



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:33 PM GMT

PDB ID : 1G59
Title : GLUTAMYL-TRNA SYNTHETASE COMPLEXED WITH TRNA(GLU).
Authors : Sekine, S.; Nureki, O.; Shimada, A.; Vassilyev, D.G.; Yokoyama, S.; RIKEN
Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2000-10-31
Resolution : 2.40 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

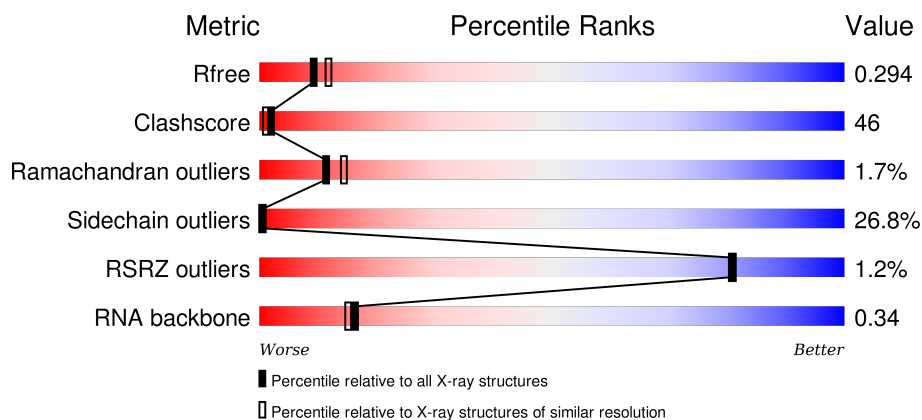
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)
RNA backbone	2183	1073 (2.90-1.90)

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	B	75	<div> <div>3%</div> <div>20% 51% 27%</div> </div>
1	D	75	<div> <div>%</div> <div>25% 48% 24%</div> </div>
2	A	468	<div> <div>38% 46% 16%</div> </div>
2	C	468	<div> <div>2%</div> <div>37% 44% 19%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11092 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 TRNA(GLU).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	75	Total	C	N	O	P	0	0	0
			1597	711	284	527	75			
1	D	75	Total	C	N	O	P	0	0	0
			1597	711	284	527	75			

- Molecule 2 is a protein called GLUTAMYL-TRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	468	Total	C	N	O	S	0	0	0
			3813	2443	674	688	8			
2	C	468	Total	C	N	O	S	0	0	0
			3813	2443	674	688	8			

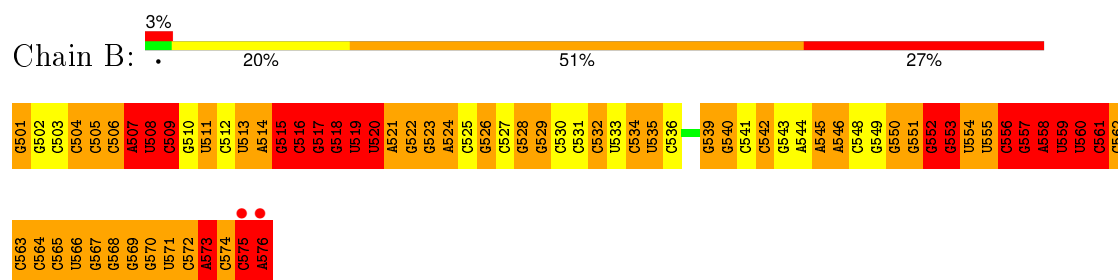
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	107	Total	O	0	0
			107	107		
3	B	34	Total	O	0	0
			34	34		
3	C	92	Total	O	0	0
			92	92		
3	D	39	Total	O	0	0
			39	39		

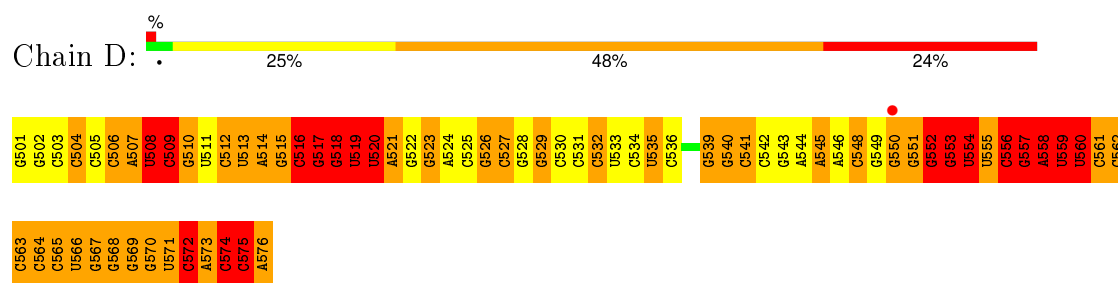
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). 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.

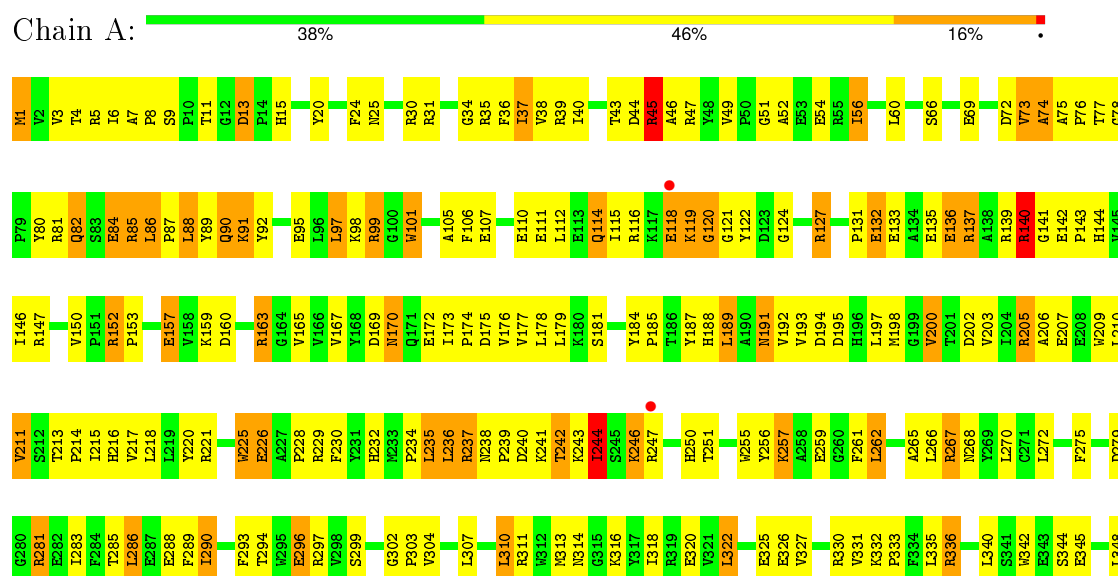
• Molecule 1: TRNA(GLU)

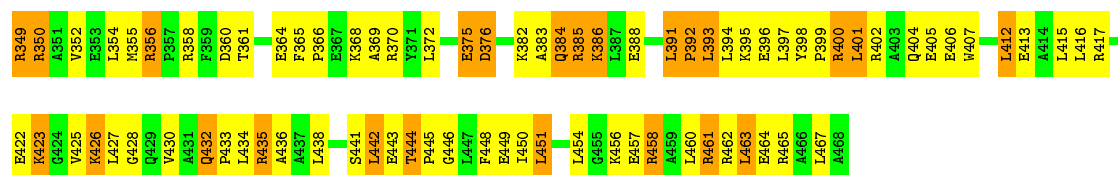


• Molecule 1: TRNA(GLU)



• Molecule 2: GLUTAMYL-TRNA SYNTHETASE





• Molecule 2: GLUTAMYL-TRNA SYNTHETASE



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	109.98Å 218.67Å 134.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40 49.13 – 2.40	Depositor EDS
% Data completeness (in resolution range)	88.4 (30.00-2.40) 88.4 (49.13-2.40)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4437.30 (at 2.39Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.218 , 0.298 0.219 , 0.294	Depositor DCC
R_{free} test set	2846 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	29.2	Xtriage
Anisotropy	0.388	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 71.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 56243 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11092	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.32% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	B	1.70	18/1782 (1.0%)	1.82	53/2774 (1.9%)
1	D	1.78	25/1782 (1.4%)	1.84	54/2774 (1.9%)
2	A	0.52	0/3908	0.67	1/5292 (0.0%)
2	C	0.49	0/3908	0.64	0/5292
All	All	1.06	43/11380 (0.4%)	1.20	108/16132 (0.7%)

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	D	0	1
2	C	0	1
All	All	0	2

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	557	G	P-O5'	8.93	1.68	1.59
1	B	557	G	P-O5'	6.88	1.66	1.59
1	B	526	G	C3'-C2'	-6.76	1.45	1.52
1	D	549	G	C3'-C2'	-6.44	1.45	1.52
1	B	555	U	C3'-C2'	-6.19	1.46	1.52
1	B	536	C	C3'-C2'	-6.03	1.46	1.52
1	B	549	G	C3'-C2'	-5.97	1.46	1.52
1	D	535	U	C3'-C2'	-5.97	1.46	1.52
1	D	514	A	C3'-C2'	-5.88	1.46	1.52
1	B	522	G	C3'-C2'	-5.82	1.46	1.52
1	B	517	G	O3'-P	5.81	1.68	1.61
1	D	518	G	C5'-C4'	5.81	1.58	1.51
1	D	522	G	C3'-C2'	-5.74	1.46	1.52
1	D	512	C	C3'-C2'	-5.69	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	505	C	P-O5'	5.65	1.65	1.59
1	B	511	U	C3'-C2'	-5.63	1.46	1.52
1	B	523	G	C3'-C2'	-5.56	1.46	1.52
1	B	518	G	P-O5'	5.54	1.65	1.59
1	D	555	U	C3'-C2'	-5.54	1.46	1.52
1	D	504	C	C3'-C2'	-5.54	1.46	1.52
1	B	504	C	C3'-C2'	-5.51	1.46	1.52
1	B	540	G	C3'-C2'	-5.51	1.46	1.52
1	B	556	C	C4'-C3'	-5.50	1.47	1.52
1	B	524	A	C3'-C2'	-5.47	1.46	1.52
1	D	557	G	O3'-P	5.42	1.67	1.61
1	D	558	A	O3'-P	5.41	1.67	1.61
1	B	535	U	C3'-C2'	-5.40	1.46	1.52
1	D	541	C	C3'-C2'	-5.38	1.46	1.52
1	D	568	G	C3'-C2'	-5.36	1.46	1.52
1	D	554	U	C3'-C2'	-5.33	1.46	1.52
1	D	536	C	C3'-C2'	-5.29	1.47	1.52
1	D	508	U	C3'-C2'	-5.23	1.47	1.52
1	D	555	U	P-O5'	5.22	1.65	1.59
1	D	556	C	C4-C5	5.17	1.47	1.43
1	D	526	G	C3'-C2'	-5.17	1.47	1.52
1	D	506	C	C3'-C2'	-5.17	1.47	1.52
1	D	545	A	C3'-C2'	-5.16	1.47	1.52
1	D	510	G	C3'-C2'	-5.11	1.47	1.52
1	B	535	U	C4'-C3'	-5.11	1.47	1.52
1	B	569	G	C3'-C2'	-5.05	1.47	1.52
1	D	527	C	C3'-C2'	-5.05	1.47	1.52
1	D	558	A	C3'-O3'	5.04	1.49	1.42
1	D	528	G	C4'-C3'	-5.02	1.47	1.52

All (108) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	556	C	C3'-C2'-C1'	6.89	107.02	101.50
1	D	576	A	C3'-C2'-C1'	6.67	106.83	101.50
1	D	557	G	C3'-C2'-C1'	6.64	106.81	101.50
1	D	558	A	C3'-C2'-C1'	6.49	106.69	101.50
1	B	576	A	C3'-C2'-C1'	6.41	106.63	101.50
1	D	575	C	C3'-C2'-C1'	6.41	106.63	101.50
1	D	572	C	C3'-C2'-C1'	6.37	106.60	101.50
1	B	515	G	C3'-C2'-C1'	6.37	106.59	101.50
1	D	515	G	C3'-C2'-C1'	6.28	106.52	101.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	556	C	C3'-C2'-C1'	6.26	106.51	101.50
1	D	560	U	C3'-C2'-C1'	6.25	106.50	101.50
1	B	517	G	C3'-C2'-C1'	6.25	106.50	101.50
1	B	518	G	C3'-C2'-C1'	6.24	106.49	101.50
1	D	518	G	C3'-C2'-C1'	6.22	106.47	101.50
1	D	557	G	N9-C1'-C2'	-6.22	105.16	112.00
1	B	575	C	C3'-C2'-C1'	6.14	106.41	101.50
1	B	573	A	C3'-C2'-C1'	6.08	106.36	101.50
1	B	558	A	C3'-C2'-C1'	6.05	106.34	101.50
1	D	520	U	C3'-C2'-C1'	6.03	106.32	101.50
1	D	517	G	C3'-C2'-C1'	5.98	106.29	101.50
1	D	559	U	C3'-C2'-C1'	5.91	106.23	101.50
1	D	569	G	C3'-C2'-C1'	5.87	106.20	101.50
1	B	563	C	C3'-C2'-C1'	5.84	106.17	101.50
1	D	563	C	C3'-C2'-C1'	5.83	106.17	101.50
1	D	532	C	C3'-C2'-C1'	5.81	106.15	101.50
1	D	574	C	C3'-C2'-C1'	5.81	106.15	101.50
1	B	520	U	C3'-C2'-C1'	5.80	106.14	101.50
1	D	571	U	C3'-C2'-C1'	5.78	106.13	101.50
1	D	570	G	C3'-C2'-C1'	5.77	106.12	101.50
1	D	506	C	C3'-C2'-C1'	5.76	106.11	101.50
1	D	541	C	O4'-C1'-N1	5.75	112.80	108.20
1	B	533	U	C3'-C2'-C1'	5.74	106.09	101.50
1	B	529	G	O4'-C1'-N9	5.74	112.79	108.20
1	D	567	G	C3'-C2'-C1'	5.74	106.09	101.50
1	B	507	A	C3'-C2'-C1'	5.72	106.07	101.50
1	D	552	G	C3'-C2'-C1'	5.67	106.04	101.50
1	D	573	A	C3'-C2'-C1'	5.65	106.02	101.50
1	D	571	U	O4'-C1'-N1	5.62	112.70	108.20
1	D	529	G	O4'-C1'-N9	5.62	112.70	108.20
1	D	519	U	C3'-C2'-C1'	5.59	105.97	101.50
1	D	514	A	C3'-C2'-C1'	5.57	105.96	101.50
1	B	519	U	C3'-C2'-C1'	5.57	105.95	101.50
1	D	564	C	C3'-C2'-C1'	5.53	105.92	101.50
1	B	506	C	C3'-C2'-C1'	5.52	105.92	101.50
1	B	532	C	C3'-C2'-C1'	5.51	105.91	101.50
1	B	560	U	O4'-C1'-N1	5.50	112.60	108.20
1	D	561	C	C3'-C2'-C1'	5.50	105.90	101.50
1	D	545	A	O4'-C1'-N9	5.47	112.58	108.20
1	B	559	U	C3'-C2'-C1'	5.44	105.85	101.50
1	B	566	U	C3'-C2'-C1'	5.44	105.85	101.50
1	B	540	G	C3'-C2'-C1'	5.42	105.84	101.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	550	G	C3'-C2'-C1'	5.42	105.83	101.50
1	B	539	G	C3'-C2'-C1'	5.42	105.83	101.50
1	B	545	A	N9-C1'-C2'	-5.41	106.05	112.00
1	D	553	G	C3'-C2'-C1'	5.41	105.83	101.50
1	D	558	A	P-O3'-C3'	5.38	126.16	119.70
1	B	560	U	C3'-C2'-C1'	5.38	105.80	101.50
1	D	568	G	C3'-C2'-C1'	5.35	105.78	101.50
1	D	507	A	C3'-C2'-C1'	5.35	105.78	101.50
1	B	568	G	C3'-C2'-C1'	5.34	105.77	101.50
1	B	551	G	C3'-C2'-C1'	5.33	105.77	101.50
1	B	513	U	O4'-C1'-N1	5.33	112.47	108.20
1	B	552	G	C3'-C2'-C1'	5.33	105.76	101.50
1	D	562	C	C3'-C2'-C1'	5.33	105.76	101.50
1	D	504	C	O4'-C1'-N1	5.33	112.46	108.20
1	B	562	C	C3'-C2'-C1'	5.31	105.75	101.50
1	D	504	C	C3'-C2'-C1'	5.31	105.75	101.50
1	D	533	U	C3'-C2'-C1'	5.29	105.73	101.50
1	B	567	G	C3'-C2'-C1'	5.29	105.73	101.50
1	D	509	C	C3'-C2'-C1'	5.29	105.73	101.50
1	B	570	G	C3'-C2'-C1'	5.28	105.72	101.50
1	D	550	G	O4'-C1'-N9	5.27	112.41	108.20
1	B	508	U	C3'-C2'-C1'	5.27	105.71	101.50
1	B	516	C	P-O3'-C3'	5.26	126.02	119.70
1	B	571	U	C3'-C2'-C1'	5.26	105.71	101.50
1	D	526	G	O4'-C1'-N9	5.26	112.41	108.20
1	B	528	G	O4'-C1'-N9	5.26	112.41	108.20
1	D	551	G	C3'-C2'-C1'	5.25	105.70	101.50
1	B	504	C	C3'-C2'-C1'	5.24	105.69	101.50
1	B	555	U	O4'-C1'-N1	5.24	112.39	108.20
1	B	514	A	C3'-C2'-C1'	5.23	105.69	101.50
1	D	560	U	O4'-C1'-N1	5.23	112.39	108.20
1	B	553	G	C3'-C2'-C1'	5.23	105.68	101.50
1	B	545	A	O4'-C1'-N9	5.21	112.37	108.20
1	B	564	C	C3'-C2'-C1'	5.21	105.67	101.50
1	B	546	A	C3'-C2'-C1'	5.18	105.65	101.50
1	D	539	G	C3'-C2'-C1'	5.18	105.64	101.50
1	D	523	G	C3'-C2'-C1'	5.17	105.64	101.50
1	B	550	G	C3'-C2'-C1'	5.17	105.64	101.50
1	D	565	C	C3'-C2'-C1'	5.16	105.63	101.50
1	B	501	G	C3'-C2'-C1'	5.15	105.62	101.50
1	B	524	A	O4'-C1'-N9	5.15	112.32	108.20
1	D	519	U	O4'-C1'-N1	5.12	112.30	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	322	LEU	CA-CB-CG	5.12	127.08	115.30
1	D	566	U	C3'-C2'-C1'	5.12	105.59	101.50
1	D	545	A	N9-C1'-C2'	-5.11	106.38	112.00
1	D	508	U	C3'-C2'-C1'	5.11	105.59	101.50
1	D	540	G	C3'-C2'-C1'	5.09	105.57	101.50
1	B	561	C	C3'-C2'-C1'	5.09	105.57	101.50
1	B	523	G	C3'-C2'-C1'	5.08	105.56	101.50
1	B	504	C	O4'-C1'-N1	5.07	112.25	108.20
1	B	572	C	C3'-C2'-C1'	5.06	105.55	101.50
1	D	516	C	C3'-C2'-C1'	5.05	105.54	101.50
1	B	542	C	O4'-C1'-N1	5.03	112.22	108.20
1	B	509	C	C3'-C2'-C1'	5.03	105.52	101.50
1	B	513	U	C3'-C2'-C1'	5.02	105.52	101.50
1	B	565	C	C3'-C2'-C1'	5.02	105.52	101.50
1	B	523	G	O4'-C1'-N9	5.02	112.22	108.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	269	TYR	Sidechain
1	D	557	G	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1597	0	813	140	0
1	D	1597	0	813	159	0
2	A	3813	0	3822	314	0
2	C	3813	0	3822	339	0
3	A	107	0	0	15	0
3	B	34	0	0	1	0
3	C	92	0	0	8	0
3	D	39	0	0	4	0
All	All	11092	0	9270	929	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 46.

All (929) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:517:G:N2	1:D:557:G:H2'	1.47	1.28
1:B:575:C:H5''	2:A:47:ARG:HH21	1.08	1.16
2:C:37:ILE:HG23	2:C:69:GLU:HB2	1.33	1.10
2:A:445:PRO:HG2	2:A:450:ILE:HD11	1.11	1.09
2:A:4:THR:HB	2:A:25:ASN:HD22	1.21	1.02
2:C:4:THR:HB	2:C:25:ASN:HD22	1.23	1.00
2:C:240:ASP:OD1	2:C:242:THR:HG22	1.61	0.99
2:C:262:LEU:H	2:C:314:ASN:HD21	1.03	0.99
2:C:267:ARG:HD2	2:C:286:LEU:HG	1.43	0.99
2:A:262:LEU:H	2:A:314:ASN:HD21	1.05	0.98
1:D:563:C:H2'	1:D:564:C:C6	1.99	0.98
2:A:112:LEU:HD23	2:A:115:ILE:HD12	1.41	0.97
1:D:574:C:H4'	1:D:575:C:OP1	1.62	0.96
1:B:550:G:O2'	1:B:551:G:H5'	1.66	0.95
2:A:460:LEU:O	2:A:464:GLU:HG3	1.66	0.94
2:A:77:THR:HG21	2:A:198:MET:HA	1.51	0.93
2:C:130:PRO:HG2	2:C:133:GLU:HB2	1.47	0.93
2:A:1:MET:HE3	2:A:35:ARG:HD3	1.50	0.93
1:D:535:U:H4'	2:C:432:GLN:HE22	1.34	0.93
1:B:556:C:C2'	1:B:557:G:H5''	1.99	0.92
1:D:550:G:O2'	1:D:551:G:H5'	1.67	0.92
2:A:445:PRO:HG2	2:A:450:ILE:CD1	2.00	0.92
2:C:238:ASN:HD22	2:C:242:THR:HG23	1.34	0.92
1:B:557:G:H5'	1:B:557:G:H8	1.33	0.91
2:A:375:GLU:HG3	2:A:465:ARG:NH1	1.86	0.91
2:A:205:ARG:HD3	2:A:232:HIS:CE1	2.06	0.90
1:D:556:C:O2	1:D:556:C:H2'	1.72	0.89
2:A:205:ARG:HD3	2:A:232:HIS:HE1	1.38	0.89
2:A:294:THR:HG22	2:A:296:GLU:H	1.37	0.89
2:A:111:GLU:O	2:A:115:ILE:HG13	1.72	0.88
2:C:137:ARG:O	2:C:142:GLU:HB2	1.72	0.88
2:C:75:ALA:HB3	2:C:80:TYR:CZ	2.09	0.88
2:A:404:GLN:HG3	2:A:415:LEU:HD22	1.54	0.88
2:A:153:PRO:HD2	3:A:506:HOH:O	1.74	0.88
2:A:205:ARG:HG3	2:A:209:TRP:HD1	1.39	0.88
1:B:563:C:H2'	1:B:564:C:C6	2.09	0.86
2:C:307:LEU:O	2:C:311:ARG:HG3	1.74	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:369:ALA:HB1	2:C:372:LEU:HD12	1.56	0.85
2:A:398:TYR:HD1	2:A:463:LEU:HD11	1.41	0.85
1:B:517:G:N2	1:B:557:G:H2'	1.92	0.84
2:A:349:ARG:HG2	2:A:349:ARG:HH21	1.41	0.84
2:A:444:THR:HG23	2:A:445:PRO:HD2	1.57	0.84
2:A:384:GLN:HE21	2:A:388:GLU:HG3	1.41	0.84
1:D:564:C:H2'	1:D:565:C:H6	1.43	0.83
2:C:3:VAL:CG1	2:C:37:ILE:HD11	2.08	0.83
2:C:463:LEU:C	2:C:463:LEU:HD23	1.99	0.82
2:A:404:GLN:CG	2:A:415:LEU:HD22	2.10	0.82
1:B:556:C:H2'	1:B:557:G:H5''	1.61	0.82
2:A:407:TRP:CE2	2:A:456:LYS:HA	2.14	0.81
2:A:152:ARG:HH11	2:A:152:ARG:HA	1.44	0.81
1:D:563:C:H2'	1:D:564:C:H6	1.40	0.81
2:C:237:ARG:NH1	2:C:302:GLY:HA3	1.96	0.81
1:D:564:C:H2'	1:D:565:C:C6	2.16	0.81
2:A:73:VAL:HG12	2:A:73:VAL:O	1.81	0.81
1:D:565:C:H2'	1:D:566:U:C6	2.16	0.80
2:A:333:PRO:HD3	3:A:493:HOH:O	1.81	0.80
2:C:205:ARG:HG3	2:C:209:TRP:HD1	1.46	0.80
1:D:535:U:C4'	2:C:432:GLN:HE22	1.94	0.80
2:C:137:ARG:HH11	2:C:137:ARG:HB3	1.46	0.80
2:C:325:GLU:HG3	2:C:349:ARG:HE	1.43	0.80
1:D:555:U:H5''	3:D:247:HOH:O	1.82	0.80
1:D:517:G:H21	1:D:557:G:H2'	1.46	0.80
2:C:95:GLU:O	2:C:99:ARG:HB2	1.82	0.80
2:A:391:LEU:HD23	2:A:395:LYS:HE3	1.63	0.79
2:C:157:GLU:HG2	2:C:167:VAL:HG22	1.63	0.79
2:A:267:ARG:HD3	3:A:529:HOH:O	1.82	0.79
2:A:205:ARG:HG3	2:A:209:TRP:CD1	2.18	0.79
1:B:570:G:H2'	1:B:571:U:C6	2.18	0.79
2:A:30:ARG:HB3	2:A:290:ILE:HD13	1.65	0.78
2:C:262:LEU:N	2:C:314:ASN:HD21	1.81	0.78
1:D:553:G:C2'	1:D:554:U:H5'	2.13	0.78
2:A:397:LEU:HG	2:A:401:LEU:HD21	1.64	0.78
1:B:566:U:O2'	1:B:567:G:H5'	1.82	0.78
2:A:226:GLU:HA	3:A:547:HOH:O	1.84	0.77
1:D:517:G:N2	1:D:557:G:C2'	2.39	0.77
2:C:205:ARG:HD3	2:C:232:HIS:CE1	2.18	0.77
2:A:445:PRO:CG	2:A:450:ILE:HD11	2.06	0.77
2:C:2:VAL:HG21	2:C:32:ASN:HD22	1.48	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:262:LEU:H	2:A:314:ASN:ND2	1.81	0.77
1:B:562:C:O2'	1:B:563:C:H5'	1.84	0.77
1:D:519:U:H2'	1:D:521:A:OP2	1.84	0.77
1:D:556:C:H5'	3:D:255:HOH:O	1.84	0.76
1:D:512:C:OP1	2:C:304:VAL:HG23	1.84	0.76
2:A:236:LEU:O	2:A:244:ILE:HG13	1.85	0.76
2:C:454:LEU:O	2:C:458:ARG:HD3	1.84	0.76
2:C:385:ARG:O	2:C:389:GLU:HB2	1.85	0.76
1:B:575:C:H5''	2:A:47:ARG:NH2	1.94	0.76
2:A:261:PHE:CE2	2:A:310:LEU:HD13	2.21	0.76
2:C:169:ASP:O	2:C:172:GLU:HG3	1.85	0.76
1:B:565:C:O2'	1:B:566:U:H5'	1.85	0.76
2:C:137:ARG:HH11	2:C:137:ARG:CB	1.99	0.76
1:B:564:C:H2'	1:B:565:C:C6	2.20	0.75
2:A:95:GLU:O	2:A:99:ARG:HB2	1.87	0.75
2:A:454:LEU:HD23	2:A:458:ARG:HE	1.52	0.75
1:B:558:A:H4'	1:B:559:U:OP1	1.85	0.75
1:B:564:C:H2'	1:B:565:C:H6	1.51	0.75
1:D:567:G:O2'	1:D:568:G:H5'	1.87	0.74
1:B:563:C:H2'	1:B:564:C:H6	1.52	0.74
2:C:262:LEU:HD22	2:C:330:ARG:HH11	1.50	0.74
2:C:236:LEU:HB2	2:C:244:ILE:HD11	1.67	0.74
2:A:163:ARG:NH2	2:A:232:HIS:O	2.20	0.74
2:C:393:LEU:HD22	2:C:419:PHE:CE1	2.22	0.73
2:A:262:LEU:N	2:A:314:ASN:HD21	1.83	0.73
2:A:383:ALA:HA	2:A:442:LEU:HD22	1.70	0.73
1:B:517:G:O2'	1:B:557:G:N2	2.20	0.73
1:B:569:G:O2'	1:B:570:G:H5'	1.88	0.73
2:C:163:ARG:NH2	2:C:232:HIS:O	2.14	0.73
1:D:565:C:H2'	1:D:566:U:H6	1.52	0.73
2:C:391:LEU:N	2:C:392:PRO:HD2	2.02	0.73
2:C:75:ALA:HB3	2:C:80:TYR:OH	1.89	0.73
1:B:566:U:H2'	1:B:567:G:H8	1.54	0.72
2:A:39:ARG:NH2	2:A:195:ASP:OD2	2.18	0.72
2:C:426:LYS:HB2	2:C:429:GLN:NE2	2.03	0.72
2:C:444:THR:HG23	2:C:445:PRO:HD2	1.71	0.72
2:C:8:PRO:HD2	2:C:39:ARG:O	1.89	0.72
2:C:235:LEU:O	2:C:237:ARG:HD3	1.89	0.72
2:C:393:LEU:HD22	2:C:419:PHE:HE1	1.54	0.72
1:B:576:A:O2'	2:A:181:SER:HB2	1.89	0.72
2:C:106:PHE:CD2	2:C:144:HIS:HB3	2.25	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:349:ARG:NH2	2:A:349:ARG:HG2	1.99	0.72
2:A:375:GLU:HG3	2:A:465:ARG:HH12	1.55	0.72
1:B:512:C:OP1	2:A:304:VAL:HG23	1.89	0.72
1:D:562:C:O2'	1:D:563:C:H5'	1.90	0.71
1:B:544:A:O2'	1:B:545:A:H5'	1.91	0.71
2:A:262:LEU:HD13	2:A:330:ARG:NH1	2.05	0.71
1:B:557:G:C8	1:B:557:G:H5'	2.23	0.71
2:C:157:GLU:CG	2:C:167:VAL:HG22	2.21	0.71
2:C:391:LEU:O	2:C:395:LYS:HG2	1.90	0.71
1:B:553:G:C2'	1:B:554:U:H5'	2.21	0.71
2:C:445:PRO:HG2	2:C:450:ILE:HD11	1.72	0.71
2:C:158:VAL:HG22	2:C:217:VAL:HG11	1.72	0.71
2:C:110:GLU:O	2:C:114:GLN:HG2	1.90	0.71
1:D:557:G:H8	1:D:557:G:H5'	1.56	0.70
2:C:355:MET:HE1	2:C:445:PRO:HD3	1.72	0.70
2:C:267:ARG:HD3	3:C:484:HOH:O	1.89	0.70
2:A:348:LEU:O	2:A:352:VAL:HG23	1.90	0.70
1:D:565:C:O2'	1:D:566:U:H5'	1.90	0.70
2:C:4:THR:HB	2:C:25:ASN:ND2	2.03	0.70
2:A:349:ARG:CG	2:A:349:ARG:HH21	2.04	0.70
1:D:561:C:H2'	1:D:562:C:C5	2.26	0.70
2:A:132:GLU:OE2	2:A:132:GLU:HA	1.91	0.70
1:D:556:C:O2'	1:D:557:G:H5''	1.90	0.70
1:D:566:U:H2'	1:D:567:G:H8	1.57	0.70
1:D:569:G:O2'	1:D:570:G:H5'	1.90	0.70
2:C:285:THR:OG1	2:C:288:GLU:HG3	1.91	0.70
2:C:205:ARG:HG3	2:C:209:TRP:CD1	2.26	0.70
2:C:107:GLU:N	2:C:107:GLU:OE2	2.22	0.70
1:D:544:A:O2'	1:D:545:A:H5'	1.92	0.70
2:A:340:LEU:HD21	2:A:370:ARG:NH1	2.06	0.70
2:C:458:ARG:CG	2:C:458:ARG:HH11	2.05	0.70
1:B:570:G:H2'	1:B:571:U:H6	1.57	0.69
2:A:370:ARG:HG3	2:A:370:ARG:HH11	1.55	0.69
2:C:262:LEU:H	2:C:314:ASN:ND2	1.85	0.69
2:A:444:THR:HG23	2:A:445:PRO:CD	2.22	0.69
1:D:566:U:O2'	1:D:567:G:H5'	1.92	0.69
2:C:131:PRO:O	2:C:135:GLU:HG2	1.93	0.69
2:A:75:ALA:HB1	2:A:76:PRO:HD2	1.75	0.69
2:A:81:ARG:HB3	2:A:84:GLU:HG2	1.75	0.69
2:A:365:PHE:HB3	2:A:366:PRO:HD3	1.75	0.69
2:A:116:ARG:HG3	2:A:121:GLY:HA2	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:444:THR:HG22	2:A:445:PRO:O	1.93	0.68
2:A:69:GLU:HB3	2:A:75:ALA:CB	2.23	0.68
2:A:441:SER:O	2:A:442:LEU:HB2	1.91	0.68
2:A:7:ALA:HA	2:A:39:ARG:O	1.93	0.68
2:C:107:GLU:HB2	2:C:112:LEU:HD21	1.76	0.68
2:A:56:ILE:O	2:A:60:LEU:HG	1.94	0.68
2:A:11:THR:HG22	2:A:47:ARG:O	1.93	0.68
2:A:463:LEU:HD22	2:A:463:LEU:O	1.94	0.68
2:A:37:ILE:HG23	2:A:69:GLU:HB2	1.75	0.68
1:D:506:C:H2'	1:D:507:A:C8	2.28	0.68
1:B:519:U:H2'	1:B:521:A:OP2	1.92	0.68
2:C:355:MET:HE2	2:C:355:MET:HA	1.73	0.68
1:D:517:G:H4'	1:D:518:G:OP1	1.93	0.68
2:C:140:ARG:HD2	2:C:140:ARG:N	2.09	0.68
2:C:7:ALA:HA	2:C:39:ARG:O	1.94	0.67
2:C:111:GLU:O	2:C:115:ILE:HD12	1.93	0.67
1:D:531:C:H2'	1:D:532:C:C6	2.29	0.67
2:A:446:GLY:O	2:A:450:ILE:HG12	1.94	0.67
2:A:393:LEU:HD23	2:A:394:LEU:N	2.09	0.67
2:A:189:LEU:O	2:A:193:VAL:HG23	1.94	0.67
1:D:562:C:H2'	1:D:563:C:C6	2.30	0.67
2:C:444:THR:HG22	2:C:445:PRO:O	1.95	0.67
2:A:384:GLN:NE2	2:A:388:GLU:HG3	2.10	0.67
1:D:567:G:H2'	1:D:568:G:H8	1.60	0.67
2:C:105:ALA:O	2:C:144:HIS:HB2	1.93	0.67
2:C:355:MET:HE3	2:C:445:PRO:HG3	1.77	0.67
1:B:567:G:O2'	1:B:568:G:H5'	1.95	0.67
1:B:506:C:H2'	1:B:507:A:C8	2.30	0.67
1:D:555:U:C2'	1:D:556:C:H5''	2.25	0.67
1:B:565:C:H2'	1:B:566:U:C6	2.30	0.67
2:C:465:ARG:HB3	2:C:465:ARG:HH11	1.60	0.67
1:B:517:G:H21	1:B:557:G:H2'	1.59	0.66
2:A:69:GLU:HB3	2:A:75:ALA:HB2	1.77	0.66
2:A:122:TYR:CE2	2:A:124:GLY:HA2	2.30	0.66
1:B:550:G:HO2'	1:B:551:G:H5'	1.57	0.66
2:A:82:GLN:HG3	2:A:89:TYR:OH	1.96	0.66
1:B:504:C:H2'	1:B:505:C:C6	2.30	0.66
2:A:139:ARG:C	2:A:141:GLY:H	1.99	0.66
2:C:355:MET:CE	2:C:358:ARG:HD2	2.24	0.66
2:A:136:GLU:HG3	2:A:140:ARG:NH1	2.11	0.66
2:A:213:THR:HA	2:A:216:HIS:HD2	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:518:G:H5''	1:D:560:U:O4	1.95	0.66
1:D:569:G:H2'	1:D:570:G:H8	1.59	0.66
2:A:397:LEU:HG	2:A:401:LEU:CD2	2.25	0.65
2:C:460:LEU:O	2:C:464:GLU:HG3	1.96	0.65
2:A:401:LEU:HB3	2:A:460:LEU:HD21	1.78	0.65
2:A:75:ALA:HB3	2:A:80:TYR:CZ	2.31	0.65
2:C:56:ILE:N	2:C:56:ILE:HD13	2.12	0.65
2:C:51:GLY:O	2:C:54:GLU:HG2	1.96	0.65
2:A:136:GLU:O	2:A:140:ARG:HG2	1.97	0.65
2:A:240:ASP:OD1	2:A:242:THR:OG1	2.14	0.65
2:C:148:LEU:HB2	2:C:178:LEU:HD11	1.78	0.65
2:A:294:THR:HG22	2:A:296:GLU:N	2.12	0.65
1:D:551:G:H2'	1:D:552:G:H8	1.61	0.65
1:B:562:C:H2'	1:B:563:C:C6	2.32	0.65
1:D:555:U:H2'	1:D:556:C:H5''	1.78	0.65
1:D:566:U:H2'	1:D:567:G:C8	2.31	0.65
2:C:435:ARG:HD2	2:C:442:LEU:HA	1.79	0.65
2:C:363:LYS:O	2:C:366:PRO:HD2	1.97	0.65
1:B:567:G:H2'	1:B:568:G:H8	1.60	0.65
2:C:147:ARG:HG2	2:C:147:ARG:HH11	1.61	0.65
2:A:184:TYR:HE1	3:A:487:HOH:O	1.80	0.65
1:D:543:G:O2'	1:D:544:A:H5'	1.97	0.64
2:C:237:ARG:HH11	2:C:302:GLY:HA3	1.60	0.64
2:C:114:GLN:O	2:C:118:GLU:HG2	1.96	0.64
2:C:44:ASP:OD2	2:C:47:ARG:HG2	1.96	0.64
1:D:517:G:O2'	1:D:557:G:N2	2.30	0.64
2:C:75:ALA:HB1	2:C:76:PRO:HD2	1.80	0.64
2:A:6:ILE:O	2:A:8:PRO:HD3	1.97	0.64
2:A:101:TRP:HH2	3:A:575:HOH:O	1.80	0.64
2:C:162:LEU:HD21	2:C:231:TYR:HD2	1.63	0.64
1:D:505:C:O2'	1:D:506:C:H5'	1.97	0.64
1:B:543:G:O2'	1:B:544:A:H5'	1.97	0.64
1:B:535:U:C4'	2:A:432:GLN:HE22	2.10	0.64
1:D:504:C:H2'	1:D:505:C:C6	2.32	0.64
2:C:398:TYR:HB3	2:C:399:PRO:HD3	1.79	0.64
1:B:566:U:H2'	1:B:567:G:C8	2.32	0.63
2:A:391:LEU:CD2	2:A:395:LYS:HE3	2.28	0.63
1:B:539:G:O2'	1:B:540:G:H5'	1.98	0.63
2:C:109:PRO:HA	2:C:112:LEU:HD12	1.81	0.63
1:D:563:C:H2'	1:D:564:C:C5	2.32	0.63
1:B:552:G:H2'	1:B:553:G:O4'	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:568:G:H2'	1:B:569:G:H8	1.64	0.63
1:B:505:C:O2'	1:B:506:C:H5'	1.99	0.62
1:B:561:C:H2'	1:B:562:C:C5	2.35	0.62
2:A:237:ARG:NH1	2:A:302:GLY:HA3	2.15	0.62
2:A:461:ARG:O	2:A:464:GLU:HB2	2.00	0.62
2:C:229:ARG:HB2	2:C:229:ARG:HH11	1.64	0.62
1:B:569:G:H2'	1:B:570:G:H8	1.62	0.62
1:B:505:C:H2'	1:B:506:C:H6	1.65	0.62
2:C:326:GLU:OE1	2:C:330:ARG:NE	2.32	0.62
2:A:398:TYR:CD1	2:A:463:LEU:HD11	2.31	0.62
2:C:147:ARG:HG2	2:C:147:ARG:NH1	2.13	0.62
1:B:576:A:H5'	2:A:45:ARG:CZ	2.28	0.62
1:B:517:G:C5	1:B:557:G:C6	2.88	0.62
2:A:81:ARG:HB3	2:A:84:GLU:CG	2.29	0.62
2:A:412:LEU:HG	2:A:451:LEU:HD13	1.80	0.62
2:A:4:THR:HB	2:A:25:ASN:ND2	2.05	0.62
1:D:505:C:H2'	1:D:506:C:H6	1.64	0.62
2:C:236:LEU:HD12	2:C:303:PRO:HG2	1.81	0.62
2:A:333:PRO:HG3	2:A:336:ARG:NH2	2.16	0.61
2:C:115:ILE:O	2:C:119:LYS:HG2	2.00	0.61
2:C:324:LEU:HD11	2:C:353:GLU:HB2	1.81	0.61
2:A:202:ASP:OD1	2:A:229:ARG:HD2	1.99	0.61
1:B:526:G:O2'	1:B:527:C:H5'	2.00	0.61
2:C:316:LYS:HE3	2:C:320:GLU:CD	2.20	0.61
1:B:517:G:H4'	1:B:518:G:OP1	2.01	0.61
2:C:398:TYR:CE2	2:C:402:ARG:HG3	2.35	0.61
1:B:502:G:H2'	1:B:503:C:C6	2.35	0.61
2:A:92:TYR:O	2:A:95:GLU:HB3	2.01	0.61
2:A:124:GLY:O	2:A:127:ARG:HB2	2.00	0.61
2:C:71:PRO:HB3	2:C:81:ARG:NH1	2.16	0.61
2:C:87:PRO:O	2:C:90:GLN:HB3	2.00	0.61
1:D:568:G:H2'	1:D:569:G:H8	1.66	0.61
1:D:558:A:H4'	1:D:559:U:OP1	2.00	0.61
2:A:370:ARG:HG3	2:A:370:ARG:NH1	2.13	0.61
2:C:89:TYR:CD2	2:C:185:PRO:HG3	2.35	0.61
1:D:501:G:H2'	1:D:502:G:C8	2.35	0.60
2:C:458:ARG:NH1	2:C:458:ARG:HG2	2.15	0.60
2:C:378:PRO:HA	3:C:530:HOH:O	2.00	0.60
2:C:75:ALA:HB3	2:C:80:TYR:CE1	2.35	0.60
2:C:45:ARG:HG2	2:C:184:TYR:CE1	2.36	0.60
1:D:556:C:C2'	1:D:556:C:O2	2.46	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:503:C:O2'	1:D:504:C:H5'	2.02	0.60
1:D:564:C:O2'	1:D:565:C:H5'	2.02	0.60
1:D:570:G:H2'	1:D:571:U:C6	2.37	0.60
2:C:136:GLU:HA	2:C:139:ARG:HD2	1.83	0.60
1:D:502:G:H2'	1:D:503:C:C6	2.37	0.60
2:A:423:LYS:HB2	2:A:423:LYS:NZ	2.16	0.60
2:C:350:ARG:O	2:C:350:ARG:HD3	2.02	0.60
1:D:534:C:O2	2:C:435:ARG:NH2	2.34	0.60
2:A:73:VAL:O	2:A:74:ALA:O	2.18	0.60
1:B:530:C:H2'	1:B:531:C:H6	1.66	0.60
1:B:564:C:O2'	1:B:565:C:H5'	2.02	0.60
1:D:541:C:O2'	1:D:542:C:H5'	2.02	0.60
2:A:333:PRO:HG3	2:A:336:ARG:HH21	1.66	0.60
2:A:170:ASN:HA	2:A:173:ILE:HD12	1.83	0.60
2:C:426:LYS:HB2	2:C:429:GLN:HE21	1.65	0.60
1:B:503:C:O2'	1:B:504:C:H5'	2.02	0.60
1:D:569:G:H4'	2:C:237:ARG:HH21	1.65	0.59
2:A:116:ARG:CG	2:A:121:GLY:HA2	2.31	0.59
2:C:423:LYS:NZ	2:C:423:LYS:HB2	2.17	0.59
2:C:238:ASN:O	2:C:304:VAL:HG13	2.03	0.59
1:D:539:G:H2'	1:D:540:G:H8	1.67	0.59
2:C:135:GLU:O	2:C:139:ARG:HD2	2.03	0.59
2:C:139:ARG:C	2:C:141:GLY:H	2.06	0.59
1:D:563:C:C2'	1:D:564:C:H6	2.15	0.59
1:D:506:C:OP1	2:C:163:ARG:HG2	2.03	0.59
1:B:523:G:O2'	1:B:524:A:H5'	2.02	0.59
2:C:435:ARG:NH1	2:C:444:THR:HG22	2.17	0.59
2:C:211:VAL:O	2:C:214:PRO:HD2	2.01	0.59
2:C:266:LEU:HD22	2:C:270:LEU:HD22	1.83	0.59
1:B:559:U:O2'	1:B:560:U:H5'	2.02	0.59
1:B:531:C:H2'	1:B:532:C:C6	2.38	0.59
2:C:355:MET:HE2	2:C:358:ARG:HD2	1.85	0.59
2:C:441:SER:O	2:C:442:LEU:HB2	2.03	0.59
2:A:85:ARG:NH1	2:A:194:ASP:OD2	2.36	0.59
2:A:327:VAL:HG12	2:A:352:VAL:HG11	1.83	0.59
1:D:539:G:O2'	1:D:540:G:H5'	2.03	0.59
1:D:530:C:H2'	1:D:531:C:H6	1.68	0.59
2:C:160:ASP:OD2	2:C:232:HIS:HD2	1.86	0.58
2:C:162:LEU:N	2:C:162:LEU:HD23	2.17	0.58
2:C:73:VAL:O	2:C:74:ALA:O	2.20	0.58
1:D:567:G:O2'	1:D:568:G:C5'	2.50	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:75:ALA:CB	2:C:80:TYR:OH	2.50	0.58
2:A:178:LEU:HB3	2:A:189:LEU:HG	1.85	0.58
2:C:135:GLU:O	2:C:139:ARG:NH1	2.36	0.58
1:D:529:G:H2'	1:D:530:C:C6	2.38	0.58
1:D:556:C:C2'	1:D:557:G:C5'	2.81	0.58
1:D:556:C:C2'	1:D:557:G:H5''	2.34	0.58
1:D:523:G:H2'	1:D:524:A:H8	1.69	0.58
1:D:531:C:H2'	1:D:532:C:H6	1.66	0.58
2:A:407:TRP:CZ2	2:A:456:LYS:HA	2.39	0.58
2:A:413:GLU:HG3	2:A:448:PHE:CZ	2.39	0.58
2:A:139:ARG:HE	2:A:140:ARG:HH21	1.51	0.58
2:A:137:ARG:O	2:A:142:GLU:HB3	2.03	0.58
2:C:220:TYR:CZ	2:C:228:PRO:HD3	2.38	0.58
2:C:404:GLN:NE2	2:C:415:LEU:HD13	2.18	0.58
1:D:544:A:C2'	1:D:545:A:H5'	2.34	0.58
2:A:75:ALA:HB3	2:A:80:TYR:OH	2.04	0.57
1:D:521:A:H61	1:D:546:A:H2'	1.69	0.57
2:A:75:ALA:HB3	2:A:80:TYR:CE1	2.39	0.57
2:A:139:ARG:HB3	2:A:140:ARG:HE	1.70	0.57
2:C:268:ASN:C	2:C:268:ASN:HD22	2.08	0.57
2:C:10:PRO:HB3	2:C:53:GLU:HA	1.86	0.57
2:C:276:SER:O	2:C:297:ARG:HD3	2.03	0.57
2:C:286:LEU:O	2:C:290:ILE:HG23	2.05	0.57
1:B:556:C:H2'	1:B:556:C:O2	2.05	0.57
2:C:3:VAL:HG11	2:C:37:ILE:HD11	1.87	0.57
1:B:556:C:H2'	1:B:557:G:C5'	2.32	0.57
2:C:205:ARG:O	2:C:232:HIS:HA	2.05	0.57
2:A:52:ALA:O	2:A:56:ILE:HG13	2.05	0.57
1:D:570:G:H2'	1:D:571:U:H6	1.70	0.56
2:A:450:ILE:HD13	2:A:450:ILE:N	2.20	0.56
1:B:554:U:H2'	1:B:555:U:C6	2.40	0.56
2:C:458:ARG:CB	2:C:458:ARG:HH11	2.18	0.56
2:A:238:ASN:HB2	2:A:240:ASP:OD1	2.04	0.56
1:B:530:C:H2'	1:B:531:C:C6	2.39	0.56
1:D:563:C:C2'	1:D:564:C:C6	2.83	0.56
1:B:525:C:H2'	1:B:526:G:C8	2.41	0.56
2:C:119:LYS:O	2:C:120:GLY:C	2.43	0.56
2:C:116:ARG:HG2	2:C:121:GLY:HA2	1.86	0.56
1:D:552:G:H2'	1:D:553:G:O4'	2.06	0.56
2:C:74:ALA:O	2:C:75:ALA:HB2	2.05	0.56
2:C:31:ARG:HD2	2:C:31:ARG:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:393:LEU:HA	2:A:396:GLU:HB2	1.88	0.56
1:D:506:C:H2'	1:D:507:A:H8	1.68	0.56
2:A:330:ARG:O	2:A:333:PRO:HD2	2.06	0.56
1:B:521:A:H61	1:B:546:A:H2'	1.70	0.56
1:D:517:G:C6	1:D:558:A:C6	2.94	0.56
2:C:207:GLU:HA	2:C:232:HIS:HB3	1.87	0.56
2:A:114:GLN:O	2:A:118:GLU:HG2	2.06	0.56
2:C:239:PRO:HA	2:C:304:VAL:CG1	2.36	0.56
2:A:152:ARG:NH1	2:A:152:ARG:HA	2.17	0.56
1:B:576:A:H5'	2:A:45:ARG:NH2	2.21	0.56
1:D:571:U:H2'	1:D:572:C:C6	2.41	0.56
2:A:350:ARG:NH1	2:A:354:LEU:HD21	2.20	0.56
2:A:398:TYR:N	2:A:399:PRO:HD2	2.20	0.56
2:A:383:ALA:CA	2:A:442:LEU:HD22	2.36	0.56
1:D:539:G:H2'	1:D:540:G:C8	2.40	0.56
2:C:458:ARG:HH11	2:C:458:ARG:HB3	1.71	0.55
2:C:396:GLU:OE1	2:C:423:LYS:HD3	2.06	0.55
2:C:260:GLY:HA2	2:C:334:PHE:CZ	2.41	0.55
2:A:427:LEU:O	2:A:430:VAL:HG12	2.06	0.55
1:D:556:C:H2'	1:D:557:G:H5'	1.88	0.55
1:D:525:C:H2'	1:D:526:G:C8	2.42	0.55
2:A:350:ARG:O	2:A:350:ARG:HD3	2.06	0.55
1:B:551:G:H2'	1:B:552:G:H8	1.71	0.55
1:B:565:C:H2'	1:B:566:U:H6	1.71	0.55
2:C:458:ARG:HG2	2:C:458:ARG:HH11	1.70	0.55
2:A:385:ARG:HH11	2:A:385:ARG:HG2	1.70	0.55
2:C:331:VAL:HG21	2:C:365:PHE:CD2	2.41	0.55
2:A:206:ALA:HB1	2:A:235:LEU:CD1	2.37	0.55
2:C:446:GLY:O	2:C:450:ILE:HG12	2.05	0.55
2:A:398:TYR:CE2	2:A:402:ARG:HD2	2.42	0.55
2:C:265:ALA:HB3	2:C:314:ASN:HD22	1.72	0.55
2:C:236:LEU:CB	2:C:244:ILE:HD11	2.35	0.55
2:A:31:ARG:NH1	2:A:293:PHE:O	2.40	0.55
1:D:523:G:H2'	1:D:524:A:C8	2.41	0.55
2:C:236:LEU:HB3	2:C:244:ILE:HG12	1.87	0.55
1:D:530:C:O2'	1:D:531:C:H5'	2.07	0.55
2:A:213:THR:N	2:A:214:PRO:HD2	2.22	0.55
2:A:214:PRO:HA	2:A:217:VAL:HG22	1.87	0.55
1:B:529:G:H2'	1:B:530:C:C6	2.42	0.55
2:A:105:ALA:HB2	2:A:147:ARG:HD2	1.89	0.55
1:D:559:U:C5	1:D:560:U:C5	2.94	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:575:C:O4'	1:D:575:C:O2	2.22	0.55
2:A:170:ASN:N	2:A:170:ASN:HD22	2.03	0.55
1:D:526:G:O2'	1:D:527:C:H5'	2.07	0.55
1:B:555:U:H2'	1:B:556:C:H5''	1.89	0.55
1:B:558:A:O2'	1:B:559:U:H3'	2.07	0.55
1:B:523:G:H2'	1:B:524:A:H8	1.72	0.55
2:A:152:ARG:NH2	2:A:173:ILE:O	2.36	0.54
2:A:74:ALA:O	2:A:75:ALA:HB2	2.07	0.54
1:B:539:G:H2'	1:B:540:G:H8	1.71	0.54
2:C:111:GLU:O	2:C:114:GLN:HB2	2.06	0.54
2:C:178:LEU:O	2:C:185:PRO:HA	2.07	0.54
2:C:423:LYS:HZ3	2:C:423:LYS:HB2	1.71	0.54
1:D:553:G:C3'	1:D:554:U:H5'	2.36	0.54
2:A:267:ARG:CD	3:A:529:HOH:O	2.50	0.54
1:B:539:G:H2'	1:B:540:G:C8	2.42	0.54
2:A:391:LEU:O	2:A:395:LYS:HG2	2.08	0.54
2:A:192:VAL:HG13	2:A:220:TYR:CE2	2.42	0.54
2:C:208:GLU:CG	2:C:235:LEU:HD11	2.37	0.54
2:C:208:GLU:HG3	2:C:235:LEU:HD11	1.88	0.54
2:C:110:GLU:H	2:C:110:GLU:CD	2.09	0.54
2:A:119:LYS:O	2:A:120:GLY:C	2.45	0.54
2:A:131:PRO:O	2:A:135:GLU:HG2	2.07	0.54
2:C:386:LYS:HE2	2:C:432:GLN:HB3	1.90	0.54
2:C:463:LEU:O	2:C:463:LEU:HD23	2.08	0.54
1:D:505:C:H2'	1:D:506:C:C6	2.42	0.54
1:B:523:G:H2'	1:B:524:A:C8	2.42	0.54
1:B:563:C:H2'	1:B:564:C:C5	2.40	0.54
1:B:502:G:O2'	1:B:503:C:H5'	2.08	0.54
1:D:553:G:H2'	1:D:554:U:H5'	1.89	0.54
2:C:238:ASN:HB3	2:C:239:PRO:HD2	1.90	0.54
2:C:147:ARG:NH1	2:C:175:ASP:O	2.41	0.54
1:B:558:A:H1'	1:B:560:U:C5	2.43	0.54
1:B:511:U:O2'	1:B:512:C:H5'	2.08	0.54
1:D:530:C:H2'	1:D:531:C:C6	2.41	0.54
2:C:407:TRP:CE2	2:C:456:LYS:HA	2.43	0.54
2:C:57:LEU:O	2:C:61:LYS:HD3	2.08	0.54
2:A:15:HIS:CE1	2:A:251:THR:HB	2.42	0.54
2:C:412:LEU:O	2:C:416:LEU:HD12	2.08	0.54
2:C:444:THR:HG23	2:C:445:PRO:CD	2.38	0.53
1:D:535:U:N3	2:C:444:THR:O	2.30	0.53
1:B:568:G:H2'	1:B:569:G:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:426:LYS:O	2:C:429:GLN:HB2	2.07	0.53
1:D:516:C:O2'	1:D:517:G:P	2.66	0.53
2:A:211:VAL:O	2:A:214:PRO:HD2	2.09	0.53
2:A:285:THR:OG1	2:A:288:GLU:HG3	2.08	0.53
2:C:238:ASN:ND2	2:C:248:LYS:HD2	2.23	0.53
2:A:152:ARG:HG3	2:A:152:ARG:HH11	1.72	0.53
2:A:391:LEU:HA	2:A:394:LEU:HD12	1.91	0.53
2:A:207:GLU:HA	2:A:232:HIS:HB3	1.91	0.53
2:A:436:ALA:HB2	2:A:442:LEU:HD13	1.90	0.53
2:C:270:LEU:O	2:C:273:MET:HB2	2.08	0.53
1:B:517:G:C6	1:B:557:G:C6	2.97	0.53
2:C:461:ARG:O	2:C:464:GLU:HB2	2.08	0.53
2:A:407:TRP:NE1	2:A:456:LYS:N	2.56	0.53
2:C:365:PHE:HB3	2:C:366:PRO:HD3	1.91	0.53
2:A:110:GLU:CD	2:A:110:GLU:H	2.12	0.53
1:B:541:C:O2'	1:B:542:C:H5'	2.08	0.53
2:C:458:ARG:NH1	2:C:458:ARG:CG	2.67	0.53
2:A:91:LYS:HG2	2:A:92:TYR:N	2.23	0.53
1:B:544:A:C2'	1:B:545:A:H5'	2.39	0.53
1:B:505:C:H2'	1:B:506:C:C6	2.44	0.53
1:D:569:G:O2'	1:D:570:G:C5'	2.58	0.52
2:A:178:LEU:O	2:A:185:PRO:HA	2.09	0.52
1:D:551:G:H2'	1:D:552:G:C8	2.43	0.52
1:D:518:G:C5'	1:D:560:U:O4	2.57	0.52
2:A:107:GLU:N	2:A:107:GLU:OE2	2.37	0.52
2:A:238:ASN:O	2:A:304:VAL:HG13	2.09	0.52
1:D:542:C:O2'	1:D:543:G:H5'	2.08	0.52
2:A:188:HIS:HA	2:A:216:HIS:HE1	1.74	0.52
1:B:556:C:C2'	1:B:557:G:C5'	2.81	0.52
2:C:388:GLU:HA	2:C:391:LEU:HD22	1.91	0.52
2:A:147:ARG:HB3	2:A:175:ASP:O	2.09	0.52
2:C:41:GLU:HA	2:C:82:GLN:HG3	1.90	0.52
2:C:375:GLU:HG3	2:C:465:ARG:HH21	1.74	0.52
2:A:435:ARG:HD2	2:A:444:THR:HB	1.91	0.52
2:A:77:THR:HG22	2:A:77:THR:O	2.10	0.52
2:A:73:VAL:CG1	2:A:73:VAL:O	2.51	0.52
2:A:92:TYR:CE2	2:A:225:TRP:HH2	2.28	0.52
1:D:561:C:H2'	1:D:562:C:C6	2.44	0.52
1:B:556:C:C3'	1:B:557:G:C5'	2.88	0.52
2:A:286:LEU:O	2:A:290:ILE:HG23	2.10	0.52
2:A:307:LEU:O	2:A:311:ARG:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:435:ARG:HD3	2:C:444:THR:HB	1.91	0.52
2:A:311:ARG:HH11	2:A:311:ARG:HB3	1.75	0.52
2:C:122:TYR:CE2	2:C:124:GLY:HA2	2.44	0.52
2:A:3:VAL:HB	2:A:200:VAL:HA	1.92	0.52
1:D:556:C:C2'	1:D:557:G:H5'	2.40	0.52
1:B:518:G:N2	1:B:557:G:H1'	2.25	0.52
1:B:556:C:C3'	1:B:557:G:H5''	2.39	0.52
2:A:401:LEU:CB	2:A:460:LEU:HD21	2.40	0.52
2:A:152:ARG:NH1	2:A:152:ARG:HG3	2.25	0.52
1:B:525:C:H2'	1:B:526:G:H8	1.75	0.52
2:A:316:LYS:HE2	2:A:320:GLU:CD	2.30	0.52
2:A:279:ASP:OD2	2:A:281:ARG:HB3	2.11	0.52
2:C:326:GLU:O	2:C:330:ARG:HG3	2.10	0.51
2:A:262:LEU:HB2	2:A:314:ASN:ND2	2.25	0.51
2:A:86:LEU:HA	2:A:89:TYR:HD2	1.75	0.51
1:B:506:C:H2'	1:B:507:A:H8	1.72	0.51
2:A:262:LEU:HB2	2:A:314:ASN:HD21	1.74	0.51
2:C:208:GLU:HG2	2:C:235:LEU:HD21	1.93	0.51
2:C:169:ASP:OD2	2:C:171:GLN:HB2	2.10	0.51
2:C:229:ARG:CG	2:C:229:ARG:HH11	2.23	0.51
2:A:112:LEU:HA	2:A:115:ILE:HD12	1.93	0.51
2:A:44:ASP:O	2:A:46:ALA:N	2.43	0.51
2:C:239:PRO:HD3	3:C:478:HOH:O	2.10	0.51
2:C:71:PRO:HB3	2:C:81:ARG:HH11	1.76	0.51
1:D:517:G:C4	1:D:558:A:C2	2.98	0.51
2:C:330:ARG:HD3	3:C:509:HOH:O	2.10	0.51
2:A:262:LEU:HD13	2:A:330:ARG:HH11	1.73	0.51
2:C:355:MET:HE1	2:C:358:ARG:HD2	1.91	0.51
2:A:194:ASP:O	2:A:198:MET:HB2	2.11	0.51
1:D:517:G:C2	1:D:558:A:C5	2.98	0.51
2:A:417:ARG:NH1	2:A:427:LEU:HD22	2.26	0.51
2:C:426:LYS:H	2:C:429:GLN:NE2	2.09	0.51
2:C:385:ARG:HH11	2:C:385:ARG:CB	2.24	0.51
2:C:261:PHE:CE2	2:C:310:LEU:HD13	2.46	0.51
1:B:508:U:C2	1:B:515:G:O6	2.64	0.50
2:C:135:GLU:HB3	2:C:139:ARG:CZ	2.41	0.50
2:A:423:LYS:HZ3	2:A:423:LYS:HB2	1.76	0.50
1:B:527:C:H2'	1:B:528:G:H8	1.76	0.50
2:C:246:LYS:O	2:C:246:LYS:HE3	2.12	0.50
2:A:257:LYS:HG2	3:A:507:HOH:O	2.11	0.50
1:D:517:G:H22	1:D:557:G:H2'	1.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:534:C:H5''	3:D:70:HOH:O	2.11	0.50
1:B:518:G:H5''	1:B:560:U:O4	2.10	0.50
2:A:461:ARG:NH2	2:A:462:ARG:HB2	2.26	0.50
1:B:561:C:H2'	1:B:562:C:C6	2.46	0.50
2:C:53:GLU:HG2	2:C:54:GLU:N	2.26	0.50
2:C:422:GLU:HG2	2:C:423:LYS:NZ	2.26	0.50
1:D:517:G:C6	1:D:557:G:C6	2.99	0.50
2:C:195:ASP:HA	2:C:200:VAL:HG13	1.92	0.50
2:A:169:ASP:HB3	2:A:172:GLU:HG3	1.94	0.50
2:A:332:LYS:O	2:A:336:ARG:HG3	2.12	0.50
1:B:553:G:C3'	1:B:554:U:H5'	2.41	0.50
2:A:404:GLN:HG2	2:A:415:LEU:HD22	1.91	0.50
1:D:505:C:H4'	2:C:163:ARG:HD2	1.93	0.50
2:C:195:ASP:O	2:C:200:VAL:HG13	2.11	0.50
2:C:246:LYS:HG3	2:C:247:ARG:N	2.23	0.50
2:C:6:ILE:O	2:C:6:ILE:HG13	2.12	0.50
2:C:358:ARG:NH1	2:C:445:PRO:HB3	2.26	0.50
1:D:508:U:H6	1:D:508:U:O5'	1.94	0.50
1:B:540:G:H2'	1:B:541:C:C6	2.47	0.50
1:B:504:C:H2'	1:B:505:C:H6	1.75	0.50
2:A:400:ARG:HH22	2:A:422:GLU:CD	2.15	0.50
2:C:348:LEU:O	2:C:352:VAL:HG23	2.12	0.50
2:C:79:PRO:HB3	2:C:84:GLU:OE1	2.12	0.50
2:A:393:LEU:C	2:A:393:LEU:HD23	2.33	0.49
1:B:542:C:O2'	1:B:543:G:H5'	2.12	0.49
2:C:238:ASN:HD22	2:C:242:THR:CG2	2.16	0.49
1:D:569:G:H2'	1:D:570:G:C8	2.45	0.49
1:D:525:C:H2'	1:D:526:G:H8	1.77	0.49
2:C:243:LYS:O	2:C:243:LYS:HG2	2.11	0.49
2:A:157:GLU:HG3	2:A:167:VAL:HG22	1.94	0.49
1:D:525:C:O2'	1:D:526:G:H5'	2.13	0.49
1:B:562:C:O2'	1:B:563:C:C5'	2.59	0.49
2:C:391:LEU:N	2:C:392:PRO:CD	2.73	0.49
2:C:116:ARG:HG2	2:C:120:GLY:O	2.12	0.49
2:A:376:ASP:O	2:A:376:ASP:CG	2.50	0.49
2:C:5:ARG:HH21	2:C:195:ASP:CG	2.15	0.49
2:A:105:ALA:O	2:A:144:HIS:HB2	2.12	0.49
1:B:508:U:O5'	1:B:508:U:H6	1.94	0.49
2:A:157:GLU:HG2	3:A:488:HOH:O	2.12	0.49
1:D:553:G:O2'	1:D:554:U:H5'	2.13	0.49
2:A:20:TYR:O	2:A:24:PHE:HD1	1.96	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:406:GLU:HG3	2:C:408:THR:HG23	1.94	0.49
2:C:238:ASN:HD21	2:C:245:SER:N	2.11	0.48
2:C:435:ARG:HH11	2:C:444:THR:CG2	2.26	0.48
2:C:385:ARG:HH11	2:C:385:ARG:HB2	1.78	0.48
2:A:239:PRO:HA	2:A:304:VAL:HG11	1.95	0.48
2:C:265:ALA:CB	2:C:314:ASN:HD22	2.25	0.48
2:C:267:ARG:NH2	2:C:284:PHE:O	2.46	0.48
2:C:465:ARG:O	2:C:468:ALA:HB3	2.14	0.48
2:A:44:ASP:C	2:A:46:ALA:H	2.17	0.48
2:C:390:GLY:C	2:C:392:PRO:HD2	2.32	0.48
2:C:122:TYR:OH	2:C:125:ARG:HG2	2.13	0.48
2:C:277:MET:HB2	3:C:549:HOH:O	2.13	0.48
2:C:213:THR:O	2:C:217:VAL:HG12	2.13	0.48
2:A:386:LYS:HE3	2:A:432:GLN:HG2	1.94	0.48
1:D:535:U:H4'	2:C:432:GLN:NE2	2.16	0.48
1:B:556:C:O2'	1:B:557:G:H5''	2.13	0.48
2:A:160:ASP:OD2	2:A:232:HIS:HD2	1.96	0.48
2:C:361:THR:O	2:C:364:GLU:HB2	2.14	0.48
1:D:511:U:O2'	1:D:512:C:H5'	2.14	0.48
2:A:314:ASN:HB3	2:A:360:ASP:O	2.12	0.48
2:C:236:LEU:O	2:C:244:ILE:HG13	2.12	0.48
2:C:425:VAL:HG22	2:C:429:GLN:OE1	2.13	0.48
2:C:196:HIS:HD2	3:C:529:HOH:O	1.97	0.48
2:C:3:VAL:HG13	2:C:37:ILE:HD11	1.94	0.48
1:D:509:C:H4'	1:D:510:G:OP2	2.13	0.48
2:C:323:SER:OG	2:C:326:GLU:HB2	2.14	0.48
2:C:125:ARG:HE	2:C:125:ARG:HB3	1.28	0.48
1:B:553:G:H2'	1:B:554:U:H5'	1.94	0.48
1:B:569:G:H2'	1:B:570:G:C8	2.47	0.48
2:C:463:LEU:CD2	2:C:463:LEU:C	2.73	0.48
2:A:396:GLU:OE1	2:A:423:LYS:HE2	2.13	0.48
2:A:6:ILE:HD11	2:A:38:VAL:HG22	1.96	0.48
1:B:530:C:O2'	1:B:531:C:H5'	2.14	0.48
1:B:531:C:H2'	1:B:532:C:H6	1.76	0.48
1:D:517:G:H21	1:D:557:G:C2'	2.18	0.48
1:B:573:A:C2	1:B:575:C:N3	2.82	0.48
1:D:504:C:H2'	1:D:505:C:H6	1.74	0.48
2:C:115:ILE:CG2	2:C:122:TYR:HA	2.44	0.48
2:C:397:LEU:HG	2:C:401:LEU:HD22	1.96	0.48
1:D:561:C:H2'	1:D:562:C:H5	1.76	0.48
2:A:333:PRO:HA	2:A:336:ARG:CZ	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:551:G:H2'	1:B:552:G:C8	2.49	0.48
1:B:509:C:H4'	1:B:510:G:OP2	2.14	0.48
1:D:568:G:H2'	1:D:569:G:C8	2.48	0.47
2:A:213:THR:HA	2:A:216:HIS:CD2	2.45	0.47
2:C:17:GLY:O	2:C:20:TYR:HB3	2.14	0.47
1:D:555:U:C3'	1:D:556:C:H5''	2.44	0.47
2:C:75:ALA:HB1	2:C:76:PRO:CD	2.43	0.47
2:A:463:LEU:HD22	2:A:467:LEU:HG	1.96	0.47
2:A:75:ALA:HB1	2:A:76:PRO:CD	2.42	0.47
2:C:229:ARG:CB	2:C:229:ARG:HH11	2.26	0.47
1:D:556:C:H2'	1:D:557:G:C5'	2.44	0.47
1:B:562:C:O5'	1:B:562:C:H6	1.96	0.47
2:C:86:LEU:N	2:C:87:PRO:HD2	2.29	0.47
2:C:96:LEU:HB3	2:C:102:ALA:HB2	1.96	0.47
2:A:255:TRP:CZ2	2:A:259:GLU:HG3	2.49	0.47
2:A:435:ARG:CD	2:A:444:THR:HB	2.43	0.47
1:D:523:G:O2'	1:D:524:A:H5'	2.15	0.47
2:A:133:GLU:HG2	2:A:137:ARG:HD2	1.95	0.47
2:C:281:ARG:HG2	2:C:281:ARG:HH11	1.80	0.47
2:A:355:MET:HG3	2:A:369:ALA:HB2	1.95	0.47
2:A:176:VAL:HG11	2:A:215:ILE:HD13	1.95	0.47
1:D:557:G:C8	1:D:557:G:H5'	2.43	0.47
1:D:540:G:H2'	1:D:541:C:C6	2.49	0.47
2:A:40:ILE:O	2:A:82:GLN:HB2	2.14	0.47
1:D:556:C:O2	1:D:557:G:C8	2.67	0.47
1:B:552:G:C4	1:B:553:G:C8	3.02	0.47
1:B:555:U:C2'	1:B:556:C:H5''	2.44	0.47
2:A:69:GLU:CB	2:A:75:ALA:HB2	2.43	0.47
2:C:140:ARG:HD2	2:C:140:ARG:H	1.80	0.47
2:C:281:ARG:HG2	2:C:281:ARG:NH1	2.29	0.47
2:C:238:ASN:HD21	2:C:245:SER:CB	2.27	0.47
2:C:383:ALA:HA	2:C:442:LEU:HD13	1.97	0.47
1:B:517:G:O6	1:B:555:U:H1'	2.13	0.47
1:B:516:C:O2'	1:B:517:G:P	2.72	0.47
1:D:505:C:O3'	2:C:163:ARG:HG2	2.15	0.47
2:C:422:GLU:HG2	2:C:423:LYS:HZ2	1.80	0.47
2:C:401:LEU:CD1	2:C:415:LEU:HD23	2.45	0.47
1:B:534:C:H4'	2:A:426:LYS:NZ	2.30	0.47
2:A:157:GLU:CG	2:A:167:VAL:HG22	2.44	0.47
2:A:51:GLY:HA2	2:A:54:GLU:OE1	2.15	0.47
2:A:275:PHE:CE2	2:A:297:ARG:HB2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:441:SER:O	2:C:442:LEU:CB	2.63	0.47
1:B:556:C:C2'	1:B:556:C:O2	2.61	0.46
2:C:110:GLU:N	2:C:110:GLU:OE2	2.38	0.46
2:A:139:ARG:C	2:A:141:GLY:N	2.66	0.46
2:A:202:ASP:CG	2:A:229:ARG:HH11	2.18	0.46
2:C:323:SER:O	2:C:327:VAL:HG23	2.15	0.46
2:A:438:LEU:O	2:A:462:ARG:HD3	2.15	0.46
2:A:1:MET:CE	2:A:35:ARG:HH11	2.28	0.46
2:A:1:MET:SD	2:A:34:GLY:HA2	2.55	0.46
2:C:402:ARG:HA	2:C:460:LEU:HD11	1.96	0.46
1:D:501:G:O5'	1:D:501:G:H8	1.99	0.46
2:A:136:GLU:HA	2:A:140:ARG:NH2	2.30	0.46
2:C:185:PRO:HB3	2:C:189:LEU:HD12	1.96	0.46
1:D:552:G:C4	1:D:553:G:C8	3.03	0.46
1:B:561:C:O2	1:B:562:C:C5	2.69	0.46
2:A:391:LEU:N	2:A:392:PRO:CD	2.79	0.46
2:A:118:GLU:HG2	2:A:118:GLU:H	1.52	0.46
2:C:355:MET:HA	2:C:358:ARG:HG3	1.97	0.46
2:C:446:GLY:O	2:C:449:GLU:HG2	2.14	0.46
2:C:314:ASN:O	2:C:318:ILE:HG13	2.16	0.46
2:A:294:THR:CG2	2:A:296:GLU:HG3	2.45	0.46
2:C:137:ARG:O	2:C:142:GLU:CB	2.55	0.46
2:C:160:ASP:OD1	2:C:162:LEU:HB2	2.14	0.46
2:A:139:ARG:O	2:A:141:GLY:N	2.48	0.46
2:A:205:ARG:O	2:A:232:HIS:HA	2.15	0.46
2:A:250:HIS:HA	3:A:572:HOH:O	2.15	0.46
2:C:107:GLU:HB2	2:C:112:LEU:CD2	2.44	0.46
2:A:335:LEU:HD13	2:A:342:TRP:CE3	2.49	0.46
1:D:524:A:H2'	1:D:525:C:C6	2.51	0.46
1:B:504:C:H3'	3:B:82:HOH:O	2.15	0.46
1:D:556:C:C2	1:D:557:G:C8	3.04	0.46
2:A:294:THR:HB	2:A:297:ARG:HG3	1.98	0.46
2:A:407:TRP:CD1	2:A:456:LYS:N	2.84	0.46
2:A:6:ILE:C	2:A:8:PRO:HD3	2.36	0.46
1:D:553:G:H2'	1:D:554:U:C6	2.51	0.46
2:C:435:ARG:HH11	2:C:444:THR:HG22	1.80	0.46
1:D:503:C:H2'	1:D:504:C:C6	2.51	0.46
2:A:88:LEU:CD1	2:A:92:TYR:HE1	2.29	0.46
2:C:178:LEU:HB3	2:C:189:LEU:HG	1.97	0.46
2:A:400:ARG:HG2	2:A:400:ARG:H	1.50	0.46
1:B:514:A:C5	1:B:522:G:C6	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:239:PRO:HA	2:A:304:VAL:CG1	2.46	0.45
2:C:147:ARG:CG	2:C:147:ARG:HH11	2.26	0.45
2:C:117:LYS:HB2	2:C:117:LYS:NZ	2.31	0.45
1:D:516:C:O2'	1:D:517:G:OP2	2.34	0.45
2:A:358:ARG:CZ	2:A:445:PRO:HA	2.46	0.45
2:A:75:ALA:CB	2:A:80:TYR:OH	2.65	0.45
1:D:506:C:P	2:C:163:ARG:HG2	2.56	0.45
1:B:534:C:H6	1:B:534:C:O5'	1.99	0.45
2:A:203:VAL:HB	2:A:230:PHE:CD1	2.51	0.45
2:A:265:ALA:CB	2:A:314:ASN:HD22	2.30	0.45
2:C:132:GLU:OE1	2:C:136:GLU:HG2	2.16	0.45
2:A:152:ARG:CG	2:A:152:ARG:HH11	2.29	0.45
2:C:97:LEU:C	2:C:99:ARG:H	2.20	0.45
1:D:520:U:H2'	1:D:521:A:H5'	1.98	0.45
1:D:517:G:C2	1:D:558:A:C4	3.04	0.45
1:D:520:U:C2'	1:D:521:A:H5'	2.47	0.45
2:A:88:LEU:HD11	2:A:92:TYR:HE1	1.81	0.45
2:C:213:THR:N	2:C:214:PRO:CD	2.79	0.45
2:C:168:TYR:CD2	2:C:214:PRO:HG3	2.51	0.45
2:A:87:PRO:O	2:A:90:GLN:HB2	2.15	0.45
2:C:382:LYS:HG2	3:C:483:HOH:O	2.15	0.45
1:D:562:C:O5'	1:D:562:C:H6	1.99	0.45
2:C:203:VAL:HG12	2:C:205:ARG:HD2	1.98	0.45
2:C:168:TYR:CE2	2:C:214:PRO:HG3	2.52	0.45
2:A:86:LEU:N	2:A:87:PRO:CD	2.79	0.45
2:C:404:GLN:NE2	2:C:404:GLN:HA	2.30	0.45
2:C:408:THR:OG1	2:C:411:ALA:CB	2.65	0.45
2:C:318:ILE:O	2:C:356:ARG:HD3	2.17	0.45
2:A:354:LEU:HD22	2:A:449:GLU:HG3	1.98	0.45
2:C:139:ARG:HG3	2:C:139:ARG:NH1	2.32	0.45
2:C:331:VAL:CG2	2:C:365:PHE:CD2	3.00	0.45
2:C:239:PRO:HA	2:C:304:VAL:HG11	1.99	0.45
1:D:501:G:H2'	1:D:502:G:H8	1.81	0.45
1:B:524:A:H2'	1:B:525:C:C6	2.52	0.45
2:A:202:ASP:OD2	2:A:229:ARG:NH1	2.49	0.45
2:A:397:LEU:C	2:A:399:PRO:HD2	2.37	0.45
2:C:426:LYS:HE2	2:C:427:LEU:H	1.82	0.45
2:C:111:GLU:O	2:C:115:ILE:CD1	2.63	0.45
2:A:13:ASP:N	2:A:13:ASP:OD1	2.49	0.45
1:B:567:G:O2'	1:B:568:G:C5'	2.64	0.44
2:A:311:ARG:NH1	2:A:311:ARG:HB3	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:89:TYR:CG	2:A:185:PRO:HG3	2.52	0.44
2:A:139:ARG:HE	2:A:140:ARG:NH2	2.15	0.44
1:D:556:C:C3'	1:D:557:G:H5'	2.48	0.44
2:A:444:THR:CG2	2:A:445:PRO:N	2.80	0.44
1:B:501:G:H2'	1:B:502:G:C8	2.52	0.44
2:C:316:LYS:HE3	2:C:320:GLU:OE1	2.16	0.44
2:A:206:ALA:HB1	2:A:235:LEU:HD11	1.99	0.44
1:D:517:G:C2	1:D:557:G:H2'	2.37	0.44
1:B:509:C:H5	1:B:523:G:O6	2.01	0.44
2:C:179:LEU:HD23	2:C:179:LEU:HA	1.70	0.44
1:D:562:C:O2'	1:D:563:C:C5'	2.62	0.44
2:A:107:GLU:HG2	2:A:115:ILE:HD11	1.99	0.44
1:B:569:G:O2'	1:B:570:G:C5'	2.63	0.44
2:A:275:PHE:HE2	2:A:297:ARG:HB2	1.83	0.44
2:A:261:PHE:HZ	2:A:311:ARG:HG2	1.82	0.44
1:D:509:C:H5	1:D:523:G:O6	2.01	0.44
1:D:502:G:O2'	1:D:503:C:H5'	2.17	0.44
2:A:142:GLU:HG3	2:A:143:PRO:HD2	2.00	0.44
2:A:246:LYS:HA	2:A:251:THR:HG23	1.99	0.44
2:A:372:LEU:HD23	2:A:372:LEU:HA	1.80	0.44
2:A:89:TYR:CD2	2:A:185:PRO:HG3	2.53	0.44
2:A:434:LEU:HD12	2:A:434:LEU:O	2.17	0.44
2:C:262:LEU:HD11	2:C:318:ILE:HG12	1.99	0.44
2:A:30:ARG:CB	2:A:290:ILE:HD13	2.41	0.44
2:A:202:ASP:CG	2:A:229:ARG:NH1	2.71	0.44
1:D:556:C:C3'	1:D:557:G:C5'	2.96	0.44
2:C:69:GLU:HB3	2:C:75:ALA:HB2	1.99	0.44
1:B:558:A:H2'	1:B:560:U:OP2	2.17	0.44
1:B:563:C:C2'	1:B:564:C:H6	2.27	0.44
1:D:517:G:C5	1:D:557:G:C6	3.06	0.44
2:A:75:ALA:N	3:A:566:HOH:O	2.51	0.44
1:D:508:U:O2'	1:D:546:A:H1'	2.18	0.44
2:C:324:LEU:HD23	2:C:324:LEU:O	2.17	0.44
2:C:332:LYS:HB2	2:C:333:PRO:CD	2.48	0.44
1:D:567:G:H2'	1:D:568:G:C8	2.47	0.43
1:B:550:G:O2'	1:B:551:G:C5'	2.53	0.43
2:C:132:GLU:OE2	2:C:132:GLU:HA	2.18	0.43
2:C:310:LEU:O	2:C:313:MET:HB3	2.18	0.43
1:B:573:A:H2	1:B:575:C:N3	2.15	0.43
2:C:124:GLY:O	2:C:127:ARG:HB2	2.18	0.43
2:C:51:GLY:O	2:C:53:GLU:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:72:ASP:OD1	2:C:72:ASP:N	2.36	0.43
1:D:560:U:H3'	1:D:561:C:C5	2.53	0.43
2:C:319:ARG:HA	2:C:356:ARG:HH11	1.82	0.43
2:A:265:ALA:HB3	2:A:314:ASN:HD22	1.83	0.43
2:A:86:LEU:HA	2:A:89:TYR:CD2	2.53	0.43
2:A:136:GLU:HG3	2:A:140:ARG:CZ	2.48	0.43
2:C:96:LEU:HB3	2:C:102:ALA:CB	2.47	0.43
2:C:355:MET:O	2:C:356:ARG:C	2.57	0.43
2:A:74:ALA:HB1	3:A:570:HOH:O	2.17	0.43
1:B:520:U:C2'	1:B:521:A:H5'	2.48	0.43
2:A:187:TYR:O	2:A:191:ASN:HB3	2.18	0.43
1:D:569:G:C4'	2:C:237:ARG:HH21	2.31	0.43
1:D:551:G:C4	1:D:552:G:C8	3.06	0.43
2:C:358:ARG:O	2:C:368:LYS:HE3	2.18	0.43
2:C:290:ILE:HG13	2:C:291:GLN:N	2.33	0.43
2:C:39:ARG:NH2	2:C:195:ASP:OD2	2.50	0.43
1:B:520:U:H2'	1:B:521:A:H5'	2.00	0.43
1:D:513:U:O2'	1:D:514:A:H5'	2.18	0.43
2:C:193:VAL:O	2:C:197:LEU:HB2	2.17	0.43
1:B:553:G:H4'	1:B:553:G:OP1	2.18	0.43
2:A:188:HIS:HA	2:A:216:HIS:CE1	2.52	0.43
2:C:188:HIS:HD2	2:C:216:HIS:CE1	2.36	0.43
2:A:318:ILE:O	2:A:356:ARG:HD3	2.17	0.43
1:B:518:G:C5'	1:B:560:U:O4	2.66	0.43
2:A:401:LEU:N	2:A:401:LEU:HD13	2.34	0.43
2:A:407:TRP:CE2	2:A:456:LYS:CA	2.97	0.43
2:A:84:GLU:HG2	2:A:84:GLU:H	1.56	0.43
2:C:31:ARG:CD	2:C:31:ARG:O	2.67	0.43
1:B:516:C:O2'	1:B:517:G:OP2	2.36	0.43
2:C:69:GLU:HB3	2:C:75:ALA:CB	2.49	0.43
1:D:574:C:O2	2:C:181:SER:OG	2.34	0.43
2:C:122:TYR:HE1	2:C:125:ARG:HD2	1.84	0.43
2:A:184:TYR:CE1	3:A:487:HOH:O	2.57	0.43
2:C:438:LEU:O	2:C:462:ARG:NH1	2.44	0.43
1:D:569:G:N3	1:D:570:G:C8	2.87	0.42
1:B:555:U:C3'	1:B:556:C:H5"	2.49	0.42
2:C:6:ILE:CD1	2:C:60:LEU:HD11	2.49	0.42
2:A:325:GLU:CD	2:A:325:GLU:H	2.22	0.42
1:D:553:G:OP1	1:D:553:G:H4'	2.18	0.42
1:B:561:C:C2	1:B:562:C:C5	3.07	0.42
2:A:236:LEU:HD12	2:A:303:PRO:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:259:HOH:O	2:C:172:GLU:HG2	2.19	0.42
2:A:220:TYR:CE1	2:A:228:PRO:HD3	2.54	0.42
2:C:355:MET:SD	2:C:369:ALA:HB2	2.59	0.42
2:A:256:TYR:O	2:A:261:PHE:HB2	2.19	0.42
2:C:314:ASN:HB3	2:C:360:ASP:O	2.20	0.42
2:C:318:ILE:O	2:C:356:ARG:NH1	2.37	0.42
2:A:345:GLU:O	2:A:349:ARG:HG3	2.19	0.42
2:C:169:ASP:OD2	2:C:169:ASP:C	2.57	0.42
2:C:229:ARG:CG	2:C:229:ARG:NH1	2.79	0.42
2:A:385:ARG:HD3	3:A:489:HOH:O	2.19	0.42
2:A:174:PRO:HG2	2:A:176:VAL:CG1	2.50	0.42
2:A:361:THR:O	2:A:364:GLU:HB2	2.20	0.42
1:D:555:U:H2'	1:D:556:C:C5'	2.47	0.42
1:D:510:G:H2'	1:D:511:U:C6	2.55	0.42
2:A:137:ARG:NH1	2:A:137:ARG:HG2	2.34	0.42
2:C:406:GLU:HG2	2:C:411:ALA:HB2	2.00	0.42
2:A:350:ARG:HH11	2:A:354:LEU:HD21	1.85	0.42
2:A:43:THR:HG23	2:A:82:GLN:HB3	2.01	0.42
2:C:462:ARG:O	2:C:465:ARG:HB2	2.19	0.42
2:C:423:LYS:NZ	2:C:423:LYS:CB	2.82	0.42
2:C:270:LEU:HD12	2:C:273:MET:HG3	2.01	0.42
2:A:426:LYS:O	2:A:427:LEU:C	2.57	0.42
2:A:20:TYR:HE2	2:A:234:PRO:O	2.03	0.42
2:C:387:LEU:CD1	2:C:437:ALA:HB2	2.50	0.42
2:C:355:MET:CE	2:C:445:PRO:HD3	2.46	0.42
1:B:544:A:HO2'	1:B:545:A:H5'	1.83	0.42
2:A:105:ALA:CB	2:A:147:ARG:HD2	2.50	0.42
2:C:85:ARG:O	2:C:88:LEU:HB2	2.20	0.42
1:D:550:G:O2'	1:D:551:G:C5'	2.55	0.42
2:C:238:ASN:HD21	2:C:245:SER:HB3	1.85	0.42
2:A:463:LEU:C	2:A:463:LEU:HD13	2.40	0.42
2:C:130:PRO:HA	2:C:131:PRO:HD2	1.86	0.42
2:C:92:TYR:O	2:C:95:GLU:HB3	2.19	0.42
2:A:6:ILE:HD13	2:A:36:PHE:HZ	1.85	0.42
2:A:442:LEU:HD12	2:A:442:LEU:HA	1.83	0.42
2:A:242:THR:O	2:A:243:LYS:C	2.58	0.42
2:A:188:HIS:CD2	2:A:216:HIS:CE1	3.08	0.42
2:C:89:TYR:HB3	2:C:189:LEU:CD1	2.50	0.42
2:C:159:LYS:HB2	2:C:165:VAL:HG22	2.02	0.42
2:C:340:LEU:HD12	2:C:366:PRO:HB3	2.02	0.41
1:D:524:A:H2'	1:D:525:C:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:558:A:H2'	1:B:561:C:H41	1.85	0.41
2:C:130:PRO:HG2	2:C:133:GLU:CB	2.35	0.41
2:C:137:ARG:HB3	2:C:137:ARG:NH1	2.23	0.41
2:C:392:PRO:HA	3:C:558:HOH:O	2.21	0.41
2:A:240:ASP:CG	2:A:242:THR:OG1	2.57	0.41
2:A:332:LYS:HB2	2:A:333:PRO:HD3	2.01	0.41
2:C:115:ILE:HG21	2:C:122:TYR:HA	2.02	0.41
2:C:169:ASP:HB3	2:C:172:GLU:CG	2.51	0.41
1:B:510:G:H2'	1:B:511:U:H6	1.85	0.41
2:A:327:VAL:CG1	2:A:352:VAL:HG11	2.50	0.41
2:C:218:LEU:O	2:C:221:ARG:HB3	2.21	0.41
2:A:11:THR:HA	2:A:49:VAL:HG23	2.03	0.41
2:A:446:GLY:O	2:A:449:GLU:HG2	2.20	0.41
2:C:395:LYS:HG2	2:C:395:LYS:H	1.42	0.41
2:C:214:PRO:HA	2:C:217:VAL:HG13	2.02	0.41
2:C:53:GLU:OE1	2:C:81:ARG:NH1	2.54	0.41
2:C:47:ARG:HG2	2:C:47:ARG:H	1.69	0.41
2:C:403:ALA:O	2:C:404:GLN:C	2.58	0.41
2:C:85:ARG:NH1	2:C:194:ASP:OD2	2.54	0.41
2:A:283:ILE:HD13	2:A:313:MET:HE3	2.02	0.41
1:D:575:C:O2	1:D:575:C:H5''	2.20	0.41
2:A:89:TYR:HB3	2:A:189:LEU:HD13	2.01	0.41
1:B:502:G:H8	1:B:502:G:O5'	2.04	0.41
2:C:48:TYR:C	2:C:48:TYR:CD1	2.93	0.41
2:A:106:PHE:N	2:A:106:PHE:CD1	2.88	0.41
2:A:275:PHE:CD1	2:A:289:PHE:HE1	2.39	0.41
2:A:150:VAL:HG21	2:A:173:ILE:HG22	2.03	0.41
2:C:107:GLU:OE1	2:C:122:TYR:CZ	2.73	0.41
2:C:113:GLU:HG3	2:C:116:ARG:NH2	2.35	0.41
2:A:370:ARG:CG	2:A:370:ARG:HH11	2.28	0.41
1:D:564:C:O2'	1:D:565:C:C5'	2.67	0.41
2:C:139:ARG:C	2:C:141:GLY:N	2.72	0.41
2:C:426:LYS:HA	2:C:426:LYS:HE2	2.02	0.41
1:B:576:A:H5'	2:A:45:ARG:NH1	2.36	0.41
2:C:119:LYS:HB3	2:C:119:LYS:HE2	1.70	0.41
2:C:432:GLN:N	2:C:433:PRO:HD2	2.35	0.41
1:B:563:C:C2'	1:B:564:C:C6	2.94	0.41
2:A:398:TYR:CE1	2:A:464:GLU:HG2	2.56	0.41
2:C:463:LEU:HD23	2:C:464:GLU:N	2.33	0.41
1:D:546:A:O2'	1:D:548:C:H4'	2.21	0.41
2:C:56:ILE:CD1	2:C:56:ILE:H	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:56:ILE:H	2:C:56:ILE:HD13	1.82	0.41
2:A:426:LYS:HD2	2:A:427:LEU:N	2.36	0.41
2:C:139:ARG:HG3	2:C:139:ARG:HH11	1.86	0.41
2:A:441:SER:O	2:A:442:LEU:CB	2.63	0.41
2:C:332:LYS:O	2:C:333:PRO:C	2.59	0.41
1:B:566:U:O2'	1:B:567:G:C5'	2.62	0.40
2:A:97:LEU:C	2:A:99:ARG:H	2.24	0.40
2:A:451:LEU:HD23	2:A:451:LEU:HA	1.83	0.40
2:C:332:LYS:O	2:C:335:LEU:N	2.54	0.40
2:C:434:LEU:HD23	2:C:447:LEU:HD21	2.03	0.40
2:C:21:ILE:HG22	2:C:22:ALA:N	2.36	0.40
2:C:426:LYS:O	2:C:427:LEU:C	2.60	0.40
2:C:116:ARG:CG	2:C:121:GLY:HA2	2.51	0.40
1:D:543:G:O2'	1:D:544:A:C5'	2.68	0.40
2:C:152:ARG:CB	2:C:153:PRO:HD3	2.51	0.40
1:B:574:C:O5'	2:A:177:VAL:CG1	2.69	0.40
2:C:319:ARG:HA	2:C:356:ARG:HD2	2.03	0.40
2:C:86:LEU:N	2:C:87:PRO:CD	2.84	0.40
2:A:283:ILE:HD13	2:A:313:MET:CE	2.52	0.40
2:A:397:LEU:O	2:A:401:LEU:HD22	2.22	0.40
2:A:398:TYR:C	2:A:398:TYR:CD2	2.94	0.40
2:A:458:ARG:O	2:A:458:ARG:HD2	2.22	0.40
2:C:115:ILE:HG21	2:C:122:TYR:HD1	1.86	0.40
1:D:555:U:C3'	1:D:556:C:C5'	2.99	0.40
2:C:319:ARG:HA	2:C:356:ARG:NH1	2.36	0.40
2:A:225:TRP:HZ3	3:A:501:HOH:O	2.04	0.40
1:B:510:G:H2'	1:B:511:U:C6	2.57	0.40
2:A:432:GLN:N	2:A:433:PRO:HD2	2.36	0.40
2:A:412:LEU:O	2:A:416:LEU:HG	2.21	0.40
2:C:180:LYS:HD3	2:C:184:TYR:O	2.21	0.40
2:C:294:THR:HG23	2:C:296:GLU:N	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	466/468 (100%)	420 (90%)	37 (8%)	9 (2%)	10	12
2	C	466/468 (100%)	415 (89%)	44 (9%)	7 (2%)	13	17
All	All	932/936 (100%)	835 (90%)	81 (9%)	16 (2%)	11	14

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	74	ALA
2	C	74	ALA
2	A	78	GLY
2	A	120	GLY
2	C	78	GLY
2	C	120	GLY
2	C	241	LYS
2	A	45	ARG
2	A	140	ARG
2	A	241	LYS
2	C	52	ALA
2	C	140	ARG
2	C	392	PRO
2	A	392	PRO
2	A	244	ILE
2	A	428	GLY

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	
2	A	393/393 (100%)	290 (74%)	103 (26%)	0	0
2	C	393/393 (100%)	285 (72%)	108 (28%)	0	0
All	All	786/786 (100%)	575 (73%)	211 (27%)	0	0

All (211) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	1	MET
2	A	5	ARG
2	A	9	SER
2	A	13	ASP
2	A	37	ILE
2	A	45	ARG
2	A	56	ILE
2	A	66	SER
2	A	72	ASP
2	A	73	VAL
2	A	82	GLN
2	A	84	GLU
2	A	85	ARG
2	A	86	LEU
2	A	88	LEU
2	A	90	GLN
2	A	91	LYS
2	A	97	LEU
2	A	98	LYS
2	A	99	ARG
2	A	101	TRP
2	A	114	GLN
2	A	118	GLU
2	A	119	LYS
2	A	127	ARG
2	A	132	GLU
2	A	136	GLU
2	A	137	ARG
2	A	140	ARG
2	A	146	ILE
2	A	152	ARG
2	A	157	GLU
2	A	159	LYS
2	A	163	ARG
2	A	165	VAL
2	A	170	ASN
2	A	179	LEU
2	A	189	LEU
2	A	191	ASN
2	A	197	LEU
2	A	200	VAL
2	A	205	ARG
2	A	210	LEU

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Mol	Chain	Res	Type
2	A	211	VAL
2	A	218	LEU
2	A	221	ARG
2	A	225	TRP
2	A	226	GLU
2	A	235	LEU
2	A	236	LEU
2	A	237	ARG
2	A	242	THR
2	A	244	ILE
2	A	246	LYS
2	A	247	ARG
2	A	257	LYS
2	A	262	LEU
2	A	266	LEU
2	A	267	ARG
2	A	268	ASN
2	A	270	LEU
2	A	272	LEU
2	A	281	ARG
2	A	286	LEU
2	A	290	ILE
2	A	296	GLU
2	A	299	SER
2	A	310	LEU
2	A	322	LEU
2	A	326	GLU
2	A	331	VAL
2	A	336	ARG
2	A	344	SER
2	A	349	ARG
2	A	350	ARG
2	A	356	ARG
2	A	368	LYS
2	A	375	GLU
2	A	376	ASP
2	A	382	LYS
2	A	384	GLN
2	A	385	ARG
2	A	386	LYS
2	A	391	LEU
2	A	393	LEU

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Mol	Chain	Res	Type
2	A	400	ARG
2	A	401	LEU
2	A	405	GLU
2	A	406	GLU
2	A	412	LEU
2	A	423	LYS
2	A	425	VAL
2	A	426	LYS
2	A	432	GLN
2	A	435	ARG
2	A	442	LEU
2	A	443	GLU
2	A	444	THR
2	A	451	LEU
2	A	457	GLU
2	A	458	ARG
2	A	461	ARG
2	A	463	LEU
2	C	13	ASP
2	C	21	ILE
2	C	35	ARG
2	C	37	ILE
2	C	43	THR
2	C	47	ARG
2	C	53	GLU
2	C	55	ARG
2	C	56	ILE
2	C	61	LYS
2	C	66	SER
2	C	72	ASP
2	C	85	ARG
2	C	86	LEU
2	C	88	LEU
2	C	96	LEU
2	C	98	LYS
2	C	99	ARG
2	C	101	TRP
2	C	108	THR
2	C	111	GLU
2	C	113	GLU
2	C	116	ARG
2	C	118	GLU

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Mol	Chain	Res	Type
2	C	119	LYS
2	C	125	ARG
2	C	132	GLU
2	C	137	ARG
2	C	139	ARG
2	C	142	GLU
2	C	147	ARG
2	C	149	LYS
2	C	152	ARG
2	C	155	THR
2	C	162	LEU
2	C	172	GLU
2	C	177	VAL
2	C	179	LEU
2	C	180	LYS
2	C	189	LEU
2	C	191	ASN
2	C	197	LEU
2	C	205	ARG
2	C	211	VAL
2	C	217	VAL
2	C	225	TRP
2	C	229	ARG
2	C	236	LEU
2	C	237	ARG
2	C	241	LYS
2	C	243	LYS
2	C	244	ILE
2	C	246	LYS
2	C	247	ARG
2	C	259	GLU
2	C	266	LEU
2	C	267	ARG
2	C	268	ASN
2	C	270	LEU
2	C	272	LEU
2	C	276	SER
2	C	281	ARG
2	C	286	LEU
2	C	290	ILE
2	C	291	GLN
2	C	294	THR

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Mol	Chain	Res	Type
2	C	307	LEU
2	C	308	GLU
2	C	309	LYS
2	C	310	LEU
2	C	313	MET
2	C	316	LYS
2	C	326	GLU
2	C	331	VAL
2	C	336	ARG
2	C	337	GLU
2	C	341	SER
2	C	349	ARG
2	C	350	ARG
2	C	355	MET
2	C	356	ARG
2	C	358	ARG
2	C	363	LYS
2	C	368	LYS
2	C	370	ARG
2	C	375	GLU
2	C	382	LYS
2	C	384	GLN
2	C	385	ARG
2	C	389	GLU
2	C	391	LEU
2	C	393	LEU
2	C	395	LYS
2	C	401	LEU
2	C	402	ARG
2	C	406	GLU
2	C	412	LEU
2	C	413	GLU
2	C	423	LYS
2	C	426	LYS
2	C	435	ARG
2	C	442	LEU
2	C	444	THR
2	C	451	LEU
2	C	458	ARG
2	C	460	LEU
2	C	463	LEU
2	C	465	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	25	ASN
2	A	114	GLN
2	A	170	ASN
2	A	216	HIS
2	A	232	HIS
2	A	314	ASN
2	A	384	GLN
2	A	429	GLN
2	C	25	ASN
2	C	170	ASN
2	C	188	HIS
2	C	196	HIS
2	C	216	HIS
2	C	232	HIS
2	C	314	ASN
2	C	404	GLN
2	C	429	GLN
2	C	432	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	74/75 (98%)	23 (31%)	14 (18%)
1	D	74/75 (98%)	22 (29%)	14 (18%)
All	All	148/150 (98%)	45 (30%)	28 (18%)

All (45) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	508	U
1	B	509	C
1	B	513	U
1	B	516	C
1	B	517	G
1	B	518	G
1	B	519	U
1	B	520	U
1	B	521	A
1	B	534	C
1	B	548	C

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Mol	Chain	Res	Type
1	B	553	G
1	B	554	U
1	B	556	C
1	B	557	G
1	B	558	A
1	B	559	U
1	B	561	C
1	B	572	C
1	B	573	A
1	B	574	C
1	B	575	C
1	B	576	A
1	D	508	U
1	D	509	C
1	D	513	U
1	D	516	C
1	D	517	G
1	D	518	G
1	D	519	U
1	D	520	U
1	D	521	A
1	D	548	C
1	D	553	G
1	D	554	U
1	D	556	C
1	D	557	G
1	D	558	A
1	D	559	U
1	D	560	U
1	D	572	C
1	D	573	A
1	D	574	C
1	D	575	C
1	D	576	A

All (28) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	B	507	A
1	B	509	C
1	B	515	G
1	B	516	C

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Mol	Chain	Res	Type
1	B	517	G
1	B	518	G
1	B	552	G
1	B	553	G
1	B	556	C
1	B	557	G
1	B	558	A
1	B	560	U
1	B	573	A
1	B	575	C
1	D	509	C
1	D	515	G
1	D	516	C
1	D	517	G
1	D	518	G
1	D	552	G
1	D	553	G
1	D	556	C
1	D	557	G
1	D	558	A
1	D	560	U
1	D	572	C
1	D	574	C
1	D	575	C

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	B	75/75 (100%)	-0.33	2 (2%) 58 57	28, 44, 77, 99	0
1	D	75/75 (100%)	-0.06	1 (1%) 79 79	26, 47, 81, 98	0
2	A	468/468 (100%)	-0.34	2 (0%) 93 93	10, 27, 50, 74	0
2	C	468/468 (100%)	-0.27	8 (1%) 73 72	10, 29, 57, 85	0
All	All	1086/1086 (100%)	-0.29	13 (1%) 81 81	10, 30, 65, 99	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	576	A	4.1
2	C	114	GLN	3.4
2	C	112	LEU	3.3
2	C	48	TYR	3.2
1	D	550	G	2.8
2	A	118	GLU	2.8
2	C	139	ARG	2.6
2	C	46	ALA	2.5
2	C	134	ALA	2.4
2	C	128	ASN	2.3
2	A	247	ARG	2.2
2	C	140	ARG	2.1
1	B	575	C	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.