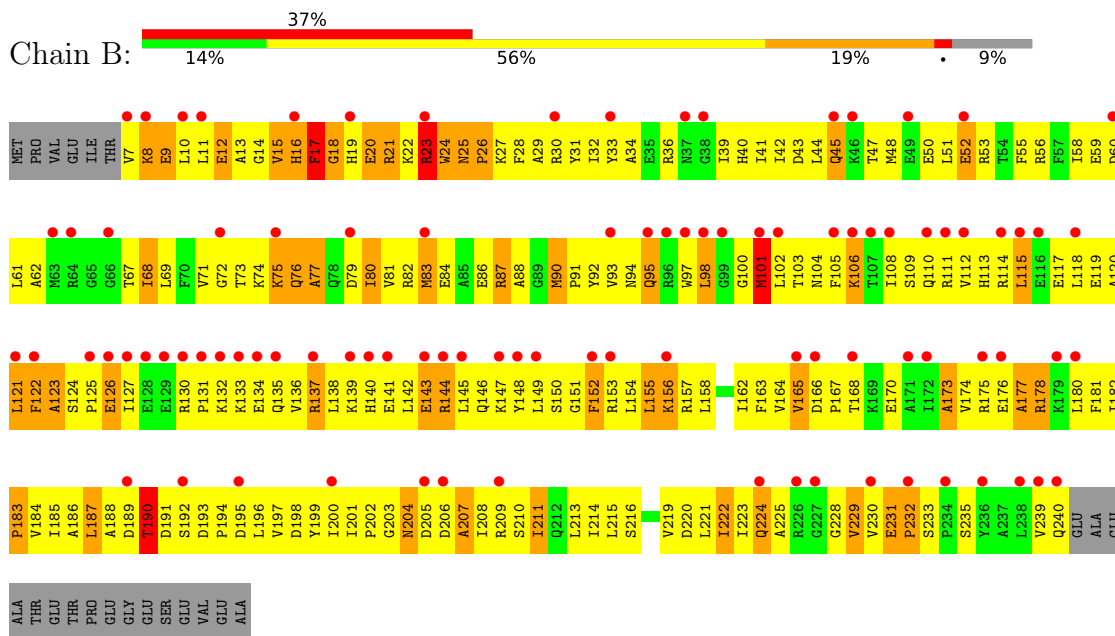
- Molecule 1: 16S RIBOSOMAL RNA



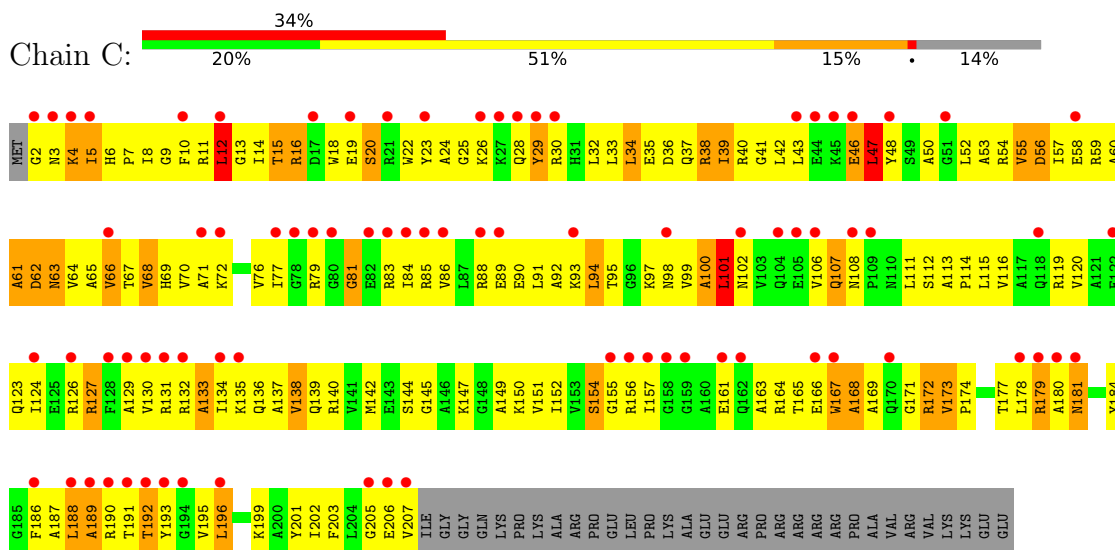




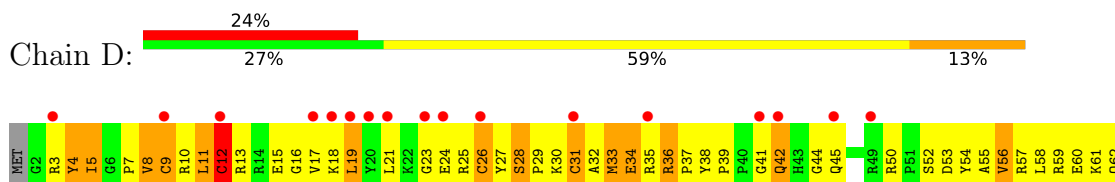
- Molecule 3: 30S RIBOSOMAL PROTEIN S2

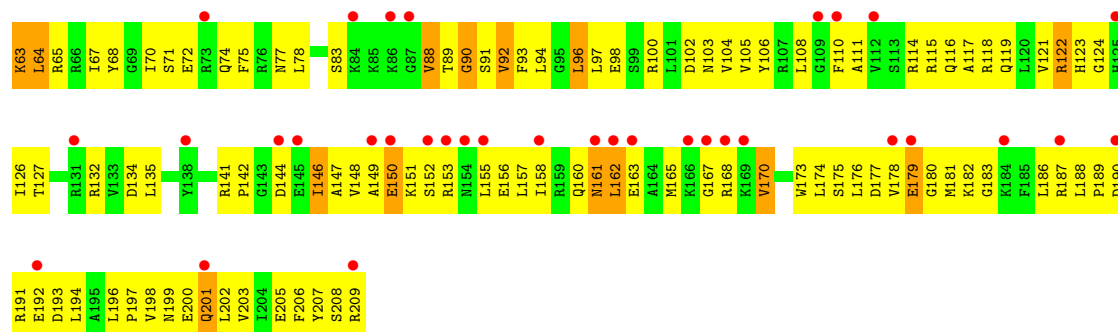


- Molecule 4: 30S RIBOSOMAL PROTEIN S3

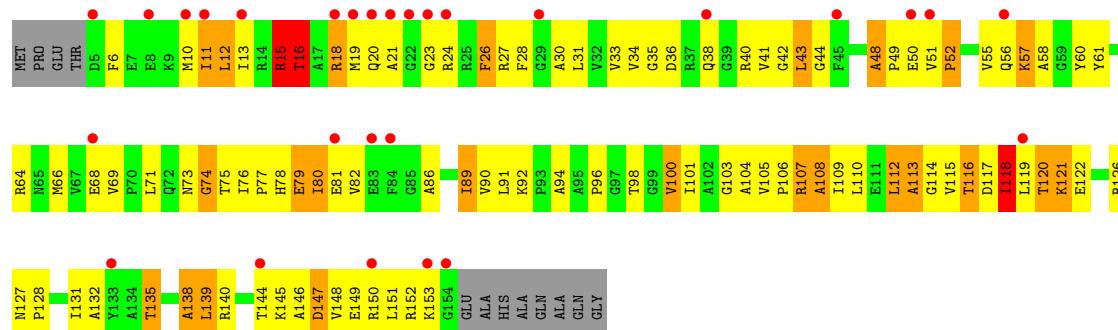


- Molecule 5: 30S RIBOSOMAL PROTEIN S4

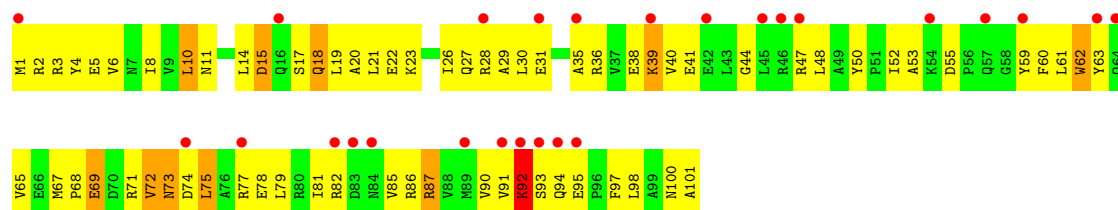




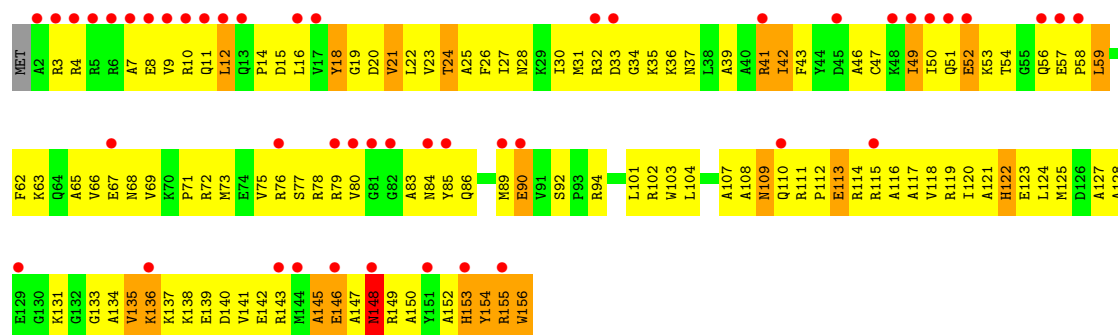
• Molecule 6: 30S RIBOSOMAL PROTEIN S5



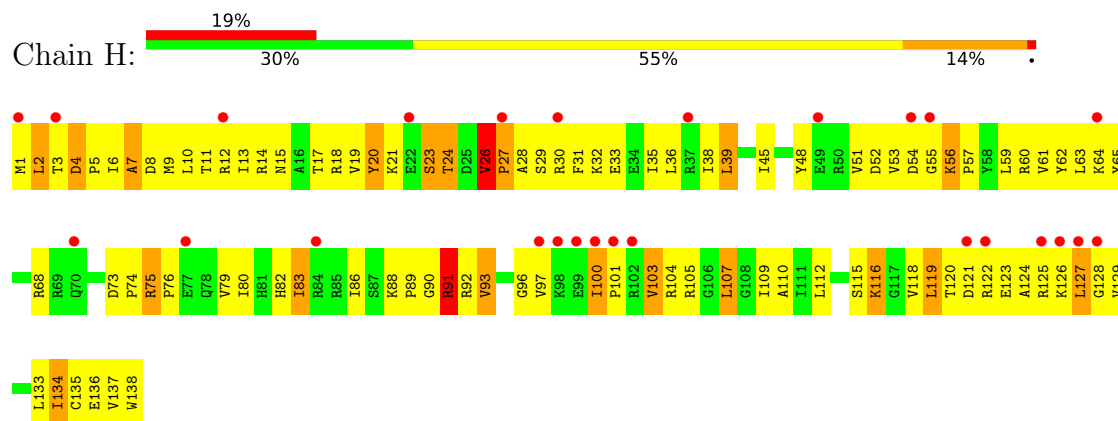
• Molecule 7: 30S RIBOSOMAL PROTEIN S6



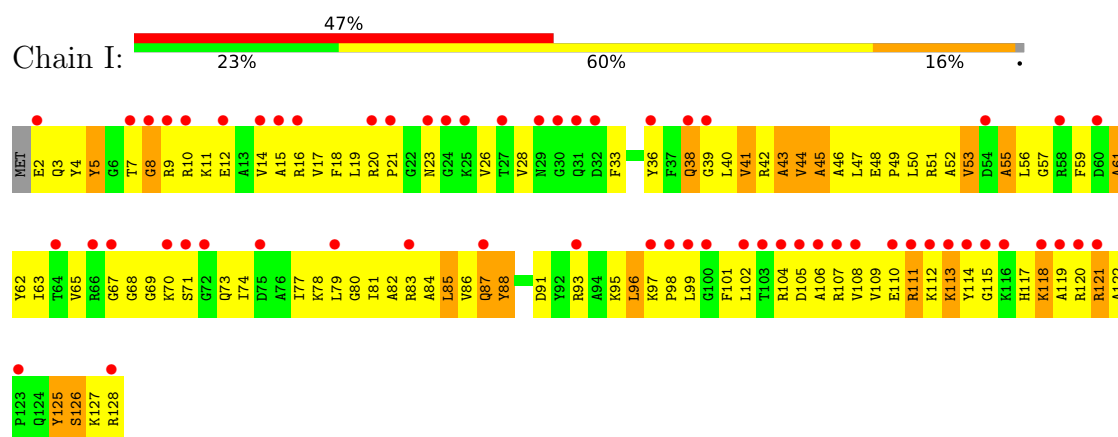
• Molecule 8: 30S RIBOSOMAL PROTEIN S7



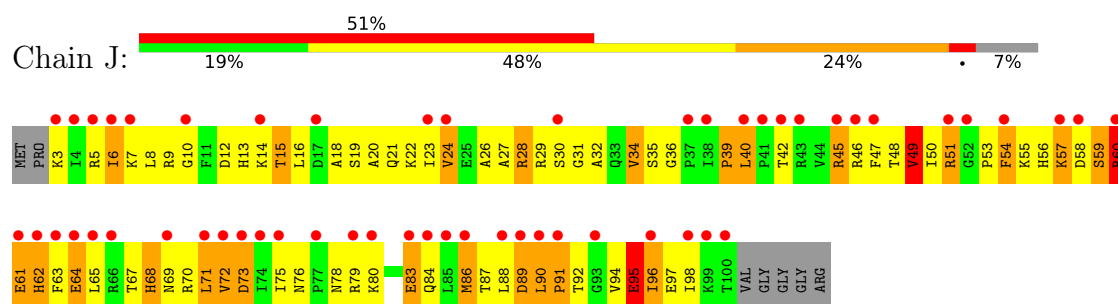
● Molecule 9: 30S RIBOSOMAL PROTEIN S8



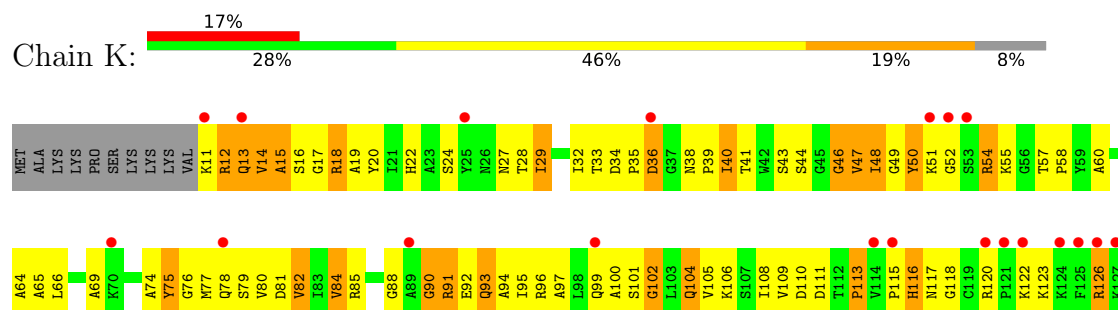
● Molecule 10: 30S RIBOSOMAL PROTEIN S9



● Molecule 11: 30S RIBOSOMAL PROTEIN S10

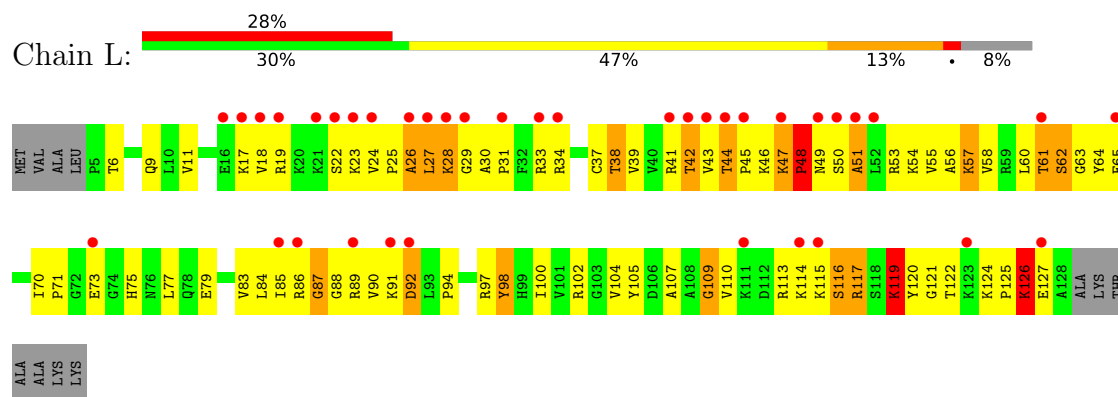


● Molecule 12: 30S RIBOSOMAL PROTEIN S11

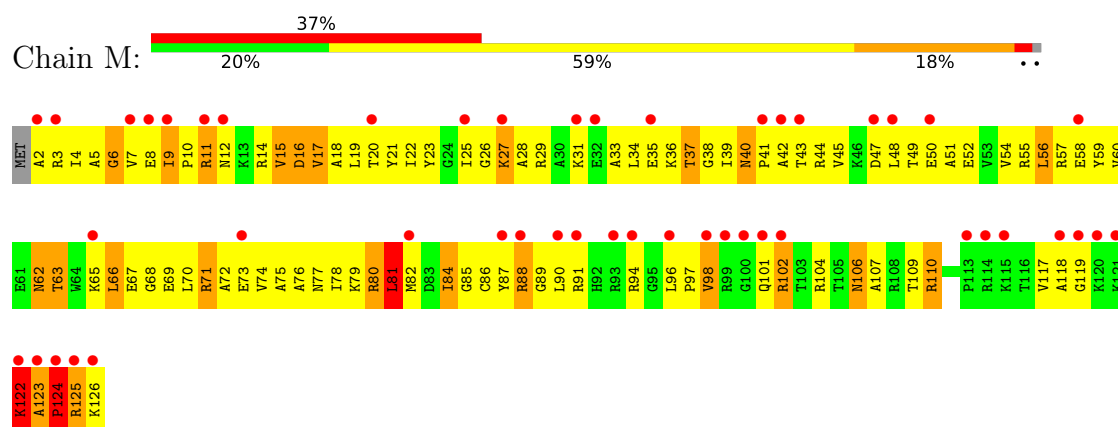




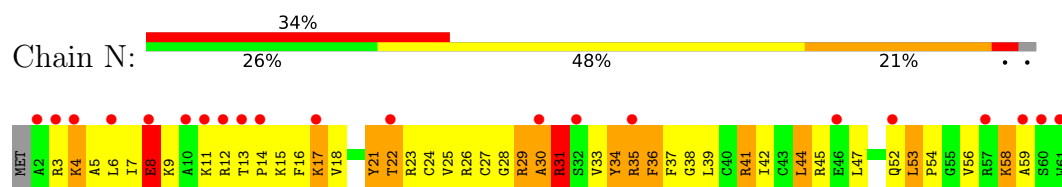
• Molecule 13: 30S RIBOSOMAL PROTEIN S12



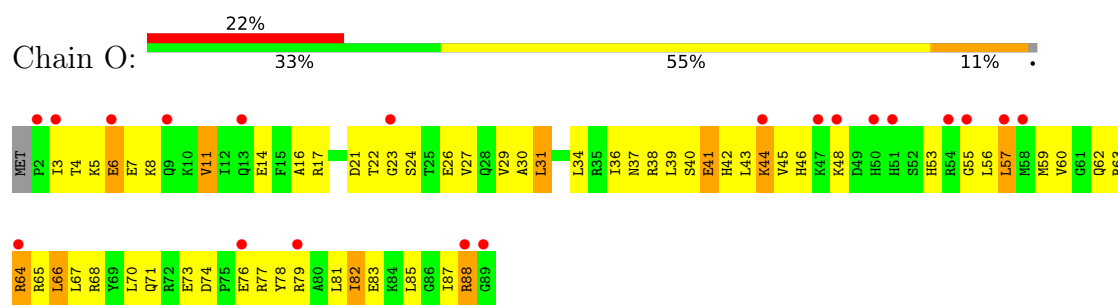
• Molecule 14: 30S RIBOSOMAL PROTEIN S13



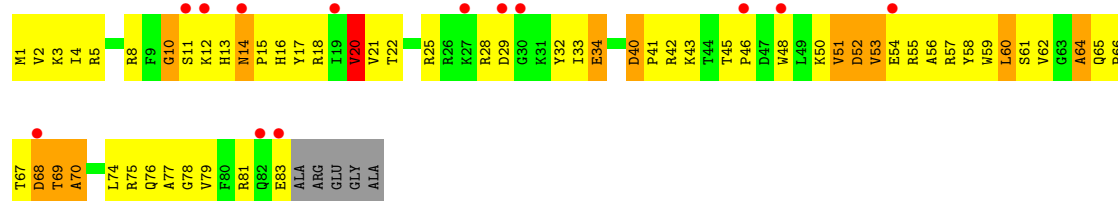
• Molecule 15: 30S RIBOSOMAL PROTEIN S14



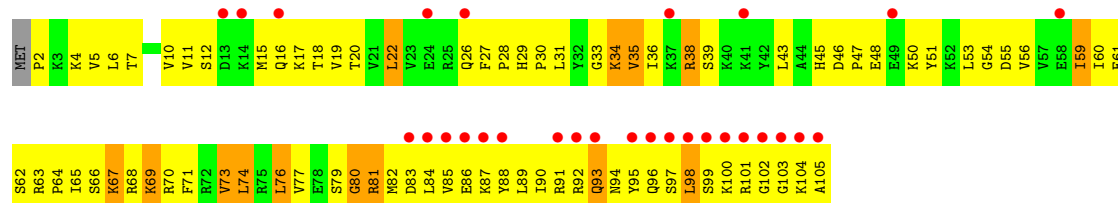
• Molecule 16: 30S RIBOSOMAL PROTEIN S15



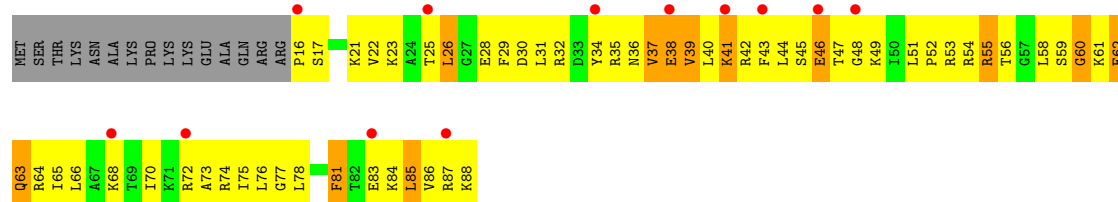
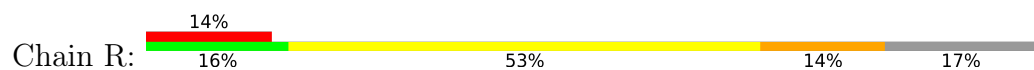
• Molecule 17: 30S RIBOSOMAL PROTEIN S16



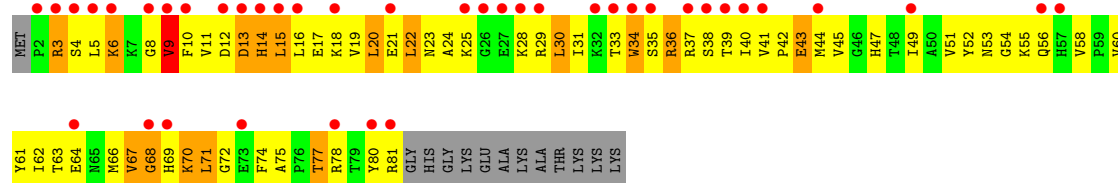
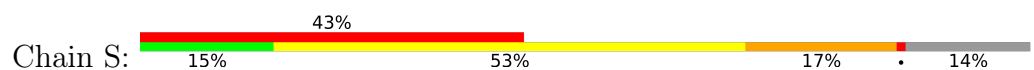
• Molecule 18: 30S RIBOSOMAL PROTEIN S17



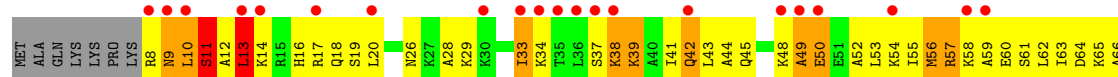
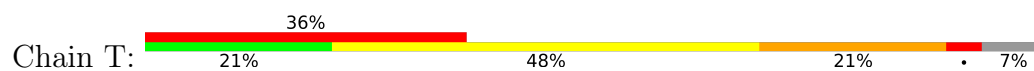
• Molecule 19: 30S RIBOSOMAL PROTEIN S18

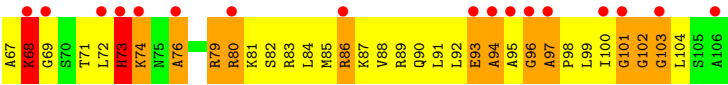


• Molecule 20: 30S RIBOSOMAL PROTEIN S19

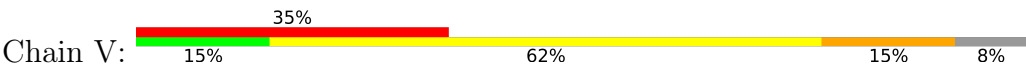


• Molecule 21: 30S RIBOSOMAL PROTEIN S20





● Molecule 22: 30S RIBOSOMAL PROTEIN THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	401.16Å 401.16Å 176.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	316.23 – 3.31 283.66 – 3.31	Depositor EDS
% Data completeness (in resolution range)	91.3 (316.23-3.31) 91.2 (283.66-3.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.52 (at 3.33Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.229 , 0.282 0.207 , 0.254	Depositor DCC
R_{free} test set	9722 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	76.7	Xtriage
Anisotropy	0.276	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 999.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	51872	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.56% 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: PAR, MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.45	0/36234	0.72	72/56554 (0.1%)
2	X	0.43	0/128	0.66	0/196
3	B	0.44	0/1935	1.03	9/2609 (0.3%)
4	C	0.46	0/1636	1.00	6/2205 (0.3%)
5	D	0.52	0/1733	0.99	6/2318 (0.3%)
6	E	0.63	0/1162	1.17	10/1564 (0.6%)
7	F	0.40	0/856	0.92	3/1154 (0.3%)
8	G	0.47	0/1276	1.07	6/1709 (0.4%)
9	H	0.60	0/1136	1.26	19/1527 (1.2%)
10	I	0.43	0/1029	1.01	7/1378 (0.5%)
11	J	0.44	0/805	1.07	3/1082 (0.3%)
12	K	0.57	0/900	1.10	8/1213 (0.7%)
13	L	0.58	0/986	1.25	8/1320 (0.6%)
14	M	0.45	0/1008	1.00	6/1347 (0.4%)
15	N	0.47	0/501	1.14	8/664 (1.2%)
16	O	0.55	0/745	0.96	1/992 (0.1%)
17	P	0.58	0/716	1.24	11/963 (1.1%)
18	Q	0.56	0/870	1.15	5/1159 (0.4%)
19	R	0.46	0/603	0.99	3/799 (0.4%)
20	S	0.38	0/659	1.07	5/886 (0.6%)
21	T	0.59	0/765	1.15	5/1007 (0.5%)
22	V	0.49	0/212	0.93	0/277
All	All	0.47	0/55895	0.85	201/82923 (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	2	36

There are no bond length outliers.

All (201) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	T	13	LEU	N-CA-C	-16.39	93.23	113.38
13	L	26	ALA	N-CA-C	-15.42	95.66	112.93
1	A	1380	U	C2'-C3'-O3'	14.22	130.83	109.50
1	A	181	G	C2'-C3'-O3'	12.99	128.99	109.50
1	A	484	G	C2'-C3'-O3'	12.84	128.76	109.50
1	A	1498	U	C2'-C3'-O3'	12.20	127.80	109.50
1	A	1528	U	C2'-C3'-O3'	12.13	127.69	109.50
16	O	44	LYS	N-CA-C	-12.03	97.88	111.71
1	A	575	G	C2'-C3'-O3'	11.96	127.45	109.50
1	A	1504	G	C2'-C3'-O3'	11.94	127.41	109.50
1	A	559	A	C2'-C3'-O3'	11.88	127.33	109.50
1	A	792	A	C2'-C3'-O3'	11.59	126.88	109.50
1	A	115	G	C2'-C3'-O3'	10.74	125.61	109.50
12	K	52	GLY	N-CA-C	10.54	119.80	110.21
1	A	366	C	C2'-C3'-O3'	10.33	125.00	109.50
8	G	148	ASN	N-CA-C	-10.28	101.00	112.72
1	A	60	A	C2'-C3'-O3'	10.27	124.91	109.50
1	A	965	A	C2'-C3'-O3'	9.86	124.29	109.50
5	D	201	GLN	OE1-CD-NE2	-9.82	112.78	122.60
1	A	243	A	C2'-C3'-O3'	9.51	123.77	109.50
9	H	75	ARG	CA-C-N	9.33	129.37	119.76
9	H	75	ARG	C-N-CA	9.33	129.37	119.76
1	A	372	C	C2'-C3'-O3'	9.10	123.15	109.50
1	A	1067	A	C2'-C3'-O3'	8.99	122.99	109.50
1	A	181	G	C4'-C3'-O3'	8.90	122.75	109.40
5	D	33	MET	N-CA-C	-8.87	102.64	113.19
19	R	81	PHE	N-CA-C	-8.79	102.68	113.41
5	D	11	LEU	N-CA-C	-8.79	100.99	112.68
1	A	687	A	C2'-C3'-O3'	8.76	122.64	109.50
4	C	192	THR	N-CA-C	-8.54	102.00	114.39
1	A	1335	C	C4'-C3'-O3'	-8.54	100.19	113.00
6	E	114	GLY	N-CA-C	-8.52	103.45	115.30
1	A	533	A	C2'-C3'-O3'	8.50	122.26	109.50
21	T	76	ALA	N-CA-C	-8.36	102.12	111.07
1	A	1301	U	C2'-C3'-O3'	8.32	121.98	109.50
11	J	60	ARG	N-CA-C	8.11	128.07	110.80
6	E	23	GLY	N-CA-C	8.05	121.51	110.56
1	A	484	G	C4'-C3'-O3'	8.04	121.46	109.40
1	A	1380	U	C4'-C3'-O3'	8.01	121.41	109.40
10	I	61	ALA	N-CA-C	7.94	121.31	108.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	H	56	LYS	CA-C-N	7.93	128.39	119.83
9	H	56	LYS	C-N-CA	7.93	128.39	119.83
1	A	1299	A	N9-C1'-C2'	7.83	123.74	112.00
1	A	1224	G	C2'-C3'-O3'	7.78	121.18	109.50
1	A	1504	G	C4'-C3'-O3'	7.76	121.04	109.40
4	C	93	LYS	N-CA-C	-7.75	102.46	112.23
17	P	40	ASP	CA-C-N	7.74	127.29	119.24
17	P	40	ASP	C-N-CA	7.74	127.29	119.24
1	A	7	G	C2'-C3'-O3'	7.73	121.10	109.50
3	B	13	ALA	N-CA-C	-7.67	103.02	112.38
8	G	49	ILE	N-CA-C	-7.64	104.48	113.42
3	B	23	ARG	N-CA-C	-7.60	104.03	113.38
1	A	1528	U	C4'-C3'-O3'	7.57	120.75	109.40
15	N	21	TYR	N-CA-C	7.54	123.49	109.24
15	N	8	GLU	N-CA-C	-7.47	104.17	113.28
17	P	65	GLN	CA-C-N	7.46	127.50	119.89
17	P	65	GLN	C-N-CA	7.46	127.50	119.89
6	E	15	ARG	N-CA-C	7.45	122.77	112.04
1	A	560	U	C2'-C3'-O3'	7.43	120.64	109.50
1	A	250	A	C2'-C3'-O3'	7.41	120.61	109.50
17	P	70	ALA	N-CA-C	-7.40	103.21	111.28
4	C	145	GLY	N-CA-C	7.39	125.52	115.32
14	M	11	ARG	N-CA-C	7.31	120.32	108.76
1	A	1201	A	C2'-C3'-O3'	7.31	120.47	109.50
1	A	960	U	C2'-C3'-O3'	7.22	120.32	109.50
1	A	1101	A	C2'-C3'-O3'	7.18	120.27	109.50
1	A	428	G	C2'-C3'-O3'	7.08	120.12	109.50
1	A	509	A	C2'-C3'-O3'	7.04	124.26	113.70
17	P	14	ASN	CA-C-N	7.04	128.64	119.84
17	P	14	ASN	C-N-CA	7.04	128.64	119.84
5	D	12	CYS	N-CA-C	-7.01	99.87	111.37
12	K	14	VAL	N-CA-C	7.01	118.01	112.12
14	M	15	VAL	N-CA-C	6.97	117.68	110.36
11	J	62	HIS	N-CA-C	6.91	121.08	109.76
4	C	25	GLY	N-CA-C	6.89	120.57	110.38
9	H	100	ILE	CA-C-N	6.81	126.84	119.89
9	H	100	ILE	C-N-CA	6.81	126.84	119.89
13	L	44	THR	CA-C-N	6.75	128.27	119.84
13	L	44	THR	C-N-CA	6.75	128.27	119.84
8	G	24	THR	N-CA-C	-6.70	102.60	111.24
1	A	748	C	C2'-C3'-O3'	6.69	119.53	109.50
13	L	119	LYS	N-CA-C	-6.68	99.64	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	S	4	SER	N-CA-C	6.67	119.09	107.49
12	K	75	TYR	N-CA-C	-6.66	105.55	113.21
9	H	26	VAL	CA-C-N	6.63	128.12	119.84
9	H	26	VAL	C-N-CA	6.63	128.12	119.84
5	D	201	GLN	CG-CD-NE2	6.62	126.33	116.40
9	H	4	ASP	CA-C-N	6.60	128.09	119.84
9	H	4	ASP	C-N-CA	6.60	128.09	119.84
10	I	96	LEU	N-CA-C	6.55	118.42	111.28
13	L	61	THR	N-CA-C	-6.55	104.22	111.36
17	P	64	ALA	N-CA-C	-6.55	101.45	110.35
1	A	266	G	C2'-C3'-O3'	6.51	123.47	113.70
20	S	22	LEU	N-CA-C	-6.48	105.33	113.18
1	A	421	U	C4'-C3'-O3'	6.47	119.11	109.40
15	N	38	GLY	N-CA-C	-6.46	106.40	115.32
15	N	4	LYS	N-CA-C	-6.43	103.55	111.33
15	N	31	ARG	N-CA-C	6.35	119.18	111.82
1	A	1182	G	C2'-C3'-O3'	6.34	119.00	109.50
1	A	976	G	C5'-C4'-O4'	6.32	118.58	109.10
1	A	119	A	C2'-C3'-O3'	6.29	118.94	109.50
18	Q	91	ARG	N-CA-C	-6.26	104.45	111.28
5	D	45	GLN	N-CA-C	6.24	120.15	112.54
13	L	92	ASP	N-CA-C	6.23	120.14	112.54
10	I	5	TYR	N-CA-C	6.21	118.61	109.24
7	F	77	ARG	N-CA-C	-6.21	104.21	110.97
10	I	115	GLY	N-CA-C	-6.20	107.12	115.36
8	G	145	ALA	N-CA-C	-6.18	100.14	109.60
9	H	115	SER	N-CA-C	-6.11	105.68	113.01
12	K	46	GLY	N-CA-C	-6.08	106.80	114.16
20	S	70	LYS	N-CA-C	6.04	118.46	108.49
13	L	117	ARG	N-CA-C	6.02	117.85	111.28
13	L	57	LYS	N-CA-C	-6.00	102.60	110.53
1	A	1065	U	C2'-C3'-O3'	5.98	118.46	109.50
20	S	36	ARG	N-CA-C	-5.97	105.08	112.90
20	S	54	GLY	N-CA-C	-5.96	99.05	113.18
1	A	413	G	C4'-C3'-O3'	-5.95	104.07	113.00
1	A	1335	C	N1-C1'-C2'	5.93	120.90	112.00
19	R	46	GLU	N-CA-C	-5.85	105.24	113.20
17	P	20	VAL	N-CA-C	5.83	118.25	108.81
1	A	1281	U	C2'-C3'-O3'	5.83	118.24	109.50
1	A	722	A	N9-C1'-C2'	5.81	120.72	112.00
3	B	137	ARG	N-CA-C	-5.79	104.96	111.28
1	A	1279	A	C2'-C3'-O3'	-5.76	105.06	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	G	154	TYR	N-CA-C	-5.75	106.60	113.21
9	H	137	VAL	CB-CA-C	-5.74	103.19	111.34
4	C	38	ARG	N-CA-C	-5.73	104.95	111.14
12	K	36	ASP	N-CA-C	-5.71	106.66	113.97
12	K	51	LYS	N-CA-C	5.71	120.25	112.04
1	A	452	A	N9-C1'-C2'	5.70	120.55	112.00
6	E	48	ALA	CA-C-N	5.70	126.97	119.84
6	E	48	ALA	C-N-CA	5.70	126.97	119.84
9	H	116	LYS	N-CA-C	-5.70	105.91	112.92
6	E	118	ILE	CB-CA-C	-5.67	103.41	111.40
9	H	93	VAL	N-CA-C	5.62	115.66	106.72
1	A	344	A	C2'-C3'-O3'	5.61	117.91	109.50
1	A	1346	A	C2'-C3'-O3'	5.58	117.87	109.50
10	I	125	TYR	N-CA-C	5.56	117.64	109.24
7	F	92	LYS	N-CA-C	-5.55	101.49	110.32
10	I	101	PHE	N-CA-C	-5.55	106.35	113.23
14	M	62	ASN	N-CA-C	-5.53	99.89	108.90
1	A	243	A	N9-C1'-C2'	5.52	122.28	114.00
12	K	82	VAL	N-CA-C	5.52	116.17	108.89
1	A	279	A	C4'-C3'-O3'	5.51	117.66	109.40
9	H	20	TYR	N-CA-C	5.51	119.30	112.58
18	Q	65	ILE	N-CA-C	-5.50	107.46	112.96
1	A	244	U	C5'-C4'-C3'	-5.50	106.96	115.20
11	J	49	VAL	N-CA-C	5.49	116.03	108.12
9	H	103	VAL	N-CA-C	5.48	116.77	109.37
7	F	18	GLN	N-CA-C	-5.48	105.23	111.14
8	G	50	ILE	N-CA-C	-5.44	104.29	111.09
1	A	572	A	N9-C1'-C2'	5.44	120.16	112.00
1	A	1285	A	C2'-C3'-O3'	5.42	117.64	109.50
1	A	976	G	C5'-C4'-C3'	5.42	123.33	115.20
14	M	40	ASN	CA-C-N	5.42	124.88	119.24
14	M	40	ASN	C-N-CA	5.42	124.88	119.24
17	P	60	LEU	N-CA-C	-5.40	105.50	111.71
1	A	1139	G	C2'-C3'-O3'	5.39	117.58	109.50
15	N	34	TYR	N-CA-C	5.39	119.56	111.81
1	A	328	C	C2'-C3'-O3'	5.34	117.51	109.50
1	A	389	A	C5'-C4'-C3'	5.34	124.01	116.00
12	K	116	HIS	N-CA-C	-5.33	105.95	113.20
9	H	7	ALA	N-CA-C	-5.33	105.12	111.03
19	R	85	LEU	N-CA-C	5.33	117.66	107.75
14	M	37	THR	N-CA-C	-5.32	101.64	109.62
1	A	913	A	C2'-C3'-O3'	5.31	117.46	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	992	U	C2'-C3'-O3'	5.30	117.45	109.50
18	Q	67	LYS	N-CA-C	-5.29	102.56	110.23
1	A	836	G	C5'-C4'-C3'	5.29	123.93	116.00
9	H	54	ASP	N-CA-C	-5.25	107.23	113.38
21	T	44	ALA	N-CA-C	-5.25	105.02	111.75
3	B	101	MET	N-CA-C	-5.24	104.62	111.02
6	E	69	VAL	CA-C-N	5.22	126.37	119.84
6	E	69	VAL	C-N-CA	5.22	126.37	119.84
1	A	389	A	C2'-C3'-O3'	-5.22	105.87	113.70
1	A	1213	A	N9-C1'-C2'	5.22	119.83	112.00
21	T	68	LYS	N-CA-C	-5.21	104.85	111.11
18	Q	39	SER	N-CA-C	5.21	116.21	108.60
6	E	57	LYS	N-CA-C	-5.20	105.73	111.71
1	A	1195	C	N1-C1'-C2'	5.16	119.74	112.00
3	B	173	ALA	N-CA-C	-5.16	105.35	110.97
1	A	413	G	N9-C1'-C2'	5.16	119.73	112.00
15	N	53	LEU	CA-C-N	5.15	125.06	119.76
15	N	53	LEU	C-N-CA	5.15	125.06	119.76
21	T	38	LYS	N-CA-C	-5.14	104.75	111.02
10	I	87	GLN	N-CA-C	-5.14	105.37	110.97
1	A	365	U	N1-C1'-C2'	5.13	119.70	112.00
1	A	1528	U	C4'-C3'-C2'	5.12	107.72	102.60
9	H	96	GLY	N-CA-C	-5.10	105.78	112.82
3	B	90	MET	CA-C-N	5.09	126.20	119.84
3	B	90	MET	C-N-CA	5.09	126.20	119.84
3	B	233	SER	CA-C-N	5.09	124.78	119.64
3	B	233	SER	C-N-CA	5.09	124.78	119.64
18	Q	93	GLN	N-CA-C	5.09	116.51	111.07
17	P	69	THR	N-CA-C	-5.09	106.42	113.18
1	A	1443	G	N9-C1'-C2'	5.05	119.58	112.00
6	E	113	ALA	N-CA-C	-5.05	106.95	113.01
1	A	129(A)	G	C2'-C3'-O3'	5.03	117.05	109.50
1	A	1195	C	C4'-C3'-O3'	-5.02	105.47	113.00
1	A	1224	G	N9-C1'-C2'	5.01	121.52	114.00
4	C	47	LEU	N-CA-C	5.00	121.46	110.80

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	181	G	C3'
1	A	1380	U	C3'

All (36) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1056	U	Sidechain
1	A	1073	U	Sidechain
1	A	1077	G	Sidechain
1	A	108	G	Sidechain
1	A	1154	G	Sidechain
1	A	1226	C	Sidechain
1	A	1281	U	Sidechain
1	A	1285	A	Sidechain
1	A	1299	A	Sidechain
1	A	1358	U	Sidechain
1	A	1360	A	Sidechain
1	A	1364	U	Sidechain
1	A	1401	G	Sidechain
1	A	1414	U	Sidechain
1	A	251	G	Sidechain
1	A	263	A	Sidechain
1	A	281	G	Sidechain
1	A	291	C	Sidechain
1	A	481	G	Sidechain
1	A	490	G	Sidechain
1	A	521	G	Sidechain
1	A	54	C	Sidechain
1	A	575	G	Sidechain
1	A	641	U	Sidechain
1	A	691	G	Sidechain
1	A	705	U	Sidechain
1	A	733	A	Sidechain
1	A	740	U	Sidechain
1	A	853	G	Sidechain
1	A	868	C	Sidechain
1	A	871	U	Sidechain
1	A	898	G	Sidechain
1	A	900	A	Sidechain
1	A	915	A	Sidechain
1	A	963	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	32369	0	16339	1341	0
2	X	117	0	64	1	0
3	B	1900	0	1951	293	0
4	C	1612	0	1677	244	0
5	D	1703	0	1764	214	0
6	E	1146	0	1207	140	0
7	F	843	0	857	86	0
8	G	1257	0	1296	151	0
9	H	1116	0	1177	106	0
10	I	1011	0	1043	154	0
11	J	792	0	835	147	0
12	K	885	0	904	92	0
13	L	970	0	1057	123	0
14	M	997	0	1072	150	0
15	N	492	0	529	86	0
16	O	734	0	771	91	0
17	P	700	0	720	77	0
18	Q	857	0	930	103	0
19	R	597	0	668	98	0
20	S	646	0	668	98	0
21	T	763	0	861	121	0
22	V	208	0	221	33	0
23	A	42	0	45	4	0
24	A	111	0	0	0	0
24	D	1	0	0	0	0
24	L	1	0	0	0	0
25	D	1	0	0	0	0
25	N	1	0	0	0	0
All	All	51872	0	36656	3661	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 41.

All (3661) 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:1443:G:H5''	1:A:1446:A:H5'	1.18	1.17
16:O:87:ILE:HG22	16:O:88:ARG:H	1.05	1.09
20:S:40:ILE:HD13	20:S:62:ILE:HD13	1.30	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:188:LEU:HD13	4:C:189:ALA:H	1.11	1.09
1:A:939:G:H5''	8:G:102:ARG:HH22	1.12	1.09
5:D:151:LYS:H	5:D:151:LYS:HD2	1.03	1.09
17:P:11:SER:HB3	17:P:14:ASN:HB3	1.36	1.08
1:A:243:A:H4'	1:A:244:U:H5'	1.37	1.06
1:A:447:G:H2'	1:A:485:G:H22	1.21	1.06
12:K:54:ARG:HB3	12:K:54:ARG:HH11	1.15	1.05
4:C:191:THR:CG2	4:C:192:THR:H	1.71	1.04
13:L:41:ARG:HG2	13:L:42:THR:H	1.19	1.04
4:C:191:THR:HG22	4:C:192:THR:N	1.69	1.03
3:B:101:MET:HA	3:B:108:ILE:HD12	1.42	1.01
11:J:94:VAL:HG12	11:J:95:GLU:H	1.22	1.01
6:E:41:VAL:CG2	6:E:113:ALA:HA	1.90	1.01
4:C:191:THR:HG22	4:C:192:THR:H	0.86	1.00
5:D:36:ARG:H	5:D:37:PRO:HD3	1.23	0.99
1:A:1286:A:H2'	1:A:1287:A:H5''	1.43	0.99
22:V:6:ARG:HD3	22:V:15:ARG:HH12	1.23	0.98
3:B:102:LEU:HD21	3:B:162:ILE:HD11	1.46	0.98
4:C:14:ILE:HG22	4:C:15:THR:H	1.25	0.98
11:J:51:ARG:HB2	11:J:59:SER:HB3	1.43	0.98
1:A:1250:A:H4'	10:I:68:GLY:H	1.29	0.97
3:B:77:ALA:HB2	3:B:211:ILE:HD13	1.45	0.97
1:A:760:G:H1	18:Q:105:ALA:HA	1.28	0.96
1:A:1286:A:C2'	1:A:1287:A:H5''	1.96	0.96
7:F:100:ASN:HD22	19:R:23:LYS:HG2	1.30	0.96
16:O:87:ILE:HG22	16:O:88:ARG:N	1.80	0.96
5:D:16:GLY:O	5:D:33:MET:HE2	1.66	0.96
3:B:178:ARG:HH11	3:B:178:ARG:HG3	1.30	0.95
11:J:15:THR:HG22	11:J:16:LEU:HD23	1.48	0.95
3:B:18:GLY:HA2	3:B:41:ILE:HA	1.49	0.94
20:S:33:THR:HG22	20:S:35:SER:H	1.31	0.94
8:G:54:THR:HG22	8:G:56:GLN:H	1.31	0.94
1:A:686:U:HO2'	1:A:687:A:H8	0.95	0.93
1:A:1195:C:H3'	1:A:1196:U:H5''	1.51	0.93
11:J:94:VAL:HG12	11:J:95:GLU:N	1.84	0.93
1:A:1116:C:H2'	1:A:1117:G:H5''	1.47	0.93
1:A:447:G:H2'	1:A:485:G:N2	1.82	0.92
1:A:975:A:H4'	1:A:976:G:OP2	1.67	0.92
1:A:1124:G:H5'	11:J:35:SER:O	1.69	0.92
10:I:19:LEU:HD23	10:I:61:ALA:HB2	1.50	0.92
13:L:46:LYS:HG2	13:L:47:LYS:H	1.35	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:22:LEU:HD13	20:S:28:LYS:HB3	1.47	0.92
1:A:1231:G:H4'	10:I:126:SER:HB3	1.51	0.92
19:R:36:ASN:ND2	19:R:38:GLU:HG2	1.85	0.92
5:D:25:ARG:C	5:D:27:TYR:H	1.74	0.92
12:K:54:ARG:HB3	12:K:54:ARG:NH1	1.85	0.92
5:D:187:ARG:HE	5:D:188:LEU:N	1.68	0.92
15:N:27:CYS:SG	15:N:29:ARG:HB2	2.10	0.92
4:C:50:ALA:HB1	4:C:70:VAL:HG11	1.52	0.91
17:P:20:VAL:HG21	17:P:32:TYR:HB2	1.52	0.91
4:C:190:ARG:HB3	4:C:190:ARG:NH1	1.85	0.91
3:B:114:ARG:HH11	3:B:118:LEU:HD21	1.35	0.91
18:Q:97:SER:HB2	18:Q:103:GLY:HA2	1.52	0.91
4:C:190:ARG:HB3	4:C:190:ARG:HH11	1.33	0.91
13:L:28:LYS:HD2	13:L:33:ARG:HH12	1.35	0.91
1:A:1391:U:H2'	1:A:1392:G:C8	2.05	0.90
3:B:23:ARG:NH1	3:B:191:ASP:HA	1.85	0.90
13:L:60:LEU:HD11	13:L:85:ILE:HD12	1.51	0.90
18:Q:53:LEU:HD22	18:Q:82:MET:HE1	1.51	0.90
1:A:954:G:H21	1:A:1227:A:H62	1.19	0.90
6:E:51:VAL:HB	6:E:52:PRO:HD3	1.53	0.90
19:R:47:THR:HA	19:R:83:GLU:HB2	1.54	0.90
1:A:1316:G:H4'	15:N:18:VAL:HG11	1.51	0.90
17:P:8:ARG:HB2	17:P:28:ARG:NH1	1.85	0.90
3:B:21:ARG:HA	3:B:39:ILE:HG12	1.53	0.89
16:O:87:ILE:CG2	16:O:88:ARG:H	1.85	0.89
1:A:1053:G:H4'	1:A:1054:C:H5'	1.55	0.89
1:A:1366:C:H2'	1:A:1367:C:H6	1.37	0.89
1:A:1053:G:C4'	1:A:1054:C:H5'	2.03	0.89
5:D:187:ARG:NE	5:D:188:LEU:H	1.71	0.89
5:D:7:PRO:HG2	5:D:10:ARG:HD2	1.53	0.88
1:A:64:G:H4'	1:A:65:U:O5'	1.73	0.88
1:A:1003(A):G:H2'	1:A:1004:A:H4'	1.56	0.88
6:E:110:LEU:HD13	6:E:118:ILE:HD12	1.55	0.88
11:J:90:LEU:H	11:J:91:PRO:HD2	1.35	0.88
5:D:151:LYS:HD2	5:D:151:LYS:N	1.87	0.87
1:A:1286:A:C3'	1:A:1287:A:H5''	2.03	0.87
13:L:33:ARG:HD3	13:L:62:SER:HB3	1.54	0.87
1:A:1480:G:H2'	1:A:1481:U:C6	2.09	0.87
4:C:107:GLN:NE2	4:C:107:GLN:H	1.71	0.87
1:A:371:G:O2'	1:A:372:C:H5'	1.75	0.87
6:E:81:GLU:HG3	6:E:90:VAL:HG22	1.55	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:117:VAL:HG12	14:M:118:ALA:H	1.38	0.87
1:A:1348:U:H2'	1:A:1349:A:H8	1.37	0.86
1:A:967:C:H4'	10:I:128:ARG:HG3	1.55	0.86
1:A:1003(A):G:H2'	1:A:1004:A:C4'	2.04	0.86
3:B:16:HIS:NE2	3:B:214:ILE:HG12	1.91	0.86
1:A:1347:G:N2	1:A:1373:G:H2'	1.90	0.86
5:D:175:SER:HB3	5:D:186:LEU:HD11	1.58	0.86
1:A:35:G:H2'	1:A:36:C:C6	2.11	0.86
11:J:6:ILE:HD11	11:J:73:ASP:H	1.40	0.86
3:B:59:GLU:HB2	3:B:221:LEU:HD11	1.58	0.86
4:C:14:ILE:HG22	4:C:15:THR:N	1.91	0.86
4:C:174:PRO:HB2	4:C:177:THR:HG22	1.57	0.86
12:K:57:THR:HG23	12:K:60:ALA:H	1.41	0.85
1:A:351:G:H4'	1:A:352:C:OP1	1.75	0.85
1:A:1285:A:H4'	1:A:1286:A:O5'	1.76	0.85
4:C:107:GLN:H	4:C:107:GLN:CD	1.82	0.85
3:B:25:ASN:HD22	3:B:25:ASN:C	1.83	0.85
17:P:22:THR:HA	17:P:33:ILE:HD12	1.57	0.85
3:B:122:PHE:HA	3:B:127:ILE:HG12	1.55	0.85
3:B:223:ILE:C	3:B:225:ALA:H	1.84	0.85
11:J:62:HIS:HB3	15:N:59:ALA:HB3	1.58	0.85
14:M:22:ILE:HD12	14:M:25:ILE:HD12	1.59	0.85
4:C:195:VAL:C	4:C:196:LEU:HD23	2.01	0.85
13:L:124:LYS:HD3	13:L:125:PRO:HD2	1.59	0.85
3:B:84:GLU:OE1	3:B:216:SER:HA	1.76	0.84
1:A:1278:U:H4'	1:A:1279:A:H5'	1.59	0.84
11:J:6:ILE:HG22	11:J:98:ILE:HG12	1.56	0.84
1:A:250:A:H4'	1:A:251:G:O5'	1.78	0.84
12:K:44:SER:H	12:K:47:VAL:HB	1.41	0.84
15:N:3:ARG:O	15:N:7:ILE:HG13	1.75	0.84
4:C:172:ARG:HB3	4:C:172:ARG:HH11	1.41	0.84
6:E:116:THR:HG23	6:E:117:ASP:OD2	1.77	0.84
1:A:1319:A:H5'	1:A:1320:C:OP1	1.78	0.83
5:D:26:CYS:HA	5:D:31:CYS:HB2	1.60	0.83
1:A:686:U:O2'	1:A:687:A:H8	1.61	0.83
13:L:75:HIS:HD2	13:L:77:LEU:H	1.26	0.83
18:Q:67:LYS:HA	18:Q:70:ARG:HH12	1.43	0.83
5:D:187:ARG:HE	5:D:188:LEU:H	0.87	0.83
21:T:13:LEU:H	21:T:13:LEU:HD12	1.42	0.83
1:A:948:C:OP1	14:M:109:THR:HG22	1.77	0.83
1:A:1250:A:C4'	10:I:68:GLY:H	1.91	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:41:ARG:HG2	13:L:42:THR:N	1.94	0.83
1:A:1060:C:O2'	1:A:1061:G:H5'	1.79	0.83
3:B:28:PHE:CZ	3:B:189:ASP:HA	2.12	0.83
11:J:51:ARG:NE	11:J:61:GLU:HB2	1.94	0.83
15:N:17:LYS:NZ	15:N:17:LYS:HB2	1.92	0.83
16:O:39:LEU:HD22	16:O:56:LEU:HD13	1.59	0.83
16:O:70:LEU:HD12	16:O:78:TYR:HB2	1.61	0.83
17:P:20:VAL:HG21	17:P:32:TYR:CB	2.08	0.83
1:A:243:A:C4'	1:A:244:U:H5'	2.08	0.82
6:E:11:ILE:HG22	6:E:12:LEU:HD12	1.58	0.82
9:H:121:ASP:HB2	9:H:125:ARG:NH2	1.94	0.82
13:L:47:LYS:HB2	13:L:48:PRO:HD3	1.58	0.82
20:S:55:LYS:HG2	20:S:56:GLN:HE21	1.44	0.82
13:L:41:ARG:CG	13:L:42:THR:H	1.88	0.82
21:T:39:LYS:HD2	21:T:55:ILE:HD13	1.61	0.82
4:C:34:LEU:HG	15:N:25:VAL:HG21	1.61	0.82
5:D:36:ARG:N	5:D:37:PRO:HD3	1.93	0.82
6:E:41:VAL:HG22	6:E:113:ALA:HA	1.61	0.82
6:E:80:ILE:CD1	6:E:91:LEU:HB2	2.09	0.82
11:J:84:GLN:HA	11:J:88:LEU:HD12	1.61	0.82
21:T:57:ARG:HH21	21:T:100:ILE:HG22	1.43	0.82
1:A:677:U:H3	1:A:713:G:H22	1.24	0.82
1:A:1250:A:H5''	10:I:68:GLY:N	1.95	0.82
1:A:977:A:H2'	1:A:978:A:H5''	1.62	0.81
11:J:96:ILE:H	11:J:96:ILE:HD12	1.46	0.81
1:A:235:C:H5'	18:Q:70:ARG:HG2	1.60	0.81
3:B:114:ARG:NH1	3:B:118:LEU:HD21	1.94	0.81
6:E:12:LEU:HD13	6:E:31:LEU:HB2	1.62	0.81
4:C:179:ARG:HD2	4:C:179:ARG:C	2.04	0.81
20:S:9:VAL:HG13	20:S:10:PHE:N	1.94	0.81
23:A:1545:PAR:H34	23:A:1545:PAR:HN61	1.45	0.81
10:I:4:TYR:CE2	10:I:88:TYR:HA	2.16	0.81
10:I:48:GLU:HA	10:I:51:ARG:HD2	1.60	0.81
1:A:1154:G:H2'	1:A:1155:G:H8	1.45	0.81
1:A:1116:C:C2'	1:A:1117:G:H5''	2.11	0.81
5:D:151:LYS:H	5:D:151:LYS:CD	1.88	0.81
12:K:43:SER:HB2	12:K:47:VAL:HG11	1.63	0.80
5:D:32:ALA:C	5:D:34:GLU:H	1.88	0.80
1:A:1137:C:H4'	1:A:1138:G:C2	2.17	0.80
1:A:1250:A:H4'	10:I:68:GLY:N	1.97	0.80
5:D:162:LEU:HD23	5:D:178:VAL:HG13	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:25:PRO:C	13:L:27:LEU:H	1.85	0.80
4:C:108:ASN:ND2	4:C:111:LEU:HG	1.95	0.80
20:S:77:THR:HG22	20:S:78:ARG:HG3	1.63	0.80
16:O:81:LEU:HD21	16:O:85:LEU:HD12	1.62	0.80
4:C:58:GLU:HB3	11:J:92:THR:HG21	1.63	0.80
11:J:6:ILE:HD12	11:J:6:ILE:H	1.47	0.80
11:J:18:ALA:O	11:J:21:GLN:HB3	1.81	0.80
1:A:839:U:H5'	1:A:840:C:C5	2.17	0.79
1:A:1112:C:O2	4:C:179:ARG:HB3	1.82	0.79
1:A:1016:A:H2'	1:A:1017:G:O4'	1.82	0.79
4:C:6:HIS:CD2	4:C:8:ILE:HB	2.17	0.79
4:C:134:ILE:HG23	4:C:151:VAL:HB	1.63	0.79
5:D:64:LEU:HG	5:D:198:VAL:HG21	1.62	0.79
1:A:243:A:H4'	1:A:244:U:C5'	2.12	0.79
1:A:1005:A:H2'	1:A:1006:C:H5'	1.64	0.79
4:C:150:LYS:HE2	4:C:152:ILE:HD11	1.65	0.79
6:E:15:ARG:HD3	6:E:26:PHE:HD2	1.46	0.79
6:E:144:THR:O	6:E:148:VAL:HG23	1.83	0.79
1:A:918:A:H2'	1:A:919:A:C8	2.18	0.79
18:Q:45:HIS:NE2	18:Q:47:PRO:HG3	1.97	0.79
1:A:1133:G:H2'	1:A:1134:G:H8	1.45	0.79
5:D:156:GLU:HG2	5:D:160:GLN:HE21	1.48	0.79
1:A:1226:C:H4'	1:A:1227:A:OP1	1.83	0.79
9:H:90:GLY:O	9:H:91:ARG:HB2	1.81	0.79
14:M:40:ASN:HD22	14:M:41:PRO:CD	1.95	0.79
3:B:36:ARG:HD2	3:B:41:ILE:HD12	1.65	0.78
4:C:188:LEU:HD13	4:C:189:ALA:N	1.95	0.78
6:E:35:GLY:HA3	6:E:112:LEU:HB3	1.65	0.78
8:G:69:VAL:HG21	8:G:104:LEU:HD21	1.65	0.78
1:A:838:G:H2'	1:A:839:U:H5''	1.64	0.78
5:D:114:ARG:HH11	5:D:114:ARG:HG3	1.47	0.78
11:J:94:VAL:CG1	11:J:95:GLU:H	1.96	0.78
16:O:26:GLU:OE1	16:O:77:ARG:HD2	1.83	0.78
1:A:972:C:H4'	11:J:57:LYS:HD2	1.65	0.78
1:A:1305:G:N2	1:A:1331:G:O2'	2.17	0.78
5:D:57:ARG:HH11	5:D:57:ARG:HG3	1.48	0.78
16:O:16:ALA:HB1	16:O:21:ASP:HB3	1.66	0.78
6:E:150:ARG:NH1	6:E:150:ARG:HB3	1.98	0.78
12:K:19:ALA:HB2	12:K:80:VAL:HG11	1.64	0.78
1:A:1236:A:H2'	1:A:1237:C:C6	2.19	0.78
4:C:6:HIS:HD2	4:C:8:ILE:H	1.28	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:103:GLY:O	6:E:106:PRO:HD2	1.84	0.78
1:A:201:C:H42	1:A:216:G:H1	1.32	0.78
1:A:392:G:H2'	1:A:393:A:H8	1.47	0.78
1:A:1139:G:H4'	1:A:1140:C:O5'	1.84	0.78
1:A:1278:U:H4'	1:A:1279:A:C5'	2.13	0.78
5:D:25:ARG:C	5:D:27:TYR:N	2.42	0.78
20:S:43:GLU:H	20:S:43:GLU:CD	1.89	0.78
1:A:532:A:N7	4:C:161:GLU:HB2	2.00	0.77
3:B:124:SER:O	3:B:127:ILE:HG13	1.84	0.77
8:G:133:GLY:HA2	8:G:136:LYS:HE3	1.66	0.77
11:J:20:ALA:O	11:J:24:VAL:HG23	1.84	0.77
21:T:76:ALA:O	21:T:80:ARG:HG2	1.84	0.77
3:B:98:LEU:HB2	3:B:101:MET:HE3	1.67	0.77
10:I:111:ARG:HD2	10:I:113:LYS:HD2	1.66	0.77
11:J:6:ILE:CD1	11:J:73:ASP:H	1.97	0.77
13:L:47:LYS:CB	13:L:48:PRO:HD3	2.13	0.77
1:A:1064:G:H4'	1:A:1065:U:C5'	2.13	0.77
6:E:115:VAL:HG11	6:E:118:ILE:HD11	1.66	0.77
21:T:54:LYS:HE3	21:T:100:ILE:HD13	1.65	0.77
1:A:382:A:H2'	1:A:383:A:C8	2.18	0.77
5:D:7:PRO:CG	5:D:10:ARG:HD2	2.14	0.77
17:P:28:ARG:HG2	17:P:28:ARG:HH11	1.49	0.77
20:S:17:GLU:HA	20:S:20:LEU:HD11	1.66	0.77
9:H:101:PRO:HG3	9:H:133:LEU:HD11	1.67	0.77
10:I:9:ARG:HG2	10:I:14:VAL:HG22	1.65	0.77
1:A:501:C:H2'	1:A:502:G:H8	1.49	0.77
1:A:983:A:H5'	1:A:984:C:OP2	1.85	0.77
5:D:13:ARG:HD2	5:D:38:TYR:O	1.84	0.77
1:A:706:A:O2'	12:K:29:ILE:HD11	1.85	0.77
5:D:36:ARG:H	5:D:37:PRO:CD	1.98	0.77
8:G:107:ALA:O	8:G:110:GLN:HB2	1.85	0.77
10:I:93:ARG:HG2	10:I:97:LYS:HE3	1.65	0.77
13:L:75:HIS:CD2	13:L:77:LEU:H	2.03	0.77
1:A:1250:A:C5'	10:I:68:GLY:H	1.98	0.77
14:M:40:ASN:HD22	14:M:41:PRO:HD2	1.49	0.77
1:A:405:U:H3'	1:A:406:G:H5'	1.66	0.76
11:J:86:MET:HA	11:J:86:MET:HE3	1.67	0.76
11:J:49:VAL:O	11:J:60:ARG:O	2.03	0.76
1:A:664:G:H22	1:A:741:G:H1	1.33	0.76
9:H:2:LEU:H	9:H:2:LEU:HD12	1.49	0.76
21:T:73:HIS:O	21:T:74:LYS:HB2	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:15:ARG:HD3	6:E:26:PHE:CD2	2.21	0.76
7:F:44:GLY:HA2	7:F:59:TYR:CE1	2.21	0.76
19:R:58:LEU:HD22	19:R:62:GLU:HB3	1.68	0.76
1:A:1158:C:H5''	3:B:133:LYS:HE3	1.66	0.76
1:A:1250:A:H5''	10:I:68:GLY:H	1.48	0.76
16:O:8:LYS:O	16:O:11:VAL:HG23	1.85	0.76
1:A:579:G:H5'	1:A:728:A:H1'	1.66	0.76
6:E:57:LYS:HG2	6:E:61:TYR:CE2	2.21	0.76
20:S:40:ILE:CD1	20:S:62:ILE:HD13	2.14	0.76
21:T:39:LYS:HD2	21:T:55:ILE:CD1	2.15	0.76
8:G:139:GLU:O	8:G:143:ARG:HG3	1.86	0.76
1:A:731:G:O2'	1:A:732:C:H5'	1.86	0.76
1:A:1286:A:H3'	1:A:1287:A:H5''	1.67	0.76
3:B:197:VAL:HB	3:B:200:ILE:HG12	1.68	0.76
10:I:65:VAL:HG21	10:I:73:GLN:HB3	1.67	0.76
1:A:1532:U:H2'	1:A:1533:C:H5''	1.68	0.76
3:B:53:ARG:HA	3:B:56:ARG:HE	1.49	0.76
5:D:150:GLU:H	5:D:150:GLU:CD	1.94	0.75
9:H:23:SER:O	9:H:24:THR:HB	1.86	0.75
1:A:129(A):G:HO2'	1:A:190(E):U:H2'	1.51	0.75
1:A:135:C:O2	17:P:1:MET:HB2	1.85	0.75
6:E:110:LEU:HD13	6:E:118:ILE:CD1	2.15	0.75
1:A:376:G:H5''	17:P:5:ARG:HD2	1.67	0.75
6:E:144:THR:HB	6:E:147:ASP:OD2	1.86	0.75
3:B:16:HIS:CE1	3:B:214:ILE:HG12	2.22	0.75
3:B:77:ALA:HB2	3:B:211:ILE:CD1	2.16	0.75
5:D:92:VAL:O	5:D:96:LEU:HD22	1.84	0.75
6:E:31:LEU:HD22	6:E:43:LEU:HD21	1.67	0.75
6:E:43:LEU:HD11	6:E:132:ALA:HB1	1.67	0.75
7:F:2:ARG:NE	7:F:69:GLU:HG2	2.01	0.75
1:A:1057:G:H5''	4:C:154:SER:HB2	1.66	0.75
4:C:14:ILE:CG2	4:C:15:THR:H	1.99	0.75
13:L:34:ARG:O	13:L:61:THR:HG23	1.86	0.75
16:O:62:GLN:HE21	16:O:66:LEU:HD21	1.52	0.75
18:Q:15:MET:HE1	18:Q:43:LEU:HD22	1.69	0.75
5:D:189:PRO:HB2	5:D:194:LEU:HD21	1.68	0.75
1:A:946:A:H2'	1:A:947:G:C8	2.21	0.75
1:A:1132:C:H2'	1:A:1133:G:C8	2.22	0.75
3:B:178:ARG:HG3	3:B:178:ARG:NH1	1.99	0.75
10:I:112:LYS:O	10:I:112:LYS:HD3	1.86	0.75
1:A:35:G:H2'	1:A:36:C:H6	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:223:ILE:HG21	3:B:230:VAL:HG23	1.69	0.74
1:A:1527:C:O2'	1:A:1528:U:H5'	1.87	0.74
11:J:24:VAL:O	11:J:28:ARG:HB2	1.87	0.74
3:B:21:ARG:O	3:B:39:ILE:HA	1.87	0.74
11:J:68:HIS:N	11:J:68:HIS:CD2	2.55	0.74
4:C:40:ARG:HH11	4:C:40:ARG:HG3	1.53	0.74
4:C:108:ASN:HD21	4:C:111:LEU:HG	1.51	0.74
10:I:8:GLY:HA2	10:I:79:LEU:HD12	1.70	0.74
9:H:119:LEU:HD12	9:H:124:ALA:HA	1.68	0.74
11:J:8:LEU:HD21	11:J:96:ILE:HG13	1.69	0.74
11:J:23:ILE:HD12	11:J:23:ILE:H	1.52	0.74
1:A:371:G:C2'	1:A:372:C:H5'	2.17	0.74
1:A:532:A:H2'	1:A:533:A:H5'	1.68	0.74
1:A:979:C:H2'	1:A:980:C:H5'	1.70	0.74
1:A:1279:A:H5''	1:A:1280:A:OP1	1.86	0.74
1:A:524:G:H2'	1:A:525:C:C6	2.23	0.74
1:A:1236:A:H4'	1:A:1304:G:H4'	1.70	0.74
16:O:36:ILE:HG12	16:O:59:MET:HE3	1.70	0.74
1:A:1241:G:H2'	1:A:1242:C:C6	2.22	0.74
3:B:23:ARG:HD3	3:B:24:TRP:N	2.03	0.74
14:M:102:ARG:HH12	14:M:104:ARG:HB3	1.53	0.74
20:S:5:LEU:O	20:S:6:LYS:HB2	1.87	0.74
17:P:20:VAL:HG21	17:P:32:TYR:CG	2.22	0.73
7:F:75:LEU:C	7:F:75:LEU:HD13	2.13	0.73
8:G:122:HIS:HA	8:G:125:MET:HE3	1.70	0.73
1:A:458:C:H2'	1:A:459:G:O4'	1.89	0.73
1:A:502:G:H2'	1:A:503:C:H6	1.52	0.73
6:E:80:ILE:HD12	6:E:91:LEU:HB2	1.71	0.73
18:Q:27:PHE:CZ	18:Q:36:ILE:HD11	2.23	0.73
17:P:20:VAL:CG2	17:P:32:TYR:HB2	2.17	0.73
3:B:118:LEU:HB2	3:B:142:LEU:HD21	1.69	0.73
5:D:162:LEU:HD13	5:D:181:MET:HE2	1.70	0.73
21:T:8:ARG:N	21:T:8:ARG:HD2	2.04	0.73
1:A:435:C:H2'	1:A:436:C:H6	1.53	0.73
1:A:839:U:O2	1:A:839:U:H2'	1.89	0.73
1:A:1066:C:O2'	1:A:1067:A:H5'	1.87	0.73
1:A:1305:G:H5'	22:V:4:GLY:C	2.14	0.73
9:H:136:GLU:HG3	9:H:136:GLU:O	1.88	0.73
13:L:120:TYR:O	13:L:122:THR:HG23	1.88	0.73
1:A:1286:A:H2'	1:A:1287:A:C5'	2.18	0.73
1:A:1142:G:H2'	1:A:1143:G:O4'	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1366:C:H2'	1:A:1367:C:C6	2.21	0.72
3:B:140:HIS:HA	3:B:143:GLU:HG2	1.71	0.72
4:C:190:ARG:HH11	4:C:190:ARG:CB	2.02	0.72
5:D:127:THR:HG22	5:D:147:ALA:O	1.89	0.72
1:A:487:A:H2'	1:A:488:C:O4'	1.89	0.72
1:A:560:U:H5'	1:A:566:G:N2	2.03	0.72
6:E:92:LYS:HB3	6:E:119:LEU:HB2	1.71	0.72
14:M:34:LEU:HD13	14:M:41:PRO:HA	1.70	0.72
18:Q:104:LYS:HE2	18:Q:104:LYS:HA	1.71	0.72
1:A:266:G:H5''	1:A:268:C:H41	1.54	0.72
1:A:970:C:H42	14:M:126:LYS:HD3	1.52	0.72
1:A:1347:G:H22	1:A:1373:G:H2'	1.55	0.72
15:N:29:ARG:HG3	15:N:30:ALA:H	1.53	0.72
17:P:10:GLY:HA3	17:P:15:PRO:HA	1.71	0.72
19:R:53:ARG:NH2	19:R:60:GLY:HA2	2.04	0.72
21:T:57:ARG:NH2	21:T:100:ILE:HG22	2.03	0.72
1:A:1352:C:H2'	1:A:1353:G:C8	2.24	0.72
1:A:1451:A:OP2	1:A:1452:C:H5	1.73	0.72
21:T:10:LEU:O	21:T:12:ALA:N	2.22	0.72
5:D:12:CYS:HA	5:D:19:LEU:HD11	1.72	0.72
7:F:40:VAL:HG12	7:F:63:TYR:HD1	1.54	0.72
11:J:15:THR:HG22	11:J:16:LEU:N	2.04	0.72
1:A:818:G:O2'	1:A:819:A:H5''	1.89	0.72
1:A:959:A:H3'	1:A:960:U:H5''	1.69	0.72
1:A:1030(B):C:H2'	1:A:1030(C):G:H8	1.54	0.72
11:J:96:ILE:HD12	11:J:96:ILE:N	2.04	0.72
3:B:151:GLY:C	3:B:153:ARG:H	1.95	0.72
20:S:49:ILE:H	20:S:49:ILE:HD12	1.54	0.72
3:B:124:SER:HB2	3:B:125:PRO:HD2	1.70	0.71
13:L:110:VAL:H	13:L:122:THR:HG22	1.54	0.71
19:R:38:GLU:H	19:R:38:GLU:CD	1.96	0.71
1:A:109:A:H2'	1:A:326:G:N2	2.06	0.71
1:A:407:G:H2'	1:A:408:A:C8	2.26	0.71
1:A:673:G:H2'	1:A:674:G:C8	2.25	0.71
1:A:1178:G:N2	1:A:1180:A:H3'	2.05	0.71
13:L:28:LYS:CD	13:L:33:ARG:HH12	2.03	0.71
1:A:564:C:C6	18:Q:31:LEU:HD11	2.26	0.71
1:A:1381:U:O2'	1:A:1382:C:H5'	1.90	0.71
15:N:47:LEU:CD2	15:N:52:GLN:HG3	2.20	0.71
1:A:1131:G:H1	1:A:1143:G:H21	1.38	0.71
1:A:1053:G:C3'	1:A:1054:C:H5'	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1241:G:H2'	1:A:1242:C:H6	1.56	0.71
4:C:70:VAL:HG12	4:C:72:LYS:H	1.54	0.71
1:A:1064:G:H4'	1:A:1065:U:H5''	1.70	0.71
4:C:131:ARG:HH21	6:E:50:GLU:HG2	1.55	0.71
5:D:39:PRO:HG2	5:D:44:GLY:HA2	1.73	0.71
5:D:146:ILE:N	5:D:146:ILE:HD12	2.06	0.71
1:A:939:G:H5''	8:G:102:ARG:NH2	1.97	0.71
3:B:77:ALA:CB	3:B:211:ILE:HD13	2.21	0.71
3:B:142:LEU:HB3	3:B:146:GLN:HE21	1.55	0.71
12:K:54:ARG:O	12:K:57:THR:HG22	1.89	0.71
4:C:50:ALA:HB1	4:C:70:VAL:CG1	2.20	0.71
5:D:156:GLU:HG2	5:D:160:GLN:NE2	2.05	0.71
11:J:90:LEU:N	11:J:91:PRO:HD2	2.05	0.71
21:T:50:GLU:HG3	21:T:99:LEU:HD12	1.71	0.71
9:H:119:LEU:HD12	9:H:124:ALA:CA	2.21	0.71
14:M:31:LYS:O	14:M:35:GLU:HB2	1.91	0.70
1:A:761:G:H4'	18:Q:103:GLY:H	1.57	0.70
4:C:19:GLU:HG2	4:C:54:ARG:NE	2.06	0.70
13:L:86:ARG:HH11	13:L:86:ARG:HG3	1.56	0.70
18:Q:18:THR:HG23	18:Q:69:LYS:HE3	1.73	0.70
1:A:80:G:H2'	1:A:81:U:H5''	1.73	0.70
1:A:168:G:O2'	1:A:169:C:H5'	1.92	0.70
1:A:1163:C:H2'	1:A:1164:G:H8	1.55	0.70
1:A:1251:A:H4'	10:I:12:GLU:CD	2.16	0.70
1:A:1307:U:H5'	14:M:109:THR:HG21	1.73	0.70
1:A:1356:G:H2'	1:A:1357:A:C8	2.27	0.70
6:E:11:ILE:CG2	6:E:12:LEU:HD12	2.21	0.70
6:E:41:VAL:HG21	6:E:113:ALA:HA	1.71	0.70
8:G:113:GLU:HG2	8:G:119:ARG:HG2	1.73	0.70
1:A:1194:U:H2'	1:A:1195:C:C6	2.27	0.70
13:L:27:LEU:C	13:L:29:GLY:H	1.98	0.70
1:A:392:G:H2'	1:A:393:A:C8	2.27	0.70
1:A:701:C:H5'	1:A:703:G:O4'	1.91	0.70
1:A:1191:A:P	4:C:3:ASN:HD21	2.14	0.70
5:D:32:ALA:C	5:D:34:GLU:N	2.46	0.70
14:M:49:THR:HG22	14:M:51:ALA:H	1.57	0.70
11:J:60:ARG:HD2	11:J:60:ARG:N	2.07	0.70
12:K:14:VAL:HG21	12:K:40:ILE:HD11	1.74	0.70
1:A:1141:C:H2'	1:A:1142:G:H8	1.57	0.70
1:A:1191:A:P	4:C:3:ASN:ND2	2.65	0.70
3:B:67:THR:HG22	3:B:68:ILE:N	2.07	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:15:VAL:HG23	14:M:43:THR:O	1.92	0.70
14:M:37:THR:O	14:M:39:ILE:HG13	1.92	0.70
1:A:918:A:H2'	1:A:919:A:H8	1.57	0.70
21:T:45:GLN:HA	21:T:91:LEU:HD22	1.71	0.70
1:A:443:C:O2'	1:A:444:C:H5'	1.92	0.70
4:C:157:ILE:CD1	4:C:166:GLU:HB2	2.21	0.70
7:F:18:GLN:O	7:F:21:LEU:HB3	1.92	0.70
11:J:89:ASP:C	11:J:90:LEU:HD12	2.16	0.70
1:A:840:C:H5''	1:A:841:U:OP1	1.92	0.69
6:E:135:THR:O	6:E:138:ALA:HB3	1.91	0.69
8:G:78:ARG:HG2	8:G:79:ARG:H	1.57	0.69
20:S:53:ASN:HD21	20:S:58:VAL:HG13	1.55	0.69
1:A:254:G:OP1	18:Q:67:LYS:O	2.10	0.69
1:A:390:C:H2'	1:A:391:G:C8	2.27	0.69
1:A:791:G:H2'	1:A:792:A:H5'	1.73	0.69
1:A:1443:G:C5'	1:A:1446:A:H5'	2.11	0.69
4:C:179:ARG:HD2	4:C:180:ALA:N	2.08	0.69
7:F:8:ILE:HD11	7:F:79:LEU:HD13	1.73	0.69
9:H:55:GLY:C	9:H:56:LYS:HD2	2.18	0.69
12:K:82:VAL:HG23	12:K:105:VAL:HG13	1.72	0.69
17:P:21:VAL:HG21	17:P:59:TRP:CD1	2.27	0.69
9:H:103:VAL:HG21	9:H:110:ALA:HB2	1.73	0.69
17:P:14:ASN:HA	17:P:42:ARG:NH2	2.07	0.69
21:T:56:MET:HE3	21:T:88:VAL:HG11	1.74	0.69
3:B:24:TRP:CH2	3:B:26:PRO:HA	2.27	0.69
3:B:139:LYS:O	3:B:143:GLU:HG2	1.92	0.69
4:C:54:ARG:HD3	4:C:56:ASP:OD1	1.91	0.69
4:C:137:ALA:HA	4:C:140:ARG:HD2	1.72	0.69
4:C:188:LEU:CD1	4:C:189:ALA:H	1.99	0.69
6:E:12:LEU:CD1	6:E:31:LEU:HB2	2.21	0.69
19:R:36:ASN:HD21	19:R:38:GLU:HG2	1.55	0.69
1:A:114:U:O2'	1:A:115:G:H5'	1.91	0.69
1:A:1412:C:H2'	1:A:1413:A:C8	2.27	0.69
3:B:10:LEU:O	3:B:10:LEU:HD23	1.93	0.69
5:D:142:PRO:HG2	5:D:187:ARG:NH2	2.08	0.69
11:J:45:ARG:HB2	11:J:65:LEU:HB3	1.74	0.69
1:A:1148:U:H2'	1:A:1149:C:O4'	1.91	0.69
1:A:1368:G:O2'	1:A:1369:C:H5'	1.93	0.69
1:A:17:U:H2'	1:A:18:C:C6	2.27	0.69
1:A:812:C:HO2'	1:A:813:U:P	2.16	0.69
11:J:3:LYS:N	11:J:75:ILE:HA	2.08	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1152:A:H5''	11:J:13:HIS:CD2	2.28	0.69
3:B:143:GLU:O	3:B:147:LYS:HG3	1.92	0.69
1:A:270:A:H2'	1:A:271:C:C6	2.28	0.68
1:A:1005:A:H62	1:A:1024:G:H1'	1.58	0.68
4:C:52:LEU:HD23	4:C:52:LEU:H	1.58	0.68
10:I:97:LYS:HG3	10:I:102:LEU:HD12	1.73	0.68
10:I:127:LYS:HB2	14:M:126:LYS:NZ	2.08	0.68
13:L:46:LYS:CG	13:L:47:LYS:H	2.06	0.68
9:H:97:VAL:HG21	9:H:128:GLY:HA2	1.75	0.68
1:A:1222:G:OP1	20:S:77:THR:HG21	1.93	0.68
3:B:36:ARG:HD2	3:B:41:ILE:CD1	2.23	0.68
3:B:140:HIS:HA	3:B:143:GLU:CG	2.23	0.68
3:B:184:VAL:HG23	3:B:198:ASP:H	1.59	0.68
15:N:17:LYS:HB2	15:N:17:LYS:HZ2	1.58	0.68
1:A:543:C:O2'	1:A:544:G:H5'	1.93	0.68
8:G:78:ARG:HG2	8:G:79:ARG:N	2.09	0.68
11:J:6:ILE:HD13	11:J:72:VAL:HB	1.75	0.68
11:J:68:HIS:CD2	11:J:68:HIS:H	2.12	0.68
18:Q:26:GLN:O	18:Q:27:PHE:HB3	1.93	0.68
19:R:55:ARG:HB3	19:R:55:ARG:HH11	1.58	0.68
1:A:662:G:H2'	1:A:663:A:C8	2.29	0.68
1:A:1281:U:H4'	1:A:1282:C:OP2	1.93	0.68
1:A:1470:G:O2'	1:A:1471:G:H5'	1.94	0.68
3:B:7:VAL:HG11	3:B:224:GLN:OE1	1.93	0.68
3:B:80:ILE:HD11	3:B:208:ILE:HG12	1.75	0.68
3:B:188:ALA:O	3:B:202:PRO:HA	1.92	0.68
4:C:32:LEU:H	4:C:32:LEU:HD12	1.57	0.68
20:S:41:VAL:HG23	20:S:43:GLU:HG2	1.76	0.68
20:S:55:LYS:HG2	20:S:56:GLN:NE2	2.08	0.68
21:T:85:MET:HE3	21:T:103:GLY:O	1.94	0.68
14:M:97:PRO:HB2	14:M:101:GLN:OE1	1.94	0.68
18:Q:53:LEU:HD23	18:Q:54:GLY:N	2.08	0.68
1:A:1425:U:H2'	1:A:1426:C:C6	2.29	0.68
21:T:41:ILE:O	21:T:45:GLN:HB2	1.94	0.68
1:A:407:G:H2'	1:A:408:A:H8	1.56	0.68
1:A:976:G:OP2	1:A:1358:U:H1'	1.94	0.68
8:G:26:PHE:CE2	8:G:30:ILE:HD11	2.29	0.68
15:N:24:CYS:HB3	15:N:28:GLY:N	2.09	0.68
1:A:753:A:C2	9:H:1:MET:HE2	2.27	0.68
4:C:150:LYS:HG3	4:C:169:ALA:HB2	1.75	0.68
10:I:118:LYS:O	10:I:119:ALA:HB3	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:G:N2	1:A:354:G:H5'	2.09	0.68
1:A:163:C:O2'	1:A:164:U:H5'	1.94	0.68
1:A:1272:G:H2'	1:A:1273:G:O4'	1.94	0.68
3:B:223:ILE:O	3:B:225:ALA:N	2.26	0.68
10:I:95:LYS:O	10:I:98:PRO:HD2	1.94	0.68
1:A:112:G:H21	1:A:354:G:H5'	1.59	0.67
10:I:97:LYS:CG	10:I:102:LEU:HD12	2.24	0.67
1:A:1054:C:O2'	1:A:1055:A:H5''	1.95	0.67
3:B:16:HIS:HE2	3:B:214:ILE:HG12	1.58	0.67
13:L:38:THR:HG22	13:L:39:VAL:HG23	1.74	0.67
3:B:223:ILE:C	3:B:225:ALA:N	2.52	0.67
9:H:116:LYS:HD2	9:H:129:VAL:HG11	1.76	0.67
15:N:8:GLU:O	15:N:11:LYS:HG2	1.94	0.67
1:A:22:G:O2'	1:A:23:C:H5'	1.94	0.67
5:D:108:LEU:HD13	5:D:183:GLY:HA3	1.77	0.67
14:M:81:LEU:HD12	14:M:88:ARG:NH1	2.09	0.67
16:O:81:LEU:HD23	16:O:81:LEU:C	2.19	0.67
1:A:797:C:O2'	1:A:798:G:H5'	1.93	0.67
3:B:53:ARG:HA	3:B:56:ARG:NE	2.10	0.67
5:D:35:ARG:O	5:D:36:ARG:HB2	1.92	0.67
11:J:32:ALA:HB2	11:J:76:ASN:HD22	1.59	0.67
7:F:36:ARG:HH12	7:F:38:GLU:HG2	1.59	0.67
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.08	0.67
1:A:393:A:O2'	1:A:394:G:H5'	1.94	0.67
1:A:1426:C:H2'	1:A:1427:U:C6	2.30	0.67
3:B:17:PHE:HB3	3:B:44:LEU:HD21	1.76	0.67
5:D:98:GLU:HG2	5:D:189:PRO:HG3	1.76	0.67
19:R:61:LYS:O	19:R:65:ILE:HG13	1.94	0.67
1:A:269:C:H2'	1:A:270:A:C8	2.28	0.67
1:A:335:C:H2'	1:A:336:C:H6	1.60	0.67
1:A:1163:C:H2'	1:A:1164:G:C8	2.30	0.67
8:G:148:ASN:HD22	8:G:148:ASN:N	1.91	0.67
11:J:8:LEU:CD2	11:J:96:ILE:HG13	2.24	0.67
13:L:70:ILE:HD13	13:L:77:LEU:HD12	1.75	0.67
14:M:88:ARG:HG3	14:M:98:VAL:CG1	2.25	0.67
3:B:88:ALA:C	3:B:90:MET:H	2.01	0.67
21:T:67:ALA:HA	21:T:73:HIS:H	1.60	0.67
1:A:839:U:H5'	1:A:840:C:H5	1.57	0.67
15:N:24:CYS:HB3	15:N:28:GLY:H	1.59	0.67
17:P:12:LYS:O	17:P:13:HIS:HB2	1.94	0.67
21:T:56:MET:HE2	21:T:85:MET:HA	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:96:GLY:O	21:T:97:ALA:HB3	1.94	0.67
1:A:1060:C:C5	4:C:2:GLY:HA3	2.30	0.66
1:A:1216:G:H5''	15:N:5:ALA:CB	2.25	0.66
11:J:45:ARG:HH22	15:N:36:PHE:HD2	1.43	0.66
13:L:97:ARG:HB2	13:L:98:TYR:CE1	2.30	0.66
5:D:149:ALA:HB3	5:D:152:SER:HB2	1.76	0.66
1:A:1005:A:C2'	1:A:1006:C:H5'	2.24	0.66
5:D:141:ARG:HB2	5:D:141:ARG:HH11	1.61	0.66
13:L:33:ARG:HG2	13:L:60:LEU:HD12	1.78	0.66
1:A:1318:A:O2'	20:S:37:ARG:HD2	1.95	0.66
6:E:138:ALA:O	6:E:139:LEU:C	2.39	0.66
1:A:1443:G:H5''	1:A:1446:A:C5'	2.11	0.66
17:P:81:ARG:HG3	17:P:83:GLU:HG2	1.78	0.66
1:A:421:U:H4'	1:A:422:C:OP2	1.93	0.66
1:A:1480:G:H2'	1:A:1481:U:H6	1.57	0.66
1:A:1518:A:H2'	1:A:1519:A:C8	2.31	0.66
5:D:19:LEU:HD12	5:D:19:LEU:H	1.59	0.66
7:F:19:LEU:C	7:F:19:LEU:HD23	2.21	0.66
12:K:14:VAL:O	12:K:15:ALA:HB3	1.96	0.66
13:L:27:LEU:O	13:L:29:GLY:N	2.29	0.66
1:A:812:C:O2'	1:A:813:U:P	2.54	0.66
1:A:1230:C:O2'	14:M:126:LYS:HG2	1.95	0.66
3:B:101:MET:HA	3:B:108:ILE:CD1	2.23	0.66
5:D:30:LYS:C	5:D:32:ALA:H	2.04	0.66
6:E:115:VAL:HG11	6:E:118:ILE:CD1	2.25	0.66
1:A:838:G:C2'	1:A:839:U:H5''	2.25	0.66
1:A:1003(A):G:C4	1:A:1004:A:H1'	2.31	0.66
6:E:110:LEU:O	6:E:113:ALA:HB3	1.96	0.66
9:H:6:ILE:HD12	9:H:35:ILE:HD11	1.78	0.66
11:J:6:ILE:HD11	11:J:73:ASP:N	2.09	0.66
13:L:27:LEU:HD23	13:L:62:SER:HB2	1.76	0.66
1:A:1254:C:OP1	11:J:45:ARG:HD3	1.96	0.66
4:C:174:PRO:HB2	4:C:177:THR:CG2	2.24	0.66
4:C:180:ALA:O	4:C:181:ASN:HB3	1.96	0.66
1:A:386:C:C2'	1:A:387:U:H5'	2.26	0.66
1:A:922:G:H5'	6:E:20:GLN:NE2	2.11	0.66
1:A:1132:C:H2'	1:A:1133:G:H8	1.59	0.66
4:C:64:VAL:H	4:C:99:VAL:HG12	1.61	0.66
4:C:157:ILE:HD11	4:C:166:GLU:HB2	1.76	0.66
5:D:17:VAL:HG12	5:D:18:LYS:N	2.11	0.66
1:A:448:A:H62	1:A:486:U:H3	1.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1229:A:H2'	1:A:1230:C:H6	1.60	0.65
4:C:20:SER:HB2	4:C:40:ARG:NH2	2.11	0.65
1:A:407:G:O2'	5:D:116:GLN:HG3	1.96	0.65
3:B:19:HIS:HD2	3:B:205:ASP:OD1	1.79	0.65
8:G:51:GLN:C	8:G:53:LYS:H	2.03	0.65
1:A:625:G:H4'	17:P:16:HIS:CD2	2.31	0.65
1:A:1006:C:H2'	1:A:1007:C:C6	2.31	0.65
1:A:1027:C:H2'	1:A:1028:C:C6	2.32	0.65
1:A:1031:G:H2'	1:A:1032:G:C8	2.31	0.65
1:A:1189:C:OP1	11:J:51:ARG:NH2	2.29	0.65
3:B:74:LYS:HE3	3:B:205:ASP:O	1.96	0.65
5:D:3:ARG:O	5:D:5:ILE:N	2.29	0.65
6:E:120:THR:HG23	6:E:121:LYS:N	2.12	0.65
8:G:79:ARG:HA	8:G:83:ALA:O	1.95	0.65
12:K:16:SER:HA	12:K:79:SER:O	1.97	0.65
14:M:52:GLU:HG2	14:M:55:ARG:HH21	1.61	0.65
16:O:29:VAL:HG12	16:O:85:LEU:CD1	2.27	0.65
1:A:440:A:H3'	1:A:442:C:C6	2.31	0.65
1:A:877:C:O2'	1:A:878:G:H5'	1.96	0.65
1:A:974:A:OP1	15:N:31:ARG:HG2	1.96	0.65
1:A:1065:U:H4'	1:A:1066:C:O5'	1.95	0.65
1:A:1367:C:H5'	11:J:60:ARG:NH1	2.11	0.65
5:D:3:ARG:HH11	5:D:118:ARG:NH1	1.94	0.65
13:L:27:LEU:C	13:L:29:GLY:N	2.51	0.65
1:A:501:C:H2'	1:A:502:G:C8	2.32	0.65
1:A:1425:U:H2'	1:A:1426:C:H6	1.59	0.65
5:D:4:TYR:HD2	5:D:115:ARG:NH2	1.94	0.65
5:D:176:LEU:HD12	5:D:182:LYS:O	1.96	0.65
9:H:51:VAL:HG11	9:H:60:ARG:HH11	1.60	0.65
14:M:117:VAL:HG12	14:M:118:ALA:N	2.10	0.65
16:O:78:TYR:CZ	16:O:82:ILE:HD11	2.31	0.65
19:R:87:ARG:HG2	19:R:87:ARG:HH11	1.61	0.65
21:T:102:GLY:O	21:T:104:LEU:N	2.28	0.65
1:A:105:G:H2'	1:A:106:C:C6	2.31	0.65
1:A:1502:A:C2	1:A:1505:G:N1	2.64	0.65
13:L:33:ARG:CG	13:L:60:LEU:HD12	2.27	0.65
21:T:68:LYS:HE3	21:T:68:LYS:HA	1.78	0.65
1:A:1028:C:H2'	1:A:1029:C:H5'	1.77	0.65
5:D:11:LEU:O	5:D:12:CYS:C	2.39	0.65
5:D:61:LYS:HD2	5:D:207:TYR:OH	1.96	0.65
6:E:55:VAL:O	6:E:58:ALA:HB3	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:42:ILE:HG23	8:G:117:ALA:HA	1.79	0.65
14:M:25:ILE:HG23	14:M:29:ARG:HB2	1.79	0.65
17:P:1:MET:HE3	17:P:3:LYS:HG2	1.78	0.65
18:Q:76:LEU:C	18:Q:76:LEU:HD23	2.22	0.65
21:T:13:LEU:HD12	21:T:13:LEU:N	2.10	0.65
21:T:72:LEU:O	21:T:73:HIS:O	2.13	0.65
1:A:148:G:H2'	1:A:149:A:H8	1.61	0.65
1:A:180:U:H2'	1:A:181:G:H5'	1.78	0.65
1:A:620:C:C2	5:D:135:LEU:HD13	2.32	0.65
14:M:80:ARG:C	14:M:82:MET:H	2.03	0.65
1:A:130:A:OP2	1:A:190(E):U:H2'	1.96	0.65
4:C:55:VAL:O	4:C:55:VAL:HG12	1.96	0.65
8:G:23:VAL:O	8:G:27:ILE:HG13	1.97	0.65
1:A:80:G:H3'	1:A:81:U:C5'	2.27	0.65
1:A:1014:A:H2'	1:A:1015:A:C8	2.31	0.65
8:G:71:PRO:HD3	8:G:103:TRP:HZ3	1.62	0.65
14:M:4:ILE:HG22	14:M:5:ALA:N	2.12	0.65
1:A:939:G:C5'	8:G:102:ARG:HH22	2.01	0.64
6:E:6:PHE:CZ	6:E:66:MET:HE2	2.31	0.64
7:F:101:ALA:HB2	19:R:28:GLU:HB2	1.79	0.64
11:J:47:PHE:HB2	11:J:63:PHE:HB2	1.78	0.64
16:O:3:ILE:HD13	16:O:34:LEU:HD22	1.78	0.64
1:A:357:G:O2'	1:A:358:U:H5'	1.97	0.64
4:C:177:THR:HG23	4:C:177:THR:O	1.96	0.64
5:D:3:ARG:HE	5:D:3:ARG:N	1.95	0.64
7:F:48:LEU:HD13	7:F:52:ILE:HG13	1.79	0.64
8:G:136:LYS:HG2	8:G:140:ASP:OD2	1.96	0.64
8:G:153:HIS:HB3	12:K:58:PRO:HG3	1.79	0.64
11:J:9:ARG:HB3	11:J:9:ARG:NH1	2.11	0.64
16:O:74:ASP:OD1	16:O:76:GLU:HB3	1.98	0.64
1:A:437:U:C2'	1:A:438:G:H5'	2.27	0.64
1:A:765:G:H1	1:A:812:C:H2'	1.62	0.64
1:A:1316:G:H4'	15:N:18:VAL:CG1	2.27	0.64
4:C:134:ILE:O	4:C:138:VAL:HG23	1.98	0.64
8:G:109:ASN:N	8:G:109:ASN:HD22	1.92	0.64
10:I:113:LYS:H	10:I:113:LYS:HD3	1.63	0.64
18:Q:89:LEU:O	18:Q:92:ARG:HB3	1.97	0.64
1:A:1057:G:H5''	4:C:154:SER:CB	2.26	0.64
3:B:178:ARG:HH21	3:B:196:LEU:C	2.04	0.64
4:C:147:LYS:HD2	4:C:203:PHE:CE2	2.33	0.64
5:D:121:VAL:O	5:D:134:ASP:HA	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:7:LYS:HD3	11:J:9:ARG:HH22	1.63	0.64
1:A:190(F):G:H4'	1:A:190(G):G:OP2	1.97	0.64
1:A:835:U:OP1	19:R:64:ARG:NH2	2.30	0.64
14:M:3:ARG:N	14:M:9:ILE:HG23	2.12	0.64
1:A:254:G:O2'	1:A:255:G:H5'	1.97	0.64
1:A:757:U:H2'	1:A:758:G:O4'	1.97	0.64
16:O:11:VAL:HG21	16:O:34:LEU:HD12	1.79	0.64
1:A:853:G:O2'	1:A:854:G:H5'	1.97	0.64
1:A:1502:A:H2	1:A:1505:G:N1	1.95	0.64
3:B:134:GLU:C	3:B:136:VAL:H	2.06	0.64
8:G:79:ARG:HE	8:G:84:ASN:HD21	1.44	0.64
9:H:36:LEU:HD12	9:H:59:LEU:HD13	1.80	0.64
16:O:60:VAL:O	16:O:64:ARG:HG2	1.97	0.64
1:A:1497:G:C2'	1:A:1498:U:H5'	2.28	0.64
3:B:15:VAL:HG11	3:B:209:ARG:C	2.23	0.64
20:S:33:THR:HG22	20:S:35:SER:N	2.08	0.64
22:V:14:TRP:C	22:V:16:GLY:H	2.05	0.64
1:A:165:C:H2'	1:A:166:G:H8	1.63	0.64
1:A:980:C:H2'	1:A:981:U:O4'	1.97	0.64
3:B:130:ARG:NH2	4:C:207:VAL:HG22	2.13	0.64
4:C:20:SER:HB2	4:C:40:ARG:HH22	1.63	0.64
4:C:134:ILE:HG22	4:C:168:ALA:HB3	1.78	0.64
8:G:43:PHE:O	8:G:47:CYS:HB2	1.98	0.64
16:O:39:LEU:HD21	16:O:43:LEU:HD11	1.80	0.64
19:R:58:LEU:HD13	19:R:63:GLN:HA	1.79	0.64
14:M:52:GLU:HG2	14:M:55:ARG:NH2	2.13	0.63
16:O:45:VAL:HG12	16:O:46:HIS:H	1.64	0.63
1:A:1489:G:O2'	1:A:1490:C:H5'	1.98	0.63
3:B:61:LEU:HD23	3:B:61:LEU:O	1.98	0.63
9:H:118:VAL:C	9:H:119:LEU:HD23	2.23	0.63
16:O:70:LEU:HD12	16:O:78:TYR:CB	2.26	0.63
18:Q:5:VAL:O	18:Q:6:LEU:HD23	1.97	0.63
21:T:53:LEU:HD21	21:T:104:LEU:HD12	1.78	0.63
1:A:1392:G:H21	1:A:1502:A:H8	1.45	0.63
1:A:1475:G:H2'	1:A:1476:G:H8	1.63	0.63
3:B:95:GLN:HG3	3:B:148:TYR:HA	1.80	0.63
3:B:130:ARG:HB3	3:B:131:PRO:HD2	1.80	0.63
6:E:51:VAL:HB	6:E:52:PRO:CD	2.27	0.63
18:Q:103:GLY:O	18:Q:104:LYS:HE3	1.97	0.63
1:A:1095:U:H2'	1:A:1096:C:C6	2.33	0.63
10:I:9:ARG:HG3	10:I:14:VAL:HG13	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:119:ALA:O	10:I:120:ARG:HG2	1.98	0.63
11:J:36:GLY:O	11:J:72:VAL:HA	1.99	0.63
1:A:1281:U:H5'	1:A:1282:C:H5	1.64	0.63
6:E:11:ILE:HB	6:E:31:LEU:HB3	1.80	0.63
12:K:13:GLN:HA	12:K:75:TYR:O	1.98	0.63
1:A:353:A:H5'	1:A:353:A:C8	2.33	0.63
1:A:1216:G:H5''	15:N:5:ALA:HB1	1.81	0.63
1:A:1397:C:H4'	1:A:1398:A:OP2	1.97	0.63
7:F:100:ASN:ND2	19:R:23:LYS:HG2	2.09	0.63
8:G:15:ASP:HB3	8:G:19:GLY:N	2.14	0.63
8:G:71:PRO:HD3	8:G:103:TRP:CZ3	2.33	0.63
14:M:78:ILE:HA	14:M:81:LEU:HD21	1.79	0.63
22:V:6:ARG:HD3	22:V:15:ARG:NH1	2.05	0.63
1:A:463:A:O2'	1:A:474:G:H5'	1.98	0.63
4:C:52:LEU:H	4:C:52:LEU:CD2	2.12	0.63
5:D:23:GLY:O	5:D:27:TYR:HD1	1.81	0.63
5:D:176:LEU:HD12	5:D:177:ASP:H	1.63	0.63
6:E:35:GLY:HA3	6:E:112:LEU:CB	2.28	0.63
6:E:80:ILE:HD12	6:E:80:ILE:H	1.62	0.63
13:L:50:SER:O	13:L:51:ALA:HB2	1.99	0.63
20:S:64:GLU:O	20:S:67:VAL:HG23	1.98	0.63
1:A:270:A:H2'	1:A:271:C:H6	1.64	0.63
13:L:28:LYS:HD2	13:L:33:ARG:NH1	2.10	0.63
1:A:1030(C):G:H2'	1:A:1030(D):A:O4'	1.98	0.63
3:B:102:LEU:HD21	3:B:162:ILE:CD1	2.26	0.63
3:B:239:VAL:HB	3:B:240:GLN:NE2	2.14	0.63
8:G:140:ASP:O	8:G:143:ARG:HB2	1.98	0.63
6:E:80:ILE:HD11	6:E:91:LEU:HD12	1.81	0.62
7:F:36:ARG:NH1	7:F:38:GLU:HG2	2.13	0.62
14:M:10:PRO:HB2	14:M:18:ALA:HB1	1.80	0.62
1:A:179:A:H2'	1:A:180:U:C6	2.35	0.62
1:A:187:C:C1'	21:T:85:MET:HE2	2.29	0.62
1:A:625:G:H2'	1:A:626:U:C6	2.34	0.62
1:A:1372:U:O2'	1:A:1373:G:H5'	1.99	0.62
4:C:54:ARG:HG2	4:C:55:VAL:N	2.13	0.62
9:H:14:ARG:O	9:H:18:ARG:HD3	1.99	0.62
9:H:82:HIS:O	9:H:83:ILE:HB	1.99	0.62
16:O:4:THR:OG1	16:O:7:GLU:HB3	2.00	0.62
1:A:1091:U:O2	1:A:1093:A:C8	2.52	0.62
7:F:23:LYS:O	7:F:27:GLN:HG2	2.00	0.62
14:M:19:LEU:O	14:M:22:ILE:HG13	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:81:ARG:HH11	17:P:81:ARG:HB2	1.64	0.62
1:A:222:U:H2'	1:A:223:U:C6	2.34	0.62
1:A:308:C:H2'	1:A:309:G:H8	1.64	0.62
1:A:1168:A:H2'	1:A:1169:A:C8	2.34	0.62
1:A:1176:A:H2'	1:A:1177:G:C8	2.34	0.62
5:D:64:LEU:O	5:D:67:ILE:HB	1.99	0.62
13:L:83:VAL:CG2	13:L:100:ILE:HG23	2.30	0.62
16:O:63:ARG:C	16:O:65:ARG:H	2.06	0.62
18:Q:95:TYR:O	18:Q:97:SER:N	2.33	0.62
20:S:58:VAL:HG21	20:S:75:ALA:HA	1.80	0.62
21:T:57:ARG:NE	21:T:102:GLY:HA3	2.14	0.62
1:A:91:C:O2'	1:A:92:C:H5'	2.00	0.62
1:A:114:U:H2'	1:A:115:G:C8	2.33	0.62
1:A:255:G:H1'	18:Q:16:GLN:NE2	2.14	0.62
5:D:152:SER:HB3	5:D:155:LEU:HD12	1.82	0.62
8:G:26:PHE:CD2	8:G:30:ILE:HD11	2.34	0.62
9:H:51:VAL:HG21	9:H:60:ARG:NH1	2.14	0.62
12:K:33:THR:OG1	12:K:38:ASN:C	2.43	0.62
14:M:50:GLU:O	14:M:54:VAL:HG23	1.98	0.62
1:A:629:G:O2'	1:A:630:G:H5'	1.99	0.62
5:D:88:VAL:O	5:D:89:THR:C	2.41	0.62
5:D:150:GLU:HA	5:D:153:ARG:HE	1.63	0.62
9:H:121:ASP:HB2	9:H:125:ARG:HH22	1.62	0.62
14:M:33:ALA:HA	14:M:59:TYR:CE2	2.35	0.62
17:P:67:THR:C	17:P:69:THR:H	2.06	0.62
1:A:192:U:H1'	21:T:103:GLY:HA2	1.81	0.62
1:A:502:G:H2'	1:A:503:C:C6	2.33	0.62
1:A:643:C:H4'	9:H:31:PHE:CE2	2.35	0.62
1:A:1026:G:H2'	1:A:1027:C:H5'	1.82	0.62
1:A:1435:G:H2'	1:A:1436:U:C6	2.35	0.62
3:B:91:PRO:HG3	3:B:154:LEU:HB2	1.80	0.62
13:L:27:LEU:HG	13:L:28:LYS:H	1.63	0.62
1:A:247:G:OP2	18:Q:100:LYS:HB2	2.00	0.62
1:A:922:G:N3	1:A:1398:A:H2	1.98	0.62
1:A:1014:A:H2	1:A:1219:U:H1'	1.65	0.62
1:A:1038:C:H2'	1:A:1039:C:C6	2.35	0.62
1:A:1338:G:H2'	1:A:1339:A:C8	2.35	0.62
1:A:1441:G:H4'	1:A:1442:G:C5	2.34	0.62
3:B:144:ARG:HA	3:B:147:LYS:HD2	1.81	0.62
8:G:65:ALA:O	8:G:69:VAL:HG23	2.00	0.62
8:G:79:ARG:HE	8:G:84:ASN:ND2	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:79:SER:HB2	12:K:106:LYS:HE2	1.82	0.62
4:C:180:ALA:HB1	4:C:203:PHE:CE1	2.34	0.62
10:I:49:PRO:O	10:I:52:ALA:HB3	2.00	0.62
1:A:52:G:O2'	1:A:53:A:H5'	1.99	0.61
1:A:166:G:O2'	1:A:167:G:H5'	2.00	0.61
1:A:370:C:O2'	1:A:371:G:H5'	2.00	0.61
1:A:1347:G:O2'	1:A:1348:U:P	2.56	0.61
1:A:1391:U:H2'	1:A:1392:G:H8	1.59	0.61
1:A:1521:G:H2'	1:A:1522:U:C6	2.35	0.61
8:G:51:GLN:OE1	8:G:51:GLN:HA	2.00	0.61
20:S:15:LEU:HA	20:S:18:LYS:HB3	1.81	0.61
1:A:338:A:H2	1:A:351:G:H22	1.48	0.61
1:A:746:A:O2'	1:A:747:C:H5'	1.99	0.61
4:C:172:ARG:HH11	4:C:172:ARG:CB	2.13	0.61
5:D:70:ILE:HD11	5:D:74:GLN:HB3	1.81	0.61
1:A:308:C:H2'	1:A:309:G:C8	2.35	0.61
1:A:753:A:H2	9:H:1:MET:HE2	1.65	0.61
5:D:57:ARG:HG3	5:D:57:ARG:NH1	2.10	0.61
9:H:107:LEU:HD23	9:H:107:LEU:N	2.14	0.61
11:J:51:ARG:HG2	11:J:51:ARG:HH11	1.66	0.61
1:A:977:A:C2'	1:A:978:A:H5''	2.30	0.61
1:A:1270:C:H2'	1:A:1271:G:H8	1.65	0.61
8:G:145:ALA:O	8:G:147:ALA:N	2.34	0.61
14:M:77:ASN:O	14:M:80:ARG:HB3	2.00	0.61
16:O:16:ALA:HA	16:O:27:VAL:HG22	1.82	0.61
1:A:975:A:C4'	1:A:976:G:OP2	2.46	0.61
4:C:22:TRP:NE1	4:C:36:ASP:OD1	2.34	0.61
5:D:12:CYS:HA	5:D:19:LEU:CD1	2.30	0.61
5:D:17:VAL:HG11	5:D:197:PRO:HG3	1.81	0.61
11:J:46:ARG:HG2	11:J:46:ARG:HH11	1.65	0.61
1:A:1349:A:OP1	10:I:120:ARG:HB2	2.01	0.61
4:C:84:ILE:HD11	4:C:88:ARG:NH1	2.16	0.61
13:L:71:PRO:O	13:L:102:ARG:HD2	2.00	0.61
17:P:14:ASN:N	17:P:15:PRO:CD	2.64	0.61
1:A:1014:A:C2	1:A:1219:U:H1'	2.35	0.61
1:A:1062:U:H2'	1:A:1063:C:C6	2.35	0.61
1:A:1296:C:H4'	1:A:1302:U:C5	2.35	0.61
6:E:12:LEU:HD22	6:E:12:LEU:C	2.24	0.61
7:F:38:GLU:O	7:F:39:LYS:HB3	2.00	0.61
8:G:46:ALA:HA	8:G:49:ILE:HD12	1.83	0.61
8:G:138:LYS:HD3	8:G:138:LYS:C	2.25	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:75:ILE:HG22	11:J:76:ASN:N	2.14	0.61
13:L:115:LYS:O	13:L:117:ARG:N	2.31	0.61
15:N:47:LEU:HD22	15:N:52:GLN:HG3	1.83	0.61
16:O:26:GLU:HG3	16:O:81:LEU:HD12	1.82	0.61
1:A:437:U:O2'	1:A:438:G:H5'	1.99	0.61
1:A:1392:G:N2	1:A:1502:A:H8	1.98	0.61
3:B:184:VAL:HG22	3:B:198:ASP:OD2	2.00	0.61
6:E:40:ARG:HG2	6:E:40:ARG:HH11	1.64	0.61
7:F:19:LEU:HD23	7:F:20:ALA:N	2.15	0.61
7:F:35:ALA:HA	7:F:67:MET:HB3	1.82	0.61
9:H:103:VAL:HG21	9:H:109:ILE:O	2.01	0.61
11:J:92:THR:C	11:J:94:VAL:H	2.09	0.61
14:M:65:LYS:HG2	14:M:69:GLU:HB3	1.82	0.61
21:T:34:LYS:HB3	21:T:38:LYS:NZ	2.14	0.61
1:A:382:A:H2'	1:A:383:A:H8	1.61	0.61
3:B:48:MET:HA	3:B:51:LEU:HD12	1.83	0.61
6:E:10:MET:SD	6:E:13:ILE:HG23	2.41	0.61
14:M:33:ALA:HA	14:M:59:TYR:CD2	2.36	0.61
19:R:35:ARG:O	19:R:37:VAL:HG23	2.00	0.61
1:A:513:C:H2'	1:A:514:C:H6	1.66	0.61
1:A:613:C:O2'	1:A:614:A:H5'	2.01	0.61
8:G:78:ARG:NH1	8:G:154:TYR:O	2.34	0.61
10:I:19:LEU:O	10:I:20:ARG:HG3	2.00	0.61
18:Q:10:VAL:HG23	18:Q:55:ASP:O	2.00	0.61
19:R:28:GLU:HG3	19:R:28:GLU:O	2.01	0.61
1:A:915:A:H2'	1:A:916:G:H5'	1.83	0.60
1:A:1072:G:H2'	1:A:1073:U:C6	2.36	0.60
5:D:162:LEU:CD2	5:D:178:VAL:HG13	2.29	0.60
9:H:10:LEU:HD23	9:H:83:ILE:HD11	1.81	0.60
12:K:110:ASP:HB2	19:R:88:LYS:NZ	2.15	0.60
1:A:440:A:H5'	1:A:442:C:OP2	2.01	0.60
1:A:1145:C:H1'	1:A:1146:A:C8	2.36	0.60
3:B:43:ASP:OD1	3:B:45:GLN:HB2	2.01	0.60
5:D:189:PRO:HB2	5:D:194:LEU:CD2	2.31	0.60
10:I:93:ARG:HB3	10:I:97:LYS:HD2	1.83	0.60
1:A:164:U:H2'	1:A:165:C:H6	1.66	0.60
1:A:765:G:H22	1:A:812:C:HO2'	1.49	0.60
5:D:173:TRP:CD2	5:D:189:PRO:HB3	2.36	0.60
13:L:24:VAL:HG13	13:L:98:TYR:CE2	2.37	0.60
18:Q:59:ILE:HD13	18:Q:73:VAL:HA	1.83	0.60
1:A:540:G:H2'	1:A:541:G:O4'	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1497:G:O2'	1:A:1498:U:H5'	2.01	0.60
4:C:134:ILE:CG2	4:C:168:ALA:HB3	2.31	0.60
9:H:2:LEU:HD12	9:H:2:LEU:N	2.16	0.60
1:A:187:C:H1'	21:T:85:MET:HE2	1.82	0.60
3:B:184:VAL:N	3:B:198:ASP:OD2	2.30	0.60
5:D:177:ASP:OD1	5:D:179:GLU:HG2	2.01	0.60
8:G:153:HIS:C	8:G:155:ARG:H	2.10	0.60
9:H:73:ASP:OD2	9:H:75:ARG:HB2	2.01	0.60
10:I:50:LEU:HB3	10:I:55:ALA:HB3	1.82	0.60
1:A:737:A:H1'	7:F:73:ASN:ND2	2.17	0.60
1:A:1300:G:HO2'	1:A:1301:U:H6	1.48	0.60
4:C:32:LEU:HD12	4:C:32:LEU:N	2.17	0.60
8:G:116:ALA:HA	8:G:119:ARG:NH1	2.17	0.60
12:K:84:VAL:HG23	12:K:109:VAL:O	2.01	0.60
20:S:81:ARG:O	20:S:81:ARG:HD3	2.02	0.60
21:T:83:ARG:O	21:T:86:ARG:HB3	2.02	0.60
1:A:192:U:O2'	1:A:193:C:H5'	2.01	0.60
1:A:706:A:HO2'	12:K:29:ILE:HD11	1.65	0.60
1:A:1158:C:C5'	3:B:133:LYS:HE3	2.32	0.60
4:C:23:TYR:C	4:C:23:TYR:CD2	2.79	0.60
8:G:46:ALA:HB1	8:G:121:ALA:HB2	1.84	0.60
9:H:138:TRP:HE3	9:H:138:TRP:OXT	1.84	0.60
13:L:83:VAL:HG21	13:L:100:ILE:HD13	1.84	0.60
16:O:41:GLU:HA	16:O:44:LYS:HG2	1.83	0.60
17:P:4:ILE:HG13	17:P:64:ALA:HB1	1.83	0.60
18:Q:53:LEU:HD23	18:Q:53:LEU:C	2.27	0.60
20:S:16:LEU:O	20:S:19:VAL:HG12	2.02	0.60
21:T:79:ARG:HH11	21:T:79:ARG:HG3	1.65	0.60
1:A:19:C:H2'	1:A:20:U:H6	1.67	0.60
1:A:235:C:C5'	18:Q:70:ARG:HG2	2.30	0.60
1:A:401:C:H2'	1:A:402:G:H8	1.66	0.60
1:A:1200:C:H1'	1:A:1204:A:N6	2.17	0.60
12:K:80:VAL:HG12	12:K:81:ASP:N	2.17	0.60
12:K:115:PRO:C	12:K:117:ASN:H	2.10	0.60
16:O:53:HIS:O	16:O:56:LEU:HB3	2.02	0.60
1:A:954:G:N2	1:A:1227:A:H62	1.94	0.60
3:B:12:GLU:C	3:B:14:GLY:N	2.57	0.60
10:I:70:LYS:O	10:I:74:ILE:HG13	2.02	0.60
17:P:51:VAL:O	17:P:53:VAL:N	2.35	0.60
21:T:92:LEU:O	21:T:94:ALA:N	2.35	0.60
1:A:932:C:H4'	8:G:4:ARG:NH2	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1003:G:H2'	1:A:1003(A):G:N7	2.17	0.59
1:A:1127:G:N2	1:A:1146:A:H62	1.99	0.59
1:A:1425:U:H3	1:A:1475:G:H1	1.50	0.59
1:A:1486:G:H2'	1:A:1487:G:O4'	2.02	0.59
1:A:107:G:C2'	1:A:108:G:H5'	2.33	0.59
1:A:451:A:N7	1:A:481:G:C2	2.71	0.59
1:A:818:G:C2'	1:A:819:A:H5''	2.33	0.59
1:A:344:A:H4'	1:A:345:C:OP2	2.02	0.59
1:A:519:C:H2'	1:A:520:A:C8	2.37	0.59
1:A:1495:U:H2'	1:A:1496:C:H6	1.67	0.59
7:F:69:GLU:OE1	7:F:69:GLU:N	2.35	0.59
10:I:49:PRO:HD3	10:I:78:LYS:HD3	1.83	0.59
11:J:68:HIS:H	11:J:68:HIS:HD2	1.50	0.59
14:M:40:ASN:HD22	14:M:41:PRO:N	2.00	0.59
15:N:35:ARG:O	15:N:37:PHE:N	2.35	0.59
16:O:87:ILE:O	16:O:88:ARG:HB2	2.02	0.59
1:A:413:G:H22	1:A:428:G:H1'	1.67	0.59
1:A:969:A:H61	14:M:126:LYS:HB2	1.66	0.59
1:A:1086:U:H3	1:A:1099:G:H22	1.49	0.59
3:B:168:THR:OG1	3:B:192:SER:HB3	2.01	0.59
8:G:76:ARG:HD2	8:G:89:MET:HE2	1.85	0.59
10:I:43:ALA:O	10:I:44:VAL:C	2.46	0.59
11:J:16:LEU:C	11:J:18:ALA:H	2.11	0.59
1:A:496:A:H4'	1:A:497:A:OP1	2.02	0.59
1:A:1003(A):G:C2'	1:A:1004:A:H4'	2.32	0.59
1:A:1238:A:N7	1:A:1303:C:H1'	2.17	0.59
3:B:180:LEU:O	3:B:181:PHE:HB2	2.03	0.59
3:B:221:LEU:O	3:B:221:LEU:HD13	2.03	0.59
4:C:40:ARG:HG3	4:C:40:ARG:NH1	2.15	0.59
4:C:206:GLU:O	4:C:207:VAL:O	2.19	0.59
11:J:59:SER:C	11:J:60:ARG:HD2	2.26	0.59
15:N:47:LEU:HD23	15:N:52:GLN:HG3	1.83	0.59
16:O:29:VAL:HG12	16:O:85:LEU:HD11	1.84	0.59
1:A:551:U:H2'	1:A:552:U:C6	2.37	0.59
1:A:1008:C:H2'	1:A:1009:G:C8	2.37	0.59
5:D:8:VAL:C	5:D:10:ARG:H	2.10	0.59
8:G:65:ALA:HB1	8:G:127:ALA:HB3	1.84	0.59
13:L:46:LYS:NZ	13:L:47:LYS:HE3	2.17	0.59
16:O:45:VAL:HG12	16:O:46:HIS:N	2.18	0.59
1:A:141:A:H1'	1:A:182:U:O2	2.03	0.59
3:B:187:LEU:HD21	3:B:203:GLY:HA3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:90:GLU:C	4:C:92:ALA:H	2.11	0.59
6:E:101:ILE:O	6:E:120:THR:HB	2.03	0.59
19:R:62:GLU:O	19:R:64:ARG:N	2.35	0.59
1:A:133:U:OP1	21:T:74:LYS:HE2	2.03	0.59
1:A:352:C:H4'	1:A:354:G:OP1	2.03	0.59
1:A:532:A:H2'	1:A:533:A:C5'	2.33	0.59
1:A:556:C:O2'	1:A:557:G:H5'	2.03	0.59
1:A:1064:G:H4'	1:A:1065:U:H5'	1.85	0.59
1:A:1190:G:OP1	4:C:4:LYS:HA	2.03	0.59
9:H:127:LEU:N	9:H:127:LEU:HD23	2.17	0.59
16:O:63:ARG:C	16:O:65:ARG:N	2.59	0.59
18:Q:66:SER:O	18:Q:70:ARG:NH1	2.36	0.59
1:A:197:A:N1	1:A:220:G:O2'	2.28	0.59
1:A:1207:G:H2'	1:A:1208:C:H6	1.66	0.59
1:A:1323:G:H2'	1:A:1324:A:C8	2.37	0.59
8:G:116:ALA:HA	8:G:119:ARG:CZ	2.32	0.59
9:H:134:ILE:HG22	9:H:135:CYS:N	2.17	0.59
14:M:33:ALA:O	14:M:37:THR:HB	2.03	0.59
21:T:66:ALA:HB3	21:T:72:LEU:HD12	1.85	0.59
1:A:243:A:C5'	1:A:244:U:H5'	2.32	0.59
1:A:921:U:O2	6:E:19:MET:HB2	2.03	0.59
1:A:1407:C:O2'	1:A:1408:A:H5'	2.03	0.59
6:E:96:PRO:HA	6:E:117:ASP:OD1	2.03	0.59
6:E:150:ARG:HB3	6:E:150:ARG:HH11	1.67	0.59
7:F:44:GLY:O	7:F:59:TYR:HA	2.03	0.59
9:H:4:ASP:OD2	9:H:7:ALA:HB2	2.03	0.59
14:M:34:LEU:CD1	14:M:41:PRO:HA	2.32	0.59
14:M:36:LYS:HD2	14:M:59:TYR:CZ	2.37	0.59
22:V:2:GLY:O	22:V:4:GLY:N	2.36	0.59
1:A:664:G:OP1	19:R:64:ARG:HD2	2.03	0.58
1:A:1251:A:H4'	10:I:12:GLU:OE2	2.03	0.58
4:C:134:ILE:HG21	4:C:167:TRP:O	2.03	0.58
5:D:196:LEU:C	5:D:198:VAL:H	2.11	0.58
9:H:9:MET:HE1	9:H:32:LYS:HA	1.85	0.58
10:I:10:ARG:HD2	10:I:11:LYS:N	2.18	0.58
16:O:34:LEU:C	16:O:34:LEU:HD23	2.28	0.58
20:S:5:LEU:O	20:S:6:LYS:CB	2.51	0.58
22:V:6:ARG:HB3	22:V:15:ARG:NH1	2.17	0.58
1:A:142:G:O2'	1:A:196:A:N1	2.31	0.58
1:A:513:C:H2'	1:A:514:C:C6	2.38	0.58
1:A:1184:G:H2'	1:A:1185:G:H8	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1193:G:O2'	1:A:1194:U:H5'	2.03	0.58
1:A:1326:C:OP1	22:V:12:LYS:NZ	2.36	0.58
1:A:1352:C:H2'	1:A:1353:G:H8	1.67	0.58
9:H:11:THR:HA	9:H:14:ARG:NH1	2.18	0.58
10:I:39:GLY:O	10:I:40:LEU:HD23	2.04	0.58
12:K:33:THR:HG1	12:K:38:ASN:C	2.10	0.58
14:M:49:THR:HB	14:M:52:GLU:HG3	1.85	0.58
17:P:75:ARG:O	17:P:78:GLY:N	2.36	0.58
21:T:59:ALA:O	21:T:63:ILE:HG13	2.03	0.58
1:A:353:A:C5'	1:A:353:A:H8	2.16	0.58
3:B:101:MET:CE	3:B:108:ILE:HD13	2.32	0.58
3:B:166:ASP:OD1	3:B:205:ASP:HB2	2.04	0.58
4:C:155:GLY:O	4:C:156:ARG:HB2	2.04	0.58
6:E:26:PHE:CD1	6:E:26:PHE:N	2.70	0.58
6:E:107:ARG:O	6:E:110:LEU:N	2.36	0.58
9:H:38:ILE:N	9:H:38:ILE:HD12	2.17	0.58
9:H:103:VAL:CG2	9:H:110:ALA:HB2	2.33	0.58
1:A:860:A:H2'	1:A:861:G:O4'	2.04	0.58
1:A:1046:A:H61	1:A:1213:A:H61	1.50	0.58
1:A:1347:G:C2'	1:A:1348:U:OP2	2.52	0.58
16:O:39:LEU:CD2	16:O:56:LEU:HB2	2.33	0.58
21:T:14:LYS:O	21:T:18:GLN:HG3	2.02	0.58
21:T:41:ILE:HG23	21:T:91:LEU:CD1	2.33	0.58
1:A:75:G:O2'	1:A:76:C:H5'	2.03	0.58
1:A:684:A:H4'	12:K:12:ARG:HH22	1.68	0.58
3:B:87:ARG:NH2	3:B:220:ASP:OD2	2.35	0.58
6:E:147:ASP:OD2	6:E:147:ASP:N	2.26	0.58
9:H:101:PRO:CG	9:H:133:LEU:HD11	2.34	0.58
10:I:19:LEU:C	10:I:20:ARG:HG3	2.29	0.58
11:J:15:THR:HG21	11:J:94:VAL:HG22	1.86	0.58
11:J:61:GLU:OE1	15:N:45:ARG:HD2	2.04	0.58
20:S:20:LEU:O	20:S:23:ASN:HB2	2.04	0.58
21:T:43:LEU:HD12	21:T:52:ALA:HA	1.84	0.58
1:A:291:C:O2'	1:A:292:G:H5'	2.04	0.58
1:A:735:C:O2'	1:A:736:C:H5'	2.04	0.58
1:A:1468:A:H2'	1:A:1469:G:O4'	2.04	0.58
1:A:1532:U:O5'	1:A:1532:U:H6	1.86	0.58
4:C:178:LEU:O	4:C:179:ARG:CB	2.51	0.58
4:C:191:THR:CG2	4:C:192:THR:N	2.43	0.58
7:F:97:PHE:N	19:R:30:ASP:OD1	2.37	0.58
18:Q:22:LEU:C	18:Q:22:LEU:HD12	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:A:H2'	1:A:102:G:H8	1.69	0.58
1:A:437:U:H2'	1:A:438:G:H5'	1.84	0.58
1:A:949:A:H2'	1:A:950:U:O4'	2.03	0.58
1:A:1285:A:H8	1:A:1285:A:OP1	1.86	0.58
1:A:1330:U:H2'	1:A:1331:G:H5'	1.84	0.58
1:A:1346:A:O2'	1:A:1347:G:OP2	2.21	0.58
3:B:84:GLU:HB3	3:B:219:VAL:HG21	1.84	0.58
3:B:101:MET:CA	3:B:108:ILE:HD12	2.25	0.58
10:I:4:TYR:CZ	10:I:88:TYR:HD1	2.22	0.58
10:I:79:LEU:O	10:I:82:ALA:HB3	2.04	0.58
17:P:28:ARG:NH1	17:P:28:ARG:HG2	2.17	0.58
1:A:80:G:C2'	1:A:81:U:H5''	2.33	0.58
1:A:657:G:O2'	1:A:658:G:H5'	2.04	0.58
1:A:807:A:H2'	1:A:808:C:C6	2.38	0.58
1:A:1164:G:H1	1:A:1172:C:H42	1.50	0.58
1:A:1230:C:H1'	14:M:126:LYS:HA	1.86	0.58
4:C:18:TRP:CD1	15:N:54:PRO:HA	2.39	0.58
9:H:6:ILE:HD12	9:H:35:ILE:CD1	2.33	0.58
14:M:94:ARG:HB3	14:M:96:LEU:HD12	1.86	0.58
14:M:122:LYS:HE3	14:M:122:LYS:HA	1.85	0.58
15:N:22:THR:OG1	15:N:33:VAL:HG21	2.04	0.58
16:O:82:ILE:O	16:O:83:GLU:C	2.46	0.58
1:A:451:A:C2	1:A:480:U:C4	2.90	0.58
1:A:663:A:O2'	1:A:664:G:H5'	2.03	0.58
1:A:684:A:H4'	12:K:12:ARG:NH2	2.19	0.58
1:A:926:G:H3'	1:A:1505:G:H21	1.68	0.58
1:A:933:G:O6	8:G:3:ARG:NH2	2.36	0.58
1:A:1182:G:O2'	1:A:1183:A:OP2	2.20	0.58
3:B:197:VAL:HB	3:B:200:ILE:CG1	2.33	0.58
6:E:94:ALA:HB1	6:E:98:THR:HG21	1.85	0.58
20:S:62:ILE:HD12	20:S:63:THR:H	1.69	0.58
1:A:353:A:C8	1:A:353:A:C5'	2.86	0.58
1:A:627:G:O2'	1:A:628:G:H5'	2.04	0.58
1:A:1229:A:H2'	1:A:1230:C:C6	2.38	0.58
1:A:1298:C:H4'	1:A:1299:A:O4'	2.03	0.58
5:D:8:VAL:C	5:D:10:ARG:N	2.59	0.58
6:E:146:ALA:O	6:E:149:GLU:HB3	2.04	0.58
15:N:29:ARG:HG3	15:N:30:ALA:N	2.19	0.58
1:A:1412:C:H2'	1:A:1413:A:H8	1.67	0.57
4:C:70:VAL:HG12	4:C:72:LYS:N	2.17	0.57
4:C:136:GLN:O	4:C:139:GLN:HB2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:2:ARG:CZ	7:F:69:GLU:HG2	2.34	0.57
14:M:78:ILE:O	14:M:81:LEU:HD23	2.04	0.57
17:P:45:THR:HB	17:P:46:PRO:HD2	1.84	0.57
20:S:40:ILE:HG21	20:S:62:ILE:CD1	2.34	0.57
1:A:335:C:H2'	1:A:336:C:C6	2.39	0.57
1:A:761:G:H4'	18:Q:103:GLY:N	2.18	0.57
3:B:48:MET:O	3:B:51:LEU:HB2	2.04	0.57
6:E:120:THR:CG2	6:E:121:LYS:N	2.67	0.57
13:L:47:LYS:CB	13:L:48:PRO:CD	2.83	0.57
18:Q:80:GLY:O	18:Q:81:ARG:HB3	2.04	0.57
1:A:112:G:H4'	1:A:389:A:H5''	1.85	0.57
1:A:328:C:H4'	1:A:329:A:O5'	2.03	0.57
1:A:921:U:O2'	6:E:19:MET:O	2.22	0.57
1:A:961:U:O2'	1:A:962:C:H5'	2.04	0.57
1:A:1202:G:H2'	1:A:1203:C:O4'	2.04	0.57
3:B:110:GLN:HA	3:B:113:HIS:HD2	1.69	0.57
4:C:116:VAL:HG21	4:C:202:ILE:HD11	1.85	0.57
10:I:127:LYS:HB2	14:M:126:LYS:HZ2	1.67	0.57
13:L:47:LYS:HB2	13:L:48:PRO:CD	2.32	0.57
1:A:179:A:H2'	1:A:180:U:H6	1.69	0.57
1:A:429:U:H4'	1:A:430:A:O5'	2.04	0.57
1:A:960:U:O2	1:A:960:U:H2'	2.03	0.57
1:A:1145:C:H1'	1:A:1146:A:H8	1.68	0.57
1:A:1238:A:H5'	1:A:1336:C:H41	1.70	0.57
16:O:6:GLU:H	16:O:6:GLU:CD	2.13	0.57
20:S:62:ILE:HD12	20:S:63:THR:N	2.19	0.57
1:A:580:U:H2'	1:A:581:G:O4'	2.05	0.57
1:A:970:C:N3	14:M:126:LYS:HB3	2.19	0.57
3:B:23:ARG:O	3:B:24:TRP:O	2.23	0.57
3:B:130:ARG:HD2	3:B:131:PRO:HD2	1.85	0.57
6:E:79:GLU:HB3	6:E:92:LYS:HA	1.86	0.57
13:L:83:VAL:HG22	13:L:84:LEU:N	2.19	0.57
1:A:791:G:H2'	1:A:792:A:C5'	2.34	0.57
1:A:1000:U:H2'	1:A:1001:A:O4'	2.04	0.57
6:E:148:VAL:CG1	6:E:152:ARG:HH21	2.16	0.57
8:G:137:LYS:O	8:G:141:VAL:HG23	2.03	0.57
21:T:50:GLU:HG2	21:T:100:ILE:HG13	1.85	0.57
1:A:440:A:H3'	1:A:442:C:H6	1.69	0.57
3:B:25:ASN:C	3:B:25:ASN:ND2	2.53	0.57
4:C:120:VAL:O	4:C:124:ILE:HG13	2.05	0.57
9:H:64:LYS:HG2	9:H:79:VAL:HG21	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:116:LYS:HD3	9:H:127:LEU:HD12	1.87	0.57
14:M:62:ASN:O	14:M:63:THR:CB	2.52	0.57
14:M:88:ARG:HG3	14:M:98:VAL:HG11	1.85	0.57
17:P:81:ARG:HB2	17:P:81:ARG:NH1	2.20	0.57
18:Q:97:SER:HB2	18:Q:103:GLY:CA	2.31	0.57
1:A:113:G:H1'	1:A:354:G:H5'	1.86	0.57
1:A:224:C:H2'	1:A:225:C:H6	1.69	0.57
1:A:309:G:O2'	1:A:310:G:H5'	2.04	0.57
1:A:1048:G:H5''	15:N:3:ARG:HG2	1.86	0.57
1:A:1497:G:H2'	1:A:1498:U:H5'	1.86	0.57
3:B:8:LYS:N	3:B:8:LYS:HD2	2.19	0.57
3:B:153:ARG:HG2	3:B:153:ARG:HH11	1.69	0.57
3:B:187:LEU:HD23	3:B:201:ILE:O	2.05	0.57
7:F:36:ARG:HG2	7:F:36:ARG:HH11	1.70	0.57
20:S:40:ILE:HG21	20:S:62:ILE:HD11	1.86	0.57
1:A:444:C:O2'	1:A:445:G:H5'	2.05	0.57
3:B:125:PRO:HG2	3:B:126:GLU:OE1	2.05	0.57
3:B:230:VAL:HG12	3:B:231:GLU:N	2.20	0.57
3:B:239:VAL:HB	3:B:240:GLN:HE22	1.67	0.57
4:C:34:LEU:HD22	4:C:38:ARG:HG2	1.87	0.57
8:G:47:CYS:SG	8:G:58:PRO:HB2	2.45	0.57
9:H:63:LEU:HD12	9:H:63:LEU:N	2.19	0.57
10:I:48:GLU:N	10:I:49:PRO:HD2	2.19	0.57
10:I:84:ALA:O	10:I:87:GLN:HB2	2.05	0.57
10:I:112:LYS:HD3	10:I:113:LYS:O	2.05	0.57
12:K:111:ASP:OD1	19:R:84:LYS:HE2	2.03	0.57
18:Q:92:ARG:O	18:Q:95:TYR:HB2	2.05	0.57
1:A:877:C:OP1	9:H:88:LYS:HE2	2.05	0.57
1:A:1495:U:H2'	1:A:1496:C:C6	2.40	0.57
5:D:7:PRO:HG2	5:D:10:ARG:CD	2.30	0.57
7:F:10:LEU:N	7:F:10:LEU:HD12	2.19	0.57
7:F:91:VAL:HG12	7:F:92:LYS:O	2.04	0.57
10:I:106:ALA:O	10:I:108:VAL:HG23	2.05	0.57
13:L:43:VAL:HG12	13:L:44:THR:N	2.19	0.57
16:O:56:LEU:HA	16:O:59:MET:HE2	1.87	0.57
20:S:16:LEU:HA	20:S:19:VAL:HG12	1.87	0.57
1:A:359:U:H2'	1:A:360:A:H8	1.70	0.56
1:A:452:A:O2'	1:A:453:A:O4'	2.21	0.56
1:A:592:G:H2'	1:A:593:G:H8	1.70	0.56
1:A:1394:A:C6	1:A:1501:C:H4'	2.40	0.56
3:B:111:ARG:HB3	3:B:149:LEU:HD11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:82:ARG:HA	7:F:82:ARG:HE	1.68	0.56
8:G:18:TYR:CD2	8:G:59:LEU:HB2	2.40	0.56
9:H:11:THR:HG22	9:H:15:ASN:ND2	2.20	0.56
1:A:129(A):G:O2'	1:A:190(E):U:H2'	2.06	0.56
1:A:356:A:H1'	1:A:368:U:O2'	2.06	0.56
4:C:10:PHE:CZ	4:C:178:LEU:HD13	2.40	0.56
10:I:8:GLY:HA2	10:I:79:LEU:HB3	1.86	0.56
11:J:45:ARG:O	11:J:64:GLU:HA	2.05	0.56
20:S:40:ILE:HD13	20:S:62:ILE:CD1	2.19	0.56
20:S:70:LYS:O	20:S:72:GLY:N	2.38	0.56
21:T:73:HIS:O	21:T:74:LYS:CB	2.51	0.56
1:A:456:C:H42	1:A:476:G:H1	1.53	0.56
1:A:474:G:H2'	1:A:475:G:H8	1.68	0.56
1:A:547:A:H4'	1:A:548:G:O5'	2.05	0.56
1:A:760:G:N1	18:Q:105:ALA:HA	2.10	0.56
1:A:999:C:O2'	1:A:1000:U:H5'	2.05	0.56
1:A:1091:U:O2	1:A:1093:A:H8	1.89	0.56
1:A:1117:G:H5'	1:A:1117:G:H8	1.68	0.56
1:A:1283:G:O2'	1:A:1284:C:H5'	2.05	0.56
1:A:1451:A:OP2	1:A:1452:C:C5	2.58	0.56
3:B:118:LEU:HB2	3:B:142:LEU:CD2	2.35	0.56
3:B:189:ASP:HB3	3:B:203:GLY:O	2.04	0.56
4:C:36:ASP:HB3	4:C:40:ARG:HH12	1.70	0.56
4:C:77:ILE:O	4:C:84:ILE:HG22	2.05	0.56
4:C:102:ASN:N	4:C:102:ASN:HD22	2.01	0.56
6:E:112:LEU:N	6:E:112:LEU:HD23	2.19	0.56
8:G:78:ARG:NH1	8:G:154:TYR:HB3	2.21	0.56
10:I:53:VAL:HG22	10:I:96:LEU:HD11	1.87	0.56
13:L:41:ARG:HH12	13:L:57:LYS:HE2	1.70	0.56
14:M:9:ILE:H	14:M:9:ILE:HD12	1.69	0.56
16:O:36:ILE:CG1	16:O:59:MET:HE3	2.36	0.56
16:O:36:ILE:HA	16:O:59:MET:HE1	1.86	0.56
16:O:55:GLY:O	16:O:59:MET:HG3	2.05	0.56
1:A:80:G:C3'	1:A:81:U:H5''	2.35	0.56
1:A:287:U:O2'	1:A:288:A:H5'	2.05	0.56
1:A:1370:G:H2'	1:A:1371:G:H8	1.70	0.56
1:A:1496:C:H2'	1:A:1497:G:O4'	2.05	0.56
1:A:1508:G:H2'	1:A:1509:C:C6	2.41	0.56
5:D:36:ARG:HG2	5:D:38:TYR:OH	2.06	0.56
5:D:110:PHE:O	5:D:161:ASN:ND2	2.38	0.56
7:F:50:TYR:CE1	19:R:77:GLY:HA2	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:8:GLY:CA	10:I:79:LEU:HD12	2.34	0.56
1:A:1133:G:H2'	1:A:1134:G:C8	2.32	0.56
1:A:1292:U:H5'	10:I:38:GLN:HE21	1.69	0.56
3:B:132:LYS:O	3:B:136:VAL:HG23	2.05	0.56
3:B:142:LEU:O	3:B:143:GLU:C	2.48	0.56
4:C:5:ILE:C	4:C:5:ILE:HD12	2.30	0.56
5:D:4:TYR:HD2	5:D:115:ARG:HH22	1.53	0.56
5:D:148:VAL:HG11	5:D:158:ILE:HG21	1.87	0.56
10:I:5:TYR:O	10:I:87:GLN:HG3	2.04	0.56
10:I:120:ARG:O	10:I:122:ALA:N	2.38	0.56
13:L:61:THR:C	13:L:63:GLY:H	2.13	0.56
19:R:53:ARG:HH22	19:R:60:GLY:HA2	1.71	0.56
20:S:19:VAL:HG13	20:S:20:LEU:N	2.20	0.56
1:A:390:C:H2'	1:A:391:G:H8	1.70	0.56
1:A:731:G:OP1	1:A:766:A:H1'	2.06	0.56
1:A:1430:C:O2'	1:A:1431:C:H5'	2.06	0.56
1:A:1515:C:O2'	1:A:1516:G:H5'	2.06	0.56
1:A:1526:G:H2'	1:A:1527:C:C6	2.41	0.56
3:B:75:LYS:C	3:B:77:ALA:H	2.13	0.56
6:E:80:ILE:HD11	6:E:91:LEU:HB2	1.88	0.56
9:H:97:VAL:HA	9:H:100:ILE:HD11	1.87	0.56
11:J:47:PHE:N	11:J:63:PHE:O	2.39	0.56
11:J:55:LYS:O	11:J:56:HIS:HB2	2.06	0.56
12:K:110:ASP:HB2	19:R:88:LYS:HZ2	1.71	0.56
13:L:75:HIS:HD2	13:L:77:LEU:N	2.01	0.56
14:M:9:ILE:HD12	14:M:9:ILE:N	2.20	0.56
15:N:22:THR:CB	15:N:33:VAL:HG21	2.35	0.56
17:P:22:THR:CA	17:P:33:ILE:HD12	2.31	0.56
1:A:1249:C:H2'	1:A:1250:A:H5'	1.88	0.56
3:B:148:TYR:CD2	3:B:148:TYR:N	2.71	0.56
4:C:129:ALA:HB3	4:C:132:ARG:HD2	1.88	0.56
4:C:139:GLN:O	4:C:142:MET:N	2.37	0.56
9:H:63:LEU:N	9:H:63:LEU:CD1	2.68	0.56
11:J:51:ARG:H	11:J:59:SER:HB3	1.69	0.56
16:O:63:ARG:O	16:O:65:ARG:N	2.39	0.56
1:A:723:U:H5'	1:A:724:G:OP2	2.06	0.56
1:A:1020:U:O2'	1:A:1021:G:H5'	2.06	0.56
1:A:1121:U:O2'	1:A:1122:U:H5'	2.06	0.56
1:A:1277:C:O2'	1:A:1279:A:H1'	2.05	0.56
3:B:33:TYR:O	3:B:34:ALA:HB2	2.05	0.56
5:D:108:LEU:CD1	5:D:183:GLY:HA3	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:12:LEU:H	8:G:12:LEU:HD12	1.70	0.56
11:J:51:ARG:CB	11:J:59:SER:HB3	2.26	0.56
16:O:81:LEU:CD2	16:O:85:LEU:HD12	2.35	0.56
1:A:151:A:H2'	1:A:152:A:O4'	2.06	0.56
1:A:543:C:C2'	1:A:544:G:H5'	2.36	0.56
1:A:559:A:P	6:E:126:ARG:HH22	2.27	0.56
1:A:1374:A:O2'	1:A:1375:A:H5'	2.05	0.56
3:B:45:GLN:O	3:B:48:MET:HB2	2.06	0.56
5:D:148:VAL:HG13	5:D:158:ILE:HD13	1.87	0.56
10:I:85:LEU:HD23	10:I:96:LEU:HD21	1.88	0.56
10:I:112:LYS:HD3	10:I:112:LYS:C	2.30	0.56
18:Q:59:ILE:HG23	18:Q:71:PHE:HB3	1.87	0.56
1:A:1491:G:H5''	13:L:46:LYS:HG3	1.88	0.56
5:D:92:VAL:HG12	5:D:96:LEU:HD21	1.88	0.56
8:G:66:VAL:O	8:G:68:ASN:N	2.39	0.56
14:M:40:ASN:ND2	14:M:41:PRO:HD2	2.19	0.56
1:A:321:A:O2'	1:A:322:C:H5'	2.06	0.55
1:A:620:C:H2'	1:A:621:A:O4'	2.06	0.55
13:L:48:PRO:C	13:L:49:ASN:HD22	2.14	0.55
18:Q:101:ARG:NE	18:Q:101:ARG:HA	2.21	0.55
19:R:47:THR:HG23	19:R:83:GLU:H	1.70	0.55
1:A:409:G:H2'	1:A:410:G:O4'	2.05	0.55
1:A:1039:C:H2'	1:A:1040:U:H6	1.70	0.55
4:C:180:ALA:HB1	4:C:203:PHE:HE1	1.71	0.55
5:D:38:TYR:HB2	5:D:39:PRO:HD2	1.88	0.55
7:F:60:PHE:CE2	19:R:78:LEU:HD21	2.41	0.55
10:I:86:VAL:HG21	10:I:102:LEU:HD11	1.86	0.55
1:A:359:U:H2'	1:A:360:A:C8	2.42	0.55
1:A:376:G:OP2	17:P:67:THR:HG21	2.05	0.55
1:A:949:A:N7	14:M:106:ASN:ND2	2.54	0.55
1:A:1346:A:C8	1:A:1348:U:C2	2.94	0.55
1:A:1346:A:C4	8:G:10:ARG:NH2	2.75	0.55
4:C:71:ALA:HA	4:C:106:VAL:HB	1.88	0.55
17:P:20:VAL:HG23	17:P:34:GLU:O	2.05	0.55
4:C:106:VAL:HG11	4:C:115:LEU:HD11	1.89	0.55
8:G:41:ARG:O	8:G:42:ILE:C	2.49	0.55
14:M:36:LYS:HD2	14:M:59:TYR:CE1	2.42	0.55
19:R:36:ASN:O	19:R:38:GLU:N	2.39	0.55
1:A:1064:G:C4'	1:A:1065:U:H5'	2.36	0.55
1:A:1211:U:H1'	1:A:1213:A:C2	2.41	0.55
3:B:7:VAL:O	3:B:8:LYS:HG3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:195:VAL:O	4:C:196:LEU:HD23	2.07	0.55
11:J:68:HIS:N	11:J:68:HIS:HD2	2.02	0.55
13:L:25:PRO:C	13:L:27:LEU:N	2.57	0.55
17:P:59:TRP:HB3	17:P:64:ALA:HB2	1.88	0.55
22:V:17:THR:O	22:V:22:ARG:NH1	2.38	0.55
1:A:80:G:H3'	1:A:81:U:H5''	1.88	0.55
1:A:386:C:H2'	1:A:387:U:H5'	1.88	0.55
1:A:1347:G:O2'	1:A:1348:U:OP2	2.24	0.55
1:A:1428:A:H2'	1:A:1429:C:C6	2.42	0.55
12:K:49:GLY:O	12:K:50:TYR:C	2.50	0.55
15:N:29:ARG:O	15:N:30:ALA:HB2	2.05	0.55
18:Q:67:LYS:CA	18:Q:70:ARG:HH12	2.16	0.55
20:S:49:ILE:HD12	20:S:49:ILE:N	2.20	0.55
1:A:851:G:H2'	1:A:852:G:H8	1.71	0.55
1:A:1250:A:H4'	10:I:68:GLY:CA	2.36	0.55
3:B:16:HIS:C	3:B:17:PHE:HD1	2.14	0.55
3:B:42:ILE:HD11	3:B:189:ASP:HB3	1.89	0.55
5:D:3:ARG:NH1	5:D:118:ARG:NH1	2.55	0.55
5:D:83:SER:HA	5:D:89:THR:HG23	1.86	0.55
6:E:80:ILE:CD1	6:E:91:LEU:HD12	2.37	0.55
6:E:92:LYS:O	6:E:118:ILE:HG22	2.07	0.55
18:Q:68:ARG:O	18:Q:69:LYS:HB2	2.06	0.55
19:R:35:ARG:C	19:R:37:VAL:H	2.15	0.55
1:A:263:A:P	21:T:79:ARG:HH12	2.29	0.55
1:A:1056:U:H5'	4:C:163:ALA:HB2	1.89	0.55
1:A:1057:G:O2'	1:A:1058:G:H5'	2.06	0.55
1:A:1191:A:OP1	4:C:4:LYS:HE3	2.07	0.55
3:B:45:GLN:OE1	3:B:45:GLN:N	2.35	0.55
3:B:135:GLN:O	3:B:135:GLN:HG2	2.07	0.55
4:C:56:ASP:O	4:C:57:ILE:HG13	2.07	0.55
5:D:157:LEU:O	5:D:161:ASN:HB2	2.07	0.55
6:E:89:ILE:HD13	6:E:90:VAL:H	1.71	0.55
9:H:51:VAL:HG11	9:H:60:ARG:NH1	2.22	0.55
13:L:98:TYR:N	13:L:98:TYR:CD1	2.74	0.55
14:M:122:LYS:CE	14:M:124:PRO:HD3	2.37	0.55
21:T:57:ARG:HE	21:T:102:GLY:HA3	1.71	0.55
1:A:164:U:H2'	1:A:165:C:C6	2.42	0.55
1:A:750:G:N3	16:O:23:GLY:HA3	2.22	0.55
1:A:794:A:H2'	1:A:795:C:C6	2.42	0.55
1:A:936:C:H2'	1:A:937:A:O4'	2.06	0.55
1:A:1504:G:OP1	1:A:1507:A:H4'	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:97:TRP:CZ3	3:B:173:ALA:HA	2.42	0.55
4:C:134:ILE:CD1	4:C:166:GLU:HB3	2.37	0.55
8:G:72:ARG:HH22	8:G:138:LYS:HZ1	1.55	0.55
9:H:104:ARG:NH2	9:H:138:TRP:CH2	2.75	0.55
1:A:148:G:H2'	1:A:149:A:C8	2.40	0.55
1:A:358:U:H2'	1:A:359:U:C6	2.42	0.55
1:A:833:U:H2'	1:A:834:C:C6	2.42	0.55
1:A:683:G:H21	12:K:38:ASN:HD22	1.56	0.54
1:A:736:C:H2'	1:A:737:A:C8	2.42	0.54
1:A:1245:A:H2'	1:A:1246:C:H6	1.71	0.54
3:B:88:ALA:HB2	3:B:219:VAL:HG13	1.89	0.54
4:C:67:THR:O	4:C:67:THR:HG22	2.07	0.54
4:C:116:VAL:O	4:C:120:VAL:HG23	2.06	0.54
5:D:30:LYS:C	5:D:32:ALA:N	2.65	0.54
5:D:141:ARG:HB2	5:D:141:ARG:NH1	2.23	0.54
8:G:15:ASP:O	8:G:19:GLY:HA2	2.07	0.54
8:G:143:ARG:O	8:G:145:ALA:O	2.25	0.54
9:H:20:TYR:CE2	9:H:75:ARG:HD2	2.42	0.54
9:H:20:TYR:HE2	9:H:75:ARG:HD2	1.71	0.54
11:J:51:ARG:H	11:J:59:SER:CB	2.20	0.54
20:S:52:TYR:HA	20:S:56:GLN:O	2.06	0.54
1:A:107:G:H2'	1:A:108:G:H5'	1.90	0.54
1:A:190(E):U:O4	18:Q:62:SER:HB3	2.07	0.54
1:A:229:U:O2'	1:A:230:G:H5'	2.08	0.54
1:A:877:C:H1'	9:H:3:THR:OG1	2.08	0.54
1:A:1300:G:O2'	1:A:1301:U:H6	1.90	0.54
3:B:144:ARG:O	3:B:147:LYS:HB2	2.07	0.54
7:F:1:MET:HG2	7:F:68:PRO:HG3	1.89	0.54
7:F:61:LEU:O	7:F:62:TRP:HB2	2.07	0.54
16:O:82:ILE:HG22	16:O:83:GLU:N	2.22	0.54
1:A:129(A):G:C2	1:A:190(E):U:H5'	2.42	0.54
1:A:224:C:H2'	1:A:225:C:C6	2.42	0.54
1:A:433:C:H2'	1:A:434:U:H6	1.72	0.54
1:A:1425:U:O2'	1:A:1426:C:H5'	2.07	0.54
5:D:119:GLN:HG2	5:D:123:HIS:CD2	2.42	0.54
6:E:110:LEU:O	6:E:115:VAL:HB	2.08	0.54
7:F:78:GLU:HA	7:F:81:ILE:HD11	1.89	0.54
7:F:100:ASN:HD22	19:R:23:LYS:CG	2.11	0.54
11:J:16:LEU:HA	11:J:19:SER:HB3	1.89	0.54
13:L:89:ARG:HA	13:L:97:ARG:HA	1.89	0.54
1:A:518:C:O2'	13:L:50:SER:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1333:A:H2'	1:A:1334:G:O4'	2.07	0.54
1:A:1370:G:H4'	10:I:12:GLU:OE1	2.08	0.54
3:B:74:LYS:HE3	3:B:166:ASP:HB2	1.90	0.54
3:B:95:GLN:HE21	3:B:147:LYS:HB3	1.73	0.54
4:C:113:ALA:HB3	4:C:114:PRO:HD3	1.90	0.54
7:F:10:LEU:HD12	7:F:10:LEU:H	1.72	0.54
7:F:91:VAL:HG13	19:R:72:ARG:NH2	2.23	0.54
10:I:111:ARG:HD3	10:I:112:LYS:C	2.32	0.54
14:M:19:LEU:HD23	14:M:22:ILE:HD11	1.89	0.54
15:N:21:TYR:HE2	15:N:23:ARG:NE	2.06	0.54
1:A:333:G:O2'	1:A:334:C:H5'	2.07	0.54
1:A:424:G:O2'	1:A:425:G:H5'	2.07	0.54
1:A:513:C:O2'	1:A:514:C:H5'	2.08	0.54
1:A:1196:U:OP1	1:A:1197:G:H5'	2.08	0.54
1:A:1286:A:H3'	1:A:1287:A:C5'	2.36	0.54
4:C:6:HIS:CD2	4:C:8:ILE:H	2.18	0.54
4:C:14:ILE:O	4:C:16:ARG:N	2.40	0.54
4:C:19:GLU:O	4:C:20:SER:HB2	2.07	0.54
4:C:22:TRP:CH2	4:C:32:LEU:HB2	2.42	0.54
10:I:8:GLY:CA	10:I:79:LEU:HB3	2.37	0.54
14:M:122:LYS:NZ	14:M:124:PRO:HD3	2.23	0.54
1:A:1004:A:N7	1:A:1037:C:N3	2.55	0.54
1:A:1096:C:O2'	1:A:1097:C:H5'	2.07	0.54
3:B:206:ASP:O	3:B:207:ALA:HB3	2.07	0.54
4:C:6:HIS:HD2	4:C:8:ILE:N	2.00	0.54
4:C:155:GLY:CA	4:C:164:ARG:H	2.21	0.54
5:D:31:CYS:O	5:D:31:CYS:SG	2.66	0.54
18:Q:86:GLU:O	18:Q:90:ILE:HG13	2.07	0.54
21:T:33:ILE:O	21:T:34:LYS:C	2.51	0.54
21:T:55:ILE:O	21:T:56:MET:C	2.48	0.54
1:A:182:U:OP2	1:A:183:G:C8	2.61	0.54
1:A:977:A:H2'	1:A:978:A:C5'	2.36	0.54
1:A:1068:G:N7	1:A:1094:G:H2'	2.23	0.54
4:C:28:GLN:O	4:C:30:ARG:N	2.41	0.54
8:G:79:ARG:NE	8:G:84:ASN:HD21	2.05	0.54
10:I:44:VAL:HG12	10:I:51:ARG:HH12	1.72	0.54
13:L:60:LEU:N	13:L:64:TYR:O	2.37	0.54
14:M:66:LEU:N	14:M:66:LEU:HD12	2.22	0.54
14:M:78:ILE:HA	14:M:81:LEU:CD2	2.38	0.54
16:O:30:ALA:HA	16:O:85:LEU:HD21	1.88	0.54
19:R:53:ARG:HA	19:R:56:THR:OG1	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:6:ARG:HB3	22:V:15:ARG:HH11	1.72	0.54
1:A:165:C:H2'	1:A:166:G:C8	2.42	0.54
1:A:266:G:H5'	1:A:266:G:C8	2.42	0.54
1:A:451:A:O5'	1:A:451:A:H8	1.90	0.54
1:A:1095:U:H2'	1:A:1096:C:H6	1.72	0.54
3:B:80:ILE:HD11	3:B:208:ILE:HG23	1.88	0.54
6:E:15:ARG:HG3	6:E:15:ARG:NH1	2.22	0.54
10:I:119:ALA:C	10:I:120:ARG:HG2	2.32	0.54
21:T:53:LEU:O	21:T:54:LYS:C	2.50	0.54
21:T:96:GLY:O	21:T:97:ALA:CB	2.56	0.54
1:A:1225:A:H2'	1:A:1225:A:N3	2.22	0.54
4:C:84:ILE:HD11	4:C:88:ARG:HH12	1.73	0.54
5:D:25:ARG:O	5:D:27:TYR:N	2.40	0.54
5:D:89:THR:O	5:D:90:GLY:C	2.51	0.54
8:G:15:ASP:HB3	8:G:19:GLY:H	1.72	0.54
8:G:21:VAL:CG2	8:G:22:LEU:N	2.70	0.54
8:G:156:TRP:CG	8:G:156:TRP:O	2.61	0.54
16:O:4:THR:HB	16:O:6:GLU:OE2	2.07	0.54
1:A:528:C:H5'	1:A:535:A:C6	2.43	0.54
1:A:781:A:H5'	1:A:782:A:OP2	2.08	0.54
1:A:913:A:H4'	1:A:914:A:O5'	2.07	0.54
1:A:1030(A):G:H3'	1:A:1030(B):C:H5''	1.89	0.54
3:B:17:PHE:HB3	3:B:44:LEU:CD2	2.38	0.54
3:B:151:GLY:C	3:B:153:ARG:N	2.61	0.54
3:B:206:ASP:O	3:B:207:ALA:CB	2.56	0.54
4:C:7:PRO:CG	4:C:184:TYR:HB2	2.38	0.54
6:E:31:LEU:HD22	6:E:43:LEU:CD2	2.38	0.54
10:I:9:ARG:CG	10:I:14:VAL:HG22	2.35	0.54
18:Q:82:MET:O	18:Q:83:ASP:C	2.50	0.54
21:T:41:ILE:HG23	21:T:91:LEU:HD13	1.90	0.54
21:T:56:MET:HE3	21:T:88:VAL:CG1	2.38	0.54
1:A:836:G:C6	1:A:851:G:C6	2.96	0.53
1:A:1106:G:H5''	4:C:172:ARG:HD3	1.89	0.53
1:A:1262:C:H42	1:A:1273:G:H1	1.55	0.53
1:A:1392:G:O2'	1:A:1502:A:H5''	2.07	0.53
3:B:12:GLU:C	3:B:14:GLY:H	2.15	0.53
3:B:45:GLN:CD	3:B:45:GLN:H	2.15	0.53
3:B:144:ARG:O	3:B:147:LYS:N	2.41	0.53
5:D:35:ARG:O	5:D:36:ARG:CB	2.56	0.53
7:F:55:ASP:HB3	7:F:86:ARG:HH12	1.73	0.53
10:I:7:THR:O	10:I:15:ALA:O	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:16:LEU:C	11:J:18:ALA:N	2.66	0.53
12:K:64:ALA:O	12:K:65:ALA:C	2.51	0.53
13:L:70:ILE:CD1	13:L:77:LEU:HD12	2.37	0.53
21:T:57:ARG:NH2	21:T:100:ILE:CG2	2.71	0.53
22:V:2:GLY:C	22:V:4:GLY:N	2.66	0.53
1:A:409:G:OP1	5:D:24:GLU:O	2.27	0.53
1:A:926:G:H5'	1:A:927:G:O5'	2.09	0.53
1:A:1313:U:OP2	20:S:6:LYS:HA	2.08	0.53
4:C:54:ARG:HG2	4:C:55:VAL:H	1.73	0.53
8:G:47:CYS:O	8:G:58:PRO:HB3	2.08	0.53
8:G:51:GLN:C	8:G:53:LYS:N	2.66	0.53
10:I:28:VAL:HG11	10:I:36:TYR:CD2	2.43	0.53
1:A:92:C:H2'	1:A:93:G:H8	1.74	0.53
1:A:437:U:H5''	5:D:155:LEU:HD22	1.90	0.53
1:A:972:C:C4'	11:J:57:LYS:HD2	2.34	0.53
1:A:1194:U:H2'	1:A:1195:C:H6	1.74	0.53
1:A:1367:C:C2	1:A:1368:G:C8	2.96	0.53
3:B:80:ILE:HG21	3:B:211:ILE:HG22	1.90	0.53
4:C:13:GLY:O	4:C:14:ILE:HD13	2.08	0.53
4:C:29:TYR:OH	15:N:54:PRO:HG2	2.08	0.53
4:C:47:LEU:CD2	4:C:68:VAL:HG11	2.38	0.53
4:C:152:ILE:HB	4:C:199:LYS:HB2	1.90	0.53
5:D:3:ARG:HD2	5:D:118:ARG:NH1	2.24	0.53
5:D:61:LYS:HA	5:D:203:VAL:HG22	1.91	0.53
7:F:48:LEU:HD13	7:F:52:ILE:CG1	2.38	0.53
10:I:65:VAL:HG13	10:I:65:VAL:O	2.08	0.53
10:I:69:GLY:O	10:I:73:GLN:HG3	2.07	0.53
10:I:112:LYS:O	10:I:112:LYS:CD	2.56	0.53
11:J:71:LEU:O	11:J:72:VAL:HB	2.07	0.53
19:R:62:GLU:O	19:R:65:ILE:N	2.40	0.53
1:A:186:C:O2	21:T:85:MET:HE1	2.08	0.53
1:A:336:C:O2'	1:A:337:C:H5'	2.08	0.53
1:A:397:A:H5'	1:A:398:C:P	2.48	0.53
1:A:401:C:H2'	1:A:402:G:C8	2.42	0.53
1:A:743:U:H2'	1:A:744:C:C6	2.44	0.53
1:A:839:U:O2	1:A:839:U:C2'	2.56	0.53
1:A:1478:C:H2'	1:A:1479:C:H6	1.73	0.53
1:A:1511:G:O2'	1:A:1512:U:H5'	2.08	0.53
4:C:139:GLN:O	4:C:140:ARG:C	2.51	0.53
15:N:14:PRO:O	15:N:15:LYS:HB3	2.08	0.53
1:A:1508:G:H2'	1:A:1509:C:H6	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:36:ASP:HA	4:C:39:ILE:HD12	1.89	0.53
5:D:3:ARG:HE	5:D:3:ARG:H	1.55	0.53
5:D:91:SER:O	5:D:92:VAL:C	2.51	0.53
9:H:119:LEU:CD1	9:H:124:ALA:HA	2.37	0.53
10:I:111:ARG:O	10:I:119:ALA:HB2	2.08	0.53
13:L:46:LYS:HG2	13:L:47:LYS:N	2.14	0.53
19:R:74:ARG:HB3	19:R:81:PHE:CE1	2.43	0.53
1:A:390:C:O3'	17:P:28:ARG:NH2	2.42	0.53
1:A:454:C:H41	1:A:478:A:H2	1.54	0.53
1:A:1320:C:N3	20:S:36:ARG:HD3	2.23	0.53
3:B:166:ASP:CG	3:B:205:ASP:HB2	2.34	0.53
5:D:19:LEU:O	5:D:21:LEU:HG	2.09	0.53
5:D:36:ARG:HG2	5:D:38:TYR:CZ	2.44	0.53
7:F:15:ASP:OD2	7:F:17:SER:HB2	2.07	0.53
7:F:29:ALA:O	7:F:30:LEU:C	2.52	0.53
11:J:39:PRO:O	11:J:70:ARG:HD3	2.09	0.53
12:K:44:SER:N	12:K:47:VAL:HB	2.19	0.53
13:L:86:ARG:HG3	13:L:86:ARG:NH1	2.23	0.53
15:N:23:ARG:HD3	15:N:29:ARG:O	2.09	0.53
22:V:5:ASP:O	22:V:11:GLY:HA3	2.08	0.53
1:A:92:C:O2'	1:A:93:G:H5'	2.09	0.53
1:A:330:C:H6	1:A:330:C:H5''	1.74	0.53
1:A:556:C:C2'	1:A:557:G:H5'	2.38	0.53
1:A:560:U:H4'	1:A:561:U:H5''	1.89	0.53
1:A:1218:C:H2'	1:A:1219:U:C6	2.43	0.53
1:A:1353:G:O2'	1:A:1354:C:H5'	2.08	0.53
3:B:121:LEU:HD22	3:B:126:GLU:HB3	1.89	0.53
4:C:52:LEU:HD23	4:C:52:LEU:N	2.24	0.53
4:C:188:LEU:O	4:C:189:ALA:HB2	2.09	0.53
5:D:3:ARG:NH2	5:D:71:SER:HB3	2.24	0.53
7:F:48:LEU:HD13	7:F:52:ILE:CD1	2.38	0.53
8:G:122:HIS:O	8:G:123:GLU:C	2.50	0.53
10:I:111:ARG:HD3	10:I:112:LYS:N	2.24	0.53
11:J:27:ALA:C	11:J:29:ARG:H	2.16	0.53
11:J:75:ILE:HG22	11:J:76:ASN:H	1.74	0.53
12:K:44:SER:H	12:K:47:VAL:CB	2.18	0.53
12:K:91:ARG:HD2	12:K:92:GLU:N	2.23	0.53
19:R:36:ASN:HD22	19:R:38:GLU:HG2	1.70	0.53
20:S:25:LYS:H	20:S:25:LYS:HD2	1.74	0.53
22:V:6:ARG:CD	22:V:15:ARG:HH12	2.10	0.53
22:V:9:ARG:O	22:V:13:ILE:HG13	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:528:C:H5'	1:A:535:A:N6	2.24	0.53
4:C:155:GLY:HA2	4:C:164:ARG:H	1.74	0.53
9:H:17:THR:HG22	9:H:63:LEU:HD23	1.90	0.53
19:R:45:SER:C	19:R:47:THR:H	2.16	0.53
21:T:16:HIS:CE1	21:T:20:LEU:HD11	2.43	0.53
1:A:124:G:C6	1:A:125:U:C4	2.97	0.53
1:A:269:C:H2'	1:A:270:A:H8	1.72	0.53
1:A:714:G:H2'	1:A:715:A:C8	2.44	0.53
1:A:897:C:H5'	18:Q:101:ARG:HH22	1.74	0.53
1:A:1263:C:H2'	1:A:1264:C:C6	2.43	0.53
3:B:182:ILE:O	3:B:183:PRO:C	2.51	0.53
6:E:15:ARG:HG3	6:E:15:ARG:HH11	1.74	0.53
8:G:125:MET:O	8:G:128:ALA:HB3	2.08	0.53
10:I:93:ARG:HD3	10:I:97:LYS:HZ2	1.74	0.53
10:I:125:TYR:CD1	10:I:128:ARG:HB2	2.43	0.53
13:L:38:THR:HG22	13:L:39:VAL:CG2	2.39	0.53
14:M:40:ASN:HD22	14:M:40:ASN:C	2.14	0.53
15:N:14:PRO:O	15:N:15:LYS:CB	2.56	0.53
16:O:70:LEU:O	16:O:71:GLN:C	2.51	0.53
18:Q:4:LYS:HE3	18:Q:6:LEU:HD21	1.91	0.53
1:A:482:A:H2'	1:A:483:C:O4'	2.08	0.53
1:A:737:A:H2'	1:A:738:C:C6	2.44	0.53
1:A:953:G:H1'	14:M:125:ARG:HA	1.89	0.53
1:A:1348:U:H2'	1:A:1349:A:C8	2.29	0.53
3:B:87:ARG:HB3	3:B:219:VAL:HG11	1.91	0.53
5:D:157:LEU:HD23	5:D:157:LEU:C	2.34	0.53
18:Q:81:ARG:HB2	18:Q:83:ASP:OD1	2.08	0.53
1:A:329:A:H4'	1:A:330:C:OP1	2.09	0.52
1:A:682:G:O2'	1:A:683:G:H5'	2.09	0.52
1:A:992:U:H4'	1:A:993:G:O5'	2.08	0.52
1:A:1278:U:C4'	1:A:1279:A:H5'	2.35	0.52
11:J:34:VAL:HG13	11:J:73:ASP:O	2.09	0.52
13:L:89:ARG:HG2	13:L:97:ARG:HA	1.90	0.52
14:M:80:ARG:C	14:M:82:MET:N	2.67	0.52
21:T:100:ILE:O	21:T:101:GLY:C	2.52	0.52
1:A:518:C:H4'	1:A:519:C:O5'	2.09	0.52
1:A:1028:C:C2'	1:A:1029:C:H5'	2.38	0.52
1:A:1154:G:H2'	1:A:1155:G:C8	2.36	0.52
1:A:1231:G:C4'	10:I:126:SER:HB3	2.32	0.52
1:A:1392:G:O2'	1:A:1393:U:H5'	2.09	0.52
4:C:132:ARG:O	4:C:133:ALA:C	2.53	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:63:LYS:O	5:D:64:LEU:C	2.52	0.52
5:D:149:ALA:HB3	5:D:152:SER:CB	2.38	0.52
8:G:18:TYR:N	8:G:18:TYR:CD1	2.77	0.52
8:G:109:ASN:HA	8:G:119:ARG:HE	1.74	0.52
16:O:82:ILE:HD13	16:O:88:ARG:HG2	1.92	0.52
18:Q:104:LYS:O	18:Q:105:ALA:HB2	2.07	0.52
20:S:36:ARG:NH2	20:S:75:ALA:HB3	2.23	0.52
1:A:666:G:H5'	1:A:726:C:H1'	1.92	0.52
1:A:818:G:C3'	1:A:819:A:H5''	2.38	0.52
1:A:1049:U:H1'	1:A:1201:A:N7	2.24	0.52
1:A:1086:U:O5'	1:A:1086:U:C6	2.62	0.52
1:A:1244:C:O2'	1:A:1245:A:H5'	2.08	0.52
6:E:107:ARG:O	6:E:108:ALA:C	2.51	0.52
9:H:23:SER:O	9:H:24:THR:CB	2.57	0.52
13:L:24:VAL:O	13:L:26:ALA:N	2.42	0.52
15:N:44:LEU:C	15:N:44:LEU:HD12	2.34	0.52
16:O:43:LEU:HA	16:O:45:VAL:O	2.10	0.52
18:Q:29:HIS:CG	18:Q:30:PRO:HD2	2.44	0.52
19:R:58:LEU:CD1	19:R:66:LEU:HD22	2.39	0.52
1:A:601:C:O2'	1:A:602:A:H5'	2.10	0.52
1:A:925:G:C2	1:A:927:G:C8	2.98	0.52
5:D:96:LEU:HD22	5:D:96:LEU:H	1.72	0.52
7:F:15:ASP:HB3	7:F:18:GLN:HG3	1.91	0.52
7:F:101:ALA:CB	19:R:28:GLU:HB2	2.39	0.52
10:I:23:ASN:HD22	10:I:23:ASN:C	2.17	0.52
11:J:15:THR:CG2	11:J:94:VAL:HG22	2.40	0.52
14:M:14:ARG:HG3	14:M:44:ARG:NH1	2.25	0.52
15:N:44:LEU:HD12	15:N:44:LEU:O	2.09	0.52
1:A:665:A:H2'	1:A:732:C:O2	2.09	0.52
1:A:1007:C:O2'	1:A:1008:C:H5'	2.10	0.52
1:A:1055:A:C2	1:A:1056:U:H1'	2.45	0.52
4:C:6:HIS:NE2	4:C:8:ILE:HB	2.24	0.52
11:J:80:LYS:HD3	11:J:83:GLU:HB2	1.91	0.52
14:M:91:ARG:HB2	14:M:98:VAL:HG13	1.92	0.52
15:N:9:LYS:HD3	15:N:9:LYS:C	2.35	0.52
16:O:36:ILE:HA	16:O:59:MET:CE	2.39	0.52
1:A:1091:U:C2	1:A:1093:A:OP2	2.62	0.52
1:A:1365:G:O2'	1:A:1366:C:H5'	2.10	0.52
1:A:1367:C:H5'	11:J:60:ARG:HH12	1.74	0.52
1:A:1392:G:H2'	1:A:1393:U:H6	1.74	0.52
3:B:7:VAL:N	3:B:8:LYS:HZ2	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:23:ARG:HH12	3:B:191:ASP:HA	1.71	0.52
3:B:130:ARG:CB	3:B:131:PRO:HD2	2.40	0.52
5:D:190:ASP:O	5:D:193:ASP:HB2	2.09	0.52
13:L:26:ALA:O	13:L:27:LEU:O	2.28	0.52
1:A:440:A:H5''	1:A:442:C:C5	2.45	0.52
1:A:481:G:O2'	1:A:482:A:C8	2.57	0.52
1:A:501:C:O2'	1:A:502:G:H5'	2.10	0.52
1:A:893:C:H2'	1:A:894:G:H8	1.73	0.52
1:A:1003(A):G:H2'	1:A:1004:A:O4'	2.08	0.52
10:I:46:ALA:O	10:I:49:PRO:HD2	2.10	0.52
15:N:12:ARG:O	15:N:13:THR:C	2.53	0.52
20:S:51:VAL:HB	20:S:75:ALA:HB2	1.92	0.52
21:T:11:SER:HA	21:T:13:LEU:HD11	1.92	0.52
1:A:1256:A:O2'	1:A:1257:U:H4'	2.10	0.52
1:A:1411:C:O2'	1:A:1412:C:H5'	2.10	0.52
3:B:97:TRP:CZ2	3:B:101:MET:HB2	2.44	0.52
5:D:191:ARG:O	5:D:191:ARG:HD2	2.10	0.52
6:E:33:VAL:HG11	6:E:109:ILE:HA	1.91	0.52
11:J:60:ARG:O	11:J:61:GLU:O	2.28	0.52
12:K:47:VAL:HG12	12:K:48:ILE:HG13	1.91	0.52
13:L:54:LYS:N	13:L:54:LYS:HD2	2.24	0.52
14:M:84:ILE:O	14:M:86:CYS:N	2.43	0.52
16:O:70:LEU:CD1	16:O:78:TYR:HB2	2.37	0.52
17:P:28:ARG:NH1	17:P:29:ASP:OD2	2.43	0.52
22:V:6:ARG:O	22:V:12:LYS:HE2	2.09	0.52
1:A:920:U:H2'	1:A:921:U:C6	2.45	0.52
1:A:939:G:H2'	1:A:940:C:C6	2.45	0.52
1:A:1528:U:O2'	1:A:1530:G:H5'	2.10	0.52
3:B:101:MET:HE2	3:B:108:ILE:HD13	1.90	0.52
4:C:131:ARG:O	4:C:135:LYS:HG3	2.10	0.52
13:L:27:LEU:HG	13:L:28:LYS:N	2.23	0.52
13:L:77:LEU:HD21	13:L:107:ALA:HB2	1.92	0.52
14:M:5:ALA:O	14:M:6:GLY:C	2.52	0.52
14:M:123:ALA:O	14:M:124:PRO:C	2.53	0.52
17:P:60:LEU:HD23	17:P:64:ALA:HB3	1.92	0.52
18:Q:98:LEU:O	18:Q:98:LEU:HD13	2.09	0.52
21:T:94:ALA:O	21:T:95:ALA:HB3	2.09	0.52
1:A:514:C:O2'	1:A:515:G:H5'	2.09	0.52
1:A:518:C:H5''	1:A:519:C:C6	2.45	0.52
1:A:713:G:H2'	1:A:714:G:C8	2.45	0.52
1:A:775:G:O2'	1:A:776:G:H5'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:960:U:H1'	1:A:1223:C:H5'	1.92	0.52
1:A:1286:A:C8	1:A:1287:A:H5''	2.45	0.52
3:B:204:ASN:HB3	3:B:206:ASP:O	2.10	0.52
4:C:10:PHE:CE2	4:C:178:LEU:HD13	2.45	0.52
10:I:93:ARG:O	10:I:98:PRO:HD3	2.10	0.52
11:J:6:ILE:CD1	11:J:72:VAL:HB	2.40	0.52
11:J:31:GLY:HA2	11:J:78:ASN:HD22	1.75	0.52
11:J:91:PRO:HB2	11:J:94:VAL:HG21	1.92	0.52
12:K:16:SER:HB3	12:K:79:SER:OG	2.10	0.52
15:N:17:LYS:HB2	15:N:17:LYS:HZ3	1.75	0.52
15:N:21:TYR:CD2	15:N:21:TYR:O	2.63	0.52
16:O:46:HIS:C	16:O:48:LYS:N	2.66	0.52
19:R:21:LYS:HD2	19:R:21:LYS:N	2.25	0.52
1:A:628:G:H2'	1:A:629:G:C8	2.45	0.51
1:A:737:A:H2'	1:A:738:C:H6	1.75	0.51
4:C:134:ILE:CG2	4:C:151:VAL:HB	2.36	0.51
5:D:10:ARG:HH11	5:D:10:ARG:HG3	1.75	0.51
5:D:25:ARG:NH1	5:D:30:LYS:HB3	2.26	0.51
6:E:13:ILE:HG22	6:E:30:ALA:CB	2.40	0.51
9:H:80:ILE:O	9:H:80:ILE:HG22	2.10	0.51
12:K:74:ALA:C	12:K:76:GLY:H	2.19	0.51
12:K:88:GLY:C	12:K:90:GLY:H	2.16	0.51
1:A:636:U:H5'	18:Q:2:PRO:HG2	1.92	0.51
1:A:1116:C:H2'	1:A:1117:G:C5'	2.30	0.51
1:A:1423:G:O2'	1:A:1424:C:H5'	2.10	0.51
3:B:80:ILE:HD11	3:B:208:ILE:CG1	2.39	0.51
3:B:82:ARG:O	3:B:86:GLU:HG3	2.10	0.51
3:B:239:VAL:O	3:B:239:VAL:HG12	2.10	0.51
4:C:23:TYR:CE2	4:C:24:ALA:O	2.63	0.51
4:C:76:VAL:O	4:C:83:ARG:HB3	2.10	0.51
4:C:137:ALA:O	4:C:138:VAL:C	2.53	0.51
9:H:83:ILE:HG23	9:H:83:ILE:O	2.11	0.51
12:K:29:ILE:HA	12:K:44:SER:HA	1.91	0.51
15:N:28:GLY:O	15:N:29:ARG:O	2.28	0.51
17:P:67:THR:C	17:P:69:THR:N	2.68	0.51
18:Q:45:HIS:HB2	18:Q:69:LYS:HE2	1.93	0.51
22:V:20:LYS:O	22:V:20:LYS:HG2	2.09	0.51
1:A:434:U:H2'	1:A:435:C:C6	2.45	0.51
1:A:765:G:N2	1:A:812:C:O2'	2.42	0.51
1:A:1032:G:H2'	1:A:1033:G:O4'	2.10	0.51
1:A:1179:A:H2'	1:A:1180:A:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1238:A:H5'	1:A:1336:C:N4	2.25	0.51
1:A:1329:A:P	14:M:28:ALA:HB3	2.51	0.51
3:B:81:VAL:O	3:B:82:ARG:C	2.52	0.51
4:C:11:ARG:O	4:C:14:ILE:O	2.28	0.51
4:C:189:ALA:HB3	4:C:196:LEU:O	2.11	0.51
5:D:28:SER:HB2	5:D:29:PRO:CD	2.40	0.51
17:P:70:ALA:O	17:P:74:LEU:HG	2.11	0.51
17:P:74:LEU:O	17:P:79:VAL:HG23	2.10	0.51
18:Q:67:LYS:O	18:Q:68:ARG:HB3	2.10	0.51
19:R:58:LEU:HD22	19:R:62:GLU:CB	2.40	0.51
20:S:45:VAL:HA	20:S:62:ILE:HG13	1.91	0.51
1:A:255:G:O6	1:A:266:G:O6	2.28	0.51
1:A:437:U:H2'	1:A:438:G:C5'	2.40	0.51
1:A:893:C:H2'	1:A:894:G:C8	2.45	0.51
1:A:993:G:H4'	1:A:994:A:OP2	2.10	0.51
1:A:1372:U:C2'	1:A:1373:G:H5'	2.41	0.51
1:A:1510:U:H2'	1:A:1511:G:C8	2.45	0.51
3:B:20:GLU:HG2	3:B:189:ASP:OD2	2.10	0.51
5:D:30:LYS:O	5:D:32:ALA:N	2.44	0.51
9:H:65:TYR:HA	9:H:79:VAL:HG23	1.93	0.51
13:L:22:SER:C	13:L:24:VAL:H	2.19	0.51
14:M:86:CYS:SG	14:M:88:ARG:HB3	2.50	0.51
1:A:539:A:H2'	1:A:540:G:C8	2.45	0.51
1:A:684:A:O2'	1:A:685:G:H5'	2.10	0.51
1:A:787:A:H2'	1:A:788:U:H6	1.74	0.51
1:A:919:A:O2'	1:A:920:U:H5'	2.10	0.51
1:A:1475:G:H2'	1:A:1476:G:C8	2.44	0.51
7:F:36:ARG:NH1	7:F:36:ARG:HG2	2.26	0.51
7:F:53:ALA:C	7:F:55:ASP:H	2.19	0.51
7:F:82:ARG:O	7:F:85:VAL:HB	2.11	0.51
8:G:15:ASP:HB3	8:G:20:ASP:H	1.76	0.51
8:G:24:THR:HG22	8:G:28:ASN:HD21	1.74	0.51
9:H:48:TYR:CD1	9:H:48:TYR:C	2.88	0.51
16:O:39:LEU:O	16:O:40:SER:C	2.54	0.51
1:A:542:G:H5'	5:D:41:GLY:HA3	1.93	0.51
1:A:620:C:N1	5:D:135:LEU:HD13	2.25	0.51
1:A:736:C:H2'	1:A:737:A:H8	1.75	0.51
1:A:1245:A:H2'	1:A:1246:C:C6	2.45	0.51
1:A:1304:G:C6	1:A:1305:G:N1	2.79	0.51
1:A:1402:C:O2	1:A:1500:A:N1	2.43	0.51
1:A:1525:G:P	12:K:120:ARG:HH22	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:154:SER:OG	4:C:155:GLY:N	2.44	0.51
11:J:12:ASP:OD2	11:J:14:LYS:HD3	2.11	0.51
14:M:59:TYR:O	14:M:59:TYR:CG	2.64	0.51
18:Q:69:LYS:C	18:Q:70:ARG:HD2	2.35	0.51
19:R:62:GLU:C	19:R:64:ARG:H	2.19	0.51
21:T:57:ARG:O	21:T:58:LYS:C	2.54	0.51
21:T:79:ARG:O	21:T:80:ARG:C	2.53	0.51
1:A:106:C:O2	1:A:379:C:H4'	2.10	0.51
1:A:156:G:O2'	1:A:157:G:H5'	2.10	0.51
1:A:252:U:H2'	1:A:253:U:C6	2.45	0.51
1:A:393:A:C2	1:A:394:G:C8	2.99	0.51
1:A:418:C:H2'	1:A:419:C:H6	1.76	0.51
1:A:475:G:H2'	1:A:476:G:C8	2.45	0.51
1:A:792:A:H4'	1:A:793:U:H5''	1.92	0.51
1:A:1086:U:O5'	1:A:1086:U:H6	1.93	0.51
1:A:1231:G:H4'	10:I:126:SER:CB	2.32	0.51
3:B:10:LEU:C	3:B:12:GLU:H	2.19	0.51
4:C:107:GLN:CD	4:C:107:GLN:N	2.57	0.51
5:D:88:VAL:O	5:D:92:VAL:HG23	2.10	0.51
8:G:79:ARG:HH21	8:G:84:ASN:HD21	1.58	0.51
1:A:403:C:H2'	1:A:404:U:H6	1.75	0.51
1:A:538:G:H2'	1:A:539:A:C8	2.45	0.51
3:B:15:VAL:O	3:B:16:HIS:O	2.29	0.51
3:B:183:PRO:HA	3:B:198:ASP:OD2	2.11	0.51
4:C:85:ARG:HD2	4:C:85:ARG:O	2.10	0.51
5:D:61:LYS:HD3	5:D:206:PHE:CE2	2.46	0.51
13:L:6:THR:OG1	13:L:9:GLN:HG3	2.10	0.51
21:T:54:LYS:O	21:T:57:ARG:HB2	2.11	0.51
1:A:129(A):G:O2'	1:A:190(E):U:H5''	2.11	0.51
1:A:149:A:O2'	1:A:150:C:H5'	2.09	0.51
1:A:1038:C:H2'	1:A:1039:C:H6	1.76	0.51
3:B:24:TRP:HB3	3:B:40:HIS:CE1	2.46	0.51
3:B:25:ASN:HD22	3:B:26:PRO:N	2.09	0.51
7:F:5:GLU:O	7:F:90:VAL:HA	2.11	0.51
8:G:108:ALA:C	8:G:110:GLN:H	2.18	0.51
8:G:147:ALA:C	8:G:149:ARG:H	2.17	0.51
12:K:94:ALA:O	12:K:97:ALA:HB3	2.09	0.51
12:K:110:ASP:HB2	19:R:88:LYS:HD3	1.93	0.51
14:M:81:LEU:O	14:M:89:GLY:HA3	2.11	0.51
16:O:11:VAL:HG21	16:O:34:LEU:CD1	2.40	0.51
19:R:52:PRO:O	19:R:56:THR:HG23	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:A:H8	1:A:143:A:O5'	1.94	0.51
1:A:913:A:O2'	1:A:914:A:OP2	2.28	0.51
1:A:1171:G:O2'	1:A:1172:C:H5'	2.11	0.51
1:A:1230:C:H2'	1:A:1231:G:H8	1.76	0.51
1:A:1478:C:H2'	1:A:1479:C:C6	2.46	0.51
4:C:5:ILE:C	4:C:5:ILE:CD1	2.84	0.51
8:G:46:ALA:HB2	8:G:117:ALA:O	2.11	0.51
14:M:44:ARG:HB2	14:M:47:ASP:OD2	2.10	0.51
16:O:39:LEU:HD22	16:O:56:LEU:HB2	1.91	0.51
20:S:20:LEU:HA	20:S:23:ASN:HB2	1.92	0.51
1:A:411:A:N9	1:A:413:G:H1'	2.27	0.50
1:A:518:C:HO2'	13:L:50:SER:HB3	1.76	0.50
1:A:1481:U:H2'	1:A:1482:G:O4'	2.11	0.50
4:C:126:ARG:C	4:C:127:ARG:HG3	2.35	0.50
5:D:56:VAL:HG12	5:D:57:ARG:N	2.25	0.50
7:F:30:LEU:C	7:F:35:ALA:HB3	2.36	0.50
10:I:118:LYS:NZ	10:I:118:LYS:CB	2.75	0.50
13:L:45:PRO:HG3	13:L:53:ARG:HD3	1.93	0.50
13:L:70:ILE:HG12	13:L:100:ILE:HD12	1.92	0.50
13:L:75:HIS:HA	13:L:102:ARG:NH2	2.25	0.50
17:P:43:LYS:HD3	17:P:48:TRP:CZ2	2.47	0.50
19:R:62:GLU:C	19:R:64:ARG:N	2.67	0.50
20:S:41:VAL:CG2	20:S:44:MET:HG3	2.41	0.50
20:S:53:ASN:HD22	20:S:53:ASN:N	2.08	0.50
21:T:50:GLU:HA	21:T:100:ILE:HG13	1.92	0.50
21:T:54:LYS:HA	21:T:57:ARG:HD3	1.94	0.50
1:A:425:G:O2'	1:A:426:G:H5'	2.12	0.50
1:A:460:A:N7	1:A:462:G:C6	2.79	0.50
1:A:1128:C:O2'	1:A:1130:A:C8	2.51	0.50
3:B:102:LEU:HB3	3:B:180:LEU:HD12	1.91	0.50
4:C:32:LEU:H	4:C:32:LEU:CD1	2.24	0.50
4:C:191:THR:HG22	4:C:193:TYR:H	1.76	0.50
5:D:25:ARG:NH2	5:D:30:LYS:HD3	2.25	0.50
5:D:162:LEU:HD13	5:D:181:MET:HG2	1.93	0.50
9:H:120:THR:HG23	9:H:123:GLU:OE2	2.10	0.50
14:M:70:LEU:O	14:M:72:ALA:N	2.44	0.50
17:P:43:LYS:HD3	17:P:48:TRP:CH2	2.47	0.50
19:R:34:TYR:CD1	19:R:34:TYR:O	2.63	0.50
1:A:489:C:H2'	1:A:490:G:H8	1.76	0.50
1:A:625:G:H2'	1:A:626:U:H6	1.75	0.50
1:A:781:A:H2	1:A:1514:C:O4'	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:915:A:C2'	1:A:916:G:H5'	2.42	0.50
1:A:971:G:C8	1:A:1365:G:H4'	2.45	0.50
1:A:1238:A:C8	1:A:1303:C:H1'	2.46	0.50
3:B:177:ALA:O	3:B:180:LEU:N	2.42	0.50
5:D:17:VAL:HG12	5:D:18:LYS:H	1.76	0.50
14:M:40:ASN:ND2	14:M:40:ASN:C	2.67	0.50
14:M:122:LYS:HE3	14:M:123:ALA:N	2.26	0.50
1:A:267:C:OP2	18:Q:67:LYS:HD2	2.11	0.50
1:A:393:A:C2'	1:A:394:G:H5'	2.42	0.50
1:A:1040:U:H2'	1:A:1041:A:C8	2.46	0.50
1:A:1056:U:O2'	1:A:1057:G:H5'	2.12	0.50
3:B:16:HIS:O	3:B:17:PHE:HD1	1.95	0.50
3:B:53:ARG:HG3	3:B:56:ARG:HH21	1.77	0.50
3:B:91:PRO:HB3	3:B:151:GLY:O	2.10	0.50
4:C:70:VAL:HG21	4:C:76:VAL:HG21	1.92	0.50
5:D:114:ARG:HG3	5:D:114:ARG:NH1	2.23	0.50
5:D:201:GLN:NE2	6:E:116:THR:OG1	2.44	0.50
7:F:78:GLU:HA	7:F:81:ILE:CD1	2.41	0.50
10:I:44:VAL:HG12	10:I:51:ARG:NH1	2.27	0.50
11:J:55:LYS:HG3	11:J:56:HIS:N	2.26	0.50
19:R:25:THR:O	19:R:26:LEU:HD13	2.10	0.50
1:A:92:C:H2'	1:A:93:G:C8	2.46	0.50
1:A:131:C:H2'	1:A:132:C:C6	2.47	0.50
1:A:967:C:H4'	10:I:128:ARG:CG	2.34	0.50
1:A:1005:A:N6	1:A:1024:G:H1'	2.25	0.50
4:C:19:GLU:HG2	4:C:54:ARG:HE	1.75	0.50
5:D:8:VAL:O	5:D:10:ARG:N	2.44	0.50
5:D:59:ARG:O	5:D:60:GLU:C	2.54	0.50
6:E:150:ARG:HH11	6:E:150:ARG:CB	2.25	0.50
8:G:22:LEU:CD1	8:G:101:LEU:HD11	2.42	0.50
8:G:124:LEU:O	8:G:127:ALA:HB3	2.11	0.50
9:H:86:ILE:HD12	9:H:135:CYS:HA	1.94	0.50
17:P:75:ARG:O	17:P:77:ALA:N	2.43	0.50
18:Q:97:SER:O	18:Q:103:GLY:N	2.45	0.50
19:R:17:SER:OG	19:R:55:ARG:HD3	2.11	0.50
19:R:58:LEU:HD11	19:R:66:LEU:HD22	1.93	0.50
1:A:411:A:C6	1:A:429:U:C4	3.00	0.50
1:A:412:A:N1	5:D:35:ARG:HB3	2.26	0.50
1:A:878:G:H5'	9:H:89:PRO:HG2	1.92	0.50
1:A:979:C:C2'	1:A:980:C:H5'	2.40	0.50
1:A:1086:U:C2'	1:A:1087:G:H5'	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1408:A:O2'	1:A:1409:C:H5'	2.12	0.50
3:B:142:LEU:HB3	3:B:146:GLN:NE2	2.25	0.50
4:C:15:THR:O	4:C:16:ARG:HB2	2.11	0.50
6:E:152:ARG:NH2	9:H:107:LEU:O	2.44	0.50
10:I:120:ARG:O	10:I:121:ARG:C	2.54	0.50
13:L:75:HIS:HA	13:L:102:ARG:HH22	1.76	0.50
13:L:119:LYS:O	13:L:120:TYR:CB	2.59	0.50
1:A:256:U:H5'	18:Q:17:LYS:NZ	2.27	0.50
1:A:1491:G:C5	23:A:1545:PAR:H21	2.47	0.50
5:D:149:ALA:O	5:D:150:GLU:C	2.55	0.50
8:G:57:GLU:O	8:G:58:PRO:C	2.54	0.50
8:G:113:GLU:CG	8:G:119:ARG:HG2	2.40	0.50
8:G:133:GLY:O	8:G:137:LYS:HG3	2.12	0.50
11:J:23:ILE:HD12	11:J:23:ILE:N	2.24	0.50
14:M:3:ARG:HA	14:M:8:GLU:O	2.12	0.50
14:M:22:ILE:HD12	14:M:25:ILE:CD1	2.36	0.50
14:M:84:ILE:HD12	20:S:66:MET:HB3	1.93	0.50
16:O:38:ARG:HG3	16:O:38:ARG:NH1	2.26	0.50
17:P:4:ILE:O	17:P:66:PRO:HA	2.11	0.50
18:Q:97:SER:CB	18:Q:103:GLY:HA2	2.31	0.50
1:A:280:C:O2	18:Q:38:ARG:HG3	2.12	0.50
3:B:24:TRP:HZ3	3:B:29:ALA:HB2	1.77	0.50
3:B:73:THR:HG23	3:B:95:GLN:O	2.12	0.50
3:B:130:ARG:HH21	4:C:207:VAL:HG22	1.76	0.50
5:D:65:ARG:HG3	5:D:75:PHE:CG	2.46	0.50
5:D:150:GLU:HA	5:D:153:ARG:NE	2.26	0.50
6:E:109:ILE:HG21	6:E:135:THR:CG2	2.42	0.50
15:N:3:ARG:O	15:N:4:LYS:C	2.52	0.50
1:A:538:G:H2'	1:A:539:A:H8	1.75	0.50
1:A:1320:C:O2'	1:A:1321:C:H5'	2.12	0.50
3:B:178:ARG:NH1	3:B:178:ARG:CG	2.69	0.50
4:C:83:ARG:C	4:C:85:ARG:N	2.68	0.50
5:D:105:VAL:HG13	5:D:110:PHE:HB2	1.94	0.50
6:E:144:THR:HG22	6:E:146:ALA:H	1.77	0.50
9:H:48:TYR:HB2	9:H:60:ARG:O	2.11	0.50
14:M:3:ARG:CA	14:M:9:ILE:HG23	2.41	0.50
18:Q:59:ILE:CD1	18:Q:73:VAL:HA	2.42	0.50
19:R:36:ASN:CG	19:R:39:VAL:HB	2.36	0.50
1:A:182:U:O4	1:A:223:U:H1'	2.12	0.49
1:A:358:U:O2'	1:A:359:U:H5'	2.12	0.49
1:A:1086:U:O2'	1:A:1087:G:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1325:C:O2'	1:A:1326:C:H5'	2.11	0.49
3:B:16:HIS:O	3:B:17:PHE:O	2.30	0.49
8:G:18:TYR:HD2	8:G:59:LEU:HB2	1.77	0.49
15:N:35:ARG:C	15:N:37:PHE:N	2.70	0.49
17:P:10:GLY:CA	17:P:16:HIS:H	2.25	0.49
18:Q:83:ASP:CG	18:Q:84:LEU:H	2.20	0.49
21:T:54:LYS:HG3	21:T:100:ILE:HD12	1.93	0.49
1:A:192:U:C1'	21:T:103:GLY:HA2	2.42	0.49
1:A:670:G:H2'	1:A:671:G:O4'	2.12	0.49
1:A:938:A:H2'	1:A:939:G:H5'	1.94	0.49
4:C:100:ALA:O	4:C:101:LEU:HB2	2.12	0.49
9:H:30:ARG:O	9:H:33:GLU:HB3	2.12	0.49
10:I:118:LYS:C	10:I:120:ARG:H	2.19	0.49
11:J:59:SER:O	11:J:60:ARG:HB2	2.11	0.49
11:J:63:PHE:HE2	15:N:58:LYS:HG2	1.77	0.49
14:M:110:ARG:HG2	14:M:110:ARG:HH11	1.76	0.49
19:R:44:LEU:HD22	19:R:48:GLY:O	2.12	0.49
20:S:34:TRP:N	20:S:34:TRP:HE3	2.11	0.49
1:A:821:G:H2'	1:A:822:C:H6	1.76	0.49
1:A:913:A:H1'	1:A:914:A:O4'	2.12	0.49
3:B:67:THR:CG2	3:B:68:ILE:N	2.74	0.49
3:B:137:ARG:HB3	3:B:137:ARG:HH11	1.77	0.49
4:C:14:ILE:O	4:C:15:THR:C	2.55	0.49
11:J:18:ALA:HA	11:J:21:GLN:HB3	1.94	0.49
1:A:560:U:O2'	1:A:561:U:OP2	2.24	0.49
1:A:1327:C:H5''	22:V:20:LYS:HB3	1.94	0.49
3:B:21:ARG:CG	3:B:22:LYS:H	2.24	0.49
8:G:77:SER:HA	8:G:86:GLN:NE2	2.27	0.49
11:J:23:ILE:H	11:J:23:ILE:CD1	2.23	0.49
14:M:17:VAL:O	14:M:20:THR:HB	2.12	0.49
17:P:53:VAL:O	17:P:54:GLU:C	2.53	0.49
1:A:39:G:N7	1:A:547:A:H8	2.11	0.49
1:A:386:C:O2'	1:A:387:U:H5'	2.13	0.49
1:A:865:A:H5'	1:A:1078:U:O4	2.13	0.49
1:A:1174:G:O2'	1:A:1175:G:H5'	2.12	0.49
6:E:74:GLY:CA	6:E:116:THR:HG22	2.42	0.49
16:O:62:GLN:NE2	16:O:66:LEU:HD21	2.24	0.49
19:R:42:ARG:NH1	19:R:42:ARG:HB3	2.26	0.49
20:S:9:VAL:CG1	20:S:10:PHE:N	2.67	0.49
20:S:80:TYR:O	20:S:81:ARG:C	2.55	0.49
1:A:397:A:H3'	1:A:397:A:N3	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:792:A:H4'	1:A:793:U:C5'	2.42	0.49
1:A:1060:C:HO2'	1:A:1061:G:H5'	1.77	0.49
1:A:1483:A:H2'	1:A:1484:C:O4'	2.12	0.49
3:B:19:HIS:O	3:B:20:GLU:O	2.30	0.49
3:B:30:ARG:HG3	3:B:31:TYR:CD2	2.47	0.49
3:B:208:ILE:C	3:B:210:SER:N	2.69	0.49
4:C:22:TRP:CE3	4:C:22:TRP:O	2.65	0.49
4:C:43:LEU:HD13	4:C:68:VAL:CG2	2.42	0.49
7:F:26:ILE:HG21	7:F:63:TYR:CE2	2.48	0.49
10:I:17:VAL:HG11	10:I:81:ILE:HA	1.95	0.49
13:L:55:VAL:CG1	13:L:56:ALA:N	2.76	0.49
17:P:13:HIS:C	17:P:15:PRO:CD	2.85	0.49
17:P:58:TYR:O	17:P:61:SER:N	2.45	0.49
1:A:105:G:H2'	1:A:106:C:H6	1.74	0.49
1:A:590:C:O2'	1:A:591:U:H5'	2.13	0.49
1:A:628:G:H2'	1:A:629:G:H8	1.78	0.49
1:A:1299:A:C8	1:A:1301:U:H1'	2.48	0.49
1:A:1488:G:O2'	1:A:1489:G:H5'	2.11	0.49
3:B:12:GLU:OE1	3:B:12:GLU:O	2.30	0.49
3:B:67:THR:HG22	3:B:68:ILE:H	1.74	0.49
4:C:56:ASP:O	4:C:57:ILE:CG1	2.60	0.49
4:C:167:TRP:O	4:C:168:ALA:HB3	2.12	0.49
5:D:100:ARG:HB3	5:D:102:ASP:OD1	2.13	0.49
6:E:73:ASN:ND2	6:E:73:ASN:C	2.70	0.49
6:E:73:ASN:C	6:E:73:ASN:HD22	2.20	0.49
10:I:15:ALA:HB2	10:I:65:VAL:HG23	1.94	0.49
11:J:51:ARG:N	11:J:59:SER:HB3	2.27	0.49
12:K:82:VAL:CG2	12:K:105:VAL:HG13	2.39	0.49
16:O:3:ILE:HA	16:O:7:GLU:OE1	2.13	0.49
21:T:84:LEU:HD23	21:T:84:LEU:C	2.38	0.49
1:A:408:A:O2'	1:A:409:G:H5'	2.12	0.49
1:A:851:G:H2'	1:A:852:G:C8	2.48	0.49
1:A:967:C:H2'	1:A:968:A:C8	2.48	0.49
1:A:1281:U:H5'	1:A:1282:C:C5	2.45	0.49
3:B:151:GLY:O	3:B:153:ARG:N	2.46	0.49
4:C:102:ASN:N	4:C:102:ASN:ND2	2.61	0.49
5:D:61:LYS:NZ	5:D:62:GLN:NE2	2.60	0.49
5:D:146:ILE:N	5:D:146:ILE:CD1	2.75	0.49
10:I:26:VAL:HG11	10:I:63:ILE:HD12	1.95	0.49
11:J:34:VAL:HG12	11:J:35:SER:N	2.27	0.49
18:Q:35:VAL:O	18:Q:35:VAL:HG12	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:81:ARG:HG3	18:Q:81:ARG:O	2.13	0.49
21:T:18:GLN:O	21:T:19:SER:C	2.54	0.49
1:A:1075:C:H5'	3:B:103:THR:HG21	1.94	0.49
1:A:1216:G:H5''	15:N:5:ALA:HB2	1.95	0.49
3:B:95:GLN:HG3	3:B:147:LYS:O	2.13	0.49
3:B:224:GLN:O	3:B:224:GLN:HG2	2.12	0.49
5:D:3:ARG:HD2	5:D:118:ARG:HH11	1.78	0.49
5:D:205:GLU:OE1	6:E:100:VAL:HG23	2.13	0.49
8:G:72:ARG:HH22	8:G:138:LYS:NZ	2.10	0.49
10:I:7:THR:HB	10:I:83:ARG:NH1	2.28	0.49
10:I:99:LEU:HD22	10:I:99:LEU:N	2.28	0.49
11:J:31:GLY:HA2	11:J:78:ASN:ND2	2.27	0.49
11:J:64:GLU:HG3	15:N:59:ALA:HA	1.95	0.49
14:M:15:VAL:HB	14:M:34:LEU:HD11	1.92	0.49
20:S:3:ARG:HH22	20:S:69:HIS:CE1	2.30	0.49
21:T:10:LEU:C	21:T:12:ALA:H	2.21	0.49
1:A:325:A:H2'	1:A:326:G:O4'	2.12	0.49
1:A:474:G:H2'	1:A:475:G:C8	2.47	0.49
1:A:707:C:O2'	1:A:708:C:H5'	2.13	0.49
1:A:1292:U:C5'	10:I:38:GLN:HE21	2.25	0.49
1:A:1330:U:C2'	1:A:1331:G:H5'	2.41	0.49
1:A:1356:G:H2'	1:A:1357:A:H8	1.73	0.49
3:B:97:TRP:CE2	3:B:101:MET:HG3	2.48	0.49
7:F:62:TRP:CD1	19:R:35:ARG:NH1	2.81	0.49
8:G:73:MET:SD	8:G:90:GLU:HA	2.53	0.49
8:G:138:LYS:C	8:G:138:LYS:CD	2.86	0.49
9:H:35:ILE:HG22	9:H:39:LEU:CD2	2.43	0.49
10:I:118:LYS:O	10:I:119:ALA:CB	2.59	0.49
11:J:12:ASP:OD1	11:J:14:LYS:N	2.46	0.49
12:K:77:MET:CE	12:K:80:VAL:HG22	2.43	0.49
15:N:35:ARG:C	15:N:37:PHE:H	2.20	0.49
16:O:67:LEU:O	16:O:68:ARG:C	2.56	0.49
19:R:16:PRO:O	19:R:17:SER:HB3	2.13	0.49
20:S:67:VAL:HG12	20:S:68:GLY:N	2.27	0.49
1:A:110:C:C4	1:A:111:G:C5	3.01	0.48
1:A:479:C:H2'	1:A:480:U:O4'	2.13	0.48
1:A:696:A:H2'	1:A:697:U:O4'	2.13	0.48
1:A:900:A:H2'	1:A:901:A:C8	2.48	0.48
1:A:1065:U:O2'	1:A:1066:C:OP2	2.25	0.48
1:A:1141:C:O2'	1:A:1142:G:H5'	2.13	0.48
1:A:1151:A:O2'	1:A:1152:A:H8	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1182:G:H4'	1:A:1183:A:O5'	2.14	0.48
1:A:1250:A:C5'	10:I:68:GLY:N	2.63	0.48
1:A:1292:U:H5'	10:I:38:GLN:NE2	2.28	0.48
4:C:39:ILE:HG22	4:C:40:ARG:N	2.28	0.48
4:C:42:LEU:HD11	4:C:94:LEU:HD13	1.95	0.48
5:D:17:VAL:CG1	5:D:18:LYS:N	2.76	0.48
5:D:196:LEU:C	5:D:198:VAL:N	2.71	0.48
6:E:116:THR:C	6:E:117:ASP:OD2	2.56	0.48
8:G:31:MET:HA	8:G:39:ALA:HB2	1.94	0.48
9:H:11:THR:O	9:H:12:ARG:C	2.56	0.48
9:H:36:LEU:CD1	9:H:59:LEU:HD13	2.43	0.48
13:L:119:LYS:O	13:L:120:TYR:HB2	2.13	0.48
15:N:22:THR:O	15:N:23:ARG:HB2	2.13	0.48
1:A:389:A:H2'	1:A:390:C:C5'	2.43	0.48
1:A:720:C:H2'	1:A:721:G:N7	2.28	0.48
1:A:1195:C:C3'	1:A:1196:U:H5''	2.34	0.48
1:A:1300:G:O2'	1:A:1301:U:P	2.70	0.48
1:A:1329:A:O2'	1:A:1330:U:H5'	2.12	0.48
1:A:1501:C:OP2	1:A:1504:G:H2'	2.13	0.48
3:B:24:TRP:CZ3	3:B:26:PRO:HA	2.48	0.48
3:B:72:GLY:HA3	3:B:81:VAL:HG21	1.95	0.48
7:F:40:VAL:HG12	7:F:63:TYR:CD1	2.41	0.48
11:J:49:VAL:HG12	15:N:41:ARG:HB2	1.94	0.48
13:L:83:VAL:HG21	13:L:100:ILE:CD1	2.43	0.48
20:S:62:ILE:HD12	20:S:66:MET:HG3	1.94	0.48
1:A:29:G:O2'	1:A:30:U:H5'	2.13	0.48
1:A:1408:A:C6	1:A:1494:G:C6	3.02	0.48
3:B:19:HIS:CG	3:B:20:GLU:H	2.30	0.48
4:C:30:ARG:HG2	4:C:30:ARG:HH11	1.78	0.48
5:D:126:ILE:HG22	5:D:127:THR:N	2.28	0.48
5:D:148:VAL:CG1	5:D:158:ILE:HD13	2.43	0.48
10:I:33:PHE:HZ	10:I:46:ALA:HB3	1.78	0.48
11:J:56:HIS:O	11:J:57:LYS:C	2.56	0.48
14:M:11:ARG:CG	14:M:12:ASN:N	2.75	0.48
17:P:67:THR:HG22	17:P:69:THR:H	1.78	0.48
22:V:12:LYS:O	22:V:13:ILE:C	2.56	0.48
1:A:19:C:H5''	6:E:86:ALA:CB	2.43	0.48
1:A:149:A:H2'	1:A:150:C:C6	2.49	0.48
1:A:194:C:H2'	1:A:195:A:H5''	1.95	0.48
1:A:411:A:C4	1:A:413:G:H1'	2.49	0.48
1:A:615:C:O2'	1:A:616:G:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:848:C:H2'	1:A:849:C:C6	2.48	0.48
1:A:965:A:O2'	1:A:966:G:OP2	2.28	0.48
1:A:976:G:H8	1:A:1358:U:H2'	1.79	0.48
1:A:1223:C:H3'	1:A:1224:G:H5''	1.95	0.48
3:B:15:VAL:HG11	3:B:209:ARG:O	2.13	0.48
3:B:97:TRP:CZ3	3:B:176:GLU:OE2	2.66	0.48
4:C:191:THR:HG21	4:C:193:TYR:CZ	2.48	0.48
6:E:6:PHE:HB3	6:E:34:VAL:HG13	1.96	0.48
10:I:17:VAL:CG2	10:I:80:GLY:HA3	2.43	0.48
13:L:38:THR:O	13:L:79:GLU:HG3	2.14	0.48
14:M:56:LEU:O	14:M:57:ARG:C	2.57	0.48
15:N:39:LEU:HD13	15:N:47:LEU:HD12	1.95	0.48
17:P:56:ALA:O	17:P:57:ARG:C	2.55	0.48
1:A:19:C:H5''	6:E:86:ALA:HB3	1.95	0.48
1:A:397:A:H5'	1:A:398:C:OP1	2.13	0.48
1:A:1131:G:H2'	1:A:1132:C:C6	2.47	0.48
3:B:93:VAL:HG11	3:B:97:TRP:HD1	1.79	0.48
8:G:72:ARG:NH2	8:G:138:LYS:NZ	2.61	0.48
10:I:50:LEU:CB	10:I:55:ALA:HB3	2.43	0.48
11:J:51:ARG:HE	11:J:61:GLU:HB2	1.74	0.48
11:J:53:PRO:HA	15:N:41:ARG:HH21	1.78	0.48
12:K:123:LYS:HA	12:K:126:ARG:HG3	1.96	0.48
13:L:110:VAL:O	13:L:122:THR:HG21	2.13	0.48
14:M:39:ILE:HG23	14:M:52:GLU:OE2	2.14	0.48
18:Q:19:VAL:HG23	18:Q:19:VAL:O	2.14	0.48
1:A:633:G:H2'	1:A:634:C:C6	2.48	0.48
1:A:951:G:O2'	1:A:952:U:H5'	2.14	0.48
1:A:1108:G:H5'	1:A:1191:A:H4'	1.94	0.48
1:A:1162:C:H2'	1:A:1163:C:C6	2.49	0.48
1:A:1202:G:C2'	1:A:1203:C:H5'	2.43	0.48
1:A:1286:A:C3'	1:A:1287:A:C5'	2.85	0.48
3:B:15:VAL:CG1	3:B:209:ARG:HG3	2.43	0.48
5:D:162:LEU:HD23	5:D:162:LEU:O	2.14	0.48
7:F:40:VAL:O	7:F:41:GLU:HG3	2.13	0.48
8:G:15:ASP:OD2	8:G:18:TYR:HD1	1.96	0.48
13:L:126:LYS:N	13:L:126:LYS:HD2	2.29	0.48
15:N:14:PRO:HB2	15:N:16:PHE:O	2.14	0.48
18:Q:16:GLN:O	18:Q:17:LYS:HB2	2.14	0.48
18:Q:63:ARG:HG2	18:Q:64:PRO:N	2.29	0.48
1:A:961:U:C2'	1:A:962:C:H5'	2.44	0.48
1:A:1345:U:C2	1:A:1377:A:C2	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1529:G:H4'	1:A:1530:G:OP2	2.14	0.48
3:B:16:HIS:CE1	3:B:210:SER:HG	2.27	0.48
3:B:76:GLN:HB2	3:B:206:ASP:OD1	2.14	0.48
5:D:173:TRP:CD1	5:D:189:PRO:HD3	2.49	0.48
6:E:139:LEU:O	6:E:140:ARG:C	2.55	0.48
8:G:77:SER:O	8:G:78:ARG:HB2	2.13	0.48
8:G:140:ASP:HA	8:G:143:ARG:HD2	1.95	0.48
10:I:127:LYS:HB2	14:M:126:LYS:HZ1	1.78	0.48
11:J:35:SER:HB2	11:J:72:VAL:O	2.14	0.48
12:K:17:GLY:O	12:K:80:VAL:HG13	2.14	0.48
15:N:41:ARG:HG3	15:N:42:ILE:N	2.29	0.48
18:Q:97:SER:HB3	18:Q:102:GLY:C	2.38	0.48
19:R:48:GLY:O	19:R:74:ARG:NH2	2.37	0.48
22:V:2:GLY:C	22:V:4:GLY:H	2.21	0.48
22:V:9:ARG:CZ	22:V:22:ARG:HG3	2.43	0.48
1:A:266:G:O2'	1:A:267:C:OP2	2.30	0.48
1:A:457:C:H2'	1:A:458:C:H6	1.78	0.48
1:A:586:C:O2'	1:A:587:G:H5'	2.13	0.48
1:A:938:A:H8	1:A:938:A:O5'	1.96	0.48
1:A:1001:A:O2'	1:A:1002:G:H8	1.96	0.48
1:A:1178:G:H22	1:A:1180:A:H3'	1.78	0.48
3:B:79:ASP:O	3:B:80:ILE:C	2.56	0.48
4:C:71:ALA:CA	4:C:106:VAL:HB	2.44	0.48
4:C:178:LEU:O	4:C:179:ARG:HB2	2.13	0.48
5:D:13:ARG:HD3	5:D:36:ARG:O	2.13	0.48
16:O:3:ILE:HD13	16:O:34:LEU:CD2	2.43	0.48
18:Q:83:ASP:CG	18:Q:84:LEU:N	2.71	0.48
21:T:57:ARG:HG2	21:T:57:ARG:NH1	2.29	0.48
21:T:59:ALA:O	21:T:60:GLU:C	2.55	0.48
21:T:60:GLU:HG3	21:T:81:LYS:HE3	1.96	0.48
1:A:401:C:O2'	1:A:402:G:H5'	2.14	0.48
1:A:421:U:C4'	1:A:422:C:OP2	2.62	0.48
1:A:619:U:N3	5:D:134:ASP:OD1	2.46	0.48
1:A:969:A:O2'	1:A:970:C:H5'	2.13	0.48
3:B:23:ARG:HH11	3:B:24:TRP:HA	1.79	0.48
4:C:83:ARG:C	4:C:85:ARG:H	2.22	0.48
8:G:20:ASP:OD2	8:G:63:LYS:NZ	2.44	0.48
8:G:110:GLN:OE1	8:G:110:GLN:HA	2.14	0.48
10:I:8:GLY:HA2	10:I:79:LEU:CD1	2.41	0.48
10:I:98:PRO:C	10:I:99:LEU:HD22	2.39	0.48
16:O:46:HIS:C	16:O:48:LYS:H	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:70:LEU:HD11	16:O:78:TYR:N	2.29	0.48
16:O:76:GLU:O	16:O:77:ARG:C	2.57	0.48
20:S:44:MET:O	20:S:47:HIS:HB2	2.14	0.48
1:A:973:G:H3'	1:A:974:A:H5''	1.96	0.48
1:A:1251:A:H4'	10:I:12:GLU:OE1	2.13	0.48
1:A:1255:G:H2'	1:A:1279:A:H62	1.79	0.48
1:A:1264:C:H2'	1:A:1265:G:C8	2.48	0.48
1:A:1420:C:H2'	1:A:1421:G:C8	2.49	0.48
1:A:1525:G:OP1	12:K:120:ARG:NH2	2.46	0.48
1:A:1531:A:O5'	1:A:1531:A:H8	1.96	0.48
9:H:86:ILE:HG21	9:H:133:LEU:HD22	1.96	0.48
17:P:18:ARG:O	17:P:20:VAL:HG12	2.14	0.48
21:T:16:HIS:HE1	21:T:20:LEU:HD11	1.78	0.48
1:A:99:C:H2'	1:A:101:A:O4'	2.14	0.47
1:A:420:U:H2'	1:A:422:C:C5	2.49	0.47
1:A:737:A:H1'	7:F:73:ASN:HD21	1.78	0.47
1:A:817:C:H1'	1:A:819:A:H5'	1.96	0.47
1:A:1030(A):G:C3'	1:A:1030(B):C:H5''	2.44	0.47
1:A:1402:C:H2'	1:A:1403:C:O4'	2.14	0.47
3:B:25:ASN:O	3:B:27:LYS:N	2.47	0.47
3:B:231:GLU:HB2	3:B:232:PRO:HD2	1.95	0.47
5:D:146:ILE:HD12	5:D:146:ILE:H	1.79	0.47
5:D:173:TRP:HB2	5:D:187:ARG:O	2.14	0.47
8:G:78:ARG:O	8:G:84:ASN:HA	2.13	0.47
9:H:93:VAL:O	9:H:93:VAL:HG12	2.14	0.47
11:J:63:PHE:CE1	15:N:45:ARG:HG3	2.49	0.47
12:K:40:ILE:HG22	12:K:41:THR:N	2.29	0.47
1:A:190:C:H2'	1:A:190(A):C:C6	2.50	0.47
1:A:302:G:N3	1:A:556:C:H4'	2.29	0.47
1:A:983:A:H3'	1:A:983:A:N3	2.29	0.47
1:A:1473:A:H2'	1:A:1474:G:C8	2.49	0.47
1:A:1494:G:OP2	23:A:1545:PAR:N32	2.46	0.47
3:B:55:PHE:O	3:B:56:ARG:C	2.58	0.47
3:B:115:LEU:HD11	3:B:146:GLN:HG2	1.94	0.47
4:C:58:GLU:O	4:C:59:ARG:CG	2.62	0.47
4:C:70:VAL:O	4:C:106:VAL:N	2.41	0.47
8:G:65:ALA:HB1	8:G:127:ALA:CB	2.43	0.47
10:I:44:VAL:O	10:I:45:ALA:C	2.57	0.47
10:I:81:ILE:O	10:I:85:LEU:HB2	2.14	0.47
11:J:91:PRO:HB2	11:J:94:VAL:CG2	2.44	0.47
17:P:50:LYS:C	17:P:50:LYS:HD3	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:76:LEU:C	18:Q:76:LEU:CD2	2.87	0.47
20:S:25:LYS:HD2	20:S:25:LYS:N	2.29	0.47
20:S:51:VAL:O	20:S:58:VAL:HG22	2.14	0.47
1:A:39:G:N7	1:A:547:A:C8	2.83	0.47
1:A:112:G:H21	1:A:354:G:C5'	2.24	0.47
1:A:160:A:H2'	1:A:161:A:O4'	2.14	0.47
1:A:633:G:H2'	1:A:634:C:H6	1.79	0.47
1:A:806:C:H2'	1:A:807:A:H8	1.78	0.47
1:A:922:G:H4'	6:E:20:GLN:HA	1.94	0.47
1:A:927:G:O2'	1:A:928:G:H5'	2.14	0.47
1:A:928:G:O2'	1:A:1533:C:OP1	2.31	0.47
3:B:25:ASN:ND2	3:B:27:LYS:H	2.11	0.47
4:C:7:PRO:HG3	4:C:184:TYR:HB2	1.96	0.47
4:C:179:ARG:NE	4:C:206:GLU:HG2	2.29	0.47
6:E:127:ASN:O	6:E:128:PRO:C	2.57	0.47
8:G:112:PRO:HD2	8:G:113:GLU:OE2	2.15	0.47
10:I:5:TYR:O	10:I:84:ALA:HA	2.14	0.47
11:J:78:ASN:O	11:J:80:LYS:N	2.47	0.47
11:J:87:THR:O	11:J:87:THR:HG22	2.13	0.47
15:N:14:PRO:C	15:N:16:PHE:H	2.21	0.47
17:P:20:VAL:CG2	17:P:21:VAL:N	2.74	0.47
17:P:67:THR:H	17:P:70:ALA:HB3	1.79	0.47
18:Q:31:LEU:HD12	18:Q:31:LEU:O	2.14	0.47
1:A:279:A:H5''	1:A:280:C:H3'	1.95	0.47
1:A:489:C:H2'	1:A:490:G:C8	2.49	0.47
1:A:650:G:O2'	1:A:651:C:H5'	2.15	0.47
1:A:992:U:O2'	1:A:993:G:P	2.72	0.47
1:A:1073:U:O2'	1:A:1074:G:H5'	2.14	0.47
1:A:1190:G:C2'	1:A:1191:A:OP2	2.62	0.47
1:A:1292:U:C5'	10:I:38:GLN:NE2	2.77	0.47
4:C:34:LEU:HG	15:N:25:VAL:CG2	2.40	0.47
6:E:15:ARG:CD	6:E:26:PHE:HD2	2.21	0.47
6:E:146:ALA:O	6:E:149:GLU:N	2.48	0.47
8:G:79:ARG:NE	8:G:84:ASN:ND2	2.62	0.47
8:G:145:ALA:C	8:G:147:ALA:N	2.70	0.47
12:K:14:VAL:O	12:K:15:ALA:CB	2.60	0.47
12:K:27:ASN:CG	12:K:28:THR:H	2.21	0.47
14:M:117:VAL:CG1	14:M:118:ALA:H	2.20	0.47
19:R:26:LEU:HD23	19:R:29:PHE:CE2	2.49	0.47
19:R:87:ARG:O	19:R:88:LYS:CB	2.62	0.47
21:T:61:SER:O	21:T:62:LEU:C	2.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:C:H2'	1:A:101:A:C8	2.50	0.47
1:A:263:A:OP1	21:T:79:ARG:NH1	2.43	0.47
1:A:519:C:O2'	1:A:520:A:H5'	2.14	0.47
1:A:1030(A):G:H2'	1:A:1030(B):C:H5''	1.96	0.47
1:A:1145:C:O2'	1:A:1146:A:O5'	2.29	0.47
3:B:59:GLU:O	3:B:62:ALA:HB3	2.15	0.47
3:B:177:ALA:O	3:B:178:ARG:C	2.58	0.47
4:C:46:GLU:O	4:C:48:TYR:N	2.44	0.47
4:C:47:LEU:N	4:C:47:LEU:HD12	2.30	0.47
4:C:130:VAL:O	4:C:131:ARG:C	2.57	0.47
5:D:52:SER:O	5:D:53:ASP:C	2.58	0.47
6:E:89:ILE:HD13	6:E:90:VAL:N	2.29	0.47
12:K:15:ALA:O	12:K:78:GLN:N	2.41	0.47
12:K:99:GLN:HA	12:K:105:VAL:HG21	1.97	0.47
14:M:70:LEU:C	14:M:72:ALA:N	2.72	0.47
15:N:3:ARG:O	15:N:6:LEU:N	2.47	0.47
17:P:21:VAL:HG21	17:P:59:TRP:CG	2.49	0.47
17:P:67:THR:HG22	17:P:68:ASP:N	2.29	0.47
1:A:21:G:H1'	1:A:914:A:N6	2.30	0.47
1:A:123:C:OP1	1:A:312:C:H5'	2.15	0.47
1:A:382:A:O2'	1:A:383:A:H5'	2.15	0.47
1:A:475:G:H2'	1:A:476:G:H8	1.78	0.47
1:A:491:G:O2'	1:A:492:G:H5'	2.15	0.47
1:A:934:C:C4	1:A:1345:U:C5	3.03	0.47
1:A:1108:G:H4'	1:A:1191:A:O4'	2.15	0.47
3:B:32:ILE:HD11	3:B:190:THR:HG22	1.96	0.47
3:B:44:LEU:O	3:B:47:THR:HB	2.14	0.47
3:B:197:VAL:CB	3:B:200:ILE:HG12	2.43	0.47
4:C:112:SER:HB3	4:C:115:LEU:HD12	1.95	0.47
5:D:60:GLU:OE2	5:D:199:ASN:HB3	2.15	0.47
5:D:162:LEU:O	5:D:165:MET:HB2	2.13	0.47
6:E:20:GLN:O	6:E:21:ALA:C	2.57	0.47
7:F:30:LEU:HB3	7:F:35:ALA:HB3	1.97	0.47
10:I:97:LYS:HB2	10:I:98:PRO:HD3	1.96	0.47
11:J:18:ALA:C	11:J:21:GLN:HB3	2.39	0.47
12:K:27:ASN:CG	12:K:28:THR:N	2.72	0.47
13:L:41:ARG:HB3	13:L:41:ARG:HH11	1.78	0.47
17:P:8:ARG:CZ	17:P:15:PRO:HB3	2.44	0.47
1:A:193:C:O2'	21:T:64:ASP:OD2	2.31	0.47
1:A:448:A:H2'	1:A:449:C:C6	2.50	0.47
1:A:774:G:O2'	1:A:775:G:H5'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:976:G:C8	1:A:1358:U:C2	3.02	0.47
1:A:1106:G:OP1	4:C:172:ARG:HD3	2.14	0.47
1:A:1346:A:C5	8:G:10:ARG:NH2	2.83	0.47
1:A:1420:C:H2'	1:A:1421:G:H8	1.78	0.47
1:A:1441:G:H4'	1:A:1442:G:C4	2.49	0.47
1:A:1514:C:H2'	1:A:1515:C:C6	2.50	0.47
3:B:10:LEU:HD23	3:B:10:LEU:C	2.39	0.47
3:B:154:LEU:O	3:B:155:LEU:C	2.58	0.47
3:B:231:GLU:HB2	3:B:232:PRO:CD	2.45	0.47
4:C:77:ILE:HA	4:C:84:ILE:HB	1.96	0.47
5:D:124:GLY:HA3	5:D:132:ARG:HD2	1.96	0.47
6:E:36:ASP:C	6:E:38:GLN:H	2.23	0.47
6:E:73:ASN:C	6:E:75:THR:H	2.22	0.47
8:G:116:ALA:O	8:G:117:ALA:C	2.58	0.47
8:G:145:ALA:O	8:G:146:GLU:C	2.58	0.47
10:I:9:ARG:CG	10:I:14:VAL:HG13	2.45	0.47
12:K:34:ASP:C	12:K:36:ASP:H	2.22	0.47
12:K:40:ILE:HG22	12:K:41:THR:HG23	1.97	0.47
13:L:60:LEU:HD21	13:L:85:ILE:HD11	1.96	0.47
14:M:37:THR:HG22	14:M:39:ILE:CD1	2.44	0.47
16:O:31:LEU:O	16:O:34:LEU:HB3	2.14	0.47
18:Q:56:VAL:HG12	18:Q:77:VAL:HB	1.96	0.47
20:S:28:LYS:HG2	20:S:29:ARG:N	2.30	0.47
21:T:93:GLU:HA	21:T:93:GLU:OE2	2.15	0.47
1:A:953:G:N7	14:M:104:ARG:NH2	2.62	0.47
1:A:1032:G:H2'	1:A:1033:G:C8	2.50	0.47
1:A:1157:A:H4'	1:A:1158:C:O5'	2.14	0.47
1:A:1226:C:N4	14:M:104:ARG:HG3	2.30	0.47
1:A:1249:C:O2'	10:I:73:GLN:NE2	2.47	0.47
1:A:1395:C:H6	1:A:1395:C:O5'	1.97	0.47
3:B:100:GLY:N	3:B:176:GLU:OE2	2.44	0.47
7:F:71:ARG:O	7:F:74:ASP:N	2.45	0.47
9:H:9:MET:HE2	9:H:32:LYS:HG2	1.97	0.47
12:K:46:GLY:C	12:K:48:ILE:N	2.71	0.47
14:M:80:ARG:O	14:M:82:MET:N	2.48	0.47
14:M:87:TYR:O	14:M:90:LEU:N	2.48	0.47
14:M:122:LYS:HE3	14:M:122:LYS:CA	2.44	0.47
14:M:122:LYS:O	14:M:123:ALA:HB2	2.15	0.47
19:R:40:LEU:C	19:R:42:ARG:N	2.72	0.47
20:S:10:PHE:C	20:S:10:PHE:CD2	2.92	0.47
21:T:58:LYS:O	21:T:59:ALA:C	2.58	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:65:LYS:O	21:T:66:ALA:C	2.56	0.47
1:A:77:G:O2'	1:A:78:G:H5'	2.15	0.47
1:A:98:U:O2'	1:A:99:C:H5'	2.15	0.47
1:A:337:C:H2'	1:A:338:A:C8	2.49	0.47
1:A:477:G:H2'	1:A:478:A:C8	2.50	0.47
1:A:878:G:H1'	9:H:3:THR:HG21	1.97	0.47
1:A:952:U:H2'	1:A:953:G:H8	1.79	0.47
1:A:959:A:C2	1:A:1222:G:O4'	2.68	0.47
1:A:1111:A:H61	4:C:177:THR:HA	1.78	0.47
1:A:1291:G:C6	1:A:1292:U:C4	3.03	0.47
1:A:1488:G:H2'	1:A:1489:G:H8	1.79	0.47
3:B:174:VAL:O	3:B:177:ALA:HB3	2.15	0.47
4:C:8:ILE:HG22	4:C:9:GLY:N	2.30	0.47
6:E:43:LEU:HD23	6:E:44:GLY:N	2.29	0.47
7:F:82:ARG:HB2	7:F:85:VAL:CG2	2.45	0.47
10:I:23:ASN:C	10:I:23:ASN:ND2	2.72	0.47
12:K:80:VAL:HG12	12:K:81:ASP:H	1.79	0.47
13:L:37:CYS:HB2	13:L:79:GLU:O	2.15	0.47
14:M:102:ARG:HB2	14:M:102:ARG:CZ	2.45	0.47
18:Q:68:ARG:HG2	18:Q:68:ARG:HH11	1.80	0.47
21:T:33:ILE:HG22	21:T:34:LYS:N	2.30	0.47
21:T:56:MET:HG3	21:T:84:LEU:CD2	2.45	0.47
1:A:44:G:OP2	17:P:12:LYS:HE3	2.15	0.47
1:A:197:A:H4'	1:A:198:G:O5'	2.13	0.47
1:A:251:G:H4'	1:A:252:U:O5'	2.15	0.47
1:A:399:G:H2'	1:A:400:C:C6	2.50	0.47
1:A:1202:G:O2'	1:A:1203:C:H5'	2.14	0.47
1:A:1466:C:H2'	1:A:1467:G:O4'	2.14	0.47
3:B:19:HIS:CD2	3:B:205:ASP:OD1	2.65	0.47
4:C:7:PRO:HG2	4:C:184:TYR:HB2	1.97	0.47
5:D:4:TYR:O	5:D:5:ILE:HB	2.15	0.47
5:D:9:CYS:HA	5:D:12:CYS:HB2	1.96	0.47
7:F:4:TYR:OH	7:F:69:GLU:HA	2.15	0.47
8:G:85:TYR:HD1	8:G:154:TYR:CE1	2.33	0.47
9:H:4:ASP:O	9:H:7:ALA:HB3	2.15	0.47
9:H:11:THR:C	9:H:13:ILE:N	2.72	0.47
10:I:44:VAL:HG13	10:I:51:ARG:NH2	2.30	0.47
12:K:54:ARG:H	12:K:54:ARG:HD2	1.80	0.47
13:L:92:ASP:O	13:L:94:PRO:HD3	2.15	0.47
14:M:17:VAL:HG12	14:M:18:ALA:N	2.30	0.47
17:P:57:ARG:HG2	17:P:57:ARG:HH11	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:41:VAL:HG23	20:S:44:MET:HG3	1.97	0.47
21:T:41:ILE:C	21:T:43:LEU:N	2.73	0.47
22:V:19:GLY:C	22:V:21:TYR:H	2.22	0.47
1:A:45:U:H2'	1:A:46:G:C8	2.50	0.46
1:A:50:A:H1'	1:A:52:G:C8	2.50	0.46
1:A:432:A:H2'	1:A:433:C:H5'	1.97	0.46
1:A:662:G:H2'	1:A:663:A:H8	1.75	0.46
1:A:908:A:H2'	1:A:909:A:C8	2.50	0.46
1:A:1063:C:H3'	1:A:1064:G:H2'	1.97	0.46
1:A:1255:G:O2'	1:A:1258:G:H1'	2.14	0.46
1:A:1393:U:O4'	1:A:1502:A:H5'	2.15	0.46
1:A:1499:A:H1'	1:A:1520:G:H5'	1.95	0.46
1:A:1514:C:H2'	1:A:1515:C:H6	1.80	0.46
3:B:222:ILE:HG22	3:B:223:ILE:N	2.29	0.46
5:D:103:ASN:O	5:D:104:VAL:C	2.58	0.46
5:D:147:ALA:HB2	5:D:182:LYS:HG2	1.97	0.46
8:G:12:LEU:HD12	8:G:12:LEU:N	2.30	0.46
9:H:75:ARG:HA	9:H:76:PRO:HD3	1.60	0.46
10:I:18:PHE:HB2	10:I:62:TYR:O	2.15	0.46
11:J:42:THR:HG23	11:J:67:THR:O	2.15	0.46
15:N:36:PHE:O	15:N:36:PHE:CD1	2.68	0.46
18:Q:101:ARG:HA	18:Q:101:ARG:HE	1.80	0.46
21:T:53:LEU:HD21	21:T:104:LEU:CD1	2.44	0.46
21:T:53:LEU:HD13	21:T:101:GLY:HA2	1.97	0.46
1:A:103:C:P	21:T:17:ARG:NH1	2.88	0.46
1:A:109:A:H2'	1:A:326:G:H21	1.80	0.46
1:A:420:U:O2'	1:A:421:U:H5''	2.15	0.46
1:A:646:U:H2'	1:A:647:C:C6	2.51	0.46
1:A:738:C:P	7:F:92:LYS:HD3	2.56	0.46
1:A:781:A:C2	1:A:1514:C:O4'	2.69	0.46
1:A:938:A:N6	1:A:939:G:C6	2.83	0.46
1:A:1054:C:H3'	1:A:1054:C:H6	1.79	0.46
1:A:1102:A:H2'	1:A:1103:C:C6	2.50	0.46
1:A:1153:C:H2'	1:A:1154:G:H8	1.80	0.46
1:A:1225:A:H5'	1:A:1226:C:OP2	2.15	0.46
1:A:1343:G:H2'	1:A:1344:C:C6	2.50	0.46
1:A:1367:C:H4'	11:J:48:THR:HG21	1.97	0.46
4:C:70:VAL:C	4:C:106:VAL:HB	2.40	0.46
14:M:18:ALA:O	14:M:21:TYR:HB2	2.16	0.46
14:M:62:ASN:O	14:M:63:THR:OG1	2.32	0.46
15:N:26:ARG:NH1	15:N:47:LEU:HD21	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:31:LEU:HA	19:R:31:LEU:HD23	1.80	0.46
20:S:30:LEU:O	20:S:31:ILE:HD13	2.15	0.46
21:T:16:HIS:O	21:T:17:ARG:C	2.56	0.46
21:T:65:LYS:O	21:T:68:LYS:HB3	2.16	0.46
1:A:226:G:O2'	1:A:227:G:H5'	2.15	0.46
1:A:959:A:H2'	1:A:960:U:O4'	2.15	0.46
1:A:1034:G:C2	1:A:1035:A:N6	2.84	0.46
1:A:1039:C:H2'	1:A:1040:U:C6	2.50	0.46
1:A:1070:U:O2'	1:A:1071:C:H5'	2.15	0.46
1:A:1275:A:O2'	1:A:1276:G:H5'	2.15	0.46
1:A:1358:U:OP1	15:N:35:ARG:HB2	2.16	0.46
4:C:39:ILE:O	4:C:40:ARG:C	2.58	0.46
4:C:181:ASN:OD1	4:C:181:ASN:C	2.58	0.46
4:C:188:LEU:HD21	4:C:195:VAL:HG11	1.97	0.46
5:D:54:TYR:O	5:D:55:ALA:C	2.57	0.46
6:E:24:ARG:HG2	6:E:24:ARG:HH11	1.80	0.46
6:E:48:ALA:HB1	6:E:49:PRO:HD2	1.97	0.46
9:H:10:LEU:CD2	9:H:83:ILE:HD11	2.46	0.46
12:K:46:GLY:C	12:K:48:ILE:H	2.22	0.46
14:M:70:LEU:O	14:M:71:ARG:C	2.57	0.46
18:Q:63:ARG:HG2	18:Q:64:PRO:HD2	1.97	0.46
19:R:40:LEU:O	19:R:41:LYS:C	2.59	0.46
21:T:39:LYS:O	21:T:43:LEU:HG	2.15	0.46
1:A:32:A:H2'	1:A:33:A:C8	2.51	0.46
1:A:706:A:H1'	12:K:29:ILE:CD1	2.45	0.46
1:A:716:A:N3	12:K:117:ASN:O	2.49	0.46
1:A:899:C:H2'	1:A:900:A:C8	2.50	0.46
1:A:922:G:H2'	1:A:923:A:C8	2.50	0.46
1:A:922:G:O2'	1:A:1398:A:N1	2.45	0.46
1:A:1196:U:H3'	1:A:1197:G:C5'	2.45	0.46
1:A:1462:G:O2'	1:A:1463:C:H5'	2.16	0.46
3:B:23:ARG:HD3	3:B:23:ARG:C	2.40	0.46
4:C:119:ARG:HG3	4:C:123:GLN:HE21	1.80	0.46
5:D:100:ARG:O	5:D:103:ASN:HB3	2.15	0.46
8:G:143:ARG:O	8:G:147:ALA:HB2	2.16	0.46
11:J:63:PHE:CZ	15:N:45:ARG:HG3	2.51	0.46
16:O:7:GLU:OE1	16:O:38:ARG:NH2	2.49	0.46
1:A:7:G:H5'	1:A:298:A:O4'	2.15	0.46
1:A:285:G:O2'	1:A:286:G:H5'	2.14	0.46
1:A:377:G:H2'	1:A:378:G:H8	1.81	0.46
1:A:765:G:N2	1:A:812:C:HO2'	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:983:A:H2	1:A:984:C:C6	2.34	0.46
1:A:1137:C:H4'	1:A:1138:G:N1	2.30	0.46
1:A:1152:A:O2'	1:A:1153:C:H5'	2.15	0.46
1:A:1349:A:OP2	10:I:118:LYS:NZ	2.49	0.46
4:C:22:TRP:CZ3	4:C:32:LEU:HB2	2.51	0.46
5:D:3:ARG:N	5:D:3:ARG:NE	2.63	0.46
10:I:28:VAL:HG13	10:I:65:VAL:HG12	1.96	0.46
10:I:127:LYS:H	14:M:126:LYS:HZ1	1.62	0.46
18:Q:12:SER:HB3	18:Q:20:THR:HB	1.96	0.46
1:A:600:C:H2'	1:A:601:C:C6	2.51	0.46
1:A:895:G:H2'	1:A:896:C:C6	2.50	0.46
1:A:930:C:O2'	1:A:931:C:H5'	2.15	0.46
1:A:1083:U:C5	1:A:1084:G:C5	3.04	0.46
1:A:1192:C:C5	1:A:1193:G:C8	3.04	0.46
1:A:1325:C:O3'	22:V:17:THR:HG21	2.16	0.46
1:A:1414:U:H2'	1:A:1415:G:H8	1.80	0.46
3:B:97:TRP:CH2	3:B:173:ALA:HA	2.51	0.46
3:B:142:LEU:O	3:B:145:LEU:N	2.49	0.46
3:B:196:LEU:HA	3:B:196:LEU:HD23	1.70	0.46
4:C:8:ILE:O	4:C:12:LEU:N	2.46	0.46
4:C:101:LEU:O	4:C:101:LEU:HD22	2.15	0.46
6:E:15:ARG:O	6:E:16:THR:O	2.34	0.46
6:E:148:VAL:O	6:E:152:ARG:HG3	2.15	0.46
8:G:51:GLN:O	8:G:53:LYS:N	2.48	0.46
8:G:152:ALA:O	8:G:154:TYR:N	2.49	0.46
10:I:93:ARG:HG2	10:I:97:LYS:CE	2.40	0.46
12:K:33:THR:HB	12:K:39:PRO:HA	1.98	0.46
13:L:24:VAL:O	13:L:24:VAL:HG12	2.14	0.46
13:L:50:SER:O	13:L:51:ALA:CB	2.63	0.46
13:L:102:ARG:NH2	13:L:109:GLY:O	2.48	0.46
22:V:24:ARG:O	22:V:25:LYS:HB2	2.14	0.46
1:A:174:C:H2'	1:A:175:C:H6	1.81	0.46
1:A:433:C:H2'	1:A:434:U:C6	2.49	0.46
1:A:521:G:OP1	13:L:73:GLU:O	2.34	0.46
1:A:718:G:C8	12:K:116:HIS:HB3	2.51	0.46
1:A:882:C:O2'	1:A:883:C:H5'	2.15	0.46
1:A:969:A:N6	14:M:126:LYS:HB2	2.31	0.46
1:A:1210:C:H5'	1:A:1214:C:N4	2.30	0.46
1:A:1251:A:H2'	1:A:1252:A:C8	2.51	0.46
1:A:1526:G:H2'	1:A:1527:C:H6	1.80	0.46
5:D:199:ASN:C	5:D:199:ASN:OD1	2.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:120:THR:O	6:E:121:LYS:HB2	2.15	0.46
7:F:3:ARG:HB3	7:F:93:SER:OG	2.16	0.46
10:I:21:PRO:HA	10:I:59:PHE:HA	1.97	0.46
11:J:53:PRO:O	11:J:54:PHE:O	2.33	0.46
12:K:18:ARG:HB2	12:K:33:THR:CG2	2.45	0.46
12:K:32:ILE:CG2	12:K:77:MET:HE2	2.45	0.46
15:N:9:LYS:HE3	15:N:21:TYR:H	1.81	0.46
20:S:9:VAL:HG22	20:S:10:PHE:H	1.81	0.46
20:S:15:LEU:O	20:S:19:VAL:HB	2.14	0.46
21:T:87:LYS:O	21:T:88:VAL:C	2.58	0.46
22:V:15:ARG:O	22:V:17:THR:HG23	2.16	0.46
1:A:178:C:O2'	1:A:179:A:H5'	2.15	0.46
1:A:771:G:H2'	1:A:772:U:C6	2.51	0.46
1:A:792:A:H1'	1:A:794:A:N7	2.31	0.46
1:A:948:C:O2'	1:A:949:A:H5'	2.16	0.46
1:A:1262:C:H2'	1:A:1263:C:C6	2.51	0.46
1:A:1364:U:O2'	1:A:1365:G:H5'	2.15	0.46
1:A:1460:A:C2	1:A:1461:G:H1'	2.51	0.46
1:A:1525:G:O2'	1:A:1526:G:H5'	2.16	0.46
3:B:69:LEU:HD22	3:B:71:VAL:HG23	1.97	0.46
8:G:65:ALA:CB	8:G:127:ALA:HB3	2.46	0.46
8:G:148:ASN:N	8:G:148:ASN:ND2	2.62	0.46
11:J:6:ILE:HD13	11:J:71:LEU:O	2.16	0.46
18:Q:17:LYS:HA	18:Q:46:ASP:O	2.16	0.46
21:T:33:ILE:HD13	21:T:63:ILE:HG12	1.98	0.46
1:A:821:G:H2'	1:A:822:C:C6	2.49	0.46
1:A:861:G:O2'	1:A:862:C:H5'	2.16	0.46
1:A:1260:C:H4'	1:A:1284:C:H5'	1.98	0.46
1:A:1263:C:H2'	1:A:1264:C:H6	1.81	0.46
3:B:7:VAL:C	3:B:8:LYS:HD2	2.40	0.46
3:B:53:ARG:NH1	3:B:199:TYR:CD2	2.84	0.46
5:D:64:LEU:HD13	5:D:75:PHE:HZ	1.80	0.46
6:E:60:TYR:O	6:E:64:ARG:HG3	2.16	0.46
8:G:15:ASP:CB	8:G:20:ASP:H	2.29	0.46
9:H:5:PRO:O	9:H:6:ILE:C	2.59	0.46
10:I:11:LYS:H	10:I:104:ARG:HH12	1.63	0.46
10:I:117:HIS:C	10:I:118:LYS:HG3	2.41	0.46
11:J:9:ARG:CB	11:J:9:ARG:HH11	2.29	0.46
12:K:95:ILE:O	12:K:96:ARG:C	2.58	0.46
1:A:129(A):G:N3	1:A:190(E):U:C5'	2.79	0.46
1:A:644:G:C5	1:A:645:C:C5	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:687:A:C2	1:A:700:G:N3	2.84	0.46
1:A:818:G:C3'	1:A:819:A:C5'	2.94	0.46
1:A:945:G:H2'	1:A:945:G:N3	2.30	0.46
1:A:949:A:C2	1:A:1233:G:N3	2.84	0.46
1:A:1057:G:C5	1:A:1204:A:C2	3.04	0.46
3:B:15:VAL:CG2	3:B:209:ARG:HG3	2.45	0.46
3:B:50:GLU:HB3	3:B:200:ILE:O	2.16	0.46
6:E:107:ARG:HG2	6:E:108:ALA:N	2.31	0.46
7:F:28:ARG:O	7:F:29:ALA:C	2.58	0.46
12:K:104:GLN:NE2	12:K:106:LYS:HD3	2.31	0.46
20:S:43:GLU:CD	20:S:43:GLU:N	2.66	0.46
20:S:61:TYR:C	20:S:61:TYR:CD2	2.93	0.46
1:A:458:C:C2	1:A:459:G:C8	3.04	0.45
1:A:736:C:OP1	19:R:68:LYS:HE2	2.16	0.45
1:A:766:A:C8	1:A:814:A:C6	3.05	0.45
1:A:1042:G:O2'	1:A:1043:C:H5'	2.15	0.45
1:A:1230:C:O2'	1:A:1231:G:H5'	2.16	0.45
5:D:61:LYS:HZ1	5:D:65:ARG:NH1	2.14	0.45
5:D:64:LEU:CG	5:D:198:VAL:HG21	2.40	0.45
5:D:141:ARG:N	5:D:144:ASP:OD2	2.49	0.45
5:D:163:GLU:C	5:D:165:MET:N	2.74	0.45
6:E:50:GLU:O	6:E:51:VAL:C	2.59	0.45
6:E:109:ILE:HG21	6:E:135:THR:HG22	1.98	0.45
7:F:22:GLU:OE2	7:F:82:ARG:HD3	2.15	0.45
13:L:73:GLU:OE2	13:L:73:GLU:HA	2.16	0.45
13:L:87:GLY:HA2	13:L:98:TYR:HA	1.98	0.45
14:M:14:ARG:CB	14:M:14:ARG:HH11	2.29	0.45
19:R:21:LYS:HE3	19:R:54:ARG:O	2.15	0.45
21:T:48:LYS:O	21:T:49:ALA:C	2.58	0.45
21:T:69:GLY:O	21:T:73:HIS:ND1	2.49	0.45
1:A:476:G:O2'	1:A:477:G:H5'	2.16	0.45
1:A:579:G:H2'	1:A:580:U:C6	2.51	0.45
1:A:802:A:H2'	1:A:803:G:O4'	2.16	0.45
1:A:824:C:H2'	1:A:825:G:H8	1.82	0.45
1:A:916:G:O2'	1:A:917:G:H5'	2.16	0.45
3:B:51:LEU:O	3:B:52:GLU:C	2.59	0.45
3:B:230:VAL:HG12	3:B:231:GLU:OE2	2.15	0.45
4:C:177:THR:HG23	4:C:180:ALA:HB2	1.98	0.45
6:E:51:VAL:CB	6:E:52:PRO:HD3	2.37	0.45
8:G:42:ILE:HG23	8:G:117:ALA:CA	2.46	0.45
8:G:79:ARG:NH2	8:G:84:ASN:HD21	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:77:ASN:O	14:M:81:LEU:HD22	2.15	0.45
17:P:40:ASP:OD2	17:P:40:ASP:C	2.58	0.45
17:P:53:VAL:HG22	17:P:54:GLU:N	2.32	0.45
18:Q:7:THR:HG23	18:Q:77:VAL:HG21	1.98	0.45
18:Q:95:TYR:C	18:Q:97:SER:N	2.75	0.45
18:Q:104:LYS:HA	18:Q:104:LYS:CE	2.44	0.45
20:S:80:TYR:CG	20:S:81:ARG:N	2.85	0.45
21:T:103:GLY:O	21:T:104:LEU:HG	2.16	0.45
1:A:389:A:H2'	1:A:390:C:H5'	1.98	0.45
1:A:542:G:O2'	1:A:543:C:H5'	2.16	0.45
1:A:687:A:O2'	1:A:688:G:OP2	2.32	0.45
1:A:990:C:H2'	1:A:991:U:O4'	2.16	0.45
1:A:1270:C:H2'	1:A:1271:G:C8	2.49	0.45
1:A:1305:G:O2'	1:A:1331:G:N2	2.49	0.45
3:B:228:GLY:O	3:B:229:VAL:C	2.58	0.45
5:D:106:TYR:HB2	5:D:117:ALA:HB2	1.98	0.45
1:A:186:C:O2'	1:A:187:C:H5'	2.16	0.45
1:A:556:C:H2'	1:A:557:G:O4'	2.16	0.45
1:A:1184:G:OP1	1:A:1184:G:H3'	2.16	0.45
1:A:1226:C:C5	14:M:104:ARG:HA	2.52	0.45
1:A:1232:U:H2'	1:A:1233:G:O4'	2.17	0.45
1:A:1279:A:C5'	1:A:1280:A:OP1	2.60	0.45
2:X:1:C:H2'	2:X:2:U:H5'	1.98	0.45
3:B:122:PHE:O	3:B:123:ALA:HB2	2.16	0.45
4:C:167:TRP:HB3	4:C:168:ALA:H	1.52	0.45
6:E:116:THR:HG23	6:E:117:ASP:CG	2.41	0.45
7:F:6:VAL:HG13	7:F:90:VAL:HG22	1.99	0.45
10:I:56:LEU:O	10:I:57:GLY:C	2.60	0.45
11:J:8:LEU:CD1	11:J:20:ALA:HB2	2.47	0.45
12:K:11:LYS:HD2	12:K:11:LYS:N	2.31	0.45
14:M:77:ASN:O	14:M:78:ILE:C	2.59	0.45
14:M:102:ARG:HB2	14:M:102:ARG:NH1	2.31	0.45
19:R:59:SER:O	19:R:60:GLY:C	2.58	0.45
20:S:20:LEU:C	20:S:23:ASN:HB2	2.42	0.45
20:S:40:ILE:HB	20:S:67:VAL:O	2.16	0.45
1:A:8:A:N6	5:D:209:ARG:HB2	2.32	0.45
1:A:640:A:O2'	1:A:641:U:H5'	2.16	0.45
1:A:647:C:H2'	1:A:648:A:H8	1.79	0.45
1:A:840:C:H5'	1:A:848:C:O2	2.16	0.45
1:A:938:A:C2'	1:A:939:G:H5'	2.46	0.45
1:A:1056:U:H5'	4:C:163:ALA:CB	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1145:C:O2'	1:A:1146:A:H8	1.99	0.45
1:A:1164:G:H1	1:A:1172:C:N4	2.14	0.45
1:A:1372:U:OP1	10:I:71:SER:HB3	2.16	0.45
4:C:3:ASN:O	4:C:4:LYS:HB2	2.17	0.45
4:C:70:VAL:HG12	4:C:71:ALA:N	2.31	0.45
7:F:28:ARG:HH11	7:F:28:ARG:HG3	1.82	0.45
13:L:28:LYS:CG	13:L:33:ARG:HH12	2.29	0.45
13:L:46:LYS:HZ1	13:L:47:LYS:CD	2.29	0.45
14:M:67:GLU:O	14:M:68:GLY:C	2.59	0.45
15:N:29:ARG:CG	15:N:30:ALA:H	2.17	0.45
16:O:70:LEU:HD13	16:O:70:LEU:C	2.41	0.45
1:A:1226:C:O2'	1:A:1227:A:O5'	2.31	0.45
3:B:114:ARG:HA	3:B:117:GLU:HB3	1.97	0.45
3:B:165:VAL:HG23	3:B:166:ASP:H	1.81	0.45
4:C:156:ARG:HD3	4:C:193:TYR:O	2.17	0.45
6:E:40:ARG:NH1	6:E:68:GLU:OE2	2.50	0.45
7:F:71:ARG:O	7:F:72:VAL:C	2.60	0.45
8:G:32:ARG:O	8:G:33:ASP:HB2	2.16	0.45
10:I:79:LEU:HD13	10:I:79:LEU:C	2.42	0.45
11:J:15:THR:HG21	11:J:94:VAL:CG2	2.46	0.45
14:M:69:GLU:O	14:M:72:ALA:HB3	2.17	0.45
16:O:24:SER:HB3	16:O:27:VAL:HG23	1.99	0.45
20:S:22:LEU:HD22	20:S:28:LYS:HB2	1.97	0.45
1:A:358:U:H2'	1:A:359:U:H6	1.82	0.45
1:A:435:C:H2'	1:A:436:C:C6	2.42	0.45
1:A:765:G:N1	1:A:812:C:H2'	2.30	0.45
1:A:848:C:H2'	1:A:849:C:H6	1.81	0.45
1:A:1353:G:C2	1:A:1370:G:C2	3.05	0.45
1:A:1472:U:O2'	1:A:1473:A:H5'	2.17	0.45
3:B:92:TYR:HE1	3:B:150:SER:OG	2.00	0.45
8:G:46:ALA:CB	8:G:117:ALA:O	2.65	0.45
8:G:135:VAL:O	8:G:139:GLU:HG3	2.17	0.45
11:J:49:VAL:O	11:J:50:ILE:C	2.59	0.45
11:J:86:MET:HA	11:J:86:MET:CE	2.43	0.45
19:R:40:LEU:O	19:R:42:ARG:N	2.50	0.45
21:T:11:SER:C	21:T:13:LEU:HD12	2.42	0.45
21:T:67:ALA:O	21:T:73:HIS:ND1	2.40	0.45
1:A:230:G:O4'	17:P:25:ARG:NH2	2.50	0.45
1:A:377:G:H2'	1:A:378:G:C8	2.52	0.45
1:A:418:C:H2'	1:A:419:C:C6	2.52	0.45
1:A:477:G:H2'	1:A:478:A:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:885:G:O2'	1:A:914:A:N1	2.47	0.45
1:A:982:U:H5''	15:N:6:LEU:CD1	2.46	0.45
1:A:1003:G:H2'	1:A:1003(A):G:C8	2.51	0.45
1:A:1130:A:H3'	1:A:1130:A:OP2	2.17	0.45
1:A:1239:A:H62	1:A:1299:A:H62	1.65	0.45
3:B:16:HIS:O	3:B:17:PHE:CD1	2.70	0.45
3:B:174:VAL:O	3:B:175:ARG:C	2.60	0.45
11:J:50:ILE:HA	11:J:60:ARG:H	1.82	0.45
19:R:73:ALA:O	19:R:74:ARG:C	2.59	0.45
1:A:222:U:H2'	1:A:223:U:H6	1.82	0.45
1:A:385:C:O2'	1:A:386:C:H5'	2.17	0.45
1:A:428:G:C6	1:A:430:A:C6	3.05	0.45
1:A:564:C:N1	18:Q:31:LEU:HD11	2.32	0.45
1:A:643:C:H4'	9:H:31:PHE:HE2	1.82	0.45
1:A:663:A:H5''	19:R:61:LYS:HE3	1.98	0.45
1:A:849:C:O2'	1:A:850:U:H5'	2.17	0.45
1:A:881:G:H2'	1:A:882:C:O4'	2.17	0.45
1:A:954:G:H2'	1:A:955:U:C6	2.52	0.45
1:A:1113:C:H1'	4:C:178:LEU:HD21	1.99	0.45
1:A:1162:C:H2'	1:A:1163:C:H6	1.81	0.45
1:A:1262:C:H2'	1:A:1263:C:H6	1.82	0.45
5:D:192:GLU:N	5:D:192:GLU:OE1	2.49	0.45
8:G:35:LYS:C	8:G:37:ASN:H	2.25	0.45
11:J:6:ILE:HG23	11:J:98:ILE:HG23	1.99	0.45
11:J:64:GLU:HG3	15:N:59:ALA:CA	2.47	0.45
19:R:40:LEU:O	19:R:43:PHE:N	2.47	0.45
19:R:53:ARG:C	19:R:55:ARG:N	2.73	0.45
19:R:87:ARG:HG2	19:R:87:ARG:NH1	2.31	0.45
1:A:319:G:O2'	1:A:320:C:H5'	2.17	0.45
1:A:458:C:O2'	1:A:459:G:H5'	2.18	0.45
1:A:479:C:O2'	1:A:480:U:H5'	2.16	0.45
1:A:518:C:O2'	1:A:519:C:OP2	2.29	0.45
1:A:579:G:H2'	1:A:580:U:H6	1.82	0.45
1:A:759:A:H2'	1:A:760:G:H5'	1.99	0.45
1:A:1030(D):A:H2'	1:A:1031:G:H5'	1.99	0.45
1:A:1138:G:C6	1:A:1140:C:H1'	2.52	0.45
1:A:1288:A:H1'	1:A:1352:C:O2'	2.17	0.45
1:A:1453:G:H2'	1:A:1454:G:O4'	2.17	0.45
3:B:101:MET:HE3	3:B:108:ILE:HD13	1.99	0.45
4:C:113:ALA:N	4:C:202:ILE:HD12	2.33	0.45
5:D:52:SER:C	5:D:54:TYR:N	2.75	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:114:ARG:HH11	5:D:114:ARG:CG	2.19	0.45
5:D:175:SER:CB	5:D:186:LEU:HD11	2.36	0.45
8:G:62:PHE:HA	8:G:124:LEU:HD22	1.99	0.45
8:G:66:VAL:C	8:G:68:ASN:H	2.25	0.45
10:I:113:LYS:HD3	10:I:113:LYS:N	2.32	0.45
11:J:94:VAL:O	11:J:95:GLU:HB2	2.17	0.45
16:O:60:VAL:HG12	16:O:64:ARG:HD2	1.97	0.45
17:P:13:HIS:C	17:P:15:PRO:HD3	2.41	0.45
18:Q:59:ILE:HG22	18:Q:71:PHE:CD1	2.52	0.45
20:S:9:VAL:HG13	20:S:10:PHE:H	1.75	0.45
21:T:37:SER:O	21:T:38:LYS:C	2.60	0.45
1:A:28:G:O2'	1:A:296:U:OP1	2.31	0.44
1:A:148:G:O2'	1:A:149:A:H5'	2.18	0.44
1:A:370:C:C2'	1:A:371:G:H5'	2.46	0.44
1:A:542:G:OP1	5:D:10:ARG:NH2	2.49	0.44
1:A:862:C:O2'	1:A:863:U:H5'	2.17	0.44
1:A:866:C:H2'	1:A:867:G:O4'	2.17	0.44
1:A:1250:A:H2'	1:A:1251:A:C8	2.52	0.44
1:A:1294:G:O2'	1:A:1295:G:H5'	2.18	0.44
3:B:17:PHE:O	3:B:18:GLY:C	2.59	0.44
3:B:138:LEU:O	3:B:139:LYS:C	2.60	0.44
4:C:180:ALA:O	4:C:181:ASN:CB	2.62	0.44
5:D:4:TYR:CD2	5:D:115:ARG:NH2	2.80	0.44
8:G:66:VAL:C	8:G:68:ASN:N	2.73	0.44
8:G:69:VAL:HG21	8:G:104:LEU:CD2	2.41	0.44
12:K:18:ARG:N	12:K:33:THR:O	2.47	0.44
13:L:34:ARG:HG3	13:L:105:TYR:CE1	2.51	0.44
14:M:37:THR:O	14:M:37:THR:HG22	2.16	0.44
14:M:49:THR:O	14:M:50:GLU:C	2.61	0.44
22:V:14:TRP:C	22:V:16:GLY:N	2.71	0.44
1:A:113:G:H1'	1:A:354:G:C5'	2.48	0.44
1:A:147:G:O2'	1:A:148:G:H5'	2.17	0.44
1:A:190(I):G:O2'	1:A:190(J):U:H5'	2.17	0.44
1:A:424:G:H2'	1:A:425:G:H8	1.82	0.44
1:A:970:C:O2	14:M:126:LYS:C	2.61	0.44
1:A:1001:A:H2'	1:A:1002:G:C8	2.53	0.44
1:A:1305:G:H5'	22:V:4:GLY:O	2.17	0.44
3:B:17:PHE:O	3:B:18:GLY:O	2.35	0.44
3:B:92:TYR:CD1	3:B:92:TYR:C	2.95	0.44
5:D:202:LEU:O	5:D:205:GLU:N	2.50	0.44
8:G:42:ILE:O	8:G:43:PHE:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:101:SER:OG	12:K:102:GLY:N	2.47	0.44
14:M:70:LEU:O	14:M:73:GLU:N	2.51	0.44
15:N:12:ARG:NH1	15:N:14:PRO:HG3	2.32	0.44
15:N:29:ARG:HG2	15:N:29:ARG:HH11	1.83	0.44
16:O:70:LEU:HD12	16:O:78:TYR:CA	2.47	0.44
1:A:448:A:OP2	1:A:485:G:N2	2.49	0.44
1:A:488:C:H2'	1:A:489:C:H6	1.82	0.44
1:A:533:A:H2'	1:A:535:A:OP2	2.16	0.44
1:A:781:A:C5	1:A:802:A:C2	3.05	0.44
1:A:930:C:C2'	1:A:931:C:H5'	2.48	0.44
1:A:1049:U:H4'	1:A:1050:G:OP2	2.18	0.44
1:A:1288:A:H2'	1:A:1289:A:O4'	2.17	0.44
3:B:23:ARG:NH1	3:B:24:TRP:C	2.75	0.44
3:B:59:GLU:O	3:B:60:ASP:C	2.61	0.44
3:B:153:ARG:HG2	3:B:153:ARG:NH1	2.30	0.44
4:C:149:ALA:HA	4:C:201:TYR:O	2.17	0.44
5:D:3:ARG:HD2	5:D:118:ARG:NE	2.32	0.44
5:D:60:GLU:OE1	5:D:60:GLU:HA	2.16	0.44
6:E:94:ALA:CB	6:E:98:THR:HG21	2.47	0.44
9:H:20:TYR:CD1	9:H:65:TYR:CD2	3.06	0.44
14:M:45:VAL:O	14:M:48:LEU:HB2	2.16	0.44
14:M:58:GLU:C	14:M:60:VAL:H	2.24	0.44
14:M:110:ARG:HH11	14:M:110:ARG:CG	2.30	0.44
16:O:38:ARG:HG3	16:O:38:ARG:HH11	1.83	0.44
18:Q:48:GLU:C	18:Q:50:LYS:N	2.72	0.44
18:Q:85:VAL:O	18:Q:86:GLU:C	2.58	0.44
20:S:12:ASP:O	20:S:14:HIS:N	2.49	0.44
20:S:63:THR:HG22	20:S:64:GLU:N	2.32	0.44
1:A:60:A:H4'	1:A:61:G:O5'	2.18	0.44
1:A:122:G:O2'	1:A:123:C:H5'	2.17	0.44
1:A:279:A:H5'	1:A:281:G:O4'	2.18	0.44
1:A:440:A:H5''	1:A:442:C:H5	1.81	0.44
1:A:462:G:C6	1:A:463:A:C5	3.06	0.44
1:A:980:C:H3'	1:A:981:U:C6	2.52	0.44
1:A:986:A:H2'	1:A:987:G:C8	2.53	0.44
1:A:1332:A:H2'	1:A:1333:A:C8	2.52	0.44
1:A:1406:U:O2'	1:A:1407:C:H5'	2.17	0.44
1:A:1488:G:H2'	1:A:1489:G:C8	2.52	0.44
3:B:44:LEU:O	3:B:45:GLN:C	2.60	0.44
3:B:114:ARG:HD2	3:B:141:GLU:OE2	2.17	0.44
5:D:3:ARG:O	5:D:5:ILE:HG13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:73:ASN:O	6:E:75:THR:N	2.46	0.44
11:J:53:PRO:O	11:J:54:PHE:C	2.59	0.44
15:N:8:GLU:OE2	15:N:9:LYS:N	2.50	0.44
19:R:30:ASP:C	19:R:32:ARG:H	2.24	0.44
19:R:86:VAL:O	19:R:87:ARG:HB2	2.18	0.44
20:S:22:LEU:HD11	20:S:31:ILE:HD11	1.99	0.44
21:T:101:GLY:O	21:T:102:GLY:O	2.36	0.44
1:A:47:C:H5''	1:A:365:U:C6	2.52	0.44
1:A:218:C:H2'	1:A:219:C:H6	1.82	0.44
1:A:582:U:O2'	1:A:583:A:H5'	2.17	0.44
1:A:676:A:H5''	12:K:113:PRO:HB2	1.99	0.44
1:A:923:A:OP1	6:E:21:ALA:HB2	2.17	0.44
3:B:156:LYS:HA	3:B:156:LYS:HE2	2.00	0.44
4:C:132:ARG:O	4:C:135:LYS:N	2.50	0.44
5:D:5:ILE:H	5:D:115:ARG:NH2	2.14	0.44
7:F:1:MET:SD	7:F:68:PRO:HG3	2.58	0.44
7:F:28:ARG:O	7:F:31:GLU:HB2	2.18	0.44
8:G:111:ARG:HB3	8:G:112:PRO:HD2	2.00	0.44
8:G:114:ARG:HG2	8:G:114:ARG:HH11	1.83	0.44
12:K:22:HIS:HB3	12:K:29:ILE:HG13	1.98	0.44
12:K:99:GLN:HA	12:K:105:VAL:CG2	2.48	0.44
13:L:97:ARG:C	13:L:98:TYR:CD1	2.96	0.44
21:T:81:LYS:O	21:T:82:SER:C	2.60	0.44
1:A:174:C:H2'	1:A:175:C:C6	2.51	0.44
1:A:248:C:C2'	1:A:249:U:H5'	2.48	0.44
1:A:522:C:O2'	1:A:523:A:H5'	2.17	0.44
1:A:652:U:O4	1:A:752:G:O2'	2.29	0.44
1:A:1015:A:H2'	1:A:1016:A:C8	2.53	0.44
1:A:1190:G:O2'	1:A:1191:A:P	2.75	0.44
1:A:1385:G:H2'	1:A:1386:G:O4'	2.17	0.44
4:C:7:PRO:CB	4:C:11:ARG:HH21	2.31	0.44
4:C:58:GLU:H	4:C:65:ALA:HB3	1.81	0.44
4:C:79:ARG:C	4:C:81:GLY:H	2.24	0.44
4:C:196:LEU:HD23	4:C:196:LEU:N	2.30	0.44
10:I:65:VAL:CG2	10:I:73:GLN:HB3	2.43	0.44
14:M:84:ILE:HG13	14:M:86:CYS:H	1.82	0.44
16:O:81:LEU:C	16:O:81:LEU:CD2	2.91	0.44
20:S:11:VAL:HA	20:S:38:SER:HB2	2.00	0.44
21:T:41:ILE:O	21:T:43:LEU:N	2.51	0.44
21:T:41:ILE:C	21:T:43:LEU:H	2.26	0.44
1:A:695:A:H2'	1:A:696:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:959:A:H2	1:A:1221:G:N3	2.16	0.44
1:A:976:G:C8	1:A:1358:U:H2'	2.52	0.44
1:A:1053:G:C3'	1:A:1054:C:C5'	2.94	0.44
1:A:1090:U:H2'	1:A:1091:U:H6	1.82	0.44
1:A:1298:C:H2'	8:G:114:ARG:HH12	1.82	0.44
1:A:1318:A:H5'	20:S:10:PHE:CE1	2.53	0.44
1:A:1499:A:O2'	1:A:1500:A:H5'	2.18	0.44
1:A:1512:U:O2'	1:A:1513:A:H5'	2.17	0.44
3:B:100:GLY:O	3:B:101:MET:C	2.60	0.44
4:C:67:THR:O	4:C:69:HIS:CD2	2.71	0.44
5:D:58:LEU:HD13	5:D:58:LEU:C	2.43	0.44
6:E:31:LEU:HA	6:E:31:LEU:HD23	1.50	0.44
6:E:78:HIS:HD2	9:H:107:LEU:HD12	1.83	0.44
11:J:32:ALA:HB2	11:J:76:ASN:ND2	2.31	0.44
11:J:63:PHE:CE2	15:N:58:LYS:HG2	2.53	0.44
11:J:75:ILE:CG2	11:J:76:ASN:N	2.81	0.44
14:M:39:ILE:HD13	14:M:52:GLU:HB3	1.99	0.44
14:M:69:GLU:O	14:M:70:LEU:C	2.61	0.44
18:Q:59:ILE:HD13	18:Q:59:ILE:HA	1.67	0.44
19:R:36:ASN:O	19:R:37:VAL:C	2.60	0.44
19:R:66:LEU:HG	19:R:70:ILE:HD11	1.99	0.44
20:S:16:LEU:O	20:S:20:LEU:HG	2.18	0.44
20:S:49:ILE:H	20:S:49:ILE:CD1	2.26	0.44
21:T:86:ARG:O	21:T:90:GLN:HG3	2.18	0.44
1:A:90:U:H2'	1:A:91:C:C6	2.53	0.44
1:A:127:G:N2	18:Q:61:GLU:OE2	2.47	0.44
1:A:193:C:H1'	21:T:60:GLU:OE1	2.17	0.44
1:A:603:U:O2'	1:A:604:G:H5'	2.18	0.44
1:A:644:G:O2'	1:A:645:C:H5'	2.17	0.44
1:A:1097:C:H2'	1:A:1098:C:C6	2.53	0.44
1:A:1125:U:O4	11:J:5:ARG:NE	2.49	0.44
1:A:1207:G:H2'	1:A:1208:C:C6	2.50	0.44
1:A:1343:G:C1'	10:I:121:ARG:HH12	2.30	0.44
3:B:12:GLU:OE2	3:B:12:GLU:HA	2.07	0.44
3:B:29:ALA:HA	3:B:32:ILE:HD12	2.00	0.44
3:B:58:ILE:O	3:B:62:ALA:HB2	2.18	0.44
3:B:134:GLU:C	3:B:136:VAL:N	2.72	0.44
5:D:36:ARG:C	5:D:38:TYR:H	2.25	0.44
5:D:114:ARG:NH1	5:D:114:ARG:CG	2.79	0.44
5:D:150:GLU:HB2	5:D:151:LYS:HD2	2.00	0.44
5:D:202:LEU:O	5:D:203:VAL:C	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:36:ASP:C	6:E:38:GLN:N	2.75	0.44
7:F:47:ARG:HG2	7:F:47:ARG:HH11	1.81	0.44
9:H:121:ASP:O	9:H:122:ARG:C	2.61	0.44
10:I:38:GLN:OE1	10:I:39:GLY:N	2.51	0.44
10:I:50:LEU:HG	10:I:81:ILE:HG21	2.00	0.44
10:I:114:TYR:CE1	11:J:59:SER:O	2.70	0.44
20:S:19:VAL:C	20:S:21:GLU:N	2.76	0.44
21:T:26:ASN:HB3	21:T:71:THR:HG23	1.99	0.44
1:A:142:G:N3	1:A:196:A:H2	2.15	0.44
1:A:255:G:O3'	18:Q:17:LYS:HD2	2.18	0.44
1:A:260:G:H2'	1:A:261:U:C6	2.53	0.44
1:A:456:C:N4	1:A:476:G:H1	2.16	0.44
1:A:778:G:C5	1:A:779:C:C5	3.06	0.44
1:A:1403:C:H2'	1:A:1404:C:C6	2.53	0.44
1:A:1519:A:H3'	1:A:1520:G:C5'	2.48	0.44
3:B:24:TRP:CG	3:B:25:ASN:N	2.82	0.44
4:C:129:ALA:O	4:C:132:ARG:HB2	2.18	0.44
5:D:150:GLU:O	5:D:153:ARG:HB2	2.18	0.44
5:D:194:LEU:HD22	5:D:194:LEU:N	2.32	0.44
5:D:205:GLU:O	5:D:208:SER:HB2	2.18	0.44
6:E:75:THR:HG23	6:E:76:ILE:N	2.31	0.44
9:H:5:PRO:HA	9:H:8:ASP:HB3	1.99	0.44
10:I:40:LEU:O	10:I:41:VAL:C	2.61	0.44
10:I:128:ARG:HG2	10:I:128:ARG:OXT	2.18	0.44
11:J:22:LYS:C	11:J:24:VAL:N	2.76	0.44
11:J:64:GLU:HG3	15:N:59:ALA:HB2	1.98	0.44
13:L:88:GLY:H	13:L:98:TYR:HA	1.82	0.44
14:M:84:ILE:C	14:M:86:CYS:H	2.26	0.44
19:R:34:TYR:O	19:R:34:TYR:HD1	2.00	0.44
19:R:46:GLU:CD	19:R:46:GLU:N	2.75	0.44
19:R:75:ILE:C	19:R:77:GLY:H	2.25	0.44
20:S:8:GLY:O	20:S:9:VAL:O	2.36	0.44
20:S:61:TYR:C	20:S:61:TYR:HD2	2.26	0.44
1:A:523:A:C2	13:L:91:LYS:HB3	2.52	0.43
1:A:538:G:P	13:L:115:LYS:HG3	2.57	0.43
1:A:542:G:C5'	5:D:41:GLY:HA3	2.48	0.43
1:A:653:A:O5'	9:H:56:LYS:NZ	2.45	0.43
1:A:911:U:H2'	1:A:912:C:C6	2.52	0.43
1:A:1085:U:H3'	1:A:1086:U:H5	1.83	0.43
1:A:1309:G:H5'	14:M:78:ILE:HD11	2.00	0.43
1:A:1422:G:O2'	1:A:1423:G:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:118:LEU:C	3:B:120:ALA:N	2.72	0.43
3:B:157:ARG:O	3:B:158:LEU:C	2.60	0.43
4:C:54:ARG:CG	4:C:55:VAL:N	2.79	0.43
5:D:78:LEU:HD21	5:D:96:LEU:HB3	2.00	0.43
8:G:31:MET:SD	8:G:34:GLY:HA2	2.57	0.43
9:H:11:THR:HG22	9:H:15:ASN:HD21	1.83	0.43
9:H:38:ILE:HD12	9:H:38:ILE:H	1.81	0.43
9:H:119:LEU:HD12	9:H:124:ALA:CB	2.48	0.43
10:I:10:ARG:HD3	10:I:105:ASP:HB3	2.00	0.43
11:J:32:ALA:C	11:J:34:VAL:H	2.26	0.43
13:L:28:LYS:HD2	13:L:33:ARG:HH22	1.83	0.43
18:Q:100:LYS:C	18:Q:101:ARG:HE	2.25	0.43
20:S:16:LEU:C	20:S:18:LYS:N	2.75	0.43
1:A:337:C:H2'	1:A:338:A:H8	1.83	0.43
1:A:416:G:H2'	1:A:417:C:C6	2.53	0.43
1:A:460:A:N7	1:A:462:G:C5	2.86	0.43
1:A:537:G:OP1	13:L:113:ARG:NH2	2.50	0.43
1:A:691:G:O2'	1:A:797:C:H4'	2.18	0.43
1:A:772:U:O2'	1:A:773:G:H5'	2.17	0.43
1:A:897:C:H5''	18:Q:101:ARG:HH12	1.82	0.43
1:A:1053:G:O2'	1:A:1199:U:H5	2.02	0.43
1:A:1131:G:H2'	1:A:1132:C:H6	1.82	0.43
1:A:1386:G:O2'	1:A:1387:G:H5'	2.17	0.43
3:B:186:ALA:HB3	3:B:197:VAL:HG11	1.99	0.43
5:D:55:ALA:O	5:D:56:VAL:C	2.61	0.43
6:E:122:GLU:HG2	6:E:131:ILE:HD12	2.00	0.43
7:F:75:LEU:C	7:F:75:LEU:CD1	2.83	0.43
8:G:30:ILE:HD13	8:G:120:ILE:CD1	2.49	0.43
8:G:133:GLY:O	8:G:136:LYS:HB3	2.18	0.43
10:I:50:LEU:CA	10:I:55:ALA:HB3	2.49	0.43
10:I:69:GLY:C	10:I:73:GLN:HG3	2.43	0.43
10:I:109:VAL:HG12	10:I:110:GLU:N	2.33	0.43
11:J:12:ASP:OD1	11:J:15:THR:N	2.49	0.43
13:L:39:VAL:H	13:L:57:LYS:HB2	1.82	0.43
14:M:49:THR:HG22	14:M:51:ALA:N	2.29	0.43
16:O:87:ILE:CG2	16:O:88:ARG:N	2.53	0.43
19:R:47:THR:HA	19:R:83:GLU:CB	2.37	0.43
21:T:33:ILE:HD11	21:T:63:ILE:HA	1.99	0.43
1:A:39:G:O2'	1:A:40:C:H5'	2.18	0.43
1:A:791:G:C2'	1:A:792:A:C5'	2.96	0.43
1:A:1111:A:N6	4:C:177:THR:HA	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1249:C:C2'	1:A:1250:A:H5'	2.49	0.43
1:A:1286:A:C8	1:A:1287:A:C5'	3.01	0.43
1:A:1316:G:N2	1:A:1318:A:H3'	2.33	0.43
3:B:15:VAL:HG11	3:B:210:SER:HA	2.01	0.43
3:B:83:MET:HB3	3:B:235:SER:HB3	1.99	0.43
4:C:30:ARG:HG2	4:C:30:ARG:NH1	2.33	0.43
4:C:35:GLU:OE2	4:C:97:LYS:HD2	2.19	0.43
4:C:111:LEU:HD11	4:C:144:SER:O	2.17	0.43
6:E:74:GLY:HA3	6:E:116:THR:HG22	2.00	0.43
7:F:19:LEU:C	7:F:19:LEU:CD2	2.90	0.43
13:L:104:VAL:HG12	13:L:105:TYR:CD1	2.52	0.43
16:O:14:GLU:HA	16:O:14:GLU:OE2	2.18	0.43
17:P:12:LYS:O	17:P:13:HIS:CB	2.64	0.43
18:Q:63:ARG:HG2	18:Q:64:PRO:CD	2.49	0.43
19:R:66:LEU:HG	19:R:70:ILE:CD1	2.48	0.43
1:A:255:G:H2'	1:A:256:U:C6	2.53	0.43
1:A:299:G:H2'	1:A:300:A:C8	2.53	0.43
1:A:340:U:H2'	1:A:341:C:C6	2.53	0.43
1:A:1022:G:O2'	1:A:1023:G:H8	2.01	0.43
3:B:97:TRP:CH2	3:B:176:GLU:CD	2.96	0.43
4:C:36:ASP:O	4:C:39:ILE:HB	2.18	0.43
4:C:179:ARG:CD	4:C:206:GLU:HG2	2.48	0.43
10:I:118:LYS:HB2	10:I:118:LYS:HZ2	1.82	0.43
11:J:6:ILE:HD12	11:J:6:ILE:N	2.20	0.43
12:K:20:TYR:HE2	12:K:85:ARG:NH2	2.15	0.43
15:N:12:ARG:HD2	15:N:14:PRO:HD3	2.00	0.43
16:O:39:LEU:HD23	16:O:39:LEU:C	2.43	0.43
20:S:19:VAL:C	20:S:21:GLU:H	2.27	0.43
20:S:38:SER:OG	20:S:71:LEU:HD12	2.18	0.43
20:S:77:THR:CG2	20:S:78:ARG:HG3	2.43	0.43
1:A:51:A:N1	1:A:314:C:O2'	2.48	0.43
1:A:142:G:H2'	1:A:143:A:C8	2.53	0.43
1:A:429:U:H3	1:A:431:A:H62	1.66	0.43
1:A:459:G:H3'	1:A:460:A:C5'	2.49	0.43
1:A:1110:A:H8	1:A:1110:A:O5'	2.02	0.43
1:A:1250:A:H5''	10:I:67:GLY:HA2	1.99	0.43
3:B:23:ARG:NH1	3:B:24:TRP:HA	2.33	0.43
4:C:157:ILE:HD13	4:C:166:GLU:HB2	1.98	0.43
5:D:65:ARG:HD2	5:D:72:GLU:HA	1.99	0.43
5:D:149:ALA:O	5:D:152:SER:N	2.52	0.43
8:G:92:SER:C	8:G:94:ARG:N	2.75	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:154:TYR:O	8:G:155:ARG:C	2.61	0.43
9:H:83:ILE:O	9:H:83:ILE:CG2	2.66	0.43
10:I:45:ALA:O	10:I:48:GLU:CB	2.66	0.43
13:L:46:LYS:CG	13:L:47:LYS:N	2.77	0.43
14:M:58:GLU:C	14:M:60:VAL:N	2.75	0.43
15:N:21:TYR:O	15:N:21:TYR:HD2	2.01	0.43
16:O:39:LEU:HD21	16:O:56:LEU:HB2	2.00	0.43
17:P:20:VAL:HG23	17:P:21:VAL:N	2.33	0.43
21:T:54:LYS:HG3	21:T:100:ILE:CD1	2.47	0.43
1:A:50:A:N6	1:A:361:G:H4'	2.34	0.43
1:A:130:A:C8	18:Q:63:ARG:HG3	2.53	0.43
1:A:166:G:C2	1:A:167:G:C8	3.07	0.43
1:A:653:A:P	9:H:56:LYS:HZ1	2.42	0.43
1:A:818:G:H3'	1:A:819:A:C5'	2.49	0.43
1:A:889:A:H8	1:A:889:A:OP1	2.00	0.43
1:A:892:A:C6	1:A:893:C:C4	3.06	0.43
1:A:974:A:OP1	1:A:974:A:H8	2.01	0.43
1:A:1128:C:H1'	1:A:1146:A:H61	1.83	0.43
1:A:1370:G:O2'	1:A:1371:G:H5'	2.18	0.43
3:B:165:VAL:O	3:B:187:LEU:O	2.37	0.43
4:C:52:LEU:CD2	4:C:52:LEU:N	2.79	0.43
4:C:61:ALA:O	4:C:62:ASP:C	2.61	0.43
6:E:36:ASP:OD2	6:E:38:GLN:HB3	2.18	0.43
6:E:41:VAL:HG12	6:E:42:GLY:N	2.33	0.43
9:H:82:HIS:CG	9:H:83:ILE:H	2.37	0.43
10:I:85:LEU:CD2	10:I:96:LEU:HD21	2.49	0.43
13:L:24:VAL:HG12	13:L:26:ALA:HB2	2.00	0.43
1:A:110:C:N4	1:A:111:G:C6	2.87	0.43
1:A:191:G:N2	21:T:85:MET:HE1	2.34	0.43
1:A:344:A:C5'	1:A:345:C:H5	2.32	0.43
1:A:410:G:C6	1:A:429:U:H1'	2.53	0.43
1:A:596:C:O2'	1:A:597:G:H5'	2.18	0.43
1:A:662:G:O2'	1:A:836:G:H5'	2.18	0.43
1:A:787:A:H2'	1:A:788:U:C6	2.54	0.43
1:A:1096:C:H2'	1:A:1097:C:H6	1.83	0.43
3:B:47:THR:HA	3:B:202:PRO:CG	2.49	0.43
3:B:130:ARG:CD	3:B:131:PRO:HD2	2.48	0.43
3:B:145:LEU:HA	3:B:145:LEU:HD23	1.74	0.43
5:D:174:LEU:C	5:D:186:LEU:HD12	2.43	0.43
6:E:41:VAL:O	6:E:66:MET:HA	2.19	0.43
10:I:50:LEU:HD22	10:I:55:ALA:HB1	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:95:LYS:C	10:I:98:PRO:HD2	2.43	0.43
11:J:15:THR:CG2	11:J:16:LEU:HD23	2.34	0.43
11:J:51:ARG:CZ	11:J:61:GLU:HB2	2.46	0.43
12:K:29:ILE:C	12:K:29:ILE:HD12	2.44	0.43
12:K:44:SER:OG	12:K:47:VAL:N	2.51	0.43
12:K:54:ARG:HH11	12:K:54:ARG:CB	2.06	0.43
13:L:113:ARG:NH1	13:L:116:SER:H	2.17	0.43
17:P:17:TYR:HE1	17:P:41:PRO:HG2	1.84	0.43
17:P:52:ASP:CG	17:P:55:ARG:HG3	2.44	0.43
19:R:59:SER:OG	19:R:62:GLU:HG3	2.19	0.43
1:A:401:C:H6	1:A:401:C:O5'	2.01	0.43
1:A:474:G:C4	1:A:475:G:C8	3.07	0.43
1:A:538:G:O2'	1:A:539:A:H5'	2.19	0.43
1:A:1279:A:O2'	1:A:1282:C:N4	2.52	0.43
1:A:1288:A:N1	1:A:1371:G:H1'	2.33	0.43
1:A:1300:G:H1'	1:A:1301:U:H5	1.84	0.43
4:C:101:LEU:O	4:C:101:LEU:CD2	2.67	0.43
4:C:134:ILE:O	4:C:135:LYS:C	2.60	0.43
5:D:65:ARG:HD2	5:D:75:PHE:HB2	2.01	0.43
7:F:78:GLU:OE2	7:F:81:ILE:HD12	2.19	0.43
9:H:29:SER:O	9:H:30:ARG:C	2.62	0.43
10:I:113:LYS:N	10:I:113:LYS:CD	2.82	0.43
12:K:122:LYS:O	12:K:123:LYS:C	2.62	0.43
14:M:87:TYR:O	14:M:88:ARG:C	2.61	0.43
15:N:34:TYR:O	15:N:35:ARG:C	2.61	0.43
16:O:43:LEU:C	16:O:45:VAL:N	2.69	0.43
17:P:5:ARG:HA	17:P:70:ALA:HB2	2.00	0.43
17:P:74:LEU:O	17:P:75:ARG:C	2.59	0.43
1:A:293:G:C5	1:A:294:U:C5	3.07	0.43
1:A:927:G:H4'	1:A:1503:A:N7	2.34	0.43
1:A:1063:C:H2'	1:A:1064:G:C8	2.54	0.43
1:A:1293:G:O2'	1:A:1294:G:H5'	2.19	0.43
1:A:1305:G:N2	1:A:1331:G:C2'	2.81	0.43
3:B:137:ARG:HB3	3:B:137:ARG:NH1	2.33	0.43
3:B:213:LEU:HD23	3:B:213:LEU:C	2.44	0.43
4:C:54:ARG:CG	4:C:55:VAL:H	2.32	0.43
4:C:179:ARG:C	4:C:179:ARG:CD	2.78	0.43
5:D:200:GLU:O	5:D:201:GLN:C	2.61	0.43
7:F:4:TYR:CZ	7:F:72:VAL:HG21	2.54	0.43
7:F:48:LEU:HD13	7:F:52:ILE:HD12	2.01	0.43
7:F:67:MET:HE2	7:F:72:VAL:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:126:LYS:C	9:H:127:LEU:HD23	2.43	0.43
1:A:21:G:H2'	1:A:22:G:C8	2.54	0.43
1:A:417:C:O2'	1:A:418:C:H5'	2.19	0.43
1:A:883:C:O2'	1:A:884:U:H5'	2.19	0.43
1:A:910:C:H5''	13:L:97:ARG:NH2	2.33	0.43
1:A:1057:G:C4	1:A:1204:A:C2	3.07	0.43
1:A:1331:G:O2'	1:A:1332:A:OP2	2.29	0.43
1:A:1347:G:C8	10:I:107:ARG:HB3	2.54	0.43
1:A:1520:G:H2'	1:A:1521:G:H8	1.84	0.43
1:A:1521:G:H2'	1:A:1522:U:H6	1.79	0.43
3:B:184:VAL:CG2	3:B:198:ASP:H	2.28	0.43
3:B:204:ASN:O	3:B:205:ASP:C	2.62	0.43
5:D:177:ASP:N	5:D:182:LYS:O	2.51	0.43
6:E:13:ILE:HG13	6:E:13:ILE:O	2.18	0.43
6:E:151:LEU:HA	6:E:151:LEU:HD23	1.73	0.43
7:F:91:VAL:HG12	7:F:92:LYS:N	2.33	0.43
10:I:5:TYR:HE2	10:I:16:ARG:HB3	1.84	0.43
10:I:45:ALA:O	10:I:48:GLU:HB2	2.19	0.43
14:M:11:ARG:HG3	14:M:12:ASN:N	2.34	0.43
14:M:78:ILE:O	14:M:81:LEU:CD2	2.64	0.43
16:O:41:GLU:C	16:O:43:LEU:N	2.77	0.43
1:A:134:A:H2'	1:A:135:C:O4'	2.19	0.42
1:A:328:C:H4'	1:A:329:A:C5'	2.49	0.42
1:A:342:C:C2'	1:A:343:U:H5'	2.48	0.42
1:A:967:C:H2'	1:A:968:A:N7	2.34	0.42
1:A:1145:C:O2'	1:A:1146:A:C8	2.72	0.42
1:A:1226:C:C4	14:M:104:ARG:HG3	2.54	0.42
1:A:1394:A:C5	1:A:1501:C:H4'	2.54	0.42
3:B:27:LYS:HD3	3:B:195:ASP:OD2	2.19	0.42
3:B:71:VAL:O	3:B:165:VAL:HG22	2.18	0.42
3:B:108:ILE:O	3:B:111:ARG:HB2	2.18	0.42
4:C:34:LEU:CG	15:N:25:VAL:HG21	2.41	0.42
8:G:22:LEU:HD11	8:G:101:LEU:HD11	2.01	0.42
8:G:43:PHE:O	8:G:47:CYS:N	2.52	0.42
8:G:118:VAL:O	8:G:121:ALA:HB3	2.19	0.42
18:Q:81:ARG:HB2	18:Q:81:ARG:HE	1.65	0.42
20:S:20:LEU:HA	20:S:23:ASN:CG	2.44	0.42
20:S:58:VAL:O	20:S:58:VAL:HG23	2.19	0.42
1:A:344:A:H5''	1:A:345:C:C5	2.54	0.42
1:A:542:G:H2'	1:A:543:C:H6	1.84	0.42
1:A:688:G:N3	1:A:704:A:C2	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:956:U:O2'	1:A:957:U:H5'	2.19	0.42
1:A:1056:U:C5'	4:C:163:ALA:HB2	2.49	0.42
1:A:1077:G:N2	1:A:1080:A:OP2	2.50	0.42
1:A:1102:A:O4'	1:A:1102:A:OP2	2.37	0.42
1:A:1327:C:OP1	22:V:20:LYS:N	2.52	0.42
3:B:110:GLN:HA	3:B:113:HIS:CD2	2.52	0.42
4:C:55:VAL:O	4:C:55:VAL:CG1	2.66	0.42
4:C:155:GLY:O	4:C:196:LEU:HD22	2.19	0.42
6:E:16:THR:HG23	6:E:27:ARG:O	2.19	0.42
8:G:138:LYS:HZ3	8:G:142:GLU:CD	2.28	0.42
11:J:57:LYS:O	11:J:60:ARG:NE	2.52	0.42
13:L:43:VAL:HG12	13:L:44:THR:H	1.84	0.42
15:N:25:VAL:O	15:N:25:VAL:HG22	2.19	0.42
17:P:20:VAL:HG21	17:P:32:TYR:CD2	2.54	0.42
19:R:56:THR:C	19:R:58:LEU:H	2.27	0.42
21:T:54:LYS:CA	21:T:57:ARG:HD3	2.49	0.42
1:A:118:U:O4	1:A:289:G:H4'	2.19	0.42
1:A:190(L):U:O2'	1:A:191:G:H5'	2.19	0.42
1:A:373:A:H1'	1:A:481:G:H1'	2.02	0.42
1:A:446:G:O2'	1:A:447:G:H5'	2.19	0.42
1:A:511:C:C2	1:A:512:U:C5	3.08	0.42
1:A:833:U:H2'	1:A:834:C:H6	1.82	0.42
1:A:1096:C:H2'	1:A:1097:C:C6	2.54	0.42
1:A:1097:C:H2'	1:A:1098:C:H6	1.83	0.42
1:A:1152:A:H2'	1:A:1153:C:C6	2.54	0.42
1:A:1287:A:H2'	1:A:1288:A:C8	2.55	0.42
1:A:1349:A:P	10:I:118:LYS:NZ	2.92	0.42
1:A:1459:C:O2'	1:A:1460:A:H5'	2.20	0.42
1:A:1508:G:O2'	1:A:1509:C:H5'	2.19	0.42
3:B:230:VAL:HG12	3:B:231:GLU:H	1.84	0.42
4:C:151:VAL:C	4:C:152:ILE:HG13	2.43	0.42
6:E:101:ILE:O	6:E:101:ILE:HG22	2.17	0.42
7:F:15:ASP:HB3	7:F:18:GLN:CG	2.49	0.42
8:G:69:VAL:CG1	8:G:134:ALA:HB1	2.49	0.42
9:H:11:THR:CG2	9:H:15:ASN:HD21	2.32	0.42
9:H:62:TYR:C	9:H:63:LEU:HD12	2.45	0.42
12:K:88:GLY:O	12:K:90:GLY:N	2.40	0.42
19:R:47:THR:C	19:R:49:LYS:H	2.27	0.42
1:A:190(E):U:O2'	18:Q:63:ARG:NH2	2.52	0.42
1:A:413:G:N2	1:A:428:G:H1'	2.32	0.42
1:A:822:C:O2'	1:A:823:G:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1130:A:OP2	1:A:1131:G:OP2	2.36	0.42
1:A:1200:C:H1'	1:A:1204:A:H61	1.85	0.42
3:B:121:LEU:O	3:B:123:ALA:N	2.52	0.42
3:B:131:PRO:C	3:B:133:LYS:N	2.78	0.42
4:C:70:VAL:N	4:C:106:VAL:HG23	2.35	0.42
4:C:180:ALA:HA	4:C:206:GLU:HG3	2.01	0.42
5:D:61:LYS:NZ	5:D:62:GLN:HE21	2.18	0.42
5:D:65:ARG:HD2	5:D:75:PHE:CB	2.49	0.42
5:D:75:PHE:HE1	5:D:97:LEU:HD11	1.84	0.42
5:D:122:ARG:C	5:D:124:GLY:H	2.28	0.42
6:E:150:ARG:HB3	6:E:150:ARG:CZ	2.48	0.42
7:F:69:GLU:CD	7:F:69:GLU:H	2.26	0.42
7:F:87:ARG:HG3	7:F:87:ARG:NH1	2.34	0.42
8:G:80:VAL:HG21	8:G:154:TYR:CE2	2.55	0.42
10:I:5:TYR:HA	10:I:17:VAL:O	2.19	0.42
10:I:47:LEU:C	10:I:49:PRO:HD2	2.43	0.42
11:J:87:THR:C	11:J:89:ASP:H	2.27	0.42
19:R:36:ASN:C	19:R:38:GLU:N	2.76	0.42
20:S:36:ARG:NH2	20:S:75:ALA:CB	2.82	0.42
21:T:57:ARG:HH11	21:T:57:ARG:CG	2.32	0.42
21:T:58:LYS:O	21:T:61:SER:HB3	2.19	0.42
21:T:72:LEU:HD23	21:T:72:LEU:HA	1.89	0.42
22:V:19:GLY:C	22:V:21:TYR:N	2.77	0.42
1:A:190(J):U:H2'	1:A:190(K):G:C8	2.55	0.42
1:A:190(K):G:H2'	1:A:190(L):U:C6	2.55	0.42
1:A:435:C:O2'	1:A:436:C:H5'	2.19	0.42
1:A:451:A:N6	1:A:481:G:C4	2.88	0.42
1:A:750:G:C2	16:O:23:GLY:HA3	2.54	0.42
1:A:878:G:C1'	9:H:3:THR:HG21	2.49	0.42
1:A:959:A:C3'	1:A:960:U:H5''	2.46	0.42
1:A:1014:A:H4'	20:S:14:HIS:CE1	2.54	0.42
1:A:1424:C:O2'	1:A:1425:U:H5'	2.20	0.42
1:A:1511:G:C2'	1:A:1512:U:H5'	2.50	0.42
3:B:23:ARG:C	3:B:23:ARG:CD	2.92	0.42
3:B:136:VAL:HA	3:B:139:LYS:HB2	2.01	0.42
3:B:166:ASP:O	3:B:170:GLU:HB2	2.20	0.42
5:D:163:GLU:C	5:D:165:MET:H	2.27	0.42
5:D:167:GLY:O	5:D:168:ARG:C	2.63	0.42
7:F:15:ASP:HB3	7:F:18:GLN:CD	2.44	0.42
10:I:11:LYS:O	10:I:11:LYS:HG2	2.19	0.42
15:N:3:ARG:C	15:N:5:ALA:N	2.74	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:77:ALA:O	17:P:78:GLY:C	2.59	0.42
19:R:47:THR:C	19:R:49:LYS:N	2.77	0.42
20:S:67:VAL:O	20:S:69:HIS:N	2.52	0.42
21:T:48:LYS:O	21:T:50:GLU:N	2.53	0.42
1:A:189:G:H2'	1:A:190:C:C6	2.55	0.42
1:A:374:A:C6	1:A:375:U:C4	3.07	0.42
1:A:482:A:C2	1:A:483:C:H1'	2.54	0.42
1:A:731:G:H2'	1:A:732:C:H6	1.85	0.42
1:A:951:G:N2	14:M:126:LYS:O	2.53	0.42
1:A:1426:C:H2'	1:A:1427:U:H6	1.81	0.42
1:A:1430:C:H2'	1:A:1431:C:H6	1.84	0.42
4:C:13:GLY:C	4:C:14:ILE:HD13	2.45	0.42
4:C:90:GLU:C	4:C:92:ALA:N	2.77	0.42
4:C:92:ALA:HA	4:C:95:THR:O	2.19	0.42
4:C:97:LYS:O	4:C:98:ASN:HB3	2.20	0.42
6:E:15:ARG:CD	6:E:26:PHE:CD2	2.98	0.42
9:H:74:PRO:O	9:H:75:ARG:C	2.61	0.42
11:J:62:HIS:C	15:N:59:ALA:HB3	2.44	0.42
12:K:66:LEU:O	12:K:69:ALA:HB3	2.19	0.42
13:L:114:LYS:HB3	13:L:114:LYS:HE2	1.88	0.42
13:L:117:ARG:CZ	13:L:124:LYS:HA	2.50	0.42
14:M:16:ASP:OD1	14:M:17:VAL:N	2.42	0.42
18:Q:11:VAL:HB	18:Q:88:TYR:CD2	2.55	0.42
19:R:35:ARG:C	19:R:37:VAL:N	2.77	0.42
1:A:135:C:C2	17:P:1:MET:HB2	2.53	0.42
1:A:718:G:H4'	12:K:117:ASN:ND2	2.35	0.42
1:A:812:C:H4'	1:A:813:U:H5'	2.02	0.42
1:A:945:G:C2	1:A:946:A:C8	3.08	0.42
1:A:1339:A:H2'	1:A:1340:A:O4'	2.20	0.42
3:B:94:ASN:O	3:B:95:GLN:C	2.63	0.42
4:C:65:ALA:O	4:C:66:VAL:C	2.62	0.42
5:D:78:LEU:HB3	5:D:93:PHE:HE2	1.85	0.42
6:E:12:LEU:C	6:E:12:LEU:CD2	2.93	0.42
7:F:94:GLN:O	7:F:95:GLU:C	2.62	0.42
9:H:53:VAL:C	9:H:55:GLY:N	2.76	0.42
10:I:108:VAL:HG12	10:I:109:VAL:N	2.35	0.42
11:J:69:ASN:O	11:J:70:ARG:CD	2.68	0.42
13:L:11:VAL:HG21	18:Q:34:LYS:HG2	2.01	0.42
14:M:88:ARG:HG3	14:M:98:VAL:HG12	2.01	0.42
18:Q:60:ILE:C	18:Q:71:PHE:HD1	2.27	0.42
21:T:84:LEU:HD23	21:T:88:VAL:CG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:92:LEU:HD23	21:T:92:LEU:HA	1.81	0.42
22:V:14:TRP:HE3	22:V:15:ARG:HG3	1.84	0.42
1:A:80:G:C3'	1:A:81:U:C5'	2.95	0.42
1:A:300:A:H8	1:A:300:A:O5'	2.02	0.42
1:A:518:C:H2'	1:A:530:G:C8	2.55	0.42
1:A:707:C:H2'	1:A:708:C:H6	1.85	0.42
1:A:748:C:O2'	1:A:749:C:P	2.78	0.42
1:A:1009:G:H1	1:A:1021:G:H1'	1.84	0.42
1:A:1193:G:C2'	1:A:1194:U:H5'	2.49	0.42
3:B:8:LYS:HB2	3:B:9:GLU:H	1.49	0.42
3:B:75:LYS:C	3:B:77:ALA:N	2.77	0.42
3:B:221:LEU:HA	3:B:224:GLN:HB3	2.02	0.42
4:C:173:VAL:N	4:C:174:PRO:CD	2.82	0.42
5:D:119:GLN:CG	5:D:123:HIS:CD2	3.03	0.42
11:J:47:PHE:CZ	15:N:37:PHE:HE1	2.37	0.42
12:K:49:GLY:O	12:K:50:TYR:O	2.38	0.42
13:L:115:LYS:O	13:L:117:ARG:HG3	2.20	0.42
14:M:78:ILE:H	14:M:78:ILE:HD12	1.83	0.42
14:M:81:LEU:HD23	14:M:81:LEU:C	2.45	0.42
16:O:22:THR:O	16:O:27:VAL:HB	2.20	0.42
17:P:75:ARG:HH11	17:P:75:ARG:HG3	1.84	0.42
19:R:65:ILE:HG13	19:R:65:ILE:H	1.66	0.42
1:A:131:C:H2'	1:A:132:C:H6	1.83	0.42
1:A:306:G:O2'	1:A:307:C:H5'	2.20	0.42
1:A:376:G:O2'	1:A:377:G:H5'	2.20	0.42
1:A:657:G:H1	1:A:749:C:H42	1.68	0.42
1:A:754:C:O2	1:A:754:C:H3'	2.19	0.42
1:A:953:G:H2'	1:A:954:G:O4'	2.20	0.42
1:A:1131:G:O2'	1:A:1132:C:H5'	2.20	0.42
1:A:1460:A:H2'	1:A:1461:G:O4'	2.20	0.42
3:B:39:ILE:HG22	3:B:40:HIS:O	2.20	0.42
3:B:93:VAL:HG11	3:B:97:TRP:CD1	2.55	0.42
3:B:119:GLU:OE1	3:B:153:ARG:NH2	2.41	0.42
4:C:35:GLU:O	4:C:38:ARG:HB2	2.19	0.42
5:D:77:ASN:O	5:D:78:LEU:C	2.62	0.42
8:G:111:ARG:HD2	8:G:123:GLU:HB2	2.02	0.42
8:G:113:GLU:CD	8:G:113:GLU:H	2.26	0.42
8:G:115:ARG:CB	8:G:115:ARG:HH11	2.33	0.42
9:H:26:VAL:HA	9:H:27:PRO:HD3	1.88	0.42
11:J:6:ILE:H	11:J:6:ILE:CD1	2.14	0.42
14:M:6:GLY:O	14:M:7:VAL:HG22	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:53:LEU:HB3	15:N:56:VAL:HG21	2.01	0.42
15:N:54:PRO:C	15:N:56:VAL:H	2.28	0.42
17:P:28:ARG:HG2	17:P:29:ASP:OD2	2.19	0.42
17:P:67:THR:CG2	17:P:68:ASP:N	2.82	0.42
19:R:22:VAL:O	19:R:26:LEU:HD22	2.20	0.42
19:R:38:GLU:N	19:R:38:GLU:OE2	2.52	0.42
19:R:53:ARG:NH2	19:R:60:GLY:CA	2.79	0.42
1:A:124:G:C5	1:A:125:U:C4	3.08	0.42
1:A:555:C:H2'	1:A:556:C:C6	2.55	0.42
1:A:877:C:H5''	9:H:88:LYS:HD3	2.01	0.42
1:A:1191:A:OP2	4:C:3:ASN:ND2	2.53	0.42
1:A:1221:G:C2'	1:A:1222:G:H5'	2.50	0.42
1:A:1237:C:H2'	1:A:1336:C:H5	1.85	0.42
1:A:1258:G:H2'	1:A:1259:C:C6	2.54	0.42
1:A:1298:C:C4	8:G:114:ARG:HD3	2.55	0.42
1:A:1405:G:P	23:A:1545:PAR:HO34	2.43	0.42
3:B:118:LEU:C	3:B:120:ALA:H	2.26	0.42
3:B:144:ARG:O	3:B:145:LEU:C	2.63	0.42
3:B:221:LEU:HD13	3:B:221:LEU:C	2.45	0.42
4:C:23:TYR:CD1	11:J:10:GLY:HA2	2.55	0.42
4:C:95:THR:O	4:C:97:LYS:N	2.46	0.42
5:D:10:ARG:HG3	5:D:10:ARG:NH1	2.35	0.42
5:D:111:ALA:HB2	5:D:117:ALA:HA	2.02	0.42
5:D:162:LEU:HD13	5:D:181:MET:CE	2.43	0.42
5:D:177:ASP:OD1	5:D:177:ASP:O	2.38	0.42
6:E:80:ILE:HD12	6:E:80:ILE:N	2.26	0.42
7:F:22:GLU:OE2	7:F:22:GLU:HA	2.20	0.42
8:G:16:LEU:HD22	8:G:16:LEU:N	2.35	0.42
8:G:72:ARG:HB2	8:G:142:GLU:OE1	2.20	0.42
9:H:9:MET:O	9:H:10:LEU:C	2.61	0.42
13:L:30:ALA:HB1	13:L:31:PRO:CD	2.50	0.42
13:L:65:GLU:CD	13:L:65:GLU:N	2.78	0.42
13:L:83:VAL:CG2	13:L:84:LEU:N	2.82	0.42
19:R:51:LEU:HA	19:R:52:PRO:HD3	1.81	0.42
20:S:15:LEU:O	20:S:19:VAL:N	2.53	0.42
20:S:20:LEU:CA	20:S:23:ASN:HB2	2.50	0.42
21:T:56:MET:O	21:T:59:ALA:HB3	2.19	0.42
21:T:63:ILE:O	21:T:66:ALA:HB3	2.19	0.42
1:A:9:G:OP1	6:E:121:LYS:HE3	2.20	0.41
1:A:180:U:C2'	1:A:181:G:H5'	2.48	0.41
1:A:913:A:O2'	1:A:914:A:P	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:928:G:O2'	1:A:929:G:H5'	2.20	0.41
1:A:960:U:O2'	1:A:1223:C:H4'	2.19	0.41
1:A:974:A:OP2	15:N:41:ARG:NH1	2.52	0.41
1:A:1305:G:OP1	22:V:2:GLY:HA3	2.21	0.41
1:A:1305:G:H5''	1:A:1305:G:H8	1.84	0.41
1:A:1305:G:H22	1:A:1331:G:C2'	2.33	0.41
1:A:1306:A:N6	1:A:1331:G:H1'	2.34	0.41
1:A:1418:A:H2'	1:A:1419:G:O4'	2.20	0.41
3:B:92:TYR:CE1	3:B:151:GLY:N	2.88	0.41
3:B:176:GLU:O	3:B:177:ALA:C	2.62	0.41
5:D:170:VAL:HG13	5:D:174:LEU:HB2	2.02	0.41
6:E:144:THR:HG22	6:E:145:LYS:N	2.35	0.41
11:J:22:LYS:NZ	11:J:91:PRO:HD3	2.34	0.41
12:K:115:PRO:C	12:K:117:ASN:N	2.77	0.41
13:L:104:VAL:O	13:L:105:TYR:HB2	2.19	0.41
16:O:64:ARG:HH11	16:O:64:ARG:HG3	1.85	0.41
18:Q:18:THR:HG23	18:Q:69:LYS:CE	2.43	0.41
20:S:16:LEU:O	20:S:17:GLU:C	2.63	0.41
1:A:39:G:H2'	1:A:40:C:H6	1.85	0.41
1:A:261:U:O2	1:A:263:A:C8	2.73	0.41
1:A:399:G:O2'	1:A:400:C:H5'	2.20	0.41
1:A:405:U:C3'	1:A:406:G:H5'	2.45	0.41
1:A:457:C:O2'	1:A:458:C:H5'	2.20	0.41
1:A:760:G:O2'	1:A:761:G:H5'	2.20	0.41
1:A:814:A:N7	1:A:816:A:C4	2.88	0.41
1:A:968:A:H4'	1:A:969:A:OP2	2.20	0.41
1:A:1349:A:H2'	1:A:1350:A:H8	1.85	0.41
3:B:88:ALA:CB	3:B:90:MET:HG2	2.49	0.41
3:B:92:TYR:CD1	3:B:151:GLY:HA3	2.56	0.41
3:B:167:PRO:CD	3:B:188:ALA:HB2	2.50	0.41
4:C:46:GLU:HB3	4:C:83:ARG:NH2	2.35	0.41
4:C:193:TYR:HE1	4:C:196:LEU:HD21	1.84	0.41
6:E:115:VAL:CG1	6:E:116:THR:N	2.81	0.41
8:G:78:ARG:HH11	8:G:154:TYR:HB3	1.85	0.41
9:H:97:VAL:HA	9:H:100:ILE:CD1	2.50	0.41
12:K:88:GLY:C	12:K:90:GLY:N	2.74	0.41
12:K:93:GLN:O	12:K:96:ARG:N	2.53	0.41
12:K:95:ILE:HG21	12:K:108:ILE:HD13	2.02	0.41
12:K:110:ASP:CB	19:R:88:LYS:HZ2	2.32	0.41
14:M:91:ARG:HA	14:M:91:ARG:HD2	1.91	0.41
19:R:30:ASP:C	19:R:32:ARG:N	2.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:2:GLY:O	22:V:3:LYS:C	2.64	0.41
1:A:246:A:O2'	18:Q:99:SER:HB2	2.19	0.41
1:A:416:G:C6	1:A:417:C:C4	3.08	0.41
1:A:450:G:N7	1:A:481:G:O6	2.53	0.41
1:A:639:G:O2'	1:A:640:A:H5'	2.20	0.41
1:A:791:G:C2'	1:A:792:A:H5'	2.44	0.41
1:A:957:U:H3	1:A:960:U:C5'	2.33	0.41
3:B:105:PHE:O	3:B:106:LYS:C	2.63	0.41
8:G:37:ASN:C	8:G:39:ALA:N	2.77	0.41
12:K:27:ASN:OD1	12:K:55:LYS:HG2	2.20	0.41
12:K:104:GLN:HE22	12:K:106:LYS:HD3	1.84	0.41
13:L:88:GLY:N	13:L:98:TYR:HA	2.36	0.41
14:M:71:ARG:HG2	14:M:71:ARG:HH11	1.86	0.41
14:M:72:ALA:O	14:M:73:GLU:C	2.64	0.41
16:O:37:ASN:O	16:O:40:SER:HB2	2.20	0.41
17:P:8:ARG:HB2	17:P:28:ARG:HH12	1.77	0.41
19:R:38:GLU:CD	19:R:38:GLU:N	2.71	0.41
19:R:87:ARG:HH11	19:R:87:ARG:CG	2.29	0.41
21:T:8:ARG:HB2	21:T:9:ASN:H	1.67	0.41
1:A:256:U:C5'	18:Q:17:LYS:NZ	2.83	0.41
1:A:636:U:O2'	1:A:637:G:H5'	2.20	0.41
1:A:663:A:C2'	1:A:664:G:H5'	2.50	0.41
1:A:851:G:O2'	1:A:852:G:H5'	2.21	0.41
1:A:940:C:C4	1:A:941:G:N7	2.89	0.41
1:A:1033:G:O2'	1:A:1034:G:H5'	2.20	0.41
1:A:1054:C:C2'	1:A:1055:A:H5''	2.50	0.41
1:A:1059:C:O2'	1:A:1060:C:H5'	2.20	0.41
1:A:1374:A:C2'	1:A:1375:A:H5'	2.49	0.41
1:A:1490:C:O2'	1:A:1491:G:H5'	2.20	0.41
3:B:9:GLU:OE1	3:B:11:LEU:C	2.64	0.41
3:B:30:ARG:HG3	3:B:31:TYR:CE2	2.56	0.41
4:C:83:ARG:O	4:C:86:VAL:N	2.53	0.41
6:E:15:ARG:O	6:E:27:ARG:O	2.39	0.41
6:E:92:LYS:HD3	6:E:119:LEU:HD12	2.02	0.41
6:E:105:VAL:HB	6:E:106:PRO:HD3	2.03	0.41
6:E:110:LEU:CD1	6:E:118:ILE:HD12	2.38	0.41
6:E:131:ILE:O	6:E:132:ALA:C	2.64	0.41
9:H:31:PHE:O	9:H:32:LYS:C	2.63	0.41
10:I:97:LYS:HG2	10:I:102:LEU:HD12	2.00	0.41
13:L:61:THR:C	13:L:63:GLY:N	2.77	0.41
14:M:39:ILE:HG12	14:M:55:ARG:NH2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:71:ARG:HG2	14:M:71:ARG:NH1	2.36	0.41
16:O:4:THR:O	16:O:5:LYS:C	2.62	0.41
16:O:57:LEU:HA	16:O:57:LEU:HD12	1.72	0.41
18:Q:27:PHE:CD1	18:Q:27:PHE:C	2.97	0.41
20:S:34:TRP:N	20:S:34:TRP:CE3	2.88	0.41
21:T:38:LYS:O	21:T:39:LYS:C	2.63	0.41
21:T:80:ARG:O	21:T:81:LYS:C	2.62	0.41
1:A:190(H):G:O2'	1:A:190(I):G:H5'	2.20	0.41
1:A:248:C:O2'	1:A:249:U:H5'	2.20	0.41
1:A:339:C:H2'	1:A:340:U:C6	2.56	0.41
1:A:344:A:H5''	1:A:345:C:H5	1.84	0.41
1:A:353:A:H5'	1:A:353:A:H8	1.77	0.41
1:A:446:G:C2'	1:A:447:G:H5'	2.51	0.41
1:A:658:G:C6	1:A:749:C:N4	2.89	0.41
1:A:977:A:C8	1:A:1223:C:N3	2.89	0.41
1:A:1104:G:P	3:B:111:ARG:HD2	2.61	0.41
1:A:1224:G:N2	1:A:1362:C:N3	2.63	0.41
1:A:1286:A:H4'	22:V:25:LYS:NZ	2.36	0.41
1:A:1342:C:H5''	10:I:125:TYR:CE1	2.55	0.41
3:B:111:ARG:NE	3:B:111:ARG:HA	2.35	0.41
3:B:138:LEU:C	3:B:140:HIS:N	2.76	0.41
3:B:164:VAL:O	3:B:186:ALA:HA	2.19	0.41
4:C:179:ARG:O	4:C:180:ALA:C	2.63	0.41
5:D:3:ARG:O	5:D:4:TYR:C	2.63	0.41
5:D:13:ARG:HA	5:D:33:MET:SD	2.60	0.41
6:E:18:ARG:HH21	6:E:27:ARG:HH21	1.67	0.41
11:J:27:ALA:C	11:J:29:ARG:N	2.78	0.41
11:J:92:THR:C	11:J:94:VAL:N	2.73	0.41
14:M:80:ARG:O	14:M:84:ILE:HG23	2.20	0.41
15:N:24:CYS:C	15:N:26:ARG:H	2.29	0.41
18:Q:27:PHE:HD1	18:Q:28:PRO:O	2.03	0.41
18:Q:51:TYR:CD1	18:Q:51:TYR:N	2.87	0.41
21:T:84:LEU:HD23	21:T:88:VAL:HG23	2.02	0.41
1:A:750:G:H1'	16:O:22:THR:OG1	2.20	0.41
1:A:777:A:C6	1:A:778:G:C4	3.08	0.41
1:A:1030(C):G:C2	1:A:1030(D):A:H1'	2.56	0.41
1:A:1101:A:H4'	1:A:1102:A:O5'	2.20	0.41
1:A:1128:C:C4	1:A:1139:G:C5	3.08	0.41
1:A:1329:A:C2'	1:A:1330:U:H5'	2.50	0.41
3:B:10:LEU:C	3:B:12:GLU:N	2.78	0.41
4:C:186:PHE:CG	4:C:187:ALA:N	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:193:TYR:CD1	4:C:193:TYR:C	2.99	0.41
5:D:10:ARG:CG	5:D:11:LEU:HD23	2.51	0.41
6:E:40:ARG:HG2	6:E:40:ARG:NH1	2.32	0.41
8:G:24:THR:O	8:G:25:ALA:C	2.63	0.41
10:I:8:GLY:HA2	10:I:79:LEU:CG	2.50	0.41
11:J:9:ARG:HB3	11:J:9:ARG:HH11	1.82	0.41
14:M:9:ILE:N	14:M:9:ILE:CD1	2.81	0.41
14:M:78:ILE:O	14:M:79:LYS:C	2.64	0.41
20:S:41:VAL:HB	20:S:42:PRO:HD2	2.03	0.41
1:A:139:G:O2'	1:A:140:A:H5'	2.20	0.41
1:A:187:C:O4'	21:T:85:MET:HE2	2.21	0.41
1:A:730:G:H2'	1:A:731:G:H5'	2.03	0.41
1:A:1147:C:O2	10:I:16:ARG:NH1	2.54	0.41
1:A:1221:G:H4'	20:S:53:ASN:O	2.20	0.41
1:A:1332:A:C2	1:A:1333:A:C4	3.08	0.41
3:B:42:ILE:HD11	3:B:203:GLY:O	2.21	0.41
3:B:103:THR:N	3:B:176:GLU:OE1	2.49	0.41
3:B:163:PHE:HA	3:B:185:ILE:HB	2.03	0.41
3:B:178:ARG:HH22	9:H:68:ARG:HH22	1.69	0.41
4:C:47:LEU:N	4:C:47:LEU:CD1	2.84	0.41
5:D:161:ASN:C	5:D:163:GLU:N	2.76	0.41
7:F:30:LEU:CA	7:F:35:ALA:HB3	2.51	0.41
7:F:98:LEU:HD22	7:F:101:ALA:HB2	2.03	0.41
8:G:58:PRO:HG2	8:G:59:LEU:H	1.86	0.41
8:G:149:ARG:HD2	8:G:149:ARG:O	2.21	0.41
8:G:150:ALA:C	8:G:152:ALA:H	2.28	0.41
11:J:6:ILE:CD1	11:J:71:LEU:O	2.69	0.41
13:L:44:THR:HA	13:L:45:PRO:HD3	1.84	0.41
13:L:117:ARG:NH2	13:L:124:LYS:HA	2.35	0.41
15:N:47:LEU:HD22	15:N:52:GLN:CG	2.51	0.41
16:O:21:ASP:OD2	16:O:24:SER:HB3	2.21	0.41
20:S:29:ARG:O	20:S:30:LEU:HB2	2.19	0.41
1:A:76:C:H2'	1:A:77:G:H8	1.85	0.41
1:A:190(B):C:H2'	1:A:190(C):C:O4'	2.20	0.41
1:A:706:A:C1'	12:K:29:ILE:HD11	2.51	0.41
1:A:938:A:C6	1:A:939:G:C5	3.08	0.41
1:A:1263:C:O2'	1:A:1264:C:H5'	2.21	0.41
1:A:1309:G:C6	1:A:1310:G:C5	3.09	0.41
1:A:1330:U:OP1	14:M:23:TYR:O	2.39	0.41
1:A:1520:G:H2'	1:A:1521:G:C8	2.56	0.41
3:B:90:MET:HA	3:B:91:PRO:HD3	1.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:38:ARG:HG3	4:C:38:ARG:HH11	1.86	0.41
4:C:177:THR:CG2	4:C:177:THR:O	2.68	0.41
5:D:17:VAL:CG1	5:D:18:LYS:H	2.33	0.41
5:D:58:LEU:HD12	5:D:59:ARG:HD2	2.02	0.41
7:F:41:GLU:HB2	7:F:62:TRP:HB3	2.03	0.41
8:G:115:ARG:HB3	8:G:115:ARG:NH1	2.36	0.41
9:H:138:TRP:OXT	9:H:138:TRP:CE3	2.70	0.41
10:I:42:ARG:O	10:I:43:ALA:C	2.64	0.41
16:O:3:ILE:HG23	16:O:7:GLU:OE1	2.20	0.41
16:O:31:LEU:HA	16:O:31:LEU:HD12	1.82	0.41
19:R:76:LEU:HB2	19:R:78:LEU:HG	2.03	0.41
20:S:33:THR:HG22	20:S:34:TRP:N	2.35	0.41
20:S:53:ASN:N	20:S:53:ASN:ND2	2.66	0.41
1:A:89:C:H2'	1:A:90:U:O4'	2.21	0.41
1:A:370:C:H2'	1:A:371:G:H8	1.85	0.41
1:A:521:G:O2'	1:A:522:C:H5'	2.21	0.41
1:A:684:A:N3	12:K:39:PRO:HG2	2.36	0.41
1:A:878:G:C5'	9:H:89:PRO:HG2	2.50	0.41
1:A:922:G:H5'	6:E:19:MET:O	2.21	0.41
1:A:941:G:N2	1:A:942:G:H1'	2.35	0.41
1:A:952:U:O2'	1:A:953:G:H5'	2.20	0.41
1:A:975:A:H5'	1:A:975:A:H8	1.85	0.41
1:A:1064:G:H1'	1:A:1190:G:N2	2.36	0.41
1:A:1121:U:H2'	1:A:1122:U:H6	1.86	0.41
1:A:1165:C:O2'	1:A:1166:G:H5'	2.20	0.41
1:A:1182:G:H4'	1:A:1183:A:C5'	2.51	0.41
1:A:1272:G:C6	1:A:1273:G:C5	3.09	0.41
1:A:1416:G:H2'	1:A:1417:G:O4'	2.21	0.41
3:B:74:LYS:CE	3:B:166:ASP:HB2	2.50	0.41
3:B:88:ALA:C	3:B:90:MET:N	2.67	0.41
4:C:19:GLU:O	4:C:40:ARG:NH2	2.48	0.41
4:C:84:ILE:O	4:C:84:ILE:HG12	2.19	0.41
5:D:93:PHE:O	5:D:94:LEU:C	2.62	0.41
6:E:28:PHE:CD1	6:E:28:PHE:N	2.88	0.41
6:E:89:ILE:CD1	6:E:90:VAL:N	2.83	0.41
7:F:15:ASP:O	7:F:18:GLN:N	2.54	0.41
8:G:16:LEU:HD22	8:G:16:LEU:H	1.86	0.41
8:G:121:ALA:O	8:G:125:MET:HG3	2.20	0.41
8:G:135:VAL:O	8:G:136:LYS:C	2.64	0.41
8:G:153:HIS:C	8:G:155:ARG:N	2.77	0.41
8:G:155:ARG:HB3	8:G:156:TRP:H	1.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:28:ALA:HB3	9:H:57:PRO:HB2	2.02	0.41
10:I:4:TYR:HB2	10:I:19:LEU:HB2	2.01	0.41
10:I:77:ILE:O	10:I:81:ILE:HG13	2.21	0.41
11:J:54:PHE:O	11:J:55:LYS:HG2	2.21	0.41
12:K:110:ASP:CB	19:R:88:LYS:NZ	2.81	0.41
13:L:28:LYS:O	13:L:29:GLY:C	2.64	0.41
14:M:2:ALA:C	14:M:9:ILE:HG23	2.46	0.41
14:M:22:ILE:CD1	14:M:25:ILE:HD12	2.39	0.41
16:O:78:TYR:O	16:O:79:ARG:C	2.62	0.41
17:P:67:THR:O	17:P:69:THR:N	2.54	0.41
17:P:75:ARG:C	17:P:77:ALA:N	2.79	0.41
18:Q:93:GLN:O	18:Q:94:ASN:C	2.64	0.41
19:R:39:VAL:HG12	19:R:40:LEU:HD23	2.03	0.41
21:T:20:LEU:HA	21:T:20:LEU:HD23	1.87	0.41
21:T:28:ALA:O	21:T:29:LYS:C	2.64	0.41
1:A:51:A:H4'	1:A:52:G:C5'	2.51	0.41
1:A:51:A:H61	1:A:314:C:H1'	1.86	0.41
1:A:267:C:P	18:Q:67:LYS:HB2	2.61	0.41
1:A:397:A:C6	1:A:548:G:N7	2.89	0.41
1:A:452:A:H2'	1:A:453:A:C8	2.56	0.41
1:A:748:C:O2'	1:A:749:C:OP2	2.36	0.41
1:A:837:G:C2	1:A:850:U:O2	2.74	0.41
1:A:1221:G:O2'	1:A:1222:G:H5'	2.21	0.41
1:A:1301:U:O2'	1:A:1302:U:P	2.79	0.41
4:C:39:ILE:O	4:C:41:GLY:N	2.54	0.41
4:C:134:ILE:HG23	4:C:151:VAL:CB	2.43	0.41
4:C:165:THR:O	4:C:165:THR:HG22	2.20	0.41
4:C:171:GLY:O	4:C:173:VAL:HG23	2.21	0.41
4:C:191:THR:HG21	4:C:193:TYR:CE2	2.56	0.41
5:D:200:GLU:OE1	5:D:200:GLU:N	2.44	0.41
6:E:18:ARG:NH2	6:E:27:ARG:HH21	2.19	0.41
7:F:67:MET:HB2	7:F:68:PRO:CD	2.50	0.41
8:G:52:GLU:HG2	8:G:52:GLU:O	2.21	0.41
9:H:31:PHE:O	9:H:35:ILE:HG13	2.20	0.41
11:J:27:ALA:O	11:J:29:ARG:N	2.48	0.41
11:J:64:GLU:HG3	15:N:59:ALA:CB	2.51	0.41
11:J:71:LEU:O	11:J:72:VAL:CB	2.69	0.41
16:O:74:ASP:OD1	16:O:77:ARG:N	2.41	0.41
17:P:43:LYS:HD3	17:P:48:TRP:CE2	2.56	0.41
19:R:39:VAL:HG12	19:R:40:LEU:N	2.36	0.41
21:T:53:LEU:HD13	21:T:101:GLY:CA	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:502:G:C4	1:A:503:C:C6	3.09	0.40
1:A:602:A:C2	1:A:637:G:C2	3.09	0.40
1:A:627:G:H2'	1:A:628:G:H8	1.86	0.40
1:A:982:U:H5''	15:N:6:LEU:HD13	2.03	0.40
1:A:1066:C:C2'	1:A:1067:A:H5'	2.51	0.40
1:A:1275:A:H2'	1:A:1276:G:O4'	2.20	0.40
1:A:1440:C:C2'	1:A:1441:G:H5'	2.51	0.40
3:B:69:LEU:HD23	3:B:69:LEU:C	2.46	0.40
3:B:84:GLU:HG3	3:B:215:LEU:HB3	2.03	0.40
3:B:144:ARG:HG3	3:B:145:LEU:H	1.85	0.40
3:B:189:ASP:O	3:B:191:ASP:N	2.55	0.40
8:G:69:VAL:HG11	8:G:134:ALA:HB1	2.03	0.40
10:I:96:LEU:HD12	10:I:96:LEU:N	2.36	0.40
11:J:10:GLY:N	11:J:16:LEU:HD11	2.36	0.40
12:K:110:ASP:HB2	19:R:88:LYS:CD	2.51	0.40
13:L:46:LYS:NZ	13:L:47:LYS:HG3	2.37	0.40
13:L:58:VAL:O	13:L:65:GLU:HA	2.21	0.40
13:L:83:VAL:HG23	13:L:100:ILE:HG23	2.00	0.40
14:M:22:ILE:HB	14:M:25:ILE:HD12	2.02	0.40
14:M:73:GLU:O	14:M:76:ALA:HB3	2.21	0.40
17:P:67:THR:HG22	17:P:69:THR:N	2.36	0.40
21:T:16:HIS:O	21:T:19:SER:N	2.54	0.40
22:V:21:TYR:O	22:V:22:ARG:HB2	2.20	0.40
1:A:68:G:H2'	1:A:69:G:O4'	2.21	0.40
1:A:104:G:C6	1:A:105:G:N7	2.90	0.40
1:A:382:A:C2	1:A:383:A:C4	3.09	0.40
1:A:668:G:C6	1:A:669:U:C4	3.10	0.40
1:A:1039:C:O2'	1:A:1040:U:H5'	2.22	0.40
1:A:1372:U:H2'	1:A:1373:G:C5'	2.51	0.40
1:A:1426:C:C2	1:A:1475:G:N2	2.89	0.40
1:A:1477:C:O2'	1:A:1478:C:H5'	2.20	0.40
3:B:95:GLN:HG3	3:B:148:TYR:HD2	1.85	0.40
3:B:104:ASN:O	3:B:105:PHE:C	2.63	0.40
3:B:109:SER:O	3:B:112:VAL:N	2.52	0.40
4:C:126:ARG:O	4:C:127:ARG:HB2	2.21	0.40
5:D:179:GLU:HG2	5:D:180:GLY:H	1.85	0.40
8:G:145:ALA:C	8:G:147:ALA:H	2.28	0.40
14:M:3:ARG:HA	14:M:9:ILE:HG23	2.04	0.40
16:O:17:ARG:HH11	16:O:17:ARG:HG3	1.85	0.40
18:Q:79:SER:O	18:Q:80:GLY:O	2.40	0.40
18:Q:86:GLU:O	18:Q:87:LYS:C	2.62	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:17:GLU:O	20:S:21:GLU:HB2	2.21	0.40
22:V:9:ARG:NH1	22:V:22:ARG:HA	2.35	0.40
1:A:126:G:H5'	1:A:633:G:N2	2.37	0.40
1:A:342:C:H2'	1:A:343:U:H5'	2.04	0.40
1:A:591:U:H2'	1:A:592:G:H8	1.86	0.40
1:A:623:C:H6	1:A:623:C:O5'	2.05	0.40
1:A:657:G:H1	1:A:749:C:N4	2.20	0.40
1:A:778:G:O2'	1:A:779:C:H5'	2.20	0.40
1:A:926:G:H3'	1:A:1505:G:N2	2.35	0.40
1:A:972:C:H4'	11:J:57:LYS:HB3	2.03	0.40
1:A:1136:U:H5''	1:A:1137:C:OP2	2.22	0.40
1:A:1195:C:H3'	1:A:1196:U:C5'	2.35	0.40
1:A:1366:C:C2	1:A:1367:C:C5	3.09	0.40
1:A:1368:G:C2	1:A:1369:C:C6	3.08	0.40
3:B:152:PHE:O	3:B:152:PHE:CD2	2.74	0.40
5:D:3:ARG:HH11	5:D:118:ARG:CZ	2.34	0.40
5:D:57:ARG:HB3	5:D:206:PHE:HB2	2.03	0.40
8:G:108:ALA:C	8:G:110:GLN:N	2.78	0.40
10:I:10:ARG:NH2	10:I:107:ARG:NH2	2.69	0.40
14:M:74:VAL:O	14:M:75:ALA:C	2.64	0.40
14:M:125:ARG:C	14:M:125:ARG:HD2	2.46	0.40
15:N:13:THR:HG22	15:N:13:THR:O	2.21	0.40
16:O:8:LYS:O	16:O:11:VAL:N	2.51	0.40
20:S:11:VAL:HG22	20:S:39:THR:O	2.21	0.40
20:S:74:PHE:CD1	20:S:74:PHE:N	2.89	0.40
21:T:89:ARG:O	21:T:92:LEU:HB2	2.21	0.40
1:A:33:A:H2'	1:A:34:C:C6	2.56	0.40
1:A:34:C:O2'	1:A:35:G:H5'	2.21	0.40
1:A:52:G:C2'	1:A:53:A:H5'	2.51	0.40
1:A:67:C:O2'	1:A:171:A:H1'	2.21	0.40
1:A:106:C:H2'	1:A:107:G:O4'	2.21	0.40
1:A:294:U:H2'	1:A:295:C:C6	2.57	0.40
1:A:344:A:O5'	1:A:345:C:H5	2.04	0.40
1:A:757:U:O2'	1:A:758:G:H5'	2.21	0.40
1:A:775:G:C2'	1:A:776:G:H5'	2.52	0.40
1:A:996:A:H2'	1:A:997:U:C6	2.57	0.40
1:A:1056:U:O2	1:A:1056:U:H2'	2.22	0.40
1:A:1068:G:OP2	1:A:1068:G:H8	2.04	0.40
1:A:1354:C:H2'	1:A:1355:G:H8	1.86	0.40
1:A:1520:G:O2'	1:A:1521:G:H5'	2.20	0.40
3:B:149:LEU:O	3:B:153:ARG:HB2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:193:ASP:HA	3:B:194:PRO:HD2	1.85	0.40
5:D:42:GLN:O	5:D:42:GLN:CG	2.69	0.40
5:D:67:ILE:HG22	5:D:68:TYR:CD1	2.56	0.40
6:E:76:ILE:HG22	6:E:78:HIS:O	2.22	0.40
6:E:79:GLU:OE2	6:E:79:GLU:O	2.39	0.40
7:F:11:ASN:O	7:F:14:LEU:HG	2.20	0.40
10:I:26:VAL:HG13	10:I:61:ALA:O	2.21	0.40
10:I:49:PRO:HD3	10:I:78:LYS:CD	2.49	0.40
11:J:9:ARG:NH1	11:J:9:ARG:CB	2.82	0.40
11:J:51:ARG:N	11:J:59:SER:CB	2.83	0.40
13:L:39:VAL:HB	13:L:57:LYS:HG2	2.03	0.40
13:L:46:LYS:O	13:L:47:LYS:C	2.64	0.40
13:L:125:PRO:O	13:L:127:GLU:N	2.54	0.40
14:M:26:GLY:O	14:M:27:LYS:C	2.63	0.40
14:M:26:GLY:O	14:M:28:ALA:N	2.54	0.40
14:M:77:ASN:O	14:M:80:ARG:N	2.53	0.40
18:Q:5:VAL:C	18:Q:6:LEU:HD23	2.46	0.40
19:R:65:ILE:O	19:R:66:LEU:C	2.63	0.40
19:R:85:LEU:C	19:R:85:LEU:HD12	2.46	0.40
20:S:13:ASP:O	20:S:14:HIS:C	2.65	0.40
1:A:102:G:H2'	1:A:103:C:H6	1.85	0.40
1:A:191:G:H22	21:T:85:MET:HE1	1.86	0.40
1:A:256:U:H5'	18:Q:17:LYS:HZ2	1.85	0.40
1:A:403:C:O2'	1:A:404:U:H5'	2.22	0.40
1:A:620:C:H2'	1:A:621:A:C8	2.56	0.40
1:A:782:A:C6	1:A:801:U:C2	3.10	0.40
1:A:787:A:C5	1:A:788:U:C5	3.10	0.40
1:A:929:G:C6	1:A:930:C:C4	3.08	0.40
1:A:957:U:O2	1:A:960:U:C2	2.75	0.40
1:A:965:A:H5'	1:A:969:A:O4'	2.21	0.40
1:A:1055:A:C6	1:A:1206:G:C5	3.10	0.40
1:A:1256:A:O3'	1:A:1257:U:H4'	2.21	0.40
1:A:1313:U:O2'	1:A:1314:C:H5'	2.21	0.40
1:A:1363:A:N3	1:A:1365:G:O6	2.55	0.40
3:B:79:ASP:C	3:B:81:VAL:N	2.78	0.40
4:C:33:LEU:HD11	15:N:53:LEU:HD23	2.03	0.40
4:C:47:LEU:HD23	4:C:68:VAL:HG11	2.03	0.40
5:D:3:ARG:HD2	5:D:118:ARG:CZ	2.51	0.40
7:F:82:ARG:HA	7:F:82:ARG:NE	2.35	0.40
8:G:72:ARG:NH2	8:G:138:LYS:HZ3	2.19	0.40
9:H:45:ILE:HB	9:H:62:TYR:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:45:ILE:HD12	9:H:61:VAL:HG13	2.02	0.40
11:J:62:HIS:O	15:N:59:ALA:N	2.53	0.40
12:K:93:GLN:O	12:K:94:ALA:C	2.62	0.40
13:L:18:VAL:HG12	13:L:19:ARG:N	2.37	0.40
13:L:90:VAL:O	13:L:91:LYS:C	2.65	0.40
13:L:116:SER:O	13:L:119:LYS:O	2.38	0.40
16:O:62:GLN:HA	16:O:65:ARG:NH2	2.36	0.40
17:P:34:GLU:OE2	17:P:55:ARG:HD3	2.21	0.40
21:T:94:ALA:O	21:T:95:ALA:CB	2.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	232/256 (91%)	146 (63%)	52 (22%)	34 (15%)	0	1
4	C	204/239 (85%)	126 (62%)	45 (22%)	33 (16%)	0	1
5	D	206/209 (99%)	141 (68%)	51 (25%)	14 (7%)	1	7
6	E	148/162 (91%)	114 (77%)	23 (16%)	11 (7%)	1	6
7	F	99/101 (98%)	72 (73%)	24 (24%)	3 (3%)	3	21
8	G	153/156 (98%)	107 (70%)	32 (21%)	14 (9%)	0	3
9	H	136/138 (99%)	114 (84%)	16 (12%)	6 (4%)	2	14
10	I	125/128 (98%)	93 (74%)	22 (18%)	10 (8%)	1	5
11	J	96/105 (91%)	50 (52%)	28 (29%)	18 (19%)	0	0
12	K	117/129 (91%)	83 (71%)	21 (18%)	13 (11%)	0	2
13	L	122/135 (90%)	88 (72%)	21 (17%)	13 (11%)	0	2
14	M	123/126 (98%)	74 (60%)	34 (28%)	15 (12%)	0	1
15	N	58/61 (95%)	34 (59%)	19 (33%)	5 (9%)	0	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	O	86/89 (97%)	59 (69%)	22 (26%)	5 (6%)	1	9
17	P	81/88 (92%)	62 (76%)	14 (17%)	5 (6%)	1	9
18	Q	102/105 (97%)	80 (78%)	16 (16%)	6 (6%)	1	9
19	R	71/88 (81%)	47 (66%)	19 (27%)	5 (7%)	1	7
20	S	78/93 (84%)	51 (65%)	17 (22%)	10 (13%)	0	1
21	T	97/106 (92%)	55 (57%)	24 (25%)	18 (19%)	0	0
22	V	22/26 (85%)	12 (54%)	6 (27%)	4 (18%)	0	0
All	All	2356/2540 (93%)	1608 (68%)	506 (22%)	242 (10%)	0	2

All (242) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	15	VAL
3	B	16	HIS
3	B	17	PHE
3	B	18	GLY
3	B	20	GLU
3	B	21	ARG
3	B	24	TRP
3	B	95	GLN
3	B	123	ALA
3	B	190	THR
3	B	224	GLN
3	B	232	PRO
4	C	15	THR
4	C	20	SER
4	C	26	LYS
4	C	39	ILE
4	C	47	LEU
4	C	56	ASP
4	C	63	ASN
4	C	101	LEU
4	C	154	SER
4	C	189	ALA
5	D	4	TYR
5	D	36	ARG
6	E	16	THR
6	E	77	PRO
7	F	72	VAL
8	G	7	ALA

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Mol	Chain	Res	Type
8	G	146	GLU
8	G	155	ARG
9	H	24	THR
9	H	83	ILE
9	H	91	ARG
10	I	126	SER
11	J	26	ALA
11	J	34	VAL
11	J	54	PHE
11	J	61	GLU
11	J	79	ARG
12	K	128	ALA
13	L	27	LEU
13	L	47	LYS
14	M	123	ALA
14	M	124	PRO
15	N	22	THR
15	N	29	ARG
15	N	30	ALA
15	N	35	ARG
15	N	36	PHE
16	O	73	GLU
16	O	82	ILE
18	Q	69	LYS
18	Q	80	GLY
18	Q	81	ARG
18	Q	96	GLN
19	R	63	GLN
20	S	6	LYS
20	S	9	VAL
20	S	14	HIS
20	S	71	LEU
21	T	9	ASN
21	T	11	SER
21	T	49	ALA
21	T	73	HIS
21	T	74	LYS
21	T	93	GLU
21	T	94	ALA
3	B	52	GLU
3	B	76	GLN
3	B	122	PHE

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Mol	Chain	Res	Type
3	B	143	GLU
3	B	165	VAL
3	B	207	ALA
3	B	229	VAL
4	C	16	ARG
4	C	53	ALA
4	C	60	ALA
4	C	62	ASP
4	C	179	ARG
4	C	205	GLY
5	D	5	ILE
5	D	56	VAL
5	D	63	LYS
5	D	179	GLU
6	E	11	ILE
6	E	71	LEU
6	E	107	ARG
6	E	138	ALA
7	F	62	TRP
8	G	41	ARG
8	G	42	ILE
8	G	67	GLU
8	G	153	HIS
9	H	134	ILE
10	I	8	GLY
10	I	43	ALA
10	I	44	VAL
10	I	45	ALA
10	I	88	TYR
10	I	121	ARG
11	J	24	VAL
11	J	57	LYS
11	J	60	ARG
12	K	12	ARG
12	K	50	TYR
12	K	91	ARG
12	K	100	ALA
12	K	126	ARG
13	L	28	LYS
13	L	51	ALA
13	L	116	SER
13	L	121	GLY

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Mol	Chain	Res	Type
13	L	126	LYS
14	M	6	GLY
14	M	38	GLY
14	M	42	ALA
14	M	63	THR
14	M	85	GLY
14	M	122	LYS
17	P	10	GLY
17	P	52	ASP
17	P	76	GLN
18	Q	74	LEU
19	R	37	VAL
20	S	13	ASP
20	S	68	GLY
21	T	50	GLU
21	T	96	GLY
21	T	101	GLY
21	T	102	GLY
21	T	103	GLY
22	V	3	LYS
22	V	6	ARG
3	B	8	LYS
3	B	77	ALA
3	B	121	LEU
3	B	152	PHE
4	C	12	LEU
4	C	29	TYR
4	C	66	VAL
4	C	81	GLY
4	C	127	ARG
5	D	31	CYS
5	D	42	GLN
6	E	74	GLY
6	E	104	ALA
7	F	39	LYS
8	G	14	PRO
8	G	36	LYS
8	G	52	GLU
8	G	136	LYS
11	J	90	LEU
11	J	91	PRO
12	K	15	ALA

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Mol	Chain	Res	Type
13	L	48	PRO
13	L	109	GLY
14	M	71	ARG
14	M	81	LEU
14	M	107	ALA
16	O	64	ARG
18	Q	33	GLY
21	T	80	ARG
3	B	9	GLU
3	B	26	PRO
3	B	83	MET
3	B	98	LEU
3	B	177	ALA
3	B	183	PRO
4	C	4	LYS
4	C	5	ILE
4	C	46	GLU
4	C	68	VAL
4	C	89	GLU
4	C	100	ALA
4	C	133	ALA
4	C	168	ALA
4	C	181	ASN
5	D	92	VAL
6	E	153	LYS
8	G	90	GLU
10	I	55	ALA
11	J	39	PRO
11	J	40	LEU
11	J	58	ASP
11	J	72	VAL
11	J	95	GLU
12	K	90	GLY
12	K	102	GLY
13	L	62	SER
14	M	125	ARG
17	P	68	ASP
20	S	3	ARG
20	S	24	ALA
21	T	42	GLN
21	T	86	ARG
3	B	155	LEU

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Mol	Chain	Res	Type
4	C	61	ALA
4	C	91	LEU
5	D	26	CYS
6	E	108	ALA
8	G	59	LEU
8	G	122	HIS
10	I	41	VAL
10	I	91	ASP
11	J	28	ARG
11	J	30	SER
11	J	59	SER
13	L	38	THR
14	M	27	LYS
14	M	80	ARG
14	M	119	GLY
16	O	42	HIS
16	O	88	ARG
19	R	41	LYS
19	R	62	GLU
20	S	30	LEU
21	T	98	PRO
22	V	15	ARG
3	B	115	LEU
5	D	150	GLU
6	E	139	LEU
9	H	23	SER
12	K	13	GLN
13	L	23	LYS
13	L	87	GLY
21	T	97	ALA
22	V	22	ARG
3	B	211	ILE
5	D	90	GLY
4	C	55	VAL
5	D	88	VAL
12	K	118	GLY
3	B	80	ILE
5	D	28	SER
9	H	27	PRO
19	R	60	GLY
21	T	33	ILE
3	B	68	ILE

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Mol	Chain	Res	Type
12	K	35	PRO
12	K	113	PRO
17	P	51	VAL
20	S	67	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	
3	B	202/220 (92%)	184 (91%)	18 (9%)	9	32
4	C	160/188 (85%)	147 (92%)	13 (8%)	11	36
5	D	180/181 (99%)	166 (92%)	14 (8%)	11	37
6	E	115/123 (94%)	95 (83%)	20 (17%)	2	9
7	F	90/90 (100%)	82 (91%)	8 (9%)	9	32
8	G	126/127 (99%)	113 (90%)	13 (10%)	7	26
9	H	119/119 (100%)	106 (89%)	13 (11%)	6	24
10	I	98/99 (99%)	90 (92%)	8 (8%)	10	36
11	J	87/92 (95%)	70 (80%)	17 (20%)	1	6
12	K	90/99 (91%)	80 (89%)	10 (11%)	6	23
13	L	104/111 (94%)	98 (94%)	6 (6%)	18	47
14	M	100/101 (99%)	86 (86%)	14 (14%)	3	15
15	N	49/50 (98%)	43 (88%)	6 (12%)	5	20
16	O	79/80 (99%)	73 (92%)	6 (8%)	12	38
17	P	72/74 (97%)	67 (93%)	5 (7%)	14	42
18	Q	96/97 (99%)	87 (91%)	9 (9%)	8	30
19	R	64/77 (83%)	60 (94%)	4 (6%)	16	44
20	S	70/80 (88%)	63 (90%)	7 (10%)	7	27
21	T	76/82 (93%)	66 (87%)	10 (13%)	4	17
22	V	19/21 (90%)	18 (95%)	1 (5%)	20	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1996/2111 (95%)	1794 (90%)	202 (10%)	7 27

All (202) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	12	GLU
3	B	17	PHE
3	B	23	ARG
3	B	25	ASN
3	B	45	GLN
3	B	75	LYS
3	B	87	ARG
3	B	101	MET
3	B	106	LYS
3	B	126	GLU
3	B	144	ARG
3	B	156	LYS
3	B	178	ARG
3	B	187	LEU
3	B	190	THR
3	B	204	ASN
3	B	222	ILE
3	B	231	GLU
4	C	12	LEU
4	C	34	LEU
4	C	37	GLN
4	C	63	ASN
4	C	94	LEU
4	C	101	LEU
4	C	107	GLN
4	C	138	VAL
4	C	167	TRP
4	C	172	ARG
4	C	173	VAL
4	C	188	LEU
4	C	196	LEU
5	D	8	VAL
5	D	9	CYS
5	D	12	CYS
5	D	15	GLU
5	D	19	LEU
5	D	34	GLU

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Mol	Chain	Res	Type
5	D	50	ARG
5	D	64	LEU
5	D	96	LEU
5	D	122	ARG
5	D	146	ILE
5	D	161	ASN
5	D	162	LEU
5	D	170	VAL
6	E	12	LEU
6	E	15	ARG
6	E	16	THR
6	E	18	ARG
6	E	26	PHE
6	E	43	LEU
6	E	52	PRO
6	E	56	GLN
6	E	79	GLU
6	E	80	ILE
6	E	82	VAL
6	E	89	ILE
6	E	100	VAL
6	E	112	LEU
6	E	116	THR
6	E	118	ILE
6	E	120	THR
6	E	121	LYS
6	E	135	THR
6	E	147	ASP
7	F	10	LEU
7	F	15	ASP
7	F	65	VAL
7	F	69	GLU
7	F	73	ASN
7	F	75	LEU
7	F	87	ARG
7	F	92	LYS
8	G	8	GLU
8	G	9	VAL
8	G	11	GLN
8	G	12	LEU
8	G	18	TYR
8	G	21	VAL

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Mol	Chain	Res	Type
8	G	75	VAL
8	G	109	ASN
8	G	113	GLU
8	G	131	LYS
8	G	135	VAL
8	G	148	ASN
8	G	156	TRP
9	H	2	LEU
9	H	19	VAL
9	H	21	LYS
9	H	26	VAL
9	H	39	LEU
9	H	52	ASP
9	H	91	ARG
9	H	92	ARG
9	H	105	ARG
9	H	107	LEU
9	H	112	LEU
9	H	119	LEU
9	H	127	LEU
10	I	2	GLU
10	I	3	GLN
10	I	38	GLN
10	I	53	VAL
10	I	85	LEU
10	I	111	ARG
10	I	113	LYS
10	I	118	LYS
11	J	6	ILE
11	J	15	THR
11	J	40	LEU
11	J	45	ARG
11	J	49	VAL
11	J	51	ARG
11	J	60	ARG
11	J	64	GLU
11	J	68	HIS
11	J	71	LEU
11	J	73	ASP
11	J	83	GLU
11	J	86	MET
11	J	89	ASP

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Mol	Chain	Res	Type
11	J	95	GLU
11	J	96	ILE
11	J	97	GLU
12	K	18	ARG
12	K	24	SER
12	K	29	ILE
12	K	40	ILE
12	K	47	VAL
12	K	48	ILE
12	K	54	ARG
12	K	84	VAL
12	K	93	GLN
12	K	104	GLN
13	L	17	LYS
13	L	42	THR
13	L	48	PRO
13	L	98	TYR
13	L	119	LYS
13	L	126	LYS
14	M	9	ILE
14	M	16	ASP
14	M	17	VAL
14	M	56	LEU
14	M	66	LEU
14	M	81	LEU
14	M	84	ILE
14	M	88	ARG
14	M	98	VAL
14	M	102	ARG
14	M	106	ASN
14	M	110	ARG
14	M	122	LYS
14	M	124	PRO
15	N	8	GLU
15	N	17	LYS
15	N	31	ARG
15	N	41	ARG
15	N	44	LEU
15	N	58	LYS
16	O	6	GLU
16	O	11	VAL
16	O	31	LEU

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Mol	Chain	Res	Type
16	O	41	GLU
16	O	57	LEU
16	O	66	LEU
17	P	2	VAL
17	P	20	VAL
17	P	34	GLU
17	P	53	VAL
17	P	62	VAL
18	Q	22	LEU
18	Q	34	LYS
18	Q	35	VAL
18	Q	38	ARG
18	Q	59	ILE
18	Q	73	VAL
18	Q	74	LEU
18	Q	76	LEU
18	Q	98	LEU
19	R	26	LEU
19	R	38	GLU
19	R	39	VAL
19	R	55	ARG
20	S	9	VAL
20	S	15	LEU
20	S	20	LEU
20	S	34	TRP
20	S	43	GLU
20	S	60	VAL
20	S	77	THR
21	T	10	LEU
21	T	11	SER
21	T	13	LEU
21	T	39	LYS
21	T	42	GLN
21	T	56	MET
21	T	57	ARG
21	T	68	LYS
21	T	73	HIS
21	T	79	ARG
22	V	8	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (64) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	19	HIS
3	B	25	ASN
3	B	40	HIS
3	B	113	HIS
3	B	135	GLN
3	B	146	GLN
3	B	204	ASN
4	C	3	ASN
4	C	6	HIS
4	C	37	GLN
4	C	102	ASN
4	C	107	GLN
4	C	108	ASN
4	C	123	GLN
4	C	136	GLN
4	C	176	HIS
5	D	42	GLN
5	D	45	GLN
5	D	62	GLN
5	D	123	HIS
5	D	160	GLN
5	D	201	GLN
6	E	20	GLN
6	E	73	ASN
7	F	18	GLN
7	F	27	GLN
7	F	32	ASN
7	F	57	GLN
7	F	100	ASN
8	G	37	ASN
8	G	84	ASN
8	G	86	GLN
8	G	96	GLN
8	G	106	GLN
8	G	109	ASN
8	G	148	ASN
9	H	82	HIS
10	I	23	ASN
10	I	73	GLN
11	J	56	HIS
11	J	69	ASN
11	J	76	ASN
11	J	78	ASN

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Mol	Chain	Res	Type
11	J	84	GLN
12	K	38	ASN
12	K	62	GLN
12	K	104	GLN
12	K	117	ASN
13	L	75	HIS
14	M	40	ASN
14	M	62	ASN
15	N	52	GLN
16	O	13	GLN
16	O	37	ASN
16	O	62	GLN
17	P	76	GLN
18	Q	16	GLN
19	R	36	ASN
20	S	53	ASN
20	S	56	GLN
20	S	57	HIS
21	T	18	GLN
21	T	42	GLN
21	T	90	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1505/1522 (98%)	212 (14%)	72 (4%)
2	X	5/6 (83%)	0	0
All	All	1510/1528 (98%)	212 (14%)	72 (4%)

All (212) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	9	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	60	A

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Mol	Chain	Res	Type
1	A	61	G
1	A	65	U
1	A	81	U
1	A	101	A
1	A	115	G
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	182	U
1	A	190(D)	U
1	A	190(E)	U
1	A	190(F)	G
1	A	195	A
1	A	197	A
1	A	198	G
1	A	201	C
1	A	203	U
1	A	204	U
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	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	345	C
1	A	352	C
1	A	353	A
1	A	354	G
1	A	366	C
1	A	367	U
1	A	373	A
1	A	384	G
1	A	397	A

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Mol	Chain	Res	Type
1	A	398	C
1	A	412	A
1	A	413	G
1	A	421	U
1	A	422	C
1	A	429	U
1	A	439	A
1	A	452	A
1	A	460	A
1	A	461	C
1	A	462	G
1	A	481	G
1	A	484	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	519	C
1	A	527	G
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	653	A
1	A	665	A
1	A	686	U
1	A	687	A
1	A	688	G
1	A	702	A
1	A	703	G
1	A	718	G

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Mol	Chain	Res	Type
1	A	721	G
1	A	723	U
1	A	724	G
1	A	731	G
1	A	749	C
1	A	755	G
1	A	777	A
1	A	792	A
1	A	793	U
1	A	813	U
1	A	817	C
1	A	819	A
1	A	820	U
1	A	828	A
1	A	839	U
1	A	841	U
1	A	859	A
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	960	U
1	A	961	U
1	A	966	G
1	A	968	A
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1005	A
1	A	1009	G
1	A	1045	C
1	A	1050	G

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Mol	Chain	Res	Type
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	1126	U
1	A	1127	G
1	A	1129	C
1	A	1130	A
1	A	1131	G
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	1191	A
1	A	1196	U
1	A	1197	G
1	A	1201	A
1	A	1202	G
1	A	1212	U
1	A	1215	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1238	A
1	A	1250	A
1	A	1256	A
1	A	1257	U
1	A	1278	U
1	A	1279	A
1	A	1280	A
1	A	1281	U

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Mol	Chain	Res	Type
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1305	G
1	A	1320	C
1	A	1347	G
1	A	1348	U
1	A	1362	C
1	A	1363	A
1	A	1379	G
1	A	1381	U
1	A	1398	A
1	A	1443	G
1	A	1446	A
1	A	1447	G
1	A	1451	A
1	A	1452	C
1	A	1454	G
1	A	1487	G
1	A	1492	A
1	A	1497	G
1	A	1498	U
1	A	1499	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1519	A
1	A	1520	G
1	A	1529	G
1	A	1530	G

All (72) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	60	A
1	A	64	G

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Mol	Chain	Res	Type
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	203	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	328	C
1	A	329	A
1	A	344	A
1	A	351	G
1	A	353	A
1	A	366	C
1	A	372	C
1	A	421	U
1	A	428	G
1	A	484	G
1	A	496	A
1	A	509	A
1	A	518	C
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A
1	A	701	C
1	A	748	C
1	A	792	A
1	A	812	C
1	A	819	A
1	A	840	C
1	A	913	A
1	A	960	U
1	A	965	A
1	A	975	A
1	A	976	G
1	A	992	U
1	A	993	G

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Mol	Chain	Res	Type
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1101	A
1	A	1117	G
1	A	1139	G
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1201	A
1	A	1214	C
1	A	1224	G
1	A	1226	C
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1301	U
1	A	1319	A
1	A	1331	G
1	A	1346	A
1	A	1347	G
1	A	1380	U
1	A	1397	C
1	A	1451	A
1	A	1498	U
1	A	1504	G
1	A	1528	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 116 ligands modelled in this entry, 115 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	$\# Z > 2$
23	PAR	A	1545	-	44,45,45	1.28	5 (11%)	63,67,67	1.21	6 (9%)

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
23	PAR	A	1545	-	-	3/18/94/94	0/4/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	1545	PAR	O54-C14	3.06	1.49	1.41
23	A	1545	PAR	C31-C21	2.86	1.57	1.53
23	A	1545	PAR	O51-C11	2.60	1.48	1.41
23	A	1545	PAR	C11-C21	2.39	1.57	1.52
23	A	1545	PAR	O54-C54	2.18	1.49	1.44

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	1545	PAR	O33-C14-C24	4.37	115.22	108.08
23	A	1545	PAR	O54-C54-C64	3.79	113.36	106.07
23	A	1545	PAR	C14-O54-C54	3.31	120.19	113.72
23	A	1545	PAR	O11-C11-C21	2.64	112.40	108.08
23	A	1545	PAR	O52-C13-O43	-2.54	108.78	111.37
23	A	1545	PAR	C11-O51-C51	2.16	117.94	113.72

There are no chirality outliers.

All (3) torsion outliers are listed below:

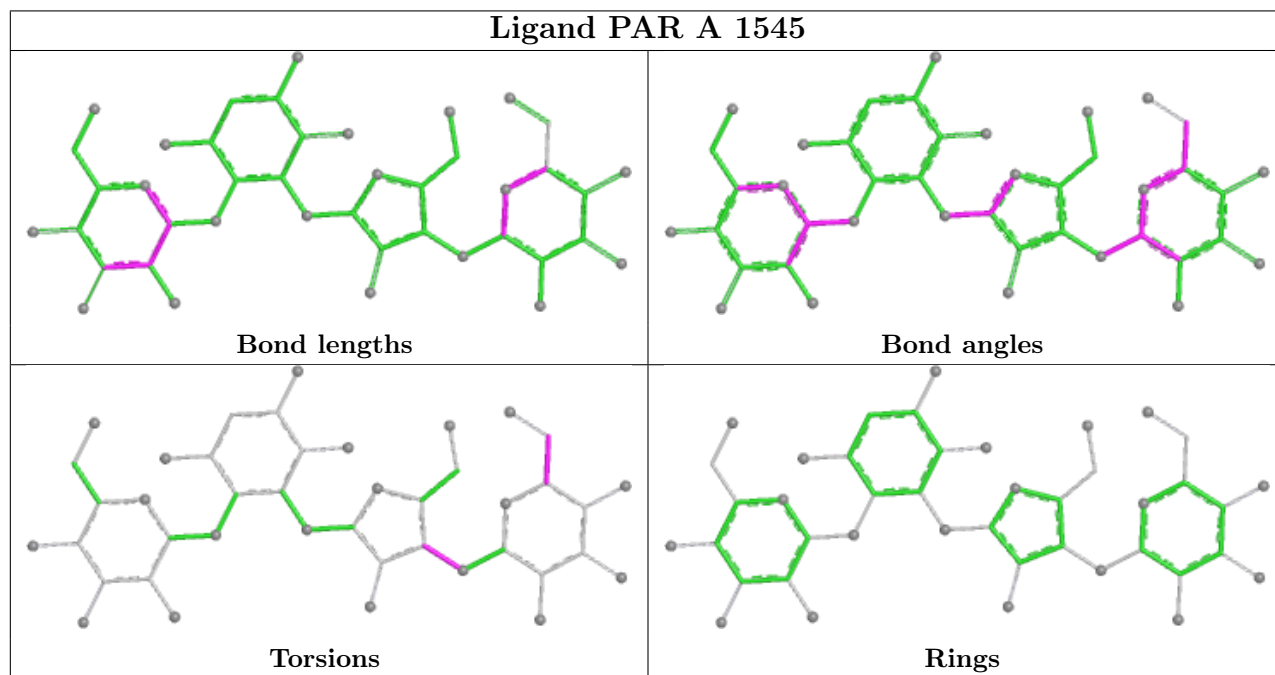
Mol	Chain	Res	Type	Atoms
23	A	1545	PAR	C44-C54-C64-N64
23	A	1545	PAR	C23-C33-O33-C14
23	A	1545	PAR	C43-C33-O33-C14

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	A	1545	PAR	4	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1506/1522 (98%)	1.21	314 (20%) 2 2	20, 53, 148, 201	0
2	X	6/6 (100%)	1.73	3 (50%) 0 0	55, 72, 99, 128	0
3	B	234/256 (91%)	1.96	94 (40%) 0 0	21, 80, 169, 201	0
4	C	206/239 (86%)	1.83	81 (39%) 1 0	21, 78, 158, 200	0
5	D	208/209 (99%)	1.24	51 (24%) 2 1	10, 56, 131, 162	0
6	E	150/162 (92%)	1.02	28 (18%) 3 3	13, 46, 111, 201	0
7	F	101/101 (100%)	1.41	26 (25%) 1 1	37, 84, 144, 170	0
8	G	155/156 (99%)	1.57	47 (30%) 1 1	27, 66, 151, 201	0
9	H	138/138 (100%)	1.13	26 (18%) 3 3	14, 43, 98, 131	0
10	I	127/128 (99%)	2.42	60 (47%) 0 0	22, 79, 146, 179	0
11	J	98/105 (93%)	2.51	54 (55%) 0 0	30, 114, 182, 201	0
12	K	119/129 (92%)	1.30	22 (18%) 3 3	19, 54, 130, 201	0
13	L	124/135 (91%)	1.45	38 (30%) 1 1	9, 53, 142, 201	0
14	M	125/126 (99%)	1.82	47 (37%) 1 0	33, 76, 152, 183	0
15	N	60/61 (98%)	1.68	21 (35%) 1 1	32, 70, 146, 178	0
16	O	88/89 (98%)	1.10	20 (22%) 2 2	16, 51, 142, 182	0
17	P	83/88 (94%)	1.01	13 (15%) 5 4	20, 45, 108, 140	0
18	Q	104/105 (99%)	1.30	29 (27%) 1 1	23, 45, 134, 201	0
19	R	73/88 (82%)	0.88	12 (16%) 4 4	36, 64, 153, 198	0
20	S	80/93 (86%)	2.11	40 (50%) 0 0	48, 95, 174, 201	0
21	T	99/106 (93%)	1.73	38 (38%) 1 0	19, 52, 129, 171	0
22	V	24/26 (92%)	2.10	9 (37%) 1 0	32, 62, 116, 155	0
All	All	3908/4068 (96%)	1.43	1073 (27%) 1 1	9, 59, 153, 201	0

All (1073) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
12	K	129	SER	25.2
12	K	128	ALA	21.0
8	G	8	GLU	16.9
8	G	5	ARG	14.1
13	L	19	ARG	12.4
1	A	532	A	11.1
8	G	11	GLN	10.8
1	A	1002	G	10.6
20	S	3	ARG	10.6
6	E	154	GLY	10.3
20	S	4	SER	10.1
1	A	81	U	10.1
3	B	128	GLU	9.8
3	B	130	ARG	8.9
8	G	13	GLN	8.8
10	I	105	ASP	8.8
13	L	28	LYS	8.7
14	M	120	LYS	8.6
1	A	1361(A)	C	8.3
8	G	81	GLY	8.0
3	B	95	GLN	7.9
14	M	125	ARG	7.8
22	V	25	LYS	7.8
4	C	132	ARG	7.7
10	I	9	ARG	7.7
1	A	1126	U	7.6
3	B	134	GLU	7.6
12	K	127	LYS	7.5
5	D	9	CYS	7.5
4	C	161	GLU	7.5
1	A	1360	A	7.5
3	B	127	ILE	7.5
10	I	114	TYR	7.5
4	C	30	ARG	7.4
14	M	88	ARG	7.4
9	H	54	ASP	7.2
9	H	126	LYS	7.2
11	J	93	GLY	7.2
14	M	124	PRO	7.2
1	A	164	U	7.1
21	T	9	ASN	7.1
13	L	44	THR	7.0
1	A	1323	G	6.9

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Mol	Chain	Res	Type	RSRZ
1	A	1361	G	6.9
1	A	1003	G	6.9
3	B	148	TYR	6.8
14	M	123	ALA	6.7
7	F	94	GLN	6.7
11	J	5	ARG	6.7
21	T	106	ALA	6.7
1	A	461	C	6.5
1	A	202	U	6.5
6	E	153	LYS	6.4
3	B	131	PRO	6.4
8	G	4	ARG	6.4
5	D	26	CYS	6.4
10	I	113	LYS	6.4
3	B	166	ASP	6.3
1	A	88	A	6.3
1	A	1026	G	6.3
10	I	119	ALA	6.2
1	A	1259	C	6.2
1	A	1314	C	6.2
3	B	129	GLU	6.2
10	I	97	LYS	6.2
1	A	394	G	6.1
1	A	1258	G	6.1
1	A	163	C	6.1
1	A	306	G	6.0
11	J	75	ILE	6.0
1	A	1034	G	6.0
1	A	1224	G	6.0
10	I	106	ALA	6.0
4	C	23	TYR	5.9
4	C	178	LEU	5.9
8	G	7	ALA	5.9
1	A	41	G	5.9
1	A	396	G	5.9
10	I	30	GLY	5.9
3	B	49	GLU	5.9
1	A	1270	C	5.9
4	C	26	LYS	5.9
4	C	193	TYR	5.8
10	I	115	GLY	5.8
5	D	31	CYS	5.8

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Mol	Chain	Res	Type	RSRZ
10	I	99	LEU	5.8
9	H	99	GLU	5.8
21	T	95	ALA	5.7
7	F	95	GLU	5.7
14	M	100	GLY	5.7
11	J	100	THR	5.7
1	A	1315	U	5.6
1	A	1140	C	5.6
8	G	82	GLY	5.6
1	A	263	A	5.6
15	N	35	ARG	5.6
18	Q	104	LYS	5.6
4	C	105	GLU	5.5
12	K	126	ARG	5.5
1	A	1269	A	5.5
14	M	87	TYR	5.5
1	A	1384	C	5.5
1	A	760	G	5.4
1	A	1138	G	5.4
1	A	978	A	5.4
8	G	79	ARG	5.4
14	M	121	LYS	5.4
5	D	24	GLU	5.4
21	T	36	LEU	5.4
10	I	118	LYS	5.4
5	D	12	CYS	5.3
4	C	27	LYS	5.3
22	V	24	ARG	5.3
3	B	144	ARG	5.3
13	L	52	LEU	5.3
1	A	1129	C	5.3
3	B	60	ASP	5.3
1	A	1281	U	5.2
4	C	131	ARG	5.2
3	B	98	LEU	5.2
1	A	1319	A	5.2
1	A	1283	G	5.2
10	I	103	THR	5.2
6	E	68	GLU	5.2
14	M	122	LYS	5.2
3	B	108	ILE	5.2
4	C	48	TYR	5.2

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Mol	Chain	Res	Type	RSRZ
8	G	33	ASP	5.2
11	J	3	LYS	5.1
8	G	12	LEU	5.1
19	R	16	PRO	5.1
11	J	45	ARG	5.1
14	M	11	ARG	5.1
1	A	460	A	5.1
8	G	143	ARG	5.1
16	O	54	ARG	5.1
18	Q	91	ARG	5.1
18	Q	13	ASP	5.0
1	A	1473	A	5.0
10	I	7	THR	5.0
3	B	111	ARG	5.0
3	B	19	HIS	5.0
1	A	1027	C	5.0
17	P	83	GLU	5.0
21	T	42	GLN	5.0
18	Q	102	GLY	5.0
11	J	71	LEU	5.0
3	B	137	ARG	4.9
1	A	1325	C	4.9
13	L	23	LYS	4.9
1	A	1255	G	4.9
10	I	104	ARG	4.9
15	N	57	ARG	4.9
3	B	8	LYS	4.8
9	H	97	VAL	4.8
10	I	8	GLY	4.8
1	A	147	G	4.8
10	I	93	ARG	4.8
21	T	54	LYS	4.8
1	A	148	G	4.8
7	F	1	MET	4.8
1	A	1324	A	4.8
9	H	84	ARG	4.8
18	Q	103	GLY	4.8
11	J	64	GLU	4.8
9	H	102	ARG	4.8
8	G	16	LEU	4.7
3	B	132	LYS	4.7
1	A	395	C	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	1001	A	4.7
10	I	98	PRO	4.7
1	A	1039	C	4.7
1	A	1209	C	4.7
5	D	187	ARG	4.7
10	I	107	ARG	4.7
5	D	192	GLU	4.7
11	J	66	ARG	4.7
10	I	2	GLU	4.7
11	J	62	HIS	4.7
10	I	100	GLY	4.7
3	B	96	ARG	4.7
11	J	43	ARG	4.7
13	L	42	THR	4.6
9	H	125	ARG	4.6
18	Q	101	ARG	4.6
5	D	18	LYS	4.6
4	C	158	GLY	4.6
3	B	147	LYS	4.6
11	J	57	LYS	4.6
1	A	1420	C	4.6
18	Q	88	TYR	4.6
4	C	51	GLY	4.6
3	B	152	PHE	4.6
12	K	125	PHE	4.6
10	I	25	LYS	4.5
1	A	1212	U	4.5
4	C	162	GLN	4.5
4	C	86	VAL	4.5
1	A	1362	C	4.5
16	O	9	GLN	4.5
3	B	106	LYS	4.5
1	A	262	A	4.5
1	A	733	A	4.5
1	A	165	C	4.5
1	A	1478	C	4.5
14	M	126	LYS	4.5
1	A	584	G	4.5
4	C	21	ARG	4.5
15	N	4	LYS	4.4
22	V	6	ARG	4.4
14	M	119	GLY	4.4

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Mol	Chain	Res	Type	RSRZ
4	C	124	ILE	4.4
3	B	114	ARG	4.4
1	A	1025	U	4.4
12	K	51	LYS	4.4
1	A	1144	G	4.4
1	A	977	A	4.4
1	A	1531	A	4.4
13	L	33	ARG	4.4
6	E	5	ASP	4.4
10	I	111	ARG	4.3
1	A	308	C	4.3
9	H	98	LYS	4.3
11	J	65	LEU	4.3
1	A	1023	G	4.3
1	A	458	C	4.3
1	A	264	U	4.3
8	G	146	GLU	4.3
18	Q	84	LEU	4.3
3	B	38	GLY	4.3
3	B	175	ARG	4.3
14	M	99	ARG	4.3
1	A	1492	A	4.3
9	H	122	ARG	4.3
14	M	73	GLU	4.3
4	C	104	GLN	4.3
1	A	260	G	4.2
21	T	37	SER	4.2
15	N	17	LYS	4.2
11	J	46	ARG	4.2
5	D	179	GLU	4.2
20	S	40	ILE	4.2
1	A	146	G	4.2
1	A	265	G	4.2
9	H	100	ILE	4.2
13	L	27	LEU	4.2
8	G	76	ARG	4.2
4	C	10	PHE	4.1
13	L	49	ASN	4.1
8	G	136	LYS	4.1
18	Q	14	LYS	4.1
1	A	1322	C	4.1
3	B	180	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
4	C	85	ARG	4.1
5	D	86	LYS	4.1
11	J	74	ILE	4.1
1	A	1006	C	4.1
1	A	1359	C	4.1
18	Q	105	ALA	4.1
7	F	31	GLU	4.1
7	F	57	GLN	4.1
4	C	190	ARG	4.1
1	A	1279	A	4.1
3	B	16	HIS	4.1
4	C	159	GLY	4.1
1	A	1423	G	4.1
4	C	28	GLN	4.1
22	V	5	ASP	4.0
16	O	58	MET	4.0
18	Q	58	GLU	4.0
1	A	204	U	4.0
1	A	1454	G	4.0
3	B	101	MET	4.0
11	J	6	ILE	4.0
1	A	1030	C	4.0
11	J	96	ILE	4.0
10	I	102	LEU	4.0
18	Q	96	GLN	4.0
11	J	4	ILE	4.0
14	M	47	ASP	4.0
20	S	2	PRO	3.9
4	C	118	GLN	3.9
16	O	57	LEU	3.9
1	A	1005	A	3.9
13	L	18	VAL	3.9
10	I	24	GLY	3.9
13	L	89	ARG	3.9
14	M	91	ARG	3.9
9	H	3	THR	3.9
1	A	759	A	3.9
1	A	1003(A)	G	3.9
1	A	1031	G	3.9
1	A	150	C	3.9
1	A	1383	C	3.9
20	S	6	LYS	3.9

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Mol	Chain	Res	Type	RSRZ
3	B	232	PRO	3.9
3	B	179	LYS	3.9
1	A	1428	A	3.9
1	A	1260	C	3.9
1	A	1443	G	3.9
5	D	3	ARG	3.8
5	D	112	VAL	3.8
3	B	125	PRO	3.8
7	F	39	LYS	3.8
1	A	307	C	3.8
1	A	1024	G	3.8
10	I	54	ASP	3.8
11	J	80	LYS	3.8
16	O	23	GLY	3.8
1	A	1318	A	3.8
20	S	37	ARG	3.8
11	J	73	ASP	3.8
17	P	29	ASP	3.8
1	A	748	C	3.8
1	A	821	G	3.8
16	O	48	LYS	3.8
21	T	34	LYS	3.8
21	T	74	LYS	3.8
6	E	144	THR	3.8
20	S	9	VAL	3.8
13	L	47	LYS	3.8
1	A	1004	A	3.8
1	A	1268	A	3.8
1	A	304	U	3.8
1	A	1479	C	3.8
1	A	1127	G	3.8
9	H	70	GLN	3.8
3	B	7	VAL	3.8
6	E	19	MET	3.8
10	I	66	ARG	3.8
10	I	110	GLU	3.8
3	B	135	GLN	3.7
14	M	98	VAL	3.7
20	S	57	HIS	3.7
1	A	993	G	3.7
1	A	1386	G	3.7
9	H	121	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
10	I	128	ARG	3.7
1	A	1257	U	3.7
10	I	14	VAL	3.7
4	C	102	ASN	3.7
1	A	1115	C	3.7
3	B	23	ARG	3.7
11	J	47	PHE	3.7
17	P	12	LYS	3.7
1	A	1419	G	3.7
1	A	1453	G	3.7
15	N	10	ALA	3.7
5	D	153	ARG	3.7
11	J	30	SER	3.7
11	J	17	ASP	3.7
1	A	131	C	3.7
8	G	48	LYS	3.7
10	I	27	THR	3.7
14	M	20	THR	3.7
1	A	157	G	3.7
1	A	1021	G	3.7
4	C	2	GLY	3.7
15	N	11	LYS	3.7
1	A	1278	U	3.7
1	A	1427	U	3.7
4	C	44	GLU	3.7
12	K	25	TYR	3.7
1	A	1256	A	3.7
10	I	12	GLU	3.6
10	I	60	ASP	3.6
17	P	54	GLU	3.6
1	A	459	G	3.6
1	A	1421	G	3.6
4	C	156	ARG	3.6
5	D	49	ARG	3.6
5	D	131	ARG	3.6
1	A	1030(D)	A	3.6
12	K	124	LYS	3.6
1	A	401	C	3.6
9	H	22	GLU	3.6
11	J	79	ARG	3.6
7	F	83	ASP	3.6
21	T	94	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
10	I	32	ASP	3.6
17	P	68	ASP	3.6
9	H	37	ARG	3.6
15	N	61	TRP	3.6
14	M	42	ALA	3.6
15	N	2	ALA	3.6
3	B	143	GLU	3.6
4	C	206	GLU	3.6
1	A	1446	A	3.6
8	G	153	HIS	3.6
4	C	80	GLY	3.6
18	Q	87	LYS	3.6
4	C	196	LEU	3.6
5	D	158	ILE	3.6
1	A	475	G	3.5
10	I	83	ARG	3.5
11	J	63	PHE	3.5
11	J	98	ILE	3.5
13	L	127	GLU	3.5
20	S	73	GLU	3.5
8	G	52	GLU	3.5
3	B	99	GLY	3.5
20	S	68	GLY	3.5
18	Q	24	GLU	3.5
21	T	17	ARG	3.5
1	A	933	G	3.5
7	F	35	ALA	3.5
8	G	115	ARG	3.5
15	N	12	ARG	3.5
18	Q	95	TYR	3.5
16	O	44	LYS	3.5
15	N	22	THR	3.5
12	K	52	GLY	3.5
1	A	1112	C	3.5
1	A	1312	G	3.5
3	B	226	ARG	3.5
1	A	261	U	3.5
5	D	154	ASN	3.4
14	M	7	VAL	3.4
4	C	129	ALA	3.4
3	B	46	LYS	3.4
19	R	83	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	723	U	3.4
8	G	9	VAL	3.4
4	C	181	ASN	3.4
14	M	113	PRO	3.4
14	M	90	LEU	3.4
8	G	32	ARG	3.4
10	I	121	ARG	3.4
1	A	1313	U	3.4
7	F	84	ASN	3.4
10	I	70	LYS	3.4
5	D	144	ASP	3.4
15	N	46	GLU	3.4
8	G	10	ARG	3.4
3	B	227	GLY	3.4
5	D	23	GLY	3.4
17	P	30	GLY	3.4
3	B	133	LYS	3.4
16	O	51	HIS	3.4
1	A	82	U	3.4
9	H	49	GLU	3.4
21	T	13	LEU	3.4
9	H	1	MET	3.4
16	O	3	ILE	3.4
8	G	84	ASN	3.3
2	X	1	C	3.3
10	I	20	ARG	3.3
13	L	43	VAL	3.3
20	S	38	SER	3.3
21	T	80	ARG	3.3
20	S	12	ASP	3.3
1	A	1009	G	3.3
22	V	9	ARG	3.3
4	C	188	LEU	3.3
1	A	382	A	3.3
1	A	412	A	3.3
4	C	4	LYS	3.3
1	A	170	U	3.3
1	A	1040	U	3.3
1	A	176	C	3.3
4	C	191	THR	3.3
6	E	20	GLN	3.3
3	B	149	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
10	I	29	ASN	3.3
3	B	156	LYS	3.3
13	L	21	LYS	3.3
4	C	82	GLU	3.3
6	E	8	GLU	3.3
8	G	57	GLU	3.3
4	C	84	ILE	3.3
8	G	2	ALA	3.3
16	O	55	GLY	3.3
1	A	1425	U	3.3
4	C	179	ARG	3.3
5	D	201	GLN	3.3
6	E	24	ARG	3.3
3	B	72	GLY	3.3
8	G	6	ARG	3.3
12	K	36	ASP	3.3
13	L	31	PRO	3.3
14	M	27	LYS	3.3
1	A	280	C	3.3
5	D	149	ALA	3.3
18	Q	49	GLU	3.3
4	C	88	ARG	3.2
10	I	10	ARG	3.2
3	B	75	LYS	3.2
6	E	38	GLN	3.2
3	B	165	VAL	3.2
4	C	109	PRO	3.2
6	E	119	LEU	3.2
20	S	35	SER	3.2
3	B	112	VAL	3.2
20	S	41	VAL	3.2
3	B	116	GLU	3.2
4	C	46	GLU	3.2
20	S	81	ARG	3.2
21	T	101	GLY	3.2
7	F	92	LYS	3.2
1	A	259	G	3.2
1	A	481	G	3.2
1	A	1035	A	3.2
1	A	1316	G	3.2
3	B	45	GLN	3.2
1	A	169	C	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	1424	C	3.2
4	C	17	ASP	3.2
13	L	92	ASP	3.2
21	T	97	ALA	3.2
7	F	42	GLU	3.2
4	C	72	LYS	3.2
12	K	114	VAL	3.2
3	B	206	ASP	3.2
10	I	75	ASP	3.2
1	A	112	G	3.2
1	A	1124	G	3.2
1	A	1174	G	3.2
8	G	89	MET	3.2
11	J	84	GLN	3.2
10	I	116	LYS	3.1
21	T	103	GLY	3.1
1	A	1349	A	3.1
3	B	239	VAL	3.1
1	A	31	G	3.1
1	A	976	G	3.1
1	A	1131	G	3.1
1	A	1141	C	3.1
4	C	83	ARG	3.1
10	I	31	GLN	3.1
10	I	87	GLN	3.1
13	L	16	GLU	3.1
3	B	64	ARG	3.1
17	P	46	PRO	3.1
12	K	11	LYS	3.1
14	M	115	LYS	3.1
14	M	58	GLU	3.1
3	B	105	PHE	3.1
14	M	25	ILE	3.1
1	A	349	A	3.1
1	A	383	A	3.1
3	B	192	SER	3.1
16	O	76	GLU	3.1
16	O	79	ARG	3.1
18	Q	37	LYS	3.1
1	A	576	G	3.1
1	A	1136	U	3.1
3	B	238	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
3	B	141	GLU	3.1
20	S	13	ASP	3.1
8	G	51	GLN	3.0
1	A	1030(A)	G	3.0
1	A	1331	G	3.0
4	C	5	ILE	3.0
14	M	41	PRO	3.0
1	A	822	C	3.0
1	A	1145	C	3.0
16	O	89	GLY	3.0
6	E	10	MET	3.0
11	J	61	GLU	3.0
1	A	1422	G	3.0
13	L	51	ALA	3.0
18	Q	92	ARG	3.0
18	Q	100	LYS	3.0
1	A	1426	C	3.0
4	C	166	GLU	3.0
11	J	86	MET	3.0
21	T	93	GLU	3.0
7	F	45	LEU	3.0
19	R	87	ARG	3.0
1	A	1485	U	3.0
5	D	169	LYS	3.0
1	A	585	G	3.0
8	G	56	GLN	3.0
17	P	82	GLN	3.0
10	I	64	THR	3.0
7	F	89	MET	3.0
21	T	50	GLU	3.0
1	A	279	A	3.0
1	A	935	A	3.0
6	E	150	ARG	3.0
22	V	18	TYR	3.0
9	H	128	GLY	3.0
12	K	13	GLN	3.0
21	T	35	THR	3.0
3	B	97	TRP	2.9
11	J	37	PRO	2.9
15	N	8	GLU	2.9
4	C	45	LYS	2.9
18	Q	83	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
3	B	52	GLU	2.9
11	J	77	PRO	2.9
17	P	27	LYS	2.9
20	S	64	GLU	2.9
6	E	21	ALA	2.9
1	A	158	G	2.9
1	A	476	G	2.9
1	A	1175	G	2.9
1	A	1508	G	2.9
1	A	1511	G	2.9
3	B	110	GLN	2.9
8	G	49	ILE	2.9
20	S	49	ILE	2.9
15	N	6	LEU	2.9
21	T	72	LEU	2.9
4	C	3	ASN	2.9
20	S	33	THR	2.9
1	A	840	C	2.9
1	A	1200	C	2.9
1	A	1020	U	2.9
6	E	133	TYR	2.9
5	D	152	SER	2.9
5	D	162	LEU	2.9
10	I	16	ARG	2.9
14	M	93	ARG	2.9
14	M	102	ARG	2.9
10	I	112	LYS	2.9
1	A	238	G	2.9
1	A	1480	G	2.9
5	D	163	GLU	2.9
1	A	1507	A	2.9
1	A	5	U	2.9
7	F	46	ARG	2.9
11	J	38	ILE	2.9
11	J	24	VAL	2.9
1	A	1385	G	2.9
5	D	19	LEU	2.9
21	T	33	ILE	2.9
1	A	83	U	2.8
1	A	848	C	2.8
1	A	1038	C	2.8
1	A	1477	C	2.8

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Mol	Chain	Res	Type	RSRZ
2	X	2	U	2.8
6	E	23	GLY	2.8
20	S	26	GLY	2.8
21	T	38	LYS	2.8
11	J	90	LEU	2.8
21	T	69	GLY	2.8
1	A	841	U	2.8
1	A	1010	G	2.8
1	A	1532	U	2.8
1	A	1284	C	2.8
13	L	111	LYS	2.8
4	C	78	GLY	2.8
13	L	29	GLY	2.8
20	S	56	GLN	2.8
11	J	91	PRO	2.8
14	M	94	ARG	2.8
11	J	42	THR	2.8
11	J	72	VAL	2.8
13	L	61	THR	2.8
1	A	859	A	2.8
5	D	73	ARG	2.8
8	G	67	GLU	2.8
20	S	8	GLY	2.8
4	C	71	ALA	2.8
4	C	79	ARG	2.8
1	A	1033	G	2.8
1	A	1120	G	2.8
11	J	88	LEU	2.8
4	C	19	GLU	2.8
6	E	13	ILE	2.8
11	J	54	PHE	2.7
19	R	43	PHE	2.7
10	I	23	ASN	2.7
1	A	250	A	2.7
1	A	1146	A	2.7
20	S	5	LEU	2.7
1	A	268	C	2.7
1	A	980	C	2.7
1	A	1533	C	2.7
14	M	50	GLU	2.7
18	Q	99	SER	2.7
21	T	100	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
19	R	25	THR	2.7
1	A	380	G	2.7
1	A	1022	G	2.7
13	L	86	ARG	2.7
4	C	29	TYR	2.7
5	D	42	GLN	2.7
3	B	118	LEU	2.7
13	L	85	ILE	2.7
4	C	167	TRP	2.7
5	D	168	ARG	2.7
11	J	51	ARG	2.7
21	T	30	LYS	2.7
1	A	1037	C	2.7
1	A	1411	C	2.7
3	B	37	ASN	2.7
22	V	23	PRO	2.7
4	C	77	ILE	2.7
5	D	109	GLY	2.7
1	A	1125	U	2.7
7	F	74	ASP	2.7
20	S	14	HIS	2.7
4	C	157	ILE	2.7
20	S	44	MET	2.7
4	C	126	ARG	2.7
14	M	3	ARG	2.7
1	A	145	G	2.7
1	A	1117	G	2.7
1	A	1248	A	2.6
1	A	1346	A	2.6
1	A	1451	A	2.6
3	B	30	ARG	2.6
9	H	30	ARG	2.6
20	S	10	PHE	2.6
5	D	166	LYS	2.6
20	S	25	LYS	2.6
21	T	14	LYS	2.6
19	R	48	GLY	2.6
1	A	1321	C	2.6
3	B	230	VAL	2.6
10	I	36	TYR	2.6
3	B	140	HIS	2.6
1	A	1032	G	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	1134	G	2.6
11	J	58	ASP	2.6
3	B	122	PHE	2.6
18	Q	93	GLN	2.6
5	D	167	GLY	2.6
1	A	397	A	2.6
6	E	50	GLU	2.6
19	R	38	GLU	2.6
3	B	93	VAL	2.6
11	J	85	LEU	2.6
1	A	233	C	2.6
1	A	1028	C	2.6
14	M	9	ILE	2.6
10	I	15	ALA	2.6
1	A	1041	A	2.6
1	A	1183	A	2.6
11	J	60	ARG	2.6
20	S	29	ARG	2.6
20	S	80	TYR	2.6
3	B	234	PRO	2.6
1	A	267	C	2.6
1	A	455	C	2.6
1	A	1029	C	2.6
1	A	1045	C	2.6
5	D	87	GLY	2.6
10	I	67	GLY	2.6
5	D	145	GLU	2.6
11	J	14	LYS	2.6
17	P	19	ILE	2.6
1	A	130	A	2.6
4	C	205	GLY	2.6
5	D	190	ASP	2.6
1	A	1114	C	2.6
1	A	1262	C	2.6
1	A	1397	C	2.6
3	B	126	GLU	2.6
7	F	91	VAL	2.6
13	L	26	ALA	2.6
8	G	151	TYR	2.5
11	J	10	GLY	2.5
12	K	99	GLN	2.5
18	Q	26	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	181	G	2.5
1	A	266	G	2.5
1	A	1030(C)	G	2.5
1	A	1104	G	2.5
1	A	1442	G	2.5
1	A	1530	G	2.5
8	G	80	VAL	2.5
11	J	83	GLU	2.5
3	B	200	ILE	2.5
1	A	48	C	2.5
1	A	732	C	2.5
1	A	1103	C	2.5
1	A	1254	C	2.5
1	A	1320	C	2.5
15	N	60	SER	2.5
4	C	170	GLN	2.5
14	M	31	LYS	2.5
3	B	205	ASP	2.5
8	G	148	ASN	2.5
12	K	89	ALA	2.5
14	M	35	GLU	2.5
14	M	118	ALA	2.5
18	Q	86	GLU	2.5
3	B	63	MET	2.5
20	S	34	TRP	2.5
1	A	42	G	2.5
1	A	1042	G	2.5
1	A	1187	G	2.5
5	D	138	TYR	2.5
8	G	85	TYR	2.5
1	A	40	C	2.5
1	A	745	C	2.5
5	D	209	ARG	2.5
8	G	3	ARG	2.5
14	M	48	LEU	2.5
13	L	22	SER	2.5
6	E	81	GLU	2.5
13	L	73	GLU	2.5
20	S	27	GLU	2.5
4	C	128	PHE	2.5
12	K	70	LYS	2.5
21	T	58	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1363	A	2.5
1	A	765	G	2.5
3	B	79	ASP	2.5
3	B	168	THR	2.5
20	S	39	THR	2.5
7	F	77	ARG	2.5
8	G	41	ARG	2.5
12	K	122	LYS	2.5
16	O	47	LYS	2.5
20	S	28	LYS	2.5
9	H	127	LEU	2.5
3	B	66	GLY	2.5
3	B	240	GLN	2.5
16	O	13	GLN	2.5
19	R	46	GLU	2.4
6	E	45	PHE	2.4
13	L	41	ARG	2.4
13	L	114	LYS	2.4
20	S	18	LYS	2.4
21	T	86	ARG	2.4
1	A	999	C	2.4
1	A	1185	G	2.4
1	A	1186	G	2.4
1	A	1476	G	2.4
21	T	10	LEU	2.4
20	S	69	HIS	2.4
18	Q	85	VAL	2.4
3	B	139	LYS	2.4
13	L	17	LYS	2.4
3	B	195	ASP	2.4
15	N	14	PRO	2.4
1	A	132	C	2.4
1	A	596	C	2.4
21	T	59	ALA	2.4
1	A	1036	G	2.4
1	A	1347	G	2.4
11	J	99	LYS	2.4
16	O	88	ARG	2.4
19	R	72	ARG	2.4
3	B	33	TYR	2.4
10	I	72	GLY	2.4
4	C	135	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
5	D	45	GLN	2.4
15	N	52	GLN	2.4
7	F	47	ARG	2.4
19	R	41	LYS	2.4
20	S	32	LYS	2.4
1	A	182	U	2.4
1	A	442	C	2.4
1	A	516	U	2.4
1	A	985	C	2.4
1	A	1019	C	2.4
1	A	1317	C	2.4
3	B	121	LEU	2.4
5	D	155	LEU	2.4
14	M	8	GLU	2.4
1	A	309	G	2.4
1	A	1387	G	2.4
10	I	123	PRO	2.4
15	N	59	ALA	2.4
9	H	64	LYS	2.4
20	S	78	ARG	2.4
1	A	313	A	2.4
5	D	178	VAL	2.4
8	G	17	VAL	2.4
1	A	457	C	2.3
4	C	192	THR	2.3
1	A	216	G	2.3
1	A	631	G	2.3
1	A	1133	G	2.3
1	A	1154	G	2.3
1	A	1305	G	2.3
3	B	11	LEU	2.3
5	D	21	LEU	2.3
11	J	40	LEU	2.3
12	K	115	PRO	2.3
1	A	583	A	2.3
22	V	7	ARG	2.3
21	T	73	HIS	2.3
21	T	76	ALA	2.3
3	B	236	TYR	2.3
3	B	102	LEU	2.3
20	S	15	LEU	2.3
16	O	6	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	326	G	2.3
1	A	384	G	2.3
1	A	485	G	2.3
1	A	597	G	2.3
1	A	1139	G	2.3
1	A	1474	G	2.3
8	G	155	ARG	2.3
10	I	58	ARG	2.3
15	N	3	ARG	2.3
5	D	110	PHE	2.3
4	C	58	GLU	2.3
9	H	77	GLU	2.3
1	A	1008	C	2.3
5	D	184	LYS	2.3
21	T	68	LYS	2.3
3	B	209	ARG	2.3
15	N	30	ALA	2.3
14	M	43	THR	2.3
18	Q	98	LEU	2.3
1	A	108	G	2.3
1	A	230	G	2.3
7	F	16	GLN	2.3
11	J	89	ASP	2.3
12	K	78	GLN	2.3
7	F	54	LYS	2.3
1	A	1285	A	2.3
5	D	35	ARG	2.3
5	D	150	GLU	2.3
1	A	518	C	2.3
1	A	995	C	2.3
3	B	115	LEU	2.3
12	K	53	SER	2.3
17	P	14	ASN	2.3
16	O	64	ARG	2.3
21	T	8	ARG	2.3
5	D	17	VAL	2.3
13	L	65	GLU	2.2
3	B	171	ALA	2.2
5	D	41	GLY	2.2
9	H	101	PRO	2.2
1	A	84	U	2.2
1	A	1130	A	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1188	A	2.2
5	D	20	TYR	2.2
13	L	50	SER	2.2
1	A	1030(B)	C	2.2
11	J	69	ASN	2.2
6	E	11	ILE	2.2
13	L	45	PRO	2.2
1	A	742	G	2.2
1	A	1142	G	2.2
3	B	107	THR	2.2
19	R	68	LYS	2.2
13	L	34	ARG	2.2
4	C	207	VAL	2.2
6	E	51	VAL	2.2
10	I	38	GLN	2.2
18	Q	16	GLN	2.2
4	C	98	ASN	2.2
4	C	134	ILE	2.2
1	A	1208	C	2.2
1	A	1382	C	2.2
4	C	155	GLY	2.2
8	G	144	MET	2.2
5	D	84	LYS	2.2
14	M	65	LYS	2.2
4	C	186	PHE	2.2
7	F	82	ARG	2.2
19	R	34	TYR	2.2
1	A	1472	U	2.2
2	X	3	U	2.2
6	E	56	GLN	2.2
7	F	64	GLN	2.2
8	G	50	ILE	2.2
1	A	413	G	2.2
1	A	761	G	2.2
1	A	1143	G	2.2
1	A	1216	G	2.2
4	C	108	ASN	2.2
5	D	161	ASN	2.2
3	B	10	LEU	2.2
14	M	32	GLU	2.2
6	E	22	GLY	2.2
10	I	21	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
11	J	52	GLY	2.2
21	T	48	LYS	2.2
6	E	18	ARG	2.2
1	A	341	C	2.2
1	A	400	C	2.2
1	A	555	C	2.2
1	A	979	C	2.2
7	F	93	SER	2.2
4	C	89	GLU	2.2
13	L	91	LYS	2.2
14	M	12	ASN	2.2
21	T	49	ALA	2.2
4	C	194	GLY	2.2
16	O	2	PRO	2.2
3	B	189	ASP	2.2
8	G	45	ASP	2.2
1	A	860	A	2.2
5	D	125	HIS	2.2
1	A	381	C	2.1
1	A	1113	C	2.1
1	A	1237	C	2.1
8	G	129	GLU	2.1
12	K	120	ARG	2.1
4	C	106	VAL	2.1
13	L	24	VAL	2.1
1	A	162	A	2.1
1	A	393	A	2.1
1	A	828	A	2.1
1	A	1280	A	2.1
3	B	172	ILE	2.1
11	J	7	LYS	2.1
21	T	20	LEU	2.1
3	B	153	ARG	2.1
3	B	224	GLN	2.1
8	G	110	GLN	2.1
14	M	101	GLN	2.1
1	A	744	C	2.1
1	A	1132	C	2.1
11	J	41	PRO	2.1
16	O	50	HIS	2.1
1	A	1414	U	2.1
10	I	79	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
13	L	115	LYS	2.1
4	C	189	ALA	2.1
3	B	176	GLU	2.1
6	E	29	GLY	2.1
10	I	39	GLY	2.1
12	K	121	PRO	2.1
20	S	21	GLU	2.1
17	P	11	SER	2.1
18	Q	97	SER	2.1
1	A	491	G	2.1
1	A	517	G	2.1
4	C	66	VAL	2.1
1	A	234	C	2.1
1	A	1076	C	2.1
13	L	123	LYS	2.1
4	C	12	LEU	2.1
4	C	43	LEU	2.1
7	F	28	ARG	2.1
9	H	12	ARG	2.1
4	C	180	ALA	2.1
1	A	30	U	2.1
1	A	997	U	2.1
4	C	93	LYS	2.1
17	P	48	TRP	2.1
22	V	10	ARG	2.1
14	M	82	MET	2.1
15	N	13	THR	2.1
1	A	1214	C	2.1
1	A	1282	C	2.1
1	A	251	G	2.1
1	A	1486	G	2.1
9	H	55	GLY	2.1
4	C	122	GLU	2.1
6	E	83	GLU	2.1
6	E	84	PHE	2.1
8	G	58	PRO	2.1
8	G	90	GLU	2.1
1	A	531	U	2.0
10	I	71	SER	2.0
15	N	32	SER	2.0
10	I	120	ARG	2.0
11	J	23	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
3	B	83	MET	2.0
1	A	228	A	2.0
1	A	1213	A	2.0
7	F	59	TYR	2.0
21	T	96	GLY	2.0
1	A	931	C	2.0
1	A	1043	C	2.0
1	A	1172	C	2.0
1	A	1400	C	2.0
1	A	1429	C	2.0
18	Q	41	LYS	2.0
4	C	130	VAL	2.0
10	I	108	VAL	2.0
1	A	425	G	2.0
20	S	16	LEU	2.0
14	M	2	ALA	2.0
7	F	63	TYR	2.0
9	H	27	PRO	2.0
1	A	149	A	2.0
14	M	114	ARG	2.0
3	B	145	LEU	2.0
14	M	96	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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
24	MG	A	1647	1/1	0.62	0.42	24,24,24,24	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	1620	1/1	0.66	0.38	24,24,24,24	1
24	MG	A	1624	1/1	0.72	0.40	24,24,24,24	1
24	MG	A	1635	1/1	0.78	0.32	24,24,24,24	1
24	MG	A	210	1/1	0.79	0.24	24,24,24,24	1
24	MG	A	1616	1/1	0.79	0.37	24,24,24,24	1
24	MG	A	1589	1/1	0.81	0.45	24,24,24,24	0
24	MG	A	1567	1/1	0.82	0.16	24,24,24,24	0
24	MG	A	1597	1/1	0.82	0.34	24,24,24,24	0
23	PAR	A	1545	42/42	0.85	0.24	58,58,58,58	0
24	MG	A	1622	1/1	0.85	0.23	24,24,24,24	1
24	MG	A	1588	1/1	0.85	0.32	24,24,24,24	0
24	MG	A	1607	1/1	0.85	0.13	24,24,24,24	0
24	MG	A	1638	1/1	0.85	0.17	24,24,24,24	1
24	MG	A	1566	1/1	0.85	0.13	24,24,24,24	0
24	MG	A	1614	1/1	0.86	0.17	24,24,24,24	0
24	MG	A	1617	1/1	0.86	0.21	24,24,24,24	0
24	MG	A	1619	1/1	0.87	0.11	24,24,24,24	1
24	MG	A	1623	1/1	0.87	0.22	24,24,24,24	1
24	MG	A	1641	1/1	0.87	0.26	24,24,24,24	1
24	MG	A	1579	1/1	0.87	0.23	24,24,24,24	1
24	MG	A	1632	1/1	0.88	0.24	24,24,24,24	1
24	MG	A	211	1/1	0.88	0.31	24,24,24,24	1
24	MG	A	1646	1/1	0.88	0.22	24,24,24,24	0
24	MG	A	1636	1/1	0.88	0.31	24,24,24,24	1
24	MG	A	1631	1/1	0.89	0.12	24,24,24,24	0
24	MG	A	1611	1/1	0.89	0.30	24,24,24,24	1
24	MG	A	1585	1/1	0.90	0.14	24,24,24,24	0
24	MG	A	1556	1/1	0.90	0.32	24,24,24,24	0
24	MG	A	1645	1/1	0.90	0.39	24,24,24,24	1
24	MG	A	1576	1/1	0.90	0.27	24,24,24,24	0
24	MG	A	1550	1/1	0.90	0.13	24,24,24,24	1
24	MG	L	464	1/1	0.90	0.43	24,24,24,24	1
24	MG	A	1561	1/1	0.91	0.22	24,24,24,24	0
24	MG	A	1626	1/1	0.91	0.19	24,24,24,24	0
24	MG	A	1591	1/1	0.91	0.20	24,24,24,24	0
24	MG	A	1613	1/1	0.92	0.11	24,24,24,24	0
24	MG	A	1587	1/1	0.92	0.20	24,24,24,24	0
24	MG	A	1562	1/1	0.92	0.27	24,24,24,24	0
24	MG	A	1640	1/1	0.92	0.25	24,24,24,24	0
24	MG	A	1581	1/1	0.92	0.08	24,24,24,24	0
24	MG	A	1643	1/1	0.92	0.11	24,24,24,24	1
24	MG	A	1644	1/1	0.92	0.09	24,24,24,24	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	1627	1/1	0.92	0.32	24,24,24,24	0
24	MG	A	1552	1/1	0.92	0.35	24,24,24,24	0
24	MG	A	1592	1/1	0.92	0.20	24,24,24,24	1
24	MG	A	1650	1/1	0.92	0.29	24,24,24,24	1
24	MG	A	1633	1/1	0.92	0.11	24,24,24,24	1
24	MG	A	1546	1/1	0.93	0.29	24,24,24,24	0
24	MG	A	1599	1/1	0.93	0.25	24,24,24,24	0
24	MG	A	1568	1/1	0.93	0.20	24,24,24,24	0
24	MG	A	1639	1/1	0.93	0.09	24,24,24,24	1
24	MG	A	1571	1/1	0.93	0.15	24,24,24,24	0
24	MG	A	1605	1/1	0.93	0.17	24,24,24,24	0
24	MG	A	1606	1/1	0.93	0.23	24,24,24,24	1
24	MG	A	1572	1/1	0.93	0.19	24,24,24,24	0
24	MG	A	1609	1/1	0.93	0.10	24,24,24,24	0
24	MG	A	1573	1/1	0.93	0.22	24,24,24,24	0
24	MG	A	1557	1/1	0.93	0.24	24,24,24,24	0
24	MG	A	1648	1/1	0.93	0.23	24,24,24,24	1
24	MG	A	1560	1/1	0.93	0.40	24,24,24,24	0
24	MG	A	1615	1/1	0.93	0.22	24,24,24,24	1
24	MG	A	1548	1/1	0.94	0.24	24,24,24,24	0
24	MG	A	1608	1/1	0.94	0.09	24,24,24,24	0
24	MG	A	1578	1/1	0.94	0.20	24,24,24,24	0
24	MG	A	1555	1/1	0.94	0.24	24,24,24,24	0
24	MG	A	1598	1/1	0.94	0.15	24,24,24,24	1
24	MG	A	1558	1/1	0.94	0.31	24,24,24,24	0
24	MG	A	1569	1/1	0.94	0.13	24,24,24,24	0
24	MG	A	1563	1/1	0.94	0.30	24,24,24,24	0
24	MG	A	1604	1/1	0.94	0.20	24,24,24,24	0
24	MG	A	71	1/1	0.94	0.28	24,24,24,24	0
24	MG	A	1565	1/1	0.94	0.27	24,24,24,24	0
24	MG	A	1637	1/1	0.95	0.15	24,24,24,24	0
24	MG	A	1574	1/1	0.95	0.18	24,24,24,24	0
24	MG	A	1625	1/1	0.95	0.16	24,24,24,24	0
24	MG	A	1600	1/1	0.95	0.20	24,24,24,24	0
24	MG	A	1582	1/1	0.95	0.16	24,24,24,24	0
24	MG	A	1628	1/1	0.95	0.08	24,24,24,24	0
24	MG	A	1629	1/1	0.95	0.11	24,24,24,24	0
24	MG	A	1630	1/1	0.95	0.06	24,24,24,24	0
24	MG	A	1593	1/1	0.95	0.16	24,24,24,24	0
24	MG	A	1601	1/1	0.95	0.17	24,24,24,24	0
24	MG	A	1621	1/1	0.95	0.14	24,24,24,24	0
24	MG	A	1580	1/1	0.95	0.18	24,24,24,24	0

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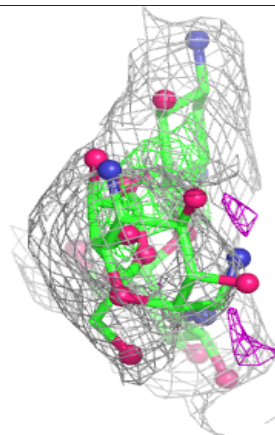
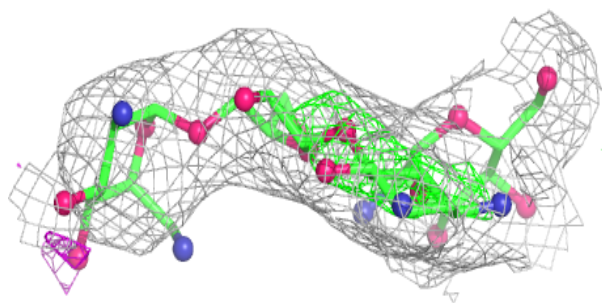
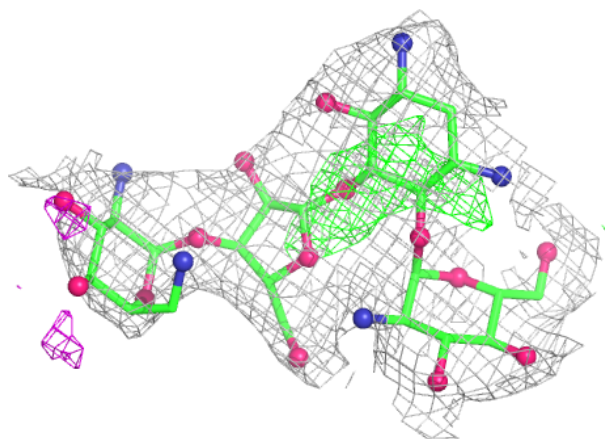
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	1590	1/1	0.95	0.15	24,24,24,24	0
25	ZN	D	306	1/1	0.95	0.23	24,24,24,24	0
24	MG	A	1642	1/1	0.96	0.06	24,24,24,24	0
24	MG	A	86	1/1	0.96	0.14	24,24,24,24	0
24	MG	A	1575	1/1	0.96	0.17	24,24,24,24	0
24	MG	A	1549	1/1	0.96	0.39	24,24,24,24	0
24	MG	A	1577	1/1	0.96	0.08	24,24,24,24	0
24	MG	A	1559	1/1	0.96	0.18	24,24,24,24	0
24	MG	A	1570	1/1	0.96	0.28	24,24,24,24	0
24	MG	A	1649	1/1	0.96	0.21	24,24,24,24	1
24	MG	A	1610	1/1	0.96	0.07	24,24,24,24	0
24	MG	A	1602	1/1	0.96	0.18	24,24,24,24	0
24	MG	A	1612	1/1	0.96	0.32	24,24,24,24	0
24	MG	A	1583	1/1	0.97	0.11	24,24,24,24	0
24	MG	A	1603	1/1	0.97	0.30	24,24,24,24	0
24	MG	A	1564	1/1	0.97	0.06	24,24,24,24	0
24	MG	A	1634	1/1	0.97	0.15	24,24,24,24	0
24	MG	A	1586	1/1	0.97	0.06	24,24,24,24	0
24	MG	A	1547	1/1	0.97	0.24	24,24,24,24	0
24	MG	A	87	1/1	0.97	0.35	24,24,24,24	1
24	MG	A	1594	1/1	0.97	0.36	24,24,24,24	0
24	MG	A	1618	1/1	0.97	0.19	24,24,24,24	0
24	MG	A	214	1/1	0.97	0.16	24,24,24,24	0
24	MG	A	1595	1/1	0.97	0.07	24,24,24,24	0
24	MG	A	1554	1/1	0.98	0.29	24,24,24,24	0
24	MG	D	215	1/1	0.98	0.05	24,24,24,24	0
24	MG	A	1584	1/1	0.98	0.25	24,24,24,24	0
24	MG	A	1551	1/1	0.98	0.23	24,24,24,24	0
24	MG	A	1553	1/1	0.99	0.25	24,24,24,24	0
24	MG	A	1596	1/1	0.99	0.40	24,24,24,24	0
25	ZN	N	307	1/1	1.00	0.01	24,24,24,24	1

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

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.