



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 04:22 AM UTC

PDB ID : 6WDI / pdb_00006wdi
EMDB ID : EMD-21637
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Non-cognate Structure IV-B2)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 4.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

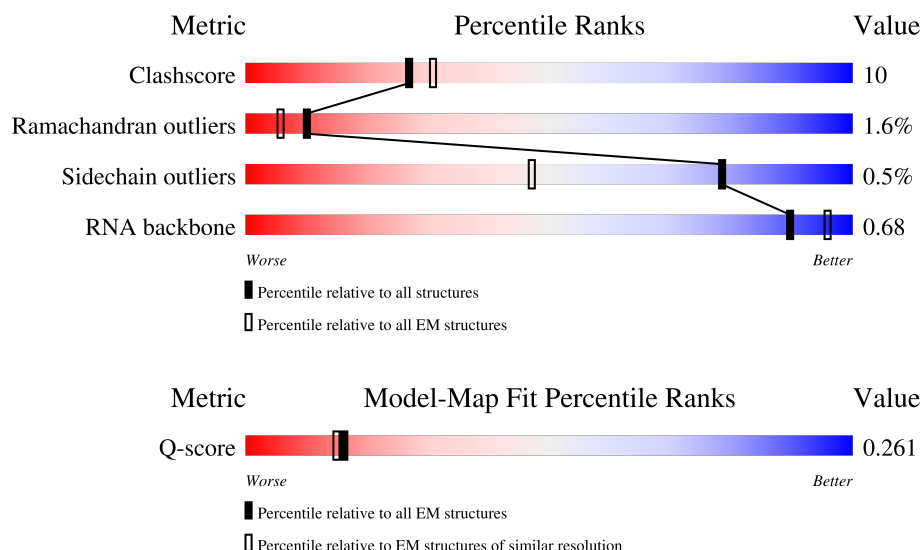
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

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



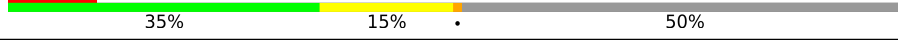
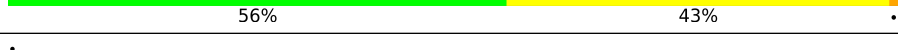
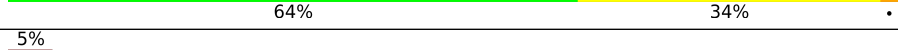
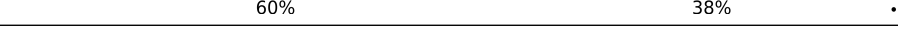
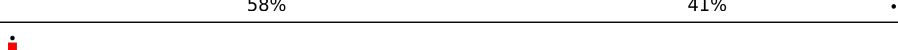
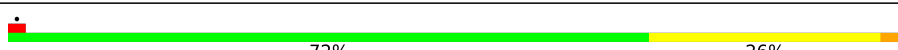
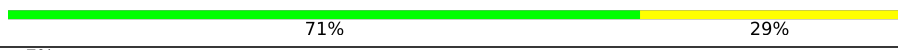
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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

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

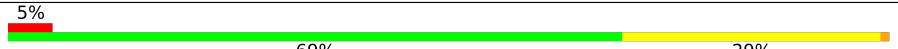
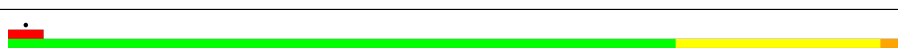
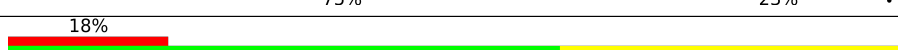
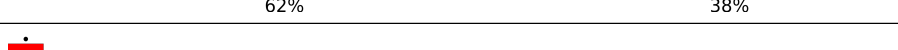
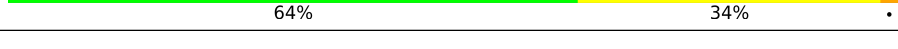
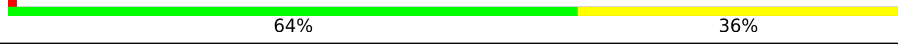
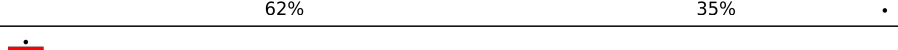
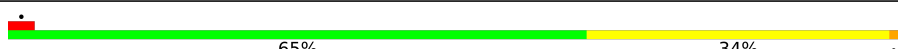
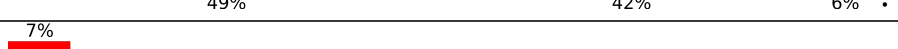
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56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

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

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Mol	Chain	Length	Quality of chain
54	2	120	53%39%8%
55	5	77	5% 66%30% .
55	6	77	8% 71%26% .
56	4	18	72%28%
57	7	76	18% 70%21%5% .

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 149628 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	71	Total	C	N	O	S	0	0
			511	313	93	102	3		

- 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		

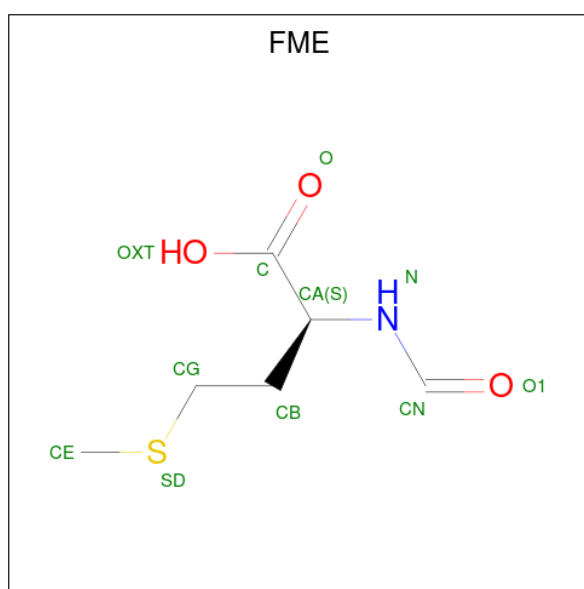
- Molecule 56 is a RNA chain called mRNA.

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	73	Total	C	N	O	P	0	0
			1557	695	279	511	72		

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

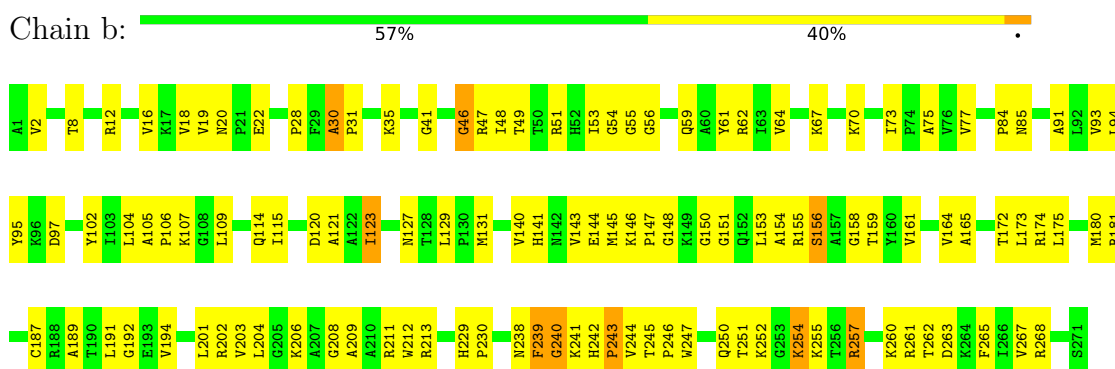


Mol	Chain	Residues	Atoms					AltConf
58	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

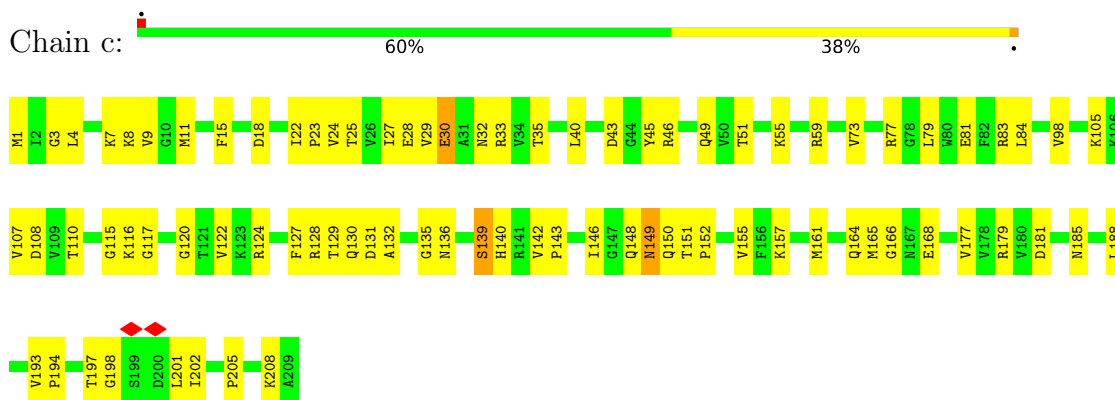
3 Residue-property plots

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

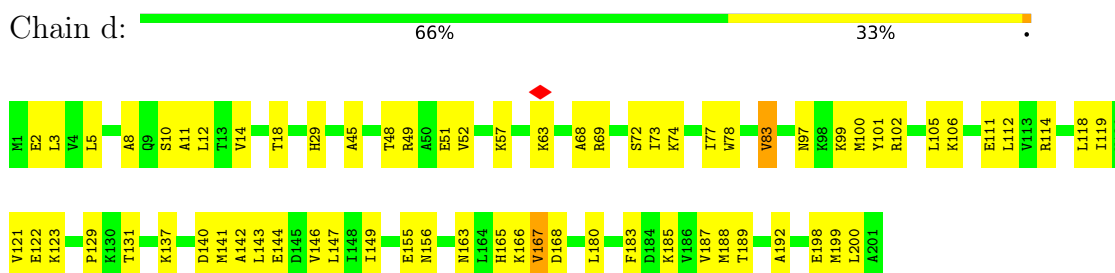
• Molecule 1: 50S ribosomal protein L2



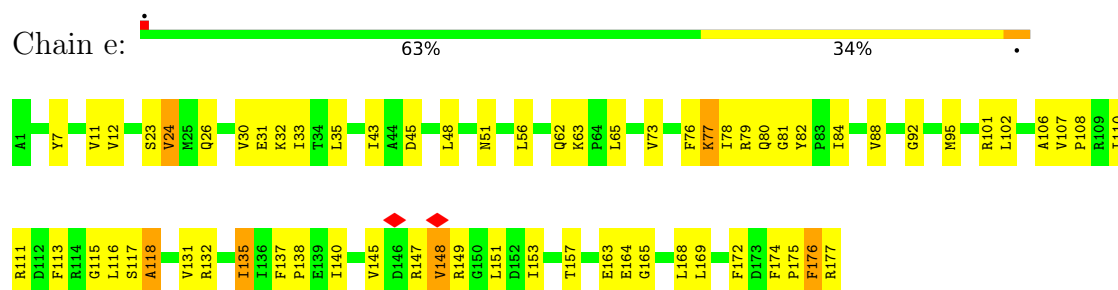
• Molecule 2: 50S ribosomal protein L3



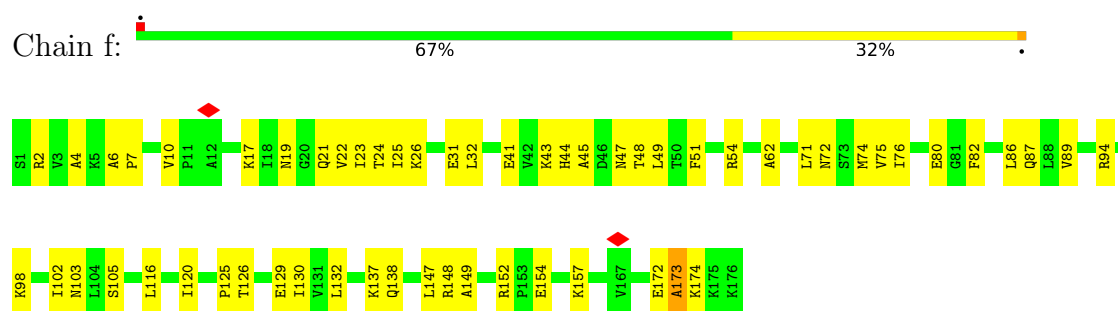
• Molecule 3: 50S ribosomal protein L4



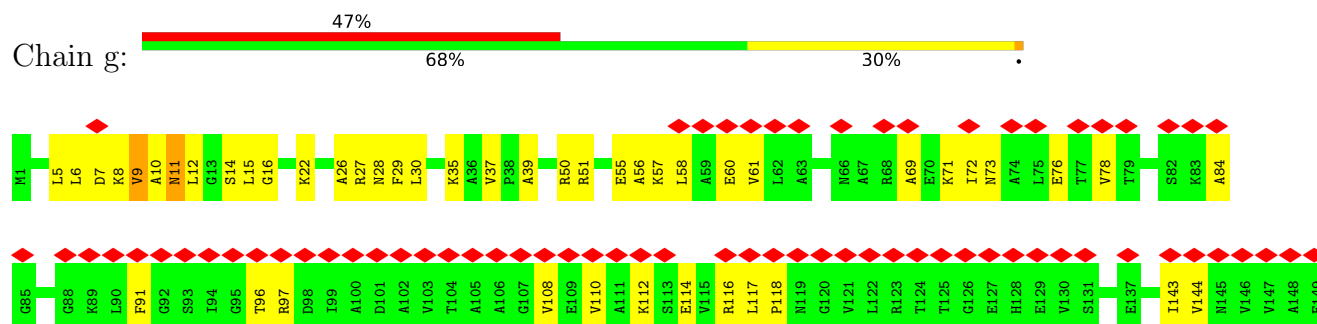
- Molecule 4: 50S ribosomal protein L5



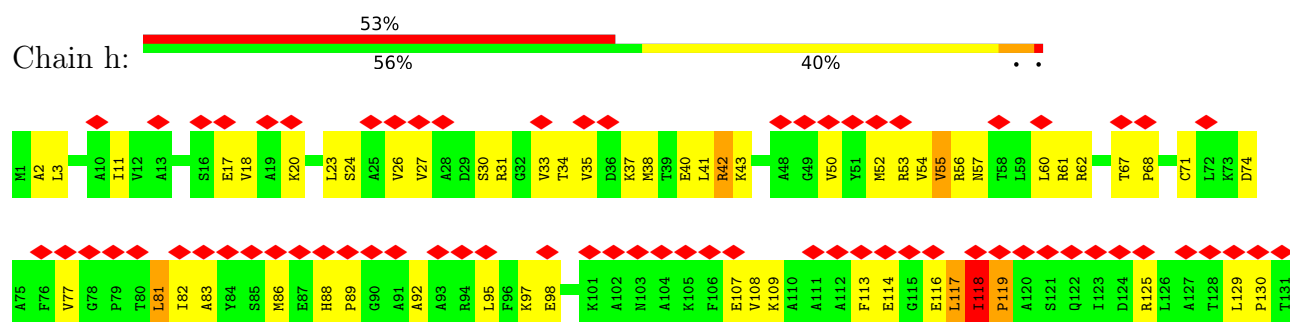
- Molecule 5: 50S ribosomal protein L6



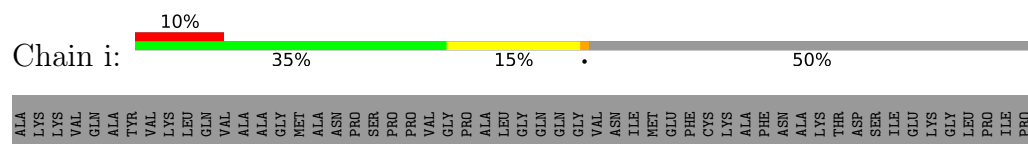
- Molecule 6: 50S ribosomal protein L9

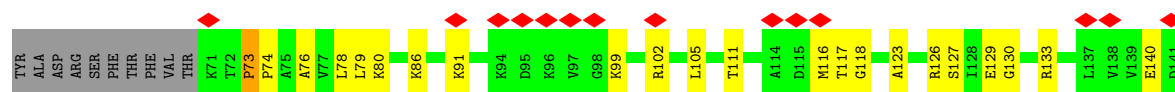


- Molecule 7: 50S ribosomal protein L10



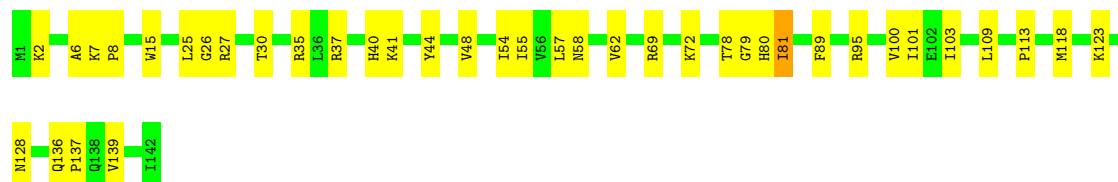
- Molecule 8: 50S ribosomal protein L11





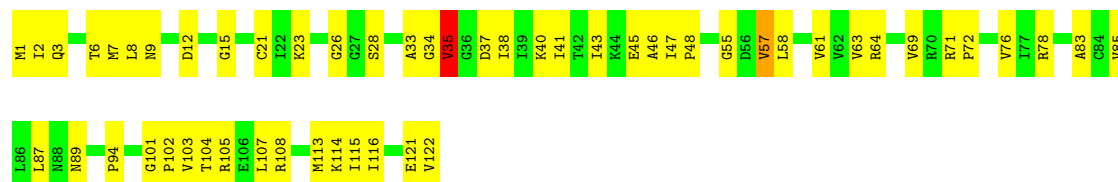
• Molecule 9: 50S ribosomal protein L13

Chain j: 73% 27%



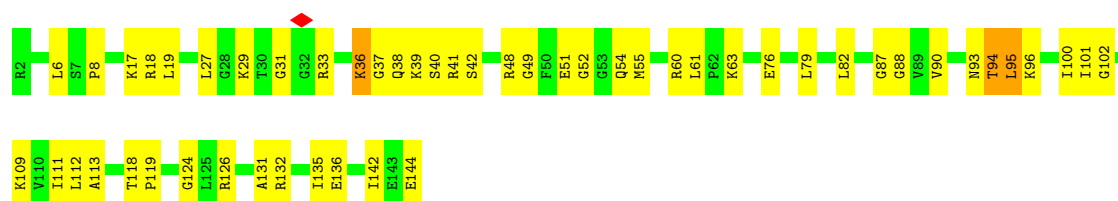
• Molecule 10: 50S ribosomal protein L14

Chain k: 56% 43%



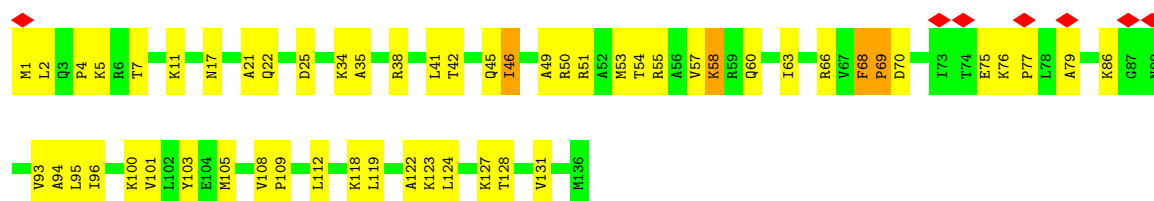
• Molecule 11: 50S ribosomal protein L15

Chain l: 64% 34%



• Molecule 12: 50S ribosomal protein L16

Chain m: 5% 60% 38%



• Molecule 13: 50S ribosomal protein L17

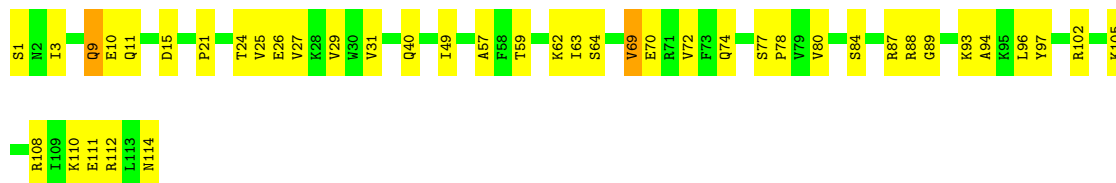
Chain n: 58% 41%



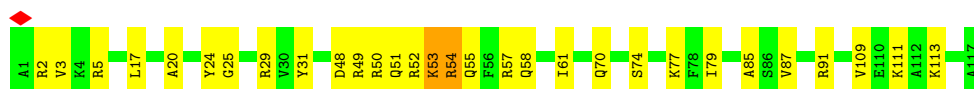
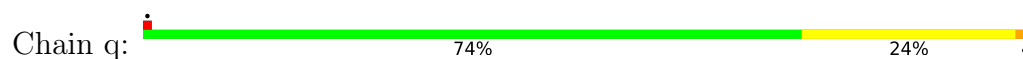
- Molecule 14: 50S ribosomal protein L18



- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23

Chain t:  72% 26%



- Molecule 20: 50S ribosomal protein L24

Chain u:  70% 28%



- Molecule 21: 50S ribosomal protein L25

Chain v:  67% 33%



- Molecule 22: 50S ribosomal protein L27

Chain w:  63% 36%



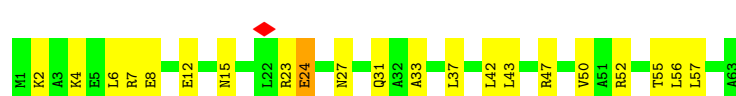
- Molecule 23: 50S ribosomal protein L28

Chain x:  61% 39%



- Molecule 24: 50S ribosomal protein L29

Chain y:  67% 32%

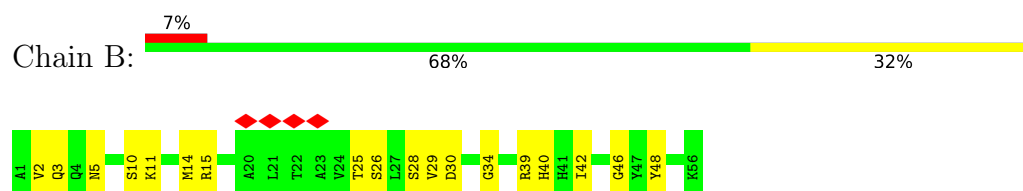


- Molecule 25: 50S ribosomal protein L30

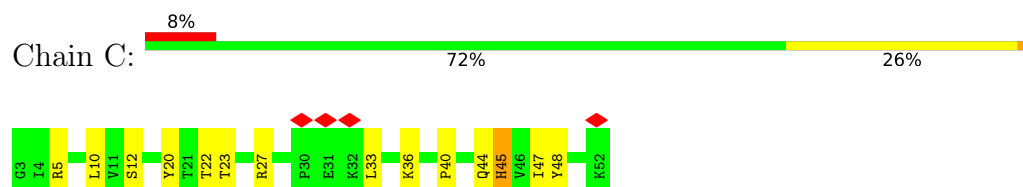
Chain z:  71% 29%



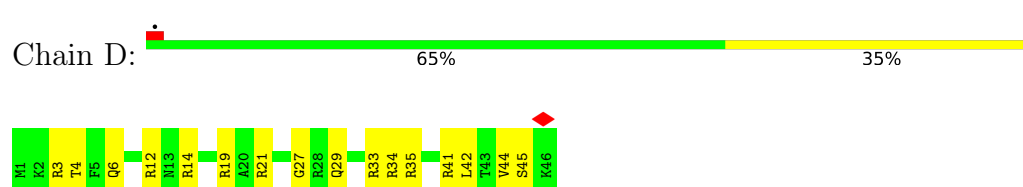
- Molecule 26: 50S ribosomal protein L32



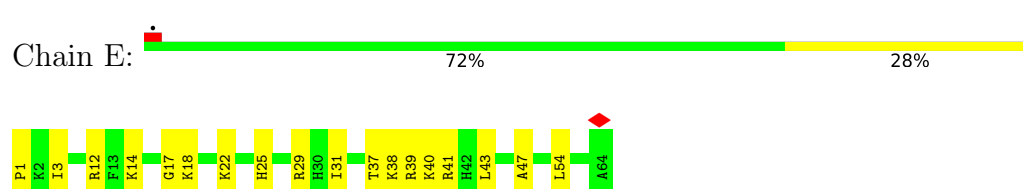
- Molecule 27: 50S ribosomal protein L33



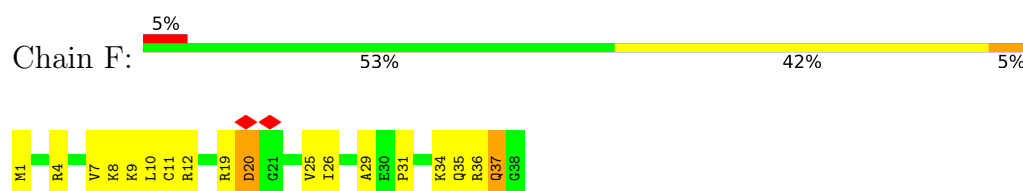
- Molecule 28: 50S ribosomal protein L34



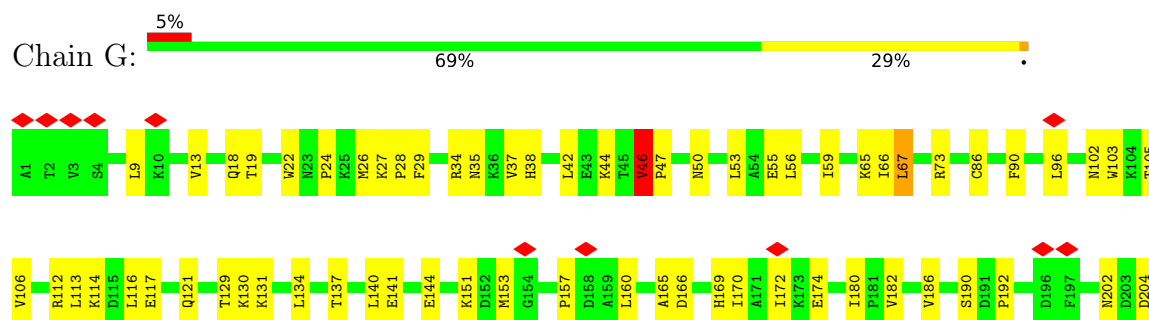
- Molecule 29: 50S ribosomal protein L35

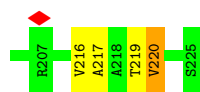


- Molecule 30: 50S ribosomal protein L36



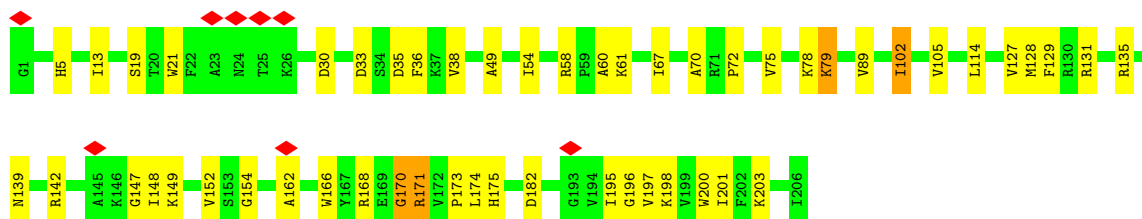
- Molecule 31: 30S ribosomal protein S2





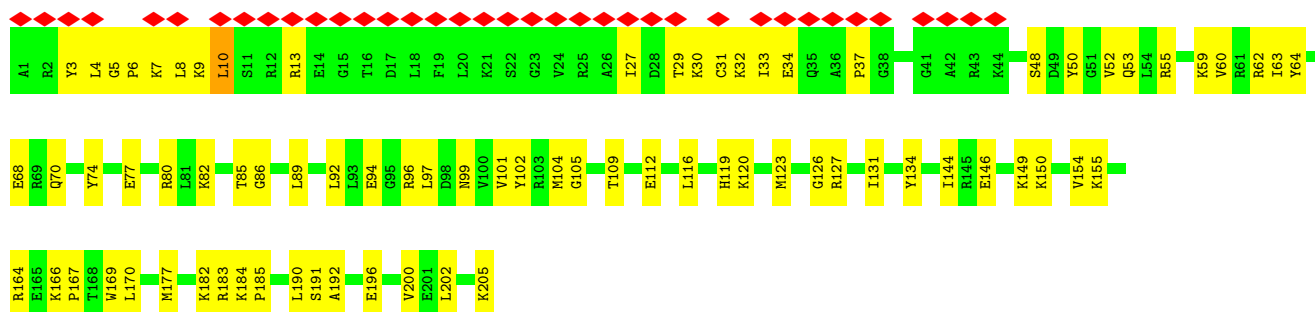
- Molecule 32: 30S ribosomal protein S3

Chain H: 75% 23%



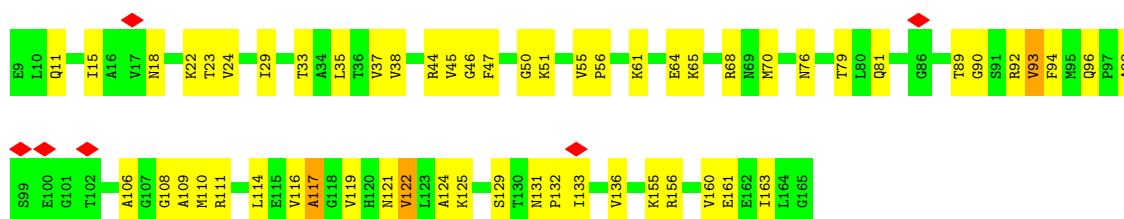
- Molecule 33: 30S ribosomal protein S4

Chain I: 18% 62% 38%



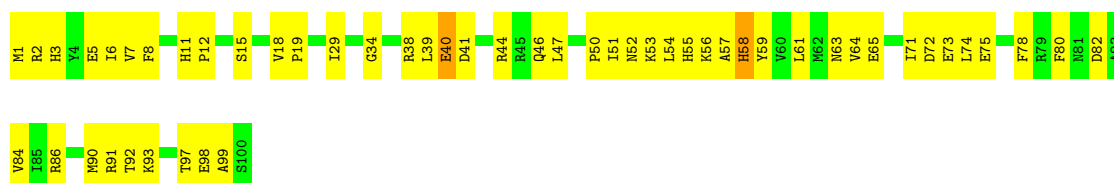
- Molecule 34: 30S ribosomal protein S5

Chain J: 64% 34%

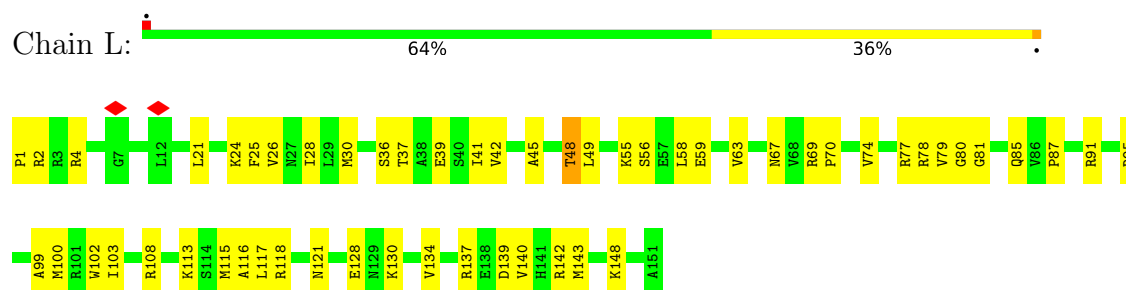


- Molecule 35: 30S ribosomal protein S6

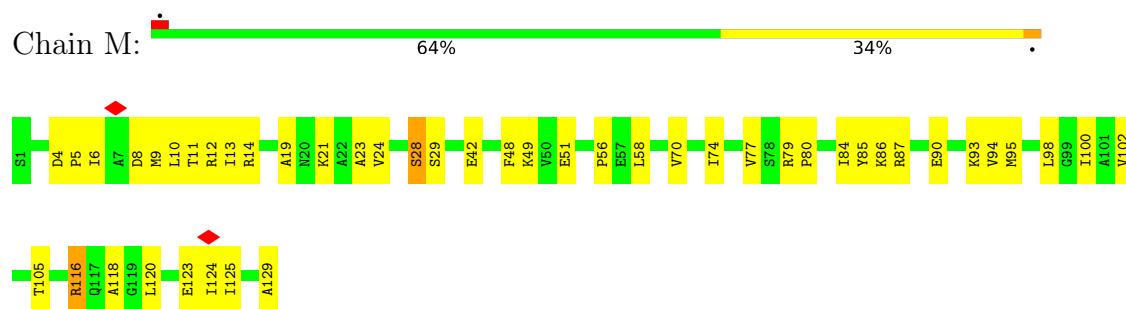
Chain K: 48% 50%



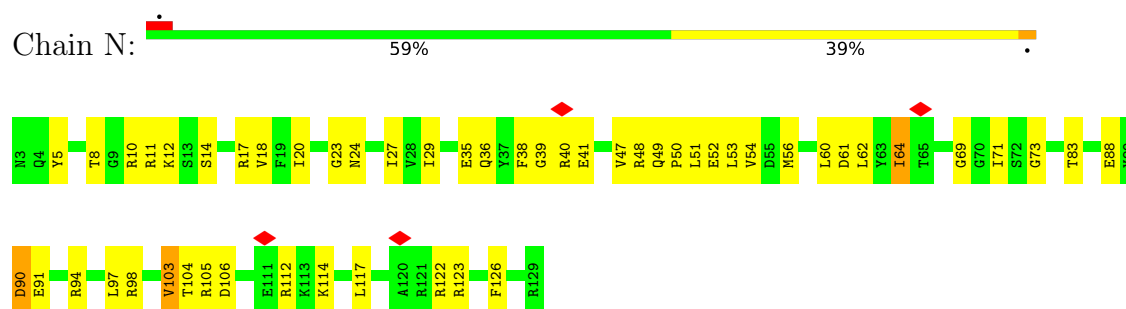
- Molecule 36: 30S ribosomal protein S7



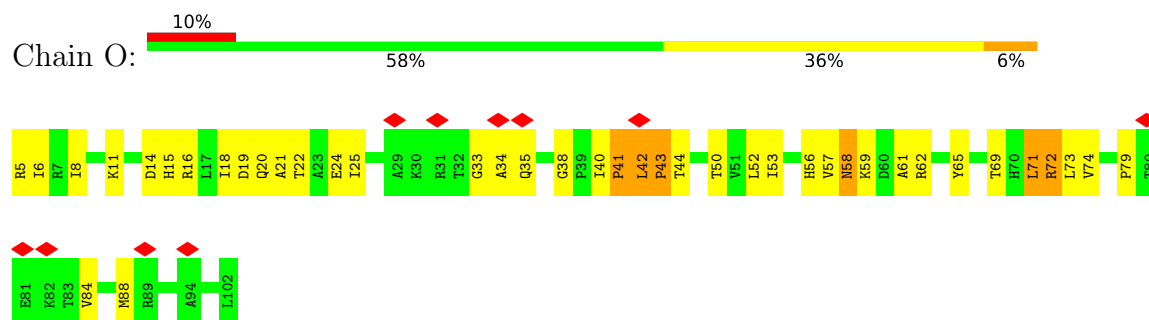
- Molecule 37: 30S ribosomal protein S8



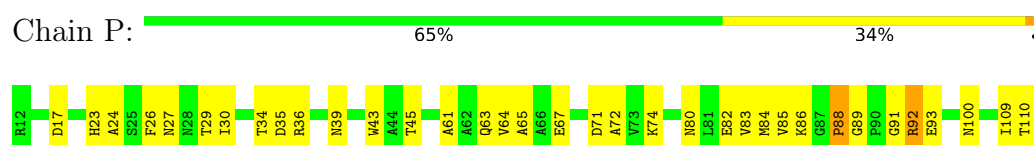
- Molecule 38: 30S ribosomal protein S9



- Molecule 39: 30S ribosomal protein S10



- Molecule 40: 30S ribosomal protein S11



P122
P123
K124
K125
R126
R127

- Molecule 41: 30S ribosomal protein S12

Chain Q:  60% 36%

A1 T2 V3 N4 R8 P10 R11 K17 L23 E24 P27 Q28 K29 R30 G31 C33 C32 T34 R35 V36 T39 T40 K43 L48 R49 K50 V51 C52 R53 V54 R55 L56 F60 G68 E69 G70 H71 N72 L73 H76 S77 V78 I79 L80 I81 R82 R85

D88 L89 R93 T96 V97 R98 G99 A100 C103 R109 K110 Q111 S114 K115 Y116 G117 V118 K119 R120 A123

- Molecule 42: 30S ribosomal protein S13

Chain R:  62% 35%

A1 R2 I3 A4 G5 I6 W7 I8 P9 V15 I16 A17 L18 I21 Y22 G23 V24 Q25 R26 T27 R28 I44 R56 V63 V64 E65 G66 D67 L68 R69 R70 S73 M74 S75 I76 K77 R78 L79 M80 D81 L82 Y85 R86 G87 L88 R89 H90 R91 R92 G93 L94 P95

Q99 R100 T101 K102 T103 R112 K113 P114

- Molecule 43: 30S ribosomal protein S14

Chain S:  59% 40%

A1 K2 Q3 S4 R5 K6 A7 R8 E9 V10 Y19 F20 A21 K22 R23 A24 E25 I29 I30 S31 D32 V33 N34 A35 S36 D37 E38 D39 R40 W41 N42 A43 V44 T49 R52 D53 S54 S55 R58 M61 R62 C63 R64 Q65 T66 G67 R68 P69 R74 K75 L78

I81 R89 G90 E91 I92 L95 M100

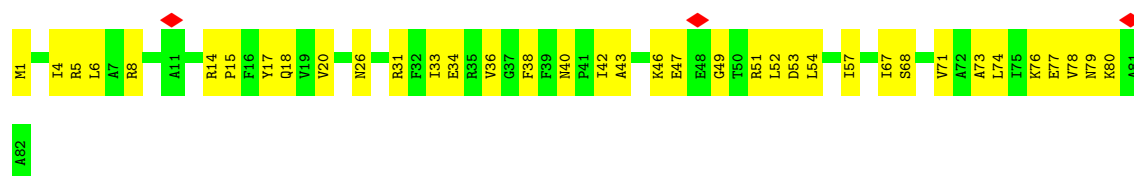
- Molecule 44: 30S ribosomal protein S15

Chain T:  70% 30%

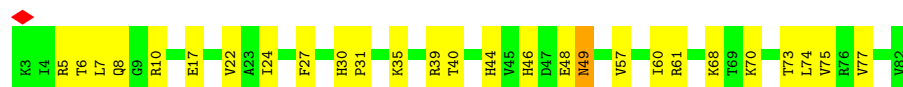
S1 L2 A18 M19 D20 V26 L30 Q34 A43 E44 H45 K46 K47 D48 H49 H50 L55 L56 L57 R58 V59 S60 Q61 R64 L65 V68 K72 A75 R76 Y77 T78 L86 R87 R88

- Molecule 45: 30S ribosomal protein S16

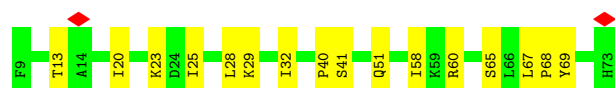
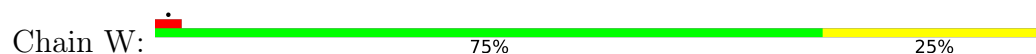
Chain U:  55% 45%



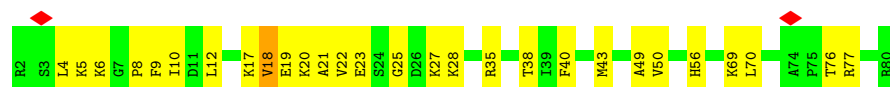
- Molecule 46: 30S ribosomal protein S17



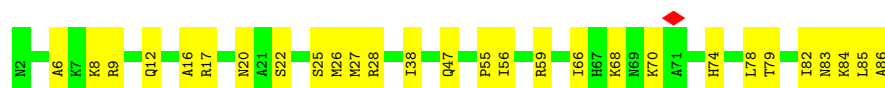
- Molecule 47: 30S ribosomal protein S18



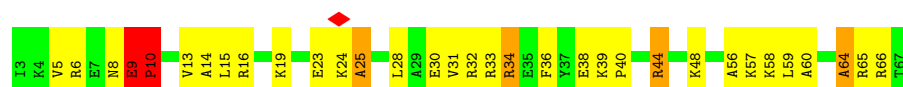
- Molecule 48: 30S ribosomal protein S19



- Molecule 49: 30S ribosomal protein S20

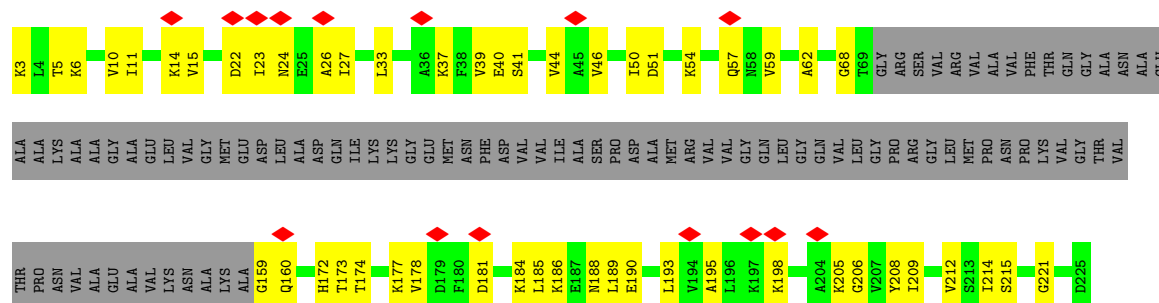


- Molecule 50: 30S ribosomal protein S21



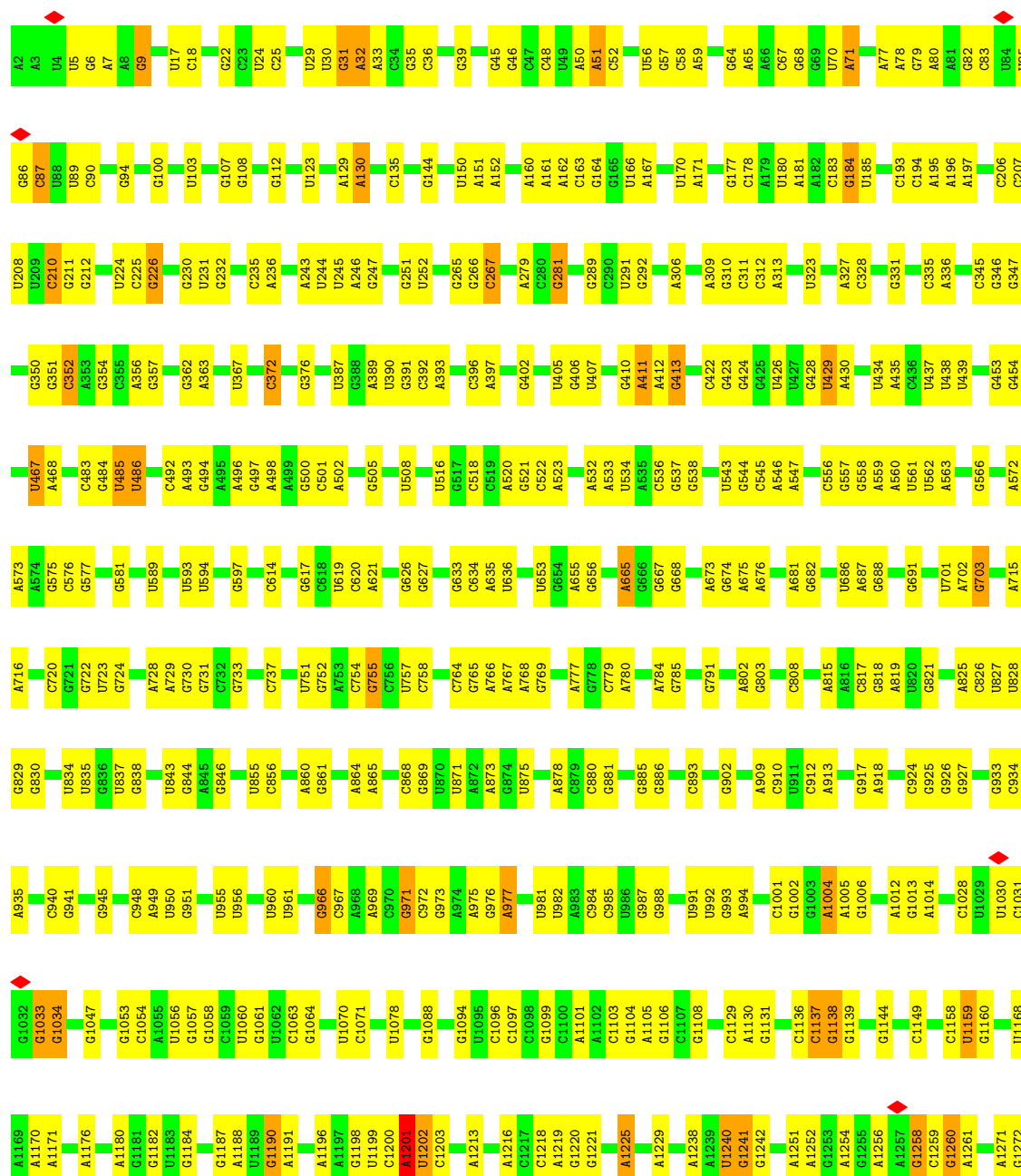
- Molecule 51: 50S ribosomal protein L1



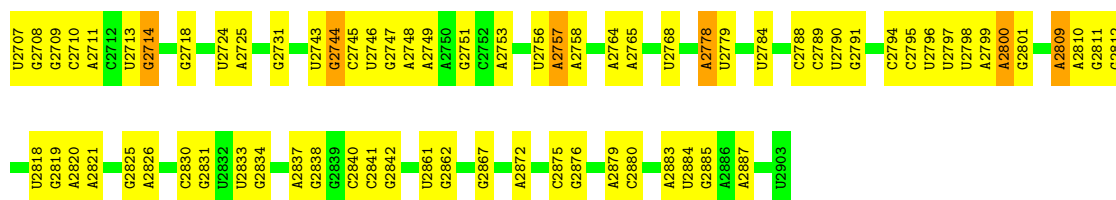


• Molecule 52: 16S ribosomal RNA

Chain 3: 63% 34% .

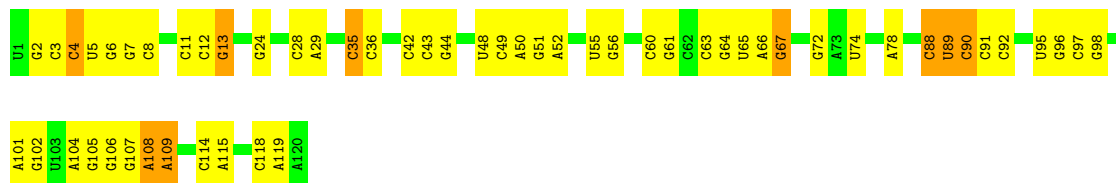






• Molecule 54: 5S ribosomal RNA

Chain 2: 53% 39% 8%



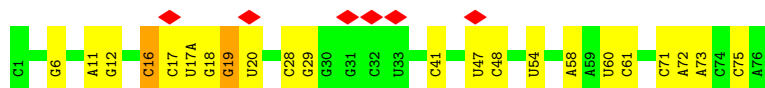
• Molecule 55: tRNA^{fMet}

Chain 5: 5% 66% 30%



• Molecule 55: tRNA^{fMet}

Chain 6: 8% 71% 26%



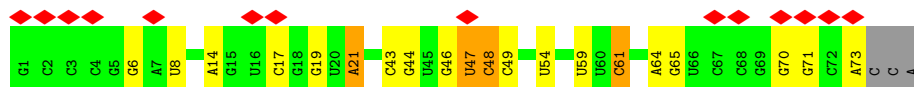
• Molecule 56: mRNA

Chain 4: 72% 28%



• Molecule 57: tRNA^{Phe}

Chain 7: 18% 70% 21% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1924	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	18.983	Depositor
Minimum map value	-10.992	Depositor
Average map value	0.128	Depositor
Map value standard deviation	0.905	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	b	0.30	0/2122	0.99	8/2852 (0.3%)
2	c	0.31	0/1586	0.88	2/2134 (0.1%)
3	d	0.29	0/1571	0.90	2/2113 (0.1%)
4	e	0.32	0/1435	0.92	6/1926 (0.3%)
5	f	0.30	0/1343	0.90	7/1816 (0.4%)
6	g	0.31	0/1122	0.94	3/1515 (0.2%)
7	h	0.35	0/1002	1.00	5/1350 (0.4%)
8	i	0.34	0/513	0.99	7/684 (1.0%)
9	j	0.29	0/1152	0.85	2/1551 (0.1%)
10	k	0.31	0/948	0.92	2/1268 (0.2%)
11	l	0.30	0/1054	0.92	5/1403 (0.4%)
12	m	0.31	0/1093	0.93	6/1460 (0.4%)
13	n	0.32	0/974	0.89	3/1301 (0.2%)
14	o	0.29	0/902	0.89	2/1209 (0.2%)
15	p	0.32	0/929	0.96	5/1242 (0.4%)
16	q	0.29	0/960	0.90	4/1278 (0.3%)
17	r	0.30	0/829	0.94	3/1107 (0.3%)
18	s	0.28	0/864	0.89	0/1156
19	t	0.29	0/745	0.88	2/994 (0.2%)
20	u	0.30	0/788	0.92	3/1051 (0.3%)
21	v	0.28	0/766	0.96	2/1025 (0.2%)
22	w	0.29	0/582	0.90	1/769 (0.1%)
23	x	0.28	0/635	0.89	1/848 (0.1%)
24	y	0.27	0/510	0.97	2/677 (0.3%)
25	z	0.28	0/453	0.83	0/605
26	B	0.31	0/450	0.95	1/599 (0.2%)
27	C	0.33	0/417	0.77	0/554
28	D	0.33	0/380	0.93	0/498
29	E	0.30	0/513	0.82	0/676
30	F	0.36	0/303	1.01	0/397
31	G	0.32	0/1788	0.96	6/2408 (0.2%)
32	H	0.30	0/1652	0.89	6/2225 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.29	0/1665	0.95	9/2227 (0.4%)
34	J	0.33	0/1170	0.99	6/1573 (0.4%)
35	K	0.31	0/836	0.98	2/1128 (0.2%)
36	L	0.30	0/1196	0.93	3/1602 (0.2%)
37	M	0.29	0/989	0.94	4/1326 (0.3%)
38	N	0.30	0/1034	0.91	2/1375 (0.1%)
39	O	0.33	0/797	0.93	3/1077 (0.3%)
40	P	0.34	0/886	0.93	3/1195 (0.3%)
41	Q	0.32	0/969	0.92	4/1300 (0.3%)
42	R	0.32	0/893	0.90	1/1193 (0.1%)
43	S	0.30	0/817	0.95	5/1088 (0.5%)
44	T	0.28	0/722	0.88	1/964 (0.1%)
45	U	0.33	0/659	0.90	1/884 (0.1%)
46	V	0.31	0/658	0.89	1/881 (0.1%)
47	W	0.32	0/545	0.99	6/731 (0.8%)
48	X	0.32	0/653	1.00	5/877 (0.6%)
49	Y	0.29	0/671	1.02	3/888 (0.3%)
50	Z	0.33	0/551	1.02	2/728 (0.3%)
51	a	0.31	0/1034	0.81	2/1387 (0.1%)
52	3	0.41	0/36963	0.51	3/57662 (0.0%)
53	1	0.40	0/69796	0.51	1/108888 (0.0%)
54	2	0.41	0/2872	0.50	0/4479
55	5	0.41	0/1832	0.50	0/2855
55	6	0.41	0/1832	0.51	0/2855
56	4	0.42	0/436	0.52	0/679
57	7	0.40	0/1740	0.49	0/2712
All	All	0.38	0/162597	0.64	163/243245 (0.1%)

There are no bond length outliers.

All (163) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	G	220	VAL	N-CA-C	-9.59	103.56	111.81
36	L	79	VAL	N-CA-C	-9.09	104.62	113.53
34	J	117	ALA	N-CA-C	-8.09	103.20	113.23
1	b	239	PHE	N-CA-C	-7.95	101.46	112.12
17	r	50	GLY	N-CA-C	-7.83	103.42	112.50
1	b	12	ARG	N-CA-C	-7.72	103.42	112.92
6	g	10	ALA	N-CA-C	7.66	120.97	109.25
15	p	94	ALA	N-CA-C	-7.61	105.94	114.62
37	M	118	ALA	N-CA-C	-7.54	104.32	113.97
34	J	161	GLU	N-CA-C	7.48	119.52	111.36

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Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	G	18	GLN	N-CA-C	7.47	120.17	110.53
21	v	80	HIS	N-CA-C	-7.40	100.32	109.65
7	h	117	LEU	N-CA-C	7.40	120.48	107.61
14	o	56	LYS	N-CA-C	7.30	119.24	111.28
16	q	31	TYR	N-CA-C	7.25	118.83	111.07
1	b	30	ALA	N-CA-C	7.24	122.32	112.55
32	H	5	HIS	CA-C-N	7.20	126.73	119.24
32	H	5	HIS	C-N-CA	7.20	126.73	119.24
1	b	123	ILE	N-CA-C	7.15	118.58	108.93
1	b	46	GLY	N-CA-C	7.07	124.40	115.42
1	b	213	ARG	N-CA-C	-7.00	104.87	113.41
35	K	73	GLU	N-CA-C	-6.85	104.40	112.89
45	U	78	VAL	N-CA-C	-6.81	104.69	111.77
6	g	51	ARG	N-CA-C	6.81	120.02	111.24
7	h	107	GLU	N-CA-C	-6.77	102.09	112.99
2	c	139	SER	N-CA-C	6.65	118.33	107.23
17	r	54	VAL	N-CA-C	6.60	123.08	109.34
46	V	8	GLN	N-CA-C	-6.50	99.95	109.63
13	n	46	ARG	N-CA-C	-6.46	105.27	112.57
44	T	43	ALA	N-CA-C	-6.46	104.88	112.89
34	J	160	VAL	N-CA-C	6.46	117.98	110.62
36	L	49	LEU	N-CA-C	-6.43	104.13	112.23
36	L	48	THR	N-CA-C	-6.37	104.99	112.89
39	O	20	GLN	N-CA-C	-6.37	105.67	113.50
50	Z	58	LYS	N-CA-C	-6.36	104.21	112.23
21	v	54	ALA	N-CA-C	6.32	118.17	111.28
17	r	18	GLN	N-CA-C	6.28	118.13	110.41
33	I	166	LYS	CA-C-N	6.24	127.64	119.84
33	I	166	LYS	C-N-CA	6.24	127.64	119.84
19	t	80	TRP	N-CA-C	6.20	119.33	109.65
49	Y	70	LYS	N-CA-C	-6.20	104.60	111.36
1	b	145	MET	N-CA-C	-6.20	106.26	113.88
33	I	94	GLU	N-CA-C	-6.18	105.78	113.38
43	S	89	ARG	N-CA-C	-6.07	106.00	113.41
9	j	139	VAL	N-CA-C	6.06	117.12	108.93
37	M	116	ARG	N-CA-C	-6.01	105.95	113.28
39	O	41	PRO	N-CA-C	6.00	121.40	114.20
47	W	23	LYS	N-CA-C	6.00	117.51	110.97
34	J	116	VAL	N-CA-C	-5.95	105.96	112.80
40	P	125	LYS	N-CA-C	5.91	123.39	110.80
35	K	82	ASP	N-CA-C	5.89	119.94	112.87
49	Y	84	LYS	N-CA-C	-5.86	104.85	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	H	89	VAL	N-CA-C	5.85	118.37	111.05
10	k	35	VAL	N-CA-C	5.85	121.51	109.34
48	X	12	LEU	N-CA-C	5.85	118.15	111.02
31	G	44	LYS	N-CA-C	-5.85	106.19	113.38
4	e	149	ARG	N-CA-C	5.83	118.80	110.10
24	y	27	ASN	N-CA-C	5.83	117.31	111.07
37	M	23	ALA	N-CA-C	5.83	118.23	108.96
16	q	70	GLN	N-CA-C	-5.80	106.16	113.18
41	Q	49	ARG	N-CA-C	5.80	118.74	110.10
5	f	173	ALA	N-CA-C	-5.79	106.84	112.97
33	I	3	TYR	N-CA-C	-5.77	105.91	113.12
7	h	42	ARG	N-CA-C	-5.76	106.22	113.18
4	e	117	SER	N-CA-C	5.75	118.57	110.23
5	f	62	ALA	N-CA-C	-5.74	106.11	113.23
11	l	49	GLY	N-CA-C	5.74	121.53	114.69
52	3	1201	A	C2'-C3'-O3'	5.73	118.09	109.50
14	o	72	ALA	N-CA-C	-5.72	105.79	112.89
43	S	22	LYS	N-CA-C	-5.72	106.35	113.55
7	h	55	VAL	N-CA-C	5.71	117.85	109.63
41	Q	43	LYS	N-CA-C	5.70	122.41	109.81
12	m	46	ILE	N-CA-C	5.70	115.89	110.53
8	i	91	LYS	CA-C-N	5.70	126.96	119.84
8	i	91	LYS	C-N-CA	5.70	126.96	119.84
41	Q	9	LYS	CA-C-N	5.68	126.94	119.84
41	Q	9	LYS	C-N-CA	5.68	126.94	119.84
2	c	150	GLN	N-CA-C	5.67	117.14	111.07
31	G	46	VAL	N-CA-C	5.67	119.15	112.35
11	l	113	ALA	N-CA-C	-5.67	106.17	114.39
4	e	118	ALA	N-CA-C	-5.64	104.02	112.54
52	3	1190	G	C2'-C3'-O3'	5.63	117.94	109.50
15	p	64	SER	N-CA-C	5.62	118.20	109.60
33	I	33	ILE	N-CA-C	5.61	116.17	110.05
5	f	47	ASN	N-CA-C	-5.61	105.16	112.23
53	1	1020	A	C2'-C3'-O3'	5.61	117.91	109.50
47	W	69	TYR	N-CA-C	-5.59	105.26	111.36
13	n	68	ALA	N-CA-C	-5.58	105.29	111.71
13	n	119	SER	N-CA-C	-5.58	104.00	111.87
33	I	5	GLY	CA-C-N	5.57	126.81	119.84
33	I	5	GLY	C-N-CA	5.57	126.81	119.84
50	Z	44	ARG	N-CA-C	-5.57	106.61	113.41
39	O	72	ARG	N-CA-C	5.54	117.39	109.14
12	m	118	LYS	N-CA-C	-5.52	104.90	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	I	10	LEU	N-CA-C	-5.52	105.42	111.82
9	j	44	TYR	N-CA-C	5.52	118.23	110.23
48	X	23	GLU	N-CA-C	-5.52	106.50	113.18
12	m	51	ARG	N-CA-C	-5.51	105.35	111.36
1	b	240	GLY	N-CA-C	5.51	126.24	113.18
48	X	9	PHE	N-CA-C	5.49	118.14	109.96
4	e	77	LYS	N-CA-C	5.48	117.33	110.91
51	a	15	VAL	N-CA-C	5.47	116.14	109.30
3	d	101	TYR	N-CA-C	-5.46	105.41	111.36
34	J	131	ASN	CA-C-N	5.46	126.67	119.84
34	J	131	ASN	C-N-CA	5.46	126.67	119.84
3	d	167	VAL	N-CA-C	5.46	115.50	107.75
48	X	18	VAL	N-CA-C	5.44	116.17	110.62
5	f	4	ALA	N-CA-C	-5.43	106.16	112.89
5	f	125	PRO	N-CA-C	-5.42	106.47	113.57
8	i	73	PRO	CA-C-N	5.42	125.42	119.89
8	i	73	PRO	C-N-CA	5.42	125.42	119.89
5	f	154	GLU	CA-C-N	5.39	126.58	119.84
5	f	154	GLU	C-N-CA	5.39	126.58	119.84
43	S	81	ILE	N-CA-C	5.39	115.59	110.53
16	q	53	LYS	N-CA-C	-5.37	106.23	112.89
11	l	136	GLU	N-CA-C	-5.37	105.59	111.82
11	l	95	LEU	N-CA-C	-5.33	106.28	112.89
48	X	20	LYS	N-CA-C	-5.33	106.73	113.18
8	i	86	LYS	N-CA-C	5.32	119.52	113.19
40	P	100	ASN	N-CA-C	-5.30	105.08	112.45
19	t	13	ALA	N-CA-C	5.29	114.93	108.11
16	q	54	ARG	N-CA-C	-5.28	105.19	111.69
49	Y	47	GLN	N-CA-C	-5.28	105.69	111.82
15	p	9	GLN	N-CA-C	5.28	120.65	113.37
51	a	6	LYS	N-CA-C	5.27	116.71	111.07
15	p	10	GLU	N-CA-C	-5.27	106.72	112.72
52	3	1300	G	N9-C1'-C2'	5.26	119.89	112.00
8	i	130	GLY	N-CA-C	-5.25	106.06	112.77
4	e	176	PHE	N-CA-C	5.24	118.35	111.28
7	h	114	GLU	N-CA-C	5.23	116.67	110.97
12	m	25	ASP	N-CA-C	5.22	118.01	110.28
47	W	20	ILE	N-CA-C	5.21	116.31	109.58
37	M	28	SER	N-CA-C	5.21	116.65	110.19
15	p	11	GLN	N-CA-C	-5.21	106.88	114.12
12	m	68	PHE	CA-C-N	5.21	126.35	119.84
12	m	68	PHE	C-N-CA	5.21	126.35	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	I	89	LEU	N-CA-C	-5.21	105.78	111.82
20	u	71	ILE	N-CA-C	5.21	116.08	108.58
24	y	57	LEU	N-CA-C	-5.21	105.67	112.23
11	l	60	ARG	N-CA-C	-5.20	106.99	113.55
23	x	5	GLN	N-CA-C	5.20	116.63	110.97
43	S	49	THR	N-CA-C	-5.19	105.80	111.82
26	B	15	ARG	N-CA-C	-5.18	106.46	112.89
20	u	75	ALA	N-CA-C	-5.18	106.49	114.16
47	W	60	ARG	N-CA-C	-5.17	105.72	111.36
22	w	40	LYS	N-CA-C	-5.14	106.96	113.18
38	N	64	ILE	N-CA-C	5.14	115.98	108.53
20	u	96	LYS	N-CA-C	-5.13	102.93	110.52
47	W	28	LEU	N-CA-C	5.12	116.86	111.28
42	R	78	ARG	N-CA-C	-5.12	105.78	112.23
8	i	111	THR	N-CA-C	-5.11	105.79	111.36
47	W	25	ILE	N-CA-C	5.10	117.47	111.09
38	N	103	VAL	N-CA-C	-5.08	105.92	113.39
32	H	170	GLY	N-CA-C	5.08	118.81	111.24
10	k	57	VAL	N-CA-C	5.07	115.21	108.11
6	g	39	ALA	N-CA-C	5.07	117.04	109.59
31	G	90	PHE	N-CA-C	5.07	116.51	108.96
40	P	65	ALA	N-CA-C	-5.07	105.84	111.36
32	H	171	ARG	N-CA-C	5.05	116.97	108.73
43	S	23	ARG	N-CA-C	-5.05	104.63	111.55
4	e	148	VAL	N-CA-C	-5.05	106.52	111.77
31	G	182	VAL	N-CA-C	5.04	115.84	108.53
32	H	129	PHE	N-CA-C	5.02	116.75	111.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2083	0	2157	90	0
2	c	1565	0	1616	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	d	1552	0	1619	53	0
4	e	1411	0	1447	58	0
5	f	1323	0	1374	38	0
6	g	1111	0	1148	42	0
7	h	989	0	1025	56	0
8	i	511	0	544	18	0
9	j	1129	0	1162	36	0
10	k	939	0	1012	48	0
11	l	1045	0	1117	41	0
12	m	1074	0	1157	40	0
13	n	961	0	1000	36	0
14	o	892	0	923	21	0
15	p	917	0	965	37	0
16	q	947	0	1022	23	0
17	r	816	0	839	30	0
18	s	857	0	922	21	0
19	t	739	0	807	22	0
20	u	780	0	834	21	0
21	v	753	0	780	22	0
22	w	575	0	592	31	0
23	x	625	0	655	24	0
24	y	509	0	543	13	0
25	z	449	0	491	13	0
26	B	444	0	461	17	0
27	C	410	0	440	13	0
28	D	377	0	418	12	0
29	E	504	0	574	18	0
30	F	302	0	343	13	0
31	G	1757	0	1787	44	0
32	H	1625	0	1699	37	0
33	I	1643	0	1710	59	0
34	J	1157	0	1199	42	0
35	K	818	0	808	37	0
36	L	1182	0	1240	37	0
37	M	979	0	1034	36	0
38	N	1022	0	1070	46	0
39	O	787	0	828	32	0
40	P	870	0	878	32	0
41	Q	955	0	1019	41	0
42	R	884	0	944	38	0
43	S	805	0	847	33	0
44	T	714	0	737	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	U	649	0	666	27	0
46	V	649	0	691	18	0
47	W	536	0	552	7	0
48	X	638	0	665	18	0
49	Y	665	0	714	25	0
50	Z	545	0	579	32	0
51	a	1027	0	1092	41	0
52	3	33012	0	16618	410	0
53	1	62317	0	31346	793	0
54	2	2568	0	1303	57	0
55	5	1640	0	836	15	0
55	6	1640	0	837	14	0
56	4	388	0	197	3	0
57	7	1557	0	789	9	0
58	5	10	0	10	0	0
All	All	149628	0	100682	2486	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (2486) 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'	1.28	1.15
11:l:48:ARG:HD2	53:1:666:A:H4'	1.44	0.99
31:G:112:ARG:HH12	52:3:1104:G:H5'	1.26	0.99
28:D:14:ARG:HG2	53:1:125:A:H5'	1.43	0.98
55:5:13:C:H2'	55:5:14:A:H5''	1.48	0.94
19:t:56:GLU:HG2	19:t:88:LYS:HG2	1.50	0.94
41:Q:56:LEU:HD12	41:Q:60:PHE:HB2	1.52	0.90
7:h:37:LYS:HG2	7:h:42:ARG:HH12	1.35	0.89
53:1:1053:C:H2'	53:1:1054:A:H5''	1.52	0.89
5:f:32:LEU:HD22	5:f:74:MET:HE3	1.56	0.88
46:V:61:ARG:HB3	46:V:75:VAL:HG22	1.56	0.88
15:p:31:VAL:HG21	15:p:40:GLN:HE21	1.39	0.87
45:U:36:VAL:HG22	45:U:53:ASP:HB3	1.58	0.86
31:G:56:LEU:HD11	31:G:216:VAL:HG13	1.59	0.85
5:f:102:ILE:HD11	5:f:116:LEU:HG	1.58	0.85
35:K:5:GLU:HB2	35:K:90:MET:HB2	1.58	0.84
15:p:21:PRO:HD3	15:p:49:ILE:HD12	1.57	0.84
12:m:127:LYS:HD3	53:1:1030:C:OP1	1.77	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:62:GLN:OE1	54:2:43:C:H5'	1.78	0.83
11:l:101:ILE:HG13	11:l:102:GLY:H	1.42	0.83
37:M:19:ALA:HB3	37:M:21:LYS:HZ2	1.43	0.83
52:3:405:U:H3'	52:3:406:G:H5'	1.60	0.83
6:g:28:ASN:HD22	53:1:2199:A:H4'	1.41	0.83
5:f:41:GLU:HB2	5:f:54:ARG:HE	1.45	0.82
29:E:18:LYS:HG3	53:1:651:G:H5'	1.62	0.82
10:k:6:THR:HG23	53:1:1666:G:H4'	1.62	0.82
52:3:1306:A:H61	52:3:1331:G:H1'	1.45	0.82
53:1:275:C:H2'	53:1:276:U:H4'	1.61	0.82
51:a:11:ILE:HG23	51:a:33:LEU:HD22	1.63	0.81
31:G:46:VAL:HG13	31:G:47:PRO:HD3	1.60	0.81
37:M:95:MET:HE2	37:M:129:ALA:HB1	1.60	0.81
8:i:123:ALA:HB1	53:1:1081:U:H4'	1.62	0.81
53:1:546:U:H2'	53:1:547:A:H4'	1.62	0.81
1:b:47:ARG:HD2	53:1:1806:C:H4'	1.63	0.80
53:1:1645:G:H5''	53:1:1646:C:H5'	1.64	0.80
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.62	0.80
24:y:2:LYS:HE2	24:y:56:LEU:HD21	1.62	0.80
53:1:1906:G:H2'	53:1:1907:G:H5''	1.65	0.79
13:n:53:THR:HG21	53:1:2840:C:H5''	1.61	0.79
22:w:8:ASN:HD21	53:1:2278:A:H5'	1.48	0.79
36:L:1:PRO:HD2	36:L:4:ARG:HB2	1.63	0.79
52:3:791:G:H22	52:3:1497:G:H4'	1.44	0.79
53:1:244:A:H62	53:1:254:G:H21	1.31	0.79
31:G:112:ARG:NH1	52:3:1104:G:H5'	1.97	0.78
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.65	0.78
22:w:66:GLU:HB2	22:w:75:PHE:HB2	1.66	0.78
2:c:1:MET:HG2	2:c:205:PRO:HG2	1.66	0.78
6:g:30:LEU:HA	6:g:35:LYS:HB2	1.62	0.78
4:e:77:LYS:HG2	55:5:57:A:H4'	1.66	0.78
51:a:172:HIS:HB2	53:1:2123:G:H4'	1.66	0.78
53:1:2286:G:H5''	53:1:2287:A:OP1	1.83	0.77
4:e:31:GLU:HG2	4:e:32:LYS:HD2	1.65	0.77
45:U:46:LYS:HD2	52:3:617:G:H5''	1.65	0.77
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.64	0.77
53:1:2055:C:H2'	53:1:2504:U:H5'	1.67	0.77
53:1:1020:A:H1'	53:1:1021:A:OP2	1.83	0.77
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.64	0.76
21:v:30:ILE:HG12	21:v:91:PHE:HB2	1.68	0.76
25:z:12:ALA:HB2	25:z:53:MET:HE1	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:109:LYS:HD2	11:l:126:ARG:HH11	1.49	0.76
3:d:69:ARG:HH22	53:1:2444:G:H5''	1.51	0.76
17:r:1:MET:HB2	17:r:43:ASN:HD22	1.50	0.76
6:g:97:ARG:HH21	53:1:2220:U:H5'	1.50	0.75
5:f:149:ALA:HA	5:f:152:ARG:HH22	1.50	0.75
1:b:28:PRO:HG3	1:b:62:ARG:HH21	1.51	0.75
44:T:68:TYR:HB2	52:3:754:C:H4'	1.69	0.75
7:h:56:ARG:HH21	53:1:1106:G:H1'	1.52	0.75
10:k:76:VAL:HG22	15:p:72:VAL:HG12	1.69	0.75
11:l:93:ASN:O	11:l:94:THR:HG22	1.87	0.75
33:l:8:LEU:HD12	52:3:429:U:H3'	1.66	0.74
52:3:1301:U:O2	52:3:1301:U:H2'	1.88	0.74
5:f:86:LEU:HB2	5:f:130:ILE:HB	1.68	0.74
34:J:55:VAL:HG23	34:J:56:PRO:HD3	1.67	0.74
50:Z:32:ARG:HG2	50:Z:33:ARG:HG2	1.70	0.74
2:c:151:THR:HB	2:c:152:PRO:HD3	1.70	0.74
38:N:23:GLY:H	38:N:60:LEU:HA	1.52	0.74
2:c:49:GLN:HE21	2:c:79:LEU:HD13	1.53	0.73
7:h:37:LYS:HG2	7:h:42:ARG:NH1	2.03	0.73
44:T:50:HIS:CE1	52:3:667:G:H4'	2.23	0.73
37:M:10:LEU:HD22	37:M:74:ILE:HD11	1.70	0.73
20:u:85:ARG:HD3	20:u:87:GLU:HG2	1.71	0.73
40:P:43:TRP:HE1	52:3:686:U:H4'	1.50	0.73
41:Q:49:ARG:HD2	41:Q:89:LEU:HD21	1.70	0.73
53:1:2391:G:H4'	53:1:2392:A:OP1	1.87	0.73
2:c:116:LYS:HG3	2:c:165:MET:HE2	1.71	0.73
7:h:26:VAL:HG13	7:h:82:ILE:HG23	1.68	0.73
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.69	0.73
3:d:63:LYS:HD2	53:1:2444:G:OP2	1.89	0.73
8:i:133:ARG:NH2	53:1:1079:C:H4'	2.03	0.73
2:c:107:VAL:HG22	2:c:108:ASP:H	1.53	0.72
2:c:33:ARG:HD3	2:c:73:VAL:HB	1.70	0.72
4:e:131:VAL:HG23	4:e:151:LEU:H	1.54	0.72
52:3:484:G:H4'	52:3:485:U:H5''	1.71	0.72
7:h:2:ALA:O	53:1:1043:C:H5''	1.90	0.72
5:f:2:ARG:HH12	53:1:1113:U:H5'	1.54	0.72
14:o:3:LYS:HE3	54:2:29:A:O3'	1.90	0.72
49:Y:9:ARG:HG3	52:3:108:G:H1	1.53	0.72
53:1:2277:G:H2'	53:1:2278:A:H5''	1.71	0.72
53:1:2298:A:H62	53:1:2318:G:H21	1.38	0.72
36:L:128:GLU:HG3	36:L:130:LYS:HE2	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:35:VAL:HG11	10:k:69:VAL:HG13	1.71	0.71
2:c:27:ILE:HD12	2:c:201:LEU:HD12	1.73	0.71
2:c:149:ASN:HD22	53:1:2575:C:H5''	1.56	0.71
1:b:238:ASN:HD21	53:1:2595:G:H1	1.38	0.71
15:p:62:LYS:HB3	15:p:69:VAL:HG13	1.72	0.71
53:1:2553:G:H3'	53:1:2554:U:H5''	1.72	0.71
52:3:1496:C:H1'	52:3:1517:G:H22	1.54	0.71
40:P:30:ILE:H	40:P:30:ILE:HD12	1.56	0.70
52:3:1200:C:H5''	52:3:1201:A:H3'	1.73	0.70
53:1:572:A:H61	53:1:2029:G:H21	1.37	0.70
43:S:25:GLU:HA	43:S:29:ILE:HD13	1.72	0.70
52:3:1259:C:H3'	52:3:1260:G:H5''	1.74	0.70
53:1:1597:A:H5''	53:1:1598:A:H5'	1.71	0.70
7:h:53:ARG:HD3	53:1:1084:A:OP1	1.92	0.70
17:r:79:ARG:NH2	53:1:572:A:H5'	2.06	0.70
12:m:50:ARG:HA	12:m:53:MET:HE3	1.72	0.70
32:H:102:ILE:H	32:H:102:ILE:HD12	1.56	0.70
36:L:80:GLY:HA3	56:4:11:U:O2'	1.92	0.70
22:w:68:LYS:HD3	22:w:69:GLY:H	1.55	0.69
35:K:3:HIS:HB2	35:K:92:THR:HA	1.74	0.69
52:3:327:A:O2'	52:3:328:C:H4'	1.92	0.69
53:1:2831:G:H1'	53:1:2883:A:H2'	1.72	0.69
53:1:2427:C:H5''	53:1:2429:G:H5'	1.75	0.69
10:k:71:ARG:HB3	10:k:72:PRO:HD2	1.74	0.69
55:5:13:C:C2'	55:5:14:A:H5''	2.21	0.69
8:i:126:ARG:O	8:i:129:GLU:HG3	1.92	0.69
10:k:2:ILE:HB	10:k:33:ALA:HB3	1.75	0.69
53:1:1837:C:H2'	53:1:1899:A:H61	1.57	0.69
11:l:101:ILE:HG13	11:l:102:GLY:N	2.07	0.69
37:M:21:LYS:HE3	52:3:827:U:H5''	1.75	0.69
28:D:34:ARG:HD3	53:1:467:G:OP2	1.92	0.69
40:P:43:TRP:NE1	52:3:686:U:H4'	2.08	0.69
31:G:103:TRP:HA	31:G:106:VAL:HG22	1.74	0.69
41:Q:79:ILE:HD12	41:Q:103:CYS:HB2	1.74	0.68
5:f:94:ARG:HB2	5:f:105:SER:HB2	1.74	0.68
4:e:23:SER:HB2	4:e:26:GLN:HG3	1.76	0.68
28:D:3:ARG:HE	28:D:4:THR:H	1.42	0.68
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.59	0.68
52:3:1306:A:N6	52:3:1331:G:H1'	2.08	0.68
53:1:1415:U:H2'	53:1:1416:G:H4'	1.74	0.68
54:2:72:G:H21	54:2:104:A:H62	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:78:A:H62	54:2:98:G:H21	1.39	0.68
10:k:102:PRO:HB3	10:k:121:GLU:HB3	1.76	0.68
28:D:12:ARG:HE	28:D:44:VAL:HG21	1.59	0.68
31:G:67:LEU:HD21	31:G:153:MET:HE1	1.74	0.68
34:J:133:ILE:H	34:J:133:ILE:HD12	1.59	0.68
53:1:2584:U:H2'	53:1:2585:U:H2'	1.75	0.68
32:H:171:ARG:HG2	32:H:173:PRO:HD3	1.74	0.68
17:r:79:ARG:O	17:r:80:ARG:HG2	1.94	0.67
45:U:31:ARG:HB2	52:3:310:G:H5''	1.77	0.67
52:3:208:U:H2'	52:3:210:C:H1'	1.75	0.67
45:U:40:ASN:HB3	45:U:43:ALA:HB2	1.76	0.67
53:1:1801:A:H5''	53:1:2203:U:H2'	1.76	0.67
53:1:1991:U:H2'	53:1:1992:G:H5''	1.76	0.67
13:n:22:ARG:HG3	13:n:70:THR:HA	1.77	0.67
31:G:134:LEU:HA	31:G:137:THR:HG22	1.75	0.67
41:Q:81:ILE:HG22	41:Q:96:THR:HG22	1.76	0.67
53:1:1912:A:H62	53:1:1917:U:H3	1.42	0.67
20:u:33:VAL:HG13	20:u:66:VAL:HG22	1.77	0.67
53:1:310:A:O2'	53:1:311:A:H5''	1.95	0.67
54:2:3:C:H3'	54:2:4:C:H5''	1.77	0.67
31:G:166:ASP:HB3	31:G:190:SER:HA	1.77	0.67
36:L:41:ILE:HG23	36:L:116:ALA:HA	1.77	0.67
52:3:1201:A:H1'	52:3:1202:U:OP2	1.94	0.67
53:1:615:U:H5''	53:1:616:A:OP2	1.95	0.67
53:1:1053:C:C2'	53:1:1054:A:H5''	2.25	0.67
53:1:1026:G:H2'	53:1:1027:A:H8	1.58	0.67
34:J:61:LYS:HE2	34:J:65:LYS:HE2	1.76	0.67
35:K:2:ARG:HD2	35:K:92:THR:HG21	1.76	0.66
53:1:1476:U:H3	53:1:1515:A:H62	1.42	0.66
9:j:58:ASN:HD21	9:j:128:ASN:HB2	1.60	0.66
32:H:196:GLY:H	52:3:1057:G:H4'	1.59	0.66
6:g:5:LEU:HD23	6:g:15:LEU:H	1.61	0.66
14:o:51:ALA:HB3	14:o:78:VAL:HG22	1.77	0.66
52:3:428:G:H4'	52:3:429:U:O5'	1.95	0.66
53:1:1796:U:H2'	53:1:1797:G:H8	1.60	0.66
22:w:68:LYS:NZ	54:2:11:C:H3'	2.10	0.66
48:X:5:LYS:HG3	48:X:6:LYS:HG2	1.77	0.66
3:d:149:ILE:HG23	3:d:188:MET:HG2	1.78	0.66
19:t:13:ALA:HB1	24:y:33:ALA:HB1	1.76	0.66
52:3:1130:A:H61	52:3:1144:G:H1'	1.60	0.66
7:h:57:ASN:HB2	7:h:62:ARG:HD2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:v:9:ARG:HH21	21:v:11:GLU:HB2	1.60	0.66
44:T:64:LYS:HD3	52:3:755:G:OP2	1.96	0.66
49:Y:68:LYS:CE	52:3:185:U:H4'	2.26	0.66
53:1:1186:G:H2'	53:1:1187:G:O4'	1.96	0.66
12:m:35:ALA:HA	12:m:128:THR:HG22	1.78	0.66
52:3:1033:G:H2'	52:3:1034:G:H5''	1.77	0.66
7:h:42:ARG:NH2	8:i:117:THR:HB	2.10	0.65
22:w:68:LYS:HZ1	54:2:11:C:H3'	1.60	0.65
53:1:49:A:H5'	53:1:51:G:O4'	1.97	0.65
53:1:310:A:C2'	53:1:311:A:H5''	2.26	0.65
20:u:17:ASP:HB3	20:u:20:LYS:HE2	1.78	0.65
45:U:14:ARG:HH22	52:3:617:G:H21	1.44	0.65
47:W:58:ILE:HG23	47:W:67:LEU:HD13	1.78	0.65
53:1:742:A:H2'	53:1:743:A:C8	2.32	0.65
7:h:61:ARG:HB3	53:1:1046:A:H4'	1.78	0.65
42:R:113:LYS:NZ	55:5:44:A:H4'	2.10	0.65
21:v:19:ARG:HG3	21:v:20:LEU:HD12	1.78	0.65
49:Y:68:LYS:HE2	52:3:185:U:H4'	1.77	0.65
50:Z:48:LYS:HG3	52:3:723:U:H5	1.61	0.65
10:k:3:GLN:HE21	53:1:1666:G:H1'	1.61	0.65
17:r:79:ARG:HG3	17:r:80:ARG:NH1	2.12	0.65
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.78	0.65
35:K:7:VAL:HG12	35:K:61:LEU:HD13	1.78	0.65
53:1:1133:A:H4'	53:1:1134:A:H5''	1.79	0.65
22:w:33:ILE:HG22	22:w:34:VAL:HG23	1.79	0.65
41:Q:23:LEU:HD22	41:Q:29:LYS:HZ1	1.61	0.65
12:m:109:PRO:HD2	12:m:112:LEU:HD23	1.78	0.65
7:h:33:VAL:HG22	7:h:34:THR:H	1.62	0.64
52:3:29:U:O2'	52:3:30:U:H5'	1.96	0.64
51:a:205:LYS:HD2	53:1:1861:G:H5''	1.77	0.64
13:n:2:ARG:HA	13:n:5:LYS:HB2	1.78	0.64
15:p:59:THR:HG22	15:p:72:VAL:HG23	1.79	0.64
35:K:29:ILE:HG22	35:K:34:GLY:HA3	1.80	0.64
35:K:52:ASN:C	35:K:53:LYS:HD3	2.22	0.64
53:1:2048:G:C3'	53:1:2049:G:H5''	2.28	0.64
1:b:153:LEU:HD13	1:b:175:LEU:HD21	1.78	0.64
4:e:84:ILE:HG21	53:1:2312:U:H5'	1.79	0.64
7:h:27:VAL:HG13	7:h:83:ALA:HB3	1.80	0.64
19:t:74:ILE:H	19:t:74:ILE:HD12	1.63	0.64
33:I:127:ARG:CZ	52:3:619:U:H4'	2.26	0.64
37:M:19:ALA:HB3	37:M:21:LYS:NZ	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:189:G:H2'	53:1:205:G:H22	1.62	0.64
17:r:35:PHE:HB2	17:r:59:ILE:HB	1.80	0.64
33:I:131:ILE:H	33:I:131:ILE:HD12	1.63	0.64
4:e:24:VAL:HG12	54:2:55:U:H4'	1.80	0.64
42:R:79:LEU:HD12	42:R:82:LEU:HD12	1.79	0.64
54:2:3:C:C3'	54:2:4:C:H5''	2.28	0.64
6:g:96:THR:OG1	6:g:112:LYS:HE3	1.97	0.64
53:1:1863:G:H4'	53:1:2411:A:H4'	1.79	0.64
4:e:107:VAL:CG1	4:e:108:PRO:HD3	2.28	0.63
10:k:55:GLY:O	53:1:1952:A:H5'	1.97	0.63
12:m:55:ARG:HD2	53:1:2469:A:H4'	1.79	0.63
15:p:31:VAL:HG21	15:p:40:GLN:NE2	2.11	0.63
40:P:116:PRO:HB3	52:3:676:A:H1'	1.80	0.63
37:M:48:PHE:HB2	37:M:58:LEU:HD11	1.80	0.63
41:Q:97:VAL:HG13	41:Q:100:ALA:HB2	1.81	0.63
52:3:758:C:H4'	52:3:880:C:H4'	1.80	0.63
6:g:116:ARG:HE	6:g:117:LEU:H	1.46	0.63
53:1:1300:G:H4'	53:1:1301:A:H5'	1.80	0.63
1:b:159:THR:HG21	53:1:1819:A:H5''	1.81	0.63
7:h:56:ARG:HH21	7:h:81:LEU:HD11	1.63	0.63
23:x:29:LEU:HD23	53:1:2230:G:H5''	1.80	0.63
15:p:27:VAL:HG12	15:p:29:VAL:HG13	1.81	0.63
35:K:78:PHE:HA	35:K:84:VAL:HG11	1.81	0.63
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.79	0.63
43:S:63:CYS:HB3	43:S:67:GLY:H	1.63	0.63
53:1:1796:U:H2'	53:1:1797:G:C8	2.34	0.63
53:1:2048:G:H2'	53:1:2049:G:H5''	1.81	0.63
32:H:128:MET:HB3	32:H:131:ARG:HB3	1.79	0.63
39:O:42:LEU:HD23	39:O:71:LEU:HD22	1.80	0.63
40:P:92:ARG:HD3	50:Z:24:LYS:HZ2	1.64	0.63
55:5:20:U:H3'	55:5:21:A:H5'	1.81	0.63
10:k:103:VAL:HB	10:k:107:LEU:HD22	1.79	0.63
19:t:51:PHE:O	19:t:52:GLU:HG2	1.99	0.63
37:M:28:SER:HB2	37:M:56:PRO:HB2	1.81	0.63
39:O:65:TYR:HB3	43:S:95:LEU:HD11	1.81	0.63
52:3:1158:C:H2'	52:3:1159:U:H4'	1.80	0.63
7:h:56:ARG:NH2	53:1:1106:G:H1'	2.14	0.62
31:G:216:VAL:O	31:G:220:VAL:HG23	1.98	0.62
7:h:38:MET:HA	7:h:42:ARG:HD3	1.82	0.62
8:i:99:LYS:HB2	8:i:140:GLU:HB2	1.81	0.62
22:w:33:ILE:HG21	22:w:76:ILE:HG21	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:4:LEU:HD22	52:3:406:G:H5''	1.80	0.62
49:Y:26:MET:HB3	52:3:1458:G:H5'	1.81	0.62
53:1:917:A:H5''	53:1:2268:A:H61	1.64	0.62
53:1:1373:A:H4'	53:1:2212:A:H1'	1.79	0.62
1:b:16:VAL:HB	1:b:203:VAL:HG12	1.81	0.62
15:p:88:ARG:HH12	15:p:114:ASN:HD21	1.47	0.62
35:K:40:GLU:HB3	35:K:61:LEU:HD23	1.81	0.62
39:O:57:VAL:O	39:O:58:ASN:HB2	1.98	0.62
40:P:122:PRO:HB2	50:Z:33:ARG:HA	1.81	0.62
43:S:19:TYR:HB2	43:S:54:SER:OG	2.00	0.62
55:6:54:U:H3	55:6:58:A:H62	1.47	0.62
18:s:83:LYS:HD3	18:s:95:ARG:HB3	1.82	0.62
38:N:114:LYS:HE2	52:3:1187:G:H5'	1.81	0.62
53:1:226:A:H2'	53:1:227:A:O4'	2.00	0.62
53:1:2834:G:H2'	53:1:2879:A:H61	1.64	0.62
7:h:55:VAL:HA	53:1:1084:A:H4'	1.82	0.62
17:r:74:ILE:HB	17:r:87:GLN:HB2	1.82	0.62
39:O:8:ILE:HB	39:O:74:VAL:HB	1.81	0.62
54:2:65:U:H3'	54:2:108:A:H61	1.63	0.62
6:g:6:LEU:HD11	6:g:37:VAL:HG23	1.80	0.62
43:S:36:SER:HA	43:S:40:ARG:HD3	1.80	0.62
31:G:22:TRP:HE1	52:3:830:G:H5'	1.64	0.62
32:H:175:HIS:CE1	52:3:1108:G:H5'	2.35	0.62
36:L:74:VAL:HB	36:L:85:GLN:HB3	1.82	0.62
52:3:396:C:H2'	52:3:397:A:H5''	1.80	0.62
52:3:1271:A:H5'	52:3:1314:C:H5''	1.82	0.62
53:1:2698:U:H2'	53:1:2699:C:C6	2.35	0.62
9:j:35:ARG:HB2	9:j:54:ILE:HD11	1.82	0.62
17:r:11:GLN:HE22	17:r:39:LEU:HD22	1.64	0.62
17:r:76:LYS:HB3	17:r:85:LYS:HB2	1.82	0.62
27:C:10:LEU:HD21	27:C:33:LEU:HB2	1.80	0.61
52:3:1481:U:H2'	52:3:1482:G:C8	2.35	0.61
53:1:2747:G:H21	53:1:2757:A:H62	1.48	0.61
53:1:215:G:H4'	53:1:216:A:H4'	1.81	0.61
32:H:175:HIS:ND1	52:3:1108:G:H5'	2.16	0.61
42:R:24:VAL:HG23	42:R:28:ARG:HB3	1.81	0.61
4:e:145:VAL:HG22	4:e:147:ARG:H	1.65	0.61
9:j:81:ILE:HG21	53:1:2514:U:H5''	1.80	0.61
19:t:40:LYS:HD3	19:t:58:VAL:HG23	1.82	0.61
21:v:60:VAL:HG22	21:v:73:LYS:HD3	1.82	0.61
52:3:516:U:H3	52:3:533:A:H62	1.47	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:542:C:H2'	53:1:543:G:H5''	1.82	0.61
15:p:93:LYS:HD2	15:p:96:LEU:HD23	1.82	0.61
24:y:47:ARG:O	24:y:50:VAL:HG12	2.01	0.61
34:J:51:LYS:H	34:J:61:LYS:HD3	1.65	0.61
37:M:12:ARG:HD3	52:3:826:C:H4'	1.82	0.61
53:1:1344:U:H3'	53:1:1345:C:H5'	1.81	0.61
5:f:172:GLU:HG2	5:f:173:ALA:N	2.14	0.61
51:a:174:THR:HB	53:1:2124:G:H5''	1.83	0.61
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.00	0.61
26:B:42:ILE:HD12	26:B:46:GLY:HA2	1.83	0.61
41:Q:36:VAL:HG13	41:Q:52:CYS:HB3	1.81	0.61
52:3:1304:G:H21	52:3:1333:A:H62	1.48	0.61
52:3:1502:A:H5'	52:3:1504:G:N7	2.15	0.61
53:1:1906:G:C2'	53:1:1907:G:H5''	2.30	0.61
1:b:8:THR:HG21	53:1:727:A:H2	1.64	0.61
27:C:5:ARG:HA	27:C:27:ARG:HH22	1.66	0.61
38:N:114:LYS:HE2	52:3:1187:G:C5'	2.30	0.61
52:3:1497:G:O2'	52:3:1498:U:H5'	2.00	0.61
5:f:173:ALA:O	5:f:174:LYS:HG2	2.00	0.61
33:I:150:LYS:HD3	33:I:154:VAL:HB	1.83	0.61
37:M:6:ILE:HD12	37:M:6:ILE:H	1.64	0.61
52:3:70:U:H5''	52:3:71:A:OP1	2.01	0.61
53:1:581:C:H2'	53:1:582:A:C8	2.36	0.61
4:e:79:ARG:HD2	4:e:80:GLN:H	1.65	0.60
4:e:102:LEU:HA	4:e:106:ALA:HB3	1.83	0.60
12:m:4:PRO:HB2	12:m:7:THR:HG22	1.83	0.60
33:I:60:VAL:O	33:I:63:ILE:HG22	2.01	0.60
42:R:3:ILE:HD13	42:R:7:ASN:HD22	1.65	0.60
51:a:37:LYS:HE2	53:1:2128:G:OP2	2.01	0.60
54:2:3:C:H2'	54:2:4:C:H5''	1.83	0.60
4:e:31:GLU:H	4:e:157:THR:HA	1.66	0.60
14:o:76:LYS:O	14:o:80:GLU:HG2	2.01	0.60
43:S:74:ARG:HH22	43:S:75:LYS:HD3	1.65	0.60
53:1:1322:A:H61	53:1:1333:G:H21	1.47	0.60
7:h:56:ARG:HB2	53:1:1084:A:H1'	1.82	0.60
33:I:119:HIS:CG	52:3:438:U:H4'	2.37	0.60
36:L:77:ARG:HG3	52:3:1381:U:O2	2.01	0.60
44:T:72:LYS:HD3	44:T:76:ARG:NH2	2.17	0.60
53:1:745:G:O2'	53:1:748:G:H1'	2.02	0.60
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.82	0.60
26:B:10:SER:HB3	26:B:14:MET:HE2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:55:MET:HE1	53:1:2392:A:N3	2.16	0.60
20:u:93:ARG:HB2	20:u:102:ILE:HD12	1.83	0.60
3:d:69:ARG:NH2	53:1:2444:G:H5''	2.15	0.60
47:W:29:LYS:O	47:W:29:LYS:HD3	2.01	0.60
2:c:146:ILE:HD13	53:1:2051:A:H4'	1.84	0.60
9:j:37:ARG:HH21	53:1:1007:C:H5''	1.67	0.60
53:1:119:A:H4'	53:1:120:U:H5'	1.83	0.60
53:1:2128:G:H21	53:1:2173:A:H1'	1.66	0.60
53:1:2514:U:H2'	53:1:2515:C:C6	2.37	0.60
53:1:2657:A:H62	53:1:2664:G:H21	1.48	0.60
1:b:165:ALA:H	1:b:172:THR:HB	1.67	0.60
5:f:86:LEU:HD22	5:f:147:LEU:HD12	1.83	0.60
9:j:37:ARG:NH2	53:1:1007:C:H5''	2.17	0.60
27:C:5:ARG:HH12	53:1:2285:C:H3'	1.66	0.60
37:M:5:PRO:HG2	37:M:6:ILE:HD12	1.82	0.60
38:N:51:LEU:HD12	38:N:56:MET:HB2	1.83	0.60
53:1:2296:U:H5''	53:1:2297:A:OP1	2.00	0.60
10:k:7:MET:HB2	53:1:1667:G:OP1	2.02	0.60
3:d:118:LEU:HD11	3:d:188:MET:HE2	1.83	0.59
30:F:19:ARG:HH22	30:F:26:ILE:HG21	1.67	0.59
33:I:70:GLN:HG3	52:3:402:G:OP1	2.02	0.59
53:1:2287:A:O2'	53:1:2288:A:H2'	2.01	0.59
4:e:84:ILE:HD11	53:1:2311:A:H1'	1.84	0.59
7:h:43:LYS:HD2	7:h:98:GLU:HG2	1.83	0.59
51:a:185:LEU:HA	51:a:188:ASN:HD22	1.67	0.59
52:3:1500:A:H5''	52:3:1508:A:H5''	1.83	0.59
53:1:2156:G:H2'	53:1:2157:G:H5'	1.84	0.59
42:R:78:ARG:HH12	42:R:82:LEU:HD11	1.68	0.59
53:1:554:U:H2'	53:1:555:G:O4'	2.02	0.59
53:1:1664:A:H61	53:1:1996:C:H42	1.49	0.59
12:m:34:LYS:HE3	12:m:131:VAL:HG11	1.84	0.59
14:o:49:VAL:HG21	14:o:82:ALA:HA	1.84	0.59
15:p:110:LYS:HD3	15:p:111:GLU:H	1.66	0.59
13:n:103:ARG:HG2	13:n:105:GLY:H	1.66	0.59
39:O:56:HIS:ND1	39:O:57:VAL:HG23	2.17	0.59
51:a:215:SER:OG	53:1:2176:A:H4'	2.02	0.59
57:7:43:C:H2'	57:7:44:G:C8	2.37	0.59
33:I:119:HIS:ND1	52:3:438:U:H4'	2.17	0.59
4:e:35:LEU:HB2	4:e:88:VAL:HB	1.83	0.59
16:q:87:VAL:HG13	17:r:49:ILE:HD11	1.85	0.59
17:r:78:ARG:HG3	17:r:81:LYS:HB2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:86:MET:HB2	18:s:96:ILE:HD13	1.83	0.59
37:M:105:THR:HB	37:M:120:LEU:HD11	1.85	0.59
13:n:101:GLY:H	13:n:110:MET:HB2	1.68	0.59
14:o:11:ALA:HB2	14:o:96:GLY:N	2.18	0.59
16:q:48:ASP:HA	16:q:51:GLN:HB3	1.85	0.59
42:R:16:ILE:HG21	52:3:1302:C:OP2	2.03	0.59
52:3:150:U:H3	52:3:171:A:H62	1.50	0.59
53:1:2480:C:H2'	53:1:2481:G:O4'	2.03	0.59
2:c:43:ASP:OD1	53:1:2784:U:H4'	2.03	0.59
23:x:17:ARG:HH11	23:x:21:LEU:HD11	1.68	0.59
31:G:46:VAL:HG13	31:G:47:PRO:CD	2.33	0.59
34:J:108:GLY:H	52:3:9:G:H5'	1.67	0.59
38:N:104:THR:HG22	38:N:106:ASP:H	1.67	0.59
52:3:1379:G:O2'	52:3:1380:U:H5'	2.03	0.59
57:7:14:A:H61	57:7:21:A:H2	1.51	0.59
19:t:61:LEU:HB3	53:1:1341:G:H5'	1.85	0.59
33:I:80:ARG:NH1	52:3:614:C:OP2	2.36	0.59
34:J:35:LEU:HD11	34:J:136:VAL:HG21	1.83	0.59
35:K:15:SER:O	35:K:18:VAL:HG22	2.03	0.59
52:3:77:A:H2'	52:3:78:A:H8	1.68	0.59
53:1:161:A:H3'	53:1:162:U:H5''	1.84	0.59
53:1:1013:C:H2'	53:1:1014:A:H8	1.66	0.59
1:b:41:GLY:HA3	1:b:53:ILE:HG21	1.85	0.58
48:X:49:ALA:HB1	48:X:56:HIS:HB3	1.85	0.58
1:b:154:ALA:HB2	1:b:161:VAL:HG23	1.84	0.58
24:y:2:LYS:HE3	53:1:77:G:O3'	2.03	0.58
32:H:166:TRP:HZ3	32:H:168:ARG:HG2	1.69	0.58
32:H:198:LYS:HE3	52:3:1058:G:H5''	1.84	0.58
33:I:32:LYS:HG3	52:3:413:G:O6	2.02	0.58
35:K:47:LEU:HD21	35:K:57:ALA:HB3	1.84	0.58
53:1:1810:A:H2'	53:1:1811:G:O4'	2.04	0.58
22:w:62:LYS:HD2	22:w:81:GLU:HG3	1.85	0.58
36:L:24:LYS:O	36:L:28:ILE:HG13	2.02	0.58
52:3:1218:C:H2'	52:3:1219:A:C8	2.38	0.58
33:I:9:LYS:HE3	52:3:428:G:H5''	1.85	0.58
43:S:92:ILE:H	43:S:92:ILE:HD12	1.67	0.58
49:Y:38:ILE:HA	49:Y:85:LEU:HD21	1.86	0.58
52:3:1005:A:H2'	52:3:1006:G:O4'	2.04	0.58
36:L:69:ARG:HE	36:L:95:ARG:NE	2.02	0.58
38:N:94:ARG:O	38:N:98:ARG:HG2	2.03	0.58
39:O:11:LYS:HB3	39:O:71:LEU:HG	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:112:ARG:HD3	52:3:1229:A:OP1	2.02	0.58
43:S:55:SER:HB3	43:S:58:ARG:HE	1.69	0.58
44:T:20:ASP:OD1	52:3:751:U:H5'	2.03	0.58
52:3:769:G:H4'	52:3:1513:A:H4'	1.85	0.58
52:3:1512:U:H2'	52:3:1513:A:C8	2.39	0.58
53:1:807:U:H2'	53:1:808:G:C8	2.38	0.58
16:q:49:ARG:HH21	17:r:72:VAL:HG13	1.68	0.58
32:H:78:LYS:HD3	32:H:79:LYS:HG2	1.85	0.58
33:I:97:LEU:HB2	33:I:134:TYR:HB3	1.86	0.58
38:N:122:ARG:HH12	52:3:1343:G:H4'	1.69	0.58
17:r:80:ARG:HG2	17:r:80:ARG:HH11	1.69	0.58
32:H:127:VAL:HG22	32:H:128:MET:H	1.67	0.58
36:L:26:VAL:HG12	36:L:42:VAL:HG21	1.85	0.58
21:v:16:ALA:HA	21:v:19:ARG:NH1	2.19	0.58
33:I:27:ILE:HG22	33:I:29:THR:HG23	1.84	0.58
50:Z:36:PHE:HB2	50:Z:40:PRO:HD3	1.86	0.58
55:6:16:C:H4'	55:6:60:U:H1'	1.86	0.58
6:g:8:LYS:O	6:g:9:VAL:C	2.46	0.58
9:j:81:ILE:H	9:j:81:ILE:HD12	1.69	0.58
10:k:1:MET:HE1	53:1:1665:A:N3	2.19	0.58
10:k:115:ILE:H	10:k:115:ILE:HD12	1.69	0.58
23:x:13:THR:HG21	53:1:188:G:H5'	1.86	0.58
34:J:79:THR:HA	34:J:121:ASN:HD21	1.69	0.58
38:N:18:VAL:HG22	38:N:64:ILE:HD13	1.86	0.58
42:R:25:GLY:H	52:3:1329:A:H5''	1.69	0.58
4:e:163:GLU:OE2	4:e:164:GLU:HG3	2.03	0.58
21:v:42:LEU:H	21:v:42:LEU:HD23	1.69	0.57
31:G:116:LEU:HG	31:G:140:LEU:HD12	1.84	0.57
35:K:97:THR:HG23	35:K:98:GLU:HG2	1.85	0.57
49:Y:25:SER:OG	52:3:1458:G:H5''	2.03	0.57
51:a:50:ILE:HD13	51:a:59:VAL:HG23	1.86	0.57
51:a:206:GLY:H	53:1:1861:G:P	2.27	0.57
53:1:792:A:H3'	53:1:793:A:H5'	1.86	0.57
1:b:147:PRO:HG3	1:b:187:CYS:HA	1.85	0.57
8:i:118:GLY:HA2	53:1:1082:U:H5'	1.87	0.57
52:3:667:G:H2'	52:3:668:G:C8	2.39	0.57
53:1:395:U:H2'	53:1:396:G:H8	1.69	0.57
4:e:135:ILE:H	4:e:135:ILE:HD12	1.69	0.57
15:p:105:LYS:HA	15:p:108:ARG:HD3	1.86	0.57
45:U:36:VAL:CG2	45:U:53:ASP:HB3	2.31	0.57
53:1:2248:C:H2'	53:1:2249:U:H5'	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:41:SER:HB2	53:1:2124:G:O2'	2.04	0.57
2:c:8:LYS:HB2	2:c:201:LEU:HD11	1.86	0.57
39:O:52:LEU:HD21	39:O:59:LYS:HD2	1.85	0.57
50:Z:30:GLU:HA	50:Z:32:ARG:HH11	1.70	0.57
3:d:167:VAL:HG22	3:d:168:ASP:N	2.20	0.57
5:f:148:ARG:HH22	53:1:2745:C:H5'	1.70	0.57
8:i:116:MET:HE1	53:1:1059:G:H4'	1.85	0.57
12:m:11:LYS:HD3	12:m:86:LYS:HG2	1.86	0.57
23:x:12:VAL:HG23	23:x:28:PHE:HD2	1.70	0.57
38:N:47:VAL:HG23	38:N:48:ARG:HE	1.69	0.57
2:c:128:ARG:NE	53:1:1995:U:OP1	2.38	0.57
31:G:165:ALA:HB3	31:G:190:SER:HB3	1.87	0.57
34:J:121:ASN:OD1	34:J:122:VAL:HG13	2.05	0.57
1:b:239:PHE:HB3	53:1:1903:G:OP1	2.05	0.57
4:e:107:VAL:HG12	4:e:108:PRO:HD3	1.87	0.57
29:E:1:PRO:H2	53:1:591:U:H1'	1.70	0.57
35:K:72:ASP:O	35:K:75:GLU:HG3	2.05	0.57
37:M:86:LYS:HE2	37:M:90:GLU:HB3	1.86	0.57
52:3:667:G:H2'	52:3:668:G:H8	1.70	0.57
11:l:17:LYS:HD3	53:1:663:G:H5''	1.87	0.57
13:n:98:LEU:HB2	13:n:112:TYR:HB2	1.86	0.57
36:L:142:ARG:HD3	55:6:41:C:H4'	1.87	0.57
53:1:2277:G:C2'	53:1:2278:A:H5''	2.35	0.57
9:j:136:GLN:N	9:j:137:PRO:HD3	2.20	0.57
13:n:3:HIS:O	13:n:4:ARG:HB2	2.03	0.57
49:Y:9:ARG:CG	52:3:108:G:H1	2.17	0.57
53:1:655:A:H4'	53:1:656:G:H5'	1.86	0.57
14:o:51:ALA:HB2	14:o:81:ARG:HD2	1.87	0.56
49:Y:38:ILE:HG23	49:Y:85:LEU:HD11	1.86	0.56
53:1:503:A:H4'	53:1:505:A:H5''	1.85	0.56
2:c:157:LYS:HE2	53:1:2619:C:OP1	2.05	0.56
12:m:42:THR:HB	12:m:93:VAL:HG12	1.87	0.56
16:q:3:VAL:HG12	53:1:1199:U:H1'	1.87	0.56
21:v:6:ALA:HB2	21:v:63:ILE:HD11	1.87	0.56
22:w:39:THR:H	53:1:2331:G:H4'	1.70	0.56
27:C:5:ARG:HE	27:C:23:THR:HG23	1.71	0.56
31:G:66:ILE:N	31:G:66:ILE:HD12	2.20	0.56
33:I:7:LYS:HA	33:I:10:LEU:HD13	1.87	0.56
38:N:12:LYS:HG2	52:3:1371:G:OP1	2.05	0.56
45:U:1:MET:HB2	52:3:135:C:N3	2.20	0.56
53:1:1201:U:H2'	53:1:1202:G:H8	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:4:LEU:HD11	52:3:405:U:C5	2.40	0.56
53:1:1827:U:O2'	53:1:1828:G:H5'	2.05	0.56
53:1:2163:A:N3	53:1:2163:A:H2'	2.21	0.56
53:1:2286:G:H4'	53:1:2287:A:O5'	2.06	0.56
5:f:157:LYS:HE2	53:1:2659:G:OP1	2.06	0.56
6:g:11:ASN:O	6:g:12:LEU:HD12	2.05	0.56
10:k:40:LYS:HD2	10:k:57:VAL:HG12	1.87	0.56
15:p:93:LYS:HE2	53:1:1754:A:OP1	2.06	0.56
16:q:109:VAL:HG12	16:q:113:LYS:HE2	1.88	0.56
53:1:1055:G:H1'	53:1:1084:A:H61	1.71	0.56
53:1:2677:G:H2'	53:1:2678:C:C6	2.40	0.56
1:b:230:PRO:HD2	1:b:246:PRO:HA	1.87	0.56
1:b:261:ARG:HG3	1:b:262:THR:HG23	1.88	0.56
10:k:35:VAL:CG1	10:k:69:VAL:HG22	2.36	0.56
21:v:33:GLY:C	21:v:34:LYS:HD3	2.30	0.56
52:3:715:A:H2'	52:3:716:A:C8	2.39	0.56
1:b:140:VAL:HG12	1:b:191:LEU:HD23	1.88	0.56
9:j:62:VAL:HG11	9:j:101:ILE:HD11	1.86	0.56
11:l:38:GLN:HG3	53:1:805:G:H5''	1.88	0.56
52:3:483:C:H2'	52:3:484:G:C8	2.41	0.56
1:b:67:LYS:HA	1:b:150:GLY:HA2	1.88	0.56
10:k:1:MET:HE1	53:1:1665:A:C2	2.41	0.56
10:k:9:ASN:O	10:k:83:ALA:HA	2.06	0.56
12:m:63:ILE:HD11	12:m:103:TYR:HB3	1.87	0.56
15:p:3:ILE:H	15:p:3:ILE:HD12	1.69	0.56
30:F:19:ARG:HA	53:1:2756:U:H5''	1.88	0.56
53:1:2628:C:H3'	53:1:2629:U:H5'	1.87	0.56
33:I:146:GLU:CD	33:I:146:GLU:H	2.14	0.56
37:M:14:ARG:HD2	52:3:875:U:O2'	2.06	0.56
6:g:11:ASN:ND2	53:1:2095:A:OP1	2.39	0.56
19:t:9:LYS:NZ	53:1:71:A:H1'	2.21	0.56
53:1:2039:U:H2'	53:1:2040:G:C8	2.41	0.56
2:c:107:VAL:HG22	2:c:108:ASP:N	2.21	0.55
13:n:2:ARG:HG2	13:n:2:ARG:O	2.06	0.55
31:G:102:ASN:ND2	31:G:105:THR:HB	2.20	0.55
41:Q:80:LEU:O	41:Q:97:VAL:HG12	2.06	0.55
1:b:208:GLY:HA3	53:1:764:A:H5'	1.87	0.55
2:c:122:VAL:HA	2:c:127:PHE:HB2	1.88	0.55
11:l:95:LEU:HD22	11:l:100:ILE:HD11	1.89	0.55
23:x:58:ILE:HG22	23:x:66:VAL:HG21	1.87	0.55
31:G:9:LEU:HD21	31:G:42:LEU:HD22	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:15:SER:HA	35:K:18:VAL:HG13	1.87	0.55
52:3:1280:A:O2'	52:3:1281:C:H5'	2.06	0.55
11:l:55:MET:HE2	53:1:2429:G:O6	2.06	0.55
34:J:50:GLY:H	34:J:65:LYS:HD2	1.72	0.55
40:P:71:ASP:HA	40:P:74:LYS:HE3	1.88	0.55
46:V:68:LYS:HE3	52:3:267:C:OP2	2.06	0.55
46:V:74:LEU:HD11	46:V:77:VAL:HG22	1.87	0.55
53:1:1357:C:H2'	53:1:1358:G:O4'	2.06	0.55
53:1:1547:C:H2'	53:1:1548:A:H8	1.71	0.55
53:1:2048:G:C2'	53:1:2049:G:H5''	2.37	0.55
23:x:70:LEU:HD12	23:x:75:GLU:OE2	2.06	0.55
27:C:22:THR:HG21	53:1:2286:G:O6	2.06	0.55
37:M:102:VAL:HG12	37:M:125:ILE:HD12	1.89	0.55
41:Q:11:ARG:HD2	52:3:562:U:H1'	1.89	0.55
52:3:405:U:O2	52:3:498:A:H2'	2.06	0.55
52:3:701:U:H4'	52:3:703:G:H1'	1.89	0.55
11:l:51:GLU:HB3	11:l:54:GLN:HB3	1.87	0.55
31:G:117:GLU:O	31:G:121:GLN:HG3	2.06	0.55
36:L:2:ARG:HB2	52:3:933:G:OP2	2.06	0.55
41:Q:39:THR:HG22	41:Q:40:THR:H	1.70	0.55
50:Z:23:GLU:HG3	50:Z:24:LYS:H	1.69	0.55
53:1:189:G:H2'	53:1:205:G:N2	2.21	0.55
7:h:18:VAL:HG22	7:h:71:CYS:SG	2.46	0.55
26:B:29:VAL:HG23	53:1:2885:G:H1	1.72	0.55
2:c:59:ARG:NH1	53:1:2830:C:H3'	2.21	0.55
14:o:15:ARG:NH2	54:2:8:C:H5''	2.22	0.55
32:H:182:ASP:HB2	32:H:201:ILE:HB	1.89	0.55
49:Y:17:ARG:HA	49:Y:20:ASN:HB2	1.88	0.55
49:Y:28:ARG:NH2	52:3:1437:A:OP1	2.39	0.55
53:1:2443:C:H2'	53:1:2444:G:C8	2.42	0.55
54:2:88:C:H5''	54:2:89:U:OP1	2.07	0.55
1:b:77:VAL:HG21	1:b:109:LEU:HD21	1.89	0.55
1:b:206:LYS:HB2	1:b:209:ALA:HB2	1.88	0.55
2:c:55:LYS:HD3	2:c:77:ARG:HB3	1.89	0.55
7:h:42:ARG:NH1	53:1:1082:U:O2'	2.40	0.55
7:h:118:ILE:HB	7:h:119:PRO:HD3	1.88	0.55
24:y:8:GLU:HB3	24:y:12:GLU:HB3	1.88	0.55
27:C:20:TYR:OH	53:1:2348:U:H5'	2.07	0.55
37:M:77:VAL:HG12	37:M:84:ILE:HD11	1.89	0.55
38:N:10:ARG:HH21	52:3:1149:C:P	2.30	0.55
50:Z:9:GLU:HB3	50:Z:10:PRO:HD3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1160:G:H1	52:3:1176:A:H61	1.54	0.55
53:1:2636:C:H2'	53:1:2637:U:C6	2.42	0.55
14:o:55:GLU:OE1	14:o:57:ALA:HB3	2.07	0.55
18:s:40:ASN:O	53:1:2009:A:H5''	2.06	0.55
18:s:82:MET:O	18:s:98:LYS:HB2	2.07	0.55
35:K:51:ILE:C	35:K:53:LYS:H	2.15	0.55
52:3:211:G:H2'	52:3:212:G:H5'	1.88	0.55
53:1:2329:U:H2'	53:1:2330:G:H8	1.71	0.55
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.72	0.55
5:f:157:LYS:HE2	53:1:2659:G:P	2.47	0.55
41:Q:30:ARG:HH22	52:3:362:G:P	2.30	0.55
42:R:15:VAL:HG23	42:R:16:ILE:HG13	1.89	0.55
53:1:1919:A:H2'	53:1:1920:C:H5'	1.89	0.54
54:2:3:C:C2'	54:2:4:C:H5''	2.37	0.54
3:d:52:VAL:HG13	53:1:452:G:OP1	2.06	0.54
5:f:21:GLN:NE2	5:f:22:VAL:HG13	2.21	0.54
10:k:121:GLU:CD	10:k:122:VAL:HG23	2.32	0.54
35:K:50:PRO:HG3	35:K:55:HIS:HE1	1.72	0.54
53:1:760:G:H2'	53:1:761:A:O4'	2.08	0.54
18:s:51:LEU:HD12	18:s:54:ALA:HB3	1.89	0.54
26:B:30:ASP:HB3	26:B:34:GLY:H	1.72	0.54
43:S:68:ARG:HD2	52:3:1202:U:H1'	1.89	0.54
13:n:28:LEU:HD23	13:n:48:VAL:HG21	1.89	0.54
35:K:92:THR:OG1	35:K:93:LYS:N	2.40	0.54
52:3:437:U:H2'	52:3:438:U:O4'	2.07	0.54
54:2:35:C:H2'	54:2:36:C:H5'	1.89	0.54
1:b:48:ILE:HD11	1:b:51:ARG:HA	1.89	0.54
9:j:123:LYS:NZ	53:1:7:G:H5''	2.23	0.54
22:w:8:ASN:HD21	53:1:2278:A:C5'	2.19	0.54
45:U:74:LEU:HA	45:U:77:GLU:HG2	1.88	0.54
51:a:26:ALA:HB1	51:a:214:ILE:HD11	1.90	0.54
53:1:742:A:H2'	53:1:743:A:H8	1.71	0.54
53:1:1360:G:H22	53:1:2214:C:H42	1.55	0.54
53:1:2710:C:H2'	53:1:2711:A:C8	2.43	0.54
13:n:12:ARG:HD2	13:n:20:MET:HE2	1.89	0.54
52:3:422:C:H5'	52:3:423:G:C2	2.42	0.54
52:3:1432:G:H1'	52:3:1468:A:N6	2.22	0.54
53:1:1326:U:H2'	53:1:1327:A:H8	1.73	0.54
2:c:157:LYS:HG2	53:1:2619:C:H5''	1.88	0.54
4:e:62:GLN:HG2	4:e:63:LYS:H	1.73	0.54
22:w:47:VAL:HG21	22:w:76:ILE:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:29:ALA:O	30:F:31:PRO:HD3	2.08	0.54
40:P:124:LYS:HD2	40:P:124:LYS:C	2.33	0.54
11:l:90:VAL:HG23	11:l:95:LEU:HD21	1.89	0.54
17:r:81:LYS:HD2	53:1:973:A:H5''	1.89	0.54
22:w:14:ALA:HB1	53:1:2271:G:H5''	1.90	0.54
53:1:1111:A:O2'	53:1:1112:G:H4'	2.06	0.54
53:1:2799:A:C2'	53:1:2800:A:H5'	2.37	0.54
8:i:133:ARG:NH2	53:1:1079:C:C4'	2.71	0.54
11:l:61:LEU:O	29:E:12:ARG:NE	2.41	0.54
20:u:27:VAL:HG12	20:u:33:VAL:HG12	1.89	0.54
22:w:68:LYS:HE3	54:2:11:C:OP2	2.08	0.54
38:N:112:ARG:HB2	52:3:1369:C:OP2	2.08	0.54
42:R:89:ARG:CZ	42:R:94:LEU:HB3	2.38	0.54
50:Z:23:GLU:HG3	50:Z:24:LYS:N	2.23	0.54
52:3:494:G:O2'	52:3:496:A:H1'	2.08	0.54
14:o:83:LEU:HD21	14:o:114:GLY:HA3	1.89	0.54
25:z:29:ARG:NE	53:1:1183:U:H5''	2.23	0.54
50:Z:6:ARG:C	50:Z:8:ASN:H	2.15	0.54
53:1:1013:C:H2'	53:1:1014:A:C8	2.43	0.54
53:1:1268:A:H2'	53:1:1269:A:O4'	2.07	0.54
53:1:2469:A:H2'	53:1:2470:G:O4'	2.07	0.54
53:1:2508:G:H1	53:1:2580:U:H3	1.54	0.54
2:c:83:ARG:NH2	53:1:2637:U:H5''	2.22	0.53
30:F:31:PRO:O	30:F:34:LYS:HB3	2.07	0.53
32:H:70:ALA:HA	32:H:105:VAL:HG12	1.89	0.53
33:I:82:LYS:HG3	52:3:5:U:O4	2.08	0.53
40:P:34:THR:OG1	40:P:35:ASP:N	2.39	0.53
43:S:7:ALA:O	43:S:10:VAL:HG12	2.08	0.53
49:Y:27:MET:HE1	49:Y:66:ILE:HD11	1.91	0.53
20:u:50:ALA:O	20:u:51:LEU:HG	2.08	0.53
33:I:170:LEU:HD12	33:I:170:LEU:O	2.08	0.53
39:O:5:ARG:HG2	39:O:79:PRO:HB3	1.89	0.53
53:1:1509:A:H2'	53:1:1510:G:C8	2.43	0.53
57:7:64:A:H2'	57:7:65:G:H8	1.73	0.53
2:c:9:VAL:HA	2:c:197:THR:HG23	1.89	0.53
37:M:12:ARG:CD	52:3:826:C:H4'	2.37	0.53
48:X:50:VAL:HG11	48:X:70:LEU:HB3	1.89	0.53
49:Y:9:ARG:HG3	52:3:108:G:N1	2.22	0.53
53:1:1827:U:C2'	53:1:1828:G:H5'	2.39	0.53
53:1:2707:U:H2'	53:1:2708:G:H8	1.74	0.53
55:5:6:G:O2'	55:5:7:G:H5'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:11:MET:HG2	2:c:25:THR:HA	1.89	0.53
52:3:235:C:H2'	52:3:236:A:C8	2.42	0.53
53:1:669:G:H2'	53:1:669:G:N3	2.24	0.53
22:w:20:LYS:HE3	53:1:2355:G:H4'	1.89	0.53
33:I:10:LEU:O	33:I:13:ARG:HG2	2.08	0.53
33:I:190:LEU:HD23	33:I:191:SER:N	2.24	0.53
53:1:1807:G:H2'	53:1:1808:A:H5'	1.90	0.53
53:1:1872:A:H2'	53:1:1873:G:O4'	2.07	0.53
53:1:2533:U:H2'	53:1:2534:A:O4'	2.08	0.53
5:f:87:GLN:HG2	5:f:89:VAL:HG23	1.91	0.53
6:g:110:VAL:HG13	6:g:114:GLU:HB2	1.89	0.53
34:J:22:LYS:HE3	34:J:29:ILE:HG23	1.89	0.53
7:h:17:GLU:HG3	7:h:86:MET:HG2	1.90	0.53
38:N:114:LYS:NZ	52:3:1187:G:H4'	2.23	0.53
50:Z:33:ARG:HG3	50:Z:34:ARG:HG2	1.91	0.53
53:1:796:C:H2'	53:1:797:G:C8	2.43	0.53
53:1:2048:G:H3'	53:1:2049:G:H5''	1.90	0.53
53:1:2749:A:H62	53:1:2753:A:H61	1.56	0.53
1:b:158:GLY:H	1:b:194:VAL:HG23	1.73	0.53
3:d:83:VAL:HG13	3:d:83:VAL:O	2.08	0.53
4:e:24:VAL:HG12	54:2:55:U:C4'	2.38	0.53
7:h:67:THR:HB	7:h:68:PRO:HD3	1.89	0.53
13:n:103:ARG:HB3	13:n:108:ALA:H	1.74	0.53
32:H:139:ASN:O	32:H:142:ARG:HG2	2.09	0.53
38:N:17:ARG:CZ	52:3:1129:C:H5''	2.38	0.53
51:a:221:GLY:N	53:1:2176:A:H5''	2.24	0.53
52:3:225:C:H2'	52:3:226:G:H5''	1.90	0.53
52:3:1316:G:H2'	52:3:1317:C:H5''	1.90	0.53
53:1:310:A:H2'	53:1:311:A:H5''	1.91	0.53
53:1:2267:A:H5''	53:1:2268:A:H5'	1.90	0.53
2:c:129:THR:HG23	2:c:140:HIS:O	2.08	0.53
3:d:68:ALA:HA	53:1:1255:U:C6	2.43	0.53
5:f:17:LYS:HB2	5:f:24:THR:HB	1.91	0.53
9:j:30:THR:HG21	53:1:1012:U:O4	2.09	0.53
15:p:1:SER:HA	53:1:2876:G:H5'	1.91	0.53
52:3:70:U:H2'	52:3:94:G:O6	2.09	0.53
52:3:880:C:H2'	52:3:881:G:H8	1.73	0.53
53:1:750:A:H2'	53:1:751:A:H5''	1.90	0.53
53:1:1054:A:H2'	53:1:1055:G:C8	2.43	0.53
53:1:1535:A:H3'	53:1:1536:C:H5'	1.91	0.53
53:1:2423:U:O2'	53:1:2425:A:H2'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:79:ARG:HB3	4:e:82:TYR:HB2	1.90	0.53
14:o:12:THR:HG21	53:1:2334:U:H5'	1.91	0.53
29:E:37:THR:HA	29:E:40:LYS:HD2	1.91	0.53
54:2:114:C:H2'	54:2:115:A:C8	2.44	0.53
1:b:62:ARG:HH12	1:b:84:PRO:HD2	1.72	0.52
1:b:255:LYS:HB3	1:b:257:ARG:HD3	1.92	0.52
4:e:115:GLY:HA2	4:e:175:PRO:HB3	1.91	0.52
9:j:72:LYS:HZ1	53:1:1139:G:P	2.32	0.52
13:n:78:LYS:HG3	13:n:82:GLU:OE2	2.09	0.52
51:a:23:ILE:HD12	51:a:186:LYS:NZ	2.25	0.52
52:3:392:C:H2'	52:3:393:A:C8	2.45	0.52
53:1:820:A:C2	53:1:943:A:H4'	2.44	0.52
21:v:49:ASN:OD1	53:1:1040:A:H5'	2.10	0.52
31:G:19:THR:HG22	31:G:38:HIS:NE2	2.23	0.52
34:J:132:PRO:O	34:J:136:VAL:HG23	2.08	0.52
34:J:155:LYS:HE3	37:M:70:VAL:HG13	1.91	0.52
37:M:87:ARG:H	37:M:90:GLU:HB2	1.75	0.52
44:T:65:LEU:HD23	52:3:754:C:O2'	2.09	0.52
51:a:51:ASP:OD2	51:a:54:LYS:HG3	2.09	0.52
1:b:61:TYR:HA	1:b:85:ASN:OD1	2.09	0.52
17:r:79:ARG:HH22	53:1:572:A:H5'	1.74	0.52
32:H:19:SER:HB2	32:H:21:TRP:HE1	1.74	0.52
50:Z:56:ALA:O	50:Z:59:LEU:HG	2.10	0.52
51:a:181:ASP:HB3	51:a:184:LYS:HG3	1.90	0.52
53:1:118:A:OP2	53:1:119:A:H5''	2.10	0.52
53:1:1023:U:O2'	53:1:1122:G:H5'	2.09	0.52
53:1:2248:C:C2'	53:1:2249:U:H5'	2.39	0.52
55:6:71:C:H2'	55:6:72:A:C8	2.44	0.52
6:g:7:ASP:OD2	6:g:35:LYS:HD3	2.10	0.52
21:v:30:ILE:HG13	21:v:40:ILE:HG13	1.92	0.52
24:y:4:LYS:HA	24:y:7:ARG:NH1	2.24	0.52
43:S:53:ASP:HA	43:S:58:ARG:HD2	1.91	0.52
48:X:10:ILE:HD13	48:X:40:PHE:CE2	2.44	0.52
52:3:1512:U:H2'	52:3:1513:A:H8	1.74	0.52
53:1:826:U:H5''	53:1:2429:G:P	2.49	0.52
53:1:2707:U:H2'	53:1:2708:G:C8	2.44	0.52
2:c:146:ILE:HD12	2:c:146:ILE:N	2.24	0.52
11:l:38:GLN:HB3	53:1:832:U:H5'	1.90	0.52
13:n:14:SER:HA	13:n:17:ARG:NH2	2.23	0.52
35:K:91:ARG:HG2	52:3:737:C:OP1	2.09	0.52
52:3:1277:C:H2'	52:3:1278:G:H5''	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2149:U:H2'	53:1:2150:C:O4'	2.09	0.52
2:c:131:ASP:HA	53:1:1994:C:OP1	2.10	0.52
3:d:189:THR:HG23	3:d:192:ALA:H	1.73	0.52
4:e:43:ILE:HD13	4:e:78:ILE:HG13	1.91	0.52
7:h:54:VAL:HG22	7:h:83:ALA:HB1	1.92	0.52
32:H:131:ARG:HG3	32:H:135:ARG:HH21	1.74	0.52
52:3:77:A:H2'	52:3:78:A:C8	2.45	0.52
52:3:163:C:H2'	52:3:164:G:O4'	2.10	0.52
52:3:352:C:H4'	52:3:354:G:OP1	2.10	0.52
53:1:776:G:H1	53:1:2072:C:H5'	1.75	0.52
53:1:873:C:H2'	53:1:874:G:C8	2.44	0.52
10:k:6:THR:CG2	53:1:1666:G:H4'	2.38	0.52
12:m:42:THR:HA	12:m:93:VAL:HA	1.90	0.52
12:m:45:GLN:OE1	53:1:2485:G:H5''	2.09	0.52
13:n:79:LEU:O	13:n:80:PHE:HB2	2.09	0.52
38:N:98:ARG:HD2	38:N:103:VAL:HG11	1.91	0.52
49:Y:16:ALA:HB3	52:3:323:U:H4'	1.92	0.52
52:3:184:G:H4'	52:3:224:U:H4'	1.90	0.52
53:1:940:G:H2'	53:1:941:A:H5''	1.92	0.52
53:1:2432:A:H1'	55:6:75:C:H5'	1.91	0.52
5:f:138:GLN:HE22	53:1:2746:U:H1'	1.75	0.52
20:u:90:LYS:NZ	53:1:101:A:H62	2.08	0.52
31:G:26:MET:HE1	31:G:192:PRO:HD3	1.91	0.52
42:R:100:ARG:HH21	42:R:102:LYS:HD3	1.75	0.52
52:3:235:C:H2'	52:3:236:A:H8	1.75	0.52
52:3:791:G:N2	52:3:1497:G:H4'	2.20	0.52
54:2:91:C:H2'	54:2:92:C:C6	2.45	0.52
4:e:45:ASP:HB2	4:e:48:LEU:HB2	1.90	0.52
7:h:55:VAL:HA	53:1:1084:A:C4'	2.39	0.52
9:j:7:LYS:NZ	53:1:538:A:H5''	2.24	0.52
34:J:108:GLY:C	34:J:110:MET:H	2.16	0.52
41:Q:73:LEU:HD12	41:Q:73:LEU:N	2.25	0.52
44:T:47:LYS:HD3	52:3:808:C:OP2	2.10	0.52
48:X:10:ILE:HD13	48:X:40:PHE:CZ	2.45	0.52
52:3:971:G:H1'	52:3:1365:G:O2'	2.10	0.52
53:1:1060:U:H4'	53:1:1061:U:H5'	1.92	0.52
10:k:108:ARG:NH1	10:k:116:ILE:HD12	2.25	0.52
12:m:41:LEU:HD22	12:m:124:LEU:HD12	1.90	0.52
21:v:37:PRO:HG2	54:2:74:U:H1'	1.92	0.52
27:C:12:SER:HB2	27:C:48:TYR:CZ	2.44	0.52
40:P:24:ALA:HA	40:P:29:THR:HA	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:987:C:H2'	53:1:988:A:O4'	2.10	0.52
53:1:1035:U:H2'	53:1:1036:G:H8	1.73	0.52
53:1:1170:C:H2'	53:1:1171:G:C8	2.45	0.52
3:d:68:ALA:HA	53:1:1255:U:C5	2.45	0.51
7:h:33:VAL:CG1	7:h:35:VAL:HG22	2.40	0.51
16:q:61:ILE:HG21	53:1:1009:A:O2'	2.10	0.51
17:r:74:ILE:HD13	53:1:992:C:H4'	1.91	0.51
20:u:97:SER:O	20:u:98:ASN:HB3	2.10	0.51
25:z:30:ARG:HD3	25:z:30:ARG:H	1.75	0.51
32:H:54:ILE:HD12	32:H:67:ILE:HG12	1.91	0.51
39:O:50:THR:HG21	52:3:1367:C:H4'	1.91	0.51
50:Z:48:LYS:HG3	52:3:723:U:C5	2.41	0.51
53:1:828:U:H2'	53:1:829:A:C8	2.44	0.51
34:J:94:PHE:O	34:J:124:ALA:HA	2.10	0.51
53:1:395:U:H2'	53:1:396:G:C8	2.46	0.51
31:G:186:VAL:HG13	31:G:190:SER:HB2	1.93	0.51
50:Z:23:GLU:C	50:Z:25:ALA:H	2.18	0.51
53:1:581:C:H2'	53:1:582:A:H8	1.75	0.51
1:b:158:GLY:N	1:b:194:VAL:HG23	2.24	0.51
3:d:45:ALA:CB	53:1:38:A:H4'	2.40	0.51
40:P:83:VAL:HB	40:P:109:ILE:HA	1.92	0.51
44:T:26:VAL:O	44:T:30:LEU:HG	2.11	0.51
52:3:1402:C:H2'	52:3:1403:C:O4'	2.11	0.51
53:1:1298:C:H2'	53:1:1299:G:O4'	2.11	0.51
53:1:1755:A:H2'	53:1:1756:G:H5'	1.92	0.51
54:2:97:C:H2'	54:2:98:G:O4'	2.10	0.51
7:h:53:ARG:HD3	53:1:1084:A:P	2.51	0.51
7:h:56:ARG:O	53:1:1106:G:H4'	2.11	0.51
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.92	0.51
22:w:56:PHE:HZ	53:1:2366:A:H5'	1.76	0.51
38:N:51:LEU:HD13	38:N:54:VAL:HG23	1.92	0.51
42:R:113:LYS:HZ1	55:5:44:A:H4'	1.75	0.51
50:Z:9:GLU:CB	50:Z:10:PRO:HD3	2.41	0.51
53:1:441:U:H2'	53:1:442:G:C8	2.45	0.51
53:1:441:U:O2'	53:1:442:G:H5'	2.11	0.51
3:d:2:GLU:HB3	3:d:11:ALA:HB1	1.92	0.51
3:d:131:THR:HG21	3:d:163:ASN:HD21	1.75	0.51
5:f:21:GLN:HE21	5:f:22:VAL:HG13	1.76	0.51
45:U:5:ARG:HH22	45:U:26:ASN:HB3	1.75	0.51
53:1:367:G:H2'	53:1:368:A:O4'	2.11	0.51
55:6:72:A:H2'	55:6:73:A:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:119:ILE:O	3:d:187:VAL:HG23	2.11	0.51
6:g:143:ILE:H	6:g:143:ILE:HD12	1.75	0.51
41:Q:109:ARG:HB2	41:Q:118:VAL:HG11	1.93	0.51
48:X:17:LYS:NZ	52:3:1014:A:OP2	2.37	0.51
52:3:1302:C:O2'	52:3:1303:C:H5'	2.11	0.51
54:2:65:U:H3'	54:2:108:A:N6	2.25	0.51
1:b:155:ARG:HB3	53:1:1818:U:H5''	1.91	0.51
11:l:93:ASN:HB2	11:l:96:LYS:HE2	1.92	0.51
53:1:2277:G:C3'	53:1:2278:A:H5''	2.39	0.51
53:1:2799:A:H2'	53:1:2800:A:H5'	1.92	0.51
12:m:46:ILE:HG23	12:m:103:TYR:OH	2.10	0.51
16:q:55:GLN:NE2	53:1:559:G:H1'	2.25	0.51
27:C:22:THR:OG1	27:C:23:THR:N	2.44	0.51
33:I:150:LYS:HD2	33:I:155:LYS:HD3	1.93	0.51
37:M:14:ARG:HE	37:M:74:ILE:HG23	1.74	0.51
37:M:79:ARG:HB2	52:3:878:A:OP1	2.11	0.51
37:M:80:PRO:HG2	52:3:878:A:H5'	1.93	0.51
48:X:27:LYS:HD2	48:X:28:LYS:N	2.26	0.51
52:3:252:U:O2	52:3:252:U:H2'	2.10	0.51
52:3:1506:U:O2'	52:3:1507:A:H5'	2.11	0.51
53:1:2638:G:H1'	53:1:2778:A:H61	1.75	0.51
1:b:156:SER:O	1:b:194:VAL:HG21	2.11	0.51
2:c:157:LYS:HD2	9:j:79:GLY:O	2.11	0.51
16:q:85:ALA:HB1	16:q:111:LYS:HE2	1.93	0.51
40:P:91:GLY:C	40:P:93:GLU:H	2.18	0.51
44:T:86:LEU:HG	44:T:87:ARG:H	1.75	0.51
45:U:33:ILE:N	45:U:33:ILE:HD12	2.25	0.51
53:1:471:A:H2'	53:1:472:A:O4'	2.11	0.51
53:1:2156:G:C2'	53:1:2157:G:H5'	2.41	0.51
55:5:51:C:H2'	55:5:52:G:C8	2.47	0.51
12:m:53:MET:O	12:m:57:VAL:HG22	2.11	0.50
12:m:79:ALA:HA	53:1:2494:G:O3'	2.11	0.50
23:x:13:THR:CG2	53:1:188:G:H5'	2.42	0.50
30:F:10:LEU:HD11	30:F:35:GLN:HE22	1.76	0.50
52:3:1413:A:H2	52:3:1487:G:H22	1.58	0.50
53:1:1363:C:H2'	53:1:1364:G:H8	1.75	0.50
53:1:1571:A:H2'	53:1:1572:A:C8	2.47	0.50
53:1:2358:A:H2'	53:1:2359:C:O4'	2.10	0.50
54:2:49:C:H2'	54:2:50:A:C8	2.45	0.50
54:2:51:G:H2'	54:2:52:A:O4'	2.11	0.50
1:b:18:VAL:H	1:b:202:ARG:HH21	1.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.93	0.50
2:c:59:ARG:HH11	53:1:2830:C:H3'	1.74	0.50
4:e:32:LYS:C	4:e:33:ILE:HD12	2.36	0.50
6:g:69:ALA:HA	6:g:72:ILE:HG12	1.93	0.50
9:j:2:LYS:HA	53:1:995:C:N3	2.26	0.50
11:l:93:ASN:C	11:l:95:LEU:H	2.20	0.50
19:t:80:TRP:HZ3	19:t:82:LYS:HB3	1.75	0.50
33:I:144:ILE:H	33:I:144:ILE:HD12	1.76	0.50
33:I:169:TRP:CD1	33:I:185:PRO:HG3	2.46	0.50
35:K:44:ARG:HB2	35:K:58:HIS:ND1	2.26	0.50
38:N:10:ARG:HG3	38:N:105:ARG:HE	1.76	0.50
40:P:63:GLN:O	40:P:67:GLU:HG3	2.12	0.50
46:V:39:ARG:HH11	46:V:40:THR:H	1.59	0.50
51:a:190:GLU:HA	51:a:193:LEU:HG	1.93	0.50
5:f:126:THR:OG1	5:f:129:GLU:HB2	2.12	0.50
10:k:43:ILE:HD12	10:k:43:ILE:N	2.26	0.50
11:l:42:SER:HB3	53:1:672:C:H5	1.76	0.50
13:n:79:LEU:HD23	13:n:83:LEU:HB2	1.93	0.50
18:s:28:LYS:HE2	18:s:70:LYS:HE3	1.93	0.50
21:v:4:ILE:O	21:v:63:ILE:HD12	2.12	0.50
33:I:97:LEU:O	33:I:101:VAL:HG23	2.11	0.50
34:J:125:LYS:HD2	52:3:9:G:OP1	2.11	0.50
39:O:53:ILE:HG22	39:O:61:ALA:O	2.11	0.50
55:6:17:C:H2'	55:6:17(A):U:C5	2.46	0.50
4:e:165:GLY:HA2	4:e:168:LEU:HD13	1.94	0.50
21:v:28:ALA:HB3	21:v:40:ILE:HB	1.94	0.50
26:B:3:GLN:HA	53:1:2615:U:C2	2.46	0.50
38:N:114:LYS:HB2	38:N:117:LEU:HD12	1.92	0.50
41:Q:48:LEU:HB2	52:3:520:A:OP1	2.11	0.50
53:1:616:A:H2'	53:1:617:G:O4'	2.12	0.50
53:1:799:G:H5''	53:1:800:A:H2'	1.94	0.50
53:1:2553:G:C3'	53:1:2554:U:H5''	2.40	0.50
8:i:133:ARG:HH21	53:1:1079:C:H4'	1.74	0.50
20:u:94:PHE:HB2	20:u:100:GLU:O	2.10	0.50
52:3:1475:G:H4'	53:1:1689:A:H4'	1.93	0.50
53:1:1528:A:H2'	53:1:1529:G:O4'	2.11	0.50
53:1:2185:U:H2'	53:1:2186:G:C8	2.46	0.50
53:1:2537:U:H2'	53:1:2538:C:C6	2.47	0.50
2:c:51:THR:HB	2:c:79:LEU:HD23	1.93	0.50
6:g:15:LEU:HD21	6:g:56:ALA:HB1	1.93	0.50
20:u:45:GLN:O	20:u:55:GLY:HA2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:w:19:VAL:HG23	22:w:34:VAL:HG22	1.93	0.50
29:E:43:LEU:HD21	53:1:2362:C:OP2	2.12	0.50
48:X:19:GLU:HA	48:X:22:VAL:HG22	1.93	0.50
51:a:209:ILE:H	51:a:209:ILE:HD12	1.75	0.50
53:1:955:U:H3	53:1:962:G:H1	1.60	0.50
53:1:2646:C:H2'	53:1:2647:U:O4'	2.12	0.50
9:j:113:PRO:HD2	53:1:558:U:OP2	2.11	0.50
10:k:69:VAL:O	10:k:76:VAL:HA	2.10	0.50
16:q:24:TYR:CE1	53:1:17:G:H4'	2.46	0.50
19:t:80:TRP:CZ3	19:t:82:LYS:HB3	2.47	0.50
27:C:36:LYS:HG2	27:C:47:ILE:HG12	1.93	0.50
34:J:92:ARG:O	34:J:93:VAL:C	2.54	0.50
34:J:96:GLN:O	34:J:122:VAL:HA	2.11	0.50
37:M:42:GLU:HG3	37:M:100:ILE:HD13	1.92	0.50
52:3:107:G:H2'	52:3:108:G:O4'	2.12	0.50
52:3:112:G:H4'	52:3:389:A:H4'	1.94	0.50
53:1:562:U:O4'	53:1:2036:C:H5'	2.12	0.50
53:1:1417:C:H4'	53:1:1587:G:H21	1.76	0.50
11:l:36:LYS:HD2	53:1:807:U:OP2	2.11	0.50
12:m:5:LYS:HG2	53:1:871:U:OP1	2.11	0.50
23:x:42:GLU:HG3	23:x:44:ARG:HG2	1.93	0.50
24:y:37:LEU:HD21	24:y:42:LEU:HD12	1.94	0.50
26:B:42:ILE:HG22	26:B:48:TYR:HB2	1.94	0.50
38:N:105:ARG:O	38:N:105:ARG:HD3	2.12	0.50
50:Z:30:GLU:HA	50:Z:32:ARG:NH1	2.26	0.50
52:3:231:U:H2'	52:3:232:G:H8	1.77	0.50
52:3:372:C:N4	52:3:387:U:H2'	2.26	0.50
53:1:548:G:H2'	53:1:549:G:O4'	2.12	0.50
53:1:2183:A:H2'	53:1:2184:A:C8	2.47	0.50
54:2:2:G:H2'	54:2:3:C:C6	2.46	0.50
1:b:95:TYR:HB2	1:b:97:ASP:OD1	2.12	0.50
3:d:73:ILE:HD12	3:d:78:TRP:CE3	2.46	0.50
13:n:72:ASP:HB3	13:n:75:ILE:HG22	1.92	0.50
19:t:30:ILE:HG23	19:t:85:VAL:HB	1.93	0.50
21:v:26:PHE:HE1	21:v:44:HIS:HA	1.77	0.50
32:H:21:TRP:HB3	32:H:58:ARG:HB3	1.93	0.50
36:L:1:PRO:HA	52:3:1379:G:O6	2.11	0.50
39:O:57:VAL:O	39:O:58:ASN:CB	2.60	0.50
46:V:27:PHE:O	52:3:597:G:H4'	2.12	0.50
52:3:885:G:H2'	52:3:886:G:H8	1.77	0.50
57:7:47:U:H3'	57:7:48:C:H5''	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:51:ARG:C	45:U:52:LEU:HD12	2.37	0.49
52:3:1301:U:O2	52:3:1301:U:C2'	2.60	0.49
53:1:2350:C:H2'	53:1:2351:G:O4'	2.11	0.49
10:k:21:CYS:HA	10:k:41:ILE:HG22	1.93	0.49
19:t:53:VAL:HG12	19:t:92:ASN:HB2	1.93	0.49
48:X:77:ARG:HH22	52:3:1322:C:P	2.35	0.49
52:3:335:C:H2'	52:3:336:A:C8	2.47	0.49
52:3:779:C:H2'	52:3:780:A:O4'	2.12	0.49
52:3:802:A:H2'	52:3:803:G:O4'	2.13	0.49
53:1:225:C:H2'	53:1:226:A:O4'	2.12	0.49
53:1:1367:A:H2'	53:1:1368:G:H5'	1.94	0.49
2:c:24:VAL:HG11	2:c:188:LEU:HB3	1.94	0.49
4:e:92:GLY:O	4:e:95:MET:HG2	2.12	0.49
5:f:44:HIS:CG	5:f:45:ALA:H	2.30	0.49
7:h:56:ARG:NH2	7:h:81:LEU:HD11	2.27	0.49
7:h:118:ILE:H	7:h:119:PRO:HD2	1.78	0.49
13:n:52:ILE:O	13:n:56:LYS:HG3	2.12	0.49
17:r:49:ILE:HG22	17:r:54:VAL:HG13	1.93	0.49
28:D:29:GLN:HG2	28:D:33:ARG:NH2	2.27	0.49
52:3:1330:U:H2'	52:3:1331:G:O4'	2.12	0.49
53:1:1837:C:H2'	53:1:1899:A:N6	2.24	0.49
3:d:146:VAL:HG12	3:d:185:LYS:HB2	1.94	0.49
7:h:33:VAL:HG22	7:h:34:THR:N	2.26	0.49
7:h:118:ILE:H	7:h:119:PRO:CD	2.25	0.49
21:v:44:HIS:O	21:v:47:VAL:HG12	2.11	0.49
23:x:10:ARG:HD2	23:x:11:PRO:N	2.27	0.49
49:Y:22:SER:HA	52:3:1458:G:O3'	2.12	0.49
53:1:2343:U:H2'	53:1:2344:U:C6	2.48	0.49
1:b:59:GLN:HB3	1:b:85:ASN:HD21	1.77	0.49
1:b:229:HIS:NE2	1:b:246:PRO:HG3	2.28	0.49
22:w:55:LEU:HD22	22:w:55:LEU:N	2.27	0.49
32:H:171:ARG:HA	52:3:1106:G:O3'	2.12	0.49
33:I:123:MET:HE3	33:I:126:GLY:HA2	1.94	0.49
34:J:64:GLU:HB3	34:J:68:ARG:HH12	1.77	0.49
35:K:1:MET:HB3	35:K:65:GLU:HG2	1.95	0.49
45:U:6:LEU:HD22	45:U:17:TYR:HB3	1.94	0.49
51:a:5:THR:HB	53:1:2130:U:OP2	2.13	0.49
53:1:523:C:H2'	53:1:524:G:H8	1.77	0.49
53:1:534:U:H2'	53:1:535:G:C8	2.47	0.49
53:1:1432:G:H2'	53:1:1433:A:C8	2.48	0.49
2:c:116:LYS:HB2	2:c:165:MET:HG3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:82:LEU:HD23	11:l:82:LEU:O	2.13	0.49
22:w:36:GLN:NE2	22:w:39:THR:HA	2.27	0.49
28:D:3:ARG:O	28:D:6:GLN:NE2	2.46	0.49
35:K:29:ILE:HD13	35:K:64:VAL:HG11	1.93	0.49
45:U:67:ILE:H	45:U:67:ILE:HD12	1.78	0.49
52:3:245:U:O2'	52:3:246:A:H5'	2.13	0.49
52:3:335:C:H2'	52:3:336:A:H8	1.78	0.49
52:3:434:U:H2'	52:3:435:A:C8	2.48	0.49
52:3:1261:A:H1'	52:3:1283:U:H5''	1.95	0.49
52:3:1346:A:O2'	52:3:1347:G:H4'	2.13	0.49
53:1:807:U:H2'	53:1:808:G:H8	1.77	0.49
53:1:1893:C:H2'	53:1:1894:C:H5'	1.93	0.49
53:1:2515:C:H2'	53:1:2516:A:C8	2.48	0.49
53:1:2633:G:H5''	53:1:2812:G:H5'	1.95	0.49
2:c:155:VAL:HG21	53:1:2618:G:H21	1.77	0.49
5:f:82:PHE:CE2	5:f:137:LYS:HB2	2.46	0.49
6:g:26:ALA:HA	6:g:30:LEU:HD12	1.95	0.49
19:t:33:LYS:HG3	19:t:80:TRP:CE3	2.48	0.49
28:D:41:ARG:HH11	28:D:45:SER:H	1.60	0.49
31:G:27:LYS:HB2	31:G:28:PRO:HD3	1.95	0.49
32:H:170:GLY:C	52:3:1106:G:H4'	2.38	0.49
37:M:87:ARG:N	37:M:90:GLU:HB2	2.27	0.49
39:O:44:THR:HG23	39:O:69:THR:O	2.13	0.49
52:3:35:G:H2'	52:3:36:C:C6	2.48	0.49
52:3:64:G:H4'	52:3:65:A:H3'	1.94	0.49
52:3:1516:G:H2'	52:3:1518:A:OP2	2.13	0.49
53:1:834:G:H1'	53:1:2358:A:N3	2.28	0.49
1:b:106:PRO:HG2	1:b:109:LEU:HB2	1.94	0.49
8:i:127:SER:HA	53:1:1080:A:H1'	1.95	0.49
9:j:78:THR:HB	53:1:2641:G:H5''	1.94	0.49
42:R:3:ILE:N	42:R:3:ILE:HD12	2.27	0.49
52:3:1354:U:H2'	52:3:1355:G:H8	1.77	0.49
53:1:69:C:H2'	53:1:70:G:C8	2.48	0.49
53:1:703:U:H2'	53:1:704:G:O4'	2.12	0.49
53:1:750:A:H5''	53:1:1615:C:H42	1.77	0.49
53:1:971:G:H2'	53:1:972:A:O4'	2.11	0.49
3:d:112:LEU:HD11	3:d:180:LEU:HD12	1.95	0.49
7:h:33:VAL:HG13	7:h:35:VAL:HG22	1.95	0.49
15:p:102:ARG:NH2	53:1:1754:A:O2'	2.46	0.49
17:r:5:PHE:O	17:r:11:GLN:HA	2.13	0.49
19:t:80:TRP:CD1	19:t:80:TRP:H	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1801:A:H62	53:1:2202:U:H5'	1.77	0.49
53:1:1856:U:H2'	53:1:1857:G:O4'	2.13	0.49
53:1:2328:A:H2'	53:1:2329:U:C6	2.48	0.49
55:6:17:C:H2'	55:6:17(A):U:H5	1.78	0.49
5:f:23:ILE:HD12	5:f:23:ILE:N	2.28	0.49
6:g:50:ARG:O	6:g:50:ARG:HD2	2.12	0.49
10:k:28:SER:HB3	53:1:2563:U:O2'	2.13	0.49
18:s:33:LEU:O	18:s:37:THR:HG23	2.13	0.49
20:u:4:ILE:HD12	20:u:4:ILE:N	2.27	0.49
22:w:72:ASN:HD21	54:2:13:G:P	2.36	0.49
33:I:109:THR:H	33:I:112:GLU:HB3	1.78	0.49
34:J:156:ARG:NH2	34:J:163:ILE:HD12	2.28	0.49
36:L:41:ILE:HG21	36:L:115:MET:HG3	1.95	0.49
52:3:730:G:H2'	52:3:731:G:H5'	1.94	0.49
53:1:346:A:H2'	53:1:346:A:N3	2.28	0.49
53:1:445:C:O2'	53:1:446:G:H5'	2.13	0.49
53:1:885:C:H2'	53:1:886:A:H8	1.78	0.49
53:1:1373:A:C5'	53:1:2212:A:H1'	2.43	0.49
53:1:2605:U:H2'	53:1:2606:C:C6	2.48	0.49
54:2:28:C:H2'	54:2:29:A:C8	2.48	0.49
1:b:20:ASN:HD21	1:b:22:GLU:HB2	1.78	0.48
1:b:146:LYS:HD3	53:1:2204:G:H1'	1.95	0.48
1:b:242:HIS:O	1:b:244:VAL:HG13	2.13	0.48
9:j:58:ASN:ND2	9:j:128:ASN:HB2	2.27	0.48
21:v:14:LYS:HB2	54:2:98:G:H1	1.78	0.48
36:L:36:SER:O	36:L:39:GLU:HG3	2.12	0.48
53:1:704:G:H1'	53:1:727:A:H61	1.78	0.48
53:1:2208:C:H2'	53:1:2209:G:C8	2.48	0.48
53:1:2553:G:H1'	53:1:2582:G:H21	1.78	0.48
3:d:57:LYS:HE2	53:1:796:C:OP1	2.13	0.48
4:e:140:ILE:HD12	4:e:140:ILE:H	1.78	0.48
10:k:38:ILE:HD13	10:k:61:VAL:HB	1.95	0.48
11:l:39:LYS:HG2	53:1:832:U:OP1	2.13	0.48
12:m:54:THR:O	12:m:58:LYS:HA	2.13	0.48
17:r:39:LEU:O	17:r:49:ILE:HG23	2.14	0.48
18:s:69:LEU:HD12	18:s:109:ASP:HA	1.96	0.48
33:I:32:LYS:HD3	52:3:426:U:P	2.53	0.48
51:a:68:GLY:HA2	51:a:159:GLY:HA2	1.96	0.48
52:3:1414:U:H2'	52:3:1415:G:H8	1.76	0.48
53:1:937:C:H2'	53:1:938:G:C8	2.48	0.48
53:1:1201:U:H2'	53:1:1202:G:C8	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:19:VAL:HG21	53:1:1565:C:OP1	2.13	0.48
2:c:193:VAL:O	53:1:2680:U:H4'	2.12	0.48
3:d:105:LEU:HD13	3:d:200:LEU:HD11	1.95	0.48
9:j:109:LEU:HD22	9:j:118:MET:SD	2.53	0.48
17:r:11:GLN:NE2	17:r:39:LEU:HD22	2.28	0.48
19:t:9:LYS:HZ2	53:1:71:A:H1'	1.79	0.48
23:x:62:GLY:O	23:x:66:VAL:HG23	2.13	0.48
32:H:149:LYS:NZ	32:H:174:LEU:HD21	2.28	0.48
33:I:131:ILE:HG12	52:3:620:C:C2	2.49	0.48
42:R:22:TYR:CE1	52:3:1330:U:H4'	2.48	0.48
52:3:78:A:H2'	52:3:79:G:O4'	2.12	0.48
52:3:1070:U:H2'	52:3:1071:C:C6	2.48	0.48
53:1:479:A:H4'	53:1:480:A:H5'	1.96	0.48
18:s:79:GLY:C	53:1:25:U:H4'	2.39	0.48
23:x:11:PRO:HG3	23:x:30:PRO:HD2	1.95	0.48
33:I:50:TYR:CD2	52:3:508:U:H4'	2.49	0.48
34:J:133:ILE:HD12	34:J:133:ILE:N	2.28	0.48
52:3:1033:G:C2'	52:3:1034:G:H5''	2.44	0.48
53:1:161:A:H62	53:1:165:A:H61	1.61	0.48
53:1:457:A:O3'	53:1:458:G:H4'	2.13	0.48
53:1:1806:C:H2'	53:1:1807:G:O4'	2.14	0.48
6:g:28:ASN:HD22	53:1:2199:A:C4'	2.17	0.48
16:q:58:GLN:HG3	53:1:1009:A:O4'	2.13	0.48
33:I:6:PRO:HA	52:3:430:A:P	2.54	0.48
41:Q:72:ASN:H	41:Q:73:LEU:HD12	1.78	0.48
52:3:1001:C:H2'	52:3:1002:G:C8	2.48	0.48
52:3:1187:G:H2'	52:3:1188:A:C8	2.48	0.48
53:1:255:A:H2'	53:1:256:A:O4'	2.13	0.48
53:1:443:A:H2'	53:1:443:A:N3	2.28	0.48
53:1:668:A:H2'	53:1:670:A:H62	1.78	0.48
27:C:40:PRO:HB3	53:1:2348:U:H4'	1.95	0.48
31:G:26:MET:HG3	31:G:29:PHE:HB2	1.94	0.48
32:H:13:ILE:N	32:H:13:ILE:HD12	2.29	0.48
49:Y:6:ALA:HB1	52:3:108:G:H21	1.78	0.48
52:3:51:A:H4'	52:3:52:C:H5''	1.96	0.48
52:3:86:G:H4'	52:3:87:C:C5	2.48	0.48
53:1:1874:C:H2'	53:1:1875:G:O4'	2.13	0.48
3:d:77:ILE:HG13	3:d:78:TRP:CD1	2.48	0.48
11:l:132:ARG:HG3	11:l:142:ILE:HD12	1.94	0.48
16:q:79:ILE:HG23	53:1:1152:C:H5''	1.96	0.48
24:y:43:LEU:H	24:y:43:LEU:HD12	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B:26:SER:HA	53:1:2887:A:H2	1.79	0.48
31:G:96:LEU:HD13	52:3:1103:C:H4'	1.95	0.48
40:P:17:ASP:CG	40:P:80:ASN:HD21	2.22	0.48
41:Q:34:THR:O	41:Q:53:ARG:HB3	2.14	0.48
45:U:54:LEU:HD13	45:U:57:ILE:HD12	1.96	0.48
52:3:1256:A:H1'	52:3:1258:G:N9	2.29	0.48
53:1:1354:A:H2'	53:1:1355:G:O4'	2.14	0.48
1:b:267:VAL:HG12	1:b:268:ARG:HG2	1.96	0.48
7:h:33:VAL:HG13	7:h:35:VAL:H	1.78	0.48
8:i:102:ARG:HH12	8:i:129:GLU:HB3	1.79	0.48
10:k:78:ARG:HB2	15:p:70:GLU:HB2	1.94	0.48
12:m:38:ARG:CZ	54:2:90:C:H4'	2.44	0.48
29:E:18:LYS:HG3	53:1:651:G:C5'	2.40	0.48
32:H:36:PHE:CE2	43:S:65:GLN:HG2	2.49	0.48
39:O:59:LYS:HD3	52:3:973:G:OP1	2.14	0.48
51:a:10:VAL:HG12	51:a:14:LYS:NZ	2.28	0.48
52:3:405:U:C3'	52:3:406:G:H5'	2.39	0.48
53:1:534:U:H2'	53:1:535:G:H8	1.79	0.48
53:1:1370:C:H2'	53:1:1371:G:O4'	2.14	0.48
1:b:120:ASP:HB2	6:g:91:PHE:CE1	2.49	0.48
1:b:148:GLY:O	53:1:2205:A:H5'	2.13	0.48
12:m:123:LYS:C	12:m:124:LEU:HD22	2.39	0.48
14:o:100:HIS:HD2	54:2:48:U:H4'	1.79	0.48
26:B:2:VAL:HG23	53:1:2056:G:H21	1.79	0.48
52:3:505:G:OP2	52:3:534:U:H2'	2.12	0.48
52:3:1258:G:H2'	52:3:1259:C:C6	2.48	0.48
53:1:1418:G:H21	53:1:1580:A:H62	1.62	0.48
53:1:1645:G:H5''	53:1:1646:C:C5'	2.38	0.48
12:m:50:ARG:HH12	57:7:54:U:H5'	1.78	0.48
17:r:89:HIS:HE1	17:r:91:GLN:HB2	1.79	0.48
40:P:88:PRO:HG2	40:P:89:GLY:H	1.78	0.48
42:R:27:THR:HG21	52:3:1328:C:H5''	1.95	0.48
52:3:1251:A:O2'	52:3:1370:G:H5'	2.14	0.48
53:1:2724:U:H2'	53:1:2725:A:C8	2.49	0.48
1:b:204:LEU:HB3	1:b:209:ALA:CB	2.44	0.47
2:c:35:THR:HG22	2:c:73:VAL:HG21	1.96	0.47
9:j:80:HIS:NE2	53:1:2642:G:H5'	2.29	0.47
10:k:57:VAL:C	10:k:58:LEU:HD12	2.39	0.47
15:p:89:GLY:O	15:p:112:ARG:NH1	2.47	0.47
31:G:53:LEU:O	31:G:56:LEU:HB3	2.14	0.47
42:R:76:ILE:HG22	42:R:80:MET:HE1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:V:30:HIS:HB3	46:V:35:LYS:H	1.79	0.47
53:1:331:C:H41	53:1:1210:G:N2	2.11	0.47
53:1:2011:U:H2'	53:1:2012:G:O4'	2.14	0.47
53:1:2128:G:H1'	53:1:2173:A:N3	2.29	0.47
53:1:2704:C:H2'	53:1:2705:A:O4'	2.14	0.47
53:1:2756:U:H3	53:1:2758:A:H62	1.62	0.47
1:b:75:ALA:HB2	1:b:95:TYR:HD1	1.78	0.47
3:d:147:LEU:HD12	3:d:168:ASP:O	2.14	0.47
15:p:89:GLY:HA2	15:p:111:GLU:HA	1.94	0.47
31:G:47:PRO:HA	31:G:50:ASN:HD21	1.79	0.47
31:G:73:ARG:HD3	31:G:73:ARG:H	1.79	0.47
35:K:46:GLN:HA	35:K:56:LYS:HD2	1.96	0.47
50:Z:44:ARG:NE	52:3:722:G:H5'	2.29	0.47
52:3:24:U:H2'	52:3:25:C:C6	2.49	0.47
52:3:193:C:H2'	52:3:194:C:C6	2.49	0.47
52:3:392:C:H2'	52:3:393:A:H8	1.79	0.47
52:3:757:U:H2'	52:3:758:C:O4'	2.14	0.47
52:3:1170:A:H2'	52:3:1171:A:O4'	2.14	0.47
53:1:69:C:O2'	53:1:70:G:H5'	2.13	0.47
53:1:2104:C:H2'	53:1:2105:U:C6	2.49	0.47
53:1:2236:U:H2'	53:1:2237:G:O4'	2.14	0.47
53:1:2372:U:H2'	53:1:2373:G:C8	2.49	0.47
54:2:3:C:H3'	54:2:4:C:C5'	2.44	0.47
2:c:46:ARG:HB2	2:c:84:LEU:HD12	1.95	0.47
14:o:29:HIS:HB3	14:o:36:TYR:HB2	1.97	0.47
16:q:24:TYR:HE1	53:1:17:G:H4'	1.80	0.47
27:C:5:ARG:NH1	53:1:2285:C:H3'	2.29	0.47
38:N:38:PHE:HA	38:N:41:GLU:HB2	1.95	0.47
40:P:61:ALA:HA	40:P:64:VAL:HG22	1.96	0.47
52:3:1001:C:H2'	52:3:1002:G:H8	1.79	0.47
52:3:1397:C:N4	56:4:22:A:H2'	2.28	0.47
53:1:1547:C:H2'	53:1:1548:A:C8	2.49	0.47
53:1:2875:C:H2'	53:1:2876:G:C8	2.49	0.47
57:7:64:A:H2'	57:7:65:G:C8	2.49	0.47
1:b:46:GLY:HA3	53:1:773:U:H5'	1.96	0.47
4:e:33:ILE:HD13	4:e:95:MET:HB2	1.97	0.47
11:l:79:LEU:HG	11:l:111:ILE:O	2.15	0.47
15:p:97:TYR:HD2	53:1:2718:G:H5'	1.80	0.47
32:H:127:VAL:HG22	32:H:128:MET:N	2.28	0.47
33:I:190:LEU:HD23	33:I:192:ALA:H	1.80	0.47
36:L:99:ALA:HA	36:L:102:TRP:CE3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:14:SER:HB2	38:N:69:GLY:HA3	1.95	0.47
49:Y:82:ILE:HA	49:Y:85:LEU:HD13	1.97	0.47
51:a:27:ILE:HD13	51:a:186:LYS:HB2	1.95	0.47
52:3:396:C:C2'	52:3:397:A:H5''	2.44	0.47
53:1:2313:C:H2'	53:1:2314:A:C8	2.49	0.47
53:1:2322:A:H2'	53:1:2323:G:O4'	2.14	0.47
54:2:106:G:H2'	54:2:107:G:O4'	2.14	0.47
57:7:47:U:H3'	57:7:48:C:C5'	2.44	0.47
1:b:209:ALA:HA	1:b:212:TRP:NE1	2.29	0.47
1:b:260:LYS:HA	1:b:263:ASP:OD2	2.14	0.47
10:k:35:VAL:HG12	10:k:69:VAL:HG22	1.97	0.47
12:m:34:LYS:HA	12:m:101:VAL:HA	1.97	0.47
15:p:25:VAL:HG22	15:p:26:GLU:N	2.29	0.47
28:D:14:ARG:HD2	53:1:771:G:OP1	2.14	0.47
28:D:42:LEU:HD12	28:D:42:LEU:H	1.78	0.47
33:I:4:LEU:HD11	52:3:405:U:C6	2.49	0.47
36:L:117:LEU:HG	36:L:121:ASN:HD21	1.80	0.47
42:R:65:GLU:HG2	42:R:66:GLY:N	2.29	0.47
42:R:79:LEU:HD11	42:R:86:ARG:HB2	1.96	0.47
44:T:2:LEU:HD23	44:T:34:GLN:OE1	2.14	0.47
49:Y:56:ILE:HD13	49:Y:59:ARG:HH12	1.79	0.47
52:3:70:U:H4'	52:3:71:A:H8	1.80	0.47
52:3:423:G:H2'	52:3:424:G:H5'	1.97	0.47
52:3:1187:G:H2'	52:3:1188:A:H8	1.79	0.47
53:1:528:A:N1	53:1:2042:A:H2'	2.29	0.47
53:1:2861:U:H2'	53:1:2862:G:H8	1.80	0.47
57:7:61:C:H5'	57:7:61:C:H6	1.79	0.47
1:b:64:VAL:HG13	1:b:102:TYR:HB3	1.97	0.47
5:f:138:GLN:NE2	53:1:2746:U:H1'	2.29	0.47
10:k:64:ARG:NH1	10:k:101:GLY:HA3	2.29	0.47
12:m:17:ASN:HB2	12:m:95:LEU:HD22	1.97	0.47
18:s:69:LEU:HG	18:s:107:VAL:HG22	1.96	0.47
25:z:2:LYS:HE2	25:z:39:ASP:HB3	1.97	0.47
34:J:55:VAL:HG23	34:J:56:PRO:CD	2.40	0.47
37:M:29:SER:HB2	52:3:589:U:H5''	1.96	0.47
41:Q:98:ARG:HA	41:Q:103:CYS:SG	2.54	0.47
42:R:3:ILE:HG23	42:R:56:ARG:HG2	1.95	0.47
52:3:151:A:H62	52:3:170:U:H3	1.62	0.47
52:3:206:C:H2'	52:3:207:C:O4'	2.15	0.47
53:1:87:U:H5''	53:1:88:G:H5'	1.97	0.47
53:1:319:G:H2'	53:1:320:A:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:208:GLY:HA2	1:b:211:ARG:HB2	1.96	0.47
2:c:208:LYS:NZ	53:1:2731:G:O3'	2.48	0.47
6:g:116:ARG:O	6:g:118:PRO:HD3	2.14	0.47
7:h:23:LEU:HB2	7:h:118:ILE:HD11	1.97	0.47
11:l:29:LYS:HD2	53:1:566:U:OP1	2.15	0.47
11:l:48:ARG:HD2	53:1:666:A:C4'	2.30	0.47
12:m:4:PRO:HB2	12:m:7:THR:CG2	2.44	0.47
12:m:75:GLU:OE2	53:1:957:C:H5'	2.15	0.47
12:m:86:LYS:HD3	53:1:955:U:H5''	1.97	0.47
30:F:4:ARG:HH22	53:1:2477:U:C2'	2.27	0.47
31:G:55:GLU:O	31:G:59:ILE:HG13	2.14	0.47
34:J:15:ILE:HD12	34:J:15:ILE:N	2.29	0.47
34:J:44:ARG:NE	34:J:70:MET:HG3	2.29	0.47
34:J:106:ALA:HB3	34:J:111:ARG:HA	1.97	0.47
36:L:100:MET:HA	36:L:103:ILE:HD13	1.95	0.47
40:P:84:MET:HG2	40:P:110:THR:OG1	2.15	0.47
42:R:85:TYR:O	42:R:88:LEU:HG	2.15	0.47
43:S:92:ILE:HD12	43:S:92:ILE:N	2.28	0.47
49:Y:8:LYS:O	49:Y:12:GLN:HG3	2.14	0.47
49:Y:83:ASN:HA	49:Y:86:ALA:HB3	1.96	0.47
50:Z:36:PHE:C	50:Z:38:GLU:H	2.23	0.47
51:a:206:GLY:HA3	53:1:1860:G:H5''	1.96	0.47
52:3:211:G:C2'	52:3:212:G:H5'	2.45	0.47
52:3:868:C:H2'	52:3:869:G:O4'	2.15	0.47
52:3:1137:C:H5'	52:3:1138:G:H5'	1.97	0.47
53:1:244:A:H62	53:1:254:G:N2	2.06	0.47
53:1:974:G:H1'	53:1:975:A:C8	2.49	0.47
53:1:2861:U:H2'	53:1:2862:G:C8	2.49	0.47
8:i:73:PRO:HA	8:i:74:PRO:HD3	1.82	0.47
12:m:45:GLN:HG2	53:1:2485:G:H5'	1.97	0.47
16:q:5:ARG:NH1	53:1:585:G:N7	2.62	0.47
37:M:77:VAL:HG11	37:M:124:ILE:HD13	1.95	0.47
46:V:24:ILE:HD12	46:V:24:ILE:N	2.29	0.47
51:a:181:ASP:HB3	51:a:184:LYS:CG	2.45	0.47
52:3:1251:A:H2'	52:3:1252:A:O4'	2.15	0.47
53:1:871:U:H2'	53:1:872:U:C6	2.50	0.47
53:1:873:C:H2'	53:1:874:G:H8	1.80	0.47
53:1:1802:A:H2'	53:1:1803:A:C8	2.50	0.47
53:1:2292:U:H2'	53:1:2293:G:C8	2.50	0.47
53:1:2623:G:H2'	53:1:2624:G:H8	1.79	0.47
54:2:49:C:H2'	54:2:50:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:146:LYS:HE2	53:1:2221:G:H21	1.80	0.47
1:b:254:LYS:O	53:1:1797:G:H4'	2.15	0.47
6:g:57:LYS:HA	6:g:60:GLU:OE1	2.14	0.47
7:h:30:SER:H	7:h:109:LYS:HZ1	1.61	0.47
11:l:33:ARG:HD3	11:l:40:SER:HA	1.97	0.47
12:m:69:PRO:O	12:m:70:ASP:HB2	2.15	0.47
34:J:38:VAL:HG23	34:J:70:MET:HE1	1.96	0.47
51:a:46:VAL:HG22	51:a:212:VAL:HG13	1.97	0.47
52:3:966:G:H2'	52:3:966:G:N3	2.29	0.47
53:1:1720:U:H2'	53:1:1721:G:O4'	2.14	0.47
53:1:2366:A:H2'	53:1:2367:G:O4'	2.15	0.47
54:2:108:A:H5'	54:2:109:A:O5'	2.15	0.47
3:d:52:VAL:HB	3:d:74:LYS:HE3	1.97	0.47
4:e:48:LEU:HA	4:e:51:ASN:HD21	1.79	0.47
4:e:65:LEU:HD22	54:2:42:C:C5	2.50	0.47
4:e:169:LEU:HD22	4:e:174:PHE:CZ	2.50	0.47
17:r:22:LEU:HD12	17:r:23:GLU:O	2.14	0.47
20:u:90:LYS:HZ3	53:1:101:A:H62	1.62	0.47
22:w:36:GLN:HE22	22:w:39:THR:HA	1.80	0.47
27:C:12:SER:HA	27:C:48:TYR:HA	1.97	0.47
50:Z:23:GLU:O	50:Z:24:LYS:HB3	2.15	0.47
52:3:501:C:H2'	52:3:502:A:C8	2.50	0.47
52:3:556:C:H2'	52:3:557:G:C8	2.50	0.47
53:1:2710:C:H2'	53:1:2711:A:H8	1.79	0.47
53:1:2818:U:H2'	53:1:2819:G:C8	2.50	0.47
1:b:70:LYS:HE3	1:b:73:ILE:HD12	1.97	0.46
3:d:111:GLU:HA	3:d:114:ARG:HE	1.80	0.46
9:j:6:ALA:O	9:j:48:VAL:HG21	2.15	0.46
30:F:8:LYS:NZ	53:1:2467:C:H5''	2.31	0.46
33:I:53:GLN:HB3	33:I:202:LEU:HB2	1.96	0.46
49:Y:55:PRO:HA	52:3:194:C:H5'	1.97	0.46
52:3:1308:U:H2'	52:3:1309:G:C8	2.49	0.46
53:1:1231:U:H2'	53:1:1232:G:H8	1.80	0.46
53:1:2013:A:H61	53:1:2613:U:H3	1.62	0.46
53:1:2329:U:H2'	53:1:2330:G:C8	2.49	0.46
53:1:2432:A:H1'	55:6:75:C:C4'	2.44	0.46
53:1:2795:C:H2'	53:1:2796:U:O4'	2.15	0.46
1:b:158:GLY:HA3	53:1:1820:U:C4	2.50	0.46
2:c:81:GLU:HB3	53:1:2636:C:H4'	1.97	0.46
5:f:41:GLU:HG2	5:f:43:LYS:HE2	1.96	0.46
29:E:1:PRO:N	53:1:591:U:H1'	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:E:54:LEU:HD23	53:1:938:G:OP1	2.14	0.46
43:S:41:TRP:HZ3	48:X:8:PRO:HD2	1.80	0.46
52:3:346:G:C2'	52:3:347:G:H5'	2.46	0.46
52:3:1053:G:O6	52:3:1199:U:H2'	2.14	0.46
53:1:2039:U:H2'	53:1:2040:G:H8	1.80	0.46
53:1:2547:A:H2'	53:1:2548:U:C6	2.50	0.46
5:f:72:ASN:O	5:f:75:VAL:HG12	2.14	0.46
6:g:58:LEU:O	6:g:61:VAL:HG22	2.14	0.46
7:h:55:VAL:HA	53:1:1084:A:C5'	2.44	0.46
8:i:133:ARG:HH21	53:1:1079:C:C4'	2.28	0.46
10:k:76:VAL:HG22	15:p:72:VAL:CG1	2.42	0.46
22:w:68:LYS:CD	22:w:69:GLY:H	2.24	0.46
30:F:36:ARG:O	30:F:37:GLN:O	2.34	0.46
40:P:30:ILE:HG13	40:P:45:THR:HG22	1.98	0.46
41:Q:88:ASP:HB2	52:3:523:A:N1	2.30	0.46
42:R:67:ASP:O	42:R:70:ARG:HG2	2.14	0.46
45:U:4:ILE:N	45:U:4:ILE:HD12	2.30	0.46
52:3:350:G:H2'	52:3:351:G:C8	2.50	0.46
52:3:940:C:H4'	52:3:1374:A:H2	1.80	0.46
53:1:560:C:H2'	53:1:561:G:O4'	2.15	0.46
53:1:662:G:H2'	53:1:663:G:H8	1.81	0.46
53:1:2800:A:H3'	53:1:2801:G:H5'	1.96	0.46
1:b:181:ARG:HG3	1:b:265:PHE:HB3	1.97	0.46
6:g:27:ARG:HD2	23:x:37:PHE:HE1	1.81	0.46
6:g:112:LYS:NZ	53:1:2220:U:O3'	2.45	0.46
9:j:113:PRO:HD2	53:1:558:U:P	2.56	0.46
13:n:14:SER:HA	13:n:17:ARG:HH22	1.79	0.46
14:o:70:ALA:O	14:o:74:VAL:HG23	2.15	0.46
15:p:57:ALA:HB2	15:p:74:GLN:HE22	1.81	0.46
16:q:53:LYS:HE2	53:1:994:C:C6	2.49	0.46
17:r:71:LYS:HE3	17:r:73:LYS:NZ	2.29	0.46
33:I:68:GLU:OE1	52:3:545:C:H5''	2.15	0.46
34:J:114:LEU:O	34:J:117:ALA:HB3	2.16	0.46
38:N:20:ILE:HG22	38:N:62:LEU:HG	1.97	0.46
38:N:83:THR:HB	38:N:97:LEU:HD21	1.97	0.46
39:O:6:ILE:H	39:O:6:ILE:HD12	1.81	0.46
40:P:36:ARG:NE	40:P:82:GLU:OE2	2.48	0.46
52:3:1137:C:H4'	52:3:1138:G:N2	2.30	0.46
53:1:639:U:H2'	53:1:640:C:C6	2.50	0.46
53:1:905:A:O2'	53:1:906:U:H5'	2.16	0.46
53:1:2087:G:H2'	53:1:2088:A:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:47:VAL:C	13:n:50:PRO:HD2	2.41	0.46
20:u:39:ASN:HB3	20:u:62:ALA:HB3	1.97	0.46
30:F:7:VAL:HG11	30:F:25:VAL:HG21	1.97	0.46
31:G:130:LYS:NZ	52:3:1160:G:H5'	2.30	0.46
35:K:40:GLU:O	35:K:61:LEU:HB3	2.15	0.46
41:Q:39:THR:HG22	41:Q:40:THR:N	2.29	0.46
48:X:76:THR:HG21	52:3:1221:G:H4'	1.97	0.46
52:3:674:G:H2'	52:3:675:A:C8	2.51	0.46
52:3:1131:G:H22	52:3:1144:G:H4'	1.80	0.46
53:1:118:A:OP2	53:1:119:A:H2'	2.15	0.46
53:1:1474:U:C2'	53:1:1475:G:H5'	2.45	0.46
53:1:2743:U:H2'	53:1:2744:G:C4'	2.45	0.46
12:m:22:GLN:H	12:m:100:LYS:HZ2	1.63	0.46
12:m:66:ARG:HB3	12:m:101:VAL:O	2.16	0.46
41:Q:23:LEU:HD22	41:Q:29:LYS:NZ	2.30	0.46
52:3:129:A:H1'	52:3:130:A:C8	2.50	0.46
13:n:2:ARG:H	13:n:5:LYS:HD3	1.79	0.46
17:r:80:ARG:N	53:1:565:C:OP2	2.48	0.46
19:t:11:LEU:HD12	19:t:50:LEU:HD12	1.97	0.46
23:x:73:ARG:HD2	23:x:75:GLU:OE1	2.16	0.46
40:P:34:THR:OG1	40:P:39:ASN:O	2.28	0.46
42:R:63:VAL:HG12	42:R:68:LEU:HG	1.98	0.46
43:S:20:PHE:O	43:S:21:ALA:HB3	2.15	0.46
52:3:59:A:N6	52:3:331:G:H1'	2.31	0.46
52:3:166:U:H2'	52:3:167:A:C8	2.51	0.46
52:3:1004:A:H2'	52:3:1005:A:O4'	2.16	0.46
53:1:511:U:H2'	53:1:512:G:H5'	1.98	0.46
53:1:1554:U:H3'	53:1:1555:G:H5'	1.97	0.46
53:1:1825:U:H2'	53:1:1826:G:H8	1.81	0.46
53:1:2487:G:H2'	53:1:2488:G:C8	2.51	0.46
53:1:2757:A:H2'	53:1:2757:A:N3	2.31	0.46
55:6:11:A:H2'	55:6:12:G:C8	2.51	0.46
7:h:97:LYS:NZ	7:h:125:ARG:HD2	2.31	0.46
7:h:118:ILE:CB	7:h:119:PRO:HD3	2.45	0.46
9:j:95:ARG:NH2	53:1:2768:U:H4'	2.31	0.46
38:N:11:ARG:HB3	38:N:73:GLY:O	2.16	0.46
38:N:53:LEU:O	38:N:53:LEU:HD23	2.16	0.46
43:S:89:ARG:NH1	43:S:89:ARG:O	2.49	0.46
45:U:15:PRO:HD2	45:U:42:ILE:HD13	1.96	0.46
52:3:834:U:H2'	52:3:835:U:C6	2.51	0.46
52:3:860:A:H2'	52:3:861:G:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1449:C:H2'	52:3:1450:U:O4'	2.15	0.46
53:1:2196:C:O2'	53:1:2197:U:H5'	2.15	0.46
53:1:2385:C:H2'	53:1:2386:A:C8	2.50	0.46
53:1:2743:U:H2'	53:1:2744:G:O4'	2.15	0.46
1:b:18:VAL:HG23	1:b:202:ARG:HE	1.81	0.46
4:e:116:LEU:O	4:e:177:ARG:N	2.41	0.46
14:o:31:THR:C	14:o:33:ARG:H	2.24	0.46
16:q:57:ARG:O	16:q:61:ILE:HG12	2.16	0.46
32:H:148:ILE:HG13	32:H:200:TRP:O	2.16	0.46
37:M:49:LYS:HB3	37:M:51:GLU:HG2	1.98	0.46
38:N:36:GLN:HA	38:N:40:ARG:HH12	1.79	0.46
38:N:61:ASP:C	38:N:62:LEU:HD12	2.41	0.46
44:T:75:ALA:O	44:T:78:THR:HG22	2.16	0.46
50:Z:39:LYS:N	50:Z:40:PRO:CD	2.79	0.46
52:3:67:C:H2'	52:3:68:G:C8	2.51	0.46
52:3:312:C:H2'	52:3:313:A:C8	2.50	0.46
52:3:390:U:H2'	52:3:391:G:C8	2.50	0.46
52:3:556:C:H2'	52:3:557:G:H8	1.81	0.46
53:1:1035:U:H2'	53:1:1036:G:C8	2.51	0.46
53:1:2475:C:C2'	53:1:2476:A:H5'	2.46	0.46
3:d:73:ILE:HD12	3:d:78:TRP:HE3	1.81	0.46
4:e:115:GLY:O	4:e:177:ARG:HB3	2.16	0.46
33:I:77:GLU:CG	33:I:92:LEU:HD11	2.45	0.46
34:J:155:LYS:HB2	37:M:70:VAL:HG13	1.98	0.46
46:V:5:ARG:HD2	52:3:636:U:OP1	2.16	0.46
46:V:6:THR:OG1	46:V:7:LEU:N	2.49	0.46
52:3:1293:C:H2'	52:3:1294:G:C8	2.51	0.46
53:1:215:G:C4'	53:1:216:A:H4'	2.46	0.46
53:1:2087:G:H2'	53:1:2088:A:C8	2.51	0.46
18:s:88:ARG:HH12	53:1:2013:A:H2	1.63	0.45
19:t:80:TRP:CD1	19:t:80:TRP:N	2.84	0.45
33:I:86:GLY:HA3	33:I:196:GLU:OE1	2.15	0.45
33:I:104:MET:SD	33:I:170:LEU:HD13	2.56	0.45
34:J:89:THR:O	52:3:864:A:H5'	2.16	0.45
36:L:134:VAL:HG23	36:L:137:ARG:HE	1.82	0.45
38:N:48:ARG:O	38:N:52:GLU:HG2	2.16	0.45
42:R:99:GLN:HG2	52:3:1307:U:OP1	2.15	0.45
50:Z:65:ARG:CZ	52:3:1088:G:H4'	2.46	0.45
51:a:177:LYS:NZ	53:1:2125:G:H5'	2.32	0.45
52:3:1494:G:H4'	53:1:1913:A:N7	2.31	0.45
53:1:468:G:H2'	53:1:469:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1394:U:H5''	53:1:1604:C:OP1	2.16	0.45
53:1:2360:G:H2'	53:1:2361:G:H5'	1.98	0.45
53:1:2583:G:H2'	53:1:2584:U:O4'	2.16	0.45
53:1:2818:U:H4'	53:1:2837:A:H4'	1.98	0.45
54:2:60:C:H2'	54:2:61:G:C8	2.51	0.45
1:b:257:ARG:HG2	1:b:257:ARG:O	2.16	0.45
2:c:30:GLU:H	2:c:30:GLU:CD	2.24	0.45
7:h:117:LEU:HD23	7:h:117:LEU:C	2.40	0.45
10:k:35:VAL:HG11	10:k:69:VAL:HG22	1.97	0.45
15:p:63:ILE:HG23	15:p:63:ILE:O	2.15	0.45
22:w:40:LYS:NZ	53:1:858:G:H5'	2.32	0.45
25:z:13:ILE:HD12	53:1:988:A:C8	2.51	0.45
28:D:35:ARG:HE	53:1:54:G:H1'	1.82	0.45
33:I:48:SER:O	33:I:52:VAL:HG23	2.15	0.45
36:L:108:ARG:O	36:L:108:ARG:HD3	2.16	0.45
39:O:14:ASP:OD2	39:O:16:ARG:HB3	2.16	0.45
42:R:65:GLU:HG2	42:R:66:GLY:H	1.82	0.45
46:V:48:GLU:O	46:V:49:ASN:C	2.59	0.45
48:X:35:ARG:NH1	52:3:1221:G:H5''	2.31	0.45
52:3:1259:C:H3'	52:3:1260:G:C5'	2.45	0.45
52:3:1354:U:H2'	52:3:1355:G:C8	2.50	0.45
53:1:1330:C:H2'	53:1:1331:G:C8	2.52	0.45
53:1:1525:A:H2'	53:1:1526:C:O4'	2.15	0.45
53:1:2398:U:H2'	53:1:2399:G:C8	2.51	0.45
53:1:2639:A:H2'	53:1:2640:G:O4'	2.16	0.45
53:1:2743:U:H2'	53:1:2744:G:H5''	1.98	0.45
3:d:45:ALA:HB2	53:1:38:A:H4'	1.98	0.45
5:f:26:LYS:HB2	5:f:31:GLU:HG2	1.98	0.45
11:l:27:LEU:C	11:l:31:GLY:HA3	2.41	0.45
31:G:56:LEU:HD22	31:G:219:THR:HG23	1.97	0.45
39:O:41:PRO:O	39:O:42:LEU:O	2.34	0.45
45:U:5:ARG:NH2	45:U:26:ASN:HB3	2.31	0.45
52:3:1202:U:C2'	52:3:1203:C:H5'	2.47	0.45
53:1:969:G:H2'	53:1:970:U:C6	2.52	0.45
53:1:1070:A:H2'	53:1:1097:U:OP1	2.17	0.45
53:1:1761:C:H2'	53:1:1762:A:O4'	2.17	0.45
53:1:1825:U:H2'	53:1:1826:G:C8	2.51	0.45
53:1:1991:U:C2'	53:1:1992:G:H5''	2.44	0.45
53:1:2163:A:N3	53:1:2164:C:H5'	2.32	0.45
53:1:2417:C:H2'	53:1:2418:A:C8	2.51	0.45
53:1:2834:G:H2'	53:1:2879:A:N6	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:144:GLU:HG3	1:b:151:GLY:N	2.32	0.45
2:c:136:ASN:ND2	2:c:139:SER:O	2.49	0.45
4:e:79:ARG:HG3	4:e:81:GLY:H	1.81	0.45
7:h:34:THR:O	7:h:37:LYS:HB3	2.16	0.45
11:l:109:LYS:HD2	11:l:126:ARG:NH1	2.25	0.45
33:I:10:LEU:HG	33:I:62:ARG:HD3	1.97	0.45
33:I:30:LYS:HD2	52:3:411:A:H8	1.82	0.45
39:O:59:LYS:HE2	39:O:62:ARG:HH21	1.81	0.45
39:O:84:VAL:O	39:O:88:MET:HE2	2.17	0.45
45:U:18:GLN:HA	45:U:38:PHE:HA	1.97	0.45
45:U:31:ARG:NH2	52:3:230:G:H5''	2.31	0.45
53:1:891:G:H2'	53:1:892:A:C8	2.52	0.45
53:1:1182:G:H2'	53:1:1183:U:O4'	2.17	0.45
53:1:1695:G:H3'	53:1:1695:G:N3	2.32	0.45
53:1:2139:U:H2'	53:1:2140:G:C8	2.51	0.45
53:1:2215:C:H2'	53:1:2216:G:C8	2.51	0.45
53:1:2705:A:H2'	53:1:2706:A:O4'	2.17	0.45
2:c:161:MET:HE1	53:1:2050:C:O2	2.17	0.45
4:e:84:ILE:HG21	53:1:2312:U:C5'	2.45	0.45
6:g:50:ARG:HD2	6:g:50:ARG:C	2.42	0.45
7:h:40:GLU:O	7:h:43:LYS:HB3	2.17	0.45
18:s:8:ARG:HD3	53:1:494:G:OP1	2.15	0.45
36:L:139:ASP:O	36:L:143:MET:HG2	2.16	0.45
38:N:104:THR:HG23	52:3:1180:A:H5'	1.97	0.45
42:R:80:MET:HG3	42:R:91:ARG:HD3	1.97	0.45
53:1:1026:G:H2'	53:1:1027:A:C8	2.47	0.45
53:1:1979:U:O2'	53:1:1980:G:H5'	2.17	0.45
53:1:2229:U:H2'	53:1:2230:G:H8	1.81	0.45
53:1:2591:C:H2'	53:1:2592:G:C8	2.52	0.45
31:G:34:ARG:O	31:G:37:VAL:HG12	2.17	0.45
34:J:76:ASN:HB2	34:J:81:GLN:NE2	2.31	0.45
35:K:38:ARG:HB2	35:K:63:ASN:HB3	1.98	0.45
35:K:71:ILE:O	35:K:74:LEU:HB3	2.17	0.45
39:O:22:THR:HA	39:O:25:ILE:HG12	1.98	0.45
40:P:91:GLY:O	40:P:93:GLU:N	2.49	0.45
43:S:38:GLU:HG3	43:S:42:ASN:ND2	2.31	0.45
46:V:39:ARG:NH1	46:V:40:THR:O	2.50	0.45
47:W:40:PRO:HB3	52:3:720:C:H5''	1.99	0.45
53:1:123:G:H2'	53:1:124:G:O4'	2.17	0.45
53:1:1079:C:H2'	53:1:1080:A:C8	2.52	0.45
53:1:1812:U:H2'	53:1:1813:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:41:GLY:HA2	53:1:1813:G:O2'	2.16	0.45
4:e:79:ARG:HD2	4:e:80:GLN:N	2.29	0.45
9:j:81:ILE:H	9:j:81:ILE:CD1	2.27	0.45
10:k:115:ILE:HD12	10:k:115:ILE:N	2.30	0.45
23:x:56:ARG:NH2	53:1:400:G:N7	2.64	0.45
31:G:86:CYS:HB2	31:G:217:ALA:HB1	1.98	0.45
34:J:90:GLY:O	34:J:129:SER:OG	2.35	0.45
38:N:122:ARG:NH1	38:N:123:ARG:O	2.49	0.45
43:S:52:ARG:NH1	52:3:1219:A:H5''	2.32	0.45
51:a:3:LYS:HE2	53:1:2151:U:H5''	1.99	0.45
52:3:977:A:H3'	52:3:977:A:N3	2.32	0.45
52:3:1514:G:H2'	52:3:1515:G:H8	1.82	0.45
53:1:475:C:H4'	53:1:510:C:H5'	1.97	0.45
53:1:599:A:H2'	53:1:600:G:H8	1.81	0.45
53:1:676:A:H62	53:1:802:A:H61	1.65	0.45
53:1:1947:C:H2'	53:1:1948:G:C8	2.52	0.45
55:5:23:C:H2'	55:5:24:U:C6	2.52	0.45
1:b:123:ILE:HG13	35:K:80:PHE:CG	2.51	0.45
11:l:18:ARG:HH12	53:1:1249:U:H2'	1.82	0.45
23:x:6:VAL:HA	23:x:73:ARG:HH22	1.81	0.45
30:F:9:LYS:HG2	30:F:11:CYS:O	2.16	0.45
36:L:118:ARG:HA	36:L:121:ASN:HD22	1.82	0.45
43:S:63:CYS:HB3	43:S:67:GLY:N	2.27	0.45
52:3:79:G:O2'	52:3:80:A:H5'	2.16	0.45
52:3:160:A:H2'	52:3:161:A:O4'	2.17	0.45
52:3:265:G:H2'	52:3:267:C:H5	1.82	0.45
52:3:1218:C:H2'	52:3:1219:A:H8	1.81	0.45
53:1:818:G:C2'	53:1:819:A:H5''	2.46	0.45
53:1:2111:U:H3	53:1:2147:A:H1'	1.82	0.45
53:1:2837:A:H2'	53:1:2838:G:C8	2.52	0.45
1:b:49:THR:HG21	53:1:1813:G:H1'	1.99	0.45
1:b:174:ARG:HA	1:b:180:MET:HG3	1.99	0.45
6:g:110:VAL:CG1	6:g:114:GLU:HB2	2.47	0.45
9:j:25:LEU:HB3	53:1:1140:C:OP1	2.17	0.45
14:o:108:ASP:HA	14:o:111:ARG:HD2	1.99	0.45
21:v:29:ILE:HD12	21:v:39:ALA:HA	1.99	0.45
21:v:64:VAL:HA	21:v:69:GLU:HA	1.98	0.45
33:I:112:GLU:O	33:I:116:LEU:HD23	2.17	0.45
35:K:3:HIS:N	35:K:92:THR:HG22	2.32	0.45
37:M:24:VAL:HG13	37:M:24:VAL:O	2.17	0.45
43:S:41:TRP:O	43:S:44:VAL:HG12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:66:ILE:HG22	49:Y:68:LYS:H	1.80	0.45
50:Z:57:LYS:HD3	50:Z:60:ALA:HB3	1.97	0.45
52:3:912:C:O2'	52:3:913:A:H5'	2.16	0.45
53:1:826:U:H2'	53:1:828:U:O4'	2.17	0.45
53:1:1161:C:H2'	53:1:1162:G:C8	2.52	0.45
53:1:1909:C:H2'	53:1:1910:G:H8	1.81	0.45
53:1:2112:G:H1'	55:6:19:G:O2'	2.17	0.45
53:1:2637:U:H2'	53:1:2638:G:O4'	2.17	0.45
54:2:35:C:C2'	54:2:36:C:H5'	2.47	0.45
2:c:120:GLY:O	2:c:124:ARG:HB2	2.16	0.45
2:c:142:VAL:HG23	2:c:143:PRO:HD2	1.98	0.45
3:d:198:GLU:OE2	3:d:199:MET:HG3	2.17	0.45
4:e:140:ILE:HD12	4:e:140:ILE:N	2.32	0.45
9:j:15:TRP:HZ3	9:j:55:ILE:HD11	1.82	0.45
16:q:55:GLN:HE21	53:1:559:G:H1'	1.81	0.45
38:N:126:PHE:HZ	52:3:967:C:H4'	1.82	0.45
39:O:19:ASP:HA	39:O:22:THR:HG22	1.98	0.45
41:Q:68:GLY:HA3	41:Q:98:ARG:HH12	1.82	0.45
43:S:2:LYS:NZ	52:3:1216:A:OP1	2.49	0.45
51:a:209:ILE:HD12	51:a:209:ILE:N	2.32	0.45
52:3:309:A:H2'	52:3:310:G:H8	1.82	0.45
52:3:909:A:H2'	52:3:910:C:O4'	2.16	0.45
53:1:158:U:H2'	53:1:159:G:O4'	2.17	0.45
53:1:611:C:H2'	53:1:612:G:O4'	2.17	0.45
53:1:644:A:H61	53:1:2349:G:H21	1.63	0.45
53:1:713:G:H21	53:1:718:A:H62	1.63	0.45
53:1:968:C:H2'	53:1:969:G:C8	2.52	0.45
53:1:1045:C:H5'	53:1:1046:A:H5''	1.99	0.45
53:1:1299:G:O6	53:1:1639:C:H5''	2.17	0.45
53:1:1363:C:H2'	53:1:1364:G:C8	2.52	0.45
54:2:101:A:H2'	54:2:102:G:O4'	2.16	0.45
2:c:3:GLY:C	2:c:4:LEU:HD12	2.42	0.44
16:q:17:LEU:HA	16:q:20:ALA:HB3	1.99	0.44
20:u:47:PRO:HG3	53:1:484:C:OP1	2.16	0.44
23:x:4:CYS:SG	23:x:50:VAL:HA	2.57	0.44
29:E:3:ILE:HD11	53:1:592:A:N3	2.32	0.44
31:G:22:TRP:CZ2	52:3:829:G:H4'	2.52	0.44
34:J:156:ARG:HH22	34:J:163:ILE:HD12	1.82	0.44
39:O:21:ALA:O	39:O:24:GLU:HG2	2.17	0.44
52:3:396:C:C3'	52:3:397:A:H5''	2.47	0.44
52:3:560:A:H5'	52:3:566:G:N2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:715:A:H2'	52:3:716:A:H8	1.81	0.44
52:3:917:G:H2'	52:3:918:A:C8	2.52	0.44
53:1:826:U:H5''	53:1:2429:G:OP1	2.17	0.44
1:b:53:ILE:HG13	1:b:54:GLY:N	2.33	0.44
2:c:135:GLY:O	53:1:2580:U:H5''	2.17	0.44
15:p:77:SER:O	15:p:80:VAL:HG22	2.17	0.44
20:u:56:GLY:N	53:1:483:A:O2'	2.48	0.44
23:x:2:ARG:HD2	23:x:29:LEU:HD11	1.99	0.44
29:E:38:LYS:O	29:E:41:ARG:HB3	2.17	0.44
31:G:160:LEU:HG	31:G:180:ILE:HG21	1.99	0.44
35:K:50:PRO:HG3	35:K:55:HIS:CE1	2.52	0.44
41:Q:76:HIS:HB3	41:Q:77:SER:H	1.62	0.44
50:Z:64:ALA:C	50:Z:66:ARG:H	2.25	0.44
52:3:655:A:H2'	52:3:656:G:H8	1.82	0.44
52:3:880:C:H2'	52:3:881:G:C8	2.52	0.44
53:1:1167:C:H2'	53:1:1168:G:H8	1.83	0.44
53:1:1877:A:H2'	53:1:1878:G:O4'	2.17	0.44
53:1:2131:U:OP1	53:1:2134:A:H5'	2.15	0.44
1:b:239:PHE:O	1:b:241:LYS:N	2.44	0.44
2:c:4:LEU:HB3	2:c:32:ASN:ND2	2.32	0.44
6:g:5:LEU:HB3	6:g:16:GLY:H	1.81	0.44
9:j:100:VAL:HA	9:j:103:ILE:HD12	1.98	0.44
12:m:58:LYS:HB2	12:m:60:GLN:HE22	1.82	0.44
31:G:170:ILE:O	31:G:174:GLU:HG3	2.18	0.44
34:J:45:VAL:HG12	34:J:46:GLY:H	1.81	0.44
37:M:4:ASP:HB2	37:M:80:PRO:HG3	1.99	0.44
45:U:8:ARG:HD3	45:U:17:TYR:CZ	2.53	0.44
52:3:246:A:H62	52:3:281:G:N2	2.15	0.44
53:1:729:G:H4'	53:1:763:G:C5'	2.47	0.44
53:1:1649:G:H2'	53:1:1650:A:H8	1.83	0.44
53:1:2128:G:H2'	53:1:2129:C:O4'	2.17	0.44
53:1:2515:C:H2'	53:1:2516:A:H8	1.82	0.44
53:1:2798:U:H4'	53:1:2799:A:C4	2.52	0.44
55:6:28:C:H2'	55:6:29:G:C8	2.52	0.44
3:d:155:GLU:HG3	3:d:156:ASN:N	2.32	0.44
4:e:7:TYR:O	4:e:12:VAL:HG23	2.17	0.44
5:f:120:ILE:HD11	5:f:132:LEU:HB2	1.99	0.44
13:n:36:THR:HG22	13:n:40:LYS:HD2	1.99	0.44
32:H:152:VAL:HG22	32:H:197:VAL:HG13	1.99	0.44
33:I:102:TYR:O	33:I:164:ARG:NH1	2.51	0.44
34:J:93:VAL:HG23	34:J:110:MET:SD	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:98:ALA:HB3	34:J:121:ASN:HB2	1.98	0.44
39:O:41:PRO:O	39:O:42:LEU:C	2.60	0.44
39:O:42:LEU:HA	39:O:43:PRO:HD2	1.79	0.44
40:P:71:ASP:O	40:P:72:ALA:HB3	2.17	0.44
41:Q:4:ASN:ND2	41:Q:8:ARG:HH22	2.15	0.44
44:T:57:ARG:HH12	44:T:61:GLN:HB2	1.81	0.44
51:a:186:LYS:HA	51:a:189:LEU:HD12	1.99	0.44
52:3:673:A:H2'	52:3:674:G:C8	2.53	0.44
52:3:1309:G:H2'	52:3:1310:G:H8	1.83	0.44
52:3:1404:C:H2'	52:3:1405:G:C8	2.51	0.44
53:1:274:C:H2'	53:1:275:C:O4'	2.18	0.44
53:1:438:G:H2'	53:1:439:A:C8	2.53	0.44
53:1:2572:A:OP1	53:1:2574:G:H4'	2.17	0.44
2:c:105:LYS:O	2:c:177:VAL:HG12	2.16	0.44
7:h:55:VAL:HA	53:1:1084:A:H5''	1.99	0.44
11:l:61:LEU:HB2	29:E:12:ARG:HD3	1.98	0.44
24:y:23:ARG:HB3	24:y:24:GLU:OE2	2.18	0.44
32:H:49:ALA:HB1	32:H:75:VAL:HG12	1.98	0.44
53:1:1020:A:C1'	53:1:1021:A:OP2	2.59	0.44
53:1:1138:G:H2'	53:1:1139:G:O4'	2.18	0.44
53:1:1297:C:H2'	53:1:1298:C:C6	2.52	0.44
53:1:2412:A:H2'	53:1:2413:G:O4'	2.18	0.44
3:d:147:LEU:HD22	3:d:183:PHE:HD2	1.83	0.44
4:e:11:VAL:HG21	4:e:172:PHE:CZ	2.53	0.44
5:f:19:ASN:O	5:f:22:VAL:HG22	2.17	0.44
7:h:88:HIS:HB3	7:h:89:PRO:HD3	2.00	0.44
11:l:124:GLY:H	11:l:144:GLU:HA	1.82	0.44
33:I:196:GLU:O	33:I:200:VAL:HG23	2.17	0.44
40:P:23:HIS:ND1	40:P:86:LYS:HE3	2.33	0.44
53:1:27:G:N2	53:1:512:G:H1'	2.32	0.44
53:1:523:C:H2'	53:1:524:G:C8	2.53	0.44
53:1:729:G:H4'	53:1:763:G:H5'	2.00	0.44
53:1:1561:C:H2'	53:1:1562:U:C6	2.52	0.44
53:1:2233:U:H2'	53:1:2234:G:C8	2.52	0.44
4:e:88:VAL:HA	54:2:42:C:O2	2.18	0.44
10:k:23:LYS:HD3	10:k:23:LYS:HA	1.82	0.44
11:l:37:GLY:O	11:l:41:ARG:HG2	2.18	0.44
13:n:14:SER:HB2	53:1:2689:U:O2'	2.17	0.44
16:q:25:GLY:O	16:q:29:ARG:NH1	2.51	0.44
27:C:44:GLN:HG3	27:C:45:HIS:H	1.83	0.44
34:J:45:VAL:HG12	34:J:46:GLY:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:3:HIS:HA	35:K:65:GLU:HA	2.00	0.44
36:L:55:LYS:HB3	36:L:59:GLU:HG3	1.99	0.44
41:Q:85:ARG:HA	41:Q:93:ARG:HA	1.99	0.44
44:T:60:SER:HB2	52:3:581:G:H5'	1.98	0.44
51:a:22:ASP:OD2	51:a:24:ASN:ND2	2.51	0.44
51:a:23:ILE:HD12	51:a:186:LYS:HZ2	1.83	0.44
52:3:945:G:H2'	52:3:945:G:N3	2.33	0.44
52:3:1486:G:H2'	52:3:1487:G:C8	2.53	0.44
53:1:543:G:H2'	53:1:544:C:O4'	2.18	0.44
53:1:909:A:H2'	53:1:912:C:C5	2.53	0.44
53:1:1071:G:OP1	53:1:1071:G:H3'	2.18	0.44
53:1:1130:U:C2	53:1:2025:C:H5''	2.53	0.44
53:1:1326:U:H2'	53:1:1327:A:C8	2.50	0.44
53:1:1686:C:H2'	53:1:1687:G:O4'	2.17	0.44
54:2:6:G:H2'	54:2:7:G:H8	1.83	0.44
4:e:30:VAL:HG13	4:e:30:VAL:O	2.18	0.44
4:e:151:LEU:HD12	4:e:151:LEU:N	2.33	0.44
6:g:78:VAL:HB	6:g:144:VAL:HG22	2.00	0.44
8:i:76:ALA:O	8:i:80:LYS:HG2	2.18	0.44
10:k:15:GLY:O	10:k:47:ILE:HG12	2.18	0.44
16:q:74:SER:HB2	16:q:77:LYS:HE3	1.99	0.44
17:r:88:GLY:HA3	53:1:1225:G:OP1	2.18	0.44
26:B:14:MET:HG2	53:1:15:G:O2'	2.17	0.44
34:J:24:VAL:HG11	52:3:1070:U:OP1	2.18	0.44
36:L:21:LEU:HD23	36:L:21:LEU:H	1.83	0.44
38:N:112:ARG:HH21	52:3:1368:A:H5''	1.82	0.44
39:O:38:GLY:O	39:O:40:ILE:HD12	2.18	0.44
45:U:76:LYS:HA	45:U:80:LYS:HZ3	1.82	0.44
49:Y:9:ARG:O	49:Y:9:ARG:HD2	2.18	0.44
51:a:177:LYS:HZ3	53:1:2125:G:H5'	1.83	0.44
52:3:58:C:O2'	52:3:59:A:H5'	2.17	0.44
52:3:291:U:H2'	52:3:292:G:C8	2.53	0.44
53:1:280:U:H2'	53:1:281:C:C6	2.52	0.44
53:1:433:C:O2'	53:1:434:U:H5'	2.18	0.44
53:1:542:C:C2'	53:1:543:G:H5''	2.47	0.44
53:1:1420:A:H5'	53:1:1421:G:OP2	2.17	0.44
53:1:1680:U:H2'	53:1:1681:G:H5'	2.00	0.44
53:1:1967:C:H2'	53:1:1968:G:O4'	2.17	0.44
53:1:2257:U:O2'	53:1:2258:C:H5'	2.18	0.44
3:d:5:LEU:HD13	3:d:8:ALA:HB3	2.00	0.44
4:e:111:ARG:HH11	42:R:69:ARG:HD2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:73:ASN:O	6:g:76:GLU:HG3	2.18	0.44
7:h:52:MET:HE2	7:h:95:LEU:HD21	1.99	0.44
20:u:48:VAL:HA	20:u:49:PRO:HD3	1.86	0.44
34:J:114:LEU:O	34:J:119:VAL:HG22	2.18	0.44
41:Q:51:VAL:HG22	41:Q:52:CYS:N	2.32	0.44
50:Z:28:LEU:HA	50:Z:31:VAL:HG12	1.99	0.44
52:3:626:G:H2'	52:3:627:G:C8	2.53	0.44
53:1:974:G:N3	53:1:974:G:H2'	2.33	0.44
53:1:1141:U:H4'	53:1:1142:A:O4'	2.17	0.44
53:1:2789:C:H2'	53:1:2790:U:H5'	2.00	0.44
1:b:251:THR:OG1	1:b:252:LYS:N	2.49	0.43
6:g:22:LYS:HD2	53:1:2094:A:P	2.58	0.43
10:k:63:VAL:HG23	10:k:64:ARG:HG3	2.00	0.43
11:l:27:LEU:O	11:l:31:GLY:HA3	2.17	0.43
13:n:22:ARG:HH22	53:1:2709:G:H5'	1.83	0.43
26:B:30:ASP:HB3	26:B:34:GLY:N	2.33	0.43
41:Q:70:GLY:O	41:Q:98:ARG:NH2	2.51	0.43
44:T:55:LEU:O	44:T:59:VAL:HG23	2.17	0.43
47:W:41:SER:HB2	47:W:51:GLN:HE21	1.83	0.43
52:3:855:U:H2'	52:3:856:C:C6	2.53	0.43
52:3:924:C:H2'	52:3:925:G:H8	1.83	0.43
52:3:1369:C:H2'	52:3:1370:G:C8	2.53	0.43
52:3:1488:G:H2'	52:3:1489:G:H8	1.83	0.43
53:1:145:C:H2'	53:1:146:A:C8	2.52	0.43
53:1:2038:G:H2'	53:1:2039:U:O4'	2.17	0.43
53:1:2818:U:H2'	53:1:2819:G:H8	1.81	0.43
54:2:66:A:H4'	54:2:67:G:N7	2.32	0.43
3:d:97:ASN:HB2	3:d:100:MET:HG3	1.99	0.43
3:d:144:GLU:HB3	3:d:166:LYS:NZ	2.33	0.43
6:g:97:ARG:NH2	53:1:2219:U:O2'	2.51	0.43
11:l:63:LYS:HA	29:E:12:ARG:HG2	2.00	0.43
15:p:108:ARG:HH12	52:3:1464:U:P	2.41	0.43
19:t:18:GLU:O	19:t:22:THR:HG23	2.18	0.43
22:w:44:GLY:H	22:w:47:VAL:HB	1.84	0.43
39:O:40:ILE:HD12	39:O:40:ILE:N	2.33	0.43
42:R:113:LYS:H	42:R:114:PRO:HD2	1.82	0.43
43:S:62:ARG:HH11	43:S:69:PRO:HD3	1.82	0.43
52:3:17:U:H2'	52:3:18:C:C6	2.53	0.43
52:3:453:G:H2'	52:3:454:G:O4'	2.18	0.43
52:3:837:U:H2'	52:3:838:G:H8	1.82	0.43
52:3:1435:G:H2'	52:3:1436:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:482:A:H1'	53:1:498:G:N2	2.33	0.43
53:1:2220:U:H2'	53:1:2221:G:H8	1.83	0.43
53:1:2238:G:H2'	53:1:2238:G:N3	2.33	0.43
54:2:48:U:H2'	54:2:49:C:C6	2.54	0.43
1:b:56:GLY:HA2	1:b:212:TRP:HA	2.00	0.43
1:b:203:VAL:HG23	53:1:1792:G:H5''	2.00	0.43
7:h:31:ARG:HH12	53:1:1054:A:H4'	1.83	0.43
10:k:87:LEU:HA	10:k:94:PRO:HA	1.99	0.43
22:w:42:HIS:CD2	22:w:73:ARG:HD3	2.53	0.43
22:w:74:LYS:HE2	53:1:857:G:H5''	2.00	0.43
24:y:52:ARG:O	24:y:55:THR:HG22	2.18	0.43
25:z:8:GLN:HE21	25:z:31:ILE:HG22	1.82	0.43
36:L:74:VAL:HA	36:L:87:PRO:HA	1.99	0.43
39:O:40:ILE:HD12	39:O:40:ILE:H	1.83	0.43
43:S:63:CYS:HB3	43:S:68:ARG:H	1.83	0.43
44:T:56:LEU:HA	44:T:59:VAL:HB	2.00	0.43
52:3:180:U:H2'	52:3:181:A:O4'	2.18	0.43
52:3:195:A:H2'	52:3:196:A:C8	2.53	0.43
52:3:485:U:H5'	52:3:486:U:OP2	2.18	0.43
52:3:837:U:H2'	52:3:838:G:C8	2.53	0.43
52:3:1352:C:H2'	52:3:1353:G:C8	2.53	0.43
53:1:45:G:H5''	53:1:46:G:C5'	2.21	0.43
53:1:598:U:H2'	53:1:599:A:C8	2.53	0.43
53:1:940:G:C3'	53:1:941:A:H5''	2.48	0.43
53:1:1001:A:H2'	53:1:1002:G:O4'	2.18	0.43
1:b:238:ASN:ND2	53:1:2595:G:H1	2.10	0.43
4:e:107:VAL:HG13	4:e:108:PRO:HD3	1.99	0.43
6:g:143:ILE:HD12	6:g:143:ILE:N	2.33	0.43
8:i:73:PRO:HG2	8:i:78:LEU:HD21	2.00	0.43
9:j:80:HIS:CD2	53:1:2642:G:H5'	2.53	0.43
12:m:105:MET:SD	12:m:108:VAL:HG21	2.59	0.43
22:w:47:VAL:HG12	22:w:55:LEU:HD12	2.00	0.43
31:G:114:LYS:HZ1	31:G:151:LYS:HB2	1.82	0.43
35:K:53:LYS:HB3	35:K:54:LEU:H	1.67	0.43
38:N:62:LEU:HD12	38:N:62:LEU:N	2.33	0.43
40:P:122:PRO:HB2	50:Z:33:ARG:CA	2.45	0.43
52:3:50:A:H4'	52:3:51:A:H5'	2.00	0.43
52:3:123:U:H5''	52:3:311:C:O2'	2.18	0.43
52:3:467:U:H5'	52:3:468:A:OP2	2.18	0.43
52:3:948:C:H2'	52:3:949:A:H8	1.83	0.43
53:1:690:G:H2'	53:1:691:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1137:G:H2'	53:1:1138:G:C8	2.52	0.43
53:1:1571:A:H2'	53:1:1572:A:H8	1.83	0.43
54:2:60:C:H2'	54:2:61:G:H8	1.83	0.43
3:d:29:HIS:HD2	11:l:6:LEU:HB3	1.83	0.43
4:e:84:ILE:CD1	53:1:2311:A:H1'	2.48	0.43
39:O:44:THR:HG23	39:O:69:THR:C	2.43	0.43
52:3:1501:C:H5''	52:3:1502:A:OP2	2.18	0.43
53:1:195:A:H2'	53:1:198:C:H41	1.83	0.43
53:1:253:C:H2'	53:1:254:G:O4'	2.18	0.43
53:1:351:C:H2'	53:1:352:A:C8	2.53	0.43
53:1:2030:A:N3	53:1:2499:C:H5''	2.33	0.43
2:c:135:GLY:HA2	53:1:743:A:OP1	2.18	0.43
9:j:35:ARG:HA	9:j:40:HIS:HD2	1.83	0.43
13:n:53:THR:HA	13:n:56:LYS:HG3	2.01	0.43
13:n:54:LEU:HD11	13:n:65:LEU:HD23	1.99	0.43
13:n:95:THR:HG22	13:n:96:ARG:H	1.82	0.43
23:x:24:THR:HG21	53:1:2081:U:H4'	2.01	0.43
25:z:29:ARG:HD3	53:1:1184:U:P	2.59	0.43
30:F:1:MET:N	53:1:2526:G:N3	2.65	0.43
32:H:154:GLY:HA3	32:H:195:ILE:HG23	2.00	0.43
33:I:77:GLU:HG3	33:I:92:LEU:HD11	2.01	0.43
34:J:108:GLY:O	34:J:109:ALA:HB3	2.18	0.43
39:O:15:HIS:HA	39:O:18:ILE:HG12	2.00	0.43
41:Q:30:ARG:HB3	52:3:363:A:OP2	2.18	0.43
42:R:70:ARG:O	42:R:74:MET:HG3	2.19	0.43
51:a:40:GLU:O	51:a:178:VAL:HG22	2.19	0.43
52:3:620:C:H2'	52:3:621:A:O4'	2.18	0.43
53:1:327:G:H2'	53:1:328:U:O4'	2.18	0.43
53:1:479:A:H1'	53:1:481:G:H5''	2.00	0.43
53:1:1161:C:H2'	53:1:1162:G:H8	1.83	0.43
53:1:1542:U:H2'	53:1:1543:G:O4'	2.18	0.43
53:1:1889:A:H2'	53:1:1890:A:C8	2.53	0.43
53:1:2118:U:H5	53:1:2149:U:H1'	1.84	0.43
53:1:2244:U:H2'	53:1:2245:U:O4'	2.19	0.43
53:1:2370:G:H2'	53:1:2371:G:O4'	2.18	0.43
54:2:65:U:O4	54:2:108:A:H2'	2.18	0.43
54:2:88:C:OP1	54:2:88:C:H3'	2.19	0.43
1:b:35:LYS:NZ	53:1:1353:A:H4'	2.32	0.43
1:b:55:GLY:N	53:1:692:C:OP1	2.52	0.43
15:p:24:THR:HB	15:p:87:ARG:HB2	2.00	0.43
17:r:79:ARG:C	17:r:80:ARG:HG2	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:7:HIS:N	18:s:103:ILE:O	2.47	0.43
25:z:40:THR:HG23	25:z:43:ILE:H	1.84	0.43
28:D:19:ARG:HB2	53:1:126:A:OP2	2.19	0.43
33:I:32:LYS:HD3	52:3:426:U:OP2	2.19	0.43
51:a:215:SER:OG	51:a:221:GLY:HA2	2.19	0.43
52:3:497:G:H2'	52:3:498:A:C8	2.53	0.43
52:3:1273:C:H2'	52:3:1274:A:O4'	2.19	0.43
53:1:133:U:H2'	53:1:134:G:C8	2.53	0.43
53:1:862:G:H2'	53:1:863:A:O4'	2.19	0.43
53:1:1093:G:H21	53:1:1098:A:H62	1.65	0.43
53:1:1736:U:H2'	53:1:1737:G:O4'	2.19	0.43
53:1:1955:U:H2'	53:1:2551:C:O2'	2.19	0.43
53:1:2019:A:H2	53:1:2035:G:H22	1.66	0.43
53:1:2215:C:H2'	53:1:2216:G:H8	1.84	0.43
2:c:4:LEU:HD23	2:c:32:ASN:HD22	1.84	0.43
2:c:181:ASP:O	2:c:185:ASN:HA	2.18	0.43
3:d:72:SER:OG	3:d:73:ILE:N	2.52	0.43
4:e:101:ARG:HB3	4:e:101:ARG:HH21	1.83	0.43
12:m:21:ALA:HB1	12:m:100:LYS:HZ2	1.84	0.43
17:r:79:ARG:HG3	17:r:80:ARG:HH12	1.81	0.43
31:G:169:HIS:HA	31:G:172:ILE:HG12	2.00	0.43
32:H:72:PRO:HA	32:H:75:VAL:HG22	2.01	0.43
32:H:182:ASP:OD2	32:H:203:LYS:HB2	2.18	0.43
36:L:113:LYS:HE3	52:3:1298:U:OP2	2.18	0.43
36:L:137:ARG:O	36:L:140:VAL:HG12	2.18	0.43
43:S:4:SER:O	43:S:8:ARG:HG3	2.18	0.43
43:S:74:ARG:HG2	43:S:74:ARG:HH11	1.84	0.43
46:V:44:HIS:O	46:V:70:LYS:HA	2.19	0.43
52:3:67:C:H2'	52:3:68:G:H8	1.83	0.43
52:3:950:U:H2'	52:3:951:G:H8	1.83	0.43
53:1:1636:U:H2'	53:1:1637:A:H8	1.84	0.43
53:1:2016:U:H2'	53:1:2017:U:C6	2.53	0.43
53:1:2837:A:H2'	53:1:2838:G:H8	1.83	0.43
53:1:2841:C:H2'	53:1:2842:G:C8	2.54	0.43
55:5:13:C:C3'	55:5:14:A:H5''	2.49	0.43
55:5:42:G:H2'	55:5:43:A:C8	2.53	0.43
1:b:131:MET:HE2	1:b:187:CYS:HB3	2.01	0.43
1:b:143:VAL:HG22	1:b:189:ALA:HB1	2.01	0.43
10:k:113:MET:SD	10:k:114:LYS:HG2	2.59	0.43
10:k:121:GLU:OE1	10:k:122:VAL:HG23	2.18	0.43
12:m:1:MET:C	12:m:2:LEU:HD12	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:80:ARG:HG2	17:r:80:ARG:NH1	2.32	0.43
24:y:12:GLU:O	24:y:15:ASN:OD1	2.36	0.43
36:L:63:VAL:O	36:L:67:ASN:ND2	2.52	0.43
37:M:8:ASP:O	37:M:11:THR:HG22	2.19	0.43
38:N:10:ARG:O	38:N:105:ARG:NE	2.51	0.43
40:P:127:ARG:NH2	52:3:1523:G:OP2	2.51	0.43
42:R:95:PRO:HB2	42:R:99:GLN:CD	2.44	0.43
52:3:356:A:H2'	52:3:357:G:O4'	2.19	0.43
53:1:1167:C:H2'	53:1:1168:G:C8	2.53	0.43
53:1:1181:U:H2'	53:1:1182:G:C8	2.54	0.43
53:1:2126:A:H2'	53:1:2162:G:C2	2.54	0.43
53:1:2197:U:H1'	53:1:2198:A:C8	2.54	0.43
53:1:2247:A:H2'	53:1:2248:C:C6	2.54	0.43
53:1:2809:A:H2'	53:1:2810:A:C8	2.54	0.43
2:c:110:THR:HB	2:c:202:ILE:HB	2.00	0.43
15:p:105:LYS:O	15:p:108:ARG:HG2	2.19	0.43
17:r:54:VAL:HG23	17:r:55:ASP:H	1.84	0.43
18:s:7:HIS:HB3	18:s:103:ILE:HB	2.00	0.43
18:s:40:ASN:O	18:s:41:LYS:HG2	2.19	0.43
30:F:20:ASP:HA	53:1:2757:A:OP2	2.18	0.43
39:O:40:ILE:HB	39:O:73:LEU:HD12	2.00	0.43
42:R:24:VAL:HA	52:3:1329:A:H5''	2.01	0.43
43:S:66:THR:HG23	52:3:1203:C:H4'	2.00	0.43
53:1:1137:G:H2'	53:1:1138:G:H8	1.83	0.43
53:1:1279:G:H2'	53:1:1280:G:C8	2.54	0.43
53:1:2209:G:H2'	53:1:2210:U:C5	2.53	0.43
53:1:2257:U:H2'	53:1:2258:C:C6	2.54	0.43
53:1:2443:C:H2'	53:1:2444:G:H8	1.82	0.43
53:1:2724:U:H2'	53:1:2725:A:H8	1.84	0.43
54:2:55:U:O2'	54:2:56:G:H5'	2.18	0.43
7:h:20:LYS:HA	7:h:20:LYS:HD3	1.90	0.42
10:k:2:ILE:HD12	10:k:8:LEU:HD21	2.00	0.42
16:q:48:ASP:O	16:q:52:ARG:HG2	2.19	0.42
17:r:38:VAL:HG11	17:r:57:GLY:HA3	2.00	0.42
20:u:5:ARG:HG2	20:u:93:ARG:NH2	2.33	0.42
42:R:113:LYS:HZ3	55:5:44:A:H4'	1.84	0.42
48:X:27:LYS:HD2	48:X:28:LYS:O	2.19	0.42
52:3:545:C:H2'	52:3:546:A:O4'	2.19	0.42
52:3:1346:A:C2'	52:3:1347:G:H4'	2.49	0.42
52:3:1453:G:H3'	52:3:1453:G:N3	2.33	0.42
53:1:403:U:O3'	53:1:404:A:H4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1054:A:H2'	53:1:1055:G:H8	1.84	0.42
53:1:1234:U:H2'	53:1:1235:G:O4'	2.18	0.42
53:1:2066:C:O2'	53:1:2067:G:H5'	2.19	0.42
53:1:2875:C:H2'	53:1:2876:G:H8	1.83	0.42
55:5:10:G:C2	55:5:26:G:H1'	2.54	0.42
1:b:229:HIS:HE2	1:b:246:PRO:HG3	1.83	0.42
2:c:22:ILE:HA	2:c:23:PRO:HD3	1.89	0.42
3:d:167:VAL:HG22	3:d:168:ASP:H	1.83	0.42
13:n:99:LYS:HE3	26:B:40:HIS:O	2.18	0.42
18:s:13:SER:OG	18:s:16:LYS:HE2	2.19	0.42
23:x:16:ASN:ND2	23:x:26:ARG:HD2	2.35	0.42
23:x:29:LEU:HD23	53:1:2230:G:C5'	2.47	0.42
26:B:28:SER:OG	26:B:39:ARG:HD2	2.19	0.42
33:I:149:LYS:NZ	33:I:177:MET:HB2	2.34	0.42
36:L:91:ARG:CZ	52:3:1378:C:H1'	2.49	0.42
38:N:5:TYR:CD2	38:N:88:GLU:HG2	2.54	0.42
39:O:41:PRO:HA	39:O:72:ARG:HD3	2.01	0.42
40:P:92:ARG:CZ	50:Z:16:ARG:HH22	2.32	0.42
43:S:41:TRP:CZ3	48:X:8:PRO:HD2	2.53	0.42
43:S:65:GLN:NE2	43:S:78:LEU:HD11	2.35	0.42
46:V:27:PHE:HB3	52:3:597:G:H4'	2.02	0.42
52:3:56:U:H2'	52:3:57:G:C8	2.54	0.42
52:3:505:G:H4'	52:3:534:U:C4	2.54	0.42
52:3:728:A:H2'	52:3:729:A:C8	2.55	0.42
52:3:1415:G:H2'	52:3:1416:G:C8	2.55	0.42
53:1:1790:C:H2'	53:1:1791:A:C5	2.54	0.42
2:c:28:GLU:HG3	2:c:30:GLU:OE2	2.19	0.42
3:d:5:LEU:HD12	3:d:10:SER:H	1.84	0.42
4:e:101:ARG:HB3	4:e:101:ARG:NH2	2.34	0.42
4:e:137:PHE:HA	4:e:138:PRO:HD3	1.92	0.42
10:k:15:GLY:O	10:k:46:ALA:HB1	2.19	0.42
10:k:41:ILE:O	10:k:57:VAL:HG13	2.18	0.42
10:k:76:VAL:H	15:p:72:VAL:HG12	1.84	0.42
11:l:63:LYS:O	29:E:29:ARG:NH1	2.52	0.42
13:n:60:VAL:HG23	53:1:1454:C:O2'	2.19	0.42
25:z:5:LYS:O	25:z:56:VAL:HG23	2.18	0.42
25:z:20:LYS:O	25:z:23:LEU:HB3	2.20	0.42
35:K:44:ARG:HA	35:K:57:ALA:O	2.19	0.42
36:L:87:PRO:HG3	36:L:148:LYS:HD3	2.01	0.42
36:L:99:ALA:O	36:L:103:ILE:HD12	2.19	0.42
39:O:6:ILE:HD12	39:O:6:ILE:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:16:ARG:HH21	50:Z:19:LYS:HG2	1.84	0.42
53:1:341:C:H2'	53:1:342:A:C8	2.54	0.42
53:1:721:A:H2'	53:1:722:A:C8	2.54	0.42
53:1:1214:A:H62	53:1:1235:G:H21	1.67	0.42
53:1:1260:A:H2'	53:1:1261:C:C6	2.54	0.42
53:1:1421:G:H1'	53:1:1494:A:H61	1.85	0.42
53:1:2055:C:H2'	53:1:2504:U:C5'	2.45	0.42
53:1:2078:C:H2'	53:1:2079:U:O4'	2.20	0.42
54:2:63:C:H2'	54:2:64:G:C8	2.54	0.42
57:7:70:G:H2'	57:7:71:G:O4'	2.19	0.42
1:b:141:HIS:ND1	1:b:192:GLY:O	2.52	0.42
3:d:3:LEU:HB2	3:d:12:LEU:HB3	2.02	0.42
3:d:99:LYS:HA	3:d:102:ARG:HH21	1.83	0.42
4:e:111:ARG:HH11	42:R:69:ARG:HE	1.67	0.42
6:g:55:GLU:HA	6:g:58:LEU:HD12	2.01	0.42
7:h:60:LEU:HD23	7:h:60:LEU:H	1.84	0.42
10:k:104:THR:HG22	10:k:105:ARG:H	1.84	0.42
15:p:69:VAL:HG13	15:p:69:VAL:O	2.19	0.42
25:z:2:LYS:HG3	25:z:39:ASP:HB3	2.00	0.42
31:G:141:GLU:O	31:G:144:GLU:HG3	2.19	0.42
33:I:74:TYR:OH	33:I:96:ARG:NH1	2.53	0.42
48:X:18:VAL:O	48:X:22:VAL:HG13	2.20	0.42
52:3:56:U:H2'	52:3:57:G:H8	1.85	0.42
52:3:665:A:O4'	52:3:733:G:H1'	2.20	0.42
52:3:1014:A:N3	52:3:1219:A:H1'	2.35	0.42
52:3:1130:A:N6	52:3:1144:G:H1'	2.31	0.42
53:1:12:U:O2'	53:1:13:A:H5'	2.20	0.42
53:1:876:C:H2'	53:1:877:A:O4'	2.20	0.42
53:1:1367:A:C2'	53:1:1368:G:H5'	2.50	0.42
1:b:46:GLY:HA3	53:1:773:U:C5'	2.50	0.42
1:b:91:ALA:HB2	1:b:105:ALA:HB2	2.01	0.42
1:b:143:VAL:HG22	1:b:189:ALA:CB	2.49	0.42
1:b:260:LYS:HD2	1:b:263:ASP:OD2	2.18	0.42
2:c:202:ILE:HD12	2:c:202:ILE:N	2.34	0.42
3:d:3:LEU:HD11	3:d:14:VAL:HG11	2.01	0.42
3:d:143:LEU:HG	3:d:185:LYS:HD2	2.00	0.42
6:g:22:LYS:CD	53:1:2093:G:H5'	2.49	0.42
6:g:29:PHE:HB2	53:1:2198:A:C2	2.54	0.42
19:t:77:ARG:CZ	53:1:63:A:H4'	2.49	0.42
21:v:7:GLU:O	21:v:41:GLU:HB3	2.20	0.42
23:x:36:ARG:HA	23:x:47:THR:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:59:TYR:OH	47:W:65:SER:HB2	2.19	0.42
36:L:78:ARG:NH2	36:L:81:GLY:O	2.52	0.42
38:N:90:ASP:HB3	38:N:91:GLU:H	1.67	0.42
38:N:114:LYS:CE	52:3:1187:G:H4'	2.49	0.42
40:P:26:PHE:HA	40:P:89:GLY:HA2	2.01	0.42
50:Z:16:ARG:HB2	50:Z:19:LYS:HD3	2.01	0.42
52:3:390:U:H2'	52:3:391:G:H8	1.84	0.42
52:3:766:A:H2'	52:3:767:A:O4'	2.19	0.42
52:3:1430:A:H2'	52:3:1431:A:O4'	2.18	0.42
52:3:1484:C:H2'	52:3:1485:U:C6	2.53	0.42
53:1:833:A:H2'	53:1:834:G:H8	1.85	0.42
53:1:1429:G:H2'	53:1:1430:G:H8	1.85	0.42
53:1:1474:U:H2'	53:1:1475:G:H5'	2.01	0.42
53:1:2788:C:H2'	53:1:2789:C:C6	2.55	0.42
54:2:95:U:H2'	54:2:96:G:C8	2.55	0.42
6:g:97:ARG:HE	53:1:2220:U:C5'	2.33	0.42
9:j:78:THR:CB	53:1:2641:G:H5''	2.49	0.42
15:p:26:GLU:HB3	15:p:84:SER:HB3	2.01	0.42
19:t:3:ARG:HD3	53:1:143:C:H1'	2.01	0.42
31:G:13:VAL:HA	31:G:202:ASN:OD1	2.19	0.42
32:H:147:GLY:HA3	32:H:171:ARG:O	2.19	0.42
39:O:57:VAL:HG13	52:3:972:C:H1'	2.02	0.42
40:P:23:HIS:HD2	40:P:30:ILE:HD13	1.85	0.42
46:V:61:ARG:HG2	46:V:73:THR:O	2.19	0.42
52:3:89:U:H2'	52:3:90:C:O4'	2.20	0.42
52:3:558:G:H2'	52:3:559:A:C2	2.55	0.42
52:3:751:U:H2'	52:3:752:G:O4'	2.19	0.42
53:1:195:A:H2'	53:1:198:C:N4	2.34	0.42
53:1:598:U:H2'	53:1:599:A:H8	1.85	0.42
53:1:687:C:H42	53:1:787:C:H4'	1.84	0.42
53:1:750:A:H5''	53:1:1615:C:N4	2.33	0.42
53:1:861:A:H2'	53:1:862:G:O4'	2.19	0.42
53:1:1465:G:H2'	53:1:1466:U:O4'	2.19	0.42
53:1:1775:U:H2'	53:1:1776:G:O4'	2.20	0.42
53:1:1880:U:H2'	53:1:1881:C:C6	2.54	0.42
2:c:132:ALA:HA	2:c:140:HIS:CE1	2.55	0.42
3:d:48:THR:OG1	3:d:51:GLU:HG3	2.19	0.42
4:e:73:VAL:HG11	4:e:76:PHE:CD2	2.54	0.42
8:i:133:ARG:NH1	53:1:1077:A:O2'	2.53	0.42
9:j:57:LEU:O	9:j:58:ASN:HB2	2.19	0.42
9:j:95:ARG:HH22	53:1:2768:U:H4'	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:x:56:ARG:HB3	53:1:372:G:N7	2.34	0.42
24:y:2:LYS:HZ1	24:y:6:LEU:HD22	1.85	0.42
26:B:14:MET:HA	53:1:15:G:O2'	2.20	0.42
32:H:152:VAL:HG13	32:H:197:VAL:HG22	2.00	0.42
33:I:64:TYR:OH	33:I:99:ASN:ND2	2.53	0.42
34:J:18:ASN:O	34:J:33:THR:HG22	2.19	0.42
34:J:44:ARG:HG3	34:J:70:MET:HG3	2.02	0.42
35:K:18:VAL:N	35:K:19:PRO:CD	2.82	0.42
41:Q:48:LEU:N	41:Q:48:LEU:HD12	2.34	0.42
44:T:45:HIS:O	44:T:47:LYS:N	2.53	0.42
45:U:33:ILE:HD12	45:U:33:ILE:H	1.85	0.42
47:W:29:LYS:HA	47:W:32:ILE:HG12	2.00	0.42
52:3:151:A:H2'	52:3:152:A:O4'	2.19	0.42
52:3:994:A:H61	52:3:1047:G:H1'	1.85	0.42
53:1:45:G:C5'	53:1:46:G:H5'	2.21	0.42
53:1:343:C:O2'	53:1:344:A:H5'	2.19	0.42
53:1:720:U:H2'	53:1:721:A:H8	1.84	0.42
53:1:1843:C:H2'	53:1:1844:C:C6	2.55	0.42
53:1:2055:C:H5'	53:1:2056:G:O5'	2.20	0.42
53:1:2417:C:H2'	53:1:2418:A:H8	1.84	0.42
53:1:2687:U:H2'	53:1:2688:G:O4'	2.20	0.42
1:b:47:ARG:HD3	53:1:778:G:OP1	2.20	0.42
1:b:164:VAL:HB	1:b:172:THR:HB	2.01	0.42
3:d:18:THR:HG23	3:d:106:LYS:HG2	2.02	0.42
4:e:110:ILE:HB	4:e:113:PHE:HB2	2.02	0.42
5:f:76:ILE:O	5:f:80:GLU:HG2	2.20	0.42
17:r:80:ARG:NH2	53:1:571:U:OP1	2.53	0.42
24:y:31:GLN:HG2	24:y:37:LEU:HB2	2.02	0.42
29:E:17:GLY:HA3	53:1:651:G:H4'	2.02	0.42
31:G:131:LYS:HD2	52:3:1158:C:O2'	2.19	0.42
32:H:102:ILE:HD12	32:H:102:ILE:N	2.30	0.42
32:H:162:ALA:CB	52:3:1056:U:H4'	2.50	0.42
38:N:29:ILE:HA	38:N:64:ILE:O	2.19	0.42
45:U:73:ALA:O	45:U:77:GLU:HG2	2.18	0.42
52:3:521:G:O2'	52:3:522:C:H5'	2.20	0.42
53:1:490:C:H4'	53:1:491:G:OP2	2.20	0.42
53:1:1570:A:H2'	53:1:1571:A:C8	2.55	0.42
53:1:1683:U:H2'	53:1:1684:G:C8	2.55	0.42
54:2:55:U:H2'	54:2:56:G:C8	2.55	0.42
54:2:63:C:H2'	54:2:64:G:H8	1.85	0.42
54:2:66:A:H4'	54:2:67:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:88:C:C5'	54:2:89:U:OP1	2.67	0.42
1:b:173:LEU:HD12	1:b:173:LEU:N	2.35	0.42
8:i:79:LEU:HD21	8:i:105:LEU:HD11	2.02	0.42
11:l:112:LEU:O	11:l:112:LEU:HD23	2.20	0.42
11:l:131:ALA:O	11:l:135:ILE:HG13	2.19	0.42
13:n:55:ALA:HA	13:n:80:PHE:CZ	2.54	0.42
21:v:34:LYS:HD3	21:v:34:LYS:N	2.34	0.42
26:B:11:LYS:HD3	26:B:11:LYS:HA	1.92	0.42
28:D:21:ARG:O	28:D:27:GLY:HA3	2.20	0.42
35:K:39:LEU:O	35:K:41:ASP:N	2.52	0.42
36:L:36:SER:HB2	52:3:1290:G:O3'	2.20	0.42
38:N:27:ILE:N	38:N:27:ILE:HD12	2.35	0.42
38:N:60:LEU:HD23	38:N:60:LEU:H	1.85	0.42
41:Q:30:ARG:NH2	52:3:362:G:O5'	2.53	0.42
52:3:243:A:H4'	52:3:244:U:H3'	2.01	0.42
52:3:1105:A:H2'	52:3:1106:G:H8	1.84	0.42
52:3:1272:G:H2'	52:3:1273:C:O4'	2.20	0.42
1:b:35:LYS:HZ1	53:1:1353:A:H4'	1.84	0.42
1:b:93:VAL:HG11	1:b:115:ILE:HD11	2.02	0.42
1:b:245:THR:C	1:b:247:TRP:H	2.26	0.42
4:e:118:ALA:HB2	4:e:176:PHE:CA	2.49	0.42
4:e:132:ARG:HD3	4:e:132:ARG:N	2.34	0.42
5:f:23:ILE:HG22	5:f:25:ILE:HG13	2.02	0.42
9:j:7:LYS:HA	9:j:8:PRO:HD3	1.86	0.42
12:m:119:LEU:O	12:m:122:ALA:HB3	2.20	0.42
30:F:11:CYS:SG	30:F:12:ARG:N	2.89	0.42
32:H:30:ASP:O	32:H:33:ASP:OD2	2.38	0.42
33:I:105:GLY:HA2	33:I:164:ARG:NH1	2.35	0.42
38:N:56:MET:SD	38:N:56:MET:C	3.03	0.42
40:P:30:ILE:H	40:P:30:ILE:CD1	2.30	0.42
45:U:68:SER:OG	45:U:71:VAL:HG22	2.20	0.42
52:3:410:G:H2'	52:3:429:U:C4	2.55	0.42
52:3:981:U:H2'	52:3:982:U:C5	2.54	0.42
52:3:1346:A:H2'	52:3:1346:A:N3	2.35	0.42
52:3:1412:C:H2'	52:3:1413:A:C8	2.54	0.42
53:1:202:U:H2'	53:1:203:A:O4'	2.19	0.42
53:1:1083:U:H2'	53:1:1085:A:OP2	2.19	0.42
53:1:1105:U:H2'	53:1:1106:G:H5''	2.00	0.42
53:1:1562:U:H2'	53:1:1563:U:O4'	2.20	0.42
53:1:2117:A:H4'	53:1:2149:U:OP1	2.20	0.42
53:1:2676:C:H2'	53:1:2677:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:203:VAL:HG23	53:1:1792:G:C5'	2.49	0.41
3:d:129:PRO:O	53:1:321:U:H5'	2.20	0.41
3:d:165:HIS:CE1	53:1:1205:A:H2'	2.55	0.41
5:f:172:GLU:C	5:f:174:LYS:H	2.27	0.41
10:k:34:GLY:H	10:k:37:ASP:CG	2.28	0.41
13:n:78:LYS:HE2	13:n:83:LEU:HD21	2.02	0.41
31:G:24:PRO:HB3	52:3:828:U:H2'	2.01	0.41
33:I:9:LYS:CE	52:3:428:G:H5''	2.49	0.41
36:L:58:LEU:HD23	36:L:58:LEU:H	1.85	0.41
43:S:3:GLN:OE1	52:3:1047:G:H5''	2.19	0.41
43:S:29:ILE:HD12	43:S:29:ILE:N	2.35	0.41
45:U:67:ILE:HD12	45:U:67:ILE:N	2.34	0.41
52:3:1434:A:H2'	52:3:1435:G:O4'	2.20	0.41
53:1:239:C:H2'	53:1:240:C:O4'	2.20	0.41
53:1:1916:A:H2'	53:1:1917:U:C6	2.54	0.41
53:1:2556:C:H2'	53:1:2557:G:O4'	2.19	0.41
1:b:243:PRO:HG2	53:1:1901:A:O2'	2.19	0.41
3:d:49:ARG:O	3:d:74:LYS:HE2	2.20	0.41
3:d:149:ILE:CG2	3:d:188:MET:HG2	2.47	0.41
5:f:51:PHE:HE1	5:f:71:LEU:HD12	1.85	0.41
7:h:74:ASP:O	7:h:77:VAL:HG22	2.20	0.41
13:n:9:GLN:HE22	13:n:17:ARG:NH2	2.19	0.41
15:p:15:ASP:OD1	15:p:15:ASP:N	2.53	0.41
18:s:11:ARG:NH2	53:1:491:G:H22	2.17	0.41
32:H:35:ASP:HA	32:H:38:VAL:HG22	2.02	0.41
35:K:6:ILE:N	35:K:6:ILE:HD12	2.36	0.41
40:P:30:ILE:HD12	40:P:30:ILE:N	2.29	0.41
42:R:70:ARG:HA	42:R:73:SER:OG	2.20	0.41
52:3:1241:G:H2'	52:3:1242:G:H8	1.85	0.41
53:1:1649:G:H2'	53:1:1650:A:C8	2.55	0.41
53:1:2345:G:H4'	53:1:2346:A:H3'	2.01	0.41
53:1:2632:A:H2'	53:1:2633:G:C8	2.55	0.41
53:1:2633:G:H5'	53:1:2811:G:O2'	2.20	0.41
55:6:16:C:O2'	55:6:17:C:H5'	2.19	0.41
1:b:75:ALA:O	1:b:114:GLN:HG3	2.20	0.41
6:g:84:ALA:HA	6:g:91:PHE:H	1.84	0.41
33:I:6:PRO:HG3	52:3:430:A:H4'	2.02	0.41
36:L:37:THR:HG21	52:3:1240:U:H4'	2.02	0.41
37:M:94:VAL:HG21	37:M:100:ILE:C	2.44	0.41
38:N:49:GLN:N	38:N:50:PRO:HD2	2.35	0.41
50:Z:13:VAL:HG23	50:Z:15:LEU:HG	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:926:G:OP2	52:3:927:G:H5''	2.20	0.41
52:3:1400:C:H5'	56:4:18:G:C6	2.55	0.41
53:1:2233:U:H2'	53:1:2234:G:H8	1.85	0.41
53:1:2398:U:H2'	53:1:2399:G:H8	1.84	0.41
53:1:2662:A:H2'	53:1:2663:G:O4'	2.19	0.41
54:2:5:U:H2'	54:2:6:G:C8	2.55	0.41
6:g:57:LYS:HA	6:g:57:LYS:HD3	1.95	0.41
20:u:81:ARG:NH1	53:1:300:A:H3'	2.35	0.41
31:G:113:LEU:O	31:G:117:GLU:HG3	2.21	0.41
33:I:169:TRP:CG	33:I:185:PRO:HG3	2.55	0.41
43:S:33:VAL:O	43:S:33:VAL:HG22	2.21	0.41
52:3:82:G:H2'	52:3:83:C:O4'	2.19	0.41
52:3:406:G:H2'	52:3:407:U:C6	2.55	0.41
52:3:984:C:H2'	52:3:985:C:C6	2.56	0.41
52:3:987:G:H2'	52:3:988:G:C8	2.56	0.41
53:1:532:A:H2'	53:1:532:A:N3	2.35	0.41
53:1:670:A:H4'	53:1:672:C:OP2	2.20	0.41
53:1:1896:G:H2'	53:1:1897:G:C8	2.56	0.41
53:1:2297:A:H62	53:1:2319:G:H1'	1.85	0.41
53:1:2432:A:H1'	55:6:75:C:C5'	2.49	0.41
5:f:10:VAL:O	5:f:10:VAL:HG13	2.20	0.41
5:f:172:GLU:CG	5:f:173:ALA:N	2.81	0.41
7:h:50:VAL:HG22	7:h:50:VAL:O	2.19	0.41
7:h:129:LEU:HA	7:h:130:PRO:HD3	1.92	0.41
9:j:40:HIS:CE1	9:j:41:LYS:HG3	2.55	0.41
12:m:49:ALA:O	12:m:53:MET:HG3	2.20	0.41
14:o:14:ALA:O	14:o:18:LEU:HD23	2.21	0.41
15:p:102:ARG:NH2	53:1:1755:A:H5'	2.36	0.41
18:s:17:VAL:O	18:s:20:VAL:HG22	2.20	0.41
18:s:31:GLN:O	18:s:34:ASP:OD1	2.38	0.41
18:s:36:LEU:HD21	18:s:47:VAL:HG13	2.02	0.41
20:u:40:LEU:N	20:u:40:LEU:HD12	2.36	0.41
22:w:20:LYS:HD2	53:1:2355:G:O3'	2.21	0.41
29:E:3:ILE:HD11	53:1:592:A:C2	2.55	0.41
33:I:182:LYS:HB3	33:I:183:ARG:H	1.64	0.41
37:M:6:ILE:HD12	37:M:6:ILE:N	2.33	0.41
37:M:93:LYS:HD2	37:M:116:ARG:NH2	2.35	0.41
41:Q:24:GLU:CD	41:Q:24:GLU:H	2.27	0.41
42:R:3:ILE:HG22	42:R:4:ALA:N	2.36	0.41
42:R:9:PRO:HG3	42:R:44:ILE:HG13	2.02	0.41
45:U:20:VAL:HG23	45:U:34:GLU:C	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:44:VAL:HG12	51:a:173:THR:O	2.21	0.41
51:a:195:ALA:O	51:a:198:LYS:HG3	2.20	0.41
52:3:70:U:H4'	52:3:71:A:C8	2.56	0.41
52:3:1254:A:H4'	52:3:1356:G:O3'	2.20	0.41
53:1:167:A:H2'	53:1:168:G:O4'	2.21	0.41
53:1:1662:U:H2'	53:1:1663:G:C8	2.55	0.41
53:1:2286:G:H4'	53:1:2287:A:O4'	2.19	0.41
55:5:59:A:O2'	55:5:60:U:H5'	2.20	0.41
3:d:141:MET:O	3:d:142:ALA:HB3	2.21	0.41
5:f:98:LYS:NZ	5:f:103:ASN:HB2	2.36	0.41
7:h:24:SER:OG	7:h:116:GLU:HB3	2.20	0.41
7:h:41:LEU:HD12	7:h:41:LEU:N	2.36	0.41
11:l:8:PRO:HD3	53:1:1244:A:H4'	2.03	0.41
14:o:29:HIS:CE1	54:2:7:G:H5'	2.55	0.41
20:u:90:LYS:NZ	53:1:101:A:N6	2.69	0.41
36:L:45:ALA:HA	36:L:48:THR:HG22	2.03	0.41
40:P:27:ASN:ND2	52:3:691:G:OP2	2.53	0.41
41:Q:11:ARG:NH1	52:3:563:A:H2	2.19	0.41
41:Q:30:ARG:HH21	52:3:362:G:H3'	1.85	0.41
41:Q:109:ARG:NH2	41:Q:111:GLN:O	2.54	0.41
42:R:113:LYS:N	42:R:114:PRO:HD2	2.35	0.41
52:3:32:A:H2'	52:3:33:A:C8	2.55	0.41
52:3:225:C:C3'	52:3:226:G:H5''	2.51	0.41
52:3:1063:C:H2'	52:3:1064:G:C8	2.56	0.41
52:3:1225:A:H2'	52:3:1225:A:N3	2.36	0.41
53:1:595:C:H2'	53:1:596:U:C6	2.56	0.41
53:1:753:A:H2'	53:1:754:U:C6	2.55	0.41
53:1:1105:U:C2'	53:1:1106:G:H5''	2.50	0.41
53:1:1434:A:H2'	53:1:1435:G:C8	2.56	0.41
53:1:1558:C:H4'	53:1:1560:G:OP2	2.21	0.41
54:2:105:G:H2'	54:2:106:G:H8	1.86	0.41
2:c:7:LYS:HE2	2:c:198:GLY:HA2	2.03	0.41
2:c:40:LEU:HD12	2:c:45:TYR:HA	2.02	0.41
4:e:31:GLU:HG2	4:e:32:LYS:CD	2.45	0.41
16:q:2:ARG:HD2	53:1:1248:G:C2	2.56	0.41
18:s:8:ARG:HA	18:s:102:HIS:ND1	2.35	0.41
19:t:21:SER:O	19:t:25:GLU:HG2	2.19	0.41
22:w:16:ARG:HD3	53:1:2356:U:O2'	2.21	0.41
29:E:25:HIS:NE2	29:E:47:ALA:HB2	2.36	0.41
35:K:8:PHE:HB2	35:K:84:VAL:HG23	2.03	0.41
38:N:83:THR:HG22	38:N:97:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:V:61:ARG:HB3	46:V:75:VAL:CG2	2.40	0.41
49:Y:79:THR:O	49:Y:82:ILE:HG12	2.21	0.41
52:3:536:C:H2'	52:3:537:G:C8	2.55	0.41
52:3:825:A:H2'	52:3:826:C:O4'	2.21	0.41
53:1:362:A:H3'	53:1:363:G:H8	1.85	0.41
53:1:691:C:O2'	53:1:692:C:H5'	2.20	0.41
53:1:828:U:H4'	53:1:831:G:N1	2.36	0.41
53:1:1563:U:H2'	53:1:1564:C:C6	2.55	0.41
53:1:1930:G:HO2'	53:1:1931:U:H5	1.66	0.41
53:1:2326:C:O2'	53:1:2327:A:OP1	2.37	0.41
53:1:2391:G:H2'	53:1:2424:C:N4	2.35	0.41
53:1:2713:U:H3'	53:1:2714:G:H5''	2.02	0.41
1:b:129:LEU:HD23	1:b:129:LEU:N	2.36	0.41
2:c:130:GLN:HE22	2:c:142:VAL:HG12	1.85	0.41
3:d:69:ARG:HH22	53:1:2444:G:C5'	2.29	0.41
5:f:6:ALA:HA	5:f:7:PRO:HD3	1.84	0.41
7:h:37:LYS:HA	7:h:41:LEU:HD13	2.03	0.41
13:n:99:LYS:NZ	26:B:40:HIS:HB2	2.35	0.41
21:v:60:VAL:HA	21:v:73:LYS:HD2	2.03	0.41
22:w:20:LYS:CE	53:1:2355:G:H4'	2.51	0.41
32:H:35:ASP:O	32:H:38:VAL:HG22	2.20	0.41
33:I:55:ARG:O	33:I:59:LYS:HB2	2.20	0.41
33:I:205:LYS:HE2	33:I:205:LYS:HB2	1.92	0.41
38:N:60:LEU:HD23	38:N:60:LEU:N	2.35	0.41
41:Q:97:VAL:HG13	41:Q:97:VAL:O	2.20	0.41
49:Y:74:HIS:O	49:Y:78:LEU:HB3	2.21	0.41
50:Z:34:ARG:HB3	50:Z:36:PHE:CE1	2.56	0.41
51:a:3:LYS:HD2	53:1:2151:U:OP1	2.21	0.41
52:3:784:A:H2'	52:3:785:G:C8	2.56	0.41
52:3:1514:G:H2'	52:3:1515:G:C8	2.55	0.41
53:1:254:G:C2'	53:1:255:A:H5''	2.50	0.41
53:1:870:U:O2'	53:1:871:U:H5'	2.20	0.41
53:1:2251:G:C8	53:1:2450:A:H4'	2.55	0.41
53:1:2404:U:H2'	53:1:2405:G:O4'	2.21	0.41
1:b:2:VAL:HG21	1:b:201:LEU:HD13	2.03	0.41
1:b:257:ARG:NH2	53:1:1845:G:OP1	2.54	0.41
2:c:166:GLY:O	2:c:168:GLU:HG3	2.21	0.41
3:d:121:VAL:HG22	3:d:122:GLU:N	2.36	0.41
6:g:71:LYS:HA	6:g:71:LYS:HD3	1.85	0.41
7:h:92:ALA:HB1	7:h:129:LEU:HD22	2.03	0.41
10:k:23:LYS:NZ	53:1:2548:U:H1'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:76:GLU:HB2	11:l:111:ILE:HD11	2.02	0.41
12:m:68:PHE:CZ	53:1:871:U:H4'	2.55	0.41
12:m:76:LYS:HA	12:m:77:PRO:HD3	1.90	0.41
12:m:94:ALA:O	12:m:96:ILE:HG12	2.21	0.41
14:o:17:LYS:HA	14:o:20:GLU:CD	2.46	0.41
14:o:18:LEU:HD13	14:o:21:LEU:HD12	2.02	0.41
14:o:85:LYS:HB2	14:o:87:ILE:HG12	2.02	0.41
15:p:9:GLN:H	15:p:9:GLN:HG2	1.57	0.41
15:p:108:ARG:NH1	52:3:1464:U:OP2	2.53	0.41
16:q:91:ARG:NH1	53:1:997:G:H5''	2.36	0.41
19:t:77:ARG:HA	19:t:77:ARG:HD2	1.83	0.41
20:u:45:GLN:HE21	20:u:45:GLN:HB3	1.71	0.41
25:z:45:GLY:HA3	53:1:852:U:H5'	2.02	0.41
26:B:5:ASN:ND2	53:1:2019:A:N7	2.69	0.41
29:E:14:LYS:HB3	29:E:22:LYS:HE2	2.02	0.41
34:J:114:LEU:HD13	34:J:122:VAL:HG21	2.02	0.41
35:K:7:VAL:CG1	35:K:61:LEU:HD13	2.47	0.41
36:L:70:PRO:HD3	36:L:102:TRP:HZ3	1.85	0.41
37:M:98:LEU:HD12	37:M:98:LEU:N	2.36	0.41
41:Q:32:VAL:HB	41:Q:55:ARG:HB3	2.03	0.41
41:Q:120:ARG:NH1	52:3:500:G:H5'	2.36	0.41
42:R:99:GLN:OE1	42:R:99:GLN:N	2.54	0.41
47:W:67:LEU:HA	47:W:68:PRO:HD3	1.87	0.41
48:X:38:THR:HG22	48:X:69:LYS:HG2	2.03	0.41
52:3:31:G:H5'	52:3:306:A:C2	2.56	0.41
52:3:45:G:H2'	52:3:46:G:C8	2.56	0.41
52:3:543:U:H2'	52:3:544:G:C8	2.56	0.41
52:3:681:A:H2'	52:3:682:G:C8	2.56	0.41
52:3:768:A:H2'	52:3:769:G:O4'	2.21	0.41
52:3:1256:A:H1'	52:3:1258:G:C4	2.55	0.41
53:1:1086:A:H3'	53:1:1086:A:N3	2.36	0.41
53:1:1386:C:H2'	53:1:1387:A:C8	2.56	0.41
53:1:1496:A:H2'	53:1:1498:C:N4	2.35	0.41
53:1:1539:U:H2'	53:1:1540:G:H8	1.85	0.41
53:1:1853:A:H1'	53:1:2233:U:O2'	2.20	0.41
53:1:1882:U:H2'	53:1:1883:U:C6	2.55	0.41
53:1:1979:U:C2'	53:1:1980:G:H5'	2.51	0.41
53:1:2185:U:H2'	53:1:2186:G:H8	1.85	0.41
4:e:79:ARG:CZ	4:e:80:GLN:HB3	2.51	0.41
10:k:1:MET:CE	53:1:1665:A:N3	2.84	0.41
10:k:57:VAL:O	10:k:58:LEU:HD12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:104:THR:HG22	10:k:105:ARG:N	2.36	0.41
11:l:118:THR:HA	11:l:119:PRO:HD3	1.87	0.41
15:p:102:ARG:NH1	53:1:1754:A:H4'	2.36	0.41
23:x:55:MET:SD	53:1:2091:C:H4'	2.61	0.41
25:z:40:THR:OG1	25:z:41:PRO:HD2	2.21	0.41
31:G:65:LYS:HD2	31:G:157:PRO:HA	2.03	0.41
33:I:4:LEU:HD22	52:3:406:G:C5'	2.48	0.41
41:Q:109:ARG:HE	52:3:538:G:P	2.43	0.41
50:Z:5:VAL:HG22	50:Z:6:ARG:N	2.36	0.41
51:a:208:TYR:HB3	51:a:209:ILE:HD12	2.03	0.41
52:3:112:G:H21	52:3:354:G:H5'	1.85	0.41
52:3:655:A:H2'	52:3:656:G:C8	2.56	0.41
52:3:764:C:H2'	52:3:765:G:O4'	2.21	0.41
52:3:924:C:H2'	52:3:925:G:C8	2.56	0.41
52:3:1220:G:H2'	52:3:1221:G:O4'	2.20	0.41
52:3:1309:G:H2'	52:3:1310:G:C8	2.55	0.41
53:1:176:A:O2'	53:1:177:G:H5'	2.20	0.41
53:1:331:C:O2'	53:1:332:A:H5'	2.21	0.41
53:1:626:A:H3'	53:1:627:A:C5'	2.50	0.41
53:1:1111:A:C2'	53:1:1112:G:H4'	2.51	0.41
53:1:1505:A:H2'	53:1:1506:U:C6	2.56	0.41
53:1:2606:C:H2'	53:1:2607:G:C8	2.56	0.41
54:2:118:C:H2'	54:2:119:A:C8	2.56	0.41
2:c:115:GLY:HA2	2:c:166:GLY:HA3	2.04	0.40
3:d:137:LYS:HA	3:d:140:ASP:OD2	2.20	0.40
9:j:69:ARG:O	9:j:89:PHE:HB3	2.21	0.40
15:p:29:VAL:HG12	15:p:80:VAL:HA	2.02	0.40
22:w:67:VAL:O	22:w:67:VAL:HG22	2.21	0.40
32:H:70:ALA:HB2	32:H:114:LEU:HD13	2.03	0.40
33:I:184:LYS:HA	33:I:185:PRO:HD3	1.86	0.40
37:M:9:MET:O	37:M:13:ILE:HG13	2.20	0.40
48:X:18:VAL:HG11	48:X:43:MET:HG2	2.03	0.40
51:a:205:LYS:HD2	53:1:1861:G:C5'	2.47	0.40
52:3:955:U:H2'	52:3:956:U:O4'	2.21	0.40
53:1:833:A:H2'	53:1:834:G:C8	2.55	0.40
53:1:1045:C:OP1	53:1:1047:G:H5'	2.21	0.40
53:1:1636:U:H2'	53:1:1637:A:C8	2.56	0.40
53:1:1786:A:H1'	53:1:1938:A:N6	2.36	0.40
53:1:2041:U:H2'	53:1:2042:A:C8	2.56	0.40
53:1:2372:U:H2'	53:1:2373:G:H8	1.85	0.40
1:b:94:LEU:HD21	53:1:1501:G:H4'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:121:ALA:HB1	1:b:127:ASN:HB3	2.03	0.40
2:c:15:PHE:HB3	15:p:78:PRO:HD3	2.03	0.40
2:c:193:VAL:HA	2:c:194:PRO:HD3	1.97	0.40
4:e:56:LEU:HD13	4:e:88:VAL:HG23	2.02	0.40
6:g:97:ARG:NH2	53:1:2220:U:H5'	2.28	0.40
14:o:14:ALA:HA	14:o:17:LYS:HE2	2.03	0.40
19:t:60:THR:O	53:1:1341:G:H4'	2.21	0.40
31:G:102:ASN:HD21	31:G:105:THR:HB	1.84	0.40
33:I:120:LYS:HE3	52:3:439:U:O3'	2.21	0.40
42:R:18:LEU:HD12	42:R:21:ILE:HD13	2.03	0.40
43:S:31:SER:HA	43:S:40:ARG:HH21	1.86	0.40
45:U:5:ARG:HB2	52:3:376:G:H5''	2.01	0.40
48:X:21:ALA:O	48:X:25:GLY:N	2.54	0.40
51:a:39:VAL:O	51:a:39:VAL:HG13	2.21	0.40
52:3:244:U:H3	52:3:893:C:H42	1.68	0.40
52:3:593:U:H2'	52:3:594:U:C6	2.57	0.40
52:3:634:C:H2'	52:3:635:A:C8	2.57	0.40
52:3:730:G:C2'	52:3:731:G:H5'	2.51	0.40
52:3:1202:U:H2'	52:3:1203:C:H5'	2.02	0.40
52:3:1324:A:H2'	52:3:1325:C:O4'	2.22	0.40
53:1:399:U:OP1	53:1:2090:A:H5''	2.21	0.40
53:1:566:U:H4'	53:1:809:G:OP2	2.21	0.40
53:1:732:C:H2'	53:1:733:G:O4'	2.21	0.40
53:1:1346:G:H2'	53:1:1347:A:O4'	2.21	0.40
53:1:1827:U:H1'	53:1:1970:A:N3	2.36	0.40
53:1:2122:U:H2'	53:1:2123:G:O4'	2.21	0.40
2:c:117:GLY:HA2	2:c:164:GLN:HE21	1.86	0.40
3:d:122:GLU:HG3	3:d:123:LYS:H	1.86	0.40
4:e:148:VAL:HG22	4:e:148:VAL:O	2.22	0.40
5:f:48:THR:OG1	5:f:49:LEU:N	2.53	0.40
6:g:108:VAL:HG12	6:g:110:VAL:HG23	2.03	0.40
11:l:19:LEU:N	11:l:19:LEU:HD12	2.37	0.40
34:J:37:VAL:HG22	34:J:47:PHE:HB2	2.04	0.40
35:K:11:HIS:HA	35:K:12:PRO:HD3	1.97	0.40
46:V:46:HIS:HA	46:V:70:LYS:HE3	2.03	0.40
49:Y:8:LYS:HE3	52:3:103:U:OP2	2.22	0.40
51:a:54:LYS:HD2	51:a:57:GLN:NE2	2.37	0.40
52:3:162:A:H2'	52:3:163:C:O4'	2.20	0.40
52:3:940:C:H2'	52:3:941:G:C8	2.56	0.40
52:3:1060:U:H2'	52:3:1061:G:H8	1.86	0.40
52:3:1497:G:C2'	52:3:1498:U:H5'	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:241:A:H61	53:1:255:A:H3'	1.86	0.40
53:1:542:C:H2'	53:1:543:G:C5'	2.51	0.40
53:1:762:U:H4'	53:1:763:G:O4'	2.21	0.40
53:1:817:C:H2'	53:1:818:G:C8	2.57	0.40
53:1:859:G:HO2'	53:1:860:U:H6	1.65	0.40
53:1:1204:A:H4'	53:1:1205:A:H5''	2.03	0.40
53:1:1431:A:H2'	53:1:1432:G:C8	2.56	0.40
53:1:2229:U:H2'	53:1:2230:G:C8	2.56	0.40
53:1:2825:G:H2'	53:1:2826:A:H5'	2.03	0.40
54:2:28:C:H2'	54:2:29:A:H8	1.86	0.40
55:5:51:C:H2'	55:5:52:G:H8	1.86	0.40
1:b:155:ARG:NH1	53:1:1818:U:H5	2.19	0.40
2:c:201:LEU:C	2:c:202:ILE:HD12	2.46	0.40
4:e:153:ILE:N	4:e:153:ILE:HD12	2.36	0.40
5:f:138:GLN:OE1	53:1:2746:U:H1'	2.21	0.40
7:h:2:ALA:HB1	7:h:3:LEU:HD12	2.03	0.40
7:h:11:ILE:HD11	7:h:62:ARG:HG2	2.02	0.40
8:i:99:LYS:HD3	8:i:140:GLU:HG2	2.04	0.40
12:m:68:PHE:CZ	53:1:871:U:H5''	2.57	0.40
13:n:36:THR:HG22	13:n:37:THR:H	1.86	0.40
16:q:50:ARG:O	16:q:54:ARG:HG3	2.22	0.40
23:x:24:THR:HG21	53:1:2081:U:C5'	2.51	0.40
29:E:39:ARG:NH1	53:1:2362:C:H5''	2.36	0.40
31:G:129:THR:HG23	31:G:131:LYS:H	1.87	0.40
36:L:25:PHE:HD1	36:L:100:MET:HB3	1.85	0.40
37:M:85:TYR:CE1	37:M:123:GLU:HB2	2.57	0.40
41:Q:23:LEU:O	41:Q:24:GLU:C	2.64	0.40
46:V:22:VAL:HG11	46:V:60:ILE:HD11	2.04	0.40
52:3:177:G:H2'	52:3:178:C:O4'	2.21	0.40
52:3:492:C:H2'	52:3:493:A:C8	2.56	0.40
52:3:1012:A:H2'	52:3:1013:G:O4'	2.21	0.40
52:3:1096:C:H2'	52:3:1097:C:C6	2.56	0.40
52:3:1458:G:H2'	52:3:1459:G:H8	1.87	0.40
3:d:69:ARG:HD3	53:1:674:G:H1'	2.03	0.40
9:j:27:ARG:NH2	53:1:1142:A:H4'	2.36	0.40
10:k:12:ASP:CG	10:k:85:VAL:HG23	2.46	0.40
21:v:64:VAL:O	21:v:64:VAL:HG13	2.22	0.40
22:w:14:ALA:O	22:w:16:ARG:NH1	2.53	0.40
40:P:83:VAL:HG12	40:P:85:VAL:HG13	2.04	0.40
41:Q:28:GLN:HE22	41:Q:82:ARG:HB3	1.86	0.40
41:Q:114:SER:HB3	52:3:35:G:H21	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:62:ARG:NH1	43:S:69:PRO:HD3	2.37	0.40
46:V:10:ARG:HA	46:V:57:VAL:HA	2.03	0.40
51:a:62:ALA:HB1	51:a:160:GLN:HE22	1.87	0.40
52:3:865:A:H5'	52:3:1078:U:O4	2.20	0.40
53:1:318:C:O2'	53:1:319:G:H5'	2.22	0.40
53:1:1331:G:C2'	53:1:1332:G:H5''	2.52	0.40
53:1:1935:G:O2'	53:1:1936:A:H5'	2.22	0.40
53:1:1936:A:H3'	53:1:1937:A:H5'	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	224 (83%)	40 (15%)	5 (2%)	6	34
2	c	207/209 (99%)	179 (86%)	25 (12%)	3 (1%)	9	39
3	d	199/201 (99%)	176 (88%)	22 (11%)	1 (0%)	24	60
4	e	175/177 (99%)	155 (89%)	20 (11%)	0	100	100
5	f	174/176 (99%)	155 (89%)	19 (11%)	0	100	100
6	g	147/149 (99%)	127 (86%)	17 (12%)	3 (2%)	6	33
7	h	129/131 (98%)	97 (75%)	27 (21%)	5 (4%)	2	22
8	i	69/141 (49%)	65 (94%)	4 (6%)	0	100	100
9	j	140/142 (99%)	122 (87%)	18 (13%)	0	100	100
10	k	120/122 (98%)	98 (82%)	18 (15%)	4 (3%)	3	24
11	l	141/143 (99%)	115 (82%)	21 (15%)	5 (4%)	3	23
12	m	134/136 (98%)	121 (90%)	11 (8%)	2 (2%)	8	38
13	n	118/120 (98%)	102 (86%)	16 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	o	114/116 (98%)	98 (86%)	14 (12%)	2 (2%)	6	34
15	p	112/114 (98%)	87 (78%)	25 (22%)	0	100	100
16	q	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
17	r	101/103 (98%)	86 (85%)	14 (14%)	1 (1%)	12	45
18	s	108/110 (98%)	93 (86%)	15 (14%)	0	100	100
19	t	91/93 (98%)	79 (87%)	12 (13%)	0	100	100
20	u	100/102 (98%)	82 (82%)	16 (16%)	2 (2%)	6	33
21	v	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
22	w	73/75 (97%)	66 (90%)	6 (8%)	1 (1%)	9	39
23	x	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
24	y	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	7	37
25	z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
26	B	54/56 (96%)	49 (91%)	4 (7%)	1 (2%)	6	34
27	C	48/50 (96%)	41 (85%)	7 (15%)	0	100	100
28	D	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
29	E	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	7	37
30	F	36/38 (95%)	29 (81%)	6 (17%)	1 (3%)	4	27
31	G	223/225 (99%)	196 (88%)	25 (11%)	2 (1%)	14	48
32	H	204/206 (99%)	186 (91%)	15 (7%)	3 (2%)	8	38
33	I	203/205 (99%)	178 (88%)	20 (10%)	5 (2%)	4	29
34	J	155/157 (99%)	124 (80%)	27 (17%)	4 (3%)	4	29
35	K	98/100 (98%)	76 (78%)	19 (19%)	3 (3%)	3	25
36	L	149/151 (99%)	126 (85%)	21 (14%)	2 (1%)	9	41
37	M	127/129 (98%)	109 (86%)	18 (14%)	0	100	100
38	N	125/127 (98%)	100 (80%)	21 (17%)	4 (3%)	3	25
39	O	96/98 (98%)	76 (79%)	14 (15%)	6 (6%)	1	15
40	P	114/116 (98%)	91 (80%)	20 (18%)	3 (3%)	4	29
41	Q	121/123 (98%)	97 (80%)	19 (16%)	5 (4%)	2	21
42	R	112/114 (98%)	98 (88%)	11 (10%)	3 (3%)	4	28
43	S	98/100 (98%)	82 (84%)	16 (16%)	0	100	100
44	T	86/88 (98%)	77 (90%)	7 (8%)	2 (2%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	U	80/82 (98%)	71 (89%)	7 (9%)	2 (2%)	4	29
46	V	78/80 (98%)	62 (80%)	13 (17%)	3 (4%)	2	22
47	W	63/65 (97%)	54 (86%)	8 (13%)	1 (2%)	7	37
48	X	77/79 (98%)	60 (78%)	16 (21%)	1 (1%)	9	41
49	Y	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
50	Z	63/65 (97%)	43 (68%)	14 (22%)	6 (10%)	0	9
51	a	130/223 (58%)	121 (93%)	9 (7%)	0	100	100
All	All	5849/6112 (96%)	5024 (86%)	732 (12%)	93 (2%)	10	37

All (93) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	240	GLY
3	d	83	VAL
6	g	9	VAL
7	h	81	LEU
12	m	58	LYS
17	r	54	VAL
29	E	31	ILE
30	F	37	GLN
34	J	93	VAL
34	J	122	VAL
35	K	40	GLU
38	N	90	ASP
39	O	42	LEU
39	O	58	ASN
44	T	46	LYS
45	U	79	ASN
46	V	49	ASN
50	Z	64	ALA
2	c	30	GLU
6	g	11	ASN
7	h	108	VAL
10	k	89	ASN
11	l	87	GLY
12	m	69	PRO
14	o	34	HIS
24	y	24	GLU
31	G	204	ASP
33	I	85	THR

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Mol	Chain	Res	Type
34	J	23	THR
35	K	86	ARG
35	K	99	ALA
36	L	30	MET
36	L	56	SER
40	P	92	ARG
41	Q	24	GLU
42	R	4	ALA
42	R	6	ILE
42	R	7	ASN
44	T	48	ASP
46	V	17	GLU
50	Z	25	ALA
1	b	107	LYS
1	b	250	GLN
10	k	35	VAL
10	k	48	PRO
20	u	98	ASN
31	G	35	ASN
32	H	60	ALA
33	I	31	CYS
34	J	11	GLN
39	O	33	GLY
39	O	34	ALA
39	O	35	GLN
41	Q	88	ASP
45	U	49	GLY
47	W	13	THR
50	Z	9	GLU
50	Z	10	PRO
50	Z	14	ALA
50	Z	34	ARG
1	b	254	LYS
6	g	14	SER
7	h	113	PHE
7	h	118	ILE
11	l	36	LYS
11	l	88	GLY
11	l	94	THR
38	N	8	THR
38	N	24	ASN
41	Q	27	PRO

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Mol	Chain	Res	Type
41	Q	77	SER
48	X	4	LEU
1	b	243	PRO
2	c	148	GLN
14	o	114	GLY
32	H	61	LYS
33	I	34	GLU
41	Q	43	LYS
2	c	149	ASN
11	l	52	GLY
26	B	25	THR
32	H	79	LYS
33	I	167	PRO
40	P	88	PRO
22	w	50	GLY
46	V	31	PRO
10	k	26	GLY
33	I	37	PRO
38	N	71	ILE
40	P	112	VAL
20	u	49	PRO
39	O	43	PRO
7	h	119	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%)	213 (99%)	3 (1%)	59	71
2	c	164/164 (100%)	161 (98%)	3 (2%)	51	68
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	146 (99%)	2 (1%)	59	71
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	h	100/100 (100%)	99 (99%)	1 (1%)	68	76
8	i	53/109 (49%)	53 (100%)	0	100	100
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	76
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	76
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	99 (99%)	1 (1%)	68	76
14	o	86/86 (100%)	86 (100%)	0	100	100
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	76
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	78 (100%)	0	100	100
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	68
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%)	44 (98%)	1 (2%)	45	65
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	33 (97%)	1 (3%)	37	58
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	74
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	81
33	I	172/172 (100%)	172 (100%)	0	100	100
34	J	119/119 (100%)	119 (100%)	0	100	100
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	74
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	85 (99%)	1 (1%)	63	73
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	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
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	70
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%)	53 (96%)	2 (4%)	31	53
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4852/4972 (98%)	4828 (100%)	24 (0%)	78	82

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	104	LEU
1	b	156	SER
1	b	257	ARG
2	c	18	ASP
2	c	29	VAL
2	c	98	VAL
4	e	24	VAL
4	e	135	ILE
7	h	118	ILE
9	j	81	ILE
10	k	45	GLU
13	n	95	THR
15	p	69	VAL
22	w	28	LEU
27	C	45	HIS
30	F	20	ASP
31	G	46	VAL
31	G	67	LEU

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Mol	Chain	Res	Type
32	H	102	ILE
35	K	58	HIS
39	O	71	LEU
45	U	47	GLU
50	Z	9	GLU
50	Z	10	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (116) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	14	HIS
1	b	20	ASN
1	b	24	HIS
1	b	85	ASN
1	b	127	ASN
1	b	196	ASN
1	b	225	ASN
1	b	231	HIS
1	b	238	ASN
1	b	250	GLN
1	b	259	ASN
2	c	32	ASN
2	c	49	GLN
2	c	94	GLN
2	c	134	HIS
2	c	140	HIS
2	c	164	GLN
2	c	173	GLN
3	d	29	HIS
3	d	90	GLN
3	d	97	ASN
3	d	165	HIS
4	e	20	ASN
4	e	80	GLN
4	e	126	ASN
5	f	63	GLN
5	f	142	GLN
6	g	28	ASN
6	g	66	ASN
6	g	145	ASN
8	i	104	GLN
9	j	40	HIS

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Mol	Chain	Res	Type
9	j	58	ASN
9	j	135	GLN
10	k	3	GLN
10	k	5	GLN
11	l	38	GLN
12	m	13	HIS
13	n	9	GLN
13	n	11	ASN
13	n	62	ASN
14	o	29	HIS
14	o	34	HIS
14	o	100	HIS
14	o	104	GLN
15	p	6	GLN
15	p	40	GLN
15	p	74	GLN
15	p	114	ASN
16	q	55	GLN
16	q	70	GLN
17	r	12	HIS
17	r	18	GLN
17	r	43	ASN
17	r	66	HIS
17	r	86	GLN
17	r	89	HIS
18	s	40	ASN
18	s	61	ASN
19	t	48	GLN
19	t	70	HIS
20	u	39	ASN
20	u	45	GLN
20	u	65	GLN
21	v	24	ASN
22	w	8	ASN
22	w	42	HIS
22	w	72	ASN
23	x	15	ASN
23	x	16	ASN
23	x	35	HIS
24	y	27	ASN
24	y	39	GLN
25	z	8	GLN

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Mol	Chain	Res	Type
26	B	4	GLN
29	E	27	ASN
31	G	57	ASN
31	G	102	ASN
31	G	169	HIS
31	G	189	ASN
32	H	139	ASN
33	I	39	GLN
33	I	99	ASN
33	I	139	ASN
34	J	11	GLN
34	J	42	ASN
34	J	72	ASN
34	J	81	GLN
34	J	134	ASN
35	K	55	HIS
36	L	27	ASN
36	L	51	GLN
36	L	121	ASN
36	L	141	HIS
36	L	147	ASN
37	M	20	ASN
38	N	24	ASN
38	N	30	ASN
38	N	49	GLN
41	Q	4	ASN
41	Q	5	GLN
42	R	7	ASN
43	S	65	GLN
44	T	19	ASN
44	T	27	GLN
44	T	39	GLN
44	T	41	HIS
44	T	61	GLN
46	V	8	GLN
47	W	51	GLN
48	X	56	HIS
49	Y	69	ASN
51	a	24	ASN
51	a	58	ASN
51	a	168	ASN
51	a	188	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	137 (8%)	2 (0%)
53	1	2902/2903 (99%)	319 (10%)	8 (0%)
54	2	119/120 (99%)	11 (9%)	1 (0%)
55	5	76/77 (98%)	11 (14%)	0
55	6	76/77 (98%)	8 (10%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	72/76 (94%)	12 (16%)	0
All	All	4800/4810 (99%)	500 (10%)	11 (0%)

All (500) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	7	A
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A
52	3	71	A
52	3	85	U
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	279	A
52	3	281	G
52	3	289	G
52	3	345	C
52	3	352	C

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Mol	Chain	Res	Type
52	3	367	U
52	3	372	C
52	3	411	A
52	3	412	A
52	3	413	G
52	3	429	U
52	3	467	U
52	3	485	U
52	3	486	U
52	3	518	C
52	3	532	A
52	3	547	A
52	3	561	U
52	3	572	A
52	3	573	A
52	3	575	G
52	3	576	C
52	3	577	G
52	3	633	G
52	3	653	U
52	3	665	A
52	3	687	A
52	3	688	G
52	3	702	A
52	3	703	G
52	3	724	G
52	3	755	G
52	3	777	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	821	G
52	3	843	U
52	3	844	G
52	3	846	G
52	3	871	U
52	3	873	A
52	3	902	G
52	3	934	C
52	3	935	A
52	3	960	U

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Mol	Chain	Res	Type
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	991	U
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1030	U
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1054	C
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1198	G
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1258	G
52	3	1260	G
52	3	1275	A
52	3	1278	G
52	3	1280	A

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Mol	Chain	Res	Type
52	3	1282	C
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1320	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1378	C
52	3	1395	C
52	3	1446	A
52	3	1448	C
52	3	1451	U
52	3	1452	C
52	3	1492	A
52	3	1502	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	49	A
53	1	51	G
53	1	71	A
53	1	74	A
53	1	75	G
53	1	119	A
53	1	120	U
53	1	138	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C

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Mol	Chain	Res	Type
53	1	181	A
53	1	196	A
53	1	216	A
53	1	221	A
53	1	222	A
53	1	228	C
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	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	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	424	G
53	1	451	U
53	1	457	A
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	530	G
53	1	531	C
53	1	532	A
53	1	543	G
53	1	545	U

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Mol	Chain	Res	Type
53	1	563	A
53	1	573	U
53	1	588	U
53	1	603	A
53	1	614	A
53	1	616	A
53	1	627	A
53	1	637	A
53	1	646	U
53	1	654	A
53	1	669	G
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	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	789	A
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	860	U
53	1	878	A
53	1	886	A
53	1	887	U
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C

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Mol	Chain	Res	Type
53	1	961	C
53	1	974	G
53	1	975	A
53	1	983	A
53	1	995	C
53	1	996	A
53	1	1009	A
53	1	1012	U
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	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	1178	C
53	1	1180	U
53	1	1212	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G

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Mol	Chain	Res	Type
53	1	1272	A
53	1	1275	A
53	1	1289	C
53	1	1301	A
53	1	1302	A
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1365	A
53	1	1379	U
53	1	1383	A
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1454	C
53	1	1461	C
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	1560	G
53	1	1569	A
53	1	1581	G
53	1	1584	U
53	1	1585	C
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1654	A
53	1	1674	G
53	1	1699	G
53	1	1715	G

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Mol	Chain	Res	Type
53	1	1729	U
53	1	1730	C
53	1	1732	C
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	1914	C
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	1993	U
53	1	1997	C
53	1	2006	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

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Mol	Chain	Res	Type
53	1	2060	A
53	1	2061	G
53	1	2062	A
53	1	2069	G
53	1	2072	C
53	1	2096	C
53	1	2110	G
53	1	2111	U
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2131	U
53	1	2132	U
53	1	2133	G
53	1	2145	C
53	1	2147	A
53	1	2162	G
53	1	2164	C
53	1	2172	U
53	1	2173	A
53	1	2198	A
53	1	2204	G
53	1	2225	A
53	1	2259	U
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2297	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2407	A
53	1	2423	U
53	1	2424	C

Continued on next page...

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Mol	Chain	Res	Type
53	1	2427	C
53	1	2429	G
53	1	2430	A
53	1	2434	A
53	1	2435	A
53	1	2441	U
53	1	2448	A
53	1	2476	A
53	1	2498	C
53	1	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
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	2603	G
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	2757	A
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	2800	A
53	1	2809	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2867	G
53	1	2872	A
53	1	2880	C
53	1	2884	U
54	2	4	C
54	2	12	C
54	2	13	G
54	2	24	G
54	2	35	C
54	2	44	G
54	2	67	G
54	2	89	U
54	2	90	C
54	2	108	A
54	2	109	A
55	5	8	U
55	5	9	G
55	5	14	A
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	56	C
55	5	57	A
55	5	61	C
55	5	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
57	7	6	G
57	7	8	U
57	7	17	C

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Mol	Chain	Res	Type
57	7	19	G
57	7	21	A
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	73	A

All (11) RNA pucker outliers are listed below:

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

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [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	0.58	0	8,9,11	0.80	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	O1-CN-N-CA

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.

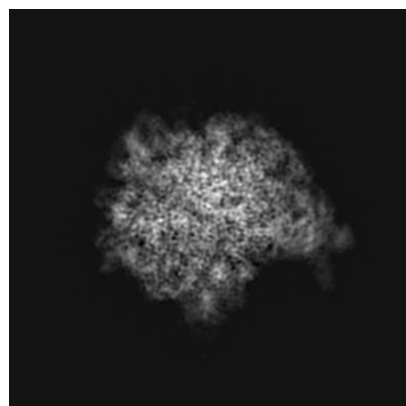
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21637. These allow visual inspection of the internal detail of the map and identification of artifacts.

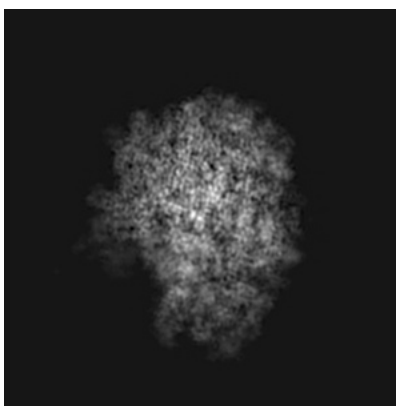
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

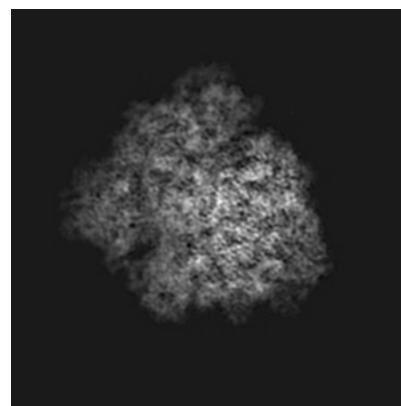
6.1.1 Primary map



X

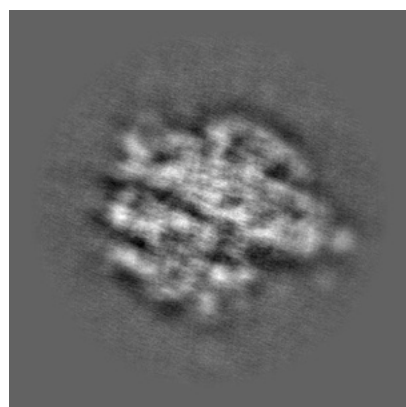


Y

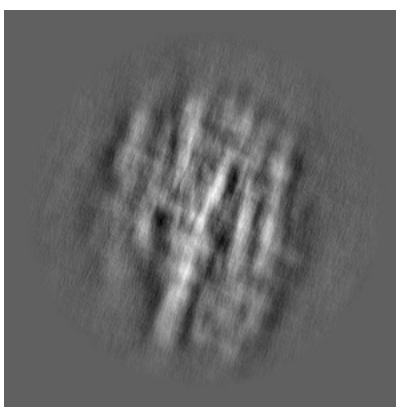


Z

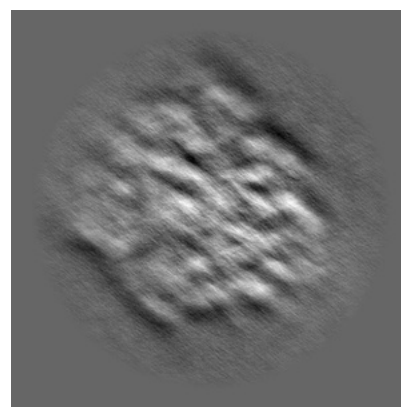
6.1.2 Raw map



X



Y

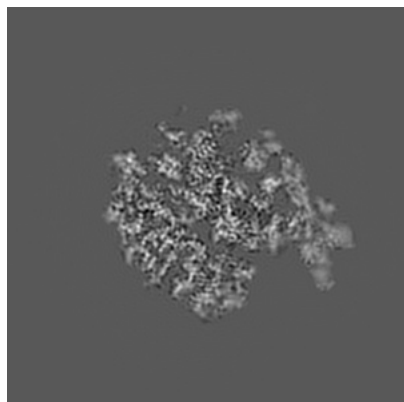


Z

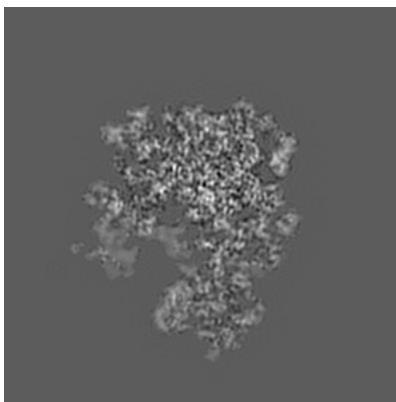
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

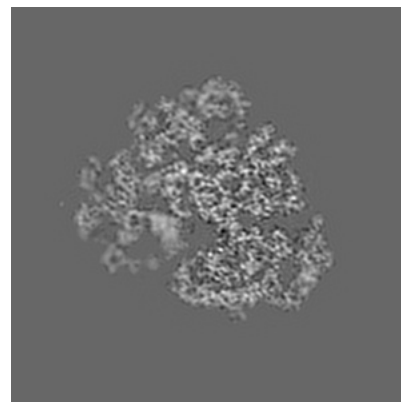
6.2.1 Primary map



X Index: 144

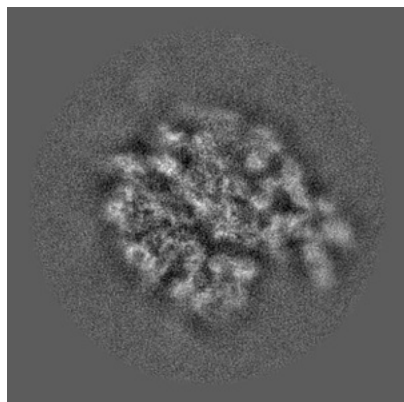


Y Index: 144

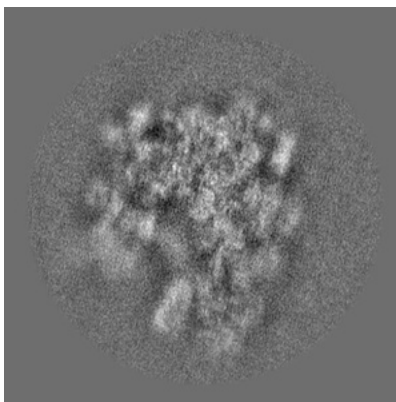


Z Index: 144

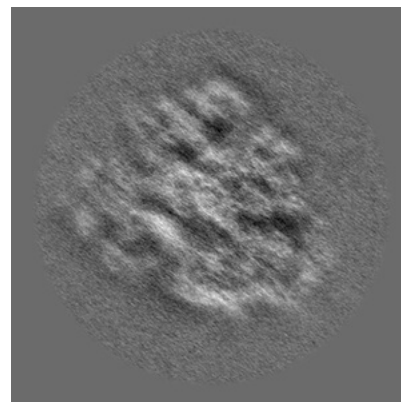
6.2.2 Raw map



X Index: 144



Y Index: 144

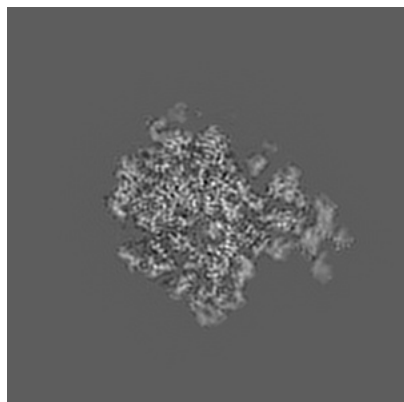


Z Index: 144

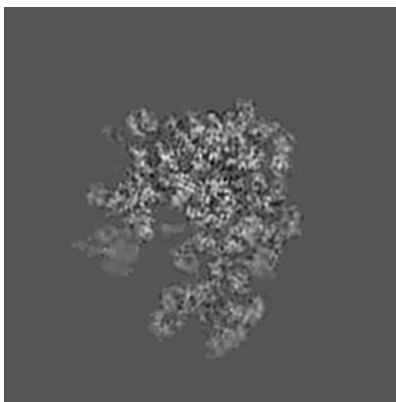
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

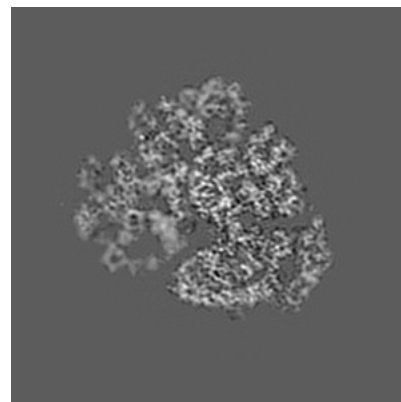
6.3.1 Primary map



X Index: 150

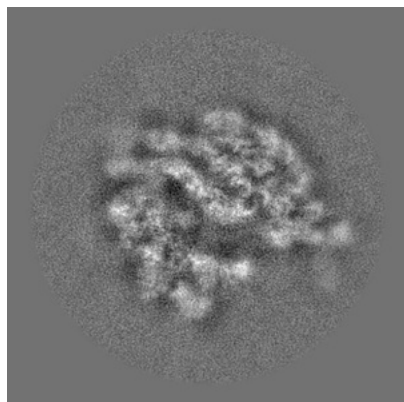


Y Index: 148

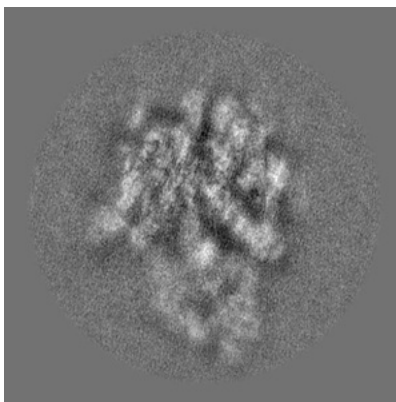


Z Index: 143

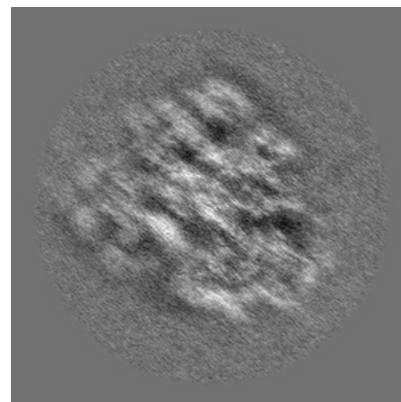
6.3.2 Raw map



X Index: 134



Y Index: 128

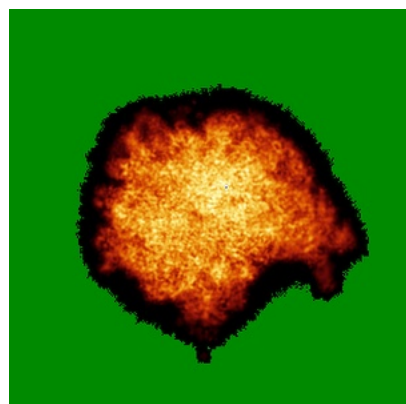


Z Index: 145

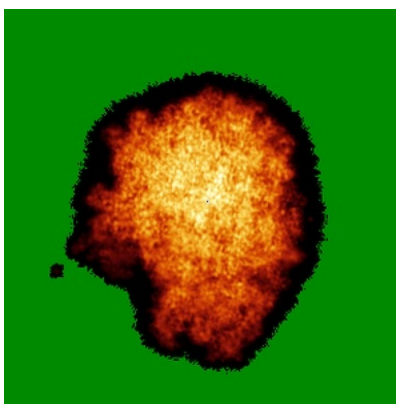
The images above show the largest variance slices of the map in three orthogonal directions.

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

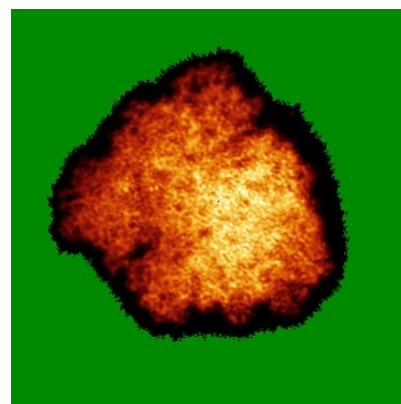
6.4.1 Primary map



X

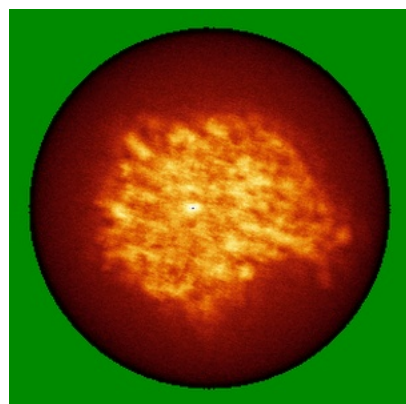


Y

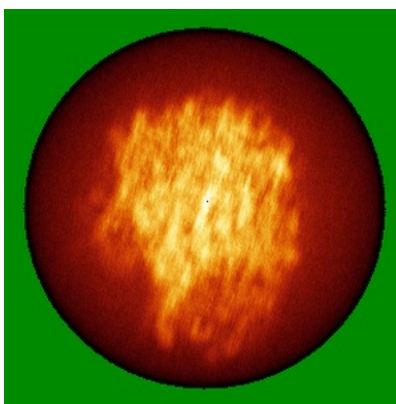


Z

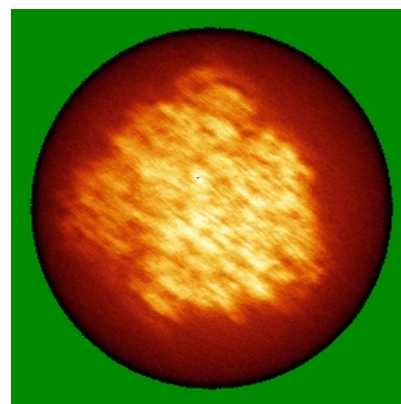
6.4.2 Raw map



X



Y



Z

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

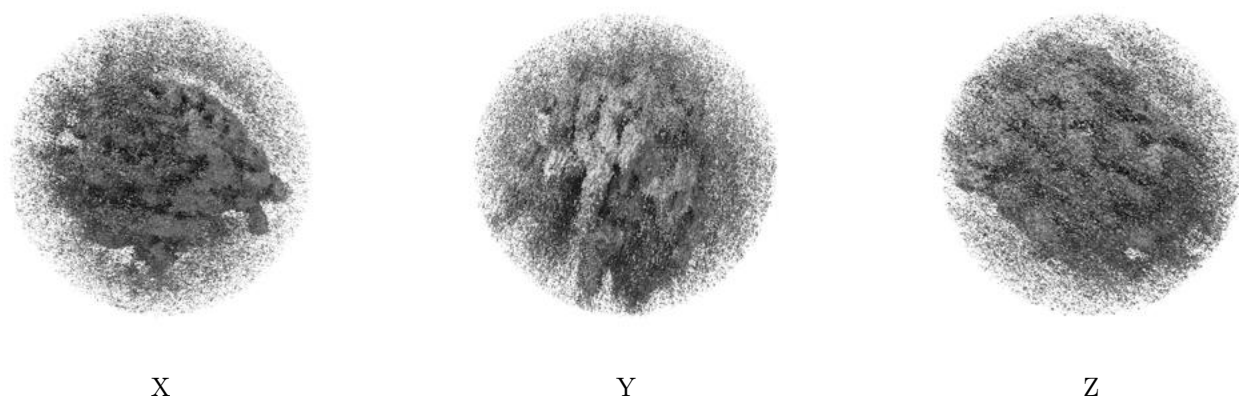
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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

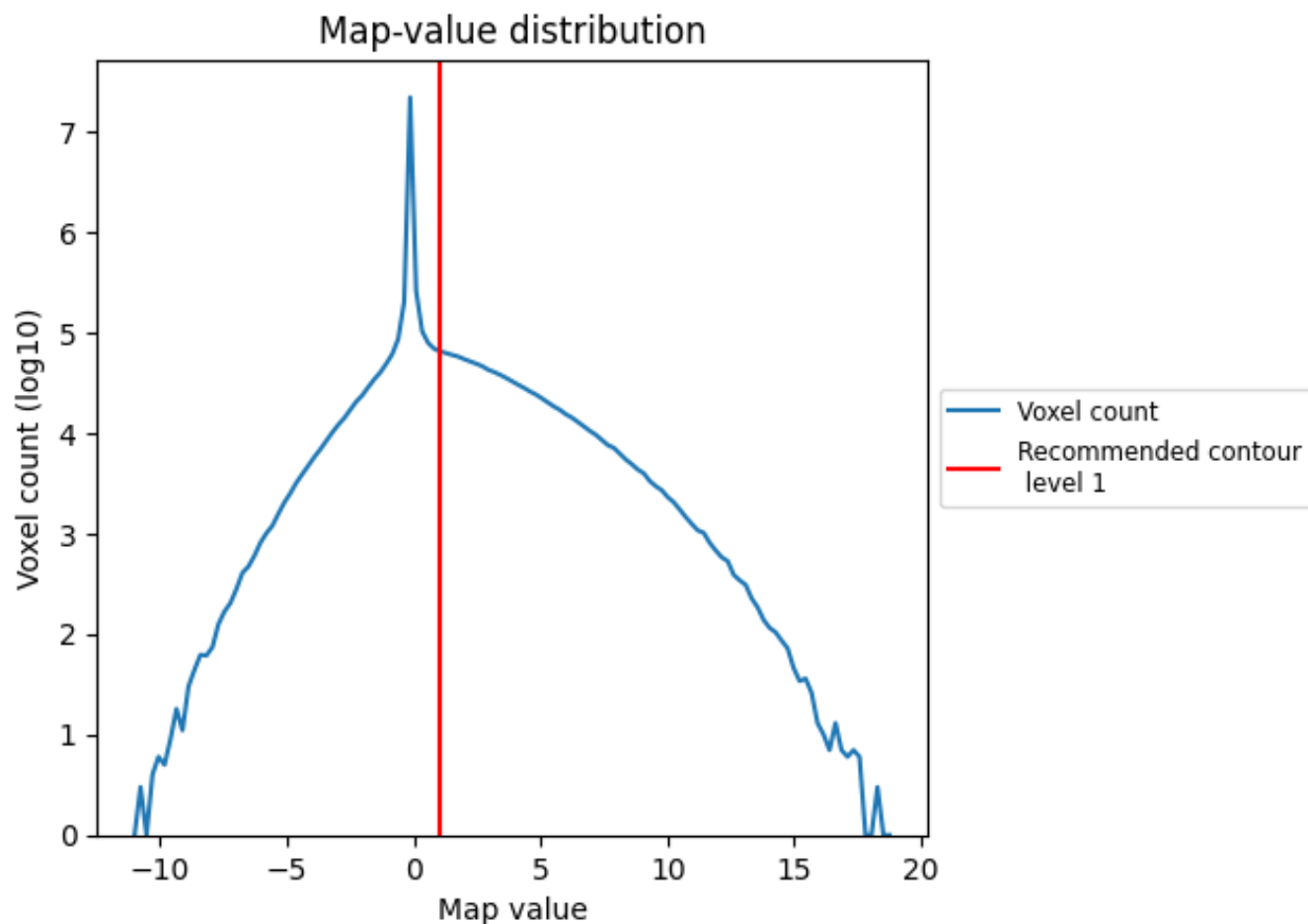
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

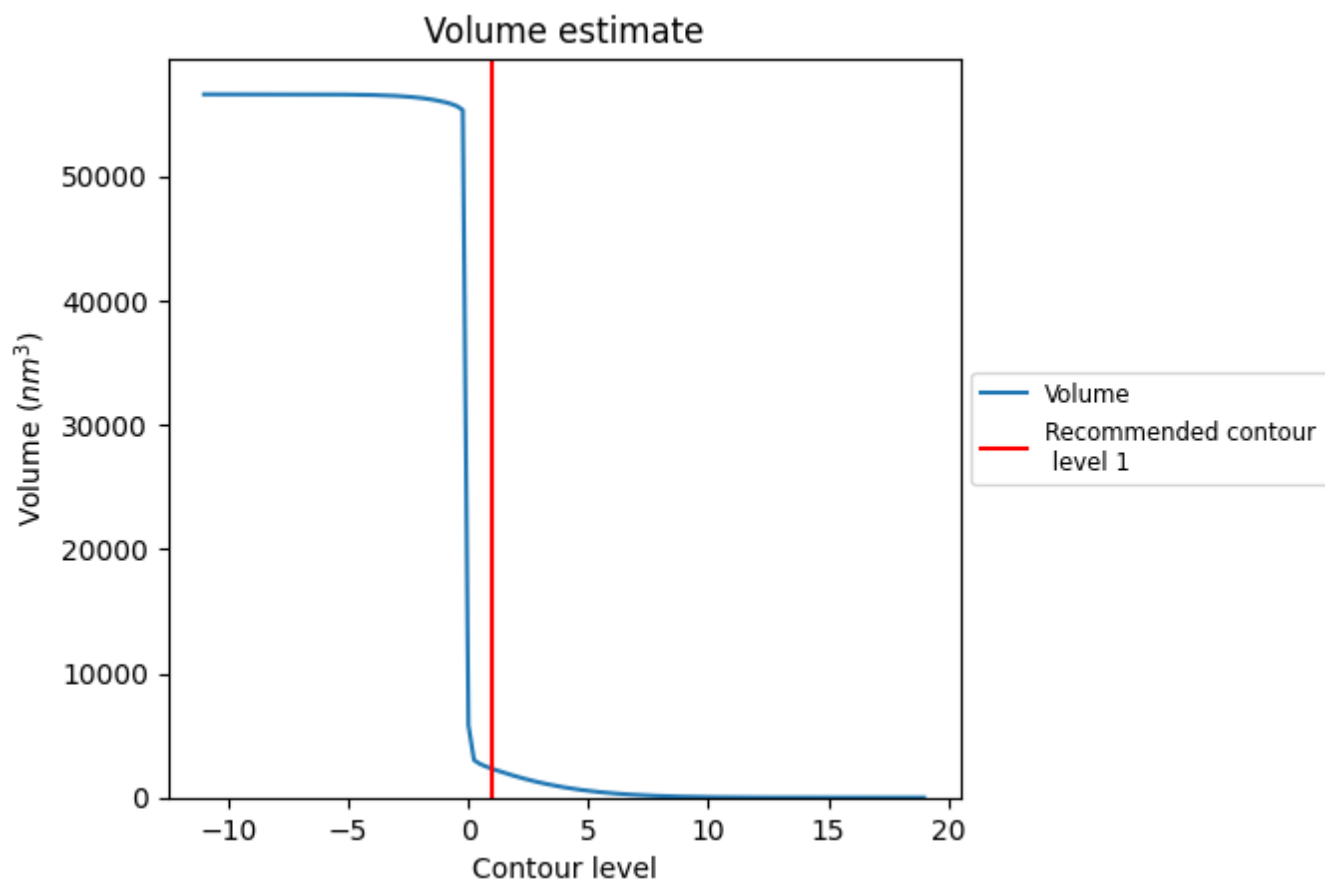
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

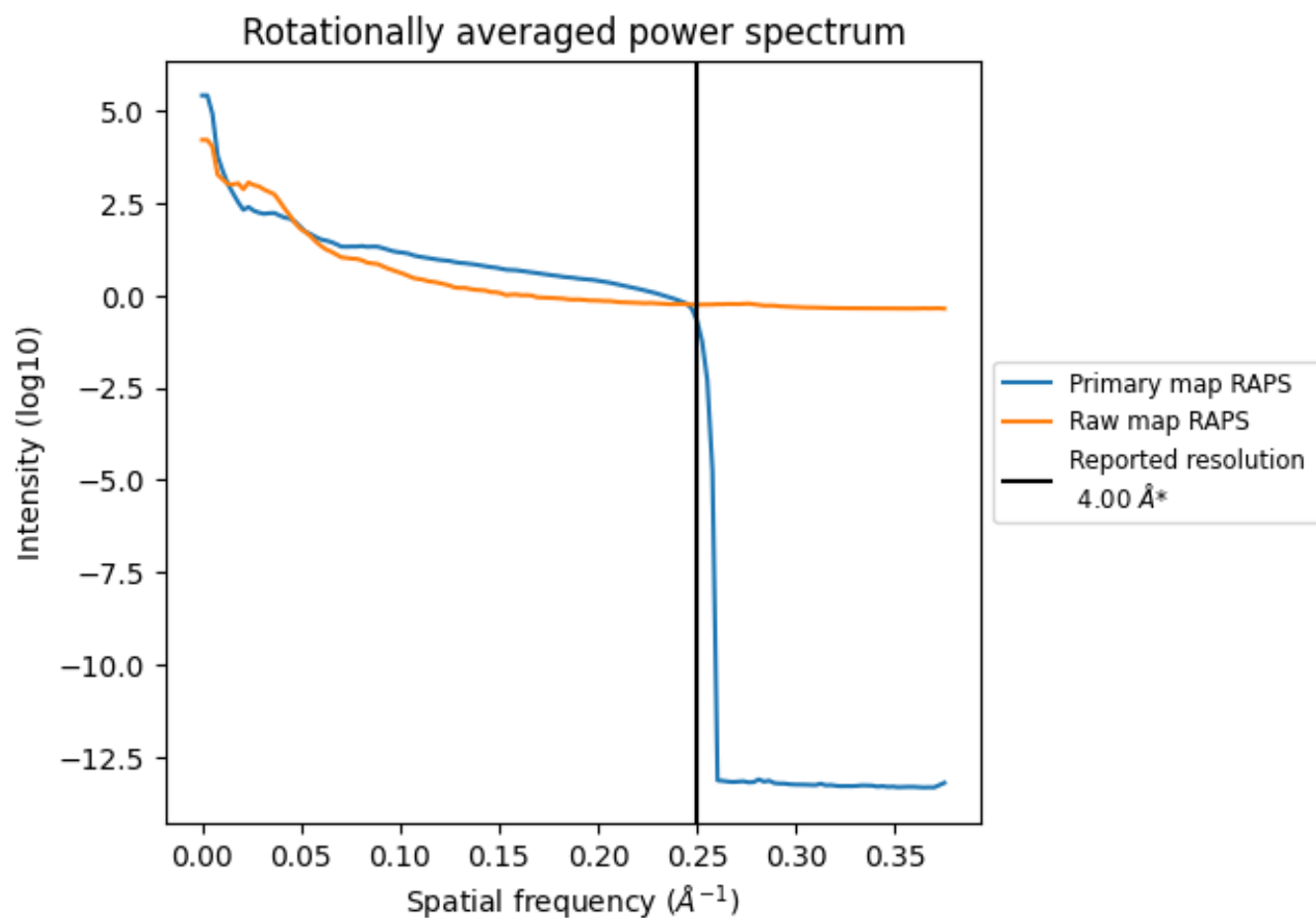
7.2 Volume estimate [i](#)



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

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

7.3 Rotationally averaged power spectrum ⓘ

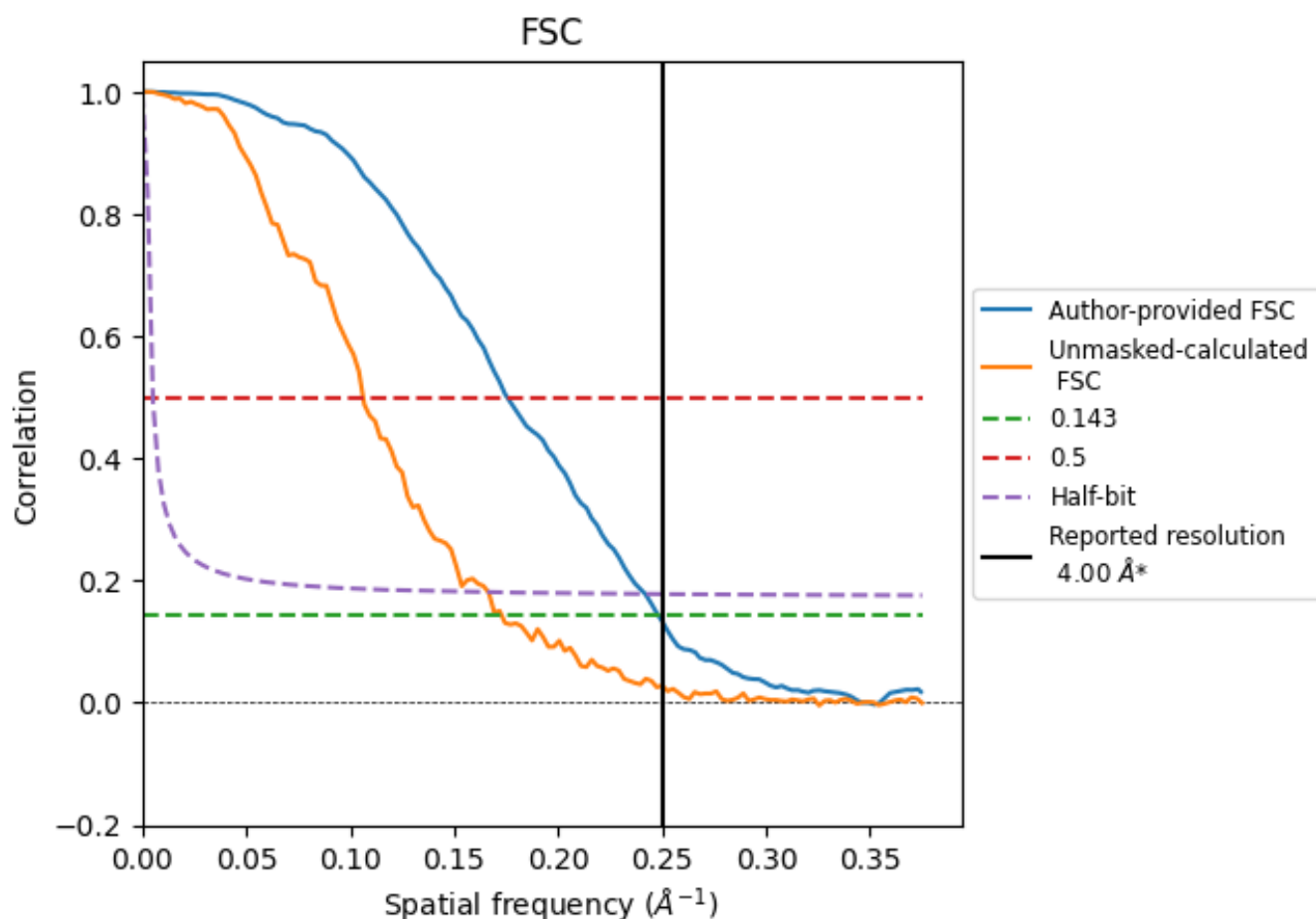


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.250 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

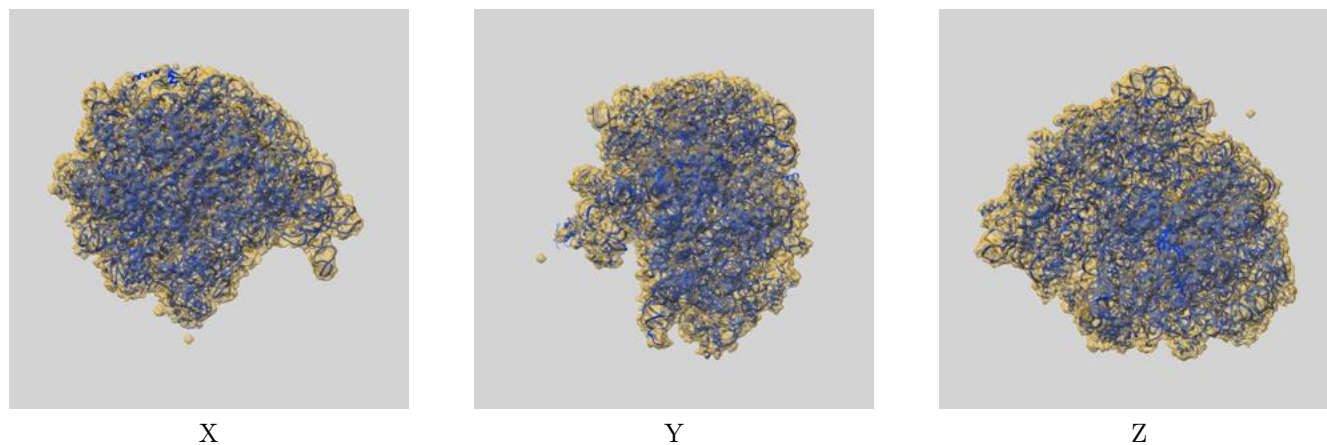
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.03	5.70	4.13
Unmasked-calculated*	5.78	9.42	6.01

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.78 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

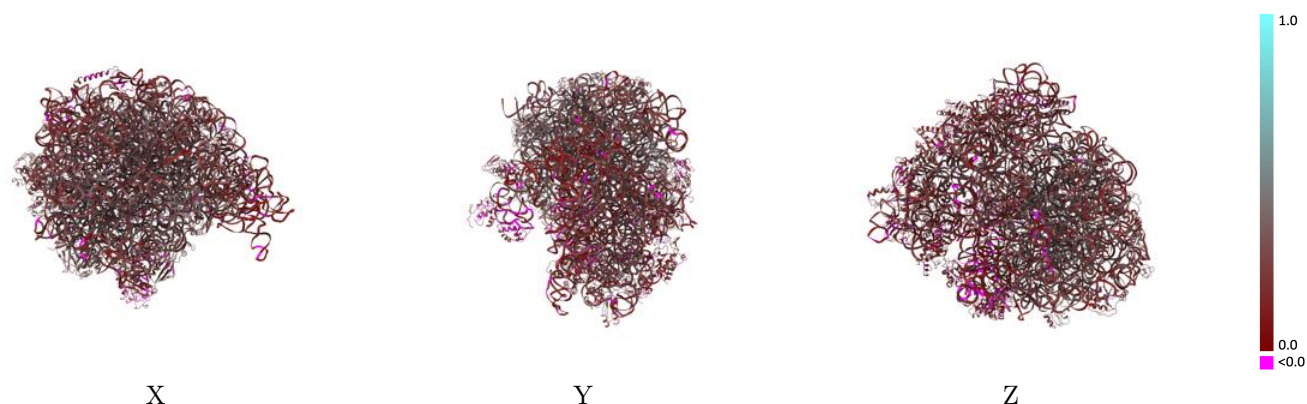
This section contains information regarding the fit between EMDB map EMD-21637 and PDB model 6WDI. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



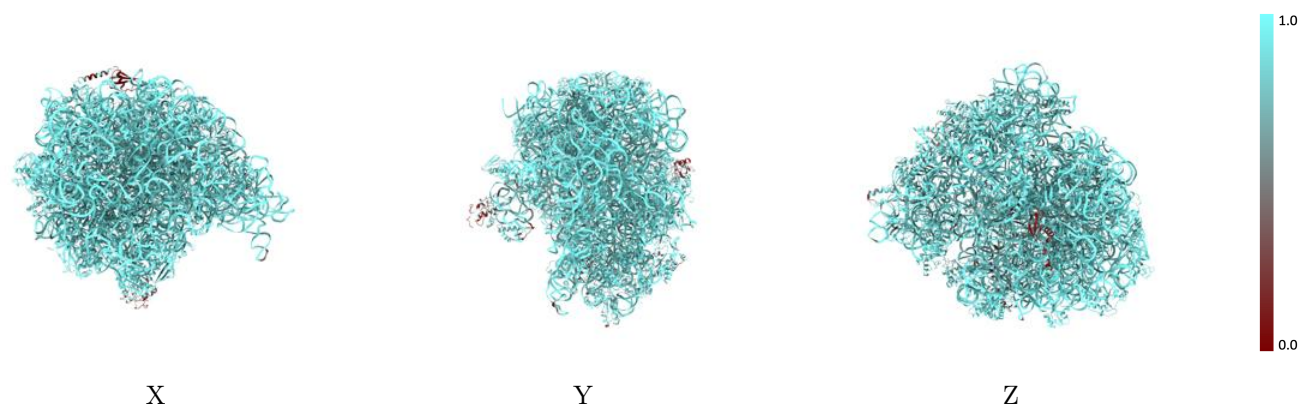
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



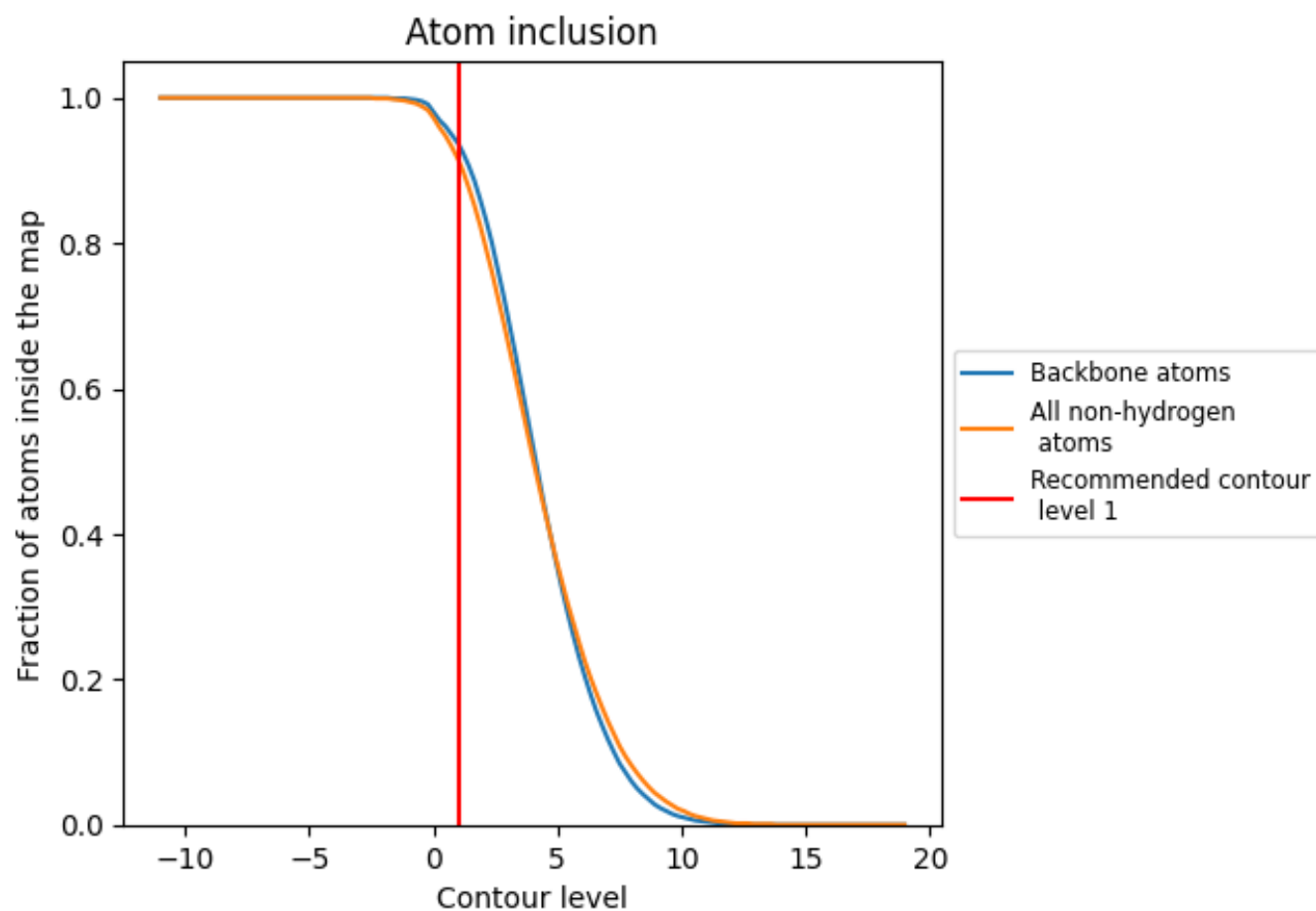
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9150	 0.2610
1	 0.9470	 0.2830
2	 0.9530	 0.2440
3	 0.9400	 0.2270
4	 0.8330	 0.1390
5	 0.8310	 0.1170
6	 0.7630	 0.1000
7	 0.6690	 0.0980
B	 0.8580	 0.3150
C	 0.7390	 0.2170
D	 0.8790	 0.3530
E	 0.8780	 0.3620
F	 0.8360	 0.3110
G	 0.8240	 0.2250
H	 0.8660	 0.2540
I	 0.7330	 0.1880
J	 0.8760	 0.2610
K	 0.9370	 0.2610
L	 0.9100	 0.2220
M	 0.8910	 0.2640
N	 0.8780	 0.2070
O	 0.7570	 0.2130
P	 0.9290	 0.2700
Q	 0.9020	 0.2940
R	 0.8870	 0.1930
S	 0.8440	 0.2250
T	 0.9410	 0.2710
U	 0.8610	 0.2170
V	 0.9070	 0.2370
W	 0.9050	 0.2820
X	 0.9030	 0.2090
Y	 0.8920	 0.2310
Z	 0.8300	 0.2430
a	 0.8130	 0.1390
b	 0.9260	 0.3630



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Chain	Atom inclusion	Q-score
c	 0.9230	 0.3620
d	 0.9130	 0.3200
e	 0.9020	 0.1870
f	 0.9360	 0.2450
g	 0.5170	 0.1680
h	 0.4110	 0.0970
i	 0.7430	 0.1220
j	 0.9190	 0.3600
k	 0.9190	 0.3530
l	 0.9310	 0.3380
m	 0.8660	 0.3360
n	 0.9190	 0.3470
o	 0.9280	 0.2960
p	 0.9240	 0.3350
q	 0.8890	 0.3510
r	 0.9210	 0.3390
s	 0.9010	 0.3360
t	 0.9020	 0.3160
u	 0.9530	 0.3280
v	 0.9360	 0.3130
w	 0.8930	 0.3460
x	 0.9220	 0.3480
y	 0.9090	 0.2830
z	 0.8950	 0.3030