Full wwPDB EM Validation Report ⓘ

Dec 18, 2022 – 07:31 am GMT

PDB ID	:	7ASN
EMDB ID	:	EMD-11901
Title	:	Staphylococcus aureus 50S after 30 minutes incubation a 37C
Authors	:	Cimicata, G.; Bashan, A.; Yonath, A.
Deposited on	:	2020-10-27
Resolution	:	2.73 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:

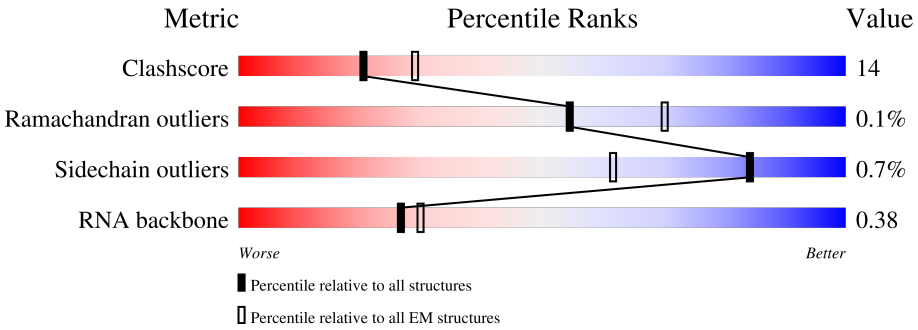
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 2.73 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	A	2742	41% 37% 20%
2	B	106	31% 42% 27%
3	1	47	34% 47% 51%
4	2	43	7% 60% 40%
5	3	64	75% 25%
6	F	274	11% 76% 24%
7	D	215	74% 24%

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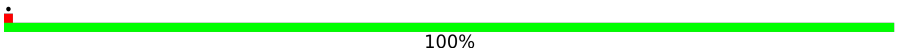
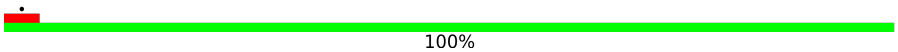
Mol	Chain	Length	Quality of chain
8	E	206	
9	H	144	
10	L	146	
11	Y	137	
12	G	122	
13	M	117	
14	N	114	
15	O	116	
16	P	102	
17	Q	112	
18	R	89	
19	S	103	
20	T	94	
21	a	79	
22	V	49	
23	W	67	
24	X	58	
25	b	48	

2 Entry composition (i)

There are 25 unique types of molecules in this entry. The entry contains 80694 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 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	2742	58787	26244	10755	19046	2742	0	0

- Molecule 2 is a RNA chain called 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	106	2260	1010	407	737	106	0	0

- Molecule 3 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	1	47	390	238	78	70	4	0	0

- Molecule 4 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	2	43	367	225	89	52	1	0	0

- Molecule 5 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	3	64	521	324	113	82	2	0	0

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	274	2094	1303	415	371	5	0	0

- Molecule 7 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	215	Total	C	N	O	S	0	0
			1627	1018	299	305	5		

- Molecule 8 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	206	Total	C	N	O	S	0	0
			1572	986	288	296	2		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	144	Total	C	N	O	S	0	0
			1132	708	204	217	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	1	MET	-	initiating methionine	UNP W8TUE6

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	146	Total	C	N	O	S	0	0
			1086	674	214	197	1		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Y	137	Total	C	N	O	S	0	0
			1071	689	203	175	4		

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	122	Total	C	N	O	S	0	0
			918	572	174	168	4		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	117	Total	C	N	O	0	0
			872	543	172	157		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	113	Total	C	N	O	0	0
			878	557	171	150		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	116	Total	C	N	O	S	0	0
			942	593	189	156	4		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	102	Total	C	N	O	S	0	0
			790	503	142	144	1		

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	112	Total	C	N	O	S	0	0
			854	534	164	153	3		

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	89	Total	C	N	O	S	0	0
			715	453	127	131	4		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	103	Total	C	N	O	S	0	0
			770	486	142	141	1		

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	94	Total 722	C 463	N 130	O 129	0	0

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	a	79	Total 597	C 369	N 117	O 111	0	0

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	V	49	Total 379	C 234	N 82	O 63	0	0

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	67	Total 541	C 333	N 102	O 106	0	0

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	X	58	Total 449	C 280	N 85	O 84	0	0

- Molecule 25 is a protein called 50S ribosomal protein L32.

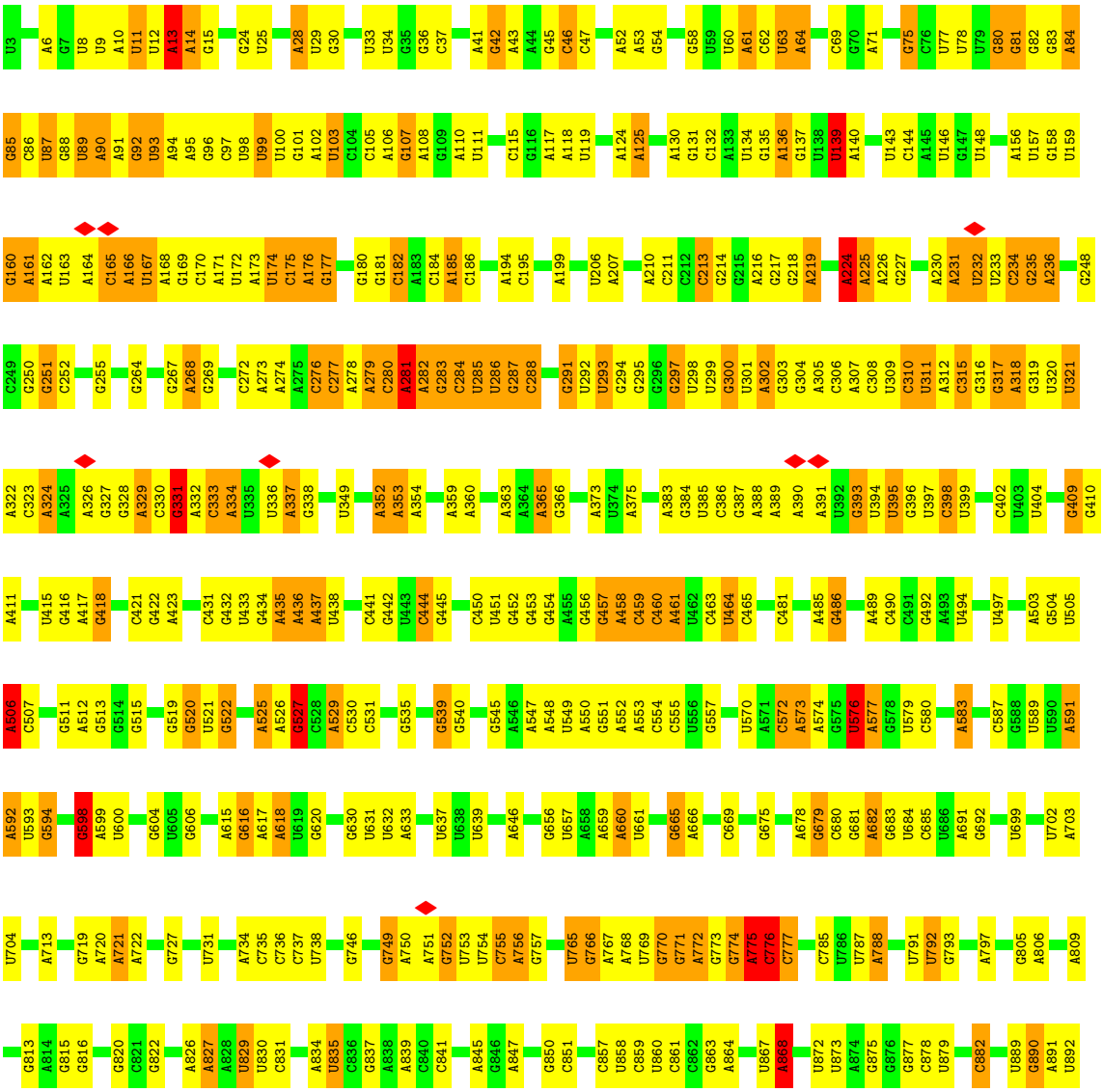
Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	48	Total 360	C 222	N 77	O 59	S 2	0	0

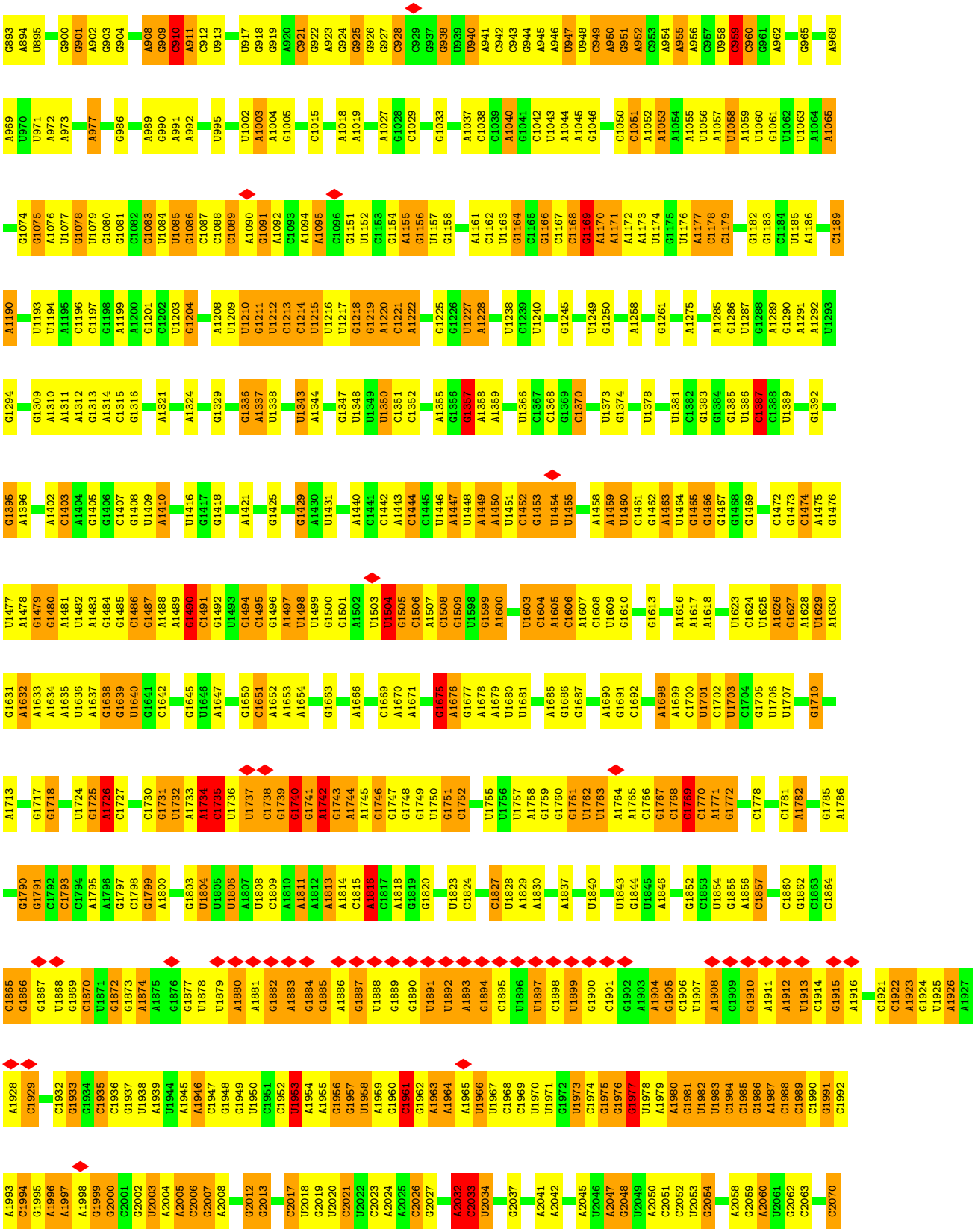
3 Residue-property plots (i)

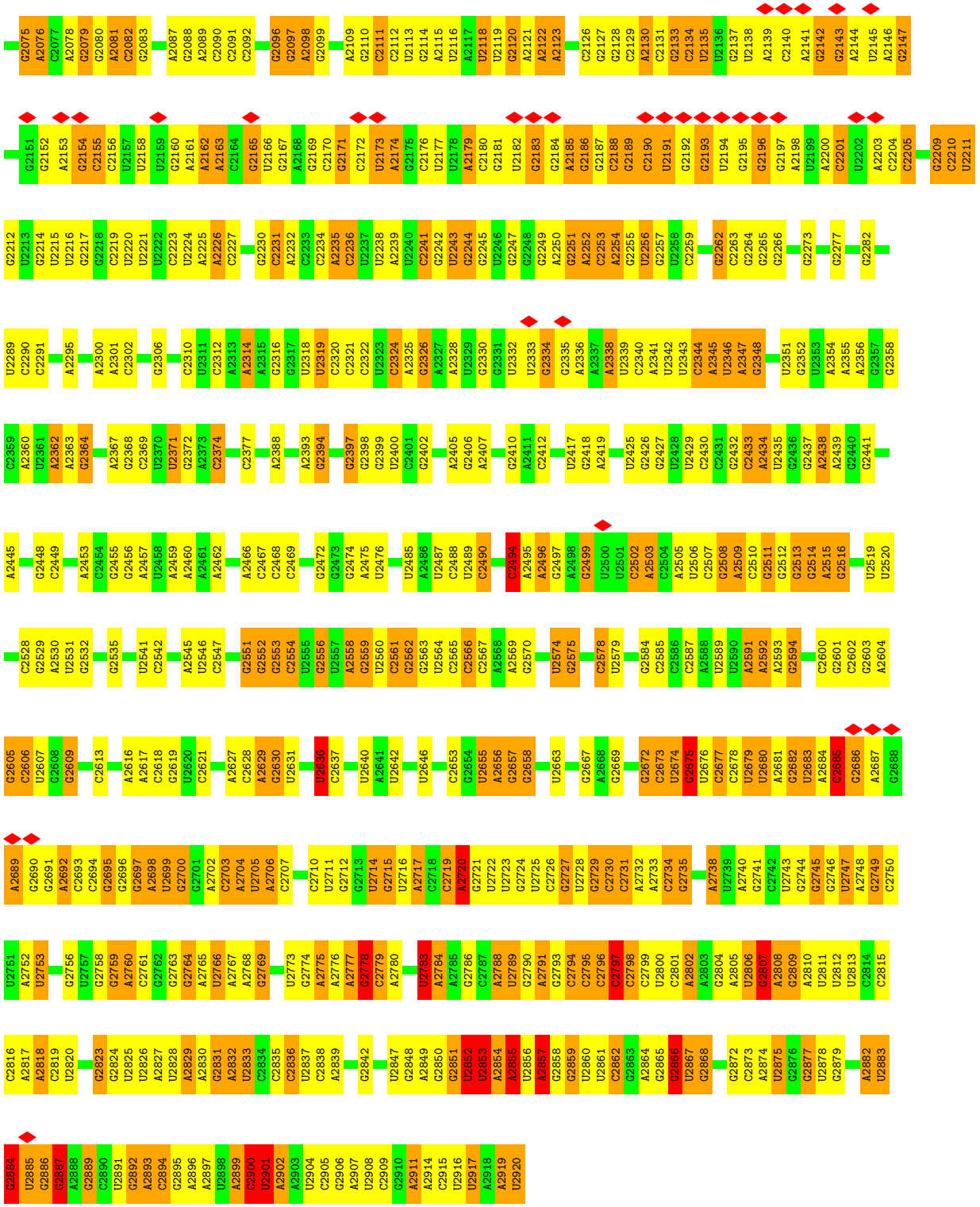
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 23S

Chain A:

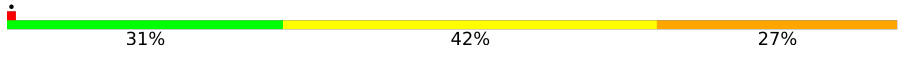


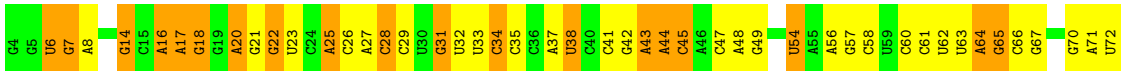


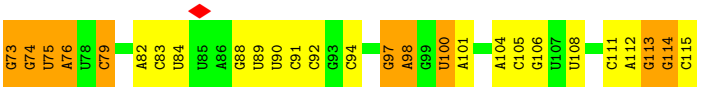


• Molecule 2: 5S

Chain B:



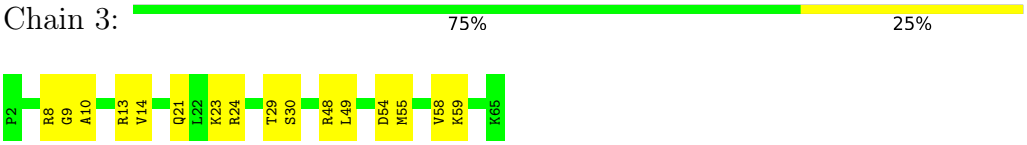




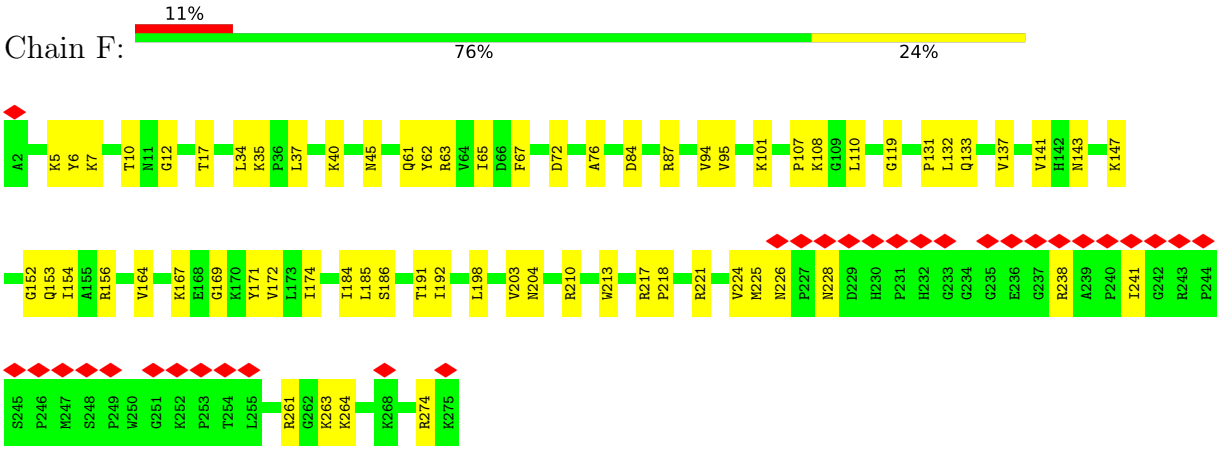
• Molecule 3: 50S ribosomal protein L33

• Molecule 4: 50S ribosomal protein L34

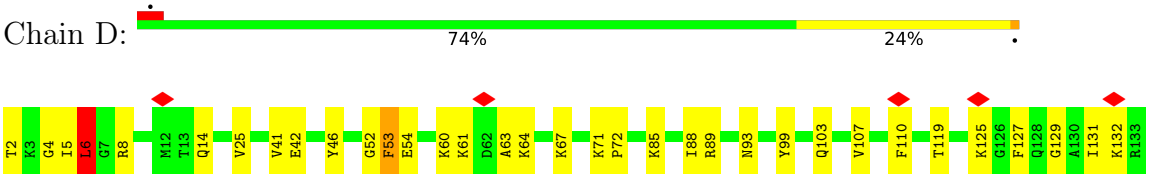
• Molecule 5: 50S ribosomal protein L35

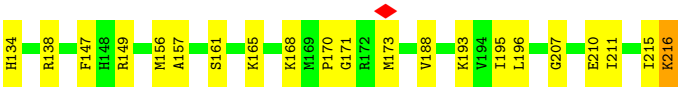


• Molecule 6: 50S ribosomal protein L2



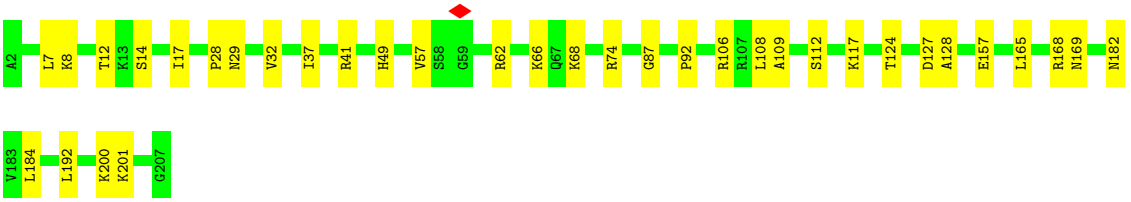
• Molecule 7: 50S ribosomal protein L3





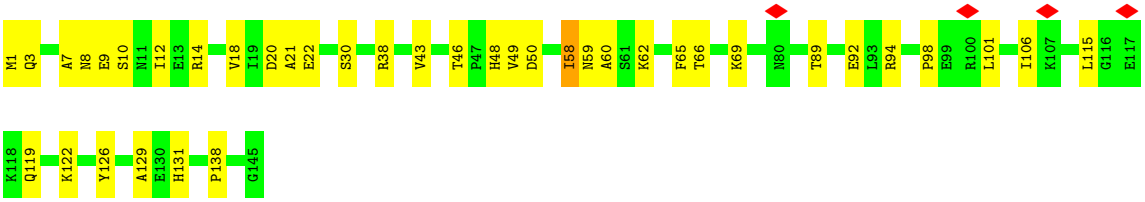
• Molecule 8: 50S ribosomal protein L4

Chain E:



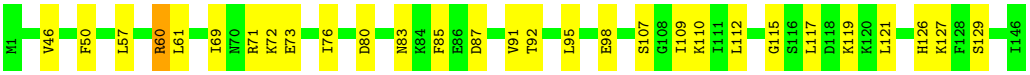
• Molecule 9: 50S ribosomal protein L13

Chain H:



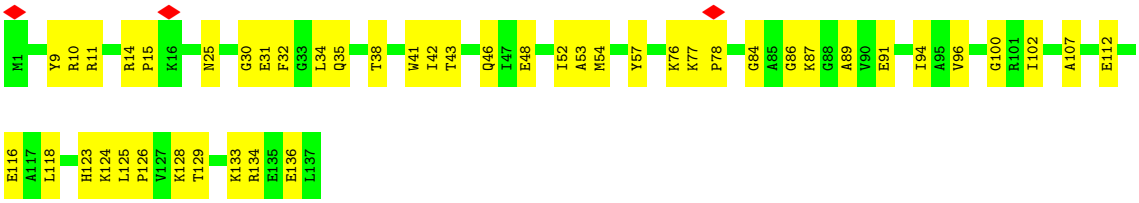
• Molecule 10: 50S ribosomal protein L15

Chain L:



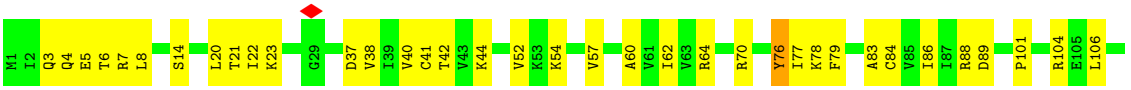
• Molecule 11: 50S ribosomal protein L16

Chain Y:



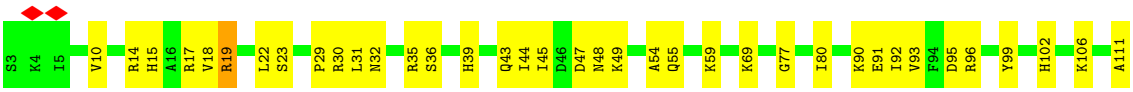
• Molecule 12: 50S ribosomal protein L14

Chain G:



• Molecule 13: 50S ribosomal protein L18

Chain M:

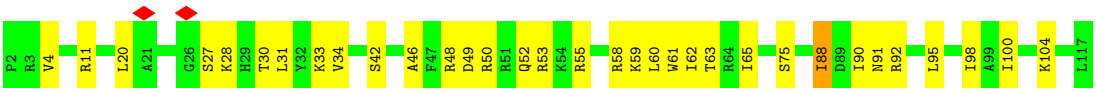


• Molecule 14: 50S ribosomal protein L19

Chain N:

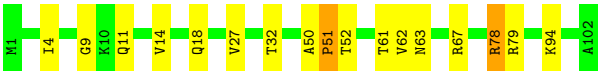
• Molecule 15: 50S ribosomal protein L20

Chain O:



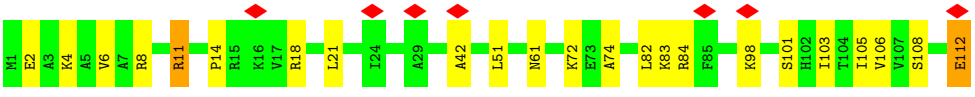
• Molecule 16: 50S ribosomal protein L21

Chain P:



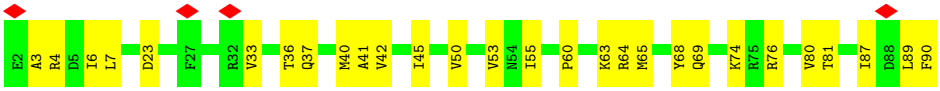
• Molecule 17: 50S ribosomal protein L22

Chain Q:



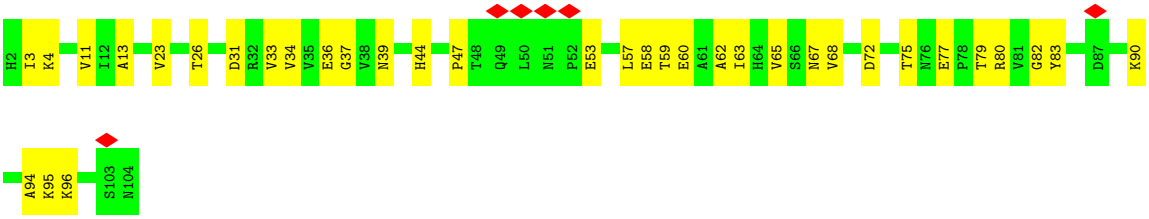
• Molecule 18: 50S ribosomal protein L23

Chain R:



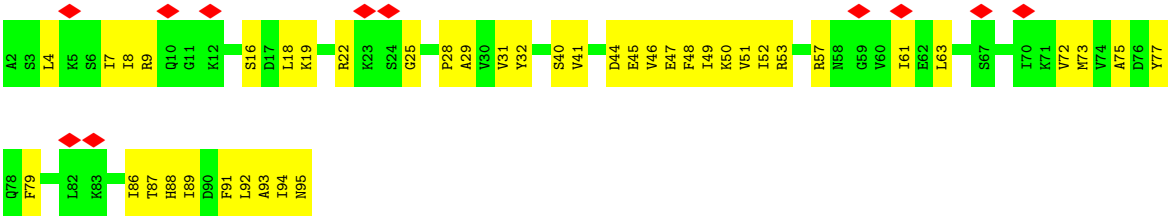
• Molecule 19: 50S ribosomal protein L24

Chain S:



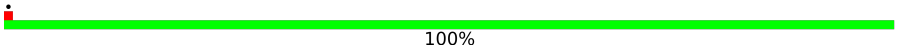
• Molecule 20: 50S ribosomal protein L25

Chain T:



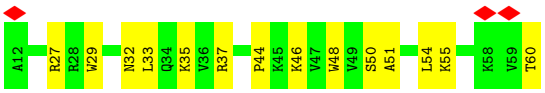
• Molecule 21: 50S ribosomal protein L27

Chain a:



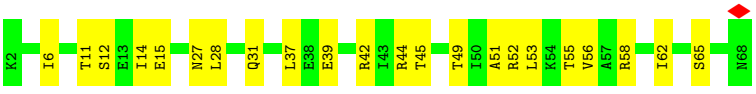
• Molecule 22: 50S ribosomal protein L28

Chain V:



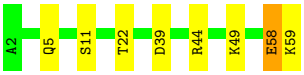
• Molecule 23: 50S ribosomal protein L29

Chain W:



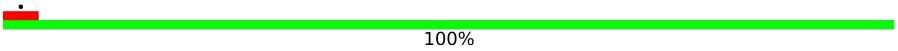
• Molecule 24: 50S ribosomal protein L30

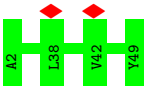
Chain X:



• Molecule 25: 50S ribosomal protein L32

Chain b:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	175844	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.029	Depositor
Minimum map value	-0.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0026	Depositor
Map size (Å)	281.42398, 281.42398, 281.42398	wwPDB
Map dimensions	328, 328, 328	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8579999, 0.8579999, 0.8579999	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, 5MU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.80	8/65753 (0.0%)	1.09	257/102527 (0.3%)
2	B	0.44	0/2523	1.01	4/3920 (0.1%)
3	1	0.37	0/395	0.80	1/530 (0.2%)
4	2	0.47	0/371	0.79	0/484
5	3	0.38	0/526	0.65	0/690
6	F	0.41	0/2129	0.65	0/2858
7	D	0.44	0/1651	0.69	0/2215
8	E	0.43	0/1595	0.63	0/2154
9	H	0.48	0/1153	0.59	0/1553
10	L	0.41	0/1100	0.69	1/1467 (0.1%)
11	Y	0.36	0/1095	0.60	0/1472
12	G	0.52	1/925 (0.1%)	0.65	0/1242
13	M	0.29	0/881	0.58	0/1180
14	N	0.44	0/889	0.65	0/1192
15	O	0.49	0/954	0.71	1/1264 (0.1%)
16	P	0.47	0/800	0.69	0/1070
17	Q	0.40	0/862	0.63	0/1161
18	R	0.37	0/723	0.59	0/966
19	S	0.35	0/779	0.59	0/1043
20	T	0.30	0/730	0.60	0/981
21	a	0.42	0/603	0.53	0/802
22	V	0.30	0/384	0.58	0/515
23	W	0.33	0/542	0.57	0/722
24	X	0.38	0/451	0.58	0/606
25	b	0.38	0/366	0.71	0/489
All	All	0.73	9/88180 (0.0%)	1.02	264/133103 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	1	0	1
7	D	0	2
8	E	0	1
9	H	0	1
All	All	0	5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2802	A	N9-C4	-7.11	1.33	1.37
1	A	2715	G	C2-N3	-6.53	1.27	1.32
1	A	2715	G	N3-C4	-6.21	1.31	1.35
1	A	2720	A	N9-C4	-6.05	1.34	1.37
1	A	882	C	N3-C4	-5.91	1.29	1.33
1	A	2715	G	N9-C4	-5.87	1.33	1.38
12	G	76	TYR	CE1-CZ	-5.36	1.31	1.38
1	A	2855	A	C5-C6	-5.33	1.36	1.41
1	A	1746	G	C6-N1	-5.01	1.36	1.39

All (264) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	2855	A	N1-C6-N6	11.88	125.73	118.60
1	A	2855	A	C5-C6-N6	-10.89	114.99	123.70
1	A	1751	G	N3-C4-N9	10.65	132.39	126.00
1	A	2715	G	N3-C4-N9	-10.63	119.62	126.00
1	A	2866	G	C2-N3-C4	-9.42	107.19	111.90
3	1	12	CYS	CA-CB-SG	9.02	130.24	114.00
1	A	2715	G	C2-N3-C4	-8.94	107.43	111.90
1	A	175	C	N1-C2-O2	8.73	124.14	118.90
1	A	2727	G	N3-C2-N2	-8.73	113.79	119.90
1	A	557	G	O4'-C1'-N9	8.71	115.17	108.20
1	A	2715	G	N3-C2-N2	-8.68	113.83	119.90
1	A	2853	U	O4'-C1'-N1	8.63	115.10	108.20
1	A	2902	A	C6-C5-N7	-8.62	126.26	132.30
1	A	2700	G	N3-C2-N2	-8.58	113.89	119.90
1	A	2802	A	C2-N3-C4	-8.57	106.31	110.60
1	A	175	C	N3-C2-O2	-8.52	115.93	121.90
1	A	2700	G	N3-C4-N9	-8.33	121.00	126.00
1	A	2855	A	N9-C4-C5	-8.30	102.48	105.80
1	A	2636	U	C2-N1-C1'	8.24	127.59	117.70
1	A	2006	C	C2-N1-C1'	8.19	127.81	118.80
1	A	2902	A	C4-C5-C6	8.11	121.06	117.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	882	C	N3-C2-O2	-7.95	116.33	121.90
1	A	2902	A	N1-C2-N3	7.94	133.27	129.30
1	A	835	U	C2-N1-C1'	7.75	127.00	117.70
1	A	2866	G	N1-C2-N3	7.75	128.55	123.90
1	A	910	C	N1-C2-O2	7.73	123.54	118.90
1	A	1168	C	N3-C2-O2	-7.64	116.55	121.90
1	A	2021	C	O5'-P-OP2	-7.61	98.85	105.70
1	A	2902	A	N7-C8-N9	7.56	117.58	113.80
1	A	1227	U	N3-C2-O2	-7.46	116.98	122.20
1	A	2727	G	N3-C4-N9	-7.42	121.55	126.00
1	A	1751	G	N9-C4-C5	-7.38	102.45	105.40
1	A	2855	A	C6-C5-N7	-7.37	127.14	132.30
1	A	1751	G	C6-C5-N7	-7.35	125.99	130.40
1	A	2902	A	N3-C4-N9	7.32	133.26	127.40
1	A	1804	U	N3-C2-O2	-7.31	117.09	122.20
1	A	2855	A	C4-C5-N7	7.30	114.35	110.70
1	A	2715	G	C8-N9-C4	-7.28	103.49	106.40
10	L	60	ARG	C-N-CA	7.23	139.77	121.70
1	A	1387	C	N3-C2-O2	-7.20	116.86	121.90
1	A	2715	G	N9-C4-C5	7.19	108.28	105.40
1	A	2189	G	C4-N9-C1'	7.17	135.82	126.50
1	A	2852	U	C2-N1-C1'	7.12	126.25	117.70
1	A	1751	G	C8-N9-C1'	-7.06	117.83	127.00
1	A	1746	G	C4-N9-C1'	7.05	135.67	126.50
1	A	1799	G	N3-C4-N9	-7.04	121.78	126.00
1	A	2006	C	O5'-P-OP2	-7.02	99.38	105.70
1	A	2715	G	N3-C4-C5	7.01	132.10	128.60
1	A	2189	G	N3-C4-C5	-6.97	125.12	128.60
1	A	1228	A	N7-C8-N9	6.96	117.28	113.80
1	A	1977	G	C8-N9-C4	-6.95	103.62	106.40
1	A	1977	G	N7-C8-N9	6.93	116.57	113.10
1	A	576	U	C2-N1-C1'	6.93	126.02	117.70
1	A	910	C	N3-C2-O2	-6.93	117.05	121.90
1	A	1751	G	N3-C4-C5	-6.88	125.16	128.60
1	A	1751	G	C4-N9-C1'	6.86	135.42	126.50
1	A	2902	A	C4-N9-C1'	6.85	138.63	126.30
1	A	2191	U	C5-C4-O4	-6.83	121.80	125.90
1	A	224	A	O4'-C1'-N9	6.83	113.67	108.20
1	A	1387	C	C6-N1-C2	-6.75	117.60	120.30
1	A	1746	G	C8-N9-C1'	-6.73	118.25	127.00
1	A	2707	C	N3-C2-O2	-6.73	117.19	121.90
1	A	2715	G	N1-C2-N3	6.71	127.93	123.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	2902	A	C6-N1-C2	-6.69	114.58	118.60
1	A	506	A	O4'-C1'-N9	6.66	113.53	108.20
1	A	1827	C	C6-N1-C2	-6.65	117.64	120.30
1	A	2877	G	O4'-C1'-N9	6.64	113.51	108.20
1	A	1228	A	C5-N7-C8	-6.63	100.59	103.90
1	A	2847	U	N3-C2-O2	-6.59	117.58	122.20
1	A	2704	A	C2-N3-C4	-6.57	107.31	110.60
1	A	1189	C	C2-N1-C1'	6.56	126.02	118.80
1	A	2720	A	C2-N3-C4	-6.56	107.32	110.60
1	A	125	A	N7-C8-N9	6.55	117.08	113.80
1	A	2738	A	O4'-C1'-N9	6.55	113.44	108.20
1	A	2889	G	C4-C5-N7	6.53	113.41	110.80
1	A	1740	G	C6-C5-N7	-6.45	126.53	130.40
1	A	506	A	C8-N9-C4	-6.44	103.22	105.80
1	A	506	A	N7-C8-N9	6.42	117.01	113.80
1	A	1746	G	C6-C5-N7	-6.42	126.55	130.40
1	A	2006	C	C6-N1-C1'	-6.41	113.10	120.80
1	A	1189	C	C6-N1-C2	-6.41	117.74	120.30
1	A	1857	C	C2-N1-C1'	6.41	125.85	118.80
1	A	2033	C	N3-C2-O2	-6.40	117.42	121.90
1	A	2706	A	C2-N3-C4	-6.38	107.41	110.60
1	A	1490	G	P-O3'-C3'	6.37	127.34	119.70
1	A	2836	C	C6-N1-C2	-6.37	117.75	120.30
1	A	464	U	C2-N1-C1'	6.34	125.31	117.70
1	A	2188	C	C2-N1-C1'	6.34	125.78	118.80
1	A	2887	G	O4'-C1'-N9	6.34	113.27	108.20
1	A	2857	A	N1-C6-N6	-6.32	114.81	118.60
1	A	2798	C	C2-N1-C1'	6.31	125.74	118.80
1	A	13	A	P-O3'-C3'	6.30	127.26	119.70
1	A	2838	C	N3-C2-O2	-6.29	117.49	121.90
1	A	2273	G	N3-C4-N9	6.26	129.76	126.00
1	A	1387	C	C2-N1-C1'	6.22	125.64	118.80
1	A	1168	C	C6-N1-C2	-6.18	117.83	120.30
1	A	2900	C	C6-N1-C2	-6.18	117.83	120.30
1	A	910	C	C2-N1-C1'	6.16	125.57	118.80
1	A	793	G	O4'-C1'-N9	6.13	113.11	108.20
1	A	1713	A	C8-N9-C4	-6.11	103.36	105.80
1	A	2326	G	N3-C4-N9	6.11	129.66	126.00
1	A	2902	A	N3-C4-C5	-6.11	122.53	126.80
1	A	1228	A	C2-N3-C4	-6.09	107.56	110.60
1	A	2090	C	C6-N1-C2	-6.08	117.87	120.30
1	A	1395	G	O4'-C1'-N9	6.05	113.04	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	776	C	O4'-C1'-N1	6.04	113.03	108.20
1	A	1168	C	N1-C2-O2	6.04	122.52	118.90
1	A	868	A	C8-N9-C4	-6.03	103.39	105.80
1	A	125	A	C5-N7-C8	-6.01	100.89	103.90
1	A	2778	G	N1-C6-O6	-6.01	116.30	119.90
1	A	1329	G	C8-N9-C1'	-6.00	119.20	127.00
1	A	1651	C	C2-N1-C1'	6.00	125.40	118.80
1	A	2026	C	N3-C2-O2	-6.00	117.70	121.90
1	A	2191	U	C5-C6-N1	5.97	125.68	122.70
1	A	2807	G	N3-C4-C5	5.96	131.58	128.60
1	A	2700	G	N9-C4-C5	5.95	107.78	105.40
1	A	1816	A	O4'-C1'-N9	5.95	112.96	108.20
1	A	2703	C	N3-C2-O2	-5.95	117.74	121.90
1	A	1740	G	C4-C5-N7	5.91	113.16	110.80
1	A	2685	C	C2-N1-C1'	5.89	125.28	118.80
1	A	2609	G	N3-C4-N9	5.88	129.53	126.00
1	A	755	C	C2-N1-C1'	5.86	125.25	118.80
1	A	2189	G	C8-N9-C1'	-5.86	119.38	127.00
1	A	1751	G	C5-C6-O6	-5.86	125.08	128.60
1	A	1988	C	N1-C2-O2	5.85	122.41	118.90
1	A	2636	U	N1-C2-O2	5.84	126.89	122.80
1	A	1799	G	N9-C4-C5	5.84	107.73	105.40
1	A	1651	C	N1-C2-O2	5.83	122.39	118.90
1	A	890	G	O4'-C1'-N9	5.82	112.86	108.20
1	A	2892	G	C8-N9-C1'	-5.82	119.43	127.00
1	A	2075	G	P-O3'-C3'	5.82	126.68	119.70
1	A	1002	U	N1-C2-O2	5.81	126.87	122.80
1	A	2033	C	N1-C2-O2	5.79	122.38	118.90
1	A	2006	C	N3-C4-N4	5.76	122.03	118.00
1	A	2636	U	C6-N1-C1'	-5.76	113.14	121.20
1	A	910	C	C6-N1-C2	-5.76	118.00	120.30
1	A	1804	U	N1-C2-O2	5.75	126.83	122.80
1	A	576	U	N1-C2-O2	5.75	126.82	122.80
1	A	589	U	C5-C4-O4	-5.73	122.46	125.90
1	A	1329	G	C4-N9-C1'	5.73	133.95	126.50
1	A	2006	C	N1-C2-O2	5.72	122.33	118.90
1	A	835	U	N3-C2-O2	-5.69	118.22	122.20
1	A	2902	A	C8-N9-C1'	-5.69	117.45	127.70
1	A	1742	A	C8-N9-C4	5.69	108.07	105.80
1	A	1228	A	C8-N9-C4	-5.67	103.53	105.80
1	A	2797	C	C2-N1-C1'	5.66	125.03	118.80
1	A	1037	A	O4'-C1'-N9	5.64	112.72	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	O	20	LEU	CA-CB-CG	5.63	128.25	115.30
1	A	2892	G	C4-N9-C1'	5.63	133.82	126.50
1	A	1351	C	C2-N1-C1'	5.62	124.99	118.80
1	A	2528	C	C6-N1-C1'	5.62	127.55	120.80
1	A	1751	G	C4-C5-N7	5.61	113.04	110.80
1	A	2866	G	N7-C8-N9	5.59	115.90	113.10
1	A	959	C	C4-C5-C6	5.59	120.20	117.40
1	A	1734	A	N7-C8-N9	5.59	116.59	113.80
1	A	2901	U	C4-C5-C6	5.58	123.05	119.70
1	A	2326	G	C4-N9-C1'	5.58	133.75	126.50
1	A	504	G	O4'-C1'-N9	5.57	112.66	108.20
1	A	2798	C	N1-C2-O2	5.56	122.24	118.90
1	A	2797	C	N1-C2-O2	5.55	122.23	118.90
2	B	100	U	N3-C2-O2	-5.54	118.32	122.20
1	A	2802	A	N3-C4-C5	5.54	130.68	126.80
1	A	2026	C	C2-N1-C1'	5.54	124.89	118.80
1	A	1726	A	N1-C6-N6	-5.54	115.28	118.60
1	A	2806	U	C5-C6-N1	5.54	125.47	122.70
1	A	2795	C	N1-C2-O2	5.51	122.21	118.90
1	A	1795	A	C8-N9-C4	-5.51	103.60	105.80
1	A	2326	G	C8-N9-C1'	-5.50	119.85	127.00
1	A	2714	U	N3-C2-O2	-5.49	118.36	122.20
1	A	459	C	C2-N1-C1'	5.49	124.84	118.80
1	A	352	A	P-O3'-C3'	5.48	126.28	119.70
1	A	1795	A	O4'-C1'-N9	5.48	112.59	108.20
1	A	13	A	O4'-C1'-N9	5.48	112.58	108.20
1	A	1769	C	C6-N1-C2	-5.48	118.11	120.30
1	A	2859	G	N3-C2-N2	-5.48	116.07	119.90
1	A	1804	U	C2-N1-C1'	5.47	124.27	117.70
1	A	1675	G	O4'-C1'-N9	5.46	112.57	108.20
1	A	959	C	O4'-C1'-N1	5.46	112.57	108.20
1	A	1734	A	N1-C6-N6	5.46	121.88	118.60
1	A	2747	U	C2-N1-C1'	5.46	124.25	117.70
1	A	2326	G	C6-C5-N7	-5.45	127.13	130.40
1	A	1953	U	C2-N1-C1'	5.44	124.23	117.70
1	A	13	A	OP1-P-O3'	5.43	117.14	105.20
1	A	1037	A	C8-N9-C4	-5.42	103.63	105.80
1	A	1378	U	N3-C2-O2	-5.42	118.41	122.20
1	A	2727	G	N3-C4-C5	5.42	131.31	128.60
1	A	527	G	O4'-C1'-N9	5.40	112.52	108.20
1	A	1357	G	C4-N9-C1'	5.39	133.51	126.50
1	A	721	A	C5-N7-C8	-5.39	101.21	103.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	2189	G	N3-C4-N9	5.38	129.23	126.00
1	A	576	U	N3-C2-O2	-5.37	118.44	122.20
1	A	1037	A	N7-C8-N9	5.37	116.48	113.80
1	A	555	C	C6-N1-C2	-5.36	118.16	120.30
1	A	1002	U	C2-N1-C1'	5.35	124.12	117.70
1	A	835	U	N1-C2-O2	5.35	126.54	122.80
1	A	1387	C	N1-C2-O2	5.34	122.11	118.90
1	A	1988	C	C2-N1-C1'	5.34	124.67	118.80
1	A	2807	G	N3-C4-N9	-5.34	122.80	126.00
1	A	1343	U	N3-C2-O2	-5.34	118.47	122.20
1	A	2705	U	N3-C2-O2	-5.34	118.47	122.20
1	A	2090	C	N3-C2-O2	-5.33	118.17	121.90
1	A	2494	C	N3-C2-O2	-5.32	118.17	121.90
1	A	1189	C	N3-C2-O2	-5.32	118.18	121.90
1	A	1778	C	N1-C2-O2	5.32	122.09	118.90
1	A	1603	U	C5-C4-O4	-5.32	122.71	125.90
1	A	1952	C	C2-N3-C4	5.31	122.56	119.90
1	A	1169	G	N9-C1'-C2'	-5.30	106.17	112.00
1	A	2855	A	N3-C4-N9	5.29	131.63	127.40
1	A	721	A	O4'-C1'-N9	5.29	112.43	108.20
1	A	2802	A	N3-C4-N9	-5.27	123.18	127.40
1	A	2070	C	C2-N1-C1'	5.27	124.59	118.80
1	A	2783	U	O4'-C1'-N1	-5.26	104.00	108.20
1	A	1816	A	C8-N9-C4	-5.24	103.70	105.80
1	A	2893	A	O4'-C1'-N9	5.24	112.39	108.20
1	A	2700	G	N3-C4-C5	5.24	131.22	128.60
1	A	2778	G	C5-C6-O6	5.23	131.74	128.60
1	A	331	G	C4-N9-C1'	5.23	133.30	126.50
1	A	1795	A	N7-C8-N9	5.22	116.41	113.80
1	A	2017	C	N3-C2-O2	-5.22	118.25	121.90
1	A	1735	C	C2-N1-C1'	5.21	124.53	118.80
1	A	1228	A	O4'-C1'-N9	5.20	112.36	108.20
1	A	2866	G	C5-N7-C8	-5.20	101.70	104.30
1	A	921	C	N1-C2-O2	5.19	122.02	118.90
1	A	793	G	C8-N9-C1'	5.19	133.74	127.00
1	A	234	C	C6-N1-C2	-5.18	118.23	120.30
1	A	598	G	C8-N9-C4	5.18	108.47	106.40
1	A	2715	G	N7-C8-N9	5.17	115.68	113.10
1	A	2606	C	C6-N1-C2	-5.16	118.23	120.30
1	A	2722	U	N3-C2-O2	-5.16	118.59	122.20
1	A	2026	C	N1-C2-O2	5.15	121.99	118.90
1	A	1504	U	O4'-C1'-N1	5.14	112.31	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1053	A	C5-N7-C8	-5.12	101.34	103.90
1	A	2806	U	C2-N1-C1'	5.12	123.84	117.70
1	A	2866	G	C3'-C2'-C1'	5.11	105.59	101.50
1	A	2857	A	N7-C8-N9	5.10	116.35	113.80
1	A	1710	G	O4'-C1'-N9	5.09	112.28	108.20
1	A	1740	G	N9-C4-C5	-5.09	103.36	105.40
1	A	281	A	P-O3'-C3'	5.09	125.81	119.70
1	A	331	G	C8-N9-C1'	-5.09	120.39	127.00
1	A	1961	C	C2-N1-C1'	5.09	124.40	118.80
1	A	2003	U	C3'-C2'-C1'	5.09	105.57	101.50
1	A	2032	A	C3'-C2'-C1'	5.08	105.56	101.50
1	A	2727	G	C2-N3-C4	-5.08	109.36	111.90
2	B	79	C	C6-N1-C2	-5.08	118.27	120.30
2	B	111	C	C2-N1-C1'	5.07	124.38	118.80
1	A	1751	G	N3-C2-N2	5.07	123.44	119.90
1	A	139	U	N1-C2-O2	5.06	126.34	122.80
1	A	1752	C	C2-N1-C1'	5.06	124.37	118.80
1	A	2715	G	C8-N9-C1'	5.06	133.58	127.00
1	A	639	U	N3-C2-O2	-5.06	118.66	122.20
1	A	2675	G	N3-C4-N9	-5.06	122.97	126.00
1	A	2700	G	C8-N9-C1'	5.06	133.57	127.00
1	A	882	C	C6-N1-C2	-5.05	118.28	120.30
1	A	1746	G	C5-C6-O6	5.05	131.63	128.60
1	A	775	A	O4'-C1'-N9	5.04	112.23	108.20
1	A	2884	G	O4'-C1'-N9	5.04	112.23	108.20
1	A	882	C	C5-C4-N4	5.03	123.72	120.20
1	A	1734	A	C6-C5-N7	-5.03	128.78	132.30
2	B	100	U	C2-N1-C1'	5.03	123.74	117.70
1	A	2714	U	N1-C2-N3	5.03	117.92	114.90
1	A	1351	C	C6-N1-C2	-5.01	118.30	120.30
1	A	125	A	C8-N9-C4	-5.01	103.80	105.80
1	A	2902	A	C8-N9-C4	-5.01	103.80	105.80
1	A	1029	C	C2-N1-C1'	5.00	124.31	118.80

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	1	11	GLU	Peptide
7	D	53	PHE	Peptide
7	D	6	LEU	Peptide
8	E	12	THR	Peptide

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Mol	Chain	Res	Type	Group
9	H	58	ILE	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	58787	0	29564	1152	0
2	B	2260	0	1148	59	0
3	1	390	0	394	23	0
4	2	367	0	415	14	0
5	3	521	0	586	13	0
6	F	2094	0	2205	56	0
7	D	1627	0	1667	46	0
8	E	1572	0	1619	23	0
9	H	1132	0	1120	33	0
10	L	1086	0	1125	21	0
11	Y	1071	0	1123	38	0
12	G	918	0	981	36	0
13	M	872	0	893	33	0
14	N	878	0	923	34	0
15	O	942	0	1014	34	0
16	P	790	0	830	13	0
17	Q	854	0	914	18	0
18	R	715	0	748	21	0
19	S	770	0	809	32	0
20	T	722	0	766	31	0
21	a	597	0	604	0	0
22	V	379	0	400	10	0
23	W	541	0	563	18	0
24	X	449	0	491	5	0
25	b	360	0	358	0	0
All	All	80694	0	51260	1646	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 14.

All (1646) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2432:G:H21	1:A:2439:A:N6	1.39	1.21
1:A:2432:G:N2	1:A:2439:A:H62	1.44	1.14
1:A:2171:G:H21	1:A:2174:A:N6	1.50	1.09
1:A:2852:U:H1'	1:A:2853:U:H5'	1.38	1.05
1:A:307:A:N6	1:A:409:G:C6	2.26	1.04
1:A:959:C:H1'	1:A:960:C:H5'	1.41	1.02
1:A:2552:G:H21	1:A:2768:A:H2	1.08	1.00
1:A:87:U:H3	1:A:95:A:H61	1.09	0.99
1:A:656:G:H21	1:A:660:A:H2	1.12	0.98
1:A:2724:G:N2	1:A:2738:A:N7	2.11	0.97
1:A:2109:A:N7	1:A:2264:G:N2	2.13	0.97
1:A:1663:G:HO2'	4:2:2:VAL:N	1.61	0.96
1:A:2724:G:H1	1:A:2738:A:N6	1.63	0.96
1:A:2855:A:H61	1:A:2902:A:H2	1.02	0.95
1:A:2769:G:H1	1:A:2789:U:H3	1.15	0.95
1:A:2675:G:H1	1:A:2700:G:H22	1.05	0.95
1:A:2494:C:HO2'	11:Y:123:HIS:HD1	1.15	0.94
13:M:90:LYS:HG3	13:M:91:GLU:H	1.33	0.94
1:A:2831:G:H1	1:A:2908:U:H3	0.96	0.93
1:A:1218:G:C6	1:A:1219:G:O6	2.21	0.93
20:T:72:VAL:HG21	20:T:91:PHE:HB3	1.51	0.92
1:A:2866:G:N2	1:A:2889:G:O6	2.02	0.91
1:A:2171:G:N2	1:A:2174:A:C6	2.38	0.91
1:A:919:G:N2	1:A:949:C:N3	2.18	0.91
1:A:2853:U:H4'	1:A:2854:A:H5'	1.53	0.90
1:A:2859:G:H22	1:A:2897:A:H2	1.14	0.90
1:A:2861:U:H3	1:A:2895:G:H1	1.04	0.90
11:Y:38:THR:HG23	11:Y:128:LYS:HE2	1.53	0.90
1:A:2706:A:H2	1:A:2756:G:H1	1.21	0.89
1:A:2727:G:H22	1:A:2735:G:H1	1.14	0.89
6:F:67:PHE:HE1	6:F:156:ARG:HD2	1.37	0.89
1:A:1705:G:H1	1:A:2026:C:H5	1.20	0.89
1:A:1459:A:H61	1:A:1631:G:H5'	1.36	0.89
1:A:1453:G:H4'	1:A:1455:U:H3	1.38	0.88
1:A:156:A:H61	1:A:172:U:H3	1.22	0.88
1:A:1675:G:H1	1:A:1725:G:HO2'	1.22	0.88
1:A:2818:A:N6	1:A:2826:U:O2	2.05	0.88
1:A:1052:A:N3	1:A:1053:A:N6	2.19	0.87
6:F:5:LYS:HD2	6:F:6:TYR:H	1.38	0.87
1:A:2171:G:N2	1:A:2174:A:N6	2.23	0.86
1:A:1179:C:N4	1:A:1182:G:OP2	2.09	0.86
12:G:104:ARG:HH12	14:N:34:ILE:HG12	1.40	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1240:U:O2'	8:E:41:ARG:NH2	2.09	0.86
5:3:21:GLN:HB3	5:3:49:LEU:HD11	1.58	0.86
1:A:1781:C:H5	14:N:96:ARG:HH21	1.21	0.86
1:A:2111:C:N3	1:A:2262:G:N1	2.23	0.86
17:Q:51:LEU:HA	17:Q:105:ILE:HD11	1.58	0.85
1:A:1092:A:N7	1:A:1155:A:N6	2.25	0.84
1:A:1497:A:H4'	1:A:1498:U:H2'	1.59	0.84
1:A:2502:C:H42	1:A:2556:G:H1	1.23	0.84
1:A:2684:A:H62	1:A:2691:G:H21	1.25	0.84
2:B:18:G:H1	2:B:61:C:H42	1.25	0.84
1:A:163:U:O4	1:A:2244:G:O2'	1.95	0.84
2:B:26:C:H2'	2:B:27:A:C8	2.12	0.84
1:A:1199:A:H5"	15:O:55:ARG:HH21	1.42	0.83
11:Y:43:THR:HG22	11:Y:94:ILE:HG22	1.61	0.83
1:A:1061:G:H22	1:A:1189:C:H5	1.25	0.83
1:A:577:A:OP1	1:A:604:G:N2	2.12	0.82
1:A:2712:G:H4'	12:G:76:TYR:HE2	1.44	0.82
18:R:53:VAL:HG22	18:R:80:VAL:HG12	1.61	0.82
1:A:2729:G:O6	1:A:2733:A:N6	2.10	0.82
1:A:1079:U:O2	1:A:1164:G:N2	2.11	0.82
19:S:39:ASN:HD22	19:S:63:ILE:HG22	1.45	0.81
1:A:2189:G:H21	1:A:2191:U:H3	1.25	0.81
1:A:273:A:N7	1:A:298:U:O2	2.13	0.81
1:A:1085:U:H3	1:A:1158:G:H22	1.25	0.81
1:A:1718:G:H1	1:A:2017:C:H5	1.24	0.81
1:A:2432:G:H21	1:A:2439:A:H62	0.81	0.81
1:A:2895:G:H1'	14:N:2:THR:HB	1.62	0.81
13:M:39:HIS:HD2	13:M:59:LYS:HB2	1.46	0.80
1:A:579:U:H5'	15:O:42:SER:HB2	1.63	0.80
1:A:1745:A:O2'	1:A:1793:C:OP1	2.00	0.80
7:D:129:GLY:HA2	7:D:170:PRO:HB3	1.61	0.80
1:A:1261:G:OP1	16:P:67:ARG:NH1	2.15	0.79
1:A:868:A:N6	1:A:879:U:O4	2.14	0.79
6:F:107:PRO:HD2	6:F:110:LEU:HD22	1.64	0.79
11:Y:30:GLY:O	11:Y:134:ARG:NH2	2.15	0.79
11:Y:77:LYS:HG3	11:Y:78:PRO:HD2	1.64	0.79
1:A:882:C:H5	1:A:986:G:H1	1.31	0.79
1:A:1741:G:C6	1:A:1742:A:H2'	2.18	0.79
1:A:927:G:N2	1:A:927:G:OP2	2.15	0.78
1:A:2866:G:H21	1:A:2889:G:H1	1.31	0.78
6:F:132:LEU:HD23	6:F:172:VAL:HB	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:G:OP2	1:A:252:C:N4	2.17	0.78
1:A:307:A:C6	1:A:409:G:C6	2.71	0.78
1:A:2675:G:H1	1:A:2700:G:N2	1.80	0.78
1:A:2672:G:H1'	1:A:2760:A:H4'	1.64	0.78
11:Y:35:GLN:HB3	11:Y:102:ILE:HD13	1.66	0.77
19:S:72:ASP:HB2	19:S:79:THR:HG21	1.65	0.77
1:A:1757:U:O2	1:A:1772:G:N2	2.16	0.77
1:A:2711:U:H3'	1:A:2712:G:H21	1.48	0.77
1:A:2728:U:H3	1:A:2734:C:H42	1.30	0.77
1:A:944:G:H2'	1:A:945:A:C8	2.19	0.77
19:S:59:THR:HG22	19:S:60:GLU:H	1.48	0.77
1:A:2554:C:O2	1:A:2563:G:N1	2.15	0.77
14:N:92:GLY:HA2	14:N:115:ILE:HG12	1.66	0.77
1:A:2553:G:N2	1:A:2564:U:O2	2.18	0.76
1:A:1818:A:N6	1:A:1855:G:O2'	2.16	0.76
17:Q:2:GLU:OE2	17:Q:72:LYS:NZ	2.13	0.76
1:A:660:A:H8	8:E:182:ASN:HB3	1.48	0.76
11:Y:77:LYS:NZ	11:Y:86:GLY:O	2.19	0.76
13:M:19:ARG:NH2	13:M:47:ASP:OD2	2.19	0.76
1:A:2726:C:H2'	1:A:2727:G:C8	2.21	0.76
4:2:25:THR:HG23	4:2:28:GLY:H	1.50	0.76
1:A:2715:G:N2	1:A:2749:G:H1	1.84	0.76
22:V:33:LEU:HD12	22:V:48:TRP:HB3	1.68	0.76
1:A:161:A:H62	1:A:167:U:H3	1.33	0.76
1:A:80:G:O2'	1:A:389:A:N7	2.19	0.76
1:A:1741:G:O3'	1:A:2005:A:H4'	1.86	0.76
1:A:1798:C:N3	1:A:1799:G:N1	2.34	0.76
15:O:98:ILE:HD11	16:P:4:ILE:HD11	1.67	0.76
12:G:70:ARG:HG3	12:G:76:TYR:HE1	1.49	0.75
1:A:2686:G:N2	1:A:2689:A:OP2	2.19	0.75
1:A:1455:U:O4	1:A:1631:G:N1	2.20	0.74
1:A:1976:G:N2	1:A:1985:C:O2	2.16	0.74
1:A:928:C:N4	1:A:938:G:OP2	2.20	0.74
1:A:1742:A:H4'	1:A:1743:G:C8	2.21	0.74
7:D:2:THR:OG1	7:D:93:ASN:O	2.05	0.74
1:A:1063:U:O2'	1:A:1065:A:N7	2.19	0.74
1:A:2712:G:H4'	12:G:76:TYR:CE2	2.22	0.74
1:A:234:C:H3'	1:A:235:G:H8	1.52	0.74
8:E:17:ILE:HD11	8:E:200:LYS:HE3	1.68	0.74
1:A:1490:G:O2'	1:A:1491:C:OP2	2.04	0.74
1:A:2121:A:H2'	1:A:2122:A:C8	2.23	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:67:PHE:CE1	6:F:156:ARG:HD2	2.20	0.74
1:A:2727:G:N2	1:A:2735:G:H1	1.86	0.73
10:L:71:ARG:NH1	10:L:72:LYS:O	2.21	0.73
1:A:2727:G:N2	1:A:2735:G:H22	1.86	0.73
1:A:2720:A:H2	1:A:2744:G:H22	1.36	0.73
1:A:775:A:O2'	1:A:776:C:OP1	2.06	0.73
1:A:131:G:N2	1:A:148:U:O2	2.20	0.73
1:A:1799:G:N2	1:A:2007:G:H22	1.85	0.73
1:A:2490:C:H42	1:A:2515:A:H61	1.36	0.73
1:A:159:U:O4	1:A:160:G:N2	2.22	0.72
1:A:136:A:H2'	1:A:137:G:O4'	1.88	0.72
1:A:1737:U:N3	1:A:1857:C:O2'	2.20	0.72
11:Y:42:ILE:HA	11:Y:46:GLN:HE21	1.54	0.72
2:B:73:G:H3'	2:B:74:G:H8	1.51	0.72
1:A:722:A:O2'	1:A:2098:A:OP1	2.06	0.72
1:A:1336:G:H21	1:A:1685:A:H62	1.37	0.72
1:A:1465:G:O6	1:A:1624:C:N4	2.18	0.72
1:A:2147:G:N2	1:A:2205:C:N3	2.36	0.72
2:B:70:G:H21	2:B:101:A:H62	1.38	0.72
1:A:1963:A:OP2	1:A:1989:C:N4	2.15	0.72
1:A:319:G:H1'	1:A:324:A:H62	1.55	0.71
1:A:78:U:H3	1:A:107:G:H1	1.37	0.71
1:A:826:A:OP1	6:F:217:ARG:NH2	2.23	0.71
17:Q:11:ARG:NH1	17:Q:98:LYS:HD2	2.05	0.71
1:A:1218:G:H2'	1:A:1219:G:C8	2.25	0.71
1:A:2496:A:N6	1:A:2508:G:N2	2.37	0.71
1:A:2552:G:N2	1:A:2768:A:C2	2.53	0.71
1:A:572:C:OP2	1:A:2807:G:N1	2.22	0.71
1:A:1675:G:N1	1:A:1725:G:O2'	2.21	0.71
3:1:8:ALA:O	3:1:46:ARG:N	2.20	0.71
1:A:1734:A:H61	1:A:1741:G:H22	1.36	0.71
1:A:2673:C:O2'	1:A:2674:U:O5'	2.09	0.71
1:A:2657:G:O2'	1:A:2658:G:OP1	2.09	0.70
1:A:2712:G:C4'	12:G:76:TYR:HE2	2.04	0.70
20:T:4:LEU:HD21	20:T:51:VAL:HG21	1.72	0.70
12:G:104:ARG:NH1	14:N:34:ILE:HG12	2.04	0.70
1:A:1482:U:OP2	1:A:1600:A:N6	2.24	0.70
12:G:104:ARG:NH2	14:N:43:GLN:OE1	2.25	0.70
14:N:8:GLU:O	14:N:12:LYS:HB2	1.91	0.70
1:A:2831:G:O6	1:A:2908:U:O4	2.09	0.70
2:B:26:C:H2'	2:B:27:A:H8	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:G:H2'	1:A:284:C:H4'	1.74	0.69
1:A:944:G:H2'	1:A:945:A:H8	1.57	0.69
1:A:2819:C:N4	1:A:2824:G:O6	2.25	0.69
1:A:2024:A:H5"	7:D:138:ARG:HD3	1.72	0.69
1:A:2510:C:H3'	1:A:2511:G:H5"	1.75	0.69
18:R:7:LEU:HD21	18:R:42:VAL:HG12	1.74	0.69
10:L:73:GLU:O	10:L:107:SER:OG	2.08	0.69
1:A:675:G:OP1	5:3:23:LYS:NZ	2.16	0.69
1:A:2703:C:H42	1:A:2759:G:H1	1.41	0.69
11:Y:76:LYS:HG2	11:Y:77:LYS:H	1.57	0.69
1:A:2872:G:N2	1:A:2883:U:O4	2.19	0.69
17:Q:11:ARG:O	17:Q:11:ARG:HD3	1.93	0.69
1:A:176:A:H1'	1:A:177:G:N7	2.08	0.68
13:M:19:ARG:NH1	13:M:22:LEU:O	2.27	0.68
1:A:2829:A:N7	1:A:2911:A:N6	2.41	0.68
1:A:2673:C:H42	1:A:2702:A:H61	1.39	0.68
1:A:80:G:H1'	1:A:389:A:C6	2.29	0.68
1:A:2347:A:O2'	1:A:2360:A:N6	2.22	0.68
1:A:2186:G:H2'	1:A:2187:G:H8	1.59	0.68
1:A:2187:G:C2	1:A:2188:C:H1'	2.28	0.68
1:A:2820:U:O2'	1:A:2823:G:N7	2.27	0.68
12:G:42:THR:HG22	12:G:57:VAL:HG22	1.75	0.68
1:A:1732:U:O2'	1:A:1744:A:N7	2.22	0.67
1:A:1899:U:H1'	1:A:1900:G:N7	2.08	0.67
2:B:16:A:O2'	2:B:17:A:OP1	2.12	0.67
13:M:15:HIS:O	13:M:19:ARG:HB2	1.94	0.67
1:A:1210:U:H3	1:A:1222:A:H61	1.41	0.67
1:A:2675:G:H22	1:A:2700:G:N2	1.92	0.67
1:A:2111:C:N4	1:A:2262:G:O6	2.19	0.67
1:A:2667:G:H22	1:A:2802:A:H2	1.41	0.67
1:A:2894:C:O2	14:N:2:THR:N	2.28	0.67
8:E:32:VAL:HG12	8:E:109:ALA:HB2	1.77	0.67
13:M:15:HIS:O	13:M:19:ARG:CB	2.43	0.67
20:T:32:TYR:O	20:T:93:ALA:N	2.27	0.67
1:A:2161:A:H61	1:A:2184:G:H1'	1.59	0.67
1:A:2768:A:H62	1:A:2790:G:H21	1.43	0.67
13:M:14:ARG:HH12	13:M:17:ARG:HH11	1.43	0.67
1:A:946:A:H2'	1:A:947:U:C6	2.30	0.67
1:A:1156:G:H2'	1:A:1157:U:C6	2.30	0.67
1:A:1451:U:N3	1:A:1633:A:N7	2.43	0.67
17:Q:21:LEU:HD22	17:Q:74:ALA:HB1	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2111:C:O2	1:A:2262:G:N2	2.16	0.66
1:A:2567:C:O2'	1:A:2767:A:N3	2.28	0.66
1:A:2684:A:H62	1:A:2691:G:N2	1.93	0.66
1:A:2226:A:H62	1:A:2251:G:H21	1.42	0.66
1:A:328:G:N2	1:A:399:U:O2'	2.28	0.66
1:A:2719:C:H2'	1:A:2720:A:C8	2.31	0.66
11:Y:53:ALA:HB2	11:Y:124:LYS:HE2	1.75	0.66
1:A:1387:C:H5	1:A:1418:G:H1	1.42	0.66
1:A:1215:U:O2'	1:A:1218:G:N1	2.28	0.66
1:A:2121:A:H2'	1:A:2122:A:H8	1.60	0.66
1:A:1959:A:C2	1:A:1960:G:H1'	2.31	0.66
9:H:58:ILE:HG22	9:H:126:TYR:HB2	1.78	0.66
1:A:940:U:H2'	1:A:941:A:C8	2.31	0.65
18:R:6:ILE:HD13	18:R:41:ALA:HB2	1.78	0.65
19:S:39:ASN:ND2	19:S:63:ILE:HG22	2.11	0.65
1:A:165:C:H3'	1:A:166:A:H8	1.60	0.65
1:A:162:A:H1'	1:A:2235:A:N3	2.11	0.65
1:A:766:G:H2'	1:A:767:A:H8	1.61	0.65
1:A:1287:U:H4'	15:O:4:VAL:HG21	1.79	0.65
1:A:139:U:H3'	1:A:140:A:C8	2.31	0.65
1:A:721:A:H8	1:A:2096:G:H21	1.43	0.65
1:A:2496:A:H62	1:A:2508:G:N2	1.95	0.65
24:X:5:GLN:HB2	24:X:59:LYS:HG3	1.78	0.65
3:1:12:CYS:SG	3:1:43:THR:OG1	2.54	0.65
20:T:18:LEU:O	20:T:22:ARG:HG3	1.97	0.65
1:A:765:U:HO2'	1:A:766:G:H8	1.43	0.64
1:A:1745:A:H3'	1:A:1746:G:H8	1.62	0.64
1:A:2697:G:C4	1:A:2698:A:H1'	2.32	0.64
1:A:227:G:N7	1:A:465:C:O2'	2.31	0.64
3:1:23:LYS:HG3	3:1:24:ARG:HD3	1.78	0.64
15:O:27:SER:HA	15:O:30:THR:HG22	1.79	0.64
1:A:2669:G:H1	1:A:2800:U:H3	1.45	0.64
1:A:2704:A:H2	1:A:2758:G:H22	1.45	0.64
6:F:63:ARG:HD2	6:F:84:ASP:OD2	1.98	0.64
1:A:160:G:O2'	1:A:169:G:N2	2.31	0.64
1:A:165:C:H3'	1:A:166:A:C8	2.33	0.64
1:A:302:A:H2'	1:A:303:G:C8	2.33	0.64
1:A:1482:U:H2'	1:A:1483:A:H8	1.63	0.64
1:A:2551:G:O3'	1:A:2790:G:O2'	2.15	0.64
1:A:2859:G:N2	1:A:2897:A:H2	1.91	0.64
6:F:95:VAL:HG12	6:F:101:LYS:HG2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:829:U:O4	6:F:228:ASN:ND2	2.30	0.64
20:T:9:ARG:HE	20:T:40:SER:HB3	1.63	0.64
1:A:331:G:H1	1:A:395:U:H3	1.44	0.63
1:A:2646:U:H5"	7:D:165:LYS:HD3	1.80	0.63
1:A:80:G:H1'	1:A:389:A:C5	2.33	0.63
1:A:2234:C:H42	1:A:2244:G:H1	1.43	0.63
1:A:2513:G:O2'	1:A:2514:G:OP1	2.15	0.63
1:A:2552:G:H1'	1:A:2768:A:H61	1.61	0.63
8:E:8:LYS:HD2	8:E:14:SER:HB2	1.79	0.63
1:A:2850:G:C5	7:D:64:LYS:HE2	2.33	0.63
1:A:460:C:H2'	1:A:461:A:H8	1.63	0.63
1:A:1724:U:N3	1:A:1791:G:OP2	2.28	0.63
1:A:1954:A:H2'	1:A:1955:A:H8	1.64	0.63
1:A:2186:G:H2'	1:A:2187:G:C8	2.33	0.63
1:A:2677:C:H2'	1:A:2678:C:C6	2.32	0.63
1:A:2760:A:O2'	1:A:2793:G:O6	2.17	0.63
2:B:22:G:N7	2:B:54:U:H2'	2.13	0.63
11:Y:42:ILE:HA	11:Y:46:GLN:NE2	2.13	0.63
1:A:91:A:H3'	1:A:92:G:H8	1.64	0.63
1:A:2851:G:N2	1:A:2899:A:H61	1.96	0.63
23:W:37:LEU:HG	23:W:39:GLU:H	1.64	0.63
1:A:307:A:N6	1:A:409:G:O6	2.30	0.63
1:A:527:G:O2'	1:A:552:A:N6	2.31	0.63
1:A:2515:A:H2'	1:A:2516:G:H8	1.63	0.63
18:R:6:ILE:HG13	18:R:33:VAL:HG21	1.80	0.63
1:A:13:A:O2'	1:A:14:A:N7	2.32	0.62
1:A:2856:U:N3	1:A:2857:A:C6	2.66	0.62
6:F:10:THR:HG22	6:F:12:GLY:H	1.64	0.62
1:A:1933:G:H8	1:A:1956:G:H2'	1.63	0.62
1:A:2855:A:N6	1:A:2902:A:H2	1.86	0.62
6:F:143:ASN:OD1	6:F:152:GLY:HA3	1.99	0.62
19:S:79:THR:HG22	19:S:96:LYS:NZ	2.14	0.62
20:T:48:PHE:O	20:T:52:ILE:HG12	1.99	0.62
3:1:9:CYS:HB2	3:1:45:HIS:CD2	2.34	0.62
1:A:776:C:O2'	1:A:777:C:OP2	2.16	0.62
1:A:1213:C:O2	1:A:1214:C:N4	2.30	0.62
1:A:1446:U:H2'	1:A:1447:A:C8	2.34	0.62
2:B:42:G:O4'	2:B:45:C:N4	2.31	0.62
1:A:2216:U:H2'	1:A:2217:G:C8	2.34	0.62
1:A:2699:U:H5'	1:A:2700:G:OP2	1.99	0.62
1:A:279:A:H62	1:A:281:A:H62	1.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2769:G:O6	1:A:2789:U:O4	2.17	0.62
1:A:80:G:H2'	1:A:81:G:C8	2.35	0.62
1:A:213:C:O2'	1:A:1403:C:O2	2.18	0.62
1:A:307:A:C6	1:A:409:G:N1	2.68	0.62
5:3:48:ARG:HG2	5:3:49:LEU:H	1.64	0.62
10:L:76:ILE:HG23	10:L:112:LEU:HD12	1.80	0.62
14:N:76:PHE:CE2	14:N:83:ILE:HD11	2.35	0.62
1:A:82:G:H2'	1:A:83:G:C8	2.35	0.62
1:A:1804:U:H5	1:A:1814:A:N1	1.98	0.62
1:A:2254:A:H4'	6:F:263:LYS:HD2	1.82	0.62
1:A:1977:G:P	1:A:1977:G:H8	2.23	0.61
1:A:2873:C:H2'	1:A:2874:A:C8	2.35	0.61
1:A:1060:U:H3	1:A:1190:A:H61	1.47	0.61
1:A:2360:A:H5"	1:A:2362:A:H1'	1.82	0.61
1:A:279:A:N6	1:A:281:A:N7	2.49	0.61
1:A:1878:U:OP2	1:A:1915:G:N2	2.33	0.61
1:A:1904:A:H2'	1:A:1905:G:C8	2.35	0.61
1:A:2682:G:N1	1:A:2692:A:OP2	2.32	0.61
1:A:2866:G:N2	1:A:2889:G:C6	2.67	0.61
1:A:2856:U:O4	1:A:2857:A:N6	2.34	0.61
1:A:943:C:H2'	1:A:944:G:C8	2.36	0.61
1:A:1084:U:H2'	1:A:1085:U:O4'	2.00	0.61
1:A:1734:A:H61	1:A:1741:G:N2	1.99	0.61
1:A:1885:G:N2	1:A:1911:A:OP2	2.30	0.61
1:A:2182:U:H3'	1:A:2183:G:C8	2.35	0.61
1:A:1448:U:O4	1:A:1449:A:N6	2.33	0.61
2:B:74:G:N2	2:B:75:U:O4	2.32	0.61
1:A:943:C:H2'	1:A:944:G:H8	1.65	0.61
1:A:513:G:OP2	4:2:35:ARG:HD3	2.01	0.61
1:A:766:G:H2'	1:A:767:A:C8	2.36	0.61
1:A:1482:U:H2'	1:A:1483:A:C8	2.36	0.61
1:A:2851:G:H4'	1:A:2852:U:O5'	2.01	0.61
13:M:48:ASN:OD1	13:M:49:LYS:N	2.34	0.61
1:A:1061:G:H1	1:A:1189:C:H41	1.46	0.60
1:A:1155:A:H4'	1:A:1156:G:OP1	1.99	0.60
1:A:1906:C:H2'	1:A:1907:U:O4'	2.01	0.60
2:B:97:G:H2'	2:B:98:A:O4'	2.01	0.60
3:1:30:ILE:H	3:1:47:GLU:HG2	1.66	0.60
1:A:115:C:HO2'	1:A:125:A:H8	1.49	0.60
1:A:291:G:H2'	1:A:292:U:C6	2.36	0.60
1:A:1085:U:H2'	1:A:1086:G:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1177:A:N6	1:A:2052:C:O2'	2.35	0.60
1:A:1732:U:O2	1:A:1744:A:H8	1.84	0.60
1:A:2259:C:OP2	22:V:27:ARG:NH2	2.32	0.60
1:A:2857:A:N1	1:A:2901:U:H5	1.98	0.60
2:B:18:G:H1	2:B:61:C:N4	1.97	0.60
9:H:7:ALA:O	9:H:9:GLU:N	2.35	0.60
1:A:276:C:H3'	1:A:277:C:H5"	1.82	0.60
3:1:6:THR:O	3:1:48:THR:OG1	2.16	0.60
1:A:684:U:H2'	1:A:685:C:C6	2.36	0.60
1:A:2807:G:H4'	1:A:2808:A:O5'	2.01	0.60
14:N:59:GLU:HG2	14:N:78:LEU:HD22	1.84	0.60
1:A:393:G:H2'	1:A:394:U:C6	2.36	0.60
1:A:2715:G:N2	1:A:2749:G:N1	2.48	0.60
1:A:353:A:O2'	1:A:354:A:H2'	2.01	0.60
1:A:389:A:H3'	1:A:390:A:C8	2.37	0.60
1:A:512:A:OP1	4:2:35:ARG:NH1	2.33	0.60
1:A:1757:U:H3	1:A:1772:G:H1	1.48	0.60
19:S:57:LEU:HD12	19:S:58:GLU:H	1.65	0.60
1:A:827:A:C2	6:F:225:MET:HG2	2.37	0.60
1:A:2343:U:H2'	1:A:2344:C:O4'	2.02	0.60
18:R:64:ARG:NH2	18:R:69:GLN:HA	2.17	0.60
1:A:1818:A:H61	1:A:1855:G:HO2'	1.44	0.60
1:A:2896:A:H2'	1:A:2897:A:C8	2.37	0.60
9:H:58:ILE:HG13	9:H:58:ILE:O	2.01	0.60
1:A:274:A:H62	1:A:297:G:H21	1.50	0.60
1:A:366:G:H2'	8:E:169:ASN:OD1	2.00	0.60
1:A:2189:G:N2	1:A:2191:U:H3	1.98	0.60
1:A:218:G:H4'	1:A:219:A:H4'	1.82	0.60
1:A:774:G:H3'	1:A:774:G:N3	2.17	0.60
1:A:1904:A:H2'	1:A:1905:G:H8	1.66	0.60
1:A:1336:G:N2	1:A:1685:A:H62	2.00	0.59
7:D:25:VAL:HG21	7:D:196:LEU:HB3	1.82	0.59
8:E:127:ASP:OD1	8:E:128:ALA:N	2.34	0.59
13:M:90:LYS:HG3	13:M:91:GLU:N	2.12	0.59
23:W:11:THR:HA	23:W:14:ILE:HD12	1.84	0.59
1:A:75:G:OP1	23:W:44:ARG:NH1	2.34	0.59
3:1:23:LYS:HE2	3:1:24:ARG:HH21	1.66	0.59
7:D:88:ILE:O	7:D:89:ARG:HD3	2.02	0.59
15:O:30:THR:HG23	15:O:31:LEU:HG	1.83	0.59
12:G:8:LEU:HG	12:G:84:CYS:HB2	1.85	0.59
1:A:2162:A:H62	1:A:2183:G:H21	1.51	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2715:G:H21	1:A:2749:G:H1	1.48	0.59
12:G:22:ILE:HB	12:G:40:VAL:HG13	1.84	0.59
1:A:1466:G:H1	1:A:1623:U:H3	1.50	0.59
10:L:112:LEU:HD23	10:L:129:SER:HB3	1.83	0.59
1:A:2171:G:O6	1:A:2173:U:H1'	2.01	0.59
13:M:30:ARG:NH2	13:M:45:ILE:HD11	2.18	0.59
1:A:1741:G:H2'	1:A:1742:A:H5'	1.85	0.59
1:A:2374:C:O2'	3:1:17:TYR:OH	2.20	0.59
1:A:2553:G:O2'	1:A:2554:C:OP1	2.18	0.59
2:B:72:U:C2	2:B:73:G:C8	2.91	0.59
9:H:58:ILE:HD13	9:H:131:HIS:HD2	1.67	0.59
1:A:1599:G:H2'	1:A:1600:A:O4'	2.03	0.59
3:1:16:ASN:OD1	3:1:17:TYR:N	2.36	0.59
1:A:157:U:H2'	1:A:158:G:C8	2.38	0.59
1:A:1033:G:OP2	24:X:11:SER:OG	2.13	0.59
1:A:1815:C:H5"	6:F:224:VAL:HG11	1.84	0.59
1:A:660:A:C8	8:E:182:ASN:HB3	2.33	0.58
1:A:1075:G:H2'	1:A:1076:A:C8	2.38	0.58
1:A:1979:A:H2	1:A:1981:G:H3'	1.68	0.58
23:W:12:SER:HA	23:W:15:GLU:HG3	1.85	0.58
1:A:2606:C:H1'	7:D:147:PHE:CD1	2.39	0.58
12:G:70:ARG:HG3	12:G:76:TYR:CE1	2.34	0.58
19:S:59:THR:HG22	19:S:60:GLU:N	2.18	0.58
20:T:44:ASP:OD1	20:T:45:GLU:N	2.36	0.58
1:A:572:C:O2'	1:A:573:A:OP2	2.21	0.58
1:A:1676:A:N1	1:A:1726:A:H4'	2.17	0.58
1:A:2302:C:O2'	11:Y:84:GLY:O	2.17	0.58
1:A:2496:A:N6	1:A:2508:G:C2	2.71	0.58
18:R:64:ARG:HH22	18:R:69:GLN:HA	1.68	0.58
1:A:2629:A:O2'	1:A:2630:G:OP2	2.19	0.58
1:A:2796:C:H2'	1:A:2797:C:O4'	2.02	0.58
7:D:52:GLY:HA3	7:D:85:LYS:HG3	1.85	0.58
1:A:1352:C:O2'	1:A:1429:G:N3	2.32	0.58
1:A:1854:U:O2'	1:A:1997:A:N3	2.36	0.58
1:A:2256:U:H2'	1:A:2257:G:H8	1.69	0.58
7:D:215:ILE:HG13	7:D:216:LYS:HG2	1.86	0.58
13:M:29:PRO:HD2	13:M:92:ILE:HG22	1.85	0.58
1:A:1494:G:H22	1:A:1504:U:H3	1.51	0.58
1:A:1798:C:N4	1:A:1799:G:O6	2.36	0.58
1:A:2727:G:H22	1:A:2735:G:H22	1.49	0.58
1:A:458:A:H3'	1:A:459:C:H6	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2253:C:H3'	1:A:2254:A:C8	2.38	0.58
1:A:2515:A:H2'	1:A:2516:G:C8	2.39	0.58
1:A:2900:C:O2'	1:A:2901:U:OP1	2.22	0.58
13:M:102:HIS:HA	13:M:106:LYS:HD2	1.84	0.58
1:A:418:G:N7	22:V:55:LYS:HE2	2.18	0.58
1:A:1075:G:OP1	11:Y:123:HIS:NE2	2.37	0.58
18:R:55:ILE:HD12	18:R:76:ARG:HH11	1.68	0.58
1:A:2499:G:H2'	1:A:2502:C:H41	1.68	0.58
1:A:2727:G:H22	1:A:2735:G:N2	2.02	0.58
1:A:1075:G:H2'	1:A:1076:A:H8	1.68	0.58
1:A:1238:U:H1'	15:O:4:VAL:HG12	1.86	0.58
1:A:2564:U:H2'	1:A:2565:C:H6	1.69	0.58
2:B:88:G:H2'	2:B:89:U:H6	1.69	0.58
1:A:6:A:H61	1:A:2915:C:H42	1.52	0.57
1:A:1474:C:H2'	1:A:1475:A:C8	2.38	0.57
1:A:2402:G:N2	1:A:2405:A:OP2	2.36	0.57
15:O:90:ILE:HG22	15:O:91:ASN:H	1.67	0.57
1:A:98:U:O2'	1:A:99:U:H5'	2.05	0.57
1:A:2432:G:N2	1:A:2439:A:N6	2.19	0.57
1:A:2788:A:H2'	1:A:2789:U:O4'	2.04	0.57
6:F:108:LYS:NZ	6:F:198:LEU:HD11	2.18	0.57
1:A:60:U:O2'	1:A:61:A:O5'	2.19	0.57
1:A:86:C:H4'	1:A:103:U:H1'	1.85	0.57
1:A:302:A:H2'	1:A:303:G:H8	1.69	0.57
1:A:986:G:HO2'	1:A:1228:A:H8	1.52	0.57
1:A:1731:G:N2	1:A:1745:A:OP2	2.37	0.57
1:A:1823:U:H2'	1:A:1824:C:C6	2.39	0.57
1:A:1980:A:O2'	1:A:1981:G:O4'	2.22	0.57
1:A:1907:U:H2'	1:A:1908:A:C8	2.39	0.57
1:A:2774:G:N2	1:A:2783:U:OP1	2.31	0.57
19:S:13:ALA:HB3	19:S:67:ASN:OD1	2.03	0.57
1:A:1964:A:H1'	1:A:1966:5MU:C4	2.38	0.57
1:A:1977:G:C8	1:A:1977:G:OP2	2.58	0.57
1:A:2715:G:N2	1:A:2749:G:C6	2.69	0.57
6:F:5:LYS:HD2	6:F:6:TYR:N	2.16	0.57
1:A:1477:U:H2'	1:A:1478:A:C8	2.40	0.57
1:A:2552:G:N3	1:A:2768:A:N1	2.53	0.57
8:E:66:LYS:HE3	8:E:68:LYS:O	2.04	0.57
18:R:60:PRO:HG3	18:R:74:LYS:HB3	1.86	0.57
20:T:49:ILE:HG22	20:T:53:ARG:HD2	1.86	0.57
1:A:276:C:O2	1:A:306:C:H5'	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:434:G:O2'	1:A:435:A:O5'	2.15	0.57
1:A:2564:U:H2'	1:A:2565:C:C6	2.40	0.57
1:A:2653:C:H42	1:A:2805:A:H61	1.51	0.57
6:F:143:ASN:HB3	6:F:191:THR:HG22	1.86	0.57
1:A:2097:G:O2'	1:A:2098:A:OP1	2.21	0.57
5:3:21:GLN:HG2	5:3:49:LEU:HD21	1.84	0.57
1:A:1732:U:H3	1:A:1744:A:H5"	1.70	0.57
1:A:2144:A:O2'	1:A:2174:A:N3	2.37	0.57
2:B:64:A:H1'	2:B:66:C:H41	1.70	0.57
3:1:39:LEU:HB2	3:1:41:LYS:HG2	1.86	0.57
8:E:49:HIS:HD2	8:E:92:PRO:CB	2.17	0.57
1:A:972:A:H3'	1:A:972:A:N3	2.20	0.57
1:A:1935:C:H2'	1:A:1936:C:O4'	2.05	0.57
13:M:30:ARG:O	13:M:44:ILE:HG13	2.04	0.57
2:B:27:A:H2'	2:B:28:C:C6	2.40	0.56
9:H:94:ARG:HB2	9:H:101:LEU:HD22	1.86	0.56
1:A:1453:G:H4'	1:A:1455:U:N3	2.16	0.56
7:D:99:TYR:HA	7:D:103:GLN:OE1	2.05	0.56
17:Q:72:LYS:HB2	17:Q:108:SER:HB2	1.87	0.56
1:A:631:U:H2'	1:A:632:U:C6	2.40	0.56
1:A:775:A:HO2'	1:A:776:C:P	2.27	0.56
1:A:858:U:H2'	1:A:859:C:C6	2.40	0.56
1:A:959:C:O2'	1:A:960:C:OP2	2.16	0.56
1:A:1051:C:H5"	9:H:38:ARG:NH1	2.21	0.56
1:A:1608:C:H2'	1:A:1609:U:C6	2.41	0.56
2:B:88:G:H2'	2:B:89:U:C6	2.40	0.56
3:1:29:ARG:HB3	3:1:47:GLU:HB3	1.88	0.56
1:A:139:U:H3'	1:A:140:A:H8	1.70	0.56
1:A:1213:C:H2'	1:A:1214:C:H5	1.70	0.56
1:A:1816:A:OP2	6:F:221:ARG:NH2	2.37	0.56
1:A:2169:G:H22	1:A:2176:C:H42	1.53	0.56
1:A:1680:U:H2'	1:A:1681:U:C6	2.41	0.56
1:A:632:U:H2'	1:A:633:A:C8	2.41	0.56
1:A:1058:U:O4	1:A:1059:A:N6	2.39	0.56
1:A:1079:U:O2	1:A:1164:G:C2	2.59	0.56
1:A:2766:U:H3	1:A:2767:A:H62	1.54	0.56
1:A:316:G:H3'	1:A:317:G:H8	1.71	0.56
1:A:1086:G:O6	1:A:1158:G:N2	2.39	0.56
1:A:2060:A:O2'	1:A:2062:G:OP2	2.16	0.56
1:A:8:U:H2'	1:A:9:U:O4'	2.06	0.56
9:H:12:ILE:HD11	9:H:14:ARG:CZ	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:841:C:H5”	8:E:62:ARG:HH12	1.71	0.56
9:H:1:MET:H1	9:H:3:GLN:HG2	1.71	0.56
1:A:460:C:H2’	1:A:461:A:C8	2.41	0.55
1:A:1986:G:H1’	1:A:1987:A:C8	2.41	0.55
1:A:2565:C:H2’	1:A:2566:C:C6	2.41	0.55
12:G:44:LYS:O	12:G:54:LYS:NZ	2.37	0.55
1:A:910:C:H5	1:A:954:A:H62	1.53	0.55
1:A:1003:A:H2’	1:A:1004:A:C8	2.40	0.55
1:A:1892:U:N3	1:A:1893:A:H1’	2.21	0.55
3:1:22:ASN:OD1	3:1:24:ARG:N	2.39	0.55
8:E:28:PRO:HA	8:E:112:SER:HB2	1.88	0.55
1:A:1178:C:H41	1:A:2054:G:H4’	1.70	0.55
3:1:9:CYS:SG	3:1:43:THR:OG1	2.62	0.55
1:A:941:A:H2’	1:A:942:C:O4’	2.06	0.55
13:M:14:ARG:O	13:M:18:VAL:HG22	2.06	0.55
1:A:583:A:N6	1:A:598:G:O2’	2.39	0.55
1:A:1870:C:H5”	1:A:1922:C:O2’	2.07	0.55
1:A:2282:G:H1	1:A:2302:C:H42	1.54	0.55
1:A:10:A:H2’	1:A:11:U:C2	2.42	0.55
1:A:1929:C:H5’	6:F:241:ILE:HG12	1.89	0.55
1:A:2560:U:H3’	1:A:2561:C:H5”	1.87	0.55
1:A:529:A:O4’	19:S:44:HIS:NE2	2.40	0.55
1:A:2818:A:N7	1:A:2827:A:N6	2.53	0.55
1:A:2853:U:H1’	1:A:2854:A:C8	2.42	0.55
1:A:2862:C:H41	1:A:2894:C:H42	1.53	0.55
8:E:49:HIS:HD2	8:E:92:PRO:HB2	1.72	0.55
10:L:117:LEU:HG	10:L:119:LYS:H	1.72	0.55
11:Y:34:LEU:HD12	11:Y:118:LEU:HB3	1.87	0.55
12:G:64:ARG:HB2	12:G:79:PHE:CG	2.42	0.55
14:N:76:PHE:CD2	14:N:83:ILE:HD11	2.41	0.55
1:A:1486:C:H2’	1:A:1487:G:N7	2.22	0.55
1:A:1973:U:H2’	1:A:1974:C:C6	2.42	0.55
15:O:91:ASN:HB2	16:P:11:GLN:OE1	2.06	0.55
19:S:47:PRO:HA	19:S:53:GLU:HA	1.89	0.55
1:A:234:C:H3’	1:A:235:G:C8	2.39	0.55
1:A:1210:U:HO2’	1:A:1211:G:P	2.30	0.55
1:A:1957:G:O2’	1:A:1958:U:OP2	2.25	0.55
1:A:1982:U:O2’	1:A:1983:U:OP2	2.22	0.55
1:A:2830:A:H61	1:A:2909:C:H42	1.55	0.55
12:G:76:TYR:O	14:N:74:ARG:HD2	2.07	0.55
12:G:78:LYS:HB2	14:N:73:GLU:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:G:H2'	1:A:292:U:N1	2.22	0.55
1:A:353:A:O2'	1:A:354:A:O5'	2.23	0.55
1:A:1698:A:N6	1:A:2076:A:OP1	2.37	0.55
7:D:107:VAL:HG11	7:D:193:LYS:HA	1.89	0.55
9:H:58:ILE:HD13	9:H:131:HIS:CD2	2.42	0.55
1:A:33:U:O4	1:A:492:G:O2'	2.22	0.54
1:A:124:A:OP2	4:2:20:ARG:NE	2.39	0.54
1:A:968:A:H2'	1:A:969:A:C8	2.42	0.54
1:A:1637:A:H2'	1:A:1638:G:O4'	2.06	0.54
1:A:2235:A:H2'	1:A:2236:C:C6	2.43	0.54
6:F:137:VAL:HG13	6:F:167:LYS:HE3	1.88	0.54
1:A:1089:C:H4'	1:A:1091:G:H1'	1.89	0.54
1:A:2696:G:H2'	1:A:2697:G:O4'	2.08	0.54
22:V:51:ALA:HA	22:V:54:LEU:HG	1.89	0.54
1:A:1737:U:H3'	1:A:1738:C:C6	2.42	0.54
1:A:1977:G:H8	1:A:1977:G:OP2	1.90	0.54
6:F:17:THR:HB	6:F:204:ASN:H	1.72	0.54
1:A:115:C:O2'	1:A:125:A:C8	2.59	0.54
1:A:280:C:O2'	1:A:281:A:H5"	2.08	0.54
1:A:421:C:H2'	1:A:422:G:H8	1.73	0.54
1:A:459:C:H2'	1:A:460:C:C5	2.41	0.54
1:A:1891:U:N3	1:A:1892:U:O4	2.40	0.54
1:A:2126:C:H2'	1:A:2127:G:C8	2.42	0.54
1:A:2706:A:H2	1:A:2756:G:N1	1.99	0.54
1:A:2801:C:H2'	1:A:2802:A:C8	2.43	0.54
16:P:14:VAL:HA	16:P:18:GLN:HE21	1.71	0.54
1:A:105:C:H2'	1:A:106:A:H8	1.72	0.54
1:A:576:U:H5	1:A:2045:A:N1	2.06	0.54
1:A:702:U:H2'	1:A:703:A:C8	2.42	0.54
1:A:924:G:H1	1:A:943:C:H42	1.56	0.54
1:A:2677:C:H42	1:A:2698:A:N6	2.06	0.54
1:A:1455:U:H3'	1:A:1629:U:OP2	2.08	0.54
1:A:1986:G:H1'	1:A:1987:A:H8	1.73	0.54
1:A:2155:C:H2'	1:A:2156:C:C6	2.42	0.54
13:M:23:SER:HA	13:M:30:ARG:HD3	1.90	0.54
14:N:84:GLU:OE1	14:N:85:LYS:HG2	2.07	0.54
1:A:115:C:O2'	1:A:125:A:H8	1.91	0.54
1:A:159:U:H3	1:A:169:G:H1	1.54	0.54
1:A:2489:U:H3	1:A:2516:G:H1	1.55	0.54
5:3:24:ARG:HD2	10:L:61:LEU:HD21	1.89	0.54
1:A:620:G:O2'	1:A:1292:A:OP1	2.26	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1151:G:H2'	1:A:1152:U:H6	1.72	0.54
1:A:2559:G:H2'	1:A:2560:U:C6	2.42	0.54
1:A:2852:U:C1'	1:A:2853:U:H5'	2.27	0.54
2:B:6:U:H2'	2:B:7:G:C8	2.43	0.54
17:Q:14:PRO:HG3	17:Q:101:SER:HB3	1.88	0.54
1:A:1676:A:H61	1:A:1726:A:H4'	1.73	0.53
1:A:1932:C:N4	1:A:1996:A:OP1	2.33	0.53
1:A:2192:G:H3'	1:A:2193:G:H8	1.73	0.53
12:G:7:ARG:HE	12:G:20:LEU:HD12	1.72	0.53
15:O:88:ILE:HG22	15:O:90:ILE:HG12	1.90	0.53
1:A:1954:A:H2'	1:A:1955:A:C8	2.43	0.53
23:W:27:ASN:O	23:W:31:GLN:HG3	2.09	0.53
1:A:181:G:H2'	1:A:182:C:O4'	2.09	0.53
1:A:1966:5MU:H1'	1:A:2619:G:H4'	1.91	0.53
1:A:2393:A:H2'	1:A:2394:G:O4'	2.08	0.53
11:Y:125:LEU:HD12	11:Y:126:PRO:HD2	1.90	0.53
1:A:530:C:H2'	1:A:531:C:C6	2.44	0.53
1:A:1699:A:H1'	7:D:127:PHE:CE2	2.44	0.53
1:A:1806:U:H5	1:A:1811:A:N7	2.07	0.53
1:A:2155:C:H2'	1:A:2156:C:H6	1.74	0.53
1:A:2864:A:H61	1:A:2891:U:H3	1.54	0.53
7:D:107:VAL:HG22	7:D:195:ILE:HD11	1.90	0.53
20:T:22:ARG:HH12	20:T:87:THR:HA	1.73	0.53
23:W:62:ILE:O	23:W:65:SER:OG	2.25	0.53
1:A:1669:C:H2'	1:A:1670:A:C8	2.44	0.53
1:A:2179:A:H2'	1:A:2180:C:C2	2.43	0.53
1:A:2862:C:N3	14:N:2:THR:OG1	2.42	0.53
2:B:73:G:H3'	2:B:74:G:C8	2.38	0.53
1:A:80:G:H2'	1:A:81:G:H8	1.72	0.53
1:A:393:G:H2'	1:A:394:U:H6	1.74	0.53
1:A:2112:C:H2'	1:A:2113:U:O4'	2.09	0.53
1:A:2367:A:H2'	1:A:2368:G:H8	1.73	0.53
11:Y:76:LYS:HB3	11:Y:91:GLU:HG3	1.89	0.53
1:A:545:G:N1	1:A:548:A:OP2	2.40	0.53
1:A:2509:A:OP2	1:A:2510:C:N4	2.38	0.53
1:A:69:C:H4'	1:A:75:G:N7	2.25	0.53
1:A:281:A:H4'	1:A:282:A:H5'	1.91	0.53
1:A:287:G:H2'	1:A:288:C:C6	2.44	0.53
1:A:2485:U:O2'	1:A:2487:U:O4	2.22	0.53
1:A:719:G:O2'	8:E:74:ARG:HD2	2.09	0.52
1:A:1169:G:H3'	1:A:1170:A:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:38:U:N3	2:B:42:G:OP2	2.42	0.52
19:S:83:TYR:CE1	19:S:90:LYS:HE3	2.45	0.52
1:A:1095:A:N1	1:A:1152:U:N3	2.53	0.52
1:A:1480:G:H2'	1:A:1481:A:C8	2.43	0.52
3:1:7:LEU:HB3	3:1:45:HIS:HB3	1.91	0.52
6:F:133:GLN:HB3	6:F:186:SER:HG	1.73	0.52
1:A:1626:A:H3'	1:A:1627:G:H8	1.74	0.52
1:A:1731:G:N1	1:A:1745:A:OP2	2.43	0.52
1:A:1884:G:O2'	1:A:1912:A:N6	2.43	0.52
5:3:9:GLY:O	5:3:13:ARG:NH1	2.42	0.52
6:F:217:ARG:HG3	6:F:218:PRO:HD2	1.90	0.52
13:M:96:ARG:NH2	13:M:99:TYR:O	2.42	0.52
1:A:901:G:H2'	1:A:902:A:C8	2.45	0.52
1:A:1506:C:H2'	1:A:1507:A:C4	2.44	0.52
1:A:2857:A:C2	1:A:2901:U:H5	2.27	0.52
1:A:2873:C:H42	1:A:2882:A:H61	1.58	0.52
2:B:25:A:H3'	2:B:26:C:C6	2.45	0.52
1:A:1700:C:H5'	7:D:149:ARG:HB2	1.91	0.52
1:A:1978:U:C2	1:A:1984:C:N3	2.78	0.52
1:A:2162:A:H62	1:A:2183:G:N2	2.07	0.52
1:A:2716:U:OP1	1:A:2740:A:N6	2.40	0.52
1:A:2728:U:H2'	1:A:2729:G:C8	2.45	0.52
11:Y:48:GLU:O	11:Y:52:ILE:HG12	2.10	0.52
12:G:77:ILE:HG13	12:G:77:ILE:O	2.10	0.52
13:M:19:ARG:O	13:M:19:ARG:HD3	2.09	0.52
13:M:90:LYS:CG	13:M:91:GLU:H	2.15	0.52
1:A:1731:G:H2'	1:A:1732:U:O4'	2.10	0.52
1:A:1739:G:H2'	1:A:1740:G:O4'	2.10	0.52
11:Y:76:LYS:CB	11:Y:91:GLU:HG3	2.39	0.52
1:A:572:C:H4'	1:A:573:A:O5'	2.10	0.52
1:A:951:G:O2'	1:A:952:A:OP1	2.22	0.52
1:A:1199:A:H5"	15:O:55:ARG:NH2	2.20	0.52
1:A:1734:A:H2'	1:A:1735:C:O4'	2.09	0.52
1:A:1737:U:H3	1:A:1857:C:HO2'	1.50	0.52
1:A:2253:C:H3'	1:A:2254:A:H8	1.73	0.52
1:A:2499:G:N2	1:A:2506:U:O4	2.42	0.52
1:A:2884:G:H2'	1:A:2886:G:H2'	1.91	0.52
19:S:26:THR:HA	19:S:33:VAL:HG12	1.92	0.52
19:S:59:THR:CG2	19:S:60:GLU:H	2.18	0.52
20:T:25:GLY:O	20:T:45:GLU:HG2	2.09	0.52
1:A:757:G:N2	1:A:765:U:H3	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:864:A:N7	1:A:1227:U:H5	2.07	0.52
1:A:1628:A:H2'	1:A:1629:U:C6	2.45	0.52
1:A:1710:G:O2'	12:G:6:THR:HG22	2.10	0.52
1:A:2171:G:N2	1:A:2174:A:C5	2.77	0.52
17:Q:14:PRO:O	17:Q:18:ARG:HG3	2.10	0.52
1:A:422:G:H2'	1:A:423:A:C8	2.45	0.52
1:A:1463:A:H5"	1:A:1465:G:N7	2.25	0.52
9:H:14:ARG:NH1	9:H:50:ASP:O	2.43	0.52
1:A:452:G:H2'	1:A:453:G:O4'	2.09	0.51
1:A:830:U:H2'	1:A:831:C:C6	2.45	0.51
1:A:1736:U:H2'	1:A:1738:C:N3	2.25	0.51
1:A:1873:G:H2'	1:A:1874:A:O4'	2.11	0.51
1:A:2091:C:H2'	1:A:2092:C:C6	2.45	0.51
1:A:2325:A:H3'	1:A:2326:G:C8	2.45	0.51
1:A:2866:G:O5'	1:A:2866:G:H8	1.93	0.51
2:B:16:A:HO2'	2:B:17:A:P	2.32	0.51
10:L:83:ASN:ND2	10:L:117:LEU:O	2.43	0.51
12:G:3:GLN:O	12:G:21:THR:HG21	2.11	0.51
1:A:908:A:H2'	1:A:909:G:H8	1.75	0.51
1:A:1699:A:H1'	7:D:127:PHE:HE2	1.74	0.51
1:A:1880:A:H2'	1:A:1881:A:O4'	2.10	0.51
1:A:2133:G:H2'	1:A:2134:C:C5	2.45	0.51
1:A:11:U:N3	1:A:2655:U:OP1	2.43	0.51
1:A:1761:G:H2'	1:A:1763:U:N3	2.25	0.51
1:A:1798:C:N3	1:A:1799:G:C6	2.78	0.51
12:G:111:PHE:O	12:G:115:VAL:HG23	2.11	0.51
1:A:435:A:H2	1:A:437:A:C8	2.29	0.51
1:A:2081:A:H5'	1:A:2082:C:H4'	1.93	0.51
1:A:2180:C:H2'	1:A:2181:G:C8	2.46	0.51
1:A:2851:G:H21	1:A:2899:A:H61	1.56	0.51
12:G:14:SER:HB3	12:G:52:VAL:HG22	1.92	0.51
1:A:28:A:H2	15:O:11:ARG:HH12	1.58	0.51
1:A:60:U:HO2'	1:A:61:A:P	2.33	0.51
1:A:1505:G:H4'	1:A:2730:C:O2'	2.10	0.51
1:A:1823:U:H2'	1:A:1824:C:H6	1.75	0.51
1:A:2728:U:H3	1:A:2734:C:N4	2.05	0.51
2:B:73:G:H2'	2:B:74:G:H5'	1.93	0.51
9:H:66:THR:O	9:H:69:LYS:HG2	2.11	0.51
22:V:37:ARG:HB3	22:V:46:LYS:HG2	1.92	0.51
7:D:8:ARG:HA	7:D:207:GLY:O	2.11	0.51
1:A:457:G:H4'	1:A:458:A:H5"	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:959:C:C2	1:A:960:C:H2'	2.46	0.51
1:A:1343:U:H5	1:A:1666:A:H61	1.58	0.51
8:E:165:LEU:HA	8:E:168:ARG:HD2	1.92	0.51
11:Y:32:PHE:CE2	11:Y:133:LYS:HG2	2.45	0.51
1:A:949:C:H2'	1:A:950:A:C8	2.45	0.51
1:A:1742:A:H4'	1:A:1743:G:H8	1.70	0.51
1:A:1960:G:H2'	1:A:1961:C:O4'	2.11	0.51
1:A:2189:G:N3	1:A:2191:U:O4	2.44	0.51
1:A:2355:A:H2'	1:A:2356:A:C8	2.46	0.51
1:A:137:G:H8	1:A:137:G:O5'	1.94	0.51
1:A:749:G:N2	1:A:772:A:N7	2.59	0.51
1:A:1350:U:H5	1:A:1647:A:N1	2.09	0.51
1:A:1458:A:N1	1:A:1459:A:N6	2.57	0.51
1:A:1989:C:O2'	1:A:1991:G:OP2	2.19	0.51
1:A:1999:G:O2'	1:A:2000:G:OP1	2.28	0.51
2:B:16:A:H2'	2:B:17:A:C8	2.45	0.51
1:A:161:A:N6	1:A:167:U:H3	2.05	0.51
1:A:1897:U:H4'	1:A:1898:C:H3'	1.93	0.51
1:A:2190:C:H3'	1:A:2191:U:C5	2.45	0.51
1:A:2758:G:H2'	1:A:2759:G:C8	2.46	0.51
6:F:217:ARG:CG	6:F:218:PRO:HD2	2.41	0.51
13:M:54:ALA:HB1	13:M:80:ILE:HD11	1.92	0.51
19:S:3:ILE:HD11	19:S:33:VAL:HG11	1.92	0.51
1:A:1167:C:H2'	1:A:1168:C:N1	2.26	0.50
16:P:14:VAL:HA	16:P:18:GLN:NE2	2.26	0.50
16:P:32:THR:HG22	16:P:61:THR:HG22	1.92	0.50
19:S:31:ASP:OD2	19:S:65:VAL:HB	2.12	0.50
1:A:2161:A:N3	1:A:2186:G:H1'	2.26	0.50
1:A:2591:A:O2'	1:A:2592:A:OP1	2.27	0.50
2:B:64:A:H4'	2:B:65:G:O5'	2.11	0.50
7:D:60:LYS:HB3	7:D:63:ALA:HB2	1.92	0.50
1:A:284:C:H3'	1:A:285:U:H5"	1.93	0.50
1:A:316:G:H2'	1:A:317:G:O4'	2.11	0.50
1:A:956:A:H2'	11:Y:9:TYR:OH	2.12	0.50
1:A:2826:U:N3	1:A:2827:A:N7	2.58	0.50
7:D:14:GLN:NE2	14:N:58:SER:HA	2.26	0.50
23:W:58:ARG:O	23:W:62:ILE:HG12	2.11	0.50
1:A:80:G:N3	1:A:389:A:N6	2.60	0.50
1:A:385:U:H2'	1:A:386:C:C6	2.47	0.50
1:A:765:U:O2'	1:A:766:G:H8	1.94	0.50
1:A:925:G:H2'	1:A:925:G:N3	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2110:G:H2'	1:A:2111:C:C6	2.46	0.50
1:A:2679:U:O2'	1:A:2695:G:N2	2.39	0.50
1:A:61:A:H2'	1:A:62:C:C6	2.47	0.50
19:S:36:GLU:OE1	19:S:60:GLU:HG3	2.12	0.50
1:A:2346:U:H4'	1:A:2348:G:N7	2.26	0.50
7:D:129:GLY:CA	7:D:170:PRO:HB3	2.38	0.50
1:A:168:A:C2	1:A:169:G:H1'	2.46	0.50
1:A:337:A:H2	1:A:389:A:H62	1.58	0.50
6:F:76:ALA:HB1	6:F:94:VAL:HB	1.94	0.50
6:F:87:ARG:HB3	6:F:87:ARG:NH1	2.27	0.50
6:F:108:LYS:HZ2	6:F:198:LEU:HD11	1.77	0.50
10:L:87:ASP:OD1	10:L:119:LYS:HD3	2.12	0.50
1:A:615:A:H5"	1:A:616:G:OP2	2.11	0.50
1:A:1921:C:O2'	1:A:1923:A:OP2	2.16	0.50
1:A:2215:U:H2'	1:A:2216:U:O4'	2.11	0.50
2:B:70:G:N2	2:B:101:A:H62	2.06	0.50
3:1:36:CYS:O	3:1:38:ARG:N	2.44	0.50
19:S:79:THR:HG22	19:S:96:LYS:HZ3	1.75	0.50
20:T:29:ALA:HB3	20:T:41:VAL:HG23	1.94	0.50
1:A:175:C:C4	1:A:176:A:C8	3.00	0.50
1:A:749:G:H21	1:A:772:A:H62	1.59	0.50
1:A:1053:A:H5'	15:O:59:LYS:HE3	1.92	0.50
7:D:129:GLY:O	7:D:131:ILE:HG22	2.11	0.50
7:D:131:ILE:HG23	7:D:132:LYS:H	1.77	0.50
9:H:22:GLU:HG2	9:H:62:LYS:HG2	1.93	0.50
1:A:274:A:H62	1:A:297:G:N2	2.10	0.49
1:A:422:G:H2'	1:A:423:A:H8	1.77	0.49
1:A:525:A:N3	1:A:527:G:H5"	2.27	0.49
1:A:1053:A:H3'	1:A:1053:A:C8	2.46	0.49
1:A:1488:A:H3'	1:A:1489:A:H8	1.77	0.49
1:A:1844:G:H5"	6:F:87:ARG:HH12	1.77	0.49
1:A:2673:C:N4	1:A:2702:A:H61	2.10	0.49
5:3:54:ASP:O	5:3:58:VAL:HG22	2.12	0.49
19:S:3:ILE:HD11	19:S:33:VAL:HG21	1.94	0.49
23:W:28:LEU:HA	23:W:31:GLN:HE21	1.77	0.49
1:A:298:U:H5'	1:A:299:U:H5'	1.95	0.49
1:A:908:A:H2'	1:A:909:G:C8	2.47	0.49
1:A:1488:A:H2'	1:A:1489:A:O4'	2.12	0.49
1:A:2371:U:H2'	3:1:32:MET:SD	2.52	0.49
1:A:2673:C:HO2'	1:A:2674:U:P	2.34	0.49
6:F:133:GLN:HB3	6:F:186:SER:OG	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:5:ILE:O	7:D:6:LEU:HB2	2.12	0.49
1:A:991:A:H2'	1:A:992:A:C8	2.47	0.49
1:A:1210:U:O2'	1:A:1211:G:OP1	2.21	0.49
1:A:1735:C:H2'	1:A:1736:U:O4'	2.12	0.49
1:A:1983:U:H5'	1:A:1984:C:OP1	2.13	0.49
6:F:210:ARG:HG3	6:F:213:TRP:CE3	2.47	0.49
1:A:2249:G:H2'	1:A:2250:A:C8	2.46	0.49
1:A:2437:G:H3'	1:A:2438:A:H8	1.77	0.49
1:A:2775:A:C2	1:A:2784:A:C4	3.00	0.49
9:H:43:VAL:HG12	15:O:100:ILE:HG13	1.94	0.49
1:A:735:C:H4'	6:F:217:ARG:HH22	1.76	0.49
1:A:1091:G:H5"	1:A:1092:A:OP1	2.13	0.49
13:M:31:LEU:HD23	13:M:93:VAL:O	2.13	0.49
1:A:734:A:H2'	1:A:735:C:C6	2.47	0.49
1:A:1079:U:N3	1:A:1080:G:N7	2.61	0.49
1:A:2192:G:H3'	1:A:2193:G:C8	2.48	0.49
1:A:2884:G:O2'	1:A:2886:G:H5"	2.13	0.49
1:A:2916:U:H2'	1:A:2917:U:C6	2.48	0.49
2:B:14:G:C2	2:B:67:G:H1'	2.48	0.49
9:H:9:GLU:HB2	9:H:49:VAL:HG11	1.95	0.49
24:X:39:ASP:OD2	24:X:44:ARG:NH2	2.44	0.49
1:A:1490:G:H1'	1:A:1491:C:C5'	2.42	0.49
1:A:1603:U:H2'	1:A:1604:C:O4'	2.13	0.49
1:A:1627:G:C2	1:A:1628:A:C8	3.01	0.49
9:H:1:MET:N	9:H:3:GLN:HG2	2.28	0.49
9:H:46:THR:OG1	9:H:49:VAL:HG12	2.12	0.49
13:M:15:HIS:O	13:M:19:ARG:HB3	2.12	0.49
14:N:65:LYS:NZ	14:N:67:SER:OG	2.44	0.49
23:W:31:GLN:HE22	23:W:37:LEU:HD13	1.76	0.49
1:A:1197:C:OP1	15:O:92:ARG:NH2	2.41	0.49
1:A:1211:G:C2	1:A:1212:U:H1'	2.48	0.49
1:A:1494:G:O2'	1:A:1495:C:OP2	2.25	0.49
1:A:2490:C:H42	1:A:2515:A:N6	2.09	0.49
1:A:2552:G:C1'	1:A:2768:A:H61	2.25	0.49
1:A:2697:G:H5'	1:A:2698:A:OP2	2.12	0.49
1:A:2902:A:H5"	1:A:2902:A:H8	1.77	0.49
13:M:43:GLN:HG2	13:M:55:GLN:HG2	1.93	0.49
1:A:174:U:H2'	1:A:175:C:H6	1.78	0.49
1:A:1799:G:N2	1:A:2007:G:H1	2.11	0.49
1:A:1963:A:H4'	1:A:1964:A:H5"	1.94	0.49
1:A:1969:C:H3'	1:A:1970:U:H2'	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2565:C:H2'	1:A:2566:C:H6	1.76	0.49
1:A:2618:C:OP2	6:F:238:ARG:HG2	2.13	0.49
1:A:2825:U:H2'	1:A:2826:U:C6	2.47	0.49
4:2:4:ARG:O	4:2:7:GLN:NE2	2.45	0.49
18:R:3:ALA:O	18:R:45:ILE:HD11	2.13	0.49
1:A:1218:G:H2'	1:A:1219:G:H8	1.76	0.49
1:A:1698:A:O2'	7:D:127:PHE:O	2.24	0.49
1:A:1741:G:N1	1:A:1742:A:H2'	2.28	0.49
6:F:17:THR:O	6:F:203:VAL:HG13	2.13	0.49
1:A:986:G:O2'	1:A:1228:A:H8	1.96	0.48
1:A:1040:A:H1'	16:P:9:GLY:O	2.13	0.48
1:A:1760:G:H3'	1:A:1761:G:H4'	1.95	0.48
1:A:2200:A:OP1	1:A:2201:C:N4	2.45	0.48
2:B:43:A:N1	2:B:44:A:H1'	2.28	0.48
5:3:55:MET:O	5:3:59:LYS:HB3	2.13	0.48
1:A:320:U:H1'	1:A:326:A:H2	1.77	0.48
1:A:1167:C:H2'	1:A:1168:C:C6	2.48	0.48
1:A:1733:A:H2'	1:A:1734:A:C8	2.48	0.48
1:A:2185:A:O2'	1:A:2186:G:H5"	2.12	0.48
1:A:2209:G:H2'	1:A:2210:C:C6	2.48	0.48
1:A:2685:C:H3'	1:A:2686:G:H5"	1.95	0.48
3:1:23:LYS:HE2	3:1:24:ARG:NH2	2.28	0.48
1:A:768:A:H2'	1:A:768:A:N3	2.27	0.48
1:A:890:G:H8	1:A:892:U:O4	1.96	0.48
1:A:1315:C:H2'	1:A:1316:G:C8	2.48	0.48
1:A:1454:U:H3'	1:A:1455:U:C6	2.48	0.48
1:A:2699:U:H3'	1:A:2700:G:C8	2.47	0.48
1:A:2865:G:H2'	1:A:2866:G:C8	2.49	0.48
4:2:31:VAL:O	4:2:35:ARG:HG2	2.13	0.48
6:F:131:PRO:HB2	6:F:133:GLN:HG2	1.95	0.48
17:Q:82:LEU:HB2	17:Q:98:LYS:HB2	1.96	0.48
1:A:1701:U:H2'	1:A:1702:C:H6	1.78	0.48
1:A:2189:G:C6	1:A:2192:G:N2	2.82	0.48
1:A:2552:G:N2	1:A:2768:A:H2	1.92	0.48
1:A:2681:A:N6	1:A:2693:C:OP2	2.28	0.48
7:D:5:ILE:HG23	7:D:6:LEU:H	1.77	0.48
1:A:224:A:N1	1:A:268:A:O2'	2.45	0.48
1:A:1168:C:H2'	1:A:1169:G:O4'	2.14	0.48
1:A:1757:U:H2'	1:A:1758:A:O4'	2.14	0.48
1:A:2126:C:H2'	1:A:2127:G:H8	1.78	0.48
9:H:65:PHE:HB3	9:H:69:LYS:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1740:G:H8	1:A:1740:G:O5'	1.96	0.48
1:A:2027:G:H21	1:A:2717:A:N6	2.11	0.48
1:A:2079:G:H4'	7:D:156:MET:O	2.13	0.48
14:N:102:LEU:HD22	14:N:112:ILE:HD12	1.95	0.48
1:A:889:U:H2'	1:A:890:G:O4'	2.14	0.48
1:A:1368:C:H2'	1:A:1370:C:C5	2.49	0.48
1:A:1443:A:H2'	1:A:1444:C:C6	2.49	0.48
1:A:1478:A:H2'	1:A:1479:G:H1'	1.94	0.48
1:A:2242:G:H2'	1:A:2243:U:C6	2.49	0.48
1:A:1887:G:C6	1:A:1910:G:C2	3.02	0.48
13:M:29:PRO:HB2	13:M:44:ILE:HD11	1.96	0.48
1:A:54:G:H1'	4:2:36:ARG:HH12	1.79	0.48
1:A:944:G:C2	1:A:945:A:C5	3.02	0.48
1:A:1605:A:H2'	1:A:1607:A:C8	2.49	0.48
24:X:22:THR:OG1	24:X:49:LYS:HD3	2.14	0.48
1:A:317:G:H2'	1:A:318:A:C8	2.49	0.48
1:A:892:U:H5	1:A:977:A:N1	2.11	0.48
1:A:2250:A:H2'	1:A:2251:G:O4'	2.14	0.48
1:A:2318:U:H2'	1:A:2319:U:C6	2.49	0.48
1:A:2676:U:C4	1:A:2677:C:N4	2.82	0.48
1:A:2684:A:N6	1:A:2691:G:H21	2.03	0.48
7:D:53:PHE:CG	7:D:54:GLU:N	2.82	0.48
9:H:50:ASP:OD1	9:H:122:LYS:NZ	2.46	0.48
13:M:77:GLY:O	13:M:80:ILE:HG22	2.14	0.48
1:A:185:A:H2'	1:A:186:C:H6	1.79	0.47
1:A:293:U:H2'	1:A:294:G:C8	2.49	0.47
1:A:1497:A:C4'	1:A:1498:U:H2'	2.37	0.47
1:A:2673:C:H42	1:A:2702:A:N6	2.10	0.47
1:A:2680:U:H3'	1:A:2681:A:H2'	1.94	0.47
1:A:2720:A:H2	1:A:2744:G:N2	2.09	0.47
3:1:9:CYS:HA	3:1:45:HIS:HA	1.96	0.47
10:L:119:LYS:HG3	10:L:121:LEU:HG	1.94	0.47
22:V:35:LYS:HD2	22:V:46:LYS:HB3	1.96	0.47
1:A:13:A:H5'	1:A:14:A:OP1	2.14	0.47
1:A:682:A:H4'	1:A:683:G:O5'	2.14	0.47
1:A:767:A:N1	1:A:768:A:H1'	2.29	0.47
1:A:1474:C:OP2	1:A:1606:C:N4	2.45	0.47
1:A:1642:C:H4'	18:R:36:THR:HG23	1.96	0.47
1:A:2211:U:H3'	1:A:2212:G:C8	2.49	0.47
1:A:2231:C:H4'	6:F:147:LYS:HD2	1.96	0.47
1:A:2511:G:H2'	1:A:2512:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:20:A:H2'	2:B:21:G:C8	2.49	0.47
8:E:117:LYS:HD3	8:E:192:LEU:HB2	1.96	0.47
1:A:305:A:H3'	1:A:306:C:C6	2.50	0.47
1:A:1203:U:H2'	1:A:1204:G:H5"	1.96	0.47
1:A:1953:U:N3	1:A:1955:A:OP1	2.46	0.47
1:A:2682:G:C2	1:A:2691:G:C2	3.02	0.47
1:A:2878:U:H2'	1:A:2879:G:C8	2.49	0.47
2:B:64:A:H5"	2:B:65:G:OP1	2.13	0.47
6:F:153:GLN:C	6:F:154:ILE:HD13	2.35	0.47
12:G:22:ILE:HD11	12:G:42:THR:HG23	1.95	0.47
1:A:1219:G:C2	1:A:1220:A:C4	3.02	0.47
1:A:1238:U:C1'	15:O:4:VAL:HG12	2.45	0.47
1:A:1628:A:O2'	1:A:1629:U:H5'	2.15	0.47
12:G:106:LEU:HB3	12:G:111:PHE:HB2	1.97	0.47
15:O:60:LEU:O	15:O:63:THR:HG22	2.14	0.47
1:A:1055:A:OP1	15:O:75:SER:OG	2.32	0.47
1:A:1083:G:C2	1:A:1161:A:C2	3.02	0.47
1:A:1798:C:C2	1:A:1799:G:C2	3.02	0.47
1:A:1980:A:N3	1:A:2587:C:O2'	2.47	0.47
1:A:2656:A:C6	1:A:2914:A:H2	2.33	0.47
14:N:101:TYR:CD2	14:N:112:ILE:HA	2.49	0.47
1:A:1314:A:H2'	1:A:1315:C:C6	2.49	0.47
1:A:1460:U:H2'	1:A:1461:C:C6	2.49	0.47
1:A:1609:U:H2'	1:A:1610:G:C8	2.49	0.47
1:A:1731:G:N2	1:A:1745:A:C8	2.82	0.47
1:A:1937:G:C6	1:A:1948:G:C6	3.03	0.47
1:A:1978:U:O2	1:A:1984:C:C2	2.67	0.47
2:B:31:G:O2'	2:B:33:U:O4	2.29	0.47
2:B:37:A:O2'	2:B:44:A:N6	2.47	0.47
9:H:9:GLU:HG3	9:H:46:THR:OG1	2.14	0.47
18:R:23:ASP:O	18:R:81:THR:HA	2.15	0.47
1:A:174:U:C2	1:A:175:C:C5	3.02	0.47
1:A:770:G:H5'	1:A:771:G:C5	2.49	0.47
1:A:911:A:H2'	1:A:911:A:N3	2.28	0.47
1:A:955:A:H2'	1:A:956:A:C8	2.50	0.47
1:A:1982:U:O2'	1:A:2578:C:O2'	2.26	0.47
1:A:2189:G:H5'	1:A:2200:A:OP2	2.15	0.47
1:A:2826:U:H3	1:A:2827:A:H62	1.63	0.47
1:A:2861:U:O4	1:A:2895:G:O6	2.33	0.47
7:D:14:GLN:HE21	14:N:58:SER:HA	1.79	0.47
8:E:7:LEU:HD12	8:E:124:THR:HG23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:59:ASN:ND2	9:H:129:ALA:HB2	2.30	0.47
11:Y:11:ARG:HH21	11:Y:89:ALA:HA	1.79	0.47
12:G:64:ARG:HH21	14:N:70:VAL:HG21	1.80	0.47
22:V:32:ASN:O	22:V:50:SER:HA	2.15	0.47
1:A:332:A:H8	1:A:332:A:O5'	1.98	0.47
1:A:1961:C:C2	1:A:1962:G:C8	3.03	0.47
1:A:1991:G:N7	1:A:1994:C:N4	2.63	0.47
1:A:2135:U:H5'	1:A:2177:U:C2	2.49	0.47
1:A:2226:A:N6	1:A:2251:G:H21	2.12	0.47
1:A:2367:A:H2'	1:A:2368:G:C8	2.50	0.47
1:A:2541:U:H2'	1:A:2542:C:H6	1.79	0.47
2:B:113:G:H2'	2:B:114:G:O4'	2.15	0.47
1:A:2144:A:O2'	1:A:2174:A:H2'	2.14	0.47
1:A:2188:C:N3	1:A:2189:G:N7	2.62	0.47
1:A:2725:U:H2'	1:A:2726:C:O4'	2.15	0.47
1:A:2828:U:C6	1:A:2911:A:N6	2.83	0.47
20:T:9:ARG:N	20:T:40:SER:O	2.39	0.47
23:W:49:THR:HG22	23:W:52:ARG:NH2	2.30	0.47
1:A:1408:G:C2	1:A:1409:U:C4	3.03	0.47
1:A:1475:A:H2'	1:A:1476:G:O4'	2.15	0.47
1:A:1725:G:H21	1:A:1790:G:H5'	1.81	0.47
1:A:1959:A:C6	1:A:1960:G:C4	3.03	0.47
1:A:2629:A:H1'	1:A:2630:G:H5"	1.97	0.47
1:A:328:G:H22	1:A:399:U:H1'	1.81	0.46
1:A:458:A:H3'	1:A:459:C:C6	2.48	0.46
1:A:1627:G:C2	1:A:1628:A:N7	2.83	0.46
11:Y:112:GLU:O	11:Y:116:GLU:OE1	2.33	0.46
19:S:75:THR:HG23	19:S:77:GLU:HB2	1.97	0.46
20:T:9:ARG:NH2	20:T:28:PRO:HB3	2.30	0.46
1:A:64:A:H4'	18:R:63:LYS:NZ	2.30	0.46
1:A:169:G:H2'	1:A:170:C:C6	2.50	0.46
1:A:194:A:H2'	1:A:195:C:C6	2.49	0.46
1:A:579:U:H2'	1:A:580:C:C6	2.50	0.46
1:A:1480:G:H2'	1:A:1481:A:H8	1.81	0.46
1:A:1813:A:OP1	1:A:2007:G:N2	2.48	0.46
1:A:1829:A:H2'	1:A:1830:A:C8	2.51	0.46
1:A:2714:U:H2'	1:A:2715:G:C8	2.50	0.46
4:2:32:LEU:O	4:2:36:ARG:HG3	2.15	0.46
1:A:1212:U:H2'	1:A:1213:C:C1'	2.45	0.46
1:A:1686:G:H2'	1:A:1687:G:O4'	2.14	0.46
1:A:2142:G:H2'	1:A:2143:G:N7	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2507:C:H2'	1:A:2508:G:C8	2.50	0.46
17:Q:72:LYS:HE3	17:Q:108:SER:HB2	1.98	0.46
20:T:29:ALA:HA	20:T:89:ILE:O	2.16	0.46
1:A:273:A:OP2	1:A:297:G:N1	2.46	0.46
1:A:736:C:H2'	1:A:737:C:H6	1.81	0.46
1:A:877:G:H2'	1:A:878:C:C6	2.51	0.46
1:A:1038:C:OP1	15:O:53:ARG:NH2	2.49	0.46
1:A:1736:U:O3'	1:A:1737:U:H2'	2.15	0.46
11:Y:41:TRP:CD1	11:Y:96:VAL:HG22	2.51	0.46
15:O:52:GLN:O	15:O:55:ARG:HG2	2.15	0.46
1:A:309:U:O2	1:A:310:C:N4	2.43	0.46
1:A:835:U:O2	1:A:835:U:H2'	2.15	0.46
1:A:918:G:H2'	1:A:919:G:O4'	2.16	0.46
1:A:1798:C:O2	1:A:1799:G:C2	2.68	0.46
1:A:1946:A:H2'	1:A:1947:C:N1	2.30	0.46
11:Y:32:PHE:HE2	11:Y:133:LYS:HG2	1.79	0.46
1:A:84:A:C8	1:A:99:U:C2	3.04	0.46
1:A:942:C:C2	1:A:943:C:H5	2.34	0.46
1:A:958:U:O2	1:A:959:C:H5	1.99	0.46
1:A:1087:C:O2'	1:A:1092:A:O2'	2.24	0.46
1:A:1458:A:H2'	1:A:1459:A:H8	1.81	0.46
1:A:1767:G:P	1:A:1768:C:H41	2.39	0.46
1:A:2799:C:H5"	7:D:215:ILE:HD12	1.96	0.46
2:B:27:A:H2	2:B:56:A:H61	1.64	0.46
23:W:49:THR:HG22	23:W:52:ARG:HH22	1.79	0.46
1:A:320:U:OP1	1:A:321:U:H5"	2.16	0.46
1:A:947:U:H2'	1:A:948:U:O4'	2.15	0.46
1:A:1092:A:C2	1:A:1157:U:H4'	2.50	0.46
1:A:1450:A:N1	1:A:1634:A:N1	2.63	0.46
1:A:2161:A:H2'	1:A:2162:A:O4'	2.16	0.46
1:A:2777:A:O2'	1:A:2780:A:N6	2.49	0.46
1:A:2884:G:O2'	1:A:2885:U:O5'	2.34	0.46
1:A:29:U:H2'	1:A:30:G:C8	2.50	0.46
1:A:166:A:H2'	1:A:167:U:C6	2.50	0.46
1:A:282:A:H5"	1:A:283:G:OP2	2.15	0.46
1:A:770:G:H2'	1:A:770:G:N3	2.30	0.46
1:A:1044:A:H2'	1:A:1045:A:C8	2.50	0.46
1:A:1218:G:H2'	1:A:1219:G:N7	2.30	0.46
1:A:2130:A:H2'	1:A:2131:C:C6	2.51	0.46
1:A:2325:A:H3'	1:A:2326:G:H8	1.81	0.46
1:A:2681:A:H62	1:A:2694:C:H41	1.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:67:G:O6	2:B:104:A:H2	1.99	0.46
3:1:30:ILE:HG13	3:1:30:ILE:O	2.15	0.46
9:H:1:MET:H1	9:H:3:GLN:N	2.14	0.46
11:Y:31:GLU:HG2	11:Y:107:ALA:HA	1.97	0.46
1:A:1080:G:N1	1:A:1163:U:C2	2.83	0.46
1:A:1169:G:C8	1:A:1170:A:C8	3.04	0.46
1:A:1481:A:H2'	1:A:1482:U:O4'	2.16	0.46
1:A:1882:G:H2'	1:A:1883:A:H8	1.81	0.46
1:A:2027:G:O2'	1:A:2717:A:OP2	2.26	0.46
1:A:2256:U:H2'	1:A:2257:G:C8	2.51	0.46
1:A:2494:C:HO2'	11:Y:123:HIS:CE1	2.28	0.46
1:A:2835:C:H42	1:A:2849:A:H61	1.63	0.46
20:T:7:ILE:HG22	20:T:8:ILE:N	2.31	0.46
1:A:522:G:N1	1:A:525:A:OP2	2.43	0.46
1:A:1447:A:OP2	1:A:1447:A:H8	1.98	0.46
1:A:2187:G:N3	1:A:2188:C:H1'	2.31	0.46
1:A:2433:C:H42	10:L:69:ILE:HD13	1.80	0.46
9:H:20:ASP:N	9:H:20:ASP:OD1	2.47	0.46
24:X:58:GLU:H	24:X:58:GLU:HG2	1.42	0.46
1:A:37:C:H4'	1:A:497:U:OP1	2.16	0.45
1:A:329:A:H2'	1:A:330:C:C6	2.51	0.45
1:A:332:A:H2'	1:A:333:C:C6	2.51	0.45
1:A:1290:G:O4'	15:O:33:LYS:HE2	2.16	0.45
1:A:1483:A:H3'	1:A:1484:G:C8	2.51	0.45
1:A:1840:U:H5"	6:F:40:LYS:HE3	1.97	0.45
1:A:1978:U:N3	1:A:1984:C:C4	2.84	0.45
1:A:2496:A:C6	1:A:2508:G:N2	2.84	0.45
1:A:2874:A:H2'	1:A:2875:U:O4'	2.16	0.45
6:F:169:GLY:O	6:F:171:TYR:HD2	2.00	0.45
14:N:46:GLU:O	14:N:65:LYS:HD3	2.16	0.45
19:S:72:ASP:HB3	19:S:75:THR:HG22	1.98	0.45
1:A:456:G:O2'	1:A:2434:A:OP2	2.28	0.45
1:A:894:A:H2'	1:A:895:U:C6	2.51	0.45
1:A:1770:C:H3'	1:A:1771:A:H4'	1.98	0.45
1:A:2397:G:H2'	1:A:2398:G:C8	2.51	0.45
1:A:2883:U:H4'	1:A:2884:G:O5'	2.16	0.45
2:B:76:A:N6	2:B:94:C:O2	2.49	0.45
12:G:4:GLN:O	12:G:5:GLU:HB2	2.16	0.45
1:A:286:U:H5'	1:A:287:G:C5	2.52	0.45
1:A:383:A:H2'	1:A:384:G:O4'	2.17	0.45
1:A:436:A:O2'	1:A:438:U:O4	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:592:A:H1'	1:A:594:G:OP2	2.17	0.45
1:A:1846:A:N1	6:F:274:ARG:NH1	2.65	0.45
1:A:2187:G:N2	1:A:2200:A:O2'	2.50	0.45
1:A:2189:G:H2'	1:A:2191:U:O4	2.16	0.45
1:A:2724:G:H1	1:A:2738:A:H62	0.78	0.45
2:B:72:U:N3	2:B:73:G:N7	2.65	0.45
17:Q:6:VAL:HA	17:Q:103:ILE:O	2.17	0.45
1:A:83:G:N2	1:A:101:G:H1'	2.32	0.45
1:A:300:G:N3	1:A:302:A:H1'	2.32	0.45
1:A:1798:C:N3	1:A:1799:G:C2	2.83	0.45
1:A:2152:G:H1'	1:A:2200:A:H61	1.81	0.45
1:A:2324:C:N3	1:A:2345:A:H2'	2.31	0.45
1:A:2791:A:H3'	1:A:2793:G:H21	1.82	0.45
5:3:10:ALA:O	5:3:14:VAL:HG12	2.17	0.45
6:F:164:VAL:HA	6:F:174:ILE:HG22	1.99	0.45
10:L:110:LYS:HD2	10:L:127:LYS:HG3	1.97	0.45
20:T:75:ALA:HB2	20:T:92:LEU:HD22	1.99	0.45
1:A:1452:C:H1'	1:A:1459:A:C2	2.51	0.45
1:A:1975:G:OP1	1:A:1975:G:H4'	2.15	0.45
1:A:2848:G:H21	1:A:2855:A:H1'	1.80	0.45
2:B:31:G:H21	2:B:34:C:N4	2.15	0.45
6:F:7:LYS:HD3	6:F:7:LYS:HA	1.79	0.45
6:F:65:ILE:HG13	6:F:67:PHE:CE2	2.51	0.45
7:D:6:LEU:HD23	7:D:53:PHE:HB2	1.97	0.45
14:N:102:LEU:CD2	14:N:112:ILE:HD12	2.46	0.45
16:P:78:ARG:HD2	16:P:79:ARG:NH1	2.31	0.45
18:R:42:VAL:HG23	18:R:50:VAL:HG21	1.97	0.45
1:A:600:U:O2'	9:H:48:HIS:O	2.25	0.45
2:B:83:C:H2'	2:B:84:U:O4'	2.17	0.45
6:F:108:LYS:HB2	6:F:108:LYS:HE2	1.67	0.45
14:N:102:LEU:HD13	14:N:112:ILE:HB	1.98	0.45
1:A:64:A:H8	18:R:65:MET:HG2	1.82	0.45
1:A:669:C:O2'	1:A:702:U:OP1	2.32	0.45
1:A:949:C:H2'	1:A:950:A:O4'	2.17	0.45
1:A:1171:A:N6	1:A:2515:A:H2	2.15	0.45
1:A:1804:U:C5	1:A:1814:A:N1	2.82	0.45
1:A:2165:G:H2'	1:A:2166:U:O4'	2.16	0.45
1:A:2223:C:O2'	1:A:2224:U:H5'	2.16	0.45
1:A:2333:U:H2'	1:A:2334:G:H4'	1.99	0.45
5:3:29:THR:HG22	5:3:30:SER:N	2.31	0.45
6:F:210:ARG:HA	6:F:213:TRP:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:91:VAL:HG13	10:L:95:LEU:HD23	1.99	0.45
1:A:312:A:H8	1:A:315:C:N4	2.13	0.45
1:A:579:U:O2'	15:O:49:ASP:OD2	2.25	0.45
1:A:908:A:HO2'	1:A:909:G:P	2.39	0.45
1:A:1197:C:H5"	15:O:62:ILE:HD13	1.99	0.45
1:A:1315:C:H2'	1:A:1316:G:H8	1.82	0.45
1:A:1488:A:H3'	1:A:1489:A:C8	2.50	0.45
1:A:1626:A:N6	1:A:1627:G:C2	2.85	0.45
1:A:1953:U:H6	1:A:1956:G:H1	1.65	0.45
1:A:2695:G:H8	1:A:2695:G:O5'	2.00	0.45
1:A:2852:U:O2'	1:A:2853:U:OP2	2.29	0.45
1:A:1926:A:O2'	1:A:1928:A:H5"	2.17	0.45
1:A:2012:G:O2'	1:A:2013:G:OP1	2.30	0.45
1:A:2254:A:H2'	1:A:2255:G:H8	1.82	0.45
1:A:2406:G:H2'	1:A:2407:A:C8	2.52	0.45
1:A:2434:A:H2'	1:A:2435:U:C6	2.52	0.45
1:A:2496:A:N6	1:A:2508:G:H21	2.15	0.45
7:D:71:LYS:HB2	7:D:72:PRO:HD3	1.98	0.45
13:M:45:ILE:HD12	13:M:47:ASP:OD1	2.17	0.45
16:P:27:VAL:HG11	16:P:62:VAL:HG21	1.98	0.45
1:A:172:U:H2'	1:A:173:A:C8	2.52	0.45
1:A:506:A:H2	1:A:515:G:H21	1.60	0.45
1:A:616:G:O2'	1:A:618:A:OP1	2.32	0.45
1:A:1092:A:H2'	1:A:1092:A:N3	2.31	0.45
1:A:1461:C:C4	1:A:1462:G:C5	3.05	0.45
1:A:1923:A:H8	1:A:1923:A:OP1	2.00	0.45
1:A:2041:A:H2'	1:A:2042:A:C8	2.52	0.45
1:A:2241:C:H2'	1:A:2242:G:O4'	2.17	0.45
2:B:7:G:H8	2:B:7:G:OP2	2.00	0.45
11:Y:57:TYR:HE1	11:Y:116:GLU:HG2	1.82	0.45
13:M:32:ASN:HA	13:M:95:ASP:O	2.16	0.45
1:A:225:A:N1	1:A:236:A:H5'	2.31	0.44
1:A:328:G:C6	1:A:329:A:N6	2.85	0.44
1:A:927:G:O6	1:A:938:G:H3'	2.17	0.44
1:A:1745:A:H3'	1:A:1746:G:C8	2.46	0.44
1:A:2120:G:N7	1:A:2252:A:H2'	2.32	0.44
1:A:2174:A:N3	1:A:2174:A:H2'	2.30	0.44
1:A:2509:A:N3	1:A:2509:A:H2'	2.32	0.44
11:Y:25:ASN:HB2	11:Y:100:GLY:O	2.17	0.44
12:G:70:ARG:CG	12:G:76:TYR:HE1	2.23	0.44
18:R:37:GLN:HA	18:R:40:MET:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:79:THR:HG22	19:S:96:LYS:HZ1	1.82	0.44
1:A:485:A:H2'	1:A:486:G:O4'	2.17	0.44
1:A:736:C:H2'	1:A:737:C:C6	2.52	0.44
1:A:1865:C:H4'	1:A:1866:G:C8	2.51	0.44
1:A:1884:G:N2	1:A:1913:U:O4	2.49	0.44
1:A:2123:A:H2	1:A:2220:U:O2	2.01	0.44
1:A:2560:U:O2	1:A:2691:G:H4'	2.16	0.44
1:A:2764:G:H2'	1:A:2765:A:O4'	2.17	0.44
1:A:2794:C:H2'	1:A:2795:C:C6	2.52	0.44
1:A:2857:A:N6	1:A:2901:U:O4	2.50	0.44
12:G:101:PRO:HB2	12:G:122:LEU:HD11	1.98	0.44
1:A:12:U:H2'	1:A:13:A:O4'	2.17	0.44
1:A:75:G:H22	1:A:110:A:H2	1.65	0.44
1:A:1078:G:H2'	1:A:1079:U:O4'	2.18	0.44
1:A:1085:U:H3	1:A:1158:G:N2	2.03	0.44
1:A:1210:U:H3	1:A:1222:A:N6	2.12	0.44
1:A:1975:G:H22	1:A:1986:G:N2	2.16	0.44
1:A:2226:A:H62	1:A:2251:G:N2	2.11	0.44
1:A:2696:G:C6	1:A:2697:G:C6	3.05	0.44
1:A:2766:U:O4	1:A:2790:G:H3'	2.17	0.44
2:B:27:A:H2'	2:B:28:C:C5	2.53	0.44
11:Y:34:LEU:HD21	11:Y:129:THR:CG2	2.47	0.44
12:G:4:GLN:HA	12:G:21:THR:HG23	1.99	0.44
1:A:131:G:H2'	1:A:132:C:C6	2.52	0.44
1:A:307:A:N1	1:A:409:G:C4	2.86	0.44
1:A:787:U:H2'	1:A:788:A:C8	2.53	0.44
1:A:1476:G:H2'	1:A:1477:U:C6	2.52	0.44
1:A:1617:A:H2'	1:A:1618:A:C8	2.52	0.44
1:A:1761:G:H2'	1:A:1763:U:C4	2.52	0.44
1:A:2340:C:H2'	1:A:2341:A:C8	2.53	0.44
1:A:2434:A:H2'	1:A:2435:U:H6	1.83	0.44
1:A:2677:C:H42	1:A:2698:A:H61	1.66	0.44
1:A:2849:A:H5'	7:D:67:LYS:HD3	2.00	0.44
10:L:109:ILE:O	10:L:126:HIS:HB2	2.18	0.44
20:T:72:VAL:HG22	20:T:73:MET:N	2.32	0.44
1:A:64:A:N6	1:A:90:A:H2'	2.32	0.44
1:A:293:U:H2'	1:A:294:G:H8	1.82	0.44
1:A:322:A:H2'	1:A:323:C:O4'	2.18	0.44
1:A:776:C:HO2'	1:A:777:C:P	2.38	0.44
1:A:1959:A:C5	1:A:1960:G:C8	3.05	0.44
1:A:2351:U:O2'	1:A:2364:G:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:131:ILE:HG23	7:D:132:LYS:N	2.32	0.44
1:A:91:A:H3'	1:A:92:G:C8	2.48	0.44
1:A:530:C:H2'	1:A:531:C:H6	1.81	0.44
1:A:703:A:H2'	1:A:704:U:C6	2.53	0.44
1:A:1337:A:OP2	1:A:1671:A:N6	2.50	0.44
1:A:2510:C:H3'	1:A:2511:G:C5'	2.44	0.44
2:B:27:A:P	13:M:36:SER:HB3	2.58	0.44
11:Y:54:MET:HE2	11:Y:54:MET:HB2	1.77	0.44
1:A:92:G:H3'	1:A:93:U:H6	1.82	0.44
1:A:398:C:H2'	1:A:399:U:H6	1.83	0.44
1:A:436:A:H4'	1:A:437:A:OP1	2.18	0.44
1:A:912:C:H2'	1:A:913:U:H6	1.83	0.44
1:A:2034:U:OP1	1:A:2842:G:N2	2.50	0.44
1:A:2051:C:H2'	1:A:2052:C:C6	2.52	0.44
1:A:2312:C:OP2	3:1:2:ARG:NH1	2.49	0.44
3:1:38:ARG:HA	3:1:38:ARG:HD3	1.82	0.44
8:E:37:ILE:HG23	8:E:184:LEU:HD12	1.99	0.44
11:Y:10:ARG:HD3	11:Y:11:ARG:NH1	2.33	0.44
16:P:27:VAL:HG21	16:P:62:VAL:HG21	2.00	0.44
1:A:577:A:H2'	1:A:577:A:N3	2.32	0.44
1:A:1781:C:H2'	1:A:1782:A:O4'	2.16	0.44
1:A:1798:C:C4	1:A:1799:G:C6	3.05	0.44
1:A:1809:C:H1'	1:A:2636:U:H5'	1.99	0.44
1:A:2448:G:H2'	1:A:2449:C:C6	2.53	0.44
1:A:2730:C:O2'	1:A:2731:C:P	2.76	0.44
1:A:2882:A:H3'	1:A:2883:U:H3'	2.00	0.44
2:B:25:A:H3'	2:B:26:C:C5	2.53	0.44
13:M:10:VAL:O	13:M:14:ARG:HG2	2.18	0.44
13:M:14:ARG:HH12	13:M:17:ARG:NH1	2.12	0.44
13:M:39:HIS:CD2	13:M:59:LYS:HB2	2.38	0.44
20:T:31:VAL:HG12	20:T:91:PHE:HB2	1.99	0.44
1:A:41:A:H2'	1:A:42:G:O4'	2.17	0.44
1:A:169:G:H2'	1:A:170:C:H6	1.83	0.44
1:A:279:A:H62	1:A:281:A:N6	2.13	0.44
1:A:1051:C:H5"	9:H:38:ARG:HH12	1.83	0.44
1:A:1490:G:HO2'	1:A:1491:C:P	2.35	0.44
1:A:1636:U:O4	1:A:1637:A:N6	2.51	0.44
1:A:1701:U:H2'	1:A:1702:C:C6	2.51	0.44
1:A:1731:G:H8	1:A:1731:G:OP2	2.01	0.44
1:A:2684:A:C5	1:A:2692:A:C8	3.06	0.44
2:B:48:A:OP1	13:M:69:LYS:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:110:PHE:O	7:D:188:VAL:HG21	2.18	0.44
9:H:18:VAL:CG2	9:H:138:PRO:HB2	2.48	0.44
14:N:101:TYR:CE2	14:N:112:ILE:HG13	2.53	0.44
20:T:31:VAL:HA	20:T:91:PHE:O	2.18	0.44
20:T:61:ILE:HG22	20:T:63:LEU:H	1.83	0.44
1:A:299:U:O4	1:A:415:U:H1'	2.18	0.43
1:A:519:G:C2'	1:A:520:G:H5'	2.48	0.43
1:A:752:G:H2'	1:A:753:U:O4'	2.18	0.43
1:A:845:A:H8	1:A:845:A:OP1	2.01	0.43
1:A:1626:A:H3'	1:A:1627:G:C8	2.53	0.43
1:A:1946:A:H8	1:A:1946:A:OP2	2.00	0.43
1:A:2497:G:N7	1:A:2503:A:H1'	2.33	0.43
2:B:31:G:C6	2:B:48:A:C6	3.06	0.43
2:B:73:G:C2'	2:B:74:G:H5'	2.47	0.43
6:F:72:ASP:OD1	6:F:119:GLY:HA2	2.18	0.43
13:M:31:LEU:HD22	13:M:92:ILE:HD12	1.99	0.43
14:N:101:TYR:O	14:N:102:LEU:HB3	2.17	0.43
1:A:111:U:OP1	23:W:58:ARG:NE	2.49	0.43
1:A:168:A:C4	1:A:169:G:H1'	2.53	0.43
1:A:1219:G:H2'	1:A:1220:A:O4'	2.18	0.43
1:A:2682:G:HO2'	1:A:2683:U:P	2.41	0.43
1:A:2808:A:O2'	1:A:2809:G:H5"	2.18	0.43
10:L:57:LEU:HA	10:L:60:ARG:NH1	2.34	0.43
12:G:38:VAL:HG13	12:G:60:ALA:O	2.19	0.43
15:O:61:TRP:O	15:O:65:ILE:HG13	2.18	0.43
20:T:72:VAL:HG23	20:T:92:LEU:O	2.17	0.43
1:A:13:A:H61	1:A:570:U:H3'	1.83	0.43
1:A:665:G:H2'	1:A:665:G:N3	2.33	0.43
1:A:1862:G:H22	1:A:1957:G:H4'	1.83	0.43
1:A:2080:G:H4'	7:D:161:SER:HB2	2.00	0.43
1:A:2683:U:H2'	1:A:2684:A:O4'	2.18	0.43
1:A:2812:U:H2'	1:A:2813:U:C6	2.53	0.43
19:S:77:GLU:O	19:S:79:THR:HG23	2.18	0.43
1:A:134:U:H2'	1:A:135:G:O4'	2.19	0.43
1:A:231:A:O2'	1:A:232:U:H2'	2.18	0.43
1:A:1221:C:H2'	1:A:1222:A:O4'	2.18	0.43
1:A:1463:A:H2'	1:A:1465:G:H8	1.82	0.43
1:A:1958:U:O2	1:A:1958:U:H2'	2.18	0.43
1:A:1980:A:O2'	1:A:1981:G:O5'	2.36	0.43
1:A:2118:U:H3'	1:A:2119:U:H2'	1.99	0.43
1:A:2541:U:H2'	1:A:2542:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2857:A:C6	1:A:2901:U:H5	2.36	0.43
23:W:51:ALA:O	23:W:55:THR:HG23	2.18	0.43
1:A:1166:G:H2'	1:A:1167:C:H5'	2.00	0.43
1:A:1769:C:H2'	1:A:1770:C:C6	2.53	0.43
1:A:2180:C:H2'	1:A:2181:G:N7	2.34	0.43
1:A:2494:C:O2'	11:Y:123:HIS:ND1	2.17	0.43
1:A:2768:A:H62	1:A:2790:G:N2	2.13	0.43
7:D:125:LYS:HG3	7:D:173:MET:HG2	1.99	0.43
9:H:115:LEU:O	9:H:119:GLN:HG3	2.18	0.43
1:A:515:G:O6	4:2:38:LYS:HE2	2.18	0.43
1:A:1639:G:H3'	1:A:1640:U:H6	1.83	0.43
1:A:1738:C:O2	1:A:1739:G:N1	2.51	0.43
1:A:1743:G:H2'	1:A:1744:A:O3'	2.19	0.43
1:A:2223:C:C2	1:A:2224:U:C5	3.06	0.43
1:A:2552:G:C2'	1:A:2768:A:H61	2.32	0.43
1:A:2562:G:C2	1:A:2563:G:C8	3.06	0.43
1:A:2584:G:H2'	1:A:2585:C:C6	2.53	0.43
7:D:60:LYS:HG2	7:D:61:LYS:N	2.34	0.43
15:O:91:ASN:OD1	15:O:92:ARG:N	2.52	0.43
23:W:49:THR:HA	23:W:52:ARG:HG2	1.99	0.43
1:A:46:C:N4	1:A:217:G:N7	2.67	0.43
1:A:460:C:C2	1:A:461:A:C8	3.07	0.43
1:A:681:G:H2'	10:L:112:LEU:HD22	2.01	0.43
1:A:749:G:N1	1:A:771:G:O2'	2.46	0.43
1:A:1358:A:H2'	1:A:1359:A:H8	1.84	0.43
1:A:1946:A:N7	1:A:1947:C:N4	2.67	0.43
1:A:2037:G:H5"	17:Q:42:ALA:HB2	2.01	0.43
1:A:2127:G:O2'	1:A:2128:G:H5'	2.19	0.43
1:A:2231:C:H2'	1:A:2232:A:H8	1.83	0.43
4:2:11:ARG:HE	4:2:15:LYS:HE3	1.84	0.43
6:F:34:LEU:HD22	6:F:61:GLN:HG3	2.00	0.43
6:F:184:ILE:HG22	6:F:185:LEU:N	2.34	0.43
8:E:57:VAL:HG21	8:E:87:GLY:H	1.83	0.43
9:H:18:VAL:HG23	9:H:138:PRO:HB2	2.00	0.43
15:O:52:GLN:HA	15:O:55:ARG:HD3	2.00	0.43
20:T:46:VAL:O	20:T:50:LYS:HG3	2.18	0.43
23:W:45:THR:O	23:W:49:THR:HG23	2.19	0.43
1:A:159:U:O2	1:A:169:G:N2	2.48	0.43
1:A:863:G:H21	1:A:1228:A:H2	1.62	0.43
1:A:1086:G:H2'	1:A:1087:C:O4'	2.19	0.43
1:A:1963:A:N7	1:A:1967:U:C2	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1986:G:O2'	1:A:1987:A:O5'	2.33	0.43
1:A:2179:A:H2'	1:A:2180:C:N1	2.33	0.43
2:B:64:A:C5	2:B:105:C:C5	3.07	0.43
14:N:77:PRO:HB2	14:N:80:THR:HB	2.00	0.43
14:N:90:ARG:HG2	14:N:91:ARG:H	1.82	0.43
16:P:50:ALA:HB3	16:P:51:PRO:HD3	2.01	0.43
1:A:165:C:OP2	1:A:166:A:N6	2.51	0.43
1:A:363:A:O2'	1:A:365:A:OP2	2.30	0.43
1:A:955:A:N6	11:Y:11:ARG:O	2.52	0.43
1:A:1642:C:H4'	18:R:36:THR:CG2	2.49	0.43
1:A:1882:G:H2'	1:A:1883:A:C8	2.53	0.43
1:A:2368:G:H2'	1:A:2369:C:C6	2.54	0.43
1:A:2783:U:H1'	1:A:2784:A:H5"	2.01	0.43
1:A:2791:A:H3'	1:A:2793:G:N2	2.34	0.43
2:B:72:U:C4	2:B:73:G:N7	2.86	0.43
2:B:91:C:OP1	20:T:16:SER:HB2	2.17	0.43
10:L:80:ASP:N	10:L:115:GLY:HA3	2.33	0.43
11:Y:11:ARG:HB3	11:Y:87:LYS:HD2	2.00	0.43
17:Q:51:LEU:HA	17:Q:105:ILE:CD1	2.39	0.43
20:T:77:TYR:HA	20:T:88:HIS:O	2.19	0.43
1:A:143:U:H2'	1:A:144:C:H6	1.82	0.43
1:A:206:U:H3'	1:A:207:A:H2'	2.00	0.43
1:A:397:U:H2'	1:A:398:C:H6	1.83	0.43
1:A:511:G:H2'	1:A:512:A:C8	2.54	0.43
1:A:591:A:H4'	1:A:592:A:H5'	2.00	0.43
1:A:1395:G:O2'	1:A:1410:A:N6	2.51	0.43
1:A:1508:C:O2'	1:A:1509:G:OP1	2.33	0.43
1:A:1771:A:H1'	1:A:1772:G:N7	2.34	0.43
1:A:2731:C:H3'	1:A:2732:A:C8	2.54	0.43
1:A:2791:A:H5'	1:A:2793:G:H21	1.82	0.43
3:1:9:CYS:HB2	3:1:45:HIS:CG	2.53	0.43
4:2:25:THR:O	4:2:29:ARG:HG3	2.18	0.43
5:3:8:ARG:HA	5:3:8:ARG:HD2	1.78	0.43
6:F:141:VAL:HG12	6:F:192:ILE:HD13	2.00	0.43
6:F:261:ARG:HE	6:F:264:LYS:HG3	1.84	0.43
14:N:66:ILE:O	14:N:68:SER:N	2.52	0.43
19:S:37:GLY:H	19:S:60:GLU:CD	2.21	0.43
20:T:4:LEU:HB2	20:T:63:LEU:HB3	1.99	0.43
20:T:72:VAL:CG2	20:T:91:PHE:HB3	2.37	0.43
1:A:64:A:C8	18:R:68:TYR:HE2	2.37	0.42
1:A:173:A:C6	1:A:174:U:C5	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:A:HO2'	1:A:354:A:P	2.42	0.42
1:A:444:C:OP1	22:V:32:ASN:ND2	2.38	0.42
1:A:1862:G:N2	1:A:1957:G:H4'	2.34	0.42
1:A:2098:A:H2'	1:A:2099:G:C8	2.54	0.42
1:A:2300:A:H2'	1:A:2301:A:C8	2.53	0.42
1:A:2488:C:H2'	1:A:2489:U:C6	2.54	0.42
1:A:2818:A:H2'	1:A:2819:C:O4'	2.19	0.42
14:N:22:PHE:CZ	14:N:86:ILE:HG21	2.54	0.42
15:O:104:LYS:HE2	15:O:104:LYS:HA	2.00	0.42
1:A:227:G:H1	1:A:234:C:H42	1.66	0.42
1:A:315:C:H1'	1:A:316:G:C8	2.54	0.42
1:A:942:C:C2	1:A:943:C:C5	3.07	0.42
1:A:2154:G:H2'	1:A:2155:C:C6	2.54	0.42
1:A:2848:G:H21	1:A:2855:A:C2'	2.31	0.42
3:1:16:ASN:O	3:1:18:ILE:HG12	2.19	0.42
9:H:30:SER:HA	9:H:106:ILE:CD1	2.48	0.42
12:G:23:LYS:HB3	12:G:40:VAL:HG12	2.01	0.42
1:A:88:G:C6	1:A:89:U:H1'	2.53	0.42
1:A:310:C:O2'	1:A:311:U:O5'	2.32	0.42
1:A:867:U:H2'	1:A:868:A:H5"	2.00	0.42
1:A:2078:A:H2'	1:A:2605:G:OP1	2.18	0.42
1:A:2188:C:O2	1:A:2188:C:H2'	2.20	0.42
12:G:60:ALA:HB2	12:G:86:ILE:HD13	2.00	0.42
19:S:82:GLY:C	19:S:83:TYR:HD2	2.23	0.42
1:A:949:C:H6	1:A:949:C:O5'	2.02	0.42
1:A:1408:G:H2'	1:A:1409:U:C6	2.55	0.42
1:A:1449:A:H3'	1:A:1449:A:N3	2.34	0.42
1:A:1913:U:H2'	1:A:1914:C:O4'	2.18	0.42
1:A:2574:U:O2'	1:A:2575:G:O5'	2.36	0.42
6:F:35:LYS:HD3	6:F:35:LYS:HA	1.81	0.42
18:R:87:ILE:HG22	18:R:89:LEU:HG	2.01	0.42
1:A:421:C:H2'	1:A:422:G:C8	2.52	0.42
1:A:434:G:N7	1:A:436:A:C8	2.87	0.42
1:A:756:A:H2'	1:A:757:G:C8	2.55	0.42
1:A:1074:G:OP1	11:Y:123:HIS:HA	2.20	0.42
1:A:2047:A:O2'	1:A:2048:G:H5'	2.18	0.42
1:A:2616:A:H2'	1:A:2617:A:C8	2.54	0.42
17:Q:112:GLU:H	17:Q:112:GLU:HG3	1.55	0.42
19:S:34:VAL:HG22	19:S:62:ALA:HA	2.00	0.42
1:A:92:G:H3'	1:A:93:U:C6	2.54	0.42
1:A:156:A:C6	1:A:173:A:C2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:U:H2'	1:A:168:A:O4'	2.19	0.42
1:A:333:C:N4	1:A:334:A:N6	2.67	0.42
1:A:349:U:HO2'	1:A:1249:U:H5	1.66	0.42
1:A:451:U:H4'	1:A:452:G:OP2	2.19	0.42
1:A:923:A:H2'	1:A:924:G:O4'	2.19	0.42
1:A:1167:C:H2'	1:A:1168:C:C2	2.54	0.42
1:A:2005:A:H8	1:A:2005:A:H5"	1.84	0.42
1:A:2196:G:H2'	1:A:2197:G:C8	2.55	0.42
1:A:2277:G:N2	11:Y:84:GLY:HA3	2.35	0.42
1:A:2627:A:H2'	1:A:2628:C:C6	2.55	0.42
1:A:2675:G:N2	1:A:2700:G:N2	2.63	0.42
1:A:2693:C:H2'	1:A:2694:C:C6	2.55	0.42
19:S:83:TYR:HE1	19:S:90:LYS:HE3	1.84	0.42
1:A:679:G:H2'	1:A:680:C:C6	2.54	0.42
1:A:1489:A:N6	1:A:1507:A:H62	2.17	0.42
1:A:1866:G:O5'	1:A:1869:G:O2'	2.37	0.42
1:A:2773:U:H3	1:A:2783:U:H5	1.68	0.42
16:P:63:ASN:O	16:P:94:LYS:HB3	2.20	0.42
1:A:92:G:H8	1:A:92:G:OP2	2.02	0.42
1:A:272:C:H41	1:A:298:U:H2'	1.85	0.42
1:A:307:A:C6	1:A:409:G:C5	3.07	0.42
1:A:572:C:HO2'	1:A:573:A:P	2.41	0.42
1:A:661:U:C5'	8:E:106:ARG:HD3	2.50	0.42
1:A:909:G:O2'	1:A:960:C:N4	2.52	0.42
1:A:1053:A:H3'	1:A:1053:A:H8	1.85	0.42
1:A:1053:A:C8	1:A:1053:A:C3'	3.03	0.42
1:A:1485:G:N2	1:A:1599:G:N2	2.67	0.42
1:A:1886:A:H62	1:A:1910:G:H21	1.67	0.42
1:A:2027:G:H21	1:A:2717:A:H62	1.68	0.42
1:A:2704:A:H2	1:A:2758:G:H1	1.57	0.42
1:A:2778:G:H5'	1:A:2779:C:H5	1.84	0.42
5:3:29:THR:HG22	5:3:30:SER:H	1.85	0.42
7:D:4:GLY:HA2	7:D:211:ILE:O	2.20	0.42
12:G:88:ARG:O	12:G:89:ASP:HB2	2.19	0.42
17:Q:83:LYS:O	17:Q:84:ARG:NH1	2.49	0.42
1:A:158:G:H1	1:A:170:C:H42	1.67	0.42
1:A:442:G:H1'	22:V:29:TRP:CD1	2.55	0.42
1:A:1080:G:N1	1:A:1163:U:N3	2.68	0.42
1:A:1169:G:H3'	1:A:1170:A:H8	1.84	0.42
1:A:1480:G:N1	1:A:1604:C:O2	2.34	0.42
1:A:1500:G:H2'	1:A:1501:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2241:C:H3'	1:A:2242:G:H8	1.85	0.42
1:A:251:G:O5'	1:A:252:C:H5"	2.20	0.42
1:A:441:C:H2'	1:A:442:G:H8	1.85	0.42
1:A:1631:G:H4'	1:A:1632:A:O4'	2.20	0.42
1:A:1982:U:H4'	1:A:1984:C:N4	2.35	0.42
1:A:2719:C:H2'	1:A:2720:A:H8	1.79	0.42
1:A:2745:G:OP1	14:N:100:TYR:HD2	2.03	0.42
2:B:71:A:H3'	2:B:72:U:H6	1.85	0.42
2:B:112:A:H2'	2:B:113:G:O4'	2.20	0.42
9:H:21:ALA:HB3	9:H:60:ALA:H	1.84	0.42
12:G:37:ASP:O	12:G:62:ILE:HD12	2.20	0.42
19:S:94:ALA:O	19:S:95:LYS:HB2	2.20	0.42
1:A:160:G:N2	1:A:169:G:O6	2.53	0.41
1:A:303:G:H2'	1:A:304:G:C8	2.55	0.41
1:A:305:A:H3'	1:A:306:C:C5	2.55	0.41
1:A:592:A:N3	1:A:592:A:O2'	2.45	0.41
1:A:632:U:H2'	1:A:633:A:H8	1.84	0.41
1:A:2783:U:C1'	1:A:2784:A:H5"	2.50	0.41
2:B:71:A:H3'	2:B:72:U:C6	2.55	0.41
1:A:143:U:H2'	1:A:144:C:C6	2.55	0.41
1:A:431:C:O2	1:A:436:A:N6	2.49	0.41
1:A:2776:A:C8	1:A:2777:A:H2'	2.54	0.41
1:A:2811:U:H2'	1:A:2812:U:C6	2.55	0.41
1:A:2868:G:O6	1:A:2887:G:H1'	2.20	0.41
7:D:127:PHE:CE1	7:D:171:GLY:HA2	2.56	0.41
15:O:95:LEU:HD23	15:O:95:LEU:HA	1.89	0.41
1:A:97:C:H2'	1:A:98:U:H6	1.86	0.41
1:A:231:A:H2'	1:A:232:U:H5"	2.02	0.41
1:A:1508:C:HO2'	1:A:1509:G:P	2.42	0.41
1:A:1702:C:H2'	1:A:1703:U:C6	2.55	0.41
1:A:2226:A:OP2	1:A:2227:C:H5	2.04	0.41
1:A:2314:A:C8	1:A:2316:G:C8	3.08	0.41
1:A:2558:A:C2	1:A:2685:C:H2'	2.54	0.41
1:A:2628:C:O2'	1:A:2629:A:O4'	2.27	0.41
1:A:2677:C:N4	1:A:2698:A:H61	2.18	0.41
1:A:2684:A:C2	1:A:2685:C:H1'	2.55	0.41
1:A:2684:A:OP2	1:A:2685:C:H5	2.04	0.41
1:A:2856:U:C4	1:A:2857:A:C6	3.08	0.41
14:N:50:ILE:HG22	14:N:99:LEU:HB2	2.01	0.41
15:O:88:ILE:HA	16:P:50:ALA:HA	2.00	0.41
18:R:4:ARG:HH12	18:R:45:ILE:HG23	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:A:N3	1:A:85:G:H1'	2.34	0.41
1:A:105:C:H2'	1:A:106:A:C8	2.54	0.41
1:A:161:A:C6	1:A:168:A:C2	3.09	0.41
1:A:302:A:H3'	1:A:411:A:H61	1.85	0.41
1:A:540:G:H21	17:Q:61:ASN:HD21	1.68	0.41
1:A:805:G:H2'	1:A:806:A:O4'	2.20	0.41
1:A:1336:G:H21	1:A:1685:A:N6	2.11	0.41
1:A:1701:U:O2'	1:A:1702:C:H5'	2.21	0.41
1:A:2223:C:H2'	1:A:2224:U:C6	2.54	0.41
1:A:2906:G:H8	1:A:2906:G:O5'	2.03	0.41
1:A:2919:A:H2'	1:A:2920:U:O4'	2.20	0.41
2:B:57:G:C2	2:B:58:C:H1'	2.55	0.41
7:D:131:ILE:HG21	7:D:149:ARG:NH1	2.35	0.41
15:O:48:ARG:O	15:O:52:GLN:HG3	2.20	0.41
1:A:210:A:H2'	1:A:211:C:O4'	2.20	0.41
1:A:225:A:C2	1:A:236:A:H4'	2.55	0.41
1:A:316:G:C2	1:A:317:G:H1'	2.55	0.41
1:A:1451:U:N3	1:A:1633:A:C8	2.88	0.41
1:A:1979:A:C2	1:A:1981:G:H3'	2.52	0.41
1:A:2768:A:H2'	1:A:2769:G:H5'	2.03	0.41
7:D:42:GLU:OE2	7:D:42:GLU:N	2.52	0.41
12:G:22:ILE:HG12	12:G:41:CYS:HA	2.02	0.41
13:M:111:ALA:O	13:M:115:SER:HB3	2.21	0.41
1:A:307:A:N6	1:A:409:G:C5	2.85	0.41
1:A:691:A:H3'	1:A:692:G:H8	1.86	0.41
1:A:1061:G:N2	1:A:1189:C:H5	2.05	0.41
1:A:1386:U:H3'	1:A:1387:C:C5'	2.51	0.41
1:A:1458:A:H2'	1:A:1459:A:C8	2.55	0.41
1:A:1700:C:O2'	1:A:1701:U:P	2.78	0.41
1:A:2855:A:H5'	1:A:2856:U:OP2	2.20	0.41
6:F:35:LYS:N	6:F:62:TYR:O	2.45	0.41
10:L:46:VAL:HG21	10:L:50:PHE:HD2	1.85	0.41
1:A:389:A:C6	1:A:390:A:C2	3.09	0.41
1:A:506:A:H2'	1:A:507:C:O4'	2.20	0.41
1:A:770:G:H2'	1:A:771:G:H5'	2.03	0.41
1:A:860:U:H2'	1:A:861:C:H6	1.86	0.41
1:A:1977:G:OP2	1:A:1977:G:O4'	2.39	0.41
1:A:2502:C:N4	1:A:2556:G:H1	2.03	0.41
1:A:2546:U:H5'	1:A:2594:G:N2	2.36	0.41
1:A:2703:C:H3'	1:A:2704:A:C8	2.54	0.41
2:B:47:C:H2'	2:B:48:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:167:LYS:HG2	6:F:172:VAL:HG22	2.03	0.41
10:L:95:LEU:HD12	10:L:98:GLU:OE2	2.21	0.41
14:N:114:GLU:O	14:N:114:GLU:HG2	2.20	0.41
1:A:63:U:H3'	1:A:63:U:OP2	2.20	0.41
1:A:331:G:C2	1:A:332:A:C5	3.08	0.41
1:A:434:G:O2'	1:A:435:A:H3'	2.21	0.41
1:A:775:A:O2'	1:A:776:C:H5'	2.20	0.41
1:A:918:G:H22	1:A:950:A:H2'	1.85	0.41
1:A:1219:G:C4	1:A:1220:A:C8	3.09	0.41
1:A:2012:G:HO2'	1:A:2013:G:P	2.44	0.41
1:A:2752:A:N3	1:A:2753:U:O2'	2.42	0.41
2:B:33:U:H2'	2:B:34:C:C2	2.56	0.41
7:D:125:LYS:HB2	7:D:173:MET:HB3	2.03	0.41
7:D:134:HIS:CE1	7:D:168:LYS:HG2	2.56	0.41
15:O:28:LYS:HD3	15:O:34:VAL:CG1	2.51	0.41
19:S:11:VAL:HG22	19:S:68:VAL:HG12	2.02	0.41
20:T:79:PHE:HD1	20:T:86:ILE:HD13	1.86	0.41
1:A:11:U:C2	1:A:2655:U:OP1	2.74	0.41
1:A:84:A:N6	1:A:99:U:O4'	2.53	0.41
1:A:752:G:C2	1:A:770:G:H5"	2.56	0.41
1:A:1196:C:H2'	1:A:1197:C:H6	1.86	0.41
1:A:1357:G:C2	1:A:1366:U:H5"	2.56	0.41
1:A:1948:G:H2'	1:A:1949:G:C8	2.56	0.41
1:A:2052:C:H2'	1:A:2053:U:C6	2.56	0.41
1:A:2432:G:H4'	1:A:2433:C:C4	2.56	0.41
1:A:2606:C:H2'	1:A:2607:U:C6	2.56	0.41
1:A:2752:A:H1'	1:A:2753:U:H2'	2.02	0.41
1:A:2777:A:C2	1:A:2780:A:H2	2.38	0.41
2:B:31:G:H21	2:B:34:C:H41	1.69	0.41
2:B:43:A:N3	2:B:43:A:H2'	2.36	0.41
2:B:91:C:P	20:T:16:SER:HB2	2.61	0.41
4:2:12:LYS:NZ	4:2:16:VAL:HG21	2.36	0.41
4:2:35:ARG:HE	4:2:40:ARG:HG2	1.86	0.41
6:F:37:LEU:HB2	6:F:62:TYR:HB2	2.03	0.41
6:F:226:ASN:O	6:F:228:ASN:N	2.48	0.41
9:H:7:ALA:O	9:H:46:THR:HG21	2.21	0.41
10:L:85:PHE:O	10:L:119:LYS:NZ	2.46	0.41
11:Y:136:GLU:HA	20:T:57:ARG:HH12	1.86	0.41
15:O:46:ALA:O	15:O:50:ARG:HG3	2.20	0.41
15:O:48:ARG:HE	15:O:48:ARG:HB3	1.76	0.41
18:R:65:MET:HG3	18:R:65:MET:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:4:LYS:O	19:S:23:VAL:HG11	2.21	0.41
20:T:94:ILE:HG13	20:T:95:ASN:N	2.36	0.41
1:A:156:A:H2'	1:A:157:U:O4'	2.21	0.41
1:A:680:C:O2'	1:A:684:U:OP1	2.39	0.41
1:A:1385:G:H2'	1:A:1386:U:O4'	2.20	0.41
1:A:1504:U:H3'	1:A:1504:U:OP2	2.21	0.41
1:A:1736:U:H2'	1:A:1738:C:C2	2.56	0.41
1:A:1741:G:H2'	1:A:1742:A:C5'	2.49	0.41
1:A:2243:U:O2'	1:A:2244:G:H5'	2.21	0.41
1:A:2439:A:P	1:A:2439:A:H8	2.44	0.41
1:A:2679:U:N3	1:A:2696:G:C6	2.89	0.41
10:L:57:LEU:HD12	10:L:60:ARG:HH11	1.85	0.41
1:A:1092:A:N1	1:A:1157:U:H4'	2.36	0.40
1:A:1094:A:H2'	1:A:1095:A:N7	2.36	0.40
1:A:1208:A:H2'	1:A:1209:U:C6	2.55	0.40
1:A:1373:U:H2'	1:A:1374:G:O4'	2.20	0.40
1:A:1786:A:H1'	1:A:2724:G:N2	2.36	0.40
1:A:1799:G:N2	1:A:2007:G:N2	2.61	0.40
1:A:1893:A:C2'	1:A:1894:G:H21	2.34	0.40
1:A:2338:A:OP2	1:A:2339:U:H5	2.03	0.40
1:A:2705:U:H2'	1:A:2706:A:C8	2.56	0.40
1:A:2764:G:H2'	1:A:2765:A:C8	2.56	0.40
1:A:2914:A:H2'	1:A:2915:C:C6	2.56	0.40
10:L:92:THR:OG1	10:L:95:LEU:N	2.50	0.40
1:A:84:A:C2	1:A:102:A:C6	3.10	0.40
1:A:539:G:OP1	17:Q:8:ARG:HD2	2.21	0.40
1:A:737:C:H2'	1:A:738:U:C6	2.56	0.40
1:A:1461:C:H2'	1:A:1462:G:O4'	2.21	0.40
1:A:1974:C:N3	1:A:1987:A:N1	2.69	0.40
1:A:2127:G:C2	1:A:2128:G:C8	3.10	0.40
1:A:2289:U:O2'	1:A:2290:C:H5'	2.21	0.40
1:A:2552:G:O2'	1:A:2768:A:N6	2.53	0.40
1:A:2602:C:H5'	7:D:157:ALA:HB2	2.03	0.40
1:A:2721:G:H1	1:A:2743:U:H3	1.70	0.40
1:A:2774:G:O5'	1:A:2774:G:H8	2.04	0.40
1:A:2866:G:O2'	1:A:2867:U:O5'	2.39	0.40
1:A:2873:C:H2'	1:A:2874:A:H8	1.84	0.40
8:E:49:HIS:CD2	8:E:92:PRO:HB2	2.55	0.40
12:G:64:ARG:HG2	12:G:83:ALA:HB3	2.03	0.40
12:G:104:ARG:HG3	12:G:122:LEU:C	2.42	0.40
19:S:65:VAL:C	19:S:67:ASN:H	2.24	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:6:ILE:HD12	23:W:53:LEU:CD2	2.52	0.40
1:A:90:A:N6	18:R:68:TYR:OH	2.54	0.40
1:A:398:C:C2	1:A:399:U:C5	3.09	0.40
1:A:912:C:H2'	1:A:913:U:C6	2.56	0.40
1:A:1479:G:C6	1:A:1480:G:C6	3.09	0.40
1:A:1742:A:H4'	1:A:1743:G:N7	2.34	0.40
1:A:1990:C:H5"	1:A:1991:G:OP1	2.22	0.40
1:A:2142:G:H2'	1:A:2143:G:C8	2.57	0.40
1:A:2704:A:H2	1:A:2758:G:N2	2.17	0.40
1:A:2816:C:H4'	1:A:2828:U:O2	2.21	0.40
1:A:2832:A:H3'	1:A:2833:U:H5"	2.02	0.40
5:3:48:ARG:HG2	5:3:49:LEU:N	2.32	0.40
6:F:45:ASN:OD1	6:F:45:ASN:N	2.53	0.40
8:E:32:VAL:HG21	8:E:108:LEU:HD23	2.03	0.40
8:E:157:GLU:HG3	8:E:201:LYS:HD2	2.03	0.40
9:H:89:THR:HG22	9:H:92:GLU:HG2	2.03	0.40
9:H:94:ARG:O	9:H:98:PRO:HB3	2.20	0.40
14:N:59:GLU:HG2	14:N:78:LEU:CD2	2.50	0.40
19:S:63:ILE:HD13	19:S:63:ILE:HG21	1.92	0.40
20:T:44:ASP:OD1	20:T:47:GLU:HG3	2.21	0.40
22:V:37:ARG:HD2	22:V:44:PRO:HB2	2.03	0.40
1:A:10:A:H2'	1:A:11:U:N3	2.37	0.40
1:A:52:A:H2'	1:A:53:A:C8	2.56	0.40
1:A:318:A:H2'	1:A:319:G:C8	2.57	0.40
1:A:576:U:H4'	1:A:577:A:H5"	2.03	0.40
1:A:959:C:O2'	1:A:959:C:O2	2.38	0.40
1:A:1762:U:C4	1:A:1768:C:C4	3.09	0.40
1:A:1872:G:O6	1:A:1921:C:H5	2.04	0.40
1:A:2032:A:H2'	1:A:2033:C:C6	2.57	0.40
1:A:2831:G:H2'	1:A:2832:A:C8	2.56	0.40
6:F:34:LEU:HD23	6:F:63:ARG:HG2	2.03	0.40
7:D:119:THR:CG2	7:D:210:GLU:HB2	2.51	0.40
11:Y:14:ARG:HA	11:Y:15:PRO:HD3	1.96	0.40
23:W:28:LEU:HD11	23:W:42:ARG:HB3	2.02	0.40
1:A:1757:U:H3'	1:A:1758:A:H8	1.86	0.40
1:A:2163:A:OP2	1:A:2179:A:N6	2.54	0.40
1:A:2667:G:N2	1:A:2802:A:H2	2.12	0.40
1:A:2827:A:H2'	1:A:2828:U:O4'	2.21	0.40
2:B:7:G:C8	2:B:7:G:OP2	2.75	0.40
2:B:90:U:H2'	2:B:91:C:C6	2.56	0.40
7:D:41:VAL:HA	7:D:46:TYR:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:8:ASN:ND2	9:H:10:SER:OG	2.54	0.40
15:O:58:ARG:HA	15:O:61:TRP:CE3	2.56	0.40
17:Q:4:LYS:HB3	17:Q:106:VAL:HG22	2.03	0.40
19:S:57:LEU:HD12	19:S:58:GLU:N	2.35	0.40
23:W:52:ARG:O	23:W:56:VAL:HG23	2.22	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	
3	1	45/47 (96%)	41 (91%)	4 (9%)	0	100	100
4	2	41/43 (95%)	40 (98%)	1 (2%)	0	100	100
5	3	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
6	F	272/274 (99%)	247 (91%)	25 (9%)	0	100	100
7	D	213/215 (99%)	172 (81%)	40 (19%)	1 (0%)	29	48
8	E	204/206 (99%)	188 (92%)	16 (8%)	0	100	100
9	H	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
10	L	144/146 (99%)	128 (89%)	16 (11%)	0	100	100
11	Y	135/137 (98%)	119 (88%)	16 (12%)	0	100	100
12	G	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
13	M	115/117 (98%)	101 (88%)	14 (12%)	0	100	100
14	N	109/114 (96%)	91 (84%)	18 (16%)	0	100	100
15	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
16	P	100/102 (98%)	88 (88%)	10 (10%)	2 (2%)	7	13
17	Q	110/112 (98%)	104 (94%)	6 (6%)	0	100	100
18	R	87/89 (98%)	77 (88%)	10 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	S	101/103 (98%)	82 (81%)	19 (19%)	0	100	100
20	T	92/94 (98%)	76 (83%)	16 (17%)	0	100	100
21	a	77/79 (98%)	70 (91%)	7 (9%)	0	100	100
22	V	47/49 (96%)	44 (94%)	3 (6%)	0	100	100
23	W	65/67 (97%)	58 (89%)	7 (11%)	0	100	100
24	X	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
25	b	46/48 (96%)	35 (76%)	11 (24%)	0	100	100
All	All	2496/2546 (98%)	2212 (89%)	281 (11%)	3 (0%)	54	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	P	51	PRO
7	D	6	LEU
16	P	78	ARG

5.3.2 Protein sidechains (i)

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	
3	1	44/45 (98%)	44 (100%)	0	100	100
4	2	39/39 (100%)	39 (100%)	0	100	100
5	3	55/55 (100%)	55 (100%)	0	100	100
6	F	221/221 (100%)	221 (100%)	0	100	100
7	D	173/173 (100%)	172 (99%)	1 (1%)	86	91
8	E	168/168 (100%)	167 (99%)	1 (1%)	86	91
9	H	121/122 (99%)	121 (100%)	0	100	100
10	L	109/112 (97%)	109 (100%)	0	100	100
11	Y	108/114 (95%)	108 (100%)	0	100	100
12	G	100/100 (100%)	99 (99%)	1 (1%)	76	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
13	M	83/93 (89%)	81 (98%)	2 (2%)	49 68
14	N	92/100 (92%)	91 (99%)	1 (1%)	73 84
15	O	96/96 (100%)	95 (99%)	1 (1%)	76 85
16	P	84/86 (98%)	83 (99%)	1 (1%)	71 83
17	Q	89/91 (98%)	87 (98%)	2 (2%)	52 71
18	R	78/80 (98%)	77 (99%)	1 (1%)	69 82
19	S	81/88 (92%)	80 (99%)	1 (1%)	71 83
20	T	78/82 (95%)	77 (99%)	1 (1%)	69 82
21	a	59/62 (95%)	59 (100%)	0	100 100
22	V	39/41 (95%)	38 (97%)	1 (3%)	46 66
23	W	58/60 (97%)	58 (100%)	0	100 100
24	X	52/52 (100%)	51 (98%)	1 (2%)	57 74
25	b	35/44 (80%)	35 (100%)	0	100 100
All	All	2062/2124 (97%)	2047 (99%)	15 (1%)	84 90

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	D	216	LYS
8	E	29	ASN
12	G	122	LEU
13	M	19	ARG
13	M	35	ARG
14	N	113	GLN
15	O	88	ILE
16	P	52	THR
17	Q	11	ARG
17	Q	112	GLU
18	R	90	PHE
19	S	80	ARG
20	T	19	LYS
22	V	60	THR
24	X	58	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
8	E	49	HIS
9	H	8	ASN
10	L	78	ASN
11	Y	46	GLN
16	P	18	GLN
19	S	39	ASN
23	W	31	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2728/2742 (99%)	946 (34%)	51 (1%)
2	B	101/106 (95%)	44 (43%)	3 (2%)
All	All	2829/2848 (99%)	990 (34%)	54 (1%)

All (990) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	U
1	A	14	A
1	A	15	G
1	A	24	G
1	A	25	U
1	A	28	A
1	A	34	U
1	A	36	G
1	A	42	G
1	A	43	A
1	A	45	G
1	A	46	C
1	A	47	C
1	A	58	G
1	A	61	A
1	A	63	U
1	A	64	A
1	A	71	A
1	A	75	G
1	A	77	U
1	A	80	G
1	A	81	G
1	A	84	A
1	A	85	G

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Mol	Chain	Res	Type
1	A	87	U
1	A	89	U
1	A	90	A
1	A	92	G
1	A	93	U
1	A	94	A
1	A	96	G
1	A	99	U
1	A	100	U
1	A	103	U
1	A	107	G
1	A	108	A
1	A	117	A
1	A	118	A
1	A	119	U
1	A	130	A
1	A	136	A
1	A	139	U
1	A	146	U
1	A	160	G
1	A	161	A
1	A	164	A
1	A	165	C
1	A	166	A
1	A	167	U
1	A	171	A
1	A	174	U
1	A	176	A
1	A	177	G
1	A	180	G
1	A	182	C
1	A	184	C
1	A	185	A
1	A	199	A
1	A	213	C
1	A	214	G
1	A	216	A
1	A	219	A
1	A	224	A
1	A	225	A
1	A	226	A
1	A	230	A

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Mol	Chain	Res	Type
1	A	231	A
1	A	232	U
1	A	233	U
1	A	235	G
1	A	236	A
1	A	248	G
1	A	251	G
1	A	255	G
1	A	264	G
1	A	267	G
1	A	268	A
1	A	269	G
1	A	276	C
1	A	277	C
1	A	278	A
1	A	279	A
1	A	280	C
1	A	281	A
1	A	282	A
1	A	283	G
1	A	284	C
1	A	285	U
1	A	286	U
1	A	287	G
1	A	288	C
1	A	291	G
1	A	293	U
1	A	295	G
1	A	297	G
1	A	300	G
1	A	301	U
1	A	302	A
1	A	308	C
1	A	310	C
1	A	311	U
1	A	315	C
1	A	317	G
1	A	318	A
1	A	321	U
1	A	324	A
1	A	327	G
1	A	329	A

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Mol	Chain	Res	Type
1	A	331	G
1	A	333	C
1	A	334	A
1	A	336	U
1	A	337	A
1	A	338	G
1	A	353	A
1	A	359	A
1	A	360	A
1	A	365	A
1	A	373	A
1	A	375	A
1	A	387	G
1	A	388	A
1	A	391	A
1	A	393	G
1	A	395	U
1	A	396	G
1	A	398	C
1	A	402	C
1	A	404	U
1	A	409	G
1	A	410	G
1	A	416	G
1	A	417	A
1	A	418	G
1	A	432	G
1	A	433	U
1	A	435	A
1	A	436	A
1	A	437	A
1	A	444	C
1	A	445	G
1	A	450	C
1	A	454	G
1	A	457	G
1	A	458	A
1	A	460	C
1	A	461	A
1	A	463	C
1	A	464	U
1	A	481	C

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Mol	Chain	Res	Type
1	A	486	G
1	A	489	A
1	A	490	C
1	A	494	U
1	A	503	A
1	A	505	U
1	A	506	A
1	A	520	G
1	A	521	U
1	A	522	G
1	A	526	A
1	A	527	G
1	A	529	A
1	A	535	G
1	A	539	G
1	A	547	A
1	A	549	U
1	A	550	A
1	A	551	G
1	A	553	A
1	A	554	C
1	A	573	A
1	A	574	A
1	A	576	U
1	A	577	A
1	A	583	A
1	A	587	C
1	A	591	A
1	A	592	A
1	A	593	U
1	A	594	G
1	A	598	G
1	A	599	A
1	A	606	G
1	A	616	G
1	A	617	A
1	A	618	A
1	A	630	G
1	A	637	U
1	A	646	A
1	A	657	U
1	A	659	A

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Mol	Chain	Res	Type
1	A	660	A
1	A	665	G
1	A	666	A
1	A	678	A
1	A	679	G
1	A	682	A
1	A	699	U
1	A	713	A
1	A	720	A
1	A	727	G
1	A	731	U
1	A	746	G
1	A	749	G
1	A	750	A
1	A	751	A
1	A	752	G
1	A	754	U
1	A	755	C
1	A	756	A
1	A	765	U
1	A	766	G
1	A	769	U
1	A	770	G
1	A	771	G
1	A	772	A
1	A	773	G
1	A	775	A
1	A	776	C
1	A	777	C
1	A	785	C
1	A	788	A
1	A	791	U
1	A	792	5MU
1	A	797	A
1	A	809	A
1	A	813	G
1	A	815	G
1	A	816	G
1	A	820	G
1	A	822	G
1	A	827	A
1	A	829	U

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Mol	Chain	Res	Type
1	A	834	A
1	A	837	G
1	A	839	A
1	A	847	A
1	A	850	G
1	A	851	C
1	A	857	C
1	A	868	A
1	A	872	U
1	A	873	U
1	A	875	G
1	A	891	A
1	A	893	G
1	A	900	G
1	A	901	G
1	A	903	G
1	A	904	G
1	A	909	G
1	A	910	C
1	A	911	A
1	A	917	U
1	A	921	C
1	A	922	G
1	A	925	G
1	A	926	G
1	A	928	C
1	A	938	G
1	A	940	U
1	A	947	U
1	A	949	C
1	A	950	A
1	A	951	G
1	A	952	A
1	A	955	A
1	A	959	C
1	A	960	C
1	A	962	A
1	A	965	G
1	A	971	U
1	A	973	A
1	A	977	A
1	A	989	A

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Mol	Chain	Res	Type
1	A	990	G
1	A	995	U
1	A	1003	A
1	A	1005	G
1	A	1015	C
1	A	1018	A
1	A	1019	A
1	A	1027	A
1	A	1040	A
1	A	1042	C
1	A	1043	U
1	A	1046	G
1	A	1050	C
1	A	1051	C
1	A	1056	U
1	A	1057	A
1	A	1058	U
1	A	1065	A
1	A	1075	G
1	A	1077	U
1	A	1078	G
1	A	1081	G
1	A	1083	G
1	A	1085	U
1	A	1086	G
1	A	1088	C
1	A	1089	C
1	A	1090	A
1	A	1091	G
1	A	1095	A
1	A	1154	G
1	A	1155	A
1	A	1156	G
1	A	1162	C
1	A	1164	G
1	A	1166	G
1	A	1169	G
1	A	1170	A
1	A	1171	A
1	A	1172	A
1	A	1173	A
1	A	1174	U

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Mol	Chain	Res	Type
1	A	1176	U
1	A	1177	A
1	A	1178	C
1	A	1179	C
1	A	1183	G
1	A	1185	U
1	A	1186	A
1	A	1190	A
1	A	1193	U
1	A	1194	U
1	A	1201	G
1	A	1204	G
1	A	1211	G
1	A	1212	U
1	A	1213	C
1	A	1214	C
1	A	1215	U
1	A	1216	U
1	A	1217	U
1	A	1218	G
1	A	1219	G
1	A	1220	A
1	A	1221	C
1	A	1222	A
1	A	1225	G
1	A	1245	G
1	A	1250	G
1	A	1258	A
1	A	1275	A
1	A	1285	A
1	A	1286	G
1	A	1289	A
1	A	1291	A
1	A	1294	G
1	A	1309	G
1	A	1310	A
1	A	1311	A
1	A	1312	A
1	A	1313	G
1	A	1321	A
1	A	1324	A
1	A	1336	G

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Mol	Chain	Res	Type
1	A	1337	A
1	A	1338	U
1	A	1344	A
1	A	1347	G
1	A	1348	U
1	A	1350	U
1	A	1355	A
1	A	1357	G
1	A	1370	C
1	A	1381	U
1	A	1383	G
1	A	1387	C
1	A	1389	U
1	A	1392	G
1	A	1396	A
1	A	1402	A
1	A	1403	C
1	A	1405	G
1	A	1407	C
1	A	1410	A
1	A	1416	U
1	A	1421	A
1	A	1425	G
1	A	1429	G
1	A	1431	U
1	A	1440	A
1	A	1442	C
1	A	1444	C
1	A	1447	A
1	A	1449	A
1	A	1450	A
1	A	1452	C
1	A	1453	G
1	A	1454	U
1	A	1455	U
1	A	1459	A
1	A	1460	U
1	A	1463	A
1	A	1464	U
1	A	1465	G
1	A	1466	G
1	A	1467	G

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Mol	Chain	Res	Type
1	A	1469	G
1	A	1472	C
1	A	1473	G
1	A	1474	C
1	A	1479	G
1	A	1480	G
1	A	1486	C
1	A	1487	G
1	A	1490	G
1	A	1491	C
1	A	1492	G
1	A	1494	G
1	A	1495	C
1	A	1496	G
1	A	1497	A
1	A	1498	U
1	A	1499	U
1	A	1503	U
1	A	1504	U
1	A	1505	G
1	A	1506	C
1	A	1508	C
1	A	1509	G
1	A	1599	G
1	A	1600	A
1	A	1604	C
1	A	1605	A
1	A	1606	C
1	A	1613	G
1	A	1616	A
1	A	1625	U
1	A	1626	A
1	A	1627	G
1	A	1629	U
1	A	1630	A
1	A	1632	A
1	A	1635	A
1	A	1638	G
1	A	1639	G
1	A	1640	U
1	A	1645	G
1	A	1650	G

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Mol	Chain	Res	Type
1	A	1651	C
1	A	1652	A
1	A	1653	A
1	A	1654	A
1	A	1675	G
1	A	1677	G
1	A	1678	A
1	A	1679	A
1	A	1690	A
1	A	1691	G
1	A	1692	C
1	A	1698	A
1	A	1701	U
1	A	1703	U
1	A	1707	U
1	A	1717	G
1	A	1718	G
1	A	1725	G
1	A	1726	A
1	A	1727	C
1	A	1730	C
1	A	1731	G
1	A	1732	U
1	A	1734	A
1	A	1735	C
1	A	1737	U
1	A	1738	C
1	A	1739	G
1	A	1740	G
1	A	1741	G
1	A	1742	A
1	A	1743	G
1	A	1744	A
1	A	1747	G
1	A	1748	G
1	A	1749	G
1	A	1750	U
1	A	1751	G
1	A	1752	C
1	A	1755	U
1	A	1759	G
1	A	1761	G

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Mol	Chain	Res	Type
1	A	1762	U
1	A	1763	U
1	A	1764	A
1	A	1765	A
1	A	1766	C
1	A	1767	G
1	A	1768	C
1	A	1769	C
1	A	1770	C
1	A	1771	A
1	A	1772	G
1	A	1782	A
1	A	1785	G
1	A	1790	G
1	A	1791	G
1	A	1793	C
1	A	1797	G
1	A	1800	A
1	A	1803	G
1	A	1806	U
1	A	1808	U
1	A	1811	A
1	A	1813	A
1	A	1816	A
1	A	1820	G
1	A	1827	C
1	A	1828	U
1	A	1837	A
1	A	1843	U
1	A	1852	G
1	A	1856	A
1	A	1860	C
1	A	1864	C
1	A	1865	C
1	A	1866	G
1	A	1867	G
1	A	1868	U
1	A	1870	C
1	A	1872	G
1	A	1874	A
1	A	1877	G
1	A	1879	U

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Mol	Chain	Res	Type
1	A	1880	A
1	A	1882	G
1	A	1883	A
1	A	1884	G
1	A	1885	G
1	A	1887	G
1	A	1888	U
1	A	1889	G
1	A	1890	G
1	A	1891	U
1	A	1892	U
1	A	1893	A
1	A	1894	G
1	A	1895	C
1	A	1897	U
1	A	1899	U
1	A	1901	C
1	A	1904	A
1	A	1905	G
1	A	1908	A
1	A	1910	G
1	A	1912	A
1	A	1913	U
1	A	1915	G
1	A	1916	A
1	A	1922	C
1	A	1923	A
1	A	1924	G
1	A	1925	U
1	A	1926	A
1	A	1929	C
1	A	1933	G
1	A	1935	C
1	A	1938	U
1	A	1939	A
1	A	1945	A
1	A	1946	A
1	A	1950	U
1	A	1953	U
1	A	1956	G
1	A	1957	G
1	A	1958	U

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Mol	Chain	Res	Type
1	A	1961	C
1	A	1963	A
1	A	1964	A
1	A	1965	A
1	A	1968	C
1	A	1971	U
1	A	1973	U
1	A	1975	G
1	A	1976	G
1	A	1977	G
1	A	1981	G
1	A	1982	U
1	A	1983	U
1	A	1984	C
1	A	1985	C
1	A	1986	G
1	A	1987	A
1	A	1988	C
1	A	1989	C
1	A	1991	G
1	A	1992	C
1	A	1993	A
1	A	1994	C
1	A	1995	G
1	A	1996	A
1	A	1997	A
1	A	1998	A
1	A	1999	G
1	A	2000	G
1	A	2002	G
1	A	2003	U
1	A	2004	A
1	A	2005	A
1	A	2006	C
1	A	2007	G
1	A	2008	A
1	A	2012	G
1	A	2013	G
1	A	2018	U
1	A	2019	G
1	A	2020	U
1	A	2021	C

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Mol	Chain	Res	Type
1	A	2023	C
1	A	2032	A
1	A	2033	C
1	A	2034	U
1	A	2047	A
1	A	2048	G
1	A	2050	A
1	A	2054	G
1	A	2058	A
1	A	2059	G
1	A	2060	A
1	A	2063	C
1	A	2070	C
1	A	2076	A
1	A	2079	G
1	A	2082	C
1	A	2083	G
1	A	2087	A
1	A	2088	G
1	A	2089	A
1	A	2096	G
1	A	2097	G
1	A	2098	A
1	A	2111	C
1	A	2114	G
1	A	2115	A
1	A	2116	U
1	A	2118	U
1	A	2120	G
1	A	2122	A
1	A	2123	A
1	A	2129	C
1	A	2130	A
1	A	2133	G
1	A	2134	C
1	A	2135	U
1	A	2137	G
1	A	2138	U
1	A	2139	A
1	A	2140	C
1	A	2141	A
1	A	2142	G

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Mol	Chain	Res	Type
1	A	2143	G
1	A	2145	U
1	A	2146	A
1	A	2147	G
1	A	2153	A
1	A	2154	G
1	A	2155	C
1	A	2158	U
1	A	2160	G
1	A	2162	A
1	A	2163	A
1	A	2165	G
1	A	2167	G
1	A	2170	C
1	A	2171	G
1	A	2172	C
1	A	2173	U
1	A	2174	A
1	A	2179	A
1	A	2183	G
1	A	2185	A
1	A	2186	G
1	A	2190	C
1	A	2193	G
1	A	2194	U
1	A	2195	G
1	A	2196	G
1	A	2198	A
1	A	2201	C
1	A	2203	A
1	A	2204	C
1	A	2205	C
1	A	2209	G
1	A	2210	C
1	A	2211	U
1	A	2214	G
1	A	2219	C
1	A	2221	U
1	A	2225	A
1	A	2226	A
1	A	2230	G
1	A	2231	C

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Mol	Chain	Res	Type
1	A	2235	A
1	A	2236	C
1	A	2238	U
1	A	2239	A
1	A	2241	C
1	A	2243	U
1	A	2244	G
1	A	2245	G
1	A	2247	G
1	A	2251	G
1	A	2252	A
1	A	2253	C
1	A	2254	A
1	A	2256	U
1	A	2262	G
1	A	2263	C
1	A	2265	G
1	A	2266	G
1	A	2291	C
1	A	2295	A
1	A	2306	G
1	A	2310	C
1	A	2314	A
1	A	2319	U
1	A	2320	C
1	A	2321	C
1	A	2322	C
1	A	2324	C
1	A	2328	A
1	A	2330	G
1	A	2332	U
1	A	2334	G
1	A	2335	G
1	A	2336	A
1	A	2338	A
1	A	2342	U
1	A	2344	C
1	A	2345	A
1	A	2346	U
1	A	2347	A
1	A	2348	G
1	A	2352	G

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Mol	Chain	Res	Type
1	A	2354	A
1	A	2358	G
1	A	2362	A
1	A	2363	A
1	A	2364	G
1	A	2371	U
1	A	2372	G
1	A	2374	C
1	A	2377	C
1	A	2388	A
1	A	2394	G
1	A	2397	G
1	A	2399	G
1	A	2400	U
1	A	2410	G
1	A	2412	C
1	A	2417	U
1	A	2418	G
1	A	2419	A
1	A	2425	U
1	A	2426	G
1	A	2427	G
1	A	2429	U
1	A	2430	C
1	A	2433	C
1	A	2434	A
1	A	2438	A
1	A	2441	G
1	A	2445	A
1	A	2453	A
1	A	2455	G
1	A	2456	G
1	A	2457	A
1	A	2459	A
1	A	2460	A
1	A	2462	A
1	A	2466	A
1	A	2467	C
1	A	2468	C
1	A	2469	C
1	A	2472	G
1	A	2474	G

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Mol	Chain	Res	Type
1	A	2475	A
1	A	2476	U
1	A	2490	C
1	A	2494	C
1	A	2495	A
1	A	2496	A
1	A	2499	G
1	A	2502	C
1	A	2503	A
1	A	2505	A
1	A	2508	G
1	A	2509	A
1	A	2511	G
1	A	2514	G
1	A	2516	G
1	A	2519	U
1	A	2520	U
1	A	2529	G
1	A	2531	U
1	A	2532	G
1	A	2535	G
1	A	2545	A
1	A	2547	C
1	A	2551	G
1	A	2552	G
1	A	2553	G
1	A	2554	C
1	A	2556	G
1	A	2558	A
1	A	2559	G
1	A	2561	C
1	A	2562	G
1	A	2566	C
1	A	2569	A
1	A	2570	G
1	A	2574	U
1	A	2575	G
1	A	2578	C
1	A	2579	U
1	A	2589	U
1	A	2591	A
1	A	2592	A

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Mol	Chain	Res	Type
1	A	2593	A
1	A	2594	G
1	A	2600	C
1	A	2601	G
1	A	2604	A
1	A	2605	G
1	A	2609	G
1	A	2613	C
1	A	2621	C
1	A	2629	A
1	A	2630	G
1	A	2631	U
1	A	2636	U
1	A	2637	C
1	A	2640	U
1	A	2642	U
1	A	2655	U
1	A	2656	A
1	A	2657	G
1	A	2658	G
1	A	2663	U
1	A	2672	G
1	A	2673	C
1	A	2674	U
1	A	2675	G
1	A	2677	C
1	A	2679	U
1	A	2680	U
1	A	2682	G
1	A	2683	U
1	A	2685	C
1	A	2686	G
1	A	2687	A
1	A	2689	A
1	A	2690	G
1	A	2692	A
1	A	2695	G
1	A	2697	G
1	A	2698	A
1	A	2699	U
1	A	2710	C
1	A	2717	A

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Mol	Chain	Res	Type
1	A	2719	C
1	A	2720	A
1	A	2723	U
1	A	2729	G
1	A	2730	C
1	A	2731	C
1	A	2734	C
1	A	2735	G
1	A	2741	G
1	A	2745	G
1	A	2747	U
1	A	2748	A
1	A	2749	G
1	A	2750	C
1	A	2753	U
1	A	2759	G
1	A	2760	A
1	A	2761	C
1	A	2763	G
1	A	2764	G
1	A	2766	U
1	A	2769	G
1	A	2775	A
1	A	2777	A
1	A	2778	G
1	A	2779	C
1	A	2784	A
1	A	2786	G
1	A	2788	A
1	A	2789	U
1	A	2791	A
1	A	2794	C
1	A	2796	C
1	A	2797	C
1	A	2798	C
1	A	2804	G
1	A	2806	U
1	A	2807	G
1	A	2808	A
1	A	2809	G
1	A	2810	A
1	A	2815	C

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Mol	Chain	Res	Type
1	A	2817	A
1	A	2818	A
1	A	2823	G
1	A	2829	A
1	A	2831	G
1	A	2832	A
1	A	2833	U
1	A	2836	C
1	A	2837	U
1	A	2839	A
1	A	2852	U
1	A	2853	U
1	A	2854	A
1	A	2855	A
1	A	2857	A
1	A	2858	G
1	A	2860	U
1	A	2862	C
1	A	2867	U
1	A	2868	G
1	A	2875	U
1	A	2877	G
1	A	2882	A
1	A	2883	U
1	A	2884	G
1	A	2885	U
1	A	2886	G
1	A	2887	G
1	A	2892	G
1	A	2893	A
1	A	2894	C
1	A	2899	A
1	A	2901	U
1	A	2904	U
1	A	2905	C
1	A	2907	A
1	A	2911	A
1	A	2917	U
1	A	2919	A
1	A	2920	U
2	B	6	U
2	B	7	G

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Mol	Chain	Res	Type
2	B	8	A
2	B	14	G
2	B	16	A
2	B	17	A
2	B	18	G
2	B	20	A
2	B	22	G
2	B	23	U
2	B	25	A
2	B	28	C
2	B	29	C
2	B	31	G
2	B	32	U
2	B	34	C
2	B	35	C
2	B	38	U
2	B	41	C
2	B	43	A
2	B	44	A
2	B	45	C
2	B	49	G
2	B	54	U
2	B	60	C
2	B	62	U
2	B	63	U
2	B	64	A
2	B	65	G
2	B	73	G
2	B	74	G
2	B	75	U
2	B	76	A
2	B	79	C
2	B	82	A
2	B	92	C
2	B	97	G
2	B	98	A
2	B	100	U
2	B	106	G
2	B	108	U
2	B	113	G
2	B	114	G
2	B	115	C

All (54) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	99	U
1	A	281	A
1	A	352	A
1	A	416	G
1	A	525	A
1	A	572	C
1	A	749	G
1	A	774	G
1	A	775	A
1	A	809	A
1	A	815	G
1	A	908	A
1	A	951	G
1	A	1155	A
1	A	1210	U
1	A	1490	G
1	A	1508	C
1	A	1676	A
1	A	1678	A
1	A	1706	U
1	A	1739	G
1	A	1742	A
1	A	1922	C
1	A	1980	A
1	A	1982	U
1	A	1989	C
1	A	1999	G
1	A	2003	U
1	A	2006	C
1	A	2007	G
1	A	2012	G
1	A	2020	U
1	A	2032	A
1	A	2075	G
1	A	2081	A
1	A	2097	G
1	A	2513	G
1	A	2515	A
1	A	2553	G
1	A	2574	U
1	A	2591	A

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Mol	Chain	Res	Type
1	A	2603	G
1	A	2657	G
1	A	2746	G
1	A	2783	U
1	A	2851	G
1	A	2854	A
1	A	2866	G
1	A	2883	U
1	A	2900	C
2	B	16	A
2	B	64	A
2	B	97	G

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

3 non-standard protein/DNA/RNA residues are 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	$\#\|Z\| > 2$
1	2MA	A	2530	1	17,25,26	2.37	5 (29%)	17,37,40	1.63	4 (23%)
1	5MU	A	792	1	19,22,23	4.90	7 (36%)	28,32,35	3.87	11 (39%)
1	5MU	A	1966	1	19,22,23	5.11	7 (36%)	28,32,35	3.57	12 (42%)

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
1	2MA	A	2530	1	-	3/3/25/26	0/3/3/3
1	5MU	A	792	1	-	0/7/25/26	0/2/2/2
1	5MU	A	1966	1	-	2/7/25/26	0/2/2/2

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1966	5MU	C2-N1	12.55	1.58	1.38
1	A	792	5MU	C2-N1	11.62	1.57	1.38
1	A	1966	5MU	C6-N1	10.75	1.56	1.38
1	A	1966	5MU	C4-C5	10.48	1.62	1.44
1	A	792	5MU	C6-N1	10.16	1.55	1.38
1	A	792	5MU	C4-C5	10.08	1.61	1.44
1	A	792	5MU	C4-N3	-7.40	1.25	1.38
1	A	1966	5MU	C4-N3	-7.23	1.25	1.38
1	A	1966	5MU	C6-C5	6.61	1.45	1.34
1	A	2530	2MA	C2-N3	6.37	1.44	1.31
1	A	792	5MU	C6-C5	6.18	1.44	1.34
1	A	2530	2MA	C4-N3	4.74	1.48	1.37
1	A	2530	2MA	C5-C4	-3.66	1.33	1.43
1	A	792	5MU	O4-C4	-3.36	1.17	1.23
1	A	792	5MU	O2-C2	-3.09	1.17	1.23
1	A	2530	2MA	C6-N1	2.97	1.44	1.38
1	A	1966	5MU	O4-C4	-2.74	1.18	1.23
1	A	1966	5MU	O2-C2	-2.34	1.18	1.23
1	A	2530	2MA	C2-N1	2.24	1.43	1.36

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	792	5MU	C5-C4-N3	12.50	125.98	115.31
1	A	1966	5MU	C5-C4-N3	11.60	125.21	115.31
1	A	792	5MU	C5-C6-N1	-10.42	112.62	123.34
1	A	1966	5MU	C5-C6-N1	-9.34	113.73	123.34
1	A	792	5MU	C4-N3-C2	-5.52	120.20	127.35
1	A	792	5MU	O4-C4-C5	-4.97	119.14	124.90
1	A	792	5MU	C5M-C5-C6	-4.77	116.47	122.85
1	A	792	5MU	N3-C2-N1	4.63	121.04	114.89
1	A	1966	5MU	C4-N3-C2	-4.57	121.44	127.35
1	A	792	5MU	C5M-C5-C4	4.47	123.69	118.77
1	A	1966	5MU	N3-C2-N1	4.42	120.75	114.89
1	A	1966	5MU	C5M-C5-C6	-4.34	117.06	122.85
1	A	1966	5MU	C5M-C5-C4	4.15	123.34	118.77
1	A	1966	5MU	O4-C4-C5	-4.01	120.25	124.90
1	A	2530	2MA	C5-C6-N1	3.54	120.12	114.02
1	A	2530	2MA	C8-N7-C5	3.47	109.60	102.99
1	A	1966	5MU	C1'-N1-C2	2.99	122.99	117.57
1	A	2530	2MA	CM2-C2-N1	2.99	122.88	116.23
1	A	1966	5MU	O4-C4-N3	-2.92	114.52	120.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	792	5MU	O4-C4-N3	-2.73	114.88	120.12
1	A	792	5MU	C1'-N1-C2	2.66	122.38	117.57
1	A	1966	5MU	O2-C2-N3	-2.47	116.91	121.50
1	A	2530	2MA	N1-C2-N3	-2.32	119.20	123.06
1	A	792	5MU	C1'-N1-C6	-2.30	117.30	121.12
1	A	792	5MU	C6-C5-C4	2.16	119.84	118.03
1	A	1966	5MU	C6-N1-C2	-2.03	119.24	121.30
1	A	1966	5MU	C1'-N1-C6	-2.03	117.75	121.12

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1966	5MU	C2'-C1'-N1-C2
1	A	2530	2MA	O4'-C4'-C5'-O5'
1	A	1966	5MU	C2'-C1'-N1-C6
1	A	2530	2MA	C3'-C4'-C5'-O5'
1	A	2530	2MA	C4'-C5'-O5'-P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1966	5MU	2	0

5.5 Carbohydrates (i)

There are no monosaccharides 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
1	A	11
2	B	4
9	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1067:U	O3'	1074:G	P	32.56
1	A	1509:G	O3'	1598:U	P	17.87
1	A	2911:A	O3'	2914:A	P	16.95
1	A	1096:C	O3'	1151:G	P	15.42
1	A	758:G	O3'	764:C	P	14.44
1	B	9:C	O3'	13:A	P	14.19
1	A	686:U	O3'	691:A	P	14.11
1	A	1939:A	O3'	1944:U	P	13.86
1	A	929:C	O3'	937:G	P	12.60
1	A	1860:C	O3'	1862:G	P	10.14
1	A	2206:C	O3'	2208:A	P	9.45
1	A	2791:A	O3'	2793:G	P	8.08
1	B	76:A	O3'	78:U	P	7.15
1	B	86:A	O3'	88:G	P	5.72
1	B	38:U	O3'	40:C	P	5.39
1	H	1:MET	C	3:GLN	N	4.35

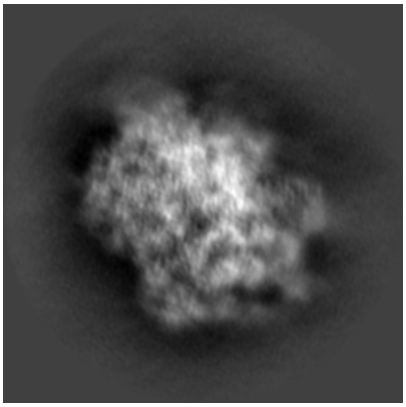
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11901. These allow visual inspection of the internal detail of the map and identification of artifacts.

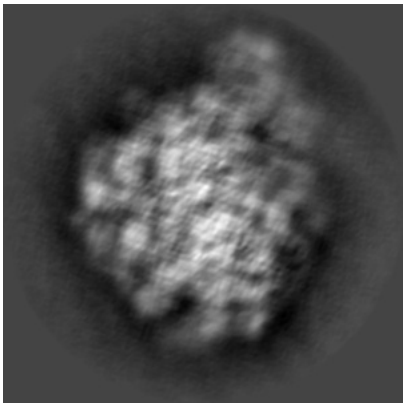
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

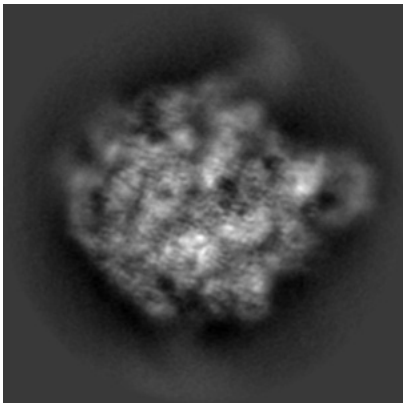
6.1.1 Primary map



X



Y

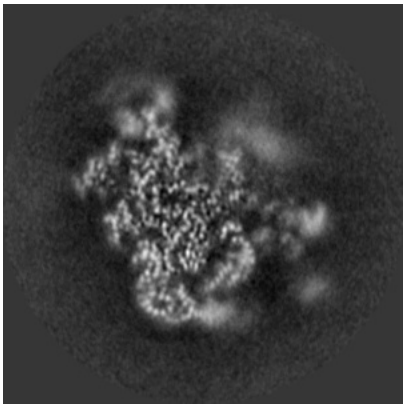


Z

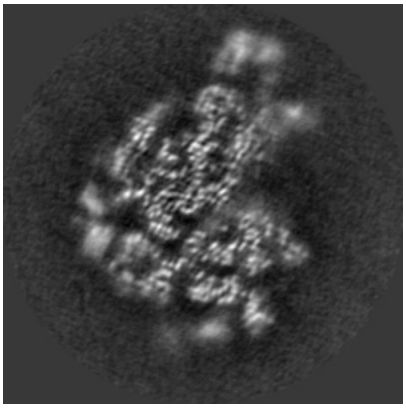
The images above show the map projected in three orthogonal directions.

6.2 Central slices

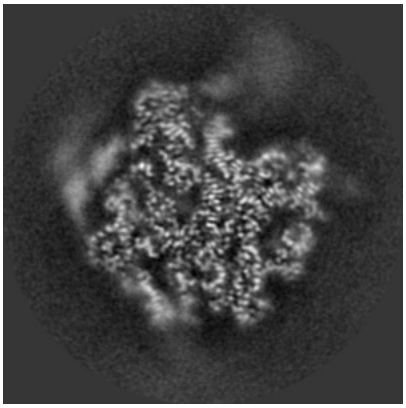
6.2.1 Primary map



X Index: 164



Y Index: 164

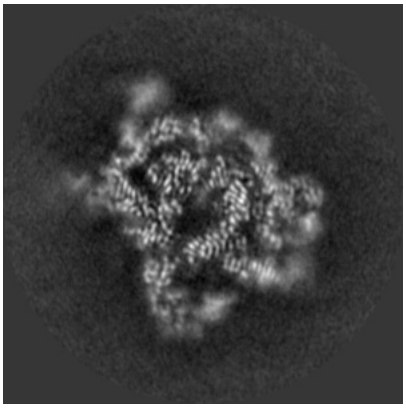


Z Index: 164

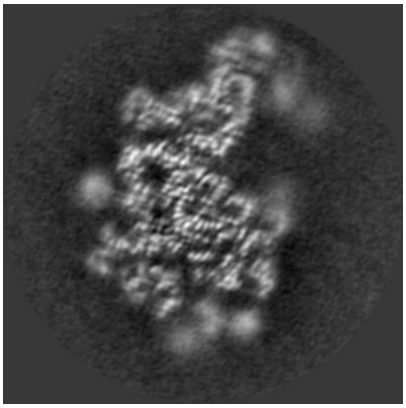
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

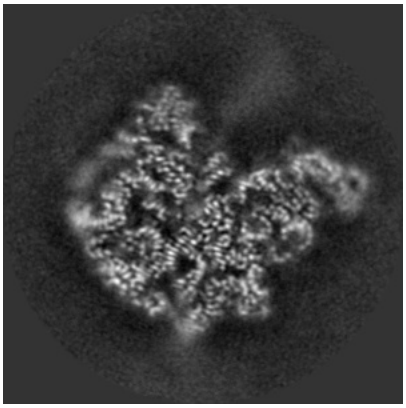
6.3.1 Primary map



X Index: 146



Y Index: 188



Z Index: 180

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.0026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

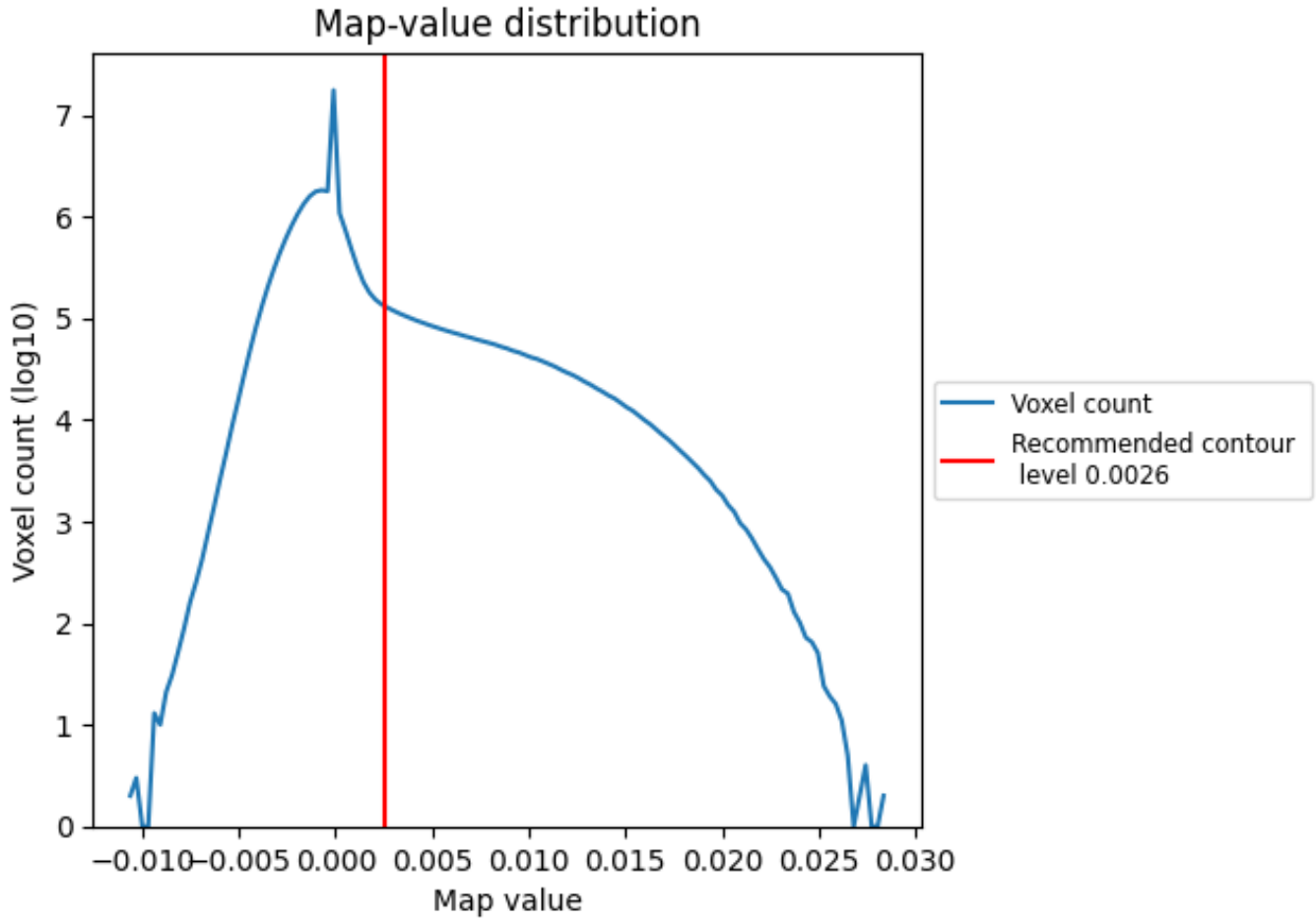
6.5 Mask visualisation (i)

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

7 Map analysis

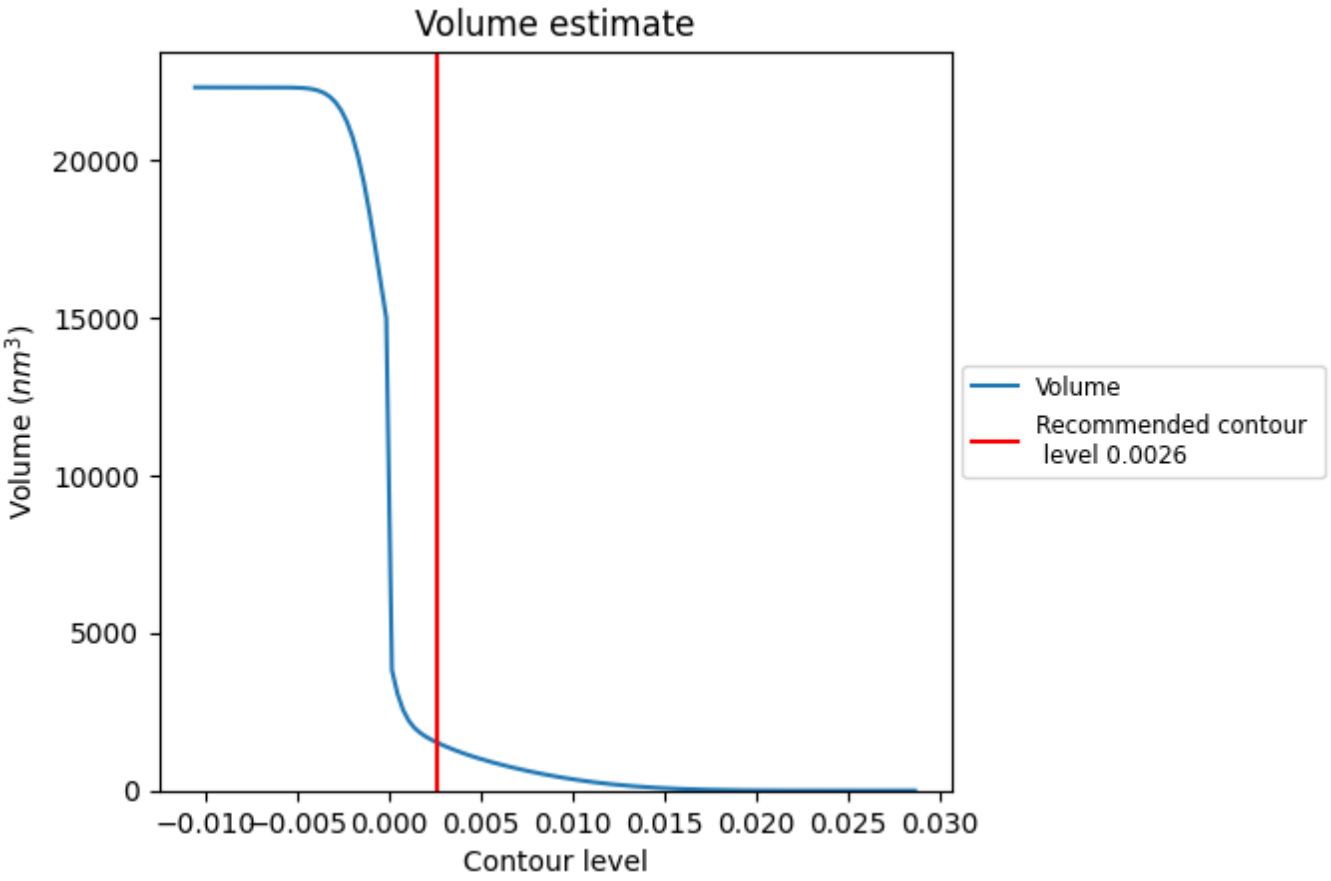
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

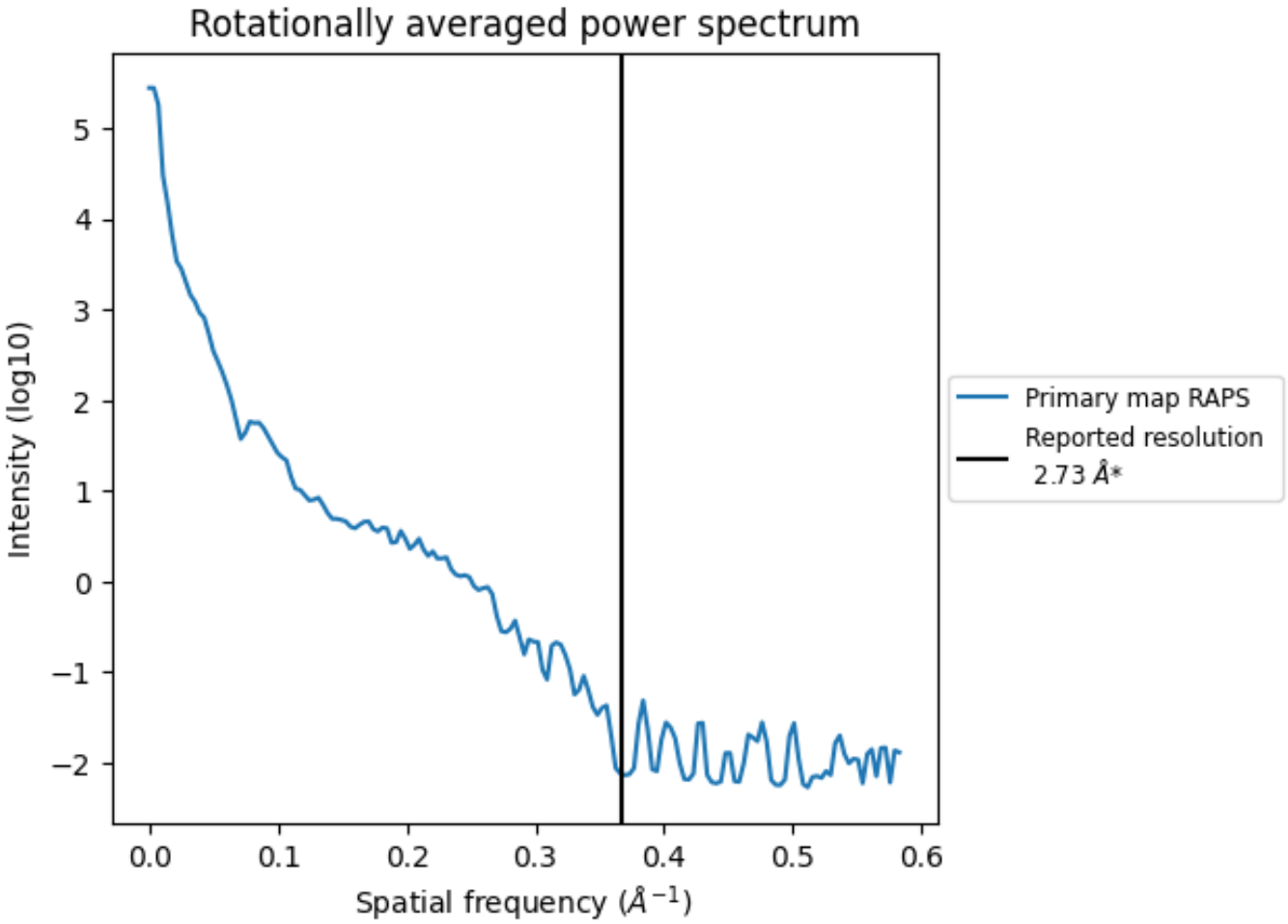
7.2 Volume estimate



The volume at the recommended contour level is 1520 nm^3; this corresponds to an approximate mass of 1373 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 (i)



*Reported resolution corresponds to spatial frequency of 0.366 Å^{-1}

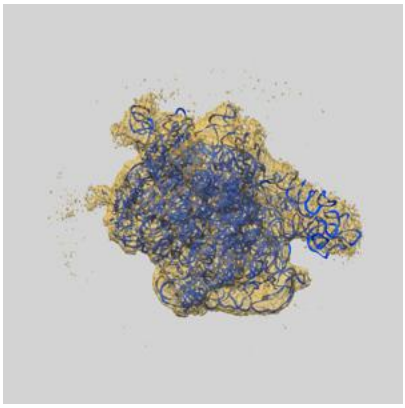
8 Fourier-Shell correlation

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

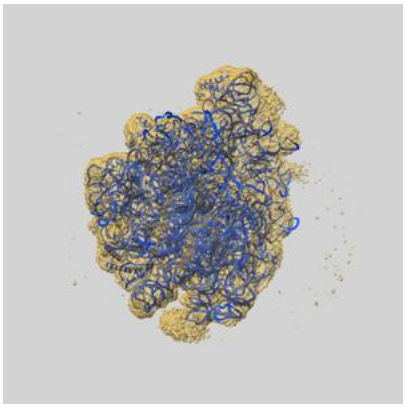
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-11901 and PDB model 7ASN. Per-residue inclusion information can be found in section 3 on page 8.

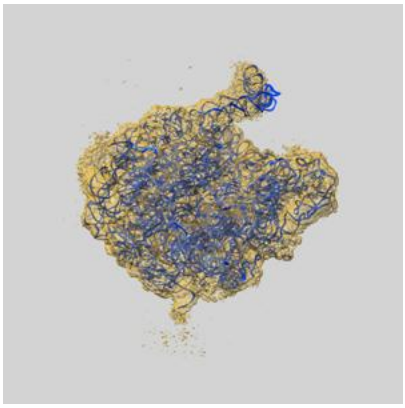
9.1 Map-model overlay



X



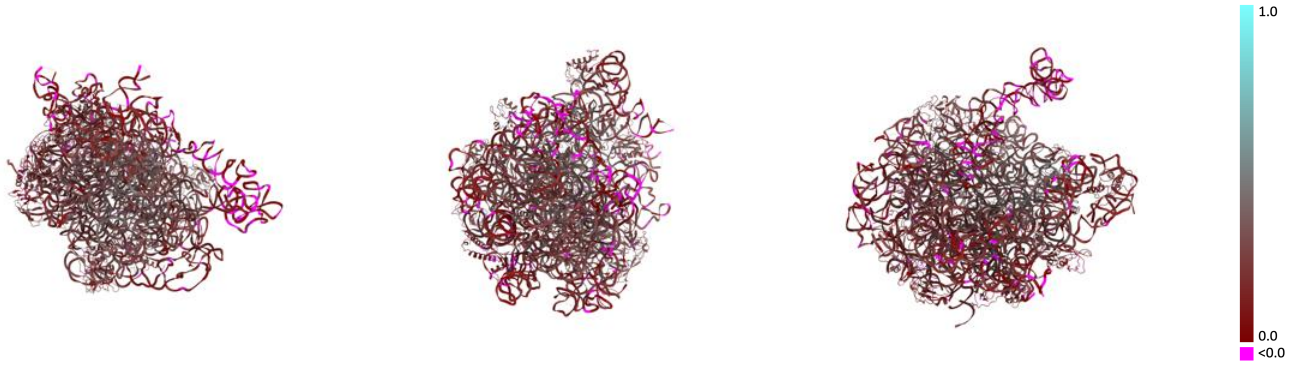
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0026 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.

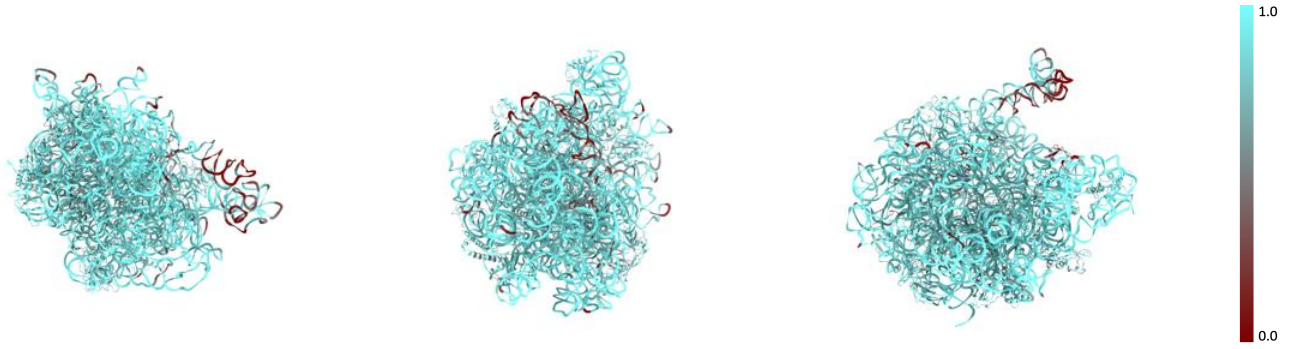
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

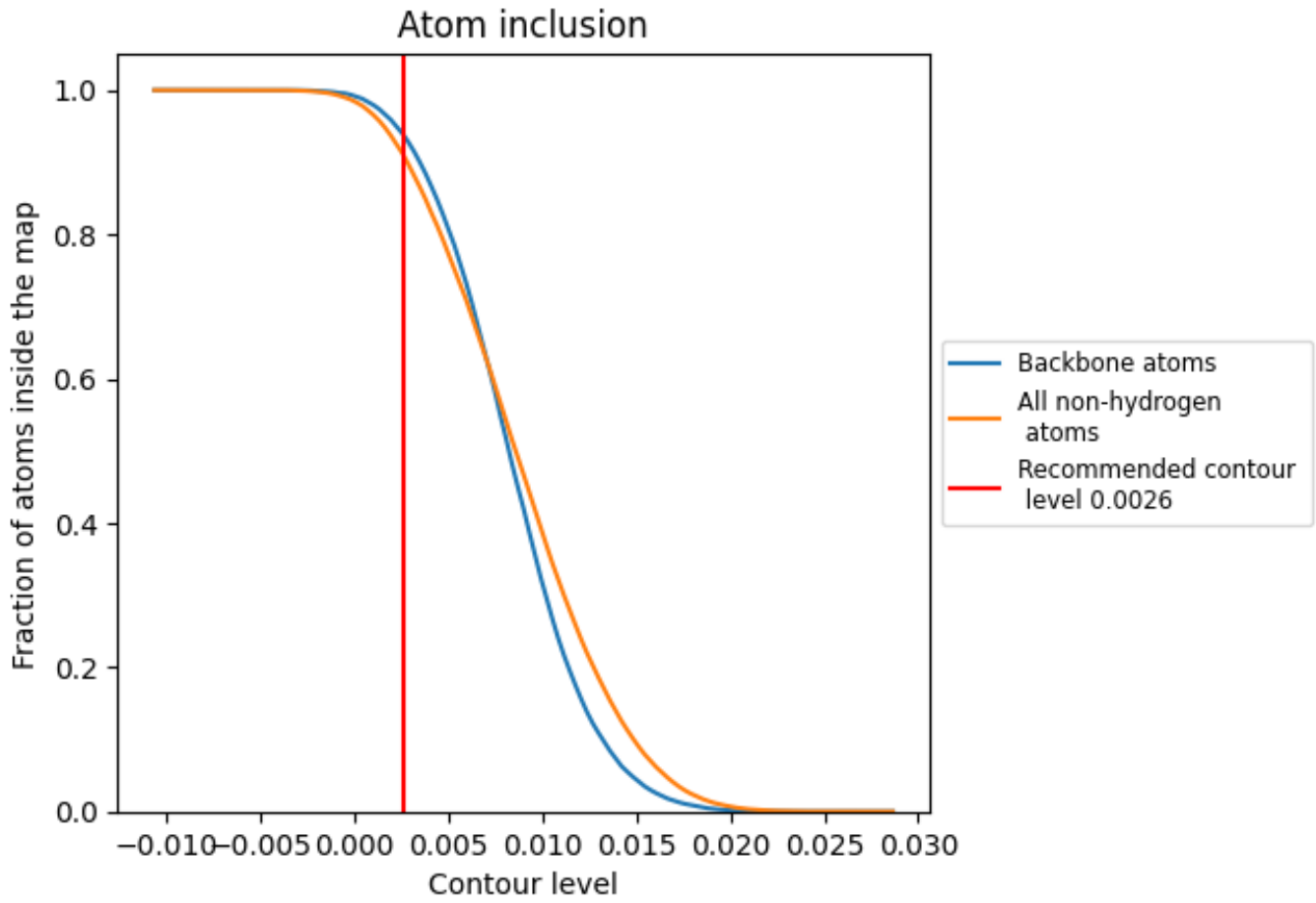
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0026).

9.4 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 91% 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 (0.0026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9116	0.2140
1	0.5333	0.1980
2	0.8092	0.2330
3	0.8645	0.2920
A	0.9334	0.2160
B	0.9850	0.1650
D	0.8366	0.1770
E	0.8877	0.2570
F	0.7900	0.2430
G	0.8559	0.2280
H	0.8285	0.1950
L	0.8881	0.2940
M	0.9235	0.2080
N	0.7812	0.1890
O	0.8306	0.2050
P	0.8676	0.2180
Q	0.8005	0.1710
R	0.8197	0.1170
S	0.8401	0.1490
T	0.7419	0.1570
V	0.8192	0.2360
W	0.8629	0.1370
X	0.8798	0.2830
Y	0.8825	0.2480
a	0.9273	0.3170
b	0.8098	0.1200