



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 11:13 AM UTC

PDB ID : 6WDB / pdb_00006wdb
EMDB ID : EMD-21630
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure IV-A)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 4.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

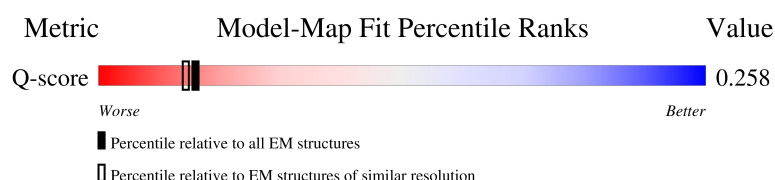
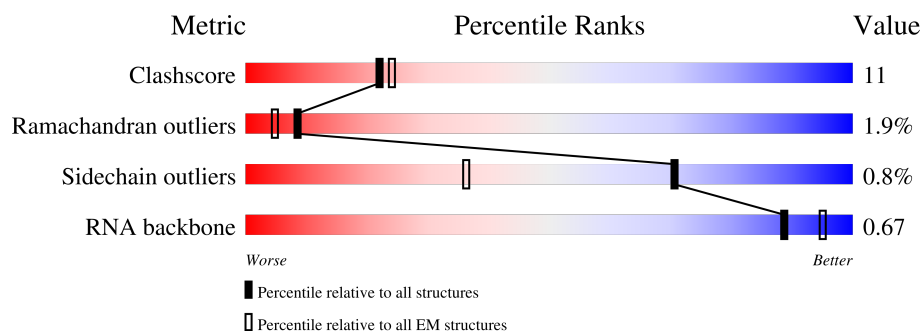
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

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



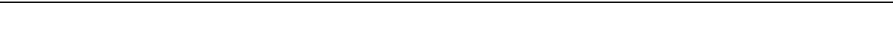
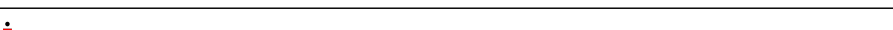
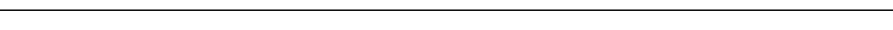
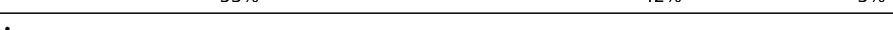
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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

Mol	Chain	Length	Quality of chain
1	b	271	
2	c	209	
3	d	201	

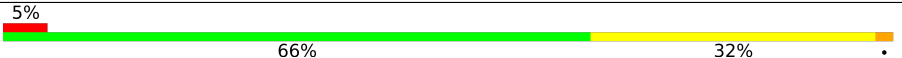
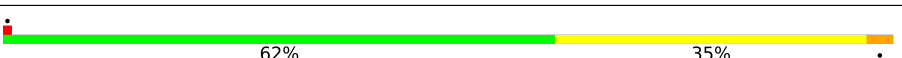
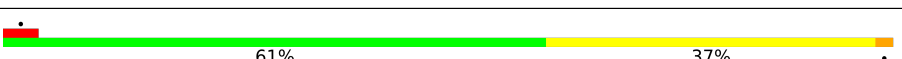
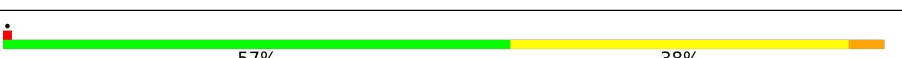
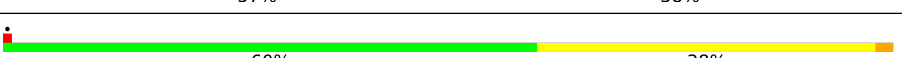
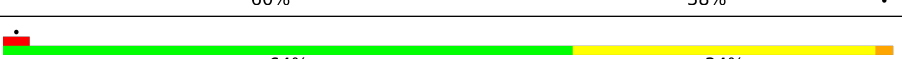
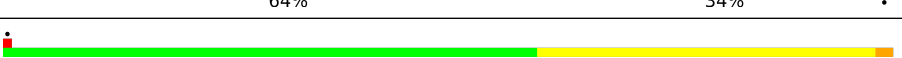
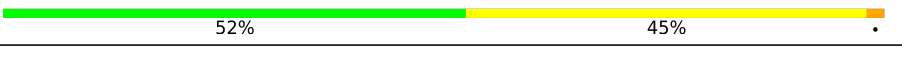
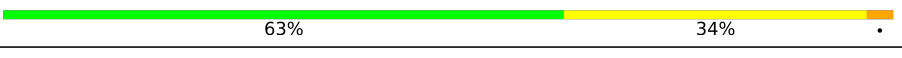
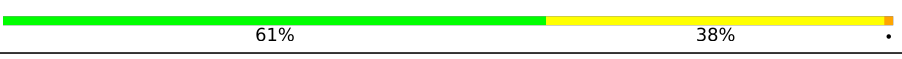
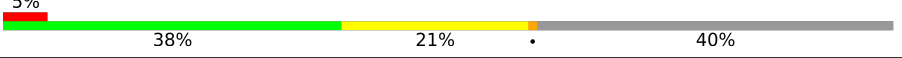
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

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Mol	Chain	Length	Quality of chain
29	E	64	
30	F	38	
31	G	225	
32	H	206	
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	223	
52	3	1539	
53	1	2903	

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Mol	Chain	Length	Quality of chain
54	2	120	56%38%7%
55	5	77	5% 60%34%6%
55	6	77	6% 61%35%.
56	4	18	78%22%
57	7	76	68%18%9%.

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 150149 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L2.

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

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

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

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

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

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

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

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

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

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	t	93	Total	C	N	O	S	0
			739	466	139	132	2	0

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O		0
			780	492	146	142		0

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

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

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

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

- Molecule 25 is a protein called 50S ribosomal protein L30.

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

- Molecule 26 is a protein called 50S ribosomal protein L32.

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

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 28 is a protein called 50S ribosomal protein L34.

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

- Molecule 29 is a protein called 50S ribosomal protein L35.

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

- Molecule 30 is a protein called 50S ribosomal protein L36.

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

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 33 is a protein called 30S ribosomal protein S4.

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

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 37 is a protein called 30S ribosomal protein S8.

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

- Molecule 38 is a protein called 30S ribosomal protein S9.

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

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 41 is a protein called 30S ribosomal protein S12.

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

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 43 is a protein called 30S ribosomal protein S14.

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

- Molecule 44 is a protein called 30S ribosomal protein S15.

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

- Molecule 45 is a protein called 30S ribosomal protein S16.

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

- Molecule 46 is a protein called 30S ribosomal protein S17.

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

- Molecule 47 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 49 is a protein called 30S ribosomal protein S20.

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

- Molecule 50 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 51 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 55 is a RNA chain called tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
55	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

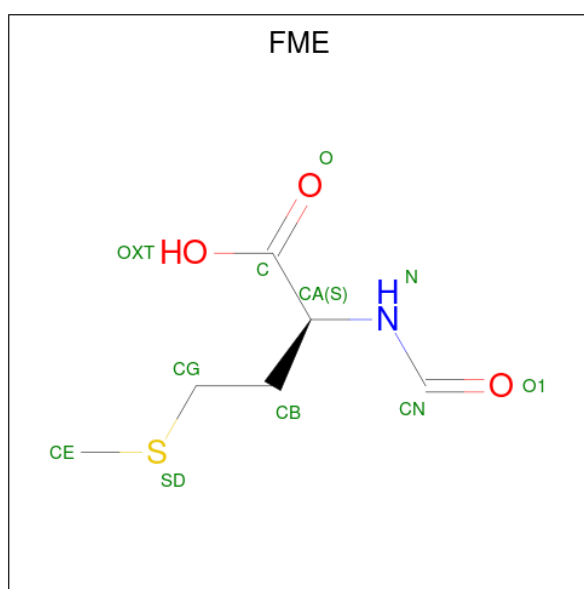
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 57 is a RNA chain called tRNA^{Phe}.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	73	Total	C	N	O	P	0	0
			1557	695	279	511	72		

- Molecule 58 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).

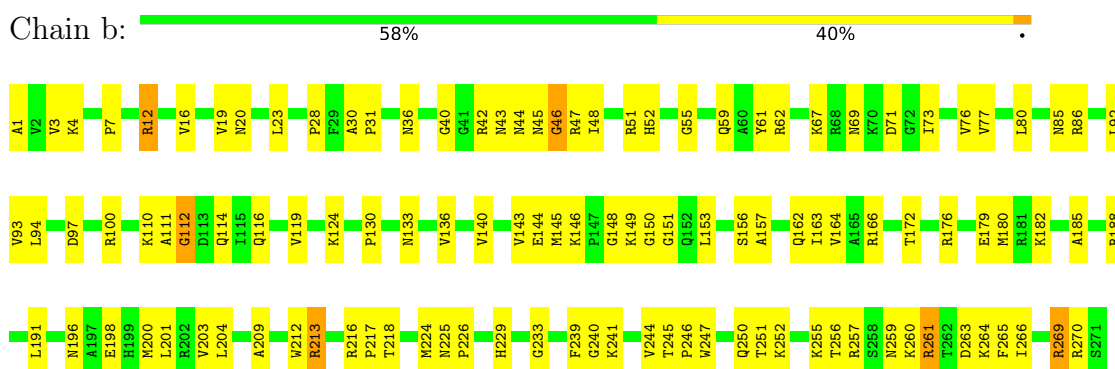


Mol	Chain	Residues	Atoms					AltConf
58	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

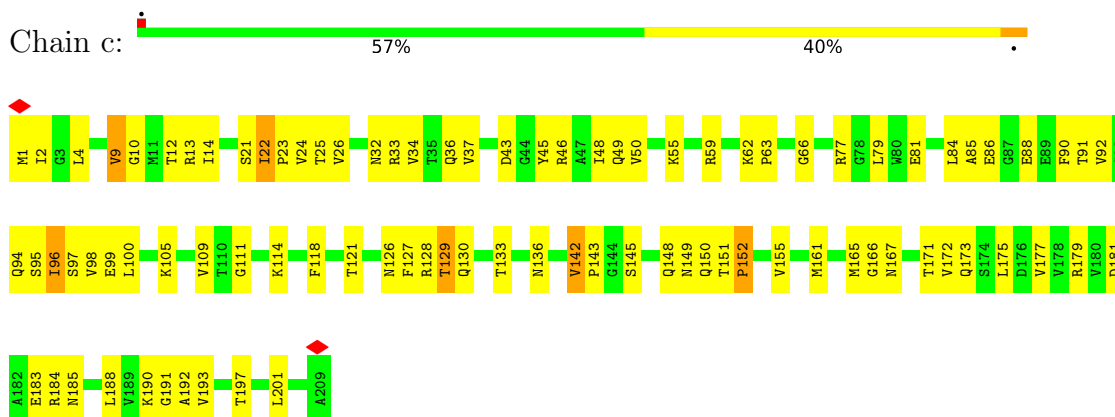
3 Residue-property plots [i](#)

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.

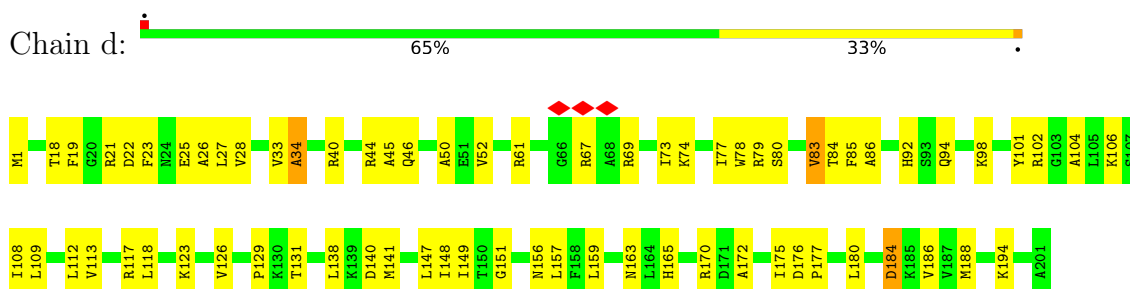
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

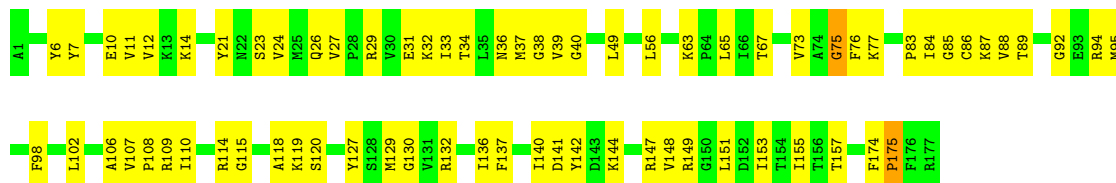


• Molecule 3: 50S ribosomal protein L4



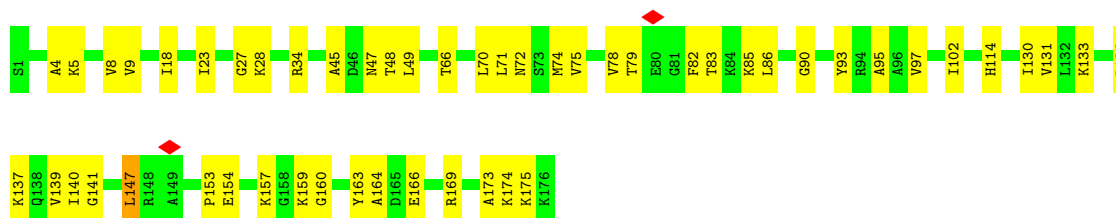
- Molecule 4: 50S ribosomal protein L5

Chain e: 



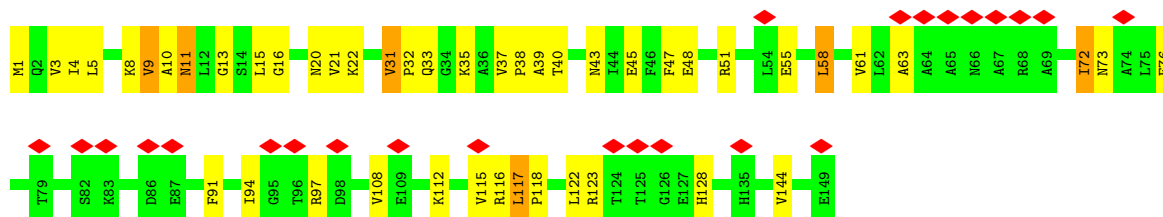
- Molecule 5: 50S ribosomal protein L6

Chain f: 

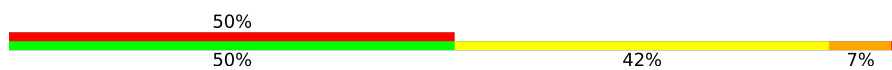


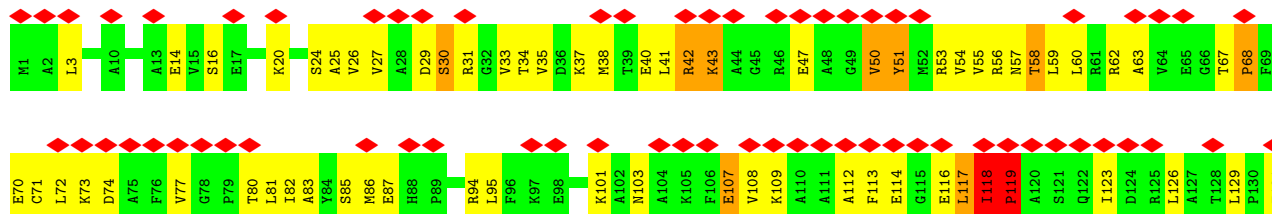
- Molecule 6: 50S ribosomal protein L9

Chain g: 



- Molecule 7: 50S ribosomal protein L10

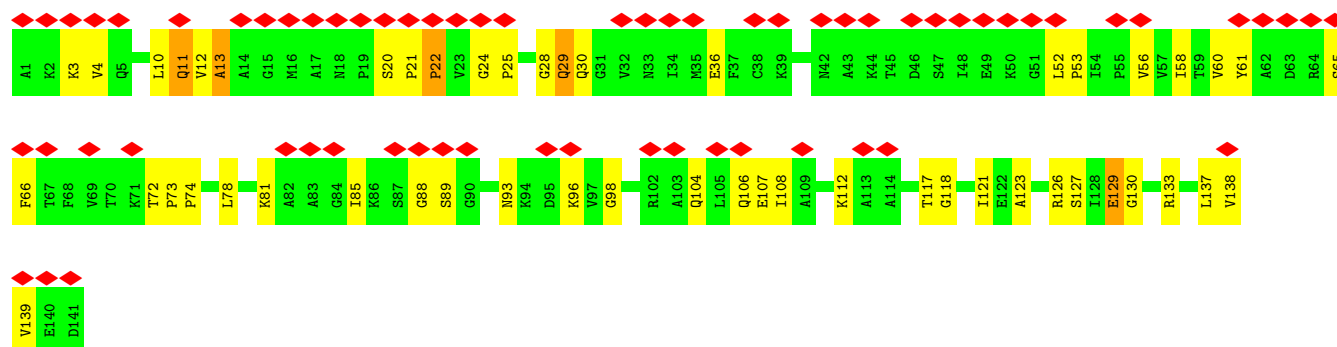
Chain h: 



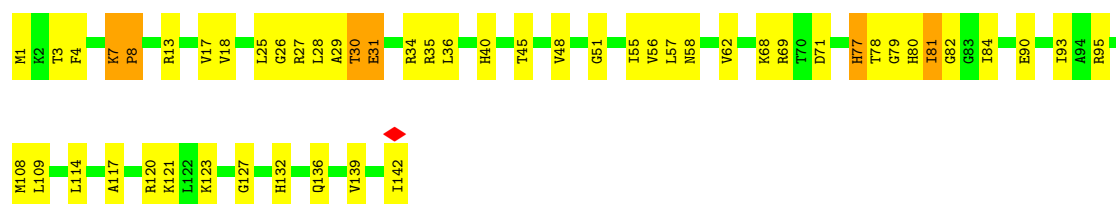
- Molecule 8: 50S ribosomal protein L11

Chain i: 

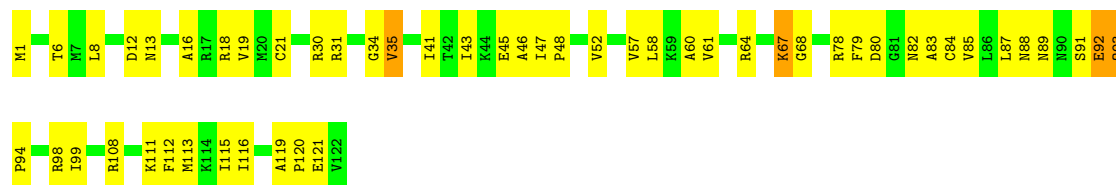




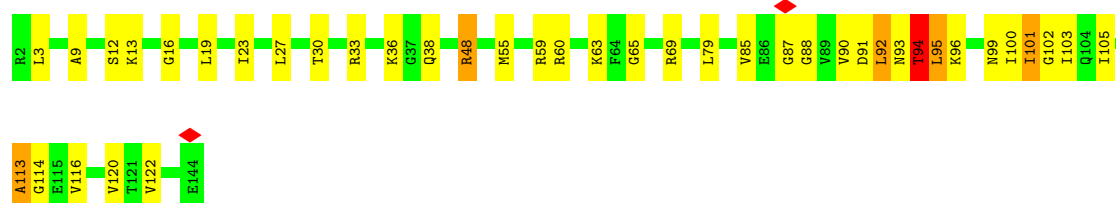
• Molecule 9: 50S ribosomal protein L13



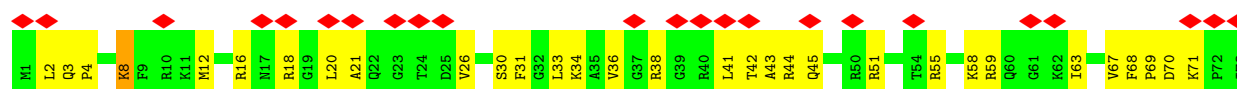
• Molecule 10: 50S ribosomal protein L14



• Molecule 11: 50S ribosomal protein L15

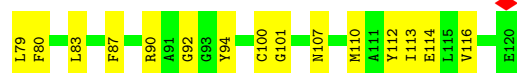
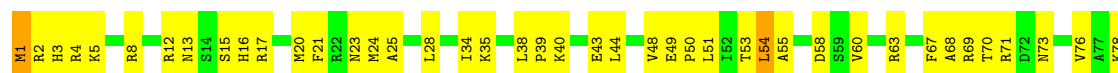


• Molecule 12: 50S ribosomal protein L16

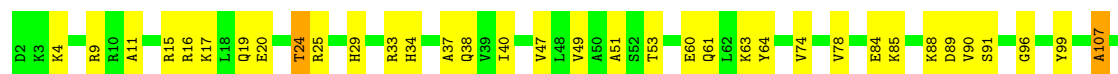




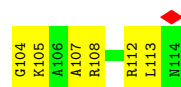
• Molecule 13: 50S ribosomal protein L17



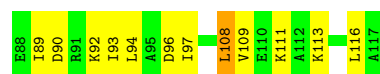
• Molecule 14: 50S ribosomal protein L18



• Molecule 15: 50S ribosomal protein L19

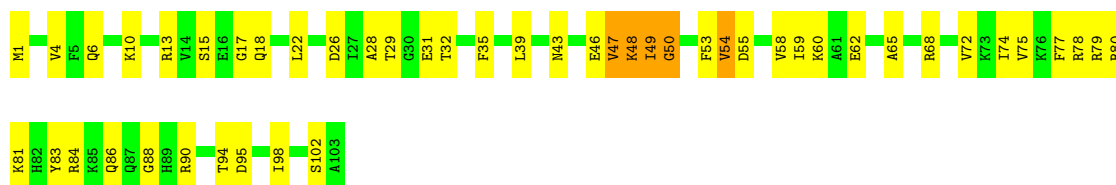


• Molecule 16: 50S ribosomal protein L20



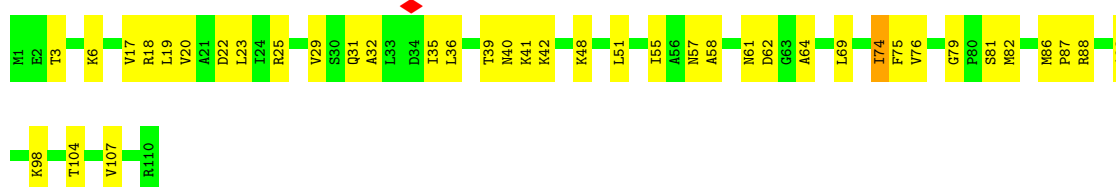
• Molecule 17: 50S ribosomal protein L21





- Molecule 18: 50S ribosomal protein L22

Chain s: 64% 35%



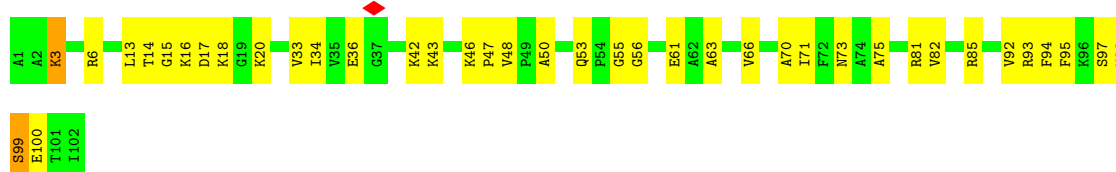
- Molecule 19: 50S ribosomal protein L23

Chain t: 60% 37%



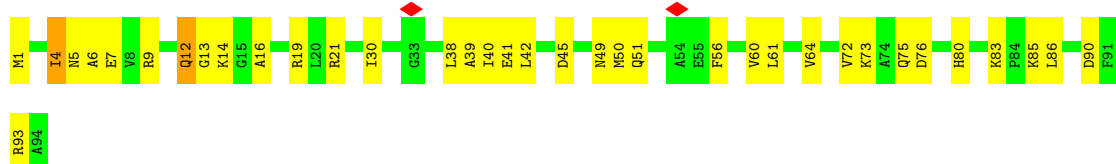
- Molecule 20: 50S ribosomal protein L24

Chain u: 62% 36%



- Molecule 21: 50S ribosomal protein L25

Chain v: 61% 37%



- Molecule 22: 50S ribosomal protein L27

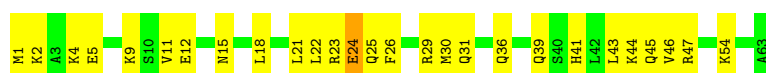
Chain w: 72% 28%



- Molecule 23: 50S ribosomal protein L28



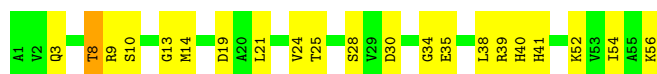
- Molecule 24: 50S ribosomal protein L29



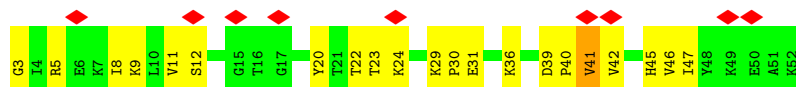
- Molecule 25: 50S ribosomal protein L30



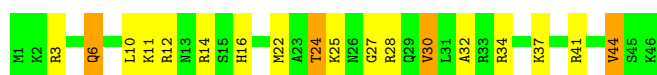
- Molecule 26: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L33

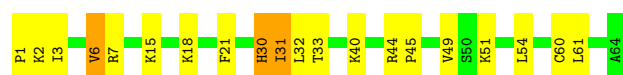


- Molecule 28: 50S ribosomal protein L34

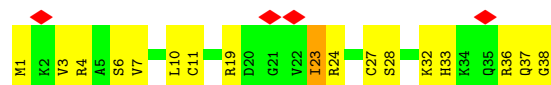


- Molecule 29: 50S ribosomal protein L35

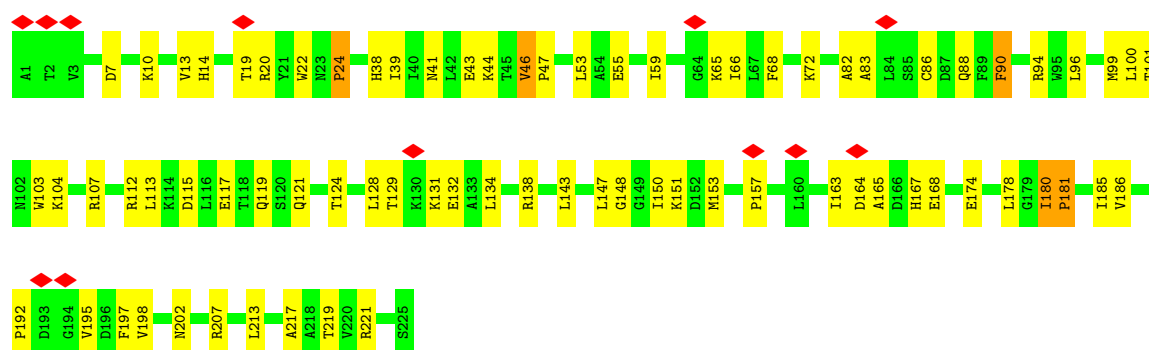




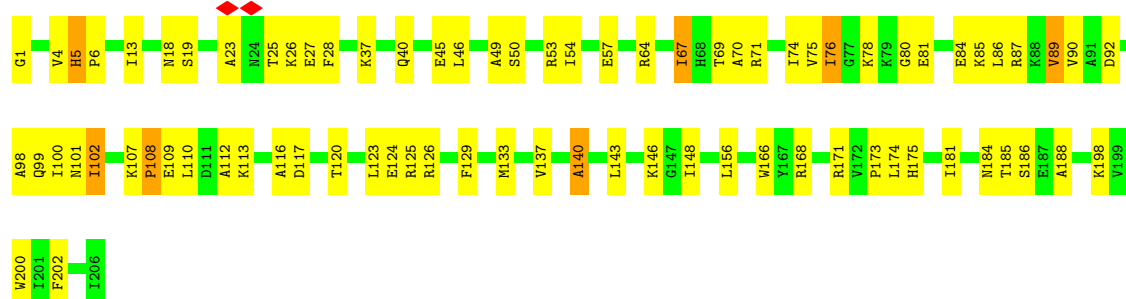
- Molecule 30: 50S ribosomal protein L36



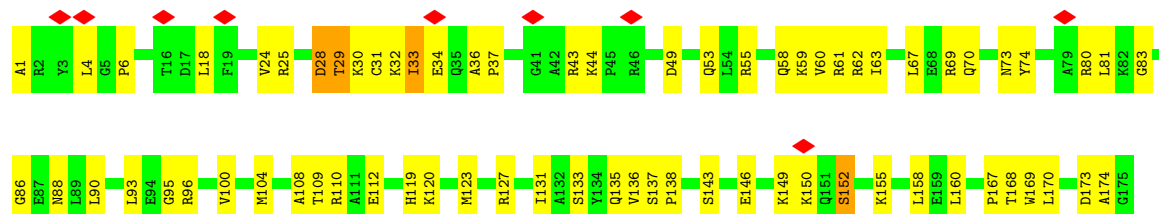
- Molecule 31: 30S ribosomal protein S2



- Molecule 32: 30S ribosomal protein S3

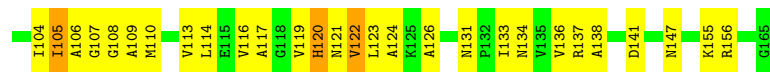
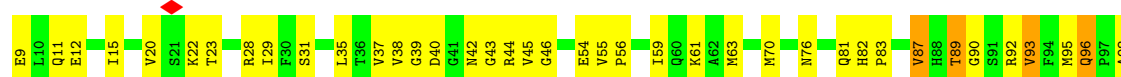


- Molecule 33: 30S ribosomal protein S4

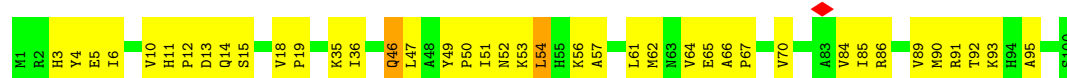




- Molecule 34: 30S ribosomal protein S5



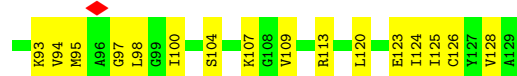
- Molecule 35: 30S ribosomal protein S6



- Molecule 36: 30S ribosomal protein S7

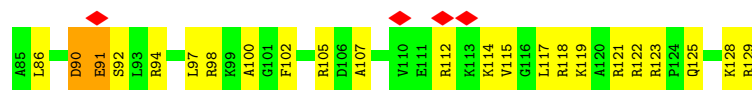


- Molecule 37: 30S ribosomal protein S8

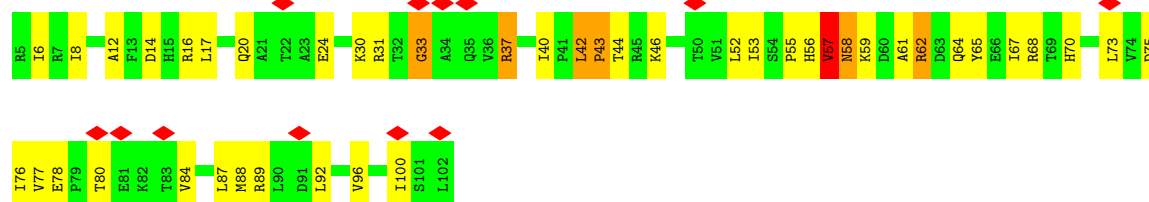


- Molecule 38: 30S ribosomal protein S9

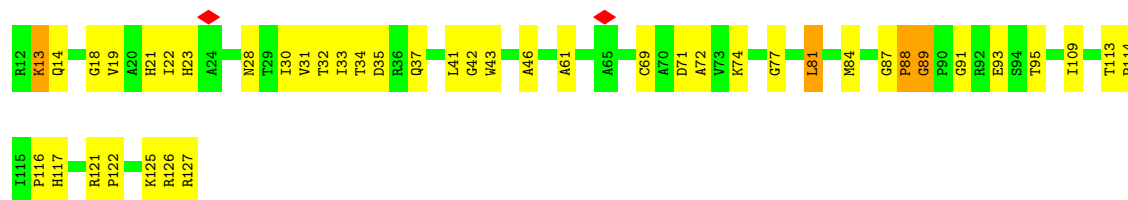




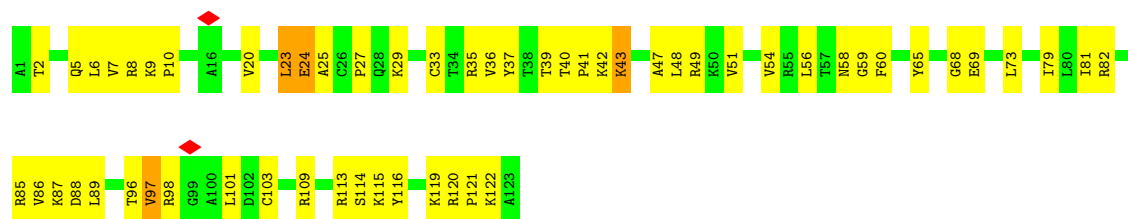
- Molecule 39: 30S ribosomal protein S10



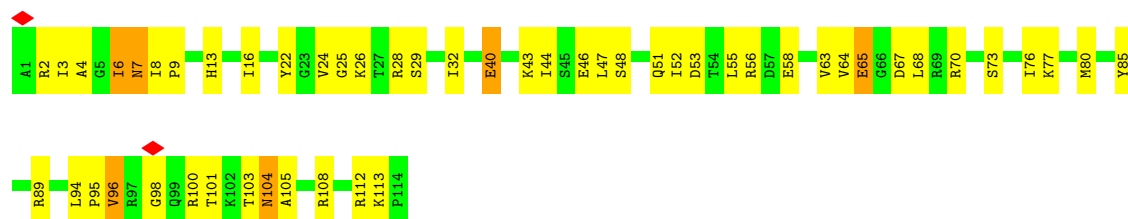
- Molecule 40: 30S ribosomal protein S11



- Molecule 41: 30S ribosomal protein S12

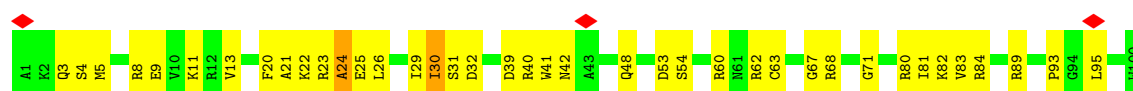


- Molecule 42: 30S ribosomal protein S13



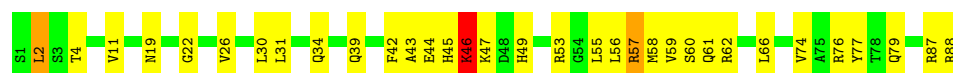
- Molecule 43: 30S ribosomal protein S14

Chain S:  61% 37%



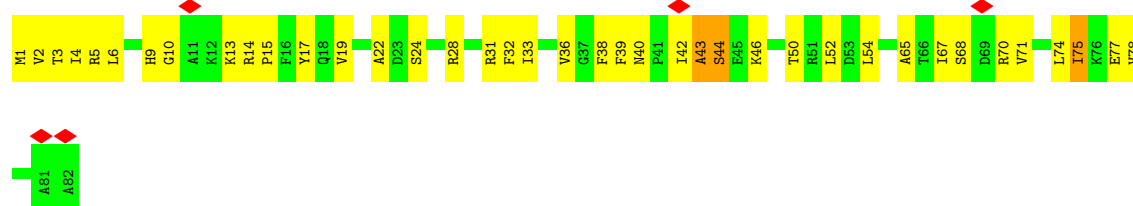
- Molecule 44: 30S ribosomal protein S15

Chain T:  63% 34%



- Molecule 45: 30S ribosomal protein S16

Chain U:  6% 52% 44%



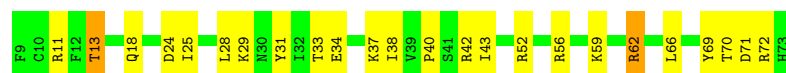
- Molecule 46: 30S ribosomal protein S17

Chain V:  52% 45%



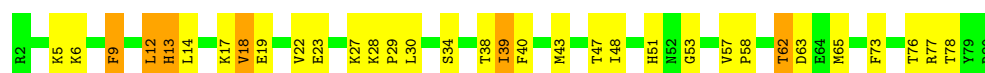
- Molecule 47: 30S ribosomal protein S18

Chain W:  63% 34%



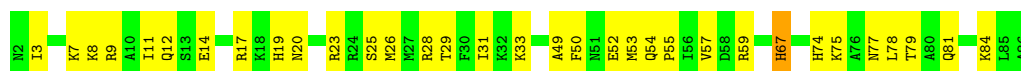
- Molecule 48: 30S ribosomal protein S19

Chain X:  58% 34% 8%



- Molecule 49: 30S ribosomal protein S20

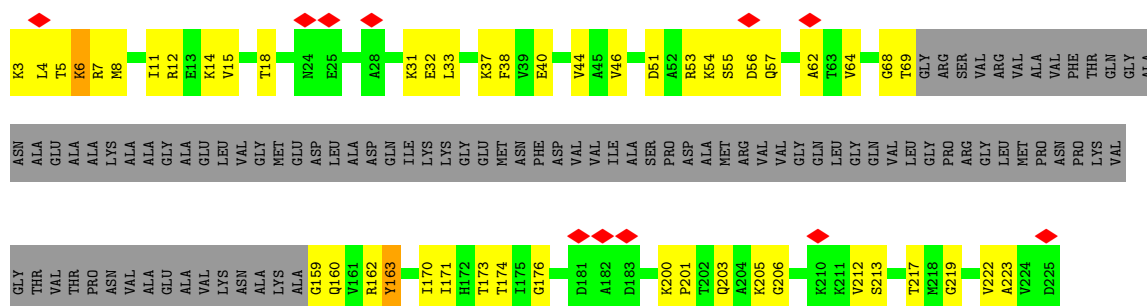
Chain Y:  61% 38%



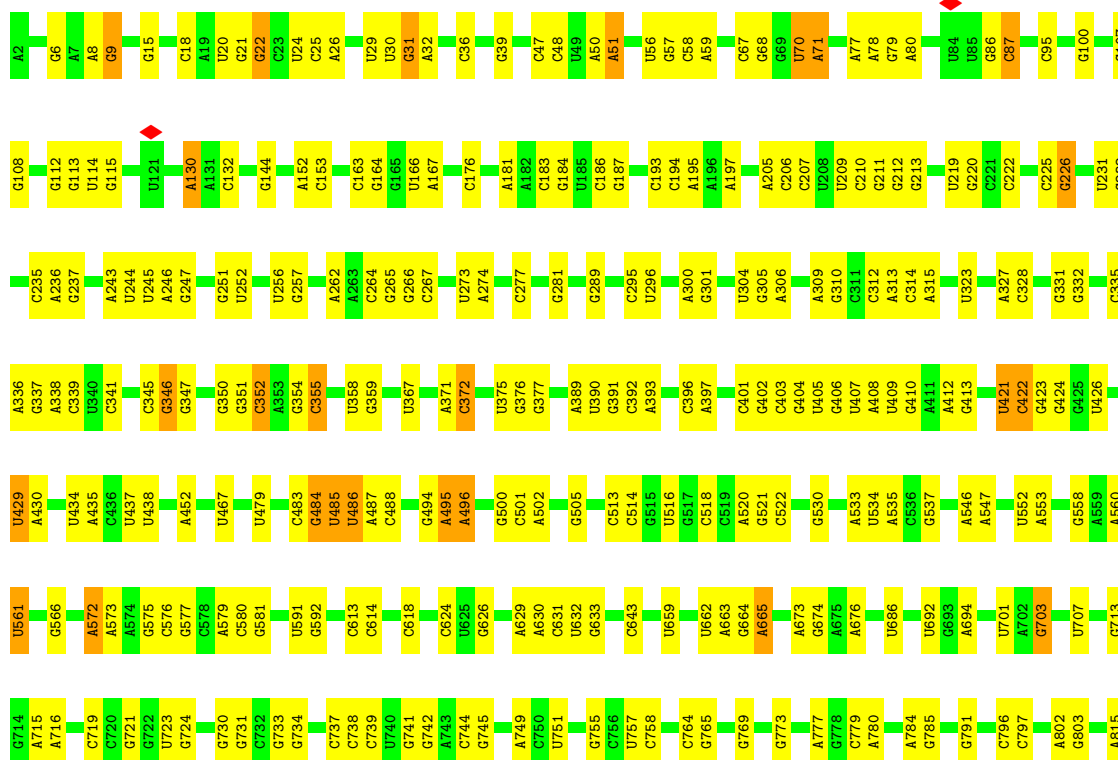
- Molecule 50: 30S ribosomal protein S21

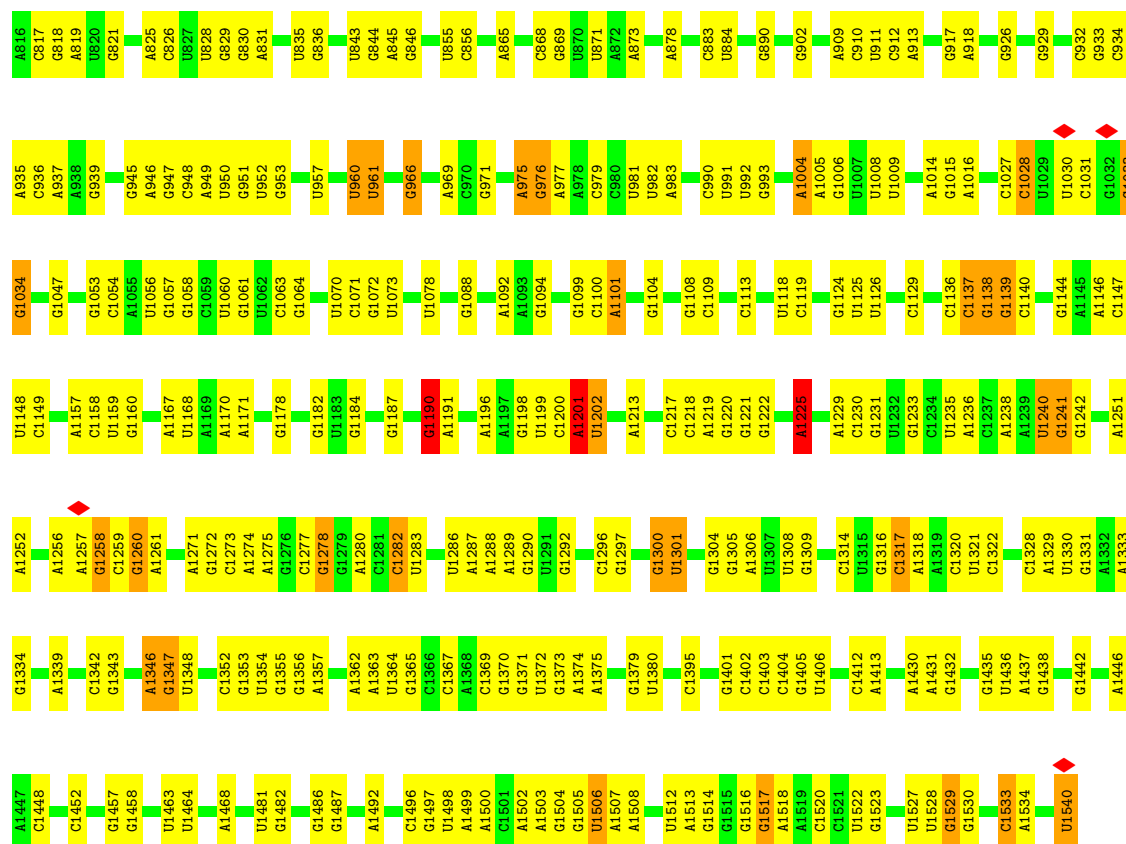


- Molecule 51: 50S ribosomal protein L1



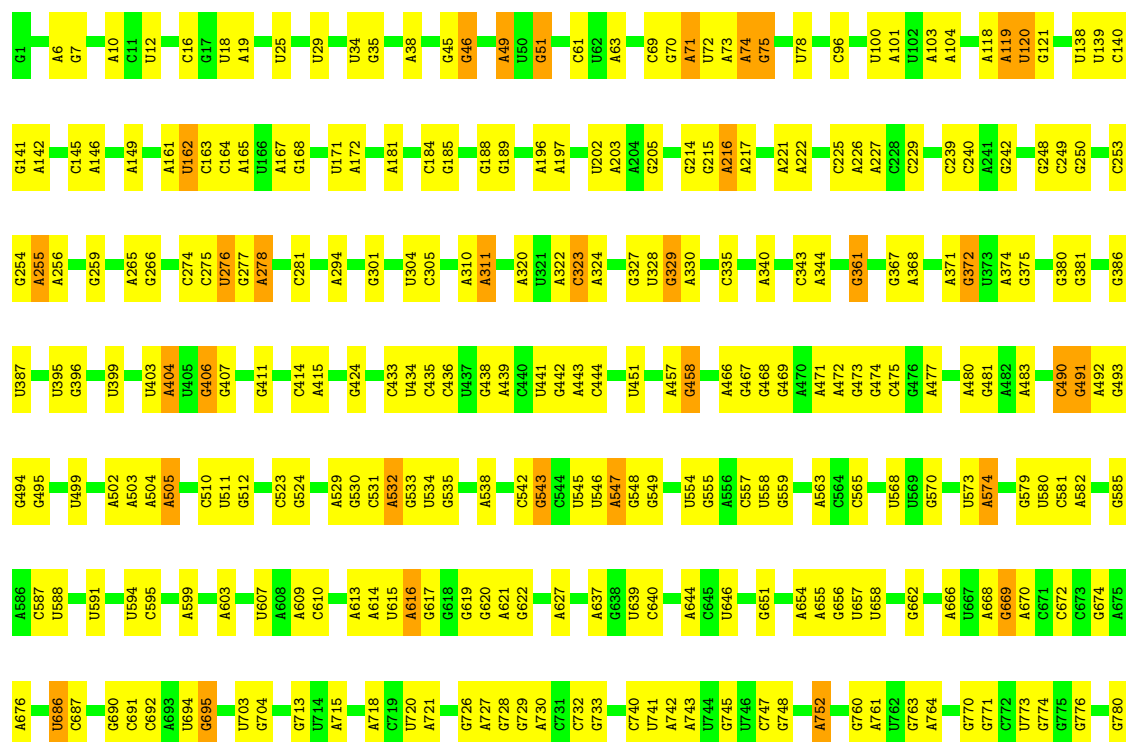
- Molecule 52: 16S ribosomal RNA

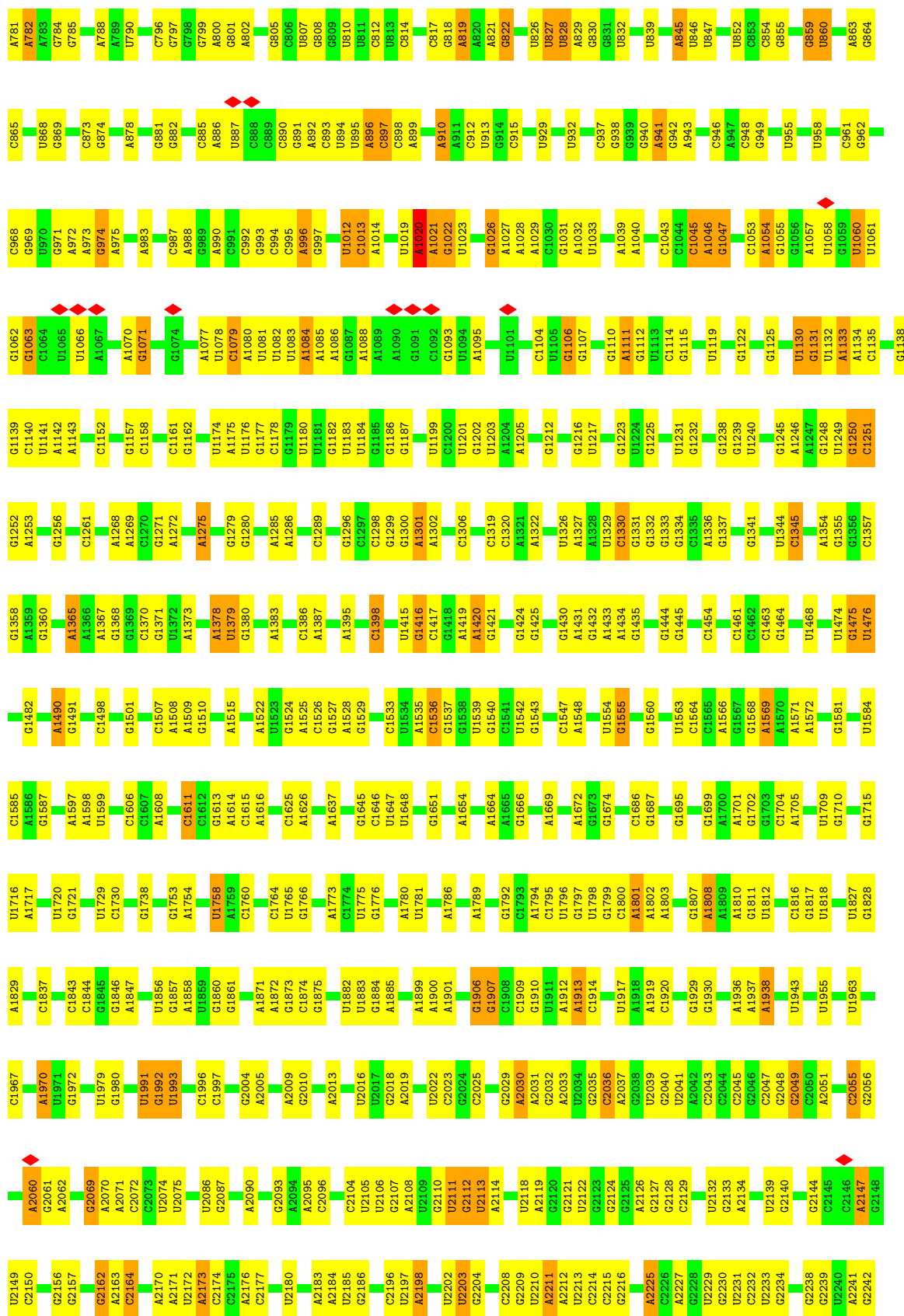


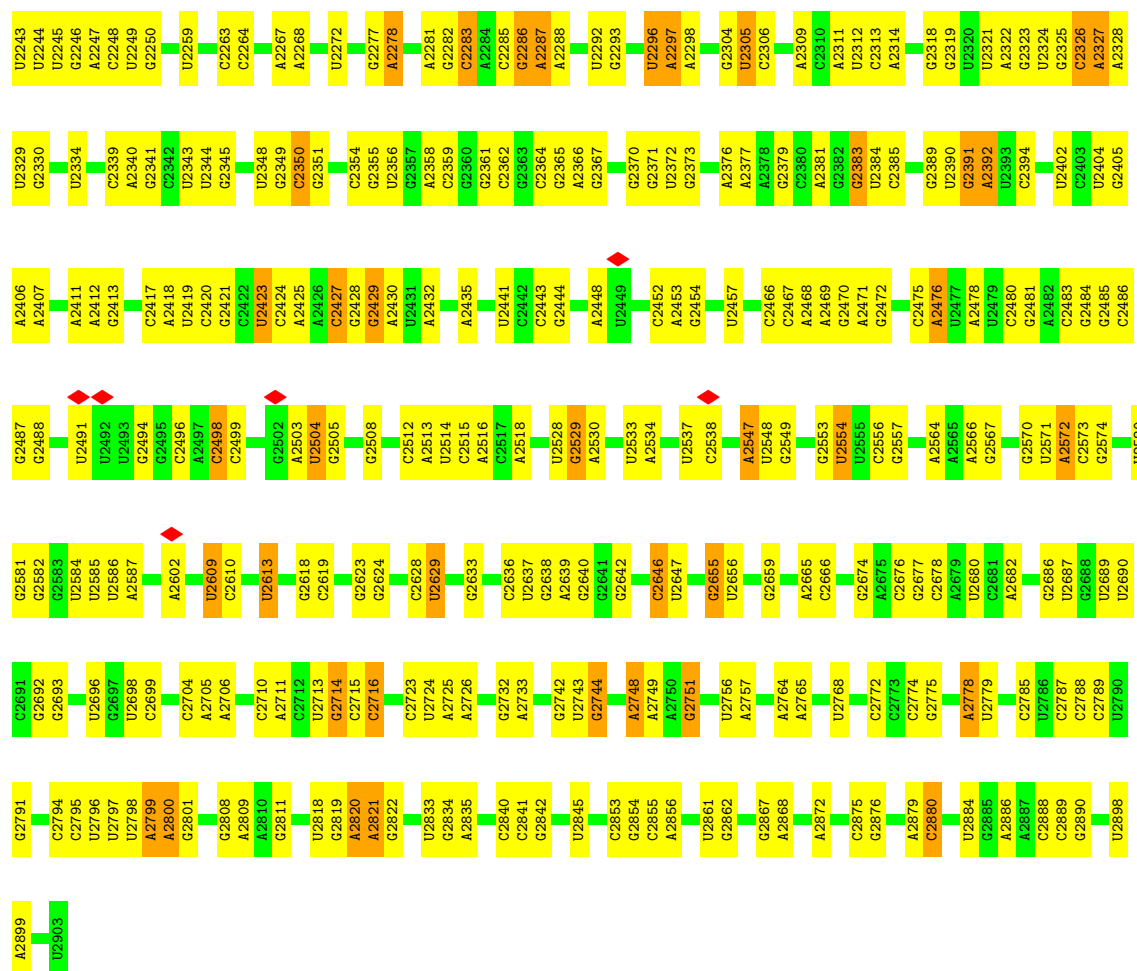


• Molecule 53: 23S ribosomal RNA

Chain 1: 60% 34% 5%







- Molecule 54: 5S ribosomal RNA

Chain 2: 56% 38% 7%



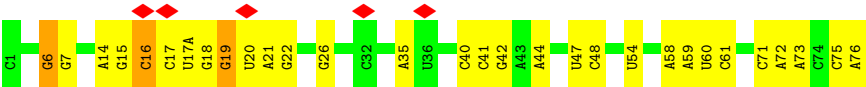
- Molecule 55: tRNA^{fMet}

Chain 5: 5% 60% 34% 6%

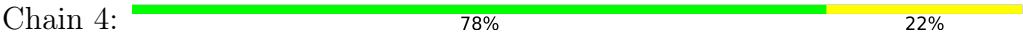


- Molecule 55: tRNA^{fMet}

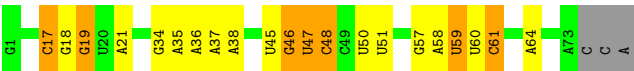
Chain 6: 6% 61% 35% 0%



• Molecule 56: mRNA



• Molecule 57: tRNAPhe



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1816	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	19.301	Depositor
Minimum map value	-10.195	Depositor
Average map value	0.124	Depositor
Map value standard deviation	0.876	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality

5.1 Standard geometry

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

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	b	0.29	0/2122	0.98	9/2852 (0.3%)
2	c	0.30	0/1586	0.92	7/2134 (0.3%)
3	d	0.29	0/1571	0.93	6/2113 (0.3%)
4	e	0.31	0/1435	0.88	3/1926 (0.2%)
5	f	0.30	0/1343	0.91	5/1816 (0.3%)
6	g	0.31	0/1122	1.00	8/1515 (0.5%)
7	h	0.32	0/1002	1.08	7/1350 (0.5%)
8	i	0.35	0/1046	0.99	7/1410 (0.5%)
9	j	0.29	0/1152	0.94	7/1551 (0.5%)
10	k	0.28	0/948	0.94	5/1268 (0.4%)
11	l	0.30	0/1054	1.01	3/1403 (0.2%)
12	m	0.33	0/1093	0.90	1/1460 (0.1%)
13	n	0.31	0/974	1.00	9/1301 (0.7%)
14	o	0.30	0/902	1.02	6/1209 (0.5%)
15	p	0.28	0/929	0.87	1/1242 (0.1%)
16	q	0.29	0/960	1.00	8/1278 (0.6%)
17	r	0.28	0/829	0.93	3/1107 (0.3%)
18	s	0.29	0/864	0.90	2/1156 (0.2%)
19	t	0.29	0/745	0.93	5/994 (0.5%)
20	u	0.28	0/788	0.87	1/1051 (0.1%)
21	v	0.29	0/766	0.83	1/1025 (0.1%)
22	w	0.28	0/582	0.89	0/769
23	x	0.28	0/635	0.92	1/848 (0.1%)
24	y	0.27	0/510	0.95	0/677
25	z	0.29	0/453	0.91	1/605 (0.2%)
26	B	0.29	0/450	0.86	1/599 (0.2%)
27	C	0.32	0/417	0.93	4/554 (0.7%)
28	D	0.32	0/380	1.08	3/498 (0.6%)
29	E	0.31	0/513	0.97	1/676 (0.1%)
30	F	0.34	0/303	0.82	0/397
31	G	0.29	0/1788	0.92	6/2408 (0.2%)
32	H	0.29	0/1652	0.95	11/2225 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.29	0/1665	0.94	6/2227 (0.3%)
34	J	0.34	0/1170	1.01	11/1573 (0.7%)
35	K	0.31	0/836	0.91	1/1128 (0.1%)
36	L	0.28	0/1196	0.98	7/1602 (0.4%)
37	M	0.29	0/989	0.91	2/1326 (0.2%)
38	N	0.31	0/1034	0.96	3/1375 (0.2%)
39	O	0.32	0/797	0.94	3/1077 (0.3%)
40	P	0.32	0/886	0.99	4/1195 (0.3%)
41	Q	0.32	0/969	1.02	5/1300 (0.4%)
42	R	0.31	0/893	1.00	3/1193 (0.3%)
43	S	0.28	0/817	1.04	5/1088 (0.5%)
44	T	0.29	0/722	1.03	7/964 (0.7%)
45	U	0.33	0/659	0.91	2/884 (0.2%)
46	V	0.32	0/658	0.91	0/881
47	W	0.32	0/545	0.97	2/731 (0.3%)
48	X	0.32	0/653	0.99	4/877 (0.5%)
49	Y	0.30	0/671	0.98	3/888 (0.3%)
50	Z	0.32	0/551	1.06	2/728 (0.3%)
51	a	0.30	0/1034	0.84	2/1387 (0.1%)
52	3	0.40	0/36963	0.51	3/57662 (0.0%)
53	1	0.39	0/69796	0.51	2/108888 (0.0%)
54	2	0.40	0/2872	0.50	0/4479
55	5	0.39	0/1832	0.50	0/2855
55	6	0.40	0/1832	0.52	0/2855
56	4	0.39	0/436	0.49	0/679
57	7	0.39	0/1740	0.48	0/2712
All	All	0.37	0/163130	0.65	209/243971 (0.1%)

There are no bond length outliers.

All (209) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	e	6	TYR	N-CA-C	-8.79	101.38	112.90
7	h	117	LEU	N-CA-C	8.33	122.48	108.90
11	l	101	ILE	N-CA-C	8.18	118.28	110.42
50	Z	58	LYS	N-CA-C	-8.12	101.70	111.69
5	f	173	ALA	N-CA-C	-7.99	103.53	113.20
14	o	116	GLN	N-CA-C	7.94	121.39	109.25
41	Q	114	SER	N-CA-C	-7.69	103.15	112.54
44	T	43	ALA	N-CA-C	-7.61	103.46	112.89
13	n	54	LEU	N-CA-C	-7.54	102.61	112.41
14	o	20	GLU	N-CA-C	-7.50	104.26	113.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	T	57	ARG	N-CA-C	-7.47	103.62	112.89
34	J	117	ALA	N-CA-C	-7.26	103.39	112.90
40	P	117	HIS	N-CA-C	-7.26	102.68	112.26
16	q	70	GLN	N-CA-C	-7.24	103.42	111.82
13	n	48	VAL	N-CA-C	7.24	118.01	110.62
17	r	49	ILE	N-CA-C	7.22	118.22	108.11
34	J	120	HIS	N-CA-C	-7.19	101.67	110.88
7	h	50	VAL	N-CA-C	7.16	118.11	111.45
36	L	49	LEU	N-CA-C	-7.14	104.55	113.55
6	g	117	LEU	CA-C-N	7.01	126.83	119.05
6	g	117	LEU	C-N-CA	7.01	126.83	119.05
38	N	71	ILE	N-CA-C	6.97	117.48	110.23
44	T	61	GLN	N-CA-C	-6.95	103.78	111.36
40	P	81	LEU	N-CA-C	6.86	118.91	109.18
11	l	95	LEU	N-CA-C	-6.85	104.89	113.18
32	H	89	VAL	N-CA-C	6.85	117.60	110.62
1	b	145	MET	N-CA-C	-6.83	103.84	112.93
42	R	96	VAL	N-CA-C	6.78	119.56	111.09
16	q	50	ARG	N-CA-C	-6.77	105.55	113.88
51	a	55	SER	N-CA-C	6.76	120.40	111.75
1	b	264	LYS	N-CA-C	6.75	119.47	111.71
34	J	105	ILE	N-CA-C	6.74	113.42	106.21
17	r	29	THR	N-CA-C	6.74	118.28	111.07
5	f	147	LEU	N-CA-C	-6.71	103.77	112.23
48	X	13	HIS	N-CA-C	6.70	119.42	111.71
39	O	42	LEU	CA-C-N	6.70	128.21	119.84
39	O	42	LEU	C-N-CA	6.70	128.21	119.84
2	c	127	PHE	N-CA-C	6.70	119.45	110.35
27	C	41	VAL	N-CA-C	6.69	116.71	110.42
14	o	113	ALA	N-CA-C	-6.65	104.99	113.23
47	W	66	LEU	N-CA-C	-6.58	104.19	111.82
28	D	30	VAL	N-CA-C	-6.54	104.11	110.72
32	H	124	GLU	N-CA-C	-6.53	105.28	113.18
14	o	84	GLU	N-CA-C	-6.52	104.02	112.23
43	S	24	ALA	N-CA-C	-6.51	105.33	113.20
3	d	73	ILE	N-CA-C	-6.50	106.18	112.29
8	i	24	GLY	CA-C-N	6.48	126.17	119.82
8	i	24	GLY	C-N-CA	6.48	126.17	119.82
16	q	49	ARG	N-CA-C	-6.48	105.00	113.17
38	N	44	ARG	N-CA-C	6.41	118.34	111.36
2	c	191	GLY	N-CA-C	6.39	118.56	112.04
8	i	28	GLY	N-CA-C	-6.39	106.73	114.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	S	41	TRP	N-CA-C	-6.38	105.46	113.18
32	H	140	ALA	N-CA-C	6.35	118.20	111.28
35	K	46	GLN	N-CA-C	6.34	119.57	110.24
44	T	26	VAL	N-CA-C	6.31	116.47	110.42
5	f	4	ALA	N-CA-C	-6.29	105.09	112.89
31	G	180	ILE	CA-C-N	6.27	127.67	119.84
31	G	180	ILE	C-N-CA	6.27	127.67	119.84
45	U	54	LEU	N-CA-C	6.24	118.88	111.71
5	f	47	ASN	N-CA-C	-6.23	104.38	112.23
43	S	22	LYS	N-CA-C	-6.23	106.31	114.04
48	X	18	VAL	N-CA-C	6.19	116.67	110.23
7	h	43	LYS	N-CA-C	-6.18	104.62	111.36
3	d	25	GLU	N-CA-C	6.16	118.53	111.02
43	S	11	LYS	N-CA-C	-6.14	104.50	112.23
2	c	128	ARG	N-CA-C	-6.13	99.16	108.67
48	X	9	PHE	N-CA-C	6.09	119.20	110.24
10	k	31	ARG	N-CA-C	6.09	118.83	111.40
42	R	113	LYS	N-CA-C	6.08	123.24	109.81
9	j	7	LYS	CA-C-N	6.05	127.40	119.84
9	j	7	LYS	C-N-CA	6.05	127.40	119.84
19	t	13	ALA	N-CA-C	6.04	113.57	108.13
44	T	39	GLN	N-CA-C	-6.03	104.79	111.36
15	p	14	GLN	N-CA-C	6.01	117.52	110.97
6	g	72	ILE	N-CA-C	-6.01	106.64	111.81
6	g	58	LEU	N-CA-C	-6.00	104.86	111.82
10	k	112	PHE	N-CA-C	-5.98	105.16	112.88
16	q	15	LYS	N-CA-C	-5.97	104.70	112.23
12	m	8	LYS	N-CA-C	5.96	119.38	111.75
25	z	44	ARG	N-CA-C	-5.96	105.27	112.54
6	g	123	ARG	N-CA-C	-5.94	105.86	113.23
7	h	30	SER	N-CA-C	-5.91	105.90	113.23
10	k	67	LYS	N-CA-C	-5.87	105.95	113.23
52	3	1190	G	C2'-C3'-O3'	5.86	118.29	109.50
14	o	63	LYS	N-CA-C	-5.85	104.27	111.40
34	J	87	VAL	N-CA-C	5.84	117.26	109.37
49	Y	78	LEU	N-CA-C	5.83	117.30	111.07
13	n	25	ALA	N-CA-C	-5.82	105.02	111.36
28	D	22	MET	N-CA-C	-5.82	105.77	112.92
33	I	83	GLY	N-CA-C	5.81	118.32	111.35
38	N	57	VAL	N-CA-C	5.80	117.23	110.62
1	b	12	ARG	N-CA-C	-5.79	106.05	113.23
44	T	46	LYS	N-CA-C	5.79	123.13	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	L	142	ARG	N-CA-C	-5.79	105.48	112.54
32	H	5	HIS	CA-C-N	5.78	125.91	119.32
32	H	5	HIS	C-N-CA	5.78	125.91	119.32
2	c	85	ALA	N-CA-C	5.78	117.45	109.54
32	H	125	ARG	N-CA-C	-5.77	105.90	113.17
19	t	19	LYS	N-CA-C	-5.77	104.96	112.23
49	Y	84	LYS	N-CA-C	-5.77	104.96	112.23
33	I	173	ASP	N-CA-C	-5.77	106.89	114.04
29	E	30	HIS	N-CA-C	5.76	116.69	108.74
49	Y	57	VAL	N-CA-C	5.76	116.50	110.62
1	b	261	ARG	N-CA-C	-5.75	106.22	113.18
41	Q	23	LEU	N-CA-C	-5.73	103.48	111.39
6	g	10	ALA	N-CA-C	5.73	118.53	108.56
52	3	1201	A	C2'-C3'-O3'	5.73	118.09	109.50
34	J	96	GLN	CA-C-N	5.70	126.97	119.84
34	J	96	GLN	C-N-CA	5.70	126.97	119.84
9	j	69	ARG	N-CA-C	-5.70	105.59	112.54
16	q	109	VAL	N-CA-C	-5.69	104.98	110.72
18	s	40	ASN	N-CA-C	5.67	118.63	107.98
8	i	130	GLY	N-CA-C	-5.65	105.80	113.37
8	i	106	GLN	N-CA-C	5.63	118.19	111.71
16	q	41	ALA	N-CA-C	-5.61	106.39	113.18
3	d	34	ALA	N-CA-C	-5.61	105.31	111.82
27	C	39	ASP	CA-C-N	5.60	125.27	119.05
27	C	39	ASP	C-N-CA	5.60	125.27	119.05
28	D	32	ALA	N-CA-C	-5.59	105.33	111.82
33	I	73	ASN	N-CA-C	-5.59	105.33	111.82
40	P	121	ARG	N-CA-C	5.58	116.86	109.93
16	q	80	ASN	N-CA-C	-5.57	105.36	111.82
50	Z	42	THR	N-CA-C	5.57	117.05	110.97
36	L	94	ARG	N-CA-C	-5.57	106.65	113.50
34	J	119	VAL	N-CA-C	5.56	116.11	110.05
41	Q	43	LYS	N-CA-C	5.54	120.04	112.55
4	e	115	GLY	N-CA-C	-5.53	104.28	111.52
1	b	185	ALA	N-CA-C	5.53	118.07	111.71
53	1	372	G	N9-C1'-C2'	5.52	120.28	112.00
34	J	122	VAL	N-CA-C	5.52	120.82	109.34
13	n	67	PHE	N-CA-C	-5.51	106.69	113.41
9	j	31	GLU	N-CA-C	-5.50	105.82	112.54
9	j	45	THR	CA-C-N	5.50	125.59	119.32
9	j	45	THR	C-N-CA	5.50	125.59	119.32
13	n	68	ALA	N-CA-C	-5.50	105.67	112.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	O	57	VAL	N-CA-C	5.49	120.75	109.34
18	s	55	ILE	N-CA-C	5.48	115.62	110.30
26	B	10	SER	N-CA-C	5.48	116.93	111.07
36	L	54	GLY	N-CA-C	-5.46	107.57	115.27
31	G	165	ALA	N-CA-C	5.46	117.68	111.02
19	t	3	ARG	N-CA-C	-5.42	105.53	111.82
33	I	187	ARG	N-CA-C	5.42	116.87	111.07
31	G	46	VAL	N-CA-C	5.42	120.58	108.88
37	M	70	VAL	N-CA-C	-5.41	106.53	111.67
36	L	135	LYS	N-CA-C	-5.40	105.47	111.36
43	S	4	SER	N-CA-C	-5.39	105.48	111.36
4	e	75	GLY	N-CA-C	-5.38	107.65	114.16
36	L	129	ASN	N-CA-C	5.38	118.62	111.30
19	t	52	GLU	N-CA-C	5.37	122.24	110.80
20	u	3	LYS	N-CA-C	5.36	117.20	111.36
8	i	129	GLU	N-CA-C	-5.35	106.25	112.89
3	d	140	ASP	N-CA-C	-5.35	106.26	112.89
10	k	111	LYS	N-CA-C	-5.34	106.77	113.28
7	h	42	ARG	N-CA-C	-5.33	106.28	112.89
44	T	11	VAL	N-CA-C	5.32	115.76	110.23
48	X	39	ILE	N-CA-C	5.32	115.56	108.11
1	b	43	ASN	N-CA-C	5.32	116.78	109.29
9	j	79	GLY	N-CA-C	-5.32	107.77	115.27
1	b	269	ARG	N-CA-C	-5.31	103.68	110.53
34	J	137	ARG	N-CA-C	-5.30	105.56	112.23
32	H	102	ILE	N-CA-C	5.29	116.41	109.21
32	H	67	ILE	N-CA-C	5.28	116.31	108.23
36	L	146	ALA	N-CA-C	5.27	117.77	111.71
6	g	63	ALA	N-CA-C	-5.26	105.72	111.82
2	c	152	PRO	N-CA-C	-5.26	106.68	113.57
1	b	213	ARG	N-CA-C	-5.25	106.46	112.92
42	R	40	GLU	N-CA-C	5.24	121.96	110.80
41	Q	97	VAL	N-CA-C	5.24	115.64	107.99
7	h	119	PRO	N-CA-C	-5.22	101.71	112.47
37	M	28	SER	N-CA-C	5.22	116.83	110.41
2	c	96	ILE	N-CA-C	5.21	115.86	107.73
13	n	101	GLY	N-CA-C	5.21	116.95	110.29
10	k	57	VAL	N-CA-C	5.20	114.79	106.88
7	h	51	TYR	N-CA-C	5.19	121.86	110.80
1	b	265	PHE	N-CA-C	5.19	118.88	112.54
2	c	22	ILE	N-CA-C	5.19	113.09	108.63
21	v	13	GLY	N-CA-C	-5.17	106.85	112.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	l	1020	A	C2'-C3'-O3'	5.17	117.26	109.50
31	G	90	PHE	N-CA-C	5.16	116.83	109.14
13	n	100	CYS	N-CA-C	5.15	119.72	113.38
34	J	95	MET	N-CA-C	5.15	116.81	108.41
3	d	92	HIS	N-CA-C	5.15	119.72	113.38
13	n	78	LYS	N-CA-C	-5.15	105.85	111.82
6	g	31	VAL	N-CA-C	5.13	119.97	108.88
13	n	60	VAL	N-CA-C	-5.12	105.42	111.00
19	t	91	GLN	N-CA-C	5.11	117.28	110.53
31	G	151	LYS	N-CA-C	-5.11	107.00	113.18
32	H	129	PHE	N-CA-C	5.11	116.85	111.28
33	I	136	VAL	N-CA-C	5.11	116.26	109.37
51	a	163	TYR	N-CA-C	5.10	116.04	108.60
17	r	50	GLY	N-CA-C	-5.10	101.10	113.18
3	d	108	ILE	N-CA-C	5.09	115.31	110.42
11	l	113	ALA	N-CA-C	-5.09	107.05	114.12
32	H	76	ILE	N-CA-C	-5.08	106.97	113.22
34	J	89	THR	N-CA-C	5.08	121.62	110.80
40	P	69	CYS	N-CA-C	-5.07	107.14	113.38
27	C	40	PRO	N-CA-C	5.07	120.58	113.53
41	Q	7	VAL	N-CA-C	-5.07	105.20	112.35
45	U	75	ILE	N-CA-C	-5.07	104.76	111.09
5	f	141	GLY	N-CA-C	-5.06	106.26	113.86
16	q	40	LYS	N-CA-C	-5.06	105.95	111.82
14	o	107	ALA	N-CA-C	5.04	116.58	111.14
47	W	62	ARG	N-CA-C	-5.03	105.88	111.36
23	x	6	VAL	N-CA-C	5.03	118.17	111.44
8	i	29	GLN	N-CA-C	-5.01	105.81	111.28
32	H	143	LEU	N-CA-C	-5.01	107.16	113.28
52	3	1225	A	N9-C1'-C2'	5.01	119.51	112.00
33	I	160	LEU	N-CA-C	-5.00	106.69	112.89

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	b	2083	0	2157	87	0
2	c	1565	0	1616	69	0
3	d	1552	0	1619	56	0
4	e	1411	0	1447	67	0
5	f	1323	0	1374	36	0
6	g	1111	0	1148	37	0
7	h	989	0	1025	64	0
8	i	1032	0	1088	44	0
9	j	1129	0	1162	44	0
10	k	939	0	1012	36	0
11	l	1045	0	1117	38	0
12	m	1074	0	1157	50	0
13	n	961	0	1000	44	0
14	o	892	0	923	34	0
15	p	917	0	965	30	0
16	q	947	0	1022	51	0
17	r	816	0	839	53	0
18	s	857	0	922	31	0
19	t	739	0	807	31	0
20	u	780	0	834	32	0
21	v	753	0	780	32	0
22	w	575	0	592	18	0
23	x	625	0	655	22	0
24	y	509	0	543	24	0
25	z	449	0	491	17	0
26	B	444	0	461	17	0
27	C	410	0	440	16	0
28	D	377	0	418	15	0
29	E	504	0	574	20	0
30	F	302	0	343	18	0
31	G	1757	0	1787	54	0
32	H	1625	0	1699	61	0
33	I	1643	0	1710	73	0
34	J	1157	0	1199	50	0
35	K	818	0	808	37	0
36	L	1182	0	1240	40	0
37	M	979	0	1034	49	0
38	N	1022	0	1070	57	0
39	O	787	0	828	33	0
40	P	870	0	878	36	0
41	Q	955	0	1019	44	0
42	R	884	0	944	46	0
43	S	805	0	847	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	T	714	0	737	27	0
45	U	649	0	666	41	0
46	V	649	0	691	30	0
47	W	536	0	552	21	0
48	X	638	0	665	33	0
49	Y	665	0	714	41	0
50	Z	545	0	579	31	0
51	a	1027	0	1092	37	0
52	3	33012	0	16618	512	0
53	1	62317	0	31346	881	0
54	2	2568	0	1303	57	0
55	5	1640	0	836	26	0
55	6	1640	0	837	24	0
56	4	388	0	196	2	0
57	7	1557	0	789	16	0
58	5	10	0	10	0	0
All	All	150149	0	101225	2879	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (2879) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:9:GLU:HG2	50:Z:10:PRO:HD3	1.30	1.09
53:1:45:G:H5''	53:1:46:G:H5'	1.24	1.08
31:G:20:ARG:HE	52:3:831:A:H5''	1.25	1.00
17:r:74:ILE:HD13	53:1:992:C:H4'	1.47	0.96
55:5:13:C:H2'	55:5:14:A:H5''	1.47	0.95
24:y:23:ARG:HG3	24:y:24:GLU:H	1.32	0.95
53:1:1906:G:H2'	53:1:1907:G:H5''	1.46	0.95
34:J:54:GLU:HG2	34:J:56:PRO:HD2	1.46	0.94
1:b:172:THR:HG22	1:b:182:LYS:HG2	1.50	0.94
53:1:821:A:H5''	53:1:822:G:H5''	1.48	0.94
37:M:80:PRO:HG2	52:3:878:A:H5'	1.51	0.92
50:Z:33:ARG:HG3	50:Z:34:ARG:HG2	1.50	0.92
33:I:190:LEU:HD12	33:I:192:ALA:H	1.36	0.90
14:o:17:LYS:HZ1	53:1:2379:G:H4'	1.36	0.90
31:G:147:LEU:HD22	31:G:150:ILE:HD11	1.52	0.90
42:R:2:ARG:HE	42:R:8:ILE:HD11	1.34	0.89
39:O:40:ILE:HD11	52:3:1124:G:H4'	1.55	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:p:1:SER:HA	53:1:2876:G:H5'	1.53	0.88
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.56	0.87
52:3:484:G:H4'	52:3:485:U:H5''	1.54	0.87
53:1:2277:G:H2'	53:1:2278:A:H5''	1.55	0.87
20:u:36:GLU:HA	20:u:61:GLU:HG2	1.55	0.87
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.54	0.87
45:U:5:ARG:HB2	52:3:376:G:H5''	1.57	0.86
4:e:23:SER:HB3	4:e:26:GLN:HB2	1.55	0.86
52:3:405:U:H3'	52:3:406:G:H5'	1.56	0.86
37:M:86:LYS:HD2	37:M:90:GLU:HB3	1.58	0.85
8:i:118:GLY:HA2	53:1:1082:U:H5'	1.59	0.85
31:G:100:LEU:HG	31:G:178:LEU:HD12	1.59	0.85
53:1:1300:G:H4'	53:1:1301:A:H5'	1.59	0.84
18:s:6:LYS:HB2	53:1:494:G:H4'	1.59	0.84
53:1:676:A:H62	53:1:802:A:H61	1.26	0.84
30:F:32:LYS:HE3	53:1:2528:U:H5'	1.60	0.84
5:f:86:LEU:HD22	5:f:147:LEU:HD23	1.58	0.83
33:I:29:THR:HG23	33:I:30:LYS:HD3	1.60	0.83
10:k:1:MET:HE1	53:1:2726:A:H1'	1.58	0.83
12:m:119:LEU:HD22	53:1:2468:A:H5'	1.58	0.83
1:b:28:PRO:HG3	1:b:62:ARG:HH21	1.41	0.83
16:q:2:ARG:HD2	53:1:1248:G:C2	2.14	0.83
20:u:42:LYS:HD3	53:1:499:U:H5''	1.60	0.83
31:G:20:ARG:HE	52:3:831:A:C5'	1.92	0.82
53:1:2553:G:H3'	53:1:2554:U:H5''	1.60	0.82
52:3:979:C:H1'	52:3:1317:C:H41	1.45	0.82
8:i:126:ARG:HD3	53:1:1080:A:H4'	1.62	0.82
9:j:108:MET:HE3	53:1:1138:G:H21	1.43	0.82
20:u:16:LYS:HG3	53:1:329:G:H1	1.45	0.82
30:F:23:ILE:H	30:F:23:ILE:HD12	1.45	0.82
49:Y:23:ARG:HH12	52:3:176:C:H5''	1.44	0.81
49:Y:28:ARG:NH2	52:3:1437:A:H5''	1.95	0.81
40:P:116:PRO:HB3	52:3:676:A:H1'	1.62	0.81
38:N:128:LYS:HD2	52:3:966:G:H21	1.44	0.80
32:H:102:ILE:H	32:H:102:ILE:HD12	1.46	0.80
54:2:3:C:H2'	54:2:4:C:H5''	1.62	0.79
36:L:46:LEU:HG	36:L:57:GLU:HG2	1.63	0.79
47:W:59:LYS:HD2	52:3:734:G:O2'	1.82	0.79
53:1:2286:G:H5''	53:1:2287:A:OP1	1.81	0.79
10:k:12:ASP:HB3	10:k:99:ILE:HG22	1.63	0.79
15:p:108:ARG:HD2	52:3:1463:U:OP1	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2452:C:H42	53:1:2504:U:H3	1.28	0.79
34:J:55:VAL:HG23	34:J:56:PRO:HD3	1.62	0.79
4:e:132:ARG:HH22	53:1:2306:C:H5'	1.47	0.79
31:G:20:ARG:HH21	52:3:831:A:H4'	1.47	0.79
33:I:55:ARG:O	33:I:59:LYS:HG3	1.82	0.79
50:Z:9:GLU:CG	50:Z:10:PRO:HD3	2.13	0.79
23:x:63:ILE:H	23:x:63:ILE:HD12	1.48	0.78
37:M:80:PRO:HG2	52:3:878:A:C5'	2.13	0.78
2:c:155:VAL:HG21	53:1:2618:G:H21	1.46	0.78
14:o:17:LYS:NZ	53:1:2379:G:H4'	1.97	0.78
4:e:107:VAL:HG12	4:e:108:PRO:HD3	1.65	0.78
41:Q:36:VAL:HG21	41:Q:73:LEU:HB3	1.65	0.78
12:m:12:MET:HA	53:1:910:A:H62	1.49	0.78
53:1:2391:G:H4'	53:1:2392:A:OP1	1.83	0.78
53:1:1020:A:H1'	53:1:1021:A:OP2	1.84	0.77
53:1:1906:G:C2'	53:1:1907:G:H5''	2.13	0.77
14:o:51:ALA:HB3	14:o:78:VAL:HG12	1.66	0.77
48:X:29:PRO:HB3	48:X:47:THR:HG23	1.65	0.77
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.49	0.77
52:3:1200:C:H5''	52:3:1201:A:H3'	1.67	0.77
38:N:33:SER:HB2	38:N:36:GLN:HG2	1.64	0.77
53:1:2427:C:H5''	53:1:2429:G:H5'	1.66	0.77
33:I:6:PRO:HG3	52:3:430:A:H4'	1.67	0.77
8:i:121:ILE:H	8:i:121:ILE:HD12	1.50	0.76
18:s:58:ALA:O	18:s:62:ASP:HB2	1.84	0.76
3:d:117:ARG:HH21	3:d:184:ASP:HA	1.49	0.76
53:1:896:A:H2'	57:7:19:G:C5	2.21	0.76
38:N:114:LYS:HD3	52:3:1187:G:H5''	1.66	0.76
4:e:147:ARG:HD3	4:e:148:VAL:H	1.51	0.76
53:1:1077:A:H2'	53:1:1078:U:H5'	1.66	0.75
38:N:8:THR:HG23	38:N:9:GLY:H	1.51	0.75
25:z:37:ARG:NH1	53:1:929:U:H5'	2.02	0.75
6:g:39:ALA:HA	6:g:43:ASN:HB2	1.68	0.75
9:j:136:GLN:HE22	53:1:2899:A:H5'	1.49	0.75
40:P:87:GLY:H	40:P:113:THR:HG22	1.51	0.75
49:Y:28:ARG:HH22	52:3:1437:A:H5''	1.50	0.75
48:X:40:PHE:HB2	48:X:43:MET:HE3	1.68	0.75
18:s:23:LEU:HD11	26:B:21:LEU:HB2	1.68	0.74
35:K:89:VAL:HG23	52:3:737:C:H5'	1.67	0.74
40:P:23:HIS:HB3	40:P:30:ILE:HG23	1.70	0.74
27:C:5:ARG:HH12	53:1:2285:C:H3'	1.52	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:112:LEU:HD22	3:d:117:ARG:HD3	1.69	0.74
2:c:173:GLN:HE21	53:1:2772:C:H5'	1.52	0.74
42:R:64:VAL:HG12	42:R:65:GLU:H	1.52	0.74
31:G:43:GLU:HG3	31:G:44:LYS:HD2	1.68	0.74
5:f:154:GLU:HB3	5:f:159:LYS:H	1.53	0.73
52:3:1502:A:H8	52:3:1505:G:H22	1.34	0.73
52:3:1259:C:H3'	52:3:1260:G:H5''	1.70	0.73
53:1:2296:U:H5''	53:1:2297:A:OP1	1.88	0.73
41:Q:69:GLU:HG2	52:3:521:G:H4'	1.71	0.73
37:M:123:GLU:OE1	52:3:643:C:H1'	1.88	0.73
5:f:174:LYS:HD2	5:f:175:LYS:HG3	1.69	0.73
9:j:30:THR:HG21	53:1:1012:U:O4	1.88	0.73
49:Y:7:LYS:HD3	52:3:332:G:OP2	1.89	0.72
32:H:45:GLU:HG2	32:H:86:LEU:HD21	1.71	0.72
47:W:37:LYS:HG2	52:3:719:C:H1'	1.71	0.72
48:X:76:THR:HG21	52:3:1221:G:H4'	1.71	0.72
8:i:129:GLU:HG2	8:i:139:VAL:HG11	1.70	0.72
13:n:53:THR:HG21	53:1:2840:C:H5''	1.72	0.72
31:G:46:VAL:HG23	31:G:47:PRO:HD3	1.71	0.72
1:b:16:VAL:HB	1:b:203:VAL:HG12	1.71	0.72
14:o:53:THR:HG22	14:o:74:VAL:HG11	1.72	0.72
7:h:33:VAL:HG13	7:h:35:VAL:H	1.55	0.72
50:Z:23:GLU:HG2	50:Z:24:LYS:H	1.55	0.72
53:1:1801:A:H5''	53:1:2203:U:H2'	1.69	0.72
32:H:116:ALA:HB1	32:H:186:SER:HB3	1.69	0.72
7:h:26:VAL:HB	7:h:82:ILE:HD11	1.72	0.71
46:V:78:VAL:O	46:V:79:GLU:HG2	1.90	0.71
16:q:4:LYS:HE2	53:1:29:U:H5''	1.70	0.71
53:1:310:A:C2'	53:1:311:A:H5''	2.20	0.71
20:u:17:ASP:HB3	20:u:20:LYS:HD3	1.72	0.71
39:O:44:THR:HG22	39:O:70:HIS:HA	1.71	0.71
43:S:5:MET:HG2	43:S:8:ARG:HH22	1.55	0.71
16:q:111:LYS:HZ1	17:r:48:LYS:CG	2.02	0.71
4:e:130:GLY:HA3	53:1:2305:U:H5''	1.71	0.71
5:f:153:PRO:HA	5:f:160:GLY:HA3	1.72	0.71
8:i:20:SER:HB3	8:i:21:PRO:HD3	1.70	0.71
52:3:70:U:H5''	52:3:71:A:OP1	1.89	0.71
53:1:1645:G:H5''	53:1:1646:C:H5'	1.72	0.71
1:b:36:ASN:HB2	1:b:61:TYR:HB2	1.71	0.71
53:1:1053:C:H2'	53:1:1054:A:H5''	1.73	0.71
9:j:81:ILE:HD11	53:1:2514:U:O3'	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:100:MET:O	36:L:103:ILE:HG22	1.90	0.71
12:m:77:PRO:HG3	12:m:88:ASN:ND2	2.06	0.70
35:K:52:ASN:O	35:K:53:LYS:HG2	1.90	0.70
3:d:33:VAL:HG21	53:1:1245:G:H4'	1.72	0.70
34:J:44:ARG:HD2	34:J:70:MET:HB3	1.72	0.70
8:i:12:VAL:HA	53:1:1061:U:H3	1.55	0.70
33:I:33:ILE:H	33:I:33:ILE:HD12	1.56	0.70
7:h:25:ALA:HB3	7:h:85:SER:HB3	1.74	0.70
11:l:93:ASN:O	11:l:94:THR:HG22	1.92	0.70
53:1:615:U:H5''	53:1:616:A:OP2	1.92	0.70
1:b:136:VAL:HG13	1:b:163:ILE:HG22	1.74	0.70
2:c:4:LEU:HD22	2:c:32:ASN:HD22	1.56	0.70
5:f:85:LYS:HB3	5:f:164:ALA:HB2	1.73	0.70
52:3:327:A:O2'	52:3:328:C:H4'	1.92	0.70
19:t:20:ALA:HB1	19:t:31:VAL:HG11	1.74	0.70
34:J:39:GLY:HA3	34:J:116:VAL:HB	1.73	0.70
37:M:29:SER:HB3	37:M:32:LYS:HG3	1.72	0.70
38:N:114:LYS:HB2	38:N:117:LEU:HD12	1.73	0.70
52:3:1201:A:H1'	52:3:1202:U:OP2	1.92	0.70
16:q:2:ARG:HA	53:1:1248:G:O2'	1.92	0.69
19:t:9:LYS:NZ	53:1:71:A:H1'	2.07	0.69
50:Z:57:LYS:HA	50:Z:60:ALA:HB3	1.73	0.69
1:b:59:GLN:HA	53:1:1568:G:H5'	1.73	0.69
11:l:63:LYS:HE3	53:1:2394:C:H5''	1.73	0.69
19:t:40:LYS:HD2	53:1:1598:A:H5''	1.74	0.69
32:H:171:ARG:HG2	32:H:173:PRO:HD3	1.73	0.69
10:k:21:CYS:HA	10:k:41:ILE:HG22	1.74	0.69
53:1:2277:G:C2'	53:1:2278:A:H5''	2.22	0.69
22:w:38:GLY:HA2	53:1:2330:G:H21	1.57	0.69
38:N:121:ARG:HG3	52:3:1348:U:H4'	1.74	0.69
40:P:43:TRP:HE1	52:3:686:U:H4'	1.57	0.69
16:q:111:LYS:NZ	17:r:48:LYS:HD2	2.08	0.69
47:W:42:ARG:HH12	52:3:721:G:H5''	1.56	0.69
6:g:128:HIS:HB2	6:g:144:VAL:HG23	1.75	0.69
53:1:655:A:H4'	53:1:656:G:H5'	1.74	0.69
17:r:17:GLY:H	17:r:98:ILE:HB	1.58	0.69
46:V:67:SER:HA	52:3:265:G:H4'	1.75	0.69
10:k:6:THR:HG23	53:1:1666:G:H4'	1.75	0.68
47:W:11:ARG:HG3	52:3:845:A:H4'	1.74	0.68
1:b:257:ARG:HH21	1:b:263:ASP:HA	1.59	0.68
22:w:33:ILE:HD11	22:w:78:ILE:HD11	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:x:9:LYS:HE2	23:x:53:LYS:HE3	1.73	0.68
45:U:70:ARG:HH11	52:3:452:A:H1'	1.59	0.68
55:5:13:C:C2'	55:5:14:A:H5''	2.23	0.68
7:h:27:VAL:HB	7:h:83:ALA:HB3	1.73	0.68
16:q:55:GLN:O	16:q:58:GLN:HG2	1.93	0.68
26:B:24:VAL:HG23	26:B:25:THR:H	1.57	0.68
32:H:140:ALA:HB3	32:H:148:ILE:HD13	1.76	0.68
48:X:18:VAL:HG11	48:X:43:MET:HG2	1.74	0.68
55:6:54:U:H3	55:6:58:A:H62	1.41	0.68
1:b:260:LYS:HE3	53:1:2227:A:H5''	1.75	0.68
14:o:16:ARG:HA	14:o:19:GLN:HG2	1.74	0.68
2:c:149:ASN:HB3	53:1:2572:A:OP2	1.93	0.68
9:j:31:GLU:HG2	9:j:142:ILE:HG12	1.76	0.68
24:y:29:ARG:HB3	24:y:30:MET:HE2	1.74	0.68
30:F:32:LYS:HE2	53:1:2478:A:H5'	1.75	0.68
50:Z:9:GLU:HG2	50:Z:10:PRO:CD	2.18	0.68
29:E:7:ARG:HH12	53:1:254:G:H22	1.41	0.67
50:Z:6:ARG:HG2	50:Z:8:ASN:H	1.59	0.67
52:3:960:U:H4'	52:3:961:U:O5'	1.93	0.67
12:m:45:GLN:HE21	12:m:124:LEU:HD22	1.58	0.67
5:f:102:ILE:HB	5:f:114:HIS:HB3	1.76	0.67
12:m:34:LYS:HD3	12:m:99:GLY:HA2	1.77	0.67
12:m:41:LEU:HD13	12:m:96:ILE:HG21	1.77	0.67
3:d:18:THR:HG23	3:d:106:LYS:HG2	1.76	0.67
17:r:22:LEU:HD23	17:r:22:LEU:H	1.60	0.67
51:a:11:ILE:HG23	51:a:33:LEU:HD22	1.76	0.67
49:Y:59:ARG:HG3	52:3:194:C:O3'	1.95	0.67
14:o:60:GLU:OE2	14:o:61:GLN:HG3	1.94	0.67
21:v:83:LYS:HB3	21:v:85:LYS:HD3	1.76	0.67
32:H:112:ALA:HB1	32:H:184:ASN:HB2	1.77	0.67
37:M:28:SER:HB2	37:M:56:PRO:HB2	1.77	0.67
53:1:310:A:O2'	53:1:311:A:H5''	1.94	0.67
53:1:2048:G:H2'	53:1:2049:G:H5''	1.77	0.67
6:g:73:ASN:ND2	6:g:76:GLU:HA	2.10	0.67
12:m:8:LYS:HD2	53:1:869:G:H1'	1.77	0.67
9:j:68:LYS:HD3	53:1:1022:G:N7	2.09	0.67
22:w:36:GLN:NE2	22:w:39:THR:HA	2.09	0.67
52:3:29:U:O2'	52:3:30:U:H5'	1.95	0.67
55:5:40:C:H4'	55:6:35:A:H4'	1.77	0.67
11:l:90:VAL:HB	11:l:122:VAL:HA	1.77	0.66
1:b:136:VAL:HG21	1:b:166:ARG:HB3	1.75	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:z:29:ARG:NE	53:1:1183:U:H5''	2.11	0.66
21:v:30:ILE:HG23	21:v:40:ILE:HG13	1.78	0.66
16:q:3:VAL:CG2	53:1:1249:U:H4'	2.26	0.66
26:B:54:ILE:HG23	26:B:56:LYS:H	1.60	0.66
39:O:59:LYS:HE2	39:O:62:ARG:HH21	1.60	0.66
49:Y:28:ARG:CZ	52:3:1437:A:H5''	2.25	0.66
3:d:69:ARG:HE	53:1:674:G:H1'	1.59	0.66
4:e:56:LEU:HD13	4:e:88:VAL:HG23	1.78	0.66
14:o:15:ARG:NH2	54:2:8:C:H5''	2.10	0.66
53:1:1026:G:H2'	53:1:1027:A:H8	1.59	0.66
53:1:1133:A:H4'	53:1:1134:A:H5''	1.78	0.66
6:g:8:LYS:HD2	6:g:9:VAL:N	2.11	0.66
9:j:136:GLN:NE2	53:1:2899:A:H5'	2.10	0.66
12:m:77:PRO:HG3	12:m:88:ASN:HD22	1.59	0.66
40:P:88:PRO:HG2	40:P:89:GLY:H	1.60	0.66
53:1:729:G:H4'	53:1:763:G:H5'	1.78	0.66
54:2:3:C:C2'	54:2:4:C:H5''	2.25	0.66
7:h:33:VAL:HG22	7:h:34:THR:H	1.61	0.65
11:l:38:GLN:HB3	53:1:832:U:H5'	1.77	0.65
21:v:45:ASP:OD2	53:1:1039:A:H4'	1.96	0.65
51:a:14:LYS:HD3	51:a:32:GLU:HB3	1.77	0.65
25:z:30:ARG:HD2	53:1:1158:C:H5''	1.78	0.65
42:R:76:ILE:HG22	42:R:80:MET:HE2	1.78	0.65
45:U:33:ILE:H	45:U:33:ILE:HD12	1.60	0.65
51:a:8:MET:HE2	53:1:2174:C:H5''	1.78	0.65
53:1:2287:A:O2'	53:1:2288:A:H2'	1.97	0.65
54:2:65:U:H3'	54:2:108:A:H61	1.61	0.65
14:o:38:GLN:HE22	54:2:7:G:H21	1.43	0.65
43:S:29:ILE:HD12	43:S:29:ILE:H	1.59	0.65
53:1:1664:A:H61	53:1:1996:C:H42	1.42	0.65
6:g:5:LEU:HD21	6:g:9:VAL:HG12	1.77	0.65
43:S:81:ILE:HG21	52:3:1202:U:N3	2.12	0.65
13:n:24:MET:HE3	13:n:44:LEU:HD13	1.79	0.65
20:u:47:PRO:HD3	20:u:55:GLY:HA2	1.79	0.65
43:S:63:CYS:HB3	43:S:67:GLY:H	1.61	0.65
13:n:79:LEU:HD23	13:n:83:LEU:HB2	1.79	0.65
50:Z:58:LYS:O	50:Z:61:ARG:HD2	1.96	0.65
53:1:310:A:H2'	53:1:311:A:H5''	1.79	0.65
55:6:16:C:O2'	55:6:17:C:H5'	1.97	0.65
32:H:76:ILE:HG22	32:H:102:ILE:HG12	1.77	0.65
51:a:38:PHE:CD1	53:1:2127:G:H4'	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2267:A:H5''	53:1:2268:A:H5'	1.78	0.65
4:e:65:LEU:HD22	54:2:42:C:C5	2.32	0.65
7:h:53:ARG:HG2	7:h:55:VAL:HG13	1.79	0.65
20:u:16:LYS:HE3	53:1:329:G:H22	1.61	0.65
42:R:25:GLY:H	52:3:1329:A:H5''	1.62	0.65
16:q:111:LYS:HZ1	17:r:48:LYS:HD2	1.63	0.64
20:u:16:LYS:CG	53:1:329:G:H1	2.10	0.64
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.78	0.64
44:T:57:ARG:HD2	44:T:58:MET:N	2.13	0.64
48:X:51:HIS:HD2	52:3:1220:G:H1'	1.62	0.64
53:1:863:A:H4'	54:2:100:G:H21	1.61	0.64
42:R:43:LYS:HE2	42:R:46:GLU:HB2	1.78	0.64
53:1:1807:G:H2'	53:1:1808:A:H5'	1.79	0.64
2:c:151:THR:HB	2:c:152:PRO:HD3	1.78	0.64
30:F:32:LYS:HE3	53:1:2528:U:C5'	2.26	0.64
33:I:112:GLU:HG2	52:3:407:U:O2'	1.97	0.64
5:f:82:PHE:HB3	5:f:140:ILE:HD13	1.78	0.64
3:d:52:VAL:HB	3:d:74:LYS:HD3	1.79	0.64
5:f:169:ARG:NH2	53:1:1093:G:H5''	2.13	0.64
48:X:77:ARG:HH11	52:3:1222:G:H5''	1.63	0.64
12:m:30:SER:HA	12:m:133:LYS:HB2	1.79	0.64
29:E:51:LYS:NZ	53:1:937:C:OP2	2.28	0.64
53:1:895:U:O2'	53:1:896:A:H5''	1.98	0.64
16:q:111:LYS:HZ1	17:r:48:LYS:CD	2.11	0.64
45:U:70:ARG:NH1	52:3:452:A:H1'	2.12	0.64
51:a:57:GLN:HE21	51:a:203:GLN:HG3	1.63	0.64
53:1:1380:G:H1'	53:1:1569:A:H61	1.63	0.64
53:1:2584:U:H2'	53:1:2585:U:H2'	1.79	0.64
47:W:56:ARG:HD2	47:W:56:ARG:N	2.13	0.64
53:1:2508:G:H1	53:1:2580:U:H3	1.46	0.64
13:n:1:MET:SD	53:1:2723:C:H4'	2.38	0.63
34:J:23:THR:HG22	34:J:28:ARG:HG2	1.78	0.63
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.79	0.63
53:1:1306:C:H41	53:1:1606:C:H2'	1.63	0.63
4:e:132:ARG:NH2	53:1:2306:C:H5'	2.14	0.63
35:K:47:LEU:HG	35:K:57:ALA:H	1.63	0.63
39:O:40:ILE:CD1	52:3:1124:G:H4'	2.26	0.63
52:3:1218:C:H2'	52:3:1219:A:C8	2.33	0.63
53:1:2423:U:O2'	53:1:2425:A:H2'	1.99	0.63
2:c:192:ALA:HB1	53:1:2680:U:H1'	1.79	0.63
17:r:35:PHE:HB2	17:r:59:ILE:HB	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:181:A:N6	52:3:194:C:H2'	2.12	0.63
1:b:216:ARG:HH22	53:1:690:G:H4'	1.62	0.63
40:P:109:ILE:HG21	50:Z:16:ARG:HD2	1.81	0.63
5:f:169:ARG:HH22	53:1:1093:G:C5'	2.11	0.63
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.80	0.63
21:v:4:ILE:HD11	21:v:50:MET:HE1	1.80	0.63
30:F:3:VAL:HG12	30:F:36:ARG:HD3	1.81	0.63
55:5:55:U:H2'	55:5:56:C:H5''	1.81	0.63
1:b:224:MET:SD	1:b:229:HIS:HB2	2.39	0.63
29:E:18:LYS:HB2	53:1:651:G:H5'	1.79	0.63
12:m:44:ARG:HB3	53:1:2484:G:H5'	1.80	0.63
20:u:73:ASN:HD21	20:u:75:ALA:HB3	1.64	0.63
25:z:40:THR:HG22	25:z:42:ALA:H	1.64	0.63
28:D:11:LYS:NZ	53:1:686:U:H5''	2.14	0.63
38:N:64:ILE:HG21	38:N:78:ILE:HD12	1.79	0.63
42:R:22:TYR:HD1	42:R:65:GLU:HG3	1.63	0.63
49:Y:28:ARG:NH1	52:3:1437:A:H5''	2.14	0.63
51:a:37:LYS:HB2	53:1:2127:G:H5'	1.81	0.63
1:b:48:ILE:HD11	1:b:51:ARG:HA	1.81	0.63
17:r:78:ARG:HD2	17:r:81:LYS:HG3	1.80	0.63
52:3:245:U:O2'	52:3:246:A:H5'	1.99	0.63
52:3:1088:G:H21	52:3:1167:A:H61	1.47	0.63
34:J:45:VAL:HG22	34:J:46:GLY:H	1.61	0.63
44:T:57:ARG:HD2	44:T:57:ARG:C	2.24	0.63
53:1:215:G:H4'	53:1:216:A:H4'	1.80	0.63
53:1:329:G:O4'	53:1:477:A:H1'	1.98	0.63
53:1:2800:A:H3'	53:1:2801:G:H5'	1.81	0.63
7:h:34:THR:HG21	53:1:1057:A:H1'	1.80	0.62
11:l:55:MET:HG2	53:1:2392:A:H2	1.63	0.62
18:s:42:LYS:HD3	53:1:2010:G:H4'	1.81	0.62
19:t:93:LEU:OXT	19:t:93:LEU:HD23	1.98	0.62
50:Z:54:ARG:HG2	50:Z:57:LYS:HE2	1.81	0.62
53:1:807:U:H2'	53:1:808:G:H8	1.64	0.62
55:5:6:G:O2'	55:5:7:G:H5'	1.99	0.62
31:G:20:ARG:NE	52:3:831:A:H5''	2.07	0.62
46:V:10:ARG:HA	46:V:57:VAL:HA	1.81	0.62
53:1:1367:A:H2'	53:1:1368:G:H5'	1.80	0.62
9:j:81:ILE:CD1	53:1:2514:U:H5''	2.28	0.62
24:y:41:HIS:CD2	53:1:96:C:H4'	2.35	0.62
35:K:36:ILE:HG13	35:K:64:VAL:HG22	1.82	0.62
52:3:769:G:H4'	52:3:1513:A:H4'	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:12:ARG:HH21	53:1:728:G:H4'	1.65	0.62
37:M:94:VAL:HG12	37:M:95:MET:HG3	1.80	0.62
1:b:20:ASN:HB3	1:b:23:LEU:HG	1.82	0.62
1:b:225:ASN:OD1	1:b:226:PRO:HD2	1.99	0.62
45:U:68:SER:OG	45:U:71:VAL:HG22	1.99	0.62
52:3:1236:A:H4'	52:3:1304:G:H4'	1.82	0.62
53:1:807:U:H2'	53:1:808:G:C8	2.34	0.62
50:Z:13:VAL:HG23	50:Z:15:LEU:HG	1.81	0.62
4:e:63:LYS:O	54:2:42:C:H1'	2.00	0.62
31:G:163:ILE:HG23	31:G:185:ILE:HD12	1.82	0.62
47:W:72:ARG:HH22	50:Z:4:LYS:HD3	1.64	0.62
53:1:542:C:H2'	53:1:543:G:H5''	1.82	0.62
4:e:40:GLY:HA2	4:e:84:ILE:HD11	1.80	0.62
23:x:16:ASN:HB3	23:x:24:THR:HB	1.82	0.62
39:O:57:VAL:O	39:O:58:ASN:HB2	2.00	0.62
48:X:12:LEU:HD23	48:X:13:HIS:N	2.14	0.62
53:1:473:G:O2'	53:1:474:G:H5'	2.00	0.62
24:y:23:ARG:HG3	24:y:24:GLU:N	2.09	0.62
26:B:8:THR:HG22	26:B:9:ARG:H	1.64	0.62
34:J:107:GLY:HA3	52:3:9:G:H5'	1.82	0.62
48:X:62:THR:HG22	48:X:63:ASP:H	1.64	0.62
53:1:2156:G:H2'	53:1:2157:G:H5'	1.81	0.62
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.65	0.61
39:O:53:ILE:HD12	43:S:84:ARG:HE	1.64	0.61
6:g:9:VAL:HG13	6:g:9:VAL:O	1.99	0.61
8:i:123:ALA:HB1	53:1:1081:U:H4'	1.82	0.61
31:G:112:ARG:NH2	52:3:1104:G:H4'	2.13	0.61
33:I:90:LEU:HD23	33:I:93:LEU:HD12	1.80	0.61
35:K:61:LEU:HD23	35:K:62:MET:N	2.14	0.61
36:L:146:ALA:HB2	55:6:40:C:H4'	1.82	0.61
7:h:33:VAL:HA	53:1:1055:G:H4'	1.82	0.61
8:i:96:LYS:HZ1	8:i:137:LEU:HA	1.65	0.61
19:t:61:LEU:HD13	53:1:1341:G:H5'	1.83	0.61
5:f:163:TYR:HB2	5:f:166:GLU:HB2	1.82	0.61
6:g:1:MET:N	6:g:20:ASN:OD1	2.29	0.61
36:L:27:ASN:HB3	52:3:1374:A:O2'	2.01	0.61
45:U:75:ILE:O	45:U:78:VAL:HG12	2.01	0.61
52:3:225:C:H2'	52:3:226:G:H5''	1.82	0.61
3:d:101:TYR:HE1	3:d:177:PRO:HD3	1.66	0.61
11:l:9:ALA:HB3	11:l:12:SER:HB2	1.82	0.61
15:p:92:ARG:HD3	53:1:1753:G:H5''	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:t:1:MET:HG3	19:t:3:ARG:H	1.66	0.61
44:T:66:LEU:HD23	44:T:87:ARG:HH21	1.63	0.61
53:1:1796:U:H2'	53:1:1797:G:H8	1.65	0.61
53:1:2646:C:H2'	53:1:2647:U:O4'	2.00	0.61
16:q:5:ARG:HD2	53:1:1251:C:OP2	2.01	0.61
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.15	0.61
23:x:73:ARG:HB2	23:x:75:GLU:HG2	1.82	0.61
33:I:131:ILE:HG22	33:I:133:SER:H	1.65	0.61
45:U:14:ARG:HH12	52:3:618:C:H1'	1.65	0.61
51:a:69:THR:HA	51:a:176:GLY:HA2	1.81	0.61
53:1:2163:A:H2'	53:1:2164:C:H5'	1.83	0.61
31:G:53:LEU:HD22	31:G:219:THR:HG21	1.82	0.61
55:6:16:C:H4'	55:6:60:U:H1'	1.82	0.61
1:b:67:LYS:HA	1:b:150:GLY:HA2	1.83	0.61
7:h:57:ASN:HB3	7:h:62:ARG:HD2	1.83	0.61
21:v:14:LYS:HE2	54:2:98:G:H22	1.64	0.61
34:J:133:ILE:O	34:J:136:VAL:HG12	2.00	0.61
19:t:12:ARG:HB2	19:t:33:LYS:HD3	1.83	0.61
34:J:107:GLY:HA2	52:3:8:A:H1'	1.83	0.61
47:W:40:PRO:HG2	47:W:43:ILE:HG12	1.82	0.61
53:1:2055:C:H2'	53:1:2504:U:H5'	1.82	0.61
17:r:79:ARG:O	17:r:80:ARG:HG2	2.00	0.60
44:T:57:ARG:HH21	52:3:742:G:H5''	1.65	0.60
49:Y:8:LYS:HG2	49:Y:12:GLN:HE21	1.65	0.60
52:3:1306:A:H61	52:3:1331:G:H1'	1.64	0.60
31:G:94:ARG:HD3	52:3:1100:C:OP2	2.01	0.60
32:H:26:LYS:HZ1	52:3:1256:A:H3'	1.66	0.60
45:U:28:ARG:HH22	52:3:391:G:H5'	1.65	0.60
53:1:2676:C:H2'	53:1:2677:G:C8	2.35	0.60
2:c:173:GLN:NE2	53:1:2772:C:H5'	2.16	0.60
33:I:108:ALA:HB3	33:I:112:GLU:OE2	2.02	0.60
1:b:55:GLY:H	53:1:692:C:P	2.24	0.60
7:h:87:GLU:HG2	7:h:95:LEU:HD12	1.83	0.60
8:i:3:LYS:HD2	8:i:4:VAL:H	1.67	0.60
28:D:11:LYS:HZ2	53:1:686:U:H5''	1.66	0.60
36:L:113:LYS:HE2	36:L:113:LYS:HA	1.82	0.60
38:N:114:LYS:HD3	52:3:1187:G:C5'	2.31	0.60
49:Y:11:ILE:H	49:Y:11:ILE:HD12	1.66	0.60
52:3:1137:C:H5'	52:3:1138:G:H5'	1.83	0.60
4:e:38:GLY:HA3	53:1:2312:U:H1'	1.84	0.60
11:l:103:ILE:HD13	53:1:259:G:H4'	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:4:PRO:HG3	12:m:68:PHE:HE2	1.66	0.60
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.83	0.60
20:u:71:ILE:H	20:u:71:ILE:HD12	1.66	0.60
27:C:41:VAL:HG13	27:C:42:VAL:HG23	1.81	0.60
52:3:1306:A:N6	52:3:1331:G:H1'	2.16	0.60
3:d:34:ALA:HA	3:d:94:GLN:HE21	1.66	0.60
11:l:102:GLY:HA3	11:l:105:ILE:HD13	1.84	0.60
17:r:49:ILE:HG22	17:r:54:VAL:HG22	1.82	0.60
18:s:36:LEU:HD13	18:s:48:LYS:HA	1.82	0.60
20:u:46:LYS:HD2	20:u:47:PRO:HD2	1.84	0.60
34:J:22:LYS:HE2	34:J:29:ILE:HG23	1.82	0.60
3:d:126:VAL:HG13	3:d:156:ASN:HB3	1.84	0.60
8:i:107:GLU:HG3	8:i:108:ILE:HG13	1.84	0.60
16:q:86:SER:HB3	17:r:50:GLY:O	2.02	0.60
17:r:68:ARG:NH1	17:r:90:ARG:HB2	2.17	0.60
33:I:112:GLU:HG3	52:3:408:A:H5'	1.83	0.60
52:3:495:A:H4'	52:3:496:A:O5'	2.02	0.60
53:1:1539:U:H2'	53:1:1540:G:H8	1.65	0.60
12:m:108:VAL:HB	12:m:112:LEU:HD23	1.84	0.60
18:s:93:ALA:HB2	53:1:1614:A:C2	2.37	0.60
21:v:4:ILE:H	21:v:4:ILE:HD12	1.66	0.60
33:I:58:GLN:O	33:I:62:ARG:HG2	2.01	0.60
34:J:56:PRO:O	34:J:59:ILE:HG22	2.01	0.60
38:N:119:LYS:HB2	38:N:122:ARG:HH21	1.66	0.60
53:1:2469:A:H2'	53:1:2470:G:O4'	2.02	0.60
1:b:140:VAL:HG12	1:b:191:LEU:HD23	1.82	0.60
6:g:5:LEU:HD23	6:g:15:LEU:H	1.67	0.60
17:r:6:GLN:HE22	17:r:39:LEU:HD21	1.66	0.60
21:v:9:ARG:HH22	21:v:12:GLN:HA	1.67	0.60
34:J:156:ARG:HH12	37:M:100:ILE:HG23	1.66	0.60
39:O:84:VAL:HA	39:O:87:LEU:HD12	1.84	0.60
52:3:390:U:H2'	52:3:391:G:H8	1.66	0.60
12:m:125:PRO:HB3	53:1:2486:C:H5'	1.83	0.59
43:S:3:GLN:NE2	52:3:1047:G:H5''	2.17	0.59
7:h:43:LYS:HE2	7:h:95:LEU:HD22	1.84	0.59
15:p:77:SER:O	15:p:80:VAL:HG22	2.02	0.59
44:T:59:VAL:HG11	53:1:715:A:H5'	1.83	0.59
53:1:1827:U:O2'	53:1:1828:G:H5'	2.01	0.59
53:1:2628:C:H3'	53:1:2629:U:H5'	1.84	0.59
7:h:81:LEU:HD22	53:1:1107:G:H1'	1.84	0.59
10:k:120:PRO:HG2	10:k:121:GLU:OE2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:3:GLN:CD	52:3:1047:G:H5''	2.27	0.59
53:1:1468:U:H2'	53:1:1522:A:H61	1.67	0.59
53:1:1872:A:H2'	53:1:1873:G:O4'	2.01	0.59
4:e:34:THR:HG21	53:1:2314:A:H5'	1.84	0.59
5:f:169:ARG:HH22	53:1:1093:G:H5''	1.67	0.59
15:p:103:THR:HA	15:p:107:ALA:HB2	1.83	0.59
53:1:161:A:H3'	53:1:162:U:H5''	1.84	0.59
53:1:503:A:H4'	53:1:505:A:H5''	1.83	0.59
53:1:955:U:H3	53:1:962:G:H1	1.50	0.59
6:g:45:GLU:HA	6:g:48:GLU:HG2	1.85	0.59
14:o:24:THR:HG23	14:o:90:VAL:HG13	1.84	0.59
38:N:74:GLN:O	38:N:78:ILE:HG12	2.02	0.59
52:3:1316:G:H2'	52:3:1317:C:H5''	1.84	0.59
52:3:1432:G:H1'	52:3:1468:A:N6	2.18	0.59
16:q:108:LEU:HG	17:r:48:LYS:HE2	1.85	0.59
43:S:8:ARG:HD3	52:3:1217:C:OP1	2.03	0.59
9:j:80:HIS:CD2	53:1:2642:G:H5'	2.37	0.59
23:x:2:ARG:HB2	53:1:1365:A:OP2	2.03	0.59
28:D:24:THR:HG22	28:D:25:LYS:H	1.67	0.59
31:G:113:LEU:HD21	31:G:143:LEU:HB2	1.85	0.59
33:I:158:LEU:HD11	33:I:174:ALA:HB1	1.84	0.59
49:Y:7:LYS:HE3	52:3:332:G:H4'	1.85	0.59
53:1:2048:G:C3'	53:1:2049:G:H5''	2.33	0.59
2:c:181:ASP:O	2:c:185:ASN:HA	2.02	0.59
3:d:98:LYS:HB3	3:d:102:ARG:HH22	1.67	0.59
53:1:895:U:C2'	53:1:896:A:H5''	2.33	0.59
6:g:33:GLN:HB2	6:g:35:LYS:HG2	1.85	0.59
30:F:19:ARG:NE	53:1:2756:U:OP2	2.35	0.59
33:I:6:PRO:HG3	52:3:430:A:C4'	2.33	0.59
40:P:43:TRP:NE1	52:3:686:U:H4'	2.17	0.59
41:Q:25:ALA:O	41:Q:27:PRO:HD3	2.03	0.59
48:X:27:LYS:HD3	48:X:28:LYS:N	2.17	0.59
53:1:1138:G:H2'	53:1:1139:G:O4'	2.03	0.59
53:1:821:A:H5''	53:1:822:G:C5'	2.28	0.59
53:1:2019:A:H2	53:1:2035:G:H22	1.50	0.59
53:1:2529:G:OP2	53:1:2530:A:H5''	2.03	0.59
15:p:113:LEU:HD22	52:3:1442:G:H1'	1.85	0.58
41:Q:56:LEU:HD12	41:Q:60:PHE:HB2	1.85	0.58
44:T:57:ARG:NH2	52:3:742:G:H5''	2.17	0.58
53:1:2298:A:H62	53:1:2318:G:H21	1.49	0.58
4:e:26:GLN:HA	54:2:57:A:H1'	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:112:LYS:O	6:g:115:VAL:HG22	2.03	0.58
12:m:20:LEU:HD23	12:m:20:LEU:H	1.67	0.58
38:N:115:VAL:HG12	52:3:1367:C:H5''	1.84	0.58
41:Q:49:ARG:NH2	52:3:522:C:H41	2.00	0.58
3:d:118:LEU:HD23	3:d:186:VAL:HG13	1.85	0.58
37:M:66:GLN:HB2	37:M:68:LYS:HG2	1.85	0.58
42:R:53:ASP:HA	42:R:56:ARG:HH11	1.68	0.58
50:Z:48:LYS:HB3	52:3:723:U:C5	2.38	0.58
2:c:149:ASN:O	2:c:152:PRO:HD2	2.02	0.58
4:e:147:ARG:HG3	4:e:149:ARG:HB2	1.86	0.58
10:k:98:ARG:NH2	52:3:341:C:H41	2.01	0.58
50:Z:54:ARG:HA	50:Z:57:LYS:HE2	1.84	0.58
52:3:390:U:H2'	52:3:391:G:C8	2.39	0.58
2:c:9:VAL:HB	2:c:26:VAL:HG23	1.86	0.58
2:c:10:GLY:HA2	2:c:197:THR:HG22	1.84	0.58
28:D:10:LEU:HD11	53:1:770:G:H5''	1.84	0.58
34:J:35:LEU:HD22	34:J:133:ILE:HG12	1.84	0.58
34:J:138:ALA:HA	34:J:141:ASP:OD2	2.03	0.58
44:T:60:SER:OG	52:3:581:G:H5''	2.02	0.58
11:l:3:LEU:HD22	53:1:1203:U:C5'	2.33	0.58
25:z:4:ILE:HG13	25:z:58:GLU:HA	1.84	0.58
37:M:21:LYS:HE2	52:3:828:U:OP1	2.04	0.58
45:U:10:GLY:HA2	52:3:624:C:H4'	1.85	0.58
52:3:78:A:H2'	52:3:79:G:O4'	2.04	0.58
53:1:639:U:H2'	53:1:640:C:C6	2.39	0.58
53:1:729:G:H4'	53:1:763:G:C5'	2.34	0.58
54:2:3:C:C3'	54:2:4:C:H5''	2.34	0.58
3:d:151:GLY:HA2	3:d:172:ALA:HB2	1.86	0.58
33:I:95:GLY:HA3	33:I:135:GLN:HE22	1.69	0.58
51:a:7:ARG:HB3	53:1:2129:C:OP1	2.03	0.58
4:e:107:VAL:CG1	4:e:108:PRO:HD3	2.33	0.58
21:v:16:ALA:O	21:v:19:ARG:HG2	2.03	0.58
28:D:37:LYS:HG3	53:1:458:G:C8	2.38	0.58
3:d:45:ALA:HB3	53:1:38:A:H4'	1.84	0.58
1:b:144:GLU:HA	1:b:151:GLY:HA2	1.85	0.58
12:m:8:LYS:NZ	53:1:868:U:O2	2.36	0.58
17:r:1:MET:N	17:r:43:ASN:HB2	2.19	0.58
39:O:53:ILE:HG23	43:S:84:ARG:NE	2.19	0.58
42:R:89:ARG:HH21	42:R:95:PRO:HG2	1.69	0.58
3:d:79:ARG:HD2	3:d:80:SER:N	2.18	0.57
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:X:17:LYS:HZ1	52:3:1014:A:H5'	1.69	0.57
55:6:17:C:H2'	55:6:17(A):U:C5	2.39	0.57
8:i:12:VAL:HG12	8:i:13:ALA:H	1.69	0.57
40:P:28:ASN:HD21	40:P:30:ILE:HB	1.69	0.57
3:d:50:ALA:HB2	53:1:801:G:C8	2.38	0.57
24:y:45:GLN:NE2	24:y:46:VAL:HG13	2.19	0.57
34:J:76:ASN:HB2	34:J:81:GLN:NE2	2.19	0.57
45:U:14:ARG:NH1	52:3:618:C:H1'	2.18	0.57
53:1:226:A:H2'	53:1:227:A:O4'	2.04	0.57
53:1:546:U:H2'	53:1:547:A:H4'	1.85	0.57
10:k:30:ARG:NE	53:1:2674:G:H4'	2.19	0.57
43:S:80:ARG:O	43:S:83:VAL:HG12	2.03	0.57
53:1:2834:G:H2'	53:1:2879:A:H61	1.69	0.57
4:e:27:VAL:O	4:e:29:ARG:NH1	2.37	0.57
6:g:117:LEU:HD23	6:g:117:LEU:H	1.70	0.57
8:i:36:GLU:HG3	8:i:66:PHE:HE1	1.69	0.57
52:3:309:A:H2'	52:3:310:G:H8	1.69	0.57
52:3:1497:G:O2'	52:3:1498:U:H5'	2.04	0.57
15:p:59:THR:HG22	15:p:72:VAL:HG12	1.87	0.57
33:I:196:GLU:HA	33:I:199:ILE:HD13	1.85	0.57
37:M:123:GLU:CD	52:3:643:C:H1'	2.30	0.57
43:S:25:GLU:HG3	43:S:26:LEU:HD12	1.86	0.57
46:V:58:VAL:HG22	46:V:59:GLU:H	1.70	0.57
45:U:22:ALA:HB2	45:U:32:PHE:HB3	1.87	0.57
49:Y:25:SER:OG	52:3:1458:G:H5''	2.04	0.57
49:Y:75:LYS:NZ	52:3:186:C:H1'	2.20	0.57
52:3:1379:G:O2'	52:3:1380:U:H5'	2.05	0.57
2:c:66:GLY:HA3	53:1:2787:C:H5'	1.87	0.57
11:l:79:LEU:H	11:l:113:ALA:HB3	1.70	0.57
38:N:71:ILE:HG13	38:N:72:SER:N	2.19	0.57
40:P:127:ARG:H	52:3:796:C:H5''	1.69	0.57
45:U:74:LEU:HA	45:U:77:GLU:HB2	1.87	0.57
53:1:2467:C:H2'	53:1:2468:A:O4'	2.04	0.57
20:u:16:LYS:HG3	53:1:329:G:N1	2.17	0.57
26:B:39:ARG:HD3	53:1:2886:A:N1	2.20	0.57
31:G:195:VAL:HG12	31:G:197:PHE:H	1.70	0.57
39:O:37:ARG:HD2	52:3:1124:G:H5''	1.86	0.57
10:k:80:ASP:HB2	15:p:67:GLU:HB3	1.86	0.57
13:n:69:ARG:O	13:n:70:THR:OG1	2.21	0.57
17:r:65:ALA:HB3	17:r:95:ASP:HB2	1.86	0.57
34:J:61:LYS:NZ	52:3:1073:U:OP2	2.31	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:X:14:LEU:HD11	48:X:34:SER:HB3	1.86	0.57
51:a:31:LYS:HE2	51:a:31:LYS:HA	1.87	0.57
52:3:966:G:N3	55:5:34:C:H5'	2.20	0.57
1:b:146:LYS:HB2	1:b:149:LYS:HB2	1.86	0.56
53:1:894:U:O2'	53:1:895:U:H5'	2.05	0.56
1:b:80:LEU:HG	1:b:111:ALA:HB2	1.85	0.56
13:n:51:LEU:HD21	13:n:69:ARG:HD3	1.87	0.56
28:D:10:LEU:HD12	28:D:11:LYS:N	2.20	0.56
48:X:5:LYS:HE2	48:X:6:LYS:HE3	1.87	0.56
52:3:437:U:H2'	52:3:438:U:O4'	2.05	0.56
52:3:715:A:H2'	52:3:716:A:C8	2.41	0.56
53:1:1322:A:H61	53:1:1333:G:H21	1.51	0.56
5:f:18:ILE:HA	5:f:23:ILE:HG12	1.86	0.56
10:k:64:ARG:HB2	10:k:83:ALA:HB3	1.87	0.56
18:s:41:LYS:HD2	53:1:2009:A:H5''	1.87	0.56
45:U:43:ALA:HB1	45:U:46:LYS:HE3	1.88	0.56
49:Y:77:ASN:O	49:Y:81:GLN:HG2	2.05	0.56
52:3:1005:A:H2'	52:3:1006:G:O4'	2.06	0.56
53:1:119:A:H4'	53:1:120:U:H5'	1.87	0.56
53:1:511:U:H2'	53:1:512:G:H5'	1.87	0.56
53:1:1045:C:OP1	53:1:1047:G:H5'	2.06	0.56
53:1:2358:A:H2'	53:1:2359:C:O4'	2.05	0.56
8:i:117:THR:HG23	53:1:1058:U:H1'	1.86	0.56
18:s:61:ASN:HD21	53:1:495:G:H21	1.54	0.56
21:v:6:ALA:HB2	21:v:42:LEU:HD13	1.88	0.56
37:M:34:ALA:HA	37:M:37:ASN:ND2	2.20	0.56
43:S:68:ARG:HD2	52:3:1202:U:H1'	1.86	0.56
45:U:1:MET:HB2	45:U:24:SER:HB3	1.87	0.56
52:3:1497:G:C2'	52:3:1498:U:H5'	2.35	0.56
16:q:43:GLN:HE21	17:r:77:PHE:HB3	1.70	0.56
43:S:20:PHE:O	43:S:21:ALA:HB3	2.05	0.56
52:3:673:A:H2'	52:3:674:G:C8	2.40	0.56
53:1:2111:U:H3	53:1:2147:A:H1'	1.70	0.56
53:1:2676:C:H2'	53:1:2677:G:H8	1.71	0.56
1:b:94:LEU:HD21	53:1:1501:G:H4'	1.87	0.56
2:c:12:THR:HG22	2:c:13:ARG:H	1.70	0.56
8:i:96:LYS:NZ	8:i:137:LEU:HA	2.20	0.56
8:i:127:SER:HA	53:1:1080:A:H1'	1.87	0.56
14:o:90:VAL:HG12	14:o:91:SER:N	2.20	0.56
42:R:100:ARG:HH12	52:3:950:U:H3'	1.71	0.56
52:3:252:U:O2	52:3:252:U:H2'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:828:U:H2'	53:1:829:A:C8	2.41	0.56
53:1:1053:C:C2'	53:1:1054:A:H5''	2.36	0.56
17:r:58:VAL:H	17:r:102:SER:HB3	1.69	0.56
22:w:7:ARG:N	22:w:7:ARG:HD3	2.21	0.56
22:w:20:LYS:HD2	53:1:2355:G:H4'	1.87	0.56
39:O:52:LEU:HB2	43:S:80:ARG:HD2	1.88	0.56
2:c:9:VAL:HG12	15:p:4:ILE:HD11	1.88	0.56
5:f:136:ASP:HB3	5:f:139:VAL:HG22	1.87	0.56
13:n:53:THR:HG21	53:1:2840:C:C5'	2.36	0.56
14:o:9:ARG:NH2	53:1:2296:U:O4	2.39	0.56
14:o:90:VAL:HG12	14:o:91:SER:H	1.71	0.56
18:s:42:LYS:HB2	53:1:2010:G:C5'	2.31	0.56
32:H:102:ILE:HD12	32:H:102:ILE:N	2.18	0.56
52:3:1502:A:H5'	52:3:1504:G:N7	2.21	0.56
53:1:1060:U:H4'	53:1:1061:U:H5'	1.88	0.56
3:d:117:ARG:NH2	3:d:184:ASP:HA	2.19	0.56
4:e:92:GLY:O	4:e:95:MET:HG2	2.06	0.56
52:3:909:A:H2'	52:3:910:C:O4'	2.06	0.56
32:H:86:LEU:HA	32:H:89:VAL:HG22	1.87	0.56
41:Q:81:ILE:HD12	41:Q:96:THR:HA	1.88	0.56
42:R:112:ARG:HD3	52:3:1229:A:P	2.46	0.56
53:1:1023:U:O2'	53:1:1122:G:H5'	2.05	0.56
4:e:36:ASN:HD21	53:1:2312:U:C2'	2.19	0.55
4:e:110:ILE:HD13	4:e:136:ILE:HG21	1.88	0.55
10:k:47:ILE:HB	10:k:48:PRO:HD2	1.88	0.55
39:O:65:TYR:HB3	43:S:95:LEU:HD11	1.88	0.55
49:Y:9:ARG:HA	49:Y:12:GLN:HG2	1.88	0.55
53:1:796:C:H2'	53:1:797:G:C8	2.40	0.55
53:1:897:C:OP1	57:7:19:G:O6	2.24	0.55
53:1:1810:A:H2'	53:1:1811:G:O4'	2.07	0.55
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.86	0.55
9:j:57:LEU:O	9:j:58:ASN:HB2	2.06	0.55
29:E:32:LEU:HD13	53:1:2419:U:OP2	2.05	0.55
41:Q:39:THR:HG22	41:Q:40:THR:H	1.70	0.55
29:E:61:LEU:HD12	29:E:61:LEU:O	2.05	0.55
53:1:948:C:H2'	53:1:949:G:C8	2.41	0.55
53:1:2421:G:H2'	55:6:76:A:N6	2.22	0.55
32:H:174:LEU:HB2	52:3:1108:G:OP1	2.06	0.55
34:J:155:LYS:HE3	37:M:70:VAL:HG13	1.88	0.55
51:a:170:ILE:HG12	53:1:2177:C:O2'	2.05	0.55
4:e:65:LEU:HD11	54:2:41:G:H5''	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:o:49:VAL:HG22	14:o:85:LYS:HG3	1.87	0.55
35:K:36:ILE:HA	35:K:64:VAL:HG13	1.88	0.55
40:P:116:PRO:HB3	52:3:676:A:C1'	2.35	0.55
48:X:5:LYS:HG3	48:X:6:LYS:HG2	1.88	0.55
52:3:350:G:H2'	52:3:351:G:C8	2.42	0.55
52:3:1404:C:H2'	52:3:1405:G:C8	2.41	0.55
53:1:1306:C:N4	53:1:1606:C:H2'	2.21	0.55
53:1:2048:G:C2'	53:1:2049:G:H5''	2.35	0.55
3:d:149:ILE:HD13	3:d:170:ARG:HB2	1.89	0.55
9:j:36:LEU:O	9:j:51:GLY:HA3	2.07	0.55
10:k:115:ILE:H	10:k:115:ILE:HD12	1.70	0.55
52:3:1506:U:O2'	52:3:1507:A:H5'	2.06	0.55
53:1:554:U:H2'	53:1:555:G:O4'	2.07	0.55
53:1:2112:G:H1'	55:6:19:G:O2'	2.06	0.55
1:b:52:HIS:HA	1:b:216:ARG:HB3	1.87	0.55
23:x:6:VAL:HG11	23:x:58:ILE:HD11	1.88	0.55
23:x:36:ARG:HA	23:x:47:THR:HA	1.89	0.55
42:R:85:TYR:CZ	52:3:1321:U:H5''	2.42	0.55
52:3:979:C:H1'	52:3:1317:C:N4	2.19	0.55
32:H:69:THR:HG21	32:H:75:VAL:HG11	1.88	0.55
52:3:1540:U:O2	52:3:1540:U:H3'	2.07	0.55
4:e:76:PHE:CE2	53:1:2311:A:H5''	2.41	0.55
11:l:3:LEU:H	11:l:3:LEU:HD12	1.72	0.55
20:u:48:VAL:HG22	20:u:50:ALA:H	1.72	0.55
24:y:39:GLN:HB3	24:y:41:HIS:CE1	2.42	0.55
33:I:25:ARG:HD3	33:I:28:ASP:HA	1.88	0.55
35:K:3:HIS:H	35:K:92:THR:HG22	1.72	0.55
53:1:2183:A:H2'	53:1:2184:A:C8	2.42	0.55
53:1:2819:G:H2'	53:1:2821:A:N7	2.22	0.55
1:b:59:GLN:HA	53:1:1568:G:C5'	2.37	0.55
11:l:96:LYS:HG3	11:l:101:ILE:HD11	1.89	0.55
31:G:66:ILE:N	31:G:66:ILE:HD12	2.22	0.55
32:H:37:LYS:HA	32:H:40:GLN:HE21	1.71	0.55
39:O:6:ILE:HB	39:O:76:ILE:HB	1.89	0.55
53:1:255:A:H2'	53:1:256:A:O4'	2.06	0.55
53:1:2350:C:H2'	53:1:2351:G:O4'	2.07	0.55
2:c:97:SER:OG	2:c:99:GLU:HG2	2.06	0.54
4:e:141:ASP:O	4:e:142:TYR:HB3	2.08	0.54
32:H:84:GLU:HA	32:H:87:ARG:HD2	1.88	0.54
52:3:1271:A:H5'	52:3:1314:C:H5''	1.87	0.54
53:1:121:G:H4'	53:1:149:A:H5'	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1344:U:H3'	53:1:1345:C:H5'	1.88	0.54
34:J:82:HIS:HD2	37:M:98:LEU:HD21	1.72	0.54
37:M:10:LEU:HD22	37:M:76:ARG:HB2	1.90	0.54
44:T:59:VAL:CG1	53:1:715:A:H5'	2.37	0.54
53:1:1360:G:H22	53:1:2214:C:H42	1.55	0.54
53:1:2180:U:H4'	55:6:17(A):U:H5'	1.90	0.54
53:1:2715:C:H2'	53:1:2716:C:H5''	1.88	0.54
3:d:61:ARG:HH12	3:d:67:ARG:HH21	1.53	0.54
4:e:38:GLY:HA2	4:e:85:GLY:HA3	1.89	0.54
9:j:17:VAL:HB	9:j:139:VAL:HA	1.88	0.54
11:l:69:ARG:NE	53:1:2406:A:H1'	2.22	0.54
21:v:4:ILE:HD12	21:v:4:ILE:N	2.22	0.54
29:E:33:THR:HG23	53:1:2420:C:OP1	2.08	0.54
33:I:170:LEU:HD12	33:I:170:LEU:O	2.07	0.54
40:P:35:ASP:OD2	40:P:37:GLN:HB3	2.06	0.54
42:R:112:ARG:HD3	52:3:1229:A:OP2	2.07	0.54
52:3:1301:U:O2	52:3:1301:U:H2'	2.07	0.54
54:2:106:G:H2'	54:2:107:G:O4'	2.07	0.54
12:m:34:LYS:HA	12:m:101:VAL:HA	1.88	0.54
29:E:51:LYS:HA	29:E:54:LEU:HG	1.89	0.54
48:X:17:LYS:NZ	52:3:1014:A:H5'	2.22	0.54
53:1:2533:U:H2'	53:1:2534:A:O4'	2.07	0.54
7:h:56:ARG:HH21	7:h:83:ALA:HB2	1.72	0.54
9:j:7:LYS:HG2	53:1:538:A:H4'	1.90	0.54
9:j:8:PRO:HG3	9:j:48:VAL:HG13	1.88	0.54
17:r:81:LYS:HD2	53:1:973:A:H5''	1.90	0.54
25:z:50:VAL:O	25:z:54:VAL:HG22	2.07	0.54
31:G:103:TRP:HE1	31:G:107:ARG:HE	1.56	0.54
33:I:95:GLY:HA3	33:I:135:GLN:NE2	2.22	0.54
41:Q:87:LYS:HE2	52:3:913:A:OP1	2.08	0.54
42:R:22:TYR:CD1	42:R:65:GLU:HG3	2.42	0.54
48:X:30:LEU:H	48:X:48:ILE:HG22	1.72	0.54
53:1:854:C:H2'	53:1:855:G:H8	1.73	0.54
53:1:1837:C:H2'	53:1:1899:A:H61	1.72	0.54
2:c:126:ASN:HD21	53:1:2678:C:P	2.30	0.54
8:i:104:GLN:O	8:i:107:GLU:HG2	2.08	0.54
16:q:51:GLN:HG2	53:1:559:G:H21	1.72	0.54
16:q:67:ALA:O	16:q:70:GLN:HB3	2.08	0.54
31:G:100:LEU:HB3	31:G:174:GLU:HB3	1.89	0.54
31:G:131:LYS:HE2	52:3:1160:G:OP1	2.08	0.54
51:a:54:LYS:HG2	51:a:56:ASP:OD1	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:45:G:H5'	53:1:46:G:C5'	2.17	0.54
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.72	0.54
16:q:23:TYR:CD1	53:1:533:G:H5'	2.43	0.54
53:1:49:A:H5'	53:1:51:G:O4'	2.08	0.54
53:1:2128:G:H21	53:1:2173:A:H1'	1.72	0.54
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.90	0.54
18:s:82:MET:HB2	18:s:98:LYS:HB2	1.90	0.54
32:H:181:ILE:HG12	32:H:202:PHE:HB2	1.90	0.54
34:J:12:GLU:HG3	34:J:38:VAL:HG12	1.88	0.54
46:V:11:VAL:HG22	46:V:22:VAL:HG22	1.89	0.54
53:1:2457:U:H3	53:1:2494:G:H1	1.55	0.54
1:b:244:VAL:HG12	1:b:250:GLN:HA	1.89	0.54
36:L:111:GLY:HA2	36:L:118:ARG:HD2	1.89	0.54
37:M:34:ALA:HA	37:M:37:ASN:HD22	1.72	0.54
41:Q:101:LEU:HD23	41:Q:101:LEU:H	1.73	0.54
43:S:9:GLU:O	43:S:13:VAL:HG23	2.08	0.54
43:S:80:ARG:HG3	43:S:81:ILE:HG13	1.90	0.54
49:Y:8:LYS:HG2	49:Y:12:GLN:NE2	2.23	0.54
53:1:745:G:O2'	53:1:748:G:H1'	2.08	0.54
4:e:24:VAL:HG12	54:2:55:U:H4'	1.89	0.54
17:r:49:ILE:CG2	17:r:54:VAL:HG22	2.38	0.54
21:v:16:ALA:HA	21:v:19:ARG:HE	1.71	0.54
32:H:26:LYS:HZ3	52:3:1257:A:P	2.30	0.54
39:O:61:ALA:HB2	52:3:1061:G:H5'	1.88	0.54
52:3:911:U:H2'	52:3:912:C:C6	2.43	0.54
52:3:1256:A:H1'	52:3:1258:G:C4	2.43	0.54
53:1:69:C:H2'	53:1:70:G:C8	2.42	0.54
53:1:441:U:O2'	53:1:442:G:H5'	2.08	0.54
53:1:2112:G:H2'	53:1:2113:U:H5'	1.89	0.54
2:c:4:LEU:HD11	2:c:97:SER:O	2.08	0.53
5:f:169:ARG:NH2	53:1:1093:G:C5'	2.71	0.53
24:y:23:ARG:CG	24:y:24:GLU:H	2.06	0.53
31:G:94:ARG:NH2	52:3:1101:A:OP2	2.40	0.53
40:P:125:LYS:HG3	40:P:126:ARG:HG3	1.90	0.53
45:U:2:VAL:HG23	45:U:65:ALA:HA	1.90	0.53
45:U:4:ILE:HB	45:U:67:ILE:HD12	1.91	0.53
53:1:1141:U:H4'	53:1:1142:A:O4'	2.07	0.53
3:d:85:PHE:HE2	53:1:587:C:H5'	1.73	0.53
4:e:120:SER:OG	53:1:2304:G:H5'	2.08	0.53
6:g:21:VAL:HG22	6:g:22:LYS:H	1.73	0.53
31:G:186:VAL:HG11	31:G:192:PRO:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:44:ILE:HA	42:R:47:LEU:HD12	1.91	0.53
45:U:19:VAL:HG11	45:U:52:LEU:HD21	1.91	0.53
52:3:501:C:H2'	52:3:502:A:C8	2.43	0.53
52:3:757:U:H2'	52:3:758:C:O4'	2.08	0.53
52:3:1229:A:H4'	55:5:29:G:H5''	1.91	0.53
3:d:1:MET:HG2	3:d:19:PHE:HB2	1.90	0.53
9:j:81:ILE:HD12	53:1:2514:U:H5''	1.90	0.53
12:m:51:ARG:HH12	53:1:2483:C:H1'	1.71	0.53
14:o:16:ARG:HA	14:o:19:GLN:CG	2.39	0.53
15:p:1:SER:HB2	15:p:4:ILE:HD12	1.89	0.53
52:3:505:G:OP2	52:3:535:A:H5'	2.08	0.53
53:1:225:C:H2'	53:1:226:A:O4'	2.09	0.53
3:d:61:ARG:NH1	3:d:67:ARG:HH21	2.07	0.53
7:h:29:ASP:HB2	7:h:56:ARG:HH22	1.73	0.53
7:h:81:LEU:HD13	53:1:1106:G:N3	2.23	0.53
16:q:3:VAL:HG21	53:1:1249:U:H4'	1.90	0.53
17:r:88:GLY:HA3	53:1:1225:G:OP1	2.08	0.53
23:x:67:LEU:HA	23:x:70:LEU:HD12	1.91	0.53
33:I:24:VAL:HG22	52:3:409:U:H5'	1.90	0.53
52:3:1251:A:O2'	52:3:1370:G:H5'	2.08	0.53
54:2:88:C:H4'	54:2:89:U:OP1	2.08	0.53
1:b:156:SER:OG	53:1:1818:U:H5'	2.08	0.53
2:c:25:THR:HG21	2:c:193:VAL:HG21	1.89	0.53
53:1:2243:U:H2'	53:1:2244:U:C6	2.43	0.53
15:p:2:ASN:ND2	53:1:2876:G:H4'	2.24	0.53
33:I:4:LEU:HD12	33:I:4:LEU:O	2.09	0.53
33:I:36:ALA:N	33:I:37:PRO:HD3	2.24	0.53
34:J:126:ALA:HB3	52:3:9:G:OP1	2.08	0.53
47:W:70:THR:HG23	47:W:72:ARG:H	1.74	0.53
49:Y:23:ARG:NH1	52:3:176:C:H5''	2.20	0.53
50:Z:28:LEU:HA	50:Z:31:VAL:HG12	1.90	0.53
51:a:68:GLY:HA2	51:a:159:GLY:HA3	1.91	0.53
53:1:669:G:H2'	53:1:669:G:N3	2.24	0.53
53:1:2197:U:H1'	53:1:2198:A:C8	2.44	0.53
8:i:133:ARG:NH1	8:i:133:ARG:HB2	2.23	0.53
16:q:111:LYS:NZ	17:r:48:LYS:CG	2.72	0.53
23:x:17:ARG:CG	53:1:380:G:H5'	2.39	0.53
25:z:16:LEU:HB2	25:z:19:HIS:CD2	2.44	0.53
37:M:79:ARG:HB2	52:3:878:A:OP1	2.09	0.53
40:P:19:VAL:HG11	40:P:84:MET:HE3	1.91	0.53
51:a:174:THR:HB	53:1:2124:G:H5''	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:948:C:H2'	52:3:949:A:H8	1.73	0.53
53:1:275:C:H2'	53:1:276:U:H4'	1.90	0.53
53:1:892:A:O2'	53:1:893:C:H5'	2.09	0.53
53:1:2156:G:C2'	53:1:2157:G:H5'	2.39	0.53
10:k:67:LYS:O	10:k:67:LYS:HD3	2.09	0.53
35:K:35:LYS:HB2	35:K:65:GLU:HB3	1.90	0.53
52:3:77:A:H2'	52:3:78:A:C8	2.43	0.53
53:1:948:C:H2'	53:1:949:G:H8	1.74	0.53
6:g:4:ILE:HG22	6:g:37:VAL:O	2.09	0.53
8:i:88:GLY:HA3	53:1:1063:G:O2'	2.09	0.53
19:t:9:LYS:HZ2	53:1:71:A:H1'	1.73	0.53
31:G:124:THR:O	31:G:128:LEU:HD13	2.09	0.53
43:S:39:ASP:HA	43:S:42:ASN:ND2	2.24	0.53
1:b:257:ARG:NE	1:b:263:ASP:OD1	2.40	0.53
13:n:79:LEU:O	13:n:80:PHE:HB2	2.07	0.53
16:q:82:LEU:HB3	16:q:87:VAL:HB	1.90	0.53
19:t:48:GLN:HE22	19:t:54:GLU:HA	1.74	0.53
24:y:31:GLN:HG2	24:y:36:GLN:HB2	1.91	0.53
36:L:9:ARG:HD3	36:L:9:ARG:N	2.24	0.53
37:M:9:MET:O	37:M:13:ILE:HG13	2.09	0.53
52:3:744:C:H2'	52:3:745:G:H8	1.72	0.53
52:3:966:G:H1'	55:5:34:C:H4'	1.90	0.53
53:1:2818:U:H2'	53:1:2819:G:H8	1.73	0.53
2:c:167:ASN:ND2	53:1:2822:G:OP1	2.43	0.52
19:t:51:PHE:O	19:t:53:VAL:HG23	2.08	0.52
21:v:56:PHE:HE1	21:v:61:LEU:HD21	1.73	0.52
27:C:8:ILE:HD13	27:C:24:LYS:HE2	1.91	0.52
31:G:217:ALA:HB1	31:G:221:ARG:HH12	1.74	0.52
36:L:3:ARG:HB2	52:3:932:C:OP1	2.09	0.52
51:a:163:TYR:HB2	51:a:171:ILE:HD11	1.91	0.52
52:3:1481:U:H2'	52:3:1482:G:C8	2.44	0.52
53:1:2033:A:H1'	53:1:2035:G:OP2	2.08	0.52
3:d:147:LEU:HB3	3:d:186:VAL:HG23	1.90	0.52
13:n:107:ASN:HD22	53:1:2009:A:C4'	2.22	0.52
46:V:78:VAL:C	46:V:79:GLU:HG2	2.34	0.52
49:Y:79:THR:HG21	52:3:187:G:H5'	1.91	0.52
53:1:690:G:H2'	53:1:691:C:C6	2.44	0.52
53:1:1357:C:H2'	53:1:1358:G:O4'	2.09	0.52
53:1:2086:U:H2'	53:1:2087:G:C8	2.44	0.52
2:c:142:VAL:HG12	2:c:143:PRO:HD2	1.91	0.52
3:d:83:VAL:HG11	53:1:1248:G:C2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:67:THR:HG22	4:e:87:LYS:HZ2	1.74	0.52
6:g:3:VAL:HA	6:g:38:PRO:HA	1.91	0.52
13:n:55:ALA:HA	13:n:80:PHE:CE1	2.45	0.52
24:y:43:LEU:HD23	53:1:61:C:H5''	1.90	0.52
28:D:12:ARG:O	28:D:16:HIS:HB2	2.10	0.52
49:Y:28:ARG:HH12	52:3:1437:A:H5''	1.74	0.52
52:3:1148:U:H2'	52:3:1149:C:O4'	2.09	0.52
53:1:1874:C:H2'	53:1:1875:G:O4'	2.10	0.52
53:1:2114:A:H2'	53:1:2114:A:N3	2.24	0.52
2:c:33:ARG:HA	2:c:95:SER:HA	1.91	0.52
6:g:47:PHE:HA	6:g:51:ARG:HB2	1.91	0.52
10:k:16:ALA:HA	10:k:46:ALA:HA	1.92	0.52
16:q:3:VAL:HG22	53:1:1249:U:H4'	1.91	0.52
37:M:76:ARG:NH1	37:M:125:ILE:HG23	2.24	0.52
52:3:312:C:H2'	52:3:313:A:C8	2.44	0.52
12:m:12:MET:HA	53:1:910:A:N6	2.22	0.52
29:E:1:PRO:HG2	53:1:591:U:O2	2.10	0.52
30:F:1:MET:HE3	53:1:2742:G:H5''	1.91	0.52
41:Q:48:LEU:HB2	52:3:520:A:OP1	2.10	0.52
42:R:25:GLY:N	52:3:1329:A:H5''	2.24	0.52
47:W:42:ARG:NH1	52:3:721:G:H5''	2.23	0.52
53:1:278:A:H2'	53:1:278:A:N3	2.23	0.52
53:1:1077:A:C2'	53:1:1078:U:H5'	2.37	0.52
1:b:179:GLU:HG3	53:1:1799:G:C8	2.45	0.52
5:f:97:VAL:HG12	5:f:102:ILE:HG12	1.92	0.52
8:i:61:TYR:HB2	8:i:65:SER:O	2.09	0.52
32:H:18:ASN:ND2	43:S:89:ARG:O	2.41	0.52
35:K:47:LEU:HD11	35:K:57:ALA:HB2	1.91	0.52
38:N:118:ARG:CZ	52:3:1233:G:H5'	2.40	0.52
38:N:118:ARG:NH2	52:3:1233:G:H5'	2.24	0.52
39:O:12:ALA:HB2	39:O:96:VAL:HG13	1.92	0.52
46:V:16:MET:HG3	46:V:19:SER:OG	2.10	0.52
49:Y:29:THR:O	49:Y:33:LYS:HG3	2.09	0.52
53:1:239:C:H2'	53:1:240:C:O4'	2.10	0.52
53:1:1319:C:O2'	53:1:1320:C:H5'	2.10	0.52
53:1:2698:U:H2'	53:1:2699:C:C6	2.45	0.52
1:b:45:ASN:O	53:1:773:U:H4'	2.10	0.52
1:b:164:VAL:HG11	1:b:180:MET:HE1	1.90	0.52
6:g:5:LEU:HB3	6:g:16:GLY:H	1.75	0.52
6:g:116:ARG:C	6:g:118:PRO:HD3	2.35	0.52
9:j:25:LEU:HB2	53:1:1140:C:OP1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:88:GLY:HA2	11:l:120:VAL:HG13	1.90	0.52
12:m:55:ARG:NH2	53:1:2469:A:O2'	2.41	0.52
19:t:69:ARG:HH21	53:1:1334:G:H5''	1.73	0.52
29:E:1:PRO:HD2	53:1:591:U:H1'	1.91	0.52
33:I:69:ARG:HH22	52:3:401:C:H3'	1.74	0.52
33:I:74:TYR:OH	33:I:96:ARG:NH1	2.41	0.52
37:M:48:PHE:HB2	37:M:58:LEU:HD11	1.92	0.52
38:N:84:ARG:HH22	52:3:1119:C:H5'	1.75	0.52
44:T:22:GLY:O	52:3:751:U:H1'	2.10	0.52
53:1:1045:C:H5'	53:1:1046:A:H5''	1.92	0.52
53:1:1856:U:H2'	53:1:1857:G:O4'	2.10	0.52
53:1:2329:U:H2'	53:1:2330:G:C8	2.44	0.52
2:c:13:ARG:HD2	2:c:21:SER:OG	2.10	0.52
3:d:84:THR:HG21	53:1:672:C:H5''	1.92	0.52
3:d:109:LEU:HD11	3:d:180:LEU:HD22	1.91	0.52
3:d:163:ASN:HB2	53:1:322:A:OP2	2.09	0.52
9:j:117:ALA:HA	9:j:120:ARG:NH2	2.24	0.52
15:p:20:ARG:HD3	15:p:112:ARG:NH1	2.25	0.52
38:N:17:ARG:NH1	52:3:1129:C:H4'	2.25	0.52
40:P:122:PRO:HG2	50:Z:35:GLU:HB2	1.91	0.52
52:3:784:A:H4'	53:1:1837:C:OP1	2.09	0.52
53:1:826:U:H5''	53:1:2429:G:P	2.50	0.52
12:m:18:ARG:HH12	54:2:80:U:P	2.33	0.52
19:t:61:LEU:N	19:t:61:LEU:HD23	2.25	0.52
23:x:11:PRO:HB3	23:x:29:LEU:HD23	1.92	0.52
31:G:24:PRO:HB3	52:3:828:U:H2'	1.92	0.52
37:M:78:SER:HB2	37:M:124:ILE:O	2.10	0.52
53:1:1060:U:H4'	53:1:1061:U:C5'	2.40	0.52
53:1:1669:A:O3'	53:1:2549:G:H5'	2.10	0.52
53:1:2285:C:O2'	53:1:2287:A:H1'	2.10	0.52
1:b:116:GLN:HE22	1:b:124:LYS:HE2	1.73	0.52
3:d:69:ARG:NH1	53:1:2060:A:H62	2.08	0.52
18:s:87:PRO:O	18:s:88:ARG:HD2	2.10	0.52
30:F:23:ILE:HD12	30:F:23:ILE:N	2.22	0.52
41:Q:49:ARG:HH21	52:3:522:C:H41	1.57	0.52
53:1:621:A:H2'	53:1:622:G:H5'	1.91	0.52
53:1:2277:G:C3'	53:1:2278:A:H5''	2.39	0.52
36:L:56:SER:OG	36:L:59:GLU:HG2	2.10	0.51
39:O:88:MET:O	39:O:89:ARG:HG2	2.11	0.51
50:Z:17:ARG:HA	50:Z:20:ARG:HH11	1.75	0.51
52:3:77:A:H2'	52:3:78:A:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:7:TYR:O	4:e:12:VAL:HG23	2.11	0.51
7:h:38:MET:HA	7:h:42:ARG:HH11	1.76	0.51
8:i:78:LEU:HD13	8:i:112:LYS:HD3	1.91	0.51
21:v:75:GLN:HB2	21:v:92:VAL:HG13	1.92	0.51
44:T:76:ARG:HA	44:T:79:GLN:HB3	1.92	0.51
52:3:1273:C:H2'	52:3:1274:A:O4'	2.10	0.51
52:3:1339:A:H2	55:5:30:G:H1'	1.76	0.51
53:1:435:C:H2'	53:1:436:C:H5'	1.92	0.51
53:1:2013:A:H61	53:1:2613:U:H3	1.58	0.51
53:1:2553:G:C3'	53:1:2554:U:H5''	2.36	0.51
4:e:11:VAL:HA	4:e:14:LYS:HD3	1.92	0.51
9:j:90:GLU:O	9:j:93:ILE:HG22	2.11	0.51
18:s:69:LEU:HG	18:s:107:VAL:HG12	1.90	0.51
52:3:730:G:H2'	52:3:731:G:H5'	1.92	0.51
53:1:987:C:H2'	53:1:988:A:O4'	2.09	0.51
53:1:2163:A:H2'	53:1:2163:A:N3	2.26	0.51
53:1:2710:C:H2'	53:1:2711:A:C8	2.46	0.51
15:p:47:ILE:HG22	15:p:99:LEU:HD12	1.93	0.51
17:r:1:MET:HE2	17:r:15:SER:HB2	1.92	0.51
19:t:50:LEU:HD13	24:y:26:PHE:CD2	2.45	0.51
20:u:82:VAL:HG23	20:u:94:PHE:O	2.10	0.51
37:M:79:ARG:HE	37:M:82:LEU:HB3	1.76	0.51
46:V:60:ILE:N	46:V:60:ILE:HD12	2.26	0.51
49:Y:20:ASN:HD21	52:3:323:U:H5''	1.75	0.51
52:3:950:U:H2'	52:3:951:G:H8	1.75	0.51
53:1:2715:C:C3'	53:1:2716:C:H5''	2.41	0.51
53:1:2756:U:H4'	53:1:2757:A:OP1	2.11	0.51
8:i:52:LEU:HG	8:i:81:LYS:HE3	1.92	0.51
10:k:60:ALA:HB1	10:k:84:CYS:SG	2.50	0.51
16:q:79:ILE:HD11	53:1:1152:C:H5''	1.93	0.51
18:s:35:ILE:O	18:s:39:THR:HG23	2.11	0.51
30:F:6:SER:OG	53:1:1031:G:H4'	2.11	0.51
31:G:164:ASP:H	31:G:185:ILE:HB	1.75	0.51
48:X:77:ARG:HD2	52:3:960:U:H5	1.75	0.51
9:j:77:HIS:NE2	53:1:1131:G:O4'	2.44	0.51
10:k:8:LEU:HD23	10:k:84:CYS:HB2	1.91	0.51
13:n:17:ARG:O	13:n:20:MET:HG3	2.10	0.51
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.92	0.51
16:q:30:VAL:HG13	53:1:580:U:O3'	2.10	0.51
16:q:94:LEU:O	16:q:97:ILE:HG22	2.11	0.51
18:s:86:MET:HE3	18:s:87:PRO:HD2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:z:6:ILE:HG12	25:z:56:VAL:HG23	1.92	0.51
26:B:38:LEU:HB2	26:B:41:HIS:HB2	1.91	0.51
31:G:13:VAL:HA	31:G:202:ASN:OD1	2.11	0.51
31:G:104:LYS:HD3	31:G:104:LYS:N	2.26	0.51
53:1:118:A:OP2	53:1:119:A:H2'	2.11	0.51
53:1:668:A:H2'	53:1:670:A:H62	1.75	0.51
53:1:859:G:H1'	53:1:860:U:H5	1.74	0.51
53:1:1919:A:H2'	53:1:1920:C:H5'	1.92	0.51
55:6:71:C:H2'	55:6:72:A:C8	2.45	0.51
4:e:132:ARG:NH2	53:1:2305:U:O2'	2.44	0.51
5:f:27:GLY:HA3	5:f:78:VAL:HB	1.92	0.51
7:h:31:ARG:HG2	7:h:109:LYS:NZ	2.26	0.51
9:j:68:LYS:HA	9:j:71:ASP:HB3	1.93	0.51
11:l:12:SER:C	11:l:13:LYS:HD2	2.35	0.51
11:l:59:ARG:HD2	53:1:250:G:H4'	1.92	0.51
12:m:21:ALA:HB2	12:m:97:GLN:HB2	1.93	0.51
16:q:21:LYS:HG2	53:1:19:A:H5''	1.92	0.51
27:C:3:GLY:N	53:1:2283:C:H5'	2.26	0.51
41:Q:20:VAL:HG21	52:3:553:A:H5''	1.92	0.51
52:3:946:A:H2'	52:3:947:G:C8	2.46	0.51
52:3:1413:A:H2	52:3:1487:G:H22	1.58	0.51
7:h:126:LEU:O	7:h:126:LEU:HD12	2.11	0.51
31:G:65:LYS:HE2	31:G:157:PRO:HA	1.93	0.51
32:H:23:ALA:HB3	32:H:28:PHE:HD1	1.74	0.51
37:M:79:ARG:HG3	37:M:82:LEU:H	1.75	0.51
44:T:74:VAL:HA	44:T:77:TYR:HB3	1.93	0.51
46:V:54:ILE:HD12	46:V:54:ILE:N	2.25	0.51
52:3:802:A:H2'	52:3:803:G:O4'	2.11	0.51
53:1:1186:G:H2'	53:1:1187:G:O4'	2.11	0.51
53:1:1509:A:H2'	53:1:1510:G:C8	2.45	0.51
53:1:2313:C:H2'	53:1:2314:A:C8	2.45	0.51
54:2:63:C:H2'	54:2:64:G:H8	1.76	0.51
54:2:66:A:H5''	54:2:67:G:OP1	2.11	0.51
1:b:143:VAL:HB	1:b:153:LEU:HD12	1.93	0.51
11:l:79:LEU:HD12	11:l:114:GLY:H	1.76	0.51
37:M:124:ILE:H	37:M:124:ILE:HD12	1.76	0.51
37:M:124:ILE:HD12	37:M:124:ILE:N	2.25	0.51
40:P:127:ARG:HB2	52:3:796:C:OP1	2.10	0.51
48:X:51:HIS:CD2	52:3:1220:G:H1'	2.45	0.51
49:Y:28:ARG:HA	49:Y:31:ILE:HG22	1.93	0.51
53:1:644:A:H61	53:1:2349:G:H21	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1053:C:C3'	53:1:1054:A:H5''	2.41	0.51
4:e:32:LYS:HD2	4:e:89:THR:CG2	2.42	0.51
14:o:9:ARG:NH2	53:1:2296:U:C5	2.79	0.51
31:G:101:THR:HA	31:G:178:LEU:HD11	1.93	0.51
33:I:6:PRO:HA	52:3:430:A:P	2.51	0.51
45:U:31:ARG:HD3	52:3:310:G:H4'	1.93	0.51
52:3:483:C:H2'	52:3:484:G:C8	2.46	0.51
52:3:715:A:H2'	52:3:716:A:H8	1.76	0.51
53:1:395:U:H2'	53:1:396:G:C8	2.46	0.51
53:1:2126:A:H2'	53:1:2162:G:C2	2.46	0.51
53:1:2799:A:C2'	53:1:2800:A:H5'	2.41	0.51
6:g:116:ARG:O	6:g:118:PRO:HD3	2.10	0.50
7:h:41:LEU:HD13	53:1:1083:U:O5'	2.10	0.50
7:h:58:THR:HG21	7:h:82:ILE:H	1.76	0.50
13:n:39:PRO:HG2	53:1:1651:G:H4'	1.93	0.50
17:r:1:MET:H1	17:r:43:ASN:HB2	1.76	0.50
19:t:54:GLU:HB2	19:t:88:LYS:HD2	1.92	0.50
21:v:7:GLU:HG2	21:v:41:GLU:HB3	1.92	0.50
21:v:76:ASP:H	21:v:90:ASP:HB2	1.76	0.50
24:y:41:HIS:NE2	53:1:96:C:H4'	2.26	0.50
35:K:6:ILE:N	35:K:6:ILE:HD12	2.26	0.50
38:N:114:LYS:CD	52:3:1187:G:H5''	2.40	0.50
41:Q:79:ILE:HD12	41:Q:103:CYS:HB2	1.92	0.50
49:Y:28:ARG:HD3	52:3:1438:G:OP1	2.11	0.50
53:1:1071:G:OP1	53:1:1071:G:H3'	2.10	0.50
53:1:2039:U:H2'	53:1:2040:G:C8	2.45	0.50
57:7:61:C:H5'	57:7:61:C:H6	1.74	0.50
10:k:19:VAL:HG12	10:k:43:ILE:HG12	1.93	0.50
32:H:185:THR:HG22	32:H:198:LYS:HG2	1.93	0.50
33:I:119:HIS:CG	52:3:438:U:H4'	2.46	0.50
41:Q:109:ARG:NH1	52:3:537:G:H5''	2.27	0.50
52:3:1014:A:H2'	52:3:1015:G:O4'	2.12	0.50
53:1:616:A:H2'	53:1:617:G:O4'	2.10	0.50
9:j:132:HIS:CE1	53:1:7:G:H5'	2.46	0.50
15:p:101:GLU:OE2	15:p:102:ARG:HG2	2.11	0.50
17:r:54:VAL:HG12	17:r:55:ASP:N	2.25	0.50
47:W:56:ARG:HD2	47:W:56:ARG:H	1.76	0.50
48:X:78:THR:HG23	52:3:957:U:H4'	1.93	0.50
52:3:195:A:H1'	52:3:222:C:O2'	2.11	0.50
52:3:392:C:H2'	52:3:393:A:C8	2.46	0.50
52:3:946:A:H2'	52:3:947:G:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1373:A:H5'	53:1:2212:A:H1'	1.93	0.50
53:1:2475:C:C2'	53:1:2476:A:H5'	2.41	0.50
2:c:133:THR:OG1	53:1:1993:U:H4'	2.12	0.50
12:m:41:LEU:HG	12:m:45:GLN:NE2	2.26	0.50
13:n:4:ARG:NH2	53:1:2820:A:C5	2.79	0.50
14:o:29:HIS:NE2	54:2:7:G:H5''	2.26	0.50
15:p:88:ARG:HB2	15:p:112:ARG:HH21	1.77	0.50
16:q:25:GLY:HA2	53:1:18:U:OP1	2.11	0.50
16:q:113:LYS:O	16:q:116:LEU:HB3	2.11	0.50
45:U:15:PRO:HD2	45:U:42:ILE:HD13	1.94	0.50
52:3:335:C:H2'	52:3:336:A:C8	2.47	0.50
53:1:367:G:H2'	53:1:368:A:O4'	2.11	0.50
53:1:1130:U:O2'	53:1:1131:G:OP1	2.27	0.50
5:f:66:THR:OG1	53:1:2748:A:H1'	2.11	0.50
8:i:12:VAL:O	8:i:13:ALA:C	2.53	0.50
8:i:74:PRO:HG3	53:1:1060:U:OP1	2.11	0.50
9:j:81:ILE:HD11	53:1:2514:U:H5''	1.93	0.50
9:j:108:MET:CE	53:1:1138:G:H21	2.19	0.50
33:I:24:VAL:HG22	52:3:409:U:C5'	2.41	0.50
36:L:114:SER:C	36:L:118:ARG:HE	2.19	0.50
39:O:14:ASP:HB3	39:O:17:LEU:HB3	1.92	0.50
52:3:501:C:H2'	52:3:502:A:H8	1.75	0.50
53:1:2366:A:H2'	53:1:2367:G:O4'	2.11	0.50
12:m:4:PRO:HG3	12:m:68:PHE:CE2	2.46	0.50
30:F:10:LEU:HD23	30:F:33:HIS:CD2	2.47	0.50
32:H:4:VAL:HG22	32:H:5:HIS:N	2.26	0.50
32:H:102:ILE:H	32:H:102:ILE:CD1	2.22	0.50
34:J:55:VAL:HG23	34:J:56:PRO:CD	2.37	0.50
41:Q:68:GLY:C	52:3:521:G:H5'	2.36	0.50
44:T:30:LEU:O	44:T:34:GLN:HG2	2.11	0.50
51:a:217:THR:HA	53:1:2124:G:H21	1.76	0.50
52:3:335:C:H2'	52:3:336:A:H8	1.76	0.50
52:3:1230:C:H5''	55:5:30:G:H5''	1.93	0.50
53:1:189:G:H2'	53:1:205:G:N2	2.27	0.50
53:1:1298:C:H2'	53:1:1299:G:O4'	2.12	0.50
53:1:2093:G:H21	53:1:2198:A:N6	2.10	0.50
54:2:63:C:H2'	54:2:64:G:C8	2.47	0.50
2:c:62:LYS:HB2	2:c:63:PRO:HD3	1.94	0.50
5:f:5:LYS:NZ	53:1:1110:G:H4'	2.27	0.50
8:i:85:ILE:HD13	8:i:98:GLY:HA3	1.94	0.50
10:k:68:GLY:HA3	10:k:78:ARG:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:19:LEU:HD13	11:l:27:LEU:HB3	1.94	0.50
21:v:16:ALA:HA	21:v:19:ARG:NE	2.26	0.50
35:K:5:GLU:HB2	35:K:90:MET:HB2	1.93	0.50
38:N:71:ILE:HG13	38:N:72:SER:H	1.76	0.50
40:P:18:GLY:HA2	40:P:35:ASP:HA	1.92	0.50
41:Q:122:LYS:HD2	41:Q:122:LYS:N	2.26	0.50
44:T:4:THR:OG1	52:3:659:U:H5''	2.11	0.50
52:3:1259:C:H3'	52:3:1260:G:C5'	2.40	0.50
53:1:1913:A:N6	57:7:38:A:H4'	2.26	0.50
4:e:151:LEU:HA	53:1:2305:U:C4	2.47	0.50
35:K:3:HIS:HB2	35:K:92:THR:HA	1.94	0.50
36:L:101:ARG:NH2	52:3:1375:A:O2'	2.41	0.50
37:M:8:ASP:O	37:M:12:ARG:HG3	2.11	0.50
42:R:63:VAL:HG12	42:R:68:LEU:HG	1.94	0.50
49:Y:53:MET:SD	49:Y:54:GLN:N	2.84	0.50
52:3:784:A:H2'	52:3:785:G:C8	2.47	0.50
52:3:1346:A:O2'	52:3:1347:G:H4'	2.12	0.50
53:1:619:G:H3'	53:1:620:G:H21	1.76	0.50
53:1:2149:U:H2'	53:1:2150:C:O4'	2.11	0.50
1:b:3:VAL:HG22	1:b:4:LYS:N	2.26	0.50
2:c:1:MET:HE2	2:c:2:ILE:HG12	1.94	0.50
9:j:108:MET:HE3	53:1:1138:G:N2	2.20	0.50
20:u:18:LYS:NZ	53:1:310:A:OP1	2.38	0.50
22:w:38:GLY:CA	53:1:2330:G:H21	2.24	0.50
29:E:2:LYS:HB2	53:1:242:G:N7	2.27	0.50
52:3:1071:C:H2'	52:3:1072:G:H8	1.77	0.50
52:3:1352:C:H2'	52:3:1353:G:C8	2.47	0.50
53:1:189:G:H2'	53:1:205:G:H22	1.76	0.50
53:1:471:A:H2'	53:1:472:A:O4'	2.12	0.50
53:1:2036:C:H2'	53:1:2037:A:C8	2.46	0.50
53:1:2286:G:H4'	53:1:2287:A:O5'	2.12	0.50
54:2:2:G:H2'	54:2:3:C:C6	2.46	0.50
54:2:3:C:H3'	54:2:4:C:H5''	1.94	0.50
2:c:55:LYS:HG3	2:c:77:ARG:HB3	1.93	0.49
12:m:31:PHE:HB2	12:m:105:MET:HB2	1.93	0.49
13:n:28:LEU:HD11	13:n:114:GLU:HA	1.94	0.49
17:r:74:ILE:CD1	53:1:992:C:H4'	2.32	0.49
33:I:182:LYS:HE3	33:I:183:ARG:HG2	1.93	0.49
36:L:25:PHE:HD2	36:L:28:ILE:HD11	1.77	0.49
39:O:8:ILE:HG12	39:O:100:ILE:HG23	1.94	0.49
39:O:33:GLY:O	39:O:80:THR:HG21	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:P:114:PRO:HB2	52:3:676:A:H5''	1.93	0.49
52:3:410:G:H2'	52:3:429:U:C4	2.47	0.49
52:3:505:G:H5'	52:3:534:U:H2'	1.94	0.49
54:2:88:C:H5''	54:2:89:U:OP1	2.12	0.49
1:b:71:ASP:O	1:b:73:ILE:HG13	2.13	0.49
3:d:26:ALA:HB3	53:1:599:A:H4'	1.93	0.49
5:f:34:ARG:HE	5:f:70:LEU:HD13	1.76	0.49
21:v:9:ARG:HH12	21:v:12:GLN:HB3	1.76	0.49
31:G:7:ASP:HA	31:G:10:LYS:HE2	1.95	0.49
35:K:51:ILE:C	35:K:53:LYS:H	2.20	0.49
36:L:70:PRO:HG3	36:L:98:LEU:HB3	1.94	0.49
38:N:14:SER:HB3	38:N:69:GLY:HA3	1.92	0.49
39:O:73:LEU:HD21	39:O:75:ASP:HB2	1.94	0.49
39:O:100:ILE:HD12	39:O:100:ILE:N	2.26	0.49
41:Q:85:ARG:HG2	41:Q:86:VAL:H	1.76	0.49
52:3:206:C:H2'	52:3:207:C:O4'	2.11	0.49
52:3:1369:C:H2'	52:3:1370:G:C8	2.47	0.49
53:1:1597:A:H5''	53:1:1598:A:H5'	1.94	0.49
53:1:2292:U:H2'	53:1:2293:G:C8	2.47	0.49
7:h:33:VAL:HG22	7:h:34:THR:N	2.25	0.49
7:h:86:MET:N	7:h:86:MET:SD	2.86	0.49
12:m:69:PRO:O	12:m:70:ASP:OD2	2.30	0.49
19:t:9:LYS:HZ1	53:1:71:A:H1'	1.76	0.49
19:t:39:THR:HG23	19:t:42:GLU:H	1.78	0.49
20:u:97:SER:O	20:u:98:ASN:HB2	2.11	0.49
24:y:1:MET:SD	24:y:1:MET:N	2.85	0.49
27:C:5:ARG:NH1	53:1:2285:C:H3'	2.26	0.49
32:H:69:THR:OG1	32:H:70:ALA:N	2.45	0.49
40:P:81:LEU:HD23	40:P:81:LEU:H	1.77	0.49
42:R:85:TYR:CE2	52:3:1321:U:H5''	2.46	0.49
53:1:2104:C:H2'	53:1:2105:U:C6	2.47	0.49
54:2:60:C:H2'	54:2:61:G:H8	1.77	0.49
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.92	0.49
4:e:21:TYR:HB3	4:e:26:GLN:HB3	1.93	0.49
13:n:35:LYS:HZ3	13:n:110:MET:HG3	1.76	0.49
15:p:98:TYR:CZ	53:1:1754:A:H5'	2.47	0.49
20:u:71:ILE:HD12	20:u:71:ILE:N	2.27	0.49
29:E:44:ARG:HB3	29:E:45:PRO:HD3	1.94	0.49
33:I:112:GLU:CG	52:3:408:A:H5'	2.43	0.49
52:3:358:U:H2'	52:3:359:G:C8	2.48	0.49
52:3:1033:G:H2'	52:3:1034:G:H5''	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:942:G:H2'	53:1:943:A:O4'	2.13	0.49
53:1:1611:C:H6	53:1:1611:C:H5'	1.76	0.49
57:7:57:G:H2'	57:7:58:A:H5'	1.95	0.49
1:b:200:MET:HE3	52:3:773:G:O3'	2.12	0.49
1:b:209:ALA:HA	1:b:212:TRP:NE1	2.28	0.49
4:e:76:PHE:C	4:e:77:LYS:HG2	2.38	0.49
4:e:127:TYR:O	4:e:155:ILE:HG22	2.13	0.49
6:g:5:LEU:HD22	6:g:13:GLY:HA3	1.95	0.49
7:h:68:PRO:HA	7:h:72:LEU:HG	1.94	0.49
8:i:29:GLN:OE1	8:i:30:GLN:NE2	2.46	0.49
14:o:29:HIS:HE2	54:2:7:G:H5''	1.77	0.49
15:p:105:LYS:O	15:p:108:ARG:HG2	2.12	0.49
29:E:32:LEU:HB3	29:E:40:LYS:HE2	1.95	0.49
34:J:105:ILE:HG13	34:J:123:LEU:HA	1.94	0.49
41:Q:42:LYS:HG2	41:Q:43:LYS:H	1.76	0.49
42:R:89:ARG:CZ	42:R:94:LEU:HB3	2.43	0.49
51:a:62:ALA:HB2	51:a:162:ARG:HG2	1.94	0.49
53:1:2233:U:H2'	53:1:2234:G:H8	1.78	0.49
20:u:43:LYS:NZ	53:1:480:A:OP2	2.46	0.49
33:I:100:VAL:O	33:I:104:MET:HG2	2.11	0.49
36:L:58:LEU:HD12	36:L:59:GLU:N	2.27	0.49
38:N:129:ARG:HH12	55:5:31:G:H3'	1.78	0.49
53:1:275:C:H3'	53:1:276:U:H5''	1.93	0.49
53:1:1110:G:H2'	53:1:1111:A:H8	1.78	0.49
1:b:148:GLY:HA2	1:b:188:ARG:HH12	1.78	0.49
5:f:71:LEU:HD13	5:f:74:MET:SD	2.52	0.49
11:l:105:ILE:HD12	11:l:105:ILE:N	2.28	0.49
21:v:21:ARG:HH22	54:2:77:U:H5'	1.78	0.49
41:Q:113:ARG:HH11	41:Q:121:PRO:HD2	1.76	0.49
52:3:950:U:H2'	52:3:951:G:C8	2.47	0.49
52:3:1277:C:H2'	52:3:1278:G:H5''	1.94	0.49
52:3:1330:U:H2'	52:3:1331:G:O4'	2.12	0.49
52:3:1486:G:H2'	52:3:1487:G:C8	2.48	0.49
53:1:184:C:H2'	53:1:185:G:C8	2.48	0.49
53:1:579:G:H4'	53:1:2018:G:H5''	1.93	0.49
53:1:799:G:H5''	53:1:800:A:H2'	1.94	0.49
53:1:2248:C:C2'	53:1:2249:U:H5'	2.43	0.49
2:c:2:ILE:HD13	2:c:90:PHE:CE2	2.48	0.49
3:d:46:GLN:HB2	3:d:86:ALA:HB1	1.94	0.49
7:h:58:THR:OG1	53:1:1107:G:H5'	2.13	0.49
7:h:73:LYS:HG3	7:h:117:LEU:HD21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:13:LEU:HD11	20:u:70:ALA:HB2	1.95	0.49
21:v:1:MET:SD	21:v:1:MET:N	2.85	0.49
32:H:1:GLY:HA3	52:3:1060:U:C5	2.47	0.49
33:I:67:LEU:HD22	52:3:546:A:OP2	2.12	0.49
34:J:45:VAL:HG22	34:J:46:GLY:N	2.27	0.49
35:K:3:HIS:N	35:K:92:THR:HG22	2.28	0.49
38:N:118:ARG:NH1	52:3:1233:G:H5'	2.28	0.49
41:Q:113:ARG:NH2	52:3:501:C:OP2	2.40	0.49
52:3:1027:C:H2'	52:3:1028:C:OP1	2.12	0.49
53:1:971:G:H2'	53:1:972:A:O4'	2.12	0.49
53:1:1474:U:H2'	53:1:1475:G:H5'	1.94	0.49
54:2:66:A:H4'	54:2:67:G:C8	2.48	0.49
1:b:7:PRO:O	53:1:1695:G:H1'	2.13	0.49
4:e:73:VAL:HG22	4:e:75:GLY:H	1.78	0.49
8:i:117:THR:CG2	53:1:1058:U:H1'	2.42	0.49
11:l:101:ILE:HG13	11:l:102:GLY:N	2.27	0.49
14:o:4:LYS:NZ	54:2:60:C:H4'	2.27	0.49
52:3:1412:C:H2'	52:3:1413:A:C8	2.48	0.49
53:1:873:C:H2'	53:1:874:G:C8	2.47	0.49
53:1:2638:G:H1'	53:1:2778:A:H61	1.77	0.49
53:1:2749:A:OP2	53:1:2751:G:H5''	2.13	0.49
8:i:72:THR:OG1	8:i:73:PRO:HD2	2.13	0.49
15:p:63:ILE:HA	15:p:68:GLY:HA2	1.95	0.49
16:q:82:LEU:HD22	16:q:87:VAL:HG21	1.95	0.49
27:C:29:LYS:HE2	53:1:2286:G:OP1	2.13	0.49
34:J:147:ASN:HD21	37:M:95:MET:HE1	1.77	0.49
38:N:5:TYR:HB2	38:N:20:ILE:HD11	1.95	0.49
40:P:71:ASP:HA	40:P:74:LYS:HD3	1.95	0.49
46:V:13:SER:HB3	46:V:21:VAL:CG1	2.43	0.49
52:3:70:U:H4'	52:3:71:A:H8	1.77	0.49
52:3:309:A:H2'	52:3:310:G:C8	2.48	0.49
53:1:2743:U:C3'	53:1:2744:G:H5''	2.42	0.49
55:5:47:U:H3'	55:5:48:C:C5'	2.43	0.49
8:i:133:ARG:HG2	53:1:1077:A:O2'	2.12	0.48
12:m:51:ARG:NH1	53:1:2483:C:H1'	2.28	0.48
13:n:1:MET:SD	13:n:1:MET:N	2.73	0.48
14:o:49:VAL:CG2	14:o:85:LYS:HG3	2.43	0.48
15:p:104:GLY:HA3	52:3:1432:G:OP1	2.13	0.48
20:u:34:ILE:HG12	20:u:63:ALA:HA	1.94	0.48
32:H:18:ASN:OD1	32:H:53:ARG:NH2	2.46	0.48
37:M:93:LYS:HE3	37:M:97:GLY:HA2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:40:ARG:NH2	52:3:1292:G:H5''	2.28	0.48
44:T:45:HIS:O	44:T:47:LYS:N	2.44	0.48
53:1:826:U:H2'	53:1:828:U:O4'	2.13	0.48
53:1:940:G:C3'	53:1:941:A:H5''	2.43	0.48
53:1:1028:A:N6	53:1:1125:G:H2'	2.28	0.48
53:1:1083:U:O2'	53:1:1084:A:H5'	2.13	0.48
53:1:2128:G:H1'	53:1:2173:A:N3	2.28	0.48
53:1:2404:U:H2'	53:1:2405:G:O4'	2.13	0.48
53:1:2623:G:H2'	53:1:2624:G:H8	1.78	0.48
4:e:31:GLU:H	4:e:157:THR:HA	1.77	0.48
21:v:49:ASN:OD1	53:1:1040:A:H5'	2.13	0.48
31:G:46:VAL:HG23	31:G:47:PRO:CD	2.41	0.48
34:J:76:ASN:HB2	34:J:81:GLN:CD	2.39	0.48
35:K:12:PRO:HA	35:K:15:SER:OG	2.13	0.48
39:O:76:ILE:H	39:O:76:ILE:HD12	1.78	0.48
50:Z:46:ARG:HA	50:Z:49:ALA:HB3	1.93	0.48
52:3:114:U:O2'	52:3:115:G:H5'	2.13	0.48
52:3:371:A:H2'	52:3:372:C:O4'	2.14	0.48
53:1:215:G:C4'	53:1:216:A:H4'	2.44	0.48
53:1:2004:G:H2'	53:1:2005:A:O4'	2.13	0.48
53:1:2818:U:H2'	53:1:2819:G:C8	2.47	0.48
2:c:150:GLN:NE2	53:1:574:A:N1	2.60	0.48
4:e:92:GLY:N	4:e:95:MET:HE2	2.29	0.48
12:m:117:PHE:HA	12:m:120:ALA:HB3	1.95	0.48
16:q:5:ARG:HD3	53:1:1250:G:H5''	1.95	0.48
17:r:46:GLU:N	17:r:46:GLU:OE2	2.46	0.48
51:a:57:GLN:NE2	51:a:203:GLN:HG3	2.28	0.48
52:3:112:G:H4'	52:3:389:A:H4'	1.95	0.48
52:3:1219:A:H2'	52:3:1220:G:C8	2.48	0.48
4:e:56:LEU:HD12	4:e:86:CYS:SG	2.53	0.48
4:e:153:ILE:HD12	4:e:153:ILE:N	2.28	0.48
11:l:36:LYS:HD2	11:l:36:LYS:N	2.28	0.48
16:q:49:ARG:HD3	17:r:72:VAL:HG11	1.95	0.48
18:s:61:ASN:ND2	53:1:495:G:H21	2.11	0.48
21:v:72:VAL:HG12	21:v:93:ARG:HA	1.95	0.48
30:F:4:ARG:HD2	53:1:2466:C:P	2.53	0.48
32:H:133:MET:O	32:H:137:VAL:HG23	2.14	0.48
33:I:108:ALA:HB3	33:I:112:GLU:CD	2.38	0.48
36:L:112:ASP:HB2	36:L:117:LEU:HD23	1.94	0.48
37:M:77:VAL:HG22	37:M:126:CYS:HA	1.93	0.48
39:O:67:ILE:HG13	39:O:67:ILE:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:P:28:ASN:ND2	40:P:30:ILE:HB	2.29	0.48
41:Q:113:ARG:NH1	41:Q:121:PRO:HD2	2.29	0.48
44:T:2:LEU:HD12	44:T:34:GLN:CD	2.38	0.48
44:T:57:ARG:HH21	52:3:742:G:C5'	2.27	0.48
45:U:6:LEU:HD22	45:U:17:TYR:HB3	1.94	0.48
52:3:352:C:H4'	52:3:354:G:OP1	2.13	0.48
1:b:198:GLU:HG3	1:b:201:LEU:HD12	1.95	0.48
2:c:121:THR:HG21	2:c:143:PRO:HB3	1.95	0.48
16:q:10:ARG:CZ	53:1:1216:G:H5''	2.43	0.48
17:r:15:SER:OG	17:r:18:GLN:NE2	2.47	0.48
21:v:45:ASP:CG	53:1:1039:A:H4'	2.38	0.48
32:H:4:VAL:HG22	32:H:5:HIS:H	1.78	0.48
37:M:50:VAL:HG22	37:M:50:VAL:O	2.13	0.48
39:O:56:HIS:ND1	39:O:57:VAL:HG13	2.27	0.48
43:S:39:ASP:O	43:S:42:ASN:HB2	2.13	0.48
49:Y:67:HIS:CB	52:3:262:A:H5'	2.43	0.48
50:Z:6:ARG:C	50:Z:8:ASN:H	2.21	0.48
52:3:406:G:O2'	52:3:407:U:H5'	2.13	0.48
53:1:2029:G:O6	53:1:2032:G:H5''	2.14	0.48
53:1:2244:U:H2'	53:1:2245:U:O4'	2.13	0.48
53:1:2515:C:H2'	53:1:2516:A:C8	2.49	0.48
55:6:26:G:H1	55:6:44:A:H61	1.61	0.48
4:e:24:VAL:HG12	54:2:55:U:C4'	2.44	0.48
6:g:40:THR:H	6:g:43:ASN:HD22	1.60	0.48
33:I:49:ASP:O	33:I:53:GLN:HG3	2.13	0.48
33:I:109:THR:OG1	33:I:112:GLU:HG3	2.12	0.48
34:J:131:ASN:HB3	34:J:134:ASN:HB2	1.94	0.48
46:V:42:LYS:HZ2	52:3:277:C:H5''	1.79	0.48
48:X:13:HIS:O	48:X:17:LYS:HG3	2.13	0.48
53:1:974:G:N3	53:1:974:G:H2'	2.29	0.48
53:1:2637:U:H2'	53:1:2638:G:O4'	2.13	0.48
53:1:2855:C:H2'	53:1:2856:A:C8	2.49	0.48
16:q:111:LYS:NZ	17:r:48:LYS:HG3	2.28	0.48
17:r:80:ARG:N	53:1:565:C:OP2	2.45	0.48
21:v:60:VAL:HA	21:v:73:LYS:HG3	1.95	0.48
26:B:52:LYS:HG3	26:B:52:LYS:O	2.13	0.48
39:O:24:GLU:OE1	39:O:92:LEU:HD22	2.14	0.48
52:3:31:G:N2	52:3:47:C:H5''	2.28	0.48
52:3:434:U:H2'	52:3:435:A:C8	2.49	0.48
52:3:1230:C:H2'	52:3:1231:G:H8	1.79	0.48
53:1:727:A:O2'	53:1:728:G:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:817:C:O2'	53:1:839:U:H5''	2.12	0.48
53:1:1796:U:H2'	53:1:1797:G:C8	2.45	0.48
54:2:88:C:C4'	54:2:89:U:OP1	2.61	0.48
2:c:49:GLN:NE2	2:c:79:LEU:HD13	2.28	0.48
4:e:76:PHE:HB3	53:1:2311:A:C4	2.49	0.48
7:h:56:ARG:O	53:1:1106:G:H4'	2.14	0.48
14:o:25:ARG:HD2	14:o:40:ILE:HD12	1.94	0.48
14:o:29:HIS:CD2	54:2:7:G:H4'	2.48	0.48
15:p:91:VAL:HG11	15:p:96:LEU:HD21	1.96	0.48
20:u:33:VAL:HG13	20:u:66:VAL:HG12	1.96	0.48
21:v:30:ILE:HD11	21:v:38:LEU:HB3	1.95	0.48
37:M:5:PRO:O	37:M:8:ASP:HB3	2.13	0.48
38:N:6:TYR:CE2	52:3:1147:C:H4'	2.48	0.48
42:R:52:ILE:HA	42:R:55:LEU:HD12	1.96	0.48
46:V:63:CYS:SG	46:V:64:ARG:N	2.84	0.48
52:3:163:C:H2'	52:3:164:G:O4'	2.13	0.48
53:1:343:C:O2'	53:1:344:A:H5'	2.14	0.48
53:1:1111:A:O2'	53:1:1112:G:H4'	2.13	0.48
53:1:2233:U:H2'	53:1:2234:G:C8	2.48	0.48
53:1:2834:G:O2'	53:1:2835:A:H5'	2.14	0.48
53:1:2861:U:H2'	53:1:2862:G:C8	2.49	0.48
54:2:30:C:H2'	54:2:31:C:O4'	2.14	0.48
2:c:88:GLU:OE1	2:c:88:GLU:N	2.47	0.48
4:e:65:LEU:CD1	54:2:41:G:H21	2.27	0.48
48:X:17:LYS:HE2	52:3:1014:A:OP2	2.13	0.48
51:a:5:THR:OG1	51:a:6:LYS:N	2.46	0.48
52:3:744:C:H2'	52:3:745:G:C8	2.49	0.48
53:1:1201:U:H2'	53:1:1202:G:H8	1.78	0.48
53:1:1420:A:H5'	53:1:1421:G:OP2	2.14	0.48
54:2:65:U:H3'	54:2:108:A:N6	2.26	0.48
57:7:46:G:O2'	57:7:48:C:H5'	2.14	0.48
6:g:11:ASN:HD21	53:1:2095:A:H4'	1.79	0.48
41:Q:82:ARG:HG2	41:Q:97:VAL:HG22	1.96	0.48
43:S:21:ALA:H	43:S:24:ALA:HB2	1.78	0.48
46:V:66:LEU:HB2	46:V:70:LYS:O	2.14	0.48
48:X:27:LYS:HD3	48:X:28:LYS:H	1.79	0.48
53:1:1326:U:H2'	53:1:1327:A:H8	1.79	0.48
53:1:1979:U:O2'	53:1:1980:G:H5'	2.14	0.48
1:b:73:ILE:HG12	53:1:1490:A:C6	2.48	0.47
4:e:147:ARG:HD3	4:e:148:VAL:N	2.26	0.47
9:j:84:ILE:HG23	9:j:84:ILE:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:115:ILE:HD12	10:k:115:ILE:N	2.29	0.47
11:l:30:THR:HG22	53:1:810:U:C4	2.49	0.47
13:n:8:ARG:N	13:n:8:ARG:HD2	2.29	0.47
17:r:58:VAL:O	17:r:58:VAL:HG13	2.14	0.47
18:s:81:SER:HB2	53:1:1261:C:OP1	2.14	0.47
31:G:117:GLU:O	31:G:121:GLN:HG2	2.13	0.47
34:J:108:GLY:O	34:J:109:ALA:HB3	2.14	0.47
35:K:51:ILE:O	35:K:52:ASN:CG	2.56	0.47
52:3:50:A:H4'	52:3:51:A:H5'	1.95	0.47
53:1:548:G:H2'	53:1:549:G:O4'	2.14	0.47
53:1:1802:A:H2'	53:1:1803:A:C8	2.48	0.47
53:1:2039:U:H2'	53:1:2040:G:H8	1.79	0.47
53:1:2297:A:N1	53:1:2321:U:H5	2.12	0.47
53:1:2704:C:H2'	53:1:2705:A:O4'	2.14	0.47
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.96	0.47
10:k:61:VAL:HG23	10:k:87:LEU:HD11	1.96	0.47
16:q:2:ARG:HB2	53:1:1248:G:C4	2.49	0.47
20:u:16:LYS:HE3	53:1:329:G:N2	2.28	0.47
26:B:54:ILE:HG13	26:B:56:LYS:HB3	1.96	0.47
32:H:156:LEU:HD22	32:H:156:LEU:H	1.78	0.47
36:L:129:ASN:HA	36:L:134:VAL:HG11	1.96	0.47
38:N:18:VAL:HG22	38:N:64:ILE:HG23	1.96	0.47
41:Q:81:ILE:HG13	41:Q:82:ARG:N	2.30	0.47
45:U:33:ILE:HD12	45:U:33:ILE:N	2.29	0.47
46:V:24:ILE:HD12	46:V:24:ILE:N	2.29	0.47
47:W:13:THR:OG1	47:W:18:GLN:N	2.46	0.47
47:W:24:ASP:O	47:W:28:LEU:HG	2.13	0.47
52:3:166:U:H2'	52:3:167:A:C8	2.49	0.47
52:3:1170:A:H2'	52:3:1171:A:O4'	2.14	0.47
52:3:1513:A:H2'	52:3:1514:G:H8	1.80	0.47
53:1:2743:U:H3'	53:1:2744:G:H5''	1.96	0.47
1:b:73:ILE:HD13	1:b:97:ASP:OD2	2.14	0.47
1:b:251:THR:OG1	1:b:252:LYS:N	2.48	0.47
10:k:99:ILE:HD11	10:k:119:ALA:HA	1.96	0.47
11:l:19:LEU:HD13	11:l:27:LEU:HD13	1.97	0.47
11:l:30:THR:HG22	53:1:810:U:O4	2.15	0.47
31:G:68:PHE:HE2	31:G:88:GLN:HB2	1.79	0.47
32:H:57:GLU:HG2	32:H:64:ARG:HH21	1.79	0.47
41:Q:120:ARG:NH1	52:3:500:G:H5'	2.29	0.47
43:S:23:ARG:HH21	43:S:26:LEU:HD21	1.79	0.47
49:Y:79:THR:HG21	52:3:186:C:O2'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:6:ARG:HG2	50:Z:8:ASN:N	2.27	0.47
52:3:982:U:H4'	52:3:983:A:O5'	2.13	0.47
52:3:1512:U:H2'	52:3:1513:A:C8	2.49	0.47
53:1:1111:A:H2'	53:1:1111:A:N3	2.28	0.47
53:1:1279:G:H2'	53:1:1280:G:C8	2.49	0.47
53:1:1367:A:C2'	53:1:1368:G:H5'	2.43	0.47
53:1:2215:C:H2'	53:1:2216:G:C8	2.49	0.47
53:1:2328:A:H2'	53:1:2329:U:C6	2.49	0.47
2:c:171:THR:HG21	53:1:2772:C:H4'	1.96	0.47
6:g:33:GLN:HB3	6:g:35:LYS:HE2	1.96	0.47
22:w:71:LYS:HE2	22:w:73:ARG:HE	1.79	0.47
24:y:31:GLN:CG	24:y:36:GLN:HB2	2.44	0.47
43:S:29:ILE:HD12	43:S:29:ILE:N	2.27	0.47
44:T:31:LEU:HD22	44:T:62:ARG:HD3	1.96	0.47
50:Z:6:ARG:O	50:Z:7:GLU:HB2	2.14	0.47
52:3:1346:A:C2'	52:3:1347:G:H4'	2.44	0.47
53:1:118:A:OP2	53:1:119:A:H5''	2.13	0.47
53:1:2480:C:H2'	53:1:2481:G:O4'	2.13	0.47
4:e:49:LEU:HD11	4:e:83:PRO:HB2	1.97	0.47
4:e:120:SER:HB3	4:e:127:TYR:CE1	2.49	0.47
7:h:58:THR:HG21	7:h:82:ILE:HG22	1.96	0.47
7:h:94:ARG:HD3	7:h:94:ARG:N	2.29	0.47
13:n:12:ARG:HH21	13:n:16:HIS:CE1	2.33	0.47
19:t:73:ARG:HG2	19:t:73:ARG:HH21	1.79	0.47
37:M:45:ILE:HD13	37:M:60:LEU:HD23	1.95	0.47
43:S:48:GLN:HB2	48:X:12:LEU:HB2	1.96	0.47
49:Y:67:HIS:CE1	52:3:132:C:H4'	2.49	0.47
52:3:784:A:H2'	52:3:785:G:H8	1.79	0.47
52:3:865:A:H5'	52:3:1078:U:O4	2.14	0.47
53:1:327:G:H2'	53:1:328:U:O4'	2.14	0.47
53:1:607:U:O4	53:1:620:G:H5'	2.13	0.47
54:2:78:A:H2'	54:2:79:G:O4'	2.15	0.47
4:e:32:LYS:NZ	53:1:2314:A:H5''	2.29	0.47
4:e:94:ARG:NH2	54:2:43:C:O3'	2.46	0.47
22:w:74:LYS:HD3	22:w:74:LYS:N	2.29	0.47
24:y:41:HIS:CE1	53:1:96:C:H4'	2.50	0.47
32:H:71:ARG:HD3	32:H:71:ARG:N	2.30	0.47
33:I:187:ARG:NE	33:I:196:GLU:OE2	2.47	0.47
34:J:82:HIS:HB2	34:J:83:PRO:HD2	1.97	0.47
45:U:38:PHE:CZ	52:3:626:G:H4'	2.49	0.47
47:W:52:ARG:HH22	52:3:835:U:H5''	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:868:C:H2'	52:3:869:G:O4'	2.14	0.47
52:3:1219:A:H2'	52:3:1220:G:H8	1.80	0.47
53:1:720:U:H2'	53:1:721:A:H8	1.79	0.47
53:1:1417:C:H4'	53:1:1587:G:H21	1.79	0.47
53:1:1765:U:H2'	53:1:1766:G:H8	1.78	0.47
53:1:2286:G:H4'	53:1:2287:A:O4'	2.15	0.47
55:6:41:C:H2'	55:6:42:G:C8	2.50	0.47
4:e:132:ARG:HG2	53:1:2305:U:O2'	2.15	0.47
9:j:78:THR:OG1	9:j:80:HIS:HB2	2.15	0.47
10:k:98:ARG:NH2	52:3:341:C:N4	2.63	0.47
16:q:93:ILE:HG13	17:r:4:VAL:HG21	1.97	0.47
18:s:74:ILE:HG23	18:s:74:ILE:O	2.15	0.47
19:t:68:LYS:HG2	19:t:69:ARG:N	2.30	0.47
22:w:73:ARG:HD2	22:w:75:PHE:CZ	2.49	0.47
32:H:23:ALA:HB1	32:H:27:GLU:HG2	1.96	0.47
33:I:63:ILE:O	33:I:110:ARG:HD2	2.15	0.47
42:R:64:VAL:HG12	42:R:65:GLU:N	2.23	0.47
44:T:31:LEU:HD13	44:T:62:ARG:HB2	1.96	0.47
45:U:13:LYS:HE3	52:3:392:C:H5'	1.95	0.47
49:Y:28:ARG:HH12	52:3:1437:A:C5'	2.28	0.47
52:3:58:C:O2'	52:3:59:A:H5'	2.15	0.47
52:3:337:G:H2'	52:3:338:A:C8	2.49	0.47
52:3:572:A:H5''	52:3:917:G:H4'	1.96	0.47
52:3:1054:C:C2	57:7:34:G:H1'	2.49	0.47
52:3:1513:A:H2'	52:3:1514:G:C8	2.49	0.47
53:1:45:G:C5'	53:1:46:G:H5'	2.17	0.47
53:1:69:C:O2'	53:1:70:G:H5'	2.15	0.47
53:1:1106:G:H2'	53:1:1107:G:O4'	2.14	0.47
53:1:1434:A:H2'	53:1:1435:G:C8	2.50	0.47
53:1:1912:A:H62	53:1:1917:U:H3	1.62	0.47
54:2:51:G:H2'	54:2:52:A:O4'	2.15	0.47
13:n:12:ARG:NE	13:n:40:LYS:HZ1	2.12	0.47
40:P:46:ALA:HB1	40:P:61:ALA:HB1	1.96	0.47
41:Q:69:GLU:HA	52:3:521:G:O5'	2.14	0.47
45:U:36:VAL:HG13	45:U:36:VAL:O	2.14	0.47
49:Y:50:PHE:HZ	49:Y:75:LYS:HG3	1.79	0.47
52:3:113:G:H2'	52:3:114:U:C6	2.49	0.47
52:3:396:C:H2'	52:3:397:A:H5''	1.97	0.47
52:3:1404:C:H2'	52:3:1405:G:H8	1.78	0.47
53:1:1300:G:C4'	53:1:1301:A:H5'	2.38	0.47
53:1:2471:A:H2'	53:1:2472:G:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2715:C:H3'	53:1:2716:C:H5''	1.97	0.47
7:h:30:SER:HB3	7:h:109:LYS:NZ	2.29	0.47
9:j:26:GLY:O	9:j:30:THR:HG22	2.15	0.47
10:k:88:ASN:HD22	10:k:93:GLN:HB2	1.80	0.47
18:s:29:VAL:HA	18:s:32:ALA:CB	2.45	0.47
21:v:56:PHE:CE1	21:v:61:LEU:HD21	2.50	0.47
32:H:126:ARG:HD3	32:H:126:ARG:N	2.30	0.47
32:H:146:LYS:HB2	32:H:202:PHE:CD2	2.50	0.47
33:I:1:ALA:HA	33:I:67:LEU:HD11	1.97	0.47
33:I:131:ILE:HD12	52:3:403:C:H5'	1.96	0.47
42:R:16:ILE:HD12	42:R:16:ILE:N	2.30	0.47
52:3:56:U:H2'	52:3:57:G:H8	1.80	0.47
52:3:331:G:OP1	52:3:332:G:H5''	2.15	0.47
52:3:1282:C:H2'	52:3:1283:U:C6	2.50	0.47
52:3:1401:G:H2'	52:3:1402:C:O4'	2.15	0.47
52:3:1432:G:H1'	52:3:1468:A:H62	1.80	0.47
53:1:254:G:C2'	53:1:255:A:H5''	2.44	0.47
53:1:1432:G:H2'	53:1:1433:A:C8	2.50	0.47
55:5:41:C:H2'	55:5:42:G:H8	1.80	0.47
1:b:77:VAL:HA	1:b:93:VAL:HA	1.96	0.47
2:c:98:VAL:HG22	2:c:98:VAL:O	2.15	0.47
2:c:129:THR:HG22	2:c:130:GLN:H	1.80	0.47
3:d:170:ARG:NH2	3:d:175:ILE:HA	2.28	0.47
5:f:28:LYS:HG2	5:f:79:THR:HA	1.96	0.47
7:h:24:SER:OG	7:h:116:GLU:HB2	2.15	0.47
9:j:18:VAL:HB	9:j:56:VAL:HG22	1.97	0.47
9:j:31:GLU:OE2	9:j:34:ARG:HD3	2.15	0.47
18:s:57:ASN:OD1	18:s:61:ASN:ND2	2.47	0.47
20:u:13:LEU:HD21	20:u:70:ALA:HB3	1.97	0.47
20:u:14:THR:HA	20:u:18:LYS:NZ	2.29	0.47
33:I:149:LYS:C	33:I:150:LYS:HG3	2.39	0.47
38:N:40:ARG:CZ	52:3:1292:G:H5''	2.45	0.47
40:P:71:ASP:O	40:P:72:ALA:HB3	2.15	0.47
41:Q:24:GLU:O	41:Q:25:ALA:HB3	2.15	0.47
52:3:24:U:H2'	52:3:25:C:C6	2.50	0.47
52:3:396:C:C3'	52:3:397:A:H5''	2.45	0.47
53:1:184:C:H2'	53:1:185:G:H8	1.79	0.47
57:7:50:U:O2'	57:7:51:U:H5'	2.15	0.47
2:c:43:ASP:HB3	2:c:45:TYR:CE1	2.51	0.46
2:c:91:THR:OG1	2:c:92:VAL:N	2.48	0.46
2:c:167:ASN:HD21	53:1:2822:G:P	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:38:MET:HE2	8:i:117:THR:HG21	1.96	0.46
23:x:15:ASN:ND2	53:1:381:G:H5''	2.30	0.46
24:y:9:LYS:HG3	24:y:12:GLU:H	1.80	0.46
25:z:45:GLY:HA3	53:1:852:U:H5'	1.96	0.46
32:H:120:THR:HG23	32:H:188:ALA:HB2	1.96	0.46
38:N:48:ARG:HA	38:N:51:LEU:HD12	1.97	0.46
40:P:32:THR:HG23	40:P:42:GLY:O	2.15	0.46
52:3:211:G:H2'	52:3:212:G:H5'	1.97	0.46
52:3:580:C:H2'	52:3:581:G:O4'	2.15	0.46
52:3:665:A:O4'	52:3:733:G:H1'	2.16	0.46
53:1:694:U:C3'	53:1:695:G:H5''	2.45	0.46
53:1:2376:A:H2'	53:1:2377:A:O4'	2.16	0.46
2:c:13:ARG:HA	2:c:24:VAL:HG22	1.97	0.46
3:d:123:LYS:HD2	3:d:123:LYS:O	2.14	0.46
10:k:12:ASP:OD2	10:k:85:VAL:HG13	2.16	0.46
38:N:129:ARG:NH1	55:5:32:C:OP2	2.49	0.46
51:a:46:VAL:HG13	51:a:212:VAL:HG22	1.97	0.46
52:3:235:C:H2'	52:3:236:A:C8	2.49	0.46
52:3:971:G:H1'	52:3:1365:G:O2'	2.16	0.46
52:3:1016:A:H4'	52:3:1218:C:H4'	1.97	0.46
53:1:1909:C:H2'	53:1:1910:G:H8	1.79	0.46
53:1:2238:G:H2'	53:1:2238:G:N3	2.30	0.46
54:2:28:C:H2'	54:2:29:A:C8	2.50	0.46
55:5:41:C:H2'	55:5:42:G:C8	2.49	0.46
1:b:204:LEU:HD12	1:b:209:ALA:HB1	1.96	0.46
3:d:40:ARG:HD2	53:1:443:A:C5	2.51	0.46
8:i:12:VAL:HA	53:1:1061:U:N3	2.25	0.46
20:u:94:PHE:HB2	20:u:100:GLU:O	2.15	0.46
24:y:2:LYS:HD3	53:1:78:U:OP1	2.15	0.46
33:I:152:SER:H	33:I:155:LYS:HZ3	1.64	0.46
35:K:11:HIS:HB3	35:K:13:ASP:OD1	2.16	0.46
35:K:49:TYR:OH	35:K:86:ARG:NH1	2.48	0.46
36:L:142:ARG:HG2	55:6:41:C:H4'	1.96	0.46
46:V:25:GLU:OE1	46:V:38:LYS:HG2	2.15	0.46
49:Y:28:ARG:HH12	52:3:1437:A:P	2.39	0.46
53:1:1201:U:H2'	53:1:1202:G:C8	2.50	0.46
53:1:2743:U:H2'	53:1:2744:G:H5''	1.97	0.46
1:b:162:GLN:NE2	52:3:713:G:OP1	2.48	0.46
10:k:113:MET:HE3	10:k:116:ILE:HG13	1.96	0.46
11:l:93:ASN:C	11:l:95:LEU:H	2.23	0.46
12:m:20:LEU:H	12:m:20:LEU:CD2	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:75:VAL:HG22	17:r:86:GLN:OE1	2.15	0.46
17:r:83:TYR:CE1	53:1:1187:G:H5''	2.51	0.46
35:K:52:ASN:HD21	35:K:85:ILE:HD13	1.80	0.46
36:L:45:ALA:HA	36:L:48:THR:OG1	2.15	0.46
38:N:42:THR:HA	38:N:44:ARG:HH11	1.81	0.46
39:O:16:ARG:O	39:O:20:GLN:HG2	2.16	0.46
45:U:67:ILE:HG13	45:U:71:VAL:HG23	1.98	0.46
50:Z:64:ALA:C	50:Z:66:ARG:H	2.24	0.46
52:3:629:A:H2'	52:3:630:A:O4'	2.16	0.46
52:3:662:U:H2'	52:3:663:A:C8	2.50	0.46
53:1:145:C:H2'	53:1:146:A:C8	2.51	0.46
53:1:581:C:H2'	53:1:582:A:C8	2.51	0.46
53:1:1322:A:N6	53:1:1333:G:H21	2.12	0.46
53:1:2036:C:H2'	53:1:2037:A:H8	1.80	0.46
53:1:2570:G:H2'	53:1:2571:U:O4'	2.16	0.46
54:2:78:A:H62	54:2:98:G:H21	1.62	0.46
24:y:24:GLU:HG3	24:y:46:VAL:HG11	1.98	0.46
31:G:134:LEU:HG	31:G:138:ARG:HE	1.81	0.46
32:H:81:GLU:O	32:H:85:LYS:HG2	2.16	0.46
40:P:114:PRO:CB	52:3:676:A:H5''	2.46	0.46
42:R:73:SER:O	42:R:77:LYS:HG2	2.16	0.46
52:3:1230:C:H2'	52:3:1231:G:C8	2.51	0.46
52:3:1372:U:H2'	52:3:1373:G:O4'	2.15	0.46
53:1:703:U:H2'	53:1:704:G:O4'	2.15	0.46
53:1:2665:A:O2'	53:1:2666:C:H5'	2.16	0.46
1:b:47:ARG:HH21	53:1:774:G:H5''	1.80	0.46
1:b:136:VAL:HB	1:b:166:ARG:HH11	1.81	0.46
12:m:55:ARG:HD2	53:1:2469:A:H4'	1.96	0.46
16:q:3:VAL:HG12	53:1:1199:U:H1'	1.97	0.46
25:z:29:ARG:CZ	53:1:1183:U:H5''	2.46	0.46
27:C:41:VAL:HG13	27:C:42:VAL:N	2.30	0.46
35:K:18:VAL:HG12	35:K:19:PRO:HD3	1.98	0.46
42:R:104:ASN:O	42:R:105:ALA:HB3	2.16	0.46
43:S:5:MET:HG2	43:S:8:ARG:NH2	2.27	0.46
45:U:43:ALA:O	45:U:44:SER:HB2	2.15	0.46
52:3:225:C:C3'	52:3:226:G:H5''	2.46	0.46
53:1:1055:G:H1'	53:1:1084:A:H61	1.81	0.46
53:1:2210:U:H4'	53:1:2211:A:C2	2.51	0.46
53:1:2795:C:H2'	53:1:2796:U:O4'	2.16	0.46
3:d:129:PRO:HB3	3:d:159:LEU:HD12	1.98	0.46
4:e:129:MET:SD	4:e:130:GLY:N	2.89	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:55:GLU:O	6:g:58:LEU:HB3	2.16	0.46
10:k:6:THR:CG2	53:1:1666:G:H4'	2.43	0.46
16:q:5:ARG:NH1	53:1:585:G:N7	2.64	0.46
17:r:47:VAL:O	17:r:47:VAL:HG12	2.15	0.46
23:x:65:THR:O	23:x:69:GLU:HG3	2.16	0.46
27:C:20:TYR:OH	53:1:2348:U:H5'	2.16	0.46
33:I:81:LEU:HD13	33:I:88:ASN:ND2	2.31	0.46
34:J:9:GLU:OE1	34:J:9:GLU:N	2.49	0.46
37:M:60:LEU:HD12	37:M:60:LEU:N	2.30	0.46
43:S:40:ARG:HH12	48:X:6:LYS:HG3	1.80	0.46
52:3:945:G:H2'	52:3:945:G:N3	2.30	0.46
53:1:532:A:H2'	53:1:532:A:N3	2.31	0.46
53:1:814:C:H1'	53:1:1225:G:N2	2.31	0.46
53:1:968:C:H2'	53:1:969:G:C8	2.51	0.46
53:1:996:A:H2'	53:1:997:G:C8	2.51	0.46
53:1:1021:A:H2'	53:1:1022:G:H4'	1.98	0.46
53:1:1900:A:H1'	53:1:1970:A:H2'	1.97	0.46
53:1:2030:A:N3	53:1:2499:C:H5''	2.30	0.46
53:1:2248:C:H2'	53:1:2249:U:H5'	1.97	0.46
53:1:2417:C:H2'	53:1:2418:A:H8	1.81	0.46
55:6:21:A:O2'	55:6:22:G:C8	2.68	0.46
1:b:42:ARG:HH12	53:1:691:C:H4'	1.80	0.46
1:b:157:ALA:HB1	1:b:196:ASN:O	2.16	0.46
2:c:105:LYS:O	2:c:177:VAL:HG12	2.15	0.46
3:d:21:ARG:HG2	3:d:22:ASP:N	2.31	0.46
7:h:33:VAL:HG13	7:h:35:VAL:N	2.28	0.46
7:h:40:GLU:O	7:h:43:LYS:HB3	2.16	0.46
16:q:50:ARG:NH2	53:1:993:G:OP2	2.48	0.46
33:I:112:GLU:OE2	52:3:408:A:H4'	2.16	0.46
37:M:17:GLN:HE21	37:M:71:VAL:HB	1.81	0.46
49:Y:9:ARG:HA	49:Y:12:GLN:CG	2.45	0.46
52:3:952:U:H2'	52:3:953:G:H8	1.81	0.46
52:3:1496:C:H1'	52:3:1517:G:H22	1.81	0.46
53:1:1268:A:H2'	53:1:1269:A:O4'	2.15	0.46
53:1:1786:A:H1'	53:1:1938:A:N6	2.31	0.46
53:1:2263:C:H2'	53:1:2264:C:O4'	2.16	0.46
7:h:118:ILE:N	7:h:119:PRO:CD	2.79	0.46
9:j:109:LEU:HD12	9:j:109:LEU:O	2.16	0.46
12:m:119:LEU:HD22	53:1:2468:A:C5'	2.39	0.46
17:r:32:THR:OG1	17:r:60:LYS:HE3	2.15	0.46
34:J:104:ILE:O	34:J:104:ILE:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:142:ARG:HB3	55:6:41:C:H4'	1.96	0.46
46:V:58:VAL:HG22	46:V:59:GLU:N	2.30	0.46
49:Y:49:ALA:O	49:Y:52:GLU:HG3	2.16	0.46
52:3:86:G:H4'	52:3:87:C:C5	2.51	0.46
52:3:130:A:O2'	52:3:264:C:H5'	2.16	0.46
52:3:1288:A:O2'	52:3:1353:G:H5'	2.16	0.46
53:1:399:U:OP1	53:1:2090:A:H5''	2.16	0.46
53:1:558:U:H2'	53:1:559:G:H8	1.80	0.46
2:c:77:ARG:HH21	2:c:77:ARG:HG3	1.80	0.46
5:f:5:LYS:HZ3	53:1:1110:G:H4'	1.80	0.46
18:s:22:ASP:HA	18:s:25:ARG:HD2	1.98	0.46
34:J:54:GLU:HG2	34:J:56:PRO:CD	2.33	0.46
37:M:80:PRO:CG	52:3:878:A:H5'	2.36	0.46
38:N:11:ARG:HD3	38:N:12:LYS:HB2	1.98	0.46
39:O:40:ILE:HB	39:O:73:LEU:HB3	1.96	0.46
43:S:31:SER:HA	43:S:40:ARG:NH2	2.31	0.46
49:Y:26:MET:HG3	52:3:1457:G:H4'	1.98	0.46
52:3:663:A:H5'	52:3:836:G:OP1	2.16	0.46
52:3:966:G:C2	55:5:34:C:H5'	2.51	0.46
52:3:981:U:H2'	52:3:982:U:C5	2.51	0.46
52:3:1435:G:H2'	52:3:1436:U:C6	2.51	0.46
53:1:468:G:H2'	53:1:469:G:O4'	2.16	0.46
53:1:818:G:O2'	53:1:819:A:H5''	2.17	0.46
53:1:2048:G:H3'	53:1:2049:G:H5''	1.96	0.46
53:1:2512:C:H2'	53:1:2513:A:O4'	2.16	0.46
3:d:148:ILE:CG2	3:d:157:LEU:HD21	2.46	0.45
7:h:54:VAL:O	7:h:54:VAL:HG22	2.16	0.45
7:h:117:LEU:O	7:h:118:ILE:HB	2.14	0.45
23:x:63:ILE:HD12	23:x:63:ILE:N	2.25	0.45
29:E:6:VAL:HG21	29:E:60:CYS:HB2	1.98	0.45
32:H:54:ILE:HG22	32:H:67:ILE:HG23	1.98	0.45
33:I:150:LYS:O	33:I:150:LYS:HD2	2.16	0.45
35:K:46:GLN:HA	35:K:56:LYS:HG2	1.98	0.45
35:K:67:PRO:O	35:K:70:VAL:HG12	2.16	0.45
43:S:39:ASP:HA	43:S:42:ASN:HD22	1.80	0.45
51:a:15:VAL:HG11	51:a:222:VAL:HG22	1.97	0.45
52:3:338:A:H2	52:3:351:G:H22	1.63	0.45
53:1:167:A:H2'	53:1:168:G:O4'	2.17	0.45
53:1:1424:G:H2'	53:1:1425:G:O4'	2.16	0.45
53:1:1528:A:H2'	53:1:1529:G:O4'	2.16	0.45
8:i:30:GLN:HG2	8:i:60:VAL:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:p:4:ILE:O	15:p:8:GLU:HG3	2.16	0.45
21:v:9:ARG:HB2	21:v:39:ALA:HB1	1.99	0.45
23:x:16:ASN:HB2	23:x:26:ARG:HD2	1.99	0.45
23:x:63:ILE:H	23:x:63:ILE:CD1	2.24	0.45
26:B:3:GLN:NE2	53:1:2016:U:O2	2.48	0.45
33:I:119:HIS:HB3	52:3:438:U:H4'	1.98	0.45
36:L:41:ILE:HD11	52:3:1240:U:O4'	2.16	0.45
45:U:22:ALA:HB2	45:U:32:PHE:CB	2.45	0.45
46:V:39:ARG:NH1	52:3:237:G:H5''	2.32	0.45
52:3:67:C:H2'	52:3:68:G:C8	2.51	0.45
53:1:406:G:H2'	53:1:407:G:C8	2.51	0.45
53:1:1430:G:H2'	53:1:1431:A:O4'	2.16	0.45
53:1:2297:A:N6	53:1:2319:G:H1'	2.31	0.45
2:c:34:VAL:HA	2:c:50:VAL:HG12	1.98	0.45
8:i:121:ILE:H	8:i:121:ILE:CD1	2.26	0.45
12:m:36:VAL:HG22	12:m:127:LYS:O	2.16	0.45
26:B:13:GLY:HA3	53:1:16:C:H5''	1.98	0.45
30:F:7:VAL:HG23	53:1:1032:A:H5'	1.98	0.45
31:G:82:ALA:HB2	31:G:213:LEU:HD13	1.98	0.45
33:I:199:ILE:HD12	33:I:199:ILE:N	2.31	0.45
35:K:10:VAL:HG12	35:K:84:VAL:HA	1.98	0.45
36:L:48:THR:O	36:L:52:ARG:HG3	2.16	0.45
37:M:113:ARG:HD2	37:M:113:ARG:O	2.16	0.45
49:Y:19:HIS:O	49:Y:23:ARG:HG3	2.16	0.45
52:3:513:C:H2'	52:3:514:C:C6	2.50	0.45
52:3:825:A:H2'	52:3:826:C:C6	2.50	0.45
52:3:939:G:H21	52:3:1375:A:H2	1.63	0.45
53:1:214:G:H2'	53:1:215:G:C8	2.51	0.45
53:1:594:U:H2'	53:1:595:C:C6	2.51	0.45
53:1:940:G:H3'	53:1:941:A:H5''	1.99	0.45
53:1:1161:C:H2'	53:1:1162:G:H8	1.81	0.45
53:1:1801:A:N6	53:1:2202:U:H5'	2.31	0.45
53:1:2834:G:H2'	53:1:2879:A:N6	2.30	0.45
1:b:204:LEU:N	1:b:204:LEU:HD22	2.31	0.45
2:c:46:ARG:NH1	2:c:86:GLU:HA	2.32	0.45
3:d:176:ASP:O	3:d:180:LEU:HD12	2.16	0.45
14:o:33:ARG:NH2	54:2:52:A:N7	2.65	0.45
15:p:54:LEU:HA	15:p:76:HIS:CD2	2.51	0.45
15:p:103:THR:OG1	15:p:104:GLY:N	2.49	0.45
24:y:23:ARG:CG	24:y:24:GLU:N	2.74	0.45
31:G:44:LYS:O	31:G:47:PRO:HD2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:60:VAL:HA	33:I:63:ILE:HD12	1.98	0.45
41:Q:29:LYS:HB3	41:Q:56:LEU:HD22	1.98	0.45
44:T:44:GLU:C	44:T:46:LYS:H	2.25	0.45
48:X:9:PHE:CD2	52:3:1318:A:H4'	2.50	0.45
52:3:779:C:H2'	52:3:780:A:O4'	2.17	0.45
52:3:1499:A:O2'	52:3:1520:C:H5'	2.16	0.45
53:1:2515:C:H2'	53:1:2516:A:H8	1.81	0.45
57:7:17:C:O5'	57:7:18:G:H5''	2.16	0.45
5:f:72:ASN:O	5:f:75:VAL:HG12	2.16	0.45
11:l:91:ASP:OD1	11:l:92:LEU:HG	2.16	0.45
12:m:71:LYS:HB3	12:m:93:VAL:O	2.16	0.45
13:n:73:ASN:HA	13:n:76:VAL:HG12	1.97	0.45
16:q:35:PHE:O	16:q:38:VAL:HG12	2.17	0.45
26:B:30:ASP:HB3	26:B:34:GLY:N	2.31	0.45
32:H:13:ILE:HG13	52:3:1113:C:H4'	1.98	0.45
52:3:273:U:H2'	52:3:274:A:H5'	1.98	0.45
52:3:764:C:H2'	52:3:765:G:O4'	2.16	0.45
52:3:1230:C:H5''	55:5:30:G:C5'	2.46	0.45
52:3:1308:U:H2'	52:3:1309:G:C8	2.51	0.45
52:3:1516:G:H2'	52:3:1518:A:OP2	2.17	0.45
53:1:171:U:H2'	53:1:172:A:H8	1.82	0.45
53:1:542:C:C2'	53:1:543:G:H5''	2.46	0.45
53:1:1083:U:H2'	53:1:1085:A:OP2	2.16	0.45
53:1:1542:U:H2'	53:1:1543:G:O4'	2.17	0.45
53:1:1637:A:H5'	53:1:1760:C:O2'	2.17	0.45
53:1:2215:C:H2'	53:1:2216:G:H8	1.82	0.45
53:1:2372:U:H2'	53:1:2373:G:H8	1.82	0.45
53:1:2514:U:H2'	53:1:2515:C:C6	2.51	0.45
54:2:49:C:H2'	54:2:50:A:C8	2.51	0.45
54:2:114:C:H2'	54:2:115:A:C8	2.51	0.45
12:m:122:ALA:HB1	53:1:2467:C:C1'	2.46	0.45
12:m:122:ALA:HB1	53:1:2467:C:H1'	1.99	0.45
20:u:85:ARG:HG3	20:u:92:VAL:HG23	1.97	0.45
33:I:86:GLY:HA3	33:I:196:GLU:HG3	1.98	0.45
34:J:98:ALA:HB2	34:J:123:LEU:CD1	2.47	0.45
41:Q:51:VAL:HG11	41:Q:89:LEU:HD22	1.98	0.45
48:X:14:LEU:HD23	48:X:17:LYS:HD2	1.99	0.45
51:a:33:LEU:HB3	51:a:219:GLY:HA2	1.98	0.45
52:3:929:G:H5''	52:3:1534:A:O2'	2.17	0.45
53:1:202:U:H2'	53:1:203:A:O4'	2.16	0.45
53:1:890:C:H2'	53:1:891:G:H5'	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1330:C:H2'	53:1:1331:G:C8	2.52	0.45
53:1:1386:C:H2'	53:1:1387:A:C8	2.51	0.45
53:1:1536:C:H4'	53:1:1537:G:C2	2.52	0.45
53:1:2471:A:O2'	57:7:64:A:H4'	2.16	0.45
2:c:49:GLN:HG2	2:c:79:LEU:HD22	1.98	0.45
2:c:118:PHE:HZ	53:1:2048:G:H21	1.65	0.45
9:j:81:ILE:HG23	9:j:82:GLY:H	1.82	0.45
13:n:107:ASN:HD22	53:1:2009:A:H4'	1.82	0.45
19:t:15:HIS:HE1	19:t:17:SER:HB3	1.80	0.45
20:u:95:PHE:O	20:u:99:SER:HA	2.16	0.45
31:G:192:PRO:HB2	31:G:198:VAL:HG11	1.99	0.45
32:H:89:VAL:HA	32:H:92:ASP:OD2	2.17	0.45
33:I:80:ARG:HH21	52:3:613:C:P	2.39	0.45
33:I:168:THR:HG22	33:I:182:LYS:NZ	2.31	0.45
34:J:92:ARG:O	34:J:93:VAL:C	2.59	0.45
34:J:104:ILE:HD11	34:J:114:LEU:HD13	1.98	0.45
35:K:6:ILE:HB	35:K:62:MET:SD	2.56	0.45
39:O:55:PRO:HA	43:S:80:ARG:HH22	1.82	0.45
42:R:9:PRO:HG2	42:R:44:ILE:CD1	2.46	0.45
52:3:1033:G:C3'	52:3:1034:G:H5''	2.47	0.45
52:3:1225:A:H2'	52:3:1225:A:N3	2.32	0.45
53:1:466:A:H2'	53:1:467:G:H5'	1.99	0.45
53:1:1020:A:C1'	53:1:1021:A:OP2	2.59	0.45
53:1:1114:C:H2'	53:1:1115:G:C8	2.52	0.45
53:1:2339:C:H2'	53:1:2340:A:C8	2.51	0.45
53:1:2556:C:H2'	53:1:2557:G:O4'	2.16	0.45
53:1:2715:C:C2'	53:1:2716:C:H5''	2.47	0.45
54:2:60:C:H2'	54:2:61:G:C8	2.52	0.45
57:7:59:U:H2'	57:7:60:U:H5'	1.98	0.45
1:b:255:LYS:HD3	1:b:269:ARG:NH2	2.32	0.45
7:h:59:LEU:HD22	7:h:62:ARG:HH21	1.81	0.45
7:h:74:ASP:OD1	7:h:117:LEU:HD13	2.17	0.45
12:m:3:GLN:HA	12:m:4:PRO:HD3	1.79	0.45
13:n:34:ILE:HG13	13:n:113:ILE:HG23	1.98	0.45
15:p:108:ARG:NH1	52:3:1464:U:OP1	2.50	0.45
17:r:32:THR:HA	17:r:62:GLU:HA	1.98	0.45
19:t:69:ARG:HA	19:t:74:ILE:HA	1.97	0.45
26:B:30:ASP:HB3	26:B:34:GLY:H	1.82	0.45
32:H:98:ALA:HB1	32:H:100:ILE:HD11	1.99	0.45
38:N:94:ARG:HA	38:N:97:LEU:HD13	1.98	0.45
45:U:24:SER:OG	52:3:377:G:H5''	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:213:SER:HA	51:a:223:ALA:HA	1.99	0.45
53:1:433:C:O2'	53:1:434:U:H5'	2.17	0.45
53:1:467:G:O2'	53:1:468:G:H5'	2.16	0.45
53:1:490:C:H4'	53:1:491:G:OP2	2.16	0.45
53:1:1765:U:H2'	53:1:1766:G:C8	2.52	0.45
1:b:100:ARG:NH1	1:b:100:ARG:HG3	2.31	0.45
4:e:137:PHE:HB2	4:e:140:ILE:HD13	1.99	0.45
8:i:25:PRO:HB2	53:1:1095:A:H61	1.81	0.45
19:t:55:VAL:HG12	19:t:87:LEU:HD12	1.99	0.45
24:y:4:LYS:HD2	24:y:5:GLU:HG2	1.98	0.45
27:C:30:PRO:HG2	27:C:31:GLU:OE1	2.17	0.45
35:K:91:ARG:HG2	52:3:737:C:OP1	2.16	0.45
36:L:2:ARG:HD2	52:3:1380:U:C4	2.52	0.45
38:N:17:ARG:HH12	52:3:1129:C:H4'	1.80	0.45
39:O:68:ARG:HB3	39:O:70:HIS:CE1	2.52	0.45
42:R:103:THR:HG22	52:3:1229:A:N6	2.32	0.45
52:3:591:U:H2'	52:3:592:G:C8	2.52	0.45
53:1:320:A:H4'	53:1:322:A:N7	2.31	0.45
53:1:962:G:H21	53:1:2250:G:H1	1.62	0.45
53:1:1301:A:H2'	53:1:1301:A:N3	2.32	0.45
53:1:1474:U:C2'	53:1:1475:G:H5'	2.47	0.45
53:1:2417:C:H2'	53:1:2418:A:C8	2.52	0.45
53:1:2743:U:H2'	53:1:2744:G:O4'	2.16	0.45
54:2:49:C:H2'	54:2:50:A:H8	1.82	0.45
1:b:257:ARG:NH2	1:b:266:ILE:HD11	2.31	0.45
2:c:149:ASN:HB2	53:1:2574:G:O2'	2.17	0.45
19:t:39:THR:O	19:t:43:ILE:HG13	2.17	0.45
34:J:120:HIS:H	34:J:121:ASN:HD22	1.65	0.45
52:3:393:A:H5'	52:3:483:C:O2'	2.17	0.45
53:1:438:G:H2'	53:1:439:A:C8	2.52	0.45
53:1:1709:U:H2'	53:1:1710:G:C8	2.52	0.45
53:1:2139:U:H2'	53:1:2140:G:C8	2.52	0.45
53:1:2799:A:H2'	53:1:2800:A:H5'	1.98	0.45
54:2:39:A:H2'	54:2:40:U:C6	2.52	0.45
54:2:88:C:C5'	54:2:89:U:OP1	2.65	0.45
1:b:100:ARG:HG3	1:b:100:ARG:HH11	1.81	0.44
3:d:1:MET:HE3	3:d:19:PHE:O	2.16	0.44
5:f:86:LEU:HA	5:f:163:TYR:HA	1.99	0.44
10:k:13:ASN:ND2	52:3:339:C:OP2	2.31	0.44
15:p:26:GLU:HA	15:p:43:GLU:HA	1.99	0.44
21:v:51:GLN:OE1	21:v:86:LEU:HD11	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:149:LYS:O	33:I:150:LYS:HG3	2.17	0.44
33:I:167:PRO:HG2	33:I:170:LEU:HD11	1.99	0.44
35:K:91:ARG:HA	35:K:91:ARG:HE	1.83	0.44
36:L:30:MET:HG3	36:L:35:LYS:HA	1.98	0.44
40:P:125:LYS:HB2	52:3:797:C:OP2	2.16	0.44
44:T:47:LYS:HD3	44:T:49:HIS:NE2	2.31	0.44
49:Y:79:THR:CG2	52:3:187:G:H5'	2.47	0.44
52:3:79:G:O2'	52:3:80:A:H5'	2.17	0.44
52:3:243:A:H4'	52:3:244:U:H3'	1.99	0.44
52:3:1405:G:O2'	52:3:1406:U:H5'	2.17	0.44
53:1:274:C:H2'	53:1:275:C:O4'	2.17	0.44
53:1:732:C:H2'	53:1:733:G:O4'	2.17	0.44
53:1:2428:G:H5''	53:1:2429:G:O5'	2.17	0.44
53:1:2498:C:O2'	53:1:2499:C:H5'	2.17	0.44
53:1:2798:U:H4'	53:1:2799:A:C4	2.52	0.44
53:1:2875:C:H2'	53:1:2876:G:C8	2.52	0.44
1:b:116:GLN:HE22	1:b:124:LYS:CE	2.30	0.44
7:h:118:ILE:HA	7:h:118:ILE:HD12	1.58	0.44
17:r:31:GLU:N	17:r:31:GLU:OE2	2.50	0.44
17:r:46:GLU:H	17:r:46:GLU:CD	2.26	0.44
29:E:18:LYS:HB3	53:1:651:G:OP1	2.17	0.44
29:E:21:PHE:O	29:E:49:VAL:HG23	2.16	0.44
35:K:13:ASP:OD2	35:K:14:GLN:NE2	2.49	0.44
38:N:105:ARG:O	38:N:105:ARG:HD3	2.17	0.44
52:3:948:C:H2'	52:3:949:A:C8	2.51	0.44
52:3:1220:G:H2'	52:3:1221:G:O4'	2.17	0.44
53:1:996:A:H2'	53:1:997:G:H8	1.82	0.44
53:1:2623:G:H2'	53:1:2624:G:C8	2.51	0.44
53:1:2774:C:H2'	53:1:2775:G:O4'	2.17	0.44
55:6:6:G:O2'	55:6:7:G:H5'	2.18	0.44
2:c:23:PRO:HD2	2:c:190:LYS:HE3	1.99	0.44
7:h:126:LEU:HD13	7:h:129:LEU:HD11	1.99	0.44
8:i:3:LYS:HD2	8:i:4:VAL:N	2.32	0.44
12:m:67:VAL:HG22	12:m:68:PHE:N	2.32	0.44
19:t:73:ARG:HG2	19:t:73:ARG:NH2	2.31	0.44
33:I:43:ARG:HG3	33:I:44:LYS:N	2.33	0.44
33:I:199:ILE:HD12	33:I:199:ILE:H	1.83	0.44
36:L:17:PHE:HE1	36:L:46:LEU:HD21	1.82	0.44
37:M:76:ARG:HH12	37:M:125:ILE:HG23	1.83	0.44
38:N:118:ARG:HB2	38:N:122:ARG:NE	2.32	0.44
41:Q:25:ALA:HA	52:3:553:A:O2'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:2:ARG:NE	42:R:8:ILE:HD11	2.17	0.44
51:a:6:LYS:HG3	51:a:7:ARG:H	1.82	0.44
52:3:205:A:H2'	52:3:206:C:O4'	2.17	0.44
52:3:1289:A:H2'	52:3:1290:G:H5'	1.99	0.44
52:3:1328:C:H2'	52:3:1329:A:O4'	2.18	0.44
53:1:713:G:H21	53:1:718:A:H62	1.64	0.44
53:1:2229:U:H2'	53:1:2230:G:H8	1.82	0.44
53:1:2313:C:H2'	53:1:2314:A:H8	1.81	0.44
53:1:2372:U:H2'	53:1:2373:G:C8	2.52	0.44
53:1:2412:A:H2'	53:1:2413:G:O4'	2.17	0.44
3:d:40:ARG:HH12	53:1:1246:A:H4'	1.83	0.44
6:g:58:LEU:O	6:g:61:VAL:HG12	2.18	0.44
7:h:31:ARG:HH22	53:1:1053:C:C2'	2.31	0.44
12:m:77:PRO:HB2	12:m:80:VAL:HG21	1.98	0.44
13:n:12:ARG:HH11	13:n:40:LYS:HZ2	1.65	0.44
14:o:107:ALA:HB1	14:o:117:PHE:HZ	1.83	0.44
17:r:28:ALA:HB3	17:r:31:GLU:OE2	2.17	0.44
32:H:166:TRP:HZ3	32:H:168:ARG:HD3	1.83	0.44
33:I:123:MET:HG3	33:I:127:ARG:C	2.42	0.44
39:O:64:GLN:OE1	39:O:64:GLN:N	2.51	0.44
52:3:487:A:H2'	52:3:488:C:O4'	2.17	0.44
52:3:976:G:N2	52:3:1362:A:H2'	2.33	0.44
52:3:1008:U:H2'	52:3:1009:U:O4'	2.17	0.44
53:1:581:C:H2'	53:1:582:A:H8	1.82	0.44
53:1:2633:G:H5'	53:1:2811:G:O2'	2.17	0.44
53:1:2692:G:H2'	53:1:2693:G:C8	2.52	0.44
55:6:72:A:H2'	55:6:73:A:O4'	2.17	0.44
1:b:52:HIS:CE1	1:b:218:THR:HG22	2.52	0.44
1:b:136:VAL:HG13	1:b:163:ILE:CG2	2.45	0.44
1:b:203:VAL:HG23	53:1:1792:G:H5''	2.00	0.44
6:g:1:MET:HG3	6:g:3:VAL:HG23	1.99	0.44
9:j:35:ARG:HD3	9:j:40:HIS:CG	2.52	0.44
16:q:33:VAL:O	16:q:36:GLN:HG2	2.18	0.44
18:s:93:ALA:HB2	53:1:1614:A:H2	1.80	0.44
25:z:40:THR:O	25:z:43:ILE:HG22	2.17	0.44
28:D:14:ARG:HG3	53:1:771:G:OP1	2.17	0.44
32:H:86:LEU:O	32:H:90:VAL:HG22	2.16	0.44
36:L:4:ARG:HB3	36:L:6:ILE:HG23	2.00	0.44
40:P:81:LEU:HD23	40:P:81:LEU:N	2.32	0.44
45:U:70:ARG:NH1	52:3:452:A:C1'	2.80	0.44
52:3:1300:G:C2'	52:3:1301:U:OP2	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:69:C:H2'	53:1:70:G:H8	1.80	0.44
53:1:720:U:H2'	53:1:721:A:C8	2.52	0.44
1:b:119:VAL:HB	6:g:91:PHE:CE1	2.52	0.44
1:b:216:ARG:NH2	53:1:781:A:OP1	2.50	0.44
5:f:137:LYS:HA	5:f:140:ILE:HG12	1.99	0.44
9:j:3:THR:OG1	9:j:4:PHE:N	2.50	0.44
14:o:116:GLN:O	14:o:117:PHE:HB3	2.17	0.44
16:q:39:ILE:O	16:q:43:GLN:HG3	2.17	0.44
33:I:32:LYS:HD2	52:3:426:U:OP1	2.17	0.44
33:I:169:TRP:HA	33:I:182:LYS:HE2	1.99	0.44
35:K:12:PRO:HD2	35:K:54:LEU:HD23	1.99	0.44
40:P:91:GLY:C	40:P:93:GLU:H	2.25	0.44
42:R:89:ARG:HB2	42:R:96:VAL:HG12	2.00	0.44
51:a:174:THR:HB	53:1:2124:G:H4'	2.00	0.44
51:a:206:GLY:CA	53:1:1860:G:H5''	2.47	0.44
52:3:26:A:H61	52:3:558:G:H1'	1.82	0.44
52:3:56:U:H2'	52:3:57:G:C8	2.53	0.44
52:3:273:U:C2'	52:3:274:A:H5'	2.48	0.44
52:3:494:G:O2'	52:3:496:A:H1'	2.18	0.44
53:1:704:G:H2'	53:1:726:G:H22	1.82	0.44
53:1:1019:U:H2'	53:1:1020:A:H8	1.82	0.44
53:1:1704:C:H2'	53:1:1705:A:C8	2.52	0.44
53:1:2070:A:O2'	53:1:2071:A:H5'	2.18	0.44
53:1:2788:C:H2'	53:1:2789:C:C6	2.52	0.44
1:b:48:ILE:HG23	1:b:48:ILE:O	2.18	0.44
1:b:270:ARG:HH12	53:1:1798:U:H5	1.65	0.44
7:h:16:SER:O	7:h:20:LYS:HG2	2.18	0.44
7:h:67:THR:HB	7:h:68:PRO:HD3	1.98	0.44
35:K:18:VAL:CG1	35:K:19:PRO:HD3	2.48	0.44
36:L:138:GLU:O	36:L:142:ARG:HD3	2.18	0.44
39:O:42:LEU:HA	39:O:43:PRO:HD2	1.80	0.44
45:U:22:ALA:HB2	45:U:32:PHE:HA	2.00	0.44
52:3:1125:U:H2'	52:3:1126:U:H2'	2.00	0.44
53:1:2121:G:H2'	53:1:2122:U:O4'	2.17	0.44
53:1:2383:G:O2'	53:1:2384:U:H5'	2.17	0.44
55:5:18:G:H22	55:5:55:U:H5	1.66	0.44
1:b:204:LEU:HB3	1:b:209:ALA:HB3	2.00	0.44
2:c:36:GLN:NE2	53:1:2785:C:H4'	2.33	0.44
3:d:138:LEU:HA	3:d:141:MET:HB2	1.99	0.44
4:e:102:LEU:HA	4:e:106:ALA:HB3	1.99	0.44
7:h:31:ARG:HG2	7:h:109:LYS:HZ3	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:15:GLY:H	20:u:18:LYS:HZ2	1.66	0.44
21:v:80:HIS:HB3	21:v:83:LYS:O	2.18	0.44
27:C:11:VAL:HG22	27:C:12:SER:N	2.33	0.44
34:J:15:ILE:HD11	34:J:37:VAL:HB	2.00	0.44
39:O:77:VAL:HG23	39:O:78:GLU:HG2	1.99	0.44
42:R:95:PRO:N	42:R:108:ARG:HG2	2.33	0.44
42:R:101:THR:OG1	52:3:1225:A:H5''	2.18	0.44
44:T:42:PHE:CE2	44:T:55:LEU:HD22	2.53	0.44
52:3:613:C:H2'	52:3:614:C:C6	2.53	0.44
52:3:855:U:H2'	52:3:856:C:C6	2.53	0.44
53:1:542:C:H2'	53:1:543:G:C5'	2.48	0.44
53:1:854:C:H2'	53:1:855:G:C8	2.50	0.44
53:1:1078:U:H4'	53:1:1079:C:H5''	1.99	0.44
54:2:87:U:H5''	54:2:88:C:OP2	2.18	0.44
6:g:8:LYS:CD	6:g:9:VAL:N	2.80	0.44
13:n:21:PHE:CZ	13:n:43:GLU:HG3	2.52	0.44
29:E:15:LYS:HA	29:E:21:PHE:CD1	2.53	0.44
31:G:167:HIS:HB3	31:G:168:GLU:OE2	2.17	0.44
32:H:50:SER:OG	32:H:71:ARG:NE	2.51	0.44
35:K:91:ARG:NH2	52:3:738:C:P	2.91	0.44
46:V:30:HIS:CD2	46:V:33:TYR:H	2.35	0.44
49:Y:75:LYS:HZ2	52:3:186:C:H1'	1.82	0.44
50:Z:66:ARG:NH2	52:3:1099:G:H4'	2.25	0.44
53:1:395:U:H2'	53:1:396:G:H8	1.83	0.44
53:1:742:A:H2'	53:1:743:A:C8	2.53	0.44
53:1:893:C:H2'	53:1:894:U:O4'	2.18	0.44
53:1:1525:A:H2'	53:1:1526:C:O4'	2.18	0.44
53:1:2281:A:O2'	53:1:2282:G:H5'	2.18	0.44
53:1:2323:G:O2'	53:1:2324:U:H5'	2.18	0.44
53:1:2861:U:H2'	53:1:2862:G:H8	1.82	0.44
12:m:38:ARG:NH2	54:2:90:C:O3'	2.51	0.43
12:m:76:LYS:HA	12:m:77:PRO:HD3	1.80	0.43
23:x:6:VAL:HG23	23:x:7:THR:HG23	2.00	0.43
24:y:54:LYS:HE3	53:1:72:U:C5	2.53	0.43
31:G:86:CYS:SG	31:G:88:GLN:HG2	2.58	0.43
38:N:40:ARG:NH1	52:3:1292:G:H4'	2.33	0.43
51:a:12:ARG:HH22	53:1:2107:G:P	2.41	0.43
52:3:701:U:H4'	52:3:703:G:H1'	2.00	0.43
53:1:103:A:H2'	53:1:104:A:O4'	2.18	0.43
53:1:1444:G:H2'	53:1:1445:G:C8	2.53	0.43
53:1:1475:G:O2'	53:1:1476:U:H6	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2485:G:O2'	53:1:2486:C:H5'	2.18	0.43
8:i:56:VAL:O	8:i:58:ILE:HD12	2.18	0.43
12:m:33:LEU:HB2	12:m:117:PHE:CE1	2.54	0.43
12:m:77:PRO:HB2	12:m:80:VAL:CG2	2.48	0.43
20:u:81:ARG:HD3	53:1:335:C:H5''	2.00	0.43
22:w:67:VAL:HB	22:w:72:ASN:OD1	2.17	0.43
26:B:39:ARG:O	26:B:40:HIS:HB2	2.18	0.43
28:D:10:LEU:HD12	28:D:10:LEU:C	2.44	0.43
40:P:91:GLY:O	40:P:93:GLU:N	2.42	0.43
43:S:26:LEU:HA	43:S:30:ILE:HD11	2.00	0.43
46:V:10:ARG:C	46:V:22:VAL:HG13	2.43	0.43
52:3:113:G:H1'	52:3:354:G:H5'	1.99	0.43
52:3:300:A:H2'	52:3:301:G:O4'	2.17	0.43
52:3:1015:G:H2'	52:3:1016:A:O4'	2.18	0.43
52:3:1256:A:H1'	52:3:1258:G:N9	2.33	0.43
53:1:974:G:H1'	53:1:975:A:C8	2.53	0.43
53:1:2371:G:O2'	53:1:2372:U:H5'	2.18	0.43
53:1:2487:G:H2'	53:1:2488:G:H8	1.84	0.43
1:b:213:ARG:HH21	53:1:1566:A:H5'	1.82	0.43
3:d:98:LYS:HB3	3:d:102:ARG:NH2	2.30	0.43
5:f:102:ILE:HD12	5:f:114:HIS:HD2	1.83	0.43
7:h:3:LEU:HD21	53:1:1043:C:OP1	2.18	0.43
10:k:108:ARG:HH12	10:k:113:MET:HE1	1.83	0.43
12:m:63:ILE:HG12	12:m:105:MET:HG2	2.01	0.43
22:w:41:PHE:O	22:w:55:LEU:HD11	2.18	0.43
27:C:41:VAL:HG13	27:C:42:VAL:H	1.83	0.43
31:G:68:PHE:HB2	31:G:90:PHE:HB2	2.00	0.43
31:G:131:LYS:HE3	52:3:1158:C:O2'	2.18	0.43
46:V:30:HIS:HD2	46:V:32:ILE:H	1.66	0.43
49:Y:9:ARG:HA	49:Y:12:GLN:CD	2.44	0.43
52:3:225:C:C2'	52:3:226:G:H5''	2.45	0.43
52:3:421:U:O2'	52:3:422:C:P	2.76	0.43
52:3:434:U:H2'	52:3:435:A:H8	1.83	0.43
52:3:692:U:H5'	52:3:797:C:H5'	2.00	0.43
52:3:1261:A:H1'	52:3:1283:U:H5''	1.99	0.43
53:1:523:C:H2'	53:1:524:G:H8	1.84	0.43
53:1:898:C:H2'	53:1:899:A:C8	2.53	0.43
53:1:912:C:O2'	53:1:913:U:H5'	2.18	0.43
53:1:1415:U:H2'	53:1:1416:G:H4'	2.01	0.43
53:1:2250:G:H21	53:1:2496:C:H4'	1.84	0.43
53:1:2354:C:H2'	53:1:2355:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2573:C:OP1	53:1:2574:G:H5''	2.18	0.43
53:1:2713:U:H3'	53:1:2714:G:H5''	2.00	0.43
1:b:1:ALA:N	1:b:19:VAL:HG13	2.33	0.43
3:d:21:ARG:HG2	3:d:22:ASP:H	1.83	0.43
7:h:70:GLU:O	7:h:71:CYS:HB2	2.19	0.43
11:l:33:ARG:HH21	11:l:33:ARG:HG3	1.83	0.43
13:n:35:LYS:HZ3	13:n:110:MET:HE2	1.84	0.43
16:q:111:LYS:NZ	17:r:48:LYS:CD	2.76	0.43
18:s:29:VAL:HA	18:s:32:ALA:HB3	2.01	0.43
18:s:82:MET:O	18:s:98:LYS:N	2.51	0.43
27:C:36:LYS:NZ	27:C:45:HIS:O	2.49	0.43
31:G:19:THR:HA	31:G:38:HIS:CE1	2.54	0.43
32:H:107:LYS:HD2	32:H:110:LEU:HD12	1.99	0.43
42:R:3:ILE:HG22	42:R:56:ARG:HG2	2.00	0.43
42:R:8:ILE:O	42:R:8:ILE:HG22	2.18	0.43
44:T:56:LEU:HD21	53:1:715:A:C5	2.53	0.43
46:V:37:ILE:H	46:V:37:ILE:HD12	1.84	0.43
47:W:28:LEU:HA	47:W:31:TYR:CD2	2.53	0.43
48:X:9:PHE:CE1	52:3:1318:A:H5'	2.53	0.43
48:X:19:GLU:O	48:X:23:GLU:HG2	2.19	0.43
50:Z:61:ARG:HD3	50:Z:62:GLU:OE2	2.18	0.43
52:3:231:U:H2'	52:3:232:G:H8	1.82	0.43
52:3:530:G:H1'	57:7:35:A:O2'	2.19	0.43
52:3:1528:U:H4'	52:3:1529:G:H21	1.83	0.43
53:1:475:C:H4'	53:1:510:C:H5'	2.01	0.43
53:1:609:A:H2'	53:1:610:C:O4'	2.18	0.43
53:1:704:G:H1'	53:1:727:A:H61	1.83	0.43
53:1:796:C:H2'	53:1:797:G:H8	1.81	0.43
53:1:940:G:H2'	53:1:941:A:H5''	1.99	0.43
57:7:59:U:C2'	57:7:60:U:H5'	2.48	0.43
9:j:114:LEU:HD13	53:1:557:C:O2'	2.18	0.43
14:o:24:THR:CG2	14:o:90:VAL:HG13	2.49	0.43
14:o:33:ARG:HH21	14:o:64:TYR:HE1	1.66	0.43
32:H:100:ILE:HD12	32:H:100:ILE:N	2.32	0.43
34:J:87:VAL:HG12	34:J:92:ARG:HA	2.00	0.43
36:L:2:ARG:HB2	52:3:933:G:OP2	2.19	0.43
36:L:63:VAL:O	36:L:67:ASN:ND2	2.51	0.43
36:L:142:ARG:CG	55:6:41:C:H4'	2.49	0.43
37:M:64:TYR:CD1	37:M:69:ALA:HA	2.54	0.43
41:Q:6:LEU:HB3	46:V:33:TYR:CZ	2.54	0.43
46:V:60:ILE:CG2	46:V:72:TRP:HB3	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:107:G:C2'	52:3:108:G:H5'	2.47	0.43
52:3:664:G:H22	52:3:741:G:H1	1.65	0.43
53:1:607:U:O4	53:1:619:G:H2'	2.18	0.43
53:1:1475:G:C2'	53:1:1476:U:OP2	2.66	0.43
53:1:1991:U:H2'	53:1:1992:G:C5'	2.48	0.43
53:1:2093:G:N7	53:1:2225:A:H2'	2.33	0.43
53:1:2296:U:C5'	53:1:2297:A:OP1	2.63	0.43
3:d:165:HIS:HE1	53:1:1205:A:H2'	1.82	0.43
7:h:47:GLU:OE2	7:h:95:LEU:HD11	2.18	0.43
8:i:96:LYS:HE2	8:i:138:VAL:HG13	2.01	0.43
9:j:28:LEU:HD12	9:j:29:ALA:N	2.34	0.43
13:n:3:HIS:CG	53:1:2820:A:H4'	2.53	0.43
14:o:88:LYS:HG3	14:o:89:ASP:H	1.82	0.43
31:G:72:LYS:NZ	31:G:163:ILE:O	2.51	0.43
32:H:76:ILE:CG2	32:H:102:ILE:HG12	2.44	0.43
33:I:44:LYS:HE3	33:I:44:LYS:HB3	1.90	0.43
33:I:81:LEU:HD13	33:I:88:ASN:HB3	2.00	0.43
35:K:4:TYR:HE1	35:K:91:ARG:HH21	1.65	0.43
38:N:59:LYS:HD2	38:N:59:LYS:HA	1.76	0.43
42:R:16:ILE:HD12	42:R:16:ILE:H	1.83	0.43
46:V:48:GLU:O	46:V:49:ASN:C	2.61	0.43
52:3:1070:U:H2'	52:3:1071:C:C6	2.54	0.43
52:3:1201:A:C1'	52:3:1202:U:OP2	2.64	0.43
53:1:1045:C:P	53:1:1047:G:H5'	2.59	0.43
53:1:1386:C:H2'	53:1:1387:A:H8	1.83	0.43
53:1:2055:C:H2'	53:1:2504:U:C5'	2.47	0.43
53:1:2134:A:N6	53:1:2157:G:H4'	2.32	0.43
54:2:28:C:H2'	54:2:29:A:H8	1.84	0.43
4:e:109:ARG:HA	4:e:109:ARG:HD2	1.89	0.43
5:f:83:THR:OG1	5:f:133:LYS:HG2	2.19	0.43
16:q:53:LYS:HE3	53:1:994:C:H3'	2.01	0.43
19:t:40:LYS:HE3	53:1:1599:U:OP2	2.19	0.43
22:w:32:ILE:HD12	22:w:32:ILE:H	1.83	0.43
26:B:30:ASP:HB3	26:B:35:GLU:H	1.84	0.43
30:F:27:CYS:SG	30:F:28:SER:N	2.92	0.43
32:H:171:ARG:CG	32:H:173:PRO:HD3	2.47	0.43
33:I:119:HIS:ND1	52:3:438:U:H4'	2.34	0.43
45:U:13:LYS:O	45:U:14:ARG:HD2	2.18	0.43
47:W:37:LYS:HE3	52:3:719:C:O2'	2.18	0.43
53:1:492:A:H2'	53:1:493:G:O4'	2.18	0.43
53:1:1354:A:H2'	53:1:1355:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:42:ARG:HG2	1:b:46:GLY:O	2.17	0.43
2:c:142:VAL:HG11	53:1:2051:A:OP1	2.19	0.43
11:l:48:ARG:HD3	53:1:666:A:H4'	2.01	0.43
18:s:31:GLN:O	18:s:35:ILE:HG13	2.19	0.43
19:t:67:VAL:HG22	19:t:76:ARG:HG2	2.01	0.43
23:x:2:ARG:O	23:x:11:PRO:HD3	2.19	0.43
25:z:17:PRO:HG3	53:1:969:G:OP1	2.19	0.43
31:G:96:LEU:O	31:G:99:MET:HG3	2.18	0.43
31:G:150:ILE:HG22	31:G:153:MET:HE2	2.00	0.43
32:H:71:ARG:HG2	32:H:74:ILE:HD12	2.00	0.43
32:H:181:ILE:HA	32:H:202:PHE:HA	1.99	0.43
35:K:66:ALA:HB1	35:K:67:PRO:HD2	2.01	0.43
36:L:73:GLU:HG2	36:L:90:VAL:HG12	2.00	0.43
41:Q:2:THR:HG22	41:Q:5:GLN:HG3	2.01	0.43
42:R:48:SER:O	42:R:52:ILE:HG13	2.18	0.43
44:T:53:ARG:HH21	52:3:579:A:H4'	1.84	0.43
45:U:19:VAL:HG23	45:U:19:VAL:O	2.17	0.43
48:X:39:ILE:HD12	48:X:39:ILE:N	2.34	0.43
52:3:256:U:H2'	52:3:257:G:C8	2.54	0.43
53:1:780:G:H2'	53:1:782:A:N7	2.33	0.43
53:1:1882:U:H2'	53:1:1883:U:C6	2.53	0.43
53:1:2229:U:H2'	53:1:2230:G:C8	2.54	0.43
55:6:16:C:H4'	55:6:60:U:C1'	2.49	0.43
56:4:17:U:H2'	56:4:18:G:C8	2.54	0.43
1:b:176:ARG:HA	1:b:176:ARG:HD2	1.79	0.43
2:c:172:VAL:O	2:c:172:VAL:HG13	2.19	0.43
17:r:68:ARG:HH21	53:1:1223:G:P	2.42	0.43
18:s:18:ARG:HG2	18:s:76:VAL:HB	2.00	0.43
26:B:14:MET:HG2	53:1:2045:C:H4'	1.99	0.43
31:G:20:ARG:NE	52:3:831:A:C5'	2.72	0.43
37:M:107:LYS:HG2	37:M:120:LEU:HD11	1.99	0.43
39:O:30:LYS:HG3	39:O:31:ARG:HD2	1.99	0.43
42:R:63:VAL:HG13	42:R:67:ASP:HB3	2.01	0.43
45:U:28:ARG:NH1	52:3:390:U:O3'	2.52	0.43
46:V:10:ARG:O	46:V:22:VAL:HG13	2.19	0.43
48:X:38:THR:OG1	48:X:39:ILE:N	2.52	0.43
50:Z:17:ARG:HA	50:Z:20:ARG:HG2	2.01	0.43
52:3:235:C:H2'	52:3:236:A:H8	1.83	0.43
52:3:990:C:H2'	52:3:991:U:O4'	2.18	0.43
52:3:1333:A:H2'	52:3:1334:G:O4'	2.19	0.43
53:1:74:A:H4'	53:1:75:G:O5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:657:U:H2'	53:1:658:U:C6	2.54	0.43
53:1:1614:A:H2'	53:1:1615:C:H5'	2.01	0.43
53:1:1720:U:H2'	53:1:1721:G:O4'	2.19	0.43
53:1:1775:U:H2'	53:1:1776:G:O4'	2.19	0.43
53:1:2487:G:H2'	53:1:2488:G:C8	2.54	0.43
53:1:2841:C:H2'	53:1:2842:G:C8	2.54	0.43
2:c:81:GLU:HG2	53:1:2636:C:O5'	2.19	0.43
10:k:52:VAL:HG11	10:k:58:LEU:HD22	1.99	0.43
11:l:116:VAL:O	11:l:116:VAL:HG13	2.19	0.43
12:m:16:ARG:HD3	53:1:958:U:O2	2.19	0.43
13:n:15:SER:HB3	53:1:2710:C:OP1	2.19	0.43
26:B:28:SER:HB2	26:B:39:ARG:HG2	2.01	0.43
33:I:69:ARG:HH12	52:3:401:C:C3'	2.32	0.43
36:L:36:SER:HA	38:N:42:THR:CG2	2.49	0.43
37:M:100:ILE:HG13	37:M:128:VAL:HB	2.01	0.43
41:Q:58:ASN:OD1	41:Q:59:GLY:N	2.51	0.43
41:Q:119:LYS:HG2	52:3:36:C:H5''	2.00	0.43
44:T:19:ASN:HB3	52:3:749:A:O2'	2.19	0.43
52:3:730:G:C2'	52:3:731:G:H5'	2.48	0.43
52:3:1354:U:H2'	52:3:1355:G:H8	1.83	0.43
53:1:1434:A:H2'	53:1:1435:G:H8	1.84	0.43
53:1:1507:C:H2'	53:1:1508:A:O4'	2.18	0.43
53:1:1547:C:H2'	53:1:1548:A:H8	1.84	0.43
53:1:2318:G:H2'	53:1:2319:G:O4'	2.18	0.43
53:1:2655:G:O2'	53:1:2656:U:H5	2.02	0.43
1:b:245:THR:C	1:b:247:TRP:H	2.27	0.42
4:e:67:THR:HG22	4:e:87:LYS:NZ	2.33	0.42
9:j:7:LYS:HA	9:j:8:PRO:HD3	1.75	0.42
11:l:23:ILE:HD13	17:r:84:ARG:HB3	2.00	0.42
11:l:103:ILE:HD13	53:1:259:G:C4'	2.48	0.42
15:p:28:LYS:HA	15:p:41:ALA:HA	2.00	0.42
21:v:14:LYS:HE2	54:2:98:G:N2	2.33	0.42
21:v:21:ARG:HH12	54:2:77:U:H5''	1.84	0.42
23:x:17:ARG:HB2	53:1:380:G:OP1	2.19	0.42
29:E:30:HIS:O	29:E:31:ILE:C	2.62	0.42
34:J:110:MET:O	34:J:113:VAL:HG12	2.19	0.42
38:N:70:GLY:O	38:N:74:GLN:HG3	2.18	0.42
38:N:125:GLN:HA	52:3:1342:C:O2'	2.18	0.42
40:P:74:LYS:N	40:P:74:LYS:HD2	2.34	0.42
42:R:13:HIS:NE2	52:3:1296:C:H5'	2.34	0.42
44:T:44:GLU:O	44:T:45:HIS:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:T:55:LEU:O	44:T:58:MET:HB3	2.19	0.42
50:Z:23:GLU:C	50:Z:25:ALA:H	2.27	0.42
52:3:21:G:H2'	52:3:22:G:C8	2.54	0.42
52:3:952:U:H2'	52:3:953:G:C8	2.54	0.42
52:3:1137:C:H4'	52:3:1138:G:N2	2.34	0.42
53:1:523:C:H2'	53:1:524:G:C8	2.54	0.42
53:1:676:A:H62	53:1:802:A:N6	2.05	0.42
53:1:1130:U:C2	53:1:2025:C:H5''	2.54	0.42
53:1:2547:A:H2'	53:1:2548:U:C6	2.54	0.42
53:1:2853:C:H2'	53:1:2854:G:C8	2.54	0.42
1:b:73:ILE:HG23	53:1:1490:A:N6	2.34	0.42
2:c:63:PRO:HA	53:1:2787:C:O4'	2.19	0.42
3:d:84:THR:HG21	53:1:672:C:C5'	2.49	0.42
9:j:95:ARG:NH2	53:1:2768:U:O3'	2.53	0.42
11:l:60:ARG:O	53:1:2392:A:O2'	2.37	0.42
16:q:96:ASP:OD2	17:r:13:ARG:NE	2.52	0.42
31:G:207:ARG:HG2	31:G:207:ARG:HH11	1.83	0.42
32:H:198:LYS:HE3	52:3:1058:G:OP1	2.19	0.42
33:I:31:CYS:O	33:I:32:LYS:C	2.61	0.42
33:I:33:ILE:HG22	33:I:34:GLU:H	1.82	0.42
35:K:12:PRO:O	35:K:15:SER:HB2	2.19	0.42
38:N:112:ARG:NH1	52:3:1187:G:H4'	2.34	0.42
40:P:22:ILE:HD13	40:P:95:THR:HG21	2.00	0.42
41:Q:39:THR:HG22	41:Q:40:THR:N	2.34	0.42
50:Z:46:ARG:HH11	52:3:1533:C:H41	1.67	0.42
53:1:1370:C:H2'	53:1:1371:G:O4'	2.19	0.42
53:1:2343:U:H2'	53:1:2344:U:C6	2.55	0.42
53:1:2853:C:H2'	53:1:2854:G:H8	1.84	0.42
1:b:36:ASN:HD22	1:b:85:ASN:HD21	1.67	0.42
6:g:8:LYS:O	6:g:9:VAL:C	2.61	0.42
12:m:2:LEU:HB3	12:m:68:PHE:CE1	2.54	0.42
14:o:37:ALA:HB3	14:o:51:ALA:O	2.19	0.42
16:q:14:LYS:HE3	53:1:1217:U:OP1	2.19	0.42
27:C:36:LYS:HD3	53:1:2344:U:OP1	2.19	0.42
36:L:113:LYS:NZ	52:3:1297:G:O2'	2.52	0.42
38:N:82:ILE:O	38:N:86:LEU:HG	2.20	0.42
41:Q:37:TYR:HD1	41:Q:37:TYR:H	1.67	0.42
41:Q:115:LYS:O	41:Q:116:TYR:HB2	2.19	0.42
42:R:52:ILE:O	42:R:56:ARG:HG3	2.20	0.42
43:S:81:ILE:HD13	52:3:1202:U:C2	2.54	0.42
51:a:3:LYS:HD2	53:1:2108:A:P	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:219:GLY:O	53:1:2176:A:H5'	2.19	0.42
52:3:31:G:H5'	52:3:306:A:C2	2.53	0.42
52:3:1235:U:O2'	52:3:1305:G:H5'	2.19	0.42
53:1:322:A:H5'	53:1:340:A:H1'	2.01	0.42
53:1:1019:U:H2'	53:1:1020:A:C8	2.55	0.42
53:1:1373:A:C5'	53:1:2212:A:H1'	2.49	0.42
53:1:2345:G:N3	53:1:2381:A:H2'	2.34	0.42
53:1:2453:A:H2'	53:1:2454:G:H8	1.84	0.42
1:b:256:THR:OG1	53:1:1798:U:H5'	2.19	0.42
1:b:260:LYS:HA	1:b:263:ASP:HB2	2.01	0.42
2:c:22:ILE:HA	2:c:23:PRO:HD3	1.84	0.42
2:c:165:MET:HE3	2:c:166:GLY:H	1.84	0.42
4:e:36:ASN:HD21	53:1:2312:U:H2'	1.83	0.42
4:e:140:ILE:N	4:e:140:ILE:HD12	2.35	0.42
8:i:10:LEU:HB3	8:i:11:GLN:H	1.51	0.42
9:j:25:LEU:HD12	9:j:62:VAL:HG22	2.01	0.42
25:z:8:GLN:NE2	25:z:53:MET:O	2.52	0.42
30:F:7:VAL:HG13	30:F:38:GLY:HA3	2.01	0.42
31:G:41:ASN:OD1	31:G:43:GLU:HG2	2.19	0.42
43:S:32:ASP:O	43:S:40:ARG:NH1	2.52	0.42
43:S:71:GLY:HA2	52:3:975:A:O2'	2.19	0.42
47:W:38:ILE:HD12	47:W:38:ILE:N	2.35	0.42
50:Z:47:ALA:O	50:Z:51:ALA:HB2	2.19	0.42
52:3:314:C:O2'	52:3:315:A:H5'	2.20	0.42
53:1:277:G:H1'	53:1:361:G:O6	2.19	0.42
53:1:752:A:O2'	53:1:1781:U:H5'	2.20	0.42
53:1:2705:A:H2'	53:1:2706:A:O4'	2.19	0.42
53:1:2732:G:O2'	53:1:2733:A:H5'	2.19	0.42
4:e:33:ILE:N	4:e:33:ILE:HD12	2.34	0.42
7:h:14:GLU:HA	7:h:53:ARG:HH22	1.83	0.42
7:h:37:LYS:NZ	53:1:1084:A:H62	2.16	0.42
7:h:50:VAL:HG13	53:1:1083:U:OP2	2.18	0.42
10:k:61:VAL:CG2	10:k:87:LEU:HD11	2.48	0.42
13:n:69:ARG:C	13:n:71:ARG:H	2.27	0.42
24:y:44:LYS:HA	24:y:47:ARG:NH2	2.34	0.42
25:z:9:THR:OG1	25:z:10:ARG:N	2.53	0.42
28:D:3:ARG:HG2	53:1:1613:G:H4'	2.01	0.42
34:J:28:ARG:NH2	52:3:15:G:H5'	2.34	0.42
37:M:17:GLN:HG2	37:M:62:LEU:HD13	2.01	0.42
43:S:5:MET:HG2	43:S:8:ARG:HH12	1.83	0.42
51:a:38:PHE:HD1	53:1:2127:G:H4'	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:791:G:N2	52:3:1497:G:H4'	2.35	0.42
53:1:171:U:H2'	53:1:172:A:C8	2.53	0.42
53:1:414:C:H2'	53:1:415:A:C8	2.55	0.42
53:1:1554:U:H3'	53:1:1555:G:H5'	2.00	0.42
53:1:2074:U:H2'	53:1:2075:U:C6	2.55	0.42
53:1:2246:G:H2'	53:1:2247:A:C8	2.54	0.42
53:1:2370:G:H2'	53:1:2371:G:O4'	2.20	0.42
56:4:17:U:O2'	56:4:18:G:H5'	2.19	0.42
1:b:110:LYS:O	1:b:112:GLY:N	2.52	0.42
1:b:164:VAL:HG21	1:b:180:MET:HE1	2.00	0.42
4:e:39:VAL:HG13	4:e:40:GLY:N	2.35	0.42
4:e:140:ILE:HA	4:e:144:LYS:HD3	2.01	0.42
5:f:8:VAL:HB	5:f:49:LEU:HD12	2.02	0.42
13:n:2:ARG:HG2	13:n:5:LYS:HB2	2.02	0.42
23:x:36:ARG:HG2	23:x:45:PHE:HB3	2.00	0.42
34:J:59:ILE:O	34:J:63:MET:HG2	2.18	0.42
43:S:20:PHE:O	43:S:21:ALA:CB	2.68	0.42
52:3:26:A:N6	52:3:558:G:H1'	2.34	0.42
52:3:354:G:C2'	52:3:355:C:H5'	2.49	0.42
52:3:1118:U:H2'	52:3:1119:C:C6	2.54	0.42
52:3:1258:G:H2'	52:3:1259:C:C6	2.54	0.42
52:3:1356:G:H2'	52:3:1357:A:C8	2.54	0.42
53:1:1378:A:H1'	53:1:1379:U:C5	2.54	0.42
53:1:2326:C:O2'	53:1:2327:A:OP1	2.33	0.42
1:b:1:ALA:N	1:b:19:VAL:O	2.46	0.42
2:c:77:ARG:HG3	2:c:77:ARG:NH2	2.35	0.42
3:d:44:ARG:HD2	53:1:444:C:OP2	2.20	0.42
3:d:44:ARG:HH12	16:q:1:ALA:HA	1.85	0.42
4:e:118:ALA:O	4:e:119:LYS:HD2	2.20	0.42
4:e:142:TYR:CE1	42:R:8:ILE:HB	2.55	0.42
14:o:15:ARG:NH1	54:2:9:G:OP2	2.52	0.42
16:q:73:ILE:HD11	16:q:77:LYS:C	2.44	0.42
17:r:10:LYS:NZ	53:1:994:C:O2	2.49	0.42
19:t:10:VAL:HG23	19:t:11:LEU:HD12	2.01	0.42
27:C:9:LYS:HZ1	53:1:2419:U:H4'	1.85	0.42
34:J:82:HIS:CD2	37:M:98:LEU:HD21	2.52	0.42
34:J:83:PRO:HB3	34:J:96:GLN:HG2	2.00	0.42
36:L:3:ARG:NH1	52:3:1092:A:H5''	2.34	0.42
37:M:104:SER:HA	37:M:109:VAL:HA	2.02	0.42
40:P:21:HIS:CD2	52:3:707:U:H5''	2.54	0.42
51:a:64:VAL:HG13	51:a:160:GLN:HE21	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1527:U:O2'	52:3:1528:U:H5'	2.20	0.42
53:1:859:G:C2'	53:1:860:U:OP2	2.67	0.42
53:1:1139:G:O2'	53:1:1140:C:H5'	2.20	0.42
53:1:1326:U:H2'	53:1:1327:A:C8	2.55	0.42
53:1:1444:G:H2'	53:1:1445:G:H8	1.84	0.42
53:1:1672:A:C2	53:1:2582:G:H5'	2.54	0.42
53:1:2326:C:O2'	53:1:2327:A:P	2.78	0.42
57:7:36:A:H2'	57:7:37:A:C8	2.55	0.42
3:d:61:ARG:HD3	3:d:61:ARG:N	2.35	0.42
4:e:114:ARG:HB3	42:R:70:ARG:NH2	2.35	0.42
5:f:90:GLY:HA3	5:f:93:TYR:CD2	2.55	0.42
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.50	0.42
13:n:20:MET:HA	13:n:23:ASN:OD1	2.20	0.42
16:q:46:TYR:HA	16:q:49:ARG:NH2	2.35	0.42
29:E:15:LYS:HA	29:E:21:PHE:HD1	1.85	0.42
32:H:113:LYS:HD2	32:H:117:ASP:OD2	2.20	0.42
38:N:8:THR:HG23	38:N:9:GLY:N	2.27	0.42
41:Q:109:ARG:CZ	52:3:537:G:H5''	2.50	0.42
43:S:62:ARG:HB3	43:S:67:GLY:HA2	2.02	0.42
52:3:152:A:H2'	52:3:153:C:H5'	2.00	0.42
52:3:403:C:H2'	52:3:404:G:C8	2.55	0.42
52:3:1060:U:H2'	52:3:1061:G:H8	1.84	0.42
52:3:1346:A:H2'	52:3:1346:A:N3	2.35	0.42
53:1:881:G:O2'	53:1:882:G:H5'	2.20	0.42
53:1:1086:A:H3'	53:1:1086:A:N3	2.35	0.42
53:1:1285:A:H2'	53:1:1286:A:H5'	2.01	0.42
53:1:2411:A:H2'	53:1:2412:A:C8	2.54	0.42
53:1:2898:U:H2'	53:1:2899:A:C8	2.54	0.42
2:c:161:MET:HG2	53:1:2049:G:H21	1.84	0.42
6:g:94:ILE:HD11	6:g:122:LEU:HD12	2.02	0.42
14:o:38:GLN:HE22	54:2:7:G:N2	2.13	0.42
18:s:17:VAL:O	18:s:20:VAL:HG12	2.20	0.42
23:x:15:ASN:HD22	53:1:381:G:C5'	2.33	0.42
28:D:27:GLY:O	28:D:30:VAL:HB	2.19	0.42
32:H:46:LEU:HB3	32:H:49:ALA:HB3	2.01	0.42
37:M:21:LYS:HE2	52:3:828:U:P	2.59	0.42
37:M:74:ILE:HG23	37:M:74:ILE:O	2.19	0.42
38:N:45:MET:HG2	38:N:48:ARG:NH2	2.35	0.42
45:U:5:ARG:HD2	52:3:376:G:H4'	2.01	0.42
45:U:71:VAL:HA	45:U:74:LEU:HB2	2.02	0.42
48:X:77:ARG:HD3	52:3:1222:G:H5''	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:358:U:H2'	52:3:359:G:H8	1.85	0.42
52:3:738:C:H2'	52:3:739:C:C6	2.54	0.42
52:3:1241:G:H2'	52:3:1242:G:H8	1.84	0.42
52:3:1430:A:H2'	52:3:1431:A:O4'	2.19	0.42
53:1:216:A:H2'	53:1:217:A:O4'	2.20	0.42
53:1:568:U:H2'	53:1:570:G:OP2	2.20	0.42
53:1:817:C:H2'	53:1:818:G:O4'	2.20	0.42
53:1:1794:A:H2'	53:1:1795:C:C6	2.55	0.42
53:1:2208:C:H2'	53:1:2209:G:C8	2.54	0.42
53:1:2322:A:H2'	53:1:2323:G:O4'	2.20	0.42
53:1:2364:C:H2'	53:1:2365:G:O4'	2.20	0.42
53:1:2586:U:H2'	53:1:2587:A:C8	2.55	0.42
53:1:2609:U:H5'	53:1:2610:C:OP2	2.19	0.42
53:1:2855:C:H2'	53:1:2856:A:H8	1.85	0.42
55:5:42:G:H2'	55:5:43:A:C8	2.55	0.42
2:c:37:VAL:HG22	2:c:48:ILE:HG22	2.02	0.42
5:f:9:VAL:HA	5:f:48:THR:HA	2.01	0.42
6:g:31:VAL:HG13	6:g:32:PRO:HD3	2.02	0.42
6:g:73:ASN:HD22	6:g:76:GLU:HA	1.83	0.42
7:h:80:THR:O	7:h:81:LEU:C	2.62	0.42
9:j:1:MET:O	16:q:92:LYS:NZ	2.51	0.42
14:o:9:ARG:NH2	53:1:2296:U:H5	2.18	0.42
24:y:18:LEU:O	24:y:22:LEU:HD13	2.19	0.42
33:I:43:ARG:NH1	33:I:44:LYS:HB3	2.34	0.42
37:M:49:LYS:O	37:M:58:LEU:HA	2.20	0.42
38:N:22:PRO:HA	38:N:59:LYS:O	2.19	0.42
42:R:32:ILE:HG23	42:R:58:GLU:HG3	2.02	0.42
42:R:51:GLN:O	42:R:55:LEU:HG	2.20	0.42
46:V:42:LYS:NZ	52:3:277:C:H5''	2.35	0.42
52:3:252:U:O2	52:3:252:U:C2'	2.68	0.42
52:3:1144:G:N2	52:3:1146:A:H62	2.17	0.42
52:3:1481:U:H2'	52:3:1482:G:H8	1.84	0.42
53:1:6:A:H2'	53:1:7:G:C8	2.55	0.42
53:1:253:C:H2'	53:1:254:G:O4'	2.20	0.42
53:1:1336:A:H2'	53:1:1337:G:C8	2.55	0.42
53:1:1463:C:H2'	53:1:1464:G:C8	2.55	0.42
53:1:2329:U:H2'	53:1:2330:G:H8	1.82	0.42
53:1:2618:G:H2'	53:1:2619:C:C6	2.54	0.42
1:b:97:ASP:HB3	53:1:1490:A:N7	2.34	0.41
2:c:55:LYS:NZ	2:c:59:ARG:HG3	2.34	0.41
3:d:131:THR:HG21	53:1:320:A:H2'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:142:TYR:HD1	42:R:8:ILE:HD12	1.83	0.41
5:f:157:LYS:HD2	53:1:2659:G:OP1	2.19	0.41
7:h:38:MET:HA	7:h:42:ARG:NH1	2.35	0.41
7:h:60:LEU:HD11	53:1:1047:G:O6	2.20	0.41
9:j:55:ILE:HD13	9:j:123:LYS:HB2	2.01	0.41
13:n:107:ASN:HD22	53:1:2009:A:C5'	2.33	0.41
28:D:25:LYS:O	28:D:28:ARG:HB2	2.19	0.41
36:L:66:GLU:HA	36:L:69:ARG:HD2	2.01	0.41
45:U:6:LEU:HD11	45:U:70:ARG:HG2	2.02	0.41
45:U:71:VAL:O	45:U:75:ILE:HG13	2.20	0.41
52:3:211:G:C2'	52:3:212:G:H5'	2.49	0.41
52:3:225:C:H2'	52:3:226:G:C5'	2.48	0.41
52:3:1064:G:H1'	52:3:1190:G:N2	2.35	0.41
52:3:1339:A:C2	55:5:30:G:H1'	2.55	0.41
53:1:164:C:H2'	53:1:165:A:O4'	2.19	0.41
53:1:1013:C:H2'	53:1:1014:A:H8	1.85	0.41
53:1:1526:C:H2'	53:1:1527:G:O4'	2.20	0.41
53:1:1846:G:H2'	53:1:1847:A:O4'	2.20	0.41
53:1:1936:A:H2	53:1:1943:U:H3	1.67	0.41
53:1:2231:U:H2'	53:1:2232:C:C6	2.55	0.41
3:d:163:ASN:OD1	53:1:323:C:H5''	2.20	0.41
5:f:174:LYS:HE3	5:f:174:LYS:HB3	1.83	0.41
6:g:5:LEU:HD21	6:g:9:VAL:CG1	2.49	0.41
10:k:8:LEU:HG	10:k:82:ASN:HB3	2.02	0.41
11:l:3:LEU:HD22	53:1:1203:U:H4'	2.02	0.41
22:w:16:ARG:HG2	53:1:2356:U:O3'	2.19	0.41
22:w:41:PHE:CD1	22:w:74:LYS:HB3	2.55	0.41
27:C:22:THR:HB	27:C:23:THR:H	1.74	0.41
29:E:3:ILE:HD12	53:1:666:A:H1'	2.02	0.41
32:H:19:SER:O	43:S:93:PRO:HG3	2.20	0.41
33:I:28:ASP:O	33:I:30:LYS:N	2.53	0.41
35:K:92:THR:OG1	35:K:93:LYS:N	2.52	0.41
36:L:65:LEU:O	36:L:69:ARG:HG3	2.21	0.41
38:N:66:VAL:HG22	38:N:67:LYS:N	2.35	0.41
42:R:24:VAL:HG23	42:R:28:ARG:HB3	2.02	0.41
49:Y:3:ILE:HG23	49:Y:3:ILE:O	2.20	0.41
52:3:212:G:H2'	52:3:213:G:H8	1.85	0.41
52:3:1004:A:H2'	52:3:1005:A:O4'	2.20	0.41
53:1:1758:U:C5	53:1:2696:U:H5'	2.55	0.41
54:2:108:A:H5'	54:2:109:A:O5'	2.20	0.41
55:6:59:A:H2'	55:6:60:U:H5'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:40:GLY:O	1:b:42:ARG:HD2	2.19	0.41
3:d:170:ARG:HH22	3:d:175:ILE:HA	1.85	0.41
6:g:97:ARG:NH1	6:g:97:ARG:HB3	2.35	0.41
8:i:12:VAL:HG22	53:1:1061:U:O2	2.20	0.41
12:m:68:PHE:HA	12:m:69:PRO:HD3	1.91	0.41
20:u:47:PRO:HB2	20:u:53:GLN:HB2	2.02	0.41
23:x:13:THR:OG1	53:1:188:G:H5'	2.21	0.41
25:z:28:LEU:HD22	25:z:33:HIS:HB3	2.02	0.41
30:F:4:ARG:HD2	53:1:2466:C:OP2	2.20	0.41
32:H:78:LYS:C	32:H:80:GLY:H	2.26	0.41
33:I:123:MET:O	33:I:143:SER:N	2.50	0.41
33:I:146:GLU:HA	33:I:149:LYS:HE2	2.02	0.41
41:Q:8:ARG:HG2	41:Q:9:LYS:HG2	2.02	0.41
52:3:181:A:H62	52:3:194:C:H2'	1.84	0.41
52:3:392:C:H2'	52:3:393:A:H8	1.84	0.41
52:3:883:C:O2'	52:3:884:U:H5'	2.19	0.41
52:3:1256:A:O2'	52:3:1257:A:H5''	2.19	0.41
53:1:1843:C:H2'	53:1:1844:C:C6	2.55	0.41
53:1:2443:C:H2'	53:1:2444:G:C8	2.55	0.41
53:1:2686:G:H2'	53:1:2687:U:C6	2.56	0.41
57:7:36:A:H2'	57:7:37:A:H8	1.85	0.41
4:e:10:GLU:OE2	4:e:14:LYS:HD2	2.20	0.41
8:i:93:ASN:HB3	53:1:1077:A:H5'	2.01	0.41
9:j:123:LYS:NZ	53:1:7:G:H5''	2.36	0.41
11:l:16:GLY:CA	53:1:662:G:H4'	2.50	0.41
11:l:105:ILE:HD12	11:l:105:ILE:H	1.85	0.41
24:y:21:LEU:HA	24:y:25:GLN:HB3	2.00	0.41
28:D:44:VAL:HG13	28:D:44:VAL:O	2.20	0.41
34:J:20:VAL:HG23	34:J:31:SER:HB3	2.02	0.41
38:N:90:ASP:O	38:N:92:SER:N	2.54	0.41
41:Q:82:ARG:HH11	52:3:552:U:H5'	1.85	0.41
45:U:70:ARG:HD3	52:3:375:U:OP1	2.20	0.41
46:V:14:ASP:HA	46:V:20:ILE:HG13	2.02	0.41
52:3:219:U:H2'	52:3:220:G:C8	2.55	0.41
52:3:631:C:H5''	52:3:632:U:O4'	2.21	0.41
52:3:1088:G:N2	52:3:1167:A:H61	2.14	0.41
52:3:1139:G:H5''	52:3:1140:C:H5	1.85	0.41
52:3:1272:G:H2'	52:3:1273:C:O4'	2.21	0.41
52:3:1522:U:H2'	52:3:1523:G:H8	1.86	0.41
53:1:863:A:H2'	53:1:864:G:C8	2.56	0.41
53:1:1239:G:H2'	53:1:1240:U:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1563:U:H2'	53:1:1564:C:C6	2.55	0.41
53:1:2580:U:H2'	53:1:2581:G:H5'	2.01	0.41
54:2:5:U:H2'	54:2:6:G:C8	2.55	0.41
54:2:104:A:H2'	54:2:105:G:O4'	2.20	0.41
1:b:217:PRO:HB3	53:1:1789:A:O3'	2.20	0.41
6:g:97:ARG:HH11	6:g:97:ARG:HA	1.85	0.41
7:h:103:ASN:HA	7:h:107:GLU:HB3	2.02	0.41
9:j:13:ARG:HD3	9:j:121:LYS:NZ	2.35	0.41
11:l:101:ILE:HG13	11:l:102:GLY:H	1.85	0.41
13:n:90:ARG:HB2	13:n:94:TYR:HE1	1.86	0.41
13:n:107:ASN:HD22	53:1:2009:A:H5'	1.84	0.41
14:o:40:ILE:HA	14:o:47:VAL:HG12	2.02	0.41
22:w:14:ALA:HB2	53:1:2272:U:OP2	2.21	0.41
24:y:11:VAL:HG12	24:y:15:ASN:HD21	1.86	0.41
29:E:15:LYS:HG3	29:E:21:PHE:HE1	1.85	0.41
31:G:207:ARG:HG2	31:G:207:ARG:NH1	2.35	0.41
32:H:99:GLN:NE2	32:H:101:ASN:OD1	2.48	0.41
34:J:98:ALA:HB2	34:J:123:LEU:HD12	2.02	0.41
35:K:18:VAL:N	35:K:19:PRO:CD	2.84	0.41
35:K:49:TYR:HA	35:K:50:PRO:HD3	1.92	0.41
40:P:34:THR:OG1	40:P:35:ASP:N	2.54	0.41
41:Q:98:ARG:NE	41:Q:103:CYS:SG	2.82	0.41
41:Q:109:ARG:HD2	41:Q:109:ARG:HA	1.95	0.41
50:Z:66:ARG:NE	50:Z:66:ARG:HA	2.34	0.41
51:a:205:LYS:HD2	53:1:1861:G:H5'	2.01	0.41
52:3:20:U:H2'	52:3:21:G:O4'	2.21	0.41
52:3:560:A:H5'	52:3:566:G:N2	2.35	0.41
52:3:1157:A:N6	52:3:1178:G:H1'	2.35	0.41
52:3:1199:U:H2'	52:3:1200:C:H5'	2.03	0.41
53:1:1182:G:H2'	53:1:1183:U:O4'	2.20	0.41
53:1:1625:C:H2'	53:1:1626:A:O4'	2.20	0.41
53:1:1827:U:H2'	53:1:1828:G:O4'	2.21	0.41
53:1:1857:G:N2	53:1:1884:G:H2'	2.35	0.41
53:1:2185:U:H2'	53:1:2186:G:C8	2.56	0.41
53:1:2389:G:H5'	53:1:2390:U:O4'	2.21	0.41
55:6:59:A:C2'	55:6:60:U:H5'	2.51	0.41
2:c:46:ARG:HE	2:c:84:LEU:HB2	1.85	0.41
3:d:113:VAL:HG13	3:d:118:LEU:HD12	2.02	0.41
7:h:101:LYS:HE3	7:h:101:LYS:HB3	1.92	0.41
7:h:114:GLU:HA	7:h:123:ILE:HG22	2.01	0.41
10:k:34:GLY:O	10:k:35:VAL:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:98:ARG:HH21	52:3:341:C:H5	1.69	0.41
16:q:89:ILE:HG12	17:r:39:LEU:HD23	2.01	0.41
16:q:90:ASP:HB2	53:1:997:G:OP1	2.20	0.41
17:r:49:ILE:O	17:r:49:ILE:HG13	2.20	0.41
18:s:75:PHE:CE2	18:s:104:THR:HB	2.56	0.41
30:F:4:ARG:NH1	53:1:2466:C:OP2	2.53	0.41
31:G:55:GLU:O	31:G:59:ILE:HG13	2.21	0.41
32:H:175:HIS:ND1	52:3:1109:C:OP2	2.53	0.41
33:I:137:SER:HA	33:I:138:PRO:HD3	1.92	0.41
43:S:60:ARG:HE	52:3:981:U:H1'	1.86	0.41
44:T:87:ARG:O	44:T:88:ARG:C	2.63	0.41
45:U:39:PHE:CE1	45:U:50:THR:HG22	2.56	0.41
45:U:40:ASN:HD22	45:U:43:ALA:HA	1.84	0.41
53:1:197:A:H4'	53:1:2069:G:OP2	2.21	0.41
53:1:441:U:H2'	53:1:442:G:C8	2.55	0.41
4:e:174:PHE:HA	4:e:175:PRO:HD3	1.94	0.41
10:k:64:ARG:HD2	10:k:79:PHE:CG	2.56	0.41
14:o:9:ARG:NH2	53:1:2296:U:C4	2.89	0.41
16:q:2:ARG:HB2	53:1:1248:G:C5	2.54	0.41
17:r:6:GLN:HE22	17:r:39:LEU:CD2	2.32	0.41
21:v:5:ASN:HA	21:v:64:VAL:HB	2.03	0.41
30:F:11:CYS:HB3	30:F:33:HIS:HE1	1.86	0.41
31:G:14:HIS:HB2	31:G:39:ILE:HG23	2.03	0.41
32:H:57:GLU:HB3	32:H:64:ARG:HB3	2.03	0.41
34:J:96:GLN:O	34:J:123:LEU:N	2.52	0.41
34:J:106:ALA:HB2	34:J:124:ALA:HB3	2.03	0.41
40:P:33:ILE:O	40:P:41:LEU:HB2	2.21	0.41
42:R:6:ILE:HG23	42:R:7:ASN:N	2.35	0.41
46:V:35:LYS:O	46:V:37:ILE:HD12	2.21	0.41
51:a:44:VAL:HG12	51:a:173:THR:H	1.86	0.41
51:a:200:LYS:HA	51:a:201:PRO:HD3	1.87	0.41
52:3:560:A:H4'	52:3:561:U:H5'	2.03	0.41
53:1:304:U:H2'	53:1:305:C:C6	2.55	0.41
53:1:760:G:H2'	53:1:761:A:O4'	2.20	0.41
53:1:2144:G:H1'	53:1:2147:A:H61	1.84	0.41
53:1:2196:C:O2'	53:1:2197:U:H5'	2.21	0.41
53:1:2241:A:H2'	53:1:2242:G:C8	2.55	0.41
55:5:57:A:H2'	55:5:58:A:H5'	2.03	0.41
2:c:111:GLY:HA3	2:c:201:LEU:HD23	2.03	0.41
2:c:114:LYS:HG3	53:1:2680:U:OP1	2.20	0.41
7:h:94:ARG:HD2	7:h:131:THR:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:112:ALA:O	7:h:113:PHE:C	2.64	0.41
12:m:38:ARG:NE	54:2:90:C:H4'	2.36	0.41
13:n:92:GLY:O	53:1:2880:C:H1'	2.20	0.41
20:u:56:GLY:N	53:1:483:A:O2'	2.53	0.41
22:w:32:ILE:HD12	22:w:32:ILE:N	2.36	0.41
22:w:61:GLY:HA3	22:w:79:GLU:O	2.20	0.41
30:F:24:ARG:HA	30:F:36:ARG:HA	2.02	0.41
32:H:123:LEU:HD23	32:H:123:LEU:HA	1.87	0.41
33:I:199:ILE:O	33:I:202:LEU:HG	2.21	0.41
38:N:98:ARG:NH2	52:3:1178:G:C8	2.80	0.41
38:N:123:ARG:HB2	52:3:1343:G:O3'	2.21	0.41
42:R:26:LYS:O	42:R:29:SER:OG	2.34	0.41
47:W:11:ARG:HB3	52:3:845:A:O2'	2.21	0.41
47:W:62:ARG:HD3	47:W:69:TYR:CE1	2.56	0.41
49:Y:14:GLU:HA	49:Y:17:ARG:HG2	2.03	0.41
52:3:295:C:H2'	52:3:296:U:O4'	2.21	0.41
52:3:917:G:H2'	52:3:918:A:C8	2.55	0.41
52:3:1014:A:C2	52:3:1219:A:H1'	2.56	0.41
52:3:1056:U:O2'	52:3:1057:G:H5'	2.20	0.41
52:3:1500:A:H5''	52:3:1508:A:H5''	2.02	0.41
53:1:534:U:H2'	53:1:535:G:C8	2.56	0.41
53:1:873:C:H2'	53:1:874:G:H8	1.85	0.41
53:1:1231:U:H2'	53:1:1232:G:H8	1.86	0.41
53:1:1341:G:C2	53:1:1398:C:H4'	2.55	0.41
55:6:14:A:H2'	55:6:15:G:O4'	2.20	0.41
1:b:67:LYS:HE3	1:b:148:GLY:O	2.21	0.41
1:b:92:LEU:HD11	1:b:100:ARG:HB3	2.03	0.41
1:b:239:PHE:O	1:b:241:LYS:N	2.54	0.41
2:c:94:GLN:HG2	2:c:96:ILE:CD1	2.51	0.41
2:c:109:VAL:HG23	2:c:175:LEU:HD12	2.03	0.41
5:f:86:LEU:HD12	5:f:86:LEU:N	2.36	0.41
7:h:77:VAL:O	7:h:77:VAL:HG22	2.21	0.41
12:m:42:THR:HG22	12:m:43:ALA:N	2.35	0.41
12:m:70:ASP:OD2	12:m:70:ASP:C	2.64	0.41
13:n:21:PHE:HZ	13:n:43:GLU:HG3	1.84	0.41
13:n:49:GLU:HB2	13:n:50:PRO:HD3	2.03	0.41
13:n:116:VAL:HG13	13:n:116:VAL:O	2.21	0.41
17:r:22:LEU:HD23	17:r:94:THR:O	2.20	0.41
18:s:79:GLY:O	53:1:25:U:H4'	2.21	0.41
19:t:1:MET:HE2	19:t:3:ARG:HB2	2.03	0.41
23:x:53:LYS:O	23:x:57:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:z:41:PRO:HA	25:z:44:ARG:HB2	2.03	0.41
31:G:22:TRP:HE1	52:3:830:G:H5'	1.86	0.41
31:G:129:THR:HG23	31:G:132:GLU:H	1.86	0.41
31:G:180:ILE:HA	31:G:181:PRO:HD2	1.82	0.41
33:I:120:LYS:HG3	33:I:120:LYS:O	2.21	0.41
33:I:176:LYS:O	33:I:177:MET:HB2	2.21	0.41
34:J:15:ILE:HD12	34:J:35:LEU:HG	2.01	0.41
34:J:40:ASP:OD2	34:J:42:ASN:HB2	2.21	0.41
35:K:51:ILE:HD11	35:K:85:ILE:HG22	2.03	0.41
36:L:4:ARG:HD3	36:L:4:ARG:N	2.36	0.41
36:L:5:VAL:HG22	36:L:5:VAL:O	2.21	0.41
38:N:114:LYS:HE3	52:3:1187:G:O3'	2.20	0.41
41:Q:41:PRO:HG2	41:Q:47:ALA:N	2.36	0.41
46:V:30:HIS:CD2	46:V:32:ILE:H	2.39	0.41
47:W:25:ILE:O	47:W:29:LYS:HG3	2.21	0.41
48:X:18:VAL:O	48:X:22:VAL:HG23	2.21	0.41
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.93	0.41
50:Z:11:PHE:C	50:Z:13:VAL:H	2.29	0.41
52:3:423:G:H2'	52:3:424:G:H5'	2.03	0.41
52:3:674:G:H1	52:3:716:A:H61	1.68	0.41
52:3:692:U:H2'	52:3:694:A:OP2	2.20	0.41
52:3:829:G:O2'	52:3:830:G:H5'	2.21	0.41
53:1:100:U:H4'	53:1:101:A:O4'	2.21	0.41
53:1:534:U:H2'	53:1:535:G:H8	1.85	0.41
53:1:864:G:O2'	53:1:865:C:H5'	2.20	0.41
53:1:937:C:H2'	53:1:938:G:C8	2.55	0.41
53:1:1161:C:H2'	53:1:1162:G:C8	2.56	0.41
53:1:2047:C:H2'	53:1:2048:G:C8	2.56	0.41
53:1:2724:U:H2'	53:1:2725:A:C8	2.56	0.41
55:5:6:G:C2'	55:5:7:G:H5'	2.50	0.41
55:5:37:A:H2'	55:5:38:A:O4'	2.20	0.41
1:b:130:PRO:HB2	1:b:133:ASN:OD1	2.21	0.41
2:c:145:SER:OG	53:1:2512:C:H1'	2.21	0.41
3:d:27:LEU:HG	3:d:104:ALA:HB2	2.03	0.41
4:e:98:PHE:O	4:e:102:LEU:HD23	2.20	0.41
4:e:140:ILE:HG22	4:e:142:TYR:H	1.86	0.41
7:h:57:ASN:O	7:h:63:ALA:HB2	2.21	0.41
7:h:81:LEU:HB3	53:1:1107:G:O4'	2.20	0.41
8:i:52:LEU:HD23	8:i:53:PRO:HD2	2.03	0.41
8:i:126:ARG:HH11	8:i:126:ARG:HG2	1.86	0.41
11:l:19:LEU:HD22	11:l:19:LEU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:51:LEU:CD2	13:n:69:ARG:HD3	2.50	0.41
13:n:58:ASP:OD1	13:n:63:ARG:HD3	2.21	0.41
15:p:28:LYS:HB2	15:p:81:ASP:HB3	2.02	0.41
15:p:77:SER:HA	15:p:78:PRO:HD3	1.95	0.41
17:r:28:ALA:HB3	17:r:31:GLU:CD	2.46	0.41
18:s:36:LEU:HD11	18:s:51:LEU:HD13	2.01	0.41
20:u:3:LYS:O	20:u:93:ARG:NH2	2.54	0.41
21:v:83:LYS:HE2	53:1:1119:U:OP1	2.20	0.41
32:H:148:ILE:HA	32:H:200:TRP:O	2.21	0.41
34:J:22:LYS:HZ2	34:J:31:SER:HB2	1.86	0.41
37:M:12:ARG:CZ	52:3:826:C:H5'	2.51	0.41
38:N:90:ASP:HB2	38:N:91:GLU:H	1.76	0.41
43:S:82:LYS:HD3	43:S:82:LYS:HA	1.89	0.41
47:W:33:THR:OG1	47:W:34:GLU:N	2.53	0.41
49:Y:55:PRO:HB3	52:3:193:C:O3'	2.22	0.41
51:a:51:ASP:OD2	51:a:53:ARG:HB2	2.20	0.41
52:3:1251:A:H2'	52:3:1252:A:O4'	2.20	0.41
53:1:1701:A:H2'	53:1:1702:G:H5'	2.03	0.41
1:b:76:VAL:HG22	1:b:114:GLN:HB2	2.02	0.40
1:b:86:ARG:NH2	53:1:1817:G:OP1	2.55	0.40
3:d:148:ILE:HG21	3:d:157:LEU:HD21	2.03	0.40
3:d:149:ILE:CG2	3:d:188:MET:HG2	2.52	0.40
5:f:95:ALA:HB1	5:f:130:ILE:HD11	2.02	0.40
5:f:102:ILE:HD12	5:f:114:HIS:CD2	2.57	0.40
7:h:67:THR:N	7:h:68:PRO:CD	2.84	0.40
13:n:3:HIS:O	13:n:4:ARG:HB2	2.21	0.40
13:n:35:LYS:HB2	13:n:112:TYR:CE1	2.56	0.40
14:o:11:ALA:HB2	14:o:96:GLY:N	2.35	0.40
19:t:53:VAL:HG11	19:t:87:LEU:HD21	2.02	0.40
22:w:7:ARG:O	22:w:8:ASN:ND2	2.54	0.40
27:C:46:VAL:HG12	27:C:47:ILE:N	2.36	0.40
28:D:6:GLN:NE2	28:D:6:GLN:N	2.69	0.40
32:H:120:THR:HG23	32:H:188:ALA:CB	2.51	0.40
33:I:61:ARG:HH12	33:I:67:LEU:C	2.29	0.40
33:I:70:GLN:OE1	52:3:402:G:OP1	2.39	0.40
37:M:45:ILE:HG21	37:M:60:LEU:HD23	2.02	0.40
39:O:46:LYS:HE2	39:O:46:LYS:HB2	1.94	0.40
41:Q:65:TYR:OH	52:3:522:C:OP2	2.39	0.40
45:U:3:THR:C	45:U:4:ILE:HD12	2.46	0.40
49:Y:28:ARG:O	49:Y:31:ILE:HG22	2.21	0.40
51:a:40:GLU:HG2	51:a:217:THR:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:936:C:H2'	52:3:937:A:O4'	2.21	0.40
52:3:1057:G:H2'	52:3:1058:G:O4'	2.22	0.40
53:1:254:G:H2'	53:1:255:A:H5''	2.02	0.40
53:1:1028:A:H2'	53:1:1029:A:C8	2.55	0.40
53:1:2106:U:H2'	53:1:2107:G:C8	2.55	0.40
53:1:2170:A:H2'	53:1:2171:A:O4'	2.21	0.40
53:1:2537:U:H2'	53:1:2538:C:C6	2.56	0.40
53:1:2639:A:H2'	53:1:2640:G:O4'	2.22	0.40
53:1:2888:C:H2'	53:1:2889:C:C6	2.56	0.40
57:7:47:U:H3'	57:7:48:C:C5'	2.52	0.40
1:b:44:ASN:HD21	53:1:1812:U:H1'	1.86	0.40
1:b:259:ASN:OD1	1:b:261:ARG:HG2	2.20	0.40
2:c:14:ILE:HD13	15:p:11:GLN:NE2	2.36	0.40
3:d:23:PHE:HE1	3:d:28:VAL:HG21	1.86	0.40
6:g:4:ILE:HD12	6:g:4:ILE:HA	1.98	0.40
10:k:91:SER:O	10:k:92:GLU:C	2.64	0.40
15:p:52:ARG:NE	53:1:2845:U:H4'	2.37	0.40
19:t:44:LYS:O	19:t:48:GLN:HG2	2.22	0.40
25:z:4:ILE:HG22	25:z:37:ARG:O	2.20	0.40
28:D:34:ARG:HH22	28:D:41:ARG:HD3	1.85	0.40
31:G:115:ASP:O	31:G:119:GLN:HG3	2.21	0.40
33:I:6:PRO:HA	52:3:430:A:O5'	2.21	0.40
34:J:134:ASN:ND2	52:3:18:C:O3'	2.54	0.40
36:L:91:ARG:O	36:L:95:ARG:N	2.53	0.40
38:N:78:ILE:O	38:N:82:ILE:HG13	2.21	0.40
40:P:125:LYS:HB2	52:3:797:C:P	2.60	0.40
42:R:98:GLY:O	52:3:1322:C:H5''	2.21	0.40
49:Y:11:ILE:HD12	49:Y:11:ILE:N	2.34	0.40
51:a:18:THR:HG22	53:1:2105:U:H5'	2.03	0.40
52:3:304:U:O2'	52:3:305:G:H5'	2.21	0.40
52:3:346:G:C2'	52:3:347:G:H5'	2.52	0.40
52:3:516:U:H3	52:3:533:A:H62	1.69	0.40
52:3:1218:C:H2'	52:3:1219:A:H8	1.83	0.40
53:1:613:A:N3	53:1:613:A:H2'	2.36	0.40
53:1:827:U:H4'	53:1:828:U:C5	2.56	0.40
53:1:845:A:H3'	53:1:845:A:N3	2.37	0.40
53:1:1716:U:H2'	53:1:1717:A:H8	1.86	0.40
53:1:1858:A:C2	53:1:1885:A:H1'	2.56	0.40
53:1:1858:A:H1'	53:1:1885:A:C2	2.56	0.40
53:1:2340:A:H2'	53:1:2341:G:H8	1.86	0.40
53:1:2361:G:O2'	53:1:2362:C:H5'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2432:A:H1'	55:6:75:C:H4'	2.02	0.40
53:1:2475:C:H2'	53:1:2476:A:H5'	2.02	0.40
55:5:44:A:H2'	55:5:45:G:O4'	2.21	0.40
2:c:9:VAL:HB	2:c:26:VAL:CG2	2.51	0.40
3:d:194:LYS:HD2	3:d:194:LYS:HA	1.92	0.40
5:f:131:VAL:HG13	5:f:131:VAL:O	2.21	0.40
7:h:29:ASP:HB2	7:h:56:ARG:HH12	1.86	0.40
10:k:18:ARG:H	10:k:45:GLU:HB2	1.87	0.40
10:k:93:GLN:HA	10:k:94:PRO:HD2	1.98	0.40
16:q:32:ARG:HB2	53:1:1252:G:N3	2.36	0.40
17:r:53:PHE:O	17:r:54:VAL:C	2.64	0.40
19:t:13:ALA:O	19:t:33:LYS:N	2.45	0.40
32:H:156:LEU:HD22	32:H:156:LEU:N	2.36	0.40
36:L:19:SER:OG	36:L:22:LEU:HD23	2.21	0.40
37:M:49:LYS:O	37:M:58:LEU:HD12	2.21	0.40
38:N:7:GLY:HA3	38:N:81:GLY:O	2.22	0.40
38:N:44:ARG:HD3	38:N:44:ARG:N	2.36	0.40
38:N:84:ARG:NH2	52:3:1119:C:H5'	2.36	0.40
40:P:13:LYS:HD2	40:P:13:LYS:N	2.35	0.40
48:X:65:MET:HE3	48:X:73:PHE:CE2	2.57	0.40
51:a:4:LEU:HD22	51:a:8:MET:HB3	2.04	0.40
52:3:113:G:H1'	52:3:354:G:C5'	2.52	0.40
52:3:219:U:H2'	52:3:220:G:H8	1.86	0.40
52:3:485:U:H5'	52:3:486:U:OP2	2.22	0.40
52:3:591:U:H2'	52:3:592:G:H8	1.86	0.40
52:3:1063:C:H2'	52:3:1064:G:C8	2.57	0.40
53:1:740:C:O2'	53:1:741:U:H5'	2.22	0.40
53:1:788:A:H5''	53:1:790:U:H5	1.87	0.40
53:1:1275:A:N6	53:1:1296:G:H4'	2.36	0.40
53:1:1279:G:H2'	53:1:1280:G:H8	1.86	0.40
53:1:2162:G:H2'	53:1:2163:A:H8	1.86	0.40
53:1:2564:A:C2	53:1:2647:U:H4'	2.56	0.40
2:c:183:GLU:OE1	2:c:184:ARG:HG3	2.22	0.40
4:e:37:MET:SD	4:e:56:LEU:HG	2.62	0.40
8:i:12:VAL:HG12	8:i:13:ALA:N	2.34	0.40
11:l:99:ASN:O	11:l:100:ILE:HD13	2.21	0.40
18:s:19:LEU:HG	26:B:21:LEU:HD12	2.03	0.40
32:H:108:PRO:HG2	32:H:109:GLU:H	1.86	0.40
36:L:16:LYS:HE2	38:N:44:ARG:NH2	2.36	0.40
41:Q:33:CYS:HA	41:Q:54:VAL:HG22	2.04	0.40
43:S:53:ASP:HB3	43:S:54:SER:H	1.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:V:46:HIS:HB2	46:V:70:LYS:HE2	2.04	0.40
52:3:354:G:O2'	52:3:355:C:H5'	2.20	0.40
52:3:1071:C:H2'	52:3:1072:G:C8	2.57	0.40
52:3:1342:C:H2'	52:3:1343:G:C8	2.56	0.40
53:1:72:U:O2'	53:1:73:A:H5'	2.21	0.40
53:1:323:C:H2'	53:1:1205:A:N1	2.37	0.40
53:1:403:U:O3'	53:1:404:A:H4'	2.21	0.40
53:1:1571:A:H2'	53:1:1572:A:C8	2.57	0.40
53:1:2808:G:H2'	53:1:2890:G:C6	2.56	0.40
55:5:36:U:H2'	55:5:37:A:C8	2.57	0.40
2:c:1:MET:CE	2:c:100:LEU:HD21	2.50	0.40
12:m:86:LYS:HG3	12:m:87:GLY:N	2.37	0.40
12:m:105:MET:HE2	12:m:117:PHE:CZ	2.57	0.40
13:n:87:PHE:HD1	13:n:87:PHE:HA	1.80	0.40
19:t:24:MET:HE3	19:t:24:MET:O	2.22	0.40
32:H:4:VAL:O	32:H:6:PRO:HD3	2.22	0.40
33:I:18:LEU:HD22	33:I:18:LEU:N	2.37	0.40
40:P:22:ILE:HG12	40:P:31:VAL:HG23	2.04	0.40
42:R:96:VAL:HG21	52:3:1309:G:P	2.61	0.40
43:S:5:MET:HE1	52:3:982:U:H5''	2.04	0.40
43:S:5:MET:HA	43:S:8:ARG:NH1	2.36	0.40
47:W:71:ASP:OD2	47:W:72:ARG:NH2	2.55	0.40
52:3:692:U:H5'	52:3:797:C:C5'	2.50	0.40
52:3:1316:G:C2'	52:3:1317:C:H5''	2.51	0.40
52:3:1402:C:H2'	52:3:1403:C:O4'	2.20	0.40
53:1:374:A:H2'	53:1:375:G:O4'	2.22	0.40
53:1:502:A:H2'	53:1:503:A:H5'	2.04	0.40
53:1:1183:U:H2'	53:1:1184:U:C6	2.56	0.40
53:1:1686:C:H2'	53:1:1687:G:O4'	2.22	0.40
53:1:2040:G:H2'	53:1:2041:U:O4'	2.22	0.40
53:1:2241:A:H2'	53:1:2242:G:H8	1.87	0.40
55:5:36:U:H2'	55:5:37:A:O4'	2.21	0.40
55:6:17:C:H2'	55:6:17(A):U:H5	1.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	b	269/271 (99%)	221 (82%)	43 (16%)	5 (2%)	6	34
2	c	207/209 (99%)	174 (84%)	32 (16%)	1 (0%)	24	60
3	d	199/201 (99%)	179 (90%)	18 (9%)	2 (1%)	12	45
4	e	175/177 (99%)	159 (91%)	15 (9%)	1 (1%)	21	57
5	f	174/176 (99%)	160 (92%)	13 (8%)	1 (1%)	21	57
6	g	147/149 (99%)	123 (84%)	22 (15%)	2 (1%)	9	39
7	h	129/131 (98%)	92 (71%)	30 (23%)	7 (5%)	1	18
8	i	139/141 (99%)	121 (87%)	14 (10%)	4 (3%)	3	26
9	j	140/142 (99%)	122 (87%)	15 (11%)	3 (2%)	5	32
10	k	120/122 (98%)	104 (87%)	12 (10%)	4 (3%)	3	24
11	l	141/143 (99%)	116 (82%)	20 (14%)	5 (4%)	3	23
12	m	134/136 (98%)	115 (86%)	17 (13%)	2 (2%)	8	38
13	n	118/120 (98%)	104 (88%)	14 (12%)	0	100	100
14	o	114/116 (98%)	105 (92%)	7 (6%)	2 (2%)	6	34
15	p	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	48
16	q	115/117 (98%)	104 (90%)	11 (10%)	0	100	100
17	r	101/103 (98%)	83 (82%)	14 (14%)	4 (4%)	2	21
18	s	108/110 (98%)	97 (90%)	8 (7%)	3 (3%)	4	27
19	t	91/93 (98%)	80 (88%)	10 (11%)	1 (1%)	11	44
20	u	100/102 (98%)	83 (83%)	15 (15%)	2 (2%)	6	33
21	v	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	w	73/75 (97%)	62 (85%)	11 (15%)	0	100	100
23	x	75/77 (97%)	67 (89%)	8 (11%)	0	100	100
24	y	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	7	37
25	z	56/58 (97%)	50 (89%)	6 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	45 (83%)	8 (15%)	1 (2%)	6	34
27	C	48/50 (96%)	40 (83%)	8 (17%)	0	100	100
28	D	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
29	E	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	37
30	F	36/38 (95%)	29 (81%)	6 (17%)	1 (3%)	4	27
31	G	223/225 (99%)	203 (91%)	16 (7%)	4 (2%)	6	34
32	H	204/206 (99%)	185 (91%)	17 (8%)	2 (1%)	12	45
33	I	203/205 (99%)	175 (86%)	26 (13%)	2 (1%)	12	45
34	J	155/157 (99%)	129 (83%)	20 (13%)	6 (4%)	2	22
35	K	98/100 (98%)	83 (85%)	13 (13%)	2 (2%)	6	33
36	L	149/151 (99%)	133 (89%)	16 (11%)	0	100	100
37	M	127/129 (98%)	115 (91%)	12 (9%)	0	100	100
38	N	125/127 (98%)	101 (81%)	18 (14%)	6 (5%)	2	19
39	O	96/98 (98%)	77 (80%)	14 (15%)	5 (5%)	1	18
40	P	114/116 (98%)	95 (83%)	14 (12%)	5 (4%)	2	20
41	Q	121/123 (98%)	93 (77%)	24 (20%)	4 (3%)	3	24
42	R	112/114 (98%)	88 (79%)	18 (16%)	6 (5%)	1	18
43	S	98/100 (98%)	83 (85%)	14 (14%)	1 (1%)	12	45
44	T	86/88 (98%)	76 (88%)	8 (9%)	2 (2%)	5	31
45	U	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	29
46	V	78/80 (98%)	64 (82%)	11 (14%)	3 (4%)	2	22
47	W	63/65 (97%)	59 (94%)	3 (5%)	1 (2%)	7	37
48	X	77/79 (98%)	65 (84%)	10 (13%)	2 (3%)	4	29
49	Y	83/85 (98%)	80 (96%)	2 (2%)	1 (1%)	10	42
50	Z	63/65 (97%)	40 (64%)	19 (30%)	4 (6%)	1	15
51	a	130/223 (58%)	122 (94%)	7 (5%)	1 (1%)	16	52
All	All	5919/6112 (97%)	5100 (86%)	706 (12%)	113 (2%)	8	34

All (113) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
6	g	9	VAL

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Mol	Chain	Res	Type
7	h	107	GLU
7	h	118	ILE
10	k	35	VAL
11	l	85	VAL
12	m	59	ARG
17	r	54	VAL
19	t	52	GLU
20	u	6	ARG
29	E	31	ILE
30	F	37	GLN
33	I	29	THR
34	J	89	THR
34	J	93	VAL
34	J	122	VAL
35	K	54	LEU
38	N	91	GLU
38	N	102	PHE
41	Q	24	GLU
42	R	4	ALA
42	R	7	ASN
42	R	40	GLU
44	T	46	LYS
45	U	43	ALA
46	V	17	GLU
46	V	49	ASN
1	b	240	GLY
5	f	45	ALA
7	h	51	TYR
9	j	81	ILE
9	j	127	GLY
11	l	65	GLY
11	l	87	GLY
14	o	99	TYR
15	p	18	SER
17	r	26	ASP
32	H	25	THR
34	J	11	GLN
38	N	90	ASP
39	O	37	ARG
39	O	43	PRO
39	O	57	VAL
40	P	77	GLY

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Mol	Chain	Res	Type
41	Q	88	ASP
45	U	44	SER
46	V	15	LYS
50	Z	9	GLU
50	Z	25	ALA
1	b	233	GLY
7	h	108	VAL
8	i	13	ALA
11	l	48	ARG
17	r	47	VAL
18	s	3	THR
26	B	19	ASP
31	G	148	GLY
35	K	95	ALA
39	O	58	ASN
40	P	13	LYS
40	P	14	GLN
41	Q	35	ARG
42	R	65	GLU
47	W	13	THR
50	Z	10	PRO
6	g	11	ASN
8	i	89	SER
10	k	92	GLU
10	k	93	GLN
11	l	94	THR
12	m	58	LYS
14	o	34	HIS
17	r	48	LYS
31	G	83	ALA
38	N	13	SER
38	N	100	ALA
38	N	107	ALA
40	P	89	GLY
42	R	104	ASN
48	X	12	LEU
51	a	6	LYS
1	b	112	GLY
1	b	246	PRO
2	c	136	ASN
4	e	175	PRO
8	i	11	GLN

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Mol	Chain	Res	Type
10	k	89	ASN
33	I	152	SER
40	P	88	PRO
49	Y	67	HIS
50	Z	34	ARG
3	d	184	ASP
7	h	58	THR
7	h	68	PRO
18	s	64	ALA
20	u	99	SER
24	y	24	GLU
32	H	108	PRO
34	J	90	GLY
39	O	33	GLY
42	R	6	ILE
44	T	2	LEU
18	s	74	ILE
31	G	24	PRO
41	Q	10	PRO
48	X	53	GLY
7	h	119	PRO
9	j	8	PRO
31	G	181	PRO
43	S	30	ILE
8	i	22	PRO
1	b	46	GLY
34	J	43	GLY

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	b	216/216 (100%)	215 (100%)	1 (0%)	81	82
2	c	164/164 (100%)	161 (98%)	3 (2%)	51	68
3	d	165/165 (100%)	165 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100
7	h	100/100 (100%)	99 (99%)	1 (1%)	68	76
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	114 (98%)	2 (2%)	53	68
10	k	103/103 (100%)	103 (100%)	0	100	100
11	l	102/102 (100%)	100 (98%)	2 (2%)	48	66
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	76
13	n	100/100 (100%)	97 (97%)	3 (3%)	36	57
14	o	86/86 (100%)	84 (98%)	2 (2%)	44	64
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	87 (98%)	2 (2%)	45	65
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	76 (97%)	2 (3%)	40	61
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	46 (98%)	1 (2%)	47	65
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	35 (92%)	3 (8%)	11	35
29	E	51/51 (100%)	50 (98%)	1 (2%)	48	66
30	F	34/34 (100%)	33 (97%)	1 (3%)	37	58
31	G	186/186 (100%)	186 (100%)	0	100	100
32	H	170/170 (100%)	170 (100%)	0	100	100
33	I	172/172 (100%)	170 (99%)	2 (1%)	63	73
34	J	119/119 (100%)	119 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	K	87/87 (100%)	87 (100%)	0	100	100
36	L	124/124 (100%)	123 (99%)	1 (1%)	73	77
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	76
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	85 (99%)	1 (1%)	63	73
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	102 (99%)	1 (1%)	68	76
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	83 (100%)	0	100	100
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	70
46	V	74/74 (100%)	72 (97%)	2 (3%)	39	60
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	69 (99%)	1 (1%)	59	71
49	Y	65/65 (100%)	64 (98%)	1 (2%)	57	70
50	Z	55/55 (100%)	53 (96%)	2 (4%)	31	53
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4908/4972 (99%)	4870 (99%)	38 (1%)	70	77

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	69	ASN
2	c	9	VAL
2	c	129	THR
2	c	142	VAL
7	h	118	ILE
9	j	30	THR
9	j	77	HIS
11	l	92	LEU
11	l	94	THR
12	m	26	VAL
13	n	1	MET
13	n	13	ASN
13	n	54	LEU
14	o	24	THR

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Mol	Chain	Res	Type
14	o	115	LEU
16	q	58	GLN
16	q	108	LEU
21	v	4	ILE
21	v	12	GLN
26	B	8	THR
28	D	6	GLN
28	D	24	THR
28	D	44	VAL
29	E	6	VAL
30	F	23	ILE
33	I	28	ASP
33	I	33	ILE
36	L	128	GLU
37	M	60	LEU
39	O	62	ARG
41	Q	23	LEU
45	U	9	HIS
46	V	17	GLU
46	V	43	LEU
48	X	62	THR
49	Y	74	HIS
50	Z	9	GLU
50	Z	10	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (125) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	14	HIS
1	b	44	ASN
1	b	59	GLN
1	b	85	ASN
1	b	89	ASN
1	b	114	GLN
1	b	116	GLN
1	b	127	ASN
2	c	49	GLN
2	c	126	ASN
2	c	149	ASN
2	c	164	GLN
2	c	167	ASN
2	c	173	GLN

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Mol	Chain	Res	Type
2	c	185	ASN
3	d	24	ASN
3	d	46	GLN
3	d	94	GLN
3	d	97	ASN
3	d	195	GLN
5	f	110	HIS
5	f	127	GLN
5	f	138	GLN
5	f	142	GLN
6	g	11	ASN
6	g	18	GLN
6	g	33	GLN
6	g	43	ASN
6	g	145	ASN
7	h	4	ASN
7	h	9	GLN
7	h	57	ASN
8	i	5	GLN
8	i	11	GLN
8	i	33	ASN
8	i	104	GLN
8	i	110	GLN
9	j	40	HIS
9	j	58	ASN
9	j	80	HIS
9	j	128	ASN
9	j	136	GLN
10	k	5	GLN
10	k	88	ASN
12	m	13	HIS
12	m	45	GLN
12	m	88	ASN
13	n	16	HIS
13	n	62	ASN
13	n	81	ASN
13	n	107	ASN
14	o	38	GLN
14	o	98	GLN
14	o	100	HIS
15	p	11	GLN
15	p	14	GLN

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Mol	Chain	Res	Type
15	p	51	ASN
16	q	43	GLN
16	q	71	ASN
17	r	6	GLN
17	r	12	HIS
18	s	7	HIS
19	t	28	ASN
19	t	48	GLN
20	u	68	ASN
20	u	73	ASN
22	w	8	ASN
23	x	15	ASN
24	y	15	ASN
24	y	25	GLN
24	y	38	GLN
24	y	58	ASN
25	z	19	HIS
26	B	4	GLN
28	D	6	GLN
28	D	26	ASN
31	G	17	HIS
31	G	38	HIS
31	G	50	ASN
31	G	88	GLN
31	G	176	ASN
32	H	2	GLN
32	H	5	HIS
32	H	7	ASN
32	H	31	ASN
32	H	40	GLN
32	H	184	ASN
33	I	39	GLN
33	I	135	GLN
34	J	11	GLN
34	J	42	ASN
34	J	81	GLN
34	J	121	ASN
34	J	131	ASN
35	K	17	GLN
36	L	27	ASN
36	L	51	GLN
36	L	67	ASN

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Mol	Chain	Res	Type
36	L	96	ASN
37	M	17	GLN
37	M	37	ASN
37	M	117	GLN
38	N	36	GLN
38	N	80	HIS
38	N	109	GLN
38	N	125	GLN
40	P	21	HIS
40	P	23	HIS
40	P	39	ASN
40	P	100	ASN
40	P	118	ASN
41	Q	45	ASN
42	R	90	HIS
43	S	70	HIS
45	U	26	ASN
45	U	40	ASN
45	U	79	ASN
47	W	18	GLN
47	W	51	GLN
49	Y	12	GLN
49	Y	47	GLN
49	Y	51	ASN
49	Y	81	GLN
51	a	58	ASN
51	a	160	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	135 (8%)	7 (0%)
53	1	2902/2903 (99%)	337 (11%)	9 (0%)
54	2	119/120 (99%)	12 (10%)	1 (0%)
55	5	76/77 (98%)	11 (14%)	0
55	6	76/77 (98%)	8 (10%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	72/76 (94%)	9 (12%)	0
All	All	4800/4810 (99%)	514 (10%)	17 (0%)

All (514) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A
52	3	71	A
52	3	87	C
52	3	95	C
52	3	100	G
52	3	130	A
52	3	144	G
52	3	183	C
52	3	184	G
52	3	197	A
52	3	209	U
52	3	210	C
52	3	226	G
52	3	247	G
52	3	251	G
52	3	266	G
52	3	267	C
52	3	281	G
52	3	289	G
52	3	345	C
52	3	346	G
52	3	352	C
52	3	355	C
52	3	367	U
52	3	372	C
52	3	412	A
52	3	413	G
52	3	422	C
52	3	429	U
52	3	467	U
52	3	479	U
52	3	484	G
52	3	485	U
52	3	486	U
52	3	496	A
52	3	518	C

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Mol	Chain	Res	Type
52	3	547	A
52	3	561	U
52	3	572	A
52	3	573	A
52	3	575	G
52	3	576	C
52	3	577	G
52	3	633	G
52	3	665	A
52	3	703	G
52	3	724	G
52	3	755	G
52	3	777	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	821	G
52	3	843	U
52	3	844	G
52	3	846	G
52	3	871	U
52	3	873	A
52	3	890	G
52	3	902	G
52	3	926	G
52	3	934	C
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1030	U
52	3	1031	C
52	3	1033	G

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Mol	Chain	Res	Type
52	3	1034	G
52	3	1053	G
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1198	G
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1258	G
52	3	1260	G
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1282	C
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1301	U
52	3	1317	C
52	3	1320	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1395	C
52	3	1446	A
52	3	1448	C
52	3	1452	C

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Mol	Chain	Res	Type
52	3	1492	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1533	C
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	46	G
53	1	49	A
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A
53	1	75	G
53	1	119	A
53	1	120	U
53	1	138	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	216	A
53	1	221	A
53	1	222	A
53	1	229	C
53	1	248	G
53	1	249	C
53	1	255	A
53	1	265	A
53	1	266	G
53	1	276	U
53	1	278	A
53	1	281	C

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Mol	Chain	Res	Type
53	1	294	A
53	1	301	G
53	1	311	A
53	1	323	C
53	1	324	A
53	1	329	G
53	1	330	A
53	1	361	G
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	424	G
53	1	451	U
53	1	457	A
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	530	G
53	1	531	C
53	1	532	A
53	1	543	G
53	1	545	U
53	1	547	A
53	1	563	A
53	1	573	U
53	1	574	A
53	1	588	U
53	1	603	A
53	1	614	A
53	1	616	A
53	1	627	A
53	1	637	A
53	1	646	U
53	1	654	A
53	1	669	G

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Mol	Chain	Res	Type
53	1	686	U
53	1	687	C
53	1	695	G
53	1	730	A
53	1	747	C
53	1	752	A
53	1	764	A
53	1	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	805	G
53	1	812	C
53	1	819	A
53	1	822	G
53	1	827	U
53	1	828	U
53	1	830	G
53	1	845	A
53	1	846	U
53	1	847	U
53	1	859	G
53	1	860	U
53	1	878	A
53	1	885	C
53	1	886	A
53	1	887	U
53	1	896	A
53	1	897	C
53	1	910	A
53	1	915	C
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	983	A
53	1	990	A
53	1	995	C
53	1	996	A
53	1	1012	U
53	1	1013	C

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Mol	Chain	Res	Type
53	1	1021	A
53	1	1022	G
53	1	1026	G
53	1	1033	U
53	1	1045	C
53	1	1046	A
53	1	1047	G
53	1	1054	A
53	1	1060	U
53	1	1062	G
53	1	1063	G
53	1	1066	U
53	1	1070	A
53	1	1071	G
53	1	1079	C
53	1	1084	A
53	1	1088	A
53	1	1104	C
53	1	1106	G
53	1	1111	A
53	1	1131	G
53	1	1132	U
53	1	1133	A
53	1	1135	C
53	1	1143	A
53	1	1157	G
53	1	1174	U
53	1	1175	A
53	1	1176	U
53	1	1177	G
53	1	1178	C
53	1	1180	U
53	1	1212	G
53	1	1238	G
53	1	1250	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A
53	1	1275	A
53	1	1289	C

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Mol	Chain	Res	Type
53	1	1301	A
53	1	1302	A
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1395	A
53	1	1398	C
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1454	C
53	1	1461	C
53	1	1476	U
53	1	1482	G
53	1	1490	A
53	1	1491	G
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1533	C
53	1	1535	A
53	1	1536	C
53	1	1555	G
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1584	U
53	1	1585	C
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1654	A
53	1	1674	G
53	1	1699	G
53	1	1715	G

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Mol	Chain	Res	Type
53	1	1729	U
53	1	1730	C
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1800	C
53	1	1801	A
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	1914	C
53	1	1929	G
53	1	1930	G
53	1	1937	A
53	1	1938	A
53	1	1955	U
53	1	1963	U
53	1	1967	C
53	1	1970	A
53	1	1972	G
53	1	1991	U
53	1	1992	G
53	1	1993	U
53	1	1997	C
53	1	2022	U
53	1	2023	C
53	1	2030	A
53	1	2031	A
53	1	2036	C
53	1	2043	C
53	1	2049	G
53	1	2055	C
53	1	2056	G
53	1	2060	A
53	1	2061	G

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Mol	Chain	Res	Type
53	1	2062	A
53	1	2069	G
53	1	2072	C
53	1	2096	C
53	1	2110	G
53	1	2111	U
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2132	U
53	1	2133	G
53	1	2147	A
53	1	2162	G
53	1	2164	C
53	1	2172	U
53	1	2173	A
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2211	A
53	1	2213	U
53	1	2225	A
53	1	2239	G
53	1	2259	U
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2297	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2407	A
53	1	2423	U
53	1	2424	C

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Mol	Chain	Res	Type
53	1	2427	C
53	1	2429	G
53	1	2430	A
53	1	2435	A
53	1	2441	U
53	1	2448	A
53	1	2476	A
53	1	2491	U
53	1	2498	C
53	1	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2529	G
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2609	U
53	1	2613	U
53	1	2629	U
53	1	2646	C
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U
53	1	2714	G
53	1	2716	C
53	1	2744	G
53	1	2748	A
53	1	2751	G
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2794	C
53	1	2797	U
53	1	2799	A
53	1	2800	A

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Mol	Chain	Res	Type
53	1	2809	A
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2880	C
53	1	2884	U
54	2	4	C
54	2	13	G
54	2	15	A
54	2	24	G
54	2	35	C
54	2	41	G
54	2	44	G
54	2	67	G
54	2	89	U
54	2	90	C
54	2	108	A
54	2	109	A
55	5	8	U
55	5	9	G
55	5	14	A
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	56	C
55	5	57	A
55	5	61	C
55	5	74	C
55	6	6	G
55	6	16	C
55	6	18	G
55	6	19	G
55	6	20	U
55	6	47	U
55	6	48	C
55	6	61	C
56	4	12	A
56	4	13	A

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Mol	Chain	Res	Type
57	7	17	C
57	7	19	G
57	7	21	A
57	7	45	U
57	7	46	G
57	7	47	U
57	7	48	C
57	7	59	U
57	7	61	C

All (17) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	70	U
52	3	421	U
52	3	495	A
52	3	960	U
52	3	1190	G
52	3	1201	A
52	3	1300	G
53	1	490	C
53	1	859	G
53	1	1020	A
53	1	1130	U
53	1	1475	G
53	1	2286	G
53	1	2296	U
53	1	2326	C
53	1	2391	G
54	2	88	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

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	FME	5	101	55	8,9,10	0.67	0	8,9,11	0.88	0

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	FME	5	101	55	-	0/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

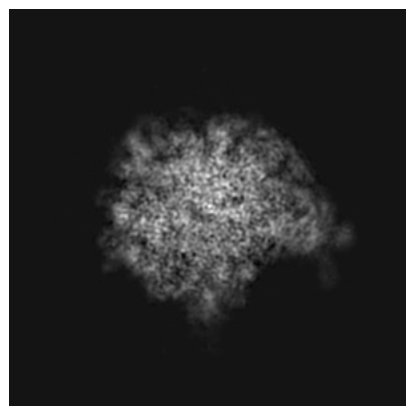
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21630. These allow visual inspection of the internal detail of the map and identification of artifacts.

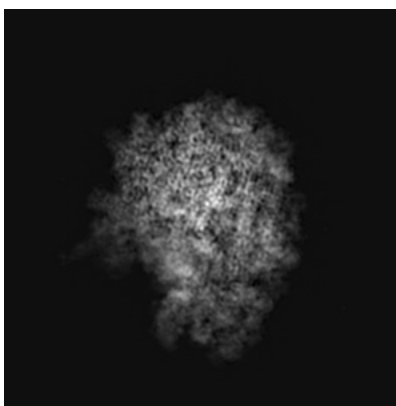
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

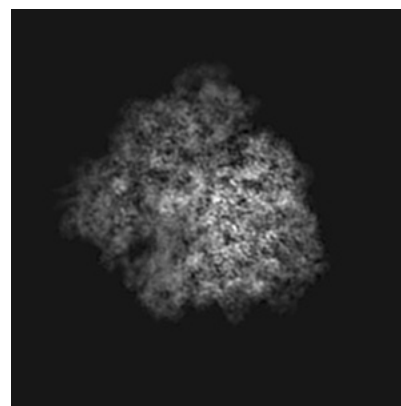
6.1.1 Primary map



X

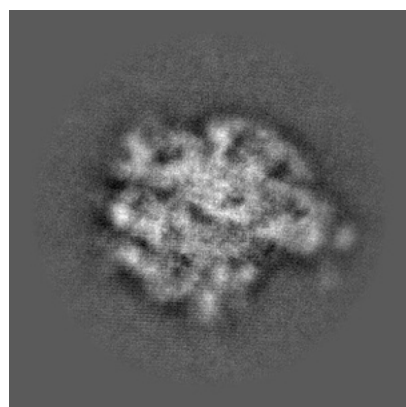


Y

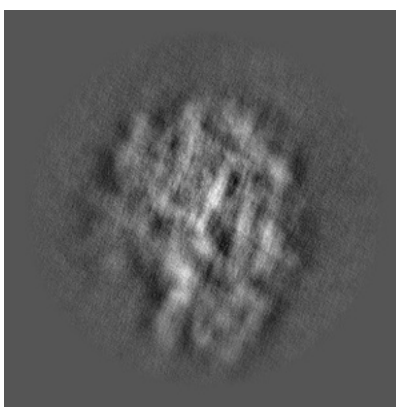


Z

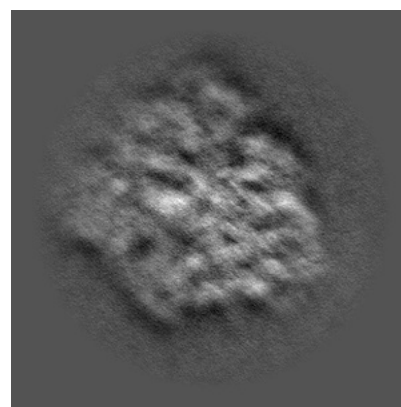
6.1.2 Raw map



X



Y

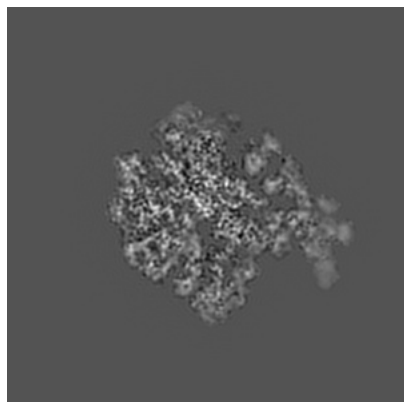


Z

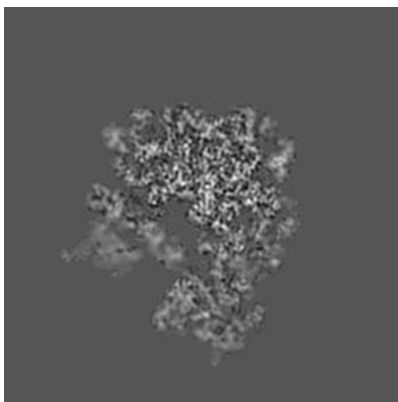
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

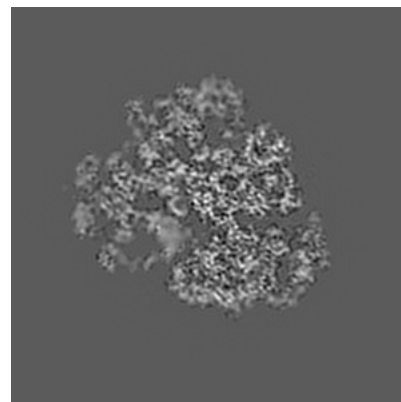
6.2.1 Primary map



X Index: 144

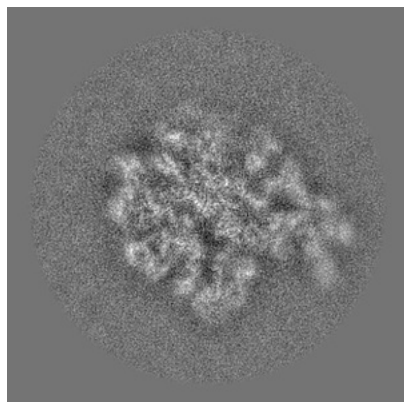


Y Index: 144

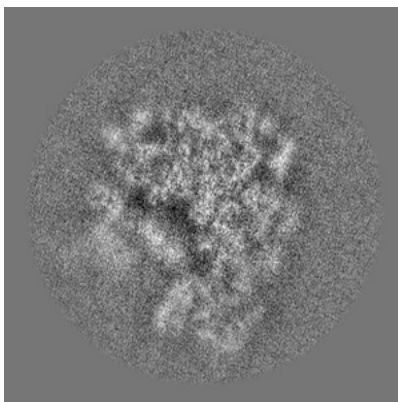


Z Index: 144

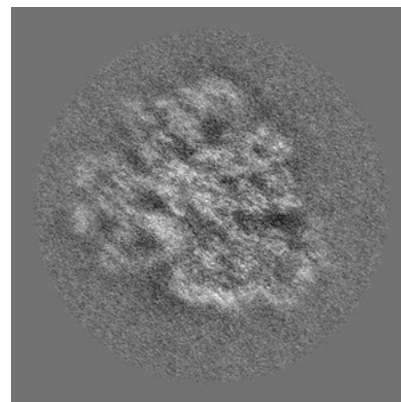
6.2.2 Raw map



X Index: 144



Y Index: 144

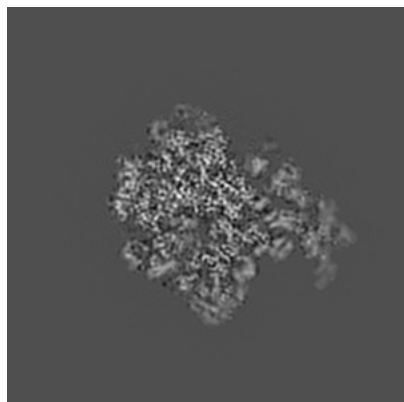


Z Index: 144

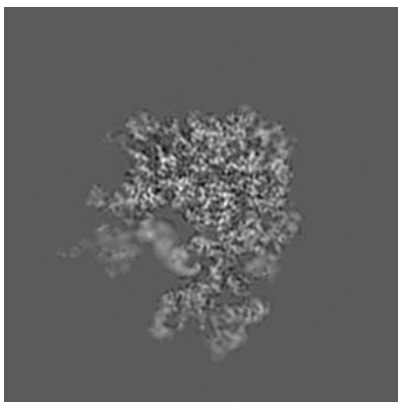
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

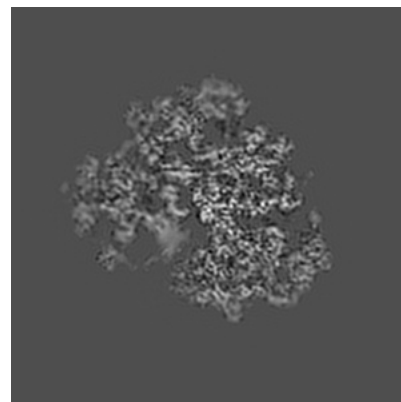
6.3.1 Primary map



X Index: 147

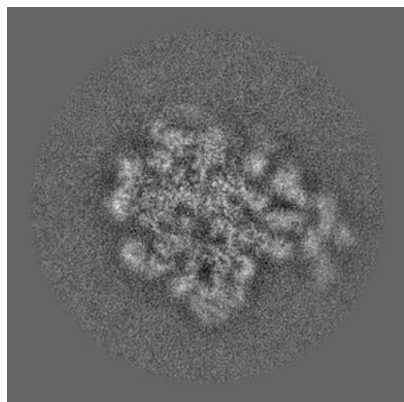


Y Index: 150

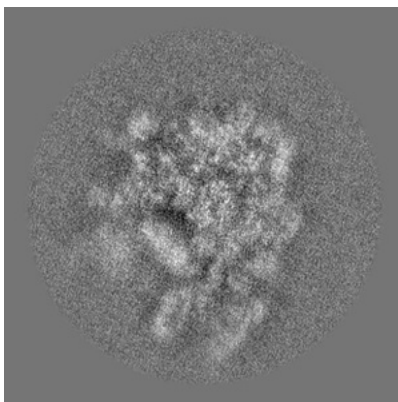


Z Index: 146

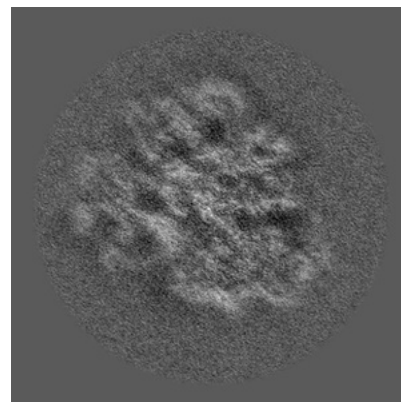
6.3.2 Raw map



X Index: 148



Y Index: 149

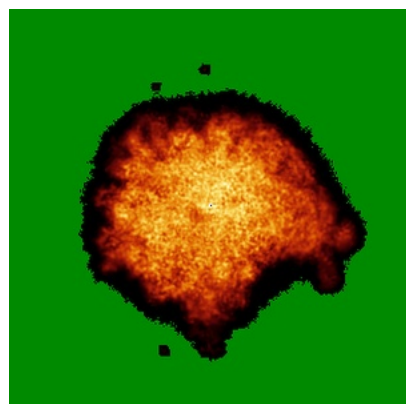


Z Index: 145

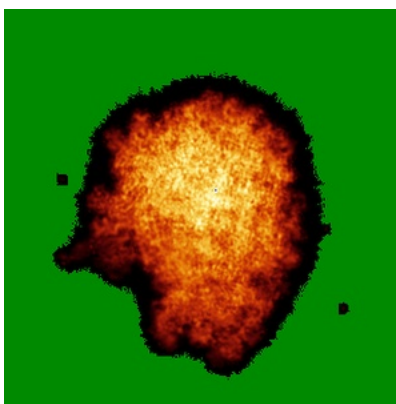
The images above show the largest variance slices of the map in three orthogonal directions.

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

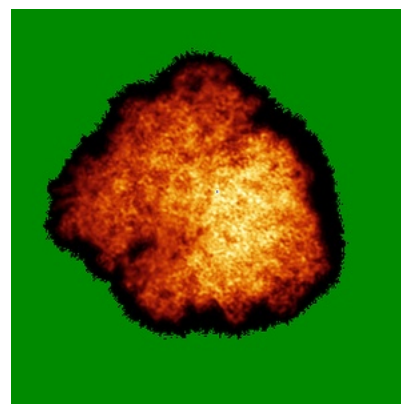
6.4.1 Primary map



X

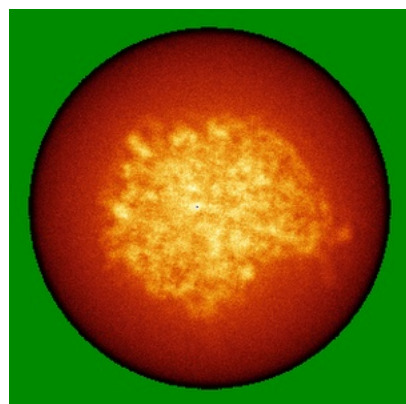


Y

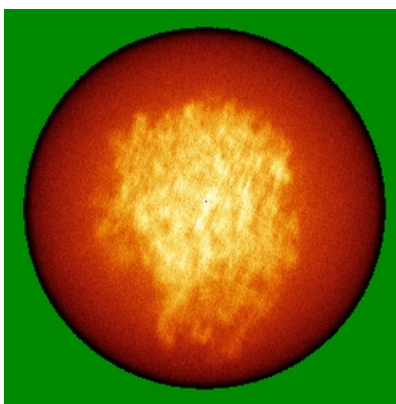


Z

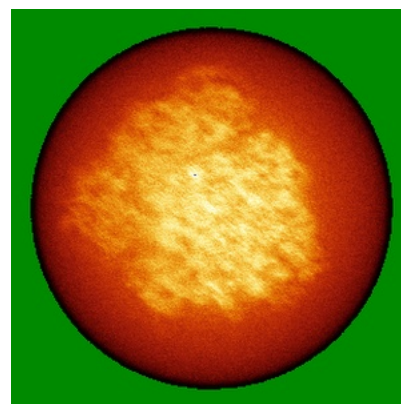
6.4.2 Raw map



X



Y



Z

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

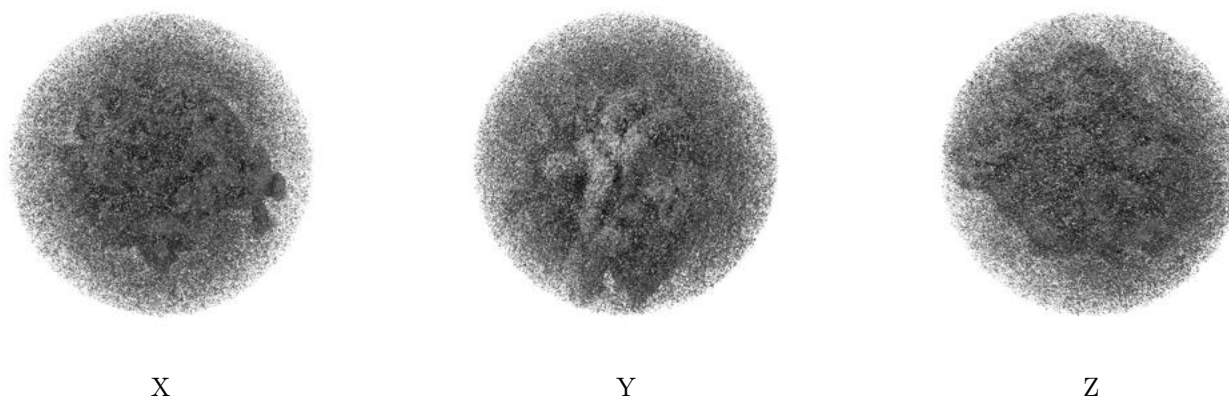
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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.

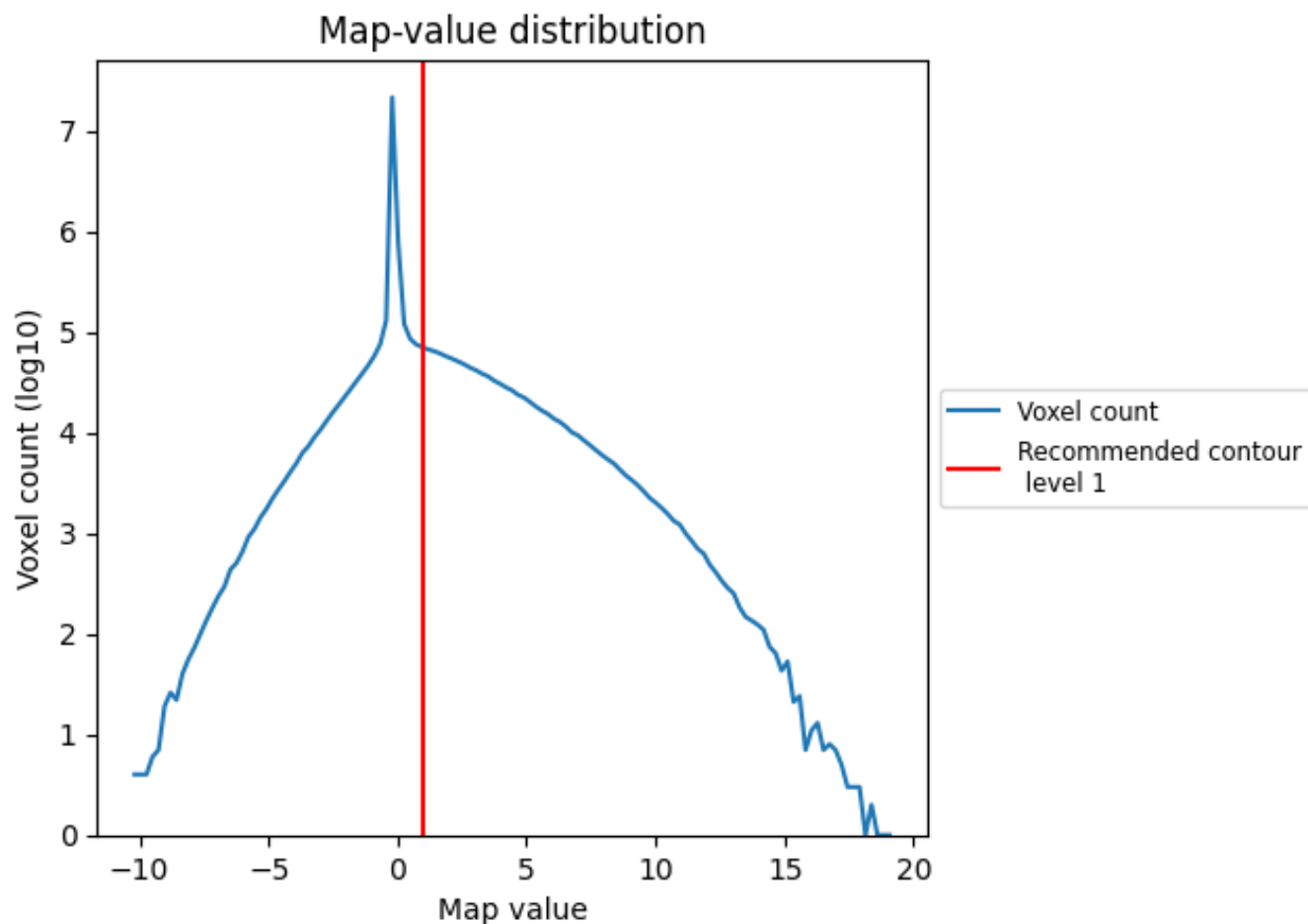
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

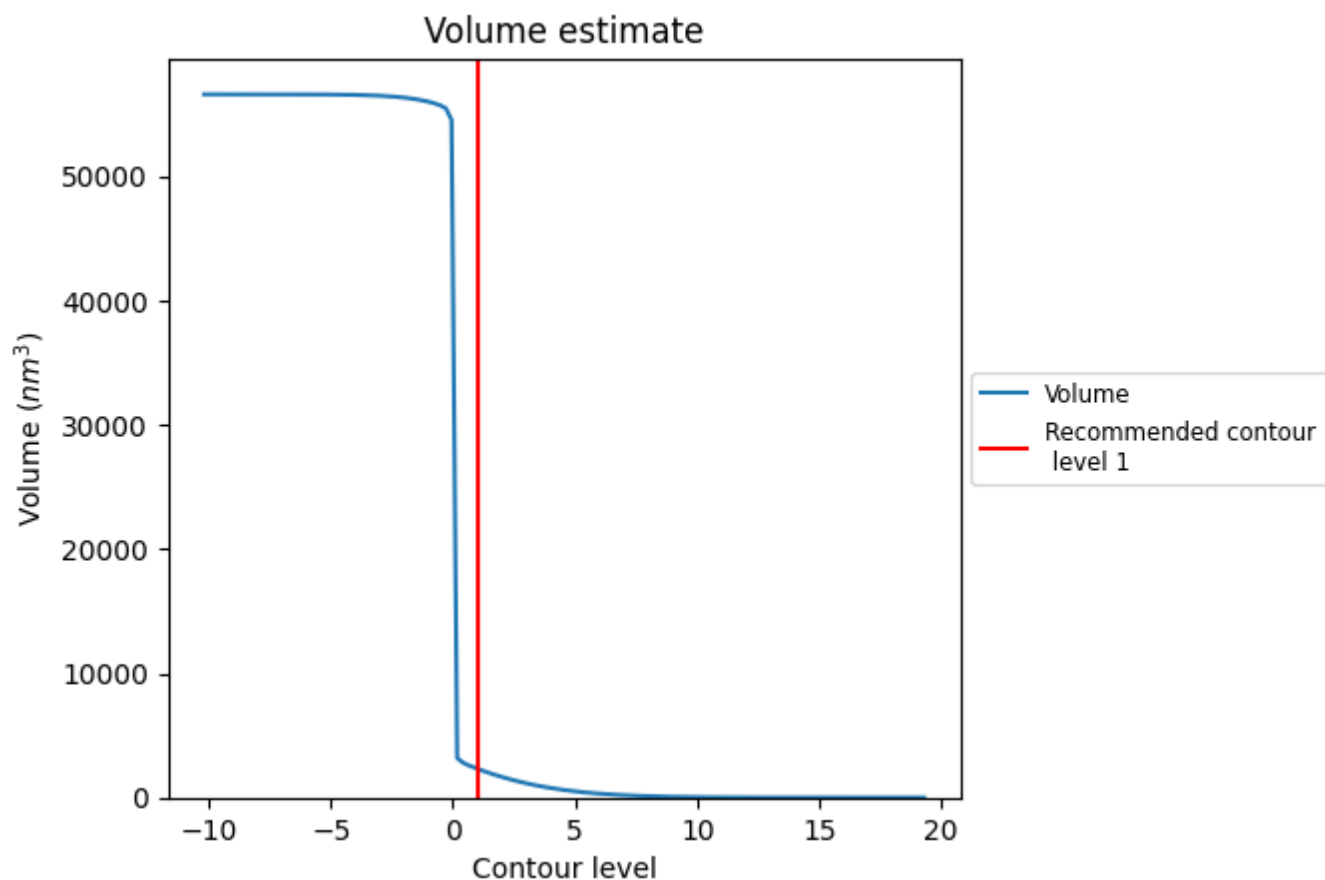
This section contains the results of statistical analysis of the map.

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.

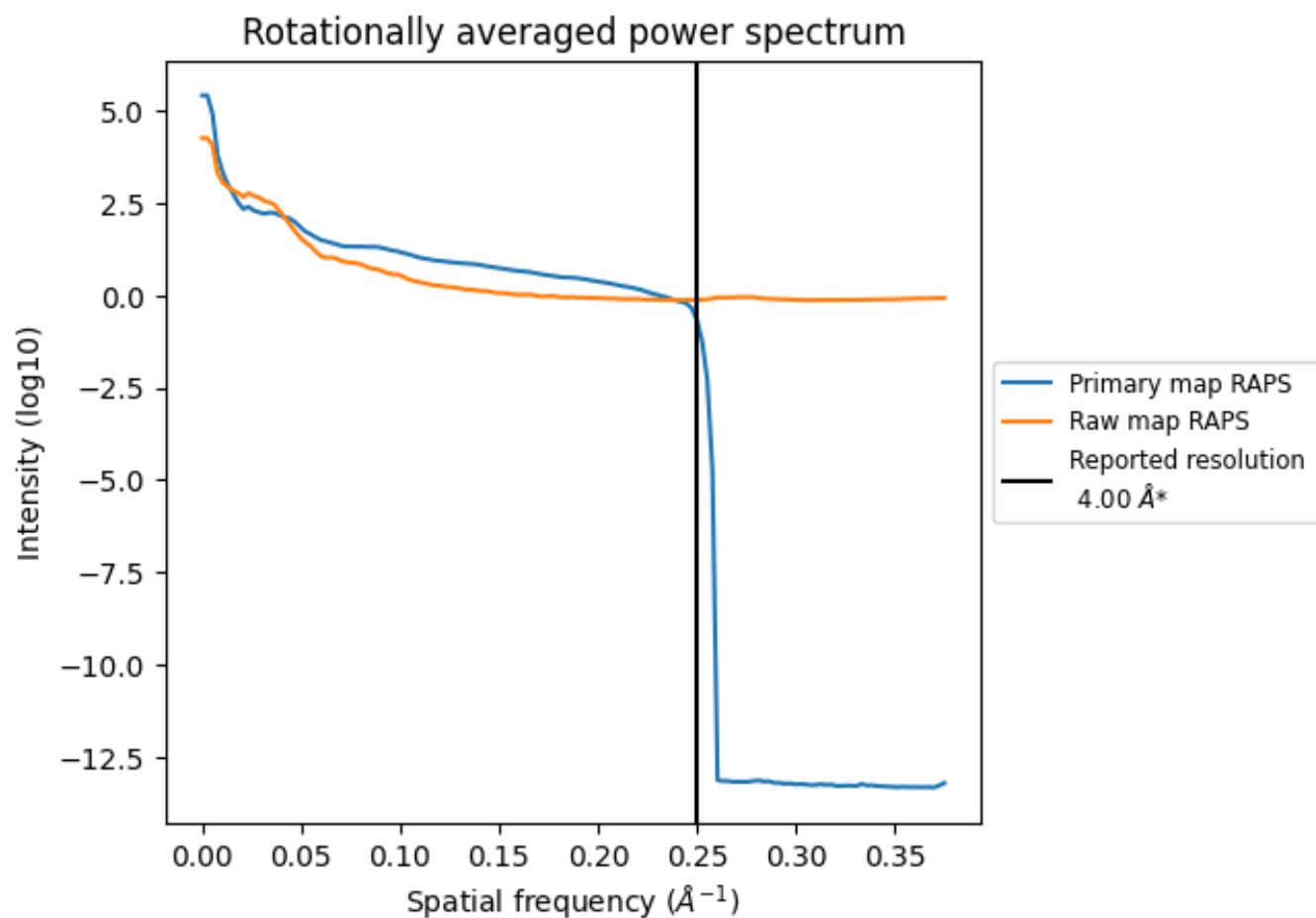
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2317 nm³; this corresponds to an approximate mass of 2093 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 ⓘ

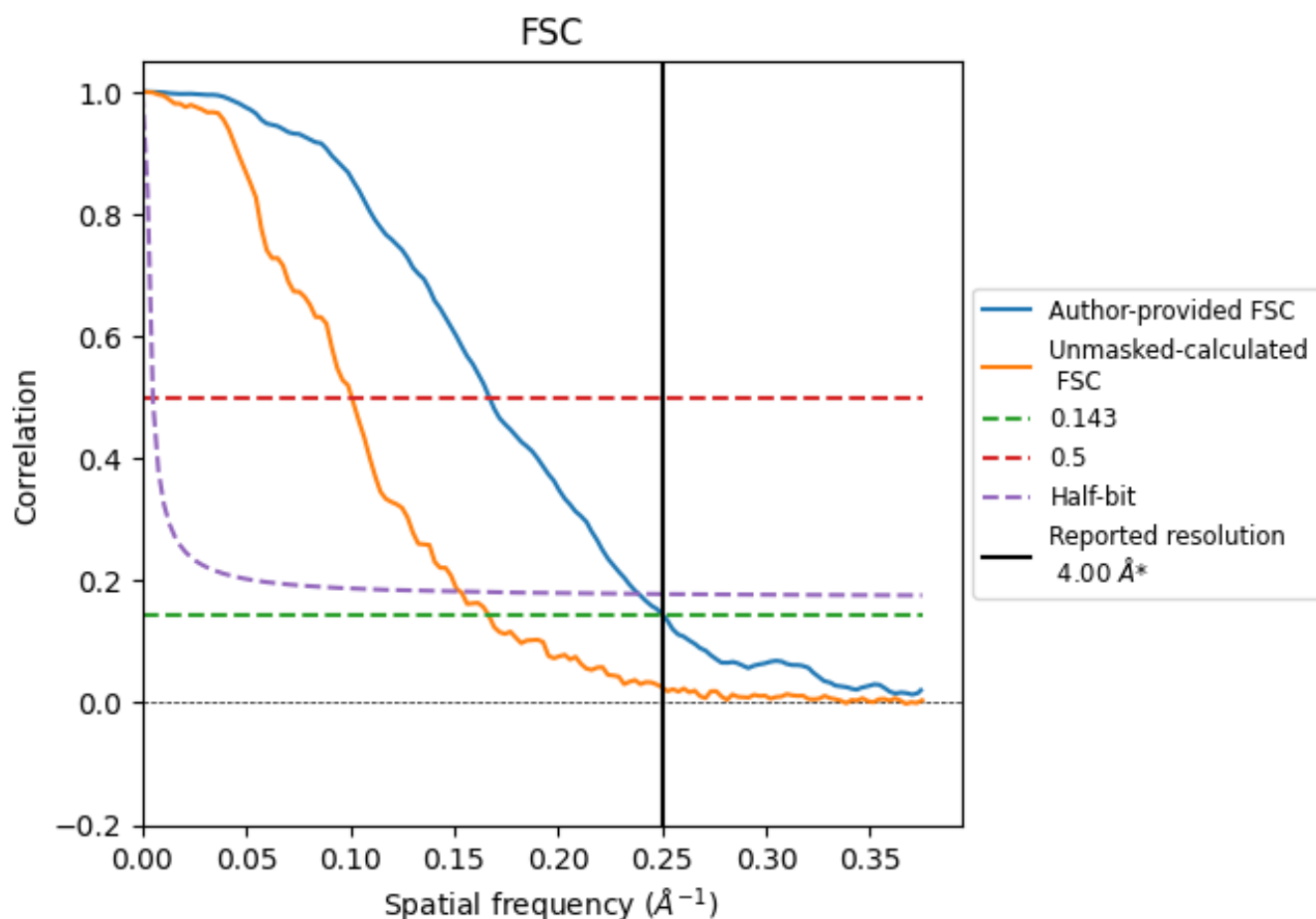


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.99	6.00	4.19
Unmasked-calculated*	6.00	9.93	6.54

*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 6.00 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21630 and PDB model 6WDB. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

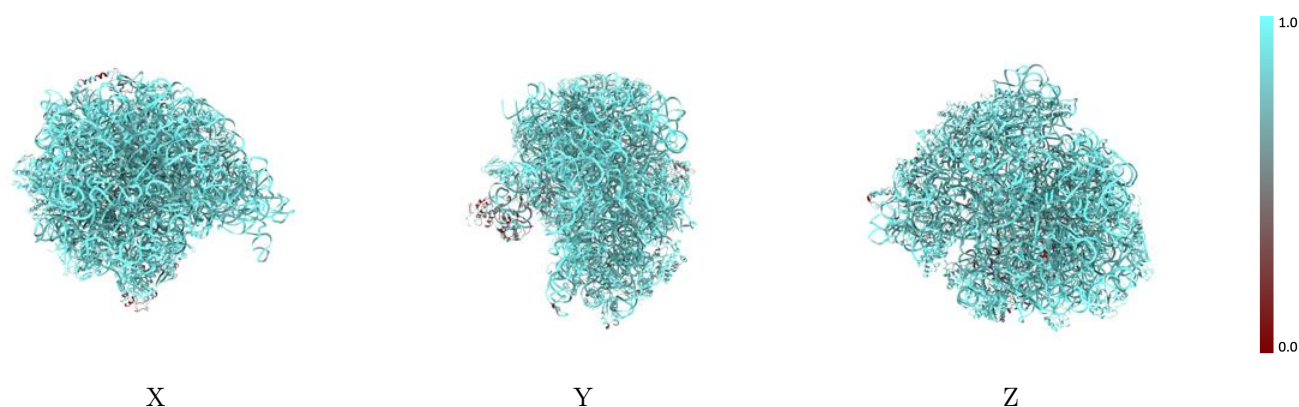
This section was not generated.

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



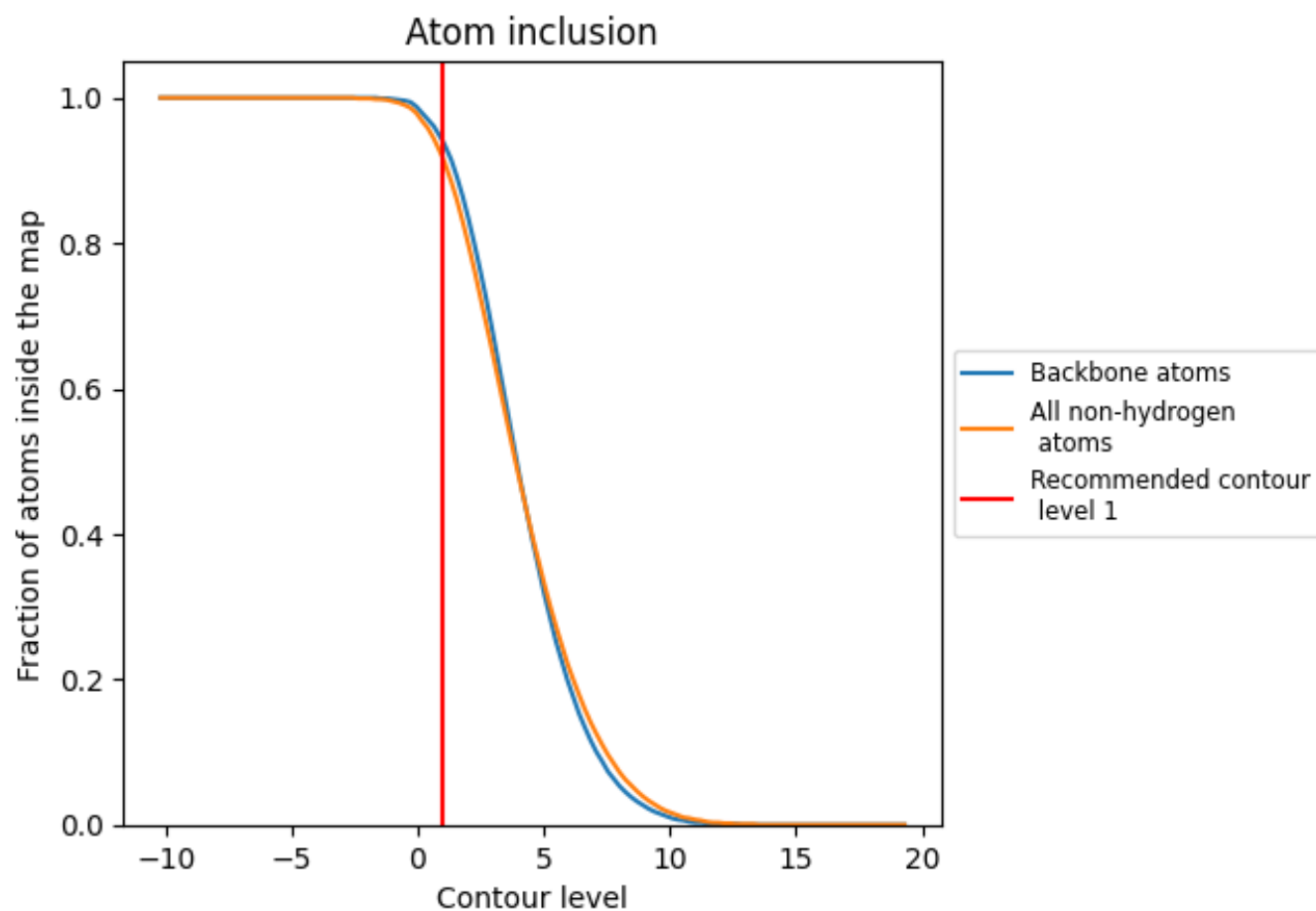
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9170	 0.2580
1	 0.9500	 0.2800
2	 0.9540	 0.2170
3	 0.9370	 0.2240
4	 0.8610	 0.1630
5	 0.8220	 0.0930
6	 0.7570	 0.1060
7	 0.9120	 0.1190
B	 0.9300	 0.3670
C	 0.6940	 0.2540
D	 0.9300	 0.3880
E	 0.9060	 0.3770
F	 0.7300	 0.2550
G	 0.8190	 0.2350
H	 0.8820	 0.2550
I	 0.8200	 0.2180
J	 0.8940	 0.2880
K	 0.9310	 0.2690
L	 0.8800	 0.2030
M	 0.8730	 0.2540
N	 0.8460	 0.2130
O	 0.7390	 0.1940
P	 0.9160	 0.2780
Q	 0.9110	 0.3160
R	 0.8940	 0.2150
S	 0.8330	 0.2270
T	 0.9260	 0.2690
U	 0.8520	 0.2610
V	 0.8810	 0.2050
W	 0.9130	 0.2750
X	 0.9210	 0.2420
Y	 0.8770	 0.2300
Z	 0.8400	 0.2380
a	 0.8540	 0.1380
b	 0.9450	 0.3820



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Chain	Atom inclusion	Q-score
c	 0.9150	 0.3620
d	 0.8960	 0.3120
e	 0.9320	 0.1840
f	 0.9270	 0.2490
g	 0.7490	 0.2260
h	 0.4390	 0.1030
i	 0.4940	 0.1010
j	 0.9210	 0.3550
k	 0.9050	 0.3690
l	 0.9260	 0.3270
m	 0.6400	 0.2320
n	 0.9230	 0.3560
o	 0.9210	 0.2610
p	 0.9220	 0.3350
q	 0.9170	 0.3720
r	 0.9470	 0.3010
s	 0.9160	 0.3510
t	 0.9110	 0.3220
u	 0.9360	 0.3200
v	 0.8820	 0.2140
w	 0.9020	 0.3370
x	 0.9520	 0.3720
y	 0.9150	 0.2400
z	 0.9180	 0.2850