



Full wwPDB EM Validation Report ⓘ

Mar 19, 2026 – 08:47 PM UTC

PDB ID : 6WDJ / pdb_00006wdj
EMDB ID : EMD-21638
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Non-cognate Structure V-A1)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.70 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 : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

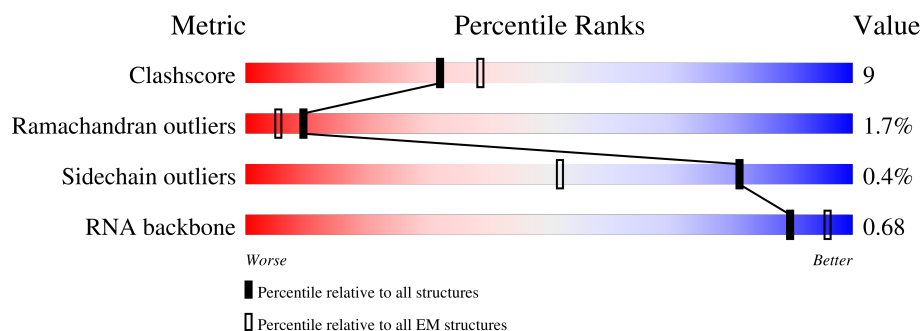
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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 $\leq 5\%$.

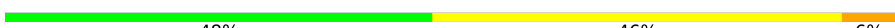
Mol	Chain	Length	Quality of chain
1	b	271	76% 23% .
2	c	209	69% 30%
3	d	201	75% 24%
4	e	177	70% 29% .
5	f	176	78% 22% .
6	g	149	68% 29% .
7	h	131	55% 37% 7% .

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Mol	Chain	Length	Quality of chain
8	i	141	67%31%
9	j	142	65%34%
10	k	122	68%30%
11	l	143	69%27%
12	m	136	74%25%
13	n	120	62%37%
14	o	116	79%21%
15	p	114	60%39%
16	q	117	81%18%
17	r	103	71%27%
18	s	110	85%15%
19	t	93	73%26%
20	u	102	74%24%
21	v	94	65%35%
22	w	75	72%28%
23	x	77	74%25%
24	y	63	73%25%
25	z	58	74%26%
26	B	56	68%32%
27	C	50	70%28%
28	D	46	80%15%
29	E	64	64%34%
30	F	38	68%29%
31	G	225	72%27%
32	H	206	74%25%



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Mol	Chain	Length	Quality of chain
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	
54	2	120	
55	5	77	
55	6	77	
56	4	18	

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Mol	Chain	Length	Quality of chain
57	7	76	72% 22% 5%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 150211 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		

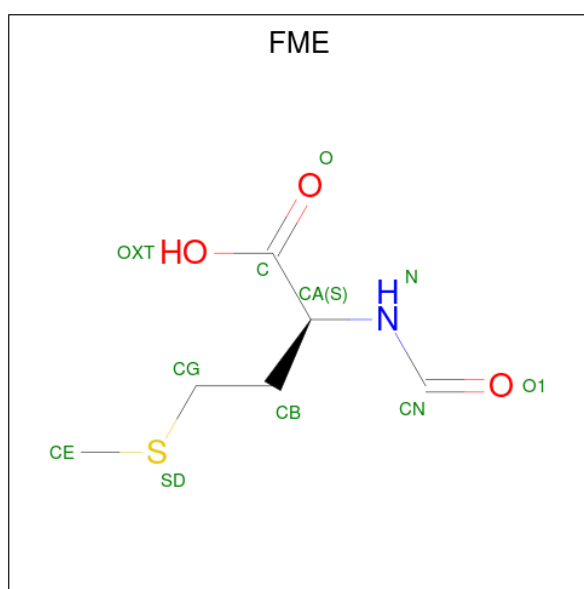
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	77	119	17		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

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

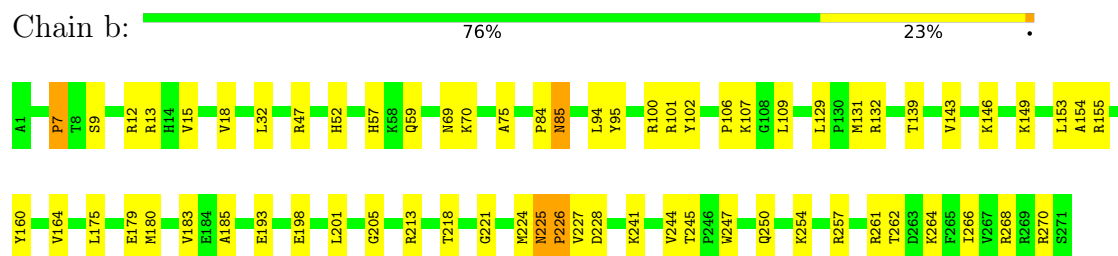


Mol	Chain	Residues	Atoms					AltConf
58	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

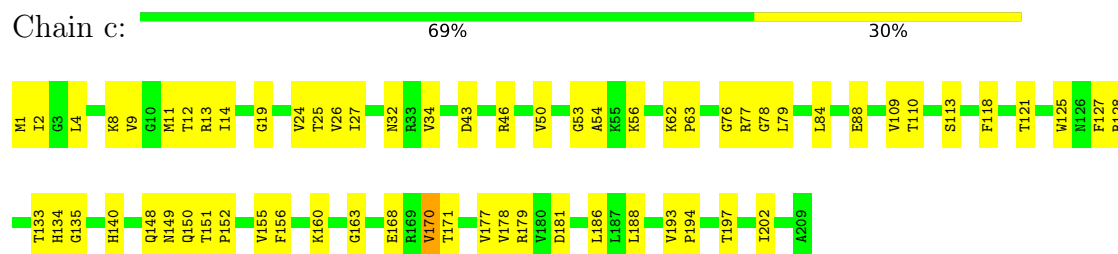
3 Residue-property plots

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. 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. 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.

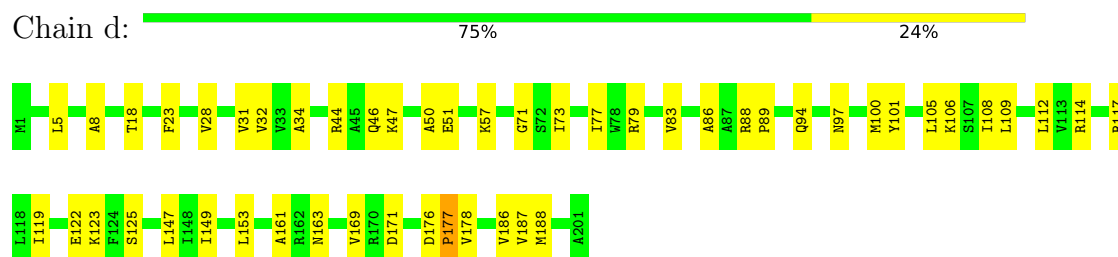
• Molecule 1: 50S ribosomal protein L2



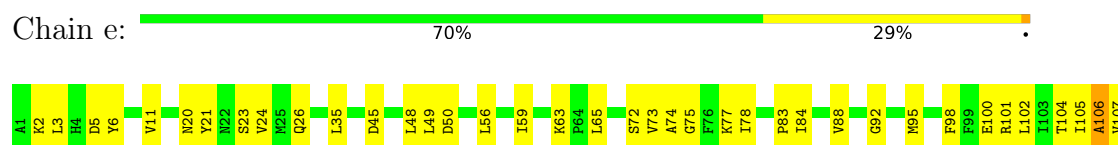
• Molecule 2: 50S ribosomal protein L3

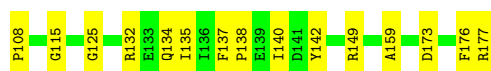


• Molecule 3: 50S ribosomal protein L4



• Molecule 4: 50S ribosomal protein L5





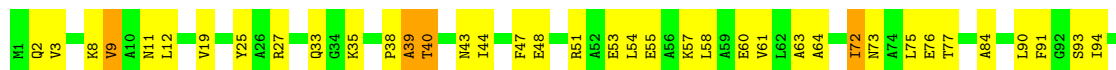
• Molecule 5: 50S ribosomal protein L6

Chain f: 78% 22% .



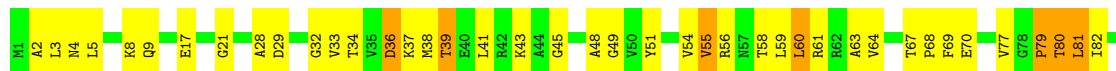
• Molecule 6: 50S ribosomal protein L9

Chain g: 68% 29% .



• Molecule 7: 50S ribosomal protein L10

Chain h: 55% 37% 7% .



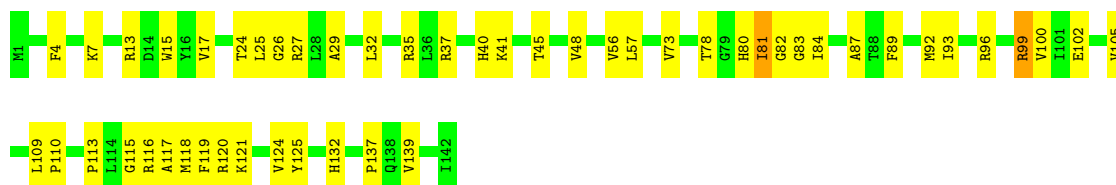
• Molecule 8: 50S ribosomal protein L11

Chain i: 67% 31% .



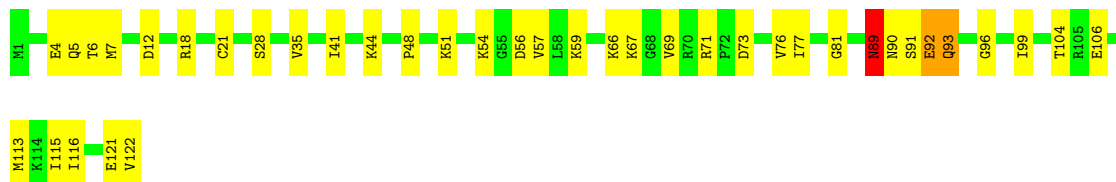
• Molecule 9: 50S ribosomal protein L13

Chain j: 65% 34% .



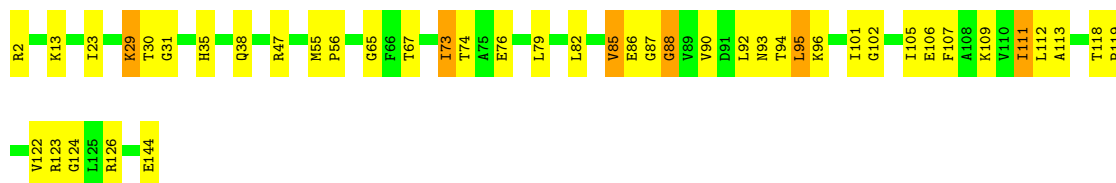
• Molecule 10: 50S ribosomal protein L14

Chain k: 68% 30% ..



• Molecule 11: 50S ribosomal protein L15

Chain l: 69% 27% .



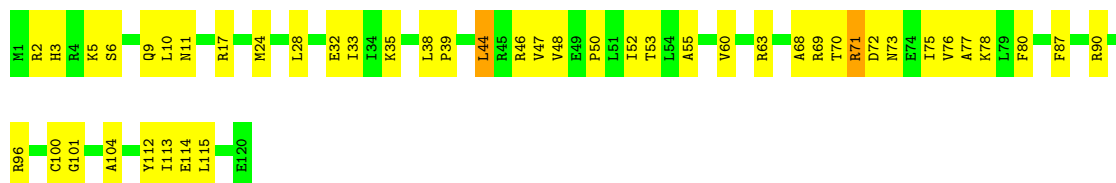
• Molecule 12: 50S ribosomal protein L16

Chain m: 74% 25% .



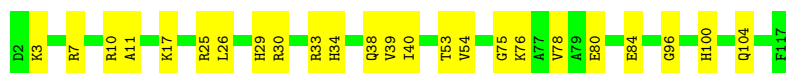
• Molecule 13: 50S ribosomal protein L17

Chain n: 62% 37% .

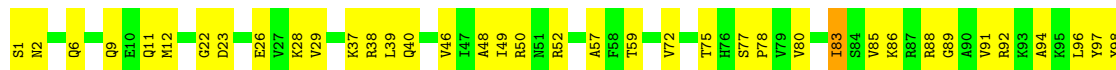


• Molecule 14: 50S ribosomal protein L18

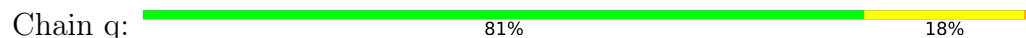
Chain o: 79% 21%



- Molecule 15: 50S ribosomal protein L19



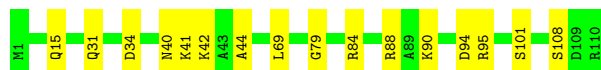
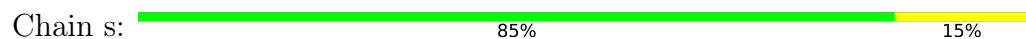
- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25

Chain v:  65% 35%



- Molecule 22: 50S ribosomal protein L27

Chain w:  72% 28%



- Molecule 23: 50S ribosomal protein L28

Chain x:  74% 25%



- Molecule 24: 50S ribosomal protein L29

Chain y:  73% 25%



- Molecule 25: 50S ribosomal protein L30

Chain z:  74% 26%



- Molecule 26: 50S ribosomal protein L32

Chain B:  68% 32%



- Molecule 27: 50S ribosomal protein L33

Chain C:  70% 28%



- Molecule 28: 50S ribosomal protein L34

Chain D:  80% 15% .



- Molecule 29: 50S ribosomal protein L35

Chain E:  64% 34% .



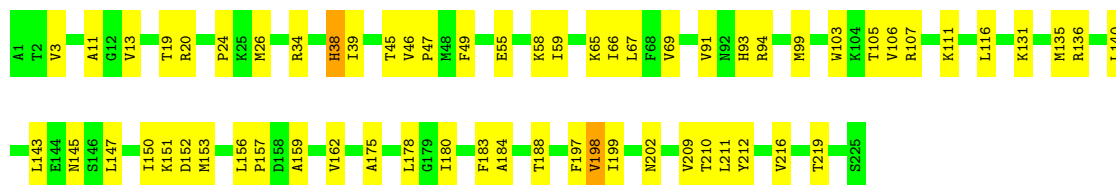
- Molecule 30: 50S ribosomal protein L36

Chain F:  68% 29% .



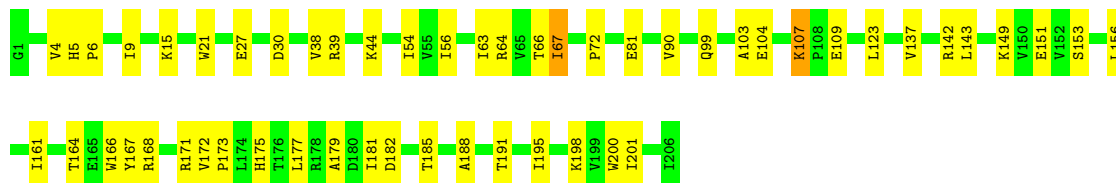
- Molecule 31: 30S ribosomal protein S2

Chain G:  72% 27% .



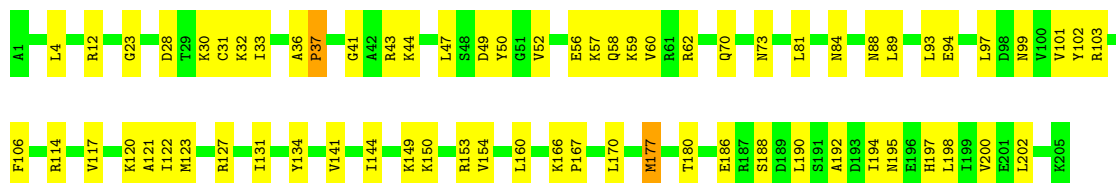
- Molecule 32: 30S ribosomal protein S3

Chain H:  74% 25% .

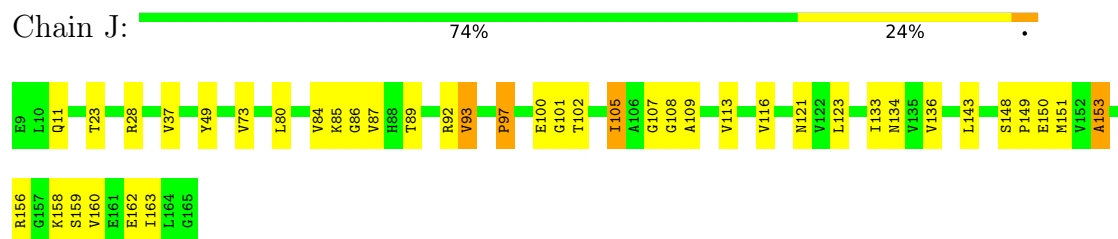


- Molecule 33: 30S ribosomal protein S4

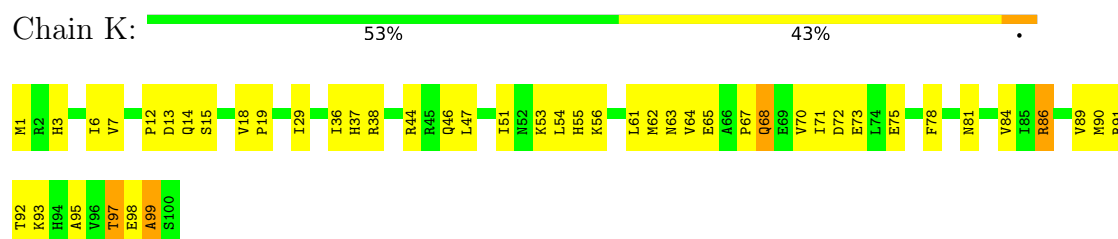
Chain I:  67% 32% .



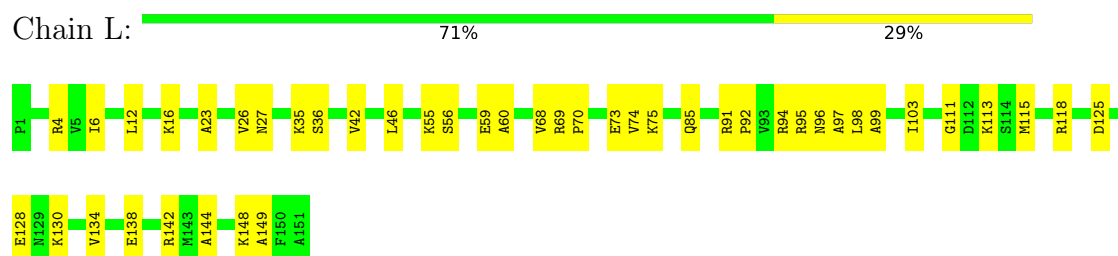
- Molecule 34: 30S ribosomal protein S5



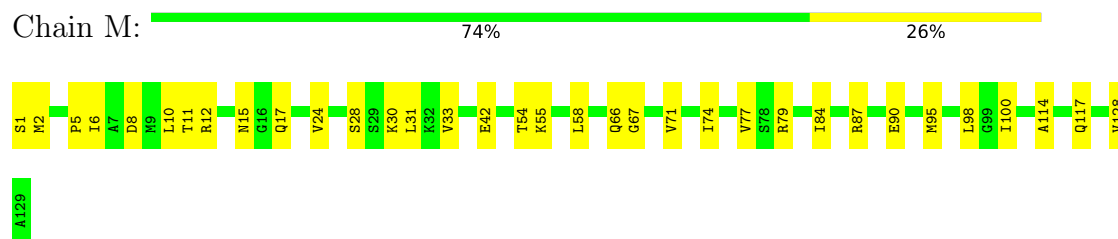
- Molecule 35: 30S ribosomal protein S6



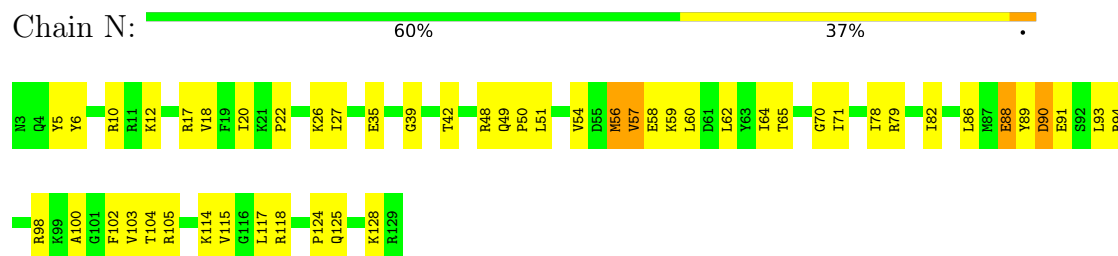
- Molecule 36: 30S ribosomal protein S7



- Molecule 37: 30S ribosomal protein S8

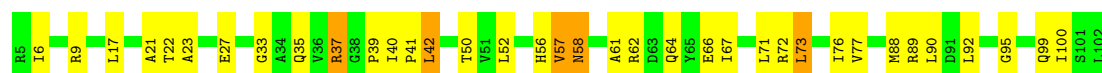


- Molecule 38: 30S ribosomal protein S9



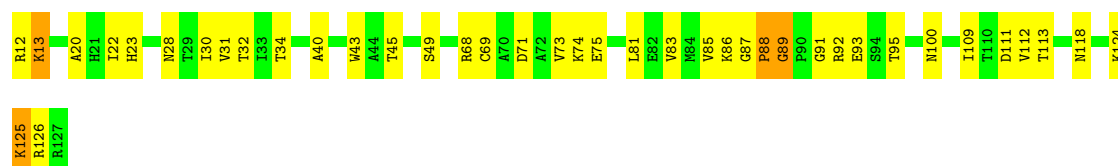
- Molecule 39: 30S ribosomal protein S10

Chain O:  63% 32% 5%



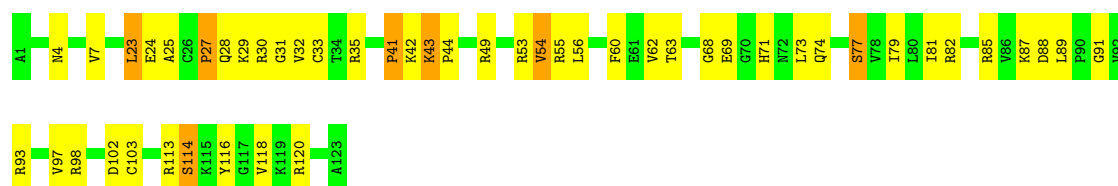
- Molecule 40: 30S ribosomal protein S11

Chain P:  66% 31% 3%



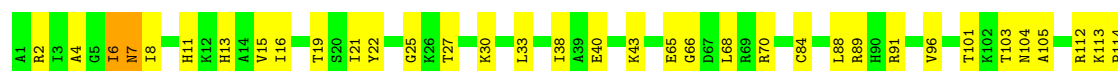
- Molecule 41: 30S ribosomal protein S12

Chain Q:  60% 34% 6%



- Molecule 42: 30S ribosomal protein S13

Chain R:  69% 29% 2%



- Molecule 43: 30S ribosomal protein S14

Chain S:  59% 38% 3%

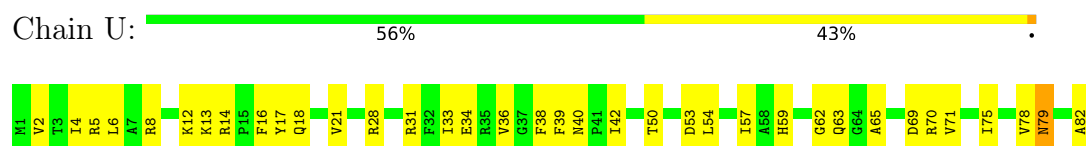


- Molecule 44: 30S ribosomal protein S15

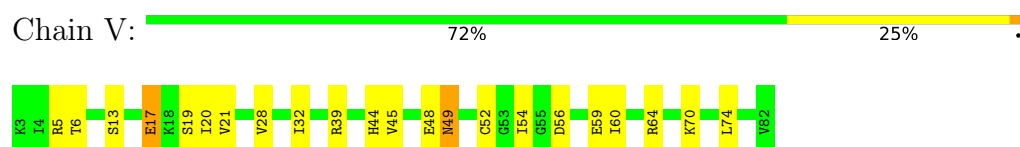
Chain T:  77% 22% 1%



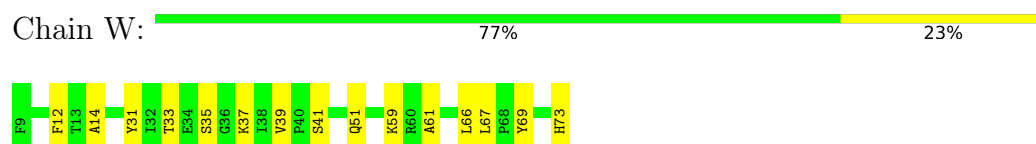
• Molecule 45: 30S ribosomal protein S16



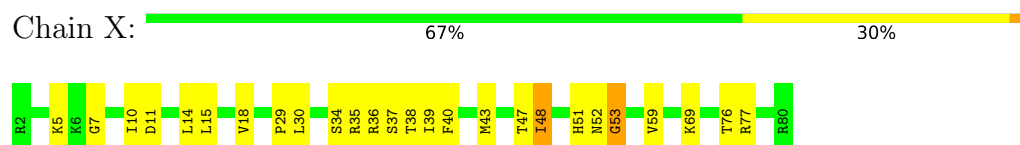
• Molecule 46: 30S ribosomal protein S17



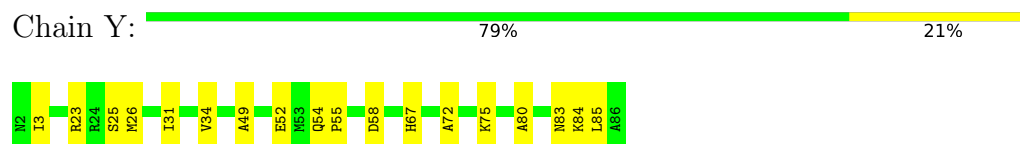
• Molecule 47: 30S ribosomal protein S18



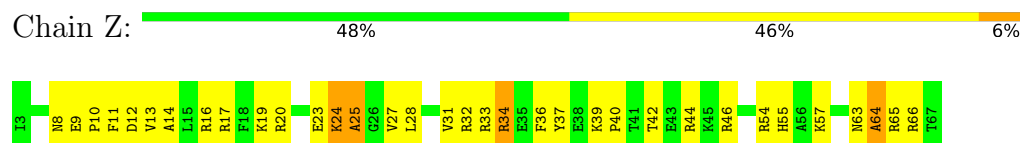
• Molecule 48: 30S ribosomal protein S19



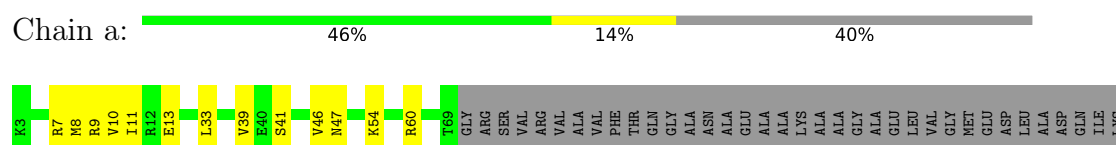
• Molecule 49: 30S ribosomal protein S20

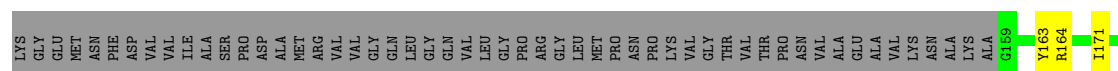


• Molecule 50: 30S ribosomal protein S21



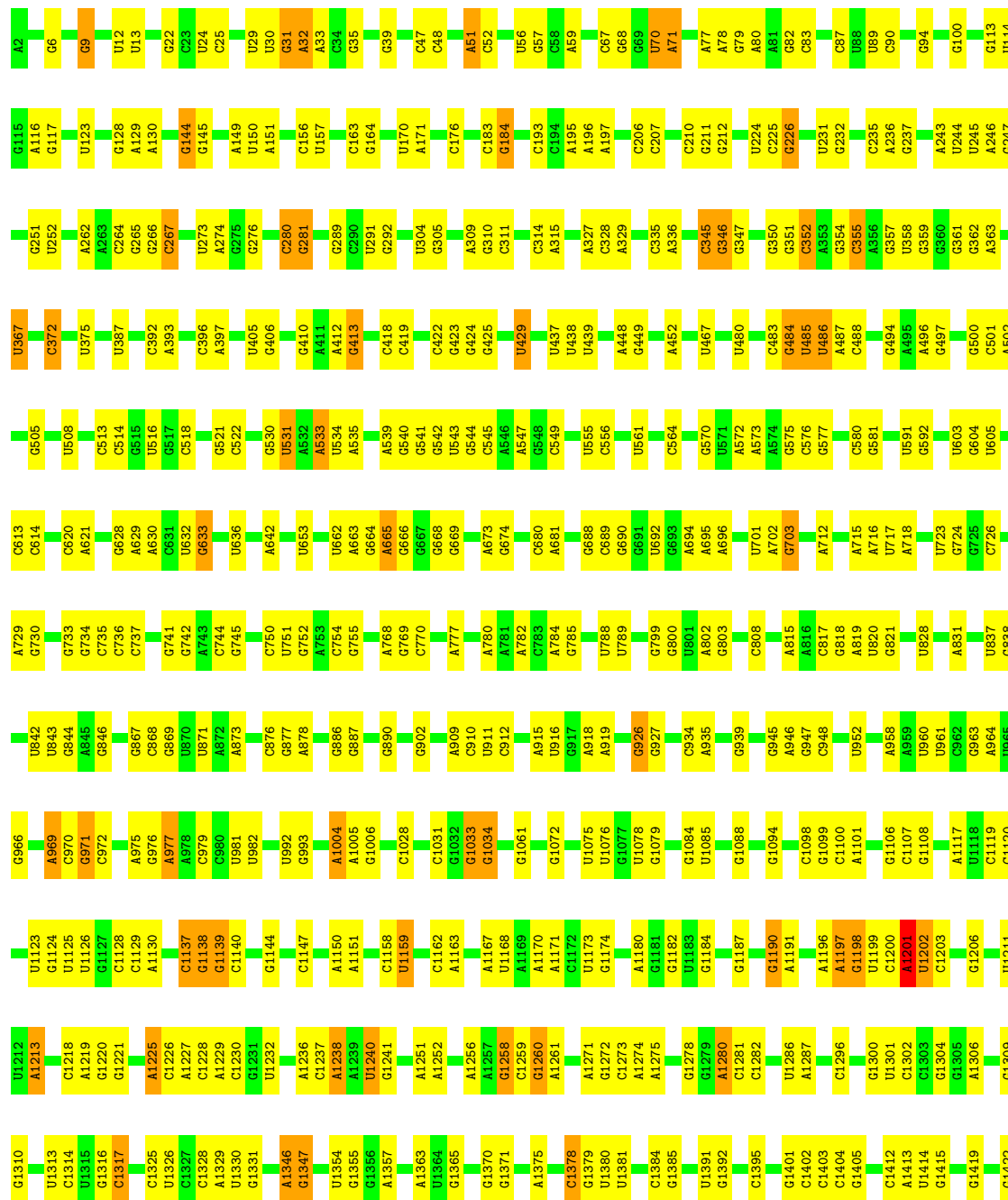
• Molecule 51: 50S ribosomal protein L1

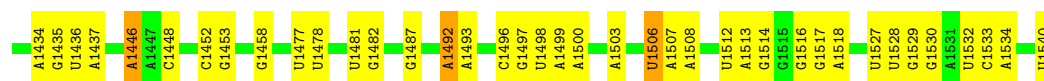




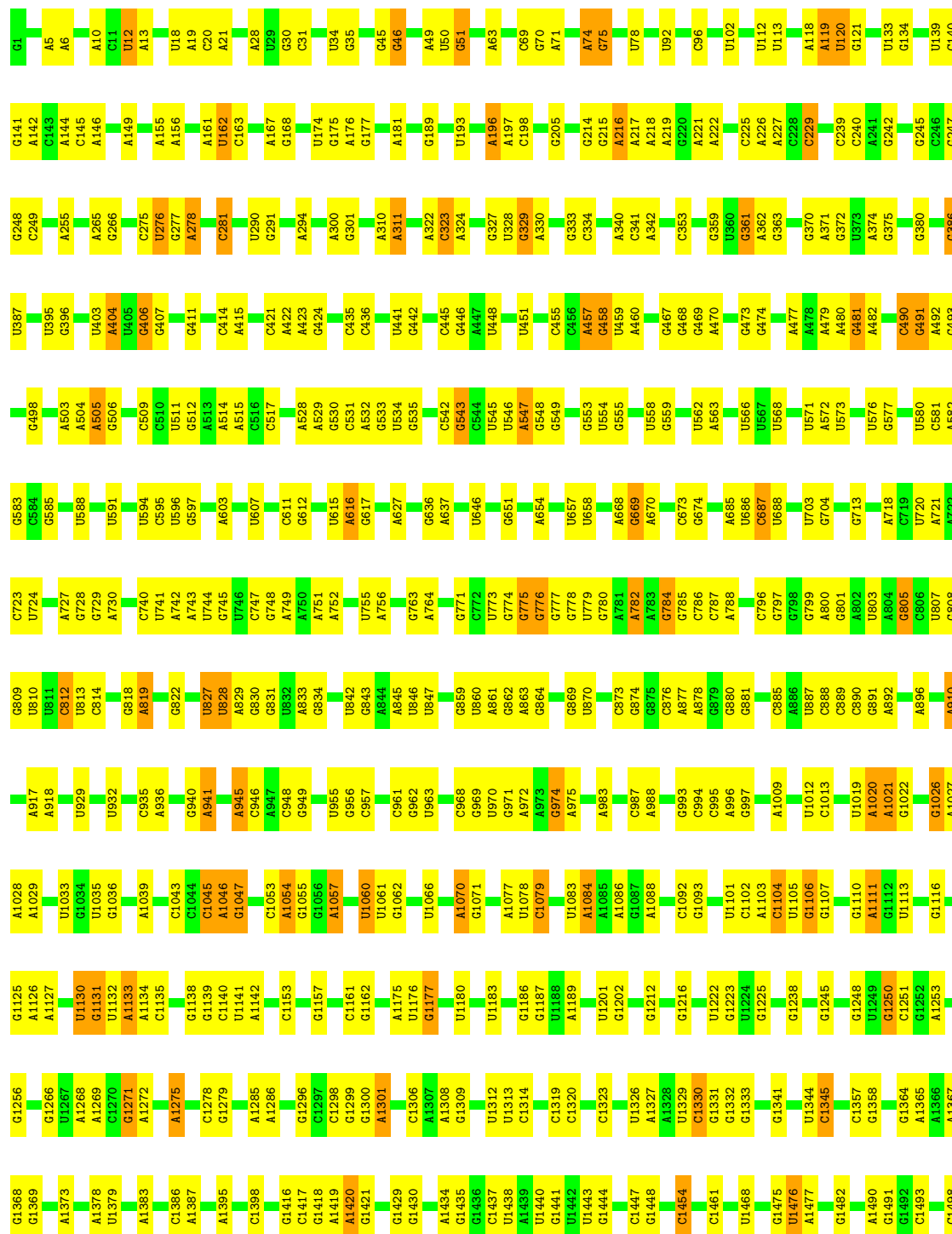
• Molecule 52: 16S ribosomal RNA

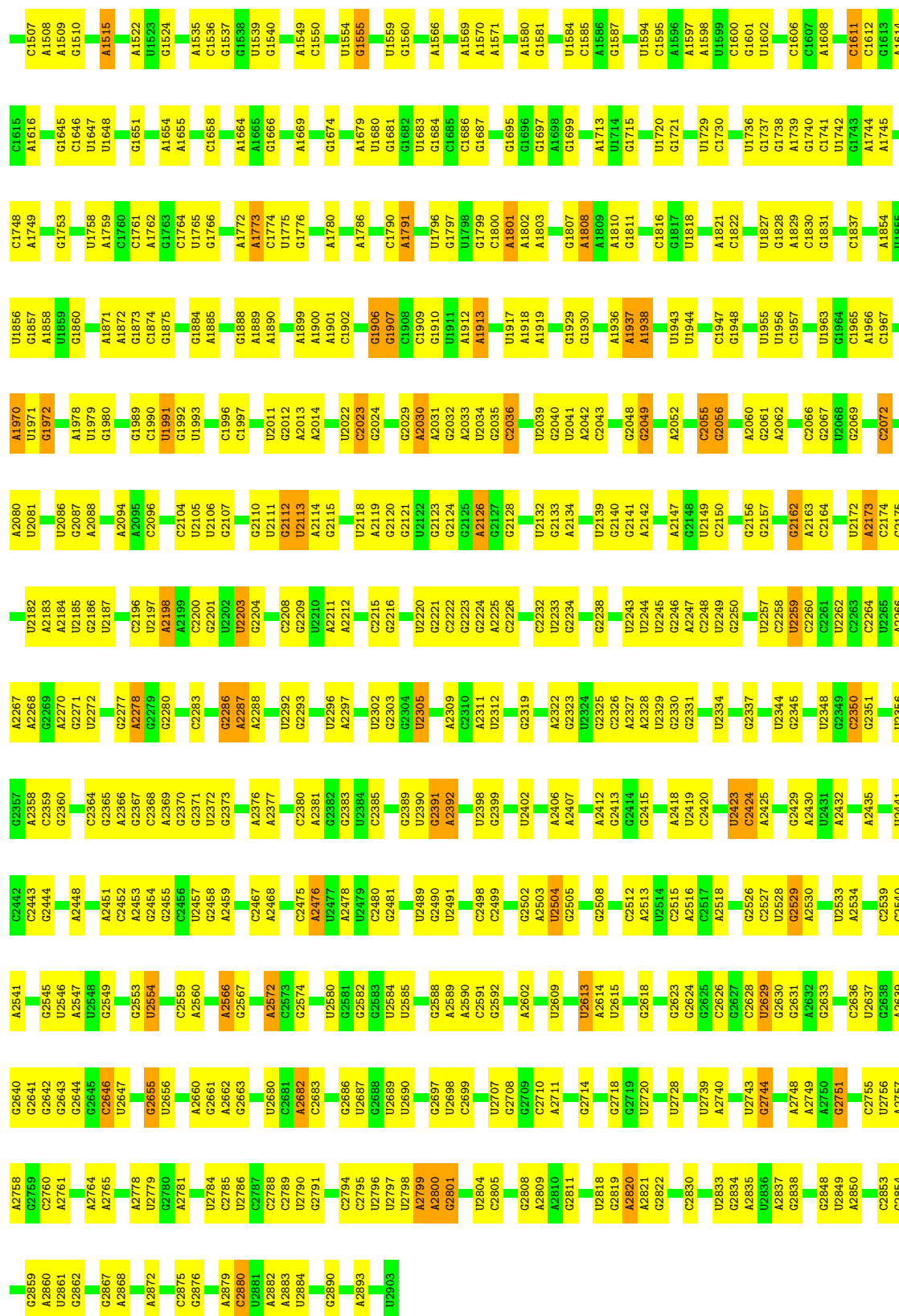
Chain 3: 66% 30% .





• Molecule 53: 23S ribosomal RNA



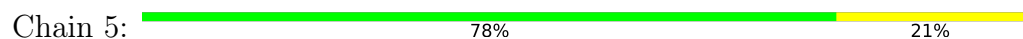


- Molecule 54: 5S ribosomal RNA

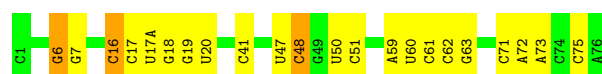




- Molecule 55: tRNA^{fMet}



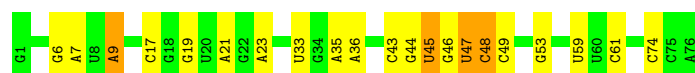
- Molecule 55: tRNA^{fMet}



- Molecule 56: mRNA



- Molecule 57: tRNA^{Phe}



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6847	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

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	0.28	0/2122	0.91	4/2852 (0.1%)
2	c	0.29	0/1586	0.88	5/2134 (0.2%)
3	d	0.29	0/1571	0.86	1/2113 (0.0%)
4	e	0.29	0/1435	0.88	4/1926 (0.2%)
5	f	0.29	0/1343	0.80	1/1816 (0.1%)
6	g	0.30	0/1122	0.98	5/1515 (0.3%)
7	h	0.34	0/1002	1.06	12/1350 (0.9%)
8	i	0.34	0/1046	1.00	8/1410 (0.6%)
9	j	0.28	0/1152	0.82	4/1551 (0.3%)
10	k	0.28	0/948	0.94	3/1268 (0.2%)
11	l	0.29	0/1054	0.97	5/1403 (0.4%)
12	m	0.29	0/1093	0.84	1/1460 (0.1%)
13	n	0.30	0/974	0.95	6/1301 (0.5%)
14	o	0.29	0/902	0.87	2/1209 (0.2%)
15	p	0.28	0/929	0.78	1/1242 (0.1%)
16	q	0.28	0/960	0.88	2/1278 (0.2%)
17	r	0.27	0/829	0.89	2/1107 (0.2%)
18	s	0.28	0/864	0.88	1/1156 (0.1%)
19	t	0.28	0/745	0.78	0/994
20	u	0.28	0/788	0.90	4/1051 (0.4%)
21	v	0.28	0/766	0.82	0/1025
22	w	0.27	0/582	0.82	0/769
23	x	0.27	0/635	0.78	1/848 (0.1%)
24	y	0.27	0/510	0.95	3/677 (0.4%)
25	z	0.28	0/453	0.81	1/605 (0.2%)
26	B	0.29	0/450	0.81	0/599
27	C	0.32	0/417	0.95	2/554 (0.4%)
28	D	0.32	0/380	0.91	0/498
29	E	0.30	0/513	0.86	1/676 (0.1%)
30	F	0.29	0/303	0.87	0/397
31	G	0.28	0/1788	0.87	5/2408 (0.2%)
32	H	0.29	0/1652	0.88	6/2225 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.29	0/1665	0.95	7/2227 (0.3%)
34	J	0.29	0/1170	0.89	3/1573 (0.2%)
35	K	0.30	0/836	0.85	1/1128 (0.1%)
36	L	0.29	0/1196	0.90	1/1602 (0.1%)
37	M	0.28	0/989	0.92	0/1326
38	N	0.30	0/1034	0.95	4/1375 (0.3%)
39	O	0.31	0/797	0.95	3/1077 (0.3%)
40	P	0.30	0/886	0.97	4/1195 (0.3%)
41	Q	0.29	0/969	0.96	3/1300 (0.2%)
42	R	0.31	0/893	0.91	2/1193 (0.2%)
43	S	0.29	0/817	0.90	4/1088 (0.4%)
44	T	0.28	0/722	0.88	4/964 (0.4%)
45	U	0.30	0/659	0.94	4/884 (0.5%)
46	V	0.28	0/658	0.87	1/881 (0.1%)
47	W	0.32	0/545	0.85	0/731
48	X	0.32	0/653	0.87	1/877 (0.1%)
49	Y	0.30	0/671	0.94	2/888 (0.2%)
50	Z	0.32	0/551	1.02	4/728 (0.5%)
51	a	0.31	0/1034	0.80	0/1387
52	3	0.40	0/36963	0.50	3/57662 (0.0%)
53	1	0.39	0/69796	0.50	0/108888
54	2	0.40	0/2872	0.50	0/4479
55	5	0.39	0/1832	0.48	0/2855
55	6	0.40	0/1832	0.51	0/2855
56	4	0.40	0/436	0.49	0/679
57	7	0.39	0/1809	0.47	0/2819
All	All	0.37	0/163199	0.63	141/244078 (0.1%)

There are no bond length outliers.

All (141) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	l	95	LEU	N-CA-C	-8.72	102.07	112.89
12	m	110	GLU	N-CA-C	7.75	121.67	111.75
2	c	150	GLN	N-CA-C	7.71	120.58	111.71
20	u	96	LYS	N-CA-C	-7.64	100.23	110.55
7	h	114	GLU	N-CA-C	7.53	119.18	110.97
42	R	68	LEU	N-CA-C	7.43	119.02	111.07
44	T	43	ALA	N-CA-C	-7.40	103.71	112.89
7	h	117	LEU	N-CA-C	7.34	120.48	109.25
2	c	19	GLY	N-CA-C	7.33	121.42	113.58
11	l	96	LYS	N-CA-C	-7.14	103.58	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	g	39	ALA	N-CA-C	7.08	119.34	109.15
33	I	36	ALA	N-CA-C	7.04	118.90	108.76
33	I	32	LYS	N-CA-C	-6.86	101.92	111.52
40	P	73	VAL	N-CA-C	-6.83	106.64	113.20
24	y	17	GLU	N-CA-C	-6.61	104.16	111.36
36	L	16	LYS	N-CA-C	-6.60	104.40	113.18
10	k	67	LYS	N-CA-C	-6.58	103.94	112.23
7	h	43	LYS	N-CA-C	-6.54	104.23	111.36
7	h	118	ILE	N-CA-C	6.50	122.92	108.88
11	l	113	ALA	N-CA-C	-6.47	105.14	113.16
40	P	69	CYS	N-CA-C	-6.45	105.57	113.50
2	c	168	GLU	N-CA-C	-6.41	100.46	109.69
45	U	69	ASP	N-CA-C	6.33	118.74	111.02
13	n	68	ALA	N-CA-C	-6.27	104.50	111.71
49	Y	85	LEU	N-CA-C	-6.26	105.47	113.23
8	i	24	GLY	CA-C-N	6.25	125.95	119.82
8	i	24	GLY	C-N-CA	6.25	125.95	119.82
1	b	225	ASN	CA-C-N	6.24	127.64	119.84
1	b	225	ASN	C-N-CA	6.24	127.64	119.84
41	Q	54	VAL	N-CA-C	6.23	116.84	108.11
7	h	55	VAL	N-CA-C	6.23	117.34	108.93
40	P	125	LYS	N-CA-C	6.16	123.91	110.80
32	H	177	LEU	N-CA-C	6.14	119.88	112.38
8	i	73	PRO	CA-C-N	6.11	126.12	119.89
8	i	73	PRO	C-N-CA	6.11	126.12	119.89
52	3	1190	G	C2'-C3'-O3'	6.08	118.62	109.50
23	x	6	VAL	N-CA-C	6.03	116.81	110.72
18	s	42	LYS	N-CA-C	-6.01	104.65	112.23
33	I	94	GLU	N-CA-C	-6.00	105.96	113.28
42	R	15	VAL	N-CA-C	5.97	116.16	110.42
13	n	77	ALA	N-CA-C	-5.96	104.72	112.23
4	e	11	VAL	N-CA-C	5.92	116.58	110.36
35	K	68	GLN	N-CA-C	5.92	117.73	111.28
10	k	90	ASN	N-CA-C	5.91	117.41	110.97
45	U	62	GLY	N-CA-C	-5.90	107.35	114.66
31	G	198	VAL	N-CA-C	5.88	117.67	109.55
7	h	118	ILE	CA-C-N	-5.87	112.51	119.84
7	h	118	ILE	C-N-CA	-5.87	112.51	119.84
4	e	173	ASP	N-CA-C	5.86	118.35	111.02
16	q	50	ARG	N-CA-C	-5.86	106.17	113.55
24	y	24	GLU	N-CA-C	5.85	118.41	111.33
11	l	111	ILE	N-CA-C	5.84	117.00	108.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	Z	55	HIS	N-CA-C	-5.83	104.89	112.23
7	h	119	PRO	N-CA-C	-5.81	100.50	112.47
44	T	53	ARG	N-CA-C	-5.80	104.86	111.07
8	i	127	SER	N-CA-C	-5.76	104.97	112.23
7	h	39	THR	N-CA-C	-5.76	106.59	113.97
52	3	1201	A	C2'-C3'-O3'	5.75	118.13	109.50
8	i	34	ILE	N-CA-C	5.75	115.94	110.42
41	Q	114	SER	N-CA-C	-5.71	105.14	111.71
31	G	38	HIS	N-CA-C	5.71	117.66	110.24
38	N	56	MET	N-CA-C	5.70	119.76	112.12
32	H	67	ILE	N-CA-C	5.68	116.28	107.99
14	o	54	VAL	N-CA-C	-5.67	105.36	113.07
9	j	99	ARG	N-CA-C	5.66	117.53	111.36
40	P	100	ASN	N-CA-C	-5.64	105.51	112.90
32	H	5	HIS	CA-C-N	5.63	125.74	119.32
32	H	5	HIS	C-N-CA	5.63	125.74	119.32
4	e	106	ALA	N-CA-C	5.63	117.11	110.97
29	E	3	ILE	N-CA-C	5.63	116.97	109.37
41	Q	43	LYS	N-CA-C	5.63	122.25	109.81
20	u	89	GLY	N-CA-C	-5.61	107.37	114.16
43	S	31	SER	N-CA-C	-5.61	105.36	113.21
14	o	84	GLU	N-CA-C	-5.60	105.70	112.54
6	g	64	ALA	N-CA-C	-5.60	105.17	112.23
2	c	113	SER	N-CA-C	5.57	117.52	110.33
7	h	79	PRO	N-CA-C	5.56	119.34	110.40
5	f	47	ASN	N-CA-C	-5.55	106.09	112.92
8	i	91	LYS	CA-C-N	5.55	126.78	119.84
8	i	91	LYS	C-N-CA	5.55	126.78	119.84
6	g	72	ILE	N-CA-C	-5.54	104.96	111.00
13	n	78	LYS	N-CA-C	-5.54	105.40	111.82
33	I	166	LYS	CA-C-N	5.51	125.51	119.89
33	I	166	LYS	C-N-CA	5.51	125.51	119.89
50	Z	37	TYR	N-CA-C	-5.51	105.90	113.56
46	V	60	ILE	N-CA-C	5.51	115.88	108.17
44	T	46	LYS	N-CA-C	5.50	122.52	110.80
20	u	75	ALA	N-CA-C	-5.50	108.35	114.62
2	c	156	PHE	N-CA-C	5.47	117.78	110.35
45	U	54	LEU	N-CA-C	5.46	117.94	111.33
43	S	49	THR	N-CA-C	-5.46	105.43	111.71
38	N	71	ILE	N-CA-C	5.46	115.66	110.42
25	z	49	ALA	N-CA-C	-5.40	107.24	113.88
27	C	43	ARG	N-CA-C	5.38	122.25	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	S	84	ARG	N-CA-C	-5.37	105.50	111.36
24	y	29	ARG	N-CA-C	-5.36	105.48	112.23
27	C	46	VAL	N-CA-C	5.35	116.94	109.55
4	e	50	ASP	N-CA-C	-5.35	105.53	111.36
43	S	50	LEU	N-CA-C	-5.34	101.51	109.42
50	Z	42	THR	N-CA-C	5.30	116.75	110.97
33	I	177	MET	N-CA-C	5.30	117.11	110.91
34	J	93	VAL	N-CA-C	5.29	120.34	109.34
45	U	78	VAL	N-CA-C	-5.29	107.32	112.29
11	l	105	ILE	N-CA-C	5.28	117.23	109.63
38	N	62	LEU	N-CA-C	5.28	117.13	108.52
34	J	116	VAL	N-CA-C	-5.27	106.74	113.22
52	3	413	G	N9-C1'-C2'	5.26	119.90	112.00
13	n	44	LEU	N-CA-C	-5.26	106.37	112.89
3	d	122	GLU	N-CA-C	5.25	117.00	111.28
44	T	59	VAL	N-CA-C	-5.25	106.02	111.58
33	I	37	PRO	N-CA-C	-5.25	106.37	113.40
17	r	24	LYS	N-CA-C	5.24	117.27	109.25
39	O	21	ALA	N-CA-C	-5.24	105.63	112.23
31	G	111	LYS	N-CA-C	-5.24	106.39	112.89
38	N	88	GLU	N-CA-C	-5.22	105.76	111.82
15	p	37	LYS	N-CA-C	-5.21	104.08	110.65
50	Z	44	ARG	N-CA-C	-5.19	106.80	113.23
31	G	210	THR	N-CA-C	-5.18	105.70	112.23
9	j	7	LYS	CA-C-N	5.18	124.85	119.56
9	j	7	LYS	C-N-CA	5.18	124.85	119.56
7	h	59	LEU	N-CA-C	-5.18	103.19	110.50
13	n	53	THR	N-CA-C	-5.16	105.83	111.82
10	k	89	ASN	N-CA-C	5.15	121.77	110.80
17	r	43	ASN	N-CA-C	-5.10	105.89	112.68
7	h	36	ASP	N-CA-C	-5.10	106.57	112.89
49	Y	3	ILE	N-CA-C	5.10	111.66	106.21
6	g	40	THR	N-CA-C	-5.10	101.57	109.72
1	b	85	ASN	N-CA-C	5.09	117.57	111.71
34	J	153	ALA	N-CA-C	-5.09	106.75	113.17
1	b	9	SER	N-CA-C	5.08	112.71	108.13
9	j	132	HIS	N-CA-C	-5.08	106.39	112.59
31	G	11	ALA	N-CA-C	-5.07	106.79	113.17
6	g	63	ALA	N-CA-C	-5.05	105.86	112.23
16	q	49	ARG	N-CA-C	-5.05	106.90	113.16
20	u	7	ASP	N-CA-C	5.05	116.93	107.99
48	X	48	ILE	N-CA-C	5.05	116.19	109.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	H	107	LYS	CA-C-N	5.05	124.77	119.82
32	H	107	LYS	C-N-CA	5.05	124.77	119.82
39	O	77	VAL	N-CA-C	5.01	119.10	111.89
39	O	17	LEU	N-CA-C	-5.00	107.83	114.04
13	n	71	ARG	N-CA-C	5.00	121.46	110.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2083	0	2157	47	0
2	c	1565	0	1616	46	0
3	d	1552	0	1619	38	0
4	e	1411	0	1447	45	0
5	f	1323	0	1374	30	0
6	g	1111	0	1148	29	0
7	h	989	0	1025	51	0
8	i	1032	0	1088	34	0
9	j	1129	0	1162	40	0
10	k	939	0	1012	25	0
11	l	1045	0	1117	33	0
12	m	1074	0	1157	23	0
13	n	961	0	1000	31	0
14	o	892	0	923	18	0
15	p	917	0	965	36	0
16	q	947	0	1022	20	0
17	r	816	0	839	23	0
18	s	857	0	922	12	0
19	t	739	0	807	19	0
20	u	780	0	834	16	0
21	v	753	0	780	23	0
22	w	575	0	592	19	0
23	x	625	0	655	15	0
24	y	509	0	543	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	z	449	0	491	14	0
26	B	444	0	461	13	0
27	C	410	0	440	9	0
28	D	377	0	418	7	0
29	E	504	0	574	18	0
30	F	302	0	343	16	0
31	G	1757	0	1787	41	0
32	H	1625	0	1699	40	0
33	I	1643	0	1710	48	0
34	J	1157	0	1199	25	0
35	K	818	0	808	40	0
36	L	1182	0	1240	32	0
37	M	979	0	1034	22	0
38	N	1022	0	1070	40	0
39	O	787	0	828	31	0
40	P	870	0	878	26	0
41	Q	955	0	1019	38	0
42	R	884	0	944	29	0
43	S	805	0	847	28	0
44	T	714	0	737	13	0
45	U	649	0	666	26	0
46	V	649	0	691	16	0
47	W	536	0	552	10	0
48	X	638	0	665	18	0
49	Y	665	0	714	14	0
50	Z	545	0	579	21	0
51	a	1027	0	1092	24	0
52	3	33012	0	16618	354	0
53	1	62317	0	31346	725	0
54	2	2568	0	1303	41	0
55	5	1640	0	836	8	0
55	6	1640	0	837	17	0
56	4	388	0	197	2	0
57	7	1619	0	822	10	0
58	5	10	0	10	0	0
All	All	150211	0	101259	2169	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (2169) 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)
53:1:45:G:H5''	53:1:46:G:H5'	1.24	1.15
42:R:113:LYS:HG3	42:R:114:PRO:HD3	1.35	1.08
34:J:107:GLY:HA3	52:3:9:G:H5'	1.43	1.00
30:F:32:LYS:HE3	53:1:2478:A:H5'	1.47	0.93
52:3:484:G:H4'	52:3:485:U:H5''	1.54	0.90
37:M:28:SER:HB2	37:M:58:LEU:HB2	1.53	0.89
53:1:2277:G:H2'	53:1:2278:A:H5''	1.55	0.87
12:m:12:MET:HA	53:1:910:A:H62	1.40	0.86
53:1:1906:G:H2'	53:1:1907:G:H5''	1.55	0.86
53:1:1103:A:H3'	53:1:1104:C:H5''	1.59	0.84
53:1:542:C:H2'	53:1:543:G:H5''	1.58	0.84
10:k:76:VAL:HG22	15:p:72:VAL:HG12	1.60	0.84
6:g:97:ARG:HG2	6:g:112:LYS:HD2	1.59	0.82
52:3:769:G:H4'	52:3:1513:A:H4'	1.61	0.80
52:3:405:U:H3'	52:3:406:G:H5'	1.63	0.80
53:1:776:G:H22	53:1:2072:C:H5'	1.46	0.80
41:Q:120:ARG:NH1	52:3:500:G:H5'	1.96	0.79
35:K:98:GLU:HG2	35:K:99:ALA:H	1.47	0.79
52:3:664:G:H22	52:3:741:G:H1	1.30	0.79
5:f:32:LEU:HD22	5:f:74:MET:HE3	1.63	0.78
8:i:12:VAL:HG12	8:i:13:ALA:H	1.48	0.78
9:j:109:LEU:HD13	9:j:110:PRO:HD2	1.66	0.77
34:J:156:ARG:HD3	37:M:42:GLU:HG3	1.66	0.77
36:L:56:SER:OG	36:L:59:GLU:HG2	1.85	0.77
27:C:7:LYS:HD3	53:1:2420:C:H5''	1.66	0.77
7:h:58:THR:HG21	7:h:82:ILE:HB	1.67	0.76
33:I:37:PRO:HD2	33:I:41:GLY:HA3	1.67	0.76
39:O:37:ARG:HD2	52:3:1124:G:H5''	1.68	0.76
52:3:1088:G:H21	52:3:1167:A:H61	1.32	0.76
53:1:1020:A:H1'	53:1:1021:A:OP2	1.86	0.76
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.66	0.76
42:R:113:LYS:HG3	42:R:114:PRO:CD	2.15	0.76
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.67	0.76
20:u:36:GLU:HA	20:u:61:GLU:HG2	1.67	0.75
31:G:34:ARG:HG2	31:G:39:ILE:HD11	1.68	0.75
7:h:117:LEU:HG	7:h:118:ILE:HG13	1.68	0.75
53:1:1053:C:H2'	53:1:1054:A:H5''	1.68	0.75
7:h:34:THR:HG21	53:1:1057:A:H1'	1.68	0.75
7:h:118:ILE:O	7:h:118:ILE:HG22	1.84	0.75
30:F:32:LYS:HD3	53:1:2528:U:H5'	1.68	0.74
39:O:40:ILE:HB	39:O:73:LEU:HG	1.69	0.74
9:j:13:ARG:HD3	9:j:121:LYS:HE2	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:v:47:VAL:HG23	21:v:48:MET:HE2	1.69	0.74
9:j:96:ARG:HD2	9:j:99:ARG:HG3	1.70	0.74
43:S:39:ASP:HA	43:S:42:ASN:HD22	1.52	0.74
46:V:5:ARG:HD3	52:3:636:U:H5''	1.68	0.74
41:Q:32:VAL:HG12	41:Q:55:ARG:HB3	1.68	0.74
10:k:48:PRO:HG3	52:3:1422:G:H5'	1.68	0.74
30:F:36:ARG:HG2	30:F:37:GLN:H	1.50	0.74
7:h:123:ILE:H	7:h:123:ILE:HD12	1.51	0.74
41:Q:43:LYS:HE2	52:3:1492:A:OP1	1.86	0.74
33:I:190:LEU:HD12	33:I:192:ALA:H	1.52	0.73
53:1:2286:G:H5''	53:1:2287:A:OP1	1.87	0.73
35:K:36:ILE:HA	35:K:64:VAL:HG23	1.69	0.73
37:M:77:VAL:HG12	37:M:84:ILE:HD12	1.71	0.73
54:2:3:C:H2'	54:2:4:C:H5''	1.70	0.73
47:W:41:SER:HB3	47:W:51:GLN:HE21	1.54	0.73
53:1:2584:U:H2'	53:1:2585:U:H2'	1.71	0.73
35:K:90:MET:HG2	35:K:91:ARG:H	1.53	0.72
37:M:54:THR:HG23	37:M:55:LYS:HD2	1.70	0.72
52:3:1158:C:H2'	52:3:1159:U:H4'	1.71	0.72
8:i:42:ASN:HA	8:i:45:THR:HG22	1.72	0.72
31:G:116:LEU:HG	31:G:140:LEU:HD13	1.71	0.72
41:Q:30:ARG:HG2	52:3:363:A:OP2	1.90	0.72
8:i:20:SER:OG	8:i:21:PRO:HD3	1.90	0.71
11:l:13:LYS:HE3	53:1:1245:G:OP1	1.90	0.71
38:N:98:ARG:HG3	38:N:103:VAL:HG21	1.70	0.71
34:J:107:GLY:HA3	52:3:9:G:C5'	2.20	0.71
49:Y:49:ALA:O	49:Y:52:GLU:HG2	1.90	0.71
53:1:713:G:H21	53:1:718:A:H62	1.38	0.71
11:l:90:VAL:HG13	11:l:95:LEU:HD11	1.73	0.71
50:Z:54:ARG:HA	50:Z:57:LYS:HG2	1.73	0.71
35:K:91:ARG:HG3	35:K:92:THR:H	1.56	0.71
43:S:63:CYS:HB2	43:S:67:GLY:H	1.56	0.71
45:U:6:LEU:HD12	45:U:17:TYR:HB3	1.72	0.71
53:1:2296:U:H5''	53:1:2297:A:OP1	1.90	0.71
4:e:107:VAL:CG1	4:e:108:PRO:HD3	2.21	0.71
53:1:310:A:C2'	53:1:311:A:H5''	2.21	0.70
9:j:81:ILE:HG23	9:j:82:GLY:H	1.56	0.70
52:3:1200:C:H5''	52:3:1201:A:H3'	1.74	0.70
52:3:1230:C:H5'	55:5:30:G:H5''	1.72	0.70
53:1:2553:G:H3'	53:1:2554:U:H5''	1.73	0.70
53:1:1141:U:H4'	53:1:1142:A:O4'	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:74:ALA:HB2	55:5:57:A:H5'	1.73	0.69
41:Q:113:ARG:HB2	41:Q:118:VAL:HB	1.72	0.69
53:1:807:U:H2'	53:1:808:G:H8	1.53	0.69
45:U:13:LYS:NZ	52:3:392:C:H5'	2.07	0.69
2:c:151:THR:HB	2:c:152:PRO:HD3	1.74	0.69
53:1:1906:G:C2'	53:1:1907:G:H5''	2.23	0.69
10:k:59:LYS:HD2	10:k:89:ASN:HA	1.74	0.69
17:r:49:ILE:HB	17:r:51:VAL:O	1.92	0.69
53:1:511:U:H2'	53:1:512:G:H5'	1.74	0.69
52:3:327:A:O2'	52:3:328:C:H4'	1.94	0.68
52:3:1306:A:H61	52:3:1331:G:H1'	1.57	0.68
53:1:685:A:H5''	53:1:788:A:H62	1.59	0.68
13:n:6:SER:HB3	13:n:46:ARG:HH22	1.55	0.68
52:3:70:U:H5''	52:3:71:A:OP1	1.93	0.68
52:3:1301:U:O2	52:3:1301:U:H2'	1.91	0.68
33:I:122:ILE:H	33:I:122:ILE:HD12	1.56	0.68
11:l:73:ILE:HG22	11:l:106:GLU:H	1.59	0.68
29:E:18:LYS:HG2	53:1:651:G:H5'	1.76	0.67
52:3:1201:A:H1'	52:3:1202:U:OP2	1.94	0.67
21:v:48:MET:HE1	21:v:86:LEU:HD12	1.75	0.67
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.75	0.67
53:1:2682:A:H61	53:1:2728:U:H1'	1.58	0.67
7:h:114:GLU:HA	7:h:123:ILE:HG23	1.75	0.67
12:m:18:ARG:HG2	12:m:19:GLY:H	1.60	0.67
15:p:52:ARG:HH21	53:1:2720:U:H5''	1.60	0.67
47:W:59:LYS:HD3	52:3:735:C:H5'	1.77	0.67
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.60	0.67
11:l:85:VAL:HG12	11:l:86:GLU:HG3	1.76	0.67
23:x:63:ILE:H	23:x:63:ILE:HD12	1.59	0.67
25:z:15:ARG:HH11	54:2:83:G:H5''	1.59	0.67
31:G:91:VAL:HG11	31:G:99:MET:HE1	1.75	0.67
53:1:1186:G:H2'	53:1:1187:G:O4'	1.94	0.67
53:1:2800:A:H3'	53:1:2801:G:H5'	1.76	0.67
10:k:104:THR:HG22	10:k:106:GLU:H	1.60	0.67
40:P:118:ASN:CG	52:3:718:A:H5'	2.20	0.67
53:1:1133:A:H4'	53:1:1134:A:H5''	1.77	0.66
7:h:61:ARG:HB3	53:1:1046:A:H4'	1.76	0.66
7:h:126:LEU:HD23	7:h:126:LEU:H	1.60	0.66
32:H:188:ALA:HB3	32:H:195:ILE:HB	1.77	0.66
48:X:10:ILE:HD12	48:X:37:SER:HB2	1.77	0.66
48:X:77:ARG:HH21	52:3:1225:A:H4'	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B:37:HIS:HB3	26:B:43:THR:HG22	1.77	0.66
9:j:27:ARG:NH2	53:1:1142:A:H4'	2.09	0.66
38:N:17:ARG:HB2	38:N:65:THR:HG23	1.78	0.66
44:T:45:HIS:O	44:T:47:LYS:N	2.29	0.66
41:Q:49:ARG:NH2	52:3:522:C:H41	1.94	0.66
41:Q:85:ARG:HA	41:Q:93:ARG:HA	1.78	0.66
24:y:9:LYS:HB3	24:y:12:GLU:HG2	1.77	0.66
33:I:195:ASN:HD22	33:I:198:LEU:HG	1.61	0.66
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.60	0.66
53:1:572:A:H61	53:1:2029:G:H21	1.43	0.66
53:1:1026:G:H2'	53:1:1027:A:H8	1.60	0.66
8:i:126:ARG:HA	8:i:129:GLU:HG2	1.78	0.66
10:k:91:SER:O	10:k:93:GLN:HG2	1.95	0.66
17:r:30:GLY:H	17:r:63:VAL:HG23	1.61	0.66
49:Y:80:ALA:HA	49:Y:83:ASN:HD21	1.60	0.66
53:1:2743:U:H2'	53:1:2744:G:H5''	1.77	0.66
4:e:107:VAL:HG12	4:e:108:PRO:HD3	1.78	0.65
33:I:144:ILE:HD12	33:I:177:MET:HB3	1.77	0.65
53:1:2086:U:H2'	53:1:2087:G:C8	2.32	0.65
45:U:14:ARG:HA	45:U:42:ILE:HD11	1.79	0.65
5:f:102:ILE:HG23	5:f:114:HIS:HB3	1.78	0.65
53:1:310:A:H2'	53:1:311:A:H5''	1.79	0.65
53:1:807:U:H2'	53:1:808:G:C8	2.31	0.65
53:1:2286:G:H4'	53:1:2287:A:O5'	1.95	0.65
35:K:46:GLN:HG2	35:K:56:LYS:HE2	1.79	0.65
21:v:4:ILE:HD12	21:v:61:LEU:HD21	1.79	0.65
52:3:516:U:H3	52:3:533:A:H62	1.44	0.65
1:b:94:LEU:HD13	1:b:100:ARG:HG2	1.78	0.64
2:c:149:ASN:HB3	53:1:2572:A:OP2	1.96	0.64
5:f:174:LYS:HE2	53:1:2529:G:H4'	1.79	0.64
6:g:12:LEU:HB2	6:g:19:VAL:HG11	1.77	0.64
52:3:352:C:H4'	52:3:354:G:OP1	1.97	0.64
5:f:88:LEU:HD11	5:f:95:ALA:HB2	1.78	0.64
8:i:89:SER:HB2	8:i:92:PRO:HG3	1.78	0.64
38:N:22:PRO:HA	38:N:60:LEU:HD13	1.79	0.64
24:y:4:LYS:HZ1	53:1:102:U:H3	1.46	0.64
19:t:15:HIS:H	19:t:32:LEU:HA	1.63	0.64
52:3:150:U:H3	52:3:171:A:H62	1.44	0.64
10:k:121:GLU:HG2	10:k:122:VAL:HG23	1.79	0.64
2:c:125:TRP:CE3	2:c:160:LYS:HE3	2.32	0.64
4:e:140:ILE:HG22	4:e:142:TYR:H	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:O:89:ARG:HD2	39:O:90:LEU:HD12	1.79	0.64
21:v:44:HIS:O	21:v:48:MET:HG2	1.98	0.64
52:3:1306:A:N6	52:3:1331:G:H1'	2.13	0.64
1:b:180:MET:HB2	1:b:268:ARG:H	1.62	0.63
37:M:95:MET:HE3	37:M:98:LEU:HD12	1.78	0.63
47:W:33:THR:HG23	47:W:35:SER:H	1.62	0.63
13:n:63:ARG:NH2	53:1:1454:C:H5'	2.14	0.63
45:U:36:VAL:HG23	45:U:53:ASP:HB2	1.81	0.63
53:1:546:U:H2'	53:1:547:A:H4'	1.81	0.63
53:1:1796:U:H2'	53:1:1797:G:H8	1.62	0.63
7:h:55:VAL:HA	53:1:1084:A:H5''	1.81	0.63
52:3:1506:U:O2'	52:3:1507:A:H5'	1.98	0.63
53:1:121:G:H4'	53:1:149:A:H5'	1.81	0.63
31:G:46:VAL:HG23	31:G:47:PRO:HD3	1.81	0.63
43:S:50:LEU:HD12	43:S:51:PRO:HD2	1.81	0.63
54:2:3:C:C2'	54:2:4:C:H5''	2.28	0.63
3:d:34:ALA:HA	3:d:94:GLN:HE21	1.63	0.62
53:1:1807:G:H2'	53:1:1808:A:H5'	1.81	0.62
53:1:49:A:H5'	53:1:51:G:O4'	1.99	0.62
53:1:329:G:O4'	53:1:477:A:H1'	1.99	0.62
53:1:729:G:H4'	53:1:763:G:H5'	1.80	0.62
53:1:2286:G:H4'	53:1:2287:A:O4'	1.99	0.62
54:2:3:C:C3'	54:2:4:C:H5''	2.29	0.62
24:y:2:LYS:HE2	53:1:102:U:H1'	1.82	0.62
35:K:53:LYS:HD2	35:K:54:LEU:O	1.99	0.62
16:q:108:LEU:HA	17:r:48:LYS:HE2	1.81	0.62
53:1:161:A:H3'	53:1:162:U:H5''	1.81	0.62
53:1:1060:U:H4'	53:1:1061:U:H5'	1.80	0.62
50:Z:32:ARG:HE	50:Z:33:ARG:HG2	1.63	0.62
51:a:163:TYR:HB2	51:a:171:ILE:HD11	1.81	0.62
22:w:19:VAL:HG22	22:w:34:VAL:HG22	1.80	0.62
1:b:12:ARG:NH2	53:1:728:G:H4'	2.14	0.62
49:Y:25:SER:OG	52:3:1458:G:H5''	2.00	0.62
53:1:1645:G:H5''	53:1:1646:C:H5'	1.82	0.62
1:b:264:LYS:HE3	53:1:2223:G:O3'	2.00	0.62
22:w:36:GLN:NE2	22:w:39:THR:HA	2.15	0.62
53:1:479:A:H4'	53:1:480:A:H5'	1.82	0.62
2:c:11:MET:HG2	2:c:25:THR:HG22	1.82	0.62
15:p:96:LEU:HB3	15:p:99:LEU:HD13	1.82	0.62
26:B:24:VAL:HG23	26:B:25:THR:H	1.64	0.62
33:I:149:LYS:O	33:I:150:LYS:HG3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:3:HIS:H	35:K:92:THR:HG22	1.64	0.62
45:U:12:LYS:HG2	45:U:13:LYS:HG2	1.81	0.62
53:1:1664:A:H61	53:1:1996:C:H42	1.47	0.62
52:3:1259:C:H3'	52:3:1260:G:H5''	1.82	0.61
53:1:2277:G:C2'	53:1:2278:A:H5''	2.28	0.61
4:e:45:ASP:OD2	4:e:48:LEU:HB2	1.99	0.61
53:1:1900:A:H1'	53:1:1970:A:H2'	1.80	0.61
52:3:1088:G:N2	52:3:1167:A:H61	1.98	0.61
53:1:112:U:H2'	53:1:113:U:H5'	1.82	0.61
53:1:275:C:H2'	53:1:276:U:H4'	1.81	0.61
16:q:53:LYS:NZ	53:1:994:C:H2'	2.14	0.61
29:E:31:ILE:O	29:E:31:ILE:HG13	1.99	0.61
40:P:86:LYS:HE2	40:P:112:VAL:HG13	1.83	0.61
53:1:310:A:O2'	53:1:311:A:H5''	2.00	0.61
7:h:5:LEU:O	7:h:9:GLN:HG2	2.00	0.61
37:M:10:LEU:HD22	37:M:74:ILE:HG21	1.82	0.61
40:P:22:ILE:HG21	40:P:95:THR:HG21	1.82	0.61
40:P:28:ASN:HD21	40:P:45:THR:HB	1.65	0.61
52:3:78:A:H2'	52:3:79:G:O4'	2.00	0.61
15:p:28:LYS:HB3	15:p:39:LEU:HD11	1.82	0.61
33:I:103:ARG:HD2	33:I:167:PRO:HG2	1.81	0.61
53:1:1045:C:H5'	53:1:1046:A:H5''	1.83	0.61
53:1:2452:C:H42	53:1:2504:U:H3	1.46	0.61
53:1:2591:C:H2'	53:1:2592:G:C8	2.35	0.61
30:F:19:ARG:HH21	53:1:2755:C:H3'	1.66	0.61
39:O:40:ILE:HD11	52:3:1124:G:H4'	1.81	0.61
32:H:39:ARG:HG3	32:H:54:ILE:HD11	1.81	0.61
53:1:615:U:H5''	53:1:616:A:OP2	2.00	0.61
15:p:92:ARG:HD3	53:1:1753:G:H5''	1.83	0.61
35:K:3:HIS:N	35:K:92:THR:HG22	2.16	0.61
39:O:92:LEU:HD23	39:O:92:LEU:H	1.65	0.60
8:i:71:LYS:HD2	8:i:72:THR:H	1.64	0.60
2:c:155:VAL:HG21	53:1:2618:G:H21	1.67	0.60
3:d:23:PHE:HB2	3:d:114:ARG:HH22	1.66	0.60
4:e:104:THR:HB	4:e:105:ILE:HD12	1.83	0.60
34:J:89:THR:HB	34:J:134:ASN:HD21	1.66	0.60
43:S:58:ARG:HH12	52:3:979:C:H2'	1.67	0.60
3:d:123:LYS:HE3	3:d:125:SER:HB2	1.83	0.60
53:1:2245:U:H5''	53:1:2246:G:H5'	1.83	0.60
9:j:57:LEU:HD23	9:j:57:LEU:H	1.67	0.60
52:3:1414:U:H2'	52:3:1415:G:H8	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.02	0.60
52:3:184:G:H4'	52:3:224:U:H4'	1.83	0.60
2:c:148:GLN:O	53:1:2052:A:H4'	2.01	0.60
19:t:57:VAL:HG12	19:t:58:VAL:H	1.67	0.60
53:1:1509:A:H2'	53:1:1510:G:C8	2.37	0.60
53:1:2623:G:H2'	53:1:2624:G:H8	1.66	0.60
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.83	0.60
22:w:39:THR:HB	53:1:2331:G:H4'	1.84	0.60
29:E:1:PRO:HD2	53:1:591:U:H1'	1.83	0.60
7:h:97:LYS:HZ1	7:h:125:ARG:HD3	1.66	0.60
9:j:113:PRO:HD2	53:1:558:U:P	2.42	0.60
53:1:971:G:H2'	53:1:972:A:O4'	2.01	0.60
53:1:2039:U:H2'	53:1:2040:G:H8	1.66	0.60
3:d:153:LEU:HB2	3:d:171:ASP:HB2	1.83	0.59
10:k:35:VAL:HG11	10:k:69:VAL:HG12	1.84	0.59
29:E:27:ASN:HB3	29:E:35:LYS:HE2	1.84	0.59
31:G:58:LYS:HG3	31:G:59:ILE:HD12	1.84	0.59
34:J:159:SER:HB3	34:J:162:GLU:HB2	1.84	0.59
40:P:12:ARG:HB3	40:P:75:GLU:HG2	1.82	0.59
42:R:27:THR:HG21	52:3:1328:C:H5''	1.82	0.59
48:X:38:THR:HG22	48:X:39:ILE:H	1.67	0.59
3:d:5:LEU:HD22	3:d:8:ALA:HB3	1.83	0.59
8:i:105:LEU:HD23	8:i:108:ILE:HD11	1.84	0.59
33:I:131:ILE:HG12	52:3:620:C:C2	2.37	0.59
37:M:12:ARG:HB3	37:M:24:VAL:HG21	1.83	0.59
51:a:11:ILE:HG23	51:a:33:LEU:HD22	1.83	0.59
14:o:25:ARG:HE	14:o:40:ILE:HD12	1.66	0.59
39:O:23:ALA:O	39:O:27:GLU:HG2	2.02	0.59
49:Y:26:MET:HB3	52:3:1458:G:H5'	1.84	0.59
7:h:34:THR:HG21	53:1:1057:A:C1'	2.33	0.59
8:i:107:GLU:OE2	8:i:108:ILE:HG23	2.01	0.59
53:1:1468:U:H2'	53:1:1522:A:H61	1.67	0.59
34:J:87:VAL:HG22	34:J:92:ARG:HD2	1.84	0.59
52:3:1391:U:H2'	52:3:1392:G:C8	2.36	0.59
54:2:3:C:H3'	54:2:4:C:H5''	1.83	0.59
53:1:1053:C:C2'	53:1:1054:A:H5''	2.33	0.59
1:b:261:ARG:HG3	1:b:262:THR:HG23	1.85	0.59
53:1:1936:A:H2	53:1:1943:U:H3	1.49	0.59
7:h:32:GLY:O	53:1:1055:G:H4'	2.03	0.59
7:h:38:MET:HE3	8:i:117:THR:HB	1.85	0.59
14:o:26:LEU:HD13	14:o:39:VAL:HG22	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:18:VAL:HG12	35:K:19:PRO:HD3	1.84	0.59
53:1:2267:A:H61	53:1:2272:U:H3	1.49	0.59
53:1:2391:G:H2'	53:1:2424:C:N4	2.18	0.59
4:e:63:LYS:O	54:2:42:C:H1'	2.03	0.59
4:e:140:ILE:N	4:e:140:ILE:HD12	2.17	0.59
29:E:2:LYS:HG3	53:1:242:G:C8	2.38	0.59
41:Q:31:GLY:HA3	41:Q:54:VAL:HG13	1.84	0.59
36:L:55:LYS:HB2	36:L:60:ALA:HB2	1.84	0.59
51:a:205:LYS:HD2	53:1:1860:G:O2'	2.03	0.58
53:1:2039:U:H2'	53:1:2040:G:C8	2.39	0.58
1:b:227:VAL:HG21	53:1:784:G:C6	2.38	0.58
38:N:54:VAL:HG12	38:N:93:LEU:HD11	1.85	0.58
41:Q:87:LYS:O	41:Q:87:LYS:HD3	2.03	0.58
52:3:346:G:H2'	52:3:347:G:H5'	1.86	0.58
4:e:24:VAL:HG12	54:2:55:U:H4'	1.85	0.58
1:b:7:PRO:O	53:1:1695:G:H1'	2.03	0.58
3:d:117:ARG:HH12	11:l:2:ARG:HG2	1.68	0.58
10:k:71:ARG:HH11	10:k:77:ILE:HD11	1.68	0.58
53:1:917:A:H5''	53:1:2268:A:H61	1.67	0.58
8:i:13:ALA:HA	8:i:53:PRO:HA	1.85	0.58
11:l:79:LEU:HD12	11:l:112:LEU:HA	1.86	0.58
20:u:65:GLN:HB2	20:u:68:ASN:ND2	2.19	0.58
35:K:98:GLU:HG2	35:K:99:ALA:N	2.17	0.58
36:L:74:VAL:HB	36:L:85:GLN:HB3	1.85	0.58
43:S:5:MET:HE1	52:3:982:U:H5''	1.83	0.58
52:3:484:G:H4'	52:3:485:U:C5'	2.30	0.58
5:f:41:GLU:HG3	5:f:54:ARG:HH21	1.68	0.58
15:p:109:ILE:N	15:p:109:ILE:HD12	2.18	0.58
19:t:48:GLN:HE22	19:t:55:VAL:H	1.51	0.58
51:a:54:LYS:NZ	55:6:63:G:H4'	2.18	0.58
17:r:98:ILE:H	17:r:98:ILE:HD12	1.69	0.58
42:R:13:HIS:NE2	52:3:1296:C:H5'	2.18	0.58
45:U:13:LYS:HZ2	52:3:392:C:H5'	1.66	0.58
52:3:1005:A:H2'	52:3:1006:G:O4'	2.04	0.58
53:1:542:C:C2'	53:1:543:G:H5''	2.30	0.58
53:1:1790:C:H2'	53:1:1791:A:C5	2.38	0.58
11:l:93:ASN:OD1	11:l:94:THR:HG23	2.04	0.58
38:N:57:VAL:HG13	38:N:58:GLU:N	2.19	0.58
52:3:1137:C:H5'	52:3:1138:G:H5'	1.86	0.58
53:1:1373:A:H5'	53:1:2212:A:H1'	1.84	0.58
8:i:78:LEU:HD21	8:i:108:ILE:HD12	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:4:GLU:HG3	10:k:5:GLN:HG2	1.86	0.58
51:a:54:LYS:HD3	55:6:63:G:H5'	1.86	0.58
52:3:265:G:H2'	52:3:267:C:H5	1.69	0.58
52:3:410:G:H2'	52:3:429:U:C4	2.39	0.58
53:1:1796:U:H2'	53:1:1797:G:C8	2.39	0.58
6:g:94:ILE:HG13	6:g:98:ASP:HB3	1.85	0.58
12:m:75:GLU:OE2	53:1:957:C:H5'	2.03	0.58
31:G:94:ARG:HH12	52:3:1100:C:H3'	1.69	0.58
36:L:148:LYS:O	36:L:148:LYS:HD3	2.04	0.58
40:P:30:ILE:HG13	40:P:45:THR:HG22	1.86	0.58
41:Q:73:LEU:HD21	41:Q:79:ILE:HG21	1.85	0.58
50:Z:23:GLU:HG3	50:Z:27:VAL:HG23	1.85	0.58
53:1:45:G:C5'	53:1:46:G:H5'	2.17	0.58
7:h:69:PHE:HD1	7:h:70:GLU:HG2	1.69	0.57
19:t:54:GLU:HB3	19:t:88:LYS:HD2	1.85	0.57
45:U:21:VAL:HG22	45:U:34:GLU:O	2.04	0.57
52:3:1492:A:H2'	53:1:1913:A:H2	1.69	0.57
53:1:2156:G:H2'	53:1:2157:G:H5'	1.84	0.57
53:1:2329:U:H2'	53:1:2330:G:C8	2.39	0.57
7:h:97:LYS:NZ	7:h:125:ARG:HD3	2.19	0.57
39:O:66:GLU:HG2	43:S:98:ALA:HB2	1.87	0.57
42:R:16:ILE:H	42:R:16:ILE:HD12	1.69	0.57
50:Z:23:GLU:O	50:Z:24:LYS:HG2	2.02	0.57
53:1:581:C:H2'	53:1:582:A:C8	2.39	0.57
2:c:109:VAL:HG11	2:c:193:VAL:HG12	1.87	0.57
38:N:57:VAL:HG13	38:N:58:GLU:H	1.69	0.57
52:3:1379:G:O2'	52:3:1380:U:H5'	2.04	0.57
54:2:88:C:H4'	54:2:89:U:OP1	2.05	0.57
5:f:136:ASP:HB3	5:f:139:VAL:HG22	1.86	0.57
7:h:33:VAL:HG12	7:h:34:THR:H	1.68	0.57
43:S:7:ALA:O	43:S:10:VAL:HG12	2.04	0.57
16:q:53:LYS:HZ3	53:1:994:C:H2'	1.69	0.57
46:V:13:SER:H	46:V:21:VAL:HG13	1.70	0.57
52:3:29:U:O2'	52:3:30:U:H5'	2.03	0.57
53:1:2114:A:H2'	53:1:2114:A:N3	2.18	0.57
53:1:2389:G:H5''	53:1:2390:U:O4'	2.04	0.57
2:c:133:THR:HG23	2:c:134:HIS:CD2	2.40	0.57
6:g:84:ALA:HB2	6:g:90:LEU:HD12	1.85	0.57
13:n:63:ARG:HH22	53:1:1454:C:H5'	1.69	0.57
53:1:435:C:H2'	53:1:436:C:H5'	1.87	0.57
53:1:1077:A:H2'	53:1:1078:U:H5'	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:t:12:ARG:HE	19:t:33:LYS:HZ1	1.53	0.57
39:O:71:LEU:O	39:O:72:ARG:HG2	2.05	0.57
20:u:24:VAL:HG22	20:u:35:VAL:HG22	1.87	0.57
41:Q:98:ARG:HB2	41:Q:116:TYR:C	2.30	0.57
52:3:225:C:C3'	52:3:226:G:H5''	2.35	0.57
52:3:971:G:H1'	52:3:1365:G:O2'	2.04	0.57
53:1:1078:U:H5''	53:1:1079:C:H5''	1.86	0.57
29:E:34:LYS:HE3	53:1:2390:U:H5''	1.87	0.57
45:U:21:VAL:HG23	45:U:33:ILE:HB	1.87	0.57
53:1:581:C:H2'	53:1:582:A:H8	1.70	0.57
53:1:2055:C:H2'	53:1:2504:U:H5'	1.86	0.57
12:m:41:LEU:HD22	12:m:124:LEU:HD22	1.87	0.57
4:e:2:LYS:HE3	4:e:100:GLU:OE2	2.05	0.56
7:h:55:VAL:HA	53:1:1084:A:C5'	2.34	0.56
53:1:2533:U:H2'	53:1:2534:A:O4'	2.05	0.56
53:1:2798:U:H4'	53:1:2799:A:C4	2.40	0.56
1:b:179:GLU:OE2	1:b:270:ARG:HB2	2.05	0.56
2:c:9:VAL:HB	2:c:26:VAL:HG23	1.87	0.56
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.86	0.56
8:i:96:LYS:HD2	8:i:138:VAL:HG23	1.86	0.56
38:N:59:LYS:C	38:N:60:LEU:HD22	2.30	0.56
38:N:128:LYS:HD3	55:5:34:C:OP2	2.05	0.56
53:1:779:U:H2'	53:1:780:G:C8	2.40	0.56
53:1:818:G:H21	53:1:1189:A:H62	1.53	0.56
57:7:44:G:H2'	57:7:45:U:O4'	2.05	0.56
6:g:40:THR:HG22	6:g:43:ASN:HD22	1.70	0.56
7:h:4:ASN:HD21	7:h:8:LYS:HD3	1.70	0.56
8:i:6:ALA:HB1	8:i:30:GLN:HG2	1.87	0.56
12:m:11:LYS:HD3	12:m:86:LYS:HG2	1.87	0.56
24:y:43:LEU:O	24:y:46:VAL:HG12	2.05	0.56
30:F:2:LYS:HB2	30:F:35:GLN:HB3	1.87	0.56
31:G:99:MET:HE3	31:G:150:ILE:HD13	1.85	0.56
37:M:17:GLN:HG3	37:M:71:VAL:HB	1.87	0.56
52:3:77:A:H2'	52:3:78:A:H8	1.70	0.56
52:3:79:G:O2'	52:3:80:A:H5'	2.04	0.56
53:1:1912:A:H62	53:1:1917:U:H3	1.53	0.56
53:1:2591:C:H2'	53:1:2592:G:H8	1.68	0.56
16:q:10:ARG:HH21	53:1:1216:G:H5''	1.69	0.56
33:I:195:ASN:HD21	33:I:197:HIS:HB3	1.68	0.56
40:P:87:GLY:H	40:P:113:THR:HG22	1.70	0.56
1:b:32:LEU:HD23	1:b:102:TYR:HD2	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:77:PRO:HB2	12:m:80:VAL:HG21	1.85	0.56
52:3:1412:C:H2'	52:3:1413:A:C8	2.40	0.56
8:i:27:LEU:HD12	8:i:28:GLY:N	2.20	0.56
35:K:38:ARG:HD3	35:K:97:THR:HA	1.87	0.56
53:1:2126:A:H2'	53:1:2162:G:N2	2.21	0.56
33:I:81:LEU:HB3	33:I:88:ASN:HD21	1.70	0.56
52:3:309:A:H2'	52:3:310:G:H8	1.70	0.56
53:1:2128:G:H21	53:1:2173:A:H1'	1.70	0.56
54:2:65:U:H3'	54:2:108:A:H61	1.71	0.56
5:f:41:GLU:HA	5:f:54:ARG:HH21	1.71	0.56
15:p:105:LYS:O	15:p:108:ARG:HG2	2.06	0.56
22:w:33:ILE:HD11	22:w:78:ILE:HD11	1.88	0.56
35:K:68:GLN:O	35:K:71:ILE:HG22	2.05	0.56
53:1:546:U:H2'	53:1:547:A:C4'	2.36	0.56
53:1:669:G:H2'	53:1:669:G:N3	2.20	0.56
54:2:65:U:H3'	54:2:108:A:N6	2.21	0.56
19:t:34:VAL:HG12	19:t:35:ALA:H	1.71	0.56
35:K:81:ASN:HB3	35:K:84:VAL:HG12	1.87	0.56
45:U:16:PHE:HD1	45:U:40:ASN:HD22	1.53	0.56
46:V:28:VAL:HG11	46:V:39:ARG:HD2	1.88	0.56
47:W:61:ALA:HB1	47:W:67:LEU:HD23	1.87	0.56
52:3:927:G:H21	52:3:1532:U:H5''	1.70	0.56
53:1:503:A:H4'	53:1:505:A:H5''	1.86	0.56
23:x:6:VAL:HG13	23:x:7:THR:HG23	1.88	0.56
33:I:167:PRO:HB2	33:I:170:LEU:CD2	2.35	0.56
36:L:68:VAL:HG21	36:L:103:ILE:HD11	1.88	0.56
40:P:126:ARG:NH2	52:3:692:U:H5''	2.21	0.56
52:3:782:A:H62	52:3:800:G:H21	1.52	0.56
4:e:105:ILE:C	4:e:108:PRO:HD2	2.31	0.55
5:f:148:ARG:HD2	5:f:161:VAL:HG23	1.86	0.55
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.88	0.55
21:v:33:GLY:O	21:v:34:LYS:HE2	2.06	0.55
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.87	0.55
53:1:300:A:H2'	53:1:334:C:H1'	1.89	0.55
1:b:155:ARG:NH1	53:1:1818:U:H5	2.03	0.55
9:j:45:THR:HB	9:j:48:VAL:HG22	1.86	0.55
24:y:4:LYS:NZ	53:1:102:U:H3	2.04	0.55
30:F:19:ARG:HE	53:1:2755:C:H2'	1.72	0.55
53:1:1837:C:H2'	53:1:1899:A:H61	1.71	0.55
2:c:8:LYS:HZ2	2:c:197:THR:HA	1.71	0.55
4:e:26:GLN:HG3	54:2:57:A:H1'	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:32:LYS:HD3	53:1:2528:U:C5'	2.33	0.55
32:H:182:ASP:HB2	32:H:201:ILE:HB	1.87	0.55
36:L:92:PRO:HA	36:L:95:ARG:HE	1.71	0.55
53:1:1772:A:H2'	53:1:1773:A:H4'	1.89	0.55
10:k:28:SER:HB2	53:1:2566:A:N1	2.21	0.55
17:r:33:VAL:HB	17:r:61:ALA:HB3	1.89	0.55
52:3:632:U:H3'	52:3:633:G:H5'	1.89	0.55
53:1:460:A:H62	53:1:469:G:H21	1.54	0.55
53:1:962:G:H21	53:1:2250:G:H1	1.54	0.55
41:Q:27:PRO:HD2	52:3:363:A:C6	2.42	0.55
43:S:92:ILE:H	43:S:92:ILE:HD12	1.71	0.55
52:3:452:A:H61	52:3:480:U:H3	1.53	0.55
52:3:1197:A:H2'	52:3:1198:G:H5''	1.89	0.55
53:1:1344:U:H3'	53:1:1345:C:H5'	1.89	0.55
53:1:2087:G:H2'	53:1:2088:A:H8	1.71	0.55
55:6:59:A:H2'	55:6:60:U:H5'	1.89	0.55
13:n:28:LEU:HD23	13:n:48:VAL:HG21	1.89	0.55
20:u:81:ARG:NH2	20:u:96:LYS:HG3	2.22	0.55
53:1:1476:U:H3	53:1:1515:A:H62	1.55	0.55
3:d:97:ASN:HA	53:1:607:U:OP1	2.06	0.55
35:K:64:VAL:HG22	35:K:65:GLU:N	2.22	0.55
41:Q:4:ASN:O	41:Q:7:VAL:HG12	2.06	0.55
42:R:25:GLY:H	52:3:1329:A:H5''	1.72	0.55
43:S:25:GLU:HB2	43:S:29:ILE:HD13	1.88	0.55
53:1:833:A:H2'	53:1:834:G:H8	1.72	0.55
53:1:2818:U:H2'	53:1:2819:G:H8	1.71	0.55
2:c:12:THR:HG22	2:c:13:ARG:H	1.71	0.55
5:f:41:GLU:HG3	5:f:54:ARG:NH2	2.22	0.55
33:I:141:VAL:HG22	33:I:180:THR:HG23	1.89	0.55
40:P:88:PRO:HG2	40:P:89:GLY:H	1.71	0.55
40:P:126:ARG:HH22	52:3:692:U:H5''	1.71	0.55
53:1:703:U:H2'	53:1:704:G:O4'	2.06	0.55
53:1:2183:A:H2'	53:1:2184:A:C8	2.42	0.55
3:d:161:ALA:HB3	3:d:169:VAL:HG23	1.88	0.55
4:e:102:LEU:HA	4:e:106:ALA:HB3	1.90	0.55
17:r:4:VAL:HG12	17:r:13:ARG:HA	1.89	0.55
53:1:1300:G:H4'	53:1:1301:A:C5'	2.37	0.55
11:l:47:ARG:HH22	53:1:196:A:H5''	1.71	0.54
15:p:112:ARG:HG2	15:p:114:ASN:HD22	1.72	0.54
33:I:57:LYS:O	33:I:60:VAL:HG12	2.07	0.54
39:O:57:VAL:O	39:O:58:ASN:HB2	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:X:14:LEU:O	48:X:18:VAL:HG23	2.07	0.54
55:5:6:G:O2'	55:5:7:G:H5'	2.05	0.54
4:e:73:VAL:HG12	4:e:75:GLY:H	1.72	0.54
30:F:32:LYS:CD	53:1:2528:U:H5'	2.35	0.54
52:3:235:C:H2'	52:3:236:A:C8	2.42	0.54
53:1:1909:C:H2'	53:1:1910:G:C8	2.42	0.54
53:1:1965:C:H5''	53:1:1966:A:H2'	1.88	0.54
1:b:132:ARG:HB3	1:b:185:ALA:HB1	1.89	0.54
11:l:93:ASN:O	11:l:94:THR:OG1	2.16	0.54
22:w:12:SER:HB3	53:1:2262:U:H5	1.72	0.54
11:l:124:GLY:H	11:l:144:GLU:HA	1.71	0.54
52:3:225:C:H3'	52:3:226:G:H5''	1.90	0.54
53:1:119:A:H4'	53:1:120:U:H5'	1.88	0.54
2:c:54:ALA:HA	2:c:76:GLY:HA2	1.90	0.54
6:g:75:LEU:HD12	6:g:77:THR:H	1.72	0.54
19:t:64:LYS:N	19:t:64:LYS:HD2	2.22	0.54
20:u:50:ALA:O	20:u:51:LEU:HG	2.08	0.54
30:F:11:CYS:HG	30:F:14:CYS:HG	1.54	0.54
52:3:1130:A:H61	52:3:1144:G:H1'	1.73	0.54
53:1:2329:U:H2'	53:1:2330:G:H8	1.72	0.54
7:h:48:ALA:HB3	7:h:51:TYR:CE1	2.43	0.54
15:p:29:VAL:HG12	15:p:80:VAL:HG12	1.90	0.54
39:O:6:ILE:HB	39:O:76:ILE:HB	1.88	0.54
53:1:528:A:C2	53:1:2042:A:H2'	2.42	0.54
6:g:33:GLN:HB2	6:g:35:LYS:HG2	1.90	0.54
7:h:64:VAL:O	7:h:67:THR:HG22	2.08	0.54
11:l:101:ILE:HG13	11:l:102:GLY:H	1.72	0.54
23:x:19:HIS:HB3	53:1:2080:A:OP1	2.07	0.54
36:L:75:LYS:NZ	52:3:1378:C:O2	2.41	0.54
43:S:20:PHE:O	43:S:21:ALA:HB3	2.08	0.54
53:1:225:C:H2'	53:1:226:A:O4'	2.08	0.54
53:1:1019:U:H3	53:1:1142:A:H62	1.56	0.54
53:1:2398:U:H2'	53:1:2399:G:C8	2.42	0.54
53:1:2443:C:H2'	53:1:2444:G:C8	2.43	0.54
53:1:473:G:O2'	53:1:474:G:H5'	2.08	0.54
54:2:65:U:H2'	54:2:66:A:H5'	1.89	0.54
20:u:93:ARG:HB2	20:u:102:ILE:HD12	1.89	0.54
24:y:21:LEU:HD23	24:y:25:GLN:HG2	1.89	0.54
33:I:190:LEU:HD12	33:I:192:ALA:N	2.22	0.54
44:T:16:ARG:HH11	44:T:16:ARG:HA	1.73	0.54
45:U:4:ILE:HG12	45:U:21:VAL:HG12	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:111:LYS:HG2	17:r:48:LYS:HD2	1.90	0.53
35:K:29:ILE:HD13	35:K:64:VAL:HG21	1.90	0.53
42:R:30:LYS:HA	42:R:40:GLU:OE1	2.08	0.53
52:3:346:G:C2'	52:3:347:G:H5'	2.37	0.53
53:1:2512:C:H2'	53:1:2513:A:O4'	2.07	0.53
56:4:17:U:O2'	56:4:18:G:H5'	2.07	0.53
6:g:55:GLU:O	6:g:58:LEU:HG	2.09	0.53
7:h:36:ASP:O	7:h:39:THR:HG22	2.07	0.53
45:U:70:ARG:HD3	52:3:375:U:OP1	2.09	0.53
53:1:729:G:H4'	53:1:763:G:C5'	2.38	0.53
53:1:1810:A:H2'	53:1:1811:G:O4'	2.07	0.53
53:1:2515:C:H2'	53:1:2516:A:C8	2.44	0.53
11:l:109:LYS:HE2	53:1:636:G:N7	2.24	0.53
15:p:22:GLY:H	15:p:46:VAL:HG23	1.73	0.53
29:E:53:ASP:OD2	53:1:2359:C:H4'	2.09	0.53
36:L:70:PRO:HG3	36:L:98:LEU:HD22	1.90	0.53
48:X:35:ARG:HD2	48:X:51:HIS:O	2.09	0.53
4:e:140:ILE:HD12	4:e:140:ILE:H	1.72	0.53
18:s:31:GLN:HA	18:s:34:ASP:OD2	2.09	0.53
26:B:38:LEU:HB2	26:B:41:HIS:HB2	1.89	0.53
33:I:195:ASN:ND2	33:I:197:HIS:HB3	2.24	0.53
52:3:1251:A:O2'	52:3:1370:G:H5'	2.08	0.53
53:1:2834:G:H2'	53:1:2879:A:H61	1.73	0.53
1:b:143:VAL:HB	1:b:153:LEU:HB2	1.90	0.53
7:h:58:THR:HA	7:h:63:ALA:HB3	1.91	0.53
10:k:7:MET:HE3	10:k:18:ARG:HD3	1.91	0.53
31:G:55:GLU:HA	31:G:58:LYS:HZ1	1.74	0.53
48:X:10:ILE:HD11	48:X:14:LEU:HD23	1.91	0.53
53:1:987:C:H2'	53:1:988:A:O4'	2.08	0.53
53:1:2066:C:O2'	53:1:2067:G:H5'	2.09	0.53
53:1:2391:G:H5'	53:1:2392:A:OP1	2.09	0.53
8:i:32:VAL:HG21	8:i:58:ILE:HD12	1.91	0.53
52:3:1357:A:H61	52:3:1365:G:H1	1.55	0.53
53:1:596:U:H2'	53:1:597:G:C8	2.43	0.53
53:1:2246:G:H2'	53:1:2247:A:C8	2.44	0.53
53:1:2292:U:H2'	53:1:2293:G:C8	2.44	0.53
54:2:60:C:H2'	54:2:61:G:H8	1.73	0.53
4:e:132:ARG:NH2	53:1:2305:U:H4'	2.23	0.53
5:f:37:ASN:O	5:f:40:VAL:HG22	2.08	0.53
7:h:55:VAL:HA	53:1:1084:A:H4'	1.90	0.53
12:m:71:LYS:HB3	12:m:93:VAL:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:156:LEU:HD12	31:G:157:PRO:HD2	1.89	0.53
53:1:2350:C:H2'	53:1:2351:G:O4'	2.09	0.53
53:1:2443:C:H2'	53:1:2444:G:H8	1.72	0.53
29:E:37:THR:HG21	53:1:2348:U:OP2	2.08	0.53
35:K:78:PHE:HA	35:K:84:VAL:HG11	1.91	0.53
38:N:115:VAL:HG21	39:O:62:ARG:HB2	1.90	0.53
52:3:31:G:N2	52:3:47:C:H5''	2.24	0.53
52:3:1330:U:H2'	52:3:1331:G:O4'	2.08	0.53
1:b:131:MET:HE1	1:b:183:VAL:HB	1.90	0.52
1:b:266:ILE:H	1:b:266:ILE:HD12	1.74	0.52
19:t:2:ILE:HD11	53:1:144:A:H4'	1.92	0.52
39:O:52:LEU:HB2	43:S:80:ARG:HD2	1.91	0.52
52:3:1497:G:C2'	52:3:1498:U:H5'	2.39	0.52
53:1:1827:U:O2'	53:1:1828:G:H5'	2.09	0.52
53:1:2112:G:H2'	53:1:2113:U:H5'	1.90	0.52
53:1:2623:G:H2'	53:1:2624:G:C8	2.43	0.52
1:b:198:GLU:HG3	1:b:201:LEU:HD12	1.91	0.52
14:o:7:ARG:HA	14:o:10:ARG:HE	1.73	0.52
23:x:39:VAL:HG22	23:x:41:SER:H	1.75	0.52
52:3:784:A:H2'	52:3:785:G:H8	1.73	0.52
52:3:1401:G:H2'	52:3:1402:C:O4'	2.09	0.52
53:1:1748:C:H2'	53:1:1749:A:C8	2.44	0.52
53:1:1909:C:H2'	53:1:1910:G:H8	1.74	0.52
53:1:2789:C:H2'	53:1:2790:U:H5'	1.91	0.52
19:t:13:ALA:HB1	24:y:33:ALA:HB1	1.89	0.52
32:H:15:LYS:HZ1	32:H:182:ASP:HA	1.74	0.52
52:3:151:A:H62	52:3:170:U:H3	1.57	0.52
8:i:48:ILE:HG13	8:i:49:GLU:H	1.75	0.52
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.92	0.52
14:o:38:GLN:HE22	14:o:40:ILE:HG12	1.74	0.52
15:p:83:ILE:HD12	15:p:83:ILE:N	2.23	0.52
22:w:36:GLN:HE22	22:w:39:THR:HA	1.73	0.52
26:B:42:ILE:HG22	26:B:48:TYR:HB2	1.90	0.52
32:H:142:ARG:HD2	32:H:142:ARG:O	2.10	0.52
33:I:122:ILE:HD12	33:I:122:ILE:N	2.24	0.52
35:K:18:VAL:CG1	35:K:19:PRO:HD3	2.39	0.52
51:a:54:LYS:HZ3	55:6:63:G:H4'	1.75	0.52
53:1:2029:G:O6	53:1:2032:G:H5''	2.09	0.52
1:b:228:ASP:CG	53:1:780:G:H1	2.17	0.52
7:h:88:HIS:HB2	7:h:89:PRO:HD3	1.92	0.52
47:W:59:LYS:HD3	52:3:734:G:O2'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2156:G:C2'	53:1:2157:G:H5'	2.40	0.52
53:1:2853:C:H2'	53:1:2854:G:H8	1.74	0.52
2:c:133:THR:OG1	2:c:134:HIS:N	2.40	0.52
24:y:2:LYS:HD2	53:1:78:U:OP2	2.10	0.52
42:R:33:LEU:HG	42:R:38:ILE:HB	1.92	0.52
52:3:225:C:H2'	52:3:226:G:H5''	1.92	0.52
53:1:596:U:H2'	53:1:597:G:H8	1.74	0.52
53:1:668:A:H2'	53:1:670:A:H62	1.75	0.52
53:1:2480:C:H2'	53:1:2481:G:O4'	2.10	0.52
9:j:78:THR:HB	53:1:2641:G:H5''	1.90	0.52
11:l:38:GLN:NE2	53:1:805:G:H5''	2.25	0.52
11:l:111:ILE:HD11	53:1:636:G:C5	2.45	0.52
32:H:149:LYS:HB3	32:H:200:TRP:HB2	1.91	0.52
53:1:774:G:O2'	53:1:775:G:H5''	2.10	0.52
53:1:1330:C:H2'	53:1:1331:G:C8	2.45	0.52
53:1:2257:U:O2'	53:1:2258:C:H5'	2.09	0.52
53:1:2475:C:C2'	53:1:2476:A:H5'	2.39	0.52
28:D:14:ARG:HD2	53:1:771:G:OP1	2.10	0.52
31:G:103:TRP:HA	31:G:106:VAL:HG12	1.91	0.52
31:G:131:LYS:O	31:G:135:MET:HG2	2.10	0.52
42:R:33:LEU:CD2	42:R:40:GLU:HG2	2.39	0.52
52:3:1273:C:H2'	52:3:1274:A:O4'	2.10	0.52
53:1:2048:G:C3'	53:1:2049:G:H5''	2.39	0.52
2:c:46:ARG:HB2	2:c:84:LEU:HD12	1.92	0.52
7:h:87:GLU:HB3	7:h:95:LEU:HD12	1.91	0.52
9:j:15:TRP:HB3	9:j:137:PRO:HB3	1.90	0.52
14:o:17:LYS:NZ	53:1:2380:C:H5'	2.25	0.52
32:H:9:ILE:HD12	32:H:9:ILE:H	1.74	0.52
52:3:483:C:H2'	52:3:484:G:C8	2.45	0.52
53:1:1418:G:H21	53:1:1580:A:H62	1.57	0.52
53:1:2875:C:H2'	53:1:2876:G:C8	2.45	0.52
4:e:125:GLY:HA3	4:e:159:ALA:HB3	1.92	0.52
13:n:96:ARG:HB3	13:n:114:GLU:OE2	2.10	0.52
16:q:5:ARG:HD2	53:1:1250:G:H5''	1.91	0.52
32:H:175:HIS:ND1	52:3:1108:G:H5'	2.25	0.52
35:K:7:VAL:HG22	35:K:61:LEU:HD13	1.92	0.52
36:L:68:VAL:HG23	36:L:99:ALA:HB1	1.92	0.52
37:M:42:GLU:HG2	37:M:100:ILE:HD13	1.92	0.52
53:1:594:U:H2'	53:1:595:C:C6	2.45	0.52
53:1:827:U:H4'	53:1:828:U:C5	2.45	0.52
2:c:135:GLY:HA2	53:1:743:A:OP1	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:z:23:LEU:HD11	25:z:53:MET:SD	2.50	0.51
34:J:133:ILE:O	34:J:136:VAL:HG12	2.10	0.51
35:K:38:ARG:HB2	35:K:63:ASN:HB3	1.93	0.51
44:T:71:ARG:O	44:T:71:ARG:HD2	2.10	0.51
53:1:2743:U:C2'	53:1:2744:G:H5''	2.40	0.51
55:6:71:C:H2'	55:6:72:A:C8	2.45	0.51
5:f:8:VAL:HG23	5:f:49:LEU:HB2	1.91	0.51
42:R:89:ARG:HB2	42:R:96:VAL:HG22	1.91	0.51
45:U:18:GLN:HA	45:U:38:PHE:HA	1.92	0.51
49:Y:23:ARG:NH1	52:3:176:C:H5''	2.25	0.51
52:3:736:C:H2'	52:3:737:C:C6	2.45	0.51
52:3:1227:A:H2'	52:3:1228:C:H5'	1.92	0.51
1:b:15:VAL:HG12	1:b:205:GLY:HA3	1.91	0.51
1:b:221:GLY:HA2	1:b:224:MET:HE2	1.92	0.51
3:d:18:THR:HG23	3:d:106:LYS:HG2	1.93	0.51
8:i:55:PRO:HD3	8:i:74:PRO:HD3	1.91	0.51
51:a:8:MET:HE3	53:1:2174:C:H5''	1.92	0.51
53:1:2163:A:N3	53:1:2163:A:H2'	2.25	0.51
53:1:2515:C:H2'	53:1:2516:A:H8	1.75	0.51
53:1:2646:C:H2'	53:1:2647:U:O4'	2.10	0.51
57:7:43:C:H2'	57:7:44:G:C8	2.46	0.51
23:x:2:ARG:HD2	23:x:29:LEU:HD22	1.92	0.51
31:G:105:THR:HG21	52:3:1072:G:H21	1.75	0.51
38:N:105:ARG:NE	52:3:1117:A:H4'	2.25	0.51
53:1:745:G:O2'	53:1:748:G:H1'	2.10	0.51
53:1:818:G:C2'	53:1:819:A:H5''	2.40	0.51
5:f:32:LEU:HD13	5:f:74:MET:HG2	1.93	0.51
12:m:51:ARG:HD3	57:7:53:G:O2'	2.11	0.51
13:n:35:LYS:HB2	13:n:112:TYR:CE1	2.46	0.51
28:D:7:PRO:HB2	53:1:1309:G:H4'	1.93	0.51
53:1:290:U:H2'	53:1:291:G:H8	1.76	0.51
53:1:1611:C:H6	53:1:1611:C:H5'	1.75	0.51
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.91	0.51
22:w:43:ALA:HB2	22:w:55:LEU:HD22	1.91	0.51
40:P:124:LYS:HG2	52:3:780:A:OP1	2.10	0.51
51:a:206:GLY:HA2	53:1:1860:G:H5''	1.92	0.51
55:6:62:C:H2'	55:6:63:G:C8	2.46	0.51
2:c:62:LYS:HB2	2:c:63:PRO:HD3	1.93	0.51
7:h:55:VAL:HA	53:1:1084:A:C4'	2.41	0.51
18:s:41:LYS:HB2	18:s:44:ALA:HB2	1.91	0.51
53:1:755:U:H2'	53:1:756:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2328:A:H2'	53:1:2329:U:C6	2.46	0.51
39:O:42:LEU:HD11	39:O:73:LEU:HB3	1.93	0.51
46:V:5:ARG:CD	52:3:636:U:H5''	2.39	0.51
53:1:2123:G:H22	53:1:2175:C:H42	1.58	0.51
10:k:48:PRO:CG	52:3:1422:G:H5'	2.40	0.51
33:I:197:HIS:O	33:I:200:VAL:HG12	2.11	0.51
35:K:6:ILE:HB	35:K:62:MET:HB3	1.92	0.51
35:K:37:HIS:HB2	35:K:63:ASN:O	2.09	0.51
52:3:206:C:H2'	52:3:207:C:O4'	2.11	0.51
53:1:1111:A:H2'	53:1:1111:A:N3	2.25	0.51
53:1:2220:U:H2'	53:1:2221:G:H8	1.76	0.51
53:1:2799:A:H2'	53:1:2800:A:H5'	1.93	0.51
13:n:24:MET:HE3	13:n:44:LEU:HD13	1.92	0.51
34:J:23:THR:HA	34:J:28:ARG:HA	1.93	0.51
39:O:9:ARG:NH1	39:O:99:GLN:HE21	2.08	0.51
53:1:2837:A:H2'	53:1:2838:G:H8	1.76	0.51
55:6:17:C:H5''	55:6:17(A):U:OP2	2.10	0.51
1:b:213:ARG:HH21	53:1:1566:A:H5'	1.76	0.50
2:c:121:THR:HB	2:c:127:PHE:CD2	2.46	0.50
11:l:74:THR:HG22	11:l:107:PHE:HB2	1.93	0.50
22:w:17:LEU:HD21	22:w:37:ARG:NH2	2.26	0.50
29:E:34:LYS:HE3	53:1:2390:U:C5'	2.42	0.50
34:J:73:VAL:HG21	34:J:143:LEU:HD22	1.92	0.50
52:3:784:A:H2'	52:3:785:G:C8	2.46	0.50
53:1:479:A:H1'	53:1:481:G:H5''	1.93	0.50
53:1:833:A:H2'	53:1:834:G:C8	2.46	0.50
53:1:1105:U:H2'	53:1:1106:G:H5''	1.92	0.50
53:1:1775:U:H2'	53:1:1776:G:O4'	2.10	0.50
53:1:1858:A:H1'	53:1:1885:A:C2	2.46	0.50
54:2:51:G:H2'	54:2:52:A:O4'	2.11	0.50
7:h:34:THR:O	7:h:37:LYS:HB3	2.11	0.50
26:B:21:LEU:HD23	26:B:22:THR:O	2.10	0.50
31:G:150:ILE:HB	31:G:153:MET:SD	2.51	0.50
48:X:29:PRO:HA	48:X:47:THR:HG23	1.93	0.50
52:3:252:U:O2	52:3:252:U:H2'	2.11	0.50
53:1:1874:C:H2'	53:1:1875:G:O4'	2.10	0.50
53:1:2215:C:H2'	53:1:2216:G:C8	2.47	0.50
5:f:22:VAL:HG22	5:f:35:THR:HG23	1.94	0.50
11:l:23:ILE:HG23	17:r:82:HIS:CE1	2.46	0.50
28:D:37:LYS:HG2	53:1:458:G:C8	2.47	0.50
33:I:59:LYS:HE3	33:I:194:ILE:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:103:THR:HG22	52:3:1229:A:N6	2.25	0.50
52:3:1211:U:H4'	52:3:1213:A:N3	2.25	0.50
53:1:1468:U:H2'	53:1:1522:A:N6	2.25	0.50
2:c:121:THR:HB	2:c:127:PHE:HD2	1.76	0.50
4:e:77:LYS:HD3	4:e:77:LYS:N	2.27	0.50
52:3:701:U:H4'	52:3:703:G:H1'	1.92	0.50
53:1:704:G:H1'	53:1:727:A:H61	1.76	0.50
53:1:1028:A:H2'	53:1:1029:A:C8	2.47	0.50
53:1:1507:C:H2'	53:1:1508:A:O4'	2.11	0.50
53:1:2055:C:H5'	53:1:2056:G:O5'	2.11	0.50
45:U:79:ASN:HB2	45:U:82:ALA:OXT	2.11	0.50
52:3:437:U:H2'	52:3:438:U:O4'	2.11	0.50
3:d:73:ILE:H	3:d:73:ILE:HD12	1.77	0.50
11:l:122:VAL:HG22	11:l:123:ARG:N	2.27	0.50
38:N:114:LYS:HB2	38:N:117:LEU:HD12	1.93	0.50
42:R:27:THR:HA	42:R:30:LYS:HE2	1.93	0.50
50:Z:20:ARG:HA	50:Z:24:LYS:HD3	1.94	0.50
52:3:77:A:H2'	52:3:78:A:C8	2.46	0.50
52:3:350:G:H2'	52:3:351:G:C8	2.47	0.50
53:1:796:C:H2'	53:1:797:G:C8	2.46	0.50
53:1:940:G:H3'	53:1:941:A:H5''	1.94	0.50
53:1:1201:U:H2'	53:1:1202:G:H8	1.77	0.50
53:1:2048:G:H3'	53:1:2049:G:H5''	1.93	0.50
53:1:2710:C:H2'	53:1:2711:A:C8	2.47	0.50
1:b:52:HIS:CG	1:b:218:THR:HG22	2.47	0.50
2:c:194:PRO:HA	53:1:2680:U:H5'	1.93	0.50
30:F:32:LYS:CE	53:1:2478:A:H5'	2.33	0.50
37:M:74:ILE:HD12	37:M:128:VAL:HG22	1.94	0.50
42:R:112:ARG:HH21	52:3:1229:A:P	2.35	0.50
51:a:181:ASP:HB3	51:a:184:LYS:HG3	1.93	0.50
53:1:774:G:H1'	53:1:777:G:H21	1.77	0.50
5:f:169:ARG:NH1	53:1:1092:C:O2'	2.44	0.50
25:z:8:GLN:NE2	25:z:23:LEU:HD13	2.26	0.50
32:H:156:LEU:HD12	32:H:156:LEU:O	2.12	0.50
33:I:131:ILE:H	33:I:131:ILE:HD12	1.77	0.50
39:O:61:ALA:HB2	52:3:1061:G:H5''	1.93	0.50
53:1:5:A:H2'	53:1:6:A:C8	2.47	0.50
53:1:247:G:H4'	53:1:386:G:C6	2.47	0.50
53:1:2287:A:O2'	53:1:2288:A:H2'	2.12	0.50
55:5:69:C:H2'	55:5:70:G:C8	2.47	0.50
1:b:47:ARG:HD3	53:1:773:U:O2'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:71:GLY:N	53:1:674:G:H5''	2.27	0.50
7:h:56:ARG:O	53:1:1106:G:H4'	2.12	0.50
32:H:151:GLU:HG3	32:H:166:TRP:HB3	1.93	0.50
40:P:20:ALA:HB2	40:P:81:LEU:HD12	1.93	0.50
50:Z:28:LEU:O	50:Z:32:ARG:HB2	2.12	0.50
51:a:7:ARG:O	51:a:10:VAL:HG12	2.12	0.50
16:q:75:TYR:HE2	53:1:1153:C:H5'	1.77	0.49
27:C:36:LYS:HD2	53:1:2344:U:OP1	2.12	0.49
35:K:93:LYS:O	35:K:93:LYS:HD3	2.12	0.49
52:3:751:U:H2'	52:3:752:G:O4'	2.11	0.49
53:1:226:A:H2'	53:1:227:A:O4'	2.12	0.49
53:1:1222:U:H2'	53:1:1223:G:C8	2.47	0.49
53:1:2391:G:H2'	53:1:2424:C:H41	1.76	0.49
53:1:2853:C:H2'	53:1:2854:G:C8	2.47	0.49
2:c:186:LEU:HD21	2:c:188:LEU:HD21	1.94	0.49
4:e:23:SER:HB3	4:e:26:GLN:HB2	1.94	0.49
7:h:3:LEU:HG	7:h:4:ASN:H	1.75	0.49
8:i:23:VAL:HG22	8:i:26:ALA:HB3	1.94	0.49
9:j:81:ILE:HG23	9:j:82:GLY:N	2.24	0.49
13:n:73:ASN:HA	13:n:76:VAL:HG22	1.93	0.49
30:F:19:ARG:HA	53:1:2756:U:H5''	1.94	0.49
43:S:26:LEU:HD11	43:S:47:LEU:HD13	1.93	0.49
52:3:357:G:OP1	52:3:367:U:H5''	2.12	0.49
8:i:12:VAL:HG12	8:i:13:ALA:N	2.24	0.49
33:I:50:TYR:CD2	52:3:508:U:H4'	2.47	0.49
42:R:2:ARG:HG2	42:R:8:ILE:HG12	1.95	0.49
46:V:52:CYS:HB2	46:V:56:ASP:OD2	2.12	0.49
52:3:24:U:H2'	52:3:25:C:C6	2.47	0.49
54:2:78:A:H2'	54:2:79:G:O4'	2.12	0.49
15:p:9:GLN:HA	15:p:12:MET:HG2	1.94	0.49
19:t:73:ARG:N	19:t:73:ARG:HD2	2.27	0.49
25:z:15:ARG:NH1	54:2:83:G:H5''	2.26	0.49
34:J:150:GLU:OE2	34:J:151:MET:HG3	2.12	0.49
38:N:12:LYS:HD3	52:3:1347:G:N7	2.28	0.49
39:O:40:ILE:HD12	39:O:73:LEU:HD11	1.93	0.49
39:O:50:THR:HG22	39:O:64:GLN:HG2	1.94	0.49
52:3:663:A:H61	52:3:742:G:H1	1.59	0.49
52:3:952:U:H4'	52:3:964:A:H61	1.77	0.49
53:1:1053:C:C3'	53:1:1054:A:H5''	2.43	0.49
53:1:1854:A:N6	53:1:1888:G:H1'	2.28	0.49
53:1:1947:C:H2'	53:1:1948:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2475:C:H2'	53:1:2476:A:H5'	1.95	0.49
7:h:118:ILE:O	7:h:118:ILE:CG2	2.56	0.49
43:S:12:ARG:HB3	43:S:59:GLN:HE21	1.78	0.49
52:3:501:C:H2'	52:3:502:A:H8	1.78	0.49
52:3:1004:A:H2'	52:3:1005:A:O4'	2.13	0.49
52:3:1513:A:H2'	52:3:1514:G:C8	2.48	0.49
53:1:2139:U:H2'	53:1:2140:G:C8	2.48	0.49
4:e:98:PHE:HD1	4:e:101:ARG:HH11	1.61	0.49
8:i:99:LYS:NZ	8:i:138:VAL:HB	2.28	0.49
31:G:26:MET:HE2	31:G:188:THR:HA	1.95	0.49
41:Q:41:PRO:HG2	41:Q:49:ARG:NH1	2.28	0.49
45:U:21:VAL:HG23	45:U:21:VAL:O	2.13	0.49
52:3:396:C:H2'	52:3:397:A:H5''	1.94	0.49
52:3:396:C:C3'	52:3:397:A:H5''	2.43	0.49
52:3:946:A:H2'	52:3:947:G:H8	1.77	0.49
53:1:459:U:H2'	53:1:460:A:H8	1.78	0.49
5:f:153:PRO:HG3	5:f:161:VAL:O	2.12	0.49
33:I:12:ARG:HG2	33:I:33:ILE:HA	1.95	0.49
34:J:105:ILE:HD11	34:J:123:LEU:HD22	1.95	0.49
40:P:112:VAL:HG22	40:P:112:VAL:O	2.13	0.49
45:U:8:ARG:HB3	45:U:28:ARG:CZ	2.42	0.49
52:3:1218:C:H2'	52:3:1219:A:C8	2.47	0.49
53:1:414:C:H2'	53:1:415:A:C8	2.48	0.49
53:1:482:A:H1'	53:1:498:G:N2	2.28	0.49
53:1:1736:U:H2'	53:1:1737:G:O4'	2.12	0.49
53:1:2526:G:H2'	53:1:2527:C:C6	2.47	0.49
7:h:41:LEU:HD13	53:1:1083:U:O5'	2.12	0.49
9:j:84:ILE:HG23	9:j:84:ILE:O	2.13	0.49
9:j:89:PHE:HE1	9:j:100:VAL:HG11	1.78	0.49
10:k:35:VAL:HG21	10:k:69:VAL:HG12	1.93	0.49
13:n:39:PRO:HG2	53:1:1651:G:H4'	1.94	0.49
41:Q:42:LYS:HG3	41:Q:44:PRO:HD2	1.93	0.49
42:R:11:HIS:HA	42:R:43:LYS:HD2	1.93	0.49
52:3:1316:G:H2'	52:3:1317:C:H5''	1.93	0.49
8:i:12:VAL:O	8:i:13:ALA:C	2.54	0.49
24:y:41:HIS:CD2	53:1:96:C:H4'	2.48	0.49
27:C:24:LYS:HZ2	27:C:26:LYS:HA	1.78	0.49
38:N:114:LYS:NZ	52:3:1187:G:H5'	2.28	0.49
52:3:1033:G:H2'	52:3:1034:G:H5''	1.93	0.49
53:1:828:U:H2'	53:1:829:A:C8	2.47	0.49
53:1:940:G:C3'	53:1:941:A:H5''	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1748:C:H2'	53:1:1749:A:H8	1.78	0.49
5:f:70:LEU:HD11	53:1:2758:A:H2	1.78	0.49
11:l:93:ASN:C	11:l:95:LEU:H	2.21	0.49
16:q:14:LYS:HA	16:q:17:LEU:HB3	1.95	0.49
17:r:40:MET:HG2	17:r:48:LYS:HA	1.95	0.49
21:v:42:LEU:H	21:v:42:LEU:HD23	1.78	0.49
31:G:3:VAL:HG11	31:G:211:LEU:HD11	1.94	0.49
43:S:29:ILE:HD12	43:S:29:ILE:N	2.28	0.49
52:3:591:U:H2'	52:3:592:G:H8	1.77	0.49
52:3:1496:C:H2'	52:3:1497:G:C8	2.47	0.49
53:1:1429:G:H2'	53:1:1430:G:H8	1.77	0.49
53:1:2267:A:H5''	53:1:2268:A:H5'	1.93	0.49
53:1:2489:U:H2'	53:1:2490:G:O4'	2.13	0.49
54:2:2:G:H2'	54:2:3:C:C6	2.48	0.49
10:k:6:THR:HG23	53:1:1666:G:H4'	1.95	0.48
10:k:99:ILE:HD13	10:k:115:ILE:HG23	1.95	0.48
14:o:29:HIS:NE2	54:2:7:G:H5''	2.28	0.48
42:R:105:ALA:HA	52:3:948:C:OP1	2.12	0.48
52:3:70:U:H4'	52:3:71:A:H8	1.77	0.48
52:3:591:U:H2'	52:3:592:G:C8	2.48	0.48
53:1:227:A:H1'	53:1:229:C:N4	2.28	0.48
53:1:1856:U:H2'	53:1:1857:G:O4'	2.13	0.48
53:1:2087:G:H2'	53:1:2088:A:C8	2.48	0.48
53:1:2297:A:N6	53:1:2319:G:H1'	2.28	0.48
53:1:2749:A:OP2	53:1:2751:G:H5''	2.13	0.48
54:2:88:C:C4'	54:2:89:U:OP1	2.61	0.48
1:b:75:ALA:HB2	1:b:95:TYR:CD1	2.48	0.48
1:b:146:LYS:HB2	1:b:149:LYS:HB2	1.95	0.48
4:e:115:GLY:HA3	4:e:177:ARG:HB2	1.95	0.48
7:h:29:ASP:HB3	7:h:32:GLY:HA3	1.94	0.48
17:r:6:GLN:HE21	17:r:9:GLY:HA2	1.78	0.48
17:r:88:GLY:HA3	53:1:1225:G:OP1	2.13	0.48
31:G:143:LEU:O	31:G:147:LEU:HB2	2.13	0.48
52:3:1402:C:H2'	52:3:1403:C:O4'	2.13	0.48
52:3:1477:U:H2'	52:3:1478:U:C6	2.48	0.48
54:2:30:C:H2'	54:2:31:C:O4'	2.13	0.48
1:b:221:GLY:HA2	1:b:224:MET:CE	2.43	0.48
6:g:58:LEU:O	6:g:61:VAL:HG12	2.14	0.48
16:q:50:ARG:NH2	53:1:993:G:OP2	2.46	0.48
17:r:35:PHE:HB2	17:r:59:ILE:HB	1.95	0.48
32:H:172:VAL:O	52:3:1107:C:H5''	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:89:LEU:O	33:I:93:LEU:HD23	2.13	0.48
48:X:5:LYS:HB3	52:3:1313:U:OP2	2.13	0.48
52:3:89:U:H2'	52:3:90:C:O4'	2.14	0.48
52:3:715:A:H2'	52:3:716:A:C8	2.48	0.48
53:1:2185:U:H2'	53:1:2186:G:C8	2.48	0.48
53:1:2345:G:N3	53:1:2381:A:H2'	2.28	0.48
3:d:176:ASP:N	3:d:176:ASP:OD1	2.46	0.48
9:j:56:VAL:HB	9:j:124:VAL:HG23	1.95	0.48
32:H:185:THR:HG22	32:H:198:LYS:HG2	1.96	0.48
45:U:31:ARG:HB2	52:3:310:G:H5''	1.95	0.48
52:3:1125:U:H2'	52:3:1126:U:H2'	1.96	0.48
53:1:5:A:H2'	53:1:6:A:H8	1.79	0.48
53:1:955:U:H3	53:1:962:G:H1	1.61	0.48
53:1:962:G:O2'	53:1:963:U:H5'	2.12	0.48
53:1:1476:U:H2'	53:1:1477:A:H8	1.78	0.48
53:1:2391:G:H4'	53:1:2392:A:OP1	2.12	0.48
53:1:2743:U:C3'	53:1:2744:G:H5''	2.43	0.48
7:h:102:ALA:O	7:h:107:GLU:HB2	2.14	0.48
12:m:27:SER:HB2	12:m:66:ARG:HH12	1.79	0.48
12:m:74:THR:HG21	53:1:956:G:OP2	2.13	0.48
31:G:66:ILE:HD12	31:G:159:ALA:HB3	1.95	0.48
35:K:3:HIS:HB2	35:K:92:THR:HA	1.95	0.48
38:N:18:VAL:HG22	38:N:64:ILE:HD12	1.94	0.48
40:P:124:LYS:HD3	52:3:780:A:H5''	1.95	0.48
52:3:945:G:H2'	52:3:945:G:N3	2.28	0.48
9:j:35:ARG:HA	9:j:40:HIS:CD2	2.49	0.48
15:p:98:TYR:HD2	15:p:102:ARG:HD3	1.79	0.48
39:O:22:THR:HG21	39:O:39:PRO:HB3	1.95	0.48
52:3:211:G:C2'	52:3:212:G:H5'	2.44	0.48
53:1:441:U:O2'	53:1:442:G:H5'	2.13	0.48
22:w:16:ARG:N	22:w:16:ARG:HD2	2.29	0.48
26:B:10:SER:O	26:B:14:MET:HG3	2.13	0.48
32:H:137:VAL:HG21	32:H:167:TYR:CD2	2.48	0.48
32:H:172:VAL:O	32:H:172:VAL:HG13	2.14	0.48
33:I:58:GLN:O	33:I:62:ARG:HG2	2.14	0.48
35:K:89:VAL:HG23	52:3:737:C:H5'	1.95	0.48
40:P:49:SER:OG	40:P:68:ARG:HD3	2.14	0.48
43:S:41:TRP:O	43:S:44:VAL:HG12	2.14	0.48
44:T:22:GLY:HA3	52:3:750:C:O2	2.14	0.48
52:3:163:C:H2'	52:3:164:G:O4'	2.13	0.48
52:3:211:G:H2'	52:3:212:G:H5'	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1078:U:C5'	53:1:1079:C:H5''	2.44	0.48
53:1:1697:G:H4'	53:1:1978:A:H5''	1.95	0.48
53:1:2266:A:H4'	53:1:2267:A:N3	2.29	0.48
53:1:2572:A:OP1	53:1:2574:G:H4'	2.14	0.48
6:g:25:TYR:CD1	53:1:2094:A:H5'	2.49	0.48
7:h:80:THR:HA	53:1:1107:G:O2'	2.13	0.48
18:s:90:LYS:HA	53:1:751:A:H5'	1.94	0.48
31:G:151:LYS:HE3	31:G:152:ASP:OD2	2.13	0.48
37:M:66:GLN:HG3	37:M:67:GLY:H	1.78	0.48
53:1:118:A:OP2	53:1:119:A:H5''	2.14	0.48
53:1:1680:U:H2'	53:1:1681:G:H5'	1.96	0.48
53:1:2423:U:O2'	53:1:2425:A:H2'	2.14	0.48
3:d:57:LYS:HB2	53:1:797:G:OP2	2.14	0.48
4:e:35:LEU:HB2	4:e:88:VAL:HB	1.95	0.48
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.96	0.48
33:I:202:LEU:O	33:I:202:LEU:HD23	2.13	0.48
35:K:92:THR:OG1	35:K:93:LYS:N	2.46	0.48
38:N:82:ILE:O	38:N:86:LEU:HG	2.14	0.48
41:Q:71:HIS:HB2	41:Q:73:LEU:HD13	1.95	0.48
53:1:2398:U:H2'	53:1:2399:G:H8	1.78	0.48
53:1:2834:G:O2'	53:1:2835:A:H5'	2.14	0.48
1:b:257:ARG:HD3	53:1:1799:G:OP1	2.14	0.48
2:c:4:LEU:HD22	2:c:32:ASN:HD22	1.79	0.48
15:p:91:VAL:HG11	15:p:96:LEU:HD21	1.96	0.48
53:1:492:A:H2'	53:1:493:G:O4'	2.14	0.48
53:1:2024:G:OP2	53:1:2034:U:H4'	2.14	0.48
4:e:107:VAL:HG13	4:e:108:PRO:HD3	1.94	0.47
31:G:156:LEU:HD21	31:G:178:LEU:HD23	1.96	0.47
33:I:4:LEU:HD21	52:3:405:U:C5	2.49	0.47
34:J:148:SER:HB2	34:J:149:PRO:HD2	1.96	0.47
44:T:44:GLU:C	44:T:46:LYS:H	2.22	0.47
52:3:1237:C:OP1	52:3:1238:A:H1'	2.14	0.47
52:3:1280:A:O2'	52:3:1281:C:H5'	2.13	0.47
53:1:528:A:N1	53:1:2042:A:H2'	2.29	0.47
53:1:1679:A:H2'	53:1:1680:U:C6	2.49	0.47
53:1:1739:A:H2'	53:1:1740:G:O4'	2.14	0.47
53:1:2633:G:H5'	53:1:2811:G:O2'	2.13	0.47
54:2:106:G:H2'	54:2:107:G:O4'	2.14	0.47
8:i:9:LYS:HE2	53:1:1070:A:N3	2.29	0.47
9:j:116:ARG:NH2	53:1:528:A:H8	2.12	0.47
25:z:10:ARG:HH21	25:z:10:ARG:HG3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:216:VAL:O	31:G:219:THR:HG22	2.13	0.47
37:M:17:GLN:HE21	37:M:71:VAL:H	1.60	0.47
42:R:66:GLY:O	42:R:70:ARG:HG2	2.14	0.47
52:3:236:A:H2'	52:3:237:G:C8	2.49	0.47
52:3:620:C:H2'	52:3:621:A:O4'	2.14	0.47
52:3:1271:A:H5'	52:3:1314:C:H5''	1.94	0.47
53:1:1765:U:H2'	53:1:1766:G:H8	1.79	0.47
4:e:26:GLN:HG3	54:2:57:A:C1'	2.44	0.47
6:g:40:THR:HG22	6:g:43:ASN:ND2	2.29	0.47
6:g:44:ILE:O	6:g:48:GLU:HG2	2.14	0.47
13:n:47:VAL:C	13:n:50:PRO:HD2	2.39	0.47
29:E:56:LEU:HD12	29:E:56:LEU:H	1.79	0.47
32:H:109:GLU:HB2	32:H:143:LEU:CD2	2.45	0.47
52:3:876:C:H2'	52:3:877:G:H8	1.79	0.47
52:3:1139:G:H5''	52:3:1140:C:H5	1.80	0.47
52:3:1202:U:H2'	52:3:1203:C:O4'	2.13	0.47
53:1:406:G:H2'	53:1:407:G:C8	2.49	0.47
53:1:445:C:O2'	53:1:446:G:H5'	2.14	0.47
53:1:1683:U:H2'	53:1:1684:G:C8	2.50	0.47
53:1:2698:U:H2'	53:1:2699:C:C6	2.49	0.47
57:7:35:A:H2'	57:7:36:A:O4'	2.14	0.47
5:f:173:ALA:O	5:f:174:LYS:HG2	2.15	0.47
9:j:4:PHE:HB3	16:q:63:ARG:HH12	1.80	0.47
13:n:32:GLU:HG2	13:n:115:LEU:HD12	1.96	0.47
14:o:75:GLY:HA2	14:o:78:VAL:HG12	1.96	0.47
52:3:328:C:H5'	52:3:329:A:H5'	1.95	0.47
52:3:392:C:H2'	52:3:393:A:H8	1.80	0.47
53:1:69:C:O2'	53:1:70:G:H5'	2.13	0.47
53:1:818:G:O2'	53:1:819:A:H5''	2.15	0.47
53:1:1300:G:H4'	53:1:1301:A:H5''	1.95	0.47
53:1:1570:A:H2'	53:1:1571:A:C8	2.49	0.47
53:1:1600:C:H2'	53:1:1601:G:H8	1.79	0.47
53:1:2233:U:H2'	53:1:2234:G:H8	1.79	0.47
53:1:2432:A:H1'	55:6:75:C:H4'	1.97	0.47
6:g:84:ALA:HA	6:g:91:PHE:H	1.80	0.47
39:O:67:ILE:HG13	39:O:67:ILE:O	2.15	0.47
41:Q:41:PRO:HG3	41:Q:49:ARG:HD2	1.96	0.47
46:V:6:THR:HG21	46:V:59:GLU:HB3	1.96	0.47
53:1:74:A:H4'	53:1:75:G:O5'	2.13	0.47
53:1:278:A:H2'	53:1:278:A:N3	2.29	0.47
53:1:1078:U:H4'	53:1:1079:C:H5''	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:114:C:H2'	54:2:115:A:H8	1.80	0.47
3:d:109:LEU:HD23	3:d:112:LEU:HD12	1.97	0.47
4:e:56:LEU:HD23	4:e:59:ILE:HD12	1.96	0.47
5:f:102:ILE:HD11	5:f:130:ILE:HD13	1.95	0.47
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.95	0.47
9:j:92:MET:HA	9:j:92:MET:HE2	1.96	0.47
15:p:59:THR:HG22	15:p:72:VAL:HG23	1.95	0.47
22:w:16:ARG:HG2	53:1:2356:U:O3'	2.15	0.47
41:Q:23:LEU:HD12	41:Q:29:LYS:NZ	2.29	0.47
52:3:1516:G:H2'	52:3:1518:A:OP2	2.14	0.47
53:1:2628:C:H3'	53:1:2629:U:H5'	1.96	0.47
53:1:2795:C:H2'	53:1:2796:U:O4'	2.14	0.47
3:d:18:THR:OG1	3:d:106:LYS:HE3	2.14	0.47
13:n:9:GLN:HA	13:n:17:ARG:NH2	2.29	0.47
14:o:3:LYS:NZ	54:2:30:C:OP1	2.46	0.47
15:p:38:ARG:HH21	15:p:38:ARG:HG3	1.79	0.47
23:x:1:SER:HA	53:1:1364:G:C8	2.49	0.47
23:x:17:ARG:HB2	53:1:380:G:OP1	2.15	0.47
29:E:61:LEU:HD12	29:E:64:ALA:HB3	1.97	0.47
31:G:116:LEU:HD13	31:G:136:ARG:HE	1.79	0.47
38:N:20:ILE:HD11	38:N:60:LEU:HG	1.97	0.47
39:O:37:ARG:CD	52:3:1124:G:H5''	2.43	0.47
46:V:48:GLU:O	46:V:49:ASN:C	2.57	0.47
50:Z:27:VAL:O	50:Z:31:VAL:HG23	2.15	0.47
51:a:193:LEU:HD23	51:a:197:LYS:HE2	1.97	0.47
52:3:70:U:H2'	52:3:94:G:O6	2.14	0.47
52:3:1497:G:O2'	52:3:1498:U:H5'	2.15	0.47
53:1:576:U:H2'	53:1:577:G:C8	2.49	0.47
53:1:1045:C:P	53:1:1047:G:H5'	2.54	0.47
53:1:1368:G:H2'	53:1:1369:G:H8	1.80	0.47
1:b:213:ARG:NH2	53:1:1566:A:H5'	2.30	0.47
12:m:36:VAL:HG13	21:v:82:TYR:CD2	2.49	0.47
14:o:17:LYS:HZ1	53:1:2380:C:H5'	1.79	0.47
17:r:20:VAL:HG23	17:r:98:ILE:HD11	1.97	0.47
17:r:98:ILE:HD12	17:r:98:ILE:N	2.30	0.47
23:x:63:ILE:HD12	23:x:63:ILE:N	2.29	0.47
48:X:53:GLY:HA3	52:3:958:A:H61	1.79	0.47
53:1:910:A:H1'	53:1:2264:C:O2'	2.14	0.47
53:1:1947:C:H2'	53:1:1948:G:C8	2.50	0.47
53:1:2032:G:OP2	53:1:2455:G:H5'	2.15	0.47
3:d:163:ASN:OD1	53:1:323:C:H5''	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:17:VAL:HG22	9:j:139:VAL:HA	1.97	0.47
15:p:2:ASN:OD1	53:1:2876:G:H4'	2.15	0.47
30:F:36:ARG:HH11	30:F:37:GLN:HG2	1.80	0.47
33:I:84:ASN:ND2	34:J:100:GLU:OE1	2.48	0.47
33:I:97:LEU:HB2	33:I:134:TYR:HB3	1.96	0.47
38:N:118:ARG:HH21	38:N:124:PRO:HB3	1.80	0.47
52:3:539:A:H2'	52:3:540:G:C8	2.49	0.47
52:3:1404:C:H2'	52:3:1405:G:C8	2.49	0.47
53:1:880:G:H2'	53:1:881:G:H8	1.79	0.47
53:1:1086:A:H3'	53:1:1086:A:N3	2.30	0.47
53:1:1440:U:H2'	53:1:1441:G:C8	2.49	0.47
1:b:47:ARG:NH2	53:1:774:G:H5''	2.30	0.47
2:c:149:ASN:HB3	53:1:2572:A:P	2.54	0.47
31:G:13:VAL:HG13	31:G:202:ASN:H	1.79	0.47
38:N:10:ARG:O	38:N:105:ARG:NH1	2.48	0.47
49:Y:23:ARG:HH12	52:3:176:C:H5''	1.78	0.47
52:3:195:A:H2'	52:3:196:A:C8	2.50	0.47
52:3:555:U:H2'	52:3:556:C:C6	2.50	0.47
52:3:946:A:H2'	52:3:947:G:C8	2.50	0.47
52:3:1170:A:H2'	52:3:1171:A:O4'	2.15	0.47
53:1:281:C:N4	53:1:359:G:H1	2.12	0.47
53:1:2162:G:H2'	53:1:2163:A:H8	1.80	0.47
53:1:2248:C:C2'	53:1:2249:U:H5'	2.45	0.47
1:b:69:ASN:OD1	1:b:101:ARG:NH1	2.48	0.46
4:e:2:LYS:HB3	4:e:100:GLU:OE2	2.15	0.46
14:o:100:HIS:HA	14:o:104:GLN:OE1	2.15	0.46
15:p:112:ARG:C	15:p:113:LEU:HD23	2.40	0.46
27:C:7:LYS:CD	53:1:2420:C:H5''	2.41	0.46
27:C:16:THR:HG21	27:C:41:VAL:HG21	1.97	0.46
31:G:198:VAL:C	31:G:199:ILE:HD12	2.40	0.46
32:H:123:LEU:HD13	32:H:195:ILE:HG21	1.96	0.46
41:Q:60:PHE:HB3	41:Q:62:VAL:HG13	1.95	0.46
50:Z:23:GLU:C	50:Z:25:ALA:H	2.23	0.46
51:a:8:MET:HA	51:a:11:ILE:HD12	1.98	0.46
52:3:981:U:H2'	52:3:982:U:C5	2.50	0.46
53:1:996:A:H2'	53:1:997:G:H8	1.79	0.46
53:1:1039:A:H2	53:1:1116:G:H22	1.61	0.46
2:c:14:ILE:HG13	15:p:11:GLN:HE22	1.80	0.46
3:d:105:LEU:O	3:d:108:ILE:HG22	2.15	0.46
40:P:34:THR:HG22	40:P:40:ALA:HA	1.97	0.46
43:S:44:VAL:HG13	43:S:45:LEU:HD22	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:V:20:ILE:HG22	46:V:45:VAL:O	2.16	0.46
46:V:32:ILE:HD12	46:V:32:ILE:N	2.29	0.46
52:3:603:U:H2'	52:3:604:G:C8	2.51	0.46
53:1:370:G:H2'	53:1:423:A:N7	2.30	0.46
53:1:1101:U:H2'	53:1:1102:C:H6	1.81	0.46
53:1:2707:U:H2'	53:1:2708:G:H8	1.79	0.46
53:1:2743:U:H2'	53:1:2744:G:C5'	2.45	0.46
6:g:73:ASN:O	6:g:76:GLU:HG3	2.15	0.46
32:H:38:VAL:HG11	32:H:90:VAL:HG23	1.97	0.46
40:P:118:ASN:OD1	52:3:717:U:H4'	2.14	0.46
43:S:6:LYS:HE2	43:S:67:GLY:HA3	1.96	0.46
45:U:2:VAL:HG23	45:U:65:ALA:HA	1.96	0.46
52:3:67:C:H2'	52:3:68:G:C8	2.50	0.46
52:3:291:U:H2'	52:3:292:G:C8	2.50	0.46
52:3:1346:A:H2'	52:3:1346:A:N3	2.30	0.46
53:1:568:U:H4'	53:1:945:A:N6	2.30	0.46
53:1:1830:C:H2'	53:1:1831:G:H8	1.81	0.46
53:1:2106:U:H2'	53:1:2107:G:C8	2.50	0.46
53:1:2451:A:H1'	55:5:76:A:O2'	2.16	0.46
14:o:33:ARG:NH2	54:2:52:A:N7	2.64	0.46
18:s:88:ARG:H	53:1:1614:A:H61	1.63	0.46
22:w:43:ALA:HB1	22:w:47:VAL:HG23	1.98	0.46
24:y:22:LEU:HB3	24:y:23:ARG:HD3	1.96	0.46
42:R:6:ILE:HG23	42:R:7:ASN:N	2.30	0.46
42:R:21:ILE:H	42:R:21:ILE:HD12	1.80	0.46
50:Z:64:ALA:C	50:Z:66:ARG:H	2.23	0.46
53:1:741:U:H2'	53:1:742:A:C8	2.51	0.46
53:1:2011:U:H2'	53:1:2012:G:O4'	2.14	0.46
53:1:2105:U:H2'	53:1:2106:U:O4'	2.15	0.46
53:1:2238:G:H2'	53:1:2238:G:N3	2.30	0.46
7:h:80:THR:HA	53:1:1107:G:HO2'	1.80	0.46
10:k:69:VAL:HG22	10:k:77:ILE:HB	1.96	0.46
20:u:5:ARG:HG3	20:u:93:ARG:NH2	2.31	0.46
24:y:21:LEU:HA	24:y:25:GLN:HB3	1.97	0.46
39:O:100:ILE:HD12	39:O:100:ILE:N	2.30	0.46
45:U:71:VAL:O	45:U:75:ILE:HG13	2.14	0.46
52:3:51:A:H4'	52:3:52:C:H5''	1.97	0.46
52:3:680:C:H2'	52:3:681:A:H8	1.81	0.46
52:3:680:C:H2'	52:3:681:A:C8	2.51	0.46
52:3:1498:U:H1'	52:3:1499:A:N7	2.31	0.46
53:1:18:U:H2'	53:1:19:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:891:G:H2'	53:1:892:A:H8	1.80	0.46
53:1:2023:C:H2'	53:1:2024:G:H8	1.80	0.46
10:k:66:LYS:HE2	10:k:81:GLY:HA2	1.98	0.46
12:m:111:GLU:HG2	12:m:112:LEU:N	2.30	0.46
25:z:29:ARG:NH2	53:1:1183:U:H5''	2.30	0.46
27:C:9:LYS:HE2	27:C:52:LYS:O	2.15	0.46
35:K:53:LYS:HD2	35:K:54:LEU:N	2.30	0.46
36:L:142:ARG:CG	55:6:41:C:H4'	2.46	0.46
37:M:79:ARG:HB3	52:3:878:A:OP1	2.16	0.46
45:U:8:ARG:HB3	45:U:28:ARG:NE	2.31	0.46
45:U:8:ARG:HD3	45:U:17:TYR:CZ	2.50	0.46
52:3:224:U:H2'	52:3:225:C:C6	2.51	0.46
52:3:422:C:H5'	52:3:423:G:N3	2.31	0.46
52:3:487:A:H2'	52:3:488:C:O4'	2.16	0.46
53:1:616:A:H2'	53:1:617:G:O4'	2.15	0.46
53:1:1773:A:H2'	53:1:1774:C:O4'	2.15	0.46
11:l:101:ILE:HG13	11:l:102:GLY:N	2.30	0.46
12:m:74:THR:HG21	12:m:86:LYS:HE2	1.97	0.46
13:n:87:PHE:CD1	13:n:90:ARG:HD3	2.51	0.46
31:G:55:GLU:HA	31:G:58:LYS:NZ	2.31	0.46
51:a:194:VAL:O	51:a:198:LYS:HG2	2.15	0.46
52:3:802:A:H2'	52:3:803:G:O4'	2.16	0.46
53:1:239:C:H2'	53:1:240:C:O4'	2.15	0.46
53:1:281:C:H42	53:1:359:G:H1	1.62	0.46
53:1:548:G:H2'	53:1:549:G:O4'	2.16	0.46
53:1:876:C:H2'	53:1:877:A:O4'	2.16	0.46
9:j:110:PRO:O	9:j:115:GLY:HA3	2.16	0.46
20:u:31:GLY:O	20:u:66:VAL:HG23	2.16	0.46
23:x:11:PRO:HG3	23:x:30:PRO:HD2	1.98	0.46
35:K:44:ARG:NH1	35:K:44:ARG:HB3	2.31	0.46
41:Q:49:ARG:HH22	52:3:522:C:H41	1.62	0.46
45:U:39:PHE:HD1	45:U:50:THR:HB	1.81	0.46
47:W:31:TYR:O	47:W:39:VAL:HG22	2.15	0.46
49:Y:55:PRO:HB3	52:3:193:C:O3'	2.16	0.46
53:1:1443:U:H2'	53:1:1444:G:H8	1.79	0.46
57:7:9:A:H62	57:7:23:A:H62	1.63	0.46
4:e:21:TYR:HB3	4:e:26:GLN:HB3	1.96	0.46
20:u:80:ASP:N	20:u:80:ASP:OD1	2.48	0.46
21:v:76:ASP:H	21:v:90:ASP:HB2	1.81	0.46
26:B:6:LYS:HA	26:B:7:PRO:HD3	1.74	0.46
31:G:65:LYS:HG3	31:G:157:PRO:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:1:MET:HE2	35:K:67:PRO:HD3	1.98	0.46
40:P:13:LYS:HD3	40:P:13:LYS:N	2.31	0.46
41:Q:114:SER:HB2	52:3:35:G:H21	1.81	0.46
42:R:91:ARG:HG2	53:1:888:C:N3	2.30	0.46
45:U:4:ILE:HD13	45:U:57:ILE:HG23	1.98	0.46
52:3:32:A:H2'	52:3:33:A:C8	2.51	0.46
52:3:886:G:H2'	52:3:887:G:O4'	2.16	0.46
52:3:1137:C:H4'	52:3:1138:G:N2	2.30	0.46
52:3:1219:A:H2'	52:3:1220:G:C8	2.50	0.46
53:1:467:G:O2'	53:1:468:G:H5'	2.16	0.46
53:1:1889:A:H2'	53:1:1890:A:C8	2.51	0.46
53:1:2508:G:H1	53:1:2580:U:H3	1.64	0.46
55:5:69:C:H2'	55:5:70:G:H8	1.81	0.46
6:g:121:VAL:HG23	6:g:123:ARG:HG3	1.98	0.46
7:h:58:THR:HA	7:h:63:ALA:CB	2.45	0.46
18:s:94:ASP:OD2	53:1:2014:A:H5'	2.16	0.46
25:z:37:ARG:HH21	53:1:929:U:H4'	1.81	0.46
33:I:43:ARG:HD2	33:I:44:LYS:O	2.16	0.46
36:L:134:VAL:O	36:L:138:GLU:HG2	2.15	0.46
38:N:105:ARG:HE	52:3:1117:A:H4'	1.80	0.46
51:a:185:LEU:HA	51:a:188:ASN:HD22	1.81	0.46
52:3:273:U:C2'	52:3:274:A:H5'	2.45	0.46
53:1:1429:G:H2'	53:1:1430:G:C8	2.50	0.46
53:1:2366:A:H2'	53:1:2367:G:O4'	2.16	0.46
53:1:2368:C:H2'	53:1:2369:A:C8	2.51	0.46
53:1:2432:A:N3	55:6:75:C:H5'	2.30	0.46
53:1:2629:U:O2'	53:1:2630:G:H5''	2.16	0.46
1:b:129:LEU:N	1:b:129:LEU:HD23	2.31	0.45
5:f:148:ARG:HE	5:f:153:PRO:HD3	1.81	0.45
39:O:88:MET:C	39:O:89:ARG:HG3	2.42	0.45
43:S:80:ARG:O	43:S:83:VAL:HG12	2.16	0.45
52:3:235:C:H2'	52:3:236:A:H8	1.81	0.45
52:3:245:U:O2'	52:3:246:A:H5'	2.17	0.45
53:1:1047:G:H2'	53:1:1110:G:H1	1.81	0.45
53:1:1437:C:H2'	53:1:1438:U:C6	2.52	0.45
53:1:2033:A:H1'	53:1:2035:G:OP2	2.16	0.45
53:1:2875:C:H2'	53:1:2876:G:H8	1.79	0.45
1:b:266:ILE:HD12	1:b:266:ILE:N	2.30	0.45
3:d:79:ARG:HH21	53:1:448:U:C4'	2.30	0.45
3:d:119:ILE:O	3:d:187:VAL:HA	2.16	0.45
8:i:71:LYS:HD2	8:i:72:THR:N	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:102:GLU:HB3	9:j:119:PHE:HZ	1.80	0.45
19:t:64:LYS:NZ	53:1:1602:U:OP2	2.43	0.45
26:B:8:THR:OG1	26:B:9:ARG:N	2.48	0.45
40:P:118:ASN:OD1	52:3:718:A:H5'	2.15	0.45
43:S:28:ALA:HB3	43:S:29:ILE:HD12	1.98	0.45
44:T:68:TYR:OH	52:3:752:G:H4'	2.17	0.45
51:a:60:ARG:HG2	51:a:164:ARG:HG3	1.98	0.45
52:3:123:U:H5''	52:3:311:C:O2'	2.16	0.45
53:1:1106:G:H2'	53:1:1107:G:O4'	2.16	0.45
53:1:1319:C:O2'	53:1:1320:C:H5'	2.16	0.45
53:1:2756:U:H4'	53:1:2757:A:OP1	2.15	0.45
1:b:70:LYS:HG2	1:b:101:ARG:NH1	2.31	0.45
5:f:32:LEU:HD23	5:f:33:THR:N	2.32	0.45
6:g:8:LYS:O	6:g:9:VAL:C	2.59	0.45
8:i:9:LYS:HG3	53:1:1070:A:H2	1.81	0.45
9:j:37:ARG:HA	9:j:118:MET:HE3	1.99	0.45
14:o:11:ALA:HB2	14:o:96:GLY:N	2.30	0.45
17:r:49:ILE:CG2	17:r:54:VAL:HG22	2.46	0.45
18:s:15:GLN:NE2	53:1:1266:G:H8	2.14	0.45
29:E:61:LEU:HG	29:E:61:LEU:O	2.16	0.45
35:K:86:ARG:CZ	52:3:673:A:H4'	2.46	0.45
52:3:79:G:H2'	52:3:80:A:O4'	2.17	0.45
52:3:358:U:H2'	52:3:359:G:C8	2.52	0.45
52:3:448:A:H3'	52:3:449:G:C8	2.51	0.45
52:3:505:G:OP2	52:3:535:A:H5'	2.16	0.45
53:1:720:U:H2'	53:1:721:A:C8	2.52	0.45
53:1:1654:A:H2'	53:1:1655:A:C8	2.51	0.45
53:1:2358:A:H2'	53:1:2359:C:O4'	2.16	0.45
57:7:47:U:H3'	57:7:48:C:C5'	2.47	0.45
1:b:153:LEU:HD13	1:b:175:LEU:HD21	1.97	0.45
11:l:30:THR:HG22	53:1:810:U:O4	2.16	0.45
17:r:80:ARG:NH2	53:1:571:U:H2'	2.31	0.45
22:w:15:LYS:HE2	22:w:15:LYS:HA	1.98	0.45
25:z:40:THR:HG23	25:z:43:ILE:H	1.81	0.45
34:J:133:ILE:HD13	52:3:1079:G:H5'	1.98	0.45
38:N:26:LYS:C	38:N:27:ILE:HD12	2.41	0.45
42:R:104:ASN:HB3	42:R:105:ALA:H	1.66	0.45
43:S:63:CYS:SG	43:S:79:SER:HB3	2.57	0.45
52:3:1513:A:H2'	52:3:1514:G:H8	1.80	0.45
53:1:554:U:H2'	53:1:555:G:O4'	2.15	0.45
53:1:657:U:H2'	53:1:658:U:C6	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1654:A:H2'	53:1:1655:A:H8	1.81	0.45
53:1:1761:C:H2'	53:1:1762:A:O4'	2.16	0.45
53:1:2023:C:H2'	53:1:2024:G:C8	2.51	0.45
53:1:2162:G:H2'	53:1:2163:A:C8	2.51	0.45
3:d:88:ARG:HB3	3:d:89:PRO:HD2	1.99	0.45
5:f:44:HIS:CG	5:f:45:ALA:H	2.34	0.45
6:g:97:ARG:HA	6:g:112:LYS:HG3	1.97	0.45
9:j:105:VAL:O	9:j:109:LEU:HD23	2.16	0.45
9:j:124:VAL:HG22	9:j:125:TYR:N	2.31	0.45
28:D:5:PHE:HD2	53:1:1612:C:H4'	1.81	0.45
36:L:144:ALA:O	36:L:148:LYS:HB2	2.16	0.45
42:R:33:LEU:HD23	42:R:40:GLU:HG2	1.98	0.45
43:S:30:ILE:HG22	43:S:40:ARG:HA	1.98	0.45
45:U:5:ARG:HH22	45:U:28:ARG:HA	1.82	0.45
52:3:59:A:H5''	52:3:387:U:H5''	1.98	0.45
52:3:505:G:H4'	52:3:534:U:C4	2.51	0.45
52:3:909:A:H2'	52:3:910:C:O4'	2.15	0.45
53:1:1744:A:H2'	53:1:1745:A:O4'	2.16	0.45
53:1:2246:G:H2'	53:1:2247:A:H8	1.82	0.45
53:1:2655:G:O2'	53:1:2656:U:H5	1.99	0.45
1:b:107:LYS:HB2	1:b:193:GLU:OE2	2.16	0.45
11:l:55:MET:HE3	53:1:2392:A:N1	2.32	0.45
13:n:69:ARG:O	13:n:70:THR:OG1	2.28	0.45
22:w:42:HIS:CD2	22:w:73:ARG:HD3	2.52	0.45
27:C:9:LYS:HG3	27:C:19:PHE:CD2	2.51	0.45
29:E:24:LYS:HD3	29:E:46:LYS:HE3	1.98	0.45
29:E:50:SER:OG	29:E:53:ASP:OD2	2.34	0.45
48:X:40:PHE:O	48:X:43:MET:HB3	2.16	0.45
52:3:1256:A:H1'	52:3:1258:G:C4	2.51	0.45
53:1:2760:C:O2'	53:1:2761:A:H5'	2.16	0.45
19:t:34:VAL:HG12	19:t:35:ALA:N	2.31	0.45
31:G:67:LEU:HD21	31:G:153:MET:HE3	1.99	0.45
35:K:47:LEU:HD12	35:K:55:HIS:HA	1.99	0.45
36:L:23:ALA:O	36:L:26:VAL:HG12	2.17	0.45
36:L:91:ARG:O	36:L:95:ARG:N	2.50	0.45
38:N:49:GLN:N	38:N:50:PRO:HD2	2.32	0.45
46:V:44:HIS:HE1	52:3:276:G:H4'	1.81	0.45
52:3:695:A:H2'	52:3:696:A:C8	2.51	0.45
52:3:1236:A:H4'	52:3:1304:G:H4'	1.98	0.45
53:1:341:C:H2'	53:1:342:A:H8	1.82	0.45
53:1:828:U:H4'	53:1:831:G:N1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1105:U:C2'	53:1:1106:G:H5''	2.47	0.45
53:1:1443:U:H2'	53:1:1444:G:C8	2.51	0.45
53:1:2376:A:H2'	53:1:2377:A:O4'	2.17	0.45
54:2:114:C:H2'	54:2:115:A:C8	2.51	0.45
1:b:84:PRO:HG2	1:b:85:ASN:H	1.82	0.45
1:b:241:LYS:O	53:1:1902:C:H4'	2.17	0.45
6:g:12:LEU:HD23	6:g:12:LEU:H	1.81	0.45
10:k:57:VAL:HG13	10:k:57:VAL:O	2.17	0.45
18:s:84:ARG:HE	53:1:1323:C:H5''	1.82	0.45
33:I:120:LYS:NZ	52:3:439:U:H4'	2.31	0.45
34:J:108:GLY:O	34:J:109:ALA:HB3	2.16	0.45
34:J:156:ARG:CD	37:M:42:GLU:HG3	2.43	0.45
40:P:91:GLY:O	40:P:93:GLU:N	2.44	0.45
41:Q:56:LEU:HD21	41:Q:81:ILE:HD11	1.99	0.45
44:T:9:LYS:HB3	44:T:9:LYS:HE2	1.80	0.45
52:3:418:C:H2'	52:3:419:C:C6	2.52	0.45
52:3:1084:G:H2'	52:3:1085:U:C5	2.52	0.45
53:1:511:U:C2'	53:1:512:G:H5'	2.45	0.45
53:1:1367:A:H2'	53:1:1368:G:H5'	1.98	0.45
53:1:2030:A:N3	53:1:2499:C:H5''	2.32	0.45
1:b:18:VAL:O	1:b:18:VAL:HG13	2.17	0.45
3:d:50:ALA:HB2	53:1:801:G:C8	2.52	0.45
4:e:49:LEU:HD22	4:e:83:PRO:HB2	1.99	0.45
13:n:3:HIS:CD2	53:1:2820:A:H4'	2.52	0.45
20:u:97:SER:O	20:u:98:ASN:HB3	2.17	0.45
41:Q:98:ARG:HD2	41:Q:103:CYS:SG	2.57	0.45
43:S:19:TYR:HB2	43:S:54:SER:OG	2.17	0.45
45:U:33:ILE:H	45:U:33:ILE:HD12	1.81	0.45
50:Z:46:ARG:HH21	52:3:1533:C:H42	1.65	0.45
52:3:225:C:C2'	52:3:226:G:H5''	2.47	0.45
53:1:917:A:H2'	53:1:918:A:O4'	2.17	0.45
53:1:1035:U:H2'	53:1:1036:G:H8	1.82	0.45
53:1:1664:A:H2'	53:1:1664:A:N3	2.32	0.45
53:1:1801:A:H5''	53:1:2203:U:H2'	1.99	0.45
53:1:2662:A:H2'	53:1:2663:G:O4'	2.16	0.45
2:c:34:VAL:HG22	2:c:50:VAL:HG12	1.99	0.45
2:c:140:HIS:HD2	53:1:1658:C:OP2	2.00	0.45
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.99	0.45
6:g:57:LYS:HA	6:g:60:GLU:OE1	2.17	0.45
17:r:22:LEU:HD12	17:r:23:GLU:O	2.17	0.45
30:F:11:CYS:HB3	30:F:33:HIS:CE1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:109:GLU:HB2	32:H:143:LEU:HD22	1.98	0.45
39:O:88:MET:O	39:O:89:ARG:HG3	2.17	0.45
41:Q:29:LYS:HA	52:3:363:A:OP1	2.17	0.45
52:3:355:C:H5'	52:3:355:C:H6	1.82	0.45
52:3:939:G:H21	52:3:1375:A:H2	1.65	0.45
53:1:873:C:H2'	53:1:874:G:C8	2.52	0.45
53:1:2788:C:H2'	53:1:2789:C:C6	2.51	0.45
53:1:2837:A:H2'	53:1:2838:G:C8	2.52	0.45
2:c:128:ARG:HA	2:c:128:ARG:HD3	1.78	0.44
3:d:44:ARG:NH1	53:1:1248:G:OP1	2.50	0.44
4:e:2:LYS:O	4:e:5:ASP:OD2	2.35	0.44
10:k:71:ARG:NH1	10:k:77:ILE:HD11	2.31	0.44
12:m:129:THR:OG1	12:m:130:PHE:N	2.50	0.44
14:o:33:ARG:HG2	14:o:34:HIS:CD2	2.51	0.44
15:p:28:LYS:HD3	15:p:39:LEU:HD21	1.99	0.44
15:p:97:TYR:HB2	53:1:2718:G:OP1	2.17	0.44
16:q:23:TYR:O	53:1:18:U:H5''	2.17	0.44
22:w:39:THR:CB	53:1:2331:G:H4'	2.48	0.44
26:B:9:ARG:NE	53:1:517:C:OP2	2.50	0.44
32:H:179:ALA:O	32:H:181:ILE:HD12	2.18	0.44
33:I:123:MET:HG3	33:I:127:ARG:C	2.42	0.44
36:L:94:ARG:HA	36:L:97:ALA:HB3	1.98	0.44
37:M:28:SER:HB2	37:M:58:LEU:CB	2.36	0.44
50:Z:34:ARG:HB3	50:Z:36:PHE:CZ	2.53	0.44
51:a:39:VAL:HG13	51:a:39:VAL:O	2.17	0.44
52:3:668:G:H2'	52:3:669:G:C8	2.52	0.44
53:1:327:G:H2'	53:1:328:U:O4'	2.18	0.44
53:1:611:C:H2'	53:1:612:G:O4'	2.17	0.44
53:1:1872:A:H2'	53:1:1873:G:O4'	2.17	0.44
53:1:2757:A:H2'	53:1:2757:A:N3	2.32	0.44
54:2:3:C:H3'	54:2:4:C:C5'	2.47	0.44
12:m:24:THR:HG22	12:m:99:GLY:O	2.17	0.44
35:K:90:MET:HG2	35:K:91:ARG:N	2.28	0.44
41:Q:41:PRO:HG2	41:Q:49:ARG:HH11	1.81	0.44
41:Q:89:LEU:HD12	41:Q:89:LEU:N	2.32	0.44
42:R:22:TYR:CZ	52:3:1330:U:H4'	2.52	0.44
52:3:280:C:O2'	52:3:281:G:P	2.75	0.44
52:3:291:U:H2'	52:3:292:G:H8	1.83	0.44
52:3:1162:C:H2'	52:3:1163:A:C8	2.52	0.44
52:3:1497:G:H2'	52:3:1498:U:H5'	1.98	0.44
52:3:1527:U:H2'	52:3:1528:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:290:U:H2'	53:1:291:G:C8	2.51	0.44
2:c:1:MET:HG3	2:c:2:ILE:H	1.82	0.44
2:c:26:VAL:HG12	2:c:186:LEU:HD11	1.99	0.44
4:e:84:ILE:HD11	53:1:2311:A:C2	2.51	0.44
4:e:177:ARG:HD2	4:e:177:ARG:C	2.42	0.44
10:k:113:MET:SD	10:k:116:ILE:HD11	2.58	0.44
12:m:82:MET:HE1	53:1:956:G:H4'	1.99	0.44
13:n:87:PHE:HD1	13:n:90:ARG:HD3	1.81	0.44
14:o:76:LYS:O	14:o:80:GLU:HG3	2.18	0.44
18:s:88:ARG:HH12	53:1:2013:A:H2	1.66	0.44
30:F:3:VAL:HG11	53:1:2539:C:H5'	1.99	0.44
31:G:45:THR:O	31:G:49:PHE:N	2.50	0.44
32:H:66:THR:HG22	32:H:103:ALA:HB2	1.99	0.44
33:I:56:GLU:HG2	33:I:198:LEU:HB2	2.00	0.44
33:I:114:ARG:O	33:I:117:VAL:HG12	2.17	0.44
33:I:190:LEU:CD1	33:I:192:ALA:H	2.26	0.44
49:Y:54:GLN:N	49:Y:55:PRO:HD2	2.32	0.44
50:Z:9:GLU:HB2	50:Z:10:PRO:HD3	1.99	0.44
52:3:673:A:H2'	52:3:674:G:C8	2.52	0.44
53:1:2459:A:H2'	53:1:2459:A:N3	2.32	0.44
53:1:2784:U:H2'	53:1:2785:C:C6	2.52	0.44
2:c:46:ARG:NH2	2:c:88:GLU:O	2.50	0.44
8:i:49:GLU:OE1	8:i:52:LEU:HD13	2.17	0.44
15:p:88:ARG:NE	15:p:112:ARG:HH21	2.16	0.44
31:G:175:ALA:HB1	31:G:180:ILE:HB	2.00	0.44
32:H:161:ILE:HD12	32:H:161:ILE:N	2.33	0.44
35:K:12:PRO:O	35:K:15:SER:OG	2.28	0.44
36:L:130:LYS:O	36:L:130:LYS:HD3	2.17	0.44
36:L:142:ARG:HG2	55:6:41:C:H4'	1.99	0.44
37:M:30:LYS:O	37:M:33:VAL:HG12	2.17	0.44
38:N:56:MET:SD	38:N:57:VAL:N	2.91	0.44
38:N:114:LYS:HZ2	52:3:1187:G:H5'	1.81	0.44
42:R:84:CYS:O	42:R:88:LEU:HD23	2.17	0.44
52:3:280:C:HO2'	52:3:281:G:P	2.40	0.44
52:3:1434:A:H2'	52:3:1435:G:O4'	2.18	0.44
53:1:1979:U:O2'	53:1:1980:G:H5'	2.17	0.44
7:h:126:LEU:H	7:h:126:LEU:CD2	2.30	0.44
14:o:29:HIS:CD2	54:2:7:G:H5''	2.52	0.44
15:p:23:ASP:OD1	15:p:89:GLY:N	2.48	0.44
15:p:38:ARG:CZ	52:3:345:C:H5'	2.47	0.44
19:t:51:PHE:O	19:t:53:VAL:HG13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:177:MET:HE2	33:I:177:MET:H	1.81	0.44
37:M:87:ARG:H	37:M:90:GLU:HB2	1.83	0.44
53:1:340:A:H2'	53:1:341:C:O4'	2.18	0.44
53:1:341:C:H2'	53:1:342:A:C8	2.52	0.44
53:1:774:G:C2'	53:1:775:G:H5''	2.48	0.44
53:1:1045:C:OP1	53:1:1047:G:H5'	2.18	0.44
53:1:1306:C:H41	53:1:1606:C:H2'	1.82	0.44
53:1:2259:U:H2'	53:1:2260:C:C6	2.53	0.44
53:1:2800:A:H3'	53:1:2801:G:C5'	2.46	0.44
54:2:63:C:H2'	54:2:64:G:C8	2.52	0.44
2:c:27:ILE:N	2:c:27:ILE:HD12	2.32	0.44
3:d:46:GLN:HB2	3:d:86:ALA:HB1	2.00	0.44
9:j:117:ALA:HA	9:j:120:ARG:HH21	1.81	0.44
13:n:90:ARG:NH2	53:1:2880:C:O2'	2.51	0.44
15:p:50:ARG:NH2	53:1:2683:C:OP1	2.51	0.44
17:r:78:ARG:HG3	17:r:81:LYS:HB2	1.98	0.44
19:t:56:GLU:OE2	19:t:88:LYS:HG2	2.18	0.44
43:S:36:SER:HA	43:S:40:ARG:HD2	2.00	0.44
46:V:74:LEU:C	46:V:74:LEU:HD23	2.42	0.44
50:Z:64:ALA:O	50:Z:65:ARG:HB2	2.18	0.44
52:3:82:G:H2'	52:3:83:C:O4'	2.17	0.44
52:3:501:C:H2'	52:3:502:A:C8	2.53	0.44
52:3:570:G:H5'	52:3:820:U:O4'	2.17	0.44
52:3:918:A:H2'	52:3:919:A:C8	2.52	0.44
52:3:971:G:H4'	52:3:972:C:H5'	1.99	0.44
53:1:935:C:H2'	53:1:936:A:H8	1.83	0.44
55:6:16:C:H4'	55:6:60:U:H1'	2.00	0.44
3:d:112:LEU:HD13	3:d:186:VAL:HG21	1.99	0.44
18:s:94:ASP:OD1	18:s:95:ARG:N	2.51	0.44
21:v:30:ILE:HG13	21:v:40:ILE:HG13	1.99	0.44
32:H:153:SER:HB2	32:H:164:THR:HG23	1.98	0.44
35:K:13:ASP:OD2	35:K:14:GLN:NE2	2.50	0.44
38:N:48:ARG:HA	38:N:51:LEU:HD12	2.00	0.44
53:1:506:G:H4'	53:1:509:C:H1'	1.99	0.44
53:1:861:A:H2'	53:1:862:G:O4'	2.17	0.44
53:1:996:A:H2'	53:1:997:G:C8	2.53	0.44
53:1:1386:C:H2'	53:1:1387:A:C8	2.53	0.44
53:1:1434:A:H2'	53:1:1435:G:H8	1.83	0.44
53:1:1720:U:H2'	53:1:1721:G:O4'	2.18	0.44
55:6:50:U:H2'	55:6:51:C:C6	2.52	0.44
2:c:56:LYS:NZ	53:1:2830:C:OP1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:102:ILE:CG2	5:f:114:HIS:HB3	2.47	0.44
6:g:47:PHE:HA	6:g:51:ARG:HB2	1.98	0.44
6:g:90:LEU:HD23	6:g:93:SER:HA	2.00	0.44
6:g:115:VAL:HG22	6:g:132:PHE:HE1	1.83	0.44
13:n:72:ASP:HB3	13:n:75:ILE:HG12	2.00	0.44
16:q:10:ARG:HH21	53:1:1216:G:C5'	2.30	0.44
31:G:69:VAL:HA	31:G:91:VAL:HG23	1.99	0.44
32:H:107:LYS:HB3	32:H:143:LEU:HD21	1.99	0.44
37:M:11:THR:O	37:M:15:ASN:ND2	2.51	0.44
38:N:79:ARG:HD2	38:N:102:PHE:CD1	2.53	0.44
38:N:104:THR:HG22	52:3:1180:A:OP1	2.18	0.44
41:Q:30:ARG:NH2	52:3:362:G:OP2	2.50	0.44
48:X:36:ARG:O	48:X:69:LYS:NZ	2.50	0.44
51:a:47:ASN:HB3	51:a:210:LYS:HE3	2.00	0.44
52:3:530:G:H3'	52:3:531:U:C5'	2.48	0.44
52:3:545:C:O2'	52:3:549:C:H5''	2.18	0.44
52:3:692:U:H2'	52:3:694:A:OP2	2.18	0.44
52:3:868:C:H2'	52:3:869:G:O4'	2.18	0.44
52:3:876:C:H2'	52:3:877:G:C8	2.52	0.44
53:1:155:A:H2'	53:1:156:A:C8	2.53	0.44
53:1:1786:A:H1'	53:1:1938:A:N6	2.33	0.44
53:1:2208:C:H2'	53:1:2209:G:C8	2.52	0.44
54:2:93:C:H2'	54:2:94:A:H8	1.83	0.44
55:6:48:C:O2'	55:6:59:A:H1'	2.17	0.44
8:i:23:VAL:CG2	8:i:26:ALA:HB3	2.48	0.44
31:G:93:HIS:ND1	31:G:145:ASN:HB2	2.32	0.44
35:K:46:GLN:HA	35:K:56:LYS:HG2	1.99	0.44
36:L:69:ARG:HH21	36:L:96:ASN:HB3	1.83	0.44
46:V:64:ARG:HD2	52:3:264:C:H4'	1.99	0.44
52:3:1384:C:H2'	52:3:1385:G:C8	2.53	0.44
53:1:30:G:H2'	53:1:31:C:O4'	2.18	0.44
53:1:214:G:H2'	53:1:215:G:C8	2.53	0.44
53:1:2048:G:H2'	53:1:2049:G:H5''	2.00	0.44
53:1:2120:G:H2'	53:1:2121:G:C8	2.53	0.44
53:1:2371:G:O2'	53:1:2372:U:H5'	2.18	0.44
53:1:2453:A:H2'	53:1:2454:G:H8	1.82	0.44
53:1:2834:G:H2'	53:1:2879:A:N6	2.33	0.44
2:c:170:VAL:HG12	2:c:171:THR:H	1.83	0.43
4:e:84:ILE:HD11	53:1:2311:A:N3	2.33	0.43
5:f:9:VAL:HA	5:f:48:THR:HA	2.00	0.43
10:k:44:LYS:O	10:k:54:LYS:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:92:VAL:HG22	20:u:93:ARG:H	1.83	0.43
29:E:18:LYS:HG2	53:1:651:G:C5'	2.44	0.43
32:H:54:ILE:HG22	32:H:67:ILE:HG12	2.00	0.43
32:H:137:VAL:HG21	32:H:167:TYR:HD2	1.83	0.43
35:K:67:PRO:HG2	35:K:70:VAL:CG2	2.48	0.43
36:L:75:LYS:NZ	52:3:1378:C:N3	2.61	0.43
40:P:32:THR:HG22	40:P:43:TRP:HB2	1.99	0.43
50:Z:17:ARG:HA	50:Z:20:ARG:HG2	1.99	0.43
52:3:128:G:O2'	52:3:129:A:H5'	2.18	0.43
52:3:372:C:N4	52:3:387:U:H2'	2.33	0.43
52:3:768:A:C2	52:3:1512:U:H4'	2.53	0.43
52:3:1384:C:H2'	52:3:1385:G:H8	1.83	0.43
53:1:1417:C:H4'	53:1:1587:G:H21	1.83	0.43
53:1:2528:U:O2'	53:1:2529:G:H3'	2.18	0.43
2:c:8:LYS:HD3	2:c:193:VAL:HG23	1.99	0.43
3:d:97:ASN:HB2	3:d:100:MET:CB	2.49	0.43
7:h:67:THR:CG2	7:h:68:PRO:HD3	2.48	0.43
9:j:87:ALA:HB1	9:j:92:MET:HE3	1.99	0.43
10:k:21:CYS:HA	10:k:41:ILE:HG22	2.00	0.43
25:z:26:LEU:HD11	25:z:46:MET:HB3	2.00	0.43
52:3:485:U:H5'	52:3:486:U:OP2	2.18	0.43
52:3:1088:G:H21	52:3:1167:A:N6	2.09	0.43
53:1:193:U:H4'	53:1:803:U:H4'	2.00	0.43
53:1:277:G:H1'	53:1:361:G:O6	2.18	0.43
53:1:403:U:O3'	53:1:404:A:H4'	2.17	0.43
53:1:786:C:O2'	53:1:787:C:H5'	2.18	0.43
53:1:1161:C:H2'	53:1:1162:G:H8	1.83	0.43
53:1:1669:A:O3'	53:1:2549:G:H5'	2.18	0.43
53:1:2134:A:N6	53:1:2157:G:H4'	2.33	0.43
13:n:2:ARG:NH1	53:1:2822:G:O6	2.51	0.43
13:n:60:VAL:HG22	53:1:1454:C:O2'	2.18	0.43
25:z:8:GLN:HB3	25:z:31:ILE:HA	2.00	0.43
52:3:314:C:O2'	52:3:315:A:H5'	2.19	0.43
52:3:668:G:H2'	52:3:669:G:H8	1.83	0.43
53:1:145:C:H2'	53:1:146:A:C8	2.53	0.43
53:1:193:U:H4'	53:1:803:U:C4'	2.48	0.43
53:1:1434:A:H2'	53:1:1435:G:C8	2.53	0.43
53:1:1906:G:C3'	53:1:1907:G:H5''	2.48	0.43
53:1:2186:G:H2'	53:1:2187:U:O4'	2.18	0.43
53:1:2220:U:H2'	53:1:2221:G:C8	2.53	0.43
53:1:2412:A:H2'	53:1:2413:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2467:C:H2'	53:1:2468:A:O4'	2.18	0.43
1:b:254:LYS:O	53:1:1797:G:H4'	2.18	0.43
2:c:43:ASP:OD1	53:1:2784:U:H4'	2.18	0.43
6:g:3:VAL:HG22	6:g:38:PRO:HA	1.99	0.43
7:h:33:VAL:HG12	7:h:34:THR:N	2.32	0.43
15:p:26:GLU:OE2	15:p:28:LYS:HG3	2.19	0.43
20:u:80:ASP:OD2	20:u:95:PHE:HB3	2.19	0.43
31:G:105:THR:HG21	52:3:1072:G:N2	2.33	0.43
34:J:80:LEU:HB2	34:J:97:PRO:HB3	2.01	0.43
38:N:78:ILE:O	38:N:82:ILE:HG13	2.19	0.43
40:P:23:HIS:HB3	40:P:30:ILE:HG23	1.99	0.43
45:U:33:ILE:HD12	45:U:33:ILE:N	2.33	0.43
52:3:788:U:H2'	52:3:789:U:O4'	2.17	0.43
52:3:1197:A:C2'	52:3:1198:G:H5''	2.48	0.43
53:1:749:A:H4'	53:1:1271:G:N3	2.32	0.43
53:1:1268:A:H2'	53:1:1269:A:O4'	2.19	0.43
53:1:1420:A:H5'	53:1:1421:G:OP2	2.17	0.43
53:1:1683:U:H2'	53:1:1684:G:H8	1.84	0.43
53:1:2391:G:C4'	53:1:2392:A:OP1	2.66	0.43
53:1:2589:A:H2'	53:1:2590:A:H8	1.83	0.43
3:d:23:PHE:HB2	3:d:114:ARG:NH2	2.31	0.43
13:n:96:ARG:HG3	53:1:2882:A:H5'	1.99	0.43
17:r:24:LYS:HA	17:r:94:THR:OG1	2.18	0.43
38:N:6:TYR:CE2	52:3:1147:C:H4'	2.53	0.43
41:Q:88:ASP:HB2	41:Q:89:LEU:HD12	2.01	0.43
51:a:41:SER:HA	51:a:177:LYS:HA	2.00	0.43
52:3:309:A:H2'	52:3:310:G:C8	2.52	0.43
52:3:494:G:O2'	52:3:496:A:H1'	2.19	0.43
52:3:694:A:H2'	52:3:695:A:O4'	2.18	0.43
52:3:1201:A:C1'	52:3:1202:U:OP2	2.65	0.43
53:1:534:U:H2'	53:1:535:G:H8	1.84	0.43
53:1:580:U:H2'	53:1:581:C:C6	2.54	0.43
53:1:2859:G:H2'	53:1:2860:A:C8	2.53	0.43
54:2:60:C:H2'	54:2:61:G:C8	2.51	0.43
1:b:57:HIS:O	1:b:59:GLN:HG3	2.18	0.43
3:d:50:ALA:HB2	53:1:801:G:H8	1.83	0.43
3:d:77:ILE:HD13	53:1:673:C:H4'	2.01	0.43
3:d:97:ASN:HB2	3:d:100:MET:HB3	2.01	0.43
13:n:33:ILE:HG13	13:n:114:GLU:HB3	2.00	0.43
34:J:101:GLY:H	34:J:121:ASN:HB2	1.83	0.43
34:J:108:GLY:H	52:3:9:G:H4'	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:153:ALA:O	34:J:158:LYS:HA	2.19	0.43
36:L:4:ARG:HG3	36:L:6:ILE:HG12	1.99	0.43
38:N:125:GLN:HB2	52:3:1232:U:H5''	2.00	0.43
52:3:513:C:H2'	52:3:514:C:C6	2.52	0.43
52:3:969:A:H2'	52:3:970:C:O4'	2.18	0.43
53:1:28:A:O2'	53:1:583:G:H5'	2.19	0.43
53:1:1601:G:C2'	53:1:1602:U:H5'	2.47	0.43
53:1:1713:A:H61	53:1:1745:A:H61	1.67	0.43
53:1:1857:G:N2	53:1:1884:G:H2'	2.33	0.43
2:c:118:PHE:CE1	2:c:163:GLY:HA2	2.54	0.43
4:e:84:ILE:HG21	53:1:2312:U:H4'	2.01	0.43
35:K:64:VAL:HG22	35:K:65:GLU:H	1.83	0.43
36:L:4:ARG:HD2	36:L:6:ILE:HG23	2.00	0.43
36:L:75:LYS:HB2	36:L:75:LYS:HE3	1.87	0.43
41:Q:77:SER:HB2	41:Q:102:ASP:OD2	2.19	0.43
52:3:156:C:H2'	52:3:157:U:O4'	2.19	0.43
53:1:723:C:H2'	53:1:724:U:C6	2.53	0.43
53:1:728:G:H3'	53:1:729:G:H5'	2.01	0.43
53:1:869:G:H2'	53:1:870:U:O4'	2.18	0.43
53:1:1078:U:C4'	53:1:1079:C:H5''	2.48	0.43
53:1:1597:A:H5''	53:1:1598:A:H5'	2.01	0.43
53:1:2104:C:H2'	53:1:2105:U:C6	2.54	0.43
53:1:2368:C:H2'	53:1:2369:A:H8	1.84	0.43
53:1:2636:C:H2'	53:1:2637:U:C6	2.53	0.43
53:1:2661:G:H2'	53:1:2662:A:O4'	2.18	0.43
54:2:87:U:H5''	54:2:88:C:OP2	2.19	0.43
6:g:2:GLN:O	6:g:39:ALA:HB3	2.18	0.43
16:q:23:TYR:CD1	53:1:533:G:H5'	2.53	0.43
19:t:61:LEU:HB3	53:1:1341:G:H4'	2.01	0.43
25:z:29:ARG:HD3	25:z:29:ARG:N	2.33	0.43
33:I:160:LEU:O	33:I:160:LEU:HD23	2.18	0.43
34:J:89:THR:HG21	52:3:1078:U:O2	2.19	0.43
52:3:335:C:H2'	52:3:336:A:C8	2.54	0.43
52:3:424:G:O2'	52:3:425:G:H5'	2.18	0.43
52:3:911:U:H2'	52:3:912:C:C6	2.54	0.43
53:1:217:A:H2'	53:1:218:A:O4'	2.18	0.43
53:1:543:G:H8	53:1:543:G:H5'	1.83	0.43
53:1:2196:C:O2'	53:1:2197:U:H5'	2.19	0.43
53:1:2370:G:H2'	53:1:2371:G:O4'	2.19	0.43
8:i:10:LEU:HB3	8:i:11:GLN:H	1.59	0.43
15:p:88:ARG:HB3	15:p:112:ARG:NH2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:32:LYS:HB3	20:u:63:ALA:HB1	2.00	0.43
22:w:16:ARG:HG3	53:1:2271:G:H5'	2.01	0.43
32:H:4:VAL:O	32:H:6:PRO:HD3	2.19	0.43
32:H:30:ASP:HA	43:S:64:ARG:NH1	2.33	0.43
52:3:1220:G:H2'	52:3:1221:G:O4'	2.19	0.43
53:1:813:U:H2'	53:1:814:C:C6	2.53	0.43
53:1:968:C:H2'	53:1:969:G:C8	2.54	0.43
1:b:224:MET:SD	53:1:782:A:C2	3.12	0.43
7:h:60:LEU:HD21	7:h:79:PRO:HB3	2.00	0.43
8:i:35:MET:SD	8:i:36:GLU:N	2.92	0.43
10:k:71:ARG:HB2	10:k:73:ASP:OD1	2.19	0.43
17:r:49:ILE:HG23	17:r:54:VAL:HG22	2.01	0.43
21:v:6:ALA:HB3	21:v:65:VAL:HB	2.01	0.43
21:v:42:LEU:HD23	21:v:42:LEU:N	2.34	0.43
36:L:113:LYS:HD3	36:L:113:LYS:HA	1.76	0.43
38:N:90:ASP:CG	38:N:91:GLU:H	2.26	0.43
52:3:70:U:H4'	52:3:71:A:C8	2.53	0.43
52:3:580:C:H2'	52:3:581:G:O4'	2.19	0.43
52:3:629:A:H2'	52:3:630:A:O4'	2.18	0.43
52:3:1296:C:H4'	52:3:1302:C:H41	1.84	0.43
53:1:20:C:H2'	53:1:21:A:C8	2.54	0.43
53:1:374:A:H2'	53:1:375:G:O4'	2.19	0.43
53:1:534:U:H2'	53:1:535:G:C8	2.54	0.43
53:1:1201:U:H2'	53:1:1202:G:C8	2.53	0.43
53:1:1357:C:H2'	53:1:1358:G:O4'	2.18	0.43
53:1:1600:C:H2'	53:1:1601:G:C8	2.54	0.43
53:1:2418:A:H2'	53:1:2419:U:O4'	2.19	0.43
53:1:2639:A:H2'	53:1:2640:G:O4'	2.18	0.43
53:1:2861:U:H2'	53:1:2862:G:C8	2.54	0.43
4:e:3:LEU:HA	4:e:6:TYR:HB3	2.00	0.42
4:e:137:PHE:HA	4:e:138:PRO:HD3	1.87	0.42
19:t:10:VAL:HG13	19:t:38:ALA:HB1	2.00	0.42
19:t:47:VAL:CG1	19:t:55:VAL:HG21	2.49	0.42
23:x:13:THR:HG21	53:1:189:G:P	2.59	0.42
25:z:52:PHE:CZ	25:z:53:MET:HE2	2.53	0.42
27:C:9:LYS:O	27:C:51:ALA:HB3	2.19	0.42
32:H:171:ARG:HG2	32:H:173:PRO:HD3	2.01	0.42
33:I:131:ILE:HD12	33:I:131:ILE:N	2.33	0.42
36:L:42:VAL:O	36:L:46:LEU:HG	2.19	0.42
52:3:915:A:H2'	52:3:916:U:H5'	2.00	0.42
52:3:1225:A:H2'	52:3:1225:A:N3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:215:G:H4'	53:1:216:A:H4'	2.01	0.42
53:1:1285:A:H2'	53:1:1286:A:H5'	2.00	0.42
53:1:2540:C:H2'	53:1:2541:A:O4'	2.19	0.42
53:1:2808:G:H2'	53:1:2890:G:C6	2.54	0.42
1:b:69:ASN:OD1	1:b:69:ASN:N	2.52	0.42
1:b:225:ASN:HA	1:b:226:PRO:HD3	1.88	0.42
16:q:16:ILE:HG21	16:q:35:PHE:HD1	1.83	0.42
21:v:9:ARG:NH1	21:v:11:GLU:O	2.52	0.42
21:v:92:VAL:HG13	21:v:92:VAL:O	2.19	0.42
34:J:84:VAL:HG22	34:J:85:LYS:N	2.34	0.42
48:X:15:LEU:HA	48:X:18:VAL:HB	2.01	0.42
52:3:116:A:H2'	52:3:117:G:O4'	2.19	0.42
52:3:1173:U:H2'	52:3:1174:G:C8	2.54	0.42
52:3:1436:U:H2'	52:3:1437:A:C8	2.54	0.42
52:3:1453:G:H3'	52:3:1453:G:N3	2.34	0.42
53:1:174:U:H2'	53:1:175:G:C8	2.55	0.42
53:1:1278:C:H2'	53:1:1279:G:C8	2.54	0.42
2:c:34:VAL:HA	2:c:50:VAL:HG12	2.00	0.42
2:c:177:VAL:HG22	2:c:178:VAL:H	1.84	0.42
9:j:80:HIS:CD2	53:1:2642:G:H5'	2.54	0.42
11:l:55:MET:HG2	53:1:2392:A:C2	2.54	0.42
13:n:28:LEU:O	13:n:32:GLU:N	2.51	0.42
15:p:57:ALA:HA	15:p:75:THR:HG23	2.01	0.42
21:v:17:SER:OG	21:v:21:ARG:NH2	2.51	0.42
32:H:27:GLU:N	32:H:27:GLU:OE1	2.52	0.42
33:I:28:ASP:O	33:I:30:LYS:HD2	2.20	0.42
37:M:1:SER:C	37:M:2:MET:HG2	2.44	0.42
39:O:41:PRO:HG3	52:3:1150:A:C2	2.54	0.42
52:3:603:U:H2'	52:3:604:G:H8	1.84	0.42
53:1:784:G:OP1	53:1:2588:G:H5''	2.19	0.42
53:1:2221:G:O2'	53:1:2222:C:H5'	2.19	0.42
54:2:13:G:N7	54:2:70:C:H4'	2.34	0.42
54:2:63:C:H2'	54:2:64:G:H8	1.85	0.42
55:5:3:C:H2'	55:5:4:G:C8	2.54	0.42
57:7:33:U:H1'	57:7:36:A:H62	1.84	0.42
57:7:47:U:H3'	57:7:48:C:H5''	2.01	0.42
3:d:28:VAL:O	3:d:31:VAL:HG12	2.19	0.42
4:e:105:ILE:O	4:e:108:PRO:HD2	2.18	0.42
9:j:113:PRO:HD2	53:1:558:U:OP1	2.18	0.42
13:n:47:VAL:O	13:n:50:PRO:HD2	2.20	0.42
19:t:80:TRP:CD1	19:t:80:TRP:H	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:v:93:ARG:NH1	21:v:93:ARG:HB2	2.34	0.42
24:y:7:ARG:H	24:y:7:ARG:HG2	1.66	0.42
31:G:20:ARG:NH2	52:3:831:A:H4'	2.34	0.42
32:H:72:PRO:HD3	32:H:104:GLU:OE1	2.19	0.42
33:I:186:GLU:HG2	33:I:188:SER:H	1.84	0.42
39:O:56:HIS:HE1	52:3:963:G:H21	1.67	0.42
42:R:33:LEU:HD22	42:R:40:GLU:HG2	2.02	0.42
44:T:5:GLU:HG2	44:T:6:ALA:N	2.34	0.42
44:T:32:THR:OG1	44:T:84:LEU:HD21	2.19	0.42
49:Y:80:ALA:HA	49:Y:83:ASN:ND2	2.32	0.42
51:a:164:ARG:NH1	51:a:164:ARG:HB3	2.35	0.42
52:3:56:U:H2'	52:3:57:G:H8	1.85	0.42
52:3:392:C:H2'	52:3:393:A:C8	2.54	0.42
52:3:926:G:H22	56:4:15:A:H3'	1.83	0.42
53:1:974:G:N3	53:1:974:G:H2'	2.35	0.42
53:1:1308:A:H2'	53:1:1309:G:O4'	2.19	0.42
53:1:1827:U:H2'	53:1:1828:G:O4'	2.19	0.42
55:6:72:A:H2'	55:6:73:A:O4'	2.19	0.42
6:g:27:ARG:HE	23:x:55:MET:HE2	1.85	0.42
12:m:3:GLN:HA	12:m:4:PRO:HD3	1.92	0.42
28:D:1:MET:HE2	28:D:3:ARG:HD3	2.01	0.42
30:F:9:LYS:NZ	30:F:14:CYS:O	2.53	0.42
31:G:20:ARG:CZ	52:3:831:A:H4'	2.49	0.42
31:G:103:TRP:HE1	31:G:107:ARG:NH2	2.17	0.42
32:H:149:LYS:O	32:H:200:TRP:HE3	2.02	0.42
32:H:191:THR:O	52:3:1206:G:H4'	2.19	0.42
33:I:99:ASN:O	33:I:102:TYR:HB3	2.20	0.42
52:3:666:G:H5'	52:3:726:C:H1'	2.00	0.42
53:1:1300:G:H4'	53:1:1301:A:H5'	2.02	0.42
53:1:1300:G:C4'	53:1:1301:A:H5''	2.49	0.42
53:1:1312:U:H4'	53:1:1313:U:O5'	2.18	0.42
53:1:2040:G:H2'	53:1:2041:U:O4'	2.20	0.42
53:1:2197:U:O2'	53:1:2198:A:H5''	2.19	0.42
53:1:2529:G:OP2	53:1:2530:A:H5''	2.19	0.42
53:1:2707:U:H2'	53:1:2708:G:C8	2.54	0.42
53:1:2799:A:C2'	53:1:2800:A:H5'	2.49	0.42
1:b:139:THR:HG23	1:b:160:TYR:CD2	2.54	0.42
2:c:181:ASP:HB3	2:c:186:LEU:HB3	2.00	0.42
3:d:101:TYR:HE1	3:d:177:PRO:HG3	1.85	0.42
4:e:177:ARG:HD2	4:e:177:ARG:O	2.20	0.42
6:g:97:ARG:NH2	53:1:2220:U:H4'	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:93:ILE:HD13	9:j:100:VAL:HG21	2.02	0.42
12:m:108:VAL:HG11	12:m:112:LEU:HD23	2.02	0.42
16:q:5:ARG:NH1	53:1:585:G:N7	2.61	0.42
16:q:65:ASN:O	16:q:69:ARG:HG3	2.20	0.42
22:w:67:VAL:HG12	22:w:74:LYS:HG2	2.02	0.42
33:I:167:PRO:HB2	33:I:170:LEU:HD21	2.01	0.42
34:J:37:VAL:HG11	34:J:113:VAL:HA	2.02	0.42
41:Q:27:PRO:HB3	41:Q:28:GLN:NE2	2.34	0.42
41:Q:82:ARG:HE	41:Q:97:VAL:HG22	1.83	0.42
50:Z:16:ARG:HD2	50:Z:19:LYS:CE	2.49	0.42
51:a:9:ARG:O	51:a:13:GLU:HG3	2.19	0.42
51:a:46:VAL:HG13	51:a:212:VAL:HG12	2.02	0.42
53:1:2128:G:H1'	53:1:2173:A:N3	2.35	0.42
53:1:2248:C:H2'	53:1:2249:U:H5'	2.00	0.42
53:1:2643:G:H2'	53:1:2644:G:O4'	2.20	0.42
2:c:24:VAL:HG12	2:c:25:THR:N	2.35	0.42
3:d:163:ASN:HB2	53:1:322:A:OP2	2.20	0.42
4:e:65:LEU:HD22	54:2:42:C:C4	2.54	0.42
4:e:92:GLY:O	4:e:95:MET:HG2	2.20	0.42
9:j:17:VAL:CG2	9:j:139:VAL:HA	2.50	0.42
11:l:67:THR:OG1	53:1:245:G:OP1	2.38	0.42
11:l:122:VAL:HG22	11:l:123:ARG:H	1.85	0.42
13:n:2:ARG:HA	13:n:5:LYS:HD2	2.02	0.42
14:o:30:ARG:HG2	14:o:30:ARG:HH11	1.85	0.42
15:p:94:ALA:HB2	53:1:2848:G:N7	2.35	0.42
15:p:105:LYS:O	15:p:108:ARG:NH2	2.47	0.42
20:u:96:LYS:O	20:u:97:SER:OG	2.36	0.42
31:G:183:PHE:HD1	31:G:197:PHE:HB2	1.85	0.42
31:G:209:VAL:HA	31:G:212:TYR:CD2	2.55	0.42
33:I:81:LEU:HB3	33:I:88:ASN:ND2	2.33	0.42
35:K:51:ILE:C	35:K:53:LYS:H	2.28	0.42
36:L:125:ASP:HA	36:L:128:GLU:OE2	2.20	0.42
37:M:5:PRO:O	37:M:8:ASP:HB3	2.18	0.42
38:N:56:MET:O	38:N:57:VAL:C	2.63	0.42
40:P:85:VAL:HG23	40:P:111:ASP:OD1	2.19	0.42
52:3:361:G:H2'	52:3:362:G:O4'	2.20	0.42
52:3:423:G:H2'	52:3:424:G:H5'	2.01	0.42
52:3:543:U:H2'	52:3:544:G:C8	2.55	0.42
52:3:1123:U:O2'	52:3:1124:G:H5'	2.20	0.42
52:3:1527:U:O2'	52:3:1528:U:H5'	2.20	0.42
53:1:12:U:C2'	53:1:13:A:H5'	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1686:C:H2'	53:1:1687:G:O4'	2.20	0.42
53:1:1971:U:H5'	53:1:1972:G:H5''	2.02	0.42
53:1:2785:C:O2'	53:1:2786:U:H5'	2.20	0.42
54:2:78:A:H62	54:2:98:G:H21	1.68	0.42
2:c:110:THR:HB	2:c:202:ILE:HB	2.01	0.42
7:h:21:GLY:HA3	7:h:86:MET:HE2	2.02	0.42
8:i:99:LYS:HZ1	8:i:138:VAL:HB	1.84	0.42
12:m:86:LYS:HD2	53:1:956:G:P	2.60	0.42
14:o:38:GLN:NE2	14:o:39:VAL:O	2.52	0.42
27:C:20:TYR:OH	53:1:2348:U:H5'	2.20	0.42
32:H:9:ILE:HD12	32:H:9:ILE:N	2.33	0.42
33:I:56:GLU:HG2	33:I:198:LEU:HD12	2.02	0.42
41:Q:68:GLY:HA3	41:Q:98:ARG:NH1	2.35	0.42
42:R:101:THR:HG21	52:3:1226:C:OP2	2.20	0.42
43:S:92:ILE:HD12	43:S:92:ILE:N	2.34	0.42
49:Y:58:ASP:CG	49:Y:75:LYS:HZ1	2.28	0.42
51:a:219:GLY:O	53:1:2175:C:H4'	2.19	0.42
52:3:231:U:H2'	52:3:232:G:H8	1.84	0.42
53:1:799:G:H5''	53:1:800:A:H2'	2.02	0.42
53:1:873:C:H2'	53:1:874:G:H8	1.83	0.42
53:1:1680:U:C2'	53:1:1681:G:H5'	2.50	0.42
7:h:129:LEU:HA	7:h:130:PRO:HD3	1.91	0.42
8:i:55:PRO:O	8:i:71:LYS:HB3	2.20	0.42
11:l:86:GLU:O	11:l:88:GLY:N	2.53	0.42
13:n:100:CYS:SG	13:n:101:GLY:N	2.93	0.42
15:p:23:ASP:O	15:p:46:VAL:HG22	2.19	0.42
15:p:85:VAL:HG12	15:p:86:LYS:N	2.35	0.42
20:u:92:VAL:HG22	20:u:93:ARG:N	2.35	0.42
23:x:26:ARG:HH12	53:1:2232:C:P	2.43	0.42
23:x:50:VAL:HG12	23:x:51:SER:O	2.19	0.42
31:G:19:THR:HG22	31:G:38:HIS:CD2	2.55	0.42
31:G:24:PRO:HB2	52:3:828:U:H2'	2.00	0.42
32:H:44:LYS:HE3	32:H:44:LYS:HB2	1.88	0.42
32:H:149:LYS:HG3	32:H:168:ARG:HB3	2.01	0.42
39:O:41:PRO:HB3	52:3:1151:A:HI'	2.01	0.42
50:Z:11:PHE:C	50:Z:13:VAL:H	2.27	0.42
52:3:1119:C:H2'	52:3:1120:C:C6	2.54	0.42
53:1:1554:U:H3'	53:1:1555:G:H5'	2.01	0.42
5:f:81:GLY:HA3	5:f:133:LYS:HZ1	1.84	0.42
7:h:45:GLY:HA2	7:h:49:GLY:HA2	2.01	0.42
15:p:1:SER:N	53:1:2875:C:O3'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:4:VAL:HG23	17:r:39:LEU:HB2	2.02	0.42
33:I:49:ASP:O	33:I:52:VAL:HG12	2.19	0.42
36:L:69:ARG:HA	36:L:99:ALA:HB2	2.01	0.42
40:P:22:ILE:HG12	40:P:31:VAL:HG23	2.01	0.42
41:Q:24:GLU:O	41:Q:25:ALA:HB3	2.20	0.42
41:Q:91:GLY:HA2	41:Q:93:ARG:NH1	2.35	0.42
48:X:52:ASN:OD1	48:X:53:GLY:N	2.43	0.42
52:3:56:U:H2'	52:3:57:G:C8	2.55	0.42
52:3:1098:C:H2'	52:3:1099:G:C8	2.55	0.42
53:1:741:U:H2'	53:1:742:A:H8	1.84	0.42
53:1:1020:A:C1'	53:1:1021:A:OP2	2.63	0.42
53:1:1330:C:H2'	53:1:1331:G:H8	1.84	0.42
53:1:1936:A:H3'	53:1:1937:A:H5'	2.00	0.42
53:1:1989:G:H2'	53:1:1990:C:O4'	2.20	0.42
53:1:2660:A:H2'	53:1:2661:G:O4'	2.20	0.42
2:c:177:VAL:HG22	2:c:178:VAL:N	2.35	0.41
4:e:65:LEU:HD11	54:2:41:G:H21	1.84	0.41
5:f:2:ARG:HH12	53:1:1113:U:H5''	1.85	0.41
7:h:86:MET:HG3	7:h:87:GLU:H	1.84	0.41
9:j:29:ALA:HA	9:j:32:LEU:HD12	2.02	0.41
11:l:65:GLY:C	53:1:2415:G:H4'	2.45	0.41
21:v:9:ARG:HD3	21:v:41:GLU:HB2	2.02	0.41
22:w:10:ARG:HD2	53:1:2280:G:O6	2.20	0.41
40:P:71:ASP:HA	40:P:74:LYS:NZ	2.35	0.41
46:V:17:GLU:C	46:V:19:SER:H	2.28	0.41
46:V:54:ILE:N	46:V:54:ILE:HD12	2.35	0.41
49:Y:67:HIS:CB	52:3:262:A:H5'	2.51	0.41
52:3:243:A:H4'	52:3:244:U:H3'	2.01	0.41
52:3:628:G:H2'	52:3:629:A:O4'	2.19	0.41
52:3:1413:A:H2	52:3:1487:G:H22	1.68	0.41
53:1:1028:A:N6	53:1:1125:G:H2'	2.35	0.41
53:1:1447:C:H2'	53:1:1448:G:C8	2.55	0.41
53:1:2628:C:O2'	53:1:2781:A:H2'	2.19	0.41
54:2:32:U:H2'	54:2:33:G:C8	2.55	0.41
55:6:6:G:O2'	55:6:7:G:H5'	2.20	0.41
2:c:9:VAL:HB	2:c:26:VAL:CG2	2.50	0.41
2:c:78:GLY:C	2:c:79:LEU:HD12	2.45	0.41
4:e:105:ILE:HD12	4:e:105:ILE:N	2.35	0.41
11:l:82:LEU:HD11	11:l:90:VAL:HG21	2.03	0.41
18:s:79:GLY:H	18:s:101:SER:HA	1.85	0.41
33:I:70:GLN:O	33:I:73:ASN:OD1	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:121:ALA:HB3	33:I:122:ILE:HD12	2.02	0.41
33:I:153:ARG:HG3	33:I:154:VAL:N	2.36	0.41
37:M:6:ILE:HD11	37:M:31:LEU:HD23	2.02	0.41
37:M:114:ALA:HA	37:M:117:GLN:HB2	2.01	0.41
41:Q:74:GLN:H	41:Q:74:GLN:HG3	1.76	0.41
43:S:56:PRO:HA	43:S:59:GLN:OE1	2.20	0.41
46:V:13:SER:HB3	46:V:21:VAL:CG1	2.50	0.41
49:Y:72:ALA:O	49:Y:75:LYS:HG2	2.21	0.41
52:3:613:C:H2'	52:3:614:C:C6	2.54	0.41
53:1:490:C:O2'	53:1:491:G:P	2.78	0.41
53:1:490:C:HO2'	53:1:491:G:P	2.43	0.41
53:1:812:C:H5''	53:1:1250:G:O2'	2.20	0.41
53:1:1821:A:H2'	53:1:1822:C:C6	2.55	0.41
53:1:2739:U:O2'	53:1:2740:A:H5'	2.20	0.41
53:1:2818:U:H2'	53:1:2819:G:C8	2.53	0.41
54:2:88:C:H5''	54:2:89:U:OP1	2.20	0.41
6:g:53:GLU:C	6:g:54:LEU:HD22	2.46	0.41
6:g:109:GLU:H	6:g:109:GLU:CD	2.28	0.41
7:h:87:GLU:HB3	7:h:95:LEU:CD1	2.50	0.41
9:j:78:THR:OG1	9:j:83:GLY:HA3	2.20	0.41
9:j:113:PRO:HD2	53:1:558:U:OP2	2.19	0.41
11:l:73:ILE:HG22	11:l:106:GLU:N	2.30	0.41
11:l:107:PHE:HB3	11:l:126:ARG:HH12	1.85	0.41
16:q:60:TRP:O	16:q:64:ILE:HG12	2.20	0.41
17:r:39:LEU:O	17:r:49:ILE:HG23	2.19	0.41
24:y:24:GLU:HB3	24:y:46:VAL:HG21	2.02	0.41
32:H:168:ARG:HH12	52:3:1106:G:H1'	1.85	0.41
33:I:170:LEU:HD23	33:I:170:LEU:H	1.86	0.41
48:X:76:THR:HG23	48:X:77:ARG:H	1.85	0.41
52:3:662:U:H2'	52:3:663:A:C8	2.54	0.41
53:1:457:A:H61	53:1:470:A:H5''	1.85	0.41
53:1:572:A:H61	53:1:2029:G:N2	2.14	0.41
53:1:968:C:H2'	53:1:969:G:H8	1.84	0.41
53:1:1138:G:H2'	53:1:1139:G:O4'	2.20	0.41
53:1:1549:A:H2'	53:1:1550:C:C6	2.55	0.41
53:1:2163:A:H2'	53:1:2164:C:H5'	2.01	0.41
53:1:2630:G:H2'	53:1:2631:G:C8	2.55	0.41
7:h:28:ALA:HB1	7:h:81:LEU:HD23	2.01	0.41
10:k:51:LYS:HE2	10:k:51:LYS:HB2	1.96	0.41
13:n:55:ALA:HA	13:n:80:PHE:CE1	2.56	0.41
21:v:1:MET:SD	21:v:1:MET:N	2.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:12:LEU:HD12	36:L:12:LEU:H	1.86	0.41
38:N:5:TYR:HB2	38:N:20:ILE:HG23	2.02	0.41
46:V:56:ASP:N	46:V:56:ASP:OD1	2.53	0.41
52:3:689:C:H2'	52:3:690:G:O4'	2.20	0.41
52:3:1075:U:H2'	52:3:1076:U:C6	2.55	0.41
52:3:1128:C:O2'	52:3:1129:C:H5'	2.20	0.41
52:3:1481:U:H2'	52:3:1482:G:C8	2.55	0.41
52:3:1500:A:H5''	52:3:1508:A:H5''	2.02	0.41
53:1:362:A:H3'	53:1:363:G:H8	1.85	0.41
53:1:582:A:H2'	53:1:583:G:C8	2.56	0.41
53:1:1019:U:H3	53:1:1142:A:N6	2.16	0.41
53:1:1956:U:H2'	53:1:1957:C:H5'	2.02	0.41
1:b:47:ARG:HD2	53:1:778:G:H5''	2.02	0.41
9:j:24:THR:CG2	9:j:27:ARG:HB2	2.50	0.41
12:m:18:ARG:HG2	12:m:19:GLY:N	2.33	0.41
23:x:24:THR:HG21	53:1:2081:U:H4'	2.02	0.41
24:y:39:GLN:HB3	24:y:41:HIS:CE1	2.56	0.41
38:N:118:ARG:HA	38:N:118:ARG:HD3	1.86	0.41
39:O:100:ILE:HD12	39:O:100:ILE:H	1.85	0.41
47:W:66:LEU:C	47:W:67:LEU:HD22	2.45	0.41
52:3:149:A:H1'	52:3:1446:A:C2	2.56	0.41
52:3:1162:C:H2'	52:3:1163:A:H8	1.86	0.41
52:3:1198:G:H2'	52:3:1199:U:C6	2.56	0.41
53:1:687:C:H2'	53:1:688:U:O4'	2.21	0.41
53:1:948:C:H2'	53:1:949:G:C8	2.55	0.41
53:1:2613:U:O2'	53:1:2614:A:H5'	2.20	0.41
57:7:9:A:H1'	57:7:45:U:O2'	2.20	0.41
3:d:147:LEU:HD23	3:d:186:VAL:HG12	2.02	0.41
4:e:3:LEU:HD22	4:e:100:GLU:HB2	2.03	0.41
4:e:72:SER:OG	4:e:78:ILE:O	2.35	0.41
9:j:17:VAL:O	9:j:17:VAL:HG23	2.21	0.41
9:j:25:LEU:HB3	53:1:1140:C:OP1	2.19	0.41
11:l:29:LYS:O	11:l:30:THR:OG1	2.35	0.41
12:m:110:GLU:HA	12:m:113:ALA:HB3	2.03	0.41
12:m:119:LEU:HD21	53:1:2468:A:H5'	2.03	0.41
21:v:79:ARG:NH1	21:v:86:LEU:HD21	2.35	0.41
21:v:83:LYS:HA	21:v:84:PRO:HD3	1.84	0.41
31:G:162:VAL:HB	31:G:184:ALA:HB2	2.02	0.41
50:Z:31:VAL:O	50:Z:31:VAL:HG12	2.20	0.41
52:3:150:U:H2'	52:3:151:A:C8	2.56	0.41
53:1:779:U:H2'	53:1:780:G:H8	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1126:A:H4'	53:1:1127:A:H5''	2.02	0.41
53:1:1326:U:H2'	53:1:1327:A:H8	1.85	0.41
53:1:2302:U:H2'	53:1:2303:G:C8	2.55	0.41
4:e:135:ILE:O	4:e:135:ILE:HG13	2.20	0.41
5:f:2:ARG:HH12	53:1:1113:U:C5'	2.33	0.41
13:n:52:ILE:HA	13:n:55:ALA:HB3	2.03	0.41
29:E:23:HIS:HD2	29:E:49:VAL:HG22	1.85	0.41
29:E:44:ARG:N	29:E:45:PRO:HD2	2.35	0.41
32:H:21:TRP:HA	39:O:95:GLY:HA2	2.03	0.41
36:L:27:ASN:OD1	36:L:35:LYS:HE3	2.20	0.41
39:O:73:LEU:C	39:O:73:LEU:HD12	2.45	0.41
42:R:25:GLY:N	52:3:1329:A:H5''	2.33	0.41
52:3:113:G:H2'	52:3:114:U:C6	2.56	0.41
52:3:144:G:O2'	52:3:145:G:H5'	2.21	0.41
52:3:729:A:H2'	52:3:730:G:C8	2.54	0.41
53:1:18:U:H2'	53:1:19:A:H8	1.84	0.41
53:1:69:C:H2'	53:1:70:G:C8	2.56	0.41
53:1:1101:U:H2'	53:1:1102:C:C6	2.56	0.41
53:1:1130:U:O2'	53:1:1131:G:OP1	2.35	0.41
53:1:1741:C:H2'	53:1:1742:U:O4'	2.21	0.41
53:1:2553:G:H1'	53:1:2582:G:H21	1.86	0.41
54:2:66:A:H4'	54:2:67:G:N7	2.36	0.41
5:f:6:ALA:HA	5:f:7:PRO:HD3	1.86	0.41
7:h:2:ALA:O	53:1:1043:C:H5''	2.21	0.41
7:h:54:VAL:O	7:h:54:VAL:HG22	2.20	0.41
21:v:79:ARG:HG2	21:v:86:LEU:CD2	2.51	0.41
25:z:52:PHE:CE2	25:z:53:MET:HE2	2.56	0.41
29:E:5:THR:HG22	29:E:62:PRO:HD2	2.02	0.41
32:H:64:ARG:HG3	32:H:99:GLN:HB3	2.02	0.41
33:I:101:VAL:HG22	33:I:106:PHE:HB2	2.02	0.41
36:L:36:SER:HA	38:N:42:THR:HG21	2.02	0.41
43:S:33:VAL:O	43:S:33:VAL:HG22	2.21	0.41
44:T:3:SER:HB3	44:T:5:GLU:OE2	2.21	0.41
52:3:12:U:H2'	52:3:13:U:H5''	2.02	0.41
52:3:977:A:H3'	52:3:977:A:N3	2.36	0.41
53:1:20:C:H2'	53:1:21:A:H8	1.86	0.41
53:1:514:A:H2'	53:1:515:A:C8	2.55	0.41
53:1:1176:U:H2'	53:1:1177:G:C8	2.56	0.41
53:1:1991:U:H2'	53:1:1992:G:C5'	2.51	0.41
53:1:2270:A:H2'	53:1:2271:G:O4'	2.21	0.41
3:d:149:ILE:CG2	3:d:188:MET:HG2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:149:ILE:HG23	3:d:188:MET:HG2	2.02	0.41
5:f:77:GLY:HA2	5:f:81:GLY:HA2	2.03	0.41
8:i:48:ILE:HG13	8:i:49:GLU:N	2.35	0.41
26:B:3:GLN:HA	53:1:2615:U:C2	2.55	0.41
28:D:42:LEU:HD12	28:D:42:LEU:H	1.85	0.41
31:G:24:PRO:CB	52:3:828:U:H2'	2.51	0.41
31:G:46:VAL:HG23	31:G:47:PRO:CD	2.46	0.41
34:J:89:THR:HB	34:J:134:ASN:ND2	2.34	0.41
35:K:98:GLU:CG	35:K:99:ALA:H	2.23	0.41
36:L:73:GLU:N	36:L:73:GLU:OE2	2.54	0.41
39:O:41:PRO:HG3	52:3:1150:A:N3	2.34	0.41
41:Q:28:GLN:CD	41:Q:28:GLN:H	2.28	0.41
42:R:22:TYR:HB3	42:R:65:GLU:HG3	2.03	0.41
44:T:7:THR:O	44:T:11:VAL:HG23	2.21	0.41
44:T:65:LEU:O	44:T:68:TYR:HB3	2.20	0.41
45:U:59:HIS:O	45:U:63:GLN:HG2	2.21	0.41
47:W:12:PHE:CZ	47:W:14:ALA:HB2	2.56	0.41
47:W:33:THR:HG22	47:W:37:LYS:H	1.84	0.41
47:W:69:TYR:HB2	47:W:73:HIS:CE1	2.56	0.41
48:X:59:VAL:O	48:X:59:VAL:HG13	2.21	0.41
51:a:41:SER:HB2	53:1:2124:G:O2'	2.21	0.41
52:3:304:U:O2'	52:3:305:G:H5'	2.21	0.41
52:3:1309:G:H2'	52:3:1310:G:C8	2.55	0.41
53:1:112:U:C2'	53:1:113:U:H5'	2.50	0.41
53:1:189:G:H2'	53:1:205:G:N2	2.36	0.41
53:1:197:A:H2'	53:1:198:C:O4'	2.21	0.41
53:1:566:U:H4'	53:1:809:G:OP2	2.21	0.41
53:1:687:C:H42	53:1:787:C:H4'	1.86	0.41
53:1:863:A:H2'	53:1:864:G:C8	2.56	0.41
53:1:889:C:H2'	53:1:890:C:O4'	2.20	0.41
53:1:1106:G:H5'	53:1:1106:G:H8	1.85	0.41
53:1:1275:A:N6	53:1:1296:G:H4'	2.35	0.41
53:1:1759:A:C2	53:1:2697:G:H1'	2.56	0.41
53:1:1918:A:H2	53:1:1919:A:H62	1.68	0.41
53:1:2120:G:H2'	53:1:2121:G:H8	1.86	0.41
53:1:2200:C:H2'	53:1:2201:G:H8	1.85	0.41
53:1:2372:U:H2'	53:1:2373:G:C8	2.56	0.41
57:7:6:G:C2'	57:7:7:A:H5'	2.51	0.41
1:b:245:THR:C	1:b:247:TRP:H	2.29	0.41
9:j:78:THR:HG22	53:1:2641:G:OP1	2.21	0.41
14:o:34:HIS:HA	14:o:53:THR:OG1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:104:ALA:HA	17:r:46:GLU:HG2	2.03	0.41
39:O:61:ALA:HB2	52:3:1061:G:C5'	2.51	0.41
41:Q:69:GLU:OE2	52:3:521:G:H4'	2.21	0.41
49:Y:80:ALA:O	49:Y:84:LYS:HG2	2.21	0.41
52:3:799:G:H2'	52:3:800:G:O4'	2.20	0.41
52:3:837:U:H2'	52:3:838:G:H8	1.86	0.41
52:3:1354:U:H2'	52:3:1355:G:H8	1.86	0.41
53:1:12:U:O2	53:1:2626:C:H4'	2.21	0.41
53:1:553:G:H2'	53:1:554:U:O4'	2.21	0.41
53:1:1298:C:H2'	53:1:1299:G:O4'	2.21	0.41
53:1:2545:G:H2'	53:1:2546:U:O4'	2.21	0.41
53:1:2559:C:H2'	53:1:2560:A:H8	1.86	0.41
55:6:16:C:O2'	55:6:17:C:H5'	2.20	0.41
1:b:244:VAL:HG12	1:b:250:GLN:HA	2.02	0.40
2:c:53:GLY:HA3	2:c:77:ARG:NH2	2.37	0.40
5:f:85:LYS:N	5:f:85:LYS:HD3	2.36	0.40
8:i:9:LYS:HE2	53:1:1070:A:C2	2.56	0.40
11:l:76:GLU:H	11:l:76:GLU:HG2	1.68	0.40
11:l:118:THR:HA	11:l:119:PRO:HD3	1.82	0.40
12:m:105:MET:HG2	12:m:106:ASP:N	2.36	0.40
15:p:77:SER:HA	15:p:78:PRO:HD3	1.93	0.40
21:v:78:GLN:HE21	21:v:88:HIS:HB3	1.86	0.40
26:B:24:VAL:HG23	26:B:25:THR:N	2.34	0.40
28:D:12:ARG:NE	28:D:44:VAL:HG21	2.36	0.40
34:J:160:VAL:O	34:J:163:ILE:HG12	2.22	0.40
36:L:115:MET:HE3	52:3:1240:U:C5	2.56	0.40
40:P:83:VAL:HB	40:P:109:ILE:HG23	2.02	0.40
44:T:47:LYS:HE2	52:3:808:C:OP2	2.20	0.40
48:X:30:LEU:HB2	48:X:48:ILE:HD12	2.02	0.40
48:X:39:ILE:HG22	48:X:40:PHE:H	1.86	0.40
50:Z:39:LYS:O	50:Z:40:PRO:C	2.64	0.40
50:Z:63:ASN:OD1	50:Z:65:ARG:HG2	2.20	0.40
51:a:200:LYS:HA	51:a:201:PRO:HD3	1.90	0.40
52:3:604:G:H2'	52:3:605:U:O4'	2.21	0.40
52:3:1272:G:H2'	52:3:1273:C:O4'	2.21	0.40
53:1:441:U:H2'	53:1:442:G:C8	2.56	0.40
53:1:744:U:H2'	53:1:745:G:O4'	2.21	0.40
53:1:1539:U:H2'	53:1:1540:G:H8	1.86	0.40
53:1:2182:U:H2'	53:1:2183:A:C8	2.55	0.40
53:1:2224:G:H4'	53:1:2226:C:O2	2.20	0.40
53:1:2457:U:O2'	53:1:2458:G:H5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:164:VAL:CG2	52:3:712:A:H5''	2.51	0.40
4:e:134:GLN:HB3	4:e:149:ARG:O	2.20	0.40
15:p:48:ALA:C	15:p:49:ILE:HD12	2.47	0.40
18:s:34:ASP:HB3	26:B:27:LEU:HD22	2.03	0.40
22:w:39:THR:N	53:1:2331:G:H4'	2.37	0.40
23:x:3:VAL:HG13	23:x:9:LYS:O	2.21	0.40
38:N:27:ILE:HD12	38:N:27:ILE:N	2.37	0.40
52:3:754:C:H3'	52:3:754:C:O2	2.21	0.40
52:3:1325:C:O2'	52:3:1326:U:H5'	2.22	0.40
53:1:558:U:H2'	53:1:559:G:C8	2.56	0.40
53:1:1092:C:H2'	53:1:1093:G:O4'	2.21	0.40
53:1:2114:A:C6	53:1:2115:G:H1'	2.56	0.40
53:1:2322:A:H2'	53:1:2323:G:O4'	2.21	0.40
53:1:2364:C:H2'	53:1:2365:G:O4'	2.21	0.40
54:2:28:C:H2'	54:2:29:A:C8	2.57	0.40
5:f:92:GLY:H	5:f:94:ARG:NH1	2.20	0.40
7:h:56:ARG:HB2	53:1:1084:A:H1'	2.02	0.40
10:k:12:ASP:HB2	10:k:96:GLY:HA3	2.04	0.40
15:p:2:ASN:O	15:p:6:GLN:HG3	2.21	0.40
18:s:69:LEU:HD12	18:s:108:SER:O	2.22	0.40
19:t:56:GLU:HG2	19:t:88:LYS:HG2	2.02	0.40
20:u:85:ARG:NH1	20:u:99:SER:HB3	2.36	0.40
22:w:35:ARG:HA	22:w:54:THR:HG23	2.03	0.40
25:z:8:GLN:HB2	25:z:28:LEU:HD22	2.03	0.40
35:K:72:ASP:O	35:K:75:GLU:HG3	2.20	0.40
38:N:86:LEU:HD22	38:N:89:TYR:HD2	1.87	0.40
38:N:88:GLU:HG2	38:N:89:TYR:N	2.36	0.40
52:3:448:A:H3'	52:3:449:G:H8	1.87	0.40
52:3:744:C:H2'	52:3:745:G:C8	2.56	0.40
52:3:1251:A:H2'	52:3:1252:A:O4'	2.21	0.40
53:1:562:U:O4'	53:1:2036:C:H5'	2.22	0.40
53:1:740:C:O5'	53:1:740:C:H6	2.05	0.40
53:1:842:U:H2'	53:1:843:G:C8	2.57	0.40
53:1:1594:U:H2'	53:1:1595:C:C6	2.56	0.40
53:1:1598:A:N3	53:1:1598:A:H2'	2.37	0.40
53:1:2141:G:H2'	53:1:2142:A:H8	1.86	0.40
53:1:2149:U:H2'	53:1:2150:C:O4'	2.21	0.40
3:d:47:LYS:HG2	3:d:51:GLU:OE1	2.21	0.40
3:d:149:ILE:HG23	3:d:149:ILE:O	2.21	0.40
9:j:40:HIS:CE1	9:j:41:LYS:HG2	2.57	0.40
16:q:2:ARG:HA	53:1:1248:G:O2'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:7:VAL:HG13	16:q:8:ILE:HG23	2.03	0.40
30:F:1:MET:HE1	30:F:36:ARG:HB2	2.02	0.40
32:H:56:ILE:HG23	32:H:63:ILE:HD11	2.03	0.40
32:H:142:ARG:HD2	32:H:142:ARG:C	2.46	0.40
41:Q:53:ARG:HG3	41:Q:63:THR:HG22	2.04	0.40
42:R:16:ILE:HA	42:R:19:THR:HG23	2.03	0.40
43:S:48:GLN:OE1	48:X:11:ASP:HA	2.21	0.40
49:Y:31:ILE:HA	49:Y:34:VAL:HG12	2.03	0.40
50:Z:66:ARG:HD2	52:3:1099:G:H4'	2.04	0.40
52:3:541:G:H2'	52:3:542:G:H8	1.86	0.40
52:3:769:G:O2'	52:3:770:C:H5'	2.22	0.40
53:1:1026:G:H2'	53:1:1027:A:C8	2.46	0.40
53:1:1161:C:H2'	53:1:1162:G:C8	2.57	0.40
53:1:1802:A:H2'	53:1:1803:A:C8	2.57	0.40
53:1:2359:C:O2'	53:1:2360:G:H5'	2.21	0.40
3:d:32:VAL:HG23	3:d:178:VAL:HG22	2.03	0.40
7:h:17:GLU:HB3	7:h:86:MET:HG2	2.03	0.40
8:i:123:ALA:O	8:i:126:ARG:HG2	2.21	0.40
11:l:92:LEU:H	11:l:92:LEU:HD23	1.87	0.40
21:v:26:PHE:HE2	21:v:89:ILE:HG13	1.87	0.40
21:v:75:GLN:HB3	21:v:90:ASP:O	2.22	0.40
35:K:53:LYS:HD2	35:K:53:LYS:C	2.47	0.40
52:3:665:A:O4'	52:3:733:G:H1'	2.22	0.40
52:3:867:G:H21	52:3:873:A:H2	1.70	0.40
52:3:1301:U:O2	52:3:1301:U:C2'	2.60	0.40
53:1:133:U:H2'	53:1:134:G:C8	2.57	0.40
53:1:167:A:H2'	53:1:168:G:O4'	2.20	0.40
53:1:176:A:O2'	53:1:177:G:H5'	2.20	0.40
53:1:395:U:H2'	53:1:396:G:H8	1.87	0.40
53:1:818:G:H2'	53:1:819:A:H5''	2.04	0.40
53:1:970:U:H2'	53:1:971:G:C8	2.57	0.40
53:1:1417:C:H2'	53:1:1418:G:O4'	2.22	0.40
53:1:2243:U:H2'	53:1:2244:U:C6	2.57	0.40
53:1:2292:U:H2'	53:1:2293:G:H8	1.86	0.40
53:1:2686:G:H2'	53:1:2687:U:O4'	2.21	0.40
53:1:2804:U:H2'	53:1:2805:C:C6	2.56	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%)	229 (85%)	36 (13%)	4 (2%)	8	36
2	c	207/209 (99%)	186 (90%)	21 (10%)	0	100	100
3	d	199/201 (99%)	178 (89%)	19 (10%)	2 (1%)	12	43
4	e	175/177 (99%)	151 (86%)	22 (13%)	2 (1%)	11	42
5	f	174/176 (99%)	159 (91%)	14 (8%)	1 (1%)	21	52
6	g	147/149 (99%)	130 (88%)	15 (10%)	2 (1%)	9	37
7	h	129/131 (98%)	100 (78%)	23 (18%)	6 (5%)	2	18
8	i	139/141 (99%)	118 (85%)	19 (14%)	2 (1%)	9	37
9	j	140/142 (99%)	130 (93%)	9 (6%)	1 (1%)	18	50
10	k	120/122 (98%)	105 (88%)	12 (10%)	3 (2%)	4	29
11	l	141/143 (99%)	117 (83%)	18 (13%)	6 (4%)	2	19
12	m	134/136 (98%)	116 (87%)	15 (11%)	3 (2%)	5	31
13	n	118/120 (98%)	101 (86%)	14 (12%)	3 (2%)	4	29
14	o	114/116 (98%)	105 (92%)	9 (8%)	0	100	100
15	p	112/114 (98%)	95 (85%)	17 (15%)	0	100	100
16	q	115/117 (98%)	106 (92%)	9 (8%)	0	100	100
17	r	101/103 (98%)	86 (85%)	13 (13%)	2 (2%)	6	32
18	s	108/110 (98%)	96 (89%)	11 (10%)	1 (1%)	14	45
19	t	91/93 (98%)	82 (90%)	8 (9%)	1 (1%)	11	42
20	u	100/102 (98%)	83 (83%)	15 (15%)	2 (2%)	6	32
21	v	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
22	w	73/75 (97%)	64 (88%)	9 (12%)	0	100	100
23	x	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
24	y	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
27	C	48/50 (96%)	44 (92%)	1 (2%)	3 (6%)	1	14
28	D	44/46 (96%)	39 (89%)	4 (9%)	1 (2%)	5	30
29	E	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	35
30	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	27
31	G	223/225 (99%)	206 (92%)	17 (8%)	0	100	100
32	H	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
33	I	203/205 (99%)	183 (90%)	18 (9%)	2 (1%)	12	43
34	J	155/157 (99%)	126 (81%)	23 (15%)	6 (4%)	2	21
35	K	98/100 (98%)	75 (76%)	20 (20%)	3 (3%)	3	26
36	L	149/151 (99%)	134 (90%)	14 (9%)	1 (1%)	18	50
37	M	127/129 (98%)	115 (91%)	12 (9%)	0	100	100
38	N	125/127 (98%)	104 (83%)	18 (14%)	3 (2%)	4	29
39	O	96/98 (98%)	73 (76%)	17 (18%)	6 (6%)	1	14
40	P	114/116 (98%)	95 (83%)	14 (12%)	5 (4%)	2	19
41	Q	121/123 (98%)	98 (81%)	17 (14%)	6 (5%)	1	17
42	R	112/114 (98%)	99 (88%)	10 (9%)	3 (3%)	4	27
43	S	98/100 (98%)	79 (81%)	16 (16%)	3 (3%)	3	26
44	T	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	40
45	U	80/82 (98%)	64 (80%)	15 (19%)	1 (1%)	9	38
46	V	78/80 (98%)	63 (81%)	12 (15%)	3 (4%)	2	22
47	W	63/65 (97%)	59 (94%)	4 (6%)	0	100	100
48	X	77/79 (98%)	63 (82%)	11 (14%)	3 (4%)	2	21
49	Y	83/85 (98%)	77 (93%)	6 (7%)	0	100	100
50	Z	63/65 (97%)	43 (68%)	13 (21%)	7 (11%)	0	5
51	a	130/223 (58%)	123 (95%)	7 (5%)	0	100	100
All	All	5919/6112 (97%)	5168 (87%)	651 (11%)	100 (2%)	9	34

All (100) 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	113	PHE
7	h	118	ILE
10	k	89	ASN
11	l	31	GLY
12	m	58	LYS
17	r	54	VAL
20	u	98	ASN
27	C	45	HIS
29	E	31	ILE
30	F	37	GLN
34	J	93	VAL
35	K	95	ALA
38	N	57	VAL
38	N	90	ASP
40	P	125	LYS
42	R	4	ALA
44	T	46	LYS
45	U	79	ASN
46	V	49	ASN
50	Z	8	ASN
1	b	154	ALA
10	k	92	GLU
11	l	87	GLY
20	u	51	LEU
27	C	43	ARG
33	I	23	GLY
34	J	11	GLN
35	K	86	ARG
38	N	100	ALA
39	O	35	GLN
40	P	89	GLY
41	Q	23	LEU
42	R	6	ILE
42	R	7	ASN
46	V	17	GLU
50	Z	25	ALA
50	Z	34	ARG
50	Z	64	ALA
5	f	174	LYS
7	h	81	LEU
8	i	13	ALA
12	m	6	ARG

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Mol	Chain	Res	Type
13	n	71	ARG
18	s	40	ASN
27	C	44	GLN
28	D	42	LEU
33	I	47	LEU
40	P	92	ARG
41	Q	27	PRO
41	Q	77	SER
43	S	3	GLN
48	X	34	SER
50	Z	14	ALA
50	Z	24	LYS
4	e	176	PHE
6	g	11	ASN
7	h	60	LEU
11	l	29	LYS
12	m	69	PRO
34	J	49	TYR
35	K	99	ALA
39	O	58	ASN
8	i	22	PRO
13	n	104	ALA
19	t	79	ASP
34	J	86	GLY
34	J	102	THR
39	O	37	ARG
40	P	13	LYS
40	P	88	PRO
41	Q	33	CYS
41	Q	35	ARG
46	V	70	LYS
50	Z	12	ASP
1	b	7	PRO
1	b	13	ARG
4	e	20	ASN
7	h	80	THR
10	k	93	GLN
11	l	56	PRO
11	l	88	GLY
13	n	11	ASN
36	L	149	ALA
39	O	57	VAL

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Mol	Chain	Res	Type
43	S	51	PRO
9	j	81	ILE
34	J	97	PRO
1	b	226	PRO
17	r	44	GLY
39	O	33	GLY
48	X	53	GLY
3	d	177	PRO
7	h	77	VAL
39	O	42	LEU
43	S	30	ILE
48	X	7	GLY
11	l	85	VAL
41	Q	41	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	165 (100%)	0	100	100
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%)	100 (100%)	0	100	100
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	75
10	k	103/103 (100%)	101 (98%)	2 (2%)	50	65
11	l	102/102 (100%)	100 (98%)	2 (2%)	48	64
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	99 (99%)	1 (1%)	68	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	o	86/86 (100%)	86 (100%)	0	100	100
15	p	99/99 (100%)	97 (98%)	2 (2%)	48	64
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	72
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	71
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	71
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%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	37 (97%)	1 (3%)	40	60
29	E	51/51 (100%)	50 (98%)	1 (2%)	48	64
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	186 (100%)	0	100	100
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	79
33	I	172/172 (100%)	171 (99%)	1 (1%)	78	79
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	76
35	K	87/87 (100%)	85 (98%)	2 (2%)	44	62
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	104 (100%)	0	100	100
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	85 (99%)	1 (1%)	63	72
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	55 (100%)	0	100	100
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4908/4972 (99%)	4888 (100%)	20 (0%)	81	81

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	c	170	VAL
9	j	73	VAL
10	k	56	ASP
10	k	92	GLU
11	l	35	HIS
11	l	73	ILE
13	n	10	LEU
15	p	40	GLN
15	p	83	ILE
17	r	54	VAL
19	t	57	VAL
21	v	20	LEU
28	D	44	VAL
29	E	28	LEU
32	H	81	GLU
33	I	31	CYS
34	J	105	ILE
35	K	73	GLU
35	K	97	THR
39	O	73	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (105) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	36	ASN
1	b	89	ASN

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Mol	Chain	Res	Type
1	b	127	ASN
2	c	32	ASN
2	c	49	GLN
2	c	140	HIS
2	c	150	GLN
2	c	185	ASN
3	d	30	GLN
3	d	94	GLN
3	d	97	ASN
3	d	195	GLN
4	e	51	ASN
5	f	29	ASN
5	f	44	HIS
5	f	72	ASN
5	f	103	ASN
6	g	33	GLN
6	g	43	ASN
7	h	4	ASN
8	i	5	GLN
8	i	33	ASN
9	j	40	HIS
9	j	58	ASN
9	j	76	HIS
9	j	130	HIS
9	j	135	GLN
11	l	38	GLN
11	l	54	GLN
12	m	13	HIS
12	m	17	ASN
12	m	22	GLN
12	m	45	GLN
14	o	38	GLN
14	o	98	GLN
15	p	6	GLN
15	p	11	GLN
15	p	114	ASN
16	q	80	ASN
17	r	6	GLN
18	s	15	GLN
18	s	40	ASN
19	t	48	GLN
20	u	73	ASN

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Mol	Chain	Res	Type
21	v	49	ASN
21	v	78	GLN
22	w	42	HIS
23	x	16	ASN
24	y	41	HIS
28	D	13	ASN
29	E	23	HIS
30	F	37	GLN
31	G	38	HIS
31	G	50	ASN
31	G	57	ASN
31	G	176	ASN
32	H	2	GLN
32	H	5	HIS
32	H	7	ASN
32	H	31	ASN
32	H	139	ASN
32	H	184	ASN
33	I	39	GLN
33	I	88	ASN
33	I	99	ASN
33	I	115	GLN
33	I	125	ASN
33	I	135	GLN
33	I	139	ASN
33	I	195	ASN
34	J	88	HIS
34	J	131	ASN
34	J	145	ASN
35	K	3	HIS
35	K	55	HIS
35	K	58	HIS
35	K	68	GLN
36	L	51	GLN
37	M	15	ASN
37	M	66	GLN
38	N	30	ASN
39	O	20	GLN
39	O	64	GLN
40	P	14	GLN
40	P	21	HIS
41	Q	4	ASN

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Mol	Chain	Res	Type
41	Q	58	ASN
43	S	3	GLN
43	S	42	ASN
44	T	36	ASN
44	T	41	HIS
44	T	49	HIS
45	U	9	HIS
45	U	63	GLN
45	U	79	ASN
46	V	30	HIS
46	V	44	HIS
47	W	51	GLN
47	W	53	GLN
48	X	68	HIS
49	Y	51	ASN
49	Y	69	ASN
49	Y	81	GLN
51	a	172	HIS
51	a	188	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	140 (9%)	4 (0%)
53	1	2902/2903 (99%)	338 (11%)	9 (0%)
54	2	119/120 (99%)	12 (10%)	1 (0%)
55	5	76/77 (98%)	8 (10%)	0
55	6	76/77 (98%)	8 (10%)	0
56	4	17/18 (94%)	3 (17%)	0
57	7	75/76 (98%)	12 (16%)	0
All	All	4803/4810 (99%)	521 (10%)	14 (0%)

All (521) 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

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Mol	Chain	Res	Type
52	3	48	C
52	3	51	A
52	3	71	A
52	3	87	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	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	429	U
52	3	467	U
52	3	484	G
52	3	485	U
52	3	486	U
52	3	497	G
52	3	518	C
52	3	531	U
52	3	533	A
52	3	547	A
52	3	561	U
52	3	564	C
52	3	572	A
52	3	573	A
52	3	575	G
52	3	576	C

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Mol	Chain	Res	Type
52	3	577	G
52	3	633	G
52	3	642	A
52	3	653	U
52	3	665	A
52	3	688	G
52	3	702	A
52	3	703	G
52	3	723	U
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	842	U
52	3	843	U
52	3	844	G
52	3	846	G
52	3	871	U
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	971	G
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	1031	C
52	3	1033	G
52	3	1034	G

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Mol	Chain	Res	Type
52	3	1094	G
52	3	1101	A
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	1197	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	1261	A
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	1317	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1378	C
52	3	1381	U
52	3	1395	C
52	3	1419	G
52	3	1446	A
52	3	1448	C
52	3	1452	C
52	3	1492	A

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Mol	Chain	Res	Type
52	3	1493	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1534	A
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	50	U
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A
53	1	75	G
53	1	92	U
53	1	119	A
53	1	120	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	219	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

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Mol	Chain	Res	Type
53	1	281	C
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	333	G
53	1	353	C
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	422	A
53	1	424	G
53	1	451	U
53	1	455	C
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	588	U
53	1	603	A
53	1	616	A
53	1	627	A
53	1	637	A

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Mol	Chain	Res	Type
53	1	646	U
53	1	654	A
53	1	669	G
53	1	686	U
53	1	687	C
53	1	730	A
53	1	747	C
53	1	752	A
53	1	764	A
53	1	775	G
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	887	U
53	1	896	A
53	1	910	A
53	1	932	U
53	1	941	A
53	1	945	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	975	A
53	1	983	A
53	1	995	C
53	1	1009	A
53	1	1012	U

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Mol	Chain	Res	Type
53	1	1013	C
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	1057	A
53	1	1060	U
53	1	1062	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	1157	G
53	1	1175	A
53	1	1177	G
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	1301	A
53	1	1314	C
53	1	1329	U
53	1	1330	C

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Mol	Chain	Res	Type
53	1	1332	G
53	1	1333	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	1493	C
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1535	A
53	1	1536	C
53	1	1537	G
53	1	1555	G
53	1	1559	U
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	1674	G
53	1	1699	G
53	1	1715	G
53	1	1729	U
53	1	1730	C

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Mol	Chain	Res	Type
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1791	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	1929	G
53	1	1930	G
53	1	1937	A
53	1	1938	A
53	1	1944	U
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	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
53	1	2062	A
53	1	2069	G

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Mol	Chain	Res	Type
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	2126	A
53	1	2132	U
53	1	2133	G
53	1	2147	A
53	1	2162	G
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	2225	A
53	1	2259	U
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2337	G
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2406	A
53	1	2407	A
53	1	2423	U
53	1	2424	C
53	1	2429	G
53	1	2430	A
53	1	2435	A

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Mol	Chain	Res	Type
53	1	2441	U
53	1	2448	A
53	1	2476	A
53	1	2491	U
53	1	2498	C
53	1	2502	G
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	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
53	1	2801	G
53	1	2809	A
53	1	2820	A
53	1	2821	A

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Mol	Chain	Res	Type
53	1	2833	U
53	1	2849	U
53	1	2850	A
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2880	C
53	1	2883	A
53	1	2884	U
53	1	2893	A
54	2	4	C
54	2	12	C
54	2	13	G
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	9	G
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	59	A
55	5	61	C
55	5	76	A
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
56	4	19	C
57	7	9	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	49	C
57	7	59	U
57	7	61	C
57	7	74	C

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	70	U
52	3	280	C
52	3	1190	G
52	3	1201	A
53	1	421	C
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	2326	C
53	1	2391	G
54	2	88	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	0.60	0	8,9,11	0.86	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	-	1/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	5	101	FME	CB-CA-N-CN

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-21638. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

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

9 Map-model fit

This section was not generated.