



Full wwPDB EM Validation Report ⓘ

Jun 21, 2026 – 09:19 am BST

PDB ID : 7AC7 / pdb_00007ac7
EMDB ID : EMD-11713
Title : Structure of accomodated trans-translation complex on E. Coli stalled ribosome.
Authors : Guyomar, C.; D'Urso, G.; Chat, S.; Giudice, E.; Gillet, R.
Deposited on : 2020-09-10
Resolution : 3.08 Å(reported)
Based on initial model : 4YBB

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

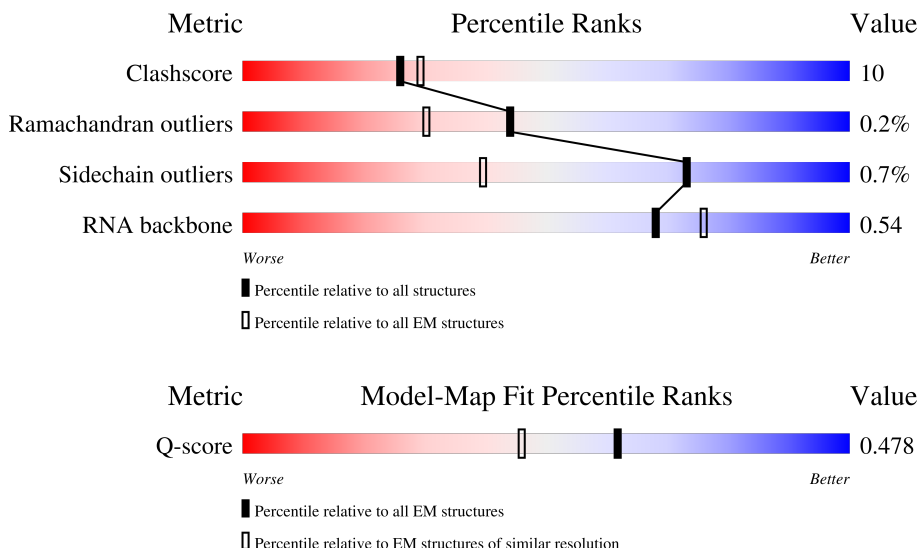
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.08 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



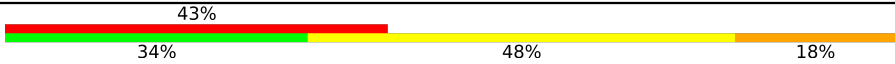
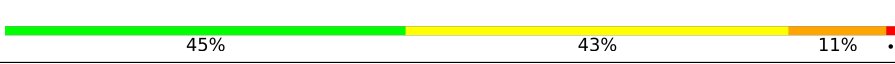
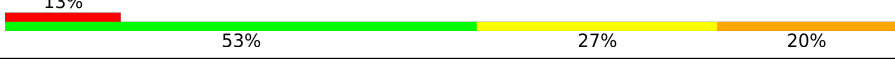
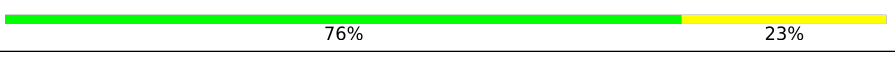
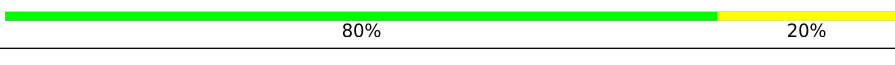
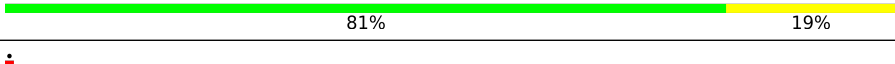
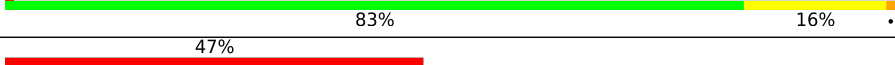
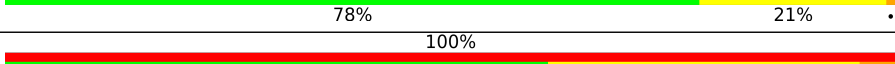
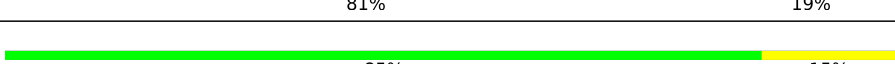
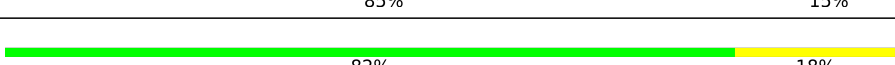
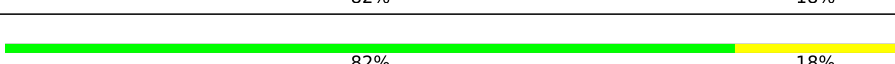
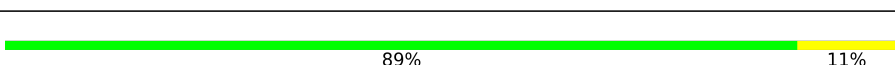
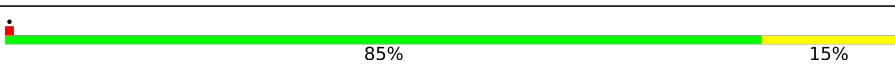
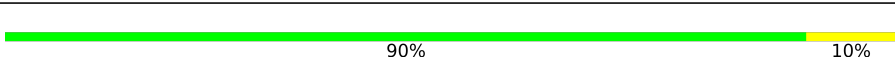
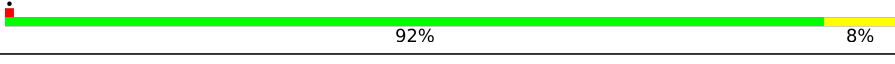
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14000 (2.58 - 3.58)

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

Mol	Chain	Length	Quality of chain
1	1	2903	
2	2	1540	
3	3	120	

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Mol	Chain	Length	Quality of chain
4	4	363	
5	5	147	
6	7	76	
7	8	15	
8	A	84	
9	B	271	
10	C	209	
11	D	201	
12	E	177	
13	F	175	
14	G	149	
15	H	130	
16	J	141	
17	K	123	
18	L	144	
19	M	136	
20	N	119	
21	O	115	
22	P	114	
23	Q	117	
24	R	103	
25	S	109	
26	T	94	
27	U	103	
28	V	94	

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Mol	Chain	Length	Quality of chain
29	W	2	100%
30	X	77	73% 27%
31	Y	58	72% 28%
32	Z	56	77% 23%
33	a	66	6% 79% 20% .
34	b	54	85% 15%
35	c	52	75% 25%
36	d	46	. 93% 7%
37	e	64	75% 22% . .
38	f	37	78% 22%
39	g	225	. 85% 15%
40	h	208	83% 17%
41	i	205	80% 20%
42	j	156	78% 22%
43	k	104	80% 20%
44	l	151	. 85% 15%
45	m	129	88% 12%
46	n	126	71% 28% .
47	o	99	68% 31% .
48	p	117	79% 21% .
49	q	123	. 76% 24%
50	r	115	78% 21% .
51	s	100	87% 13%
52	t	87	90% 10%
53	u	81	85% 14% .

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Mol	Chain	Length	Quality of chain
54	v	80	 90% 10%
55	w	65	 86% 14%
56	x	82	 71% 29%
57	y	85	 82% 18%
58	z	70	 10% 89% 11%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	3TD	1	1915	-	-	X	-

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 154883 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62336	27816	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1540	Total	C	N	O	P	0	0
			33049	14747	6057	10705	1540		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called transfer-messenger RNA (tmRNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	363	Total	C	N	O	P	0	0
			7759	3466	1410	2520	363		

- Molecule 5 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	147	Total	C	N	O	S	0	0
			1191	753	223	211	4		

- Molecule 6 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	7	76	Total	C	N	O	P	S	0	0
			1635	735	291	532	75	2		

- Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	8	15	Total	C	N	O	P	0	0
			324	145	60	105	14		

- Molecule 8 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 14 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 15 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	130	Total	C	N	O	S	0	0
			980	620	174	182	4		

- Molecule 16 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	141	Total	C	N	O	S	0	0
			1121	709	211	198	3		

- Molecule 17 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 19 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	136	Total	C	N	O	S	0	0
			1075	686	205	178	6		

- Molecule 20 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 21 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	O	115	Total	C	N	O	0	0
			884	548	177	159		

- Molecule 22 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 23 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 24 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 25 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	109	Total	C	N	O	S	0	0
			849	527	165	155	2		

- Molecule 26 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	U	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 28 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 29 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	W	2	Total	C	N	O	0	0
			16	12	2	2		

- Molecule 30 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	58	Total	C	N	O	S	0	0
			477	294	93	89	1		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	56	Total	C	N	O	S	0	0
			434	272	84	76	2		

- Molecule 33 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 34 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	54	Total	C	N	O	S	0	0
			429	260	91	77	1		

- Molecule 35 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 36 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 37 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 38 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	37	Total	C	N	O	S	0	0
			297	183	64	46	4		

- Molecule 39 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 40 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 41 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 42 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 43 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 44 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 45 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 46 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	126	Total	C	N	O	S	0	0
			1010	628	202	177	3		

- Molecule 47 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 48 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 49 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 50 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 51 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 52 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	87	Total	C	N	O	S	0	0
			708	436	143	128	1		

- Molecule 53 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 54 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 55 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 56 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 57 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

- Molecule 58 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	1	303	Total	Mg	0
			303	303	
59	2	118	Total	Mg	0
			118	118	
59	3	9	Total	Mg	0
			9	9	
59	7	1	Total	Mg	0
			1	1	
59	B	2	Total	Mg	0
			2	2	
59	C	1	Total	Mg	0
			1	1	
59	D	1	Total	Mg	0
			1	1	
59	L	1	Total	Mg	0
			1	1	
59	Q	2	Total	Mg	0
			2	2	
59	Z	1	Total	Mg	0
			1	1	
59	b	2	Total	Mg	0
			2	2	

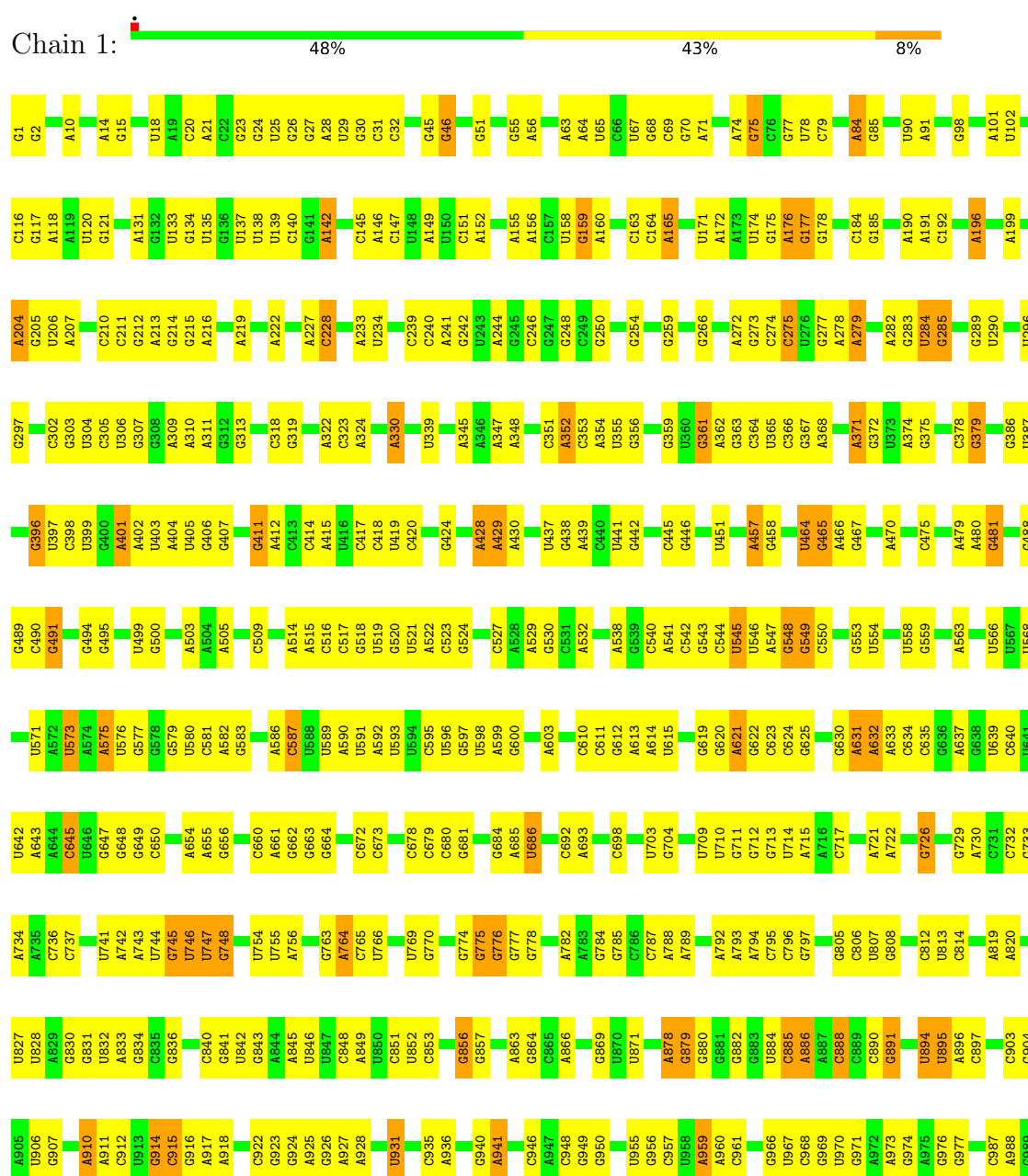
- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	a	1	Total 1	Zn 1	0
60	f	1	Total 1	Zn 1	0

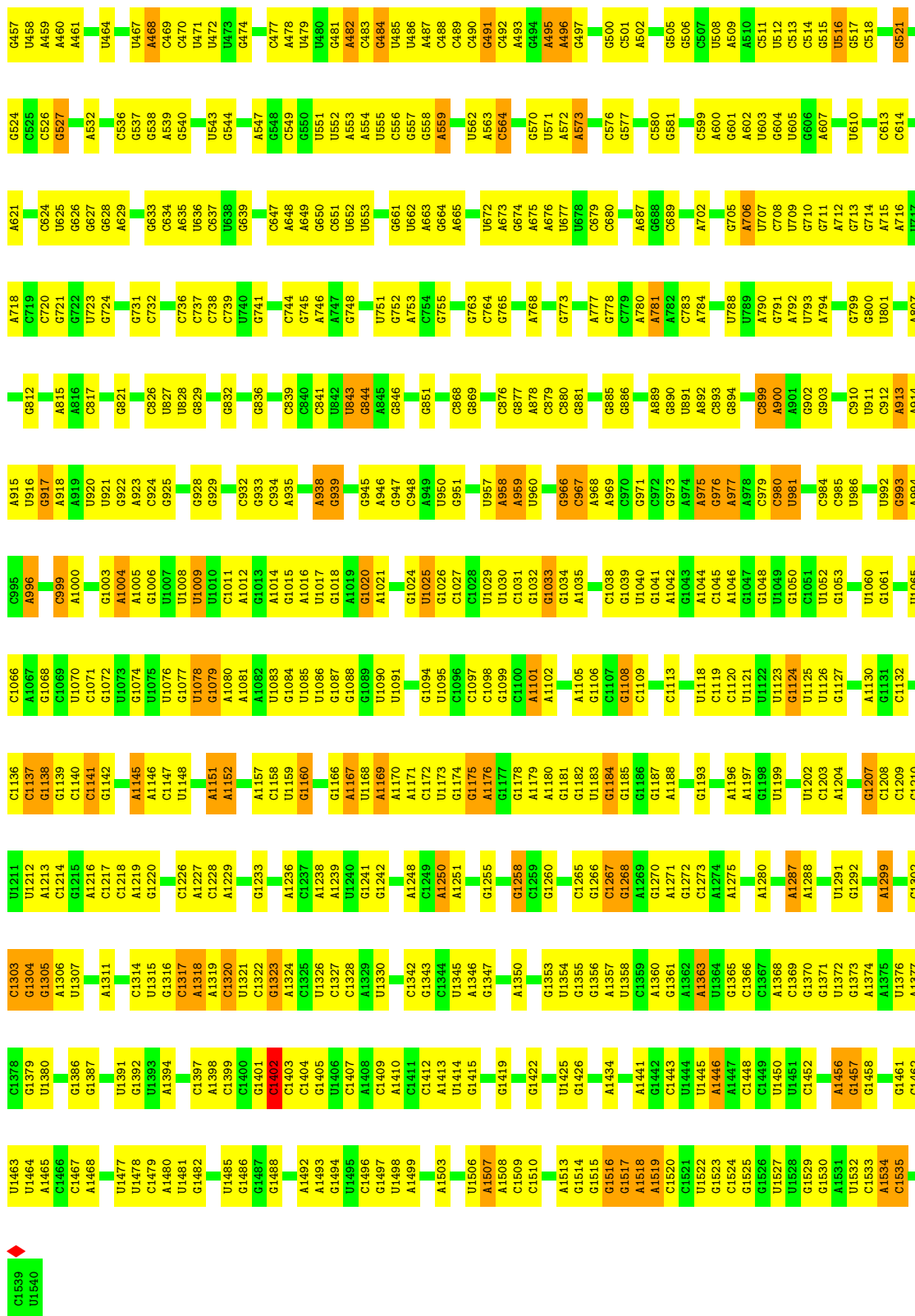
3 Residue-property plots

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

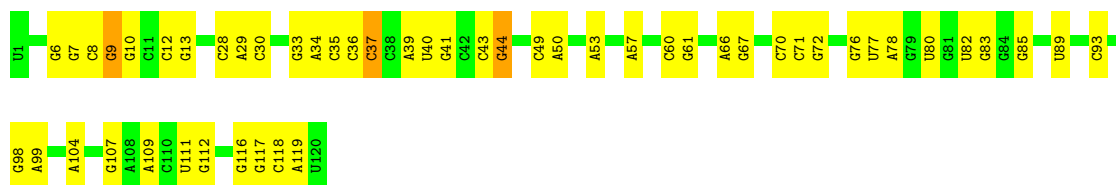


U2099	U2100	A2101	G2102	C2103	C2104	U2105	U2106	U2109	G2110	U2111	G2112	U2113	U2114	U2115	U2116	U2117	U2118	U2119	U2120	U2121	U2122	G2123	G2124	G2125	A2126	G2127	G2128	G2129	G2130	G2131	G2132	G2133	G2134	G2135	G2136	G2137	G2138	G2139	G2140	G2141	G2142	G2143	G2144	G2145	G2146	G2147	G2148	G2149	G2150	U2151	G2152	G2153	A2154	U2155	G2156	G2157	A2158	G2159																																																																																																																																																																																																																																																																																																																																																																																						
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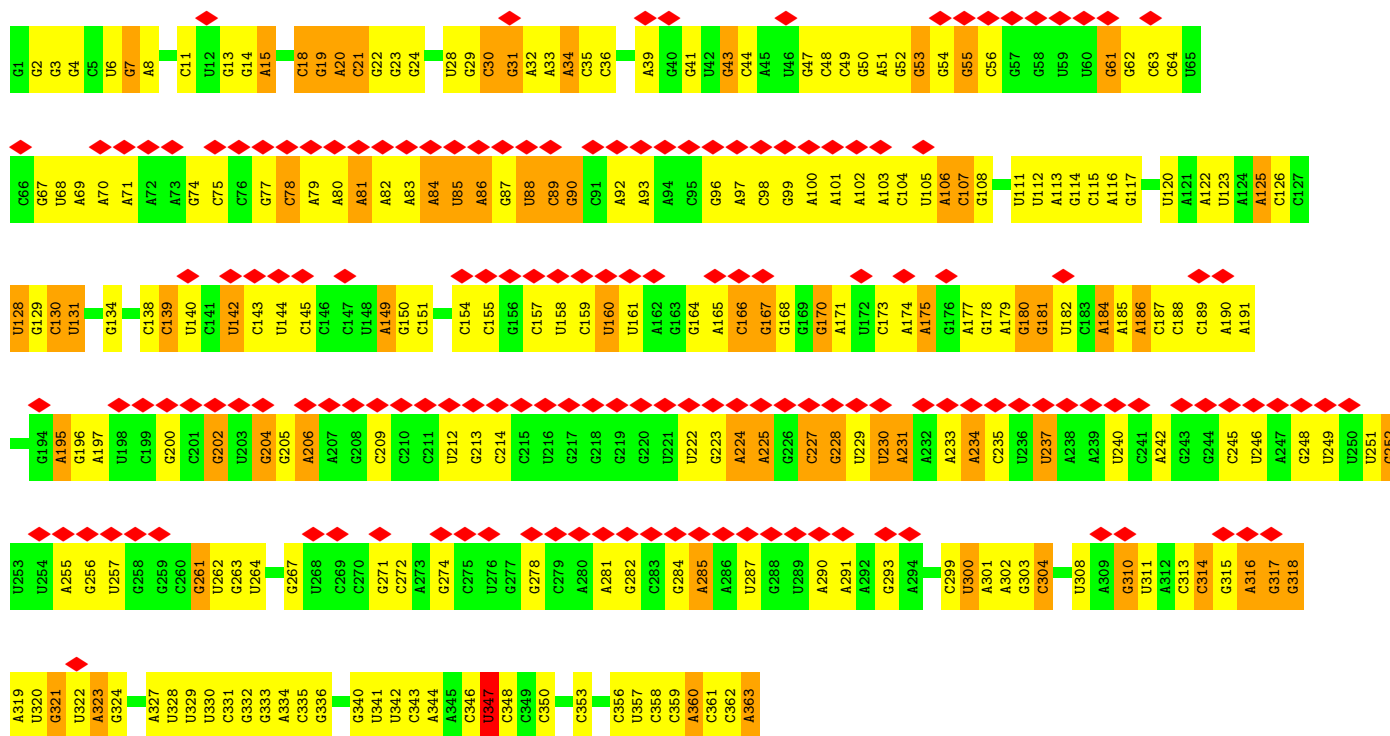


• Molecule 3: 5S ribosomal RNA

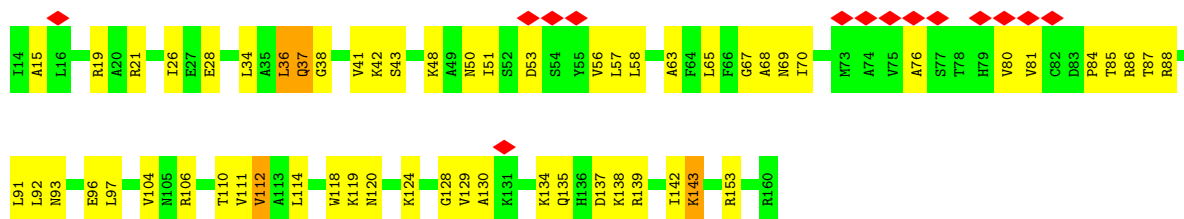
Chain 3: 58% 40%



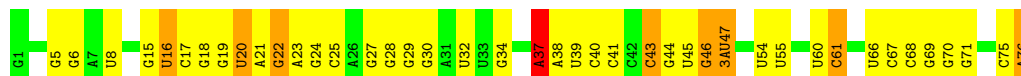
• Molecule 4: transfer-messenger RNA (tmRNA)



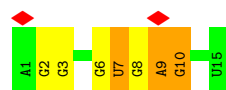
• Molecule 5: SsrA-binding protein



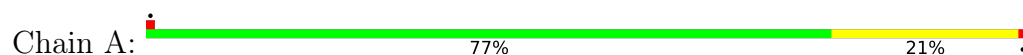
• Molecule 6: tRNA-Phe



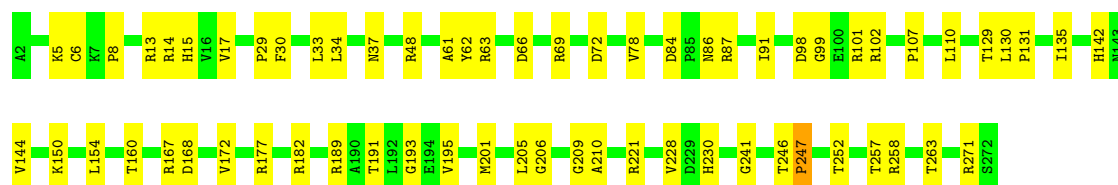
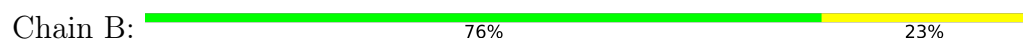
- Molecule 7: mRNA



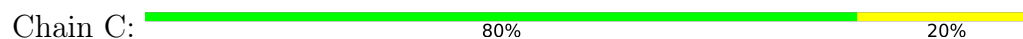
- Molecule 8: 50S ribosomal protein L27



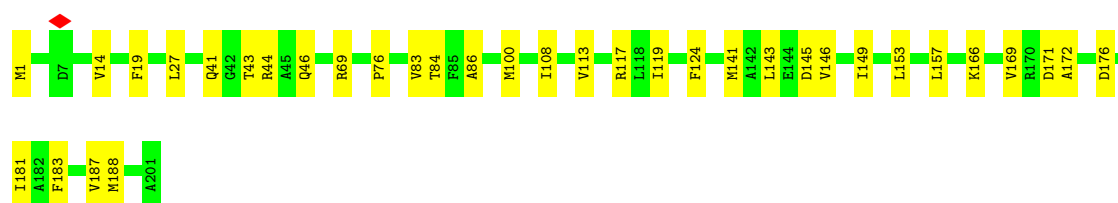
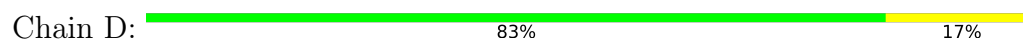
- Molecule 9: 50S ribosomal protein L2



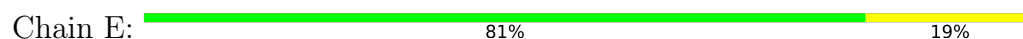
- Molecule 10: 50S ribosomal protein L3



- Molecule 11: 50S ribosomal protein L4



- Molecule 12: 50S ribosomal protein L5





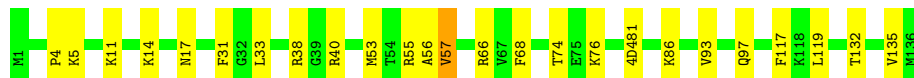
• Molecule 17: 50S ribosomal protein L14

Chain K:  81% 19%

• Molecule 18: 50S ribosomal protein L15

Chain L:  85% 15%

• Molecule 19: 50S ribosomal protein L16

Chain M:  82% 18%

• Molecule 20: 50S ribosomal protein L17

Chain N:  82% 18%

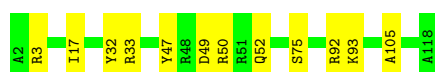
• Molecule 21: 50S ribosomal protein L18

Chain O:  89% 11%

• Molecule 22: 50S ribosomal protein L19

Chain P:  85% 15%

• Molecule 23: 50S ribosomal protein L20

Chain Q:  90% 10%

- Molecule 24: 50S ribosomal protein L21

Chain R:  79% 21%



- Molecule 25: 50S ribosomal protein L22

Chain S:  75% 25%



- Molecule 26: 50S ribosomal protein L23

Chain T:  82% 18%



- Molecule 27: 50S ribosomal protein L24

Chain U:  92% 8%



- Molecule 28: 50S ribosomal protein L25

Chain V:  84% 16%



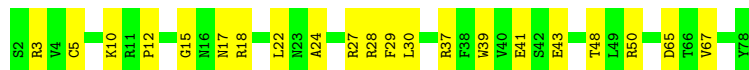
- Molecule 29: Nascent peptide

Chain W:  100%



- Molecule 30: 50S ribosomal protein L28

Chain X:  73% 27%



- Molecule 31: 50S ribosomal protein L29

Chain Y:  72% 28%



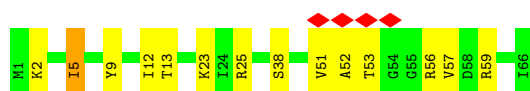
- Molecule 32: 50S ribosomal protein L30

Chain Z:  77% 23%



- Molecule 33: 50S ribosomal protein L31

Chain a:  6% 79% 20%



- Molecule 34: 50S ribosomal protein L32

Chain b:  85% 15%



- Molecule 35: 50S ribosomal protein L33

Chain c:  75% 25%



- Molecule 36: 50S ribosomal protein L34

Chain d:  93% 7%



- Molecule 37: 50S ribosomal protein L35

Chain e:  75% 22%



- Molecule 38: 50S ribosomal protein L36

Chain f:  78% 22%



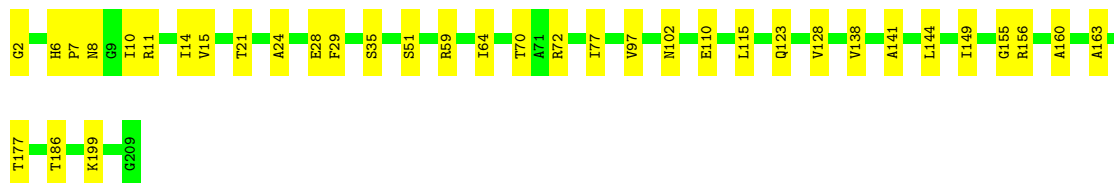
- Molecule 39: 30S ribosomal protein S2

Chain g:  85% 15%



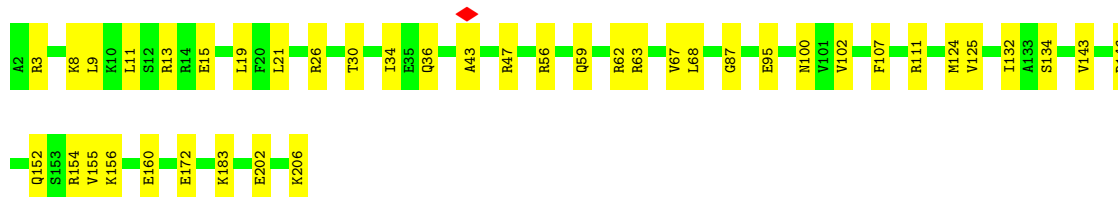
- Molecule 40: 30S ribosomal protein S3

Chain h:  83% 17%



- Molecule 41: 30S ribosomal protein S4

Chain i:  80% 20%



- Molecule 42: 30S ribosomal protein S5

Chain j:  78% 22%

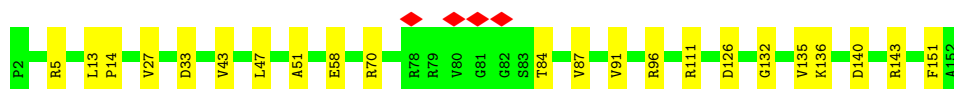
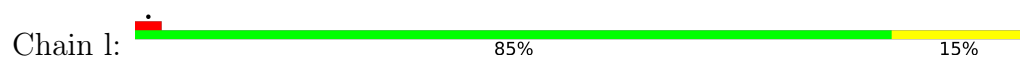


- Molecule 43: 30S ribosomal protein S6

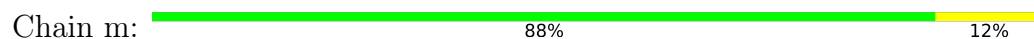
Chain k:  80% 20%



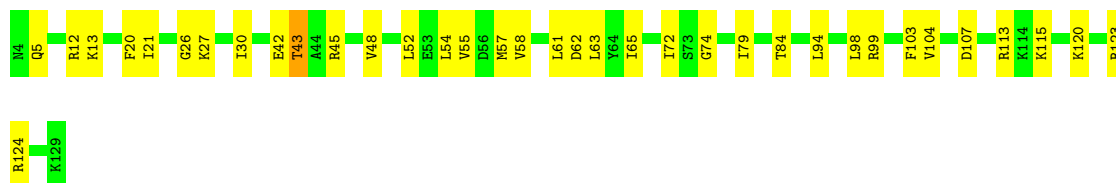
- Molecule 44: 30S ribosomal protein S7



- Molecule 45: 30S ribosomal protein S8



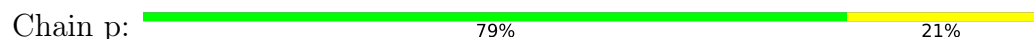
- Molecule 46: 30S ribosomal protein S9



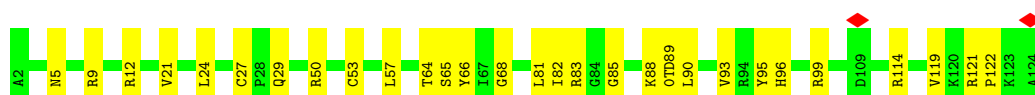
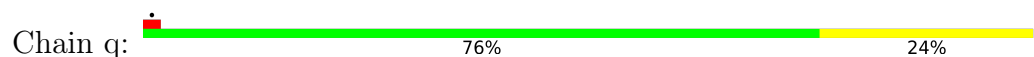
- Molecule 47: 30S ribosomal protein S10



- Molecule 48: 30S ribosomal protein S11



- Molecule 49: 30S ribosomal protein S12



- Molecule 50: 30S ribosomal protein S13

Chain r:  78% 21%



- Molecule 51: 30S ribosomal protein S14

Chain s:  87% 13%



- Molecule 52: 30S ribosomal protein S15

Chain t:  90% 10%



- Molecule 53: 30S ribosomal protein S16

Chain u:  85% 14%



- Molecule 54: 30S ribosomal protein S17

Chain v:  90% 10%



- Molecule 55: 30S ribosomal protein S18

Chain w:  86% 14%

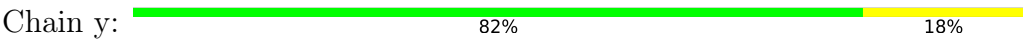


- Molecule 56: 30S ribosomal protein S19

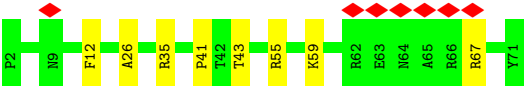
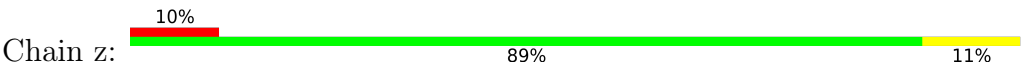
Chain x:  71% 29%



- Molecule 57: 30S ribosomal protein S20



• Molecule 58: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36069	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 ($e^-/\text{\AA}^2$)	29	Depositor
Minimum defocus (nm)	-700	Depositor
Maximum defocus (nm)	-2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	27.267	Depositor
Minimum map value	-12.720	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	499.20026, 499.20026, 499.20026	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0400006, 1.0400006, 1.0400006	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 1MG, OMC, OMU, MG, 3AU, MIA, 6MZ, 0TD, 5MU, 4SU, G7M, H2U, MA6, PSU, 4OC, UR3, OMG, 3TD, 2MG, 4D4, 5MC, ZN, 2MA

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	1	0.11	0/69286	0.23	1/108087 (0.0%)
2	2	0.10	0/36722	0.21	0/57278
3	3	0.07	0/2872	0.19	0/4478
4	4	0.18	1/8615 (0.0%)	0.38	4/13430 (0.0%)
5	5	0.40	0/1213	0.90	5/1630 (0.3%)
6	7	0.19	0/1580	0.27	0/2459
7	8	0.11	0/363	0.35	0/566
8	A	0.20	0/642	0.49	1/848 (0.1%)
9	B	0.18	1/2122 (0.0%)	0.37	0/2852
10	C	0.13	0/1586	0.36	0/2134
11	D	0.10	0/1571	0.32	0/2113
12	E	0.13	0/1435	0.40	1/1926 (0.1%)
13	F	0.28	1/1333 (0.1%)	0.48	2/1805 (0.1%)
14	G	0.28	1/1122 (0.1%)	0.54	4/1515 (0.3%)
15	H	0.38	0/993	0.80	0/1340
16	J	0.11	0/1144	0.33	0/1541
17	K	0.12	0/955	0.35	0/1279
18	L	0.11	0/1062	0.35	0/1413
19	M	0.13	0/1081	0.35	0/1443
20	N	0.13	0/964	0.36	0/1289
21	O	0.12	0/894	0.33	0/1198
22	P	0.13	0/929	0.40	0/1242
23	Q	0.12	0/960	0.36	0/1278
24	R	0.12	0/829	0.35	0/1107
25	S	0.12	0/856	0.40	0/1146
26	T	0.10	0/752	0.41	1/1005 (0.1%)
27	U	0.11	0/796	0.34	0/1062
28	V	0.11	0/766	0.34	0/1025
29	W	1.11	0/16	1.59	1/20 (5.0%)
30	X	0.16	0/635	0.59	3/848 (0.4%)
31	Y	0.10	0/478	0.33	0/637

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Z	0.12	0/438	0.34	0/587
33	a	0.13	0/531	0.49	2/709 (0.3%)
34	b	0.10	0/435	0.33	0/581
35	c	0.12	0/433	0.53	1/576 (0.2%)
36	d	0.14	0/380	0.47	0/498
37	e	0.34	1/513 (0.2%)	0.54	1/676 (0.1%)
38	f	0.12	0/298	0.41	0/392
39	g	0.12	0/1791	0.35	0/2413
40	h	0.15	0/1663	0.37	0/2241
41	i	0.11	0/1665	0.39	1/2227 (0.0%)
42	j	0.12	0/1165	0.40	0/1568
43	k	0.19	0/867	0.44	0/1171
44	l	0.11	0/1195	0.34	0/1602
45	m	0.12	0/989	0.39	0/1326
46	n	0.24	0/1022	0.55	1/1361 (0.1%)
47	o	0.14	0/800	0.42	0/1082
48	p	0.30	1/893 (0.1%)	0.41	1/1205 (0.1%)
49	q	0.13	0/960	0.42	0/1286
50	r	0.13	0/900	0.47	2/1204 (0.2%)
51	s	0.11	0/817	0.34	0/1088
52	t	0.10	0/716	0.35	0/956
53	u	0.13	0/653	0.46	1/877 (0.1%)
54	v	0.11	0/658	0.33	0/881
55	w	0.11	0/544	0.34	0/731
56	x	0.11	0/675	0.39	0/908
57	y	0.11	0/670	0.34	0/888
58	z	0.15	0/597	0.53	2/792 (0.3%)
All	All	0.13	6/166840 (0.0%)	0.30	35/249820 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	p	117	PRO	N-CD	-8.03	1.36	1.47
14	G	38	PRO	N-CD	-7.95	1.36	1.47
37	e	33	LEU	CA-C	7.11	1.62	1.52
13	F	12	PRO	N-CD	-6.63	1.38	1.47
4	4	363	A	C3'-O3'	5.99	1.51	1.42
9	B	247	PRO	N-CD	-5.76	1.39	1.47

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	5	112	VAL	N-CA-CB	-10.85	98.71	110.53
30	X	67	VAL	N-CA-C	9.41	120.22	110.62
13	F	9	VAL	N-CA-C	7.84	119.19	107.51
58	z	43	THR	N-CA-C	7.82	119.81	111.28
4	4	316	A	C2'-C3'-O3'	7.75	121.12	109.50
5	5	56	VAL	N-CA-C	7.17	118.36	108.89
5	5	142	ILE	N-CA-C	-6.92	105.09	111.67
46	n	43	THR	N-CA-C	-6.81	103.94	111.36
4	4	78	C	C2'-C3'-O3'	6.32	118.98	109.50
14	G	71	LYS	N-CA-C	-6.21	104.61	111.82
33	a	57	VAL	N-CA-C	6.20	116.37	110.42
12	E	148	ARG	N-CA-C	-6.15	100.18	108.86
35	c	33	LYS	N-CA-C	-6.11	102.90	110.41
30	X	65	ASP	N-CA-C	-6.04	104.77	111.36
4	4	314	C	C2'-C3'-O3'	5.96	118.44	109.50
14	G	91	PHE	N-CA-CB	-5.94	101.07	110.28
29	W	2	ALA	CA-C-O	-5.87	110.83	120.80
5	5	57	LEU	N-CA-CB	5.82	119.92	110.43
37	e	34	THR	N-CA-C	5.74	123.03	110.80
26	T	16	VAL	N-CA-C	5.61	115.94	107.80
41	i	87	GLY	N-CA-C	5.51	119.35	112.73
4	4	363	A	C2'-C3'-O3'	5.40	121.80	113.70
50	r	66	GLU	N-CA-C	5.39	117.85	111.33
50	r	70	ARG	N-CA-C	5.38	117.14	111.28
13	F	10	VAL	N-CA-CB	5.36	117.96	110.56
58	z	41	PRO	N-CA-C	-5.35	106.43	113.65
8	A	3	HIS	CA-C-O	-5.32	116.72	121.67
1	1	1070	A	C2'-C3'-O3'	5.25	117.37	109.50
5	5	112	VAL	N-CA-C	5.24	115.81	108.89
14	G	38	PRO	N-CA-CB	-5.17	98.71	103.31
48	p	117	PRO	CA-N-CD	5.15	119.21	112.00
30	X	67	VAL	N-CA-CB	-5.14	103.55	110.54
14	G	38	PRO	CA-N-CD	5.10	119.14	112.00
33	a	5	ILE	N-CA-C	-5.04	108.92	113.71
53	u	36	VAL	N-CA-C	5.01	113.98	106.42

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	62336	0	31369	1105	0
2	2	33049	0	16651	561	0
3	3	2569	0	1301	34	0
4	4	7759	0	3919	117	0
5	5	1191	0	1209	65	0
6	7	1635	0	848	26	0
7	8	324	0	162	5	0
8	A	634	0	653	12	0
9	B	2083	0	2154	62	0
10	C	1565	0	1616	31	0
11	D	1552	0	1619	22	0
12	E	1411	0	1444	22	0
13	F	1313	0	1358	25	0
14	G	1111	0	1148	38	0
15	H	980	0	1013	85	0
16	J	1121	0	1150	19	0
17	K	946	0	1023	18	0
18	L	1053	0	1129	17	0
19	M	1075	0	1154	18	0
20	N	951	0	994	15	0
21	O	884	0	919	11	0
22	P	917	0	962	16	0
23	Q	947	0	1019	12	0
24	R	816	0	839	15	0
25	S	849	0	910	19	0
26	T	746	0	811	11	0
27	U	788	0	844	8	0
28	V	753	0	780	12	0
29	W	16	0	16	13	0
30	X	625	0	652	13	0
31	Y	477	0	505	9	0
32	Z	434	0	470	8	0
33	a	522	0	520	27	0
34	b	429	0	440	10	0
35	c	426	0	464	8	0
36	d	377	0	418	3	0
37	e	504	0	572	19	0
38	f	297	0	338	5	0
39	g	1760	0	1787	20	0
40	h	1636	0	1710	27	0
41	i	1643	0	1707	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	j	1152	0	1196	22	0
43	k	848	0	846	28	0
44	l	1181	0	1238	13	0
45	m	979	0	1031	23	0
46	n	1010	0	1055	32	0
47	o	790	0	831	37	0
48	p	877	0	887	19	0
49	q	957	0	1017	27	0
50	r	891	0	952	31	0
51	s	805	0	844	9	0
52	t	708	0	729	6	0
53	u	643	0	661	9	0
54	v	649	0	691	5	0
55	w	535	0	552	6	0
56	x	658	0	683	36	0
57	y	664	0	714	14	0
58	z	589	0	629	8	0
59	1	303	0	0	0	0
59	2	118	0	0	0	0
59	3	9	0	0	0	0
59	7	1	0	0	0	0
59	B	2	0	0	0	0
59	C	1	0	0	0	0
59	D	1	0	0	0	0
59	L	1	0	0	0	0
59	Q	2	0	0	0	0
59	Z	1	0	0	0	0
59	b	2	0	0	0	0
60	a	1	0	0	0	0
60	f	1	0	0	0	0
All	All	154883	0	103153	2556	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 10.

All (2556) 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)
50:r:23:TYR:CE1	50:r:69:LEU:HD22	1.20	1.68
50:r:23:TYR:HE1	50:r:69:LEU:CD2	1.08	1.60
5:5:50:ASN:HB3	5:5:69:ASN:CG	1.25	1.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:246:THR:HG23	9:B:252:THR:CG2	1.47	1.44
1:1:1084:A:OP1	15:H:54:VAL:CG1	1.73	1.34
5:5:50:ASN:HB3	5:5:69:ASN:OD1	1.19	1.33
45:m:106:THR:HB	45:m:121:LEU:CD1	1.59	1.32
1:1:1083:U:O5'	15:H:41:LEU:HD13	1.25	1.28
5:5:50:ASN:CB	5:5:69:ASN:OD1	1.82	1.27
47:o:86:ALA:HA	47:o:89:ARG:CD	1.67	1.25
50:r:23:TYR:CE1	50:r:69:LEU:CD2	1.92	1.23
1:1:1915:3TD:O2'	5:5:48:LYS:HD2	1.36	1.21
50:r:23:TYR:CD1	50:r:69:LEU:HD22	1.76	1.19
13:F:9:VAL:CG1	13:F:50:LEU:HB2	1.71	1.19
43:k:18:VAL:CG2	43:k:19:PRO:HD3	1.74	1.17
1:1:1084:A:OP1	15:H:54:VAL:HG12	1.40	1.16
9:B:246:THR:CG2	9:B:252:THR:CG2	2.24	1.15
43:k:18:VAL:HG23	43:k:19:PRO:HD3	1.16	1.14
5:5:50:ASN:CB	5:5:69:ASN:CG	2.20	1.14
46:n:42:GLU:OE1	46:n:45:ARG:HD2	1.49	1.13
47:o:86:ALA:HA	47:o:89:ARG:CG	1.81	1.10
47:o:86:ALA:O	47:o:89:ARG:HG2	1.48	1.10
1:1:1107:G:OP1	15:H:57:ASN:HA	1.51	1.09
47:o:86:ALA:C	47:o:89:ARG:HG2	1.75	1.09
45:m:106:THR:HB	45:m:121:LEU:HD13	1.25	1.08
1:1:1046:A:H1'	15:H:61:ARG:O	1.52	1.07
50:r:65:VAL:HG12	50:r:66:GLU:H	1.18	1.07
1:1:2585:U:N3	29:W:1:PHE:CD2	2.23	1.06
56:x:12:ASP:CB	56:x:14:HIS:CE1	2.38	1.06
4:4:24:G:H1	4:4:329:U:H3	1.04	1.03
41:i:152:GLN:HB2	41:i:155:VAL:HG12	1.36	1.03
37:e:31:HIS:O	37:e:33:LEU:N	1.91	1.02
47:o:86:ALA:CA	47:o:89:ARG:HG2	1.89	1.02
1:1:1047:G:OP2	15:H:59:LEU:CD2	2.06	1.02
9:B:246:THR:CG2	9:B:252:THR:HG21	1.88	1.01
1:1:1915:3TD:O3'	5:5:48:LYS:HD3	1.61	1.00
41:i:152:GLN:HB2	41:i:155:VAL:CG1	1.90	1.00
1:1:1824:G:O2'	9:B:246:THR:HG22	1.62	1.00
5:5:51:ILE:N	5:5:69:ASN:HD21	1.60	0.99
1:1:2585:U:H3	29:W:1:PHE:HD2	1.08	0.99
45:m:106:THR:CB	45:m:121:LEU:CD1	2.40	0.99
14:G:90:LEU:HD21	14:G:124:THR:H	1.28	0.98
33:a:56:ARG:NH2	33:a:59:ARG:NH2	2.10	0.98
1:1:1107:G:C1'	15:H:81:LEU:HD12	1.92	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:o:86:ALA:HA	47:o:89:ARG:HG2	1.42	0.98
56:x:12:ASP:HB3	56:x:14:HIS:CE1	1.99	0.98
1:1:1082:U:O2'	15:H:37:LYS:HG2	1.62	0.97
45:m:106:THR:CB	45:m:121:LEU:HD11	1.94	0.97
5:5:50:ASN:HB3	5:5:69:ASN:ND2	1.78	0.96
45:m:106:THR:HB	45:m:121:LEU:HD11	1.44	0.96
1:1:1083:U:O5'	15:H:41:LEU:CD1	2.14	0.95
9:B:246:THR:HG23	9:B:252:THR:HG23	1.44	0.95
9:B:130:LEU:HD11	9:B:135:ILE:HG13	1.47	0.94
14:G:70:GLU:OE2	14:G:138:VAL:CG1	2.15	0.94
1:1:1107:G:O4'	15:H:81:LEU:HD12	1.68	0.93
43:k:64:VAL:HG12	43:k:66:ALA:H	1.34	0.93
9:B:246:THR:HG23	9:B:252:THR:HG21	1.44	0.92
1:1:1047:G:OP2	15:H:59:LEU:HD22	1.66	0.92
1:1:1050:A:C2	1:1:2751:G:C5	2.58	0.92
1:1:1050:A:C2	1:1:2751:G:C4	2.57	0.91
1:1:1046:A:C1'	15:H:61:ARG:O	2.18	0.91
9:B:246:THR:HG23	9:B:252:THR:HG22	1.52	0.91
1:1:196:A:H61	1:1:831:G:H21	1.17	0.91
47:o:86:ALA:O	47:o:89:ARG:CG	2.19	0.90
1:1:1915:3TD:H4'	5:5:48:LYS:HB2	1.52	0.90
9:B:130:LEU:CD1	9:B:135:ILE:HG13	2.02	0.90
43:k:18:VAL:HG23	43:k:19:PRO:CD	2.01	0.90
1:1:1046:A:OP2	15:H:61:ARG:CG	2.20	0.90
50:r:65:VAL:HG12	50:r:66:GLU:N	1.87	0.89
6:7:76:A:O3'	29:W:1:PHE:O	1.88	0.89
14:G:90:LEU:CD2	14:G:124:THR:N	2.36	0.89
5:5:51:ILE:H	5:5:69:ASN:HD21	1.15	0.89
14:G:37:VAL:HG22	14:G:38:PRO:HD2	1.55	0.89
33:a:56:ARG:NH2	33:a:59:ARG:HH22	1.71	0.88
5:5:67:GLY:O	5:5:85:THR:CG2	2.20	0.88
47:o:10:LEU:HG	47:o:98:VAL:HG12	1.53	0.88
1:1:1107:G:H4'	15:H:81:LEU:CG	2.03	0.88
33:a:56:ARG:CZ	33:a:59:ARG:NH2	2.37	0.88
50:r:23:TYR:CE1	50:r:69:LEU:HD21	2.09	0.88
14:G:90:LEU:HD21	14:G:124:THR:N	1.88	0.87
41:i:152:GLN:CB	41:i:155:VAL:HG12	2.04	0.87
1:1:1046:A:OP2	15:H:61:ARG:HG3	1.75	0.87
50:r:65:VAL:CG1	50:r:66:GLU:H	1.87	0.86
1:1:2585:U:O2	29:W:1:PHE:CG	2.29	0.86
2:2:765:G:H1	2:2:812:G:HO2'	0.90	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1107:G:H4'	15:H:81:LEU:HG	1.58	0.85
5:5:86:ARG:HG3	5:5:87:THR:H	1.42	0.85
1:1:1107:G:C4'	15:H:81:LEU:HD12	2.06	0.85
1:1:2451:A:N3	29:W:2:ALA:HB2	1.91	0.85
13:F:9:VAL:HG11	13:F:50:LEU:HB2	1.59	0.85
1:1:1084:A:OP1	15:H:54:VAL:HG13	1.77	0.85
9:B:130:LEU:HD11	9:B:135:ILE:CG1	2.05	0.85
13:F:9:VAL:HG13	13:F:50:LEU:HB2	1.57	0.84
1:1:1047:G:OP2	15:H:62:ARG:NH2	2.11	0.83
47:o:86:ALA:HA	47:o:89:ARG:HD2	1.59	0.83
1:1:1084:A:P	15:H:54:VAL:HG12	2.19	0.83
12:E:135:GLN:HE22	12:E:149:VAL:HA	1.45	0.81
43:k:64:VAL:HG12	43:k:66:ALA:N	1.95	0.81
27:U:98:SER:O	27:U:99:ASN:OD1	1.98	0.81
37:e:31:HIS:C	37:e:33:LEU:H	1.88	0.81
2:2:1086:U:H3	2:2:1099:G:H22	1.26	0.81
14:G:37:VAL:CG2	14:G:38:PRO:HD2	2.10	0.81
14:G:90:LEU:HD23	14:G:124:THR:C	2.06	0.81
1:1:1915:3TD:O3'	5:5:48:LYS:CD	2.29	0.80
27:U:98:SER:O	27:U:99:ASN:CG	2.25	0.80
2:2:319:G:H1	2:2:334:C:H42	1.26	0.80
22:P:27:GLU:HB3	22:P:85:SER:OG	1.82	0.80
1:1:1085:A:H61	15:H:34:THR:HG22	1.46	0.80
1:1:2585:U:O2	29:W:1:PHE:CB	2.30	0.80
1:1:1082:U:O2'	15:H:37:LYS:CG	2.31	0.79
56:x:12:ASP:OD2	56:x:14:HIS:HE1	1.64	0.79
1:1:1057:A:O2'	15:H:37:LYS:NZ	2.16	0.79
56:x:12:ASP:HB2	56:x:14:HIS:CE1	2.16	0.79
2:2:1412:C:H42	2:2:1488:G:H1	1.31	0.79
5:5:67:GLY:O	5:5:85:THR:HG22	1.82	0.78
47:o:86:ALA:HA	47:o:89:ARG:HD3	1.65	0.78
14:G:70:GLU:OE2	14:G:138:VAL:HG12	1.82	0.78
50:r:23:TYR:HE1	50:r:69:LEU:HD23	1.39	0.78
40:h:110:GLU:HB2	40:h:144:LEU:CD1	2.13	0.78
49:q:50:ARG:HG3	49:q:90:LEU:HD11	1.65	0.78
14:G:90:LEU:HD12	14:G:90:LEU:O	1.84	0.78
56:x:12:ASP:CB	56:x:14:HIS:HE1	1.96	0.78
33:a:56:ARG:HH11	56:x:68:GLY:CA	1.98	0.77
43:k:97:THR:HG22	43:k:97:THR:O	1.83	0.77
47:o:86:ALA:CA	47:o:89:ARG:CD	2.58	0.77
14:G:70:GLU:HG3	14:G:140:ALA:HB2	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1239:A:H61	2:2:1299:A:H61	1.30	0.77
14:G:90:LEU:HD21	14:G:122:LEU:O	1.86	0.76
47:o:6:ILE:CG2	47:o:76:ILE:HB	2.15	0.76
1:1:475:C:O2	1:1:479:A:N6	2.19	0.76
1:1:2585:U:O2	29:W:1:PHE:HB2	1.84	0.76
22:P:33:VAL:HG12	22:P:38:LYS:HG2	1.68	0.76
1:1:1483:G:H1	1:1:1506:U:H3	1.32	0.76
4:4:47:G:H21	4:4:48:C:H41	1.32	0.76
33:a:56:ARG:NH1	56:x:68:GLY:CA	2.50	0.75
15:H:87:GLU:HG2	15:H:95:LEU:HD12	1.66	0.75
1:1:196:A:H61	1:1:831:G:N2	1.84	0.75
14:G:125:THR:HG23	14:G:125:THR:O	1.86	0.74
1:1:2304:G:H22	1:1:2312:U:H3	1.35	0.74
33:a:56:ARG:NH1	56:x:68:GLY:HA3	2.03	0.74
3:3:30:C:H1'	3:3:57:A:H61	1.53	0.73
1:1:1070:A:H2'	1:1:1097:U:H4'	1.69	0.73
1:1:196:A:N6	1:1:831:G:H21	1.86	0.73
5:5:51:ILE:N	5:5:69:ASN:ND2	2.36	0.73
2:2:673:A:H2'	2:2:674:G:C8	2.24	0.72
33:a:56:ARG:HH22	33:a:59:ARG:HH22	1.37	0.72
1:1:1050:A:H2	1:1:2751:G:C4	2.07	0.72
2:2:744:C:H2'	2:2:745:G:H8	1.53	0.72
1:1:1047:G:P	15:H:62:ARG:HH21	2.12	0.72
43:k:18:VAL:CG2	43:k:19:PRO:CD	2.63	0.72
6:7:15:G:H2'	6:7:16:H2U:H62	1.70	0.72
14:G:72:ILE:HD13	14:G:108:VAL:HG22	1.70	0.72
40:h:21:THR:O	40:h:21:THR:HG22	1.89	0.72
56:x:12:ASP:HB3	56:x:14:HIS:ND1	2.05	0.72
1:1:2419:U:OP2	37:e:33:LEU:HD13	1.90	0.71
5:5:19:ARG:HD3	5:5:53:ASP:HB3	1.70	0.71
1:1:1054:A:H4'	15:H:31:ARG:HA	1.71	0.71
1:1:2585:U:C2	29:W:1:PHE:CD2	2.78	0.71
1:1:2482:A:HO2'	4:4:350:C:HO2'	1.34	0.71
2:2:297:G:N2	2:2:300:A:OP2	2.24	0.71
5:5:67:GLY:O	5:5:85:THR:HG21	1.89	0.71
4:4:49:C:N4	4:4:304:C:OP2	2.24	0.71
4:4:89:C:H2'	4:4:90:G:C8	2.25	0.71
9:B:29:PRO:HG2	9:B:34:LEU:HD11	1.72	0.71
2:2:61:G:N7	57:y:6:SER:OG	2.23	0.70
1:1:1107:G:OP1	15:H:57:ASN:CA	2.34	0.70
37:e:29:LEU:HA	37:e:33:LEU:HD21	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:568:U:H1'	1:1:2030:6MZ:H9C1	1.73	0.70
41:i:152:GLN:O	41:i:155:VAL:HG12	1.91	0.70
1:1:1047:G:OP2	15:H:59:LEU:HD23	1.90	0.70
1:1:2233:U:H2'	1:1:2234:G:H8	1.56	0.70
1:1:2451:A:C2	29:W:2:ALA:HB2	2.26	0.70
1:1:2100:G:H22	1:1:2190:G:H1	1.37	0.70
2:2:21:G:H5'	2:2:573:A:H61	1.57	0.70
47:o:5:ARG:N	47:o:76:ILE:O	2.25	0.70
1:1:832:U:H2'	1:1:833:A:H8	1.56	0.70
1:1:1927:A:H2'	1:1:1928:A:C8	2.26	0.70
9:B:246:THR:CG2	9:B:252:THR:HG22	2.11	0.70
40:h:110:GLU:HB2	40:h:144:LEU:HD12	1.74	0.69
4:4:334:A:C8	5:5:36:LEU:HB2	2.26	0.69
1:1:175:G:H2'	1:1:176:A:C8	2.27	0.69
1:1:2659:G:N2	1:1:2662:A:OP2	2.25	0.69
14:G:30:LEU:HB3	14:G:36:ALA:HB3	1.74	0.69
1:1:2618:G:H21	10:C:155:VAL:HG21	1.58	0.69
2:2:1409:C:H2'	2:2:1410:A:H8	1.57	0.69
22:P:106:LYS:O	22:P:109:ARG:NH2	2.25	0.69
1:1:1915:3TD:H4'	5:5:48:LYS:CB	2.22	0.69
4:4:142:U:C4	4:4:175:A:N1	2.61	0.69
2:2:501:C:OP1	49:q:114:ARG:NH2	2.25	0.69
5:5:92:LEU:HB3	5:5:97:LEU:HD12	1.75	0.69
1:1:2419:U:OP2	37:e:33:LEU:CD1	2.41	0.69
12:E:16:LEU:HD23	12:E:29:PRO:HD2	1.75	0.69
1:1:1085:A:N6	15:H:34:THR:HG22	2.08	0.68
22:P:60:THR:HG22	22:P:73:VAL:HG22	1.75	0.68
1:1:2368:C:H2'	1:1:2369:A:H8	1.58	0.68
3:3:43:C:O2	12:E:92:ARG:NH2	2.27	0.68
4:4:184:A:N3	4:4:185:A:N6	2.41	0.68
5:5:36:LEU:HA	5:5:86:ARG:NH2	2.09	0.68
5:5:119:LYS:HD3	5:5:124:LYS:HG3	1.76	0.68
1:1:2595:G:N2	1:1:2598:A:OP2	2.25	0.68
14:G:90:LEU:CD2	14:G:124:THR:H	1.96	0.68
1:1:1107:G:O2'	15:H:81:LEU:HB2	1.93	0.68
1:1:1386:C:H2'	1:1:1387:A:H8	1.58	0.68
9:B:144:VAL:HB	9:B:154:LEU:HB2	1.75	0.68
9:B:246:THR:HG22	9:B:252:THR:HG21	1.72	0.68
56:x:45:ILE:HA	56:x:62:VAL:HG13	1.76	0.68
2:2:664:G:H22	2:2:741:G:H1	1.42	0.68
43:k:43:GLY:H	43:k:58:HIS:CD2	2.11	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:674:G:H2'	2:2:675:A:H8	1.59	0.68
14:G:12:LEU:HD13	14:G:19:VAL:HG21	1.76	0.68
2:2:718:A:O2'	58:z:35:ARG:NH2	2.26	0.68
25:S:48:LYS:NZ	25:S:52:GLU:OE2	2.25	0.68
1:1:2400:G:H1	1:1:2416:C:H42	1.40	0.68
3:3:37:C:O2	21:O:100:HIS:NE2	2.27	0.67
33:a:56:ARG:CZ	33:a:59:ARG:HH22	2.03	0.67
46:n:21:ILE:HD13	46:n:63:LEU:HB3	1.75	0.67
2:2:166:U:H2'	2:2:167:A:H8	1.58	0.67
2:2:673:A:H2'	2:2:674:G:H8	1.58	0.67
2:2:1497:G:H1'	2:2:1518:MA6:H2	1.76	0.67
45:m:11:LEU:HD22	45:m:75:ILE:HD11	1.76	0.67
38:f:14:CYS:SG	38:f:27:CYS:HB2	2.33	0.67
1:1:575:A:OP2	1:1:2499:C:O2'	2.13	0.67
1:1:1432:G:H2'	1:1:1433:A:H8	1.59	0.67
1:1:2285:C:OP2	35:c:6:ARG:NH1	2.27	0.67
43:k:18:VAL:HG22	43:k:19:PRO:HD3	1.70	0.67
1:1:2258:C:O2'	1:1:2427:C:OP2	2.13	0.67
1:1:1433:A:H61	1:1:1560:G:H1	1.41	0.67
1:1:1462:C:O2'	1:1:2702:G:O2'	2.11	0.67
1:1:2126:A:H61	1:1:2162:G:H1'	1.60	0.67
1:1:210:C:OP1	36:d:29:GLN:NE2	2.27	0.66
1:1:1084:A:OP1	15:H:54:VAL:HG11	1.87	0.66
2:2:1071:C:H2'	2:2:1072:G:H8	1.60	0.66
56:x:51:VAL:HG11	56:x:71:LEU:HD21	1.76	0.66
1:1:542:C:H2'	1:1:543:G:C8	2.30	0.66
2:2:1522:U:H2'	2:2:1523:G:H8	1.61	0.66
2:2:946:A:H2'	2:2:947:G:H8	1.61	0.66
5:5:86:ARG:CG	5:5:87:THR:H	2.09	0.66
56:x:12:ASP:CG	56:x:14:HIS:HE1	2.04	0.66
1:1:2683:C:O2	17:K:70:ARG:NH2	2.29	0.66
26:T:9:LYS:O	26:T:12:ARG:NH2	2.29	0.66
2:2:1218:C:H2'	2:2:1219:A:H8	1.61	0.66
1:1:1107:G:C4'	15:H:81:LEU:CD1	2.74	0.66
9:B:129:THR:HG22	9:B:191:THR:HG22	1.78	0.65
14:G:66:ASN:HA	14:G:138:VAL:HG11	1.78	0.65
4:4:142:U:O2'	4:4:177:A:N6	2.30	0.65
17:K:7:MET:HG2	17:K:18:ARG:HH11	1.60	0.65
10:C:11:MET:HG2	10:C:25:THR:HG22	1.77	0.65
42:j:142:ASP:O	42:j:146:ASN:ND2	2.30	0.65
1:1:581:C:H2'	1:1:582:A:H8	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:143:A:H2	2:2:220:G:H1	1.43	0.65
1:1:2250:G:O2'	1:1:2496:C:OP1	2.13	0.65
14:G:90:LEU:HD23	14:G:124:THR:N	2.10	0.65
2:2:1027:C:H5	2:2:1034:G:H1	1.43	0.65
2:2:1126:U:OP1	47:o:7:ARG:NH1	2.30	0.65
2:2:1270:G:H2'	2:2:1271:A:H8	1.62	0.65
5:5:50:ASN:HB2	5:5:69:ASN:OD1	1.90	0.65
5:5:65:LEU:HG	5:5:67:GLY:H	1.62	0.65
14:G:70:GLU:OE2	14:G:138:VAL:HG13	1.95	0.65
5:5:28:GLU:H	5:5:129:VAL:HG22	1.62	0.64
20:N:99:LYS:HB3	34:b:42:HIS:CD2	2.32	0.64
20:N:103:ARG:O	20:N:107:ASN:HA	1.97	0.64
1:1:1107:G:O4'	15:H:81:LEU:CD1	2.45	0.64
9:B:258:ARG:NH2	9:B:263:THR:OG1	2.30	0.64
1:1:2581:G:N2	1:1:2581:G:OP2	2.31	0.64
20:N:56:LYS:HE3	20:N:88:ALA:HA	1.79	0.64
1:1:1518:C:H2'	1:1:1519:G:H8	1.62	0.64
1:1:1687:G:N2	1:1:1702:G:O6	2.30	0.64
1:1:2692:G:H1'	1:1:2847:U:H1'	1.79	0.64
2:2:902:G:H2'	2:2:903:G:H8	1.63	0.64
2:2:1183:U:O2'	2:2:1185:G:OP2	2.14	0.64
2:2:957:U:H2'	2:2:958:A:H3'	1.79	0.64
1:1:1666:G:H4'	17:K:6:THR:HG23	1.79	0.64
33:a:56:ARG:HH11	56:x:68:GLY:N	1.96	0.64
1:1:275:C:N3	1:1:362:A:N6	2.46	0.64
1:1:820:A:H4'	1:1:836:G:H22	1.62	0.64
2:2:626:G:OP1	53:u:35:ARG:NH2	2.31	0.64
5:5:86:ARG:HG3	5:5:87:THR:N	2.11	0.64
12:E:119:ALA:HB1	12:E:167:ARG:HE	1.62	0.64
2:2:1317:C:N3	56:x:37:ARG:NH1	2.37	0.64
1:1:693:A:O2'	1:1:1353:A:N3	2.31	0.63
1:1:1107:G:H1'	15:H:81:LEU:HD12	1.80	0.63
1:1:621:A:OP2	18:L:99:ASN:ND2	2.31	0.63
2:2:1445:U:O2	2:2:1458:G:N1	2.31	0.63
2:2:18:C:OP1	42:j:132:ASN:ND2	2.32	0.63
28:V:31:TYR:HE1	28:V:90:ASP:HB3	1.62	0.63
43:k:64:VAL:HG11	43:k:66:ALA:HB2	1.78	0.63
1:1:1046:A:OP2	15:H:61:ARG:CB	2.46	0.63
1:1:2822:G:OP1	10:C:164:GLN:NE2	2.32	0.63
14:G:37:VAL:CG2	14:G:38:PRO:CD	2.77	0.63
1:1:324:A:OP2	1:1:1205:A:N6	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:363:A:N6	49:q:27:CYS:SG	2.71	0.63
42:j:115:LEU:HD13	42:j:123:VAL:HG11	1.80	0.63
1:1:710:U:H2'	1:1:711:G:C8	2.33	0.63
48:p:86:VAL:HG11	48:p:93:ARG:HG3	1.81	0.63
1:1:1779:U:OP2	1:1:1784:A:N6	2.32	0.63
2:2:1356:G:H2'	2:2:1357:A:C8	2.34	0.63
41:i:102:VAL:HG13	41:i:107:PHE:HB2	1.80	0.63
1:1:353:C:H2'	1:1:354:A:C8	2.34	0.63
1:1:2140:G:N2	1:1:2141:G:O6	2.32	0.63
1:1:2497:A:H1'	1:1:2498:OMC:H5	1.63	0.63
25:S:82:MET:HB2	25:S:98:LYS:HB2	1.81	0.63
1:1:2692:G:N3	1:1:2847:U:O2'	2.32	0.63
2:2:1397:C:OP2	42:j:29:ARG:NH2	2.32	0.63
2:2:1457:G:OP1	57:y:34:LYS:NZ	2.32	0.63
5:5:67:GLY:C	5:5:85:THR:HG22	2.24	0.63
43:k:43:GLY:CA	43:k:58:HIS:CD2	2.82	0.63
46:n:84:THR:HG21	46:n:103:PHE:HB3	1.81	0.63
1:1:1107:G:H4'	15:H:81:LEU:CD1	2.29	0.62
2:2:843:U:OP1	2:2:844:G:N2	2.31	0.62
46:n:42:GLU:CD	46:n:45:ARG:HD2	2.21	0.62
1:1:164:C:OP2	1:1:165:A:N6	2.28	0.62
1:1:1223:G:N2	1:1:1226:A:OP2	2.29	0.62
1:1:1987:A:H2'	1:1:1988:G:H8	1.64	0.62
1:1:1248:G:OP1	11:D:44:ARG:NH2	2.23	0.62
1:1:1386:C:H2'	1:1:1387:A:C8	2.33	0.62
20:N:99:LYS:CB	34:b:42:HIS:CD2	2.82	0.62
13:F:9:VAL:HG13	13:F:9:VAL:O	1.99	0.62
44:l:111:ARG:NH2	44:l:126:ASP:OD2	2.32	0.62
1:1:1026:G:OP2	1:1:1134:A:O2'	2.17	0.62
1:1:1791:A:O2'	9:B:206:GLY:N	2.31	0.62
15:H:73:LYS:HB3	15:H:117:LEU:HD11	1.81	0.62
28:V:9:ARG:HD3	28:V:39:ALA:HB1	1.80	0.62
48:p:116:ILE:O	48:p:116:ILE:HG13	1.99	0.62
1:1:1046:A:OP2	15:H:61:ARG:HB3	1.98	0.62
1:1:1824:G:HO2'	9:B:246:THR:HG22	1.65	0.62
2:2:206:C:H41	2:2:213:G:H1	1.48	0.62
41:i:62:ARG:HH21	41:i:68:LEU:HA	1.64	0.62
2:2:1227:A:OP2	50:r:110:LYS:NZ	2.33	0.62
14:G:37:VAL:HG22	14:G:38:PRO:CD	2.29	0.62
18:L:48:ARG:NH2	37:e:5:LYS:O	2.33	0.62
4:4:47:G:H1'	4:4:300:U:H3	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:22:GLN:NE2	13:F:38:ASN:O	2.33	0.62
47:o:32:THR:O	47:o:83:THR:OG1	2.18	0.62
2:2:790:A:OP1	6:7:38:A:O2'	2.18	0.61
37:e:31:HIS:O	37:e:33:LEU:HG	2.00	0.61
50:r:16:VAL:HG23	50:r:17:ILE:HD12	1.82	0.61
2:2:891:U:H2'	2:2:892:A:H8	1.65	0.61
2:2:1229:A:O2'	6:7:30:G:OP1	2.14	0.61
38:f:16:ILE:HG12	38:f:25:VAL:HG22	1.83	0.61
1:1:2232:C:OP1	30:X:27:ARG:NH1	2.32	0.61
4:4:34:A:H4'	4:4:324:G:H1'	1.82	0.61
13:F:107:LEU:HD13	13:F:152:ARG:HB2	1.83	0.61
16:J:17:VAL:HG12	16:J:55:ILE:HB	1.82	0.61
1:1:968:C:H2'	1:1:969:G:H8	1.65	0.61
1:1:2564:A:OP1	1:1:2648:G:O2'	2.17	0.61
1:1:2585:U:C2	29:W:1:PHE:CG	2.87	0.61
1:1:2857:G:N2	1:1:2860:A:OP2	2.29	0.61
11:D:108:ILE:HG12	18:L:1:MET:HE1	1.83	0.61
1:1:527:C:N4	1:1:2779:U:OP2	2.31	0.61
1:1:1954:G:O2'	1:1:1956:U:O4	2.15	0.61
4:4:31:G:OP2	4:4:34:A:N6	2.33	0.61
47:o:53:ILE:HD11	47:o:61:ALA:HB1	1.83	0.61
1:1:1807:G:OP1	9:B:48:ARG:NH1	2.34	0.61
2:2:1305:G:HO2'	2:2:1306:A:H8	1.46	0.61
4:4:6:U:HO2'	4:4:7:G:H8	1.48	0.61
41:i:100:ASN:OD1	41:i:111:ARG:NH1	2.32	0.61
47:o:86:ALA:CA	47:o:89:ARG:CG	2.58	0.61
1:1:278:A:N6	1:1:361:G:O2'	2.34	0.61
2:2:1323:G:H1'	2:2:1361:G:H21	1.66	0.61
9:B:130:LEU:HD12	9:B:131:PRO:O	2.00	0.61
1:1:516:C:OP1	34:b:10:ARG:NH1	2.34	0.61
1:1:2506:U:N3	1:1:2585:U:O4	2.33	0.61
2:2:358:U:H2'	2:2:359:G:H8	1.66	0.61
2:2:946:A:H2'	2:2:947:G:C8	2.35	0.61
2:2:1464:U:H2'	2:2:1465:A:H8	1.66	0.61
5:5:50:ASN:C	5:5:69:ASN:OD1	2.43	0.61
10:C:35:THR:HB	10:C:49:GLN:HG3	1.83	0.61
1:1:1264:A:N6	1:1:2014:A:OP2	2.33	0.61
31:Y:11:VAL:O	31:Y:15:ASN:ND2	2.32	0.61
32:Z:9:GLN:HB2	32:Z:29:LEU:HD13	1.82	0.61
50:r:23:TYR:HB3	50:r:66:GLU:HG2	1.82	0.61
1:1:1050:A:C2	1:1:2751:G:C6	2.88	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1734:G:H2'	1:1:1735:A:C8	2.36	0.60
1:1:2898:U:H2'	1:1:2899:A:H8	1.65	0.60
1:1:213:A:H2'	1:1:214:G:C8	2.37	0.60
1:1:1915:3TD:O2'	5:5:48:LYS:CD	2.31	0.60
1:1:1926:U:H2'	1:1:1927:A:H3'	1.81	0.60
45:m:5:ASP:OD1	45:m:77:ARG:NH1	2.33	0.60
1:1:1432:G:H2'	1:1:1433:A:C8	2.35	0.60
1:1:2357:G:N2	1:1:2360:G:OP2	2.26	0.60
2:2:711:G:H2'	2:2:712:A:H8	1.66	0.60
2:2:924:C:H2'	2:2:925:G:H8	1.67	0.60
2:2:1166:G:N1	2:2:1169:A:OP2	2.33	0.60
9:B:5:LYS:HG2	9:B:17:VAL:HG22	1.82	0.60
15:H:53:ARG:HB3	15:H:55:VAL:HG13	1.82	0.60
39:g:163:VAL:HG21	39:g:173:ILE:HD11	1.81	0.60
1:1:1518:C:H2'	1:1:1519:G:C8	2.37	0.60
1:1:2293:G:H5''	21:O:94:ARG:HH22	1.66	0.60
1:1:2298:A:OP1	12:E:71:ARG:NH2	2.33	0.60
2:2:490:C:H2'	2:2:491:G:H8	1.66	0.60
2:2:624:C:H4'	53:u:10:GLY:HA2	1.81	0.60
4:4:61:G:N2	4:4:62:G:O6	2.35	0.60
53:u:50:THR:HG23	53:u:52:LEU:HD13	1.82	0.60
1:1:2831:G:OP2	10:C:59:ARG:NH1	2.35	0.60
2:2:312:C:H2'	2:2:313:A:H8	1.66	0.60
2:2:1126:U:O4	47:o:9:ARG:NH1	2.34	0.60
44:l:27:VAL:HG12	44:l:43:VAL:HG21	1.83	0.60
1:1:441:U:H2'	1:1:442:G:C8	2.37	0.60
1:1:1601:G:OP1	26:T:64:LYS:NZ	2.34	0.60
46:n:12:ARG:HG2	46:n:74:GLY:HA2	1.83	0.60
1:1:576:U:H2'	1:1:577:G:C8	2.37	0.60
2:2:21:G:H2'	2:2:22:G:H8	1.67	0.60
2:2:337:G:H2'	2:2:338:A:H8	1.67	0.60
14:G:90:LEU:HD23	14:G:124:THR:CA	2.32	0.60
22:P:90:GLY:O	22:P:113:ARG:NH1	2.34	0.60
1:1:24:G:O2'	25:S:78:GLU:O	2.19	0.60
1:1:1082:U:O2'	15:H:37:LYS:CD	2.49	0.60
1:1:2446:G:N2	1:1:2449:U:O2	2.33	0.60
2:2:193:C:H1'	57:y:55:GLN:HE22	1.66	0.60
2:2:339:C:OP2	17:K:98:ARG:NH1	2.34	0.60
2:2:1524:C:H2'	2:2:1525:G:H8	1.67	0.60
39:g:22:TYR:OH	58:z:67:ARG:NH1	2.34	0.60
2:2:398:U:H2'	2:2:399:G:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2220:U:H2'	1:1:2221:G:H8	1.66	0.60
1:1:2731:G:H2'	1:1:2732:G:C8	2.37	0.60
2:2:713:G:H2'	2:2:714:G:C8	2.36	0.60
2:2:886:G:O2'	2:2:915:A:O2'	2.19	0.60
12:E:58:ALA:HB2	12:E:65:PRO:HD3	1.84	0.60
18:L:101:ILE:HB	18:L:105:ILE:HG13	1.82	0.60
1:1:177:G:H3'	1:1:178:G:H8	1.67	0.59
1:1:1105:U:H2'	1:1:1106:G:C8	2.36	0.59
1:1:2095:A:OP1	14:G:11:ASN:ND2	2.35	0.59
2:2:714:G:H2'	2:2:715:A:C8	2.37	0.59
2:2:1448:C:O2	2:2:1456:A:N6	2.35	0.59
11:D:149:ILE:HD12	11:D:188:MET:HE2	1.83	0.59
1:1:1668:A:N3	1:1:1670:C:N4	2.51	0.59
1:1:2036:C:H2'	1:1:2037:A:H8	1.67	0.59
1:1:2246:G:H2'	1:1:2247:A:H8	1.67	0.59
2:2:521:G:HO2'	2:2:536:C:HO2'	1.42	0.59
3:3:72:G:H21	3:3:104:A:H62	1.50	0.59
25:S:23:LEU:HD12	25:S:24:ILE:HG23	1.83	0.59
40:h:11:ARG:NH2	40:h:177:THR:O	2.33	0.59
49:q:64:THR:HG22	49:q:93:VAL:CG2	2.32	0.59
2:2:459:A:H2'	2:2:460:A:H8	1.67	0.59
4:4:261:G:N2	4:4:271:G:O2'	2.35	0.59
5:5:36:LEU:HD23	5:5:38:GLY:H	1.67	0.59
1:1:411:G:OP2	1:1:2406:A:O2'	2.15	0.59
1:1:465:G:H2'	1:1:466:A:C8	2.37	0.59
1:1:2215:C:H2'	1:1:2216:G:H8	1.67	0.59
1:1:2312:U:O2	12:E:37:ASN:ND2	2.35	0.59
1:1:2840:C:H5''	20:N:53:THR:HG21	1.83	0.59
2:2:715:A:H2'	2:2:716:A:C8	2.38	0.59
2:2:738:C:OP1	43:k:2:ARG:NH2	2.35	0.59
42:j:159:LYS:NZ	45:m:42:GLU:O	2.28	0.59
45:m:78:VAL:HG21	45:m:128:TYR:CZ	2.37	0.59
41:i:152:GLN:CA	41:i:155:VAL:HG12	2.33	0.59
1:1:151:C:H2'	1:1:152:A:H8	1.67	0.59
1:1:1704:C:H2'	1:1:1705:A:H8	1.68	0.59
2:2:1025:U:O2'	2:2:1026:G:O4'	2.19	0.59
10:C:46:ARG:NH2	10:C:89:GLU:OE1	2.35	0.59
12:E:108:VAL:HG11	12:E:176:PRO:HG2	1.82	0.59
1:1:244:A:H62	1:1:254:G:H21	1.50	0.59
1:1:437:U:H2'	1:1:438:G:H8	1.67	0.59
1:1:1266:G:N2	1:1:2013:A:OP2	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1651:G:H5''	20:N:39:PRO:HG2	1.85	0.59
2:2:104:G:N7	57:y:9:LYS:NZ	2.45	0.59
2:2:460:A:H2'	2:2:461:A:H8	1.66	0.59
2:2:1251:A:N3	2:2:1369:C:O2'	2.32	0.59
3:3:49:C:H2'	3:3:50:A:H8	1.68	0.59
41:i:125:VAL:HG22	41:i:143:VAL:HG22	1.84	0.59
46:n:123:ARG:NH1	46:n:124:ARG:O	2.35	0.59
57:y:55:GLN:NE2	57:y:59:ASP:OD2	2.35	0.59
2:2:390:U:H2'	2:2:391:G:H8	1.68	0.59
2:2:916:U:H2'	2:2:917:G:H8	1.68	0.59
2:2:1356:G:H2'	2:2:1357:A:H8	1.67	0.59
45:m:106:THR:CG2	45:m:121:LEU:CD1	2.81	0.59
1:1:1058:U:H3	1:1:1080:A:H2	1.49	0.58
1:1:1394:U:H4'	1:1:1603:A:H4'	1.85	0.58
2:2:20:U:O2'	2:2:573:A:N6	2.36	0.58
4:4:115:C:H2'	4:4:116:A:H8	1.67	0.58
17:K:2:ILE:HB	17:K:33:ALA:HB3	1.84	0.58
1:1:2443:C:H2'	1:1:2444:G:H8	1.67	0.58
2:2:309:A:H2'	2:2:310:G:H8	1.68	0.58
2:2:551:U:O2'	49:q:83:ARG:NH2	2.35	0.58
49:q:68:GLY:O	49:q:99:ARG:NH1	2.36	0.58
1:1:176:A:O2'	1:1:177:G:OP1	2.21	0.58
1:1:302:C:H2'	1:1:303:G:H8	1.68	0.58
1:1:950:G:H1	1:1:967:U:H3	1.49	0.58
1:1:1050:A:N3	1:1:2751:G:C2	2.72	0.58
1:1:1704:C:H2'	1:1:1705:A:C8	2.38	0.58
2:2:429:U:H3'	41:i:9:LEU:HD23	1.82	0.58
1:1:814:C:H1'	1:1:1225:G:H21	1.67	0.58
2:2:269:C:H2'	2:2:270:A:H8	1.67	0.58
2:2:526:C:OP1	49:q:88:LYS:NZ	2.37	0.58
5:5:70:ILE:HG13	5:5:84:PRO:HA	1.85	0.58
1:1:1007:C:OP1	16:J:37:ARG:NH2	2.37	0.58
1:1:2696:U:H2'	1:1:2697:G:H8	1.68	0.58
2:2:1307:U:OP1	50:r:100:GLN:NE2	2.36	0.58
14:G:125:THR:HA	14:G:146:VAL:HB	1.85	0.58
41:i:36:GLN:HG3	41:i:43:ALA:H	1.68	0.58
46:n:52:LEU:HB3	46:n:58:VAL:HG22	1.86	0.58
1:1:926:G:H2'	1:1:927:A:C8	2.38	0.58
2:2:1077:G:N2	2:2:1080:A:OP2	2.23	0.58
2:2:1209:C:O2'	2:2:1214:C:N4	2.37	0.58
41:i:172:GLU:HG2	41:i:183:LYS:HD2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2789:C:H42	1:1:2894:G:H22	1.52	0.58
2:2:1524:C:H2'	2:2:1525:G:C8	2.38	0.58
4:4:256:G:OP2	4:4:272:C:N4	2.36	0.58
33:a:13:THR:HG22	33:a:23:LYS:HG2	1.84	0.58
1:1:1734:G:H2'	1:1:1735:A:H8	1.67	0.58
1:1:1825:U:H2'	1:1:1826:G:H8	1.69	0.58
1:1:1921:G:H2'	1:1:1922:G:H8	1.69	0.58
2:2:712:A:H2'	2:2:713:G:C8	2.39	0.58
2:2:1463:U:OP1	22:P:109:ARG:NE	2.34	0.58
1:1:428:A:O2'	1:1:429:A:OP1	2.22	0.58
1:1:1123:C:H2'	1:1:1124:G:C8	2.39	0.58
1:1:1181:U:H2'	1:1:1182:G:C8	2.38	0.58
1:1:1392:A:N6	26:T:18:GLU:OE1	2.37	0.58
1:1:1788:C:OP1	9:B:221:ARG:NH2	2.36	0.58
2:2:362:G:N2	2:2:365:U:OP2	2.30	0.58
2:2:1458:G:OP1	57:y:30:THR:OG1	2.22	0.58
56:x:19:VAL:HG21	56:x:44:MET:HG2	1.86	0.58
5:5:80:VAL:HG13	5:5:81:VAL:HG13	1.86	0.58
6:7:68:C:H2'	6:7:69:G:H8	1.68	0.58
1:1:521:U:H2'	1:1:522:A:H8	1.69	0.57
1:1:581:C:H2'	1:1:582:A:C8	2.38	0.57
1:1:755:U:H2'	1:1:756:A:H8	1.68	0.57
1:1:775:G:H4'	1:1:776:G:H5'	1.86	0.57
49:q:50:ARG:HB3	49:q:66:TYR:HE1	1.68	0.57
1:1:307:G:H21	1:1:330:A:H61	1.52	0.57
1:1:566:U:H5''	18:L:29:LYS:HE3	1.85	0.57
1:1:796:C:H2'	1:1:797:G:H8	1.67	0.57
1:1:1636:U:H2'	1:1:1637:A:H8	1.68	0.57
1:1:1693:U:O2'	9:B:14:ARG:NH1	2.37	0.57
1:1:2777:G:OP2	1:1:2781:A:O2'	2.22	0.57
2:2:263:A:OP1	57:y:74:ARG:NE	2.34	0.57
2:2:713:G:H2'	2:2:714:G:H8	1.69	0.57
5:5:50:ASN:CA	5:5:69:ASN:OD1	2.51	0.57
18:L:55:MET:SD	18:L:59:ARG:NE	2.73	0.57
1:1:711:G:O6	1:1:721:A:N6	2.37	0.57
1:1:2314:A:H1'	12:E:155:THR:HG21	1.85	0.57
2:2:401:C:O2'	2:2:621:A:N3	2.36	0.57
2:2:1404:C:H2'	2:2:1405:G:C8	2.38	0.57
4:4:131:U:O4	40:h:72:ARG:NH1	2.38	0.57
47:o:86:ALA:CA	47:o:89:ARG:HD3	2.31	0.57
1:1:2623:G:H2'	1:1:2624:G:H8	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:235:C:H2'	2:2:236:A:H8	1.67	0.57
2:2:269:C:H2'	2:2:270:A:C8	2.40	0.57
2:2:788:U:O2'	7:8:10:G:N2	2.37	0.57
1:1:589:U:H2'	1:1:590:A:H8	1.68	0.57
1:1:796:C:H2'	1:1:797:G:C8	2.40	0.57
2:2:552:U:O2'	49:q:83:ARG:O	2.19	0.57
12:E:13:VAL:HG12	12:E:28:VAL:HG11	1.85	0.57
1:1:704:G:O2'	1:1:726:G:N2	2.36	0.57
4:4:359:C:H3'	4:4:360:A:H5''	1.87	0.57
19:M:33:LEU:HD13	19:M:117:PHE:HB3	1.86	0.57
44:l:140:ASP:OD1	44:l:143:ARG:NH2	2.35	0.57
50:r:87:ARG:HG3	50:r:97:VAL:HB	1.87	0.57
56:x:3:ARG:HH12	56:x:10:PHE:HB2	1.69	0.57
56:x:50:ALA:HB1	56:x:57:HIS:HB3	1.86	0.57
1:1:582:A:H2'	1:1:583:G:H8	1.69	0.57
1:1:1299:G:H5'	1:1:1300:G:H5'	1.85	0.57
2:2:166:U:H2'	2:2:167:A:C8	2.38	0.57
2:2:1016:A:HO2'	2:2:1217:C:HO2'	1.50	0.57
2:2:1534:A:H2	7:8:7:U:H3	1.52	0.57
24:R:63:VAL:HA	24:R:96:VAL:HG12	1.87	0.57
46:n:63:LEU:HD13	46:n:65:ILE:HD11	1.86	0.57
1:1:903:C:H2'	1:1:904:G:H8	1.69	0.57
1:1:926:G:H2'	1:1:927:A:H8	1.70	0.57
4:4:52:G:H2'	4:4:53:G:C8	2.40	0.57
7:8:2:G:H5''	58:z:59:LYS:HE2	1.87	0.57
15:H:27:VAL:HG13	15:H:83:ALA:HB3	1.87	0.57
1:1:379:G:H1'	1:1:2232:C:H5''	1.86	0.57
1:1:576:U:H2'	1:1:577:G:H8	1.69	0.57
1:1:1067:A:H2'	1:1:1068:G:C8	2.40	0.57
2:2:958:A:C6	56:x:55:ARG:HB2	2.40	0.57
2:2:1218:C:H2'	2:2:1219:A:C8	2.38	0.57
43:k:64:VAL:CG1	43:k:66:ALA:HB2	2.34	0.57
1:1:848:C:H2'	1:1:849:A:H8	1.70	0.57
1:1:1082:U:HO2'	15:H:37:LYS:HG2	1.68	0.57
1:1:2836:U:H2'	1:1:2837:A:H8	1.70	0.57
2:2:662:U:H2'	2:2:663:A:C8	2.40	0.57
1:1:631:A:O2'	1:1:632:A:OP1	2.23	0.56
1:1:755:U:H2'	1:1:756:A:C8	2.40	0.56
1:1:1123:C:H2'	1:1:1124:G:H8	1.68	0.56
1:1:1270:C:H5''	1:1:1271:G:H5'	1.87	0.56
1:1:2039:U:H2'	1:1:2040:G:H8	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2788:C:O2'	1:1:2809:A:N3	2.38	0.56
18:L:63:LYS:HA	37:e:13:ARG:HG2	1.87	0.56
24:R:38:VAL:HG11	24:R:57:GLY:HA3	1.86	0.56
30:X:18:ARG:HH21	30:X:24:ALA:HB2	1.70	0.56
41:i:124:MET:HE3	41:i:146:ARG:HG2	1.87	0.56
1:1:549:G:H2'	1:1:550:C:H6	1.69	0.56
1:1:1649:G:H2'	1:1:1650:A:H8	1.69	0.56
2:2:314:C:H2'	2:2:315:A:C8	2.40	0.56
4:4:139:C:H41	4:4:180:G:H21	1.52	0.56
9:B:205:LEU:HB3	9:B:210:ALA:HB3	1.87	0.56
15:H:34:THR:O	15:H:37:LYS:HB3	2.04	0.56
19:M:135:VAL:HG23	19:M:135:VAL:O	2.05	0.56
1:1:966:G:O4'	1:1:2267:A:N6	2.38	0.56
1:1:1368:G:H2'	1:1:1369:G:H8	1.70	0.56
1:1:2122:U:H2'	1:1:2123:G:C8	2.40	0.56
2:2:7:A:N7	42:j:97:GLN:NE2	2.54	0.56
2:2:1179:A:OP2	46:n:99:ARG:NH1	2.39	0.56
2:2:1291:U:H2'	2:2:1292:G:H8	1.70	0.56
12:E:93:GLY:H	12:E:96:MET:HE2	1.71	0.56
12:E:102:ARG:NH1	33:a:25:ARG:O	2.34	0.56
15:H:56:ARG:HD3	15:H:81:LEU:HD21	1.87	0.56
16:J:114:LEU:HG	16:J:118:MET:HE3	1.87	0.56
25:S:38:TYR:OH	34:b:37:LYS:O	2.23	0.56
40:h:186:THR:HG22	40:h:199:LYS:HG2	1.86	0.56
42:j:133:PRO:HA	42:j:136:VAL:HG12	1.85	0.56
1:1:1107:G:H4'	15:H:81:LEU:HD12	1.87	0.56
2:2:674:G:H2'	2:2:675:A:C8	2.40	0.56
2:2:1255:G:O2'	2:2:1258:G:N3	2.29	0.56
3:3:49:C:H2'	3:3:50:A:C8	2.40	0.56
4:4:34:A:O2'	4:4:323:A:N3	2.36	0.56
4:4:149:A:H1'	4:4:151:C:H41	1.70	0.56
8:A:18:ALA:O	8:A:20:ARG:NH1	2.39	0.56
1:1:1287:A:O2'	1:1:1288:G:OP1	2.20	0.56
1:1:1798:U:O2'	1:1:1802:A:N3	2.38	0.56
1:1:1830:C:H42	1:1:1975:G:H1	1.54	0.56
1:1:2065:C:H42	1:1:2445:2MG:HN1	1.54	0.56
2:2:1355:G:H2'	2:2:1356:G:H8	1.69	0.56
2:2:745:G:H2'	2:2:746:A:H8	1.70	0.56
2:2:1517:G:H2'	2:2:1518:MA6:H8	1.88	0.56
4:4:284:G:N2	4:4:284:G:OP2	2.39	0.56
5:5:21:ARG:HD3	5:5:26:ILE:HD13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:37:LYS:HG3	15:H:41:LEU:HD12	1.88	0.56
45:m:106:THR:CG2	45:m:121:LEU:HD11	2.35	0.56
1:1:171:U:H2'	1:1:172:A:H8	1.69	0.56
1:1:1098:A:H3'	1:1:1099:G:H8	1.71	0.56
1:1:1429:G:H2'	1:1:1430:G:H8	1.70	0.56
1:1:1568:G:OP2	9:B:63:ARG:NH1	2.38	0.56
1:1:1839:G:C2	1:1:1840:G:C8	2.94	0.56
2:2:107:G:O6	57:y:10:ARG:NE	2.38	0.56
2:2:1088:G:H21	2:2:1167:A:H61	1.53	0.56
4:4:31:G:H5''	4:4:35:C:H42	1.70	0.56
40:h:35:SER:OG	40:h:59:ARG:NH2	2.39	0.56
1:1:806:C:O2	1:1:2444:G:O2'	2.24	0.56
1:1:924:G:H2'	1:1:925:A:H8	1.71	0.56
1:1:1223:G:OP1	24:R:68:ARG:NH2	2.39	0.56
1:1:1607:C:N4	1:1:1622:G:OP2	2.35	0.56
1:1:2777:G:H5'	1:1:2781:A:H1'	1.88	0.56
2:2:110:C:O2'	53:u:25:ARG:O	2.23	0.56
2:2:390:U:H2'	2:2:391:G:C8	2.41	0.56
9:B:130:LEU:HD11	9:B:135:ILE:HG12	1.88	0.56
45:m:78:VAL:HG21	45:m:128:TYR:CE2	2.41	0.56
1:1:1046:A:OP2	15:H:61:ARG:CD	2.53	0.56
1:1:1050:A:N1	1:1:2751:G:C5	2.73	0.56
1:1:1364:G:N2	1:1:1367:A:OP2	2.35	0.56
1:1:1752:C:H2'	1:1:1753:G:C8	2.40	0.56
1:1:1812:U:H2'	1:1:1813:G:H8	1.71	0.56
1:1:2039:U:H2'	1:1:2040:G:C8	2.41	0.56
1:1:2193:G:H2'	1:1:2194:U:C6	2.41	0.56
2:2:1457:G:H5''	57:y:30:THR:HG21	1.88	0.56
4:4:331:C:H2'	4:4:332:G:H8	1.70	0.56
9:B:84:ASP:OD2	9:B:87:ARG:NH1	2.39	0.56
53:u:36:VAL:HG23	53:u:36:VAL:O	2.05	0.56
2:2:1083:U:H3'	2:2:1084:G:C8	2.40	0.56
2:2:1508:A:H61	2:2:1527:U:H3	1.54	0.56
4:4:331:C:H2'	4:4:332:G:C8	2.40	0.56
49:q:53:CYS:SG	49:q:65:SER:OG	2.63	0.56
1:1:2515:C:H2'	1:1:2516:A:H8	1.72	0.55
9:B:142:HIS:ND1	9:B:193:GLY:O	2.39	0.55
19:M:17:ASN:O	19:M:38:ARG:NH1	2.39	0.55
1:1:1131:G:HO2'	1:1:2025:C:HO2'	1.52	0.55
2:2:672:U:H2'	2:2:673:A:H8	1.71	0.55
2:2:1513:A:H2'	2:2:1514:G:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:23:G:H1	4:4:330:U:H3	1.55	0.55
4:4:195:A:O2'	4:4:196:G:O4'	2.18	0.55
10:C:109:VAL:HG22	10:C:203:VAL:HG12	1.87	0.55
15:H:29:ASP:HB2	15:H:56:ARG:HH12	1.71	0.55
21:O:110:ALA:HB1	21:O:115:LEU:HD12	1.88	0.55
42:j:157:ARG:NH1	45:m:43:GLU:OE1	2.39	0.55
49:q:121:ARG:HD2	49:q:122:PRO:HD2	1.87	0.55
55:w:37:GLY:O	55:w:63:ARG:NH2	2.39	0.55
1:1:571:U:O2'	1:1:573:U:OP2	2.24	0.55
2:2:1074:G:H1	2:2:1083:U:H3	1.53	0.55
2:2:1485:U:H2'	2:2:1486:G:H8	1.71	0.55
6:7:23:A:H2'	6:7:24:G:H8	1.72	0.55
1:1:840:C:H2'	1:1:841:G:H8	1.72	0.55
1:1:1864:U:OP1	1:1:2410:G:O2'	2.24	0.55
1:1:2529:G:H4'	13:F:175:LYS:HD3	1.88	0.55
2:2:552:U:H2'	2:2:553:A:H8	1.72	0.55
2:2:996:A:N1	2:2:1045:C:O2'	2.32	0.55
2:2:1463:U:H5''	22:P:109:ARG:HH11	1.71	0.55
43:k:43:GLY:N	43:k:58:HIS:CD2	2.74	0.55
2:2:481:G:O2'	2:2:483:C:N4	2.39	0.55
16:J:18:VAL:HG22	16:J:140:LEU:HB3	1.89	0.55
22:P:27:GLU:HB3	22:P:85:SER:HG	1.69	0.55
35:c:25:LYS:NZ	35:c:32:GLU:O	2.40	0.55
1:1:1278:C:H2'	1:1:1279:G:H8	1.72	0.55
1:1:2233:U:H2'	1:1:2234:G:C8	2.39	0.55
2:2:950:U:H2'	2:2:951:G:C8	2.42	0.55
2:2:1173:U:H2'	2:2:1174:G:H8	1.71	0.55
2:2:1345:U:O2'	44:l:5:ARG:NH2	2.40	0.55
4:4:7:G:H22	4:4:353:C:H5	1.53	0.55
11:D:157:LEU:HG	11:D:169:VAL:HG21	1.89	0.55
12:E:102:ARG:NH1	33:a:9:TYR:OH	2.39	0.55
16:J:32:LEU:HD22	16:J:54:ILE:HG21	1.89	0.55
53:u:4:ILE:HG12	53:u:21:VAL:HG22	1.89	0.55
1:1:672:C:OP2	18:L:42:SER:OG	2.21	0.55
1:1:1631:G:N2	1:1:1634:A:OP2	2.33	0.55
2:2:21:G:H2'	2:2:22:G:C8	2.41	0.55
2:2:193:C:H2'	2:2:194:C:C6	2.42	0.55
41:i:8:LYS:HD3	41:i:21:LEU:HB3	1.87	0.55
47:o:52:LEU:HD23	47:o:62:ARG:HG2	1.89	0.55
1:1:619:G:OP2	1:1:620:G:N2	2.38	0.55
1:1:1427:A:N6	1:1:1571:A:OP2	2.28	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:741:G:OP1	52:t:35:GLN:NE2	2.40	0.55
2:2:876:C:H2'	2:2:877:G:H8	1.72	0.55
2:2:1005:A:H3'	2:2:1006:G:H8	1.72	0.55
2:2:1127:G:H1	2:2:1145:A:H61	1.55	0.55
2:2:1479:C:H2'	2:2:1480:A:H8	1.71	0.55
4:4:186:A:C2	40:h:102:ASN:HA	2.42	0.55
45:m:3:MET:HE1	45:m:9:ASP:OD2	2.07	0.55
1:1:467:G:OP1	36:d:33:ARG:NH2	2.39	0.55
1:1:1654:A:N6	1:1:2049:G:OP1	2.40	0.55
1:1:2591:C:H2'	1:1:2592:G:C8	2.42	0.55
1:1:2836:U:H2'	1:1:2837:A:C8	2.42	0.55
15:H:88:HIS:HB2	15:H:89:PRO:HD3	1.88	0.55
47:o:45:ARG:HB3	47:o:69:THR:HB	1.89	0.55
1:1:1807:G:N2	1:1:1810:A:OP2	2.31	0.54
2:2:337:G:H2'	2:2:338:A:C8	2.42	0.54
2:2:634:C:H2'	2:2:635:A:H8	1.71	0.54
2:2:993:G:O2'	2:2:994:A:N7	2.39	0.54
12:E:31:VAL:HA	12:E:158:THR:HG22	1.88	0.54
19:M:56:ALA:HB2	19:M:119:LEU:HD12	1.89	0.54
21:O:111:ARG:NH2	21:O:117:PHE:OXT	2.40	0.54
31:Y:16:THR:O	31:Y:20:ASN:ND2	2.41	0.54
2:2:459:A:H2'	2:2:460:A:C8	2.42	0.54
2:2:1425:U:H2'	2:2:1426:G:H8	1.73	0.54
47:o:47:GLU:OE1	51:s:76:LYS:NZ	2.39	0.54
1:1:523:C:H2'	1:1:524:G:H8	1.72	0.54
1:1:743:A:O2'	1:1:1659:G:OP1	2.26	0.54
1:1:1696:G:N2	1:1:1977:A:O2'	2.39	0.54
1:1:2246:G:H2'	1:1:2247:A:C8	2.42	0.54
2:2:745:G:H2'	2:2:746:A:C8	2.43	0.54
2:2:950:U:H2'	2:2:951:G:H8	1.73	0.54
2:2:1151:A:O2'	2:2:1152:A:H8	1.89	0.54
3:3:77:U:H5''	28:V:21:ARG:HH12	1.72	0.54
33:a:56:ARG:HH22	33:a:59:ARG:NH2	1.97	0.54
1:1:1:G:H2'	1:1:2:G:H8	1.72	0.54
1:1:160:A:N3	1:1:2208:C:O2'	2.37	0.54
1:1:698:C:O2'	1:1:734:A:N6	2.33	0.54
1:1:987:C:O2'	1:1:1000:A:N3	2.32	0.54
1:1:1062:G:H22	1:1:1088:A:H2'	1.72	0.54
2:2:107:G:C2	2:2:108:G:H1'	2.43	0.54
2:2:222:C:H2'	2:2:223:A:H8	1.72	0.54
2:2:1355:G:H2'	2:2:1356:G:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1801:A:OP2	9:B:150:LYS:NZ	2.39	0.54
2:2:1088:G:N2	2:2:1167:A:H61	2.06	0.54
14:G:133:GLN:NE2	14:G:135:HIS:O	2.41	0.54
1:1:480:A:OP2	27:U:44:LYS:NZ	2.39	0.54
1:1:1819:A:H5''	9:B:160:THR:HG21	1.88	0.54
1:1:2064:C:H2'	1:1:2065:C:H6	1.73	0.54
1:1:2137:U:N3	1:1:2138:G:O6	2.40	0.54
27:U:25:VAL:HG12	27:U:36:VAL:HG22	1.89	0.54
1:1:1046:A:OP2	15:H:61:ARG:HD2	2.08	0.54
1:1:1083:U:C5'	15:H:41:LEU:HD13	2.33	0.54
1:1:1754:A:N1	1:1:2716:C:O2'	2.41	0.54
1:1:1812:U:H2'	1:1:1813:G:C8	2.43	0.54
2:2:460:A:H2'	2:2:461:A:C8	2.43	0.54
2:2:881:G:OP2	49:q:9:ARG:NH1	2.41	0.54
56:x:12:ASP:OD2	56:x:14:HIS:CE1	2.53	0.54
1:1:589:U:H2'	1:1:590:A:C8	2.43	0.54
1:1:1744:A:H3'	1:1:1745:A:H8	1.72	0.54
2:2:672:U:H2'	2:2:673:A:C8	2.43	0.54
2:2:720:C:OP2	2:2:721:G:O2'	2.19	0.54
16:J:77:HIS:NE2	16:J:80:HIS:O	2.40	0.54
25:S:17:VAL:HG21	25:S:76:VAL:HG11	1.90	0.54
41:i:11:LEU:HB3	41:i:63:ARG:HD3	1.89	0.54
41:i:152:GLN:C	41:i:155:VAL:HG12	2.32	0.54
1:1:296:U:H2'	1:1:297:G:C8	2.43	0.54
1:1:1083:U:P	15:H:41:LEU:HD13	2.44	0.54
1:1:1915:3TD:C2'	5:5:48:LYS:HD2	2.32	0.54
1:1:2646:C:OP2	1:1:2732:G:O2'	2.26	0.54
2:2:298:A:O2'	2:2:299:G:OP1	2.25	0.54
2:2:312:C:H2'	2:2:313:A:C8	2.43	0.54
1:1:305:C:H2'	1:1:306:U:C6	2.43	0.54
2:2:178:C:H2'	2:2:179:A:H8	1.73	0.54
4:4:320:U:H2'	4:4:321:G:C4	2.43	0.54
1:1:970:U:H2'	1:1:971:G:C8	2.44	0.53
1:1:1413:A:N7	1:1:1414:C:N4	2.55	0.53
2:2:1041:G:H2'	2:2:1042:A:C8	2.43	0.53
22:P:14:LYS:HE2	22:P:77:HIS:HA	1.90	0.53
1:1:366:C:H2'	1:1:367:G:H8	1.73	0.53
1:1:548:G:H5'	1:1:549:G:C8	2.43	0.53
1:1:1316:U:H2'	1:1:1317:G:H8	1.73	0.53
1:1:1463:C:H2'	1:1:1464:G:H8	1.72	0.53
1:1:1636:U:H2'	1:1:1637:A:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1715:G:O2'	1:1:1743:G:O6	2.23	0.53
1:1:2008:C:H2'	1:1:2009:A:H8	1.73	0.53
1:1:2487:G:H2'	1:1:2488:G:H8	1.72	0.53
1:1:2591:C:H2'	1:1:2592:G:H8	1.73	0.53
2:2:923:A:O2'	2:2:1399:C:OP2	2.25	0.53
32:Z:16:ARG:HG3	32:Z:54:MET:HE1	1.89	0.53
42:j:101:GLU:OE1	42:j:122:ASN:ND2	2.41	0.53
46:n:63:LEU:HD13	46:n:65:ILE:CD1	2.38	0.53
47:o:86:ALA:CB	47:o:89:ARG:HD3	2.38	0.53
1:1:538:A:H4'	16:J:7:LYS:HG3	1.90	0.53
1:1:1107:G:H4'	15:H:81:LEU:CB	2.39	0.53
1:1:1161:C:H2'	1:1:1162:G:H8	1.73	0.53
1:1:2428:G:H5''	1:1:2429:G:H5'	1.90	0.53
1:1:2730:C:O3'	10:C:174:SER:OG	2.26	0.53
2:2:1026:G:O6	2:2:1035:A:N1	2.42	0.53
2:2:1118:U:H2'	2:2:1119:C:H6	1.72	0.53
5:5:48:LYS:HG3	5:5:48:LYS:O	2.08	0.53
41:i:26:ARG:NH2	41:i:30:THR:O	2.41	0.53
43:k:97:THR:O	43:k:97:THR:CG2	2.54	0.53
44:l:87:VAL:HG12	44:l:151:PHE:HB3	1.89	0.53
1:1:31:C:H2'	1:1:32:C:C6	2.44	0.53
1:1:1046:A:O2'	15:H:61:ARG:O	2.26	0.53
1:1:2898:U:O2'	16:J:134:ALA:O	2.19	0.53
2:2:1173:U:H2'	2:2:1174:G:C8	2.43	0.53
3:3:40:U:N3	3:3:44:G:OP2	2.39	0.53
6:7:43:C:N4	6:7:44:G:O6	2.41	0.53
1:1:856:G:H2'	1:1:857:G:C8	2.44	0.53
1:1:1980:G:O2'	1:1:1982:U:OP2	2.20	0.53
2:2:783:C:H2'	2:2:784:A:H8	1.72	0.53
5:5:58:LEU:HD22	5:5:104:VAL:HG11	1.90	0.53
15:H:114:GLU:HA	15:H:123:ILE:HB	1.90	0.53
24:R:28:ALA:HB3	24:R:31:GLU:HG3	1.91	0.53
1:1:1162:G:N2	24:R:91:GLN:OE1	2.42	0.53
1:1:1365:A:OP1	30:X:28:ARG:NH2	2.35	0.53
1:1:1791:A:H4'	9:B:205:LEU:HB2	1.90	0.53
1:1:2157:G:H2'	1:1:2158:A:H8	1.74	0.53
2:2:945:G:C2	2:2:946:A:C8	2.97	0.53
2:2:1248:A:H2	46:n:72:ILE:HD11	1.73	0.53
12:E:103:LEU:HD12	12:E:107:ALA:HB3	1.89	0.53
24:R:19:THR:OG1	24:R:95:ASP:OD1	2.27	0.53
46:n:63:LEU:HD13	46:n:65:ILE:HG13	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:57:ASN:HD22	15:H:63:ALA:HB2	1.74	0.53
1:1:968:C:H2'	1:1:969:G:C8	2.43	0.53
1:1:1357:C:H2'	1:1:1358:G:O4'	2.09	0.53
2:2:973:G:OP1	47:o:59:LYS:NZ	2.30	0.53
2:2:1009:U:H3	2:2:1020:G:H1	1.57	0.53
11:D:171:ASP:OD1	11:D:172:ALA:N	2.42	0.53
28:V:6:ALA:HB3	28:V:65:VAL:HG22	1.90	0.53
51:s:2:ALA:N	51:s:67:THR:O	2.42	0.53
56:x:3:ARG:HH21	56:x:7:LYS:HB3	1.73	0.53
1:1:643:A:OP1	35:c:44:ARG:NH1	2.32	0.53
1:1:1264:A:OP1	34:b:16:ARG:NH1	2.41	0.53
1:1:2443:C:H2'	1:1:2444:G:C8	2.42	0.53
1:1:2468:A:OP2	1:1:2476:A:N6	2.42	0.53
2:2:45:G:H2'	2:2:46:G:H8	1.73	0.53
2:2:126:G:OP1	2:2:605:U:O2'	2.14	0.53
2:2:544:G:OP1	41:i:56:ARG:NH2	2.39	0.53
2:2:1179:A:H2'	2:2:1180:A:C8	2.43	0.53
4:4:86:A:H8	4:4:90:G:H5''	1.73	0.53
15:H:37:LYS:O	15:H:41:LEU:HB2	2.08	0.53
40:h:51:SER:HB3	40:h:115:LEU:HD22	1.91	0.53
41:i:132:ILE:HG22	41:i:134:SER:H	1.74	0.53
50:r:17:ILE:O	50:r:20:THR:OG1	2.26	0.53
1:1:1847:A:H2	1:1:1848:A:H62	1.57	0.53
1:1:2245:U:H5''	1:1:2246:G:H5'	1.90	0.53
9:B:130:LEU:HD12	9:B:135:ILE:HG13	1.86	0.53
10:C:35:THR:OG1	10:C:51:THR:OG1	2.27	0.53
17:K:40:LYS:NZ	17:K:89:ASN:OD1	2.41	0.53
38:f:2:LYS:NZ	38:f:32:LYS:O	2.41	0.53
39:g:77:SER:OG	39:g:78:GLU:OE1	2.26	0.53
43:k:6:ILE:HG12	43:k:89:VAL:HG12	1.90	0.53
44:l:84:THR:HG23	44:l:84:THR:O	2.09	0.53
1:1:466:A:OP1	36:d:34:ARG:NH1	2.42	0.52
1:1:2148:G:H2'	1:1:2149:U:C6	2.44	0.52
1:1:2329:U:H2'	1:1:2330:G:C8	2.43	0.52
33:a:56:ARG:NH1	33:a:59:ARG:NH2	2.57	0.52
1:1:598:U:H2'	1:1:599:A:H8	1.75	0.52
1:1:662:G:H2'	1:1:663:G:H8	1.73	0.52
1:1:1469:A:OP2	1:1:1522:A:N6	2.41	0.52
1:1:1808:A:H3'	1:1:1809:A:C8	2.45	0.52
1:1:2728:U:O2'	1:1:2729:G:H8	1.92	0.52
2:2:1513:A:H2'	2:2:1514:G:H8	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:57:ASN:HB2	15:H:62:ARG:HD2	1.91	0.52
33:a:56:ARG:NH1	33:a:59:ARG:HH22	2.07	0.52
44:l:91:VAL:HG12	44:l:96:ARG:HG3	1.92	0.52
1:1:441:U:H2'	1:1:442:G:H8	1.73	0.52
1:1:1040:A:H4'	28:V:49:ASN:HD22	1.74	0.52
1:1:1046:A:O2'	15:H:61:ARG:C	2.53	0.52
1:1:2441:U:OP2	1:1:2586:U:O2'	2.27	0.52
1:1:1379:U:O2'	1:1:1380:G:OP1	2.27	0.52
1:1:1563:U:H2'	1:1:1564:C:C6	2.45	0.52
1:1:1797:G:O2'	9:B:257:THR:OG1	2.28	0.52
1:1:2188:U:O2'	1:1:2189:U:OP1	2.26	0.52
1:1:2328:A:H2'	1:1:2329:U:C6	2.45	0.52
37:e:36:LYS:HB3	37:e:40:ARG:HD3	1.91	0.52
1:1:580:U:H2'	1:1:581:C:C6	2.44	0.52
1:1:630:G:N2	1:1:633:A:OP2	2.33	0.52
1:1:754:U:H2'	1:1:755:U:C6	2.44	0.52
1:1:1431:A:H2'	1:1:1432:G:H8	1.74	0.52
2:2:536:C:H2'	2:2:537:G:H8	1.74	0.52
2:2:677:U:O2	2:2:777:A:O2'	2.28	0.52
4:4:20:A:C8	5:5:91:LEU:HD22	2.45	0.52
6:7:23:A:H2'	6:7:24:G:C8	2.44	0.52
10:C:3:GLY:HA3	10:C:204:LYS:HG2	1.91	0.52
55:w:30:LYS:HA	55:w:33:ILE:HG12	1.91	0.52
1:1:318:C:H2'	1:1:319:G:H8	1.74	0.52
1:1:1550:C:H2'	1:1:1551:A:C8	2.44	0.52
1:1:1550:C:H2'	1:1:1551:A:H8	1.74	0.52
1:1:2087:G:H2'	1:1:2088:A:H8	1.74	0.52
1:1:2329:U:H2'	1:1:2330:G:H8	1.75	0.52
1:1:2417:C:H2'	1:1:2418:A:H8	1.74	0.52
11:D:145:ASP:HA	11:D:166:LYS:HB3	1.91	0.52
1:1:1196:C:C2	1:1:1197:G:C8	2.98	0.52
1:1:1665:A:H2'	1:1:1666:G:H8	1.74	0.52
1:1:2339:C:H2'	1:1:2340:A:H8	1.75	0.52
1:1:2647:U:H2'	1:1:2648:G:H8	1.74	0.52
1:1:2682:A:C2	10:C:23:PRO:HB3	2.43	0.52
55:w:38:LYS:NZ	58:z:26:ALA:O	2.41	0.52
2:2:501:C:O2	2:2:549:C:O2'	2.27	0.52
1:1:23:G:H2'	1:1:24:G:H8	1.75	0.52
1:1:1435:G:H2'	1:1:1436:G:C8	2.44	0.52
1:1:1548:A:H2'	1:1:1549:A:H8	1.74	0.52
2:2:334:C:O2	2:2:1434:A:O2'	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:227:C:H3'	4:4:228:G:C8	2.45	0.52
30:X:39:TRP:NE1	30:X:41:GLU:OE1	2.39	0.52
1:1:2817:U:OP1	20:N:42:LYS:NZ	2.30	0.52
1:1:2821:A:OP2	10:C:115:GLY:N	2.43	0.52
2:2:274:A:H1'	2:2:275:G:C8	2.44	0.52
4:4:202:G:H1	4:4:228:G:H1'	1.74	0.52
8:A:56:ASP:HB3	8:A:58:THR:HG23	1.92	0.52
15:H:48:ALA:HB3	15:H:51:TYR:HE2	1.75	0.52
42:j:94:VAL:HG13	42:j:111:MET:HE3	1.92	0.52
50:r:33:ILE:HD12	50:r:59:GLU:HB3	1.92	0.52
1:1:976:G:H2'	1:1:977:G:H8	1.74	0.51
1:1:1709:U:H2'	1:1:1710:G:C8	2.45	0.51
1:1:1857:G:N2	1:1:1884:G:N3	2.58	0.51
1:1:1942:C:OP2	1:1:1943:U:O2'	2.20	0.51
2:2:1363:A:H2'	2:2:1365:G:N7	2.25	0.51
9:B:66:ASP:OD2	9:B:102:ARG:NH1	2.42	0.51
1:1:176:A:H3'	1:1:177:G:N2	2.25	0.51
1:1:190:A:H3'	1:1:204:A:H61	1.75	0.51
1:1:347:A:H2'	1:1:348:A:H8	1.75	0.51
1:1:686:U:H6	1:1:788:A:H61	1.58	0.51
1:1:1282:U:H3	1:1:1286:A:H62	1.58	0.51
1:1:1335:C:H2'	1:1:1336:A:H8	1.75	0.51
1:1:1463:C:H2'	1:1:1464:G:C8	2.46	0.51
1:1:2031:A:N3	1:1:2455:G:O2'	2.33	0.51
1:1:2034:U:H2'	1:1:2035:G:C8	2.44	0.51
2:2:564:C:OP2	49:q:12:ARG:NH2	2.33	0.51
2:2:744:C:H2'	2:2:745:G:C8	2.40	0.51
9:B:78:VAL:HG21	9:B:110:LEU:HD11	1.92	0.51
1:1:464:U:O4	1:1:684:G:O2'	2.28	0.51
1:1:514:A:N3	1:1:581:C:O2'	2.39	0.51
1:1:1592:C:H2'	1:1:1593:A:H8	1.74	0.51
2:2:555:U:H2'	2:2:556:C:C6	2.45	0.51
2:2:634:C:H2'	2:2:635:A:C8	2.46	0.51
46:n:57:MET:HE2	46:n:61:LEU:HD11	1.93	0.51
50:r:65:VAL:CG1	50:r:66:GLU:N	2.55	0.51
1:1:1:G:H2'	1:1:2:G:C8	2.46	0.51
1:1:259:G:HO2'	1:1:621:A:HO2'	1.58	0.51
1:1:296:U:H2'	1:1:297:G:H8	1.74	0.51
1:1:304:U:H3	1:1:313:G:H1	1.57	0.51
1:1:518:G:O5'	25:S:18:ARG:NH1	2.44	0.51
1:1:1047:G:H8	15:H:59:LEU:HD21	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2365:G:N7	37:e:39:LYS:NZ	2.51	0.51
2:2:1267:C:O2'	2:2:1268:G:OP1	2.28	0.51
4:4:142:U:O4	4:4:175:A:N1	2.43	0.51
4:4:202:G:O2'	4:4:234:A:OP1	2.29	0.51
4:4:249:U:O2	4:4:285:A:N6	2.43	0.51
4:4:330:U:H2'	4:4:331:C:C6	2.45	0.51
12:E:64:LYS:HE3	33:a:5:ILE:HD12	1.93	0.51
16:J:20:ALA:HA	16:J:23:LYS:HD2	1.93	0.51
1:1:438:G:H2'	1:1:439:A:H8	1.75	0.51
1:1:517:C:OP1	34:b:13:ARG:NH2	2.42	0.51
1:1:648:G:H2'	1:1:649:G:H8	1.75	0.51
1:1:715:A:C8	52:t:60:VAL:HG21	2.45	0.51
1:1:918:A:N3	3:3:80:U:O2'	2.38	0.51
1:1:1013:C:H2'	1:1:1014:A:C8	2.45	0.51
1:1:2204:G:OP2	9:B:150:LYS:NZ	2.42	0.51
1:1:2898:U:H2'	1:1:2899:A:C8	2.45	0.51
2:2:74:A:O2'	2:2:75:G:H8	1.94	0.51
4:4:31:G:OP2	4:4:321:G:N2	2.43	0.51
1:1:151:C:H2'	1:1:152:A:C8	2.45	0.51
1:1:378:C:H2'	1:1:379:G:C8	2.45	0.51
1:1:2229:U:H2'	1:1:2230:G:H8	1.75	0.51
2:2:600:A:H2'	2:2:601:G:H8	1.76	0.51
22:P:33:VAL:O	22:P:33:VAL:HG23	2.10	0.51
54:v:62:ARG:N	54:v:74:THR:O	2.43	0.51
1:1:935:C:H2'	1:1:936:A:H8	1.76	0.51
1:1:1059:G:H3'	1:1:1060:U:H2'	1.93	0.51
1:1:1431:A:H2'	1:1:1432:G:C8	2.45	0.51
1:1:1965:C:H5''	1:1:1966:A:H2'	1.92	0.51
1:1:2216:G:H2'	1:1:2217:G:H8	1.76	0.51
1:1:2707:U:H2'	1:1:2708:G:C8	2.45	0.51
15:H:48:ALA:HB3	15:H:51:TYR:CE2	2.45	0.51
17:K:58:LEU:HD12	17:K:59:LYS:O	2.09	0.51
1:1:190:A:N3	1:1:679:C:O2'	2.39	0.51
1:1:807:U:O2'	1:1:2060:A:N1	2.41	0.51
1:1:2411:A:H2'	1:1:2412:A:H8	1.76	0.51
1:1:2756:U:OP2	38:f:19:ARG:NE	2.44	0.51
1:1:2841:C:H2'	1:1:2842:G:C8	2.46	0.51
2:2:1217:C:OP1	51:s:5:SER:OG	2.29	0.51
4:4:205:G:O6	4:4:206:A:N6	2.44	0.51
13:F:9:VAL:HG12	13:F:50:LEU:HB2	1.83	0.51
14:G:90:LEU:HD11	14:G:123:ARG:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:709:U:H2'	2:2:710:G:C8	2.46	0.51
6:7:60:U:H5''	6:7:61:C:H5	1.76	0.51
26:T:25:GLU:HG3	26:T:26:LYS:HG3	1.93	0.51
33:a:56:ARG:NH2	33:a:59:ARG:CZ	2.73	0.51
47:o:11:LYS:HG2	47:o:71:LEU:HD13	1.93	0.51
1:1:2215:C:H2'	1:1:2216:G:C8	2.46	0.51
1:1:2691:C:H2'	1:1:2692:G:H8	1.74	0.51
1:1:2723:C:OP1	10:C:114:LYS:NZ	2.38	0.51
2:2:917:G:H2'	2:2:918:A:C8	2.46	0.51
2:2:1342:C:H2'	2:2:1343:G:C8	2.46	0.51
58:z:55:ARG:O	58:z:59:LYS:HG2	2.11	0.51
1:1:1844:C:H2'	1:1:1845:G:H8	1.76	0.50
1:1:1882:U:H2'	1:1:1883:U:C6	2.46	0.50
1:1:2680:U:O2'	10:C:11:MET:SD	2.70	0.50
2:2:178:C:H2'	2:2:179:A:C8	2.45	0.50
2:2:924:C:H2'	2:2:925:G:C8	2.45	0.50
2:2:966:2MG:H2'	2:2:967:5MC:C6	2.46	0.50
2:2:1287:A:H2'	2:2:1288:A:C8	2.47	0.50
2:2:1354:U:H2'	2:2:1355:G:H8	1.75	0.50
5:5:112:VAL:O	5:5:128:GLY:N	2.38	0.50
31:Y:17:GLU:HA	31:Y:20:ASN:HD21	1.75	0.50
50:r:86:TYR:O	50:r:90:ARG:HG2	2.10	0.50
1:1:1483:G:O6	1:1:1506:U:O4	2.29	0.50
1:1:2698:U:H2'	1:1:2699:C:C6	2.46	0.50
2:2:45:G:H2'	2:2:46:G:C8	2.46	0.50
2:2:768:A:H4'	2:2:1523:G:N2	2.26	0.50
2:2:1287:A:H2	2:2:1353:G:H1'	1.75	0.50
4:4:222:U:O2'	4:4:237:U:O2	2.27	0.50
10:C:5:VAL:HB	10:C:52:THR:HG21	1.93	0.50
40:h:7:PRO:HA	40:h:10:ILE:HG22	1.94	0.50
1:1:45:G:N7	1:1:215:G:O2'	2.40	0.50
1:1:211:C:H2'	1:1:212:G:C8	2.47	0.50
1:1:1153:C:OP1	23:Q:92:ARG:NH2	2.44	0.50
1:1:1720:U:H2'	1:1:1721:G:O4'	2.11	0.50
2:2:123:U:H2'	2:2:124:C:H6	1.76	0.50
23:Q:105:ALA:HB1	24:R:40:MET:HE1	1.92	0.50
25:S:25:ARG:NH1	25:S:74:ILE:O	2.44	0.50
1:1:84:A:N1	1:1:98:G:O2'	2.38	0.50
1:1:464:U:O2'	1:1:465:G:OP1	2.30	0.50
1:1:2372:U:H2'	1:1:2373:G:H8	1.77	0.50
4:4:43:G:N7	4:4:310:G:N2	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:167:ARG:HG3	9:B:172:VAL:HG22	1.94	0.50
41:i:152:GLN:O	41:i:155:VAL:CG1	2.58	0.50
43:k:3:HIS:ND1	43:k:65:GLU:OE1	2.44	0.50
1:1:527:C:H41	1:1:2777:G:HO2'	1.55	0.50
1:1:582:A:H2'	1:1:583:G:C8	2.46	0.50
1:1:1363:C:O2'	1:1:1809:A:N3	2.36	0.50
1:1:1576:U:H2'	1:1:1577:C:C6	2.46	0.50
1:1:2298:A:H62	1:1:2318:G:H21	1.58	0.50
1:1:2339:C:H2'	1:1:2340:A:C8	2.46	0.50
1:1:2417:C:H2'	1:1:2418:A:C8	2.47	0.50
27:U:86:ARG:NH1	27:U:100:SER:OG	2.42	0.50
42:j:57:PRO:O	42:j:60:ILE:HG13	2.12	0.50
46:n:12:ARG:HG3	46:n:13:LYS:H	1.76	0.50
1:1:69:C:H2'	1:1:70:G:C8	2.47	0.50
1:1:592:A:O2'	37:e:64:TYR:OH	2.28	0.50
1:1:1131:G:H4'	16:J:84:ILE:HD12	1.93	0.50
1:1:2705:A:O2'	1:1:2852:G:OP1	2.25	0.50
1:1:2841:C:H2'	1:1:2842:G:H8	1.75	0.50
2:2:647:C:H2'	2:2:648:A:H8	1.75	0.50
2:2:709:U:H2'	2:2:710:G:H8	1.77	0.50
2:2:1316:G:N1	2:2:1319:A:OP2	2.44	0.50
4:4:86:A:C8	4:4:90:G:H5''	2.46	0.50
4:4:116:A:H61	4:4:126:C:H42	1.58	0.50
25:S:73:LYS:HB3	25:S:106:VAL:HB	1.92	0.50
1:1:586:A:O2'	1:1:672:C:O4'	2.28	0.50
1:1:624:C:H2'	1:1:625:G:C8	2.47	0.50
1:1:863:A:H2'	1:1:864:G:C8	2.47	0.50
2:2:458:U:H2'	2:2:459:A:C8	2.46	0.50
4:4:47:G:H1'	4:4:300:U:N3	2.27	0.50
4:4:282:G:N2	4:4:287:U:O4	2.45	0.50
9:B:37:ASN:HB2	9:B:62:TYR:HB2	1.94	0.50
9:B:72:ASP:OD2	9:B:189:ARG:NH1	2.44	0.50
17:K:121:GLU:OE1	22:P:65:SER:OG	2.29	0.50
1:1:155:A:H2'	1:1:156:A:C8	2.47	0.50
1:1:175:G:H2'	1:1:176:A:H8	1.72	0.50
1:1:1710:G:H2'	1:1:1711:A:C8	2.47	0.50
2:2:543:U:H2'	2:2:544:G:H8	1.76	0.50
2:2:999:C:N3	2:2:1042:A:N6	2.59	0.50
2:2:1137:C:O2	2:2:1138:G:N2	2.45	0.50
4:4:317:G:H2'	4:4:318:G:H8	1.77	0.50
10:C:1:MET:HB3	10:C:205:PRO:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Q:49:ASP:HA	23:Q:52:GLN:HB2	1.94	0.50
1:1:2036:C:H2'	1:1:2037:A:C8	2.47	0.50
2:2:512:U:H2'	2:2:513:C:H6	1.76	0.50
2:2:521:G:N7	49:q:50:ARG:NH2	2.60	0.50
2:2:958:A:N7	56:x:55:ARG:NH2	2.60	0.50
2:2:1368:A:OP1	46:n:113:ARG:NH2	2.45	0.50
3:3:93:C:OP2	28:V:18:ARG:NH1	2.42	0.50
4:4:224:A:H4'	4:4:225:A:O5'	2.11	0.50
12:E:110:ARG:O	50:r:3:ARG:NH2	2.45	0.50
40:h:24:ALA:HB1	40:h:28:GLU:HB2	1.93	0.50
46:n:63:LEU:HD13	46:n:65:ILE:CG1	2.42	0.50
1:1:1265:A:H61	1:1:2013:A:H3'	1.77	0.49
1:1:1385:A:O2'	1:1:1396:U:O2	2.25	0.49
1:1:1915:3TD:HO2'	5:5:48:LYS:HD2	1.69	0.49
1:1:2812:G:H2'	1:1:2813:A:H8	1.75	0.49
2:2:123:U:H2'	2:2:124:C:C6	2.47	0.49
2:2:204:G:H2'	2:2:205:A:C8	2.47	0.49
2:2:967:5MC:OP2	2:2:968:A:O2'	2.24	0.49
2:2:1011:C:H2'	2:2:1012:A:H8	1.77	0.49
52:t:36:ILE:O	52:t:40:GLN:HG2	2.11	0.49
56:x:36:ARG:HA	56:x:71:LEU:HD22	1.93	0.49
57:y:35:VAL:HG11	57:y:79:LEU:HD13	1.93	0.49
1:1:145:C:H2'	1:1:146:A:C8	2.47	0.49
1:1:191:A:H2'	1:1:192:C:C6	2.47	0.49
1:1:2683:C:OP1	22:P:51:ARG:NH2	2.33	0.49
2:2:320:A:H2'	2:2:321:A:C8	2.46	0.49
16:J:7:LYS:HB2	16:J:10:THR:HG22	1.94	0.49
46:n:99:ARG:HD3	46:n:104:VAL:HB	1.94	0.49
49:q:64:THR:HG22	49:q:93:VAL:HG23	1.94	0.49
1:1:417:C:H2'	1:1:418:C:H6	1.77	0.49
1:1:499:U:H5''	27:U:43:LYS:HD3	1.93	0.49
1:1:1697:G:OP2	1:1:1698:A:O2'	2.23	0.49
1:1:1709:U:H2'	1:1:1710:G:H8	1.77	0.49
1:1:2626:C:H2'	1:1:2627:G:C8	2.46	0.49
1:1:2818:U:H2'	1:1:2819:G:C8	2.47	0.49
2:2:562:U:H1'	49:q:12:ARG:HD2	1.94	0.49
2:2:1507:A:H2'	2:2:1508:A:H8	1.77	0.49
4:4:166:C:O2	4:4:167:G:N1	2.45	0.49
11:D:143:LEU:HD13	11:D:146:VAL:HG21	1.95	0.49
14:G:3:VAL:CG2	14:G:36:ALA:HB1	2.42	0.49
1:1:31:C:O2'	1:1:1238:G:OP1	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:888:C:OP1	50:r:93:ARG:NH1	2.45	0.49
1:1:1548:A:H2'	1:1:1549:A:C8	2.47	0.49
1:1:2419:U:OP2	37:e:33:LEU:HD12	2.13	0.49
2:2:1157:A:N7	2:2:1180:A:N6	2.61	0.49
4:4:170:G:O6	4:4:171:A:N6	2.46	0.49
32:Z:24:LEU:HG	32:Z:29:LEU:HD12	1.93	0.49
39:g:136:MET:HA	39:g:139:ARG:HE	1.78	0.49
46:n:55:VAL:HG21	46:n:94:LEU:HD23	1.95	0.49
47:o:6:ILE:HG22	47:o:76:ILE:HB	1.93	0.49
48:p:98:ARG:HD2	58:z:12:PHE:HE2	1.77	0.49
53:u:19:VAL:HB	53:u:36:VAL:O	2.12	0.49
53:u:76:LYS:HG2	53:u:80:LYS:HE3	1.95	0.49
1:1:523:C:H2'	1:1:524:G:C8	2.47	0.49
1:1:924:G:H2'	1:1:925:A:C8	2.47	0.49
1:1:1283:G:N1	1:1:1286:A:OP2	2.44	0.49
2:2:405:U:OP2	41:i:3:ARG:NH1	2.45	0.49
2:2:876:C:H1'	45:m:12:THR:HG21	1.94	0.49
2:2:1291:U:H2'	2:2:1292:G:C8	2.46	0.49
6:7:68:C:H2'	6:7:69:G:C8	2.47	0.49
13:F:89:LEU:HD21	13:F:94:TYR:HB3	1.93	0.49
15:H:5:LEU:O	15:H:9:GLN:HB2	2.13	0.49
48:p:46:THR:HG23	48:p:49:GLY:H	1.78	0.49
1:1:764:A:H5'	9:B:209:GLY:HA2	1.94	0.49
1:1:828:U:O2'	1:1:831:G:O6	2.30	0.49
1:1:2117:A:O2'	1:1:2119:A:OP2	2.30	0.49
1:1:2126:A:H62	1:1:2163:A:H8	1.61	0.49
1:1:2696:U:H2'	1:1:2697:G:C8	2.47	0.49
1:1:2865:U:OP2	1:1:2866:U:O2'	2.25	0.49
2:2:932:C:H2'	2:2:933:G:H8	1.77	0.49
2:2:999:C:H2'	2:2:1000:A:C8	2.47	0.49
3:3:39:A:H2'	3:3:40:U:C6	2.48	0.49
4:4:186:A:H2	40:h:102:ASN:HA	1.76	0.49
5:5:36:LEU:HA	5:5:86:ARG:HH21	1.77	0.49
13:F:137:ASP:OD1	13:F:138:LYS:N	2.45	0.49
17:K:21:CYS:HA	17:K:41:ILE:HG22	1.93	0.49
1:1:1093:G:H2'	1:1:1094:U:O4'	2.12	0.49
1:1:1825:U:H2'	1:1:1826:G:C8	2.47	0.49
1:1:2385:C:H2'	1:1:2386:A:C8	2.48	0.49
1:1:2451:A:N3	29:W:2:ALA:CB	2.72	0.49
1:1:2845:U:H2'	1:1:2846:G:C8	2.48	0.49
2:2:1497:G:H1'	2:2:1518:MA6:C2	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:7:22:G:H2'	6:7:23:A:H8	1.77	0.49
19:M:135:VAL:HG23	28:V:57:TYR:CD2	2.47	0.49
1:1:55:G:H2'	1:1:56:A:H8	1.77	0.49
1:1:417:C:H2'	1:1:418:C:C6	2.48	0.49
1:1:832:U:H2'	1:1:833:A:C8	2.42	0.49
1:1:2194:U:H2'	1:1:2195:U:C6	2.47	0.49
2:2:543:U:H2'	2:2:544:G:C8	2.47	0.49
2:2:1496:C:H2'	2:2:1497:G:C8	2.47	0.49
5:5:15:ALA:HB1	5:5:51:ILE:HD12	1.93	0.49
25:S:6:LYS:HG2	25:S:104:THR:HG22	1.95	0.49
39:g:11:LYS:O	39:g:208:ARG:NH1	2.46	0.49
5:5:153:ARG:O	41:i:47:ARG:NH1	2.32	0.49
11:D:176:ASP:N	11:D:176:ASP:OD1	2.45	0.49
28:V:77:VAL:HG23	28:V:89:ILE:HG12	1.95	0.49
46:n:120:LYS:HB2	46:n:123:ARG:HB3	1.94	0.49
51:s:64:CYS:HB3	51:s:68:GLY:H	1.78	0.49
1:1:587:C:H42	18:L:33:ARG:HD2	1.78	0.49
1:1:599:A:H2'	1:1:600:G:H8	1.78	0.49
1:1:1469:A:H2'	1:1:1470:A:H8	1.78	0.49
1:1:2599:G:H2'	1:1:2600:A:H8	1.77	0.49
2:2:17:U:H2'	2:2:18:C:H6	1.78	0.49
2:2:19:A:H2'	2:2:20:U:C6	2.48	0.49
2:2:424:G:H2'	2:2:425:G:H8	1.78	0.49
2:2:879:C:OP1	49:q:5:ASN:ND2	2.45	0.49
19:M:40:ARG:HD3	19:M:93:VAL:HG11	1.95	0.49
1:1:244:A:OP2	37:e:8:ARG:NH2	2.33	0.48
1:1:729:G:O2'	1:1:763:G:H4'	2.13	0.48
1:1:1181:U:H2'	1:1:1182:G:H8	1.74	0.48
1:1:1958:C:H2'	1:1:1959:G:H8	1.77	0.48
1:1:2513:A:H2'	1:1:2514:U:C6	2.48	0.48
2:2:899:C:O2'	2:2:900:A:OP1	2.26	0.48
2:2:1287:A:H2'	2:2:1288:A:H8	1.77	0.48
2:2:1314:C:H2'	2:2:1315:U:C6	2.48	0.48
3:3:28:C:H2'	3:3:29:A:H8	1.78	0.48
4:4:225:A:H61	4:4:235:C:H42	1.61	0.48
5:5:112:VAL:HG23	5:5:130:ALA:HB2	1.95	0.48
39:g:186:ILE:HD13	39:g:200:ILE:HB	1.94	0.48
50:r:65:VAL:HG12	50:r:66:GLU:HG3	1.95	0.48
1:1:2101:A:H2'	1:1:2102:G:O4'	2.14	0.48
1:1:2487:G:H2'	1:1:2488:G:C8	2.48	0.48
2:2:304:U:H2'	2:2:305:G:C8	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:539:A:H2'	2:2:540:G:C8	2.48	0.48
9:B:130:LEU:HD12	9:B:130:LEU:C	2.37	0.48
11:D:1:MET:HB3	11:D:14:VAL:HG23	1.94	0.48
14:G:37:VAL:HG23	14:G:38:PRO:HD2	1.95	0.48
43:k:59:TYR:OH	55:w:66:SER:OG	2.32	0.48
1:1:2355:G:H1'	8:A:39:ARG:HH21	1.79	0.48
1:1:2368:C:H2'	1:1:2369:A:C8	2.42	0.48
1:1:2583:G:N2	4:4:363:A:H1'	2.28	0.48
2:2:215:C:H2'	2:2:216:U:H6	1.77	0.48
10:C:33:ARG:NH1	10:C:53:GLY:O	2.45	0.48
14:G:115:VAL:O	14:G:116:ARG:NE	2.47	0.48
26:T:69:ARG:HG2	26:T:74:ILE:HG22	1.94	0.48
43:k:86:ARG:NH1	55:w:64:TYR:O	2.44	0.48
1:1:284:U:N3	1:1:285:G:O6	2.47	0.48
1:1:428:A:HO2'	1:1:429:A:P	2.37	0.48
1:1:686:U:H2'	1:1:788:A:N1	2.28	0.48
1:1:1316:U:H2'	1:1:1317:G:C8	2.48	0.48
1:1:2514:U:H2'	1:1:2515:C:C6	2.48	0.48
1:1:2751:G:OP1	1:1:2751:G:N2	2.38	0.48
2:2:736:C:H2'	2:2:737:C:H6	1.79	0.48
2:2:1088:G:H21	2:2:1167:A:N6	2.10	0.48
4:4:15:A:OP1	4:4:15:A:H4'	2.14	0.48
16:J:118:MET:HA	16:J:121:LYS:HE2	1.94	0.48
26:T:8:LEU:HD23	26:T:50:LEU:HD21	1.94	0.48
55:w:50:LYS:HA	55:w:53:ARG:HH21	1.77	0.48
1:1:212:G:H2'	1:1:213:A:C8	2.47	0.48
1:1:347:A:H2'	1:1:348:A:C8	2.49	0.48
1:1:596:U:H2'	1:1:597:G:H8	1.79	0.48
1:1:1335:C:H2'	1:1:1336:A:C8	2.48	0.48
1:1:2425:A:H4'	1:1:2426:A:O5'	2.12	0.48
41:i:13:ARG:HG2	41:i:34:ILE:HA	1.95	0.48
1:1:494:G:H4'	25:S:6:LYS:HB2	1.96	0.48
1:1:680:C:H2'	1:1:681:G:H8	1.78	0.48
1:1:1564:C:H2'	1:1:1565:C:C6	2.48	0.48
1:1:2463:C:H2'	1:1:2464:G:H8	1.78	0.48
1:1:2897:U:H2'	1:1:2898:U:H6	1.78	0.48
12:E:4:LEU:HG	12:E:101:GLU:HB2	1.95	0.48
12:E:44:ILE:HD11	12:E:79:ILE:HG22	1.96	0.48
13:F:9:VAL:CG1	13:F:50:LEU:CB	2.66	0.48
19:M:4:PRO:HG3	19:M:68:PHE:HE2	1.79	0.48
47:o:52:LEU:HB2	51:s:81:ARG:HD2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:545:U:O2'	1:1:548:G:OP2	2.32	0.48
1:1:571:U:N3	1:1:575:A:N7	2.61	0.48
1:1:793:A:OP2	1:1:2071:A:O2'	2.32	0.48
1:1:970:U:H2'	1:1:971:G:H8	1.78	0.48
1:1:1345:C:H2'	1:1:1346:G:H8	1.77	0.48
1:1:2241:A:H2'	1:1:2242:G:C8	2.49	0.48
1:1:2291:U:H2'	1:1:2292:U:C6	2.48	0.48
1:1:2804:U:H2'	1:1:2805:C:H6	1.78	0.48
2:2:451:A:H4'	2:2:452:A:O4'	2.13	0.48
4:4:117:G:H21	4:4:125:A:H62	1.60	0.48
11:D:46:GLN:HB2	11:D:86:ALA:HB1	1.96	0.48
40:h:110:GLU:HB2	40:h:144:LEU:HD11	1.93	0.48
50:r:11:ASP:HA	50:r:45:ILE:HB	1.94	0.48
1:1:24:G:H2'	1:1:25:U:C6	2.49	0.48
1:1:680:C:H2'	1:1:681:G:C8	2.48	0.48
1:1:1447:C:H2'	1:1:1448:G:H8	1.78	0.48
1:1:2011:U:H2'	1:1:2012:G:O4'	2.14	0.48
1:1:2438:U:O2'	1:1:2440:C:OP1	2.29	0.48
2:2:1003:G:N2	2:2:1005:A:O5'	2.47	0.48
4:4:24:G:O6	4:4:329:U:O4	2.32	0.48
4:4:51:A:N6	4:4:62:G:OP2	2.47	0.48
11:D:124:PHE:HE2	11:D:141:MET:HE1	1.79	0.48
32:Z:56:LYS:NZ	32:Z:58:GLU:OE2	2.47	0.48
33:a:51:VAL:HG11	50:r:75:MET:HG3	1.96	0.48
1:1:142:A:O2'	26:T:1:MET:N	2.47	0.48
1:1:596:U:H2'	1:1:597:G:C8	2.49	0.48
1:1:611:C:H2'	1:1:612:G:O4'	2.14	0.48
1:1:2044:C:H42	1:1:2624:G:H1	1.62	0.48
2:2:8:A:N6	41:i:202:GLU:O	2.44	0.48
2:2:539:A:H2'	2:2:540:G:H8	1.78	0.48
2:2:676:A:H1'	48:p:117:PRO:HB3	1.96	0.48
10:C:179:ARG:HB3	10:C:188:LEU:HD12	1.96	0.48
15:H:44:ALA:HB2	15:H:52:MET:HE2	1.95	0.48
17:K:18:ARG:HB2	17:K:45:GLU:HB3	1.96	0.48
19:M:53:MET:O	19:M:57:VAL:HG23	2.13	0.48
30:X:15:GLY:HA3	30:X:29:PHE:HE2	1.77	0.48
42:j:76:LEU:HD21	42:j:120:VAL:HG22	1.95	0.48
1:1:228:C:N3	1:1:417:C:O2'	2.45	0.48
1:1:371:A:H61	1:1:401:A:H3'	1.78	0.48
1:1:948:C:H2'	1:1:949:G:H8	1.79	0.48
1:1:967:U:H2'	1:1:968:C:H6	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1999:C:H1'	1:1:2687:U:H1'	1.96	0.48
1:1:2419:U:H4'	35:c:22:THR:HG21	1.96	0.48
1:1:2661:G:O2'	1:1:2662:A:O4'	2.25	0.48
2:2:358:U:H2'	2:2:359:G:C8	2.47	0.48
2:2:977:A:O2'	2:2:979:C:OP2	2.31	0.48
9:B:69:ARG:HG3	9:B:129:THR:HG21	1.96	0.48
9:B:130:LEU:CD1	9:B:131:PRO:O	2.61	0.48
13:F:42:GLU:HB2	13:F:55:ARG:HE	1.79	0.48
40:h:156:ARG:NE	40:h:160:ALA:O	2.47	0.48
48:p:23:ILE:HD12	48:p:86:VAL:HG22	1.96	0.48
1:1:2023:C:H2'	1:1:2024:G:H8	1.79	0.47
2:2:1068:G:N1	2:2:1108:G:H1'	2.28	0.47
2:2:1187:G:H5''	46:n:115:LYS:HD3	1.96	0.47
2:2:1372:U:H2'	2:2:1373:G:O4'	2.13	0.47
3:3:116:G:H2'	3:3:117:G:H8	1.78	0.47
8:A:37:ILE:HG22	8:A:38:VAL:HG23	1.95	0.47
11:D:83:VAL:HB	11:D:86:ALA:HB2	1.96	0.47
19:M:31:PHE:HD1	19:M:132:THR:HG22	1.78	0.47
23:Q:3:ARG:HG3	23:Q:3:ARG:O	2.14	0.47
40:h:138:VAL:HA	40:h:149:ILE:HD13	1.95	0.47
43:k:43:GLY:O	43:k:58:HIS:HA	2.14	0.47
46:n:21:ILE:HD13	46:n:63:LEU:CB	2.44	0.47
1:1:1143:A:N6	16:J:26:GLY:O	2.47	0.47
2:2:1160:G:H1	2:2:1176:A:N6	2.12	0.47
2:2:1414:U:H2'	2:2:1415:G:H8	1.79	0.47
4:4:212:U:H3	4:4:242:A:H62	1.62	0.47
4:4:330:U:H2'	4:4:331:C:H6	1.78	0.47
1:1:1114:C:H2'	1:1:1115:G:C8	2.48	0.47
1:1:1426:G:OP2	1:1:1427:A:O2'	2.23	0.47
1:1:1475:G:O2'	1:1:1514:G:O6	2.31	0.47
1:1:1918:A:O2'	1:1:1920:C:N4	2.47	0.47
1:1:2027:G:H2'	1:1:2028:U:H6	1.79	0.47
2:2:355:C:H1'	2:2:388:G:H1'	1.94	0.47
2:2:1441:A:H62	2:2:1461:G:H21	1.63	0.47
4:4:19:G:N3	5:5:93:ASN:HB2	2.29	0.47
13:F:52:PHE:HZ	13:F:72:LEU:HD12	1.78	0.47
39:g:35:ARG:O	39:g:38:VAL:HG22	2.14	0.47
1:1:1417:C:H2'	1:1:1418:G:O4'	2.14	0.47
1:1:2414:G:C2	1:1:2415:G:C8	3.03	0.47
1:1:2684:U:O4'	17:K:70:ARG:NH1	2.47	0.47
2:2:309:A:H2'	2:2:310:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:600:A:H2'	2:2:601:G:C8	2.49	0.47
2:2:879:C:H2'	2:2:880:C:H6	1.80	0.47
2:2:1020:G:H2'	2:2:1021:A:C8	2.49	0.47
2:2:1038:C:H2'	2:2:1039:G:C8	2.50	0.47
2:2:1241:G:H2'	2:2:1242:G:H8	1.79	0.47
2:2:1412:C:H2'	2:2:1413:A:C8	2.49	0.47
3:3:60:C:H2'	3:3:61:G:C8	2.49	0.47
14:G:3:VAL:HG22	14:G:36:ALA:HB1	1.95	0.47
43:k:2:ARG:HG3	43:k:4:TYR:CE2	2.49	0.47
1:1:306:U:H3	1:1:310:A:H62	1.63	0.47
1:1:1443:U:H2'	1:1:1444:G:H8	1.79	0.47
1:1:2030:6MZ:H5'2	1:1:2031:A:C8	2.49	0.47
1:1:2774:C:H2'	1:1:2775:G:O4'	2.14	0.47
2:2:254:G:H2'	2:2:255:G:H8	1.80	0.47
2:2:495:A:H4'	2:2:496:A:H5'	1.95	0.47
3:3:33:G:H2'	3:3:34:A:C8	2.49	0.47
15:H:41:LEU:O	15:H:44:ALA:HB3	2.15	0.47
52:t:39:LEU:HD23	52:t:43:PHE:HE2	1.80	0.47
1:1:171:U:H2'	1:1:172:A:C8	2.47	0.47
1:1:1050:A:N1	1:1:2751:G:C6	2.83	0.47
1:1:1281:G:H2'	1:1:1282:U:C6	2.49	0.47
1:1:1999:C:O2	1:1:2687:U:O2'	2.28	0.47
1:1:2063:C:N4	1:1:2501:C:O2	2.47	0.47
1:1:2685:G:H21	1:1:2726:A:N6	2.12	0.47
3:3:28:C:H2'	3:3:29:A:C8	2.50	0.47
3:3:66:A:H61	3:3:107:G:H2'	1.79	0.47
14:G:90:LEU:CD2	14:G:124:THR:C	2.81	0.47
20:N:87:PHE:HD1	20:N:90:ARG:HD2	1.78	0.47
45:m:78:VAL:CG2	45:m:128:TYR:CD2	2.97	0.47
48:p:70:CYS:O	48:p:74:VAL:HG23	2.14	0.47
1:1:307:G:H22	1:1:309:A:H3'	1.78	0.47
1:1:365:U:H2'	1:1:366:C:C6	2.50	0.47
1:1:519:U:H2'	1:1:520:G:H8	1.79	0.47
1:1:685:A:N1	1:1:787:C:H1'	2.30	0.47
1:1:692:C:H2'	1:1:693:A:H8	1.80	0.47
1:1:1046:A:O2'	15:H:59:LEU:HD23	2.14	0.47
1:1:1107:G:C2'	15:H:81:LEU:HD12	2.44	0.47
1:1:1330:C:H2'	1:1:1331:G:C8	2.49	0.47
1:1:1541:C:H2'	1:1:1542:U:C6	2.50	0.47
1:1:1651:G:H2'	1:1:1652:A:H8	1.80	0.47
1:1:2086:U:H2'	1:1:2087:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2243:U:H2'	1:1:2244:U:C6	2.49	0.47
1:1:2376:A:N3	21:O:111:ARG:NH1	2.62	0.47
1:1:2853:C:H2'	1:1:2854:G:C8	2.50	0.47
2:2:34:C:H2'	2:2:35:G:H8	1.80	0.47
2:2:555:U:H2'	2:2:556:C:H6	1.79	0.47
2:2:1317:C:H3'	2:2:1318:A:H8	1.80	0.47
4:4:19:G:O2'	4:4:20:A:OP1	2.24	0.47
11:D:27:LEU:HD11	11:D:100:MET:HB3	1.97	0.47
16:J:19:ASP:OD1	16:J:19:ASP:N	2.46	0.47
47:o:36:VAL:HG12	47:o:38:GLY:H	1.80	0.47
1:1:401:A:H2'	1:1:402:A:C8	2.50	0.47
1:1:521:U:H2'	1:1:522:A:C8	2.48	0.47
1:1:1418:G:N2	1:1:1579:A:N7	2.62	0.47
1:1:1649:G:H2'	1:1:1650:A:C8	2.48	0.47
1:1:1992:G:N2	1:1:1996:C:O2'	2.43	0.47
1:1:2111:U:O4'	1:1:2147:A:N6	2.47	0.47
1:1:2496:C:H2'	1:1:2497:A:O4'	2.15	0.47
1:1:2597:G:OP1	9:B:241:GLY:HA3	2.14	0.47
1:1:2699:C:H2'	1:1:2700:A:C8	2.50	0.47
2:2:490:C:H2'	2:2:491:G:C8	2.47	0.47
2:2:1060:U:H5	40:h:2:GLY:HA3	1.79	0.47
2:2:1305:G:O2'	2:2:1306:A:H8	1.96	0.47
2:2:1368:A:OP1	47:o:64:GLN:NE2	2.41	0.47
2:2:1422:G:O2'	17:K:49:ARG:NH2	2.48	0.47
13:F:52:PHE:CZ	13:F:72:LEU:HD12	2.49	0.47
40:h:64:ILE:HG22	40:h:97:VAL:HG23	1.96	0.47
1:1:1164:C:H2'	1:1:1165:A:H8	1.79	0.47
1:1:1848:A:O2'	2:2:702:A:OP2	2.29	0.47
1:1:2052:A:O2'	10:C:148:GLN:O	2.30	0.47
1:1:2494:G:C2	1:1:2495:G:C8	3.02	0.47
1:1:2649:C:H2'	1:1:2650:U:H6	1.79	0.47
2:2:647:C:H2'	2:2:648:A:C8	2.49	0.47
2:2:1040:U:H2'	2:2:1041:G:C8	2.50	0.47
2:2:1178:G:N2	2:2:1181:G:OP2	2.48	0.47
2:2:1314:C:H2'	2:2:1315:U:H6	1.80	0.47
4:4:317:G:H2'	4:4:318:G:C8	2.50	0.47
4:4:323:A:O2'	4:4:324:G:O4'	2.33	0.47
13:F:26:ILE:HD12	13:F:75:MET:HE2	1.96	0.47
1:1:544:C:H42	1:1:549:G:H1	1.63	0.47
1:1:632:A:H2'	1:1:633:A:C8	2.50	0.47
1:1:741:U:H2'	1:1:742:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:871:U:OP1	19:M:5:LYS:NZ	2.38	0.47
1:1:2438:U:H2'	1:1:2441:U:C5	2.50	0.47
1:1:2699:C:H2'	1:1:2700:A:H8	1.80	0.47
2:2:237:G:H4'	54:v:27:ARG:HH22	1.80	0.47
2:2:707:U:H2'	2:2:708:C:H6	1.80	0.47
2:2:1068:G:OP1	2:2:1387:G:O2'	2.33	0.47
2:2:1090:U:H2'	2:2:1091:U:C6	2.50	0.47
3:3:60:C:H2'	3:3:61:G:H8	1.80	0.47
11:D:181:ILE:HG12	18:L:1:MET:HE2	1.96	0.47
20:N:73:ASN:HA	20:N:76:VAL:HG12	1.95	0.47
25:S:4:ILE:HG22	25:S:106:VAL:HG22	1.97	0.47
32:Z:41:THR:HG23	32:Z:44:ILE:H	1.80	0.47
39:g:66:LYS:HB2	39:g:158:PRO:HA	1.97	0.47
47:o:6:ILE:HG23	47:o:76:ILE:HB	1.96	0.47
1:1:227:A:C2	1:1:2407:A:H1'	2.50	0.46
1:1:744:U:H2'	1:1:745:1MG:O4'	2.15	0.46
1:1:1141:U:H4'	1:1:1142:A:O4'	2.15	0.46
1:1:2025:C:H2'	1:1:2026:U:C6	2.50	0.46
1:1:2111:U:O2'	1:1:2112:G:O3'	2.32	0.46
2:2:148:G:N2	2:2:175:C:O2	2.48	0.46
2:2:603:U:H2'	2:2:604:G:C8	2.50	0.46
2:2:1171:A:H2'	2:2:1172:C:H6	1.80	0.46
13:F:24:ILE:HD13	13:F:72:LEU:HD11	1.97	0.46
23:Q:17:ILE:HG13	23:Q:32:TYR:HE1	1.80	0.46
1:1:67:U:C2	1:1:68:G:C8	3.03	0.46
2:2:1038:C:H2'	2:2:1039:G:H8	1.79	0.46
2:2:1141:C:HO2'	2:2:1142:G:H8	1.63	0.46
4:4:142:U:H2'	4:4:143:C:C5	2.50	0.46
4:4:179:A:H2'	4:4:179:A:N3	2.31	0.46
4:4:340:G:H5''	19:M:55:ARG:HH12	1.80	0.46
49:q:114:ARG:HG3	49:q:119:VAL:HB	1.96	0.46
1:1:732:C:H2'	1:1:733:G:O4'	2.16	0.46
1:1:1609:A:O2'	1:1:1610:A:H5''	2.14	0.46
1:1:1713:A:N6	1:1:1746:A:N1	2.63	0.46
1:1:2222:C:H2'	1:1:2223:G:H8	1.80	0.46
1:1:2445:2MG:P	11:D:69:ARG:HH22	2.37	0.46
2:2:912:C:H2'	2:2:913:A:C8	2.50	0.46
2:2:948:C:H42	2:2:1233:G:H1	1.63	0.46
2:2:1534:A:H1'	2:2:1535:C:C5	2.51	0.46
3:3:76:G:H5'	28:V:9:ARG:HH12	1.79	0.46
17:K:1:MET:HG3	17:K:67:LYS:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Z:47:MET:O	32:Z:51:VAL:HG22	2.15	0.46
40:h:14:ILE:HG22	40:h:15:VAL:HG23	1.97	0.46
56:x:17:LYS:HA	56:x:20:GLU:HG2	1.96	0.46
1:1:714:U:OP2	52:t:88:ARG:NH2	2.29	0.46
1:1:906:U:O2'	19:M:66:ARG:NH2	2.41	0.46
1:1:1219:U:H2'	1:1:1220:G:C8	2.51	0.46
1:1:1330:C:H2'	1:1:1331:G:H8	1.80	0.46
1:1:1591:A:H2'	1:1:1592:C:H6	1.80	0.46
1:1:1869:G:N2	1:1:1871:A:O2'	2.48	0.46
1:1:2075:U:O2'	1:1:2596:U:O4	2.33	0.46
1:1:2222:C:H2'	1:1:2223:G:C8	2.50	0.46
2:2:966:2MG:N2	6:7:34:G:H5'	2.31	0.46
2:2:1016:A:O2'	2:2:1217:C:O2'	2.26	0.46
2:2:1228:C:H2'	2:2:1229:A:C8	2.49	0.46
4:4:145:C:H5'	4:4:174:A:H61	1.80	0.46
10:C:133:THR:OG1	10:C:134:HIS:N	2.48	0.46
14:G:90:LEU:HD12	14:G:90:LEU:C	2.39	0.46
20:N:34:ILE:HG13	20:N:113:ILE:HG23	1.96	0.46
46:n:30:ILE:HG12	46:n:65:ILE:HB	1.97	0.46
1:1:158:U:O4	1:1:159:G:N2	2.46	0.46
1:1:935:C:H2'	1:1:936:A:C8	2.51	0.46
1:1:2522:U:O2'	1:1:2647:U:OP1	2.29	0.46
1:1:2625:G:H2'	1:1:2626:C:C6	2.51	0.46
1:1:2649:C:H2'	1:1:2650:U:C6	2.51	0.46
1:1:2824:C:OP2	1:1:2825:G:N2	2.49	0.46
1:1:2895:G:H2'	1:1:2896:C:H6	1.80	0.46
2:2:910:C:H2'	2:2:911:U:H6	1.80	0.46
2:2:1118:U:H2'	2:2:1119:C:C6	2.51	0.46
2:2:1350:A:O2'	44:l:33:ASP:OD1	2.31	0.46
5:5:92:LEU:O	5:5:97:LEU:HB2	2.15	0.46
30:X:18:ARG:HH11	30:X:22:LEU:HD12	1.80	0.46
31:Y:54:LYS:O	31:Y:58:ASN:ND2	2.45	0.46
41:i:95:GLU:OE1	41:i:100:ASN:ND2	2.38	0.46
46:n:26:GLY:N	46:n:62:ASP:OD1	2.49	0.46
1:1:285:G:H22	1:1:355:U:H2'	1.80	0.46
1:1:548:G:H3'	1:1:549:G:O4'	2.15	0.46
1:1:549:G:H2'	1:1:550:C:C6	2.49	0.46
1:1:631:A:HO2'	1:1:632:A:P	2.38	0.46
1:1:1106:G:O3'	15:H:56:ARG:O	2.34	0.46
1:1:1435:G:H2'	1:1:1436:G:H8	1.79	0.46
1:1:2027:G:H2'	1:1:2028:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2796:U:O2'	1:1:2797:U:H5''	2.15	0.46
2:2:488:C:H2'	2:2:489:C:H6	1.80	0.46
2:2:501:C:H1'	2:2:549:C:H1'	1.98	0.46
2:2:1004:A:H2'	2:2:1005:A:O4'	2.15	0.46
5:5:50:ASN:CB	5:5:69:ASN:ND2	2.64	0.46
30:X:3:ARG:O	30:X:12:PRO:HD3	2.14	0.46
48:p:29:ASN:HD21	48:p:57:LYS:HD2	1.81	0.46
1:1:519:U:C2	1:1:520:G:C8	3.04	0.46
1:1:639:U:H2'	1:1:640:C:C6	2.50	0.46
1:1:840:C:H2'	1:1:841:G:C8	2.51	0.46
1:1:931:U:N3	1:1:1167:C:O2	2.48	0.46
1:1:1083:U:P	15:H:41:LEU:CD1	3.02	0.46
1:1:1800:C:OP2	9:B:182:ARG:NH1	2.43	0.46
1:1:2074:U:H2'	1:1:2075:U:C6	2.51	0.46
1:1:2395:C:H2'	1:1:2396:G:C8	2.50	0.46
1:1:2516:A:O2'	1:1:2517:C:OP1	2.30	0.46
2:2:603:U:H2'	2:2:604:G:H8	1.80	0.46
2:2:651:C:H2'	2:2:652:U:C6	2.50	0.46
2:2:1008:U:H2'	2:2:1009:U:C6	2.51	0.46
4:4:19:G:O2'	5:5:93:ASN:HA	2.15	0.46
5:5:143:LYS:HE3	5:5:143:LYS:HB3	1.45	0.46
15:H:26:VAL:HG21	15:H:114:GLU:HG2	1.98	0.46
42:j:23:LYS:HB3	42:j:30:ILE:HB	1.98	0.46
43:k:51:ILE:O	43:k:54:LEU:HG	2.15	0.46
1:1:1076:C:H2'	1:1:1077:A:O4'	2.15	0.46
1:1:1401:G:H2'	1:1:1402:U:C6	2.49	0.46
1:1:1604:C:H2'	1:1:1605:C:C6	2.51	0.46
1:1:1710:G:H2'	1:1:1711:A:H8	1.81	0.46
1:1:2419:U:OP1	37:e:41:LYS:NZ	2.37	0.46
2:2:309:A:O2'	2:2:607:A:N1	2.49	0.46
2:2:501:C:H2'	2:2:502:A:C8	2.50	0.46
2:2:928:G:H2'	2:2:929:G:H8	1.80	0.46
2:2:1181:G:H1'	2:2:1182:G:C4	2.50	0.46
45:m:78:VAL:CG2	45:m:128:TYR:CE2	2.99	0.46
50:r:16:VAL:HA	50:r:30:SER:OG	2.16	0.46
1:1:25:U:H2'	1:1:26:G:O4'	2.16	0.46
1:1:151:C:N3	1:1:176:A:N6	2.63	0.46
1:1:239:C:O2'	1:1:622:G:O2'	2.25	0.46
1:1:438:G:H2'	1:1:439:A:C8	2.51	0.46
1:1:597:G:H2'	1:1:598:U:C6	2.50	0.46
1:1:1179:G:H3'	1:1:1180:U:H5''	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1682:G:H2'	1:1:1683:U:C6	2.51	0.46
1:1:2142:A:N6	1:1:2151:U:H3	2.14	0.46
1:1:2896:C:H2'	1:1:2897:U:H6	1.79	0.46
2:2:113:G:H2'	2:2:114:U:C6	2.51	0.46
2:2:1199:U:O2'	2:2:1202:U:OP2	2.33	0.46
2:2:1272:G:H2'	2:2:1273:C:C6	2.51	0.46
2:2:1391:U:H2'	2:2:1392:G:C8	2.51	0.46
2:2:1517:G:H2'	2:2:1518:MA6:C8	2.46	0.46
3:3:77:U:OP1	28:V:21:ARG:NH1	2.49	0.46
4:4:160:U:N3	4:4:161:U:O4	2.49	0.46
38:f:25:VAL:HB	38:f:35:GLN:HB2	1.98	0.46
46:n:65:ILE:HD13	46:n:79:ILE:HG23	1.97	0.46
1:1:18:U:O2'	1:1:554:U:OP1	2.32	0.46
1:1:419:U:H2'	1:1:420:C:C6	2.50	0.46
1:1:1276:A:O2'	20:N:16:HIS:NE2	2.33	0.46
1:1:1614:A:H61	25:S:88:ARG:H	1.63	0.46
1:1:2086:U:H2'	1:1:2087:G:C8	2.50	0.46
1:1:2182:U:O2'	1:1:2183:A:H8	1.99	0.46
2:2:199:A:H2'	2:2:200:G:H8	1.81	0.46
2:2:215:C:H2'	2:2:216:U:C6	2.51	0.46
2:2:458:U:H2'	2:2:459:A:H8	1.80	0.46
2:2:553:A:H2'	2:2:554:A:H8	1.81	0.46
2:2:922:G:H2'	2:2:923:A:H8	1.81	0.46
2:2:999:C:H2'	2:2:1000:A:H8	1.81	0.46
2:2:1118:U:H1'	2:2:1179:A:C5	2.51	0.46
2:2:1404:C:H2'	2:2:1405:G:H8	1.79	0.46
3:3:6:G:H2'	3:3:7:G:H8	1.81	0.46
4:4:335:C:H4'	5:5:42:LYS:HE3	1.97	0.46
15:H:118:ILE:H	15:H:119:PRO:CD	2.29	0.46
21:O:116:GLN:OE1	21:O:116:GLN:N	2.49	0.46
25:S:107:VAL:O	25:S:107:VAL:HG23	2.16	0.46
56:x:36:ARG:HH12	56:x:77:THR:HG22	1.81	0.46
1:1:632:A:H4'	18:L:68:SER:HB3	1.97	0.45
1:1:806:C:H2'	1:1:807:U:H6	1.81	0.45
1:1:922:C:C2	1:1:923:G:C8	3.04	0.45
1:1:1061:U:H5''	1:1:1070:A:C4	2.50	0.45
1:1:1091:G:H2'	1:1:1092:C:C6	2.52	0.45
1:1:1140:C:H5'	16:J:26:GLY:HA3	1.98	0.45
1:1:1906:G:H2'	1:1:1907:G:H8	1.81	0.45
1:1:2452:C:H2'	1:1:2453:A:O4'	2.16	0.45
1:1:2855:C:H2'	1:1:2856:A:H8	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:613:C:H2'	2:2:614:C:C6	2.50	0.45
2:2:923:A:H2'	2:2:924:C:C6	2.51	0.45
2:2:1250:A:H2	2:2:1370:G:H1'	1.80	0.45
4:4:2:G:H2'	4:4:3:G:H8	1.81	0.45
6:7:66:U:H2'	6:7:67:C:H6	1.80	0.45
39:g:43:LEU:HA	39:g:46:THR:HB	1.98	0.45
48:p:87:LYS:HB2	48:p:113:VAL:HG23	1.97	0.45
1:1:363:G:H2'	1:1:364:C:H6	1.81	0.45
1:1:1608:A:O2'	1:1:1610:A:OP2	2.34	0.45
1:1:2193:G:O2'	1:1:2194:U:OP1	2.31	0.45
1:1:2585:U:N3	29:W:1:PHE:HD2	1.84	0.45
2:2:17:U:H2'	2:2:18:C:C6	2.52	0.45
2:2:921:U:C2	2:2:922:G:C8	3.04	0.45
2:2:1078:U:O2'	2:2:1079:G:OP1	2.31	0.45
2:2:1187:G:H2'	2:2:1188:A:H8	1.82	0.45
2:2:1477:U:H2'	2:2:1478:U:C6	2.52	0.45
6:7:40:C:H2'	6:7:41:C:C6	2.51	0.45
6:7:66:U:H2'	6:7:67:C:C6	2.52	0.45
7:8:2:G:H2'	7:8:3:G:H8	1.81	0.45
9:B:30:PHE:HD2	9:B:33:LEU:HG	1.81	0.45
18:L:92:LEU:HG	18:L:96:LYS:HE3	1.99	0.45
33:a:56:ARG:HG3	56:x:65:GLU:O	2.16	0.45
42:j:86:LYS:HG2	42:j:95:PHE:HD1	1.81	0.45
50:r:91:HIS:CD2	50:r:97:VAL:HG11	2.51	0.45
1:1:45:G:H5'	1:1:46:G:H5'	1.98	0.45
1:1:500:G:N1	1:1:503:A:OP2	2.46	0.45
1:1:672:C:H2'	1:1:673:C:H6	1.81	0.45
1:1:1159:U:N3	1:1:1160:G:N7	2.64	0.45
1:1:1547:C:H2'	1:1:1548:A:H8	1.82	0.45
1:1:1654:A:O2'	10:C:118:PHE:O	2.26	0.45
1:1:2636:C:H2'	1:1:2637:U:C6	2.50	0.45
2:2:599:C:H2'	2:2:600:A:H8	1.81	0.45
2:2:601:G:H2'	2:2:602:A:H8	1.81	0.45
2:2:628:G:H2'	2:2:629:A:H8	1.82	0.45
2:2:652:U:O4	2:2:752:G:O2'	2.33	0.45
2:2:674:G:N2	48:p:118:HIS:HB2	2.30	0.45
2:2:751:U:H2'	2:2:752:G:O4'	2.15	0.45
2:2:780:A:N6	2:2:801:U:OP2	2.37	0.45
2:2:1169:A:H2'	2:2:1170:A:C8	2.52	0.45
25:S:88:ARG:NE	25:S:94:ASP:OD2	2.49	0.45
31:Y:32:ALA:HB2	31:Y:37:LEU:HD23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:52:ALA:O	33:a:53:THR:OG1	2.28	0.45
44:l:13:LEU:HD12	44:l:14:PRO:HD2	1.96	0.45
47:o:80:THR:OG1	47:o:83:THR:OG1	2.35	0.45
51:s:3:LYS:HB2	51:s:6:MET:HG2	1.98	0.45
1:1:1055:G:H1	1:1:1104:C:H42	1.64	0.45
1:1:1331:G:C5	1:1:1333:G:N7	2.85	0.45
1:1:2228:G:H2'	1:1:2229:U:H6	1.81	0.45
1:1:2895:G:H2'	1:1:2896:C:C6	2.52	0.45
2:2:436:C:H2'	2:2:437:U:C6	2.52	0.45
2:2:945:G:N3	2:2:945:G:H2'	2.31	0.45
2:2:1172:C:C2	2:2:1173:U:C5	3.05	0.45
9:B:107:PRO:HD2	9:B:110:LEU:HD22	1.99	0.45
40:h:123:GLN:HB3	40:h:128:VAL:HB	1.98	0.45
40:h:141:ALA:HB3	40:h:149:ILE:HD12	1.98	0.45
43:k:43:GLY:C	43:k:58:HIS:CD2	2.95	0.45
1:1:176:A:H3'	1:1:177:G:C2	2.51	0.45
1:1:306:U:H2'	1:1:307:G:O4'	2.17	0.45
1:1:1222:U:H2'	1:1:1223:G:C8	2.51	0.45
1:1:1597:A:H5''	1:1:1598:A:H5'	1.97	0.45
1:1:2784:U:H2'	1:1:2785:C:H6	1.81	0.45
2:2:154:U:H2'	2:2:155:A:C8	2.52	0.45
2:2:335:C:H2'	2:2:336:A:H8	1.80	0.45
2:2:407:U:H2'	2:2:408:A:H8	1.80	0.45
2:2:477:C:H2'	2:2:478:A:C8	2.51	0.45
2:2:899:C:HO2'	2:2:900:A:P	2.39	0.45
2:2:958:A:H4'	2:2:959:A:OP1	2.16	0.45
3:3:72:G:N2	3:3:104:A:H62	2.14	0.45
42:j:72:ILE:HD11	42:j:145:GLU:HG3	1.99	0.45
1:1:414:C:H2'	1:1:415:A:H8	1.81	0.45
1:1:754:U:H2'	1:1:755:U:H6	1.80	0.45
1:1:863:A:H2'	1:1:864:G:H8	1.81	0.45
1:1:1159:U:C2	1:1:1160:G:C8	3.04	0.45
1:1:1501:G:OP1	9:B:101:ARG:NH2	2.50	0.45
1:1:1682:G:H2'	1:1:1683:U:H6	1.80	0.45
1:1:2071:A:H2'	1:1:2072:C:C6	2.52	0.45
2:2:1463:U:H5''	22:P:109:ARG:NH1	2.31	0.45
4:4:185:A:H62	40:h:77:ILE:HD12	1.82	0.45
19:M:17:ASN:OD1	19:M:97:GLN:NE2	2.50	0.45
48:p:35:THR:HG1	48:p:40:ASN:C	2.22	0.45
50:r:83:LEU:HD13	56:x:66:MET:HG2	1.99	0.45
1:1:397:U:H2'	1:1:398:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:842:U:H2'	1:1:843:G:C8	2.52	0.45
1:1:915:C:H2'	1:1:916:G:O4'	2.16	0.45
1:1:1103:A:H3'	1:1:1104:C:H5''	1.98	0.45
1:1:1416:G:H1	1:1:1582:C:H42	1.65	0.45
1:1:1645:G:H5''	1:1:1646:C:H5'	1.99	0.45
1:1:1922:G:O2'	6:7:25:C:O2'	2.28	0.45
1:1:2290:G:H2'	1:1:2291:U:C6	2.51	0.45
1:1:2677:G:H2'	1:1:2678:C:C6	2.51	0.45
1:1:2804:U:H2'	1:1:2805:C:C6	2.52	0.45
2:2:470:C:H2'	2:2:471:U:C6	2.52	0.45
2:2:471:U:H2'	2:2:472:U:C6	2.52	0.45
2:2:1074:G:O2'	2:2:1101:A:N1	2.45	0.45
2:2:1180:A:OP2	46:n:99:ARG:NH2	2.50	0.45
20:N:103:ARG:NH2	20:N:106:ASP:OD2	2.49	0.45
57:y:31:PHE:HB3	57:y:54:MET:HB2	1.99	0.45
1:1:541:A:N6	1:1:553:G:O6	2.50	0.45
1:1:1103:A:H3'	1:1:1104:C:C5'	2.47	0.45
1:1:2645:G:OP2	1:1:2645:G:N2	2.21	0.45
1:1:2748:A:H5'	13:F:4:VAL:HG21	1.98	0.45
1:1:2896:C:H2'	1:1:2897:U:C6	2.52	0.45
2:2:763:G:H2'	2:2:764:C:C6	2.52	0.45
2:2:1130:A:O2'	46:n:5:GLN:OE1	2.34	0.45
2:2:1219:A:H2'	2:2:1220:G:H8	1.82	0.45
2:2:1509:C:H2'	2:2:1510:C:H6	1.80	0.45
3:3:9:G:C2	3:3:10:G:C8	3.04	0.45
4:4:81:A:OP1	4:4:84:A:H2'	2.16	0.45
49:q:29:GLN:HB3	49:q:81:LEU:HD11	1.98	0.45
52:t:78:TYR:OH	52:t:89:ARG:O	2.28	0.45
56:x:3:ARG:NH1	56:x:10:PHE:HB2	2.31	0.45
1:1:414:C:H2'	1:1:415:A:C8	2.52	0.45
1:1:465:G:O2'	1:1:466:A:O4'	2.25	0.45
1:1:2183:A:H2'	1:1:2184:A:C8	2.52	0.45
1:1:2636:C:H2'	1:1:2637:U:H6	1.82	0.45
2:2:73:C:H2'	2:2:74:A:C8	2.52	0.45
2:2:149:A:H1'	2:2:1446:A:C2	2.51	0.45
4:4:88:U:H2'	4:4:89:C:O4'	2.17	0.45
57:y:10:ARG:HA	57:y:13:GLN:HB2	1.98	0.45
1:1:78:U:H2'	1:1:79:C:C6	2.52	0.45
1:1:679:C:H2'	1:1:680:C:H6	1.81	0.45
1:1:1028:A:N6	1:1:1125:G:H2'	2.32	0.45
1:1:1484:U:H2'	1:1:1485:U:H6	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1581:G:H2'	1:1:1582:C:C6	2.51	0.45
1:1:2698:U:H2'	1:1:2699:C:H6	1.81	0.45
2:2:994:A:C5	2:2:1216:A:H4'	2.52	0.45
6:7:27:G:H2'	6:7:28:G:H8	1.81	0.45
21:O:33:ARG:O	21:O:65:THR:OG1	2.28	0.45
31:Y:31:GLN:HG2	31:Y:37:LEU:HB2	1.99	0.45
39:g:50:PHE:HD1	39:g:200:ILE:HG21	1.80	0.45
39:g:69:PHE:HD1	39:g:162:PHE:HB3	1.82	0.45
42:j:89:HIS:CG	42:j:90:THR:H	2.35	0.45
1:1:418:C:H2'	1:1:419:U:C6	2.52	0.44
1:1:741:U:H2'	1:1:742:A:C8	2.52	0.44
1:1:992:C:OP1	23:Q:47:TYR:OH	2.25	0.44
1:1:1014:A:H2'	1:1:1015:U:C6	2.52	0.44
1:1:1252:G:N2	23:Q:33:ARG:O	2.50	0.44
1:1:1291:C:H2'	1:1:1292:G:H8	1.82	0.44
1:1:1429:G:H2'	1:1:1430:G:C8	2.51	0.44
1:1:1462:C:H2'	1:1:1463:C:H6	1.82	0.44
2:2:323:U:H2'	2:2:324:G:O4'	2.17	0.44
2:2:501:C:H2'	2:2:502:A:H8	1.83	0.44
2:2:1173:U:C2	2:2:1174:G:C8	3.06	0.44
4:4:113:A:H62	4:4:129:G:H22	1.65	0.44
16:J:37:ARG:HG3	16:J:118:MET:HE1	1.99	0.44
35:c:11:LEU:HD21	35:c:34:LEU:HD23	1.99	0.44
1:1:26:G:H1'	1:1:515:A:H61	1.82	0.44
1:1:146:A:H2'	1:1:147:C:C6	2.53	0.44
1:1:479:A:H4'	1:1:480:A:H5'	1.99	0.44
1:1:593:U:H3	1:1:664:G:H1	1.65	0.44
1:1:885:C:O2'	1:1:886:A:OP1	2.32	0.44
1:1:1153:C:H2'	1:1:1154:G:O4'	2.17	0.44
1:1:1827:U:H2'	1:1:1828:G:O4'	2.17	0.44
1:1:1923:U:H5''	6:7:24:G:O2'	2.17	0.44
2:2:455:G:H2'	2:2:456:A:H8	1.82	0.44
2:2:513:C:H2'	2:2:514:C:H6	1.83	0.44
2:2:928:G:H2'	2:2:929:G:C8	2.53	0.44
2:2:1060:U:H2'	2:2:1061:G:H8	1.82	0.44
2:2:1174:G:O2'	2:2:1175:G:H5'	2.17	0.44
2:2:1481:U:H2'	2:2:1482:G:H8	1.82	0.44
4:4:186:A:N3	4:4:186:A:H2'	2.31	0.44
18:L:61:LEU:O	37:e:13:ARG:NH2	2.51	0.44
51:s:88:ALA:HB2	51:s:96:LEU:HD23	1.99	0.44
1:1:365:U:H2'	1:1:366:C:H6	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1291:C:C2	1:1:1292:G:C8	3.06	0.44
1:1:1345:C:H2'	1:1:1346:G:C8	2.52	0.44
1:1:1542:U:H2'	1:1:1543:G:O4'	2.17	0.44
1:1:2533:U:H2'	1:1:2534:A:O4'	2.18	0.44
2:2:1097:C:H2'	2:2:1098:C:C6	2.53	0.44
2:2:1219:A:H2'	2:2:1220:G:C8	2.53	0.44
2:2:1250:A:H2'	2:2:1251:A:C8	2.52	0.44
2:2:1467:C:H2'	2:2:1468:A:H8	1.82	0.44
4:4:113:A:H62	4:4:129:G:H1	1.63	0.44
11:D:117:ARG:NH2	11:D:183:PHE:O	2.45	0.44
14:G:41:LYS:HA	14:G:44:ILE:HD12	2.00	0.44
39:g:77:SER:HB2	39:g:93:ASN:HB2	1.99	0.44
43:k:47:LEU:HD21	43:k:57:ALA:HB3	2.00	0.44
57:y:28:MET:HE1	57:y:67:ILE:HG21	2.00	0.44
1:1:90:U:OP2	1:1:91:A:O2'	2.29	0.44
1:1:307:G:N2	1:1:309:A:H3'	2.32	0.44
1:1:428:A:O2'	1:1:429:A:P	2.75	0.44
1:1:488:G:H22	1:1:491:G:H5''	1.82	0.44
1:1:769:U:H2'	1:1:770:G:H8	1.83	0.44
1:1:990:A:N1	24:R:78:ARG:NH1	2.63	0.44
1:1:993:G:OP1	23:Q:50:ARG:NH1	2.51	0.44
1:1:1952:A:N6	1:1:1953:A:N1	2.66	0.44
1:1:1971:U:H5'	1:1:1972:G:H5''	1.99	0.44
1:1:2100:G:N2	1:1:2190:G:H1	2.09	0.44
2:2:236:A:H2'	2:2:237:G:C8	2.52	0.44
2:2:486:U:H2'	2:2:487:A:H8	1.83	0.44
2:2:512:U:H2'	2:2:513:C:C6	2.52	0.44
2:2:556:C:H2'	2:2:557:G:C8	2.52	0.44
2:2:885:G:H2'	2:2:886:G:H8	1.82	0.44
3:3:118:C:H2'	3:3:119:A:H8	1.81	0.44
9:B:6:CYS:SG	9:B:13:ARG:NH2	2.91	0.44
19:M:74:THR:HG21	19:M:86:LYS:HE3	1.99	0.44
39:g:165:ASP:HB3	39:g:168:HIS:HB3	1.98	0.44
42:j:123:VAL:HG22	42:j:124:LEU:N	2.32	0.44
49:q:90:LEU:HB3	49:q:93:VAL:HG12	1.98	0.44
1:1:29:U:H2'	1:1:30:G:H8	1.83	0.44
1:1:206:U:C2	1:1:207:A:C8	3.05	0.44
1:1:396:G:OP2	30:X:10:LYS:NZ	2.40	0.44
1:1:959:A:H2'	1:1:960:A:C8	2.53	0.44
1:1:1025:G:N2	1:1:1139:G:O6	2.48	0.44
1:1:1589:U:O2'	1:1:1590:A:H8	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2100:G:H1	1:1:2190:G:H1	1.63	0.44
1:1:2100:G:O2'	1:1:2101:A:O4'	2.33	0.44
1:1:2359:C:H2'	1:1:2360:G:C8	2.53	0.44
1:1:2888:C:H2'	1:1:2889:C:C6	2.53	0.44
1:1:2889:C:H2'	1:1:2890:G:O4'	2.18	0.44
2:2:1303:C:O2'	2:2:1304:G:OP1	2.33	0.44
3:3:118:C:H2'	3:3:119:A:C8	2.51	0.44
4:4:357:U:H2'	4:4:358:C:C6	2.52	0.44
5:5:69:ASN:OD1	5:5:69:ASN:O	2.35	0.44
5:5:93:ASN:O	5:5:96:GLU:HG2	2.17	0.44
8:A:41:ARG:NH2	8:A:56:ASP:OD1	2.48	0.44
1:1:20:C:H2'	1:1:21:A:H8	1.82	0.44
1:1:24:G:H2'	1:1:25:U:H6	1.82	0.44
1:1:155:A:H2'	1:1:156:A:H8	1.81	0.44
1:1:184:C:H2'	1:1:185:G:C8	2.53	0.44
1:1:598:U:H2'	1:1:599:A:C8	2.53	0.44
1:1:1054:A:O4'	15:H:30:SER:O	2.35	0.44
1:1:1167:C:H2'	1:1:1168:G:H8	1.83	0.44
1:1:1255:U:H5''	1:1:1256:G:H5''	2.00	0.44
1:1:1340:U:OP1	26:T:19:LYS:NZ	2.50	0.44
1:1:2035:G:H5''	1:1:2036:C:H5	1.82	0.44
1:1:2143:C:H1'	1:1:2150:C:H42	1.82	0.44
1:1:2686:G:H2'	1:1:2687:U:C6	2.53	0.44
1:1:2802:G:H2'	1:1:2803:G:H8	1.82	0.44
2:2:159:G:N2	2:2:162:A:OP2	2.50	0.44
2:2:298:A:HO2'	2:2:299:G:P	2.40	0.44
2:2:322:C:H2'	2:2:323:U:C6	2.52	0.44
2:2:328:C:H4'	2:2:329:A:H5'	1.98	0.44
2:2:1228:C:H2'	2:2:1229:A:H8	1.82	0.44
3:3:6:G:H2'	3:3:7:G:C8	2.53	0.44
3:3:12:C:O2'	8:A:74:PRO:O	2.34	0.44
5:5:36:LEU:HD13	5:5:41:VAL:HB	2.00	0.44
33:a:56:ARG:NH1	56:x:68:GLY:C	2.76	0.44
1:1:324:A:N6	1:1:339:U:O4'	2.51	0.44
1:1:639:U:H2'	1:1:640:C:H6	1.83	0.44
1:1:679:C:H2'	1:1:680:C:C6	2.52	0.44
1:1:833:A:H2'	1:1:834:G:H8	1.82	0.44
1:1:851:C:H2'	1:1:852:U:C6	2.53	0.44
1:1:1130:U:C2	1:1:2025:C:H5''	2.52	0.44
1:1:1161:C:H2'	1:1:1162:G:C8	2.52	0.44
1:1:1462:C:H2'	1:1:1463:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2143:C:H1'	1:1:2150:C:N4	2.33	0.44
1:1:2292:U:H2'	1:1:2293:G:H8	1.81	0.44
1:1:2494:G:OP1	8:A:3:HIS:HB2	2.17	0.44
1:1:2543:G:H2'	1:1:2544:G:C8	2.53	0.44
1:1:2623:G:H2'	1:1:2624:G:C8	2.52	0.44
2:2:392:C:C2	2:2:393:A:C8	3.06	0.44
2:2:536:C:H2'	2:2:537:G:C8	2.52	0.44
2:2:1070:U:H2'	2:2:1071:C:C6	2.53	0.44
3:3:82:U:H2'	3:3:83:G:H8	1.82	0.44
4:4:251:U:H2'	4:4:252:G:N7	2.33	0.44
4:4:340:G:H5''	19:M:55:ARG:NH1	2.33	0.44
5:5:43:SER:N	5:5:76:ALA:HB2	2.32	0.44
27:U:25:VAL:HA	27:U:36:VAL:HA	1.99	0.44
30:X:5:CYS:SG	30:X:10:LYS:HB2	2.58	0.44
1:1:579:G:H2'	1:1:580:U:C6	2.53	0.44
1:1:996:A:OP2	23:Q:93:LYS:NZ	2.44	0.44
1:1:1167:C:H2'	1:1:1168:G:C8	2.53	0.44
1:1:1266:G:O2'	1:1:2012:G:O6	2.33	0.44
1:1:2217:G:H2'	1:1:2218:G:H8	1.83	0.44
1:1:2241:A:H2'	1:1:2242:G:H8	1.83	0.44
1:1:2438:U:H2'	1:1:2441:U:H5	1.83	0.44
1:1:2467:C:H2'	1:1:2468:A:O4'	2.17	0.44
1:1:2840:C:H2'	1:1:2841:C:H6	1.83	0.44
2:2:224:U:H2'	2:2:225:C:C6	2.53	0.44
2:2:424:G:H2'	2:2:425:G:C8	2.52	0.44
2:2:791:G:O6	2:2:792:A:N6	2.50	0.44
2:2:1250:A:H2'	2:2:1251:A:H8	1.83	0.44
2:2:1463:U:H2'	2:2:1464:U:C6	2.53	0.44
4:4:18:C:H3'	4:4:19:G:C8	2.53	0.44
5:5:112:VAL:HB	5:5:128:GLY:C	2.43	0.44
9:B:8:PRO:HB3	9:B:14:ARG:HG3	2.00	0.44
13:F:86:LYS:HG2	13:F:132:VAL:HG23	1.99	0.44
15:H:40:GLU:O	15:H:43:LYS:HB3	2.18	0.44
30:X:12:PRO:HB3	30:X:30:LEU:HD13	2.00	0.44
35:c:11:LEU:HB3	35:c:49:TYR:HB3	1.99	0.44
49:q:85:GLY:O	49:q:96:HIS:ND1	2.43	0.44
1:1:650:C:H5''	37:e:49:MET:SD	2.58	0.44
1:1:678:C:H2'	1:1:679:C:H6	1.82	0.44
1:1:927:A:H2'	1:1:928:A:C8	2.53	0.44
1:1:1287:A:HO2'	1:1:1288:G:P	2.39	0.44
1:1:1708:C:H2'	1:1:1709:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:628:G:H2'	2:2:629:A:C8	2.53	0.44
5:5:21:ARG:HH21	5:5:114:LEU:HD13	1.83	0.44
5:5:69:ASN:OD1	5:5:69:ASN:C	2.59	0.44
10:C:132:ALA:HA	10:C:140:HIS:HD1	1.83	0.44
11:D:41:GLN:HG2	11:D:43:THR:HG23	1.99	0.44
41:i:15:GLU:HG3	41:i:19:LEU:HD11	1.99	0.44
45:m:78:VAL:HG21	45:m:128:TYR:CE1	2.52	0.44
1:1:134:G:H2'	1:1:135:U:C6	2.53	0.43
1:1:219:A:N3	1:1:234:U:O2'	2.49	0.43
1:1:742:A:H2'	1:1:743:A:C8	2.53	0.43
1:1:967:U:H2'	1:1:968:C:C6	2.53	0.43
1:1:1295:C:H2'	1:1:1296:G:H8	1.83	0.43
1:1:1663:G:O2'	1:1:2686:G:H4'	2.18	0.43
1:1:1829:A:N3	9:B:15:HIS:NE2	2.63	0.43
1:1:2087:G:H2'	1:1:2088:A:C8	2.53	0.43
1:1:2100:G:H4'	1:1:2101:A:OP1	2.18	0.43
1:1:2202:U:O2'	1:1:2204:G:OP1	2.31	0.43
1:1:2606:C:H2'	1:1:2607:G:C8	2.52	0.43
1:1:2615:U:H1'	34:b:4:GLN:HB3	2.00	0.43
1:1:2897:U:H2'	1:1:2898:U:C6	2.53	0.43
2:2:958:A:N1	56:x:55:ARG:HB2	2.33	0.43
2:2:1171:A:H2'	2:2:1172:C:C6	2.53	0.43
2:2:1379:G:H2'	2:2:1380:U:C6	2.53	0.43
24:R:17:GLY:O	24:R:97:LYS:NZ	2.39	0.43
41:i:152:GLN:HB2	41:i:155:VAL:HG11	1.91	0.43
50:r:83:LEU:HD21	56:x:65:GLU:HB2	1.99	0.43
1:1:304:U:H2'	1:1:305:C:C6	2.52	0.43
1:1:1199:U:H2'	1:1:1200:C:H6	1.83	0.43
1:1:1561:C:H2'	1:1:1562:U:C6	2.52	0.43
1:1:1594:U:H2'	1:1:1595:C:C6	2.53	0.43
1:1:1680:U:H3'	1:1:1681:G:H8	1.83	0.43
2:2:28:A:O2'	2:2:296:U:OP1	2.33	0.43
2:2:216:U:H2'	2:2:217:C:H6	1.82	0.43
2:2:235:C:H2'	2:2:236:A:C8	2.51	0.43
2:2:254:G:H2'	2:2:255:G:C8	2.53	0.43
2:2:393:A:C2	2:2:394:G:C8	3.07	0.43
2:2:556:C:H2'	2:2:557:G:H8	1.82	0.43
4:4:111:U:H2'	4:4:112:U:C6	2.52	0.43
6:7:67:C:H2'	6:7:68:C:H6	1.83	0.43
10:C:12:THR:OG1	10:C:13:ARG:N	2.48	0.43
10:C:13:ARG:HG2	22:P:56:HIS:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:3:LEU:HB2	15:H:4:ASN:H	1.68	0.43
15:H:87:GLU:OE2	15:H:95:LEU:HB2	2.17	0.43
16:J:117:ALA:HA	16:J:120:ARG:HD2	2.00	0.43
17:K:77:ILE:HG12	22:P:72:ARG:HG3	2.00	0.43
1:1:174:U:H2'	1:1:175:G:C8	2.52	0.43
1:1:445:C:O3'	23:Q:3:ARG:HG2	2.19	0.43
1:1:592:A:H4'	37:e:3:LYS:HG2	2.00	0.43
1:1:710:U:H2'	1:1:711:G:H8	1.81	0.43
1:1:848:C:H2'	1:1:849:A:C8	2.53	0.43
1:1:1315:C:H2'	1:1:1316:U:H6	1.83	0.43
1:1:2349:G:OP1	37:e:45:ARG:NH2	2.37	0.43
1:1:2597:G:O2'	1:1:2598:A:O4'	2.23	0.43
2:2:1347:G:N7	46:n:13:LYS:HE2	2.33	0.43
10:C:133:THR:HG23	10:C:134:HIS:CD2	2.54	0.43
26:T:56:GLU:HG2	26:T:57:VAL:H	1.83	0.43
31:Y:21:LEU:HD22	31:Y:46:VAL:HG23	1.98	0.43
49:q:21:VAL:HG13	49:q:95:TYR:HE1	1.84	0.43
1:1:64:A:H2'	1:1:65:U:H6	1.83	0.43
1:1:289:G:H2'	1:1:290:U:C6	2.53	0.43
1:1:538:A:H5''	16:J:7:LYS:HE3	2.00	0.43
1:1:623:C:H2'	1:1:624:C:C6	2.54	0.43
1:1:777:G:H2'	1:1:778:G:H8	1.83	0.43
1:1:806:C:H2'	1:1:807:U:C6	2.53	0.43
1:1:1050:A:C2	1:1:2751:G:C2	3.07	0.43
1:1:1539:U:H2'	1:1:1540:G:C8	2.54	0.43
1:1:1849:G:H2'	1:1:1850:G:H8	1.84	0.43
1:1:2567:G:H2'	1:1:2568:U:C6	2.54	0.43
2:2:227:G:H2'	2:2:228:A:H8	1.83	0.43
2:2:636:U:H2'	2:2:637:C:C6	2.53	0.43
2:2:764:C:H2'	2:2:765:G:O4'	2.17	0.43
2:2:878:A:H2'	2:2:879:C:H6	1.82	0.43
2:2:921:U:O2'	42:j:23:LYS:NZ	2.45	0.43
2:2:950:U:OP2	50:r:101:ARG:HD2	2.17	0.43
2:2:1123:U:H2'	2:2:1124:G:O4'	2.18	0.43
3:3:111:U:H2'	3:3:112:G:H8	1.83	0.43
11:D:153:LEU:HD21	11:D:171:ASP:HB2	2.00	0.43
25:S:86:MET:HE3	25:S:88:ARG:HH11	1.83	0.43
33:a:2:LYS:HD2	33:a:5:ILE:HD13	2.00	0.43
39:g:117:LEU:HB3	39:g:141:LEU:HD13	2.00	0.43
41:i:36:GLN:HG3	41:i:43:ALA:N	2.32	0.43
43:k:43:GLY:H	43:k:58:HIS:HD2	1.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:145:C:H2'	1:1:146:A:H8	1.82	0.43
1:1:1084:A:H2'	1:1:1085:A:C8	2.54	0.43
1:1:1231:U:H2'	1:1:1232:G:H8	1.83	0.43
1:1:1387:A:H2'	1:1:1388:G:C8	2.54	0.43
1:1:1534:U:N3	1:1:1536:C:N3	2.67	0.43
1:1:2064:C:H2'	1:1:2065:C:C6	2.52	0.43
1:1:2333:A:P	8:A:77:ARG:HH22	2.42	0.43
1:1:2838:G:C4	1:1:2839:G:C8	3.07	0.43
1:1:2899:A:H2'	1:1:2900:A:H8	1.83	0.43
2:2:407:U:C2	2:2:408:A:C8	3.06	0.43
2:2:773:G:O6	2:2:807:A:N6	2.52	0.43
2:2:1014:A:C2	2:2:1219:A:H1'	2.54	0.43
2:2:1060:U:C5	40:h:2:GLY:HA3	2.53	0.43
3:3:78:A:H62	3:3:98:G:H21	1.66	0.43
4:4:149:A:N3	4:4:151:C:N4	2.66	0.43
35:c:10:LYS:HE3	35:c:20:PHE:CD2	2.53	0.43
45:m:121:LEU:C	45:m:121:LEU:HD12	2.44	0.43
46:n:20:PHE:O	46:n:63:LEU:HA	2.18	0.43
1:1:190:A:H2'	1:1:191:A:C8	2.54	0.43
1:1:351:C:H2'	1:1:352:A:H8	1.84	0.43
1:1:956:G:N7	19:M:14:LYS:NZ	2.64	0.43
1:1:1190:G:H2'	1:1:1191:G:H8	1.84	0.43
1:1:1219:U:H2'	1:1:1220:G:H8	1.83	0.43
2:2:538:G:H2'	2:2:539:A:H8	1.82	0.43
2:2:980:C:HO2'	2:2:981:U:P	2.41	0.43
2:2:985:C:H2'	2:2:986:U:C6	2.53	0.43
2:2:1515:G:H2'	2:2:1516:2MG:C8	2.53	0.43
4:4:318:G:H2'	4:4:319:A:H8	1.84	0.43
13:F:9:VAL:HG12	13:F:50:LEU:O	2.18	0.43
13:F:89:LEU:HD13	13:F:162:VAL:HG22	1.99	0.43
17:K:65:THR:HG22	17:K:67:LYS:H	1.83	0.43
39:g:57:LEU:HD13	39:g:217:VAL:HG13	2.01	0.43
1:1:307:G:N2	1:1:330:A:H61	2.15	0.43
1:1:580:U:H2'	1:1:581:C:H6	1.83	0.43
1:1:692:C:H2'	1:1:693:A:C8	2.53	0.43
1:1:1675:C:H2'	1:1:1676:A:O4'	2.18	0.43
1:1:1858:A:H2'	1:1:1859:U:O4'	2.19	0.43
1:1:1874:C:H2'	1:1:1875:G:O4'	2.19	0.43
1:1:2061:G:H2'	1:1:2501:C:O2'	2.19	0.43
1:1:2372:U:H2'	1:1:2373:G:C8	2.54	0.43
1:1:2547:A:H2'	1:1:2548:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2704:C:H2'	1:1:2705:A:O4'	2.19	0.43
1:1:2853:C:H2'	1:1:2854:G:H8	1.84	0.43
2:2:180:U:H2'	2:2:181:A:H5'	2.01	0.43
2:2:492:C:H2'	2:2:493:A:C4	2.54	0.43
2:2:878:A:H2'	2:2:879:C:C6	2.54	0.43
2:2:1184:G:C2	2:2:1185:G:C8	3.07	0.43
2:2:1354:U:H2'	2:2:1355:G:C8	2.52	0.43
3:3:82:U:H2'	3:3:83:G:C8	2.53	0.43
4:4:181:G:H2'	4:4:181:G:N3	2.34	0.43
7:8:9:A:O2'	7:8:10:G:OP1	2.29	0.43
21:O:31:THR:HG22	21:O:33:ARG:H	1.84	0.43
33:a:12:ILE:HD12	33:a:12:ILE:HA	1.92	0.43
40:h:51:SER:O	40:h:70:THR:OG1	2.26	0.43
41:i:59:GLN:OE1	41:i:62:ARG:NH1	2.51	0.43
45:m:7:ILE:O	45:m:11:LEU:HG	2.18	0.43
54:v:61:ILE:HA	54:v:75:LEU:HA	2.00	0.43
1:1:414:C:H1'	1:1:1864:U:H1'	2.00	0.43
1:1:558:U:H2'	1:1:559:G:H8	1.83	0.43
1:1:590:A:H2'	1:1:591:U:C6	2.54	0.43
1:1:795:C:C2	1:1:796:C:C5	3.06	0.43
1:1:1295:C:C2	1:1:1296:G:C8	3.07	0.43
1:1:1336:A:OP2	26:T:68:LYS:NZ	2.43	0.43
1:1:1368:G:H2'	1:1:1369:G:C8	2.52	0.43
1:1:1664:A:H2'	1:1:1664:A:N3	2.34	0.43
1:1:1800:C:H42	1:1:1817:G:H22	1.67	0.43
1:1:2100:G:H2'	1:1:2101:A:C8	2.54	0.43
1:1:2395:C:H2'	1:1:2396:G:H8	1.84	0.43
1:1:2626:C:H2'	1:1:2627:G:H8	1.84	0.43
2:2:434:U:O4	2:2:435:A:N6	2.51	0.43
2:2:920:U:HO2'	2:2:1081:A:HO2'	1.58	0.43
2:2:1479:C:H2'	2:2:1480:A:C8	2.51	0.43
25:S:80:PRO:O	25:S:100:THR:OG1	2.31	0.43
43:k:64:VAL:HG12	43:k:65:GLU:N	2.33	0.43
44:l:47:LEU:HB3	44:l:58:GLU:HB3	2.01	0.43
1:1:914:G:H3'	1:1:915:C:H5''	2.01	0.43
1:1:1011:G:OP1	23:Q:75:SER:OG	2.36	0.43
1:1:1166:G:H2'	1:1:1167:C:C6	2.54	0.43
1:1:2015:A:C6	34:b:3:VAL:HG23	2.53	0.43
1:1:2259:U:H2'	1:1:2260:C:H6	1.83	0.43
1:1:2687:U:H2'	1:1:2688:G:O4'	2.19	0.43
1:1:2799:A:O2'	1:1:2801:G:OP2	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:75:G:H2'	2:2:76:G:O4'	2.19	0.43
2:2:81:A:N7	2:2:83:C:N4	2.67	0.43
2:2:154:U:H2'	2:2:155:A:H8	1.83	0.43
2:2:626:G:H2'	2:2:627:G:C8	2.54	0.43
2:2:783:C:H2'	2:2:784:A:C8	2.53	0.43
2:2:1147:C:H2'	2:2:1148:U:H6	1.83	0.43
5:5:58:LEU:HG	5:5:63:ALA:HB2	2.00	0.43
9:B:160:THR:HG22	9:B:177:ARG:HG2	2.01	0.43
1:1:279:A:C2	1:1:362:A:H4'	2.54	0.43
1:1:494:G:H2'	1:1:495:G:H8	1.84	0.43
1:1:703:U:H3'	1:1:704:G:H8	1.84	0.43
1:1:1132:U:H2'	1:1:1133:A:C8	2.54	0.43
1:1:2691:C:H2'	1:1:2692:G:C8	2.52	0.43
2:2:186:C:N4	2:2:192:A:H61	2.17	0.43
2:2:406:G:H2'	2:2:407:U:C6	2.54	0.43
2:2:484:G:H4'	2:2:485:U:H3'	2.01	0.43
2:2:625:U:H2'	2:2:626:G:H8	1.84	0.43
2:2:778:G:H21	48:p:122:ARG:HD2	1.84	0.43
2:2:1011:C:H2'	2:2:1012:A:C8	2.54	0.43
2:2:1071:C:H2'	2:2:1072:G:C8	2.46	0.43
2:2:1180:A:O2'	2:2:1184:G:H1'	2.18	0.43
4:4:35:C:O2	4:4:320:U:O2'	2.36	0.43
4:4:61:G:H4'	4:4:62:G:H5'	2.01	0.43
4:4:158:U:N3	4:4:196:G:N1	2.67	0.43
5:5:67:GLY:HA2	5:5:88:ARG:HG2	2.01	0.43
8:A:50:ASN:HB2	8:A:82:ILE:HB	2.00	0.43
10:C:116:LYS:HD3	10:C:123:LYS:HE3	2.01	0.43
14:G:125:THR:O	14:G:125:THR:CG2	2.59	0.43
18:L:56:PRO:O	18:L:60:ARG:HB2	2.19	0.43
1:1:479:A:O2'	1:1:481:G:H5'	2.19	0.42
1:1:1841:U:C2	1:1:1842:G:C8	3.07	0.42
1:1:2128:G:H21	1:1:2129:C:H41	1.66	0.42
1:1:2638:G:O2'	1:1:2775:G:N2	2.42	0.42
1:1:2721:A:H1'	1:1:2873:A:O2'	2.19	0.42
1:1:2818:U:H2'	1:1:2819:G:H8	1.84	0.42
2:2:202:G:O2'	2:2:468:A:H8	2.02	0.42
2:2:246:A:N6	2:2:281:G:C2	2.87	0.42
2:2:266:G:H1'	2:2:268:U:OP2	2.18	0.42
2:2:294:U:OP1	2:2:610:U:O2'	2.30	0.42
2:2:482:A:H2'	2:2:483:C:O4'	2.18	0.42
2:2:661:G:H2'	2:2:662:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:738:C:H2'	2:2:739:C:C6	2.54	0.42
2:2:932:C:H2'	2:2:933:G:C8	2.53	0.42
2:2:1004:A:N6	2:2:1026:G:H1'	2.33	0.42
2:2:1270:G:H2'	2:2:1271:A:C8	2.48	0.42
4:4:107:C:H2'	4:4:108:G:H8	1.83	0.42
4:4:204:G:P	4:4:234:A:H62	2.42	0.42
28:V:65:VAL:O	28:V:68:LYS:HG2	2.19	0.42
1:1:541:A:H2'	1:1:542:C:C6	2.54	0.42
1:1:765:C:H2'	1:1:766:U:C6	2.55	0.42
1:1:992:C:H2'	1:1:993:G:H8	1.83	0.42
1:1:2303:G:O6	1:1:2314:A:N6	2.52	0.42
1:1:2600:A:H2'	1:1:2601:C:C6	2.54	0.42
2:2:1034:G:C2	2:2:1035:A:C8	3.06	0.42
2:2:1326:U:H2'	2:2:1327:C:C6	2.55	0.42
2:2:1327:C:H2'	2:2:1328:C:C6	2.54	0.42
2:2:1330:U:H4'	50:r:23:TYR:CE2	2.54	0.42
4:4:30:C:H3'	4:4:34:A:H62	1.83	0.42
4:4:129:G:H2'	4:4:130:C:H4'	2.01	0.42
12:E:135:GLN:OE1	12:E:135:GLN:N	2.46	0.42
24:R:43:ASN:OD1	24:R:46:GLU:HB2	2.19	0.42
45:m:7:ILE:HB	45:m:77:ARG:NH1	2.34	0.42
50:r:90:ARG:HB2	50:r:97:VAL:HG12	2.00	0.42
1:1:184:C:H2'	1:1:185:G:H8	1.84	0.42
1:1:418:C:H2'	1:1:419:U:H6	1.83	0.42
1:1:591:U:H2'	1:1:592:A:H8	1.83	0.42
1:1:634:C:H2'	1:1:635:C:C6	2.55	0.42
1:1:903:C:H2'	1:1:904:G:C8	2.53	0.42
1:1:1446:C:H2'	1:1:1447:C:C6	2.54	0.42
1:1:1447:C:H2'	1:1:1448:G:C8	2.54	0.42
1:1:2251:OMG:C8	1:1:2450:A:H4'	2.54	0.42
1:1:2619:C:H2'	1:1:2620:C:C6	2.53	0.42
1:1:2783:U:H2'	1:1:2784:U:H6	1.84	0.42
1:1:2855:C:H2'	1:1:2856:A:C8	2.54	0.42
2:2:187:G:N1	2:2:191:G:O6	2.53	0.42
2:2:321:A:H2	2:2:332:G:H22	1.67	0.42
2:2:676:A:H2'	2:2:677:U:H6	1.84	0.42
2:2:1102:A:H4'	39:g:95:ARG:HH22	1.85	0.42
2:2:1462:C:H2'	2:2:1463:U:C6	2.54	0.42
2:2:1496:C:H2'	2:2:1497:G:H8	1.83	0.42
4:4:2:G:H2'	4:4:3:G:C8	2.54	0.42
12:E:105:THR:HA	33:a:38:SER:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:94:ILE:HB	14:G:122:LEU:HD12	2.00	0.42
15:H:71:CYS:HB3	15:H:117:LEU:HD12	2.02	0.42
1:1:813:U:H2'	1:1:814:C:H6	1.84	0.42
1:1:922:C:H2'	1:1:923:G:H8	1.84	0.42
1:1:1161:C:C2	1:1:1162:G:C8	3.07	0.42
1:1:1395:A:H4'	1:1:1397:U:C5	2.55	0.42
1:1:1485:U:H2'	1:1:1486:U:H6	1.84	0.42
1:1:1594:U:H2'	1:1:1595:C:H6	1.83	0.42
1:1:1843:C:H2'	1:1:1844:C:H6	1.83	0.42
1:1:2030:6MZ:H2	1:1:2499:C:O3'	2.20	0.42
1:1:2585:U:C2	29:W:1:PHE:HB2	2.52	0.42
1:1:2802:G:H2'	1:1:2803:G:C8	2.54	0.42
2:2:322:C:H2'	2:2:323:U:H6	1.84	0.42
2:2:356:A:N3	2:2:368:U:H1'	2.34	0.42
2:2:1098:C:H2'	2:2:1099:G:C8	2.54	0.42
15:H:57:ASN:ND2	15:H:63:ALA:HB2	2.33	0.42
42:j:74:VAL:HG11	42:j:144:LEU:HB3	2.01	0.42
1:1:77:G:H2'	1:1:78:U:H6	1.84	0.42
1:1:133:U:H2'	1:1:134:G:C8	2.54	0.42
1:1:1751:U:H2'	1:1:1752:C:C6	2.54	0.42
1:1:2548:U:O2	17:K:23:LYS:NZ	2.30	0.42
1:1:2685:G:H1	1:1:2724:U:H3	1.68	0.42
1:1:2837:A:H2'	1:1:2838:G:H8	1.85	0.42
2:2:136:C:O2'	53:u:64:GLY:O	2.35	0.42
2:2:213:G:H2'	2:2:213:G:N3	2.35	0.42
2:2:389:A:H3'	2:2:390:U:H6	1.84	0.42
2:2:922:G:H2'	2:2:923:A:C8	2.54	0.42
2:2:976:G:C8	2:2:1358:U:H2'	2.55	0.42
2:2:1307:U:H5''	50:r:100:GLN:HE22	1.83	0.42
2:2:1412:C:H2'	2:2:1413:A:H8	1.84	0.42
4:4:143:C:N4	4:4:175:A:H2	2.17	0.42
4:4:145:C:H5'	4:4:174:A:N6	2.35	0.42
1:1:116:C:H2'	1:1:117:G:O4'	2.19	0.42
1:1:244:A:H62	1:1:254:G:N2	2.16	0.42
1:1:246:C:N4	37:e:8:ARG:HG3	2.34	0.42
1:1:577:G:O2'	1:1:1254:A:OP1	2.37	0.42
1:1:1387:A:H2'	1:1:1388:G:H8	1.85	0.42
1:1:2537:U:H2'	1:1:2538:C:H6	1.84	0.42
1:1:2810:A:H4'	10:C:62:LYS:HD3	2.01	0.42
2:2:147:G:H2'	2:2:148:G:C8	2.55	0.42
2:2:1090:U:H4'	2:2:1171:A:O2'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1120:C:H2'	2:2:1121:U:C6	2.55	0.42
5:5:70:ILE:HG12	5:5:88:ARG:HH12	1.83	0.42
6:7:28:G:H2'	6:7:29:G:O4'	2.18	0.42
11:D:19:PHE:HD2	11:D:113:VAL:HG21	1.85	0.42
25:S:19:LEU:HB3	34:b:22:LEU:HG	2.00	0.42
56:x:12:ASP:HB3	56:x:14:HIS:HD1	1.84	0.42
1:1:272:A:H2'	1:1:273:G:H8	1.84	0.42
1:1:364:C:H2'	1:1:365:U:H6	1.84	0.42
1:1:540:C:H2'	1:1:541:A:H8	1.84	0.42
1:1:927:A:O2'	32:Z:39:GLU:OE2	2.29	0.42
1:1:1292:G:H2'	1:1:1293:C:H6	1.84	0.42
1:1:1967:C:H2'	1:1:1968:G:O4'	2.20	0.42
1:1:2340:A:H2'	1:1:2341:G:H8	1.85	0.42
1:1:2349:G:O6	1:1:2369:A:N6	2.53	0.42
1:1:2847:U:H2'	1:1:2848:G:O4'	2.20	0.42
2:2:113:G:H2'	2:2:114:U:H6	1.85	0.42
2:2:358:U:C2	2:2:359:G:C8	3.08	0.42
2:2:799:G:H2'	2:2:800:G:O4'	2.20	0.42
2:2:980:C:O2'	2:2:981:U:OP1	2.28	0.42
2:2:984:C:H2'	2:2:985:C:H6	1.83	0.42
2:2:985:C:H2'	2:2:986:U:H6	1.84	0.42
2:2:1113:C:H4'	40:h:14:ILE:HG12	2.02	0.42
2:2:1360:A:OP2	51:s:75:ARG:NH2	2.52	0.42
6:7:37:MIA:H121	6:7:37:MIA:H162	1.71	0.42
6:7:70:G:H2'	6:7:71:G:H8	1.85	0.42
9:B:84:ASP:HB2	9:B:91:ILE:HG13	2.01	0.42
47:o:8:ILE:HG13	47:o:74:VAL:HB	2.01	0.42
1:1:595:C:H2'	1:1:596:U:H6	1.84	0.42
1:1:969:G:H2'	1:1:970:U:C6	2.55	0.42
1:1:1069:A:H1'	1:1:1096:A:H4'	2.01	0.42
1:1:1186:G:H2'	1:1:1187:G:O4'	2.19	0.42
1:1:1520:U:H2'	1:1:1521:G:O4'	2.20	0.42
1:1:1683:U:H2'	1:1:1684:G:H8	1.84	0.42
1:1:1824:G:O2'	9:B:252:THR:HG21	2.20	0.42
1:1:2073:C:H5''	9:B:228:VAL:HG22	2.02	0.42
2:2:171:A:H2'	2:2:172:A:C8	2.55	0.42
2:2:455:G:H2'	2:2:456:A:C8	2.54	0.42
2:2:1217:C:P	51:s:9:ARG:HH21	2.43	0.42
2:2:1402:4OC:HM22	2:2:1403:C:H5'	2.00	0.42
4:4:167:G:N2	4:4:168:G:N7	2.68	0.42
4:4:204:G:H8	4:4:205:G:C4	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:33:ALA:N	8:A:64:ASP:OD1	2.52	0.42
13:F:9:VAL:CG1	13:F:9:VAL:O	2.67	0.42
42:j:91:GLY:O	42:j:130:SER:OG	2.32	0.42
48:p:29:ASN:ND2	48:p:57:LYS:HD2	2.35	0.42
49:q:21:VAL:HG13	49:q:95:TYR:CE1	2.55	0.42
49:q:24:LEU:HB3	49:q:27:CYS:O	2.20	0.42
1:1:366:C:C2	1:1:367:G:C8	3.08	0.42
1:1:940:G:H2'	1:1:941:A:O4'	2.19	0.42
1:1:1047:G:C8	15:H:59:LEU:HD21	2.55	0.42
1:1:1464:G:H2'	1:1:1465:G:C8	2.55	0.42
1:1:2267:A:H5''	1:1:2268:A:H5''	2.02	0.42
1:1:2815:C:C2	1:1:2816:G:C8	3.08	0.42
1:1:2841:C:C2	1:1:2842:G:C8	3.08	0.42
1:1:2845:U:H2'	1:1:2846:G:H8	1.84	0.42
2:2:131:A:H2'	2:2:132:C:C6	2.54	0.42
2:2:662:U:O2'	2:2:836:G:OP1	2.37	0.42
2:2:1033:G:H2'	2:2:1034:G:H8	1.84	0.42
5:5:51:ILE:C	5:5:69:ASN:ND2	2.78	0.42
13:F:148:LEU:HD22	13:F:148:LEU:HA	1.87	0.42
15:H:117:LEU:HD22	15:H:120:ALA:HA	2.02	0.42
20:N:45:ARG:HA	20:N:48:VAL:HG22	2.02	0.42
49:q:57:LEU:HD11	49:q:82:ILE:HD11	2.01	0.42
1:1:77:G:H2'	1:1:78:U:C6	2.55	0.42
1:1:833:A:H2'	1:1:834:G:C8	2.55	0.42
1:1:1056:G:O3'	1:1:1057:A:H8	2.01	0.42
1:1:1322:A:N1	1:1:1333:G:O2'	2.42	0.42
1:1:1509:A:O2'	1:1:1510:G:H8	2.02	0.42
1:1:1658:C:H2'	1:1:1659:G:H8	1.85	0.42
1:1:1922:G:HO2'	6:7:25:C:HO2'	1.64	0.42
2:2:373:A:C2	2:2:374:A:C8	3.08	0.42
2:2:375:U:H2'	2:2:376:G:O4'	2.20	0.42
2:2:500:G:H5''	49:q:121:ARG:HH12	1.84	0.42
2:2:1105:A:H2'	2:2:1106:G:H8	1.85	0.42
15:H:24:SER:HA	15:H:85:SER:O	2.19	0.42
45:m:89:LYS:HA	45:m:92:LEU:HG	2.02	0.42
47:o:11:LYS:HB2	47:o:97:ASP:OD1	2.19	0.42
1:1:250:G:H4'	18:L:59:ARG:HD3	2.02	0.41
1:1:842:U:H2'	1:1:843:G:H8	1.83	0.41
1:1:927:A:H2'	1:1:928:A:H8	1.84	0.41
1:1:1391:U:N3	1:1:1394:U:H5	2.17	0.41
1:1:1562:U:H2'	1:1:1563:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1652:A:OP1	20:N:8:ARG:HD3	2.20	0.41
1:1:1662:U:H2'	1:1:1663:G:C8	2.55	0.41
1:1:2220:U:H2'	1:1:2221:G:C8	2.52	0.41
1:1:2703:C:C2	1:1:2704:C:C5	3.08	0.41
2:2:508:U:H1'	2:2:509:A:N7	2.35	0.41
2:2:707:U:H2'	2:2:708:C:C6	2.54	0.41
2:2:790:A:H62	6:7:37:MIA:H111	1.84	0.41
2:2:1048:G:C2	2:2:1050:G:C6	3.08	0.41
2:2:1120:C:H2'	2:2:1121:U:H6	1.83	0.41
2:2:1152:A:P	47:o:72:ARG:HH22	2.42	0.41
9:B:98:ASP:OD1	9:B:99:GLY:N	2.53	0.41
10:C:131:ASP:OD1	10:C:131:ASP:N	2.52	0.41
18:L:36:LYS:HA	18:L:41:ARG:HH11	1.83	0.41
24:R:78:ARG:HB3	24:R:81:LYS:HB2	2.02	0.41
56:x:27:ASP:OD1	56:x:27:ASP:N	2.49	0.41
1:1:521:U:C2	1:1:522:A:N7	2.88	0.41
1:1:645:C:N4	1:1:2349:G:N3	2.67	0.41
1:1:775:G:C5	1:1:794:A:C8	3.08	0.41
1:1:1275:A:O2'	1:1:1645:G:N3	2.53	0.41
1:1:2216:G:H2'	1:1:2217:G:C8	2.55	0.41
1:1:2391:G:C6	1:1:2427:C:H1'	2.55	0.41
1:1:2787:C:H2'	1:1:2788:C:C6	2.54	0.41
2:2:147:G:N2	2:2:176:C:C2	2.88	0.41
2:2:570:G:H2'	2:2:571:U:C6	2.55	0.41
2:2:689:C:OP2	48:p:53:ARG:NH1	2.49	0.41
2:2:868:C:H2'	2:2:869:G:O4'	2.20	0.41
2:2:1311:A:OP1	33:a:59:ARG:NH1	2.41	0.41
5:5:37:GLN:HB2	5:5:86:ARG:NE	2.35	0.41
9:B:230:HIS:CD2	9:B:247:PRO:HG3	2.54	0.41
14:G:101:ASP:O	14:G:104:THR:OG1	2.37	0.41
15:H:18:VAL:HG11	15:H:70:GLU:HB3	2.01	0.41
15:H:49:GLY:H	15:H:51:TYR:HE2	1.68	0.41
18:L:112:LEU:HD23	18:L:112:LEU:O	2.20	0.41
39:g:50:PHE:CD1	39:g:200:ILE:HD13	2.55	0.41
43:k:25:TYR:O	43:k:29:ILE:HG12	2.20	0.41
44:l:51:ALA:HB2	44:l:58:GLU:HG3	2.02	0.41
46:n:27:LYS:HG2	46:n:62:ASP:CG	2.45	0.41
47:o:21:ALA:HB1	47:o:92:LEU:HD13	2.02	0.41
1:1:176:A:O2'	1:1:177:G:P	2.79	0.41
1:1:379:G:N1	1:1:396:G:C6	2.89	0.41
1:1:402:A:H2	1:1:407:G:H4'	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:736:C:H2'	1:1:737:C:H6	1.85	0.41
1:1:956:G:H5'	19:M:76:LYS:HG3	2.02	0.41
1:1:1012:U:O4	16:J:30:THR:HG21	2.20	0.41
1:1:1398:C:C2	1:1:1399:C:C5	3.08	0.41
1:1:1712:U:OP2	1:1:1713:A:O2'	2.30	0.41
1:1:1979:U:O2'	1:1:1980:G:H5'	2.20	0.41
1:1:2408:U:C2	1:1:2409:G:N7	2.89	0.41
1:1:2806:C:H2'	1:1:2807:U:O4'	2.20	0.41
2:2:191:G:H2'	2:2:192:A:C8	2.55	0.41
2:2:1015:G:H2'	2:2:1016:A:C8	2.55	0.41
2:2:1346:A:N1	2:2:1374:A:H5''	2.35	0.41
4:4:120:U:H3	42:j:60:ILE:HD13	1.85	0.41
4:4:227:C:H3'	4:4:228:G:H8	1.83	0.41
4:4:359:C:H3'	4:4:360:A:C5'	2.50	0.41
8:A:38:VAL:HB	8:A:59:LEU:HD12	2.02	0.41
21:O:39:VAL:HG22	21:O:49:VAL:HG22	2.02	0.41
22:P:9:GLU:OE2	22:P:56:HIS:NE2	2.51	0.41
27:U:98:SER:C	27:U:99:ASN:CG	2.88	0.41
1:1:69:C:H2'	1:1:70:G:H8	1.84	0.41
1:1:746:PSU:H1'	1:1:748:G:H21	1.85	0.41
1:1:878:A:C6	1:1:879:G:H1'	2.56	0.41
1:1:890:C:C2	1:1:891:G:H1'	2.55	0.41
1:1:917:A:H5''	1:1:2268:A:H61	1.85	0.41
1:1:2033:A:O2'	1:1:2035:G:OP1	2.30	0.41
1:1:2066:C:H2'	1:1:2067:G:C8	2.54	0.41
1:1:2507:C:C2	1:1:2583:G:N2	2.88	0.41
1:1:2596:U:O4	1:1:2597:G:N2	2.53	0.41
1:1:2661:G:H2'	1:1:2662:A:C8	2.55	0.41
2:2:580:C:H2'	2:2:581:G:O4'	2.21	0.41
2:2:826:C:H2'	2:2:827:U:C6	2.55	0.41
2:2:893:C:C2	2:2:894:G:C8	3.09	0.41
2:2:1209:C:N3	2:2:1210:C:N4	2.67	0.41
2:2:1320:C:H1'	56:x:73:GLU:HG3	2.01	0.41
4:4:55:G:N3	4:4:55:G:H2'	2.34	0.41
58:z:59:LYS:HA	58:z:59:LYS:HD3	1.92	0.41
1:1:733:G:N2	1:1:734:A:N7	2.69	0.41
1:1:910:A:H2'	1:1:911:A:C8	2.55	0.41
1:1:1364:G:OP2	30:X:50:ARG:NH2	2.45	0.41
1:1:1386:C:H1'	1:1:1470:A:H1'	2.02	0.41
1:1:1414:C:O2'	1:1:1415:U:O4'	2.31	0.41
1:1:1958:C:H2'	1:1:1959:G:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2327:A:H2'	1:1:2328:A:C8	2.55	0.41
1:1:2445:2MG:OP1	11:D:69:ARG:NH2	2.43	0.41
1:1:2594:C:H2'	1:1:2595:G:C8	2.55	0.41
2:2:736:C:H2'	2:2:737:C:C6	2.56	0.41
2:2:781:A:O2'	2:2:1522:U:O2	2.35	0.41
2:2:1317:C:H3'	2:2:1318:A:C8	2.55	0.41
2:2:1320:C:H2'	2:2:1321:U:C6	2.55	0.41
3:3:8:C:O2'	21:O:40:ILE:HD13	2.20	0.41
4:4:230:U:H4'	4:4:231:A:C8	2.56	0.41
26:T:80:TRP:CD1	26:T:80:TRP:H	2.37	0.41
46:n:63:LEU:C	46:n:63:LEU:HD12	2.45	0.41
48:p:34:ILE:HB	48:p:74:VAL:HG21	2.03	0.41
1:1:494:G:H2'	1:1:495:G:C8	2.56	0.41
1:1:527:C:N4	1:1:2777:G:O2'	2.27	0.41
1:1:660:C:H2'	1:1:661:A:C8	2.55	0.41
1:1:678:C:H2'	1:1:679:C:C6	2.55	0.41
1:1:852:U:H2'	1:1:853:C:C6	2.56	0.41
1:1:894:U:O2'	1:1:895:U:H2'	2.20	0.41
1:1:987:C:H2'	1:1:988:A:O4'	2.21	0.41
1:1:1013:C:H2'	1:1:1014:A:H8	1.85	0.41
1:1:1082:U:O2'	15:H:37:LYS:HD2	2.21	0.41
1:1:1234:U:H2'	1:1:1235:G:O4'	2.19	0.41
1:1:1315:C:H2'	1:1:1316:U:C6	2.55	0.41
1:1:1443:U:H2'	1:1:1444:G:C8	2.55	0.41
1:1:1796:U:H2'	1:1:1797:G:C8	2.54	0.41
1:1:2126:A:N6	1:1:2163:A:H8	2.18	0.41
1:1:2143:C:H5''	1:1:2144:G:H5'	2.02	0.41
1:1:2305:U:H2'	1:1:2306:C:C6	2.55	0.41
1:1:2504:PSU:H2'	1:1:2505:G:H5''	2.03	0.41
1:1:2683:C:O2'	10:C:13:ARG:NH1	2.53	0.41
1:1:2784:U:H2'	1:1:2785:C:C6	2.56	0.41
2:2:402:G:H2'	2:2:403:C:C6	2.56	0.41
2:2:437:U:O2'	41:i:154:ARG:NH2	2.51	0.41
2:2:562:U:H5'	2:2:563:A:C5	2.55	0.41
2:2:885:G:H2'	2:2:886:G:C8	2.55	0.41
2:2:1014:A:N3	2:2:1219:A:H1'	2.36	0.41
2:2:1323:G:H2'	2:2:1324:A:H8	1.85	0.41
2:2:1386:G:C2	2:2:1387:G:C8	3.09	0.41
9:B:61:ALA:O	9:B:86:ASN:ND2	2.48	0.41
14:G:76:GLU:O	14:G:143:ILE:HG12	2.20	0.41
19:M:11:LYS:HD2	19:M:86:LYS:HD3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:S:9:HIS:H	25:S:102:HIS:CE1	2.39	0.41
30:X:37:ARG:HG2	30:X:48:THR:HG22	2.03	0.41
45:m:3:MET:CE	45:m:9:ASP:OD2	2.68	0.41
57:y:9:LYS:HE2	57:y:13:GLN:NE2	2.36	0.41
1:1:354:A:H2'	1:1:355:U:C6	2.55	0.41
1:1:610:C:H2'	1:1:611:C:C6	2.56	0.41
1:1:807:U:C2	1:1:808:G:C8	3.08	0.41
1:1:966:G:H2'	1:1:967:U:H6	1.84	0.41
1:1:1027:A:C2	1:1:2488:G:H5'	2.55	0.41
1:1:1299:G:O2'	1:1:1301:A:N7	2.52	0.41
1:1:1345:C:C2	1:1:1346:G:C8	3.09	0.41
1:1:1591:A:H2'	1:1:1592:C:C6	2.55	0.41
1:1:1809:A:H2'	1:1:1810:A:C8	2.56	0.41
1:1:2053:G:H5'	10:C:150:GLN:H	1.85	0.41
1:1:2065:C:N4	1:1:2445:2MG:HN1	2.19	0.41
1:1:2317:A:H2'	1:1:2318:G:O4'	2.21	0.41
1:1:2743:U:OP2	1:1:2755:C:N4	2.54	0.41
1:1:2899:A:H2'	1:1:2900:A:C8	2.56	0.41
2:2:514:C:C2	2:2:515:G:N7	2.89	0.41
2:2:679:C:H2'	2:2:680:C:H6	1.86	0.41
2:2:1187:G:H2'	2:2:1188:A:C8	2.56	0.41
2:2:1203:C:H2'	2:2:1204:A:H8	1.86	0.41
3:3:116:G:H2'	3:3:117:G:C8	2.56	0.41
17:K:58:LEU:CD1	17:K:59:LYS:O	2.68	0.41
30:X:17:ASN:CG	30:X:27:ARG:HD2	2.46	0.41
33:a:56:ARG:HH11	56:x:68:GLY:H	1.67	0.41
42:j:153:VAL:HA	42:j:156:LYS:HE2	2.02	0.41
48:p:64:GLN:HB3	48:p:95:SER:OG	2.21	0.41
1:1:55:G:H2'	1:1:56:A:C8	2.55	0.41
1:1:367:G:H2'	1:1:368:A:H8	1.86	0.41
1:1:721:A:H2'	1:1:722:A:C8	2.56	0.41
1:1:1418:G:N1	1:1:1579:A:OP2	2.47	0.41
1:1:1561:C:H2'	1:1:1562:U:H6	1.85	0.41
1:1:1703:G:H2'	1:1:1704:C:C6	2.56	0.41
1:1:1823:G:H2'	1:1:1824:G:H8	1.85	0.41
1:1:1825:U:C2	1:1:1826:G:C8	3.09	0.41
1:1:1973:G:H2'	1:1:1974:C:C6	2.55	0.41
1:1:2050:C:H2'	1:1:2051:A:O4'	2.20	0.41
1:1:2801:G:H2'	1:1:2802:G:H8	1.85	0.41
1:1:2812:G:H2'	1:1:2813:A:C8	2.54	0.41
2:2:916:U:H2'	2:2:917:G:C8	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:C:91:THR:OG1	10:C:94:GLN:HG3	2.20	0.41
40:h:6:HIS:CE1	40:h:8:ASN:HB3	2.55	0.41
56:x:44:MET:O	56:x:62:VAL:HG11	2.20	0.41
1:1:540:C:H2'	1:1:541:A:C8	2.56	0.41
1:1:1198:U:H2'	1:1:1199:U:H6	1.86	0.41
1:1:1263:U:OP1	34:b:13:ARG:NH1	2.52	0.41
1:1:1324:G:H3'	1:1:1325:U:H4'	2.03	0.41
1:1:1443:U:C2	1:1:1444:G:C8	3.09	0.41
1:1:1665:A:H2'	1:1:1666:G:C8	2.53	0.41
1:1:1672:A:C6	1:1:2582:G:H5'	2.56	0.41
1:1:1726:C:H42	1:1:1735:A:H61	1.68	0.41
1:1:1736:U:C4	1:1:1737:G:C2	3.08	0.41
1:1:1820:U:H1'	9:B:201:MET:HB3	2.03	0.41
1:1:1824:G:H2'	1:1:1825:U:H6	1.85	0.41
1:1:1987:A:H2'	1:1:1988:G:C8	2.51	0.41
1:1:1992:G:O2'	1:1:1997:C:N4	2.54	0.41
1:1:2535:G:C2	1:1:2536:G:C8	3.09	0.41
1:1:2601:C:H2'	1:1:2603:G:C8	2.55	0.41
1:1:2746:U:H2'	1:1:2747:G:O4'	2.20	0.41
1:1:2766:A:N3	1:1:2766:A:H2'	2.36	0.41
1:1:2773:C:H2'	1:1:2774:C:H6	1.86	0.41
1:1:2888:C:H2'	1:1:2889:C:H6	1.84	0.41
2:2:73:C:H2'	2:2:74:A:H8	1.86	0.41
2:2:333:U:H2'	2:2:334:C:H5''	2.03	0.41
2:2:437:U:H2'	2:2:438:U:H5'	2.03	0.41
2:2:489:C:C2	2:2:490:C:C5	3.09	0.41
2:2:648:A:H2'	2:2:649:A:C8	2.56	0.41
2:2:679:C:H2'	2:2:680:C:C6	2.55	0.41
2:2:705:G:C5	2:2:706:A:C8	3.08	0.41
2:2:714:G:H1'	2:2:777:A:C8	2.56	0.41
2:2:1086:U:C2	2:2:1087:G:C8	3.08	0.41
2:2:1207:2MG:HM23	2:2:1208:C:H1'	2.03	0.41
2:2:1376:U:H2'	2:2:1377:A:C8	2.56	0.41
4:4:7:G:H1	4:4:353:C:H5	1.68	0.41
4:4:21:C:H2'	4:4:22:G:C8	2.55	0.41
4:4:114:G:H1	4:4:128:U:H3	1.69	0.41
4:4:185:A:C5	40:h:77:ILE:HG21	2.55	0.41
4:4:255:A:H5''	4:4:271:G:N7	2.36	0.41
17:K:43:ILE:HD12	17:K:56:ASP:HB2	2.03	0.41
20:N:30:ARG:HB2	20:N:75:ILE:HD11	2.02	0.41
44:l:70:ARG:HD3	44:l:96:ARG:HH21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:l:132:GLY:O	44:l:136:LYS:HG2	2.21	0.41
47:o:86:ALA:O	47:o:89:ARG:HG3	2.13	0.41
48:p:97:ILE:HG22	58:z:12:PHE:CZ	2.56	0.41
54:v:57:ASP:OD1	54:v:58:VAL:N	2.54	0.41
1:1:272:A:H2'	1:1:273:G:C8	2.56	0.41
1:1:345:A:N3	1:1:347:A:N6	2.69	0.41
1:1:374:A:C5	1:1:375:G:C8	3.09	0.41
1:1:437:U:H2'	1:1:438:G:C8	2.50	0.41
1:1:1007:C:OP2	1:1:1008:A:O2'	2.28	0.41
1:1:1054:A:C4'	15:H:31:ARG:HA	2.48	0.41
1:1:1814:G:OP2	1:1:1815:A:O2'	2.33	0.41
1:1:1927:A:O2'	1:1:1928:A:P	2.79	0.41
1:1:2026:U:C2	1:1:2027:G:C8	3.09	0.41
1:1:2128:G:N2	1:1:2129:C:H41	2.19	0.41
1:1:2384:U:H5''	1:1:2386:A:OP1	2.21	0.41
2:2:219:U:C2	2:2:220:G:C8	3.09	0.41
2:2:711:G:H2'	2:2:712:A:C8	2.50	0.41
2:2:975:A:N1	2:2:1366:C:O2'	2.49	0.41
2:2:984:C:H2'	2:2:985:C:C6	2.56	0.41
4:4:84:A:H1'	4:4:85:U:C5	2.56	0.41
4:4:248:G:H2'	4:4:249:U:O4'	2.21	0.41
24:R:1:MET:HE2	24:R:1:MET:HB2	1.98	0.41
54:v:46:VAL:HG21	54:v:61:ILE:HG21	2.03	0.41
1:1:45:G:H5'	1:1:46:G:OP1	2.21	0.40
1:1:306:U:O4	1:1:310:A:N7	2.54	0.40
1:1:457:A:N1	1:1:470:A:H5''	2.37	0.40
1:1:1056:G:H4'	1:1:1086:A:C8	2.56	0.40
1:1:1441:G:H2'	1:1:1442:U:C6	2.56	0.40
1:1:1686:C:H2'	1:1:1687:G:O4'	2.21	0.40
1:1:1928:A:H2'	1:1:1929:G:O4'	2.21	0.40
1:1:2292:U:H2'	1:1:2293:G:C8	2.56	0.40
1:1:2328:A:H2'	1:1:2329:U:H6	1.83	0.40
1:1:2647:U:O2	1:1:2674:G:O6	2.39	0.40
2:2:8:A:N7	41:i:206:LYS:HA	2.36	0.40
2:2:42:G:H2'	2:2:43:C:C6	2.56	0.40
2:2:296:U:O2'	2:2:556:C:O2	2.38	0.40
2:2:337:G:C2	2:2:338:A:C5	3.08	0.40
2:2:359:G:C4	2:2:360:G:C8	3.09	0.40
2:2:1076:U:H2'	2:2:1077:G:C8	2.56	0.40
2:2:1141:C:O2'	2:2:1142:G:H8	2.03	0.40
11:D:119:ILE:HD11	11:D:187:VAL:HG22	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Q:47:TYR:HA	23:Q:50:ARG:NH1	2.36	0.40
31:Y:26:PHE:HD1	31:Y:29:ARG:HH11	1.68	0.40
33:a:56:ARG:HH11	56:x:68:GLY:C	2.28	0.40
35:c:6:ARG:NH2	35:c:24:THR:O	2.54	0.40
39:g:28:LYS:HB3	39:g:29:PRO:HD3	2.02	0.40
39:g:103:ASN:O	39:g:107:VAL:HG23	2.21	0.40
46:n:45:ARG:HA	46:n:48:VAL:HG12	2.03	0.40
47:o:89:ARG:HG3	47:o:90:LEU:N	2.35	0.40
48:p:18:ASP:OD1	48:p:18:ASP:N	2.43	0.40
1:1:239:C:H2'	1:1:240:C:O4'	2.22	0.40
1:1:371:A:N6	1:1:402:A:OP2	2.53	0.40
1:1:736:C:H2'	1:1:737:C:C6	2.57	0.40
1:1:1152:C:H2'	1:1:1153:C:H6	1.86	0.40
1:1:1229:C:H2'	1:1:1230:A:C8	2.56	0.40
1:1:1528:A:OP2	1:1:1543:G:N2	2.55	0.40
1:1:1541:C:H2'	1:1:1542:U:H6	1.86	0.40
1:1:2840:C:C2	1:1:2841:C:C5	3.09	0.40
2:2:304:U:H2'	2:2:305:G:H8	1.84	0.40
2:2:505:G:H2'	2:2:506:G:C8	2.56	0.40
2:2:1214:C:O4'	5:5:106:ARG:NH2	2.55	0.40
4:4:106:A:N3	4:4:106:A:H2'	2.36	0.40
4:4:150:G:H2'	4:4:150:G:N3	2.35	0.40
6:7:5:G:H2'	6:7:6:G:H8	1.86	0.40
9:B:69:ARG:O	9:B:189:ARG:NH2	2.54	0.40
13:F:11:VAL:O	13:F:11:VAL:HG13	2.21	0.40
48:p:64:GLN:HB2	48:p:99:ALA:HB2	2.02	0.40
1:1:211:C:H2'	1:1:212:G:H8	1.84	0.40
1:1:307:G:N1	1:1:310:A:OP2	2.33	0.40
1:1:366:C:H2'	1:1:367:G:C8	2.53	0.40
1:1:1071:G:H2'	1:1:1072:C:C6	2.56	0.40
1:1:1107:G:P	15:H:57:ASN:HA	2.56	0.40
1:1:1988:G:H2'	1:1:1989:G:C8	2.57	0.40
1:1:2377:A:O2'	21:O:117:PHE:O	2.26	0.40
1:1:2800:A:C2	1:1:2895:G:H1'	2.57	0.40
2:2:357:G:C2	2:2:358:U:C5	3.10	0.40
2:2:558:G:OP2	2:2:559:A:O2'	2.31	0.40
2:2:910:C:H2'	2:2:911:U:C6	2.56	0.40
2:2:1326:U:H2'	2:2:1327:C:H6	1.87	0.40
4:4:13:G:O2'	4:4:347:PSU:O2	2.38	0.40
4:4:178:G:H2'	4:4:179:A:H8	1.86	0.40
8:A:24:LYS:N	8:A:37:ILE:O	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:E:33:LYS:HG2	12:E:157:THR:HB	2.03	0.40
24:R:79:ARG:O	24:R:81:LYS:HG2	2.21	0.40
31:Y:4:LYS:O	31:Y:6:LEU:HG	2.22	0.40
32:Z:6:LYS:HB2	32:Z:58:GLU:HB2	2.02	0.40
39:g:105:LYS:HG3	39:g:108:ARG:HH21	1.87	0.40
41:i:156:LYS:O	41:i:160:GLU:HG2	2.22	0.40
43:k:2:ARG:HG3	43:k:4:TYR:HE2	1.86	0.40
49:q:50:ARG:HB3	49:q:66:TYR:CE1	2.53	0.40
1:1:23:G:H2'	1:1:24:G:C8	2.55	0.40
1:1:121:G:H4'	1:1:149:A:H5'	2.03	0.40
1:1:1039:A:H2'	1:1:1040:A:O4'	2.22	0.40
1:1:1083:U:H2'	1:1:1084:A:H3'	2.04	0.40
1:1:1687:G:H2'	1:1:1688:U:C6	2.57	0.40
1:1:1798:U:OP2	9:B:271:ARG:NH2	2.53	0.40
1:1:2507:C:C2	1:1:2508:G:C8	3.09	0.40
2:2:234:C:H2'	2:2:235:C:C6	2.56	0.40
2:2:285:C:H2'	2:2:286:C:H6	1.86	0.40
2:2:406:G:H2'	2:2:407:U:H6	1.86	0.40
2:2:938:A:O2'	2:2:939:G:P	2.78	0.40
2:2:1401:G:H2'	2:2:1402:4OC:O4'	2.22	0.40
3:3:70:C:H2'	3:3:71:C:H6	1.85	0.40
4:4:112:U:H2'	4:4:113:A:N3	2.37	0.40
6:7:67:C:H2'	6:7:68:C:C6	2.57	0.40
13:F:2:SER:OG	13:F:3:ARG:N	2.53	0.40
13:F:72:LEU:HD23	13:F:72:LEU:HA	1.91	0.40
14:G:125:THR:OG1	14:G:146:VAL:HG12	2.21	0.40
40:h:155:GLY:HA2	40:h:163:ALA:HB1	2.03	0.40
46:n:54:LEU:HD23	46:n:98:LEU:HD23	2.03	0.40
1:1:75:G:N3	1:1:75:G:H2'	2.37	0.40
1:1:1030:C:N3	1:1:1125:G:N2	2.70	0.40
1:1:1058:U:H2'	1:1:1059:G:O4'	2.22	0.40
1:1:1574:C:C2	1:1:1575:C:C5	3.10	0.40
1:1:2133:G:H1'	1:1:2158:A:N6	2.36	0.40
1:1:2398:U:H2'	1:1:2399:G:C8	2.56	0.40
1:1:2506:U:O2'	1:1:2507:C:OP1	2.33	0.40
1:1:2507:C:H2'	1:1:2508:G:O4'	2.21	0.40
2:2:35:G:H2'	2:2:36:C:C6	2.57	0.40
2:2:60:A:N6	2:2:110:C:C4	2.90	0.40
2:2:211:G:C6	2:2:212:G:H1'	2.56	0.40
2:2:514:C:H2'	2:2:515:G:H8	1.87	0.40
2:2:737:C:H2'	2:2:738:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1265:C:H2'	2:2:1266:G:C8	2.57	0.40
2:2:1288:A:H61	2:2:1371:G:H1'	1.86	0.40
2:2:1319:A:O2'	2:2:1323:G:N7	2.46	0.40
2:2:1481:U:H2'	2:2:1482:G:C8	2.56	0.40
4:4:318:G:H2'	4:4:319:A:C8	2.56	0.40
5:5:118:TRP:CD1	5:5:120:ASN:HA	2.56	0.40
9:B:168:ASP:OD1	9:B:168:ASP:N	2.54	0.40
11:D:76:PRO:HG3	11:D:84:THR:HG22	2.03	0.40
24:R:68:ARG:NH1	24:R:90:ARG:HB2	2.36	0.40
24:R:76:LYS:HD2	24:R:85:LYS:HD3	2.03	0.40
28:V:7:GLU:HB2	28:V:41:GLU:HB2	2.03	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	
5	5	145/147 (99%)	114 (79%)	29 (20%)	2 (1%)	9	31
8	A	82/84 (98%)	80 (98%)	2 (2%)	0	100	100
9	B	269/271 (99%)	266 (99%)	3 (1%)	0	100	100
10	C	207/209 (99%)	204 (99%)	3 (1%)	0	100	100
11	D	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
12	E	175/177 (99%)	168 (96%)	7 (4%)	0	100	100
13	F	173/175 (99%)	165 (95%)	8 (5%)	0	100	100
14	G	147/149 (99%)	137 (93%)	10 (7%)	0	100	100
15	H	128/130 (98%)	98 (77%)	23 (18%)	7 (6%)	1	8
16	J	139/141 (99%)	138 (99%)	1 (1%)	0	100	100
17	K	121/123 (98%)	120 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	L	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
19	M	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
20	N	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
21	O	113/115 (98%)	111 (98%)	2 (2%)	0	100	100
22	P	112/114 (98%)	112 (100%)	0	0	100	100
23	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
24	R	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
25	S	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
26	T	92/94 (98%)	92 (100%)	0	0	100	100
27	U	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
28	V	92/94 (98%)	92 (100%)	0	0	100	100
30	X	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
31	Y	56/58 (97%)	56 (100%)	0	0	100	100
32	Z	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
33	a	64/66 (97%)	61 (95%)	3 (5%)	0	100	100
34	b	52/54 (96%)	52 (100%)	0	0	100	100
35	c	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
36	d	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
37	e	62/64 (97%)	57 (92%)	2 (3%)	3 (5%)	2	10
38	f	35/37 (95%)	35 (100%)	0	0	100	100
39	g	223/225 (99%)	219 (98%)	4 (2%)	0	100	100
40	h	206/208 (99%)	202 (98%)	4 (2%)	0	100	100
41	i	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
42	j	154/156 (99%)	147 (96%)	7 (4%)	0	100	100
43	k	102/104 (98%)	102 (100%)	0	0	100	100
44	l	149/151 (99%)	147 (99%)	2 (1%)	0	100	100
45	m	127/129 (98%)	127 (100%)	0	0	100	100
46	n	124/126 (98%)	120 (97%)	4 (3%)	0	100	100
47	o	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
48	p	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
49	q	120/123 (98%)	114 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	r	113/115 (98%)	111 (98%)	2 (2%)	0	100	100
51	s	98/100 (98%)	98 (100%)	0	0	100	100
52	t	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
53	u	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
54	v	78/80 (98%)	72 (92%)	6 (8%)	0	100	100
55	w	63/65 (97%)	63 (100%)	0	0	100	100
56	x	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
57	y	83/85 (98%)	82 (99%)	1 (1%)	0	100	100
58	z	68/70 (97%)	68 (100%)	0	0	100	100
All	All	5869/5973 (98%)	5678 (97%)	179 (3%)	12 (0%)	44	71

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
37	e	32	ILE
15	H	55	VAL
15	H	88	HIS
15	H	118	ILE
37	e	33	LEU
15	H	22	ALA
15	H	90	GLY
15	H	130	PRO
37	e	34	THR
5	5	111	VAL
5	5	68	ALA
15	H	108	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	5	123/123 (100%)	113 (92%)	10 (8%)	11	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	A	62/62 (100%)	59 (95%)	3 (5%)	23	51
9	B	216/216 (100%)	215 (100%)	1 (0%)	81	83
10	C	164/164 (100%)	164 (100%)	0	100	100
11	D	165/165 (100%)	165 (100%)	0	100	100
12	E	148/148 (100%)	148 (100%)	0	100	100
13	F	136/136 (100%)	133 (98%)	3 (2%)	45	68
14	G	114/114 (100%)	113 (99%)	1 (1%)	70	78
15	H	99/99 (100%)	96 (97%)	3 (3%)	36	62
16	J	115/115 (100%)	115 (100%)	0	100	100
17	K	104/104 (100%)	104 (100%)	0	100	100
18	L	103/103 (100%)	102 (99%)	1 (1%)	68	77
19	M	108/108 (100%)	107 (99%)	1 (1%)	70	78
20	N	99/99 (100%)	99 (100%)	0	100	100
21	O	85/85 (100%)	85 (100%)	0	100	100
22	P	99/99 (100%)	99 (100%)	0	100	100
23	Q	89/89 (100%)	89 (100%)	0	100	100
24	R	84/84 (100%)	84 (100%)	0	100	100
25	S	92/92 (100%)	92 (100%)	0	100	100
26	T	81/81 (100%)	81 (100%)	0	100	100
27	U	84/84 (100%)	84 (100%)	0	100	100
28	V	78/78 (100%)	78 (100%)	0	100	100
29	W	1/1 (100%)	0	1 (100%)	0	0
30	X	67/67 (100%)	66 (98%)	1 (2%)	57	73
31	Y	53/53 (100%)	53 (100%)	0	100	100
32	Z	47/47 (100%)	47 (100%)	0	100	100
33	a	59/59 (100%)	59 (100%)	0	100	100
34	b	46/46 (100%)	46 (100%)	0	100	100
35	c	47/47 (100%)	46 (98%)	1 (2%)	47	68
36	d	38/38 (100%)	38 (100%)	0	100	100
37	e	51/51 (100%)	51 (100%)	0	100	100
38	f	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	g	187/187 (100%)	187 (100%)	0	100	100
40	h	171/171 (100%)	170 (99%)	1 (1%)	78	81
41	i	172/172 (100%)	171 (99%)	1 (1%)	78	81
42	j	119/119 (100%)	119 (100%)	0	100	100
43	k	91/91 (100%)	91 (100%)	0	100	100
44	l	124/124 (100%)	123 (99%)	1 (1%)	73	79
45	m	104/104 (100%)	104 (100%)	0	100	100
46	n	104/104 (100%)	102 (98%)	2 (2%)	50	70
47	o	86/86 (100%)	85 (99%)	1 (1%)	63	75
48	p	90/90 (100%)	90 (100%)	0	100	100
49	q	102/102 (100%)	102 (100%)	0	100	100
50	r	93/93 (100%)	93 (100%)	0	100	100
51	s	83/83 (100%)	83 (100%)	0	100	100
52	t	75/75 (100%)	75 (100%)	0	100	100
53	u	65/65 (100%)	65 (100%)	0	100	100
54	v	74/74 (100%)	74 (100%)	0	100	100
55	w	56/56 (100%)	56 (100%)	0	100	100
56	x	72/72 (100%)	72 (100%)	0	100	100
57	y	65/65 (100%)	65 (100%)	0	100	100
58	z	60/60 (100%)	60 (100%)	0	100	100
All	All	4884/4884 (100%)	4852 (99%)	32 (1%)	73	80

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	5	34	LEU
5	5	36	LEU
5	5	37	GLN
5	5	110	THR
5	5	134	LYS
5	5	135	GLN
5	5	137	ASP
5	5	138	LYS
5	5	139	ARG
5	5	143	LYS

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Mol	Chain	Res	Type
8	A	3	HIS
8	A	4	LYS
8	A	5	LYS
9	B	195	VAL
13	F	19	ILE
13	F	148	LEU
13	F	149	ARG
14	G	72	ILE
15	H	3	LEU
15	H	57	ASN
15	H	122	GLN
18	L	77	ILE
19	M	57	VAL
29	W	1	PHE
30	X	43	GLU
35	c	43	VAL
40	h	29	PHE
41	i	67	VAL
44	l	135	VAL
46	n	43	THR
46	n	107	ASP
47	o	59	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
5	5	37	GLN
10	C	130	GLN
10	C	148	GLN
11	D	92	HIS
11	D	165	HIS
13	F	128	GLN
14	G	28	ASN
16	J	58	ASN
18	L	104	GLN
21	O	38	GLN
27	U	45	HIS
27	U	74	ASN
28	V	49	ASN
30	X	36	HIS
31	Y	20	ASN
31	Y	45	GLN

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Mol	Chain	Res	Type
33	a	20	ASN
33	a	48	GLN
34	b	42	HIS
37	e	28	ASN
38	f	35	GLN
39	g	227	GLN
40	h	102	ASN
41	i	54	GLN
43	k	58	HIS
46	n	37	GLN
46	n	75	GLN
48	p	22	HIS
48	p	29	ASN
48	p	38	GLN
50	r	100	GLN
50	r	105	ASN
53	u	59	HIS
56	x	14	HIS
57	y	13	GLN
57	y	55	GLN
58	z	9	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	540 (18%)	25 (0%)
2	2	1538/1540 (99%)	247 (16%)	13 (0%)
3	3	119/120 (99%)	13 (10%)	0
4	4	362/363 (99%)	164 (45%)	14 (3%)
6	7	75/76 (98%)	14 (18%)	2 (2%)
7	8	14/15 (93%)	4 (28%)	2 (14%)
All	All	5010/5017 (99%)	982 (19%)	56 (1%)

All (982) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	14	A
1	1	15	G
1	1	27	G
1	1	28	A

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Mol	Chain	Res	Type
1	1	46	G
1	1	51	G
1	1	63	A
1	1	71	A
1	1	74	A
1	1	75	G
1	1	84	A
1	1	85	G
1	1	101	A
1	1	102	U
1	1	118	A
1	1	120	U
1	1	131	A
1	1	137	U
1	1	138	U
1	1	139	U
1	1	140	C
1	1	142	A
1	1	159	G
1	1	163	C
1	1	165	A
1	1	177	G
1	1	196	A
1	1	199	A
1	1	204	A
1	1	205	G
1	1	216	A
1	1	222	A
1	1	228	C
1	1	233	A
1	1	241	A
1	1	242	G
1	1	248	G
1	1	266	G
1	1	274	C
1	1	275	C
1	1	277	G
1	1	279	A
1	1	282	A
1	1	283	G
1	1	284	U
1	1	285	G

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Mol	Chain	Res	Type
1	1	311	A
1	1	322	A
1	1	323	C
1	1	330	A
1	1	352	A
1	1	356	G
1	1	359	G
1	1	361	G
1	1	371	A
1	1	372	G
1	1	379	G
1	1	386	G
1	1	387	U
1	1	396	G
1	1	399	U
1	1	401	A
1	1	403	U
1	1	405	U
1	1	406	G
1	1	411	G
1	1	412	A
1	1	424	G
1	1	429	A
1	1	430	A
1	1	446	G
1	1	451	U
1	1	457	A
1	1	458	G
1	1	464	U
1	1	465	G
1	1	481	G
1	1	489	G
1	1	490	C
1	1	491	G
1	1	505	A
1	1	509	C
1	1	529	A
1	1	530	G
1	1	532	A
1	1	545	U
1	1	546	U
1	1	547	A

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Mol	Chain	Res	Type
1	1	548	G
1	1	549	G
1	1	563	A
1	1	573	U
1	1	575	A
1	1	587	C
1	1	603	A
1	1	613	A
1	1	614	A
1	1	615	U
1	1	621	A
1	1	632	A
1	1	637	A
1	1	642	U
1	1	645	C
1	1	647	G
1	1	654	A
1	1	655	A
1	1	656	G
1	1	686	U
1	1	709	U
1	1	712	G
1	1	713	G
1	1	717	C
1	1	726	G
1	1	730	A
1	1	747	5MU
1	1	748	G
1	1	764	A
1	1	775	G
1	1	776	G
1	1	782	A
1	1	784	G
1	1	785	G
1	1	789	A
1	1	792	A
1	1	805	G
1	1	812	C
1	1	819	A
1	1	827	U
1	1	830	G
1	1	845	A

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Mol	Chain	Res	Type
1	1	846	U
1	1	856	G
1	1	866	A
1	1	869	G
1	1	878	A
1	1	879	G
1	1	880	G
1	1	882	G
1	1	884	U
1	1	885	C
1	1	886	A
1	1	888	C
1	1	891	G
1	1	894	U
1	1	895	U
1	1	896	A
1	1	897	C
1	1	907	G
1	1	910	A
1	1	912	C
1	1	914	G
1	1	915	C
1	1	931	U
1	1	941	A
1	1	946	C
1	1	957	C
1	1	959	A
1	1	961	C
1	1	973	A
1	1	974	G
1	1	995	C
1	1	996	A
1	1	999	U
1	1	1009	A
1	1	1012	U
1	1	1013	C
1	1	1017	G
1	1	1022	G
1	1	1023	U
1	1	1026	G
1	1	1033	U
1	1	1035	U

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Mol	Chain	Res	Type
1	1	1040	A
1	1	1043	C
1	1	1044	C
1	1	1045	C
1	1	1047	G
1	1	1049	C
1	1	1050	A
1	1	1051	G
1	1	1053	C
1	1	1055	G
1	1	1056	G
1	1	1058	U
1	1	1059	G
1	1	1060	U
1	1	1061	U
1	1	1062	G
1	1	1064	C
1	1	1065	U
1	1	1066	U
1	1	1067	A
1	1	1068	G
1	1	1070	A
1	1	1071	G
1	1	1072	C
1	1	1073	A
1	1	1074	G
1	1	1075	C
1	1	1076	C
1	1	1078	U
1	1	1080	A
1	1	1081	U
1	1	1082	U
1	1	1083	U
1	1	1084	A
1	1	1085	A
1	1	1087	G
1	1	1088	A
1	1	1089	A
1	1	1090	A
1	1	1092	C
1	1	1093	G
1	1	1094	U

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Mol	Chain	Res	Type
1	1	1095	A
1	1	1098	A
1	1	1099	G
1	1	1100	C
1	1	1101	U
1	1	1103	A
1	1	1104	C
1	1	1105	U
1	1	1106	G
1	1	1110	G
1	1	1111	A
1	1	1112	G
1	1	1115	G
1	1	1116	G
1	1	1119	U
1	1	1126	A
1	1	1132	U
1	1	1135	C
1	1	1142	A
1	1	1147	A
1	1	1155	A
1	1	1171	G
1	1	1173	U
1	1	1174	U
1	1	1175	A
1	1	1176	U
1	1	1177	G
1	1	1178	C
1	1	1180	U
1	1	1204	A
1	1	1236	G
1	1	1238	G
1	1	1247	A
1	1	1248	G
1	1	1250	G
1	1	1253	A
1	1	1256	G
1	1	1266	G
1	1	1271	G
1	1	1272	A
1	1	1288	G
1	1	1299	G

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Mol	Chain	Res	Type
1	1	1300	G
1	1	1301	A
1	1	1306	C
1	1	1314	C
1	1	1321	A
1	1	1325	U
1	1	1329	U
1	1	1345	C
1	1	1352	U
1	1	1365	A
1	1	1368	G
1	1	1378	A
1	1	1379	U
1	1	1380	G
1	1	1383	A
1	1	1394	U
1	1	1403	A
1	1	1409	U
1	1	1414	C
1	1	1416	G
1	1	1417	C
1	1	1427	A
1	1	1428	C
1	1	1434	A
1	1	1455	G
1	1	1458	U
1	1	1482	G
1	1	1490	A
1	1	1493	C
1	1	1494	A
1	1	1497	U
1	1	1508	A
1	1	1509	A
1	1	1510	G
1	1	1515	A
1	1	1524	G
1	1	1534	U
1	1	1535	A
1	1	1536	C
1	1	1538	G
1	1	1558	C
1	1	1569	A

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Mol	Chain	Res	Type
1	1	1578	U
1	1	1590	A
1	1	1603	A
1	1	1610	A
1	1	1615	C
1	1	1618	6MZ
1	1	1619	G
1	1	1627	G
1	1	1630	A
1	1	1634	A
1	1	1646	C
1	1	1647	U
1	1	1648	U
1	1	1654	A
1	1	1674	G
1	1	1681	G
1	1	1715	G
1	1	1726	C
1	1	1729	U
1	1	1730	C
1	1	1732	C
1	1	1733	G
1	1	1738	G
1	1	1756	G
1	1	1764	C
1	1	1773	A
1	1	1786	A
1	1	1791	A
1	1	1800	C
1	1	1801	A
1	1	1802	A
1	1	1808	A
1	1	1815	A
1	1	1816	C
1	1	1820	U
1	1	1833	C
1	1	1847	A
1	1	1848	A
1	1	1858	A
1	1	1859	U
1	1	1869	G
1	1	1906	G

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Mol	Chain	Res	Type
1	1	1914	C
1	1	1919	A
1	1	1924	C
1	1	1927	A
1	1	1928	A
1	1	1929	G
1	1	1936	A
1	1	1955	U
1	1	1967	C
1	1	1970	A
1	1	1971	U
1	1	1972	G
1	1	1991	U
1	1	1992	G
1	1	1993	U
1	1	1997	C
1	1	2013	A
1	1	2022	U
1	1	2023	C
1	1	2030	6MZ
1	1	2031	A
1	1	2033	A
1	1	2034	U
1	1	2043	C
1	1	2049	G
1	1	2052	A
1	1	2055	C
1	1	2056	G
1	1	2060	A
1	1	2061	G
1	1	2062	A
1	1	2064	C
1	1	2068	U
1	1	2069	G7M
1	1	2080	A
1	1	2093	G
1	1	2099	U
1	1	2100	G
1	1	2101	A
1	1	2102	G
1	1	2104	C
1	1	2105	U

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Mol	Chain	Res	Type
1	1	2106	U
1	1	2109	U
1	1	2110	G
1	1	2111	U
1	1	2112	G
1	1	2113	U
1	1	2114	A
1	1	2115	G
1	1	2117	A
1	1	2118	U
1	1	2120	G
1	1	2122	U
1	1	2123	G
1	1	2124	G
1	1	2125	G
1	1	2126	A
1	1	2128	G
1	1	2130	U
1	1	2131	U
1	1	2132	U
1	1	2134	A
1	1	2136	G
1	1	2138	G
1	1	2139	U
1	1	2144	G
1	1	2146	C
1	1	2147	A
1	1	2151	U
1	1	2154	A
1	1	2155	U
1	1	2156	G
1	1	2157	G
1	1	2158	A
1	1	2159	G
1	1	2161	C
1	1	2163	A
1	1	2165	C
1	1	2166	U
1	1	2168	G
1	1	2170	A
1	1	2171	A
1	1	2172	U

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Mol	Chain	Res	Type
1	1	2174	C
1	1	2178	C
1	1	2181	U
1	1	2182	U
1	1	2183	A
1	1	2186	G
1	1	2188	U
1	1	2189	U
1	1	2190	G
1	1	2191	A
1	1	2193	G
1	1	2194	U
1	1	2198	A
1	1	2199	A
1	1	2204	G
1	1	2211	A
1	1	2212	A
1	1	2225	A
1	1	2238	G
1	1	2239	G
1	1	2250	G
1	1	2266	A
1	1	2268	A
1	1	2279	G
1	1	2283	C
1	1	2287	A
1	1	2297	A
1	1	2305	U
1	1	2308	G
1	1	2309	A
1	1	2315	G
1	1	2322	A
1	1	2325	G
1	1	2327	A
1	1	2333	A
1	1	2347	C
1	1	2350	C
1	1	2361	G
1	1	2383	G
1	1	2385	C
1	1	2402	U
1	1	2403	C

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Mol	Chain	Res	Type
1	1	2423	U
1	1	2425	A
1	1	2426	A
1	1	2428	G
1	1	2429	G
1	1	2430	A
1	1	2441	U
1	1	2445	2MG
1	1	2448	A
1	1	2469	A
1	1	2470	G
1	1	2475	C
1	1	2476	A
1	1	2491	U
1	1	2498	OMC
1	1	2499	C
1	1	2501	C
1	1	2503	2MA
1	1	2504	PSU
1	1	2506	U
1	1	2507	C
1	1	2517	C
1	1	2518	A
1	1	2519	U
1	1	2520	C
1	1	2529	G
1	1	2535	G
1	1	2554	U
1	1	2555	U
1	1	2564	A
1	1	2566	A
1	1	2567	G
1	1	2572	A
1	1	2585	U
1	1	2586	U
1	1	2597	G
1	1	2602	A
1	1	2609	U
1	1	2613	U
1	1	2615	U
1	1	2629	U
1	1	2630	G

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Mol	Chain	Res	Type
1	1	2646	C
1	1	2682	A
1	1	2689	U
1	1	2690	U
1	1	2712	C
1	1	2714	G
1	1	2725	A
1	1	2726	A
1	1	2729	G
1	1	2733	A
1	1	2744	G
1	1	2748	A
1	1	2750	A
1	1	2765	A
1	1	2776	A
1	1	2777	G
1	1	2778	A
1	1	2790	U
1	1	2794	C
1	1	2795	C
1	1	2797	U
1	1	2798	U
1	1	2818	U
1	1	2820	A
1	1	2849	U
1	1	2867	G
1	1	2873	A
1	1	2874	C
1	1	2880	C
1	1	2884	U
1	1	2903	U
2	2	4	U
2	2	6	G
2	2	8	A
2	2	9	G
2	2	14	U
2	2	31	G
2	2	32	A
2	2	39	G
2	2	47	C
2	2	48	C
2	2	51	A

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Mol	Chain	Res	Type
2	2	70	U
2	2	71	A
2	2	72	A
2	2	73	C
2	2	75	G
2	2	76	G
2	2	81	A
2	2	82	G
2	2	83	C
2	2	84	U
2	2	85	U
2	2	87	C
2	2	88	U
2	2	89	U
2	2	91	U
2	2	95	C
2	2	108	G
2	2	110	C
2	2	120	A
2	2	128	G
2	2	130	A
2	2	131	A
2	2	177	G
2	2	179	A
2	2	181	A
2	2	188	C
2	2	197	A
2	2	204	G
2	2	207	C
2	2	209	U
2	2	211	G
2	2	212	G
2	2	226	G
2	2	245	U
2	2	247	G
2	2	251	G
2	2	266	G
2	2	267	C
2	2	280	C
2	2	289	G
2	2	299	G
2	2	328	C

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Mol	Chain	Res	Type
2	2	332	G
2	2	334	C
2	2	347	G
2	2	351	G
2	2	352	C
2	2	354	G
2	2	367	U
2	2	369	G
2	2	372	C
2	2	373	A
2	2	392	C
2	2	397	A
2	2	406	G
2	2	412	A
2	2	413	G
2	2	414	A
2	2	421	U
2	2	424	G
2	2	429	U
2	2	457	G
2	2	464	U
2	2	467	U
2	2	468	A
2	2	469	C
2	2	474	G
2	2	479	U
2	2	482	A
2	2	484	G
2	2	491	G
2	2	495	A
2	2	496	A
2	2	497	G
2	2	511	C
2	2	517	G
2	2	518	C
2	2	521	G
2	2	524	G
2	2	527	G7M
2	2	532	A
2	2	547	A
2	2	559	A
2	2	564	C

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Mol	Chain	Res	Type
2	2	572	A
2	2	573	A
2	2	576	C
2	2	577	G
2	2	633	G
2	2	639	G
2	2	650	G
2	2	653	U
2	2	665	A
2	2	687	A
2	2	706	A
2	2	723	U
2	2	724	G
2	2	731	G
2	2	732	C
2	2	748	G
2	2	753	A
2	2	755	G
2	2	781	A
2	2	793	U
2	2	794	A
2	2	815	A
2	2	817	C
2	2	821	G
2	2	828	U
2	2	829	G
2	2	832	G
2	2	839	C
2	2	841	C
2	2	843	U
2	2	844	G
2	2	846	G
2	2	851	G
2	2	889	A
2	2	890	G
2	2	900	A
2	2	913	A
2	2	914	A
2	2	917	G
2	2	934	C
2	2	935	A
2	2	939	G

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Mol	Chain	Res	Type
2	2	959	A
2	2	960	U
2	2	969	A
2	2	971	G
2	2	975	A
2	2	976	G
2	2	977	A
2	2	981	U
2	2	992	U
2	2	993	G
2	2	996	A
2	2	999	C
2	2	1004	A
2	2	1009	U
2	2	1017	U
2	2	1018	G
2	2	1020	G
2	2	1024	G
2	2	1025	U
2	2	1029	U
2	2	1030	U
2	2	1031	C
2	2	1032	G
2	2	1033	G
2	2	1044	A
2	2	1046	A
2	2	1052	U
2	2	1053	G
2	2	1065	U
2	2	1066	C
2	2	1078	U
2	2	1079	G
2	2	1085	U
2	2	1094	G
2	2	1095	U
2	2	1101	A
2	2	1108	G
2	2	1124	G
2	2	1125	U
2	2	1132	C
2	2	1136	C
2	2	1137	C

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Mol	Chain	Res	Type
2	2	1138	G
2	2	1139	G
2	2	1140	C
2	2	1141	C
2	2	1146	A
2	2	1151	A
2	2	1152	A
2	2	1158	C
2	2	1159	U
2	2	1160	G
2	2	1167	A
2	2	1168	U
2	2	1169	A
2	2	1175	G
2	2	1176	A
2	2	1184	G
2	2	1193	G
2	2	1196	A
2	2	1197	A
2	2	1212	U
2	2	1213	A
2	2	1226	C
2	2	1236	A
2	2	1238	A
2	2	1250	A
2	2	1258	G
2	2	1260	G
2	2	1267	C
2	2	1268	G
2	2	1275	A
2	2	1280	A
2	2	1287	A
2	2	1299	A
2	2	1302	C
2	2	1304	G
2	2	1305	G
2	2	1317	C
2	2	1318	A
2	2	1320	C
2	2	1322	C
2	2	1323	G
2	2	1363	A

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Mol	Chain	Res	Type
2	2	1394	A
2	2	1398	A
2	2	1402	4OC
2	2	1419	G
2	2	1443	C
2	2	1446	A
2	2	1450	U
2	2	1452	C
2	2	1456	A
2	2	1457	G
2	2	1492	A
2	2	1493	A
2	2	1494	G
2	2	1499	A
2	2	1503	A
2	2	1506	U
2	2	1507	A
2	2	1517	G
2	2	1519	MA6
2	2	1520	C
2	2	1529	G
2	2	1530	G
2	2	1532	U
2	2	1533	C
2	2	1534	A
2	2	1535	C
3	3	9	G
3	3	13	G
3	3	35	C
3	3	36	C
3	3	37	C
3	3	41	G
3	3	44	G
3	3	53	A
3	3	67	G
3	3	85	G
3	3	89	U
3	3	99	A
3	3	109	A
4	4	4	G
4	4	7	G
4	4	8	A

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Mol	Chain	Res	Type
4	4	11	C
4	4	14	G
4	4	15	A
4	4	18	C
4	4	20	A
4	4	21	C
4	4	28	U
4	4	29	G
4	4	30	C
4	4	31	G
4	4	32	A
4	4	33	A
4	4	34	A
4	4	36	C
4	4	39	A
4	4	41	G
4	4	44	C
4	4	50	G
4	4	53	G
4	4	54	G
4	4	55	G
4	4	56	C
4	4	61	G
4	4	63	C
4	4	64	C
4	4	67	G
4	4	68	U
4	4	69	A
4	4	70	A
4	4	71	A
4	4	74	G
4	4	75	C
4	4	77	G
4	4	78	C
4	4	79	A
4	4	80	A
4	4	81	A
4	4	82	A
4	4	83	A
4	4	84	A
4	4	85	U
4	4	86	A

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Mol	Chain	Res	Type
4	4	87	G
4	4	88	U
4	4	89	C
4	4	90	G
4	4	93	A
4	4	96	G
4	4	97	A
4	4	98	C
4	4	99	G
4	4	100	A
4	4	101	A
4	4	102	A
4	4	103	A
4	4	104	C
4	4	105	U
4	4	106	A
4	4	107	C
4	4	122	A
4	4	123	U
4	4	125	A
4	4	128	U
4	4	130	C
4	4	131	U
4	4	134	G
4	4	138	C
4	4	139	C
4	4	140	U
4	4	142	U
4	4	144	U
4	4	149	A
4	4	154	C
4	4	155	C
4	4	157	C
4	4	159	C
4	4	160	U
4	4	164	G
4	4	165	A
4	4	166	C
4	4	167	G
4	4	170	G
4	4	173	C
4	4	175	A

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Mol	Chain	Res	Type
4	4	180	G
4	4	181	G
4	4	182	U
4	4	184	A
4	4	186	A
4	4	187	C
4	4	188	C
4	4	189	C
4	4	190	A
4	4	191	A
4	4	195	A
4	4	197	A
4	4	200	G
4	4	202	G
4	4	204	G
4	4	206	A
4	4	209	C
4	4	213	G
4	4	214	C
4	4	223	G
4	4	224	A
4	4	225	A
4	4	227	C
4	4	228	G
4	4	229	U
4	4	230	U
4	4	231	A
4	4	233	A
4	4	234	A
4	4	237	U
4	4	240	U
4	4	245	C
4	4	246	U
4	4	252	G
4	4	257	U
4	4	261	G
4	4	262	U
4	4	263	G
4	4	264	U
4	4	267	G
4	4	274	G
4	4	278	G

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Mol	Chain	Res	Type
4	4	281	A
4	4	285	A
4	4	290	A
4	4	291	A
4	4	293	G
4	4	299	C
4	4	300	U
4	4	301	A
4	4	302	A
4	4	303	G
4	4	304	C
4	4	308	U
4	4	310	G
4	4	311	U
4	4	313	C
4	4	314	C
4	4	315	G
4	4	316	A
4	4	317	G
4	4	318	G
4	4	321	G
4	4	322	U
4	4	323	A
4	4	327	A
4	4	328	U
4	4	333	G
4	4	336	G
4	4	344	A
4	4	346	C
4	4	347	PSU
4	4	348	C
4	4	356	C
4	4	360	A
4	4	361	C
4	4	362	C
6	7	17	C
6	7	18	G
6	7	19	G
6	7	20	H2U
6	7	21	A
6	7	22	G
6	7	37	MIA

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Mol	Chain	Res	Type
6	7	43	C
6	7	45	U
6	7	46	G7M
6	7	47	3AU
6	7	61	C
6	7	75	C
6	7	76	A
7	8	6	G
7	8	8	G
7	8	9	A
7	8	10	G

All (56) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	176	A
1	1	404	A
1	1	428	A
1	1	464	U
1	1	631	A
1	1	774	G
1	1	784	G
1	1	894	U
1	1	1070	A
1	1	1088	A
1	1	1109	C
1	1	1287	A
1	1	1379	U
1	1	1614	A
1	1	1680	U
1	1	1927	A
1	1	2048	G
1	1	2100	G
1	1	2150	C
1	1	2193	G
1	1	2425	A
1	1	2505	G
1	1	2506	U
1	1	2516	A
1	1	2596	U
2	2	298	A
2	2	516	PSU

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Mol	Chain	Res	Type
2	2	899	C
2	2	938	A
2	2	958	A
2	2	980	C
2	2	1078	U
2	2	1109	C
2	2	1145	A
2	2	1267	C
2	2	1303	C
2	2	1492	A
2	2	1533	C
4	4	14	G
4	4	19	G
4	4	43	G
4	4	78	C
4	4	79	A
4	4	80	A
4	4	92	A
4	4	96	G
4	4	101	A
4	4	224	A
4	4	310	G
4	4	314	C
4	4	316	A
4	4	343	C
6	7	19	G
6	7	20	H2U
7	8	7	U
7	8	9	A

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

48 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
6	PSU	7	39	6	18,21,22	1.08	1 (5%)	22,30,33	1.70	4 (18%)
1	2MG	1	1835	1	23,26,27	3.01	7 (30%)	32,38,41	2.17	9 (28%)
19	4D4	M	81	19	9,11,12	2.05	2 (22%)	8,13,15	1.84	3 (37%)
2	2MG	2	1207	2	23,26,27	3.01	7 (30%)	32,38,41	2.11	9 (28%)
6	5MU	7	54	6	19,22,23	4.88	7 (36%)	28,32,35	3.56	9 (32%)
6	H2U	7	20	6	18,21,22	1.10	2 (11%)	21,30,33	2.54	2 (9%)
1	G7M	1	2069	1	23,26,27	2.53	9 (39%)	35,39,42	2.16	10 (28%)
49	0TD	q	89	49	7,9,10	1.43	0	6,11,13	1.98	2 (33%)
2	2MG	2	1516	2	23,26,27	3.01	7 (30%)	32,38,41	2.13	10 (31%)
2	5MC	2	967	2	18,22,23	3.60	7 (38%)	26,32,35	0.98	1 (3%)
1	PSU	1	2457	1	18,21,22	1.04	1 (5%)	22,30,33	1.71	3 (13%)
1	1MG	1	745	1	22,26,27	2.69	6 (27%)	33,39,42	1.68	6 (18%)
1	PSU	1	1911	1	18,21,22	1.10	1 (5%)	22,30,33	1.76	4 (18%)
1	PSU	1	2504	1	18,21,22	1.08	1 (5%)	22,30,33	1.76	4 (18%)
2	UR3	2	1498	2	19,22,23	2.99	6 (31%)	26,32,35	1.31	1 (3%)
2	PSU	2	516	2	18,21,22	1.07	1 (5%)	22,30,33	1.69	5 (22%)
6	MIA	7	37	6	28,31,32	2.62	6 (21%)	40,44,47	3.14	17 (42%)
1	PSU	1	2580	1	18,21,22	1.07	1 (5%)	22,30,33	1.65	4 (18%)
6	PSU	7	32	6	18,21,22	1.07	1 (5%)	22,30,33	1.74	4 (18%)
1	6MZ	1	2030	1	22,25,26	2.81	2 (9%)	30,36,39	2.37	10 (33%)
1	5MU	1	1939	1	19,22,23	4.87	7 (36%)	28,32,35	3.63	9 (32%)
1	2MG	1	2445	1	23,26,27	2.99	7 (30%)	32,38,41	2.11	9 (28%)
2	MA6	2	1519	2	23,26,27	1.23	3 (13%)	34,38,41	4.03	14 (41%)
4	PSU	4	342	4	18,21,22	1.11	1 (5%)	22,30,33	1.74	4 (18%)
6	PSU	7	55	6	18,21,22	1.10	1 (5%)	22,30,33	1.73	4 (18%)
1	OMG	1	2251	6,1	23,26,27	2.47	8 (34%)	33,38,41	2.69	10 (30%)
4	5MU	4	341	4	19,22,23	4.89	7 (36%)	28,32,35	3.56	9 (32%)
2	MA6	2	1518	2	23,26,27	1.22	3 (13%)	34,38,41	4.02	15 (44%)
2	4OC	2	1402	2	20,23,24	3.28	9 (45%)	26,32,35	0.91	1 (3%)
2	G7M	2	527	2	23,26,27	2.55	8 (34%)	35,39,42	2.20	10 (28%)
1	PSU	1	1917	1	18,21,22	1.11	1 (5%)	22,30,33	1.77	4 (18%)
4	PSU	4	347	4	18,21,22	1.12	1 (5%)	22,30,33	1.75	4 (18%)
1	OMU	1	2552	1	19,22,23	3.21	7 (36%)	26,31,34	1.67	5 (19%)
6	3AU	7	47	6	24,28,29	3.03	9 (37%)	33,40,43	1.30	3 (9%)
1	PSU	1	955	1	18,21,22	1.07	1 (5%)	22,30,33	1.75	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	1	2498	1,59	19,22,23	3.05	8 (42%)	26,31,34	0.77	0
1	PSU	1	746	1,59	18,21,22	1.10	1 (5%)	22,30,33	1.79	5 (22%)
2	2MG	2	966	2	23,26,27	3.02	7 (30%)	32,38,41	2.13	9 (28%)
6	H2U	7	16	6	18,21,22	1.22	3 (16%)	21,30,33	1.79	3 (14%)
1	2MA	1	2503	1,59	22,25,26	3.68	7 (31%)	33,37,40	2.00	9 (27%)
1	3TD	1	1915	1	18,22,23	4.33	7 (38%)	22,32,35	1.60	3 (13%)
2	5MC	2	1407	2	18,22,23	3.62	7 (38%)	26,32,35	1.00	2 (7%)
1	5MC	1	1962	1	18,22,23	3.61	7 (38%)	26,32,35	1.04	2 (7%)
1	PSU	1	2605	1	18,21,22	1.10	1 (5%)	22,30,33	1.76	4 (18%)
1	6MZ	1	1618	1	22,25,26	2.86	2 (9%)	30,36,39	2.32	10 (33%)
1	5MU	1	747	1	19,22,23	4.90	7 (36%)	28,32,35	3.62	8 (28%)
6	G7M	7	46	6	23,26,27	3.68	12 (52%)	35,39,42	1.66	6 (17%)
6	4SU	7	8	6	18,21,22	3.74	8 (44%)	26,30,33	2.20	4 (15%)

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
6	PSU	7	39	6	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
19	4D4	M	81	19	-	5/11/12/14	-
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
6	5MU	7	54	6	-	2/7/25/26	0/2/2/2
6	H2U	7	20	6	-	6/7/38/39	0/2/2/2
1	G7M	1	2069	1	-	2/7/25/26	0/3/3/3
49	0TD	q	89	49	-	4/7/12/14	-
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
2	UR3	2	1498	2	-	2/7/25/26	0/2/2/2
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
6	MIA	7	37	6	-	5/15/33/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1	2580	1	-	3/7/25/26	0/2/2/2
6	PSU	7	32	6	-	0/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	2/9/27/28	0/3/3/3
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
4	PSU	4	342	4	-	1/7/25/26	0/2/2/2
6	PSU	7	55	6	-	0/7/25/26	0/2/2/2
1	OMG	1	2251	6,1	-	0/9/27/28	0/3/3/3
4	5MU	4	341	4	-	0/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	G7M	2	527	2	-	3/7/25/26	0/3/3/3
1	PSU	1	1917	1	-	2/7/25/26	0/2/2/2
4	PSU	4	347	4	-	2/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
6	3AU	7	47	6	-	2/16/34/35	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	OMC	1	2498	1,59	-	2/9/27/28	0/2/2/2
1	PSU	1	746	1,59	-	0/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
6	H2U	7	16	6	-	1/7/38/39	0/2/2/2
1	2MA	1	2503	1,59	-	2/7/25/26	0/3/3/3
1	3TD	1	1915	1	-	2/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	3/9/27/28	0/3/3/3
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
6	G7M	7	46	6	-	3/7/25/26	0/3/3/3
6	4SU	7	8	6	-	0/7/25/26	0/2/2/2

All (225) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	12.55	1.49	1.35
1	1	1618	6MZ	C6-N6	12.49	1.47	1.34
1	1	2030	6MZ	C6-N6	12.23	1.47	1.34
1	1	2503	2MA	C4-N3	11.55	1.48	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	747	5MU	C2-N1	11.45	1.56	1.38
6	7	54	5MU	C2-N1	11.29	1.56	1.38
4	4	341	5MU	C2-N1	11.23	1.56	1.38
1	1	1939	5MU	C2-N1	11.12	1.56	1.38
6	7	54	5MU	C6-N1	10.73	1.56	1.38
4	4	341	5MU	C6-N1	10.63	1.56	1.38
1	1	1939	5MU	C6-N1	10.59	1.56	1.38
1	1	747	5MU	C6-N1	10.52	1.56	1.38
6	7	46	G7M	C8-N7	10.30	1.51	1.33
1	1	1939	5MU	C4-C5	10.26	1.61	1.44
4	4	341	5MU	C4-C5	10.20	1.61	1.44
1	1	747	5MU	C4-C5	10.15	1.61	1.44
6	7	54	5MU	C4-C5	10.09	1.61	1.44
1	1	1915	3TD	C2-N1	9.37	1.49	1.37
2	2	1407	5MC	C6-C5	9.23	1.49	1.34
1	1	1962	5MC	C6-C5	9.16	1.49	1.34
2	2	967	5MC	C6-C5	9.15	1.49	1.34
6	7	47	3AU	C2-N1	8.48	1.50	1.38
6	7	8	4SU	C4-N3	7.90	1.46	1.37
1	1	1835	2MG	C2-N3	7.78	1.46	1.31
1	1	747	5MU	C4-N3	-7.78	1.24	1.38
2	2	966	2MG	C2-N3	7.76	1.46	1.31
1	1	1939	5MU	C4-N3	-7.74	1.24	1.38
2	2	1516	2MG	C2-N3	7.74	1.46	1.31
2	2	1207	2MG	C2-N3	7.74	1.46	1.31
4	4	341	5MU	C4-N3	-7.72	1.24	1.38
6	7	54	5MU	C4-N3	-7.69	1.24	1.38
1	1	2445	2MG	C2-N3	7.68	1.46	1.31
2	2	1498	UR3	C2-N1	7.57	1.49	1.38
1	1	2503	2MA	C2-N3	7.52	1.47	1.34
1	1	2552	OMU	C2-N3	7.50	1.51	1.38
6	7	37	MIA	C2-S10	7.48	1.82	1.75
1	1	2552	OMU	C2-N1	7.46	1.50	1.38
6	7	37	MIA	C13-C14	7.30	1.53	1.32
6	7	37	MIA	C6-N6	7.13	1.45	1.34
6	7	8	4SU	C2-N1	7.08	1.49	1.38
2	2	966	2MG	C2-N2	6.88	1.48	1.33
6	7	8	4SU	C2-N3	6.86	1.50	1.38
2	2	1207	2MG	C2-N2	6.86	1.48	1.33
2	2	1516	2MG	C2-N2	6.85	1.48	1.33
1	1	1835	2MG	C2-N2	6.83	1.48	1.33
1	1	745	1MG	C2-N3	6.77	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1498	UR3	C6-C5	6.77	1.50	1.35
1	1	1835	2MG	C4-N3	6.77	1.50	1.34
1	1	2445	2MG	C2-N2	6.76	1.48	1.33
2	2	1207	2MG	C4-N3	6.72	1.50	1.34
2	2	966	2MG	C4-N3	6.68	1.50	1.34
6	7	47	3AU	C6-C5	6.66	1.50	1.35
2	2	1516	2MG	C4-N3	6.63	1.50	1.34
1	1	1962	5MC	C4-N3	6.63	1.45	1.34
2	2	967	5MC	C4-N3	6.62	1.45	1.34
2	2	1407	5MC	C4-N3	6.59	1.45	1.34
2	2	1402	4OC	C4-N3	6.58	1.44	1.32
1	1	2445	2MG	C4-N3	6.56	1.49	1.34
1	1	2251	OMG	C4-N3	6.48	1.49	1.34
1	1	745	1MG	C4-N3	6.47	1.49	1.34
1	1	2498	OMC	C2-N3	6.46	1.49	1.36
1	1	745	1MG	C2-N2	6.26	1.45	1.34
1	1	1962	5MC	C2-N3	6.25	1.49	1.36
2	2	1407	5MC	C2-N3	6.24	1.49	1.36
2	2	967	5MC	C2-N3	6.22	1.49	1.36
2	2	1498	UR3	C2-N3	6.16	1.50	1.39
2	2	1402	4OC	C2-N3	6.11	1.48	1.36
1	1	2498	OMC	C6-C5	6.05	1.49	1.35
6	7	46	G7M	C2-N3	6.05	1.47	1.33
4	4	341	5MU	C6-C5	6.04	1.44	1.34
6	7	47	3AU	C2-N3	6.04	1.49	1.38
1	1	2503	2MA	C2-N1	6.02	1.44	1.34
2	2	527	G7M	C4-N3	6.01	1.48	1.34
1	1	2552	OMU	C6-C5	6.00	1.49	1.35
1	1	1939	5MU	C6-C5	6.00	1.44	1.34
1	1	747	5MU	C6-C5	6.00	1.44	1.34
1	1	2069	G7M	C4-N3	5.95	1.48	1.34
6	7	54	5MU	C6-C5	5.89	1.44	1.34
2	2	1402	4OC	C6-C5	5.86	1.48	1.35
1	1	1915	3TD	C6-N1	5.84	1.45	1.36
1	1	2503	2MA	C6-N1	5.81	1.43	1.35
6	7	8	4SU	C6-C5	5.77	1.48	1.35
6	7	46	G7M	C8-N9	5.73	1.51	1.35
6	7	46	G7M	C4-N3	5.72	1.47	1.34
2	2	1402	4OC	C4-N4	5.65	1.47	1.35
1	1	2251	OMG	C2-N3	5.63	1.46	1.33
2	2	966	2MG	C2-N1	5.53	1.45	1.36
2	2	1207	2MG	C2-N1	5.52	1.45	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1516	2MG	C2-N1	5.52	1.45	1.36
1	1	2445	2MG	C2-N1	5.49	1.45	1.36
1	1	1835	2MG	C2-N1	5.47	1.45	1.36
19	M	81	4D4	CZ-NE	5.27	1.43	1.33
1	1	1915	3TD	C2-N3	5.20	1.50	1.38
1	1	2498	OMC	C4-N3	5.16	1.44	1.34
2	2	527	G7M	C2-N2	5.09	1.46	1.34
1	1	2069	G7M	C2-N2	5.07	1.46	1.34
1	1	2498	OMC	C4-N4	4.96	1.45	1.33
6	7	8	4SU	C5-C4	4.94	1.48	1.42
6	7	46	G7M	C5-N7	4.87	1.44	1.39
1	1	2251	OMG	C2-N2	4.84	1.45	1.34
6	7	46	G7M	C2-N2	4.83	1.45	1.34
2	2	527	G7M	C5-N7	-4.74	1.33	1.39
1	1	2069	G7M	C5-N7	-4.70	1.33	1.39
1	1	2498	OMC	C2-N1	4.62	1.50	1.40
2	2	1407	5MC	C6-N1	4.61	1.45	1.38
1	1	1962	5MC	C6-N1	4.59	1.45	1.38
2	2	967	5MC	C6-N1	4.57	1.45	1.38
2	2	527	G7M	C2-N3	4.47	1.43	1.33
1	1	1962	5MC	C4-N4	4.45	1.45	1.34
1	1	2503	2MA	C5-C6	4.45	1.53	1.41
2	2	967	5MC	C4-N4	4.44	1.45	1.34
2	2	1407	5MC	C4-N4	4.43	1.45	1.34
6	7	8	4SU	C4-S4	-4.40	1.60	1.68
2	2	1402	4OC	C2-N1	4.40	1.49	1.40
1	1	2069	G7M	C2-N3	4.39	1.43	1.33
1	1	2552	OMU	C4-N3	4.38	1.46	1.38
6	7	47	3AU	C4-N3	4.26	1.47	1.40
2	2	967	5MC	C2-N1	4.26	1.49	1.40
2	2	1407	5MC	C2-N1	4.24	1.49	1.40
1	1	1962	5MC	C2-N1	4.20	1.49	1.40
2	2	1402	4OC	C5-C4	4.07	1.49	1.40
6	7	46	G7M	C2-N1	3.81	1.47	1.37
1	1	1915	3TD	O2-C2	-3.78	1.16	1.23
4	4	347	PSU	C6-C5	3.68	1.39	1.35
2	2	516	PSU	C6-C5	3.66	1.39	1.35
4	4	342	PSU	C6-C5	3.65	1.39	1.35
1	1	1911	PSU	C6-C5	3.62	1.39	1.35
1	1	1917	PSU	C6-C5	3.62	1.39	1.35
1	1	2580	PSU	C6-C5	3.61	1.39	1.35
1	1	2605	PSU	C6-C5	3.61	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	7	55	PSU	C6-C5	3.60	1.39	1.35
1	1	2504	PSU	C6-C5	3.60	1.39	1.35
6	7	39	PSU	C6-C5	3.60	1.39	1.35
2	2	1402	4OC	CM4-N4	3.59	1.52	1.45
1	1	746	PSU	C6-C5	3.58	1.39	1.35
2	2	1402	4OC	O2-C2	-3.53	1.17	1.23
6	7	32	PSU	C6-C5	3.52	1.39	1.35
1	1	955	PSU	C6-C5	3.46	1.39	1.35
6	7	47	3AU	C6-N1	3.43	1.46	1.38
6	7	46	G7M	C5-C6	3.42	1.52	1.43
1	1	2457	PSU	C6-C5	3.41	1.39	1.35
6	7	46	G7M	C6-N1	3.35	1.45	1.38
2	2	527	G7M	O6-C6	-3.34	1.17	1.23
1	1	2069	G7M	O6-C6	-3.34	1.17	1.23
1	1	745	1MG	C5-C6	3.30	1.53	1.45
1	1	2498	OMC	C6-N1	3.25	1.45	1.38
1	1	2552	OMU	C6-N1	3.24	1.45	1.38
2	2	1498	UR3	C6-N1	3.20	1.45	1.38
2	2	527	G7M	C5-C6	3.18	1.52	1.43
1	1	2069	G7M	C5-C6	3.15	1.52	1.43
6	7	16	H2U	C2-N3	-3.12	1.32	1.38
1	1	2069	G7M	C2-N1	3.11	1.45	1.37
2	2	527	G7M	C2-N1	3.10	1.45	1.37
2	2	1519	MA6	C5-C4	-3.00	1.33	1.39
6	7	20	H2U	C2-N3	-2.98	1.32	1.38
6	7	8	4SU	C6-N1	2.95	1.45	1.38
2	2	1518	MA6	C5-C4	-2.93	1.33	1.39
1	1	2552	OMU	C5-C4	2.86	1.50	1.43
6	7	47	3AU	C5-C4	2.84	1.51	1.43
1	1	745	1MG	C5-N7	-2.83	1.33	1.39
1	1	2251	OMG	C2-N1	2.78	1.44	1.37
1	1	2251	OMG	C5-N7	-2.78	1.33	1.39
2	2	1518	MA6	C6-N6	2.74	1.44	1.36
6	7	47	3AU	C11-C10	2.73	1.58	1.52
6	7	16	H2U	C4-N3	-2.72	1.33	1.37
2	2	1519	MA6	C6-N6	2.71	1.44	1.36
6	7	37	MIA	C5-C4	-2.69	1.34	1.39
6	7	20	H2U	C4-N3	-2.68	1.33	1.37
2	2	1516	2MG	C5-C6	2.65	1.54	1.44
2	2	966	2MG	C5-C6	2.65	1.54	1.44
1	1	1835	2MG	C5-C6	2.65	1.54	1.44
2	2	1207	2MG	C5-C6	2.64	1.54	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2445	2MG	C5-C6	2.64	1.54	1.44
2	2	966	2MG	C6-N1	2.62	1.43	1.38
2	2	1516	2MG	C6-N1	2.61	1.43	1.38
6	7	47	3AU	O4-C4	-2.59	1.18	1.23
1	1	2498	OMC	O2-C2	-2.59	1.18	1.23
2	2	1207	2MG	C6-N1	2.59	1.43	1.38
1	1	1962	5MC	O2-C2	-2.58	1.18	1.23
6	7	54	5MU	O4-C4	-2.57	1.18	1.23
1	1	2251	OMG	C6-N1	2.57	1.43	1.38
1	1	2251	OMG	C5-C6	2.57	1.53	1.44
2	2	967	5MC	O2-C2	-2.55	1.19	1.23
1	1	2445	2MG	C6-N1	2.55	1.43	1.38
1	1	1939	5MU	O4-C4	-2.55	1.18	1.23
1	1	747	5MU	O4-C4	-2.54	1.18	1.23
1	1	2498	OMC	C5-C4	2.54	1.48	1.42
2	2	1407	5MC	O2-C2	-2.53	1.19	1.23
4	4	341	5MU	O4-C4	-2.52	1.18	1.23
1	1	2503	2MA	C5-N7	-2.51	1.34	1.39
6	7	46	G7M	C4-N9	2.51	1.44	1.38
1	1	1835	2MG	C6-N1	2.49	1.43	1.38
2	2	1519	MA6	C8-N7	2.46	1.36	1.31
1	1	2251	OMG	O6-C6	-2.45	1.18	1.23
6	7	47	3AU	O2-C2	-2.44	1.18	1.22
6	7	46	G7M	O6-C6	-2.44	1.18	1.23
6	7	37	MIA	C5-N7	-2.44	1.34	1.39
2	2	1518	MA6	C8-N7	2.42	1.36	1.31
1	1	2552	OMU	O4-C4	-2.42	1.19	1.24
2	2	1498	UR3	C5-C4	2.41	1.50	1.43
19	M	81	4D4	CZ-NH1	2.41	1.44	1.34
1	1	1835	2MG	C5-N7	-2.38	1.34	1.39
1	1	2445	2MG	C5-N7	-2.37	1.34	1.39
6	7	46	G7M	C5-C4	2.33	1.44	1.38
2	2	1516	2MG	C5-N7	-2.33	1.34	1.39
2	2	966	2MG	C5-N7	-2.33	1.34	1.39
1	1	1939	5MU	O2-C2	-2.32	1.18	1.23
4	4	341	5MU	O2-C2	-2.32	1.18	1.23
6	7	54	5MU	O2-C2	-2.31	1.18	1.23
2	2	1498	UR3	C4-N3	2.29	1.45	1.40
2	2	1402	4OC	C6-N1	2.29	1.43	1.38
6	7	16	H2U	C2-N1	-2.28	1.32	1.35
2	2	1207	2MG	C5-N7	-2.28	1.34	1.39
1	1	747	5MU	O2-C2	-2.27	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2069	G7M	C4-N9	-2.26	1.32	1.38
1	1	1915	3TD	C4-N3	2.24	1.45	1.40
2	2	527	G7M	C4-N9	-2.22	1.32	1.38
6	7	8	4SU	O2-C2	-2.18	1.19	1.23
1	1	2503	2MA	C8-N7	2.18	1.35	1.31
1	1	1915	3TD	O4-C4	-2.15	1.18	1.23
1	1	2069	G7M	C6-N1	2.05	1.42	1.38
1	1	2030	6MZ	C5-N7	-2.04	1.35	1.39
1	1	1618	6MZ	C5-N7	-2.03	1.35	1.39
1	1	745	1MG	O6-C6	-2.02	1.18	1.23
6	7	37	MIA	C8-N9	-2.02	1.33	1.37

All (287) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1939	5MU	C5-C4-N3	12.03	125.58	115.31
1	1	747	5MU	C5-C4-N3	11.95	125.52	115.31
6	7	54	5MU	C5-C4-N3	11.93	125.50	115.31
4	4	341	5MU	C5-C4-N3	11.82	125.40	115.31
2	2	1518	MA6	C1'-N9-C8	-11.70	100.71	127.14
2	2	1519	MA6	C1'-N9-C8	-11.61	100.91	127.14
2	2	1519	MA6	N1-C6-N6	-11.31	104.72	117.08
2	2	1518	MA6	N1-C6-N6	-11.26	104.78	117.08
6	7	20	H2U	C4-N3-C2	-10.62	116.98	125.79
2	2	1518	MA6	C4-N9-C1'	10.38	151.33	126.59
1	1	1939	5MU	C5-C6-N1	-10.23	112.81	123.34
2	2	1519	MA6	C4-N9-C1'	10.17	150.82	126.59
1	1	747	5MU	C5-C6-N1	-10.08	112.96	123.34
4	4	341	5MU	C5-C6-N1	-9.70	113.36	123.34
6	7	54	5MU	C5-C6-N1	-9.55	113.52	123.34
6	7	37	MIA	C11-S10-C2	9.02	109.00	102.27
6	7	37	MIA	C12-C13-C14	-8.63	110.34	127.14
1	1	2251	OMG	C1'-N9-C8	-8.58	102.27	126.70
6	7	8	4SU	C4-N3-C2	-7.73	119.83	127.34
1	1	2251	OMG	C1'-N9-C4	7.23	147.96	126.50
1	1	1835	2MG	C2-N3-C4	6.72	120.38	112.04
6	7	37	MIA	C5-C4-N3	-6.53	119.85	127.19
2	2	1516	2MG	C2-N3-C4	6.46	120.05	112.04
2	2	1207	2MG	C2-N3-C4	6.46	120.05	112.04
2	2	966	2MG	C2-N3-C4	6.43	120.01	112.04
1	1	2445	2MG	C2-N3-C4	6.39	119.96	112.04
1	1	2503	2MA	C5-C4-N3	-6.37	120.02	127.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1518	MA6	C5-C6-N6	5.81	135.43	125.30
2	2	1519	MA6	C5-C6-N6	5.75	135.31	125.30
6	7	16	H2U	C4-N3-C2	-5.61	121.14	125.79
2	2	1519	MA6	N1-C2-N3	-5.54	119.93	128.60
1	1	1835	2MG	C5-C4-N3	-5.51	119.52	128.46
1	1	2030	6MZ	N1-C2-N3	-5.49	120.01	128.60
1	1	1618	6MZ	N1-C2-N3	-5.47	120.04	128.60
6	7	8	4SU	C5-C4-N3	5.44	119.74	114.69
2	2	1518	MA6	N1-C2-N3	-5.27	120.36	128.60
1	1	1618	6MZ	C5-C4-N3	-5.23	119.92	126.75
1	1	2030	6MZ	C9-N6-C6	-5.17	118.42	122.87
1	1	2552	OMU	C4-N3-C2	-5.16	119.77	126.58
2	2	1207	2MG	C5-C4-N3	-5.12	120.16	128.46
2	2	1519	MA6	C5-C4-N3	-5.10	120.10	126.75
6	7	54	5MU	O4-C4-C5	-5.09	119.00	124.90
2	2	1516	2MG	C5-C4-N3	-5.09	120.21	128.46
1	1	2445	2MG	C5-C4-N3	-5.05	120.28	128.46
2	2	1518	MA6	C5-C4-N3	-5.04	120.18	126.75
2	2	966	2MG	C5-C4-N3	-5.02	120.31	128.46
1	1	745	1MG	C5-C4-N3	-4.99	120.36	128.46
1	1	2030	6MZ	C5-C4-N3	-4.97	120.27	126.75
1	1	1915	3TD	N1-C2-N3	4.93	120.03	116.14
1	1	2251	OMG	C5-C4-N3	-4.90	120.51	128.46
2	2	1498	UR3	C4-N3-C2	-4.89	119.96	124.56
1	1	1939	5MU	C4-N3-C2	-4.84	121.09	127.35
1	1	1939	5MU	O4-C4-C5	-4.82	119.31	124.90
1	1	747	5MU	O4-C4-C5	-4.82	119.32	124.90
4	4	341	5MU	O4-C4-C5	-4.76	119.39	124.90
1	1	747	5MU	C4-N3-C2	-4.71	121.25	127.35
6	7	37	MIA	C15-C14-C13	-4.70	109.06	122.65
2	2	527	G7M	C1'-N9-C4	4.68	140.42	126.50
6	7	54	5MU	C4-N3-C2	-4.67	121.30	127.35
4	4	341	5MU	C4-N3-C2	-4.66	121.32	127.35
1	1	2069	G7M	CN7-N7-C5	4.61	132.49	126.77
2	2	527	G7M	C1'-N9-C8	-4.59	111.23	126.74
2	2	527	G7M	CN7-N7-C5	4.59	132.47	126.77
1	1	746	PSU	C4-N3-C2	-4.57	119.75	126.34
1	1	2605	PSU	C4-N3-C2	-4.53	119.82	126.34
1	1	2504	PSU	C4-N3-C2	-4.52	119.82	126.34
1	1	1911	PSU	C4-N3-C2	-4.52	119.83	126.34
4	4	341	5MU	N3-C2-N1	4.51	120.87	114.89
4	4	342	PSU	C4-N3-C2	-4.50	119.85	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1917	PSU	C4-N3-C2	-4.49	119.87	126.34
2	2	1519	MA6	N9-C8-N7	-4.49	107.78	113.91
6	7	55	PSU	C4-N3-C2	-4.48	119.88	126.34
1	1	955	PSU	C4-N3-C2	-4.48	119.88	126.34
4	4	347	PSU	N1-C2-N3	4.48	120.20	115.13
6	7	32	PSU	C4-N3-C2	-4.47	119.90	126.34
1	1	2069	G7M	C1'-N9-C4	4.47	139.77	126.50
6	7	54	5MU	N3-C2-N1	4.47	120.82	114.89
1	1	2457	PSU	C4-N3-C2	-4.46	119.91	126.34
1	1	746	PSU	N1-C2-N3	4.45	120.17	115.13
6	7	46	G7M	C2-N3-C4	4.45	120.22	112.30
2	2	527	G7M	C2-N3-C4	4.45	120.22	112.30
4	4	347	PSU	C4-N3-C2	-4.45	119.93	126.34
1	1	2069	G7M	C2-N3-C4	4.44	120.21	112.30
1	1	1917	PSU	N1-C2-N3	4.44	120.16	115.13
1	1	2504	PSU	N1-C2-N3	4.43	120.15	115.13
1	1	2030	6MZ	N9-C8-N7	-4.42	107.86	113.91
1	1	1939	5MU	N3-C2-N1	4.41	120.74	114.89
1	1	1911	PSU	N1-C2-N3	4.41	120.12	115.13
6	7	32	PSU	N1-C2-N3	4.41	120.12	115.13
1	1	1618	6MZ	N9-C8-N7	-4.40	107.90	113.91
1	1	2605	PSU	N1-C2-N3	4.39	120.11	115.13
6	7	55	PSU	N1-C2-N3	4.38	120.09	115.13
6	7	39	PSU	C4-N3-C2	-4.37	120.04	126.34
1	1	955	PSU	N1-C2-N3	4.37	120.09	115.13
1	1	2069	G7M	C1'-N9-C8	-4.36	112.01	126.74
6	7	39	PSU	N1-C2-N3	4.35	120.06	115.13
4	4	342	PSU	N1-C2-N3	4.34	120.05	115.13
1	1	2503	2MA	N9-C8-N7	-4.33	107.99	113.91
1	1	747	5MU	N3-C2-N1	4.32	120.63	114.89
6	7	37	MIA	C16-C14-C13	-4.32	110.16	122.65
1	1	1835	2MG	C2-N1-C6	-4.32	119.51	124.48
1	1	2251	OMG	C2-N3-C4	4.31	119.98	112.30
6	7	37	MIA	N9-C8-N7	-4.31	108.02	113.91
1	1	2457	PSU	N1-C2-N3	4.29	119.99	115.13
1	1	2580	PSU	N1-C2-N3	4.25	119.95	115.13
2	2	1518	MA6	N9-C8-N7	-4.24	108.11	113.91
6	7	37	MIA	N6-C6-N1	4.24	123.91	118.50
2	2	516	PSU	C4-N3-C2	-4.22	120.27	126.34
1	1	2445	2MG	C2-N1-C6	-4.21	119.63	124.48
1	1	747	5MU	C5M-C5-C6	-4.20	117.24	122.85
2	2	516	PSU	N1-C2-N3	4.18	119.86	115.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2580	PSU	C4-N3-C2	-4.18	120.32	126.34
6	7	46	G7M	C5-C4-N3	-4.17	120.16	128.15
2	2	1516	2MG	C2-N1-C6	-4.16	119.69	124.48
2	2	966	2MG	C2-N1-C6	-4.15	119.71	124.48
6	7	16	H2U	O4'-C1'-N1	4.05	114.82	109.30
4	4	341	5MU	C5M-C5-C6	-4.04	117.45	122.85
2	2	1207	2MG	C2-N1-C6	-4.04	119.83	124.48
1	1	1939	5MU	C5M-C5-C6	-3.99	117.52	122.85
4	4	341	5MU	C5M-C5-C4	3.99	123.16	118.77
2	2	527	G7M	C5-C4-N3	-3.98	120.51	128.15
6	7	54	5MU	C5M-C5-C6	-3.96	117.56	122.85
6	7	37	MIA	C4-C5-C6	3.96	119.88	116.81
1	1	747	5MU	C5M-C5-C4	3.95	123.12	118.77
1	1	2069	G7M	C5-C4-N3	-3.94	120.58	128.15
6	7	54	5MU	C5M-C5-C4	3.93	123.09	118.77
2	2	527	G7M	C5-C6-N1	3.90	119.93	111.79
1	1	1915	3TD	C4-N3-C2	-3.87	120.41	124.61
1	1	1618	6MZ	C4-C5-C6	3.84	119.78	116.81
1	1	2069	G7M	C5-C6-N1	3.84	119.81	111.79
6	7	46	G7M	C5-C6-N1	3.82	119.76	111.79
6	7	37	MIA	N3-C4-N9	3.77	132.22	126.99
1	1	1939	5MU	C5M-C5-C4	3.77	122.91	118.77
1	1	2552	OMU	N3-C2-N1	3.75	119.87	114.89
6	7	8	4SU	N3-C2-N1	3.75	119.87	114.89
1	1	2503	2MA	N3-C4-N9	3.72	132.15	126.99
6	7	47	3AU	C4-N3-C2	-3.70	119.99	124.63
6	7	37	MIA	N3-C2-N1	-3.67	120.22	126.95
6	7	37	MIA	S10-C2-N1	3.63	128.57	116.01
1	1	1618	6MZ	C9-N6-C6	-3.59	119.78	122.87
1	1	1618	6MZ	C2-N3-C4	3.59	120.24	111.75
1	1	2251	OMG	N9-C8-N7	-3.57	106.66	113.39
2	2	1518	MA6	C4-C5-C6	3.57	119.88	115.88
1	1	745	1MG	C2-N3-C4	3.57	120.00	111.98
1	1	2030	6MZ	C2-N3-C4	3.56	120.15	111.75
49	q	89	0TD	OD2-CG-CB	3.55	120.81	113.15
2	2	1519	MA6	C2-N3-C4	3.55	120.13	111.75
2	2	1519	MA6	C2-N1-C6	3.54	120.12	111.75
1	1	2069	G7M	CN7-N7-C8	-3.54	119.38	124.84
2	2	527	G7M	CN7-N7-C8	-3.53	119.39	124.84
2	2	1518	MA6	C2-N1-C6	3.47	119.94	111.75
6	7	37	MIA	C5-C6-N6	-3.46	115.92	121.76
2	2	1519	MA6	C4-C5-C6	3.45	119.74	115.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	527	G7M	O6-C6-C5	-3.45	120.27	128.06
19	M	81	4D4	NE-CZ-NH2	3.43	126.73	120.70
2	2	1518	MA6	C2-N3-C4	3.42	119.84	111.75
1	1	1835	2MG	N9-C4-N3	3.41	132.78	125.94
1	1	2069	G7M	O6-C6-C5	-3.39	120.40	128.06
1	1	1962	5MC	C5-C6-N1	-3.39	119.85	123.34
6	7	8	4SU	C5-C4-S4	-3.37	120.13	124.47
1	1	2251	OMG	N9-C4-N3	3.32	132.60	125.94
1	1	2030	6MZ	C4-C5-C6	3.31	119.37	116.81
6	7	47	3AU	C5-C4-N3	3.30	119.85	115.50
6	7	46	G7M	O6-C6-C5	-3.28	120.67	128.06
1	1	2552	OMU	C5-C4-N3	3.27	119.73	114.84
2	2	1519	MA6	C5-N7-C8	3.25	108.12	103.51
1	1	745	1MG	N9-C8-N7	-3.22	107.33	113.39
1	1	2503	2MA	C5-N7-C8	3.21	108.07	103.51
1	1	1618	6MZ	C5-N7-C8	3.20	108.06	103.51
1	1	2030	6MZ	C5-N7-C8	3.19	108.04	103.51
2	2	1407	5MC	C5-C6-N1	-3.16	120.08	123.34
6	7	37	MIA	C5-N7-C8	3.16	108.00	103.51
1	1	1618	6MZ	N3-C4-N9	3.15	132.28	127.08
2	2	1518	MA6	C5-N7-C8	3.14	107.96	103.51
1	1	745	1MG	N9-C4-N3	3.13	132.22	125.94
1	1	2503	2MA	N3-C2-N1	-3.12	119.99	125.72
2	2	1207	2MG	N9-C4-N3	3.05	132.06	125.94
2	2	967	5MC	C5-C6-N1	-2.96	120.30	123.34
6	7	37	MIA	C2-N3-C4	2.93	120.07	112.35
2	2	1516	2MG	N9-C4-N3	2.92	131.80	125.94
2	2	527	G7M	C2-N1-C6	-2.91	119.79	125.10
2	2	1519	MA6	N3-C4-N9	2.91	131.88	127.08
1	1	2251	OMG	C2-N1-C6	-2.91	119.79	125.10
1	1	2069	G7M	C2-N1-C6	-2.90	119.81	125.10
2	2	966	2MG	N9-C4-N3	2.89	131.75	125.94
1	1	2445	2MG	N9-C4-N3	2.87	131.71	125.94
1	1	2030	6MZ	N3-C4-N9	2.86	131.79	127.08
1	1	2552	OMU	O4-C4-C5	-2.83	120.19	125.16
2	2	966	2MG	N9-C8-N7	-2.81	108.09	113.39
2	2	1207	2MG	N9-C8-N7	-2.77	108.17	113.39
2	2	527	G7M	N9-C4-N3	2.77	131.49	125.94
2	2	1518	MA6	N3-C4-N9	2.76	131.63	127.08
6	7	46	G7M	C2-N1-C6	-2.76	120.07	125.10
2	2	1516	2MG	N9-C8-N7	-2.74	108.23	113.39
1	1	1917	PSU	O2-C2-N1	-2.73	119.79	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2445	2MG	N9-C8-N7	-2.72	108.28	113.39
1	1	1835	2MG	C5-C6-N1	2.71	120.06	113.19
1	1	2251	OMG	C5-C6-N1	2.68	120.00	113.19
2	2	966	2MG	C5-C6-N1	2.66	119.96	113.19
4	4	342	PSU	O2-C2-N1	-2.65	119.88	122.79
4	4	347	PSU	O2-C2-N1	-2.64	119.89	122.79
1	1	745	1MG	C5-C6-N1	2.64	120.01	114.91
1	1	2069	G7M	N9-C4-N3	2.64	131.23	125.94
1	1	2445	2MG	C5-C6-N1	2.63	119.88	113.19
2	2	1516	2MG	C5-C6-N1	2.63	119.88	113.19
1	1	1835	2MG	N9-C8-N7	-2.62	108.45	113.39
1	1	955	PSU	O2-C2-N1	-2.62	119.91	122.79
1	1	1939	5MU	O4-C4-N3	-2.61	115.11	120.12
1	1	1911	PSU	O2-C2-N1	-2.61	119.92	122.79
2	2	1207	2MG	C5-C6-N1	2.60	119.80	113.19
1	1	2605	PSU	O2-C2-N1	-2.60	119.92	122.79
1	1	747	5MU	O4-C4-N3	-2.58	115.17	120.12
6	7	32	PSU	O2-C2-N1	-2.58	119.95	122.79
2	2	1207	2MG	N1-C2-N3	-2.57	119.98	123.95
1	1	746	PSU	O2-C2-N1	-2.56	119.97	122.79
1	1	2457	PSU	O2-C2-N1	-2.56	119.97	122.79
4	4	341	5MU	O4-C4-N3	-2.56	115.21	120.12
6	7	55	PSU	O2-C2-N1	-2.56	119.97	122.79
6	7	39	PSU	O2-C2-N1	-2.56	119.97	122.79
2	2	966	2MG	N1-C2-N3	-2.56	120.00	123.95
1	1	2504	PSU	O2-C2-N1	-2.54	119.99	122.79
2	2	1516	2MG	N1-C2-N3	-2.52	120.06	123.95
1	1	2580	PSU	O2-C2-N1	-2.50	120.04	122.79
1	1	1835	2MG	O6-C6-C5	-2.49	119.98	126.60
2	2	966	2MG	O6-C6-C5	-2.49	119.99	126.60
1	1	1835	2MG	N1-C2-N3	-2.49	120.10	123.95
1	1	2445	2MG	O6-C6-C5	-2.49	120.01	126.60
1	1	1939	5MU	O2-C2-N1	-2.48	119.49	122.79
6	7	37	MIA	C16-C14-C15	-2.47	109.16	114.60
2	2	1516	2MG	O6-C6-C5	-2.46	120.07	126.60
1	1	2251	OMG	O6-C6-C5	-2.46	120.08	126.60
1	1	2445	2MG	N1-C2-N3	-2.45	120.17	123.95
2	2	1207	2MG	O6-C6-C5	-2.44	120.13	126.60
4	4	341	5MU	O2-C2-N1	-2.41	119.58	122.79
6	7	54	5MU	O4-C4-N3	-2.41	115.50	120.12
6	7	54	5MU	O2-C2-N1	-2.39	119.61	122.79
1	1	2251	OMG	C8-N7-C5	2.37	108.54	104.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2030	6MZ	C4-N9-C8	2.36	108.29	105.73
2	2	1402	4OC	C6-C5-C4	2.35	119.84	116.96
1	1	2580	PSU	C6-N1-C2	-2.35	120.28	122.68
1	1	1618	6MZ	C4-N9-C8	2.35	108.27	105.73
2	2	1519	MA6	C4-N9-C8	2.34	108.26	105.73
2	2	1518	MA6	C4-C5-N7	-2.32	107.79	110.62
4	4	347	PSU	C6-N1-C2	-2.31	120.32	122.68
19	M	81	4D4	CB-CA-C	-2.30	108.10	111.77
2	2	1519	MA6	C4-C5-N7	-2.30	107.82	110.62
2	2	516	PSU	C6-N1-C2	-2.29	120.34	122.68
1	1	2030	6MZ	C4-C5-N7	-2.26	107.86	110.62
1	1	746	PSU	C6-C5-C4	2.24	119.77	118.20
49	q	89	0TD	OD1-CG-CB	-2.24	117.76	122.44
1	1	2503	2MA	C6-C5-C4	2.23	120.18	117.18
1	1	745	1MG	C8-N7-C5	2.23	108.27	104.24
6	7	39	PSU	C6-N1-C2	-2.22	120.41	122.68
1	1	1917	PSU	C6-N1-C2	-2.22	120.42	122.68
6	7	16	H2U	O2-C2-N1	-2.21	120.33	123.11
1	1	955	PSU	C6-N1-C2	-2.21	120.42	122.68
19	M	81	4D4	O-C-CA	-2.20	119.02	124.78
1	1	2445	2MG	CM2-N2-C2	-2.19	119.03	123.86
1	1	2605	PSU	C6-N1-C2	-2.19	120.45	122.68
6	7	37	MIA	C4-C5-N7	-2.19	107.95	110.62
1	1	1962	5MC	CM5-C5-C6	-2.19	119.93	122.85
1	1	2503	2MA	N6-C6-N1	2.19	120.12	117.03
6	7	37	MIA	C4-N9-C8	2.18	108.09	105.73
1	1	2504	PSU	C6-N1-C2	-2.18	120.46	122.68
1	1	1618	6MZ	C4-C5-N7	-2.17	107.97	110.62
6	7	46	G7M	N9-C8-N7	-2.17	106.83	112.21
6	7	32	PSU	C6-N1-C2	-2.16	120.47	122.68
1	1	2503	2MA	C4-N9-C8	2.15	108.05	105.73
6	7	20	H2U	C3'-C2'-C1'	2.14	105.50	101.43
2	2	516	PSU	O4'-C1'-C2'	2.13	108.15	105.14
1	1	1911	PSU	C6-N1-C2	-2.13	120.50	122.68
1	1	2503	2MA	C4-C5-N7	-2.11	108.05	110.62
6	7	55	PSU	C6-N1-C2	-2.10	120.53	122.68
2	2	516	PSU	O2-C2-N1	-2.10	120.48	122.79
4	4	342	PSU	C6-N1-C2	-2.09	120.55	122.68
1	1	746	PSU	C6-N1-C2	-2.09	120.55	122.68
2	2	1518	MA6	C5-C4-N9	2.07	108.19	105.78
1	1	1915	3TD	O4'-C1'-C2'	2.06	108.05	105.14
1	1	2552	OMU	O2-C2-N1	-2.06	120.05	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	966	2MG	C8-N7-C5	2.05	107.95	104.24
2	2	1518	MA6	C4-N9-C8	2.05	107.95	105.73
1	1	1835	2MG	C8-N7-C5	2.05	107.95	104.24
2	2	1407	5MC	CM5-C5-C6	-2.04	120.12	122.85
2	2	1516	2MG	C8-N7-C5	2.03	107.92	104.24
2	2	1207	2MG	C8-N7-C5	2.03	107.91	104.24
6	7	47	3AU	C6-N1-C2	-2.01	119.99	121.79
2	2	1516	2MG	C1'-N9-C4	-2.01	120.54	126.50

There are no chirality outliers.

All (67) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	M	81	4D4	C-CA-CB-OB
19	M	81	4D4	C-CA-CB-CG
19	M	81	4D4	N-CA-CB-OB
19	M	81	4D4	N-CA-CB-CG
49	q	89	0TD	SB-CB-CG-OD2
1	1	1618	6MZ	O4'-C4'-C5'-O5'
1	1	1618	6MZ	C3'-C4'-C5'-O5'
1	1	1915	3TD	O4'-C1'-C5-C4
1	1	1915	3TD	O4'-C1'-C5-C6
1	1	2030	6MZ	O4'-C4'-C5'-O5'
1	1	2445	2MG	C3'-C4'-C5'-O5'
1	1	2504	PSU	O4'-C4'-C5'-O5'
1	1	2552	OMU	C1'-C2'-O2'-CM2
1	1	2580	PSU	O4'-C1'-C5-C4
1	1	2580	PSU	C2'-C1'-C5-C6
1	1	2580	PSU	O4'-C1'-C5-C6
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	1402	4OC	O4'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'
2	2	1519	MA6	C3'-C4'-C5'-O5'
4	4	347	PSU	C3'-C4'-C5'-O5'
4	4	347	PSU	O4'-C4'-C5'-O5'
6	7	20	H2U	O4'-C4'-C5'-O5'
6	7	20	H2U	O4'-C1'-N1-C6
6	7	37	MIA	O4'-C4'-C5'-O5'
6	7	37	MIA	C3'-C4'-C5'-O5'
6	7	37	MIA	C5-C6-N6-C12
6	7	37	MIA	C12-C13-C14-C16

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Mol	Chain	Res	Type	Atoms
6	7	47	3AU	C10-C11-C12-C13
6	7	47	3AU	C10-C11-C12-N40
1	1	2503	2MA	O4'-C4'-C5'-O5'
1	1	2503	2MA	C3'-C4'-C5'-O5'
1	1	2504	PSU	C3'-C4'-C5'-O5'
2	2	527	G7M	C3'-C4'-C5'-O5'
2	2	1402	4OC	C3'-C4'-C5'-O5'
6	7	20	H2U	C3'-C4'-C5'-O5'
6	7	46	G7M	C3'-C4'-C5'-O5'
1	1	2445	2MG	O4'-C4'-C5'-O5'
6	7	20	H2U	C2'-C1'-N1-C6
6	7	20	H2U	C2'-C1'-N1-C2
6	7	37	MIA	N1-C6-N6-C12
1	1	1835	2MG	O4'-C4'-C5'-O5'
1	1	1917	PSU	C3'-C4'-C5'-O5'
2	2	527	G7M	O4'-C4'-C5'-O5'
6	7	46	G7M	O4'-C4'-C5'-O5'
1	1	1835	2MG	C3'-C4'-C5'-O5'
2	2	1498	UR3	O4'-C4'-C5'-O5'
1	1	2498	OMC	O4'-C4'-C5'-O5'
6	7	54	5MU	O4'-C4'-C5'-O5'
2	2	527	G7M	C4'-C5'-O5'-P
1	1	1917	PSU	O4'-C4'-C5'-O5'
49	q	89	0TD	SB-CB-CG-OD1
6	7	54	5MU	C3'-C4'-C5'-O5'
1	1	2069	G7M	C4'-C5'-O5'-P
6	7	46	G7M	C4'-C5'-O5'-P
2	2	1498	UR3	C3'-C4'-C5'-O5'
6	7	20	H2U	O4'-C1'-N1-C2
19	M	81	4D4	CA-CB-CG-CD
1	1	2069	G7M	O4'-C4'-C5'-O5'
4	4	342	PSU	C3'-C4'-C5'-O5'
1	1	2030	6MZ	C3'-C4'-C5'-O5'
49	q	89	0TD	CA-CB-SB-CSB
1	1	1618	6MZ	C4'-C5'-O5'-P
1	1	2498	OMC	C3'-C4'-C5'-O5'
6	7	16	H2U	C3'-C4'-C5'-O5'
49	q	89	0TD	CG-CB-SB-CSB

There are no ring outliers.

17 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	1207	2MG	1	0
2	2	1516	2MG	1	0
2	2	967	5MC	2	0
1	1	745	1MG	1	0
1	1	2504	PSU	1	0
6	7	37	MIA	2	0
1	1	2030	6MZ	3	0
1	1	2445	2MG	4	0
1	1	2251	OMG	1	0
2	2	1518	MA6	4	0
2	2	1402	4OC	2	0
4	4	347	PSU	1	0
1	1	2498	OMC	1	0
1	1	746	PSU	1	0
2	2	966	2MG	2	0
6	7	16	H2U	1	0
1	1	1915	3TD	8	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 443 ligands modelled in this entry, 443 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

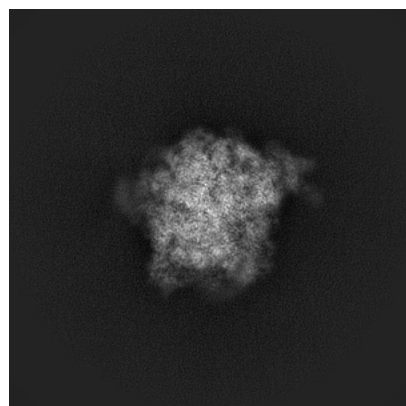
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11713. These allow visual inspection of the internal detail of the map and identification of artifacts.

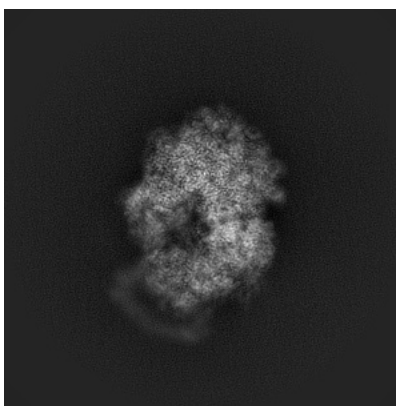
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

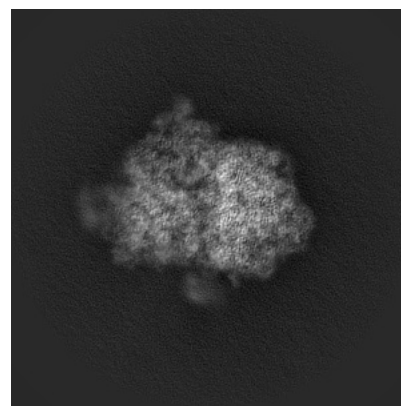
6.1.1 Primary map



X

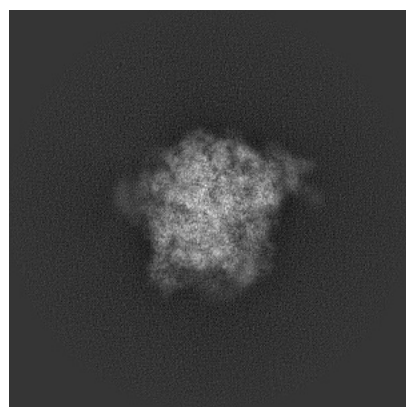


Y

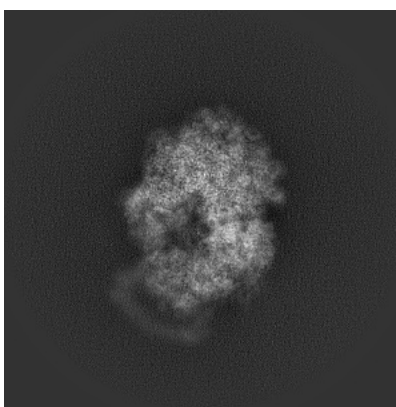


Z

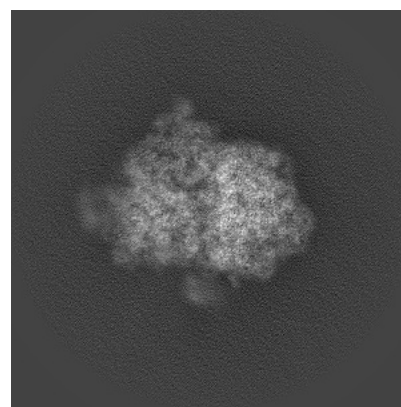
6.1.2 Raw map



X



Y

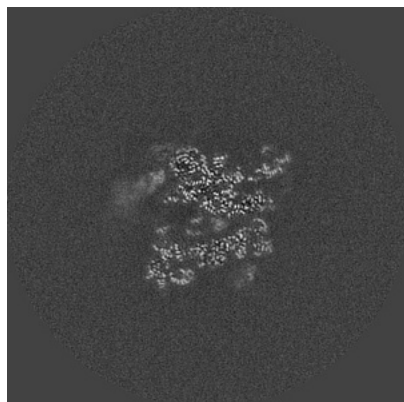


Z

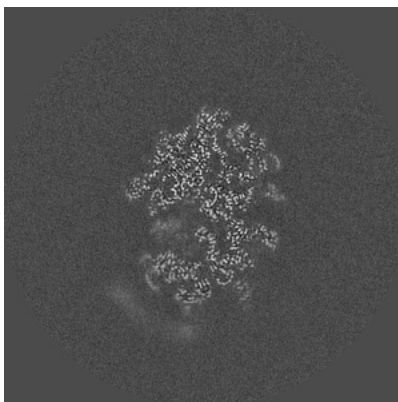
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

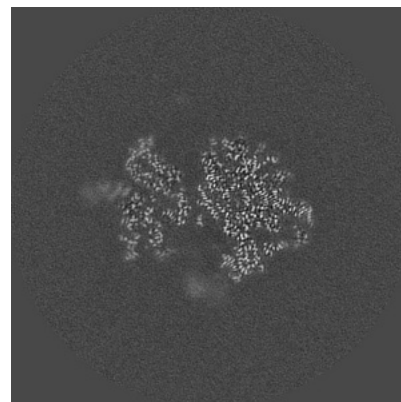
6.2.1 Primary map



X Index: 240

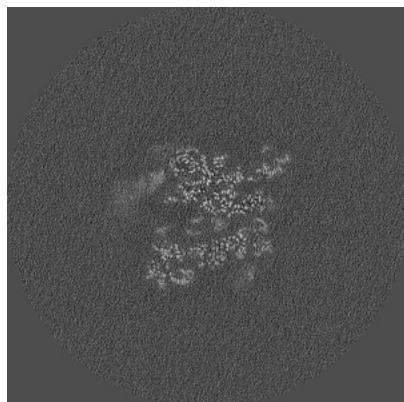


Y Index: 240

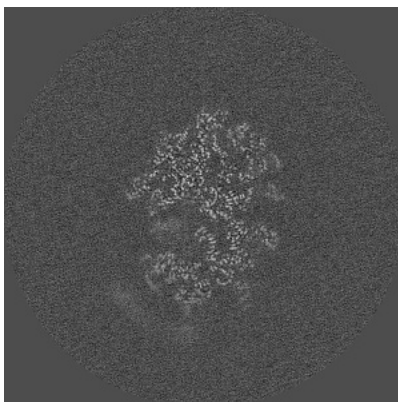


Z Index: 240

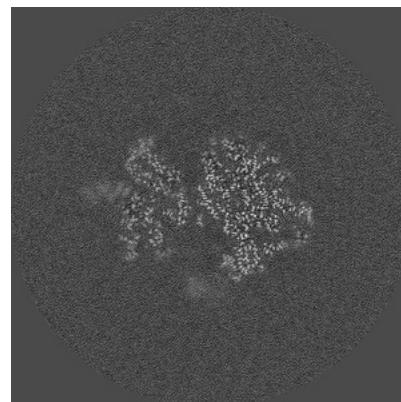
6.2.2 Raw map



X Index: 240



Y Index: 240

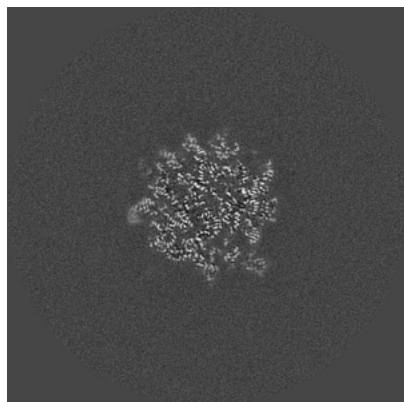


Z Index: 240

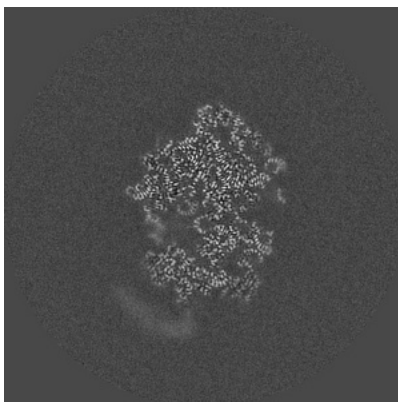
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

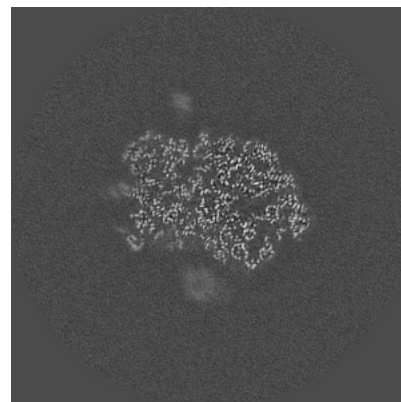
6.3.1 Primary map



X Index: 269

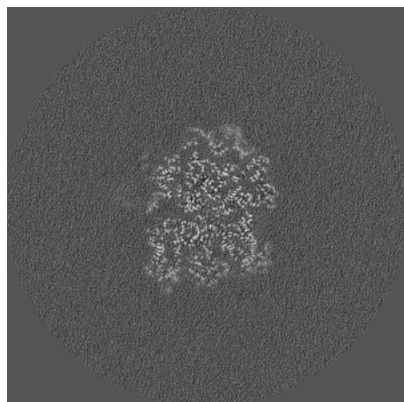


Y Index: 231

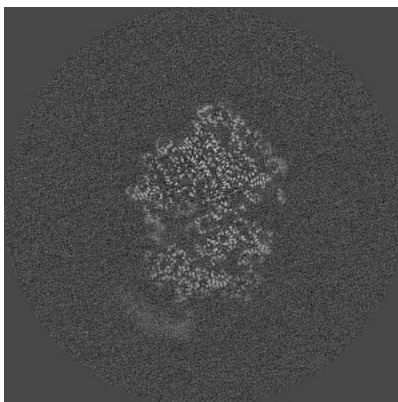


Z Index: 252

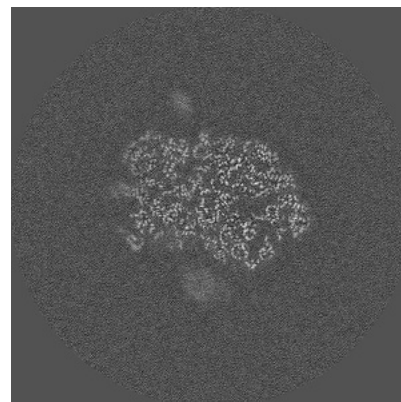
6.3.2 Raw map



X Index: 258



Y Index: 230

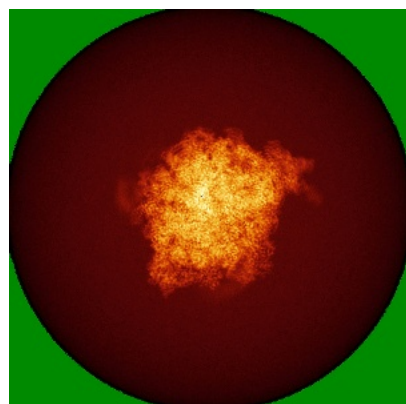


Z Index: 252

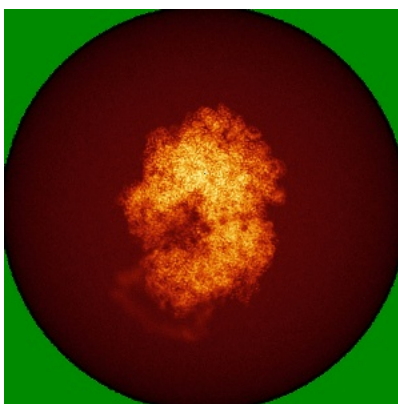
The images above show the largest variance slices of the map in three orthogonal directions.

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

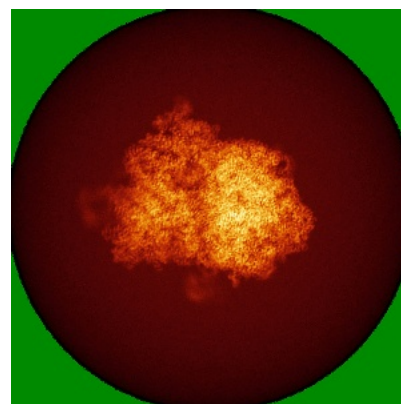
6.4.1 Primary map



X

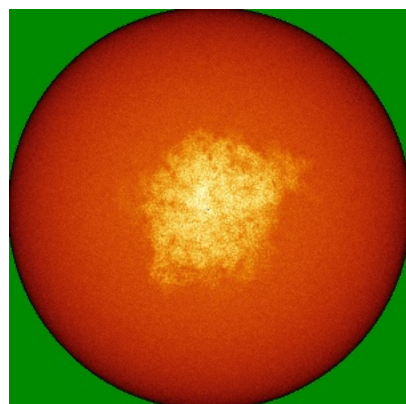


Y

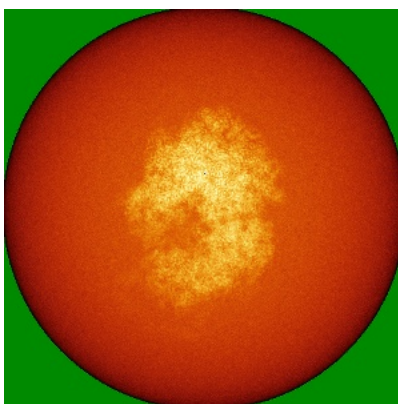


Z

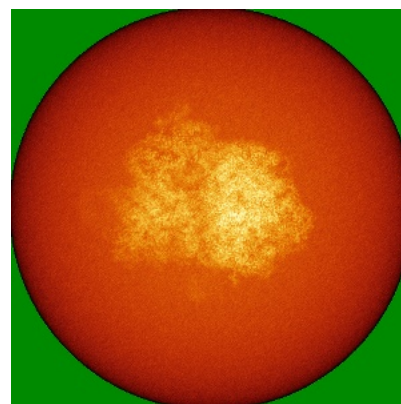
6.4.2 Raw map



X



Y

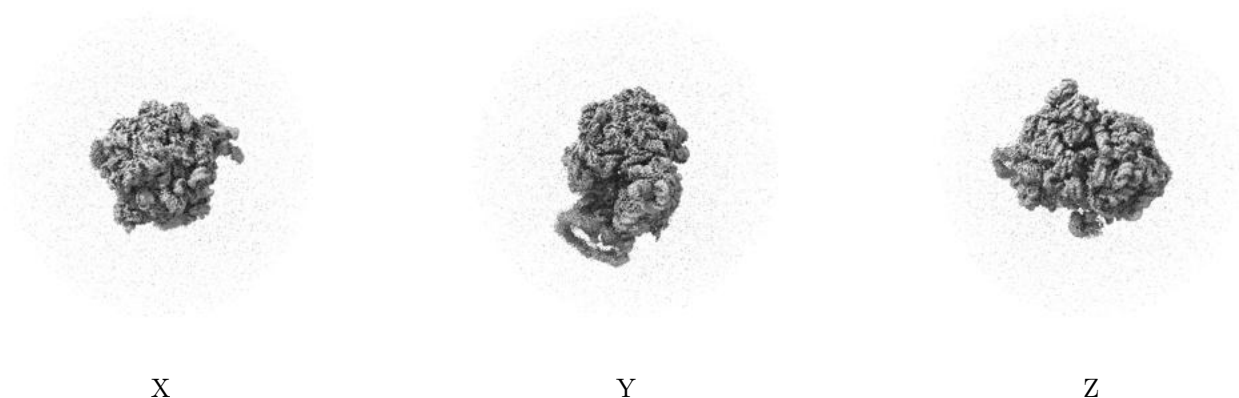


Z

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

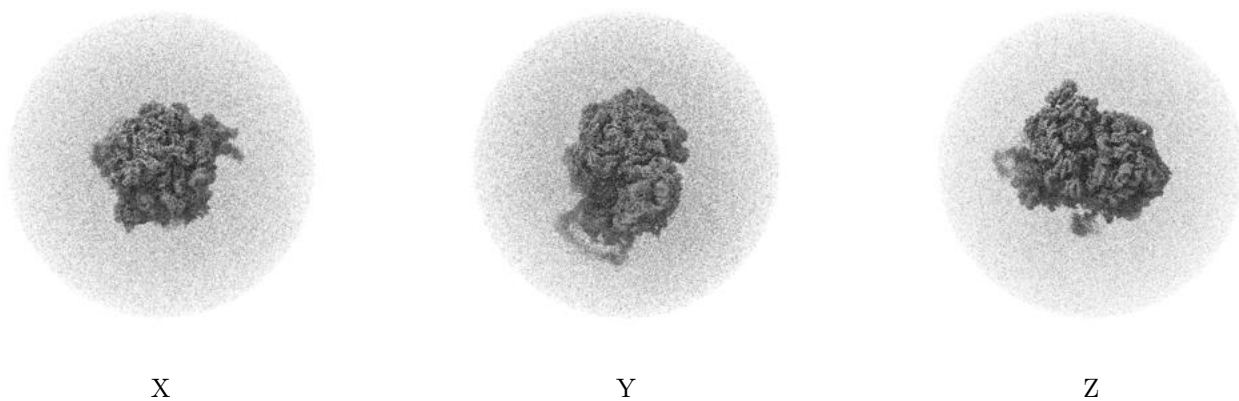
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

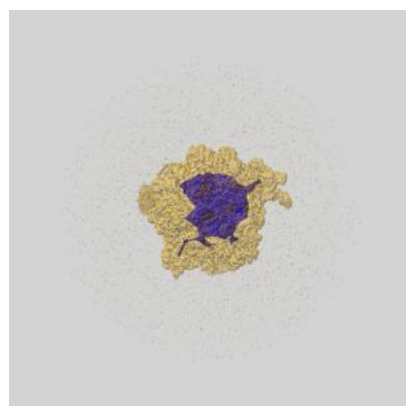
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

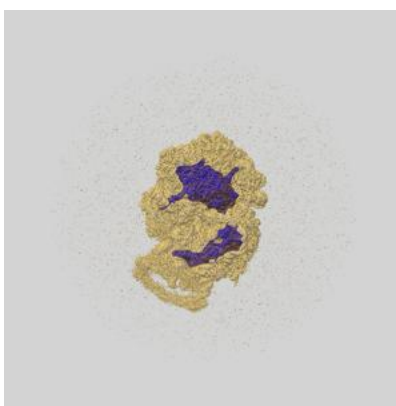
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

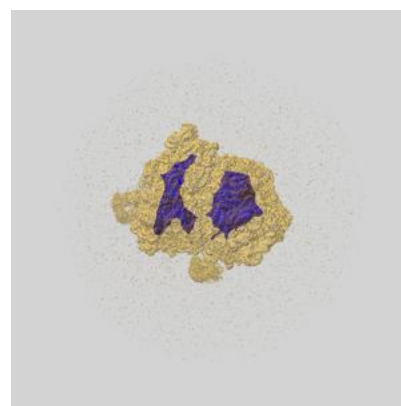
6.6.1 emd_11713_msk_1.map [i](#)



X



Y

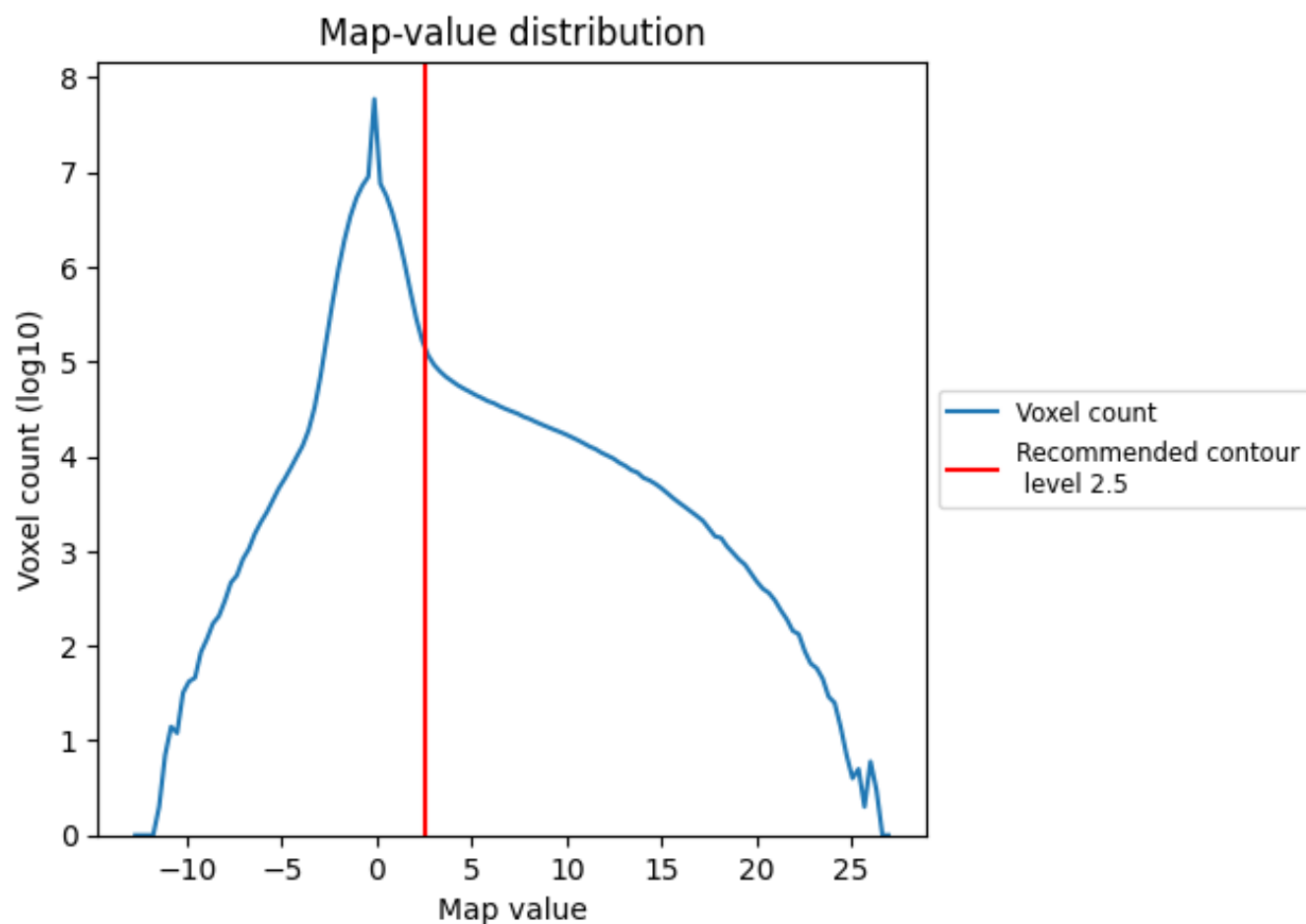


Z

7 Map analysis [i](#)

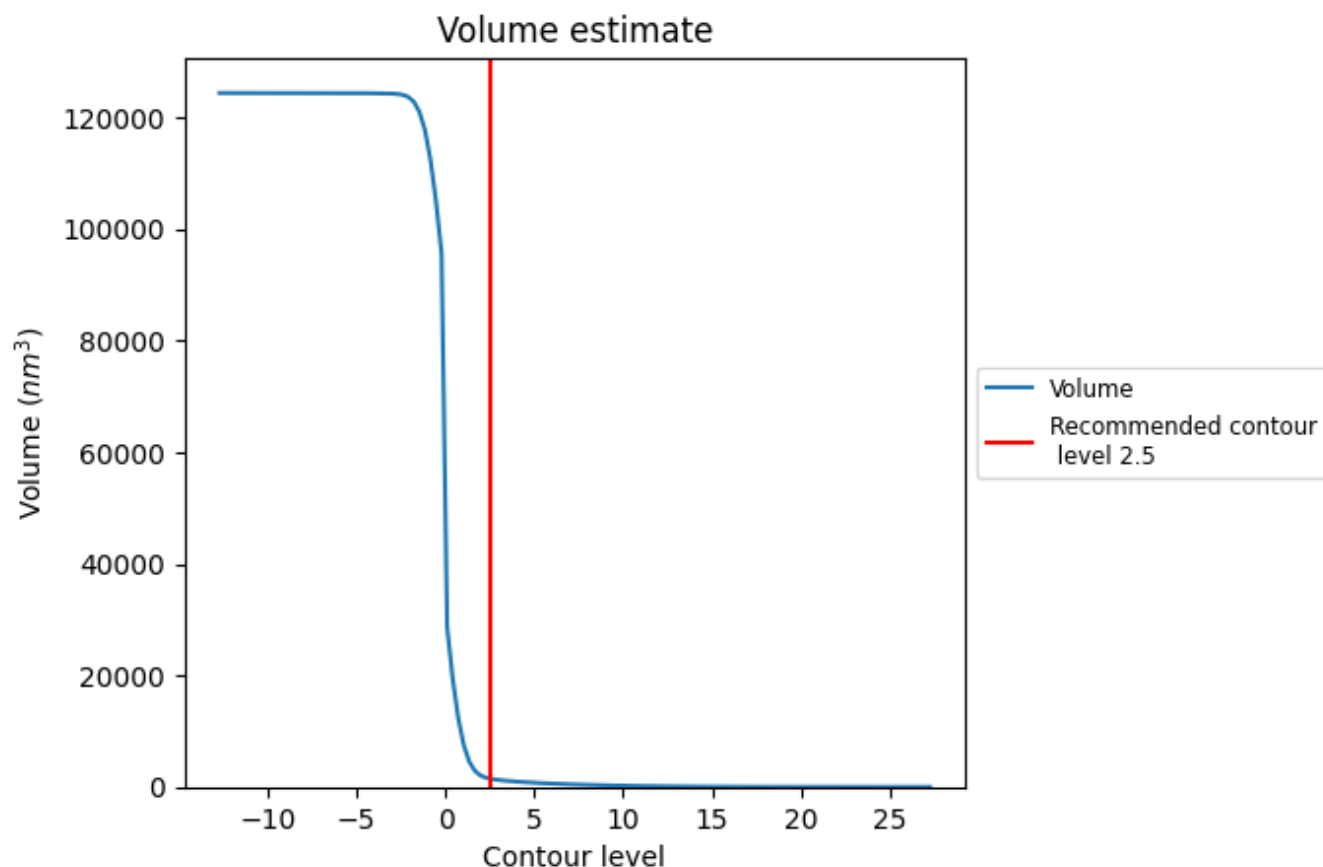
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

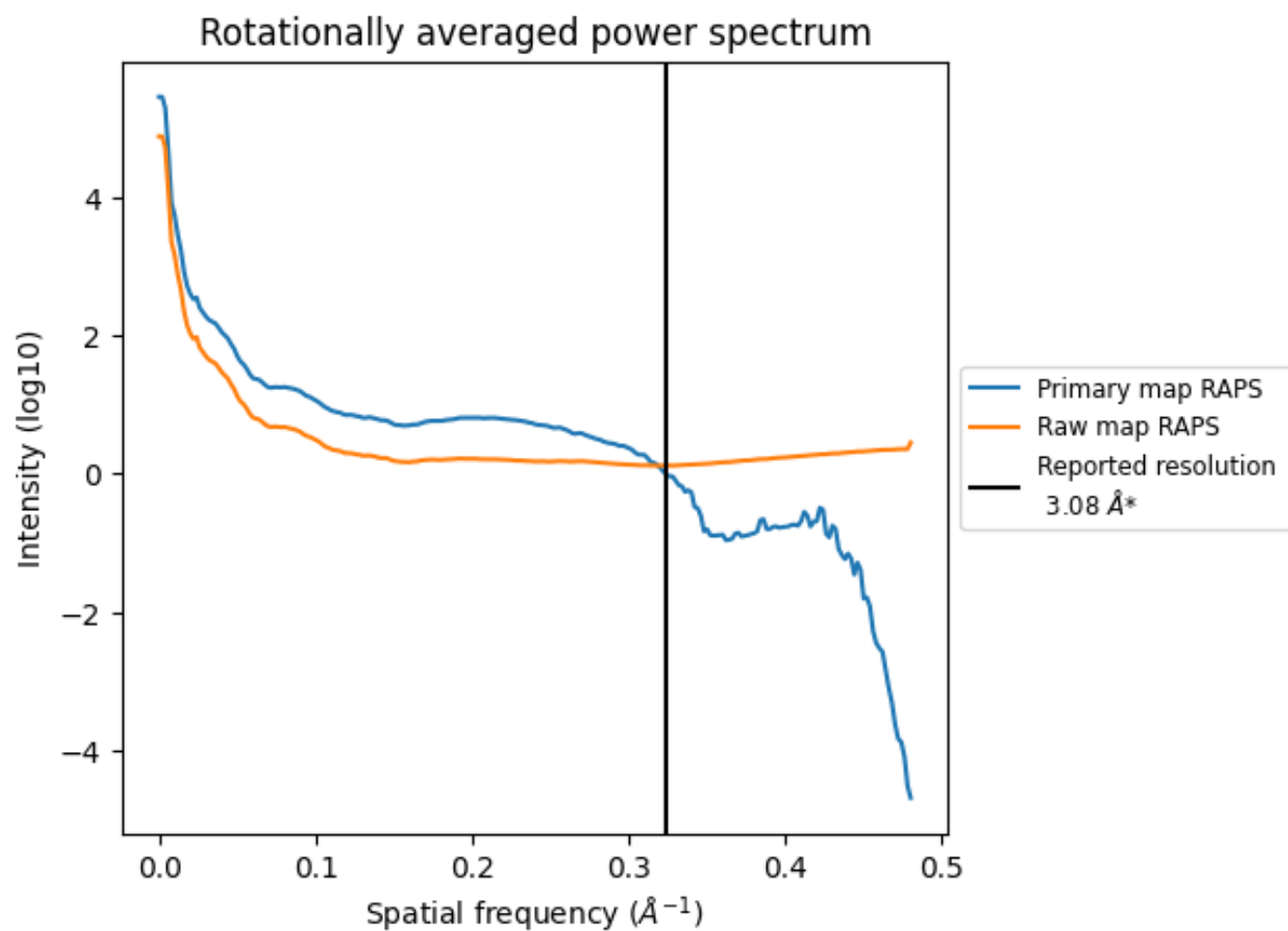
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1491 nm^3 ; this corresponds to an approximate mass of 1347 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

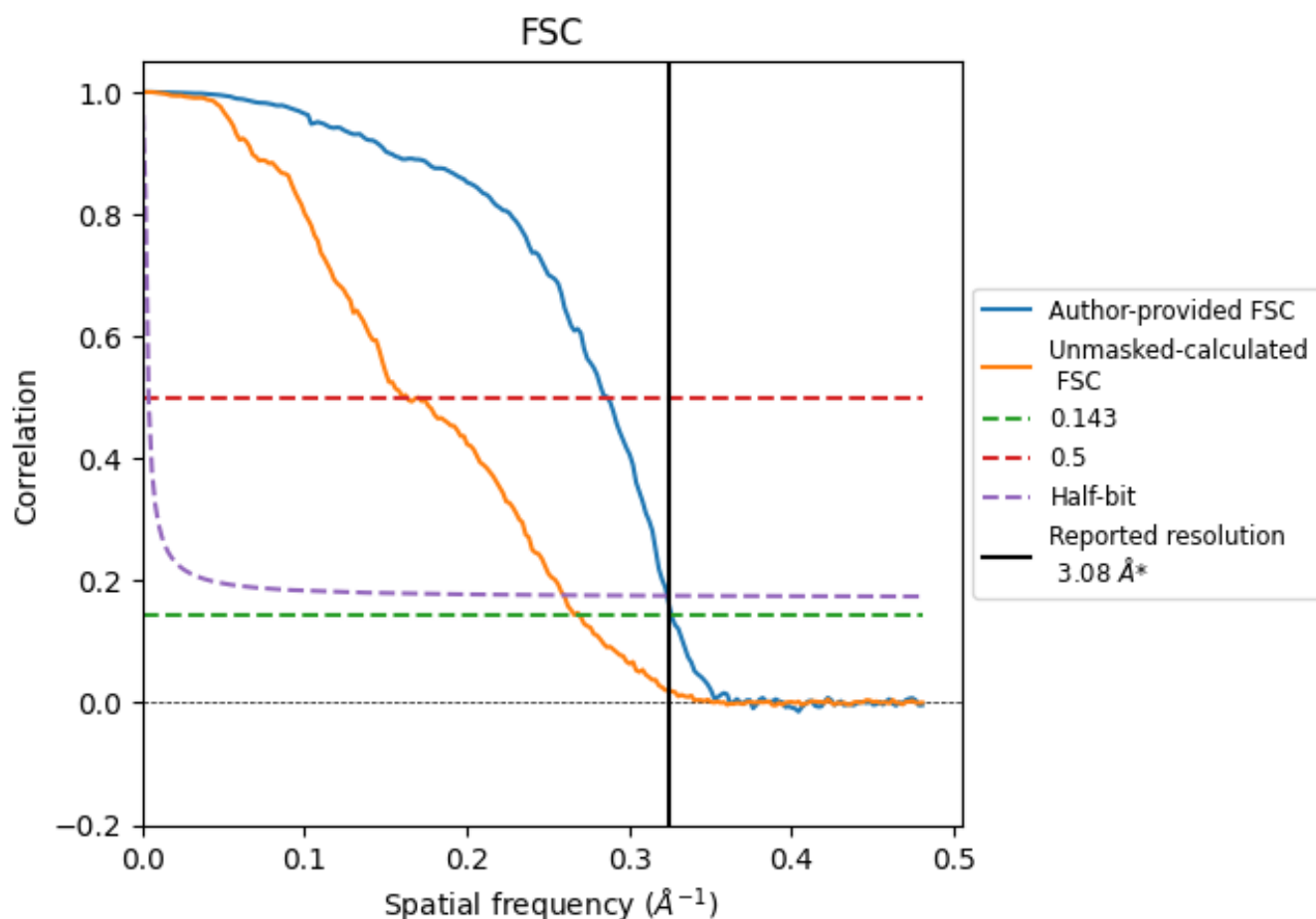


*Reported resolution corresponds to spatial frequency of 0.325 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.325 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

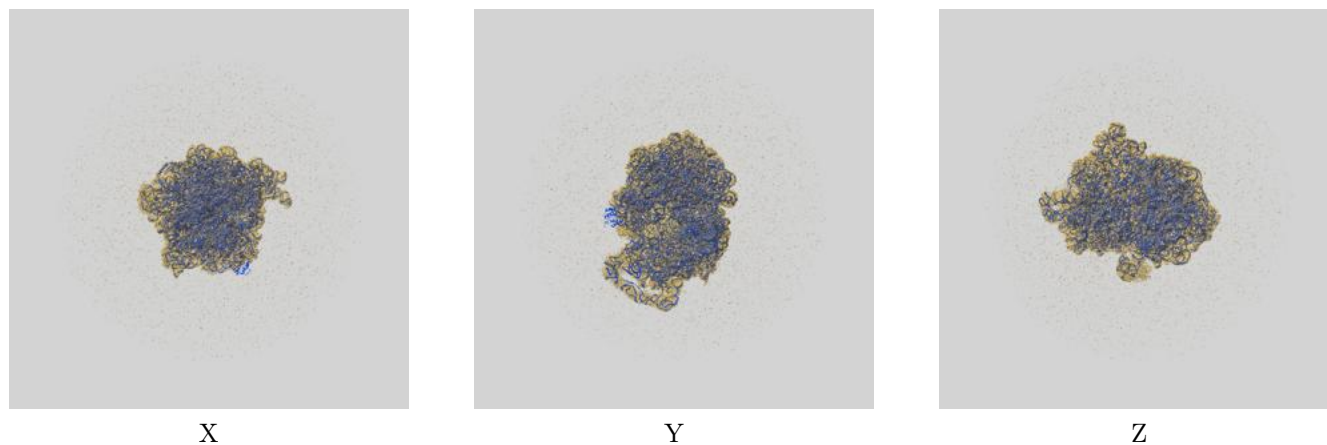
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.08	-	-
Author-provided FSC curve	3.06	3.49	3.09
Unmasked-calculated*	3.71	6.13	3.85

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.71 differs from the reported value 3.08 by more than 10 %

9 Map-model fit [i](#)

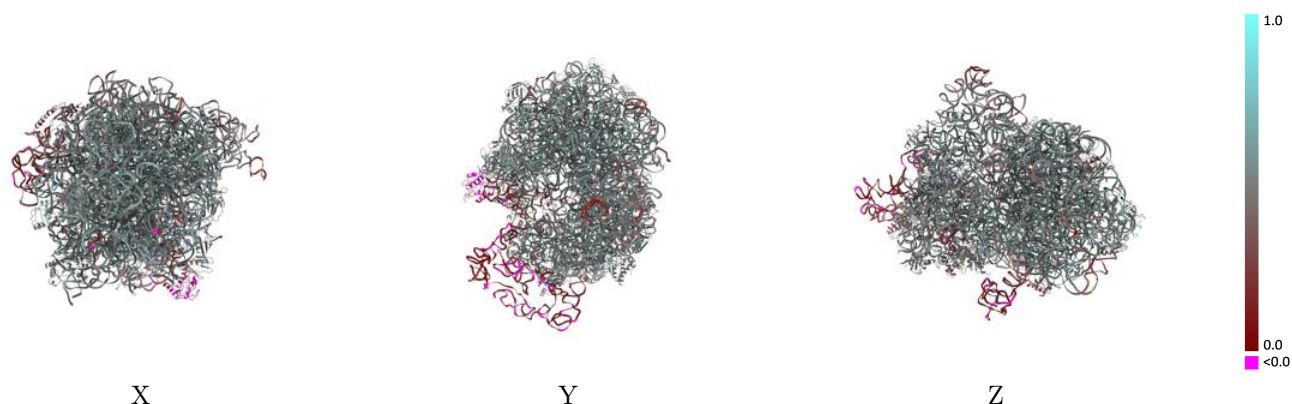
This section contains information regarding the fit between EMDB map EMD-11713 and PDB model 7AC7. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



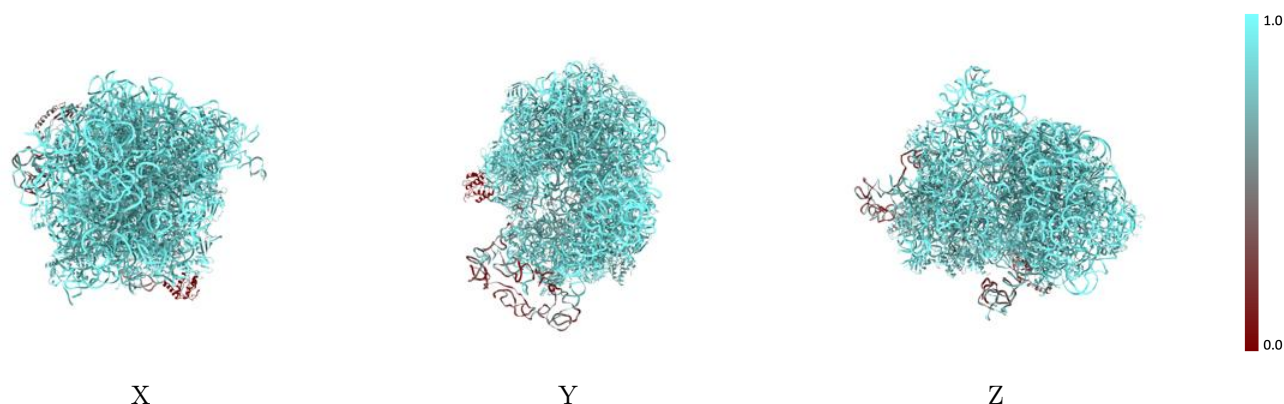
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



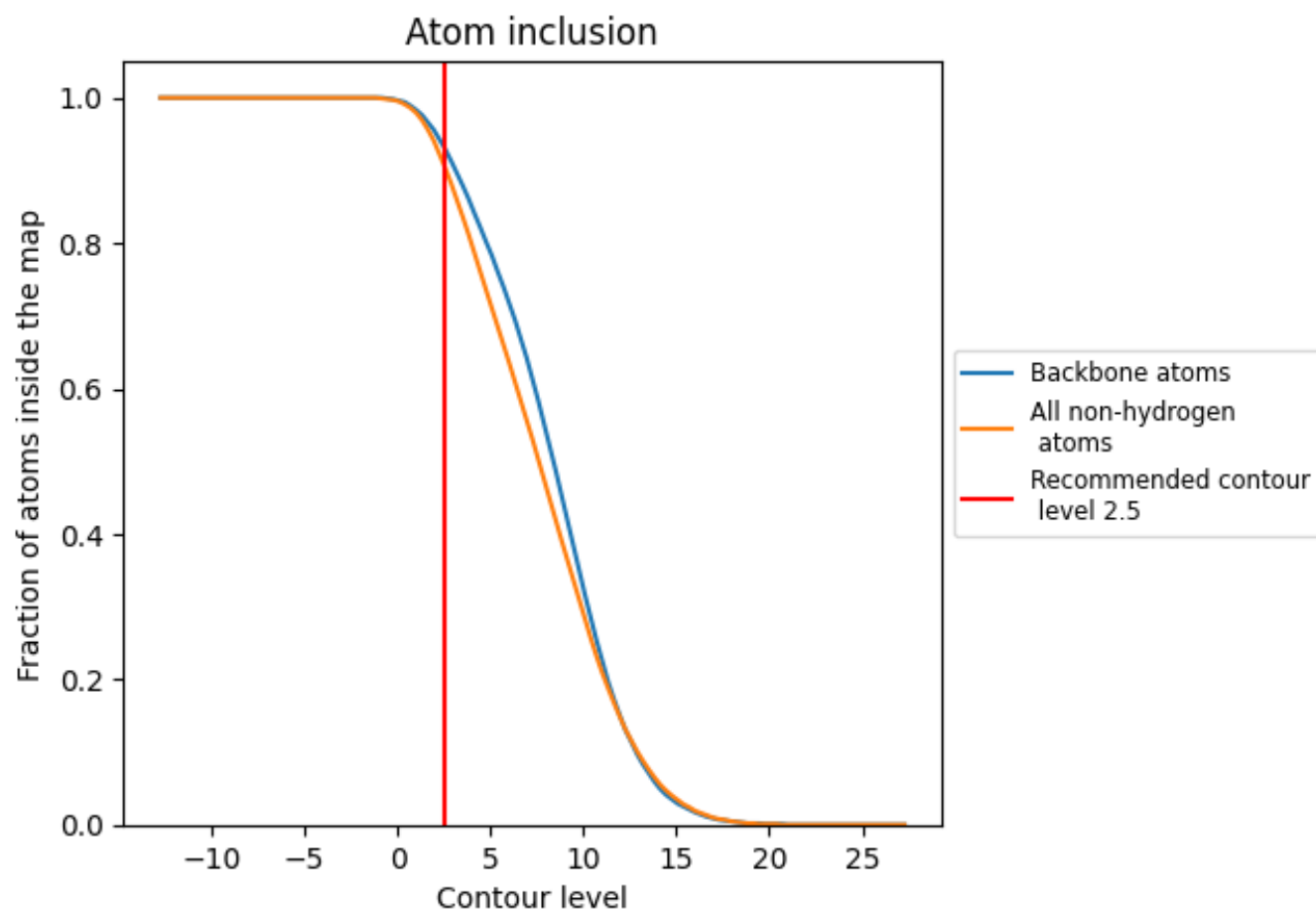
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.4780
1	 0.9590	 0.5010
2	 0.9710	 0.4960
3	 0.9790	 0.5140
4	 0.5090	 0.1570
5	 0.7440	 0.3550
7	 0.9390	 0.5020
8	 0.6850	 0.2610
A	 0.9130	 0.5380
B	 0.9250	 0.5440
C	 0.9140	 0.5270
D	 0.9050	 0.5150
E	 0.8920	 0.4880
F	 0.8810	 0.4740
G	 0.4570	 0.3420
H	 0.0090	 0.0260
J	 0.9070	 0.5240
K	 0.9110	 0.5380
L	 0.9110	 0.5180
M	 0.9150	 0.5370
N	 0.9240	 0.5370
O	 0.9160	 0.5040
P	 0.9140	 0.5300
Q	 0.9190	 0.5300
R	 0.9160	 0.5250
S	 0.8860	 0.5090
T	 0.8860	 0.5110
U	 0.9100	 0.5100
V	 0.9160	 0.5240
W	 0.6880	 0.4110
X	 0.9130	 0.5340
Y	 0.9140	 0.4810
Z	 0.9240	 0.5240
a	 0.8460	 0.4550
b	 0.9200	 0.5280



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Chain	Atom inclusion	Q-score
c	 0.8920	 0.5180
d	 0.9240	 0.5260
e	 0.9040	 0.5340
f	 0.9620	 0.5560
g	 0.7650	 0.4510
h	 0.8900	 0.4950
i	 0.8870	 0.4930
j	 0.9070	 0.5140
k	 0.8790	 0.4710
l	 0.7970	 0.4310
m	 0.9210	 0.5290
n	 0.9080	 0.4780
o	 0.8630	 0.4600
p	 0.8990	 0.4910
q	 0.8890	 0.5090
r	 0.8910	 0.4660
s	 0.9070	 0.4980
t	 0.9080	 0.5030
u	 0.9070	 0.5020
v	 0.8830	 0.4990
w	 0.8790	 0.4890
x	 0.8970	 0.4770
y	 0.8870	 0.4890
z	 0.6830	 0.4030