



Full wwPDB EM Validation Report ⓘ

Jun 19, 2026 – 02:33 am BST

PDB ID : 6YSS / pdb_00006yss
EMDB ID : EMD-10906
Title : Structure of the P+9 ArfB-ribosome complex in the post-hydrolysis state
Authors : Chan, K.-H.; Petrychenko, V.; Mueller, C.; Maracci, C.; Holtkamp, W.; Wilson, D.N.; Fischer, N.; Rodnina, M.V.
Deposited on : 2020-04-23
Resolution : 2.60 Å(reported)
Based on initial models : 4V95, 4RB7, 5AFI, 5O2R

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:

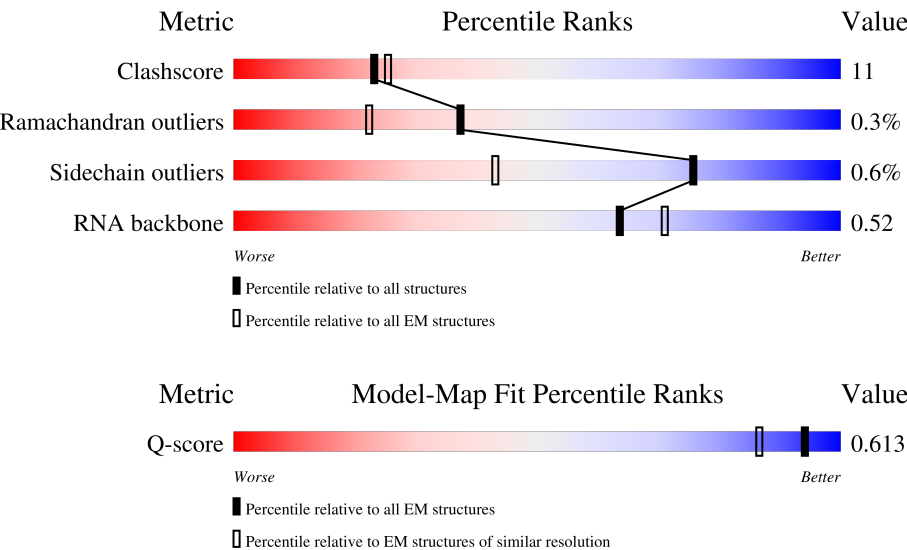
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal 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 i

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

The reported resolution of this entry is 2.60 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.



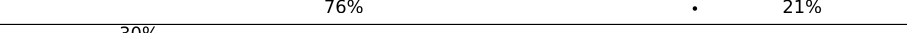
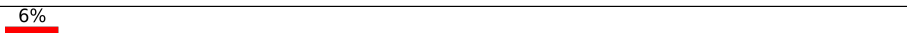
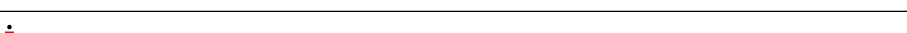
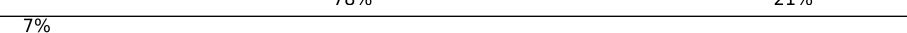
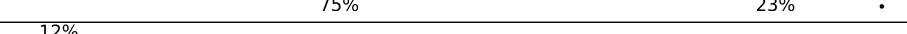
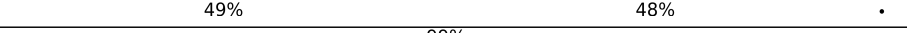
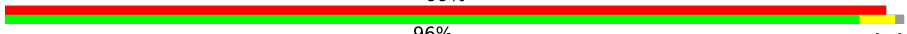
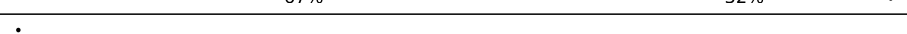
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	0	57	75% 23%
2	1	55	5% 58% 33% 9%
3	2	46	78% 22%

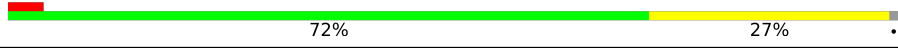
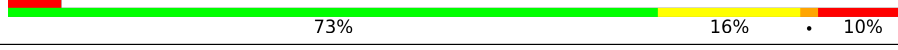
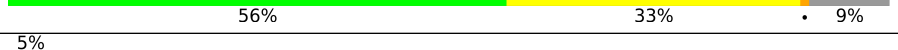
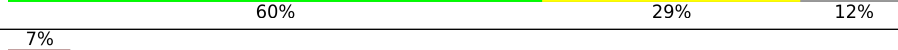
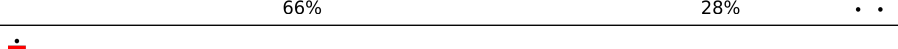
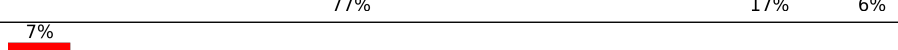
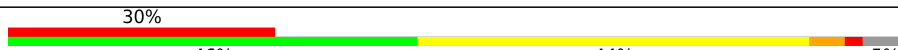
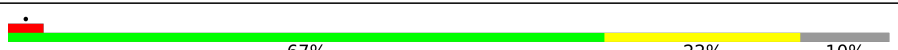
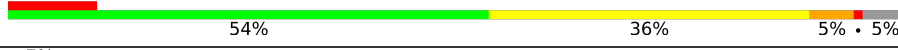
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Mol	Chain	Length	Quality of chain
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R	103	
26	S	110	
27	T	100	
28	U	104	

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Mol	Chain	Length	Quality of chain
29	V	94	
30	W	85	
31	X	78	
32	Y	63	
33	Z	59	
34	a	1542	
35	b	240	
36	c	233	
37	d	206	
38	e	167	
39	f	135	
40	g	179	
41	h	130	
42	i	130	
43	j	103	
44	k	129	
45	l	124	
46	m	118	
47	n	102	
48	o	89	
49	p	82	
50	q	84	
51	r	75	
52	s	92	
53	t	87	

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Mol	Chain	Length	Quality of chain
54	u	71	28% 56% 25% 7% 8%
55	v	14	14% 71% 29%
56	w	76	5% 57% 33% 7%
57	x	15	7% 33% 13% 53%
58	y	140	8% 73% 25%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 147046 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 protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	2903	Total	C	N	O	P	0	0
			62336	27815	11468	20150	2903		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 10 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 11 is a protein called 50S ribosomal protein L3.

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

- Molecule 12 is a protein called 50S ribosomal protein L4.

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

- Molecule 13 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 14 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 15 is a protein called 50S ribosomal protein L9.

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

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	141	Total	C	N	O	S	0	0
			693	411	141	141			

- Molecule 17 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 23 is a protein called 50S ribosomal protein L19.

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

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

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

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	U	102	Total	C	N	O		
			779	492	146	141	0	0

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	75	Total	C	N	O	S		
			575	356	116	102	1	0	0

- Molecule 31 is a protein called 50S ribosomal protein L28.

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

- Molecule 32 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	63	Total	C	N	O	S		
			509	313	99	95	2	0	0

- Molecule 33 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	58	Total	C	N	O	S		
			449	281	87	79	2	0	0

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1540	Total	C	N	O	P		
			33050	14748	6057	10705	1540	0	0

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 47 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	36	ALA	-	insertion	UNP I2X5X6

- Molecule 48 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 49 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 51 is a protein called 30S ribosomal protein S18.

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

- Molecule 52 is a protein called 30S ribosomal protein S19.

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

- Molecule 53 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 55 is a protein called Api137.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	v	14	Total	C	N	O	0	0
			121	80	25	16		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	10	ARG	GLN	conflict	UNP Q8WSY8

- Molecule 56 is a RNA chain called P-site tRNAPhe.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	76	Total	C	N	O	P	S	0	0
			1631	731	291	531	76	2		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	7	Total	C	N	O	P	0	0
			147	66	24	50	7		

- Molecule 58 is a protein called Alternative stalled-ribosome rescue factor B.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	139	Total	C	N	O	S	0	0
			1078	666	215	195	2		

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

Mol	Chain	Residues	Atoms		AltConf
59	0	1	Total	Mg	0
			1	1	
59	A	269	Total	Mg	0
			269	269	
59	B	7	Total	Mg	0
			7	7	
59	C	3	Total	Mg	0
			3	3	
59	D	1	Total	Mg	0
			1	1	
59	M	1	Total	Mg	0
			1	1	
59	O	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
59	P	1	Total 1	Mg 1	0
59	W	1	Total 1	Mg 1	0
59	a	95	Total 95	Mg 95	0
59	m	1	Total 1	Mg 1	0
59	n	1	Total 1	Mg 1	0
59	w	4	Total 4	Mg 4	0
59	y	1	Total 1	Mg 1	0

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

Mol	Chain	Residues	Atoms		AltConf
60	4	1	Total 1	Zn 1	0
60	6	1	Total 1	Zn 1	0

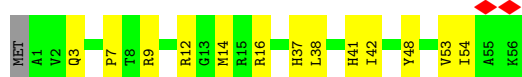
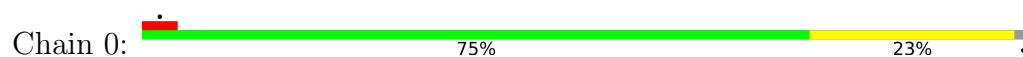
- Molecule 61 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
61	A	1	Total 1	Na 1	0
61	V	1	Total 1	Na 1	0

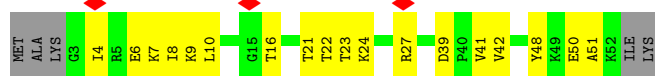
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

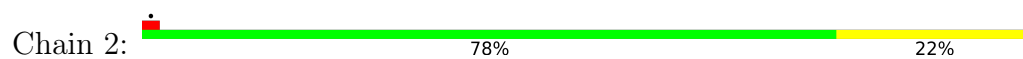
- Molecule 1: 50S ribosomal protein L32



- Molecule 2: 50S ribosomal protein L33



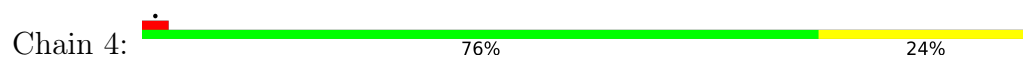
- Molecule 3: 50S ribosomal protein L34



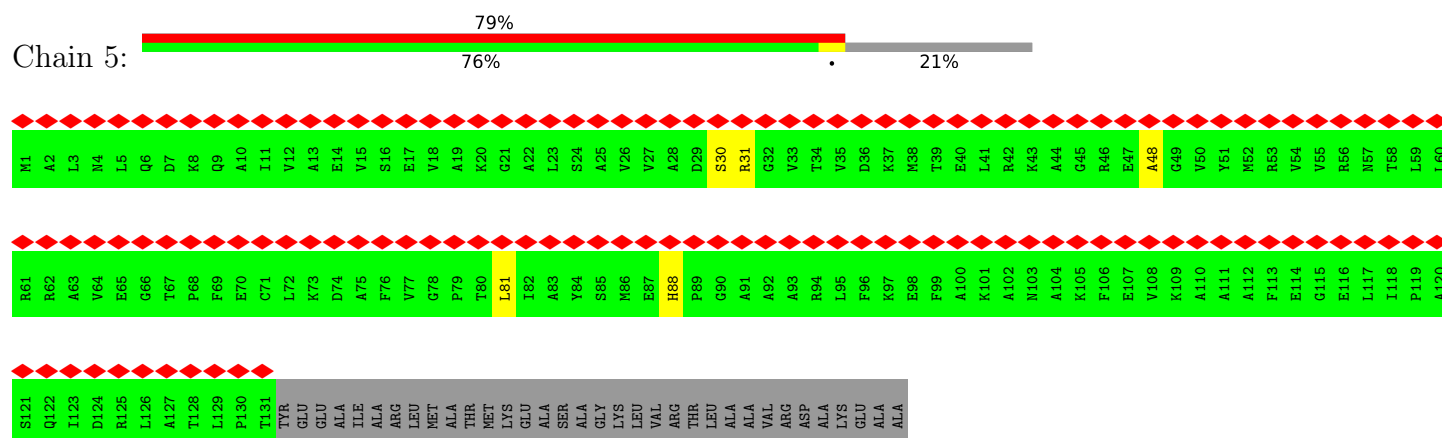
- Molecule 4: 50S ribosomal protein L35



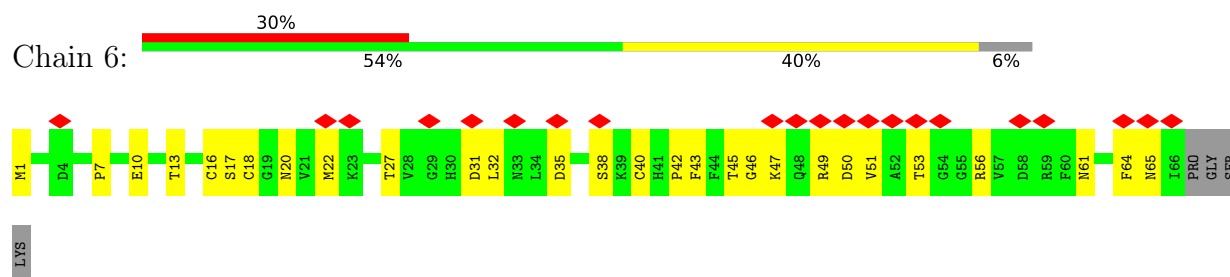
- Molecule 5: 50S ribosomal protein L36



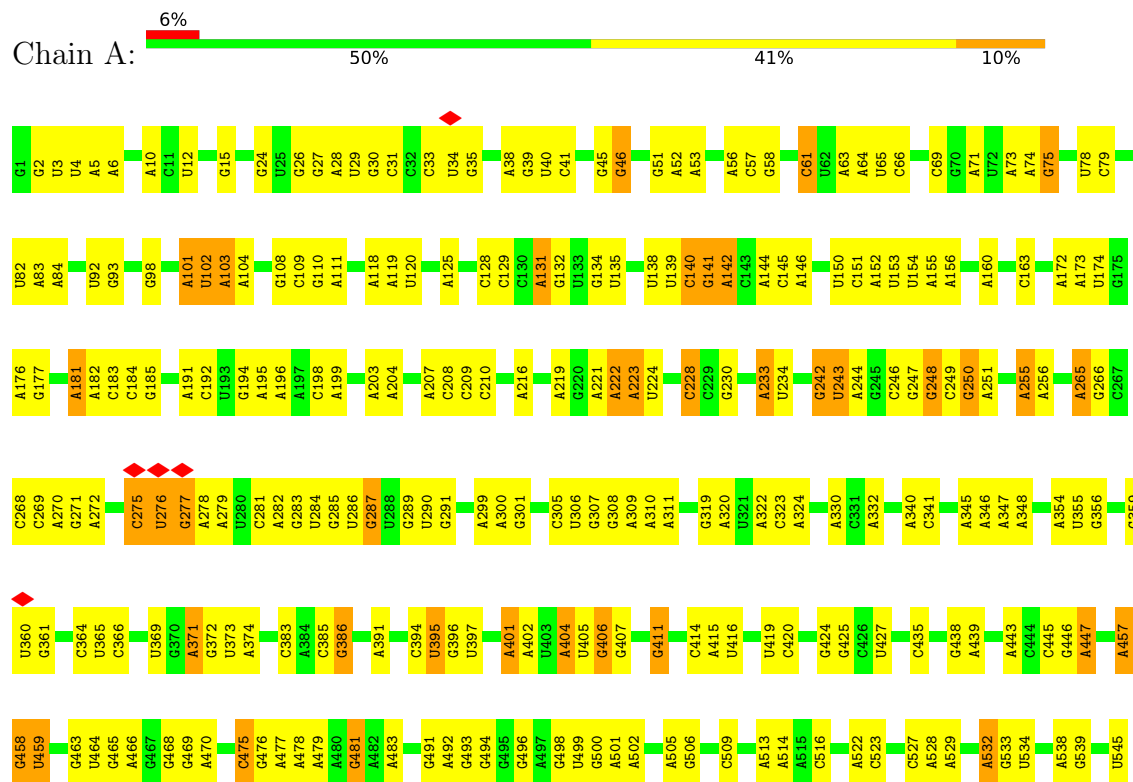
- Molecule 6: 50S ribosomal protein L10



- Molecule 7: 50S ribosomal protein L31



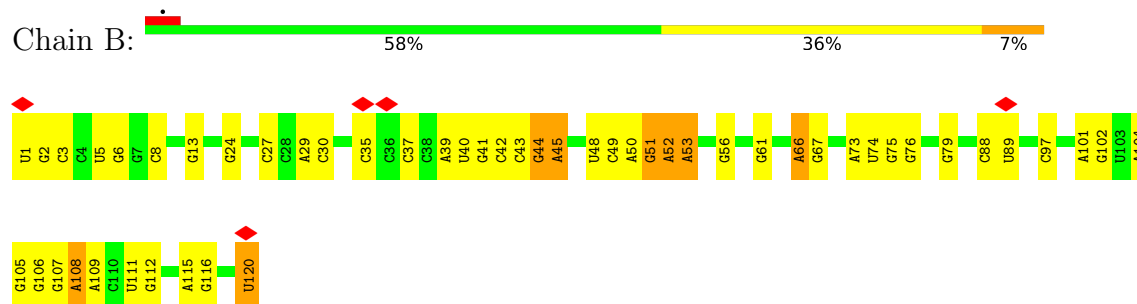
- Molecule 8: 23S ribosomal RNA



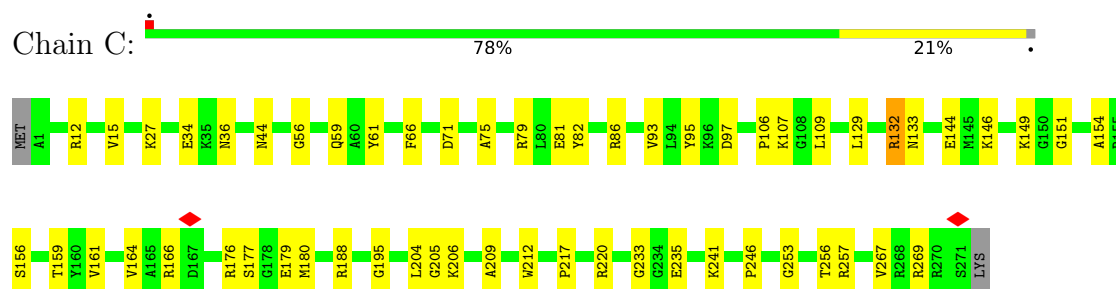




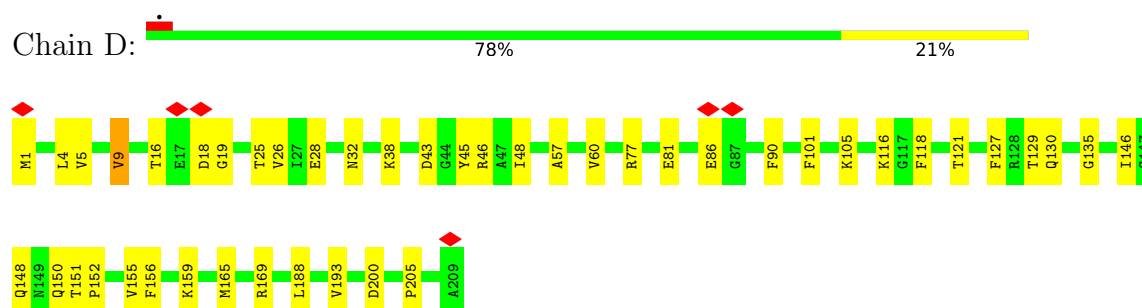
- Molecule 9: 5S ribosomal RNA



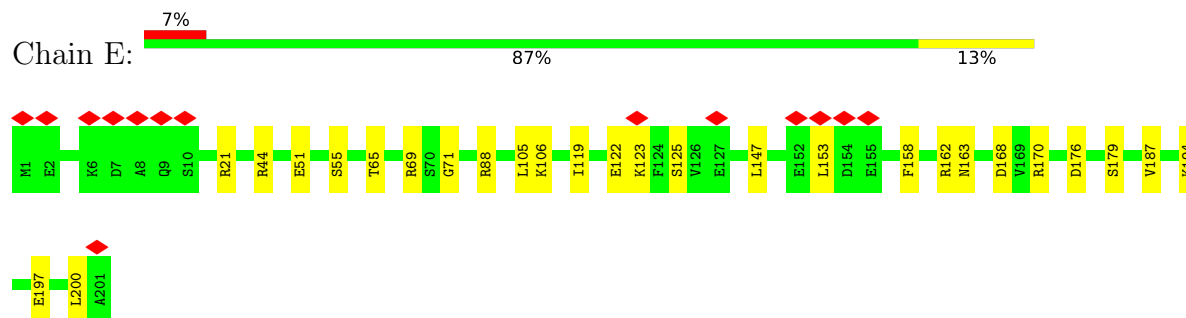
- Molecule 10: 50S ribosomal protein L2



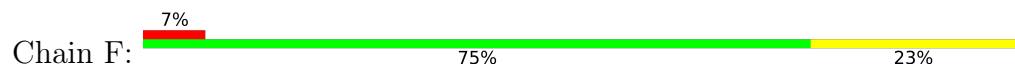
- Molecule 11: 50S ribosomal protein L3

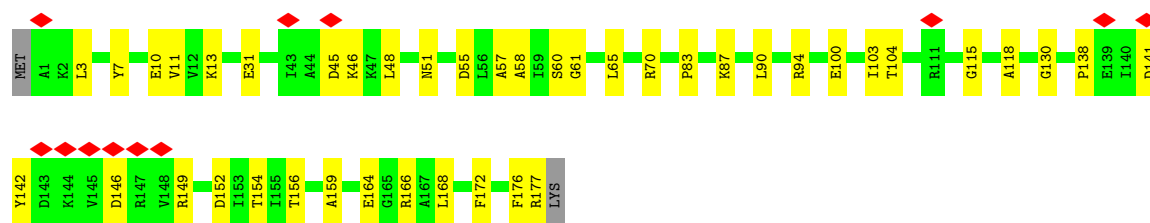


- Molecule 12: 50S ribosomal protein L4

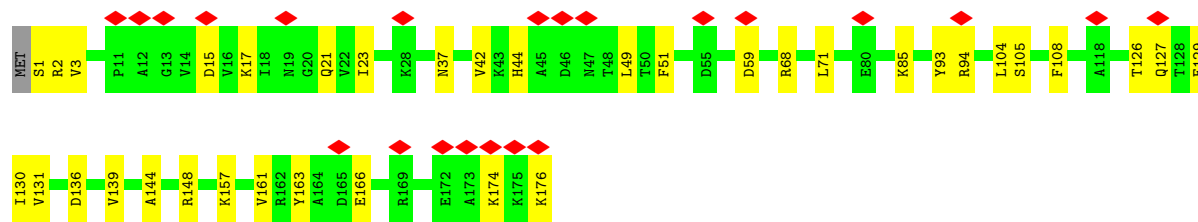
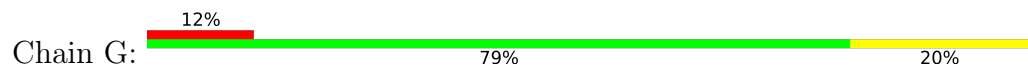


- Molecule 13: 50S ribosomal protein L5

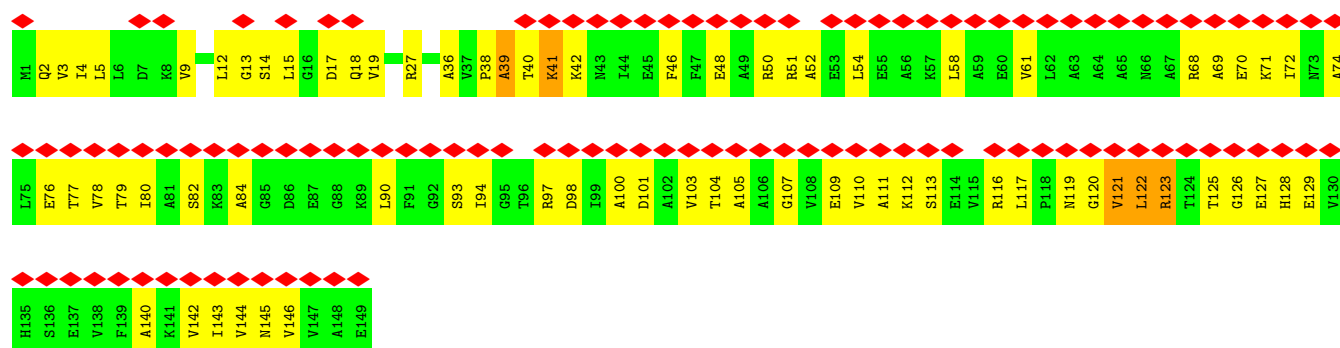
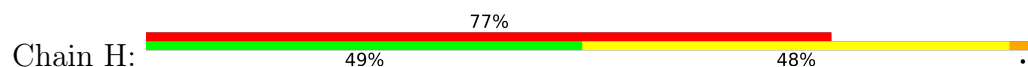




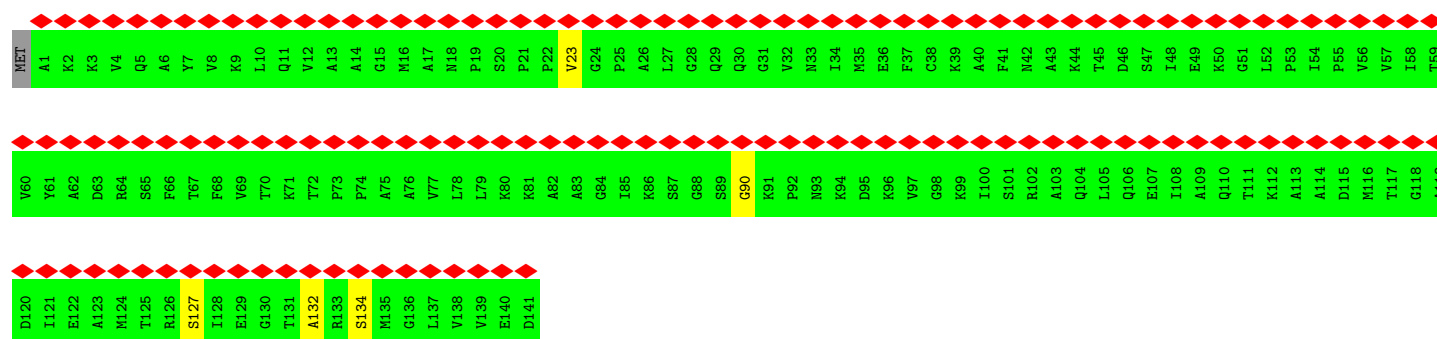
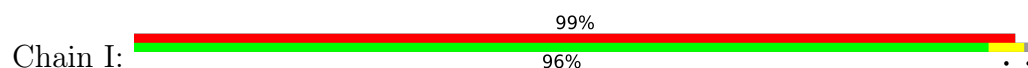
- Molecule 14: 50S ribosomal protein L6



- Molecule 15: 50S ribosomal protein L9

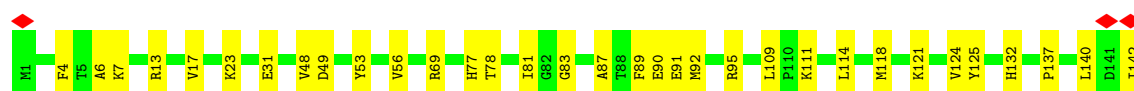


- Molecule 16: 50S ribosomal protein L11



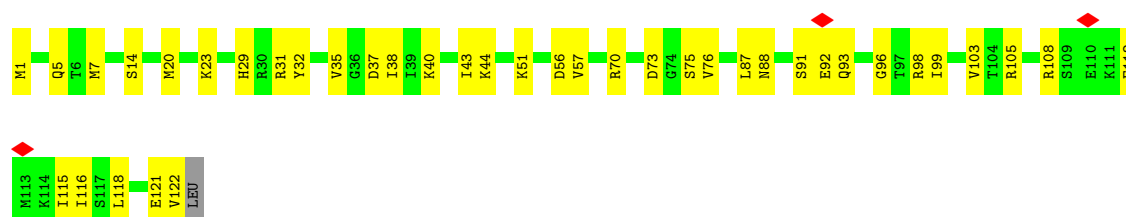
- Molecule 17: 50S ribosomal protein L13

Chain J:  77% 23%



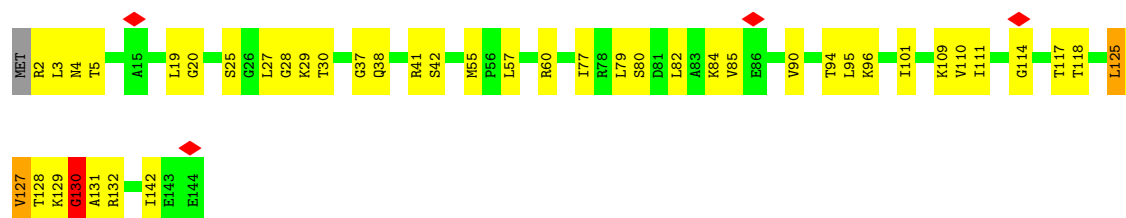
- Molecule 18: 50S ribosomal protein L14

Chain K:  67% 32%



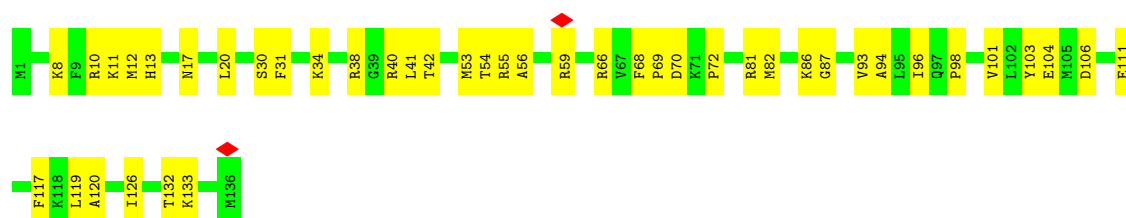
- Molecule 19: 50S ribosomal protein L15

Chain L:  69% 28%



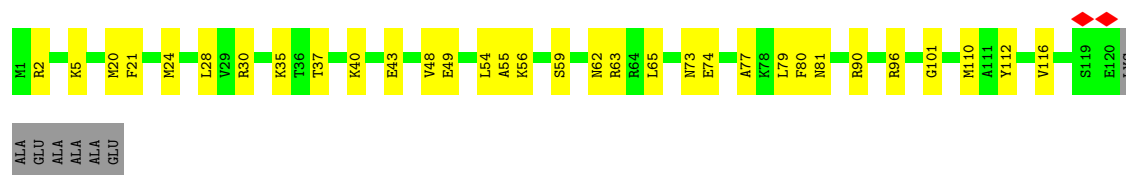
- Molecule 20: 50S ribosomal protein L16

Chain M:  68% 32%

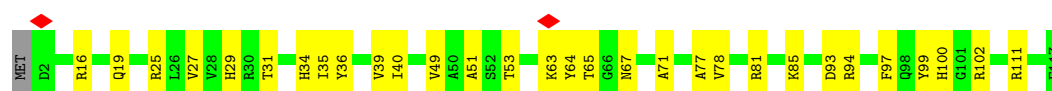


- Molecule 21: 50S ribosomal protein L17

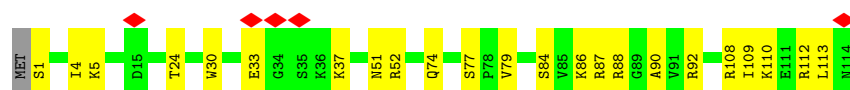
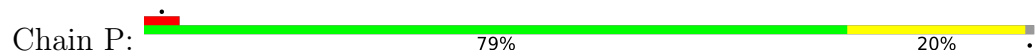
Chain N:  69% 25% 6%



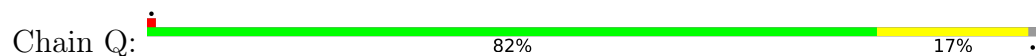
- Molecule 22: 50S ribosomal protein L18



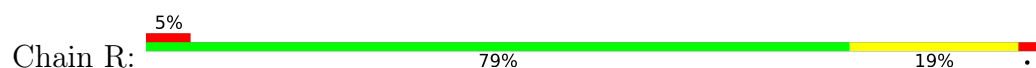
- Molecule 23: 50S ribosomal protein L19



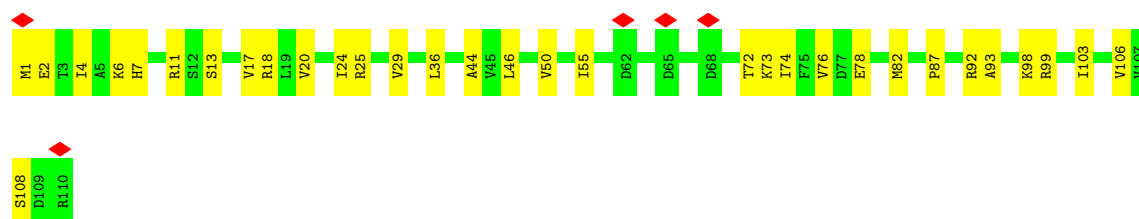
- Molecule 24: 50S ribosomal protein L20



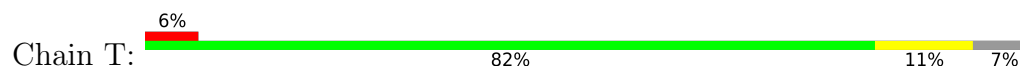
- Molecule 25: 50S ribosomal protein L21



- Molecule 26: 50S ribosomal protein L22

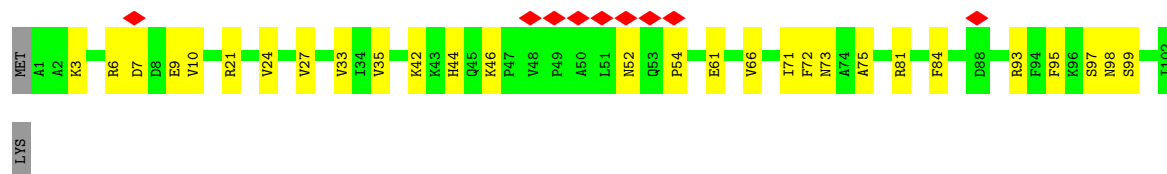


- Molecule 27: 50S ribosomal protein L23

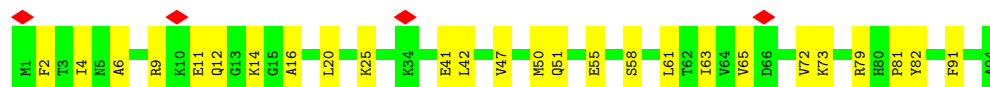


- Molecule 28: 50S ribosomal protein L24

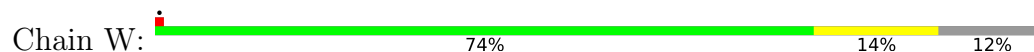




- Molecule 29: 50S ribosomal protein L25



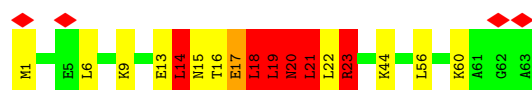
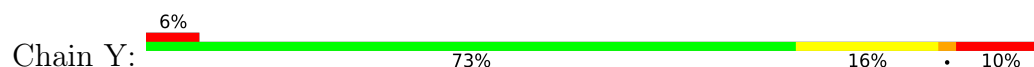
- Molecule 30: 50S ribosomal protein L27



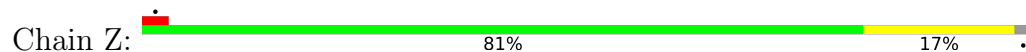
- Molecule 31: 50S ribosomal protein L28



- Molecule 32: 50S ribosomal protein L29

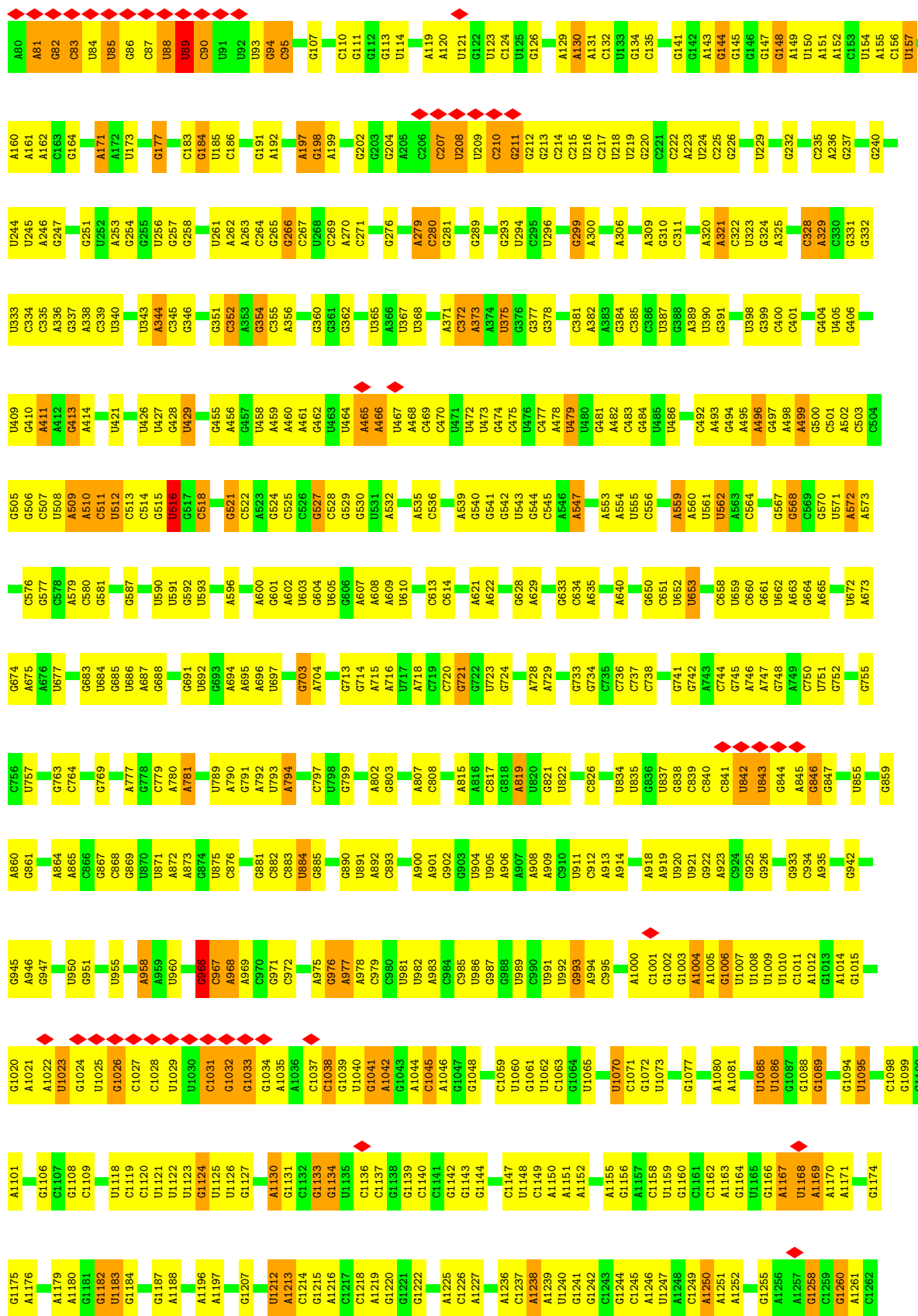


- Molecule 33: 50S ribosomal protein L30

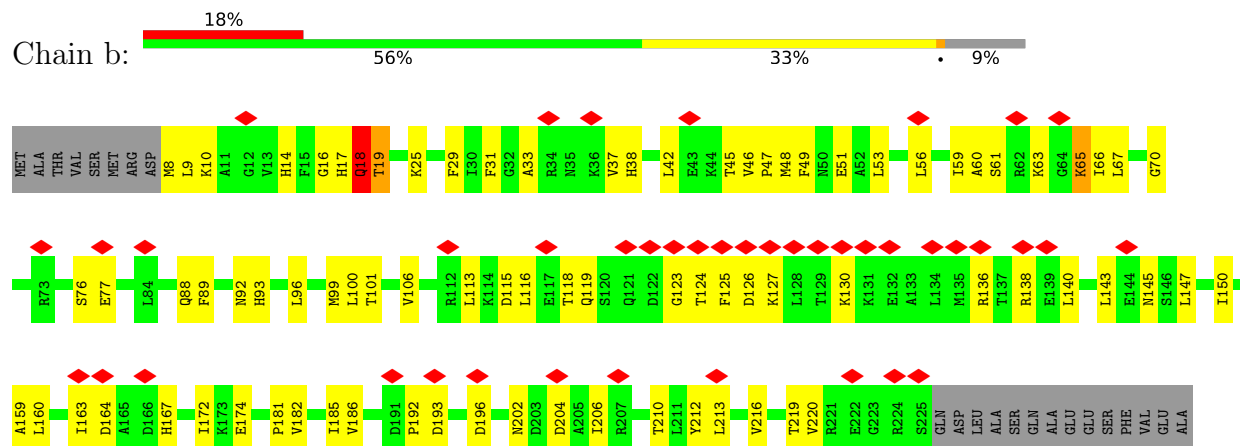


- Molecule 34: 16S ribosomal RNA

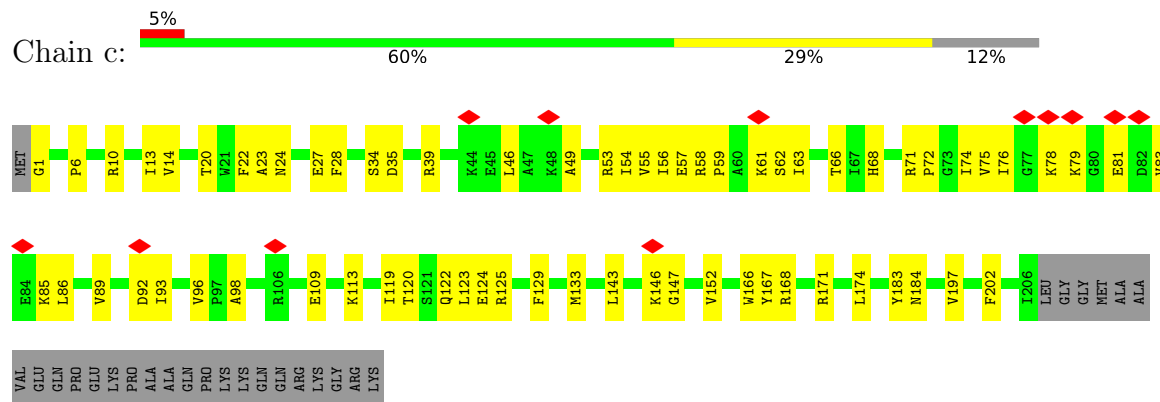




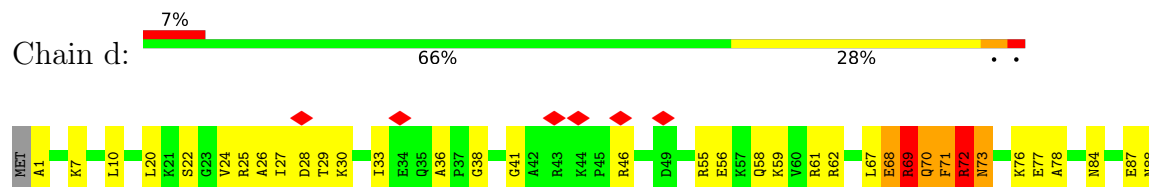
- Molecule 35: 30S ribosomal protein S2

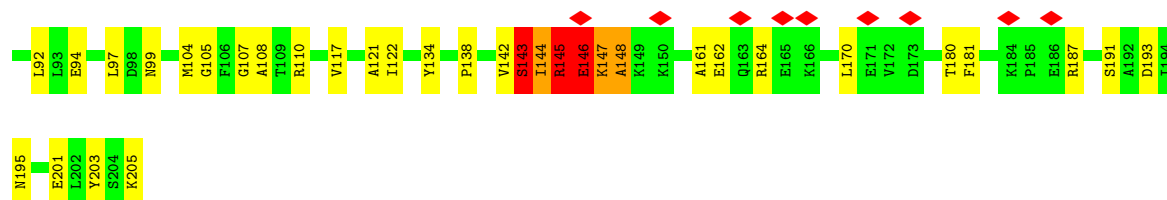


- Molecule 36: 30S ribosomal protein S3

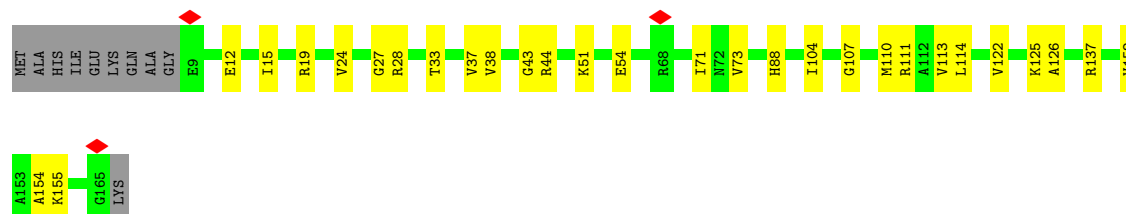
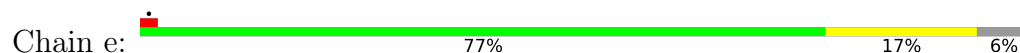


- Molecule 37: 30S ribosomal protein S4

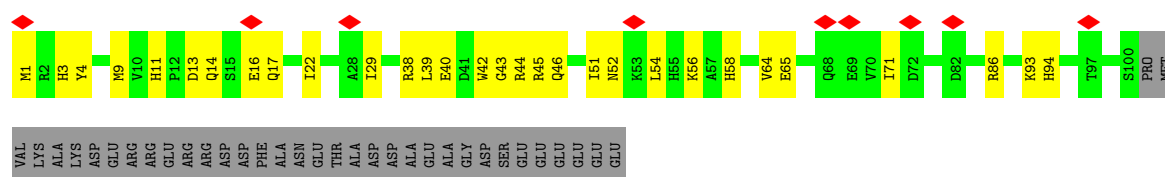




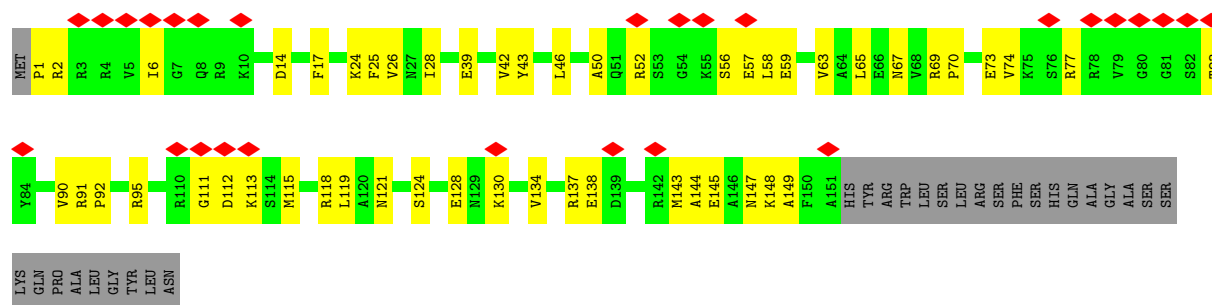
- Molecule 38: 30S ribosomal protein S5



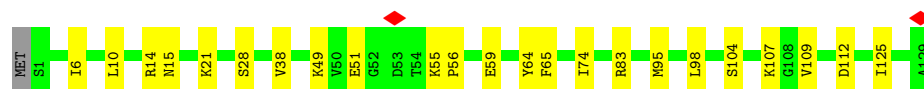
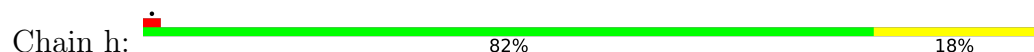
- Molecule 39: 30S ribosomal protein S6



- Molecule 40: 30S ribosomal protein S7

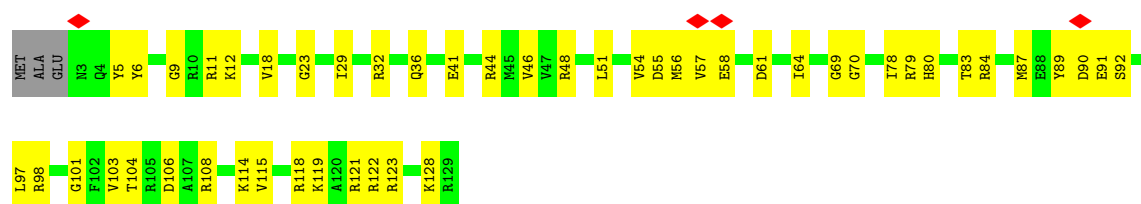


- Molecule 41: 30S ribosomal protein S8



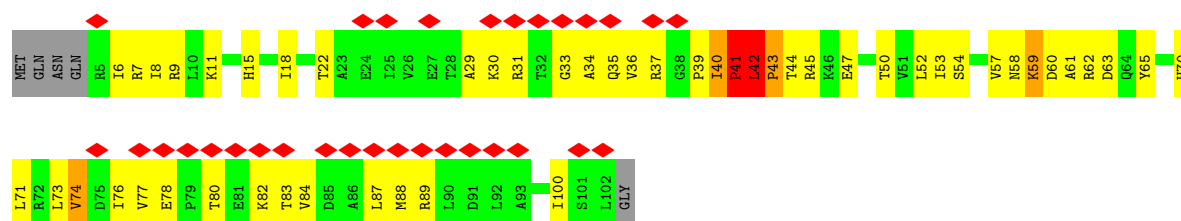
- Molecule 42: 30S ribosomal protein S9

Chain i: 



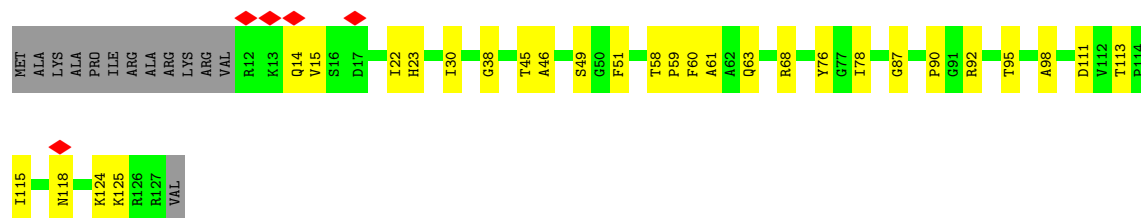
- Molecule 43: 30S ribosomal protein S10

Chain j: 



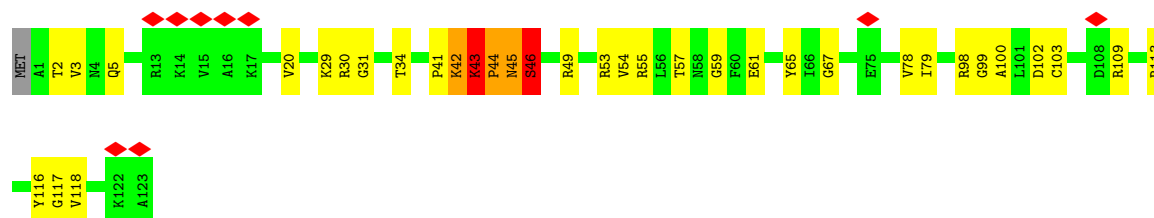
- Molecule 44: 30S ribosomal protein S11

Chain k: 



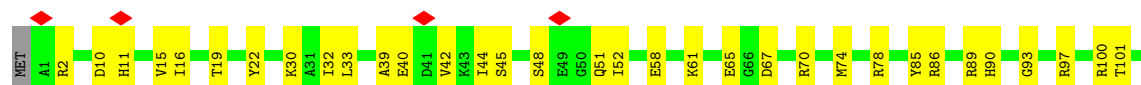
- Molecule 45: 30S ribosomal protein S12

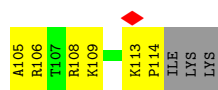
Chain l: 



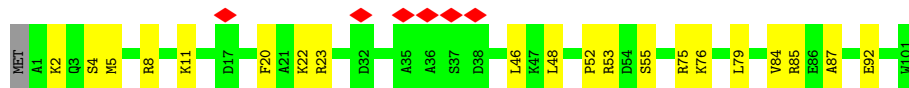
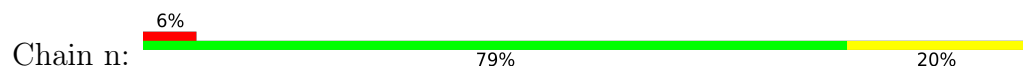
- Molecule 46: 30S ribosomal protein S13

Chain m: 

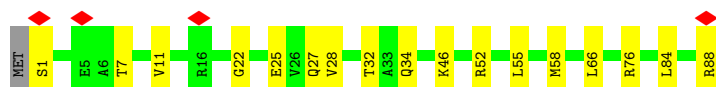
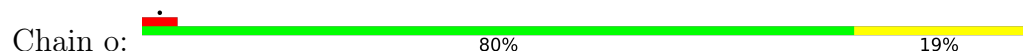




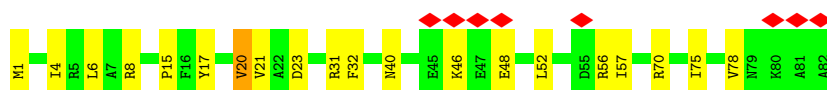
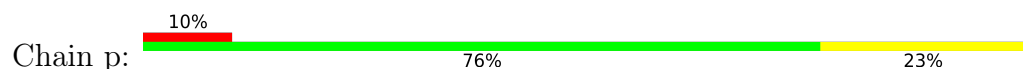
- Molecule 47: 30S ribosomal protein S14



- Molecule 48: 30S ribosomal protein S15



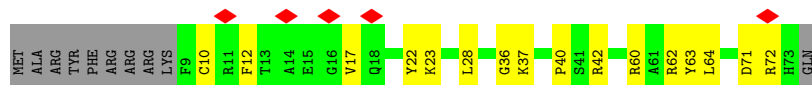
- Molecule 49: 30S ribosomal protein S16



- Molecule 50: 30S ribosomal protein S17



- Molecule 51: 30S ribosomal protein S18

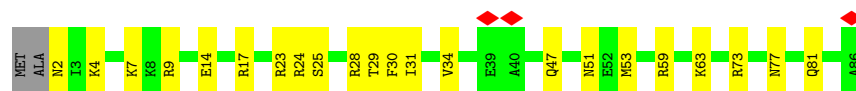


- Molecule 52: 30S ribosomal protein S19

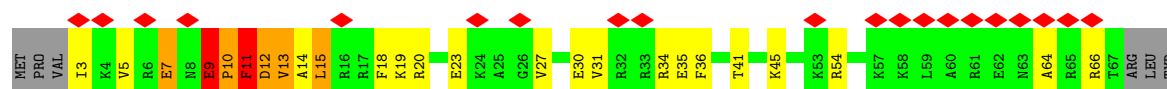




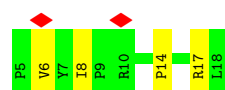
- Molecule 53: 30S ribosomal protein S20



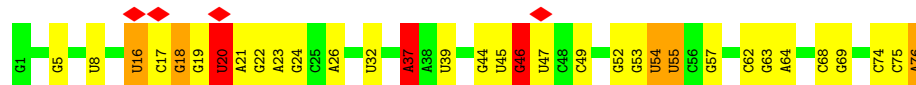
- Molecule 54: 30S ribosomal protein S21



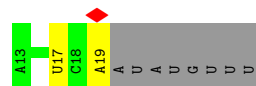
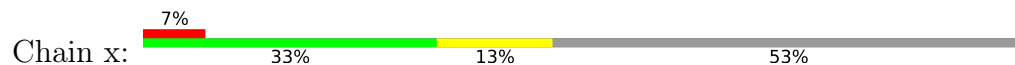
- Molecule 55: Api137



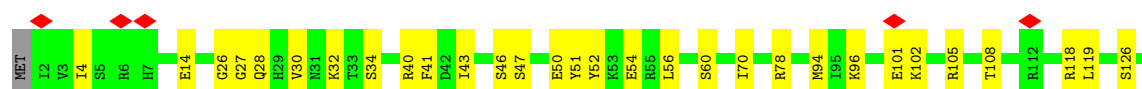
- Molecule 56: P-site tRNA^{Phe}



- Molecule 57: mRNA



- Molecule 58: Alternative stalled-ribosome rescue factor B





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	282252	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2.5	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	23.880	Depositor
Minimum map value	-9.666	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3	Depositor
Map size (Å)	334.08, 334.08, 334.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.6525, 0.6525, 0.6525	Depositor

5 Model quality

5.1 Standard geometry

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

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	0	0.35	0/450	0.48	0/599
2	1	0.31	0/416	0.40	0/554
3	2	0.37	0/380	0.42	0/498
4	3	0.34	0/513	0.46	0/676
5	4	0.38	0/303	0.51	0/397
6	5	0.14	0/646	0.43	0/898
7	6	0.21	0/531	0.43	0/709
8	A	0.41	4/69263 (0.0%)	0.34	0/108050
9	B	0.34	1/2873 (0.0%)	0.31	0/4478
10	C	0.38	0/2121	0.49	1/2852 (0.0%)
11	D	0.35	0/1586	0.43	0/2134
12	E	0.31	0/1571	0.40	0/2113
13	F	0.26	0/1434	0.42	0/1926
14	G	0.25	0/1343	0.40	0/1816
15	H	0.73	6/1122 (0.5%)	0.69	3/1515 (0.2%)
16	I	0.15	0/692	0.40	0/960
17	J	0.34	0/1152	0.38	0/1551
18	K	0.36	0/947	0.43	0/1268
19	L	2.06	14/1054 (1.3%)	0.88	6/1403 (0.4%)
20	M	0.34	0/1093	0.44	0/1460
21	N	0.36	0/973	0.49	0/1301
22	O	0.28	0/902	0.46	0/1209
23	P	0.34	0/929	0.40	0/1242
24	Q	0.37	0/960	0.40	0/1278
25	R	0.38	0/829	1.38	6/1107 (0.5%)
26	S	0.34	0/864	0.44	0/1156
27	T	0.29	0/744	0.40	0/994
28	U	0.29	0/787	0.41	0/1051
29	V	0.29	0/766	0.37	0/1025
30	W	0.35	0/582	0.38	0/769
31	X	0.36	0/635	0.39	0/848

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	2.63	35/510 (6.9%)	1.40	17/677 (2.5%)
33	Z	0.30	0/453	0.38	0/605
34	a	0.36	1/36725 (0.0%)	0.37	4/57285 (0.0%)
35	b	0.69	7/1735 (0.4%)	0.68	4/2338 (0.2%)
36	c	0.28	0/1651	0.40	0/2225
37	d	1.19	25/1665 (1.5%)	0.86	14/2227 (0.6%)
38	e	0.30	0/1154	0.42	0/1554
39	f	0.27	0/835	0.47	0/1128
40	g	0.24	0/1195	0.40	0/1602
41	h	0.29	0/989	0.37	0/1326
42	i	0.27	0/1034	0.47	0/1375
43	j	1.66	31/796 (3.9%)	0.99	7/1077 (0.6%)
44	k	0.27	0/885	0.44	0/1195
45	l	1.31	17/969 (1.8%)	0.92	5/1300 (0.4%)
46	m	0.27	0/892	0.49	0/1193
47	n	0.27	0/811	0.41	0/1081
48	o	0.27	0/722	0.38	0/964
49	p	0.31	0/659	0.44	0/884
50	q	1.54	18/657 (2.7%)	0.92	5/881 (0.6%)
51	r	0.30	0/544	0.46	0/731
52	s	0.26	0/675	0.43	0/908
53	t	0.28	0/671	0.39	0/888
54	u	1.20	9/512 (1.8%)	1.21	8/683 (1.2%)
55	v	0.33	0/128	0.60	1/175 (0.6%)
56	w	0.60	6/1650 (0.4%)	0.33	0/2569
57	x	0.31	0/163	0.31	0/251
58	y	0.31	0/1090	0.59	4/1461 (0.3%)
All	All	0.49	174/158231 (0.1%)	0.42	85/236420 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
19	L	0	1
37	d	0	1
58	y	0	1
All	All	0	3

All (174) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	L	130	GLY	C-O	-33.07	0.79	1.23
19	L	129	LYS	C-O	-29.46	0.89	1.24
19	L	126	ARG	C-O	-24.52	0.93	1.24
19	L	129	LYS	CA-C	-19.32	1.26	1.52
19	L	126	ARG	CA-C	-17.63	1.31	1.52
45	l	43	LYS	CA-C	-16.85	1.31	1.52
32	Y	19	LEU	C-O	-16.63	1.03	1.24
45	l	44	PRO	C-O	-16.38	1.04	1.24
19	L	130	GLY	CA-C	-14.70	1.31	1.51
35	b	16	GLY	C-O	-14.27	1.08	1.23
15	H	123	ARG	C-O	-14.10	1.07	1.23
50	q	70	LYS	C-O	-14.09	1.06	1.24
32	Y	21	LEU	C-O	-13.95	1.07	1.24
32	Y	23	ARG	C-O	-13.93	1.08	1.24
32	Y	14	LEU	C-O	-13.83	1.05	1.24
32	Y	19	LEU	CA-C	-13.34	1.34	1.52
37	d	70	GLN	CA-C	-13.00	1.35	1.52
37	d	71	PHE	C-O	-12.99	1.08	1.24
19	L	126	ARG	CA-CB	-12.70	1.31	1.53
15	H	39	ALA	C-O	-12.68	1.08	1.24
32	Y	14	LEU	CA-C	-12.28	1.35	1.52
45	l	46	SER	C-O	-12.24	1.08	1.24
19	L	129	LYS	CA-CB	-11.99	1.34	1.53
37	d	72	ARG	C-O	-11.39	1.09	1.24
32	Y	17	GLU	C-O	-11.26	1.10	1.24
32	Y	22	LEU	C-O	-11.22	1.10	1.24
37	d	70	GLN	C-O	-11.12	1.09	1.24
32	Y	15	ASN	C-O	-11.04	1.09	1.24
43	j	61	ALA	C-O	-10.90	1.11	1.24
50	q	69	THR	C-O	-10.68	1.09	1.24
32	Y	18	LEU	C-O	-10.43	1.10	1.24
50	q	71	SER	CA-C	-10.33	1.40	1.52
43	j	42	LEU	C-O	-10.33	1.11	1.24
50	q	70	LYS	CA-C	-10.32	1.40	1.52
50	q	68	LYS	CA-CB	-10.31	1.37	1.53
32	Y	16	THR	CA-C	-10.29	1.39	1.52
43	j	45	ARG	C-O	-10.21	1.11	1.24
43	j	60	ASP	C-O	-9.94	1.10	1.24
35	b	19	THR	C-O	-9.89	1.11	1.24
43	j	58	ASN	CA-C	-9.82	1.43	1.53
32	Y	18	LEU	CA-C	-9.74	1.39	1.52
19	L	126	ARG	CD-NE	-9.73	1.32	1.46
43	j	43	PRO	C-O	-9.69	1.12	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	Y	23	ARG	CA-C	-9.68	1.40	1.52
32	Y	23	ARG	N-CA	-9.52	1.35	1.46
37	d	71	PHE	CA-C	-9.40	1.40	1.52
54	u	13	VAL	C-O	-9.36	1.13	1.24
37	d	73	ASN	C-O	-9.26	1.11	1.24
37	d	72	ARG	CA-CB	-9.24	1.37	1.53
35	b	17	HIS	C-O	-9.21	1.12	1.24
45	l	44	PRO	CA-C	-9.17	1.42	1.52
32	Y	22	LEU	CA-C	-9.12	1.41	1.52
19	L	130	GLY	C-N	-9.01	1.22	1.33
19	L	130	GLY	N-CA	-8.94	1.32	1.45
37	d	73	ASN	CA-C	-8.80	1.40	1.52
50	q	67	SER	C-O	-8.80	1.17	1.24
32	Y	23	ARG	CA-CB	-8.75	1.39	1.53
37	d	143	SER	C-O	-8.67	1.13	1.24
19	L	125	LEU	C-N	-8.47	1.21	1.33
32	Y	17	GLU	CA-CB	-8.41	1.42	1.53
35	b	18	GLN	C-O	-8.29	1.12	1.23
19	L	129	LYS	C-N	-8.28	1.21	1.33
37	d	72	ARG	N-CA	-8.25	1.35	1.46
37	d	144	ILE	CA-CB	-8.20	1.44	1.54
45	l	45	ASN	CG-OD1	-8.18	1.08	1.23
45	l	45	ASN	CA-C	-8.16	1.42	1.52
50	q	66	LEU	CA-C	-8.08	1.42	1.52
43	j	42	LEU	CA-C	-8.02	1.42	1.52
43	j	60	ASP	N-CA	-7.96	1.35	1.46
32	Y	20	ASN	C-O	-7.94	1.13	1.24
43	j	61	ALA	CA-C	-7.90	1.42	1.52
43	j	60	ASP	CA-C	-7.89	1.40	1.52
32	Y	20	ASN	N-CA	-7.86	1.35	1.46
56	w	20	U	N1-C2	7.86	1.54	1.38
37	d	148	ALA	CA-C	-7.76	1.42	1.52
32	Y	22	LEU	CA-CB	-7.69	1.41	1.53
50	q	68	LYS	CA-C	-7.65	1.42	1.52
50	q	67	SER	CA-C	-7.61	1.43	1.53
32	Y	16	THR	N-CA	-7.59	1.37	1.46
32	Y	20	ASN	CA-C	-7.55	1.42	1.52
56	w	20	U	C5-C6	7.51	1.49	1.34
45	l	43	LYS	C-O	-7.45	1.14	1.24
56	w	16	U	C5-C6	7.44	1.49	1.34
50	q	68	LYS	C-O	-7.42	1.15	1.24
50	q	71	SER	C-O	-7.41	1.14	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	w	16	U	N1-C2	7.38	1.53	1.38
35	b	18	GLN	CA-C	-7.36	1.43	1.53
43	j	54	SER	C-O	-7.35	1.14	1.24
37	d	72	ARG	CA-C	-7.33	1.42	1.52
54	u	13	VAL	N-CA	-7.29	1.37	1.46
37	d	69	ARG	N-CA	-7.27	1.37	1.46
32	Y	21	LEU	CA-C	-7.26	1.43	1.52
54	u	15	LEU	C-O	-7.23	1.15	1.24
43	j	59	LYS	CA-C	-7.19	1.43	1.52
50	q	67	SER	CA-CB	-7.15	1.45	1.54
32	Y	19	LEU	CA-CB	-7.10	1.41	1.53
43	j	58	ASN	CA-CB	-7.06	1.44	1.53
45	l	42	LYS	C-O	-7.06	1.14	1.23
8	A	2449	U	C5-C6	7.06	1.48	1.34
43	j	41	PRO	C-O	-7.04	1.14	1.24
54	u	15	LEU	N-CA	-7.02	1.38	1.46
43	j	58	ASN	CG-OD1	-7.01	1.10	1.23
37	d	73	ASN	CA-CB	-6.98	1.41	1.53
37	d	145	ARG	CA-C	-6.98	1.43	1.52
43	j	44	THR	CA-C	-6.95	1.43	1.52
37	d	70	GLN	CD-OE1	-6.91	1.10	1.23
8	A	2449	U	N1-C2	6.85	1.52	1.38
50	q	71	SER	N-CA	-6.83	1.38	1.46
45	l	42	LYS	N-CA	-6.82	1.37	1.45
50	q	70	LYS	CA-CB	-6.82	1.43	1.53
45	l	45	ASN	CG-ND2	-6.82	1.19	1.33
37	d	69	ARG	CA-C	-6.70	1.44	1.52
37	d	73	ASN	N-CA	-6.67	1.37	1.46
37	d	71	PHE	CA-CB	-6.66	1.42	1.53
43	j	59	LYS	C-O	-6.63	1.16	1.24
50	q	66	LEU	C-O	-6.61	1.15	1.23
43	j	41	PRO	CA-CB	-6.60	1.44	1.53
43	j	45	ARG	N-CA	-6.57	1.37	1.46
19	L	129	LYS	N-CA	-6.51	1.38	1.46
54	u	10	PRO	C-O	-6.51	1.16	1.24
43	j	44	THR	C-O	-6.50	1.16	1.24
34	a	89	U	O3'-P	6.46	1.70	1.61
45	l	42	LYS	CA-C	-6.37	1.44	1.53
32	Y	15	ASN	CG-ND2	-6.30	1.20	1.33
32	Y	17	GLU	CA-C	-6.23	1.45	1.52
8	A	887	U	C1'-N1	6.22	1.56	1.47
37	d	145	ARG	C-O	-6.19	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	j	60	ASP	CA-CB	-6.08	1.43	1.53
54	u	14	ALA	C-O	-6.01	1.17	1.24
56	w	20	U	C2-N3	6.00	1.49	1.37
37	d	148	ALA	C-O	-5.97	1.15	1.24
43	j	44	THR	CB-CG2	-5.92	1.33	1.52
15	H	123	ARG	CD-NE	-5.91	1.38	1.46
9	B	120	U	C1'-N1	5.89	1.57	1.48
45	l	45	ASN	N-CA	-5.89	1.39	1.46
56	w	16	U	C2-N3	5.83	1.49	1.37
32	Y	16	THR	C-O	-5.83	1.17	1.24
43	j	58	ASN	C-O	-5.78	1.15	1.23
54	u	15	LEU	CA-C	-5.77	1.45	1.52
43	j	54	SER	CA-CB	-5.72	1.43	1.53
43	j	41	PRO	N-CA	-5.69	1.40	1.47
45	l	41	PRO	CA-C	-5.65	1.44	1.52
43	j	58	ASN	CG-ND2	-5.65	1.21	1.33
45	l	45	ASN	C-O	-5.65	1.17	1.24
32	Y	16	THR	CA-CB	-5.64	1.44	1.53
35	b	17	HIS	CA-C	-5.64	1.45	1.52
43	j	58	ASN	CB-CG	-5.64	1.38	1.52
43	j	61	ALA	CA-CB	-5.58	1.45	1.53
43	j	45	ARG	CA-CB	-5.56	1.45	1.53
50	q	68	LYS	N-CA	-5.56	1.39	1.46
15	H	39	ALA	CA-C	-5.50	1.45	1.52
32	Y	16	THR	CB-CG2	-5.49	1.34	1.52
45	l	42	LYS	CA-CB	-5.46	1.45	1.53
8	A	2449	U	C2-N3	5.44	1.48	1.37
32	Y	17	GLU	N-CA	-5.44	1.39	1.46
15	H	123	ARG	CA-C	-5.41	1.46	1.52
32	Y	21	LEU	CA-CB	-5.39	1.44	1.53
43	j	41	PRO	CA-C	-5.39	1.44	1.52
37	d	146	GLU	CA-C	-5.38	1.45	1.52
32	Y	18	LEU	C-N	-5.37	1.26	1.33
37	d	70	GLN	CD-NE2	-5.32	1.22	1.33
37	d	68	GLU	C-N	-5.32	1.25	1.33
32	Y	15	ASN	CA-CB	-5.28	1.45	1.53
35	b	18	GLN	CA-CB	-5.26	1.44	1.53
15	H	123	ARG	C-N	-5.21	1.25	1.33
45	l	44	PRO	C-N	-5.20	1.26	1.33
32	Y	22	LEU	C-N	-5.19	1.27	1.33
32	Y	21	LEU	N-CA	-5.17	1.39	1.46
50	q	66	LEU	CA-CB	-5.17	1.46	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	u	12	ASP	CB-CG	-5.12	1.39	1.52
54	u	7	GLU	N-CA	-5.09	1.40	1.46
50	q	69	THR	CA-C	-5.08	1.46	1.52
45	l	44	PRO	N-CA	-5.05	1.41	1.47
43	j	43	PRO	CA-C	-5.04	1.46	1.52

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	89	U	O3'-P-O5'	36.78	159.17	104.00
25	R	51	VAL	CA-C-N	27.44	154.14	119.84
25	R	51	VAL	C-N-CA	27.44	154.14	119.84
45	l	45	ASN	N-CA-C	18.33	131.34	111.36
34	a	89	U	OP1-P-O3'	-17.47	55.59	108.00
19	L	130	GLY	CA-C-N	13.53	138.92	120.38
19	L	130	GLY	C-N-CA	13.53	138.92	120.38
34	a	89	U	P-O3'-C3'	13.33	140.19	120.20
35	b	16	GLY	N-CA-C	12.99	135.42	110.73
54	u	10	PRO	N-CA-C	12.29	130.62	113.53
25	R	51	VAL	C-N-CD	-11.87	76.34	125.00
43	j	40	ILE	CA-C-N	11.43	134.13	119.84
43	j	40	ILE	C-N-CA	11.43	134.13	119.84
32	Y	18	LEU	N-CA-C	-10.90	87.58	110.80
50	q	48	GLU	N-CA-C	10.43	122.23	111.07
45	l	43	LYS	CA-C-N	10.21	133.25	120.89
45	l	43	LYS	C-N-CA	10.21	133.25	120.89
45	l	46	SER	N-CA-C	9.44	130.91	110.80
37	d	70	GLN	N-CA-CB	9.23	126.09	110.49
58	y	136	ARG	CA-C-N	9.05	138.83	121.54
58	y	136	ARG	C-N-CA	9.05	138.83	121.54
19	L	130	GLY	CA-C-O	-8.79	105.27	120.57
43	j	41	PRO	CA-C-O	-8.37	105.37	120.60
54	u	9	GLU	N-CA-C	8.27	128.09	109.81
32	Y	18	LEU	N-CA-CB	8.09	124.16	110.49
32	Y	15	ASN	N-CA-C	-7.99	103.32	113.23
35	b	16	GLY	CA-C-N	7.90	136.63	121.54
35	b	16	GLY	C-N-CA	7.90	136.63	121.54
25	R	51	VAL	N-CA-C	-7.89	91.83	108.88
37	d	148	ALA	N-CA-C	-7.86	102.77	113.30
50	q	49	ASN	N-CA-C	-7.73	96.67	108.96
54	u	10	PRO	CA-C-O	-7.63	107.96	119.86
37	d	143	SER	N-CA-C	7.61	127.01	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	Y	17	GLU	CA-C-N	7.58	136.01	121.54
32	Y	17	GLU	C-N-CA	7.58	136.01	121.54
54	u	13	VAL	N-CA-C	-7.39	103.58	110.53
32	Y	19	LEU	CB-CA-C	-7.25	95.98	110.42
35	b	19	THR	N-CA-C	7.22	120.01	111.71
10	C	132	ARG	N-CA-C	-7.14	105.49	114.56
19	L	126	ARG	CG-CD-NE	-7.10	96.37	112.00
37	d	69	ARG	N-CA-C	-7.10	96.97	108.41
58	y	137	SER	N-CA-C	-7.03	95.84	110.80
32	Y	19	LEU	N-CA-CB	6.96	122.25	110.49
50	q	71	SER	N-CA-C	-6.79	102.47	113.19
54	u	7	GLU	N-CA-C	6.63	119.09	108.41
37	d	73	ASN	N-CA-C	-6.59	104.72	112.89
32	Y	14	LEU	N-CA-CB	6.58	120.80	110.46
32	Y	13	GLU	O-C-N	6.49	131.13	122.43
37	d	144	ILE	N-CA-C	6.43	117.18	110.62
32	Y	18	LEU	CA-C-N	6.39	133.75	121.54
32	Y	18	LEU	C-N-CA	6.39	133.75	121.54
37	d	146	GLU	CA-C-N	6.38	133.72	121.54
37	d	146	GLU	C-N-CA	6.38	133.72	121.54
19	L	129	LYS	CA-C-O	-6.28	113.85	120.63
43	j	60	ASP	N-CA-C	6.28	120.55	113.02
54	u	11	PHE	CA-C-N	6.23	133.43	121.54
54	u	11	PHE	C-N-CA	6.23	133.43	121.54
50	q	49	ASN	CA-C-N	-6.04	112.39	122.17
50	q	49	ASN	C-N-CA	-6.04	112.39	122.17
54	u	11	PHE	N-CA-CB	6.03	120.69	110.49
45	l	43	LYS	O-C-N	6.01	128.23	121.32
37	d	145	ARG	N-CA-CB	5.76	120.22	110.49
58	y	137	SER	N-CA-CB	5.73	120.17	110.49
25	R	52	PRO	N-CA-C	-5.63	100.86	112.47
55	v	6	VAL	N-CA-C	-5.61	108.38	113.71
37	d	69	ARG	NE-CZ-NH2	5.57	124.21	119.20
32	Y	19	LEU	N-CA-C	-5.55	98.97	110.80
37	d	69	ARG	CA-C-N	5.53	132.10	121.54
37	d	69	ARG	C-N-CA	5.53	132.10	121.54
32	Y	20	ASN	CB-CA-C	5.50	120.29	109.72
43	j	54	SER	N-CA-CB	-5.49	103.39	110.03
32	Y	19	LEU	CA-C-O	-5.42	112.76	120.51
37	d	70	GLN	CB-CA-C	-5.40	99.67	110.42
32	Y	14	LEU	CB-CG-CD1	-5.40	94.51	110.70
32	Y	19	LEU	CB-CG-CD2	-5.31	94.78	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	H	123	ARG	CB-CA-C	-5.25	102.28	110.37
32	Y	23	ARG	N-CA-CB	-5.24	102.26	109.91
34	a	89	U	OP2-P-O3'	-5.18	92.45	108.00
37	d	69	ARG	NE-CZ-NH1	-5.17	116.33	121.50
15	H	119	ASN	N-CA-C	-5.16	108.01	114.56
43	j	59	LYS	N-CA-C	5.14	116.88	111.28
25	R	55	ASP	N-CA-C	5.10	116.84	111.28
19	L	129	LYS	CA-CB-CG	-5.09	103.91	114.10
43	j	42	LEU	N-CA-CB	5.08	119.42	110.37
15	H	123	ARG	CG-CD-NE	-5.04	100.92	112.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	L	130	GLY	Mainchain
37	d	143	SER	Mainchain
58	y	136	ARG	Mainchain

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	0	444	0	461	11	0
2	1	409	0	440	15	0
3	2	377	0	418	8	0
4	3	504	0	574	16	0
5	4	302	0	340	8	0
6	5	647	0	336	4	0
7	6	522	0	521	27	0
8	A	62336	0	31365	1043	0
9	B	2570	0	1300	34	0
10	C	2082	0	2157	47	0
11	D	1565	0	1616	34	0
12	E	1552	0	1618	21	0
13	F	1410	0	1447	32	0
14	G	1323	0	1374	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	H	1111	0	1148	64	0
16	I	693	0	347	5	0
17	J	1129	0	1162	26	0
18	K	938	0	1012	32	0
19	L	1045	0	1116	33	0
20	M	1074	0	1157	45	0
21	N	960	0	1000	21	0
22	O	892	0	923	21	0
23	P	917	0	965	18	0
24	Q	947	0	1022	18	0
25	R	816	0	839	16	0
26	S	857	0	922	26	0
27	T	738	0	807	9	0
28	U	779	0	834	21	0
29	V	753	0	780	19	0
30	W	575	0	592	9	0
31	X	625	0	655	17	0
32	Y	509	0	543	11	0
33	Z	449	0	491	6	0
34	a	33050	0	16653	617	0
35	b	1704	0	1732	62	0
36	c	1624	0	1699	41	0
37	d	1643	0	1710	63	0
38	e	1141	0	1170	21	0
39	f	817	0	808	21	0
40	g	1181	0	1240	35	0
41	h	979	0	1034	17	0
42	i	1022	0	1070	41	0
43	j	786	0	828	44	0
44	k	869	0	878	23	0
45	l	955	0	1019	31	0
46	m	883	0	944	30	0
47	n	799	0	841	18	0
48	o	714	0	737	10	0
49	p	649	0	666	15	0
50	q	648	0	691	37	0
51	r	535	0	552	14	0
52	s	658	0	685	22	0
53	t	665	0	714	22	0
54	u	506	0	502	22	0
55	v	121	0	128	3	0
56	w	1631	0	837	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	x	147	0	75	1	0
58	y	1078	0	1134	36	0
59	0	1	0	0	0	0
59	A	269	0	0	0	0
59	B	7	0	0	0	0
59	C	3	0	0	0	0
59	D	1	0	0	0	0
59	M	1	0	0	1	0
59	O	1	0	0	0	0
59	P	1	0	0	0	0
59	W	1	0	0	0	0
59	a	95	0	0	0	0
59	m	1	0	0	0	0
59	n	1	0	0	0	0
59	w	4	0	0	0	0
59	y	1	0	0	0	0
60	4	1	0	0	0	0
60	6	1	0	0	0	0
61	A	1	0	0	0	0
61	V	1	0	0	0	0
All	All	147046	0	98629	2663	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 11.

All (2663) 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)
45:l:43:LYS:HB3	45:l:44:PRO:CD	1.53	1.39
45:l:43:LYS:CB	45:l:44:PRO:CD	1.97	1.38
19:L:130:GLY:O	19:L:130:GLY:CA	1.69	1.38
37:d:46:ARG:NH2	58:y:137:SER:O	1.60	1.32
34:a:89:U:O2'	34:a:90:C:C6	1.81	1.32
34:a:89:U:C2'	34:a:90:C:C5	2.21	1.24
50:q:18:LYS:CG	50:q:48:GLU:HA	1.69	1.21
19:L:130:GLY:O	19:L:131:ALA:N	1.73	1.19
37:d:46:ARG:CZ	58:y:137:SER:O	1.89	1.19
34:a:89:U:C2'	34:a:90:C:H5	1.53	1.19
45:l:43:LYS:CB	45:l:44:PRO:HD3	1.66	1.18
50:q:18:LYS:HG2	50:q:48:GLU:HA	1.24	1.14
45:l:43:LYS:HB2	45:l:44:PRO:HD2	1.16	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:q:18:LYS:HD3	50:q:48:GLU:HG3	1.14	1.08
15:H:42:LYS:O	15:H:46:PHE:CD2	2.07	1.08
37:d:72:ARG:NH1	37:d:76:LYS:HD2	1.68	1.08
35:b:65:LYS:HG2	35:b:89:PHE:CE2	1.90	1.06
45:l:43:LYS:CB	45:l:44:PRO:HD2	1.75	1.05
19:L:130:GLY:O	19:L:130:GLY:C	0.79	1.04
34:a:89:U:C1'	34:a:90:C:H5	1.71	1.03
34:a:89:U:HO2'	34:a:90:C:H6	1.06	0.97
34:a:89:U:O2'	34:a:90:C:C5	1.98	0.95
50:q:19:SER:HB3	50:q:70:LYS:NZ	1.81	0.94
34:a:89:U:O2	34:a:90:C:N4	1.99	0.94
8:A:2102:G:H1	8:A:2187:U:H3	1.15	0.94
50:q:18:LYS:HG3	50:q:48:GLU:HA	1.50	0.93
37:d:73:ASN:O	37:d:77:GLU:OE1	1.85	0.92
40:g:111:GLY:HA2	40:g:118:ARG:HD3	1.52	0.92
15:H:93:SER:HB2	15:H:123:ARG:NH1	1.84	0.92
35:b:65:LYS:CG	35:b:89:PHE:HE2	1.83	0.92
35:b:65:LYS:HG2	35:b:89:PHE:HE2	1.33	0.92
34:a:89:U:H2'	34:a:90:C:C5	2.05	0.91
8:A:1105:U:H2'	8:A:1106:G:H8	1.34	0.91
46:m:105:ALA:O	46:m:109:LYS:HB2	1.71	0.91
45:l:42:LYS:HG3	45:l:43:LYS:HG2	1.53	0.91
15:H:42:LYS:O	15:H:46:PHE:HD2	1.50	0.90
37:d:121:ALA:O	37:d:144:ILE:O	1.89	0.89
34:a:89:U:H1'	34:a:90:C:C5	2.09	0.88
8:A:585:G:N7	24:Q:5:ARG:NH1	2.21	0.88
50:q:18:LYS:HG3	50:q:48:GLU:O	1.74	0.88
56:w:5:G:N2	56:w:68:C:O2	2.08	0.86
34:a:79:G:N2	34:a:90:C:O2	2.09	0.86
34:a:89:U:C1'	34:a:90:C:C5	2.52	0.85
8:A:285:G:H1	8:A:355:U:H3	1.17	0.85
37:d:72:ARG:NH1	37:d:76:LYS:CD	2.40	0.85
8:A:1936:A:H2	8:A:1943:U:H3	1.21	0.85
34:a:664:G:H22	34:a:741:G:H1	1.21	0.84
8:A:2105:U:H2'	8:A:2106:U:H5	1.44	0.83
15:H:78:VAL:HG21	15:H:103:VAL:HG23	1.59	0.82
34:a:79:G:N1	34:a:90:C:N3	2.26	0.82
42:i:98:ARG:HG2	42:i:103:VAL:HG11	1.60	0.82
8:A:1056:G:H21	8:A:1103:A:H62	1.25	0.82
37:d:72:ARG:HH11	37:d:76:LYS:HD2	1.43	0.82
34:a:76:G:H1	34:a:93:U:H3	0.85	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:284:U:H3	8:A:356:G:H1	1.28	0.81
45:l:43:LYS:HB3	45:l:44:PRO:HD3	0.82	0.81
8:A:1171:G:H22	8:A:1177:G:H1	1.26	0.81
36:c:39:ARG:NH1	36:c:54:ILE:O	2.14	0.81
34:a:673:A:H2'	34:a:674:G:C8	2.15	0.81
34:a:89:U:C2'	34:a:90:C:C6	2.57	0.80
34:a:677:U:H3	34:a:713:G:H22	1.29	0.80
8:A:1047:G:N2	8:A:1110:G:O2'	2.14	0.80
14:G:23:ILE:HD11	14:G:42:VAL:HG11	1.62	0.79
8:A:545:U:O2	8:A:548:G:O6	2.00	0.79
56:w:52:G:N2	56:w:62:C:O2	2.12	0.78
17:J:125:TYR:HH	17:J:132:HIS:HE2	1.30	0.78
50:q:18:LYS:CG	50:q:48:GLU:CA	2.58	0.78
50:q:19:SER:HB3	50:q:70:LYS:HZ2	1.49	0.78
34:a:1086:U:H3	34:a:1099:G:H22	1.29	0.77
34:a:76:G:N2	34:a:93:U:O2	2.16	0.77
37:d:147:LYS:HG2	37:d:147:LYS:O	1.84	0.77
8:A:1799:G:OP2	10:C:269:ARG:NH2	2.18	0.77
34:a:718:A:H5'	44:k:118:ASN:HB2	1.64	0.77
8:A:1059:G:H22	8:A:1080:A:H1'	1.50	0.77
8:A:84:A:H62	8:A:101:A:H2	1.32	0.77
50:q:18:LYS:CD	50:q:48:GLU:HG3	2.08	0.76
8:A:2305:U:H5''	13:F:130:GLY:HA3	1.64	0.76
10:C:66:PHE:HZ	10:C:86:ARG:HH12	1.34	0.76
34:a:1305:G:N2	34:a:1332:A:OP2	2.18	0.76
3:2:39:ARG:NH2	8:A:468:G:N7	2.33	0.76
15:H:50:ARG:HG2	15:H:51:ARG:HG3	1.66	0.76
8:A:475:C:O2	8:A:479:A:N6	2.19	0.76
2:1:7:LYS:HE2	4:3:33:THR:HG21	1.67	0.75
8:A:880:G:N2	8:A:897:C:O2	2.14	0.75
8:A:1076:C:H1'	16:I:90:GLY:HA2	1.67	0.75
8:A:2123:G:H1	8:A:2170:A:H5'	1.51	0.75
8:A:1802:A:H2'	8:A:1803:A:C8	2.22	0.75
8:A:880:G:N1	8:A:897:C:N3	2.28	0.75
35:b:65:LYS:CG	35:b:89:PHE:CE2	2.64	0.75
8:A:2558:C:OP1	58:y:40:ARG:NH1	2.19	0.75
34:a:147:G:H2'	34:a:148:G:C8	2.21	0.75
34:a:544:G:OP1	37:d:55:ARG:NH2	2.18	0.74
50:q:19:SER:HB3	50:q:70:LYS:HZ1	1.51	0.74
37:d:99:ASN:OD1	37:d:110:ARG:NH2	2.19	0.74
54:u:30:GLU:OE2	54:u:34:ARG:NH2	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1060:U:H4'	8:A:1062:G:H5'	1.70	0.74
10:C:106:PRO:HD2	10:C:109:LEU:HD22	1.67	0.74
34:a:529:G:O6	45:l:45:ASN:O	2.05	0.74
8:A:1434:A:H2'	8:A:1435:G:C8	2.22	0.74
18:K:121:GLU:HG2	18:K:122:VAL:HG23	1.70	0.74
34:a:946:A:H2'	34:a:947:G:C8	2.23	0.74
35:b:10:LYS:HB2	35:b:14:HIS:CE1	2.22	0.74
36:c:76:ILE:HA	36:c:83:VAL:HG13	1.70	0.74
8:A:270:A:N1	8:A:369:U:O2'	2.21	0.74
53:t:34:VAL:HG21	53:t:53:MET:HG2	1.69	0.73
20:M:69:PRO:O	20:M:93:VAL:O	2.06	0.73
8:A:1176:U:H2'	8:A:1177:G:C8	2.24	0.73
36:c:109:GLU:HB2	36:c:143:LEU:HD22	1.70	0.73
2:l:7:LYS:CE	4:3:33:THR:HG21	2.19	0.72
35:b:119:GLN:HA	35:b:123:GLY:HA3	1.70	0.72
19:L:130:GLY:O	19:L:130:GLY:HA2	1.87	0.72
36:c:34:SER:HB3	36:c:58:ARG:HH12	1.55	0.72
40:g:145:GLU:HA	40:g:148:LYS:HB2	1.71	0.72
52:s:35:ARG:NH2	52:s:74:ALA:O	2.23	0.72
41:h:49:LYS:HE3	41:h:59:GLU:HG2	1.72	0.72
56:w:52:G:N1	56:w:62:C:N3	2.28	0.71
1:0:53:VAL:HG23	1:0:54:ILE:HG12	1.72	0.71
7:6:42:PRO:HB2	7:6:47:LYS:HB3	1.73	0.71
8:A:2278:A:OP1	20:M:10:ARG:NH2	2.23	0.71
15:H:14:SER:HB2	15:H:17:ASP:HB2	1.71	0.71
45:l:2:THR:HG22	45:l:5:GLN:H	1.55	0.71
8:A:1478:G:H1	8:A:1513:U:H3	1.38	0.71
44:k:59:PRO:HD3	44:k:90:PRO:HB2	1.71	0.71
21:N:56:LYS:NZ	21:N:90:ARG:O	2.24	0.71
18:K:98:ARG:NH2	34:a:340:U:OP2	2.23	0.71
8:A:2584:U:H3'	8:A:2585:U:H5''	1.72	0.71
8:A:1250:G:H5''	24:Q:5:ARG:HD3	1.73	0.70
43:j:30:LYS:HE3	43:j:36:VAL:HB	1.71	0.70
50:q:24:ILE:HD11	50:q:60:ILE:HD11	1.72	0.70
8:A:499:U:H5''	28:U:42:LYS:HE2	1.72	0.70
8:A:1028:A:H2'	8:A:1029:A:C8	2.27	0.70
8:A:652:U:OP1	8:A:654:A:N6	2.24	0.70
8:A:1056:G:N2	8:A:1103:A:H62	1.90	0.70
8:A:2847:U:H2'	8:A:2848:G:O4'	1.92	0.70
15:H:48:GLU:HA	15:H:52:ALA:HB2	1.72	0.70
34:a:507:C:OP1	58:y:134:LYS:NZ	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:q:18:LYS:HG3	50:q:48:GLU:CA	2.21	0.69
2:1:7:LYS:NZ	4:3:33:THR:HG21	2.07	0.69
8:A:568:U:H1'	8:A:2030:6MZ:H9C1	1.75	0.69
43:j:41:PRO:O	43:j:71:LEU:O	2.10	0.69
22:O:39:VAL:HB	22:O:49:VAL:HG22	1.72	0.69
34:a:1356:G:H2'	34:a:1357:A:C8	2.28	0.69
8:A:1817:G:OP1	10:C:86:ARG:NH2	2.24	0.69
26:S:24:ILE:HD13	26:S:36:LEU:HD11	1.75	0.69
35:b:125:PHE:O	35:b:130:LYS:NZ	2.26	0.69
8:A:704:G:H1'	8:A:727:A:H61	1.57	0.69
8:A:2635:A:O2'	11:D:81:GLU:OE1	2.11	0.69
50:q:51:GLU:O	50:q:80:LYS:NZ	2.26	0.69
9:B:51:G:OP1	22:O:63:LYS:NZ	2.20	0.69
8:A:1454:C:N4	21:N:73:ASN:OD1	2.26	0.69
32:Y:9:LYS:O	32:Y:60:LYS:NZ	2.26	0.69
34:a:1009:U:O2	34:a:1020:G:N2	2.25	0.69
34:a:1026:G:O6	34:a:1035:A:N6	2.25	0.69
8:A:2638:G:H1'	8:A:2778:A:H61	1.58	0.68
15:H:104:THR:HG23	15:H:105:ALA:H	1.58	0.68
5:4:23:ILE:HD13	8:A:1032:A:H1'	1.75	0.68
8:A:301:G:OP2	28:U:81:ARG:NH1	2.26	0.68
34:a:85:U:H5'	34:a:86:G:H5'	1.74	0.68
8:A:1715:G:HO2'	8:A:1716:U:H6	1.38	0.68
11:D:1:MET:HG2	11:D:205:PRO:HG2	1.75	0.68
15:H:97:ARG:HA	15:H:112:LYS:HD2	1.75	0.68
9:B:1:U:H2'	9:B:2:G:H8	1.59	0.68
8:A:1063:G:N2	16:I:132:ALA:O	2.27	0.68
46:m:22:TYR:HB3	46:m:65:GLU:HG3	1.75	0.68
8:A:1172:C:N3	8:A:1176:U:O4	2.26	0.68
34:a:1347:G:O6	42:i:11:ARG:NH2	2.26	0.68
34:a:1377:A:OP1	40:g:91:ARG:NH2	2.27	0.68
7:6:51:VAL:HG13	7:6:53:THR:H	1.58	0.68
29:V:58:SER:O	29:V:73:LYS:NZ	2.26	0.68
49:p:46:LYS:O	49:p:48:GLU:N	2.27	0.68
8:A:639:U:H2'	8:A:640:C:C6	2.29	0.68
8:A:856:G:H2'	8:A:857:G:C8	2.28	0.68
7:6:45:THR:HG22	7:6:46:GLY:H	1.58	0.68
8:A:319:G:H1	8:A:323:C:H5	1.41	0.68
35:b:14:HIS:HB2	35:b:202:ASN:HB3	1.74	0.68
8:A:1022:G:N2	8:A:1023:U:O4	2.22	0.67
8:A:848:C:H2'	8:A:849:A:H8	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1391:U:H2'	34:a:1392:G:C8	2.28	0.67
51:r:71:ASP:OD2	54:u:3:ILE:N	2.27	0.67
11:D:9:VAL:O	23:P:4:ILE:HD11	1.94	0.67
14:G:1:SER:OG	14:G:2:ARG:N	2.26	0.67
1:0:12:ARG:NH1	8:A:1263:U:OP1	2.28	0.67
8:A:1434:A:H2'	8:A:1435:G:H8	1.58	0.67
11:D:5:VAL:H	11:D:32:ASN:HD21	1.42	0.67
14:G:23:ILE:HD13	14:G:71:LEU:HD21	1.76	0.67
15:H:42:LYS:HG2	15:H:46:PHE:CE2	2.30	0.67
6:5:48:ALA:HB1	6:5:88:HIS:H	1.60	0.67
8:A:1843:C:O2'	10:C:253:GLY:O	2.11	0.67
25:R:73:LYS:NZ	25:R:86:GLN:OE1	2.28	0.67
8:A:138:U:O2'	8:A:141:G:O6	2.12	0.67
8:A:994:C:OP1	24:Q:52:ARG:NH2	2.28	0.67
8:A:1059:G:N2	8:A:1080:A:H1'	2.10	0.67
34:a:501:C:OP1	45:l:113:ARG:NH2	2.28	0.67
8:A:1779:U:H5	8:A:1784:A:N7	1.93	0.66
34:a:1005:A:N6	34:a:1024:G:O2'	2.29	0.66
8:A:704:G:H1'	8:A:727:A:N6	2.11	0.66
8:A:2308:G:O6	8:A:2311:A:N6	2.19	0.66
20:M:69:PRO:HA	20:M:94:ALA:CA	2.24	0.66
34:a:1106:G:H5''	36:c:171:ARG:HG2	1.78	0.66
50:q:49:ASN:OD1	50:q:49:ASN:N	2.25	0.66
34:a:966:2MG:HM21	42:i:128:LYS:HD2	1.77	0.66
1:0:14:MET:HE3	8:A:2045:C:H5''	1.77	0.66
36:c:92:ASP:OD1	36:c:93:ILE:N	2.28	0.66
20:M:69:PRO:HA	20:M:94:ALA:N	2.10	0.66
9:B:37:C:O2	22:O:100:HIS:NE2	2.29	0.66
8:A:2271:G:H5'	30:W:16:ARG:HD3	1.77	0.66
39:f:45:ARG:O	39:f:56:LYS:HA	1.95	0.66
8:A:1181:U:H2'	8:A:1182:G:C8	2.31	0.66
35:b:25:LYS:NZ	35:b:193:ASP:OD2	2.27	0.66
40:g:92:PRO:HA	40:g:95:ARG:HD2	1.78	0.66
53:t:2:ASN:HB2	53:t:7:LYS:HG2	1.76	0.66
8:A:310:A:O2'	8:A:311:A:O5'	2.13	0.65
34:a:521:G:N7	45:l:49:ARG:NH1	2.43	0.65
43:j:33:GLY:HA3	43:j:80:THR:HG21	1.78	0.65
8:A:2391:G:O2'	8:A:2429:G:N2	2.29	0.65
9:B:48:U:H4'	22:O:100:HIS:HD2	1.61	0.65
34:a:88:U:O5'	34:a:88:U:H6	1.79	0.65
8:A:1799:G:OP1	10:C:257:ARG:NH1	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2405:G:O2'	8:A:2411:A:N6	2.29	0.65
28:U:95:PHE:O	28:U:99:SER:HA	1.96	0.65
34:a:781:A:OP1	44:k:124:LYS:NZ	2.28	0.65
34:a:933:G:O6	40:g:2:ARG:NH2	2.30	0.65
45:l:3:VAL:HG23	50:q:33:TYR:HB3	1.78	0.65
34:a:1040:U:H2'	34:a:1041:G:H8	1.61	0.65
8:A:340:A:O2'	12:E:162:ARG:NH1	2.29	0.65
50:q:18:LYS:HG2	50:q:48:GLU:CA	2.15	0.65
56:w:18:G:O2'	56:w:57:G:N2	2.27	0.65
8:A:1366:A:OP1	31:X:1:SER:OG	2.15	0.65
23:P:90:ALA:HB3	23:P:110:LYS:HG3	1.78	0.65
33:Z:8:GLN:NE2	33:Z:10:ARG:O	2.25	0.65
34:a:713:G:H2'	34:a:714:G:C8	2.32	0.65
35:b:10:LYS:HG3	35:b:42:LEU:HD13	1.79	0.65
50:q:18:LYS:HD3	50:q:48:GLU:CG	2.08	0.65
10:C:132:ARG:O	10:C:166:ARG:NH2	2.30	0.65
34:a:28:A:O2'	34:a:296:U:OP1	2.12	0.65
34:a:264:C:O2'	50:q:65:PRO:O	2.14	0.65
8:A:955:PSU:OP1	20:M:86:LYS:NZ	2.26	0.65
36:c:78:LYS:HB3	36:c:79:LYS:HD3	1.77	0.65
50:q:18:LYS:HG3	50:q:48:GLU:C	2.21	0.65
8:A:886:A:H1'	8:A:887:U:H2'	1.79	0.65
8:A:887:U:OP2	8:A:890:C:N4	2.30	0.65
8:A:1057:A:H8	8:A:1060:U:H3	1.43	0.64
34:a:1119:C:OP1	42:i:84:ARG:NH1	2.30	0.64
8:A:2233:U:H2'	8:A:2234:G:C8	2.32	0.64
8:A:2452:C:H4'	58:y:32:LYS:HG3	1.79	0.64
5:4:4:ARG:HH22	8:A:2477:U:H2'	1.63	0.64
8:A:887:U:H5''	8:A:890:C:H42	1.63	0.64
8:A:1858:A:N6	8:A:1884:G:O2'	2.29	0.64
34:a:769:G:H4'	34:a:1513:A:H4'	1.79	0.64
2:1:21:THR:HG21	8:A:2419:U:H4'	1.79	0.64
8:A:881:G:O6	8:A:895:U:O2	2.15	0.64
9:B:27:C:OP1	22:O:34:HIS:NE2	2.27	0.64
34:a:1317:C:O2	52:s:36:ARG:NH2	2.31	0.64
40:g:73:GLU:HG2	40:g:90:VAL:HG22	1.78	0.64
40:g:77:ARG:O	40:g:83:THR:HA	1.97	0.64
8:A:458:G:O2'	8:A:459:U:OP2	2.15	0.64
8:A:483:A:H5''	28:U:46:LYS:HD2	1.80	0.64
8:A:1102:C:H3'	8:A:1103:A:H8	1.63	0.64
8:A:2032:G:O2'	11:D:150:GLN:NE2	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2327:A:H2'	8:A:2328:A:C8	2.33	0.64
13:F:159:ALA:HB1	13:F:164:GLU:HG3	1.80	0.64
48:o:55:LEU:HA	48:o:58:MET:HE2	1.79	0.64
54:u:9:GLU:CB	54:u:10:PRO:HD3	2.27	0.64
56:w:18:G:O6	56:w:55:PSU:H1'	1.98	0.64
7:6:18:CYS:HB2	7:6:40:CYS:CB	2.28	0.64
8:A:2328:A:H2'	8:A:2329:U:C6	2.32	0.64
44:k:87:GLY:O	44:k:92:ARG:NH1	2.31	0.64
8:A:1176:U:H2'	8:A:1177:G:H8	1.63	0.64
8:A:2638:G:H1'	8:A:2778:A:N6	2.13	0.64
15:H:71:LYS:HA	15:H:74:ALA:HB2	1.77	0.64
18:K:43:ILE:HD12	18:K:56:ASP:HB2	1.80	0.64
34:a:94:G:H4'	34:a:95:C:H5'	1.80	0.64
8:A:1105:U:H2'	8:A:1106:G:C8	2.25	0.63
8:A:1796:U:H2'	8:A:1797:G:C8	2.33	0.63
8:A:2329:U:H2'	8:A:2330:G:C8	2.33	0.63
10:C:79:ARG:NH1	10:C:81:GLU:OE2	2.31	0.63
25:R:6:GLN:HB3	25:R:11:GLN:HG2	1.79	0.63
34:a:736:C:OP1	51:r:60:ARG:NH1	2.30	0.63
43:j:35:GLN:NE2	43:j:78:GLU:O	2.30	0.63
8:A:639:U:H2'	8:A:640:C:H6	1.63	0.63
8:A:2183:A:H2'	8:A:2184:A:H8	1.62	0.63
15:H:38:PRO:O	15:H:40:THR:HG23	1.97	0.63
15:H:113:SER:O	15:H:116:ARG:NH2	2.26	0.63
19:L:20:GLY:HA2	19:L:28:GLY:HA2	1.78	0.63
56:w:5:G:N1	56:w:68:C:N3	2.34	0.63
8:A:547:A:O2'	8:A:548:G:N7	2.31	0.63
8:A:2298:A:OP1	13:F:70:ARG:NH2	2.30	0.63
34:a:89:U:O2'	34:a:90:C:H6	1.56	0.63
8:A:275:C:C4	8:A:276:U:H1'	2.33	0.63
8:A:1469:A:H2'	8:A:1470:A:C8	2.33	0.63
15:H:84:ALA:HB2	15:H:90:LEU:HD12	1.81	0.63
34:a:1323:G:H2'	34:a:1324:A:C8	2.34	0.63
35:b:116:LEU:HB3	35:b:140:LEU:HD12	1.81	0.63
42:i:90:ASP:OD1	42:i:92:SER:OG	2.16	0.63
34:a:143:A:H5''	34:a:144:G:H5''	1.81	0.63
8:A:2820:A:O2'	8:A:2821:A:OP1	2.11	0.63
18:K:99:ILE:HD13	18:K:115:ILE:HG23	1.80	0.63
19:L:96:LYS:HG3	19:L:101:ILE:HD11	1.81	0.63
19:L:110:VAL:HB	19:L:127:VAL:HG13	1.79	0.63
8:A:880:G:H2'	8:A:881:G:H8	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:51:ARG:HD2	15:H:54:LEU:HD23	1.81	0.63
27:T:48:GLN:HE21	27:T:55:VAL:H	1.46	0.63
8:A:1141:U:H4'	8:A:1142:A:O4'	1.99	0.63
8:A:1900:A:H1'	8:A:1970:A:H2'	1.81	0.63
8:A:2110:G:N2	8:A:2118:U:O2'	2.28	0.63
22:O:34:HIS:HA	22:O:53:THR:OG1	1.99	0.63
34:a:1028:C:N3	34:a:1034:G:N2	2.47	0.63
34:a:1320:C:O2	52:s:35:ARG:NH1	2.32	0.63
34:a:1218:C:H2'	34:a:1219:A:C8	2.34	0.62
35:b:119:GLN:OE1	35:b:136:ARG:NH2	2.32	0.62
8:A:2728:U:H2'	8:A:2729:G:C8	2.34	0.62
42:i:46:VAL:HG13	42:i:79:ARG:HE	1.63	0.62
8:A:1171:G:N2	8:A:1177:G:H1	1.96	0.62
19:L:80:SER:O	19:L:84:LYS:NZ	2.33	0.62
41:h:10:LEU:HD22	41:h:74:ILE:HD11	1.81	0.62
56:w:23:A:H2'	56:w:24:G:C8	2.34	0.62
4:3:34:LYS:HE2	8:A:2390:U:OP2	2.00	0.62
35:b:60:ALA:HB2	35:b:220:VAL:HG13	1.79	0.62
39:f:44:ARG:HG2	39:f:56:LYS:HG2	1.81	0.62
34:a:83:C:O2'	34:a:85:U:OP2	2.17	0.62
44:k:92:ARG:NH2	44:k:111:ASP:OD1	2.24	0.62
8:A:2167:U:O4	8:A:2171:A:N6	2.32	0.62
15:H:77:THR:OG1	15:H:143:ILE:O	2.15	0.62
34:a:67:C:H2'	34:a:68:G:C8	2.35	0.62
8:A:1059:G:H5'	8:A:1060:U:C5	2.35	0.62
8:A:2116:G:N2	8:A:2163:A:OP2	2.23	0.62
8:A:2720:U:OP1	23:P:52:ARG:NH2	2.32	0.62
34:a:216:U:H2'	34:a:217:C:C6	2.35	0.62
34:a:261:U:OP2	53:t:73:ARG:NH2	2.32	0.62
43:j:47:GLU:OE2	47:n:76:LYS:NZ	2.32	0.62
34:a:458:U:H2'	34:a:459:A:C8	2.35	0.62
34:a:499:A:H61	34:a:547:A:H5''	1.63	0.62
38:e:37:VAL:HG11	38:e:113:VAL:HG22	1.80	0.62
42:i:83:THR:HG23	42:i:97:LEU:HD13	1.80	0.62
8:A:743:A:O2'	8:A:1659:G:OP1	2.18	0.62
8:A:2291:U:H2'	8:A:2292:U:C6	2.35	0.62
8:A:2845:U:H5''	23:P:51:ASN:O	2.00	0.62
34:a:1071:C:H2'	34:a:1072:G:H8	1.65	0.62
8:A:284:U:O2	8:A:356:G:N2	2.29	0.62
8:A:974:G:H8	8:A:990:A:H62	1.46	0.62
8:A:2183:A:H2'	8:A:2184:A:C8	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:O:31:THR:O	22:O:102:ARG:NH1	2.21	0.62
8:A:555:G:O2'	8:A:556:A:H8	1.83	0.61
34:a:958:A:C4	52:s:54:ARG:HD3	2.35	0.61
37:d:104:MET:HE1	37:d:142:VAL:HB	1.81	0.61
53:t:73:ARG:O	53:t:77:ASN:ND2	2.33	0.61
5:4:2:LYS:HE3	5:4:4:ARG:NH2	2.15	0.61
8:A:1794:A:H2'	8:A:1795:C:C6	2.35	0.61
8:A:2391:G:H2'	8:A:2424:C:H41	1.64	0.61
17:J:23:LYS:NZ	17:J:142:ILE:OXT	2.32	0.61
38:e:12:GLU:HG2	38:e:38:VAL:HG12	1.82	0.61
8:A:1796:U:H2'	8:A:1797:G:H8	1.64	0.61
53:t:14:GLU:OE2	53:t:17:ARG:NH2	2.32	0.61
53:t:24:ARG:O	53:t:28:ARG:HG2	1.99	0.61
8:A:704:G:H2'	8:A:726:G:H22	1.64	0.61
22:O:99:TYR:OH	22:O:111:ARG:NH2	2.33	0.61
34:a:41:G:H2'	34:a:42:G:C8	2.35	0.61
48:o:25:GLU:OE2	48:o:76:ARG:NH1	2.33	0.61
34:a:337:G:H2'	34:a:338:A:C8	2.35	0.61
37:d:72:ARG:HH12	37:d:76:LYS:CD	2.11	0.61
8:A:715:A:OP2	48:o:88:ARG:NH2	2.30	0.61
15:H:12:LEU:HD12	15:H:19:VAL:HG11	1.81	0.61
34:a:1147:C:HO2'	42:i:6:TYR:HH	1.47	0.61
42:i:83:THR:HG22	42:i:87:MET:HE2	1.82	0.61
35:b:18:GLN:HA	35:b:37:VAL:HA	1.81	0.61
8:A:2689:U:OP1	8:A:2719:G:N1	2.24	0.61
34:a:333:U:P	53:t:2:ASN:HD21	2.23	0.61
34:a:492:C:H2'	34:a:493:A:C8	2.36	0.61
34:a:1060:U:C5	36:c:1:GLY:HA3	2.35	0.61
43:j:8:ILE:HB	43:j:74:VAL:HG22	1.80	0.61
45:l:55:ARG:NH2	45:l:59:GLY:O	2.33	0.61
56:w:74:C:H3'	58:y:78:ARG:HH12	1.65	0.61
8:A:1509:A:H2'	8:A:1510:G:C8	2.36	0.61
8:A:2273:A:H2'	8:A:2274:A:C8	2.36	0.61
8:A:2848:G:H2'	8:A:2867:G:H22	1.64	0.61
30:W:13:GLU:O	30:W:15:LYS:NZ	2.34	0.61
2:1:7:LYS:NZ	4:3:33:THR:CG2	2.64	0.61
7:6:43:PHE:HB2	7:6:47:LYS:HE3	1.83	0.61
8:A:2637:U:H2'	8:A:2638:G:O4'	1.99	0.61
10:C:164:VAL:HG21	10:C:180:MET:HE1	1.83	0.61
20:M:66:ARG:NH1	20:M:104:GLU:OE2	2.34	0.61
34:a:344:A:H5''	34:a:345:C:H5	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:603:U:H5	34:a:635:A:N1	1.98	0.61
34:a:1028:C:H1'	34:a:1033:G:H22	1.65	0.61
29:V:4:ILE:HG12	29:V:50:MET:HE1	1.81	0.60
36:c:122:GLN:HG2	36:c:125:ARG:HH21	1.65	0.60
8:A:2638:G:HO2'	8:A:2639:A:H8	1.46	0.60
15:H:82:SER:HB2	15:H:94:ILE:HD11	1.83	0.60
34:a:662:U:H2'	34:a:663:A:C8	2.36	0.60
34:a:1152:A:OP1	43:j:70:HIS:ND1	2.26	0.60
40:g:128:GLU:HG3	40:g:130:LYS:HG2	1.84	0.60
8:A:581:C:H2'	8:A:582:A:C8	2.36	0.60
8:A:881:G:O6	8:A:895:U:C2	2.54	0.60
8:A:2788:C:H2'	8:A:2789:C:C6	2.36	0.60
8:A:2848:G:H2'	8:A:2867:G:N2	2.17	0.60
24:Q:71:ASN:HB3	24:Q:109:VAL:HG11	1.83	0.60
25:R:51:VAL:O	25:R:51:VAL:HG23	2.01	0.60
34:a:714:G:H2'	34:a:715:A:C8	2.36	0.60
34:a:1071:C:H2'	34:a:1072:G:C8	2.37	0.60
6:5:81:LEU:HA	8:A:1107:G:H5''	1.83	0.60
34:a:1040:U:H2'	34:a:1041:G:C8	2.37	0.60
8:A:848:C:H2'	8:A:849:A:C8	2.37	0.60
8:A:1386:C:H2'	8:A:1387:A:C8	2.36	0.60
8:A:1405:U:H2'	8:A:1406:U:C6	2.36	0.60
8:A:2032:G:N2	11:D:151:THR:OG1	2.35	0.60
13:F:46:LYS:NZ	13:F:83:PRO:HG2	2.17	0.60
18:K:7:MET:HE1	18:K:44:LYS:HG3	1.82	0.60
24:Q:99:VAL:O	24:Q:102:LYS:NZ	2.35	0.60
31:X:5:GLN:O	31:X:73:ARG:NH2	2.34	0.60
34:a:1004:A:H61	34:a:1025:U:H4'	1.67	0.60
40:g:26:VAL:HG22	40:g:42:VAL:HG21	1.84	0.60
8:A:1068:G:H22	16:I:23:VAL:HA	1.66	0.60
8:A:2000:C:OP1	21:N:5:LYS:NZ	2.32	0.60
8:A:2676:C:OP2	18:K:31:ARG:NH2	2.34	0.60
9:B:5:U:OP1	9:B:61:G:O2'	2.16	0.60
34:a:539:A:H2'	34:a:540:G:C8	2.37	0.60
34:a:1143:G:H2'	34:a:1144:G:H8	1.65	0.60
34:a:1432:G:H1'	34:a:1468:A:H62	1.67	0.60
53:t:47:GLN:O	53:t:51:ASN:ND2	2.35	0.60
8:A:84:A:N1	8:A:98:G:O2'	2.28	0.60
30:W:55:LEU:HD12	30:W:76:ILE:HD12	1.84	0.60
34:a:107:G:O6	53:t:9:ARG:HD3	2.02	0.60
4:3:11:LYS:NZ	8:A:249:C:O2	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:881:G:H2'	8:A:882:G:H8	1.67	0.60
8:A:2728:U:H2'	8:A:2729:G:H8	1.66	0.60
9:B:8:C:O3'	22:O:25:ARG:NH1	2.34	0.60
15:H:93:SER:HB2	15:H:123:ARG:HH11	1.67	0.60
35:b:124:THR:HA	35:b:127:LYS:HE2	1.83	0.60
8:A:481:G:O2'	8:A:506:G:N2	2.34	0.59
8:A:1857:G:O2'	8:A:1885:A:N6	2.35	0.59
37:d:68:GLU:OE2	37:d:203:TYR:OH	2.19	0.59
8:A:2125:G:N2	8:A:2172:U:OP1	2.35	0.59
11:D:45:TYR:OH	11:D:81:GLU:OE2	2.18	0.59
13:F:46:LYS:HZ3	13:F:83:PRO:HG2	1.67	0.59
20:M:56:ALA:HB2	20:M:119:LEU:HD12	1.83	0.59
34:a:1003:G:O2'	34:a:1004:A:OP1	2.19	0.59
52:s:27:LYS:HG3	52:s:28:LYS:HG3	1.83	0.59
8:A:155:A:H2'	8:A:156:A:C8	2.37	0.59
8:A:1746:A:H2'	8:A:1747:U:C6	2.36	0.59
18:K:14:SER:HA	18:K:51:LYS:HE2	1.83	0.59
34:a:31:G:O2'	34:a:48:C:N4	2.34	0.59
34:a:459:A:H2'	34:a:460:A:C8	2.38	0.59
3:2:29:GLN:NE2	8:A:210:C:OP1	2.30	0.59
8:A:1028:A:H61	8:A:1125:G:H2'	1.67	0.59
8:A:1028:A:N6	8:A:1125:G:H2'	2.17	0.59
8:A:2178:C:O2'	8:A:2180:U:O4	2.20	0.59
8:A:2591:C:H2'	8:A:2592:G:C8	2.37	0.59
15:H:116:ARG:HB2	15:H:131:SER:HB3	1.84	0.59
34:a:1347:G:HO2'	34:a:1348:U:P	2.24	0.59
9:B:1:U:H2'	9:B:2:G:C8	2.38	0.59
18:K:38:ILE:HD11	18:K:112:PHE:HZ	1.68	0.59
34:a:1062:U:H2'	34:a:1063:C:C6	2.38	0.59
42:i:57:VAL:HG23	42:i:58:GLU:H	1.68	0.59
8:A:172:A:H2'	8:A:173:A:C8	2.37	0.59
8:A:191:A:H2'	8:A:192:C:C6	2.37	0.59
14:G:94:ARG:HG2	14:G:105:SER:HB3	1.85	0.59
20:M:82:MET:O	59:M:201:MG:MG	1.44	0.59
33:Z:44:ARG:NH1	33:Z:58:GLU:OE2	2.28	0.59
34:a:9:G:H5'	38:e:107:GLY:HA3	1.84	0.59
34:a:41:G:H2'	34:a:42:G:H8	1.68	0.59
8:A:64:A:H2'	8:A:65:U:C6	2.37	0.59
8:A:1108:U:H2'	8:A:1109:C:C6	2.38	0.59
8:A:1497:U:H5''	8:A:1498:C:H5	1.68	0.59
34:a:17:U:H2'	34:a:18:C:C6	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1130:A:H2'	34:a:1131:G:H8	1.67	0.59
35:b:101:THR:HG23	35:b:174:GLU:HG3	1.83	0.59
8:A:281:C:H2'	8:A:282:A:H8	1.68	0.59
8:A:833:A:H2'	8:A:834:G:C8	2.38	0.59
8:A:1432:G:H2'	8:A:1433:A:C8	2.38	0.59
8:A:2012:G:OP1	26:S:11:ARG:NH2	2.26	0.59
34:a:458:U:H3	34:a:474:G:H1	1.51	0.59
7:6:20:ASN:ND2	7:6:22:MET:SD	2.76	0.59
8:A:2641:G:H5''	17:J:78:THR:HB	1.84	0.59
13:F:7:TYR:HB2	13:F:172:PHE:HZ	1.68	0.59
34:a:496:A:N3	34:a:496:A:H2'	2.18	0.59
2:1:9:LYS:O	2:1:51:ALA:N	2.35	0.58
34:a:746:A:H2'	34:a:747:A:C8	2.38	0.58
34:a:1238:A:H2	34:a:1241:G:N3	2.01	0.58
35:b:96:LEU:HB2	35:b:99:MET:HG3	1.84	0.58
49:p:52:LEU:HD12	49:p:57:ILE:HD11	1.83	0.58
8:A:593:U:H2'	8:A:594:U:C6	2.38	0.58
8:A:1322:A:H5''	26:S:82:MET:HE1	1.83	0.58
11:D:16:THR:OG1	11:D:18:ASP:OD1	2.14	0.58
15:H:125:THR:HA	15:H:146:VAL:HB	1.84	0.58
20:M:53:MET:HE1	20:M:103:TYR:CD1	2.37	0.58
8:A:75:G:H22	8:A:111:A:H2	1.51	0.58
8:A:1451:C:O2'	8:A:1452:G:N2	2.36	0.58
34:a:77:A:O2'	34:a:78:A:OP1	2.18	0.58
34:a:723:U:OP1	54:u:54:ARG:NH2	2.35	0.58
36:c:13:ILE:HG22	36:c:14:VAL:HG13	1.84	0.58
5:4:1:MET:HE2	5:4:34:LYS:HG2	1.83	0.58
8:A:414:C:H2'	8:A:415:A:C8	2.37	0.58
8:A:721:A:H2'	8:A:722:A:C8	2.38	0.58
8:A:930:G:H1'	33:Z:24:LEU:HD21	1.85	0.58
8:A:2547:A:H2'	8:A:2548:U:C6	2.39	0.58
21:N:30:ARG:NH1	21:N:74:GLU:OE1	2.35	0.58
34:a:59:A:H5''	34:a:387:U:H5''	1.85	0.58
34:a:390:U:H2'	34:a:391:G:C8	2.38	0.58
34:a:404:G:O2'	34:a:498:A:N1	2.36	0.58
8:A:871:U:H2'	8:A:872:U:C6	2.38	0.58
34:a:1366:C:O2'	43:j:62:ARG:NH2	2.36	0.58
8:A:1808:A:H3'	8:A:1809:A:C8	2.38	0.58
9:B:48:U:H2'	9:B:49:C:C6	2.38	0.58
34:a:1125:U:OP1	43:j:37:ARG:NH1	2.36	0.58
8:A:832:U:H2'	8:A:833:A:C8	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2086:U:H2'	8:A:2087:G:C8	2.39	0.58
8:A:2666:C:N4	14:G:108:PHE:O	2.36	0.58
34:a:867:G:O2'	34:a:873:A:N1	2.36	0.58
40:g:112:ASP:OD2	40:g:121:ASN:ND2	2.36	0.58
8:A:971:G:OP1	8:A:974:G:O2'	2.19	0.58
8:A:1087:G:H21	8:A:1102:C:H41	1.52	0.58
34:a:135:C:O2	49:p:1:MET:HB2	2.04	0.58
37:d:84:ASN:HB3	37:d:87:GLU:HG2	1.86	0.58
8:A:887:U:OP1	8:A:891:G:N2	2.37	0.58
34:a:1226:C:H2'	46:m:101:THR:HG22	1.85	0.58
8:A:910:A:H2'	8:A:911:A:C8	2.39	0.57
11:D:77:ARG:NH2	11:D:200:ASP:OD1	2.36	0.57
17:J:125:TYR:OH	17:J:132:HIS:NE2	2.24	0.57
18:K:99:ILE:HD12	18:K:118:LEU:HB2	1.84	0.57
21:N:24:MET:HE1	21:N:40:LYS:HD3	1.86	0.57
34:a:1287:A:H2'	34:a:1288:A:C8	2.39	0.57
41:h:28:SER:HB3	41:h:56:PRO:HB2	1.87	0.57
8:A:1000:A:H2'	8:A:1001:A:C8	2.39	0.57
8:A:1826:G:O2'	8:A:1971:U:OP2	2.21	0.57
8:A:1937:A:O2'	8:A:1939:5MU:OP2	2.22	0.57
8:A:1149:G:H2'	8:A:1150:C:C6	2.40	0.57
8:A:1703:G:H2'	8:A:1704:C:C6	2.39	0.57
8:A:2425:A:H4'	8:A:2426:A:H5''	1.86	0.57
8:A:2636:C:O2'	11:D:45:TYR:OH	2.22	0.57
34:a:780:A:H5''	44:k:124:LYS:HD3	1.86	0.57
34:a:1004:A:OP2	34:a:1024:G:N2	2.36	0.57
37:d:144:ILE:HG22	37:d:148:ALA:HB3	1.86	0.57
34:a:459:A:H2'	34:a:460:A:H8	1.69	0.57
7:6:42:PRO:O	7:6:45:THR:C	2.47	0.57
8:A:1902:C:H4'	10:C:241:LYS:O	2.04	0.57
18:K:73:ASP:OD2	18:K:75:SER:OG	2.20	0.57
34:a:1001:C:H2'	34:a:1002:G:C8	2.40	0.57
5:4:16:ILE:HD13	5:4:25:VAL:HG22	1.86	0.57
13:F:55:ASP:OD2	13:F:149:ARG:NH1	2.37	0.57
26:S:24:ILE:HG13	26:S:24:ILE:O	2.04	0.57
42:i:9:GLY:HA2	42:i:80:HIS:ND1	2.19	0.57
8:A:674:G:H1'	12:E:69:ARG:HD2	1.86	0.57
40:g:24:LYS:O	40:g:28:ILE:HG12	2.05	0.57
44:k:49:SER:OG	44:k:68:ARG:NH1	2.33	0.57
44:k:111:ASP:O	51:r:72:ARG:NH1	2.37	0.57
46:m:70:ARG:O	46:m:74:MET:HG3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:880:G:H2'	8:A:881:G:C8	2.39	0.57
8:A:1059:G:N2	16:I:127:SER:O	2.38	0.57
35:b:65:LYS:HG3	35:b:89:PHE:HE2	1.65	0.57
49:p:6:LEU:HB3	49:p:17:TYR:HB3	1.86	0.57
8:A:219:A:N3	8:A:234:U:O2'	2.33	0.57
8:A:2125:G:H1	8:A:2171:A:H5'	1.69	0.57
11:D:148:GLN:HB2	11:D:152:PRO:HG2	1.87	0.57
12:E:21:ARG:HD3	12:E:106:LYS:HB3	1.87	0.57
21:N:37:THR:HG22	21:N:110:MET:HE1	1.85	0.57
8:A:2880:C:O2'	21:N:90:ARG:NH1	2.37	0.57
33:Z:15:ARG:O	33:Z:20:LYS:NZ	2.38	0.57
39:f:22:ILE:HG23	39:f:39:LEU:HD11	1.87	0.57
51:r:40:PRO:HB2	51:r:42:ARG:HG2	1.86	0.57
17:J:91:GLU:O	17:J:95:ARG:HD3	2.05	0.56
19:L:117:THR:HG23	19:L:118:THR:HG23	1.87	0.56
34:a:842:U:H3'	34:a:843:U:H4'	1.86	0.56
35:b:100:LEU:HB2	35:b:174:GLU:HG2	1.85	0.56
6:5:31:ARG:HA	8:A:1054:A:O2'	2.05	0.56
8:A:2204:G:H4'	10:C:149:LYS:HD3	1.87	0.56
8:A:2898:U:H2'	8:A:2899:A:C8	2.40	0.56
34:a:258:G:H5''	53:t:81:GLN:NE2	2.20	0.56
34:a:343:U:O2'	34:a:346:G:O6	2.16	0.56
34:a:1273:C:H2'	34:a:1274:A:O4'	2.04	0.56
45:l:109:ARG:HB2	45:l:118:VAL:HG21	1.87	0.56
8:A:1086:A:H4'	8:A:1087:G:C4	2.40	0.56
8:A:1528:A:OP2	8:A:1543:G:N2	2.38	0.56
8:A:1889:A:H2'	8:A:1890:A:C8	2.40	0.56
8:A:2469:A:H4'	20:M:55:ARG:HD2	1.87	0.56
8:A:2514:U:H2'	8:A:2515:C:C6	2.41	0.56
9:B:75:G:OP1	29:V:12:GLN:NE2	2.39	0.56
20:M:69:PRO:HA	20:M:94:ALA:HB2	1.87	0.56
34:a:89:U:H2'	34:a:90:C:C6	2.33	0.56
34:a:640:A:O2'	41:h:107:LYS:NZ	2.38	0.56
34:a:1356:G:H2'	34:a:1357:A:H8	1.69	0.56
39:f:43:GLY:O	39:f:58:HIS:HA	2.04	0.56
7:6:49:ARG:HD3	7:6:49:ARG:H	1.70	0.56
8:A:887:U:H5''	8:A:890:C:N4	2.20	0.56
8:A:2140:G:H4'	8:A:2152:G:H22	1.70	0.56
34:a:310:G:H5''	49:p:31:ARG:HB2	1.88	0.56
34:a:390:U:H2'	34:a:391:G:H8	1.71	0.56
34:a:744:C:H2'	34:a:745:G:C8	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:i:64:ILE:HG21	42:i:78:ILE:HG12	1.88	0.56
8:A:359:G:H2'	8:A:360:U:C6	2.39	0.56
20:M:30:SER:OG	20:M:106:ASP:OD1	2.22	0.56
26:S:72:THR:HG21	26:S:108:SER:HB3	1.88	0.56
28:U:3:LYS:O	28:U:93:ARG:NH2	2.36	0.56
34:a:524:G:H2'	34:a:525:C:C6	2.41	0.56
34:a:1120:C:H2'	34:a:1121:U:H6	1.70	0.56
42:i:32:ARG:HB3	42:i:36:GLN:HG3	1.87	0.56
43:j:84:VAL:O	43:j:88:MET:HG2	2.06	0.56
43:j:88:MET:O	43:j:89:ARG:HG2	2.05	0.56
8:A:1428:C:O2'	8:A:1569:A:OP2	2.18	0.56
8:A:1926:U:O2'	8:A:1928:A:N7	2.35	0.56
8:A:2071:A:H2'	8:A:2072:C:C6	2.41	0.56
8:A:2584:U:H3'	8:A:2585:U:C5'	2.35	0.56
21:N:2:ARG:O	21:N:2:ARG:HD3	2.05	0.56
34:a:177:G:OP2	53:t:63:LYS:NZ	2.39	0.56
34:a:600:A:H2'	34:a:601:G:C8	2.41	0.56
34:a:922:G:H2'	34:a:923:A:C8	2.41	0.56
34:a:1081:A:OP2	38:e:51:LYS:NZ	2.38	0.56
8:A:720:U:H2'	8:A:721:A:C8	2.40	0.56
8:A:2251:OMG:OP1	20:M:81:ARG:NH1	2.38	0.56
15:H:58:LEU:HA	15:H:61:VAL:HG12	1.88	0.56
20:M:53:MET:HE2	20:M:117:PHE:CD1	2.41	0.56
8:A:882:G:N2	8:A:884:U:H3	2.04	0.56
8:A:1300:G:H4'	8:A:1301:A:H5''	1.88	0.56
8:A:2144:G:O2'	8:A:2148:G:N2	2.38	0.56
18:K:108:ARG:HG2	18:K:116:ILE:HG12	1.88	0.56
32:Y:14:LEU:C	32:Y:14:LEU:HD12	2.31	0.56
34:a:51:A:N7	34:a:114:U:O2'	2.38	0.56
38:e:33:THR:HG22	38:e:51:LYS:HE3	1.88	0.56
43:j:8:ILE:HD11	43:j:87:LEU:HD13	1.87	0.56
8:A:310:A:O2'	8:A:311:A:H2'	2.05	0.56
8:A:837:C:N3	8:A:941:A:N6	2.53	0.56
8:A:905:A:H2'	8:A:906:U:H5'	1.88	0.56
8:A:1797:G:O2'	10:C:256:THR:OG1	2.18	0.56
8:A:2340:A:H5'	9:B:41:G:H21	1.71	0.56
8:A:2804:U:H2'	8:A:2805:C:C6	2.40	0.56
21:N:77:ALA:O	21:N:81:ASN:HB2	2.05	0.56
34:a:509:A:N3	34:a:543:U:O2'	2.36	0.56
34:a:1477:U:H2'	34:a:1478:U:C6	2.41	0.56
40:g:63:VAL:O	40:g:67:ASN:ND2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:g:74:VAL:HG11	40:g:147:ASN:HD22	1.71	0.56
58:y:43:ILE:O	58:y:46:SER:OG	2.23	0.56
8:A:1105:U:O2'	8:A:1106:G:H5'	2.05	0.56
34:a:555:U:H2'	34:a:556:C:C6	2.41	0.56
34:a:744:C:H2'	34:a:745:G:H8	1.70	0.56
35:b:93:HIS:ND1	35:b:145:ASN:O	2.38	0.56
8:A:657:U:H2'	8:A:658:U:C6	2.41	0.55
8:A:894:U:O2'	8:A:896:A:N7	2.39	0.55
8:A:1654:A:O2'	11:D:118:PHE:O	2.22	0.55
10:C:209:ALA:HA	10:C:212:TRP:CE2	2.41	0.55
13:F:3:LEU:HD13	13:F:100:GLU:HB2	1.87	0.55
22:O:64:TYR:O	22:O:67:ASN:ND2	2.39	0.55
34:a:89:U:H2'	34:a:90:C:H5	1.44	0.55
34:a:216:U:H4'	34:a:464:U:H4'	1.87	0.55
8:A:1509:A:H2'	8:A:1510:G:H8	1.71	0.55
8:A:2014:A:H2'	8:A:2015:A:C8	2.41	0.55
8:A:2898:U:H2'	8:A:2899:A:H8	1.70	0.55
34:a:126:G:OP1	34:a:605:U:O2'	2.18	0.55
34:a:981:U:OP1	47:n:8:ARG:NH1	2.39	0.55
39:f:38:ARG:HG2	39:f:40:GLU:HG3	1.89	0.55
8:A:846:U:H4'	8:A:847:U:H5	1.71	0.55
8:A:1125:G:OP2	8:A:1126:A:O2'	2.23	0.55
8:A:1475:G:HO2'	8:A:1476:U:H6	1.52	0.55
8:A:1548:A:H2'	8:A:1549:A:C8	2.40	0.55
8:A:2141:G:H2'	8:A:2142:A:C8	2.42	0.55
17:J:118:MET:HA	17:J:121:LYS:HE2	1.89	0.55
43:j:50:THR:HG22	43:j:62:ARG:HD3	1.88	0.55
18:K:88:ASN:HB3	18:K:91:SER:O	2.06	0.55
28:U:97:SER:O	28:U:97:SER:OG	2.18	0.55
29:V:2:PHE:HB2	29:V:61:LEU:HD22	1.88	0.55
29:V:51:GLN:OE1	29:V:79:ARG:NH2	2.35	0.55
34:a:477:C:H2'	34:a:478:A:C8	2.42	0.55
34:a:728:A:H2'	34:a:729:A:C8	2.42	0.55
34:a:1187:G:H5'	42:i:114:LYS:HE3	1.87	0.55
34:a:1300:G:O2'	34:a:1303:C:N4	2.39	0.55
51:r:12:PHE:HD1	51:r:17:VAL:HG21	1.72	0.55
4:3:18:LYS:HG3	8:A:651:G:H5'	1.88	0.55
8:A:1490:A:HO2'	8:A:1491:G:P	2.30	0.55
20:M:17:ASN:O	20:M:38:ARG:NH1	2.39	0.55
28:U:33:VAL:HG13	28:U:66:VAL:HG12	1.88	0.55
30:W:33:ILE:HG21	30:W:76:ILE:HG21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:384:G:H2'	34:a:385:C:C6	2.42	0.55
34:a:1412:C:H2'	34:a:1413:A:C8	2.41	0.55
8:A:1570:A:H2'	8:A:1571:A:C8	2.42	0.55
8:A:2698:U:H2'	8:A:2699:C:C6	2.41	0.55
12:E:105:LEU:HB3	12:E:200:LEU:HD21	1.88	0.55
34:a:673:A:O3'	39:f:86:ARG:NH2	2.39	0.55
34:a:1305:G:H22	34:a:1331:G:H1'	1.72	0.55
34:a:1331:G:H4'	34:a:1332:A:O5'	2.07	0.55
40:g:65:LEU:O	40:g:69:ARG:HB2	2.06	0.55
8:A:5:A:H2'	8:A:6:A:C8	2.41	0.55
8:A:181:A:H1'	8:A:435:C:H5'	1.89	0.55
8:A:608:A:H2'	8:A:609:A:C8	2.42	0.55
8:A:871:U:H5''	20:M:68:PHE:CE2	2.42	0.55
8:A:886:A:H4'	8:A:887:U:OP1	2.07	0.55
15:H:76:GLU:OE1	15:H:77:THR:HG22	2.07	0.55
15:H:132:PHE:HB2	15:H:140:ALA:HB3	1.89	0.55
22:O:27:VAL:HA	22:O:93:ASP:HB3	1.88	0.55
34:a:197:A:N1	34:a:220:G:O2'	2.31	0.55
34:a:229:U:O2'	49:p:23:ASP:OD1	2.24	0.55
34:a:634:C:H2'	34:a:635:A:C8	2.42	0.55
34:a:1028:C:O2'	34:a:1033:G:N2	2.40	0.55
37:d:94:GLU:O	37:d:99:ASN:ND2	2.39	0.55
39:f:3:HIS:HD2	39:f:65:GLU:HB2	1.71	0.55
4:3:33:THR:HG22	8:A:2420:C:OP1	2.06	0.55
8:A:281:C:H2'	8:A:282:A:C8	2.42	0.55
8:A:880:G:O6	8:A:897:C:N4	2.30	0.55
8:A:1171:G:H2'	8:A:1172:C:H5'	1.88	0.55
34:a:993:G:O2'	34:a:994:A:N7	2.39	0.55
37:d:73:ASN:O	37:d:77:GLU:CD	2.49	0.55
14:G:94:ARG:HB2	14:G:127:GLN:HG2	1.88	0.55
34:a:405:U:O4	37:d:1:ALA:N	2.40	0.55
47:n:46:LEU:HD13	52:s:12:LEU:HD21	1.88	0.55
8:A:851:C:H2'	8:A:852:U:C6	2.42	0.55
8:A:1932:A:H2'	8:A:1933:G:O4'	2.07	0.55
8:A:839:U:H2'	8:A:840:C:C6	2.42	0.54
34:a:1011:C:H2'	34:a:1012:A:C8	2.42	0.54
34:a:1251:A:H2'	34:a:1252:A:C8	2.42	0.54
8:A:580:U:H2'	8:A:581:C:C6	2.42	0.54
8:A:1482:G:H2'	8:A:1483:G:H8	1.71	0.54
8:A:2682:A:H61	8:A:2728:U:H1'	1.71	0.54
17:J:114:LEU:HG	17:J:118:MET:HE3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:S:73:LYS:HB2	26:S:106:VAL:HB	1.89	0.54
34:a:82:G:N2	34:a:83:C:O2'	2.40	0.54
34:a:213:G:H2'	34:a:214:C:H5'	1.88	0.54
34:a:652:U:O2'	34:a:653:U:O5'	2.25	0.54
46:m:78:ARG:HD2	52:s:64:GLU:OE2	2.07	0.54
8:A:191:A:H2'	8:A:192:C:H6	1.73	0.54
8:A:396:G:H1'	31:X:28:PHE:HB3	1.89	0.54
8:A:581:C:H2'	8:A:582:A:H8	1.73	0.54
8:A:910:A:H62	20:M:12:MET:HA	1.72	0.54
8:A:2439:A:N6	56:w:76:A:OP1	2.41	0.54
45:l:67:GLY:O	45:l:98:ARG:NH1	2.37	0.54
47:n:52:PRO:O	47:n:55:SER:OG	2.16	0.54
56:w:20:U:O2	56:w:20:U:H2'	2.05	0.54
56:w:62:C:H2'	56:w:63:G:H8	1.72	0.54
8:A:831:G:O2'	19:L:38:GLN:OE1	2.24	0.54
8:A:1753:G:H5''	23:P:92:ARG:HD3	1.90	0.54
34:a:144:G:H2'	34:a:145:G:O4'	2.06	0.54
34:a:269:C:H2'	34:a:270:A:C8	2.42	0.54
35:b:113:LEU:HD13	35:b:143:LEU:HB3	1.88	0.54
37:d:78:ALA:HB2	37:d:92:LEU:HD22	1.89	0.54
42:i:122:ARG:NH1	42:i:123:ARG:O	2.41	0.54
8:A:714:U:H1'	8:A:717:C:H5	1.73	0.54
8:A:959:A:H2'	8:A:960:A:C8	2.42	0.54
8:A:1198:U:H2'	8:A:1199:U:C6	2.42	0.54
8:A:1199:U:H1'	24:Q:3:VAL:HG22	1.89	0.54
14:G:85:LYS:HG3	14:G:131:VAL:HG22	1.88	0.54
25:R:27:ILE:HG22	25:R:31:GLU:HB2	1.89	0.54
34:a:613:C:H2'	34:a:614:C:C6	2.42	0.54
34:a:976:G:OP2	34:a:1358:U:O2'	2.25	0.54
34:a:1240:U:C5	40:g:115:MET:HG2	2.43	0.54
8:A:306:U:H2'	8:A:307:G:O4'	2.07	0.54
8:A:882:G:H22	8:A:894:U:H1'	1.72	0.54
8:A:1197:G:H2'	8:A:1198:U:H6	1.73	0.54
8:A:1809:A:H2'	8:A:1810:A:C8	2.43	0.54
8:A:2687:U:H2'	8:A:2688:G:O4'	2.08	0.54
14:G:21:GLN:NE2	14:G:37:ASN:O	2.40	0.54
33:Z:5:LYS:HB2	33:Z:57:GLU:HG2	1.90	0.54
34:a:1034:G:H2'	34:a:1035:A:C8	2.43	0.54
8:A:1071:G:O2'	8:A:1088:A:O2'	2.21	0.54
4:3:30:HIS:N	4:3:30:HIS:CD2	2.73	0.54
8:A:1715:G:O2'	8:A:1716:U:O5'	2.26	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2297:A:N1	8:A:2321:U:H5	2.06	0.54
30:W:29:ALA:N	30:W:60:ASP:OD1	2.39	0.54
34:a:945:G:C2	34:a:946:A:C8	2.96	0.54
48:o:22:GLY:O	48:o:27:GLN:NE2	2.37	0.54
54:u:11:PHE:CD1	54:u:11:PHE:C	2.85	0.54
56:w:75:C:OP2	58:y:78:ARG:NH1	2.41	0.54
7:6:43:PHE:C	7:6:45:THR:H	2.14	0.54
8:A:807:U:OP2	19:L:41:ARG:NH1	2.40	0.54
8:A:1715:G:O2'	8:A:1716:U:H6	1.90	0.54
8:A:2160:C:O2'	8:A:2161:C:O4'	2.24	0.54
35:b:56:LEU:HD13	35:b:216:VAL:HG23	1.89	0.54
36:c:46:LEU:HB3	36:c:49:ALA:HB3	1.89	0.54
1:0:9:ARG:NH1	8:A:516:C:OP1	2.41	0.54
8:A:1292:G:H2'	8:A:1293:C:C6	2.43	0.54
34:a:1120:C:H2'	34:a:1121:U:C6	2.42	0.54
34:a:1352:C:H2'	34:a:1353:G:C8	2.43	0.54
34:a:1397:C:OP2	38:e:28:ARG:NH2	2.41	0.54
35:b:206:ILE:O	35:b:210:THR:HG23	2.07	0.54
37:d:69:ARG:HG2	37:d:69:ARG:HH21	1.72	0.54
50:q:53:GLY:N	50:q:56:ASP:OD2	2.35	0.54
8:A:815:C:OP2	25:R:85:LYS:HD2	2.08	0.53
8:A:1052:C:O5'	8:A:1052:C:H6	1.92	0.53
8:A:1089:A:O2'	8:A:1090:A:H5''	2.08	0.53
14:G:44:HIS:HA	14:G:49:LEU:HD23	1.90	0.53
34:a:1182:G:H4'	34:a:1183:U:O5'	2.07	0.53
34:a:1498:UR3:H6	34:a:1499:A:H62	1.73	0.53
36:c:152:VAL:HG12	36:c:197:VAL:HG22	1.90	0.53
38:e:43:GLY:O	38:e:73:VAL:N	2.38	0.53
46:m:106:ARG:NH2	46:m:109:LYS:HD3	2.23	0.53
47:n:23:ARG:HG3	47:n:48:LEU:HD11	1.89	0.53
52:s:29:PRO:HA	52:s:47:THR:HG23	1.89	0.53
8:A:1130:U:C2	8:A:2025:C:H5''	2.44	0.53
8:A:1187:G:OP1	25:R:85:LYS:NZ	2.25	0.53
8:A:1486:U:H2'	8:A:1487:U:C6	2.44	0.53
8:A:1799:G:O2'	10:C:179:GLU:OE2	2.23	0.53
20:M:38:ARG:HB2	20:M:98:PRO:HD3	1.90	0.53
32:Y:17:GLU:O	32:Y:17:GLU:HG2	2.05	0.53
34:a:56:U:H2'	34:a:57:G:C8	2.43	0.53
36:c:120:THR:O	36:c:124:GLU:HG2	2.08	0.53
8:A:742:A:H2'	8:A:743:A:C8	2.43	0.53
8:A:849:A:H2'	8:A:850:U:H6	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1790:C:H2'	8:A:1791:A:C5	2.43	0.53
15:H:104:THR:OG1	15:H:109:GLU:HG2	2.08	0.53
34:a:545:C:H5''	37:d:68:GLU:HG2	1.91	0.53
34:a:1011:C:H2'	34:a:1012:A:H8	1.73	0.53
8:A:155:A:H2'	8:A:156:A:H8	1.74	0.53
8:A:788:A:OP1	8:A:791:C:N4	2.34	0.53
8:A:1447:C:H2'	8:A:1448:G:C8	2.44	0.53
8:A:1720:U:H2'	8:A:1721:G:O4'	2.09	0.53
19:L:55:MET:O	19:L:60:ARG:NH1	2.41	0.53
22:O:53:THR:HB	22:O:65:THR:HB	1.91	0.53
34:a:202:G:H1	34:a:215:C:H41	1.56	0.53
45:l:98:ARG:HB2	45:l:116:TYR:HA	1.89	0.53
8:A:871:U:H4'	20:M:68:PHE:CE2	2.44	0.53
8:A:2467:C:H2'	8:A:2468:A:O4'	2.09	0.53
8:A:2618:G:H21	11:D:155:VAL:HG21	1.74	0.53
8:A:365:U:H2'	8:A:366:C:C6	2.44	0.53
8:A:674:G:O2'	12:E:69:ARG:HD3	2.08	0.53
8:A:889:C:H3'	8:A:890:C:C6	2.44	0.53
8:A:1415:U:H3	8:A:1587:G:H1	1.57	0.53
10:C:129:LEU:HD12	10:C:133:ASN:HB2	1.88	0.53
26:S:20:VAL:HG11	26:S:44:ALA:HA	1.91	0.53
26:S:82:MET:HB2	26:S:98:LYS:HB2	1.91	0.53
35:b:65:LYS:HE2	35:b:89:PHE:CZ	2.43	0.53
39:f:1:MET:HE3	39:f:65:GLU:HG2	1.91	0.53
47:n:46:LEU:HB3	52:s:12:LEU:HD11	1.91	0.53
7:6:13:THR:HG22	7:6:31:ASP:CG	2.34	0.53
7:6:38:SER:HB3	13:F:104:THR:HA	1.90	0.53
8:A:141:G:H4'	8:A:142:A:OP1	2.09	0.53
8:A:282:A:H2'	8:A:283:G:C8	2.44	0.53
8:A:805:G:N2	8:A:829:A:OP1	2.39	0.53
8:A:882:G:H2'	8:A:884:U:O4	2.09	0.53
8:A:2039:U:H2'	8:A:2040:G:C8	2.44	0.53
17:J:13:ARG:NH1	17:J:49:ASP:O	2.38	0.53
21:N:54:LEU:HD21	21:N:65:LEU:HB3	1.90	0.53
25:R:34:GLU:HG2	25:R:60:LYS:HG2	1.90	0.53
34:a:515:G:O2'	34:a:516:PSU:O4'	2.26	0.53
35:b:126:ASP:HA	35:b:130:LYS:HZ2	1.74	0.53
42:i:54:VAL:HG23	42:i:55:ASP:H	1.72	0.53
52:s:49:ALA:HB1	52:s:56:HIS:HB3	1.91	0.53
1:O:41:HIS:HD2	21:N:101:GLY:H	1.57	0.53
8:A:1490:A:O2'	8:A:1491:G:OP1	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:48:U:H4'	22:O:100:HIS:CD2	2.43	0.53
12:E:51:GLU:OE2	12:E:88:ARG:NH1	2.42	0.53
20:M:53:MET:HE1	20:M:103:TYR:CG	2.43	0.53
22:O:35:ILE:HG21	22:O:71:ALA:HA	1.90	0.53
34:a:244:U:O4	34:a:906:A:H1'	2.08	0.53
34:a:652:U:O4	34:a:752:G:O2'	2.26	0.53
34:a:1077:G:N2	34:a:1080:A:OP2	2.37	0.53
34:a:455:G:H2'	34:a:456:A:C8	2.44	0.53
34:a:481:G:O2'	34:a:483:C:N4	2.42	0.53
35:b:59:ILE:HD13	35:b:159:ALA:HB2	1.91	0.53
36:c:56:ILE:HG23	36:c:63:ILE:HD11	1.90	0.53
36:c:146:LYS:HB2	36:c:202:PHE:CD2	2.44	0.53
8:A:1604:C:O2'	8:A:1610:A:N1	2.38	0.53
8:A:1710:G:H4'	8:A:2858:C:O2	2.09	0.53
10:C:144:GLU:HA	10:C:151:GLY:HA2	1.91	0.53
19:L:85:VAL:HG22	19:L:94:THR:HG22	1.90	0.53
8:A:849:A:H2'	8:A:850:U:C6	2.43	0.52
8:A:869:G:H1'	20:M:8:LYS:HE3	1.91	0.52
8:A:1475:G:H1'	8:A:1732:C:H41	1.74	0.52
8:A:1812:U:O2'	10:C:44:ASN:N	2.40	0.52
8:A:2319:G:HO2'	8:A:2320:U:H6	1.56	0.52
34:a:542:G:H5'	37:d:38:GLY:HA3	1.91	0.52
8:A:242:G:N2	8:A:255:A:OP2	2.33	0.52
8:A:2059:A:H2	55:v:14:PRO:HB3	1.75	0.52
36:c:59:PRO:O	36:c:62:SER:OG	2.25	0.52
45:l:78:VAL:O	45:l:102:ASP:HB3	2.08	0.52
46:m:58:GLU:OE1	46:m:61:LYS:NZ	2.35	0.52
46:m:90:HIS:HA	46:m:108:ARG:HH22	1.73	0.52
5:4:32:LYS:HE2	8:A:2478:A:H5'	1.91	0.52
8:A:45:G:H5'	8:A:46:G:OP1	2.09	0.52
8:A:248:G:O5'	8:A:249:C:H5''	2.10	0.52
8:A:1568:G:H5'	10:C:59:GLN:HA	1.92	0.52
8:A:1794:A:H2'	8:A:1795:C:H6	1.74	0.52
8:A:2804:U:H2'	8:A:2805:C:H6	1.74	0.52
12:E:168:ASP:OD2	12:E:170:ARG:NE	2.38	0.52
15:H:46:PHE:O	15:H:50:ARG:HB3	2.08	0.52
34:a:747:A:H2'	34:a:748:G:O4'	2.09	0.52
39:f:86:ARG:NH1	51:r:63:TYR:O	2.43	0.52
40:g:74:VAL:HG21	40:g:143:MET:HE2	1.92	0.52
8:A:2243:U:H2'	8:A:2244:U:C6	2.45	0.52
8:A:2313:C:H5''	13:F:87:LYS:HD3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:29:LYS:O	19:L:30:THR:OG1	2.25	0.52
1:O:37:HIS:ND1	1:O:38:LEU:O	2.42	0.52
8:A:534:U:O2'	24:Q:48:ASP:OD2	2.16	0.52
41:h:49:LYS:NZ	41:h:51:GLU:OE1	2.41	0.52
42:i:104:THR:HG22	42:i:106:ASP:H	1.74	0.52
8:A:569:U:O2'	8:A:983:A:N1	2.38	0.52
8:A:1179:G:OP2	8:A:1180:U:H5''	2.08	0.52
34:a:918:A:H2'	34:a:919:A:C8	2.45	0.52
43:j:7:ARG:HD2	43:j:73:LEU:HD11	1.91	0.52
44:k:124:LYS:HG3	44:k:125:LYS:H	1.75	0.52
50:q:7:LEU:HD13	50:q:72:TRP:HH2	1.75	0.52
8:A:645:C:H2'	8:A:647:G:C8	2.45	0.52
8:A:1086:A:H5''	8:A:1087:G:H5'	1.92	0.52
8:A:1490:A:C8	10:C:97:ASP:HB3	2.45	0.52
23:P:24:THR:HB	23:P:87:ARG:HB3	1.91	0.52
34:a:131:A:H2'	34:a:132:C:C6	2.45	0.52
34:a:332:G:O3'	53:t:2:ASN:ND2	2.32	0.52
34:a:600:A:H2'	34:a:601:G:H8	1.75	0.52
37:d:72:ARG:HH12	37:d:76:LYS:HD2	1.62	0.52
56:w:62:C:H2'	56:w:63:G:C8	2.44	0.52
56:w:76:A:H3'	58:y:27:GLY:HA3	1.92	0.52
8:A:250:G:H2'	8:A:251:A:C8	2.45	0.52
8:A:476:G:N1	8:A:479:A:OP2	2.41	0.52
8:A:522:A:H2'	8:A:523:C:C6	2.45	0.52
8:A:2127:G:H2'	8:A:2128:G:C8	2.44	0.52
8:A:2899:A:H2'	8:A:2900:A:H8	1.74	0.52
11:D:57:ALA:HA	11:D:60:VAL:HG12	1.91	0.52
34:a:79:G:O6	34:a:90:C:N4	2.34	0.52
34:a:1220:G:P	47:n:53:ARG:HH12	2.32	0.52
34:a:1330:U:H2'	34:a:1331:G:H5'	1.92	0.52
38:e:104:ILE:O	38:e:111:ARG:NH2	2.42	0.52
43:j:80:THR:C	43:j:82:LYS:H	2.18	0.52
45:l:54:VAL:HG21	45:l:79:ILE:HD11	1.92	0.52
54:u:5:VAL:HG21	54:u:18:PHE:HA	1.90	0.52
19:L:25:SER:OG	19:L:27:LEU:O	2.27	0.52
35:b:126:ASP:HA	35:b:130:LYS:NZ	2.25	0.52
4:3:53:ASP:HB3	19:L:57:LEU:HD22	1.91	0.52
8:A:892:A:O2'	8:A:893:C:H5''	2.10	0.52
8:A:909:A:H2'	8:A:912:C:H5	1.74	0.52
8:A:1278:C:H2'	8:A:1279:G:H8	1.75	0.52
8:A:2051:A:H4'	11:D:146:ILE:HG12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2590:A:H2'	8:A:2591:C:H6	1.75	0.52
34:a:1048:G:H5''	47:n:2:LYS:HD2	1.92	0.52
37:d:10:LEU:HD13	37:d:62:ARG:HG2	1.92	0.52
39:f:4:TYR:CE2	39:f:71:ILE:HG13	2.45	0.52
45:l:43:LYS:HB2	45:l:44:PRO:CD	1.83	0.52
8:A:299:A:N3	8:A:319:G:O2'	2.38	0.51
8:A:394:C:H2'	8:A:395:U:O4'	2.10	0.51
8:A:739:A:H1'	8:A:740:C:H5	1.74	0.51
8:A:813:U:H2'	8:A:814:C:C6	2.45	0.51
8:A:1109:C:H2'	8:A:1110:G:O4'	2.10	0.51
8:A:1946:U:H2'	8:A:1947:C:C6	2.45	0.51
13:F:3:LEU:HD21	13:F:103:ILE:HD11	1.90	0.51
19:L:2:ARG:HB2	19:L:5:THR:HG23	1.92	0.51
30:W:37:ARG:HA	30:W:37:ARG:HE	1.75	0.51
34:a:263:A:H2'	34:a:264:C:C6	2.45	0.51
34:a:1530:G:H2'	34:a:1531:A:C8	2.45	0.51
37:d:22:SER:HB2	37:d:108:ALA:HB1	1.91	0.51
43:j:6:ILE:HB	43:j:76:ILE:HG23	1.91	0.51
52:s:2:ARG:NH2	52:s:9:PHE:HB2	2.25	0.51
8:A:33:C:N4	8:A:446:G:O2'	2.38	0.51
8:A:181:A:H2'	8:A:182:A:C8	2.45	0.51
8:A:414:C:H2'	8:A:415:A:H8	1.74	0.51
8:A:1683:U:H2'	8:A:1684:G:C8	2.45	0.51
8:A:2468:A:O2'	8:A:2469:A:O5'	2.27	0.51
8:A:2700:A:H2'	8:A:2701:U:C6	2.45	0.51
34:a:1151:A:HO2'	34:a:1152:A:H8	1.59	0.51
34:a:1500:A:H5''	34:a:1508:A:H5''	1.91	0.51
36:c:63:ILE:HG22	36:c:96:VAL:HG23	1.92	0.51
8:A:1816:C:H41	10:C:34:GLU:CD	2.19	0.51
34:a:191:G:H2'	34:a:192:A:C8	2.44	0.51
34:a:309:A:O2'	34:a:607:A:N1	2.39	0.51
34:a:793:U:H5'	34:a:794:A:H5''	1.92	0.51
2:1:16:THR:HG21	2:1:41:VAL:HB	1.92	0.51
8:A:242:G:O2'	8:A:243:U:P	2.69	0.51
8:A:594:U:H2'	8:A:595:C:C6	2.45	0.51
8:A:644:A:H2'	8:A:645:C:O4'	2.10	0.51
8:A:1353:A:H2'	8:A:1354:A:C8	2.45	0.51
8:A:2788:C:O2'	8:A:2809:A:N3	2.40	0.51
15:H:46:PHE:HB3	15:H:50:ARG:NH2	2.25	0.51
34:a:1124:G:N2	34:a:1125:U:O4	2.25	0.51
34:a:1513:A:H2'	34:a:1514:G:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:e:15:ILE:HD11	38:e:37:VAL:HG22	1.93	0.51
38:e:114:LEU:HD13	38:e:122:VAL:HG11	1.92	0.51
8:A:714:U:O2'	8:A:716:A:N7	2.41	0.51
34:a:50:A:O2'	34:a:360:G:N2	2.42	0.51
34:a:579:A:H2'	34:a:580:C:C6	2.46	0.51
34:a:715:A:H2'	34:a:716:A:C8	2.45	0.51
34:a:1133:G:H2'	34:a:1134:G:C8	2.46	0.51
37:d:10:LEU:HB3	37:d:62:ARG:HD3	1.92	0.51
3:2:37:LYS:HE2	8:A:469:G:O6	2.10	0.51
8:A:1545:A:H2'	8:A:1546:G:O4'	2.11	0.51
8:A:1680:U:H2'	8:A:1681:G:O4'	2.11	0.51
8:A:1853:A:H2'	8:A:1854:A:C8	2.44	0.51
8:A:2120:G:H1	8:A:2172:U:H3	1.57	0.51
18:K:38:ILE:HD11	18:K:112:PHE:CZ	2.46	0.51
34:a:745:G:H2'	34:a:746:A:C8	2.46	0.51
34:a:868:C:H2'	34:a:869:G:O4'	2.10	0.51
34:a:1150:A:C2	43:j:41:PRO:HG2	2.45	0.51
34:a:1314:C:H2'	34:a:1315:U:C6	2.46	0.51
34:a:1507:A:H2'	34:a:1508:A:C8	2.46	0.51
37:d:97:LEU:HB2	37:d:134:TYR:HB3	1.93	0.51
8:A:576:U:H2'	8:A:577:G:C8	2.46	0.51
8:A:1003:G:O2'	8:A:1010:A:N1	2.38	0.51
8:A:1442:U:H2'	8:A:1443:U:C6	2.46	0.51
8:A:2025:C:H2'	8:A:2026:U:C6	2.46	0.51
8:A:2096:C:H2'	8:A:2097:A:H8	1.76	0.51
15:H:77:THR:OG1	15:H:143:ILE:HG23	2.10	0.51
26:S:2:GLU:HG2	26:S:108:SER:HB2	1.93	0.51
34:a:751:U:H2'	34:a:752:G:O4'	2.09	0.51
8:A:579:G:O2'	8:A:2019:A:OP1	2.28	0.51
8:A:1394:U:H2'	8:A:1395:A:O4'	2.11	0.51
8:A:1563:U:H2'	8:A:1564:C:C6	2.45	0.51
8:A:2064:C:H2'	8:A:2065:C:C6	2.45	0.51
8:A:2104:C:C5	8:A:2105:U:H1'	2.45	0.51
8:A:2118:U:N3	8:A:2143:C:O2	2.43	0.51
8:A:2812:G:H2'	8:A:2813:A:C8	2.46	0.51
12:E:119:ILE:HB	12:E:187:VAL:HG22	1.92	0.51
15:H:127:GLU:HG3	15:H:145:ASN:HB3	1.92	0.51
20:M:42:THR:HG22	20:M:93:VAL:HG12	1.93	0.51
34:a:35:G:H2'	34:a:36:C:C6	2.46	0.51
34:a:683:G:N2	44:k:38:GLY:O	2.42	0.51
36:c:72:PRO:HA	36:c:75:VAL:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:q:59:GLU:OE1	50:q:76:ARG:NH1	2.43	0.51
7:6:65:ASN:ND2	52:s:7:GLY:HA2	2.26	0.51
8:A:549:G:H2'	8:A:550:C:H6	1.76	0.51
8:A:2308:G:H2'	8:A:2310:C:H5	1.75	0.51
8:A:2857:G:N2	8:A:2860:A:OP2	2.30	0.51
28:U:21:ARG:HD2	28:U:72:PHE:CG	2.46	0.51
31:X:38:TRP:NE1	31:X:40:GLU:OE1	2.25	0.51
32:Y:14:LEU:C	32:Y:14:LEU:CD1	2.82	0.51
34:a:1007:U:H2'	34:a:1008:U:C6	2.45	0.51
34:a:1464:U:H2'	34:a:1465:A:H8	1.75	0.51
37:d:72:ARG:HH11	37:d:76:LYS:CD	2.12	0.51
38:e:88:HIS:CE1	38:e:137:ARG:HD3	2.46	0.51
8:A:285:G:H2'	8:A:286:U:H6	1.75	0.51
8:A:973:A:H5'	8:A:1188:U:H1'	1.93	0.51
15:H:101:ASP:HB2	15:H:107:GLY:N	2.26	0.51
21:N:28:LEU:HD23	21:N:48:VAL:HG11	1.92	0.51
34:a:276:G:OP1	50:q:13:SER:OG	2.27	0.51
34:a:955:U:O2'	52:s:82:HIS:HD2	1.94	0.51
43:j:8:ILE:HG12	43:j:100:ILE:HG23	1.93	0.51
44:k:22:ILE:HG21	44:k:95:THR:HG21	1.92	0.51
8:A:150:U:H2'	8:A:151:C:C6	2.45	0.50
8:A:397:U:H5''	31:X:31:ASN:HB2	1.92	0.50
8:A:528:A:N1	8:A:2042:A:H2'	2.26	0.50
8:A:1782:U:H1'	8:A:2609:U:H5''	1.93	0.50
8:A:2102:G:O6	8:A:2187:U:O4	2.29	0.50
8:A:2809:A:H2'	8:A:2810:A:C8	2.46	0.50
8:A:2899:A:H2'	8:A:2900:A:C8	2.46	0.50
34:a:76:G:O6	34:a:93:U:O4	2.29	0.50
34:a:692:U:O2'	34:a:694:A:N7	2.32	0.50
34:a:946:A:O2'	34:a:1333:A:N3	2.40	0.50
8:A:634:C:H2'	8:A:635:C:C6	2.46	0.50
8:A:749:A:H4'	8:A:1271:G:N3	2.26	0.50
8:A:995:C:OP2	24:Q:53:LYS:NZ	2.37	0.50
8:A:2074:U:H2'	8:A:2075:U:C6	2.46	0.50
8:A:2241:A:H2'	8:A:2242:G:C8	2.46	0.50
9:B:29:A:H2'	9:B:30:C:C6	2.46	0.50
21:N:59:SER:O	21:N:63:ARG:HG2	2.10	0.50
34:a:580:C:H2'	34:a:581:G:O4'	2.11	0.50
34:a:859:G:H2'	34:a:860:A:C8	2.46	0.50
34:a:1345:U:OP1	42:i:121:ARG:NH1	2.44	0.50
35:b:125:PHE:HE1	35:b:136:ARG:HE	1.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:y:134:LYS:HE2	58:y:136:ARG:HD3	1.93	0.50
8:A:2038:G:H2'	8:A:2039:U:O4'	2.12	0.50
22:O:51:ALA:HB3	22:O:78:VAL:HB	1.93	0.50
34:a:33:A:H2'	34:a:34:C:C6	2.47	0.50
34:a:410:G:OP1	37:d:25:ARG:NH2	2.45	0.50
34:a:1038:C:N4	34:a:1039:G:O6	2.45	0.50
36:c:167:TYR:OH	38:e:54:GLU:OE2	2.22	0.50
38:e:19:ARG:HD3	58:y:131:MET:HE3	1.93	0.50
42:i:41:GLU:HG3	42:i:44:ARG:NH1	2.26	0.50
8:A:784:G:H5'	8:A:785:G:OP1	2.12	0.50
8:A:2123:G:N1	8:A:2170:A:H5'	2.23	0.50
8:A:2705:A:O2'	8:A:2852:G:OP1	2.28	0.50
13:F:118:ALA:HB1	13:F:166:ARG:HE	1.77	0.50
26:S:17:VAL:HG11	26:S:103:ILE:HG12	1.92	0.50
34:a:156:C:H2'	34:a:157:U:O4'	2.12	0.50
34:a:1031:C:H5'	34:a:1032:G:C8	2.47	0.50
34:a:1118:U:H2'	34:a:1119:C:H6	1.76	0.50
46:m:85:TYR:O	46:m:89:ARG:HG2	2.11	0.50
50:q:46:HIS:HB2	50:q:66:LEU:CD1	2.40	0.50
8:A:324:A:OP2	8:A:1205:A:N6	2.44	0.50
8:A:538:A:H5''	17:J:7:LYS:HE3	1.93	0.50
8:A:580:U:H2'	8:A:581:C:H6	1.76	0.50
8:A:1041:G:H2'	8:A:1042:G:H8	1.76	0.50
8:A:1093:G:N2	8:A:1097:U:O5'	2.45	0.50
8:A:1156:A:C8	24:Q:50:ARG:HG2	2.47	0.50
8:A:1703:G:H2'	8:A:1704:C:H6	1.77	0.50
8:A:1874:C:H2'	8:A:1875:G:O4'	2.12	0.50
8:A:2590:A:H2'	8:A:2591:C:C6	2.46	0.50
8:A:2591:C:H2'	8:A:2592:G:H8	1.74	0.50
17:J:17:VAL:HG23	17:J:137:PRO:HB2	1.94	0.50
35:b:186:VAL:HG11	35:b:192:PRO:HB3	1.93	0.50
45:l:79:ILE:HG22	45:l:103:CYS:HB2	1.93	0.50
8:A:728:G:H4'	10:C:12:ARG:HD3	1.92	0.50
8:A:1168:G:H2'	8:A:1169:A:H8	1.77	0.50
8:A:1262:A:P	26:S:99:ARG:HH22	2.35	0.50
8:A:1447:C:H2'	8:A:1448:G:H8	1.77	0.50
8:A:1631:G:N1	8:A:1634:A:OP2	2.35	0.50
8:A:2638:G:O2'	8:A:2639:A:H8	1.93	0.50
8:A:2801:G:H2'	8:A:2802:G:C8	2.47	0.50
9:B:106:G:H2'	9:B:107:G:O4'	2.12	0.50
34:a:501:C:H2'	34:a:502:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:k:30:ILE:HG12	44:k:45:THR:HG22	1.92	0.50
58:y:138:GLY:C	58:y:140:GLU:N	2.70	0.50
1:0:42:ILE:HG22	1:0:48:TYR:HB2	1.93	0.50
8:A:29:U:H2'	8:A:30:G:C8	2.47	0.50
8:A:285:G:N2	8:A:355:U:O2	2.42	0.50
8:A:642:U:O2'	8:A:644:A:N7	2.37	0.50
8:A:1614:A:C6	26:S:87:PRO:HB3	2.47	0.50
8:A:2573:C:N4	58:y:34:SER:OG	2.45	0.50
17:J:49:ASP:OD1	17:J:121:LYS:NZ	2.36	0.50
34:a:331:G:H2'	53:t:4:LYS:HZ2	1.76	0.50
34:a:500:G:H2'	34:a:501:C:C6	2.47	0.50
34:a:1118:U:H2'	34:a:1119:C:C6	2.46	0.50
39:f:14:GLN:OE1	39:f:14:GLN:N	2.45	0.50
8:A:151:C:H2'	8:A:152:A:H8	1.77	0.50
8:A:1327:A:H2'	8:A:1328:A:O4'	2.12	0.50
8:A:1747:U:H2'	8:A:1748:C:C6	2.47	0.50
28:U:97:SER:O	28:U:98:ASN:HB3	2.12	0.50
34:a:977:A:O2'	34:a:979:C:OP2	2.27	0.50
34:a:1238:A:N7	34:a:1303:C:H1'	2.27	0.50
34:a:1250:A:H2'	34:a:1251:A:C8	2.47	0.50
34:a:1347:G:O2'	34:a:1348:U:P	2.70	0.50
56:w:53:G:H2'	56:w:54:5MU:C6	2.47	0.50
8:A:568:U:O4	25:R:81:LYS:NZ	2.45	0.50
8:A:1084:A:O3'	8:A:1104:C:O2'	2.30	0.50
8:A:1416:G:H2'	8:A:1417:C:H6	1.77	0.50
34:a:236:A:H2'	34:a:237:G:C8	2.47	0.50
34:a:328:C:H4'	34:a:329:A:H5''	1.94	0.50
34:a:401:C:O2'	34:a:621:A:N3	2.42	0.50
34:a:908:A:H2'	34:a:909:A:C8	2.47	0.50
34:a:920:U:H2'	34:a:921:U:C6	2.47	0.50
34:a:1006:G:O6	34:a:1023:U:O2	2.30	0.50
34:a:1007:U:H2'	34:a:1008:U:H6	1.77	0.50
34:a:1302:C:C5	46:m:16:ILE:HG13	2.47	0.50
34:a:1371:G:O3'	42:i:70:GLY:HA3	2.12	0.50
36:c:22:PHE:CZ	43:j:11:LYS:HD3	2.46	0.50
41:h:38:VAL:HG21	41:h:109:VAL:HG12	1.94	0.50
43:j:34:ALA:O	43:j:35:GLN:HG2	2.12	0.50
8:A:577:G:O2'	8:A:1254:A:OP1	2.29	0.49
8:A:667:U:H2'	8:A:668:A:O4'	2.10	0.49
8:A:1269:A:H2'	8:A:1270:C:C6	2.47	0.49
8:A:1494:A:H2'	8:A:1495:A:C8	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:C:180:MET:HB2	10:C:267:VAL:HB	1.94	0.49
15:H:98:ASP:HA	15:H:101:ASP:OD2	2.11	0.49
15:H:100:ALA:O	15:H:103:VAL:HG12	2.12	0.49
34:a:323:U:H2'	34:a:324:G:O4'	2.12	0.49
8:A:33:C:O2	8:A:447:A:N6	2.45	0.49
8:A:182:A:H2'	8:A:183:C:H6	1.77	0.49
10:C:36:ASN:HB2	10:C:61:TYR:HB2	1.93	0.49
34:a:224:U:H2'	34:a:225:C:C6	2.46	0.49
34:a:587:G:OP1	41:h:83:ARG:NH2	2.43	0.49
34:a:1119:C:H2'	34:a:1120:C:H6	1.77	0.49
34:a:1347:G:HO2'	34:a:1373:G:H1	1.60	0.49
35:b:33:ALA:HB2	35:b:38:HIS:HA	1.92	0.49
44:k:63:GLN:HG3	44:k:98:ALA:HB2	1.93	0.49
8:A:481:G:H1'	8:A:506:G:N2	2.27	0.49
8:A:843:G:H2'	8:A:844:A:C8	2.47	0.49
8:A:1441:G:H2'	8:A:1442:U:C6	2.47	0.49
8:A:2202:U:O2'	8:A:2204:G:OP1	2.20	0.49
8:A:2537:U:H2'	8:A:2538:C:C6	2.47	0.49
27:T:54:GLU:N	27:T:54:GLU:OE1	2.44	0.49
34:a:62:U:H2'	34:a:63:C:C6	2.47	0.49
34:a:68:G:H5'	34:a:171:A:O2'	2.12	0.49
34:a:413:G:H1'	34:a:428:G:H21	1.77	0.49
34:a:736:C:H2'	34:a:737:C:C6	2.47	0.49
34:a:946:A:H2'	34:a:947:G:H8	1.76	0.49
8:A:948:C:H1'	8:A:984:A:C8	2.47	0.49
8:A:1085:A:O2'	8:A:1086:A:OP1	2.28	0.49
8:A:1177:G:H2'	8:A:1178:C:H5''	1.94	0.49
8:A:2599:G:C8	10:C:235:GLU:HG2	2.48	0.49
17:J:109:LEU:O	17:J:111:LYS:NZ	2.39	0.49
19:L:95:LEU:HD11	19:L:125:LEU:HD21	1.94	0.49
23:P:108:ARG:NH1	34:a:1464:U:OP2	2.46	0.49
34:a:864:A:H2'	34:a:865:A:C8	2.47	0.49
34:a:1125:U:C6	43:j:40:ILE:HG12	2.47	0.49
39:f:9:MET:HE3	39:f:86:ARG:HB2	1.93	0.49
43:j:9:ARG:HG3	43:j:73:LEU:HD13	1.93	0.49
8:A:1104:C:H2'	8:A:1105:U:C6	2.48	0.49
8:A:1688:U:O2'	8:A:1700:A:N7	2.39	0.49
8:A:2230:G:H5''	31:X:29:LEU:HD12	1.94	0.49
8:A:2246:G:H2'	8:A:2247:A:C8	2.48	0.49
8:A:2522:U:O2'	8:A:2647:U:OP1	2.16	0.49
8:A:2684:U:O4'	18:K:70:ARG:NH1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:R:6:GLN:HG2	25:R:37:GLU:OE1	2.13	0.49
27:T:33:LYS:HG2	27:T:80:TRP:CZ3	2.47	0.49
34:a:148:G:O2'	34:a:1446:A:N3	2.38	0.49
34:a:474:G:H2'	34:a:475:C:C6	2.47	0.49
34:a:1020:G:H2'	34:a:1021:A:C8	2.48	0.49
34:a:1166:G:H2'	34:a:1168:U:OP2	2.12	0.49
34:a:1527:U:OP2	54:u:41:THR:HG22	2.12	0.49
37:d:46:ARG:NH1	58:y:137:SER:O	2.42	0.49
8:A:354:A:H2'	8:A:355:U:O4'	2.12	0.49
8:A:391:A:H1'	8:A:411:G:O4'	2.12	0.49
8:A:1077:A:O2'	16:I:134:SER:O	2.27	0.49
8:A:1266:G:O2'	8:A:2012:G:O6	2.26	0.49
8:A:1416:G:H2'	8:A:1417:C:C6	2.48	0.49
8:A:2037:A:H2'	8:A:2038:G:C8	2.47	0.49
20:M:69:PRO:HA	20:M:94:ALA:CB	2.42	0.49
34:a:21:G:H2'	34:a:22:G:C8	2.48	0.49
34:a:950:U:H2'	34:a:951:G:C8	2.47	0.49
34:a:951:G:OP2	46:m:100:ARG:NH1	2.40	0.49
8:A:954:G:H5''	20:M:13:HIS:CG	2.47	0.49
9:B:79:G:N7	29:V:14:LYS:NZ	2.61	0.49
14:G:163:TYR:HB2	14:G:166:GLU:HB2	1.95	0.49
34:a:107:G:OP1	34:a:325:A:N6	2.43	0.49
34:a:993:G:H2'	34:a:995:C:H41	1.77	0.49
34:a:1244:G:H2'	34:a:1245:C:C6	2.48	0.49
34:a:1493:A:N7	58:y:108:THR:OG1	2.40	0.49
40:g:144:ALA:O	40:g:145:GLU:HB3	2.13	0.49
8:A:52:A:H2'	8:A:53:A:C8	2.47	0.49
8:A:145:C:H2'	8:A:146:A:C8	2.48	0.49
8:A:672:C:OP2	19:L:42:SER:OG	2.25	0.49
8:A:2118:U:H5	8:A:2148:G:H4'	1.78	0.49
8:A:2649:C:H2'	8:A:2650:U:C6	2.48	0.49
19:L:77:ILE:N	19:L:109:LYS:O	2.34	0.49
20:M:41:LEU:HG	20:M:96:ILE:HG13	1.94	0.49
34:a:1530:G:N7	54:u:45:LYS:NZ	2.60	0.49
35:b:130:LYS:HE2	35:b:130:LYS:HA	1.94	0.49
36:c:63:ILE:HG23	36:c:98:ALA:HA	1.94	0.49
36:c:166:TRP:HZ3	36:c:168:ARG:HB2	1.77	0.49
42:i:87:MET:O	42:i:91:GLU:HG3	2.13	0.49
44:k:115:ILE:HD11	54:u:27:VAL:HG23	1.93	0.49
56:w:75:C:H2'	56:w:76:A:O4'	2.12	0.49
8:A:972:A:OP2	8:A:973:A:O2'	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2233:U:H2'	8:A:2234:G:H8	1.78	0.49
34:a:371:A:H2'	34:a:372:C:O4'	2.13	0.49
34:a:518:C:O2	58:y:118:ARG:NH2	2.42	0.49
8:A:103:A:H2'	8:A:104:A:O4'	2.13	0.49
8:A:285:G:H2'	8:A:286:U:C6	2.48	0.49
8:A:395:U:H2'	8:A:396:G:N7	2.28	0.49
8:A:1645:G:H5''	8:A:1646:C:H5'	1.94	0.49
8:A:1715:G:N2	8:A:1744:A:OP2	2.43	0.49
28:U:6:ARG:NH2	28:U:7:ASP:OD1	2.46	0.49
34:a:512:U:H2'	34:a:513:C:C6	2.48	0.49
34:a:522:C:H41	45:l:49:ARG:NH2	2.11	0.49
34:a:1350:A:N7	42:i:119:LYS:NZ	2.61	0.49
37:d:69:ARG:HG2	37:d:69:ARG:NH2	2.27	0.49
54:u:11:PHE:CD1	54:u:11:PHE:O	2.65	0.49
7:6:7:PRO:HG3	13:F:57:ALA:O	2.12	0.48
8:A:909:A:H2'	8:A:912:C:C5	2.48	0.48
8:A:1168:G:H2'	8:A:1169:A:C8	2.48	0.48
8:A:1730:C:O2'	8:A:1731:G:O5'	2.31	0.48
8:A:2377:A:H2'	8:A:2378:A:C8	2.48	0.48
12:E:170:ARG:NH1	12:E:179:SER:OG	2.44	0.48
34:a:130:A:C8	50:q:64:ARG:HG3	2.48	0.48
34:a:202:G:H22	34:a:215:C:H5	1.59	0.48
37:d:27:ILE:HG13	37:d:33:ILE:HG21	1.95	0.48
40:g:39:GLU:HA	40:g:42:VAL:HG22	1.95	0.48
40:g:46:LEU:HD23	40:g:57:GLU:HB3	1.95	0.48
40:g:70:PRO:O	40:g:95:ARG:HG2	2.12	0.48
8:A:1915:3TD:H10A	58:y:105:ARG:CZ	2.43	0.48
13:F:7:TYR:HB2	13:F:172:PHE:CZ	2.46	0.48
17:J:69:ARG:O	17:J:90:GLU:HG3	2.13	0.48
34:a:202:G:H1	34:a:215:C:H5	1.60	0.48
34:a:344:A:H5''	34:a:345:C:C5	2.47	0.48
34:a:972:C:O3'	43:j:59:LYS:HD3	2.14	0.48
34:a:1010:U:H2'	34:a:1011:C:C6	2.48	0.48
34:a:1060:U:H5''	43:j:53:ILE:HD12	1.95	0.48
34:a:1163:A:H2'	34:a:1164:G:C8	2.48	0.48
34:a:1432:G:H1'	34:a:1468:A:N6	2.27	0.48
39:f:16:GLU:HB2	39:f:17:GLN:HE21	1.77	0.48
8:A:208:C:H2'	8:A:209:C:C6	2.48	0.48
8:A:1199:U:H2'	8:A:1200:C:C6	2.48	0.48
8:A:1231:U:H2'	8:A:1232:G:H8	1.78	0.48
8:A:1315:C:O2'	8:A:1392:A:N3	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2146:C:O2'	8:A:2147:A:N7	2.37	0.48
8:A:2554:U:H2'	8:A:2555:U:C6	2.48	0.48
15:H:129:GLU:HA	15:H:143:ILE:HA	1.95	0.48
34:a:1180:A:P	42:i:98:ARG:HH22	2.36	0.48
35:b:172:ILE:HG12	35:b:182:VAL:HG11	1.95	0.48
8:A:468:G:H5''	12:E:55:SER:HB3	1.96	0.48
8:A:851:C:H2'	8:A:852:U:H6	1.78	0.48
8:A:1429:G:H2'	8:A:1430:G:H8	1.78	0.48
8:A:1527:G:N1	8:A:1544:A:OP2	2.38	0.48
8:A:1682:G:H2'	8:A:1683:U:C6	2.49	0.48
8:A:1689:A:H2'	8:A:1690:A:C8	2.48	0.48
8:A:2109:U:N3	8:A:2120:G:N7	2.61	0.48
24:Q:75:TYR:CZ	24:Q:79:ILE:HG13	2.48	0.48
34:a:113:G:H1'	34:a:354:G:H5'	1.94	0.48
34:a:779:C:H2'	34:a:780:A:O4'	2.14	0.48
34:a:1004:A:N6	34:a:1025:U:H4'	2.28	0.48
34:a:1330:U:C2'	34:a:1331:G:H5'	2.44	0.48
56:w:37:MIA:H162	56:w:37:MIA:H121	1.64	0.48
6:5:30:SER:O	8:A:1054:A:H1'	2.13	0.48
8:A:871:U:C5'	20:M:68:PHE:CE2	2.96	0.48
8:A:1084:A:C1'	8:A:1105:U:HO2'	2.25	0.48
8:A:1843:C:H2'	8:A:1844:C:C6	2.48	0.48
8:A:2649:C:H2'	8:A:2650:U:H6	1.78	0.48
15:H:93:SER:OG	15:H:122:LEU:O	2.14	0.48
34:a:49:U:O4	34:a:365:U:H5	1.95	0.48
34:a:198:G:H2'	34:a:199:A:H8	1.78	0.48
34:a:802:A:H3'	34:a:803:G:H8	1.79	0.48
34:a:911:U:H2'	34:a:912:C:C6	2.48	0.48
37:d:78:ALA:HB1	37:d:88:ASN:HB3	1.96	0.48
43:j:50:THR:CG2	43:j:62:ARG:HD3	2.43	0.48
44:k:58:THR:HG22	44:k:60:PHE:H	1.78	0.48
8:A:265:A:N1	8:A:427:U:O2'	2.46	0.48
8:A:322:A:OP2	12:E:163:ASN:HB2	2.14	0.48
8:A:1429:G:H2'	8:A:1430:G:C8	2.49	0.48
8:A:1923:U:H2'	8:A:1924:C:C6	2.47	0.48
8:A:2314:A:OP1	13:F:87:LYS:NZ	2.45	0.48
8:A:2469:A:N6	8:A:2481:G:O2'	2.47	0.48
9:B:42:C:C6	13:F:65:LEU:HB2	2.48	0.48
20:M:53:MET:HG3	20:M:120:ALA:HB2	1.94	0.48
20:M:111:GLU:H	20:M:111:GLU:CD	2.21	0.48
21:N:79:LEU:O	21:N:80:PHE:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:352:C:H4'	34:a:354:G:OP1	2.12	0.48
34:a:465:A:H4'	34:a:466:A:OP1	2.14	0.48
43:j:35:GLN:HG3	43:j:77:VAL:O	2.14	0.48
49:p:4:ILE:HG12	49:p:21:VAL:HG22	1.95	0.48
8:A:1370:C:H2'	8:A:1371:G:O4'	2.13	0.48
8:A:2680:U:O2'	8:A:2681:C:H5'	2.13	0.48
8:A:2683:C:O2	18:K:70:ARG:NH2	2.47	0.48
8:A:2748:A:H5'	14:G:3:VAL:HG21	1.96	0.48
26:S:25:ARG:NH2	26:S:74:ILE:O	2.37	0.48
29:V:42:LEU:HB3	29:V:47:VAL:HG21	1.96	0.48
34:a:455:G:H2'	34:a:456:A:H8	1.79	0.48
34:a:602:A:H2'	34:a:603:U:O2	2.14	0.48
35:b:96:LEU:H	35:b:99:MET:HE3	1.79	0.48
35:b:99:MET:HA	35:b:106:VAL:HG21	1.95	0.48
36:c:53:ARG:HB2	36:c:68:HIS:HB2	1.95	0.48
58:y:4:ILE:O	58:y:96:LYS:NZ	2.46	0.48
8:A:494:G:H4'	26:S:6:LYS:HB2	1.95	0.48
8:A:2193:G:H2'	8:A:2194:U:C6	2.49	0.48
11:D:121:THR:HB	11:D:127:PHE:CD2	2.49	0.48
13:F:45:ASP:HB3	13:F:48:LEU:HG	1.95	0.48
15:H:18:GLN:HE21	15:H:39:ALA:CB	2.26	0.48
32:Y:6:LEU:HB3	32:Y:56:LEU:HD13	1.95	0.48
34:a:1000:A:H2'	34:a:1001:C:C6	2.48	0.48
34:a:1001:C:H2'	34:a:1002:G:H8	1.79	0.48
34:a:1347:G:O2'	34:a:1348:U:OP2	2.19	0.48
35:b:19:THR:HG22	35:b:38:HIS:CD2	2.48	0.48
37:d:61:ARG:HG2	37:d:71:PHE:CD1	2.49	0.48
8:A:1056:G:H4'	8:A:1086:A:H8	1.78	0.48
8:A:2773:C:OP1	11:D:169:ARG:NH2	2.46	0.48
9:B:5:U:H2'	9:B:6:G:H8	1.78	0.48
14:G:136:ASP:HB3	14:G:139:VAL:HB	1.96	0.48
15:H:2:GLN:HB3	15:H:18:GLN:HE22	1.79	0.48
18:K:105:ARG:NH1	23:P:33:GLU:OE2	2.47	0.48
37:d:56:GLU:OE2	37:d:195:ASN:N	2.40	0.48
8:A:12:U:O2	8:A:2626:C:H4'	2.13	0.48
8:A:308:G:H2'	8:A:309:A:C8	2.49	0.48
8:A:546:U:O2	8:A:547:A:H1'	2.14	0.48
8:A:729:G:C6	10:C:206:LYS:HB2	2.49	0.48
8:A:2567:G:H2'	8:A:2568:U:C6	2.49	0.48
34:a:3:A:H5''	34:a:4:U:O4'	2.14	0.48
34:a:82:G:C2	34:a:83:C:H1'	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:982:U:H4'	34:a:983:A:O4'	2.14	0.48
34:a:985:C:H2'	34:a:986:U:C6	2.49	0.48
34:a:1060:U:H2'	34:a:1061:G:H8	1.79	0.48
50:q:46:HIS:NE2	50:q:48:GLU:HB2	2.29	0.48
8:A:145:C:H2'	8:A:146:A:H8	1.79	0.47
8:A:498:G:H1'	28:U:44:HIS:HE1	1.79	0.47
8:A:704:G:H2'	8:A:726:G:N2	2.29	0.47
8:A:1094:U:O2'	8:A:1095:A:H3'	2.14	0.47
8:A:1830:C:H2'	8:A:1831:G:H8	1.79	0.47
10:C:159:THR:HG22	10:C:176:ARG:HG2	1.95	0.47
14:G:59:ASP:OD1	14:G:59:ASP:N	2.47	0.47
29:V:9:ARG:HG2	29:V:41:GLU:HG3	1.95	0.47
34:a:736:C:H2'	34:a:737:C:H6	1.79	0.47
34:a:1464:U:H2'	34:a:1465:A:C8	2.49	0.47
40:g:56:SER:HB3	40:g:59:GLU:HG2	1.96	0.47
41:h:104:SER:HB2	41:h:125:ILE:HD11	1.95	0.47
44:k:15:VAL:HG13	44:k:78:ILE:HD11	1.95	0.47
8:A:871:U:H5''	20:M:68:PHE:CZ	2.48	0.47
8:A:1187:G:H5''	25:R:83:TYR:CE1	2.49	0.47
8:A:1199:U:H2'	8:A:1200:C:H6	1.80	0.47
8:A:2079:U:H2'	8:A:2080:A:O4'	2.15	0.47
8:A:2443:C:H2'	8:A:2444:G:C8	2.49	0.47
8:A:2455:G:H2'	8:A:2456:C:C6	2.49	0.47
8:A:2556:C:H2'	8:A:2557:G:O4'	2.13	0.47
20:M:11:LYS:HE3	20:M:87:GLY:O	2.14	0.47
29:V:11:GLU:HG3	29:V:16:ALA:HB1	1.95	0.47
34:a:1130:A:H2'	34:a:1131:G:C8	2.49	0.47
34:a:1414:U:H2'	34:a:1415:G:H8	1.80	0.47
34:a:1496:C:H2'	34:a:1497:G:O4'	2.14	0.47
46:m:10:ASP:HB2	46:m:45:SER:HB3	1.96	0.47
46:m:48:SER:O	46:m:52:ILE:HD12	2.14	0.47
56:w:46:G7M:H5''	56:w:46:G7M:H8	1.95	0.47
8:A:476:G:H4'	8:A:502:A:N1	2.29	0.47
8:A:1044:C:O2'	8:A:1111:A:N1	2.47	0.47
8:A:2175:C:N4	8:A:2176:A:N7	2.62	0.47
15:H:41:LYS:HD2	15:H:41:LYS:HA	1.49	0.47
29:V:55:GLU:OE1	29:V:55:GLU:N	2.43	0.47
34:a:1360:A:OP2	47:n:75:ARG:NH2	2.48	0.47
58:y:138:GLY:C	58:y:140:GLU:H	2.22	0.47
7:6:49:ARG:HH11	46:m:67:ASP:HB3	1.79	0.47
8:A:144:A:H2'	8:A:145:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:151:C:H2'	8:A:152:A:C8	2.48	0.47
8:A:760:G:H2'	8:A:761:A:O4'	2.15	0.47
8:A:1087:G:N2	8:A:1102:C:H41	2.12	0.47
8:A:1338:G:O2'	8:A:1393:A:N1	2.36	0.47
8:A:1443:U:H2'	8:A:1444:G:C8	2.49	0.47
8:A:2047:C:H2'	8:A:2048:G:H8	1.78	0.47
19:L:132:ARG:HG3	19:L:142:ILE:HD12	1.95	0.47
20:M:20:LEU:HD13	29:V:81:PRO:HG2	1.94	0.47
34:a:890:G:O2'	34:a:906:A:N6	2.46	0.47
34:a:1006:G:C6	34:a:1023:U:O2	2.68	0.47
34:a:1436:U:H2'	34:a:1437:A:C8	2.49	0.47
43:j:11:LYS:HA	43:j:70:HIS:O	2.14	0.47
5:4:1:MET:SD	5:4:36:ARG:HB2	2.54	0.47
8:A:78:U:H2'	8:A:79:C:C6	2.50	0.47
8:A:102:U:O2'	8:A:103:A:OP1	2.23	0.47
8:A:975:A:H1'	8:A:990:A:C2	2.50	0.47
8:A:2109:U:H1'	8:A:2180:U:H3	1.80	0.47
8:A:2573:C:OP2	58:y:32:LYS:NZ	2.41	0.47
15:H:126:GLY:O	15:H:145:ASN:HA	2.14	0.47
22:O:27:VAL:HG21	22:O:40:ILE:HD12	1.96	0.47
31:X:41:SER:OG	31:X:64:ASP:OD2	2.31	0.47
34:a:521:G:O2'	34:a:536:C:O2'	2.29	0.47
34:a:686:U:O2'	34:a:687:A:O4'	2.32	0.47
34:a:1338:G:H2'	34:a:1339:A:C8	2.49	0.47
34:a:1478:U:H2'	34:a:1479:C:C6	2.50	0.47
37:d:36:ALA:HB3	37:d:41:GLY:HA2	1.97	0.47
39:f:29:ILE:HD13	39:f:64:VAL:HG11	1.96	0.47
41:h:6:ILE:O	41:h:10:LEU:HG	2.13	0.47
43:j:52:LEU:HD23	43:j:62:ARG:HG2	1.96	0.47
2:1:8:ILE:HD13	2:1:24:LYS:HB2	1.97	0.47
8:A:754:U:H2'	8:A:755:U:C6	2.49	0.47
8:A:1930:G:O2'	8:A:1968:G:O6	2.29	0.47
8:A:2848:G:O2'	8:A:2868:A:N6	2.48	0.47
13:F:51:ASN:ND2	13:F:146:ASP:OD2	2.48	0.47
26:S:46:LEU:O	26:S:50:VAL:HG23	2.14	0.47
34:a:515:G:O2'	34:a:516:PSU:O5'	2.30	0.47
34:a:1009:U:H2'	34:a:1010:U:C6	2.49	0.47
34:a:1305:G:N2	34:a:1331:G:H1'	2.30	0.47
41:h:112:ASP:N	41:h:112:ASP:OD1	2.47	0.47
8:A:172:A:H2'	8:A:173:A:H8	1.78	0.47
8:A:632:A:H2'	8:A:633:A:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:645:C:O2'	8:A:646:U:H5''	2.14	0.47
8:A:1019:U:OP1	8:A:1035:U:O2'	2.19	0.47
8:A:2292:U:H2'	8:A:2293:G:C8	2.49	0.47
9:B:104:A:H2'	9:B:105:G:O4'	2.15	0.47
11:D:156:PHE:CE1	17:J:81:ILE:HD13	2.50	0.47
13:F:115:GLY:HA3	13:F:177:ARG:HB2	1.96	0.47
15:H:2:GLN:HB3	15:H:18:GLN:NE2	2.29	0.47
19:L:19:LEU:HD12	19:L:27:LEU:HD13	1.96	0.47
23:P:77:SER:OG	23:P:79:VAL:HG12	2.15	0.47
31:X:2:ARG:O	31:X:11:PRO:HD3	2.14	0.47
34:a:235:C:H2'	34:a:236:A:C8	2.50	0.47
34:a:687:A:N6	34:a:703:G:H1'	2.28	0.47
34:a:1059:C:O3'	47:n:85:ARG:NH1	2.39	0.47
34:a:1143:G:H2'	34:a:1144:G:C8	2.47	0.47
34:a:1435:G:H2'	34:a:1436:U:C6	2.49	0.47
40:g:17:PHE:HB3	40:g:58:LEU:HD11	1.97	0.47
42:i:18:VAL:HG22	42:i:64:ILE:HG23	1.96	0.47
54:u:9:GLU:HB3	54:u:10:PRO:HD3	1.97	0.47
8:A:134:G:H2'	8:A:135:U:C6	2.50	0.47
8:A:577:G:H2'	8:A:578:G:C8	2.50	0.47
8:A:792:A:N3	8:A:2072:C:O2'	2.44	0.47
8:A:1857:G:H22	8:A:1884:G:H2'	1.78	0.47
8:A:2104:C:C4	8:A:2105:U:H1'	2.49	0.47
8:A:2151:U:H2'	8:A:2152:G:N7	2.29	0.47
34:a:161:A:H2'	34:a:162:A:C8	2.50	0.47
34:a:527:G7M:O2'	34:a:535:A:N1	2.41	0.47
34:a:1006:G:O6	34:a:1023:U:C2	2.68	0.47
36:c:85:LYS:O	36:c:89:VAL:HG12	2.14	0.47
39:f:4:TYR:CD2	39:f:71:ILE:HG13	2.50	0.47
8:A:153:U:H2'	8:A:154:U:C6	2.49	0.47
8:A:419:U:H2'	8:A:420:C:C6	2.50	0.47
8:A:1593:A:H2'	8:A:1594:U:C6	2.50	0.47
8:A:2055:C:H5'	8:A:2056:G:H5''	1.97	0.47
8:A:2110:G:H21	8:A:2118:U:HO2'	1.59	0.47
8:A:2646:C:H2'	8:A:2647:U:O4'	2.15	0.47
8:A:2848:G:H1'	8:A:2868:A:N6	2.30	0.47
12:E:170:ARG:NH2	12:E:176:ASP:OD1	2.28	0.47
15:H:15:LEU:O	15:H:15:LEU:HD23	2.15	0.47
28:U:10:VAL:HA	28:U:71:ILE:HA	1.97	0.47
34:a:210:C:H4'	34:a:211:G:C2	2.49	0.47
34:a:1297:G:N3	40:g:113:LYS:HD2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:b:46:VAL:HG13	35:b:47:PRO:HD3	1.96	0.47
36:c:147:GLY:HA3	36:c:171:ARG:O	2.15	0.47
8:A:223:A:N1	8:A:407:G:O2'	2.39	0.47
8:A:360:U:H2'	8:A:361:G:O4'	2.15	0.47
8:A:364:C:H2'	8:A:365:U:C6	2.49	0.47
8:A:438:G:H2'	8:A:439:A:C8	2.50	0.47
8:A:1656:C:H2'	8:A:1657:U:H6	1.80	0.47
8:A:1824:G:O3'	10:C:246:PRO:HD3	2.15	0.47
8:A:1842:G:H2'	8:A:1843:C:C6	2.50	0.47
8:A:1864:U:OP1	8:A:2410:G:O2'	2.23	0.47
8:A:2373:G:H2'	8:A:2374:C:C6	2.50	0.47
20:M:53:MET:HE2	20:M:117:PHE:HD1	1.79	0.47
34:a:409:U:H5''	37:d:24:VAL:HG11	1.97	0.47
34:a:553:A:H5''	45:l:20:VAL:HG21	1.96	0.47
34:a:1002:G:H2'	34:a:1003:G:O4'	2.14	0.47
34:a:1236:A:H2'	34:a:1237:C:C6	2.50	0.47
53:t:47:GLN:HG3	53:t:51:ASN:HD21	1.79	0.47
8:A:5:A:H2'	8:A:6:A:H8	1.80	0.46
8:A:222:A:N1	8:A:233:A:H5''	2.30	0.46
8:A:305:C:H2'	8:A:306:U:C6	2.51	0.46
8:A:640:C:H2'	8:A:641:U:C6	2.50	0.46
8:A:993:G:OP2	24:Q:50:ARG:NH2	2.48	0.46
8:A:1905:C:H3'	8:A:1930:G:C8	2.49	0.46
8:A:2801:G:H2'	8:A:2802:G:H8	1.79	0.46
19:L:80:SER:N	19:L:114:GLY:O	2.48	0.46
23:P:84:SER:OG	23:P:86:LYS:HE3	2.16	0.46
34:a:1148:U:H2'	34:a:1149:C:O4'	2.15	0.46
34:a:1463:U:H2'	34:a:1464:U:C6	2.51	0.46
50:q:11:VAL:HG21	50:q:52:CYS:HB3	1.97	0.46
58:y:50:GLU:O	58:y:51:TYR:HB3	2.14	0.46
8:A:492:A:H2'	8:A:493:G:O4'	2.14	0.46
8:A:493:G:H2'	8:A:494:G:O4'	2.15	0.46
8:A:1083:U:H4'	8:A:1084:A:N7	2.31	0.46
8:A:2474:U:H3'	8:A:2475:C:C6	2.50	0.46
8:A:2684:U:H4'	18:K:76:VAL:HG21	1.96	0.46
8:A:2808:G:O2'	8:A:2809:A:H8	1.98	0.46
13:F:152:ASP:N	13:F:152:ASP:OD1	2.48	0.46
14:G:93:TYR:HA	14:G:105:SER:O	2.15	0.46
15:H:42:LYS:HG2	15:H:46:PHE:HE2	1.80	0.46
34:a:22:G:O2'	34:a:913:A:N1	2.47	0.46
34:a:381:C:H2'	34:a:382:A:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:399:G:H2'	34:a:400:C:C6	2.51	0.46
34:a:672:U:H2'	34:a:673:A:C8	2.50	0.46
34:a:1216:A:H5''	47:n:4:SER:HB3	1.97	0.46
34:a:1309:G:N7	46:m:97:ARG:NH2	2.62	0.46
58:y:26:GLY:HA3	58:y:30:VAL:HB	1.98	0.46
8:A:184:C:H2'	8:A:185:G:C8	2.50	0.46
8:A:499:U:H2'	8:A:500:G:O4'	2.15	0.46
8:A:1419:A:O2'	8:A:1421:G:N7	2.40	0.46
8:A:2515:C:H2'	8:A:2516:A:H8	1.80	0.46
8:A:2655:G:O2'	8:A:2656:U:P	2.73	0.46
8:A:2839:G:O2'	21:N:49:GLU:OE1	2.26	0.46
15:H:80:ILE:O	15:H:146:VAL:HA	2.16	0.46
34:a:684:U:H2'	34:a:685:G:O4'	2.14	0.46
43:j:29:ALA:C	43:j:31:ARG:H	2.23	0.46
45:l:99:GLY:HA3	45:l:117:GLY:HA3	1.98	0.46
49:p:70:ARG:HD2	49:p:70:ARG:HA	1.74	0.46
7:6:10:GLU:OE1	7:6:10:GLU:N	2.39	0.46
7:6:18:CYS:HB2	7:6:40:CYS:HB3	1.95	0.46
8:A:24:G:O2'	26:S:78:GLU:O	2.34	0.46
8:A:871:U:H4'	20:M:68:PHE:CD2	2.51	0.46
8:A:1723:G:H2'	8:A:1724:G:O4'	2.15	0.46
8:A:2130:U:H2'	8:A:2131:U:H4'	1.98	0.46
34:a:4:U:H2'	34:a:5:U:H3'	1.96	0.46
34:a:294:U:OP1	34:a:610:U:O2'	2.30	0.46
34:a:607:A:H2'	34:a:608:A:C8	2.51	0.46
37:d:187:ARG:NH1	37:d:187:ARG:O	2.48	0.46
56:w:18:G:HO2'	56:w:57:G:H22	1.58	0.46
8:A:586:A:N1	8:A:809:G:O2'	2.34	0.46
8:A:1354:A:H2'	8:A:1355:G:O4'	2.16	0.46
8:A:1856:U:H2'	8:A:1857:G:O4'	2.16	0.46
13:F:60:SER:HB2	13:F:90:LEU:HD21	1.98	0.46
15:H:9:VAL:H	15:H:13:GLY:HA3	1.81	0.46
34:a:1266:G:N2	34:a:1269:A:OP2	2.41	0.46
34:a:1404:C:H2'	34:a:1405:G:C8	2.50	0.46
37:d:180:THR:OG1	37:d:181:PHE:N	2.49	0.46
46:m:11:HIS:ND1	46:m:11:HIS:O	2.49	0.46
4:3:29:ARG:HG2	8:A:2393:U:P	2.56	0.46
8:A:173:A:H2'	8:A:174:U:C6	2.51	0.46
8:A:630:G:N2	8:A:633:A:OP2	2.38	0.46
8:A:905:A:C2'	8:A:906:U:H5'	2.45	0.46
8:A:918:A:H5''	9:B:97:C:O2'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:947:A:H2'	8:A:948:C:C6	2.50	0.46
8:A:1057:A:C2	8:A:1086:A:C6	3.04	0.46
8:A:1843:C:H2'	8:A:1844:C:H6	1.81	0.46
8:A:1914:C:OP1	8:A:1915:3TD:H10	2.16	0.46
8:A:2125:G:H1'	8:A:2173:A:H62	1.81	0.46
8:A:2636:C:H2'	8:A:2637:U:C6	2.50	0.46
8:A:2740:A:H2'	8:A:2741:A:C8	2.51	0.46
34:a:967:5MC:OP2	34:a:968:A:O2'	2.26	0.46
36:c:10:ARG:NH2	36:c:174:LEU:O	2.45	0.46
8:A:58:G:O2'	8:A:73:A:N1	2.39	0.46
8:A:228:C:N4	8:A:2407:A:N3	2.63	0.46
8:A:527:C:N4	8:A:2779:U:OP2	2.47	0.46
8:A:589:U:H2'	8:A:590:A:C8	2.51	0.46
8:A:598:U:H2'	8:A:599:A:C8	2.51	0.46
8:A:675:A:N3	8:A:2443:C:O2'	2.46	0.46
8:A:857:G:H2'	8:A:858:G:O4'	2.15	0.46
8:A:1827:U:H5'	8:A:1971:U:H4'	1.97	0.46
8:A:2391:G:C2'	8:A:2424:C:H41	2.28	0.46
8:A:2747:G:O6	8:A:2755:C:H5''	2.15	0.46
10:C:204:LEU:O	10:C:206:LYS:N	2.48	0.46
23:P:87:ARG:NH2	23:P:109:ILE:O	2.35	0.46
24:Q:85:ALA:HB2	24:Q:115:ALA:HB2	1.98	0.46
34:a:218:U:H2'	34:a:219:U:O4'	2.15	0.46
34:a:628:G:H2'	34:a:629:A:C8	2.51	0.46
34:a:1000:A:H2'	34:a:1001:C:H6	1.79	0.46
34:a:1428:A:H2'	34:a:1429:A:O4'	2.15	0.46
37:d:67:LEU:O	37:d:71:PHE:HB2	2.14	0.46
46:m:16:ILE:O	46:m:19:THR:OG1	2.34	0.46
46:m:32:ILE:HD12	46:m:58:GLU:HG3	1.97	0.46
50:q:6:THR:OG1	50:q:60:ILE:O	2.20	0.46
8:A:1827:U:H2'	8:A:1828:G:O4'	2.15	0.46
8:A:2848:G:H1'	8:A:2868:A:H61	1.81	0.46
31:X:12:VAL:HG22	31:X:28:PHE:HB2	1.96	0.46
34:a:160:A:H2'	34:a:161:A:O4'	2.16	0.46
34:a:335:C:H2'	34:a:336:A:H8	1.80	0.46
34:a:978:A:C2	34:a:1319:A:C4	3.03	0.46
34:a:1316:G:H2'	34:a:1317:C:H5''	1.96	0.46
37:d:144:ILE:HG23	37:d:144:ILE:HD12	1.47	0.46
40:g:25:PHE:HE2	40:g:119:LEU:HD21	1.81	0.46
56:w:26:A:H61	56:w:44:G:H1	1.62	0.46
1:0:3:GLN:HA	8:A:2615:U:C2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:1:MET:HB3	9:B:43:C:H5''	1.97	0.46
8:A:222:A:C2	8:A:233:A:H5''	2.51	0.46
8:A:282:A:H2'	8:A:283:G:H8	1.80	0.46
8:A:832:U:H2'	8:A:833:A:H8	1.79	0.46
8:A:1278:C:H2'	8:A:1279:G:C8	2.51	0.46
8:A:1319:C:O2'	8:A:1320:C:H5'	2.16	0.46
8:A:2598:A:H5''	10:C:233:GLY:HA3	1.97	0.46
8:A:2751:G:H4'	14:G:3:VAL:HG23	1.97	0.46
11:D:129:THR:HG22	11:D:130:GLN:O	2.16	0.46
13:F:10:GLU:O	13:F:13:LYS:HG3	2.16	0.46
15:H:117:LEU:HG	15:H:120:GLY:O	2.16	0.46
34:a:875:U:O2'	41:h:14:ARG:NH1	2.42	0.46
34:a:1037:C:H2'	34:a:1038:C:O4'	2.16	0.46
34:a:1347:G:H1'	34:a:1348:U:H5	1.81	0.46
34:a:1390:U:H2'	34:a:1391:U:C6	2.50	0.46
37:d:138:PRO:HA	37:d:181:PHE:HD2	1.80	0.46
41:h:95:MET:HE2	41:h:98:LEU:HB2	1.97	0.46
43:j:63:ASP:HB3	43:j:65:TYR:CZ	2.51	0.46
8:A:708:G:H2'	8:A:709:U:C6	2.51	0.46
8:A:1009:A:N3	8:A:1153:C:O2'	2.47	0.46
8:A:1251:C:OP2	24:Q:5:ARG:HD2	2.16	0.46
8:A:1485:U:H2'	8:A:1486:U:C6	2.51	0.46
8:A:2065:C:H2'	8:A:2066:C:C6	2.51	0.46
21:N:35:LYS:HD2	21:N:112:TYR:CZ	2.51	0.46
34:a:299:G:H2'	34:a:300:A:C8	2.51	0.46
34:a:696:A:H2'	34:a:697:U:H6	1.80	0.46
34:a:1041:G:H2'	34:a:1042:A:C8	2.51	0.46
34:a:1150:A:H2	43:j:41:PRO:HG2	1.81	0.46
45:l:29:LYS:HD3	45:l:29:LYS:HA	1.79	0.46
49:p:40:ASN:HD22	49:p:46:LYS:HD2	1.80	0.46
8:A:1316:U:H2'	8:A:1317:G:C8	2.51	0.45
8:A:1357:C:H2'	8:A:1358:G:O4'	2.17	0.45
8:A:1704:C:H2'	8:A:1705:A:C8	2.51	0.45
8:A:2087:G:H2'	8:A:2088:A:C8	2.52	0.45
8:A:2808:G:H2'	8:A:2890:G:O6	2.16	0.45
12:E:153:LEU:HD11	12:E:158:PHE:HB2	1.99	0.45
14:G:126:THR:HB	14:G:129:GLU:CD	2.41	0.45
15:H:68:ARG:HG2	15:H:70:GLU:HB2	1.98	0.45
17:J:31:GLU:HG2	17:J:142:ILE:HB	1.97	0.45
25:R:68:ARG:HB3	25:R:90:ARG:HB3	1.98	0.45
34:a:604:G:H2'	34:a:605:U:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:608:A:H2'	34:a:609:A:O4'	2.16	0.45
34:a:1149:C:H2'	34:a:1150:A:C8	2.52	0.45
42:i:23:GLY:HA3	42:i:61:ASP:CG	2.41	0.45
46:m:93:GLY:HA2	46:m:108:ARG:HH12	1.81	0.45
48:o:1:SER:HB2	48:o:34:GLN:HE22	1.81	0.45
7:6:43:PHE:HZ	13:F:177:ARG:HA	1.81	0.45
8:A:373:U:H2'	8:A:374:A:H8	1.81	0.45
8:A:709:U:H2'	8:A:710:U:C6	2.51	0.45
8:A:868:U:O2	20:M:8:LYS:NZ	2.44	0.45
8:A:1045:C:H41	8:A:1111:A:H2'	1.82	0.45
8:A:1224:U:H2'	8:A:1225:G:C8	2.51	0.45
8:A:1485:U:H2'	8:A:1486:U:H6	1.82	0.45
8:A:1769:U:O2'	8:A:1958:C:OP1	2.32	0.45
8:A:2405:G:H1'	8:A:2412:A:N6	2.31	0.45
8:A:2723:C:H2'	8:A:2724:U:O4'	2.17	0.45
15:H:18:GLN:HE21	15:H:39:ALA:HB1	1.81	0.45
15:H:93:SER:CB	15:H:123:ARG:NH1	2.67	0.45
34:a:270:A:H2'	34:a:271:C:C6	2.52	0.45
34:a:458:U:H2'	34:a:459:A:H8	1.77	0.45
34:a:505:G:H2'	34:a:506:G:C8	2.50	0.45
34:a:1085:U:H3'	34:a:1086:U:C5	2.51	0.45
34:a:1155:A:H2'	34:a:1156:G:O4'	2.16	0.45
35:b:163:ILE:HD11	35:b:213:LEU:HD21	1.99	0.45
36:c:129:PHE:O	36:c:133:MET:HG3	2.16	0.45
37:d:7:LYS:HB3	37:d:20:LEU:HB3	1.98	0.45
8:A:1672:A:C2	8:A:2582:G:H5'	2.52	0.45
8:A:1786:A:H1'	8:A:1938:A:N6	2.31	0.45
8:A:2105:U:H2'	8:A:2106:U:C5	2.35	0.45
8:A:2262:U:OP1	8:A:2387:U:O2'	2.26	0.45
8:A:2661:G:H2'	8:A:2662:A:C8	2.52	0.45
8:A:2895:G:H2'	8:A:2896:C:C6	2.52	0.45
18:K:103:VAL:O	18:K:122:VAL:HB	2.16	0.45
21:N:21:PHE:CZ	21:N:43:GLU:HB3	2.52	0.45
27:T:54:GLU:HG2	27:T:88:LYS:HB2	1.99	0.45
34:a:119:A:H4'	34:a:120:A:C4	2.52	0.45
34:a:494:G:H2'	34:a:496:A:H8	1.80	0.45
34:a:846:G:H2'	34:a:847:G:C8	2.51	0.45
34:a:1417:G:N2	34:a:1482:G:H2'	2.31	0.45
36:c:23:ALA:HB1	36:c:27:GLU:HG2	1.97	0.45
36:c:61:LYS:O	36:c:61:LYS:HD3	2.17	0.45
52:s:15:LEU:O	52:s:19:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:964:C:O2'	8:A:2273:A:N3	2.38	0.45
8:A:1443:U:H2'	8:A:1444:G:H8	1.81	0.45
8:A:1853:A:N1	8:A:2087:G:H1'	2.32	0.45
8:A:2819:G:H2'	8:A:2821:A:N7	2.31	0.45
10:C:56:GLY:HA2	10:C:212:TRP:HA	1.98	0.45
15:H:27:ARG:NH1	31:X:59:ASP:OD2	2.49	0.45
15:H:100:ALA:O	15:H:104:THR:HG22	2.16	0.45
34:a:89:U:H3'	34:a:89:U:H6	1.81	0.45
34:a:826:C:O2	41:h:15:ASN:ND2	2.50	0.45
34:a:834:U:H2'	34:a:835:U:C6	2.51	0.45
34:a:1003:G:HO2'	34:a:1004:A:P	2.38	0.45
34:a:1004:A:H2	34:a:1026:G:C5	2.34	0.45
34:a:1060:U:P	47:n:85:ARG:HH12	2.38	0.45
34:a:1241:G:H2'	34:a:1242:G:H8	1.81	0.45
34:a:1348:U:H4'	42:i:121:ARG:HG3	1.98	0.45
35:b:53:LEU:HD22	35:b:219:THR:HG21	1.99	0.45
43:j:15:HIS:HA	43:j:18:ILE:HG22	1.97	0.45
7:6:56:ARG:HG3	52:s:64:GLU:HA	1.98	0.45
8:A:242:G:O2'	8:A:243:U:OP2	2.34	0.45
8:A:588:U:H2'	8:A:589:U:C6	2.52	0.45
8:A:640:C:H2'	8:A:641:U:H6	1.81	0.45
8:A:687:C:H2'	8:A:688:U:O4'	2.17	0.45
8:A:1070:A:H5'	8:A:1072:C:OP1	2.15	0.45
8:A:1086:A:H3'	8:A:1086:A:N3	2.30	0.45
8:A:1183:U:H2'	8:A:1184:U:C6	2.51	0.45
8:A:1857:G:N2	8:A:1884:G:H2'	2.30	0.45
8:A:2520:C:C6	8:A:2567:G:H1'	2.51	0.45
8:A:2700:A:H2'	8:A:2701:U:H6	1.80	0.45
34:a:335:C:H2'	34:a:336:A:C8	2.50	0.45
34:a:1070:U:H2'	34:a:1071:C:C6	2.51	0.45
34:a:1319:A:C8	34:a:1323:G:C6	3.05	0.45
34:a:1326:U:H2'	34:a:1327:C:C6	2.52	0.45
39:f:51:ILE:O	39:f:54:LEU:HB3	2.17	0.45
43:j:34:ALA:C	43:j:35:GLN:HG2	2.42	0.45
7:6:42:PRO:O	7:6:45:THR:O	2.35	0.45
8:A:92:U:H2'	8:A:93:G:O4'	2.17	0.45
8:A:1028:A:H2'	8:A:1029:A:H8	1.78	0.45
8:A:1341:G:H1'	27:T:59:ASN:HB3	1.98	0.45
8:A:2096:C:H2'	8:A:2097:A:C8	2.52	0.45
9:B:66:A:N6	9:B:108:A:OP2	2.49	0.45
15:H:72:ILE:HA	15:H:142:VAL:HG22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:U:84:PHE:CE1	28:U:93:ARG:HG2	2.52	0.45
34:a:513:C:H2'	34:a:514:C:C6	2.52	0.45
34:a:855:U:OP2	34:a:871:U:N3	2.46	0.45
35:b:70:GLY:O	35:b:92:ASN:HA	2.17	0.45
43:j:40:ILE:HA	43:j:41:PRO:HD2	1.60	0.45
51:r:36:GLY:O	51:r:62:ARG:NH2	2.36	0.45
8:A:279:A:N6	8:A:361:G:O2'	2.46	0.45
8:A:300:A:OP2	28:U:81:ARG:NH2	2.36	0.45
8:A:361:G:H8	8:A:361:G:OP2	2.00	0.45
8:A:532:A:H4'	8:A:533:G:C8	2.52	0.45
8:A:1496:A:H2'	8:A:1498:C:C5	2.51	0.45
8:A:2193:G:H2'	8:A:2194:U:H6	1.82	0.45
34:a:559:A:H4'	34:a:560:A:H3'	1.97	0.45
34:a:571:U:H5''	34:a:819:A:C5	2.52	0.45
35:b:126:ASP:C	35:b:127:LYS:HD3	2.42	0.45
37:d:46:ARG:HH21	37:d:46:ARG:HB2	1.82	0.45
37:d:162:GLU:C	37:d:164:ARG:H	2.25	0.45
38:e:152:VAL:HA	38:e:155:LYS:HE2	1.98	0.45
45:l:31:GLY:O	45:l:78:VAL:HA	2.17	0.45
58:y:41:PHE:HD2	58:y:70:ILE:HD12	1.82	0.45
5:4:2:LYS:NZ	8:A:2478:A:OP2	2.35	0.45
8:A:208:C:H2'	8:A:209:C:H6	1.82	0.45
8:A:445:C:H2'	8:A:446:G:O4'	2.16	0.45
8:A:475:C:N3	8:A:479:A:N7	2.65	0.45
8:A:549:G:H2'	8:A:550:C:C6	2.52	0.45
8:A:641:U:O2'	8:A:2350:C:OP1	2.34	0.45
8:A:828:U:H4'	8:A:831:G:N1	2.32	0.45
8:A:1053:C:H42	8:A:1106:G:H1	1.65	0.45
8:A:1059:G:C8	8:A:1060:U:H6	2.34	0.45
8:A:2577:A:H5''	8:A:2578:G:H5'	1.99	0.45
11:D:25:THR:HG21	11:D:193:VAL:HG22	1.99	0.45
19:L:37:GLY:O	19:L:41:ARG:HG2	2.17	0.45
22:O:81:ARG:O	22:O:85:LYS:HG2	2.17	0.45
34:a:20:U:H2'	34:a:21:G:O4'	2.17	0.45
34:a:148:G:H2'	34:a:149:A:O4'	2.16	0.45
34:a:411:A:P	37:d:25:ARG:HH22	2.40	0.45
34:a:695:A:H2'	34:a:696:A:C8	2.52	0.45
34:a:1413:A:H2	34:a:1487:G:H22	1.65	0.45
58:y:51:TYR:HA	58:y:54:GLU:HB3	1.99	0.45
8:A:569:U:H2'	8:A:570:G:O4'	2.17	0.45
8:A:674:G:H2'	8:A:804:A:H61	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1632:A:H2'	8:A:1633:G:C8	2.52	0.45
8:A:2237:G:H5''	8:A:2238:G:OP1	2.17	0.45
8:A:2238:G:H2'	8:A:2238:G:N3	2.32	0.45
18:K:92:GLU:OE1	18:K:92:GLU:N	2.50	0.45
30:W:33:ILE:HD11	30:W:78:ILE:HD11	1.99	0.45
34:a:198:G:H2'	34:a:199:A:C8	2.51	0.45
34:a:409:U:OP1	37:d:22:SER:HB3	2.17	0.45
34:a:528:C:OP1	58:y:126:SER:OG	2.26	0.45
34:a:1308:U:H2'	34:a:1309:G:H8	1.82	0.45
34:a:1347:G:O2'	34:a:1373:G:N1	2.46	0.45
42:i:18:VAL:HG13	42:i:64:ILE:HG12	1.99	0.45
52:s:2:ARG:HE	52:s:6:LYS:HB2	1.81	0.45
8:A:242:G:H1'	8:A:243:U:H5	1.82	0.45
8:A:679:C:H2'	8:A:680:C:C6	2.51	0.45
8:A:1182:G:H2'	8:A:1183:U:O4'	2.15	0.45
8:A:1275:A:N1	8:A:1295:C:O2'	2.47	0.45
8:A:1282:U:H2'	8:A:1283:G:O4'	2.18	0.45
8:A:2011:U:H2'	8:A:2012:G:O4'	2.17	0.45
8:A:2115:G:H5''	8:A:2116:G:H5'	1.99	0.45
8:A:2343:U:O2'	8:A:2373:G:O2'	2.30	0.45
9:B:48:U:H2'	9:B:49:C:H6	1.78	0.45
14:G:15:ASP:OD2	14:G:17:LYS:NZ	2.47	0.45
34:a:413:G:H1'	34:a:428:G:N2	2.32	0.45
34:a:1014:A:C2	34:a:1219:A:H1'	2.52	0.45
34:a:1255:G:O2'	34:a:1258:G:N3	2.43	0.45
34:a:1410:A:H2'	34:a:1411:C:C6	2.52	0.45
34:a:1491:G:H2'	34:a:1492:A:O4'	2.17	0.45
8:A:881:G:H2'	8:A:882:G:O4'	2.18	0.44
8:A:898:C:H2'	8:A:899:A:O4'	2.17	0.44
8:A:1062:G:N3	8:A:1062:G:H2'	2.33	0.44
8:A:1106:G:C4	8:A:1107:G:C8	3.05	0.44
8:A:1197:G:H2'	8:A:1198:U:C6	2.53	0.44
8:A:1198:U:H2'	8:A:1199:U:H6	1.83	0.44
8:A:1361:G:H2'	8:A:1362:C:C6	2.52	0.44
8:A:1667:G:H5''	18:K:5:GLN:O	2.17	0.44
8:A:1683:U:H2'	8:A:1684:G:H8	1.82	0.44
8:A:1744:A:H3'	8:A:1745:A:H8	1.82	0.44
9:B:5:U:H2'	9:B:6:G:C8	2.52	0.44
10:C:106:PRO:HG2	10:C:109:LEU:HD13	1.99	0.44
11:D:116:LYS:HB2	11:D:165:MET:HB3	1.98	0.44
15:H:82:SER:HB3	15:H:90:LEU:HD11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Y:1:MET:HE3	32:Y:6:LEU:HD21	2.00	0.44
34:a:958:A:C5	52:s:54:ARG:HD3	2.52	0.44
34:a:1169:A:H2'	34:a:1170:A:C8	2.52	0.44
34:a:1300:G:O2'	34:a:1301:U:P	2.75	0.44
35:b:29:PHE:CE1	35:b:48:MET:HE1	2.52	0.44
35:b:66:ILE:N	35:b:88:GLN:OE1	2.43	0.44
37:d:26:ALA:HB3	37:d:29:THR:OG1	2.17	0.44
42:i:29:ILE:HD13	42:i:78:ILE:HD13	1.99	0.44
47:n:2:LYS:HB3	47:n:5:MET:HG3	1.98	0.44
54:u:7:GLU:OE1	54:u:7:GLU:HA	2.16	0.44
8:A:57:C:H2'	8:A:58:G:O4'	2.16	0.44
8:A:717:C:H3'	8:A:718:A:H8	1.80	0.44
8:A:753:A:H2'	8:A:754:U:C6	2.53	0.44
8:A:814:C:H2'	8:A:815:C:H6	1.82	0.44
8:A:871:U:H2'	8:A:872:U:H6	1.80	0.44
8:A:1599:U:H2'	8:A:1600:C:C6	2.52	0.44
8:A:2247:A:H2'	8:A:2248:C:H6	1.82	0.44
8:A:2328:A:H2'	8:A:2329:U:H6	1.78	0.44
10:C:107:LYS:HA	10:C:195:GLY:HA2	1.98	0.44
11:D:5:VAL:H	11:D:32:ASN:ND2	2.10	0.44
11:D:5:VAL:N	11:D:32:ASN:HD21	2.13	0.44
13:F:61:GLY:O	13:F:94:ARG:NH1	2.40	0.44
32:Y:19:LEU:HD12	32:Y:19:LEU:HA	1.83	0.44
34:a:991:U:C4	34:a:1212:U:H1'	2.52	0.44
34:a:1167:A:H4'	34:a:1168:U:H5	1.81	0.44
34:a:1218:C:H2'	34:a:1219:A:H8	1.80	0.44
34:a:1440:U:O2'	34:a:1441:A:H5''	2.16	0.44
37:d:105:GLY:HA2	37:d:161:ALA:HB2	1.99	0.44
46:m:78:ARG:HH22	52:s:68:HIS:CE1	2.34	0.44
50:q:68:LYS:O	50:q:68:LYS:HG2	2.14	0.44
8:A:184:C:H2'	8:A:185:G:H8	1.82	0.44
8:A:415:A:H2'	8:A:416:U:C6	2.53	0.44
8:A:590:A:H2'	8:A:591:U:C6	2.52	0.44
8:A:1027:A:C2	8:A:2488:G:H5'	2.52	0.44
8:A:1090:A:H4'	8:A:1091:G:OP1	2.17	0.44
8:A:1722:A:N6	8:A:1738:G:H1'	2.33	0.44
8:A:1799:G:N7	10:C:177:SER:OG	2.45	0.44
8:A:1812:U:H2'	8:A:1813:G:C8	2.52	0.44
8:A:1814:G:OP2	8:A:1815:A:O2'	2.26	0.44
8:A:2684:U:H4'	18:K:76:VAL:CG2	2.47	0.44
13:F:141:ASP:O	13:F:142:TYR:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:M:40:ARG:HD3	20:M:93:VAL:HG21	2.00	0.44
25:R:69:GLY:O	25:R:90:ARG:HG2	2.18	0.44
26:S:18:ARG:HG3	26:S:76:VAL:HB	1.98	0.44
34:a:123:U:OP1	34:a:311:C:O2'	2.32	0.44
34:a:389:A:H3'	34:a:390:U:H6	1.82	0.44
34:a:560:A:H4'	34:a:561:U:H5''	1.98	0.44
34:a:904:U:H2'	34:a:905:U:C6	2.52	0.44
34:a:1175:G:H2'	34:a:1176:A:H8	1.81	0.44
34:a:1222:G:OP2	34:a:1322:C:N4	2.39	0.44
49:p:20:VAL:HG13	49:p:32:PHE:HB2	1.98	0.44
49:p:75:ILE:HA	49:p:78:VAL:HG22	1.99	0.44
8:A:876:C:H2'	8:A:877:A:O4'	2.17	0.44
8:A:2215:C:H2'	8:A:2216:G:C8	2.52	0.44
8:A:2245:U:H5''	8:A:2246:G:H5'	1.99	0.44
10:C:156:SER:O	10:C:159:THR:OG1	2.29	0.44
12:E:147:LEU:HD11	12:E:170:ARG:HG2	1.99	0.44
34:a:34:C:H2'	34:a:35:G:H8	1.81	0.44
34:a:343:U:H2'	34:a:345:C:C5	2.53	0.44
34:a:718:A:C2	51:r:37:LYS:HG2	2.52	0.44
35:b:48:MET:HA	35:b:51:GLU:HG2	1.99	0.44
37:d:191:SER:C	37:d:193:ASP:H	2.25	0.44
37:d:201:GLU:CD	38:e:111:ARG:HH12	2.25	0.44
40:g:50:ALA:HB2	40:g:57:GLU:HG3	2.00	0.44
50:q:62:GLU:OE1	50:q:72:TRP:NE1	2.51	0.44
8:A:30:G:H2'	8:A:31:C:C6	2.53	0.44
8:A:401:A:H2'	8:A:402:A:C8	2.53	0.44
8:A:457:A:N1	8:A:470:A:H5''	2.33	0.44
8:A:972:A:H3'	8:A:973:A:H2'	2.00	0.44
8:A:1054:A:N1	8:A:1106:G:C6	2.85	0.44
8:A:1179:G:H2'	8:A:1179:G:N3	2.32	0.44
8:A:1203:U:OP2	8:A:1204:A:O2'	2.25	0.44
8:A:2558:C:H2'	8:A:2559:C:O4'	2.17	0.44
13:F:31:GLU:HG3	13:F:156:THR:O	2.17	0.44
15:H:4:ILE:HA	15:H:17:ASP:O	2.17	0.44
20:M:30:SER:HA	20:M:133:LYS:HE3	1.99	0.44
23:P:74:GLN:HB2	23:P:77:SER:HB2	1.98	0.44
34:a:134:G:H1'	34:a:325:A:C5	2.53	0.44
34:a:223:A:H2'	34:a:224:U:C6	2.52	0.44
40:g:134:VAL:O	40:g:138:GLU:HG2	2.17	0.44
44:k:113:THR:HG21	54:u:31:VAL:HG11	1.98	0.44
47:n:87:ALA:HB1	47:n:92:GLU:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:u:35:GLU:HG3	54:u:36:PHE:CD2	2.52	0.44
4:3:7:ARG:NH2	8:A:244:A:OP2	2.42	0.44
8:A:75:G:N3	8:A:75:G:H2'	2.32	0.44
8:A:340:A:H2'	8:A:341:C:O4'	2.16	0.44
8:A:881:G:H2'	8:A:882:G:C8	2.49	0.44
8:A:967:U:H2'	8:A:968:C:C6	2.53	0.44
8:A:1930:G:N2	8:A:1931:U:O4	2.37	0.44
8:A:2030:6MZ:C2	8:A:2499:C:H5''	2.47	0.44
17:J:91:GLU:HB3	17:J:95:ARG:NH2	2.32	0.44
24:Q:57:ARG:HA	24:Q:60:TRP:CE3	2.52	0.44
29:V:72:VAL:HB	29:V:91:PHE:HB3	1.99	0.44
34:a:530:G:C2	58:y:119:LEU:HD13	2.52	0.44
34:a:995:C:N3	34:a:1046:A:O2'	2.48	0.44
34:a:1028:C:H2'	34:a:1029:U:C2	2.52	0.44
34:a:1150:A:H4'	43:j:43:PRO:HG3	1.99	0.44
34:a:1458:G:OP1	53:t:29:THR:OG1	2.34	0.44
39:f:46:GLN:HA	39:f:56:LYS:HA	2.00	0.44
8:A:131:A:H2'	8:A:132:G:C8	2.53	0.44
8:A:566:U:H5''	19:L:29:LYS:HE2	2.00	0.44
8:A:573:U:O4	8:A:2029:G:O2'	2.34	0.44
8:A:1070:A:O2'	8:A:1096:A:O3'	2.28	0.44
8:A:1365:A:OP1	31:X:2:ARG:NH1	2.40	0.44
8:A:1912:A:N1	34:a:1407:5MC:O2'	2.50	0.44
8:A:2564:A:OP1	8:A:2648:G:O2'	2.27	0.44
8:A:2655:G:O2'	8:A:2656:U:O5'	2.36	0.44
17:J:4:PHE:O	24:Q:63:ARG:NH1	2.41	0.44
17:J:87:ALA:HB3	17:J:92:MET:HE2	2.00	0.44
34:a:45:G:H2'	34:a:46:G:C8	2.53	0.44
34:a:1310:G:OP2	46:m:86:ARG:NH2	2.34	0.44
34:a:1342:C:H2'	34:a:1343:G:C8	2.53	0.44
52:s:38:THR:OG1	52:s:69:LYS:NZ	2.51	0.44
2:1:22:THR:OG1	2:1:23:THR:N	2.51	0.44
4:3:25:HIS:NE2	4:3:47:ALA:HB2	2.33	0.44
8:A:320:A:H4'	8:A:322:A:N7	2.33	0.44
8:A:796:C:H2'	8:A:797:G:C8	2.53	0.44
8:A:871:U:H4'	20:M:68:PHE:CZ	2.53	0.44
8:A:936:A:H2'	8:A:937:C:C6	2.52	0.44
10:C:154:ALA:HB2	10:C:161:VAL:HG23	2.00	0.44
11:D:26:VAL:HG22	11:D:188:LEU:HD22	2.00	0.44
11:D:48:ILE:HG21	11:D:90:PHE:HB2	1.99	0.44
20:M:31:PHE:HD1	20:M:132:THR:HG22	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:U:73:ASN:C	28:U:75:ALA:H	2.26	0.44
29:V:20:LEU:HD21	29:V:41:GLU:HG2	2.00	0.44
34:a:123:U:H2'	34:a:124:C:C6	2.52	0.44
34:a:151:A:H3'	34:a:152:A:H8	1.82	0.44
34:a:473:U:H2'	34:a:474:G:H8	1.82	0.44
35:b:8:MET:C	35:b:9:LEU:HD23	2.42	0.44
53:t:59:ARG:O	53:t:63:LYS:HG2	2.18	0.44
58:y:14:GLU:CD	58:y:47:SER:H	2.26	0.44
4:3:22:LYS:NZ	8:A:631:A:OP2	2.49	0.44
8:A:463:G:N2	8:A:466:A:OP2	2.39	0.44
8:A:593:U:H2'	8:A:594:U:H6	1.82	0.44
8:A:1013:C:H2'	8:A:1014:A:H8	1.83	0.44
8:A:1248:G:OP1	12:E:44:ARG:NH1	2.51	0.44
8:A:1372:U:O2'	8:A:2212:A:N3	2.50	0.44
8:A:1475:G:O2'	8:A:1476:U:H6	2.01	0.44
8:A:2250:G:O2'	8:A:2496:C:OP1	2.34	0.44
10:C:15:VAL:HG22	10:C:205:GLY:HA3	1.98	0.44
11:D:19:GLY:O	18:K:73:ASP:HB3	2.18	0.44
15:H:69:ALA:C	15:H:71:LYS:H	2.26	0.44
29:V:63:ILE:HG22	29:V:65:VAL:HG23	2.00	0.44
34:a:377:G:H2'	34:a:378:G:H8	1.83	0.44
34:a:789:U:O2'	34:a:791:G:N7	2.47	0.44
34:a:1149:C:H2'	34:a:1150:A:H8	1.83	0.44
42:i:5:TYR:CG	42:i:89:TYR:HB2	2.52	0.44
51:r:22:TYR:HE2	51:r:64:LEU:HD12	1.82	0.44
8:A:26:G:H2'	8:A:27:G:O4'	2.18	0.43
8:A:38:A:H2'	8:A:39:G:O4'	2.17	0.43
8:A:598:U:H2'	8:A:599:A:H8	1.83	0.43
8:A:645:C:H2'	8:A:647:G:N7	2.33	0.43
8:A:1056:G:H2'	8:A:1087:G:H22	1.83	0.43
8:A:1567:G:OP2	10:C:82:TYR:OH	2.33	0.43
8:A:1677:A:H2'	8:A:1678:A:C8	2.53	0.43
8:A:1771:C:H2'	8:A:1772:A:C8	2.53	0.43
8:A:1869:G:H2'	8:A:1871:A:C2	2.53	0.43
8:A:2364:C:H2'	8:A:2365:G:O4'	2.18	0.43
8:A:2443:C:H2'	8:A:2444:G:H8	1.83	0.43
9:B:39:A:H2'	9:B:40:U:C6	2.53	0.43
17:J:6:ALA:O	17:J:48:VAL:HG21	2.17	0.43
18:K:1:MET:HE3	18:K:32:TYR:CZ	2.53	0.43
34:a:266:G:H3'	50:q:68:LYS:HB2	1.99	0.43
34:a:375:U:H5''	49:p:70:ARG:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1225:A:H2'	34:a:1225:A:N3	2.32	0.43
36:c:6:PRO:HD2	36:c:183:TYR:CD2	2.53	0.43
44:k:14:GLN:HG2	44:k:76:TYR:O	2.18	0.43
45:l:30:ARG:HE	45:l:57:THR:CG2	2.31	0.43
8:A:1542:U:H2'	8:A:1543:G:O4'	2.18	0.43
8:A:2514:U:H2'	8:A:2515:C:H6	1.81	0.43
8:A:2783:U:H2'	8:A:2784:U:C6	2.52	0.43
10:C:75:ALA:HB2	10:C:95:TYR:CD1	2.52	0.43
10:C:75:ALA:HB1	10:C:93:VAL:CG1	2.48	0.43
14:G:51:PHE:CE2	14:G:71:LEU:HD22	2.53	0.43
17:J:49:ASP:CG	17:J:121:LYS:HZ3	2.24	0.43
34:a:472:U:H2'	34:a:473:U:C6	2.52	0.43
34:a:567:G:H2'	34:a:568:G:O4'	2.18	0.43
34:a:674:G:H2'	34:a:675:A:H8	1.83	0.43
34:a:720:C:H2'	34:a:721:G:C8	2.53	0.43
34:a:821:G:H2'	34:a:822:U:C6	2.53	0.43
34:a:1260:G:O2'	34:a:1275:A:N6	2.48	0.43
35:b:65:LYS:HG2	35:b:89:PHE:CD2	2.48	0.43
42:i:44:ARG:NH2	42:i:48:ARG:HH22	2.15	0.43
51:r:64:LEU:HD23	51:r:64:LEU:HA	1.85	0.43
8:A:3:U:H2'	8:A:4:U:C6	2.53	0.43
8:A:753:A:H2'	8:A:754:U:H6	1.82	0.43
8:A:1170:C:H2'	8:A:1171:G:C8	2.53	0.43
8:A:1597:A:H5''	8:A:1598:A:H5'	1.99	0.43
8:A:1819:A:H5''	10:C:159:THR:HG21	2.00	0.43
8:A:2271:G:OP1	30:W:14:ALA:HB1	2.18	0.43
8:A:2462:C:H2'	8:A:2463:C:C6	2.52	0.43
20:M:34:LYS:HD3	29:V:82:TYR:HA	1.99	0.43
21:N:55:ALA:HA	21:N:80:PHE:CE1	2.53	0.43
29:V:6:ALA:HB3	29:V:65:VAL:HG22	1.99	0.43
34:a:515:G:HO2'	34:a:516:PSU:P	2.41	0.43
34:a:603:U:C5	34:a:635:A:N1	2.84	0.43
34:a:1425:U:H2'	34:a:1426:G:H8	1.82	0.43
36:c:119:ILE:O	36:c:123:LEU:HG	2.17	0.43
37:d:201:GLU:OE1	38:e:111:ARG:NH1	2.50	0.43
39:f:42:TRP:HZ2	51:r:23:LYS:HD2	1.82	0.43
44:k:23:HIS:HB3	44:k:30:ILE:HB	1.99	0.43
46:m:33:LEU:HD13	46:m:40:GLU:HA	2.01	0.43
52:s:14:LEU:O	52:s:18:VAL:HG13	2.19	0.43
8:A:69:C:O2	8:A:73:A:O2'	2.29	0.43
8:A:203:A:OP2	8:A:204:A:O2'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:711:G:H1	8:A:720:U:H3	1.67	0.43
8:A:933:A:H5'	8:A:934:U:OP2	2.19	0.43
8:A:1339:G:P	27:T:15:HIS:HE2	2.40	0.43
8:A:1413:A:H2'	8:A:1414:C:C6	2.53	0.43
8:A:1484:U:H2'	8:A:1485:U:C6	2.54	0.43
8:A:2230:G:H2'	8:A:2231:U:C6	2.54	0.43
8:A:2498:OMC:HM22	8:A:2499:C:H5'	2.01	0.43
8:A:2836:U:H2'	8:A:2837:A:C8	2.54	0.43
15:H:121:VAL:HG21	15:H:123:ARG:HH21	1.83	0.43
18:K:40:LYS:HE3	18:K:57:VAL:HG12	2.00	0.43
21:N:96:ARG:CZ	21:N:116:VAL:HG12	2.47	0.43
29:V:2:PHE:HB3	29:V:50:MET:HE3	1.99	0.43
31:X:21:LEU:HD23	31:X:21:LEU:HA	1.91	0.43
34:a:154:U:H2'	34:a:155:A:C8	2.52	0.43
34:a:280:C:O4'	50:q:39:ARG:NH2	2.50	0.43
34:a:737:C:H2'	34:a:738:C:H6	1.83	0.43
34:a:741:G:H2'	34:a:742:G:O4'	2.19	0.43
35:b:115:ASP:O	35:b:118:THR:HG22	2.18	0.43
35:b:212:TYR:O	35:b:216:VAL:HG12	2.18	0.43
37:d:30:LYS:HE2	37:d:30:LYS:HB3	1.78	0.43
48:o:7:THR:O	48:o:11:VAL:HG23	2.18	0.43
50:q:14:ASP:OD2	50:q:53:GLY:HA2	2.19	0.43
56:w:22:G:H2'	56:w:23:A:H8	1.84	0.43
7:6:32:LEU:HD21	13:F:138:PRO:HB2	2.00	0.43
7:6:61:ASN:O	7:6:64:PHE:HB2	2.17	0.43
8:A:152:A:H2'	8:A:153:U:C6	2.53	0.43
8:A:582:A:H2'	8:A:583:G:C8	2.53	0.43
8:A:1081:U:O2'	8:A:1082:U:OP1	2.30	0.43
8:A:1083:U:O3'	8:A:1084:A:H3'	2.18	0.43
8:A:1316:U:H2'	8:A:1317:G:H8	1.82	0.43
8:A:1444:G:H2'	8:A:1445:G:H8	1.84	0.43
8:A:1536:C:H4'	8:A:1537:G:C4	2.53	0.43
8:A:1915:3TD:H2'	8:A:1916:A:O4'	2.18	0.43
8:A:2284:A:O2'	8:A:2288:A:N1	2.47	0.43
8:A:2627:G:N2	8:A:2777:G:OP2	2.45	0.43
9:B:115:A:H2'	9:B:116:G:C8	2.54	0.43
20:M:54:THR:HG22	20:M:59:ARG:HH11	1.82	0.43
34:a:69:G:H2'	34:a:70:U:C6	2.53	0.43
34:a:81:A:N6	34:a:86:G:H21	2.17	0.43
34:a:737:C:H2'	34:a:738:C:C6	2.54	0.43
34:a:837:U:H2'	34:a:838:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1072:G:H2'	34:a:1073:U:C6	2.54	0.43
34:a:1244:G:H2'	34:a:1245:C:H6	1.84	0.43
34:a:1312:G:H5'	52:s:4:LEU:HD11	2.00	0.43
35:b:42:LEU:HA	35:b:45:THR:HB	1.99	0.43
8:A:671:C:H2'	8:A:672:C:C6	2.53	0.43
8:A:1081:U:HO2'	8:A:1082:U:P	2.42	0.43
8:A:1394:U:H4'	8:A:1603:A:H4'	2.00	0.43
8:A:1668:A:H4'	8:A:1669:A:O5'	2.19	0.43
8:A:2070:A:H2'	8:A:2071:A:O4'	2.19	0.43
8:A:2728:U:O2'	8:A:2729:G:O5'	2.30	0.43
17:J:56:VAL:HB	17:J:124:VAL:HA	2.01	0.43
19:L:127:VAL:HG21	19:L:142:ILE:HD13	2.01	0.43
31:X:11:PRO:HB3	31:X:29:LEU:HD23	2.00	0.43
34:a:362:G:N1	34:a:365:U:OP2	2.51	0.43
56:w:44:G:H2'	56:w:45:U:C6	2.53	0.43
8:A:286:U:H2'	8:A:287:G:C8	2.54	0.43
8:A:723:C:H2'	8:A:724:U:O4'	2.18	0.43
8:A:989:G:OP2	33:Z:11:SER:OG	2.21	0.43
8:A:1430:G:H2'	8:A:1431:A:O4'	2.19	0.43
8:A:1640:A:H2'	8:A:1641:A:C8	2.53	0.43
8:A:1857:G:HO2'	8:A:1885:A:N6	2.17	0.43
8:A:2012:G:OP1	26:S:98:LYS:HD2	2.19	0.43
8:A:2545:G:H2'	8:A:2546:U:O4'	2.18	0.43
34:a:204:G:O6	34:a:465:A:H2	2.00	0.43
34:a:279:A:H5''	34:a:281:G:O4'	2.18	0.43
34:a:539:A:H2'	34:a:540:G:H8	1.82	0.43
34:a:652:U:HO2'	34:a:653:U:P	2.42	0.43
34:a:860:A:H2'	34:a:861:G:O4'	2.18	0.43
34:a:1118:U:H1'	34:a:1179:A:C5	2.53	0.43
34:a:1147:C:O2'	42:i:6:TYR:OH	2.25	0.43
34:a:1308:U:H2'	34:a:1309:G:C8	2.53	0.43
34:a:1444:U:H2'	34:a:1445:U:C6	2.54	0.43
34:a:1530:G:O6	54:u:45:LYS:NZ	2.50	0.43
42:i:51:LEU:HB3	42:i:56:MET:HB3	2.00	0.43
47:n:2:LYS:O	47:n:5:MET:N	2.49	0.43
8:A:2:G:H2'	8:A:3:U:C6	2.54	0.43
8:A:1469:A:H2'	8:A:1470:A:H8	1.78	0.43
8:A:2298:A:H2'	8:A:2299:U:O4'	2.17	0.43
8:A:2314:A:H1'	13:F:154:THR:HG21	1.99	0.43
8:A:2676:C:P	18:K:31:ARG:HH22	2.40	0.43
8:A:2698:U:H2'	8:A:2699:C:H6	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2806:C:H2'	8:A:2807:U:O4'	2.19	0.43
11:D:105:LYS:HD3	11:D:105:LYS:HA	1.77	0.43
13:F:176:PHE:HD1	13:F:176:PHE:HA	1.72	0.43
14:G:104:LEU:HD21	14:G:130:ILE:HD11	1.99	0.43
27:T:54:GLU:HB2	27:T:88:LYS:HD2	2.01	0.43
34:a:1127:G:H5'	34:a:1280:A:O2'	2.18	0.43
34:a:1512:U:H2'	34:a:1513:A:C8	2.54	0.43
41:h:21:LYS:O	41:h:64:TYR:OH	2.34	0.43
44:k:46:ALA:HB1	44:k:61:ALA:HB1	2.01	0.43
51:r:10:CYS:C	51:r:12:PHE:H	2.26	0.43
53:t:28:ARG:HA	53:t:31:ILE:HD12	2.00	0.43
54:u:20:ARG:HA	54:u:23:GLU:HG2	2.01	0.43
8:A:207:A:H2'	8:A:208:C:O4'	2.19	0.43
8:A:755:U:H2'	8:A:756:A:C8	2.54	0.43
8:A:1667:G:O2'	8:A:1991:U:O4	2.23	0.43
8:A:2039:U:H2'	8:A:2040:G:H8	1.84	0.43
8:A:2099:U:H3	8:A:2190:G:H1	1.65	0.43
8:A:2119:A:H2'	8:A:2168:G:C6	2.54	0.43
8:A:2143:C:N4	8:A:2148:G:N3	2.63	0.43
8:A:2291:U:H2'	8:A:2292:U:H6	1.83	0.43
8:A:2389:G:H5''	8:A:2390:U:O4'	2.19	0.43
9:B:44:G:H5''	9:B:45:A:N7	2.33	0.43
12:E:123:LYS:HE2	12:E:125:SER:HB2	2.00	0.43
15:H:3:VAL:HG22	15:H:36:ALA:HB1	2.01	0.43
34:a:373:A:H1'	34:a:481:G:C8	2.53	0.43
34:a:474:G:H2'	34:a:475:C:H6	1.83	0.43
34:a:1098:C:OP1	35:b:138:ARG:NH2	2.52	0.43
34:a:1315:U:O2'	34:a:1360:A:N3	2.41	0.43
35:b:61:SER:C	35:b:63:LYS:H	2.27	0.43
35:b:76:SER:HB3	35:b:92:ASN:HB2	2.01	0.43
39:f:11:HIS:C	39:f:13:ASP:H	2.25	0.43
8:A:128:C:H2'	8:A:129:C:C6	2.54	0.43
8:A:706:A:H2'	8:A:707:G:O4'	2.19	0.43
8:A:1001:A:H2'	8:A:1002:G:O4'	2.19	0.43
8:A:1102:C:H2'	8:A:1103:A:O4'	2.18	0.43
8:A:1212:G:H1'	8:A:1237:A:N6	2.34	0.43
8:A:1999:C:H5''	8:A:2723:C:O2'	2.19	0.43
12:E:65:THR:HG22	55:v:8:ILE:HG21	2.01	0.43
19:L:82:LEU:HG	19:L:90:VAL:HG21	2.01	0.43
30:W:34:VAL:HG12	30:W:55:LEU:HB2	2.00	0.43
31:X:6:VAL:HG21	31:X:58:ILE:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:81:A:H5'	34:a:82:G:N7	2.34	0.43
34:a:337:G:H2'	34:a:338:A:H8	1.81	0.43
34:a:427:U:O2'	34:a:541:G:OP1	2.30	0.43
34:a:509:A:H2'	34:a:510:A:C8	2.54	0.43
34:a:790:A:H2'	34:a:791:G:C8	2.54	0.43
34:a:1125:U:H2'	34:a:1126:U:H2'	2.01	0.43
36:c:79:LYS:HE2	36:c:79:LYS:HB2	1.79	0.43
37:d:72:ARG:HH12	37:d:76:LYS:HD3	1.83	0.43
47:n:79:LEU:HB2	47:n:84:VAL:HG23	2.01	0.43
8:A:766:U:H2'	8:A:767:U:C6	2.54	0.42
8:A:1386:C:H2'	8:A:1387:A:H8	1.83	0.42
8:A:2480:C:H2'	8:A:2481:G:O4'	2.19	0.42
8:A:2896:C:H2'	8:A:2897:U:C6	2.54	0.42
10:C:66:PHE:HZ	10:C:86:ARG:NH1	2.11	0.42
23:P:90:ALA:HB2	23:P:112:ARG:HA	2.01	0.42
34:a:253:A:H2'	34:a:254:G:C8	2.54	0.42
34:a:356:A:N3	34:a:368:U:O2'	2.41	0.42
34:a:892:A:H2'	34:a:893:C:C6	2.54	0.42
34:a:1347:G:C8	42:i:108:ARG:HG3	2.53	0.42
36:c:61:LYS:O	36:c:96:VAL:HB	2.19	0.42
37:d:59:LYS:HB3	37:d:59:LYS:HE2	1.78	0.42
58:y:94:MET:HE2	58:y:94:MET:HB3	1.84	0.42
2:l:39:ASP:HB3	2:l:42:VAL:HG22	2.01	0.42
8:A:141:G:H1	27:T:1:MET:HE2	1.85	0.42
8:A:290:U:H2'	8:A:291:G:O4'	2.19	0.42
8:A:477:A:H2'	8:A:478:A:C8	2.54	0.42
8:A:885:C:H2'	8:A:886:A:H5'	1.99	0.42
8:A:1383:A:H2'	8:A:1384:A:C8	2.54	0.42
8:A:1405:U:H2'	8:A:1406:U:H6	1.83	0.42
8:A:1915:3TD:H6	58:y:102:LYS:HE3	2.01	0.42
8:A:2319:G:O2'	8:A:2320:U:O5'	2.34	0.42
8:A:2468:A:HO2'	8:A:2469:A:P	2.41	0.42
9:B:76:G:OP1	29:V:9:ARG:NH1	2.44	0.42
14:G:144:ALA:HB1	14:G:163:TYR:HE1	1.84	0.42
15:H:5:LEU:CD2	15:H:13:GLY:HA2	2.49	0.42
15:H:109:GLU:HG3	15:H:110:VAL:HG13	2.01	0.42
17:J:125:TYR:HH	17:J:132:HIS:CD2	2.36	0.42
34:a:501:C:H2'	34:a:502:A:H8	1.83	0.42
34:a:1005:A:H4'	34:a:1037:C:O2'	2.18	0.42
35:b:202:ASN:ND2	35:b:204:ASP:OD1	2.52	0.42
40:g:134:VAL:HG13	40:g:137:ARG:HH21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:g:149:ALA:HB1	44:k:58:THR:HG21	1.99	0.42
53:t:23:ARG:HA	53:t:23:ARG:HD3	1.79	0.42
8:A:64:A:H2'	8:A:65:U:H6	1.81	0.42
8:A:176:A:O2'	8:A:177:G:H5'	2.19	0.42
8:A:247:G:H4'	8:A:386:G:C5	2.54	0.42
8:A:310:A:HO2'	8:A:311:A:P	2.42	0.42
8:A:674:G:H1'	12:E:69:ARG:CD	2.47	0.42
8:A:1058:U:H2'	8:A:1059:G:H5''	2.01	0.42
17:J:69:ARG:HD3	17:J:89:PHE:HD2	1.85	0.42
21:N:20:MET:HE2	21:N:20:MET:HB3	1.92	0.42
24:Q:47:ARG:HH11	24:Q:48:ASP:CG	2.27	0.42
29:V:20:LEU:HG	29:V:25:LYS:HB2	2.01	0.42
34:a:110:C:H2'	34:a:111:G:O4'	2.19	0.42
34:a:222:C:H2'	34:a:223:A:H8	1.84	0.42
34:a:384:G:H2'	34:a:385:C:H6	1.84	0.42
34:a:502:A:H2'	34:a:503:C:O4'	2.19	0.42
34:a:651:C:H2'	34:a:652:U:C6	2.54	0.42
34:a:1095:U:H5'	34:a:1109:C:O2	2.19	0.42
34:a:1237:C:O3'	34:a:1300:G:N2	2.52	0.42
34:a:1313:U:H2'	34:a:1314:C:C6	2.53	0.42
40:g:113:LYS:HA	40:g:113:LYS:HD3	1.80	0.42
47:n:11:LYS:HB2	47:n:11:LYS:HE3	1.66	0.42
56:w:68:C:H2'	56:w:69:G:C8	2.53	0.42
2:1:10:LEU:HB3	2:1:48:TYR:HB3	2.01	0.42
3:2:3:ARG:HD3	3:2:3:ARG:HA	1.86	0.42
8:A:39:G:H2'	8:A:40:U:C6	2.54	0.42
8:A:56:A:H2'	8:A:57:C:O4'	2.19	0.42
8:A:194:G:H2'	8:A:195:A:O4'	2.19	0.42
8:A:705:A:C2	8:A:727:A:H1'	2.54	0.42
8:A:1093:G:N7	8:A:1098:A:N6	2.68	0.42
8:A:1614:A:C2	26:S:93:ALA:HB2	2.54	0.42
8:A:2163:A:O2'	8:A:2172:U:OP2	2.26	0.42
8:A:2192:U:HO2'	8:A:2193:G:P	2.42	0.42
8:A:2701:U:H3'	8:A:2702:G:H5''	2.01	0.42
8:A:2834:G:H2'	8:A:2879:A:H61	1.84	0.42
11:D:9:VAL:O	23:P:4:ILE:CD1	2.64	0.42
18:K:51:LYS:HE3	18:K:96:GLY:HA2	2.00	0.42
20:M:53:MET:HE3	20:M:120:ALA:CB	2.49	0.42
32:Y:21:LEU:HD12	32:Y:21:LEU:HA	1.65	0.42
34:a:410:G:H2'	34:a:429:U:C4	2.54	0.42
34:a:1006:G:N3	34:a:1006:G:H2'	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1026:G:H3'	34:a:1026:G:N3	2.35	0.42
34:a:1401:G:H2'	34:a:1402:4OC:O4'	2.18	0.42
35:b:31:PHE:O	35:b:31:PHE:CG	2.73	0.42
42:i:101:GLY:C	42:i:103:VAL:H	2.27	0.42
42:i:118:ARG:HD3	42:i:122:ARG:HG3	2.01	0.42
46:m:15:VAL:HG13	46:m:33:LEU:HD12	2.01	0.42
8:A:653:U:C4	8:A:654:A:H1'	2.54	0.42
8:A:1056:G:H21	8:A:1103:A:N6	2.05	0.42
8:A:1068:G:O2'	8:A:1070:A:O4'	2.37	0.42
8:A:1089:A:H2	8:A:1090:A:H62	1.68	0.42
8:A:1281:G:H2'	8:A:1282:U:C6	2.54	0.42
8:A:1480:C:H2'	8:A:1481:U:O4'	2.19	0.42
8:A:1641:A:H2'	8:A:1642:G:O4'	2.18	0.42
8:A:2033:A:H1'	8:A:2035:G:OP2	2.20	0.42
8:A:2292:U:H2'	8:A:2293:G:H8	1.83	0.42
14:G:49:LEU:HD13	14:G:71:LEU:HD23	2.00	0.42
15:H:78:VAL:O	15:H:144:VAL:HA	2.19	0.42
26:S:1:MET:SD	26:S:2:GLU:HG3	2.59	0.42
34:a:56:U:H2'	34:a:57:G:H8	1.82	0.42
34:a:653:U:C2	41:h:55:LYS:HG2	2.55	0.42
34:a:1031:C:H5'	34:a:1032:G:N9	2.34	0.42
34:a:1373:G:N7	42:i:12:LYS:NZ	2.66	0.42
35:b:164:ASP:OD1	35:b:167:HIS:N	2.44	0.42
35:b:181:PRO:HA	35:b:196:ASP:OD2	2.19	0.42
50:q:7:LEU:HD23	50:q:24:ILE:HD13	2.02	0.42
53:t:25:SER:O	53:t:29:THR:OG1	2.37	0.42
7:6:35:ASP:OD2	46:m:2:ARG:HB3	2.19	0.42
8:A:150:U:H2'	8:A:151:C:H6	1.85	0.42
8:A:555:G:O2'	8:A:556:A:O5'	2.38	0.42
8:A:567:U:H2'	8:A:568:U:O4'	2.20	0.42
8:A:1084:A:O4'	8:A:1105:U:O2'	2.28	0.42
8:A:1486:U:H2'	8:A:1487:U:H6	1.83	0.42
8:A:1792:G:O2'	8:A:1830:C:OP1	2.34	0.42
8:A:2301:C:H2'	8:A:2302:U:C6	2.53	0.42
8:A:2358:A:H2'	8:A:2359:C:O4'	2.19	0.42
14:G:51:PHE:HE2	14:G:71:LEU:HD22	1.84	0.42
34:a:8:A:C4	37:d:205:LYS:HD3	2.53	0.42
34:a:925:G:H1'	34:a:1502:A:C4	2.55	0.42
36:c:113:LYS:HB2	36:c:184:ASN:ND2	2.35	0.42
43:j:83:THR:O	43:j:87:LEU:HG	2.20	0.42
48:o:46:LYS:HA	48:o:52:ARG:HH22	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:u:30:GLU:O	54:u:34:ARG:HG3	2.19	0.42
8:A:61:C:OP1	32:Y:44:LYS:HB2	2.19	0.42
8:A:277:G:O2'	8:A:361:G:N1	2.53	0.42
8:A:514:A:N3	8:A:581:C:O2'	2.43	0.42
8:A:624:C:O2'	8:A:657:U:OP1	2.36	0.42
8:A:703:U:H2'	8:A:704:G:O4'	2.19	0.42
8:A:1444:G:H2'	8:A:1445:G:C8	2.55	0.42
8:A:1923:U:H2'	8:A:1924:C:H6	1.83	0.42
8:A:2097:A:H2'	8:A:2098:U:C6	2.54	0.42
11:D:38:LYS:HG2	11:D:43:ASP:CG	2.44	0.42
28:U:9:GLU:OE2	28:U:21:ARG:HG2	2.19	0.42
28:U:27:VAL:HG22	28:U:33:VAL:HG12	2.02	0.42
31:X:39:VAL:HG12	31:X:42:GLU:H	1.84	0.42
34:a:123:U:H2'	34:a:124:C:H6	1.85	0.42
34:a:185:U:H2'	34:a:186:C:C6	2.54	0.42
34:a:592:G:H2'	34:a:593:U:C6	2.54	0.42
34:a:673:A:H2'	34:a:674:G:H8	1.80	0.42
34:a:1213:A:O2'	34:a:1215:G:N7	2.47	0.42
35:b:49:PHE:O	35:b:53:LEU:HG	2.20	0.42
37:d:105:GLY:O	37:d:107:GLY:N	2.52	0.42
37:d:146:GLU:OE1	37:d:147:LYS:N	2.52	0.42
44:k:46:ALA:O	44:k:51:PHE:HB2	2.20	0.42
54:u:11:PHE:O	54:u:11:PHE:HD1	2.00	0.42
3:2:25:LYS:HE3	3:2:25:LYS:HB3	1.88	0.42
8:A:248:G:H5'	8:A:250:G:N7	2.35	0.42
8:A:347:A:H2'	8:A:348:A:C8	2.55	0.42
8:A:545:U:O2	8:A:548:G:C6	2.73	0.42
8:A:697:G:H2'	8:A:698:C:C6	2.55	0.42
8:A:839:U:H2'	8:A:840:C:H6	1.84	0.42
8:A:1209:U:O2'	8:A:1237:A:N1	2.46	0.42
8:A:1213:A:H2'	8:A:1214:A:C8	2.55	0.42
8:A:1791:A:N6	8:A:1828:G:O2'	2.46	0.42
8:A:1838:C:N4	8:A:1898:U:H2'	2.34	0.42
8:A:2405:G:O2'	8:A:2406:A:P	2.78	0.42
23:P:30:TRP:CD2	23:P:37:LYS:HE3	2.55	0.42
27:T:6:ARG:HH22	27:T:37:ASP:HB2	1.85	0.42
34:a:256:U:H2'	34:a:257:G:C8	2.55	0.42
34:a:559:A:H1'	34:a:561:U:O2'	2.20	0.42
34:a:1346:A:OP1	34:a:1346:A:H4'	2.19	0.42
37:d:117:VAL:HG22	37:d:122:ILE:HG13	2.02	0.42
40:g:52:ARG:NH1	40:g:121:ASN:OD1	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:p:56:ARG:HA	49:p:56:ARG:HD2	1.80	0.42
8:A:1341:G:OP1	8:A:1397:U:N3	2.47	0.42
8:A:1827:U:OP2	10:C:220:ARG:HD2	2.19	0.42
8:A:2852:G:H2'	8:A:2853:C:O4'	2.20	0.42
18:K:87:LEU:HB3	18:K:92:GLU:O	2.20	0.42
26:S:29:VAL:HB	26:S:55:ILE:HD11	2.02	0.42
34:a:207:C:H2'	34:a:208:U:H4'	2.01	0.42
34:a:258:G:H5''	53:t:81:GLN:HE22	1.84	0.42
34:a:333:U:H2'	34:a:334:C:H6	1.85	0.42
34:a:718:A:H2	51:r:37:LYS:HG2	1.84	0.42
34:a:1225:A:H5''	34:a:1226:C:OP2	2.20	0.42
35:b:67:LEU:HB3	35:b:160:LEU:HD12	2.01	0.42
36:c:71:ARG:HB3	36:c:74:ILE:HB	2.01	0.42
54:u:15:LEU:HD12	54:u:15:LEU:HA	1.51	0.42
58:y:43:ILE:HD13	58:y:56:LEU:HB3	2.00	0.42
8:A:108:G:H2'	8:A:109:C:O4'	2.20	0.42
8:A:594:U:H2'	8:A:595:C:H6	1.83	0.42
8:A:828:U:H2'	8:A:829:A:C8	2.55	0.42
8:A:1048:A:OP2	8:A:1110:G:N2	2.47	0.42
8:A:1722:A:H61	8:A:1738:G:H1'	1.85	0.42
8:A:2267:A:H5''	8:A:2268:A:H5'	2.01	0.42
10:C:27:LYS:HA	10:C:27:LYS:HD3	1.83	0.42
20:M:12:MET:HG2	20:M:72:PRO:HD2	2.02	0.42
22:O:94:ARG:O	22:O:97:PHE:HD2	2.03	0.42
34:a:16:A:N1	34:a:919:A:H2	2.17	0.42
34:a:320:A:H2'	34:a:321:A:O4'	2.20	0.42
34:a:333:U:H2'	34:a:334:C:C6	2.54	0.42
34:a:908:A:H2'	34:a:909:A:H8	1.85	0.42
38:e:44:ARG:HA	38:e:71:ILE:O	2.20	0.42
45:l:53:ARG:HG3	45:l:61:GLU:OE2	2.18	0.42
58:y:60:SER:O	58:y:60:SER:OG	2.36	0.42
1:0:12:ARG:HD3	1:0:16:ARG:CZ	2.50	0.41
1:0:38:LEU:HB2	1:0:41:HIS:HB2	2.02	0.41
8:A:285:G:C6	8:A:356:G:C6	3.08	0.41
8:A:570:G:H2'	8:A:2030:6MZ:N7	2.34	0.41
8:A:1052:C:O5'	8:A:1052:C:C6	2.72	0.41
8:A:1348:C:C5	8:A:1349:C:C5	3.08	0.41
8:A:1538:G:H2'	8:A:1539:U:H6	1.84	0.41
8:A:2047:C:H2'	8:A:2048:G:C8	2.54	0.41
9:B:111:U:H2'	9:B:112:G:H8	1.84	0.41
10:C:146:LYS:HB2	10:C:149:LYS:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:D:46:ARG:HH21	11:D:86:GLU:H	1.66	0.41
17:J:140:LEU:HG	17:J:142:ILE:HG23	2.02	0.41
28:U:35:VAL:O	28:U:61:GLU:HG2	2.20	0.41
32:Y:18:LEU:O	32:Y:18:LEU:HD23	2.19	0.41
34:a:34:C:H2'	34:a:35:G:C8	2.55	0.41
34:a:846:G:H2'	34:a:847:G:H8	1.85	0.41
34:a:921:U:H2'	34:a:922:G:O4'	2.20	0.41
34:a:994:A:C5	34:a:1216:A:H4'	2.55	0.41
34:a:1158:C:C4	34:a:1160:G:C8	3.08	0.41
35:b:66:ILE:HG13	35:b:220:VAL:HG11	2.01	0.41
36:c:20:THR:HB	36:c:57:GLU:HG2	2.02	0.41
40:g:1:PRO:HG2	40:g:6:ILE:HD11	2.02	0.41
53:t:2:ASN:HD22	53:t:2:ASN:HA	1.68	0.41
8:A:138:U:H2'	8:A:140:C:C5	2.55	0.41
8:A:289:G:H2'	8:A:290:U:C6	2.55	0.41
8:A:878:A:N6	8:A:899:A:O2'	2.53	0.41
8:A:987:C:H2'	8:A:988:A:O4'	2.20	0.41
8:A:1321:A:C4	8:A:1322:A:C8	3.08	0.41
8:A:1440:U:H2'	8:A:1441:G:C8	2.55	0.41
15:H:122:LEU:HD11	15:H:128:HIS:CB	2.50	0.41
28:U:6:ARG:O	28:U:24:VAL:HB	2.19	0.41
34:a:410:G:H2'	34:a:429:U:C5	2.55	0.41
34:a:839:C:H2'	34:a:840:C:C6	2.56	0.41
34:a:1249:C:O2'	42:i:69:GLY:O	2.35	0.41
34:a:1498:UR3:H3U2	57:x:17:U:H4'	2.02	0.41
36:c:55:VAL:HB	36:c:66:THR:HB	2.02	0.41
38:e:154:ALA:HB1	41:h:65:PHE:CZ	2.55	0.41
39:f:51:ILE:HG22	39:f:52:ASN:ND2	2.34	0.41
41:h:49:LYS:HG3	41:h:59:GLU:HG3	2.02	0.41
44:k:124:LYS:O	44:k:125:LYS:HB2	2.20	0.41
45:l:46:SER:HB2	58:y:118:ARG:CZ	2.50	0.41
48:o:28:VAL:HG11	48:o:66:LEU:HD21	2.01	0.41
50:q:29:LYS:HB2	50:q:36:PHE:CE2	2.54	0.41
3:2:35:ARG:HG3	3:2:42:LEU:HD11	2.02	0.41
7:6:43:PHE:C	7:6:45:THR:N	2.79	0.41
8:A:404:A:H1'	8:A:406:G:C4	2.55	0.41
8:A:819:A:H5'	8:A:973:A:N1	2.35	0.41
8:A:1091:G:H2'	8:A:1092:C:O4'	2.20	0.41
8:A:1180:U:H2'	8:A:1181:U:O4'	2.21	0.41
8:A:1526:C:H2'	8:A:1527:G:O4'	2.19	0.41
8:A:1656:C:H2'	8:A:1657:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2078:C:H2'	8:A:2079:U:C6	2.55	0.41
8:A:2087:G:H2'	8:A:2088:A:H8	1.85	0.41
8:A:2192:U:O2'	8:A:2193:G:OP1	2.32	0.41
15:H:79:THR:HA	15:H:145:ASN:O	2.20	0.41
15:H:113:SER:O	15:H:113:SER:OG	2.37	0.41
18:K:23:LYS:HB2	18:K:23:LYS:HE2	1.82	0.41
19:L:3:LEU:HD12	19:L:3:LEU:HA	1.87	0.41
21:N:62:ASN:HD22	21:N:62:ASN:HA	1.68	0.41
23:P:88:ARG:HH11	23:P:113:LEU:HA	1.86	0.41
25:R:74:ILE:HB	25:R:87:GLN:HB3	2.02	0.41
34:a:634:C:H2'	34:a:635:A:H8	1.84	0.41
34:a:950:U:H2'	34:a:951:G:H8	1.85	0.41
34:a:1162:C:H2'	34:a:1163:A:H8	1.85	0.41
34:a:1236:A:H4'	34:a:1304:G:H4'	2.01	0.41
35:b:147:LEU:HD22	35:b:150:ILE:HD11	2.03	0.41
35:b:163:ILE:O	35:b:185:ILE:HB	2.21	0.41
45:l:34:THR:N	45:l:53:ARG:O	2.53	0.41
49:p:52:LEU:HD23	49:p:78:VAL:HG11	2.02	0.41
2:1:4:ILE:HB	2:1:27:ARG:NH1	2.36	0.41
7:6:27:THR:OG1	13:F:58:ALA:O	2.37	0.41
8:A:82:U:H2'	8:A:83:A:C8	2.55	0.41
8:A:255:A:H2'	8:A:256:A:O4'	2.20	0.41
8:A:743:A:OP1	11:D:135:GLY:HA2	2.20	0.41
8:A:1292:G:H2'	8:A:1293:C:H6	1.85	0.41
8:A:1378:A:O2'	8:A:1380:G:N7	2.53	0.41
8:A:1378:A:O2'	8:A:1379:U:OP2	2.37	0.41
8:A:1831:G:H2'	8:A:1832:C:C6	2.56	0.41
8:A:1935:G:H3'	8:A:1962:5MC:HN41	1.86	0.41
8:A:2105:U:H3	8:A:2185:U:H3	1.68	0.41
8:A:2554:U:H2'	8:A:2555:U:H6	1.85	0.41
11:D:4:LEU:HD23	11:D:101:PHE:CE2	2.55	0.41
19:L:111:ILE:HG22	19:L:128:THR:CG2	2.50	0.41
20:M:66:ARG:HB2	20:M:101:VAL:O	2.20	0.41
22:O:16:ARG:NH1	22:O:19:GLN:OE1	2.42	0.41
22:O:77:ALA:O	22:O:81:ARG:HG3	2.20	0.41
25:R:6:GLN:HA	25:R:11:GLN:HA	2.02	0.41
26:S:13:SER:O	26:S:17:VAL:HG23	2.19	0.41
32:Y:20:ASN:HA	32:Y:23:ARG:HB2	2.01	0.41
34:a:35:G:H2'	34:a:36:C:H6	1.85	0.41
34:a:81:A:H61	34:a:86:G:H21	1.68	0.41
34:a:232:G:H1'	34:a:262:A:N1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:482:A:H2'	34:a:483:C:O4'	2.20	0.41
34:a:544:G:P	37:d:58:GLN:HE21	2.43	0.41
34:a:1142:G:H2'	34:a:1143:G:O4'	2.21	0.41
43:j:59:LYS:O	43:j:59:LYS:HG3	2.18	0.41
46:m:30:LYS:HE2	46:m:30:LYS:HB3	1.81	0.41
50:q:7:LEU:HD13	50:q:72:TRP:CH2	2.53	0.41
54:u:9:GLU:CB	54:u:10:PRO:CD	2.98	0.41
7:6:50:ASP:OD1	7:6:51:VAL:N	2.54	0.41
8:A:69:C:H4'	8:A:75:G:N7	2.35	0.41
8:A:246:C:O2'	8:A:385:C:H4'	2.20	0.41
8:A:538:A:H2'	8:A:539:G:O4'	2.20	0.41
8:A:674:G:H5''	12:E:71:GLY:N	2.35	0.41
8:A:1171:G:H2'	8:A:1171:G:N3	2.35	0.41
8:A:1438:U:H2'	8:A:1439:A:H8	1.85	0.41
8:A:1724:G:H1	8:A:1736:U:H3	1.68	0.41
8:A:2191:A:H2'	8:A:2192:U:C6	2.56	0.41
8:A:2646:C:OP2	8:A:2732:G:O2'	2.37	0.41
12:E:194:LYS:O	12:E:197:GLU:HG3	2.20	0.41
34:a:426:U:H2'	34:a:427:U:C6	2.55	0.41
34:a:802:A:H3'	34:a:803:G:C8	2.55	0.41
34:a:1238:A:C8	34:a:1303:C:H1'	2.55	0.41
34:a:1486:G:H2'	34:a:1487:G:O4'	2.20	0.41
34:a:1510:C:H2'	34:a:1511:G:C8	2.54	0.41
35:b:216:VAL:HA	35:b:219:THR:HG22	2.00	0.41
36:c:35:ASP:OD1	36:c:58:ARG:NH1	2.28	0.41
40:g:128:GLU:HG3	40:g:130:LYS:HE3	2.01	0.41
56:w:54:5MU:H2'	56:w:55:PSU:O4'	2.21	0.41
8:A:371:A:H1'	31:X:60:LYS:NZ	2.36	0.41
8:A:395:U:H2'	8:A:396:G:C8	2.56	0.41
8:A:739:A:N3	8:A:740:C:N4	2.57	0.41
8:A:858:G:H3'	8:A:859:G:C8	2.56	0.41
8:A:1260:A:H2'	8:A:1261:C:O4'	2.20	0.41
8:A:1754:A:N1	8:A:2716:C:O2'	2.39	0.41
8:A:1954:G:O2'	8:A:1956:U:O4	2.38	0.41
8:A:2157:G:H21	8:A:2158:A:H61	1.68	0.41
8:A:2228:G:H2'	8:A:2229:U:C6	2.55	0.41
34:a:212:G:H2'	34:a:213:G:C8	2.56	0.41
34:a:478:A:H2'	34:a:479:U:O4'	2.21	0.41
34:a:757:U:OP1	34:a:822:U:O2'	2.32	0.41
34:a:883:C:O2'	34:a:884:U:H5'	2.21	0.41
34:a:1124:G:H3'	43:j:37:ARG:NH2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1179:A:H2'	34:a:1180:A:O4'	2.21	0.41
43:j:59:LYS:HE2	43:j:62:ARG:NH2	2.35	0.41
54:u:19:LYS:HD2	54:u:19:LYS:O	2.21	0.41
2:1:7:LYS:HZ1	4:3:33:THR:CG2	2.32	0.41
3:2:44:VAL:O	3:2:44:VAL:HG23	2.21	0.41
8:A:740:C:H5'	8:A:1784:A:H3'	2.02	0.41
8:A:764:A:H2	10:C:217:PRO:HG3	1.86	0.41
8:A:1243:C:H1'	19:L:4:ASN:O	2.20	0.41
8:A:1586:A:H2'	8:A:1587:G:O4'	2.21	0.41
8:A:2247:A:H2'	8:A:2248:C:C6	2.55	0.41
8:A:2547:A:H4'	18:K:29:HIS:NE2	2.36	0.41
8:A:2897:U:H2'	8:A:2898:U:C6	2.56	0.41
10:C:176:ARG:HD2	10:C:176:ARG:HA	1.87	0.41
11:D:9:VAL:CG2	11:D:28:GLU:H	2.33	0.41
14:G:3:VAL:O	14:G:68:ARG:HG2	2.19	0.41
15:H:122:LEU:HD11	15:H:128:HIS:HB2	2.03	0.41
17:J:53:TYR:CE2	17:J:121:LYS:HG2	2.56	0.41
23:P:110:LYS:HB2	23:P:110:LYS:HE2	1.84	0.41
26:S:7:HIS:HB2	26:S:50:VAL:HG22	2.03	0.41
34:a:398:U:H2'	34:a:399:G:C8	2.55	0.41
34:a:691:G:O2'	34:a:797:C:H4'	2.21	0.41
34:a:1032:G:H2'	34:a:1033:G:O4'	2.21	0.41
43:j:42:LEU:HD23	43:j:42:LEU:HA	1.68	0.41
48:o:32:THR:HG21	48:o:84:LEU:HG	2.02	0.41
49:p:8:ARG:NE	49:p:15:PRO:HB3	2.35	0.41
54:u:64:ALA:C	54:u:66:ARG:H	2.27	0.41
56:w:23:A:H2'	56:w:24:G:H8	1.83	0.41
56:w:63:G:H2'	56:w:64:A:H8	1.86	0.41
2:1:24:LYS:NZ	2:1:50:GLU:OE1	2.33	0.41
4:3:30:HIS:N	4:3:30:HIS:HD2	2.19	0.41
8:A:287:G:H2'	8:A:287:G:N3	2.36	0.41
8:A:464:U:H2'	8:A:465:G:O4'	2.20	0.41
8:A:610:C:H2'	8:A:611:C:C6	2.55	0.41
8:A:679:C:H2'	8:A:680:C:H6	1.85	0.41
8:A:702:U:H2'	8:A:703:U:C6	2.56	0.41
8:A:747:5MC:O2'	26:S:92:ARG:NH2	2.54	0.41
8:A:1059:G:N7	8:A:1088:A:N6	2.68	0.41
8:A:1579:A:H2'	8:A:1580:A:C8	2.56	0.41
8:A:1779:U:OP2	8:A:1784:A:N6	2.39	0.41
8:A:1833:C:O2'	8:A:1969:A:N1	2.50	0.41
8:A:2688:G:H1'	8:A:2721:A:N6	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:42:C:C5	13:F:65:LEU:HD22	2.56	0.41
15:H:50:ARG:CZ	15:H:51:ARG:HH11	2.34	0.41
18:K:35:VAL:C	18:K:37:ASP:H	2.29	0.41
18:K:92:GLU:O	18:K:93:GLN:C	2.64	0.41
25:R:51:VAL:HB	25:R:52:PRO:HD2	1.92	0.41
34:a:522:C:OP2	45:l:65:TYR:OH	2.28	0.41
34:a:554:A:H2'	34:a:555:U:C6	2.56	0.41
34:a:590:U:H2'	34:a:591:U:C6	2.55	0.41
34:a:692:U:H1'	34:a:695:A:N7	2.35	0.41
34:a:763:G:H2'	34:a:764:C:C6	2.56	0.41
34:a:1372:U:H2'	34:a:1373:G:O4'	2.20	0.41
35:b:77:GLU:H	35:b:77:GLU:CD	2.25	0.41
37:d:28:ASP:OD1	37:d:29:THR:N	2.54	0.41
37:d:77:GLU:O	37:d:78:ALA:HB3	2.21	0.41
38:e:24:VAL:N	38:e:27:GLY:O	2.53	0.41
40:g:124:SER:O	40:g:128:GLU:HG2	2.20	0.41
43:j:8:ILE:HB	43:j:74:VAL:CG2	2.47	0.41
55:v:17:ARG:NH1	58:y:28:GLN:OE1	2.53	0.41
8:A:40:U:H2'	8:A:41:C:C6	2.56	0.41
8:A:65:U:H2'	8:A:66:C:H6	1.86	0.41
8:A:195:A:H61	8:A:198:C:H3'	1.85	0.41
8:A:595:C:H2'	8:A:596:U:H6	1.86	0.41
8:A:610:C:H2'	8:A:611:C:H6	1.85	0.41
8:A:634:C:H2'	8:A:635:C:H6	1.86	0.41
8:A:698:C:O2'	8:A:734:A:N6	2.54	0.41
8:A:744:U:H2'	8:A:745:1MG:O4'	2.21	0.41
8:A:984:A:H2'	8:A:984:A:N3	2.36	0.41
8:A:1057:A:H2'	8:A:1058:U:H5'	2.03	0.41
8:A:2070:A:H2'	8:A:2071:A:C8	2.55	0.41
8:A:2141:G:H2'	8:A:2142:A:H8	1.83	0.41
8:A:2205:A:H2'	8:A:2206:C:C6	2.56	0.41
8:A:2246:G:H2'	8:A:2247:A:H8	1.85	0.41
8:A:2395:C:H2'	8:A:2396:G:O4'	2.21	0.41
8:A:2646:C:O5'	8:A:2646:C:H6	2.04	0.41
8:A:2813:A:H2'	8:A:2814:A:C8	2.56	0.41
9:B:2:G:H2'	9:B:3:C:C6	2.56	0.41
10:C:71:ASP:OD2	10:C:188:ARG:NH2	2.54	0.41
14:G:174:LYS:HB2	14:G:176:LYS:H	1.85	0.41
15:H:110:VAL:HG23	15:H:111:ALA:O	2.21	0.41
18:K:20:MET:HE2	18:K:20:MET:HB3	1.99	0.41
19:L:79:LEU:O	19:L:82:LEU:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:85:VAL:HG21	19:L:90:VAL:HG22	2.03	0.41
23:P:1:SER:O	23:P:5:LYS:HG2	2.21	0.41
34:a:35:G:H5'	45:l:100:ALA:HB2	2.03	0.41
34:a:184:G:H2'	34:a:185:U:H6	1.86	0.41
34:a:505:G:H2'	34:a:506:G:H8	1.86	0.41
34:a:507:C:OP2	34:a:508:U:O2'	2.37	0.41
34:a:511:C:O2'	34:a:512:U:O5'	2.34	0.41
34:a:660:C:H2'	34:a:661:G:O4'	2.21	0.41
34:a:807:A:H2'	34:a:808:C:C6	2.55	0.41
34:a:1014:A:H2'	34:a:1015:G:C8	2.56	0.41
34:a:1121:U:H2'	34:a:1122:U:C6	2.55	0.41
34:a:1350:A:OP2	42:i:119:LYS:HD3	2.20	0.41
34:a:1451:U:H5''	34:a:1452:C:H5	1.86	0.41
34:a:1513:A:H2'	34:a:1514:G:H8	1.86	0.41
43:j:15:HIS:HB3	43:j:70:HIS:CE1	2.56	0.41
46:m:39:ALA:HB3	46:m:42:VAL:HG13	2.02	0.41
46:m:113:LYS:HB2	46:m:114:PRO:HD3	2.02	0.41
47:n:20:PHE:C	47:n:22:LYS:H	2.29	0.41
58:y:51:TYR:OH	58:y:101:GLU:OE1	2.33	0.41
8:A:595:C:H2'	8:A:596:U:C6	2.56	0.41
8:A:722:A:H2'	8:A:723:C:C6	2.56	0.41
8:A:747:5MC:O2	8:A:2014:A:H1'	2.20	0.41
8:A:911:A:N6	20:M:11:LYS:O	2.48	0.41
8:A:1012:U:OP2	24:Q:69:ARG:NH1	2.46	0.41
8:A:1183:U:H2'	8:A:1184:U:H6	1.86	0.41
8:A:1918:A:O2'	8:A:1919:A:N7	2.36	0.41
8:A:2794:C:H2'	8:A:2795:C:C6	2.56	0.41
9:B:74:U:H2'	9:B:75:G:O4'	2.21	0.41
12:E:122:GLU:HB3	12:E:123:LYS:H	1.73	0.41
19:L:111:ILE:HG22	19:L:128:THR:HG21	2.01	0.41
22:O:29:HIS:HB3	22:O:36:TYR:HB2	2.03	0.41
26:S:17:VAL:HB	26:S:76:VAL:HG11	2.03	0.41
28:U:10:VAL:HG12	28:U:71:ILE:HG22	2.02	0.41
34:a:5:U:H5''	34:a:6:G:OP1	2.21	0.41
34:a:19:A:O2'	34:a:572:A:N1	2.46	0.41
34:a:184:G:H2'	34:a:185:U:C6	2.56	0.41
34:a:621:A:H2'	34:a:622:A:C8	2.55	0.41
34:a:986:U:H2'	34:a:987:G:O4'	2.21	0.41
34:a:1187:G:H2'	34:a:1188:A:C8	2.56	0.41
34:a:1260:G:H4'	34:a:1283:U:O2'	2.20	0.41
34:a:1280:A:OP1	43:j:9:ARG:NH1	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1532:U:H2'	34:a:1533:C:O4'	2.21	0.41
37:d:104:MET:HG2	37:d:170:LEU:HD13	2.02	0.41
38:e:110:MET:HE2	38:e:126:ALA:HB2	2.03	0.41
52:s:2:ARG:HE	52:s:6:LYS:CB	2.33	0.41
2:1:6:GLU:OE1	2:1:6:GLU:N	2.53	0.40
8:A:28:A:H1'	8:A:513:A:C2	2.56	0.40
8:A:268:C:H2'	8:A:269:C:H6	1.86	0.40
8:A:558:U:H2'	8:A:559:G:C8	2.56	0.40
8:A:644:A:C2	8:A:2369:A:H1'	2.56	0.40
8:A:753:A:OP2	8:A:753:A:H8	2.04	0.40
8:A:814:C:H1'	8:A:1225:G:N2	2.36	0.40
8:A:1091:G:O2'	8:A:1092:C:OP1	2.36	0.40
8:A:1171:G:H22	8:A:1177:G:H22	1.68	0.40
8:A:1296:G:OP1	8:A:2709:G:O2'	2.21	0.40
8:A:1739:A:H2'	8:A:1740:G:O4'	2.21	0.40
8:A:2297:A:N6	8:A:2319:G:H1'	2.35	0.40
8:A:2350:C:H2'	8:A:2351:G:O4'	2.20	0.40
8:A:2658:C:OP1	14:G:157:LYS:HE2	2.21	0.40
9:B:52:A:O2'	9:B:53:A:P	2.79	0.40
28:U:52:ASN:C	28:U:54:PRO:HD3	2.46	0.40
34:a:339:C:H2'	34:a:340:U:C6	2.56	0.40
34:a:881:G:H2'	34:a:882:C:O4'	2.21	0.40
34:a:1122:U:H2'	34:a:1123:U:C6	2.56	0.40
34:a:1263:C:H2'	34:a:1264:U:C6	2.56	0.40
34:a:1267:C:O2	34:a:1327:C:H4'	2.21	0.40
34:a:1300:G:H1'	34:a:1301:U:H5	1.86	0.40
34:a:1347:G:H5''	42:i:108:ARG:HB2	2.02	0.40
36:c:24:ASN:O	36:c:28:PHE:HB2	2.21	0.40
40:g:14:ASP:OD1	40:g:43:TYR:OH	2.27	0.40
43:j:22:THR:HG21	43:j:39:PRO:HB3	2.04	0.40
46:m:10:ASP:HA	46:m:44:ILE:HB	2.03	0.40
8:A:26:G:H1'	8:A:514:A:N6	2.36	0.40
8:A:736:C:H2'	8:A:737:C:C6	2.56	0.40
8:A:861:A:H2'	8:A:862:G:O4'	2.21	0.40
8:A:864:G:O2'	8:A:865:C:H5'	2.22	0.40
8:A:1083:U:H4'	8:A:1084:A:C8	2.57	0.40
8:A:1385:A:H1'	8:A:1386:C:C6	2.56	0.40
8:A:1538:G:H2'	8:A:1539:U:C6	2.56	0.40
8:A:2081:U:H2'	8:A:2082:A:H8	1.86	0.40
34:a:628:G:H2'	34:a:629:A:H8	1.86	0.40
34:a:658:C:H2'	34:a:659:U:H6	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1044:A:C5	34:a:1045:C:H1'	2.56	0.40
34:a:1119:C:H2'	34:a:1120:C:C6	2.56	0.40
34:a:1163:A:H2'	34:a:1164:G:H8	1.85	0.40
34:a:1246:A:H2'	34:a:1247:U:C6	2.56	0.40
34:a:1367:C:H5''	42:i:115:VAL:HG22	2.02	0.40
34:a:1446:A:O2'	34:a:1447:A:H5'	2.22	0.40
42:i:54:VAL:HG23	42:i:55:ASP:N	2.34	0.40
58:y:27:GLY:O	58:y:30:VAL:HG12	2.21	0.40
7:6:16:CYS:SG	7:6:17:SER:N	2.94	0.40
8:A:277:G:H4'	8:A:361:G:O6	2.20	0.40
8:A:825:A:H2'	8:A:826:U:O4'	2.21	0.40
8:A:1039:A:H2'	8:A:1040:A:O4'	2.20	0.40
8:A:1436:G:H2'	8:A:1437:C:O4'	2.21	0.40
8:A:1496:A:H2'	8:A:1498:C:C4	2.56	0.40
8:A:2468:A:O2'	8:A:2469:A:H8	2.04	0.40
8:A:2638:G:O2'	8:A:2639:A:O5'	2.39	0.40
17:J:77:HIS:HA	17:J:83:GLY:O	2.21	0.40
34:a:9:G:OP2	38:e:125:LYS:NZ	2.41	0.40
34:a:264:C:H2'	34:a:265:G:O4'	2.22	0.40
34:a:950:U:H3'	46:m:100:ARG:HH12	1.86	0.40
34:a:1088:G:H2'	34:a:1089:G:O4'	2.21	0.40
34:a:1162:C:H2'	34:a:1163:A:C8	2.56	0.40
34:a:1326:U:H2'	34:a:1327:C:H6	1.86	0.40
34:a:1402:4OC:H2'	34:a:1403:C:O4'	2.21	0.40
46:m:48:SER:O	46:m:51:GLN:N	2.54	0.40
58:y:50:GLU:C	58:y:52:TYR:H	2.29	0.40
1:O:7:PRO:HD2	8:A:1263:U:O2'	2.22	0.40
8:A:501:A:H2'	8:A:502:A:C8	2.56	0.40
8:A:561:G:O2'	24:Q:44:TYR:OH	2.26	0.40
8:A:882:G:C6	8:A:883:G:N1	2.90	0.40
8:A:1138:G:H2'	8:A:1139:G:O4'	2.22	0.40
8:A:1847:G:O2'	8:A:1848:A:P	2.79	0.40
8:A:2141:G:H1	8:A:2150:C:H42	1.70	0.40
8:A:2473:U:H6	8:A:2473:U:H2'	1.69	0.40
8:A:2552:OMU:HM23	8:A:2554:U:C6	2.56	0.40
9:B:49:C:H2'	9:B:50:A:C8	2.57	0.40
9:B:101:A:H2'	9:B:102:G:O4'	2.22	0.40
14:G:148:ARG:HG3	14:G:161:VAL:O	2.21	0.40
20:M:126:ILE:HA	20:M:126:ILE:HD12	1.78	0.40
34:a:321:A:H2'	34:a:322:C:C6	2.57	0.40
34:a:562:U:H2'	34:a:562:U:OP1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:579:A:H2'	34:a:580:C:H6	1.87	0.40
34:a:900:A:H2'	34:a:901:A:C8	2.56	0.40
36:c:81:GLU:O	36:c:85:LYS:HG3	2.22	0.40
39:f:93:LYS:O	39:f:94:HIS:ND1	2.54	0.40
51:r:22:TYR:HA	51:r:28:LEU:HD21	2.02	0.40
3:2:18:PHE:HA	3:2:43:THR:HG21	2.04	0.40
8:A:528:A:C2	8:A:2043:C:H4'	2.56	0.40
8:A:721:A:H2'	8:A:722:A:H8	1.83	0.40
8:A:880:G:C2	8:A:898:C:C2	3.10	0.40
8:A:1057:A:C8	8:A:1060:U:N3	2.87	0.40
8:A:2079:U:O2'	31:X:22:ASN:OD1	2.27	0.40
8:A:2128:G:H1'	8:A:2173:A:H1'	2.02	0.40
8:A:2266:A:H4'	8:A:2267:A:N3	2.37	0.40
8:A:2515:C:H2'	8:A:2516:A:C8	2.57	0.40
11:D:146:ILE:HA	11:D:159:LYS:HE3	2.04	0.40
13:F:11:VAL:HG11	13:F:168:LEU:HD12	2.04	0.40
25:R:5:PHE:HB3	25:R:59:ILE:HD12	2.04	0.40
26:S:4:ILE:HG13	26:S:106:VAL:HG22	2.03	0.40
34:a:509:A:H4'	34:a:510:A:OP1	2.21	0.40
34:a:750:C:O2	48:o:22:GLY:HA3	2.22	0.40
34:a:891:U:H2'	34:a:892:A:H8	1.87	0.40
36:c:46:LEU:HD21	36:c:86:LEU:HD11	2.04	0.40
40:g:6:ILE:HD13	40:g:6:ILE:HA	1.87	0.40
50:q:16:MET:HE1	50:q:44:HIS:HD2	1.87	0.40
53:t:30:PHE:O	53:t:34:VAL:HG23	2.22	0.40
56:w:63:G:H2'	56:w:64:A:C8	2.57	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	
1	0	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
2	1	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
3	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
4	3	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
5	4	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
6	5	129/165 (78%)	103 (80%)	26 (20%)	0	100	100
7	6	64/70 (91%)	51 (80%)	13 (20%)	0	100	100
10	C	269/273 (98%)	254 (94%)	15 (6%)	0	100	100
11	D	207/209 (99%)	194 (94%)	13 (6%)	0	100	100
12	E	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
13	F	175/179 (98%)	163 (93%)	12 (7%)	0	100	100
14	G	174/177 (98%)	160 (92%)	14 (8%)	0	100	100
15	H	147/149 (99%)	116 (79%)	31 (21%)	0	100	100
16	I	139/142 (98%)	121 (87%)	18 (13%)	0	100	100
17	J	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
18	K	120/123 (98%)	109 (91%)	11 (9%)	0	100	100
19	L	141/144 (98%)	126 (89%)	15 (11%)	0	100	100
20	M	134/136 (98%)	130 (97%)	3 (2%)	1 (1%)	18	38
21	N	118/127 (93%)	108 (92%)	10 (8%)	0	100	100
22	O	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
23	P	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
24	Q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
25	R	101/103 (98%)	96 (95%)	4 (4%)	1 (1%)	12	28
26	S	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
27	T	91/100 (91%)	82 (90%)	9 (10%)	0	100	100
28	U	100/104 (96%)	91 (91%)	9 (9%)	0	100	100
29	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
30	W	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
31	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
32	Y	61/63 (97%)	59 (97%)	0	2 (3%)	3	5
33	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
35	b	216/240 (90%)	198 (92%)	18 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	c	204/233 (88%)	196 (96%)	8 (4%)	0	100	100
37	d	203/206 (98%)	176 (87%)	23 (11%)	4 (2%)	6	12
38	e	155/167 (93%)	139 (90%)	16 (10%)	0	100	100
39	f	98/135 (73%)	90 (92%)	8 (8%)	0	100	100
40	g	149/179 (83%)	141 (95%)	8 (5%)	0	100	100
41	h	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
42	i	125/130 (96%)	108 (86%)	17 (14%)	0	100	100
43	j	96/103 (93%)	81 (84%)	12 (12%)	3 (3%)	3	5
44	k	114/129 (88%)	102 (90%)	12 (10%)	0	100	100
45	l	121/124 (98%)	112 (93%)	8 (7%)	1 (1%)	16	34
46	m	112/118 (95%)	102 (91%)	10 (9%)	0	100	100
47	n	99/102 (97%)	90 (91%)	9 (9%)	0	100	100
48	o	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
49	p	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
50	q	78/84 (93%)	69 (88%)	9 (12%)	0	100	100
51	r	63/75 (84%)	55 (87%)	8 (13%)	0	100	100
52	s	80/92 (87%)	74 (92%)	6 (8%)	0	100	100
53	t	83/87 (95%)	80 (96%)	3 (4%)	0	100	100
54	u	63/71 (89%)	52 (82%)	8 (13%)	3 (5%)	2	2
55	v	12/14 (86%)	9 (75%)	3 (25%)	0	100	100
58	y	137/140 (98%)	129 (94%)	6 (4%)	2 (2%)	8	18
All	All	5999/6374 (94%)	5518 (92%)	464 (8%)	17 (0%)	37	58

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	M	70	ASP
25	R	52	PRO
32	Y	18	LEU
37	d	143	SER
45	l	43	LYS
54	u	9	GLU
58	y	137	SER
32	Y	19	LEU
37	d	70	GLN

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Mol	Chain	Res	Type
54	u	12	ASP
43	j	41	PRO
43	j	57	VAL
54	u	11	PHE
58	y	139	ARG
37	d	145	ARG
37	d	147	LYS
43	j	42	LEU

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	
1	0	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	47 (92%)	4 (8%)	11	26
5	4	34/34 (100%)	34 (100%)	0	100	100
7	6	59/62 (95%)	59 (100%)	0	100	100
10	C	216/218 (99%)	216 (100%)	0	100	100
11	D	164/164 (100%)	163 (99%)	1 (1%)	78	91
12	E	165/165 (100%)	165 (100%)	0	100	100
13	F	148/150 (99%)	148 (100%)	0	100	100
14	G	137/138 (99%)	137 (100%)	0	100	100
15	H	114/114 (100%)	111 (97%)	3 (3%)	40	68
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	103 (100%)	0	100	100
19	L	102/103 (99%)	101 (99%)	1 (1%)	68	86
20	M	109/109 (100%)	109 (100%)	0	100	100
21	N	100/103 (97%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	O	86/87 (99%)	86 (100%)	0	100	100
23	P	99/100 (99%)	99 (100%)	0	100	100
24	Q	89/90 (99%)	89 (100%)	0	100	100
25	R	84/84 (100%)	82 (98%)	2 (2%)	43	70
26	S	93/93 (100%)	93 (100%)	0	100	100
27	T	80/84 (95%)	80 (100%)	0	100	100
28	U	83/85 (98%)	83 (100%)	0	100	100
29	V	78/78 (100%)	78 (100%)	0	100	100
30	W	57/63 (90%)	57 (100%)	0	100	100
31	X	67/68 (98%)	67 (100%)	0	100	100
32	Y	55/55 (100%)	50 (91%)	5 (9%)	9	19
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	178 (99%)	2 (1%)	65	84
36	c	170/190 (90%)	170 (100%)	0	100	100
37	d	172/173 (99%)	167 (97%)	5 (3%)	37	65
38	e	114/126 (90%)	114 (100%)	0	100	100
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	124 (100%)	0	100	100
41	h	104/105 (99%)	104 (100%)	0	100	100
42	i	105/107 (98%)	105 (100%)	0	100	100
43	j	86/90 (96%)	84 (98%)	2 (2%)	44	71
44	k	89/99 (90%)	89 (100%)	0	100	100
45	l	103/104 (99%)	101 (98%)	2 (2%)	50	75
46	m	92/96 (96%)	92 (100%)	0	100	100
47	n	79/84 (94%)	79 (100%)	0	100	100
48	o	76/77 (99%)	76 (100%)	0	100	100
49	p	65/65 (100%)	64 (98%)	1 (2%)	57	80
50	q	74/78 (95%)	73 (99%)	1 (1%)	59	81
51	r	56/65 (86%)	56 (100%)	0	100	100
52	s	72/79 (91%)	72 (100%)	0	100	100
53	t	65/66 (98%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	u	46/61 (75%)	45 (98%)	1 (2%)	45	72
55	v	14/14 (100%)	14 (100%)	0	100	100
58	y	112/115 (97%)	112 (100%)	0	100	100
All	All	4752/4958 (96%)	4722 (99%)	30 (1%)	76	91

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	3	28	LEU
4	3	30	HIS
4	3	31	ILE
4	3	32	LEU
11	D	9	VAL
15	H	41	LYS
15	H	121	VAL
15	H	122	LEU
19	L	127	VAL
25	R	51	VAL
25	R	52	PRO
32	Y	14	LEU
32	Y	18	LEU
32	Y	20	ASN
32	Y	21	LEU
32	Y	23	ARG
35	b	18	GLN
35	b	65	LYS
37	d	69	ARG
37	d	72	ARG
37	d	143	SER
37	d	145	ARG
37	d	146	GLU
43	j	41	PRO
43	j	74	VAL
45	l	43	LYS
45	l	46	SER
49	p	20	VAL
50	q	49	ASN
54	u	13	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (67) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	4	GLN
1	0	5	ASN
1	0	41	HIS
4	3	30	HIS
7	6	61	ASN
7	6	65	ASN
10	C	52	HIS
10	C	114	GLN
10	C	133	ASN
11	D	32	ASN
11	D	150	GLN
11	D	173	GLN
12	E	90	GLN
12	E	136	GLN
13	F	36	ASN
13	F	80	GLN
14	G	19	ASN
14	G	29	ASN
14	G	115	GLN
15	H	18	GLN
15	H	73	ASN
15	H	128	HIS
17	J	47	HIS
18	K	9	ASN
18	K	88	ASN
18	K	90	ASN
19	L	104	GLN
20	M	13	HIS
21	N	62	ASN
23	P	14	GLN
23	P	40	GLN
27	T	48	GLN
27	T	92	ASN
28	U	26	ASN
28	U	73	ASN
30	W	8	ASN
31	X	35	HIS
35	b	14	HIS
35	b	108	GLN
36	c	18	ASN
36	c	101	ASN
36	c	175	HIS
37	d	73	ASN

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Mol	Chain	Res	Type
38	e	131	ASN
38	e	147	ASN
39	f	17	GLN
39	f	52	ASN
39	f	63	ASN
40	g	8	GLN
41	h	17	GLN
41	h	66	GLN
43	j	56	HIS
44	k	21	HIS
44	k	23	HIS
44	k	39	ASN
44	k	118	ASN
45	l	76	HIS
45	l	111	GLN
47	n	49	GLN
47	n	60	GLN
48	o	79	GLN
49	p	40	ASN
49	p	59	HIS
52	s	82	HIS
53	t	2	ASN
53	t	51	ASN
53	t	77	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1539/1542 (99%)	253 (16%)	0
56	w	75/76 (98%)	11 (14%)	0
57	x	6/15 (40%)	1 (16%)	0
8	A	2902/2903 (99%)	515 (17%)	35 (1%)
9	B	119/120 (99%)	15 (12%)	3 (2%)
All	All	4641/4656 (99%)	795 (17%)	38 (0%)

All (795) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	15	G
8	A	34	U

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Mol	Chain	Res	Type
8	A	35	G
8	A	46	G
8	A	51	G
8	A	61	C
8	A	63	A
8	A	71	A
8	A	74	A
8	A	75	G
8	A	101	A
8	A	102	U
8	A	103	A
8	A	110	G
8	A	118	A
8	A	119	A
8	A	120	U
8	A	125	A
8	A	131	A
8	A	139	U
8	A	140	C
8	A	141	G
8	A	142	A
8	A	160	A
8	A	163	C
8	A	181	A
8	A	196	A
8	A	199	A
8	A	216	A
8	A	221	A
8	A	222	A
8	A	223	A
8	A	224	U
8	A	228	C
8	A	230	G
8	A	233	A
8	A	242	G
8	A	243	U
8	A	248	G
8	A	250	G
8	A	255	A
8	A	265	A
8	A	266	G
8	A	271	G

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Mol	Chain	Res	Type
8	A	272	A
8	A	275	C
8	A	276	U
8	A	277	G
8	A	278	A
8	A	287	G
8	A	330	A
8	A	332	A
8	A	345	A
8	A	346	A
8	A	371	A
8	A	372	G
8	A	383	C
8	A	386	G
8	A	395	U
8	A	401	A
8	A	404	A
8	A	405	U
8	A	406	G
8	A	411	G
8	A	424	G
8	A	425	G
8	A	443	A
8	A	447	A
8	A	457	A
8	A	458	G
8	A	459	U
8	A	475	C
8	A	481	G
8	A	491	G
8	A	496	G
8	A	505	A
8	A	509	C
8	A	529	A
8	A	532	A
8	A	549	G
8	A	556	A
8	A	563	A
8	A	568	U
8	A	571	U
8	A	573	U
8	A	575	A

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Mol	Chain	Res	Type
8	A	603	A
8	A	613	A
8	A	614	A
8	A	615	U
8	A	622	G
8	A	627	A
8	A	637	A
8	A	645	C
8	A	647	G
8	A	655	A
8	A	669	G
8	A	670	A
8	A	677	A
8	A	682	G
8	A	686	U
8	A	705	A
8	A	717	C
8	A	729	G
8	A	730	A
8	A	738	G
8	A	740	C
8	A	747	5MC
8	A	752	A
8	A	753	A
8	A	764	A
8	A	774	G
8	A	775	G
8	A	776	G
8	A	782	A
8	A	784	G
8	A	785	G
8	A	789	A
8	A	791	C
8	A	792	A
8	A	805	G
8	A	812	C
8	A	819	A
8	A	827	U
8	A	828	U
8	A	845	A
8	A	846	U
8	A	847	U

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Mol	Chain	Res	Type
8	A	856	G
8	A	858	G
8	A	859	G
8	A	869	G
8	A	878	A
8	A	880	G
8	A	883	G
8	A	884	U
8	A	885	C
8	A	886	A
8	A	887	U
8	A	888	C
8	A	892	A
8	A	894	U
8	A	895	U
8	A	896	A
8	A	897	C
8	A	906	U
8	A	910	A
8	A	913	U
8	A	914	G
8	A	927	A
8	A	941	A
8	A	946	C
8	A	961	C
8	A	974	G
8	A	975	A
8	A	983	A
8	A	990	A
8	A	995	C
8	A	996	A
8	A	999	U
8	A	1012	U
8	A	1013	C
8	A	1026	G
8	A	1033	U
8	A	1040	A
8	A	1046	A
8	A	1047	G
8	A	1057	A
8	A	1058	U
8	A	1059	G

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Mol	Chain	Res	Type
8	A	1060	U
8	A	1061	U
8	A	1062	G
8	A	1063	G
8	A	1064	C
8	A	1065	U
8	A	1066	U
8	A	1067	A
8	A	1068	G
8	A	1069	A
8	A	1070	A
8	A	1072	C
8	A	1073	A
8	A	1074	G
8	A	1075	C
8	A	1078	U
8	A	1079	C
8	A	1080	A
8	A	1082	U
8	A	1083	U
8	A	1084	A
8	A	1085	A
8	A	1086	A
8	A	1088	A
8	A	1089	A
8	A	1090	A
8	A	1091	G
8	A	1092	C
8	A	1093	G
8	A	1095	A
8	A	1097	U
8	A	1098	A
8	A	1099	G
8	A	1100	C
8	A	1101	U
8	A	1102	C
8	A	1105	U
8	A	1106	G
8	A	1107	G
8	A	1111	A
8	A	1112	G
8	A	1115	G

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Mol	Chain	Res	Type
8	A	1116	G
8	A	1130	U
8	A	1132	U
8	A	1135	C
8	A	1142	A
8	A	1171	G
8	A	1172	C
8	A	1174	U
8	A	1175	A
8	A	1176	U
8	A	1178	C
8	A	1179	G
8	A	1180	U
8	A	1206	G
8	A	1227	G
8	A	1247	A
8	A	1250	G
8	A	1253	A
8	A	1256	G
8	A	1271	G
8	A	1272	A
8	A	1300	G
8	A	1301	A
8	A	1321	A
8	A	1329	U
8	A	1341	G
8	A	1352	U
8	A	1365	A
8	A	1368	G
8	A	1378	A
8	A	1379	U
8	A	1383	A
8	A	1395	A
8	A	1416	G
8	A	1419	A
8	A	1420	A
8	A	1421	G
8	A	1427	A
8	A	1428	C
8	A	1437	C
8	A	1452	G
8	A	1453	A

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Mol	Chain	Res	Type
8	A	1454	C
8	A	1455	G
8	A	1458	U
8	A	1460	U
8	A	1461	C
8	A	1482	G
8	A	1490	A
8	A	1491	G
8	A	1493	C
8	A	1497	U
8	A	1508	A
8	A	1509	A
8	A	1515	A
8	A	1523	U
8	A	1534	U
8	A	1535	A
8	A	1536	C
8	A	1560	G
8	A	1566	A
8	A	1569	A
8	A	1578	U
8	A	1583	A
8	A	1584	U
8	A	1585	C
8	A	1607	C
8	A	1608	A
8	A	1610	A
8	A	1626	A
8	A	1634	A
8	A	1647	U
8	A	1648	U
8	A	1649	G
8	A	1667	G
8	A	1674	G
8	A	1715	G
8	A	1716	U
8	A	1725	U
8	A	1729	U
8	A	1730	C
8	A	1731	G
8	A	1738	G
8	A	1744	A

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Mol	Chain	Res	Type
8	A	1764	C
8	A	1773	A
8	A	1776	G
8	A	1782	U
8	A	1784	A
8	A	1786	A
8	A	1800	C
8	A	1801	A
8	A	1807	G
8	A	1808	A
8	A	1811	G
8	A	1816	C
8	A	1829	A
8	A	1848	A
8	A	1857	G
8	A	1869	G
8	A	1876	A
8	A	1884	G
8	A	1900	A
8	A	1906	G
8	A	1907	G
8	A	1913	A
8	A	1914	C
8	A	1927	A
8	A	1929	G
8	A	1930	G
8	A	1937	A
8	A	1938	A
8	A	1939	5MU
8	A	1955	U
8	A	1965	C
8	A	1967	C
8	A	1970	A
8	A	1971	U
8	A	1972	G
8	A	1975	G
8	A	1982	U
8	A	1991	U
8	A	1992	G
8	A	1993	U
8	A	1997	C
8	A	2020	A

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Mol	Chain	Res	Type
8	A	2022	U
8	A	2023	C
8	A	2030	6MZ
8	A	2031	A
8	A	2032	G
8	A	2033	A
8	A	2036	C
8	A	2043	C
8	A	2055	C
8	A	2056	G
8	A	2060	A
8	A	2061	G
8	A	2062	A
8	A	2069	G7M
8	A	2072	C
8	A	2080	A
8	A	2093	G
8	A	2100	G
8	A	2104	C
8	A	2106	U
8	A	2107	G
8	A	2108	A
8	A	2109	U
8	A	2111	U
8	A	2112	G
8	A	2115	G
8	A	2116	G
8	A	2118	U
8	A	2120	G
8	A	2123	G
8	A	2124	G
8	A	2125	G
8	A	2129	C
8	A	2131	U
8	A	2132	U
8	A	2133	G
8	A	2134	A
8	A	2135	A
8	A	2136	G
8	A	2140	G
8	A	2141	G
8	A	2143	C

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Mol	Chain	Res	Type
8	A	2144	G
8	A	2145	C
8	A	2146	C
8	A	2147	A
8	A	2149	U
8	A	2154	A
8	A	2155	U
8	A	2156	G
8	A	2157	G
8	A	2158	A
8	A	2163	A
8	A	2164	C
8	A	2165	C
8	A	2166	U
8	A	2170	A
8	A	2171	A
8	A	2172	U
8	A	2176	A
8	A	2180	U
8	A	2181	U
8	A	2183	A
8	A	2185	U
8	A	2186	G
8	A	2188	U
8	A	2193	G
8	A	2198	A
8	A	2204	G
8	A	2211	A
8	A	2225	A
8	A	2238	G
8	A	2239	G
8	A	2268	A
8	A	2273	A
8	A	2278	A
8	A	2280	G
8	A	2283	C
8	A	2287	A
8	A	2288	A
8	A	2297	A
8	A	2305	U
8	A	2309	A
8	A	2320	U

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Mol	Chain	Res	Type
8	A	2322	A
8	A	2325	G
8	A	2336	A
8	A	2347	C
8	A	2350	C
8	A	2361	G
8	A	2382	G
8	A	2383	G
8	A	2385	C
8	A	2396	G
8	A	2402	U
8	A	2406	A
8	A	2407	A
8	A	2410	G
8	A	2423	U
8	A	2425	A
8	A	2426	A
8	A	2429	G
8	A	2435	A
8	A	2436	G
8	A	2441	U
8	A	2445	2MG
8	A	2447	G
8	A	2448	A
8	A	2469	A
8	A	2470	G
8	A	2474	U
8	A	2475	C
8	A	2476	A
8	A	2487	G
8	A	2494	G
8	A	2498	OMC
8	A	2502	G
8	A	2503	2MA
8	A	2505	G
8	A	2518	A
8	A	2520	C
8	A	2525	G
8	A	2529	G
8	A	2547	A
8	A	2554	U
8	A	2566	A

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Mol	Chain	Res	Type
8	A	2567	G
8	A	2572	A
8	A	2573	C
8	A	2582	G
8	A	2585	U
8	A	2586	U
8	A	2602	A
8	A	2609	U
8	A	2613	U
8	A	2614	A
8	A	2615	U
8	A	2629	U
8	A	2630	G
8	A	2646	C
8	A	2655	G
8	A	2656	U
8	A	2689	U
8	A	2690	U
8	A	2702	G
8	A	2714	G
8	A	2716	C
8	A	2718	G
8	A	2726	A
8	A	2729	G
8	A	2732	G
8	A	2733	A
8	A	2744	G
8	A	2748	A
8	A	2765	A
8	A	2778	A
8	A	2779	U
8	A	2780	G
8	A	2791	G
8	A	2798	U
8	A	2799	A
8	A	2800	A
8	A	2809	A
8	A	2818	U
8	A	2820	A
8	A	2821	A
8	A	2835	A
8	A	2849	U

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Mol	Chain	Res	Type
8	A	2861	U
8	A	2867	G
8	A	2873	A
8	A	2880	C
8	A	2884	U
8	A	2886	A
8	A	2891	U
8	A	2902	C
9	B	13	G
9	B	24	G
9	B	35	C
9	B	44	G
9	B	45	A
9	B	51	G
9	B	53	A
9	B	56	G
9	B	67	G
9	B	73	A
9	B	88	C
9	B	89	U
9	B	108	A
9	B	109	A
9	B	120	U
34	a	6	G
34	a	7	A
34	a	9	G
34	a	31	G
34	a	32	A
34	a	39	G
34	a	47	C
34	a	48	C
34	a	50	A
34	a	51	A
34	a	71	A
34	a	74	A
34	a	78	A
34	a	79	G
34	a	81	A
34	a	82	G
34	a	83	C
34	a	84	U
34	a	85	U

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Mol	Chain	Res	Type
34	a	87	C
34	a	88	U
34	a	89	U
34	a	90	C
34	a	94	G
34	a	95	C
34	a	121	U
34	a	129	A
34	a	130	A
34	a	141	G
34	a	144	G
34	a	148	G
34	a	150	U
34	a	157	U
34	a	164	G
34	a	171	A
34	a	173	U
34	a	177	G
34	a	183	C
34	a	184	G
34	a	197	A
34	a	198	G
34	a	207	C
34	a	208	U
34	a	209	U
34	a	210	C
34	a	211	G
34	a	226	G
34	a	240	G
34	a	245	U
34	a	246	A
34	a	247	G
34	a	251	G
34	a	266	G
34	a	267	C
34	a	279	A
34	a	280	C
34	a	289	G
34	a	293	G
34	a	299	G
34	a	306	A
34	a	321	A

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Mol	Chain	Res	Type
34	a	328	C
34	a	329	A
34	a	344	A
34	a	351	G
34	a	352	C
34	a	354	G
34	a	355	C
34	a	367	U
34	a	372	C
34	a	373	A
34	a	375	U
34	a	406	G
34	a	411	A
34	a	413	G
34	a	414	A
34	a	421	U
34	a	429	U
34	a	461	A
34	a	462	G
34	a	465	A
34	a	466	A
34	a	467	U
34	a	468	A
34	a	469	C
34	a	470	C
34	a	479	U
34	a	484	G
34	a	486	U
34	a	495	A
34	a	496	A
34	a	497	G
34	a	499	A
34	a	509	A
34	a	510	A
34	a	511	C
34	a	512	U
34	a	516	PSU
34	a	518	C
34	a	521	G
34	a	532	A
34	a	547	A
34	a	559	A

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Mol	Chain	Res	Type
34	a	562	U
34	a	564	C
34	a	568	G
34	a	570	G
34	a	572	A
34	a	573	A
34	a	576	C
34	a	577	G
34	a	596	A
34	a	633	G
34	a	650	G
34	a	653	U
34	a	665	A
34	a	688	G
34	a	703	G
34	a	704	A
34	a	721	G
34	a	724	G
34	a	733	G
34	a	734	G
34	a	755	G
34	a	777	A
34	a	781	A
34	a	792	A
34	a	794	A
34	a	799	G
34	a	815	A
34	a	817	C
34	a	819	A
34	a	841	C
34	a	842	U
34	a	843	U
34	a	844	G
34	a	845	A
34	a	846	G
34	a	872	A
34	a	876	C
34	a	884	U
34	a	885	G
34	a	902	G
34	a	914	A
34	a	926	G

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Mol	Chain	Res	Type
34	a	934	C
34	a	935	A
34	a	942	G
34	a	958	A
34	a	960	U
34	a	966	2MG
34	a	968	A
34	a	969	A
34	a	971	G
34	a	975	A
34	a	976	G
34	a	977	A
34	a	989	U
34	a	992	U
34	a	993	G
34	a	1004	A
34	a	1006	G
34	a	1022	A
34	a	1023	U
34	a	1026	G
34	a	1027	C
34	a	1031	C
34	a	1032	G
34	a	1033	G
34	a	1038	C
34	a	1041	G
34	a	1042	A
34	a	1045	C
34	a	1065	U
34	a	1070	U
34	a	1085	U
34	a	1086	U
34	a	1089	G
34	a	1094	G
34	a	1095	U
34	a	1101	A
34	a	1108	G
34	a	1124	G
34	a	1130	A
34	a	1133	G
34	a	1134	G
34	a	1136	C

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Mol	Chain	Res	Type
34	a	1137	C
34	a	1139	G
34	a	1140	C
34	a	1159	U
34	a	1167	A
34	a	1168	U
34	a	1169	A
34	a	1171	A
34	a	1174	G
34	a	1182	G
34	a	1183	U
34	a	1184	G
34	a	1196	A
34	a	1197	A
34	a	1212	U
34	a	1213	A
34	a	1214	C
34	a	1227	A
34	a	1238	A
34	a	1239	A
34	a	1250	A
34	a	1258	G
34	a	1260	G
34	a	1261	A
34	a	1275	A
34	a	1280	A
34	a	1287	A
34	a	1299	A
34	a	1300	G
34	a	1301	U
34	a	1302	C
34	a	1305	G
34	a	1317	C
34	a	1320	C
34	a	1331	G
34	a	1332	A
34	a	1338	G
34	a	1346	A
34	a	1347	G
34	a	1348	U
34	a	1353	G
34	a	1363	A

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Mol	Chain	Res	Type
34	a	1368	A
34	a	1370	G
34	a	1379	G
34	a	1381	U
34	a	1399	C
34	a	1400	C
34	a	1419	G
34	a	1441	A
34	a	1446	A
34	a	1451	U
34	a	1493	A
34	a	1494	G
34	a	1497	G
34	a	1503	A
34	a	1506	U
34	a	1517	G
34	a	1519	MA6
34	a	1520	C
34	a	1529	G
34	a	1530	G
34	a	1535	C
34	a	1536	C
34	a	1538	C
34	a	1540	U
56	w	16	U
56	w	17	C
56	w	18	G
56	w	19	G
56	w	20	U
56	w	21	A
56	w	37	MIA
56	w	46	G7M
56	w	47	U
56	w	49	C
56	w	76	A
57	x	19	A

All (38) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	102	U
8	A	141	G

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Mol	Chain	Res	Type
8	A	242	G
8	A	555	G
8	A	704	G
8	A	746	PSU
8	A	752	A
8	A	784	G
8	A	886	A
8	A	1003	G
8	A	1081	U
8	A	1085	A
8	A	1090	A
8	A	1091	G
8	A	1173	U
8	A	1182	G
8	A	1300	G
8	A	1331	G
8	A	1399	C
8	A	1490	A
8	A	1715	G
8	A	1730	C
8	A	1847	G
8	A	2192	U
8	A	2287	A
8	A	2308	G
8	A	2319	G
8	A	2324	U
8	A	2405	G
8	A	2406	A
8	A	2468	A
8	A	2655	G
8	A	2728	U
8	A	2808	G
8	A	2820	A
9	B	44	G
9	B	52	A
9	B	66	A

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

41 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
8	2MA	A	2503	8,59	22,25,26	3.77	8 (36%)	33,37,40	2.14	10 (30%)
8	OMC	A	2498	8,59	19,22,23	2.82	8 (42%)	26,31,34	0.86	0
8	PSU	A	955	8	18,21,22	1.07	1 (5%)	22,30,33	1.89	4 (18%)
34	5MC	a	967	34	18,22,23	3.43	7 (38%)	26,32,35	1.00	2 (7%)
8	6MZ	A	1618	8	22,25,26	2.31	7 (31%)	30,36,39	2.42	10 (33%)
34	UR3	a	1498	34	19,22,23	2.70	6 (31%)	26,32,35	1.54	3 (11%)
8	PSU	A	1917	8	18,21,22	1.05	1 (5%)	22,30,33	1.79	4 (18%)
56	4SU	w	8	56	18,21,22	3.67	8 (44%)	26,30,33	2.26	5 (19%)
8	6MZ	A	2030	8	22,25,26	2.30	8 (36%)	30,36,39	2.53	12 (40%)
8	G7M	A	2069	8	23,26,27	3.34	10 (43%)	35,39,42	1.64	6 (17%)
8	PSU	A	2580	8	18,21,22	1.13	3 (16%)	22,30,33	1.97	6 (27%)
56	MIA	w	37	56	28,31,32	2.59	7 (25%)	40,44,47	2.86	16 (40%)
8	3TD	A	1915	8	18,22,23	4.46	7 (38%)	22,32,35	1.83	4 (18%)
8	OMG	A	2251	56,8,59	23,26,27	2.33	8 (34%)	33,38,41	2.62	10 (30%)
34	2MG	a	1516	34	23,26,27	2.70	9 (39%)	32,38,41	2.28	12 (37%)
8	5MC	A	1962	8	18,22,23	3.37	7 (38%)	26,32,35	1.08	2 (7%)
8	PSU	A	2504	8	18,21,22	1.09	1 (5%)	22,30,33	1.76	4 (18%)
34	G7M	a	527	34	23,26,27	3.39	10 (43%)	35,39,42	1.61	6 (17%)
8	2MG	A	2445	8	23,26,27	2.65	8 (34%)	32,38,41	2.23	10 (31%)
56	PSU	w	55	56	18,21,22	1.02	1 (5%)	22,30,33	2.09	5 (22%)
34	PSU	a	516	34,59	18,21,22	0.96	1 (5%)	22,30,33	1.73	5 (22%)
8	5MU	A	1939	8	19,22,23	4.69	7 (36%)	28,32,35	3.78	9 (32%)
56	PSU	w	39	56	18,21,22	1.04	1 (5%)	22,30,33	1.75	2 (9%)
34	2MG	a	966	34	23,26,27	2.71	7 (30%)	32,38,41	2.31	8 (25%)
34	MA6	a	1518	34	23,26,27	1.61	2 (8%)	34,38,41	3.15	11 (32%)
8	5MC	A	747	8	18,22,23	3.35	7 (38%)	26,32,35	1.24	2 (7%)
8	PSU	A	2457	8	18,21,22	1.08	1 (5%)	22,30,33	2.02	6 (27%)
34	2MG	a	1207	34	23,26,27	2.71	9 (39%)	32,38,41	2.14	11 (34%)
34	MA6	a	1519	34	23,26,27	1.59	2 (8%)	34,38,41	3.23	11 (32%)
8	PSU	A	746	8,59	18,21,22	1.04	1 (5%)	22,30,33	1.76	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	PSU	A	1911	8	18,21,22	1.05	1 (5%)	22,30,33	1.90	5 (22%)
8	PSU	A	2604	8	18,21,22	1.04	1 (5%)	22,30,33	1.98	5 (22%)
34	4OC	a	1402	34	20,23,24	3.06	8 (40%)	26,32,35	0.94	1 (3%)
8	1MG	A	745	8	22,26,27	2.57	7 (31%)	33,39,42	1.63	6 (18%)
34	5MC	a	1407	34	18,22,23	3.35	7 (38%)	26,32,35	1.07	2 (7%)
56	5MU	w	54	56	19,22,23	4.76	7 (36%)	28,32,35	3.74	9 (32%)
8	OMU	A	2552	8,59	19,22,23	2.88	7 (36%)	26,31,34	1.97	6 (23%)
8	2MG	A	1835	8	23,26,27	2.67	8 (34%)	32,38,41	2.23	9 (28%)
56	PSU	w	32	56	18,21,22	1.07	1 (5%)	22,30,33	1.71	3 (13%)
56	G7M	w	46	56	23,26,27	2.26	7 (30%)	35,39,42	3.16	10 (28%)
8	PSU	A	2605	8	18,21,22	1.04	1 (5%)	22,30,33	1.88	4 (18%)

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
8	2MA	A	2503	8,59	-	2/7/25/26	0/3/3/3
8	OMC	A	2498	8,59	-	0/9/27/28	0/2/2/2
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
34	5MC	a	967	34	-	0/7/25/26	0/2/2/2
8	6MZ	A	1618	8	-	0/9/27/28	0/3/3/3
34	UR3	a	1498	34	-	2/7/25/26	0/2/2/2
8	PSU	A	1917	8	-	0/7/25/26	0/2/2/2
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
8	6MZ	A	2030	8	-	2/9/27/28	0/3/3/3
8	G7M	A	2069	8	-	1/7/25/26	0/3/3/3
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2
56	MIA	w	37	56	-	8/15/33/34	0/3/3/3
8	3TD	A	1915	8	-	3/7/25/26	0/2/2/2
8	OMG	A	2251	56,8,59	-	1/9/27/28	0/3/3/3
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
8	5MC	A	1962	8	-	0/7/25/26	0/2/2/2
8	PSU	A	2504	8	-	2/7/25/26	0/2/2/2
34	G7M	a	527	34	-	1/7/25/26	0/3/3/3
8	2MG	A	2445	8	-	2/9/27/28	0/3/3/3
56	PSU	w	55	56	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	PSU	a	516	34,59	-	0/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	2/7/25/26	0/2/2/2
56	PSU	w	39	56	-	3/7/25/26	0/2/2/2
34	2MG	a	966	34	-	2/9/27/28	0/3/3/3
34	MA6	a	1518	34	-	1/11/29/30	0/3/3/3
8	5MC	A	747	8	-	0/7/25/26	0/2/2/2
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
34	2MG	a	1207	34	-	0/9/27/28	0/3/3/3
34	MA6	a	1519	34	-	1/11/29/30	0/3/3/3
8	PSU	A	746	8,59	-	1/7/25/26	0/2/2/2
8	PSU	A	1911	8	-	0/7/25/26	0/2/2/2
8	PSU	A	2604	8	-	0/7/25/26	0/2/2/2
34	4OC	a	1402	34	-	1/9/29/30	0/2/2/2
8	1MG	A	745	8	-	0/7/25/26	0/3/3/3
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
56	5MU	w	54	56	-	0/7/25/26	0/2/2/2
8	OMU	A	2552	8,59	-	2/9/27/28	0/2/2/2
8	2MG	A	1835	8	-	2/9/27/28	0/3/3/3
56	PSU	w	32	56	-	3/7/25/26	0/2/2/2
56	G7M	w	46	56	-	3/7/25/26	0/3/3/3
8	PSU	A	2605	8	-	0/7/25/26	0/2/2/2

All (218) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	C6-C5	14.22	1.51	1.35
8	A	2503	2MA	C4-N3	11.60	1.49	1.34
56	w	54	5MU	C2-N1	10.85	1.55	1.38
56	w	54	5MU	C6-N1	10.23	1.55	1.38
8	A	1939	5MU	C6-N1	10.06	1.55	1.38
8	A	1939	5MU	C2-N1	10.06	1.54	1.38
56	w	54	5MU	C4-C5	9.83	1.61	1.44
34	a	527	G7M	C8-N7	9.79	1.50	1.33
8	A	1939	5MU	C4-C5	9.72	1.60	1.44
8	A	2069	G7M	C8-N7	9.64	1.50	1.33
34	a	967	5MC	C6-C5	8.80	1.49	1.34
34	a	1407	5MC	C6-C5	8.79	1.49	1.34
8	A	1962	5MC	C6-C5	8.70	1.48	1.34
8	A	747	5MC	C6-C5	8.55	1.48	1.34
8	A	1939	5MU	C4-N3	-8.40	1.23	1.38
8	A	1915	3TD	C2-N1	8.32	1.48	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	w	8	4SU	C4-N3	8.17	1.46	1.37
56	w	54	5MU	C4-N3	-8.07	1.23	1.38
8	A	1618	6MZ	C6-N6	7.99	1.42	1.34
8	A	2030	6MZ	C6-N6	7.75	1.42	1.34
56	w	37	MIA	C13-C14	7.43	1.53	1.32
34	a	966	2MG	C2-N3	7.27	1.45	1.31
34	a	1498	UR3	C2-N1	7.19	1.48	1.38
8	A	2503	2MA	C2-N3	7.16	1.46	1.34
8	A	2552	OMU	C2-N1	7.14	1.49	1.38
34	a	1207	2MG	C2-N3	7.05	1.45	1.31
8	A	2445	2MG	C2-N3	6.96	1.45	1.31
34	a	1516	2MG	C2-N3	6.94	1.45	1.31
8	A	1835	2MG	C2-N3	6.90	1.45	1.31
56	w	37	MIA	C2-S10	6.78	1.81	1.75
56	w	8	4SU	C2-N3	6.67	1.49	1.38
56	w	37	MIA	C6-N6	6.61	1.44	1.34
34	a	1402	4OC	C4-N3	6.56	1.44	1.32
56	w	46	G7M	C4-N3	6.32	1.49	1.34
8	A	2552	OMU	C2-N3	6.26	1.49	1.38
34	a	1402	4OC	C6-C5	6.22	1.49	1.35
56	w	8	4SU	C2-N1	6.17	1.48	1.38
34	a	1207	2MG	C4-N3	6.10	1.48	1.34
8	A	1835	2MG	C4-N3	6.08	1.48	1.34
34	a	967	5MC	C4-N3	6.08	1.44	1.34
34	a	966	2MG	C4-N3	6.06	1.48	1.34
8	A	745	1MG	C2-N3	6.06	1.45	1.34
8	A	745	1MG	C4-N3	6.05	1.48	1.34
8	A	2503	2MA	C6-N1	5.96	1.43	1.35
8	A	747	5MC	C4-N3	5.95	1.44	1.34
8	A	2552	OMU	C6-C5	5.93	1.48	1.35
34	a	1516	2MG	C4-N3	5.92	1.48	1.34
34	a	967	5MC	C2-N3	5.89	1.48	1.36
8	A	2445	2MG	C4-N3	5.85	1.48	1.34
8	A	2251	OMG	C4-N3	5.83	1.48	1.34
8	A	1962	5MC	C4-N3	5.83	1.44	1.34
8	A	745	1MG	C2-N2	5.77	1.44	1.34
34	a	1498	UR3	C6-C5	5.76	1.48	1.35
8	A	2503	2MA	C2-N1	5.74	1.44	1.34
8	A	1962	5MC	C2-N3	5.74	1.48	1.36
8	A	747	5MC	C2-N3	5.72	1.48	1.36
34	a	1407	5MC	C2-N3	5.64	1.47	1.36
56	w	8	4SU	C6-C5	5.64	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	2498	OMC	C6-C5	5.62	1.48	1.35
34	a	1402	4OC	C2-N3	5.57	1.47	1.36
34	a	1407	5MC	C4-N3	5.52	1.43	1.34
8	A	2498	OMC	C2-N3	5.51	1.47	1.36
8	A	1939	5MU	C6-C5	5.49	1.43	1.34
56	w	54	5MU	C6-C5	5.42	1.43	1.34
8	A	1915	3TD	C2-N3	5.41	1.50	1.38
34	a	527	G7M	C8-N9	5.39	1.50	1.35
8	A	2069	G7M	C8-N9	5.33	1.50	1.35
34	a	527	G7M	C2-N3	5.29	1.45	1.33
34	a	527	G7M	C4-N3	5.18	1.46	1.34
8	A	1915	3TD	C6-N1	5.16	1.44	1.36
8	A	2069	G7M	C2-N3	5.14	1.45	1.33
8	A	2069	G7M	C4-N3	5.14	1.46	1.34
34	a	1207	2MG	C2-N2	5.09	1.44	1.33
34	a	1516	2MG	C2-N2	5.01	1.44	1.33
8	A	2445	2MG	C2-N2	4.96	1.44	1.33
8	A	1835	2MG	C2-N2	4.94	1.44	1.33
8	A	2498	OMC	C4-N4	4.88	1.45	1.33
34	a	966	2MG	C2-N2	4.85	1.44	1.33
56	w	8	4SU	C4-S4	-4.82	1.59	1.68
34	a	1402	4OC	C4-N4	4.81	1.45	1.35
8	A	2498	OMC	C4-N3	4.75	1.44	1.34
8	A	2503	2MA	C5-C6	4.69	1.54	1.41
34	a	1498	UR3	C2-N3	4.68	1.48	1.39
34	a	1518	MA6	C6-N6	4.67	1.50	1.36
8	A	2251	OMG	C2-N3	4.65	1.44	1.33
34	a	1519	MA6	C6-N6	4.63	1.50	1.36
8	A	2251	OMG	C2-N2	4.48	1.44	1.34
34	a	527	G7M	C2-N2	4.42	1.44	1.34
56	w	8	4SU	C5-C4	4.40	1.48	1.42
34	a	967	5MC	C6-N1	4.37	1.45	1.38
34	a	1516	2MG	C2-N1	4.31	1.43	1.36
34	a	966	2MG	C2-N1	4.31	1.43	1.36
34	a	1207	2MG	C2-N1	4.30	1.43	1.36
8	A	2069	G7M	C2-N2	4.30	1.44	1.34
34	a	967	5MC	C4-N4	4.29	1.45	1.34
8	A	2069	G7M	C5-N7	4.23	1.44	1.39
56	w	46	G7M	C5-N7	-4.23	1.34	1.39
8	A	747	5MC	C4-N4	4.21	1.45	1.34
8	A	1962	5MC	C6-N1	4.17	1.45	1.38
8	A	2498	OMC	C2-N1	4.16	1.49	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1962	5MC	C4-N4	4.14	1.44	1.34
34	a	1407	5MC	C6-N1	4.13	1.45	1.38
34	a	1407	5MC	C4-N4	4.12	1.44	1.34
34	a	527	G7M	C5-N7	4.12	1.44	1.39
56	w	46	G7M	C2-N2	4.10	1.43	1.34
8	A	747	5MC	C6-N1	4.08	1.45	1.38
8	A	1835	2MG	C2-N1	4.03	1.43	1.36
34	a	1407	5MC	C2-N1	4.00	1.48	1.40
56	w	46	G7M	C2-N3	3.93	1.42	1.33
8	A	1962	5MC	C2-N1	3.93	1.48	1.40
34	a	1402	4OC	C5-C4	3.85	1.49	1.40
8	A	747	5MC	C2-N1	3.84	1.48	1.40
34	a	967	5MC	C2-N1	3.82	1.48	1.40
34	a	1518	MA6	C5-C4	-3.76	1.32	1.39
8	A	2445	2MG	C2-N1	3.74	1.42	1.36
34	a	1402	4OC	C2-N1	3.67	1.47	1.40
34	a	1519	MA6	C5-C4	-3.61	1.32	1.39
56	w	37	MIA	C5-C4	-3.58	1.32	1.39
8	A	2030	6MZ	C5-N7	-3.57	1.32	1.39
8	A	1618	6MZ	C5-N7	-3.56	1.32	1.39
8	A	2445	2MG	C5-N7	-3.45	1.32	1.39
34	a	966	2MG	C5-N7	-3.44	1.32	1.39
34	a	527	G7M	C2-N1	3.40	1.46	1.37
34	a	1402	4OC	O2-C2	-3.37	1.17	1.23
8	A	745	1MG	C5-N7	-3.34	1.32	1.39
8	A	1835	2MG	C5-N7	-3.33	1.32	1.39
8	A	2069	G7M	C2-N1	3.30	1.45	1.37
8	A	1915	3TD	O2-C2	-3.29	1.17	1.23
34	a	1516	2MG	C5-N7	-3.29	1.32	1.39
8	A	2251	OMG	C5-N7	-3.25	1.32	1.39
8	A	2552	OMU	C4-N3	3.24	1.44	1.38
34	a	1207	2MG	C5-N7	-3.24	1.32	1.39
8	A	2069	G7M	O6-C6	-3.13	1.17	1.23
8	A	2030	6MZ	C5-C4	-3.11	1.33	1.39
8	A	1618	6MZ	C5-C4	-3.07	1.33	1.39
8	A	747	5MC	O2-C2	-3.06	1.18	1.23
8	A	2498	OMC	C6-N1	3.05	1.45	1.38
34	a	1402	4OC	C6-N1	3.04	1.45	1.38
56	w	55	PSU	C6-C5	3.04	1.38	1.35
8	A	2251	OMG	O6-C6	-3.00	1.17	1.23
34	a	1407	5MC	O2-C2	-2.99	1.18	1.23
8	A	2445	2MG	O6-C6	-2.99	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1835	2MG	O6-C6	-2.98	1.17	1.23
56	w	8	4SU	C6-N1	2.98	1.45	1.38
34	a	527	G7M	O6-C6	-2.97	1.17	1.23
8	A	1962	5MC	O2-C2	-2.97	1.18	1.23
34	a	527	G7M	C5-C6	2.96	1.51	1.43
8	A	1939	5MU	O4-C4	-2.96	1.18	1.23
8	A	2504	PSU	C6-C5	2.95	1.38	1.35
8	A	2503	2MA	C5-N7	-2.95	1.33	1.39
8	A	1917	PSU	C6-C5	2.94	1.38	1.35
8	A	1939	5MU	O2-C2	-2.93	1.17	1.23
8	A	2503	2MA	C6-N6	-2.88	1.26	1.34
56	w	54	5MU	O4-C4	-2.85	1.18	1.23
8	A	2498	OMC	O2-C2	-2.85	1.18	1.23
8	A	2069	G7M	C5-C6	2.85	1.51	1.43
34	a	1498	UR3	C6-N1	2.84	1.44	1.38
8	A	1911	PSU	C6-C5	2.83	1.38	1.35
8	A	2030	6MZ	C6-N1	-2.83	1.30	1.35
34	a	1516	2MG	O6-C6	-2.82	1.18	1.23
8	A	2604	PSU	C6-C5	2.81	1.38	1.35
56	w	39	PSU	C6-C5	2.80	1.38	1.35
8	A	2605	PSU	C6-C5	2.79	1.38	1.35
8	A	955	PSU	C6-C5	2.79	1.38	1.35
34	a	527	G7M	C6-N1	2.78	1.44	1.38
34	a	1207	2MG	O6-C6	-2.78	1.18	1.23
34	a	967	5MC	O2-C2	-2.77	1.18	1.23
56	w	32	PSU	C6-C5	2.77	1.38	1.35
34	a	966	2MG	O6-C6	-2.76	1.18	1.23
8	A	1618	6MZ	C6-N1	-2.72	1.30	1.35
56	w	37	MIA	C5-N7	-2.72	1.33	1.39
8	A	745	1MG	C5-C6	2.70	1.52	1.45
8	A	2069	G7M	C6-N1	2.69	1.43	1.38
34	a	1498	UR3	O4-C4	-2.68	1.17	1.23
56	w	46	G7M	C5-C6	2.67	1.50	1.43
56	w	46	G7M	C6-N1	2.66	1.43	1.38
8	A	746	PSU	C6-C5	2.66	1.38	1.35
8	A	2580	PSU	C6-C5	2.66	1.38	1.35
56	w	8	4SU	O2-C2	-2.66	1.18	1.23
34	a	1498	UR3	O2-C2	-2.64	1.17	1.22
8	A	2457	PSU	C6-C5	2.64	1.38	1.35
8	A	2251	OMG	C4-N9	-2.64	1.31	1.38
8	A	1915	3TD	C4-N3	2.62	1.46	1.40
34	a	516	PSU	C6-C5	2.59	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	O4-C4	-2.56	1.17	1.23
8	A	2030	6MZ	C9-N6	-2.56	1.40	1.45
8	A	2030	6MZ	C8-N9	-2.53	1.33	1.37
8	A	1618	6MZ	C9-N6	-2.45	1.40	1.45
8	A	2251	OMG	C2-N1	2.44	1.43	1.37
8	A	745	1MG	O6-C6	-2.43	1.18	1.23
8	A	2552	OMU	C6-N1	2.41	1.43	1.38
56	w	54	5MU	O2-C2	-2.40	1.18	1.23
34	a	1516	2MG	C4-N9	-2.40	1.31	1.38
8	A	1618	6MZ	C8-N9	-2.37	1.33	1.37
8	A	2251	OMG	C5-C6	2.35	1.53	1.44
8	A	2445	2MG	C4-N9	-2.34	1.32	1.38
34	a	1207	2MG	C5-C6	2.33	1.53	1.44
56	w	46	G7M	C2-N1	2.32	1.43	1.37
34	a	966	2MG	C5-C6	2.32	1.53	1.44
8	A	745	1MG	C4-N9	-2.30	1.32	1.38
8	A	1618	6MZ	C5-C6	-2.28	1.36	1.41
8	A	2445	2MG	C5-C6	2.28	1.52	1.44
8	A	2580	PSU	O4'-C1'	-2.27	1.40	1.43
34	a	1516	2MG	C5-C6	2.26	1.52	1.44
8	A	1835	2MG	C5-C6	2.25	1.52	1.44
56	w	37	MIA	C8-N9	-2.24	1.33	1.37
34	a	1207	2MG	C4-N9	-2.22	1.32	1.38
8	A	2552	OMU	O4-C4	-2.20	1.20	1.24
56	w	37	MIA	C4-N9	-2.20	1.32	1.37
8	A	1835	2MG	C4-N9	-2.19	1.32	1.38
8	A	2030	6MZ	C5-C6	-2.17	1.36	1.41
8	A	2552	OMU	C5-C4	2.16	1.48	1.43
8	A	2030	6MZ	C4-N9	-2.15	1.32	1.37
8	A	2498	OMC	C5-C4	2.13	1.47	1.42
34	a	1516	2MG	C6-N1	2.05	1.42	1.38
8	A	2503	2MA	C8-N7	2.05	1.35	1.31
8	A	2580	PSU	C4-C5	-2.01	1.38	1.44
34	a	1207	2MG	C6-N1	2.01	1.42	1.38

All (259) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1519	MA6	N1-C6-N6	-12.91	102.97	117.08
56	w	54	5MU	C5-C4-N3	12.67	126.12	115.31
8	A	1939	5MU	C5-C4-N3	12.46	125.94	115.31
34	a	1518	MA6	N1-C6-N6	-12.17	103.78	117.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1939	5MU	C5-C6-N1	-10.78	112.25	123.34
56	w	54	5MU	C5-C6-N1	-9.99	113.06	123.34
56	w	46	G7M	CN7-N7-C5	9.13	138.12	126.77
8	A	2251	OMG	C1'-N9-C8	-8.40	102.79	126.70
56	w	37	MIA	C11-S10-C2	8.25	108.43	102.27
56	w	46	G7M	C1'-N9-C4	8.18	150.80	126.50
56	w	37	MIA	C12-C13-C14	-7.92	111.72	127.14
56	w	8	4SU	C4-N3-C2	-7.89	119.68	127.34
8	A	2251	OMG	C1'-N9-C4	7.57	148.99	126.50
56	w	46	G7M	C1'-N9-C8	-7.53	101.32	126.74
56	w	46	G7M	CN7-N7-C8	-7.08	113.92	124.84
8	A	1835	2MG	C2-N3-C4	6.71	120.36	112.04
34	a	1519	MA6	C5-C6-N6	6.71	136.99	125.30
34	a	1516	2MG	C2-N3-C4	6.61	120.23	112.04
8	A	2445	2MG	C2-N3-C4	6.56	120.17	112.04
34	a	966	2MG	C2-N3-C4	6.55	120.16	112.04
34	a	1518	MA6	C5-C6-N6	6.43	136.50	125.30
34	a	1207	2MG	C2-N3-C4	6.36	119.92	112.04
8	A	2030	6MZ	C9-N6-C6	-6.22	117.51	122.87
8	A	1915	3TD	N1-C2-N3	6.02	120.89	116.14
8	A	2503	2MA	C5-C4-N3	-5.95	120.50	127.19
8	A	2552	OMU	C4-N3-C2	-5.82	118.90	126.58
34	a	966	2MG	C5-C4-N3	-5.71	119.19	128.46
56	w	37	MIA	C5-C4-N3	-5.67	120.81	127.19
8	A	1618	6MZ	C5-C4-N3	-5.63	119.40	126.75
34	a	1518	MA6	N1-C2-N3	-5.62	119.81	128.60
34	a	1519	MA6	N1-C2-N3	-5.54	119.94	128.60
8	A	1618	6MZ	N1-C2-N3	-5.48	120.02	128.60
8	A	2030	6MZ	N1-C2-N3	-5.48	120.03	128.60
56	w	54	5MU	O4-C4-C5	-5.47	118.57	124.90
8	A	2445	2MG	C5-C4-N3	-5.44	119.64	128.46
8	A	1835	2MG	C5-C4-N3	-5.41	119.68	128.46
8	A	2457	PSU	N1-C2-N3	5.34	121.18	115.13
34	a	966	2MG	C2-N1-C6	-5.25	118.44	124.48
56	w	8	4SU	C5-C4-N3	5.23	119.55	114.69
8	A	1939	5MU	C4-N3-C2	-5.17	120.65	127.35
8	A	2503	2MA	N9-C8-N7	-5.17	106.84	113.91
8	A	2604	PSU	N1-C2-N3	5.17	120.98	115.13
56	w	55	PSU	N1-C2-N3	5.08	120.89	115.13
8	A	2604	PSU	C4-N3-C2	-5.04	119.08	126.34
56	w	54	5MU	C4-N3-C2	-5.03	120.84	127.35
8	A	2030	6MZ	C5-C4-N3	-5.01	120.21	126.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2580	PSU	N1-C2-N3	4.98	120.77	115.13
8	A	2457	PSU	C4-N3-C2	-4.98	119.16	126.34
8	A	2605	PSU	C4-N3-C2	-4.97	119.18	126.34
34	a	1516	2MG	C5-C4-N3	-4.95	120.44	128.46
8	A	955	PSU	N1-C2-N3	4.94	120.73	115.13
8	A	1911	PSU	N1-C2-N3	4.94	120.73	115.13
34	a	1207	2MG	C5-C4-N3	-4.92	120.47	128.46
8	A	955	PSU	C4-N3-C2	-4.90	119.28	126.34
56	w	32	PSU	C4-N3-C2	-4.90	119.28	126.34
34	a	1518	MA6	N9-C8-N7	-4.89	107.22	113.91
56	w	37	MIA	N9-C8-N7	-4.86	107.27	113.91
8	A	1911	PSU	C4-N3-C2	-4.85	119.36	126.34
56	w	39	PSU	C4-N3-C2	-4.84	119.37	126.34
8	A	745	1MG	C5-C4-N3	-4.84	120.61	128.46
8	A	2605	PSU	N1-C2-N3	4.83	120.60	115.13
34	a	1516	2MG	C2-N1-C6	-4.81	118.94	124.48
8	A	2580	PSU	C4-N3-C2	-4.80	119.42	126.34
8	A	1835	2MG	C2-N1-C6	-4.77	118.99	124.48
8	A	1917	PSU	C4-N3-C2	-4.77	119.47	126.34
8	A	746	PSU	C4-N3-C2	-4.75	119.49	126.34
34	a	1519	MA6	N9-C8-N7	-4.75	107.42	113.91
8	A	2445	2MG	C2-N1-C6	-4.73	119.04	124.48
8	A	2552	OMU	N3-C2-N1	4.67	121.08	114.89
8	A	2504	PSU	C4-N3-C2	-4.66	119.62	126.34
8	A	1939	5MU	O4-C4-C5	-4.66	119.50	124.90
8	A	2504	PSU	N1-C2-N3	4.65	120.40	115.13
8	A	1939	5MU	N3-C2-N1	4.60	121.00	114.89
8	A	1917	PSU	N1-C2-N3	4.57	120.30	115.13
56	w	37	MIA	C15-C14-C13	-4.56	109.46	122.65
34	a	1519	MA6	C5-C4-N3	-4.47	120.91	126.75
56	w	39	PSU	N1-C2-N3	4.46	120.19	115.13
8	A	746	PSU	N1-C2-N3	4.45	120.18	115.13
8	A	2030	6MZ	N9-C8-N7	-4.45	107.83	113.91
34	a	516	PSU	C4-N3-C2	-4.40	120.00	126.34
34	a	1518	MA6	C5-C4-N3	-4.39	121.02	126.75
56	w	55	PSU	O2-C2-N1	-4.39	117.96	122.79
34	a	1207	2MG	C2-N1-C6	-4.37	119.45	124.48
8	A	1618	6MZ	N9-C8-N7	-4.36	107.95	113.91
34	a	516	PSU	N1-C2-N3	4.35	120.06	115.13
8	A	2069	G7M	C2-N3-C4	4.34	120.03	112.30
56	w	54	5MU	N3-C2-N1	4.26	120.55	114.89
56	w	54	5MU	C5M-C5-C4	4.25	123.45	118.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	46	G7M	C2-N3-C4	4.25	119.88	112.30
34	a	527	G7M	C2-N3-C4	4.25	119.86	112.30
34	a	1498	UR3	C4-N3-C2	-4.24	120.57	124.56
56	w	55	PSU	C4-N3-C2	-4.24	120.23	126.34
8	A	747	5MC	C5-C6-N1	-4.20	119.02	123.34
8	A	2251	OMG	C2-N3-C4	4.13	119.66	112.30
56	w	54	5MU	C5M-C5-C6	-4.12	117.34	122.85
34	a	1498	UR3	C1'-N1-C2	4.12	123.94	116.99
56	w	32	PSU	N1-C2-N3	4.11	119.79	115.13
56	w	37	MIA	S10-C2-N1	4.10	130.18	116.01
56	w	46	G7M	C5-C4-N3	-4.08	120.33	128.15
8	A	2251	OMG	C5-C4-N3	-4.06	121.88	128.46
8	A	1939	5MU	C5M-C5-C6	-4.05	117.45	122.85
8	A	1618	6MZ	C4-C5-C6	4.04	119.94	116.81
8	A	2069	G7M	C5-C6-N1	4.03	120.20	111.79
56	w	8	4SU	N3-C2-N1	3.94	120.12	114.89
34	a	527	G7M	C5-C6-N1	3.89	119.92	111.79
56	w	46	G7M	C5-C6-N1	3.85	119.84	111.79
8	A	1618	6MZ	C9-N6-C6	-3.85	119.56	122.87
8	A	1939	5MU	C5M-C5-C4	3.84	123.00	118.77
56	w	55	PSU	C6-C5-C4	3.80	120.86	118.20
56	w	37	MIA	N3-C2-N1	-3.77	120.04	126.95
34	a	966	2MG	CM2-N2-C2	-3.77	115.53	123.86
56	w	37	MIA	C16-C14-C13	-3.74	111.83	122.65
34	a	527	G7M	C5-C4-N3	-3.74	120.97	128.15
56	w	8	4SU	C5-C4-S4	-3.73	119.66	124.47
8	A	1915	3TD	C4-N3-C2	-3.72	120.57	124.61
8	A	2069	G7M	C5-C4-N3	-3.70	121.05	128.15
8	A	1618	6MZ	N3-C4-N9	3.67	133.12	127.08
8	A	2503	2MA	N3-C4-N9	3.66	132.07	126.99
34	a	1518	MA6	C2-N1-C6	3.66	120.40	111.75
8	A	2503	2MA	C5-N7-C8	3.64	108.68	103.51
8	A	1618	6MZ	C2-N3-C4	3.64	120.34	111.75
34	a	1519	MA6	C2-N1-C6	3.62	120.30	111.75
8	A	2552	OMU	C5-C4-N3	3.61	120.24	114.84
56	w	46	G7M	O6-C6-C5	-3.56	120.03	128.06
34	a	967	5MC	C5-C6-N1	-3.52	119.71	123.34
34	a	966	2MG	N9-C4-N3	3.51	132.99	125.94
8	A	2030	6MZ	C2-N3-C4	3.48	119.97	111.75
8	A	745	1MG	C2-N3-C4	3.47	119.78	111.98
34	a	1519	MA6	C2-N3-C4	3.37	119.70	111.75
34	a	527	G7M	O6-C6-C5	-3.37	120.47	128.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2069	G7M	O6-C6-C5	-3.36	120.49	128.06
34	a	1518	MA6	C2-N3-C4	3.30	119.54	111.75
56	w	37	MIA	C5-N7-C8	3.28	108.17	103.51
8	A	2503	2MA	C4-N9-C8	3.27	109.27	105.73
8	A	1962	5MC	C5-C6-N1	-3.27	119.98	123.34
34	a	1518	MA6	C4-C5-C6	3.25	119.51	115.88
8	A	1835	2MG	N9-C4-N3	3.24	132.44	125.94
34	a	1518	MA6	C4-N9-C8	3.24	109.23	105.73
34	a	1407	5MC	C5-C6-N1	-3.20	120.05	123.34
8	A	2030	6MZ	C5-N7-C8	3.18	108.03	103.51
8	A	2503	2MA	N3-C2-N1	-3.18	119.88	125.72
8	A	2030	6MZ	C4-C5-C6	3.17	119.27	116.81
8	A	2445	2MG	N9-C4-N3	3.13	132.23	125.94
8	A	2030	6MZ	C4-N9-C1'	-3.12	119.15	126.59
8	A	1618	6MZ	C5-N7-C8	3.12	107.94	103.51
8	A	2251	OMG	N9-C8-N7	-3.11	107.53	113.39
56	w	46	G7M	C2-N1-C6	-3.11	119.43	125.10
34	a	1516	2MG	N9-C8-N7	-3.10	107.56	113.39
8	A	1939	5MU	O2-C2-N1	-3.07	118.70	122.79
34	a	1498	UR3	C6-N1-C2	-3.07	119.04	121.79
8	A	745	1MG	N9-C8-N7	-3.05	107.64	113.39
34	a	1519	MA6	C5-N7-C8	3.05	107.84	103.51
34	a	1518	MA6	C5-N7-C8	3.01	107.79	103.51
8	A	745	1MG	N9-C4-N3	3.01	131.98	125.94
8	A	746	PSU	O2-C2-N1	-2.99	119.50	122.79
34	a	1516	2MG	C5-C6-N1	2.94	120.65	113.19
56	w	37	MIA	C4-C5-C6	2.94	119.08	116.81
8	A	2457	PSU	O2-C2-N1	-2.92	119.57	122.79
8	A	2030	6MZ	N3-C4-N9	2.92	131.90	127.08
8	A	2445	2MG	N9-C8-N7	-2.92	107.90	113.39
56	w	55	PSU	C6-N1-C2	-2.91	119.71	122.68
56	w	37	MIA	C2-N3-C4	2.90	119.99	112.35
8	A	1939	5MU	O4-C4-N3	-2.90	114.56	120.12
8	A	1835	2MG	C5-C6-N1	2.89	120.54	113.19
34	a	1519	MA6	C4-C5-C6	2.89	119.11	115.88
34	a	516	PSU	O2-C2-N1	-2.87	119.64	122.79
34	a	966	2MG	C5-C6-N1	2.86	120.46	113.19
34	a	1207	2MG	N9-C8-N7	-2.85	108.02	113.39
34	a	1518	MA6	N3-C4-N9	2.84	131.76	127.08
8	A	2069	G7M	C2-N1-C6	-2.83	119.94	125.10
34	a	1519	MA6	C4-N9-C8	2.82	108.78	105.73
8	A	2552	OMU	C1'-N1-C2	2.82	122.67	117.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2251	OMG	C2-N1-C6	-2.82	119.96	125.10
34	a	1516	2MG	CM2-N2-C2	-2.81	117.64	123.86
8	A	2445	2MG	CM2-N2-C2	-2.81	117.66	123.86
8	A	2445	2MG	C5-C6-N1	2.81	120.32	113.19
8	A	2580	PSU	O2-C2-N1	-2.78	119.73	122.79
34	a	527	G7M	C2-N1-C6	-2.77	120.05	125.10
34	a	1207	2MG	C5-C6-N1	2.76	120.21	113.19
8	A	1835	2MG	N9-C8-N7	-2.74	108.23	113.39
8	A	2251	OMG	C5-C6-N1	2.70	120.03	113.19
34	a	1516	2MG	C1'-N9-C4	-2.69	118.51	126.50
8	A	2604	PSU	O2-C2-N1	-2.69	119.83	122.79
34	a	966	2MG	N9-C8-N7	-2.68	108.34	113.39
8	A	745	1MG	C5-C6-N1	2.67	120.07	114.91
34	a	1516	2MG	O6-C6-C5	-2.66	119.54	126.60
34	a	1207	2MG	N9-C4-N3	2.66	131.27	125.94
8	A	2457	PSU	C6-C5-C4	2.63	120.04	118.20
8	A	1962	5MC	CM5-C5-C6	-2.63	119.34	122.85
56	w	46	G7M	N9-C4-N3	2.61	131.17	125.94
8	A	1911	PSU	O2-C2-N1	-2.60	119.93	122.79
8	A	2503	2MA	C4-N9-C1'	-2.60	120.40	126.59
34	a	1519	MA6	N3-C4-N9	2.59	131.35	127.08
8	A	1835	2MG	O6-C6-C5	-2.59	119.74	126.60
8	A	2580	PSU	C6-C5-C4	2.58	120.00	118.20
8	A	747	5MC	CM5-C5-C6	-2.57	119.41	122.85
34	a	1516	2MG	N9-C4-N3	2.57	131.09	125.94
34	a	966	2MG	O6-C6-C5	-2.56	119.80	126.60
8	A	2552	OMU	O4-C4-C5	-2.56	120.66	125.16
8	A	1835	2MG	CM2-N2-C2	-2.54	118.24	123.86
8	A	2457	PSU	C6-N1-C2	-2.54	120.08	122.68
56	w	37	MIA	C16-C14-C15	-2.54	108.99	114.60
8	A	1618	6MZ	C5-C6-N1	2.53	120.90	118.20
8	A	1915	3TD	C10-N3-C4	2.53	121.56	117.69
56	w	37	MIA	C5-C4-N9	2.52	108.71	105.78
56	w	37	MIA	N3-C4-N9	2.51	130.47	126.99
56	w	54	5MU	O4-C4-N3	-2.51	115.31	120.12
8	A	2030	6MZ	C1'-N9-C8	2.50	132.79	127.14
34	a	516	PSU	C6-N1-C2	-2.50	120.13	122.68
56	w	37	MIA	C4-C5-N7	-2.47	107.61	110.62
8	A	1917	PSU	O2-C2-N1	-2.42	120.13	122.79
8	A	2580	PSU	O4'-C1'-C2'	2.41	108.55	105.14
34	a	1516	2MG	N1-C2-N3	-2.41	120.22	123.95
8	A	2069	G7M	N9-C8-N7	-2.40	106.27	112.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	54	5MU	O2-C2-N1	-2.39	119.61	122.79
34	a	1207	2MG	N1-C2-N3	-2.38	120.28	123.95
8	A	2251	OMG	O6-C6-C5	-2.37	120.31	126.60
34	a	1207	2MG	O6-C6-C5	-2.36	120.34	126.60
8	A	1911	PSU	C6-N1-C2	-2.35	120.28	122.68
34	a	1407	5MC	CM5-C5-C6	-2.34	119.72	122.85
8	A	2503	2MA	C4-C5-N7	-2.34	107.77	110.62
8	A	955	PSU	C6-N1-C2	-2.34	120.29	122.68
8	A	2604	PSU	C6-C5-C4	2.33	119.83	118.20
8	A	955	PSU	O2-C2-N1	-2.32	120.23	122.79
34	a	1207	2MG	C1'-N9-C4	-2.32	119.61	126.50
8	A	2604	PSU	C6-N1-C2	-2.31	120.32	122.68
8	A	2251	OMG	N2-C2-N1	2.31	121.64	116.71
34	a	527	G7M	N9-C8-N7	-2.31	106.50	112.21
56	w	37	MIA	C4-N9-C8	2.31	108.23	105.73
34	a	1516	2MG	C1'-N9-C8	2.30	133.24	126.70
8	A	1835	2MG	N1-C2-N3	-2.28	120.42	123.95
8	A	2503	2MA	N6-C6-N1	2.28	120.26	117.03
8	A	2580	PSU	C6-N1-C2	-2.28	120.36	122.68
34	a	1402	4OC	C6-C5-C4	2.28	119.75	116.96
8	A	2504	PSU	C6-N1-C2	-2.26	120.38	122.68
8	A	2504	PSU	O2-C2-N1	-2.25	120.32	122.79
8	A	2030	6MZ	C5-C6-N1	2.24	120.59	118.20
8	A	2445	2MG	O6-C6-C5	-2.23	120.67	126.60
8	A	2605	PSU	O2-C2-N1	-2.23	120.33	122.79
56	w	32	PSU	C5-C4-N3	2.19	121.54	116.58
8	A	2445	2MG	N1-C2-N3	-2.17	120.59	123.95
34	a	1207	2MG	CM2-N2-C2	-2.16	119.10	123.86
8	A	2030	6MZ	C4-N9-C8	2.15	108.06	105.73
8	A	1911	PSU	C6-C5-C4	2.14	119.70	118.20
34	a	967	5MC	CM5-C5-C6	-2.13	120.00	122.85
8	A	2503	2MA	CM2-C2-N1	2.13	120.48	117.15
34	a	1516	2MG	C8-N7-C5	2.12	108.07	104.24
8	A	1915	3TD	C6-C5-C4	2.12	119.68	118.22
8	A	1618	6MZ	C4-N9-C8	2.11	108.02	105.73
56	w	8	4SU	O2-C2-N1	-2.11	119.98	122.79
8	A	2445	2MG	C8-N7-C5	2.11	108.05	104.24
8	A	2552	OMU	O2-C2-N3	-2.09	117.62	121.50
8	A	2605	PSU	C6-C5-C4	2.05	119.63	118.20
8	A	2251	OMG	C8-N7-C5	2.04	107.94	104.24
8	A	2457	PSU	O4'-C1'-C2'	2.04	108.02	105.14
8	A	1917	PSU	C6-N1-C2	-2.03	120.60	122.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1207	2MG	C1'-N9-C8	2.03	132.46	126.70
8	A	745	1MG	C8-N7-C5	2.01	107.89	104.24
34	a	516	PSU	O4'-C1'-C2'	2.00	107.97	105.14

There are no chirality outliers.

All (45) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1915	3TD	C2'-C1'-C5-C4
8	A	1915	3TD	O4'-C1'-C5-C4
8	A	1915	3TD	O4'-C1'-C5-C6
8	A	1939	5MU	O4'-C4'-C5'-O5'
8	A	2251	OMG	C1'-C2'-O2'-CM2
8	A	2552	OMU	O4'-C1'-N1-C2
8	A	2552	OMU	O4'-C1'-N1-C6
34	a	966	2MG	C3'-C4'-C5'-O5'
34	a	1498	UR3	O4'-C1'-N1-C6
34	a	1498	UR3	O4'-C1'-N1-C2
56	w	32	PSU	O4'-C1'-C5-C4
56	w	32	PSU	C2'-C1'-C5-C6
56	w	32	PSU	O4'-C1'-C5-C6
56	w	37	MIA	O4'-C4'-C5'-O5'
56	w	37	MIA	C3'-C4'-C5'-O5'
56	w	37	MIA	N1-C2-S10-C11
56	w	37	MIA	N3-C2-S10-C11
56	w	37	MIA	C12-C13-C14-C15
56	w	37	MIA	C12-C13-C14-C16
56	w	39	PSU	O4'-C1'-C5-C4
56	w	39	PSU	C2'-C1'-C5-C6
56	w	39	PSU	O4'-C1'-C5-C6
8	A	2030	6MZ	O4'-C4'-C5'-O5'
8	A	2030	6MZ	C3'-C4'-C5'-O5'
8	A	2503	2MA	O4'-C4'-C5'-O5'
8	A	2503	2MA	C3'-C4'-C5'-O5'
34	a	966	2MG	O4'-C4'-C5'-O5'
8	A	1939	5MU	C3'-C4'-C5'-O5'
8	A	2445	2MG	C3'-C4'-C5'-O5'
8	A	2504	PSU	O4'-C4'-C5'-O5'
8	A	2504	PSU	C3'-C4'-C5'-O5'
56	w	46	G7M	C3'-C4'-C5'-O5'
56	w	37	MIA	C5-C6-N6-C12
56	w	37	MIA	N1-C6-N6-C12

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Mol	Chain	Res	Type	Atoms
8	A	2445	2MG	O4'-C4'-C5'-O5'
56	w	46	G7M	C4'-C5'-O5'-P
34	a	1402	4OC	O4'-C4'-C5'-O5'
34	a	527	G7M	C4'-C5'-O5'-P
8	A	1835	2MG	O4'-C4'-C5'-O5'
8	A	1835	2MG	C3'-C4'-C5'-O5'
56	w	46	G7M	O4'-C4'-C5'-O5'
8	A	746	PSU	O4'-C1'-C5-C6
8	A	2069	G7M	O4'-C4'-C5'-O5'
34	a	1518	MA6	C3'-C4'-C5'-O5'
34	a	1519	MA6	C4'-C5'-O5'-P

There are no ring outliers.

21 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	2498	OMC	1	0
8	A	955	PSU	1	0
34	a	967	5MC	1	0
34	a	1498	UR3	2	0
8	A	2030	6MZ	3	0
56	w	37	MIA	1	0
8	A	1915	3TD	4	0
8	A	2251	OMG	1	0
8	A	1962	5MC	1	0
34	a	527	G7M	1	0
56	w	55	PSU	2	0
34	a	516	PSU	3	0
8	A	1939	5MU	1	0
34	a	966	2MG	1	0
8	A	747	5MC	2	0
34	a	1402	4OC	2	0
8	A	745	1MG	1	0
34	a	1407	5MC	1	0
56	w	54	5MU	2	0
8	A	2552	OMU	1	0
56	w	46	G7M	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 391 ligands modelled in this entry, 391 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

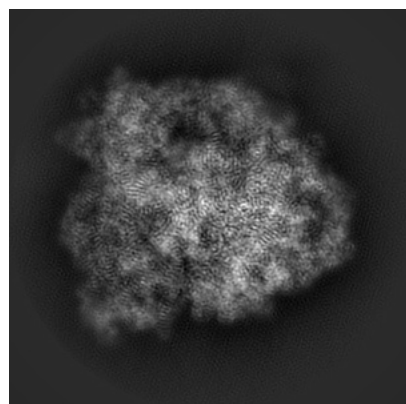
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10906. These allow visual inspection of the internal detail of the map and identification of artifacts.

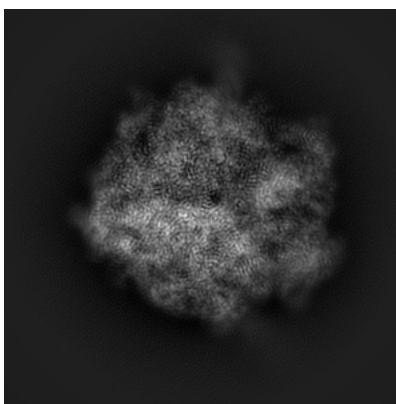
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

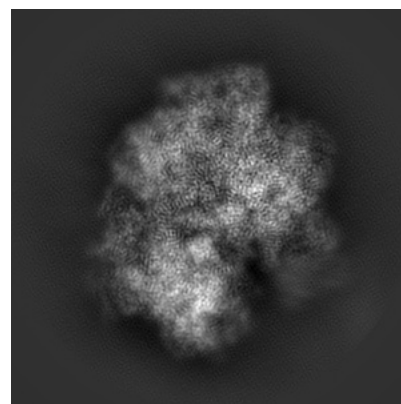
6.1.1 Primary map



X

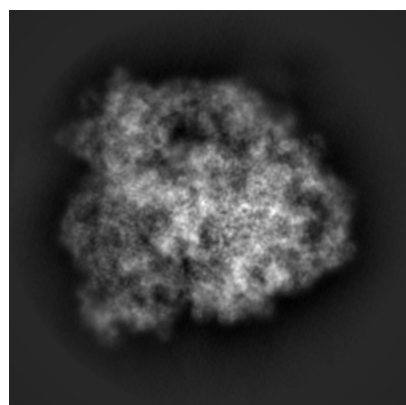


Y

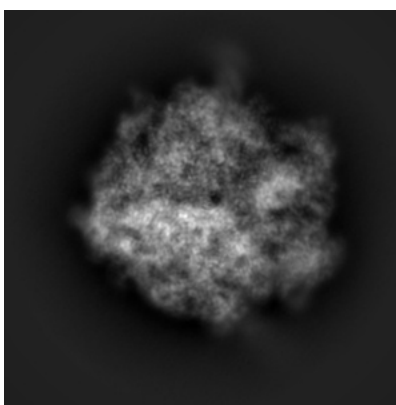


Z

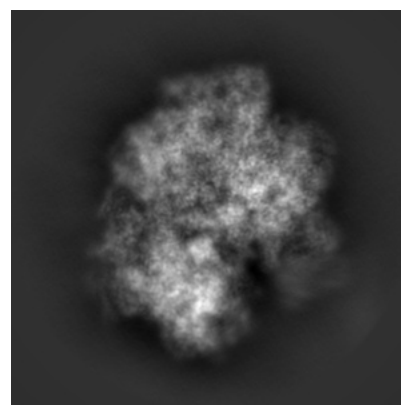
6.1.2 Raw map



X



Y

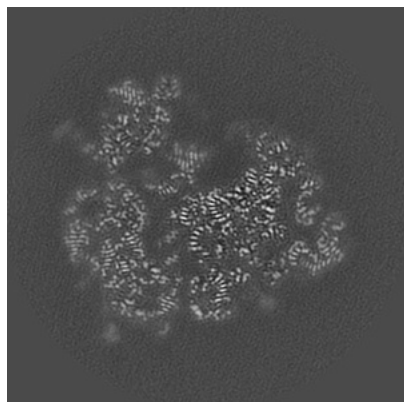


Z

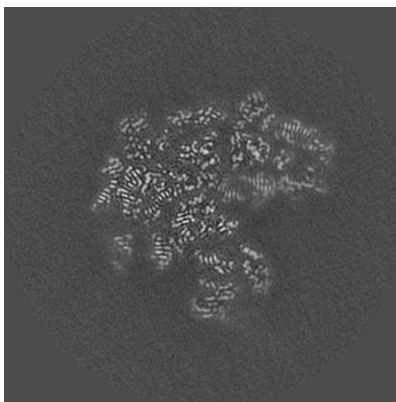
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

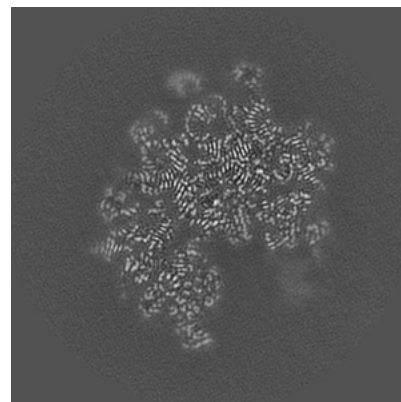
6.2.1 Primary map



X Index: 256

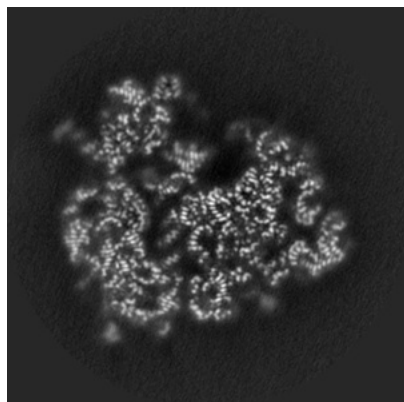


Y Index: 256

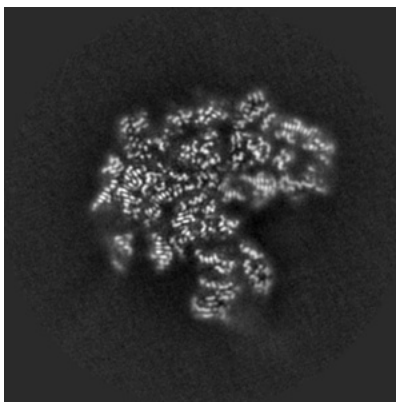


Z Index: 256

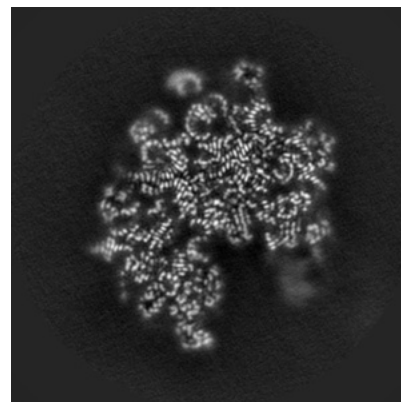
6.2.2 Raw map



X Index: 144



Y Index: 144

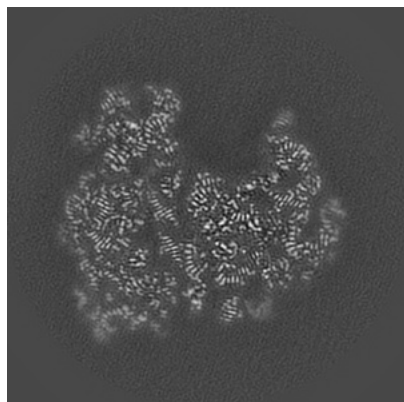


Z Index: 144

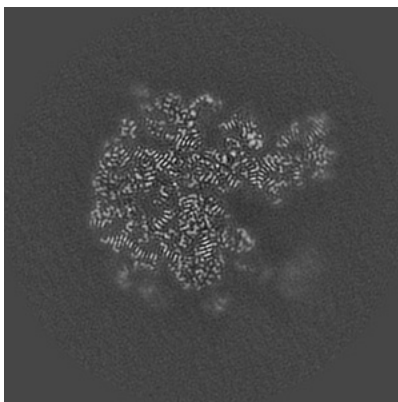
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

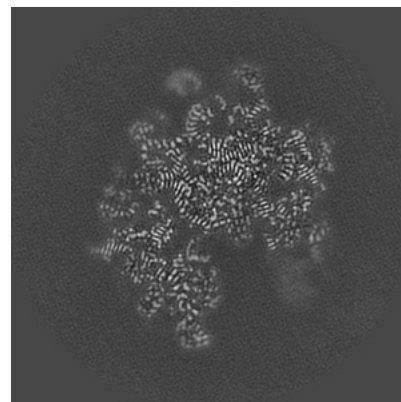
6.3.1 Primary map



X Index: 236

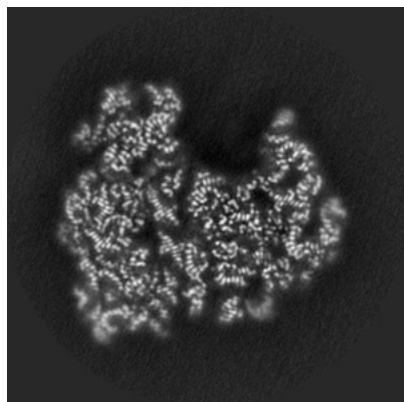


Y Index: 284

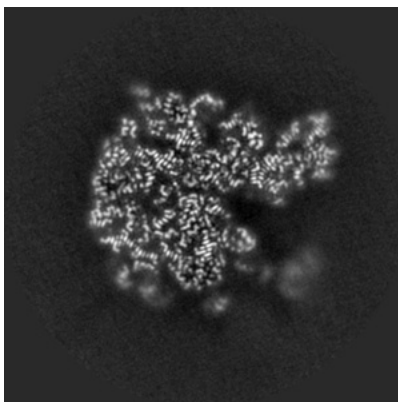


Z Index: 258

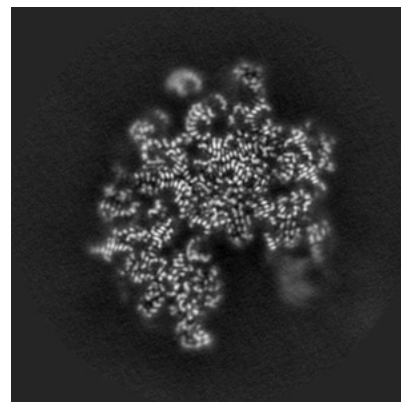
6.3.2 Raw map



X Index: 133



Y Index: 160

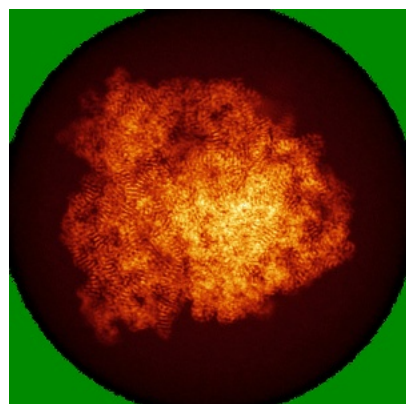


Z Index: 145

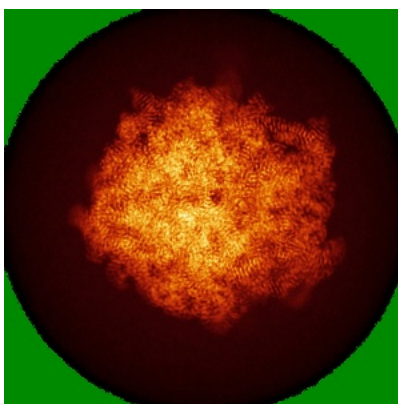
The images above show the largest variance slices of the map in three orthogonal directions.

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

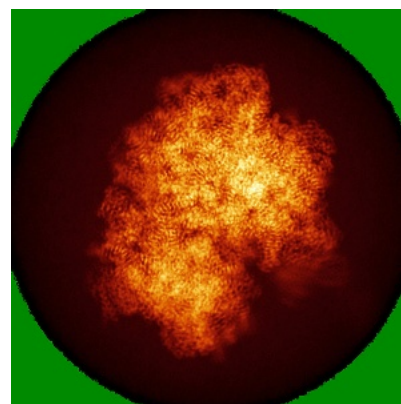
6.4.1 Primary map



X

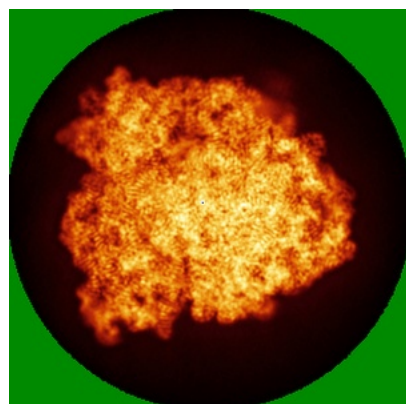


Y

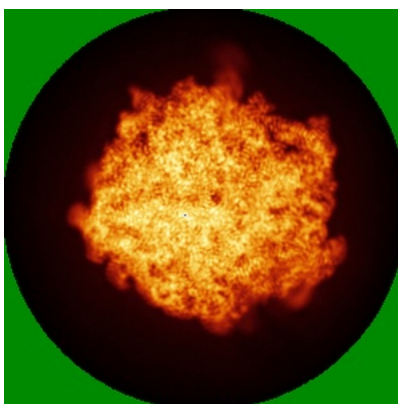


Z

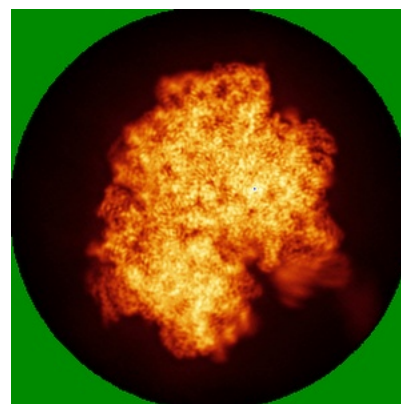
6.4.2 Raw map



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](#)

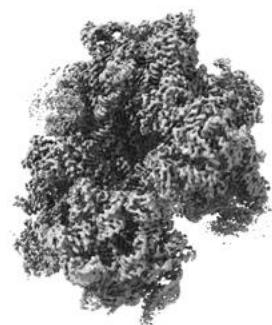
6.5.1 Primary map



X



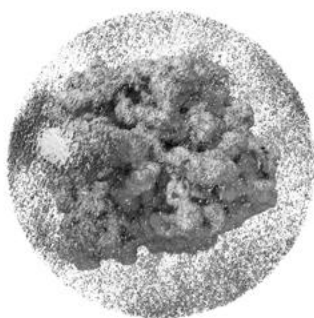
Y



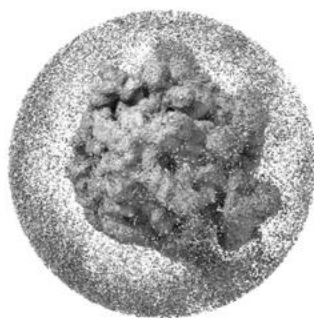
Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

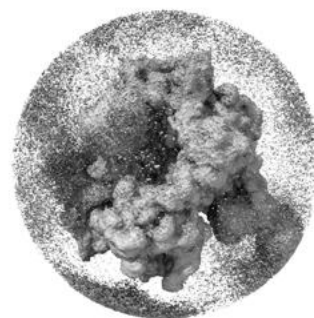
6.5.2 Raw map



X



Y



Z

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.

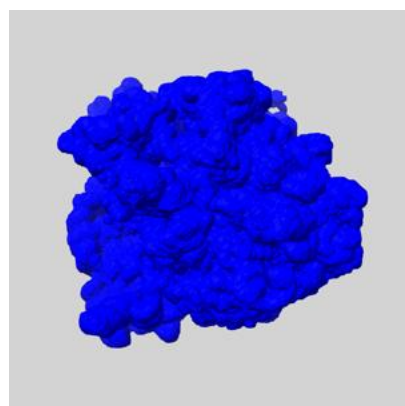
6.6 Mask visualisation [i](#)

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

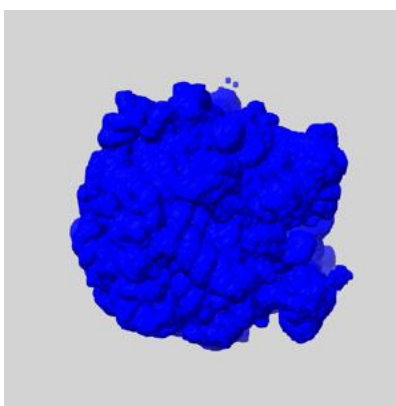
A mask typically either:

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

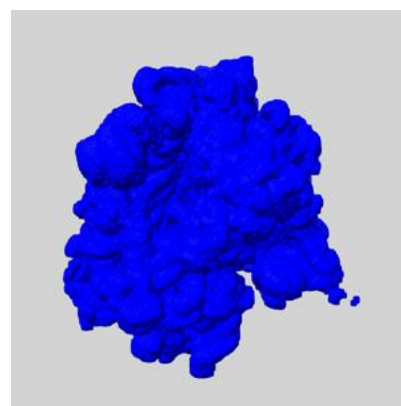
6.6.1 emd_10906_msk_1.map [i](#)



X



Y

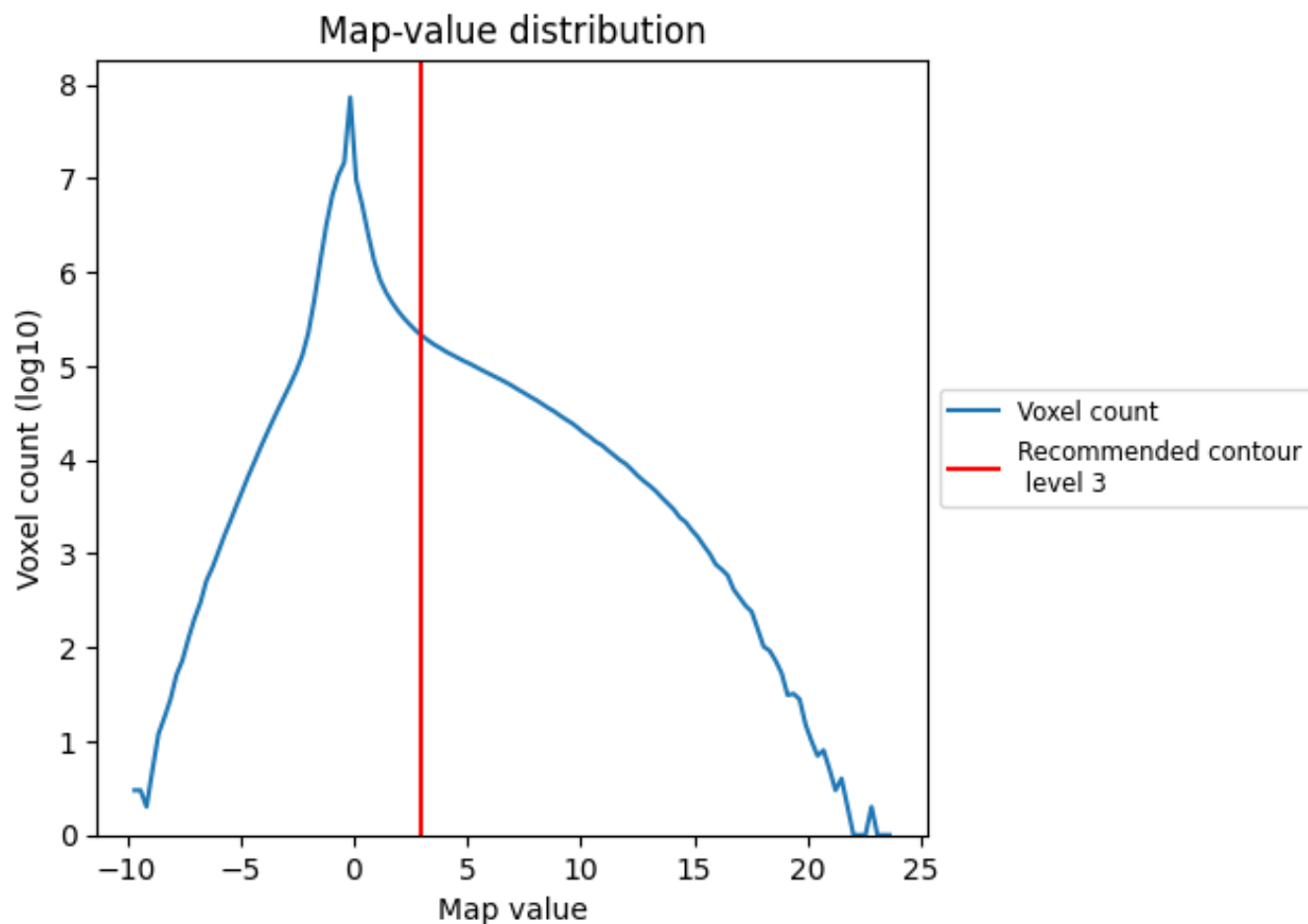


Z

7 Map analysis [i](#)

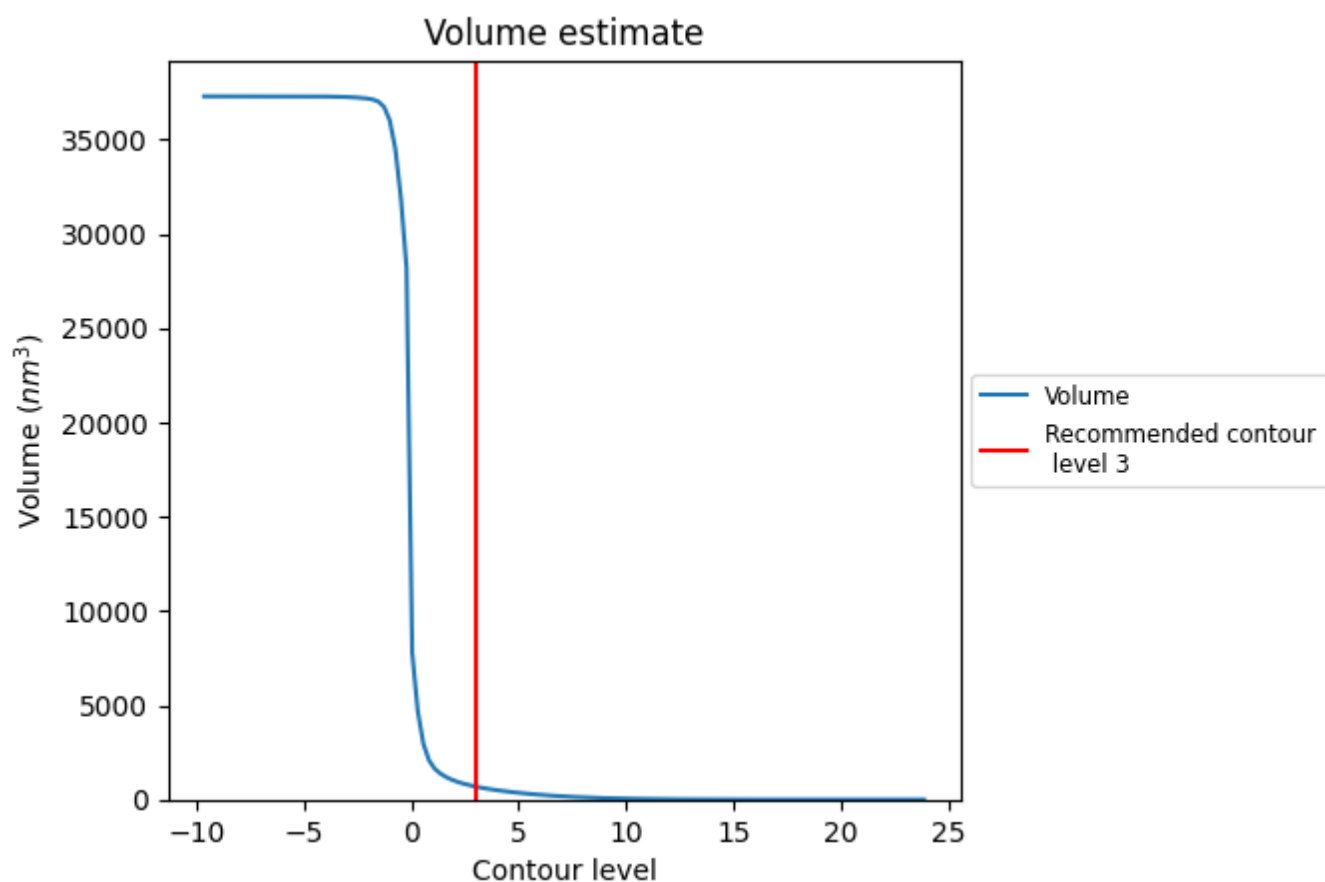
This section contains the results of statistical analysis of the map.

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.

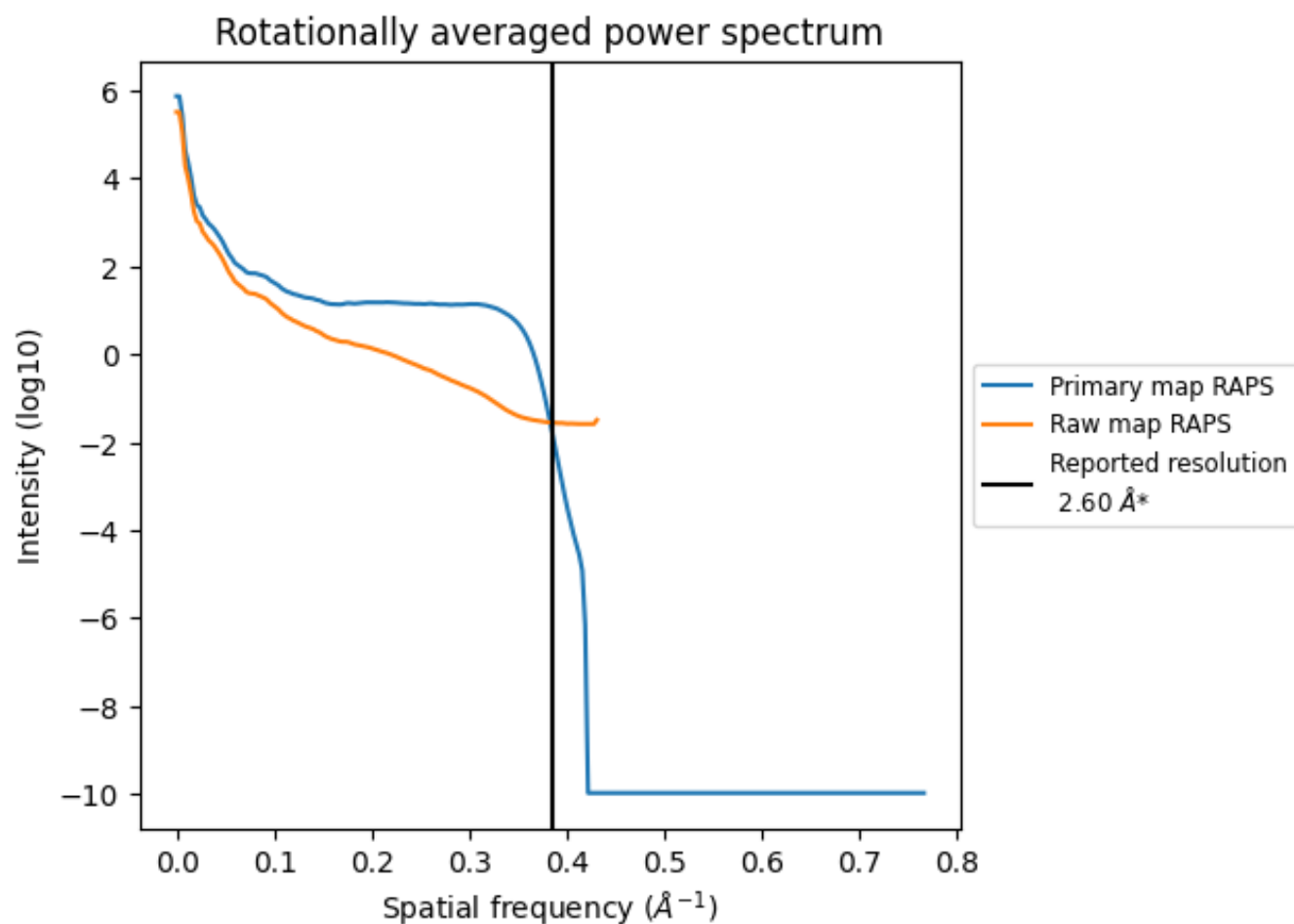
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 684 nm³; this corresponds to an approximate mass of 618 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 ⓘ

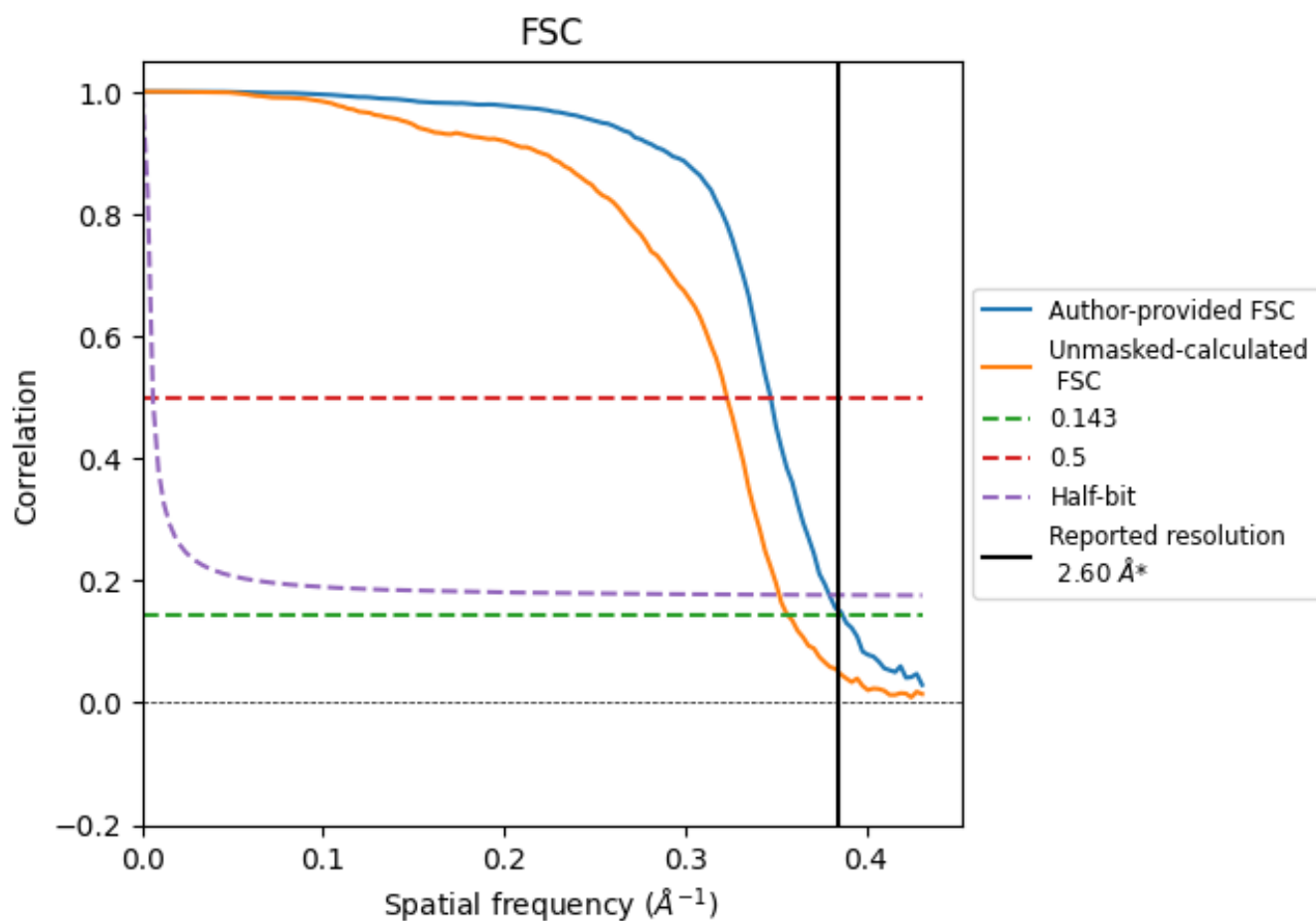


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

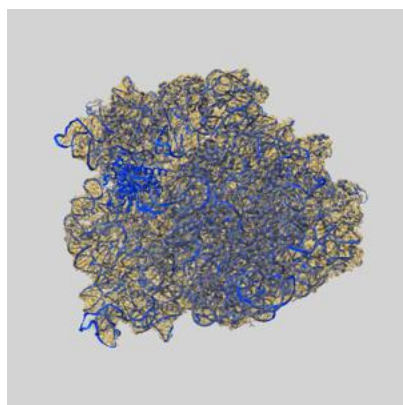
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.58	2.88	2.63
Unmasked-calculated*	2.80	3.10	2.84

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

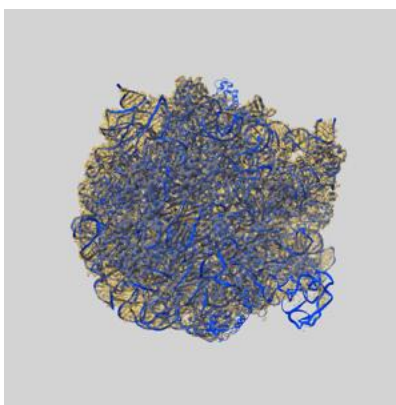
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10906 and PDB model 6YSS. Per-residue inclusion information can be found in section [3](#) on page [16](#).

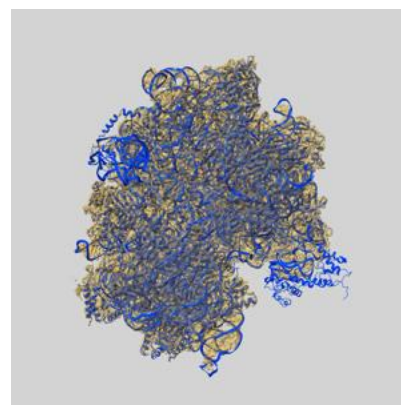
9.1 Map-model overlay [i](#)



X



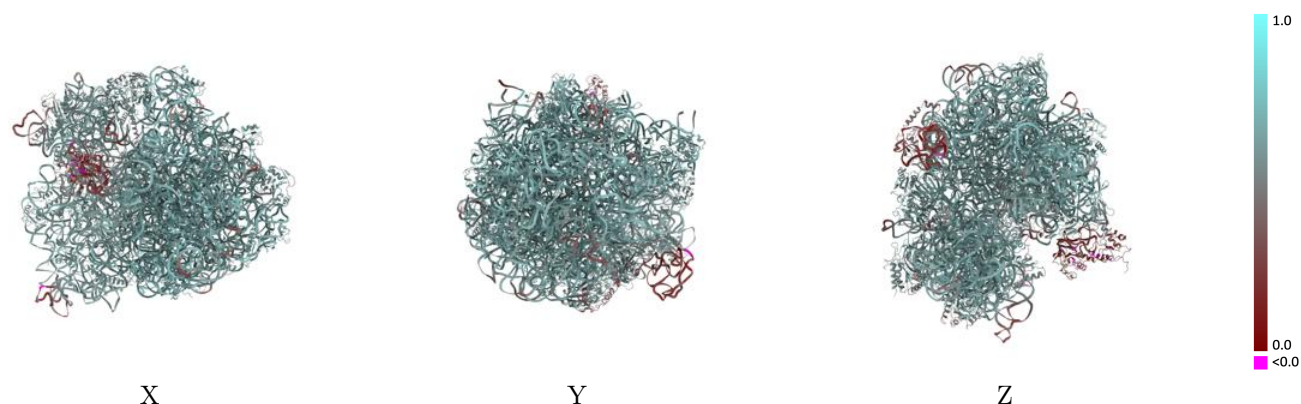
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0 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](#)



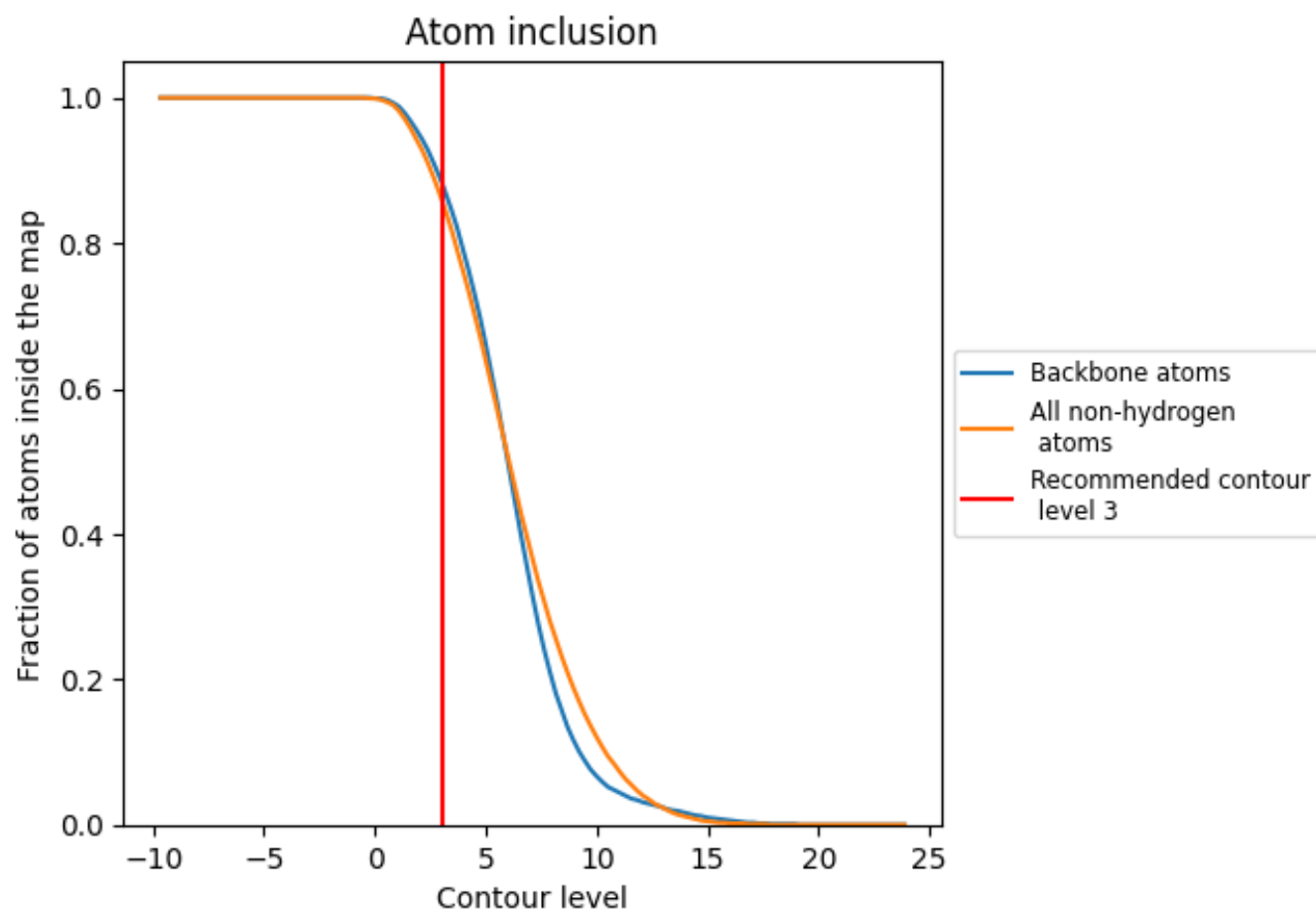
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8610	 0.6130
0	 0.8420	 0.6350
1	 0.7760	 0.6330
2	 0.9130	 0.6610
3	 0.9100	 0.6550
4	 0.8800	 0.6260
5	 0.0220	 0.2620
6	 0.5180	 0.5170
A	 0.9070	 0.6190
B	 0.9310	 0.6300
C	 0.8950	 0.6580
D	 0.8910	 0.6470
E	 0.7850	 0.6180
F	 0.7310	 0.5890
G	 0.6900	 0.5820
H	 0.2110	 0.4620
I	 0.0060	 0.2640
J	 0.8910	 0.6480
K	 0.8410	 0.6460
L	 0.8460	 0.6360
M	 0.8500	 0.6430
N	 0.9130	 0.6540
O	 0.8330	 0.6150
P	 0.8370	 0.6420
Q	 0.9340	 0.6620
R	 0.8420	 0.6260
S	 0.8490	 0.6390
T	 0.7890	 0.6100
U	 0.7720	 0.6000
V	 0.8170	 0.6300
W	 0.8960	 0.6530
X	 0.8500	 0.6390
Y	 0.7430	 0.6000
Z	 0.8490	 0.6390
a	 0.9190	 0.6190



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Chain	Atom inclusion	Q-score
b	 0.5960	 0.5570
c	 0.7590	 0.6080
d	 0.7600	 0.6060
e	 0.8450	 0.6310
f	 0.7190	 0.5820
g	 0.6260	 0.5560
h	 0.8240	 0.6350
i	 0.7650	 0.5890
j	 0.5820	 0.5460
k	 0.7880	 0.6050
l	 0.8260	 0.6250
m	 0.7570	 0.6050
n	 0.7880	 0.6060
o	 0.7960	 0.6080
p	 0.7860	 0.6000
q	 0.7550	 0.6090
r	 0.7880	 0.6090
s	 0.7730	 0.5960
t	 0.8000	 0.6050
u	 0.5590	 0.5610
v	 0.7810	 0.6420
w	 0.8450	 0.6010
x	 0.8160	 0.5840
y	 0.7540	 0.6170