



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 12:43 PM UTC

PDB ID : 1RY1 / pdb_00001ry1
EMDB ID : EMD-1063
Title : Structure of the signal recognition particle interacting with the elongation-arrested ribosome
Authors : Halic, M.; Becker, T.; Pool, M.R.; Spahn, C.M.; Grassucci, R.A.; Frank, J.; Beckmann, R.
Deposited on : 2003-12-19
Resolution : 12.00 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

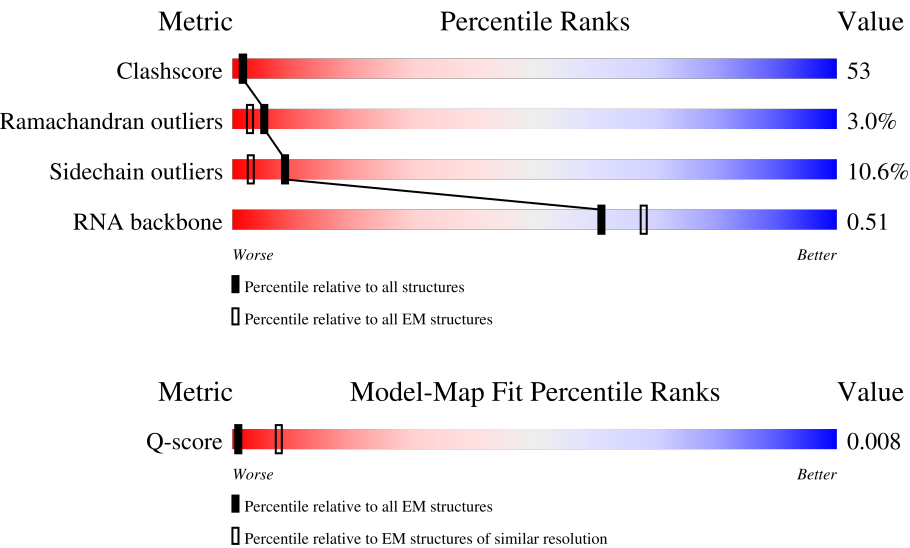
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 12.00 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	93 (11.50 - 12.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	E	50	96% 22% 56% 16% . .
2	A	128	100% 36% 52% 12% .
3	M	27	100% 15% 41% 22% 22%

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Mol	Chain	Length	Quality of chain
4	N	31	
5	O	24	
6	P	20	
7	Q	12	
8	R	12	
9	C	85	
10	D	106	
11	B	108	
12	U	296	
13	W	109	
14	S	18	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 11794 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 SRP Alu domain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	49	Total	C	N	O	P	0	0
			1051	466	190	346	49		

- Molecule 2 is a RNA chain called SRP S domain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	128	Total	C	N	O	P	0	0
			2751	1226	511	886	128		

- Molecule 3 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	27	Total	C	N	O	P	0	0
			585	260	110	188	27		

- Molecule 4 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	31	Total	C	N	O	P	0	0
			649	291	109	218	31		

- Molecule 5 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	O	24	Total	C	N	O	P	0	0
			511	227	86	174	24		

- Molecule 6 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	P	19	Total	C	N	O	P	0	0
			401	180	72	130	19		

- Molecule 7 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Q	12	Total	C	N	O	P	0	0
			257	114	45	86	12		

- Molecule 8 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	R	12	Total	C	N	O	P	0	0
			254	113	43	86	12		

- Molecule 9 is a protein called SRP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	71	Total	C	N	O	S	0	0
			580	369	101	105	5		

- Molecule 10 is a protein called SRP14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	76	Total	C	N	O	S	0	0
			604	382	105	113	4		

- Molecule 11 is a protein called SRP19.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	107	Total	C	N	O	S	0	0
			870	549	159	156	6		

- Molecule 12 is a protein called SRP54NG.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	U	294	Total	C	N	O	S	0	0
			2266	1424	413	423	6		

- Molecule 13 is a protein called SRP54M.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	W	109	Total	C	N	O	S	0	0
			865	540	150	164	11		

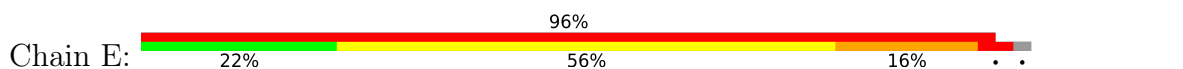
- Molecule 14 is a protein called signal sequence peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	S	18	Total	C	N	O	0	0
			150	103	24	23		

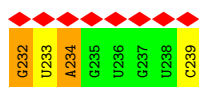
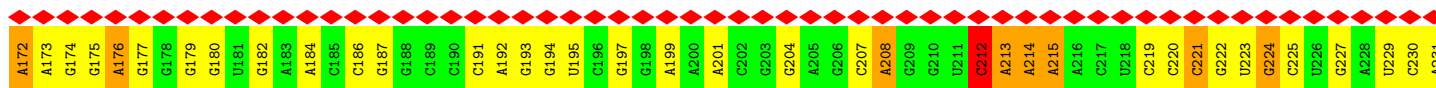
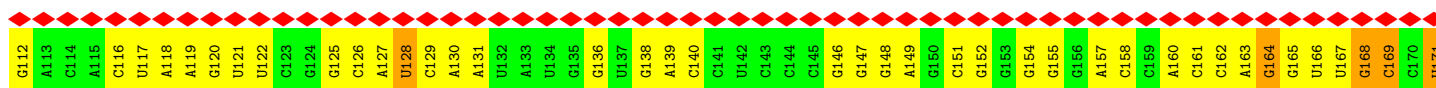
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: SRP Alu domain



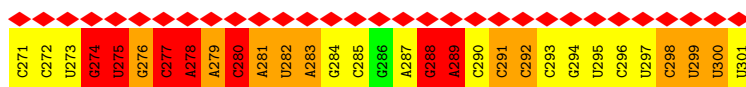
- Molecule 2: SRP S domain



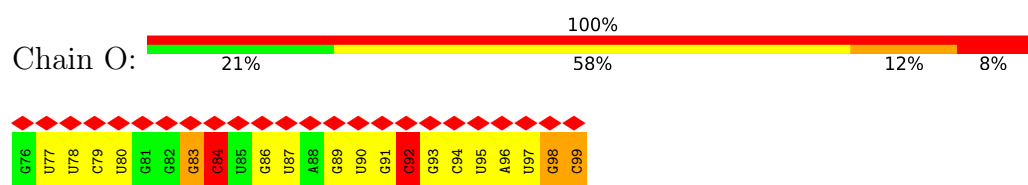
- Molecule 3: SRP RNA



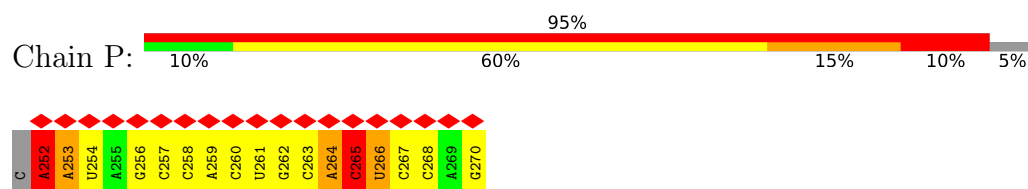
- Molecule 4: SRP RNA



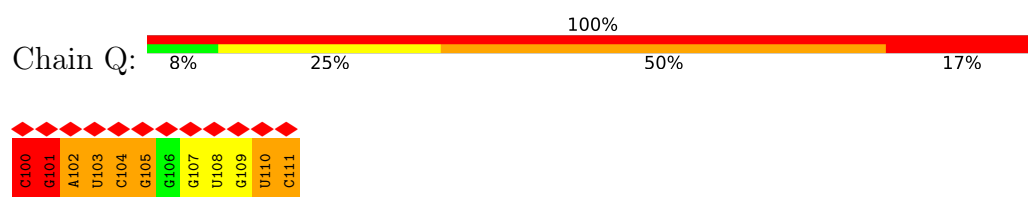
- Molecule 5: SRP RNA



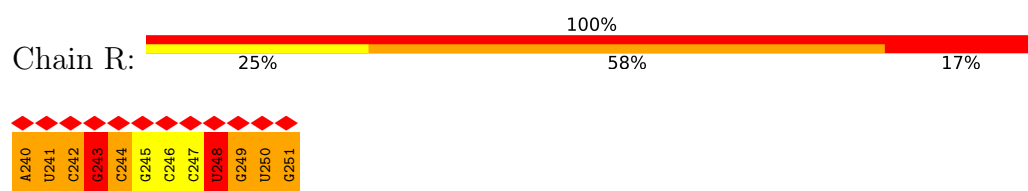
- Molecule 6: SRP RNA



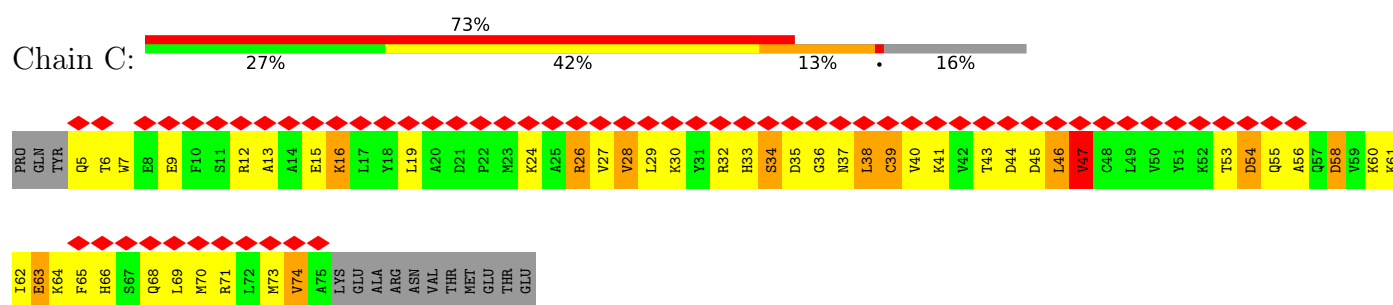
- Molecule 7: SRP RNA



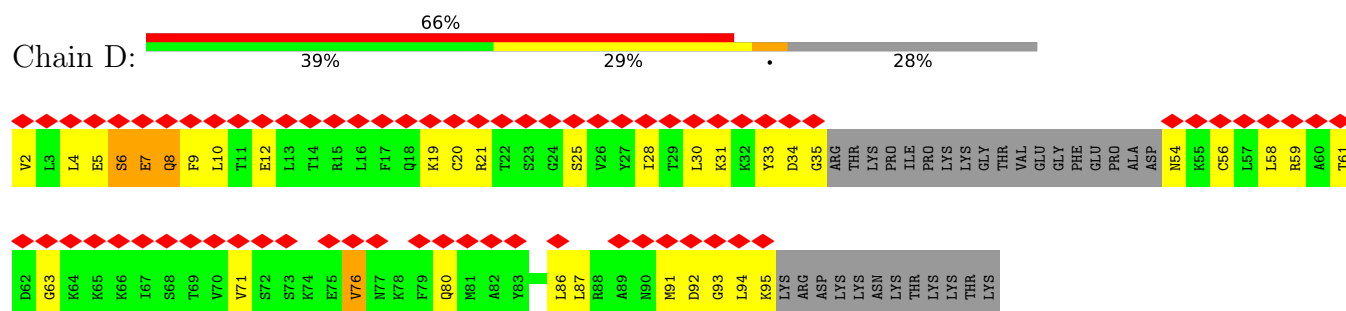
- Molecule 8: SRP RNA



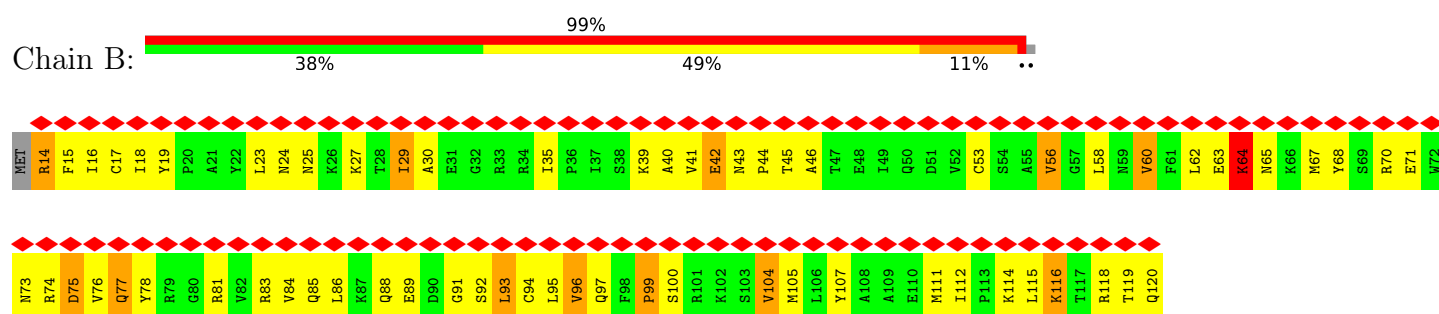
- Molecule 9: SRP9



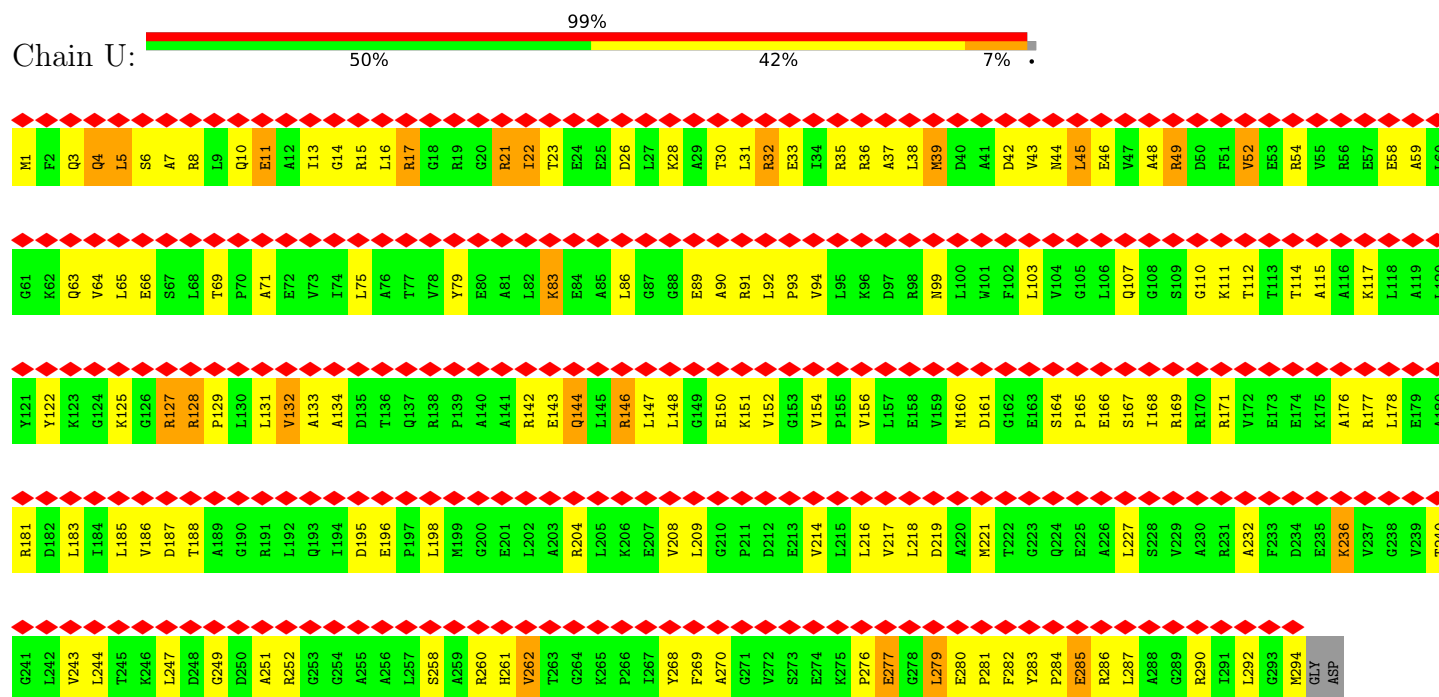
- Molecule 10: SRP14



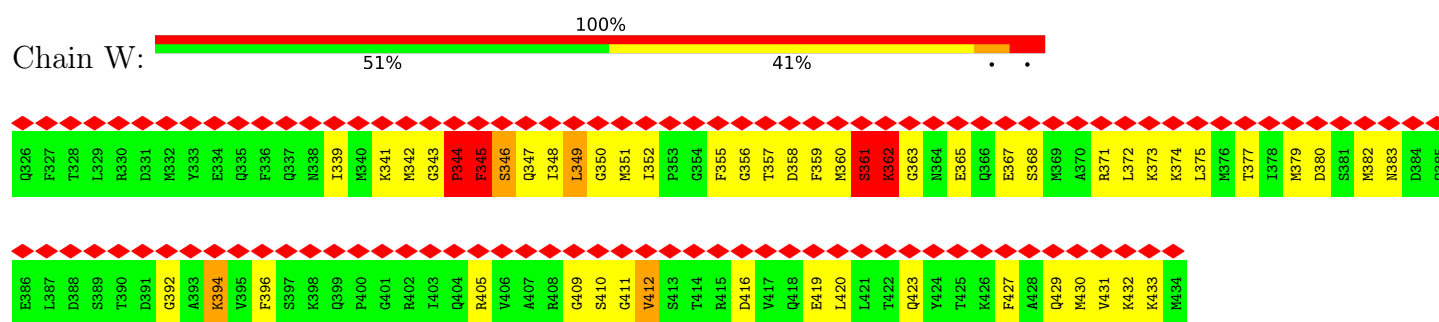
- Molecule 11: SRP19



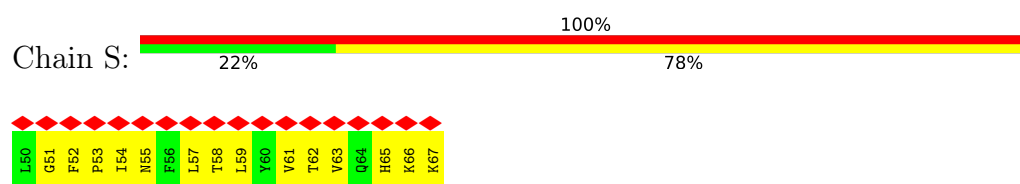
• Molecule 12: SRP54NG



• Molecule 13: SRP54M



• Molecule 14: signal sequence peptide



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	160	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	10000	Depositor
Maximum defocus (nm)	45000	Depositor
Magnification	52000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.002	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.00055	Depositor
Map size ($\text{\AA}$)	423.8, 423.8, 423.8	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	3.26, 3.26, 3.26	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CCC

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	E	0.40	0/1173	0.73	3/1829 (0.2%)
2	A	0.36	0/3055	0.69	1/4766 (0.0%)
3	M	0.94	2/651 (0.3%)	1.98	9/1005 (0.9%)
4	N	1.77	4/721 (0.6%)	2.44	16/1116 (1.4%)
5	O	0.65	0/567	2.36	6/877 (0.7%)
6	P	0.67	0/446	1.99	4/689 (0.6%)
7	Q	1.99	2/284 (0.7%)	3.15	8/436 (1.8%)
8	R	1.03	1/282 (0.4%)	2.51	7/437 (1.6%)
9	C	0.50	0/589	1.03	4/791 (0.5%)
10	D	0.48	0/608	0.92	1/809 (0.1%)
11	B	0.57	0/884	1.05	1/1188 (0.1%)
12	U	0.33	0/2291	0.83	2/3086 (0.1%)
13	W	1.34	3/876 (0.3%)	1.82	9/1165 (0.8%)
14	S	0.69	0/154	1.12	1/208 (0.5%)
All	All	0.78	12/12581 (0.1%)	1.43	72/18402 (0.4%)

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
2	A	0	3
13	W	0	5
All	All	0	8

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	N	288	G	O3'-P	32.48	2.09	1.61
7	Q	110	U	O3'-P	30.94	2.07	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	W	345	PHE	C-N	-29.96	0.91	1.33
4	N	292	C	O3'-P	27.79	2.02	1.61
13	W	362	LYS	C-N	21.42	1.64	1.33
3	M	74	G	O3'-P	15.83	1.84	1.61
8	R	248	U	O3'-P	13.54	1.81	1.61
4	N	275	U	O3'-P	8.91	1.74	1.61
13	W	344	PRO	C-N	7.30	1.44	1.33
7	Q	103	U	O3'-P	-7.03	1.50	1.61
3	M	56	A	O3'-P	6.66	1.71	1.61
4	N	287	A	O3'-P	-5.35	1.53	1.61

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	O	92	C	P-O3'-C3'	-52.62	41.28	120.20
4	N	280	C	P-O3'-C3'	-46.14	50.99	120.20
3	M	69	U	O3'-P-O5'	-45.94	35.09	104.00
6	P	252	A	P-O3'-C3'	-36.61	65.29	120.20
7	Q	100	C	O3'-P-O5'	35.99	157.99	104.00
7	Q	103	U	O3'-P-O5'	-35.49	50.76	104.00
5	O	83	G	O3'-P-O5'	34.42	155.62	104.00
4	N	277	C	O3'-P-O5'	33.81	154.72	104.00
8	R	248	U	O3'-P-O5'	-33.12	54.33	104.00
7	Q	101	G	P-O3'-C3'	-32.56	71.36	120.20
13	W	362	LYS	CA-C-N	-30.04	62.53	121.41
13	W	362	LYS	C-N-CA	-30.04	62.53	121.41
4	N	289	A	O3'-P-O5'	29.40	148.11	104.00
6	P	264	A	O3'-P-O5'	-25.68	65.47	104.00
4	N	275	U	P-O3'-C3'	23.32	155.18	120.20
8	R	250	U	O3'-P-O5'	21.48	136.22	104.00
8	R	240	A	O3'-P-O5'	-19.34	74.98	104.00
3	M	56	A	O3'-P-O5'	19.16	132.74	104.00
6	P	265	C	P-O3'-C3'	-19.01	91.69	120.20
3	M	65	U	P-O3'-C3'	-18.58	92.32	120.20
4	N	278	A	O3'-P-O5'	-16.40	79.40	104.00
13	W	362	LYS	O-C-N	15.39	143.05	122.59
13	W	345	PHE	CA-C-N	15.32	150.81	121.54
13	W	345	PHE	C-N-CA	15.32	150.81	121.54
4	N	274	G	O3'-P-O5'	-15.17	81.25	104.00
5	O	84	C	P-O3'-C3'	-14.81	97.99	120.20
8	R	243	G	P-O3'-C3'	14.22	141.53	120.20
8	R	248	U	OP1-P-O3'	14.12	150.35	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	N	288	G	O3'-P-O5'	-13.80	83.29	104.00
7	Q	110	U	P-O3'-C3'	13.71	140.77	120.20
3	M	58	G	O3'-P-O5'	-13.50	83.75	104.00
3	M	59	A	P-O3'-C3'	12.90	139.55	120.20
3	M	57	G	P-O3'-C3'	-12.66	101.21	120.20
13	W	361	SER	O-C-N	12.40	137.35	123.33
4	N	287	A	O3'-P-O5'	12.23	122.35	104.00
5	O	91	G	O3'-P-O5'	11.80	121.70	104.00
8	R	248	U	P-O3'-C3'	11.14	136.91	120.20
7	Q	110	U	O3'-P-O5'	-10.87	87.69	104.00
7	Q	100	C	OP2-P-O3'	-9.53	79.42	108.00
4	N	288	G	P-O3'-C3'	-9.47	106.00	120.20
5	O	83	G	OP2-P-O3'	-9.17	80.49	108.00
4	N	277	C	OP2-P-O3'	-9.04	80.87	108.00
7	Q	100	C	OP1-P-O3'	-8.63	82.11	108.00
13	W	361	SER	CA-C-N	-8.47	105.36	121.54
13	W	361	SER	C-N-CA	-8.47	105.36	121.54
5	O	83	G	OP1-P-O3'	-8.16	83.52	108.00
4	N	277	C	OP1-P-O3'	-8.05	83.86	108.00
4	N	289	A	OP2-P-O3'	-7.98	84.07	108.00
13	W	344	PRO	O-C-N	-7.70	112.25	122.64
14	S	66	LYS	N-CA-C	6.96	121.38	112.34
4	N	298	C	O3'-P-O5'	6.85	114.28	104.00
4	N	289	A	OP1-P-O3'	-6.72	87.82	108.00
3	M	74	G	P-O3'-C3'	-6.71	110.14	120.20
9	C	30	LYS	N-CA-C	6.69	119.64	108.20
12	U	110	GLY	N-CA-C	-6.48	105.97	115.63
8	R	250	U	OP2-P-O3'	-6.06	89.81	108.00
9	C	54	ASP	N-CA-C	-5.97	107.23	114.75
4	N	292	C	O3'-P-O5'	5.89	112.84	104.00
7	Q	103	U	OP1-P-O3'	5.80	125.39	108.00
1	E	137	C	C2'-C3'-O3'	5.72	122.27	113.70
12	U	262	VAL	N-CA-C	5.62	115.81	110.53
1	E	132	A	C2'-C3'-O3'	5.57	117.85	109.50
3	M	56	A	OP2-P-O3'	-5.56	91.32	108.00
6	P	264	A	OP1-P-O3'	5.54	124.62	108.00
4	N	277	C	P-O3'-C3'	5.48	128.42	120.20
2	A	212	C	C2'-C3'-O3'	5.38	117.58	109.50
9	C	16	LYS	N-CA-C	-5.21	105.28	111.69
11	B	60	VAL	N-CA-C	5.17	115.01	107.88
10	D	33	TYR	N-CA-C	5.08	117.53	109.50
1	E	132	A	C5'-C4'-C3'	-5.08	107.58	115.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	69	U	OP1-P-O3'	5.07	123.22	108.00
9	C	58	ASP	N-CA-C	5.01	119.40	113.28

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	197	G	Sidechain
2	A	201	A	Sidechain
2	A	208	A	Sidechain
13	W	344	PRO	Peptide,Mainchain
13	W	361	SER	Peptide,Mainchain
13	W	362	LYS	Peptide

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	E	1051	0	528	84	0
2	A	2751	0	1387	98	0
3	M	585	0	289	99	0
4	N	649	0	330	150	0
5	O	511	0	258	25	0
6	P	401	0	208	107	0
7	Q	257	0	129	83	0
8	R	254	0	128	75	0
9	C	580	0	594	88	0
10	D	604	0	638	36	0
11	B	870	0	901	85	0
12	U	2266	0	2367	231	0
13	W	865	0	865	237	0
14	S	150	0	158	66	0
All	All	11794	0	8780	1090	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 53.

All (1090) 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)
6:P:252:A:C2	8:R:250:U:H2'	1.25	1.63
12:U:281:PRO:CB	13:W:347:GLN:HG3	1.15	1.61
4:N:274:G:H2'	4:N:275:U:C5	1.11	1.59
12:U:283:TYR:CE1	13:W:360:MET:HB2	1.05	1.56
7:Q:104:C:H1'	7:Q:105:G:C8	1.36	1.56
4:N:274:G:C2'	4:N:275:U:C5	1.89	1.54
12:U:283:TYR:HE1	13:W:360:MET:CB	1.19	1.50
13:W:339:ILE:HD11	14:S:54:ILE:CG2	1.36	1.50
6:P:252:A:H5'	7:Q:102:A:N7	1.25	1.49
6:P:263:C:H3'	6:P:265:C:N4	1.21	1.48
12:U:283:TYR:CE1	13:W:360:MET:HE3	1.46	1.48
4:N:290:C:C2'	4:N:291:C:H5'	1.46	1.46
6:P:252:A:N3	8:R:250:U:C2	1.80	1.46
6:P:252:A:C2	8:R:250:U:C2'	1.95	1.45
13:W:339:ILE:CD1	14:S:54:ILE:CG2	1.91	1.45
12:U:283:TYR:OH	13:W:359:PHE:CD2	1.68	1.44
12:U:286:ARG:NH2	13:W:360:MET:HB3	1.15	1.44
6:P:252:A:N1	8:R:250:U:C2'	1.82	1.43
6:P:252:A:C4	8:R:250:U:C2	2.08	1.41
12:U:285:GLU:CD	13:W:359:PHE:HB2	1.44	1.41
6:P:252:A:C2	8:R:250:U:C2	2.09	1.39
12:U:281:PRO:HB3	13:W:347:GLN:CG	0.93	1.39
6:P:263:C:C3'	6:P:265:C:H41	1.31	1.39
6:P:264:A:O5'	6:P:265:C:C5	1.75	1.37
12:U:286:ARG:HH21	13:W:360:MET:CB	1.38	1.37
6:P:264:A:O5'	6:P:265:C:H5	1.04	1.36
7:Q:104:C:O2	7:Q:105:G:N7	1.59	1.36
4:N:281:A:OP2	4:N:281:A:C8	1.78	1.36
3:M:56:A:C8	9:C:45:ASP:O	1.80	1.35
1:E:105:G:C4'	4:N:290:C:H1'	1.57	1.34
4:N:290:C:H2'	4:N:291:C:C5'	1.57	1.34
1:E:123:U:C2'	3:M:57:G:O2'	1.68	1.34
6:P:252:A:N1	8:R:250:U:H2'	1.04	1.34
12:U:285:GLU:CB	13:W:359:PHE:H	1.41	1.33
12:U:283:TYR:CZ	13:W:360:MET:HE2	1.66	1.31
6:P:257:C:O3'	6:P:258:C:H5'	1.22	1.30
7:Q:104:C:C1'	7:Q:105:G:C8	2.13	1.30
12:U:283:TYR:CE1	13:W:360:MET:CE	2.15	1.29
6:P:252:A:C5'	7:Q:102:A:N7	1.95	1.28
13:W:372:LEU:HD11	14:S:58:THR:CG2	1.62	1.28
13:W:423:GLN:NE2	14:S:65:HIS:NE2	1.82	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:124:G:P	3:M:57:G:H4'	1.73	1.27
7:Q:104:C:O2'	7:Q:105:G:H8	1.08	1.27
1:E:124:G:P	3:M:57:G:C4'	2.22	1.27
8:R:250:U:C5'	8:R:251:G:OP2	1.80	1.27
13:W:339:ILE:CD1	14:S:54:ILE:HG23	1.58	1.26
8:R:250:U:H5''	8:R:251:G:OP2	1.13	1.26
1:E:101:G:O2'	3:M:49:A:OP2	1.53	1.24
4:N:288:G:O4'	4:N:288:G:OP2	1.55	1.23
12:U:283:TYR:CZ	13:W:360:MET:CE	2.21	1.23
13:W:343:GLY:O	13:W:346:SER:HB2	1.05	1.22
4:N:271:C:H5'	6:P:270:G:C3'	1.70	1.22
6:P:264:A:P	6:P:265:C:C5	2.32	1.22
2:A:112:G:N3	7:Q:111:C:O2	1.72	1.22
13:W:423:GLN:HE22	14:S:65:HIS:CD2	1.55	1.22
7:Q:103:U:H3'	7:Q:104:C:C5	1.74	1.21
6:P:252:A:C5	8:R:250:U:O2	1.91	1.21
12:U:281:PRO:HB3	13:W:347:GLN:CB	1.70	1.21
1:E:123:U:H2'	3:M:57:G:O2'	1.24	1.21
13:W:419:GLU:HB3	14:S:65:HIS:CE1	1.76	1.20
7:Q:104:C:C6	7:Q:104:C:OP2	1.94	1.20
6:P:252:A:C4	8:R:250:U:N3	2.10	1.20
13:W:372:LEU:CG	14:S:58:THR:HG23	1.72	1.20
12:U:285:GLU:CD	13:W:359:PHE:CB	2.16	1.18
13:W:361:SER:O	13:W:362:LYS:HG3	1.43	1.18
4:N:298:C:H5''	4:N:299:U:OP1	1.43	1.18
3:M:57:G:C5'	3:M:58:G:OP1	1.90	1.18
4:N:299:U:C2'	4:N:300:U:O5'	1.92	1.18
12:U:283:TYR:CE1	13:W:360:MET:CB	2.02	1.17
12:U:283:TYR:OH	13:W:360:MET:HE2	1.42	1.17
7:Q:104:C:C2'	7:Q:105:G:H8	1.58	1.17
1:E:105:G:H4'	4:N:290:C:C1'	1.74	1.16
3:M:57:G:H5''	3:M:58:G:OP1	1.01	1.16
12:U:286:ARG:NH2	13:W:360:MET:CB	1.97	1.16
4:N:292:C:O3'	4:N:293:C:P	2.02	1.16
13:W:372:LEU:CD1	14:S:58:THR:HG23	1.76	1.15
6:P:252:A:C2	8:R:250:U:N1	2.13	1.15
1:E:125:U:O2'	4:N:292:C:H4'	1.48	1.14
12:U:283:TYR:CE2	13:W:350:GLY:HA2	1.79	1.14
13:W:427:PHE:CD1	14:S:57:LEU:HD21	1.82	1.14
6:P:264:A:C8	6:P:265:C:C5	2.35	1.14
6:P:264:A:H8	6:P:265:C:C5	1.65	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:P:252:A:C6	8:R:250:U:O2	2.01	1.13
7:Q:110:U:O3'	7:Q:111:C:P	2.07	1.13
6:P:252:A:H1'	8:R:250:U:C4	1.84	1.12
12:U:285:GLU:HB3	13:W:359:PHE:N	1.64	1.11
4:N:274:G:N3	4:N:275:U:O4	1.82	1.11
12:U:285:GLU:CG	13:W:359:PHE:HB2	1.81	1.11
13:W:343:GLY:O	13:W:346:SER:CB	1.97	1.11
4:N:280:C:O2	4:N:281:A:C5'	1.99	1.11
13:W:339:ILE:HD13	14:S:54:ILE:HG22	1.31	1.11
6:P:252:A:O5'	7:Q:102:A:C5	2.04	1.10
6:P:257:C:O3'	6:P:258:C:C5'	1.98	1.10
4:N:299:U:O2'	4:N:300:U:O5'	1.67	1.10
12:U:281:PRO:CB	13:W:347:GLN:CG	1.90	1.10
13:W:423:GLN:CD	14:S:65:HIS:NE2	2.10	1.10
12:U:89:GLU:HB3	13:W:351:MET:C	1.75	1.09
5:O:98:G:H4'	5:O:99:C:OP1	1.30	1.09
6:P:264:A:C8	6:P:265:C:C6	2.41	1.09
4:N:288:G:O3'	4:N:289:A:P	2.09	1.08
4:N:271:C:H5'	6:P:270:G:H3'	1.29	1.08
7:Q:104:C:O2'	7:Q:105:G:O5'	1.71	1.08
4:N:301:U:OP2	4:N:301:U:C3'	2.00	1.08
13:W:374:LYS:NZ	14:S:67:LYS:HB3	1.69	1.08
12:U:286:ARG:HH21	13:W:360:MET:CA	1.56	1.08
6:P:252:A:C5'	7:Q:102:A:C5	2.28	1.07
13:W:427:PHE:CE1	14:S:57:LEU:CD2	2.37	1.07
7:Q:104:C:P	7:Q:104:C:H3'	1.94	1.07
3:M:57:G:OP2	9:C:43:THR:HG21	1.53	1.06
7:Q:104:C:OP2	7:Q:104:C:H3'	1.54	1.06
12:U:285:GLU:HB3	13:W:359:PHE:H	1.17	1.06
6:P:252:A:C4	8:R:250:U:O2	2.03	1.06
1:E:123:U:O3'	3:M:57:G:H4'	1.52	1.05
12:U:285:GLU:CB	13:W:359:PHE:N	2.18	1.05
4:N:301:U:C3'	4:N:301:U:P	2.45	1.05
12:U:285:GLU:CG	13:W:359:PHE:CB	2.32	1.05
13:W:372:LEU:CD1	14:S:58:THR:CG2	2.32	1.05
4:N:280:C:C2	4:N:281:A:H5'	1.90	1.04
6:P:252:A:P	7:Q:102:A:C8	2.51	1.04
4:N:280:C:O2	4:N:281:A:H5''	1.54	1.03
6:P:252:A:C2	8:R:250:U:C1'	2.40	1.03
6:P:265:C:O2'	6:P:266:U:O5'	1.66	1.03
12:U:281:PRO:CB	13:W:347:GLN:CB	2.34	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:P:252:A:H1'	8:R:250:U:O4	1.56	1.03
6:P:264:A:OP2	6:P:265:C:C4	2.11	1.02
13:W:339:ILE:HD13	14:S:54:ILE:CG2	1.86	1.02
6:P:265:C:HO2'	6:P:266:U:H6	1.02	1.02
12:U:283:TYR:CE1	13:W:359:PHE:O	2.13	1.02
1:E:105:G:H4'	4:N:290:C:H1'	1.02	1.02
6:P:264:A:OP2	6:P:265:C:C5	2.11	1.02
12:U:285:GLU:CB	13:W:359:PHE:HB3	1.90	1.02
9:C:38:LEU:HD12	9:C:39:CYS:H	1.17	1.02
8:R:242:C:H5'	8:R:243:G:OP2	1.61	1.01
4:N:280:C:C2	4:N:281:A:C5'	2.43	1.01
2:A:112:G:C2	7:Q:111:C:O2	2.12	1.01
6:P:252:A:N3	8:R:250:U:N3	2.04	1.01
7:Q:104:C:C2'	7:Q:105:G:C8	2.38	1.01
12:U:283:TYR:CZ	13:W:359:PHE:O	2.13	1.00
4:N:271:C:C5'	6:P:270:G:O3'	2.09	1.00
4:N:281:A:OP2	4:N:281:A:H3'	1.62	1.00
13:W:372:LEU:HD11	14:S:58:THR:HG21	1.39	1.00
12:U:91:ARG:HG2	13:W:351:MET:HB3	1.42	1.00
7:Q:104:C:O3'	7:Q:105:G:P	2.20	0.99
13:W:339:ILE:CD1	14:S:54:ILE:HG22	1.80	0.99
9:C:28:VAL:HG22	9:C:41:LYS:HB3	1.44	0.99
12:U:125:LYS:HE3	13:W:344:PRO:CB	1.91	0.99
12:U:125:LYS:CE	13:W:344:PRO:HB3	1.91	0.99
12:U:283:TYR:OH	13:W:359:PHE:CE2	2.09	0.99
12:U:285:GLU:HG2	13:W:359:PHE:N	1.77	0.99
12:U:285:GLU:CG	13:W:359:PHE:H	1.76	0.98
6:P:264:A:P	6:P:265:C:H5	1.76	0.98
1:E:124:G:OP1	3:M:57:G:C4'	2.10	0.98
7:Q:103:U:H3'	7:Q:104:C:C6	1.99	0.98
6:P:264:A:H3'	6:P:265:C:H6	1.24	0.97
13:W:372:LEU:HD11	14:S:58:THR:HG23	1.30	0.97
13:W:371:ARG:NH2	14:S:63:VAL:HA	1.37	0.96
13:W:372:LEU:CD2	14:S:58:THR:HG23	1.95	0.96
2:A:220:C:H2'	2:A:221:C:H5''	1.45	0.96
8:R:240:A:O3'	8:R:242:C:H5''	1.64	0.95
6:P:252:A:H5'	7:Q:102:A:C5	1.98	0.95
2:A:112:G:C4	7:Q:111:C:O2	2.20	0.95
3:M:55:G:H5''	9:C:46:LEU:HD11	1.48	0.95
12:U:285:GLU:HB3	13:W:359:PHE:CA	1.95	0.95
1:E:124:G:OP1	3:M:57:G:H4'	1.67	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:278:A:H2'	4:N:279:A:H5''	1.48	0.94
3:M:55:G:O3'	3:M:56:A:OP1	1.85	0.94
9:C:55:GLN:HA	10:D:95:LYS:HB2	1.49	0.94
12:U:281:PRO:HB3	13:W:347:GLN:CD	1.92	0.94
4:N:274:G:C2'	4:N:275:U:H5	1.45	0.94
4:N:299:U:H2'	4:N:300:U:O5'	1.68	0.94
12:U:89:GLU:CB	13:W:351:MET:C	2.40	0.94
6:P:252:A:H2	8:R:250:U:C2'	1.62	0.94
13:W:374:LYS:NZ	14:S:67:LYS:CB	2.27	0.94
4:N:271:C:H4'	6:P:270:G:O3'	1.67	0.93
12:U:285:GLU:CB	13:W:359:PHE:CB	2.46	0.93
13:W:427:PHE:CE1	14:S:57:LEU:HD21	2.01	0.93
12:U:281:PRO:CG	13:W:347:GLN:HB2	1.98	0.93
7:Q:103:U:H3'	7:Q:104:C:H5	1.33	0.93
4:N:281:A:OP2	4:N:281:A:H8	1.36	0.93
11:B:60:VAL:HG23	11:B:83:ARG:O	1.67	0.93
4:N:271:C:C5'	6:P:270:G:C3'	2.46	0.93
8:R:250:U:C4'	8:R:251:G:OP2	2.11	0.93
13:W:427:PHE:CE1	14:S:57:LEU:HD23	2.03	0.93
4:N:274:G:O2'	4:N:275:U:C5	2.20	0.92
1:E:123:U:C2'	3:M:57:G:C2'	2.42	0.92
12:U:89:GLU:HB3	13:W:352:ILE:N	1.52	0.92
13:W:423:GLN:NE2	14:S:65:HIS:CD2	2.28	0.92
12:U:283:TYR:CE2	13:W:350:GLY:CA	2.51	0.92
12:U:281:PRO:CA	13:W:347:GLN:HG3	1.99	0.91
12:U:89:GLU:CB	13:W:352:ILE:N	2.28	0.91
13:W:367:GLU:O	14:S:62:THR:HG21	1.71	0.91
3:M:57:G:P	9:C:26:ARG:NH2	2.44	0.91
2:A:112:G:C2	7:Q:111:C:C2	2.58	0.91
8:R:242:C:H5'	8:R:244:C:H5'	1.53	0.91
12:U:125:LYS:HE3	13:W:344:PRO:HB3	0.96	0.90
12:U:286:ARG:HH22	13:W:360:MET:HB3	1.34	0.90
7:Q:103:U:C3'	7:Q:104:C:C5	2.54	0.90
7:Q:104:C:OP2	7:Q:104:C:C3'	2.18	0.90
6:P:257:C:HO3'	6:P:258:C:H5'	1.10	0.90
2:A:127:A:C2'	2:A:128:U:H5''	2.02	0.89
11:B:64:LYS:HD3	11:B:64:LYS:N	1.88	0.89
10:D:61:THR:HG22	10:D:63:GLY:H	1.36	0.89
4:N:281:A:OP2	4:N:281:A:C3'	2.21	0.89
7:Q:103:U:C3'	7:Q:104:C:C6	2.55	0.89
12:U:285:GLU:CG	13:W:359:PHE:N	2.33	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:280:C:O2	4:N:281:A:H5'	1.68	0.89
12:U:92:LEU:HD12	13:W:348:ILE:N	1.85	0.88
6:P:252:A:C2	8:R:250:U:O2	2.26	0.88
13:W:372:LEU:HD21	14:S:58:THR:HG23	1.55	0.88
4:N:298:C:C5'	4:N:299:U:OP1	2.22	0.88
4:N:299:U:O2'	4:N:300:U:C5'	2.21	0.88
7:Q:100:C:O2'	7:Q:101:G:P	2.31	0.88
11:B:94:CYS:O	11:B:95:LEU:HD23	1.74	0.88
4:N:274:G:C2'	4:N:275:U:C6	2.51	0.88
4:N:281:A:C8	4:N:281:A:P	2.67	0.87
12:U:283:TYR:CD1	13:W:360:MET:HB2	2.04	0.87
5:O:83:G:H1	6:P:266:U:H3	1.22	0.87
12:U:89:GLU:OE1	13:W:352:ILE:HG22	1.73	0.87
6:P:264:A:H5''	6:P:265:C:OP2	1.73	0.87
5:O:84:C:H2'	5:O:86:G:OP2	1.74	0.87
13:W:419:GLU:HB3	14:S:65:HIS:HE1	1.23	0.87
2:A:127:A:H2'	2:A:128:U:H5''	1.57	0.87
4:N:271:C:C5'	6:P:270:G:H3'	2.04	0.87
3:M:51:G:H1	4:N:295:U:H3	1.22	0.87
12:U:268:TYR:O	13:W:347:GLN:NE2	2.06	0.87
3:M:69:U:H3	4:N:276:G:H1	1.22	0.86
1:E:122:C:O2	3:M:58:G:N7	2.05	0.86
5:O:84:C:C2'	5:O:86:G:OP2	2.24	0.86
9:C:5:GLN:HG3	9:C:6:THR:H	1.40	0.86
4:N:282:U:H4'	4:N:282:U:OP2	1.73	0.86
13:W:372:LEU:CG	14:S:58:THR:CG2	2.53	0.86
9:C:38:LEU:HD12	9:C:39:CYS:N	1.91	0.85
12:U:90:ALA:N	13:W:350:GLY:O	1.91	0.85
13:W:427:PHE:CD1	14:S:57:LEU:CD2	2.57	0.85
4:N:271:C:C4'	6:P:270:G:O3'	2.24	0.85
3:M:59:A:O2'	3:M:60:U:C5	2.30	0.85
3:M:55:G:H5''	9:C:46:LEU:CD1	2.06	0.85
4:N:280:C:O2'	4:N:281:A:H3'	1.77	0.85
2:A:184:A:N3	13:W:405:ARG:NH1	2.24	0.85
13:W:344:PRO:C	13:W:346:SER:N	2.34	0.85
7:Q:105:G:H1	8:R:248:U:H3	1.22	0.85
13:W:375:LEU:HD11	14:S:61:VAL:HG11	1.57	0.85
8:R:241:U:O2'	8:R:245:G:H5'	1.76	0.84
7:Q:103:U:H3	8:R:249:G:H1	1.22	0.84
12:U:285:GLU:OE1	13:W:359:PHE:HB2	1.76	0.84
4:N:278:A:O2'	4:N:279:A:P	2.35	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:O:87:U:H3	6:P:262:G:H1	1.22	0.84
12:U:132:VAL:HG13	12:U:186:VAL:HA	1.59	0.84
12:U:285:GLU:OE1	13:W:355:PHE:C	2.21	0.83
7:Q:103:U:C5	7:Q:104:C:N4	2.46	0.83
11:B:24:ASN:HD22	11:B:27:LYS:HG3	1.42	0.83
7:Q:104:C:H1'	7:Q:105:G:N7	1.94	0.83
12:U:16:LEU:HD22	12:U:22:ILE:HD12	1.61	0.83
12:U:285:GLU:HB3	13:W:359:PHE:CB	2.06	0.83
7:Q:108:U:H3	8:R:245:G:H1	1.22	0.83
12:U:89:GLU:HB3	13:W:351:MET:O	1.77	0.83
7:Q:109:G:H3'	7:Q:110:U:P	2.18	0.82
3:M:57:G:P	9:C:26:ARG:HH22	2.01	0.82
1:E:127:G:O6	4:N:293:C:P	2.37	0.82
4:N:274:G:C2	4:N:275:U:O4	2.32	0.82
4:N:278:A:O2'	4:N:279:A:O5'	1.96	0.82
12:U:89:GLU:CB	13:W:351:MET:O	2.28	0.82
13:W:419:GLU:OE2	14:S:65:HIS:ND1	2.13	0.81
13:W:394:LYS:HZ3	13:W:394:LYS:HB3	1.45	0.81
4:N:278:A:C2'	4:N:279:A:C5'	2.59	0.81
13:W:339:ILE:HD11	14:S:54:ILE:HG23	0.81	0.81
6:P:264:A:O5'	6:P:265:C:C6	2.33	0.81
4:N:288:G:O2'	4:N:289:A:OP2	1.99	0.81
10:D:4:LEU:HD22	10:D:8:GLN:HG2	1.60	0.81
13:W:339:ILE:HD11	14:S:54:ILE:HG21	1.58	0.81
2:A:112:G:C4	7:Q:111:C:C2	2.69	0.81
4:N:278:A:C2'	4:N:279:A:H5''	2.10	0.81
1:E:123:U:O3'	3:M:57:G:C4'	2.25	0.81
11:B:14:ARG:NH1	11:B:14:ARG:HB3	1.96	0.80
6:P:252:A:H1'	8:R:250:U:N3	1.97	0.80
12:U:285:GLU:HB3	13:W:359:PHE:HB3	1.63	0.80
13:W:361:SER:O	13:W:362:LYS:CG	2.27	0.80
12:U:79:TYR:HE1	13:W:358:ASP:CG	1.90	0.80
12:U:92:LEU:HD12	13:W:348:ILE:H	1.45	0.80
5:O:98:G:C4'	5:O:99:C:OP1	2.22	0.80
4:N:289:A:O4'	4:N:289:A:OP1	2.00	0.80
8:R:241:U:P	8:R:242:C:H5''	2.22	0.80
3:M:56:A:N9	9:C:45:ASP:O	2.13	0.79
4:N:279:A:H4'	4:N:280:C:OP2	1.82	0.79
7:Q:100:C:O2'	7:Q:101:G:H5'	1.82	0.79
1:E:104:G:N2	3:M:57:G:N2	2.29	0.79
12:U:281:PRO:HB2	13:W:347:GLN:HG3	1.56	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:U:283:TYR:CZ	13:W:359:PHE:CD2	2.69	0.79
13:W:371:ARG:NH1	14:S:63:VAL:C	2.37	0.79
12:U:283:TYR:OH	13:W:359:PHE:CG	2.34	0.79
3:M:57:G:H5''	3:M:58:G:P	2.22	0.79
4:N:278:A:C3'	4:N:279:A:C5'	2.59	0.79
5:O:84:C:N3	5:O:86:G:OP1	2.06	0.79
6:P:252:A:N9	8:R:250:U:N3	2.31	0.78
4:N:278:A:C2'	4:N:279:A:O5'	2.32	0.78
4:N:277:C:H4'	4:N:278:A:OP2	1.83	0.78
8:R:240:A:C5	8:R:242:C:N3	2.43	0.78
2:A:220:C:C2'	2:A:221:C:H5''	2.14	0.78
4:N:288:G:C2'	4:N:289:A:P	2.72	0.77
9:C:70:MET:HB2	10:D:30:LEU:HD21	1.65	0.77
12:U:6:SER:O	12:U:10:GLN:HG2	1.84	0.77
14:S:52:PHE:HB3	14:S:53:PRO:HD3	1.65	0.77
1:E:122:C:C6	3:M:58:G:O6	2.22	0.77
12:U:268:TYR:CD1	13:W:351:MET:HE1	2.19	0.77
8:R:242:C:H5'	8:R:244:C:C5'	2.14	0.77
13:W:344:PRO:O	13:W:346:SER:N	2.18	0.77
4:N:288:G:H2'	4:N:288:G:N3	2.00	0.77
7:Q:103:U:H2'	7:Q:104:C:C6	2.20	0.77
7:Q:104:C:OP2	7:Q:104:C:N1	2.17	0.77
6:P:263:C:H3'	6:P:265:C:C4	2.16	0.77
3:M:70:C:O2'	3:M:71:C:C5	2.39	0.76
6:P:252:A:N1	8:R:250:U:O2	2.18	0.76
3:M:56:A:O2'	3:M:57:G:P	2.44	0.76
3:M:70:C:O2'	3:M:71:C:H5	1.66	0.76
6:P:264:A:H3'	6:P:265:C:C6	2.15	0.76
3:M:59:A:O2'	3:M:60:U:H5	1.68	0.76
12:U:91:ARG:CG	13:W:351:MET:HB3	2.13	0.76
12:U:290:ARG:HD2	13:W:362:LYS:H	1.50	0.76
6:P:265:C:O2'	6:P:266:U:C5'	2.33	0.76
12:U:285:GLU:OE1	13:W:355:PHE:CB	2.34	0.76
3:M:55:G:O3'	9:C:46:LEU:HG	1.86	0.76
9:C:53:THR:HG21	9:C:58:ASP:HB2	1.67	0.76
12:U:42:ASP:HB2	12:U:252:ARG:HH11	1.49	0.75
12:U:290:ARG:HG3	13:W:361:SER:HB3	1.66	0.75
2:A:175:G:H3'	2:A:176:A:H5'	1.68	0.75
4:N:278:A:H2'	4:N:279:A:C5'	2.16	0.75
4:N:282:U:OP2	4:N:282:U:C4'	2.33	0.75
12:U:283:TYR:CD2	13:W:350:GLY:HA3	2.22	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:W:371:ARG:HH12	14:S:63:VAL:C	1.94	0.75
4:N:290:C:H2'	4:N:291:C:H5'	0.77	0.75
9:C:56:ALA:HB2	10:D:95:LYS:O	1.87	0.75
13:W:339:ILE:CD1	14:S:54:ILE:HG21	2.14	0.75
1:E:124:G:O4'	3:M:57:G:H2'	1.86	0.75
3:M:57:G:OP2	9:C:43:THR:CG2	2.34	0.75
3:M:57:G:OP1	9:C:26:ARG:NH2	2.18	0.75
6:P:264:A:C8	6:P:265:C:C4	2.74	0.75
12:U:31:LEU:HD22	12:U:52:VAL:HG23	1.67	0.75
1:E:124:G:OP1	3:M:57:G:O4'	2.04	0.74
7:Q:109:G:O3'	7:Q:110:U:P	2.44	0.74
4:N:281:A:H2'	4:N:282:U:OP1	1.87	0.74
11:B:14:ARG:HB3	11:B:14:ARG:CZ	2.17	0.74
2:A:127:A:H2'	2:A:128:U:C5'	2.17	0.74
13:W:371:ARG:NH2	14:S:63:VAL:CA	2.29	0.74
7:Q:104:C:O2'	7:Q:105:G:C8	1.97	0.74
12:U:89:GLU:OE1	13:W:352:ILE:CG2	2.21	0.74
4:N:282:U:H4'	4:N:283:A:OP2	1.87	0.73
7:Q:104:C:C6	7:Q:104:C:P	2.81	0.73
3:M:69:U:H5''	3:M:70:C:OP2	1.88	0.73
3:M:55:G:O2'	3:M:56:A:O4'	2.05	0.73
12:U:32:ARG:O	12:U:36:ARG:HG3	1.88	0.73
13:W:361:SER:C	13:W:362:LYS:HG3	2.13	0.73
4:N:282:U:H2'	4:N:283:A:C8	2.23	0.73
12:U:285:GLU:CA	13:W:359:PHE:H	2.02	0.73
13:W:375:LEU:HD11	14:S:61:VAL:CG1	2.19	0.73
3:M:57:G:O4'	9:C:26:ARG:NH2	2.21	0.73
4:N:288:G:H21	4:N:289:A:H5'	1.53	0.73
4:N:290:C:H2'	4:N:291:C:C4'	2.18	0.73
12:U:283:TYR:HH	13:W:360:MET:HE2	1.51	0.73
12:U:285:GLU:HG2	13:W:359:PHE:HB2	1.71	0.73
1:E:132:A:O2'	1:E:133:G:H8	1.72	0.73
12:U:285:GLU:CD	13:W:359:PHE:HB3	2.13	0.72
2:A:117:U:H3	2:A:234:A:H61	1.37	0.72
13:W:372:LEU:CD1	14:S:58:THR:HG21	2.11	0.72
4:N:278:A:O2'	4:N:279:A:OP1	2.08	0.72
2:A:148:G:H4'	11:B:15:PHE:O	1.89	0.72
12:U:283:TYR:HE2	13:W:350:GLY:HA2	1.48	0.72
12:U:285:GLU:OE1	13:W:355:PHE:HB2	1.88	0.72
1:E:123:U:H4'	3:M:57:G:O3'	1.88	0.71
4:N:281:A:OP2	4:N:281:A:N9	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:U:283:TYR:CD2	13:W:350:GLY:CA	2.73	0.71
7:Q:103:U:C3'	7:Q:104:C:H6	2.03	0.71
8:R:241:U:O3'	8:R:244:C:H4'	1.89	0.71
3:M:58:G:H1'	4:N:280:C:N4	2.06	0.71
13:W:423:GLN:OE1	14:S:65:HIS:NE2	2.22	0.71
4:N:281:A:C2'	4:N:282:U:OP1	2.39	0.71
4:N:274:G:O2'	4:N:275:U:C6	2.38	0.71
8:R:240:A:C6	8:R:242:C:N3	2.59	0.70
7:Q:109:G:C3'	7:Q:110:U:P	2.79	0.70
12:U:14:GLY:HA2	12:U:17:ARG:HH21	1.56	0.70
13:W:372:LEU:HG	14:S:58:THR:HG23	1.71	0.70
9:C:28:VAL:CG2	9:C:41:LYS:HB3	2.19	0.70
7:Q:103:U:C2'	7:Q:104:C:C6	2.74	0.70
2:A:151:C:OP1	2:A:204:G:H4'	1.90	0.70
1:E:129:C:OP1	10:D:2:VAL:HG23	1.92	0.70
12:U:283:TYR:HE1	13:W:360:MET:CG	2.01	0.70
3:M:67:A:O3'	3:M:68:G:P	2.50	0.69
8:R:242:C:C5'	8:R:244:C:H5'	2.21	0.69
6:P:252:A:H2	8:R:250:U:C3'	2.03	0.69
6:P:252:A:C1'	8:R:250:U:N3	2.55	0.69
11:B:73:ASN:ND2	11:B:75:ASP:H	1.89	0.69
12:U:285:GLU:OE1	13:W:355:PHE:O	2.10	0.69
5:O:92:C:OP2	5:O:93:G:H8	1.75	0.69
12:U:8:ARG:HG2	12:U:37:ALA:CB	2.23	0.69
12:U:169:ARG:HG3	12:U:209:LEU:HD13	1.73	0.69
12:U:283:TYR:CZ	13:W:360:MET:HE3	2.02	0.69
2:A:130:A:H2'	2:A:131:A:C8	2.26	0.69
6:P:252:A:O5'	7:Q:102:A:N7	2.16	0.69
13:W:374:LYS:HZ1	14:S:67:LYS:HB3	1.55	0.69
2:A:125:G:H1	2:A:225:C:H42	1.39	0.69
4:N:282:U:H2'	4:N:282:U:O2	1.90	0.69
12:U:221:MET:HE3	12:U:249:GLY:O	1.93	0.69
1:E:123:U:H4'	3:M:58:G:P	2.34	0.68
4:N:282:U:C2'	4:N:283:A:H8	1.95	0.68
11:B:60:VAL:HG23	11:B:83:ARG:C	2.18	0.68
8:R:241:U:O2'	8:R:244:C:O3'	2.11	0.68
9:C:15:GLU:O	9:C:19:LEU:HG	1.92	0.68
2:A:175:G:H1	2:A:221:C:H42	1.42	0.68
13:W:339:ILE:CG1	14:S:54:ILE:CG2	2.71	0.68
4:N:290:C:C2'	4:N:291:C:C5'	2.37	0.68
7:Q:110:U:O3'	7:Q:111:C:H5'	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:65:U:H4'	3:M:66:G:OP1	1.89	0.68
4:N:288:G:C3'	4:N:289:A:P	2.82	0.68
12:U:112:THR:HG21	12:U:144:GLN:CD	2.18	0.67
2:A:154:G:O2'	2:A:155:G:H5'	1.93	0.67
6:P:252:A:C1'	8:R:250:U:H3	2.08	0.67
12:U:35:ARG:HH21	12:U:49:ARG:HD2	1.58	0.67
11:B:93:LEU:HD23	11:B:93:LEU:N	2.08	0.67
1:E:122:C:P	9:C:32:ARG:HH21	2.17	0.67
4:N:282:U:C4'	4:N:283:A:OP2	2.42	0.67
7:Q:104:C:C2	7:Q:105:G:N7	2.57	0.67
6:P:264:A:OP2	6:P:265:C:N4	2.27	0.67
12:U:89:GLU:CA	13:W:352:ILE:N	2.56	0.67
1:E:123:U:C4'	3:M:57:G:O3'	2.43	0.67
1:E:123:U:H5'	3:M:58:G:C8	2.30	0.67
11:B:15:PHE:CE1	11:B:85:GLN:HB2	2.30	0.67
8:R:248:U:H2'	8:R:249:G:C8	2.29	0.66
12:U:79:TYR:CE1	13:W:358:ASP:CG	2.73	0.66
13:W:419:GLU:CB	14:S:65:HIS:HE1	2.06	0.66
3:M:66:G:H2'	3:M:67:A:OP2	1.96	0.66
2:A:127:A:O2'	2:A:128:U:H5'	1.93	0.66
2:A:215:A:O5'	2:A:215:A:H8	1.78	0.66
5:O:97:U:O3'	5:O:98:G:P	2.53	0.66
12:U:285:GLU:C	13:W:359:PHE:N	2.52	0.66
9:C:5:GLN:HG3	9:C:6:THR:N	2.09	0.66
12:U:268:TYR:HD1	13:W:351:MET:HE1	1.58	0.66
11:B:14:ARG:O	11:B:14:ARG:HG2	1.95	0.65
6:P:265:C:O2'	6:P:266:U:H6	1.73	0.65
13:W:372:LEU:HG	14:S:58:THR:CG2	2.23	0.65
7:Q:103:U:C3'	7:Q:104:C:H5	2.03	0.65
2:A:157:A:H2'	2:A:158:C:H6	1.62	0.65
2:A:157:A:H2'	2:A:158:C:C6	2.32	0.65
12:U:131:LEU:HB2	12:U:156:VAL:HG22	1.79	0.65
12:U:17:ARG:N	12:U:71:ALA:HB2	2.12	0.65
1:E:123:U:H4'	3:M:58:G:O5'	1.97	0.65
13:W:349:LEU:HD22	13:W:359:PHE:HE2	1.62	0.65
1:E:126:A:N7	4:N:293:C:C5'	2.61	0.64
12:U:286:ARG:HB2	13:W:360:MET:O	1.97	0.64
1:E:123:U:O3'	3:M:57:G:C3'	2.45	0.64
7:Q:100:C:O2'	7:Q:101:G:C5'	2.44	0.64
8:R:241:U:OP2	8:R:242:C:H3'	1.98	0.64
11:B:88:GLN:HE21	11:B:92:SER:HB2	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:271:C:H5'	6:P:270:G:C5'	2.28	0.64
1:E:148:C:C5'	1:E:148:C:H6	2.11	0.63
2:A:139:A:H2'	2:A:140:C:H6	1.63	0.63
2:A:148:G:O2'	11:B:83:ARG:NH2	2.31	0.63
11:B:76:VAL:HG13	11:B:77:GLN:N	2.14	0.63
12:U:44:ASN:OD1	12:U:46:GLU:HB3	1.98	0.63
12:U:285:GLU:HG2	13:W:359:PHE:CB	2.24	0.63
10:D:76:VAL:O	10:D:80:GLN:HG3	1.99	0.63
12:U:260:ARG:HH21	12:U:261:HIS:HB2	1.63	0.63
13:W:341:LYS:O	13:W:345:PHE:CD1	2.52	0.63
9:C:74:VAL:HG11	10:D:76:VAL:HG11	1.81	0.63
13:W:419:GLU:CB	14:S:65:HIS:CE1	2.68	0.63
7:Q:104:C:H1'	7:Q:105:G:N9	2.08	0.63
2:A:149:A:H4'	11:B:17:CYS:SG	2.39	0.62
4:N:282:U:H2'	4:N:283:A:H8	1.58	0.62
1:E:121:C:O2'	1:E:122:C:H5'	1.99	0.62
2:A:117:U:H3	2:A:234:A:N6	1.98	0.62
12:U:281:PRO:HB2	13:W:347:GLN:HA	1.79	0.62
12:U:285:GLU:HB2	13:W:359:PHE:HB3	1.79	0.62
1:E:105:G:C5'	4:N:290:C:H1'	2.29	0.62
1:E:123:U:O3'	3:M:57:G:O3'	2.17	0.62
1:E:114:G:O2'	1:E:115:C:H5'	2.00	0.62
6:P:252:A:P	7:Q:102:A:N9	2.72	0.62
3:M:70:C:O3'	3:M:71:C:P	2.57	0.62
11:B:107:TYR:CZ	11:B:111:MET:HG3	2.35	0.62
12:U:283:TYR:CD1	13:W:359:PHE:O	2.53	0.62
1:E:105:G:O4'	4:N:290:C:H1'	2.00	0.61
4:N:288:G:O2'	4:N:289:A:P	2.58	0.61
4:N:278:A:C3'	4:N:279:A:H5''	2.30	0.61
1:E:125:U:O2'	4:N:292:C:C4'	2.38	0.61
13:W:344:PRO:O	13:W:346:SER:HB3	1.99	0.61
2:A:120:G:N2	2:A:230:C:O2	2.32	0.61
10:D:4:LEU:HD22	10:D:8:GLN:CG	2.29	0.61
2:A:195:U:O4'	13:W:411:GLY:HA3	1.99	0.61
3:M:65:U:O4'	3:M:65:U:O2	2.16	0.61
12:U:283:TYR:OH	13:W:360:MET:CE	2.28	0.61
12:U:286:ARG:O	13:W:361:SER:CB	2.44	0.61
1:E:137:C:H3'	1:E:137:C:O2	2.01	0.61
1:E:138:U:H4'	1:E:139:C:OP2	2.01	0.61
2:A:139:A:H2'	2:A:140:C:C6	2.35	0.61
12:U:283:TYR:CD1	13:W:360:MET:HE3	2.26	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:P:252:A:N3	8:R:250:U:N1	2.32	0.61
9:C:53:THR:HG22	9:C:54:ASP:N	2.15	0.61
1:E:122:C:O2'	1:E:123:U:H5'	2.01	0.60
3:M:55:G:O2'	9:C:45:ASP:HB2	2.01	0.60
4:N:279:A:O2'	4:N:280:C:OP2	2.14	0.60
12:U:21:ARG:NH1	12:U:66:GLU:HA	2.15	0.60
4:N:271:C:C4'	6:P:270:G:C3'	2.79	0.60
10:D:4:LEU:HD11	10:D:12:GLU:HG3	1.83	0.60
9:C:5:GLN:CG	9:C:6:THR:H	2.11	0.60
12:U:48:ALA:O	12:U:52:VAL:HG12	2.00	0.60
13:W:344:PRO:O	13:W:346:SER:CB	2.50	0.60
12:U:59:ALA:O	12:U:64:VAL:HG13	2.02	0.60
2:A:193:G:N1	13:W:409:GLY:O	2.32	0.60
4:N:288:G:C2'	4:N:289:A:OP2	2.49	0.60
1:E:110:G:C2'	1:E:111:G:H5'	2.31	0.60
6:P:252:A:O5'	7:Q:102:A:C4	2.53	0.60
8:R:240:A:C6	8:R:242:C:C2	2.69	0.60
12:U:285:GLU:HG2	13:W:359:PHE:CA	2.32	0.60
3:M:55:G:O3'	9:C:46:LEU:CG	2.50	0.60
9:C:12:ARG:CG	9:C:13:ALA:N	2.65	0.60
3:M:55:G:O3'	9:C:46:LEU:CD1	2.50	0.60
1:E:126:A:N7	4:N:293:C:H5''	2.17	0.59
2:A:233:U:H2'	2:A:234:A:H5''	1.84	0.59
8:R:242:C:H5'	8:R:243:G:P	2.42	0.59
4:N:290:C:C2	4:N:291:C:O4'	2.55	0.59
11:B:73:ASN:HD21	11:B:75:ASP:H	1.50	0.59
1:E:132:A:O2'	1:E:133:G:C8	2.50	0.59
9:C:46:LEU:O	9:C:47:VAL:HG13	2.02	0.59
13:W:372:LEU:HD21	14:S:58:THR:HA	1.85	0.59
10:D:19:LYS:HG2	10:D:19:LYS:O	2.01	0.59
11:B:73:ASN:HD21	11:B:75:ASP:CB	2.16	0.59
6:P:264:A:N7	6:P:265:C:C2	2.71	0.59
7:Q:103:U:C6	7:Q:104:C:C5	2.91	0.59
12:U:92:LEU:HB2	13:W:348:ILE:CG1	2.33	0.59
7:Q:103:U:C2'	7:Q:104:C:C5	2.86	0.59
14:S:51:GLY:O	14:S:55:ASN:HB2	2.01	0.59
7:Q:104:C:O2'	7:Q:105:G:P	2.60	0.59
1:E:141:G:O2'	1:E:142:G:H5'	2.03	0.58
4:N:277:C:O2'	4:N:278:A:OP2	2.14	0.58
4:N:288:G:C2'	4:N:288:G:N3	2.66	0.58
2:A:212:C:H4'	2:A:213:A:OP1	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:271:C:C4'	6:P:270:G:H3'	2.33	0.58
2:A:112:G:C5	7:Q:111:C:C2	2.91	0.58
12:U:281:PRO:HG2	13:W:347:GLN:HB2	1.84	0.58
12:U:285:GLU:CG	13:W:359:PHE:CA	2.81	0.58
2:A:214:A:H5'	2:A:215:A:P	2.43	0.58
6:P:264:A:H8	6:P:265:C:C4	2.17	0.58
4:N:271:C:H5'	6:P:270:G:C4'	2.31	0.58
8:R:243:G:OP2	8:R:244:C:C5'	2.51	0.58
9:C:29:LEU:HD11	9:C:38:LEU:HD11	1.86	0.58
12:U:35:ARG:NE	12:U:49:ARG:HG3	2.19	0.58
12:U:42:ASP:HB2	12:U:252:ARG:NH1	2.18	0.58
8:R:241:U:H5'	8:R:242:C:OP1	2.03	0.58
12:U:268:TYR:CE1	13:W:351:MET:HE1	2.39	0.58
1:E:101:G:O2'	3:M:49:A:P	2.61	0.58
2:A:128:U:H5'	2:A:128:U:H6	1.68	0.58
2:A:163:A:O5'	2:A:163:A:H8	1.87	0.58
12:U:8:ARG:HG2	12:U:37:ALA:HB2	1.86	0.58
12:U:22:ILE:HG12	12:U:23:THR:N	2.18	0.58
4:N:288:G:H21	4:N:289:A:C5'	2.15	0.57
6:P:252:A:N1	8:R:250:U:C1'	2.62	0.57
7:Q:100:C:H4'	7:Q:101:G:OP1	2.02	0.57
1:E:110:G:O2'	1:E:111:G:H5'	2.04	0.57
1:E:132:A:HO2'	1:E:133:G:H8	1.47	0.57
5:O:92:C:OP2	5:O:93:G:C8	2.55	0.57
11:B:73:ASN:ND2	11:B:75:ASP:N	2.51	0.57
11:B:112:ILE:HG23	11:B:115:LEU:HD12	1.87	0.57
3:M:67:A:O2'	3:M:68:G:OP2	2.21	0.57
7:Q:104:C:P	7:Q:104:C:C3'	2.71	0.57
11:B:77:GLN:O	11:B:77:GLN:HG2	2.05	0.57
12:U:283:TYR:CE2	13:W:359:PHE:O	2.54	0.57
3:M:56:A:C8	9:C:46:LEU:HG	2.38	0.57
9:C:12:ARG:HG2	9:C:13:ALA:H	1.68	0.57
9:C:32:ARG:O	9:C:32:ARG:HG2	2.04	0.57
12:U:167:SER:O	12:U:171:ARG:HG3	2.04	0.57
13:W:361:SER:C	13:W:362:LYS:CG	2.67	0.57
4:N:277:C:C4'	4:N:278:A:OP2	2.48	0.57
7:Q:104:C:C1'	7:Q:104:C:OP2	2.53	0.57
9:C:53:THR:HG21	9:C:58:ASP:CB	2.34	0.57
12:U:86:LEU:HD13	12:U:287:LEU:HB2	1.87	0.57
12:U:286:ARG:NH2	13:W:360:MET:CA	2.38	0.57
13:W:371:ARG:CA	14:S:62:THR:HG23	1.91	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:W:379:MET:HA	13:W:382:MET:HG3	1.87	0.57
1:E:105:G:H5'	4:N:290:C:O2'	2.05	0.57
2:A:233:U:H3'	2:A:234:A:H5'	1.86	0.57
7:Q:110:U:O3'	7:Q:111:C:C5'	2.53	0.57
6:P:252:A:N1	8:R:250:U:O2'	2.37	0.57
6:P:252:A:OP2	7:Q:102:A:C8	2.58	0.56
7:Q:100:C:HO2'	7:Q:101:G:P	2.25	0.56
4:N:281:A:OP2	4:N:281:A:C1'	2.53	0.56
10:D:7:GLU:O	10:D:8:GLN:C	2.47	0.56
2:A:171:U:C3'	2:A:172:A:H5''	2.35	0.56
12:U:279:LEU:HG	12:U:280:GLU:N	2.20	0.56
12:U:285:GLU:C	13:W:359:PHE:H	2.10	0.56
10:D:5:GLU:O	10:D:6:SER:C	2.48	0.56
11:B:86:LEU:HD13	11:B:99:PRO:O	2.05	0.56
9:C:12:ARG:HG2	9:C:13:ALA:N	2.20	0.56
11:B:64:LYS:HZ3	11:B:65:ASN:HB2	1.71	0.56
11:B:112:ILE:C	11:B:114:LYS:H	2.13	0.56
12:U:69:THR:HG23	12:U:69:THR:O	2.06	0.56
9:C:29:LEU:HD13	9:C:40:VAL:HG22	1.87	0.56
10:D:34:ASP:CG	10:D:35:GLY:H	2.13	0.56
1:E:148:C:H6	1:E:148:C:H5''	1.70	0.56
3:M:56:A:C8	3:M:56:A:OP1	2.59	0.56
3:M:56:A:N7	9:C:46:LEU:HG	2.21	0.56
3:M:55:G:H2'	3:M:56:A:N9	2.20	0.55
3:M:56:A:H8	9:C:45:ASP:O	1.75	0.55
9:C:7:TRP:CD1	9:C:61:LYS:HD3	2.42	0.55
11:B:60:VAL:CG2	11:B:84:VAL:HG12	2.35	0.55
3:M:67:A:O2'	3:M:68:G:P	2.64	0.55
6:P:264:A:C5'	6:P:265:C:OP2	2.51	0.55
12:U:283:TYR:CE1	13:W:360:MET:CG	2.83	0.55
13:W:375:LEU:CD1	14:S:61:VAL:HG11	2.33	0.55
12:U:128:ARG:HH11	12:U:181:ARG:NH2	2.05	0.55
2:A:112:G:C5	7:Q:111:C:N1	2.73	0.55
8:R:242:C:C5'	8:R:243:G:OP2	2.45	0.55
9:C:13:ALA:O	9:C:16:LYS:HB3	2.05	0.55
4:N:274:G:H2'	4:N:275:U:C4	2.17	0.55
4:N:290:C:O2'	4:N:291:C:H5'	2.00	0.55
2:A:112:G:N1	7:Q:111:C:C2	2.75	0.55
11:B:62:LEU:HD12	11:B:81:ARG:O	2.07	0.55
12:U:281:PRO:HG3	13:W:347:GLN:HB2	1.85	0.55
1:E:106:G:N2	3:M:58:G:C6	2.75	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:220:C:H2'	2:A:221:C:C5'	2.29	0.55
6:P:252:A:P	7:Q:102:A:N7	2.80	0.55
12:U:4:GLN:HB3	12:U:251:ALA:O	2.07	0.55
9:C:5:GLN:O	9:C:9:GLU:N	2.34	0.55
13:W:429:GLN:O	13:W:432:LYS:HG2	2.06	0.55
1:E:105:G:O4'	4:N:290:C:O2	2.25	0.54
2:A:220:C:C3'	2:A:221:C:H5''	2.36	0.54
7:Q:110:U:HO3'	7:Q:111:C:P	2.25	0.54
11:B:116:LYS:N	11:B:116:LYS:HD2	2.23	0.54
4:N:299:U:O2'	4:N:300:U:P	2.65	0.54
12:U:8:ARG:HG2	12:U:37:ALA:HB1	1.89	0.54
12:U:290:ARG:HD2	13:W:362:LYS:N	2.20	0.54
1:E:125:U:OP2	10:D:59:ARG:NH2	2.41	0.54
3:M:57:G:H2'	3:M:57:G:N3	2.20	0.54
12:U:283:TYR:CD1	13:W:360:MET:O	2.60	0.54
1:E:102:C:O2'	1:E:103:C:H5'	2.08	0.54
2:A:127:A:C2'	2:A:128:U:C5'	2.79	0.54
11:B:64:LYS:NZ	11:B:65:ASN:H	2.06	0.54
11:B:73:ASN:HD21	11:B:75:ASP:N	2.06	0.54
6:P:257:C:O3'	6:P:258:C:P	2.65	0.54
3:M:57:G:C4'	3:M:58:G:OP1	2.55	0.54
5:O:92:C:C5	5:O:94:C:OP2	2.61	0.54
12:U:281:PRO:CB	13:W:347:GLN:CA	2.87	0.53
12:U:35:ARG:NH2	12:U:49:ARG:HH11	2.05	0.53
2:A:130:A:H2'	2:A:131:A:H8	1.72	0.53
2:A:172:A:H2	2:A:225:C:H1'	1.73	0.53
2:A:195:U:H4'	13:W:411:GLY:O	2.08	0.53
3:M:57:G:OP2	9:C:26:ARG:NH2	2.41	0.53
7:Q:103:U:C6	7:Q:104:C:H5	2.26	0.53
9:C:65:PHE:CZ	9:C:69:LEU:HD11	2.44	0.53
12:U:269:PHE:CE2	13:W:347:GLN:OE1	2.62	0.53
2:A:208:A:H1'	13:W:380:ASP:O	2.08	0.53
2:A:233:U:H3'	2:A:234:A:C5'	2.39	0.53
6:P:252:A:N3	8:R:250:U:C4	2.76	0.53
4:N:288:G:HO3'	4:N:289:A:P	2.29	0.53
11:B:76:VAL:HG13	11:B:77:GLN:H	1.71	0.53
11:B:116:LYS:O	11:B:120:GLN:HG2	2.09	0.53
1:E:105:G:O2'	1:E:106:G:H5'	2.08	0.53
4:N:271:C:H4'	6:P:270:G:HO3'	1.73	0.53
12:U:83:LYS:CE	13:W:356:GLY:O	2.57	0.53
13:W:341:LYS:O	13:W:345:PHE:CE1	2.62	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:109:G:O3'	7:Q:110:U:OP2	2.27	0.53
12:U:134:ALA:HB3	12:U:188:THR:HA	1.90	0.53
12:U:91:ARG:HG2	13:W:351:MET:CB	2.28	0.53
2:A:164:G:OP2	2:A:164:G:H8	1.92	0.53
10:D:30:LEU:HD13	10:D:58:LEU:HD13	1.90	0.53
9:C:34:SER:C	9:C:36:GLY:N	2.65	0.52
12:U:112:THR:O	12:U:115:ALA:HB3	2.10	0.52
9:C:32:ARG:NH2	10:D:25:SER:OG	2.42	0.52
4:N:271:C:H5''	6:P:270:G:O3'	2.04	0.52
4:N:290:C:C3'	4:N:291:C:H5'	2.33	0.52
4:N:301:U:C3'	4:N:301:U:OP1	2.56	0.52
4:N:274:G:N2	4:N:275:U:O4	2.42	0.52
10:D:61:THR:HG22	10:D:63:GLY:N	2.16	0.52
11:B:60:VAL:HB	11:B:84:VAL:HG12	1.90	0.52
12:U:92:LEU:HB2	13:W:348:ILE:HG13	1.91	0.52
4:N:280:C:C2	4:N:281:A:H5''	2.28	0.52
3:M:57:G:H8	9:C:26:ARG:HH22	1.58	0.52
13:W:371:ARG:HH22	14:S:63:VAL:HA	1.60	0.52
11:B:41:VAL:CG1	11:B:42:GLU:N	2.72	0.52
11:B:71:GLU:OE2	11:B:78:TYR:HD2	1.92	0.52
12:U:247:LEU:CD1	12:U:270:ALA:HB1	2.39	0.52
11:B:88:GLN:O	11:B:91:GLY:N	2.42	0.52
6:P:252:A:O5'	7:Q:102:A:C8	2.60	0.52
7:Q:104:C:H3'	7:Q:104:C:OP1	2.09	0.52
3:M:67:A:HO2'	3:M:68:G:P	2.32	0.51
8:R:243:G:OP2	8:R:244:C:H5''	2.10	0.51
9:C:63:GLU:C	9:C:63:GLU:CD	2.78	0.51
10:D:92:ASP:OD1	10:D:92:ASP:O	2.27	0.51
9:C:40:VAL:HG21	9:C:62:ILE:HG23	1.91	0.51
9:C:70:MET:CB	10:D:30:LEU:HD21	2.38	0.51
10:D:56:CYS:SG	10:D:71:VAL:HB	2.50	0.51
2:A:112:G:C6	7:Q:111:C:C2	2.98	0.51
12:U:152:VAL:HG23	12:U:154:VAL:HG23	1.92	0.51
3:M:55:G:O3'	9:C:46:LEU:HD12	2.09	0.51
3:M:55:G:H2'	3:M:56:A:C1'	2.40	0.51
7:Q:103:U:C2'	7:Q:104:C:H6	2.18	0.51
8:R:250:U:H4'	8:R:251:G:OP2	2.06	0.51
9:C:40:VAL:CG2	9:C:62:ILE:HG23	2.40	0.51
11:B:93:LEU:HD23	11:B:93:LEU:H	1.75	0.51
13:W:374:LYS:CD	14:S:67:LYS:C	2.81	0.51
2:A:199:A:H8	2:A:199:A:OP1	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:281:A:OP2	4:N:281:A:C4'	2.58	0.51
12:U:22:ILE:CG1	12:U:26:ASP:HB2	2.40	0.51
1:E:121:C:H5''	9:C:32:ARG:HH22	1.76	0.51
2:A:121:U:H2'	2:A:122:U:C6	2.46	0.51
11:B:56:VAL:HG21	11:B:107:TYR:CE2	2.45	0.51
12:U:196:GLU:OE1	12:U:196:GLU:HA	2.11	0.51
12:U:270:ALA:HB2	12:U:282:PHE:HD1	1.76	0.51
12:U:92:LEU:HB2	13:W:348:ILE:HG12	1.93	0.51
13:W:339:ILE:CG1	14:S:54:ILE:HG21	2.40	0.51
2:A:125:G:H1	2:A:225:C:N4	2.08	0.50
9:C:33:HIS:CD2	10:D:21:ARG:HG3	2.46	0.50
11:B:15:PHE:CZ	11:B:85:GLN:HB2	2.45	0.50
12:U:22:ILE:HG12	12:U:26:ASP:HB2	1.92	0.50
12:U:128:ARG:HH11	12:U:181:ARG:HH22	1.59	0.50
1:E:119:C:O2'	1:E:120:G:H5'	2.12	0.50
2:A:136:G:N3	2:A:214:A:H2	2.09	0.50
4:N:280:C:O3'	4:N:281:A:C8	2.64	0.50
4:N:282:U:OP2	4:N:283:A:OP2	2.29	0.50
12:U:93:PRO:HG3	12:U:268:TYR:CD2	2.46	0.50
7:Q:104:C:O2'	7:Q:105:G:C5'	2.58	0.50
10:D:28:ILE:HA	10:D:59:ARG:O	2.11	0.50
11:B:68:TYR:CE2	11:B:70:ARG:HB2	2.46	0.50
6:P:263:C:C3'	6:P:265:C:N4	2.15	0.50
12:U:13:ILE:HD13	12:U:75:LEU:HD12	1.93	0.50
1:E:127:G:C6	4:N:293:C:P	3.05	0.50
1:E:147:U:H2'	1:E:148:C:H5''	1.94	0.50
3:M:58:G:H1'	4:N:280:C:H41	1.75	0.50
8:R:248:U:C3'	8:R:249:G:H8	2.24	0.50
11:B:43:ASN:C	11:B:118:ARG:HH22	2.20	0.50
1:E:105:G:H4'	4:N:290:C:O4'	2.12	0.50
11:B:60:VAL:CG2	11:B:83:ARG:O	2.52	0.50
13:W:349:LEU:HD22	13:W:359:PHE:CE2	2.45	0.50
7:Q:104:C:OP2	7:Q:104:C:C2'	2.59	0.49
8:R:240:A:O3'	8:R:242:C:C5'	2.50	0.49
1:E:126:A:N7	4:N:293:C:P	2.83	0.49
4:N:280:C:O2'	4:N:281:A:C3'	2.44	0.49
4:N:288:G:O4'	4:N:288:G:P	2.65	0.49
7:Q:103:U:H2'	7:Q:104:C:H6	1.74	0.49
12:U:281:PRO:HB3	13:W:347:GLN:HG3	0.53	0.49
12:U:281:PRO:CB	13:W:347:GLN:HA	2.43	0.49
13:W:344:PRO:C	13:W:346:SER:CB	2.85	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:W:344:PRO:O	13:W:345:PHE:C	2.53	0.49
2:A:175:G:H1	2:A:221:C:N4	2.08	0.49
2:A:231:A:H5''	2:A:232:G:OP2	2.12	0.49
12:U:214:VAL:HB	12:U:240:THR:HG23	1.95	0.49
12:U:258:SER:O	12:U:262:VAL:HG23	2.13	0.49
12:U:281:PRO:CG	13:W:347:GLN:CB	2.68	0.49
2:A:125:G:H2'	2:A:126:C:C6	2.48	0.49
11:B:14:ARG:CZ	11:B:14:ARG:CB	2.88	0.49
6:P:252:A:H2	8:R:250:U:H3'	1.78	0.49
9:C:44:ASP:HB3	9:C:47:VAL:HG23	1.95	0.49
12:U:285:GLU:OE2	13:W:359:PHE:CB	2.56	0.49
13:W:392:GLY:O	13:W:396:PHE:HD1	1.95	0.49
1:E:142:G:O2'	1:E:143:A:H5'	2.12	0.49
3:M:52:C:H2'	3:M:53:U:C6	2.48	0.49
3:M:55:G:C2'	3:M:56:A:O4'	2.61	0.49
5:O:96:A:H2'	5:O:97:U:C6	2.48	0.49
12:U:83:LYS:HE2	13:W:356:GLY:O	2.13	0.49
12:U:92:LEU:HG	13:W:347:GLN:HG2	1.36	0.49
12:U:285:GLU:HG3	13:W:356:GLY:O	2.13	0.49
13:W:423:GLN:CD	14:S:65:HIS:CD2	2.84	0.49
1:E:145:G:O2'	1:E:146:C:H5'	2.13	0.48
8:R:247:C:H2'	8:R:248:U:C6	2.48	0.48
10:D:4:LEU:HD13	10:D:8:GLN:HG3	1.95	0.48
13:W:373:LYS:O	13:W:377:THR:HG23	2.13	0.48
5:O:94:C:H2'	5:O:95:U:C6	2.49	0.48
10:D:4:LEU:HB3	10:D:8:GLN:HB3	1.95	0.48
14:S:57:LEU:O	14:S:61:VAL:HG23	2.14	0.48
3:M:68:G:H2'	3:M:69:U:C6	2.48	0.48
12:U:227:LEU:HB3	12:U:262:VAL:HG11	1.95	0.48
2:A:172:A:H2	2:A:225:C:C1'	2.26	0.48
4:N:272:C:H2'	4:N:273:U:C6	2.49	0.48
5:O:79:C:H2'	5:O:80:U:C6	2.49	0.48
5:O:86:G:H2'	5:O:87:U:C6	2.49	0.48
7:Q:107:G:H2'	7:Q:108:U:C6	2.49	0.48
8:R:249:G:H2'	8:R:250:U:C6	2.49	0.48
11:B:64:LYS:HD3	11:B:64:LYS:H	1.71	0.48
1:E:107:C:O2'	1:E:108:G:H5'	2.12	0.48
4:N:282:U:O4	4:N:283:A:N6	2.46	0.48
4:N:288:G:OP2	4:N:288:G:C4'	2.57	0.48
4:N:296:C:H2'	4:N:297:U:C6	2.49	0.48
5:O:89:G:H2'	5:O:90:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:94:CYS:C	11:B:95:LEU:HD23	2.38	0.48
4:N:294:G:H2'	4:N:295:U:C6	2.48	0.48
5:O:84:C:C1'	5:O:86:G:OP2	2.62	0.48
6:P:260:C:H2'	6:P:261:U:C6	2.49	0.48
8:R:240:A:C5	8:R:242:C:C4	3.02	0.48
12:U:8:ARG:HA	12:U:11:GLU:OE1	2.13	0.48
12:U:122:TYR:O	12:U:127:ARG:HB2	2.13	0.48
12:U:129:PRO:HA	12:U:183:LEU:O	2.13	0.48
5:O:93:G:H2'	5:O:94:C:C6	2.49	0.48
6:P:256:G:H2'	6:P:257:C:C6	2.49	0.48
6:P:267:C:H2'	6:P:268:C:C6	2.49	0.48
12:U:21:ARG:HH11	12:U:66:GLU:HA	1.78	0.48
12:U:114:THR:HG21	12:U:243:VAL:HG11	1.96	0.48
12:U:177:ARG:NH2	12:U:178:LEU:HD21	2.28	0.48
4:N:276:G:H2'	4:N:277:C:C6	2.49	0.48
6:P:253:A:H2'	6:P:254:U:C6	2.48	0.48
11:B:29:ILE:HG22	11:B:30:ALA:N	2.29	0.48
12:U:283:TYR:CZ	13:W:359:PHE:C	2.90	0.48
2:A:192:A:H2'	2:A:193:G:O4'	2.13	0.47
7:Q:102:A:H2'	7:Q:103:U:C6	2.48	0.47
1:E:148:C:C5'	1:E:148:C:C6	2.96	0.47
2:A:224:G:H8	2:A:224:G:H5'	1.79	0.47
3:M:63:C:H2'	3:M:64:U:C6	2.48	0.47
4:N:295:U:H2'	4:N:296:C:C6	2.49	0.47
5:O:79:C:H2'	5:O:80:U:H6	1.79	0.47
7:Q:104:C:P	7:Q:104:C:H6	2.32	0.47
12:U:1:MET:HE2	12:U:247:LEU:HB3	1.95	0.47
12:U:79:TYR:HE1	13:W:358:ASP:CB	2.26	0.47
2:A:165:G:N7	2:A:176:A:C6	2.82	0.47
3:M:63:C:H2'	3:M:64:U:H6	1.79	0.47
5:O:94:C:H2'	5:O:95:U:H6	1.79	0.47
9:C:5:GLN:O	9:C:9:GLU:HB2	2.14	0.47
9:C:34:SER:O	9:C:36:GLY:N	2.47	0.47
12:U:134:ALA:HB3	12:U:187:ASP:O	2.14	0.47
2:A:160:A:H2'	2:A:161:C:O4'	2.14	0.47
2:A:160:A:H2'	2:A:161:C:C6	2.49	0.47
3:M:70:C:HO2'	3:M:71:C:H5	1.53	0.47
6:P:267:C:H2'	6:P:268:C:H6	1.80	0.47
11:B:62:LEU:HD12	11:B:63:GLU:N	2.30	0.47
4:N:276:G:H2'	4:N:277:C:H6	1.80	0.47
5:O:93:G:H2'	5:O:94:C:H6	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:P:266:U:H2'	6:P:267:C:C6	2.49	0.47
8:R:246:C:H2'	8:R:247:C:C6	2.49	0.47
3:M:52:C:H2'	3:M:53:U:H6	1.79	0.47
4:N:271:C:H2'	4:N:272:C:C6	2.49	0.47
6:P:257:C:O3'	6:P:258:C:O5'	2.29	0.47
3:M:62:G:H2'	3:M:63:C:C6	2.49	0.47
4:N:284:G:H2'	4:N:285:C:C6	2.49	0.47
4:N:291:C:H2'	4:N:292:C:C6	2.49	0.47
4:N:294:G:H2'	4:N:295:U:H6	1.79	0.47
4:N:295:U:H2'	4:N:296:C:H6	1.80	0.47
4:N:296:C:H2'	4:N:297:U:H6	1.79	0.47
4:N:297:U:H2'	4:N:298:C:H6	1.80	0.47
5:O:89:G:H2'	5:O:90:U:H6	1.80	0.47
6:P:259:A:H2'	6:P:260:C:C6	2.49	0.47
6:P:262:G:H2'	6:P:263:C:C6	2.49	0.47
8:R:245:G:H2'	8:R:246:C:H6	1.80	0.47
9:C:32:ARG:HH11	9:C:32:ARG:HG3	1.79	0.47
9:C:46:LEU:C	9:C:47:VAL:HG22	2.39	0.47
11:B:73:ASN:HD21	11:B:75:ASP:HB3	1.80	0.47
12:U:208:VAL:HG12	12:U:209:LEU:HD22	1.96	0.47
12:U:219:ASP:C	12:U:219:ASP:OD1	2.58	0.47
1:E:121:C:C2'	1:E:122:C:H5'	2.43	0.47
4:N:272:C:H2'	4:N:273:U:H6	1.80	0.47
7:Q:102:A:H2'	7:Q:103:U:H6	1.79	0.47
7:Q:107:G:H2'	7:Q:108:U:H6	1.80	0.47
9:C:5:GLN:O	9:C:9:GLU:CB	2.63	0.47
9:C:53:THR:CG2	9:C:54:ASP:N	2.78	0.47
4:N:271:C:H2'	4:N:272:C:H6	1.80	0.47
11:B:45:THR:O	11:B:46:ALA:C	2.56	0.47
5:O:96:A:H2'	5:O:97:U:H6	1.79	0.47
6:P:253:A:H2'	6:P:254:U:H6	1.79	0.47
8:R:245:G:H2'	8:R:246:C:C6	2.49	0.46
8:R:246:C:H2'	8:R:247:C:H6	1.80	0.46
12:U:284:PRO:HD2	13:W:350:GLY:O	2.15	0.46
2:A:146:G:C6	2:A:147:G:C5	3.03	0.46
2:A:167:U:H2'	2:A:168:G:O4'	2.15	0.46
3:M:60:U:H2'	3:M:61:C:C6	2.49	0.46
4:N:297:U:H2'	4:N:298:C:C6	2.49	0.46
6:P:252:A:O2'	6:P:253:A:H8	1.98	0.46
6:P:262:G:H2'	6:P:263:C:H6	1.80	0.46
10:D:87:LEU:HB3	10:D:91:MET:HE3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:88:GLN:O	11:B:89:GLU:C	2.58	0.46
12:U:247:LEU:HD12	12:U:270:ALA:HB1	1.98	0.46
3:M:55:G:O3'	3:M:56:A:P	2.73	0.46
3:M:62:G:H2'	3:M:63:C:H6	1.80	0.46
3:M:68:G:H2'	3:M:69:U:H6	1.79	0.46
4:N:290:C:C3'	4:N:291:C:C5'	2.93	0.46
12:U:90:ALA:HB1	13:W:347:GLN:O	2.16	0.46
12:U:216:LEU:HD21	12:U:218:LEU:HD21	1.98	0.46
12:U:285:GLU:OE2	13:W:359:PHE:HB3	2.14	0.46
1:E:116:G:H2'	1:E:117:C:H5'	1.98	0.46
4:N:291:C:H2'	4:N:292:C:H6	1.80	0.46
5:O:86:G:H2'	5:O:87:U:H6	1.79	0.46
6:P:259:A:H2'	6:P:260:C:H6	1.80	0.46
7:Q:104:C:O2	7:Q:105:G:C5	2.59	0.46
8:R:241:U:OP2	8:R:242:C:H5''	2.15	0.46
2:A:116:C:H2'	2:A:117:U:C6	2.50	0.46
6:P:256:G:H2'	6:P:257:C:H6	1.80	0.46
9:C:61:LYS:HE2	9:C:61:LYS:HB3	1.71	0.46
12:U:11:GLU:O	12:U:15:ARG:HB2	2.15	0.46
12:U:176:ALA:HA	12:U:181:ARG:CG	2.45	0.46
12:U:286:ARG:O	13:W:361:SER:HB2	2.14	0.46
2:A:207:C:C4	2:A:208:A:N7	2.84	0.46
3:M:51:G:H2'	3:M:52:C:C6	2.50	0.46
4:N:284:G:H2'	4:N:285:C:H6	1.80	0.46
10:D:30:LEU:HD12	10:D:31:LYS:H	1.79	0.46
11:B:76:VAL:C	11:B:78:TYR:N	2.70	0.46
12:U:285:GLU:CD	13:W:355:PHE:HB2	2.39	0.46
2:A:125:G:H2'	2:A:126:C:H6	1.81	0.46
2:A:171:U:H3'	2:A:172:A:H5''	1.96	0.46
6:P:260:C:H2'	6:P:261:U:H6	1.80	0.46
12:U:283:TYR:CE2	13:W:359:PHE:CD2	3.03	0.46
12:U:281:PRO:CB	13:W:347:GLN:CD	2.70	0.46
3:M:60:U:H2'	3:M:61:C:H6	1.80	0.46
8:R:247:C:H2'	8:R:248:U:H6	1.79	0.46
12:U:83:LYS:HE3	13:W:356:GLY:O	2.16	0.46
8:R:249:G:H2'	8:R:250:U:H6	1.80	0.45
11:B:35:ILE:HD11	11:B:40:ALA:HA	1.98	0.45
6:P:266:U:H2'	6:P:267:C:H6	1.80	0.45
9:C:44:ASP:HB3	9:C:47:VAL:CG2	2.46	0.45
8:R:242:C:C5'	8:R:243:G:P	3.04	0.45
11:B:75:ASP:OD1	11:B:76:VAL:N	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:U:21:ARG:HD2	12:U:65:LEU:O	2.16	0.45
3:M:56:A:OP1	3:M:56:A:H8	1.98	0.45
6:P:264:A:C8	6:P:265:C:N1	2.82	0.45
2:A:229:U:H2'	2:A:230:C:C6	2.51	0.45
3:M:51:G:H2'	3:M:52:C:H6	1.80	0.45
3:M:57:G:H8	9:C:26:ARG:NH2	2.14	0.45
9:C:5:GLN:CG	9:C:6:THR:N	2.76	0.45
13:W:372:LEU:HD21	14:S:58:THR:CG2	2.35	0.45
1:E:105:G:C4'	4:N:290:C:C1'	2.49	0.45
12:U:39:MET:HE1	12:U:45:LEU:HD23	1.98	0.45
2:A:168:G:H3'	2:A:169:C:H5'	1.99	0.45
2:A:194:G:O2'	13:W:410:SER:O	2.30	0.45
12:U:133:ALA:HB1	12:U:142:ARG:HA	1.99	0.45
12:U:269:PHE:CE2	13:W:347:GLN:CD	2.95	0.45
1:E:105:G:C2'	1:E:106:G:H5'	2.47	0.45
1:E:148:C:H5''	1:E:148:C:C6	2.50	0.45
2:A:223:U:C2'	2:A:224:G:H5''	2.47	0.45
2:A:223:U:H2'	2:A:224:G:H5''	1.98	0.45
11:B:24:ASN:ND2	11:B:27:LYS:HG3	2.22	0.45
12:U:269:PHE:CE2	13:W:347:GLN:NE2	2.85	0.45
14:S:52:PHE:CB	14:S:53:PRO:HD3	2.40	0.45
4:N:282:U:C4	4:N:283:A:N6	2.84	0.45
4:N:288:G:H2'	4:N:289:A:OP2	2.16	0.45
9:C:37:ASN:CA	10:D:94:LEU:HD11	2.47	0.45
11:B:112:ILE:C	11:B:114:LYS:N	2.74	0.45
12:U:195:ASP:HB3	12:U:198:LEU:HB3	1.97	0.45
13:W:427:PHE:O	13:W:431:VAL:HG23	2.17	0.45
12:U:143:GLU:OE2	12:U:146:ARG:NH1	2.50	0.45
2:A:166:U:H2'	2:A:167:U:O4'	2.17	0.44
9:C:29:LEU:CD1	9:C:38:LEU:HD11	2.46	0.44
11:B:116:LYS:N	11:B:116:LYS:CD	2.80	0.44
12:U:111:LYS:HA	12:U:217:VAL:HG21	2.00	0.44
13:W:339:ILE:HG12	14:S:54:ILE:HG21	1.99	0.44
13:W:423:GLN:NE2	14:S:61:VAL:HG13	2.32	0.44
4:N:279:A:O2'	4:N:280:C:P	2.75	0.44
4:N:279:A:C4'	4:N:280:C:OP2	2.57	0.44
6:P:252:A:P	7:Q:102:A:C4	3.10	0.44
8:R:242:C:C5'	8:R:244:C:C5'	2.89	0.44
11:B:76:VAL:O	11:B:78:TYR:N	2.50	0.44
12:U:132:VAL:HG11	12:U:186:VAL:HG22	1.99	0.44
12:U:144:GLN:O	12:U:148:LEU:HG	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:163:A:H2'	2:A:164:G:N9	2.32	0.44
3:M:55:G:C5'	9:C:46:LEU:HD11	2.32	0.44
3:M:66:G:C2'	3:M:67:A:OP2	2.55	0.44
8:R:243:G:OP2	8:R:244:C:H5'	2.17	0.44
9:C:26:ARG:HG2	9:C:26:ARG:HH11	1.82	0.44
12:U:131:LEU:O	12:U:156:VAL:HA	2.17	0.44
1:E:128:U:C2	1:E:129:C:C5	3.05	0.44
3:M:65:U:O2	3:M:65:U:O5'	2.35	0.44
12:U:164:SER:O	12:U:168:ILE:HG13	2.17	0.44
9:C:32:ARG:HG3	9:C:32:ARG:NH1	2.33	0.44
9:C:68:GLN:O	9:C:71:ARG:N	2.50	0.44
11:B:104:VAL:O	11:B:105:MET:C	2.60	0.44
9:C:29:LEU:CD1	9:C:40:VAL:HG22	2.47	0.44
12:U:89:GLU:HB2	13:W:351:MET:O	2.17	0.44
6:P:252:A:C1'	8:R:250:U:C4	2.76	0.44
9:C:34:SER:C	9:C:36:GLY:H	2.24	0.44
2:A:138:G:H2'	2:A:139:A:H8	1.83	0.44
9:C:33:HIS:C	9:C:33:HIS:HD1	2.26	0.44
11:B:76:VAL:CG1	11:B:77:GLN:N	2.80	0.44
12:U:16:LEU:HD21	12:U:30:THR:OG1	2.18	0.44
13:W:420:LEU:C	13:W:420:LEU:HD23	2.42	0.44
2:A:117:U:H2'	2:A:118:A:C8	2.53	0.44
3:M:55:G:C5'	9:C:46:LEU:CD1	2.88	0.44
8:R:248:U:C2'	8:R:249:G:C8	3.01	0.44
11:B:64:LYS:HZ2	11:B:65:ASN:H	1.66	0.44
4:N:292:C:C3'	4:N:293:C:P	3.01	0.43
13:W:368:SER:O	14:S:62:THR:OG1	2.36	0.43
11:B:93:LEU:N	11:B:93:LEU:CD2	2.77	0.43
2:A:162:C:H2'	2:A:163:A:C8	2.52	0.43
10:D:7:GLU:O	10:D:10:LEU:N	2.47	0.43
13:W:347:GLN:O	13:W:351:MET:HG3	2.18	0.43
11:B:73:ASN:ND2	11:B:74:ARG:N	2.67	0.43
14:S:54:ILE:O	14:S:58:THR:OG1	2.35	0.43
2:A:179:G:N2	2:A:180:G:H1'	2.33	0.43
2:A:186:C:O5'	2:A:186:C:H6	2.01	0.43
12:U:90:ALA:O	13:W:348:ILE:O	2.36	0.43
12:U:128:ARG:NH1	12:U:181:ARG:HH22	2.16	0.43
2:A:221:C:H2'	2:A:222:G:O4'	2.18	0.43
4:N:288:G:H2'	4:N:289:A:P	2.53	0.43
11:B:96:VAL:HG23	11:B:97:GLN:N	2.33	0.43
1:E:121:C:H5''	9:C:32:ARG:NH2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:117:U:H2'	2:A:118:A:H8	1.83	0.43
11:B:15:PHE:O	11:B:83:ARG:NH2	2.52	0.43
11:B:88:GLN:HG3	11:B:92:SER:O	2.18	0.43
13:W:427:PHE:CZ	14:S:57:LEU:HD23	2.52	0.43
2:A:160:A:H2'	2:A:161:C:H6	1.84	0.43
11:B:76:VAL:C	11:B:78:TYR:H	2.25	0.43
9:C:27:VAL:CG1	10:D:30:LEU:HB3	2.49	0.43
11:B:42:GLU:HG3	11:B:43:ASN:N	2.34	0.43
12:U:5:LEU:HD11	12:U:38:LEU:HD23	2.00	0.43
13:W:344:PRO:HB2	13:W:345:PHE:H	1.69	0.43
1:E:124:G:O4'	3:M:57:G:C2'	2.54	0.42
5:O:92:C:H5	5:O:94:C:OP2	2.00	0.42
10:D:7:GLU:O	10:D:9:PHE:N	2.52	0.42
11:B:116:LYS:HE3	11:B:116:LYS:H	1.83	0.42
12:U:7:ALA:O	12:U:11:GLU:HG3	2.19	0.42
12:U:17:ARG:HE	12:U:17:ARG:HB2	1.37	0.42
12:U:89:GLU:C	13:W:351:MET:O	2.32	0.42
9:C:27:VAL:HG13	10:D:30:LEU:HB3	2.00	0.42
12:U:285:GLU:CG	13:W:356:GLY:O	2.67	0.42
2:A:223:U:H2'	2:A:224:G:C5'	2.49	0.42
13:W:423:GLN:OE1	14:S:65:HIS:CD2	2.71	0.42
1:E:138:U:O2	1:E:138:U:C2'	2.67	0.42
2:A:127:A:H2'	2:A:128:U:H5'	1.99	0.42
3:M:55:G:C4'	9:C:46:LEU:HD12	2.50	0.42
11:B:16:ILE:HG12	11:B:84:VAL:HG22	2.02	0.42
12:U:227:LEU:HD13	12:U:262:VAL:HB	2.01	0.42
12:U:283:TYR:CE2	13:W:359:PHE:HD2	2.38	0.42
13:W:339:ILE:HG12	14:S:54:ILE:CG2	2.49	0.42
13:W:430:MET:HA	13:W:433:LYS:HB3	2.00	0.42
1:E:126:A:N7	4:N:293:C:H5'	2.34	0.42
2:A:171:U:H3'	2:A:172:A:C5'	2.49	0.42
2:A:195:U:C4'	13:W:411:GLY:HA3	2.50	0.42
11:B:53:CYS:O	11:B:58:LEU:HB2	2.19	0.42
10:D:86:LEU:C	10:D:86:LEU:HD23	2.45	0.42
11:B:19:TYR:CE2	11:B:81:ARG:HD3	2.55	0.42
11:B:24:ASN:HD22	11:B:27:LYS:CG	2.22	0.42
2:A:161:C:HO2'	2:A:214:A:HO2'	1.66	0.42
11:B:107:TYR:O	11:B:111:MET:HG2	2.19	0.42
12:U:132:VAL:HG12	12:U:185:LEU:O	2.20	0.42
8:R:240:A:C8	8:R:242:C:C5	3.08	0.42
11:B:56:VAL:O	11:B:56:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:41:VAL:HG12	11:B:42:GLU:N	2.34	0.42
12:U:79:TYR:HA	12:U:292:LEU:HD11	2.02	0.42
1:E:110:G:H2'	1:E:111:G:H5'	2.02	0.41
9:C:5:GLN:OE1	9:C:5:GLN:HA	2.20	0.41
9:C:37:ASN:N	10:D:94:LEU:HD11	2.34	0.41
9:C:63:GLU:O	9:C:66:HIS:HB3	2.20	0.41
13:W:412:VAL:HG22	13:W:416:ASP:OD2	2.20	0.41
2:A:182:G:H21	2:A:215:A:H62	1.67	0.41
4:N:271:C:H5'	6:P:270:G:O5'	2.20	0.41
12:U:31:LEU:HB3	12:U:52:VAL:CG2	2.51	0.41
2:A:171:U:H5'	2:A:172:A:OP2	2.20	0.41
11:B:25:ASN:OD1	11:B:25:ASN:C	2.63	0.41
12:U:260:ARG:NH2	12:U:261:HIS:HB2	2.31	0.41
11:B:60:VAL:CB	11:B:84:VAL:HG12	2.49	0.41
12:U:35:ARG:O	12:U:39:MET:CG	2.69	0.41
12:U:147:LEU:O	12:U:150:GLU:HB3	2.21	0.41
1:E:104:G:C2	3:M:57:G:N2	2.87	0.41
1:E:124:G:O3'	3:M:57:G:C5	2.71	0.41
6:P:264:A:N7	6:P:265:C:C4	2.88	0.41
11:B:23:LEU:HB2	11:B:44:PRO:HG3	2.01	0.41
11:B:116:LYS:H	11:B:116:LYS:CE	2.34	0.41
12:U:221:MET:HE3	12:U:249:GLY:C	2.46	0.41
2:A:118:A:H2'	2:A:119:A:H5'	2.02	0.41
2:A:193:G:H2'	2:A:194:G:O4'	2.21	0.41
9:C:70:MET:HE2	10:D:30:LEU:HD13	2.01	0.41
12:U:43:VAL:O	12:U:44:ASN:C	2.62	0.41
12:U:117:LYS:HD2	12:U:279:LEU:HB2	2.01	0.41
12:U:269:PHE:CZ	13:W:347:GLN:OE1	2.73	0.41
1:E:114:G:C2'	1:E:115:C:H5'	2.49	0.41
10:D:5:GLU:O	10:D:7:GLU:N	2.54	0.41
9:C:65:PHE:O	9:C:69:LEU:HG	2.21	0.41
9:C:68:GLN:O	9:C:69:LEU:C	2.63	0.41
11:B:18:ILE:HD12	11:B:105:MET:HG2	2.02	0.41
11:B:99:PRO:HB2	11:B:100:SER:H	1.59	0.41
12:U:59:ALA:HB1	12:U:64:VAL:HG11	2.02	0.41
12:U:232:ALA:O	12:U:236:LYS:HD2	2.21	0.41
1:E:105:G:O4'	4:N:290:C:C2	2.74	0.41
2:A:233:U:C3'	2:A:234:A:C5'	2.98	0.41
11:B:16:ILE:CG1	11:B:84:VAL:HG22	2.51	0.41
12:U:35:ARG:CZ	12:U:49:ARG:HG3	2.51	0.41
13:W:344:PRO:C	13:W:346:SER:HB2	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:105:G:C5'	4:N:290:C:O2'	2.69	0.41
8:R:243:G:P	8:R:244:C:H5'	2.61	0.41
11:B:67:MET:HE1	11:B:74:ARG:HG3	2.02	0.41
13:W:342:MET:O	13:W:345:PHE:HB2	2.21	0.41
1:E:138:U:O2	1:E:138:U:H2'	2.19	0.40
1:E:148:C:H6	1:E:148:C:H5'	1.86	0.40
9:C:69:LEU:O	9:C:73:MET:HG3	2.21	0.40
12:U:79:TYR:O	13:W:357:THR:HG23	2.21	0.40
2:A:151:C:H2'	2:A:152:G:H8	1.86	0.40
8:R:240:A:H5''	8:R:241:U:H3'	2.04	0.40
11:B:76:VAL:CG1	11:B:77:GLN:H	2.34	0.40
12:U:276:PRO:HD2	12:U:277:GLU:OE2	2.21	0.40
12:U:283:TYR:HB3	12:U:286:ARG:HB3	2.02	0.40
1:E:116:G:C2'	1:E:117:C:H5'	2.51	0.40
9:C:60:LYS:O	9:C:64:LYS:HG3	2.20	0.40
12:U:165:PRO:HD2	12:U:166:GLU:OE1	2.21	0.40
12:U:283:TYR:HD1	13:W:360:MET:O	2.04	0.40
12:U:285:GLU:OE1	13:W:355:PHE:CA	2.69	0.40
2:A:172:A:C2	2:A:225:C:H1'	2.56	0.40
3:M:69:U:C5'	3:M:70:C:OP2	2.63	0.40
1:E:124:G:O3'	3:M:57:G:C8	2.75	0.40
2:A:126:C:H2'	2:A:127:A:O4'	2.21	0.40
11:B:119:THR:O	11:B:120:GLN:OXT	2.40	0.40
12:U:35:ARG:O	12:U:39:MET:HG3	2.21	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 PDB entries followed by that with respect to all EM entries.

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
9	C	69/85 (81%)	57 (83%)	9 (13%)	3 (4%)	2 17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	D	72/106 (68%)	63 (88%)	5 (7%)	4 (6%)	1	14
11	B	105/108 (97%)	87 (83%)	11 (10%)	7 (7%)	1	12
12	U	292/296 (99%)	273 (94%)	18 (6%)	1 (0%)	36	72
13	W	107/109 (98%)	100 (94%)	2 (2%)	5 (5%)	2	16
14	S	16/18 (89%)	14 (88%)	2 (12%)	0	100	100
All	All	661/722 (92%)	594 (90%)	47 (7%)	20 (3%)	5	23

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	C	34	SER
9	C	47	VAL
10	D	6	SER
11	B	42	GLU
11	B	75	ASP
13	W	344	PRO
13	W	345	PHE
13	W	362	LYS
10	D	7	GLU
10	D	8	GLN
11	B	99	PRO
13	W	346	SER
12	U	21	ARG
9	C	35	ASP
11	B	64	LYS
11	B	77	GLN
10	D	93	GLY
13	W	363	GLY
11	B	56	VAL
11	B	96	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	
9	C	64/77 (83%)	55 (86%)	9 (14%)	3	13
10	D	69/96 (72%)	66 (96%)	3 (4%)	26	47
11	B	96/97 (99%)	89 (93%)	7 (7%)	13	34
12	U	233/234 (100%)	197 (84%)	36 (16%)	2	12
13	W	96/96 (100%)	91 (95%)	5 (5%)	21	42
14	S	17/17 (100%)	16 (94%)	1 (6%)	18	39
All	All	575/617 (93%)	514 (89%)	61 (11%)	9	21

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	C	24	LYS
9	C	26	ARG
9	C	28	VAL
9	C	38	LEU
9	C	39	CYS
9	C	46	LEU
9	C	47	VAL
9	C	63	GLU
9	C	74	VAL
10	D	20	CYS
10	D	54	ASN
10	D	76	VAL
11	B	14	ARG
11	B	29	ILE
11	B	39	LYS
11	B	64	LYS
11	B	93	LEU
11	B	104	VAL
11	B	116	LYS
12	U	3	GLN
12	U	4	GLN
12	U	5	LEU
12	U	11	GLU
12	U	17	ARG
12	U	22	ILE
12	U	28	LYS
12	U	32	ARG
12	U	33	GLU
12	U	39	MET
12	U	45	LEU

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Mol	Chain	Res	Type
12	U	49	ARG
12	U	52	VAL
12	U	54	ARG
12	U	58	GLU
12	U	63	GLN
12	U	83	LYS
12	U	94	VAL
12	U	99	ASN
12	U	103	LEU
12	U	107	GLN
12	U	127	ARG
12	U	128	ARG
12	U	132	VAL
12	U	144	GLN
12	U	146	ARG
12	U	151	LYS
12	U	160	MET
12	U	161	ASP
12	U	204	ARG
12	U	236	LYS
12	U	244	LEU
12	U	277	GLU
12	U	279	LEU
12	U	285	GLU
12	U	294	MET
13	W	349	LEU
13	W	365	GLU
13	W	383	ASN
13	W	394	LYS
13	W	412	VAL
14	S	59	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
10	D	18	GLN
10	D	54	ASN
10	D	85	ASN
11	B	43	ASN
11	B	59	ASN
11	B	65	ASN
11	B	73	ASN

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Mol	Chain	Res	Type
11	B	88	GLN
12	U	3	GLN
12	U	144	GLN
13	W	383	ASN
13	W	385	GLN
13	W	399	GLN
13	W	423	GLN
13	W	429	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	48/50 (96%)	11 (22%)	2 (4%)
2	A	127/128 (99%)	22 (17%)	1 (0%)
3	M	26/27 (96%)	12 (46%)	3 (11%)
4	N	29/31 (93%)	13 (44%)	8 (27%)
5	O	23/24 (95%)	6 (26%)	1 (4%)
6	P	19/20 (95%)	2 (10%)	2 (10%)
7	Q	12/12 (100%)	5 (41%)	2 (16%)
8	R	11/12 (91%)	6 (54%)	3 (27%)
All	All	295/304 (97%)	77 (26%)	22 (7%)

All (77) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	E	101	G
1	E	104	G
1	E	128	U
1	E	129	C
1	E	132	A
1	E	133	G
1	E	136	A
1	E	137	C
1	E	138	U
1	E	139	C
1	E	148	C
2	A	128	U
2	A	129	C
2	A	164	G
2	A	168	G
2	A	169	C

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Mol	Chain	Res	Type
2	A	171	U
2	A	172	A
2	A	173	A
2	A	174	G
2	A	176	A
2	A	177	G
2	A	187	G
2	A	191	C
2	A	213	A
2	A	214	A
2	A	215	A
2	A	219	C
2	A	221	C
2	A	224	G
2	A	227	G
2	A	232	G
2	A	234	A
3	M	56	A
3	M	57	G
3	M	58	G
3	M	59	A
3	M	60	U
3	M	65	U
3	M	66	G
3	M	67	A
3	M	68	G
3	M	70	C
3	M	71	C
3	M	75	A
4	N	275	U
4	N	276	G
4	N	278	A
4	N	279	A
4	N	280	C
4	N	281	A
4	N	282	U
4	N	283	A
4	N	288	G
4	N	289	A
4	N	291	C
4	N	299	U
4	N	300	U

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Mol	Chain	Res	Type
5	O	77	U
5	O	78	U
5	O	84	C
5	O	92	C
5	O	98	G
5	O	99	C
6	P	253	A
6	P	266	U
7	Q	101	G
7	Q	102	A
7	Q	104	C
7	Q	105	G
7	Q	111	C
8	R	241	U
8	R	242	C
8	R	243	G
8	R	244	C
8	R	249	G
8	R	251	G

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	E	136	A
1	E	137	C
2	A	212	C
3	M	56	A
3	M	65	U
3	M	69	U
4	N	274	G
4	N	275	U
4	N	277	C
4	N	278	A
4	N	279	A
4	N	280	C
4	N	281	A
4	N	299	U
5	O	98	G
6	P	252	A
6	P	265	C
7	Q	100	C
7	Q	101	G

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Mol	Chain	Res	Type
8	R	242	C
8	R	243	G
8	R	248	U

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	$\# Z > 2$
2	CCC	A	239	8,2	20,25,26	0.63	0	27,38,41	2.81	4 (14%)

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
2	CCC	A	239	8,2	-	0/7/35/36	0/3/3/3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	239	CCC	O2C-PC-O1C	11.05	145.57	109.89
2	A	239	CCC	O3'-PC-O1C	-7.07	97.11	115.76
2	A	239	CCC	O2'-PC-O1C	-5.43	101.44	115.76
2	A	239	CCC	O2'-C2'-C3'	2.01	112.79	104.34

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	M	5
7	Q	3
4	N	3
5	O	2
13	W	2
6	P	1
8	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	O	77:U	O3'	78:U	P	3.09
1	M	64:U	O3'	65:U	P	2.87
1	M	55:G	O3'	56:A	P	2.73
1	P	257:C	O3'	258:C	P	2.65
1	M	70:C	O3'	71:C	P	2.57
1	O	97:U	O3'	98:G	P	2.53
1	M	67:A	O3'	68:G	P	2.50
1	Q	109:G	O3'	110:U	P	2.44
1	N	282:U	O3'	283:A	P	2.31
1	Q	104:C	O3'	105:G	P	2.20
1	N	288:G	O3'	289:A	P	2.09
1	Q	110:U	O3'	111:C	P	2.07

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	N	292:C	O3'	293:C	P	2.02
1	M	74:G	O3'	75:A	P	1.84
1	R	248:U	O3'	249:G	P	1.81
1	W	362:LYS	C	363:GLY	N	1.64
1	W	345:PHE	C	346:SER	N	0.91

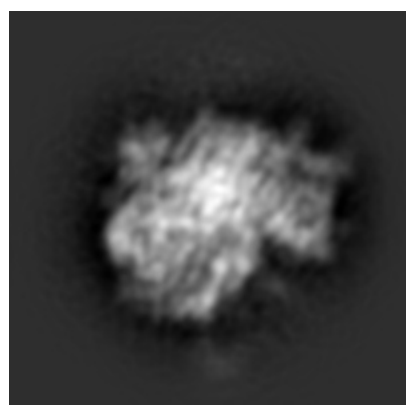
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1063. These allow visual inspection of the internal detail of the map and identification of artifacts.

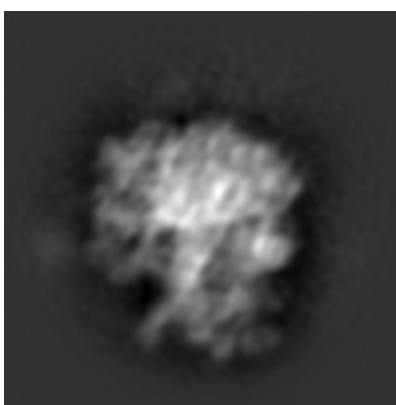
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

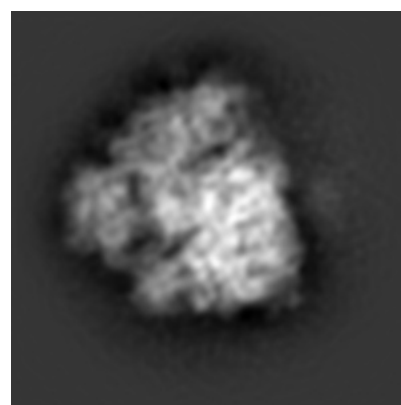
6.1.1 Primary map



X



Y

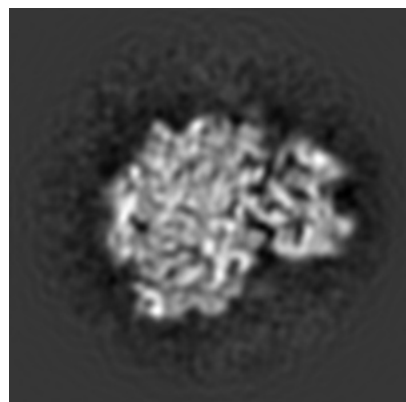


Z

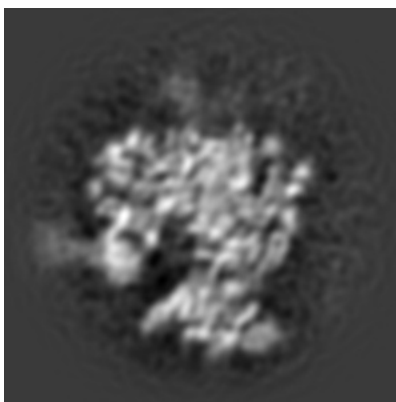
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

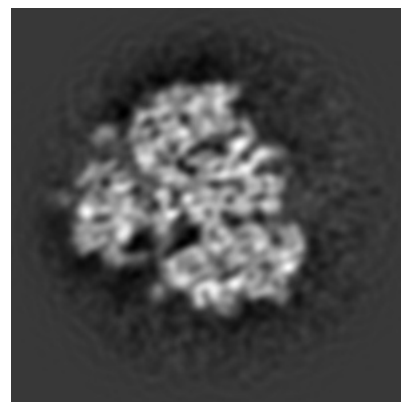
6.2.1 Primary map



X Index: 65



Y Index: 65

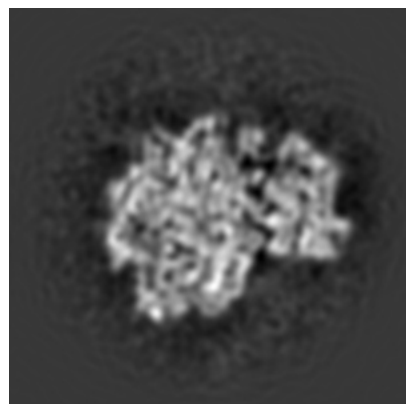


Z Index: 65

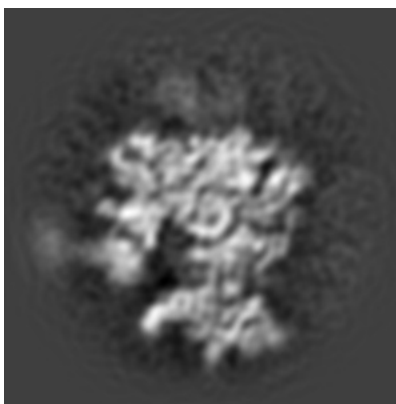
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

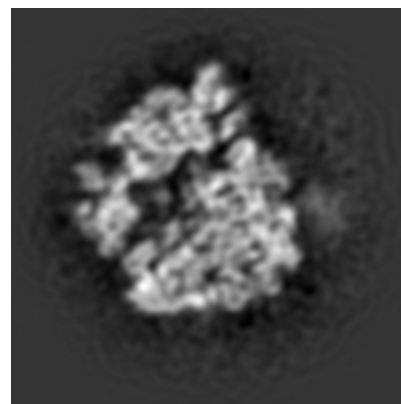
6.3.1 Primary map



X Index: 63



Y Index: 67

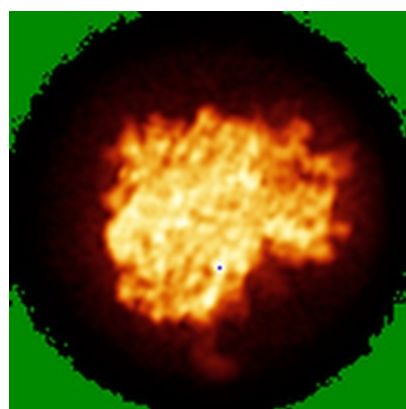


Z Index: 59

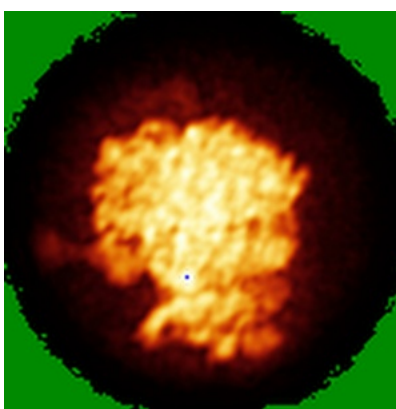
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

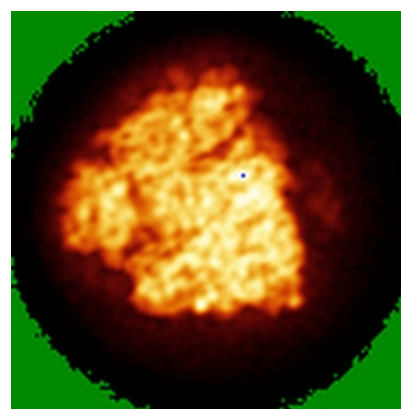
6.4.1 Primary map



X



Y

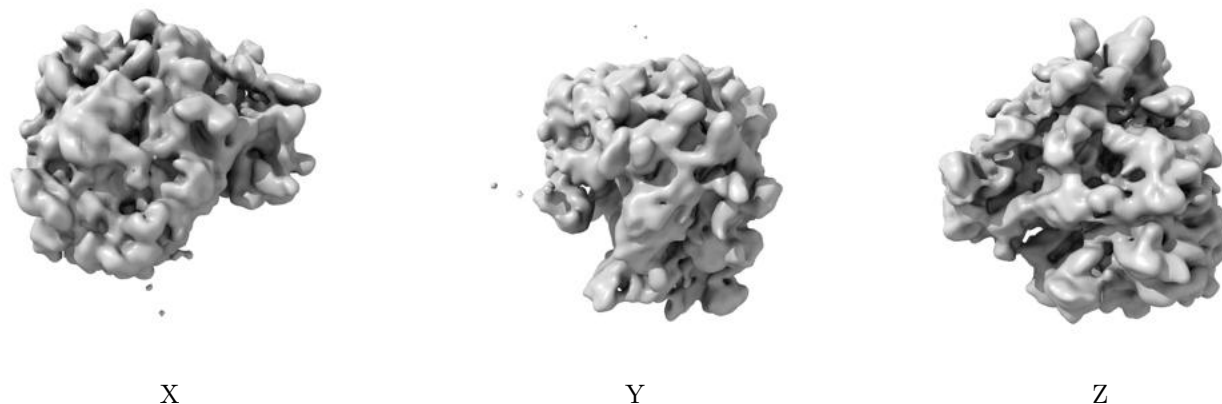


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

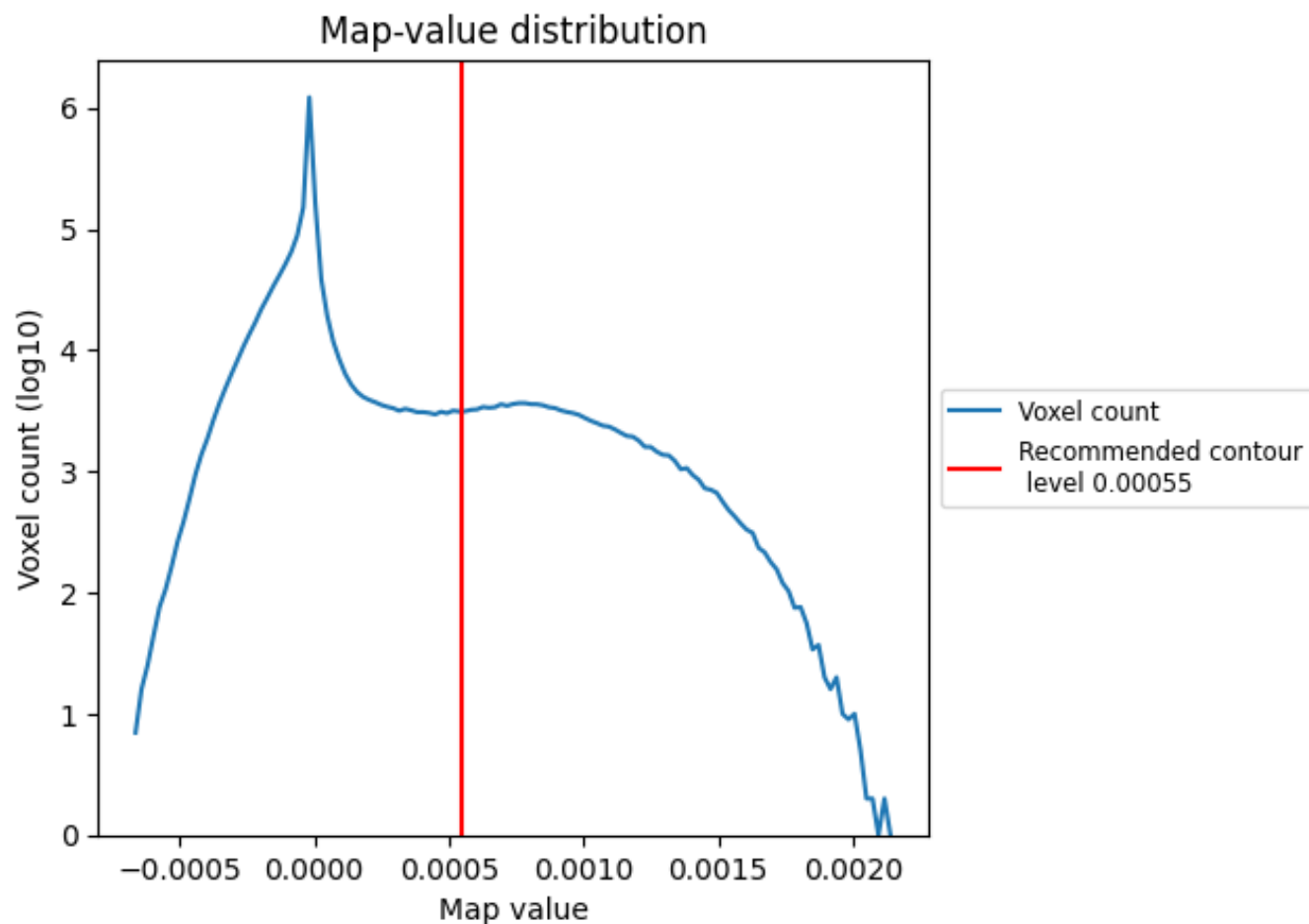
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

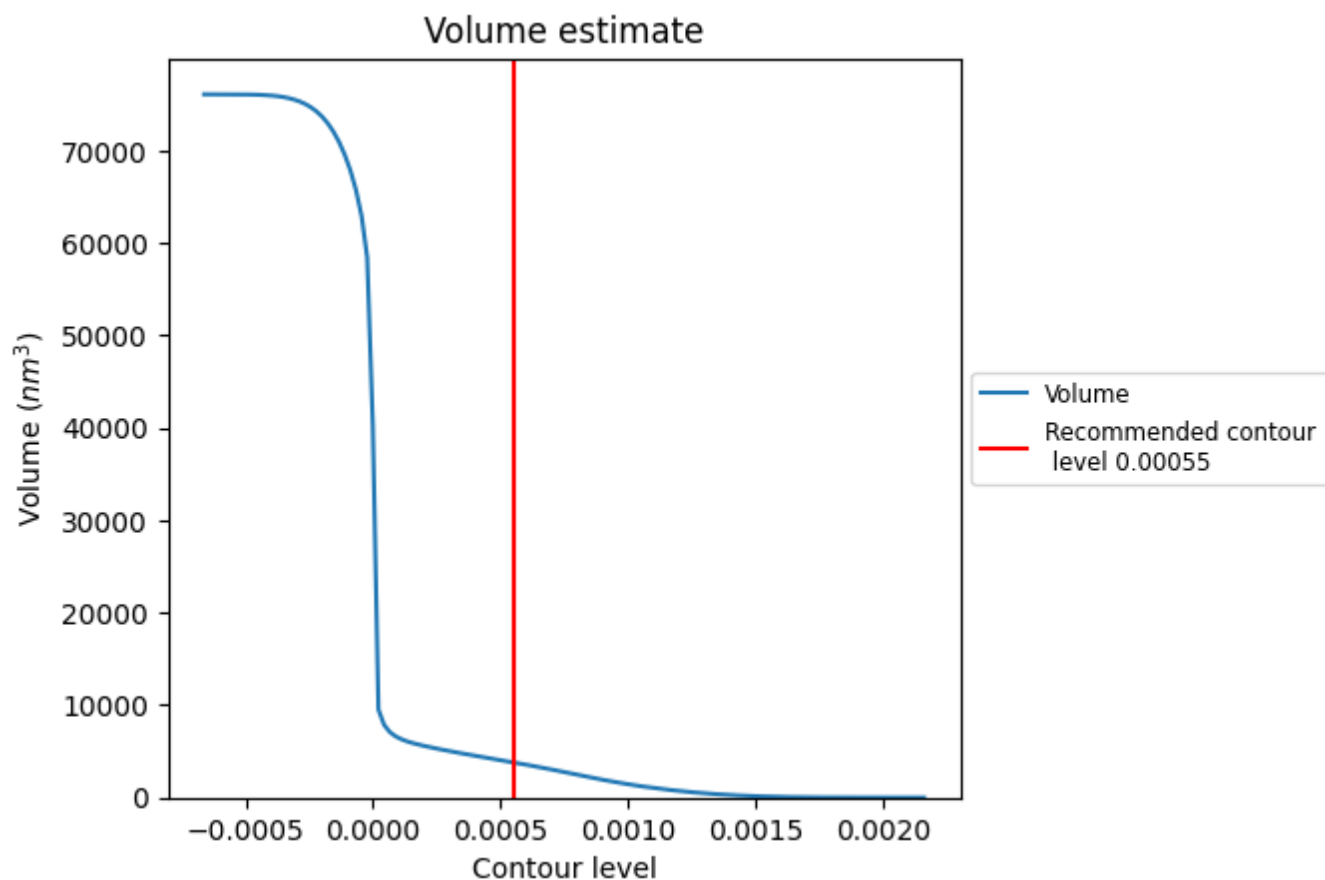
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

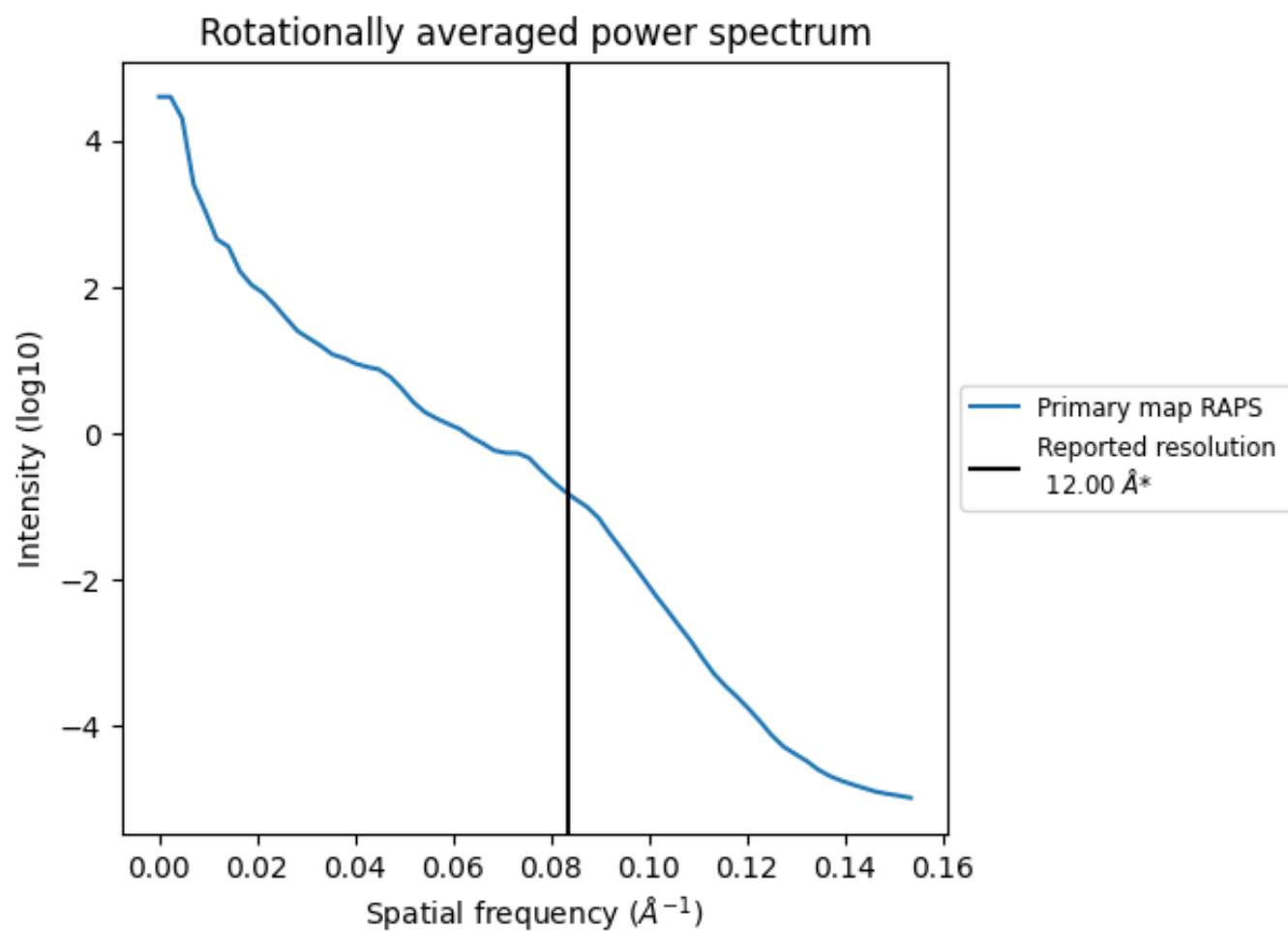
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3809 nm³; this corresponds to an approximate mass of 3440 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.083 Å⁻¹

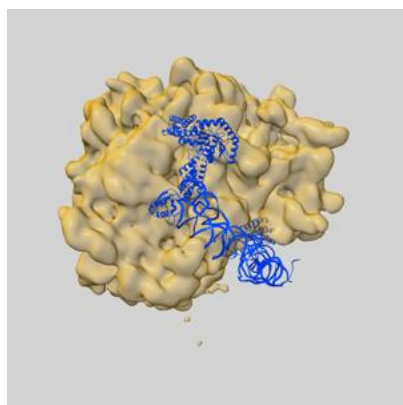
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

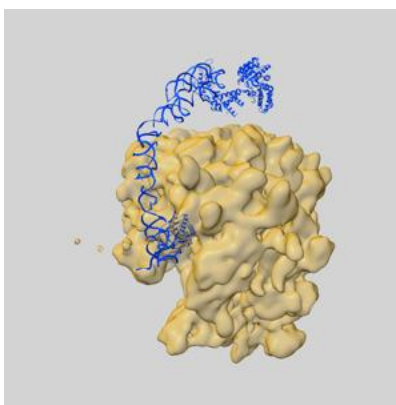
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1063 and PDB model 1RY1. Per-residue inclusion information can be found in section [3](#) on page [7](#).

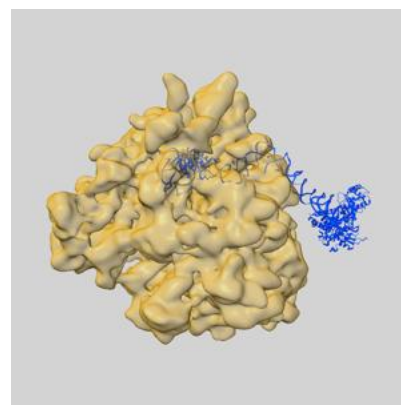
9.1 Map-model overlay [i](#)



X



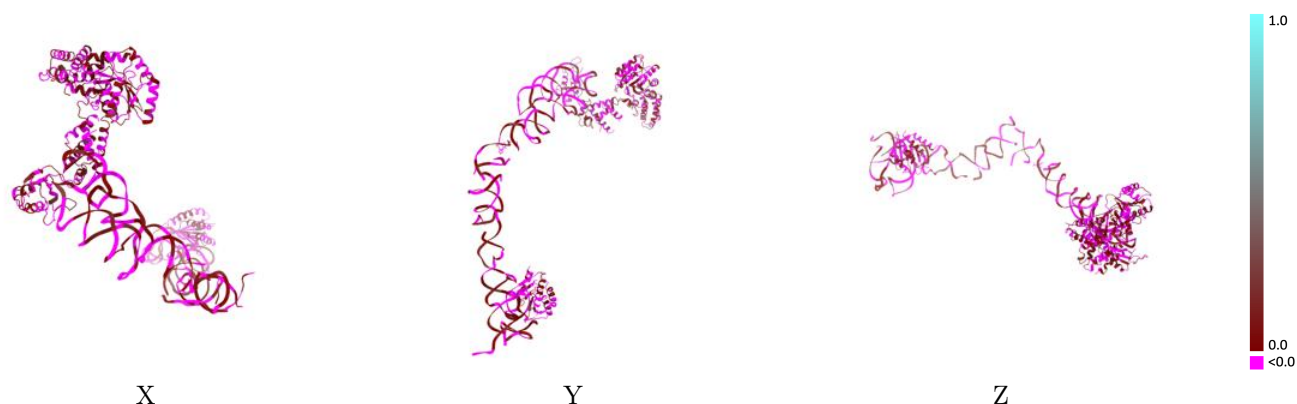
Y



Z

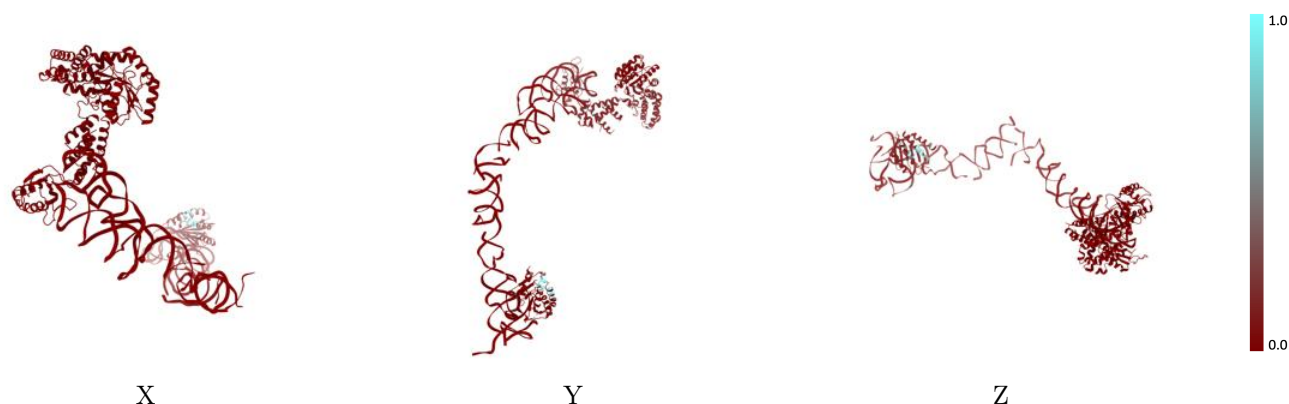
The images above show the 3D surface view of the map at the recommended contour level 0.00055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



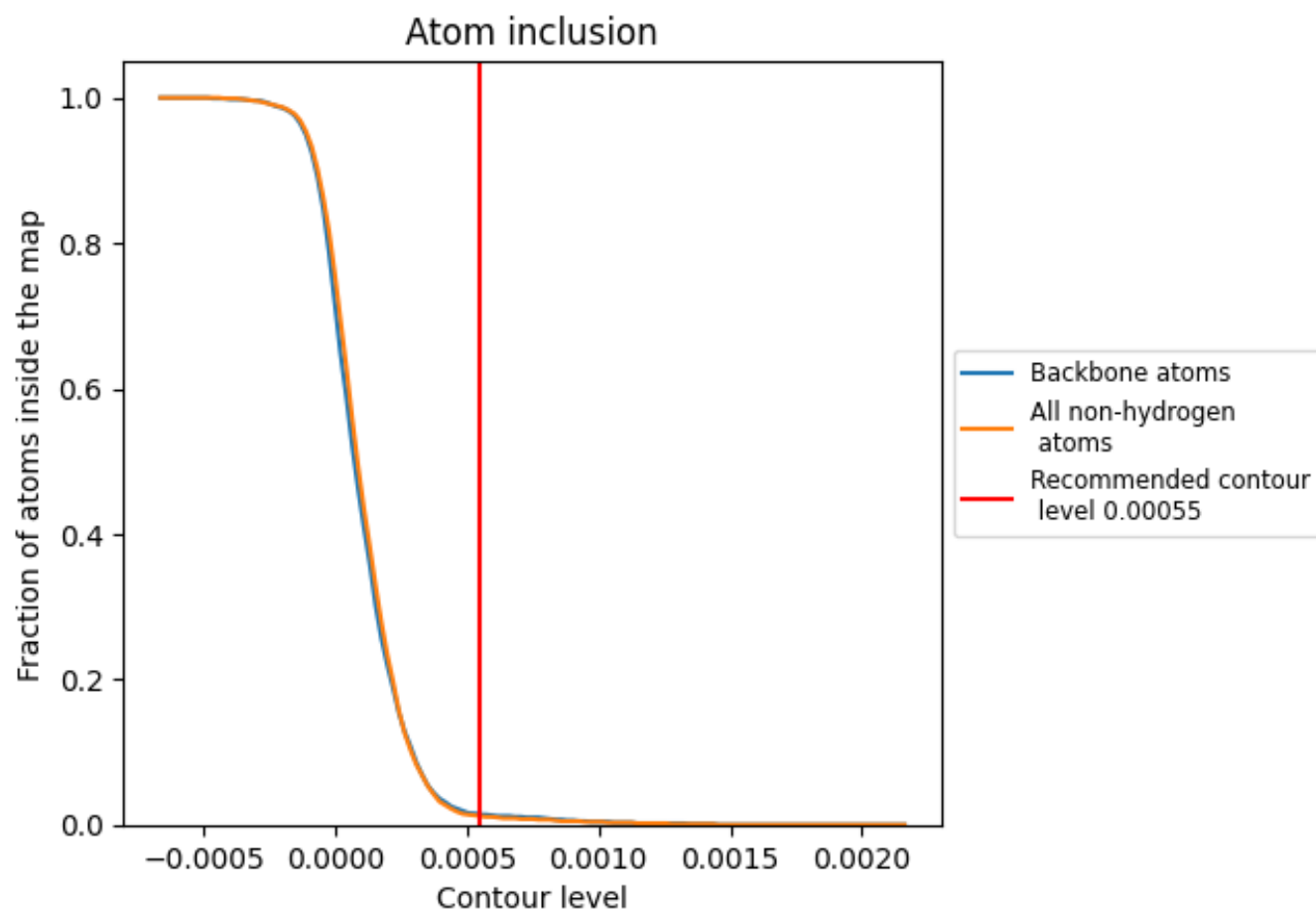
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00055).

9.4 Atom inclusion [i](#)



At the recommended contour level, 2% of all backbone atoms, 1% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.00055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.0120	 0.0080
A	 0.0000	 0.0050
B	 0.0000	 0.0140
C	 0.1360	 -0.0390
D	 0.0690	 -0.0040
E	 0.0230	 -0.0010
M	 0.0000	 0.0300
N	 0.0000	 0.0490
O	 0.0000	 0.0520
P	 0.0000	 0.0240
Q	 0.0000	 0.0130
R	 0.0000	 0.0060
S	 0.0000	 -0.1010
U	 0.0000	 -0.0010
W	 0.0000	 0.0310

