



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 05:57 am GMT

PDB ID : 1HNW
Title : STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL
SUBUNIT IN COMPLEX WITH TETRACYCLINE
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 : 3.40 Å(reported)

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

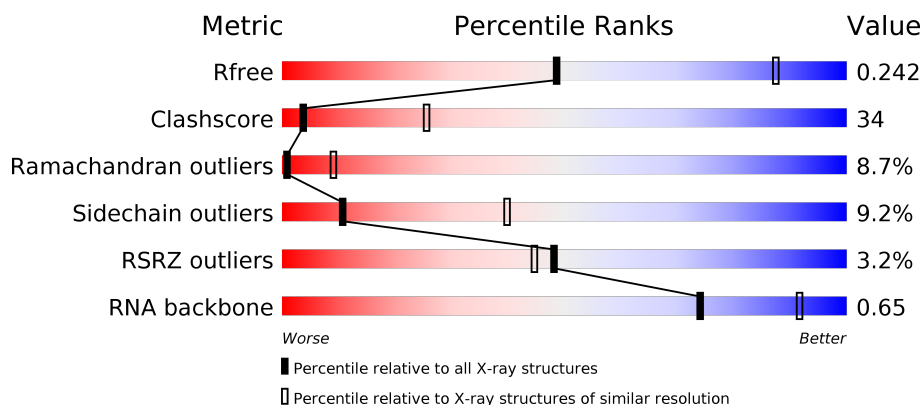
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	100719	1679 (3.50-3.30)
Clashscore	112137	1832 (3.50-3.30)
Ramachandran outliers	110173	1789 (3.50-3.30)
Sidechain outliers	110143	1789 (3.50-3.30)
RSRZ outliers	101464	1709 (3.50-3.30)
RNA backbone	2435	1009 (3.96-2.84)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	<div> <div>5%</div> <div> <div></div> <div>30%</div> <div>56%</div> <div>12%</div> <div>..</div> </div> </div>
2	X	6	<div> <div>33%</div> <div>100%</div> </div>
3	B	256	<div> <div>4%</div> <div>18%</div> <div>54%</div> <div>16%</div> <div>•</div> <div>9%</div> </div>
4	C	239	<div> <div>23%</div> <div>45%</div> <div>17%</div> <div>•</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
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	1553	-	-	-	X
23	MG	A	1557	-	-	-	X
23	MG	A	1562	-	-	-	X
23	MG	A	1575	-	-	-	X
23	MG	A	1576	-	-	-	X
23	MG	A	1580	-	-	-	X
23	MG	A	1587	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	MG	A	1592	-	-	-	X
23	MG	A	1594	-	-	-	X
23	MG	A	1599	-	-	-	X
23	MG	A	1600	-	-	-	X
23	MG	A	1602	-	-	-	X
23	MG	A	1604	-	-	-	X
23	MG	A	1606	-	-	-	X
23	MG	A	1612	-	-	-	X
23	MG	A	1613	-	-	-	X
23	MG	A	1619	-	-	-	X
23	MG	A	1624	-	-	-	X
23	MG	A	1625	-	-	-	X
23	MG	A	1628	-	-	-	X
23	MG	A	211	-	-	-	X
25	TAC	A	1633	-	-	-	X

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 51934 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			

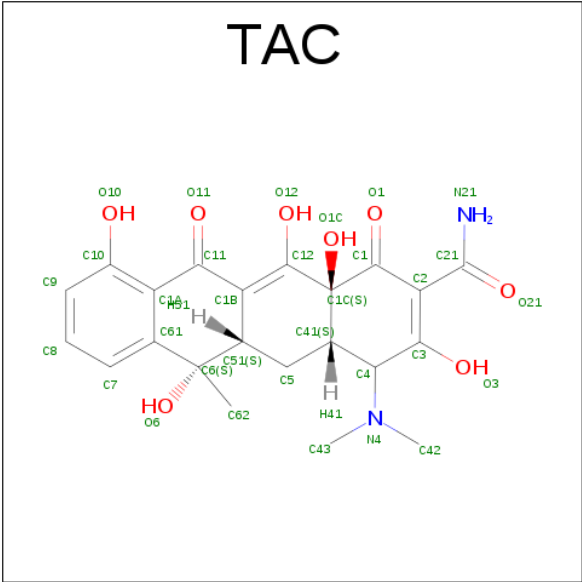
- Molecule 23 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

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

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

- Molecule 25 is TETRACYCLINE (three-letter code: TAC) (formula: C₂₂H₂₄N₂O₈).

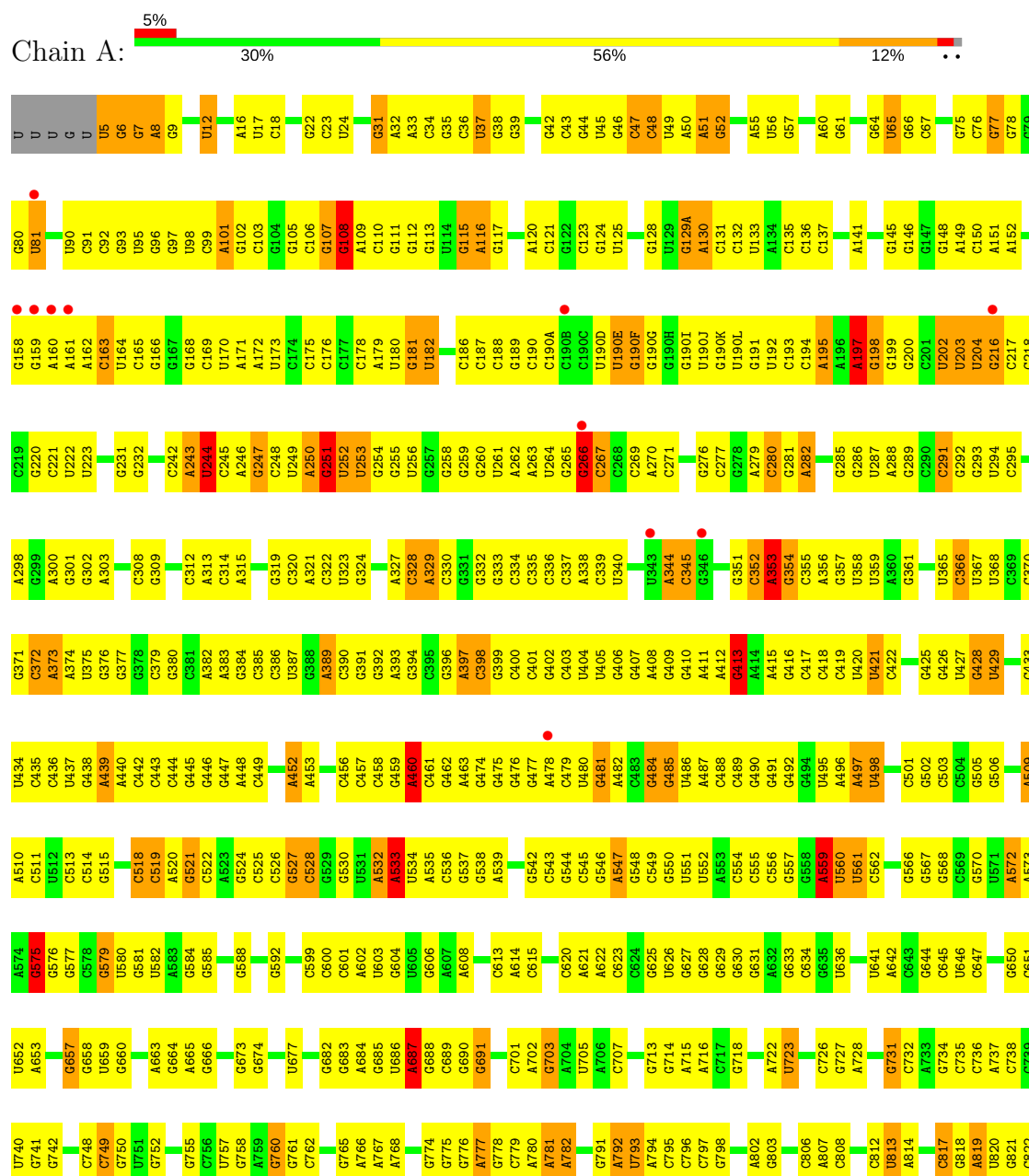


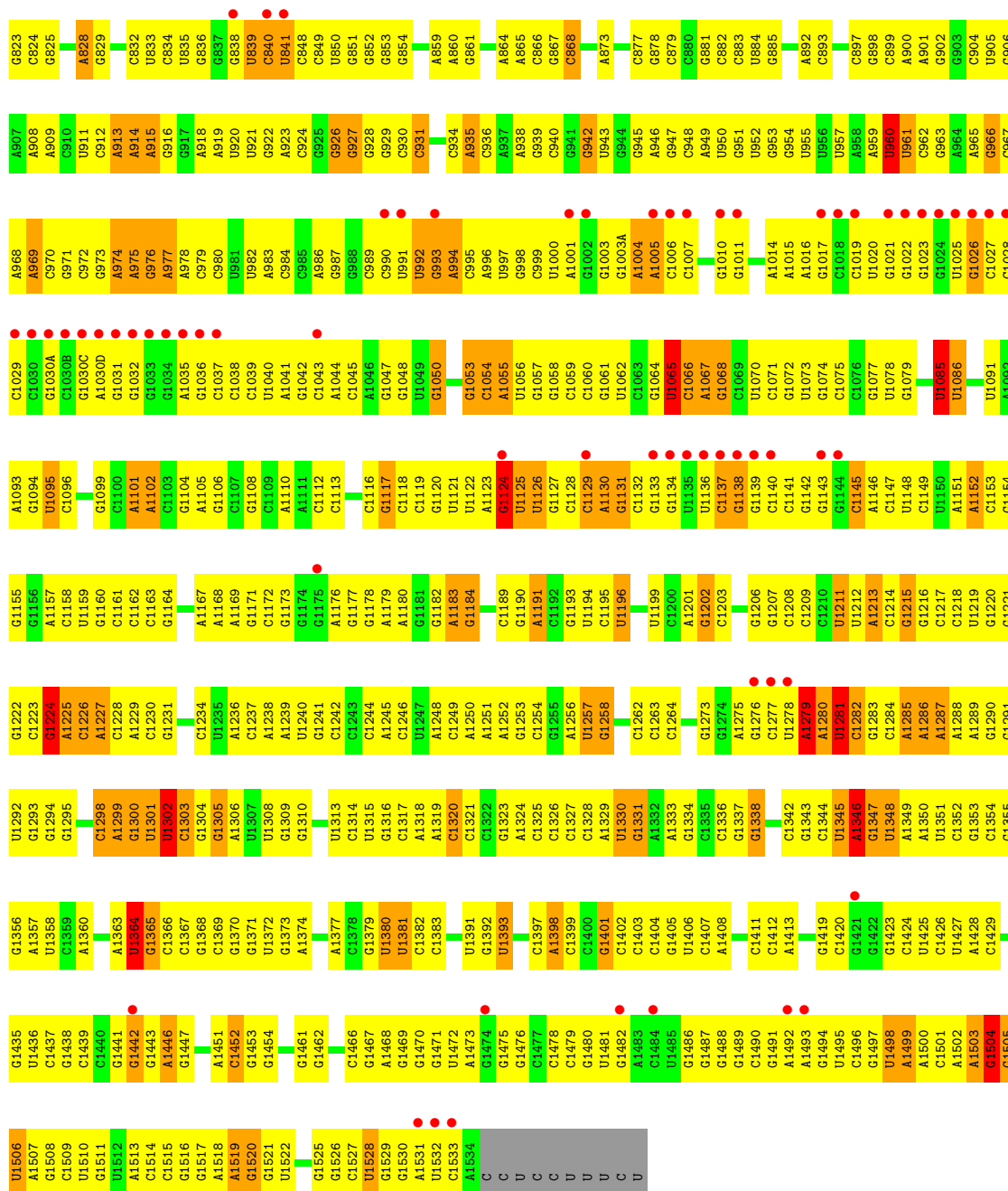
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
25	A	1	Total	C	N	O	0	0
			32	22	2	8		
25	A	1	Total	C	N	O	0	0
			32	22	2	8		

3 Residue-property plots

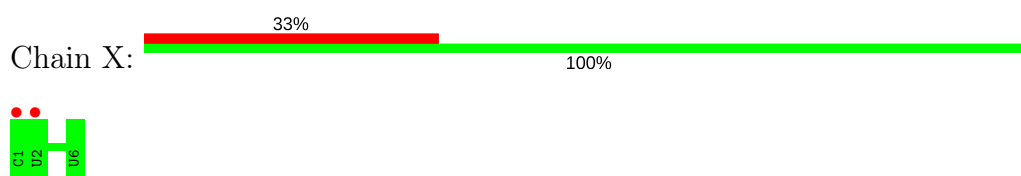
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

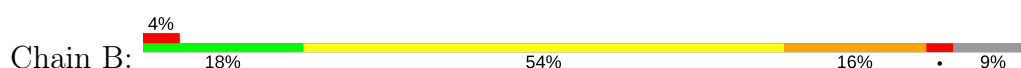


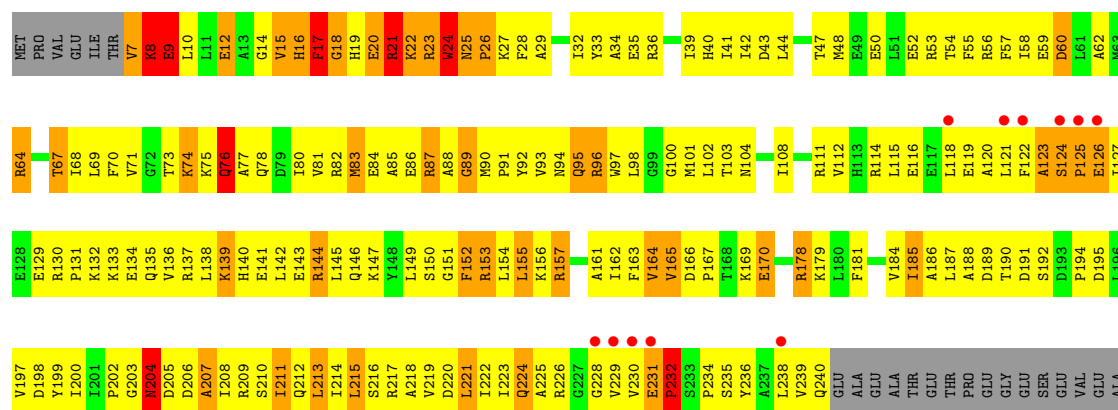


• Molecule 2: FRAGMENT OF MESSENGER RNA



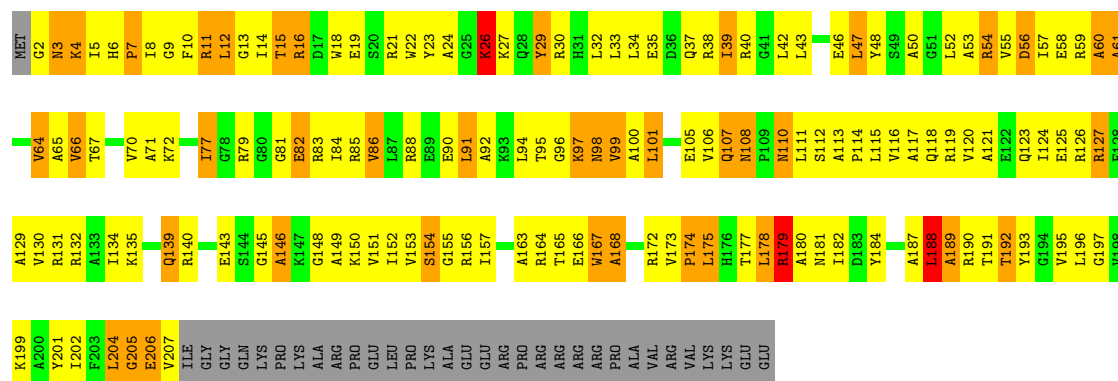
• Molecule 3: 30S RIBOSOMAL PROTEIN S2





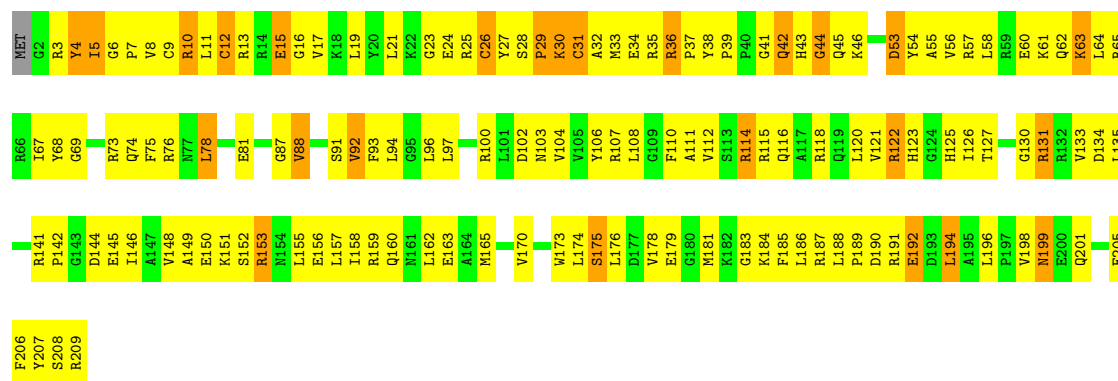
• Molecule 4: 30S RIBOSOMAL PROTEIN S3

Chain C: 23% 45% 17% 14%



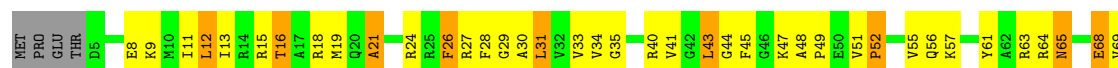
• Molecule 5: 30S RIBOSOMAL PROTEIN S4

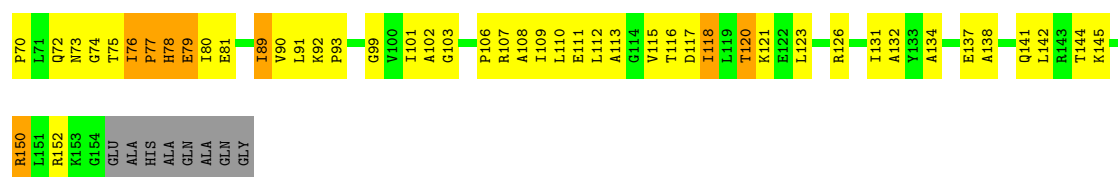
Chain D: 32% 56% 12%



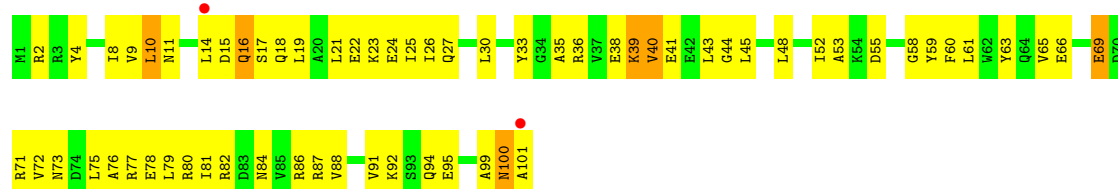
• Molecule 6: 30S RIBOSOMAL PROTEIN S5

Chain E: 40% 43% 10% 7%

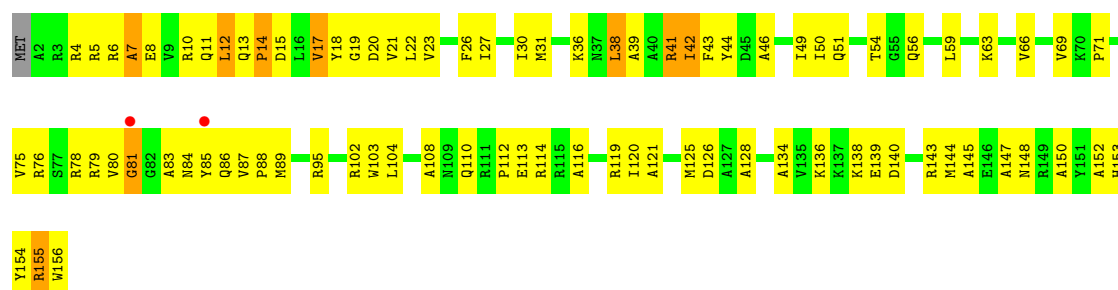
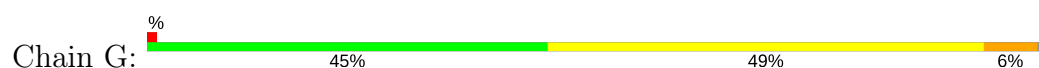




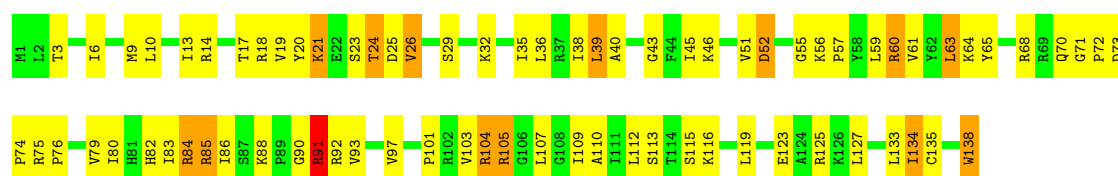
• Molecule 7: 30S RIBOSOMAL PROTEIN S6



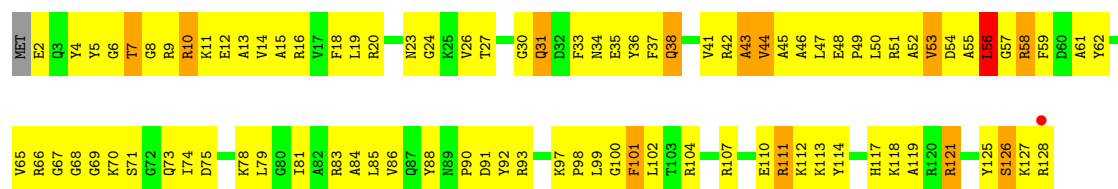
• Molecule 8: 30S RIBOSOMAL PROTEIN S7



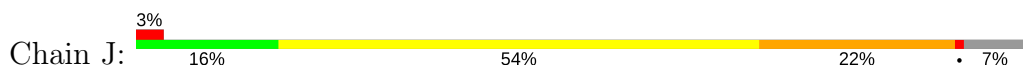
• Molecule 9: 30S RIBOSOMAL PROTEIN S8



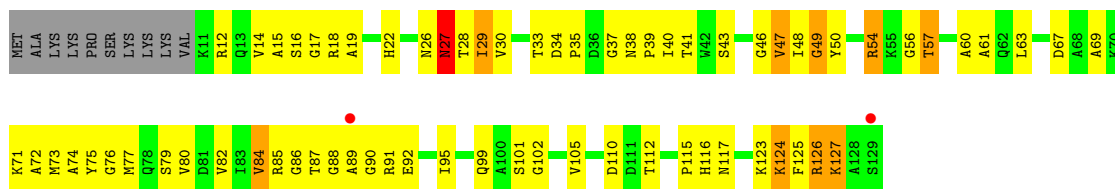
• Molecule 10: 30S RIBOSOMAL PROTEIN S9



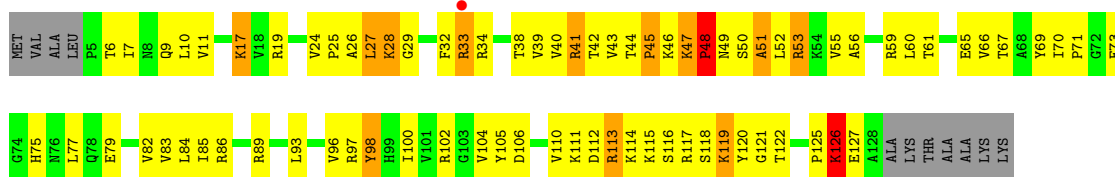
• Molecule 11: 30S RIBOSOMAL PROTEIN S10



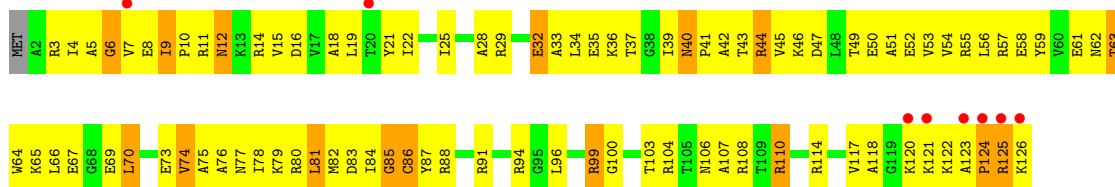
• Molecule 12: 30S RIBOSOMAL PROTEIN S11



• Molecule 13: 30S RIBOSOMAL PROTEIN S12



• Molecule 14: 30S RIBOSOMAL PROTEIN S13



• Molecule 15: 30S RIBOSOMAL PROTEIN S14

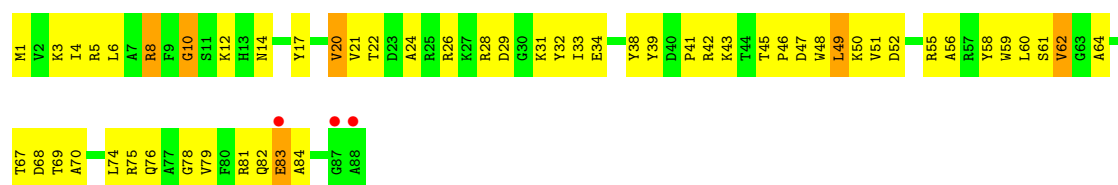


• Molecule 16: 30S RIBOSOMAL PROTEIN S15

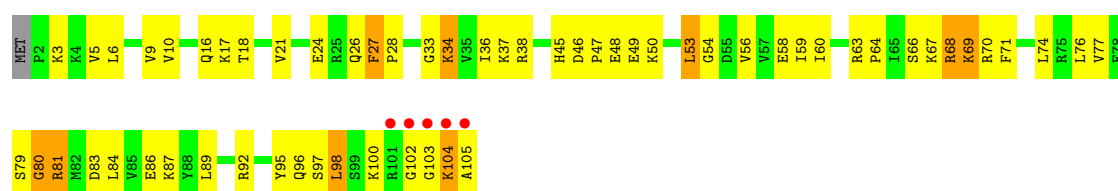
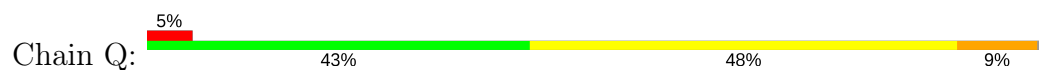




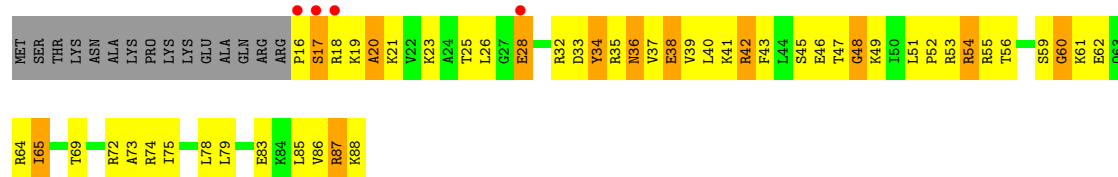
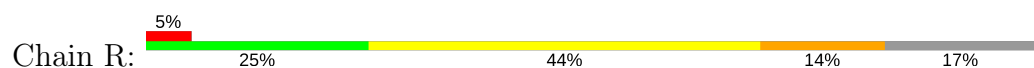
• Molecule 17: 30S RIBOSOMAL PROTEIN S16



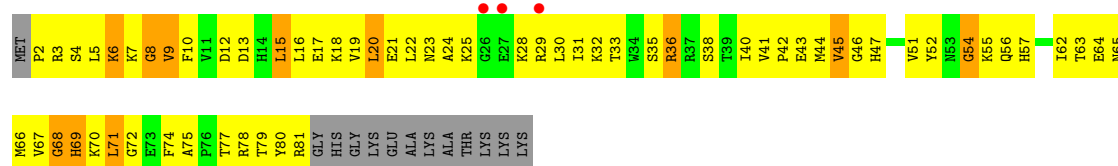
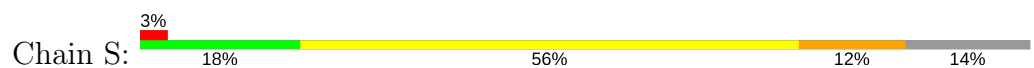
• Molecule 18: 30S RIBOSOMAL PROTEIN S17



• Molecule 19: 30S RIBOSOMAL PROTEIN S18

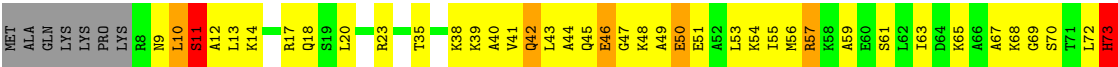


• Molecule 20: 30S RIBOSOMAL PROTEIN S19

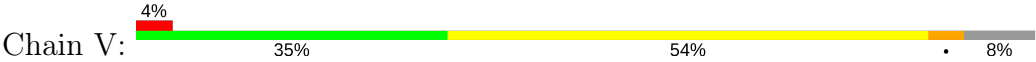


• Molecule 21: 30S RIBOSOMAL PROTEIN S20





● Molecule 22: 30S RIBOSOMAL PROTEIN THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	401.16Å 401.16Å 176.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.75 – 3.40 29.64 – 2.99	Depositor EDS
% Data completeness (in resolution range)	92.5 (29.75-3.40) 83.7 (29.64-2.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 3.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.222 , 0.264 0.201 , 0.242	Depositor DCC
R_{free} test set	9130 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	65.2	Xtriage
Anisotropy	0.419	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 69.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	51934	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.51	0/36259	0.76	47/56593 (0.1%)
2	X	0.54	0/128	0.69	0/196
3	B	0.38	0/1935	0.68	0/2609
4	C	0.38	0/1636	0.67	0/2205
5	D	0.42	0/1733	0.68	1/2318 (0.0%)
6	E	0.47	0/1162	0.78	1/1564 (0.1%)
7	F	0.34	0/856	0.64	0/1154
8	G	0.37	0/1276	0.63	0/1709
9	H	0.46	0/1136	0.75	0/1527
10	I	0.36	0/1029	0.65	0/1378
11	J	0.38	0/805	0.70	0/1082
12	K	0.39	0/900	0.71	0/1213
13	L	0.44	0/986	0.78	1/1320 (0.1%)
14	M	0.35	0/1008	0.64	0/1347
15	N	0.44	0/501	0.76	0/664
16	O	0.36	0/745	0.62	0/992
17	P	0.44	0/751	0.76	0/1008
18	Q	0.47	0/870	0.78	0/1159
19	R	0.38	0/603	0.64	0/799
20	S	0.34	0/661	0.72	1/890 (0.1%)
21	T	0.40	0/764	0.73	0/1006
22	V	0.47	0/212	0.73	0/277
All	All	0.47	0/55956	0.74	51/83010 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	3	50

There are no bond length outliers.

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1498	U	C2'-C3'-O3'	10.26	132.07	109.50
1	A	1085	U	C2'-C3'-O3'	9.36	130.08	109.50
1	A	559	A	C2'-C3'-O3'	9.22	129.78	109.50
1	A	181	G	C2'-C3'-O3'	9.18	129.70	109.50
1	A	1528	U	C2'-C3'-O3'	8.97	129.24	109.50
1	A	243	A	C2'-C3'-O3'	8.97	129.23	109.50
1	A	1299	A	N9-C1'-C2'	8.60	125.17	114.00
1	A	60	A	C2'-C3'-O3'	8.34	127.84	109.50
1	A	687	A	C2'-C3'-O3'	7.90	126.88	109.50
1	A	1302	U	C2'-C3'-O3'	7.83	126.73	109.50
1	A	108	G	O4'-C1'-N9	7.75	114.40	108.20
1	A	575	G	C2'-C3'-O3'	7.70	126.43	109.50
1	A	7	G	C2'-C3'-O3'	7.64	126.32	109.50
1	A	1504	G	C2'-C3'-O3'	7.53	126.07	109.50
1	A	792	A	C2'-C3'-O3'	7.27	125.50	109.50
1	A	484	G	C2'-C3'-O3'	7.01	124.93	109.50
1	A	197	A	N9-C1'-C2'	6.99	123.09	114.00
1	A	366	C	C2'-C3'-O3'	6.96	124.84	113.70
1	A	115	G	C2'-C3'-O3'	6.90	124.73	113.70
1	A	1364	U	C2'-C3'-O3'	6.52	124.13	113.70
1	A	509	A	C2'-C3'-O3'	6.48	124.06	113.70
1	A	960	U	C2'-C3'-O3'	6.45	124.02	113.70
1	A	1346	A	C2'-C3'-O3'	6.33	123.83	113.70
1	A	244	U	C5'-C4'-C3'	-6.30	105.92	116.00
1	A	372	C	C2'-C3'-O3'	6.27	123.73	113.70
1	A	266	G	C2'-C3'-O3'	6.25	123.70	113.70
1	A	266	G	O4'-C1'-N9	-6.23	103.22	108.20
1	A	1065	U	C1'-O4'-C4'	-6.16	104.97	109.90
1	A	353	A	C5'-C4'-O4'	-5.96	101.95	109.10
1	A	1279	A	N9-C1'-C2'	5.58	121.25	114.00
13	L	119	LYS	N-CA-C	-5.56	95.98	111.00
5	D	12	CYS	CA-CB-SG	5.54	123.97	114.00
1	A	1281	U	N1-C1'-C2'	5.52	121.17	114.00
1	A	533	A	N9-C1'-C2'	5.50	121.15	114.00
1	A	760	G	N9-C1'-C2'	-5.47	105.98	112.00
1	A	1224	G	N9-C1'-C2'	5.46	121.11	114.00
1	A	5	U	N1-C1'-C2'	5.46	121.10	114.00
20	S	54	GLY	N-CA-C	-5.38	99.64	113.10
1	A	266	G	C5'-C4'-C3'	-5.38	107.39	116.00
1	A	1380	U	C2'-C3'-O3'	5.37	122.30	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	413	G	N9-C1'-C2'	5.36	120.96	114.00
6	E	21	ALA	N-CA-C	-5.33	96.61	111.00
1	A	1124	G	N9-C1'-C2'	5.29	120.88	114.00
1	A	1305	G	N9-C1'-C2'	5.26	120.84	114.00
1	A	428	G	C2'-C3'-O3'	5.19	122.00	113.70
1	A	530	G	N9-C1'-C2'	5.09	120.61	114.00
1	A	1050	G	C5'-C4'-C3'	5.05	124.08	116.00
1	A	389	A	C5'-C4'-C3'	5.03	124.04	116.00
1	A	1067	A	C2'-C3'-O3'	5.02	121.73	113.70
1	A	115	G	N9-C1'-C2'	5.01	120.52	114.00
1	A	460	A	N9-C1'-C2'	5.01	120.52	114.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1085	U	C3'
1	A	1498	U	C3'
1	A	1528	U	C3'

All (50) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	107	G	Sidechain
1	A	1077	G	Sidechain
1	A	1079	G	Sidechain
1	A	108	G	Sidechain
1	A	12	U	Sidechain
1	A	1281	U	Sidechain
1	A	1298	C	Sidechain
1	A	1299	A	Sidechain
1	A	1330	U	Sidechain
1	A	1331	G	Sidechain
1	A	1345	U	Sidechain
1	A	1360	A	Sidechain
1	A	1393	U	Sidechain
1	A	1401	G	Sidechain
1	A	1519	A	Sidechain
1	A	197	A	Sidechain
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	253	U	Sidechain

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Mol	Chain	Res	Type	Group
1	A	266	G	Sidechain
1	A	291	C	Sidechain
1	A	303	A	Sidechain
1	A	37	U	Sidechain
1	A	380	G	Sidechain
1	A	481	G	Sidechain
1	A	521	G	Sidechain
1	A	528	C	Sidechain
1	A	561	U	Sidechain
1	A	572	A	Sidechain
1	A	575	G	Sidechain
1	A	592	G	Sidechain
1	A	636	U	Sidechain
1	A	641	U	Sidechain
1	A	657	G	Sidechain
1	A	691	G	Sidechain
1	A	705	U	Sidechain
1	A	727	G	Sidechain
1	A	77	G	Sidechain
1	A	868	C	Sidechain
1	A	873	A	Sidechain
1	A	879	C	Sidechain
1	A	897	C	Sidechain
1	A	898	G	Sidechain
1	A	915	A	Sidechain
1	A	931	C	Sidechain
1	A	942	G	Sidechain
1	A	960	U	Sidechain
1	A	963	G	Sidechain
1	A	982	U	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	1178	0
2	X	117	0	64	0	0
3	B	1900	0	1951	258	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	1612	0	1677	236	0
5	D	1703	0	1764	173	0
6	E	1146	0	1207	120	0
7	F	843	0	857	80	0
8	G	1257	0	1296	90	0
9	H	1116	0	1177	85	0
10	I	1011	0	1043	135	0
11	J	792	0	835	138	0
12	K	885	0	904	60	0
13	L	970	0	1057	98	0
14	M	997	0	1072	119	0
15	N	492	0	529	62	0
16	O	734	0	771	52	0
17	P	735	0	752	71	0
18	Q	857	0	930	72	0
19	R	597	0	668	89	0
20	S	647	0	673	89	0
21	T	762	0	859	80	0
22	V	208	0	221	22	0
23	A	94	0	0	0	0
23	D	1	0	0	0	0
23	H	1	0	0	0	0
24	D	1	0	0	0	0
24	N	1	0	0	0	0
25	A	64	0	45	4	0
All	All	51934	0	36701	3016	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 34.

All (3016) 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)
4:C:94:LEU:HD23	4:C:95:THR:HG23	1.27	1.16
1:A:1443:G:H5''	1:A:1446:A:H5'	1.21	1.12
13:L:41:ARG:HG2	13:L:42:THR:H	1.03	1.12
5:D:36:ARG:H	5:D:37:PRO:HD3	1.09	1.11
3:B:77:ALA:HB2	3:B:211:ILE:HD13	1.26	1.11
6:E:110:LEU:HD13	6:E:118:ILE:HD12	1.33	1.10
10:I:8:GLY:HA2	10:I:79:LEU:HD12	1.24	1.10
20:S:55:LYS:HG2	20:S:56:GLN:HE21	1.13	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1057:G:H5''	4:C:154:SER:HB2	1.36	1.07
11:J:51:ARG:HB2	11:J:59:SER:HB3	1.30	1.07
1:A:243:A:H4'	1:A:244:U:H5'	1.30	1.06
14:M:117:VAL:HG12	14:M:118:ALA:H	1.21	1.05
1:A:1060:C:C5	4:C:2:GLY:HA3	1.93	1.04
11:J:45:ARG:HH11	11:J:45:ARG:HB3	1.18	1.04
19:R:53:ARG:HH11	19:R:59:SER:HA	1.15	1.03
1:A:1250:A:H4'	10:I:68:GLY:H	1.21	1.02
6:E:81:GLU:HG2	6:E:90:VAL:HG22	1.40	1.01
1:A:953:G:H1'	14:M:125:ARG:HA	1.41	1.00
12:K:40:ILE:HG22	12:K:41:THR:HG23	1.40	0.99
21:T:39:LYS:HD2	21:T:55:ILE:HD13	1.44	0.99
3:B:84:GLU:HB3	3:B:219:VAL:HG21	1.44	0.99
11:J:31:GLY:HA2	11:J:78:ASN:HD22	1.25	0.98
8:G:69:VAL:HG21	8:G:104:LEU:HD21	1.45	0.98
1:A:761:G:H4'	18:Q:103:GLY:N	1.79	0.97
4:C:91:LEU:HD21	4:C:99:VAL:HG13	1.42	0.97
1:A:1047:G:H5''	15:N:4:LYS:HD2	1.47	0.96
4:C:174:PRO:HB2	4:C:177:THR:HG22	1.48	0.96
1:A:351:G:H4'	1:A:352:C:OP1	1.63	0.95
6:E:80:ILE:HD11	6:E:91:LEU:HD12	1.46	0.95
19:R:53:ARG:NH1	19:R:60:GLY:H	1.64	0.95
1:A:1086:U:H3	1:A:1099:G:H22	1.01	0.94
14:M:10:PRO:HB2	14:M:18:ALA:HB1	1.47	0.94
1:A:1190:G:OP1	4:C:4:LYS:HA	1.68	0.94
3:B:200:ILE:HG22	3:B:202:PRO:HD3	1.50	0.94
1:A:1060:C:H5	4:C:2:GLY:HA3	1.30	0.93
4:C:110:ASN:HD21	4:C:140:ARG:HB3	1.33	0.93
8:G:75:VAL:HG11	8:G:86:GLN:HB3	1.50	0.93
21:T:54:LYS:HG3	21:T:100:ILE:HD13	1.50	0.93
22:V:6:ARG:HH11	22:V:15:ARG:HH12	1.17	0.92
1:A:1238:A:H5'	1:A:1336:C:H41	1.33	0.92
12:K:110:ASP:HB2	19:R:88:LYS:HD2	1.51	0.92
1:A:64:G:H4'	1:A:65:U:O5'	1.69	0.92
9:H:10:LEU:HD22	9:H:83:ILE:HD11	1.48	0.92
19:R:39:VAL:HG13	19:R:40:LEU:HD23	1.52	0.92
11:J:96:ILE:HG22	11:J:97:GLU:H	1.34	0.90
3:B:77:ALA:HB2	3:B:211:ILE:CD1	2.01	0.90
14:M:49:THR:HG22	14:M:51:ALA:H	1.35	0.89
1:A:99:C:H2'	1:A:101:A:C8	2.07	0.88
1:A:141:A:H1'	1:A:182:U:O2	1.73	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:150:LYS:HE2	4:C:152:ILE:HD11	1.54	0.88
1:A:1141:C:H2'	1:A:1142:G:H8	1.37	0.88
4:C:14:ILE:HG22	4:C:15:THR:H	1.36	0.88
5:D:156:GLU:HG2	5:D:160:GLN:HE21	1.38	0.88
1:A:1298:C:H2'	8:G:114:ARG:HH12	1.36	0.88
11:J:32:ALA:HB2	11:J:75:ILE:O	1.74	0.87
13:L:41:ARG:HG2	13:L:42:THR:N	1.87	0.87
5:D:23:GLY:HA3	5:D:112:VAL:HG12	1.54	0.87
1:A:80:G:H3'	1:A:81:U:H5''	1.54	0.87
1:A:761:G:C2	18:Q:105:ALA:HB3	2.09	0.86
6:E:110:LEU:HD13	6:E:118:ILE:CD1	2.03	0.86
6:E:51:VAL:HB	6:E:52:PRO:HD3	1.57	0.86
1:A:1125:U:H3	11:J:5:ARG:HH21	1.19	0.86
11:J:38:ILE:HG13	11:J:71:LEU:HB3	1.55	0.86
1:A:1116:C:H2'	1:A:1117:G:H5''	1.54	0.86
1:A:664:G:H22	1:A:741:G:H1	1.16	0.86
3:B:132:LYS:HA	3:B:135:GLN:HB3	1.57	0.86
3:B:88:ALA:O	3:B:90:MET:N	2.09	0.86
1:A:1101:A:H4'	1:A:1102:A:O5'	1.76	0.85
5:D:36:ARG:N	5:D:37:PRO:HD3	1.91	0.85
13:L:75:HIS:HD2	13:L:77:LEU:H	1.21	0.85
1:A:1497:G:C2'	1:A:1498:U:H5'	2.07	0.85
4:C:179:ARG:O	4:C:179:ARG:HG2	1.76	0.84
1:A:1040:U:H2'	1:A:1041:A:C8	2.12	0.84
1:A:1053:G:C4'	1:A:1054:C:H5'	2.07	0.84
1:A:1305:G:HO2'	1:A:1306:A:H8	0.86	0.84
4:C:131:ARG:HG2	4:C:135:LYS:HE3	1.57	0.84
11:J:53:PRO:HA	15:N:41:ARG:HH21	1.39	0.84
1:A:1305:G:O2'	1:A:1306:A:H8	1.60	0.84
11:J:90:LEU:H	11:J:91:PRO:HD2	1.41	0.84
14:M:50:GLU:O	14:M:54:VAL:HG23	1.77	0.84
3:B:77:ALA:CB	3:B:211:ILE:HD13	2.06	0.84
3:B:80:ILE:HD11	3:B:208:ILE:HG23	1.60	0.83
11:J:28:ARG:NH1	11:J:33:GLN:HG2	1.93	0.83
17:P:58:TYR:O	17:P:61:SER:HB3	1.77	0.83
6:E:43:LEU:HD11	6:E:132:ALA:HB1	1.59	0.83
1:A:1226:C:H4'	1:A:1227:A:OP1	1.78	0.83
1:A:438:G:H4'	1:A:439:A:OP1	1.78	0.83
6:E:11:ILE:HB	6:E:31:LEU:HB3	1.60	0.83
14:M:3:ARG:HA	14:M:8:GLU:O	1.77	0.83
8:G:78:ARG:HB2	8:G:156:TRP:HZ3	1.42	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:117:VAL:HG12	14:M:118:ALA:N	1.92	0.83
1:A:195:A:H4'	21:T:68:LYS:HE2	1.58	0.83
1:A:760:G:O6	18:Q:105:ALA:HB2	1.77	0.83
11:J:45:ARG:HH11	11:J:45:ARG:CB	1.91	0.83
13:L:41:ARG:CG	13:L:42:THR:H	1.84	0.83
20:S:16:LEU:O	20:S:19:VAL:HG12	1.77	0.83
10:I:8:GLY:CA	10:I:79:LEU:HD12	2.07	0.82
11:J:60:ARG:N	11:J:60:ARG:HD2	1.92	0.82
10:I:93:ARG:HD3	10:I:97:LYS:HE3	1.60	0.82
12:K:54:ARG:O	12:K:57:THR:HG22	1.78	0.82
13:L:27:LEU:O	13:L:29:GLY:N	2.11	0.82
14:M:78:ILE:HA	14:M:81:LEU:HD21	1.61	0.82
1:A:1195:C:H3'	1:A:1196:U:H5''	1.59	0.82
1:A:501:C:H2'	1:A:502:G:H8	1.41	0.82
4:C:191:THR:HG22	4:C:192:THR:N	1.92	0.82
1:A:1443:G:C5'	1:A:1446:A:H5'	2.08	0.82
3:B:124:SER:HB2	3:B:125:PRO:HD2	1.62	0.82
4:C:70:VAL:HG12	4:C:72:LYS:H	1.44	0.82
14:M:40:ASN:HD22	14:M:41:PRO:CD	1.92	0.82
1:A:1137:C:H4'	1:A:1138:G:C2	2.14	0.82
5:D:150:GLU:CD	5:D:150:GLU:H	1.83	0.82
6:E:64:ARG:O	6:E:65:ASN:HB3	1.78	0.81
3:B:91:PRO:HG3	3:B:154:LEU:HB2	1.63	0.81
1:A:243:A:C4'	1:A:244:U:H5'	2.10	0.81
5:D:36:ARG:H	5:D:37:PRO:CD	1.91	0.81
14:M:120:LYS:HE2	14:M:123:ALA:HB2	1.62	0.81
4:C:58:GLU:HB3	11:J:92:THR:HG21	1.62	0.81
1:A:1250:A:C4'	10:I:68:GLY:H	1.93	0.81
5:D:114:ARG:HG3	5:D:114:ARG:HH11	1.45	0.81
13:L:46:LYS:HG2	13:L:47:LYS:H	1.45	0.81
1:A:1497:G:O2'	1:A:1498:U:H5'	1.80	0.80
17:P:74:LEU:O	17:P:79:VAL:HG23	1.81	0.80
1:A:1356:G:H2'	1:A:1357:A:C8	2.17	0.80
1:A:353:A:H5'	1:A:353:A:H8	1.46	0.80
1:A:405:U:H3'	1:A:406:G:H5'	1.61	0.80
3:B:114:ARG:HH11	3:B:118:LEU:HD21	1.45	0.80
12:K:57:THR:HG23	12:K:60:ALA:H	1.46	0.80
12:K:87:THR:HA	12:K:91:ARG:HH21	1.45	0.80
4:C:110:ASN:O	4:C:111:LEU:HD23	1.79	0.80
4:C:134:ILE:HG23	4:C:151:VAL:HB	1.63	0.80
1:A:1256:A:H4'	1:A:1257:U:H5'	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:28:LYS:HD2	13:L:33:ARG:HH22	1.46	0.80
19:R:36:ASN:HD22	19:R:38:GLU:HG2	1.47	0.80
20:S:17:GLU:HA	20:S:20:LEU:HD11	1.61	0.80
3:B:21:ARG:HG3	3:B:23:ARG:HD2	1.64	0.80
13:L:6:THR:OG1	13:L:9:GLN:HG3	1.82	0.80
13:L:55:VAL:HG12	13:L:56:ALA:H	1.47	0.80
3:B:68:ILE:H	3:B:90:MET:HE3	1.47	0.79
4:C:83:ARG:HA	4:C:86:VAL:HG23	1.63	0.79
7:F:21:LEU:O	7:F:24:GLU:HB3	1.81	0.79
21:T:53:LEU:HD21	21:T:104:LEU:HD12	1.64	0.79
13:L:27:LEU:C	13:L:29:GLY:H	1.86	0.79
20:S:33:THR:HG22	20:S:35:SER:H	1.44	0.79
9:H:51:VAL:HG21	9:H:60:ARG:HG3	1.64	0.79
3:B:150:SER:O	3:B:153:ARG:HB2	1.82	0.79
5:D:148:VAL:HG11	5:D:158:ILE:HG21	1.64	0.79
1:A:1117:G:H4'	10:I:104:ARG:NH1	1.97	0.79
18:Q:97:SER:HB2	18:Q:103:GLY:N	1.97	0.79
1:A:1250:A:H4'	10:I:68:GLY:N	1.95	0.79
16:O:78:TYR:CZ	16:O:82:ILE:HD11	2.17	0.79
1:A:1053:G:H4'	1:A:1054:C:H5'	1.64	0.78
1:A:1064:G:H4'	1:A:1065:U:H5'	1.64	0.78
11:J:39:PRO:HA	11:J:70:ARG:HH11	1.48	0.78
1:A:197:A:H4'	1:A:198:G:O5'	1.82	0.78
11:J:44:VAL:HG22	11:J:66:ARG:HB3	1.64	0.78
4:C:195:VAL:O	4:C:196:LEU:HD23	1.82	0.78
6:E:12:LEU:HD13	6:E:31:LEU:HB2	1.64	0.78
15:N:26:ARG:NH1	15:N:47:LEU:HG	1.98	0.78
11:J:39:PRO:O	11:J:40:LEU:HB2	1.83	0.78
1:A:839:U:H5'	1:A:840:C:H5	1.48	0.78
15:N:24:CYS:HB3	15:N:28:GLY:H	1.47	0.78
6:E:57:LYS:HG2	6:E:61:TYR:CE2	2.18	0.78
13:L:24:VAL:HG13	13:L:98:TYR:CE2	2.17	0.78
1:A:1443:G:H5''	1:A:1446:A:C5'	2.07	0.78
3:B:143:GLU:O	3:B:147:LYS:HG3	1.84	0.78
13:L:55:VAL:HG12	13:L:56:ALA:N	1.99	0.78
9:H:36:LEU:HD12	9:H:59:LEU:HD13	1.66	0.78
9:H:84:ARG:HD2	9:H:85:ARG:O	1.84	0.78
11:J:22:LYS:HE2	11:J:90:LEU:HD12	1.64	0.78
12:K:27:ASN:HA	12:K:56:GLY:HA2	1.66	0.78
12:K:54:ARG:HH11	12:K:54:ARG:HB3	1.47	0.78
14:M:110:ARG:HG2	14:M:110:ARG:HH11	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:A:H4'	1:A:251:G:O5'	1.84	0.77
6:E:75:THR:HG23	6:E:76:ILE:N	1.98	0.77
1:A:953:G:C1'	14:M:125:ARG:HA	2.13	0.77
1:A:1168:A:H2'	1:A:1169:A:C8	2.19	0.77
1:A:370:C:O2'	1:A:371:G:H5'	1.83	0.77
3:B:17:PHE:HB3	3:B:44:LEU:HD11	1.65	0.77
3:B:23:ARG:N	3:B:23:ARG:HD3	2.00	0.77
14:M:65:LYS:HG3	14:M:69:GLU:OE2	1.85	0.77
1:A:1251:A:H2'	1:A:1252:A:C8	2.19	0.77
18:Q:97:SER:HB2	18:Q:102:GLY:C	2.05	0.77
1:A:923:A:OP1	6:E:21:ALA:HB2	1.84	0.77
7:F:8:ILE:HD11	7:F:79:LEU:HD13	1.67	0.77
1:A:1152:A:H5''	11:J:13:HIS:CD2	2.19	0.77
13:L:27:LEU:HG	13:L:28:LYS:H	1.48	0.77
15:N:23:ARG:NH1	15:N:30:ALA:HB2	2.00	0.77
7:F:101:ALA:HB2	19:R:28:GLU:HB3	1.67	0.77
4:C:108:ASN:ND2	4:C:111:LEU:HG	2.00	0.77
9:H:10:LEU:CD2	9:H:83:ILE:HD11	2.15	0.77
1:A:1236:A:H4'	1:A:1304:G:H4'	1.67	0.76
1:A:80:G:C3'	1:A:81:U:H5''	2.15	0.76
1:A:877:C:O2	9:H:3:THR:HG21	1.85	0.76
3:B:101:MET:HA	3:B:108:ILE:HD12	1.66	0.76
3:B:209:ARG:HE	3:B:239:VAL:HG11	1.50	0.76
1:A:1132:C:H2'	1:A:1133:G:C8	2.20	0.76
1:A:839:U:H5'	1:A:840:C:C5	2.20	0.76
4:C:50:ALA:HB1	4:C:70:VAL:HG11	1.66	0.76
6:E:89:ILE:HD13	6:E:90:VAL:H	1.50	0.76
13:L:24:VAL:HG13	13:L:98:TYR:HE2	1.51	0.76
18:Q:24:GLU:OE2	18:Q:37:LYS:HD3	1.86	0.76
1:A:1116:C:C2'	1:A:1117:G:H5''	2.14	0.76
1:A:474:G:H2'	1:A:475:G:H8	1.49	0.76
3:B:23:ARG:HH11	3:B:24:TRP:N	1.82	0.76
11:J:62:HIS:HB3	15:N:59:ALA:HB3	1.66	0.76
3:B:185:ILE:HG23	3:B:199:TYR:HB2	1.66	0.76
9:H:29:SER:OG	9:H:32:LYS:HB2	1.86	0.76
13:L:25:PRO:C	13:L:27:LEU:H	1.85	0.76
4:C:26:LYS:H	4:C:26:LYS:HD3	1.50	0.76
17:P:21:VAL:HG21	17:P:59:TRP:CD1	2.21	0.76
21:T:50:GLU:HG2	21:T:100:ILE:HG13	1.67	0.75
1:A:192:U:H1'	21:T:103:GLY:HA2	1.69	0.75
18:Q:21:VAL:HG21	18:Q:59:ILE:HD11	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190(F):G:H4'	1:A:190(G):G:OP2	1.84	0.75
4:C:188:LEU:CD1	4:C:189:ALA:H	1.99	0.75
6:E:31:LEU:HD22	6:E:43:LEU:HD21	1.68	0.75
1:A:1035:A:H2'	1:A:1036:G:H8	1.51	0.75
1:A:1281:U:H5'	1:A:1282:C:H5	1.51	0.75
1:A:579:G:H5'	1:A:728:A:H1'	1.68	0.75
4:C:52:LEU:H	4:C:52:LEU:HD23	1.51	0.75
11:J:96:ILE:HG22	11:J:97:GLU:N	2.01	0.75
1:A:650:G:O2'	1:A:651:C:H5'	1.86	0.75
1:A:371:G:O2'	1:A:372:C:H5'	1.87	0.74
12:K:18:ARG:HB2	12:K:33:THR:HG23	1.69	0.74
1:A:382:A:H2'	1:A:383:A:C8	2.21	0.74
10:I:5:TYR:O	10:I:84:ALA:HA	1.87	0.74
12:K:19:ALA:HB2	12:K:80:VAL:HG11	1.68	0.74
3:B:114:ARG:NH1	3:B:118:LEU:HD21	2.01	0.74
5:D:35:ARG:O	5:D:36:ARG:HB2	1.86	0.74
8:G:23:VAL:O	8:G:27:ILE:HG13	1.87	0.74
3:B:223:ILE:C	3:B:225:ALA:H	1.91	0.74
13:L:97:ARG:HB2	13:L:98:TYR:CE1	2.22	0.74
5:D:29:PRO:O	5:D:30:LYS:HG3	1.87	0.74
1:A:80:G:H3'	1:A:81:U:C5'	2.16	0.74
1:A:840:C:H5''	1:A:841:U:OP1	1.88	0.74
4:C:5:ILE:HD13	4:C:10:PHE:HB2	1.68	0.74
4:C:7:PRO:O	4:C:11:ARG:HD2	1.87	0.74
11:J:28:ARG:HH12	11:J:33:GLN:HG2	1.53	0.74
11:J:51:ARG:CB	11:J:59:SER:HB3	2.15	0.74
1:A:673:G:H2'	1:A:674:G:C8	2.22	0.74
9:H:60:ARG:HG3	9:H:60:ARG:HH11	1.51	0.74
10:I:118:LYS:O	10:I:119:ALA:HB3	1.86	0.74
16:O:29:VAL:HG12	16:O:85:LEU:HD11	1.68	0.74
1:A:173:U:H5'	1:A:197:A:O4'	1.87	0.74
16:O:29:VAL:HG12	16:O:85:LEU:CD1	2.17	0.74
1:A:7:G:H5'	1:A:298:A:O4'	1.87	0.73
4:C:15:THR:O	4:C:16:ARG:HB2	1.87	0.73
13:L:47:LYS:CB	13:L:48:PRO:HD3	2.17	0.73
1:A:1057:G:H5''	4:C:154:SER:CB	2.15	0.73
14:M:49:THR:HG22	14:M:51:ALA:N	2.03	0.73
1:A:1167:A:H2'	1:A:1168:A:C8	2.24	0.73
7:F:9:VAL:HB	7:F:87:ARG:HB2	1.70	0.73
17:P:26:ARG:HD2	17:P:31:LYS:O	1.87	0.73
1:A:1352:C:H2'	1:A:1353:G:C8	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:61:LYS:HD2	5:D:207:TYR:OH	1.87	0.73
1:A:1281:U:H4'	1:A:1282:C:OP2	1.88	0.73
3:B:164:VAL:HG12	3:B:186:ALA:HB2	1.70	0.73
11:J:38:ILE:CG1	11:J:71:LEU:HB3	2.19	0.73
11:J:4:ILE:HA	11:J:100:THR:HA	1.69	0.73
1:A:390:C:O3'	17:P:28:ARG:NH2	2.22	0.73
3:B:139:LYS:O	3:B:143:GLU:HG2	1.87	0.73
5:D:25:ARG:C	5:D:27:TYR:H	1.90	0.72
10:I:97:LYS:CG	10:I:102:LEU:HD12	2.19	0.72
10:I:97:LYS:HG2	10:I:102:LEU:HD12	1.71	0.72
1:A:1323:G:H2'	1:A:1324:A:C8	2.24	0.72
1:A:1117:G:H4'	10:I:104:ARG:HH11	1.54	0.72
8:G:78:ARG:HB2	8:G:156:TRP:CZ3	2.25	0.72
19:R:36:ASN:ND2	19:R:38:GLU:HG2	2.03	0.72
4:C:149:ALA:HA	4:C:201:TYR:O	1.89	0.72
7:F:38:GLU:O	7:F:39:LYS:HB3	1.88	0.72
11:J:6:ILE:HG23	11:J:98:ILE:HG12	1.72	0.72
20:S:25:LYS:HD2	20:S:25:LYS:H	1.54	0.72
1:A:1279:A:H5''	1:A:1280:A:OP1	1.89	0.72
16:O:30:ALA:HA	16:O:85:LEU:HD21	1.71	0.72
1:A:1086:U:H3	1:A:1099:G:N2	1.83	0.72
1:A:1497:G:H2'	1:A:1498:U:H5'	1.71	0.72
18:Q:59:ILE:CG2	18:Q:71:PHE:HB3	2.19	0.72
1:A:1142:G:H2'	1:A:1143:G:O4'	1.90	0.72
1:A:1053:G:C3'	1:A:1054:C:H5'	2.19	0.72
1:A:149:A:H2'	1:A:150:C:C6	2.24	0.72
3:B:22:LYS:HD2	3:B:35:GLU:OE1	1.89	0.72
1:A:1319:A:H5'	1:A:1320:C:OP1	1.90	0.71
1:A:992:U:H4'	1:A:993:G:O5'	1.88	0.71
1:A:953:G:H1'	14:M:125:ARG:CA	2.18	0.71
3:B:197:VAL:HB	3:B:200:ILE:HG13	1.72	0.71
4:C:179:ARG:HD3	4:C:206:GLU:HG2	1.71	0.71
3:B:36:ARG:HD2	3:B:41:ILE:HD12	1.73	0.71
11:J:35:SER:HB2	11:J:72:VAL:O	1.91	0.71
14:M:40:ASN:HD22	14:M:41:PRO:HD2	1.53	0.71
19:R:53:ARG:HH11	19:R:59:SER:CA	1.99	0.71
1:A:1065:U:H4'	1:A:1066:C:O5'	1.90	0.71
1:A:839:U:O2	1:A:839:U:H2'	1.90	0.71
4:C:191:THR:HG22	4:C:192:THR:H	1.53	0.71
15:N:27:CYS:SG	15:N:29:ARG:HB2	2.31	0.71
16:O:16:ALA:HB1	16:O:21:ASP:HB3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1125:U:H3	11:J:5:ARG:NH2	1.88	0.71
1:A:35:G:H2'	1:A:36:C:C6	2.25	0.71
4:C:190:ARG:HB3	4:C:190:ARG:NH1	2.05	0.71
1:A:977:A:H2'	1:A:978:A:H5''	1.73	0.71
3:B:68:ILE:N	3:B:90:MET:HE3	2.06	0.71
4:C:110:ASN:ND2	4:C:140:ARG:HB3	2.04	0.71
9:H:19:VAL:HG23	9:H:21:LYS:HD3	1.71	0.71
1:A:1251:A:H4'	10:I:12:GLU:OE2	1.90	0.71
13:L:83:VAL:HG21	13:L:100:ILE:HD13	1.72	0.71
1:A:353:A:H5'	1:A:353:A:C8	2.26	0.71
1:A:761:G:H4'	18:Q:103:GLY:H	1.55	0.71
6:E:80:ILE:HD12	6:E:80:ILE:O	1.91	0.71
10:I:19:LEU:HD11	10:I:85:LEU:HD12	1.71	0.71
1:A:1161:C:H2'	1:A:1162:C:H6	1.55	0.71
1:A:328:C:H4'	1:A:329:A:O5'	1.90	0.71
1:A:411:A:C4	1:A:413:G:H1'	2.26	0.71
4:C:11:ARG:HH12	4:C:179:ARG:H	1.35	0.71
4:C:96:GLY:O	4:C:98:ASN:N	2.24	0.71
9:H:138:TRP:OXT	9:H:138:TRP:HE3	1.73	0.71
11:J:31:GLY:HA2	11:J:78:ASN:ND2	2.05	0.71
1:A:328:C:O2	1:A:328:C:H2'	1.89	0.71
1:A:1038:C:H2'	1:A:1039:C:C5	2.26	0.70
14:M:117:VAL:CG1	14:M:118:ALA:H	2.01	0.70
1:A:975:A:H5'	1:A:975:A:H8	1.56	0.70
4:C:6:HIS:HD2	4:C:8:ILE:H	1.38	0.70
13:L:47:LYS:HB2	13:L:48:PRO:HD3	1.71	0.70
1:A:1131:G:H1	1:A:1143:G:H21	1.38	0.70
1:A:8:A:N6	5:D:209:ARG:HB2	2.06	0.70
18:Q:27:PHE:CZ	18:Q:36:ILE:HD11	2.26	0.70
1:A:1025:U:H2'	1:A:1026:G:C8	2.26	0.70
17:P:28:ARG:HG3	17:P:29:ASP:OD2	1.91	0.70
1:A:1064:G:H4'	1:A:1065:U:C5'	2.22	0.70
4:C:10:PHE:CZ	4:C:178:LEU:HD13	2.25	0.70
5:D:8:VAL:O	5:D:10:ARG:N	2.24	0.70
1:A:1487:G:O2'	1:A:1488:G:H5'	1.91	0.70
1:A:269:C:H2'	1:A:270:A:H8	1.57	0.70
1:A:701:C:H5'	1:A:703:G:O4'	1.91	0.70
13:L:75:HIS:CD2	13:L:77:LEU:H	2.08	0.70
4:C:29:TYR:OH	15:N:54:PRO:HG2	1.92	0.70
1:A:1208:C:H2'	1:A:1209:C:H6	1.56	0.70
1:A:1493:A:O2'	1:A:1494:G:H5'	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1499:A:O2'	1:A:1500:A:H5'	1.92	0.70
1:A:939:G:H5''	8:G:102:ARG:HH22	1.57	0.70
10:I:26:VAL:HB	10:I:33:PHE:HB2	1.74	0.70
21:T:70:SER:HA	21:T:73:HIS:CD2	2.26	0.70
3:B:151:GLY:C	3:B:153:ARG:H	1.94	0.70
3:B:222:ILE:O	3:B:226:ARG:HG3	1.92	0.70
15:N:14:PRO:C	15:N:16:PHE:H	1.95	0.70
18:Q:63:ARG:HG2	18:Q:64:PRO:HD2	1.74	0.70
1:A:1028:C:H2'	1:A:1029:C:C6	2.26	0.70
1:A:107:G:C2'	1:A:108:G:H5'	2.21	0.70
1:A:1256:A:N6	1:A:1278:U:H1'	2.07	0.70
1:A:1298:C:C5	8:G:114:ARG:HD3	2.27	0.70
8:G:26:PHE:CE2	8:G:30:ILE:HD11	2.26	0.70
20:S:15:LEU:HD12	20:S:16:LEU:N	2.07	0.70
1:A:135:C:O2	17:P:1:MET:HB2	1.92	0.69
1:A:1475:G:H2'	1:A:1476:G:H8	1.56	0.69
3:B:16:HIS:CE1	3:B:214:ILE:HG12	2.26	0.69
11:J:39:PRO:HA	11:J:70:ARG:NH1	2.07	0.69
1:A:1250:A:C5'	10:I:68:GLY:H	2.05	0.69
4:C:38:ARG:HH11	4:C:38:ARG:HG3	1.56	0.69
7:F:33:TYR:HA	7:F:71:ARG:NH2	2.07	0.69
10:I:93:ARG:HH11	10:I:97:LYS:HZ2	1.38	0.69
20:S:70:LYS:O	20:S:72:GLY:N	2.25	0.69
1:A:551:U:H2'	1:A:552:U:C6	2.27	0.69
3:B:71:VAL:HB	3:B:164:VAL:HG23	1.75	0.69
4:C:108:ASN:HD22	4:C:111:LEU:HG	1.57	0.69
14:M:4:ILE:HG22	14:M:5:ALA:N	2.07	0.69
8:G:46:ALA:O	8:G:50:ILE:HG13	1.93	0.69
12:K:18:ARG:HB2	12:K:33:THR:CG2	2.23	0.69
11:J:78:ASN:O	11:J:80:LYS:N	2.25	0.69
16:O:26:GLU:OE1	16:O:77:ARG:HD2	1.93	0.69
20:S:63:THR:HG22	20:S:64:GLU:H	1.56	0.69
1:A:1128:C:H1'	1:A:1146:A:H61	1.57	0.69
1:A:397:A:H5'	1:A:398:C:OP1	1.93	0.69
3:B:76:GLN:HG3	3:B:206:ASP:OD1	1.93	0.69
21:T:10:LEU:O	21:T:12:ALA:N	2.26	0.69
1:A:1128:C:H4'	10:I:16:ARG:NH1	2.08	0.69
14:M:15:VAL:HG23	14:M:43:THR:O	1.92	0.69
14:M:78:ILE:HG22	14:M:82:MET:HE3	1.74	0.69
11:J:3:LYS:HG3	11:J:75:ILE:HG23	1.73	0.69
12:K:110:ASP:CB	19:R:88:LYS:HD2	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1157:A:H4'	1:A:1158:C:O5'	1.92	0.69
1:A:620:C:N1	5:D:135:LEU:HD13	2.08	0.69
5:D:30:LYS:C	5:D:32:ALA:H	1.95	0.69
8:G:78:ARG:NH1	8:G:154:TYR:HB3	2.08	0.69
8:G:38:LEU:HD12	8:G:38:LEU:O	1.93	0.69
17:P:82:GLN:O	17:P:84:ALA:N	2.26	0.69
1:A:113:G:H1'	1:A:354:G:H5'	1.75	0.68
14:M:81:LEU:HD22	14:M:81:LEU:H	1.58	0.68
20:S:64:GLU:O	20:S:67:VAL:HG23	1.93	0.68
1:A:107:G:H2'	1:A:108:G:H5'	1.74	0.68
4:C:113:ALA:HB3	4:C:114:PRO:HD3	1.72	0.68
13:L:17:LYS:HE3	13:L:17:LYS:HA	1.75	0.68
20:S:55:LYS:HG2	20:S:56:GLN:NE2	1.98	0.68
21:T:45:GLN:HB2	21:T:91:LEU:HD22	1.74	0.68
1:A:1428:A:H2'	1:A:1429:C:C6	2.28	0.68
9:H:113:SER:HB2	9:H:134:ILE:HD11	1.75	0.68
4:C:35:GLU:HG2	4:C:59:ARG:HH22	1.58	0.68
13:L:45:PRO:HG3	13:L:53:ARG:HD3	1.74	0.68
1:A:922:G:H5'	6:E:19:MET:O	1.93	0.68
11:J:61:GLU:OE1	15:N:45:ARG:NH1	2.27	0.68
1:A:1038:C:H2'	1:A:1039:C:C6	2.29	0.68
1:A:1148:U:H2'	1:A:1149:C:O4'	1.93	0.68
7:F:76:ALA:O	7:F:80:ARG:HG3	1.92	0.68
19:R:48:GLY:O	19:R:74:ARG:NH2	2.26	0.68
1:A:1257:U:H4'	1:A:1258:G:O5'	1.94	0.68
3:B:124:SER:HB2	3:B:125:PRO:CD	2.24	0.68
1:A:1533:C:H2'	1:A:1533:C:O2	1.92	0.68
1:A:853:G:O2'	1:A:854:G:H5'	1.94	0.68
11:J:38:ILE:CD1	11:J:71:LEU:HB3	2.23	0.68
13:L:46:LYS:NZ	13:L:47:LYS:HE3	2.09	0.68
15:N:24:CYS:HB3	15:N:28:GLY:N	2.08	0.68
7:F:4:TYR:OH	7:F:69:GLU:HB3	1.92	0.68
11:J:51:ARG:H	11:J:59:SER:HB2	1.59	0.68
1:A:418:C:H2'	1:A:419:C:H6	1.59	0.67
1:A:664:G:OP1	19:R:64:ARG:HD2	1.94	0.67
3:B:102:LEU:HD21	3:B:162:ILE:HD11	1.75	0.67
9:H:23:SER:OG	9:H:60:ARG:HD3	1.94	0.67
9:H:63:LEU:H	9:H:63:LEU:HD22	1.58	0.67
1:A:1141:C:H2'	1:A:1142:G:C8	2.25	0.67
1:A:882:C:O2'	1:A:883:C:H5'	1.94	0.67
3:B:178:ARG:O	9:H:71:GLY:HA2	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:C:H2'	1:A:270:A:C8	2.29	0.67
10:I:24:GLY:HA2	10:I:59:PHE:O	1.94	0.67
1:A:1330:U:H2'	1:A:1331:G:H5'	1.75	0.67
1:A:677:U:H3	1:A:713:G:H22	1.39	0.67
6:E:24:ARG:HH11	6:E:24:ARG:HG2	1.60	0.67
3:B:178:ARG:HG3	3:B:178:ARG:HH11	1.59	0.67
5:D:152:SER:HB3	5:D:155:LEU:HD12	1.76	0.67
1:A:1133:G:H2'	1:A:1134:G:H8	1.60	0.67
4:C:107:GLN:H	4:C:107:GLN:CD	1.97	0.67
4:C:11:ARG:HH11	4:C:11:ARG:HG2	1.58	0.67
6:E:80:ILE:HD11	6:E:91:LEU:CD1	2.25	0.67
1:A:1152:A:H5''	11:J:13:HIS:HD2	1.59	0.67
1:A:31:G:N1	1:A:48:C:H5''	2.10	0.67
19:R:34:TYR:CD1	19:R:35:ARG:HG3	2.30	0.67
1:A:1502:A:H2	1:A:1505:G:H1	1.42	0.67
9:H:9:MET:SD	9:H:32:LYS:HG2	2.35	0.67
18:Q:67:LYS:O	18:Q:68:ARG:HB3	1.94	0.67
20:S:40:ILE:HA	20:S:44:MET:HE3	1.77	0.67
1:A:1369:C:H2'	1:A:1370:G:C8	2.29	0.66
1:A:77:G:O2'	1:A:78:G:H5'	1.94	0.66
4:C:112:SER:HB3	4:C:115:LEU:HD12	1.77	0.66
13:L:27:LEU:C	13:L:29:GLY:N	2.45	0.66
3:B:28:PHE:CD2	3:B:190:THR:HA	2.30	0.66
7:F:36:ARG:HH11	7:F:36:ARG:HG2	1.60	0.66
14:M:110:ARG:HH11	14:M:110:ARG:CG	2.07	0.66
1:A:1392:G:N2	1:A:1502:A:H8	1.93	0.66
3:B:144:ARG:HG3	3:B:145:LEU:N	2.11	0.66
1:A:1298:C:H2'	8:G:114:ARG:NH1	2.08	0.66
15:N:22:THR:O	15:N:23:ARG:HB2	1.95	0.66
21:T:86:ARG:O	21:T:90:GLN:HG3	1.95	0.66
1:A:524:G:H2'	1:A:525:C:C6	2.30	0.66
4:C:52:LEU:HD21	4:C:118:GLN:HE22	1.59	0.66
4:C:191:THR:HG21	4:C:193:TYR:CZ	2.31	0.66
1:A:1223:C:OP1	1:A:1224:G:H3'	1.94	0.66
11:J:62:HIS:CB	15:N:59:ALA:HB3	2.24	0.66
1:A:1006:C:H2'	1:A:1007:C:H6	1.60	0.66
1:A:1256:A:H61	1:A:1278:U:H1'	1.61	0.66
1:A:686:U:HO2'	1:A:687:A:H8	1.43	0.66
1:A:939:G:H2'	1:A:940:C:C6	2.30	0.66
7:F:36:ARG:HH12	7:F:38:GLU:HG2	1.60	0.66
18:Q:18:THR:HG23	18:Q:69:LYS:HE3	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:975:A:O5'	1:A:976:G:H5'	1.95	0.66
11:J:45:ARG:NH2	15:N:36:PHE:CD2	2.64	0.66
1:A:1124:G:H5'	11:J:35:SER:O	1.96	0.66
1:A:761:G:N3	18:Q:105:ALA:HB3	2.11	0.66
1:A:781:A:H2'	1:A:782:A:H5'	1.77	0.66
4:C:179:ARG:O	4:C:179:ARG:CG	2.44	0.66
1:A:1250:A:H5''	10:I:68:GLY:N	2.11	0.66
16:O:87:ILE:HG22	16:O:88:ARG:HG2	1.77	0.66
4:C:52:LEU:HD23	4:C:52:LEU:N	2.12	0.65
10:I:100:GLY:O	10:I:102:LEU:N	2.28	0.65
1:A:723:U:O2	1:A:723:U:H2'	1.94	0.65
3:B:71:VAL:O	3:B:165:VAL:HG23	1.96	0.65
9:H:60:ARG:NH1	9:H:60:ARG:HG3	2.11	0.65
1:A:1250:A:H5''	10:I:68:GLY:H	1.61	0.65
3:B:116:GLU:HG2	3:B:153:ARG:NH2	2.09	0.65
4:C:188:LEU:CD1	4:C:195:VAL:HG13	2.27	0.65
8:G:15:ASP:OD2	8:G:23:VAL:HG11	1.96	0.65
11:J:45:ARG:O	11:J:64:GLU:HA	1.95	0.65
1:A:1238:A:N7	1:A:1303:C:H1'	2.12	0.65
1:A:1521:G:H2'	1:A:1522:U:C6	2.31	0.65
4:C:91:LEU:HD21	4:C:99:VAL:CG1	2.23	0.65
6:E:150:ARG:HH11	6:E:150:ARG:HG3	1.61	0.65
14:M:81:LEU:CD2	14:M:81:LEU:H	2.09	0.65
1:A:1493:A:C2'	1:A:1494:G:H5'	2.26	0.65
3:B:8:LYS:HD3	3:B:9:GLU:H	1.62	0.65
5:D:176:LEU:HA	5:D:183:GLY:HA2	1.78	0.65
5:D:92:VAL:O	5:D:96:LEU:HD13	1.97	0.65
21:T:50:GLU:O	21:T:100:ILE:HD12	1.96	0.65
3:B:23:ARG:NH1	3:B:24:TRP:N	2.44	0.65
4:C:120:VAL:O	4:C:124:ILE:HG13	1.96	0.65
5:D:24:GLU:HG2	5:D:25:ARG:H	1.61	0.65
1:A:1347:G:O2'	1:A:1348:U:P	2.54	0.65
1:A:1366:C:H2'	1:A:1367:C:H6	1.60	0.65
4:C:191:THR:CG2	4:C:192:THR:N	2.59	0.65
6:E:57:LYS:HG2	6:E:61:TYR:HE2	1.62	0.65
8:G:15:ASP:OD1	8:G:17:VAL:N	2.30	0.65
14:M:79:LYS:HD3	14:M:83:ASP:OD2	1.96	0.65
1:A:321:A:O2'	1:A:322:C:H5'	1.97	0.65
3:B:25:ASN:C	3:B:25:ASN:HD22	1.99	0.65
5:D:127:THR:HG23	5:D:130:GLY:O	1.97	0.65
5:D:57:ARG:HB3	5:D:206:PHE:HB2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1016:A:H2'	1:A:1017:G:O4'	1.96	0.65
1:A:287:U:O2'	1:A:288:A:H5'	1.95	0.65
1:A:860:A:H2'	1:A:861:G:O4'	1.96	0.65
11:J:12:ASP:HB3	11:J:15:THR:HB	1.79	0.65
19:R:47:THR:HA	19:R:83:GLU:HB2	1.79	0.65
20:S:40:ILE:HD13	20:S:62:ILE:HD13	1.79	0.65
1:A:761:G:H5''	18:Q:102:GLY:HA3	1.78	0.65
17:P:67:THR:HG22	17:P:68:ASP:N	2.11	0.64
1:A:1262:C:H2'	1:A:1263:C:C6	2.32	0.64
19:R:32:ARG:HH21	19:R:65:ILE:HG21	1.60	0.64
1:A:1117:G:H5'	1:A:1117:G:H8	1.59	0.64
1:A:1498:U:H4'	1:A:1519:A:C2	2.32	0.64
1:A:657:G:H4'	16:O:28:GLN:HG2	1.78	0.64
3:B:102:LEU:HD21	3:B:162:ILE:CD1	2.27	0.64
4:C:64:VAL:HG23	4:C:99:VAL:HB	1.80	0.64
10:I:8:GLY:HA2	10:I:79:LEU:CD1	2.14	0.64
6:E:120:THR:HG23	6:E:121:LYS:N	2.12	0.64
14:M:14:ARG:HG3	14:M:44:ARG:NH1	2.11	0.64
3:B:132:LYS:C	3:B:134:GLU:H	2.00	0.64
8:G:18:TYR:CD2	8:G:59:LEU:HB2	2.32	0.64
11:J:49:VAL:O	11:J:60:ARG:O	2.16	0.64
13:L:53:ARG:HD2	13:L:53:ARG:N	2.11	0.64
1:A:101:A:O2'	1:A:102:G:H5'	1.97	0.64
1:A:195:A:H4'	21:T:68:LYS:CE	2.27	0.64
1:A:883:C:O2'	1:A:884:U:H5'	1.98	0.64
4:C:139:GLN:O	4:C:143:GLU:N	2.29	0.64
1:A:939:G:H5''	8:G:102:ARG:NH2	2.13	0.64
19:R:34:TYR:HD1	19:R:35:ARG:HG3	1.63	0.64
19:R:53:ARG:NH1	19:R:59:SER:HA	2.00	0.64
1:A:1495:U:H2'	1:A:1496:C:C6	2.31	0.64
1:A:17:U:H2'	1:A:18:C:C6	2.31	0.64
11:J:30:SER:O	11:J:78:ASN:HB2	1.97	0.64
1:A:253:U:H2'	1:A:254:G:H8	1.61	0.64
3:B:156:LYS:O	3:B:156:LYS:HD3	1.98	0.64
5:D:39:PRO:HG2	5:D:44:GLY:HA2	1.80	0.64
19:R:55:ARG:HB3	19:R:55:ARG:NH1	2.13	0.64
1:A:1031:G:H2'	1:A:1032:G:H8	1.63	0.64
1:A:983:A:H5'	1:A:984:C:OP2	1.98	0.64
1:A:1498:U:H4'	1:A:1519:A:H2	1.61	0.64
1:A:188:C:H4'	21:T:89:ARG:NH1	2.13	0.64
1:A:477:G:H2'	1:A:478:A:H8	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:34:ARG:O	13:L:61:THR:HG23	1.97	0.64
18:Q:53:LEU:C	18:Q:53:LEU:HD12	2.18	0.64
19:R:25:THR:O	19:R:26:LEU:HB2	1.97	0.64
1:A:1305:G:H5'	22:V:4:GLY:HA3	1.80	0.64
3:B:97:TRP:HZ2	3:B:102:LEU:HD13	1.63	0.63
4:C:64:VAL:O	4:C:99:VAL:HG23	1.97	0.63
6:E:115:VAL:HG11	6:E:118:ILE:CD1	2.28	0.63
1:A:1231:G:H4'	10:I:126:SER:HB3	1.81	0.63
16:O:87:ILE:O	16:O:88:ARG:HB2	1.97	0.63
1:A:1035:A:H2'	1:A:1036:G:C8	2.32	0.63
1:A:797:C:O2'	1:A:798:G:H5'	1.96	0.63
11:J:8:LEU:HD23	11:J:96:ILE:HG12	1.81	0.63
1:A:1289:A:H2'	1:A:1290:G:H5'	1.80	0.63
1:A:1305:G:N2	1:A:1331:G:H1'	2.13	0.63
6:E:116:THR:HG23	6:E:117:ASP:OD2	1.99	0.63
11:J:8:LEU:HB2	11:J:70:ARG:HB2	1.80	0.63
13:L:27:LEU:HG	13:L:28:LYS:N	2.14	0.63
1:A:742:G:H5''	16:O:58:MET:HE1	1.79	0.63
16:O:87:ILE:CG2	16:O:88:ARG:N	2.62	0.63
1:A:1132:C:H2'	1:A:1133:G:H8	1.62	0.63
11:J:96:ILE:CG2	11:J:97:GLU:H	2.10	0.63
16:O:41:GLU:OE2	16:O:41:GLU:HA	1.97	0.63
17:P:17:TYR:HE1	17:P:41:PRO:HG2	1.62	0.63
18:Q:97:SER:OG	18:Q:98:LEU:N	2.29	0.63
14:M:88:ARG:HD2	20:S:3:ARG:HH21	1.64	0.63
1:A:291:C:O2'	1:A:292:G:H5'	1.97	0.63
1:A:818:G:C3'	1:A:819:A:H5''	2.28	0.63
3:B:57:PHE:O	3:B:60:ASP:HB3	1.98	0.63
4:C:195:VAL:C	4:C:196:LEU:HD23	2.18	0.63
9:H:56:LYS:N	9:H:56:LYS:HD2	2.14	0.63
10:I:4:TYR:CD2	10:I:88:TYR:HA	2.33	0.63
14:M:40:ASN:HD22	14:M:41:PRO:N	1.95	0.63
21:T:44:ALA:HB2	21:T:88:VAL:HG13	1.80	0.63
1:A:1176:A:H2'	1:A:1177:G:C8	2.33	0.63
1:A:1347:G:N2	1:A:1373:G:H2'	2.14	0.63
1:A:501:C:H2'	1:A:502:G:C8	2.30	0.63
5:D:61:LYS:NZ	5:D:62:GLN:HE21	1.97	0.63
13:L:55:VAL:CG1	13:L:56:ALA:H	2.12	0.63
13:L:55:VAL:CG1	13:L:67:THR:HG23	2.29	0.63
19:R:52:PRO:HB2	19:R:54:ARG:HD3	1.79	0.63
22:V:9:ARG:NH1	22:V:22:ARG:HA	2.13	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:865:A:H5'	1:A:1078:U:O4	1.98	0.63
3:B:101:MET:CA	3:B:108:ILE:HD12	2.28	0.63
15:N:31:ARG:O	15:N:33:VAL:HG22	1.99	0.63
16:O:17:ARG:HH11	16:O:17:ARG:HG3	1.62	0.63
1:A:129(A):G:O2'	1:A:190(E):U:H2'	1.99	0.63
5:D:162:LEU:HD22	5:D:178:VAL:HG13	1.80	0.63
10:I:19:LEU:CD1	10:I:85:LEU:HD12	2.29	0.63
1:A:1230:C:H1'	14:M:126:LYS:HA	1.80	0.63
1:A:1368:G:O2'	1:A:1369:C:H5'	1.98	0.63
1:A:1527:C:O2'	1:A:1528:U:H5'	1.99	0.63
1:A:539:A:OP1	13:L:114:LYS:HE2	1.99	0.63
1:A:954:G:H2'	1:A:955:U:H6	1.64	0.63
4:C:64:VAL:HB	4:C:99:VAL:CG2	2.29	0.63
19:R:33:ASP:OD2	19:R:36:ASN:HB2	1.99	0.63
1:A:1064:G:C4'	1:A:1065:U:H5'	2.28	0.62
1:A:1343:G:H2'	1:A:1344:C:C6	2.34	0.62
1:A:560:U:H5'	1:A:566:G:N2	2.14	0.62
4:C:70:VAL:C	4:C:106:VAL:HG23	2.18	0.62
13:L:47:LYS:HB2	13:L:48:PRO:CD	2.29	0.62
14:M:81:LEU:HD12	14:M:88:ARG:HD3	1.79	0.62
17:P:81:ARG:CG	17:P:83:GLU:HG2	2.29	0.62
1:A:474:G:H2'	1:A:475:G:C8	2.33	0.62
10:I:4:TYR:CE2	10:I:88:TYR:HA	2.33	0.62
14:M:57:ARG:HG2	14:M:61:GLU:OE2	1.99	0.62
19:R:61:LYS:O	19:R:65:ILE:HG12	1.98	0.62
1:A:1003(A):G:H2'	1:A:1004:A:H4'	1.79	0.62
1:A:1172:C:H2'	1:A:1173:G:H8	1.63	0.62
1:A:1303:C:H2'	1:A:1304:G:H5'	1.81	0.62
1:A:490:G:H2'	1:A:491:G:H8	1.65	0.62
4:C:180:ALA:O	4:C:181:ASN:HB3	1.98	0.62
4:C:53:ALA:O	4:C:54:ARG:HB2	1.98	0.62
6:E:77:PRO:O	6:E:78:HIS:HB3	2.00	0.62
1:A:1128:C:H4'	10:I:16:ARG:HH12	1.63	0.62
3:B:184:VAL:N	3:B:198:ASP:OD2	2.32	0.62
3:B:73:THR:HG23	3:B:95:GLN:O	1.99	0.62
5:D:150:GLU:HA	5:D:153:ARG:HE	1.63	0.62
11:J:3:LYS:N	11:J:77:PRO:HD3	2.15	0.62
1:A:434:U:H2'	1:A:435:C:C6	2.34	0.62
1:A:959:A:H3'	1:A:960:U:H5''	1.80	0.62
4:C:34:LEU:HD23	4:C:34:LEU:O	1.99	0.62
14:M:37:THR:O	14:M:37:THR:HG22	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:70:LYS:O	10:I:74:ILE:HG13	1.99	0.62
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.34	0.62
1:A:179:A:H2'	1:A:180:U:C6	2.35	0.62
1:A:246:A:N6	1:A:281:G:H1'	2.15	0.62
3:B:21:ARG:CG	3:B:23:ARG:HD2	2.30	0.62
3:B:68:ILE:H	3:B:90:MET:CE	2.12	0.62
3:B:88:ALA:C	3:B:90:MET:H	2.02	0.62
4:C:7:PRO:HG2	4:C:184:TYR:HB2	1.80	0.62
15:N:11:LYS:O	15:N:13:THR:N	2.32	0.62
19:R:59:SER:O	19:R:60:GLY:C	2.38	0.62
1:A:1278:U:H5''	1:A:1279:A:O4'	1.98	0.62
1:A:1441:G:H4'	1:A:1442:G:C5	2.35	0.62
3:B:162:ILE:O	3:B:185:ILE:HG13	1.99	0.62
4:C:23:TYR:CD2	4:C:24:ALA:N	2.67	0.62
7:F:19:LEU:HD23	7:F:19:LEU:C	2.20	0.62
10:I:48:GLU:HA	10:I:51:ARG:HH11	1.65	0.62
13:L:47:LYS:CB	13:L:48:PRO:CD	2.78	0.62
1:A:112:G:H4'	1:A:389:A:H5''	1.82	0.62
10:I:48:GLU:N	10:I:49:PRO:HD2	2.14	0.62
14:M:62:ASN:O	14:M:63:THR:HB	1.99	0.62
17:P:48:TRP:O	17:P:49:LEU:HB2	2.00	0.62
1:A:1425:U:H2'	1:A:1426:C:C6	2.35	0.62
1:A:1392:G:H21	1:A:1502:A:H8	1.46	0.62
21:T:45:GLN:CB	21:T:91:LEU:HD22	2.30	0.62
1:A:339:C:H2'	1:A:340:U:H6	1.65	0.61
4:C:77:ILE:HG22	4:C:81:GLY:HA2	1.82	0.61
5:D:131:ARG:H	5:D:131:ARG:HD2	1.65	0.61
5:D:199:ASN:ND2	5:D:201:GLN:HB3	2.15	0.61
11:J:80:LYS:HA	11:J:83:GLU:HB2	1.82	0.61
1:A:537:G:OP1	13:L:113:ARG:NH2	2.33	0.61
1:A:1182:G:H4'	1:A:1183:A:O5'	2.00	0.61
3:B:23:ARG:C	3:B:23:ARG:HH11	2.03	0.61
10:I:127:LYS:HB2	14:M:126:LYS:NZ	2.15	0.61
1:A:835:U:OP1	19:R:64:ARG:NH2	2.33	0.61
21:T:96:GLY:O	21:T:97:ALA:HB3	1.98	0.61
1:A:202:U:H4'	1:A:203:U:OP1	2.00	0.61
1:A:908:A:H2'	1:A:909:A:C8	2.36	0.61
6:E:80:ILE:HD13	6:E:138:ALA:HB1	1.82	0.61
13:L:60:LEU:HD21	13:L:66:VAL:HG22	1.80	0.61
1:A:376:G:H5''	17:P:5:ARG:HD2	1.81	0.61
21:T:53:LEU:O	21:T:57:ARG:HD3	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:6:ARG:HD2	22:V:15:ARG:NH1	2.15	0.61
1:A:1229:A:OP2	14:M:114:ARG:HD3	1.99	0.61
1:A:538:G:H2'	1:A:539:A:H8	1.64	0.61
4:C:129:ALA:HB3	4:C:132:ARG:HD2	1.82	0.61
1:A:1343:G:H1'	10:I:121:ARG:HH12	1.66	0.61
13:L:86:ARG:HG3	13:L:86:ARG:HH11	1.64	0.61
1:A:1000:U:H2'	1:A:1001:A:C8	2.35	0.61
1:A:1300:G:HO2'	1:A:1301:U:H6	1.48	0.61
1:A:393:A:O2'	1:A:394:G:H5'	2.01	0.61
8:G:116:ALA:HA	8:G:119:ARG:CZ	2.31	0.61
1:A:64:G:H4'	1:A:65:U:C5'	2.30	0.61
1:A:757:U:H2'	1:A:758:G:O4'	1.98	0.61
1:A:838:G:H2'	1:A:839:U:H5''	1.81	0.61
3:B:84:GLU:OE1	3:B:216:SER:HA	2.01	0.61
6:E:92:LYS:O	6:E:118:ILE:HG22	2.00	0.61
1:A:1056:U:H5'	4:C:163:ALA:HB2	1.82	0.61
1:A:437:U:H5''	5:D:155:LEU:HD22	1.82	0.61
1:A:818:G:C2'	1:A:819:A:H5''	2.30	0.61
4:C:3:ASN:C	4:C:4:LYS:HG2	2.21	0.61
8:G:85:TYR:HD1	8:G:154:TYR:HE1	1.46	0.61
8:G:18:TYR:HD2	8:G:59:LEU:HD22	1.64	0.61
1:A:686:U:O2'	1:A:687:A:H8	1.81	0.61
3:B:34:ALA:O	3:B:41:ILE:N	2.34	0.61
11:J:56:HIS:O	11:J:58:ASP:N	2.34	0.61
19:R:16:PRO:O	19:R:17:SER:HB3	2.01	0.61
1:A:620:C:C2	5:D:135:LEU:HD13	2.36	0.61
4:C:46:GLU:O	4:C:48:TYR:N	2.26	0.61
15:N:53:LEU:HB3	15:N:56:VAL:HG21	1.83	0.61
22:V:17:THR:O	22:V:22:ARG:HD3	2.01	0.61
1:A:344:A:H4'	1:A:345:C:OP2	2.01	0.60
1:A:559:A:P	6:E:126:ARG:HH22	2.24	0.60
1:A:818:G:O2'	1:A:819:A:H5''	2.01	0.60
18:Q:26:GLN:O	18:Q:27:PHE:HB3	2.00	0.60
20:S:17:GLU:O	20:S:21:GLU:HG3	2.01	0.60
1:A:448:A:OP2	1:A:485:G:N2	2.26	0.60
10:I:117:HIS:HB2	10:I:121:ARG:HD2	1.82	0.60
1:A:1137:C:H4'	1:A:1138:G:N2	2.15	0.60
1:A:190(E):U:O2'	18:Q:63:ARG:NH2	2.34	0.60
3:B:132:LYS:HA	3:B:135:GLN:CB	2.31	0.60
5:D:23:GLY:HA3	5:D:112:VAL:CG1	2.31	0.60
6:E:13:ILE:HG22	6:E:30:ALA:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:3:LYS:HA	11:J:75:ILE:HA	1.83	0.60
13:L:89:ARG:HG2	13:L:97:ARG:HA	1.83	0.60
1:A:1262:C:H2'	1:A:1263:C:H6	1.63	0.60
1:A:575:G:OP1	1:A:575:G:H4'	1.99	0.60
19:R:45:SER:C	19:R:47:THR:H	2.03	0.60
21:T:43:LEU:HA	21:T:46:GLU:OE2	2.01	0.60
1:A:1241:G:H2'	1:A:1242:C:H6	1.65	0.60
5:D:25:ARG:C	5:D:27:TYR:N	2.55	0.60
1:A:738:C:OP1	7:F:92:LYS:HE3	2.02	0.60
1:A:738:C:P	7:F:92:LYS:HE3	2.42	0.60
10:I:10:ARG:HG2	10:I:75:ASP:CB	2.32	0.60
1:A:1241:G:H2'	1:A:1242:C:C6	2.36	0.60
1:A:1381:U:O2'	1:A:1382:C:H5'	2.02	0.60
1:A:1435:G:H2'	1:A:1436:U:C6	2.37	0.60
1:A:538:G:H2'	1:A:539:A:C8	2.37	0.60
1:A:734:G:H21	19:R:75:ILE:HD11	1.67	0.60
5:D:64:LEU:HD12	5:D:75:PHE:HZ	1.67	0.60
8:G:12:LEU:N	8:G:12:LEU:HD12	2.17	0.60
8:G:75:VAL:CG1	8:G:86:GLN:HE21	2.15	0.60
14:M:36:LYS:HD2	14:M:59:TYR:CZ	2.36	0.60
21:T:87:LYS:O	21:T:91:LEU:HD12	2.01	0.60
1:A:1502:A:H2	1:A:1505:G:N1	1.99	0.60
4:C:190:ARG:HH11	4:C:190:ARG:CB	2.14	0.60
5:D:28:SER:O	5:D:30:LYS:N	2.34	0.60
17:P:43:LYS:HG3	17:P:48:TRP:CE3	2.37	0.60
3:B:53:ARG:NH1	3:B:199:TYR:HD2	2.00	0.60
10:I:50:LEU:HG	10:I:81:ILE:HG21	1.84	0.60
20:S:7:LYS:HG3	20:S:7:LYS:O	2.02	0.60
1:A:1154:G:H2'	1:A:1155:G:H8	1.67	0.60
1:A:1182:G:O2'	1:A:1183:A:OP2	2.19	0.60
1:A:1490:C:O2'	1:A:1491:G:H5'	2.02	0.60
3:B:18:GLY:CA	3:B:41:ILE:HA	2.32	0.60
4:C:97:LYS:O	4:C:98:ASN:HB3	2.00	0.60
13:L:82:VAL:O	13:L:106:ASP:HB2	2.02	0.60
14:M:86:CYS:SG	14:M:88:ARG:HB3	2.42	0.60
1:A:959:A:C2	1:A:1222:G:O4'	2.54	0.60
1:A:1225:A:N3	1:A:1225:A:H2'	2.16	0.60
1:A:1285:A:H4'	1:A:1286:A:O5'	2.02	0.60
1:A:1372:U:OP1	10:I:71:SER:HB3	2.02	0.60
1:A:765:G:H1	1:A:812:C:H2'	1.66	0.60
3:B:125:PRO:HG2	3:B:126:GLU:H	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:43:LEU:HD12	4:C:55:VAL:HG11	1.84	0.60
10:I:110:GLU:OE2	10:I:113:LYS:NZ	2.35	0.60
11:J:55:LYS:O	11:J:56:HIS:HB2	2.02	0.60
18:Q:24:GLU:CD	18:Q:37:LYS:HD3	2.23	0.60
7:F:101:ALA:HB2	19:R:28:GLU:CB	2.31	0.60
1:A:1039:C:O2'	1:A:1040:U:H5'	2.02	0.59
9:H:119:LEU:HD23	9:H:119:LEU:N	2.17	0.59
15:N:45:ARG:HG3	15:N:45:ARG:HH11	1.67	0.59
20:S:67:VAL:HG12	20:S:68:GLY:N	2.17	0.59
21:T:14:LYS:O	21:T:18:GLN:HG3	2.02	0.59
1:A:1263:C:H2'	1:A:1264:C:C6	2.37	0.59
1:A:253:U:H2'	1:A:254:G:C8	2.37	0.59
3:B:132:LYS:HG2	3:B:135:GLN:OE1	2.01	0.59
1:A:1191:A:P	4:C:3:ASN:ND2	2.74	0.59
17:P:52:ASP:OD2	17:P:55:ARG:HB2	2.02	0.59
20:S:20:LEU:HA	20:S:23:ASN:ND2	2.17	0.59
1:A:1066:C:O2'	1:A:1067:A:H5'	2.03	0.59
4:C:174:PRO:HB2	4:C:177:THR:CG2	2.28	0.59
8:G:71:PRO:HD3	8:G:103:TRP:HZ3	1.67	0.59
8:G:154:TYR:O	8:G:156:TRP:N	2.35	0.59
10:I:125:TYR:CD1	10:I:128:ARG:HB2	2.37	0.59
1:A:1148:U:H4'	10:I:14:VAL:HG11	1.84	0.59
1:A:1392:G:H2'	1:A:1393:U:H6	1.67	0.59
1:A:1531:A:O5'	1:A:1531:A:H8	1.85	0.59
5:D:142:PRO:HG2	5:D:187:ARG:NH1	2.16	0.59
12:K:14:VAL:HG21	12:K:40:ILE:HD11	1.82	0.59
14:M:81:LEU:CD2	14:M:81:LEU:N	2.65	0.59
1:A:1288:A:H2'	1:A:1289:A:C8	2.38	0.59
18:Q:59:ILE:HG22	18:Q:71:PHE:CD1	2.37	0.59
18:Q:95:TYR:C	18:Q:97:SER:H	2.06	0.59
21:T:38:LYS:O	21:T:42:GLN:HB2	2.03	0.59
1:A:149:A:H2'	1:A:150:C:H6	1.68	0.59
1:A:189:G:H2'	1:A:190:C:C6	2.38	0.59
5:D:187:ARG:NH2	5:D:188:LEU:HD12	2.18	0.59
1:A:1193:G:O2'	1:A:1194:U:H5'	2.02	0.59
1:A:1226:C:H5''	14:M:103:THR:OG1	2.03	0.59
1:A:254:G:OP1	18:Q:67:LYS:O	2.20	0.59
1:A:551:U:H2'	1:A:552:U:H6	1.66	0.59
4:C:107:GLN:O	4:C:108:ASN:HB3	2.03	0.59
5:D:3:ARG:HD2	5:D:69:GLY:O	2.02	0.59
8:G:54:THR:CG2	8:G:56:GLN:HE21	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:71:PRO:HD3	8:G:103:TRP:CZ3	2.38	0.59
1:A:1238:A:H2	1:A:1241:G:N3	2.01	0.59
1:A:1342:C:O2'	1:A:1343:G:H5'	2.03	0.59
1:A:918:A:H2'	1:A:919:A:C8	2.38	0.59
3:B:19:HIS:CD2	3:B:205:ASP:OD1	2.56	0.59
4:C:191:THR:CG2	4:C:192:THR:H	2.14	0.59
4:C:26:LYS:N	4:C:26:LYS:HD3	2.14	0.59
20:S:13:ASP:O	20:S:17:GLU:HG2	2.03	0.59
1:A:722:A:H4'	1:A:723:U:C5	2.38	0.59
3:B:93:VAL:HG11	3:B:97:TRP:HD1	1.68	0.59
4:C:127:ARG:HG2	4:C:127:ARG:HH11	1.68	0.59
6:E:115:VAL:HG11	6:E:118:ILE:HD11	1.85	0.59
1:A:1367:C:H4'	11:J:48:THR:HG21	1.84	0.59
1:A:254:G:O2'	1:A:255:G:H5'	2.03	0.59
1:A:370:C:H2'	1:A:371:G:H8	1.68	0.59
3:B:75:LYS:HA	3:B:78:GLN:HB2	1.85	0.59
7:F:36:ARG:NH1	7:F:36:ARG:HG2	2.17	0.59
9:H:123:GLU:O	9:H:127:LEU:HD23	2.03	0.59
18:Q:45:HIS:NE2	18:Q:47:PRO:HG3	2.18	0.59
8:G:50:ILE:O	8:G:54:THR:HB	2.03	0.58
11:J:4:ILE:HG12	11:J:100:THR:CB	2.33	0.58
11:J:51:ARG:H	11:J:59:SER:CB	2.16	0.58
19:R:37:VAL:O	19:R:41:LYS:HB2	2.03	0.58
1:A:613:C:O2'	1:A:614:A:H5'	2.04	0.58
3:B:12:GLU:C	3:B:14:GLY:H	2.05	0.58
3:B:169:LYS:HD3	3:B:169:LYS:O	2.02	0.58
4:C:35:GLU:HG3	4:C:95:THR:HG21	1.85	0.58
6:E:12:LEU:C	6:E:12:LEU:HD22	2.23	0.58
7:F:36:ARG:NH1	7:F:38:GLU:HG2	2.17	0.58
10:I:48:GLU:HA	10:I:51:ARG:NH1	2.19	0.58
13:L:25:PRO:C	13:L:27:LEU:N	2.56	0.58
4:C:34:LEU:CD1	15:N:25:VAL:HG21	2.33	0.58
20:S:41:VAL:HG23	20:S:43:GLU:HG2	1.85	0.58
1:A:1292:U:H5'	10:I:38:GLN:HE22	1.69	0.58
1:A:202:U:H5''	1:A:203:U:OP2	2.03	0.58
1:A:314:C:O2'	1:A:315:A:H5'	2.04	0.58
1:A:357:G:O2'	1:A:358:U:H5'	2.03	0.58
4:C:188:LEU:HD11	4:C:195:VAL:HG13	1.84	0.58
1:A:735:C:O2'	1:A:736:C:H5'	2.02	0.58
1:A:939:G:H2'	1:A:940:C:H6	1.66	0.58
4:C:107:GLN:NE2	4:C:107:GLN:H	2.00	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:58:GLU:H	4:C:65:ALA:HB3	1.68	0.58
10:I:111:ARG:HD3	10:I:111:ARG:C	2.24	0.58
11:J:53:PRO:HA	15:N:41:ARG:NH2	2.15	0.58
1:A:222:U:H2'	1:A:223:U:C6	2.39	0.58
3:B:95:GLN:O	3:B:96:ARG:HD2	2.03	0.58
14:M:9:ILE:N	14:M:9:ILE:HD12	2.18	0.58
3:B:122:PHE:O	3:B:123:ALA:HB2	2.03	0.58
4:C:47:LEU:CD1	4:C:47:LEU:H	2.17	0.58
8:G:75:VAL:HG12	8:G:86:GLN:HE21	1.68	0.58
15:N:12:ARG:O	15:N:14:PRO:N	2.35	0.58
19:R:53:ARG:NH1	19:R:60:GLY:N	2.43	0.58
19:R:86:VAL:O	19:R:87:ARG:HG2	2.04	0.58
1:A:628:G:O2'	1:A:629:G:H5'	2.03	0.58
1:A:954:G:H2'	1:A:955:U:C6	2.38	0.58
3:B:181:PHE:CD2	9:H:70:GLN:HB3	2.38	0.58
13:L:55:VAL:CG1	13:L:56:ALA:N	2.67	0.58
21:T:87:LYS:C	21:T:91:LEU:HD12	2.25	0.58
1:A:1053:G:HO2'	1:A:1199:U:H5	1.50	0.58
17:P:22:THR:CA	17:P:33:ILE:HD12	2.34	0.58
1:A:1320:C:N3	20:S:36:ARG:HG3	2.19	0.58
21:T:56:MET:HE3	21:T:88:VAL:HG11	1.86	0.58
1:A:731:G:OP1	1:A:766:A:H1'	2.04	0.58
1:A:975:A:H4'	1:A:976:G:H5'	1.86	0.58
3:B:188:ALA:O	3:B:202:PRO:HA	2.03	0.58
5:D:64:LEU:HD12	5:D:75:PHE:CZ	2.39	0.58
1:A:1257:U:H4'	1:A:1258:G:C5'	2.34	0.57
4:C:188:LEU:O	4:C:189:ALA:HB2	2.03	0.57
4:C:188:LEU:HD13	4:C:189:ALA:H	1.69	0.57
7:F:80:ARG:NH1	7:F:88:VAL:HB	2.19	0.57
15:N:8:GLU:O	15:N:11:LYS:HB3	2.04	0.57
1:A:1070:U:H2'	1:A:1071:C:C6	2.39	0.57
1:A:1091:U:O2	1:A:1093:A:C8	2.57	0.57
1:A:1277:C:C2'	1:A:1278:U:H5'	2.34	0.57
1:A:959:A:H2'	1:A:960:U:O4'	2.04	0.57
5:D:30:LYS:O	5:D:32:ALA:N	2.38	0.57
6:E:51:VAL:O	6:E:55:VAL:HG23	2.04	0.57
8:G:108:ALA:O	8:G:119:ARG:HD2	2.04	0.57
8:G:21:VAL:HG23	8:G:22:LEU:N	2.19	0.57
14:M:11:ARG:CG	14:M:12:ASN:N	2.66	0.57
14:M:78:ILE:O	14:M:81:LEU:HD23	2.03	0.57
19:R:19:LYS:O	19:R:20:ALA:HB2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:C:O2	21:T:105:SER:HB3	2.04	0.57
1:A:103:C:P	21:T:17:ARG:HH11	2.26	0.57
21:T:61:SER:O	21:T:65:LYS:HG3	2.03	0.57
1:A:1191:A:P	4:C:3:ASN:HD22	2.26	0.57
25:A:1633:TAC:H8	13:L:19:ARG:HH22	1.70	0.57
1:A:163:C:O2'	1:A:164:U:H5'	2.04	0.57
1:A:382:A:H2'	1:A:383:A:H8	1.64	0.57
1:A:627:G:O2'	1:A:628:G:H5'	2.04	0.57
4:C:35:GLU:CG	4:C:59:ARG:HH22	2.17	0.57
4:C:32:LEU:HD21	4:C:59:ARG:HD2	1.86	0.57
17:P:17:TYR:CE1	17:P:41:PRO:HG2	2.39	0.57
3:B:53:ARG:NH1	3:B:199:TYR:CD2	2.72	0.57
3:B:223:ILE:O	3:B:225:ALA:N	2.36	0.57
6:E:15:ARG:O	6:E:15:ARG:HD2	2.03	0.57
6:E:72:GLN:NE2	6:E:144:THR:HG23	2.20	0.57
6:E:80:ILE:CD1	6:E:138:ALA:HB1	2.34	0.57
11:J:94:VAL:HG12	11:J:95:GLU:N	2.17	0.57
13:L:120:TYR:O	13:L:122:THR:HG23	2.04	0.57
1:A:1300:G:O2'	1:A:1301:U:H6	1.87	0.57
1:A:1380:U:O2'	1:A:1381:U:OP2	2.19	0.57
1:A:1412:C:H2'	1:A:1413:A:C8	2.40	0.57
1:A:252:U:H2'	1:A:253:U:C6	2.39	0.57
4:C:99:VAL:HG22	4:C:100:ALA:O	2.04	0.57
11:J:3:LYS:HG2	11:J:75:ILE:HG12	1.85	0.57
14:M:8:GLU:OE1	14:M:22:ILE:HA	2.04	0.57
16:O:70:LEU:HD12	16:O:78:TYR:HB2	1.85	0.57
1:A:103:C:P	21:T:17:ARG:NH1	2.77	0.57
1:A:543:C:O2'	1:A:544:G:H5'	2.04	0.57
9:H:101:PRO:HG3	9:H:133:LEU:HD11	1.86	0.57
14:M:106:ASN:O	14:M:107:ALA:HB3	2.04	0.57
14:M:29:ARG:HB3	14:M:64:TRP:CH2	2.39	0.57
19:R:73:ALA:HB3	19:R:79:LEU:HD12	1.87	0.57
1:A:1250:A:H2'	1:A:1251:A:C8	2.39	0.57
1:A:555:C:H2'	1:A:556:C:C6	2.39	0.57
6:E:103:GLY:O	6:E:106:PRO:HD2	2.05	0.57
13:L:46:LYS:NZ	13:L:47:LYS:HG3	2.18	0.57
18:Q:103:GLY:O	18:Q:104:LYS:O	2.23	0.57
1:A:1060:C:O2'	1:A:1061:G:H5'	2.04	0.57
1:A:433:C:H2'	1:A:434:U:H6	1.70	0.57
1:A:996:A:H2'	1:A:997:U:C6	2.39	0.57
3:B:124:SER:CB	3:B:125:PRO:HD2	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:174:PRO:CB	4:C:177:THR:HG22	2.29	0.57
11:J:49:VAL:O	11:J:60:ARG:HA	2.05	0.57
10:I:127:LYS:HB2	14:M:126:LYS:HZ3	1.68	0.57
1:A:954:G:H21	1:A:1227:A:H62	1.53	0.57
1:A:1263:C:H2'	1:A:1264:C:H6	1.69	0.57
1:A:339:C:H2'	1:A:340:U:C6	2.39	0.57
1:A:392:G:H2'	1:A:393:A:H8	1.69	0.57
4:C:18:TRP:O	4:C:54:ARG:NH2	2.38	0.57
9:H:51:VAL:HG12	9:H:52:ASP:N	2.20	0.57
9:H:90:GLY:O	9:H:91:ARG:HB2	2.04	0.57
12:K:48:ILE:HD13	12:K:63:LEU:HB3	1.85	0.57
14:M:8:GLU:HG3	14:M:22:ILE:HG23	1.87	0.57
21:T:57:ARG:HH21	21:T:100:ILE:CG2	2.17	0.57
21:T:67:ALA:HA	21:T:73:HIS:H	1.70	0.57
1:A:180:U:H2'	1:A:181:G:H5'	1.87	0.57
1:A:519:C:O2'	1:A:520:A:H5'	2.05	0.57
6:E:11:ILE:HG22	6:E:12:LEU:HD12	1.87	0.57
7:F:69:GLU:N	7:F:69:GLU:OE1	2.38	0.57
10:I:85:LEU:HB3	10:I:92:TYR:HD1	1.70	0.57
14:M:123:ALA:O	14:M:125:ARG:N	2.38	0.57
20:S:51:VAL:HB	20:S:75:ALA:HB2	1.87	0.57
1:A:1194:U:H2'	1:A:1195:C:C6	2.41	0.56
1:A:164:U:H2'	1:A:165:C:C6	2.40	0.56
1:A:556:C:O2'	1:A:557:G:H5'	2.05	0.56
6:E:102:ALA:HB1	6:E:120:THR:HG21	1.87	0.56
6:E:99:GLY:O	6:E:117:ASP:HA	2.04	0.56
16:O:17:ARG:NH1	16:O:77:ARG:NH1	2.52	0.56
19:R:26:LEU:HD21	19:R:39:VAL:CG2	2.35	0.56
1:A:1057:G:O2'	1:A:1058:G:H5'	2.05	0.56
1:A:1126:U:OP2	1:A:1281:U:O2	2.22	0.56
1:A:149:A:O2'	1:A:150:C:H5'	2.05	0.56
4:C:188:LEU:HD12	4:C:189:ALA:H	1.70	0.56
8:G:144:MET:O	8:G:148:ASN:ND2	2.38	0.56
1:A:689:C:P	12:K:46:GLY:HA3	2.44	0.56
19:R:47:THR:C	19:R:49:LYS:H	2.08	0.56
1:A:521:G:O2'	1:A:522:C:H5'	2.04	0.56
1:A:502:G:H4'	1:A:550:G:H4'	1.86	0.56
3:B:12:GLU:C	3:B:14:GLY:N	2.57	0.56
3:B:189:ASP:OD1	3:B:205:ASP:HB3	2.04	0.56
3:B:16:HIS:NE2	3:B:214:ILE:HG12	2.20	0.56
16:O:38:ARG:O	16:O:41:GLU:HB3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:U:H2'	1:A:165:C:H6	1.70	0.56
1:A:130:A:OP2	1:A:190(E):U:H2'	2.04	0.56
1:A:502:G:H2'	1:A:503:C:H6	1.69	0.56
1:A:502:G:H1'	1:A:550:G:H5'	1.87	0.56
6:E:43:LEU:HD23	6:E:44:GLY:H	1.71	0.56
8:G:38:LEU:HD12	8:G:38:LEU:C	2.25	0.56
1:A:1060:C:H2'	1:A:1061:G:H8	1.71	0.56
1:A:1329:A:P	14:M:28:ALA:HB3	2.46	0.56
1:A:418:C:H2'	1:A:419:C:C6	2.39	0.56
1:A:748:C:H1'	1:A:749:C:H5	1.70	0.56
3:B:230:VAL:HG13	3:B:231:GLU:OE2	2.05	0.56
3:B:96:ARG:O	3:B:98:LEU:HD23	2.06	0.56
1:A:1112:C:O2	4:C:179:ARG:HB3	2.05	0.56
5:D:3:ARG:NH2	5:D:74:GLN:OE1	2.38	0.56
13:L:84:LEU:HD22	13:L:104:VAL:HG11	1.86	0.56
13:L:60:LEU:HD11	13:L:85:ILE:HD12	1.87	0.56
1:A:1207:G:O2'	1:A:1208:C:H5'	2.04	0.56
1:A:828:A:H2'	1:A:829:G:O4'	2.05	0.56
1:A:838:G:C2'	1:A:839:U:H5''	2.35	0.56
3:B:15:VAL:CG1	3:B:209:ARG:HG3	2.36	0.56
6:E:8:GLU:HG2	6:E:34:VAL:HG22	1.88	0.56
1:A:135:C:C2	17:P:1:MET:HB2	2.40	0.56
1:A:1314:C:H2'	1:A:1315:U:C6	2.41	0.56
1:A:392:G:H2'	1:A:393:A:C8	2.40	0.56
1:A:476:G:O2'	1:A:477:G:H5'	2.05	0.56
4:C:26:LYS:CD	4:C:26:LYS:N	2.67	0.56
8:G:143:ARG:O	8:G:145:ALA:O	2.24	0.56
8:G:78:ARG:O	8:G:84:ASN:HA	2.06	0.56
9:H:104:ARG:NH2	9:H:138:TRP:CH2	2.74	0.56
10:I:9:ARG:HA	10:I:13:ALA:O	2.04	0.56
14:M:11:ARG:HG3	14:M:12:ASN:H	1.68	0.56
1:A:1003(A):G:H2'	1:A:1004:A:C4'	2.34	0.56
1:A:1278:U:C5'	1:A:1279:A:O4'	2.54	0.56
1:A:160:A:H1'	1:A:344:A:C5	2.41	0.56
1:A:774:G:O2'	1:A:775:G:H5'	2.05	0.56
4:C:167:TRP:O	4:C:168:ALA:HB3	2.05	0.56
4:C:70:VAL:O	4:C:106:VAL:HG23	2.06	0.56
14:M:22:ILE:HB	14:M:25:ILE:HD12	1.88	0.56
1:A:1003:G:N2	1:A:1039:C:C2	2.73	0.56
1:A:1020:U:H2'	1:A:1021:G:H8	1.70	0.56
1:A:1202:G:C2'	1:A:1203:C:H5'	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:C:H4'	1:A:354:G:OP1	2.06	0.56
4:C:47:LEU:HD12	4:C:47:LEU:H	1.71	0.56
4:C:94:LEU:CD2	4:C:95:THR:HG23	2.19	0.56
1:A:427:U:OP1	5:D:13:ARG:NH2	2.38	0.56
6:E:33:VAL:HG11	6:E:109:ILE:HA	1.88	0.56
6:E:15:ARG:HD3	6:E:26:PHE:HB3	1.86	0.56
13:L:126:LYS:HD2	13:L:126:LYS:N	2.21	0.56
19:R:39:VAL:O	19:R:42:ARG:HB2	2.05	0.56
1:A:1342:C:H5''	10:I:125:TYR:CE1	2.41	0.56
1:A:942:G:C2	1:A:943:U:C6	2.93	0.56
1:A:975:A:O2'	15:N:32:SER:HB2	2.06	0.56
4:C:148:GLY:HA3	4:C:172:ARG:O	2.05	0.56
4:C:191:THR:HG22	4:C:193:TYR:H	1.70	0.56
14:M:52:GLU:HG2	14:M:55:ARG:HH21	1.70	0.56
17:P:52:ASP:O	17:P:52:ASP:OD2	2.22	0.56
1:A:1238:A:C8	1:A:1303:C:H1'	2.41	0.56
1:A:192:U:O2'	1:A:193:C:H5'	2.06	0.56
1:A:42:G:H2'	1:A:43:C:C6	2.40	0.56
1:A:794:A:H2'	1:A:795:C:C6	2.40	0.56
4:C:190:ARG:NH1	4:C:190:ARG:CB	2.69	0.56
4:C:60:ALA:O	4:C:61:ALA:HB2	2.06	0.56
7:F:53:ALA:C	7:F:55:ASP:H	2.10	0.56
9:H:14:ARG:O	9:H:18:ARG:HD3	2.06	0.56
3:B:9:GLU:OE1	3:B:10:LEU:N	2.38	0.55
3:B:178:ARG:NH1	3:B:178:ARG:HG3	2.20	0.55
1:A:1256:A:H8	4:C:27:LYS:NZ	2.04	0.55
4:C:77:ILE:O	4:C:83:ARG:HB3	2.06	0.55
12:K:22:HIS:HB3	12:K:29:ILE:HG23	1.88	0.55
1:A:199:G:O2'	1:A:200:G:H5'	2.06	0.55
1:A:411:A:N9	1:A:413:G:H1'	2.21	0.55
1:A:992:U:O2'	1:A:993:G:OP2	2.23	0.55
3:B:206:ASP:CG	3:B:207:ALA:H	2.10	0.55
5:D:151:LYS:N	5:D:151:LYS:HD2	2.21	0.55
6:E:12:LEU:CD1	6:E:31:LEU:HB2	2.36	0.55
13:L:98:TYR:N	13:L:98:TYR:CD1	2.74	0.55
14:M:54:VAL:O	14:M:58:GLU:HG2	2.06	0.55
22:V:9:ARG:HH12	22:V:23:PRO:HD2	1.71	0.55
11:J:30:SER:HB3	11:J:84:GLN:HE21	1.72	0.55
13:L:83:VAL:HG22	13:L:84:LEU:H	1.71	0.55
1:A:463:A:C4'	17:P:82:GLN:HE21	2.20	0.55
17:P:81:ARG:HG3	17:P:83:GLU:HG2	1.86	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:24:GLU:HG2	5:D:25:ARG:N	2.21	0.55
6:E:31:LEU:HD22	6:E:43:LEU:CD2	2.35	0.55
8:G:18:TYR:HD2	8:G:59:LEU:HB2	1.71	0.55
1:A:1250:A:OP1	10:I:66:ARG:HG2	2.07	0.55
11:J:30:SER:OG	11:J:81:THR:HA	2.06	0.55
1:A:1238:A:H5'	1:A:1336:C:N4	2.12	0.55
3:B:17:PHE:HD1	3:B:17:PHE:C	2.10	0.55
4:C:10:PHE:CE2	4:C:178:LEU:HD13	2.42	0.55
4:C:30:ARG:HG2	4:C:30:ARG:HH11	1.70	0.55
6:E:43:LEU:HD23	6:E:44:GLY:N	2.21	0.55
13:L:6:THR:HG1	13:L:9:GLN:HG3	1.71	0.55
12:K:84:VAL:HG21	19:R:88:LYS:HD3	1.87	0.55
1:A:1238:A:C2	1:A:1241:G:N3	2.75	0.55
1:A:438:G:C4'	1:A:439:A:OP1	2.53	0.55
1:A:75:G:O2'	1:A:76:C:H5'	2.07	0.55
10:I:11:LYS:O	10:I:11:LYS:HG2	2.06	0.55
18:Q:53:LEU:HD12	18:Q:54:GLY:N	2.22	0.55
19:R:40:LEU:N	19:R:40:LEU:HD23	2.21	0.55
1:A:1257:U:O2'	1:A:1258:G:OP2	2.21	0.55
1:A:1489:G:O2'	1:A:1490:C:H5'	2.06	0.55
1:A:192:U:H2'	1:A:193:C:H6	1.72	0.55
1:A:401:C:H2'	1:A:402:G:H8	1.72	0.55
3:B:68:ILE:HB	3:B:90:MET:HE3	1.88	0.55
4:C:9:GLY:HA2	4:C:12:LEU:HD12	1.89	0.55
1:A:542:G:OP1	5:D:10:ARG:NH2	2.40	0.55
10:I:112:LYS:HD3	10:I:112:LYS:O	2.07	0.55
17:P:4:ILE:HG13	17:P:64:ALA:HB1	1.88	0.55
3:B:116:GLU:HG2	3:B:153:ARG:HH22	1.71	0.55
3:B:23:ARG:NH1	3:B:23:ARG:HB2	2.22	0.55
5:D:104:VAL:HG11	5:D:146:ILE:HD12	1.88	0.55
11:J:38:ILE:HG13	11:J:71:LEU:CB	2.32	0.55
4:C:13:GLY:HA3	15:N:57:ARG:NH2	2.22	0.55
16:O:87:ILE:HG22	16:O:88:ARG:N	2.22	0.55
18:Q:45:HIS:HB2	18:Q:69:LYS:HE2	1.89	0.55
1:A:1229:A:H2'	1:A:1230:C:H6	1.72	0.55
1:A:1355:G:O2'	1:A:1356:G:H5'	2.07	0.55
1:A:791:G:H2'	1:A:792:A:H5'	1.88	0.55
1:A:920:U:H2'	1:A:921:U:C6	2.41	0.55
7:F:2:ARG:NE	7:F:69:GLU:HG2	2.21	0.55
13:L:71:PRO:O	13:L:102:ARG:HD2	2.06	0.55
15:N:9:LYS:HD3	15:N:9:LYS:C	2.28	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1222:G:P	20:S:77:THR:HG21	2.47	0.55
1:A:1278:U:H5''	1:A:1279:A:C5'	2.36	0.55
1:A:1294:G:O2'	1:A:1295:G:H5'	2.07	0.55
1:A:1316:G:H4'	15:N:18:VAL:CG1	2.36	0.55
1:A:929:G:O2'	1:A:930:C:H5'	2.06	0.55
4:C:172:ARG:HH12	4:C:174:PRO:HG3	1.71	0.55
4:C:79:ARG:HE	4:C:82:GLU:HG2	1.71	0.55
8:G:51:GLN:OE1	8:G:51:GLN:HA	2.08	0.55
16:O:33:THR:HG23	16:O:63:ARG:HH12	1.71	0.55
1:A:1521:G:H2'	1:A:1522:U:H6	1.70	0.54
3:B:124:SER:CB	3:B:125:PRO:CD	2.85	0.54
3:B:32:ILE:HD13	3:B:40:HIS:CD2	2.42	0.54
4:C:26:LYS:CD	4:C:26:LYS:H	2.19	0.54
1:A:1256:A:H8	4:C:27:LYS:HZ1	1.53	0.54
5:D:173:TRP:HB2	5:D:187:ARG:O	2.07	0.54
5:D:6:GLY:O	5:D:7:PRO:C	2.45	0.54
8:G:75:VAL:CG1	8:G:86:GLN:HB3	2.30	0.54
11:J:11:PHE:CE2	11:J:65:LEU:HD21	2.41	0.54
20:S:43:GLU:H	20:S:43:GLU:CD	2.10	0.54
4:C:64:VAL:CG2	4:C:99:VAL:HB	2.37	0.54
20:S:80:TYR:CE2	20:S:81:ARG:HB2	2.42	0.54
21:T:76:ALA:O	21:T:80:ARG:HG2	2.06	0.54
1:A:1478:C:H2'	1:A:1479:C:H6	1.73	0.54
1:A:463:A:O4'	17:P:82:GLN:NE2	2.37	0.54
3:B:217:ARG:HA	3:B:220:ASP:OD2	2.07	0.54
4:C:38:ARG:NH1	4:C:38:ARG:HG3	2.23	0.54
7:F:44:GLY:HA2	7:F:59:TYR:CE1	2.42	0.54
7:F:80:ARG:HH11	7:F:80:ARG:HG2	1.72	0.54
8:G:15:ASP:HB3	8:G:19:GLY:N	2.23	0.54
11:J:80:LYS:O	11:J:83:GLU:HB3	2.08	0.54
14:M:34:LEU:CD1	14:M:41:PRO:HA	2.37	0.54
17:P:42:ARG:O	17:P:43:LYS:C	2.45	0.54
1:A:818:G:H3'	1:A:819:A:C5'	2.38	0.54
4:C:155:GLY:O	4:C:156:ARG:HB2	2.07	0.54
5:D:130:GLY:O	5:D:131:ARG:C	2.46	0.54
5:D:187:ARG:HH21	5:D:188:LEU:HD12	1.73	0.54
6:E:101:ILE:O	6:E:120:THR:HB	2.07	0.54
12:K:99:GLN:HG2	12:K:105:VAL:HG21	1.89	0.54
13:L:119:LYS:O	13:L:120:TYR:HB2	2.08	0.54
13:L:83:VAL:HG22	13:L:84:LEU:N	2.21	0.54
15:N:21:TYR:HE2	15:N:23:ARG:NE	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:29:ARG:HH11	15:N:29:ARG:HG2	1.73	0.54
4:C:29:TYR:CZ	15:N:54:PRO:HG2	2.42	0.54
21:T:82:SER:O	21:T:86:ARG:HB2	2.06	0.54
1:A:1472:U:O2'	1:A:1473:A:H5'	2.08	0.54
1:A:765:G:N2	1:A:812:C:O2'	2.40	0.54
3:B:16:HIS:CE1	3:B:210:SER:HG	2.26	0.54
4:C:52:LEU:H	4:C:52:LEU:CD2	2.19	0.54
6:E:19:MET:HE2	6:E:24:ARG:HH12	1.73	0.54
7:F:30:LEU:HD11	7:F:63:TYR:CD2	2.43	0.54
20:S:18:LYS:HG2	20:S:18:LYS:O	2.08	0.54
20:S:24:ALA:HB3	20:S:25:LYS:NZ	2.23	0.54
14:M:94:ARG:HH12	20:S:81:ARG:HD3	1.72	0.54
1:A:1138:G:N3	1:A:1138:G:H3'	2.22	0.54
1:A:376:G:P	17:P:67:THR:HG21	2.47	0.54
1:A:435:C:H2'	1:A:436:C:H6	1.72	0.54
1:A:663:A:H2'	1:A:664:G:O4'	2.07	0.54
1:A:761:G:H4'	18:Q:102:GLY:C	2.27	0.54
3:B:53:ARG:HH12	3:B:199:TYR:HD2	1.56	0.54
5:D:61:LYS:NZ	5:D:62:GLN:NE2	2.56	0.54
20:S:5:LEU:O	20:S:6:LYS:CB	2.56	0.54
1:A:1037:C:H2'	1:A:1038:C:C6	2.42	0.54
1:A:1095:U:H2'	1:A:1096:C:C6	2.43	0.54
3:B:137:ARG:HB3	3:B:137:ARG:NH1	2.23	0.54
5:D:114:ARG:NH1	5:D:114:ARG:HG3	2.20	0.54
6:E:93:PRO:HG2	9:H:105:ARG:HH21	1.73	0.54
11:J:22:LYS:CE	11:J:90:LEU:HD12	2.37	0.54
18:Q:74:LEU:C	18:Q:74:LEU:HD23	2.28	0.54
19:R:42:ARG:HG3	19:R:42:ARG:NH1	2.23	0.54
1:A:1412:C:H2'	1:A:1413:A:H8	1.73	0.54
1:A:475:G:H2'	1:A:476:G:H8	1.72	0.54
1:A:659:U:O2'	1:A:660:G:H5'	2.07	0.54
7:F:75:LEU:O	7:F:79:LEU:HG	2.08	0.54
11:J:8:LEU:CD1	11:J:20:ALA:HB2	2.37	0.54
1:A:1221:G:O3'	20:S:77:THR:HG21	2.07	0.54
1:A:1347:G:O2'	1:A:1348:U:OP2	2.23	0.54
1:A:1404:C:H2'	1:A:1405:G:C8	2.42	0.54
1:A:824:C:H2'	1:A:825:G:H8	1.73	0.54
3:B:10:LEU:HG	3:B:48:MET:CE	2.38	0.54
3:B:115:LEU:HD11	3:B:146:GLN:HG3	1.90	0.54
7:F:14:LEU:HD21	7:F:84:ASN:OD1	2.08	0.54
11:J:19:SER:O	11:J:22:LYS:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1316:G:H4'	15:N:18:VAL:HG11	1.89	0.54
1:A:974:A:OP1	15:N:31:ARG:HG2	2.08	0.54
1:A:1347:G:C8	10:I:107:ARG:HB3	2.42	0.54
1:A:42:G:H2'	1:A:43:C:H6	1.72	0.54
3:B:17:PHE:CD1	3:B:17:PHE:C	2.81	0.54
5:D:150:GLU:HA	5:D:153:ARG:NE	2.22	0.54
13:L:28:LYS:HD2	13:L:33:ARG:NH2	2.20	0.54
17:P:1:MET:O	17:P:24:ALA:HB2	2.08	0.54
1:A:1006:C:H2'	1:A:1007:C:C6	2.43	0.53
1:A:1172:C:H2'	1:A:1173:G:C8	2.42	0.53
1:A:1497:G:H2'	1:A:1498:U:C5'	2.37	0.53
1:A:760:G:O6	18:Q:105:ALA:CB	2.54	0.53
1:A:922:G:N3	1:A:1398:A:H2	2.06	0.53
1:A:930:C:O2'	1:A:931:C:H5'	2.08	0.53
3:B:118:LEU:HB2	3:B:142:LEU:HD21	1.90	0.53
3:B:124:SER:O	3:B:127:ILE:HG13	2.08	0.53
4:C:191:THR:HG21	4:C:193:TYR:CE1	2.42	0.53
4:C:5:ILE:O	4:C:5:ILE:HD12	2.08	0.53
5:D:151:LYS:H	5:D:151:LYS:HD2	1.73	0.53
8:G:79:ARG:HD3	8:G:84:ASN:OD1	2.08	0.53
9:H:51:VAL:HG11	9:H:60:ARG:NH1	2.22	0.53
11:J:82:ILE:O	11:J:86:MET:HB2	2.08	0.53
12:K:26:ASN:O	12:K:27:ASN:CB	2.56	0.53
20:S:22:LEU:CD2	20:S:28:LYS:HD2	2.38	0.53
1:A:1224:G:H2'	20:S:78:ARG:HH12	1.72	0.53
21:T:93:GLU:OE2	21:T:93:GLU:HA	2.09	0.53
1:A:1364:U:H5'	22:V:14:TRP:CH2	2.43	0.53
1:A:112:G:H21	1:A:354:G:H5'	1.72	0.53
1:A:1405:G:O2'	1:A:1406:U:H5'	2.08	0.53
3:B:134:GLU:C	3:B:136:VAL:H	2.11	0.53
3:B:144:ARG:HG3	3:B:145:LEU:H	1.72	0.53
3:B:27:LYS:HD3	3:B:195:ASP:OD2	2.08	0.53
4:C:3:ASN:OD1	4:C:3:ASN:N	2.41	0.53
5:D:115:ARG:O	5:D:118:ARG:HB3	2.08	0.53
5:D:15:GLU:O	5:D:17:VAL:N	2.40	0.53
6:E:24:ARG:NH1	6:E:24:ARG:HG2	2.22	0.53
9:H:134:ILE:HG22	9:H:135:CYS:N	2.22	0.53
17:P:45:THR:HB	17:P:46:PRO:HD2	1.90	0.53
1:A:130:A:C8	18:Q:63:ARG:HG3	2.43	0.53
7:F:101:ALA:CB	19:R:28:GLU:HB3	2.38	0.53
20:S:74:PHE:N	20:S:74:PHE:CD1	2.76	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1234:C:H5'	1:A:1365:G:OP1	2.08	0.53
1:A:514:C:H2'	1:A:515:G:C8	2.42	0.53
1:A:736:C:H2'	1:A:737:A:C8	2.43	0.53
4:C:179:ARG:HD3	4:C:206:GLU:CG	2.37	0.53
7:F:43:LEU:N	7:F:43:LEU:HD22	2.22	0.53
1:A:1226:C:N4	14:M:104:ARG:HD2	2.23	0.53
1:A:1310:G:O6	20:S:2:PRO:HB3	2.08	0.53
20:S:40:ILE:CD1	20:S:62:ILE:HD13	2.38	0.53
1:A:1129:C:O2'	1:A:1130:A:OP2	2.24	0.53
1:A:244:U:O4	1:A:906:G:H1'	2.08	0.53
4:C:175:LEU:HD11	4:C:201:TYR:CE2	2.44	0.53
5:D:111:ALA:HB2	5:D:120:LEU:HD12	1.88	0.53
8:G:156:TRP:OXT	8:G:156:TRP:HD1	1.91	0.53
9:H:24:THR:HG22	9:H:61:VAL:O	2.08	0.53
12:K:74:ALA:C	12:K:76:GLY:H	2.12	0.53
14:M:77:ASN:O	14:M:80:ARG:HB3	2.07	0.53
19:R:34:TYR:HA	19:R:69:THR:HG23	1.89	0.53
1:A:447:G:H2'	1:A:485:G:N2	2.23	0.53
3:B:23:ARG:O	3:B:24:TRP:O	2.26	0.53
4:C:88:ARG:O	4:C:91:LEU:HD22	2.09	0.53
6:E:35:GLY:HA3	6:E:112:LEU:HB3	1.91	0.53
7:F:10:LEU:HD13	7:F:59:TYR:HD2	1.73	0.53
1:A:737:A:H1'	7:F:73:ASN:HD21	1.74	0.53
1:A:1123:A:O3'	11:J:36:GLY:HA3	2.08	0.53
17:P:67:THR:HG22	17:P:68:ASP:H	1.72	0.53
1:A:1004:A:H5''	1:A:1025:U:C5	2.44	0.53
1:A:115:G:H1'	1:A:116:A:N7	2.24	0.53
1:A:308:C:H2'	1:A:309:G:H8	1.73	0.53
1:A:452:A:HO2'	1:A:453:A:H8	1.55	0.53
1:A:833:U:H2'	1:A:834:C:C6	2.43	0.53
3:B:187:LEU:HD13	3:B:187:LEU:O	2.09	0.53
3:B:229:VAL:O	3:B:229:VAL:HG12	2.09	0.53
6:E:19:MET:CE	6:E:24:ARG:HH12	2.21	0.53
8:G:20:ASP:OD2	8:G:22:LEU:HB3	2.08	0.53
10:I:12:GLU:O	10:I:12:GLU:HG2	2.08	0.53
1:A:1249:C:O2'	10:I:73:GLN:NE2	2.42	0.53
15:N:21:TYR:CD2	15:N:21:TYR:O	2.61	0.53
17:P:8:ARG:HB2	17:P:28:ARG:NH1	2.24	0.53
1:A:1145:C:O2'	1:A:1146:A:H8	1.92	0.53
1:A:1236:A:H2'	1:A:1237:C:C6	2.43	0.53
1:A:496:A:H4'	1:A:497:A:OP1	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:151:GLY:C	3:B:153:ARG:N	2.60	0.53
3:B:26:PRO:O	3:B:29:ALA:HB2	2.09	0.53
4:C:123:GLN:HE22	4:C:140:ARG:HH22	1.56	0.53
4:C:33:LEU:O	4:C:33:LEU:HD23	2.08	0.53
20:S:63:THR:HG22	20:S:64:GLU:N	2.22	0.53
22:V:5:ASP:O	22:V:11:GLY:HA3	2.09	0.53
1:A:1042:G:O2'	1:A:1043:C:H5'	2.08	0.53
1:A:1106:G:H5''	4:C:172:ARG:HG2	1.90	0.53
1:A:1231:G:O3'	10:I:126:SER:HB3	2.09	0.53
1:A:1277:C:HO2'	1:A:1279:A:H8	1.52	0.53
1:A:1317:C:H2'	1:A:1318:A:O4'	2.09	0.53
1:A:336:C:O2'	1:A:337:C:H5'	2.09	0.53
1:A:913:A:H1'	1:A:914:A:O4'	2.09	0.53
3:B:141:GLU:O	3:B:145:LEU:HG	2.09	0.53
3:B:223:ILE:C	3:B:225:ALA:N	2.60	0.53
3:B:223:ILE:HG22	3:B:228:GLY:HA3	1.91	0.53
5:D:118:ARG:HG3	5:D:118:ARG:HH21	1.73	0.53
12:K:69:ALA:O	12:K:73:MET:HG2	2.09	0.53
16:O:29:VAL:HG11	16:O:67:LEU:HD21	1.91	0.53
20:S:29:ARG:O	20:S:30:LEU:HB2	2.08	0.53
1:A:1366:C:H2'	1:A:1367:C:C6	2.42	0.53
1:A:477:G:H2'	1:A:478:A:C8	2.44	0.53
4:C:35:GLU:OE2	4:C:97:LYS:HE3	2.08	0.53
5:D:60:GLU:HA	5:D:60:GLU:OE1	2.09	0.53
17:P:28:ARG:NH1	17:P:29:ASP:OD2	2.40	0.53
20:S:5:LEU:O	20:S:6:LYS:HB2	2.08	0.53
1:A:1072:G:H2'	1:A:1073:U:C6	2.44	0.53
1:A:1229:A:H2'	1:A:1230:C:C6	2.43	0.53
1:A:1240:U:P	8:G:116:ALA:HB2	2.49	0.53
1:A:1292:U:O2'	1:A:1293:G:H5'	2.09	0.53
1:A:433:C:H2'	1:A:434:U:C6	2.44	0.53
1:A:993:G:H4'	1:A:994:A:OP2	2.09	0.53
3:B:137:ARG:HH11	3:B:137:ARG:HB3	1.74	0.53
5:D:151:LYS:H	5:D:151:LYS:CD	2.22	0.53
5:D:152:SER:O	5:D:158:ILE:HD12	2.08	0.53
5:D:191:ARG:O	5:D:191:ARG:HD2	2.09	0.53
6:E:69:VAL:HG21	6:E:113:ALA:HB1	1.91	0.53
7:F:75:LEU:HD13	7:F:75:LEU:C	2.30	0.53
8:G:18:TYR:CD2	8:G:59:LEU:HD13	2.44	0.53
9:H:36:LEU:CD1	9:H:59:LEU:HD13	2.37	0.53
10:I:112:LYS:HD3	10:I:112:LYS:C	2.29	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:117:HIS:O	10:I:118:LYS:HG3	2.09	0.53
1:A:1128:C:C4'	10:I:16:ARG:HH12	2.22	0.53
11:J:19:SER:HB2	11:J:91:PRO:HG3	1.90	0.53
17:P:22:THR:HA	17:P:33:ILE:HD12	1.91	0.53
20:S:40:ILE:HG21	20:S:62:ILE:HD11	1.90	0.53
21:T:57:ARG:CG	21:T:57:ARG:HH11	2.22	0.53
1:A:440:A:H5'	1:A:442:C:OP2	2.08	0.52
10:I:19:LEU:C	10:I:20:ARG:HG3	2.30	0.52
10:I:93:ARG:NH1	10:I:97:LYS:HZ2	2.07	0.52
12:K:43:SER:HA	12:K:47:VAL:HG21	1.91	0.52
14:M:108:ARG:NE	14:M:108:ARG:HA	2.24	0.52
15:N:26:ARG:HH12	15:N:47:LEU:HG	1.69	0.52
1:A:266:G:O3'	18:Q:67:LYS:HB2	2.08	0.52
21:T:85:MET:HE3	21:T:103:GLY:O	2.10	0.52
1:A:967:C:H2'	1:A:968:A:C8	2.45	0.52
3:B:206:ASP:CG	3:B:207:ALA:N	2.63	0.52
4:C:33:LEU:HD23	4:C:33:LEU:C	2.30	0.52
6:E:72:GLN:O	6:E:75:THR:HG22	2.09	0.52
14:M:78:ILE:O	14:M:82:MET:HB2	2.08	0.52
18:Q:27:PHE:HB2	18:Q:28:PRO:HD2	1.91	0.52
22:V:3:LYS:HB3	22:V:14:TRP:CD1	2.44	0.52
1:A:1133:G:H2'	1:A:1134:G:C8	2.43	0.52
1:A:1161:C:H2'	1:A:1162:C:C6	2.40	0.52
4:C:11:ARG:HH12	4:C:179:ARG:N	2.07	0.52
5:D:33:MET:O	5:D:37:PRO:HG3	2.09	0.52
11:J:47:PHE:HB2	11:J:63:PHE:HB2	1.92	0.52
16:O:77:ARG:O	16:O:80:ALA:HB3	2.10	0.52
1:A:1106:G:OP1	4:C:172:ARG:HD3	2.08	0.52
1:A:1451:A:OP2	1:A:1452:C:H5	1.93	0.52
1:A:396:G:O2'	1:A:398:C:OP1	2.21	0.52
3:B:18:GLY:HA2	3:B:41:ILE:HA	1.90	0.52
19:R:36:ASN:CG	19:R:39:VAL:HG12	2.30	0.52
21:T:54:LYS:HG3	21:T:100:ILE:CD1	2.33	0.52
21:T:57:ARG:HH11	21:T:57:ARG:CB	2.22	0.52
1:A:217:C:O2'	1:A:218:C:H5'	2.10	0.52
1:A:628:G:H2'	1:A:629:G:H8	1.74	0.52
1:A:666:G:H5'	1:A:726:C:H1'	1.90	0.52
5:D:118:ARG:HG3	5:D:118:ARG:NH2	2.24	0.52
5:D:32:ALA:C	5:D:34:GLU:N	2.62	0.52
6:E:51:VAL:HB	6:E:52:PRO:CD	2.35	0.52
10:I:13:ALA:HA	10:I:67:GLY:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:40:ILE:HG23	12:K:75:TYR:CD2	2.44	0.52
21:T:44:ALA:CB	21:T:88:VAL:HG13	2.40	0.52
1:A:1285:A:O2'	1:A:1286:A:OP2	2.27	0.52
1:A:1333:A:H2'	1:A:1334:G:O4'	2.10	0.52
1:A:1402:C:O2	1:A:1500:A:N1	2.42	0.52
1:A:1532:U:H6	1:A:1532:U:O5'	1.93	0.52
1:A:162:A:H8	1:A:162:A:O5'	1.92	0.52
1:A:260:G:H2'	1:A:261:U:C6	2.45	0.52
1:A:399:G:O2'	1:A:400:C:H5'	2.10	0.52
9:H:80:ILE:HG22	9:H:80:ILE:O	2.09	0.52
11:J:8:LEU:HD12	11:J:20:ALA:HB2	1.92	0.52
14:M:110:ARG:CG	14:M:110:ARG:NH1	2.70	0.52
20:S:21:GLU:O	20:S:25:LYS:HE2	2.10	0.52
20:S:67:VAL:O	20:S:69:HIS:N	2.42	0.52
1:A:1121:U:O2'	1:A:1122:U:H5'	2.10	0.52
1:A:1163:C:H2'	1:A:1164:G:H8	1.75	0.52
5:D:103:ASN:O	5:D:106:TYR:HB3	2.09	0.52
12:K:19:ALA:HB2	12:K:80:VAL:CG1	2.39	0.52
21:T:53:LEU:HD21	21:T:104:LEU:CD1	2.37	0.52
21:T:79:ARG:O	21:T:80:ARG:C	2.48	0.52
1:A:1195:C:H3'	1:A:1196:U:C5'	2.35	0.52
6:E:102:ALA:HB2	6:E:120:THR:HB	1.92	0.52
7:F:4:TYR:CZ	7:F:72:VAL:HG21	2.45	0.52
10:I:47:LEU:C	10:I:49:PRO:HD2	2.30	0.52
11:J:51:ARG:CZ	11:J:61:GLU:HB2	2.38	0.52
1:A:56:U:O2'	1:A:57:G:H5'	2.10	0.52
1:A:682:G:O2'	1:A:683:G:H5'	2.09	0.52
1:A:80:G:C2'	1:A:81:U:H5''	2.39	0.52
3:B:194:PRO:HA	3:B:200:ILE:HD11	1.91	0.52
3:B:15:VAL:CG2	3:B:209:ARG:HG3	2.40	0.52
11:J:45:ARG:NH1	11:J:45:ARG:HB3	2.03	0.52
11:J:87:THR:O	11:J:88:LEU:HG	2.09	0.52
14:M:39:ILE:HD13	14:M:52:GLU:HB3	1.91	0.52
14:M:5:ALA:O	14:M:6:GLY:C	2.48	0.52
17:P:34:GLU:OE2	17:P:55:ARG:HD3	2.08	0.52
12:K:84:VAL:CG2	19:R:88:LYS:HD3	2.40	0.52
20:S:10:PHE:HE2	20:S:12:ASP:OD1	1.93	0.52
1:A:1216:G:H2'	1:A:1217:C:C6	2.45	0.52
1:A:1231:G:C4'	10:I:126:SER:HB3	2.40	0.52
1:A:279:A:H5''	1:A:280:C:H3'	1.91	0.52
1:A:975:A:H4'	1:A:976:G:C5'	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:986:A:H2'	1:A:987:G:C8	2.45	0.52
3:B:231:GLU:HB2	3:B:232:PRO:HD2	1.92	0.52
5:D:64:LEU:HD11	5:D:97:LEU:HD11	1.92	0.52
7:F:25:ILE:HD12	7:F:82:ARG:HH11	1.75	0.52
10:I:10:ARG:HG2	10:I:75:ASP:HB2	1.91	0.52
10:I:118:LYS:O	10:I:119:ALA:CB	2.53	0.52
10:I:5:TYR:CG	10:I:6:GLY:N	2.77	0.52
12:K:123:LYS:O	12:K:125:PHE:N	2.43	0.52
14:M:79:LYS:O	14:M:83:ASP:OD2	2.27	0.52
1:A:1021:G:C2	1:A:1022:G:H1'	2.46	0.51
1:A:1248:A:H1'	10:I:70:LYS:NZ	2.24	0.51
1:A:179:A:H2'	1:A:180:U:H6	1.74	0.51
1:A:216:G:H2'	1:A:217:C:C6	2.45	0.51
1:A:31:G:H1	1:A:48:C:H5''	1.75	0.51
1:A:633:G:H2'	1:A:634:C:C6	2.45	0.51
1:A:812:C:O2'	1:A:813:U:P	2.69	0.51
3:B:54:THR:O	3:B:58:ILE:HG13	2.11	0.51
11:J:61:GLU:CD	15:N:45:ARG:HH12	2.12	0.51
1:A:707:C:OP1	12:K:85:ARG:NH1	2.44	0.51
12:K:95:ILE:O	12:K:99:GLN:HG3	2.10	0.51
1:A:1426:C:H2'	1:A:1427:U:C6	2.45	0.51
1:A:514:C:H2'	1:A:515:G:H8	1.75	0.51
5:D:8:VAL:HG13	5:D:11:LEU:HD12	1.92	0.51
9:H:86:ILE:HD12	9:H:133:LEU:HD22	1.93	0.51
14:M:73:GLU:O	14:M:76:ALA:HB3	2.10	0.51
19:R:34:TYR:O	19:R:34:TYR:HD1	1.94	0.51
19:R:46:GLU:CD	19:R:46:GLU:H	2.14	0.51
21:T:11:SER:C	21:T:13:LEU:H	2.13	0.51
1:A:1391:U:H2'	1:A:1392:G:C8	2.45	0.51
1:A:373:A:O2'	1:A:374:A:H5'	2.10	0.51
1:A:922:G:H2'	1:A:923:A:C8	2.45	0.51
1:A:965:A:C2	1:A:969:A:C2	2.98	0.51
3:B:223:ILE:HG21	3:B:230:VAL:CG2	2.40	0.51
3:B:73:THR:HB	3:B:169:LYS:HE3	1.90	0.51
3:B:8:LYS:HD3	3:B:9:GLU:N	2.24	0.51
5:D:157:LEU:C	5:D:157:LEU:HD23	2.31	0.51
1:A:16:A:O2'	1:A:17:U:H5'	2.10	0.51
1:A:489:C:H2'	1:A:490:G:H8	1.75	0.51
3:B:197:VAL:HB	3:B:200:ILE:CG1	2.39	0.51
5:D:142:PRO:HA	5:D:185:PHE:HD2	1.75	0.51
6:E:137:GLU:O	6:E:141:GLN:HG3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:13:ILE:HG22	6:E:30:ALA:CB	2.39	0.51
6:E:40:ARG:HG2	6:E:68:GLU:OE2	2.10	0.51
1:A:1298:C:C4	8:G:114:ARG:HD3	2.45	0.51
1:A:1147:C:O2	10:I:16:ARG:NH1	2.44	0.51
11:J:51:ARG:HB2	11:J:59:SER:CB	2.21	0.51
14:M:40:ASN:ND2	14:M:41:PRO:HD2	2.22	0.51
15:N:14:PRO:C	15:N:16:PHE:N	2.64	0.51
20:S:41:VAL:H	20:S:44:MET:HE3	1.76	0.51
1:A:1123:A:H4'	11:J:37:PRO:HD2	1.91	0.51
1:A:1277:C:H2'	1:A:1278:U:H5'	1.91	0.51
1:A:1425:U:H2'	1:A:1426:C:H6	1.76	0.51
1:A:203:U:H5''	1:A:204:U:OP1	2.09	0.51
1:A:393:A:OP2	17:P:12:LYS:HE2	2.11	0.51
1:A:748:C:OP2	1:A:748:C:H6	1.93	0.51
4:C:112:SER:CB	4:C:115:LEU:HD12	2.39	0.51
4:C:130:VAL:HG21	4:C:157:ILE:HG23	1.92	0.51
6:E:120:THR:CG2	6:E:121:LYS:N	2.71	0.51
22:V:15:ARG:O	22:V:17:THR:HG23	2.11	0.51
1:A:1313:U:O4	20:S:4:SER:OG	2.24	0.51
1:A:259:G:O2'	1:A:260:G:H5'	2.09	0.51
1:A:324:G:N2	1:A:327:A:C8	2.79	0.51
1:A:836:G:C6	1:A:851:G:C6	2.99	0.51
3:B:7:VAL:HG11	3:B:221:LEU:HD23	1.91	0.51
4:C:11:ARG:O	4:C:13:GLY:N	2.44	0.51
4:C:164:ARG:HB3	4:C:164:ARG:HH11	1.76	0.51
5:D:199:ASN:HD21	5:D:201:GLN:CB	2.23	0.51
5:D:19:LEU:HD22	5:D:67:ILE:HG12	1.93	0.51
15:N:53:LEU:HB3	15:N:56:VAL:CG2	2.40	0.51
16:O:26:GLU:HG3	16:O:81:LEU:HD12	1.91	0.51
18:Q:68:ARG:O	18:Q:69:LYS:HB2	2.11	0.51
18:Q:76:LEU:HD23	18:Q:76:LEU:C	2.30	0.51
21:T:63:ILE:HD13	21:T:80:ARG:HB3	1.92	0.51
1:A:1021:G:H2'	1:A:1022:G:O4'	2.11	0.51
1:A:1279:A:O2'	1:A:1281:U:OP2	2.26	0.51
1:A:1470:G:O2'	1:A:1471:G:H5'	2.10	0.51
1:A:248:C:C2'	1:A:249:U:H5'	2.41	0.51
1:A:437:U:H5''	5:D:155:LEU:CD2	2.40	0.51
1:A:900:A:H2'	1:A:901:A:C8	2.46	0.51
5:D:209:ARG:HG2	5:D:209:ARG:HH11	1.74	0.51
5:D:42:GLN:CG	5:D:42:GLN:O	2.59	0.51
8:G:14:PRO:HB2	8:G:19:GLY:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:23:SER:O	9:H:24:THR:HB	2.10	0.51
1:A:953:G:H1'	14:M:125:ARG:CB	2.40	0.51
1:A:370:C:C2'	1:A:371:G:H5'	2.40	0.51
1:A:742:G:C5'	16:O:58:MET:HE1	2.39	0.51
1:A:812:C:O2'	1:A:813:U:OP2	2.28	0.51
3:B:8:LYS:CD	3:B:9:GLU:N	2.74	0.51
5:D:121:VAL:O	5:D:134:ASP:HA	2.11	0.51
5:D:5:ILE:HG22	5:D:5:ILE:O	2.11	0.51
8:G:54:THR:HG22	8:G:56:GLN:H	1.74	0.51
12:K:86:GLY:H	12:K:112:THR:HG23	1.75	0.51
18:Q:56:VAL:HG12	18:Q:77:VAL:HB	1.92	0.51
19:R:52:PRO:O	19:R:56:THR:HG23	2.10	0.51
20:S:22:LEU:HD13	20:S:28:LYS:HB3	1.92	0.51
1:A:1070:U:H2'	1:A:1071:C:H6	1.75	0.51
1:A:1095:U:H2'	1:A:1096:C:H6	1.75	0.51
1:A:443:C:H2'	1:A:444:C:H6	1.76	0.51
1:A:731:G:O2'	1:A:732:C:H5'	2.10	0.51
1:A:924:C:H5'	1:A:1399:C:OP2	2.11	0.51
3:B:25:ASN:O	3:B:27:LYS:N	2.44	0.51
5:D:199:ASN:HD21	5:D:201:GLN:HB3	1.76	0.51
5:D:4:TYR:O	5:D:5:ILE:HB	2.11	0.51
5:D:61:LYS:HZ2	5:D:62:GLN:HE21	1.59	0.51
10:I:81:ILE:O	10:I:85:LEU:HD13	2.11	0.51
13:L:117:ARG:HB3	13:L:122:THR:OG1	2.10	0.51
13:L:50:SER:O	13:L:51:ALA:HB2	2.10	0.51
19:R:46:GLU:CD	19:R:46:GLU:N	2.63	0.51
1:A:1510:U:H2'	1:A:1511:G:C8	2.46	0.51
1:A:193:C:H2'	1:A:194:C:C6	2.46	0.51
1:A:319:G:O2'	1:A:320:C:H5'	2.11	0.51
1:A:446:G:C2'	1:A:447:G:H5'	2.41	0.51
4:C:6:HIS:CD2	4:C:8:ILE:HB	2.46	0.51
7:F:10:LEU:HD12	7:F:10:LEU:H	1.76	0.51
10:I:4:TYR:CZ	10:I:88:TYR:HD1	2.29	0.51
11:J:34:VAL:HG22	11:J:74:ILE:CG2	2.41	0.51
13:L:125:PRO:O	13:L:127:GLU:N	2.43	0.51
16:O:34:LEU:HD23	16:O:34:LEU:C	2.31	0.51
18:Q:17:LYS:HA	18:Q:46:ASP:O	2.11	0.51
19:R:18:ARG:NH1	19:R:21:LYS:NZ	2.58	0.51
1:A:1194:U:O2'	1:A:1195:C:H5'	2.11	0.50
1:A:1253:G:H2'	1:A:1254:C:C6	2.47	0.50
1:A:1518:A:H2'	1:A:1519:A:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:C:O2'	1:A:249:U:H5'	2.11	0.50
1:A:975:A:H5'	1:A:975:A:C8	2.42	0.50
4:C:83:ARG:HA	4:C:86:VAL:CG2	2.38	0.50
4:C:84:ILE:O	4:C:88:ARG:HB2	2.11	0.50
6:E:102:ALA:CB	6:E:120:THR:HG21	2.40	0.50
9:H:38:ILE:N	9:H:38:ILE:HD12	2.26	0.50
14:M:40:ASN:ND2	14:M:41:PRO:N	2.60	0.50
21:T:72:LEU:O	21:T:73:HIS:O	2.29	0.50
1:A:67:C:O2'	1:A:171:A:H1'	2.11	0.50
1:A:382:A:C2	1:A:383:A:C4	3.00	0.50
1:A:554:C:H2'	1:A:555:C:C6	2.46	0.50
4:C:47:LEU:N	4:C:47:LEU:HD12	2.25	0.50
18:Q:63:ARG:HG2	18:Q:64:PRO:CD	2.40	0.50
1:A:23:C:H2'	1:A:24:U:H6	1.76	0.50
1:A:778:G:O2'	1:A:779:C:H5'	2.11	0.50
1:A:812:C:H4'	1:A:813:U:H5'	1.94	0.50
3:B:80:ILE:HG21	3:B:211:ILE:HG22	1.93	0.50
4:C:11:ARG:CG	4:C:11:ARG:HH11	2.24	0.50
4:C:91:LEU:HD23	4:C:92:ALA:N	2.26	0.50
5:D:3:ARG:NH1	5:D:118:ARG:HH12	2.10	0.50
7:F:78:GLU:HA	7:F:81:ILE:HD12	1.92	0.50
3:B:178:ARG:NH2	9:H:68:ARG:HH22	2.09	0.50
1:A:1411:C:H2'	1:A:1412:C:C6	2.46	0.50
1:A:1425:U:H3	1:A:1475:G:H1	1.60	0.50
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.27	0.50
1:A:270:A:H2'	1:A:271:C:C6	2.47	0.50
1:A:818:G:C3'	1:A:819:A:C5'	2.89	0.50
3:B:93:VAL:HG11	3:B:97:TRP:CD1	2.46	0.50
4:C:14:ILE:O	4:C:16:ARG:N	2.45	0.50
6:E:15:ARG:HD3	6:E:26:PHE:CD2	2.47	0.50
11:J:59:SER:O	11:J:60:ARG:HB2	2.12	0.50
10:I:114:TYR:CE1	11:J:60:ARG:HB2	2.47	0.50
12:K:115:PRO:C	12:K:117:ASN:H	2.14	0.50
13:L:38:THR:HG22	13:L:39:VAL:HG23	1.93	0.50
1:A:103:C:OP2	21:T:17:ARG:NH1	2.44	0.50
1:A:1287:A:H2'	1:A:1288:A:C8	2.46	0.50
1:A:1305:G:O2'	1:A:1306:A:C8	2.46	0.50
1:A:132:C:O2'	1:A:133:U:H5'	2.12	0.50
1:A:542:G:O2'	1:A:543:C:H5'	2.12	0.50
5:D:130:GLY:O	5:D:131:ARG:O	2.30	0.50
5:D:25:ARG:O	5:D:27:TYR:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:32:ALA:C	5:D:34:GLU:H	2.15	0.50
7:F:30:LEU:HD11	7:F:63:TYR:CE2	2.45	0.50
14:M:37:THR:O	14:M:39:ILE:HG13	2.11	0.50
15:N:50:LYS:HD3	15:N:52:GLN:NE2	2.26	0.50
19:R:59:SER:O	19:R:62:GLU:N	2.44	0.50
22:V:9:ARG:HH12	22:V:23:PRO:CD	2.24	0.50
1:A:1010:G:O2'	1:A:1011:G:H5'	2.11	0.50
1:A:1413:A:H2	1:A:1487:G:H22	1.59	0.50
1:A:929:G:H5''	1:A:1533:C:H41	1.76	0.50
1:A:51:A:H4'	1:A:52:G:C5'	2.42	0.50
1:A:545:C:O2'	1:A:549:C:OP1	2.30	0.50
1:A:559:A:OP2	6:E:126:ARG:NH2	2.43	0.50
1:A:818:G:H3'	1:A:819:A:H5''	1.94	0.50
3:B:8:LYS:CD	3:B:9:GLU:H	2.24	0.50
4:C:64:VAL:HB	4:C:99:VAL:HG21	1.93	0.50
5:D:58:LEU:C	5:D:58:LEU:HD13	2.32	0.50
9:H:29:SER:OG	9:H:32:LYS:HE3	2.11	0.50
20:S:20:LEU:C	20:S:22:LEU:H	2.13	0.50
1:A:1005:A:C2'	1:A:1006:C:H5'	2.40	0.50
1:A:1288:A:H2'	1:A:1289:A:H8	1.75	0.50
1:A:1316:G:N2	1:A:1318:A:H3'	2.26	0.50
1:A:1347:G:C2'	1:A:1348:U:OP2	2.60	0.50
1:A:448:A:H2'	1:A:449:C:H6	1.77	0.50
1:A:487:A:H2'	1:A:488:C:O4'	2.12	0.50
1:A:714:G:H2'	1:A:715:A:C8	2.46	0.50
1:A:792:A:H4'	1:A:793:U:C5'	2.42	0.50
1:A:986:A:H1'	20:S:54:GLY:O	2.12	0.50
4:C:177:THR:O	4:C:177:THR:HG23	2.12	0.50
5:D:150:GLU:N	5:D:150:GLU:CD	2.60	0.50
5:D:194:LEU:HD22	5:D:194:LEU:N	2.26	0.50
5:D:91:SER:O	5:D:93:PHE:N	2.45	0.50
6:E:18:ARG:HG2	6:E:19:MET:N	2.26	0.50
6:E:89:ILE:CD1	6:E:90:VAL:H	2.23	0.50
8:G:26:PHE:CD2	8:G:30:ILE:HD11	2.47	0.50
9:H:116:LYS:NZ	9:H:127:LEU:HD12	2.27	0.50
13:L:32:PHE:HB3	13:L:84:LEU:HD11	1.94	0.50
1:A:449:C:O2	17:P:42:ARG:HD2	2.12	0.50
1:A:1085:U:H3'	1:A:1086:U:C5	2.46	0.50
1:A:1281:U:H5'	1:A:1282:C:C5	2.38	0.50
1:A:1424:C:O2'	1:A:1425:U:H5'	2.12	0.50
1:A:243:A:H4'	1:A:244:U:C5'	2.21	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:488:C:H2'	1:A:489:C:C6	2.46	0.50
3:B:16:HIS:NE2	3:B:214:ILE:CG1	2.74	0.50
6:E:15:ARG:O	6:E:16:THR:O	2.30	0.50
7:F:18:GLN:O	7:F:21:LEU:HB3	2.12	0.50
7:F:8:ILE:HB	7:F:61:LEU:HB2	1.93	0.50
10:I:111:ARG:HD3	10:I:112:LYS:N	2.27	0.50
1:A:1208:C:H2'	1:A:1209:C:C6	2.42	0.50
1:A:927:G:H4'	1:A:1503:A:N7	2.27	0.50
3:B:140:HIS:HA	3:B:143:GLU:HG2	1.94	0.50
4:C:116:VAL:O	4:C:120:VAL:HG23	2.12	0.50
4:C:11:ARG:NH1	4:C:179:ARG:H	2.07	0.50
5:D:53:ASP:O	5:D:57:ARG:HD3	2.11	0.50
1:A:1346:A:C4	8:G:10:ARG:NH2	2.80	0.50
8:G:21:VAL:CG2	8:G:22:LEU:N	2.75	0.50
13:L:71:PRO:HG2	13:L:102:ARG:HG3	1.94	0.50
20:S:22:LEU:HD22	20:S:28:LYS:HD2	1.94	0.50
1:A:1054:C:H5''	25:A:1632:TAC:O10	2.11	0.49
1:A:384:G:H2'	1:A:385:C:C6	2.47	0.49
1:A:555:C:H2'	1:A:556:C:H6	1.77	0.49
1:A:973:G:H3'	1:A:974:A:H5''	1.94	0.49
3:B:50:GLU:HB3	3:B:200:ILE:O	2.11	0.49
5:D:174:LEU:O	5:D:186:LEU:HD12	2.12	0.49
6:E:9:LYS:CD	6:E:112:LEU:HD21	2.42	0.49
1:A:716:A:N3	12:K:117:ASN:O	2.45	0.49
1:A:251:G:H4'	1:A:252:U:O5'	2.11	0.49
1:A:946:A:H2'	1:A:947:G:C8	2.46	0.49
1:A:979:C:H2'	1:A:980:C:H5'	1.93	0.49
3:B:130:ARG:NH2	4:C:207:VAL:HG22	2.26	0.49
3:B:25:ASN:HB2	3:B:191:ASP:O	2.13	0.49
4:C:35:GLU:HG2	4:C:59:ARG:NH2	2.26	0.49
5:D:3:ARG:HH22	5:D:74:GLN:CD	2.16	0.49
11:J:34:VAL:HG22	11:J:74:ILE:HG23	1.94	0.49
11:J:75:ILE:O	11:J:76:ASN:HB2	2.12	0.49
12:K:126:ARG:O	12:K:127:LYS:C	2.51	0.49
12:K:40:ILE:HG23	12:K:75:TYR:CE2	2.46	0.49
1:A:1026:G:H2'	1:A:1027:C:H5'	1.94	0.49
1:A:1178:G:P	10:I:97:LYS:NZ	2.85	0.49
1:A:37:U:O2'	1:A:38:G:H5'	2.12	0.49
1:A:848:C:O2'	1:A:849:C:H5'	2.13	0.49
1:A:965:A:O2'	1:A:966:G:OP2	2.28	0.49
5:D:173:TRP:CD2	5:D:189:PRO:HB3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:10:LEU:HD12	7:F:59:TYR:O	2.12	0.49
18:Q:95:TYR:O	18:Q:97:SER:N	2.45	0.49
21:T:94:ALA:O	21:T:95:ALA:HB3	2.11	0.49
1:A:327:A:HO2'	1:A:328:C:H6	1.59	0.49
4:C:134:ILE:HG22	4:C:168:ALA:HB3	1.93	0.49
4:C:154:SER:OG	4:C:155:GLY:N	2.45	0.49
4:C:178:LEU:O	4:C:179:ARG:HB3	2.11	0.49
4:C:42:LEU:HD12	4:C:94:LEU:CD1	2.42	0.49
5:D:205:GLU:O	5:D:208:SER:HB2	2.12	0.49
8:G:18:TYR:HB3	8:G:59:LEU:HD22	1.94	0.49
16:O:17:ARG:HG3	16:O:17:ARG:NH1	2.26	0.49
17:P:28:ARG:HH11	17:P:28:ARG:HG3	1.77	0.49
18:Q:59:ILE:HG23	18:Q:71:PHE:HB3	1.91	0.49
20:S:20:LEU:C	20:S:22:LEU:N	2.66	0.49
21:T:56:MET:O	21:T:59:ALA:HB3	2.13	0.49
1:A:1015:A:H2'	1:A:1016:A:C8	2.48	0.49
1:A:1136:U:H5''	1:A:1137:C:OP2	2.12	0.49
1:A:686:U:O2'	1:A:687:A:C8	2.55	0.49
1:A:995:C:H2'	1:A:995:C:O2	2.12	0.49
5:D:156:GLU:CG	5:D:160:GLN:HE21	2.18	0.49
6:E:150:ARG:NH1	6:E:150:ARG:HG3	2.23	0.49
7:F:22:GLU:OE1	7:F:22:GLU:HA	2.13	0.49
18:Q:9:VAL:HG21	18:Q:84:LEU:HD13	1.95	0.49
19:R:47:THR:O	19:R:49:LYS:N	2.45	0.49
1:A:110:C:C4	1:A:111:G:C5	3.01	0.49
1:A:1126:U:H2'	1:A:1127:G:O4'	2.12	0.49
1:A:1230:C:O2	14:M:126:LYS:O	2.30	0.49
1:A:393:A:C2'	1:A:394:G:H5'	2.42	0.49
4:C:180:ALA:HB3	4:C:182:ILE:HG13	1.95	0.49
5:D:30:LYS:C	5:D:32:ALA:N	2.65	0.49
1:A:1025:U:H4'	1:A:1025:U:OP1	2.12	0.49
1:A:1515:C:O2'	1:A:1516:G:H5'	2.13	0.49
1:A:168:G:O2'	1:A:169:C:H5'	2.11	0.49
1:A:285:G:O2'	1:A:286:G:H5'	2.13	0.49
1:A:961:U:O2'	1:A:962:C:H5'	2.12	0.49
6:E:89:ILE:HD13	6:E:90:VAL:N	2.24	0.49
11:J:51:ARG:N	11:J:59:SER:HB2	2.27	0.49
12:K:33:THR:OG1	12:K:34:ASP:N	2.45	0.49
1:A:1466:C:H2'	1:A:1467:G:O4'	2.12	0.49
1:A:490:G:H2'	1:A:491:G:C8	2.47	0.49
3:B:17:PHE:HD1	3:B:18:GLY:N	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:215:LEU:O	3:B:218:ALA:N	2.45	0.49
5:D:68:TYR:OH	5:D:196:LEU:HD11	2.13	0.49
3:B:178:ARG:NH2	9:H:68:ARG:NH2	2.60	0.49
14:M:6:GLY:O	14:M:7:VAL:HG22	2.13	0.49
17:P:59:TRP:HB3	17:P:64:ALA:HB2	1.94	0.49
18:Q:95:TYR:C	18:Q:97:SER:N	2.66	0.49
20:S:16:LEU:O	20:S:20:LEU:HG	2.12	0.49
1:A:1305:G:C5'	22:V:4:GLY:HA3	2.42	0.49
1:A:105:G:H2'	1:A:106:C:C6	2.47	0.49
1:A:252:U:H2'	1:A:253:U:C5	2.48	0.49
1:A:403:C:H2'	1:A:404:U:H6	1.77	0.49
1:A:518:C:H5''	1:A:519:C:C6	2.48	0.49
1:A:627:G:H2'	1:A:628:G:H8	1.78	0.49
1:A:865:A:O2'	1:A:866:C:H5'	2.12	0.49
1:A:22:G:H4'	1:A:885:G:C8	2.48	0.49
3:B:69:LEU:HD12	3:B:155:LEU:HD11	1.95	0.49
4:C:14:ILE:HG22	4:C:15:THR:N	2.16	0.49
5:D:57:ARG:NH2	5:D:205:GLU:OE2	2.44	0.49
9:H:6:ILE:HD12	9:H:35:ILE:HD12	1.94	0.49
10:I:121:ARG:HH11	10:I:121:ARG:HG2	1.78	0.49
11:J:91:PRO:HB2	11:J:94:VAL:HG23	1.95	0.49
20:S:22:LEU:HD22	20:S:28:LYS:HB2	1.94	0.49
20:S:44:MET:O	20:S:47:HIS:HB2	2.12	0.49
1:A:1220:G:H1'	20:S:52:TYR:HD2	1.77	0.49
1:A:1222:G:O2'	1:A:1223:C:H5'	2.12	0.49
1:A:300:A:H2'	1:A:301:G:O4'	2.13	0.49
1:A:439:A:C4	1:A:497:A:C2	3.01	0.49
1:A:532:A:H2'	1:A:533:A:C5'	2.42	0.49
1:A:737:A:H2'	1:A:738:C:C6	2.48	0.49
3:B:223:ILE:CG2	3:B:228:GLY:HA3	2.42	0.49
3:B:18:GLY:HA2	3:B:42:ILE:H	1.76	0.49
4:C:175:LEU:HD21	4:C:201:TYR:CD2	2.48	0.49
5:D:29:PRO:O	5:D:30:LYS:CG	2.61	0.49
9:H:107:LEU:N	9:H:107:LEU:HD23	2.28	0.49
11:J:26:ALA:HB1	11:J:84:GLN:HB3	1.95	0.49
12:K:124:LYS:HD3	12:K:125:PHE:HE1	1.77	0.49
13:L:46:LYS:HZ3	13:L:47:LYS:HE3	1.75	0.49
15:N:12:ARG:O	15:N:13:THR:C	2.51	0.49
21:T:42:GLN:O	21:T:45:GLN:HB3	2.13	0.49
1:A:1189:C:P	11:J:51:ARG:HH22	2.35	0.48
1:A:1468:A:H2'	1:A:1469:G:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:C:O2'	1:A:170:U:H5'	2.13	0.48
1:A:460:A:N7	1:A:462:G:C6	2.81	0.48
4:C:91:LEU:C	4:C:91:LEU:HD23	2.33	0.48
8:G:41:ARG:O	8:G:44:TYR:N	2.46	0.48
10:I:93:ARG:NH1	10:I:97:LYS:NZ	2.61	0.48
1:A:580:U:H5''	16:O:58:MET:HG2	1.93	0.48
1:A:761:G:C5'	18:Q:102:GLY:HA3	2.43	0.48
1:A:491:G:O2'	1:A:492:G:H5'	2.12	0.48
3:B:85:ALA:O	3:B:88:ALA:O	2.31	0.48
4:C:105:GLU:HG2	4:C:106:VAL:N	2.28	0.48
5:D:100:ARG:O	5:D:104:VAL:HG23	2.13	0.48
7:F:40:VAL:CG2	7:F:41:GLU:N	2.75	0.48
14:M:124:PRO:C	14:M:126:LYS:H	2.16	0.48
7:F:94:GLN:HB2	19:R:32:ARG:HD3	1.94	0.48
7:F:60:PHE:CE2	19:R:78:LEU:HD21	2.48	0.48
1:A:1005:A:H2'	1:A:1006:C:O4'	2.13	0.48
1:A:1278:U:H5''	1:A:1279:A:H5'	1.94	0.48
1:A:231:G:O2'	1:A:232:G:H5'	2.14	0.48
1:A:806:C:O2'	1:A:807:A:H5'	2.12	0.48
1:A:892:A:O2'	1:A:893:C:H5'	2.13	0.48
1:A:911:U:H2'	1:A:912:C:C6	2.49	0.48
5:D:163:GLU:C	5:D:165:MET:N	2.66	0.48
17:P:20:VAL:HG13	17:P:21:VAL:O	2.13	0.48
17:P:43:LYS:HG3	17:P:48:TRP:CD2	2.48	0.48
18:Q:76:LEU:HD23	18:Q:77:VAL:N	2.28	0.48
7:F:99:ALA:O	19:R:28:GLU:HA	2.13	0.48
19:R:36:ASN:ND2	19:R:38:GLU:CG	2.76	0.48
20:S:15:LEU:O	20:S:19:VAL:N	2.47	0.48
21:T:50:GLU:C	21:T:100:ILE:HD12	2.34	0.48
21:T:96:GLY:O	21:T:97:ALA:CB	2.61	0.48
1:A:301:G:O2'	1:A:302:G:H5'	2.13	0.48
1:A:452:A:O2'	1:A:453:A:H8	1.94	0.48
1:A:929:G:C5'	1:A:1533:C:H41	2.26	0.48
5:D:157:LEU:HD23	5:D:157:LEU:O	2.14	0.48
7:F:45:LEU:HA	7:F:58:GLY:O	2.13	0.48
8:G:41:ARG:O	8:G:42:ILE:C	2.51	0.48
8:G:83:ALA:HB3	8:G:85:TYR:CE2	2.48	0.48
12:K:48:ILE:O	12:K:49:GLY:C	2.52	0.48
13:L:115:LYS:O	13:L:117:ARG:N	2.39	0.48
21:T:45:GLN:HA	21:T:91:LEU:HB3	1.94	0.48
1:A:1191:A:OP1	4:C:3:ASN:ND2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1356:G:H2'	1:A:1357:A:H8	1.72	0.48
1:A:567:G:H2'	1:A:568:G:O4'	2.13	0.48
1:A:839:U:C2'	1:A:839:U:O2	2.61	0.48
1:A:972:C:OP1	11:J:57:LYS:NZ	2.31	0.48
3:B:67:THR:HA	3:B:90:MET:HE1	1.95	0.48
4:C:188:LEU:HD13	4:C:195:VAL:HG13	1.94	0.48
4:C:33:LEU:HD11	15:N:53:LEU:CD2	2.43	0.48
1:A:1194:U:H2'	1:A:1195:C:H6	1.78	0.48
1:A:1405:G:O4'	1:A:1519:A:H4'	2.14	0.48
1:A:371:G:C2'	1:A:372:C:H5'	2.43	0.48
1:A:416:G:H2'	1:A:417:C:C6	2.48	0.48
1:A:51:A:H4'	1:A:52:G:O5'	2.14	0.48
3:B:132:LYS:C	3:B:134:GLU:N	2.66	0.48
3:B:35:GLU:HA	3:B:39:ILE:O	2.14	0.48
3:B:42:ILE:HD12	3:B:203:GLY:HA2	1.95	0.48
4:C:19:GLU:O	4:C:40:ARG:NH2	2.47	0.48
5:D:8:VAL:CG1	5:D:21:LEU:HD13	2.43	0.48
6:E:80:ILE:CD1	6:E:91:LEU:HB2	2.44	0.48
3:B:181:PHE:HD2	9:H:70:GLN:HB3	1.79	0.48
1:A:972:C:O5'	11:J:57:LYS:HD2	2.13	0.48
14:M:3:ARG:HG2	14:M:9:ILE:HG23	1.95	0.48
18:Q:48:GLU:O	18:Q:49:GLU:C	2.51	0.48
7:F:94:GLN:NE2	19:R:32:ARG:HD3	2.28	0.48
1:A:1128:C:O2'	1:A:1130:A:C8	2.64	0.48
1:A:1227:A:OP1	20:S:80:TYR:OH	2.21	0.48
1:A:1325:C:O2'	1:A:1326:C:H5'	2.13	0.48
1:A:22:G:O2'	1:A:23:C:H5'	2.13	0.48
1:A:386:C:C2'	1:A:387:U:H5'	2.44	0.48
1:A:877:C:OP1	9:H:88:LYS:NZ	2.43	0.48
3:B:78:GLN:O	3:B:94:ASN:OD1	2.31	0.48
3:B:95:GLN:OE1	3:B:95:GLN:HA	2.12	0.48
4:C:99:VAL:CG2	4:C:100:ALA:N	2.76	0.48
3:B:130:ARG:HH22	4:C:207:VAL:HG22	1.78	0.48
5:D:110:PHE:CD1	5:D:110:PHE:N	2.82	0.48
6:E:115:VAL:HG12	6:E:116:THR:N	2.27	0.48
10:I:48:GLU:N	10:I:49:PRO:CD	2.76	0.48
1:A:1280:A:O4'	11:J:41:PRO:HG3	2.14	0.48
11:J:54:PHE:O	11:J:55:LYS:HG2	2.13	0.48
19:R:74:ARG:HA	19:R:79:LEU:O	2.14	0.48
1:A:1305:G:H5''	22:V:4:GLY:C	2.34	0.48
1:A:1190:G:HO2'	1:A:1191:A:P	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1305:G:H2'	1:A:1331:G:N2	2.28	0.48
1:A:16:A:C2'	1:A:17:U:H5'	2.43	0.48
1:A:255:G:H2'	1:A:256:U:C6	2.48	0.48
1:A:344:A:O2'	1:A:345:C:OP1	2.29	0.48
1:A:434:U:H2'	1:A:435:C:H6	1.78	0.48
1:A:488:C:H2'	1:A:489:C:H6	1.77	0.48
1:A:80:G:H2'	1:A:81:U:H5''	1.96	0.48
1:A:832:C:O2'	1:A:833:U:H5'	2.13	0.48
11:J:72:VAL:O	11:J:73:ASP:HB2	2.13	0.48
13:L:75:HIS:HD2	13:L:77:LEU:N	2.01	0.48
14:M:66:LEU:HD12	14:M:66:LEU:N	2.29	0.48
1:A:376:G:OP2	17:P:67:THR:HG21	2.14	0.48
1:A:1005:A:H2'	1:A:1006:C:H5'	1.96	0.48
1:A:1067:A:N3	1:A:1068:G:H1'	2.28	0.48
1:A:927:G:O2'	1:A:928:G:H5'	2.14	0.48
4:C:5:ILE:HD13	4:C:10:PHE:CB	2.40	0.48
5:D:133:VAL:HG12	5:D:133:VAL:O	2.13	0.48
8:G:121:ALA:O	8:G:125:MET:HG3	2.13	0.48
10:I:50:LEU:HD23	10:I:85:LEU:HD11	1.96	0.48
10:I:56:LEU:C	10:I:58:ARG:H	2.17	0.48
10:I:69:GLY:O	10:I:73:GLN:HG3	2.13	0.48
11:J:48:THR:OG1	11:J:62:HIS:CD2	2.67	0.48
12:K:67:ASP:OD1	12:K:71:LYS:HE3	2.14	0.48
14:M:52:GLU:HG2	14:M:55:ARG:NH2	2.28	0.48
1:A:974:A:OP2	15:N:41:ARG:NH1	2.46	0.48
1:A:116:A:H2'	1:A:117:G:O4'	2.13	0.48
1:A:266:G:C8	1:A:266:G:H5''	2.47	0.48
1:A:377:G:OP1	17:P:3:LYS:HD2	2.13	0.48
1:A:390:C:H2'	1:A:391:G:C8	2.49	0.48
1:A:513:C:O2'	1:A:514:C:H5'	2.14	0.48
1:A:527:G:O2'	1:A:535:A:N1	2.42	0.48
1:A:599:C:O2'	1:A:600:C:H5'	2.13	0.48
4:C:117:ALA:HB1	4:C:187:ALA:HB2	1.96	0.48
15:N:41:ARG:HG3	15:N:42:ILE:N	2.29	0.48
21:T:65:LYS:O	21:T:68:LYS:HB2	2.13	0.48
1:A:1436:U:O2'	1:A:1437:C:H5'	2.14	0.47
7:F:91:VAL:HG12	7:F:92:LYS:O	2.14	0.47
9:H:103:VAL:CG2	9:H:110:ALA:HB2	2.44	0.47
10:I:46:ALA:HA	10:I:78:LYS:HB2	1.96	0.47
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.49	0.47
1:A:1031:G:H2'	1:A:1032:G:C8	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:G:H1'	18:Q:16:GLN:NE2	2.29	0.47
1:A:281:G:O2'	1:A:282:A:OP2	2.24	0.47
1:A:294:U:H2'	1:A:295:C:H6	1.79	0.47
1:A:409:G:H2'	1:A:410:G:O4'	2.14	0.47
1:A:435:C:O2'	1:A:436:C:H5'	2.14	0.47
1:A:485:G:C2'	1:A:486:U:OP2	2.62	0.47
1:A:822:C:O2'	1:A:823:G:H5'	2.15	0.47
1:A:851:G:O2'	1:A:852:G:H5'	2.14	0.47
3:B:44:LEU:HD23	3:B:47:THR:OG1	2.14	0.47
4:C:116:VAL:HG21	4:C:202:ILE:HD11	1.95	0.47
6:E:15:ARG:CZ	6:E:26:PHE:CD2	2.97	0.47
8:G:23:VAL:HG13	8:G:43:PHE:CE2	2.49	0.47
12:K:110:ASP:HB3	19:R:85:LEU:HB3	1.97	0.47
15:N:27:CYS:SG	15:N:29:ARG:CB	3.01	0.47
1:A:264:U:O2'	18:Q:64:PRO:HB2	2.13	0.47
19:R:87:ARG:HG2	19:R:87:ARG:HH11	1.79	0.47
1:A:1454:G:H5''	21:T:35:THR:HG21	1.96	0.47
1:A:1068:G:H8	1:A:1068:G:OP2	1.97	0.47
1:A:1075:C:H5'	3:B:103:THR:HG21	1.95	0.47
1:A:1250:A:C5'	10:I:68:GLY:N	2.72	0.47
1:A:265:G:H2'	1:A:267:C:H5	1.78	0.47
3:B:154:LEU:O	3:B:155:LEU:C	2.52	0.47
10:I:86:VAL:HG13	10:I:90:PRO:HA	1.96	0.47
12:K:16:SER:HA	12:K:79:SER:O	2.13	0.47
22:V:6:ARG:HD3	22:V:15:ARG:NH2	2.29	0.47
1:A:1056:U:H5'	4:C:163:ALA:CB	2.45	0.47
1:A:1220:G:H1'	20:S:52:TYR:CD2	2.49	0.47
1:A:124:G:C6	1:A:125:U:C4	3.03	0.47
1:A:397:A:N3	1:A:397:A:H3'	2.28	0.47
1:A:446:G:H2'	1:A:447:G:H5'	1.96	0.47
1:A:603:U:O2'	1:A:604:G:H5'	2.14	0.47
3:B:23:ARG:C	3:B:23:ARG:NH1	2.67	0.47
3:B:59:GLU:O	3:B:62:ALA:HB3	2.14	0.47
3:B:68:ILE:N	3:B:90:MET:CE	2.73	0.47
7:F:43:LEU:H	7:F:43:LEU:HD22	1.78	0.47
8:G:110:GLN:OE1	8:G:110:GLN:HA	2.14	0.47
11:J:42:THR:HG23	11:J:68:HIS:HA	1.96	0.47
13:L:104:VAL:O	13:L:105:TYR:HB2	2.14	0.47
14:M:85:GLY:O	14:M:86:CYS:C	2.52	0.47
20:S:38:SER:O	20:S:70:LYS:HB3	2.14	0.47
1:A:1004:A:N7	1:A:1036:G:O6	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1486:G:H2'	1:A:1487:G:O4'	2.15	0.47
1:A:246:A:C2	1:A:282:A:C5	3.03	0.47
1:A:1056:U:C5'	4:C:163:ALA:HB2	2.45	0.47
8:G:148:ASN:C	8:G:150:ALA:H	2.16	0.47
10:I:126:SER:OG	10:I:127:LYS:N	2.45	0.47
10:I:79:LEU:HD13	10:I:79:LEU:O	2.14	0.47
18:Q:27:PHE:CE1	18:Q:36:ILE:HD11	2.49	0.47
1:A:1481:U:O2'	1:A:1482:G:H5'	2.14	0.47
1:A:459:G:H3'	1:A:460:A:H5''	1.95	0.47
1:A:620:C:H2'	1:A:621:A:O4'	2.13	0.47
1:A:767:A:H2'	1:A:768:A:C8	2.50	0.47
3:B:129:GLU:O	3:B:130:ARG:HB2	2.15	0.47
6:E:77:PRO:O	6:E:78:HIS:CB	2.63	0.47
1:A:1298:C:C2'	8:G:114:ARG:HH12	2.18	0.47
9:H:40:ALA:O	9:H:43:GLY:N	2.36	0.47
11:J:57:LYS:HE2	11:J:58:ASP:OD1	2.13	0.47
14:M:121:LYS:O	14:M:123:ALA:N	2.47	0.47
1:A:1202:G:H2'	1:A:1203:C:H5'	1.96	0.47
1:A:1231:G:H4'	10:I:126:SER:CB	2.44	0.47
1:A:1245:A:H2'	1:A:1246:C:C6	2.49	0.47
4:C:151:VAL:HA	4:C:199:LYS:O	2.15	0.47
4:C:84:ILE:O	4:C:84:ILE:HG12	2.15	0.47
5:D:112:VAL:N	5:D:116:GLN:OE1	2.39	0.47
6:E:80:ILE:HD12	6:E:80:ILE:C	2.34	0.47
7:F:25:ILE:HD12	7:F:82:ARG:NH1	2.30	0.47
14:M:74:VAL:O	14:M:77:ASN:N	2.48	0.47
16:O:3:ILE:HD13	16:O:34:LEU:HD22	1.96	0.47
16:O:75:PRO:O	16:O:78:TYR:HB3	2.15	0.47
17:P:48:TRP:O	17:P:49:LEU:CB	2.63	0.47
18:Q:84:LEU:HD23	18:Q:84:LEU:HA	1.68	0.47
21:T:42:GLN:O	21:T:46:GLU:HG3	2.14	0.47
1:A:458:C:H2'	1:A:459:G:H8	1.79	0.47
1:A:580:U:H2'	1:A:581:G:O4'	2.15	0.47
1:A:740:U:O2'	1:A:741:G:H5'	2.15	0.47
1:A:908:A:H2'	1:A:909:A:H8	1.78	0.47
3:B:224:GLN:O	3:B:224:GLN:HG2	2.14	0.47
3:B:84:GLU:OE2	3:B:235:SER:HB3	2.14	0.47
3:B:33:TYR:HB2	3:B:43:ASP:HB2	1.96	0.47
3:B:84:GLU:HB3	3:B:219:VAL:CG2	2.31	0.47
5:D:199:ASN:ND2	5:D:201:GLN:CB	2.77	0.47
8:G:138:LYS:HD3	8:G:138:LYS:C	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:156:TRP:OXT	8:G:156:TRP:CD1	2.68	0.47
9:H:51:VAL:HG21	9:H:60:ARG:NH1	2.30	0.47
1:A:965:A:H2	14:M:124:PRO:HB2	1.79	0.47
16:O:75:PRO:HB2	16:O:79:ARG:NH2	2.29	0.47
18:Q:5:VAL:O	18:Q:6:LEU:HD23	2.14	0.47
20:S:62:ILE:HD12	20:S:66:MET:HG3	1.97	0.47
1:A:1030(A):G:N2	1:A:1030(C):G:H3'	2.29	0.47
1:A:1054:C:O2'	1:A:1055:A:H5''	2.15	0.47
1:A:266:G:O2'	1:A:267:C:P	2.73	0.47
1:A:437:U:C5'	5:D:155:LEU:HD22	2.44	0.47
1:A:761:G:H2'	1:A:762:C:C6	2.50	0.47
3:B:101:MET:N	3:B:108:ILE:HD12	2.29	0.47
1:A:1112:C:N3	4:C:178:LEU:N	2.63	0.47
1:A:404:U:H5'	5:D:122:ARG:HD2	1.97	0.47
6:E:64:ARG:O	6:E:65:ASN:CB	2.55	0.47
1:A:1231:G:H5''	10:I:126:SER:HB2	1.96	0.47
13:L:119:LYS:O	13:L:120:TYR:CB	2.62	0.47
1:A:1055:A:C2	1:A:1056:U:H1'	2.50	0.47
1:A:1126:U:H6	1:A:1126:U:P	2.38	0.47
1:A:1230:C:O2'	1:A:1231:G:H5'	2.15	0.47
1:A:243:A:C2	1:A:245:C:C2	3.02	0.47
1:A:370:C:H2'	1:A:371:G:C8	2.50	0.47
1:A:393:A:C2	1:A:394:G:C8	3.02	0.47
3:B:19:HIS:CE1	3:B:206:ASP:HB3	2.50	0.47
3:B:75:LYS:C	3:B:77:ALA:H	2.18	0.47
5:D:191:ARG:NH2	5:D:198:VAL:O	2.48	0.47
7:F:86:ARG:O	7:F:87:ARG:HG2	2.15	0.47
13:L:24:VAL:O	13:L:24:VAL:HG12	2.15	0.47
15:N:26:ARG:NH1	15:N:47:LEU:CG	2.74	0.47
20:S:13:ASP:HA	20:S:16:LEU:CB	2.45	0.47
20:S:45:VAL:HG12	20:S:46:GLY:N	2.30	0.47
21:T:40:ALA:O	21:T:41:VAL:C	2.52	0.47
1:A:1108:G:H4'	1:A:1191:A:O4'	2.15	0.47
1:A:650:G:C2'	1:A:651:C:H5'	2.44	0.47
1:A:915:A:H2'	1:A:916:G:H5'	1.95	0.47
3:B:120:ALA:O	3:B:124:SER:HB3	2.15	0.47
3:B:17:PHE:CD1	3:B:18:GLY:N	2.82	0.47
4:C:83:ARG:C	4:C:85:ARG:H	2.17	0.47
7:F:48:LEU:HD13	7:F:52:ILE:HG13	1.96	0.47
9:H:20:TYR:CE1	9:H:76:PRO:HD2	2.50	0.47
9:H:91:ARG:CG	13:L:7:ILE:HG13	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:93:ARG:HH11	10:I:97:LYS:NZ	2.11	0.47
14:M:32:GLU:O	14:M:35:GLU:HB3	2.15	0.47
14:M:8:GLU:C	14:M:9:ILE:HG13	2.36	0.47
17:P:14:ASN:OD1	17:P:42:ARG:NH2	2.48	0.47
19:R:42:ARG:HH11	19:R:42:ARG:HG3	1.80	0.47
1:A:1222:G:OP1	20:S:77:THR:HG21	2.15	0.47
1:A:1492:A:H2'	1:A:1493:A:C8	2.50	0.46
1:A:1506:U:O2'	1:A:1507:A:H5'	2.15	0.46
1:A:437:U:O2'	5:D:123:HIS:CD2	2.68	0.46
1:A:45:U:H2'	1:A:46:G:C8	2.49	0.46
1:A:813:U:OP1	1:A:904:C:H5'	2.15	0.46
3:B:83:MET:HG3	3:B:238:LEU:HD12	1.97	0.46
3:B:23:ARG:C	3:B:24:TRP:HD1	2.18	0.46
5:D:64:LEU:HD13	5:D:64:LEU:C	2.35	0.46
7:F:100:ASN:ND2	19:R:23:LYS:HG3	2.30	0.46
10:I:47:LEU:HB3	10:I:50:LEU:HD12	1.97	0.46
10:I:5:TYR:CD2	10:I:6:GLY:N	2.79	0.46
11:J:6:ILE:HA	11:J:98:ILE:HG23	1.96	0.46
12:K:26:ASN:O	12:K:27:ASN:HB3	2.15	0.46
20:S:13:ASP:HA	20:S:16:LEU:HB3	1.97	0.46
1:A:1305:G:C5'	22:V:4:GLY:C	2.83	0.46
1:A:1065:U:C5	1:A:1190:G:C4	3.03	0.46
1:A:448:A:H2'	1:A:449:C:C6	2.50	0.46
1:A:47:C:C6	1:A:365:U:H2'	2.49	0.46
1:A:606:G:H2'	1:A:631:G:H22	1.80	0.46
1:A:953:G:N7	14:M:104:ARG:NH2	2.62	0.46
3:B:166:ASP:O	3:B:170:GLU:HB2	2.15	0.46
4:C:23:TYR:CD2	4:C:23:TYR:C	2.89	0.46
7:F:95:GLU:H	7:F:95:GLU:CD	2.18	0.46
8:G:18:TYR:CD2	8:G:59:LEU:HD22	2.47	0.46
11:J:3:LYS:CA	11:J:75:ILE:HA	2.44	0.46
15:N:22:THR:OG1	15:N:33:VAL:HG21	2.15	0.46
1:A:1044:A:H2'	1:A:1045:C:C4'	2.45	0.46
1:A:1392:G:N2	1:A:1502:A:C8	2.81	0.46
1:A:1480:G:H2'	1:A:1481:U:C6	2.51	0.46
1:A:386:C:O2'	1:A:387:U:H5'	2.15	0.46
1:A:547:A:H4'	1:A:548:G:O5'	2.14	0.46
3:B:20:GLU:HG2	3:B:189:ASP:OD2	2.15	0.46
4:C:139:GLN:NE2	4:C:143:GLU:HB2	2.31	0.46
5:D:191:ARG:HH12	5:D:196:LEU:HB2	1.79	0.46
8:G:95:ARG:HG3	8:G:95:ARG:HH11	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:117:HIS:C	10:I:118:LYS:HG3	2.36	0.46
14:M:81:LEU:HA	14:M:84:ILE:HG12	1.97	0.46
16:O:27:VAL:O	16:O:30:ALA:HB3	2.15	0.46
1:A:581:G:HO2'	18:Q:105:ALA:C	2.18	0.46
19:R:39:VAL:HG13	19:R:40:LEU:N	2.30	0.46
1:A:106:C:O2'	1:A:379:C:H5''	2.16	0.46
1:A:112:G:N2	1:A:354:G:H5'	2.30	0.46
1:A:1217:C:O2'	1:A:1218:C:H5'	2.16	0.46
1:A:1309:G:N7	14:M:99:ARG:NH2	2.60	0.46
1:A:1346:A:H2'	8:G:10:ARG:HH22	1.80	0.46
1:A:491:G:H2'	1:A:492:G:H8	1.81	0.46
1:A:950:U:H2'	1:A:951:G:C8	2.51	0.46
3:B:206:ASP:O	3:B:207:ALA:HB3	2.16	0.46
3:B:36:ARG:HD2	3:B:41:ILE:CD1	2.44	0.46
5:D:61:LYS:HZ1	5:D:62:GLN:NE2	2.13	0.46
7:F:65:VAL:HG23	7:F:66:GLU:N	2.29	0.46
13:L:113:ARG:HB2	13:L:122:THR:HG21	1.97	0.46
14:M:22:ILE:HD12	14:M:25:ILE:HD12	1.98	0.46
14:M:77:ASN:O	14:M:81:LEU:HD22	2.15	0.46
16:O:29:VAL:HG21	16:O:67:LEU:CD2	2.45	0.46
18:Q:66:SER:O	18:Q:70:ARG:NH1	2.48	0.46
19:R:62:GLU:O	19:R:65:ILE:HG13	2.16	0.46
1:A:421:U:H5'	1:A:422:C:H5	1.80	0.46
1:A:413:G:H22	1:A:428:G:H1'	1.81	0.46
1:A:601:C:O2'	1:A:602:A:H5'	2.16	0.46
3:B:130:ARG:HH22	4:C:179:ARG:HH12	1.62	0.46
3:B:134:GLU:C	3:B:136:VAL:N	2.69	0.46
3:B:23:ARG:O	3:B:24:TRP:HD1	1.98	0.46
3:B:33:TYR:HB3	3:B:41:ILE:O	2.16	0.46
5:D:102:ASP:OD1	5:D:103:ASN:N	2.48	0.46
9:H:103:VAL:HG23	9:H:110:ALA:HB2	1.97	0.46
12:K:72:ALA:HB1	12:K:77:MET:HG3	1.98	0.46
16:O:55:GLY:HA2	16:O:58:MET:HE2	1.96	0.46
17:P:6:LEU:HD23	17:P:17:TYR:CG	2.50	0.46
17:P:5:ARG:HA	17:P:70:ALA:HB2	1.98	0.46
1:A:188:C:C4'	21:T:89:ARG:NH1	2.78	0.46
1:A:1218:C:H2'	1:A:1219:U:C6	2.51	0.46
1:A:1372:U:O2'	1:A:1373:G:H5'	2.15	0.46
1:A:294:U:H2'	1:A:295:C:C6	2.51	0.46
1:A:502:G:C1'	1:A:550:G:H5'	2.45	0.46
1:A:974:A:P	15:N:29:ARG:HH22	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:19:HIS:HD2	3:B:189:ASP:OD2	1.98	0.46
3:B:84:GLU:HA	3:B:87:ARG:HB2	1.97	0.46
5:D:7:PRO:HG2	5:D:10:ARG:HD2	1.98	0.46
7:F:23:LYS:HE2	7:F:23:LYS:HB3	1.70	0.46
10:I:42:ARG:O	10:I:43:ALA:C	2.54	0.46
10:I:49:PRO:HD3	10:I:78:LYS:HG2	1.96	0.46
13:L:111:LYS:O	13:L:112:ASP:HB2	2.15	0.46
13:L:47:LYS:HB3	13:L:48:PRO:HD3	1.93	0.46
16:O:81:LEU:HD21	16:O:85:LEU:CD1	2.46	0.46
1:A:957:U:H4'	20:S:79:THR:HB	1.97	0.46
1:A:1349:A:H1'	1:A:1374:A:N6	2.31	0.46
1:A:443:C:O2'	1:A:444:C:H5'	2.16	0.46
1:A:98:U:O2'	1:A:99:C:H5'	2.16	0.46
3:B:20:GLU:O	3:B:39:ILE:HG23	2.16	0.46
3:B:18:GLY:HA3	3:B:41:ILE:HA	1.98	0.46
5:D:152:SER:HB3	5:D:158:ILE:HD11	1.97	0.46
6:E:107:ARG:O	6:E:111:GLU:HG3	2.15	0.46
7:F:27:GLN:HA	7:F:30:LEU:HD12	1.98	0.46
10:I:78:LYS:HD3	10:I:101:PHE:CD2	2.51	0.46
12:K:14:VAL:O	12:K:15:ALA:HB3	2.16	0.46
13:L:11:VAL:HG21	18:Q:34:LYS:HG2	1.98	0.46
13:L:42:THR:CG2	13:L:52:LEU:HB3	2.46	0.46
19:R:38:GLU:OE1	19:R:38:GLU:N	2.47	0.46
21:T:43:LEU:HD13	21:T:51:GLU:HG3	1.98	0.46
1:A:33:A:H2'	1:A:34:C:C6	2.51	0.46
1:A:690:G:H2'	1:A:691:G:O4'	2.16	0.46
3:B:125:PRO:HG2	3:B:126:GLU:N	2.29	0.46
4:C:100:ALA:O	4:C:101:LEU:HB2	2.16	0.46
4:C:177:THR:HG23	4:C:180:ALA:HB2	1.98	0.46
14:M:49:THR:CG2	14:M:51:ALA:H	2.18	0.46
16:O:10:LYS:HD2	16:O:10:LYS:O	2.16	0.46
16:O:17:ARG:CZ	16:O:77:ARG:NH1	2.79	0.46
19:R:55:ARG:HB3	19:R:55:ARG:HH11	1.79	0.46
19:R:60:GLY:O	19:R:64:ARG:HB2	2.16	0.46
1:A:407:G:H2'	1:A:408:A:C8	2.50	0.46
3:B:33:TYR:O	3:B:34:ALA:HB2	2.15	0.46
4:C:127:ARG:HG2	4:C:127:ARG:NH1	2.30	0.46
7:F:22:GLU:OE1	7:F:82:ARG:HD3	2.16	0.46
8:G:85:TYR:O	8:G:87:VAL:HG23	2.16	0.46
8:G:87:VAL:HG13	8:G:88:PRO:HD2	1.98	0.46
9:H:103:VAL:HG21	9:H:109:ILE:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1368:G:OP1	11:J:62:HIS:HE1	1.99	0.46
13:L:115:LYS:C	13:L:117:ARG:H	2.19	0.46
1:A:521:G:OP1	13:L:73:GLU:O	2.34	0.46
12:K:91:ARG:CD	19:R:88:LYS:HE2	2.46	0.46
1:A:108:G:N2	1:A:109:A:N1	2.64	0.46
1:A:1130:A:OP2	1:A:1130:A:H3'	2.16	0.46
1:A:1216:G:H2'	1:A:1217:C:H6	1.80	0.46
1:A:1300:G:O2'	1:A:1301:U:P	2.73	0.46
1:A:1366:C:O2'	1:A:1367:C:H5'	2.16	0.46
1:A:1493:A:H2'	1:A:1494:G:H5'	1.96	0.46
1:A:308:C:H2'	1:A:309:G:C8	2.50	0.46
1:A:420:U:H2'	1:A:422:C:C5	2.51	0.46
1:A:644:G:C5	1:A:645:C:C5	3.04	0.46
1:A:652:U:O4	1:A:752:G:O2'	2.29	0.46
3:B:112:VAL:O	3:B:116:GLU:HG3	2.16	0.46
3:B:130:ARG:HB3	3:B:131:PRO:HD2	1.98	0.46
3:B:53:ARG:HG2	3:B:53:ARG:NH1	2.31	0.46
4:C:167:TRP:O	4:C:168:ALA:CB	2.64	0.46
4:C:178:LEU:O	4:C:179:ARG:CB	2.64	0.46
4:C:30:ARG:HG2	4:C:30:ARG:NH1	2.30	0.46
6:E:15:ARG:CD	6:E:26:PHE:CD2	2.99	0.46
7:F:9:VAL:HG22	7:F:60:PHE:CD2	2.51	0.46
11:J:71:LEU:O	11:J:72:VAL:HB	2.15	0.46
11:J:82:ILE:O	11:J:82:ILE:HG22	2.16	0.46
13:L:46:LYS:HZ1	13:L:47:LYS:HG3	1.81	0.46
12:K:91:ARG:NH1	19:R:88:LYS:HE2	2.30	0.46
21:T:56:MET:HE2	21:T:88:VAL:HB	1.97	0.46
1:A:1004:A:H3'	1:A:1025:U:O4	2.16	0.45
1:A:1345:U:C2	1:A:1377:A:C2	3.04	0.45
1:A:186:C:O3'	21:T:82:SER:HB3	2.16	0.45
1:A:792:A:H1'	1:A:794:A:N7	2.30	0.45
1:A:948:C:O2'	1:A:949:A:H5'	2.16	0.45
3:B:69:LEU:HB3	3:B:162:ILE:HG12	1.99	0.45
5:D:158:ILE:O	5:D:162:LEU:HB2	2.15	0.45
1:A:921:U:O2	6:E:19:MET:HB2	2.15	0.45
9:H:138:TRP:CE3	9:H:138:TRP:OXT	2.60	0.45
11:J:75:ILE:O	11:J:76:ASN:CB	2.63	0.45
13:L:7:ILE:HA	13:L:7:ILE:HD13	1.85	0.45
19:R:87:ARG:HB3	19:R:88:LYS:H	1.56	0.45
21:T:50:GLU:HG2	21:T:100:ILE:CG1	2.43	0.45
1:A:1056:U:O2'	1:A:1057:G:H5'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1397:C:H4'	1:A:1398:A:OP2	2.15	0.45
1:A:1525:G:O2'	1:A:1526:G:H5'	2.15	0.45
1:A:113:G:C1'	1:A:354:G:H5'	2.44	0.45
1:A:415:A:H2'	1:A:416:G:C8	2.51	0.45
1:A:50:A:H4'	1:A:51:A:H5'	1.98	0.45
1:A:302:G:N3	1:A:556:C:H4'	2.31	0.45
3:B:90:MET:HA	3:B:91:PRO:HD3	1.73	0.45
5:D:153:ARG:HG2	5:D:181:MET:SD	2.55	0.45
5:D:78:LEU:O	5:D:81:GLU:HB3	2.16	0.45
7:F:77:ARG:O	7:F:81:ILE:HG13	2.16	0.45
8:G:116:ALA:HA	8:G:119:ARG:NH2	2.31	0.45
10:I:121:ARG:C	10:I:121:ARG:HD3	2.37	0.45
10:I:55:ALA:O	10:I:57:GLY:N	2.49	0.45
10:I:79:LEU:CD1	10:I:83:ARG:HD2	2.46	0.45
15:N:25:VAL:HG12	15:N:39:LEU:HD23	1.98	0.45
16:O:74:ASP:OD1	16:O:76:GLU:HB3	2.15	0.45
17:P:38:TYR:CE2	17:P:50:LYS:HB3	2.50	0.45
20:S:7:LYS:CG	20:S:7:LYS:O	2.64	0.45
1:A:1179:A:H2'	1:A:1180:A:O4'	2.15	0.45
1:A:242:C:H2'	1:A:243:A:H5'	1.99	0.45
1:A:458:C:H2'	1:A:459:G:O4'	2.17	0.45
1:A:489:C:H2'	1:A:490:G:C8	2.51	0.45
1:A:904:C:H2'	1:A:905:U:O4'	2.16	0.45
1:A:922:G:O2'	1:A:923:A:H5'	2.17	0.45
3:B:16:HIS:O	3:B:17:PHE:O	2.34	0.45
4:C:121:ALA:O	4:C:125:GLU:HG3	2.16	0.45
4:C:57:ILE:HG23	4:C:64:VAL:HG12	1.98	0.45
5:D:148:VAL:CG1	5:D:158:ILE:HD13	2.46	0.45
6:E:15:ARG:O	6:E:27:ARG:O	2.33	0.45
8:G:6:ARG:O	8:G:7:ALA:C	2.55	0.45
11:J:65:LEU:C	11:J:65:LEU:HD23	2.36	0.45
16:O:87:ILE:O	16:O:88:ARG:CB	2.62	0.45
17:P:6:LEU:HB3	17:P:17:TYR:CD2	2.51	0.45
1:A:187:C:C2	21:T:105:SER:HB3	2.50	0.45
1:A:1130:A:OP2	1:A:1131:G:OP2	2.34	0.45
1:A:1402:C:H2'	1:A:1403:C:O4'	2.16	0.45
1:A:926:G:H3'	1:A:1505:G:H21	1.81	0.45
1:A:1507:A:C2	1:A:1508:G:C4	3.04	0.45
1:A:425:G:O2'	1:A:426:G:H5'	2.17	0.45
1:A:502:G:H2'	1:A:503:C:C6	2.51	0.45
1:A:538:G:O2'	1:A:539:A:H5'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:187:LEU:HD11	3:B:204:ASN:O	2.15	0.45
4:C:40:ARG:HH11	4:C:40:ARG:HG3	1.81	0.45
5:D:114:ARG:CG	5:D:114:ARG:HH11	2.19	0.45
5:D:42:GLN:HG2	5:D:42:GLN:O	2.16	0.45
6:E:144:THR:HG22	6:E:145:LYS:N	2.32	0.45
7:F:48:LEU:HD21	7:F:60:PHE:CZ	2.51	0.45
10:I:71:SER:O	10:I:74:ILE:HB	2.15	0.45
11:J:49:VAL:HG12	15:N:41:ARG:HB2	1.98	0.45
16:O:70:LEU:HD12	16:O:78:TYR:CB	2.47	0.45
16:O:81:LEU:C	16:O:81:LEU:HD23	2.37	0.45
7:F:91:VAL:HG11	19:R:72:ARG:NH1	2.31	0.45
21:T:57:ARG:NE	21:T:102:GLY:HA3	2.31	0.45
1:A:1501:C:OP2	1:A:1504:G:H2'	2.17	0.45
25:A:1633:TAC:H8	13:L:19:ARG:NH2	2.31	0.45
1:A:279:A:H5'	1:A:281:G:O4'	2.16	0.45
1:A:312:C:H2'	1:A:313:A:C8	2.51	0.45
4:C:42:LEU:HD12	4:C:94:LEU:HD12	1.98	0.45
10:I:26:VAL:HA	10:I:61:ALA:O	2.16	0.45
12:K:86:GLY:N	12:K:112:THR:HG23	2.32	0.45
1:A:965:A:C2	14:M:124:PRO:HB2	2.50	0.45
22:V:6:ARG:CD	22:V:15:ARG:NH1	2.79	0.45
1:A:1044:A:C2'	1:A:1045:C:H5'	2.47	0.45
1:A:258:G:H2'	1:A:259:G:H8	1.81	0.45
1:A:344:A:H5''	1:A:345:C:H5	1.81	0.45
1:A:90:U:H2'	1:A:91:C:C6	2.52	0.45
3:B:115:LEU:O	3:B:119:GLU:HG3	2.17	0.45
3:B:89:GLY:O	3:B:154:LEU:HD13	2.17	0.45
6:E:110:LEU:CD1	6:E:118:ILE:HD12	2.25	0.45
7:F:38:GLU:OE1	7:F:66:GLU:HB2	2.17	0.45
10:I:45:ALA:O	10:I:48:GLU:HB2	2.16	0.45
12:K:91:ARG:NH1	19:R:88:LYS:CE	2.80	0.45
14:M:15:VAL:HG12	14:M:19:LEU:CD1	2.46	0.45
15:N:17:LYS:HB2	15:N:17:LYS:HE2	1.74	0.45
1:A:1116:C:H2'	1:A:1117:G:C5'	2.38	0.45
1:A:1250:A:H4'	10:I:68:GLY:CA	2.46	0.45
1:A:457:C:H2'	1:A:458:C:H6	1.82	0.45
1:A:614:A:H2'	1:A:615:C:C6	2.52	0.45
1:A:625:G:H2'	1:A:626:U:C6	2.51	0.45
1:A:877:C:O2'	1:A:878:G:H5'	2.17	0.45
4:C:70:VAL:O	4:C:105:GLU:HA	2.17	0.45
4:C:117:ALA:HB1	4:C:187:ALA:CB	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:11:LEU:O	5:D:12:CYS:C	2.55	0.45
5:D:174:LEU:O	5:D:186:LEU:CD1	2.65	0.45
5:D:192:GLU:OE1	5:D:192:GLU:N	2.50	0.45
6:E:43:LEU:CD1	6:E:132:ALA:HB1	2.39	0.45
6:E:43:LEU:CD2	6:E:44:GLY:N	2.80	0.45
11:J:5:ARG:HA	11:J:73:ASP:OD1	2.17	0.45
13:L:26:ALA:O	13:L:27:LEU:O	2.34	0.45
14:M:96:LEU:O	14:M:110:ARG:NH1	2.50	0.45
1:A:101:A:H2'	1:A:102:G:H8	1.81	0.45
1:A:1499:A:H1'	1:A:1520:G:H5'	1.98	0.45
1:A:781:A:H2	1:A:1514:C:C4'	2.30	0.45
3:B:68:ILE:HG12	3:B:161:ALA:HB3	1.99	0.45
4:C:107:GLN:O	4:C:108:ASN:CB	2.63	0.45
4:C:119:ARG:HG2	4:C:140:ARG:NH1	2.32	0.45
8:G:113:GLU:HG2	8:G:119:ARG:HG2	1.97	0.45
8:G:75:VAL:HA	8:G:87:VAL:O	2.16	0.45
9:H:63:LEU:HD22	9:H:63:LEU:N	2.28	0.45
9:H:68:ARG:HH11	9:H:68:ARG:HG2	1.81	0.45
13:L:110:VAL:O	13:L:122:THR:CG2	2.65	0.45
14:M:70:LEU:O	14:M:73:GLU:N	2.50	0.45
16:O:36:ILE:CG1	16:O:59:MET:HE3	2.46	0.45
1:A:1347:G:HO2'	1:A:1373:G:H1	1.64	0.45
1:A:1475:G:H2'	1:A:1476:G:C8	2.43	0.45
1:A:232:G:H1'	1:A:262:A:N1	2.32	0.45
1:A:287:U:C2'	1:A:288:A:H5'	2.47	0.45
1:A:570:G:H1'	1:A:820:U:C4	2.52	0.45
1:A:952:U:H2'	1:A:953:G:H8	1.81	0.45
3:B:15:VAL:HG11	3:B:209:ARG:HG3	1.99	0.45
3:B:23:ARG:N	3:B:23:ARG:CD	2.71	0.45
3:B:81:VAL:O	3:B:82:ARG:C	2.56	0.45
4:C:154:SER:O	4:C:165:THR:HA	2.16	0.45
4:C:154:SER:HB3	4:C:197:GLY:H	1.82	0.45
4:C:58:GLU:HB3	11:J:92:THR:CG2	2.41	0.45
8:G:36:LYS:O	8:G:36:LYS:HG2	2.17	0.45
14:M:3:ARG:CG	14:M:9:ILE:HG23	2.47	0.45
19:R:59:SER:O	19:R:61:LYS:N	2.49	0.45
21:T:102:GLY:O	21:T:104:LEU:N	2.44	0.45
1:A:1019:C:H2'	1:A:1020:U:O4'	2.17	0.45
1:A:1292:U:C5'	10:I:38:GLN:HE22	2.29	0.45
1:A:1314:C:H2'	1:A:1315:U:H6	1.82	0.45
1:A:1337:G:H5''	1:A:1338:G:OP1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1423:G:O2'	1:A:1424:C:H5'	2.16	0.45
1:A:497:A:O2'	1:A:498:U:OP1	2.30	0.45
1:A:867:G:O2'	1:A:868:C:H5'	2.17	0.45
3:B:167:PRO:HG2	3:B:192:SER:CB	2.47	0.45
3:B:20:GLU:OE1	3:B:20:GLU:HA	2.17	0.45
3:B:80:ILE:HD13	3:B:212:GLN:HB2	1.98	0.45
4:C:167:TRP:HB3	4:C:168:ALA:H	1.38	0.45
4:C:97:LYS:O	4:C:98:ASN:CB	2.65	0.45
5:D:125:HIS:ND1	5:D:152:SER:OG	2.40	0.45
6:E:19:MET:CE	6:E:24:ARG:NH1	2.80	0.45
8:G:80:VAL:O	8:G:81:GLY:C	2.53	0.45
10:I:99:LEU:N	10:I:99:LEU:HD22	2.32	0.45
12:K:54:ARG:HH11	12:K:54:ARG:CB	2.24	0.45
1:A:528:C:H41	13:L:49:ASN:CG	2.19	0.45
14:M:77:ASN:O	14:M:80:ARG:N	2.50	0.45
15:N:11:LYS:HG2	15:N:11:LYS:O	2.17	0.45
1:A:129(A):G:O2'	1:A:130:A:OP2	2.35	0.44
1:A:1489:G:H2'	1:A:1490:C:H6	1.82	0.44
1:A:374:A:C6	1:A:375:U:C4	3.05	0.44
4:C:191:THR:HG21	4:C:193:TYR:CE2	2.52	0.44
8:G:88:PRO:HG3	8:G:152:ALA:HB2	1.99	0.44
11:J:72:VAL:HG12	11:J:73:ASP:N	2.31	0.44
12:K:88:GLY:O	12:K:90:GLY:N	2.50	0.44
14:M:81:LEU:HD23	14:M:81:LEU:N	2.32	0.44
1:A:1152:A:O2'	1:A:1153:C:H5'	2.17	0.44
1:A:1330:U:C2'	1:A:1331:G:H5'	2.44	0.44
1:A:327:A:O2'	1:A:328:C:H6	2.00	0.44
1:A:50:A:N6	1:A:361:G:H4'	2.32	0.44
1:A:938:A:N6	1:A:939:G:C6	2.85	0.44
3:B:126:GLU:O	3:B:129:GLU:HB2	2.18	0.44
3:B:134:GLU:O	3:B:138:LEU:HG	2.17	0.44
3:B:223:ILE:HG21	3:B:230:VAL:HG23	1.99	0.44
3:B:239:VAL:O	3:B:239:VAL:HG12	2.17	0.44
6:E:48:ALA:HB1	6:E:49:PRO:HD2	1.99	0.44
9:H:45:ILE:HG13	9:H:45:ILE:O	2.16	0.44
11:J:3:LYS:N	11:J:76:ASN:H	2.15	0.44
15:N:57:ARG:HG2	15:N:58:LYS:H	1.82	0.44
1:A:1053:G:C3'	1:A:1054:C:C5'	2.93	0.44
1:A:1119:C:O2'	1:A:1120:G:H5'	2.18	0.44
1:A:12:U:H4'	1:A:526:C:H4'	1.99	0.44
1:A:1320:C:H2'	1:A:1321:C:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:A:H1'	1:A:198:G:O4'	2.17	0.44
1:A:458:C:C2	1:A:459:G:C8	3.05	0.44
1:A:628:G:H2'	1:A:629:G:C8	2.51	0.44
1:A:851:G:H2'	1:A:852:G:H8	1.82	0.44
3:B:25:ASN:ND2	3:B:25:ASN:C	2.69	0.44
4:C:123:GLN:NE2	4:C:140:ARG:HH22	2.15	0.44
5:D:110:PHE:HD1	5:D:110:PHE:N	2.15	0.44
5:D:152:SER:HB3	5:D:158:ILE:CD1	2.46	0.44
5:D:187:ARG:HD2	5:D:187:ARG:HA	1.75	0.44
7:F:69:GLU:HA	7:F:72:VAL:HG23	1.98	0.44
11:J:60:ARG:O	11:J:61:GLU:HB3	2.16	0.44
19:R:51:LEU:HA	19:R:52:PRO:HD3	1.81	0.44
20:S:40:ILE:HB	20:S:67:VAL:O	2.17	0.44
1:A:1041:A:H2'	1:A:1042:G:H8	1.83	0.44
1:A:1508:G:O2'	1:A:1509:C:H5'	2.17	0.44
1:A:186:C:H2'	1:A:187:C:H6	1.82	0.44
1:A:35:G:H2'	1:A:36:C:H6	1.79	0.44
1:A:398:C:O2'	1:A:399:G:H5'	2.17	0.44
1:A:405:U:C3'	1:A:406:G:H5'	2.41	0.44
3:B:121:LEU:O	3:B:127:ILE:HG12	2.18	0.44
8:G:139:GLU:O	8:G:143:ARG:HG3	2.18	0.44
10:I:11:LYS:O	10:I:12:GLU:HB3	2.17	0.44
10:I:4:TYR:CE1	10:I:88:TYR:HD1	2.35	0.44
16:O:55:GLY:O	16:O:59:MET:HG3	2.17	0.44
19:R:43:PHE:C	19:R:51:LEU:HD12	2.38	0.44
21:T:39:LYS:HD2	21:T:55:ILE:CD1	2.32	0.44
21:T:83:ARG:O	21:T:87:LYS:HG3	2.17	0.44
22:V:2:GLY:O	22:V:4:GLY:N	2.51	0.44
1:A:1108:G:H5'	1:A:1191:A:H4'	1.99	0.44
1:A:807:A:H2'	1:A:808:C:C6	2.52	0.44
3:B:47:THR:HA	3:B:202:PRO:HG2	2.00	0.44
4:C:11:ARG:CG	4:C:11:ARG:NH1	2.80	0.44
1:A:1113:C:H1'	4:C:178:LEU:HD21	2.00	0.44
4:C:70:VAL:HG12	4:C:71:ALA:N	2.33	0.44
11:J:47:PHE:CE2	15:N:37:PHE:HE1	2.36	0.44
17:P:10:GLY:HA3	17:P:14:ASN:O	2.18	0.44
19:R:18:ARG:NH1	19:R:21:LYS:HZ1	2.15	0.44
1:A:1231:G:H5''	10:I:126:SER:CB	2.47	0.44
1:A:1392:G:H2'	1:A:1393:U:C6	2.49	0.44
1:A:123:C:OP1	1:A:312:C:H5'	2.18	0.44
1:A:406:G:H2'	1:A:407:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:A:O2'	1:A:56:U:H5'	2.18	0.44
1:A:606:G:H2'	1:A:631:G:N2	2.33	0.44
1:A:960:U:H2'	1:A:960:U:O2	2.16	0.44
4:C:83:ARG:C	4:C:85:ARG:N	2.70	0.44
5:D:145:GLU:HG2	5:D:184:LYS:HG2	1.98	0.44
6:E:12:LEU:O	6:E:12:LEU:HD22	2.18	0.44
6:E:131:ILE:O	6:E:134:ALA:HB3	2.18	0.44
6:E:31:LEU:HA	6:E:31:LEU:HD23	1.55	0.44
8:G:152:ALA:C	8:G:154:TYR:H	2.20	0.44
9:H:45:ILE:HD12	9:H:61:VAL:HG13	1.99	0.44
10:I:48:GLU:OE1	10:I:51:ARG:HD2	2.18	0.44
14:M:62:ASN:HA	14:M:62:ASN:HD22	1.64	0.44
15:N:31:ARG:O	15:N:33:VAL:N	2.50	0.44
16:O:39:LEU:HD23	16:O:39:LEU:O	2.18	0.44
16:O:81:LEU:O	16:O:81:LEU:HD23	2.18	0.44
1:A:1230:C:H2'	1:A:1231:G:H8	1.83	0.44
1:A:1327:C:O2'	1:A:1328:C:H5'	2.18	0.44
1:A:1490:C:C2'	1:A:1491:G:H5'	2.47	0.44
1:A:479:C:O2'	1:A:480:U:H5'	2.18	0.44
1:A:575:G:C5	1:A:881:G:C2	3.06	0.44
3:B:213:LEU:HD23	3:B:213:LEU:C	2.38	0.44
4:C:134:ILE:HD11	4:C:153:VAL:CG2	2.48	0.44
4:C:188:LEU:HD13	4:C:189:ALA:N	2.32	0.44
5:D:159:ARG:O	5:D:163:GLU:N	2.50	0.44
6:E:107:ARG:HG2	6:E:108:ALA:N	2.31	0.44
8:G:136:LYS:O	8:G:140:ASP:OD1	2.34	0.44
11:J:46:ARG:HH11	11:J:64:GLU:CB	2.31	0.44
11:J:81:THR:C	11:J:83:GLU:H	2.21	0.44
20:S:3:ARG:O	20:S:4:SER:HB3	2.18	0.44
20:S:41:VAL:HG22	20:S:44:MET:CE	2.48	0.44
20:S:70:LYS:O	20:S:71:LEU:C	2.55	0.44
1:A:1364:U:H5'	22:V:14:TRP:CZ2	2.53	0.44
1:A:1124:G:C8	1:A:1145:C:C5	3.06	0.44
1:A:259:G:C2'	1:A:260:G:H5'	2.48	0.44
1:A:358:U:H2'	1:A:359:U:C6	2.53	0.44
1:A:518:C:O2'	1:A:519:C:OP2	2.32	0.44
1:A:972:C:P	11:J:57:LYS:HD2	2.58	0.44
1:A:976:G:C8	1:A:1358:U:C2	3.06	0.44
3:B:100:GLY:O	3:B:104:ASN:N	2.43	0.44
5:D:107:ARG:HG2	5:D:107:ARG:HH11	1.83	0.44
5:D:63:LYS:O	5:D:64:LEU:C	2.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:76:ILE:HD13	6:E:142:LEU:HD11	1.99	0.44
6:E:45:PHE:CE2	6:E:47:LYS:HE2	2.53	0.44
9:H:45:ILE:O	9:H:46:LYS:C	2.55	0.44
12:K:33:THR:OG1	12:K:37:GLY:C	2.57	0.44
12:K:54:ARG:HG2	12:K:54:ARG:H	1.59	0.44
13:L:43:VAL:HG12	13:L:44:THR:N	2.32	0.44
14:M:58:GLU:OE2	14:M:58:GLU:HA	2.18	0.44
7:F:101:ALA:CA	19:R:28:GLU:HB3	2.48	0.44
19:R:26:LEU:HD21	19:R:39:VAL:HG23	2.00	0.44
1:A:1327:C:OP1	22:V:20:LYS:N	2.50	0.44
1:A:1438:G:H2'	1:A:1439:C:C6	2.53	0.44
1:A:791:G:H2'	1:A:792:A:C5'	2.47	0.44
4:C:145:GLY:O	4:C:146:ALA:O	2.36	0.44
5:D:8:VAL:HG13	5:D:21:LEU:HD13	2.00	0.44
7:F:26:ILE:CG2	7:F:63:TYR:HE2	2.30	0.44
8:G:104:LEU:HD23	8:G:134:ALA:CB	2.48	0.44
17:P:60:LEU:C	17:P:62:VAL:H	2.21	0.44
1:A:1003(A):G:C4	1:A:1004:A:H1'	2.53	0.43
1:A:1250:A:H5'	10:I:68:GLY:O	2.18	0.43
1:A:1250:A:H61	1:A:1354:C:C1'	2.30	0.43
1:A:1251:A:H2'	1:A:1252:A:H8	1.80	0.43
1:A:1275:A:H2'	1:A:1276:G:O4'	2.18	0.43
1:A:1285:A:HO2'	1:A:1286:A:P	2.39	0.43
1:A:1305:G:H5'	22:V:4:GLY:CA	2.47	0.43
1:A:1520:G:O2'	1:A:1521:G:H5'	2.18	0.43
1:A:190(J):U:H2'	1:A:190(K):G:C8	2.53	0.43
1:A:505:G:H2'	1:A:506:G:C8	2.53	0.43
1:A:781:A:H2	1:A:1514:C:O4'	2.00	0.43
1:A:970:C:O2	14:M:126:LYS:C	2.56	0.43
3:B:52:GLU:O	3:B:56:ARG:HB2	2.18	0.43
4:C:195:VAL:HG12	4:C:196:LEU:N	2.33	0.43
4:C:46:GLU:C	4:C:48:TYR:H	2.16	0.43
6:E:40:ARG:NH1	6:E:68:GLU:OE1	2.51	0.43
7:F:52:ILE:O	7:F:53:ALA:HB3	2.18	0.43
9:H:17:THR:HG22	9:H:63:LEU:HG	2.00	0.43
10:I:128:ARG:CG	10:I:128:ARG:OXT	2.65	0.43
10:I:19:LEU:HD11	10:I:85:LEU:CD1	2.46	0.43
11:J:55:LYS:O	11:J:56:HIS:CB	2.66	0.43
17:P:20:VAL:HG21	17:P:32:TYR:CG	2.53	0.43
18:Q:86:GLU:O	18:Q:87:LYS:C	2.56	0.43
1:A:192:U:C1'	21:T:103:GLY:HA2	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:90:GLN:O	21:T:93:GLU:HB2	2.18	0.43
1:A:1014:A:C2	1:A:1219:U:H1'	2.53	0.43
1:A:1058:G:H2'	1:A:1059:C:C6	2.53	0.43
1:A:1315:U:H5	20:S:6:LYS:HZ1	1.65	0.43
1:A:1497:G:C2'	1:A:1498:U:C5'	2.87	0.43
1:A:438:G:O2'	1:A:495:U:O4	2.24	0.43
1:A:767:A:H2'	1:A:768:A:H8	1.83	0.43
1:A:994:A:H8	1:A:994:A:OP1	2.02	0.43
3:B:53:ARG:HH11	3:B:53:ARG:HG2	1.82	0.43
5:D:163:GLU:O	5:D:165:MET:N	2.51	0.43
8:G:125:MET:O	8:G:128:ALA:HB3	2.18	0.43
11:J:48:THR:HG1	11:J:62:HIS:CD2	2.36	0.43
13:L:7:ILE:O	13:L:11:VAL:HG23	2.17	0.43
14:M:16:ASP:N	14:M:16:ASP:OD1	2.49	0.43
16:O:36:ILE:HA	16:O:59:MET:CE	2.48	0.43
1:A:1044:A:H2'	1:A:1045:C:C5'	2.49	0.43
1:A:1117:G:H5'	1:A:1117:G:C8	2.47	0.43
1:A:1257:U:H4'	1:A:1258:G:H5'	1.99	0.43
1:A:1283:G:O2'	1:A:1284:C:H5'	2.18	0.43
1:A:1426:C:H2'	1:A:1427:U:H6	1.83	0.43
1:A:194:C:H2'	1:A:195:A:H5''	2.00	0.43
1:A:356:A:H1'	1:A:368:U:O2'	2.18	0.43
1:A:795:C:H5''	1:A:796:C:OP2	2.18	0.43
1:A:914:A:O2'	1:A:915:A:H5'	2.19	0.43
3:B:10:LEU:HG	3:B:48:MET:HE2	1.99	0.43
4:C:79:ARG:HG3	4:C:79:ARG:O	2.17	0.43
4:C:35:GLU:CG	4:C:95:THR:HG21	2.47	0.43
6:E:15:ARG:CZ	6:E:26:PHE:CE2	3.01	0.43
8:G:18:TYR:CE2	8:G:59:LEU:HB2	2.53	0.43
9:H:13:ILE:O	9:H:17:THR:HG23	2.18	0.43
20:S:5:LEU:HA	20:S:5:LEU:HD23	1.80	0.43
1:A:107:G:O2'	1:A:108:G:H5'	2.19	0.43
1:A:1293:G:O2'	1:A:1294:G:H5'	2.18	0.43
1:A:1397:C:O2'	1:A:1398:A:P	2.76	0.43
1:A:333:G:O2'	1:A:334:C:H5'	2.18	0.43
1:A:407:G:H2'	1:A:408:A:H8	1.84	0.43
1:A:554:C:H2'	1:A:555:C:H6	1.82	0.43
1:A:919:A:O2'	1:A:920:U:H5'	2.17	0.43
1:A:970:C:O2	14:M:126:LYS:O	2.37	0.43
1:A:975:A:H4'	1:A:976:G:O5'	2.18	0.43
3:B:15:VAL:HG11	3:B:209:ARG:C	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:108:ASN:C	4:C:110:ASN:H	2.21	0.43
4:C:152:ILE:HB	4:C:199:LYS:HB2	1.99	0.43
4:C:204:LEU:O	4:C:205:GLY:C	2.57	0.43
5:D:162:LEU:O	5:D:165:MET:HB2	2.19	0.43
5:D:174:LEU:O	5:D:175:SER:HB3	2.18	0.43
10:I:36:TYR:CD2	10:I:37:PHE:CE2	3.06	0.43
11:J:35:SER:OG	11:J:73:ASP:HB3	2.18	0.43
12:K:17:GLY:O	12:K:80:VAL:HA	2.19	0.43
18:Q:10:VAL:HG12	18:Q:53:LEU:HA	2.00	0.43
1:A:1190:G:OP1	4:C:4:LYS:CA	2.55	0.43
1:A:1498:U:C4'	1:A:1519:A:H2	2.29	0.43
1:A:244:U:O2	25:A:1633:TAC:O21	2.36	0.43
1:A:913:A:O2'	1:A:914:A:P	2.77	0.43
1:A:989:C:O2'	1:A:990:C:H5'	2.19	0.43
3:B:108:ILE:HG22	3:B:152:PHE:CE2	2.54	0.43
4:C:108:ASN:OD1	4:C:110:ASN:HB2	2.19	0.43
5:D:163:GLU:C	5:D:165:MET:H	2.20	0.43
6:E:13:ILE:HA	6:E:29:GLY:O	2.19	0.43
6:E:40:ARG:HH11	6:E:40:ARG:HG2	1.82	0.43
6:E:9:LYS:HD2	6:E:112:LEU:HD21	2.00	0.43
8:G:18:TYR:N	8:G:18:TYR:CD1	2.86	0.43
9:H:91:ARG:HG2	13:L:7:ILE:HG13	2.01	0.43
11:J:45:ARG:CG	11:J:45:ARG:HH11	2.32	0.43
11:J:6:ILE:O	11:J:71:LEU:HD22	2.17	0.43
11:J:85:LEU:O	11:J:87:THR:N	2.52	0.43
14:M:14:ARG:HB3	14:M:16:ASP:OD1	2.18	0.43
16:O:7:GLU:O	16:O:11:VAL:HG23	2.18	0.43
17:P:6:LEU:HB3	17:P:17:TYR:HD2	1.84	0.43
18:Q:97:SER:CB	18:Q:103:GLY:N	2.76	0.43
21:T:56:MET:CE	21:T:88:VAL:HG11	2.48	0.43
1:A:1142:G:C2	1:A:1143:G:H1'	2.54	0.43
1:A:1308:U:H2'	1:A:1309:G:H8	1.83	0.43
1:A:1346:A:C8	1:A:1348:U:C2	3.07	0.43
1:A:158:G:H2'	1:A:159:G:H8	1.82	0.43
1:A:293:G:O2'	1:A:294:U:H5'	2.18	0.43
1:A:684:A:N6	1:A:685:G:C6	2.86	0.43
4:C:175:LEU:HD11	4:C:201:TYR:HE2	1.84	0.43
4:C:94:LEU:HD23	4:C:95:THR:CG2	2.20	0.43
5:D:194:LEU:CD2	5:D:194:LEU:N	2.81	0.43
5:D:91:SER:O	5:D:92:VAL:C	2.57	0.43
1:A:921:U:O2'	6:E:19:MET:O	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:30:LEU:O	7:F:35:ALA:HB3	2.19	0.43
8:G:75:VAL:HG21	8:G:144:MET:HB3	2.01	0.43
15:N:53:LEU:HA	15:N:54:PRO:HD2	1.79	0.43
16:O:29:VAL:HG21	16:O:67:LEU:HD21	2.01	0.43
20:S:77:THR:HG22	20:S:78:ARG:N	2.32	0.43
1:A:1206:G:C6	1:A:1207:G:C5	3.07	0.43
1:A:1350:A:C6	1:A:1351:U:C4	3.06	0.43
1:A:821:G:H2'	1:A:822:C:H6	1.84	0.43
3:B:91:PRO:CG	3:B:154:LEU:HB2	2.41	0.43
5:D:149:ALA:HB3	5:D:152:SER:HB2	2.01	0.43
5:D:58:LEU:HD23	5:D:206:PHE:CE1	2.53	0.43
11:J:15:THR:HG23	11:J:94:VAL:HG22	2.01	0.43
11:J:94:VAL:CG1	11:J:95:GLU:N	2.81	0.43
14:M:11:ARG:CG	14:M:12:ASN:H	2.25	0.43
18:Q:89:LEU:O	18:Q:92:ARG:HB3	2.19	0.43
1:A:1314:C:OP2	20:S:6:LYS:CD	2.67	0.43
1:A:145:G:O2'	1:A:146:G:H5'	2.19	0.43
1:A:186:C:H2'	1:A:187:C:C6	2.53	0.43
1:A:243:A:N6	1:A:281:G:O2'	2.52	0.43
1:A:462:G:C6	1:A:463:A:C5	3.07	0.43
1:A:947:G:H2'	1:A:948:C:O4'	2.18	0.43
1:A:960:U:O2	1:A:960:U:H5'	2.19	0.43
5:D:3:ARG:NH1	5:D:118:ARG:NH1	2.67	0.43
6:E:72:GLN:HE22	6:E:144:THR:HG23	1.81	0.43
6:E:79:GLU:N	6:E:79:GLU:OE1	2.51	0.43
8:G:13:GLN:HA	8:G:14:PRO:HD2	1.78	0.43
11:J:71:LEU:O	11:J:71:LEU:HD13	2.18	0.43
12:K:28:THR:HG22	12:K:29:ILE:H	1.84	0.43
14:M:75:ALA:HA	14:M:78:ILE:HD12	2.00	0.43
14:M:87:TYR:CE1	14:M:91:ARG:HD3	2.54	0.43
17:P:20:VAL:HG21	17:P:32:TYR:CD1	2.54	0.43
18:Q:59:ILE:HG22	18:Q:71:PHE:HD1	1.83	0.43
19:R:47:THR:C	19:R:49:LYS:N	2.72	0.43
20:S:32:LYS:O	20:S:32:LYS:HG3	2.18	0.43
1:A:1020:U:H2'	1:A:1021:G:C8	2.51	0.43
1:A:1129:C:HO2'	1:A:1130:A:P	2.40	0.43
1:A:1227:A:H2'	1:A:1228:C:O5'	2.19	0.43
1:A:1438:G:H2'	1:A:1439:C:H6	1.84	0.43
3:B:111:ARG:NE	3:B:111:ARG:HA	2.34	0.43
1:A:1190:G:P	4:C:4:LYS:HA	2.58	0.43
5:D:151:LYS:N	5:D:151:LYS:CD	2.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:33:TYR:C	7:F:71:ARG:HH21	2.22	0.43
13:L:59:ARG:HD3	13:L:65:GLU:HG3	2.01	0.43
14:M:37:THR:CG2	14:M:37:THR:O	2.67	0.43
15:N:12:ARG:O	15:N:14:PRO:HD3	2.18	0.43
19:R:18:ARG:HH11	19:R:21:LYS:HZ3	1.67	0.43
19:R:35:ARG:O	19:R:37:VAL:HG23	2.19	0.43
19:R:87:ARG:HG2	19:R:87:ARG:NH1	2.33	0.43
21:T:94:ALA:O	21:T:95:ALA:CB	2.66	0.43
1:A:960:U:H1'	1:A:1223:C:H5'	2.01	0.43
1:A:1291:G:H2'	1:A:1292:U:C6	2.54	0.43
1:A:161:A:H2'	1:A:162:A:C8	2.53	0.43
1:A:188:C:H4'	21:T:89:ARG:HH12	1.82	0.43
4:C:134:ILE:HG21	4:C:167:TRP:O	2.19	0.43
6:E:11:ILE:HG22	6:E:12:LEU:N	2.34	0.43
3:B:181:PHE:CE2	9:H:70:GLN:HB3	2.53	0.43
3:B:179:LYS:HA	9:H:72:PRO:HD3	2.01	0.43
9:H:75:ARG:HA	9:H:76:PRO:HD3	1.71	0.43
10:I:19:LEU:O	10:I:20:ARG:HG3	2.18	0.43
14:M:84:ILE:O	14:M:86:CYS:N	2.51	0.43
15:N:45:ARG:NH1	15:N:45:ARG:HG3	2.33	0.43
19:R:42:ARG:HH11	19:R:42:ARG:CG	2.31	0.43
21:T:51:GLU:HA	21:T:54:LYS:HB2	2.00	0.43
1:A:1254:C:OP1	11:J:45:ARG:HD2	2.18	0.42
1:A:622:A:C8	1:A:623:C:C5	3.07	0.42
3:B:124:SER:O	3:B:127:ILE:CD1	2.67	0.42
3:B:69:LEU:C	3:B:69:LEU:HD23	2.38	0.42
6:E:28:PHE:O	6:E:47:LYS:HA	2.19	0.42
7:F:25:ILE:CD1	7:F:82:ARG:NH1	2.82	0.42
17:P:51:VAL:O	17:P:51:VAL:CG1	2.66	0.42
1:A:128:G:O2'	18:Q:3:LYS:HE3	2.18	0.42
20:S:22:LEU:C	20:S:24:ALA:H	2.22	0.42
1:A:1172:C:O2'	1:A:1173:G:H5'	2.19	0.42
1:A:1451:A:O2'	1:A:1452:C:OP1	2.33	0.42
1:A:319:G:C2'	1:A:320:C:H5'	2.48	0.42
1:A:626:U:O2'	1:A:627:G:H5'	2.20	0.42
1:A:935:A:C2	1:A:936:C:C2	3.06	0.42
3:B:83:MET:HE3	3:B:234:PRO:HG2	2.01	0.42
5:D:96:LEU:CD1	5:D:96:LEU:N	2.82	0.42
7:F:43:LEU:H	7:F:43:LEU:CD2	2.31	0.42
9:H:25:ASP:C	9:H:26:VAL:HG12	2.39	0.42
3:B:178:ARG:NH1	9:H:71:GLY:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:93:VAL:HG12	9:H:93:VAL:O	2.19	0.42
1:A:1216:G:H5''	15:N:5:ALA:HB2	2.01	0.42
1:A:1495:U:H2'	1:A:1496:C:H6	1.80	0.42
1:A:538:G:H5''	13:L:114:LYS:HB2	2.00	0.42
1:A:613:C:H2'	1:A:614:A:H8	1.83	0.42
3:B:41:ILE:HG22	3:B:41:ILE:O	2.18	0.42
5:D:64:LEU:HD21	5:D:94:LEU:HD21	2.01	0.42
6:E:69:VAL:HA	6:E:70:PRO:HD3	1.87	0.42
7:F:38:GLU:O	7:F:39:LYS:CB	2.60	0.42
8:G:155:ARG:O	8:G:156:TRP:HB3	2.19	0.42
10:I:7:THR:O	10:I:15:ALA:O	2.38	0.42
11:J:3:LYS:N	11:J:75:ILE:HA	2.33	0.42
13:L:10:LEU:HA	13:L:10:LEU:HD23	1.85	0.42
13:L:85:ILE:HG23	13:L:98:TYR:HB3	2.02	0.42
14:M:33:ALA:HB2	14:M:64:TRP:CH2	2.54	0.42
17:P:74:LEU:HB3	17:P:79:VAL:HG21	2.01	0.42
17:P:75:ARG:HH11	17:P:75:ARG:HG3	1.84	0.42
20:S:15:LEU:HD12	20:S:16:LEU:H	1.82	0.42
20:S:20:LEU:HD12	20:S:21:GLU:N	2.33	0.42
1:A:110:C:N4	1:A:111:G:C6	2.87	0.42
1:A:397:A:H5'	1:A:398:C:P	2.60	0.42
1:A:403:C:O2'	1:A:404:U:H5'	2.20	0.42
1:A:613:C:H2'	1:A:614:A:C8	2.55	0.42
1:A:64:G:C4'	1:A:65:U:O5'	2.54	0.42
1:A:792:A:H4'	1:A:793:U:H5''	2.01	0.42
3:B:230:VAL:CG1	3:B:231:GLU:N	2.82	0.42
6:E:74:GLY:O	6:E:116:THR:HG22	2.18	0.42
7:F:78:GLU:HA	7:F:81:ILE:CD1	2.49	0.42
13:L:69:TYR:CD2	13:L:70:ILE:N	2.88	0.42
14:M:46:LYS:HE2	14:M:47:ASP:OD1	2.19	0.42
17:P:21:VAL:HG21	17:P:59:TRP:NE1	2.35	0.42
21:T:47:GLY:O	21:T:49:ALA:N	2.53	0.42
1:A:1133:G:N1	1:A:1142:G:C6	2.87	0.42
1:A:1461:G:O2'	1:A:1462:G:H5'	2.19	0.42
1:A:824:C:O2'	1:A:825:G:H5'	2.18	0.42
5:D:43:HIS:CE1	5:D:46:LYS:HZ2	2.38	0.42
11:J:90:LEU:N	11:J:91:PRO:HD2	2.17	0.42
15:N:12:ARG:O	15:N:14:PRO:CD	2.67	0.42
17:P:43:LYS:CG	17:P:48:TRP:CD2	3.02	0.42
18:Q:95:TYR:N	18:Q:95:TYR:CD1	2.88	0.42
14:M:84:ILE:HG22	20:S:65:ASN:ND2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:57:ARG:CG	21:T:57:ARG:NH1	2.80	0.42
21:T:73:HIS:C	21:T:74:LYS:HG2	2.39	0.42
1:A:1256:A:O2'	1:A:1257:U:P	2.78	0.42
1:A:1442:G:H2'	1:A:1442:G:N3	2.34	0.42
1:A:1513:A:H2'	1:A:1514:C:C6	2.54	0.42
1:A:67:C:H4'	1:A:172:A:O4'	2.20	0.42
1:A:748:C:O2'	1:A:749:C:OP2	2.35	0.42
3:B:140:HIS:O	3:B:143:GLU:HB2	2.20	0.42
3:B:195:ASP:O	9:H:74:PRO:HG3	2.18	0.42
3:B:98:LEU:N	3:B:98:LEU:HD23	2.34	0.42
4:C:154:SER:OG	4:C:196:LEU:HA	2.19	0.42
5:D:148:VAL:HG11	5:D:158:ILE:HD13	2.00	0.42
1:A:542:G:H5'	5:D:41:GLY:HA3	2.01	0.42
6:E:11:ILE:HD11	6:E:108:ALA:HB3	2.01	0.42
7:F:15:ASP:O	7:F:16:GLN:C	2.57	0.42
7:F:48:LEU:HD13	7:F:52:ILE:CG1	2.49	0.42
9:H:65:TYR:CD1	9:H:65:TYR:N	2.87	0.42
10:I:97:LYS:HG3	10:I:102:LEU:HD12	1.96	0.42
10:I:97:LYS:HB2	10:I:98:PRO:HD3	2.02	0.42
1:A:1123:A:H2	11:J:39:PRO:HG3	1.85	0.42
17:P:55:ARG:O	17:P:56:ALA:C	2.55	0.42
20:S:24:ALA:HB3	20:S:25:LYS:HZ3	1.83	0.42
1:A:1000:U:H2'	1:A:1001:A:H8	1.82	0.42
1:A:1074:G:O2'	3:B:103:THR:HG22	2.19	0.42
1:A:865:A:H5'	1:A:1078:U:C4	2.53	0.42
1:A:1157:A:O4'	1:A:1158:C:C2	2.73	0.42
1:A:1214:C:H5''	1:A:1215:G:OP2	2.20	0.42
1:A:1370:G:O2'	1:A:1371:G:H5'	2.20	0.42
1:A:502:G:OP1	13:L:118:SER:HB2	2.20	0.42
1:A:5:U:HO2'	1:A:6:G:P	2.43	0.42
1:A:642:A:N7	9:H:115:SER:HA	2.35	0.42
3:B:122:PHE:O	3:B:123:ALA:CB	2.66	0.42
3:B:133:LYS:O	3:B:137:ARG:HG3	2.19	0.42
3:B:165:VAL:HB	3:B:166:ASP:H	1.71	0.42
4:C:52:LEU:HG	4:C:52:LEU:O	2.20	0.42
4:C:35:GLU:OE2	4:C:97:LYS:HG3	2.20	0.42
5:D:190:ASP:O	5:D:194:LEU:HD23	2.19	0.42
5:D:65:ARG:HB2	5:D:75:PHE:CE1	2.55	0.42
6:E:80:ILE:HD11	6:E:91:LEU:HB2	2.02	0.42
7:F:48:LEU:HD21	7:F:60:PHE:HZ	1.85	0.42
9:H:73:ASP:OD2	9:H:75:ARG:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1178:G:P	10:I:97:LYS:HZ3	2.42	0.42
11:J:12:ASP:OD1	11:J:14:LYS:N	2.45	0.42
12:K:82:VAL:HG23	12:K:105:VAL:HG13	2.00	0.42
13:L:69:TYR:HE2	13:L:71:PRO:HA	1.85	0.42
17:P:60:LEU:C	17:P:62:VAL:N	2.71	0.42
18:Q:48:GLU:C	18:Q:50:LYS:N	2.72	0.42
18:Q:68:ARG:HH11	18:Q:68:ARG:HG2	1.85	0.42
20:S:52:TYR:HA	20:S:56:GLN:O	2.18	0.42
21:T:20:LEU:O	21:T:23:ARG:HB3	2.19	0.42
1:A:1014:A:H2'	1:A:1015:A:C8	2.55	0.42
1:A:1151:A:O2'	1:A:1152:A:H8	2.03	0.42
1:A:1211:U:H1'	1:A:1213:A:C2	2.55	0.42
1:A:1319:A:P	20:S:5:LEU:HD21	2.60	0.42
1:A:1329:A:O2'	1:A:1330:U:H5'	2.20	0.42
1:A:1399:C:O2	1:A:1401:G:C5	2.72	0.42
1:A:178:C:O2'	1:A:179:A:H5'	2.20	0.42
1:A:335:C:H2'	1:A:336:C:C6	2.53	0.42
1:A:390:C:H6	1:A:390:C:O5'	2.02	0.42
1:A:685:G:C2	1:A:686:U:C4	3.08	0.42
1:A:998:G:O2'	1:A:999:C:H5'	2.19	0.42
3:B:86:GLU:C	3:B:88:ALA:H	2.22	0.42
4:C:126:ARG:O	4:C:127:ARG:HB2	2.20	0.42
9:H:104:ARG:HG3	9:H:138:TRP:CG	2.55	0.42
6:E:152:ARG:HA	9:H:64:LYS:NZ	2.35	0.42
10:I:49:PRO:O	10:I:52:ALA:HB3	2.19	0.42
14:M:46:LYS:HE3	14:M:46:LYS:HB2	1.81	0.42
17:P:75:ARG:O	17:P:78:GLY:N	2.50	0.42
19:R:16:PRO:O	19:R:17:SER:CB	2.67	0.42
1:A:1202:G:H2'	1:A:1203:C:O4'	2.20	0.42
1:A:1262:C:H42	1:A:1273:G:H1	1.66	0.42
1:A:276:G:O2'	1:A:277:C:H5'	2.19	0.42
1:A:663:A:O2'	1:A:664:G:H5'	2.20	0.42
3:B:24:TRP:CG	3:B:25:ASN:N	2.87	0.42
3:B:130:ARG:NH2	4:C:179:ARG:HH12	2.17	0.42
7:F:75:LEU:O	7:F:75:LEU:HD22	2.19	0.42
9:H:23:SER:OG	9:H:24:THR:N	2.50	0.42
10:I:53:VAL:O	10:I:54:ASP:HB2	2.19	0.42
10:I:78:LYS:HE2	10:I:78:LYS:HB3	1.92	0.42
13:L:46:LYS:HZ2	13:L:47:LYS:HG3	1.83	0.42
13:L:60:LEU:HD21	13:L:66:VAL:CG2	2.48	0.42
14:M:9:ILE:N	14:M:9:ILE:CD1	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:70:LEU:HD12	16:O:78:TYR:CA	2.50	0.42
1:A:1244:C:O2'	1:A:1245:A:H5'	2.20	0.42
1:A:1496:C:H2'	1:A:1497:G:O4'	2.19	0.42
1:A:190(K):G:H2'	1:A:190(L):U:C6	2.55	0.42
1:A:456:C:H2'	1:A:457:C:C6	2.55	0.42
1:A:821:G:H2'	1:A:822:C:C6	2.55	0.42
1:A:952:U:O2'	1:A:953:G:H5'	2.20	0.42
1:A:96:G:O2'	1:A:97:G:H5'	2.20	0.42
3:B:97:TRP:CZ2	3:B:102:LEU:HD13	2.48	0.42
3:B:126:GLU:O	3:B:127:ILE:C	2.56	0.42
3:B:64:ARG:HB2	3:B:64:ARG:HE	1.49	0.42
3:B:92:TYR:CD1	3:B:151:GLY:HA3	2.54	0.42
5:D:126:ILE:HG22	5:D:127:THR:N	2.33	0.42
5:D:15:GLU:C	5:D:17:VAL:N	2.73	0.42
7:F:15:ASP:O	7:F:17:SER:N	2.53	0.42
17:P:5:ARG:CB	17:P:67:THR:OG1	2.68	0.42
18:Q:6:LEU:O	18:Q:58:GLU:HA	2.20	0.42
18:Q:79:SER:O	18:Q:80:GLY:O	2.37	0.42
18:Q:81:ARG:O	18:Q:81:ARG:HG3	2.20	0.42
19:R:53:ARG:HA	19:R:56:THR:OG1	2.20	0.42
20:S:41:VAL:HG22	20:S:44:MET:HE2	2.00	0.42
1:A:1005:A:H2'	1:A:1006:C:C5'	2.49	0.41
1:A:1382:C:H2'	1:A:1383:C:H6	1.85	0.41
1:A:1487:G:HO2'	1:A:1488:G:H5'	1.82	0.41
1:A:66:G:H4'	1:A:173:U:C5	2.55	0.41
1:A:190(I):G:O2'	1:A:190(J):U:H5'	2.20	0.41
1:A:777:A:C6	1:A:778:G:C5	3.08	0.41
1:A:92:C:O2'	1:A:93:G:H5'	2.20	0.41
1:A:986:A:H2'	1:A:987:G:O4'	2.19	0.41
1:A:994:A:C8	1:A:994:A:OP1	2.73	0.41
3:B:115:LEU:HD23	3:B:153:ARG:HE	1.85	0.41
3:B:122:PHE:HE2	3:B:139:LYS:HG2	1.85	0.41
3:B:151:GLY:O	3:B:153:ARG:N	2.53	0.41
5:D:64:LEU:HD11	5:D:97:LEU:CD1	2.49	0.41
5:D:68:TYR:N	5:D:68:TYR:CD1	2.88	0.41
10:I:113:LYS:H	10:I:113:LYS:HD2	1.85	0.41
10:I:114:TYR:CD1	11:J:60:ARG:HG2	2.54	0.41
10:I:33:PHE:C	10:I:35:GLU:H	2.23	0.41
12:K:46:GLY:O	12:K:47:VAL:C	2.58	0.41
14:M:10:PRO:O	14:M:45:VAL:HG11	2.20	0.41
17:P:50:LYS:HG2	17:P:51:VAL:N	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:97:SER:HB3	18:Q:103:GLY:HA3	2.01	0.41
21:T:72:LEU:HD23	21:T:72:LEU:HA	1.79	0.41
1:A:109:A:H4'	1:A:110:C:OP2	2.20	0.41
1:A:1183:A:C2'	1:A:1184:G:OP1	2.67	0.41
1:A:1238:A:N7	1:A:1303:C:C1'	2.83	0.41
1:A:1407:C:O2'	1:A:1408:A:H5'	2.20	0.41
1:A:44:G:H2'	1:A:45:U:C6	2.55	0.41
1:A:997:U:H2'	1:A:998:G:O4'	2.20	0.41
3:B:7:VAL:C	3:B:8:LYS:HG3	2.40	0.41
4:C:67:THR:HG22	4:C:67:THR:O	2.20	0.41
5:D:107:ARG:CD	5:D:173:TRP:HZ2	2.33	0.41
5:D:189:PRO:HB2	5:D:194:LEU:HD21	2.02	0.41
5:D:76:ARG:HH11	5:D:76:ARG:HG2	1.86	0.41
5:D:8:VAL:HG21	5:D:115:ARG:CZ	2.50	0.41
6:E:115:VAL:CG1	6:E:116:THR:N	2.83	0.41
10:I:79:LEU:HD13	10:I:79:LEU:C	2.41	0.41
11:J:38:ILE:O	11:J:70:ARG:HA	2.20	0.41
13:L:46:LYS:CG	13:L:47:LYS:H	2.18	0.41
14:M:108:ARG:HD3	14:M:114:ARG:NH1	2.35	0.41
15:N:3:ARG:O	15:N:4:LYS:C	2.56	0.41
11:J:64:GLU:HG2	15:N:59:ALA:CB	2.50	0.41
16:O:45:VAL:HB	16:O:46:HIS:ND1	2.35	0.41
17:P:39:TYR:O	17:P:41:PRO:HD3	2.21	0.41
18:Q:56:VAL:CG1	18:Q:77:VAL:HB	2.49	0.41
1:A:267:C:P	18:Q:67:LYS:HB2	2.59	0.41
21:T:57:ARG:NH1	21:T:57:ARG:HG2	2.36	0.41
1:A:1064:G:C2	1:A:1066:C:N4	2.88	0.41
1:A:190:C:H2'	1:A:190(A):C:C6	2.55	0.41
1:A:197:A:N1	1:A:220:G:O2'	2.50	0.41
1:A:247:G:OP2	18:Q:100:LYS:HG3	2.21	0.41
1:A:262:A:C6	1:A:263:A:C6	3.08	0.41
1:A:445:G:O2'	1:A:446:G:H5'	2.20	0.41
3:B:25:ASN:O	3:B:26:PRO:C	2.58	0.41
4:C:173:VAL:N	4:C:174:PRO:CD	2.81	0.41
4:C:22:TRP:O	4:C:22:TRP:CE3	2.73	0.41
9:H:56:LYS:HB3	9:H:57:PRO:HD2	2.03	0.41
14:M:40:ASN:ND2	14:M:40:ASN:C	2.73	0.41
14:M:87:TYR:CZ	14:M:91:ARG:HD3	2.55	0.41
20:S:22:LEU:HD11	20:S:31:ILE:HD11	2.02	0.41
20:S:8:GLY:O	20:S:9:VAL:C	2.58	0.41
1:A:1441:G:H4'	1:A:1442:G:N7	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1478:C:H2'	1:A:1479:C:C6	2.53	0.41
1:A:264:U:H2'	1:A:265:G:O4'	2.20	0.41
1:A:322:C:O2'	1:A:323:U:H5'	2.21	0.41
1:A:401:C:H2'	1:A:402:G:C8	2.53	0.41
1:A:657:G:O2'	1:A:658:G:H5'	2.19	0.41
1:A:780:A:O2'	1:A:781:A:H5''	2.20	0.41
1:A:828:A:H5''	1:A:859:A:C2	2.55	0.41
3:B:137:ARG:O	3:B:140:HIS:HB2	2.20	0.41
4:C:47:LEU:N	4:C:47:LEU:CD1	2.83	0.41
4:C:79:ARG:C	4:C:81:GLY:H	2.24	0.41
5:D:78:LEU:HB3	5:D:93:PHE:HE2	1.85	0.41
7:F:45:LEU:HD23	7:F:59:TYR:HD1	1.85	0.41
11:J:12:ASP:O	11:J:15:THR:HG22	2.20	0.41
12:K:127:LYS:HA	12:K:127:LYS:HD3	1.71	0.41
14:M:49:THR:HB	14:M:52:GLU:HG3	2.01	0.41
14:M:58:GLU:O	14:M:62:ASN:HB2	2.20	0.41
14:M:7:VAL:O	14:M:9:ILE:HD11	2.20	0.41
20:S:47:HIS:O	20:S:62:ILE:HG22	2.20	0.41
1:A:1118:C:H1'	1:A:1179:A:C4	2.56	0.41
1:A:1257:U:HO2'	1:A:1258:G:P	2.40	0.41
1:A:165:C:H2'	1:A:166:G:H8	1.85	0.41
1:A:175:C:H2'	1:A:176:C:H6	1.84	0.41
1:A:584:G:H2'	1:A:585:G:C8	2.55	0.41
1:A:817:C:H4'	1:A:818:G:OP1	2.21	0.41
1:A:838:G:C2	1:A:849:C:N3	2.88	0.41
1:A:965:A:H4'	1:A:966:G:O5'	2.21	0.41
3:B:92:TYR:CE1	3:B:151:GLY:HA3	2.55	0.41
5:D:43:HIS:O	5:D:44:GLY:C	2.59	0.41
6:E:93:PRO:CG	9:H:105:ARG:HE	2.33	0.41
8:G:116:ALA:HA	8:G:119:ARG:NH1	2.36	0.41
10:I:111:ARG:HD2	10:I:113:LYS:HG3	2.01	0.41
10:I:44:VAL:HG13	10:I:51:ARG:NH2	2.35	0.41
1:A:1248:A:H1'	10:I:70:LYS:HZ1	1.84	0.41
12:K:60:ALA:O	12:K:61:ALA:C	2.59	0.41
13:L:28:LYS:HD2	13:L:33:ARG:HH12	1.86	0.41
15:N:21:TYR:CE2	15:N:23:ARG:NE	2.87	0.41
16:O:36:ILE:HA	16:O:59:MET:HE3	2.01	0.41
17:P:55:ARG:O	17:P:58:TYR:N	2.53	0.41
18:Q:97:SER:CB	18:Q:103:GLY:HA3	2.50	0.41
1:A:191:G:H21	21:T:103:GLY:C	2.23	0.41
1:A:1110:A:H8	1:A:1110:A:O5'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1145:C:O2'	1:A:1146:A:C8	2.73	0.41
1:A:1015:A:H1'	1:A:1218:C:O2'	2.21	0.41
1:A:1226:C:HO2'	1:A:1227:A:P	2.42	0.41
1:A:1301:U:O2'	1:A:1302:U:P	2.79	0.41
1:A:1367:C:H5'	11:J:60:ARG:NH1	2.35	0.41
1:A:220:G:O2'	1:A:221:C:H5'	2.21	0.41
1:A:411:A:C6	1:A:429:U:C4	3.09	0.41
1:A:766:A:C8	1:A:814:A:C6	3.09	0.41
3:B:19:HIS:NE2	3:B:206:ASP:HB3	2.35	0.41
3:B:69:LEU:HD23	3:B:70:PHE:N	2.36	0.41
5:D:31:CYS:C	5:D:33:MET:H	2.22	0.41
5:D:87:GLY:O	5:D:88:VAL:C	2.58	0.41
8:G:145:ALA:C	8:G:147:ALA:N	2.74	0.41
11:J:64:GLU:HG2	15:N:59:ALA:HB2	2.02	0.41
1:A:1061:G:O2'	1:A:1062:U:H5'	2.20	0.41
1:A:1137:C:H5'	1:A:1138:G:C6	2.56	0.41
1:A:646:U:H2'	1:A:647:C:C6	2.55	0.41
6:E:11:ILE:HG12	6:E:33:VAL:HG23	2.02	0.41
6:E:15:ARG:CD	6:E:26:PHE:HD2	2.33	0.41
9:H:51:VAL:CG1	9:H:52:ASP:N	2.84	0.41
9:H:91:ARG:HG2	13:L:7:ILE:HG21	2.02	0.41
10:I:111:ARG:HD3	10:I:112:LYS:C	2.41	0.41
10:I:27:THR:HG23	10:I:30:GLY:O	2.21	0.41
1:A:1371:G:O3'	10:I:69:GLY:HA3	2.21	0.41
13:L:40:VAL:O	13:L:40:VAL:HG12	2.21	0.41
17:P:43:LYS:HG2	17:P:48:TRP:CE2	2.56	0.41
17:P:81:ARG:HB2	17:P:81:ARG:NH1	2.36	0.41
1:A:1003(A):G:C5	1:A:1004:A:N3	2.88	0.41
1:A:1427:U:O2'	1:A:1428:A:H5'	2.21	0.41
1:A:248:C:H2'	1:A:249:U:H5'	2.02	0.41
1:A:354:G:C2	1:A:355:C:C6	3.09	0.41
1:A:546:G:OP1	5:D:73:ARG:HB2	2.21	0.41
1:A:942:G:H2'	1:A:943:U:H6	1.86	0.41
1:A:960:U:O2'	1:A:1223:C:H4'	2.20	0.41
3:B:208:ILE:HG21	3:B:239:VAL:HA	2.02	0.41
4:C:188:LEU:HD22	4:C:188:LEU:HA	1.94	0.41
4:C:56:ASP:O	4:C:57:ILE:HG13	2.20	0.41
5:D:141:ARG:N	5:D:144:ASP:OD2	2.53	0.41
5:D:43:HIS:O	5:D:45:GLN:N	2.53	0.41
6:E:15:ARG:HG2	6:E:28:PHE:CE2	2.56	0.41
9:H:6:ILE:HD12	9:H:35:ILE:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:92:TYR:O	10:I:93:ARG:C	2.59	0.41
1:A:502:G:OP1	13:L:118:SER:CB	2.69	0.41
14:M:73:GLU:O	14:M:74:VAL:C	2.59	0.41
17:P:69:THR:O	17:P:70:ALA:C	2.59	0.41
1:A:187:C:N3	21:T:105:SER:HB3	2.36	0.41
1:A:1112:C:O2	4:C:178:LEU:O	2.39	0.41
1:A:151:A:H2'	1:A:152:A:O4'	2.21	0.41
1:A:399:G:H2'	1:A:400:C:C6	2.55	0.41
1:A:625:G:C6	1:A:626:U:C4	3.09	0.41
1:A:838:G:N2	1:A:849:C:C2	2.89	0.41
3:B:215:LEU:O	3:B:216:SER:C	2.59	0.41
5:D:54:TYR:O	5:D:55:ALA:C	2.59	0.41
6:E:112:LEU:N	6:E:112:LEU:HD23	2.35	0.41
6:E:78:HIS:CE1	6:E:80:ILE:HG23	2.56	0.41
8:G:31:MET:HA	8:G:39:ALA:HB2	2.03	0.41
9:H:35:ILE:HG22	9:H:39:LEU:HD23	2.02	0.41
11:J:56:HIS:C	11:J:58:ASP:N	2.75	0.41
12:K:87:THR:HG23	12:K:91:ARG:NH2	2.35	0.41
13:L:84:LEU:CD2	13:L:104:VAL:HG11	2.50	0.41
16:O:11:VAL:HG21	16:O:34:LEU:HD12	2.02	0.41
16:O:84:LYS:O	16:O:85:LEU:C	2.59	0.41
19:R:34:TYR:C	19:R:34:TYR:CD1	2.94	0.41
20:S:36:ARG:NH2	20:S:75:ALA:HB3	2.35	0.41
20:S:41:VAL:HB	20:S:42:PRO:HD2	2.01	0.41
22:V:2:GLY:C	22:V:4:GLY:N	2.74	0.41
1:A:1003:G:N1	1:A:1003(A):G:C6	2.89	0.41
1:A:1038:C:H2'	1:A:1039:C:H6	1.83	0.41
1:A:1053:G:C5'	1:A:1054:C:H5'	2.50	0.41
1:A:1104:G:H2'	1:A:1105:A:H8	1.86	0.41
1:A:113:G:H1'	1:A:354:G:C5'	2.48	0.41
1:A:1419:G:H2'	1:A:1420:C:C6	2.55	0.41
1:A:6:G:H4'	1:A:298:A:H4'	2.03	0.41
1:A:309:G:H1'	1:A:608:A:C2	2.56	0.41
1:A:457:C:H2'	1:A:458:C:C6	2.55	0.41
1:A:459:G:H3'	1:A:460:A:C5'	2.51	0.41
1:A:93:G:H2'	1:A:95:U:O4'	2.21	0.41
3:B:144:ARG:HA	3:B:147:LYS:HD2	2.03	0.41
4:C:15:THR:O	4:C:16:ARG:CB	2.61	0.41
5:D:162:LEU:HA	5:D:162:LEU:HD23	1.81	0.41
5:D:6:GLY:O	5:D:8:VAL:HG23	2.21	0.41
6:E:131:ILE:HD13	6:E:131:ILE:HA	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:26:PHE:CD1	6:E:26:PHE:N	2.82	0.41
7:F:27:GLN:NE2	7:F:27:GLN:HA	2.35	0.41
9:H:24:THR:HG23	9:H:61:VAL:HB	2.03	0.41
1:A:877:C:H1'	9:H:3:THR:CG2	2.51	0.41
9:H:56:LYS:CD	9:H:56:LYS:N	2.83	0.41
1:A:600:C:OP1	9:H:97:VAL:HG12	2.20	0.41
11:J:29:ARG:HB2	11:J:84:GLN:HE22	1.85	0.41
12:K:99:GLN:HA	12:K:105:VAL:CG2	2.51	0.41
14:M:18:ALA:O	14:M:21:TYR:HB2	2.21	0.41
14:M:53:VAL:O	14:M:57:ARG:HB2	2.21	0.41
17:P:52:ASP:OD2	17:P:55:ARG:CB	2.69	0.41
19:R:34:TYR:O	19:R:34:TYR:CD1	2.71	0.41
19:R:73:ALA:CB	19:R:79:LEU:HD12	2.49	0.41
1:A:242:C:C2'	1:A:243:A:H5'	2.50	0.41
1:A:664:G:N2	1:A:741:G:H1	2.00	0.41
1:A:899:C:H2'	1:A:900:A:C8	2.56	0.41
3:B:55:PHE:CZ	3:B:218:ALA:HB2	2.56	0.41
4:C:34:LEU:O	4:C:34:LEU:CD2	2.66	0.41
4:C:39:ILE:HD12	4:C:57:ILE:HD13	2.03	0.41
5:D:114:ARG:CG	5:D:114:ARG:NH1	2.78	0.41
6:E:123:LEU:HA	6:E:123:LEU:HD23	1.82	0.41
6:E:76:ILE:HG12	6:E:77:PRO:HD2	2.02	0.41
6:E:89:ILE:CD1	6:E:90:VAL:N	2.84	0.41
8:G:136:LYS:HG2	8:G:140:ASP:OD1	2.21	0.41
6:E:152:ARG:NH2	9:H:107:LEU:O	2.54	0.41
18:Q:80:GLY:O	18:Q:81:ARG:HB3	2.22	0.41
1:A:1041:A:H2'	1:A:1042:G:C8	2.56	0.40
1:A:1072:G:C5	1:A:1073:U:C4	3.08	0.40
1:A:1277:C:O2'	1:A:1279:A:H1'	2.21	0.40
1:A:321:A:H2'	1:A:322:C:C6	2.55	0.40
1:A:446:G:O2'	1:A:447:G:H5'	2.21	0.40
1:A:528:C:H5'	1:A:535:A:C6	2.55	0.40
1:A:622:A:C8	1:A:623:C:C6	3.10	0.40
1:A:802:A:H2'	1:A:803:G:O4'	2.20	0.40
1:A:818:G:HO2'	1:A:819:A:H5''	1.86	0.40
1:A:930:C:C2'	1:A:931:C:H5'	2.51	0.40
3:B:132:LYS:O	3:B:136:VAL:HG23	2.21	0.40
3:B:188:ALA:HB1	3:B:192:SER:OG	2.20	0.40
3:B:230:VAL:HG12	3:B:231:GLU:N	2.35	0.40
4:C:56:ASP:O	4:C:66:VAL:HA	2.21	0.40
5:D:209:ARG:HG2	5:D:209:ARG:NH1	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:11:ASN:O	7:F:14:LEU:HG	2.21	0.40
7:F:48:LEU:HD13	7:F:52:ILE:HD12	2.03	0.40
10:I:10:ARG:HG2	10:I:75:ASP:HB3	2.01	0.40
10:I:125:TYR:CE1	10:I:128:ARG:HB2	2.56	0.40
10:I:47:LEU:O	10:I:50:LEU:HB2	2.21	0.40
11:J:16:LEU:C	11:J:18:ALA:H	2.25	0.40
11:J:34:VAL:C	11:J:36:GLY:H	2.25	0.40
16:O:8:LYS:O	16:O:11:VAL:N	2.50	0.40
17:P:47:ASP:OD2	17:P:47:ASP:C	2.60	0.40
18:Q:81:ARG:HB2	18:Q:83:ASP:OD1	2.22	0.40
20:S:44:MET:O	20:S:62:ILE:HG21	2.20	0.40
1:A:1004:A:N7	1:A:1037:C:N3	2.69	0.40
1:A:1152:A:H2'	1:A:1153:C:C6	2.56	0.40
1:A:136:C:H2'	1:A:137:C:H6	1.86	0.40
1:A:148:G:H2'	1:A:149:A:H8	1.87	0.40
1:A:204:U:H4'	1:A:216:G:O5'	2.20	0.40
1:A:33:A:H2'	1:A:34:C:H6	1.85	0.40
1:A:488:C:O5'	1:A:488:C:H6	2.03	0.40
1:A:491:G:C2	1:A:492:G:C8	3.09	0.40
1:A:630:G:O2'	1:A:631:G:H5'	2.22	0.40
1:A:775:G:O2'	1:A:776:G:H5'	2.21	0.40
1:A:865:A:H2'	1:A:866:C:C6	2.56	0.40
1:A:951:G:O2'	1:A:952:U:H5'	2.21	0.40
1:A:961:U:C2'	1:A:962:C:H5'	2.51	0.40
1:A:969:A:O2'	1:A:970:C:H5'	2.21	0.40
3:B:142:LEU:HD22	3:B:146:GLN:NE2	2.36	0.40
3:B:213:LEU:C	3:B:213:LEU:CD2	2.89	0.40
3:B:239:VAL:HB	3:B:240:GLN:HE22	1.85	0.40
5:D:108:LEU:HA	5:D:108:LEU:HD23	1.85	0.40
11:J:16:LEU:C	11:J:18:ALA:N	2.74	0.40
11:J:22:LYS:HE2	11:J:90:LEU:CD1	2.44	0.40
12:K:38:ASN:HA	12:K:39:PRO:HD2	1.76	0.40
12:K:87:THR:CA	12:K:91:ARG:HH21	2.25	0.40
19:R:36:ASN:C	19:R:38:GLU:N	2.74	0.40
1:A:1314:C:OP2	20:S:6:LYS:HG2	2.21	0.40
21:T:14:LYS:O	21:T:17:ARG:HB2	2.21	0.40
1:A:1070:U:OP1	6:E:18:ARG:NH1	2.54	0.40
1:A:1169:A:H2'	1:A:1171:G:O4'	2.22	0.40
1:A:1239:A:C4	1:A:1298:C:N4	2.89	0.40
1:A:1245:A:C2	1:A:1293:G:C2	3.10	0.40
1:A:1287:A:C6	1:A:1288:A:C6	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:A:H2'	1:A:409:G:H8	1.86	0.40
1:A:999:C:H2'	1:A:1000:U:C6	2.56	0.40
3:B:83:MET:CE	3:B:234:PRO:HG2	2.51	0.40
8:G:76:ARG:HD2	8:G:89:MET:SD	2.60	0.40
9:H:55:GLY:C	9:H:56:LYS:HD2	2.41	0.40
10:I:18:PHE:HD1	10:I:62:TYR:HD2	1.69	0.40
10:I:9:ARG:HG2	10:I:14:VAL:HG22	2.03	0.40
12:K:91:ARG:HD3	19:R:88:LYS:HE2	2.02	0.40
14:M:63:THR:HG23	14:M:64:TRP:CD2	2.57	0.40
19:R:86:VAL:HG12	19:R:86:VAL:O	2.21	0.40
20:S:25:LYS:HD2	20:S:25:LYS:N	2.29	0.40
21:T:10:LEU:O	21:T:13:LEU:HD12	2.22	0.40
1:A:1190:G:C2'	1:A:1191:A:OP2	2.69	0.40
1:A:1504:G:OP1	1:A:1507:A:H4'	2.22	0.40
1:A:179:A:C2	1:A:180:U:C2	3.10	0.40
1:A:279:A:H4'	1:A:280:C:OP2	2.21	0.40
1:A:416:G:H2'	1:A:417:C:H6	1.86	0.40
1:A:421:U:H5'	1:A:422:C:C5	2.57	0.40
1:A:750:G:H1'	16:O:22:THR:OG1	2.21	0.40
1:A:820:U:H4'	1:A:821:G:OP2	2.22	0.40
1:A:849:C:O2'	1:A:850:U:H5'	2.22	0.40
3:B:111:ARG:HB3	3:B:149:LEU:HD11	2.02	0.40
3:B:74:LYS:HG2	3:B:74:LYS:O	2.21	0.40
4:C:155:GLY:O	4:C:196:LEU:HD22	2.21	0.40
6:E:79:GLU:HA	6:E:91:LEU:O	2.21	0.40
8:G:59:LEU:O	8:G:63:LYS:HG3	2.22	0.40
9:H:138:TRP:CE3	9:H:138:TRP:C	2.95	0.40
9:H:82:HIS:C	9:H:82:HIS:CD2	2.94	0.40
10:I:30:GLY:O	10:I:31:GLN:C	2.60	0.40
13:L:67:THR:HG22	13:L:96:VAL:HG13	2.03	0.40
17:P:20:VAL:HG22	17:P:34:GLU:O	2.22	0.40
17:P:51:VAL:HG12	17:P:51:VAL:O	2.22	0.40
19:R:36:ASN:O	19:R:38:GLU:N	2.55	0.40
20:S:51:VAL:O	20:S:57:HIS:HA	2.21	0.40
1:A:1003:G:H2'	1:A:1003(A):G:C8	2.56	0.40
1:A:1277:C:O2'	1:A:1278:U:H5'	2.21	0.40
1:A:1308:U:H2'	1:A:1309:G:C8	2.57	0.40
1:A:1369:C:H2'	1:A:1370:G:H8	1.83	0.40
1:A:129(A):G:C2	1:A:190(E):U:H5'	2.57	0.40
1:A:337:C:H2'	1:A:338:A:C8	2.56	0.40
1:A:533:A:C5	1:A:536:C:C4	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:582:U:C2	1:A:760:G:C6	3.09	0.40
1:A:864:A:H2'	1:A:865:A:C8	2.56	0.40
4:C:134:ILE:CG2	4:C:168:ALA:HB3	2.52	0.40
4:C:6:HIS:HA	4:C:7:PRO:HD2	1.83	0.40
5:D:150:GLU:HG3	5:D:153:ARG:NH2	2.36	0.40
5:D:36:ARG:HG3	5:D:38:TYR:CZ	2.56	0.40
8:G:153:HIS:NE2	8:G:154:TYR:CE2	2.89	0.40
8:G:49:ILE:HG22	8:G:49:ILE:O	2.22	0.40
10:I:118:LYS:NZ	10:I:118:LYS:CB	2.85	0.40
11:J:51:ARG:NE	11:J:61:GLU:HB2	2.37	0.40
11:J:62:HIS:HB3	15:N:59:ALA:CB	2.46	0.40
13:L:53:ARG:CB	13:L:93:LEU:HD11	2.52	0.40
17:P:33:ILE:O	17:P:34:GLU:HB2	2.22	0.40
21:T:69:GLY:O	21:T:73:HIS:CE1	2.74	0.40
22:V:24:ARG:O	22:V:25:LYS:CB	2.69	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]	1.76	0.44

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%)	161 (69%)	41 (18%)	30 (13%)	0	3
4	C	204/239 (85%)	131 (64%)	45 (22%)	28 (14%)	0	3
5	D	206/209 (99%)	158 (77%)	30 (15%)	18 (9%)	1	9
6	E	148/162 (91%)	131 (88%)	13 (9%)	4 (3%)	6	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	F	99/101 (98%)	82 (83%)	15 (15%)	2 (2%)	9	44
8	G	153/156 (98%)	105 (69%)	37 (24%)	11 (7%)	1	12
9	H	136/138 (99%)	115 (85%)	18 (13%)	3 (2%)	8	42
10	I	125/128 (98%)	87 (70%)	29 (23%)	9 (7%)	1	12
11	J	96/105 (91%)	57 (59%)	23 (24%)	16 (17%)	0	2
12	K	117/129 (91%)	84 (72%)	19 (16%)	14 (12%)	0	4
13	L	122/135 (90%)	94 (77%)	18 (15%)	10 (8%)	1	10
14	M	123/126 (98%)	84 (68%)	27 (22%)	12 (10%)	1	7
15	N	58/61 (95%)	41 (71%)	10 (17%)	7 (12%)	0	4
16	O	86/89 (97%)	69 (80%)	13 (15%)	4 (5%)	3	23
17	P	86/88 (98%)	65 (76%)	18 (21%)	3 (4%)	4	32
18	Q	102/105 (97%)	81 (79%)	13 (13%)	8 (8%)	1	11
19	R	71/88 (81%)	47 (66%)	19 (27%)	5 (7%)	1	13
20	S	78/93 (84%)	56 (72%)	15 (19%)	7 (9%)	1	8
21	T	97/106 (92%)	62 (64%)	22 (23%)	13 (13%)	0	3
22	V	22/26 (85%)	18 (82%)	3 (14%)	1 (4%)	3	24
All	All	2361/2540 (93%)	1728 (73%)	428 (18%)	205 (9%)	1	9

All (205) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	8	LYS
3	B	15	VAL
3	B	16	HIS
3	B	17	PHE
3	B	21	ARG
3	B	24	TRP
3	B	89	GLY
3	B	123	ALA
3	B	165	VAL
4	C	4	LYS
4	C	15	THR
4	C	16	ARG
4	C	26	LYS
4	C	29	TYR
4	C	47	LEU

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Mol	Chain	Res	Type
4	C	61	ALA
4	C	97	LYS
4	C	146	ALA
4	C	154	SER
4	C	179	ARG
4	C	189	ALA
5	D	4	TYR
5	D	36	ARG
6	E	16	THR
8	G	7	ALA
8	G	14	PRO
8	G	155	ARG
9	H	91	ARG
9	H	134	ILE
10	I	43	ALA
10	I	101	PHE
11	J	32	ALA
11	J	54	PHE
11	J	57	LYS
11	J	79	ARG
11	J	86	MET
12	K	27	ASN
12	K	49	GLY
12	K	57	THR
12	K	89	ALA
13	L	27	LEU
13	L	28	LYS
13	L	47	LYS
13	L	126	LYS
14	M	63	THR
14	M	67	GLU
14	M	124	PRO
15	N	22	THR
15	N	32	SER
16	O	88	ARG
17	P	49	LEU
17	P	83	GLU
18	Q	69	LYS
18	Q	80	GLY
18	Q	98	LEU
18	Q	104	LYS
19	R	20	ALA

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Mol	Chain	Res	Type
19	R	60	GLY
19	R	87	ARG
20	S	6	LYS
20	S	9	VAL
20	S	71	LEU
21	T	11	SER
21	T	48	LYS
21	T	73	HIS
3	B	18	GLY
3	B	20	GLU
3	B	60	ASP
3	B	83	MET
3	B	204	ASN
3	B	224	GLN
4	C	12	LEU
4	C	54	ARG
4	C	77	ILE
4	C	101	LEU
4	C	205	GLY
5	D	16	GLY
5	D	31	CYS
5	D	42	GLN
5	D	44	GLY
5	D	88	VAL
5	D	92	VAL
5	D	131	ARG
5	D	175	SER
6	E	78	HIS
7	F	16	GLN
7	F	39	LYS
8	G	42	ILE
9	H	24	THR
10	I	126	SER
11	J	30	SER
11	J	34	VAL
11	J	72	VAL
11	J	90	LEU
12	K	50	TYR
12	K	124	LYS
12	K	127	LYS
13	L	41	ARG
13	L	51	ALA

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Mol	Chain	Res	Type
13	L	121	GLY
14	M	6	GLY
14	M	74	VAL
14	M	85	GLY
14	M	99	ARG
14	M	122	LYS
15	N	31	ARG
15	N	36	PHE
16	O	84	LYS
17	P	10	GLY
18	Q	81	ARG
18	Q	96	GLN
20	S	68	GLY
20	S	69	HIS
21	T	96	GLY
21	T	99	LEU
21	T	102	GLY
3	B	26	PRO
3	B	76	GLN
3	B	95	GLN
3	B	124	SER
3	B	125	PRO
3	B	155	LEU
3	B	211	ILE
4	C	168	ALA
4	C	188	LEU
5	D	153	ARG
6	E	65	ASN
8	G	4	ARG
11	J	39	PRO
11	J	60	ARG
11	J	61	GLU
12	K	101	SER
12	K	102	GLY
12	K	126	ARG
13	L	48	PRO
14	M	86	CYS
14	M	100	GLY
15	N	12	ARG
15	N	13	THR
15	N	29	ARG
18	Q	33	GLY

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Mol	Chain	Res	Type
21	T	9	ASN
21	T	50	GLU
21	T	95	ALA
22	V	3	LYS
3	B	9	GLU
3	B	22	LYS
3	B	215	LEU
3	B	232	PRO
4	C	98	ASN
4	C	108	ASN
5	D	10	ARG
5	D	26	CYS
5	D	29	PRO
5	D	30	LYS
5	D	63	LYS
8	G	41	ARG
8	G	81	GLY
8	G	112	PRO
10	I	7	THR
10	I	44	VAL
10	I	56	LEU
11	J	40	LEU
14	M	42	ALA
19	R	17	SER
19	R	48	GLY
20	S	45	VAL
21	T	74	LYS
21	T	98	PRO
3	B	126	GLU
3	B	152	PHE
3	B	213	LEU
4	C	60	ALA
4	C	178	LEU
8	G	5	ARG
10	I	31	GLN
10	I	34	ASN
11	J	26	ALA
11	J	55	LYS
12	K	12	ARG
12	K	29	ILE
12	K	47	VAL
14	M	12	ASN

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Mol	Chain	Res	Type
3	B	207	ALA
4	C	7	PRO
4	C	206	GLU
5	D	5	ILE
13	L	45	PRO
13	L	116	SER
16	O	73	GLU
18	Q	27	PHE
4	C	39	ILE
4	C	66	VAL
5	D	56	VAL
8	G	17	VAL
11	J	76	ASN
12	K	35	PRO
16	O	82	ILE
8	G	66	VAL
20	S	8	GLY
21	T	101	GLY
6	E	77	PRO
10	I	41	VAL
4	C	174	PRO
21	T	97	ALA

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%)	173 (86%)	29 (14%)	4	20
4	C	160/188 (85%)	137 (86%)	23 (14%)	4	20
5	D	180/181 (99%)	168 (93%)	12 (7%)	19	57
6	E	115/123 (94%)	99 (86%)	16 (14%)	4	21
7	F	90/90 (100%)	86 (96%)	4 (4%)	33	69
8	G	126/127 (99%)	120 (95%)	6 (5%)	30	67
9	H	119/119 (100%)	103 (87%)	16 (13%)	4	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	I	98/99 (99%)	87 (89%)	11 (11%)	7	30
11	J	87/92 (95%)	77 (88%)	10 (12%)	6	29
12	K	90/99 (91%)	84 (93%)	6 (7%)	19	57
13	L	104/111 (94%)	96 (92%)	8 (8%)	15	49
14	M	100/101 (99%)	91 (91%)	9 (9%)	11	41
15	N	49/50 (98%)	45 (92%)	4 (8%)	13	47
16	O	79/80 (99%)	77 (98%)	2 (2%)	53	81
17	P	74/74 (100%)	70 (95%)	4 (5%)	26	63
18	Q	96/97 (99%)	91 (95%)	5 (5%)	27	64
19	R	64/77 (83%)	57 (89%)	7 (11%)	7	32
20	S	71/80 (89%)	68 (96%)	3 (4%)	34	70
21	T	76/82 (93%)	67 (88%)	9 (12%)	6	27
22	V	19/21 (90%)	19 (100%)	0	100	100
All	All	1999/2111 (95%)	1815 (91%)	184 (9%)	11	40

All (184) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	7	VAL
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	24	TRP
3	B	25	ASN
3	B	64	ARG
3	B	67	THR
3	B	74	LYS
3	B	76	GLN
3	B	87	ARG
3	B	96	ARG
3	B	139	LYS
3	B	144	ARG
3	B	153	ARG
3	B	157	ARG

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Mol	Chain	Res	Type
3	B	163	PHE
3	B	164	VAL
3	B	170	GLU
3	B	178	ARG
3	B	185	ILE
3	B	204	ASN
3	B	221	LEU
3	B	231	GLU
3	B	232	PRO
3	B	236	TYR
4	C	3	ASN
4	C	11	ARG
4	C	21	ARG
4	C	26	LYS
4	C	37	GLN
4	C	56	ASP
4	C	64	VAL
4	C	82	GLU
4	C	86	VAL
4	C	90	GLU
4	C	91	LEU
4	C	99	VAL
4	C	107	GLN
4	C	110	ASN
4	C	127	ARG
4	C	139	GLN
4	C	166	GLU
4	C	167	TRP
4	C	175	LEU
4	C	179	ARG
4	C	188	LEU
4	C	192	THR
4	C	204	LEU
5	D	9	CYS
5	D	15	GLU
5	D	26	CYS
5	D	53	ASP
5	D	78	LEU
5	D	114	ARG
5	D	122	ARG
5	D	170	VAL
5	D	179	GLU

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Mol	Chain	Res	Type
5	D	192	GLU
5	D	194	LEU
5	D	199	ASN
6	E	12	LEU
6	E	26	PHE
6	E	31	LEU
6	E	41	VAL
6	E	43	LEU
6	E	52	PRO
6	E	56	GLN
6	E	63	ARG
6	E	68	GLU
6	E	73	ASN
6	E	76	ILE
6	E	79	GLU
6	E	89	ILE
6	E	118	ILE
6	E	120	THR
6	E	150	ARG
7	F	10	LEU
7	F	40	VAL
7	F	69	GLU
7	F	100	ASN
8	G	8	GLU
8	G	11	GLN
8	G	12	LEU
8	G	38	LEU
8	G	120	ILE
8	G	126	ASP
9	H	21	LYS
9	H	26	VAL
9	H	39	LEU
9	H	52	ASP
9	H	60	ARG
9	H	63	LEU
9	H	79	VAL
9	H	84	ARG
9	H	85	ARG
9	H	91	ARG
9	H	92	ARG
9	H	104	ARG
9	H	105	ARG

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Mol	Chain	Res	Type
9	H	112	LEU
9	H	125	ARG
9	H	138	TRP
10	I	2	GLU
10	I	10	ARG
10	I	23	ASN
10	I	38	GLN
10	I	53	VAL
10	I	56	LEU
10	I	58	ARG
10	I	65	VAL
10	I	91	ASP
10	I	111	ARG
10	I	121	ARG
11	J	38	ILE
11	J	45	ARG
11	J	49	VAL
11	J	60	ARG
11	J	64	GLU
11	J	66	ARG
11	J	71	LEU
11	J	73	ASP
11	J	74	ILE
11	J	95	GLU
12	K	27	ASN
12	K	30	VAL
12	K	54	ARG
12	K	84	VAL
12	K	92	GLU
12	K	116	HIS
13	L	17	LYS
13	L	33	ARG
13	L	48	PRO
13	L	53	ARG
13	L	79	GLU
13	L	98	TYR
13	L	113	ARG
13	L	126	LYS
14	M	9	ILE
14	M	32	GLU
14	M	40	ASN
14	M	44	ARG

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Mol	Chain	Res	Type
14	M	56	LEU
14	M	70	LEU
14	M	81	LEU
14	M	110	ARG
14	M	125	ARG
15	N	17	LYS
15	N	31	ARG
15	N	33	VAL
15	N	41	ARG
16	O	3	ILE
16	O	83	GLU
17	P	8	ARG
17	P	20	VAL
17	P	62	VAL
17	P	76	GLN
18	Q	34	LYS
18	Q	38	ARG
18	Q	53	LEU
18	Q	60	ILE
18	Q	68	ARG
19	R	28	GLU
19	R	34	TYR
19	R	36	ASN
19	R	38	GLU
19	R	42	ARG
19	R	54	ARG
19	R	65	ILE
20	S	15	LEU
20	S	20	LEU
20	S	36	ARG
21	T	10	LEU
21	T	11	SER
21	T	42	GLN
21	T	46	GLU
21	T	57	ARG
21	T	73	HIS
21	T	75	ASN
21	T	84	LEU
21	T	86	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	19	HIS
3	B	25	ASN
3	B	40	HIS
3	B	94	ASN
3	B	140	HIS
3	B	204	ASN
3	B	240	GLN
4	C	6	HIS
4	C	31	HIS
4	C	69	HIS
4	C	98	ASN
4	C	104	GLN
4	C	110	ASN
4	C	118	GLN
4	C	123	GLN
4	C	139	GLN
4	C	181	ASN
5	D	62	GLN
5	D	123	HIS
5	D	160	GLN
5	D	199	ASN
6	E	72	GLN
6	E	73	ASN
7	F	13	ASN
7	F	18	GLN
7	F	27	GLN
7	F	57	GLN
7	F	73	ASN
7	F	94	GLN
7	F	100	ASN
8	G	37	ASN
8	G	56	GLN
8	G	86	GLN
8	G	106	GLN
8	G	122	HIS
10	I	23	ASN
10	I	38	GLN
10	I	73	GLN
11	J	56	HIS
11	J	62	HIS
11	J	78	ASN
11	J	84	GLN
12	K	22	HIS

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Mol	Chain	Res	Type
12	K	93	GLN
12	K	117	ASN
13	L	49	ASN
13	L	75	HIS
14	M	12	ASN
14	M	40	ASN
14	M	62	ASN
14	M	77	ASN
16	O	13	GLN
16	O	37	ASN
18	Q	16	GLN
18	Q	26	GLN
19	R	36	ASN
20	S	53	ASN
20	S	56	GLN
21	T	42	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1522 (98%)	218 (14%)	0
2	X	5/6 (83%)	0	0
All	All	1511/1528 (98%)	218 (14%)	0

All (218) RNA backbone outliers are listed below:

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

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Mol	Chain	Res	Type
1	A	101	A
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	163	C
1	A	182	U
1	A	190(D)	U
1	A	190(E)	U
1	A	190(F)	G
1	A	195	A
1	A	197	A
1	A	198	G
1	A	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	366	C
1	A	367	U
1	A	373	A
1	A	397	A
1	A	398	C

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Mol	Chain	Res	Type
1	A	412	A
1	A	413	G
1	A	421	U
1	A	429	U
1	A	439	A
1	A	452	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	579	G
1	A	588	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

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Mol	Chain	Res	Type
1	A	723	U
1	A	731	G
1	A	749	C
1	A	755	G
1	A	777	A
1	A	781	A
1	A	782	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	902	G
1	A	913	A
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1005	A
1	A	1023	G
1	A	1026	G
1	A	1050	G
1	A	1053	G

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Mol	Chain	Res	Type
1	A	1054	C
1	A	1055	A
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1085	U
1	A	1086	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1145	C
1	A	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	1201	A
1	A	1202	G
1	A	1211	U
1	A	1212	U
1	A	1213	A
1	A	1215	G
1	A	1224	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1257	U
1	A	1258	G

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Mol	Chain	Res	Type
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1320	C
1	A	1338	G
1	A	1346	A
1	A	1347	G
1	A	1348	U
1	A	1363	A
1	A	1364	U
1	A	1365	G
1	A	1379	G
1	A	1381	U
1	A	1398	A
1	A	1442	G
1	A	1446	A
1	A	1447	G
1	A	1452	C
1	A	1453	G
1	A	1499	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

There are no RNA pucker outliers to report.

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 100 ligands modelled in this entry, 98 are monoatomic - leaving 2 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	$\# Z > 2$
25	TAC	A	1632	23	33,35,35	2.58	18 (54%)	41,58,58	1.01	2 (4%)
25	TAC	A	1633	-	33,35,35	4.45	25 (75%)	41,58,58	1.25	5 (12%)

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
25	TAC	A	1632	23	-	0/8/74/74	0/4/4/4
25	TAC	A	1633	-	-	0/8/74/74	0/4/4/4

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1633	TAC	C9-C10	2.03	1.43	1.39
25	A	1632	TAC	C1A-C10	2.09	1.45	1.41
25	A	1633	TAC	C42-N4	2.10	1.54	1.46
25	A	1632	TAC	C43-N4	2.17	1.54	1.46
25	A	1633	TAC	C8-C9	2.19	1.43	1.38
25	A	1633	TAC	O21-C21	2.23	1.30	1.24
25	A	1632	TAC	C5-C51	2.24	1.58	1.54
25	A	1632	TAC	C7-C61	2.35	1.42	1.39
25	A	1633	TAC	C2-C3	2.36	1.46	1.40
25	A	1632	TAC	O21-C21	2.38	1.30	1.24
25	A	1633	TAC	C1B-C11	2.43	1.52	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1632	TAC	C6-C61	2.50	1.55	1.53
25	A	1632	TAC	C51-C1B	2.59	1.56	1.51
25	A	1633	TAC	C1A-C11	2.70	1.53	1.46
25	A	1632	TAC	C21-N21	2.78	1.41	1.33
25	A	1632	TAC	C8-C7	2.86	1.44	1.38
25	A	1632	TAC	C4-N4	2.86	1.53	1.47
25	A	1633	TAC	C2-C21	2.89	1.53	1.47
25	A	1633	TAC	C5-C51	2.91	1.59	1.54
25	A	1632	TAC	C62-C6	2.94	1.55	1.53
25	A	1633	TAC	C1A-C61	3.29	1.48	1.41
25	A	1633	TAC	C51-C1B	3.36	1.57	1.51
25	A	1632	TAC	O11-C11	3.57	1.31	1.23
25	A	1633	TAC	O6-C6	3.60	1.48	1.43
25	A	1632	TAC	C1C-C41	3.73	1.56	1.53
25	A	1633	TAC	C8-C7	3.74	1.46	1.38
25	A	1632	TAC	O6-C6	3.96	1.49	1.43
25	A	1632	TAC	O1C-C1C	4.08	1.48	1.42
25	A	1633	TAC	C7-C61	4.23	1.45	1.39
25	A	1633	TAC	C1B-C12	4.25	1.41	1.36
25	A	1632	TAC	C4-C3	4.34	1.60	1.52
25	A	1632	TAC	C1C-C1	4.44	1.61	1.55
25	A	1633	TAC	C62-C6	4.49	1.57	1.53
25	A	1633	TAC	O11-C11	4.73	1.33	1.23
25	A	1632	TAC	C1C-C12	4.90	1.56	1.52
25	A	1633	TAC	C1C-C1	4.92	1.62	1.55
25	A	1633	TAC	C1A-C10	5.49	1.50	1.41
25	A	1633	TAC	C4-N4	5.79	1.60	1.47
25	A	1633	TAC	O1C-C1C	5.82	1.50	1.42
25	A	1633	TAC	C4-C3	5.97	1.63	1.52
25	A	1633	TAC	C1C-C41	8.60	1.60	1.53
25	A	1633	TAC	C1C-C12	10.25	1.61	1.52
25	A	1633	TAC	C6-C61	10.90	1.61	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	1633	TAC	O1C-C1C-C1	-2.88	99.37	106.78
25	A	1633	TAC	O21-C21-N21	-2.64	116.50	122.92
25	A	1633	TAC	C1C-C41-C4	-2.16	108.68	111.64
25	A	1632	TAC	C1C-C41-C4	-2.04	108.85	111.64
25	A	1632	TAC	C21-C2-C1	2.43	123.66	120.89
25	A	1633	TAC	O21-C21-C2	2.47	124.57	120.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	1633	TAC	C42-N4-C4	3.45	122.11	114.09

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	A	1632	TAC	1	0
25	A	1633	TAC	3	0

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%)	0.32	75 (4%) 30 27	28, 61, 137, 198	0
2	X	6/6 (100%)	1.06	2 (33%) 0 0	49, 60, 101, 115	0
3	B	234/256 (91%)	-0.06	11 (4%) 32 30	29, 83, 142, 189	0
4	C	206/239 (86%)	-0.21	0 100 100	41, 81, 136, 152	0
5	D	208/209 (99%)	-0.26	0 100 100	34, 65, 117, 161	0
6	E	150/162 (92%)	-0.37	0 100 100	30, 52, 100, 154	0
7	F	101/101 (100%)	-0.13	2 (1%) 65 61	52, 87, 135, 168	0
8	G	155/156 (99%)	-0.22	2 (1%) 77 73	34, 75, 132, 187	0
9	H	138/138 (100%)	-0.37	0 100 100	22, 48, 84, 137	0
10	I	127/128 (99%)	-0.20	1 (0%) 86 82	37, 86, 126, 152	0
11	J	98/105 (93%)	0.08	3 (3%) 49 46	47, 106, 168, 186	0
12	K	119/129 (92%)	-0.29	2 (1%) 70 66	33, 64, 111, 178	0
13	L	124/135 (91%)	-0.22	1 (0%) 86 82	17, 64, 108, 156	0
14	M	125/126 (99%)	0.15	8 (6%) 20 20	43, 80, 146, 194	0
15	N	60/61 (98%)	-0.08	1 (1%) 70 66	47, 77, 127, 153	0
16	O	88/89 (98%)	-0.25	1 (1%) 80 76	32, 66, 126, 186	0
17	P	88/88 (100%)	-0.07	3 (3%) 46 41	32, 55, 144, 198	0
18	Q	104/105 (99%)	0.11	5 (4%) 31 28	29, 58, 126, 198	0
19	R	73/88 (82%)	-0.00	4 (5%) 26 24	42, 69, 143, 187	0
20	S	80/93 (86%)	0.17	3 (3%) 41 37	64, 100, 151, 189	0
21	T	99/106 (93%)	-0.22	1 (1%) 82 78	36, 65, 110, 161	0
22	V	24/26 (92%)	-0.28	1 (4%) 37 34	36, 71, 104, 118	0
All	All	3913/4068 (96%)	0.03	126 (3%) 48 45	17, 67, 138, 198	0

All (126) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
18	Q	103	GLY	13.4
18	Q	105	ALA	13.2
18	Q	104	LYS	12.1
18	Q	102	GLY	9.9
14	M	124	PRO	9.3
1	A	1129	C	8.7
14	M	123	ALA	8.1
12	K	129	SER	6.0
17	P	87	GLY	5.8
1	A	1006	C	5.1
1	A	1029	C	5.0
14	M	125	ARG	5.0
1	A	1030	C	4.8
1	A	1533	C	4.7
17	P	88	ALA	4.6
1	A	1036	G	4.6
1	A	1030(A)	G	4.6
1	A	1023	G	4.5
1	A	1033	G	4.4
1	A	1030(B)	C	4.4
14	M	121	LYS	4.4
1	A	1137	C	4.3
1	A	1278	U	4.3
1	A	1135	U	4.2
1	A	1026	G	4.2
14	M	120	LYS	4.2
1	A	1277	C	4.2
1	A	1027	C	4.2
1	A	1024	G	4.1
7	F	101	ALA	4.1
1	A	1492	A	3.9
1	A	840	C	3.9
1	A	1531	A	3.8
3	B	122	PHE	3.8
1	A	1037	C	3.8
1	A	1022	G	3.7
1	A	159	G	3.7
1	A	1001	A	3.7
1	A	1442	G	3.7
19	R	16	PRO	3.6
16	O	89	GLY	3.5
1	A	1032	G	3.5
1	A	1030(C)	G	3.5

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Mol	Chain	Res	Type	RSRZ
14	M	126	LYS	3.5
1	A	1034	G	3.5
1	A	158	G	3.4
1	A	1043	C	3.3
1	A	1144	G	3.3
1	A	1140	C	3.3
3	B	125	PRO	3.2
1	A	1028	C	3.1
2	X	2	U	3.1
1	A	1030(D)	A	3.1
1	A	1035	A	3.1
1	A	1011	G	3.0
1	A	841	U	3.0
1	A	1421	G	3.0
19	R	28	GLU	3.0
3	B	238	LEU	3.0
1	A	1005	A	3.0
1	A	1010	G	3.0
7	F	14	LEU	2.9
3	B	228	GLY	2.9
1	A	1138	G	2.9
8	G	81	GLY	2.9
1	A	1139	G	2.8
1	A	1532	U	2.8
1	A	1021	G	2.7
1	A	1124	G	2.7
14	M	7	VAL	2.7
1	A	1134	G	2.7
11	J	33	GLN	2.6
1	A	216	G	2.6
1	A	1031	G	2.6
1	A	1175	G	2.6
1	A	991	U	2.6
1	A	1007	C	2.5
2	X	1	C	2.5
1	A	1133	G	2.5
1	A	160	A	2.5
3	B	124	SER	2.5
19	R	17	SER	2.5
1	A	838	G	2.5
1	A	993	G	2.5
1	A	1493	A	2.5

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Mol	Chain	Res	Type	RSRZ
17	P	83	GLU	2.5
18	Q	101	ARG	2.5
1	A	1276	G	2.4
3	B	118	LEU	2.4
1	A	1025	U	2.4
1	A	1143	G	2.4
1	A	1474	G	2.4
3	B	121	LEU	2.4
1	A	161	A	2.4
1	A	81	U	2.4
1	A	1136	U	2.3
1	A	1002	G	2.3
1	A	1482	G	2.3
21	T	106	ALA	2.3
1	A	1018	C	2.3
1	A	1484	C	2.3
12	K	89	ALA	2.3
1	A	190(B)	C	2.3
20	S	29	ARG	2.3
1	A	1019	C	2.3
1	A	343	U	2.3
11	J	81	THR	2.2
3	B	229	VAL	2.2
1	A	478	A	2.2
20	S	27	GLU	2.2
1	A	990	C	2.2
3	B	230	VAL	2.2
10	I	128	ARG	2.1
3	B	126	GLU	2.1
15	N	18	VAL	2.1
1	A	266	G	2.1
19	R	18	ARG	2.1
1	A	346	G	2.1
1	A	1017	G	2.1
8	G	85	TYR	2.1
20	S	26	GLY	2.1
13	L	33	ARG	2.0
22	V	25	LYS	2.0
14	M	20	THR	2.0
3	B	231	GLU	2.0
11	J	89	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å ²)	Q<0.9
23	MG	A	1599	1/1	0.98	0.71	36.87	35,35,35,35	0
23	MG	A	1628	1/1	0.80	0.74	19.82	35,35,35,35	1
23	MG	A	1602	1/1	0.94	0.39	18.95	35,35,35,35	0
23	MG	A	1606	1/1	0.97	0.82	17.29	35,35,35,35	0
23	MG	A	1557	1/1	0.97	0.54	17.11	35,35,35,35	0
23	MG	A	1562	1/1	0.94	0.42	15.82	35,35,35,35	0
23	MG	A	1553	1/1	0.97	0.58	12.96	35,35,35,35	0
23	MG	A	1604	1/1	0.98	0.47	11.72	35,35,35,35	0
23	MG	A	1625	1/1	0.95	0.34	11.14	35,35,35,35	0
23	MG	A	211	1/1	0.53	0.37	7.27	35,35,35,35	0
23	MG	A	1592	1/1	0.96	0.31	4.84	35,35,35,35	0
25	TAC	A	1633	32/32	0.84	0.37	4.71	19,19,19,19	0
23	MG	A	1613	1/1	0.70	0.30	4.60	35,35,35,35	1
23	MG	A	1594	1/1	0.98	0.30	4.52	35,35,35,35	0
23	MG	A	1587	1/1	0.95	0.31	3.98	35,35,35,35	0
23	MG	A	1580	1/1	0.83	0.26	3.32	35,35,35,35	0
23	MG	A	1612	1/1	0.67	0.42	3.20	35,35,35,35	1
23	MG	A	1600	1/1	0.92	0.26	2.74	35,35,35,35	1
23	MG	A	1575	1/1	0.89	0.29	2.59	35,35,35,35	1
23	MG	A	1619	1/1	0.92	0.26	2.58	35,35,35,35	0
23	MG	A	1624	1/1	0.99	0.24	2.17	35,35,35,35	1
23	MG	A	1576	1/1	0.96	0.43	1.70	35,35,35,35	0
25	TAC	A	1632	32/32	0.92	0.26	1.28	19,19,19,19	0
23	MG	A	1566	1/1	0.74	0.23	0.77	35,35,35,35	0
23	MG	A	1577	1/1	0.95	0.23	0.53	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
24	ZN	D	300	1/1	0.99	0.30	0.31	44,44,44,44	0
23	MG	A	1570	1/1	0.92	0.18	-0.04	35,35,35,35	1
23	MG	A	1591	1/1	0.88	0.17	-0.11	35,35,35,35	0
24	ZN	N	190	1/1	0.99	0.14	-0.55	44,44,44,44	1
23	MG	D	215	1/1	0.83	0.17	-0.61	35,35,35,35	1
23	MG	A	1560	1/1	0.90	0.17	-0.98	35,35,35,35	0
23	MG	A	1603	1/1	0.78	0.17	-1.16	35,35,35,35	1
23	MG	A	1618	1/1	0.90	0.17	-1.24	35,35,35,35	1
23	MG	A	1605	1/1	0.92	0.14	-1.59	35,35,35,35	0
23	MG	A	1578	1/1	0.97	0.14	-2.09	35,35,35,35	0
23	MG	A	1610	1/1	0.82	0.12	-2.10	35,35,35,35	1
23	MG	A	1598	1/1	0.91	0.12	-3.19	35,35,35,35	0
23	MG	A	1589	1/1	0.91	0.16	-	35,35,35,35	0
23	MG	A	1559	1/1	0.91	0.20	-	35,35,35,35	0
23	MG	A	1584	1/1	0.71	0.33	-	35,35,35,35	1
23	MG	A	1551	1/1	0.92	0.72	-	35,35,35,35	0
23	MG	A	1595	1/1	0.94	0.27	-	35,35,35,35	1
23	MG	A	1571	1/1	0.97	0.54	-	35,35,35,35	0
23	MG	A	1586	1/1	0.94	0.17	-	35,35,35,35	0
23	MG	A	1554	1/1	0.93	0.62	-	35,35,35,35	0
23	MG	A	1555	1/1	0.92	0.66	-	35,35,35,35	0
23	MG	A	1622	1/1	0.69	0.72	-	35,35,35,35	1
23	MG	A	1565	1/1	0.98	0.44	-	35,35,35,35	0
23	MG	A	1601	1/1	0.96	0.55	-	35,35,35,35	0
23	MG	A	1609	1/1	0.86	0.34	-	35,35,35,35	1
23	MG	A	210	1/1	0.80	0.32	-	35,35,35,35	1
23	MG	A	1620	1/1	0.99	0.12	-	35,35,35,35	1
23	MG	A	1593	1/1	0.95	0.41	-	35,35,35,35	0
23	MG	A	1582	1/1	0.96	0.23	-	35,35,35,35	0
23	MG	A	1597	1/1	0.96	0.16	-	35,35,35,35	1
23	MG	A	1627	1/1	0.99	0.24	-	35,35,35,35	1
23	MG	A	1607	1/1	0.89	0.35	-	35,35,35,35	0
23	MG	A	1546	1/1	0.97	0.49	-	35,35,35,35	0
23	MG	A	1596	1/1	0.86	0.15	-	35,35,35,35	0
23	MG	A	1549	1/1	0.76	0.16	-	35,35,35,35	1
23	MG	A	1561	1/1	0.95	0.24	-	35,35,35,35	0
23	MG	A	1630	1/1	0.97	0.64	-	35,35,35,35	1
23	MG	A	1617	1/1	0.76	0.31	-	35,35,35,35	1
23	MG	A	1615	1/1	0.97	0.30	-	35,35,35,35	0
23	MG	A	1550	1/1	0.36	0.84	-	35,35,35,35	1
23	MG	A	1579	1/1	0.93	0.22	-	35,35,35,35	0
23	MG	A	1631	1/1	0.95	0.06	-	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
23	MG	A	212	1/1	0.91	1.45	-	35,35,35,35	1
23	MG	A	1588	1/1	0.95	0.27	-	35,35,35,35	0
23	MG	A	1545	1/1	0.92	0.12	-	35,35,35,35	1
23	MG	A	1574	1/1	0.97	0.29	-	35,35,35,35	0
23	MG	A	1567	1/1	0.93	0.36	-	35,35,35,35	0
23	MG	A	1621	1/1	0.94	0.60	-	35,35,35,35	1
23	MG	A	1585	1/1	0.96	0.29	-	35,35,35,35	0
23	MG	A	1547	1/1	0.97	0.61	-	35,35,35,35	0
23	MG	A	1556	1/1	0.95	0.28	-	35,35,35,35	1
23	MG	A	214	1/1	0.95	0.20	-	35,35,35,35	0
23	MG	A	1552	1/1	0.98	0.20	-	35,35,35,35	0
23	MG	A	1614	1/1	0.92	1.38	-	35,35,35,35	1
23	MG	A	1608	1/1	0.70	0.77	-	35,35,35,35	1
23	MG	A	71	1/1	0.93	0.20	-	35,35,35,35	0
23	MG	A	1616	1/1	0.96	0.20	-	35,35,35,35	1
23	MG	A	1563	1/1	0.88	0.09	-	35,35,35,35	0
23	MG	A	1581	1/1	0.88	0.49	-	35,35,35,35	1
23	MG	A	1558	1/1	0.96	0.41	-	35,35,35,35	0
23	MG	A	86	1/1	0.98	0.52	-	35,35,35,35	0
23	MG	A	1629	1/1	0.98	0.75	-	35,35,35,35	1
23	MG	A	1573	1/1	0.98	0.27	-	35,35,35,35	0
23	MG	A	1590	1/1	0.96	0.45	-	35,35,35,35	0
23	MG	A	1548	1/1	0.77	0.47	-	35,35,35,35	0
23	MG	A	1623	1/1	0.66	0.20	-	35,35,35,35	1
23	MG	A	1564	1/1	0.96	0.16	-	35,35,35,35	0
23	MG	A	87	1/1	0.97	0.32	-	35,35,35,35	1
23	MG	A	1611	1/1	0.79	0.41	-	35,35,35,35	1
23	MG	A	1572	1/1	0.95	0.47	-	35,35,35,35	0
23	MG	A	1568	1/1	0.89	0.35	-	35,35,35,35	0
23	MG	A	1569	1/1	0.97	0.34	-	35,35,35,35	1
23	MG	A	1583	1/1	0.98	0.40	-	35,35,35,35	0
23	MG	H	213	1/1	0.81	0.59	-	35,35,35,35	1
23	MG	A	1626	1/1	0.93	0.34	-	35,35,35,35	1

6.5 Other polymers [i](#)

There are no such residues in this entry.