



# Full wwPDB EM Validation Report ⓘ

Oct 19, 2025 – 01:42 AM JST

PDB ID : 9WNR / pdb\_00009wnr  
EMDB ID : EMD-66122  
Title : Structure of E.coli ribosome in complex with an engineered arrest peptide and trigger factor  
Authors : Sriramoju, M.K.; Ko, T.P.; Draczkowski, P.; Hsu, S.T.D.  
Deposited on : 2025-09-05  
Resolution : 2.76 Å(reported)  
Based on initial model : 3JBU

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev129  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
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) : 2.46

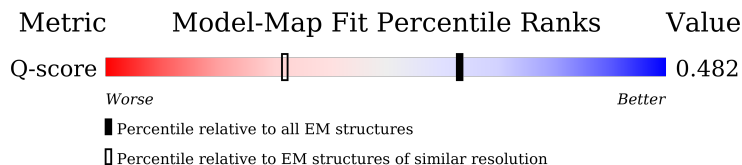
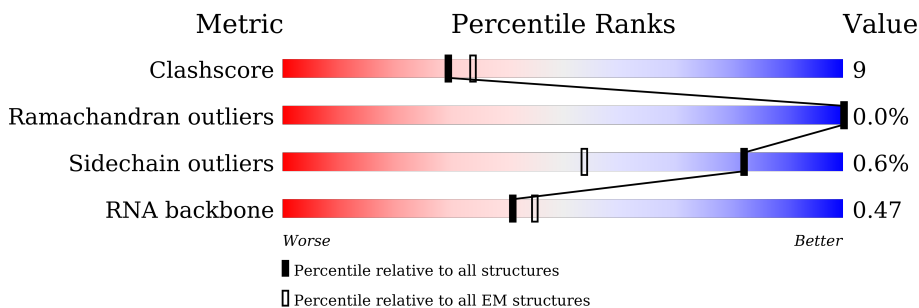
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.76 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.





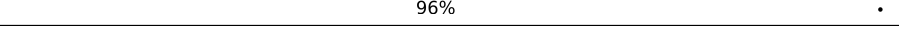
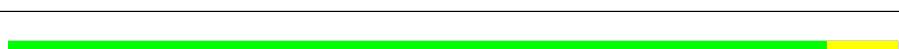
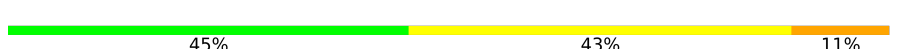


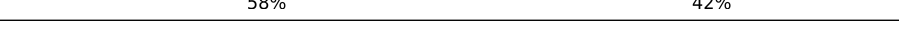



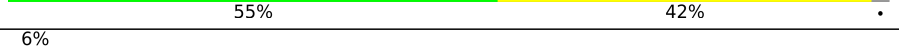

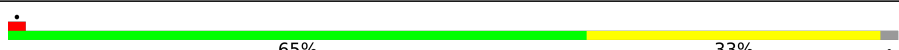


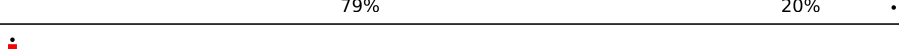







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	10642 ( 2.26 - 3.26 )

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  $\geq 3$ , 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	78	
2	1	63	
3	2	59	



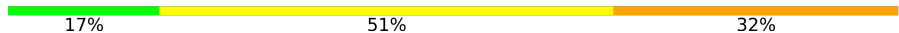
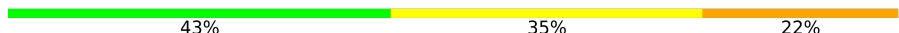
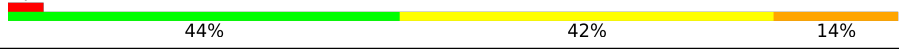















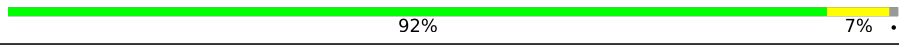
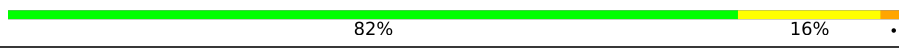
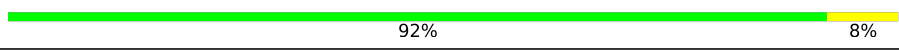


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Mol	Chain	Length	Quality of chain
4	4	57	
5	5	55	
6	6	46	
7	7	65	
8	8	38	
9	A	1533	
10	B	241	
11	C	233	
12	D	206	
13	E	167	
14	F	135	
15	G	179	
16	H	130	
17	I	130	
18	J	103	
19	K	129	
20	L	124	
21	M	118	
22	N	101	
23	O	89	
24	P	82	
25	Q	84	
26	R	75	
27	S	92	
28	T	87	





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Mol	Chain	Length	Quality of chain
29	U	71	
30	V	432	
31	X	76	
32	Y	77	
32	Z	77	
33	a	120	
34	b	2904	
35	c	273	
36	d	209	
37	e	201	
38	f	179	
39	g	177	
40	h	149	
41	k	142	
42	l	123	
43	m	144	
44	n	136	
45	o	127	
46	p	117	
47	q	115	
48	r	118	
49	s	103	
50	t	110	
51	u	100	
52	v	104	

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Mol	Chain	Length	Quality of chain
53	w	94	 88% 11% .
54	x	14	 50% 29% 21%
55	y	85	 7% 85% 14% .
56	z	39	 44% 44% 13%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
58	PRO	Z	101	-	-	X	-

## 2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 148018 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 Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 4 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 5 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	5	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 9 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	1533	Total	C	N	O	P	0	0
			32895	14671	6036	10655	1533		

- Molecule 10 is a protein called 30S ribosomal protein S2.

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

- Molecule 11 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	207	Total	C	N	O	S	0	0
			1632	1034	306	289	3		

- Molecule 12 is a protein called 30S ribosomal protein S4.

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

- Molecule 13 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 14 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 15 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 16 is a protein called 30S ribosomal protein S8.

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

- Molecule 17 is a protein called 30S ribosomal protein S9.

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

- Molecule 18 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	100	Total	C	N	O	S	0	0
			803	502	154	146	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 20 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	122	Total	C	N	O	S	0	0
			949	587	195	163	4		

- Molecule 21 is a protein called 30S ribosomal protein S13.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 22 is a protein called 30S ribosomal protein S14.

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

- Molecule 23 is a protein called 30S ribosomal protein S15.

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

- Molecule 24 is a protein called 30S ribosomal protein S16.

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

- Molecule 25 is a protein called 30S ribosomal protein S17.

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

- Molecule 26 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 27 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 28 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 29 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	64	Total	C	N	O	S	0	0
			529	329	110	89	1		

- Molecule 30 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	59	Total	C	N	O	S	0	0
			454	284	84	84	2		

- Molecule 31 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	76	Total	C	N	O	P	0	0
			1621	722	287	536	76		

- Molecule 32 is a RNA chain called P-tRNA(PRO), A-tRNA(PRO).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		
32	Z	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 33 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	120	Total	C	N	O	P	0	0
			2568	1144	468	837	119		

- Molecule 34 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

- Molecule 35 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 36 is a protein called 50S ribosomal protein L3.

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

- Molecule 37 is a protein called 50S ribosomal protein L4.

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

- Molecule 38 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	178	Total	C	N	O	S	0	0
			1419	905	251	257	6		

- Molecule 39 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 40 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 41 is a protein called 50S ribosomal protein L13.

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

- Molecule 42 is a protein called 50S ribosomal protein L14.

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

- Molecule 43 is a protein called 50S ribosomal protein L15.

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

- Molecule 44 is a protein called 50S ribosomal protein L16.

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

- Molecule 45 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 46 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 47 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 48 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 49 is a protein called 50S ribosomal protein L21.

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

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

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

- Molecule 51 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	100	Total	C	N	O	S	0	0
			786	496	146	142	2		

- Molecule 52 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	103	Total	C	N	O	S	0	0
			788	498	148	142			

- Molecule 53 is a protein called 50S ribosomal protein L25.

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

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	14	Total	C	N	O	P	0	0
			299	133	55	97	14		

- Molecule 55 is a protein called Large ribosomal subunit protein bL27.

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

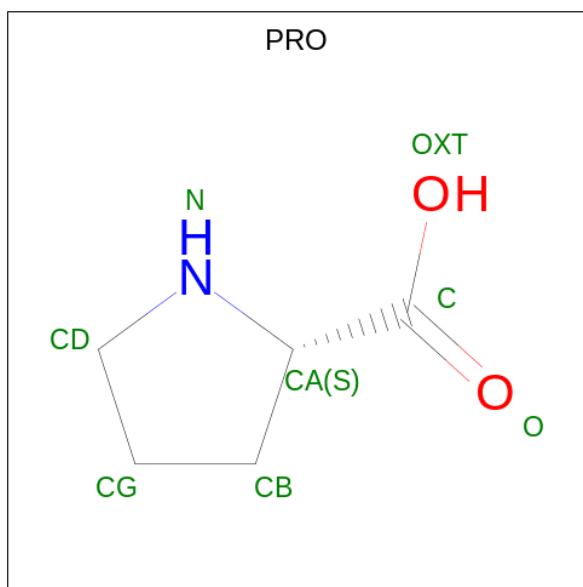
- Molecule 56 is a protein called eRAP-NC.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	39	Total	C	N	O	S	8	0
			397	259	72	64	2		

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	8	1	Total	Zn	0
			1	1	

- Molecule 58 is PROLINE (CCD ID: PRO) (formula: C<sub>5</sub>H<sub>9</sub>NO<sub>2</sub>).




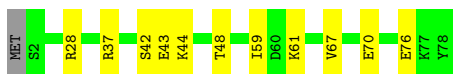
Mol	Chain	Residues	Atoms				AltConf
58	Z	1	Total	C	N	O	0
			7	5	1	1	

### 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: Large ribosomal subunit protein bL28

Chain 0:  85% 14% .



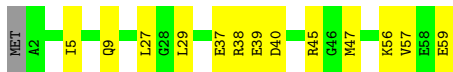
- Molecule 2: Large ribosomal subunit protein uL29

Chain 1:  70% 27% .



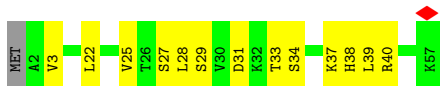
- Molecule 3: Large ribosomal subunit protein uL30

Chain 2:  76% 22% .




- Molecule 4: Large ribosomal subunit protein bL32

Chain 4:  75% 23% .



- Molecule 5: Large ribosomal subunit protein bL33

Chain 5:  84% 11% 5%



- Molecule 6: 50S ribosomal protein L34

Chain 6:  96% .



- Molecule 7: Large ribosomal subunit protein bL35

Chain 7:  89% 9% .



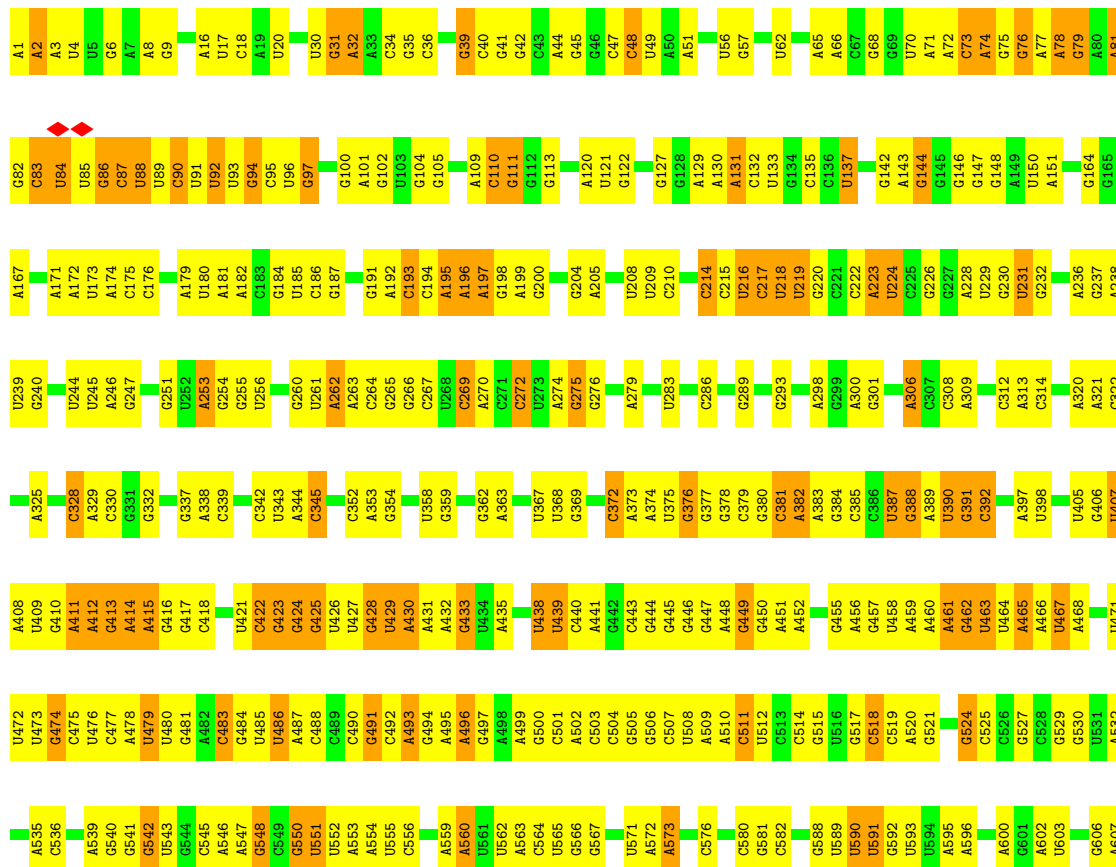
- Molecule 8: 50S ribosomal protein L36

Chain 8:  92% 8% .

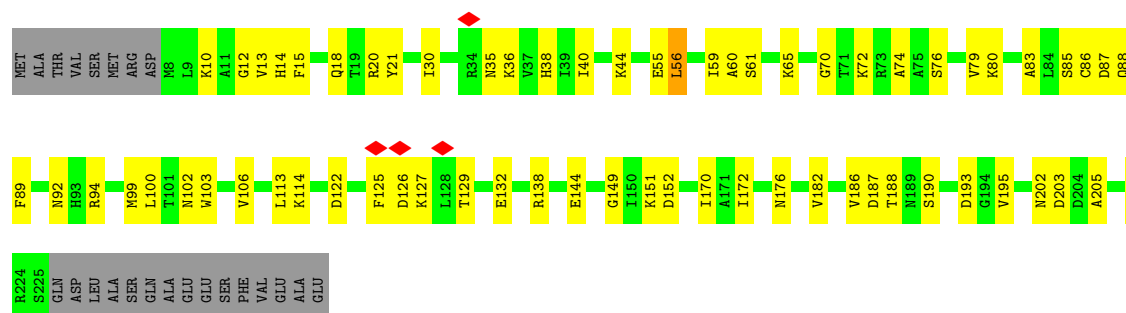
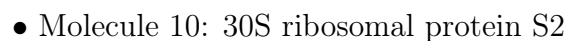


- Molecule 9: 16S rRNA

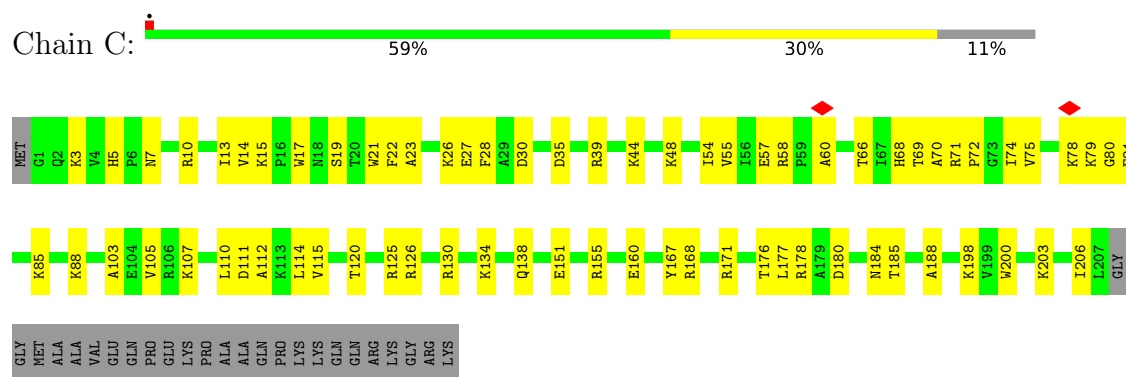
Chain A:  45% 43% 11% .



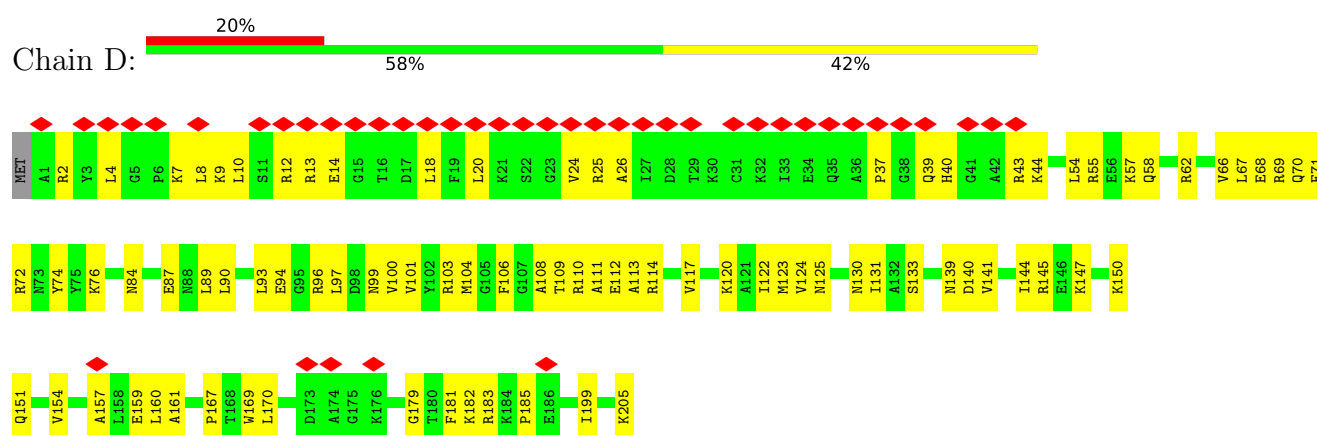




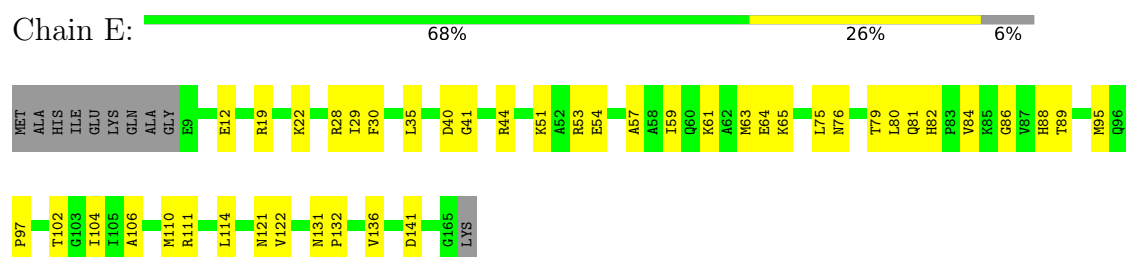
- Molecule 11: 30S ribosomal protein S3



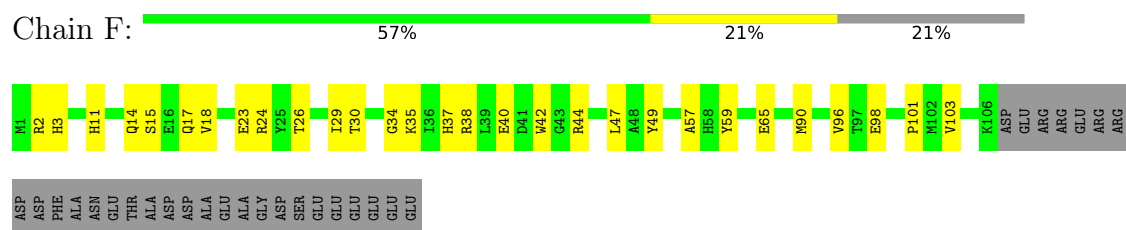
- Molecule 12: 30S ribosomal protein S4



- Molecule 13: 30S ribosomal protein S5

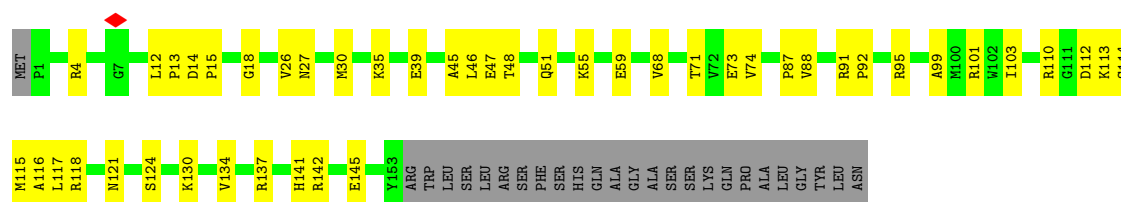


- Molecule 14: 30S ribosomal protein S6, fully modified isoform



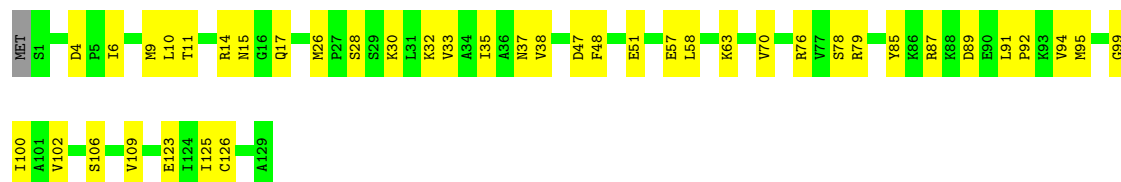
- Molecule 15: 30S ribosomal protein S7





• Molecule 16: 30S ribosomal protein S8

Chain H: 68% 32%



• Molecule 17: 30S ribosomal protein S9

Chain I: 55% 42%



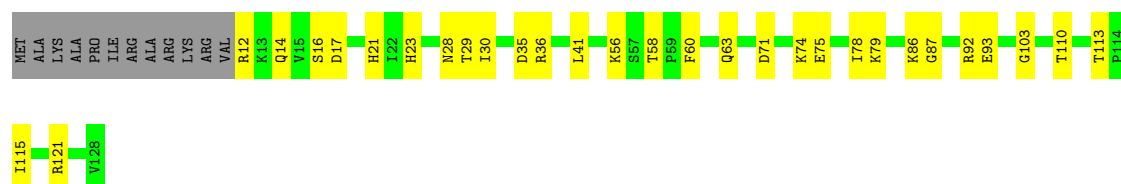
• Molecule 18: 30S ribosomal protein S10

Chain J: 6% 60% 37%

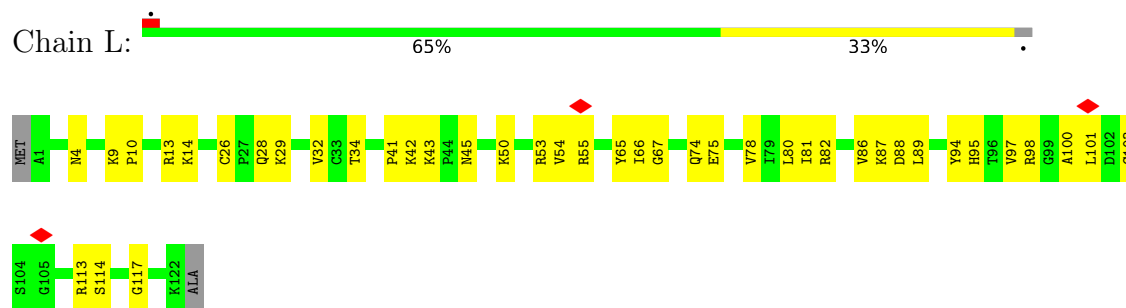


• Molecule 19: Small ribosomal subunit protein uS11

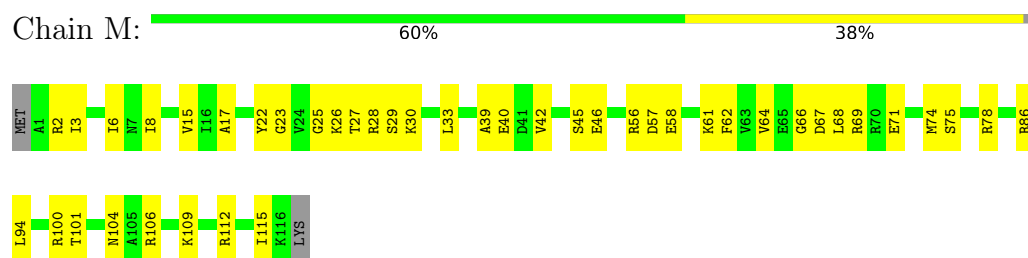
Chain K: 67% 23% 9%



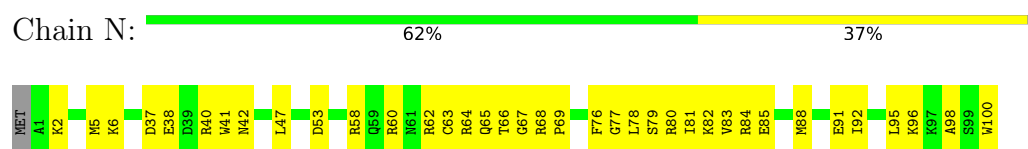
• Molecule 20: Small ribosomal subunit protein uS12



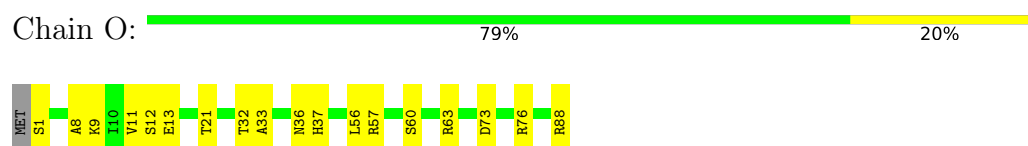
- Molecule 21: 30S ribosomal protein S13



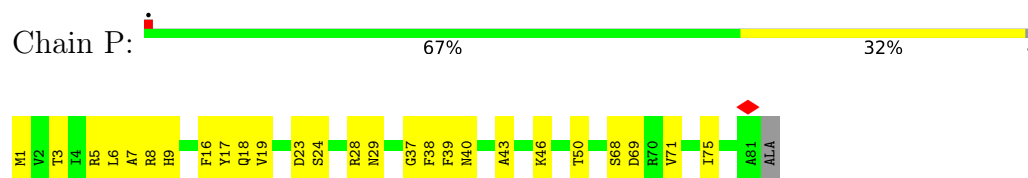
- Molecule 22: 30S ribosomal protein S14



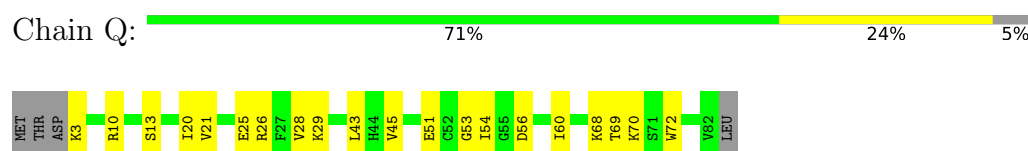
- Molecule 23: 30S ribosomal protein S15



- Molecule 24: 30S ribosomal protein S16



- Molecule 25: 30S ribosomal protein S17



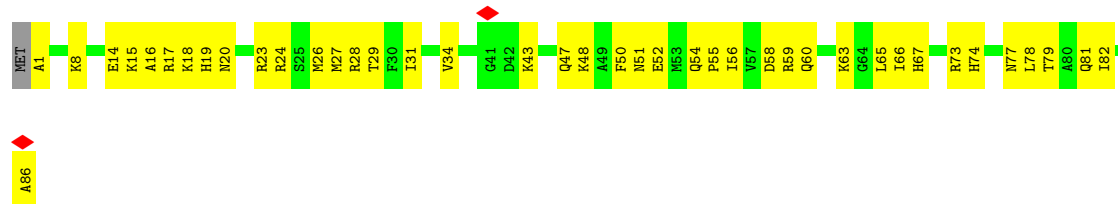
- Molecule 26: 30S ribosomal protein S18



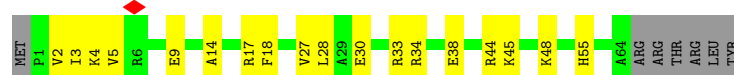
- Molecule 27: 30S ribosomal protein S19



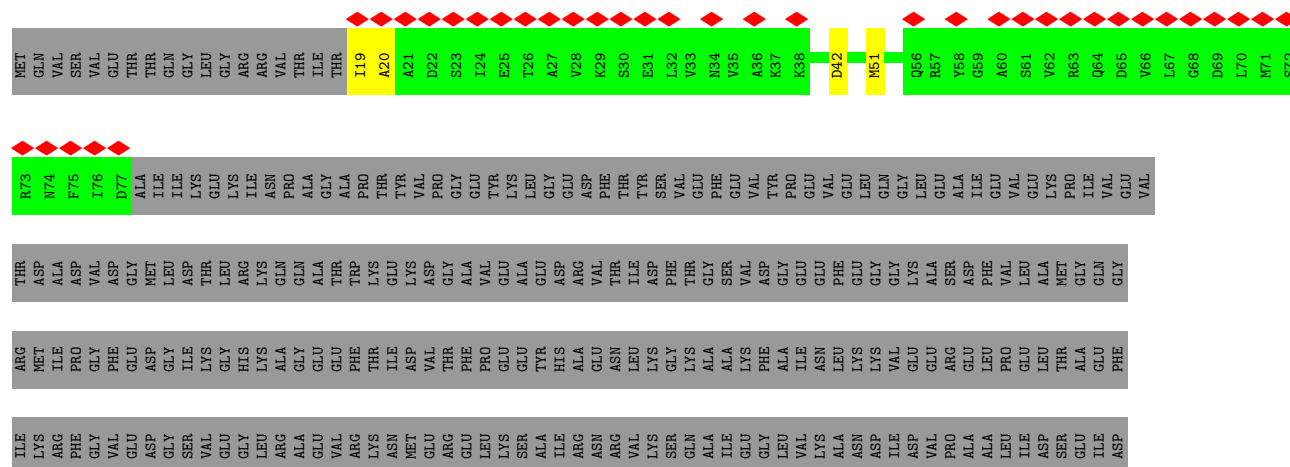
- Molecule 28: 30S ribosomal protein S20



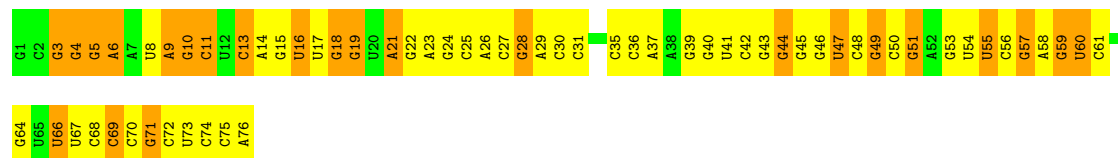
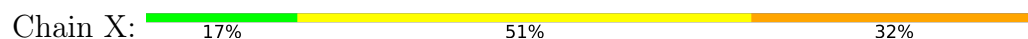
- Molecule 29: 30S ribosomal protein S21



- Molecule 30: Trigger factor



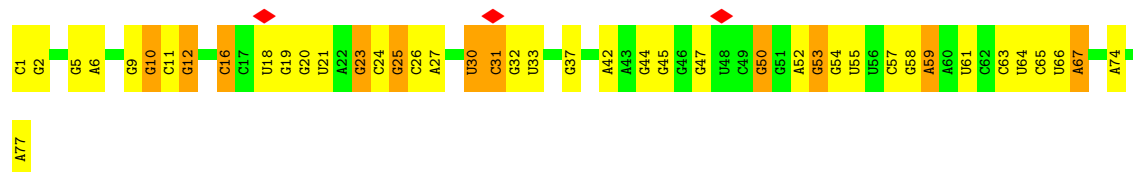
- Molecule 31: E-tRNA



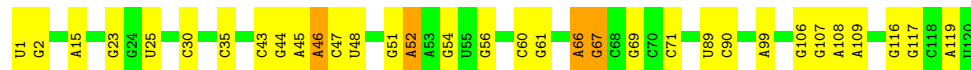
- Molecule 32: P-tRNA(PRO), A-tRNA(PRO)



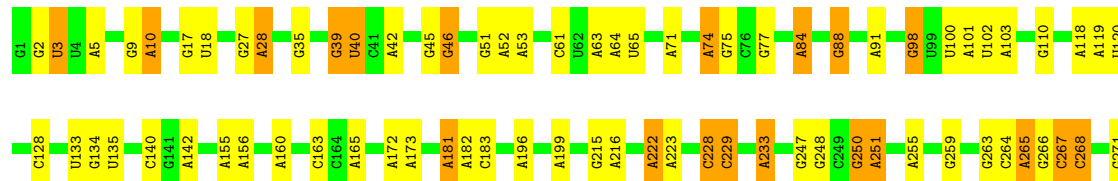
- Molecule 32: P-tRNA(PRO), A-tRNA(PRO)



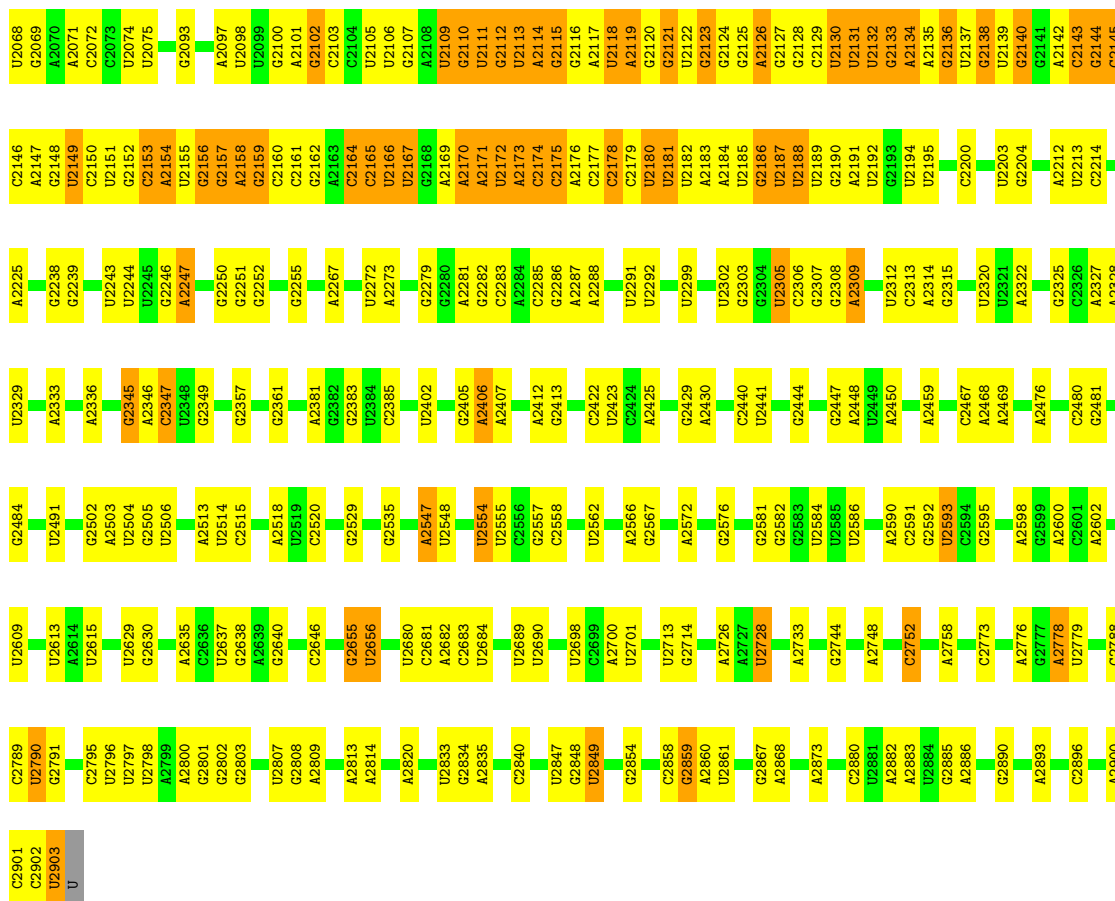
- Molecule 33: 5S rRNA



- Molecule 34: 23S rRNA

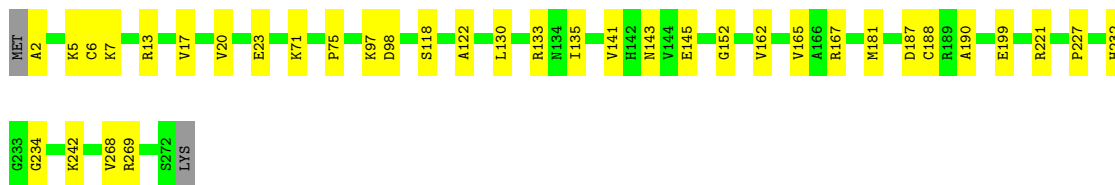






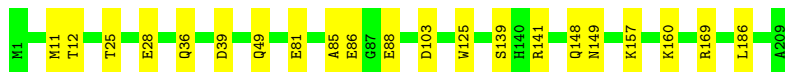
- Molecule 35: Large ribosomal subunit protein uL2

Chain c: 86% 13%



- Molecule 36: 50S ribosomal protein L3

Chain d: 90% 10%



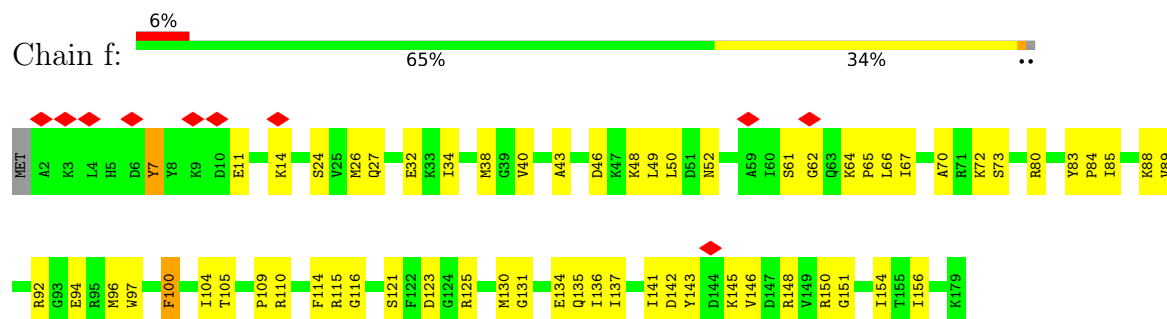
- Molecule 37: 50S ribosomal protein L4

Chain e: 88% 12%

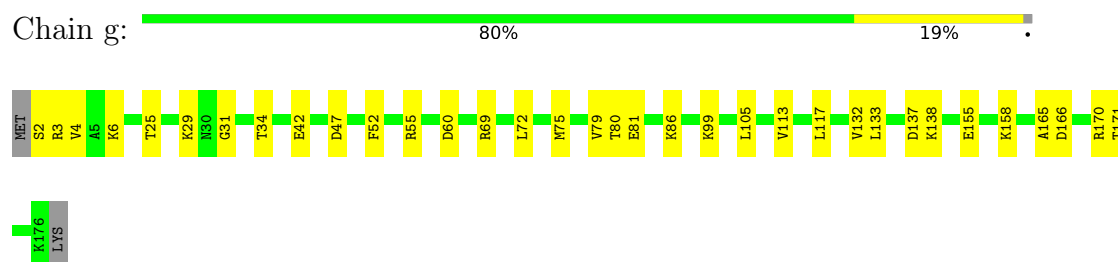




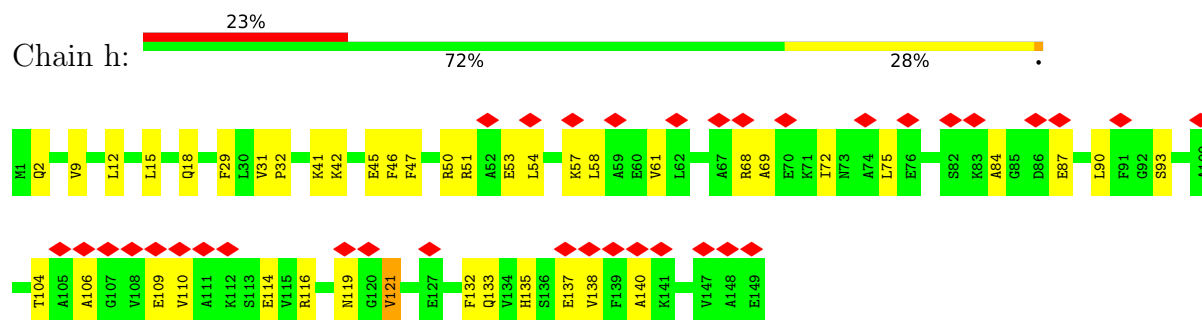
- Molecule 38: Large ribosomal subunit protein uL5



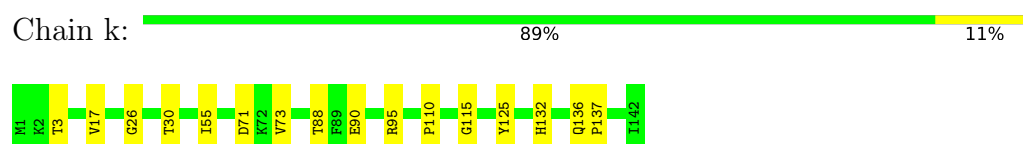
- Molecule 39: Large ribosomal subunit protein uL6



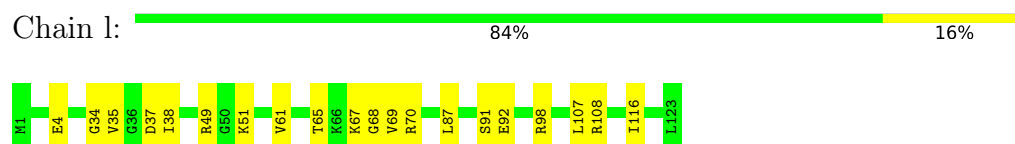
- Molecule 40: 50S ribosomal protein L9



- Molecule 41: 50S ribosomal protein L13



- Molecule 42: 50S ribosomal protein L14



- Molecule 43: 50S ribosomal protein L15





- Molecule 44: 50S ribosomal protein L16

Chain n: 83% 15% ..



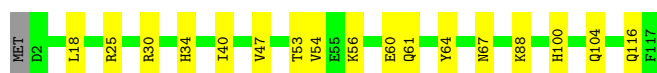
- Molecule 45: Large ribosomal subunit protein bL17

Chain o: 84% 10% 6%



- Molecule 46: Large ribosomal subunit protein uL18

Chain p: 85% 15% .



- Molecule 47: Large ribosomal subunit protein bL19

Chain q: 88% 11% .



- Molecule 48: Large ribosomal subunit protein bL20

Chain r: 92% 7% .



- Molecule 49: 50S ribosomal protein L21

Chain s: 82% 16% .

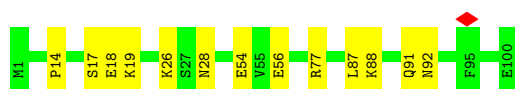
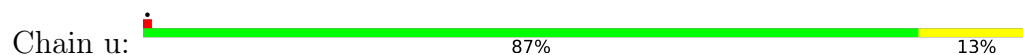


- Molecule 50: 50S ribosomal protein L22

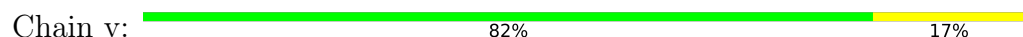
Chain t: 92% 8%



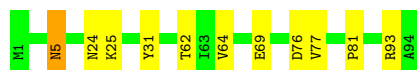
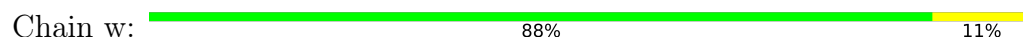
- Molecule 51: Large ribosomal subunit protein uL23



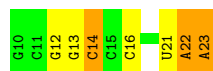
- Molecule 52: 50S ribosomal protein L24



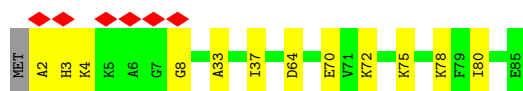
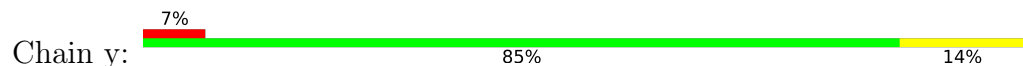
- Molecule 53: 50S ribosomal protein L25



- Molecule 54: mRNA



- Molecule 55: Large ribosomal subunit protein bL27



- Molecule 56: eRAP-NC



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72313	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 ( $e^-/\text{\AA}^2$ )	38	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.235	Depositor
Minimum map value	-0.701	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.096	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	682.0, 682.0, 682.0	wwPDB
Map dimensions	620, 620, 620	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.19	0/635	0.30	0/848
2	1	0.18	0/496	0.29	0/660
3	2	0.21	0/453	0.29	0/605
4	4	0.22	0/450	0.33	0/599
5	5	0.18	0/433	0.28	0/576
6	6	0.23	0/380	0.32	0/498
7	7	0.22	0/513	0.27	0/676
8	8	0.24	0/303	0.24	0/397
9	A	0.15	0/36834	0.27	0/57462
10	B	0.12	0/1735	0.29	0/2338
11	C	0.13	0/1659	0.27	0/2236
12	D	0.11	0/1665	0.28	0/2227
13	E	0.16	0/1169	0.31	0/1573
14	F	0.16	0/881	0.31	0/1189
15	G	0.11	0/1219	0.25	0/1635
16	H	0.15	0/989	0.29	0/1326
17	I	0.12	0/1034	0.32	0/1375
18	J	0.13	0/813	0.35	0/1100
19	K	0.15	0/893	0.27	0/1205
20	L	0.15	0/963	0.33	0/1293
21	M	0.12	0/909	0.28	0/1215
22	N	0.12	0/817	0.24	0/1088
23	O	0.15	0/722	0.26	0/964
24	P	0.11	0/653	0.26	0/877
25	Q	0.13	0/657	0.31	0/881
26	R	0.14	0/553	0.27	0/742
27	S	0.12	0/680	0.33	0/915
28	T	0.16	0/676	0.28	0/895
29	U	0.12	0/536	0.35	0/711
30	V	0.15	0/457	0.42	0/612
31	X	0.12	0/1810	0.27	0/2820
32	Y	0.14	0/1840	0.27	0/2866

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	Z	0.12	0/1840	0.25	0/2866
33	a	0.17	0/2869	0.26	0/4474
34	b	0.21	0/69800	0.30	0/108892
35	c	0.22	0/2121	0.30	0/2852
36	d	0.22	0/1586	0.33	0/2134
37	e	0.21	0/1571	0.28	0/2113
38	f	0.15	0/1443	0.36	0/1937
39	g	0.15	0/1333	0.26	0/1805
40	h	0.12	0/1121	0.26	0/1515
41	k	0.28	1/1152 (0.1%)	0.27	0/1551
42	l	0.20	0/955	0.34	0/1279
43	m	0.21	0/1062	0.31	0/1413
44	n	0.23	0/1093	0.49	2/1460 (0.1%)
45	o	0.22	0/973	0.30	0/1301
46	p	0.16	0/902	0.26	0/1209
47	q	0.21	0/929	0.27	0/1242
48	r	0.24	0/960	0.28	0/1278
49	s	0.22	0/829	0.35	0/1107
50	t	0.23	0/864	0.26	0/1156
51	u	0.19	0/793	0.29	0/1060
52	v	0.20	0/796	0.36	0/1062
53	w	0.18	0/766	0.30	0/1025
54	x	0.14	0/333	0.27	0/517
55	y	0.21	0/642	0.27	0/848
56	z	0.26	0/415	0.37	0/567
All	All	0.19	1/160975 (0.0%)	0.29	2/241067 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	k	136	GLN	C-O	-5.86	1.21	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	n	69	PRO	CA-N-CD	-9.77	98.32	112.00
44	n	68	PHE	C-N-CD	-5.81	101.18	125.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	625	0	652	9	0
2	1	495	0	526	13	0
3	2	449	0	488	8	0
4	4	444	0	458	11	0
5	5	426	0	464	4	0
6	6	377	0	418	1	0
7	7	504	0	572	3	0
8	8	302	0	341	2	0
9	A	32895	0	16553	612	0
10	B	1704	0	1732	53	0
11	C	1632	0	1710	58	0
12	D	1643	0	1710	85	0
13	E	1156	0	1199	32	0
14	F	862	0	864	30	0
15	G	1203	0	1256	40	0
16	H	979	0	1034	37	0
17	I	1022	0	1070	54	0
18	J	803	0	842	40	0
19	K	877	0	887	24	0
20	L	949	0	1014	37	0
21	M	900	0	968	38	0
22	N	805	0	847	40	0
23	O	714	0	737	19	0
24	P	643	0	661	28	0
25	Q	648	0	691	17	0
26	R	544	0	565	16	0
27	S	663	0	690	26	0
28	T	670	0	722	36	0
29	U	529	0	565	14	0
30	V	454	0	476	3	0
31	X	1621	0	820	56	0
32	Y	1647	0	832	42	0
32	Z	1647	0	832	26	0
33	a	2568	0	1302	21	0
34	b	62321	0	31344	518	0
35	c	2082	0	2154	23	0
36	d	1565	0	1616	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	e	1552	0	1619	18	0
38	f	1419	0	1457	56	0
39	g	1313	0	1358	22	0
40	h	1110	0	1148	28	0
41	k	1129	0	1162	11	0
42	l	946	0	1023	18	0
43	m	1053	0	1129	12	0
44	n	1074	0	1157	24	0
45	o	960	0	1000	19	0
46	p	892	0	923	15	0
47	q	917	0	962	10	0
48	r	947	0	1019	6	0
49	s	816	0	839	13	0
50	t	857	0	922	9	0
51	u	786	0	846	12	0
52	v	788	0	844	12	0
53	w	753	0	780	6	0
54	x	299	0	154	6	0
55	y	634	0	653	10	0
56	z	397	0	368	25	0
57	8	1	0	0	0	0
58	Z	7	0	7	4	0
All	All	148018	0	98982	2157	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 9.

All (2157) 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)
36:d:11:MET:CG	36:d:25:THR:HG22	1.67	1.23
24:P:6:LEU:CD1	24:P:71:VAL:CG2	2.20	1.19
26:R:32:ILE:HG23	26:R:37:LYS:O	1.43	1.17
32:Y:77:A:O3'	56:z:162:PRO:C	1.90	1.14
24:P:6:LEU:HD13	24:P:71:VAL:CG2	1.80	1.10
15:G:68:VAL:HG22	15:G:134:VAL:HG23	1.36	1.06
36:d:11:MET:HG2	36:d:25:THR:HG22	1.09	1.03
44:n:68:PHE:CD2	44:n:69:PRO:HD3	1.95	1.02
11:C:110:LEU:HD11	11:C:203:LYS:HE2	1.39	1.01
13:E:132:PRO:O	13:E:136:VAL:HG23	1.61	0.99
36:d:11:MET:HG2	36:d:25:THR:CG2	1.91	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:H:35:ILE:HD13	16:H:109:VAL:HG11	1.43	0.99
34:b:1352:U:HO2'	34:b:1570:A:H8	1.12	0.98
34:b:1277:G:H5'	45:o:20:MET:CE	1.92	0.98
34:b:1277:G:O4'	45:o:20:MET:HE1	1.64	0.97
44:n:68:PHE:CG	44:n:69:PRO:HD3	2.00	0.97
12:D:18:LEU:HD13	12:D:20:LEU:HG	1.45	0.97
32:Z:77:A:O3'	58:Z:101:PRO:C	2.08	0.95
34:b:1040:A:H61	34:b:1115:G:H1	1.11	0.95
11:C:15:LYS:NZ	11:C:180:ASP:OD1	2.00	0.94
9:A:954:G:H21	9:A:1227:A:H62	1.15	0.94
24:P:6:LEU:CD1	24:P:71:VAL:HG22	1.97	0.94
26:R:32:ILE:HD11	26:R:58:ILE:HD12	1.49	0.93
32:Z:77:A:HO3'	58:Z:101:PRO:C	1.75	0.93
14:F:47:LEU:CD1	14:F:49:TYR:O	2.18	0.92
42:l:61:VAL:HG23	42:l:87:LEU:HD11	1.49	0.92
9:A:76:G:H1	9:A:93:U:H3	1.18	0.92
33:a:54:G:H21	38:f:26:MET:HE1	1.31	0.92
24:P:6:LEU:CD1	24:P:71:VAL:HG21	1.97	0.91
34:b:2102:G:H22	34:b:2188:U:H3	1.19	0.90
34:b:1277:G:H5'	45:o:20:MET:HE2	1.53	0.90
46:p:40:ILE:CD1	46:p:47:VAL:HG22	2.02	0.88
34:b:1321:A:N1	56:z:129:ARG:NH1	2.23	0.87
24:P:6:LEU:HD11	24:P:71:VAL:HG22	1.53	0.87
36:d:28:GLU:HG2	36:d:186:LEU:CD2	2.05	0.87
24:P:6:LEU:HD11	24:P:71:VAL:CG2	2.05	0.85
16:H:35:ILE:CD1	16:H:109:VAL:HG11	2.05	0.85
36:d:28:GLU:OE2	47:q:4:ILE:HG21	1.76	0.85
24:P:6:LEU:HD13	24:P:71:VAL:HG23	1.58	0.83
32:Z:27:A:H61	32:Z:45:G:H1	1.25	0.83
9:A:973:G:H5'	18:J:59:LYS:HE2	1.60	0.83
9:A:1151:A:H5''	18:J:44:THR:HG23	1.59	0.83
32:Y:75:C:N4	55:y:4:LYS:O	2.12	0.82
12:D:109:THR:HG22	12:D:112:GLU:HG2	1.60	0.82
15:G:68:VAL:CG2	15:G:134:VAL:HG23	2.09	0.82
31:X:3:G:H3'	31:X:4:G:H21	1.45	0.81
34:b:2144:G:O2'	34:b:2147:A:N6	2.13	0.81
16:H:35:ILE:HD12	16:H:102:VAL:HG11	1.60	0.81
17:I:114:LYS:HB2	17:I:117:LEU:HD12	1.63	0.81
34:b:1277:G:C5'	45:o:20:MET:CE	2.59	0.80
34:b:1277:G:C4'	45:o:20:MET:HE1	2.12	0.80
42:l:38:ILE:HG12	42:l:61:VAL:HG22	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:l:61:VAL:HG23	42:l:87:LEU:CD1	2.12	0.79
11:C:69:THR:HG22	11:C:71:ARG:H	1.47	0.79
14:F:47:LEU:HD11	14:F:49:TYR:O	1.80	0.79
34:b:1276:A:O2'	45:o:20:MET:SD	2.40	0.79
31:X:15:G:H5'	31:X:16:U:H2'	1.63	0.79
42:l:61:VAL:CG2	42:l:87:LEU:HD11	2.12	0.79
32:Z:59:A:O2'	32:Z:61:U:OP2	2.01	0.79
11:C:110:LEU:HG	11:C:111:ASP:H	1.48	0.78
44:n:68:PHE:CD2	44:n:69:PRO:CD	2.67	0.78
9:A:546:A:H4'	9:A:548:G:H4'	1.66	0.77
34:b:1040:A:N6	34:b:1115:G:H1	1.82	0.77
34:b:1061:U:O2	34:b:1070:A:N6	2.17	0.77
9:A:1349:A:H1'	9:A:1374:A:H61	1.46	0.77
14:F:90:MET:SD	26:R:60:ARG:NH2	2.58	0.77
38:f:105:THR:O	38:f:105:THR:HG22	1.84	0.77
9:A:363:A:N6	20:L:26:CYS:SG	2.57	0.77
34:b:1277:G:C5'	45:o:20:MET:HE1	2.15	0.76
17:I:26:LYS:HE2	17:I:61:ASP:HB3	1.66	0.76
34:b:1439:A:H62	34:b:1552:A:H8	1.34	0.75
9:A:1441:A:H62	9:A:1461:G:H21	1.32	0.75
9:A:1009:U:H3	9:A:1020:G:H1	1.34	0.75
34:b:2134:A:OP2	34:b:2158:A:N6	2.20	0.74
46:p:40:ILE:HD13	46:p:47:VAL:HG22	1.70	0.74
34:b:1277:G:C4'	45:o:20:MET:CE	2.65	0.74
34:b:1753:G:N2	34:b:1756:G:OP2	2.20	0.74
9:A:625:U:H2'	9:A:626:G:H8	1.52	0.74
32:Y:33:U:H3	32:Y:39:A:H61	1.36	0.74
9:A:1055:A:O2'	11:C:155:ARG:NH1	2.21	0.74
31:X:54:U:H3	31:X:58:A:H62	1.34	0.74
15:G:30:MET:HE2	15:G:35:LYS:HG2	1.70	0.73
9:A:552:U:H2'	9:A:553:A:H8	1.53	0.73
34:b:858:G:OP1	55:y:78:LYS:NZ	2.20	0.73
17:I:51:LEU:HG	17:I:56:MET:HG3	1.69	0.73
34:b:1080:A:H8	34:b:1081:U:H4'	1.54	0.73
29:U:9:GLU:HG2	29:U:14:ALA:HB2	1.70	0.73
17:I:112:ARG:NH1	17:I:113:LYS:O	2.21	0.72
13:E:102:THR:O	13:E:121:ASN:ND2	2.22	0.72
9:A:392:C:OP2	24:P:8:ARG:NH2	2.23	0.72
9:A:477:C:H2'	9:A:478:A:C8	2.24	0.72
22:N:63:CYS:SG	22:N:65:GLN:NE2	2.63	0.72
9:A:1227:A:OP2	21:M:109:LYS:NZ	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:d:28:GLU:HG2	36:d:186:LEU:HD23	1.71	0.71
28:T:16:ALA:O	28:T:20:ASN:ND2	2.23	0.71
34:b:1433:A:H61	34:b:1560:G:H1	1.39	0.71
9:A:31:G:O2'	9:A:48:C:N4	2.24	0.71
32:Z:30:U:N3	32:Z:32:G:O6	2.24	0.70
4:4:22:LEU:HD11	50:t:23:LEU:HD11	1.73	0.70
9:A:1186:G:N2	22:N:100:TRP:OXT	2.24	0.70
9:A:1014:A:C8	27:S:33:TRP:CD1	2.78	0.70
38:f:142:ASP:H	38:f:145:LYS:HZ3	1.37	0.70
50:t:85:ILE:HB	56:z:137:VAL:HG23	1.73	0.70
36:d:11:MET:SD	36:d:25:THR:HG22	2.30	0.70
23:O:88:ARG:NH2	34:b:714:U:OP2	2.24	0.70
9:A:993:G:O2'	9:A:994:A:N7	2.23	0.70
17:I:38:PHE:O	17:I:44:ARG:NH1	2.25	0.70
32:Z:23:G:N7	32:Z:47:G:N2	2.30	0.70
9:A:518:C:H41	9:A:529:G:H3'	1.56	0.70
34:b:1482:G:O6	34:b:1508:A:N6	2.25	0.70
46:p:40:ILE:HD12	46:p:47:VAL:HG22	1.72	0.70
9:A:474:G:H2'	9:A:475:C:C6	2.27	0.69
12:D:14:GLU:OE1	12:D:62:ARG:NH1	2.25	0.69
24:P:39:PHE:HD1	24:P:50:THR:HB	1.58	0.69
9:A:148:G:H1	9:A:174:A:H61	1.38	0.69
34:b:1315:C:HO2'	34:b:1392:A:H8	1.38	0.69
9:A:1175:G:H2'	9:A:1176:A:H8	1.57	0.69
9:A:1405:G:O2'	9:A:1518:A:O2'	2.10	0.69
27:S:31:ARG:NH1	27:S:32:THR:O	2.25	0.69
34:b:956:G:N7	44:n:14:LYS:NZ	2.41	0.69
34:b:1056:G:O2'	34:b:1104:C:N4	2.25	0.69
18:J:5:ARG:HA	18:J:77:VAL:HA	1.75	0.68
34:b:1936:A:H2	34:b:1943:U:H5	1.40	0.68
34:b:2164:C:H42	34:b:2171:A:H2'	1.58	0.68
38:f:38:MET:SD	38:f:150:ARG:NH1	2.65	0.68
40:h:84:ALA:HB2	40:h:90:LEU:HD12	1.75	0.68
37:e:125:SER:O	37:e:137:LYS:NZ	2.25	0.68
34:b:1133:A:N6	34:b:2025:C:O2'	2.27	0.68
9:A:78:A:N6	9:A:88:U:O2'	2.26	0.68
34:b:281:C:H2'	34:b:282:A:C8	2.29	0.68
9:A:88:U:O2	9:A:90:C:N4	2.26	0.68
12:D:120:LYS:HA	12:D:130:ASN:OD1	1.94	0.68
32:Y:6:A:O2'	32:Y:7:U:O4'	2.12	0.68
34:b:1069:A:H1'	34:b:1096:A:H1'	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:b:1105:U:H2'	34:b:1106:G:C8	2.29	0.68
9:A:514:C:H2'	9:A:515:G:C8	2.28	0.67
31:X:26:A:H61	31:X:44:G:H1	1.41	0.67
34:b:886:A:N3	34:b:890:C:N4	2.41	0.67
23:O:73:ASP:HB3	23:O:76:ARG:HB2	1.76	0.67
9:A:673:A:H2'	9:A:674:G:C8	2.29	0.67
29:U:4:LYS:O	29:U:17:ARG:NH2	2.28	0.67
46:p:64:TYR:O	46:p:67:ASN:ND2	2.27	0.67
31:X:21:A:H2'	31:X:22:G:H8	1.58	0.67
34:b:878:A:H3'	34:b:879:G:H8	1.60	0.67
9:A:44:A:H2'	9:A:45:G:C8	2.30	0.67
28:T:43:LYS:HG3	28:T:86:ALA:HA	1.76	0.67
34:b:713:G:H21	34:b:718:A:H2	1.41	0.67
38:f:109:PRO:HA	38:f:114:PHE:HE2	1.58	0.67
9:A:1356:G:H2'	9:A:1357:A:H8	1.60	0.66
17:I:25:GLY:N	17:I:61:ASP:OD1	2.27	0.66
9:A:41:G:H2'	9:A:42:G:H8	1.60	0.66
9:A:73:C:H41	9:A:97:G:H1	1.43	0.66
9:A:1039:G:H2'	9:A:1040:U:C6	2.29	0.66
9:A:622:A:H5''	9:A:623:C:H5	1.60	0.66
35:c:122:ALA:HB3	35:c:130:LEU:HD21	1.78	0.66
9:A:1192:C:OP2	11:C:3:LYS:NZ	2.27	0.66
16:H:35:ILE:HD13	16:H:109:VAL:CG1	2.24	0.66
34:b:952:G:H21	34:b:2267:A:H2	1.44	0.66
37:e:146:VAL:HG12	37:e:147:LEU:N	2.10	0.66
9:A:1309:G:OP1	21:M:86:ARG:NH2	2.27	0.66
12:D:139:ASN:N	12:D:181:PHE:O	2.28	0.66
35:c:2:ALA:N	35:c:20:VAL:O	2.29	0.66
9:A:1405:G:HO2'	9:A:1518:A:HO2'	1.44	0.66
31:X:19:G:H5'	31:X:57:G:H21	1.60	0.66
31:X:48:C:H5''	31:X:49:G:H5''	1.77	0.66
34:b:2165:C:O2	34:b:2171:A:N6	2.29	0.66
9:A:745:G:H2'	9:A:746:A:H8	1.60	0.66
9:A:1107:C:OP2	11:C:171:ARG:NH2	2.29	0.66
9:A:1397:C:N4	54:x:22:A:OP2	2.28	0.66
12:D:18:LEU:CD1	12:D:20:LEU:HG	2.25	0.66
12:D:124:VAL:HG12	12:D:125:ASN:HD22	1.61	0.65
33:a:1:U:H2'	33:a:2:G:H8	1.61	0.65
9:A:193:C:H2'	9:A:194:C:C6	2.30	0.65
9:A:514:C:H2'	9:A:515:G:H8	1.60	0.65
9:A:1007:U:N3	9:A:1023:U:O2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:142:ARG:NH2	31:X:42:C:O5'	2.26	0.65
18:J:57:VAL:HA	18:J:59:LYS:HZ2	1.60	0.65
34:b:1277:G:O4'	45:o:20:MET:CE	2.42	0.65
34:b:1865:U:O2	34:b:1876:A:N6	2.30	0.65
34:b:1172:C:OP2	34:b:1174:U:N3	2.29	0.65
9:A:994:A:N1	9:A:1216:A:H4'	2.11	0.65
9:A:844:G:H2'	9:A:845:A:H2'	1.78	0.65
9:A:1320:C:H42	27:S:35:ARG:HG3	1.61	0.65
31:X:47:U:H4'	31:X:48:C:H5'	1.78	0.65
9:A:938:A:N3	9:A:1376:U:O2'	2.28	0.65
9:A:1218:C:H2'	9:A:1219:A:C8	2.31	0.65
34:b:1315:C:O2'	34:b:1392:A:H8	1.79	0.65
34:b:2189:U:H2'	34:b:2190:G:H8	1.62	0.65
9:A:92:U:H2'	9:A:93:U:C2	2.32	0.65
9:A:581:G:O3'	23:O:63:ARG:NH2	2.29	0.65
22:N:40:ARG:NH1	27:S:5:LYS:O	2.29	0.65
4:4:38:HIS:ND1	4:4:39:LEU:O	2.30	0.65
34:b:627:A:OP1	43:m:78:ARG:NH1	2.30	0.65
34:b:2133:G:H1'	34:b:2157:G:H1	1.62	0.65
9:A:93:U:H2'	9:A:94:G:H4'	1.79	0.64
18:J:6:ILE:HB	18:J:76:ILE:HG23	1.79	0.64
34:b:1532:A:N6	34:b:1540:G:O6	2.30	0.64
9:A:137:U:H3	9:A:226:G:H1	1.42	0.64
9:A:545:C:O3'	12:D:69:ARG:NH2	2.29	0.64
34:b:1789:A:OP2	35:c:221:ARG:NH1	2.30	0.64
16:H:33:VAL:O	16:H:37:ASN:ND2	2.31	0.64
17:I:34:LEU:HD11	17:I:48:ARG:HH22	1.63	0.64
34:b:63:A:O2'	51:u:77:ARG:NH1	2.30	0.64
34:b:1428:C:H42	34:b:1570:A:H2	1.46	0.64
29:U:30:GLU:OE1	29:U:33:ARG:NH2	2.29	0.64
2:1:52:ARG:NH1	34:b:77:G:OP1	2.30	0.64
39:g:105:LEU:HB2	39:g:113:VAL:HG23	1.78	0.64
9:A:68:G:H22	9:A:101:A:H2	1.46	0.64
19:K:110:THR:HG23	29:U:2:VAL:HG22	1.79	0.64
24:P:9:HIS:N	24:P:16:PHE:O	2.30	0.64
34:b:2102:G:N2	34:b:2188:U:H3	1.94	0.64
9:A:447:G:O2'	9:A:487:A:N6	2.27	0.63
31:X:68:C:N3	31:X:69:C:N4	2.45	0.63
34:b:2148:G:H2'	34:b:2149:U:C6	2.32	0.63
2:1:23:ARG:O	2:1:27:ASN:ND2	2.30	0.63
35:c:6:CYS:SG	35:c:13:ARG:NH2	2.71	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:166:U:H2'	9:A:167:A:C8	2.33	0.63
33:a:66:A:OP2	33:a:108:A:N6	2.30	0.63
15:G:112:ASP:HB3	15:G:118:ARG:HG2	1.79	0.63
9:A:674:G:H2'	9:A:675:A:H8	1.64	0.63
10:B:30:ILE:HD11	10:B:38:HIS:HB3	1.79	0.63
19:K:28:ASN:OD1	19:K:29:THR:N	2.32	0.63
34:b:1352:U:O2'	34:b:1570:A:H8	1.81	0.63
12:D:18:LEU:HD13	12:D:20:LEU:CG	2.26	0.63
34:b:2255:G:N2	55:y:8:GLY:O	2.25	0.63
34:b:2303:G:O2'	38:f:121:SER:O	2.15	0.63
4:4:25:VAL:HG12	4:4:27:SER:H	1.63	0.63
9:A:236:A:H2'	9:A:237:G:H8	1.64	0.63
9:A:1038:C:H2'	9:A:1039:G:C8	2.34	0.63
15:G:15:PRO:HG3	17:I:42:THR:HG22	1.80	0.63
34:b:1055:G:N2	34:b:1084:A:O2'	2.32	0.63
40:h:68:ARG:NH2	40:h:109:GLU:O	2.32	0.63
14:F:17:GLN:NE2	40:h:87:GLU:OE1	2.31	0.62
18:J:52:LEU:O	22:N:80:ARG:NH1	2.32	0.62
33:a:44:G:H21	33:a:47:C:H5	1.46	0.62
34:b:1039:A:H61	34:b:1116:G:H1	1.45	0.62
29:U:30:GLU:OE2	29:U:34:ARG:NE	2.31	0.62
40:h:51:ARG:HD3	40:h:54:LEU:HD12	1.81	0.62
6:6:44:VAL:HG23	6:6:45:SER:H	1.64	0.62
22:N:2:LYS:O	22:N:6:LYS:NZ	2.30	0.62
34:b:1649:G:O2'	45:o:106:ASP:OD2	2.17	0.62
9:A:384:G:H2'	9:A:385:C:C6	2.34	0.62
9:A:462:G:H2'	9:A:463:U:H5	1.63	0.62
9:A:41:G:H2'	9:A:42:G:C8	2.35	0.62
34:b:1509:A:O2'	34:b:1510:G:O4'	2.18	0.62
9:A:462:G:H2'	9:A:463:U:C5	2.34	0.62
13:E:64:GLU:OE1	13:E:64:GLU:N	2.29	0.62
9:A:691:G:O6	19:K:56:LYS:NZ	2.33	0.62
21:M:15:VAL:HG21	21:M:40:GLU:HB3	1.81	0.62
24:P:6:LEU:HD12	24:P:71:VAL:HG21	1.82	0.62
9:A:1013:G:N2	9:A:1016:A:OP2	2.33	0.62
16:H:76:ARG:NH2	16:H:78:SER:O	2.33	0.62
42:l:107:LEU:C	42:l:116:ILE:HD11	2.24	0.62
34:b:2118:U:O2	34:b:2145:C:N4	2.33	0.61
34:b:2902:C:N4	34:b:2903:U:O4	2.33	0.61
40:h:135:HIS:HB3	40:h:138:VAL:HG22	1.80	0.61
40:h:104:THR:HG22	40:h:109:GLU:HA	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:u:54:GLU:OE1	51:u:92:ASN:ND2	2.32	0.61
12:D:96:ARG:HG3	12:D:133:SER:HA	1.82	0.61
34:b:2115:G:H4'	34:b:2166:U:H4'	1.81	0.61
56:z:129:ARG:HA	56:z:132:ASN:HB2	1.82	0.61
9:A:407:U:H2'	9:A:408:A:C8	2.35	0.61
16:H:11:THR:HG22	16:H:14:ARG:HH12	1.65	0.61
29:U:38:GLU:OE1	29:U:38:GLU:N	2.33	0.61
35:c:199:GLU:OE1	35:c:199:GLU:N	2.30	0.61
24:P:18:GLN:HA	24:P:38:PHE:HA	1.82	0.61
27:S:28:LYS:HD2	27:S:29:PRO:HD2	1.82	0.61
34:b:310:A:O2'	34:b:311:A:H2'	2.00	0.61
9:A:380:G:N2	9:A:383:A:OP2	2.34	0.61
11:C:110:LEU:HG	11:C:111:ASP:N	2.14	0.61
14:F:47:LEU:HD13	14:F:49:TYR:O	2.00	0.61
28:T:24:ARG:O	28:T:28:ARG:HG2	2.01	0.61
31:X:14:A:C2	31:X:15:G:H1'	2.36	0.61
34:b:2790:U:H2'	34:b:2893:A:N7	2.16	0.61
17:I:5:TYR:HB2	17:I:20:ILE:HG22	1.83	0.61
22:N:65:GLN:HE22	22:N:82:LYS:HG3	1.66	0.61
9:A:589:U:H3	9:A:650:G:H1	1.49	0.61
25:Q:10:ARG:NH1	25:Q:56:ASP:O	2.34	0.61
36:d:11:MET:SD	36:d:25:THR:CG2	2.89	0.61
46:p:18:LEU:HD21	46:p:25:ARG:HB3	1.82	0.61
31:X:49:G:H2'	31:X:50:C:C6	2.35	0.61
32:Y:77:A:N6	55:y:2:ALA:O	2.20	0.61
35:c:71:LYS:O	35:c:118:SER:OG	2.19	0.61
9:A:1179:A:H4'	17:I:104:THR:HA	1.82	0.60
9:A:1219:A:H2'	9:A:1220:G:H8	1.66	0.60
13:E:61:LYS:O	13:E:65:LYS:NZ	2.31	0.60
37:e:5:LEU:HD12	37:e:10:SER:HB3	1.82	0.60
53:w:76:ASP:OD1	53:w:77:VAL:N	2.34	0.60
9:A:1323:G:H2'	9:A:1324:A:H8	1.65	0.60
12:D:90:LEU:HD13	12:D:93:LEU:HD12	1.83	0.60
34:b:2681:C:H5'	36:d:11:MET:CE	2.31	0.60
9:A:977:A:N6	9:A:1224:U:OP1	2.29	0.60
14:F:11:HIS:HB3	14:F:14:GLN:HG2	1.84	0.60
9:A:958:A:H62	27:S:54:ARG:HH21	1.47	0.60
9:A:976:G:N2	9:A:1362:A:HO2'	2.00	0.60
19:K:71:ASP:HA	19:K:74:LYS:HD2	1.83	0.60
9:A:1222:G:H5''	27:S:77:ARG:HE	1.66	0.60
12:D:99:ASN:OD1	12:D:110:ARG:NH2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:I:56:MET:HG2	17:I:57:VAL:H	1.67	0.60
26:R:32:ILE:HD11	26:R:58:ILE:CD1	2.28	0.60
9:A:82:G:N7	9:A:83:C:N4	2.50	0.60
9:A:222:C:H2'	9:A:223:A:H8	1.67	0.60
9:A:1323:G:H2'	9:A:1324:A:C8	2.36	0.60
9:A:236:A:H2'	9:A:237:G:C8	2.37	0.60
9:A:1003:G:H21	9:A:1037:C:H2'	1.67	0.60
13:E:81:GLN:HA	13:E:97:PRO:HG2	1.83	0.60
31:X:9:A:OP2	31:X:13:C:N4	2.35	0.60
34:b:2136:G:H22	34:b:2156:G:H1	1.49	0.60
9:A:269:C:H2'	9:A:270:A:C8	2.36	0.60
11:C:160:GLU:HG3	54:x:23:A:H5''	1.83	0.60
14:F:38:ARG:HD2	14:F:101:PRO:HD3	1.82	0.60
31:X:56:C:O2'	31:X:57:G:O4'	2.19	0.60
34:b:2305:U:H3	38:f:151:GLY:HA3	1.67	0.60
34:b:2683:C:O2	42:l:70:ARG:NH2	2.34	0.60
9:A:438:U:O2'	9:A:493:A:N6	2.35	0.60
9:A:1027:C:N3	9:A:1035:A:N6	2.50	0.60
28:T:51:ASN:HA	28:T:54:GLN:HE22	1.66	0.60
39:g:31:GLY:H	39:g:79:VAL:HG13	1.66	0.60
9:A:40:C:H2'	9:A:41:G:H8	1.67	0.60
9:A:954:G:N2	9:A:1227:A:H62	1.94	0.60
9:A:1357:A:O2'	9:A:1358:U:OP1	2.20	0.60
9:A:1424:U:H3	9:A:1476:A:H62	1.50	0.60
10:B:10:LYS:HD2	10:B:12:GLY:H	1.67	0.60
11:C:30:ASP:N	11:C:30:ASP:OD1	2.35	0.60
34:b:2188:U:H2'	34:b:2189:U:C6	2.37	0.60
9:A:486:U:H2'	9:A:487:A:H8	1.66	0.59
31:X:22:G:H2'	31:X:23:A:H8	1.67	0.59
9:A:426:U:O2	12:D:39:GLN:NE2	2.36	0.59
18:J:10:LEU:HB2	18:J:72:ARG:HB2	1.84	0.59
32:Z:31:C:N4	32:Z:42:A:O2'	2.35	0.59
34:b:1057:A:N6	34:b:1081:U:O2	2.36	0.59
35:c:141:VAL:HG11	35:c:190:ALA:HB1	1.84	0.59
44:n:106:ASP:OD1	44:n:107:GLY:N	2.34	0.59
9:A:321:A:H2'	9:A:322:C:H6	1.68	0.59
9:A:475:C:H2'	9:A:476:U:H6	1.66	0.59
13:E:95:MET:HE1	13:E:114:LEU:HD21	1.84	0.59
9:A:981:U:O2'	22:N:60:ARG:NH1	2.34	0.59
19:K:12:ARG:O	19:K:14:GLN:NE2	2.35	0.59
32:Z:57:C:OP2	44:n:59:ARG:NH2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:b:845:A:N6	34:b:932:U:H3	2.01	0.59
9:A:308:C:H2'	9:A:309:A:H8	1.68	0.59
9:A:1317:C:H4'	22:N:47:LEU:HG	1.84	0.59
9:A:1373:G:H5''	15:G:35:LYS:HE2	1.83	0.59
15:G:112:ASP:OD1	15:G:113:LYS:N	2.34	0.59
34:b:359:G:H2'	34:b:360:U:C6	2.38	0.59
47:q:2:SER:OG	47:q:3:ASN:N	2.35	0.59
34:b:704:G:O2'	34:b:726:G:N2	2.28	0.59
34:b:882:G:N2	34:b:895:U:O2'	2.32	0.59
34:b:955:U:OP1	44:n:86:LYS:NZ	2.35	0.59
9:A:1374:A:O3'	15:G:27:ASN:ND2	2.35	0.59
34:b:1858:A:N6	34:b:1884:G:O2'	2.36	0.59
9:A:580:C:O3'	23:O:57:ARG:NH1	2.36	0.59
15:G:14:ASP:HB2	15:G:18:GLY:H	1.68	0.59
40:h:2:GLN:HE21	40:h:18:GLN:HE21	1.51	0.59
9:A:86:G:OP1	9:A:86:G:N2	2.36	0.59
9:A:1250:A:H2'	9:A:1251:A:C8	2.37	0.59
13:E:35:LEU:HD21	13:E:136:VAL:HG21	1.84	0.59
32:Y:69:C:H2'	32:Y:70:A:H8	1.67	0.59
34:b:1021:A:H62	34:b:1141:U:H3	1.51	0.59
9:A:779:C:H1'	19:K:121:ARG:NH2	2.18	0.59
12:D:104:MET:HG2	12:D:170:LEU:HD11	1.83	0.59
2:1:5:GLU:OE1	2:1:5:GLU:N	2.37	0.58
23:O:32:THR:O	23:O:36:ASN:ND2	2.36	0.58
34:b:845:A:H61	34:b:932:U:H3	1.51	0.58
44:n:66:ARG:NH2	44:n:104:GLU:OE2	2.36	0.58
9:A:1151:A:H5'	18:J:43:PRO:HA	1.85	0.58
12:D:96:ARG:HB3	12:D:99:ASN:HB3	1.84	0.58
13:E:40:ASP:HB2	13:E:44:ARG:HB2	1.86	0.58
34:b:856:G:H2'	34:b:857:G:C8	2.39	0.58
9:A:486:U:H2'	9:A:487:A:C8	2.38	0.58
9:A:582:C:OP2	9:A:758:C:N4	2.28	0.58
34:b:389:G:C8	34:b:2413:G:H4'	2.38	0.58
35:c:145:GLU:HB2	35:c:188:CYS:HB2	1.84	0.58
34:b:1853:A:H2'	34:b:1854:A:C8	2.37	0.58
36:d:103:ASP:OD1	36:d:103:ASP:N	2.36	0.58
9:A:332:G:OP2	28:T:1:ALA:N	2.34	0.58
34:b:2180:U:O2'	34:b:2181:U:O5'	2.20	0.58
2:1:10:SER:N	2:1:13:GLU:OE2	2.35	0.58
9:A:229:U:O2'	24:P:23:ASP:OD2	2.21	0.58
9:A:1219:A:H2'	9:A:1220:G:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:76:SER:O	10:B:92:ASN:ND2	2.35	0.58
22:N:5:MET:SD	22:N:6:LYS:N	2.76	0.58
22:N:64:ARG:NH2	22:N:76:PHE:O	2.36	0.58
34:b:1802:A:H2'	34:b:1803:A:C8	2.39	0.58
42:l:35:VAL:HG21	42:l:69:VAL:HG21	1.85	0.58
9:A:473:U:H2'	9:A:474:G:C8	2.39	0.58
11:C:39:ARG:NH1	11:C:54:ILE:O	2.37	0.58
34:b:2882:A:OP1	45:o:96:ARG:NH1	2.37	0.58
38:f:64:LYS:HD3	38:f:64:LYS:H	1.68	0.58
40:h:47:PHE:HD1	40:h:50:ARG:HH21	1.51	0.58
9:A:274:A:H4'	9:A:275:G:H5'	1.84	0.58
9:A:613:C:H2'	9:A:614:C:C6	2.38	0.58
9:A:1423:G:OP1	42:l:49:ARG:NH2	2.35	0.58
15:G:68:VAL:HG13	15:G:137:ARG:HG2	1.85	0.58
17:I:105:ARG:NH1	17:I:106:ASP:O	2.36	0.58
26:R:35:SER:HA	26:R:71:ASP:HB2	1.86	0.58
28:T:74:HIS:O	28:T:78:LEU:HG	2.03	0.58
31:X:36:C:H5	54:x:12:G:H22	1.49	0.58
34:b:74:A:O2'	34:b:88:G:OP2	2.21	0.58
9:A:222:C:H2'	9:A:223:A:C8	2.38	0.58
9:A:1038:C:H2'	9:A:1039:G:H8	1.68	0.58
20:L:13:ARG:HE	20:L:14:LYS:H	1.51	0.58
34:b:307:G:N1	34:b:310:A:OP2	2.35	0.58
34:b:870:U:OP1	44:n:6:ARG:NH1	2.36	0.58
34:b:1276:A:O2'	45:o:20:MET:CE	2.52	0.58
9:A:1015:G:H2'	9:A:1016:A:C8	2.39	0.58
47:q:68:GLU:OE1	47:q:68:GLU:N	2.37	0.58
2:l:10:SER:OG	2:l:13:GLU:OE1	2.22	0.57
9:A:1441:A:N6	9:A:1461:G:H21	2.00	0.57
34:b:1509:A:O2'	34:b:1510:G:O5'	2.22	0.57
1:0:42:SER:OG	1:0:43:GLU:OE1	2.22	0.57
9:A:475:C:H2'	9:A:476:U:C6	2.39	0.57
14:F:30:THR:HA	14:F:34:GLY:H	1.69	0.57
9:A:113:G:N3	9:A:353:A:O2'	2.36	0.57
11:C:19:SER:OG	22:N:91:GLU:O	2.18	0.57
46:p:61:GLN:N	46:p:61:GLN:OE1	2.37	0.57
51:u:91:GLN:NE2	51:u:92:ASN:OD1	2.37	0.57
3:2:40:ASP:OD2	3:2:45:ARG:NH2	2.34	0.57
9:A:424:G:H2'	9:A:425:G:H8	1.69	0.57
9:A:483:C:H2'	9:A:484:G:C8	2.39	0.57
9:A:1086:U:H3	9:A:1099:G:H22	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:H:35:ILE:CD1	16:H:109:VAL:CG1	2.80	0.57
18:J:10:LEU:O	18:J:72:ARG:N	2.31	0.57
23:O:12:SER:OG	23:O:13:GLU:OE1	2.21	0.57
34:b:487:C:O2'	50:t:52:GLU:OE1	2.22	0.57
9:A:147:G:H2'	9:A:148:G:C8	2.39	0.57
9:A:382:A:O2'	9:A:383:A:O4'	2.14	0.57
9:A:714:G:H2'	9:A:715:A:C8	2.40	0.57
31:X:15:G:H22	31:X:48:C:H42	1.53	0.57
31:X:18:G:O2'	31:X:57:G:N2	2.35	0.57
9:A:263:A:H2'	9:A:264:C:C6	2.40	0.57
9:A:792:A:H4'	9:A:793:U:H5'	1.86	0.57
9:A:1299:A:C8	9:A:1301:U:H1'	2.40	0.57
17:I:107:ALA:O	17:I:109:GLN:NE2	2.38	0.57
31:X:3:G:H3'	31:X:4:G:N2	2.19	0.57
34:b:45:G:H5'	34:b:46:G:OP1	2.05	0.57
34:b:1051:G:H4'	34:b:1052:C:OP1	2.04	0.57
34:b:2159:G:H2'	34:b:2160:C:C6	2.40	0.57
42:l:91:SER:OG	42:l:92:GLU:N	2.38	0.57
16:H:28:SER:HB3	16:H:58:LEU:HB2	1.85	0.57
21:M:46:GLU:OE1	21:M:46:GLU:N	2.33	0.57
31:X:16:U:OP1	31:X:59:G:N2	2.37	0.57
33:a:1:U:H2'	33:a:2:G:C8	2.40	0.57
56:z:127:ASN:ND2	56:z:131:MET:SD	2.78	0.57
9:A:565:U:H3'	9:A:566:G:H2'	1.86	0.57
9:A:958:A:N7	27:S:54:ARG:NH2	2.53	0.57
16:H:87:ARG:NH1	16:H:89:ASP:OD1	2.37	0.57
34:b:279:A:C4	34:b:280:U:H1'	2.39	0.57
34:b:1862:G:H1	34:b:1880:U:H5	1.53	0.57
9:A:1107:C:H5'	11:C:168:ARG:HH22	1.69	0.57
13:E:86:GLY:HA3	13:E:141:ASP:HB3	1.87	0.57
28:T:48:LYS:HA	28:T:51:ASN:HD21	1.69	0.57
28:T:52:GLU:N	28:T:52:GLU:OE1	2.37	0.57
34:b:511:U:O2'	34:b:512:G:OP1	2.22	0.57
9:A:1251:A:H2'	9:A:1252:A:C8	2.40	0.57
16:H:94:VAL:HG11	16:H:100:ILE:C	2.30	0.57
28:T:47:GLN:O	28:T:51:ASN:ND2	2.37	0.57
32:Z:6:A:H5'	32:Z:16:C:H42	1.70	0.57
34:b:2112:G:H5'	34:b:2113:U:C5	2.40	0.57
38:f:24:SER:HB3	38:f:27:GLN:HB2	1.86	0.57
52:v:77:THR:O	52:v:79:LYS:NZ	2.38	0.57
9:A:444:G:N1	9:A:491:G:O6	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:T:19:HIS:O	28:T:23:ARG:HG2	2.04	0.56
32:Y:18:U:O2'	32:Y:19:G:O5'	2.23	0.56
34:b:1079:C:H41	34:b:1088:A:H5'	1.70	0.56
9:A:263:A:OP1	28:T:73:ARG:NH1	2.38	0.56
9:A:1328:C:H5''	21:M:27:THR:HG21	1.87	0.56
12:D:125:ASN:ND2	12:D:140:ASP:OD1	2.37	0.56
21:M:26:LYS:O	21:M:30:LYS:HG2	2.05	0.56
24:P:19:VAL:N	24:P:37:GLY:O	2.38	0.56
25:Q:13:SER:OG	25:Q:21:VAL:N	2.37	0.56
34:b:27:G:O2'	34:b:28:A:O5'	2.24	0.56
34:b:2161:C:H4'	34:b:2172:U:OP2	2.05	0.56
34:b:2306:C:OP2	34:b:2307:G:O2'	2.18	0.56
34:b:2313:C:H2'	34:b:2314:A:H8	1.71	0.56
34:b:2315:G:N3	38:f:125:ARG:NH2	2.53	0.56
39:g:166:ASP:N	39:g:166:ASP:OD1	2.38	0.56
9:A:1316:G:N1	9:A:1319:A:OP2	2.36	0.56
12:D:101:VAL:HG23	12:D:113:ALA:HB1	1.87	0.56
15:G:26:VAL:HG21	15:G:39:GLU:HG3	1.87	0.56
18:J:66:GLU:OE1	22:N:98:ALA:N	2.38	0.56
34:b:826:U:O2'	43:m:53:GLY:HA3	2.05	0.56
34:b:2773:C:OP1	36:d:169:ARG:NH1	2.38	0.56
9:A:411:A:N3	9:A:430:A:N6	2.54	0.56
9:A:463:U:H2'	9:A:464:U:C6	2.40	0.56
12:D:12:ARG:HD3	12:D:37:PRO:HB3	1.87	0.56
21:M:71:GLU:HA	21:M:74:MET:HG3	1.86	0.56
24:P:69:ASP:OD1	24:P:69:ASP:N	2.34	0.56
32:Y:77:A:O3'	56:z:162:PRO:CA	2.54	0.56
34:b:883:G:O2'	34:b:884:U:O5'	2.21	0.56
21:M:15:VAL:O	21:M:29:SER:OG	2.23	0.56
22:N:63:CYS:HB3	22:N:67:GLY:H	1.70	0.56
34:b:2125:G:O2'	34:b:2173:A:N1	2.38	0.56
34:b:2328:A:H2'	34:b:2329:U:C6	2.41	0.56
39:g:155:GLU:OE1	39:g:158:LYS:N	2.37	0.56
56:z:152[A]:GLY:C	56:z:154[A]:TRP:H	2.11	0.56
9:A:1303:C:H2'	9:A:1304:G:O4'	2.06	0.56
17:I:3:ASN:HB3	17:I:5:TYR:HE1	1.71	0.56
32:Y:77:A:O3'	56:z:162:PRO:O	2.21	0.56
34:b:278:A:O2'	34:b:279:A:N7	2.38	0.56
34:b:2154:A:H2'	34:b:2155:U:C6	2.41	0.56
9:A:2:A:H1'	9:A:613:C:O2'	2.06	0.56
9:A:337:G:H2'	9:A:338:A:H8	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:K:16:SER:HA	19:K:78:ILE:HA	1.88	0.56
9:A:427:U:OP1	12:D:12:ARG:NH1	2.39	0.56
9:A:955:U:O2'	27:S:80:ARG:NH2	2.38	0.56
9:A:1305:G:N2	9:A:1332:A:OP2	2.37	0.56
34:b:2858:C:O2'	34:b:2859:G:O5'	2.22	0.56
9:A:600:A:P	16:H:87:ARG:HB2	2.46	0.56
34:b:1114:C:H2'	34:b:1115:G:C8	2.41	0.56
34:b:1339:G:H5''	51:u:19:LYS:HD3	1.88	0.56
9:A:219:U:H2'	9:A:220:G:C8	2.40	0.55
9:A:1312:G:H5'	27:S:4:LEU:HD21	1.88	0.55
9:A:1357:A:H2'	9:A:1358:U:C6	2.41	0.55
17:I:20:ILE:HD11	17:I:60:LEU:HD11	1.87	0.55
28:T:14:GLU:HA	28:T:17:ARG:HD3	1.87	0.55
34:b:404:A:N6	34:b:421:C:O2'	2.39	0.55
34:b:2848:G:O2'	34:b:2849:U:O5'	2.23	0.55
38:f:40:VAL:HG21	38:f:50:LEU:HD23	1.87	0.55
9:A:1152:A:OP1	18:J:70:HIS:ND1	2.39	0.55
9:A:1492:A:H5''	20:L:43:LYS:HD2	1.88	0.55
14:F:14:GLN:HB3	14:F:17:GLN:NE2	2.21	0.55
21:M:45:SER:OG	21:M:46:GLU:OE1	2.24	0.55
26:R:32:ILE:CD1	26:R:58:ILE:HD12	2.30	0.55
34:b:2302:U:O2'	38:f:123:ASP:O	2.23	0.55
5:5:6:ARG:NH1	34:b:2285:C:OP2	2.33	0.55
9:A:197:A:N1	9:A:220:G:O2'	2.37	0.55
15:G:48:THR:HA	15:G:51:GLN:HE22	1.71	0.55
18:J:49:PHE:HB2	18:J:65:TYR:HB2	1.89	0.55
19:K:92:ARG:HH12	29:U:27:VAL:HG21	1.72	0.55
32:Z:5:G:H2'	32:Z:6:A:N3	2.21	0.55
34:b:1055:G:O2'	34:b:1056:G:O5'	2.23	0.55
34:b:2186:G:H2'	34:b:2187:U:C5	2.41	0.55
42:l:65:THR:HG22	42:l:67:LYS:H	1.72	0.55
51:u:17:SER:OG	51:u:18:GLU:N	2.39	0.55
5:5:7:GLU:N	5:5:7:GLU:OE1	2.39	0.55
11:C:10:ARG:NH2	11:C:176:THR:O	2.32	0.55
17:I:29:ILE:HG23	17:I:64:ILE:HG13	1.88	0.55
34:b:1854:A:H62	34:b:1888:G:H8	1.53	0.55
38:f:34:ILE:HG12	38:f:96:MET:HE2	1.88	0.55
40:h:47:PHE:HA	40:h:50:ARG:HE	1.71	0.55
9:A:405:U:OP2	12:D:2:ARG:NH1	2.39	0.55
34:b:740:C:H5	34:b:757:G:H22	1.54	0.55
34:b:1485:U:H2'	34:b:1486:U:H6	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:439:U:OP1	12:D:120:LYS:NZ	2.32	0.55
9:A:1060:U:OP1	22:N:84:ARG:NH2	2.39	0.55
11:C:111:ASP:O	11:C:114:LEU:N	2.39	0.55
11:C:130:ARG:NH2	11:C:167:TYR:OH	2.32	0.55
32:Y:63:C:H2'	32:Y:64:U:C6	2.41	0.55
34:b:878:A:N6	34:b:900:A:OP1	2.39	0.55
34:b:2175:C:H3'	34:b:2176:A:H2	1.71	0.55
9:A:131:A:H2'	9:A:132:C:C6	2.42	0.55
25:Q:20:ILE:HG13	25:Q:45:VAL:HB	1.89	0.55
31:X:36:C:H41	54:x:12:G:H1	1.55	0.55
32:Y:69:C:H2'	32:Y:70:A:C8	2.42	0.55
34:b:1070:A:OP2	34:b:1075:C:N4	2.40	0.55
9:A:636:U:H2'	9:A:637:C:C6	2.42	0.55
9:A:1492:A:H2'	9:A:1493:A:C8	2.41	0.55
35:c:232:HIS:HA	35:c:242:LYS:HE3	1.88	0.55
1:0:37:ARG:HA	1:0:48:THR:HA	1.89	0.55
1:0:61:LYS:NZ	34:b:372:G:O4'	2.40	0.55
9:A:337:G:H2'	9:A:338:A:C8	2.42	0.55
9:A:429:U:H5'	12:D:8:LEU:HD12	1.88	0.55
10:B:60:ALA:HB3	10:B:223:GLY:HA3	1.89	0.55
32:Y:20:G:O6	38:f:80:ARG:NH2	2.40	0.55
32:Z:19:G:O2'	32:Z:58:G:N2	2.32	0.55
34:b:1534:U:N3	34:b:1537:G:O6	2.39	0.55
9:A:49:U:H3	9:A:362:G:H1'	1.72	0.55
9:A:1377:A:OP1	15:G:91:ARG:NH2	2.39	0.55
13:E:12:GLU:HB2	13:E:63:MET:HE1	1.89	0.55
13:E:53:ARG:HH11	13:E:54:GLU:HB3	1.71	0.55
24:P:68:SER:OG	24:P:69:ASP:OD1	2.25	0.55
9:A:745:G:H2'	9:A:746:A:C8	2.40	0.54
58:Z:101:PRO:HG2	56:z:160:ARG:HG2	1.88	0.54
34:b:1042:G:H1	34:b:1113:U:H3	1.55	0.54
34:b:2484:G:OP1	44:n:44:ARG:NH1	2.40	0.54
41:k:88:THR:OG1	41:k:90:GLU:OE1	2.22	0.54
11:C:78:LYS:HD2	11:C:79:LYS:HB2	1.89	0.54
34:b:2137:U:H5''	34:b:2138:G:C8	2.42	0.54
39:g:52:PHE:HE1	39:g:72:LEU:HD12	1.71	0.54
22:N:65:GLN:HG3	22:N:78:LEU:HD11	1.89	0.54
34:b:172:A:H2'	34:b:173:A:C8	2.41	0.54
34:b:445:C:OP1	48:r:2:ALA:N	2.39	0.54
34:b:881:G:H3'	34:b:882:G:H8	1.73	0.54
34:b:2136:G:N2	34:b:2156:G:H22	2.04	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:t:77:ASP:N	50:t:77:ASP:OD1	2.37	0.54
14:F:23:GLU:OE1	14:F:23:GLU:N	2.40	0.54
34:b:2291:U:H2'	34:b:2292:U:C6	2.43	0.54
9:A:542:G:O3'	12:D:13:ARG:NH2	2.41	0.54
10:B:65:LYS:HG3	10:B:89:PHE:HE2	1.73	0.54
15:G:110:ARG:NH2	15:G:121:ASN:OD1	2.37	0.54
17:I:111:GLU:OE1	17:I:111:GLU:N	2.40	0.54
34:b:752:A:N1	56:z:151[A]:LYS:HE2	2.22	0.54
34:b:1149:G:H2'	34:b:1150:C:C6	2.43	0.54
37:e:146:VAL:CG1	37:e:147:LEU:N	2.70	0.54
1:0:59:ILE:HD13	1:0:67:VAL:HG21	1.89	0.54
9:A:184:G:H2'	9:A:185:U:C6	2.43	0.54
9:A:878:A:OP1	16:H:79:ARG:NH1	2.40	0.54
9:A:1397:C:OP2	13:E:28:ARG:NH2	2.33	0.54
16:H:11:THR:O	16:H:15:ASN:ND2	2.41	0.54
34:b:475:C:O2	34:b:479:A:N6	2.41	0.54
37:e:7:ASP:OD1	37:e:7:ASP:N	2.41	0.54
9:A:192:A:H2'	9:A:193:C:C6	2.43	0.54
9:A:269:C:H2'	9:A:270:A:H8	1.73	0.54
11:C:177:LEU:HD23	11:C:177:LEU:H	1.73	0.54
15:G:13:PRO:HB2	15:G:18:GLY:HA2	1.89	0.54
32:Y:16:C:O2'	32:Y:61:U:O3'	2.21	0.54
40:h:15:LEU:HD21	40:h:54:LEU:HD13	1.89	0.54
9:A:494:G:C8	9:A:496:A:H1'	2.43	0.54
20:L:101:LEU:HD23	20:L:101:LEU:H	1.73	0.54
9:A:673:A:H2'	9:A:674:G:H8	1.72	0.54
9:A:1464:U:H2'	9:A:1465:A:H8	1.72	0.54
10:B:83:ALA:HA	10:B:88:GLN:HG2	1.90	0.54
12:D:2:ARG:HG2	12:D:4:LEU:HG	1.90	0.54
34:b:1936:A:H2	34:b:1943:U:C5	2.23	0.54
2:1:30:MET:HE3	51:u:14:PRO:HD3	1.89	0.53
16:H:4:ASP:OD2	16:H:76:ARG:NH1	2.41	0.53
34:b:534:U:O2'	48:r:49:ASP:OD2	2.15	0.53
34:b:1089:A:H1'	34:b:1090:A:N1	2.23	0.53
34:b:2109:U:O2	34:b:2180:U:N3	2.40	0.53
38:f:105:THR:O	38:f:105:THR:CG2	2.55	0.53
39:g:137:ASP:OD1	39:g:138:LYS:N	2.41	0.53
42:l:4:GLU:OE1	42:l:4:GLU:N	2.40	0.53
9:A:1073:U:O2	10:B:102:ASN:ND2	2.35	0.53
14:F:3:HIS:ND1	14:F:65:GLU:OE2	2.41	0.53
14:F:40:GLU:OE2	14:F:42:TRP:NE1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:T:77:ASN:O	28:T:81:GLN:NE2	2.42	0.53
34:b:1762:A:O2'	34:b:1763:G:OP1	2.26	0.53
9:A:260:G:H2'	9:A:261:U:C6	2.44	0.53
12:D:18:LEU:CD1	12:D:20:LEU:HB2	2.39	0.53
14:F:49:TYR:HB3	26:R:73:HIS:CE1	2.44	0.53
18:J:35:GLN:OE1	18:J:35:GLN:N	2.42	0.53
30:V:19:ILE:HG13	30:V:20:ALA:H	1.74	0.53
31:X:70:C:H2'	31:X:71:G:C8	2.43	0.53
34:b:1056:G:H2'	34:b:1102:C:N4	2.24	0.53
38:f:7:TYR:H	38:f:7:TYR:HD1	1.54	0.53
2:1:20:ASN:O	2:1:24:GLU:HG2	2.08	0.53
21:M:68:LEU:HA	21:M:71:GLU:CD	2.34	0.53
52:v:101:GLU:OE1	52:v:101:GLU:N	2.42	0.53
9:A:166:U:H2'	9:A:167:A:H8	1.72	0.53
9:A:1187:G:O2'	9:A:1188:A:OP1	2.23	0.53
9:A:1307:U:O4	9:A:1331:G:N2	2.41	0.53
10:B:85:SER:OG	10:B:88:GLN:NE2	2.42	0.53
32:Y:17:C:OP2	32:Y:18:U:O2'	2.19	0.53
34:b:1779:U:H5	34:b:1784:A:N7	2.06	0.53
34:b:2130:U:N3	34:b:2158:A:OP1	2.40	0.53
35:c:141:VAL:CG1	35:c:190:ALA:HB1	2.38	0.53
9:A:976:G:H1	9:A:1362:A:HO2'	1.53	0.53
13:E:106:ALA:O	13:E:111:ARG:NH2	2.41	0.53
26:R:12:PHE:O	26:R:17:VAL:N	2.41	0.53
29:U:28:LEU:HD23	29:U:28:LEU:H	1.74	0.53
33:a:60:C:H2'	33:a:61:G:H8	1.74	0.53
34:b:1475:G:H1'	34:b:1476:U:H5	1.74	0.53
34:b:2305:U:H5''	38:f:131:GLY:HA3	1.91	0.53
40:h:9:VAL:HB	40:h:12:LEU:HB2	1.90	0.53
9:A:487:A:OP2	9:A:488:C:N4	2.42	0.53
9:A:582:C:P	23:O:63:ARG:HH22	2.30	0.53
9:A:1136:C:H3'	9:A:1137:C:H5''	1.91	0.53
9:A:1218:C:H2'	9:A:1219:A:H8	1.74	0.53
9:A:1451:U:OP2	9:A:1452:C:N4	2.42	0.53
12:D:18:LEU:CD1	12:D:20:LEU:CG	2.86	0.53
18:J:25:ILE:HA	18:J:28:THR:HG22	1.89	0.53
27:S:80:ARG:HD3	27:S:80:ARG:H	1.74	0.53
34:b:27:G:O2'	34:b:28:A:H8	1.92	0.53
34:b:2315:G:O2'	38:f:125:ARG:NE	2.42	0.53
40:h:41:LYS:O	40:h:45:GLU:HG3	2.09	0.53
9:A:198:G:H2'	9:A:199:A:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:928:G:O2'	9:A:1533:C:OP1	2.25	0.53
10:B:15:PHE:HD1	10:B:40:ILE:HG22	1.73	0.53
12:D:167:PRO:HB2	12:D:169:TRP:CD1	2.44	0.53
24:P:68:SER:OG	24:P:69:ASP:N	2.42	0.53
32:Z:19:G:N2	32:Z:59:A:O4'	2.42	0.53
35:c:23:GLU:OE1	35:c:23:GLU:N	2.42	0.53
52:v:96:PHE:O	52:v:100:SER:HA	2.08	0.53
9:A:148:G:H1	9:A:174:A:N6	2.05	0.53
9:A:738:C:OP1	14:F:2:ARG:NH1	2.43	0.53
9:A:1187:G:HO2'	9:A:1188:A:P	2.31	0.53
9:A:1240:U:H5'	9:A:1241:G:C8	2.44	0.53
34:b:272:A:H2'	34:b:273:G:H8	1.73	0.53
9:A:320:A:H2'	9:A:321:A:C8	2.44	0.52
9:A:417:G:N2	9:A:426:U:O2	2.38	0.52
10:B:18:GLN:HG3	10:B:20:ARG:HB3	1.90	0.52
10:B:70:GLY:HA3	10:B:79:VAL:HG11	1.89	0.52
16:H:95:MET:HB3	16:H:99:GLY:H	1.74	0.52
20:L:86:VAL:HG23	20:L:95:HIS:HE1	1.73	0.52
37:e:143:LEU:HD23	37:e:146:VAL:HG21	1.92	0.52
9:A:191:G:H2'	9:A:192:A:C8	2.45	0.52
9:A:1107:C:H5'	11:C:168:ARG:NH2	2.24	0.52
9:A:1116:U:H3	9:A:1184:G:H1	1.55	0.52
11:C:79:LYS:HG2	11:C:80:GLY:H	1.73	0.52
14:F:96:VAL:HG23	14:F:98:GLU:HG2	1.91	0.52
17:I:114:LYS:HD2	17:I:117:LEU:HD12	1.92	0.52
34:b:2177:C:H2'	34:b:2178:C:C6	2.44	0.52
31:X:22:G:H2'	31:X:23:A:C8	2.43	0.52
32:Y:6:A:O2'	32:Y:7:U:O5'	2.28	0.52
1:O:37:ARG:NH1	34:b:2200:C:OP2	2.42	0.52
9:A:198:G:H2'	9:A:199:A:H8	1.74	0.52
9:A:1412:C:H2'	9:A:1413:A:C8	2.45	0.52
21:M:57:ASP:OD1	21:M:58:GLU:N	2.42	0.52
34:b:549:G:H2'	34:b:550:C:H6	1.74	0.52
34:b:549:G:H2'	34:b:550:C:C6	2.44	0.52
42:l:108:ARG:N	42:l:116:ILE:HD11	2.23	0.52
46:p:88:LYS:HZ3	46:p:116:GLN:HE21	1.56	0.52
9:A:428:G:H8	9:A:430:A:H1'	1.75	0.52
12:D:18:LEU:HD11	12:D:20:LEU:HD12	1.91	0.52
12:D:122:ILE:HD12	12:D:144:ILE:HG22	1.92	0.52
34:b:593:U:H2'	34:b:594:U:C6	2.44	0.52
34:b:1495:A:O2'	34:b:1496:A:O4'	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:b:2119:A:H61	34:b:2167:U:H1'	1.75	0.52
38:f:65:PRO:HB3	38:f:89:VAL:HG22	1.92	0.52
9:A:458:U:H2'	9:A:459:A:C8	2.45	0.52
9:A:979:C:O2	22:N:58:ARG:NH1	2.43	0.52
9:A:1039:G:H2'	9:A:1040:U:H6	1.74	0.52
11:C:110:LEU:CG	11:C:111:ASP:H	2.20	0.52
12:D:70:GLN:H	12:D:70:GLN:CD	2.15	0.52
31:X:58:A:N3	31:X:60:U:H5''	2.24	0.52
32:Y:77:A:C3'	56:z:162:PRO:C	2.82	0.52
34:b:401:A:H2'	34:b:402:A:H8	1.75	0.52
38:f:114:PHE:HE1	38:f:116:GLY:HA2	1.74	0.52
44:n:55:ARG:NE	44:n:55:ARG:O	2.41	0.52
9:A:946:A:H2'	9:A:947:G:H8	1.74	0.52
18:J:11:LYS:HB3	18:J:71:LEU:HD23	1.92	0.52
31:X:44:G:H2'	31:X:45:G:C4	2.45	0.52
31:X:66:U:H2'	31:X:67:U:C6	2.45	0.52
34:b:2144:G:H21	34:b:2147:A:H8	1.58	0.52
34:b:2180:U:H2'	34:b:2181:U:C6	2.45	0.52
34:b:2640:G:P	41:k:95:ARG:HH12	2.32	0.52
49:s:51:VAL:HB	49:s:52:PRO:HD3	1.91	0.52
9:A:958:A:N6	9:A:959:A:N1	2.58	0.52
11:C:13:ILE:HG22	11:C:14:VAL:HG13	1.91	0.52
17:I:3:ASN:OD1	17:I:4:GLN:N	2.42	0.52
32:Y:52:A:O2'	32:Y:53:G:H5''	2.10	0.52
32:Y:73:G:H2'	32:Y:74:A:C8	2.44	0.52
34:b:27:G:H22	34:b:512:G:H2'	1.75	0.52
34:b:84:A:C2	34:b:98:G:H8	2.28	0.52
34:b:878:A:H3'	34:b:879:G:C8	2.44	0.52
34:b:1724:G:O6	34:b:1737:G:N2	2.43	0.52
39:g:52:PHE:CE1	39:g:72:LEU:HD12	2.45	0.52
9:A:553:A:H2'	9:A:554:A:H8	1.75	0.52
9:A:674:G:H2'	9:A:675:A:C8	2.45	0.52
10:B:99:MET:HG2	10:B:100:LEU:HD12	1.91	0.52
10:B:126:ASP:N	10:B:126:ASP:OD1	2.38	0.52
11:C:79:LYS:N	11:C:81:GLU:OE2	2.43	0.52
14:F:35:LYS:HB3	14:F:37:HIS:CE1	2.45	0.52
25:Q:53:GLY:N	25:Q:56:ASP:OD2	2.37	0.52
33:a:51:G:H2'	33:a:52:A:C8	2.44	0.52
34:b:2840:C:H5''	45:o:53:THR:HG21	1.91	0.52
39:g:75:MET:O	39:g:79:VAL:HG23	2.08	0.52
56:z:125:THR:O	56:z:129:ARG:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:447:G:N2	9:A:486:U:OP1	2.43	0.52
28:T:15:LYS:HG2	28:T:19:HIS:CE1	2.45	0.52
46:p:100:HIS:O	46:p:104:GLN:NE2	2.42	0.52
9:A:191:G:H2'	9:A:192:A:H8	1.74	0.51
11:C:134:LYS:O	11:C:138:GLN:HG2	2.11	0.51
17:I:35:GLU:HA	17:I:44:ARG:NH2	2.25	0.51
18:J:5:ARG:HH11	18:J:7:ARG:HG3	1.75	0.51
28:T:15:LYS:HG2	28:T:19:HIS:HE1	1.75	0.51
32:Z:1:C:H2'	32:Z:2:G:C8	2.45	0.51
33:a:117:G:P	46:p:56:LYS:HZ3	2.33	0.51
34:b:740:C:H5	34:b:757:G:H1	1.59	0.51
36:d:148:GLN:OE1	36:d:148:GLN:N	2.44	0.51
44:n:2:LEU:H	44:n:2:LEU:HD12	1.75	0.51
9:A:459:A:H2'	9:A:460:A:H8	1.75	0.51
9:A:481:G:H1'	9:A:483:C:N4	2.25	0.51
12:D:68:GLU:HG3	12:D:72:ARG:HH21	1.75	0.51
27:S:28:LYS:NZ	27:S:29:PRO:O	2.43	0.51
32:Y:22:A:C6	32:Y:47:G:H2'	2.45	0.51
34:b:983:A:N6	34:b:984:A:N1	2.58	0.51
34:b:2847:U:H2'	34:b:2848:G:O4'	2.09	0.51
44:n:69:PRO:HD2	44:n:70:ASP:N	2.24	0.51
45:o:86:ARG:NH2	45:o:117:ASP:OD1	2.36	0.51
51:u:28:ASN:ND2	51:u:88:LYS:O	2.42	0.51
2:1:38:GLN:OE1	2:1:38:GLN:N	2.41	0.51
12:D:120:LYS:HD3	12:D:120:LYS:H	1.75	0.51
18:J:44:THR:HG22	18:J:70:HIS:HA	1.91	0.51
29:U:5:VAL:HG13	29:U:9:GLU:HB3	1.92	0.51
32:Z:1:C:H2'	32:Z:2:G:H8	1.76	0.51
32:Z:11:C:H2'	32:Z:12:G:C8	2.46	0.51
50:t:17:VAL:HG11	50:t:103:ILE:HD11	1.91	0.51
9:A:978:A:C2	9:A:1319:A:C4	2.97	0.51
9:A:1241:G:H2'	9:A:1242:G:H8	1.74	0.51
9:A:1349:A:H1'	9:A:1374:A:N6	2.22	0.51
47:q:65:SER:OG	47:q:66:ASN:OD1	2.26	0.51
49:s:32:THR:HA	49:s:62:GLU:HA	1.93	0.51
1:0:28:ARG:HH22	34:b:1365:A:H5''	1.75	0.51
9:A:81:A:H2'	9:A:82:G:C8	2.45	0.51
9:A:1036:A:H2'	9:A:1037:C:C6	2.45	0.51
34:b:1597:A:H5''	34:b:1598:A:H5'	1.92	0.51
34:b:2312:U:H5'	38:f:85:ILE:HD11	1.92	0.51
2:1:8:GLU:OE1	2:1:8:GLU:N	2.32	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1013:G:H2'	9:A:1015:G:OP2	2.11	0.51
9:A:1176:A:H2'	9:A:1177:G:C8	2.46	0.51
34:b:401:A:H2'	34:b:402:A:C8	2.45	0.51
34:b:546:U:H2'	34:b:547:A:N3	2.25	0.51
12:D:68:GLU:OE1	12:D:68:GLU:N	2.37	0.51
34:b:2111:U:O2'	34:b:2117:A:O2'	2.29	0.51
38:f:100:PHE:CE1	38:f:104:ILE:HD11	2.46	0.51
4:4:3:VAL:HG12	34:b:2015:A:C2	2.46	0.51
9:A:180:U:O2	9:A:196:A:N6	2.43	0.51
9:A:976:G:H22	9:A:1362:A:HO2'	1.58	0.51
9:A:1317:C:H2'	9:A:1318:A:O4'	2.11	0.51
17:I:26:LYS:HE3	17:I:62:LEU:C	2.36	0.51
20:L:74:GLN:HG3	20:L:75:GLU:H	1.75	0.51
22:N:79:SER:HB2	22:N:82:LYS:HG2	1.91	0.51
31:X:27:C:N3	31:X:44:G:N2	2.58	0.51
31:X:69:C:H2'	31:X:70:C:C6	2.46	0.51
32:Y:14:A:N1	32:Y:22:A:O2'	2.38	0.51
34:b:873:C:N4	34:b:899:A:H62	2.09	0.51
34:b:1796:U:H2'	34:b:1797:G:H8	1.76	0.51
34:b:2187:U:H2'	34:b:2188:U:C6	2.46	0.51
34:b:2681:C:H5'	36:d:11:MET:HE1	1.93	0.51
9:A:426:U:H1'	12:D:39:GLN:HG2	1.92	0.51
9:A:478:A:H3'	9:A:479:U:H5'	1.91	0.51
15:G:74:VAL:HA	15:G:87:PRO:HA	1.93	0.51
26:R:40:PRO:HG2	26:R:43:ILE:HG12	1.92	0.51
33:a:116:G:O3'	46:p:56:LYS:NZ	2.43	0.51
34:b:874:G:N7	34:b:899:A:N6	2.50	0.51
34:b:1425:G:O2'	34:b:1426:G:OP1	2.27	0.51
34:b:1469:A:H2'	34:b:1470:A:C8	2.46	0.51
36:d:28:GLU:OE2	47:q:4:ILE:HG12	2.11	0.51
38:f:34:ILE:HD12	38:f:156:ILE:HG13	1.93	0.51
13:E:104:ILE:HD12	13:E:122:VAL:HG12	1.93	0.51
34:b:1506:U:H5'	34:b:1507:C:OP2	2.11	0.51
9:A:1212:U:H5'	9:A:1213:A:N7	2.26	0.50
12:D:71:PHE:HE1	12:D:89:LEU:HD11	1.76	0.50
34:b:1168:G:H1	34:b:1181:U:H3	1.58	0.50
34:b:1485:U:H2'	34:b:1486:U:C6	2.46	0.50
39:g:4:VAL:HG12	39:g:69:ARG:HD2	1.92	0.50
7:7:31:HIS:ND1	7:7:32:ILE:HG13	2.26	0.50
9:A:320:A:HO2'	9:A:1435:G:HO2'	1.54	0.50
9:A:1356:G:H2'	9:A:1357:A:C8	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:88:GLN:H	10:B:88:GLN:CD	2.17	0.50
13:E:53:ARG:NH1	13:E:54:GLU:HB3	2.26	0.50
17:I:19:PHE:HB2	17:I:63:TYR:HD2	1.76	0.50
32:Z:24:C:H2'	32:Z:25:G:C8	2.45	0.50
34:b:272:A:H2'	34:b:273:G:C8	2.46	0.50
34:b:705:A:N6	34:b:726:G:H1'	2.26	0.50
43:m:136:GLU:OE1	43:m:136:GLU:N	2.43	0.50
9:A:171:A:H2'	9:A:172:A:C8	2.45	0.50
9:A:338:A:H2'	9:A:339:C:H6	1.75	0.50
9:A:1111:A:N1	11:C:176:THR:OG1	2.44	0.50
9:A:1347:G:N2	9:A:1373:G:H2'	2.27	0.50
9:A:1492:A:O2'	9:A:1493:A:O4'	2.22	0.50
12:D:101:VAL:HA	12:D:104:MET:HB2	1.92	0.50
28:T:59:ARG:O	28:T:63:LYS:HG2	2.10	0.50
9:A:3:A:N3	9:A:613:C:H1'	2.25	0.50
9:A:455:G:H2'	9:A:456:A:C8	2.46	0.50
9:A:552:U:H2'	9:A:553:A:C8	2.42	0.50
9:A:580:C:O2'	23:O:57:ARG:NH2	2.44	0.50
10:B:86:CYS:SG	10:B:87:ASP:N	2.81	0.50
17:I:114:LYS:HD2	17:I:117:LEU:CD1	2.41	0.50
34:b:1998:A:OP2	36:d:141:ARG:NH2	2.45	0.50
34:b:2062:A:C6	56:z:158:ARG:HD2	2.46	0.50
34:b:2114:A:C6	34:b:2115:G:H1'	2.46	0.50
34:b:2171:A:H4'	34:b:2171:A:OP1	2.11	0.50
34:b:2246:G:H2'	34:b:2247:A:H8	1.76	0.50
9:A:1304:G:C2	9:A:1305:G:N2	2.80	0.50
32:Y:15:G:O2'	32:Y:21:U:N3	2.44	0.50
33:a:43:C:O2	38:f:92:ARG:NH2	2.39	0.50
34:b:1484:U:H2'	34:b:1485:U:C6	2.47	0.50
34:b:2132:U:H2'	34:b:2133:G:C8	2.45	0.50
34:b:2243:U:H2'	34:b:2244:U:C6	2.47	0.50
38:f:109:PRO:HA	38:f:114:PHE:CE2	2.45	0.50
9:A:144:G:C2	9:A:179:A:C8	2.99	0.50
9:A:253:A:H2'	9:A:254:G:H8	1.77	0.50
9:A:519:C:H2'	9:A:520:A:O4'	2.12	0.50
9:A:613:C:H2'	9:A:614:C:H6	1.76	0.50
9:A:1279:G:H5''	18:J:9:ARG:HH12	1.77	0.50
9:A:1467:C:H2'	9:A:1468:A:C8	2.45	0.50
9:A:1467:C:H2'	9:A:1468:A:H8	1.77	0.50
20:L:9:LYS:NZ	20:L:10:PRO:O	2.37	0.50
21:M:2:ARG:HH21	38:f:136:ILE:HD12	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:S:11:ASP:OD2	27:S:13:HIS:NE2	2.45	0.50
31:X:55:U:H2'	31:X:56:C:H2'	1.93	0.50
32:Y:16:C:O2'	32:Y:17:C:OP1	2.30	0.50
34:b:1482:G:H2'	34:b:1483:G:H8	1.77	0.50
34:b:2635:A:O2'	36:d:81:GLU:OE2	2.25	0.50
9:A:415:A:H2'	9:A:416:G:O4'	2.12	0.50
9:A:465:A:H2'	9:A:466:A:C8	2.47	0.50
34:b:64:A:H2'	34:b:65:U:C6	2.47	0.50
34:b:1727:C:H2'	34:b:1728:C:H6	1.77	0.50
38:f:94:GLU:HA	38:f:97:TRP:NE1	2.26	0.50
8:8:11:CYS:SG	8:8:33:HIS:HE1	2.35	0.50
9:A:1202:U:O2'	22:N:66:THR:HG21	2.12	0.50
10:B:18:GLN:HG3	10:B:20:ARG:H	1.77	0.50
12:D:94:GLU:HA	12:D:99:ASN:ND2	2.27	0.50
31:X:27:C:H2'	31:X:28:G:H8	1.76	0.50
34:b:1727:C:H2'	34:b:1728:C:C6	2.47	0.50
36:d:88:GLU:N	36:d:88:GLU:OE1	2.45	0.50
40:h:53:GLU:OE1	40:h:53:GLU:N	2.41	0.50
3:2:5:ILE:N	3:2:38:ARG:O	2.45	0.50
20:L:65:TYR:N	20:L:94:TYR:O	2.43	0.50
30:V:51:MET:N	30:V:51:MET:SD	2.85	0.50
31:X:71:G:O2'	34:b:1851:U:O2'	2.25	0.50
34:b:883:G:N2	34:b:894:U:O2'	2.44	0.50
34:b:1087:G:H5'	34:b:1090:A:N7	2.27	0.50
34:b:1434:A:H1'	34:b:1435:G:C8	2.47	0.50
9:A:308:C:H2'	9:A:309:A:C8	2.47	0.49
9:A:1253:G:H2'	9:A:1254:A:H8	1.76	0.49
9:A:1516:G:H2'	9:A:1518:A:OP2	2.11	0.49
12:D:109:THR:HG23	12:D:111:ALA:H	1.77	0.49
31:X:27:C:H2'	31:X:28:G:C8	2.47	0.49
40:h:93:SER:OG	40:h:121:VAL:O	2.30	0.49
9:A:214:C:H2'	9:A:215:C:H6	1.76	0.49
15:G:12:LEU:HD12	15:G:13:PRO:HD2	1.94	0.49
20:L:50:LYS:HG3	20:L:66:ILE:HG23	1.94	0.49
31:X:41:U:H2'	31:X:42:C:C6	2.47	0.49
34:b:1115:G:H2'	34:b:1116:G:H8	1.76	0.49
34:b:2100:G:C6	34:b:2101:A:C6	3.00	0.49
34:b:2130:U:H5'	34:b:2131:U:H2'	1.94	0.49
34:b:2469:A:N6	34:b:2481:G:O2'	2.45	0.49
9:A:44:A:H2'	9:A:45:G:H8	1.74	0.49
9:A:1147:C:H4'	17:I:6:TYR:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:54:LEU:HD11	12:D:55:ARG:HH21	1.77	0.49
20:L:53:ARG:C	20:L:54:VAL:HG23	2.36	0.49
21:M:39:ALA:HB3	21:M:42:VAL:HG13	1.94	0.49
34:b:2126:A:N6	34:b:2162:G:O5'	2.38	0.49
34:b:2132:U:O2'	34:b:2133:G:O4'	2.30	0.49
36:d:39:ASP:OD1	36:d:39:ASP:N	2.46	0.49
9:A:214:C:H2'	9:A:215:C:C6	2.48	0.49
9:A:880:C:P	20:L:4:ASN:HD21	2.35	0.49
15:G:73:GLU:O	15:G:88:VAL:N	2.41	0.49
15:G:115:MET:HA	15:G:118:ARG:HD3	1.94	0.49
17:I:33:SER:O	17:I:37:TYR:N	2.40	0.49
22:N:37:ASP:O	22:N:41:TRP:N	2.44	0.49
24:P:28:ARG:NH2	24:P:29:ASN:OD1	2.34	0.49
27:S:13:HIS:HA	27:S:16:LYS:HZ2	1.76	0.49
27:S:62:THR:OG1	27:S:65:MET:SD	2.61	0.49
31:X:36:C:H2'	31:X:37:A:O4'	2.12	0.49
34:b:2112:G:OP2	34:b:2114:A:N6	2.46	0.49
39:g:2:SER:OG	39:g:3:ARG:N	2.46	0.49
9:A:231:U:H2'	9:A:232:G:H8	1.77	0.49
9:A:416:G:N2	9:A:427:U:O2	2.35	0.49
9:A:1004:A:O2'	9:A:1036:A:N3	2.46	0.49
9:A:1175:G:H2'	9:A:1176:A:C8	2.44	0.49
31:X:41:U:H2'	31:X:42:C:H6	1.77	0.49
34:b:1040:A:N1	34:b:1115:G:N2	2.48	0.49
38:f:134:GLU:HG3	38:f:135:GLN:H	1.77	0.49
40:h:58:LEU:HA	40:h:61:VAL:HG12	1.94	0.49
9:A:427:U:H5''	12:D:9:LYS:HD2	1.94	0.49
9:A:456:A:H2'	9:A:457:G:C8	2.47	0.49
13:E:104:ILE:O	13:E:111:ARG:NH1	2.45	0.49
17:I:18:VAL:HG22	17:I:64:ILE:HG22	1.94	0.49
18:J:9:ARG:HE	18:J:42:LEU:HD21	1.78	0.49
34:b:27:G:HO2'	34:b:28:A:P	2.36	0.49
34:b:2251:G:OP1	44:n:81:ARG:NH1	2.45	0.49
9:A:215:C:H2'	9:A:216:U:C6	2.48	0.49
9:A:622:A:H8	9:A:623:C:C5	2.30	0.49
9:A:1343:G:H2'	9:A:1344:C:C6	2.48	0.49
13:E:82:HIS:HB3	13:E:84:VAL:HG13	1.93	0.49
20:L:45:ASN:ND2	20:L:88:ASP:OD2	2.46	0.49
22:N:65:GLN:NE2	22:N:82:LYS:HG3	2.28	0.49
34:b:285:G:H2'	34:b:286:U:C6	2.48	0.49
34:b:310:A:O2'	34:b:311:A:O5'	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:b:2135:A:N6	34:b:2156:G:O2'	2.46	0.49
38:f:148:ARG:HA	38:f:148:ARG:NH1	2.27	0.49
9:A:859:G:H2'	9:A:860:A:C8	2.48	0.49
10:B:186:VAL:HG13	10:B:190:SER:HB2	1.94	0.49
17:I:29:ILE:N	17:I:32:ARG:O	2.33	0.49
26:R:10:CYS:HB2	26:R:46:THR:HA	1.94	0.49
34:b:461:C:O2'	56:z:143:GLU:OE2	2.27	0.49
34:b:2126:A:C5	34:b:2161:C:H2'	2.48	0.49
5:5:7:GLU:OE2	5:5:27:LYS:NZ	2.39	0.49
9:A:223:A:O2'	9:A:224:U:OP1	2.25	0.49
9:A:642:A:C5	16:H:106:SER:HA	2.47	0.49
9:A:1014:A:N7	27:S:33:TRP:NE1	2.61	0.49
10:B:10:LYS:HZ1	10:B:13:VAL:HG23	1.78	0.49
11:C:85:LYS:O	11:C:88:LYS:HG3	2.13	0.49
13:E:12:GLU:N	13:E:12:GLU:OE1	2.45	0.49
18:J:35:GLN:HG2	18:J:77:VAL:HG13	1.93	0.49
28:T:47:GLN:HE22	28:T:82:ILE:HD12	1.76	0.49
32:Y:24:C:H2'	32:Y:25:G:H8	1.78	0.49
32:Y:76:C:H41	55:y:3:HIS:HA	1.78	0.49
33:a:66:A:H4'	33:a:67:G:O5'	2.12	0.49
4:4:22:LEU:C	4:4:22:LEU:HD12	2.37	0.49
9:A:30:U:O4	9:A:32:A:N6	2.46	0.49
9:A:181:A:O2'	9:A:194:C:N4	2.39	0.49
9:A:778:G:H21	19:K:121:ARG:NH1	2.11	0.49
11:C:35:ASP:OD1	11:C:58:ARG:NH2	2.28	0.49
32:Y:67:A:H2'	32:Y:68:U:C4'	2.43	0.49
9:A:34:C:O4'	20:L:28:GLN:NE2	2.46	0.48
9:A:104:G:N7	28:T:8:LYS:NZ	2.60	0.48
9:A:373:A:O2'	9:A:451:A:N7	2.46	0.48
9:A:505:G:H2'	9:A:506:G:H8	1.78	0.48
9:A:1130:A:H2'	9:A:1131:G:H8	1.77	0.48
27:S:3:SER:HB3	27:S:5:LYS:NZ	2.28	0.48
27:S:31:ARG:HH22	27:S:51:HIS:HB2	1.78	0.48
34:b:1541:C:H2'	34:b:1542:U:C6	2.48	0.48
34:b:2123:G:O6	34:b:2176:A:N6	2.46	0.48
34:b:2848:G:H1'	34:b:2868:A:H61	1.78	0.48
9:A:74:A:H2'	9:A:75:G:H8	1.78	0.48
9:A:543:U:OP1	12:D:13:ARG:NE	2.45	0.48
9:A:643:C:H2'	9:A:644:U:H6	1.78	0.48
18:J:52:LEU:HD23	18:J:52:LEU:H	1.77	0.48
22:N:92:ILE:HD11	22:N:95:LEU:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:h:114:GLU:OE2	40:h:133:GLN:N	2.45	0.48
9:A:142:G:H2'	9:A:143:A:C8	2.48	0.48
9:A:1040:U:H2'	9:A:1041:G:C8	2.48	0.48
9:A:1450:U:H2'	9:A:1452:C:C4	2.48	0.48
9:A:1513:A:H2'	9:A:1514:G:C8	2.48	0.48
12:D:43:ARG:CZ	12:D:44:LYS:H	2.26	0.48
13:E:59:ILE:O	13:E:63:MET:HG2	2.13	0.48
17:I:51:LEU:HA	17:I:54:VAL:HG22	1.93	0.48
34:b:721:A:H2'	34:b:722:A:C8	2.48	0.48
34:b:2136:G:H22	34:b:2156:G:H22	1.61	0.48
41:k:125:TYR:OH	41:k:132:HIS:NE2	2.44	0.48
44:n:20:LEU:HD13	53:w:81:PRO:HG2	1.94	0.48
9:A:81:A:N6	9:A:87:C:O3'	2.46	0.48
9:A:184:G:H2'	9:A:185:U:H6	1.78	0.48
9:A:328:C:H4'	9:A:329:A:H5'	1.94	0.48
9:A:449:G:H2'	9:A:450:G:C8	2.49	0.48
9:A:592:G:H2'	9:A:593:U:H6	1.79	0.48
9:A:746:A:H2'	9:A:747:A:C8	2.48	0.48
10:B:80:LYS:HA	10:B:83:ALA:HB3	1.95	0.48
10:B:122:ASP:N	10:B:122:ASP:OD1	2.45	0.48
40:h:72:ILE:HD11	40:h:140:ALA:HB1	1.96	0.48
41:k:17:VAL:HG13	41:k:137:PRO:HB2	1.96	0.48
49:s:32:THR:HG22	49:s:62:GLU:HB3	1.95	0.48
53:w:5:ASN:OD1	53:w:5:ASN:N	2.46	0.48
9:A:501:C:P	20:L:113:ARG:HH21	2.37	0.48
9:A:1065:U:H4'	9:A:1066:C:O5'	2.12	0.48
17:I:129:ARG:NH2	32:Y:36:G:OP2	2.36	0.48
22:N:68:ARG:HH12	22:N:81:ILE:HD12	1.79	0.48
32:Y:77:A:C3'	56:z:162:PRO:O	2.61	0.48
34:b:706:A:OP1	35:c:7:LYS:NZ	2.46	0.48
34:b:722:A:H2'	34:b:723:C:C6	2.49	0.48
34:b:1019:U:H3	34:b:1142:A:H62	1.62	0.48
9:A:411:A:H61	9:A:428:G:H1'	1.78	0.48
9:A:520:A:H61	9:A:529:G:H1'	1.79	0.48
9:A:1222:G:OP2	9:A:1322:C:N4	2.36	0.48
10:B:122:ASP:HA	10:B:125:PHE:HD2	1.78	0.48
11:C:70:ALA:HB2	11:C:105:VAL:HB	1.95	0.48
11:C:120:THR:OG1	11:C:188:ALA:HB2	2.14	0.48
16:H:38:VAL:HG21	16:H:109:VAL:HG12	1.95	0.48
17:I:80:HIS:HA	17:I:83:THR:HG22	1.96	0.48
21:M:23:GLY:HA3	21:M:64:VAL:HG13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:b:414:C:H2'	34:b:415:A:C8	2.48	0.48
34:b:1281:G:H2'	34:b:1282:U:C6	2.48	0.48
9:A:389:A:H3'	9:A:389:A:N3	2.29	0.48
9:A:407:U:O2'	12:D:112:GLU:OE1	2.20	0.48
9:A:723:U:O4	29:U:55:HIS:ND1	2.36	0.48
12:D:106:PHE:HA	12:D:154:VAL:HG13	1.95	0.48
13:E:88:HIS:CG	13:E:89:THR:H	2.31	0.48
15:G:142:ARG:HH12	31:X:42:C:P	2.36	0.48
19:K:87:GLY:H	19:K:113:THR:HG22	1.78	0.48
34:b:1087:G:H4'	34:b:1089:A:H4'	1.95	0.48
34:b:2174:C:H2'	34:b:2175:C:C6	2.49	0.48
51:u:54:GLU:HB2	51:u:88:LYS:HG3	1.95	0.48
9:A:78:A:N3	9:A:79:G:N1	2.61	0.48
9:A:501:C:H2'	9:A:502:A:C8	2.49	0.48
9:A:592:G:H2'	9:A:593:U:C6	2.49	0.48
9:A:1100:C:H3'	10:B:94:ARG:HH12	1.79	0.48
9:A:1381:U:H2'	9:A:1382:C:H6	1.79	0.48
11:C:39:ARG:NE	22:N:91:GLU:OE2	2.47	0.48
20:L:86:VAL:HG23	20:L:95:HIS:CE1	2.49	0.48
20:L:97:VAL:O	20:L:98:ARG:HD2	2.14	0.48
31:X:19:G:H5'	31:X:57:G:N2	2.25	0.48
31:X:71:G:HO2'	34:b:1851:U:HO2'	1.58	0.48
34:b:251:A:OP1	43:m:58:TYR:OH	2.32	0.48
34:b:2315:G:H21	38:f:125:ARG:HH22	1.61	0.48
41:k:3:THR:HG21	48:r:61:TRP:HE1	1.78	0.48
9:A:338:A:H2'	9:A:339:C:C6	2.48	0.48
9:A:1004:A:H61	9:A:1024:G:H1'	1.79	0.48
34:b:1476:U:H2'	34:b:1477:A:H8	1.78	0.48
34:b:1754:A:O3'	47:q:103:ARG:NH2	2.42	0.48
42:l:35:VAL:HG21	42:l:69:VAL:CG2	2.44	0.48
9:A:74:A:H2'	9:A:75:G:C8	2.49	0.48
9:A:424:G:H2'	9:A:425:G:C8	2.48	0.48
9:A:580:C:H4'	23:O:57:ARG:CZ	2.44	0.48
9:A:1130:A:O2'	17:I:4:GLN:OE1	2.21	0.48
12:D:10:LEU:HG	12:D:62:ARG:HE	1.79	0.48
31:X:54:U:O4	31:X:58:A:N7	2.47	0.48
34:b:572:A:OP2	49:s:80:ARG:NH2	2.41	0.48
34:b:1051:G:OP1	34:b:2752:C:H1'	2.14	0.48
34:b:2064:C:H2'	34:b:2065:C:C6	2.49	0.48
34:b:2345:G:N3	34:b:2381:A:H2'	2.29	0.48
34:b:2591:C:H2'	34:b:2592:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:217:C:H5'	9:A:218:U:OP2	2.14	0.47
9:A:1162:C:H2'	9:A:1163:A:H8	1.79	0.47
9:A:1368:A:OP1	17:I:112:ARG:NH1	2.44	0.47
11:C:72:PRO:HA	11:C:75:VAL:HB	1.96	0.47
18:J:10:LEU:HB3	18:J:18:ILE:HD11	1.96	0.47
22:N:5:MET:SD	22:N:6:LYS:HG3	2.54	0.47
34:b:172:A:H2'	34:b:173:A:H8	1.78	0.47
34:b:345:A:H1'	34:b:346:A:H2	1.79	0.47
34:b:832:U:H2'	34:b:833:A:H8	1.78	0.47
34:b:2176:A:H2'	34:b:2177:C:C6	2.49	0.47
34:b:2680:U:O2'	36:d:11:MET:HE1	2.14	0.47
38:f:67:ILE:HG21	38:f:84:PRO:HB3	1.96	0.47
9:A:416:G:H2'	9:A:417:G:H8	1.78	0.47
9:A:490:C:H2'	9:A:491:G:C8	2.49	0.47
9:A:602:A:H2'	9:A:603:U:C6	2.49	0.47
9:A:1124:G:H5'	18:J:37:ARG:NH1	2.29	0.47
9:A:1229:A:OP2	21:M:112:ARG:HD3	2.14	0.47
35:c:227:PRO:HG3	35:c:234:GLY:H	1.80	0.47
38:f:46:ASP:OD2	38:f:49:LEU:N	2.47	0.47
3:2:39:GLU:OE1	3:2:39:GLU:N	2.34	0.47
9:A:432:A:H3'	9:A:433:G:C8	2.48	0.47
9:A:1314:C:H2'	9:A:1315:U:C6	2.49	0.47
12:D:169:TRP:N	12:D:183:ARG:HH21	2.11	0.47
19:K:23:HIS:HB3	19:K:30:ILE:HG13	1.95	0.47
21:M:106:ARG:HH22	21:M:109:LYS:HD3	1.79	0.47
23:O:33:ALA:HA	23:O:36:ASN:HD21	1.79	0.47
24:P:6:LEU:HD23	24:P:17:TYR:HB3	1.96	0.47
34:b:418:C:H2'	34:b:419:U:C6	2.49	0.47
34:b:2637:U:H2'	34:b:2638:G:O4'	2.14	0.47
9:A:1010:U:H2'	9:A:1011:C:H6	1.79	0.47
9:A:1035:A:N7	9:A:1036:A:N6	2.62	0.47
12:D:159:GLU:OE1	12:D:159:GLU:N	2.40	0.47
19:K:86:LYS:HA	19:K:113:THR:HG22	1.96	0.47
22:N:81:ILE:O	22:N:85:GLU:HG2	2.13	0.47
24:P:71:VAL:O	24:P:75:ILE:N	2.46	0.47
26:R:25:ILE:O	26:R:29:LYS:HG2	2.14	0.47
34:b:645:C:N4	34:b:2349:G:N3	2.63	0.47
34:b:2246:G:H2'	34:b:2247:A:C8	2.50	0.47
37:e:147:LEU:HD11	37:e:170:ARG:HD2	1.96	0.47
41:k:17:VAL:HG12	41:k:55:ILE:HB	1.97	0.47
42:l:108:ARG:HA	42:l:116:ILE:CD1	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:X:5:G:C6	31:X:68:C:C2	3.03	0.47
31:X:72:C:H2'	31:X:73:U:O4'	2.15	0.47
34:b:289:G:H2'	34:b:290:U:C6	2.50	0.47
34:b:1531:C:H2'	34:b:1532:A:C8	2.48	0.47
34:b:2166:U:O2'	34:b:2167:U:O4'	2.28	0.47
9:A:146:G:H2'	9:A:147:G:C8	2.49	0.47
9:A:590:U:H5	9:A:649:A:N1	2.13	0.47
9:A:1256:A:H62	9:A:1279:G:N2	2.11	0.47
11:C:184:ASN:OD1	11:C:185:THR:N	2.39	0.47
12:D:25:ARG:HG2	12:D:26:ALA:H	1.78	0.47
16:H:51:GLU:H	16:H:51:GLU:CD	2.22	0.47
16:H:125:ILE:HG22	16:H:126:CYS:SG	2.54	0.47
27:S:38:THR:HG2	27:S:69:LYS:HG2	1.96	0.47
34:b:2308:G:O2'	34:b:2309:A:OP1	2.28	0.47
37:e:119:ILE:HB	37:e:187:VAL:HG12	1.95	0.47
9:A:175:C:H2'	9:A:176:C:C6	2.49	0.47
9:A:418:C:O2'	9:A:540:G:O2'	2.20	0.47
9:A:939:G:H4'	15:G:101:ARG:HH12	1.79	0.47
9:A:1033:G:H5''	9:A:1033:G:H8	1.79	0.47
9:A:1080:A:OP1	13:E:51:LYS:HE2	2.14	0.47
34:b:1090:A:H8	34:b:1103:A:P	2.38	0.47
50:t:2:GLU:OE1	50:t:2:GLU:N	2.48	0.47
9:A:623:C:H2'	9:A:624:C:H6	1.80	0.47
9:A:626:G:H2'	9:A:627:G:C8	2.50	0.47
9:A:1004:A:N1	9:A:1024:G:O2'	2.44	0.47
9:A:1060:U:P	22:N:84:ARG:HH22	2.38	0.47
9:A:1361:G:O6	9:A:1362:A:N6	2.47	0.47
14:F:42:TRP:CD2	14:F:103:VAL:HG11	2.49	0.47
23:O:60:SER:O	23:O:63:ARG:HG3	2.14	0.47
34:b:2591:C:H2'	34:b:2592:G:C8	2.48	0.47
38:f:38:MET:SD	38:f:150:ARG:HD2	2.55	0.47
8:8:8:LYS:NZ	34:b:2467:C:OP1	2.43	0.47
18:J:21:ALA:O	18:J:24:GLU:HG3	2.15	0.47
19:K:75:GLU:OE1	19:K:75:GLU:N	2.37	0.47
21:M:66:GLY:HA2	21:M:69:ARG:HH11	1.79	0.47
22:N:62:ARG:HE	22:N:69:PRO:HG3	1.79	0.47
39:g:86:LYS:HG2	39:g:132:VAL:HG12	1.97	0.47
9:A:627:G:H2'	9:A:628:G:H8	1.80	0.47
13:E:40:ASP:OD1	13:E:41:GLY:N	2.46	0.47
17:I:44:ARG:O	17:I:48:ARG:NH1	2.48	0.47
20:L:32:VAL:HA	20:L:78:VAL:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:M:23:GLY:O	21:M:28:ARG:NH1	2.44	0.47
34:b:727:A:OP1	34:b:1431:A:O2'	2.33	0.47
40:h:69:ALA:O	40:h:72:ILE:HG13	2.15	0.47
3:2:27:LEU:HG	3:2:47:MET:HE2	1.97	0.46
9:A:842:U:H5''	9:A:843:U:O4'	2.14	0.46
9:A:1152:A:H2'	9:A:1153:G:H8	1.81	0.46
9:A:1347:G:H22	9:A:1373:G:H2'	1.78	0.46
11:C:57:GLU:OE1	11:C:57:GLU:N	2.49	0.46
12:D:108:ALA:HB3	12:D:112:GLU:HG3	1.96	0.46
13:E:75:LEU:HA	13:E:80:LEU:HB2	1.97	0.46
20:L:53:ARG:O	20:L:54:VAL:HG23	2.15	0.46
22:N:64:ARG:NE	22:N:77:GLY:O	2.48	0.46
34:b:721:A:H2'	34:b:722:A:H8	1.80	0.46
34:b:869:G:H1'	44:n:8:LYS:HE2	1.97	0.46
34:b:1321:A:C2	56:z:126:ALA:HA	2.50	0.46
34:b:1353:A:H2'	34:b:1354:A:C8	2.50	0.46
34:b:1936:A:C2	34:b:1943:U:H5	2.27	0.46
34:b:2139:U:H5'	34:b:2140:G:OP1	2.15	0.46
9:A:1402:C:H2'	9:A:1403:C:O4'	2.14	0.46
10:B:14:HIS:HB3	10:B:202:ASN:ND2	2.30	0.46
10:B:127:LYS:HE3	10:B:132:GLU:HG2	1.96	0.46
16:H:6:ILE:HB	16:H:76:ARG:NH1	2.29	0.46
34:b:668:A:H2'	34:b:670:A:H62	1.79	0.46
40:h:75:LEU:HD11	40:h:106:ALA:HB1	1.96	0.46
9:A:996:A:H2'	9:A:997:U:C6	2.51	0.46
9:A:1237:C:H3'	9:A:1336:C:H41	1.80	0.46
22:N:78:LEU:HB3	22:N:83:VAL:HG23	1.96	0.46
34:b:1083:U:O2	34:b:1085:A:H2'	2.16	0.46
9:A:230:G:H2'	9:A:231:U:O4'	2.15	0.46
9:A:830:G:O3'	10:B:20:ARG:NH1	2.49	0.46
9:A:1314:C:H2'	9:A:1315:U:H6	1.79	0.46
11:C:68:HIS:HA	11:C:103:ALA:HB3	1.97	0.46
12:D:97:LEU:HD23	12:D:97:LEU:HA	1.84	0.46
12:D:104:MET:HA	12:D:170:LEU:HD21	1.97	0.46
18:J:81:GLU:OE1	18:J:82:LYS:N	2.33	0.46
32:Y:77:A:H3'	56:z:162:PRO:O	2.16	0.46
34:b:1433:A:N6	34:b:1560:G:H1	2.10	0.46
34:b:1883:U:H2'	34:b:1884:G:O4'	2.15	0.46
38:f:61:SER:OG	38:f:62:GLY:N	2.48	0.46
9:A:218:U:H4'	9:A:218:U:OP1	2.15	0.46
9:A:237:G:H5''	25:Q:26:ARG:HH12	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:358:U:H2'	9:A:359:G:H8	1.81	0.46
9:A:376:G:H4'	24:P:5:ARG:HE	1.80	0.46
9:A:430:A:P	12:D:7:LYS:HG2	2.55	0.46
11:C:71:ARG:NH2	11:C:74:ILE:HG13	2.30	0.46
16:H:10:LEU:HD11	16:H:126:CYS:SG	2.56	0.46
28:T:15:LYS:O	28:T:19:HIS:ND1	2.35	0.46
28:T:31:ILE:HA	28:T:34:VAL:HG12	1.96	0.46
28:T:54:GLN:CD	28:T:54:GLN:H	2.23	0.46
28:T:56:ILE:HA	28:T:59:ARG:NH1	2.30	0.46
34:b:2166:U:O2	34:b:2170:A:N6	2.48	0.46
34:b:2307:G:H5'	34:b:2308:G:C4	2.50	0.46
34:b:2813:A:H2'	34:b:2814:A:H8	1.81	0.46
38:f:94:GLU:HA	38:f:97:TRP:CD1	2.51	0.46
39:g:31:GLY:H	39:g:79:VAL:CG1	2.29	0.46
9:A:562:U:H2'	20:L:13:ARG:CZ	2.46	0.46
9:A:1060:U:H2'	9:A:1061:G:H8	1.80	0.46
9:A:1112:C:O2'	11:C:178:ARG:HD3	2.16	0.46
10:B:182:VAL:H	10:B:195:VAL:HB	1.80	0.46
12:D:54:LEU:O	12:D:58:GLN:HG2	2.15	0.46
20:L:28:GLN:HB3	20:L:80:LEU:HD11	1.98	0.46
31:X:3:G:H2'	31:X:4:G:H5'	1.98	0.46
34:b:548:G:H2'	34:b:549:G:O4'	2.15	0.46
34:b:2444:G:OP2	37:e:63:LYS:NZ	2.38	0.46
38:f:100:PHE:O	38:f:104:ILE:HG12	2.15	0.46
53:w:31:TYR:O	53:w:93:ARG:N	2.45	0.46
9:A:237:G:H5''	25:Q:26:ARG:HH22	1.80	0.46
9:A:410:G:H2'	9:A:429:U:O4	2.16	0.46
9:A:607:A:H2'	9:A:608:A:O4'	2.15	0.46
9:A:1152:A:H2'	9:A:1153:G:C8	2.50	0.46
9:A:1391:U:H2'	9:A:1392:G:C8	2.50	0.46
34:b:1000:A:H2'	34:b:1001:A:C8	2.50	0.46
34:b:1059:G:H2'	34:b:1060:U:O4'	2.16	0.46
34:b:1198:U:H2'	34:b:1199:U:C6	2.51	0.46
34:b:1796:U:H2'	34:b:1797:G:C8	2.51	0.46
49:s:26:ASP:OD1	49:s:26:ASP:N	2.34	0.46
55:y:37:ILE:HD13	55:y:80:ILE:HG21	1.97	0.46
9:A:443:C:H3'	9:A:444:G:H8	1.79	0.46
9:A:1181:G:H1'	9:A:1182:G:C4	2.50	0.46
9:A:1240:U:O5'	15:G:115:MET:HE1	2.16	0.46
9:A:1441:A:H62	9:A:1461:G:N2	2.08	0.46
12:D:2:ARG:HE	12:D:4:LEU:HD21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:120:LYS:HE2	12:D:145:ARG:NH1	2.31	0.46
15:G:141:HIS:O	15:G:145:GLU:HG2	2.15	0.46
21:M:74:MET:O	21:M:78:ARG:HG2	2.15	0.46
24:P:3:THR:HG21	24:P:24:SER:HB3	1.96	0.46
32:Y:24:C:H2'	32:Y:25:G:C8	2.51	0.46
32:Y:67:A:H2'	32:Y:68:U:O4'	2.16	0.46
34:b:548:G:H2'	34:b:549:G:C4'	2.46	0.46
34:b:1047:G:O2'	34:b:1110:G:N2	2.44	0.46
34:b:2183:A:H2'	34:b:2184:A:C8	2.51	0.46
36:d:85:ALA:O	36:d:86:GLU:HG3	2.15	0.46
9:A:71:A:C8	9:A:72:A:C8	3.04	0.46
9:A:255:G:N1	9:A:272:C:N3	2.64	0.46
9:A:412:A:OP1	9:A:414:A:O2'	2.29	0.46
9:A:475:C:C2	9:A:476:U:C5	3.04	0.46
9:A:778:G:H21	19:K:121:ARG:CZ	2.28	0.46
9:A:1329:A:H5'	21:M:25:GLY:N	2.31	0.46
28:T:56:ILE:O	28:T:60:GLN:HG2	2.16	0.46
34:b:871:U:H2'	34:b:872:U:C6	2.51	0.46
34:b:2684:U:O4'	42:l:70:ARG:NH1	2.49	0.46
39:g:86:LYS:HB2	39:g:165:ALA:HB2	1.97	0.46
44:n:4:PRO:HD3	44:n:69:PRO:HG2	1.97	0.46
9:A:608:A:H3'	9:A:609:A:H8	1.80	0.46
9:A:876:C:H1'	16:H:11:THR:HG21	1.98	0.46
9:A:1210:C:N4	9:A:1211:U:O4	2.48	0.46
9:A:1279:G:H5''	18:J:9:ARG:NH1	2.31	0.46
34:b:866:A:C8	34:b:914:G:C6	3.04	0.46
34:b:1062:G:H2'	34:b:1063:G:C8	2.50	0.46
40:h:114:GLU:O	40:h:116:ARG:NH2	2.49	0.46
9:A:1460:C:H2'	9:A:1461:G:C8	2.50	0.45
10:B:10:LYS:NZ	10:B:13:VAL:HG23	2.30	0.45
10:B:113:LEU:HD11	10:B:144:GLU:HB3	1.98	0.45
14:F:26:THR:HA	14:F:29:ILE:HG12	1.99	0.45
17:I:78:ILE:O	17:I:82:ILE:HG12	2.16	0.45
20:L:26:CYS:HB2	20:L:29:LYS:HE3	1.98	0.45
20:L:53:ARG:O	20:L:54:VAL:CG2	2.64	0.45
21:M:15:VAL:CG2	21:M:40:GLU:HB3	2.46	0.45
34:b:84:A:OP1	52:v:6:ARG:NH2	2.50	0.45
34:b:580:U:H2'	34:b:581:C:C6	2.51	0.45
34:b:1060:U:H1'	34:b:1062:G:OP2	2.15	0.45
34:b:1533:C:O2'	34:b:1534:U:O4'	2.33	0.45
35:c:143:ASN:OD1	35:c:152:GLY:HA3	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:f:142:ASP:H	38:f:145:LYS:NZ	2.10	0.45
9:A:150:U:H2'	9:A:151:A:H8	1.81	0.45
9:A:193:C:O2'	28:T:58:ASP:OD2	2.33	0.45
9:A:472:U:H2'	9:A:473:U:H6	1.81	0.45
9:A:763:G:H2'	9:A:764:C:C6	2.51	0.45
9:A:946:A:H2'	9:A:947:G:C8	2.49	0.45
12:D:84:ASN:OD1	12:D:87:GLU:HB2	2.16	0.45
15:G:99:ALA:O	15:G:103:ILE:HG12	2.16	0.45
19:K:17:ASP:OD2	19:K:36:ARG:NH1	2.49	0.45
34:b:2053:G:H5'	36:d:149:ASN:O	2.16	0.45
34:b:2133:G:O3'	34:b:2157:G:N2	2.49	0.45
38:f:114:PHE:HD1	38:f:115:ARG:N	2.15	0.45
9:A:511:C:O2	12:D:40:HIS:NE2	2.49	0.45
9:A:925:G:C2	9:A:927:G:C8	3.05	0.45
9:A:1199:U:H4'	18:J:56:HIS:NE2	2.32	0.45
9:A:1300:G:N2	9:A:1301:U:O4	2.42	0.45
9:A:1342:C:HO2'	9:A:1343:G:H8	1.62	0.45
20:L:50:LYS:HD2	20:L:67:GLY:HA2	1.98	0.45
21:M:74:MET:SD	21:M:75:SER:N	2.89	0.45
31:X:35:C:H2'	31:X:36:C:O2	2.16	0.45
34:b:718:A:H5''	34:b:719:C:C5	2.51	0.45
34:b:1410:G:H2'	34:b:1411:U:C6	2.51	0.45
34:b:2071:A:H2'	34:b:2072:C:C6	2.51	0.45
38:f:135:GLN:C	38:f:137:ILE:H	2.24	0.45
49:s:6:GLN:HG2	49:s:11:GLN:HG2	1.97	0.45
9:A:143:A:H5''	9:A:144:G:H5'	1.97	0.45
9:A:179:A:H2'	9:A:179:A:N3	2.32	0.45
9:A:253:A:N6	9:A:274:A:C6	2.85	0.45
9:A:501:C:H2'	9:A:502:A:H8	1.81	0.45
9:A:1242:G:H1	9:A:1295:U:H3	1.63	0.45
9:A:1349:A:N3	9:A:1374:A:N1	2.65	0.45
9:A:1445:U:H3	9:A:1457:G:H1	1.62	0.45
10:B:56:LEU:HA	10:B:59:ILE:HB	1.99	0.45
10:B:103:TRP:HA	10:B:106:VAL:HG22	1.97	0.45
10:B:187:ASP:OD1	10:B:188:THR:N	2.41	0.45
11:C:198:LYS:HB3	11:C:200:TRP:CH2	2.52	0.45
13:E:53:ARG:HD3	13:E:54:GLU:HG2	1.98	0.45
14:F:35:LYS:HB2	14:F:65:GLU:HB2	1.98	0.45
17:I:5:TYR:CD2	17:I:88:GLU:HB3	2.50	0.45
31:X:21:A:H2'	31:X:22:G:C8	2.46	0.45
34:b:613:A:H5'	34:b:614:A:H2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:b:1114:C:H2'	34:b:1115:G:H8	1.81	0.45
1:0:67:VAL:O	1:0:70:GLU:HG3	2.17	0.45
9:A:999:C:N4	9:A:1042:A:H61	2.14	0.45
34:b:1094:U:O3'	34:b:1098:A:N6	2.48	0.45
34:b:1115:G:H2'	34:b:1116:G:C8	2.50	0.45
4:4:22:LEU:CD1	50:t:23:LEU:HD11	2.44	0.45
9:A:35:G:H1'	20:L:114:SER:O	2.17	0.45
9:A:133:U:H4'	9:A:325:A:H1'	1.97	0.45
9:A:389:A:N3	9:A:390:U:H5''	2.32	0.45
9:A:1477:U:H2'	9:A:1478:U:C6	2.52	0.45
10:B:18:GLN:NE2	10:B:36:LYS:O	2.49	0.45
10:B:20:ARG:HG3	10:B:21:TYR:CD1	2.51	0.45
16:H:6:ILE:H	16:H:6:ILE:HD12	1.82	0.45
17:I:60:LEU:HD22	17:I:61:ASP:H	1.82	0.45
18:J:37:ARG:NH1	18:J:38:GLY:H	2.14	0.45
27:S:10:ILE:O	27:S:15:LEU:HD23	2.17	0.45
29:U:44:ARG:O	29:U:48:LYS:HG2	2.17	0.45
34:b:882:G:O2'	34:b:883:G:H5'	2.16	0.45
34:b:1067:A:H2'	34:b:1096:A:N6	2.32	0.45
34:b:2136:G:N2	34:b:2156:G:H1	2.13	0.45
34:b:2164:C:H4'	34:b:2165:C:H5'	1.98	0.45
44:n:12:MET:HE3	44:n:12:MET:HB2	1.88	0.45
49:s:42:ALA:HB1	49:s:46:GLU:HB3	1.98	0.45
54:x:13:G:H4'	54:x:14:C:OP1	2.17	0.45
9:A:62:U:O2'	9:A:379:C:O2	2.33	0.45
9:A:748:G:H2'	9:A:749:A:C8	2.52	0.45
9:A:1119:C:OP1	17:I:84:ARG:NH1	2.31	0.45
9:A:1163:A:H2'	9:A:1164:G:H8	1.81	0.45
9:A:1246:A:N6	9:A:1292:G:O6	2.50	0.45
9:A:1435:G:H2'	9:A:1436:U:C6	2.52	0.45
9:A:1513:A:H2'	9:A:1514:G:H8	1.82	0.45
14:F:42:TRP:HB2	14:F:59:TYR:HB2	1.99	0.45
14:F:49:TYR:HB3	26:R:73:HIS:CG	2.52	0.45
20:L:34:THR:OG1	20:L:55:ARG:HG3	2.17	0.45
28:T:66:ILE:HG22	28:T:67:HIS:N	2.31	0.45
31:X:9:A:H1'	31:X:45:G:N7	2.32	0.45
32:Y:22:A:N6	32:Y:48:U:OP2	2.50	0.45
34:b:1509:A:H2'	34:b:1510:G:C8	2.52	0.45
34:b:2144:G:N2	34:b:2148:G:N7	2.65	0.45
35:c:75:PRO:HD2	35:c:97:LYS:HD3	1.99	0.45
38:f:11:GLU:HA	38:f:14:LYS:HE3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:z:154[B]:TRP:CE3	56:z:154[B]:TRP:HA	2.52	0.45
56:z:155[A]:TRP:CD1	56:z:155[A]:TRP:H	2.33	0.45
9:A:237:G:C5'	25:Q:26:ARG:HH12	2.29	0.45
9:A:440:C:C2	9:A:441:A:C8	3.05	0.45
9:A:948:C:H3'	21:M:104:ASN:HD22	1.82	0.45
9:A:982:U:OP2	22:N:69:PRO:HG2	2.17	0.45
9:A:1333:A:H2'	9:A:1334:G:O4'	2.17	0.45
22:N:65:GLN:HE21	22:N:78:LEU:HG	1.81	0.45
31:X:5:G:H2'	31:X:6:A:H8	1.82	0.45
32:Z:27:A:N6	32:Z:45:G:H1	2.04	0.45
33:a:54:G:N2	38:f:26:MET:HE1	2.15	0.45
34:b:39:G:H2'	34:b:40:U:O2	2.16	0.45
34:b:1038:G:H2'	34:b:1039:A:C8	2.51	0.45
34:b:1425:G:H2'	34:b:1426:G:C8	2.51	0.45
34:b:2405:G:O2'	34:b:2406:A:OP1	2.32	0.45
36:d:125:TRP:CD1	36:d:160:LYS:HB3	2.51	0.45
46:p:60:GLU:OE1	46:p:60:GLU:N	2.50	0.45
55:y:70:GLU:OE1	55:y:70:GLU:N	2.50	0.45
3:2:37:GLU:O	3:2:38:ARG:NH1	2.46	0.45
4:4:28:LEU:HD12	4:4:37:LYS:HB3	1.99	0.45
9:A:36:C:H5'	20:L:117:GLY:HA2	1.99	0.45
9:A:129:A:H2	9:A:232:G:H22	1.64	0.45
9:A:344:A:H3'	9:A:345:C:C6	2.52	0.45
9:A:476:U:H2'	9:A:477:C:C6	2.52	0.45
9:A:859:G:H2'	9:A:860:A:H8	1.80	0.45
9:A:1192:C:P	11:C:3:LYS:HZ1	2.40	0.45
9:A:1202:U:O2'	22:N:68:ARG:HD2	2.16	0.45
11:C:112:ALA:HA	11:C:115:VAL:HG12	1.98	0.45
16:H:51:GLU:OE2	16:H:57:GLU:HB3	2.17	0.45
21:M:58:GLU:N	21:M:58:GLU:OE1	2.46	0.45
34:b:388:G:O6	34:b:390:U:O2'	2.31	0.45
34:b:1539:U:H2'	34:b:1540:G:C8	2.52	0.45
34:b:2111:U:H5''	34:b:2112:G:H4'	1.99	0.45
38:f:40:VAL:HG11	38:f:43:ALA:HB2	1.98	0.45
9:A:372:C:N4	9:A:388:G:OP2	2.43	0.45
9:A:1107:C:C4	9:A:1108:G:C8	3.05	0.45
9:A:1280:A:OP1	18:J:9:ARG:NH2	2.50	0.45
9:A:1436:U:H2'	9:A:1437:A:C8	2.51	0.45
12:D:150:LYS:HE2	12:D:151:GLN:HE21	1.82	0.45
13:E:79:THR:OG1	13:E:80:LEU:N	2.50	0.45
14:F:49:TYR:HB3	26:R:73:HIS:CD2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:116:G:H4'	46:p:54:VAL:HG12	1.99	0.45
34:b:974:G:H8	34:b:990:A:H62	1.64	0.45
34:b:2055:C:O2'	34:b:2504:U:H4'	2.16	0.45
34:b:2064:C:H2'	34:b:2065:C:H6	1.82	0.45
37:e:22:ASP:OD1	37:e:22:ASP:N	2.50	0.45
56:z:148:LEU:C	56:z:150[A]:TYR:H	2.25	0.45
9:A:413:G:H4'	9:A:414:A:H4'	1.99	0.44
9:A:539:A:H2'	9:A:540:G:O4'	2.17	0.44
9:A:1309:G:C6	9:A:1329:A:C6	3.05	0.44
12:D:125:ASN:HA	12:D:141:VAL:HG23	1.98	0.44
14:F:3:HIS:CD2	14:F:3:HIS:H	2.34	0.44
17:I:26:LYS:HB3	17:I:61:ASP:HB3	1.99	0.44
27:S:62:THR:OG1	27:S:64:GLU:OE1	2.35	0.44
32:Z:10:G:H2'	32:Z:11:C:C6	2.52	0.44
34:b:642:U:H2'	34:b:643:A:H2'	1.99	0.44
34:b:1847:A:H2'	34:b:1848:A:C8	2.51	0.44
34:b:2299:U:OP1	38:f:72:LYS:NZ	2.35	0.44
39:g:170:ARG:NH1	39:g:171:THR:H	2.15	0.44
45:o:38:LEU:HB3	45:o:39:PRO:HD3	1.99	0.44
4:4:31:ASP:OD1	4:4:33:THR:N	2.50	0.44
9:A:438:U:OP2	12:D:147:LYS:NZ	2.50	0.44
9:A:634:C:H2'	9:A:635:A:H8	1.82	0.44
9:A:1320:C:H2'	9:A:1321:U:C6	2.52	0.44
9:A:1441:A:C2	9:A:1442:G:H1'	2.52	0.44
10:B:202:ASN:HD22	10:B:205:ALA:HB2	1.82	0.44
16:H:47:ASP:OD1	16:H:48:PHE:N	2.49	0.44
16:H:48:PHE:HB2	16:H:58:LEU:HD11	1.99	0.44
32:Z:52:A:O2'	32:Z:53:G:H8	2.00	0.44
34:b:634:C:H2'	34:b:635:C:C6	2.52	0.44
34:b:1107:G:H2'	34:b:1108:U:C6	2.52	0.44
34:b:1361:G:H2'	34:b:1362:C:C6	2.52	0.44
34:b:1735:A:H2'	34:b:1736:U:C6	2.52	0.44
34:b:2052:A:H4'	36:d:148:GLN:O	2.18	0.44
34:b:2859:G:H2'	34:b:2860:A:C8	2.52	0.44
2:1:26:PHE:HD1	2:1:29:ARG:HH21	1.64	0.44
9:A:559:A:H4'	9:A:560:A:H3'	2.00	0.44
9:A:627:G:H2'	9:A:628:G:C8	2.52	0.44
9:A:970:C:H41	17:I:128:LYS:HD2	1.82	0.44
9:A:1071:C:H2'	9:A:1072:G:H8	1.82	0.44
9:A:1163:A:H2'	9:A:1164:G:C8	2.52	0.44
11:C:22:PHE:CE2	18:J:12:ALA:HA	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:X:23:A:H2'	31:X:24:G:C8	2.52	0.44
34:b:832:U:H2'	34:b:833:A:C8	2.52	0.44
34:b:1857:G:O2'	34:b:1885:A:N6	2.51	0.44
34:b:2109:U:H1'	34:b:2180:U:H3	1.82	0.44
34:b:2547:A:H2'	34:b:2548:U:C6	2.52	0.44
35:c:5:LYS:HG2	35:c:17:VAL:HG22	1.99	0.44
5:5:23:THR:OG1	5:5:24:THR:N	2.51	0.44
9:A:135:C:O2	24:P:1:MET:HB2	2.16	0.44
9:A:554:A:H2'	9:A:555:U:C6	2.53	0.44
9:A:1372:U:OP1	17:I:72:SER:OG	2.33	0.44
10:B:72:LYS:HE3	10:B:74:ALA:HB3	1.98	0.44
11:C:22:PHE:HB2	18:J:95:GLY:HA2	2.00	0.44
15:G:121:ASN:O	15:G:124:SER:OG	2.32	0.44
16:H:85:TYR:CE2	16:H:123:GLU:HG2	2.52	0.44
34:b:182:A:H2'	34:b:183:C:H6	1.82	0.44
34:b:713:G:H2'	34:b:714:U:C6	2.53	0.44
34:b:1292:G:H2'	34:b:1293:C:C6	2.53	0.44
34:b:1319:C:O2'	34:b:1320:C:H5'	2.17	0.44
34:b:1484:U:H2'	34:b:1485:U:H6	1.81	0.44
34:b:2514:U:H2'	34:b:2515:C:C6	2.52	0.44
52:v:62:GLU:OE1	52:v:62:GLU:N	2.41	0.44
9:A:456:A:H2'	9:A:457:G:H8	1.83	0.44
9:A:622:A:C8	9:A:623:C:C5	3.05	0.44
9:A:978:A:C5	9:A:1318:A:C6	3.06	0.44
19:K:79:LYS:NZ	19:K:103:GLY:O	2.50	0.44
32:Y:5:G:N1	32:Y:6:A:N1	2.65	0.44
34:b:285:G:H2'	34:b:286:U:N1	2.33	0.44
34:b:1406:U:H2'	34:b:1407:G:H8	1.82	0.44
34:b:1585:C:H2'	34:b:1586:A:O4'	2.17	0.44
36:d:139:SER:O	36:d:139:SER:OG	2.22	0.44
37:e:6:LYS:HB3	37:e:121:VAL:HG12	1.99	0.44
37:e:119:ILE:O	37:e:187:VAL:HA	2.17	0.44
40:h:46:PHE:CE2	40:h:50:ARG:HD2	2.53	0.44
45:o:35:LYS:HB2	45:o:112:TYR:CE1	2.52	0.44
52:v:7:ARG:O	52:v:25:VAL:HG13	2.17	0.44
3:2:56:LYS:HD3	3:2:57:VAL:N	2.33	0.44
9:A:374:A:O2'	9:A:375:U:O4'	2.31	0.44
9:A:936:C:C2	9:A:937:A:C8	3.05	0.44
9:A:1169:A:H3'	9:A:1170:A:C8	2.53	0.44
9:A:1253:G:H2'	9:A:1254:A:C8	2.52	0.44
9:A:1306:A:H61	9:A:1331:G:H1'	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:152:ASP:OD1	10:B:152:ASP:N	2.49	0.44
12:D:57:LYS:HB2	12:D:199:ILE:HD12	1.99	0.44
12:D:72:ARG:O	12:D:76:LYS:HG3	2.18	0.44
12:D:157:ALA:O	12:D:161:ALA:N	2.51	0.44
32:Z:32:G:H2'	32:Z:32:G:N3	2.32	0.44
34:b:372:G:O2'	34:b:400:G:O6	2.26	0.44
34:b:635:C:OP2	43:m:126:ARG:NH1	2.51	0.44
34:b:900:A:H2'	34:b:901:C:O4'	2.17	0.44
36:d:11:MET:HG2	36:d:25:THR:HA	2.00	0.44
40:h:137:GLU:OE1	40:h:137:GLU:N	2.51	0.44
44:n:69:PRO:HB2	44:n:92:TRP:HB3	1.99	0.44
9:A:439:U:H5'	12:D:120:LYS:H	1.83	0.44
9:A:620:C:C4	12:D:131:ILE:HG13	2.52	0.44
9:A:883:C:H2'	9:A:884:U:C6	2.53	0.44
9:A:1254:A:H2'	9:A:1255:G:C8	2.53	0.44
9:A:1345:U:H5''	17:I:121:ARG:HH11	1.83	0.44
9:A:1346:A:H61	9:A:1374:A:H3'	1.81	0.44
18:J:37:ARG:CZ	18:J:38:GLY:H	2.30	0.44
20:L:41:PRO:HB2	20:L:45:ASN:HB3	1.99	0.44
20:L:42:LYS:HG2	20:L:43:LYS:H	1.82	0.44
21:M:33:LEU:HA	21:M:33:LEU:HD23	1.82	0.44
22:N:53:ASP:OD1	22:N:58:ARG:NE	2.36	0.44
30:V:42:ASP:O	34:b:1337:G:O2'	2.23	0.44
31:X:5:G:H2'	31:X:6:A:C8	2.53	0.44
32:Z:65:C:N4	32:Z:66:U:O4	2.51	0.44
34:b:1721:G:N2	34:b:1738:G:H2'	2.32	0.44
34:b:2194:U:H2'	34:b:2195:U:H6	1.83	0.44
9:A:31:G:N3	9:A:306:A:O2'	2.51	0.44
9:A:562:U:H2'	20:L:13:ARG:NH2	2.32	0.44
9:A:643:C:H2'	9:A:644:U:C6	2.52	0.44
9:A:660:C:N3	9:A:746:A:N6	2.65	0.44
9:A:662:U:O2'	9:A:836:G:OP1	2.35	0.44
9:A:806:C:H2'	9:A:807:A:H8	1.82	0.44
12:D:124:VAL:HG12	12:D:125:ASN:ND2	2.30	0.44
15:G:91:ARG:O	15:G:95:ARG:HG3	2.18	0.44
16:H:17:GLN:HE21	16:H:17:GLN:HA	1.83	0.44
17:I:38:PHE:HZ	17:I:75:ALA:HB2	1.83	0.44
34:b:27:G:N2	34:b:512:G:H2'	2.33	0.44
34:b:882:G:N1	34:b:895:U:O2'	2.50	0.44
34:b:1496:A:H2'	34:b:1498:C:C5	2.53	0.44
38:f:130:MET:HG3	38:f:154:ILE:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:41:G:C2	9:A:42:G:C5	3.06	0.44
9:A:372:C:H41	9:A:387:U:H3'	1.83	0.44
9:A:750:C:H2'	9:A:751:U:H6	1.83	0.44
9:A:833:G:H2'	9:A:834:U:C6	2.53	0.44
12:D:103:ARG:HB2	12:D:170:LEU:HD13	1.99	0.44
15:G:114:SER:O	15:G:117:LEU:N	2.44	0.44
15:G:115:MET:HE2	15:G:115:MET:HB2	1.84	0.44
27:S:3:SER:HB3	27:S:5:LYS:HZ1	1.81	0.44
28:T:14:GLU:O	28:T:18:LYS:HG2	2.18	0.44
32:Y:50:G:C5	32:Y:67:A:C6	3.06	0.44
34:b:259:G:HO2'	34:b:621:A:HO2'	1.63	0.44
34:b:740:C:H41	34:b:757:G:H1	1.66	0.44
34:b:1387:A:H5'	34:b:1469:A:H1'	2.00	0.44
34:b:1548:A:H2'	34:b:1549:A:C8	2.53	0.44
34:b:2788:C:H2'	34:b:2789:C:C6	2.53	0.44
46:p:34:HIS:ND1	46:p:53:THR:OG1	2.39	0.44
48:r:58:ARG:O	48:r:62:ILE:HG12	2.18	0.44
9:A:100:G:C4	9:A:101:A:C8	3.05	0.43
9:A:390:U:H4'	24:P:28:ARG:NH2	2.33	0.43
9:A:606:G:H21	9:A:631:C:H3'	1.83	0.43
9:A:713:G:H2'	9:A:714:G:C8	2.53	0.43
9:A:875:U:O2'	16:H:14:ARG:NH1	2.51	0.43
9:A:1072:G:H2'	9:A:1073:U:C6	2.52	0.43
9:A:1432:G:OP2	47:q:106:LYS:NZ	2.30	0.43
10:B:61:SER:OG	10:B:223:GLY:O	2.26	0.43
10:B:89:PHE:HB3	10:B:149:GLY:O	2.17	0.43
21:M:58:GLU:O	21:M:61:LYS:HG2	2.18	0.43
26:R:12:PHE:HA	26:R:17:VAL:HB	2.00	0.43
27:S:45:GLY:HA2	27:S:60:PHE:CZ	2.52	0.43
31:X:18:G:C8	31:X:60:U:C5	3.06	0.43
34:b:63:A:H2'	34:b:64:A:H8	1.83	0.43
34:b:2100:G:H2'	34:b:2101:A:C8	2.53	0.43
34:b:2164:C:O2'	34:b:2166:U:O4	2.35	0.43
38:f:110:ARG:HH21	38:f:137:ILE:C	2.26	0.43
38:f:141:ILE:HG13	38:f:146:VAL:HG22	2.00	0.43
40:h:132:PHE:HB2	40:h:140:ALA:HB3	2.00	0.43
52:v:14:LEU:HD11	52:v:71:ALA:HB2	1.99	0.43
9:A:950:U:OP2	21:M:100:ARG:HD2	2.17	0.43
9:A:1057:G:H2'	9:A:1058:G:O4'	2.18	0.43
9:A:1309:G:O6	9:A:1329:A:N6	2.50	0.43
11:C:21:TRP:HB3	11:C:58:ARG:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:109:THR:HG23	12:D:111:ALA:N	2.33	0.43
15:G:137:ARG:O	15:G:141:HIS:ND1	2.50	0.43
19:K:35:ASP:OD1	19:K:41:LEU:HD21	2.18	0.43
26:R:33:THR:HG22	26:R:34:GLU:H	1.83	0.43
34:b:17:G:H2'	34:b:18:U:C6	2.53	0.43
34:b:1277:G:C4'	45:o:20:MET:HE3	2.48	0.43
34:b:2114:A:N6	34:b:2119:A:N7	2.66	0.43
34:b:2813:A:H2'	34:b:2814:A:C8	2.53	0.43
38:f:48:LYS:HE3	38:f:52:ASN:HB2	2.00	0.43
4:4:29:SER:OG	4:4:40:ARG:HD3	2.18	0.43
9:A:312:C:H2'	9:A:313:A:C8	2.53	0.43
9:A:414:A:H2'	9:A:414:A:N3	2.34	0.43
9:A:461:A:H2'	9:A:462:G:N7	2.32	0.43
9:A:1287:A:H2	9:A:1353:G:H1'	1.84	0.43
14:F:24:ARG:NH1	14:F:24:ARG:HA	2.34	0.43
14:F:44:ARG:HA	14:F:57:ALA:O	2.18	0.43
33:a:60:C:H2'	33:a:61:G:C8	2.52	0.43
34:b:365:U:H2'	34:b:366:C:C6	2.53	0.43
34:b:1535:A:N1	34:b:1538:G:H1'	2.33	0.43
34:b:1722:A:H2'	34:b:1722:A:N3	2.32	0.43
34:b:2148:G:H2'	34:b:2149:U:C5	2.53	0.43
39:g:42:GLU:OE1	39:g:55:ARG:HG2	2.18	0.43
47:q:4:ILE:H	47:q:4:ILE:HD12	1.84	0.43
48:r:98:ILE:HG22	48:r:106:PHE:HD2	1.83	0.43
9:A:987:G:H2'	9:A:988:G:H8	1.83	0.43
9:A:1130:A:H2'	9:A:1131:G:C8	2.53	0.43
9:A:1319:A:C4	9:A:1323:G:C8	3.07	0.43
9:A:1321:U:OP2	9:A:1322:C:O2'	2.21	0.43
11:C:5:HIS:CG	22:N:88:MET:SD	3.11	0.43
11:C:23:ALA:HB1	11:C:27:GLU:HG2	2.00	0.43
12:D:123:MET:H	12:D:144:ILE:HA	1.84	0.43
14:F:15:SER:HA	14:F:18:VAL:HG23	2.00	0.43
19:K:93:GLU:N	19:K:93:GLU:OE1	2.51	0.43
20:L:82:ARG:HB2	20:L:97:VAL:HG22	2.00	0.43
32:Y:16:C:H5''	32:Y:17:C:C5	2.54	0.43
32:Y:76:C:H5''	32:Y:77:A:OP2	2.18	0.43
34:b:465:G:H2'	34:b:466:A:C8	2.53	0.43
34:b:745:G:O2'	34:b:748:G:O2'	2.29	0.43
34:b:2132:U:O2'	34:b:2133:G:O5'	2.37	0.43
41:k:71:ASP:O	41:k:73:VAL:HG23	2.19	0.43
9:A:20:U:O2'	9:A:573:A:N6	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:146:G:H2'	9:A:147:G:H8	1.81	0.43
9:A:254:G:O3'	25:Q:70:LYS:NZ	2.49	0.43
9:A:1227:A:H2'	21:M:115:ILE:HD11	2.01	0.43
9:A:1266:G:N2	9:A:1269:A:OP2	2.44	0.43
10:B:138:ARG:CZ	10:B:138:ARG:HA	2.49	0.43
21:M:89:ARG:NH2	21:M:94:LEU:HB3	2.33	0.43
26:R:56:ARG:HB3	26:R:56:ARG:NH1	2.34	0.43
34:b:265:A:N6	34:b:428:A:C8	2.87	0.43
34:b:1019:U:O2'	34:b:1021:A:H2	2.01	0.43
34:b:1744:A:C2	34:b:1745:A:H1'	2.54	0.43
34:b:2137:U:H5''	34:b:2138:G:N7	2.33	0.43
34:b:2153:C:H2'	34:b:2154:A:N7	2.32	0.43
42:l:34:GLY:N	42:l:37:ASP:OD2	2.25	0.43
45:o:72:ASP:OD1	45:o:74:GLU:N	2.50	0.43
9:A:262:A:N7	9:A:263:A:C5	2.87	0.43
9:A:313:A:H2'	9:A:314:C:C6	2.54	0.43
9:A:510:A:H5''	9:A:511:C:OP2	2.19	0.43
9:A:687:A:C2	9:A:704:A:C5	3.07	0.43
9:A:746:A:H2'	9:A:747:A:H8	1.82	0.43
9:A:1254:A:OP1	18:J:45:ARG:NH2	2.44	0.43
11:C:14:VAL:HB	11:C:206:ILE:HD12	2.00	0.43
11:C:17:TRP:HZ2	22:N:96:LYS:HZ3	1.65	0.43
11:C:26:LYS:HE3	11:C:26:LYS:HB3	1.82	0.43
11:C:28:PHE:HE2	22:N:76:PHE:HA	1.83	0.43
17:I:46:VAL:HA	17:I:49:GLN:CD	2.43	0.43
21:M:8:ILE:HG21	21:M:17:ALA:HB1	2.01	0.43
34:b:285:G:N1	34:b:356:G:C6	2.87	0.43
34:b:1332:G:N7	34:b:1609:A:O2'	2.43	0.43
34:b:1417:C:H2'	34:b:1418:G:O4'	2.19	0.43
34:b:1779:U:O2	34:b:1783:A:N6	2.52	0.43
34:b:2111:U:C5'	34:b:2112:G:H4'	2.47	0.43
34:b:2194:U:H2'	34:b:2195:U:C6	2.54	0.43
35:c:165:VAL:HG21	35:c:181:MET:HE1	2.01	0.43
39:g:2:SER:O	39:g:6:LYS:HG2	2.18	0.43
51:u:26:LYS:HE2	51:u:26:LYS:HB2	1.87	0.43
7:7:51:SER:OG	7:7:52:LYS:N	2.52	0.43
9:A:186:C:N4	9:A:187:G:O6	2.52	0.43
9:A:500:G:H2'	9:A:501:C:H6	1.83	0.43
9:A:1306:A:N6	9:A:1331:G:H1'	2.33	0.43
12:D:9:LYS:HE3	12:D:9:LYS:HB3	1.87	0.43
21:M:62:PHE:HB3	21:M:64:VAL:HG23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:O:8:ALA:O	23:O:11:VAL:HG12	2.19	0.43
33:a:106:G:H2'	33:a:107:G:O4'	2.19	0.43
34:b:2:G:O2'	34:b:3:U:H5'	2.18	0.43
34:b:964:C:O2'	34:b:2273:A:N3	2.48	0.43
34:b:1589:U:H2'	34:b:1590:A:H8	1.83	0.43
34:b:2809:A:OP2	34:b:2890:G:N1	2.39	0.43
9:A:185:U:H2'	9:A:186:C:C6	2.54	0.43
9:A:185:U:H2'	9:A:186:C:H6	1.82	0.43
9:A:625:U:H2'	9:A:626:G:C8	2.42	0.43
9:A:985:C:H2'	9:A:986:U:C6	2.53	0.43
9:A:1003:G:H2'	9:A:1037:C:O2	2.18	0.43
9:A:1434:A:H2'	9:A:1435:G:O4'	2.19	0.43
15:G:71:THR:OG1	15:G:95:ARG:NH2	2.52	0.43
17:I:40:ARG:HD3	17:I:44:ARG:HG3	2.01	0.43
21:M:33:LEU:HD13	21:M:40:GLU:HA	2.01	0.43
28:T:43:LYS:O	28:T:47:GLN:HG2	2.18	0.43
31:X:10:G:H2'	31:X:11:C:C6	2.53	0.43
32:Y:49:C:H5''	32:Y:50:G:OP1	2.18	0.43
32:Z:44:G:H2'	32:Z:45:G:C8	2.54	0.43
34:b:2184:A:H2'	34:b:2185:U:H6	1.83	0.43
34:b:2581:G:OP2	34:b:2581:G:N2	2.46	0.43
34:b:2901:C:H2'	34:b:2902:C:C6	2.54	0.43
53:w:62:THR:HG23	53:w:69:GLU:OE2	2.18	0.43
9:A:104:G:H2'	9:A:105:G:C8	2.53	0.43
9:A:502:A:H2'	9:A:503:C:C6	2.53	0.43
9:A:1109:C:C2	9:A:1110:A:C8	3.07	0.43
9:A:1277:C:H1'	9:A:1282:C:O2	2.18	0.43
9:A:1316:G:N2	9:A:1318:A:H3'	2.34	0.43
14:F:23:GLU:HA	14:F:26:THR:HG22	2.00	0.43
16:H:9:MET:HE2	16:H:9:MET:HB2	1.72	0.43
33:a:46:A:H3'	33:a:47:C:O2	2.19	0.43
34:b:9:G:O2'	34:b:10:A:O5'	2.34	0.43
34:b:9:G:H4'	34:b:10:A:OP1	2.19	0.43
34:b:1965:C:H5''	34:b:1966:A:H2'	2.01	0.43
34:b:2313:C:H2'	34:b:2314:A:C8	2.53	0.43
36:d:36:GLN:HB3	36:d:49:GLN:HE21	1.84	0.43
37:e:21:ARG:HD3	37:e:106:LYS:HB3	2.01	0.43
38:f:142:ASP:O	38:f:146:VAL:HG23	2.18	0.43
46:p:60:GLU:H	46:p:60:GLU:CD	2.26	0.43
9:A:1127:G:H5'	9:A:1280:A:O2'	2.19	0.43
9:A:1256:A:H62	9:A:1279:G:H21	1.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:129:THR:O	10:B:132:GLU:HG3	2.19	0.43
13:E:131:ASN:OD1	13:E:131:ASN:N	2.52	0.43
34:b:228:C:H4'	34:b:229:C:O5'	2.18	0.43
34:b:608:A:H2'	34:b:609:A:C8	2.53	0.43
34:b:2179:C:H2'	34:b:2180:U:C5	2.53	0.43
34:b:2802:G:H2'	34:b:2803:G:H8	1.84	0.43
43:m:1:MET:SD	43:m:2:ARG:N	2.92	0.43
56:z:152[A]:GLY:C	56:z:154[A]:TRP:N	2.77	0.43
9:A:1:A:H2'	9:A:2:A:N3	2.34	0.42
9:A:551:U:H6	20:L:82:ARG:NH2	2.17	0.42
9:A:707:U:H4'	19:K:21:HIS:CD2	2.54	0.42
9:A:1042:A:H2'	9:A:1043:G:C4	2.54	0.42
17:I:87:MET:N	17:I:87:MET:SD	2.92	0.42
25:Q:54:ILE:HD12	25:Q:54:ILE:HA	1.87	0.42
32:Z:1:C:H6	32:Z:1:C:O5'	2.02	0.42
32:Z:50:G:O6	32:Z:67:A:N6	2.52	0.42
34:b:247:G:N2	34:b:250:G:O2'	2.52	0.42
34:b:280:U:O4	34:b:360:U:N3	2.52	0.42
34:b:288:U:H2'	34:b:289:G:C8	2.54	0.42
34:b:639:U:H2'	34:b:640:C:C6	2.53	0.42
34:b:969:G:H2'	34:b:970:U:C6	2.54	0.42
34:b:1917:U:O4	34:b:1918:A:N6	2.52	0.42
34:b:2111:U:OP1	34:b:2119:A:H5'	2.19	0.42
34:b:2327:A:H2'	34:b:2328:A:C8	2.53	0.42
38:f:66:LEU:HD21	38:f:88:LYS:HD3	2.01	0.42
39:g:80:THR:OG1	39:g:81:GLU:OE1	2.25	0.42
9:A:65:A:C5	9:A:381:C:N3	2.87	0.42
9:A:405:U:O5'	12:D:2:ARG:NH2	2.52	0.42
9:A:1048:G:H5''	22:N:2:LYS:HG2	2.01	0.42
9:A:1123:U:O2'	18:J:37:ARG:NH1	2.52	0.42
10:B:72:LYS:NZ	10:B:203:ASP:O	2.45	0.42
11:C:5:HIS:HE1	11:C:7:ASN:OD1	2.02	0.42
23:O:9:LYS:O	23:O:12:SER:OG	2.36	0.42
34:b:285:G:O2'	34:b:286:U:OP1	2.27	0.42
34:b:368:A:H2'	34:b:369:U:C6	2.54	0.42
34:b:1021:A:H8	34:b:1022:G:H5''	1.83	0.42
34:b:1410:G:H2'	34:b:1411:U:H6	1.83	0.42
34:b:2074:U:H2'	34:b:2075:U:C6	2.55	0.42
34:b:2110:G:H3'	34:b:2118:U:O2'	2.19	0.42
34:b:2305:U:N3	38:f:151:GLY:HA3	2.32	0.42
9:A:195:A:O2'	9:A:196:A:O5'	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:524:G:H2'	9:A:525:C:H6	1.84	0.42
9:A:1226:C:H2'	21:M:101:THR:HG23	2.01	0.42
9:A:1448:C:H2'	9:A:1449:C:C6	2.54	0.42
12:D:71:PHE:HA	12:D:74:TYR:CD2	2.54	0.42
16:H:26:MET:HE1	16:H:32:LYS:NZ	2.34	0.42
27:S:23:GLU:OE2	27:S:24:SER:OG	2.34	0.42
32:Y:52:A:HO2'	32:Y:53:G:H5''	1.83	0.42
34:b:555:G:O2'	34:b:556:A:H8	2.02	0.42
34:b:1176:U:H3'	34:b:1177:G:H8	1.84	0.42
34:b:2112:G:H5'	34:b:2113:U:C6	2.54	0.42
44:n:14:LYS:HE3	44:n:14:LYS:HB2	1.88	0.42
44:n:69:PRO:CD	44:n:70:ASP:N	2.82	0.42
9:A:506:G:H2'	9:A:507:C:C6	2.54	0.42
9:A:623:C:H2'	9:A:624:C:C6	2.53	0.42
9:A:908:A:H2'	9:A:909:A:H8	1.83	0.42
10:B:55:GLU:O	10:B:59:ILE:N	2.49	0.42
12:D:139:ASN:H	12:D:182:LYS:HA	1.85	0.42
13:E:106:ALA:HB1	13:E:110:MET:HB3	2.01	0.42
15:G:12:LEU:HD21	17:I:49:GLN:HE22	1.84	0.42
19:K:60:PHE:O	19:K:63:GLN:HG2	2.19	0.42
28:T:54:GLN:N	28:T:55:PRO:HD2	2.35	0.42
34:b:263:G:H2'	34:b:264:C:O4'	2.20	0.42
34:b:267:C:HO2'	34:b:268:C:P	2.42	0.42
34:b:900:A:H2'	34:b:901:C:C6	2.54	0.42
34:b:1321:A:N3	34:b:1321:A:H2'	2.34	0.42
34:b:1884:G:OP2	34:b:1884:G:H8	2.03	0.42
34:b:2557:G:H2'	34:b:2558:C:C6	2.54	0.42
45:o:72:ASP:OD1	45:o:73:ASN:N	2.53	0.42
9:A:39:G:H2'	9:A:40:C:C6	2.53	0.42
10:B:20:ARG:O	10:B:20:ARG:NE	2.43	0.42
10:B:59:ILE:HD13	10:B:59:ILE:HA	1.89	0.42
15:G:114:SER:O	15:G:116:ALA:N	2.52	0.42
29:U:4:LYS:HE2	29:U:4:LYS:HB3	1.77	0.42
32:Y:56:U:O2'	32:Y:58:G:N7	2.39	0.42
32:Y:72:C:H2'	32:Y:73:G:C8	2.54	0.42
34:b:1071:G:N2	34:b:1091:G:OP2	2.52	0.42
43:m:123:ARG:NH1	43:m:143:GLU:OE2	2.52	0.42
9:A:101:A:H2'	9:A:102:G:C8	2.55	0.42
9:A:195:A:H2'	9:A:196:A:C8	2.54	0.42
9:A:253:A:H2'	9:A:254:G:C8	2.54	0.42
9:A:553:A:H2'	9:A:554:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:778:G:N3	19:K:121:ARG:NH1	2.65	0.42
9:A:949:A:N6	9:A:1233:G:C6	2.88	0.42
9:A:994:A:C2	9:A:1216:A:H4'	2.54	0.42
9:A:1030:U:H3'	9:A:1031:C:C6	2.54	0.42
9:A:1125:U:O2'	9:A:1126:U:O5'	2.31	0.42
23:O:56:LEU:HG	23:O:57:ARG:HH21	1.84	0.42
23:O:57:ARG:NE	23:O:57:ARG:HA	2.34	0.42
25:Q:51:GLU:OE1	25:Q:51:GLU:N	2.38	0.42
31:X:58:A:C2	31:X:60:U:H5''	2.55	0.42
34:b:181:A:H2'	34:b:182:A:H8	1.84	0.42
34:b:345:A:H1'	34:b:346:A:C2	2.55	0.42
34:b:571:U:H3'	49:s:80:ARG:NH2	2.34	0.42
34:b:784:G:H5'	34:b:785:G:OP1	2.19	0.42
34:b:1589:U:H2'	34:b:1590:A:C8	2.55	0.42
34:b:2100:G:C6	34:b:2190:G:C6	3.07	0.42
34:b:2700:A:H2'	34:b:2701:U:C6	2.54	0.42
37:e:15:SER:N	37:e:197:GLU:OE2	2.51	0.42
37:e:61:ARG:HE	37:e:65:THR:HG23	1.84	0.42
38:f:143:TYR:HA	38:f:146:VAL:HB	2.02	0.42
44:n:69:PRO:CG	44:n:70:ASP:H	2.32	0.42
9:A:274:A:H1'	9:A:275:G:C8	2.55	0.42
9:A:1148:U:H2'	9:A:1149:C:O4'	2.20	0.42
10:B:44:LYS:HA	10:B:44:LYS:HD2	1.84	0.42
11:C:55:VAL:HB	11:C:66:THR:HB	2.00	0.42
12:D:24:VAL:HG22	12:D:160:LEU:HD22	2.02	0.42
23:O:88:ARG:HH22	34:b:714:U:P	2.42	0.42
25:Q:10:ARG:HA	25:Q:10:ARG:HH11	1.85	0.42
34:b:1392:A:O2'	34:b:1393:A:O4'	2.38	0.42
34:b:1443:U:H2'	34:b:1444:G:H8	1.85	0.42
34:b:1532:A:C6	34:b:1533:C:C4	3.08	0.42
37:e:3:LEU:HD12	37:e:3:LEU:HA	1.84	0.42
39:g:117:LEU:HD12	39:g:117:LEU:HA	1.85	0.42
40:h:119:ASN:OD1	40:h:119:ASN:N	2.52	0.42
2:1:4:LYS:HG3	2:1:5:GLU:OE1	2.20	0.42
9:A:504:C:H1'	9:A:510:A:H2'	2.01	0.42
17:I:45:MET:HA	17:I:48:ARG:HD3	2.01	0.42
32:Y:16:C:H4'	32:Y:17:C:OP2	2.19	0.42
34:b:1205:A:O2'	34:b:1206:G:OP1	2.38	0.42
34:b:1537:G:H2'	34:b:1538:G:O4'	2.20	0.42
43:m:2:ARG:HA	43:m:2:ARG:HD3	1.87	0.42
49:s:43:ASN:OD1	49:s:43:ASN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:263:A:P	28:T:73:ARG:HH12	2.43	0.42
9:A:1125:U:HO2'	9:A:1126:U:P	2.42	0.42
9:A:1360:A:H2'	9:A:1361:G:O4'	2.20	0.42
11:C:44:LYS:HB3	11:C:44:LYS:HE2	1.78	0.42
17:I:40:ARG:CZ	17:I:44:ARG:HE	2.32	0.42
17:I:83:THR:HG21	17:I:102:PHE:HB3	2.02	0.42
34:b:52:A:H2'	34:b:53:A:C8	2.55	0.42
34:b:134:G:H2'	34:b:135:U:C6	2.54	0.42
34:b:581:C:H2'	34:b:582:A:H8	1.85	0.42
34:b:1060:U:H1'	34:b:1062:G:P	2.60	0.42
34:b:1403:A:HO2'	34:b:1471:G:HO2'	1.62	0.42
34:b:1790:C:H2'	34:b:1791:A:C8	2.55	0.42
34:b:2142:A:H2'	34:b:2143:C:C2	2.54	0.42
34:b:2267:A:N6	34:b:2272:U:H3	2.18	0.42
34:b:2554:U:C2	34:b:2555:U:C5	3.07	0.42
9:A:17:U:H2'	9:A:18:C:C6	2.55	0.42
9:A:504:C:H4'	9:A:510:A:N7	2.34	0.42
9:A:590:U:C4	9:A:650:G:C6	3.08	0.42
9:A:1124:G:H4'	18:J:37:ARG:HD3	2.02	0.42
18:J:14:ASP:OD2	18:J:17:LEU:N	2.44	0.42
22:N:38:GLU:OE2	22:N:42:ASN:ND2	2.52	0.42
34:b:581:C:H2'	34:b:582:A:C8	2.55	0.42
34:b:640:C:H2'	34:b:641:U:H6	1.84	0.42
34:b:880:G:N2	34:b:897:C:H42	2.18	0.42
34:b:1069:A:O2'	34:b:1072:C:OP2	2.31	0.42
34:b:2281:A:O2'	34:b:2282:G:H5'	2.20	0.42
34:b:2655:G:O2'	34:b:2656:U:P	2.78	0.42
35:c:268:VAL:HG12	35:c:269:ARG:HG2	2.02	0.42
38:f:72:LYS:HG2	38:f:73:SER:H	1.83	0.42
39:g:99:LYS:HB3	39:g:99:LYS:HE3	1.78	0.42
40:h:29:PHE:C	40:h:32:PRO:HD2	2.45	0.42
9:A:477:C:H2'	9:A:478:A:H8	1.78	0.41
9:A:939:G:H4'	15:G:101:ARG:NH1	2.35	0.41
15:G:130:LYS:HB3	15:G:130:LYS:HE3	1.82	0.41
24:P:46:LYS:HB2	24:P:46:LYS:HE2	1.78	0.41
25:Q:28:VAL:HG22	25:Q:29:LYS:H	1.85	0.41
32:Y:52:A:O2'	32:Y:53:G:H8	2.03	0.41
34:b:729:G:H5'	34:b:730:A:H5''	2.02	0.41
34:b:871:U:H2'	34:b:872:U:H6	1.85	0.41
34:b:1538:G:H2'	34:b:1539:U:H6	1.84	0.41
34:b:2119:A:N6	34:b:2167:U:H1'	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:x:13:G:H2'	54:x:14:C:C6	2.55	0.41
2:1:47:ARG:NH2	34:b:61:C:OP2	2.52	0.41
9:A:56:U:H2'	9:A:57:G:C8	2.55	0.41
9:A:339:C:OP2	42:l:98:ARG:NH2	2.53	0.41
9:A:422:C:H4'	9:A:423:G:C4	2.54	0.41
9:A:492:C:O2'	9:A:493:A:H5'	2.20	0.41
9:A:690:G:H2'	9:A:691:G:C8	2.55	0.41
9:A:721:G:H4'	9:A:722:G:O4'	2.20	0.41
9:A:985:C:H2'	9:A:986:U:H6	1.85	0.41
11:C:48:LYS:HB2	11:C:48:LYS:HE2	1.84	0.41
12:D:66:VAL:HG21	12:D:74:TYR:HE2	1.84	0.41
14:F:47:LEU:HD12	14:F:47:LEU:C	2.45	0.41
20:L:34:THR:O	20:L:75:GLU:HB3	2.20	0.41
20:L:89:LEU:HD23	20:L:89:LEU:HA	1.94	0.41
23:O:11:VAL:HG21	23:O:21:THR:HG22	2.02	0.41
31:X:53:G:H2'	31:X:54:U:C6	2.55	0.41
58:Z:101:PRO:CG	56:z:160:ARG:HG2	2.51	0.41
34:b:276:U:O2'	34:b:278:A:N6	2.53	0.41
34:b:1082:U:H2'	34:b:1083:U:H4'	2.01	0.41
34:b:1406:U:H2'	34:b:1407:G:C8	2.54	0.41
34:b:2638:G:H1'	34:b:2778:A:H61	1.85	0.41
35:c:141:VAL:N	35:c:162:VAL:O	2.50	0.41
37:e:188:MET:HE3	37:e:193:VAL:HG22	2.02	0.41
41:k:26:GLY:O	41:k:30:THR:HG23	2.20	0.41
43:m:29:LYS:O	43:m:30:THR:OG1	2.31	0.41
44:n:58:LYS:O	44:n:60:GLN:NE2	2.53	0.41
9:A:8:A:N1	12:D:205:LYS:NZ	2.68	0.41
9:A:110:C:H5	9:A:111:G:C5	2.38	0.41
9:A:550:G:N3	20:L:114:SER:OG	2.53	0.41
9:A:954:G:H21	9:A:1227:A:N6	1.98	0.41
9:A:981:U:H2'	9:A:982:U:C5	2.55	0.41
9:A:1115:U:H2'	9:A:1116:U:C6	2.55	0.41
9:A:1238:A:H2	9:A:1241:G:N3	2.18	0.41
14:F:35:LYS:HB2	14:F:35:LYS:HE2	1.80	0.41
15:G:92:PRO:HA	15:G:95:ARG:HD3	2.01	0.41
20:L:100:ALA:HB3	20:L:103:CYS:SG	2.60	0.41
27:S:13:HIS:O	27:S:17:LYS:NZ	2.39	0.41
34:b:222:A:N1	34:b:233:A:H5''	2.36	0.41
34:b:892:A:C8	34:b:893:C:C4	3.08	0.41
34:b:1386:C:H2'	34:b:1387:A:C8	2.55	0.41
34:b:1596:A:H2'	34:b:1597:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:b:1713:A:H61	34:b:1745:A:N6	2.18	0.41
36:d:12:THR:HB	47:q:5:ILE:HD11	2.02	0.41
38:f:80:ARG:HB2	38:f:83:TYR:CE2	2.55	0.41
39:g:47:ASP:N	39:g:47:ASP:OD1	2.51	0.41
40:h:110:VAL:HG13	40:h:114:GLU:HG2	2.03	0.41
41:k:90:GLU:OE1	41:k:90:GLU:N	2.54	0.41
49:s:41:ILE:HG13	49:s:48:LYS:HG3	2.02	0.41
49:s:43:ASN:O	49:s:45:GLU:N	2.49	0.41
49:s:69:GLY:N	49:s:91:GLN:O	2.43	0.41
51:u:54:GLU:OE1	51:u:54:GLU:N	2.53	0.41
9:A:101:A:H2'	9:A:102:G:H8	1.85	0.41
9:A:507:C:OP2	9:A:508:U:O2'	2.28	0.41
9:A:860:A:H2'	9:A:861:G:O4'	2.20	0.41
9:A:945:G:H21	9:A:1334:G:H4'	1.85	0.41
9:A:1309:G:H2'	9:A:1310:G:H8	1.85	0.41
9:A:1435:G:H2'	9:A:1436:U:H6	1.86	0.41
12:D:94:GLU:OE2	12:D:185:PRO:HB3	2.20	0.41
17:I:45:MET:HE3	17:I:45:MET:H	1.85	0.41
19:K:12:ARG:HA	19:K:12:ARG:HD3	1.95	0.41
19:K:58:THR:HG22	19:K:60:PHE:H	1.84	0.41
21:M:92:ARG:HB2	21:M:94:LEU:HD13	2.03	0.41
28:T:59:ARG:HG2	28:T:63:LYS:HE2	2.02	0.41
32:Z:63:C:H2'	32:Z:64:U:C6	2.56	0.41
34:b:279:A:N3	34:b:280:U:H1'	2.35	0.41
34:b:280:U:H6	34:b:280:U:H2'	1.70	0.41
34:b:1361:G:H2'	34:b:1362:C:H6	1.86	0.41
34:b:1401:G:H2'	34:b:1402:U:C6	2.56	0.41
34:b:2328:A:H2'	34:b:2329:U:H6	1.83	0.41
51:u:56:GLU:N	51:u:56:GLU:OE1	2.53	0.41
55:y:33:ALA:N	55:y:64:ASP:OD1	2.54	0.41
3:2:9:GLN:HB2	3:2:29:LEU:HD13	2.02	0.41
3:2:45:ARG:NH2	3:2:59:GLU:OE1	2.50	0.41
9:A:219:U:H2'	9:A:220:G:H8	1.82	0.41
9:A:500:G:P	9:A:500:G:H8	2.42	0.41
9:A:600:A:OP2	16:H:87:ARG:NE	2.54	0.41
9:A:855:U:H2'	9:A:856:C:C6	2.55	0.41
9:A:1378:C:H5'	15:G:4:ARG:HH12	1.85	0.41
12:D:114:ARG:HA	12:D:117:VAL:HG22	2.02	0.41
29:U:3:ILE:HD13	29:U:18:PHE:HB2	2.02	0.41
34:b:1636:U:H2'	34:b:1637:A:C8	2.55	0.41
34:b:2586:U:C2	56:z:154[B]:TRP:CZ2	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:d:157:LYS:HE3	36:d:157:LYS:HB2	1.75	0.41
40:h:54:LEU:HA	40:h:57:LYS:HZ3	1.86	0.41
1:0:44:LYS:HA	1:0:44:LYS:HD3	1.93	0.41
9:A:87:C:HO2'	9:A:88:U:H5	1.67	0.41
9:A:264:C:H2'	9:A:265:G:C8	2.56	0.41
9:A:298:A:H8	9:A:298:A:OP1	2.03	0.41
9:A:590:U:H5'	16:H:30:LYS:HE3	2.03	0.41
9:A:648:A:H2'	9:A:649:A:H8	1.85	0.41
9:A:1124:G:O2'	9:A:1127:G:N1	2.53	0.41
9:A:1169:A:H3'	9:A:1170:A:H8	1.85	0.41
10:B:114:LYS:HE3	10:B:151:LYS:O	2.20	0.41
10:B:170:ILE:H	10:B:170:ILE:HD12	1.86	0.41
17:I:38:PHE:CZ	17:I:75:ALA:HB2	2.55	0.41
17:I:112:ARG:NH1	17:I:114:LYS:HA	2.35	0.41
28:T:28:ARG:HA	28:T:31:ILE:HG22	2.01	0.41
28:T:65:LEU:HD13	28:T:65:LEU:HA	1.87	0.41
34:b:827:U:O2'	34:b:2068:U:N3	2.52	0.41
34:b:1050:A:C6	34:b:1051:G:C6	3.08	0.41
34:b:1050:A:N6	34:b:1051:G:C6	2.88	0.41
34:b:2682:A:H61	34:b:2728:U:H1'	1.85	0.41
43:m:20:GLY:HA2	43:m:28:GLY:HA2	2.02	0.41
49:s:3:ALA:HB2	49:s:41:ILE:HG22	2.03	0.41
50:t:29:VAL:HG21	50:t:55:ILE:HD11	2.03	0.41
4:4:22:LEU:HD12	50:t:23:LEU:HD21	2.03	0.41
9:A:84:U:C2'	9:A:86:G:H22	2.34	0.41
9:A:104:G:H2'	9:A:105:G:H8	1.86	0.41
9:A:682:G:H2'	9:A:683:G:H8	1.85	0.41
9:A:685:G:C2	9:A:686:U:C4	3.08	0.41
9:A:1147:C:H4'	17:I:6:TYR:CZ	2.55	0.41
9:A:1272:G:H2'	9:A:1273:C:C6	2.55	0.41
9:A:1357:A:HO2'	9:A:1358:U:P	2.42	0.41
17:I:33:SER:OG	17:I:35:GLU:OE1	2.38	0.41
18:J:21:ALA:O	18:J:25:ILE:HG12	2.20	0.41
20:L:81:ILE:HD13	20:L:81:ILE:HA	1.92	0.41
21:M:3:ILE:O	21:M:6:ILE:HG13	2.20	0.41
25:Q:43:LEU:HD23	25:Q:43:LEU:HA	1.93	0.41
34:b:880:G:H22	34:b:897:C:H42	1.68	0.41
34:b:1437:C:H2'	34:b:1438:U:C6	2.56	0.41
34:b:2097:A:H2'	34:b:2098:U:C6	2.55	0.41
35:c:130:LEU:HB2	35:c:135:ILE:HD11	2.02	0.41
52:v:103:ILE:HG22	52:v:104:LYS:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1048:G:OP1	22:N:2:LYS:HA	2.20	0.41
9:A:1070:U:H2'	9:A:1071:C:H6	1.86	0.41
9:A:1357:A:O2'	9:A:1358:U:P	2.78	0.41
10:B:76:SER:C	10:B:92:ASN:HD21	2.29	0.41
10:B:193:ASP:OD1	10:B:193:ASP:N	2.53	0.41
11:C:125:ARG:HH21	11:C:126:ARG:NE	2.19	0.41
28:T:50:PHE:HD2	28:T:82:ILE:HG21	1.86	0.41
34:b:483:A:H5''	52:v:47:LYS:HD2	2.02	0.41
34:b:570:G:H2'	34:b:2030:A:N7	2.36	0.41
34:b:1013:C:H2'	34:b:1014:A:H8	1.85	0.41
34:b:1405:U:H2'	34:b:1406:U:C6	2.56	0.41
34:b:1564:C:H2'	34:b:1565:C:C6	2.56	0.41
39:g:60:ASP:OD1	39:g:60:ASP:N	2.50	0.41
52:v:27:ASN:OD1	52:v:27:ASN:N	2.54	0.41
56:z:129:ARG:HG3	56:z:129:ARG:H	1.57	0.41
9:A:175:C:H2'	9:A:176:C:H6	1.85	0.41
9:A:215:C:O2'	9:A:464:U:O2'	2.37	0.41
9:A:391:G:H5'	24:P:8:ARG:NH2	2.36	0.41
9:A:466:A:H2'	9:A:467:U:H5''	2.03	0.41
9:A:555:U:H2'	9:A:556:C:C6	2.56	0.41
9:A:591:U:H2'	9:A:592:G:H8	1.85	0.41
9:A:705:G:C5	9:A:706:A:C8	3.09	0.41
9:A:953:G:C6	9:A:1229:A:C6	3.09	0.41
9:A:1123:U:H1'	18:J:39:PRO:HD2	2.03	0.41
9:A:1521:C:H2'	9:A:1522:U:C6	2.56	0.41
9:A:1530:G:O6	29:U:45:LYS:NZ	2.53	0.41
10:B:172:ILE:O	10:B:176:ASN:ND2	2.48	0.41
11:C:151:GLU:HB3	11:C:198:LYS:HB2	2.03	0.41
12:D:104:MET:SD	12:D:179:GLY:HA3	2.61	0.41
12:D:106:PHE:O	12:D:154:VAL:HG22	2.20	0.41
15:G:55:LYS:HB3	15:G:59:GLU:HG3	2.02	0.41
16:H:89:ASP:OD1	16:H:89:ASP:N	2.48	0.41
18:J:80:THR:OG1	18:J:81:GLU:N	2.53	0.41
20:L:87:LYS:HA	20:L:87:LYS:HD2	1.76	0.41
21:M:3:ILE:CD1	21:M:56:ARG:HG2	2.50	0.41
22:N:88:MET:HE3	22:N:88:MET:HB3	1.86	0.41
25:Q:60:ILE:HG22	25:Q:72:TRP:HE3	1.86	0.41
25:Q:68:LYS:HG3	25:Q:69:THR:HG23	2.03	0.41
28:T:27:MET:HE3	28:T:28:ARG:HD3	2.02	0.41
31:X:3:G:C2	31:X:71:G:O6	2.74	0.41
31:X:50:C:N4	31:X:51:G:O6	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:48:U:OP1	46:p:30:ARG:NH2	2.54	0.41
34:b:155:A:H2'	34:b:156:A:H8	1.86	0.41
34:b:289:G:H2'	34:b:290:U:H6	1.86	0.41
34:b:817:C:H2'	34:b:818:G:O4'	2.21	0.41
34:b:881:G:H3'	34:b:882:G:C8	2.54	0.41
34:b:1230:A:H2'	34:b:1231:U:C6	2.56	0.41
34:b:1542:U:H2'	34:b:1543:G:O4'	2.21	0.41
34:b:1636:U:H2'	34:b:1637:A:H8	1.85	0.41
34:b:1779:U:OP2	34:b:1784:A:N6	2.47	0.41
34:b:2590:A:H2'	34:b:2591:C:H6	1.86	0.41
34:b:2640:G:OP1	41:k:95:ARG:NH2	2.51	0.41
47:q:60:THR:HG22	47:q:73:VAL:HG22	2.02	0.41
52:v:97:LYS:O	52:v:98:SER:OG	2.37	0.41
1:0:76:GLU:N	1:0:76:GLU:OE1	2.54	0.41
2:1:50:VAL:O	2:1:54:LYS:HG2	2.21	0.41
9:A:40:C:H2'	9:A:41:G:C8	2.50	0.41
9:A:321:A:H4'	9:A:1436:U:H5'	2.01	0.41
9:A:1120:C:H2'	9:A:1121:U:C6	2.56	0.41
9:A:1235:U:H2'	9:A:1236:A:C8	2.56	0.41
9:A:1464:U:H2'	9:A:1465:A:C8	2.54	0.41
10:B:35:ASN:O	10:B:35:ASN:ND2	2.54	0.41
13:E:19:ARG:HD2	13:E:30:PHE:HB3	2.03	0.41
13:E:76:ASN:N	13:E:79:THR:O	2.49	0.41
19:K:115:ILE:HD13	19:K:115:ILE:HA	1.91	0.41
23:O:1:SER:OG	23:O:37:HIS:ND1	2.52	0.41
28:T:26:MET:O	28:T:29:THR:OG1	2.32	0.41
28:T:79:THR:HA	28:T:82:ILE:HG12	2.03	0.41
31:X:71:G:O2'	34:b:1852:U:H5'	2.21	0.41
33:a:67:G:O6	33:a:108:A:H2	2.04	0.41
34:b:2136:G:H1	34:b:2156:G:H1	1.69	0.41
34:b:2655:G:HO2'	34:b:2656:U:P	2.43	0.41
34:b:2700:A:H2'	34:b:2701:U:H6	1.85	0.41
38:f:70:ALA:C	38:f:72:LYS:H	2.29	0.41
4:4:31:ASP:OD1	4:4:34:SER:N	2.54	0.40
9:A:425:G:N2	12:D:39:GLN:OE1	2.54	0.40
9:A:651:C:H2'	9:A:652:U:C6	2.56	0.40
9:A:1100:C:OP2	10:B:94:ARG:NH1	2.54	0.40
9:A:1231:G:H2'	9:A:1232:U:C6	2.56	0.40
12:D:169:TRP:CE3	12:D:170:LEU:HB2	2.56	0.40
16:H:91:LEU:HD13	16:H:92:PRO:HD2	2.03	0.40
21:M:22:TYR:O	21:M:22:TYR:CG	2.75	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:M:67:ASP:OD1	21:M:67:ASP:N	2.53	0.40
34:b:2593:U:H5	34:b:2600:A:N1	2.19	0.40
38:f:100:PHE:HD1	38:f:100:PHE:HA	1.66	0.40
39:g:25:THR:HG22	39:g:34:THR:HG23	2.03	0.40
48:r:72:ASN:OD1	48:r:72:ASN:N	2.54	0.40
9:A:275:G:H2'	9:A:276:G:H8	1.85	0.40
9:A:648:A:H2'	9:A:649:A:C8	2.56	0.40
9:A:736:C:H2'	9:A:737:C:C6	2.56	0.40
9:A:738:C:H2'	9:A:739:C:H6	1.85	0.40
9:A:958:A:N6	27:S:54:ARG:HH21	2.17	0.40
9:A:986:U:H2'	9:A:987:G:C8	2.55	0.40
9:A:1125:U:C2	9:A:1127:G:C8	3.10	0.40
9:A:1405:G:H2'	9:A:1406:U:H6	1.86	0.40
11:C:58:ARG:C	11:C:60:ALA:H	2.28	0.40
11:C:107:LYS:HG2	11:C:110:LEU:H	1.86	0.40
12:D:96:ARG:O	12:D:100:VAL:HG13	2.21	0.40
13:E:81:GLN:HA	13:E:97:PRO:CG	2.51	0.40
14:F:14:GLN:HB3	14:F:17:GLN:HE22	1.84	0.40
16:H:63:LYS:HE2	16:H:70:VAL:HG11	2.02	0.40
24:P:40:ASN:O	24:P:43:ALA:HB2	2.21	0.40
25:Q:25:GLU:OE1	25:Q:25:GLU:N	2.54	0.40
32:Y:29:U:H2'	32:Y:30:U:H6	1.87	0.40
33:a:45:A:C5	33:a:46:A:C2	3.09	0.40
34:b:181:A:H2'	34:b:182:A:C8	2.55	0.40
34:b:613:A:N3	34:b:613:A:H3'	2.37	0.40
34:b:874:G:O6	34:b:899:A:N6	2.55	0.40
34:b:1009:A:N3	34:b:1153:C:O2'	2.53	0.40
34:b:1535:A:O2'	34:b:1536:C:O4'	2.39	0.40
34:b:1703:G:H2'	34:b:1704:C:C6	2.56	0.40
34:b:2177:C:H2'	34:b:2178:C:H6	1.86	0.40
34:b:2267:A:H62	34:b:2272:U:H3	1.68	0.40
34:b:2595:G:N2	34:b:2598:A:OP2	2.47	0.40
37:e:10:SER:OG	37:e:11:ALA:N	2.52	0.40
40:h:42:LYS:HB2	40:h:42:LYS:HE2	1.84	0.40
42:l:68:GLY:C	42:l:69:VAL:HG23	2.46	0.40
43:m:128:THR:HG23	43:m:131:ALA:H	1.86	0.40
53:w:24:ASN:O	53:w:25:LYS:HG3	2.21	0.40
7:7:14:PHE:O	7:7:15:LYS:HD2	2.20	0.40
9:A:524:G:H2'	9:A:525:C:C6	2.56	0.40
9:A:615:G:H1	9:A:625:U:H3	1.70	0.40
9:A:840:C:N4	9:A:842:U:O2	2.43	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Q:3:LYS:HA	25:Q:3:LYS:HD2	1.85	0.40
33:a:51:G:HO2'	33:a:52:A:P	2.44	0.40
34:b:2:G:H2'	34:b:3:U:C6	2.57	0.40
34:b:657:U:H2'	34:b:658:U:C6	2.56	0.40
34:b:900:A:H2'	34:b:901:C:H6	1.87	0.40
34:b:1593:A:H2'	34:b:1594:U:O4'	2.21	0.40
34:b:2121:G:OP1	34:b:2169:A:O2'	2.39	0.40
34:b:2795:C:H2'	34:b:2796:U:O4'	2.21	0.40
35:c:98:ASP:OD1	35:c:98:ASP:N	2.55	0.40
35:c:133:ARG:NH2	35:c:187:ASP:OD1	2.44	0.40
43:m:109:LYS:HG2	43:m:126:ARG:HB2	2.03	0.40
44:n:69:PRO:O	44:n:93:VAL:O	2.39	0.40
51:u:54:GLU:CB	51:u:88:LYS:HG3	2.51	0.40
9:A:253:A:N6	9:A:274:A:N1	2.70	0.40
9:A:416:G:H2'	9:A:417:G:C8	2.56	0.40
9:A:444:G:C6	9:A:491:G:O6	2.74	0.40
9:A:502:A:H4'	9:A:550:G:O4'	2.22	0.40
9:A:957:U:O2'	9:A:959:A:N7	2.52	0.40
9:A:1106:G:H2'	9:A:1107:C:C6	2.56	0.40
9:A:1127:G:C2	9:A:1128:C:C5	3.09	0.40
12:D:71:PHE:CE1	12:D:89:LEU:HD11	2.55	0.40
13:E:54:GLU:HG3	13:E:57:ALA:HB3	2.02	0.40
15:G:45:ALA:HB2	15:G:116:ALA:HA	2.03	0.40
15:G:46:LEU:HD12	15:G:47:GLU:N	2.37	0.40
23:O:13:GLU:CD	23:O:13:GLU:H	2.29	0.40
24:P:7:ALA:O	24:P:17:TYR:HA	2.22	0.40
31:X:66:U:H2'	31:X:67:U:H6	1.86	0.40
33:a:46:A:C5	33:a:47:C:C2	3.10	0.40
34:b:1656:C:H2'	34:b:1657:U:H6	1.87	0.40
34:b:1746:A:H2'	34:b:1747:U:C6	2.56	0.40
34:b:2118:U:H1'	34:b:2145:C:N3	2.37	0.40
34:b:2130:U:H3'	34:b:2131:U:C6	2.57	0.40
34:b:2155:U:H5''	34:b:2156:G:OP2	2.22	0.40
41:k:110:PRO:O	41:k:115:GLY:HA3	2.22	0.40
55:y:75:LYS:HE2	55:y:75:LYS:HB3	1.88	0.40
56:z:146:ARG:NE	56:z:149[B]:GLY:H	2.19	0.40
9:A:1054:C:H4'	9:A:1055:A:H5''	2.04	0.40
9:A:1207:G:C6	9:A:1208:C:C5	3.10	0.40
9:A:1278:G:H4'	9:A:1279:G:O4'	2.22	0.40
10:B:122:ASP:HA	10:B:125:PHE:CD2	2.57	0.40
11:C:22:PHE:HE2	18:J:12:ALA:HA	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:C:78:LYS:HE3	11:C:78:LYS:HB3	1.85	0.40
12:D:67:LEU:HB2	12:D:70:GLN:CD	2.47	0.40
13:E:22:LYS:HD3	13:E:29:ILE:HD11	2.03	0.40
32:Z:54:G:H2'	32:Z:55:U:C6	2.56	0.40
34:b:278:A:H2	34:b:361:G:H1'	1.87	0.40
34:b:892:A:O2'	34:b:893:C:O4'	2.36	0.40
34:b:1353:A:H2'	34:b:1354:A:H8	1.85	0.40
34:b:2252:G:O6	55:y:4:LYS:HB3	2.22	0.40
34:b:2346:A:H3'	34:b:2347:C:H5''	2.03	0.40
34:b:2467:C:H2'	34:b:2468:A:O4'	2.21	0.40
34:b:2480:C:H2'	34:b:2481:G:O4'	2.21	0.40
35:c:133:ARG:O	35:c:167:ARG:NH1	2.55	0.40
38:f:32:GLU:N	38:f:32:GLU:OE1	2.54	0.40
52:v:104:LYS:HE2	52:v:104:LYS:HB2	1.86	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	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
2	1	59/63 (94%)	57 (97%)	2 (3%)	0	100	100
3	2	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
4	4	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
5	5	50/55 (91%)	47 (94%)	3 (6%)	0	100	100
6	6	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
7	7	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
8	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
10	B	216/241 (90%)	197 (91%)	19 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	C	205/233 (88%)	190 (93%)	15 (7%)	0	100	100
12	D	203/206 (98%)	183 (90%)	20 (10%)	0	100	100
13	E	155/167 (93%)	141 (91%)	14 (9%)	0	100	100
14	F	104/135 (77%)	98 (94%)	6 (6%)	0	100	100
15	G	151/179 (84%)	143 (95%)	8 (5%)	0	100	100
16	H	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
17	I	125/130 (96%)	113 (90%)	12 (10%)	0	100	100
18	J	98/103 (95%)	83 (85%)	15 (15%)	0	100	100
19	K	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
20	L	120/124 (97%)	105 (88%)	15 (12%)	0	100	100
21	M	114/118 (97%)	106 (93%)	8 (7%)	0	100	100
22	N	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
23	O	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
24	P	79/82 (96%)	68 (86%)	11 (14%)	0	100	100
25	Q	78/84 (93%)	71 (91%)	7 (9%)	0	100	100
26	R	64/75 (85%)	62 (97%)	2 (3%)	0	100	100
27	S	81/92 (88%)	73 (90%)	8 (10%)	0	100	100
28	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
29	U	62/71 (87%)	54 (87%)	8 (13%)	0	100	100
30	V	57/432 (13%)	54 (95%)	3 (5%)	0	100	100
35	c	269/273 (98%)	256 (95%)	13 (5%)	0	100	100
36	d	207/209 (99%)	194 (94%)	13 (6%)	0	100	100
37	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
38	f	176/179 (98%)	159 (90%)	17 (10%)	0	100	100
39	g	173/177 (98%)	164 (95%)	9 (5%)	0	100	100
40	h	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
41	k	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
42	l	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
43	m	142/144 (99%)	125 (88%)	17 (12%)	0	100	100
44	n	134/136 (98%)	126 (94%)	7 (5%)	1 (1%)	19	32
45	o	118/127 (93%)	111 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	p	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
47	q	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
48	r	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
49	s	101/103 (98%)	85 (84%)	16 (16%)	0	100	100
50	t	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
51	u	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
52	v	101/104 (97%)	88 (87%)	13 (13%)	0	100	100
53	w	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
55	y	82/85 (96%)	82 (100%)	0	0	100	100
56	z	45/39 (115%)	37 (82%)	8 (18%)	0	100	100
All	All	5652/6314 (90%)	5264 (93%)	387 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
44	n	69	PRO

### 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	67/68 (98%)	67 (100%)	0	100	100
2	1	54/55 (98%)	54 (100%)	0	100	100
3	2	48/49 (98%)	48 (100%)	0	100	100
4	4	47/48 (98%)	47 (100%)	0	100	100
5	5	47/49 (96%)	46 (98%)	1 (2%)	48	69
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	51 (100%)	0	100	100
8	8	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	B	180/199 (90%)	179 (99%)	1 (1%)	84	90
11	C	171/190 (90%)	171 (100%)	0	100	100
12	D	172/173 (99%)	172 (100%)	0	100	100
13	E	119/126 (94%)	119 (100%)	0	100	100
14	F	92/116 (79%)	92 (100%)	0	100	100
15	G	126/147 (86%)	126 (100%)	0	100	100
16	H	104/105 (99%)	104 (100%)	0	100	100
17	I	105/107 (98%)	105 (100%)	0	100	100
18	J	88/90 (98%)	88 (100%)	0	100	100
19	K	90/99 (91%)	90 (100%)	0	100	100
20	L	103/104 (99%)	103 (100%)	0	100	100
21	M	94/96 (98%)	94 (100%)	0	100	100
22	N	83/84 (99%)	83 (100%)	0	100	100
23	O	76/77 (99%)	76 (100%)	0	100	100
24	P	65/65 (100%)	65 (100%)	0	100	100
25	Q	74/78 (95%)	74 (100%)	0	100	100
26	R	57/65 (88%)	57 (100%)	0	100	100
27	S	72/79 (91%)	72 (100%)	0	100	100
28	T	65/66 (98%)	65 (100%)	0	100	100
29	U	54/61 (88%)	54 (100%)	0	100	100
30	V	49/359 (14%)	49 (100%)	0	100	100
35	c	216/218 (99%)	216 (100%)	0	100	100
36	d	164/164 (100%)	164 (100%)	0	100	100
37	e	165/165 (100%)	165 (100%)	0	100	100
38	f	149/150 (99%)	147 (99%)	2 (1%)	65	80
39	g	136/138 (99%)	134 (98%)	2 (2%)	60	76
40	h	114/114 (100%)	112 (98%)	2 (2%)	54	72
41	k	116/116 (100%)	116 (100%)	0	100	100
42	l	104/104 (100%)	103 (99%)	1 (1%)	73	84
43	m	103/103 (100%)	103 (100%)	0	100	100
44	n	109/109 (100%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	o	100/103 (97%)	100 (100%)	0	100	100
46	p	86/87 (99%)	86 (100%)	0	100	100
47	q	99/100 (99%)	97 (98%)	2 (2%)	50	70
48	r	89/90 (99%)	89 (100%)	0	100	100
49	s	84/84 (100%)	79 (94%)	5 (6%)	16	29
50	t	93/93 (100%)	93 (100%)	0	100	100
51	u	84/84 (100%)	83 (99%)	1 (1%)	67	81
52	v	84/85 (99%)	83 (99%)	1 (1%)	67	81
53	w	78/78 (100%)	76 (97%)	2 (3%)	41	63
55	y	62/63 (98%)	61 (98%)	1 (2%)	58	75
56	z	39/33 (118%)	29 (74%)	10 (26%)	0	0
All	All	4699/5160 (91%)	4668 (99%)	31 (1%)	82	89

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	5	51	GLU
10	B	56	LEU
38	f	7	TYR
38	f	100	PHE
39	g	29	LYS
39	g	133	LEU
40	h	31	VAL
40	h	121	VAL
42	l	51	LYS
47	q	13	MET
47	q	16	ASP
49	s	45	GLU
49	s	46	GLU
49	s	51	VAL
49	s	54	VAL
49	s	55	ASP
51	u	87	LEU
52	v	66	GLN
53	w	5	ASN
53	w	64	VAL
55	y	72	LYS
56	z	124	MET

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Mol	Chain	Res	Type
56	z	127	ASN
56	z	129	ARG
56	z	132	ASN
56	z	146	ARG
56	z	148	LEU
56	z	153[A]	SER
56	z	153[B]	SER
56	z	156[A]	TRP
56	z	156[B]	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	23	ASN
2	1	20	ASN
3	2	34	HIS
8	8	35	GLN
10	B	145	ASN
10	B	202	ASN
12	D	125	ASN
12	D	135	GLN
13	E	88	HIS
13	E	121	ASN
14	F	14	GLN
14	F	17	GLN
14	F	46	GLN
14	F	52	ASN
15	G	129	ASN
15	G	147	ASN
15	G	152	HIS
16	H	37	ASN
16	H	117	GLN
17	I	49	GLN
18	J	20	GLN
18	J	58	ASN
19	K	21	HIS
19	K	100	ASN
20	L	95	HIS
22	N	65	GLN
23	O	34	GLN
23	O	36	ASN
23	O	49	HIS

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Mol	Chain	Res	Type
24	P	63	GLN
26	R	30	ASN
28	T	2	ASN
28	T	51	ASN
30	V	52	ASN
35	c	15	HIS
36	d	49	GLN
36	d	130	GLN
37	e	29	HIS
37	e	90	GLN
40	h	18	GLN
40	h	145	ASN
42	l	3	GLN
42	l	29	HIS
42	l	93	GLN
43	m	54	GLN
46	p	100	HIS
46	p	116	GLN
47	q	56	HIS
50	t	60	HIS
50	t	61	ASN
52	v	66	GLN
53	w	87	GLN
56	z	147	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	X	75/76 (98%)	39 (52%)	0
32	Y	76/77 (98%)	20 (26%)	2 (2%)
32	Z	76/77 (98%)	19 (25%)	0
33	a	119/120 (99%)	17 (14%)	0
34	b	2902/2904 (99%)	599 (20%)	0
54	x	13/14 (92%)	5 (38%)	0
9	A	1532/1533 (99%)	362 (23%)	12 (0%)
All	All	4793/4801 (99%)	1061 (22%)	14 (0%)

All (1061) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	2	A

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Mol	Chain	Res	Type
9	A	4	U
9	A	6	G
9	A	9	G
9	A	16	A
9	A	31	G
9	A	32	A
9	A	39	G
9	A	47	C
9	A	48	C
9	A	51	A
9	A	70	U
9	A	73	C
9	A	74	A
9	A	76	G
9	A	77	A
9	A	78	A
9	A	79	G
9	A	81	A
9	A	83	C
9	A	84	U
9	A	85	U
9	A	86	G
9	A	87	C
9	A	88	U
9	A	89	U
9	A	90	C
9	A	91	U
9	A	92	U
9	A	94	G
9	A	95	C
9	A	96	U
9	A	97	G
9	A	109	A
9	A	110	C
9	A	111	G
9	A	120	A
9	A	121	U
9	A	122	G
9	A	127	G
9	A	130	A
9	A	131	A
9	A	137	U

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Mol	Chain	Res	Type
9	A	144	G
9	A	164	G
9	A	173	U
9	A	182	A
9	A	193	C
9	A	196	A
9	A	197	A
9	A	200	G
9	A	204	G
9	A	205	A
9	A	208	U
9	A	209	U
9	A	210	C
9	A	214	C
9	A	216	U
9	A	217	C
9	A	218	U
9	A	219	U
9	A	224	U
9	A	228	A
9	A	231	U
9	A	239	U
9	A	240	G
9	A	244	U
9	A	245	U
9	A	246	A
9	A	247	G
9	A	251	G
9	A	253	A
9	A	256	U
9	A	262	A
9	A	266	G
9	A	267	C
9	A	269	C
9	A	272	C
9	A	275	G
9	A	279	A
9	A	283	U
9	A	286	C
9	A	289	G
9	A	293	G
9	A	300	A

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Mol	Chain	Res	Type
9	A	301	G
9	A	306	A
9	A	328	C
9	A	330	C
9	A	342	C
9	A	343	U
9	A	345	C
9	A	352	C
9	A	354	G
9	A	367	U
9	A	368	U
9	A	369	G
9	A	372	C
9	A	376	G
9	A	377	G
9	A	378	G
9	A	381	C
9	A	382	A
9	A	387	U
9	A	388	G
9	A	390	U
9	A	391	G
9	A	392	C
9	A	397	A
9	A	398	U
9	A	406	G
9	A	407	U
9	A	409	U
9	A	411	A
9	A	412	A
9	A	413	G
9	A	414	A
9	A	415	A
9	A	421	U
9	A	422	C
9	A	423	G
9	A	424	G
9	A	425	G
9	A	428	G
9	A	429	U
9	A	430	A
9	A	431	A

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Mol	Chain	Res	Type
9	A	433	G
9	A	435	A
9	A	438	U
9	A	439	U
9	A	445	G
9	A	446	G
9	A	448	A
9	A	449	G
9	A	452	A
9	A	461	A
9	A	462	G
9	A	463	U
9	A	465	A
9	A	467	U
9	A	468	A
9	A	471	U
9	A	474	G
9	A	479	U
9	A	480	U
9	A	483	C
9	A	485	U
9	A	486	U
9	A	491	G
9	A	493	A
9	A	495	A
9	A	496	A
9	A	497	G
9	A	499	A
9	A	509	A
9	A	511	C
9	A	512	U
9	A	517	G
9	A	518	C
9	A	521	G
9	A	524	G
9	A	527	G
9	A	530	G
9	A	532	A
9	A	535	A
9	A	536	C
9	A	541	G
9	A	542	G

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Mol	Chain	Res	Type
9	A	547	A
9	A	548	G
9	A	550	G
9	A	551	U
9	A	560	A
9	A	563	A
9	A	564	C
9	A	567	G
9	A	571	U
9	A	572	A
9	A	573	A
9	A	576	C
9	A	588	G
9	A	590	U
9	A	591	U
9	A	595	A
9	A	596	A
9	A	610	U
9	A	615	G
9	A	619	U
9	A	622	A
9	A	632	U
9	A	633	G
9	A	653	U
9	A	665	A
9	A	666	G
9	A	687	A
9	A	709	U
9	A	720	C
9	A	721	G
9	A	723	U
9	A	724	G
9	A	731	G
9	A	755	G
9	A	777	A
9	A	787	A
9	A	793	U
9	A	794	A
9	A	815	A
9	A	817	C
9	A	820	U
9	A	821	G

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Mol	Chain	Res	Type
9	A	828	U
9	A	829	G
9	A	831	A
9	A	832	G
9	A	841	C
9	A	842	U
9	A	843	U
9	A	844	G
9	A	845	A
9	A	846	G
9	A	848	C
9	A	849	G
9	A	869	G
9	A	872	A
9	A	889	A
9	A	891	U
9	A	900	A
9	A	902	G
9	A	914	A
9	A	919	A
9	A	927	G
9	A	933	G
9	A	934	C
9	A	935	A
9	A	939	G
9	A	945	G
9	A	958	A
9	A	960	U
9	A	961	U
9	A	966	G
9	A	969	A
9	A	975	A
9	A	976	G
9	A	978	A
9	A	979	C
9	A	992	U
9	A	993	G
9	A	994	A
9	A	996	A
9	A	998	C
9	A	999	C
9	A	1001	C

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Mol	Chain	Res	Type
9	A	1003	G
9	A	1004	A
9	A	1006	G
9	A	1007	U
9	A	1017	U
9	A	1020	G
9	A	1022	A
9	A	1027	C
9	A	1028	C
9	A	1032	G
9	A	1034	G
9	A	1036	A
9	A	1039	G
9	A	1042	A
9	A	1045	C
9	A	1049	U
9	A	1053	G
9	A	1058	G
9	A	1065	U
9	A	1066	C
9	A	1081	A
9	A	1085	U
9	A	1094	G
9	A	1095	U
9	A	1100	C
9	A	1101	A
9	A	1104	G
9	A	1108	G
9	A	1124	G
9	A	1125	U
9	A	1136	C
9	A	1137	C
9	A	1139	G
9	A	1151	A
9	A	1152	A
9	A	1157	A
9	A	1159	U
9	A	1160	G
9	A	1167	A
9	A	1168	U
9	A	1169	A
9	A	1173	U

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Mol	Chain	Res	Type
9	A	1174	G
9	A	1183	U
9	A	1184	G
9	A	1188	A
9	A	1196	A
9	A	1197	A
9	A	1206	G
9	A	1207	G
9	A	1208	C
9	A	1210	C
9	A	1212	U
9	A	1213	A
9	A	1225	A
9	A	1227	A
9	A	1238	A
9	A	1240	U
9	A	1241	G
9	A	1248	A
9	A	1257	A
9	A	1258	G
9	A	1259	C
9	A	1260	G
9	A	1266	G
9	A	1268	G
9	A	1280	A
9	A	1286	U
9	A	1287	A
9	A	1300	G
9	A	1301	U
9	A	1303	C
9	A	1305	G
9	A	1316	G
9	A	1323	G
9	A	1336	C
9	A	1338	G
9	A	1340	A
9	A	1343	G
9	A	1347	G
9	A	1348	U
9	A	1358	U
9	A	1360	A
9	A	1362	A

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Mol	Chain	Res	Type
9	A	1363	A
9	A	1364	U
9	A	1378	C
9	A	1398	A
9	A	1419	G
9	A	1441	A
9	A	1446	A
9	A	1450	U
9	A	1451	U
9	A	1452	C
9	A	1454	G
9	A	1461	G
9	A	1471	U
9	A	1487	G
9	A	1492	A
9	A	1494	G
9	A	1497	G
9	A	1503	A
9	A	1506	U
9	A	1517	G
9	A	1519	A
9	A	1520	C
9	A	1529	G
9	A	1530	G
9	A	1533	C
31	X	3	G
31	X	4	G
31	X	5	G
31	X	6	A
31	X	8	U
31	X	9	A
31	X	10	G
31	X	11	C
31	X	13	C
31	X	16	U
31	X	17	U
31	X	18	G
31	X	19	G
31	X	21	A
31	X	25	C
31	X	28	G
31	X	29	A

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Mol	Chain	Res	Type
31	X	30	C
31	X	31	C
31	X	39	G
31	X	40	G
31	X	43	G
31	X	44	G
31	X	46	G
31	X	47	U
31	X	49	G
31	X	51	G
31	X	55	U
31	X	57	G
31	X	59	G
31	X	60	U
31	X	61	C
31	X	64	G
31	X	66	U
31	X	69	C
31	X	71	G
31	X	74	C
31	X	75	C
31	X	76	A
32	Y	2	G
32	Y	3	G
32	Y	5	G
32	Y	7	U
32	Y	9	G
32	Y	16	C
32	Y	17	C
32	Y	18	U
32	Y	19	G
32	Y	21	U
32	Y	47	G
32	Y	48	U
32	Y	49	C
32	Y	50	G
32	Y	51	G
32	Y	63	C
32	Y	64	U
32	Y	68	U
32	Y	69	C
32	Y	77	A

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Mol	Chain	Res	Type
32	Z	9	G
32	Z	10	G
32	Z	12	G
32	Z	16	C
32	Z	18	U
32	Z	20	G
32	Z	21	U
32	Z	23	G
32	Z	25	G
32	Z	26	C
32	Z	30	U
32	Z	31	C
32	Z	33	U
32	Z	37	G
32	Z	50	G
32	Z	53	G
32	Z	59	A
32	Z	67	A
32	Z	74	A
33	a	15	A
33	a	23	G
33	a	25	U
33	a	30	C
33	a	35	C
33	a	46	A
33	a	52	A
33	a	56	G
33	a	66	A
33	a	67	G
33	a	69	G
33	a	71	C
33	a	89	U
33	a	90	C
33	a	99	A
33	a	109	A
33	a	119	A
34	b	3	U
34	b	5	A
34	b	10	A
34	b	28	A
34	b	35	G
34	b	39	G

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Mol	Chain	Res	Type
34	b	40	U
34	b	42	A
34	b	46	G
34	b	51	G
34	b	71	A
34	b	74	A
34	b	75	G
34	b	84	A
34	b	88	G
34	b	91	A
34	b	98	G
34	b	100	U
34	b	101	A
34	b	102	U
34	b	103	A
34	b	110	G
34	b	118	A
34	b	119	A
34	b	120	U
34	b	128	C
34	b	133	U
34	b	140	C
34	b	142	A
34	b	160	A
34	b	163	C
34	b	165	A
34	b	181	A
34	b	196	A
34	b	199	A
34	b	215	G
34	b	216	A
34	b	222	A
34	b	223	A
34	b	228	C
34	b	229	C
34	b	233	A
34	b	248	G
34	b	250	G
34	b	251	A
34	b	255	A
34	b	265	A
34	b	266	G

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Mol	Chain	Res	Type
34	b	267	C
34	b	268	C
34	b	271	G
34	b	272	A
34	b	276	U
34	b	278	A
34	b	279	A
34	b	280	U
34	b	282	A
34	b	284	U
34	b	286	U
34	b	295	G
34	b	330	A
34	b	349	U
34	b	356	G
34	b	357	C
34	b	359	G
34	b	361	G
34	b	364	C
34	b	368	A
34	b	369	U
34	b	371	A
34	b	372	G
34	b	386	G
34	b	387	U
34	b	391	A
34	b	395	U
34	b	396	G
34	b	404	A
34	b	405	U
34	b	411	G
34	b	412	A
34	b	417	C
34	b	424	G
34	b	428	A
34	b	430	A
34	b	451	U
34	b	457	A
34	b	473	G
34	b	481	G
34	b	491	G
34	b	493	G

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Mol	Chain	Res	Type
34	b	505	A
34	b	508	A
34	b	509	C
34	b	510	C
34	b	512	G
34	b	529	A
34	b	530	G
34	b	531	C
34	b	532	A
34	b	538	A
34	b	546	U
34	b	548	G
34	b	549	G
34	b	557	C
34	b	563	A
34	b	568	U
34	b	573	U
34	b	574	A
34	b	575	A
34	b	587	C
34	b	595	C
34	b	603	A
34	b	604	G
34	b	613	A
34	b	614	A
34	b	615	U
34	b	621	A
34	b	627	A
34	b	637	A
34	b	639	U
34	b	644	A
34	b	645	C
34	b	646	U
34	b	647	G
34	b	653	U
34	b	654	A
34	b	655	A
34	b	670	A
34	b	686	U
34	b	701	G
34	b	709	U
34	b	713	G

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Mol	Chain	Res	Type
34	b	716	A
34	b	717	C
34	b	718	A
34	b	719	C
34	b	727	A
34	b	730	A
34	b	738	G
34	b	747	U
34	b	748	G
34	b	757	G
34	b	764	A
34	b	765	C
34	b	774	G
34	b	775	G
34	b	776	G
34	b	782	A
34	b	784	G
34	b	785	G
34	b	792	A
34	b	805	G
34	b	812	C
34	b	819	A
34	b	827	U
34	b	828	U
34	b	845	A
34	b	846	U
34	b	859	G
34	b	869	G
34	b	877	A
34	b	879	G
34	b	880	G
34	b	881	G
34	b	883	G
34	b	884	U
34	b	885	C
34	b	886	A
34	b	887	U
34	b	888	C
34	b	889	C
34	b	890	C
34	b	891	G
34	b	892	A

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Mol	Chain	Res	Type
34	b	893	C
34	b	894	U
34	b	895	U
34	b	896	A
34	b	897	C
34	b	898	C
34	b	899	A
34	b	900	A
34	b	902	C
34	b	910	A
34	b	912	C
34	b	914	G
34	b	927	A
34	b	932	U
34	b	938	G
34	b	941	A
34	b	946	C
34	b	959	A
34	b	961	C
34	b	972	A
34	b	974	G
34	b	981	A
34	b	983	A
34	b	996	A
34	b	999	U
34	b	1009	A
34	b	1012	U
34	b	1013	C
34	b	1022	G
34	b	1026	G
34	b	1033	U
34	b	1040	A
34	b	1047	G
34	b	1048	A
34	b	1051	G
34	b	1052	C
34	b	1053	C
34	b	1056	G
34	b	1057	A
34	b	1058	U
34	b	1059	G
34	b	1060	U

*Continued on next page...*

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Mol	Chain	Res	Type
34	b	1061	U
34	b	1062	G
34	b	1064	C
34	b	1065	U
34	b	1066	U
34	b	1067	A
34	b	1068	G
34	b	1069	A
34	b	1070	A
34	b	1072	C
34	b	1073	A
34	b	1074	G
34	b	1076	C
34	b	1078	U
34	b	1080	A
34	b	1081	U
34	b	1083	U
34	b	1084	A
34	b	1085	A
34	b	1086	A
34	b	1087	G
34	b	1088	A
34	b	1090	A
34	b	1092	C
34	b	1093	G
34	b	1094	U
34	b	1095	A
34	b	1096	A
34	b	1099	G
34	b	1102	C
34	b	1103	A
34	b	1104	C
34	b	1105	U
34	b	1106	G
34	b	1108	U
34	b	1110	G
34	b	1111	A
34	b	1112	G
34	b	1132	U
34	b	1133	A
34	b	1134	A
34	b	1135	C

*Continued on next page...*

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Mol	Chain	Res	Type
34	b	1136	G
34	b	1141	U
34	b	1142	A
34	b	1166	G
34	b	1174	U
34	b	1175	A
34	b	1179	G
34	b	1186	G
34	b	1195	G
34	b	1205	A
34	b	1206	G
34	b	1210	G
34	b	1223	G
34	b	1224	U
34	b	1234	U
34	b	1236	G
34	b	1238	G
34	b	1241	A
34	b	1250	G
34	b	1253	A
34	b	1256	G
34	b	1266	G
34	b	1267	U
34	b	1269	A
34	b	1271	G
34	b	1272	A
34	b	1273	U
34	b	1276	A
34	b	1291	C
34	b	1300	G
34	b	1301	A
34	b	1321	A
34	b	1341	G
34	b	1365	A
34	b	1366	A
34	b	1379	U
34	b	1383	A
34	b	1384	A
34	b	1386	C
34	b	1393	A
34	b	1395	A
34	b	1416	G

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Mol	Chain	Res	Type
34	b	1420	A
34	b	1421	G
34	b	1426	G
34	b	1427	A
34	b	1428	C
34	b	1433	A
34	b	1453	A
34	b	1459	G
34	b	1461	C
34	b	1482	G
34	b	1484	U
34	b	1487	U
34	b	1488	C
34	b	1490	A
34	b	1491	G
34	b	1493	C
34	b	1494	A
34	b	1496	A
34	b	1497	U
34	b	1498	C
34	b	1504	A
34	b	1505	A
34	b	1506	U
34	b	1507	C
34	b	1509	A
34	b	1510	G
34	b	1520	U
34	b	1523	U
34	b	1534	U
34	b	1535	A
34	b	1536	C
34	b	1540	G
34	b	1541	C
34	b	1552	A
34	b	1553	A
34	b	1560	G
34	b	1562	U
34	b	1566	A
34	b	1568	G
34	b	1569	A
34	b	1576	U
34	b	1578	U

*Continued on next page...*

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Mol	Chain	Res	Type
34	b	1584	U
34	b	1585	C
34	b	1607	C
34	b	1610	A
34	b	1618	A
34	b	1646	C
34	b	1647	U
34	b	1648	U
34	b	1674	G
34	b	1675	C
34	b	1677	A
34	b	1710	G
34	b	1713	A
34	b	1716	U
34	b	1722	A
34	b	1729	U
34	b	1730	C
34	b	1733	G
34	b	1736	U
34	b	1738	G
34	b	1744	A
34	b	1745	A
34	b	1758	U
34	b	1763	G
34	b	1764	C
34	b	1773	A
34	b	1776	G
34	b	1799	G
34	b	1800	C
34	b	1801	A
34	b	1802	A
34	b	1808	A
34	b	1810	A
34	b	1811	G
34	b	1816	C
34	b	1829	A
34	b	1847	A
34	b	1857	G
34	b	1866	A
34	b	1870	C
34	b	1871	A
34	b	1875	G

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Mol	Chain	Res	Type
34	b	1876	A
34	b	1901	A
34	b	1906	G
34	b	1913	A
34	b	1914	C
34	b	1916	A
34	b	1919	A
34	b	1927	A
34	b	1929	G
34	b	1930	G
34	b	1931	U
34	b	1936	A
34	b	1937	A
34	b	1938	A
34	b	1955	U
34	b	1960	A
34	b	1963	U
34	b	1967	C
34	b	1970	A
34	b	1971	U
34	b	1972	G
34	b	1977	A
34	b	1992	G
34	b	1993	U
34	b	1997	C
34	b	2023	C
34	b	2031	A
34	b	2032	G
34	b	2033	A
34	b	2043	C
34	b	2055	C
34	b	2056	G
34	b	2060	A
34	b	2061	G
34	b	2062	A
34	b	2069	G
34	b	2093	G
34	b	2102	G
34	b	2103	C
34	b	2105	U
34	b	2106	U
34	b	2107	G

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Mol	Chain	Res	Type
34	b	2109	U
34	b	2110	G
34	b	2111	U
34	b	2112	G
34	b	2113	U
34	b	2114	A
34	b	2115	G
34	b	2116	G
34	b	2118	U
34	b	2119	A
34	b	2120	G
34	b	2121	G
34	b	2122	U
34	b	2123	G
34	b	2124	G
34	b	2126	A
34	b	2127	G
34	b	2128	G
34	b	2129	C
34	b	2130	U
34	b	2131	U
34	b	2132	U
34	b	2133	G
34	b	2134	A
34	b	2136	G
34	b	2138	G
34	b	2140	G
34	b	2143	C
34	b	2144	G
34	b	2145	C
34	b	2146	C
34	b	2149	U
34	b	2150	C
34	b	2151	U
34	b	2152	G
34	b	2153	C
34	b	2154	A
34	b	2156	G
34	b	2157	G
34	b	2158	A
34	b	2159	G
34	b	2164	C

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Mol	Chain	Res	Type
34	b	2165	C
34	b	2166	U
34	b	2167	U
34	b	2170	A
34	b	2171	A
34	b	2172	U
34	b	2173	A
34	b	2174	C
34	b	2175	C
34	b	2178	C
34	b	2180	U
34	b	2181	U
34	b	2182	U
34	b	2186	G
34	b	2187	U
34	b	2188	U
34	b	2191	A
34	b	2192	U
34	b	2203	U
34	b	2204	G
34	b	2212	A
34	b	2213	U
34	b	2214	C
34	b	2225	A
34	b	2238	G
34	b	2239	G
34	b	2247	A
34	b	2250	G
34	b	2279	G
34	b	2283	C
34	b	2286	G
34	b	2287	A
34	b	2288	A
34	b	2305	U
34	b	2309	A
34	b	2320	U
34	b	2322	A
34	b	2325	G
34	b	2333	A
34	b	2336	A
34	b	2345	G
34	b	2347	C

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Mol	Chain	Res	Type
34	b	2357	G
34	b	2361	G
34	b	2383	G
34	b	2385	C
34	b	2402	U
34	b	2406	A
34	b	2407	A
34	b	2412	A
34	b	2422	C
34	b	2423	U
34	b	2425	A
34	b	2429	G
34	b	2430	A
34	b	2440	C
34	b	2441	U
34	b	2447	G
34	b	2448	A
34	b	2450	A
34	b	2459	A
34	b	2476	A
34	b	2491	U
34	b	2502	G
34	b	2503	A
34	b	2505	G
34	b	2506	U
34	b	2513	A
34	b	2518	A
34	b	2520	C
34	b	2529	G
34	b	2535	G
34	b	2547	A
34	b	2554	U
34	b	2562	U
34	b	2566	A
34	b	2567	G
34	b	2572	A
34	b	2576	G
34	b	2582	G
34	b	2584	U
34	b	2593	U
34	b	2602	A
34	b	2609	U

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Mol	Chain	Res	Type
34	b	2613	U
34	b	2615	U
34	b	2629	U
34	b	2630	G
34	b	2646	C
34	b	2655	G
34	b	2656	U
34	b	2689	U
34	b	2690	U
34	b	2698	U
34	b	2713	U
34	b	2714	G
34	b	2726	A
34	b	2728	U
34	b	2733	A
34	b	2744	G
34	b	2748	A
34	b	2752	C
34	b	2758	A
34	b	2776	A
34	b	2778	A
34	b	2779	U
34	b	2790	U
34	b	2791	G
34	b	2797	U
34	b	2798	U
34	b	2800	A
34	b	2801	G
34	b	2807	U
34	b	2808	G
34	b	2820	A
34	b	2833	U
34	b	2834	G
34	b	2835	A
34	b	2849	U
34	b	2854	G
34	b	2859	G
34	b	2861	U
34	b	2867	G
34	b	2873	A
34	b	2880	C
34	b	2883	A

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Mol	Chain	Res	Type
34	b	2885	G
34	b	2886	A
34	b	2896	C
34	b	2900	A
34	b	2903	U
54	x	14	C
54	x	16	C
54	x	21	U
54	x	22	A
54	x	23	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	66	A
9	A	195	A
9	A	223	A
9	A	238	A
9	A	428	G
9	A	429	U
9	A	719	C
9	A	1003	G
9	A	1065	U
9	A	1187	G
9	A	1357	A
9	A	1493	A
32	Y	6	A
32	Y	16	C

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	$\# Z  > 2$
58	PRO	Z	101	32	5,7,8	0.46	0	7,8,10	1.44	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	PRO	Z	101	32	-	0/0/9/11	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	Z	101	PRO	O-C-CA	-2.35	118.62	124.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	Z	101	PRO	4	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

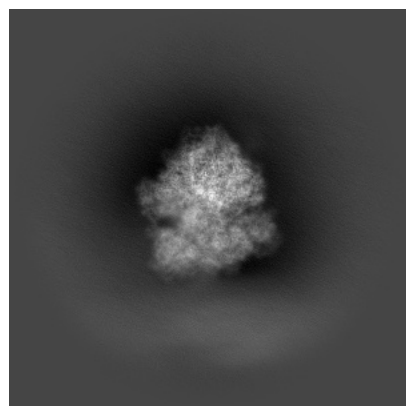
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66122. These allow visual inspection of the internal detail of the map and identification of artifacts.

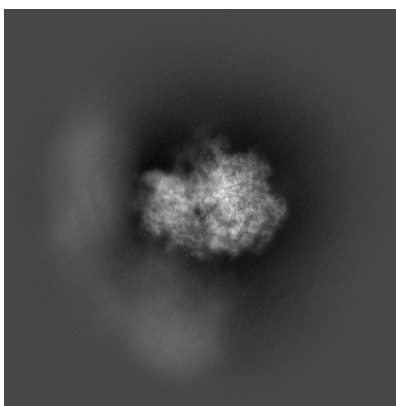
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

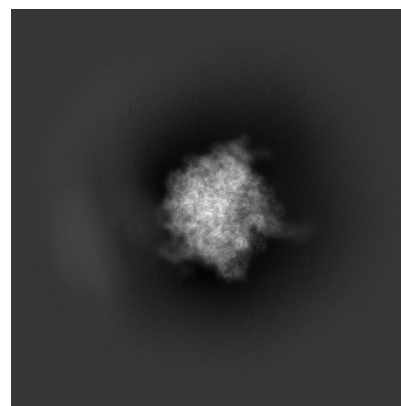
#### 6.1.1 Primary map



X

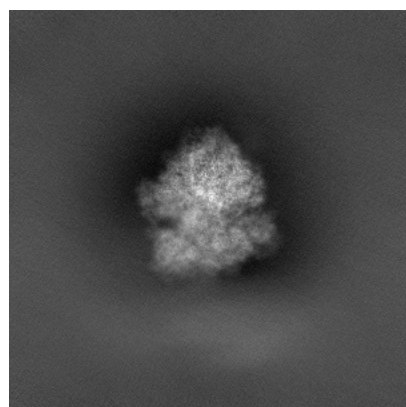


Y

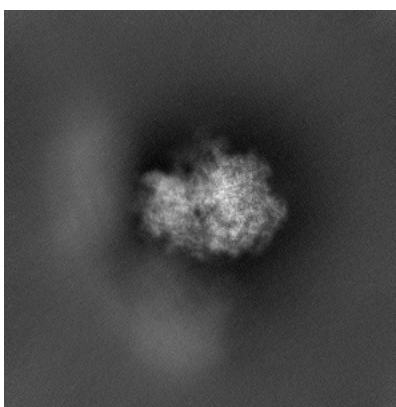


Z

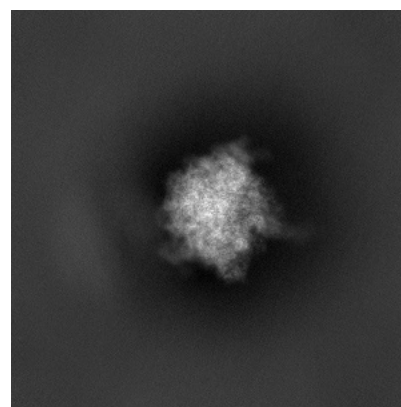
#### 6.1.2 Raw map



X



Y

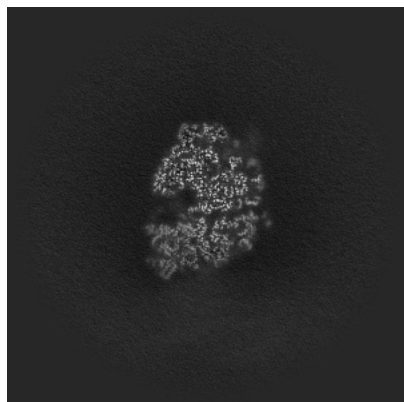


Z

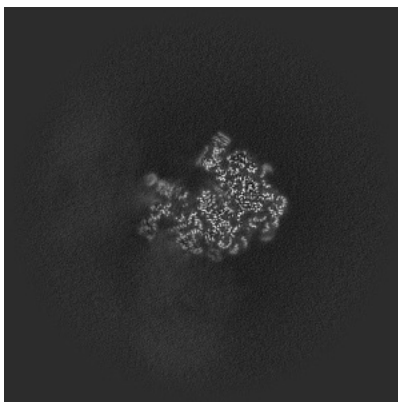
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

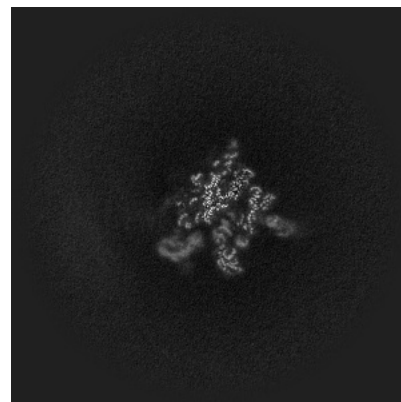
### 6.2.1 Primary map



X Index: 310

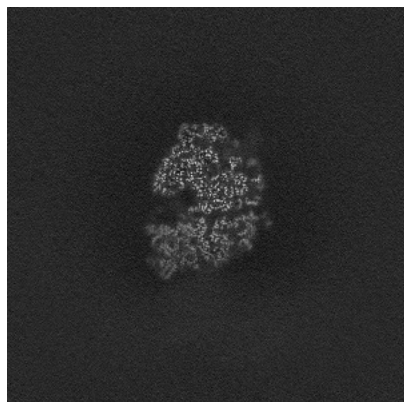


Y Index: 310

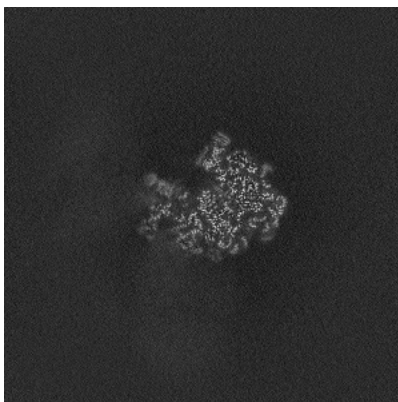


Z Index: 310

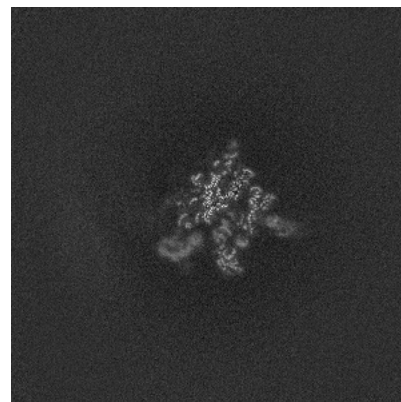
### 6.2.2 Raw map



X Index: 310



Y Index: 310



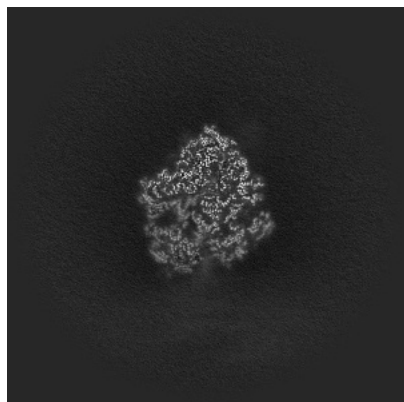
Z Index: 310

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

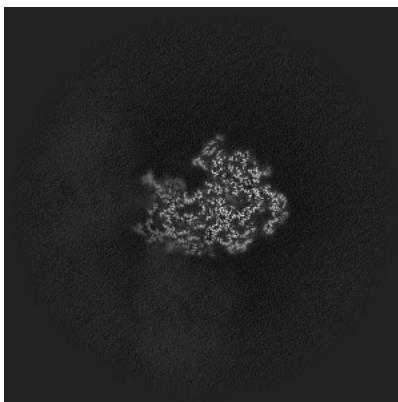


## 6.3 Largest variance slices [i](#)

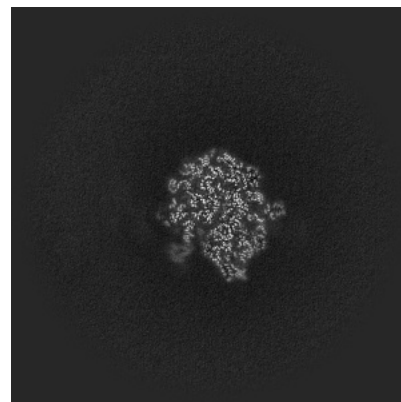
### 6.3.1 Primary map



X Index: 324

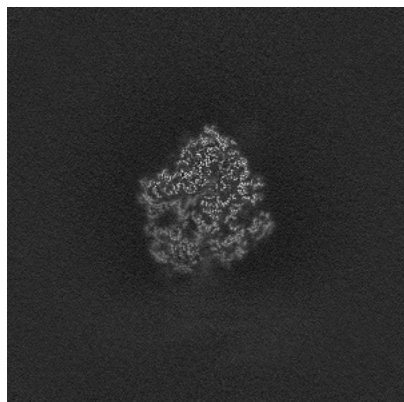


Y Index: 318

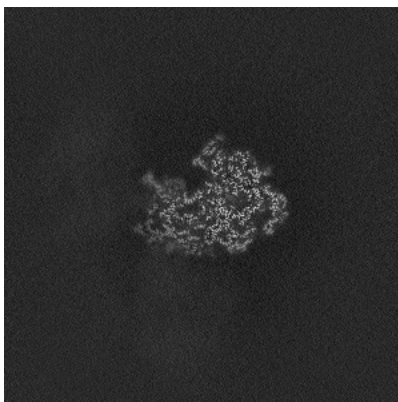


Z Index: 340

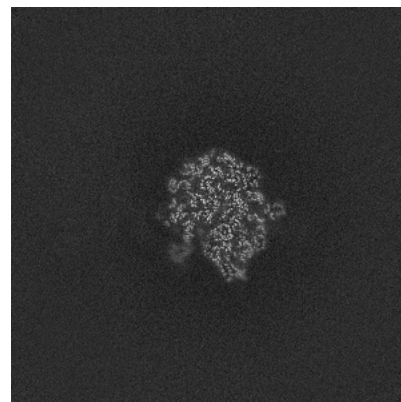
### 6.3.2 Raw map



X Index: 324



Y Index: 318

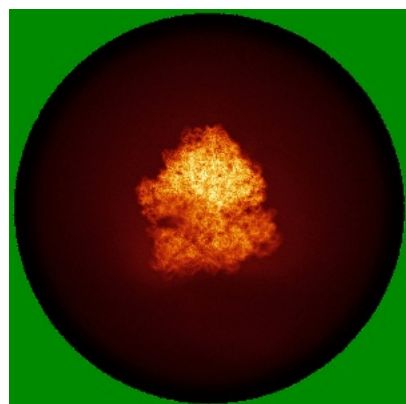


Z Index: 340

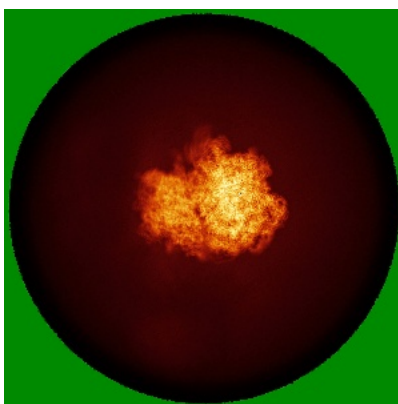
The images above show the largest variance slices of the map in three orthogonal directions.

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

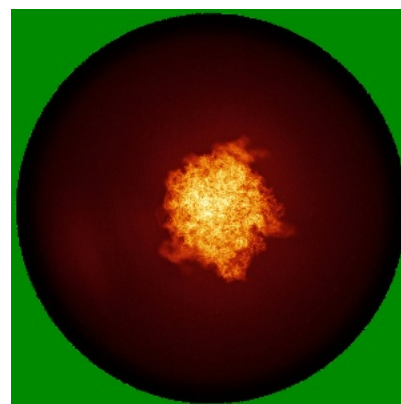
### 6.4.1 Primary map



X

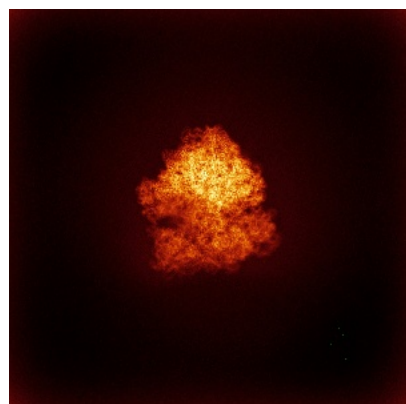


Y

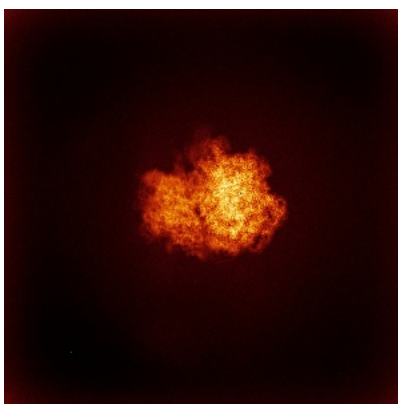


Z

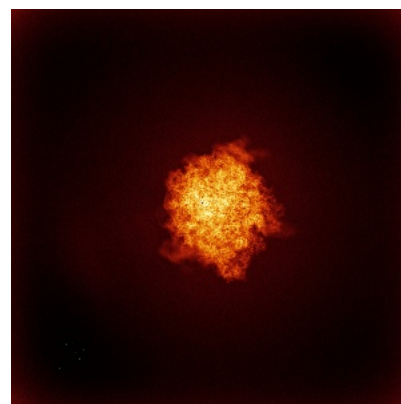
### 6.4.2 Raw map



X



Y

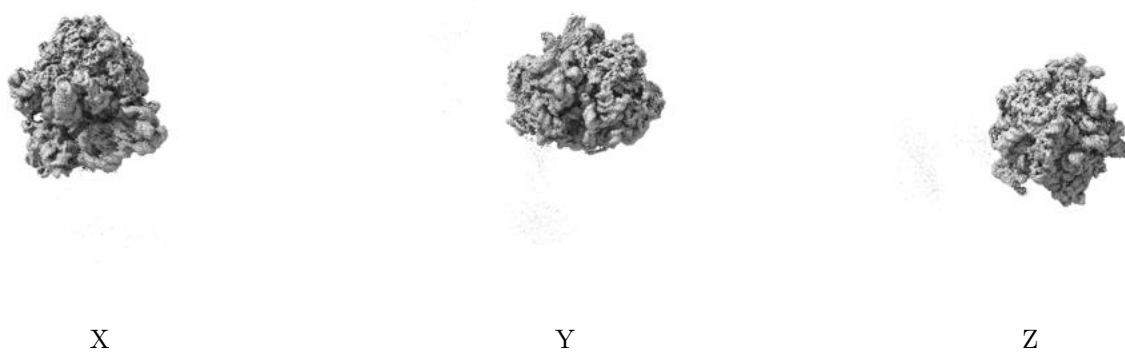


Z

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

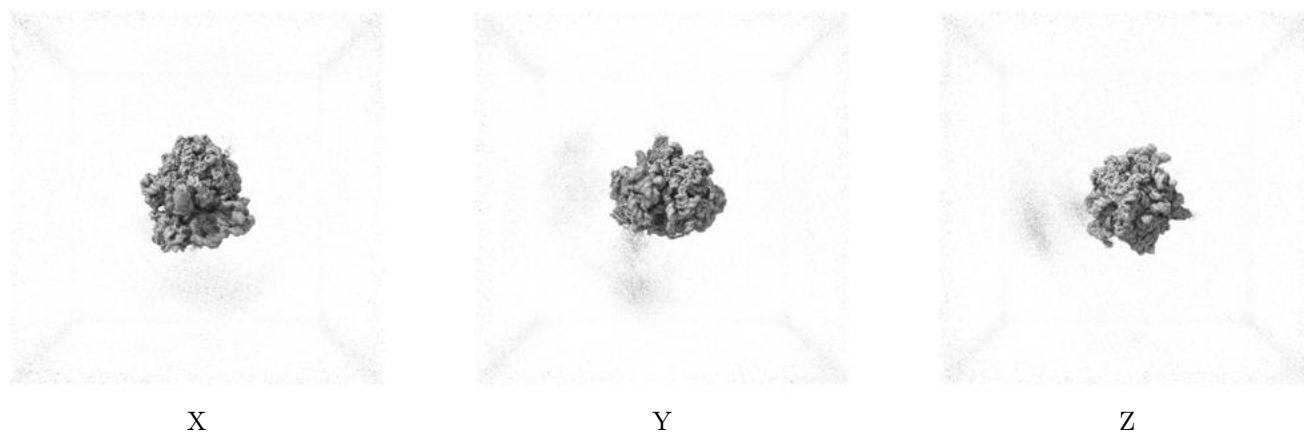
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.33. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

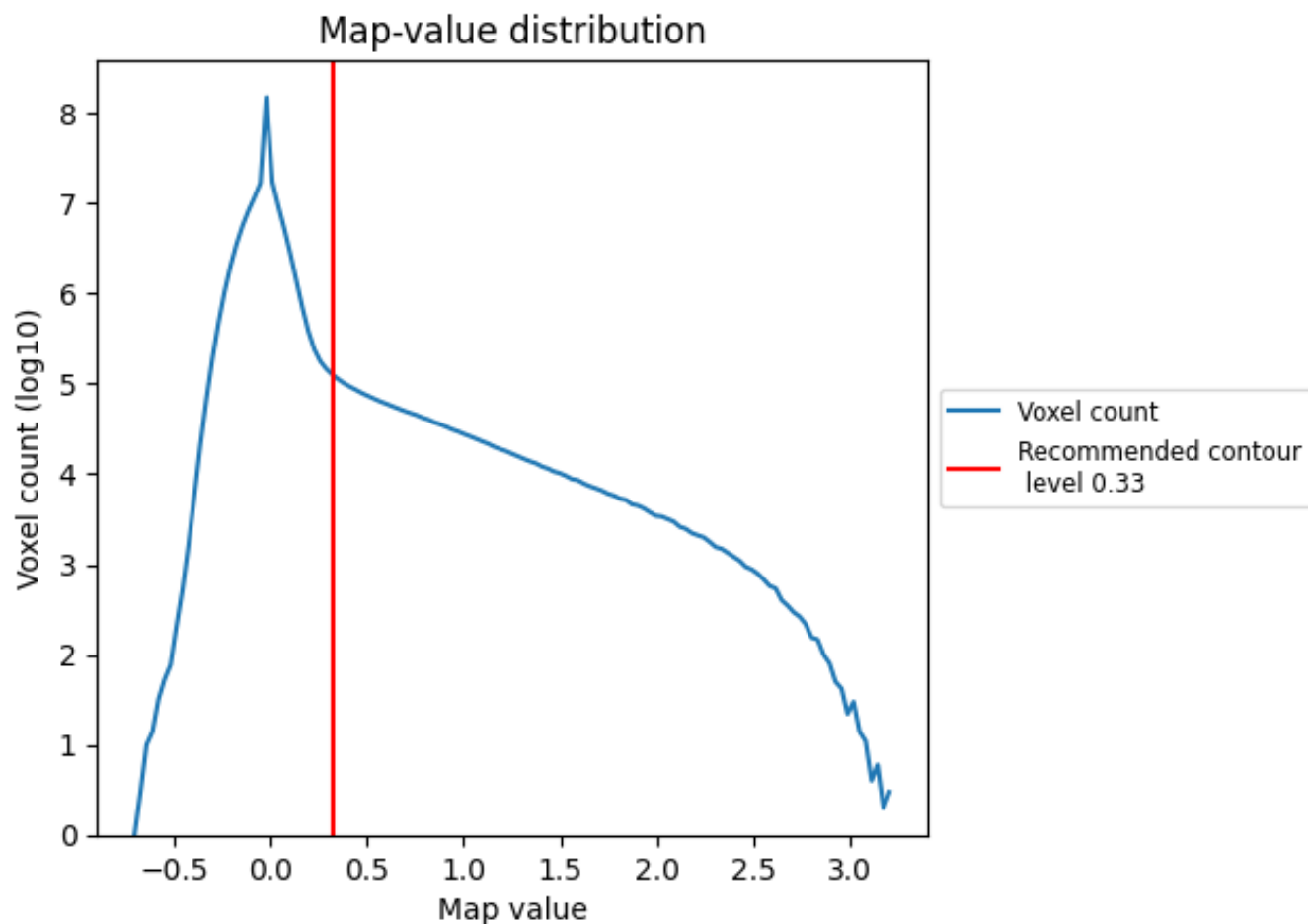
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

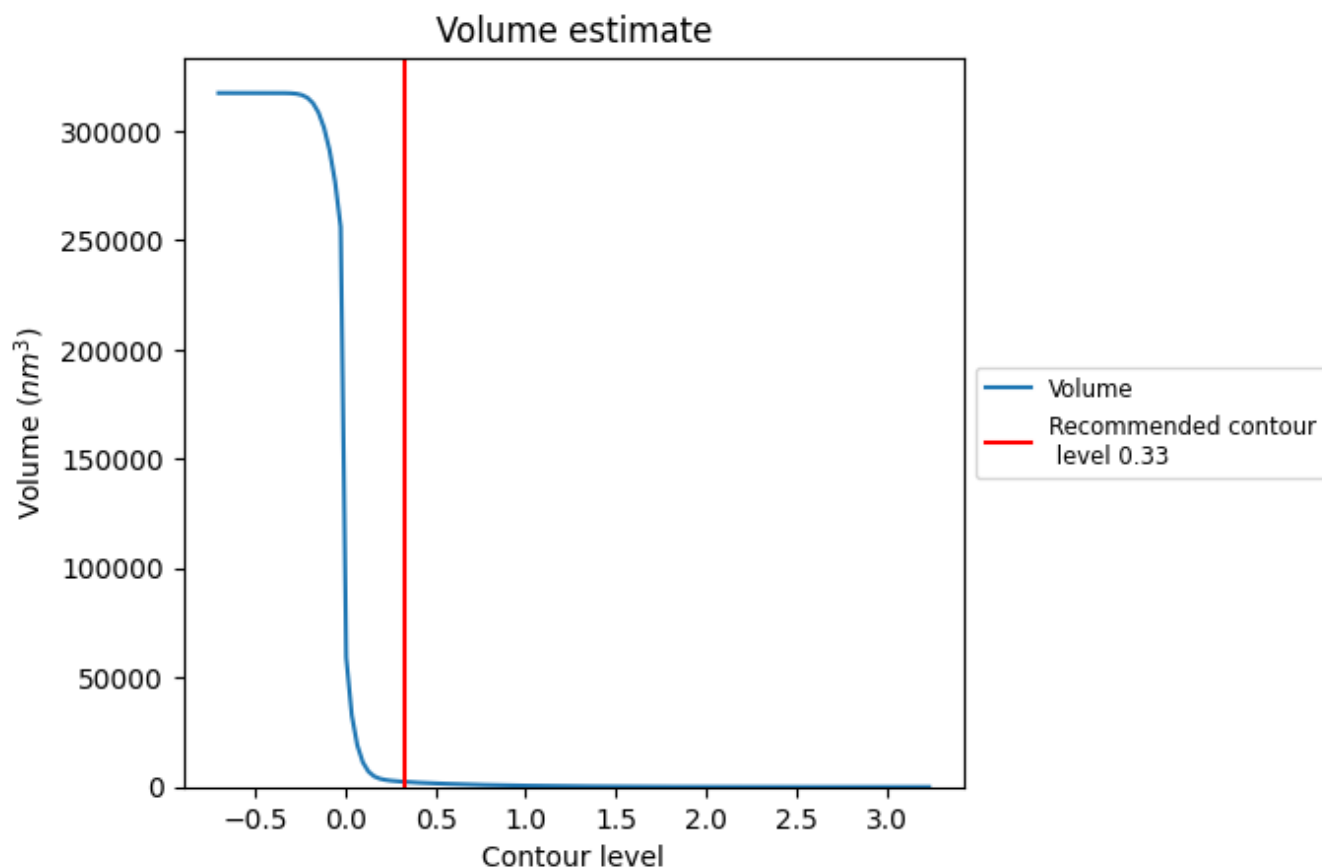
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

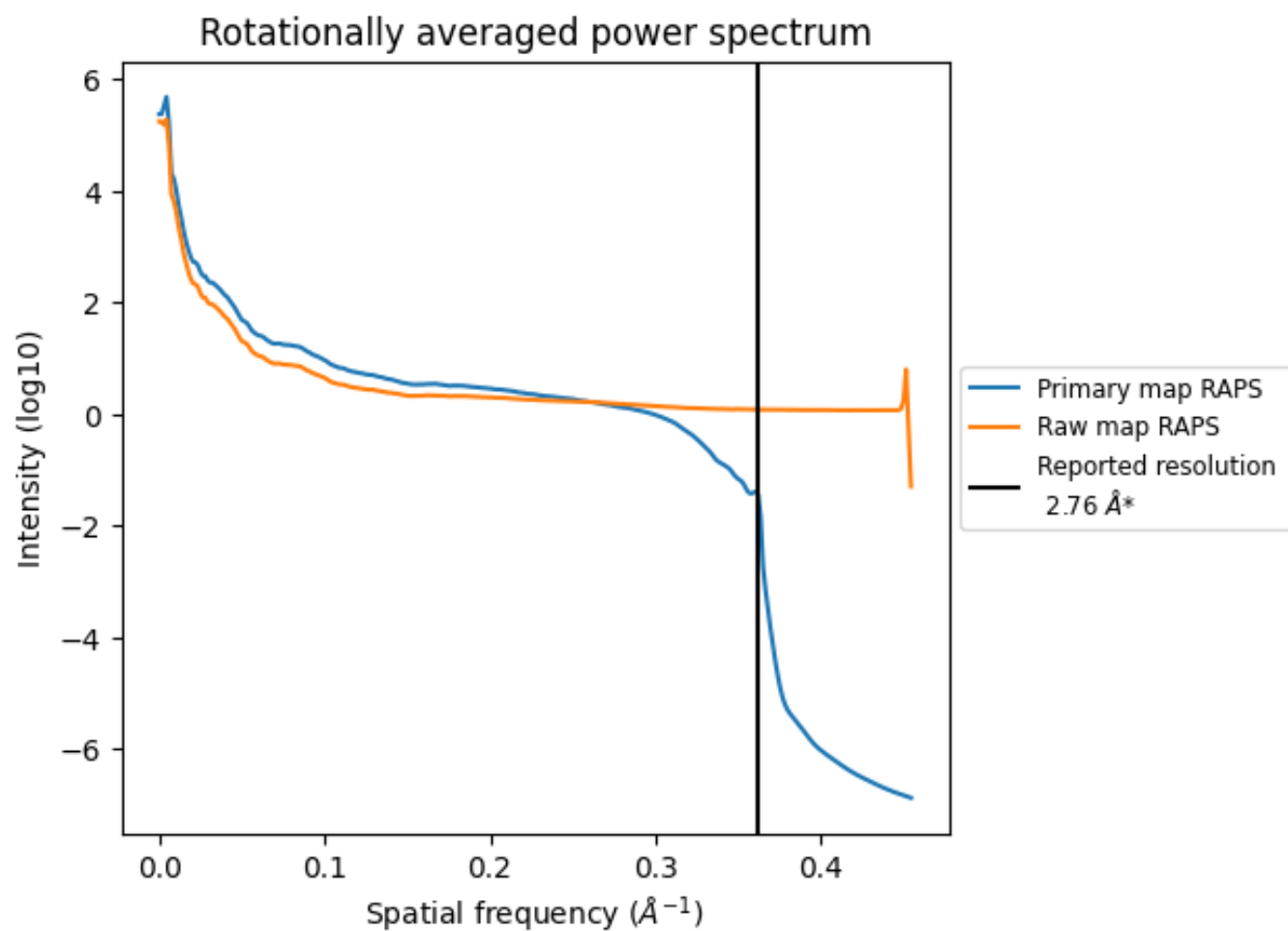
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2344 nm<sup>3</sup>; this corresponds to an approximate mass of 2118 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 ⓘ

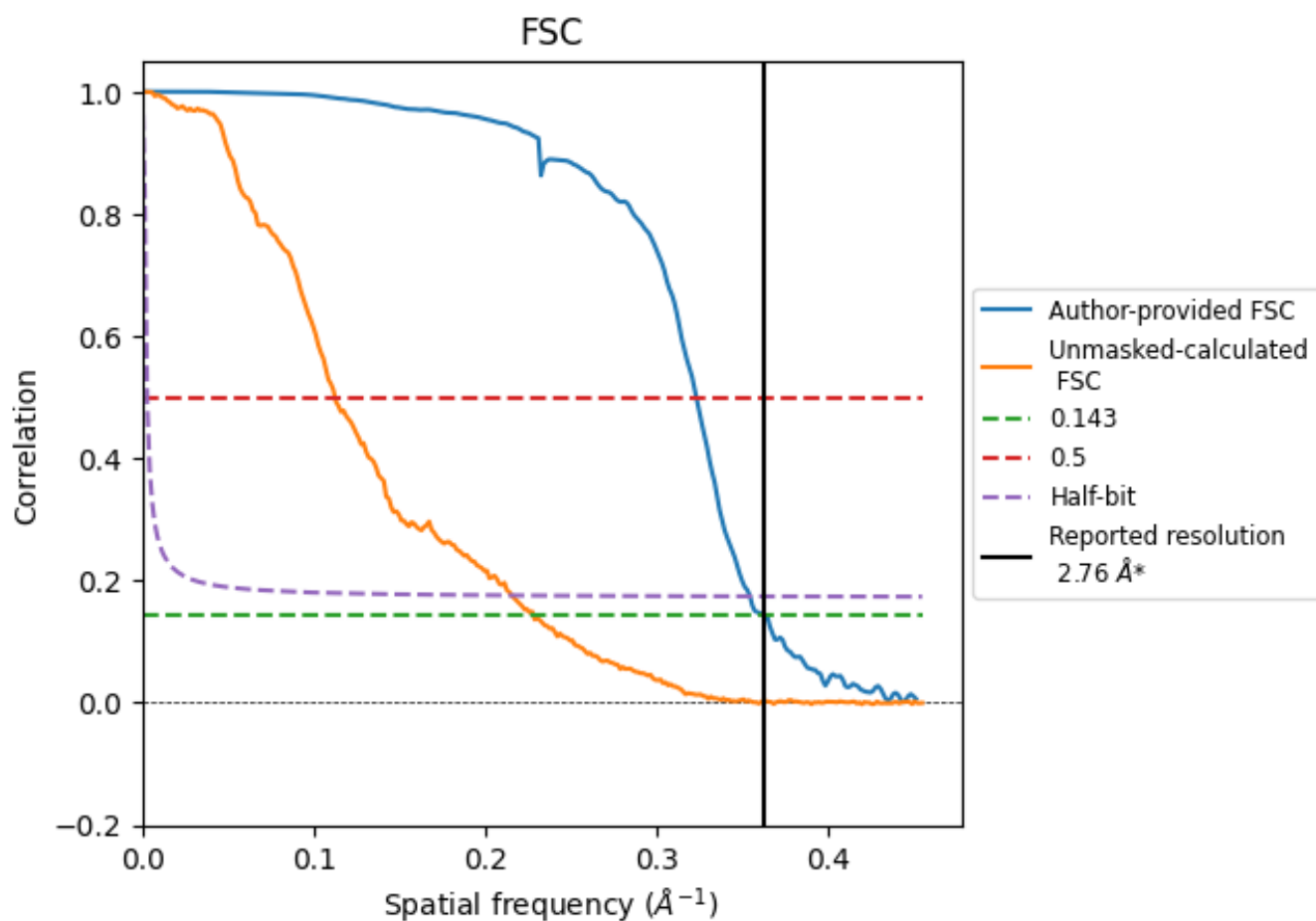


\*Reported resolution corresponds to spatial frequency of 0.362 Å<sup>-1</sup>

## 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 0.362  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	2.75	3.10	2.82
Unmasked-calculated*	4.39	8.90	4.64

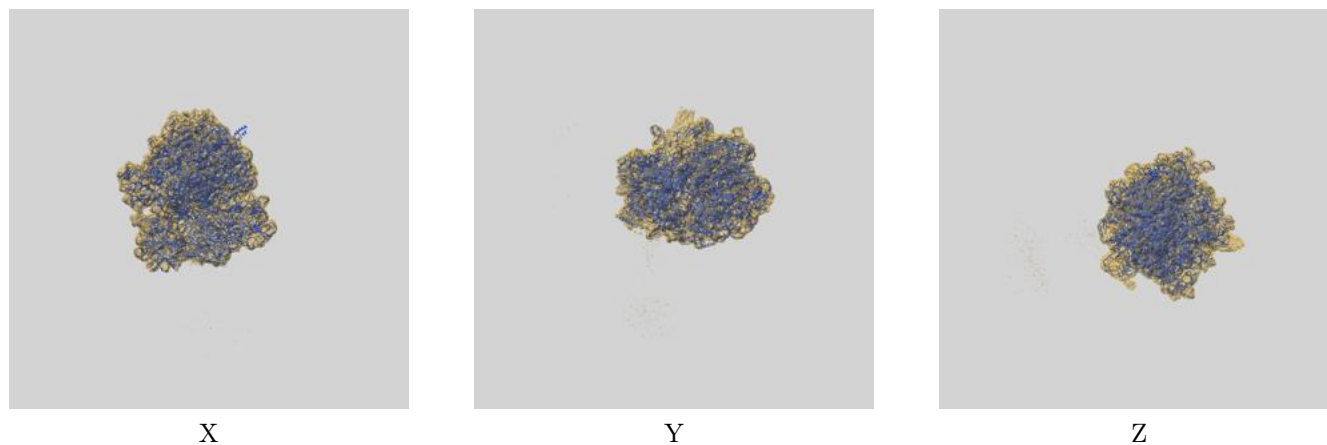
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.39 differs from the reported value 2.76 by more than 10 %



## 9 Map-model fit [i](#)

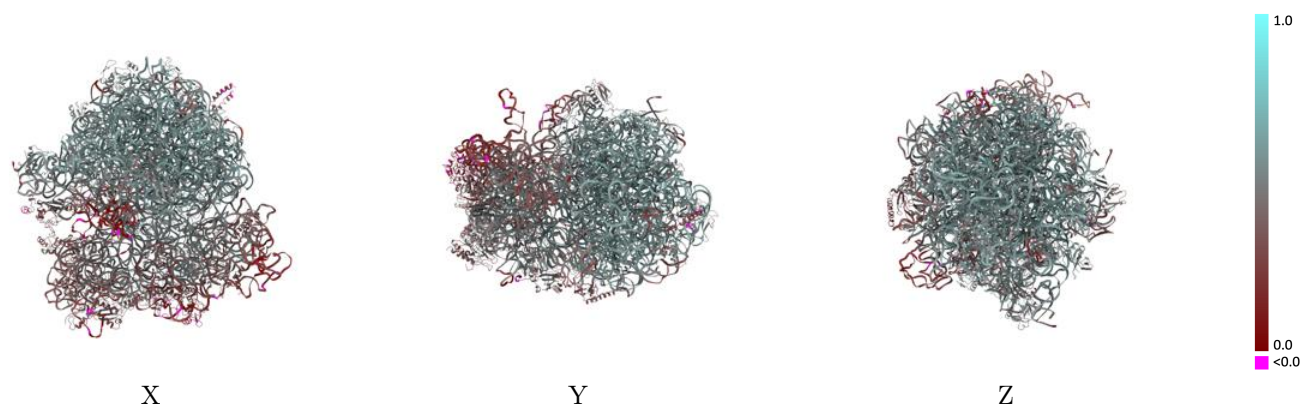
This section contains information regarding the fit between EMDB map EMD-66122 and PDB model 9WNR. Per-residue inclusion information can be found in section [3](#) on page [15](#).

### 9.1 Map-model overlay [i](#)



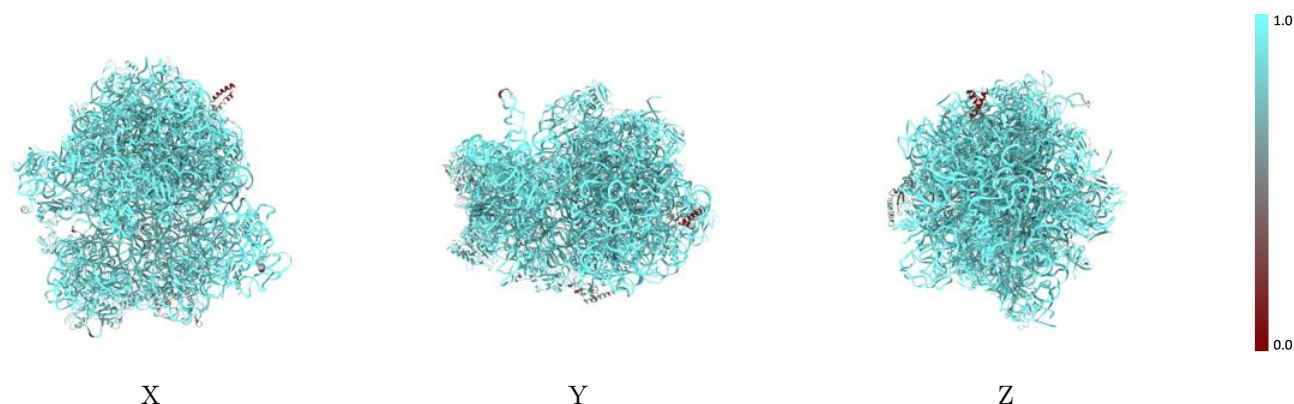
The images above show the 3D surface view of the map at the recommended contour level 0.33 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



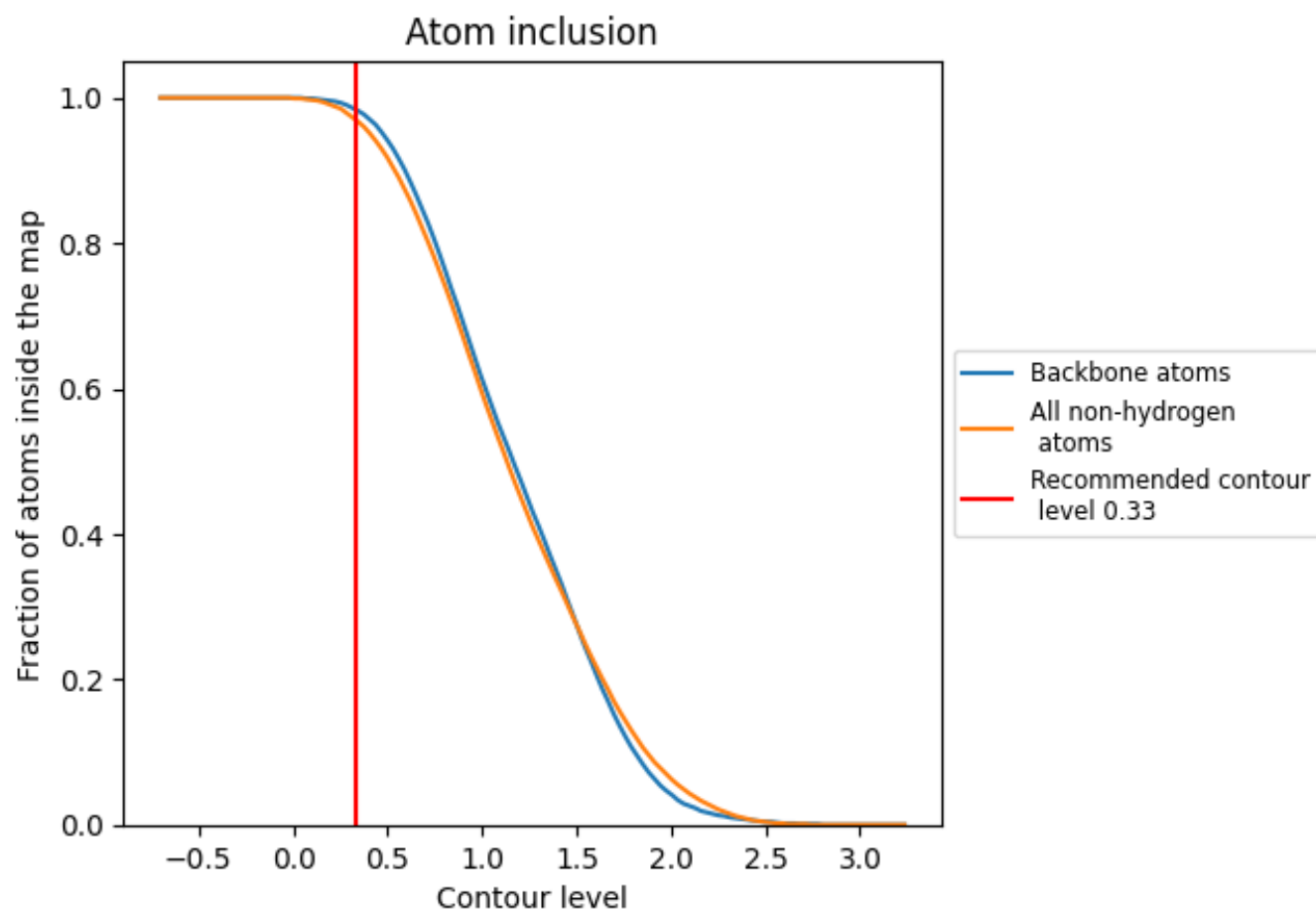
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.33).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ















































The table lists the average atom inclusion at the recommended contour level (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.4820
0	 0.9880	 0.5130
1	 0.9730	 0.4920
2	 0.9680	 0.5400
4	 0.9670	 0.5490
5	 0.9620	 0.5210
6	 0.9920	 0.5930
7	 0.9820	 0.5840
8	 0.9930	 0.5450
A	 0.9900	 0.4270
B	 0.8290	 0.3650
C	 0.8600	 0.3910
D	 0.6820	 0.1910
E	 0.9140	 0.4540
F	 0.9350	 0.4170
G	 0.9220	 0.3340
H	 0.9410	 0.4540
I	 0.9380	 0.3400
J	 0.8140	 0.3390
K	 0.9640	 0.4470
L	 0.8620	 0.3340
M	 0.9350	 0.3440
N	 0.9110	 0.3390
O	 0.9540	 0.4500
P	 0.9260	 0.3750
Q	 0.9160	 0.3730
R	 0.8890	 0.3790
S	 0.9260	 0.3200
T	 0.9330	 0.3290
U	 0.8360	 0.3610
V	 0.3210	 0.2590
X	 0.9800	 0.2460
Y	 0.9930	 0.3930
Z	 0.9360	 0.4260
a	 0.9990	 0.5180



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Chain	Atom inclusion	Q-score
b	 0.9960	 0.5430
c	 0.9870	 0.5740
d	 0.9800	 0.5530
e	 0.9690	 0.5350
f	 0.8800	 0.3300
g	 0.9650	 0.4550
h	 0.6750	 0.3620
k	 0.9790	 0.5600
l	 0.9670	 0.5410
m	 0.9760	 0.5500
n	 0.9720	 0.5410
o	 0.9860	 0.5710
p	 0.9630	 0.4900
q	 0.9630	 0.5280
r	 0.9860	 0.5730
s	 0.9620	 0.5520
t	 0.9710	 0.5530
u	 0.9550	 0.5050
v	 0.9700	 0.5130
w	 0.9660	 0.5120
x	 0.9830	 0.4290
y	 0.9130	 0.5190
z	 0.9120	 0.3920