



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 24, 2026 – 07:45 PM UTC

PDB ID : 1HNZ / pdb_00001hnz
Title : STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL
SUBUNIT IN COMPLEX WITH HYGROMYCIN B
Authors : Brodersen, D.E.; Clemons Jr., W.M.; Carter, A.P.; Morgan-Warren, R.; Wim-
berly, B.T.; Ramakrishnan, V.
Deposited on : 2000-12-08
Resolution : 3.30 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

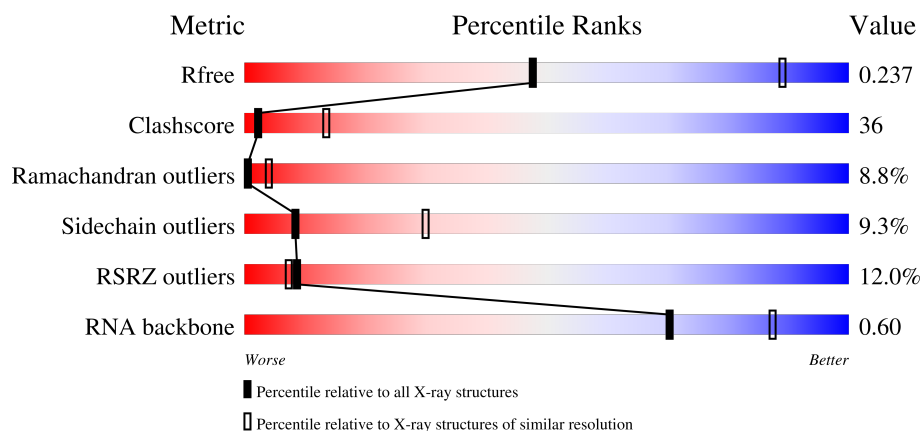
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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.



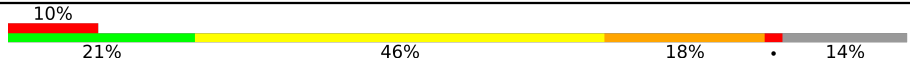
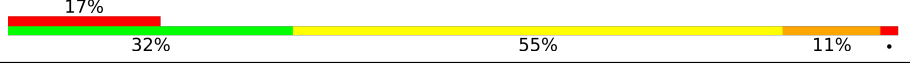
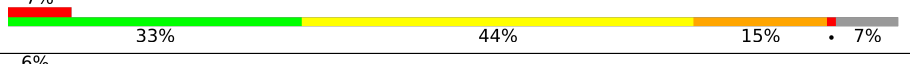
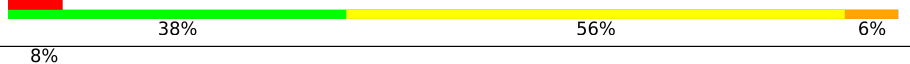
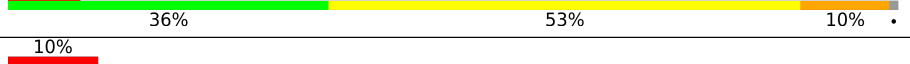
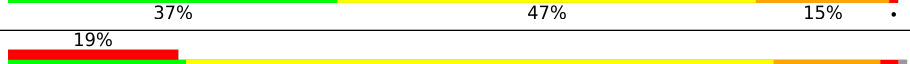
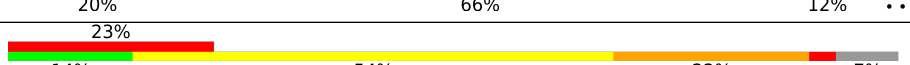
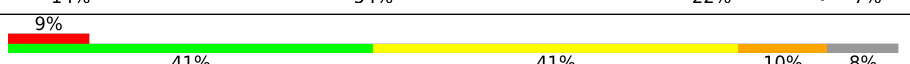
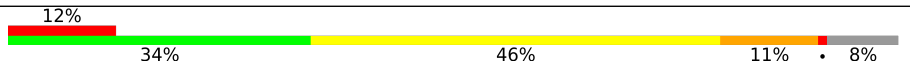
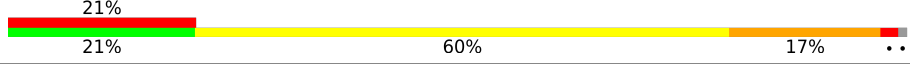
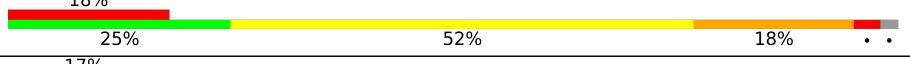
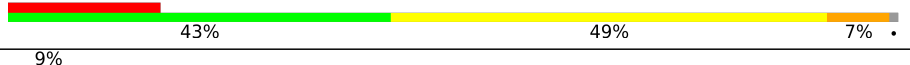
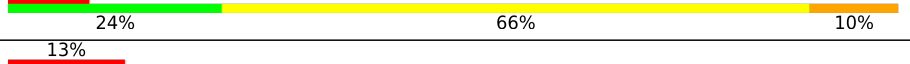
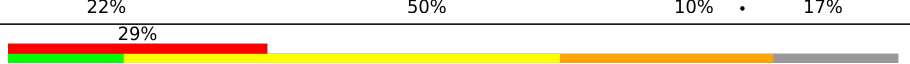
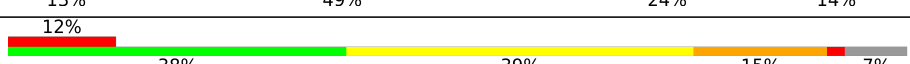
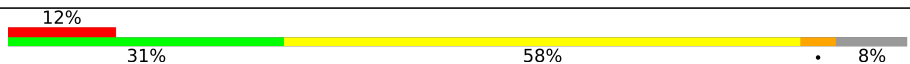
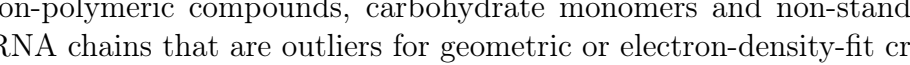
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)
RNA backbone	3983	1048 (3.60-3.00)

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	9% 28% 56% 11% • •
2	X	6	17% 100%
3	B	256	13% 17% 55% 16% • 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
23	MG	A	1547	-	-	-	X
23	MG	A	1550	-	-	-	X
23	MG	A	1556	-	-	-	X
23	MG	A	1557	-	-	-	X
23	MG	A	1566	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	MG	A	1585	-	-	-	X
23	MG	A	1586	-	-	-	X
23	MG	A	1614	-	-	-	X
23	MG	A	1615	-	-	-	X
23	MG	A	1618	-	-	-	X
23	MG	A	1623	-	-	-	X
23	MG	A	210	-	-	-	X
23	MG	A	212	-	-	-	X
23	MG	A	214	-	-	-	X
24	HYG	A	1632	X	-	-	-

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 51906 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1507	Total	C	N	O	P	22	0	0
			32391	14418	6002	10465	1506			

- Molecule 2 is a RNA chain called FRAGMENT OF MESSENGER RNA.

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	88	Total	C	N	O	S	0	0	0
			735	462	147	125	1			

- 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
			647	414	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
			762	469	162	129	2			

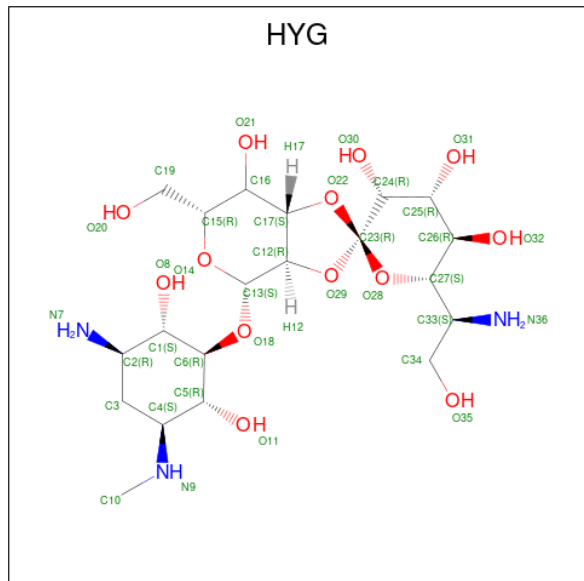
- Molecule 22 is a protein called 30S RIBOSOMAL PROTEIN THX.

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

- Molecule 23 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
23	A	94	Total Mg 94 94	0	0
23	D	1	Total Mg 1 1	0	0
23	H	1	Total Mg 1 1	0	0

- Molecule 24 is HYGROMYCIN B (CCD ID: HYG) (formula: $C_{20}H_{37}N_3O_{13}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
24	A	1	Total	C	N	O	0	0
			36	20	3	13		

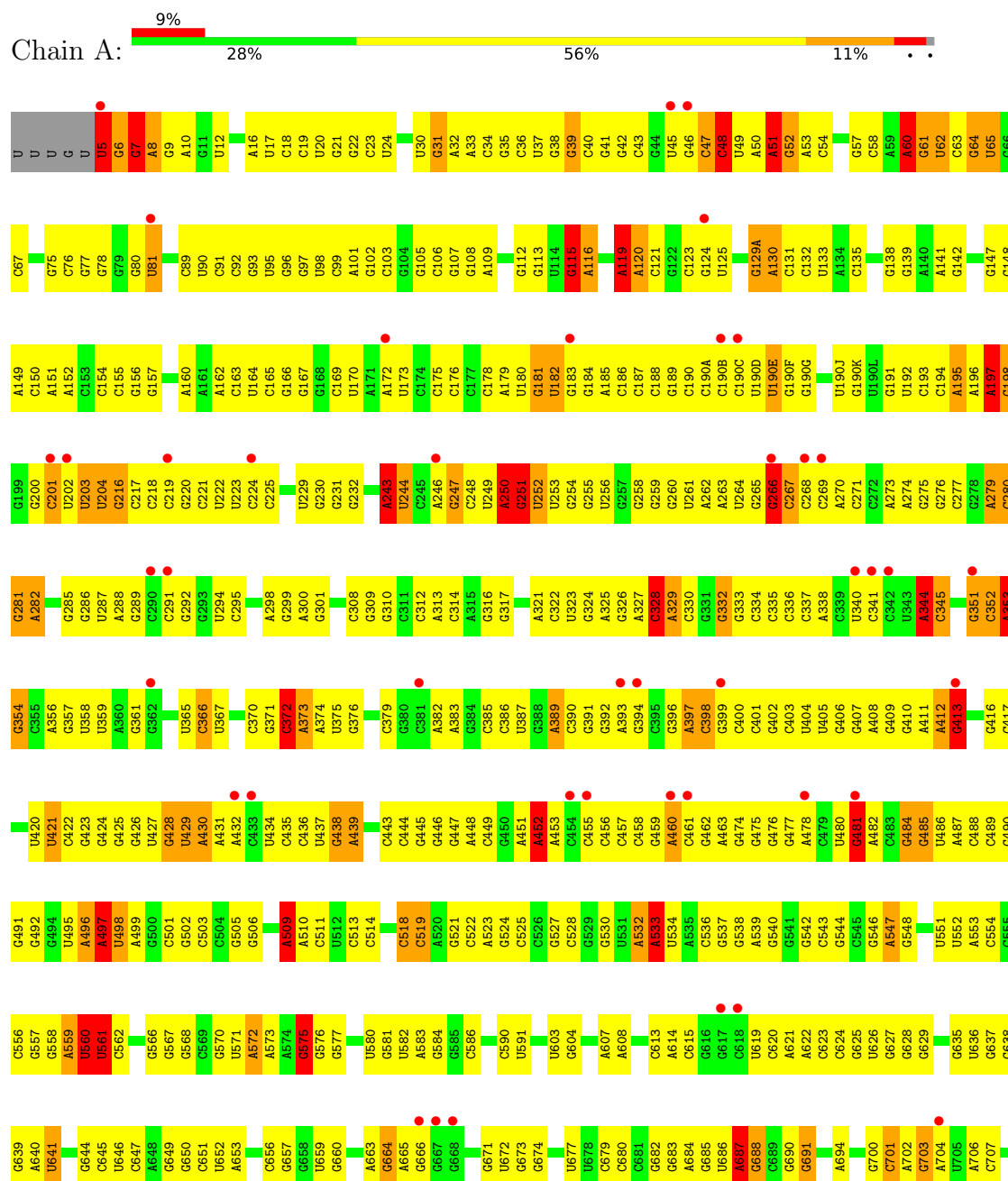
- Molecule 25 is ZINC ION (CCD ID: ZN) (formula: Zn).

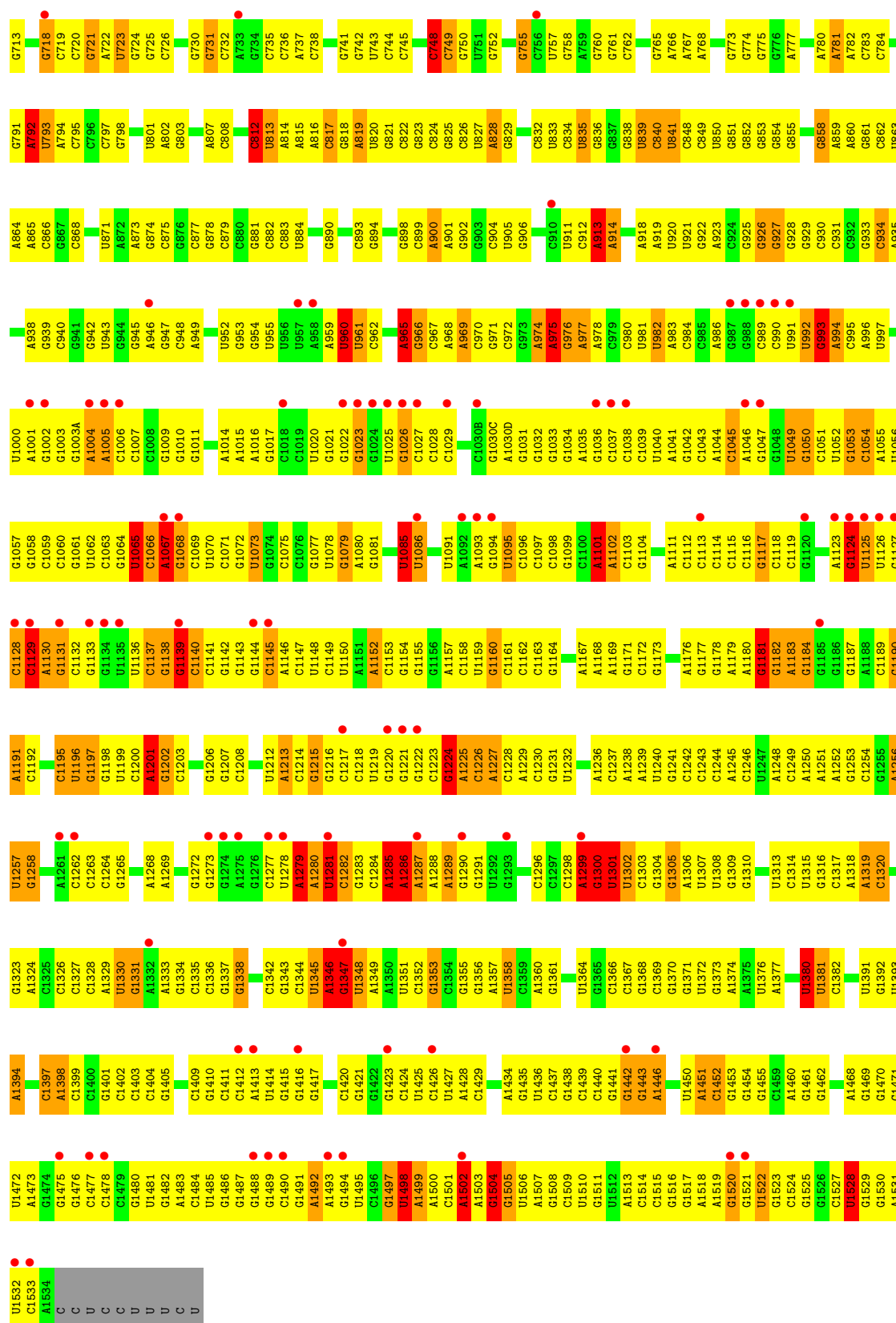
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	D	1	Total 1	Zn 1	0	0
25	N	1	Total 1	Zn 1	0	0

3 Residue-property plots

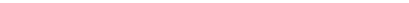
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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



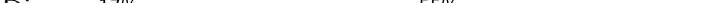


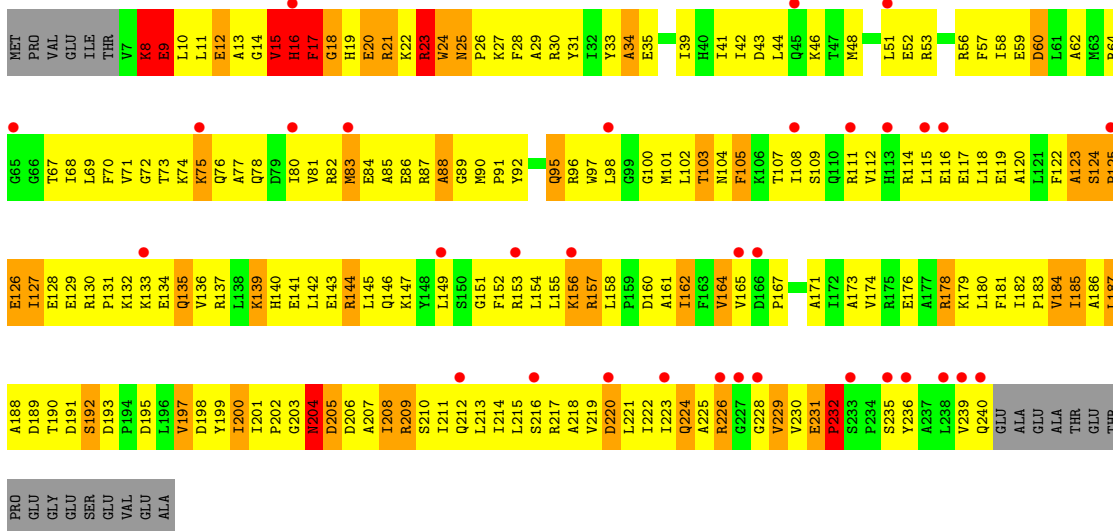
• Molecule 2: FRAGMENT OF MESSENGER RNA

Chain X:  17% 100%

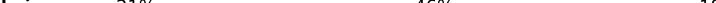


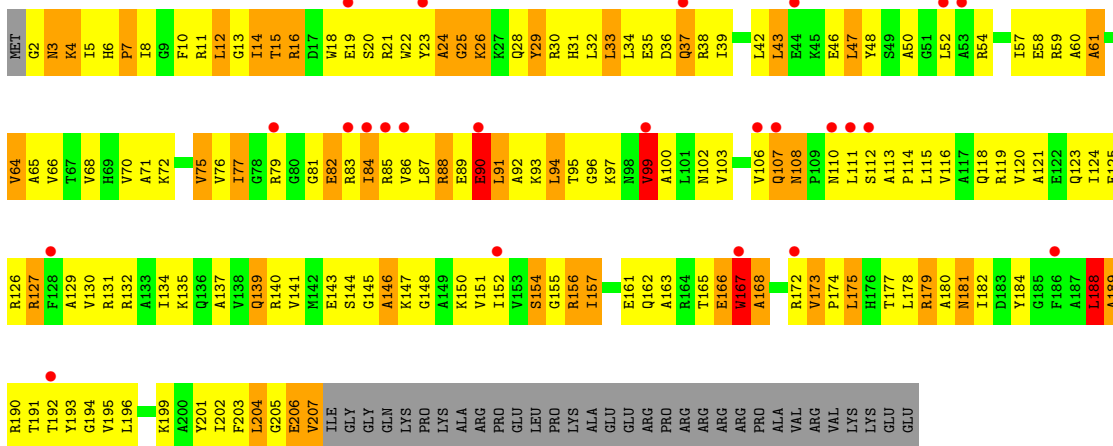
- Molecule 3: 30S RIBOSOMAL PROTEIN S2

Chain B: 

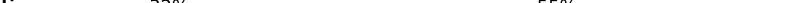


- Molecule 4: 30S RIBOSOMAL PROTEIN S3

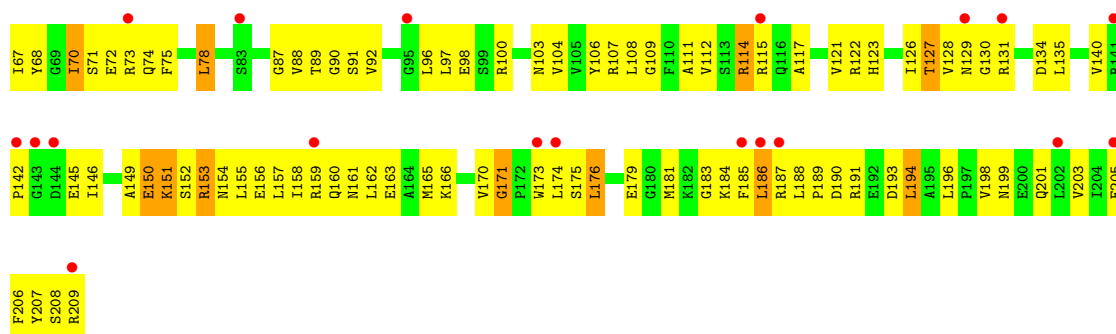
Chain C:  10% 21% 46% 18% 14%



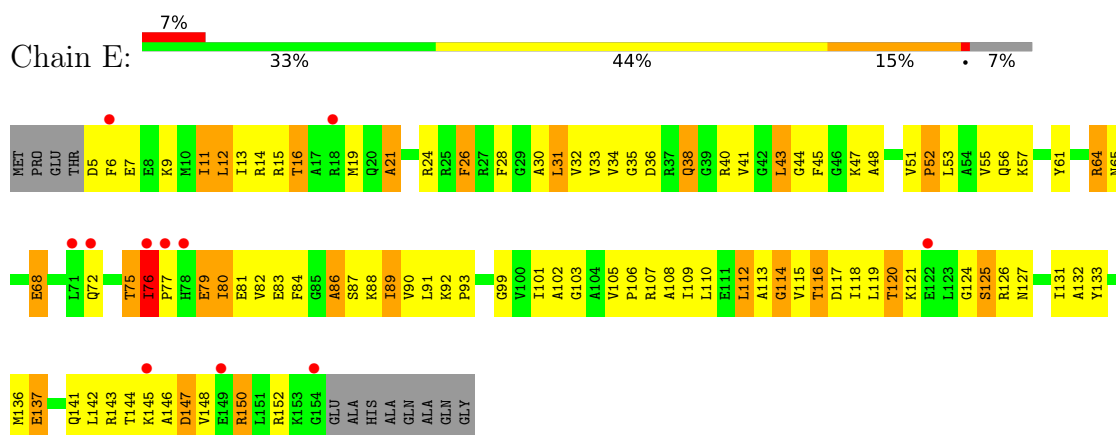
- Molecule 5: 30S RIBOSOMAL PROTEIN S4

Chain D: 

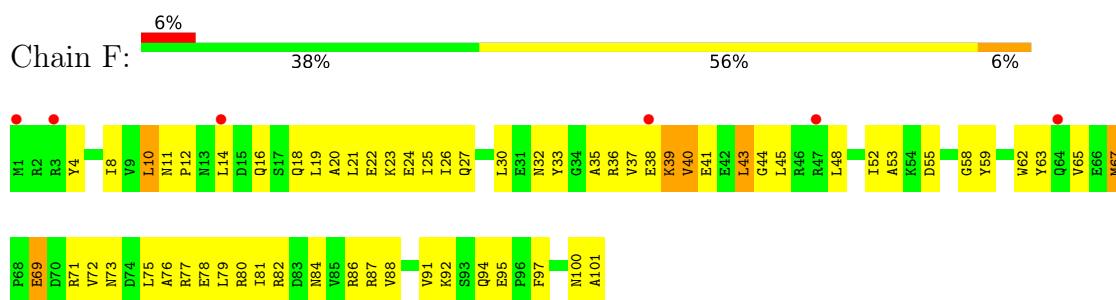




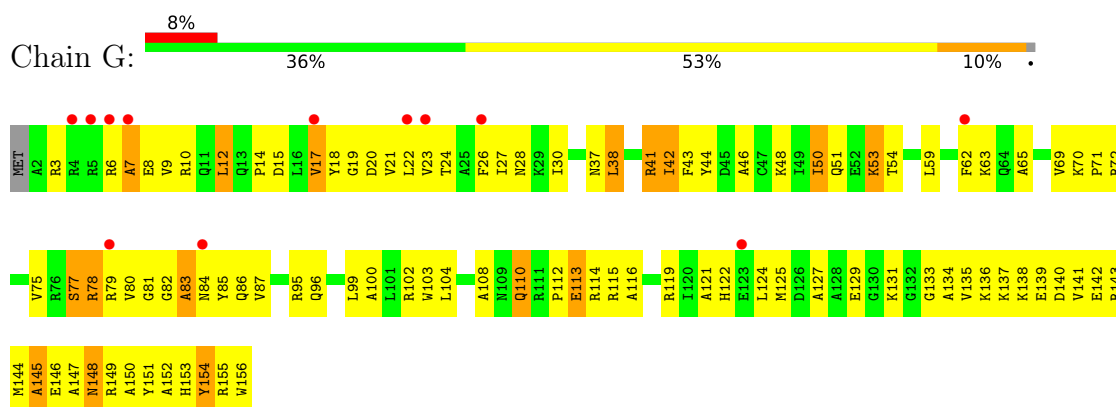
• Molecule 6: 30S RIBOSOMAL PROTEIN S5



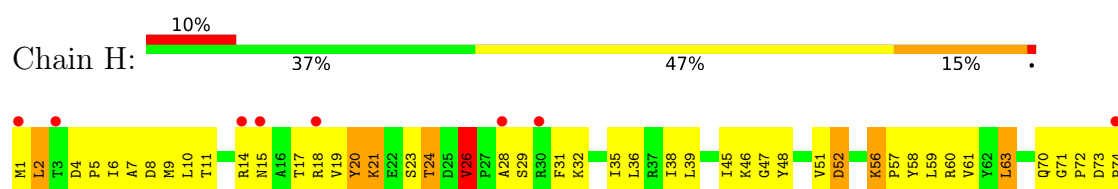
• Molecule 7: 30S RIBOSOMAL PROTEIN S6



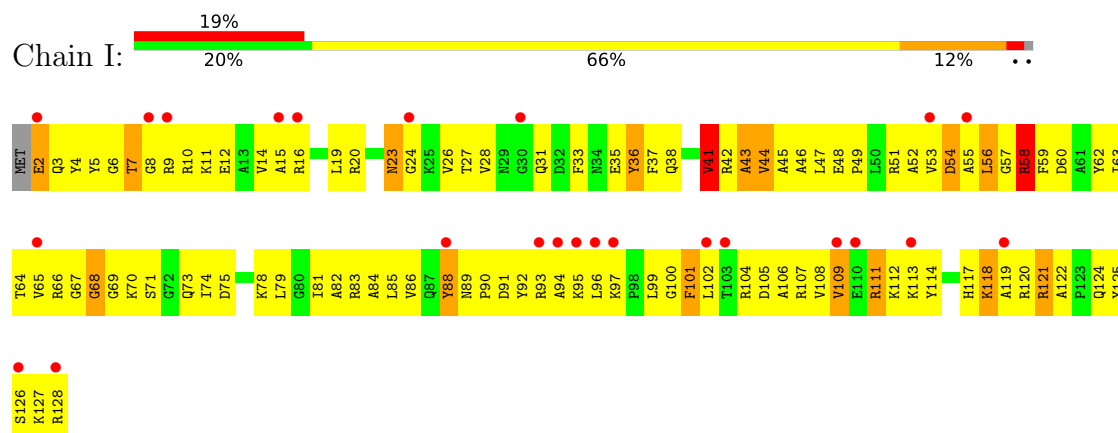
• Molecule 8: 30S RIBOSOMAL PROTEIN S7



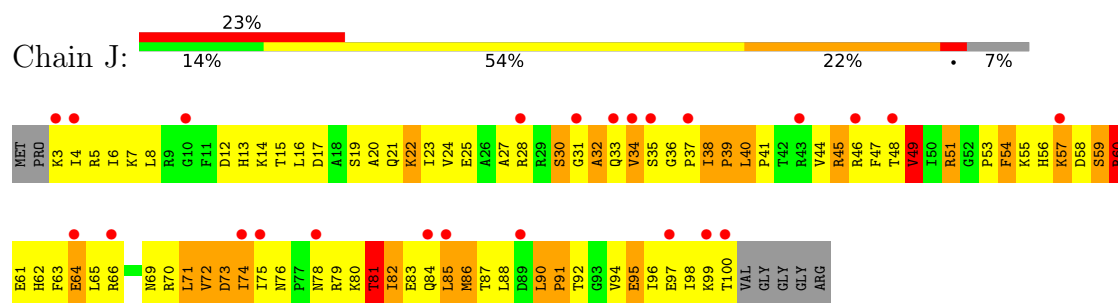
• Molecule 9: 30S RIBOSOMAL PROTEIN S8



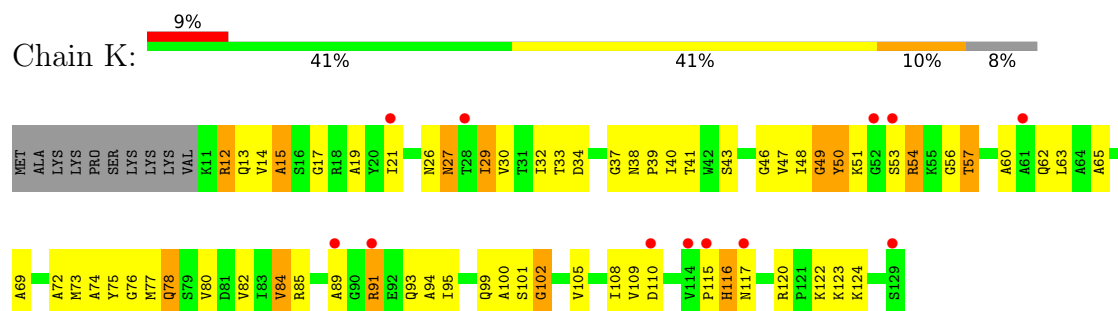
• Molecule 10: 30S RIBOSOMAL PROTEIN S9



• Molecule 11: 30S RIBOSOMAL PROTEIN S10

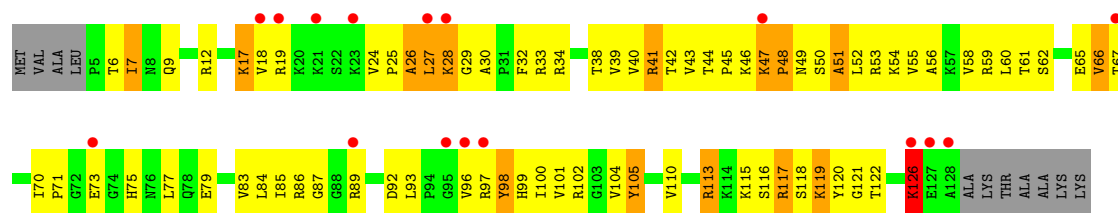


• Molecule 12: 30S RIBOSOMAL PROTEIN S11

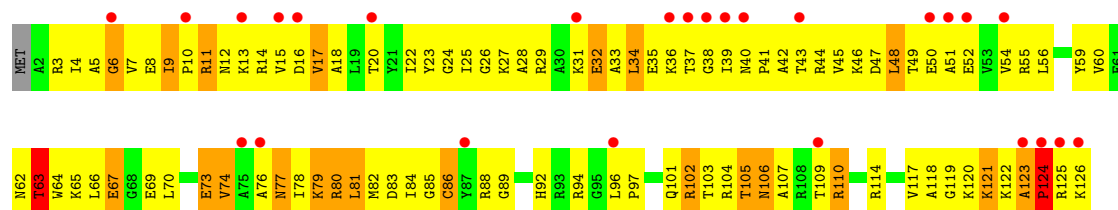


• Molecule 13: 30S RIBOSOMAL PROTEIN S12

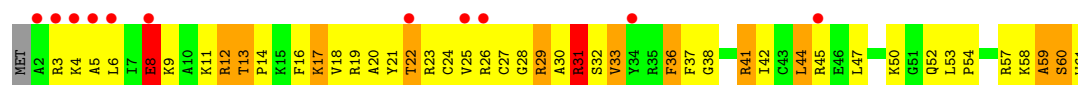




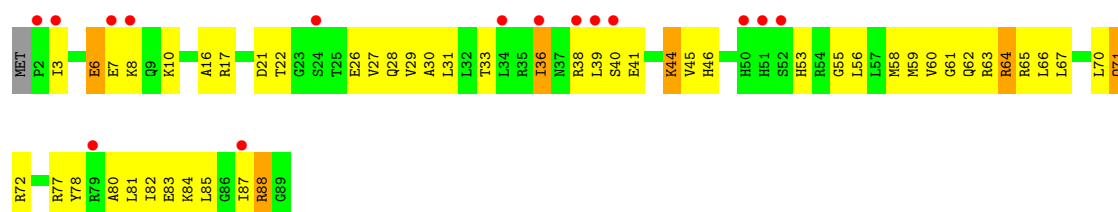
● Molecule 14: 30S RIBOSOMAL PROTEIN S13



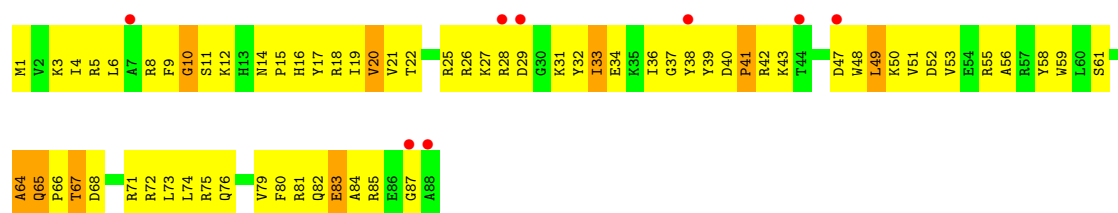
● Molecule 15: 30S RIBOSOMAL PROTEIN S14



● Molecule 16: 30S RIBOSOMAL PROTEIN S15

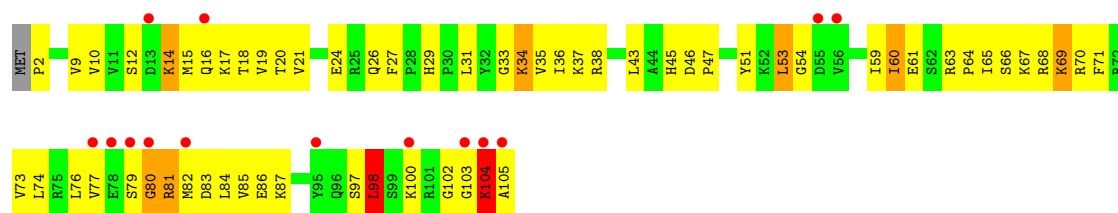


● Molecule 17: 30S RIBOSOMAL PROTEIN S16

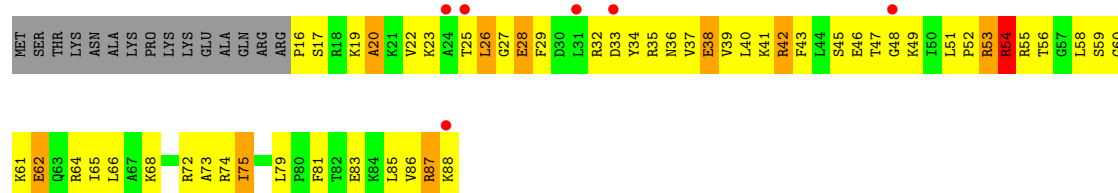


● Molecule 18: 30S RIBOSOMAL PROTEIN S17

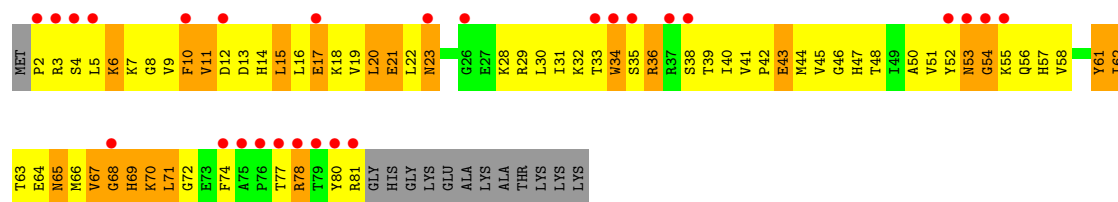
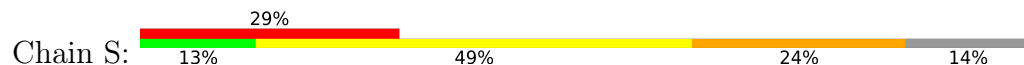




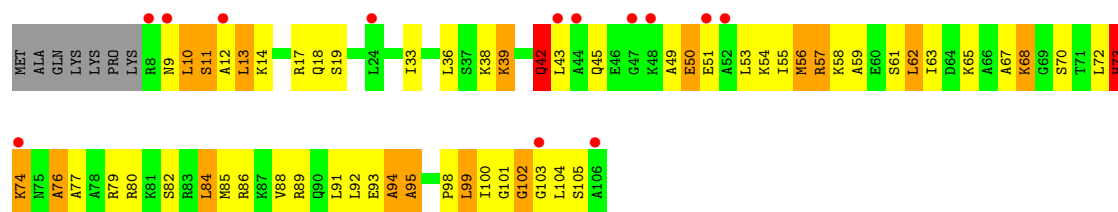
• Molecule 19: 30S RIBOSOMAL PROTEIN S18



• 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	402.06Å 402.06Å 175.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.30 50.00 – 3.30	Depositor EDS
% Data completeness (in resolution range)	88.0 (50.00-3.30) 88.0 (50.00-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 3.07Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.218 , 0.261 0.199 , 0.237	Depositor DCC
R_{free} test set	10985 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	88.1	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 105.4	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	0.90	EDS
Total number of atoms	51906	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.46% 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: MG, HYG, 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	0.46	0/36259	0.74	76/56593 (0.1%)
2	X	0.44	0/128	0.65	0/196
3	B	0.46	0/1935	1.07	14/2609 (0.5%)
4	C	0.44	0/1636	1.00	9/2205 (0.4%)
5	D	0.48	0/1733	1.02	6/2318 (0.3%)
6	E	0.58	0/1162	1.21	11/1564 (0.7%)
7	F	0.41	0/856	1.01	3/1154 (0.3%)
8	G	0.44	0/1276	0.99	8/1709 (0.5%)
9	H	0.56	0/1136	1.24	15/1527 (1.0%)
10	I	0.43	0/1029	1.00	6/1378 (0.4%)
11	J	0.44	0/805	1.01	6/1082 (0.6%)
12	K	0.49	0/900	1.06	3/1213 (0.2%)
13	L	0.54	0/986	1.13	6/1320 (0.5%)
14	M	0.46	0/1008	1.04	5/1347 (0.4%)
15	N	0.45	0/501	1.18	4/664 (0.6%)
16	O	0.48	0/745	0.90	1/992 (0.1%)
17	P	0.53	0/751	1.23	9/1008 (0.9%)
18	Q	0.53	0/870	1.09	2/1159 (0.2%)
19	R	0.45	0/603	1.01	1/799 (0.1%)
20	S	0.47	0/661	1.21	10/890 (1.1%)
21	T	0.51	0/764	1.09	3/1006 (0.3%)
22	V	0.54	0/212	1.05	1/277 (0.4%)
All	All	0.47	0/55956	0.86	199/83010 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	3	39

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	H	0	1
All	All	3	40

There are no bond length outliers.

All (199) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1498	U	C2'-C3'-O3'	15.40	132.60	109.50
1	A	559	A	C2'-C3'-O3'	13.34	129.51	109.50
1	A	181	G	C2'-C3'-O3'	12.99	128.99	109.50
1	A	1528	U	C2'-C3'-O3'	12.91	128.87	109.50
13	L	26	ALA	N-CA-C	-12.67	98.64	113.21
1	A	575	G	C2'-C3'-O3'	11.92	127.38	109.50
1	A	60	A	C2'-C3'-O3'	11.85	127.27	109.50
1	A	366	C	C2'-C3'-O3'	11.62	126.94	109.50
1	A	792	A	C2'-C3'-O3'	11.59	126.88	109.50
1	A	7	G	C2'-C3'-O3'	11.23	126.35	109.50
21	T	13	LEU	N-CA-C	-10.72	98.72	112.23
7	F	77	ARG	N-CA-C	-10.47	99.87	111.07
1	A	266	G	C2'-C3'-O3'	10.16	124.74	109.50
9	H	134	ILE	N-CA-C	10.08	120.72	110.23
1	A	372	C	C2'-C3'-O3'	9.97	124.45	109.50
1	A	48	C	C2'-C3'-O3'	9.95	124.43	109.50
1	A	1504	G	C2'-C3'-O3'	9.75	124.12	109.50
5	D	11	LEU	N-CA-C	-9.71	99.75	111.69
1	A	1528	U	C4'-C3'-O3'	9.51	123.67	109.40
9	H	56	LYS	CA-C-N	9.43	130.92	119.98
9	H	56	LYS	C-N-CA	9.43	130.92	119.98
5	D	12	CYS	N-CA-C	-9.36	99.87	111.11
1	A	243	A	C2'-C3'-O3'	9.25	123.38	109.50
1	A	960	U	C2'-C3'-O3'	9.22	123.34	109.50
15	N	8	GLU	N-CA-C	-9.18	102.08	113.28
1	A	115	G	C2'-C3'-O3'	9.12	123.18	109.50
16	O	44	LYS	N-CA-C	-9.07	101.28	111.71
1	A	533	A	C2'-C3'-O3'	8.92	122.88	109.50
1	A	687	A	C2'-C3'-O3'	8.84	122.76	109.50
1	A	484	G	C2'-C3'-O3'	8.76	122.64	109.50
1	A	1067	A	C2'-C3'-O3'	8.70	122.56	109.50
6	E	26	PHE	N-CA-C	8.60	120.98	110.41
1	A	181	G	C4'-C3'-O3'	8.58	122.27	109.40
17	P	27	LYS	N-CA-C	-8.35	100.14	110.41
1	A	560	U	C2'-C3'-O3'	8.24	121.86	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1380	U	C2'-C3'-O3'	8.09	121.63	109.50
1	A	428	G	C2'-C3'-O3'	8.08	121.62	109.50
3	B	13	ALA	N-CA-C	-8.02	103.25	112.87
1	A	1101	A	C2'-C3'-O3'	7.99	121.49	109.50
9	H	20	TYR	N-CA-C	7.97	122.44	112.24
21	T	76	ALA	N-CA-C	-7.95	102.57	111.07
8	G	154	TYR	N-CA-C	-7.91	101.49	112.25
1	A	1335	C	C4'-C3'-O3'	-7.87	101.19	113.00
1	A	1201	A	C2'-C3'-O3'	7.75	121.12	109.50
20	S	14	HIS	N-CA-C	-7.71	101.30	111.24
1	A	1301	U	C2'-C3'-O3'	7.60	120.90	109.50
1	A	328	C	C2'-C3'-O3'	7.57	120.85	109.50
1	A	559	A	C4'-C3'-O3'	7.52	120.67	109.40
20	S	36	ARG	N-CA-C	-7.49	103.41	112.54
6	E	21	ALA	N-CA-C	-7.41	99.06	110.10
1	A	1139	G	C2'-C3'-O3'	7.35	120.52	109.50
1	A	1224	G	C2'-C3'-O3'	7.32	120.49	109.50
1	A	748	C	C2'-C3'-O3'	7.23	120.34	109.50
5	D	186	LEU	N-CA-C	7.22	118.93	111.14
12	K	51	LYS	N-CA-C	7.12	122.10	113.41
1	A	1498	U	C4'-C3'-O3'	7.12	120.08	109.40
5	D	33	MET	N-CA-C	-7.08	103.59	113.37
1	A	60	A	C4'-C3'-O3'	7.04	119.97	109.40
1	A	1299	A	N9-C1'-C2'	6.99	122.48	112.00
20	S	10	PHE	N-CA-C	6.93	119.78	110.35
1	A	965	A	C2'-C3'-O3'	6.92	119.88	109.50
12	K	116	HIS	N-CA-C	-6.90	102.86	112.25
1	A	1124	G	N9-C1'-C2'	6.90	122.34	112.00
1	A	250	A	C2'-C3'-O3'	6.88	119.82	109.50
20	S	34	TRP	N-CA-C	-6.80	104.88	113.72
1	A	1281	U	C2'-C3'-O3'	6.78	119.66	109.50
17	P	67	THR	N-CA-C	-6.71	102.16	110.41
6	E	64	ARG	N-CA-C	-6.69	99.68	110.32
1	A	509	A	C2'-C3'-O3'	6.68	123.72	113.70
8	G	50	ILE	N-CA-C	-6.68	104.32	113.00
10	I	63	ILE	N-CA-C	6.66	117.90	108.17
9	H	79	VAL	N-CA-C	-6.66	102.52	111.44
1	A	413	G	C4'-C3'-O3'	-6.58	103.14	113.00
20	S	21	GLU	N-CA-C	-6.54	105.16	113.01
1	A	975	A	C2'-C3'-O3'	6.48	119.22	109.50
15	N	31	ARG	N-CA-C	6.47	122.05	111.37
20	S	38	SER	N-CA-C	6.47	119.29	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	P	25	ARG	N-CA-C	6.46	120.90	112.89
1	A	1285	A	C2'-C3'-O3'	6.45	119.17	109.50
1	A	913	A	C2'-C3'-O3'	6.40	119.10	109.50
6	E	76	ILE	CA-C-N	6.40	126.89	119.47
6	E	76	ILE	C-N-CA	6.40	126.89	119.47
13	L	119	LYS	N-CA-C	-6.36	99.33	109.76
14	M	17	VAL	CB-CA-C	-6.33	105.42	111.05
1	A	1085	U	C2'-C3'-O3'	6.29	118.94	109.50
1	A	1346	A	C2'-C3'-O3'	6.26	118.89	109.50
9	H	75	ARG	CA-C-N	6.26	127.66	119.84
9	H	75	ARG	C-N-CA	6.26	127.66	119.84
22	V	13	ILE	CB-CA-C	-6.26	103.69	111.70
1	A	1065	U	C2'-C3'-O3'	6.25	118.87	109.50
9	H	87	SER	N-CA-C	-6.24	100.60	109.96
8	G	153	HIS	N-CA-C	-6.19	105.83	113.19
1	A	119	A	C2'-C3'-O3'	6.18	118.77	109.50
1	A	1129	C	C2'-C3'-O3'	6.17	118.75	109.50
8	G	145	ALA	N-CA-C	-6.16	102.55	110.19
1	A	197	A	N9-C1'-C2'	6.14	123.21	114.00
1	A	1347	G	C1'-C2'-O2'	-6.13	102.61	111.80
4	C	173	VAL	CA-C-N	6.12	127.49	119.84
4	C	173	VAL	C-N-CA	6.12	127.49	119.84
20	S	53	ASN	N-CA-C	-6.11	105.96	113.41
1	A	366	C	C4'-C3'-O3'	6.10	118.55	109.40
21	T	68	LYS	N-CA-C	-6.09	104.27	111.03
13	L	79	GLU	N-CA-C	6.07	120.23	112.34
19	R	42	ARG	N-CA-C	6.06	118.68	111.71
13	L	61	THR	N-CA-C	-6.06	105.15	112.54
17	P	65	GLN	CA-C-N	6.05	126.00	119.76
17	P	65	GLN	C-N-CA	6.05	126.00	119.76
20	S	70	LYS	N-CA-C	6.05	121.05	108.53
1	A	1331	G	C4'-C3'-O3'	-5.99	104.01	113.00
14	M	11	ARG	N-CA-C	5.96	118.12	109.07
1	A	1300	G	N9-C1'-C2'	5.94	120.91	112.00
3	B	135	GLN	N-CA-C	-5.93	106.14	113.19
5	D	13	ARG	N-CA-C	5.91	117.52	111.14
20	S	54	GLY	N-CA-C	-5.91	99.18	113.18
1	A	452	A	N9-C1'-C2'	5.86	120.79	112.00
1	A	1181	G	N9-C1'-C2'	5.84	120.77	112.00
15	N	33	VAL	N-CA-C	5.83	116.59	108.89
3	B	156	LYS	N-CA-C	-5.77	106.86	114.31
13	L	105	TYR	CB-CA-C	-5.75	109.96	116.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	S	23	ASN	N-CA-C	-5.73	106.24	113.18
14	M	119	GLY	N-CA-C	5.72	119.48	111.19
1	A	1200	C	C2'-C3'-O3'	-5.72	105.12	113.70
11	J	38	ILE	CA-C-N	5.71	126.98	119.84
11	J	38	ILE	C-N-CA	5.71	126.98	119.84
3	B	220	ASP	N-CA-C	-5.71	104.06	111.02
18	Q	104	LYS	N-CA-C	5.68	122.90	110.80
1	A	51	A	C2'-C3'-O3'	5.67	118.00	109.50
4	C	99	VAL	N-CA-C	5.65	117.47	108.89
10	I	36	TYR	N-CA-C	-5.64	105.13	111.28
13	L	66	VAL	N-CA-C	5.63	118.23	108.95
8	G	110	GLN	N-CA-C	-5.62	106.46	113.38
17	P	50	LYS	N-CA-C	-5.62	101.71	110.42
6	E	48	ALA	CA-C-N	5.61	125.97	119.47
6	E	48	ALA	C-N-CA	5.61	125.97	119.47
9	H	96	GLY	N-CA-C	-5.59	105.11	112.82
11	J	60	ARG	N-CA-C	5.57	122.67	110.80
1	A	344	A	C2'-C3'-O3'	5.56	117.83	109.50
8	G	148	ASN	N-CA-C	-5.53	104.79	113.02
3	B	152	PHE	N-CA-C	-5.52	106.87	113.21
3	B	192	SER	N-CA-C	5.51	118.62	110.46
9	H	26	VAL	CA-C-N	5.51	126.72	119.84
9	H	26	VAL	C-N-CA	5.51	126.72	119.84
1	A	1286	A	O3'-P-O5'	5.50	112.25	104.00
1	A	1331	G	N9-C1'-C2'	5.49	120.24	112.00
15	N	38	GLY	N-CA-C	-5.49	108.06	115.36
3	B	105	PHE	N-CA-C	5.48	117.69	111.11
4	C	93	LYS	N-CA-C	-5.46	105.83	113.37
4	C	25	GLY	N-CA-C	5.45	120.89	112.45
3	B	88	ALA	N-CA-C	-5.44	101.68	110.32
18	Q	14	LYS	N-CA-C	5.42	119.37	112.87
17	P	64	ALA	N-CA-C	-5.38	102.08	110.10
10	I	117	HIS	N-CA-C	5.38	117.90	111.71
14	M	34	LEU	N-CA-C	-5.37	105.34	111.14
4	C	94	LEU	N-CA-C	-5.37	106.66	113.43
12	K	91	ARG	N-CA-C	-5.36	104.41	111.96
11	J	22	LYS	N-CA-C	-5.36	105.36	111.14
10	I	27	THR	N-CA-C	-5.35	102.36	110.28
1	A	530	G	N9-C1'-C2'	5.34	120.02	112.00
1	A	993	G	C2'-C3'-O3'	5.34	117.51	109.50
1	A	1195	C	C4'-C3'-O3'	-5.33	105.01	113.00
14	M	79	LYS	N-CA-C	-5.33	104.89	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	P	33	ILE	N-CA-C	5.33	117.75	111.09
6	E	86	ALA	N-CA-C	-5.30	106.58	113.16
7	F	67	MET	N-CA-C	5.30	114.40	108.25
1	A	353	A	C5'-C4'-O4'	-5.28	101.88	109.80
6	E	32	VAL	N-CA-C	5.27	115.49	108.11
1	A	1195	C	N1-C1'-C2'	5.26	119.89	112.00
17	P	20	VAL	N-CA-C	5.26	115.13	107.88
9	H	103	VAL	N-CA-C	5.24	116.45	109.37
3	B	11	LEU	N-CA-C	-5.23	106.09	113.20
3	B	200	ILE	N-CA-C	5.22	116.49	108.71
11	J	81	THR	N-CA-C	-5.22	105.51	111.14
5	D	150	GLU	N-CA-C	-5.20	104.68	111.02
1	A	497	A	C2'-C3'-O3'	5.20	117.29	109.50
1	A	1279	A	N9-C1'-C2'	5.20	119.79	112.00
3	B	15	VAL	N-CA-C	5.18	120.12	109.34
3	B	205	ASP	N-CA-C	-5.18	105.81	111.82
1	A	389	A	C2'-C3'-O3'	-5.17	105.95	113.70
6	E	114	GLY	N-CA-C	-5.17	107.12	115.08
11	J	49	VAL	N-CA-C	5.15	116.07	108.45
10	I	60	ASP	N-CA-C	-5.14	101.30	108.96
6	E	75	THR	CB-CA-C	-5.14	107.98	114.40
1	A	993	G	N9-C1'-C2'	5.13	121.70	114.00
1	A	812	C	C2'-C3'-O3'	5.12	117.18	109.50
9	H	116	LYS	N-CA-C	-5.10	105.78	112.41
3	B	16	HIS	N-CA-C	5.09	121.65	110.80
1	A	1502	A	N9-C1'-C2'	5.09	121.64	114.00
4	C	12	LEU	N-CA-C	5.09	118.96	112.34
9	H	120	THR	N-CA-C	-5.08	102.54	110.42
9	H	46	LYS	N-CA-C	-5.08	106.35	112.54
4	C	84	ILE	N-CA-C	-5.07	106.32	112.76
7	F	37	VAL	N-CA-C	5.06	115.77	108.93
4	C	90	GLU	N-CA-C	-5.06	105.89	111.71
3	B	34	ALA	N-CA-C	5.06	115.87	107.73
1	A	389	A	C5'-C4'-C3'	5.04	123.56	116.00
1	A	5	U	N1-C1'-C2'	5.03	119.54	112.00
8	G	9	VAL	N-CA-C	5.03	115.53	108.89
8	G	115	ARG	N-CA-C	5.01	116.92	109.25
10	I	68	GLY	N-CA-C	5.01	120.08	110.86

All (3) chirality outliers are listed below:

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Mol	Chain	Res	Type	Atom
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Mol	Chain	Res	Type	Atom
1	A	181	G	C3'
1	A	1498	U	C3'
1	A	1528	U	C3'

All (40) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1073	U	Sidechain
1	A	1077	G	Sidechain
1	A	1079	G	Sidechain
1	A	1085	U	Sidechain
1	A	1181	G	Sidechain
1	A	12	U	Sidechain
1	A	1281	U	Sidechain
1	A	1289	A	Sidechain
1	A	1299	A	Sidechain
1	A	1301	U	Sidechain
1	A	1330	U	Sidechain
1	A	1345	U	Sidechain
1	A	1358	U	Sidechain
1	A	1401	G	Sidechain
1	A	1434	A	Sidechain
1	A	1522	U	Sidechain
1	A	197	A	Sidechain
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	263	A	Sidechain
1	A	266	G	Sidechain
1	A	413	G	Sidechain
1	A	452	A	Sidechain
1	A	481	G	Sidechain
1	A	561	U	Sidechain
1	A	572	A	Sidechain
1	A	575	G	Sidechain
1	A	641	U	Sidechain
1	A	664	G	Sidechain
1	A	691	G	Sidechain
1	A	773	G	Sidechain
1	A	835	U	Sidechain
1	A	868	C	Sidechain
1	A	871	U	Sidechain

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Mol	Chain	Res	Type	Group
1	A	873	A	Sidechain
1	A	879	C	Sidechain
1	A	898	G	Sidechain
1	A	900	A	Sidechain
1	A	982	U	Sidechain
9	H	58	TYR	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	32391	0	16349	1229	0
2	X	117	0	64	0	0
3	B	1900	0	1951	272	1
4	C	1612	0	1677	242	0
5	D	1703	0	1763	190	0
6	E	1146	0	1207	118	0
7	F	843	0	857	70	0
8	G	1257	0	1296	101	0
9	H	1116	0	1177	103	0
10	I	1011	0	1043	148	0
11	J	792	0	835	150	0
12	K	885	0	904	73	0
13	L	970	0	1057	114	0
14	M	997	0	1072	131	0
15	N	492	0	529	71	0
16	O	734	0	771	69	0
17	P	735	0	752	69	0
18	Q	857	0	930	82	0
19	R	597	0	668	85	0
20	S	647	0	673	85	0
21	T	762	0	859	70	0
22	V	208	0	221	23	0
23	A	94	0	0	0	0
23	D	1	0	0	0	0
23	H	1	0	0	0	0
24	A	36	0	36	7	0
25	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	N	1	0	0	0	0
All	All	51906	0	36691	3195	1

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

All (3195) 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)
13:L:28:LYS:HD2	13:L:33:ARG:HH22	1.08	1.12
1:A:1443:G:H5''	1:A:1446:A:H5'	1.21	1.11
5:D:36:ARG:H	5:D:37:PRO:HD3	1.02	1.10
3:B:84:GLU:HB3	3:B:219:VAL:HG21	1.30	1.09
11:J:45:ARG:HB3	11:J:45:ARG:HH11	1.01	1.09
13:L:41:ARG:HG2	13:L:42:THR:H	1.10	1.09
1:A:80:G:H3'	1:A:81:U:H5''	1.33	1.08
3:B:77:ALA:HB2	3:B:211:ILE:HD13	1.15	1.08
4:C:25:GLY:HA2	4:C:29:TYR:HB2	1.32	1.07
12:K:110:ASP:HB2	19:R:88:LYS:HD2	1.33	1.07
10:I:8:GLY:HA2	10:I:79:LEU:HD12	1.34	1.06
11:J:51:ARG:HB2	11:J:59:SER:HB3	1.32	1.05
16:O:56:LEU:HA	16:O:59:MET:HE2	1.34	1.04
1:A:761:G:H4'	18:Q:103:GLY:H	1.21	1.04
20:S:33:THR:HG22	20:S:35:SER:H	1.15	1.04
9:H:119:LEU:HD12	9:H:124:ALA:HA	1.36	1.04
18:Q:104:LYS:H	18:Q:104:LYS:HZ3	1.05	1.02
1:A:1047:G:H5''	15:N:4:LYS:HD2	1.41	1.02
4:C:91:LEU:HD21	4:C:99:VAL:HG13	1.41	1.01
1:A:1057:G:H5''	4:C:154:SER:HB2	1.41	1.01
11:J:45:ARG:HB3	11:J:45:ARG:NH1	1.75	1.01
14:M:49:THR:HG22	14:M:51:ALA:H	1.24	1.01
4:C:94:LEU:HD23	4:C:95:THR:HG23	1.43	1.00
14:M:10:PRO:HB2	14:M:18:ALA:HB1	1.43	0.99
5:D:187:ARG:HE	5:D:188:LEU:H	1.02	0.99
13:L:60:LEU:HD11	13:L:85:ILE:HD12	1.40	0.99
21:T:39:LYS:HD2	21:T:55:ILE:HD13	1.43	0.99
6:E:51:VAL:HB	6:E:52:PRO:HD3	1.44	0.99
5:D:187:ARG:HH21	5:D:188:LEU:HG	1.29	0.98
5:D:16:GLY:O	5:D:33:MET:HE2	1.63	0.98
13:L:33:ARG:HG2	13:L:60:LEU:HD12	1.46	0.98
1:A:1131:G:H1	1:A:1143:G:H21	1.03	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:761:G:H4'	18:Q:103:GLY:N	1.78	0.97
3:B:74:LYS:NZ	3:B:206:ASP:HA	1.81	0.96
1:A:64:G:H4'	1:A:65:U:O5'	1.65	0.96
5:D:36:ARG:N	5:D:37:PRO:HD3	1.82	0.95
5:D:140:VAL:HG11	5:D:146:ILE:HD11	1.46	0.95
12:K:54:ARG:HB3	12:K:54:ARG:HH11	1.31	0.94
1:A:1305:G:HO2'	1:A:1306:A:H8	0.96	0.94
1:A:1125:U:H3	11:J:5:ARG:HH21	1.08	0.94
4:C:3:ASN:HD22	4:C:3:ASN:N	1.65	0.93
1:A:1137:C:H4'	1:A:1138:G:C2	2.04	0.93
3:B:91:PRO:HG3	3:B:154:LEU:HB2	1.48	0.93
7:F:8:ILE:HD11	7:F:79:LEU:HD13	1.47	0.93
1:A:1305:G:O2'	1:A:1306:A:H8	1.52	0.93
9:H:19:VAL:HG23	9:H:21:LYS:HD3	1.51	0.92
13:L:75:HIS:HD2	13:L:77:LEU:H	1.16	0.92
12:K:40:ILE:HG22	12:K:41:THR:HG23	1.49	0.92
5:D:162:LEU:HD12	5:D:181:MET:HE2	1.52	0.91
13:L:24:VAL:HG13	13:L:98:TYR:HE2	1.34	0.91
1:A:1286:A:C3'	1:A:1287:A:H5''	2.00	0.91
1:A:1286:A:C2'	1:A:1287:A:H5''	2.02	0.90
18:Q:104:LYS:H	18:Q:104:LYS:NZ	1.69	0.90
1:A:1281:U:H5'	1:A:1282:C:H5	1.34	0.90
1:A:243:A:H4'	1:A:244:U:H5'	1.54	0.90
8:G:78:ARG:HB2	8:G:156:TRP:HZ3	1.35	0.90
1:A:686:U:HO2'	1:A:687:A:H8	0.90	0.90
19:R:36:ASN:ND2	19:R:38:GLU:HG2	1.87	0.90
1:A:7:G:H5'	1:A:298:A:O4'	1.72	0.90
1:A:1230:C:H1'	14:M:126:LYS:HA	1.52	0.90
1:A:351:G:H4'	1:A:352:C:OP1	1.71	0.89
1:A:1086:U:H3	1:A:1099:G:H22	0.93	0.89
5:D:25:ARG:NH1	5:D:30:LYS:HB3	1.88	0.89
1:A:1116:C:H2'	1:A:1117:G:H5''	1.52	0.89
3:B:77:ALA:HB2	3:B:211:ILE:CD1	2.03	0.89
4:C:3:ASN:HD22	4:C:3:ASN:H	1.19	0.88
1:A:1286:A:H2'	1:A:1287:A:H5''	1.54	0.88
5:D:150:GLU:H	5:D:150:GLU:CD	1.82	0.88
4:C:195:VAL:O	4:C:196:LEU:HD23	1.74	0.87
1:A:1250:A:H4'	10:I:68:GLY:N	1.90	0.87
18:Q:15:MET:HE1	18:Q:43:LEU:HD22	1.55	0.87
18:Q:97:SER:HB2	18:Q:103:GLY:N	1.90	0.87
5:D:199:ASN:HD21	5:D:201:GLN:HB3	1.40	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1226:C:H4'	1:A:1227:A:OP1	1.72	0.86
4:C:108:ASN:ND2	4:C:111:LEU:HG	1.89	0.86
4:C:52:LEU:HD23	4:C:52:LEU:H	1.39	0.86
19:R:55:ARG:NH1	19:R:55:ARG:HB3	1.90	0.86
1:A:1152:A:H5''	11:J:13:HIS:HD2	1.40	0.85
3:B:178:ARG:HH11	3:B:178:ARG:HG3	1.39	0.85
5:D:187:ARG:HE	5:D:188:LEU:N	1.72	0.85
8:G:78:ARG:HB2	8:G:156:TRP:CZ3	2.12	0.85
11:J:62:HIS:HB3	15:N:59:ALA:HB3	1.57	0.85
1:A:954:G:H21	1:A:1227:A:H62	1.25	0.85
1:A:974:A:OP1	15:N:31:ARG:HG2	1.76	0.85
5:D:23:GLY:HA3	5:D:112:VAL:HG12	1.57	0.84
5:D:36:ARG:H	5:D:37:PRO:CD	1.85	0.84
6:E:80:ILE:CD1	6:E:91:LEU:HB2	2.08	0.84
1:A:438:G:H4'	1:A:439:A:OP1	1.75	0.84
1:A:664:G:H22	1:A:741:G:H1	1.20	0.84
3:B:124:SER:HB2	3:B:125:PRO:HD2	1.60	0.84
1:A:371:G:O2'	1:A:372:C:H5'	1.77	0.84
1:A:975:A:H5'	1:A:975:A:H8	1.40	0.84
4:C:131:ARG:HG2	4:C:135:LYS:HE3	1.59	0.84
9:H:1:MET:HG2	9:H:2:LEU:H	1.43	0.84
5:D:156:GLU:HG2	5:D:160:GLN:HE21	1.42	0.84
11:J:19:SER:HB2	11:J:91:PRO:HG3	1.58	0.84
7:F:10:LEU:HD12	7:F:59:TYR:HB3	1.60	0.84
1:A:1356:G:H2'	1:A:1357:A:C8	2.13	0.83
1:A:1286:A:H3'	1:A:1287:A:H5''	1.57	0.83
13:L:41:ARG:HG2	13:L:42:THR:N	1.93	0.83
3:B:130:ARG:HH22	4:C:207:VAL:HG23	1.43	0.83
4:C:112:SER:HB2	4:C:115:LEU:HD12	1.59	0.83
12:K:91:ARG:NH1	19:R:88:LYS:HE2	1.94	0.83
11:J:39:PRO:HA	11:J:70:ARG:HH11	1.44	0.82
20:S:55:LYS:HG2	20:S:56:GLN:HE21	1.43	0.82
1:A:1117:G:H4'	10:I:104:ARG:NH1	1.93	0.82
1:A:1443:G:C5'	1:A:1446:A:H5'	2.07	0.82
13:L:70:ILE:HD13	13:L:77:LEU:HD12	1.59	0.82
1:A:1347:G:N2	1:A:1373:G:H2'	1.92	0.82
3:B:197:VAL:HB	3:B:200:ILE:HG12	1.59	0.82
13:L:28:LYS:HD2	13:L:33:ARG:NH2	1.91	0.82
4:C:58:GLU:HB3	11:J:92:THR:HG21	1.62	0.82
6:E:9:LYS:HD2	6:E:112:LEU:HD21	1.61	0.82
1:A:1060:C:C5	4:C:2:GLY:HA3	2.14	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:174:PRO:HB2	4:C:177:THR:HG22	1.60	0.81
1:A:80:G:H3'	1:A:81:U:C5'	2.09	0.81
1:A:1137:C:H4'	1:A:1138:G:N2	1.95	0.81
13:L:25:PRO:C	13:L:27:LEU:H	1.86	0.81
1:A:1065:U:H4'	1:A:1066:C:O5'	1.79	0.81
20:S:64:GLU:O	20:S:67:VAL:HG23	1.80	0.81
1:A:1412:C:H2'	1:A:1413:A:H8	1.44	0.81
3:B:74:LYS:HZ1	3:B:206:ASP:HA	1.43	0.81
1:A:80:G:C3'	1:A:81:U:H5''	2.10	0.80
1:A:686:U:O2'	1:A:687:A:H8	1.64	0.80
6:E:81:GLU:HG2	6:E:90:VAL:HG22	1.61	0.80
8:G:95:ARG:HG2	8:G:99:LEU:HD11	1.62	0.80
10:I:9:ARG:HG2	10:I:14:VAL:HG22	1.64	0.80
11:J:51:ARG:HG2	11:J:51:ARG:HH11	1.46	0.80
14:M:50:GLU:O	14:M:54:VAL:HG23	1.81	0.80
3:B:80:ILE:HD11	3:B:208:ILE:HG23	1.62	0.80
1:A:1025:U:H2'	1:A:1026:G:C8	2.16	0.80
1:A:1236:A:H4'	1:A:1304:G:H4'	1.62	0.80
1:A:1493:A:O2'	1:A:1494:G:H5'	1.82	0.80
20:S:33:THR:HG22	20:S:35:SER:N	1.95	0.80
1:A:1238:A:H5'	1:A:1336:C:H41	1.44	0.80
1:A:1190:G:OP1	4:C:4:LYS:HA	1.80	0.80
5:D:61:LYS:HD2	5:D:207:TYR:OH	1.81	0.80
1:A:839:U:H5'	1:A:840:C:C5	2.16	0.80
1:A:1279:A:H5''	1:A:1280:A:OP1	1.82	0.80
3:B:132:LYS:HA	3:B:135:GLN:HB3	1.63	0.80
1:A:953:G:H1'	14:M:125:ARG:CB	2.12	0.79
1:A:1182:G:H4'	1:A:1183:A:O5'	1.82	0.79
5:D:199:ASN:ND2	5:D:201:GLN:HB3	1.96	0.79
1:A:1006:C:H2'	1:A:1007:C:H6	1.46	0.79
1:A:328:C:O2	1:A:328:C:H2'	1.82	0.79
14:M:11:ARG:HG3	14:M:12:ASN:N	1.96	0.79
3:B:22:LYS:HD2	3:B:35:GLU:OE1	1.83	0.79
4:C:58:GLU:H	4:C:65:ALA:HB3	1.48	0.79
12:K:57:THR:HG23	12:K:60:ALA:H	1.48	0.79
13:L:27:LEU:HG	13:L:28:LYS:H	1.48	0.79
1:A:1132:C:H2'	1:A:1133:G:C8	2.18	0.79
1:A:1251:A:H2'	1:A:1252:A:C8	2.17	0.79
1:A:1366:C:H2'	1:A:1367:C:H6	1.47	0.79
3:B:16:HIS:NE2	3:B:214:ILE:HG12	1.97	0.79
13:L:24:VAL:HG13	13:L:98:TYR:CE2	2.18	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:52:GLU:HG2	14:M:55:ARG:HH21	1.48	0.79
1:A:1502:A:H2	1:A:1505:G:H1	1.31	0.79
6:E:110:LEU:HD13	6:E:118:ILE:HD12	1.65	0.79
15:N:26:ARG:NH1	15:N:47:LEU:HG	1.98	0.79
1:A:1475:G:H2'	1:A:1476:G:H8	1.46	0.78
9:H:138:TRP:HE3	9:H:138:TRP:OXT	1.65	0.78
11:J:37:PRO:HA	11:J:72:VAL:HG22	1.62	0.78
1:A:435:C:H2'	1:A:436:C:H6	1.49	0.78
1:A:1488:G:H2'	1:A:1489:G:C8	2.19	0.78
15:N:14:PRO:C	15:N:16:PHE:H	1.88	0.78
4:C:15:THR:O	4:C:16:ARG:HB2	1.80	0.78
16:O:29:VAL:HG12	16:O:85:LEU:CD1	2.13	0.78
1:A:620:C:C2	5:D:135:LEU:HD13	2.17	0.78
4:C:52:LEU:HD21	4:C:118:GLN:HE22	1.46	0.78
21:T:14:LYS:O	21:T:18:GLN:HG3	1.84	0.78
1:A:1343:G:H1'	10:I:121:ARG:HH12	1.49	0.78
1:A:1116:C:C2'	1:A:1117:G:H5''	2.13	0.78
1:A:975:A:H4'	1:A:976:G:H5'	1.66	0.78
8:G:79:ARG:HG2	8:G:84:ASN:OD1	1.81	0.78
13:L:41:ARG:CG	13:L:42:THR:H	1.93	0.78
16:O:16:ALA:HB1	16:O:21:ASP:HB3	1.65	0.78
20:S:17:GLU:HA	20:S:20:LEU:HD11	1.66	0.78
1:A:1487:G:O2'	1:A:1488:G:H5'	1.83	0.78
3:B:161:ALA:HB1	3:B:185:ILE:HD11	1.64	0.78
4:C:108:ASN:HD22	4:C:111:LEU:HG	1.46	0.78
5:D:104:VAL:HG11	5:D:146:ILE:HD13	1.66	0.78
1:A:393:A:O2'	1:A:394:G:H5'	1.84	0.77
1:A:1086:U:H3	1:A:1099:G:N2	1.76	0.77
1:A:538:G:OP2	13:L:115:LYS:HG3	1.84	0.77
1:A:706:A:H1'	12:K:29:ILE:HD11	1.65	0.77
6:E:93:PRO:HG2	9:H:105:ARG:HE	1.48	0.77
1:A:250:A:H4'	1:A:251:G:O5'	1.82	0.77
8:G:18:TYR:HB3	8:G:59:LEU:HD22	1.66	0.77
5:D:32:ALA:C	5:D:34:GLU:H	1.93	0.77
17:P:58:TYR:O	17:P:61:SER:HB3	1.85	0.77
3:B:67:THR:HA	3:B:90:MET:HE1	1.66	0.77
10:I:86:VAL:HG13	10:I:90:PRO:HA	1.65	0.77
1:A:382:A:H2'	1:A:383:A:C8	2.19	0.77
1:A:1443:G:H5''	1:A:1446:A:C5'	2.08	0.77
3:B:142:LEU:HB3	3:B:146:GLN:HE21	1.50	0.77
5:D:70:ILE:HD11	5:D:100:ARG:CZ	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:27:LEU:O	13:L:29:GLY:N	2.18	0.76
7:F:33:TYR:HB2	7:F:75:LEU:HD23	1.67	0.76
1:A:1256:A:H4'	1:A:1257:U:H5'	1.67	0.76
1:A:1497:G:H2'	1:A:1498:U:H5'	1.68	0.76
1:A:1495:U:O4	24:A:1632:HYG:H2	1.86	0.76
9:H:51:VAL:HG21	9:H:60:ARG:HG2	1.66	0.76
13:L:33:ARG:CD	13:L:62:SER:HB3	2.15	0.76
17:P:21:VAL:HG21	17:P:59:TRP:CD1	2.21	0.76
1:A:939:G:H2'	1:A:940:C:C6	2.21	0.76
4:C:177:THR:HG23	4:C:180:ALA:HB2	1.68	0.76
1:A:141:A:H1'	1:A:182:U:O2	1.86	0.76
3:B:102:LEU:HD21	3:B:162:ILE:CD1	2.15	0.76
10:I:16:ARG:HB2	10:I:64:THR:HB	1.68	0.76
18:Q:24:GLU:OE2	18:Q:37:LYS:HD3	1.85	0.76
21:T:56:MET:HG3	21:T:88:VAL:HG21	1.68	0.76
3:B:10:LEU:HG	3:B:48:MET:HE2	1.68	0.76
12:K:77:MET:O	12:K:78:GLN:HG3	1.86	0.76
13:L:110:VAL:O	13:L:122:THR:HG21	1.85	0.76
1:A:1004:A:H5''	1:A:1025:U:C5	2.20	0.75
1:A:1278:U:H5''	1:A:1279:A:H5'	1.68	0.75
21:T:53:LEU:HD23	21:T:56:MET:HE3	1.66	0.75
7:F:100:ASN:HD22	19:R:23:LYS:HG2	1.51	0.75
1:A:1064:G:H4'	1:A:1065:U:H5'	1.68	0.75
1:A:1152:A:H5''	11:J:13:HIS:CD2	2.21	0.75
1:A:1391:U:H2'	1:A:1392:G:C8	2.21	0.75
10:I:10:ARG:HG2	10:I:75:ASP:HB2	1.68	0.75
20:S:70:LYS:O	20:S:72:GLY:N	2.20	0.75
1:A:501:C:H2'	1:A:502:G:H8	1.52	0.75
1:A:761:G:C2	18:Q:105:ALA:HB3	2.21	0.75
1:A:1281:U:H5'	1:A:1282:C:C5	2.20	0.75
4:C:191:THR:HG22	4:C:192:THR:N	1.99	0.75
1:A:1497:G:C2'	1:A:1498:U:H5'	2.16	0.75
3:B:80:ILE:HD13	3:B:212:GLN:HB2	1.69	0.75
4:C:174:PRO:HB2	4:C:177:THR:CG2	2.17	0.75
10:I:48:GLU:HA	10:I:51:ARG:NH1	2.02	0.75
11:J:61:GLU:OE1	15:N:45:ARG:NH1	2.19	0.75
4:C:38:ARG:HH11	4:C:38:ARG:HG3	1.52	0.75
5:D:8:VAL:HG21	5:D:115:ARG:NH1	2.02	0.74
21:T:54:LYS:HG3	21:T:100:ILE:HD13	1.67	0.74
1:A:1064:G:H4'	1:A:1065:U:C5'	2.18	0.74
4:C:107:GLN:H	4:C:107:GLN:CD	1.95	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:36:ASN:HD22	19:R:38:GLU:HG2	1.50	0.74
1:A:8:A:N6	5:D:209:ARG:HB2	2.03	0.74
3:B:122:PHE:HE2	3:B:139:LYS:HG2	1.51	0.74
18:Q:21:VAL:HG21	18:Q:59:ILE:HD11	1.70	0.74
1:A:839:U:O2	1:A:839:U:H2'	1.87	0.74
14:M:4:ILE:HG22	14:M:5:ALA:N	2.03	0.74
1:A:434:U:H2'	1:A:435:C:C6	2.23	0.74
5:D:191:ARG:O	5:D:191:ARG:HD2	1.87	0.74
10:I:70:LYS:O	10:I:74:ILE:HG13	1.88	0.74
14:M:88:ARG:HD2	20:S:3:ARG:HH21	1.52	0.74
1:A:129(A):G:O2'	1:A:190(E):U:H2'	1.88	0.74
1:A:1278:U:H5''	1:A:1279:A:C5'	2.18	0.74
7:F:101:ALA:HA	19:R:28:GLU:HB3	1.69	0.74
8:G:46:ALA:O	8:G:50:ILE:HG13	1.87	0.74
12:K:54:ARG:O	12:K:57:THR:HG22	1.86	0.74
1:A:1498:U:H4'	1:A:1519:A:H2	1.51	0.74
5:D:35:ARG:O	5:D:36:ARG:HB2	1.87	0.74
11:J:86:MET:O	11:J:86:MET:HE3	1.88	0.74
14:M:14:ARG:HG3	14:M:44:ARG:NH1	2.03	0.74
1:A:975:A:H5'	1:A:975:A:C8	2.23	0.74
7:F:26:ILE:HG21	7:F:63:TYR:HE2	1.53	0.74
4:C:107:GLN:H	4:C:107:GLN:NE2	1.86	0.73
6:E:93:PRO:CG	9:H:105:ARG:HE	2.01	0.73
1:A:1250:A:H4'	10:I:68:GLY:H	1.51	0.73
5:D:114:ARG:HH11	5:D:114:ARG:HG3	1.51	0.73
8:G:138:LYS:HD3	8:G:138:LYS:C	2.13	0.73
11:J:53:PRO:HA	15:N:41:ARG:HH21	1.53	0.73
1:A:1490:C:H2'	1:A:1491:G:H8	1.51	0.73
13:L:33:ARG:HD3	13:L:62:SER:HB3	1.70	0.73
4:C:110:ASN:HD21	4:C:140:ARG:HB3	1.53	0.73
11:J:30:SER:O	11:J:78:ASN:HB2	1.89	0.73
14:M:59:TYR:O	14:M:63:THR:HB	1.89	0.73
7:F:101:ALA:HB2	19:R:28:GLU:HB2	1.69	0.73
8:G:18:TYR:CD2	8:G:59:LEU:HB2	2.24	0.73
19:R:43:PHE:C	19:R:51:LEU:HD12	2.14	0.73
1:A:173:U:H5'	1:A:197:A:O4'	1.89	0.73
1:A:1298:C:C5	8:G:114:ARG:HD3	2.23	0.73
15:N:27:CYS:SG	15:N:29:ARG:HB2	2.29	0.73
18:Q:45:HIS:NE2	18:Q:47:PRO:HG3	2.02	0.73
20:S:22:LEU:HD22	20:S:28:LYS:HB2	1.69	0.73
1:A:1241:G:H2'	1:A:1242:C:C6	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:25:ASN:HD22	3:B:25:ASN:C	1.96	0.73
4:C:43:LEU:N	4:C:43:LEU:HD23	2.04	0.73
5:D:170:VAL:HG12	5:D:174:LEU:HB2	1.70	0.73
1:A:405:U:H3'	1:A:406:G:H5'	1.71	0.72
4:C:23:TYR:CD2	4:C:24:ALA:N	2.57	0.72
5:D:24:GLU:HG2	5:D:25:ARG:H	1.52	0.72
10:I:78:LYS:HD3	10:I:101:PHE:HD2	1.55	0.72
19:R:45:SER:C	19:R:47:THR:H	1.96	0.72
9:H:9:MET:SD	9:H:32:LYS:HG2	2.29	0.72
14:M:78:ILE:HA	14:M:81:LEU:HD21	1.71	0.72
5:D:25:ARG:HH12	5:D:30:LYS:HB3	1.54	0.72
16:O:45:VAL:HG12	16:O:46:HIS:H	1.53	0.72
1:A:1040:U:H2'	1:A:1041:A:C8	2.23	0.72
5:D:187:ARG:NE	5:D:188:LEU:H	1.84	0.72
12:K:84:VAL:HG21	19:R:88:LYS:HD3	1.71	0.72
1:A:1226:C:H5''	14:M:103:THR:OG1	1.89	0.72
12:K:110:ASP:HB2	19:R:88:LYS:CD	2.14	0.72
1:A:992:U:H4'	1:A:993:G:O5'	1.89	0.72
6:E:80:ILE:HD12	6:E:91:LEU:HB2	1.69	0.72
10:I:79:LEU:HD13	10:I:83:ARG:HD2	1.72	0.72
11:J:22:LYS:HE2	11:J:90:LEU:HB2	1.72	0.72
1:A:701:C:H5'	1:A:703:G:O4'	1.90	0.72
3:B:8:LYS:O	3:B:9:GLU:HB2	1.87	0.72
3:B:15:VAL:HG11	3:B:209:ARG:C	2.15	0.72
19:R:74:ARG:HB3	19:R:81:PHE:CE1	2.25	0.72
1:A:243:A:C4'	1:A:244:U:H5'	2.20	0.71
1:A:1355:G:O2'	1:A:1356:G:H5'	1.90	0.71
1:A:1372:U:OP1	10:I:71:SER:HB3	1.89	0.71
3:B:84:GLU:HB3	3:B:219:VAL:CG2	2.17	0.71
17:P:28:ARG:HG3	17:P:29:ASP:OD2	1.90	0.71
1:A:1475:G:H2'	1:A:1476:G:C8	2.25	0.71
5:D:29:PRO:O	5:D:30:LYS:HG3	1.90	0.71
9:H:1:MET:HG2	9:H:2:LEU:N	2.05	0.71
1:A:840:C:H5''	1:A:841:U:OP1	1.89	0.71
1:A:1189:C:OP1	11:J:51:ARG:NH2	2.23	0.71
1:A:953:G:H1'	14:M:125:ARG:HB3	1.71	0.71
3:B:116:GLU:HG2	3:B:153:ARG:NH1	2.04	0.71
1:A:195:A:H4'	21:T:68:LYS:HE2	1.71	0.71
4:C:29:TYR:OH	15:N:54:PRO:HG2	1.91	0.71
4:C:188:LEU:CD1	4:C:189:ALA:H	2.04	0.71
20:S:15:LEU:HA	20:S:18:LYS:HB3	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:382:A:H2'	1:A:383:A:H8	1.55	0.71
1:A:448:A:OP2	1:A:485:G:N2	2.24	0.71
3:B:42:ILE:HD11	3:B:189:ASP:HB2	1.72	0.71
11:J:5:ARG:HA	11:J:73:ASP:OD1	1.91	0.71
1:A:923:A:OP1	6:E:21:ALA:HB2	1.90	0.71
4:C:188:LEU:HD13	4:C:189:ALA:H	1.56	0.71
13:L:83:VAL:HG22	13:L:84:LEU:H	1.55	0.71
1:A:135:C:O2	17:P:1:MET:HB2	1.90	0.71
1:A:791:G:H2'	1:A:792:A:H5'	1.73	0.71
11:J:39:PRO:O	11:J:40:LEU:HB2	1.89	0.71
21:T:57:ARG:HH21	21:T:100:ILE:CG2	2.03	0.71
1:A:254:G:O2'	1:A:255:G:H5'	1.91	0.70
11:J:32:ALA:HB2	11:J:75:ILE:O	1.91	0.70
16:O:39:LEU:HD22	16:O:56:LEU:HD13	1.71	0.70
18:Q:76:LEU:HD23	18:Q:77:VAL:N	2.06	0.70
21:T:85:MET:HE3	21:T:103:GLY:O	1.90	0.70
1:A:1028:C:H2'	1:A:1029:C:C6	2.25	0.70
1:A:760:G:O6	18:Q:105:ALA:HB2	1.91	0.70
1:A:1006:C:H2'	1:A:1007:C:C6	2.26	0.70
7:F:86:ARG:O	7:F:87:ARG:HG2	1.92	0.70
12:K:27:ASN:HA	12:K:56:GLY:HA2	1.73	0.70
6:E:12:LEU:HD13	6:E:31:LEU:HB2	1.70	0.70
16:O:26:GLU:OE1	16:O:77:ARG:HD2	1.90	0.70
1:A:1141:C:H2'	1:A:1142:G:H8	1.57	0.70
3:B:74:LYS:HZ2	3:B:206:ASP:HA	1.55	0.70
19:R:86:VAL:O	19:R:87:ARG:HB2	1.90	0.70
1:A:1498:U:H4'	1:A:1519:A:C2	2.26	0.70
3:B:139:LYS:O	3:B:143:GLU:HG2	1.90	0.70
7:F:21:LEU:O	7:F:24:GLU:HB3	1.91	0.70
1:A:1148:U:H2'	1:A:1149:C:O4'	1.91	0.70
4:C:120:VAL:O	4:C:124:ILE:HG13	1.90	0.70
13:L:47:LYS:CB	13:L:48:PRO:HD3	2.22	0.70
4:C:6:HIS:CD2	4:C:8:ILE:HB	2.27	0.70
14:M:78:ILE:HG22	14:M:82:MET:HE3	1.74	0.70
20:S:17:GLU:O	20:S:21:GLU:HG3	1.91	0.70
3:B:76:GLN:HG3	3:B:206:ASP:OD1	1.92	0.69
4:C:64:VAL:HB	4:C:99:VAL:CG2	2.22	0.69
4:C:179:ARG:HD3	4:C:206:GLU:HG2	1.72	0.69
10:I:108:VAL:HG12	10:I:109:VAL:N	2.07	0.69
1:A:1426:C:H2'	1:A:1427:U:C6	2.27	0.69
12:K:84:VAL:HG11	12:K:95:ILE:HD11	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:677:U:H3	1:A:713:G:H22	1.41	0.69
1:A:939:G:H5''	8:G:102:ARG:NH2	2.08	0.69
1:A:1132:C:H2'	1:A:1133:G:H8	1.54	0.69
1:A:1167:A:H2'	1:A:1168:A:C8	2.28	0.69
1:A:918:A:H2'	1:A:919:A:C8	2.28	0.69
4:C:35:GLU:HG3	4:C:95:THR:HG21	1.74	0.69
4:C:180:ALA:O	4:C:181:ASN:HB3	1.91	0.69
14:M:3:ARG:HA	14:M:8:GLU:O	1.92	0.69
7:F:80:ARG:NH1	7:F:88:VAL:HB	2.07	0.69
11:J:34:VAL:HG22	11:J:74:ILE:HG23	1.75	0.69
18:Q:53:LEU:HD11	18:Q:85:VAL:HG11	1.73	0.69
1:A:824:C:H2'	1:A:825:G:H8	1.58	0.69
14:M:65:LYS:HG3	14:M:69:GLU:OE2	1.93	0.69
10:I:2:GLU:OE1	10:I:3:GLN:HB2	1.92	0.69
1:A:149:A:H2'	1:A:150:C:C6	2.26	0.69
1:A:401:C:H2'	1:A:402:G:H8	1.57	0.69
1:A:1113:C:H4'	4:C:14:ILE:HD11	1.74	0.69
1:A:1250:A:H4'	10:I:68:GLY:CA	2.23	0.69
1:A:1415:G:H2'	1:A:1416:G:H8	1.58	0.69
4:C:130:VAL:HG12	4:C:134:ILE:HD11	1.73	0.69
8:G:23:VAL:O	8:G:27:ILE:HG13	1.93	0.69
13:L:47:LYS:CB	13:L:48:PRO:CD	2.71	0.69
13:L:83:VAL:HG22	13:L:84:LEU:N	2.07	0.69
14:M:49:THR:HG22	14:M:51:ALA:N	2.04	0.69
19:R:39:VAL:O	19:R:42:ARG:HB2	1.93	0.69
1:A:946:A:H2'	1:A:947:G:C8	2.27	0.69
1:A:948:C:OP1	14:M:109:THR:HG22	1.92	0.69
8:G:95:ARG:HG2	8:G:99:LEU:CD1	2.23	0.69
14:M:11:ARG:HG3	14:M:12:ASN:H	1.54	0.69
17:P:20:VAL:HG23	17:P:34:GLU:O	1.93	0.69
1:A:99:C:H2'	1:A:101:A:C8	2.27	0.69
4:C:52:LEU:HD23	4:C:52:LEU:N	2.07	0.69
6:E:51:VAL:O	6:E:55:VAL:HG23	1.93	0.69
12:K:43:SER:HA	12:K:47:VAL:HG21	1.74	0.68
1:A:113:G:H1'	1:A:354:G:H5'	1.75	0.68
1:A:243:A:H4'	1:A:244:U:C5'	2.22	0.68
1:A:476:G:H2'	1:A:477:G:H8	1.58	0.68
1:A:1004:A:H5''	1:A:1025:U:C4	2.27	0.68
1:A:1241:G:H2'	1:A:1242:C:H6	1.58	0.68
1:A:1343:G:H2'	1:A:1344:C:C6	2.28	0.68
1:A:1412:C:H2'	1:A:1413:A:C8	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:8:GLY:HA2	10:I:79:LEU:CD1	2.18	0.68
10:I:48:GLU:HA	10:I:51:ARG:HH11	1.57	0.68
18:Q:63:ARG:HG2	18:Q:64:PRO:HD2	1.75	0.68
19:R:37:VAL:O	19:R:41:LYS:HB2	1.93	0.68
1:A:1163:C:H2'	1:A:1164:G:H8	1.58	0.68
1:A:1499:A:O2'	1:A:1500:A:H5'	1.94	0.68
4:C:50:ALA:HB1	4:C:70:VAL:HG11	1.75	0.68
7:F:38:GLU:O	7:F:39:LYS:HB3	1.92	0.68
4:C:95:THR:C	4:C:97:LYS:H	2.02	0.68
1:A:1411:C:H2'	1:A:1412:C:C6	2.28	0.68
3:B:143:GLU:O	3:B:147:LYS:HG3	1.93	0.68
6:E:79:GLU:CD	6:E:79:GLU:H	2.00	0.68
21:T:54:LYS:HG3	21:T:100:ILE:CD1	2.23	0.68
1:A:1256:A:N6	1:A:1278:U:H1'	2.09	0.68
4:C:3:ASN:N	4:C:3:ASN:ND2	2.32	0.68
5:D:24:GLU:HG2	5:D:25:ARG:N	2.08	0.68
13:L:126:LYS:N	13:L:126:LYS:HD2	2.06	0.68
1:A:285:G:O2'	1:A:286:G:H5'	1.93	0.68
1:A:1281:U:H4'	1:A:1282:C:OP2	1.93	0.68
11:J:49:VAL:HG11	15:N:41:ARG:O	1.92	0.68
11:J:51:ARG:CB	11:J:59:SER:HB3	2.17	0.68
1:A:1160:G:O2'	1:A:1161:C:H5'	1.94	0.68
20:S:62:ILE:HD12	20:S:66:MET:HG3	1.76	0.68
1:A:1053:G:C3'	1:A:1054:C:H5'	2.23	0.68
4:C:79:ARG:HG2	4:C:82:GLU:HG2	1.74	0.68
14:M:40:ASN:HD22	14:M:41:PRO:CD	2.07	0.68
13:L:45:PRO:HD3	13:L:51:ALA:O	1.94	0.68
1:A:1257:U:H4'	1:A:1258:G:C5'	2.24	0.67
19:R:53:ARG:HH21	19:R:60:GLY:N	1.91	0.67
1:A:1286:A:H2'	1:A:1287:A:C5'	2.23	0.67
9:H:7:ALA:HA	9:H:85:ARG:HG3	1.76	0.67
18:Q:59:ILE:HG23	18:Q:71:PHE:HB3	1.75	0.67
1:A:996:A:H2'	1:A:997:U:C6	2.30	0.67
1:A:1124:G:H5'	11:J:35:SER:O	1.95	0.67
11:J:54:PHE:O	11:J:55:LYS:HG2	1.94	0.67
17:P:67:THR:HG22	17:P:68:ASP:N	2.09	0.67
1:A:1262:C:H2'	1:A:1263:C:C6	2.29	0.67
1:A:1289:A:H2'	1:A:1290:G:H5'	1.77	0.67
1:A:1533:C:O2	1:A:1533:C:H2'	1.93	0.67
4:C:8:ILE:HG23	4:C:16:ARG:HG2	1.75	0.67
6:E:80:ILE:HD12	6:E:80:ILE:H	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:6:ARG:CD	22:V:15:ARG:NH1	2.57	0.67
1:A:255:G:H1'	18:Q:16:GLN:NE2	2.09	0.67
6:E:43:LEU:HD11	6:E:132:ALA:HB1	1.77	0.67
14:M:36:LYS:HD2	14:M:59:TYR:CZ	2.30	0.67
6:E:40:ARG:HG2	6:E:68:GLU:OE2	1.95	0.67
19:R:55:ARG:HB3	19:R:55:ARG:HH11	1.58	0.67
19:R:87:ARG:HG2	19:R:87:ARG:HH11	1.60	0.67
1:A:560:U:H5'	1:A:566:G:N2	2.10	0.67
11:J:45:ARG:NH2	15:N:36:PHE:CD2	2.62	0.67
12:K:19:ALA:HB2	12:K:80:VAL:HG11	1.75	0.67
14:M:40:ASN:HD22	14:M:41:PRO:HD2	1.60	0.67
16:O:17:ARG:NH1	16:O:77:ARG:NH1	2.43	0.67
20:S:42:PRO:O	20:S:45:VAL:HG23	1.94	0.67
1:A:975:A:O2'	15:N:32:SER:HB2	1.94	0.67
1:A:1510:U:H2'	1:A:1511:G:C8	2.30	0.67
3:B:68:ILE:H	3:B:90:MET:HE3	1.60	0.67
12:K:69:ALA:O	12:K:73:MET:HG2	1.95	0.67
18:Q:59:ILE:HG22	18:Q:71:PHE:CD1	2.29	0.67
1:A:130:A:OP2	1:A:190(E):U:H2'	1.95	0.67
1:A:1502:A:H2	1:A:1505:G:N1	1.92	0.67
4:C:150:LYS:HE2	4:C:152:ILE:HD11	1.76	0.67
6:E:64:ARG:O	6:E:65:ASN:HB3	1.95	0.67
7:F:95:GLU:CD	7:F:95:GLU:H	2.03	0.67
9:H:36:LEU:HD12	9:H:59:LEU:HD13	1.77	0.67
1:A:1305:G:H5'	22:V:4:GLY:HA3	1.75	0.67
13:L:47:LYS:HB2	13:L:48:PRO:CD	2.25	0.67
1:A:107:G:C2'	1:A:108:G:H5'	2.25	0.66
1:A:650:G:O2'	1:A:651:C:H5'	1.95	0.66
1:A:1285:A:H4'	1:A:1286:A:O5'	1.94	0.66
3:B:102:LEU:HD21	3:B:162:ILE:HD11	1.75	0.66
5:D:196:LEU:C	5:D:198:VAL:H	2.02	0.66
11:J:39:PRO:HA	11:J:70:ARG:NH1	2.10	0.66
22:V:6:ARG:HD3	22:V:15:ARG:NH1	2.10	0.66
1:A:972:C:P	11:J:57:LYS:HD3	2.35	0.66
3:B:84:GLU:OE1	3:B:216:SER:HA	1.95	0.66
1:A:1248:A:H1'	10:I:70:LYS:NZ	2.11	0.66
5:D:25:ARG:C	5:D:27:TYR:H	2.01	0.66
11:J:4:ILE:HG22	11:J:6:ILE:HG23	1.76	0.66
11:J:8:LEU:CD2	11:J:96:ILE:HG12	2.24	0.66
13:L:6:THR:OG1	13:L:9:GLN:HG3	1.96	0.66
3:B:124:SER:HB2	3:B:125:PRO:CD	2.26	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:4:TYR:CE2	10:I:88:TYR:HA	2.30	0.66
1:A:838:G:H2'	1:A:839:U:H5''	1.77	0.66
1:A:1202:G:C2'	1:A:1203:C:H5'	2.26	0.66
1:A:1425:U:H2'	1:A:1426:C:C6	2.31	0.66
3:B:23:ARG:NH1	3:B:24:TRP:HA	2.11	0.66
16:O:29:VAL:HG11	16:O:67:LEU:HD21	1.78	0.66
1:A:723:U:O2	1:A:723:U:H2'	1.95	0.66
1:A:1195:C:H3'	1:A:1196:U:H5''	1.76	0.66
1:A:1347:G:O2'	1:A:1348:U:OP2	2.13	0.66
16:O:26:GLU:HA	16:O:81:LEU:HD11	1.76	0.66
17:P:39:TYR:CD2	17:P:73:LEU:HD11	2.30	0.66
1:A:1037:C:H2'	1:A:1038:C:C6	2.31	0.66
4:C:6:HIS:HD2	4:C:8:ILE:HB	1.60	0.66
9:H:31:PHE:O	9:H:35:ILE:HG13	1.96	0.66
17:P:34:GLU:OE2	17:P:55:ARG:HD3	1.95	0.66
22:V:5:ASP:O	22:V:11:GLY:HA3	1.96	0.66
1:A:390:C:O3'	17:P:28:ARG:NH2	2.29	0.66
1:A:1040:U:H2'	1:A:1041:A:H8	1.60	0.66
11:J:40:LEU:HD22	11:J:41:PRO:HD2	1.77	0.66
16:O:31:LEU:HD12	16:O:31:LEU:H	1.59	0.66
18:Q:74:LEU:HD23	18:Q:74:LEU:C	2.21	0.66
1:A:1142:G:H2'	1:A:1143:G:O4'	1.96	0.66
1:A:1145:C:O2'	1:A:1146:A:H8	1.79	0.66
4:C:113:ALA:HB3	4:C:114:PRO:HD3	1.77	0.66
9:H:60:ARG:HH11	9:H:60:ARG:HG3	1.59	0.66
16:O:87:ILE:O	16:O:88:ARG:HB2	1.93	0.66
1:A:130:A:C8	18:Q:63:ARG:HG3	2.31	0.66
1:A:197:A:H4'	1:A:198:G:O5'	1.96	0.65
1:A:1202:G:O2'	1:A:1203:C:H5'	1.96	0.65
1:A:1423:G:O2'	1:A:1424:C:H5'	1.97	0.65
18:Q:15:MET:HE1	18:Q:43:LEU:CD2	2.27	0.65
6:E:115:VAL:HG11	6:E:118:ILE:CD1	2.25	0.65
13:L:75:HIS:CD2	13:L:77:LEU:H	2.06	0.65
20:S:52:TYR:HA	20:S:56:GLN:O	1.96	0.65
1:A:489:C:H2'	1:A:490:G:H8	1.60	0.65
1:A:953:G:O4'	14:M:125:ARG:HA	1.95	0.65
9:H:103:VAL:CG2	9:H:110:ALA:HB2	2.27	0.65
5:D:30:LYS:C	5:D:32:ALA:H	2.03	0.65
11:J:8:LEU:HB3	11:J:16:LEU:HD22	1.78	0.65
13:L:59:ARG:HD3	13:L:65:GLU:HG3	1.77	0.65
3:B:23:ARG:HH11	3:B:24:TRP:HA	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:190:ARG:HB3	4:C:190:ARG:NH1	2.12	0.65
5:D:140:VAL:CG1	5:D:146:ILE:HD11	2.24	0.65
6:E:35:GLY:HA3	6:E:112:LEU:HB3	1.76	0.65
13:L:27:LEU:C	13:L:29:GLY:N	2.53	0.65
16:O:17:ARG:HG3	16:O:17:ARG:HH11	1.61	0.65
18:Q:18:THR:OG1	18:Q:69:LYS:HE3	1.96	0.65
22:V:6:ARG:HD3	22:V:15:ARG:HH12	1.60	0.65
1:A:1527:C:O2'	1:A:1528:U:H5'	1.97	0.65
3:B:97:TRP:HZ2	3:B:102:LEU:HD13	1.61	0.65
1:A:1195:C:H2'	1:A:1197:G:H5'	1.79	0.65
5:D:4:TYR:O	5:D:5:ILE:HB	1.95	0.65
1:A:353:A:H5'	1:A:353:A:H8	1.62	0.65
1:A:1021:G:H2'	1:A:1022:G:O4'	1.97	0.65
1:A:1225:A:H2'	1:A:1225:A:N3	2.12	0.65
1:A:1348:U:H2'	1:A:1349:A:H8	1.60	0.65
1:A:1428:A:H2'	1:A:1429:C:C6	2.31	0.65
5:D:121:VAL:O	5:D:134:ASP:HA	1.96	0.65
3:B:215:LEU:O	3:B:219:VAL:HG23	1.97	0.65
5:D:142:PRO:HG2	5:D:187:ARG:NH2	2.12	0.65
10:I:81:ILE:O	10:I:85:LEU:HB2	1.97	0.65
19:R:53:ARG:HH21	19:R:60:GLY:H	1.45	0.65
3:B:206:ASP:CG	3:B:207:ALA:H	2.04	0.64
1:A:509:A:H5'	5:D:54:TYR:HD2	1.62	0.64
1:A:761:G:N3	18:Q:105:ALA:HB3	2.12	0.64
10:I:78:LYS:HD3	10:I:101:PHE:CD2	2.32	0.64
1:A:1037:C:H2'	1:A:1038:C:H6	1.62	0.64
10:I:118:LYS:O	10:I:119:ALA:HB3	1.95	0.64
14:M:102:ARG:HB2	14:M:102:ARG:HH11	1.62	0.64
14:M:117:VAL:HG12	14:M:118:ALA:N	2.12	0.64
17:P:8:ARG:HB2	17:P:28:ARG:NH1	2.12	0.64
5:D:70:ILE:HD11	5:D:100:ARG:NE	2.12	0.64
6:E:12:LEU:HD22	6:E:12:LEU:C	2.23	0.64
13:L:120:TYR:O	13:L:122:THR:HG23	1.98	0.64
1:A:1323:G:H2'	1:A:1324:A:C8	2.32	0.64
1:A:1411:C:H2'	1:A:1412:C:H6	1.61	0.64
13:L:60:LEU:CD1	13:L:85:ILE:HD12	2.22	0.64
18:Q:12:SER:HB3	18:Q:20:THR:HB	1.80	0.64
21:T:54:LYS:HE3	21:T:100:ILE:HD11	1.79	0.64
6:E:15:ARG:HD2	6:E:15:ARG:O	1.98	0.64
6:E:51:VAL:HB	6:E:52:PRO:CD	2.25	0.64
9:H:6:ILE:HD11	9:H:31:PHE:CD2	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:78:ASN:O	11:J:80:LYS:N	2.30	0.64
12:K:73:MET:HE1	12:K:102:GLY:HA3	1.79	0.64
1:A:1251:A:H4'	10:I:12:GLU:OE2	1.98	0.64
3:B:184:VAL:N	3:B:198:ASP:OD2	2.31	0.64
4:C:92:ALA:C	4:C:94:LEU:H	2.05	0.64
21:T:67:ALA:HA	21:T:73:HIS:H	1.62	0.64
1:A:920:U:H2'	1:A:921:U:C6	2.33	0.64
1:A:939:G:H2'	1:A:940:C:H6	1.63	0.64
1:A:1368:G:O2'	1:A:1369:C:H5'	1.98	0.64
5:D:190:ASP:HB2	5:D:193:ASP:OD2	1.98	0.64
6:E:31:LEU:HD22	6:E:43:LEU:HD21	1.79	0.64
1:A:735:C:O2'	1:A:736:C:H5'	1.98	0.64
1:A:1117:G:H5'	1:A:1117:G:H8	1.62	0.64
17:P:59:TRP:HB3	17:P:64:ALA:HB2	1.80	0.64
1:A:1306:A:N6	1:A:1331:G:H1'	2.13	0.64
5:D:3:ARG:HH22	5:D:74:GLN:CD	2.06	0.64
6:E:75:THR:HG23	6:E:76:ILE:N	2.12	0.64
6:E:86:ALA:HB3	6:E:125:SER:HB2	1.80	0.64
6:E:118:ILE:HG22	6:E:119:LEU:N	2.10	0.64
18:Q:97:SER:HB2	18:Q:102:GLY:C	2.23	0.64
20:S:16:LEU:C	20:S:18:LYS:H	2.04	0.64
3:B:69:LEU:HD12	3:B:155:LEU:HD11	1.80	0.63
4:C:14:ILE:HG22	4:C:15:THR:H	1.62	0.63
4:C:26:LYS:HD3	4:C:26:LYS:N	2.13	0.63
14:M:37:THR:HG22	14:M:37:THR:O	1.98	0.63
15:N:57:ARG:HG2	15:N:58:LYS:H	1.63	0.63
21:T:89:ARG:HE	21:T:104:LEU:HD22	1.63	0.63
5:D:55:ALA:O	5:D:59:ARG:HG2	1.98	0.63
1:A:328:C:H4'	1:A:329:A:O5'	1.98	0.63
3:B:95:GLN:O	3:B:96:ARG:HD2	1.98	0.63
4:C:155:GLY:O	4:C:156:ARG:HB2	1.97	0.63
1:A:254:G:OP1	18:Q:67:LYS:O	2.14	0.63
1:A:411:A:N9	1:A:413:G:H1'	2.14	0.63
1:A:620:C:N1	5:D:135:LEU:HD13	2.13	0.63
1:A:1131:G:H1	1:A:1143:G:N2	1.86	0.63
1:A:1329:A:P	14:M:28:ALA:HB3	2.38	0.63
8:G:71:PRO:HD3	8:G:103:TRP:HZ3	1.62	0.63
1:A:190(F):G:H4'	1:A:190(G):G:OP2	1.98	0.63
3:B:28:PHE:CZ	3:B:189:ASP:HA	2.34	0.63
5:D:104:VAL:HG11	5:D:146:ILE:CD1	2.29	0.63
10:I:100:GLY:O	10:I:102:LEU:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:G:N1	1:A:48:C:H5''	2.14	0.63
1:A:1053:G:HO2'	1:A:1199:U:H5	1.46	0.63
19:R:47:THR:HG23	19:R:83:GLU:H	1.64	0.63
1:A:657:G:H4'	16:O:28:GLN:HG2	1.80	0.63
1:A:1484:C:H2'	1:A:1485:U:H6	1.63	0.63
4:C:34:LEU:HD23	4:C:34:LEU:O	1.98	0.63
19:R:25:THR:O	19:R:26:LEU:HB2	1.98	0.63
1:A:149:A:O2'	1:A:150:C:H5'	1.99	0.63
1:A:267:C:H2'	1:A:268:C:C6	2.34	0.63
1:A:1250:A:H2'	1:A:1251:A:C8	2.33	0.63
1:A:1520:G:O2'	1:A:1521:G:H5'	1.99	0.63
6:E:115:VAL:HG11	6:E:118:ILE:HD11	1.80	0.63
7:F:30:LEU:HB3	7:F:35:ALA:HB3	1.80	0.63
11:J:35:SER:HB2	11:J:72:VAL:O	1.98	0.63
11:J:90:LEU:H	11:J:91:PRO:HD2	1.62	0.63
12:K:77:MET:HE3	12:K:80:VAL:HG22	1.80	0.63
13:L:27:LEU:C	13:L:29:GLY:H	2.07	0.63
17:P:43:LYS:HG3	17:P:48:TRP:CD2	2.34	0.63
1:A:1216:G:H5''	15:N:5:ALA:CB	2.29	0.63
1:A:1257:U:H4'	1:A:1258:G:H5'	1.80	0.63
4:C:52:LEU:H	4:C:52:LEU:CD2	2.11	0.63
6:E:80:ILE:HD13	6:E:91:LEU:HD12	1.80	0.63
15:N:59:ALA:O	15:N:60:SER:CB	2.47	0.62
3:B:75:LYS:HE3	3:B:78:GLN:OE1	1.98	0.62
3:B:88:ALA:C	3:B:90:MET:H	2.07	0.62
4:C:84:ILE:O	4:C:88:ARG:HB2	1.98	0.62
4:C:108:ASN:C	4:C:110:ASN:H	2.06	0.62
7:F:19:LEU:C	7:F:19:LEU:HD23	2.24	0.62
11:J:54:PHE:CD2	11:J:55:LYS:HD3	2.33	0.62
1:A:476:G:H2'	1:A:477:G:C8	2.34	0.62
1:A:1413:A:O2'	1:A:1414:U:H5'	1.98	0.62
1:A:1425:U:H2'	1:A:1426:C:H6	1.63	0.62
3:B:142:LEU:HB3	3:B:146:GLN:NE2	2.14	0.62
10:I:111:ARG:HD3	10:I:112:LYS:N	2.14	0.62
13:L:42:THR:CG2	13:L:52:LEU:HB3	2.29	0.62
20:S:16:LEU:O	20:S:19:VAL:HG12	1.99	0.62
1:A:175:C:H2'	1:A:176:C:H6	1.64	0.62
1:A:1298:C:H2'	8:G:114:ARG:HH12	1.65	0.62
3:B:42:ILE:HD12	3:B:203:GLY:HA2	1.80	0.62
18:Q:79:SER:O	18:Q:80:GLY:O	2.17	0.62
3:B:27:LYS:HD3	3:B:195:ASP:OD2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:178:ARG:O	9:H:71:GLY:HA2	2.00	0.62
13:L:47:LYS:HB3	13:L:48:PRO:HD3	1.79	0.62
14:M:62:ASN:O	14:M:63:THR:HB	2.00	0.62
1:A:107:G:H2'	1:A:108:G:H5'	1.81	0.62
1:A:370:C:O2'	1:A:371:G:H5'	1.98	0.62
1:A:477:G:H2'	1:A:478:A:H8	1.65	0.62
1:A:1347:G:H22	1:A:1373:G:H2'	1.64	0.62
24:A:1632:HYG:O14	24:A:1632:HYG:H1	1.98	0.62
24:A:1632:HYG:O30	24:A:1632:HYG:H12	1.99	0.62
6:E:120:THR:HG23	6:E:121:LYS:N	2.13	0.62
14:M:45:VAL:O	14:M:48:LEU:HB2	1.99	0.62
20:S:29:ARG:O	20:S:30:LEU:HB2	2.00	0.62
1:A:664:G:OP1	19:R:64:ARG:HD2	2.00	0.62
3:B:132:LYS:C	3:B:134:GLU:H	2.07	0.62
4:C:11:ARG:HG2	4:C:11:ARG:HH11	1.65	0.62
14:M:77:ASN:O	14:M:80:ARG:HB3	1.98	0.62
1:A:1216:G:H5''	15:N:5:ALA:HB2	1.82	0.62
1:A:1305:G:C5'	22:V:4:GLY:HA3	2.29	0.62
1:A:1314:C:H2'	1:A:1315:U:C6	2.34	0.62
1:A:1366:C:H2'	1:A:1367:C:C6	2.32	0.62
11:J:38:ILE:HG13	11:J:72:VAL:H	1.65	0.62
16:O:55:GLY:O	16:O:59:MET:HG3	1.99	0.62
1:A:791:G:H2'	1:A:792:A:C5'	2.29	0.62
4:C:195:VAL:C	4:C:196:LEU:HD23	2.24	0.62
13:L:55:VAL:HG12	13:L:56:ALA:N	2.14	0.62
1:A:835:U:OP1	19:R:64:ARG:NH2	2.33	0.61
3:B:213:LEU:HD23	3:B:213:LEU:C	2.26	0.61
4:C:83:ARG:C	4:C:85:ARG:H	2.07	0.61
7:F:69:GLU:OE1	7:F:69:GLU:N	2.33	0.61
8:G:139:GLU:O	8:G:143:ARG:HG3	2.00	0.61
13:L:38:THR:HG22	13:L:39:VAL:HG23	1.81	0.61
14:M:14:ARG:HB3	14:M:16:ASP:OD1	2.00	0.61
14:M:117:VAL:HG12	14:M:118:ALA:H	1.65	0.61
19:R:72:ARG:O	19:R:75:ILE:HG22	2.00	0.61
1:A:614:A:H2'	1:A:615:C:C6	2.34	0.61
3:B:18:GLY:CA	3:B:41:ILE:HA	2.30	0.61
5:D:32:ALA:C	5:D:34:GLU:N	2.54	0.61
11:J:8:LEU:HB2	11:J:70:ARG:HB2	1.81	0.61
19:R:38:GLU:OE1	19:R:38:GLU:N	2.33	0.61
4:C:47:LEU:N	4:C:47:LEU:HD12	2.16	0.61
6:E:24:ARG:HG2	6:E:24:ARG:HH11	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:36:ARG:HG2	7:F:36:ARG:HH11	1.64	0.61
1:A:524:G:H2'	1:A:525:C:C6	2.35	0.61
1:A:1346:A:N1	1:A:1374:A:H5''	2.15	0.61
1:A:1356:G:H2'	1:A:1357:A:H8	1.62	0.61
3:B:12:GLU:C	3:B:14:GLY:N	2.58	0.61
5:D:173:TRP:HB2	5:D:187:ARG:O	2.00	0.61
15:N:11:LYS:O	15:N:13:THR:N	2.33	0.61
1:A:1397:C:H4'	1:A:1398:A:OP2	2.00	0.61
1:A:1425:U:O2'	1:A:1426:C:H5'	2.00	0.61
13:L:17:LYS:HA	13:L:17:LYS:HE3	1.80	0.61
17:P:22:THR:HA	17:P:33:ILE:HG13	1.81	0.61
17:P:52:ASP:OD2	17:P:55:ARG:HB2	2.01	0.61
19:R:16:PRO:O	19:R:17:SER:HB3	2.00	0.61
1:A:373:A:O2'	1:A:374:A:H5'	2.00	0.61
1:A:1307:U:H5'	14:M:109:THR:HG21	1.83	0.61
1:A:1352:C:H2'	1:A:1353:G:C8	2.36	0.61
3:B:53:ARG:NH1	3:B:199:TYR:CD2	2.69	0.61
14:M:11:ARG:CG	14:M:12:ASN:N	2.62	0.61
1:A:953:G:C1'	14:M:125:ARG:HA	2.31	0.61
1:A:1016:A:H2'	1:A:1017:G:O4'	2.01	0.61
1:A:1057:G:H5''	4:C:154:SER:CB	2.23	0.61
1:A:1112:C:O2	4:C:179:ARG:HB3	1.99	0.61
1:A:1218:C:H2'	1:A:1219:U:C6	2.35	0.61
1:A:1489:G:H2'	1:A:1490:C:C6	2.35	0.61
3:B:68:ILE:N	3:B:90:MET:HE3	2.16	0.61
16:O:38:ARG:O	16:O:41:GLU:HB3	2.00	0.61
20:S:30:LEU:HD23	20:S:48:THR:O	2.00	0.61
22:V:6:ARG:CD	22:V:15:ARG:HH12	2.14	0.61
1:A:344:A:H4'	1:A:345:C:OP2	2.01	0.61
1:A:646:U:H2'	1:A:647:C:C6	2.36	0.61
4:C:46:GLU:O	4:C:48:TYR:N	2.32	0.61
8:G:12:LEU:H	8:G:12:LEU:HD12	1.65	0.61
9:H:118:VAL:C	9:H:119:LEU:HD23	2.26	0.61
13:L:33:ARG:HD2	13:L:62:SER:HB3	1.82	0.61
1:A:1320:C:N3	20:S:36:ARG:HG3	2.16	0.61
3:B:23:ARG:O	3:B:24:TRP:O	2.19	0.61
4:C:47:LEU:H	4:C:47:LEU:CD1	2.14	0.61
4:C:91:LEU:CD2	4:C:99:VAL:HG13	2.24	0.61
10:I:65:VAL:HG21	10:I:73:GLN:HB3	1.81	0.61
11:J:62:HIS:HB3	15:N:59:ALA:CB	2.30	0.61
1:A:35:G:H2'	1:A:36:C:C6	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1195:C:H3'	1:A:1196:U:C5'	2.30	0.61
11:J:49:VAL:HG12	15:N:41:ARG:HD2	1.82	0.61
14:M:88:ARG:HD2	20:S:3:ARG:NH2	2.16	0.61
19:R:47:THR:HA	19:R:83:GLU:HB2	1.81	0.61
1:A:580:U:H2'	1:A:581:G:O4'	2.01	0.60
14:M:22:ILE:HD12	14:M:25:ILE:HD12	1.83	0.60
18:Q:53:LEU:C	18:Q:53:LEU:HD12	2.26	0.60
1:A:437:U:H5''	5:D:155:LEU:HD22	1.82	0.60
1:A:1163:C:H2'	1:A:1164:G:C8	2.36	0.60
3:B:17:PHE:HB3	3:B:44:LEU:HD11	1.83	0.60
4:C:13:GLY:HA3	15:N:57:ARG:CZ	2.30	0.60
4:C:112:SER:CB	4:C:115:LEU:HD12	2.31	0.60
8:G:85:TYR:HD1	8:G:154:TYR:HE1	1.48	0.60
14:M:52:GLU:HG2	14:M:55:ARG:NH2	2.15	0.60
1:A:232:G:H1'	1:A:262:A:N1	2.16	0.60
1:A:765:G:H1	1:A:812:C:H2'	1.66	0.60
1:A:1066:C:O2'	1:A:1067:A:H5'	2.01	0.60
4:C:110:ASN:ND2	4:C:140:ARG:HB3	2.15	0.60
6:E:12:LEU:CD1	6:E:31:LEU:HB2	2.31	0.60
1:A:1223:C:P	20:S:78:ARG:HH12	2.24	0.60
5:D:209:ARG:HG2	5:D:209:ARG:HH11	1.66	0.60
9:H:138:TRP:OXT	9:H:138:TRP:CE3	2.51	0.60
11:J:31:GLY:HA2	11:J:78:ASN:HD22	1.66	0.60
11:J:82:ILE:O	11:J:86:MET:HB2	2.01	0.60
1:A:474:G:H2'	1:A:475:G:H8	1.66	0.60
1:A:1111:A:H2'	1:A:1112:C:C6	2.35	0.60
4:C:191:THR:CG2	4:C:192:THR:N	2.64	0.60
5:D:3:ARG:HE	5:D:71:SER:HB3	1.67	0.60
9:H:51:VAL:HG21	9:H:60:ARG:CG	2.31	0.60
17:P:21:VAL:HG21	17:P:59:TRP:CG	2.36	0.60
1:A:513:C:H2'	1:A:514:C:H6	1.66	0.60
1:A:761:G:H5''	18:Q:102:GLY:HA3	1.82	0.60
1:A:1047:G:C5'	15:N:4:LYS:HD2	2.27	0.60
1:A:1053:G:C4'	1:A:1054:C:H5'	2.31	0.60
3:B:18:GLY:HA3	3:B:41:ILE:HA	1.84	0.60
4:C:47:LEU:HD12	4:C:47:LEU:H	1.66	0.60
9:H:14:ARG:O	9:H:18:ARG:HD3	2.00	0.60
11:J:38:ILE:HB	11:J:71:LEU:HB3	1.83	0.60
17:P:20:VAL:HG21	17:P:32:TYR:CG	2.37	0.60
1:A:10:A:OP2	6:E:126:ARG:HG2	2.02	0.60
1:A:1409:C:H2'	1:A:1410:G:H8	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:176:LEU:HA	5:D:183:GLY:HA2	1.83	0.60
10:I:49:PRO:HD3	10:I:78:LYS:HG2	1.83	0.60
13:L:55:VAL:HG12	13:L:56:ALA:H	1.66	0.60
14:M:33:ALA:HA	14:M:59:TYR:HE2	1.66	0.60
1:A:969:A:N6	14:M:124:PRO:HB3	2.16	0.60
1:A:1168:A:H2'	1:A:1169:A:C8	2.36	0.60
1:A:1522:U:O2'	1:A:1523:G:H5'	2.02	0.60
7:F:14:LEU:HA	7:F:18:GLN:NE2	2.16	0.60
10:I:24:GLY:HA2	10:I:59:PHE:O	2.02	0.60
11:J:69:ASN:O	11:J:70:ARG:HD3	2.02	0.60
19:R:53:ARG:HE	19:R:59:SER:C	2.10	0.60
19:R:61:LYS:O	19:R:65:ILE:HG13	2.01	0.60
20:S:33:THR:HG22	20:S:34:TRP:N	2.17	0.60
1:A:765:G:N2	1:A:812:C:O2'	2.34	0.60
5:D:13:ARG:HA	5:D:33:MET:SD	2.42	0.60
5:D:150:GLU:HG3	5:D:153:ARG:NH2	2.16	0.60
1:A:1521:G:H2'	1:A:1522:U:C6	2.37	0.60
8:G:71:PRO:HD3	8:G:103:TRP:CZ3	2.37	0.60
12:K:72:ALA:HB1	12:K:77:MET:HG3	1.84	0.60
13:L:46:LYS:NZ	13:L:47:LYS:HG3	2.17	0.60
1:A:16:A:O2'	1:A:17:U:H5'	2.01	0.59
1:A:518:C:O2'	13:L:50:SER:HB3	2.02	0.59
1:A:1223:C:OP1	1:A:1224:G:H3'	2.02	0.59
1:A:1229:A:OP2	14:M:114:ARG:HD3	2.02	0.59
14:M:14:ARG:HG3	14:M:44:ARG:HH12	1.65	0.59
14:M:60:VAL:HG12	14:M:66:LEU:HD11	1.83	0.59
20:S:44:MET:O	20:S:47:HIS:HB2	2.02	0.59
1:A:222:U:H2'	1:A:223:U:C6	2.37	0.59
1:A:532:A:H2'	1:A:533:A:C5'	2.32	0.59
1:A:673:G:H2'	1:A:674:G:C8	2.37	0.59
3:B:178:ARG:HG3	3:B:178:ARG:NH1	2.08	0.59
8:G:145:ALA:C	8:G:147:ALA:H	2.08	0.59
11:J:53:PRO:HA	15:N:41:ARG:NH2	2.17	0.59
1:A:164:U:H2'	1:A:165:C:H6	1.67	0.59
3:B:74:LYS:HZ3	3:B:76:GLN:HB2	1.67	0.59
3:B:101:MET:N	3:B:108:ILE:HD12	2.17	0.59
4:C:179:ARG:CD	4:C:206:GLU:HG2	2.32	0.59
7:F:25:ILE:HD12	7:F:82:ARG:HD2	1.83	0.59
9:H:29:SER:OG	9:H:32:LYS:HB2	2.03	0.59
11:J:12:ASP:HB3	11:J:15:THR:CG2	2.32	0.59
21:T:82:SER:O	21:T:86:ARG:HB2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:547:A:H4'	1:A:548:G:O5'	2.02	0.59
4:C:33:LEU:HD23	4:C:33:LEU:O	2.01	0.59
6:E:9:LYS:CD	6:E:112:LEU:HD21	2.31	0.59
16:O:29:VAL:HG12	16:O:85:LEU:HD12	1.84	0.59
21:T:76:ALA:O	21:T:80:ARG:HG2	2.02	0.59
1:A:22:G:O2'	1:A:23:C:H5'	2.02	0.59
1:A:1054:C:OP1	1:A:1197:G:OP1	2.21	0.59
15:N:9:LYS:HD3	15:N:9:LYS:C	2.28	0.59
16:O:56:LEU:HA	16:O:59:MET:CE	2.23	0.59
17:P:51:VAL:O	17:P:52:ASP:HB3	2.00	0.59
21:T:59:ALA:O	21:T:63:ILE:HG13	2.01	0.59
1:A:321:A:O2'	1:A:322:C:H5'	2.03	0.59
1:A:731:G:O2'	1:A:732:C:H5'	2.03	0.59
8:G:116:ALA:HA	8:G:119:ARG:CZ	2.32	0.59
11:J:81:THR:C	11:J:83:GLU:H	2.11	0.59
18:Q:67:LYS:O	18:Q:68:ARG:HB3	2.01	0.59
1:A:1369:C:H2'	1:A:1370:G:C8	2.38	0.59
1:A:1392:G:H21	1:A:1502:A:H8	1.48	0.59
5:D:127:THR:HG23	5:D:128:VAL:N	2.18	0.59
16:O:41:GLU:OE2	16:O:41:GLU:HA	2.02	0.59
1:A:187:C:O2	21:T:105:SER:HB3	2.01	0.59
1:A:392:G:H2'	1:A:393:A:C8	2.37	0.59
1:A:427:U:OP1	5:D:13:ARG:NH2	2.35	0.59
1:A:627:G:O2'	1:A:628:G:H5'	2.02	0.59
1:A:1226:C:H5''	14:M:103:THR:HG1	1.65	0.59
1:A:1226:C:N4	14:M:104:ARG:HD2	2.17	0.59
1:A:1283:G:O2'	1:A:1284:C:H5'	2.02	0.59
4:C:42:LEU:O	4:C:46:GLU:HG2	2.03	0.59
1:A:1236:A:H2'	1:A:1237:C:C6	2.38	0.59
1:A:1305:G:N2	1:A:1331:G:O2'	2.35	0.59
3:B:230:VAL:HG13	3:B:231:GLU:OE2	2.02	0.59
8:G:38:LEU:HD12	8:G:38:LEU:O	2.03	0.59
9:H:119:LEU:HD12	9:H:124:ALA:CA	2.23	0.59
11:J:40:LEU:HD12	11:J:69:ASN:HB3	1.85	0.59
16:O:3:ILE:HD12	16:O:3:ILE:N	2.18	0.59
1:A:1064:G:C4'	1:A:1065:U:H5'	2.33	0.59
1:A:1172:C:H2'	1:A:1173:G:H8	1.65	0.59
10:I:125:TYR:CD1	10:I:128:ARG:HB2	2.38	0.59
1:A:266:G:C8	1:A:266:G:H5''	2.38	0.58
1:A:371:G:C2'	1:A:372:C:H5'	2.33	0.58
3:B:124:SER:CB	3:B:125:PRO:HD2	2.32	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:25:GLY:CA	4:C:29:TYR:HB2	2.21	0.58
10:I:4:TYR:CD2	10:I:88:TYR:HA	2.38	0.58
10:I:49:PRO:O	10:I:52:ALA:HB3	2.02	0.58
11:J:8:LEU:HD23	11:J:96:ILE:HG12	1.83	0.58
1:A:17:U:H2'	1:A:18:C:C6	2.38	0.58
3:B:97:TRP:HZ3	3:B:176:GLU:OE2	1.86	0.58
11:J:49:VAL:O	11:J:60:ARG:HA	2.04	0.58
12:K:48:ILE:HD13	12:K:63:LEU:CB	2.33	0.58
14:M:102:ARG:HB2	14:M:102:ARG:NH1	2.17	0.58
20:S:43:GLU:H	20:S:43:GLU:CD	2.09	0.58
1:A:1238:A:C8	1:A:1303:C:H1'	2.39	0.58
3:B:124:SER:O	3:B:127:ILE:HG13	2.03	0.58
4:C:64:VAL:HB	4:C:99:VAL:HG21	1.85	0.58
5:D:28:SER:O	5:D:30:LYS:N	2.36	0.58
12:K:95:ILE:O	12:K:99:GLN:HG3	2.03	0.58
17:P:6:LEU:HB3	17:P:17:TYR:CD2	2.38	0.58
18:Q:76:LEU:HD23	18:Q:76:LEU:C	2.28	0.58
1:A:37:U:O2'	1:A:38:G:H5'	2.03	0.58
1:A:683:G:H2'	1:A:684:A:C8	2.38	0.58
1:A:828:A:H2'	1:A:829:G:O4'	2.03	0.58
1:A:911:U:H2'	1:A:912:C:C6	2.39	0.58
1:A:977:A:H2'	1:A:978:A:H5''	1.84	0.58
1:A:1278:U:H5	11:J:99:LYS:NZ	2.01	0.58
3:B:114:ARG:NH1	3:B:118:LEU:HD21	2.17	0.58
11:J:38:ILE:HD12	11:J:71:LEU:HD12	1.85	0.58
1:A:178:C:O2'	1:A:179:A:H5'	2.03	0.58
1:A:255:G:H2'	1:A:256:U:C6	2.39	0.58
1:A:1038:C:H2'	1:A:1039:C:C6	2.39	0.58
1:A:1333:A:H2'	1:A:1334:G:O4'	2.03	0.58
1:A:1343:G:H1'	10:I:121:ARG:NH1	2.18	0.58
3:B:12:GLU:OE2	3:B:213:LEU:HD11	2.04	0.58
3:B:134:GLU:C	3:B:136:VAL:H	2.11	0.58
3:B:228:GLY:O	3:B:229:VAL:C	2.47	0.58
4:C:155:GLY:O	4:C:196:LEU:HD22	2.03	0.58
7:F:33:TYR:HA	7:F:71:ARG:NH2	2.17	0.58
11:J:46:ARG:NH1	11:J:64:GLU:HG2	2.18	0.58
18:Q:26:GLN:O	18:Q:27:PHE:HB3	2.03	0.58
4:C:177:THR:HG23	4:C:177:THR:O	2.03	0.58
10:I:48:GLU:N	10:I:49:PRO:HD2	2.18	0.58
17:P:19:ILE:HG22	17:P:36:ILE:HG13	1.86	0.58
1:A:403:C:O2'	1:A:404:U:H5'	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:761:G:C4'	18:Q:103:GLY:H	2.08	0.58
3:B:52:GLU:O	3:B:56:ARG:HB2	2.03	0.58
8:G:113:GLU:HG2	8:G:119:ARG:HG2	1.85	0.58
1:A:1039:C:O2'	1:A:1040:U:H5'	2.03	0.58
1:A:1113:C:H1'	4:C:178:LEU:HD21	1.86	0.58
3:B:16:HIS:NE2	3:B:214:ILE:CG1	2.67	0.58
1:A:243:A:C5'	1:A:244:U:H5'	2.34	0.58
1:A:1262:C:H2'	1:A:1263:C:H6	1.68	0.58
1:A:1515:C:O2'	1:A:1516:G:H5'	2.04	0.58
4:C:60:ALA:O	4:C:61:ALA:HB3	2.03	0.58
7:F:10:LEU:HD11	7:F:59:TYR:HD2	1.69	0.58
7:F:94:GLN:HE21	19:R:32:ARG:HD3	1.68	0.58
1:A:1239:A:H62	1:A:1299:A:H62	1.50	0.58
3:B:162:ILE:C	3:B:185:ILE:HD12	2.29	0.58
3:B:179:LYS:HA	9:H:72:PRO:HD3	1.85	0.58
5:D:8:VAL:O	5:D:10:ARG:N	2.37	0.58
6:E:105:VAL:HB	6:E:106:PRO:HD3	1.86	0.58
9:H:101:PRO:HG3	9:H:133:LEU:HD11	1.85	0.57
17:P:20:VAL:HG22	17:P:21:VAL:O	2.03	0.57
1:A:1286:A:C8	1:A:1287:A:H5''	2.39	0.57
3:B:116:GLU:HG2	3:B:153:ARG:HH12	1.70	0.57
4:C:35:GLU:CD	4:C:95:THR:HG21	2.29	0.57
10:I:11:LYS:O	10:I:11:LYS:HG2	2.03	0.57
1:A:542:G:O2'	1:A:543:C:H5'	2.04	0.57
1:A:959:A:H3'	1:A:960:U:H5''	1.84	0.57
17:P:20:VAL:HG23	17:P:34:GLU:C	2.29	0.57
1:A:105:G:H2'	1:A:106:C:C6	2.39	0.57
1:A:1026:G:H2'	1:A:1027:C:H5'	1.85	0.57
1:A:1101:A:H4'	1:A:1102:A:O5'	2.04	0.57
1:A:1310:G:O6	20:S:2:PRO:HB3	2.04	0.57
1:A:1347:G:O2'	1:A:1348:U:P	2.62	0.57
8:G:69:VAL:HG21	8:G:104:LEU:HD21	1.86	0.57
9:H:83:ILE:HG23	9:H:83:ILE:O	2.03	0.57
14:M:5:ALA:O	14:M:6:GLY:C	2.48	0.57
16:O:70:LEU:HD12	16:O:78:TYR:HB2	1.84	0.57
1:A:5:U:O2	1:A:5:U:H2'	2.04	0.57
1:A:129(A):G:O2'	1:A:130:A:OP2	2.23	0.57
1:A:203:U:H5''	1:A:204:U:OP1	2.04	0.57
1:A:1153:C:H2'	1:A:1154:G:H8	1.69	0.57
7:F:4:TYR:OH	7:F:69:GLU:HB3	2.04	0.57
1:A:376:G:H5''	17:P:5:ARG:HD2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:824:C:H2'	1:A:825:G:C8	2.38	0.57
1:A:930:C:O2'	1:A:931:C:H5'	2.04	0.57
3:B:97:TRP:CZ2	3:B:101:MET:HB2	2.39	0.57
22:V:24:ARG:O	22:V:25:LYS:HB2	2.05	0.57
1:A:881:G:P	13:L:12:ARG:HH22	2.27	0.57
1:A:993:G:H4'	1:A:994:A:OP2	2.03	0.57
3:B:221:LEU:O	3:B:221:LEU:HD13	2.05	0.57
4:C:157:ILE:HD11	4:C:166:GLU:HB2	1.87	0.57
5:D:142:PRO:HA	5:D:185:PHE:O	2.04	0.57
5:D:152:SER:O	5:D:158:ILE:HD12	2.04	0.57
6:E:116:THR:HG23	6:E:117:ASP:OD2	2.03	0.57
9:H:103:VAL:HG21	9:H:110:ALA:HB2	1.86	0.57
13:L:86:ARG:HB3	13:L:101:VAL:HG23	1.87	0.57
17:P:10:GLY:HA3	17:P:15:PRO:HA	1.86	0.57
1:A:164:U:H2'	1:A:165:C:C6	2.39	0.57
1:A:736:C:H2'	1:A:737:A:C8	2.39	0.57
1:A:1117:G:H4'	10:I:104:ARG:HH12	1.66	0.57
1:A:1229:A:H2'	1:A:1230:C:H6	1.69	0.57
3:B:19:HIS:NE2	3:B:206:ASP:HB3	2.20	0.57
4:C:83:ARG:C	4:C:85:ARG:N	2.59	0.57
10:I:97:LYS:HG2	10:I:102:LEU:HD12	1.87	0.57
1:A:448:A:O2'	1:A:449:C:H5'	2.05	0.57
1:A:1286:A:H3'	1:A:1287:A:C5'	2.32	0.57
3:B:132:LYS:HG2	3:B:135:GLN:OE1	2.05	0.57
14:M:94:ARG:HH12	20:S:81:ARG:HD3	1.70	0.57
20:S:63:THR:O	20:S:66:MET:HG2	2.05	0.57
1:A:812:C:O2'	1:A:813:U:OP2	2.23	0.57
1:A:826:C:H2'	1:A:827:U:H6	1.70	0.57
1:A:974:A:OP2	15:N:41:ARG:NH1	2.38	0.57
4:C:35:GLU:CG	4:C:95:THR:HG21	2.35	0.57
4:C:188:LEU:CD1	4:C:195:VAL:HG13	2.35	0.57
10:I:43:ALA:O	10:I:45:ALA:N	2.38	0.57
11:J:49:VAL:HG13	15:N:41:ARG:HB2	1.85	0.57
12:K:84:VAL:HG23	12:K:110:ASP:HA	1.86	0.57
1:A:188:C:H4'	21:T:89:ARG:NH1	2.19	0.56
1:A:780:A:O2'	1:A:781:A:H5''	2.04	0.56
1:A:1072:G:H2'	1:A:1073:U:C6	2.39	0.56
1:A:1182:G:O2'	1:A:1183:A:OP2	2.23	0.56
6:E:72:GLN:O	6:E:75:THR:HG22	2.05	0.56
7:F:22:GLU:OE2	7:F:84:ASN:HB2	2.04	0.56
16:O:36:ILE:HD11	16:O:60:VAL:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:6:LEU:HB3	17:P:17:TYR:HD2	1.70	0.56
22:V:6:ARG:HD2	22:V:15:ARG:NH1	2.19	0.56
22:V:7:ARG:O	22:V:7:ARG:HG3	2.05	0.56
3:B:88:ALA:O	3:B:90:MET:N	2.37	0.56
3:B:119:GLU:CD	3:B:153:ARG:HH22	2.13	0.56
3:B:122:PHE:O	3:B:123:ALA:HB2	2.04	0.56
6:E:41:VAL:HG13	6:E:113:ALA:HA	1.86	0.56
22:V:17:THR:O	22:V:22:ARG:HD3	2.05	0.56
1:A:112:G:H4'	1:A:389:A:H5''	1.87	0.56
1:A:149:A:H2'	1:A:150:C:H6	1.70	0.56
1:A:435:C:H2'	1:A:436:C:C6	2.36	0.56
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.41	0.56
1:A:1231:G:O3'	10:I:126:SER:HB3	2.05	0.56
3:B:12:GLU:C	3:B:14:GLY:H	2.12	0.56
3:B:73:THR:HG23	3:B:95:GLN:O	2.05	0.56
3:B:101:MET:HA	3:B:108:ILE:HD12	1.88	0.56
5:D:112:VAL:HG23	5:D:161:ASN:HD21	1.68	0.56
6:E:80:ILE:CD1	6:E:91:LEU:HD12	2.35	0.56
15:N:14:PRO:C	15:N:16:PHE:N	2.59	0.56
15:N:21:TYR:HE2	15:N:23:ARG:NE	2.03	0.56
17:P:81:ARG:CG	17:P:83:GLU:HG2	2.34	0.56
20:S:41:VAL:HG23	20:S:43:GLU:HG2	1.86	0.56
1:A:477:G:H2'	1:A:478:A:C8	2.39	0.56
1:A:1117:G:H21	1:A:1180:A:H1'	1.71	0.56
1:A:1245:A:H2'	1:A:1246:C:C6	2.40	0.56
3:B:130:ARG:HH22	4:C:207:VAL:CG2	2.17	0.56
8:G:41:ARG:O	8:G:42:ILE:C	2.47	0.56
14:M:81:LEU:HD22	14:M:81:LEU:N	2.20	0.56
20:S:5:LEU:O	20:S:6:LYS:CB	2.52	0.56
1:A:838:G:C2'	1:A:839:U:H5''	2.34	0.56
1:A:1141:C:H2'	1:A:1142:G:C8	2.40	0.56
1:A:1263:C:H2'	1:A:1264:C:C6	2.40	0.56
3:B:111:ARG:HB3	3:B:149:LEU:HD11	1.88	0.56
4:C:137:ALA:O	4:C:141:VAL:HG23	2.06	0.56
4:C:177:THR:CG2	4:C:180:ALA:HB2	2.36	0.56
9:H:120:THR:H	9:H:123:GLU:HB2	1.71	0.56
9:H:123:GLU:O	9:H:127:LEU:HD23	2.05	0.56
10:I:93:ARG:HD3	10:I:97:LYS:HE3	1.88	0.56
13:L:50:SER:O	13:L:51:ALA:HB2	2.05	0.56
14:M:82:MET:HE2	14:M:92:HIS:HB3	1.88	0.56
15:N:59:ALA:O	15:N:60:SER:HB2	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:882:C:O2'	1:A:883:C:H5'	2.05	0.56
6:E:150:ARG:HG3	6:E:150:ARG:HH11	1.71	0.56
8:G:26:PHE:CE2	8:G:30:ILE:HD11	2.41	0.56
12:K:48:ILE:HD13	12:K:63:LEU:HB3	1.86	0.56
20:S:15:LEU:O	20:S:19:VAL:N	2.38	0.56
20:S:20:LEU:HA	20:S:23:ASN:ND2	2.20	0.56
1:A:112:G:N2	1:A:354:G:H5'	2.21	0.56
1:A:151:A:H2'	1:A:152:A:O4'	2.06	0.56
1:A:390:C:H2'	1:A:391:G:C8	2.41	0.56
1:A:818:G:C3'	1:A:819:A:H5''	2.35	0.56
5:D:43:HIS:CE1	5:D:46:LYS:HZ2	2.22	0.56
21:T:43:LEU:HD13	21:T:51:GLU:HG3	1.88	0.56
1:A:193:C:H2'	1:A:194:C:C6	2.41	0.56
1:A:883:C:O2'	1:A:884:U:H5'	2.06	0.56
1:A:1257:U:H4'	1:A:1258:G:O5'	2.06	0.56
8:G:21:VAL:HG23	8:G:22:LEU:N	2.20	0.56
13:L:60:LEU:CD2	13:L:66:VAL:HG22	2.36	0.56
18:Q:80:GLY:O	18:Q:81:ARG:HB3	2.06	0.56
19:R:48:GLY:O	19:R:74:ARG:NH2	2.37	0.56
1:A:353:A:H5'	1:A:353:A:C8	2.41	0.56
1:A:1268:A:H2'	1:A:1269:A:C8	2.41	0.56
17:P:4:ILE:HG13	17:P:64:ALA:HB1	1.88	0.56
1:A:407:G:H2'	1:A:408:A:H8	1.71	0.56
1:A:877:C:O2'	1:A:878:G:H5'	2.05	0.56
1:A:1316:G:N2	1:A:1318:A:H3'	2.21	0.56
5:D:107:ARG:HD2	5:D:173:TRP:CZ2	2.41	0.56
6:E:11:ILE:HB	6:E:31:LEU:HB3	1.88	0.56
11:J:96:ILE:HG22	11:J:97:GLU:H	1.69	0.56
13:L:126:LYS:N	13:L:126:LYS:CD	2.69	0.56
19:R:22:VAL:HG23	19:R:55:ARG:O	2.05	0.56
1:A:743:U:H2'	1:A:744:C:C6	2.42	0.55
1:A:1347:G:H3'	10:I:108:VAL:O	2.06	0.55
3:B:15:VAL:CG2	3:B:209:ARG:HG3	2.35	0.55
19:R:33:ASP:OD2	19:R:36:ASN:HB2	2.06	0.55
1:A:755:G:OP2	16:O:65:ARG:HD2	2.06	0.55
1:A:969:A:H61	14:M:124:PRO:HB3	1.70	0.55
1:A:1287:A:H2'	1:A:1288:A:C8	2.41	0.55
16:O:53:HIS:O	16:O:56:LEU:HB3	2.06	0.55
19:R:86:VAL:O	19:R:87:ARG:CB	2.53	0.55
1:A:187:C:C2	21:T:105:SER:HB3	2.41	0.55
1:A:358:U:H2'	1:A:359:U:C6	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:223:ILE:HG21	3:B:230:VAL:CG2	2.37	0.55
4:C:130:VAL:O	4:C:134:ILE:HG13	2.06	0.55
6:E:43:LEU:HB2	6:E:136:MET:HE2	1.88	0.55
9:H:19:VAL:CG2	9:H:21:LYS:HD3	2.32	0.55
10:I:53:VAL:O	10:I:54:ASP:HB2	2.06	0.55
1:A:357:G:O2'	1:A:358:U:H5'	2.07	0.55
1:A:501:C:H2'	1:A:502:G:C8	2.37	0.55
1:A:513:C:H2'	1:A:514:C:C6	2.42	0.55
1:A:1003:G:N2	1:A:1039:C:C2	2.75	0.55
3:B:188:ALA:O	3:B:202:PRO:HA	2.06	0.55
5:D:19:LEU:HD22	5:D:67:ILE:HG12	1.88	0.55
5:D:111:ALA:HB3	5:D:117:ALA:HB2	1.88	0.55
7:F:8:ILE:CD1	7:F:79:LEU:HD13	2.29	0.55
9:H:7:ALA:HB2	9:H:85:ARG:HD2	1.88	0.55
15:N:24:CYS:HB3	15:N:28:GLY:H	1.71	0.55
18:Q:97:SER:HB2	18:Q:103:GLY:CA	2.36	0.55
1:A:268:C:H2'	1:A:269:C:H6	1.71	0.55
1:A:730:G:N2	1:A:765:G:H5''	2.22	0.55
1:A:1091:U:O2	1:A:1093:A:C8	2.60	0.55
1:A:1427:U:H2'	1:A:1428:A:C8	2.41	0.55
3:B:17:PHE:H	3:B:44:LEU:HD21	1.71	0.55
5:D:131:ARG:H	5:D:131:ARG:HD2	1.71	0.55
6:E:102:ALA:HB1	6:E:120:THR:HG21	1.88	0.55
10:I:65:VAL:CG2	10:I:73:GLN:HB3	2.35	0.55
11:J:46:ARG:HH11	11:J:64:GLU:HB3	1.71	0.55
1:A:382:A:C2	1:A:383:A:C4	2.94	0.55
1:A:1000:U:H2'	1:A:1001:A:C8	2.41	0.55
1:A:1130:A:H3'	1:A:1130:A:OP2	2.07	0.55
3:B:15:VAL:HG11	3:B:210:SER:N	2.21	0.55
3:B:17:PHE:HD1	3:B:17:PHE:C	2.15	0.55
3:B:160:ASP:O	3:B:183:PRO:HD2	2.06	0.55
4:C:38:ARG:HG3	4:C:38:ARG:NH1	2.22	0.55
4:C:191:THR:HG21	4:C:193:TYR:CZ	2.42	0.55
5:D:6:GLY:O	5:D:7:PRO:C	2.47	0.55
8:G:133:GLY:O	8:G:137:LYS:HG3	2.07	0.55
10:I:10:ARG:HG2	10:I:75:ASP:CB	2.35	0.55
11:J:51:ARG:H	11:J:59:SER:CB	2.20	0.55
16:O:71:GLN:HB2	16:O:78:TYR:CD1	2.41	0.55
1:A:101:A:O2'	1:A:102:G:H5'	2.06	0.55
1:A:532:A:H2'	1:A:533:A:H5'	1.87	0.55
1:A:1154:G:O2'	1:A:1155:G:H5'	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:77:ALA:CB	3:B:211:ILE:HD13	2.10	0.55
4:C:76:VAL:HG11	4:C:103:VAL:HG21	1.89	0.55
4:C:116:VAL:HG21	4:C:202:ILE:HD11	1.87	0.55
7:F:76:ALA:O	7:F:80:ARG:HG3	2.06	0.55
11:J:27:ALA:HB2	11:J:85:LEU:HD21	1.89	0.55
13:L:70:ILE:CD1	13:L:77:LEU:HD12	2.36	0.55
14:M:3:ARG:HG2	14:M:9:ILE:HG23	1.89	0.55
20:S:67:VAL:O	20:S:69:HIS:N	2.40	0.55
1:A:546:G:OP1	5:D:73:ARG:HB2	2.07	0.55
1:A:659:U:O2'	1:A:660:G:H5'	2.07	0.55
1:A:748:C:H1'	1:A:749:C:H5	1.72	0.55
1:A:954:G:H5''	14:M:120:LYS:HD3	1.88	0.55
3:B:101:MET:CA	3:B:108:ILE:HD12	2.37	0.55
7:F:36:ARG:HG2	7:F:36:ARG:NH1	2.21	0.55
10:I:97:LYS:CG	10:I:102:LEU:HD12	2.36	0.55
16:O:29:VAL:HG12	16:O:85:LEU:HD11	1.88	0.55
19:R:73:ALA:CB	19:R:79:LEU:HD12	2.37	0.55
22:V:7:ARG:HA	22:V:12:LYS:HE2	1.89	0.55
1:A:162:A:O5'	1:A:162:A:H8	1.90	0.55
3:B:209:ARG:HE	3:B:239:VAL:HG11	1.71	0.55
6:E:83:GLU:HG3	6:E:88:LYS:HG3	1.88	0.55
6:E:152:ARG:NH2	9:H:107:LEU:O	2.39	0.55
12:K:14:VAL:O	12:K:15:ALA:HB3	2.06	0.55
15:N:59:ALA:HB1	15:N:61:TRP:CZ3	2.42	0.55
16:O:28:GLN:OE1	16:O:66:LEU:HD11	2.07	0.55
20:S:7:LYS:HG3	20:S:7:LYS:O	2.07	0.55
1:A:192:U:H1'	21:T:103:GLY:HA2	1.88	0.55
1:A:972:C:O5'	11:J:57:LYS:HD3	2.07	0.55
1:A:1381:U:O2'	1:A:1382:C:H5'	2.07	0.55
3:B:178:ARG:NH1	9:H:71:GLY:O	2.40	0.55
5:D:36:ARG:N	5:D:37:PRO:CD	2.58	0.55
8:G:108:ALA:O	8:G:119:ARG:HD2	2.06	0.55
13:L:55:VAL:CG1	13:L:67:THR:HG23	2.36	0.55
1:A:204:U:H4'	1:A:216:G:O5'	2.05	0.54
1:A:972:C:OP1	11:J:57:LYS:NZ	2.37	0.54
1:A:1060:C:O2'	1:A:1061:G:H5'	2.07	0.54
3:B:17:PHE:C	3:B:17:PHE:CD1	2.85	0.54
3:B:103:THR:HB	3:B:176:GLU:CD	2.32	0.54
6:E:15:ARG:HD3	6:E:26:PHE:CD2	2.41	0.54
6:E:84:PHE:CE2	6:E:133:TYR:HD1	2.25	0.54
8:G:53:LYS:O	8:G:54:THR:HG23	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:93:ARG:NH1	10:I:97:LYS:NZ	2.54	0.54
11:J:45:ARG:NH1	11:J:45:ARG:CB	2.63	0.54
13:L:126:LYS:CD	13:L:126:LYS:H	2.20	0.54
19:R:26:LEU:HD11	19:R:39:VAL:HG23	1.89	0.54
1:A:921:U:O2	6:E:19:MET:HB2	2.07	0.54
1:A:1454:G:O2'	1:A:1455:G:H5'	2.06	0.54
5:D:145:GLU:HG3	5:D:184:LYS:HE2	1.88	0.54
6:E:87:SER:HB3	6:E:131:ILE:HD13	1.89	0.54
11:J:23:ILE:N	11:J:23:ILE:HD12	2.22	0.54
11:J:96:ILE:HG22	11:J:97:GLU:N	2.22	0.54
16:O:17:ARG:NH1	16:O:77:ARG:HH11	2.05	0.54
1:A:694:A:H5'	12:K:53:SER:HB2	1.89	0.54
1:A:706:A:C1'	12:K:29:ILE:HD11	2.37	0.54
1:A:742:G:H5''	16:O:58:MET:HE3	1.89	0.54
1:A:794:A:H2'	1:A:795:C:C6	2.42	0.54
1:A:911:U:H2'	1:A:912:C:H6	1.72	0.54
1:A:1202:G:H2'	1:A:1203:C:H5'	1.90	0.54
1:A:1251:A:H4'	10:I:12:GLU:CD	2.32	0.54
4:C:29:TYR:CZ	15:N:54:PRO:HG2	2.42	0.54
5:D:63:LYS:O	5:D:64:LEU:C	2.51	0.54
5:D:173:TRP:CD2	5:D:189:PRO:HB3	2.42	0.54
11:J:36:GLY:O	11:J:72:VAL:HA	2.07	0.54
16:O:60:VAL:O	16:O:64:ARG:HG2	2.07	0.54
20:S:40:ILE:HG21	20:S:62:ILE:CD1	2.38	0.54
1:A:542:G:OP1	5:D:10:ARG:NH2	2.40	0.54
1:A:965:A:C2	14:M:124:PRO:HB2	2.42	0.54
1:A:983:A:H5'	1:A:984:C:OP2	2.06	0.54
4:C:147:LYS:HE2	4:C:205:GLY:HA2	1.89	0.54
6:E:101:ILE:O	6:E:120:THR:HB	2.07	0.54
7:F:4:TYR:CZ	7:F:72:VAL:HG21	2.43	0.54
12:K:32:ILE:CG2	12:K:77:MET:HE2	2.37	0.54
16:O:87:ILE:CG2	16:O:88:ARG:N	2.70	0.54
21:T:50:GLU:HG2	21:T:100:ILE:HG13	1.89	0.54
1:A:189:G:H2'	1:A:190:C:C6	2.43	0.54
1:A:443:C:O2'	1:A:444:C:H5'	2.07	0.54
1:A:1308:U:H2'	1:A:1309:G:C8	2.42	0.54
4:C:191:THR:HG22	4:C:193:TYR:H	1.73	0.54
6:E:15:ARG:O	6:E:16:THR:O	2.25	0.54
8:G:15:ASP:OD1	8:G:17:VAL:HB	2.07	0.54
8:G:37:ASN:ND2	10:I:41:VAL:HG23	2.22	0.54
8:G:122:HIS:HA	8:G:125:MET:HE3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:44:VAL:HG22	11:J:66:ARG:HB3	1.88	0.54
14:M:8:GLU:HG3	14:M:22:ILE:HG23	1.88	0.54
16:O:26:GLU:HA	16:O:81:LEU:CD1	2.37	0.54
16:O:39:LEU:HD22	16:O:56:LEU:HB2	1.89	0.54
1:A:187:C:C1'	21:T:85:MET:HE2	2.38	0.54
3:B:119:GLU:CD	3:B:153:ARG:NH2	2.66	0.54
4:C:48:TYR:HA	4:C:52:LEU:HD22	1.90	0.54
10:I:111:ARG:HG3	10:I:111:ARG:NH1	2.22	0.54
14:M:6:GLY:O	14:M:7:VAL:HG22	2.08	0.54
15:N:3:ARG:NH2	15:N:6:LEU:HG	2.22	0.54
18:Q:34:LYS:HD3	18:Q:35:VAL:O	2.08	0.54
18:Q:66:SER:O	18:Q:70:ARG:NH1	2.40	0.54
19:R:73:ALA:HB3	19:R:79:LEU:HD12	1.89	0.54
20:S:45:VAL:C	20:S:47:HIS:H	2.15	0.54
1:A:865:A:H5'	1:A:1078:U:O4	2.07	0.54
1:A:974:A:OP1	1:A:974:A:H8	1.91	0.54
1:A:1425:U:H3	1:A:1475:G:H1	1.54	0.54
3:B:144:ARG:HG3	3:B:145:LEU:H	1.72	0.54
4:C:188:LEU:O	4:C:189:ALA:HB2	2.07	0.54
9:H:103:VAL:HB	9:H:108:GLY:O	2.08	0.54
11:J:3:LYS:N	11:J:75:ILE:HA	2.23	0.54
11:J:84:GLN:O	11:J:88:LEU:HD12	2.08	0.54
13:L:75:HIS:HD2	13:L:77:LEU:N	1.97	0.54
14:M:81:LEU:HA	14:M:84:ILE:HG12	1.89	0.54
15:N:9:LYS:HD3	15:N:9:LYS:O	2.07	0.54
15:N:12:ARG:O	15:N:13:THR:C	2.51	0.54
17:P:74:LEU:O	17:P:79:VAL:HG23	2.07	0.54
18:Q:68:ARG:O	18:Q:69:LYS:HB2	2.06	0.54
1:A:106:C:O2	1:A:379:C:H4'	2.07	0.54
1:A:1014:A:H2'	1:A:1015:A:C8	2.43	0.54
9:H:56:LYS:HD2	9:H:56:LYS:N	2.22	0.54
14:M:16:ASP:HB3	14:M:41:PRO:HB3	1.88	0.54
15:N:41:ARG:HG3	15:N:42:ILE:N	2.22	0.54
19:R:46:GLU:H	19:R:46:GLU:CD	2.16	0.54
1:A:807:A:H2'	1:A:808:C:C6	2.42	0.54
1:A:818:G:C2'	1:A:819:A:H5''	2.37	0.54
3:B:92:TYR:CD1	3:B:151:GLY:HA3	2.43	0.54
6:E:112:LEU:N	6:E:112:LEU:HD23	2.22	0.54
7:F:53:ALA:C	7:F:55:ASP:H	2.16	0.54
7:F:75:LEU:C	7:F:75:LEU:HD13	2.33	0.54
8:G:83:ALA:HB3	8:G:85:TYR:CE2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:108:VAL:CG1	10:I:109:VAL:N	2.70	0.54
16:O:78:TYR:CZ	16:O:82:ILE:HD11	2.42	0.54
18:Q:60:ILE:HD13	18:Q:61:GLU:N	2.23	0.54
1:A:187:C:N3	21:T:105:SER:HB3	2.23	0.54
1:A:336:C:O2'	1:A:337:C:H5'	2.07	0.54
1:A:1524:C:OP1	12:K:120:ARG:NH1	2.41	0.54
4:C:32:LEU:HD21	4:C:59:ARG:HD2	1.90	0.54
9:H:18:ARG:HD2	9:H:18:ARG:N	2.23	0.54
9:H:23:SER:OG	9:H:60:ARG:HD2	2.08	0.54
11:J:16:LEU:HD13	11:J:70:ARG:HG2	1.88	0.54
11:J:45:ARG:O	11:J:64:GLU:HA	2.08	0.54
16:O:39:LEU:HD13	16:O:59:MET:CE	2.38	0.54
1:A:148:G:H2'	1:A:149:A:C8	2.43	0.53
1:A:613:C:O2'	1:A:614:A:H5'	2.08	0.53
1:A:1004:A:H5''	1:A:1025:U:O4	2.08	0.53
1:A:1232:U:H5''	10:I:124:GLN:O	2.08	0.53
1:A:1417:G:H2'	1:A:1482:G:H22	1.72	0.53
1:A:1441:G:H4'	1:A:1442:G:C5	2.44	0.53
1:A:1521:G:H2'	1:A:1522:U:H6	1.73	0.53
4:C:179:ARG:HD2	4:C:179:ARG:C	2.33	0.53
5:D:39:PRO:HG2	5:D:44:GLY:HA2	1.90	0.53
5:D:187:ARG:NH2	5:D:188:LEU:HG	2.12	0.53
9:H:17:THR:HB	9:H:78:GLN:OE1	2.08	0.53
12:K:15:ALA:HA	12:K:77:MET:HA	1.88	0.53
13:L:43:VAL:HG12	13:L:44:THR:N	2.23	0.53
19:R:55:ARG:HH11	19:R:55:ARG:CB	2.21	0.53
20:S:5:LEU:O	20:S:6:LYS:HB2	2.08	0.53
21:T:79:ARG:O	21:T:80:ARG:C	2.51	0.53
3:B:19:HIS:CE1	3:B:206:ASP:HB3	2.43	0.53
4:C:152:ILE:HB	4:C:199:LYS:HB2	1.90	0.53
5:D:17:VAL:HG12	5:D:18:LYS:N	2.22	0.53
6:E:89:ILE:HD13	6:E:90:VAL:N	2.23	0.53
11:J:24:VAL:HG12	11:J:28:ARG:HE	1.73	0.53
11:J:30:SER:OG	11:J:81:THR:HA	2.07	0.53
21:T:10:LEU:O	21:T:12:ALA:N	2.40	0.53
1:A:200:G:H2'	1:A:201:C:O4'	2.08	0.53
1:A:505:G:H2'	1:A:506:G:C8	2.43	0.53
1:A:812:C:O2'	1:A:813:U:P	2.66	0.53
1:A:913:A:H1'	1:A:914:A:O4'	2.09	0.53
1:A:1102:A:H2'	1:A:1103:C:C6	2.43	0.53
3:B:144:ARG:HG3	3:B:145:LEU:N	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:87:LEU:C	4:C:89:GLU:N	2.65	0.53
4:C:145:GLY:O	4:C:146:ALA:O	2.26	0.53
4:C:191:THR:HG22	4:C:192:THR:H	1.71	0.53
5:D:107:ARG:HD2	5:D:173:TRP:HZ2	1.72	0.53
11:J:47:PHE:CE2	15:N:37:PHE:HE1	2.26	0.53
13:L:48:PRO:HG2	13:L:49:ASN:H	1.73	0.53
18:Q:29:HIS:CE1	18:Q:31:LEU:H	2.27	0.53
1:A:556:C:O2'	1:A:557:G:H5'	2.08	0.53
1:A:959:A:C2	1:A:1222:G:O4'	2.62	0.53
3:B:97:TRP:CZ3	3:B:176:GLU:OE2	2.61	0.53
3:B:162:ILE:O	3:B:185:ILE:HD12	2.09	0.53
4:C:33:LEU:HD23	4:C:33:LEU:C	2.33	0.53
4:C:180:ALA:HB1	4:C:203:PHE:CE1	2.43	0.53
6:E:102:ALA:CB	6:E:120:THR:HG21	2.38	0.53
8:G:145:ALA:C	8:G:147:ALA:N	2.66	0.53
1:A:490:G:H2'	1:A:491:G:H8	1.74	0.53
1:A:826:C:H2'	1:A:827:U:C6	2.44	0.53
1:A:954:G:C5'	14:M:120:LYS:HD3	2.39	0.53
3:B:25:ASN:HD22	3:B:27:LYS:H	1.56	0.53
4:C:106:VAL:HG11	4:C:115:LEU:CD1	2.38	0.53
5:D:127:THR:CG2	5:D:128:VAL:N	2.71	0.53
6:E:120:THR:CG2	6:E:121:LYS:N	2.72	0.53
16:O:30:ALA:HA	16:O:85:LEU:HD21	1.90	0.53
16:O:39:LEU:CD2	16:O:56:LEU:HB2	2.38	0.53
19:R:27:GLY:O	19:R:29:PHE:HD2	1.90	0.53
21:T:57:ARG:HH21	21:T:100:ILE:HG23	1.72	0.53
1:A:260:G:H2'	1:A:261:U:C6	2.44	0.53
1:A:614:A:H2'	1:A:615:C:H6	1.74	0.53
1:A:986:A:H1'	20:S:54:GLY:O	2.09	0.53
3:B:53:ARG:NH1	3:B:199:TYR:HD2	2.06	0.53
3:B:69:LEU:HD22	3:B:71:VAL:HG22	1.90	0.53
14:M:81:LEU:O	14:M:89:GLY:HA3	2.08	0.53
15:N:8:GLU:O	15:N:11:LYS:HB2	2.09	0.53
1:A:229:U:H5''	17:P:33:ILE:HD13	1.89	0.53
1:A:392:G:H2'	1:A:393:A:H8	1.72	0.53
1:A:797:C:O2'	1:A:798:G:H5'	2.09	0.53
1:A:818:G:O2'	1:A:819:A:H5''	2.08	0.53
3:B:137:ARG:NH1	3:B:137:ARG:HB3	2.24	0.53
5:D:64:LEU:HG	5:D:198:VAL:HG11	1.91	0.53
8:G:12:LEU:HD12	8:G:12:LEU:N	2.24	0.53
9:H:23:SER:O	9:H:24:THR:HB	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:81:LEU:O	16:O:81:LEU:HD23	2.08	0.53
17:P:81:ARG:NH1	17:P:81:ARG:HB2	2.23	0.53
1:A:255:G:H2'	1:A:256:U:H6	1.72	0.53
1:A:258:G:O2'	1:A:259:G:H5'	2.09	0.53
1:A:268:C:H2'	1:A:269:C:C6	2.43	0.53
1:A:476:G:O2'	1:A:477:G:H5'	2.09	0.53
1:A:1070:U:H2'	1:A:1071:C:H6	1.72	0.53
3:B:187:LEU:O	3:B:187:LEU:HD13	2.09	0.53
4:C:37:GLN:NE2	15:N:52:GLN:OE1	2.39	0.53
4:C:172:ARG:HH12	4:C:174:PRO:HG3	1.73	0.53
14:M:15:VAL:C	14:M:17:VAL:H	2.16	0.53
15:N:14:PRO:HB2	15:N:16:PHE:O	2.09	0.53
18:Q:18:THR:HG23	18:Q:69:LYS:HE2	1.91	0.53
20:S:51:VAL:O	20:S:57:HIS:HA	2.09	0.53
1:A:650:G:C2'	1:A:651:C:H5'	2.39	0.53
1:A:1044:A:H2'	1:A:1045:C:C4'	2.39	0.53
1:A:1288:A:H1'	1:A:1352:C:O2'	2.08	0.53
3:B:182:ILE:O	3:B:183:PRO:C	2.50	0.53
10:I:105:ASP:OD1	10:I:107:ARG:HG3	2.09	0.53
13:L:45:PRO:HB2	13:L:49:ASN:O	2.09	0.53
13:L:85:ILE:HG23	13:L:98:TYR:HB2	1.91	0.53
15:N:12:ARG:O	15:N:14:PRO:N	2.42	0.53
1:A:287:U:O2'	1:A:288:A:H5'	2.09	0.53
1:A:403:C:H2'	1:A:404:U:H6	1.73	0.53
1:A:420:U:H2'	1:A:422:C:C5	2.44	0.53
1:A:853:G:O2'	1:A:854:G:H5'	2.09	0.53
1:A:948:C:O2'	1:A:949:A:H5'	2.09	0.53
1:A:1053:G:H4'	1:A:1054:C:H5'	1.91	0.53
1:A:1498:U:O4	24:A:1632:HYG:H24	2.09	0.53
4:C:10:PHE:CZ	4:C:178:LEU:HD13	2.44	0.53
4:C:204:LEU:O	4:C:205:GLY:C	2.51	0.53
8:G:70:LYS:HB3	8:G:96:GLN:HG2	1.91	0.53
19:R:19:LYS:O	19:R:20:ALA:HB3	2.09	0.53
21:T:53:LEU:CD2	21:T:56:MET:HE3	2.36	0.53
1:A:575:G:OP1	1:A:575:G:H4'	2.08	0.52
3:B:124:SER:CB	3:B:125:PRO:CD	2.87	0.52
7:F:44:GLY:HA2	7:F:59:TYR:CE1	2.44	0.52
11:J:7:LYS:NZ	11:J:40:LEU:HD11	2.24	0.52
11:J:46:ARG:HH11	11:J:64:GLU:CB	2.22	0.52
13:L:97:ARG:HB2	13:L:98:TYR:CE1	2.44	0.52
1:A:217:C:O2'	1:A:218:C:H5'	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1319:A:H5'	1:A:1320:C:OP1	2.09	0.52
1:A:1438:G:H2'	1:A:1439:C:C6	2.43	0.52
3:B:19:HIS:HB2	3:B:204:ASN:OD1	2.09	0.52
9:H:9:MET:HB2	9:H:32:LYS:HD3	1.91	0.52
9:H:126:LYS:C	9:H:128:GLY:H	2.17	0.52
14:M:33:ALA:HB2	14:M:64:TRP:CH2	2.44	0.52
14:M:78:ILE:HG22	14:M:82:MET:CE	2.39	0.52
1:A:190(E):U:O2'	18:Q:63:ARG:NH2	2.42	0.52
1:A:393:A:C2'	1:A:394:G:H5'	2.39	0.52
1:A:1370:G:O2'	1:A:1371:G:H5'	2.10	0.52
1:A:1453:G:H2'	1:A:1454:G:O4'	2.10	0.52
3:B:10:LEU:CG	3:B:48:MET:HE2	2.38	0.52
5:D:162:LEU:HD12	5:D:181:MET:CE	2.33	0.52
5:D:190:ASP:O	5:D:194:LEU:HD23	2.09	0.52
7:F:100:ASN:ND2	19:R:23:LYS:HG2	2.22	0.52
8:G:85:TYR:HD1	8:G:154:TYR:CE1	2.27	0.52
11:J:6:ILE:HD11	11:J:72:VAL:CG1	2.39	0.52
19:R:46:GLU:CD	19:R:46:GLU:N	2.67	0.52
22:V:7:ARG:O	22:V:8:THR:HG23	2.09	0.52
1:A:757:U:H2'	1:A:758:G:O4'	2.09	0.52
1:A:1126:U:H1'	1:A:1280:A:C6	2.44	0.52
1:A:1172:C:O2'	1:A:1173:G:H5'	2.09	0.52
1:A:1248:A:H1'	10:I:70:LYS:HZ2	1.73	0.52
5:D:25:ARG:C	5:D:27:TYR:N	2.60	0.52
7:F:18:GLN:O	7:F:21:LEU:HB3	2.10	0.52
14:M:84:ILE:HG22	20:S:65:ASN:HD22	1.74	0.52
16:O:27:VAL:O	16:O:30:ALA:HB3	2.09	0.52
16:O:87:ILE:O	16:O:88:ARG:CB	2.57	0.52
17:P:55:ARG:O	17:P:56:ALA:C	2.51	0.52
1:A:103:C:P	21:T:17:ARG:HH11	2.33	0.52
1:A:1136:U:H5''	1:A:1137:C:OP2	2.10	0.52
1:A:1414:U:H2'	1:A:1415:G:C8	2.44	0.52
3:B:15:VAL:HG21	3:B:209:ARG:HG3	1.90	0.52
3:B:126:GLU:O	3:B:129:GLU:HB2	2.09	0.52
4:C:110:ASN:O	4:C:111:LEU:HD23	2.10	0.52
8:G:15:ASP:HB3	8:G:19:GLY:N	2.24	0.52
11:J:60:ARG:HD2	11:J:60:ARG:N	2.24	0.52
1:A:567:G:H2'	1:A:568:G:O4'	2.10	0.52
1:A:663:A:O2'	1:A:664:G:H5'	2.10	0.52
3:B:72:GLY:HA3	3:B:81:VAL:HG21	1.91	0.52
6:E:112:LEU:C	6:E:114:GLY:N	2.65	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:144:THR:HG22	6:E:145:LYS:N	2.25	0.52
11:J:62:HIS:CB	15:N:59:ALA:HB3	2.35	0.52
13:L:119:LYS:O	13:L:120:TYR:HB2	2.10	0.52
17:P:67:THR:CG2	17:P:68:ASP:N	2.73	0.52
18:Q:97:SER:OG	18:Q:98:LEU:N	2.35	0.52
1:A:47:C:C6	1:A:365:U:H2'	2.44	0.52
1:A:690:G:H2'	1:A:691:G:O4'	2.10	0.52
1:A:989:C:O2'	1:A:990:C:H5'	2.10	0.52
1:A:1250:A:H5''	10:I:67:GLY:C	2.35	0.52
3:B:19:HIS:HD2	3:B:205:ASP:OD1	1.92	0.52
3:B:71:VAL:O	3:B:165:VAL:HG23	2.09	0.52
4:C:46:GLU:C	4:C:48:TYR:H	2.16	0.52
4:C:151:VAL:HG12	4:C:152:ILE:N	2.24	0.52
4:C:154:SER:OG	4:C:155:GLY:N	2.39	0.52
7:F:95:GLU:CD	7:F:95:GLU:N	2.68	0.52
8:G:48:LYS:O	8:G:51:GLN:HB2	2.10	0.52
18:Q:17:LYS:HA	18:Q:46:ASP:O	2.10	0.52
21:T:33:ILE:HD13	21:T:63:ILE:HG12	1.92	0.52
1:A:913:A:O2'	1:A:914:A:OP2	2.28	0.52
1:A:1460:A:H2'	1:A:1461:G:O4'	2.10	0.52
4:C:107:GLN:O	4:C:108:ASN:CB	2.57	0.52
9:H:121:ASP:HB2	9:H:125:ARG:HH21	1.74	0.52
10:I:9:ARG:CG	10:I:14:VAL:HG22	2.37	0.52
13:L:85:ILE:HG23	13:L:98:TYR:CB	2.39	0.52
1:A:543:C:O2'	1:A:544:G:H5'	2.09	0.52
1:A:744:C:H2'	1:A:745:C:C6	2.45	0.52
1:A:1306:A:H2'	1:A:1307:U:O4'	2.10	0.52
4:C:13:GLY:HA3	15:N:57:ARG:NH2	2.24	0.52
5:D:70:ILE:HD11	5:D:100:ARG:HD2	1.92	0.52
5:D:196:LEU:C	5:D:198:VAL:N	2.68	0.52
1:A:1264:C:H2'	1:A:1265:G:H8	1.75	0.52
3:B:18:GLY:HA2	3:B:42:ILE:H	1.75	0.52
6:E:112:LEU:C	6:E:114:GLY:H	2.18	0.52
13:L:46:LYS:HZ3	13:L:47:LYS:HG3	1.74	0.52
14:M:15:VAL:HG23	14:M:43:THR:O	2.10	0.52
18:Q:59:ILE:CG2	18:Q:71:PHE:CD1	2.93	0.52
1:A:1286:A:H8	1:A:1287:A:H5''	1.75	0.51
4:C:23:TYR:O	4:C:24:ALA:HB2	2.09	0.51
4:C:190:ARG:CB	4:C:190:ARG:HH11	2.22	0.51
5:D:70:ILE:HD11	5:D:100:ARG:CD	2.40	0.51
6:E:103:GLY:O	6:E:107:ARG:HB3	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:97:PHE:HB2	19:R:32:ARG:NH1	2.25	0.51
12:K:46:GLY:O	12:K:47:VAL:C	2.52	0.51
12:K:54:ARG:HH11	12:K:54:ARG:CB	2.15	0.51
13:L:60:LEU:HD21	13:L:66:VAL:HG22	1.92	0.51
18:Q:104:LYS:NZ	18:Q:104:LYS:N	2.50	0.51
1:A:459:G:H3'	1:A:460:A:C5'	2.39	0.51
1:A:1028:C:H2'	1:A:1029:C:H6	1.71	0.51
1:A:1222:G:P	20:S:77:THR:HG21	2.49	0.51
1:A:1250:A:H5''	10:I:68:GLY:N	2.25	0.51
1:A:1368:G:P	10:I:112:LYS:O	2.68	0.51
1:A:1405:G:O6	24:A:1632:HYG:N7	2.42	0.51
1:A:1491:G:N2	1:A:1492:A:H62	2.06	0.51
3:B:10:LEU:HD23	3:B:48:MET:HG3	1.92	0.51
14:M:5:ALA:O	14:M:7:VAL:N	2.43	0.51
19:R:39:VAL:HG13	19:R:40:LEU:N	2.25	0.51
20:S:20:LEU:C	20:S:22:LEU:N	2.68	0.51
20:S:22:LEU:HD21	20:S:28:LYS:HD2	1.92	0.51
1:A:316:G:H2'	1:A:317:G:H8	1.75	0.51
1:A:393:A:OP2	17:P:12:LYS:HE2	2.11	0.51
1:A:738:C:OP1	7:F:92:LYS:HE3	2.10	0.51
1:A:860:A:H2'	1:A:861:G:O4'	2.11	0.51
3:B:151:GLY:C	3:B:153:ARG:H	2.17	0.51
4:C:26:LYS:N	4:C:26:LYS:CD	2.73	0.51
9:H:11:THR:HG22	9:H:15:ASN:ND2	2.26	0.51
9:H:119:LEU:CD1	9:H:124:ALA:HA	2.23	0.51
10:I:36:TYR:CD2	10:I:37:PHE:CE2	2.98	0.51
15:N:22:THR:O	15:N:23:ARG:HB2	2.09	0.51
19:R:53:ARG:C	19:R:55:ARG:H	2.18	0.51
21:T:53:LEU:O	21:T:57:ARG:HD2	2.11	0.51
1:A:190(B):C:H2'	1:A:190(C):C:O4'	2.10	0.51
1:A:761:G:H1'	18:Q:104:LYS:O	2.11	0.51
1:A:1038:C:H2'	1:A:1039:C:H6	1.76	0.51
1:A:1127:G:H5''	10:I:66:ARG:HH22	1.75	0.51
3:B:197:VAL:CB	3:B:200:ILE:HG12	2.38	0.51
6:E:47:LYS:N	6:E:47:LYS:HD2	2.25	0.51
13:L:54:LYS:N	13:L:54:LYS:HD2	2.25	0.51
1:A:308:C:H2'	1:A:309:G:H8	1.75	0.51
1:A:328:C:O2	1:A:328:C:C2'	2.56	0.51
1:A:736:C:H2'	1:A:737:A:H8	1.76	0.51
1:A:737:A:H1'	7:F:73:ASN:HD21	1.75	0.51
1:A:1036:G:H2'	1:A:1037:C:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1346:A:O2'	1:A:1347:G:OP2	2.27	0.51
1:A:1348:U:H2'	1:A:1349:A:C8	2.45	0.51
3:B:102:LEU:HD21	3:B:162:ILE:HD12	1.90	0.51
3:B:239:VAL:O	3:B:239:VAL:HG12	2.11	0.51
4:C:108:ASN:C	4:C:110:ASN:N	2.69	0.51
7:F:94:GLN:NE2	19:R:32:ARG:HD3	2.25	0.51
9:H:45:ILE:HG13	9:H:47:GLY:N	2.26	0.51
13:L:38:THR:HG22	13:L:39:VAL:CG2	2.39	0.51
14:M:78:ILE:O	14:M:81:LEU:CD2	2.58	0.51
18:Q:12:SER:HB3	18:Q:20:THR:CB	2.41	0.51
1:A:407:G:H2'	1:A:408:A:C8	2.45	0.51
1:A:652:U:O4	1:A:752:G:O2'	2.23	0.51
1:A:1415:G:H2'	1:A:1416:G:C8	2.43	0.51
3:B:137:ARG:HB3	3:B:137:ARG:HH11	1.76	0.51
9:H:114:THR:C	9:H:116:LYS:H	2.19	0.51
14:M:37:THR:HG23	14:M:55:ARG:HB3	1.93	0.51
16:O:27:VAL:HG12	16:O:31:LEU:CD1	2.41	0.51
18:Q:63:ARG:HG2	18:Q:64:PRO:CD	2.41	0.51
20:S:20:LEU:C	20:S:22:LEU:H	2.17	0.51
1:A:881:G:OP2	13:L:12:ARG:NH2	2.44	0.51
1:A:953:G:H1'	14:M:125:ARG:HA	1.92	0.51
1:A:1153:C:P	11:J:13:HIS:HE2	2.33	0.51
1:A:1222:G:OP1	20:S:77:THR:HG21	2.11	0.51
4:C:20:SER:HB3	4:C:22:TRP:NE1	2.25	0.51
4:C:33:LEU:HD11	15:N:53:LEU:CD2	2.41	0.51
4:C:52:LEU:CD2	4:C:118:GLN:HE22	2.21	0.51
6:E:13:ILE:HG22	6:E:30:ALA:HA	1.92	0.51
9:H:104:ARG:HG2	9:H:104:ARG:HH11	1.76	0.51
16:O:56:LEU:O	16:O:60:VAL:HG23	2.11	0.51
20:S:45:VAL:HG12	20:S:46:GLY:N	2.26	0.51
1:A:279:A:H5''	1:A:280:C:H3'	1.93	0.51
1:A:399:G:H2'	1:A:400:C:C6	2.45	0.51
1:A:848:C:H2'	1:A:849:C:C6	2.46	0.51
1:A:1057:G:O2'	1:A:1058:G:H5'	2.11	0.51
4:C:157:ILE:CD1	4:C:166:GLU:HB2	2.40	0.51
9:H:60:ARG:HG3	9:H:60:ARG:NH1	2.25	0.51
13:L:83:VAL:CG2	13:L:84:LEU:H	2.21	0.51
14:M:33:ALA:HA	14:M:59:TYR:CE2	2.45	0.51
14:M:78:ILE:HA	14:M:81:LEU:CD2	2.40	0.51
18:Q:74:LEU:C	18:Q:74:LEU:CD2	2.83	0.51
1:A:332:G:O2'	1:A:333:G:H5'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1003(A):G:H2'	1:A:1004:A:H4'	1.93	0.51
1:A:1153:C:H2'	1:A:1154:G:C8	2.46	0.51
1:A:1207:G:O2'	1:A:1208:C:H5'	2.11	0.51
3:B:97:TRP:CH2	3:B:176:GLU:CD	2.89	0.51
4:C:106:VAL:HG11	4:C:115:LEU:HD11	1.93	0.51
20:S:16:LEU:C	20:S:18:LYS:N	2.68	0.51
1:A:112:G:H21	1:A:354:G:H5'	1.76	0.51
1:A:411:A:C4	1:A:413:G:H1'	2.46	0.51
1:A:424:G:O2'	1:A:425:G:H5'	2.11	0.51
1:A:459:G:H3'	1:A:460:A:H5''	1.93	0.51
1:A:501:C:OP1	13:L:117:ARG:NH2	2.43	0.51
1:A:1504:G:OP1	1:A:1507:A:H4'	2.11	0.51
4:C:14:ILE:O	4:C:16:ARG:N	2.43	0.51
5:D:153:ARG:HG2	5:D:181:MET:SD	2.50	0.51
6:E:92:LYS:O	6:E:118:ILE:HG23	2.11	0.51
6:E:144:THR:HB	6:E:147:ASP:OD2	2.11	0.51
7:F:14:LEU:HA	7:F:18:GLN:HE21	1.74	0.51
7:F:75:LEU:HD13	7:F:75:LEU:O	2.09	0.51
8:G:72:ARG:HG2	8:G:142:GLU:OE1	2.11	0.51
8:G:85:TYR:O	8:G:87:VAL:HG23	2.11	0.51
10:I:111:ARG:HD3	10:I:112:LYS:H	1.74	0.51
15:N:26:ARG:HH12	15:N:47:LEU:HG	1.72	0.51
21:T:50:GLU:HG3	21:T:99:LEU:HD12	1.93	0.51
1:A:731:G:H5'	1:A:766:A:H4'	1.93	0.50
4:C:11:ARG:HG2	4:C:11:ARG:NH1	2.27	0.50
5:D:3:ARG:HH22	5:D:74:GLN:CG	2.23	0.50
8:G:143:ARG:O	8:G:145:ALA:O	2.29	0.50
11:J:20:ALA:O	11:J:24:VAL:HG23	2.10	0.50
13:L:46:LYS:O	13:L:47:LYS:C	2.54	0.50
16:O:31:LEU:HD12	16:O:31:LEU:N	2.25	0.50
21:T:73:HIS:C	21:T:74:LYS:HG2	2.37	0.50
1:A:142:G:O2'	1:A:196:A:N1	2.32	0.50
1:A:1238:A:N7	1:A:1303:C:H1'	2.26	0.50
3:B:97:TRP:HH2	3:B:176:GLU:CD	2.20	0.50
4:C:107:GLN:O	4:C:108:ASN:HB3	2.10	0.50
5:D:130:GLY:O	5:D:131:ARG:C	2.53	0.50
11:J:12:ASP:HB3	11:J:15:THR:HG22	1.93	0.50
11:J:45:ARG:HH11	11:J:45:ARG:CB	1.95	0.50
15:N:24:CYS:HB3	15:N:28:GLY:N	2.26	0.50
17:P:1:MET:HE3	17:P:3:LYS:HG2	1.91	0.50
19:R:42:ARG:HG3	19:R:42:ARG:NH1	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:U:O2'	5:D:123:HIS:CD2	2.64	0.50
1:A:861:G:O2'	1:A:862:C:H5'	2.11	0.50
1:A:1477:C:H2'	1:A:1478:C:H6	1.76	0.50
3:B:224:GLN:C	3:B:226:ARG:H	2.20	0.50
4:C:34:LEU:HG	15:N:25:VAL:HG21	1.93	0.50
4:C:139:GLN:O	4:C:140:ARG:C	2.54	0.50
11:J:6:ILE:HG22	11:J:98:ILE:HG12	1.93	0.50
13:L:119:LYS:O	13:L:120:TYR:CB	2.60	0.50
19:R:42:ARG:HG3	19:R:42:ARG:HH11	1.77	0.50
1:A:337:C:H2'	1:A:338:A:H8	1.76	0.50
1:A:509:A:N3	1:A:543:C:O2'	2.36	0.50
1:A:551:U:H2'	1:A:552:U:C6	2.47	0.50
1:A:707:C:OP1	12:K:85:ARG:NH1	2.45	0.50
1:A:961:U:O2'	1:A:962:C:H5'	2.11	0.50
1:A:1149:C:H2'	1:A:1150:U:C6	2.47	0.50
1:A:1176:A:H2'	1:A:1177:G:C8	2.46	0.50
4:C:8:ILE:C	4:C:10:PHE:N	2.69	0.50
4:C:188:LEU:HD11	4:C:195:VAL:HG13	1.92	0.50
10:I:58:ARG:HD2	10:I:58:ARG:O	2.11	0.50
13:L:84:LEU:HD22	13:L:104:VAL:HG11	1.94	0.50
1:A:933:G:OP2	8:G:3:ARG:HB3	2.11	0.50
1:A:1326:C:OP1	22:V:12:LYS:NZ	2.44	0.50
3:B:98:LEU:O	3:B:101:MET:HG3	2.11	0.50
6:E:65:ASN:CG	6:E:65:ASN:O	2.55	0.50
10:I:42:ARG:O	10:I:43:ALA:C	2.54	0.50
10:I:120:ARG:O	10:I:121:ARG:C	2.54	0.50
11:J:56:HIS:O	11:J:58:ASP:N	2.44	0.50
12:K:99:GLN:HG2	12:K:105:VAL:HG21	1.93	0.50
14:M:80:ARG:C	14:M:82:MET:H	2.18	0.50
18:Q:27:PHE:CE1	18:Q:36:ILE:HD11	2.47	0.50
18:Q:81:ARG:HG3	18:Q:81:ARG:O	2.12	0.50
20:S:61:TYR:HD2	20:S:61:TYR:C	2.19	0.50
1:A:281:G:O2'	1:A:282:A:OP2	2.24	0.50
1:A:624:C:H2'	1:A:625:G:H8	1.76	0.50
1:A:918:A:H2'	1:A:919:A:H8	1.75	0.50
9:H:91:ARG:CG	13:L:7:ILE:HG13	2.41	0.50
13:L:26:ALA:O	13:L:27:LEU:O	2.30	0.50
21:T:94:ALA:O	21:T:95:ALA:HB3	2.10	0.50
1:A:187:C:H1'	21:T:85:MET:HE2	1.92	0.50
1:A:505:G:H2'	1:A:506:G:H8	1.77	0.50
3:B:19:HIS:CD2	3:B:205:ASP:OD1	2.64	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:134:GLU:C	3:B:136:VAL:N	2.69	0.50
3:B:208:ILE:C	3:B:210:SER:N	2.70	0.50
5:D:151:LYS:H	5:D:151:LYS:HD2	1.77	0.50
14:M:29:ARG:HB3	14:M:64:TRP:CH2	2.47	0.50
14:M:78:ILE:O	14:M:81:LEU:HD22	2.12	0.50
18:Q:59:ILE:CG2	18:Q:71:PHE:HB3	2.42	0.50
21:T:102:GLY:O	21:T:104:LEU:N	2.39	0.50
1:A:91:C:O2'	1:A:92:C:H5'	2.11	0.50
1:A:190:C:H2'	1:A:190(A):C:C6	2.47	0.50
1:A:190(J):U:H2'	1:A:190(K):G:C8	2.47	0.50
1:A:276:G:C2'	1:A:277:C:H5'	2.42	0.50
1:A:522:C:H41	13:L:53:ARG:HH22	1.60	0.50
1:A:965:A:H2	14:M:124:PRO:HB2	1.77	0.50
1:A:1113:C:O5'	1:A:1113:C:H6	1.95	0.50
1:A:1250:A:H5'	10:I:68:GLY:O	2.12	0.50
1:A:1392:G:H2'	1:A:1393:U:H6	1.77	0.50
3:B:187:LEU:HD23	3:B:201:ILE:HG22	1.92	0.50
6:E:148:VAL:O	6:E:152:ARG:HG3	2.12	0.50
19:R:52:PRO:HB2	19:R:54:ARG:HD3	1.93	0.50
20:S:61:TYR:C	20:S:61:TYR:CD2	2.89	0.50
21:T:39:LYS:CD	21:T:55:ILE:HD13	2.31	0.50
1:A:270:A:H2'	1:A:271:C:C6	2.47	0.50
1:A:298:A:H2'	1:A:299:G:O4'	2.12	0.50
1:A:628:G:O2'	1:A:629:G:H5'	2.11	0.50
1:A:1002:G:H2'	1:A:1003:G:O4'	2.12	0.50
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.47	0.50
1:A:1116:C:H2'	1:A:1117:G:C5'	2.34	0.50
1:A:1306:A:C2	1:A:1307:U:H1'	2.47	0.50
4:C:167:TRP:O	4:C:168:ALA:HB3	2.12	0.50
8:G:135:VAL:O	8:G:139:GLU:HG3	2.12	0.50
9:H:20:TYR:CE1	9:H:76:PRO:HD2	2.47	0.50
11:J:24:VAL:CG1	11:J:28:ARG:HE	2.25	0.50
12:K:85:ARG:HH11	12:K:85:ARG:HG3	1.77	0.50
17:P:47:ASP:C	17:P:47:ASP:OD2	2.54	0.50
22:V:24:ARG:O	22:V:25:LYS:CB	2.60	0.50
1:A:521:G:OP1	13:L:73:GLU:O	2.29	0.49
1:A:666:G:H5'	1:A:726:C:H1'	1.92	0.49
1:A:1277:C:H2'	1:A:1278:U:H5'	1.94	0.49
1:A:1330:U:H2'	1:A:1331:G:H5'	1.94	0.49
3:B:137:ARG:O	3:B:140:HIS:HB2	2.12	0.49
3:B:181:PHE:CD2	9:H:70:GLN:HB3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:170:VAL:O	5:D:171:GLY:C	2.55	0.49
7:F:36:ARG:HH12	7:F:38:GLU:HG2	1.77	0.49
10:I:93:ARG:NH1	10:I:97:LYS:HZ2	2.09	0.49
12:K:13:GLN:HA	12:K:75:TYR:O	2.11	0.49
12:K:49:GLY:O	12:K:50:TYR:C	2.54	0.49
13:L:27:LEU:O	13:L:28:LYS:C	2.55	0.49
19:R:58:LEU:HD22	19:R:62:GLU:HB3	1.93	0.49
1:A:109:A:H2'	1:A:326:G:N2	2.27	0.49
1:A:1042:G:O2'	1:A:1043:C:H5'	2.12	0.49
1:A:1139:G:O2'	1:A:1140:C:P	2.70	0.49
1:A:1420:C:H2'	1:A:1421:G:H8	1.76	0.49
3:B:57:PHE:O	3:B:60:ASP:HB3	2.12	0.49
3:B:130:ARG:NH2	4:C:207:VAL:HG23	2.22	0.49
4:C:22:TRP:CZ3	4:C:32:LEU:HD22	2.46	0.49
4:C:191:THR:CG2	4:C:192:THR:H	2.24	0.49
9:H:104:ARG:NH2	9:H:138:TRP:CH2	2.80	0.49
19:R:51:LEU:HB2	19:R:56:THR:HG22	1.94	0.49
1:A:444:C:O2'	1:A:445:G:H5'	2.12	0.49
1:A:625:G:H4'	17:P:16:HIS:CD2	2.48	0.49
1:A:818:G:H3'	1:A:819:A:C5'	2.42	0.49
1:A:1498:U:C4'	1:A:1519:A:H2	2.24	0.49
3:B:17:PHE:HD1	3:B:18:GLY:N	2.10	0.49
3:B:23:ARG:NH1	3:B:24:TRP:CA	2.75	0.49
3:B:164:VAL:HG12	3:B:186:ALA:CB	2.42	0.49
4:C:87:LEU:C	4:C:89:GLU:H	2.20	0.49
11:J:34:VAL:CG2	11:J:74:ILE:HG23	2.43	0.49
12:K:19:ALA:HB2	12:K:80:VAL:CG1	2.43	0.49
13:L:25:PRO:C	13:L:27:LEU:N	2.58	0.49
16:O:45:VAL:O	16:O:46:HIS:C	2.54	0.49
1:A:443:C:H2'	1:A:444:C:H6	1.78	0.49
1:A:448:A:H62	1:A:486:U:H3	1.59	0.49
1:A:1061:G:C2'	1:A:1062:U:H5'	2.43	0.49
1:A:1442:G:N3	1:A:1442:G:H2'	2.26	0.49
4:C:91:LEU:HD23	4:C:91:LEU:C	2.38	0.49
8:G:110:GLN:OE1	8:G:110:GLN:HA	2.11	0.49
11:J:51:ARG:HG2	11:J:51:ARG:NH1	2.21	0.49
13:L:53:ARG:CB	13:L:93:LEU:HD11	2.43	0.49
21:T:53:LEU:HD13	21:T:101:GLY:N	2.27	0.49
1:A:6:G:C4	6:E:119:LEU:HD11	2.47	0.49
1:A:77:G:O2'	1:A:78:G:H5'	2.13	0.49
1:A:141:A:H1'	1:A:182:U:C2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1305:G:H5''	22:V:4:GLY:C	2.37	0.49
3:B:16:HIS:CE1	3:B:214:ILE:HG12	2.47	0.49
4:C:131:ARG:O	4:C:135:LYS:HG3	2.12	0.49
10:I:89:ASN:ND2	10:I:91:ASP:HB2	2.28	0.49
10:I:111:ARG:HG3	10:I:111:ARG:HH11	1.77	0.49
11:J:54:PHE:CE2	11:J:55:LYS:HD3	2.48	0.49
19:R:45:SER:C	19:R:47:THR:N	2.66	0.49
1:A:123:C:OP1	1:A:312:C:H5'	2.12	0.49
1:A:447:G:H2'	1:A:485:G:N2	2.27	0.49
1:A:537:G:OP1	13:L:113:ARG:NH2	2.46	0.49
1:A:687:A:H4'	1:A:688:G:O5'	2.11	0.49
1:A:1085:U:O3'	1:A:1086:U:H6	1.96	0.49
1:A:1256:A:H5'	1:A:1258:G:O4'	2.13	0.49
1:A:1413:A:H2	1:A:1487:G:H22	1.58	0.49
3:B:26:PRO:O	3:B:29:ALA:HB2	2.13	0.49
3:B:103:THR:HB	3:B:176:GLU:OE1	2.12	0.49
3:B:109:SER:O	3:B:112:VAL:N	2.42	0.49
3:B:144:ARG:O	3:B:147:LYS:N	2.44	0.49
4:C:70:VAL:C	4:C:106:VAL:HG23	2.37	0.49
4:C:88:ARG:O	4:C:91:LEU:HD22	2.11	0.49
10:I:46:ALA:HA	10:I:78:LYS:HB2	1.95	0.49
10:I:65:VAL:HG13	10:I:65:VAL:O	2.12	0.49
11:J:51:ARG:N	11:J:59:SER:CB	2.76	0.49
11:J:71:LEU:O	11:J:72:VAL:HB	2.13	0.49
15:N:18:VAL:C	15:N:20:ALA:H	2.20	0.49
20:S:62:ILE:CD1	20:S:66:MET:HG3	2.42	0.49
1:A:485:G:C2'	1:A:486:U:OP2	2.61	0.49
1:A:929:G:O2'	1:A:930:C:H5'	2.12	0.49
1:A:1023:G:H2'	1:A:1023:G:N3	2.26	0.49
1:A:1053:G:O2'	1:A:1199:U:H5	1.96	0.49
1:A:1118:C:H1'	1:A:1179:A:C4	2.48	0.49
1:A:1399:C:C2	1:A:1502:A:N6	2.80	0.49
1:A:1470:G:O2'	1:A:1471:G:H5'	2.13	0.49
4:C:20:SER:HB3	4:C:22:TRP:HE1	1.78	0.49
4:C:87:LEU:O	4:C:89:GLU:N	2.46	0.49
4:C:95:THR:O	4:C:97:LYS:N	2.44	0.49
9:H:11:THR:HA	9:H:14:ARG:NH1	2.28	0.49
10:I:43:ALA:C	10:I:45:ALA:H	2.20	0.49
11:J:65:LEU:HD23	11:J:65:LEU:C	2.38	0.49
15:N:44:LEU:HD12	15:N:44:LEU:O	2.12	0.49
16:O:70:LEU:HD12	16:O:78:TYR:CB	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:C:H2'	1:A:391:G:H8	1.77	0.49
1:A:646:U:H2'	1:A:647:C:H6	1.78	0.49
1:A:1417:G:O2'	1:A:1483:A:N6	2.45	0.49
3:B:58:ILE:O	3:B:59:GLU:C	2.56	0.49
3:B:209:ARG:HG2	3:B:209:ARG:HH11	1.78	0.49
5:D:38:TYR:HB2	5:D:39:PRO:HD2	1.95	0.49
5:D:92:VAL:O	5:D:96:LEU:HD13	2.12	0.49
8:G:72:ARG:HA	8:G:96:GLN:NE2	2.27	0.49
9:H:120:THR:O	9:H:121:ASP:C	2.55	0.49
10:I:118:LYS:O	10:I:119:ALA:CB	2.61	0.49
11:J:80:LYS:O	11:J:84:GLN:HG3	2.12	0.49
21:T:42:GLN:CA	21:T:42:GLN:HE21	2.24	0.49
1:A:552:U:H4'	13:L:86:ARG:O	2.12	0.49
1:A:1128:C:O2'	1:A:1130:A:C8	2.65	0.49
3:B:109:SER:C	3:B:111:ARG:H	2.20	0.49
5:D:3:ARG:NE	5:D:71:SER:H	2.11	0.49
7:F:19:LEU:HD23	7:F:20:ALA:N	2.28	0.49
14:M:31:LYS:O	14:M:35:GLU:HB2	2.12	0.49
14:M:80:ARG:C	14:M:82:MET:N	2.70	0.49
14:M:97:PRO:HB2	14:M:101:GLN:OE1	2.12	0.49
15:N:29:ARG:HG2	15:N:29:ARG:HH11	1.77	0.49
20:S:51:VAL:HG12	20:S:52:TYR:N	2.28	0.49
1:A:246:A:N6	1:A:281:G:H1'	2.27	0.49
1:A:420:U:O2'	1:A:421:U:H5''	2.13	0.49
1:A:1216:G:H2'	1:A:1217:C:H6	1.78	0.49
1:A:1238:A:H2	1:A:1241:G:N3	2.10	0.49
1:A:1487:G:H2'	1:A:1488:G:H8	1.77	0.49
3:B:125:PRO:C	3:B:127:ILE:H	2.20	0.49
4:C:172:ARG:HB3	4:C:172:ARG:HH11	1.78	0.49
5:D:24:GLU:O	5:D:25:ARG:HB3	2.13	0.49
7:F:94:GLN:HB2	19:R:32:ARG:HD3	1.95	0.49
8:G:95:ARG:O	8:G:96:GLN:C	2.56	0.49
14:M:73:GLU:O	14:M:74:VAL:C	2.56	0.49
14:M:84:ILE:O	14:M:86:CYS:N	2.46	0.49
15:N:3:ARG:O	15:N:4:LYS:C	2.53	0.49
1:A:5:U:O2	1:A:5:U:C2'	2.61	0.48
1:A:1075:C:H5'	3:B:103:THR:HG21	1.95	0.48
1:A:1346:A:C4	8:G:10:ARG:NH2	2.81	0.48
3:B:59:GLU:O	3:B:62:ALA:HB3	2.12	0.48
4:C:42:LEU:HD12	4:C:94:LEU:CD1	2.43	0.48
4:C:52:LEU:HG	4:C:52:LEU:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:58:GLU:HB2	4:C:65:ALA:HB2	1.95	0.48
4:C:123:GLN:HE22	4:C:140:ARG:HH22	1.61	0.48
5:D:68:TYR:CD2	5:D:97:LEU:HB3	2.48	0.48
5:D:68:TYR:CE2	5:D:97:LEU:HB3	2.48	0.48
6:E:107:ARG:HG2	6:E:108:ALA:N	2.27	0.48
8:G:15:ASP:O	8:G:19:GLY:HA2	2.12	0.48
11:J:4:ILE:HG23	11:J:98:ILE:HG21	1.95	0.48
16:O:27:VAL:HG12	16:O:31:LEU:HD11	1.94	0.48
19:R:36:ASN:HB3	19:R:39:VAL:HG12	1.94	0.48
20:S:74:PHE:CD1	20:S:74:PHE:N	2.80	0.48
20:S:80:TYR:CD2	20:S:81:ARG:N	2.80	0.48
21:T:53:LEU:HD21	21:T:104:LEU:HD12	1.95	0.48
1:A:248:C:O2'	1:A:249:U:H5'	2.13	0.48
1:A:783:C:O2'	1:A:784:C:H5'	2.13	0.48
1:A:959:A:H2	1:A:1221:G:N3	2.11	0.48
1:A:1095:U:H2'	1:A:1096:C:C6	2.48	0.48
1:A:1202:G:H2'	1:A:1203:C:C5'	2.42	0.48
1:A:1238:A:C2	1:A:1241:G:N3	2.81	0.48
1:A:1514:C:H2'	1:A:1515:C:C6	2.47	0.48
3:B:239:VAL:HB	3:B:240:GLN:NE2	2.28	0.48
4:C:18:TRP:HE3	4:C:18:TRP:H	1.59	0.48
5:D:24:GLU:CG	5:D:25:ARG:H	2.25	0.48
5:D:98:GLU:HA	5:D:103:ASN:ND2	2.28	0.48
6:E:43:LEU:CD2	6:E:44:GLY:N	2.76	0.48
14:M:36:LYS:HD2	14:M:59:TYR:OH	2.13	0.48
19:R:47:THR:C	19:R:49:LYS:H	2.21	0.48
1:A:75:G:O2'	1:A:76:C:H5'	2.14	0.48
1:A:108:G:N2	1:A:109:A:N1	2.61	0.48
1:A:162:A:H2'	1:A:163:C:O4'	2.13	0.48
1:A:425:G:O2'	1:A:426:G:H5'	2.13	0.48
1:A:622:A:C8	1:A:623:C:C5	3.01	0.48
1:A:832:C:O2'	1:A:833:U:H5'	2.13	0.48
1:A:1172:C:H2'	1:A:1173:G:C8	2.47	0.48
1:A:1197:G:C2'	1:A:1198:G:H5'	2.44	0.48
1:A:1296:C:H4'	1:A:1302:U:C5	2.48	0.48
1:A:1472:U:O2'	1:A:1473:A:H5'	2.12	0.48
3:B:82:ARG:O	3:B:86:GLU:HG3	2.13	0.48
3:B:109:SER:C	3:B:111:ARG:N	2.70	0.48
3:B:125:PRO:HG2	3:B:126:GLU:H	1.78	0.48
4:C:43:LEU:N	4:C:43:LEU:CD2	2.73	0.48
14:M:26:GLY:C	14:M:28:ALA:N	2.71	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:639:G:O2'	1:A:640:A:H5'	2.12	0.48
1:A:1020:U:H2'	1:A:1021:G:H8	1.78	0.48
1:A:1231:G:H4'	10:I:126:SER:CB	2.44	0.48
1:A:1492:A:H2'	1:A:1493:A:C8	2.48	0.48
3:B:130:ARG:HB3	3:B:131:PRO:HD2	1.96	0.48
4:C:7:PRO:HG2	4:C:184:TYR:HB2	1.96	0.48
6:E:102:ALA:HB2	6:E:120:THR:HB	1.96	0.48
10:I:93:ARG:CD	10:I:97:LYS:HE3	2.44	0.48
13:L:47:LYS:HB2	13:L:48:PRO:HD3	1.92	0.48
14:M:60:VAL:CG1	14:M:66:LEU:HD11	2.44	0.48
14:M:110:ARG:HG2	14:M:110:ARG:HH11	1.78	0.48
17:P:39:TYR:O	17:P:41:PRO:HD3	2.13	0.48
18:Q:59:ILE:HG22	18:Q:71:PHE:HD1	1.76	0.48
21:T:45:GLN:CB	21:T:91:LEU:HD22	2.42	0.48
1:A:553:A:H2'	1:A:554:C:C6	2.48	0.48
1:A:1230:C:O2'	1:A:1231:G:H5'	2.14	0.48
1:A:1248:A:H1'	10:I:70:LYS:HZ1	1.78	0.48
1:A:1269:A:C2	1:A:1313:U:O4'	2.67	0.48
1:A:1402:C:O2	1:A:1500:A:N1	2.47	0.48
1:A:1531:A:O5'	1:A:1531:A:H8	1.96	0.48
1:A:1532:U:O5'	1:A:1532:U:H6	1.97	0.48
3:B:17:PHE:CD1	3:B:18:GLY:N	2.81	0.48
3:B:33:TYR:O	3:B:34:ALA:HB2	2.13	0.48
3:B:230:VAL:CG1	3:B:231:GLU:N	2.77	0.48
4:C:5:ILE:C	4:C:5:ILE:HD12	2.38	0.48
4:C:5:ILE:HD12	4:C:5:ILE:O	2.14	0.48
6:E:57:LYS:HG2	6:E:61:TYR:CE2	2.48	0.48
11:J:32:ALA:HB2	11:J:76:ASN:HD22	1.79	0.48
11:J:46:ARG:HH11	11:J:64:GLU:HG2	1.78	0.48
11:J:51:ARG:HH11	11:J:51:ARG:CG	2.20	0.48
13:L:98:TYR:N	13:L:98:TYR:CD1	2.81	0.48
14:M:40:ASN:HD22	14:M:41:PRO:N	2.11	0.48
1:A:33:A:H2'	1:A:34:C:C6	2.48	0.48
1:A:218:C:H2'	1:A:219:C:C6	2.49	0.48
1:A:267:C:H2'	1:A:268:C:H6	1.78	0.48
1:A:875:C:H1'	9:H:15:ASN:OD1	2.14	0.48
1:A:1488:G:H2'	1:A:1489:G:H8	1.73	0.48
3:B:115:LEU:O	3:B:119:GLU:HG3	2.13	0.48
9:H:38:ILE:N	9:H:38:ILE:HD12	2.27	0.48
12:K:48:ILE:O	12:K:49:GLY:C	2.55	0.48
14:M:110:ARG:HH11	14:M:110:ARG:CG	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:A:N1	1:A:220:G:O2'	2.45	0.48
1:A:244:U:O4	1:A:906:G:H1'	2.13	0.48
1:A:458:C:H2'	1:A:459:G:O4'	2.14	0.48
1:A:737:A:H1'	7:F:73:ASN:ND2	2.29	0.48
1:A:1305:G:H2'	1:A:1331:G:N2	2.28	0.48
3:B:8:LYS:O	3:B:9:GLU:CB	2.60	0.48
3:B:84:GLU:CB	3:B:219:VAL:HG21	2.22	0.48
4:C:70:VAL:HG12	4:C:72:LYS:H	1.78	0.48
4:C:77:ILE:HG22	4:C:81:GLY:HA2	1.95	0.48
5:D:65:ARG:HA	5:D:75:PHE:CE1	2.48	0.48
6:E:5:ASP:CG	6:E:6:PHE:H	2.22	0.48
6:E:144:THR:HG22	6:E:146:ALA:H	1.79	0.48
6:E:150:ARG:HG3	6:E:150:ARG:NH1	2.29	0.48
12:K:26:ASN:O	12:K:27:ASN:HB2	2.14	0.48
14:M:121:LYS:O	14:M:123:ALA:N	2.47	0.48
18:Q:104:LYS:O	18:Q:105:ALA:HB2	2.14	0.48
1:A:41:G:H2'	1:A:42:G:H8	1.78	0.48
1:A:635:G:O2'	1:A:636:U:H5'	2.13	0.48
1:A:1420:C:H2'	1:A:1421:G:C8	2.49	0.48
4:C:8:ILE:C	4:C:10:PHE:H	2.22	0.48
5:D:64:LEU:HD13	5:D:75:PHE:HZ	1.79	0.48
8:G:152:ALA:C	8:G:154:TYR:H	2.22	0.48
9:H:108:GLY:HA3	9:H:138:TRP:HB3	1.96	0.48
10:I:23:ASN:ND2	10:I:23:ASN:C	2.72	0.48
10:I:108:VAL:HG12	10:I:109:VAL:H	1.78	0.48
11:J:48:THR:OG1	11:J:62:HIS:CD2	2.66	0.48
13:L:40:VAL:O	13:L:40:VAL:HG12	2.13	0.48
14:M:79:LYS:O	14:M:83:ASP:OD2	2.32	0.48
15:N:23:ARG:HD3	15:N:30:ALA:HB2	1.96	0.48
16:O:39:LEU:HD13	16:O:59:MET:HE1	1.96	0.48
21:T:72:LEU:HD23	21:T:72:LEU:HA	1.72	0.48
1:A:39:G:O2'	1:A:40:C:H5'	2.13	0.48
1:A:256:U:H5'	18:Q:17:LYS:HZ1	1.79	0.48
1:A:308:C:H2'	1:A:309:G:C8	2.48	0.48
1:A:523:A:H61	13:L:92:ASP:HB2	1.78	0.48
1:A:736:C:OP2	19:R:68:LYS:HE2	2.14	0.48
1:A:760:G:O6	18:Q:105:ALA:CB	2.59	0.48
1:A:862:C:O2'	1:A:863:U:H5'	2.14	0.48
1:A:913:A:O2'	1:A:914:A:P	2.72	0.48
1:A:934:C:C4	1:A:1345:U:C5	3.02	0.48
1:A:959:A:H2'	1:A:960:U:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1096:C:O2'	1:A:1097:C:H5'	2.14	0.48
1:A:1256:A:H61	1:A:1278:U:H1'	1.75	0.48
1:A:1380:U:O2'	1:A:1381:U:OP2	2.31	0.48
1:A:1426:C:H2'	1:A:1427:U:H6	1.78	0.48
4:C:32:LEU:HD23	4:C:32:LEU:O	2.14	0.48
5:D:174:LEU:C	5:D:186:LEU:HD12	2.39	0.48
6:E:137:GLU:O	6:E:141:GLN:HG3	2.13	0.48
6:E:143:ARG:NH1	9:H:77:GLU:OE2	2.46	0.48
11:J:19:SER:O	11:J:23:ILE:HD13	2.14	0.48
11:J:51:ARG:N	11:J:59:SER:HB3	2.29	0.48
13:L:67:THR:HG22	13:L:96:VAL:HG13	1.96	0.48
14:M:96:LEU:O	14:M:110:ARG:NH1	2.47	0.48
17:P:82:GLN:O	17:P:83:GLU:C	2.56	0.48
20:S:5:LEU:O	20:S:6:LYS:HG3	2.14	0.48
1:A:197:A:H1'	1:A:198:G:O4'	2.14	0.48
1:A:1005:A:H2'	1:A:1006:C:H5'	1.94	0.48
1:A:1152:A:H2'	1:A:1153:C:C6	2.49	0.48
1:A:1306:A:O2'	14:M:109:THR:HG21	2.13	0.48
1:A:1392:G:H2'	1:A:1393:U:C6	2.49	0.48
5:D:162:LEU:HD23	5:D:165:MET:HG3	1.96	0.48
7:F:11:ASN:O	7:F:14:LEU:HG	2.13	0.48
8:G:124:LEU:O	8:G:127:ALA:HB3	2.14	0.48
18:Q:24:GLU:CD	18:Q:37:LYS:HD3	2.38	0.48
21:T:50:GLU:O	21:T:100:ILE:HD12	2.14	0.48
1:A:953:G:H1'	14:M:125:ARG:CA	2.44	0.47
1:A:1277:C:C2'	1:A:1278:U:H5'	2.43	0.47
3:B:92:TYR:CE1	3:B:151:GLY:HA3	2.48	0.47
3:B:208:ILE:O	3:B:210:SER:N	2.47	0.47
3:B:208:ILE:O	3:B:209:ARG:C	2.57	0.47
4:C:60:ALA:O	4:C:61:ALA:CB	2.61	0.47
4:C:108:ASN:OD1	4:C:110:ASN:HB2	2.14	0.47
12:K:56:GLY:O	12:K:57:THR:O	2.32	0.47
13:L:58:VAL:O	13:L:65:GLU:HA	2.14	0.47
16:O:87:ILE:HG22	16:O:88:ARG:N	2.29	0.47
1:A:255:G:H1'	18:Q:16:GLN:HE22	1.79	0.47
1:A:498:U:O2'	1:A:499:A:H5'	2.14	0.47
1:A:920:U:H2'	1:A:921:U:H6	1.78	0.47
1:A:1056:U:O2	1:A:1056:U:H2'	2.13	0.47
1:A:1064:G:H4'	1:A:1065:U:H5''	1.92	0.47
1:A:1065:U:H5''	1:A:1066:C:H5'	1.97	0.47
1:A:1298:C:C4	8:G:114:ARG:HD3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1516:G:H2'	1:A:1518:A:OP2	2.14	0.47
5:D:33:MET:HE3	5:D:37:PRO:HB3	1.96	0.47
5:D:88:VAL:O	5:D:92:VAL:HG23	2.14	0.47
10:I:58:ARG:HD2	10:I:58:ARG:C	2.39	0.47
1:A:216:G:H2'	1:A:217:C:C6	2.49	0.47
1:A:409:G:H2'	1:A:410:G:O4'	2.13	0.47
1:A:518:C:H5''	1:A:519:C:C6	2.49	0.47
1:A:994:A:OP1	1:A:994:A:H8	1.97	0.47
4:C:190:ARG:NH1	4:C:190:ARG:CB	2.78	0.47
6:E:115:VAL:HG11	6:E:118:ILE:HG13	1.97	0.47
10:I:5:TYR:O	10:I:84:ALA:HA	2.14	0.47
20:S:63:THR:HG22	20:S:64:GLU:N	2.30	0.47
1:A:792:A:H4'	1:A:793:U:H5''	1.97	0.47
1:A:1286:A:C8	1:A:1287:A:C5'	2.96	0.47
1:A:1513:A:H2'	1:A:1514:C:C6	2.49	0.47
4:C:42:LEU:HD12	4:C:94:LEU:HD12	1.97	0.47
4:C:188:LEU:HD13	4:C:189:ALA:N	2.27	0.47
5:D:53:ASP:O	5:D:57:ARG:HD3	2.14	0.47
7:F:91:VAL:HG12	7:F:92:LYS:O	2.14	0.47
8:G:114:ARG:HG2	8:G:114:ARG:HH11	1.79	0.47
14:M:13:LYS:O	14:M:14:ARG:C	2.57	0.47
14:M:32:GLU:O	14:M:35:GLU:HB3	2.15	0.47
1:A:31:G:C2	1:A:48:C:H5''	2.50	0.47
1:A:60:A:H4'	1:A:61:G:O5'	2.14	0.47
1:A:160:A:H1'	1:A:344:A:N7	2.28	0.47
1:A:276:G:O2'	1:A:277:C:H5'	2.14	0.47
1:A:356:A:O2'	1:A:357:G:H5'	2.15	0.47
1:A:438:G:C4'	1:A:439:A:OP1	2.55	0.47
1:A:582:U:C2	1:A:760:G:C6	3.02	0.47
1:A:802:A:H2'	1:A:803:G:O4'	2.15	0.47
4:C:79:ARG:CG	4:C:82:GLU:HG2	2.42	0.47
4:C:151:VAL:C	4:C:152:ILE:HG13	2.40	0.47
5:D:67:ILE:HG22	5:D:68:TYR:CD1	2.49	0.47
10:I:23:ASN:C	10:I:23:ASN:HD22	2.22	0.47
10:I:69:GLY:O	10:I:73:GLN:HG3	2.14	0.47
14:M:34:LEU:CD1	14:M:41:PRO:HA	2.45	0.47
17:P:26:ARG:HE	17:P:31:LYS:HB3	1.78	0.47
1:A:67:C:H4'	1:A:172:A:O4'	2.14	0.47
1:A:103:C:OP1	21:T:17:ARG:HD2	2.14	0.47
1:A:488:C:O2'	1:A:489:C:H5'	2.15	0.47
1:A:730:G:H21	1:A:765:G:H5''	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:743:U:H2'	1:A:744:C:H6	1.78	0.47
1:A:836:G:C6	1:A:851:G:C6	3.02	0.47
1:A:1327:C:O2'	1:A:1328:C:H5'	2.14	0.47
1:A:1367:C:H5'	11:J:60:ARG:NH1	2.29	0.47
3:B:195:ASP:O	9:H:74:PRO:HG3	2.14	0.47
4:C:47:LEU:N	4:C:47:LEU:CD1	2.76	0.47
4:C:77:ILE:CG2	4:C:81:GLY:HA2	2.45	0.47
4:C:110:ASN:HB3	4:C:144:SER:OG	2.13	0.47
4:C:205:GLY:O	4:C:206:GLU:HB2	2.13	0.47
5:D:160:GLN:O	5:D:163:GLU:HB3	2.14	0.47
5:D:163:GLU:C	5:D:165:MET:N	2.71	0.47
6:E:24:ARG:HG2	6:E:24:ARG:NH1	2.27	0.47
9:H:51:VAL:HG12	9:H:52:ASP:N	2.29	0.47
9:H:103:VAL:HG23	9:H:110:ALA:HB2	1.96	0.47
10:I:89:ASN:C	10:I:91:ASP:H	2.21	0.47
10:I:120:ARG:O	10:I:122:ALA:N	2.47	0.47
1:A:6:G:H4'	1:A:298:A:H4'	1.95	0.47
1:A:781:A:H2	1:A:1514:C:C4'	2.28	0.47
1:A:854:G:C6	1:A:855:G:N7	2.82	0.47
1:A:974:A:P	15:N:31:ARG:HG2	2.55	0.47
1:A:1213:A:N1	1:A:1215:G:H1'	2.29	0.47
1:A:1238:A:H5'	1:A:1336:C:N4	2.21	0.47
1:A:1279:A:O2'	1:A:1282:C:N4	2.48	0.47
1:A:1298:C:H2'	8:G:114:ARG:NH1	2.29	0.47
1:A:1303:C:H2'	1:A:1304:G:H5'	1.97	0.47
1:A:1366:C:HO2'	11:J:60:ARG:HH22	1.61	0.47
3:B:23:ARG:HH12	3:B:191:ASP:HA	1.79	0.47
4:C:28:GLN:O	4:C:31:HIS:N	2.40	0.47
4:C:71:ALA:HA	4:C:106:VAL:HB	1.96	0.47
4:C:156:ARG:NH2	4:C:161:GLU:HA	2.29	0.47
5:D:30:LYS:O	5:D:32:ALA:N	2.48	0.47
5:D:78:LEU:CD1	5:D:97:LEU:HD23	2.44	0.47
6:E:19:MET:HE2	6:E:24:ARG:HH12	1.80	0.47
6:E:31:LEU:HD22	6:E:43:LEU:CD2	2.44	0.47
6:E:33:VAL:HG11	6:E:109:ILE:HA	1.97	0.47
7:F:43:LEU:HD22	7:F:43:LEU:N	2.29	0.47
8:G:18:TYR:HD2	8:G:59:LEU:HD22	1.80	0.47
8:G:59:LEU:O	8:G:63:LYS:HG3	2.15	0.47
11:J:49:VAL:CG1	15:N:41:ARG:HB2	2.44	0.47
13:L:33:ARG:HH11	13:L:62:SER:HB3	1.80	0.47
14:M:46:LYS:HE2	14:M:47:ASP:OD1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:10:LYS:O	16:O:10:LYS:HD2	2.14	0.47
17:P:42:ARG:O	17:P:43:LYS:C	2.58	0.47
1:A:649:G:O2'	1:A:650:G:H5'	2.14	0.47
1:A:1523:G:OP1	12:K:123:LYS:HD2	2.15	0.47
3:B:119:GLU:OE1	3:B:153:ARG:NH2	2.37	0.47
3:B:132:LYS:C	3:B:134:GLU:N	2.70	0.47
4:C:70:VAL:HG21	4:C:76:VAL:HG21	1.96	0.47
7:F:12:PRO:HG3	7:F:55:ASP:OD1	2.15	0.47
7:F:62:TRP:CD1	19:R:35:ARG:NH1	2.83	0.47
9:H:84:ARG:HD2	9:H:85:ARG:O	2.14	0.47
1:A:42:G:H2'	1:A:43:C:C6	2.50	0.47
1:A:115:G:H1'	1:A:116:A:N7	2.29	0.47
1:A:138:G:O2'	1:A:139:G:H5'	2.15	0.47
1:A:953:G:N7	14:M:104:ARG:NH2	2.62	0.47
1:A:1060:C:C4	4:C:2:GLY:HA3	2.50	0.47
1:A:1138:G:H2'	1:A:1140:C:H5'	1.97	0.47
1:A:1440:C:H2'	1:A:1441:G:H5'	1.97	0.47
13:L:71:PRO:O	13:L:102:ARG:HD2	2.15	0.47
13:L:89:ARG:HG2	13:L:97:ARG:HA	1.95	0.47
17:P:9:PHE:CE2	17:P:18:ARG:HD2	2.50	0.47
1:A:148:G:H2'	1:A:149:A:H8	1.79	0.47
1:A:337:C:H2'	1:A:338:A:C8	2.50	0.47
1:A:760:G:H2'	1:A:761:G:H5'	1.97	0.47
1:A:1187:G:OP1	10:I:113:LYS:HE2	2.15	0.47
3:B:95:GLN:OE1	3:B:95:GLN:HA	2.14	0.47
4:C:121:ALA:O	4:C:125:GLU:HG3	2.15	0.47
6:E:31:LEU:HD23	6:E:31:LEU:HA	1.66	0.47
6:E:76:ILE:O	6:E:93:PRO:HB3	2.15	0.47
15:N:60:SER:H	15:N:61:TRP:HE3	1.63	0.47
18:Q:27:PHE:CZ	18:Q:36:ILE:HD11	2.50	0.47
1:A:189:G:H2'	1:A:190:C:H6	1.80	0.46
1:A:264:U:O2'	18:Q:64:PRO:HB2	2.14	0.46
1:A:266:G:O3'	18:Q:67:LYS:HB2	2.14	0.46
1:A:965:A:H4'	1:A:966:G:O5'	2.15	0.46
1:A:1058:G:O2'	1:A:1059:C:H5'	2.15	0.46
1:A:1253:G:H2'	1:A:1254:C:C6	2.50	0.46
1:A:1347:G:HO2'	1:A:1373:G:H1	1.62	0.46
1:A:1480:G:O2'	1:A:1481:U:H5'	2.16	0.46
3:B:59:GLU:HG2	3:B:221:LEU:HD11	1.96	0.46
3:B:107:THR:C	3:B:109:SER:N	2.73	0.46
4:C:182:ILE:HG12	4:C:203:PHE:HD1	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:30:LYS:C	5:D:32:ALA:N	2.70	0.46
5:D:109:GLY:HA3	5:D:165:MET:SD	2.55	0.46
8:G:152:ALA:C	8:G:154:TYR:N	2.74	0.46
12:K:109:VAL:HG13	19:R:85:LEU:O	2.15	0.46
14:M:9:ILE:HD12	14:M:9:ILE:N	2.30	0.46
1:A:93:G:O2'	1:A:95:U:H5'	2.15	0.46
1:A:163:C:O2'	1:A:164:U:H5'	2.16	0.46
1:A:243:A:H5''	1:A:244:U:H5'	1.97	0.46
1:A:373:A:H1'	1:A:481:G:H1'	1.96	0.46
1:A:426:G:O2'	1:A:427:U:H5'	2.15	0.46
1:A:590:C:O2'	1:A:591:U:H5'	2.15	0.46
1:A:774:G:O2'	1:A:775:G:H5'	2.16	0.46
1:A:781:A:H2'	1:A:782:A:H5'	1.96	0.46
1:A:814:A:N7	1:A:816:A:C4	2.83	0.46
1:A:1020:U:H2'	1:A:1021:G:C8	2.50	0.46
1:A:1123:A:H4'	11:J:37:PRO:HD2	1.96	0.46
1:A:1145:C:O2'	1:A:1146:A:O5'	2.34	0.46
5:D:58:LEU:HD23	5:D:206:PHE:CE1	2.50	0.46
6:E:79:GLU:OE1	6:E:79:GLU:N	2.47	0.46
9:H:75:ARG:HA	9:H:76:PRO:HD3	1.67	0.46
18:Q:15:MET:CE	18:Q:43:LEU:HD22	2.37	0.46
21:T:45:GLN:HB2	21:T:91:LEU:HD22	1.97	0.46
1:A:338:A:H2	1:A:351:G:H22	1.62	0.46
1:A:977:A:C2'	1:A:978:A:H5''	2.45	0.46
1:A:1049:U:H1'	1:A:1201:A:N7	2.30	0.46
1:A:1138:G:H3'	1:A:1138:G:N3	2.31	0.46
3:B:103:THR:HA	3:B:180:LEU:HD11	1.97	0.46
3:B:236:TYR:HA	3:B:239:VAL:HG23	1.96	0.46
6:E:76:ILE:HG23	6:E:142:LEU:HD22	1.97	0.46
8:G:24:THR:HG22	8:G:28:ASN:HD21	1.80	0.46
14:M:40:ASN:HD22	14:M:40:ASN:C	2.22	0.46
15:N:45:ARG:HH11	15:N:45:ARG:HG3	1.80	0.46
19:R:59:SER:OG	19:R:62:GLU:HG3	2.15	0.46
19:R:87:ARG:HG2	19:R:87:ARG:NH1	2.29	0.46
1:A:269:C:H2'	1:A:270:A:C8	2.49	0.46
1:A:750:G:H1'	16:O:22:THR:OG1	2.15	0.46
1:A:938:A:H8	1:A:938:A:O5'	1.98	0.46
1:A:954:G:H2'	1:A:955:U:C6	2.50	0.46
1:A:1005:A:C2'	1:A:1006:C:H5'	2.46	0.46
1:A:1068:G:N2	1:A:1191:A:N3	2.61	0.46
5:D:54:TYR:O	5:D:55:ALA:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:102:ALA:HA	6:E:120:THR:CG2	2.45	0.46
9:H:28:ALA:HB3	9:H:57:PRO:HB2	1.96	0.46
10:I:113:LYS:H	10:I:113:LYS:HD2	1.79	0.46
12:K:54:ARG:HB3	12:K:54:ARG:NH1	2.14	0.46
1:A:89:C:O2'	1:A:90:U:H5'	2.15	0.46
1:A:247:G:OP2	18:Q:100:LYS:HG3	2.16	0.46
1:A:397:A:H5'	1:A:398:C:P	2.56	0.46
1:A:452:A:H2'	1:A:453:A:H8	1.81	0.46
1:A:722:A:H4'	1:A:723:U:C5	2.50	0.46
1:A:761:G:H2'	1:A:762:C:C6	2.51	0.46
1:A:791:G:C2'	1:A:792:A:C5'	2.94	0.46
1:A:865:A:H2'	1:A:866:C:C6	2.51	0.46
1:A:960:U:H1'	1:A:1223:C:H5'	1.98	0.46
1:A:1256:A:H4'	1:A:1257:U:C5'	2.40	0.46
4:C:83:ARG:HA	4:C:86:VAL:HG23	1.98	0.46
7:F:40:VAL:CG2	7:F:41:GLU:N	2.79	0.46
8:G:141:VAL:O	8:G:144:MET:HB2	2.16	0.46
9:H:48:TYR:CD1	9:H:48:TYR:C	2.93	0.46
10:I:111:ARG:O	10:I:119:ALA:HB2	2.16	0.46
11:J:54:PHE:HD2	11:J:55:LYS:HD3	1.77	0.46
13:L:28:LYS:HG3	13:L:33:ARG:HH12	1.79	0.46
13:L:28:LYS:O	13:L:29:GLY:C	2.57	0.46
18:Q:10:VAL:HG13	18:Q:19:VAL:HB	1.98	0.46
20:S:41:VAL:HG22	20:S:44:MET:HE3	1.97	0.46
21:T:42:GLN:O	21:T:45:GLN:HB3	2.16	0.46
1:A:16:A:N1	1:A:919:A:H2	2.12	0.46
1:A:51:A:H4'	1:A:52:G:C5'	2.46	0.46
1:A:135:C:C2	17:P:1:MET:HB2	2.50	0.46
1:A:154:C:H2'	1:A:155:C:H6	1.81	0.46
1:A:619:U:N3	5:D:134:ASP:OD1	2.48	0.46
1:A:980:C:H2'	1:A:981:U:O4'	2.16	0.46
1:A:995:C:O2	1:A:995:C:H2'	2.14	0.46
1:A:1003(A):G:N1	1:A:1004:A:H1'	2.30	0.46
1:A:1063:C:H2'	1:A:1064:G:C8	2.50	0.46
3:B:88:ALA:C	3:B:90:MET:N	2.71	0.46
4:C:50:ALA:HB2	4:C:75:VAL:HB	1.96	0.46
4:C:141:VAL:O	4:C:146:ALA:HB3	2.16	0.46
4:C:173:VAL:N	4:C:174:PRO:CD	2.78	0.46
10:I:19:LEU:C	10:I:20:ARG:HG3	2.40	0.46
11:J:85:LEU:O	11:J:86:MET:C	2.58	0.46
13:L:27:LEU:HG	13:L:28:LYS:N	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:26:GLY:O	14:M:28:ALA:N	2.49	0.46
15:N:50:LYS:HD3	15:N:52:GLN:NE2	2.31	0.46
21:T:56:MET:HG2	21:T:84:LEU:HD11	1.98	0.46
1:A:98:U:O2'	1:A:99:C:H5'	2.15	0.46
1:A:815:A:H4'	1:A:817:C:C4	2.51	0.46
1:A:1070:U:O2'	1:A:1071:C:H5'	2.16	0.46
1:A:1244:C:O2'	1:A:1245:A:H5'	2.16	0.46
1:A:1494:G:OP2	24:A:1632:HYG:O11	2.30	0.46
1:A:1525:G:P	12:K:120:ARG:HH22	2.39	0.46
3:B:208:ILE:HG22	3:B:209:ARG:N	2.31	0.46
3:B:224:GLN:O	3:B:226:ARG:N	2.48	0.46
5:D:98:GLU:HG2	5:D:189:PRO:HG3	1.98	0.46
5:D:196:LEU:O	5:D:198:VAL:N	2.42	0.46
7:F:30:LEU:HA	7:F:75:LEU:HD21	1.96	0.46
18:Q:15:MET:HB2	18:Q:18:THR:HB	1.98	0.46
18:Q:81:ARG:NH2	18:Q:83:ASP:OD2	2.47	0.46
19:R:59:SER:O	19:R:60:GLY:C	2.59	0.46
22:V:8:THR:O	22:V:9:ARG:C	2.58	0.46
1:A:106:C:O2'	1:A:379:C:H5''	2.16	0.46
1:A:192:U:O2'	1:A:193:C:H5'	2.16	0.46
1:A:193:C:H2'	1:A:194:C:H6	1.80	0.46
1:A:259:G:O2'	1:A:260:G:H5'	2.15	0.46
1:A:463:A:H2'	1:A:474:G:O4'	2.15	0.46
1:A:583:A:H2'	1:A:584:G:O4'	2.16	0.46
1:A:839:U:O2	1:A:839:U:C2'	2.60	0.46
1:A:1085:U:O3'	1:A:1086:U:C6	2.69	0.46
1:A:1127:G:N2	1:A:1144:G:N2	2.64	0.46
3:B:23:ARG:C	3:B:23:ARG:HD3	2.41	0.46
3:B:197:VAL:HB	3:B:200:ILE:CG1	2.39	0.46
4:C:174:PRO:O	4:C:177:THR:HG22	2.16	0.46
5:D:52:SER:O	5:D:53:ASP:C	2.59	0.46
5:D:58:LEU:HD13	5:D:58:LEU:C	2.41	0.46
6:E:76:ILE:HG23	6:E:77:PRO:HD2	1.97	0.46
13:L:86:ARG:HH11	13:L:86:ARG:HG3	1.80	0.46
14:M:120:LYS:HE2	14:M:123:ALA:HB2	1.98	0.46
17:P:17:TYR:CE1	17:P:41:PRO:HG2	2.51	0.46
19:R:53:ARG:HE	19:R:60:GLY:N	2.13	0.46
20:S:5:LEU:O	20:S:6:LYS:CG	2.64	0.46
21:T:38:LYS:O	21:T:42:GLN:HB2	2.15	0.46
1:A:1056:U:H5'	4:C:163:ALA:CB	2.46	0.46
1:A:1145:C:O2'	1:A:1146:A:C8	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1285:A:H8	1:A:1285:A:OP1	1.99	0.46
3:B:105:PHE:HB2	3:B:158:LEU:HD21	1.97	0.46
3:B:206:ASP:CG	3:B:207:ALA:N	2.68	0.46
4:C:3:ASN:C	4:C:4:LYS:HG2	2.40	0.46
4:C:139:GLN:O	4:C:143:GLU:N	2.37	0.46
5:D:17:VAL:CG1	5:D:18:LYS:N	2.79	0.46
5:D:103:ASN:O	5:D:106:TYR:HB3	2.16	0.46
6:E:115:VAL:HG11	6:E:118:ILE:CG1	2.46	0.46
21:T:67:ALA:HB2	21:T:77:ALA:HB2	1.97	0.46
1:A:21:G:H2'	1:A:22:G:C8	2.50	0.46
1:A:253:U:H2'	1:A:254:G:H8	1.79	0.46
1:A:960:U:O2'	1:A:1223:C:H4'	2.16	0.46
1:A:1004:A:C8	1:A:1037:C:O2	2.69	0.46
1:A:1044:A:H2'	1:A:1045:C:C5'	2.46	0.46
1:A:1118:C:H2'	1:A:1119:C:H6	1.80	0.46
1:A:1183:A:C2'	1:A:1184:G:OP1	2.64	0.46
1:A:1343:G:C1'	10:I:121:ARG:HH12	2.25	0.46
4:C:28:GLN:O	4:C:29:TYR:C	2.58	0.46
4:C:64:VAL:HB	4:C:99:VAL:HB	1.98	0.46
5:D:114:ARG:HG3	5:D:114:ARG:NH1	2.26	0.46
7:F:67:MET:HE2	7:F:72:VAL:HA	1.98	0.46
10:I:43:ALA:C	10:I:45:ALA:N	2.74	0.46
10:I:108:VAL:CG1	10:I:109:VAL:H	2.29	0.46
14:M:40:ASN:C	14:M:40:ASN:ND2	2.74	0.46
14:M:94:ARG:HH12	20:S:81:ARG:CD	2.29	0.46
15:N:59:ALA:HB1	15:N:61:TRP:HZ3	1.79	0.46
1:A:101:A:H2'	1:A:102:G:H8	1.81	0.45
1:A:248:C:C2'	1:A:249:U:H5'	2.46	0.45
1:A:406:G:H2'	1:A:407:G:H8	1.82	0.45
1:A:421:U:H5'	1:A:422:C:H5	1.80	0.45
1:A:767:A:H2'	1:A:768:A:C8	2.51	0.45
1:A:1150:U:O5'	1:A:1150:U:H6	2.00	0.45
1:A:1220:G:H1'	20:S:52:TYR:HD2	1.82	0.45
5:D:52:SER:C	5:D:54:TYR:N	2.73	0.45
6:E:9:LYS:HG3	6:E:112:LEU:HD11	1.97	0.45
6:E:93:PRO:HG3	9:H:105:ARG:HE	1.79	0.45
11:J:40:LEU:HB3	11:J:69:ASN:HB2	1.98	0.45
19:R:39:VAL:CG1	19:R:40:LEU:N	2.78	0.45
1:A:437:U:C5'	5:D:155:LEU:HD22	2.45	0.45
1:A:1256:A:H2	1:A:1258:G:C2	2.33	0.45
1:A:1286:A:C3'	1:A:1287:A:C5'	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1514:C:H2'	1:A:1515:C:H6	1.80	0.45
4:C:35:GLU:CG	4:C:59:ARG:HH22	2.29	0.45
4:C:156:ARG:HH21	4:C:161:GLU:HA	1.82	0.45
4:C:172:ARG:HB3	4:C:172:ARG:NH1	2.32	0.45
5:D:68:TYR:OH	5:D:196:LEU:HD11	2.16	0.45
5:D:145:GLU:CG	5:D:184:LYS:HE2	2.47	0.45
6:E:102:ALA:HA	6:E:120:THR:HG22	1.98	0.45
7:F:43:LEU:N	7:F:43:LEU:CD2	2.79	0.45
7:F:101:ALA:CA	19:R:28:GLU:HB3	2.42	0.45
8:G:156:TRP:OXT	8:G:156:TRP:HD1	2.00	0.45
9:H:126:LYS:C	9:H:128:GLY:N	2.74	0.45
11:J:21:GLN:O	11:J:25:GLU:HG3	2.16	0.45
14:M:94:ARG:NH1	20:S:81:ARG:HD3	2.30	0.45
22:V:15:ARG:O	22:V:17:THR:HG23	2.17	0.45
1:A:1286:A:H8	1:A:1287:A:C5'	2.29	0.45
1:A:1308:U:H2'	1:A:1309:G:H8	1.81	0.45
1:A:1313:U:OP2	20:S:6:LYS:HA	2.16	0.45
1:A:1366:C:C2	1:A:1367:C:C5	3.04	0.45
4:C:7:PRO:O	4:C:11:ARG:HD2	2.15	0.45
4:C:91:LEU:HD23	4:C:92:ALA:N	2.31	0.45
6:E:28:PHE:O	6:E:47:LYS:HA	2.16	0.45
8:G:78:ARG:HD2	8:G:156:TRP:CE3	2.50	0.45
11:J:8:LEU:HD21	11:J:96:ILE:HG12	1.97	0.45
13:L:32:PHE:CE1	13:L:86:ARG:HB2	2.52	0.45
14:M:20:THR:C	14:M:22:ILE:H	2.24	0.45
16:O:45:VAL:HB	16:O:46:HIS:ND1	2.31	0.45
16:O:71:GLN:HG3	16:O:78:TYR:CE2	2.52	0.45
1:A:334:C:H2'	1:A:335:C:C6	2.52	0.45
1:A:429:U:H4'	1:A:430:A:O5'	2.16	0.45
1:A:682:G:O2'	1:A:683:G:H5'	2.16	0.45
1:A:1149:C:OP1	10:I:9:ARG:HD3	2.15	0.45
1:A:1229:A:H2'	1:A:1230:C:C6	2.50	0.45
5:D:24:GLU:CG	5:D:25:ARG:N	2.78	0.45
5:D:162:LEU:HD13	5:D:181:MET:HG2	1.98	0.45
6:E:115:VAL:HG12	6:E:116:THR:N	2.31	0.45
7:F:35:ALA:HA	7:F:67:MET:HB3	1.97	0.45
7:F:45:LEU:HA	7:F:58:GLY:O	2.16	0.45
10:I:7:THR:HG22	10:I:8:GLY:N	2.31	0.45
10:I:97:LYS:O	10:I:100:GLY:N	2.39	0.45
22:V:2:GLY:O	22:V:3:LYS:C	2.59	0.45
1:A:96:G:O2'	1:A:97:G:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:C:O2'	1:A:292:G:H5'	2.17	0.45
1:A:818:G:C3'	1:A:819:A:C5'	2.94	0.45
1:A:1021:G:C2	1:A:1022:G:H1'	2.52	0.45
1:A:1051:C:O2'	1:A:1052:U:H5'	2.16	0.45
1:A:1063:C:H3'	1:A:1064:G:H2'	1.99	0.45
1:A:1486:G:H2'	1:A:1487:G:C8	2.52	0.45
5:D:3:ARG:NH2	5:D:74:GLN:HG3	2.31	0.45
5:D:205:GLU:O	5:D:208:SER:HB2	2.16	0.45
10:I:44:VAL:HG13	10:I:51:ARG:NH2	2.31	0.45
10:I:118:LYS:NZ	10:I:118:LYS:CB	2.80	0.45
13:L:42:THR:HG22	13:L:52:LEU:HB3	1.96	0.45
13:L:87:GLY:H	13:L:98:TYR:HB3	1.81	0.45
17:P:81:ARG:HB2	17:P:81:ARG:HH11	1.82	0.45
1:A:375:U:C2	1:A:376:G:C8	3.05	0.45
1:A:538:G:H2'	1:A:539:A:C8	2.52	0.45
1:A:975:A:C8	1:A:975:A:C5'	2.97	0.45
1:A:1070:U:H2'	1:A:1071:C:C6	2.51	0.45
1:A:1392:G:N2	1:A:1502:A:H8	2.14	0.45
1:A:1435:G:H2'	1:A:1436:U:C6	2.51	0.45
3:B:100:GLY:O	3:B:104:ASN:N	2.48	0.45
3:B:107:THR:C	3:B:109:SER:H	2.25	0.45
3:B:112:VAL:O	3:B:116:GLU:HG3	2.16	0.45
3:B:117:GLU:O	3:B:120:ALA:HB3	2.16	0.45
5:D:60:GLU:OE1	5:D:60:GLU:HA	2.17	0.45
7:F:48:LEU:HD13	7:F:52:ILE:HD12	1.99	0.45
8:G:26:PHE:O	8:G:30:ILE:HG13	2.16	0.45
10:I:19:LEU:CD1	10:I:85:LEU:HD12	2.47	0.45
16:O:70:LEU:HD12	16:O:78:TYR:CA	2.47	0.45
19:R:47:THR:HA	19:R:83:GLU:CB	2.47	0.45
21:T:18:GLN:O	21:T:19:SER:C	2.58	0.45
1:A:45:U:H2'	1:A:46:G:C8	2.52	0.45
1:A:113:G:C1'	1:A:354:G:H5'	2.45	0.45
1:A:528:C:H41	13:L:49:ASN:CG	2.24	0.45
1:A:1181:G:O2'	1:A:1182:G:O4'	2.34	0.45
1:A:1300:G:O2'	1:A:1301:U:H6	2.00	0.45
1:A:1533:C:O2	1:A:1533:C:C2'	2.64	0.45
3:B:10:LEU:C	3:B:12:GLU:H	2.24	0.45
3:B:103:THR:N	3:B:176:GLU:OE1	2.44	0.45
3:B:132:LYS:HE2	3:B:135:GLN:OE1	2.17	0.45
4:C:12:LEU:HD23	4:C:12:LEU:HA	1.63	0.45
4:C:152:ILE:N	4:C:199:LYS:O	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:112:LEU:HD23	9:H:112:LEU:H	1.82	0.45
10:I:97:LYS:HE2	10:I:102:LEU:HD12	1.98	0.45
11:J:12:ASP:OD1	11:J:14:LYS:N	2.49	0.45
11:J:34:VAL:C	11:J:36:GLY:H	2.24	0.45
12:K:38:ASN:HA	12:K:39:PRO:HD2	1.78	0.45
14:M:15:VAL:C	14:M:17:VAL:N	2.75	0.45
16:O:40:SER:O	16:O:44:LYS:HG2	2.17	0.45
18:Q:9:VAL:HG21	18:Q:84:LEU:HD13	1.97	0.45
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.31	0.45
1:A:147:G:O2'	1:A:148:G:H5'	2.17	0.45
1:A:231:G:O2'	1:A:232:G:H5'	2.17	0.45
1:A:300:A:H2'	1:A:301:G:O4'	2.17	0.45
1:A:640:A:O2'	1:A:641:U:H5'	2.17	0.45
1:A:792:A:H4'	1:A:793:U:C5'	2.47	0.45
1:A:838:G:N2	1:A:849:C:C2	2.85	0.45
1:A:893:C:H2'	1:A:894:G:C8	2.51	0.45
1:A:953:G:H2'	1:A:954:G:O4'	2.16	0.45
1:A:1003(A):G:C6	1:A:1004:A:H1'	2.52	0.45
1:A:1069:C:O2'	1:A:1192:C:H1'	2.17	0.45
1:A:1221:G:O3'	20:S:77:THR:HG21	2.15	0.45
1:A:1440:C:C2'	1:A:1441:G:H5'	2.47	0.45
3:B:25:ASN:ND2	3:B:27:LYS:H	2.14	0.45
3:B:187:LEU:HA	3:B:201:ILE:O	2.17	0.45
4:C:126:ARG:C	4:C:127:ARG:HG3	2.42	0.45
4:C:129:ALA:HB3	4:C:132:ARG:HD2	1.99	0.45
5:D:151:LYS:HD2	5:D:151:LYS:N	2.32	0.45
5:D:189:PRO:HB2	5:D:194:LEU:HD21	1.98	0.45
7:F:67:MET:CE	7:F:72:VAL:HA	2.46	0.45
8:G:46:ALA:HB1	8:G:121:ALA:HB2	1.99	0.45
10:I:4:TYR:CZ	10:I:88:TYR:HD1	2.35	0.45
11:J:30:SER:HB3	11:J:80:LYS:CG	2.47	0.45
13:L:59:ARG:NH1	13:L:65:GLU:HG2	2.32	0.45
17:P:81:ARG:HH11	17:P:81:ARG:CB	2.30	0.45
20:S:13:ASP:HA	20:S:16:LEU:HB3	1.98	0.45
1:A:130:A:N7	18:Q:63:ARG:HG3	2.32	0.45
1:A:385:C:H2'	1:A:386:C:C6	2.52	0.45
1:A:560:U:H4'	1:A:561:U:H5''	1.97	0.45
1:A:822:C:O2'	1:A:823:G:H5'	2.17	0.45
1:A:986:A:C2	1:A:1220:G:C2	3.05	0.45
1:A:1217:C:O2'	1:A:1218:C:H5'	2.17	0.45
1:A:1409:C:H2'	1:A:1410:G:C8	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1509:C:C2'	1:A:1510:U:H5'	2.46	0.45
3:B:75:LYS:O	3:B:75:LYS:HD3	2.17	0.45
3:B:167:PRO:O	3:B:171:ALA:N	2.50	0.45
7:F:69:GLU:C	7:F:71:ARG:H	2.25	0.45
9:H:91:ARG:HG2	13:L:7:ILE:HG13	1.98	0.45
10:I:46:ALA:O	10:I:49:PRO:HD2	2.17	0.45
10:I:127:LYS:C	10:I:128:ARG:O	2.58	0.45
11:J:34:VAL:HG12	11:J:36:GLY:N	2.31	0.45
11:J:51:ARG:H	11:J:59:SER:HB3	1.80	0.45
15:N:21:TYR:CD2	15:N:21:TYR:O	2.70	0.45
16:O:27:VAL:O	16:O:30:ALA:N	2.50	0.45
1:A:61:G:O2'	1:A:62:U:H5'	2.17	0.45
1:A:243:A:N6	1:A:281:G:O2'	2.50	0.45
1:A:456:C:H2'	1:A:457:C:C6	2.52	0.45
1:A:967:C:H2'	1:A:968:A:C8	2.52	0.45
1:A:1129:C:O2'	1:A:1130:A:OP2	2.27	0.45
1:A:1176:A:H2'	1:A:1177:G:O4'	2.16	0.45
4:C:43:LEU:HD23	4:C:43:LEU:H	1.79	0.45
4:C:180:ALA:O	4:C:181:ASN:CB	2.62	0.45
5:D:199:ASN:HD21	5:D:201:GLN:CB	2.19	0.45
10:I:79:LEU:CD1	10:I:83:ARG:HD2	2.45	0.45
10:I:118:LYS:C	10:I:120:ARG:H	2.25	0.45
11:J:94:VAL:HG12	11:J:95:GLU:N	2.32	0.45
13:L:53:ARG:N	13:L:53:ARG:HD2	2.32	0.45
21:T:10:LEU:O	21:T:13:LEU:HD12	2.17	0.45
1:A:16:A:C2'	1:A:17:U:H5'	2.47	0.44
1:A:281:G:O2'	1:A:282:A:P	2.74	0.44
1:A:437:U:H5''	5:D:155:LEU:CD2	2.44	0.44
1:A:446:G:O2'	1:A:447:G:H5'	2.17	0.44
1:A:836:G:C6	1:A:851:G:C5	3.05	0.44
1:A:900:A:H2'	1:A:901:A:C8	2.52	0.44
1:A:922:G:N3	1:A:1398:A:H2	2.15	0.44
1:A:939:G:H5''	8:G:102:ARG:HH22	1.78	0.44
1:A:1055:A:C6	1:A:1056:U:C6	3.04	0.44
1:A:1115:C:H1'	15:N:61:TRP:O	2.17	0.44
3:B:46:LYS:C	3:B:48:MET:N	2.72	0.44
3:B:101:MET:HG2	3:B:108:ILE:HD13	1.97	0.44
3:B:108:ILE:O	3:B:108:ILE:CG2	2.65	0.44
4:C:82:GLU:O	4:C:85:ARG:HB3	2.17	0.44
11:J:34:VAL:HG12	11:J:36:GLY:H	1.82	0.44
11:J:38:ILE:O	11:J:70:ARG:HA	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:24:VAL:O	13:L:24:VAL:HG12	2.17	0.44
14:M:48:LEU:HD23	14:M:48:LEU:HA	1.85	0.44
14:M:82:MET:HE2	14:M:92:HIS:CB	2.47	0.44
19:R:43:PHE:HD1	19:R:66:LEU:HD11	1.81	0.44
21:T:53:LEU:HD21	21:T:104:LEU:CD1	2.46	0.44
1:A:19:C:OP1	6:E:125:SER:OG	2.24	0.44
1:A:412:A:N1	5:D:35:ARG:HB3	2.32	0.44
1:A:491:G:H2'	1:A:492:G:H8	1.82	0.44
1:A:1059:C:O2'	1:A:1060:C:H5'	2.17	0.44
1:A:1129:C:O2'	1:A:1130:A:P	2.75	0.44
1:A:1216:G:H2'	1:A:1217:C:C6	2.52	0.44
1:A:1477:C:H2'	1:A:1478:C:C6	2.51	0.44
3:B:83:MET:HE3	3:B:235:SER:N	2.32	0.44
3:B:156:LYS:O	3:B:156:LYS:HD3	2.17	0.44
5:D:25:ARG:HA	5:D:28:SER:OG	2.17	0.44
6:E:118:ILE:CG2	6:E:119:LEU:N	2.79	0.44
8:G:20:ASP:OD1	8:G:21:VAL:N	2.50	0.44
9:H:112:LEU:HD23	9:H:112:LEU:N	2.33	0.44
1:A:538:G:O2'	1:A:539:A:H5'	2.17	0.44
1:A:1096:C:H2'	1:A:1097:C:H6	1.82	0.44
1:A:1129:C:OP1	10:I:62:TYR:CE2	2.71	0.44
1:A:1161:C:H2'	1:A:1162:C:H6	1.83	0.44
1:A:1162:C:H2'	1:A:1163:C:C6	2.52	0.44
3:B:10:LEU:CD2	3:B:48:MET:HE2	2.47	0.44
4:C:30:ARG:HG2	4:C:30:ARG:HH11	1.83	0.44
5:D:150:GLU:HG3	5:D:153:ARG:HH21	1.83	0.44
5:D:162:LEU:HD23	5:D:162:LEU:HA	1.66	0.44
9:H:39:LEU:HD11	9:H:137:VAL:HG21	2.00	0.44
12:K:30:VAL:HG21	12:K:65:ALA:HA	1.98	0.44
12:K:110:ASP:HB3	19:R:85:LEU:HB3	2.00	0.44
18:Q:27:PHE:CD1	18:Q:27:PHE:C	2.96	0.44
19:R:55:ARG:HB3	19:R:55:ARG:CZ	2.46	0.44
1:A:294:U:H2'	1:A:295:C:H6	1.83	0.44
1:A:337:C:O2'	1:A:338:A:H5'	2.18	0.44
1:A:452:A:H2'	1:A:453:A:C8	2.53	0.44
1:A:818:G:H3'	1:A:819:A:H5''	2.00	0.44
1:A:1231:G:H4'	10:I:126:SER:HB3	1.98	0.44
3:B:10:LEU:CD2	3:B:48:MET:HG3	2.48	0.44
3:B:80:ILE:CD1	3:B:212:GLN:HB2	2.43	0.44
3:B:132:LYS:O	3:B:136:VAL:HG23	2.17	0.44
3:B:140:HIS:O	3:B:143:GLU:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:178:ARG:NH1	3:B:178:ARG:CG	2.76	0.44
3:B:231:GLU:OE1	3:B:232:PRO:O	2.35	0.44
5:D:150:GLU:CD	5:D:150:GLU:N	2.61	0.44
7:F:94:GLN:CB	19:R:32:ARG:HD3	2.46	0.44
8:G:6:ARG:O	8:G:7:ALA:C	2.59	0.44
10:I:44:VAL:O	10:I:44:VAL:HG12	2.16	0.44
12:K:17:GLY:O	12:K:80:VAL:HA	2.17	0.44
13:L:18:VAL:CG1	13:L:19:ARG:N	2.80	0.44
20:S:50:ALA:HA	20:S:58:VAL:O	2.18	0.44
1:A:179:A:H2'	1:A:180:U:C6	2.52	0.44
1:A:252:U:H2'	1:A:253:U:C6	2.53	0.44
1:A:313:A:H2'	1:A:314:C:C6	2.53	0.44
1:A:396:G:O2'	1:A:398:C:OP1	2.27	0.44
1:A:1127:G:H1'	1:A:1148:U:H3	1.81	0.44
1:A:1221:G:H1'	20:S:54:GLY:HA3	2.00	0.44
1:A:1461:G:O2'	1:A:1462:G:H5'	2.17	0.44
3:B:97:TRP:CZ2	3:B:102:LEU:HD13	2.48	0.44
3:B:122:PHE:CE2	3:B:139:LYS:HG2	2.41	0.44
5:D:33:MET:HE1	5:D:37:PRO:O	2.17	0.44
5:D:91:SER:O	5:D:92:VAL:C	2.59	0.44
5:D:151:LYS:H	5:D:151:LYS:CD	2.31	0.44
5:D:165:MET:HE2	5:D:176:LEU:HD13	2.00	0.44
8:G:38:LEU:O	8:G:42:ILE:HG13	2.17	0.44
9:H:24:THR:HG22	9:H:61:VAL:O	2.18	0.44
12:K:12:ARG:O	12:K:13:GLN:HB2	2.18	0.44
14:M:24:GLY:HA3	14:M:66:LEU:HD22	1.99	0.44
17:P:11:SER:O	17:P:12:LYS:C	2.61	0.44
17:P:71:ARG:HD3	17:P:75:ARG:HH21	1.83	0.44
18:Q:66:SER:O	18:Q:67:LYS:C	2.61	0.44
20:S:28:LYS:HG2	20:S:29:ARG:N	2.32	0.44
20:S:30:LEU:O	20:S:31:ILE:HD13	2.18	0.44
1:A:113:G:H1'	1:A:354:G:C5'	2.45	0.44
1:A:166:G:O2'	1:A:167:G:H5'	2.18	0.44
1:A:224:C:H2'	1:A:225:C:H6	1.83	0.44
1:A:424:G:H2'	1:A:425:G:H8	1.83	0.44
1:A:518:C:H4'	1:A:519:C:O5'	2.18	0.44
1:A:636:U:C5'	18:Q:2:PRO:HG2	2.47	0.44
1:A:942:G:C2	1:A:943:U:C6	3.05	0.44
1:A:952:U:O2'	1:A:953:G:H5'	2.17	0.44
1:A:1190:G:C2'	1:A:1191:A:OP2	2.65	0.44
1:A:1427:U:H2'	1:A:1428:A:H8	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1632:HYG:O14	24:A:1632:HYG:C1	2.65	0.44
4:C:79:ARG:HG3	4:C:79:ARG:O	2.16	0.44
8:G:138:LYS:HE2	8:G:142:GLU:OE1	2.17	0.44
10:I:58:ARG:CG	10:I:58:ARG:HH11	2.31	0.44
11:J:30:SER:HB3	11:J:80:LYS:HG3	1.99	0.44
11:J:69:ASN:O	11:J:70:ARG:CD	2.66	0.44
12:K:69:ALA:O	12:K:73:MET:N	2.50	0.44
13:L:28:LYS:C	13:L:30:ALA:N	2.74	0.44
14:M:74:VAL:O	14:M:77:ASN:HB2	2.18	0.44
15:N:3:ARG:CZ	15:N:6:LEU:HG	2.48	0.44
19:R:52:PRO:HB2	19:R:54:ARG:CD	2.47	0.44
21:T:53:LEU:O	21:T:54:LYS:C	2.60	0.44
1:A:52:G:H2'	1:A:53:A:H8	1.82	0.44
1:A:191:G:H22	21:T:85:MET:HE1	1.82	0.44
1:A:375:U:H4'	17:P:17:TYR:CE2	2.51	0.44
1:A:411:A:C8	1:A:413:G:H1'	2.53	0.44
1:A:1115:C:O2'	1:A:1116:C:H5'	2.17	0.44
1:A:1272:G:H2'	1:A:1273:G:H8	1.82	0.44
3:B:8:LYS:HD3	3:B:9:GLU:N	2.32	0.44
3:B:87:ARG:NH2	3:B:220:ASP:OD1	2.39	0.44
3:B:181:PHE:HD2	9:H:70:GLN:HB3	1.81	0.44
5:D:108:LEU:O	5:D:165:MET:HE2	2.18	0.44
6:E:43:LEU:HD23	6:E:44:GLY:H	1.82	0.44
7:F:44:GLY:O	7:F:59:TYR:HA	2.17	0.44
16:O:71:GLN:HB2	16:O:78:TYR:CE1	2.52	0.44
17:P:52:ASP:O	17:P:52:ASP:CG	2.61	0.44
1:A:409:G:O2'	1:A:410:G:H5'	2.18	0.44
1:A:458:C:O2'	1:A:459:G:H5'	2.18	0.44
1:A:781:A:H2	1:A:1514:C:H4'	1.82	0.44
1:A:1352:C:H2'	1:A:1353:G:O4'	2.17	0.44
3:B:167:PRO:HG2	3:B:192:SER:OG	2.18	0.44
4:C:30:ARG:HG2	4:C:30:ARG:NH1	2.32	0.44
5:D:4:TYR:CG	5:D:5:ILE:N	2.79	0.44
12:K:48:ILE:HD13	12:K:63:LEU:HB2	1.99	0.44
19:R:52:PRO:O	19:R:56:THR:HG23	2.18	0.44
1:A:160:A:H1'	1:A:344:A:C5	2.52	0.44
1:A:186:C:H2'	1:A:187:C:H6	1.83	0.44
1:A:250:A:C2	1:A:274:A:C6	3.06	0.44
1:A:438:G:O2'	1:A:495:U:O4	2.28	0.44
1:A:1347:G:C2'	1:A:1348:U:OP2	2.65	0.44
1:A:1417:G:N2	1:A:1484:C:N4	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:23:ARG:HH11	3:B:24:TRP:CA	2.30	0.44
3:B:53:ARG:HG2	3:B:53:ARG:HH11	1.83	0.44
5:D:31:CYS:C	5:D:33:MET:H	2.25	0.44
5:D:68:TYR:CD1	5:D:68:TYR:N	2.85	0.44
8:G:18:TYR:CD1	8:G:18:TYR:N	2.85	0.44
9:H:4:ASP:HB3	9:H:7:ALA:HB3	2.00	0.44
9:H:119:LEU:HD23	9:H:119:LEU:N	2.33	0.44
10:I:49:PRO:CD	10:I:78:LYS:HG2	2.48	0.44
12:K:82:VAL:HG23	12:K:105:VAL:HG13	2.00	0.44
14:M:37:THR:O	14:M:37:THR:CG2	2.65	0.44
18:Q:80:GLY:O	18:Q:81:ARG:CB	2.66	0.44
1:A:253:U:H2'	1:A:254:G:C8	2.53	0.43
1:A:489:C:H2'	1:A:490:G:C8	2.46	0.43
1:A:718:G:H5'	1:A:719:C:OP2	2.18	0.43
1:A:864:A:H2'	1:A:865:A:C8	2.53	0.43
1:A:1202:G:O4'	15:N:29:ARG:HD3	2.18	0.43
1:A:1249:C:O2'	10:I:73:GLN:NE2	2.51	0.43
1:A:1272:G:O2'	1:A:1273:G:H5'	2.18	0.43
1:A:1394:A:C5	1:A:1501:C:H4'	2.53	0.43
1:A:1490:C:O2'	1:A:1491:G:H5'	2.18	0.43
6:E:11:ILE:HG23	6:E:105:VAL:HG22	2.00	0.43
12:K:74:ALA:C	12:K:76:GLY:H	2.26	0.43
16:O:70:LEU:C	16:O:72:ARG:N	2.76	0.43
1:A:115:G:O2'	1:A:116:A:OP2	2.33	0.43
1:A:182:U:O4	1:A:223:U:H1'	2.18	0.43
1:A:521:G:O2'	1:A:522:C:H5'	2.18	0.43
1:A:890:G:O2'	1:A:906:G:O6	2.36	0.43
1:A:1054:C:O2'	1:A:1055:A:H5''	2.18	0.43
1:A:1157:A:H4'	1:A:1158:C:O5'	2.18	0.43
1:A:1223:C:P	20:S:78:ARG:NH1	2.90	0.43
1:A:1353:G:OP2	22:V:3:LYS:HE2	2.18	0.43
1:A:1376:U:H2'	1:A:1377:A:C8	2.53	0.43
1:A:1519:A:H2'	1:A:1520:G:H5'	2.00	0.43
3:B:84:GLU:HG3	3:B:215:LEU:HB3	2.00	0.43
5:D:162:LEU:CD1	5:D:181:MET:HG2	2.48	0.43
8:G:18:TYR:CD2	8:G:59:LEU:HD22	2.52	0.43
10:I:47:LEU:C	10:I:49:PRO:HD2	2.42	0.43
11:J:12:ASP:O	11:J:15:THR:HG22	2.18	0.43
1:A:169:C:O2'	1:A:170:U:H5'	2.18	0.43
1:A:264:U:H4'	18:Q:63:ARG:HD3	1.99	0.43
1:A:352:C:H4'	1:A:354:G:OP1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:586:C:O2'	1:A:878:G:H4'	2.18	0.43
1:A:992:U:O2'	1:A:993:G:OP2	2.31	0.43
1:A:1301:U:O2'	1:A:1302:U:P	2.77	0.43
3:B:81:VAL:O	3:B:82:ARG:C	2.61	0.43
4:C:92:ALA:C	4:C:94:LEU:N	2.70	0.43
4:C:99:VAL:CG2	4:C:100:ALA:N	2.81	0.43
5:D:11:LEU:O	5:D:12:CYS:C	2.61	0.43
5:D:191:ARG:HD2	5:D:191:ARG:C	2.42	0.43
7:F:36:ARG:NH1	7:F:38:GLU:HG2	2.34	0.43
8:G:151:TYR:N	8:G:151:TYR:CD1	2.85	0.43
11:J:12:ASP:HB3	11:J:15:THR:HB	2.00	0.43
11:J:90:LEU:N	11:J:91:PRO:HD2	2.29	0.43
13:L:34:ARG:HB3	13:L:105:TYR:HE1	1.83	0.43
21:T:54:LYS:HA	21:T:57:ARG:HD3	2.00	0.43
1:A:186:C:H2'	1:A:187:C:C6	2.53	0.43
1:A:926:G:H3'	1:A:1505:G:H21	1.83	0.43
1:A:1003(A):G:H2'	1:A:1004:A:C4'	2.47	0.43
1:A:1111:A:H2'	1:A:1112:C:H6	1.82	0.43
1:A:1117:G:N2	1:A:1180:A:H1'	2.33	0.43
1:A:1426:C:O2'	1:A:1427:U:H5'	2.19	0.43
3:B:17:PHE:N	3:B:44:LEU:HD21	2.33	0.43
3:B:100:GLY:C	3:B:108:ILE:HD12	2.43	0.43
8:G:129:GLU:CB	8:G:131:LYS:HE2	2.49	0.43
9:H:1:MET:CG	9:H:2:LEU:N	2.77	0.43
17:P:38:TYR:O	17:P:49:LEU:HD12	2.19	0.43
20:S:51:VAL:HG12	20:S:52:TYR:H	1.82	0.43
1:A:1298:C:N4	8:G:114:ARG:HB3	2.33	0.43
1:A:1417:G:N2	1:A:1484:C:H42	2.17	0.43
1:A:1509:C:O2'	1:A:1510:U:H5'	2.18	0.43
3:B:85:ALA:O	3:B:90:MET:O	2.37	0.43
3:B:129:GLU:O	3:B:130:ARG:HB2	2.19	0.43
4:C:46:GLU:HB2	4:C:47:LEU:HD12	2.01	0.43
4:C:147:LYS:HE2	4:C:205:GLY:CA	2.48	0.43
5:D:209:ARG:HG2	5:D:209:ARG:NH1	2.32	0.43
10:I:97:LYS:CE	10:I:102:LEU:HD12	2.49	0.43
11:J:15:THR:HG23	11:J:94:VAL:HG22	2.01	0.43
14:M:117:VAL:CG1	14:M:118:ALA:N	2.81	0.43
15:N:53:LEU:HA	15:N:54:PRO:HD2	1.85	0.43
17:P:36:ILE:O	17:P:51:VAL:O	2.36	0.43
20:S:3:ARG:O	20:S:4:SER:HB3	2.18	0.43
22:V:2:GLY:C	22:V:4:GLY:N	2.73	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:755:G:H1'	9:H:1:MET:CE	2.48	0.43
1:A:1014:A:C2	1:A:1219:U:H1'	2.53	0.43
1:A:1243:C:H2'	1:A:1244:C:C6	2.54	0.43
1:A:1329:A:O2'	1:A:1330:U:H5'	2.19	0.43
3:B:12:GLU:CD	3:B:213:LEU:HD11	2.44	0.43
3:B:16:HIS:CD2	3:B:210:SER:OG	2.71	0.43
3:B:131:PRO:C	3:B:133:LYS:H	2.26	0.43
3:B:217:ARG:HA	3:B:220:ASP:OD2	2.19	0.43
5:D:174:LEU:O	5:D:186:LEU:HD12	2.18	0.43
5:D:189:PRO:HB2	5:D:194:LEU:CD2	2.48	0.43
8:G:80:VAL:O	8:G:82:GLY:N	2.51	0.43
9:H:39:LEU:HD13	9:H:39:LEU:HA	1.87	0.43
10:I:55:ALA:O	10:I:57:GLY:N	2.51	0.43
10:I:89:ASN:CG	10:I:91:ASP:HB2	2.43	0.43
11:J:53:PRO:O	11:J:54:PHE:O	2.37	0.43
11:J:85:LEU:O	11:J:87:THR:N	2.52	0.43
17:P:84:ALA:O	17:P:85:ARG:C	2.61	0.43
19:R:39:VAL:HG13	19:R:40:LEU:HD23	2.00	0.43
1:A:156:G:O2'	1:A:157:G:H5'	2.19	0.43
1:A:230:G:H2'	1:A:231:G:O4'	2.19	0.43
1:A:250:A:H2	1:A:274:A:C6	2.36	0.43
1:A:518:C:O2'	1:A:519:C:OP2	2.30	0.43
1:A:570:G:H1'	1:A:820:U:C4	2.53	0.43
1:A:718:G:H4'	12:K:117:ASN:HD21	1.84	0.43
1:A:741:G:H5''	16:O:39:LEU:HD12	2.00	0.43
1:A:1118:C:H2'	1:A:1119:C:C6	2.54	0.43
3:B:69:LEU:C	3:B:69:LEU:HD23	2.43	0.43
4:C:5:ILE:C	4:C:5:ILE:CD1	2.92	0.43
4:C:34:LEU:HD23	4:C:34:LEU:C	2.43	0.43
4:C:114:PRO:O	4:C:118:GLN:HG3	2.18	0.43
4:C:188:LEU:HD22	4:C:188:LEU:HA	1.84	0.43
6:E:43:LEU:HD22	6:E:44:GLY:N	2.34	0.43
6:E:124:GLY:O	6:E:126:ARG:N	2.52	0.43
10:I:92:TYR:O	10:I:93:ARG:C	2.62	0.43
13:L:83:VAL:CG2	13:L:84:LEU:N	2.74	0.43
14:M:26:GLY:C	14:M:28:ALA:H	2.26	0.43
20:S:40:ILE:HB	20:S:67:VAL:O	2.19	0.43
21:T:61:SER:O	21:T:65:LYS:HG3	2.18	0.43
1:A:386:C:C2'	1:A:387:U:H5'	2.49	0.43
1:A:448:A:O2'	1:A:449:C:C5'	2.66	0.43
1:A:502:G:OP1	13:L:118:SER:CB	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:542:G:H2'	1:A:543:C:H6	1.83	0.43
1:A:976:G:C8	1:A:1358:U:C2	3.07	0.43
1:A:1009:G:C6	1:A:1021:G:C6	3.07	0.43
1:A:1034:G:O2'	1:A:1035:A:H5'	2.19	0.43
1:A:1064:G:C2	1:A:1066:C:N4	2.87	0.43
1:A:1127:G:H21	1:A:1147:C:N4	2.17	0.43
1:A:1402:C:H2'	1:A:1403:C:O4'	2.18	0.43
1:A:1424:C:O2'	1:A:1425:U:H5'	2.19	0.43
3:B:131:PRO:C	3:B:133:LYS:N	2.77	0.43
5:D:156:GLU:HG2	5:D:160:GLN:NE2	2.21	0.43
5:D:163:GLU:OE2	5:D:166:LYS:HE3	2.19	0.43
8:G:151:TYR:OH	12:K:54:ARG:NE	2.52	0.43
9:H:60:ARG:CG	9:H:60:ARG:NH1	2.80	0.43
13:L:60:LEU:HD21	13:L:85:ILE:CD1	2.48	0.43
16:O:6:GLU:O	16:O:7:GLU:C	2.62	0.43
16:O:17:ARG:HD3	16:O:26:GLU:CD	2.44	0.43
16:O:39:LEU:HD23	16:O:39:LEU:C	2.43	0.43
1:A:31:G:H1	1:A:48:C:H5''	1.83	0.43
1:A:129(A):G:C2	1:A:190(E):U:H5'	2.54	0.43
1:A:421:U:H5'	1:A:422:C:C5	2.54	0.43
1:A:446:G:C2'	1:A:447:G:H5'	2.49	0.43
3:B:34:ALA:O	3:B:41:ILE:N	2.51	0.43
3:B:120:ALA:O	3:B:124:SER:HB3	2.19	0.43
3:B:218:ALA:O	3:B:222:ILE:HG13	2.18	0.43
4:C:7:PRO:CG	4:C:184:TYR:HB2	2.49	0.43
5:D:61:LYS:HA	5:D:203:VAL:HG22	2.00	0.43
5:D:114:ARG:NH1	5:D:114:ARG:CG	2.82	0.43
11:J:6:ILE:HG13	11:J:71:LEU:O	2.19	0.43
11:J:55:LYS:O	11:J:56:HIS:HB2	2.18	0.43
13:L:102:ARG:HE	13:L:102:ARG:HB3	1.69	0.43
20:S:20:LEU:HB3	20:S:23:ASN:HD22	1.84	0.43
21:T:72:LEU:O	21:T:73:HIS:O	2.36	0.43
1:A:92:C:O2'	1:A:93:G:H5'	2.19	0.43
1:A:386:C:O2'	1:A:387:U:H5'	2.18	0.43
1:A:434:U:H2'	1:A:435:C:H6	1.78	0.43
1:A:452:A:O2'	1:A:453:A:O4'	2.24	0.43
1:A:620:C:H2'	1:A:621:A:O4'	2.18	0.43
1:A:688:G:N3	1:A:704:A:C2	2.87	0.43
1:A:761:G:H2'	1:A:762:C:H6	1.83	0.43
1:A:1060:C:OP1	15:N:45:ARG:NH2	2.49	0.43
1:A:1097:C:H2'	1:A:1098:C:C6	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1221:G:H4'	20:S:53:ASN:O	2.18	0.43
1:A:1227:A:OP1	20:S:80:TYR:OH	2.34	0.43
5:D:150:GLU:C	5:D:152:SER:N	2.77	0.43
7:F:78:GLU:O	7:F:81:ILE:HG13	2.18	0.43
10:I:7:THR:O	10:I:15:ALA:O	2.37	0.43
10:I:36:TYR:HD2	10:I:37:PHE:CE2	2.37	0.43
10:I:44:VAL:CG1	10:I:51:ARG:NH2	2.82	0.43
11:J:3:LYS:HG3	11:J:75:ILE:HG23	2.01	0.43
11:J:30:SER:HB2	11:J:80:LYS:HB3	2.00	0.43
11:J:39:PRO:O	11:J:69:ASN:O	2.37	0.43
11:J:51:ARG:H	11:J:59:SER:HB2	1.83	0.43
12:K:84:VAL:CG2	19:R:88:LYS:HD3	2.44	0.43
14:M:37:THR:CG2	14:M:39:ILE:HD11	2.49	0.43
14:M:123:ALA:O	14:M:125:ARG:N	2.51	0.43
17:P:12:LYS:C	17:P:14:ASN:H	2.27	0.43
17:P:65:GLN:HA	17:P:66:PRO:HD2	1.85	0.43
21:T:92:LEU:HD23	21:T:92:LEU:HA	1.88	0.43
1:A:54:C:H2'	1:A:352:C:H41	1.84	0.42
1:A:720:C:H2'	1:A:721:G:C8	2.54	0.42
1:A:849:C:O2'	1:A:850:U:H5'	2.19	0.42
1:A:1262:C:O2'	1:A:1263:C:H5'	2.19	0.42
1:A:1280:A:O4'	11:J:41:PRO:HG3	2.19	0.42
8:G:69:VAL:HG12	8:G:69:VAL:O	2.19	0.42
8:G:75:VAL:CG1	8:G:86:GLN:HB3	2.49	0.42
10:I:100:GLY:O	10:I:101:PHE:C	2.62	0.42
16:O:8:LYS:HE3	16:O:31:LEU:HD23	2.01	0.42
17:P:19:ILE:N	17:P:37:GLY:O	2.52	0.42
17:P:21:VAL:HG12	17:P:22:THR:N	2.33	0.42
17:P:40:ASP:OD2	17:P:40:ASP:C	2.62	0.42
21:T:57:ARG:HH11	21:T:57:ARG:CG	2.32	0.42
1:A:370:C:H2'	1:A:371:G:H8	1.83	0.42
1:A:815:A:N6	1:A:1509:C:H1'	2.34	0.42
1:A:923:A:O4'	1:A:1398:A:C2	2.72	0.42
1:A:1250:A:C4'	10:I:68:GLY:H	2.28	0.42
1:A:1360:A:H2'	1:A:1361:G:O4'	2.18	0.42
1:A:1368:G:OP2	10:I:112:LYS:HD2	2.19	0.42
4:C:7:PRO:HG2	4:C:184:TYR:CB	2.49	0.42
4:C:188:LEU:HD13	4:C:195:VAL:HG13	2.01	0.42
6:E:15:ARG:CD	6:E:26:PHE:CD2	3.01	0.42
8:G:99:LEU:O	8:G:100:ALA:C	2.62	0.42
8:G:145:ALA:O	8:G:147:ALA:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:32:PHE:HE1	13:L:86:ARG:HB2	1.84	0.42
20:S:10:PHE:O	20:S:39:THR:HB	2.19	0.42
20:S:67:VAL:HG12	20:S:68:GLY:N	2.33	0.42
1:A:265:G:H2'	1:A:267:C:H5	1.85	0.42
1:A:656:C:O2'	16:O:28:GLN:OE1	2.30	0.42
1:A:738:C:P	7:F:92:LYS:HE3	2.59	0.42
1:A:748:C:H1'	1:A:749:C:C5	2.53	0.42
1:A:1222:G:O2'	1:A:1223:C:H5'	2.19	0.42
1:A:1279:A:O2'	1:A:1281:U:OP2	2.37	0.42
3:B:19:HIS:NE2	3:B:206:ASP:CB	2.82	0.42
3:B:213:LEU:C	3:B:213:LEU:CD2	2.92	0.42
4:C:175:LEU:HD11	4:C:201:TYR:CE2	2.54	0.42
6:E:36:ASP:C	6:E:38:GLN:N	2.75	0.42
7:F:23:LYS:HE2	7:F:23:LYS:HB3	1.86	0.42
7:F:80:ARG:HG2	7:F:80:ARG:HH11	1.84	0.42
8:G:148:ASN:C	8:G:150:ALA:N	2.77	0.42
11:J:51:ARG:N	11:J:59:SER:HB2	2.34	0.42
17:P:17:TYR:HE1	17:P:41:PRO:HG2	1.83	0.42
18:Q:65:ILE:O	18:Q:65:ILE:HG22	2.19	0.42
20:S:71:LEU:O	20:S:74:PHE:N	2.39	0.42
21:T:58:LYS:O	21:T:62:LEU:HG	2.19	0.42
1:A:20:U:O2'	1:A:21:G:H5'	2.19	0.42
1:A:41:G:H2'	1:A:42:G:C8	2.54	0.42
1:A:496:A:H4'	1:A:497:A:OP1	2.19	0.42
1:A:925:G:C2	1:A:927:G:C8	3.07	0.42
1:A:1010:G:H2'	1:A:1011:G:H8	1.84	0.42
1:A:1033:G:H2'	1:A:1034:G:C8	2.54	0.42
1:A:1061:G:H2'	1:A:1062:U:H5'	2.00	0.42
1:A:1501:C:OP2	1:A:1504:G:H2'	2.19	0.42
3:B:70:PHE:O	3:B:92:TYR:HA	2.19	0.42
3:B:90:MET:HA	3:B:91:PRO:HD3	1.85	0.42
3:B:164:VAL:HG12	3:B:186:ALA:HB1	2.01	0.42
3:B:208:ILE:HG21	3:B:239:VAL:HA	2.01	0.42
4:C:86:VAL:O	4:C:90:GLU:HB2	2.20	0.42
5:D:152:SER:O	5:D:154:ASN:N	2.53	0.42
5:D:199:ASN:C	5:D:199:ASN:HD22	2.27	0.42
6:E:43:LEU:N	6:E:136:MET:HE2	2.34	0.42
7:F:33:TYR:CB	7:F:75:LEU:HD23	2.45	0.42
8:G:75:VAL:HG11	8:G:86:GLN:HB3	2.01	0.42
10:I:5:TYR:CG	10:I:6:GLY:N	2.87	0.42
10:I:99:LEU:HB3	10:I:101:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:46:ARG:HD3	11:J:64:GLU:HB3	2.01	0.42
15:N:27:CYS:SG	15:N:29:ARG:CB	3.04	0.42
17:P:52:ASP:OD2	17:P:55:ARG:HG3	2.19	0.42
17:P:71:ARG:HG3	17:P:80:PHE:CZ	2.54	0.42
19:R:87:ARG:HH11	19:R:87:ARG:CG	2.28	0.42
21:T:11:SER:C	21:T:13:LEU:H	2.27	0.42
22:V:2:GLY:O	22:V:4:GLY:N	2.53	0.42
1:A:42:G:H2'	1:A:43:C:H6	1.85	0.42
1:A:220:G:O2'	1:A:221:C:H5'	2.19	0.42
1:A:376:G:OP2	17:P:67:THR:HG21	2.20	0.42
1:A:397:A:H3'	1:A:397:A:N3	2.34	0.42
1:A:401:C:O2'	1:A:402:G:H5'	2.19	0.42
1:A:439:A:C4	1:A:497:A:C2	3.08	0.42
1:A:1240:U:P	8:G:116:ALA:HB2	2.59	0.42
1:A:1256:A:H5'	1:A:1258:G:C1'	2.49	0.42
1:A:1391:U:H2'	1:A:1392:G:H8	1.79	0.42
3:B:142:LEU:O	3:B:143:GLU:C	2.60	0.42
4:C:33:LEU:C	4:C:33:LEU:CD2	2.92	0.42
7:F:78:GLU:HA	7:F:81:ILE:CD1	2.49	0.42
12:K:40:ILE:HG23	12:K:75:TYR:CE2	2.55	0.42
13:L:89:ARG:O	13:L:99:HIS:HE1	2.02	0.42
17:P:48:TRP:O	17:P:49:LEU:HB2	2.20	0.42
1:A:344:A:H5''	1:A:345:C:H5	1.85	0.42
1:A:644:G:C5	1:A:645:C:C5	3.08	0.42
1:A:782:A:C6	1:A:801:U:C2	3.08	0.42
1:A:1113:C:H4'	4:C:14:ILE:CD1	2.46	0.42
1:A:1113:C:O2'	1:A:1114:C:H5'	2.19	0.42
4:C:84:ILE:O	4:C:84:ILE:HG12	2.19	0.42
4:C:178:LEU:O	4:C:179:ARG:CB	2.66	0.42
5:D:61:LYS:NZ	5:D:62:GLN:NE2	2.67	0.42
5:D:150:GLU:O	5:D:152:SER:N	2.53	0.42
6:E:125:SER:C	6:E:127:ASN:H	2.27	0.42
10:I:33:PHE:C	10:I:35:GLU:H	2.27	0.42
10:I:127:LYS:N	10:I:127:LYS:HD2	2.35	0.42
14:M:10:PRO:HB3	14:M:18:ALA:O	2.19	0.42
14:M:49:THR:HB	14:M:52:GLU:HG3	2.00	0.42
17:P:58:TYR:C	17:P:61:SER:HB3	2.43	0.42
20:S:22:LEU:CD2	20:S:28:LYS:HD2	2.49	0.42
20:S:31:ILE:HG22	20:S:32:LYS:N	2.35	0.42
20:S:40:ILE:HG21	20:S:62:ILE:HD13	2.02	0.42
21:T:56:MET:HE2	21:T:88:VAL:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:U:H2'	1:A:91:C:C6	2.55	0.42
1:A:323:U:H2'	1:A:324:G:O4'	2.20	0.42
1:A:411:A:C2	1:A:431:A:N6	2.88	0.42
1:A:449:C:O2	17:P:42:ARG:HD2	2.20	0.42
1:A:687:A:N1	1:A:700:G:O2'	2.48	0.42
1:A:731:G:OP1	1:A:766:A:H1'	2.20	0.42
1:A:1031:G:H2'	1:A:1032:G:H8	1.85	0.42
1:A:1206:G:C6	1:A:1207:G:C5	3.08	0.42
1:A:1403:C:H1'	1:A:1500:A:N1	2.35	0.42
4:C:134:ILE:HG23	4:C:151:VAL:HB	2.01	0.42
6:E:124:GLY:O	6:E:125:SER:C	2.63	0.42
7:F:27:GLN:HA	7:F:27:GLN:NE2	2.34	0.42
8:G:116:ALA:HA	8:G:119:ARG:NH2	2.35	0.42
9:H:45:ILE:HG13	9:H:47:GLY:H	1.85	0.42
10:I:93:ARG:O	10:I:95:LYS:N	2.53	0.42
11:J:8:LEU:CD1	11:J:20:ALA:HB2	2.49	0.42
1:A:275:G:H5'	18:Q:14:LYS:HD3	2.02	0.42
1:A:429:U:OP2	5:D:36:ARG:NH1	2.52	0.42
1:A:460:A:N7	1:A:462:G:C6	2.88	0.42
1:A:851:G:H2'	1:A:852:G:H8	1.85	0.42
1:A:862:C:O4'	1:A:874:G:H4'	2.20	0.42
1:A:1041:A:H2'	1:A:1042:G:C8	2.55	0.42
1:A:1131:G:H2'	1:A:1132:C:C6	2.54	0.42
1:A:1231:G:OP1	10:I:127:LYS:NZ	2.53	0.42
1:A:1342:C:O2'	1:A:1343:G:H5'	2.20	0.42
3:B:85:ALA:CB	3:B:92:TYR:HB3	2.50	0.42
4:C:19:GLU:HG2	4:C:54:ARG:HE	1.85	0.42
4:C:64:VAL:HB	4:C:99:VAL:CB	2.49	0.42
4:C:116:VAL:O	4:C:119:ARG:HB3	2.20	0.42
5:D:57:ARG:HB3	5:D:206:PHE:HB2	2.00	0.42
5:D:126:ILE:HG22	5:D:127:THR:N	2.35	0.42
9:H:7:ALA:HB2	9:H:85:ARG:CD	2.50	0.42
10:I:26:VAL:HG12	10:I:28:VAL:HG23	2.01	0.42
10:I:48:GLU:N	10:I:49:PRO:CD	2.81	0.42
10:I:114:TYR:CD1	11:J:60:ARG:HB2	2.55	0.42
11:J:34:VAL:HG22	11:J:74:ILE:CG2	2.48	0.42
11:J:81:THR:C	11:J:83:GLU:N	2.78	0.42
12:K:50:TYR:HD1	12:K:60:ALA:HB2	1.85	0.42
12:K:56:GLY:O	12:K:57:THR:C	2.63	0.42
13:L:60:LEU:HD23	13:L:66:VAL:HG22	2.00	0.42
14:M:13:LYS:O	14:M:45:VAL:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:C:H5''	18:Q:68:ARG:NH2	2.35	0.42
1:A:321:A:H2'	1:A:322:C:C6	2.55	0.42
1:A:858:G:O2'	1:A:859:A:H5'	2.20	0.42
1:A:975:A:C4'	1:A:976:G:H5'	2.42	0.42
1:A:1006:C:O2'	1:A:1007:C:H5'	2.20	0.42
1:A:1015:A:H2'	1:A:1016:A:C8	2.55	0.42
1:A:1231:G:H5''	10:I:126:SER:CB	2.49	0.42
1:A:1508:G:O2'	1:A:1509:C:H5'	2.18	0.42
3:B:97:TRP:HH2	3:B:176:GLU:OE1	2.03	0.42
3:B:126:GLU:O	3:B:127:ILE:C	2.62	0.42
3:B:189:ASP:OD1	3:B:205:ASP:HB3	2.20	0.42
4:C:126:ARG:O	4:C:127:ARG:HB2	2.20	0.42
5:D:78:LEU:HA	5:D:78:LEU:HD23	1.73	0.42
5:D:170:VAL:CG1	5:D:174:LEU:HB2	2.45	0.42
6:E:80:ILE:HD12	6:E:80:ILE:N	2.29	0.42
10:I:82:ALA:O	10:I:96:LEU:HD21	2.19	0.42
10:I:89:ASN:C	10:I:91:ASP:N	2.77	0.42
11:J:47:PHE:N	11:J:63:PHE:O	2.48	0.42
12:K:115:PRO:C	12:K:117:ASN:H	2.28	0.42
12:K:122:LYS:O	12:K:123:LYS:C	2.62	0.42
14:M:73:GLU:O	14:M:76:ALA:N	2.52	0.42
16:O:59:MET:HE3	16:O:59:MET:HB2	1.92	0.42
17:P:10:GLY:HA3	17:P:14:ASN:O	2.19	0.42
20:S:7:LYS:O	20:S:7:LYS:CG	2.68	0.42
21:T:93:GLU:HA	21:T:93:GLU:OE2	2.19	0.42
1:A:557:G:C6	1:A:558:G:C6	3.08	0.42
1:A:724:G:O2'	1:A:725:G:H5'	2.20	0.42
1:A:930:C:C2'	1:A:931:C:H5'	2.50	0.42
1:A:965:A:C2	1:A:969:A:C2	3.08	0.42
1:A:992:U:O2'	1:A:993:G:P	2.78	0.42
4:C:191:THR:HG21	4:C:193:TYR:CE1	2.55	0.42
6:E:7:GLU:O	6:E:34:VAL:HA	2.20	0.42
6:E:144:THR:N	6:E:147:ASP:OD2	2.48	0.42
9:H:4:ASP:CG	9:H:85:ARG:HH11	2.28	0.42
11:J:22:LYS:NZ	11:J:91:PRO:HD3	2.34	0.42
13:L:50:SER:O	13:L:51:ALA:CB	2.68	0.42
14:M:23:TYR:HB3	14:M:67:GLU:HA	2.02	0.42
1:A:50:A:N6	1:A:361:G:H4'	2.35	0.41
1:A:431:A:O2'	1:A:432:A:H5'	2.20	0.41
1:A:833:U:H2'	1:A:834:C:C6	2.55	0.41
1:A:1239:A:H62	1:A:1299:A:N6	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:110:LEU:O	6:E:113:ALA:HB3	2.20	0.41
12:K:60:ALA:C	12:K:62:GLN:N	2.75	0.41
13:L:73:GLU:OE2	13:L:73:GLU:HA	2.19	0.41
14:M:80:ARG:O	14:M:82:MET:N	2.53	0.41
21:T:45:GLN:C	21:T:45:GLN:CD	2.87	0.41
21:T:62:LEU:N	21:T:62:LEU:HD23	2.35	0.41
1:A:57:G:H2'	1:A:58:C:O4'	2.19	0.41
1:A:124:G:C6	1:A:125:U:C4	3.08	0.41
1:A:182:U:H6	1:A:182:U:H5'	1.85	0.41
1:A:281:G:HO2'	1:A:282:A:P	2.43	0.41
1:A:285:G:C2'	1:A:286:G:H5'	2.50	0.41
1:A:312:C:H2'	1:A:313:A:C8	2.55	0.41
1:A:397:A:C6	1:A:548:G:N7	2.88	0.41
1:A:401:C:H2'	1:A:402:G:C8	2.46	0.41
1:A:637:G:O2'	1:A:638:G:H5'	2.20	0.41
3:B:69:LEU:HB3	3:B:162:ILE:HG12	2.02	0.41
3:B:127:ILE:HB	3:B:128:GLU:OE1	2.19	0.41
3:B:173:ALA:O	3:B:174:VAL:C	2.63	0.41
4:C:47:LEU:CD2	4:C:68:VAL:HG11	2.51	0.41
8:G:14:PRO:HB2	8:G:19:GLY:O	2.19	0.41
17:P:26:ARG:HG2	17:P:26:ARG:HH11	1.85	0.41
18:Q:45:HIS:HB2	18:Q:69:LYS:HZ3	1.85	0.41
20:S:33:THR:HG22	20:S:34:TRP:H	1.84	0.41
20:S:33:THR:CG2	20:S:34:TRP:N	2.81	0.41
21:T:102:GLY:C	21:T:104:LEU:H	2.26	0.41
1:A:224:C:H2'	1:A:225:C:C6	2.54	0.41
1:A:416:G:C5	1:A:417:C:C4	3.09	0.41
1:A:626:U:O2'	1:A:627:G:H5'	2.19	0.41
1:A:767:A:H2'	1:A:768:A:H8	1.85	0.41
1:A:820:U:H4'	1:A:821:G:OP2	2.20	0.41
1:A:1103:C:H2'	1:A:1104:G:O4'	2.21	0.41
1:A:1169:A:H2'	1:A:1171:G:O4'	2.20	0.41
1:A:1351:U:O2'	1:A:1352:C:H5'	2.19	0.41
3:B:53:ARG:NH1	3:B:53:ARG:HG2	2.35	0.41
3:B:109:SER:O	3:B:111:ARG:N	2.53	0.41
3:B:115:LEU:HG	3:B:153:ARG:NH2	2.36	0.41
3:B:130:ARG:NH2	4:C:207:VAL:CG2	2.81	0.41
5:D:43:HIS:O	5:D:45:GLN:N	2.53	0.41
5:D:61:LYS:NZ	5:D:72:GLU:OE2	2.53	0.41
5:D:65:ARG:HB2	5:D:75:PHE:CE1	2.55	0.41
5:D:96:LEU:N	5:D:96:LEU:CD1	2.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:144:THR:C	6:E:146:ALA:N	2.75	0.41
9:H:1:MET:CG	9:H:2:LEU:H	2.21	0.41
9:H:24:THR:HG23	9:H:61:VAL:HB	2.02	0.41
10:I:19:LEU:HB3	10:I:59:PHE:CE2	2.54	0.41
10:I:83:ARG:C	10:I:85:LEU:N	2.77	0.41
21:T:94:ALA:O	21:T:95:ALA:CB	2.68	0.41
1:A:255:G:O6	1:A:266:G:O6	2.38	0.41
1:A:309:G:O2'	1:A:310:G:H5'	2.19	0.41
1:A:448:A:C4	1:A:487:A:C2	3.08	0.41
1:A:926:G:H5'	1:A:927:G:O5'	2.20	0.41
1:A:1198:G:O2'	1:A:1199:U:H5'	2.21	0.41
1:A:1468:A:H2'	1:A:1469:G:O4'	2.20	0.41
5:D:65:ARG:HE	5:D:72:GLU:N	2.17	0.41
5:D:114:ARG:HH11	5:D:114:ARG:CG	2.23	0.41
7:F:101:ALA:HB2	19:R:28:GLU:CB	2.46	0.41
8:G:23:VAL:HG13	8:G:43:PHE:CE2	2.56	0.41
9:H:119:LEU:HB3	9:H:123:GLU:HB3	2.02	0.41
18:Q:51:TYR:CD1	18:Q:73:VAL:HG11	2.56	0.41
1:A:281:G:O2'	1:A:282:A:C8	2.73	0.41
1:A:325:A:OP2	21:T:70:SER:HB3	2.21	0.41
1:A:393:A:OP2	17:P:12:LYS:CE	2.67	0.41
1:A:393:A:C2	1:A:394:G:C8	3.08	0.41
1:A:451:A:C2	1:A:480:U:C4	3.08	0.41
1:A:607:A:O2'	1:A:608:A:H5'	2.21	0.41
1:A:622:A:C8	1:A:623:C:C6	3.09	0.41
1:A:1221:G:O2'	1:A:1222:G:H5'	2.20	0.41
3:B:16:HIS:HE1	3:B:213:LEU:HB3	1.85	0.41
3:B:67:THR:HA	3:B:90:MET:CE	2.44	0.41
3:B:180:LEU:HD23	3:B:180:LEU:HA	1.78	0.41
4:C:24:ALA:O	4:C:26:LYS:HE2	2.20	0.41
6:E:92:LYS:HB3	6:E:119:LEU:HB2	2.01	0.41
8:G:75:VAL:HG21	8:G:144:MET:HB3	2.02	0.41
8:G:77:SER:O	8:G:78:ARG:HB2	2.19	0.41
8:G:136:LYS:O	8:G:140:ASP:OD1	2.38	0.41
9:H:73:ASP:OD2	9:H:75:ARG:HB2	2.21	0.41
12:K:100:ALA:O	12:K:102:GLY:N	2.53	0.41
14:M:6:GLY:C	14:M:7:VAL:HG22	2.46	0.41
14:M:22:ILE:HD12	14:M:25:ILE:CD1	2.49	0.41
14:M:105:THR:O	14:M:106:ASN:C	2.64	0.41
14:M:120:LYS:HE2	14:M:123:ALA:CB	2.50	0.41
1:A:401:C:H1'	1:A:622:A:H1'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:C:C5	1:A:459:G:N7	2.89	0.41
1:A:560:U:O2'	1:A:561:U:OP2	2.28	0.41
1:A:603:U:O2'	1:A:604:G:H5'	2.20	0.41
1:A:899:C:H2'	1:A:900:A:C8	2.55	0.41
1:A:1050:G:O2'	1:A:1051:C:H5'	2.20	0.41
1:A:1079:G:O3'	6:E:14:ARG:NH2	2.53	0.41
3:B:43:ASP:OD1	3:B:43:ASP:C	2.62	0.41
3:B:140:HIS:O	3:B:141:GLU:C	2.63	0.41
3:B:155:LEU:HD23	3:B:155:LEU:HA	1.90	0.41
5:D:3:ARG:HA	5:D:3:ARG:HD3	1.80	0.41
5:D:43:HIS:O	5:D:44:GLY:C	2.63	0.41
5:D:87:GLY:O	5:D:88:VAL:C	2.64	0.41
5:D:159:ARG:O	5:D:163:GLU:N	2.54	0.41
5:D:199:ASN:ND2	5:D:199:ASN:C	2.79	0.41
6:E:143:ARG:HA	6:E:143:ARG:HD3	1.78	0.41
9:H:61:VAL:O	9:H:63:LEU:HD13	2.20	0.41
12:K:85:ARG:NH1	12:K:85:ARG:HG3	2.34	0.41
16:O:33:THR:OG1	16:O:85:LEU:HD13	2.21	0.41
17:P:81:ARG:HD3	17:P:83:GLU:HG2	2.03	0.41
20:S:78:ARG:H	20:S:78:ARG:HG2	1.57	0.41
1:A:184:G:H2'	1:A:185:A:H8	1.86	0.41
1:A:426:G:OP1	5:D:38:TYR:OH	2.38	0.41
1:A:463:A:O2'	1:A:474:G:H5'	2.21	0.41
1:A:685:G:C2	1:A:686:U:C4	3.08	0.41
1:A:970:C:O2	14:M:126:LYS:C	2.64	0.41
4:C:148:GLY:HA3	4:C:172:ARG:O	2.21	0.41
4:C:191:THR:HB	4:C:194:GLY:H	1.86	0.41
6:E:52:PRO:O	6:E:53:LEU:C	2.64	0.41
6:E:144:THR:CG2	6:E:145:LYS:N	2.84	0.41
8:G:18:TYR:H	8:G:18:TYR:HD1	1.67	0.41
9:H:5:PRO:O	9:H:8:ASP:HB3	2.21	0.41
9:H:6:ILE:O	9:H:10:LEU:HG	2.21	0.41
10:I:106:ALA:O	10:I:108:VAL:HG23	2.20	0.41
10:I:126:SER:OG	10:I:127:LYS:N	2.52	0.41
12:K:33:THR:OG1	12:K:34:ASP:N	2.53	0.41
12:K:84:VAL:CG1	12:K:95:ILE:HD11	2.46	0.41
12:K:99:GLN:HA	12:K:105:VAL:CG2	2.51	0.41
16:O:33:THR:HG23	16:O:63:ARG:HH12	1.86	0.41
16:O:61:GLY:O	16:O:62:GLN:C	2.64	0.41
16:O:77:ARG:O	16:O:80:ALA:HB3	2.20	0.41
18:Q:53:LEU:HD12	18:Q:54:GLY:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:10:PHE:CD2	20:S:11:VAL:N	2.88	0.41
1:A:141:A:O2'	1:A:142:G:H5'	2.21	0.41
1:A:324:G:N2	1:A:327:A:H8	2.19	0.41
1:A:370:C:C2'	1:A:371:G:H5'	2.50	0.41
1:A:452:A:O2'	17:P:72:ARG:HD2	2.20	0.41
1:A:502:G:H2'	1:A:503:C:H6	1.86	0.41
1:A:522:C:H2'	1:A:523:A:O4'	2.20	0.41
1:A:982:U:H5''	15:N:6:LEU:CD1	2.51	0.41
3:B:60:ASP:O	3:B:64:ARG:HB2	2.21	0.41
4:C:23:TYR:CD2	4:C:23:TYR:C	2.98	0.41
4:C:34:LEU:C	4:C:34:LEU:CD2	2.94	0.41
4:C:179:ARG:HD2	4:C:179:ARG:O	2.20	0.41
6:E:45:PHE:CE2	6:E:47:LYS:HE3	2.56	0.41
6:E:79:GLU:HA	6:E:91:LEU:O	2.21	0.41
8:G:15:ASP:C	8:G:17:VAL:H	2.28	0.41
8:G:51:GLN:OE1	8:G:51:GLN:HA	2.20	0.41
8:G:71:PRO:HG3	8:G:103:TRP:CH2	2.56	0.41
9:H:9:MET:HG3	9:H:26:VAL:HG21	2.02	0.41
15:N:36:PHE:O	15:N:36:PHE:CD1	2.74	0.41
19:R:40:LEU:C	19:R:42:ARG:N	2.76	0.41
21:T:56:MET:HG2	21:T:84:LEU:CD1	2.50	0.41
1:A:5:U:O2'	1:A:6:G:P	2.79	0.41
1:A:62:U:H2'	1:A:63:C:C6	2.56	0.41
1:A:132:C:H2'	1:A:133:U:O4'	2.21	0.41
1:A:273:A:N6	1:A:274:A:C6	2.89	0.41
1:A:645:C:O2'	1:A:646:U:H5'	2.21	0.41
1:A:652:U:H2'	1:A:752:G:N1	2.36	0.41
1:A:718:G:H1'	12:K:116:HIS:HA	2.03	0.41
1:A:821:G:H2'	1:A:822:C:C6	2.55	0.41
1:A:904:C:H2'	1:A:905:U:O4'	2.21	0.41
1:A:961:U:C2'	1:A:962:C:H5'	2.51	0.41
1:A:1080:A:C8	1:A:1081:G:H1'	2.56	0.41
1:A:1117:G:H4'	10:I:104:ARG:HH11	1.81	0.41
1:A:1126:U:H2'	1:A:1127:G:C8	2.56	0.41
1:A:1227:A:H2'	1:A:1228:C:O5'	2.21	0.41
1:A:1254:C:OP1	11:J:45:ARG:HD2	2.20	0.41
1:A:1257:U:O2'	1:A:1258:G:OP2	2.28	0.41
1:A:1442:G:N3	1:A:1442:G:C2'	2.84	0.41
3:B:73:THR:O	3:B:74:LYS:C	2.64	0.41
3:B:122:PHE:O	3:B:123:ALA:CB	2.67	0.41
3:B:224:GLN:C	3:B:226:ARG:N	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:25:GLY:C	4:C:26:LYS:HG2	2.46	0.41
5:D:149:ALA:O	5:D:150:GLU:C	2.64	0.41
6:E:143:ARG:NH1	9:H:77:GLU:CD	2.79	0.41
9:H:51:VAL:CG1	9:H:52:ASP:N	2.84	0.41
9:H:136:GLU:O	9:H:136:GLU:HG2	2.19	0.41
10:I:42:ARG:O	10:I:44:VAL:N	2.53	0.41
10:I:48:GLU:CA	10:I:51:ARG:NH1	2.79	0.41
10:I:93:ARG:HH11	10:I:97:LYS:HZ2	1.69	0.41
10:I:99:LEU:CB	10:I:101:PHE:CE1	3.03	0.41
11:J:4:ILE:HA	11:J:100:THR:HA	2.01	0.41
11:J:22:LYS:HE2	11:J:90:LEU:HD12	2.02	0.41
11:J:23:ILE:O	11:J:23:ILE:HG22	2.21	0.41
14:M:22:ILE:HG21	14:M:66:LEU:HD13	2.02	0.41
15:N:26:ARG:HH11	15:N:47:LEU:HG	1.80	0.41
18:Q:82:MET:O	18:Q:83:ASP:C	2.63	0.41
18:Q:86:GLU:O	18:Q:87:LYS:C	2.64	0.41
20:S:13:ASP:O	20:S:17:GLU:HG2	2.21	0.41
1:A:33:A:N3	13:L:32:PHE:HE2	2.18	0.41
1:A:586:C:O3'	9:H:89:PRO:HB2	2.20	0.41
1:A:922:G:H2'	1:A:923:A:C8	2.56	0.41
1:A:954:G:H2'	1:A:955:U:H6	1.85	0.41
1:A:994:A:OP1	1:A:994:A:C8	2.74	0.41
1:A:995:C:N3	1:A:1046:A:O2'	2.50	0.41
1:A:1006:C:N3	1:A:1023:G:O6	2.53	0.41
1:A:1317:C:C6	15:N:16:PHE:CD2	3.09	0.41
1:A:1337:G:H5''	1:A:1338:G:OP1	2.21	0.41
1:A:1450:U:H2'	1:A:1452:C:C5	2.56	0.41
1:A:1499:A:H1'	1:A:1520:G:H5'	2.03	0.41
3:B:20:GLU:O	3:B:39:ILE:HG23	2.21	0.41
3:B:33:TYR:HB3	3:B:41:ILE:O	2.21	0.41
4:C:8:ILE:O	4:C:10:PHE:N	2.54	0.41
5:D:8:VAL:HG11	5:D:21:LEU:HB3	2.03	0.41
8:G:41:ARG:O	8:G:44:TYR:N	2.54	0.41
9:H:60:ARG:HA	9:H:60:ARG:HD3	1.93	0.41
9:H:86:ILE:HD12	9:H:133:LEU:CD2	2.51	0.41
11:J:84:GLN:O	11:J:88:LEU:HB2	2.21	0.41
12:K:15:ALA:CA	12:K:77:MET:HA	2.50	0.41
14:M:8:GLU:C	14:M:9:ILE:HG13	2.46	0.41
1:A:7:G:H5''	1:A:298:A:H5'	2.03	0.40
1:A:8:A:C6	5:D:209:ARG:HB2	2.55	0.40
1:A:23:C:H2'	1:A:24:U:H6	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:G:OP2	17:P:75:ARG:NH1	2.53	0.40
1:A:893:C:H2'	1:A:894:G:H8	1.86	0.40
1:A:1033:G:H2'	1:A:1034:G:H8	1.86	0.40
1:A:1062:U:H2'	1:A:1063:C:C6	2.56	0.40
1:A:1158:C:C5	1:A:1160:G:C8	3.10	0.40
1:A:1256:A:O2'	1:A:1257:U:P	2.79	0.40
1:A:1305:G:OP1	22:V:2:GLY:N	2.53	0.40
3:B:126:GLU:HG2	3:B:129:GLU:OE1	2.20	0.40
4:C:206:GLU:O	4:C:207:VAL:O	2.39	0.40
6:E:127:ASN:O	6:E:131:ILE:HG12	2.20	0.40
8:G:104:LEU:HD23	8:G:134:ALA:CB	2.50	0.40
9:H:88:LYS:O	9:H:89:PRO:C	2.64	0.40
9:H:114:THR:C	9:H:116:LYS:N	2.78	0.40
10:I:86:VAL:CG1	10:I:90:PRO:HA	2.44	0.40
11:J:13:HIS:O	11:J:17:ASP:OD2	2.39	0.40
11:J:82:ILE:O	11:J:82:ILE:HG22	2.20	0.40
13:L:110:VAL:O	13:L:122:THR:CG2	2.63	0.40
14:M:44:ARG:HA	14:M:44:ARG:HD2	1.88	0.40
19:R:51:LEU:HA	19:R:52:PRO:HD3	1.91	0.40
19:R:87:ARG:NH1	19:R:87:ARG:CG	2.83	0.40
1:A:322:C:O2'	1:A:323:U:H5'	2.20	0.40
1:A:340:U:H2'	1:A:341:C:C6	2.56	0.40
1:A:423:G:C2'	1:A:424:G:H5'	2.52	0.40
1:A:791:G:C2'	1:A:792:A:H5'	2.48	0.40
1:A:1097:C:O2'	1:A:1168:A:N3	2.46	0.40
1:A:1152:A:H2'	1:A:1153:C:H6	1.86	0.40
1:A:1285:A:O2'	1:A:1286:A:OP2	2.36	0.40
1:A:1288:A:H2'	1:A:1289:A:C8	2.56	0.40
1:A:1291:G:H5''	8:G:41:ARG:NH2	2.37	0.40
1:A:1346:A:C5	8:G:10:ARG:NH2	2.89	0.40
3:B:96:ARG:O	3:B:98:LEU:HD23	2.21	0.40
3:B:200:ILE:HG22	3:B:201:ILE:N	2.36	0.40
3:B:236:TYR:HA	3:B:239:VAL:CG2	2.51	0.40
4:C:155:GLY:O	4:C:156:ARG:CB	2.68	0.40
5:D:187:ARG:HH21	5:D:188:LEU:CG	2.15	0.40
6:E:115:VAL:CG1	6:E:116:THR:N	2.85	0.40
8:G:156:TRP:OXT	8:G:156:TRP:CD1	2.75	0.40
10:I:78:LYS:CD	10:I:101:PHE:HD2	2.29	0.40
10:I:112:LYS:C	10:I:112:LYS:HD3	2.46	0.40
10:I:113:LYS:HD2	10:I:113:LYS:N	2.36	0.40
10:I:118:LYS:HB2	10:I:118:LYS:HZ2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:6:GLY:O	14:M:7:VAL:CG2	2.69	0.40
14:M:110:ARG:CG	14:M:110:ARG:NH1	2.84	0.40
18:Q:76:LEU:HD23	18:Q:77:VAL:C	2.46	0.40
19:R:16:PRO:O	19:R:17:SER:CB	2.68	0.40
20:S:45:VAL:C	20:S:47:HIS:N	2.79	0.40
21:T:36:LEU:HA	21:T:39:LYS:HB2	2.03	0.40
1:A:182:U:OP2	1:A:183:G:C8	2.74	0.40
1:A:294:U:H2'	1:A:295:C:C6	2.56	0.40
1:A:309:G:H1'	1:A:608:A:C2	2.57	0.40
1:A:344:A:O2'	1:A:345:C:OP1	2.34	0.40
1:A:474:G:H2'	1:A:475:G:C8	2.50	0.40
1:A:536:C:H2'	1:A:537:G:C8	2.56	0.40
1:A:671:G:H2'	1:A:672:U:O4'	2.22	0.40
1:A:679:C:H2'	1:A:680:C:C6	2.56	0.40
1:A:922:G:O2'	1:A:1398:A:N1	2.51	0.40
1:A:1152:A:O2'	1:A:1153:C:H5'	2.21	0.40
1:A:1404:C:H2'	1:A:1405:G:C8	2.56	0.40
1:A:1451:A:H4'	1:A:1452:C:OP2	2.22	0.40
3:B:18:GLY:HA2	3:B:41:ILE:HA	2.03	0.40
3:B:20:GLU:OE2	3:B:205:ASP:OD1	2.39	0.40
3:B:192:SER:OG	3:B:193:ASP:N	2.54	0.40
4:C:145:GLY:O	4:C:146:ALA:C	2.64	0.40
5:D:108:LEU:HD23	5:D:108:LEU:HA	1.89	0.40
6:E:99:GLY:O	6:E:117:ASP:HA	2.21	0.40
6:E:115:VAL:CG1	6:E:118:ILE:HG13	2.51	0.40
8:G:21:VAL:CG2	8:G:22:LEU:N	2.84	0.40
9:H:84:ARG:HE	9:H:84:ARG:HB3	1.51	0.40
9:H:133:LEU:C	9:H:133:LEU:HD23	2.46	0.40
10:I:89:ASN:OD1	10:I:91:ASP:HB2	2.21	0.40
11:J:23:ILE:CD1	11:J:23:ILE:H	2.33	0.40
11:J:38:ILE:CG2	11:J:39:PRO:HD2	2.52	0.40
13:L:83:VAL:CG2	13:L:100:ILE:HG23	2.51	0.40
21:T:42:GLN:CA	21:T:42:GLN:NE2	2.84	0.40
1:A:119:A:H4'	1:A:120:A:O5'	2.21	0.40
1:A:335:C:H2'	1:A:336:C:H6	1.86	0.40
1:A:455:C:H6	1:A:455:C:O5'	2.04	0.40
1:A:539:A:H2'	1:A:540:G:C8	2.57	0.40
1:A:760:G:H2'	1:A:761:G:C5'	2.51	0.40
1:A:981:U:H5'	15:N:21:TYR:CE1	2.55	0.40
1:A:1068:G:H8	1:A:1068:G:OP2	2.05	0.40
1:A:1139:G:O2'	1:A:1140:C:OP2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1481:U:H2'	1:A:1482:G:C8	2.56	0.40
3:B:14:GLY:C	3:B:15:VAL:CG2	2.94	0.40
3:B:30:ARG:HG3	3:B:31:TYR:CD2	2.56	0.40
3:B:85:ALA:HB1	3:B:92:TYR:HB3	2.04	0.40
4:C:36:ASP:HA	4:C:39:ILE:HD12	2.03	0.40
4:C:107:GLN:CD	4:C:107:GLN:N	2.70	0.40
5:D:70:ILE:HD11	5:D:100:ARG:NH1	2.36	0.40
5:D:163:GLU:C	5:D:165:MET:H	2.29	0.40
7:F:22:GLU:O	7:F:26:ILE:HG13	2.22	0.40
8:G:18:TYR:HD2	8:G:59:LEU:HB2	1.77	0.40
8:G:62:PHE:O	8:G:65:ALA:HB3	2.20	0.40
8:G:148:ASN:C	8:G:150:ALA:H	2.30	0.40
9:H:10:LEU:HD22	9:H:83:ILE:HD11	2.03	0.40
9:H:24:THR:HG23	9:H:24:THR:O	2.21	0.40
9:H:56:LYS:CB	9:H:57:PRO:HD2	2.51	0.40
9:H:91:ARG:HG3	13:L:7:ILE:HG13	2.03	0.40
10:I:97:LYS:C	10:I:99:LEU:N	2.77	0.40
11:J:51:ARG:NH1	11:J:51:ARG:CG	2.80	0.40
12:K:32:ILE:HG22	12:K:77:MET:HE2	2.03	0.40
12:K:33:THR:HG1	12:K:37:GLY:C	2.24	0.40
12:K:77:MET:CE	12:K:80:VAL:HG22	2.51	0.40
12:K:108:ILE:C	12:K:109:VAL:HG23	2.46	0.40
13:L:47:LYS:HB2	13:L:48:PRO:HD2	2.02	0.40
15:N:8:GLU:HB2	15:N:11:LYS:HD2	2.04	0.40
19:R:36:ASN:C	19:R:38:GLU:N	2.78	0.40
19:R:40:LEU:O	19:R:41:LYS:C	2.64	0.40
1:A:61:G:C2'	1:A:62:U:H5'	2.52	0.40
1:A:179:A:H2'	1:A:180:U:H6	1.86	0.40
1:A:420:U:C2'	1:A:421:U:H5''	2.51	0.40
1:A:570:G:N2	1:A:571:U:C2	2.90	0.40
1:A:928:G:O2'	1:A:929:G:H5'	2.20	0.40
1:A:1127:G:H1'	1:A:1148:U:N3	2.37	0.40
1:A:1178:G:P	10:I:97:LYS:NZ	2.95	0.40
1:A:1282:C:O2'	1:A:1283:G:H5'	2.21	0.40
1:A:1436:U:O2'	1:A:1437:C:H5'	2.22	0.40
3:B:8:LYS:CD	3:B:9:GLU:N	2.84	0.40
3:B:204:ASN:HD22	3:B:207:ALA:CB	2.35	0.40
4:C:108:ASN:HD22	4:C:111:LEU:CG	2.27	0.40
5:D:24:GLU:C	5:D:26:CYS:H	2.28	0.40
5:D:78:LEU:HD13	5:D:97:LEU:HD23	2.02	0.40
5:D:89:THR:O	5:D:90:GLY:C	2.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:34:VAL:HA	11:J:74:ILE:HG23	2.03	0.40
12:K:21:ILE:HD13	12:K:94:ALA:HB3	2.03	0.40
16:O:17:ARG:HH11	16:O:17:ARG:CG	2.30	0.40
16:O:31:LEU:H	16:O:31:LEU:CD1	2.31	0.40
19:R:34:TYR:CD1	19:R:35:ARG:HG3	2.56	0.40
19:R:36:ASN:O	19:R:39:VAL:HG12	2.21	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:157:ARG:NH1	3:B:157:ARG:NH1[7_555]	1.94	0.26

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%)	172 (74%)	34 (15%)	26 (11%)	0	2
4	C	204/239 (85%)	132 (65%)	44 (22%)	28 (14%)	0	1
5	D	206/209 (99%)	153 (74%)	37 (18%)	16 (8%)	1	5
6	E	148/162 (91%)	130 (88%)	15 (10%)	3 (2%)	6	27
7	F	99/101 (98%)	83 (84%)	13 (13%)	3 (3%)	3	20
8	G	153/156 (98%)	119 (78%)	23 (15%)	11 (7%)	1	6
9	H	136/138 (99%)	118 (87%)	15 (11%)	3 (2%)	5	26
10	I	125/128 (98%)	86 (69%)	26 (21%)	13 (10%)	0	2
11	J	96/105 (91%)	59 (62%)	19 (20%)	18 (19%)	0	0
12	K	117/129 (91%)	84 (72%)	23 (20%)	10 (8%)	0	4
13	L	122/135 (90%)	90 (74%)	22 (18%)	10 (8%)	0	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	M	123/126 (98%)	87 (71%)	20 (16%)	16 (13%)	0	1
15	N	58/61 (95%)	40 (69%)	9 (16%)	9 (16%)	0	1
16	O	86/89 (97%)	66 (77%)	18 (21%)	2 (2%)	5	25
17	P	86/88 (98%)	67 (78%)	14 (16%)	5 (6%)	1	9
18	Q	102/105 (97%)	83 (81%)	13 (13%)	6 (6%)	1	9
19	R	71/88 (81%)	51 (72%)	15 (21%)	5 (7%)	1	7
20	S	78/93 (84%)	56 (72%)	12 (15%)	10 (13%)	0	1
21	T	97/106 (92%)	66 (68%)	19 (20%)	12 (12%)	0	1
22	V	22/26 (85%)	17 (77%)	4 (18%)	1 (4%)	2	13
All	All	2361/2540 (93%)	1759 (74%)	395 (17%)	207 (9%)	0	4

All (207) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	8	LYS
3	B	16	HIS
3	B	17	PHE
3	B	21	ARG
3	B	24	TRP
3	B	123	ALA
4	C	4	LYS
4	C	15	THR
4	C	16	ARG
4	C	24	ALA
4	C	29	TYR
4	C	47	LEU
4	C	108	ASN
4	C	146	ALA
4	C	154	SER
4	C	179	ARG
4	C	189	ALA
4	C	206	GLU
5	D	29	PRO
5	D	36	ARG
6	E	16	THR
9	H	24	THR
9	H	83	ILE
9	H	91	ARG
10	I	7	THR

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Mol	Chain	Res	Type
10	I	43	ALA
10	I	44	VAL
10	I	101	PHE
11	J	30	SER
11	J	32	ALA
11	J	54	PHE
11	J	57	LYS
11	J	79	ARG
11	J	86	MET
12	K	57	THR
12	K	101	SER
13	L	27	LEU
13	L	28	LYS
13	L	47	LYS
14	M	63	THR
14	M	67	GLU
14	M	107	ALA
14	M	122	LYS
14	M	124	PRO
15	N	22	THR
15	N	29	ARG
15	N	59	ALA
15	N	60	SER
16	O	88	ARG
17	P	83	GLU
18	Q	69	LYS
18	Q	80	GLY
18	Q	81	ARG
18	Q	98	LEU
18	Q	104	LYS
19	R	87	ARG
20	S	6	LYS
20	S	9	VAL
20	S	71	LEU
21	T	11	SER
21	T	73	HIS
21	T	99	LEU
3	B	9	GLU
3	B	18	GLY
3	B	20	GLU
3	B	23	ARG
3	B	126	GLU

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Mol	Chain	Res	Type
3	B	127	ILE
3	B	190	THR
3	B	204	ASN
3	B	225	ALA
4	C	61	ALA
5	D	4	TYR
5	D	31	CYS
5	D	44	GLY
5	D	63	LYS
5	D	153	ARG
5	D	175	SER
6	E	11	ILE
6	E	125	SER
7	F	16	GLN
7	F	39	LYS
8	G	7	ALA
8	G	53	LYS
8	G	155	ARG
10	I	23	ASN
10	I	41	VAL
10	I	94	ALA
11	J	33	GLN
11	J	34	VAL
11	J	59	SER
11	J	60	ARG
11	J	72	VAL
12	K	49	GLY
12	K	50	TYR
12	K	78	GLN
12	K	89	ALA
13	L	48	PRO
13	L	51	ALA
13	L	121	GLY
14	M	6	GLY
14	M	42	ALA
14	M	85	GLY
14	M	123	ALA
15	N	17	LYS
17	P	10	GLY
17	P	49	LEU
19	R	26	LEU
20	S	67	VAL

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Mol	Chain	Res	Type
20	S	68	GLY
20	S	69	HIS
21	T	9	ASN
21	T	49	ALA
21	T	50	GLU
21	T	94	ALA
21	T	102	GLY
3	B	124	SER
3	B	232	PRO
4	C	26	LYS
4	C	88	ARG
4	C	167	TRP
4	C	168	ALA
5	D	10	ARG
5	D	151	LYS
5	D	179	GLU
8	G	77	SER
10	I	31	GLN
10	I	54	ASP
10	I	56	LEU
10	I	58	ARG
10	I	121	ARG
11	J	39	PRO
11	J	90	LEU
12	K	15	ALA
13	L	117	ARG
14	M	27	LYS
14	M	38	GLY
14	M	80	ARG
15	N	12	ARG
15	N	13	THR
15	N	36	PHE
19	R	54	ARG
21	T	95	ALA
21	T	98	PRO
22	V	9	ARG
3	B	15	VAL
3	B	224	GLN
4	C	181	ASN
4	C	188	LEU
5	D	30	LYS
5	D	64	LEU

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Mol	Chain	Res	Type
8	G	41	ARG
8	G	42	ILE
8	G	78	ARG
8	G	81	GLY
11	J	73	ASP
11	J	85	LEU
12	K	12	ARG
12	K	27	ASN
12	K	102	GLY
13	L	41	ARG
13	L	126	LYS
14	M	73	GLU
14	M	74	VAL
14	M	86	CYS
14	M	121	LYS
15	N	19	ARG
18	Q	33	GLY
21	T	42	GLN
3	B	60	ASP
3	B	83	MET
3	B	95	GLN
3	B	125	PRO
4	C	127	ARG
4	C	156	ARG
5	D	5	ILE
5	D	32	ALA
7	F	32	ASN
10	I	88	TYR
16	O	84	LYS
19	R	20	ALA
19	R	62	GLU
20	S	65	ASN
21	T	74	LYS
3	B	209	ARG
4	C	96	GLY
4	C	157	ILE
8	G	83	ALA
13	L	116	SER
20	S	17	GLU
4	C	66	VAL
5	D	171	GLY
11	J	40	LEU

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Mol	Chain	Res	Type
3	B	89	GLY
3	B	229	VAL
4	C	77	ILE
8	G	112	PRO
11	J	91	PRO
20	S	11	VAL
4	C	14	ILE
8	G	17	VAL
20	S	8	GLY
4	C	57	ILE
11	J	82	ILE
17	P	41	PRO
17	P	87	GLY
4	C	7	PRO

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%)	177 (88%)	25 (12%)	4	19
4	C	160/188 (85%)	138 (86%)	22 (14%)	3	15
5	D	180/181 (99%)	163 (91%)	17 (9%)	8	30
6	E	115/123 (94%)	97 (84%)	18 (16%)	2	12
7	F	90/90 (100%)	85 (94%)	5 (6%)	19	47
8	G	126/127 (99%)	120 (95%)	6 (5%)	23	52
9	H	119/119 (100%)	104 (87%)	15 (13%)	4	18
10	I	98/99 (99%)	90 (92%)	8 (8%)	10	35
11	J	87/92 (95%)	79 (91%)	8 (9%)	8	30
12	K	90/99 (91%)	85 (94%)	5 (6%)	19	47
13	L	104/111 (94%)	99 (95%)	5 (5%)	23	52
14	M	100/101 (99%)	87 (87%)	13 (13%)	4	17
15	N	49/50 (98%)	43 (88%)	6 (12%)	5	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	O	79/80 (99%)	74 (94%)	5 (6%)	16	44
17	P	74/74 (100%)	72 (97%)	2 (3%)	39	63
18	Q	96/97 (99%)	90 (94%)	6 (6%)	16	44
19	R	64/77 (83%)	59 (92%)	5 (8%)	11	36
20	S	71/80 (89%)	64 (90%)	7 (10%)	7	27
21	T	76/82 (93%)	68 (90%)	8 (10%)	6	25
22	V	19/21 (90%)	19 (100%)	0	100	100
All	All	1999/2111 (95%)	1813 (91%)	186 (9%)	8	30

All (186) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	8	LYS
3	B	9	GLU
3	B	12	GLU
3	B	17	PHE
3	B	21	ARG
3	B	23	ARG
3	B	25	ASN
3	B	51	LEU
3	B	75	LYS
3	B	103	THR
3	B	139	LYS
3	B	144	ARG
3	B	157	ARG
3	B	162	ILE
3	B	164	VAL
3	B	178	ARG
3	B	184	VAL
3	B	185	ILE
3	B	187	LEU
3	B	197	VAL
3	B	204	ASN
3	B	208	ILE
3	B	226	ARG
3	B	231	GLU
3	B	232	PRO
4	C	3	ASN
4	C	21	ARG
4	C	33	LEU

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Mol	Chain	Res	Type
4	C	37	GLN
4	C	43	LEU
4	C	64	VAL
4	C	75	VAL
4	C	82	GLU
4	C	90	GLU
4	C	91	LEU
4	C	99	VAL
4	C	102	ASN
4	C	107	GLN
4	C	139	GLN
4	C	162	GLN
4	C	165	THR
4	C	166	GLU
4	C	167	TRP
4	C	175	LEU
4	C	188	LEU
4	C	204	LEU
4	C	207	VAL
5	D	9	CYS
5	D	10	ARG
5	D	12	CYS
5	D	15	GLU
5	D	29	PRO
5	D	34	GLU
5	D	59	ARG
5	D	64	LEU
5	D	70	ILE
5	D	78	LEU
5	D	114	ARG
5	D	122	ARG
5	D	127	THR
5	D	129	ASN
5	D	157	LEU
5	D	176	LEU
5	D	194	LEU
6	E	12	LEU
6	E	31	LEU
6	E	38	GLN
6	E	43	LEU
6	E	52	PRO
6	E	56	GLN

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Mol	Chain	Res	Type
6	E	68	GLU
6	E	76	ILE
6	E	79	GLU
6	E	80	ILE
6	E	82	VAL
6	E	89	ILE
6	E	112	LEU
6	E	116	THR
6	E	120	THR
6	E	137	GLU
6	E	147	ASP
6	E	150	ARG
7	F	10	LEU
7	F	40	VAL
7	F	43	LEU
7	F	65	VAL
7	F	69	GLU
8	G	8	GLU
8	G	12	LEU
8	G	38	LEU
8	G	113	GLU
8	G	146	GLU
8	G	149	ARG
9	H	2	LEU
9	H	21	LYS
9	H	26	VAL
9	H	52	ASP
9	H	63	LEU
9	H	79	VAL
9	H	81	HIS
9	H	84	ARG
9	H	85	ARG
9	H	92	ARG
9	H	104	ARG
9	H	105	ARG
9	H	112	LEU
9	H	119	LEU
9	H	136	GLU
10	I	2	GLU
10	I	38	GLN
10	I	41	VAL
10	I	56	LEU

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Mol	Chain	Res	Type
10	I	58	ARG
10	I	109	VAL
10	I	111	ARG
10	I	118	LYS
11	J	45	ARG
11	J	49	VAL
11	J	51	ARG
11	J	64	GLU
11	J	71	LEU
11	J	74	ILE
11	J	81	THR
11	J	95	GLU
12	K	29	ILE
12	K	54	ARG
12	K	84	VAL
12	K	93	GLN
12	K	124	LYS
13	L	7	ILE
13	L	17	LYS
13	L	98	TYR
13	L	113	ARG
13	L	126	LYS
14	M	9	ILE
14	M	32	GLU
14	M	48	LEU
14	M	56	LEU
14	M	63	THR
14	M	70	LEU
14	M	77	ASN
14	M	81	LEU
14	M	102	ARG
14	M	105	THR
14	M	106	ASN
14	M	110	ARG
14	M	124	PRO
15	N	8	GLU
15	N	17	LYS
15	N	31	ARG
15	N	33	VAL
15	N	41	ARG
15	N	44	LEU
16	O	6	GLU

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Mol	Chain	Res	Type
16	O	36	ILE
16	O	64	ARG
16	O	71	GLN
16	O	83	GLU
17	P	53	VAL
17	P	76	GLN
18	Q	34	LYS
18	Q	38	ARG
18	Q	53	LEU
18	Q	60	ILE
18	Q	98	LEU
18	Q	104	LYS
19	R	28	GLU
19	R	38	GLU
19	R	53	ARG
19	R	54	ARG
19	R	75	ILE
20	S	12	ASP
20	S	15	LEU
20	S	20	LEU
20	S	43	GLU
20	S	61	TYR
20	S	62	ILE
20	S	78	ARG
21	T	10	LEU
21	T	39	LYS
21	T	42	GLN
21	T	56	MET
21	T	57	ARG
21	T	62	LEU
21	T	73	HIS
21	T	84	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	16	HIS
3	B	25	ASN
3	B	94	ASN
3	B	113	HIS
3	B	140	HIS
3	B	146	GLN

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Mol	Chain	Res	Type
3	B	204	ASN
3	B	240	GLN
4	C	3	ASN
4	C	6	HIS
4	C	31	HIS
4	C	69	HIS
4	C	104	GLN
4	C	107	GLN
4	C	110	ASN
4	C	118	GLN
4	C	123	GLN
4	C	136	GLN
4	C	139	GLN
4	C	162	GLN
4	C	176	HIS
5	D	62	GLN
5	D	77	ASN
5	D	123	HIS
5	D	160	GLN
5	D	199	ASN
6	E	38	GLN
6	E	73	ASN
7	F	18	GLN
7	F	27	GLN
7	F	32	ASN
7	F	57	GLN
7	F	94	GLN
7	F	100	ASN
8	G	37	ASN
8	G	86	GLN
8	G	96	GLN
10	I	73	GLN
10	I	117	HIS
11	J	56	HIS
11	J	62	HIS
11	J	76	ASN
11	J	78	ASN
11	J	84	GLN
12	K	117	ASN
13	L	75	HIS
14	M	12	ASN
14	M	40	ASN

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Mol	Chain	Res	Type
14	M	62	ASN
16	O	13	GLN
16	O	37	ASN
17	P	16	HIS
18	Q	16	GLN
19	R	36	ASN
20	S	14	HIS
20	S	23	ASN
20	S	56	GLN
21	T	16	HIS
21	T	42	GLN
21	T	90	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1507/1522 (99%)	215 (14%)	88 (5%)
2	X	5/6 (83%)	0	0
All	All	1512/1528 (98%)	215 (14%)	88 (5%)

All (215) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	51	A
1	A	52	G
1	A	61	G
1	A	62	U
1	A	65	U
1	A	81	U
1	A	116	A
1	A	120	A

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Mol	Chain	Res	Type
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	182	U
1	A	190(D)	U
1	A	190(E)	U
1	A	195	A
1	A	197	A
1	A	198	G
1	A	201	C
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	282	A
1	A	289	G
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	344	A
1	A	345	C
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	397	A
1	A	398	C
1	A	412	A
1	A	413	G
1	A	421	U
1	A	429	U
1	A	430	A

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Mol	Chain	Res	Type
1	A	439	A
1	A	460	A
1	A	461	C
1	A	481	G
1	A	482	A
1	A	484	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	519	C
1	A	527	G
1	A	532	A
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	653	A
1	A	665	A
1	A	687	A
1	A	688	G
1	A	702	A
1	A	703	G
1	A	718	G
1	A	721	G
1	A	723	U
1	A	731	G
1	A	749	C
1	A	755	G
1	A	777	A
1	A	781	A

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Mol	Chain	Res	Type
1	A	792	A
1	A	793	U
1	A	813	U
1	A	817	C
1	A	819	A
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	858	G
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1005	A
1	A	1023	G
1	A	1026	G
1	A	1045	C
1	A	1050	G
1	A	1053	G
1	A	1054	C
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1085	U

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Mol	Chain	Res	Type
1	A	1086	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1128	C
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1145	C
1	A	1152	A
1	A	1159	U
1	A	1160	G
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	1213	A
1	A	1215	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1257	U
1	A	1258	G
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A

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Mol	Chain	Res	Type
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1305	G
1	A	1320	C
1	A	1338	G
1	A	1347	G
1	A	1348	U
1	A	1353	G
1	A	1364	U
1	A	1381	U
1	A	1394	A
1	A	1398	A
1	A	1442	G
1	A	1443	G
1	A	1446	A
1	A	1452	C
1	A	1492	A
1	A	1497	G
1	A	1499	A
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G

All (88) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	7	G
1	A	30	U
1	A	48	C
1	A	51	A
1	A	60	A
1	A	64	G
1	A	115	G
1	A	119	A

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Mol	Chain	Res	Type
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	202	U
1	A	204	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	281	G
1	A	328	C
1	A	329	A
1	A	344	A
1	A	351	G
1	A	353	A
1	A	366	C
1	A	372	C
1	A	428	G
1	A	429	U
1	A	438	G
1	A	484	G
1	A	496	A
1	A	497	A
1	A	509	A
1	A	518	C
1	A	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	945	G
1	A	960	U
1	A	965	A
1	A	975	A

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Mol	Chain	Res	Type
1	A	976	G
1	A	992	U
1	A	993	G
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1085	U
1	A	1101	A
1	A	1117	G
1	A	1129	C
1	A	1139	G
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1196	U
1	A	1201	A
1	A	1212	U
1	A	1214	C
1	A	1224	G
1	A	1225	A
1	A	1226	C
1	A	1256	A
1	A	1257	U
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1301	U
1	A	1319	A
1	A	1346	A
1	A	1347	G
1	A	1380	U
1	A	1397	C
1	A	1451	A
1	A	1498	U
1	A	1502	A
1	A	1504	G
1	A	1528	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 99 ligands modelled in this entry, 98 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
24	HYG	A	1632	-	36,39,39	2.88	16 (44%)	44,60,60	2.01	12 (27%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	HYG	A	1632	-	1/1/16/17	10/12/87/87	0/4/4/4

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1632	HYG	O28-C23	7.73	1.49	1.40
24	A	1632	HYG	C27-C33	6.83	1.61	1.52
24	A	1632	HYG	C4-N9	6.66	1.55	1.47
24	A	1632	HYG	O28-C27	4.68	1.51	1.44
24	A	1632	HYG	C26-C27	3.53	1.61	1.52
24	A	1632	HYG	O30-C24	3.39	1.49	1.42
24	A	1632	HYG	C1-C6	3.25	1.61	1.52
24	A	1632	HYG	C3-C4	3.16	1.58	1.53
24	A	1632	HYG	C26-C25	3.03	1.60	1.52
24	A	1632	HYG	O29-C12	-2.94	1.38	1.43
24	A	1632	HYG	C10-N9	2.76	1.53	1.46
24	A	1632	HYG	C25-C24	2.54	1.57	1.53
24	A	1632	HYG	C19-C15	2.23	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1632	HYG	C16-C15	2.21	1.57	1.53
24	A	1632	HYG	O14-C13	2.08	1.47	1.41
24	A	1632	HYG	C34-C33	2.02	1.55	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1632	HYG	O21-C16-C15	5.36	122.53	109.32
24	A	1632	HYG	O28-C27-C26	5.35	115.97	108.50
24	A	1632	HYG	O21-C16-C17	4.26	120.85	109.94
24	A	1632	HYG	C23-O28-C27	3.45	118.57	112.00
24	A	1632	HYG	C16-C17-C12	-3.34	105.53	113.50
24	A	1632	HYG	C26-C25-C24	-3.29	106.48	111.18
24	A	1632	HYG	C17-C16-C15	3.09	116.17	109.57
24	A	1632	HYG	O18-C6-C1	2.72	114.15	107.23
24	A	1632	HYG	C10-N9-C4	2.47	117.34	114.39
24	A	1632	HYG	O29-C12-C13	2.47	117.20	110.89
24	A	1632	HYG	O22-C17-C16	2.35	116.83	111.22
24	A	1632	HYG	C25-C26-C27	2.06	114.36	109.68

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
24	A	1632	HYG	C16

All (10) torsion outliers are listed below:

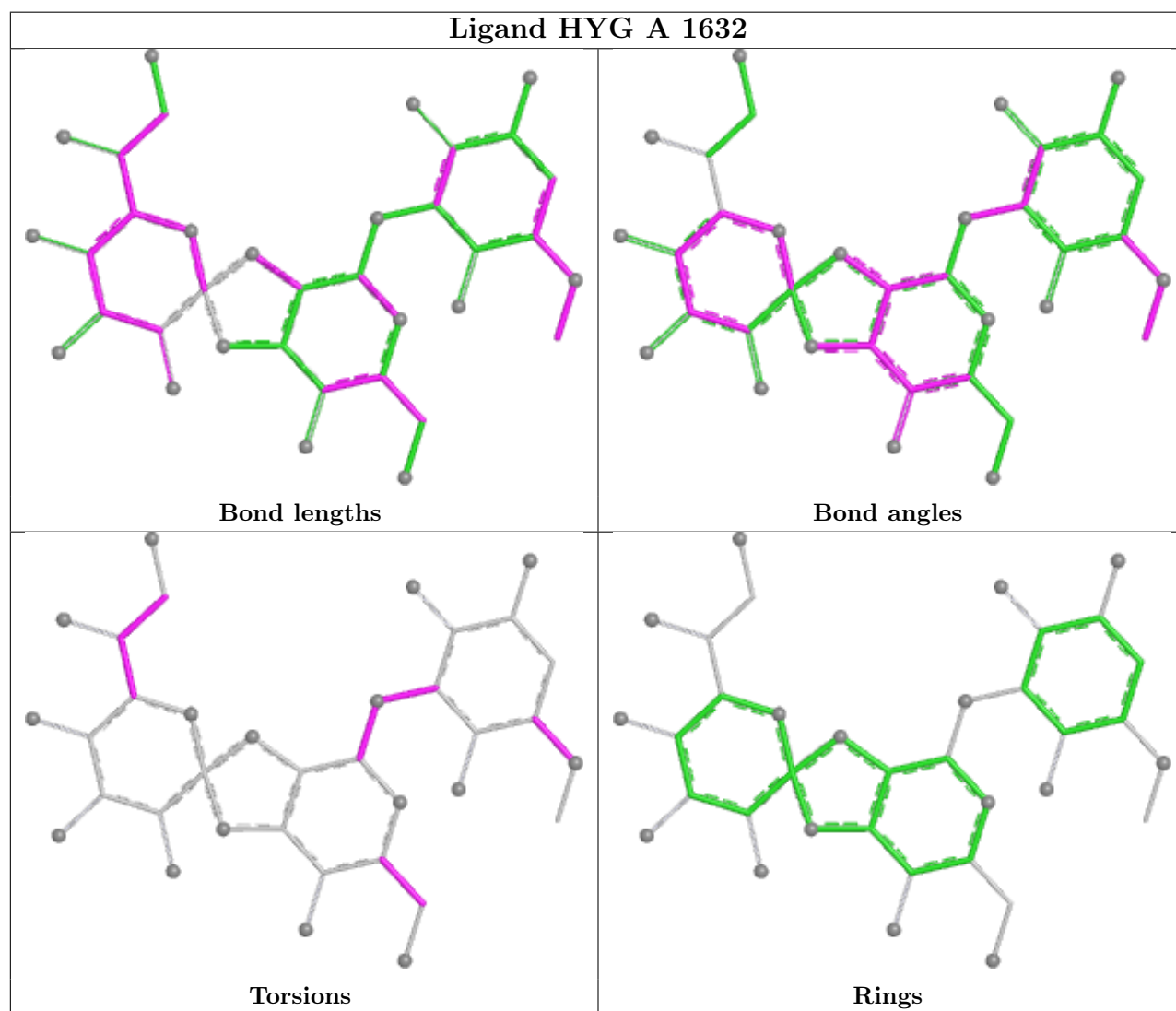
Mol	Chain	Res	Type	Atoms
24	A	1632	HYG	C5-C4-N9-C10
24	A	1632	HYG	C26-C27-C33-C34
24	A	1632	HYG	O28-C27-C33-C34
24	A	1632	HYG	N36-C33-C34-O35
24	A	1632	HYG	O14-C13-O18-C6
24	A	1632	HYG	C1-C6-O18-C13
24	A	1632	HYG	O14-C15-C19-O20
24	A	1632	HYG	C16-C15-C19-O20
24	A	1632	HYG	C27-C33-C34-O35
24	A	1632	HYG	C5-C6-O18-C13

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	1632	HYG	7	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1506/1522 (98%)	0.56	135 (8%) 15 11	53, 82, 169, 199	0
2	X	6/6 (100%)	1.72	1 (16%) 4 4	78, 84, 140, 155	0
3	B	234/256 (91%)	0.88	33 (14%) 6 5	51, 102, 165, 199	0
4	C	206/239 (86%)	0.77	24 (11%) 9 8	59, 103, 158, 177	0
5	D	208/209 (99%)	0.83	36 (17%) 4 4	55, 85, 131, 175	0
6	E	150/162 (92%)	0.39	11 (7%) 21 15	50, 73, 114, 192	0
7	F	101/101 (100%)	0.65	6 (5%) 28 19	66, 109, 144, 174	0
8	G	155/156 (99%)	0.59	12 (7%) 19 14	58, 100, 150, 177	0
9	H	138/138 (100%)	0.42	14 (10%) 12 10	41, 70, 106, 152	0
10	I	127/128 (99%)	1.09	24 (18%) 3 3	62, 109, 150, 175	0
11	J	98/105 (93%)	1.18	24 (24%) 2 1	59, 128, 184, 199	0
12	K	119/129 (92%)	0.68	12 (10%) 12 10	57, 85, 140, 191	0
13	L	124/135 (91%)	0.74	16 (12%) 7 6	44, 83, 128, 182	0
14	M	125/126 (99%)	1.04	26 (20%) 2 2	61, 99, 158, 193	0
15	N	60/61 (98%)	1.31	11 (18%) 3 3	64, 96, 150, 162	0
16	O	88/89 (98%)	0.86	15 (17%) 4 4	52, 83, 136, 185	0
17	P	88/88 (100%)	0.57	8 (9%) 15 11	53, 77, 158, 199	0
18	Q	104/105 (99%)	0.80	14 (13%) 7 6	55, 77, 140, 199	0
19	R	73/88 (82%)	0.41	6 (8%) 17 13	56, 87, 148, 191	0
20	S	80/93 (86%)	1.68	27 (33%) 1 1	84, 119, 170, 198	0
21	T	99/106 (93%)	0.99	13 (13%) 7 6	59, 86, 135, 199	0
22	V	24/26 (92%)	1.05	3 (12%) 8 6	60, 91, 127, 143	0
All	All	3913/4068 (96%)	0.71	471 (12%) 9 7	41, 88, 161, 199	0

All (471) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
20	S	79	THR	10.6
21	T	51	GLU	10.1
13	L	95	GLY	9.6
13	L	23	LYS	9.5
20	S	77	THR	9.0
8	G	79	ARG	8.2
14	M	124	PRO	7.8
18	Q	104	LYS	7.8
18	Q	78	GLU	7.8
13	L	89	ARG	7.5
16	O	40	SER	7.4
16	O	7	GLU	7.2
18	Q	80	GLY	7.2
18	Q	105	ALA	7.0
20	S	3	ARG	6.8
1	A	989	C	6.7
1	A	1036	G	6.6
3	B	235	SER	6.5
1	A	990	C	6.3
5	D	33	MET	6.3
1	A	1489	G	6.3
15	N	8	GLU	6.3
15	N	4	LYS	6.2
21	T	48	LYS	6.1
3	B	227	GLY	6.1
6	E	72	GLN	6.1
11	J	33	GLN	6.1
14	M	123	ALA	6.0
3	B	166	ASP	6.0
21	T	12	ALA	5.9
22	V	6	ARG	5.7
3	B	156	LYS	5.7
1	A	1124	G	5.7
1	A	1488	G	5.6
1	A	1273	G	5.5
20	S	54	GLY	5.5
6	E	76	ILE	5.5
14	M	125	ARG	5.5
18	Q	103	GLY	5.4
20	S	76	PRO	5.4
12	K	114	VAL	5.4
1	A	1005	A	5.2
14	M	109	THR	5.2

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Mol	Chain	Res	Type	RSRZ
18	Q	82	MET	5.2
6	E	149	GLU	5.2
18	Q	79	SER	5.2
3	B	233	SER	5.2
1	A	991	U	5.1
1	A	455	C	5.1
1	A	1006	C	5.1
1	A	1027	C	5.1
15	N	2	ALA	5.0
4	C	53	ALA	5.0
3	B	220	ASP	5.0
11	J	57	LYS	5.0
5	D	185	PHE	5.0
21	T	44	ALA	5.0
8	G	62	PHE	4.9
1	A	1129	C	4.9
7	F	38	GLU	4.9
3	B	133	LYS	4.8
4	C	172	ARG	4.8
3	B	212	GLN	4.8
1	A	958	A	4.8
18	Q	77	VAL	4.8
14	M	43	THR	4.7
6	E	77	PRO	4.7
15	N	6	LEU	4.7
16	O	39	LEU	4.7
16	O	3	ILE	4.7
5	D	187	ARG	4.7
5	D	5	ILE	4.7
4	C	86	VAL	4.7
9	H	18	ARG	4.6
21	T	43	LEU	4.6
1	A	1126	U	4.6
12	K	115	PRO	4.6
8	G	5	ARG	4.6
5	D	31	CYS	4.6
20	S	78	ARG	4.6
8	G	26	PHE	4.6
21	T	47	GLY	4.6
13	L	97	ARG	4.5
1	A	454	C	4.5
1	A	1037	C	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	1023	G	4.5
16	O	51	HIS	4.5
3	B	226	ARG	4.5
20	S	37	ARG	4.5
3	B	108	ILE	4.5
3	B	238	LEU	4.5
22	V	25	LYS	4.5
14	M	20	THR	4.4
3	B	98	LEU	4.4
8	G	4	ARG	4.4
1	A	667	G	4.4
14	M	51	ALA	4.3
20	S	5	LEU	4.3
1	A	1093	A	4.3
1	A	1123	A	4.3
10	I	110	GLU	4.3
20	S	2	PRO	4.3
9	H	1	MET	4.3
11	J	89	ASP	4.3
20	S	75	ALA	4.3
1	A	1024	G	4.2
1	A	433	C	4.1
1	A	1026	G	4.1
13	L	96	VAL	4.1
10	I	97	LYS	4.1
1	A	1275	A	4.1
1	A	1477	C	4.0
1	A	1493	A	4.0
1	A	1533	C	4.0
17	P	29	ASP	4.0
8	G	22	LEU	4.0
14	M	38	GLY	3.9
1	A	432	A	3.9
1	A	481	G	3.8
2	X	1	C	3.8
15	N	3	ARG	3.8
1	A	461	C	3.8
17	P	28	ARG	3.8
1	A	1025	U	3.7
19	R	31	LEU	3.7
1	A	666	G	3.7
5	D	3	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	1281	U	3.7
5	D	115	ARG	3.6
1	A	1067	A	3.6
14	M	126	LYS	3.6
17	P	87	GLY	3.6
1	A	1022	G	3.6
1	A	1018	C	3.6
14	M	37	THR	3.6
21	T	9	ASN	3.6
1	A	478	A	3.5
1	A	1220	G	3.5
1	A	1217	C	3.5
5	D	28	SER	3.5
18	Q	56	VAL	3.5
10	I	94	ALA	3.5
1	A	1134	G	3.5
4	C	52	LEU	3.5
20	S	53	ASN	3.5
1	A	733	A	3.5
3	B	216	SER	3.5
1	A	341	C	3.4
5	D	23	GLY	3.4
7	F	64	GLN	3.4
9	H	28	ALA	3.4
3	B	239	VAL	3.4
1	A	190(B)	C	3.4
5	D	129	ASN	3.4
1	A	1274	G	3.4
5	D	19	LEU	3.4
4	C	37	GLN	3.4
21	T	52	ALA	3.4
1	A	1125	U	3.3
4	C	192	THR	3.3
4	C	23	TYR	3.3
7	F	3	ARG	3.3
20	S	10	PHE	3.3
13	L	21	LYS	3.2
11	J	78	ASN	3.2
1	A	183	G	3.2
1	A	1221	G	3.2
11	J	64	GLU	3.2
5	D	142	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
5	D	26	CYS	3.2
10	I	24	GLY	3.2
6	E	71	LEU	3.2
1	A	1139	G	3.2
4	C	84	ILE	3.2
11	J	100	THR	3.2
15	N	22	THR	3.2
1	A	988	G	3.2
21	T	74	LYS	3.1
20	S	80	TYR	3.1
13	L	19	ARG	3.1
4	C	99	VAL	3.1
8	G	23	VAL	3.1
1	A	1478	C	3.1
1	A	399	G	3.1
1	A	1047	G	3.1
1	A	1127	G	3.1
20	S	81	ARG	3.1
5	D	16	GLY	3.1
1	A	219	C	3.1
1	A	1145	C	3.1
5	D	9	CYS	3.1
3	B	16	HIS	3.1
1	A	957	U	3.1
10	I	102	LEU	3.1
16	O	24	SER	3.1
1	A	1001	A	3.1
1	A	1502	A	3.1
4	C	107	GLN	3.0
1	A	1290	G	3.0
9	H	90	GLY	3.0
9	H	98	LYS	3.0
5	D	205	GLU	3.0
1	A	290	C	3.0
3	B	228	GLY	3.0
14	M	39	ILE	3.0
1	A	393	A	3.0
11	J	43	ARG	3.0
1	A	202	U	3.0
16	O	2	PRO	3.0
11	J	46	ARG	3.0
13	L	128	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
11	J	99	LYS	2.9
10	I	128	ARG	2.9
12	K	89	ALA	2.9
20	S	4	SER	2.9
20	S	12	ASP	2.9
16	O	87	ILE	2.9
7	F	47	ARG	2.9
9	H	136	GLU	2.9
5	D	54	TYR	2.9
5	D	73	ARG	2.9
1	A	1520	G	2.9
8	G	17	VAL	2.9
1	A	618	C	2.9
1	A	1262	C	2.9
19	R	48	GLY	2.9
9	H	116	LYS	2.9
15	N	26	ARG	2.9
1	A	1144	G	2.9
21	T	106	ALA	2.8
4	C	167	TRP	2.8
13	L	18	VAL	2.8
1	A	460	A	2.8
1	A	1092	A	2.8
10	I	126	SER	2.8
12	K	129	SER	2.8
5	D	209	ARG	2.8
10	I	93	ARG	2.8
20	S	74	PHE	2.8
5	D	202	LEU	2.8
1	A	756	C	2.8
14	M	76	ALA	2.8
20	S	35	SER	2.8
13	L	67	THR	2.8
3	B	236	TYR	2.8
10	I	65	VAL	2.8
5	D	24	GLU	2.8
9	H	3	THR	2.8
5	D	30	LYS	2.7
13	L	126	LYS	2.7
1	A	81	U	2.7
20	S	38	SER	2.7
20	S	33	THR	2.7

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Mol	Chain	Res	Type	RSRZ
20	S	26	GLY	2.7
19	R	88	LYS	2.7
20	S	23	ASN	2.7
11	J	75	ILE	2.7
12	K	28	THR	2.7
12	K	21	ILE	2.7
1	A	1261	A	2.7
1	A	1446	A	2.7
12	K	110	ASP	2.7
17	P	47	ASP	2.7
1	A	201	C	2.7
6	E	154	GLY	2.7
18	Q	100	LYS	2.7
1	A	1002	G	2.7
1	A	1222	G	2.7
4	C	106	VAL	2.7
9	H	15	ASN	2.7
11	J	74	ILE	2.6
14	M	36	LYS	2.6
14	M	87	TYR	2.6
6	E	78	HIS	2.6
4	C	79	ARG	2.6
14	M	40	ASN	2.6
4	C	111	LEU	2.6
1	A	1113	C	2.6
1	A	1133	G	2.6
10	I	119	ALA	2.6
3	B	75	LYS	2.6
12	K	53	SER	2.6
1	A	1030(B)	C	2.6
1	A	1426	C	2.6
1	A	1490	C	2.6
12	K	52	GLY	2.6
14	M	52	GLU	2.6
10	I	55	ALA	2.6
3	B	153	ARG	2.6
5	D	159	ARG	2.6
6	E	18	ARG	2.6
10	I	103	THR	2.6
1	A	1004	A	2.6
10	I	96	LEU	2.6
11	J	85	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
14	M	54	VAL	2.6
19	R	25	THR	2.6
1	A	45	U	2.5
1	A	1135	U	2.5
16	O	50	HIS	2.5
20	S	52	TYR	2.5
1	A	718	G	2.5
13	L	28	LYS	2.5
16	O	8	LYS	2.5
16	O	79	ARG	2.5
3	B	223	ILE	2.5
1	A	1029	C	2.5
1	A	1277	C	2.5
3	B	113	HIS	2.5
13	L	27	LEU	2.5
20	S	68	GLY	2.5
6	E	145	LYS	2.5
4	C	90	GLU	2.5
8	G	7	ALA	2.5
15	N	5	ALA	2.5
11	J	4	ILE	2.5
4	C	186	PHE	2.5
1	A	124	G	2.5
11	J	37	PRO	2.5
5	D	95	GLY	2.5
15	N	45	ARG	2.5
4	C	44	GLU	2.5
11	J	34	VAL	2.5
10	I	113	LYS	2.5
5	D	143	GLY	2.5
5	D	131	ARG	2.4
10	I	30	GLY	2.4
12	K	61	ALA	2.4
3	B	51	LEU	2.4
3	B	65	GLY	2.4
10	I	53	VAL	2.4
15	N	34	TYR	2.4
1	A	351	G	2.4
1	A	1094	G	2.4
1	A	1347	G	2.4
11	J	97	GLU	2.4
20	S	34	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
9	H	74	PRO	2.4
3	B	83	MET	2.4
1	A	910	C	2.4
1	A	1532	U	2.4
13	L	127	GLU	2.4
1	A	46	G	2.4
1	A	668	G	2.4
1	A	1120	G	2.4
1	A	1494	G	2.4
18	Q	55	ASP	2.4
8	G	6	ARG	2.4
16	O	34	LEU	2.4
14	M	50	GLU	2.4
1	A	362	G	2.3
1	A	1185	G	2.3
5	D	21	LEU	2.3
4	C	112	SER	2.3
11	J	84	GLN	2.3
10	I	2	GLU	2.3
20	S	17	GLU	2.3
1	A	394	G	2.3
1	A	413	G	2.3
10	I	109	VAL	2.3
5	D	141	ARG	2.3
11	J	31	GLY	2.3
16	O	52	SER	2.3
1	A	946	A	2.3
8	G	123	GLU	2.3
14	M	31	LYS	2.3
3	B	111	ARG	2.3
16	O	38	ARG	2.3
22	V	23	PRO	2.3
14	M	75	ALA	2.3
3	B	115	LEU	2.3
3	B	149	LEU	2.3
1	A	1068	G	2.3
4	C	128	PHE	2.3
1	A	1287	A	2.3
9	H	117	GLY	2.3
1	A	1038	C	2.3
5	D	173	TRP	2.3
6	E	6	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
11	J	35	SER	2.3
4	C	85	ARG	2.3
11	J	66	ARG	2.3
13	L	73	GLU	2.2
10	I	15	ALA	2.2
19	R	24	ALA	2.2
1	A	246	A	2.2
1	A	1046	A	2.2
1	A	1128	C	2.2
8	G	84	ASN	2.2
1	A	266	G	2.2
1	A	617	G	2.2
1	A	1131	G	2.2
1	A	1416	G	2.2
1	A	1521	G	2.2
1	A	1413	A	2.2
4	C	152	ILE	2.2
1	A	268	C	2.2
1	A	269	C	2.2
1	A	291	C	2.2
21	T	24	LEU	2.2
14	M	15	VAL	2.2
1	A	1278	U	2.2
1	A	704	A	2.2
1	A	1293	G	2.2
1	A	1299	A	2.2
1	A	1442	G	2.2
5	D	174	LEU	2.2
7	F	14	LEU	2.2
17	P	7	ALA	2.2
14	M	16	ASP	2.2
18	Q	13	ASP	2.2
3	B	165	VAL	2.2
12	K	117	ASN	2.2
1	A	5	U	2.2
1	A	340	U	2.2
1	A	1423	G	2.2
17	P	38	TYR	2.1
1	A	342	C	2.1
3	B	240	GLN	2.1
14	M	96	LEU	2.1
4	C	83	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
9	H	14	ARG	2.1
5	D	12	CYS	2.1
15	N	25	VAL	2.1
11	J	48	THR	2.1
11	J	3	LYS	2.1
10	I	9	ARG	2.1
18	Q	16	GLN	2.1
4	C	19	GLU	2.1
11	J	10	GLY	2.1
17	P	44	THR	2.1
14	M	6	GLY	2.1
1	A	190(C)	C	2.1
1	A	224	C	2.1
1	A	1412	C	2.1
19	R	33	ASP	2.1
12	K	91	ARG	2.1
18	Q	95	TYR	2.1
17	P	88	ALA	2.1
5	D	83	SER	2.1
13	L	47	LYS	2.1
10	I	16	ARG	2.1
7	F	1	MET	2.1
5	D	4	TYR	2.1
3	B	125	PRO	2.1
6	E	122	GLU	2.1
14	M	10	PRO	2.1
5	D	22	LYS	2.0
20	S	55	LYS	2.0
5	D	186	LEU	2.0
9	H	105	ARG	2.0
11	J	28	ARG	2.0
16	O	36	ILE	2.0
21	T	8	ARG	2.0
1	A	172	A	2.0
5	D	144	ASP	2.0
10	I	88	TYR	2.0
10	I	8	GLY	2.0
14	M	13	LYS	2.0
1	A	987	G	2.0
1	A	1475	G	2.0
1	A	1086	U	2.0
4	C	110	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
21	T	103	GLY	2.0
3	B	45	GLN	2.0
10	I	95	LYS	2.0
1	A	1332	A	2.0
3	B	116	GLU	2.0
9	H	30	ARG	2.0
3	B	80	ILE	2.0
1	A	381	C	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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(Å ²)	Q<0.9
23	MG	A	1585	1/1	0.45	0.60	58,58,58,58	1
23	MG	A	1615	1/1	0.45	0.99	58,58,58,58	1
23	MG	D	215	1/1	0.51	0.31	58,58,58,58	1
23	MG	A	210	1/1	0.53	0.64	58,58,58,58	1
23	MG	A	1595	1/1	0.55	0.38	58,58,58,58	0
23	MG	A	214	1/1	0.58	0.54	58,58,58,58	0
23	MG	A	1566	1/1	0.59	0.44	58,58,58,58	0
23	MG	A	1623	1/1	0.61	0.90	58,58,58,58	1
23	MG	A	1550	1/1	0.61	0.40	58,58,58,58	1
23	MG	A	1582	1/1	0.70	0.25	58,58,58,58	1
23	MG	A	1586	1/1	0.72	0.44	58,58,58,58	0
23	MG	A	212	1/1	0.72	1.02	58,58,58,58	1
23	MG	A	1618	1/1	0.73	0.47	58,58,58,58	1
23	MG	A	1548	1/1	0.73	0.25	58,58,58,58	0
23	MG	A	1549	1/1	0.73	0.30	58,58,58,58	1

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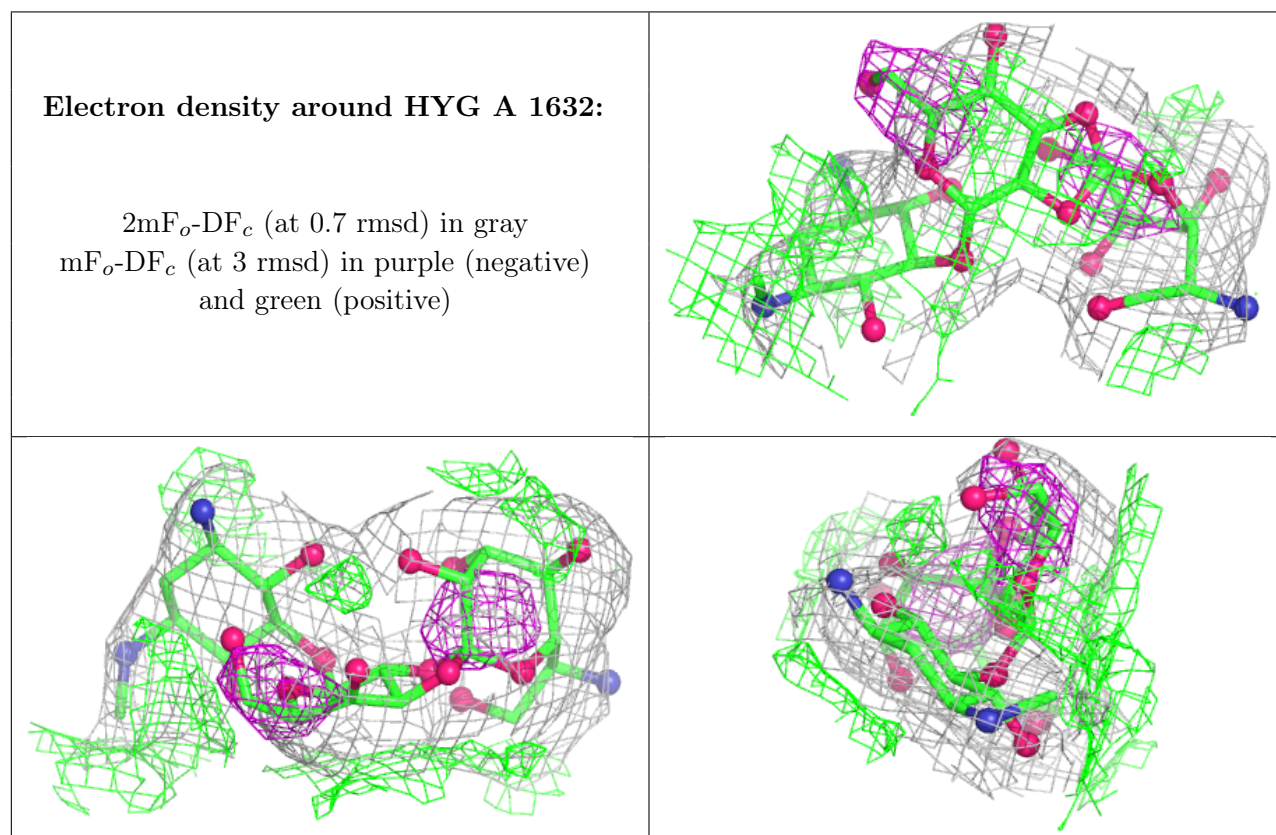
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	MG	A	1577	1/1	0.74	0.32	58,58,58,58	0
23	MG	A	1616	1/1	0.75	0.28	58,58,58,58	0
23	MG	A	1574	1/1	0.75	0.34	58,58,58,58	0
23	MG	A	1620	1/1	0.75	0.37	58,58,58,58	0
23	MG	A	1612	1/1	0.75	0.24	58,58,58,58	1
23	MG	A	1556	1/1	0.75	0.89	58,58,58,58	1
23	MG	A	1578	1/1	0.76	0.27	58,58,58,58	0
23	MG	A	1557	1/1	0.76	0.60	58,58,58,58	0
23	MG	A	86	1/1	0.76	0.36	58,58,58,58	0
23	MG	A	1619	1/1	0.78	0.10	58,58,58,58	0
23	MG	A	1547	1/1	0.78	0.50	58,58,58,58	0
23	MG	A	1599	1/1	0.79	0.39	58,58,58,58	0
23	MG	A	1552	1/1	0.80	0.26	58,58,58,58	0
23	MG	A	1614	1/1	0.80	0.52	58,58,58,58	1
23	MG	A	1568	1/1	0.80	0.28	58,58,58,58	0
24	HYG	A	1632	36/36	0.80	0.15	41,41,41,41	0
23	MG	A	1567	1/1	0.81	0.40	58,58,58,58	0
23	MG	A	71	1/1	0.81	0.36	58,58,58,58	0
23	MG	A	1559	1/1	0.81	0.33	58,58,58,58	0
23	MG	A	1562	1/1	0.82	0.48	58,58,58,58	0
23	MG	A	1584	1/1	0.82	0.36	58,58,58,58	0
23	MG	A	1624	1/1	0.82	1.10	58,58,58,58	1
23	MG	A	1601	1/1	0.82	0.24	58,58,58,58	0
23	MG	A	1590	1/1	0.82	0.59	58,58,58,58	0
23	MG	A	1553	1/1	0.83	0.43	58,58,58,58	0
23	MG	A	211	1/1	0.83	0.38	58,58,58,58	0
23	MG	H	213	1/1	0.83	0.44	58,58,58,58	1
23	MG	A	1603	1/1	0.83	0.47	58,58,58,58	0
23	MG	A	1626	1/1	0.84	0.19	58,58,58,58	0
23	MG	A	1611	1/1	0.84	0.18	58,58,58,58	1
23	MG	A	1600	1/1	0.85	0.51	58,58,58,58	0
23	MG	A	1597	1/1	0.85	0.43	58,58,58,58	0
23	MG	A	1560	1/1	0.85	0.32	58,58,58,58	0
23	MG	A	1554	1/1	0.86	0.49	58,58,58,58	0
23	MG	A	1570	1/1	0.86	0.29	58,58,58,58	1
23	MG	A	1571	1/1	0.86	0.51	58,58,58,58	0
23	MG	A	1545	1/1	0.86	0.14	58,58,58,58	1
23	MG	A	1564	1/1	0.86	0.31	58,58,58,58	0
23	MG	A	1576	1/1	0.86	0.53	58,58,58,58	0
23	MG	A	1629	1/1	0.86	0.76	58,58,58,58	1
23	MG	A	1589	1/1	0.86	0.23	58,58,58,58	0
23	MG	A	1604	1/1	0.86	0.14	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	MG	A	1605	1/1	0.86	0.35	58,58,58,58	0
23	MG	A	1579	1/1	0.87	0.32	58,58,58,58	0
23	MG	A	1575	1/1	0.87	0.15	58,58,58,58	1
23	MG	A	1563	1/1	0.88	0.24	58,58,58,58	0
23	MG	A	1596	1/1	0.88	0.49	58,58,58,58	1
23	MG	A	1592	1/1	0.89	0.19	58,58,58,58	0
23	MG	A	1594	1/1	0.89	0.22	58,58,58,58	0
23	MG	A	1573	1/1	0.89	0.55	58,58,58,58	0
23	MG	A	1551	1/1	0.89	0.45	58,58,58,58	0
23	MG	A	87	1/1	0.89	0.46	58,58,58,58	1
23	MG	A	1591	1/1	0.90	0.37	58,58,58,58	0
23	MG	A	1561	1/1	0.90	0.28	58,58,58,58	0
23	MG	A	1581	1/1	0.90	0.17	58,58,58,58	1
23	MG	A	1606	1/1	0.90	0.21	58,58,58,58	0
23	MG	A	1609	1/1	0.90	0.47	58,58,58,58	0
23	MG	A	1593	1/1	0.91	0.41	58,58,58,58	0
23	MG	A	1572	1/1	0.91	0.31	58,58,58,58	0
23	MG	A	1588	1/1	0.91	0.18	58,58,58,58	0
23	MG	A	1546	1/1	0.91	0.28	58,58,58,58	0
23	MG	A	1610	1/1	0.92	0.33	58,58,58,58	0
23	MG	A	1617	1/1	0.92	0.23	58,58,58,58	1
23	MG	A	1558	1/1	0.93	0.52	58,58,58,58	0
23	MG	A	1607	1/1	0.93	0.42	58,58,58,58	0
23	MG	A	1608	1/1	0.93	0.40	58,58,58,58	0
23	MG	A	1598	1/1	0.94	0.09	58,58,58,58	0
23	MG	A	1583	1/1	0.94	0.16	58,58,58,58	0
23	MG	A	1613	1/1	0.95	0.33	58,58,58,58	1
23	MG	A	1580	1/1	0.95	0.14	58,58,58,58	0
23	MG	A	1587	1/1	0.95	0.12	58,58,58,58	0
23	MG	A	1602	1/1	0.96	0.60	58,58,58,58	0
25	ZN	D	300	1/1	0.96	0.21	66,66,66,66	0
23	MG	A	1631	1/1	0.97	0.16	58,58,58,58	1
23	MG	A	1621	1/1	0.97	0.20	58,58,58,58	1
23	MG	A	1627	1/1	0.97	0.17	58,58,58,58	1
23	MG	A	1625	1/1	0.97	0.21	58,58,58,58	1
23	MG	A	1630	1/1	0.97	0.25	58,58,58,58	1
23	MG	A	1628	1/1	0.98	0.07	58,58,58,58	1
23	MG	A	1622	1/1	0.98	0.09	58,58,58,58	1
23	MG	A	1555	1/1	0.98	0.76	58,58,58,58	0
23	MG	A	1565	1/1	0.98	0.34	58,58,58,58	0
23	MG	A	1569	1/1	0.99	0.20	58,58,58,58	1
25	ZN	N	190	1/1	1.00	0.03	66,66,66,66	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.