



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 12:00 PM UTC

PDB ID : 6WD9 / pdb_00006wd9
EMDB ID : EMD-21628
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure III-B)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

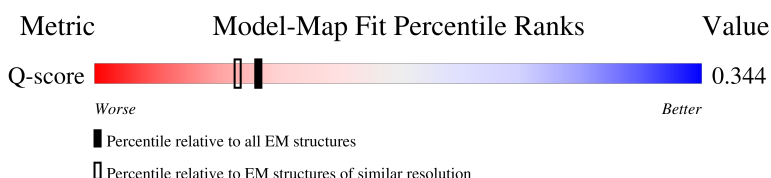
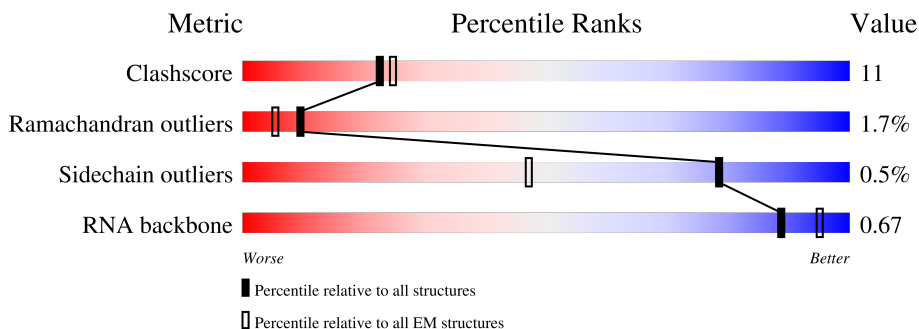
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

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



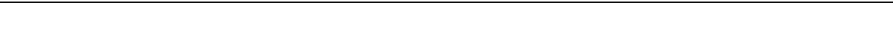
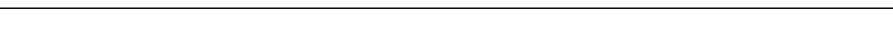
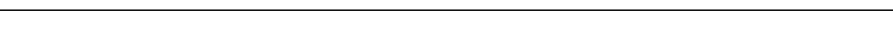
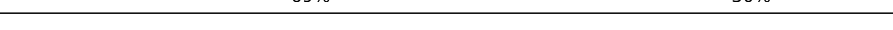
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	 67% 32% .
2	c	209	 74% 25%
3	d	201	 76% 24%

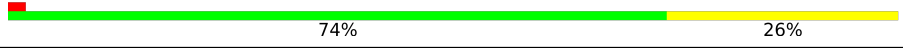
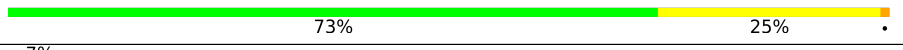
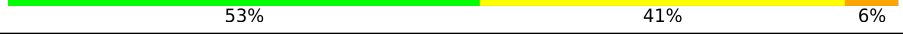
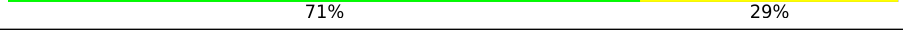
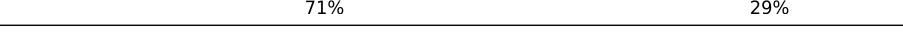
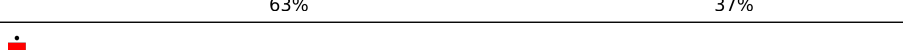
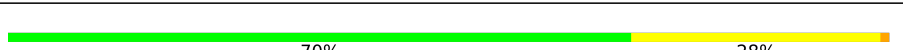
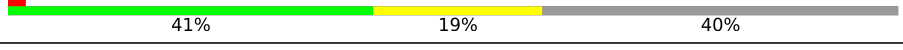
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Mol	Chain	Length	Quality of chain
4	e	177	 67% 33%
5	f	176	 69% 31%
6	g	149	 13% 66% 30%
7	h	131	 18% 49% 44% 6%
8	i	141	 13% 62% 35%
9	j	142	 70% 29%
10	k	122	 62% 33% 5%
11	l	143	 69% 26% 5%
12	m	136	 66% 33%
13	n	120	 66% 33%
14	o	116	 70% 29%
15	p	114	 68% 31%
16	q	117	 76% 21%
17	r	103	 69% 30%
18	s	110	 75% 23%
19	t	93	 77% 22%
20	u	102	 72% 26%
21	v	94	 68% 31%
22	w	75	 68% 31%
23	x	77	 66% 32%
24	y	63	 67% 32%
25	z	58	 78% 22%
26	B	56	 75% 21%
27	C	50	 74% 24%
28	D	46	 67% 30%

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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	55% 38% 7%
55	5	77	53% 43%
55	6	77	5% 49% 48%
56	4	18	6% 50% 50%
57	7	76	49% 46% 5%
58	8	400	56% 29% 14%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 152927 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1036415628

- 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 1370526515

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

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

- Molecule 56 is a RNA chain called mRNA.

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

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

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

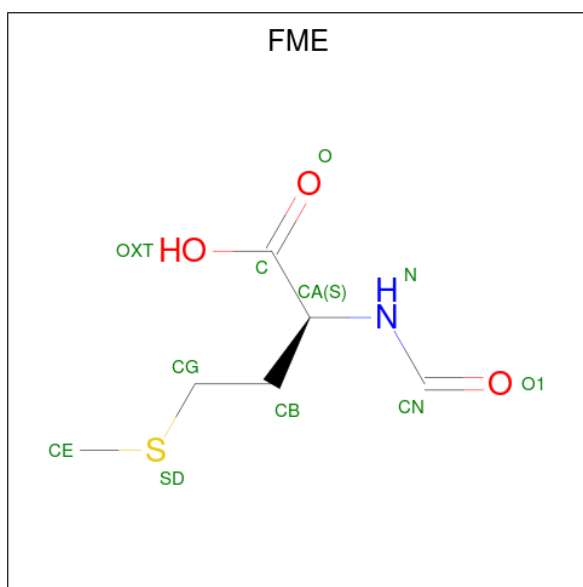
- Molecule 58 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	346	Total	C	N	O	S	0	0
			2677	1698	459	508	12		

There are 7 discrepancies between the modelled and reference sequences:

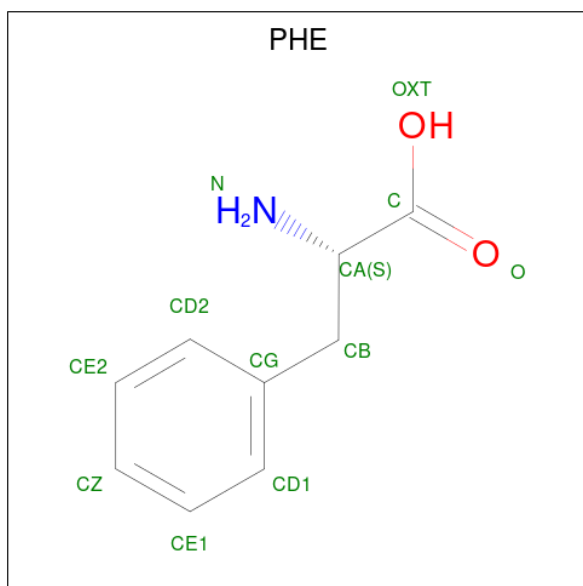
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag	UNP E2QFJ4

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



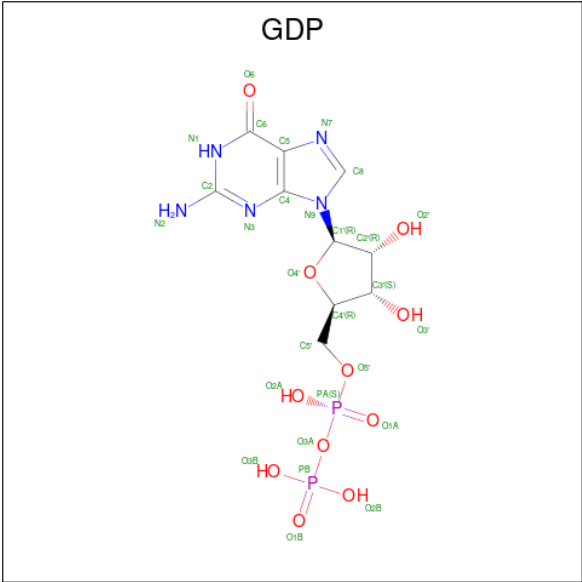
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 60 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms					AltConf
60	7	1	Total	C	N	O		0
			11	9	1	1		

- Molecule 61 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

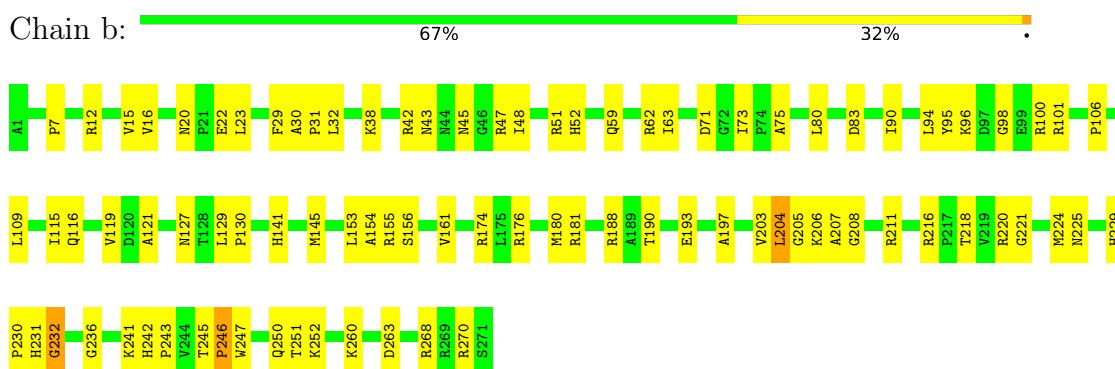


Mol	Chain	Residues	Atoms					AltConf
61	8	1	Total	C	N	O	P	0
			28	10	5	11	2	

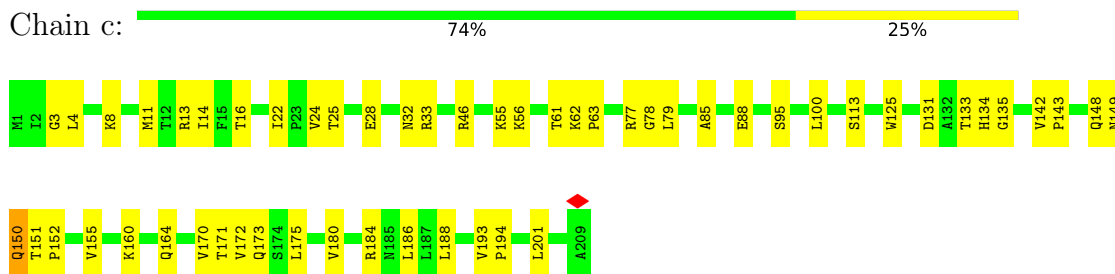
3 Residue-property plots

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.

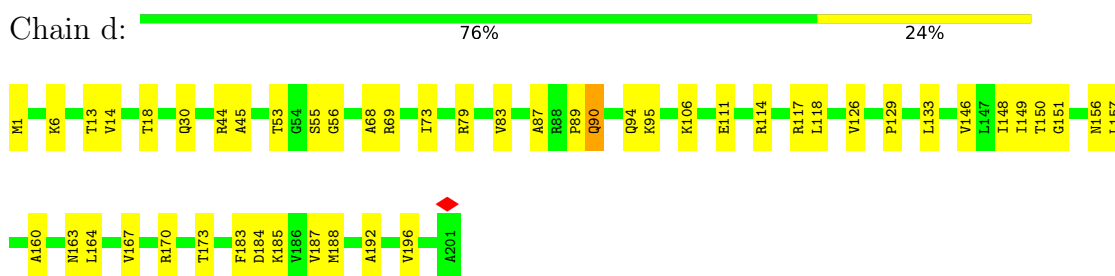
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

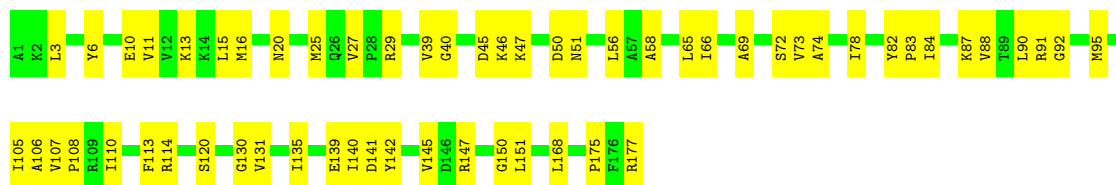


• Molecule 3: 50S ribosomal protein L4



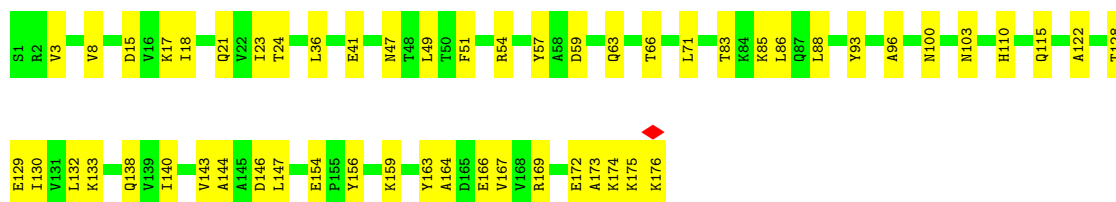
• Molecule 4: 50S ribosomal protein L5

Chain e:  67% 33%



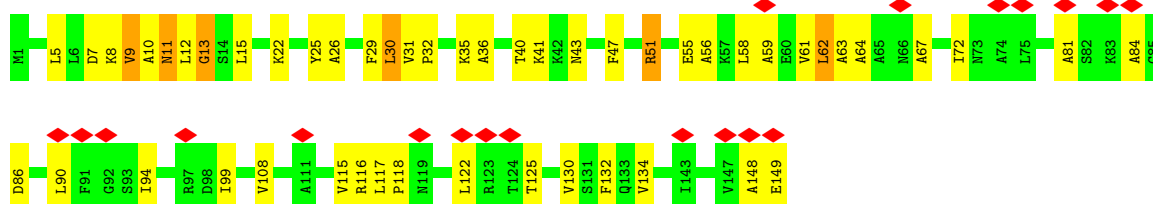
• Molecule 5: 50S ribosomal protein L6

Chain f:  69% 31%



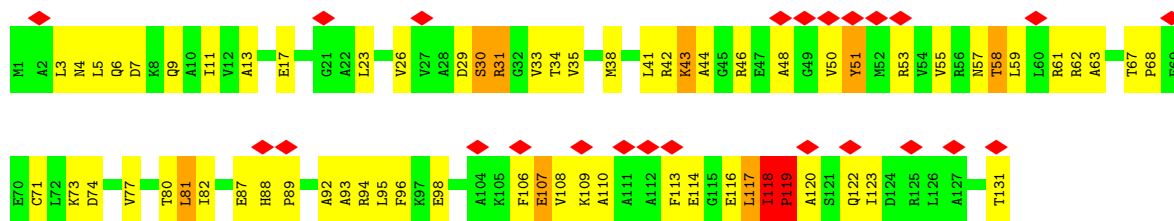
• Molecule 6: 50S ribosomal protein L9

Chain g:  13% 66% 30%



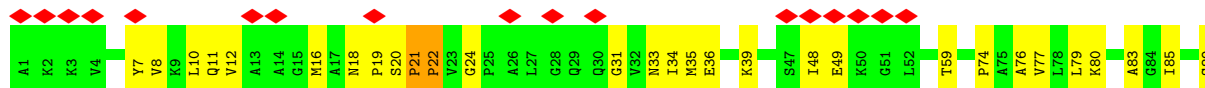
• Molecule 7: 50S ribosomal protein L10

Chain h:  18% 49% 44% 6%

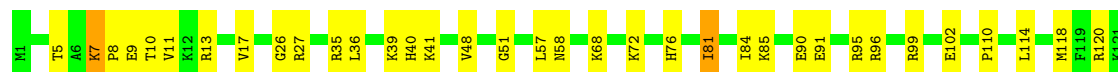


• Molecule 8: 50S ribosomal protein L11

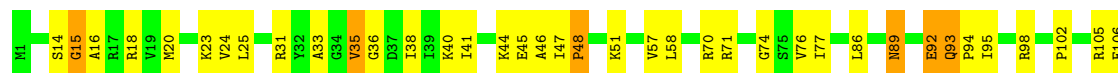
Chain i:  13% 62% 35%



- Molecule 9: 50S ribosomal protein L13



- Molecule 10: 50S ribosomal protein L14



- Molecule 11: 50S ribosomal protein L15

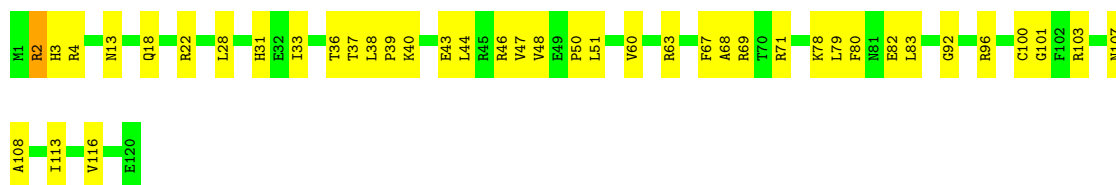


- Molecule 12: 50S ribosomal protein L16



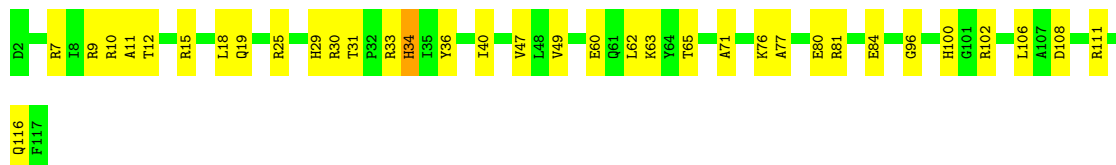
- Molecule 13: 50S ribosomal protein L17





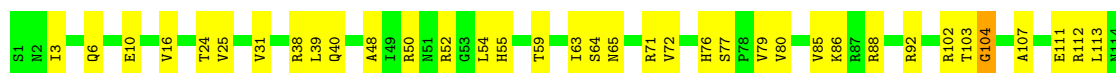
- Molecule 14: 50S ribosomal protein L18

Chain o: 70% 29%



- Molecule 15: 50S ribosomal protein L19

Chain p: 68% 31%



- Molecule 16: 50S ribosomal protein L20

Chain q: 76% 21%



- Molecule 17: 50S ribosomal protein L21

Chain r: 69% 30%



- Molecule 18: 50S ribosomal protein L22

Chain s: 75% 23%

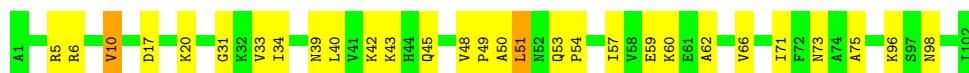


- Molecule 19: 50S ribosomal protein L23

Chain t: 77% 22%



- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25



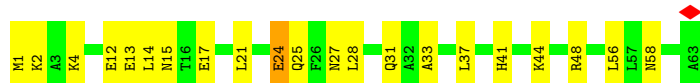
- Molecule 22: 50S ribosomal protein L27



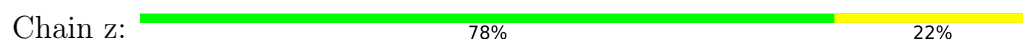
- Molecule 23: 50S ribosomal protein L28



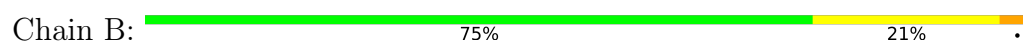
- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30

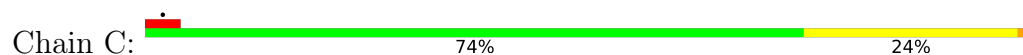


- Molecule 26: 50S ribosomal protein L32

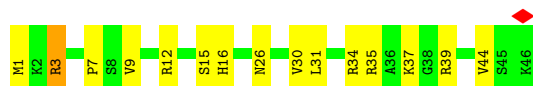




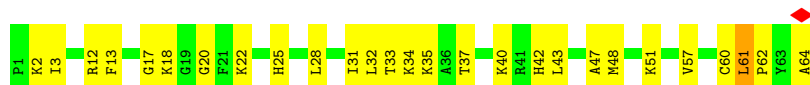
- Molecule 27: 50S ribosomal protein L33



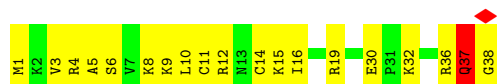
- Molecule 28: 50S ribosomal protein L34



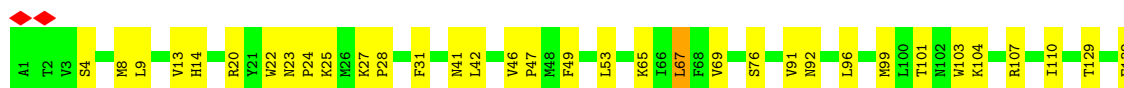
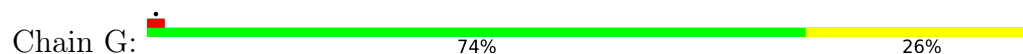
- Molecule 29: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L36

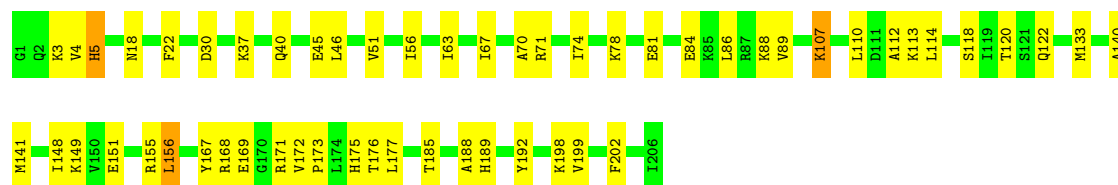


- Molecule 31: 30S ribosomal protein S2

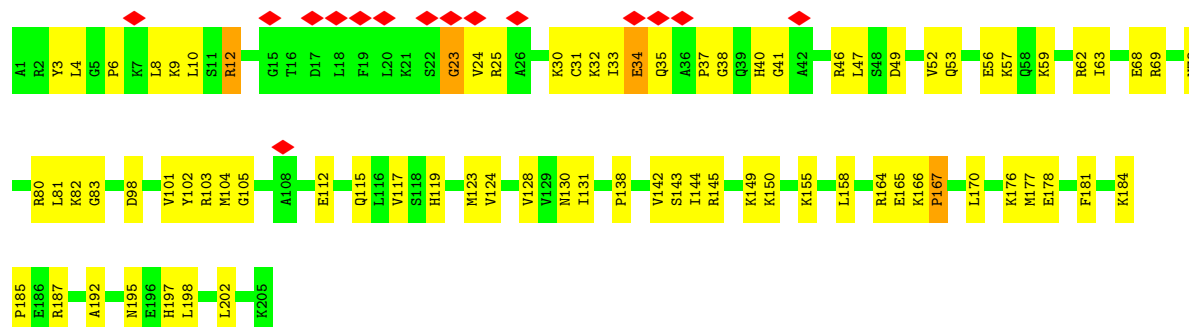


- Molecule 32: 30S ribosomal protein S3

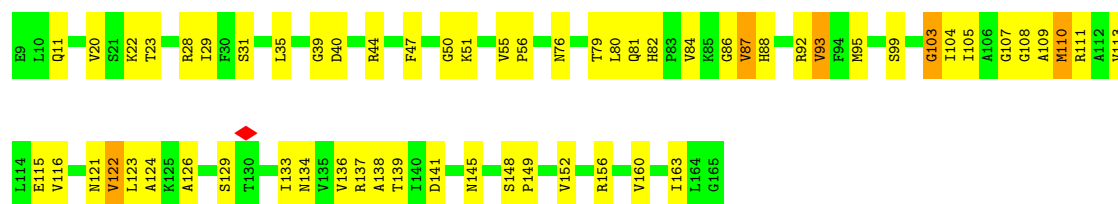




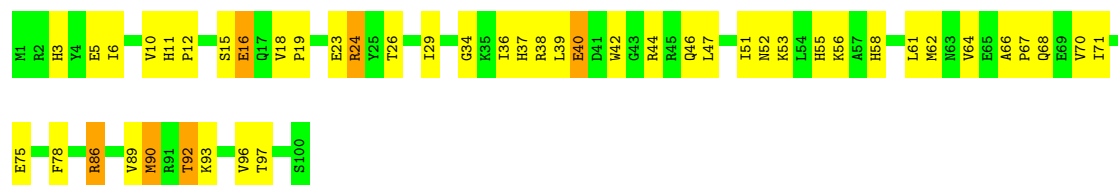
- Molecule 33: 30S ribosomal protein S4



- Molecule 34: 30S ribosomal protein S5



- Molecule 35: 30S ribosomal protein S6



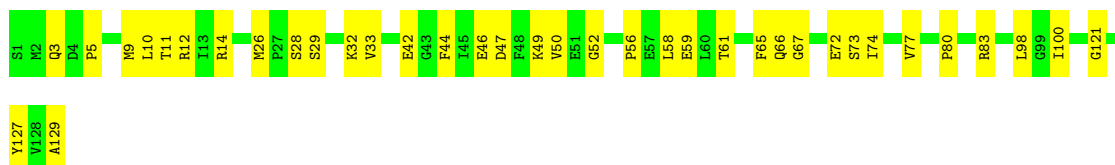
- Molecule 36: 30S ribosomal protein S7





- Molecule 37: 30S ribosomal protein S8

Chain M: 71% 29%



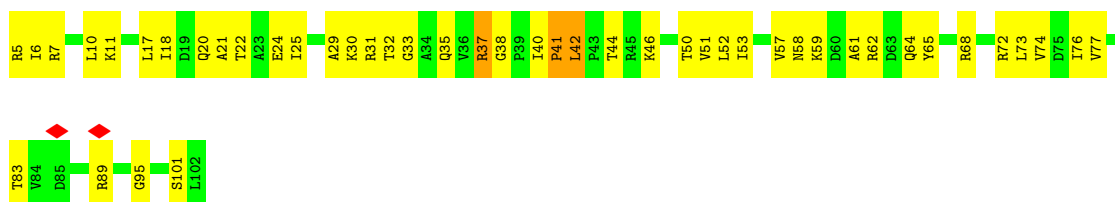
- Molecule 38: 30S ribosomal protein S9

Chain N: 63% 37%



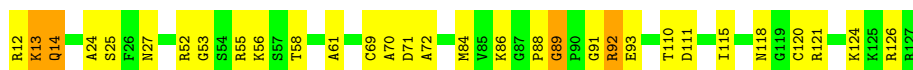
- Molecule 39: 30S ribosomal protein S10

Chain O: 53% 44%



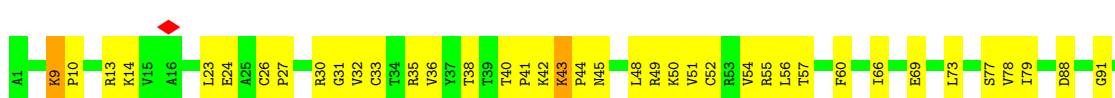
- Molecule 40: 30S ribosomal protein S11

Chain P: 73% 23%



- Molecule 41: 30S ribosomal protein S12

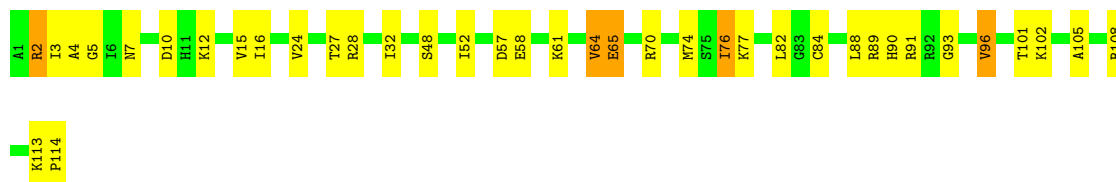
Chain Q: 58% 41%





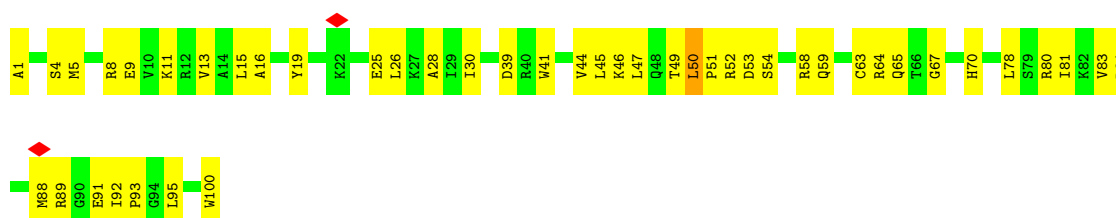
- Molecule 42: 30S ribosomal protein S13

Chain R: 67% 29%



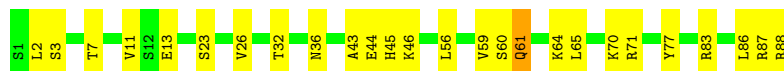
- Molecule 43: 30S ribosomal protein S14

Chain S: 55% 44%



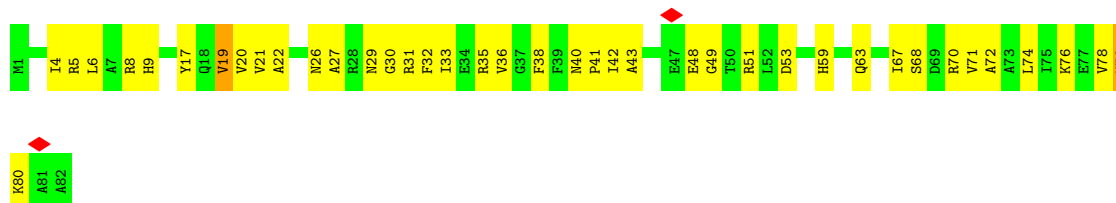
- Molecule 44: 30S ribosomal protein S15

Chain T: 70% 28%



- Molecule 45: 30S ribosomal protein S16

Chain U: 51% 46%



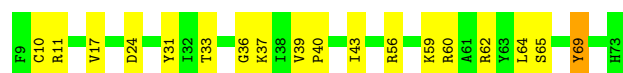
- Molecule 46: 30S ribosomal protein S17

Chain V: 68% 31%



- Molecule 47: 30S ribosomal protein S18

Chain W:  72% 26%



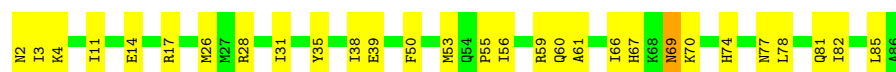
- Molecule 48: 30S ribosomal protein S19

Chain X:  72% 28%



- Molecule 49: 30S ribosomal protein S20

Chain Y:  66% 33%

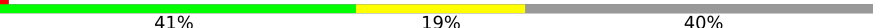


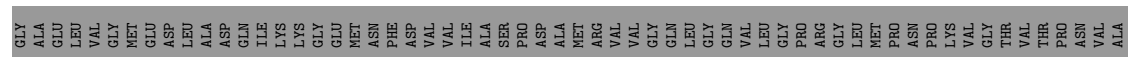
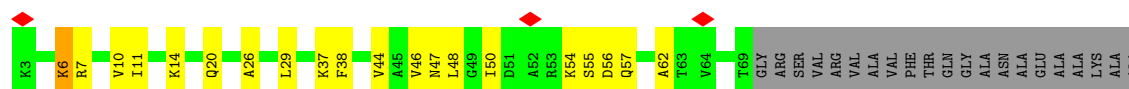
- Molecule 50: 30S ribosomal protein S21

Chain Z:  52% 37% 11%



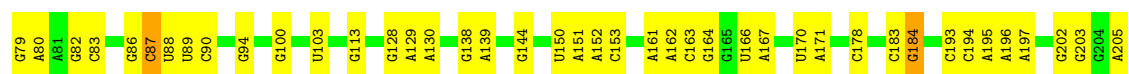
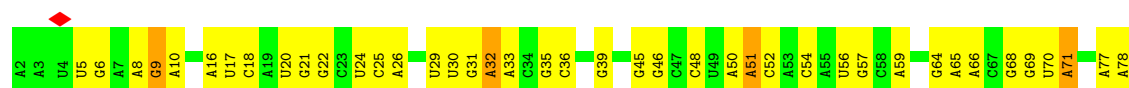
- Molecule 51: 50S ribosomal protein L1

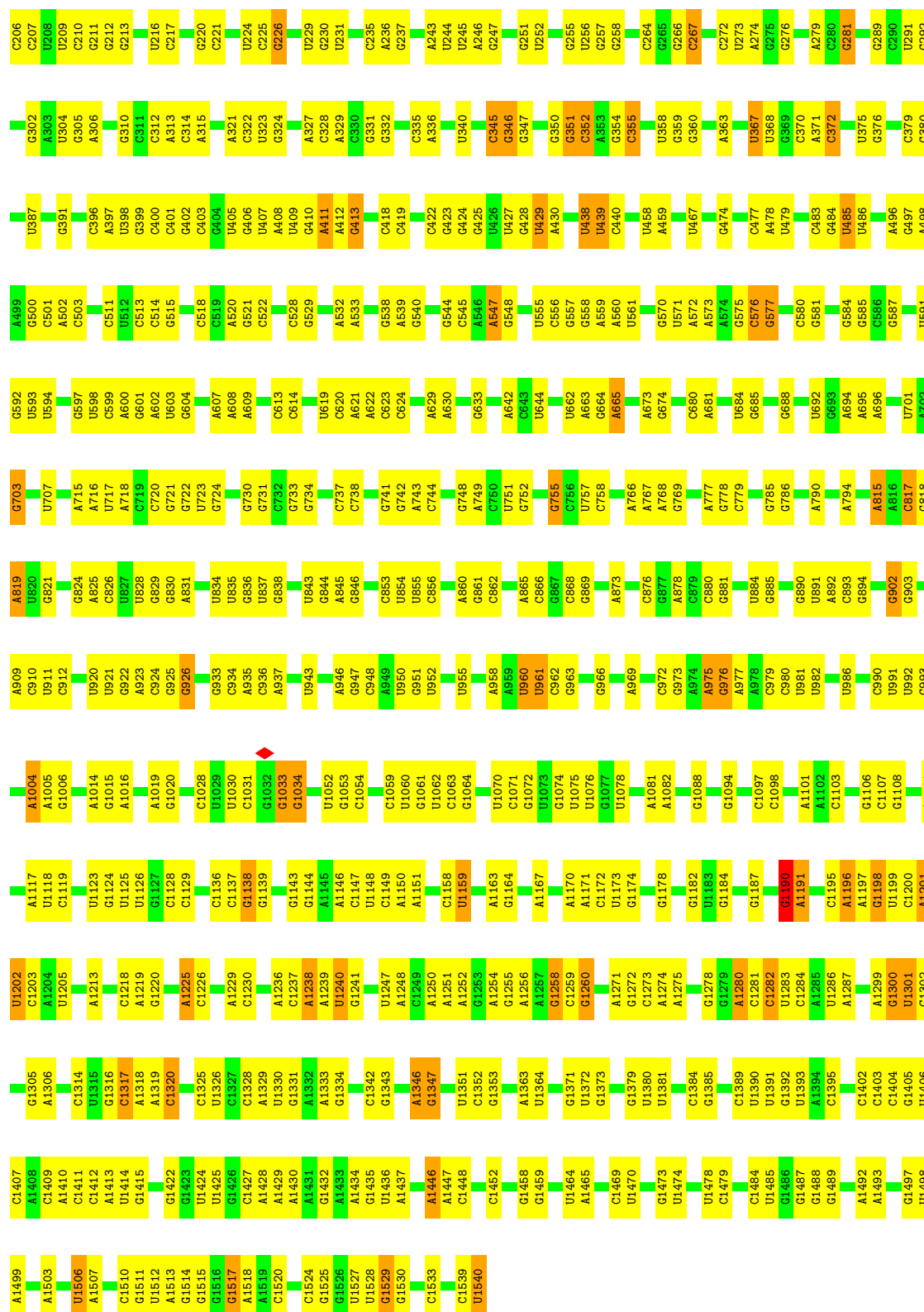
Chain a:  41% 19% 40%



- Molecule 52: 16S ribosomal RNA

Chain 3:  57% 39%





• Molecule 53: 23S ribosomal RNA

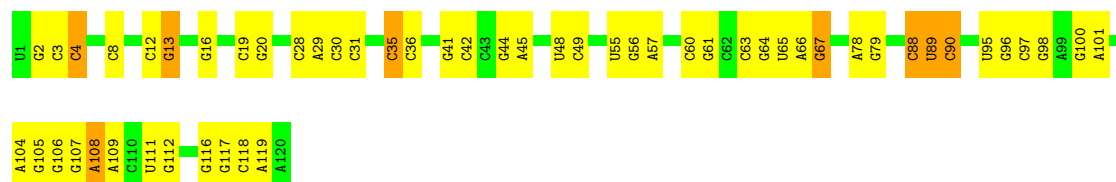


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G1416	G2	A119	A324	G530	A614	G704	U807	A917	A1012	U1101	G1200	U1313	G1416
A1419	A10	A120	G325	C531	U615	U714	G808	C922	U1013	U1102	U1201	C1314	A1419
G1420	G11	G121	A426	A532	A616	A715	C812	G923	C1013	A1103	G1202	C1320	A1419
A1429	U12	G122	G227	G533	G617	G726	C817	U929	U1019	C1104	A1204	A1321	A1429
G1430	U18	G123	C228	G536	G618	G727	C818	G930	A1020	U1105	A1205	U1326	G1430
A1434	A19	U138	C229	A537	G619	A728	A819	U931	A1021	G1106	G1210	U1327	A1434
G1435	A20	U139	G230	G538	G622	G729	C822	U932	U1022	G1107	G1211	A1327	G1435
C1437	A21	G141	G232	A539	G623	A730	C827	U933	U1023	A1111	G1212	A1328	G1437
U1438	G22	A142	C239	C540	A627	G737	A825	C937	G1026	U1119	G1213	U1329	U1438
G1441	G23	A145	A241	C541	A628	G738	U826	G938	A1027	U1120	G1214	U1330	G1441
U1442	G24	A146	G242	C544	A629	U741	U827	G939	U1028	U1121	G1215	C1331	U1442
G1443	G25	A147	G243	C545	A633	U742	C829	A941	A1029	U1122	G1216	C1332	G1443
U1444	G26	A148	G244	C546	A634	A743	U830	A942	U1032	U1123	U1219	U1333	U1444
G1445	G27	U148	G245	C547	A635	U744	C831	A943	U1033	U1124	U1220	G1334	U1445
C1454	A28	U149	G246	C548	A636	G745	U832	C946	A1034	U1125	G1221	U1335	C1454
U1458	U34	U150	G247	C549	A637	U746	U833	A947	U1035	U1126	U1222	U1336	U1458
G1459	G35	U151	G248	C550	A638	C747	C834	A948	A1036	U1127	U1223	U1337	G1459
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U1461	C37	A161	A256	C552	A640	U750	U846	G953	G1038	U1129	U1225	U1339	U1461
G1464	G45	U162	A257	C553	A641	A751	U847	G954	G1039	U1130	U1226	U1340	G1464
G1465	G46	U163	A258	C554	A642	A752	C851	U955	C1040	U1131	U1227	U1341	G1465
U1468	A49	U164	A259	C555	A643	A753	U852	U956	A1041	U1132	U1228	U1342	U1468
A1470	U50	U165	A260	C556	A644	U754	C853	U957	A1042	U1133	U1229	U1343	A1470
G1475	G51	U166	A261	C557	A645	U755	C854	C961	A1043	U1134	U1230	U1344	G1475
U1476	C61	U167	A262	C558	A646	U756	C855	C962	A1044	U1135	U1231	U1345	U1476
G1482	U62	U168	A263	C559	A647	G757	U856	G963	A1045	U1136	U1232	U1346	G1482
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G1489	U65	U171	A266	C562	A650	G760	U859	U966	G1048	U1139	U1235	U1349	G1489
A1490	C68	U172	A267	C563	A651	A761	U860	U967	U1049	U1140	U1236	U1350	A1490
C1498	G70	U173	A268	C564	A652	U762	U861	C968	U1050	U1141	U1237	U1351	C1498
U1500	A74	U174	A269	C565	A653	G763	U862	C969	U1051	U1142	U1238	U1352	U1500
U1506	G75	U175	A270	C566	A654	A764	U863	U970	C1052	U1143	U1239	U1353	U1506
C1507	C76	U176	A271	C567	A655	G765	U864	C971	C1053	U1144	U1240	U1354	C1507
A1508	G77	U177	A272	C568	A656	U766	U865	C972	U1054	U1145	U1241	U1355	A1508
G1510	A84	U178	A273	C569	A657	G767	U866	C973	A1055	U1146	U1242	U1356	G1510
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A1515	C88	U182	A277	C573	A661	G771	U870	C977	U1059	U1150	U1246	U1360	A1515
G1516	C89	U183	A278	C574	A662	U772	U871	C978	U1060	U1151	U1247	U1361	G1516
A1522	C90	U184	A279	C575	A663	G773	U872	C979	U1061	U1152	U1248	U1362	A1522
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		U186	A281	C577	A665	G775	U874	C981	U1063	U1154	U1250	U1364	
		U187	A282	C578	A666	U776	U875	C982	U1064	U1155	U1251	U1365	
		U188	A283	C579	A667	G777	U876	C983	U1065	U1156	U1252	U1366	
		U189	A284	C580	A668	U778	U877	C984	U1066	U1157	U1253	U1367	
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		U194	A289	C585	A673	G783	U882	C989	U1071	U1162	U1258	U1372	
		U195	A290	C586	A674	U784	U883	C990	U1072	U1163	U1259	U1373	
		U196	A291	C587	A675	G785	U884	C991	U1073	U1164	U1260	U1374	
		U197	A292	C588	A676	U786	U885	C992	U1074	U1165	U1261	U1375	
		U198	A293	C589	A677	G787	U886	C993	U1075	U1166	U1262	U1376	
		U199	A294	C590	A678	U788	U887	C994	U1076	U1167	U1263	U1377	
		U200	A295	C591	A679	G789	U888	C995	U1077	U1168	U1264	U1378	
		U201	A296	C592	A680	U790	U889	C996	U1078	U1169	U1265	U1379	
		U202	A297	C593	A681	G791	U890	C997	U1079	U1170	U1266	U1380	
		U203	A298	C594	A682	U792	U891	C998	U1080	U1171	U1267	U1381	
		U204	A299	C595	A683	G793	U892	C999	U1081	U1172	U1268	U1382	
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		U206	A301	C597	A685	G795	U894	C1001	U1083	U1174	U1270	U1384	
		U207	A302	C598	A686	U796	U895	C1002	U1084	U1175	U1271	U1385	
		U208	A303	C599	A687	G797	U896	C1003	U1085	U1176	U1272	U1386	
		U209	A304	C600	A688	U798	U897	C1004	U1086	U1177	U1273	U1387	
		U210	A305	C601	A689	G799	U898	C1005	U1087	U1178	U1274	U1388	
		U211	A306	C602	A690	U800	U899	C1006	U1088	U1179	U1275	U1389	
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		U213	A308	C604	A692	U802	U901	C1008	U1090	U1181	U1277	U1391	
		U214	A309	C605	A693	U803	U902	C1009	U1091	U1182	U1278	U1392	
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		U216	A311	C607	A695	U805	U904	C1011	U1093	U1184	U1280	U1394	
		U217	A312	C608	A696	U806	U905	C1012	U1094	U1185	U1281	U1395	
		U218	A313	C609	A697	U807	U906	C1013	U1095	U1186	U1282	U1396	
		U219	A314	C610	A698	U808	U907	C1014	U1096	U1187	U1283	U1397	
		U220	A315	C611	A699	U809	U908	C1015	U1097	U1188	U1284	U1398	
		U221	A316	C612	A700	U810	U909	C1016	U1098	U1189	U1285	U1399	
		U222	A317	C613	A701	U811	U910	C1017	U1099	U1190	U1286	U1400	
		U223	A318	C614	A702	U812	U911	C1018	U1100	U1191	U1287	U1401	
		U224	A319	C615	A703	U813	U912	C1019	U1101	U1192	U1288	U1402	
		U225	A320	C616	A704	U814	U913	C1020	U1102	U1193	U1289	U1403	
		U226	A321	C617	A705	U815	U914	C1021	U1103	U1194	U1290	U1404	
		U227	A322	C618	A706	U816	U915	C1022	U1104	U1195	U1291	U1405	
		U228	A323	C619	A707	U817	U916	C1023	U1105	U1196	U1292	U1406	
		U229	A324	C620	A708	U818	U917	C1024	U1106	U1197	U1293	U1407	
		U230	A325	C621	A709	U819	U918	C1025	U1107	U1198	U1294	U1408	
		U231	A326	C622	A710	U820	U919	C1026	U1108	U1199	U1295	U1409	
		U232	A327	C623	A711	U821	U920	C1027	U1109	U1200	U1296	U1410	
		U233	A328	C624	A712	U822	U921	C1028	U1110	U1201	U1297	U1411	
		U234	A329	C625	A713	U823	U922	C1029	U1111	U1202	U1298	U1412	
		U235	A330	C626	A714	U824	U923	C1030	U1112	U1203	U1299	U1413	
		U236	A331	C627	A715	U825	U924	C1031	U1113	U1204	U1300	U1414	
		U237	A332	C628	A716	U826	U925	C1032	U1114	U1205	U1301	U1415	
		U238	A333	C629	A717	U827	U926	C1033	U1115	U1206	U1302	U1416	
		U239	A334	C630	A718	U828	U927	C1034	U1116	U1207	U1303	U1417	
		U240	A335	C631	A719	U829	U928	C1035	U1117	U1208	U1304	U1418	
		U241	A336	C632	A720	U830	U929	C1036	U1118	U1209	U1305	U1419	
		U242	A337	C633	A721	U831	U930	C1037	U1119	U1210	U1306	U1420	
		U243	A338	C634	A722	U832	U931	C1038	U1120	U1211	U1307	U1421	

U1523	G1524	C1605	A1744	U1827	C1924	A2031	G2126	G2218	U2296	A2369	C2452	G2553	G2641	U2754	U2849
C1525	C1526	C1606	A1745	G1828	C1925	U2034	U2127	U2219	A2297	G2370	G2455	U2554	C2646	C2755	C2849
C1527	A1608	C1607	U1751	A1829	A1928	G2035	U2132	U2220	A2298	G2371	G2456	U2555	U2647	U2756	C2853
A1528	A1609	A1610	U1752	C1833	G1929	C2036	G2133	G2221	C2304	G2372	U2457	C2556	U2648	A2757	C2854
G1529	C1611	C1611	G1753	U1834	G1930	A2042	A2134	A2225	U2305	C2373	G2458	C2557	G2655	G2759	G2859
C1533	A1614	A1615	A1754	C1843	G1935	C2043	U2139	C2226	U2306	A2375	G2464	C2558	G2656	A2764	U2860
U1534	A1616	A1616	A1755	C1844	A1936	A2052	G2140	A2228	G2315	G2385	C2465	C2559	C2658	A2765	A2861
C1536	U1636	U1637	G1756	A1847	A1937	A2056	A2142	G2228	G2316	A2386	C2466	U2561	G2659	C2772	C2862
G1537	A1637	A1637	U1758	U1851	A1938	C2055	A2147	U2233	U2317	U2387	A2468	C2562	A2665	C2773	C2863
G1538	U1637	U1637	G1764	U1856	U1943	C2056	G2156	U2234	G2318	A2388	A2469	A2566	A2666	A2778	U2865
U1539	G1645	G1645	C1771	G1857	U1944	A2060	G2157	U2235	G2319	U2389	G2470	C2567	C2667	U2779	U2866
C1541	A1646	A1646	A1772	C1874	A1952	G2061	G2158	U2236	G2320	G2390	C2471	U2568	C2668	C2785	C2867
U1542	U1647	U1647	A1773	G1875	A1953	A2062	G2159	G2237	U2321	A2391	G2472	C2569	C2669	U2786	A2868
G1543	U1648	U1648	C1774	G1860	G1954	C2066	C2161	G2238	U2322	U2392	A2473	G2570	A2670	C2787	C2869
C1550	G1651	G1651	U1775	A1871	U1955	C2067	G2162	G2239	A2323	C2394	C2475	U2571	A2682	C2788	C2870
A1551	C1658	C1658	U1776	A1872	U1963	U2068	G2163	U2244	G2324	U2395	A2476	C2572	U2683	C2789	G2791
G1555	U1662	U1662	U1779	G1873	A1964	G2069	A2163	A2247	U2325	U2396	U2477	C2573	A2684	U2790	C2875
C1558	A1664	A1664	A1788	C1874	G1965	A2070	G2164	C2248	U2326	U2397	A2478	C2574	U2685	U2791	C2876
U1559	G1666	G1666	C1789	G1875	A1966	C2071	C2165	C2249	U2327	C2398	C2479	C2575	G2693	A2792	A2879
C1563	G1667	G1667	U1781	A1876	G1967	C2072	G2166	G2250	A2328	U2398	U2482	C2576	G2694	C2794	C2880
C1564	A1672	A1672	U1790	C1881	U1970	C2073	A2167	U2257	A2329	G2399	C2483	U2579	C2695	C2795	C2875
C1565	U1673	U1673	A1791	U1882	G1971	C2074	C2168	C2258	G2330	U2402	C2484	U2580	U2696	U2796	C2876
U1566	G1674	G1674	C1792	U1883	G1972	U2081	U2169	U2262	U2331	A2406	U2485	C2581	C2697	U2797	U2884
G1567	G1674	G1674	U1794	A1885	U1973	A2082	A2183	C2263	C2332	A2411	G2494	C2582	C2698	U2798	C2885
G1568	A1677	A1677	A1795	A1889	U1991	G2087	A2184	C2264	U2333	A2412	C2495	C2583	C2699	U2799	C2886
A1569	U1678	U1678	U1796	A1890	U1992	U2087	U2185	C2265	U2334	C2417	C2496	C2584	A2700	A2800	C2887
A1570	A1679	A1679	G1797	G1891	C1994	C2087	U2186	U2266	U2335	C2418	C2497	C2585	C2710	A2801	C2888
A1571	U1680	U1680	A1801	A1900	U1995	C2091	G2189	A2270	A2340	U2423	C2498	U2586	U2720	G2801	C2889
G1581	G1681	G1681	A1806	A1901	C1996	U2092	G2190	U2271	A2341	C2424	G2499	C2587	A2721	C2794	C2890
U1584	U1682	U1682	C1806	A1806	C1997	U2093	A2191	U2272	G2342	C2425	G2502	U2588	C2722	C2795	A2893
G1587	C1684	C1684	G1807	G1906	G2010	G2011	U2192	A2273	C2343	A2426	A2503	C2589	C2723	A2724	U2898
G1588	C1685	C1685	A1808	C1908	G2012	G2012	U2193	C2275	U2344	A2427	U2504	C2590	U2724	A2725	A2899
U1589	G1695	G1695	A1809	G1909	G2013	U2017	U2194	C2276	C2345	G2428	G2505	C2591	C2725	A2726	U2903
A1590	G1696	G1696	A1810	G1910	G2014	U2018	U2195	A2277	G2346	A2429	G2506	C2592	U2726	U2727	U2818
A1591	U1686	U1686	G1811	U1911	G2015	G2015	U2196	A2278	U2347	U2430	C2507	C2593	A2728	A2729	G2819
C1592	G1699	G1699	A1812	A1912	A2019	G2016	U2197	G2280	G2348	U2431	C2508	C2594	A2730	A2731	U2820
U1594	U1709	U1709	C1816	C1914	A2020	G2017	U2198	G2281	U2349	A2432	A2514	C2595	A2732	A2733	A2821
C1595	G1710	G1710	G1817	U1915	G2018	U2019	U2199	G2282	C2350	A2433	C2515	C2596	A2734	A2735	G2822
A1596	U1715	U1715	A1818	A1916	G2019	U2020	U2200	G2283	C2351	A2434	C2516	C2597	A2736	A2737	C2830
A1597	G1715	G1715	A1819	U1917	G2023	G2023	A2212	G2284	U2352	U2441	C2517	C2598	A2738	A2739	G2831
A1598	U1729	U1729	U1820	A1918	G2024	U2025	C2213	A2285	C2353	C2442	C2518	C2599	G2744	A2740	U2832
G1601	C1730	C1730	G1823	A1919	G2026	G2027	C2214	G2286	C2354	C2443	C2519	C2600	A2745	A2746	U2833
U1602	U1730	U1730	G1824	A1920	G2028	U2028	C2215	G2287	C2355	C2444	C2520	C2601	A2747	A2748	U2834
A1603	G1738	G1738	G1825	G1921	G2029	G2029	C2216	U2290	C2356	C2445	C2521	C2602	A2749	A2750	U2835
C1604	U1738	U1738	U1826	G1922	G2030	G2030	C2217	U2291	C2357	A2446	C2522	C2603	C2752	C2753	G2846
				U1923	A2030	A2030		U2292	C2368	A2448	G2549	G2640	A2753	A2754	

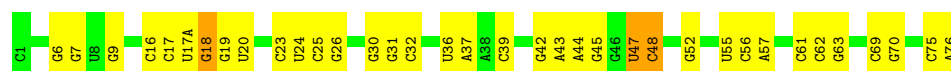
- Molecule 54: 5S ribosomal RNA

Chain 2: 



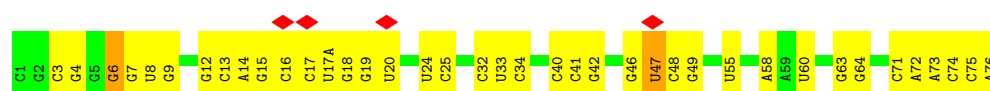
- Molecule 55: tRNA^{fMet}

Chain 5: 



- Molecule 55: tRNA^{fMet}

Chain 6: 



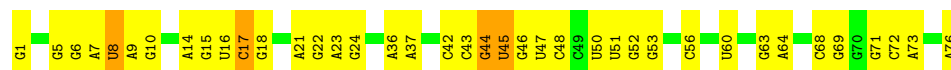
- Molecule 56: mRNA

Chain 4: 



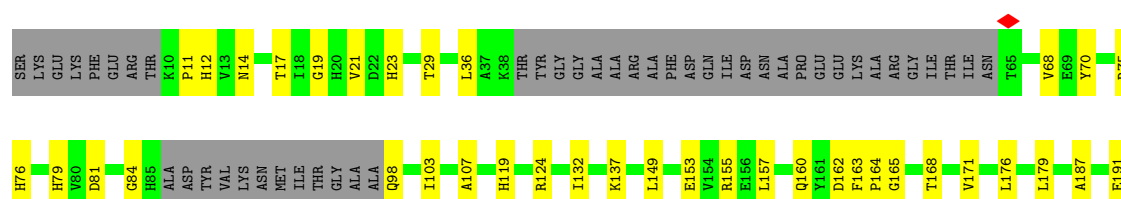
- Molecule 57: tRNA^{Phe}

Chain 7: 



- Molecule 58: Elongation factor Tu

Chain 8: 





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	7974	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	18.424	Depositor
Minimum map value	-10.090	Depositor
Average map value	0.118	Depositor
Map value standard deviation	0.851	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, GDP

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	0.94	4/2852 (0.1%)
2	c	0.29	0/1586	0.86	3/2134 (0.1%)
3	d	0.28	0/1571	0.86	3/2113 (0.1%)
4	e	0.30	0/1435	0.91	6/1926 (0.3%)
5	f	0.30	0/1343	0.87	4/1816 (0.2%)
6	g	0.32	0/1122	0.96	8/1515 (0.5%)
7	h	0.36	0/1002	1.11	9/1350 (0.7%)
8	i	0.36	0/1046	0.96	4/1410 (0.3%)
9	j	0.29	0/1152	0.88	3/1551 (0.2%)
10	k	0.29	0/948	0.91	1/1268 (0.1%)
11	l	0.30	0/1054	0.93	4/1403 (0.3%)
12	m	0.29	0/1093	0.86	1/1460 (0.1%)
13	n	0.29	0/974	0.91	3/1301 (0.2%)
14	o	0.27	0/902	0.86	2/1209 (0.2%)
15	p	0.29	0/929	0.81	1/1242 (0.1%)
16	q	0.29	0/960	0.91	3/1278 (0.2%)
17	r	0.30	0/829	0.87	4/1107 (0.4%)
18	s	0.29	0/864	0.84	1/1156 (0.1%)
19	t	0.29	0/745	0.87	1/994 (0.1%)
20	u	0.30	0/788	0.94	2/1051 (0.2%)
21	v	0.28	0/766	0.91	2/1025 (0.2%)
22	w	0.27	0/582	0.87	3/769 (0.4%)
23	x	0.27	0/635	0.89	3/848 (0.4%)
24	y	0.26	0/510	0.91	1/677 (0.1%)
25	z	0.28	0/453	0.79	0/605
26	B	0.27	0/450	0.84	1/599 (0.2%)
27	C	0.33	0/417	0.80	0/554
28	D	0.31	0/380	0.96	2/498 (0.4%)
29	E	0.27	0/513	0.91	3/676 (0.4%)
30	F	0.32	0/303	0.82	0/397
31	G	0.29	0/1788	0.88	2/2408 (0.1%)
32	H	0.31	0/1652	0.91	5/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.92	4/2227 (0.2%)
34	J	0.32	0/1170	1.02	7/1573 (0.4%)
35	K	0.31	0/836	0.93	2/1128 (0.2%)
36	L	0.29	0/1196	0.93	2/1602 (0.1%)
37	M	0.30	0/989	0.88	1/1326 (0.1%)
38	N	0.30	0/1034	0.92	0/1375
39	O	0.33	0/797	0.99	5/1077 (0.5%)
40	P	0.31	0/886	0.90	3/1195 (0.3%)
41	Q	0.33	0/969	1.03	7/1300 (0.5%)
42	R	0.31	0/893	0.96	5/1193 (0.4%)
43	S	0.29	0/817	0.91	3/1088 (0.3%)
44	T	0.28	0/722	0.83	2/964 (0.2%)
45	U	0.32	0/659	0.91	1/884 (0.1%)
46	V	0.30	0/658	0.92	3/881 (0.3%)
47	W	0.32	0/545	0.90	1/731 (0.1%)
48	X	0.31	0/653	0.93	0/877
49	Y	0.29	0/671	0.90	3/888 (0.3%)
50	Z	0.32	0/551	1.04	6/728 (0.8%)
51	a	0.31	0/1034	0.85	1/1387 (0.1%)
52	3	0.41	0/36963	0.47	2/57662 (0.0%)
53	1	0.40	0/69796	0.48	2/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.40	0/1832	0.46	0/2855
55	6	0.41	0/1832	0.47	0/2855
56	4	0.41	0/436	0.46	0/679
57	7	0.39	0/1809	0.47	0/2819
58	8	0.31	0/2726	0.92	7/3689 (0.2%)
All	All	0.37	0/165925	0.62	156/247767 (0.1%)

There are no bond length outliers.

All (156) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	B	53	VAL	N-CA-C	8.86	119.67	110.72
7	h	117	LEU	N-CA-C	8.36	123.20	109.24
32	H	5	HIS	CA-C-N	7.95	127.51	119.24
32	H	5	HIS	C-N-CA	7.95	127.51	119.24
35	K	24	ARG	N-CA-C	-7.86	103.29	113.12
43	S	49	THR	N-CA-C	-7.52	103.09	111.82
20	u	96	LYS	N-CA-C	-7.48	99.45	110.52
31	G	222	GLU	N-CA-C	-7.35	103.78	112.89
50	Z	21	SER	N-CA-C	-7.24	103.92	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	x	68	ALA	N-CA-C	-7.22	103.13	112.23
7	h	30	SER	N-CA-C	-6.98	104.38	113.17
13	n	68	ALA	N-CA-C	-6.91	103.81	111.82
42	R	64	VAL	N-CA-C	6.80	117.12	108.82
58	8	200	ILE	N-CA-C	6.80	114.89	108.15
2	c	85	ALA	N-CA-C	6.79	118.59	110.44
19	t	92	ASN	N-CA-C	-6.76	104.91	113.43
51	a	55	SER	N-CA-C	6.72	119.46	111.33
41	Q	117	GLY	N-CA-C	6.68	123.23	113.48
6	g	63	ALA	N-CA-C	-6.62	103.89	112.23
33	I	166	LYS	CA-C-N	6.61	128.10	119.84
33	I	166	LYS	C-N-CA	6.61	128.10	119.84
24	y	14	LEU	N-CA-C	-6.60	104.16	111.82
18	s	24	ILE	N-CA-C	6.56	115.77	106.53
7	h	50	VAL	N-CA-C	6.50	117.29	110.72
41	Q	114	SER	N-CA-C	-6.46	104.28	111.71
50	Z	30	GLU	N-CA-C	-6.46	106.61	114.75
32	H	107	LYS	CA-C-N	6.46	126.38	119.28
32	H	107	LYS	C-N-CA	6.46	126.38	119.28
39	O	20	GLN	N-CA-C	-6.46	105.56	113.50
41	Q	43	LYS	N-CA-C	6.45	124.06	109.81
7	h	43	LYS	N-CA-C	-6.44	104.12	112.23
34	J	84	VAL	N-CA-C	6.43	118.30	108.71
58	8	336	THR	N-CA-C	6.43	120.53	110.17
7	h	106	PHE	N-CA-C	6.40	118.40	110.91
53	l	1130	U	C2'-C3'-O3'	6.38	119.08	109.50
4	e	25	MET	N-CA-C	-6.38	105.53	113.38
8	i	127	SER	N-CA-C	-6.38	104.42	111.82
2	c	150	GLN	N-CA-C	6.30	118.67	111.11
47	W	69	TYR	N-CA-C	-6.28	104.06	111.03
49	Y	70	LYS	N-CA-C	-6.27	103.98	111.69
4	e	106	ALA	N-CA-C	6.24	117.77	110.97
32	H	177	LEU	N-CA-C	6.20	119.95	112.38
23	x	71	ARG	N-CA-C	-6.19	104.64	111.82
41	Q	54	VAL	N-CA-C	6.17	117.58	108.45
34	J	145	ASN	N-CA-C	-6.16	105.53	113.16
46	V	30	HIS	CA-C-N	6.14	126.60	119.47
46	V	30	HIS	C-N-CA	6.14	126.60	119.47
40	P	61	ALA	N-CA-C	-6.14	104.50	112.23
1	b	12	ARG	N-CA-C	-6.13	105.75	113.72
6	g	13	GLY	N-CA-C	6.12	122.74	113.02
13	n	67	PHE	N-CA-C	-6.08	106.19	113.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R	3	ILE	N-CA-C	6.03	117.20	109.30
23	x	6	VAL	N-CA-C	6.01	118.56	111.05
4	e	11	VAL	N-CA-C	6.00	116.66	110.36
58	8	196	LEU	N-CA-C	-5.98	105.47	112.89
7	h	44	ALA	N-CA-C	-5.98	104.34	111.69
21	v	40	ILE	N-CA-C	5.98	116.48	108.11
41	Q	42	LYS	N-CA-C	5.96	118.58	110.35
37	M	67	GLY	N-CA-C	-5.96	105.38	113.37
8	i	21	PRO	N-CA-C	5.94	117.95	110.70
4	e	10	GLU	N-CA-C	5.93	117.61	111.03
34	J	87	VAL	N-CA-C	5.85	116.97	109.30
42	R	76	ILE	N-CA-C	5.84	116.02	110.53
14	o	63	LYS	N-CA-C	-5.82	104.85	111.14
52	3	1190	G	C2'-C3'-O3'	5.81	118.22	109.50
49	Y	82	ILE	N-CA-C	5.79	116.57	110.72
9	j	7	LYS	CA-C-N	5.79	127.08	119.84
9	j	7	LYS	C-N-CA	5.79	127.08	119.84
39	O	74	VAL	N-CA-C	-5.78	106.83	111.81
39	O	77	VAL	N-CA-C	5.77	119.18	111.44
17	r	9	GLY	N-CA-C	-5.76	107.31	115.43
17	r	50	GLY	N-CA-C	-5.76	99.52	113.18
5	f	144	ALA	N-CA-C	-5.75	104.98	112.23
58	8	337	ASP	N-CA-C	-5.74	104.02	111.71
3	d	73	ILE	N-CA-C	-5.74	107.15	112.83
33	I	12	ARG	N-CA-C	-5.73	105.01	112.23
34	J	141	ASP	N-CA-C	-5.73	105.18	111.82
10	k	15	GLY	N-CA-C	-5.72	106.76	115.00
6	g	30	LEU	N-CA-C	5.68	117.15	111.07
21	v	45	ASP	N-CA-C	5.67	118.19	111.33
11	l	95	LEU	N-CA-C	-5.67	105.09	112.23
58	8	23	HIS	N-CA-C	-5.67	106.24	114.12
44	T	61	GLN	N-CA-C	-5.67	104.72	111.69
33	I	46	ARG	N-CA-C	-5.66	105.25	111.82
53	1	1020	A	C2'-C3'-O3'	5.66	117.99	109.50
50	Z	44	ARG	N-CA-C	-5.65	105.11	112.23
58	8	309	VAL	N-CA-C	5.64	116.07	108.17
4	e	51	ASN	N-CA-C	-5.63	105.22	111.36
46	V	15	LYS	N-CA-C	5.62	119.42	110.70
1	b	197	ALA	N-CA-C	5.60	118.14	111.71
7	h	107	GLU	N-CA-C	-5.58	104.37	113.19
29	E	61	LEU	CA-C-N	5.58	126.81	119.84
29	E	61	LEU	C-N-CA	5.58	126.81	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	Z	9	GLU	N-CA-C	5.55	122.08	109.81
9	j	120	ARG	N-CA-C	-5.54	106.47	113.18
5	f	47	ASN	N-CA-C	-5.50	106.73	113.50
44	T	43	ALA	N-CA-C	-5.50	105.44	111.82
6	g	51	ARG	N-CA-C	5.47	117.68	111.11
15	p	25	VAL	N-CA-C	5.47	116.11	108.89
35	K	90	MET	N-CA-C	5.46	115.60	108.07
16	q	92	LYS	N-CA-C	-5.45	105.50	111.82
41	Q	9	LYS	CA-C-N	5.45	125.75	119.92
41	Q	9	LYS	C-N-CA	5.45	125.75	119.92
6	g	64	ALA	N-CA-C	-5.44	105.38	112.23
40	P	70	ALA	N-CA-C	-5.43	105.52	111.82
34	J	134	ASN	N-CA-C	5.43	116.88	111.07
42	R	2	ARG	N-CA-C	-5.42	105.62	113.21
3	d	13	THR	N-CA-C	5.41	116.94	109.15
34	J	103	GLY	N-CA-C	5.40	122.30	112.58
29	E	17	GLY	N-CA-C	5.38	118.75	112.50
13	n	2	ARG	N-CA-C	5.37	119.03	111.52
2	c	16	THR	N-CA-C	-5.36	102.12	110.42
17	r	29	THR	N-CA-C	5.36	117.20	111.36
39	O	95	GLY	N-CA-C	-5.36	107.72	115.27
20	u	10	VAL	N-CA-C	5.35	115.06	108.53
36	L	58	LEU	N-CA-C	5.34	116.79	110.97
28	D	3	ARG	N-CA-C	5.33	117.76	109.60
3	d	90	GLN	N-CA-C	5.33	118.75	110.17
16	q	24	TYR	N-CA-C	5.29	118.18	109.76
58	8	332	TYR	N-CA-C	5.29	117.28	108.02
4	e	114	ARG	N-CA-C	-5.29	107.48	114.04
11	l	60	ARG	N-CA-C	-5.29	107.49	114.31
17	r	75	VAL	N-CA-C	5.27	114.34	106.85
5	f	18	ILE	N-CA-C	5.27	114.33	106.85
11	l	23	ILE	N-CA-C	-5.27	107.26	113.42
43	S	41	TRP	N-CA-C	-5.25	105.61	112.23
39	O	44	THR	N-CA-C	5.24	118.61	110.17
1	b	225	ASN	CA-C-N	5.24	126.39	119.84
1	b	225	ASN	C-N-CA	5.24	126.39	119.84
31	G	4	SER	N-CA-C	5.23	116.85	110.41
22	w	69	GLY	CA-C-N	5.22	124.84	119.56
22	w	69	GLY	C-N-CA	5.22	124.84	119.56
6	g	134	VAL	N-CA-C	-5.22	105.45	110.72
36	L	43	TYR	N-CA-C	5.22	116.65	111.07
45	U	72	ALA	N-CA-C	-5.21	105.66	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	f	147	LEU	N-CA-C	-5.21	105.67	112.23
22	w	52	ASP	N-CA-C	-5.21	106.69	112.57
11	l	137	ALA	N-CA-C	-5.19	105.69	112.23
16	q	80	ASN	N-CA-C	-5.17	105.76	111.71
7	h	31	ARG	N-CA-C	-5.16	106.94	114.12
50	Z	8	ASN	N-CA-C	5.15	121.77	110.80
42	R	96	VAL	N-CA-C	5.13	118.32	111.44
50	Z	45	LYS	N-CA-C	-5.09	105.91	111.82
7	h	29	ASP	N-CA-C	5.09	117.06	110.65
6	g	62	LEU	N-CA-C	-5.09	106.58	112.89
14	o	116	GLN	N-CA-C	5.08	116.55	108.67
28	D	7	PRO	N-CA-C	5.08	119.06	111.14
52	3	1301	U	N1-C1'-C2'	5.07	119.61	112.00
40	P	69	CYS	N-CA-C	-5.07	107.15	113.38
8	i	24	GLY	CA-C-N	5.06	125.13	119.87
8	i	24	GLY	C-N-CA	5.06	125.13	119.87
49	Y	69	ASN	N-CA-C	-5.06	107.24	113.41
12	m	59	ARG	N-CA-C	5.03	121.52	110.80
6	g	67	ALA	N-CA-C	-5.02	106.00	111.82
43	S	50	LEU	N-CA-C	-5.01	103.34	109.65
34	J	110	MET	N-CA-C	-5.00	106.02	111.82

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	71	0
2	c	1565	0	1616	43	0
3	d	1552	0	1619	36	0
4	e	1411	0	1447	40	0
5	f	1323	0	1374	37	0
6	g	1111	0	1148	43	0
7	h	989	0	1025	67	0
8	i	1032	0	1088	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	j	1129	0	1162	36	0
10	k	939	0	1012	42	0
11	l	1045	0	1117	40	0
12	m	1074	0	1157	32	0
13	n	961	0	1000	31	0
14	o	892	0	923	28	0
15	p	917	0	965	33	0
16	q	947	0	1022	26	0
17	r	816	0	839	23	0
18	s	857	0	922	18	0
19	t	739	0	807	19	0
20	u	780	0	834	20	0
21	v	753	0	780	22	0
22	w	575	0	592	20	0
23	x	625	0	655	19	0
24	y	509	0	543	21	0
25	z	449	0	491	9	0
26	B	444	0	461	15	0
27	C	410	0	440	11	0
28	D	377	0	418	12	0
29	E	504	0	574	21	0
30	F	302	0	343	25	0
31	G	1757	0	1787	43	0
32	H	1625	0	1699	39	0
33	I	1643	0	1710	69	0
34	J	1157	0	1199	44	0
35	K	818	0	808	47	0
36	L	1182	0	1240	40	0
37	M	979	0	1034	31	0
38	N	1022	0	1070	42	0
39	O	787	0	828	43	0
40	P	870	0	878	25	0
41	Q	955	0	1019	40	0
42	R	884	0	944	35	0
43	S	805	0	847	38	0
44	T	714	0	737	18	0
45	U	649	0	666	38	0
46	V	649	0	691	19	0
47	W	536	0	552	18	0
48	X	638	0	665	17	0
49	Y	665	0	714	20	0
50	Z	545	0	579	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	a	1027	0	1092	37	0
52	3	33012	0	16618	559	0
53	1	62317	0	31346	941	0
54	2	2568	0	1303	47	0
55	5	1640	0	836	27	0
55	6	1640	0	837	33	0
56	4	388	0	196	5	0
57	7	1619	0	821	29	0
58	8	2677	0	2699	93	0
59	5	10	0	10	0	0
60	7	11	0	8	4	0
61	8	28	0	12	1	0
All	All	152927	0	103976	2898	0

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

All (2898) 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)
52:3:405:U:H3'	52:3:406:G:H5'	1.33	1.10
7:h:73:LYS:HB3	7:h:117:LEU:HD21	1.40	1.04
53:1:1053:C:H2'	53:1:1054:A:H5''	1.45	0.98
45:U:41:PRO:HG2	45:U:42:ILE:HD12	1.45	0.98
52:3:484:G:H4'	52:3:485:U:H5''	1.46	0.97
52:3:1259:C:H3'	52:3:1260:G:H5''	1.45	0.96
1:b:145:MET:HE1	1:b:181:ARG:HH22	1.31	0.96
43:S:11:LYS:HZ1	43:S:15:LEU:HG	1.30	0.95
39:O:57:VAL:HG22	39:O:58:ASN:H	1.31	0.95
35:K:3:HIS:H	35:K:92:THR:HG22	1.30	0.95
53:1:1300:G:H4'	53:1:1301:A:H5''	1.48	0.94
55:5:75:C:H2'	55:5:76:A:H5''	1.49	0.94
1:b:116:GLN:HE21	1:b:121:ALA:HA	1.31	0.93
34:J:55:VAL:HG23	34:J:56:PRO:HD3	1.48	0.93
45:U:36:VAL:HG23	45:U:53:ASP:HB3	1.51	0.92
7:h:71:CYS:SG	7:h:117:LEU:HD13	2.09	0.92
53:1:1906:G:H2'	53:1:1907:G:H5''	1.51	0.92
2:c:148:GLN:O	53:1:2052:A:H4'	1.70	0.91
53:1:45:G:H5''	53:1:46:G:H5'	1.53	0.90
52:3:1033:G:H2'	52:3:1034:G:H5''	1.51	0.89
47:W:40:PRO:HB3	52:3:720:C:H5''	1.53	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2277:G:H2'	53:1:2278:A:H5''	1.57	0.87
53:1:2432:A:H1'	55:6:75:C:H5'	1.58	0.86
38:N:46:VAL:HA	38:N:49:GLN:HG3	1.57	0.86
19:t:47:VAL:HG13	19:t:55:VAL:HG21	1.58	0.85
32:H:171:ARG:HG2	32:H:173:PRO:HD3	1.60	0.84
39:O:6:ILE:HB	39:O:76:ILE:HG23	1.60	0.83
10:k:121:GLU:HG2	10:k:122:VAL:HG23	1.56	0.83
7:h:48:ALA:HB3	7:h:51:TYR:HE2	1.43	0.83
53:1:2553:G:H3'	53:1:2554:U:H5''	1.61	0.82
39:O:7:ARG:HB3	39:O:101:SER:HB3	1.62	0.82
52:3:1201:A:H1'	52:3:1202:U:OP2	1.80	0.82
53:1:275:C:H2'	53:1:276:U:H4'	1.62	0.81
10:k:35:VAL:HG13	10:k:36:GLY:H	1.44	0.81
10:k:98:ARG:HH21	52:3:340:U:H5''	1.45	0.81
49:Y:11:ILE:H	49:Y:11:ILE:HD12	1.45	0.81
53:1:1020:A:H1'	53:1:1021:A:OP2	1.80	0.81
42:R:27:THR:HG21	52:3:1328:C:H5''	1.62	0.81
35:K:23:GLU:HA	35:K:26:THR:HG22	1.61	0.81
42:R:64:VAL:HG22	42:R:65:GLU:H	1.45	0.81
55:5:75:C:C2'	55:5:76:A:H5''	2.10	0.81
35:K:96:VAL:HG22	35:K:97:THR:H	1.46	0.80
52:3:955:U:H3	52:3:1225:A:H61	1.29	0.80
43:S:11:LYS:NZ	43:S:15:LEU:HG	1.95	0.80
52:3:150:U:H3	52:3:171:A:H62	1.27	0.80
10:k:40:LYS:HE3	10:k:57:VAL:HG12	1.61	0.80
32:H:140:ALA:HB3	32:H:148:ILE:HD11	1.63	0.79
39:O:37:ARG:NH2	52:3:1125:U:H5'	1.95	0.79
53:1:2800:A:H3'	53:1:2801:G:H5'	1.62	0.79
2:c:155:VAL:HG21	53:1:2618:G:H21	1.48	0.79
53:1:189:G:H2'	53:1:205:G:H22	1.47	0.79
53:1:2423:U:O2'	53:1:2425:A:H2'	1.83	0.78
8:i:48:ILE:HG13	8:i:49:GLU:HG2	1.63	0.78
54:2:3:C:H3'	54:2:4:C:H5''	1.64	0.78
38:N:126:PHE:HB3	52:3:1342:C:H4'	1.65	0.78
23:x:63:ILE:H	23:x:63:ILE:HD12	1.49	0.77
53:1:2715:C:H2'	53:1:2716:C:H5''	1.65	0.77
2:c:135:GLY:HA2	53:1:743:A:OP1	1.85	0.77
8:i:12:VAL:HG22	53:1:1061:U:O2	1.85	0.77
49:Y:38:ILE:HG23	49:Y:85:LEU:HD11	1.66	0.77
54:2:3:C:C3'	54:2:4:C:H5''	2.15	0.77
53:1:1807:G:H2'	53:1:1808:A:H5'	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M:10:LEU:HD11	37:M:74:ILE:HD13	1.66	0.76
49:Y:77:ASN:O	49:Y:81:GLN:HG2	1.84	0.76
45:U:6:LEU:HD12	52:3:375:U:H4'	1.66	0.76
5:f:173:ALA:O	5:f:174:LYS:HG2	1.85	0.76
53:1:1645:G:H5''	53:1:1646:C:H5'	1.66	0.76
35:K:3:HIS:N	35:K:92:THR:HG22	2.00	0.76
53:1:1133:A:H4'	53:1:1134:A:H5''	1.68	0.76
53:1:2156:G:H2'	53:1:2157:G:H5'	1.68	0.76
53:1:322:A:H5'	53:1:340:A:H1'	1.67	0.76
12:m:12:MET:HA	53:1:910:A:H62	1.52	0.75
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.68	0.75
57:7:50:U:H3	57:7:64:A:H61	1.33	0.75
53:1:215:G:H4'	53:1:216:A:H4'	1.67	0.75
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.50	0.74
30:F:12:ARG:NH1	53:1:1091:G:H1'	2.02	0.74
52:3:50:A:H4'	52:3:51:A:H5'	1.67	0.74
1:b:250:GLN:OE1	53:1:1843:C:H5'	1.88	0.74
39:O:37:ARG:HH22	52:3:1125:U:H5'	1.53	0.74
31:G:206:ILE:H	31:G:206:ILE:HD12	1.51	0.74
39:O:65:TYR:HB3	43:S:95:LEU:HD11	1.68	0.74
58:8:36:LEU:HD13	58:8:70:TYR:HB2	1.69	0.74
4:e:107:VAL:HG12	4:e:108:PRO:HD3	1.70	0.74
41:Q:23:LEU:HB3	41:Q:26:CYS:SG	2.28	0.74
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.70	0.74
7:h:55:VAL:HA	53:1:1084:A:H4'	1.67	0.74
58:8:343:GLU:HB2	58:8:360:VAL:HB	1.68	0.74
16:q:5:ARG:HD2	53:1:1250:G:H5''	1.70	0.73
4:e:13:LYS:HA	4:e:16:MET:HE3	1.70	0.73
52:3:730:G:H2'	52:3:731:G:H5'	1.69	0.73
53:1:329:G:O4'	53:1:477:A:H1'	1.88	0.73
6:g:5:LEU:HD12	6:g:36:ALA:HB2	1.71	0.73
33:I:131:ILE:HG23	52:3:403:C:H5'	1.71	0.73
52:3:960:U:H4'	52:3:961:U:O5'	1.89	0.73
11:l:38:GLN:NE2	11:l:45:GLY:H	1.87	0.72
14:o:40:ILE:HG12	14:o:47:VAL:HG12	1.72	0.72
40:P:118:ASN:OD1	52:3:718:A:H5'	1.90	0.72
16:q:23:TYR:CD1	53:1:533:G:H5'	2.24	0.72
30:F:37:GLN:HG2	30:F:38:GLY:N	2.04	0.72
43:S:13:VAL:HG22	43:S:59:GLN:HE22	1.54	0.72
5:f:96:ALA:HB3	5:f:103:ASN:HB3	1.71	0.72
43:S:50:LEU:HD12	43:S:51:PRO:HD2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:V:12:VAL:HB	46:V:21:VAL:HG23	1.71	0.72
7:h:48:ALA:HB3	7:h:51:TYR:CE2	2.23	0.72
53:1:2682:A:H61	53:1:2728:U:H1'	1.54	0.71
53:1:1053:C:C2'	53:1:1054:A:H5''	2.20	0.71
11:l:38:GLN:HE22	11:l:45:GLY:H	1.38	0.71
34:J:107:GLY:HA3	52:3:9:G:H5'	1.72	0.71
2:c:25:THR:HG21	2:c:193:VAL:HG22	1.73	0.71
27:C:7:LYS:HD2	29:E:33:THR:HG21	1.72	0.71
38:N:98:ARG:HG3	38:N:103:VAL:HG11	1.72	0.71
50:Z:16:ARG:HH21	50:Z:19:LYS:HG2	1.53	0.71
53:1:528:A:N1	53:1:2042:A:H2'	2.04	0.71
53:1:1141:U:H4'	53:1:1142:A:O4'	1.91	0.71
34:J:111:ARG:O	34:J:115:GLU:HG3	1.91	0.71
33:I:33:ILE:HG13	33:I:34:GLU:H	1.57	0.70
34:J:104:ILE:HD13	34:J:115:GLU:HG2	1.73	0.70
8:i:91:LYS:HB3	8:i:94:LYS:HB2	1.74	0.70
21:v:4:ILE:HD13	21:v:47:VAL:HG22	1.74	0.70
34:J:80:LEU:HG	34:J:122:VAL:HG11	1.72	0.70
52:3:1197:A:H2'	52:3:1198:G:H5''	1.73	0.70
53:1:2277:G:C2'	53:1:2278:A:H5''	2.20	0.70
5:f:174:LYS:HE3	53:1:2529:G:H4'	1.72	0.70
53:1:1906:G:C2'	53:1:1907:G:H5''	2.22	0.70
16:q:49:ARG:HH22	17:r:72:VAL:HG13	1.57	0.69
55:6:6:G:O2'	55:6:7:G:H5'	1.92	0.69
27:C:8:ILE:HD13	27:C:24:LYS:HB3	1.73	0.69
32:H:45:GLU:HG2	32:H:86:LEU:HD21	1.73	0.69
38:N:114:LYS:HD3	52:3:1187:G:H5''	1.74	0.69
51:a:174:THR:HB	53:1:2124:G:H4'	1.74	0.69
52:3:1033:G:C2'	52:3:1034:G:H5''	2.22	0.69
14:o:30:ARG:HH11	14:o:102:ARG:HH11	1.38	0.69
33:I:119:HIS:HB3	52:3:438:U:H4'	1.75	0.69
42:R:113:LYS:HG3	42:R:114:PRO:HD3	1.73	0.69
43:S:63:CYS:HB3	43:S:67:GLY:H	1.58	0.69
53:1:2134:A:N6	53:1:2157:G:H4'	2.07	0.69
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.74	0.69
34:J:110:MET:HE2	34:J:126:ALA:HB2	1.74	0.69
36:L:4:ARG:H	36:L:4:ARG:HD3	1.57	0.69
53:1:917:A:H5''	53:1:2268:A:H61	1.58	0.69
4:e:65:LEU:HD22	54:2:42:C:C5	2.28	0.69
52:3:1379:G:O2'	52:3:1380:U:H5'	1.93	0.69
52:3:1158:C:H2'	52:3:1159:U:H4'	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:3:C:H2'	54:2:4:C:H5''	1.75	0.69
7:h:6:GLN:O	7:h:9:GLN:HG3	1.93	0.68
34:J:55:VAL:HG23	34:J:56:PRO:CD	2.22	0.68
52:3:59:A:H5''	52:3:387:U:H5''	1.74	0.68
53:1:2266:A:H4'	53:1:2267:A:C2	2.28	0.68
53:1:2743:U:H2'	53:1:2744:G:H5''	1.74	0.68
50:Z:34:ARG:HB3	50:Z:36:PHE:CE2	2.28	0.68
53:1:859:G:H1'	53:1:860:U:H5	1.58	0.68
1:b:52:HIS:HA	1:b:216:ARG:HB2	1.75	0.68
4:e:56:LEU:HD13	4:e:88:VAL:HG23	1.75	0.68
6:g:25:TYR:O	6:g:30:LEU:HD23	1.93	0.68
40:P:126:ARG:HH22	52:3:692:U:H5''	1.58	0.68
8:i:20:SER:HB2	8:i:21:PRO:HD3	1.73	0.68
33:I:105:GLY:HA2	33:I:164:ARG:HH12	1.58	0.68
43:S:80:ARG:O	43:S:83:VAL:HG12	1.93	0.68
51:a:37:LYS:HB2	53:1:2127:G:H5'	1.74	0.68
3:d:18:THR:HG22	3:d:106:LYS:HE3	1.75	0.68
52:3:327:A:O2'	52:3:328:C:H4'	1.93	0.68
24:y:2:LYS:HZ1	24:y:56:LEU:HG	1.58	0.68
23:x:33:HIS:CE1	53:1:2228:G:H21	2.11	0.68
50:Z:9:GLU:HB2	50:Z:10:PRO:HD3	1.74	0.68
4:e:135:ILE:H	4:e:135:ILE:HD12	1.57	0.68
33:I:57:LYS:HD3	33:I:202:LEU:HD13	1.76	0.68
1:b:48:ILE:HD11	1:b:51:ARG:HA	1.76	0.67
53:1:1300:G:C4'	53:1:1301:A:H5''	2.21	0.67
53:1:2092:U:H4'	53:1:2093:G:H5''	1.74	0.67
2:c:194:PRO:HA	53:1:2680:U:H5'	1.77	0.67
8:i:106:GLN:O	8:i:110:GLN:HG3	1.94	0.67
13:n:47:VAL:C	13:n:50:PRO:HD2	2.19	0.67
52:3:1199:U:H2'	52:3:1200:C:H5'	1.76	0.67
54:2:3:C:C2'	54:2:4:C:H5''	2.25	0.67
33:I:37:PRO:HD2	33:I:41:GLY:HA3	1.74	0.67
52:3:225:C:H2'	52:3:226:G:H5''	1.76	0.67
51:a:47:ASN:HB2	51:a:211:LYS:H	1.59	0.67
1:b:154:ALA:HB2	1:b:161:VAL:HG23	1.77	0.67
39:O:37:ARG:HH21	52:3:1124:G:H4'	1.57	0.67
42:R:2:ARG:HD2	42:R:2:ARG:O	1.95	0.67
42:R:64:VAL:HG22	42:R:65:GLU:N	2.10	0.67
52:3:346:G:H2'	52:3:347:G:H5'	1.76	0.67
7:h:117:LEU:HD23	7:h:120:ALA:HA	1.77	0.67
5:f:83:THR:HG22	5:f:133:LYS:HG2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:279:A:H5'	52:3:281:G:H5'	1.75	0.67
52:3:1346:A:O2'	52:3:1347:G:H4'	1.95	0.67
53:1:1077:A:H2'	53:1:1078:U:H5'	1.77	0.67
1:b:203:VAL:HG23	53:1:1792:G:H5''	1.76	0.67
39:O:40:ILE:HB	39:O:73:LEU:HB2	1.76	0.67
42:R:10:ASP:H	42:R:12:LYS:HE3	1.60	0.67
52:3:235:C:H2'	52:3:236:A:C8	2.30	0.67
7:h:73:LYS:CB	7:h:117:LEU:HD21	2.21	0.66
41:Q:13:ARG:HH11	41:Q:14:LYS:H	1.40	0.66
45:U:78:VAL:HG23	45:U:79:ASN:H	1.58	0.66
53:1:2233:U:H2'	53:1:2234:G:C8	2.30	0.66
46:V:16:MET:HG2	46:V:19:SER:HB3	1.76	0.66
53:1:1801:A:H5''	53:1:2203:U:H2'	1.77	0.66
58:8:328:ARG:HH22	58:8:364:ILE:HG23	1.60	0.66
14:o:62:LEU:HD12	14:o:62:LEU:O	1.96	0.66
52:3:1301:U:O2	52:3:1301:U:H2'	1.96	0.66
15:p:88:ARG:HE	15:p:112:ARG:HH21	1.43	0.66
14:o:31:THR:HG23	54:2:29:A:OP2	1.95	0.66
21:v:61:LEU:HD22	21:v:63:ILE:HG13	1.78	0.66
53:1:310:A:C2'	53:1:311:A:H5''	2.25	0.66
1:b:95:TYR:HE2	1:b:101:ARG:HD2	1.59	0.66
1:b:231:HIS:HA	1:b:241:LYS:HD2	1.77	0.66
22:w:35:ARG:HA	22:w:54:THR:HG23	1.78	0.66
39:O:57:VAL:HG22	39:O:58:ASN:N	2.09	0.66
55:5:6:G:O2'	55:5:7:G:H5'	1.96	0.66
2:c:151:THR:HB	2:c:152:PRO:HD3	1.77	0.66
41:Q:73:LEU:HD12	41:Q:73:LEU:H	1.61	0.66
10:k:98:ARG:NH2	52:3:340:U:H5''	2.11	0.66
48:X:5:LYS:HD2	52:3:1314:C:OP2	1.95	0.66
53:1:615:U:H5''	53:1:616:A:OP2	1.95	0.65
53:1:2298:A:H62	53:1:2318:G:H21	1.42	0.65
7:h:33:VAL:HG12	7:h:34:THR:H	1.61	0.65
11:l:9:ALA:HB3	11:l:12:SER:OG	1.96	0.65
33:I:33:ILE:HG13	33:I:34:GLU:N	2.11	0.65
50:Z:13:VAL:HG13	50:Z:15:LEU:HG	1.77	0.65
53:1:2715:C:C2'	53:1:2716:C:H5''	2.26	0.65
2:c:56:LYS:NZ	53:1:2830:C:H5''	2.11	0.65
11:l:17:LYS:HE3	11:l:27:LEU:HD11	1.78	0.65
52:3:715:A:H2'	52:3:716:A:H8	1.62	0.65
55:6:34:C:H2'	55:6:34:C:O2	1.95	0.65
53:1:161:A:H3'	53:1:162:U:H5''	1.76	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:o:12:THR:HA	14:o:15:ARG:HB2	1.79	0.65
52:3:715:A:H2'	52:3:716:A:C8	2.32	0.65
53:1:310:A:O2'	53:1:311:A:H5''	1.96	0.65
45:U:4:ILE:HG13	45:U:4:ILE:O	1.96	0.65
57:7:7:A:H3'	57:7:8:U:H5''	1.77	0.65
6:g:40:THR:HB	6:g:43:ASN:HD22	1.61	0.65
31:G:20:ARG:HD3	52:3:831:A:C5'	2.27	0.65
38:N:17:ARG:HH12	52:3:1129:C:H4'	1.62	0.65
39:O:6:ILE:H	39:O:6:ILE:HD12	1.62	0.65
51:a:54:LYS:HD3	51:a:57:GLN:NE2	2.12	0.65
6:g:5:LEU:HD22	6:g:13:GLY:HA3	1.79	0.64
14:o:15:ARG:HH22	54:2:8:C:H5''	1.62	0.64
14:o:108:ASP:HA	14:o:111:ARG:HD2	1.79	0.64
33:I:53:GLN:HE22	52:3:8:A:H61	1.45	0.64
34:J:82:HIS:HD2	37:M:98:LEU:HD21	1.62	0.64
53:1:2636:C:H2'	53:1:2637:U:C6	2.33	0.64
2:c:184:ARG:HB3	2:c:186:LEU:HD23	1.79	0.64
16:q:5:ARG:NH1	53:1:585:G:N7	2.44	0.64
31:G:104:LYS:HA	31:G:107:ARG:HE	1.62	0.64
45:U:67:ILE:H	45:U:67:ILE:HD12	1.63	0.64
53:1:2345:G:N3	53:1:2381:A:H2'	2.12	0.64
19:t:51:PHE:O	19:t:52:GLU:HG2	1.98	0.64
53:1:1078:U:H5''	53:1:1079:C:H5''	1.77	0.64
55:6:16:C:H4'	55:6:60:U:H1'	1.79	0.64
7:h:88:HIS:HB2	7:h:89:PRO:HD3	1.79	0.64
26:B:9:ARG:H	26:B:9:ARG:HD2	1.61	0.64
33:I:23:GLY:HA3	52:3:409:U:OP1	1.98	0.64
53:1:1796:U:H2'	53:1:1797:G:H8	1.62	0.64
53:1:2156:G:C2'	53:1:2157:G:H5'	2.28	0.64
8:i:48:ILE:HG23	8:i:49:GLU:H	1.63	0.64
46:V:69:THR:HG22	46:V:70:LYS:H	1.63	0.64
53:1:1176:U:H2'	53:1:1177:G:C8	2.33	0.64
12:m:74:THR:HG21	12:m:86:LYS:HE2	1.79	0.64
44:T:64:LYS:HD3	52:3:755:G:OP2	1.98	0.64
52:3:29:U:O2'	52:3:30:U:H5'	1.98	0.64
52:3:423:G:H2'	52:3:424:G:H5'	1.80	0.64
57:7:44:G:H1'	57:7:45:U:H2'	1.79	0.64
22:w:67:VAL:HG22	22:w:74:LYS:HG3	1.79	0.64
45:U:31:ARG:NH2	52:3:230:G:H5''	2.13	0.64
53:1:1045:C:H5'	53:1:1046:A:H5''	1.80	0.64
54:2:65:U:H3'	54:2:108:A:H61	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:303:THR:HG22	58:8:366:PRO:HB3	1.80	0.64
42:R:24:VAL:HG13	42:R:28:ARG:HB3	1.79	0.63
53:1:1186:G:H2'	53:1:1187:G:O4'	1.97	0.63
33:I:155:LYS:O	33:I:158:LEU:HG	1.98	0.63
45:U:31:ARG:HH22	52:3:230:G:H5''	1.63	0.63
53:1:2849:U:H4'	53:1:2868:A:C2	2.33	0.63
26:B:49:ARG:HG2	53:1:2884:U:C6	2.34	0.63
45:U:20:VAL:HG23	45:U:35:ARG:HA	1.80	0.63
53:1:2163:A:H2'	53:1:2164:C:H5'	1.80	0.63
58:8:17:THR:HG23	58:8:79:HIS:CE1	2.33	0.63
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.13	0.63
49:Y:4:LYS:HD3	52:3:332:G:OP1	1.98	0.63
9:j:7:LYS:HG3	53:1:538:A:H4'	1.78	0.63
53:1:639:U:H2'	53:1:640:C:C6	2.34	0.63
53:1:1326:U:H2'	53:1:1327:A:H8	1.64	0.63
58:8:98:GLN:HA	58:8:231:ARG:HD3	1.78	0.63
58:8:103:ILE:HG12	58:8:132:ILE:HB	1.81	0.63
2:c:13:ARG:HH11	15:p:55:HIS:HA	1.62	0.63
24:y:28:LEU:HD22	24:y:37:LEU:HD12	1.80	0.63
53:1:2238:G:H2'	53:1:2238:G:N3	2.14	0.63
4:e:107:VAL:CG1	4:e:108:PRO:HD3	2.29	0.63
52:3:1230:C:H5'	55:5:30:G:H5''	1.81	0.63
6:g:31:VAL:HG13	6:g:32:PRO:HD3	1.81	0.63
29:E:61:LEU:HD12	29:E:61:LEU:O	1.98	0.63
53:1:1067:A:H1'	57:7:56:C:O4'	1.98	0.63
34:J:20:VAL:HG23	34:J:31:SER:HB2	1.80	0.63
1:b:260:LYS:HA	1:b:263:ASP:OD2	1.98	0.62
24:y:31:GLN:HG2	24:y:37:LEU:HB2	1.80	0.62
29:E:2:LYS:HG3	53:1:242:G:C8	2.34	0.62
44:T:13:GLU:HG2	44:T:83:ARG:HH21	1.64	0.62
53:1:2432:A:H1'	55:6:75:C:C5'	2.29	0.62
41:Q:73:LEU:HD21	41:Q:79:ILE:HG21	1.80	0.62
42:R:91:ARG:NH2	53:1:888:C:OP1	2.32	0.62
52:3:1060:U:H3	52:3:1197:A:H61	1.47	0.62
53:1:2834:G:H2'	53:1:2879:A:H61	1.64	0.62
58:8:203:PRO:HG2	58:8:205:ARG:HE	1.64	0.62
20:u:73:ASN:HD21	20:u:75:ALA:HB3	1.65	0.62
35:K:18:VAL:CG1	35:K:19:PRO:HD3	2.29	0.62
1:b:43:ASN:ND2	1:b:45:ASN:HD22	1.97	0.62
11:l:101:ILE:HG13	11:l:102:GLY:H	1.65	0.62
13:n:2:ARG:HG2	13:n:2:ARG:O	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2114:A:H61	53:1:2117:A:H62	1.47	0.62
32:H:70:ALA:HB2	32:H:114:LEU:HD21	1.81	0.62
52:3:664:G:H22	52:3:741:G:H1	1.48	0.62
53:1:1611:C:H6	53:1:1611:C:H5'	1.65	0.62
12:m:85:GLY:HA2	53:1:2276:G:H5'	1.80	0.62
34:J:108:GLY:H	52:3:9:G:H4'	1.64	0.62
52:3:130:A:O2'	52:3:264:C:H5'	1.98	0.62
52:3:1218:C:H2'	52:3:1219:A:C8	2.35	0.62
53:1:2715:C:C3'	53:1:2716:C:H5''	2.30	0.62
33:I:104:MET:HE2	33:I:170:LEU:HD22	1.82	0.62
52:3:701:U:H5''	52:3:703:G:H1'	1.81	0.62
53:1:2233:U:H2'	53:1:2234:G:H8	1.64	0.62
10:k:114:LYS:HE3	10:k:118:LEU:HD11	1.81	0.62
52:3:335:C:H2'	52:3:336:A:C8	2.35	0.62
53:1:2277:G:C3'	53:1:2278:A:H5''	2.28	0.62
58:8:213:LEU:HB3	58:8:293:LEU:HB2	1.82	0.62
5:f:23:ILE:HD13	5:f:71:LEU:HD11	1.81	0.62
5:f:154:GLU:OE2	5:f:156:TYR:HB2	1.99	0.62
14:o:100:HIS:HD2	54:2:48:U:H4'	1.64	0.62
30:F:1:MET:HE2	30:F:36:ARG:HB3	1.80	0.62
38:N:123:ARG:HB2	52:3:1343:G:H4'	1.81	0.62
52:3:1052:U:H2'	52:3:1200:C:H41	1.65	0.62
53:1:2267:A:H5''	53:1:2268:A:H5'	1.82	0.62
7:h:73:LYS:HB3	7:h:117:LEU:CD2	2.25	0.61
9:j:35:ARG:HD3	9:j:40:HIS:CD2	2.34	0.61
52:3:501:C:H2'	52:3:502:A:C8	2.35	0.61
43:S:9:GLU:O	43:S:13:VAL:HG23	1.99	0.61
24:y:24:GLU:HB3	24:y:28:LEU:HG	1.81	0.61
33:I:37:PRO:HD2	33:I:41:GLY:CA	2.30	0.61
33:I:115:GLN:HE22	52:3:406:G:H1'	1.64	0.61
52:3:501:C:H2'	52:3:502:A:H8	1.66	0.61
1:b:15:VAL:HG12	1:b:205:GLY:HA3	1.83	0.61
4:e:140:ILE:HG12	4:e:142:TYR:H	1.65	0.61
9:j:9:GLU:HG2	9:j:10:THR:HG23	1.81	0.61
38:N:46:VAL:HA	38:N:49:GLN:CG	2.31	0.61
18:s:88:ARG:HG3	18:s:94:ASP:OD2	2.00	0.61
28:D:1:MET:HE1	53:1:1781:U:H5	1.66	0.61
30:F:15:LYS:NZ	53:1:2754:U:H1'	2.15	0.61
32:H:155:ARG:HD3	32:H:192:TYR:HB3	1.82	0.61
39:O:53:ILE:HG13	43:S:84:ARG:HD2	1.83	0.61
58:8:391:LYS:HD3	58:8:392:VAL:H	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1300:G:H4'	53:1:1301:A:C5'	2.27	0.61
53:1:2086:U:H2'	53:1:2087:G:C8	2.35	0.61
25:z:37:ARG:NH2	53:1:929:U:H4'	2.16	0.61
52:3:407:U:H2'	52:3:408:A:C8	2.35	0.61
52:3:1306:A:N6	52:3:1331:G:H1'	2.16	0.61
16:q:90:ASP:OD1	17:r:11:GLN:HG3	2.01	0.61
45:U:41:PRO:HG2	45:U:42:ILE:CD1	2.27	0.61
53:1:572:A:H61	53:1:2029:G:H21	1.49	0.61
53:1:2710:C:H2'	53:1:2711:A:C8	2.35	0.61
15:p:38:ARG:CZ	52:3:345:C:H5'	2.31	0.61
18:s:93:ALA:HB2	53:1:1614:A:N1	2.16	0.61
24:y:41:HIS:CG	53:1:96:C:H4'	2.36	0.61
45:U:31:ARG:HB2	52:3:310:G:H5''	1.83	0.61
52:3:1497:G:C2'	52:3:1498:U:H5'	2.31	0.61
57:7:7:A:H3'	57:7:8:U:C5'	2.31	0.61
11:l:17:LYS:HD3	53:1:663:G:H5''	1.83	0.60
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.81	0.60
53:1:45:G:H5''	53:1:46:G:C5'	2.28	0.60
53:1:69:C:O2'	53:1:70:G:H5'	2.01	0.60
60:7:101:PHE:HA	58:8:229:THR:HG21	1.82	0.60
7:h:13:ALA:O	7:h:17:GLU:HG2	2.01	0.60
37:M:12:ARG:CZ	52:3:826:C:H5'	2.30	0.60
7:h:58:THR:HG23	53:1:1107:G:C5'	2.31	0.60
52:3:225:C:C3'	52:3:226:G:H5''	2.31	0.60
1:b:52:HIS:CE1	1:b:218:THR:HG22	2.36	0.60
9:j:81:ILE:HD11	53:1:2514:U:C5'	2.31	0.60
52:3:1280:A:O2'	52:3:1281:C:H5'	2.02	0.60
53:1:473:G:O2'	53:1:474:G:H5'	2.01	0.60
53:1:703:U:H2'	53:1:704:G:O4'	2.02	0.60
53:1:704:G:H2'	53:1:726:G:N2	2.15	0.60
53:1:1810:A:H2'	53:1:1811:G:O4'	2.01	0.60
31:G:46:VAL:HG23	31:G:47:PRO:HD3	1.83	0.60
52:3:769:G:H4'	52:3:1513:A:H4'	1.83	0.60
15:p:24:THR:HB	15:p:86:LYS:HB2	1.83	0.60
50:Z:23:GLU:O	50:Z:24:LYS:HB2	2.01	0.60
5:f:140:ILE:HA	5:f:143:VAL:HG22	1.84	0.60
29:E:3:ILE:HD13	29:E:62:PRO:HG2	1.84	0.60
31:G:8:MET:HE3	31:G:13:VAL:HG11	1.83	0.60
50:Z:23:GLU:C	50:Z:25:ALA:H	2.09	0.60
1:b:73:ILE:HG23	53:1:1490:A:C6	2.37	0.60
15:p:48:ALA:HB3	15:p:59:THR:HG22	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:39:LEU:O	17:r:49:ILE:HG23	2.02	0.60
30:F:36:ARG:O	30:F:38:GLY:N	2.35	0.60
35:K:18:VAL:HG13	35:K:19:PRO:HD3	1.81	0.60
41:Q:101:LEU:HD23	41:Q:101:LEU:H	1.67	0.60
52:3:321:A:H4'	52:3:1436:U:H5'	1.84	0.60
53:1:121:G:H4'	53:1:149:A:H5'	1.81	0.60
37:M:42:GLU:HG2	37:M:100:ILE:HD13	1.84	0.60
52:3:824:G:H2'	52:3:825:A:H8	1.67	0.60
52:3:1527:U:H2'	52:3:1528:U:C6	2.37	0.60
53:1:974:G:H5''	53:1:1186:G:H21	1.67	0.60
55:5:24:U:H2'	55:5:25:C:C6	2.36	0.60
2:c:55:LYS:HD2	2:c:77:ARG:HA	1.84	0.59
52:3:539:A:H2'	52:3:540:G:C8	2.37	0.59
53:1:1919:A:H2'	53:1:1920:C:H5'	1.84	0.59
53:1:2884:U:H2'	53:1:2885:G:C8	2.37	0.59
4:e:66:ILE:H	4:e:66:ILE:HD12	1.66	0.59
7:h:30:SER:HB3	7:h:109:LYS:NZ	2.17	0.59
32:H:189:HIS:CD2	52:3:1205:U:H4'	2.37	0.59
39:O:46:LYS:HG2	39:O:68:ARG:HG2	1.83	0.59
7:h:26:VAL:HG13	7:h:116:GLU:HG3	1.84	0.59
7:h:55:VAL:HA	53:1:1084:A:C4'	2.32	0.59
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.85	0.59
10:k:48:PRO:HB3	52:3:1422:G:H5'	1.85	0.59
22:w:16:ARG:HG2	53:1:2356:U:H4'	1.82	0.59
1:b:7:PRO:O	53:1:1695:G:H1'	2.02	0.59
1:b:20:ASN:HB3	1:b:23:LEU:HG	1.83	0.59
4:e:92:GLY:O	4:e:95:MET:HG2	2.03	0.59
39:O:59:LYS:HD2	39:O:62:ARG:NH2	2.16	0.59
57:7:15:G:H2'	57:7:16:U:H5'	1.85	0.59
8:i:107:GLU:OE2	8:i:108:ILE:HG23	2.03	0.59
11:l:101:ILE:HG13	11:l:102:GLY:N	2.16	0.59
53:1:387:U:H5'	53:1:387:U:H6	1.68	0.59
53:1:1434:A:H2'	53:1:1435:G:C8	2.38	0.59
53:1:1790:C:H2'	53:1:1791:A:C8	2.38	0.59
11:l:38:GLN:HE22	11:l:45:GLY:N	2.00	0.59
2:c:142:VAL:CG1	2:c:143:PRO:HD2	2.33	0.59
2:c:149:ASN:HD22	53:1:2572:A:H2'	1.66	0.59
42:R:113:LYS:N	42:R:114:PRO:HD2	2.17	0.59
53:1:1900:A:H1'	53:1:1970:A:H2'	1.84	0.59
7:h:94:ARG:O	7:h:98:GLU:HG2	2.03	0.59
11:l:93:ASN:OD1	11:l:94:THR:HG23	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:176:LYS:HZ3	33:I:178:GLU:HB3	1.66	0.59
35:K:75:GLU:HA	35:K:78:PHE:HD2	1.68	0.59
53:1:2296:U:H5''	53:1:2297:A:OP1	2.02	0.59
53:1:2472:G:H2'	53:1:2475:C:H42	1.67	0.59
53:1:2636:C:H2'	53:1:2637:U:H6	1.64	0.59
4:e:73:VAL:HG22	4:e:78:ILE:HD11	1.84	0.59
33:I:3:TYR:O	33:I:4:LEU:HG	2.02	0.59
44:T:71:ARG:O	44:T:71:ARG:HD2	2.02	0.59
52:3:372:C:N4	52:3:387:U:H2'	2.17	0.59
4:e:177:ARG:OXT	4:e:177:ARG:HD2	2.02	0.59
10:k:35:VAL:HG13	10:k:36:GLY:N	2.17	0.59
41:Q:45:ASN:HD22	52:3:528:C:H41	1.51	0.59
43:S:30:ILE:HD11	43:S:39:ASP:HB3	1.84	0.59
52:3:1118:U:H2'	52:3:1119:C:C6	2.38	0.59
53:1:2475:C:C2'	53:1:2476:A:H5'	2.33	0.59
58:8:312:LEU:HD23	58:8:312:LEU:H	1.67	0.59
13:n:79:LEU:O	13:n:80:PHE:HB2	2.02	0.58
52:3:692:U:H2'	52:3:694:A:OP2	2.03	0.58
53:1:1149:G:H2'	53:1:1150:C:C6	2.38	0.58
53:1:2248:C:C2'	53:1:2249:U:H5'	2.33	0.58
53:1:2799:A:C2'	53:1:2800:A:H5'	2.32	0.58
3:d:164:LEU:HB2	3:d:167:VAL:HG22	1.84	0.58
15:p:111:GLU:HG3	15:p:113:LEU:HD23	1.83	0.58
41:Q:113:ARG:HB2	41:Q:118:VAL:O	2.03	0.58
1:b:220:ARG:NH1	53:1:1827:U:OP2	2.36	0.58
5:f:51:PHE:HZ	5:f:71:LEU:HD12	1.68	0.58
5:f:128:THR:HG23	5:f:129:GLU:CD	2.28	0.58
39:O:50:THR:HG22	39:O:64:GLN:HG2	1.84	0.58
22:w:39:THR:H	53:1:2331:G:H4'	1.67	0.58
34:J:156:ARG:HD2	37:M:44:PHE:CZ	2.38	0.58
42:R:88:LEU:HA	42:R:91:ARG:HD3	1.85	0.58
42:R:113:LYS:H	42:R:114:PRO:HD2	1.68	0.58
53:1:554:U:H2'	53:1:555:G:O4'	2.04	0.58
53:1:1662:U:H2'	53:1:1663:G:O4'	2.02	0.58
2:c:173:GLN:NE2	53:1:2772:C:H5'	2.19	0.58
52:3:358:U:H2'	52:3:359:G:H8	1.68	0.58
53:1:435:C:H2'	53:1:436:C:H5'	1.85	0.58
53:1:669:G:H2'	53:1:669:G:N3	2.19	0.58
53:1:1213:A:N6	53:1:1236:G:H1'	2.18	0.58
53:1:2427:C:H5''	53:1:2429:G:H5'	1.85	0.58
58:8:29:THR:HG21	58:8:81:ASP:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:101:THR:HG21	52:3:1226:C:OP2	2.03	0.58
47:W:56:ARG:HE	47:W:60:ARG:HH21	1.52	0.58
48:X:35:ARG:HH21	48:X:74:ALA:HB3	1.68	0.58
52:3:584:G:H2'	52:3:585:G:H8	1.67	0.58
53:1:49:A:H5'	53:1:51:G:O4'	2.03	0.58
58:8:257:THR:HG21	58:8:280:ARG:HE	1.67	0.58
9:j:122:LEU:HD23	9:j:123:LYS:N	2.18	0.58
52:3:54:C:H2'	52:3:352:C:H41	1.68	0.58
52:3:405:U:C3'	52:3:406:G:H5'	2.22	0.58
52:3:730:G:C2'	52:3:731:G:H5'	2.34	0.58
53:1:598:U:H2'	53:1:599:A:H8	1.69	0.58
53:1:2024:G:OP2	53:1:2034:U:H4'	2.03	0.58
53:1:2287:A:O2'	53:1:2288:A:H2'	2.02	0.58
53:1:2329:U:H2'	53:1:2330:G:C8	2.37	0.58
1:b:73:ILE:HG23	53:1:1490:A:N6	2.19	0.58
13:n:63:ARG:NH1	53:1:1454:C:H5'	2.18	0.58
24:y:1:MET:HA	24:y:4:LYS:HE3	1.85	0.58
37:M:10:LEU:HD11	37:M:74:ILE:CD1	2.34	0.58
47:W:31:TYR:O	47:W:39:VAL:HG12	2.04	0.58
52:3:1125:U:H2'	52:3:1126:U:H2'	1.86	0.58
52:3:1259:C:H3'	52:3:1260:G:C5'	2.28	0.58
53:1:2467:C:H2'	53:1:2468:A:O4'	2.03	0.58
55:6:71:C:H2'	55:6:72:A:C8	2.39	0.58
6:g:11:ASN:HB3	6:g:12:LEU:HD23	1.86	0.58
17:r:26:ASP:C	17:r:27:ILE:HD12	2.28	0.58
34:J:39:GLY:HA3	34:J:116:VAL:HB	1.83	0.58
42:R:70:ARG:O	42:R:74:MET:HG2	2.03	0.58
52:3:70:U:H2'	52:3:94:G:O6	2.04	0.58
52:3:555:U:H2'	52:3:556:C:C6	2.39	0.58
53:1:704:G:H2'	53:1:726:G:H22	1.69	0.58
53:1:2066:C:O2'	53:1:2067:G:H5'	2.03	0.58
9:j:99:ARG:HA	9:j:102:GLU:HB3	1.84	0.58
34:J:82:HIS:CD2	37:M:98:LEU:HD21	2.39	0.58
53:1:1285:A:H2'	53:1:1286:A:H5'	1.86	0.58
1:b:245:THR:HG23	1:b:247:TRP:H	1.69	0.57
7:h:3:LEU:HG	7:h:5:LEU:H	1.68	0.57
39:O:5:ARG:HB3	39:O:6:ILE:HD12	1.85	0.57
53:1:2480:C:H2'	53:1:2481:G:O4'	2.04	0.57
5:f:88:LEU:HB3	5:f:93:TYR:HB3	1.86	0.57
6:g:15:LEU:HD21	6:g:56:ALA:HB1	1.86	0.57
10:k:48:PRO:HB3	52:3:1422:G:C5'	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:6:ARG:N	53:1:85:G:OP1	2.36	0.57
40:P:115:ILE:HG12	50:Z:28:LEU:HD21	1.86	0.57
51:a:215:SER:HB2	51:a:221:GLY:HA2	1.84	0.57
53:1:2398:U:H2'	53:1:2399:G:C8	2.39	0.57
55:5:75:C:C3'	55:5:76:A:H5''	2.33	0.57
7:h:55:VAL:HA	53:1:1084:A:C5'	2.34	0.57
7:h:116:GLU:C	7:h:117:LEU:HG	2.29	0.57
24:y:2:LYS:HE2	53:1:77:G:H4'	1.86	0.57
29:E:20:GLY:HA3	29:E:48:MET:HE1	1.87	0.57
35:K:96:VAL:HG22	35:K:97:THR:N	2.17	0.57
52:3:256:U:H2'	52:3:257:G:C8	2.39	0.57
52:3:1342:C:H2'	52:3:1343:G:H8	1.68	0.57
53:1:458:G:O2'	53:1:459:U:H5	1.87	0.57
9:j:35:ARG:HD3	9:j:40:HIS:NE2	2.18	0.57
25:z:40:THR:HG23	25:z:43:ILE:H	1.69	0.57
52:3:346:G:C2'	52:3:347:G:H5'	2.34	0.57
52:3:1540:U:O2	52:3:1540:U:H3'	2.04	0.57
16:q:116:LEU:O	16:q:116:LEU:HD23	2.04	0.57
45:U:6:LEU:HD22	45:U:17:TYR:HB3	1.84	0.57
15:p:102:ARG:NH2	53:1:1754:A:O2'	2.37	0.57
34:J:107:GLY:HA2	52:3:8:A:H1'	1.85	0.57
53:1:1909:C:H2'	53:1:1910:G:H8	1.69	0.57
53:1:2266:A:H4'	53:1:2267:A:N3	2.20	0.57
27:C:49:LYS:HD3	27:C:50:GLU:H	1.69	0.57
32:H:140:ALA:HB3	32:H:148:ILE:CD1	2.32	0.57
46:V:24:ILE:HD12	46:V:24:ILE:N	2.19	0.57
52:3:195:A:H2'	52:3:196:A:C8	2.40	0.57
52:3:211:G:C2'	52:3:212:G:H5'	2.34	0.57
52:3:1316:G:H2'	52:3:1317:C:H5''	1.87	0.57
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.86	0.57
38:N:64:ILE:HG21	38:N:78:ILE:HD12	1.87	0.57
42:R:105:ALA:HA	52:3:948:C:OP1	2.05	0.57
46:V:59:GLU:HG3	46:V:75:VAL:HB	1.86	0.57
2:c:24:VAL:HG21	2:c:188:LEU:HB3	1.86	0.57
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.87	0.57
52:3:70:U:H5''	52:3:71:A:OP1	2.04	0.57
29:E:25:HIS:NE2	29:E:47:ALA:HB2	2.20	0.57
38:N:74:GLN:O	38:N:78:ILE:HG12	2.04	0.57
43:S:92:ILE:HD12	43:S:93:PRO:HD2	1.86	0.57
45:U:5:ARG:HB2	52:3:376:G:H5''	1.86	0.57
52:3:304:U:O2'	52:3:305:G:H5'	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:542:C:H2'	53:1:543:G:H5''	1.87	0.57
4:e:87:LYS:HD2	53:1:2313:C:H4'	1.87	0.56
32:H:151:GLU:HB3	32:H:198:LYS:HB2	1.87	0.56
39:O:6:ILE:HD12	39:O:6:ILE:N	2.19	0.56
42:R:91:ARG:HH21	53:1:887:U:H5'	1.70	0.56
52:3:680:C:H2'	52:3:681:A:C8	2.40	0.56
52:3:1346:A:H2'	52:3:1346:A:N3	2.19	0.56
53:1:1874:C:H2'	53:1:1875:G:O4'	2.04	0.56
9:j:27:ARG:NH2	53:1:1142:A:H4'	2.19	0.56
18:s:86:MET:HE3	18:s:87:PRO:HD2	1.85	0.56
47:W:37:LYS:HE2	52:3:718:A:C2	2.40	0.56
47:W:37:LYS:HE2	52:3:718:A:H2	1.70	0.56
53:1:2475:C:O2'	53:1:2476:A:H5'	2.05	0.56
58:8:132:ILE:HG13	58:8:196:LEU:HD22	1.86	0.56
20:u:17:ASP:HB3	20:u:20:LYS:HD2	1.88	0.56
35:K:3:HIS:H	35:K:92:THR:CG2	2.10	0.56
35:K:68:GLN:O	35:K:71:ILE:HG22	2.05	0.56
38:N:73:GLY:N	52:3:1372:U:OP1	2.39	0.56
41:Q:106:VAL:HG23	41:Q:109:ARG:HG3	1.87	0.56
45:U:8:ARG:HE	52:3:391:G:H5''	1.71	0.56
52:3:211:G:H2'	52:3:212:G:H5'	1.85	0.56
52:3:1384:C:H2'	52:3:1385:G:C8	2.40	0.56
52:3:1412:C:H2'	52:3:1413:A:C8	2.39	0.56
53:1:1368:G:H2'	53:1:1369:G:H8	1.69	0.56
53:1:1872:A:H2'	53:1:1873:G:O4'	2.05	0.56
53:1:2698:U:H2'	53:1:2699:C:C6	2.40	0.56
52:3:225:C:C2'	52:3:226:G:H5''	2.34	0.56
55:6:24:U:H2'	55:6:25:C:C6	2.40	0.56
58:8:226:THR:HG21	58:8:287:ILE:HD11	1.88	0.56
1:b:206:LYS:HD3	53:1:729:G:OP2	2.05	0.56
5:f:172:GLU:HG3	5:f:174:LYS:H	1.71	0.56
10:k:18:ARG:HB3	10:k:45:GLU:HG2	1.87	0.56
10:k:92:GLU:O	10:k:93:GLN:C	2.49	0.56
11:l:79:LEU:HB3	11:l:116:VAL:HG13	1.87	0.56
12:m:20:LEU:HD23	21:v:81:PRO:HG2	1.87	0.56
25:z:11:SER:HB2	53:1:989:G:OP2	2.04	0.56
31:G:67:LEU:HD23	31:G:157:PRO:HB3	1.88	0.56
52:3:66:A:H61	52:3:103:U:H3	1.53	0.56
52:3:673:A:H2'	52:3:674:G:C8	2.40	0.56
53:1:226:A:H2'	53:1:227:A:O4'	2.05	0.56
53:1:2327:A:H2'	53:1:2328:A:C8	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2391:G:H4'	53:1:2392:A:OP1	2.05	0.56
53:1:2743:U:C2'	53:1:2744:G:H5''	2.35	0.56
58:8:206:ALA:HB1	58:8:209:LYS:HD2	1.86	0.56
1:b:224:MET:O	1:b:232:GLY:HA2	2.06	0.56
7:h:59:LEU:HD21	53:1:1047:G:H8	1.70	0.56
21:v:75:GLN:HB2	21:v:92:VAL:HG23	1.87	0.56
32:H:107:LYS:HB3	32:H:110:LEU:HD13	1.87	0.56
36:L:149:ALA:HB1	40:P:58:THR:HG21	1.88	0.56
52:3:113:G:H1'	52:3:354:G:H5''	1.86	0.56
52:3:291:U:H2'	52:3:292:G:H8	1.69	0.56
53:1:828:U:H4'	53:1:831:G:N1	2.20	0.56
53:1:833:A:H2'	53:1:834:G:C8	2.40	0.56
54:2:2:G:H2'	54:2:3:C:C6	2.41	0.56
55:5:76:A:H5'	55:5:76:A:C8	2.41	0.56
57:7:16:U:H1'	57:7:60:U:H1'	1.87	0.56
3:d:94:GLN:HB2	53:1:660:C:OP1	2.06	0.56
7:h:23:LEU:HD22	7:h:92:ALA:HA	1.87	0.56
30:F:15:LYS:HZ1	53:1:2754:U:H1'	1.71	0.56
35:K:90:MET:HA	52:3:737:C:OP1	2.05	0.56
52:3:946:A:H2'	52:3:947:G:H8	1.71	0.56
53:1:310:A:H2'	53:1:311:A:H5''	1.86	0.56
4:e:145:VAL:HG22	4:e:147:ARG:H	1.70	0.56
9:j:68:LYS:HD3	53:1:1022:G:N7	2.21	0.56
39:O:37:ARG:CZ	52:3:1125:U:H5'	2.36	0.56
41:Q:52:CYS:SG	41:Q:66:ILE:HD11	2.45	0.56
52:3:243:A:H4'	52:3:244:U:H3'	1.87	0.56
52:3:367:U:O2'	52:3:368:U:H4'	2.06	0.56
52:3:695:A:H2'	52:3:696:A:C8	2.40	0.56
54:2:106:G:H2'	54:2:107:G:O4'	2.06	0.56
42:R:113:LYS:N	42:R:114:PRO:CD	2.69	0.56
43:S:65:GLN:NE2	43:S:78:LEU:HD21	2.21	0.56
47:W:11:ARG:HB3	52:3:845:A:H4'	1.87	0.56
52:3:235:C:H2'	52:3:236:A:H8	1.71	0.56
53:1:872:U:H2'	53:1:873:C:C6	2.41	0.56
54:2:55:U:H2'	54:2:56:G:C8	2.39	0.56
17:r:49:ILE:HD12	17:r:52:PRO:HA	1.87	0.56
32:H:18:ASN:ND2	43:S:89:ARG:O	2.38	0.56
40:P:118:ASN:OD1	52:3:717:U:H4'	2.06	0.56
53:1:367:G:H2'	53:1:368:A:O4'	2.05	0.56
54:2:66:A:N1	54:2:107:G:H2'	2.20	0.56
36:L:29:LEU:HD23	36:L:29:LEU:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2247:A:H2'	53:1:2248:C:C6	2.41	0.55
53:1:2605:U:H2'	53:1:2606:C:C6	2.41	0.55
53:1:2743:U:C3'	53:1:2744:G:H5''	2.37	0.55
4:e:105:ILE:C	4:e:108:PRO:HD2	2.32	0.55
32:H:120:THR:HG23	32:H:188:ALA:HB2	1.88	0.55
43:S:92:ILE:HG21	43:S:95:LEU:HD23	1.88	0.55
52:3:950:U:H2'	52:3:951:G:C8	2.41	0.55
53:1:441:U:O2'	53:1:442:G:H5'	2.06	0.55
53:1:1367:A:H2'	53:1:1368:G:H5'	1.88	0.55
53:1:2208:C:H2'	53:1:2209:G:C8	2.41	0.55
41:Q:38:THR:HG23	41:Q:49:ARG:O	2.06	0.55
41:Q:120:ARG:HH12	52:3:500:G:H5'	1.70	0.55
52:3:1429:A:H2'	52:3:1430:A:H8	1.70	0.55
53:1:580:U:H2'	53:1:581:C:C6	2.41	0.55
53:1:613:A:H2'	53:1:613:A:N3	2.20	0.55
55:5:69:C:H2'	55:5:70:G:C8	2.41	0.55
6:g:5:LEU:HG	6:g:7:ASP:H	1.71	0.55
9:j:8:PRO:HG3	9:j:48:VAL:HG13	1.88	0.55
14:o:77:ALA:HB1	14:o:81:ARG:HH11	1.70	0.55
18:s:17:VAL:HG12	18:s:76:VAL:HG21	1.89	0.55
28:D:26:ASN:CG	53:1:682:G:H5'	2.31	0.55
49:Y:61:ALA:HA	49:Y:66:ILE:HB	1.87	0.55
51:a:190:GLU:O	51:a:194:VAL:HG22	2.07	0.55
1:b:129:LEU:N	1:b:129:LEU:HD23	2.22	0.55
48:X:12:LEU:HD12	48:X:13:HIS:N	2.22	0.55
52:3:884:U:H4'	52:3:885:G:H5''	1.88	0.55
53:1:962:G:H21	53:1:2250:G:H1	1.54	0.55
53:1:2329:U:H2'	53:1:2330:G:H8	1.70	0.55
53:1:2743:U:H2'	53:1:2744:G:C5'	2.36	0.55
53:1:2853:C:H2'	53:1:2854:G:H8	1.71	0.55
6:g:55:GLU:O	6:g:58:LEU:HG	2.07	0.55
16:q:58:GLN:HG2	53:1:1009:A:O4'	2.06	0.55
17:r:22:LEU:HD23	17:r:22:LEU:H	1.71	0.55
20:u:39:ASN:HB3	20:u:62:ALA:HB3	1.87	0.55
32:H:22:PHE:CE2	39:O:11:LYS:HG3	2.42	0.55
33:I:56:GLU:HG2	33:I:198:LEU:HD12	1.88	0.55
53:1:1921:G:O2'	53:1:1922:G:H5'	2.05	0.55
58:8:149:LEU:O	58:8:153:GLU:HG3	2.06	0.55
58:8:328:ARG:NH2	58:8:364:ILE:HG23	2.21	0.55
22:w:19:VAL:HG22	22:w:34:VAL:HG22	1.89	0.55
11:l:29:LYS:O	11:l:30:THR:OG1	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:195:ASN:ND2	33:I:198:LEU:HG	2.21	0.55
38:N:62:LEU:HB3	38:N:64:ILE:HD11	1.88	0.55
41:Q:73:LEU:CD2	41:Q:79:ILE:HD13	2.37	0.55
52:3:216:U:H2'	52:3:217:C:C6	2.42	0.55
11:l:74:THR:HG22	11:l:107:PHE:HB2	1.89	0.55
35:K:89:VAL:HG23	52:3:737:C:H5'	1.88	0.55
50:Z:49:ALA:HA	52:3:723:U:O4	2.07	0.55
52:3:224:U:H2'	52:3:225:C:C6	2.42	0.55
52:3:406:G:O2'	52:3:407:U:H5'	2.07	0.55
52:3:1458:G:H2'	52:3:1459:G:H8	1.72	0.55
53:1:146:A:H2'	53:1:147:C:C6	2.42	0.55
53:1:225:C:H2'	53:1:226:A:O4'	2.06	0.55
53:1:744:U:H4'	53:1:1658:C:H4'	1.88	0.55
53:1:2220:U:H2'	53:1:2221:G:H8	1.72	0.55
53:1:2443:C:H2'	53:1:2444:G:C8	2.41	0.55
3:d:45:ALA:HA	3:d:87:ALA:O	2.05	0.55
5:f:8:VAL:HB	5:f:49:LEU:HB2	1.89	0.55
15:p:92:ARG:HD3	53:1:1753:G:OP1	2.07	0.55
16:q:18:LYS:HE2	53:1:1219:U:OP2	2.05	0.55
32:H:175:HIS:ND1	52:3:1108:G:H5'	2.22	0.55
34:J:93:VAL:HG21	34:J:139:THR:HG22	1.89	0.55
34:J:123:LEU:HD12	34:J:123:LEU:O	2.06	0.55
35:K:29:ILE:HG22	35:K:34:GLY:HA3	1.89	0.55
41:Q:50:LYS:HD2	41:Q:50:LYS:N	2.21	0.55
42:R:27:THR:HG21	52:3:1328:C:OP1	2.06	0.55
52:3:1219:A:H2'	52:3:1220:G:C8	2.42	0.55
53:1:189:G:H2'	53:1:205:G:N2	2.19	0.55
53:1:948:C:H2'	53:1:949:G:C8	2.42	0.55
53:1:2071:A:H2'	53:1:2072:C:C6	2.41	0.55
53:1:2800:A:H3'	53:1:2801:G:C5'	2.34	0.55
5:f:143:VAL:O	5:f:146:ASP:OD2	2.24	0.54
22:w:14:ALA:HB1	53:1:2271:G:OP1	2.07	0.54
26:B:9:ARG:NH1	53:1:516:C:OP1	2.41	0.54
52:3:911:U:H2'	52:3:912:C:C6	2.42	0.54
53:1:742:A:H2'	53:1:743:A:C8	2.42	0.54
53:1:745:G:O2'	53:1:748:G:H1'	2.07	0.54
53:1:890:C:H2'	53:1:891:G:H5'	1.89	0.54
54:2:3:C:H3'	54:2:4:C:C5'	2.36	0.54
58:8:211:PHE:HA	58:8:235:GLY:HA3	1.89	0.54
58:8:215:ILE:HD11	58:8:293:LEU:HD22	1.88	0.54
24:y:2:LYS:HE2	53:1:77:G:H5''	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:118:SER:O	32:H:122:GLN:HG3	2.06	0.54
52:3:352:C:H4'	52:3:354:G:OP1	2.07	0.54
53:1:565:C:H2'	53:1:566:U:C6	2.42	0.54
53:1:596:U:H2'	53:1:597:G:H8	1.72	0.54
6:g:22:LYS:HD2	53:1:2094:A:P	2.47	0.54
12:m:93:VAL:HG22	12:m:94:ALA:H	1.72	0.54
52:3:1497:G:O2'	52:3:1498:U:H5'	2.07	0.54
6:g:99:ILE:HG21	6:g:115:VAL:HG11	1.90	0.54
7:h:33:VAL:HA	53:1:1055:G:H4'	1.88	0.54
25:z:50:VAL:O	25:z:54:VAL:HG12	2.07	0.54
35:K:36:ILE:N	35:K:36:ILE:HD12	2.22	0.54
37:M:80:PRO:HG2	52:3:878:A:H5''	1.89	0.54
51:a:7:ARG:O	51:a:11:ILE:HG13	2.07	0.54
52:3:291:U:H2'	52:3:292:G:C8	2.43	0.54
52:3:662:U:H2'	52:3:663:A:C8	2.43	0.54
52:3:1258:G:H2'	52:3:1259:C:C6	2.42	0.54
53:1:1817:G:C2	53:1:1818:U:H1'	2.43	0.54
2:c:61:THR:OG1	2:c:63:PRO:HD2	2.08	0.54
9:j:81:ILE:HD11	53:1:2514:U:H5'	1.89	0.54
35:K:68:GLN:NE2	52:3:738:C:H5''	2.23	0.54
40:P:12:ARG:O	40:P:13:LYS:HG2	2.07	0.54
52:3:663:A:H5'	52:3:836:G:OP1	2.06	0.54
53:1:2788:C:H2'	53:1:2789:C:C6	2.43	0.54
53:1:2834:G:H2'	53:1:2879:A:N6	2.22	0.54
58:8:308:GLU:HA	58:8:358:LYS:HA	1.88	0.54
11:l:23:ILE:HD12	11:l:23:ILE:N	2.22	0.54
12:m:40:ARG:HH22	53:1:958:U:H5	1.55	0.54
30:F:5:ALA:HA	30:F:38:GLY:HA2	1.89	0.54
33:I:164:ARG:HG2	33:I:165:GLU:H	1.73	0.54
35:K:11:HIS:CG	35:K:12:PRO:HD2	2.42	0.54
44:T:7:THR:O	44:T:11:VAL:HG23	2.07	0.54
46:V:18:LYS:HD3	52:3:255:G:H4'	1.89	0.54
53:1:532:A:H2'	53:1:532:A:N3	2.22	0.54
53:1:1036:G:H1	53:1:1119:U:H3	1.55	0.54
53:1:1067:A:H1'	57:7:56:C:C1'	2.37	0.54
53:1:1775:U:H2'	53:1:1776:G:O4'	2.05	0.54
53:1:2286:G:H4'	53:1:2287:A:C4	2.43	0.54
53:1:2457:U:O2'	53:1:2458:G:H5'	2.07	0.54
25:z:8:GLN:HB2	25:z:28:LEU:HD13	1.88	0.54
33:I:30:LYS:HZ3	52:3:411:A:H8	1.53	0.54
52:3:1384:C:H2'	52:3:1385:G:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2073:C:O2'	53:1:2074:U:H5'	2.07	0.54
53:1:2297:A:N6	53:1:2319:G:H1'	2.22	0.54
20:u:48:VAL:HG22	20:u:50:ALA:H	1.72	0.54
26:B:30:ASP:HB3	26:B:34:GLY:H	1.73	0.54
38:N:33:SER:OG	38:N:36:GLN:HG2	2.07	0.54
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.90	0.54
53:1:1570:A:H2'	53:1:1571:A:C8	2.43	0.54
7:h:114:GLU:HA	7:h:123:ILE:HA	1.90	0.54
20:u:50:ALA:O	20:u:51:LEU:HG	2.07	0.54
31:G:65:LYS:N	31:G:158:ASP:OD2	2.41	0.54
31:G:174:GLU:HA	31:G:177:ASN:HD21	1.71	0.54
32:H:3:LYS:NZ	52:3:1191:A:H5''	2.23	0.54
32:H:133:MET:HE2	32:H:167:TYR:HB3	1.90	0.54
49:Y:14:GLU:O	49:Y:17:ARG:HG3	2.06	0.54
51:a:205:LYS:HD3	53:1:1860:G:O2'	2.08	0.54
53:1:2537:U:H2'	53:1:2538:C:C6	2.42	0.54
55:5:69:C:H2'	55:5:70:G:H8	1.73	0.54
7:h:46:ARG:HH21	7:h:95:LEU:HD21	1.73	0.54
10:k:94:PRO:HG3	10:k:115:ILE:HG12	1.89	0.54
16:q:24:TYR:HE2	53:1:2020:A:H4'	1.73	0.54
31:G:20:ARG:HG3	52:3:830:G:O2'	2.08	0.54
40:P:71:ASP:O	40:P:72:ALA:HB3	2.08	0.54
52:3:166:U:H2'	52:3:167:A:C8	2.43	0.54
52:3:1352:C:H2'	52:3:1353:G:C8	2.43	0.54
53:1:2679:A:O2'	53:1:2680:U:H5'	2.07	0.54
58:8:283:LYS:HD2	58:8:284:ARG:H	1.73	0.54
1:b:94:LEU:HD21	1:b:98:GLY:HA2	1.89	0.53
7:h:58:THR:HG23	53:1:1107:G:H5''	1.88	0.53
12:m:119:LEU:HD22	53:1:2468:A:H5'	1.90	0.53
37:M:73:SER:O	37:M:129:ALA:HB3	2.08	0.53
45:U:4:ILE:HD11	45:U:67:ILE:HG23	1.89	0.53
49:Y:3:ILE:H	49:Y:3:ILE:HD12	1.74	0.53
51:a:26:ALA:HB1	51:a:214:ILE:HD11	1.89	0.53
52:3:225:C:H3'	52:3:226:G:H5''	1.90	0.53
52:3:405:U:H3'	52:3:406:G:C5'	2.22	0.53
53:1:466:A:H2'	53:1:467:G:H5'	1.90	0.53
53:1:1071:G:OP1	53:1:1071:G:H3'	2.07	0.53
6:g:12:LEU:HG	6:g:13:GLY:N	2.23	0.53
8:i:101:SER:HA	8:i:140:GLU:O	2.08	0.53
33:I:197:HIS:CE1	34:J:103:GLY:HA3	2.43	0.53
40:P:52:ARG:HE	40:P:53:GLY:H	1.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:64:VAL:CG2	42:R:65:GLU:H	2.19	0.53
52:3:1071:C:H2'	52:3:1072:G:H8	1.73	0.53
53:1:598:U:H2'	53:1:599:A:C8	2.42	0.53
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.90	0.53
29:E:18:LYS:HG2	53:1:651:G:H5'	1.90	0.53
30:F:12:ARG:HH12	53:1:1091:G:H1'	1.72	0.53
33:I:10:LEU:HD23	33:I:10:LEU:H	1.73	0.53
52:3:621:A:H2'	52:3:622:A:C8	2.43	0.53
52:3:1005:A:H2'	52:3:1006:G:O4'	2.09	0.53
52:3:1138:G:H3'	52:3:1138:G:N3	2.24	0.53
53:1:511:U:H2'	53:1:512:G:H5'	1.90	0.53
53:1:2026:U:H2'	53:1:2027:G:C8	2.43	0.53
53:1:2248:C:H2'	53:1:2249:U:H5'	1.89	0.53
53:1:2861:U:H2'	53:1:2862:G:H8	1.73	0.53
11:l:27:LEU:O	11:l:31:GLY:HA2	2.08	0.53
12:m:112:LEU:O	12:m:115:GLU:HG3	2.08	0.53
36:L:142:ARG:HG2	55:6:41:C:H4'	1.89	0.53
41:Q:56:LEU:HD12	41:Q:60:PHE:HB2	1.90	0.53
51:a:175:ILE:HD13	51:a:189:LEU:HD21	1.91	0.53
52:3:458:U:H2'	52:3:459:A:C8	2.44	0.53
53:1:1201:U:H2'	53:1:1202:G:H8	1.72	0.53
53:1:1936:A:H2	53:1:1943:U:H3	1.56	0.53
54:2:118:C:H2'	54:2:119:A:H8	1.74	0.53
58:8:17:THR:HG22	58:8:103:ILE:HB	1.90	0.53
58:8:236:ILE:HG22	58:8:270:ARG:HA	1.90	0.53
58:8:333:PHE:O	58:8:334:ARG:HG2	2.09	0.53
7:h:41:LEU:HD13	53:1:1083:U:O5'	2.09	0.53
29:E:32:LEU:HD22	29:E:40:LYS:HD3	1.91	0.53
35:K:66:ALA:HB1	35:K:67:PRO:HD2	1.89	0.53
52:3:1060:U:H2'	52:3:1061:G:H8	1.74	0.53
52:3:1306:A:H62	52:3:1331:G:H1'	1.73	0.53
58:8:283:LYS:HB3	58:8:286:GLU:OE1	2.07	0.53
5:f:51:PHE:CZ	5:f:71:LEU:HD12	2.44	0.53
9:j:114:LEU:O	9:j:118:MET:HG2	2.08	0.53
16:q:109:VAL:HG12	16:q:113:LYS:HE2	1.90	0.53
36:L:4:ARG:HD3	36:L:4:ARG:N	2.20	0.53
40:P:25:SER:O	40:P:89:GLY:HA2	2.09	0.53
52:3:757:U:H2'	52:3:758:C:O4'	2.08	0.53
53:1:18:U:H2'	53:1:19:A:C8	2.44	0.53
53:1:119:A:H4'	53:1:120:U:H5'	1.91	0.53
53:1:854:C:H2'	53:1:855:G:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:49:ILE:HG22	17:r:54:VAL:HG22	1.89	0.53
30:F:12:ARG:CZ	53:1:1091:G:H1'	2.39	0.53
39:O:42:LEU:HD11	39:O:73:LEU:HG	1.91	0.53
40:P:126:ARG:HH22	52:3:692:U:C5'	2.20	0.53
46:V:13:SER:H	46:V:21:VAL:HG23	1.74	0.53
46:V:61:ARG:HD3	46:V:75:VAL:HG22	1.89	0.53
52:3:26:A:N6	52:3:558:G:H1'	2.22	0.53
52:3:399:G:H2'	52:3:400:C:C6	2.44	0.53
53:1:616:A:H2'	53:1:617:G:O4'	2.08	0.53
53:1:1268:A:H2'	53:1:1269:A:O4'	2.08	0.53
53:1:1213:A:H62	53:1:1236:G:H1'	1.72	0.53
53:1:2498:C:O2'	53:1:2499:C:H5'	2.09	0.53
53:1:2888:C:H2'	53:1:2889:C:H6	1.73	0.53
55:5:24:U:H2'	55:5:25:C:H6	1.72	0.53
1:b:47:ARG:HD3	53:1:778:G:H5''	1.91	0.53
8:i:79:LEU:HD21	8:i:135:MET:HG3	1.89	0.53
11:l:54:GLN:OE1	53:1:825:A:H1'	2.09	0.53
34:J:133:ILE:O	34:J:136:VAL:HG12	2.09	0.53
39:O:52:LEU:HD21	39:O:59:LYS:HA	1.90	0.53
53:1:467:G:O2'	53:1:468:G:H5'	2.09	0.53
53:1:1827:U:O2'	53:1:1828:G:H5'	2.08	0.53
1:b:29:PHE:CD2	1:b:32:LEU:HD23	2.44	0.53
11:l:60:ARG:O	53:1:2393:U:H5'	2.09	0.53
26:B:4:GLN:HG3	26:B:5:ASN:HD22	1.74	0.53
33:I:4:LEU:HD12	33:I:4:LEU:O	2.08	0.53
34:J:76:ASN:H	34:J:81:GLN:HE22	1.57	0.53
52:3:398:U:H2'	52:3:399:G:H8	1.73	0.53
52:3:1163:A:H2'	52:3:1164:G:C8	2.44	0.53
53:1:1060:U:H4'	53:1:1061:U:H5'	1.91	0.53
53:1:2196:C:O2'	53:1:2197:U:H5'	2.09	0.53
53:1:2257:U:O2'	53:1:2258:C:H5'	2.09	0.53
1:b:203:VAL:O	1:b:205:GLY:N	2.42	0.52
3:d:117:ARG:HH21	3:d:184:ASP:HA	1.74	0.52
4:e:105:ILE:O	4:e:108:PRO:HD2	2.09	0.52
28:D:34:ARG:NH1	53:1:467:G:OP2	2.41	0.52
33:I:59:LYS:O	33:I:63:ILE:HG13	2.09	0.52
34:J:23:THR:HA	34:J:28:ARG:HA	1.91	0.52
35:K:67:PRO:HG2	35:K:70:VAL:HG12	1.90	0.52
38:N:17:ARG:NH1	52:3:1129:C:H4'	2.23	0.52
51:a:167:LYS:HD2	55:6:55:U:H5'	1.91	0.52
53:1:2236:U:H2'	53:1:2237:G:O4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:146:VAL:HG12	3:d:185:LYS:HB2	1.90	0.52
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.90	0.52
31:G:22:TRP:HE1	52:3:830:G:H5'	1.73	0.52
52:3:151:A:H62	52:3:170:U:H3	1.55	0.52
52:3:331:G:OP1	52:3:332:G:H5''	2.10	0.52
52:3:1512:U:H2'	52:3:1513:A:C8	2.43	0.52
53:1:45:G:C5'	53:1:46:G:H5'	2.33	0.52
53:1:503:A:H4'	53:1:505:A:H5''	1.92	0.52
57:7:14:A:H2'	57:7:15:G:O4'	2.09	0.52
1:b:94:LEU:HD23	1:b:95:TYR:O	2.10	0.52
8:i:113:ALA:HA	8:i:124:MET:HE2	1.91	0.52
9:j:136:GLN:NE2	53:1:2899:A:H5'	2.23	0.52
11:l:135:ILE:HD12	11:l:142:ILE:HD11	1.91	0.52
14:o:71:ALA:HB1	14:o:106:LEU:HB2	1.92	0.52
15:p:77:SER:OG	15:p:79:VAL:HG12	2.09	0.52
33:I:24:VAL:HG12	52:3:409:U:H5''	1.90	0.52
33:I:62:ARG:HH22	52:3:544:G:P	2.32	0.52
39:O:29:ALA:O	39:O:33:GLY:HA3	2.10	0.52
39:O:41:PRO:HG3	52:3:1150:A:N3	2.23	0.52
42:R:27:THR:CG2	52:3:1328:C:H5''	2.36	0.52
53:1:1138:G:H2'	53:1:1139:G:O4'	2.10	0.52
4:e:66:ILE:HD12	4:e:66:ILE:N	2.25	0.52
6:g:51:ARG:HA	6:g:55:GLU:HB2	1.91	0.52
10:k:76:VAL:H	15:p:72:VAL:HG12	1.75	0.52
19:t:61:LEU:HB3	53:1:1341:G:H5'	1.90	0.52
21:v:26:PHE:HE2	21:v:89:ILE:HG13	1.74	0.52
33:I:81:LEU:HD12	33:I:82:LYS:H	1.75	0.52
52:3:423:G:C2'	52:3:424:G:H5'	2.39	0.52
53:1:277:G:H4'	53:1:278:A:N7	2.24	0.52
53:1:1140:C:H2'	53:1:1141:U:H5'	1.91	0.52
8:i:93:ASN:ND2	53:1:1077:A:H5''	2.25	0.52
20:u:57:ILE:HG23	20:u:57:ILE:O	2.08	0.52
21:v:3:THR:HG22	21:v:62:THR:HB	1.92	0.52
53:1:2443:C:H2'	53:1:2444:G:H8	1.72	0.52
53:1:2646:C:H2'	53:1:2647:U:O4'	2.09	0.52
54:2:118:C:H2'	54:2:119:A:C8	2.45	0.52
7:h:26:VAL:HG13	7:h:116:GLU:CG	2.39	0.52
34:J:108:GLY:O	34:J:109:ALA:HB3	2.10	0.52
34:J:110:MET:O	34:J:113:VAL:HG12	2.10	0.52
35:K:51:ILE:C	35:K:53:LYS:H	2.17	0.52
45:U:19:VAL:HG23	45:U:36:VAL:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:V:4:ILE:H	46:V:4:ILE:HD12	1.74	0.52
52:3:570:G:HO2'	52:3:819:A:H2'	1.75	0.52
53:1:215:G:C4'	53:1:216:A:H4'	2.39	0.52
53:1:1083:U:H2'	53:1:1085:A:OP2	2.10	0.52
57:7:68:C:H2'	57:7:69:G:H8	1.74	0.52
23:x:18:SER:OG	23:x:19:HIS:N	2.43	0.52
31:G:76:SER:HB2	31:G:92:ASN:HD22	1.74	0.52
52:3:855:U:H2'	52:3:856:C:C6	2.45	0.52
53:1:634:C:H2'	53:1:635:C:C6	2.44	0.52
53:1:1979:U:O2'	53:1:1980:G:H5'	2.10	0.52
53:1:2799:A:H2'	53:1:2800:A:H5'	1.91	0.52
58:8:325:LYS:NZ	58:8:349:GLU:HA	2.24	0.52
1:b:42:ARG:HH12	53:1:690:G:H21	1.58	0.52
26:B:9:ARG:HD2	26:B:9:ARG:N	2.24	0.52
39:O:50:THR:OG1	52:3:975:A:N6	2.43	0.52
52:3:1342:C:H2'	52:3:1343:G:C8	2.44	0.52
52:3:1391:U:H2'	52:3:1392:G:C8	2.45	0.52
53:1:227:A:H61	53:1:410:G:H21	1.57	0.52
53:1:513:A:H2	53:1:582:A:H4'	1.75	0.52
53:1:863:A:H2'	53:1:864:G:C8	2.45	0.52
53:1:1078:U:C5'	53:1:1079:C:H5''	2.40	0.52
53:1:2285:C:C2'	53:1:2286:G:H5'	2.40	0.52
5:f:86:LEU:HB2	5:f:130:ILE:HG23	1.92	0.52
6:g:11:ASN:HD22	6:g:12:LEU:CD2	2.23	0.52
8:i:7:TYR:HB3	8:i:59:THR:HA	1.92	0.52
10:k:14:SER:HB2	10:k:86:LEU:HD12	1.92	0.52
14:o:11:ALA:HB2	14:o:96:GLY:N	2.25	0.52
32:H:3:LYS:HZ2	52:3:1191:A:H5''	1.74	0.52
41:Q:36:VAL:HG22	41:Q:52:CYS:HB3	1.91	0.52
52:3:580:C:H2'	52:3:581:G:O4'	2.09	0.52
52:3:880:C:H2'	52:3:881:G:H8	1.75	0.52
52:3:1004:A:H2'	52:3:1005:A:O4'	2.10	0.52
52:3:1347:G:N2	52:3:1373:G:H2'	2.25	0.52
52:3:1412:C:H2'	52:3:1413:A:H8	1.75	0.52
53:1:445:C:O2'	53:1:446:G:H5'	2.10	0.52
53:1:1190:G:H2'	53:1:1191:G:H8	1.74	0.52
1:b:59:GLN:HA	53:1:1568:G:H5'	1.92	0.52
27:C:46:VAL:HG12	27:C:47:ILE:H	1.75	0.52
38:N:10:ARG:NH2	52:3:1148:U:H5''	2.25	0.52
39:O:21:ALA:O	39:O:24:GLU:HG3	2.10	0.52
41:Q:32:VAL:HG22	41:Q:55:ARG:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1170:A:H2'	52:3:1171:A:O4'	2.10	0.52
53:1:352:A:H2'	53:1:353:C:C6	2.45	0.52
53:1:1965:C:H5''	53:1:1966:A:H2'	1.91	0.52
1:b:203:VAL:O	1:b:203:VAL:HG22	2.10	0.51
15:p:38:ARG:NE	52:3:345:C:H5'	2.24	0.51
15:p:64:SER:OG	15:p:65:ASN:N	2.42	0.51
30:F:9:LYS:NZ	30:F:12:ARG:HA	2.25	0.51
41:Q:13:ARG:HH12	41:Q:14:LYS:HB3	1.75	0.51
51:a:10:VAL:O	51:a:14:LYS:HG3	2.10	0.51
53:1:1856:U:H2'	53:1:1857:G:O4'	2.10	0.51
53:1:2208:C:H2'	53:1:2209:G:H8	1.75	0.51
53:1:2243:U:H2'	53:1:2244:U:C6	2.45	0.51
53:1:2795:C:H2'	53:1:2796:U:O4'	2.09	0.51
58:8:12:HIS:HA	58:8:76:HIS:HB3	1.92	0.51
1:b:29:PHE:HD2	1:b:32:LEU:HD23	1.76	0.51
5:f:93:TYR:CZ	5:f:159:LYS:HE3	2.45	0.51
37:M:83:ARG:NH2	52:3:644:U:H4'	2.26	0.51
52:3:570:G:O2'	52:3:819:A:H2'	2.10	0.51
53:1:1683:U:H2'	53:1:1684:G:C8	2.45	0.51
53:1:2417:C:H2'	53:1:2418:A:H8	1.74	0.51
53:1:2560:A:H2'	53:1:2561:U:C6	2.45	0.51
54:2:60:C:H2'	54:2:61:G:H8	1.74	0.51
58:8:333:PHE:HB3	58:8:375:PHE:HB3	1.91	0.51
7:h:3:LEU:HD23	7:h:3:LEU:H	1.76	0.51
10:k:15:GLY:O	10:k:46:ALA:HB1	2.11	0.51
32:H:78:LYS:O	32:H:81:GLU:HG2	2.11	0.51
43:S:26:LEU:O	43:S:26:LEU:HD23	2.10	0.51
52:3:16:A:O2'	52:3:17:U:H5'	2.10	0.51
52:3:584:G:H2'	52:3:585:G:C8	2.44	0.51
53:1:704:G:H1'	53:1:727:A:H61	1.75	0.51
53:1:827:U:H4'	53:1:828:U:C5	2.45	0.51
53:1:2027:G:O2'	53:1:2028:U:H5'	2.10	0.51
53:1:2350:C:H2'	53:1:2351:G:O4'	2.10	0.51
58:8:334:ARG:O	58:8:335:THR:HG23	2.11	0.51
3:d:44:ARG:HE	53:1:444:C:H4'	1.76	0.51
7:h:23:LEU:HD21	7:h:96:PHE:HB2	1.92	0.51
13:n:4:ARG:HB2	53:1:2722:G:H4'	1.92	0.51
52:3:438:U:HO2'	52:3:439:U:H6	1.58	0.51
53:1:796:C:H2'	53:1:797:G:C8	2.46	0.51
53:1:2291:U:H2'	53:1:2292:U:C6	2.45	0.51
53:1:2724:U:H2'	53:1:2725:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:6:8:U:H2'	55:6:46:G:H21	1.75	0.51
58:8:311:ILE:N	58:8:311:ILE:HD12	2.25	0.51
58:8:340:GLY:HA3	58:8:363:LEU:HD23	1.91	0.51
33:I:6:PRO:HG3	52:3:430:A:H4'	1.91	0.51
36:L:4:ARG:HB3	36:L:6:ILE:HG23	1.92	0.51
52:3:868:C:H2'	52:3:869:G:O4'	2.11	0.51
53:1:279:A:H2'	53:1:280:U:H5'	1.92	0.51
53:1:593:U:H2'	53:1:594:U:C6	2.45	0.51
53:1:633:A:H2'	53:1:634:C:H5'	1.92	0.51
53:1:668:A:H2'	53:1:670:A:H62	1.75	0.51
53:1:744:U:H2'	53:1:745:G:O4'	2.10	0.51
53:1:1068:G:H2'	53:1:1069:A:O4'	2.09	0.51
53:1:1563:U:H2'	53:1:1564:C:C6	2.45	0.51
53:1:2861:U:H2'	53:1:2862:G:C8	2.46	0.51
53:1:2888:C:H2'	53:1:2889:C:C6	2.45	0.51
1:b:42:ARG:N	1:b:42:ARG:HD2	2.26	0.51
21:v:14:LYS:HB2	54:2:98:G:H1	1.75	0.51
21:v:20:LEU:HD11	21:v:27:PRO:HD3	1.93	0.51
32:H:141:MET:HE2	32:H:169:GLU:HG3	1.92	0.51
35:K:38:ARG:HE	35:K:40:GLU:HB2	1.76	0.51
47:W:62:ARG:HB3	47:W:69:TYR:CE2	2.45	0.51
50:Z:66:ARG:NH1	52:3:1167:A:C4	2.78	0.51
53:1:1357:C:H2'	53:1:1358:G:O4'	2.11	0.51
9:j:36:LEU:HD11	9:j:122:LEU:HD12	1.92	0.51
9:j:90:GLU:HG2	9:j:91:GLU:N	2.26	0.51
11:l:33:ARG:HD3	11:l:40:SER:HA	1.92	0.51
36:L:115:MET:HE3	52:3:1240:U:C4	2.45	0.51
39:O:57:VAL:CG2	39:O:58:ASN:H	2.14	0.51
45:U:20:VAL:HG22	45:U:21:VAL:N	2.25	0.51
52:3:865:A:H2'	52:3:866:C:C6	2.44	0.51
52:3:955:U:H3	52:3:1225:A:N6	2.05	0.51
53:1:974:G:H1'	53:1:975:A:C8	2.46	0.51
53:1:1344:U:H3'	53:1:1345:C:H5'	1.91	0.51
53:1:1672:A:C2	53:1:2582:G:H5'	2.45	0.51
53:1:2516:A:O2'	53:1:2517:C:H5'	2.11	0.51
53:1:2756:U:H4'	53:1:2757:A:OP1	2.10	0.51
1:b:208:GLY:HA2	1:b:211:ARG:HB2	1.93	0.51
5:f:3:VAL:HG11	53:1:2748:A:H5'	1.92	0.51
20:u:42:LYS:HD2	53:1:499:U:H5''	1.93	0.51
22:w:70:PRO:HD3	54:2:12:C:H42	1.75	0.51
25:z:13:ILE:HD12	53:1:988:A:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:76:ASN:O	34:J:79:THR:HG22	2.10	0.51
50:Z:49:ALA:O	50:Z:53:LYS:HG3	2.11	0.51
52:3:1236:A:H2'	52:3:1237:C:C6	2.45	0.51
53:1:1609:A:H1'	53:1:1616:A:O4'	2.10	0.51
58:8:124:ARG:NE	58:8:162:ASP:OD1	2.44	0.51
3:d:173:THR:OG1	53:1:616:A:H1'	2.10	0.51
6:g:29:PHE:HB2	53:1:2198:A:C2	2.46	0.51
29:E:42:HIS:HE1	53:1:2351:G:N7	2.09	0.51
52:3:1254:A:H2'	52:3:1255:G:C8	2.46	0.51
53:1:323:C:H2'	53:1:1205:A:N1	2.25	0.51
53:1:796:C:H2'	53:1:797:G:H8	1.75	0.51
53:1:967:U:H2'	53:1:968:C:C6	2.46	0.51
53:1:1065:U:H5'	53:1:1066:U:OP2	2.11	0.51
53:1:2623:G:H2'	53:1:2624:G:H8	1.76	0.51
57:7:16:U:H2'	57:7:17:C:H4'	1.92	0.51
58:8:155:ARG:NH1	58:8:165:GLY:O	2.42	0.51
58:8:312:LEU:HD12	58:8:316:GLU:HG2	1.90	0.51
27:C:8:ILE:N	27:C:8:ILE:HD12	2.26	0.51
35:K:12:PRO:O	35:K:15:SER:OG	2.26	0.51
50:Z:11:PHE:C	50:Z:13:VAL:H	2.19	0.51
57:7:52:G:H4'	58:8:319:ARG:HH12	1.75	0.51
58:8:224:ARG:HH21	58:8:224:ARG:HA	1.76	0.51
2:c:28:GLU:HA	2:c:186:LEU:HD13	1.93	0.50
15:p:102:ARG:HG2	15:p:102:ARG:HH11	1.76	0.50
30:F:3:VAL:HG12	30:F:36:ARG:HD3	1.91	0.50
31:G:20:ARG:CD	52:3:831:A:H5'	2.41	0.50
34:J:148:SER:HB2	34:J:149:PRO:HD2	1.93	0.50
52:3:1514:G:O2'	52:3:1515:G:H5'	2.11	0.50
53:1:458:G:HO2'	53:1:459:U:H5	1.58	0.50
53:1:876:C:H2'	53:1:877:A:O4'	2.11	0.50
53:1:1434:A:H2'	53:1:1435:G:H8	1.76	0.50
55:5:42:G:H2'	55:5:43:A:C8	2.46	0.50
1:b:145:MET:SD	1:b:153:LEU:HD11	2.52	0.50
4:e:141:ASP:O	4:e:142:TYR:HB3	2.10	0.50
10:k:106:GLU:N	10:k:106:GLU:OE2	2.43	0.50
23:x:5:GLN:HE22	23:x:49:ARG:HB3	1.75	0.50
33:I:131:ILE:H	33:I:131:ILE:HD12	1.77	0.50
36:L:24:LYS:HD2	36:L:27:ASN:HD22	1.76	0.50
49:Y:26:MET:HB2	52:3:1458:G:H5'	1.93	0.50
49:Y:28:ARG:NH1	52:3:1437:A:H5''	2.26	0.50
52:3:79:G:O2'	52:3:80:A:H5'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1197:A:C2'	52:3:1198:G:H5''	2.41	0.50
53:1:1857:G:H1'	53:1:1885:A:N6	2.27	0.50
12:m:36:VAL:HG22	21:v:82:TYR:HB2	1.93	0.50
22:w:20:LYS:HG3	53:1:2355:G:H4'	1.94	0.50
26:B:30:ASP:HB3	26:B:34:GLY:N	2.27	0.50
31:G:198:VAL:C	31:G:199:ILE:HD12	2.37	0.50
38:N:49:GLN:O	38:N:52:GLU:HG3	2.10	0.50
41:Q:38:THR:HG21	41:Q:48:LEU:HG	1.92	0.50
41:Q:78:VAL:O	41:Q:102:ASP:HB2	2.11	0.50
48:X:27:LYS:HG2	48:X:28:LYS:H	1.76	0.50
52:3:205:A:H2'	52:3:206:C:O4'	2.12	0.50
52:3:206:C:H2'	52:3:207:C:O4'	2.12	0.50
53:1:833:A:H2'	53:1:834:G:H8	1.76	0.50
53:1:942:G:H2'	53:1:943:A:O4'	2.11	0.50
53:1:2841:C:H2'	53:1:2842:G:H8	1.76	0.50
26:B:4:GLN:HG3	26:B:5:ASN:ND2	2.26	0.50
37:M:65:PHE:CD2	37:M:66:GLN:HG2	2.47	0.50
41:Q:48:LEU:HB3	52:3:520:A:OP1	2.12	0.50
44:T:2:LEU:HG	44:T:7:THR:HG22	1.93	0.50
44:T:86:LEU:HD12	44:T:87:ARG:N	2.26	0.50
52:3:1524:C:H2'	52:3:1525:G:C8	2.46	0.50
53:1:1916:A:H2'	53:1:1917:U:C6	2.46	0.50
14:o:25:ARG:HE	14:o:40:ILE:HD12	1.77	0.50
32:H:5:HIS:HB3	43:S:88:MET:HE3	1.93	0.50
33:I:12:ARG:HG2	33:I:33:ILE:HD12	1.93	0.50
36:L:2:ARG:HA	52:3:1380:U:C5	2.46	0.50
42:R:113:LYS:H	42:R:114:PRO:CD	2.25	0.50
53:1:23:G:H2'	53:1:24:G:H8	1.76	0.50
53:1:2126:A:H2'	53:1:2162:G:N2	2.27	0.50
10:k:31:ARG:NH2	53:1:1996:C:OP2	2.44	0.50
19:t:74:ILE:HG13	19:t:74:ILE:O	2.11	0.50
35:K:92:THR:OG1	35:K:93:LYS:N	2.43	0.50
38:N:117:LEU:CD2	38:N:123:ARG:HD3	2.42	0.50
49:Y:56:ILE:O	49:Y:60:GLN:HG2	2.11	0.50
51:a:44:VAL:HG22	51:a:214:ILE:HG22	1.94	0.50
52:3:358:U:H2'	52:3:359:G:C8	2.47	0.50
52:3:1427:C:H2'	52:3:1428:A:C8	2.47	0.50
52:3:1506:U:O2'	52:3:1507:A:H5'	2.11	0.50
53:1:971:G:H2'	53:1:972:A:O4'	2.11	0.50
53:1:1020:A:C1'	53:1:1021:A:OP2	2.55	0.50
4:e:58:ALA:O	4:e:139:GLU:HG2	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:100:CYS:SG	13:n:101:GLY:N	2.83	0.50
14:o:60:GLU:OE1	14:o:60:GLU:N	2.45	0.50
36:L:110:ARG:HG2	36:L:110:ARG:O	2.11	0.50
45:U:38:PHE:CE1	45:U:51:ARG:HB2	2.46	0.50
52:3:398:U:H2'	52:3:399:G:C8	2.46	0.50
52:3:1247:U:O2'	52:3:1248:A:H5'	2.12	0.50
52:3:1458:G:H2'	52:3:1459:G:C8	2.47	0.50
53:1:272:A:H2'	53:1:273:G:H8	1.77	0.50
53:1:755:U:H2'	53:1:756:A:C8	2.46	0.50
53:1:828:U:H2'	53:1:829:A:C8	2.46	0.50
53:1:1021:A:H3'	53:1:1021:A:N3	2.27	0.50
53:1:1319:C:O2'	53:1:1320:C:H5'	2.12	0.50
53:1:2715:C:H3'	53:1:2716:C:H5''	1.94	0.50
2:c:125:TRP:CG	2:c:160:LYS:HB3	2.46	0.50
3:d:117:ARG:NH2	3:d:183:PHE:O	2.45	0.50
6:g:26:ALA:HA	6:g:30:LEU:HB2	1.93	0.50
13:n:92:GLY:O	53:1:2880:C:H1'	2.12	0.50
16:q:108:LEU:HD23	17:r:48:LYS:HE3	1.92	0.50
33:I:131:ILE:HD11	52:3:619:U:C4	2.47	0.50
50:Z:36:PHE:C	50:Z:38:GLU:H	2.20	0.50
52:3:70:U:H4'	52:3:71:A:H8	1.76	0.50
52:3:458:U:H2'	52:3:459:A:H8	1.77	0.50
52:3:1391:U:H2'	52:3:1392:G:H8	1.76	0.50
52:3:1464:U:H2'	52:3:1465:A:C8	2.47	0.50
52:3:1497:G:H2'	52:3:1498:U:H5'	1.93	0.50
53:1:595:C:H2'	53:1:596:U:C6	2.47	0.50
53:1:783:A:H2'	53:1:784:G:H5'	1.94	0.50
53:1:1068:G:H2'	53:1:1069:A:C1'	2.42	0.50
53:1:1509:A:H2'	53:1:1510:G:C8	2.46	0.50
53:1:1590:A:H2'	53:1:1591:A:C8	2.47	0.50
53:1:2345:G:H21	53:1:2381:A:H3'	1.76	0.50
53:1:2628:C:H3'	53:1:2629:U:H5'	1.94	0.50
53:1:2853:C:H2'	53:1:2854:G:C8	2.47	0.50
54:2:63:C:H2'	54:2:64:G:C8	2.47	0.50
2:c:133:THR:OG1	2:c:134:HIS:N	2.44	0.50
11:l:93:ASN:C	11:l:95:LEU:H	2.20	0.50
13:n:43:GLU:OE2	13:n:46:ARG:HD3	2.12	0.50
38:N:125:GLN:HE22	52:3:943:U:H1'	1.77	0.50
45:U:76:LYS:HA	45:U:80:LYS:NZ	2.27	0.50
52:3:78:A:H2'	52:3:79:G:O4'	2.12	0.50
52:3:891:U:H2'	52:3:892:A:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:135:ILE:HD12	4:e:135:ILE:N	2.26	0.49
6:g:41:LYS:H	6:g:41:LYS:HD3	1.76	0.49
16:q:56:PHE:CE2	53:1:536:G:H4'	2.47	0.49
32:H:30:ASP:HA	43:S:64:ARG:HH12	1.77	0.49
38:N:49:GLN:N	38:N:50:PRO:HD2	2.27	0.49
42:R:101:THR:OG1	52:3:1225:A:H5''	2.12	0.49
52:3:502:A:H2'	52:3:503:C:O4'	2.11	0.49
52:3:1163:A:H2'	52:3:1164:G:H8	1.77	0.49
53:1:145:C:H2'	53:1:146:A:C8	2.47	0.49
53:1:457:A:H5'	53:1:459:U:H1'	1.94	0.49
55:5:36:U:H2'	55:5:37:A:C8	2.47	0.49
1:b:245:THR:OG1	1:b:246:PRO:HD2	2.12	0.49
6:g:47:PHE:HA	6:g:51:ARG:HB2	1.93	0.49
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.93	0.49
33:I:40:HIS:NE2	52:3:511:C:O2'	2.45	0.49
41:Q:30:ARG:HH11	41:Q:78:VAL:HG11	1.77	0.49
42:R:91:ARG:NH2	53:1:887:U:H5'	2.27	0.49
43:S:44:VAL:HG13	43:S:45:LEU:HD22	1.93	0.49
47:W:40:PRO:HG2	47:W:43:ILE:HG12	1.92	0.49
52:3:979:C:H2'	52:3:980:C:H5'	1.94	0.49
53:1:96:C:H2'	53:1:97:C:H6	1.78	0.49
53:1:688:U:H2'	53:1:689:A:C8	2.46	0.49
3:d:6:LYS:HD2	3:d:6:LYS:N	2.27	0.49
4:e:47:LYS:O	4:e:50:ASP:OD1	2.29	0.49
10:k:18:ARG:HB3	10:k:45:GLU:CG	2.42	0.49
18:s:88:ARG:NH2	18:s:94:ASP:OD2	2.45	0.49
24:y:41:HIS:CD2	53:1:96:C:H4'	2.47	0.49
36:L:55:LYS:HB2	36:L:60:ALA:HB2	1.93	0.49
52:3:1271:A:H5'	52:3:1314:C:H5''	1.93	0.49
53:1:426:C:H2'	53:1:427:U:C6	2.47	0.49
57:7:53:G:OP1	58:8:321:THR:HB	2.13	0.49
2:c:142:VAL:HG13	2:c:143:PRO:HD2	1.93	0.49
9:j:39:LYS:NZ	53:1:1009:A:OP1	2.45	0.49
14:o:40:ILE:HA	14:o:47:VAL:HA	1.94	0.49
15:p:54:LEU:HA	15:p:76:HIS:HD2	1.76	0.49
31:G:20:ARG:HD3	52:3:831:A:H5'	1.94	0.49
32:H:45:GLU:HG3	32:H:46:LEU:HD22	1.93	0.49
34:J:87:VAL:HG22	34:J:92:ARG:HA	1.95	0.49
45:U:59:HIS:O	45:U:63:GLN:HG2	2.11	0.49
52:3:785:G:O2'	52:3:786:G:H5'	2.12	0.49
52:3:860:A:H2'	52:3:861:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:326:G:H2'	53:1:327:G:H8	1.77	0.49
53:1:2389:G:H5''	53:1:2390:U:O4'	2.12	0.49
58:8:305:PHE:CE1	58:8:361:VAL:HB	2.48	0.49
2:c:62:LYS:HB2	2:c:63:PRO:HD3	1.94	0.49
6:g:12:LEU:HD23	6:g:12:LEU:H	1.77	0.49
40:P:91:GLY:O	40:P:93:GLU:N	2.45	0.49
52:3:623:C:H2'	52:3:624:C:C6	2.47	0.49
52:3:1271:A:H2'	52:3:1272:G:C8	2.48	0.49
53:1:729:G:H4'	53:1:763:G:C5'	2.43	0.49
53:1:2455:G:H2'	53:1:2456:C:C6	2.47	0.49
55:5:36:U:H2'	55:5:37:A:H8	1.77	0.49
19:t:58:VAL:HG12	19:t:85:VAL:HG13	1.94	0.49
21:v:61:LEU:HD23	21:v:62:THR:H	1.77	0.49
21:v:82:TYR:CE2	21:v:83:LYS:HE2	2.47	0.49
31:G:195:VAL:HB	31:G:198:VAL:HG12	1.94	0.49
45:U:42:ILE:O	45:U:42:ILE:HG22	2.11	0.49
52:3:599:C:H2'	52:3:600:A:H8	1.77	0.49
52:3:1271:A:H2'	52:3:1272:G:H8	1.78	0.49
53:1:576:U:H2'	53:1:577:G:C8	2.48	0.49
53:1:1019:U:H2'	53:1:1020:A:C8	2.48	0.49
53:1:1278:C:H2'	53:1:1279:G:H8	1.77	0.49
53:1:2579:C:O2'	53:1:2580:U:H5'	2.12	0.49
54:2:88:C:H5''	54:2:89:U:OP1	2.13	0.49
2:c:164:GLN:HE22	53:1:2822:G:H5''	1.78	0.49
5:f:122:ALA:HB1	5:f:130:ILE:HD11	1.94	0.49
8:i:48:ILE:HG23	8:i:49:GLU:N	2.26	0.49
8:i:126:ARG:HE	53:1:1081:U:P	2.36	0.49
24:y:24:GLU:HA	24:y:27:ASN:HB2	1.95	0.49
36:L:110:ARG:HD3	36:L:122:GLU:OE2	2.12	0.49
40:P:84:MET:SD	40:P:110:THR:OG1	2.70	0.49
52:3:680:C:H2'	52:3:681:A:H8	1.76	0.49
52:3:1402:C:H2'	52:3:1403:C:O4'	2.13	0.49
53:1:2220:U:H2'	53:1:2221:G:C8	2.48	0.49
53:1:2281:A:O2'	53:1:2282:G:H5'	2.13	0.49
53:1:2699:C:H2'	53:1:2700:A:C8	2.48	0.49
53:1:2841:C:H2'	53:1:2842:G:C8	2.48	0.49
5:f:122:ALA:HA	5:f:132:LEU:HA	1.95	0.49
5:f:138:GLN:HE21	53:1:2759:G:N2	2.10	0.49
8:i:8:VAL:HG13	8:i:10:LEU:HD22	1.94	0.49
9:j:11:VAL:O	9:j:13:ARG:NH2	2.46	0.49
9:j:58:ASN:HD21	9:j:128:ASN:HB2	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:96:ARG:HB2	13:n:116:VAL:HG22	1.94	0.49
18:s:62:ASP:N	18:s:62:ASP:OD1	2.45	0.49
27:C:22:THR:HG21	53:1:2286:G:O6	2.12	0.49
33:I:32:LYS:HB3	33:I:35:GLN:HE22	1.78	0.49
35:K:12:PRO:HG3	35:K:56:LYS:O	2.13	0.49
35:K:86:ARG:NH1	52:3:673:A:H4'	2.28	0.49
51:a:185:LEU:HA	51:a:188:ASN:HD22	1.77	0.49
52:3:1070:U:H2'	52:3:1071:C:C6	2.48	0.49
53:1:471:A:H2'	53:1:472:A:O4'	2.12	0.49
53:1:1779:U:H5	53:1:1784:A:N7	2.10	0.49
1:b:116:GLN:H	1:b:127:ASN:ND2	2.10	0.49
17:r:63:VAL:HA	17:r:96:VAL:HA	1.94	0.49
39:O:38:GLY:O	39:O:40:ILE:HD12	2.13	0.49
43:S:81:ILE:HD13	52:3:1202:U:N3	2.28	0.49
52:3:163:C:H2'	52:3:164:G:O4'	2.13	0.49
52:3:909:A:H2'	52:3:910:C:O4'	2.12	0.49
52:3:924:C:H2'	52:3:925:G:H8	1.76	0.49
52:3:1410:A:H2'	52:3:1411:C:C6	2.48	0.49
53:1:214:G:O2'	53:1:215:G:H5'	2.13	0.49
53:1:278:A:H2'	53:1:278:A:N3	2.28	0.49
53:1:522:A:H2'	53:1:523:C:C6	2.48	0.49
53:1:1550:C:H2'	53:1:1551:A:H8	1.78	0.49
53:1:1664:A:H61	53:1:1996:C:H42	1.59	0.49
53:1:2584:U:H2'	53:1:2585:U:H2'	1.95	0.49
54:2:63:C:H2'	54:2:64:G:H8	1.78	0.49
4:e:15:LEU:HD23	4:e:27:VAL:HG23	1.95	0.49
6:g:86:ASP:OD2	35:K:24:ARG:NH1	2.46	0.49
8:i:125:THR:O	8:i:129:GLU:HG3	2.13	0.49
32:H:172:VAL:O	32:H:172:VAL:HG13	2.13	0.49
38:N:98:ARG:HG3	38:N:103:VAL:CG1	2.41	0.49
42:R:82:LEU:HD22	42:R:84:CYS:HB3	1.95	0.49
52:3:815:A:H5''	52:3:817:C:N4	2.28	0.49
53:1:1278:C:H2'	53:1:1279:G:C8	2.48	0.49
53:1:1935:G:H1'	53:1:1964:G:N2	2.28	0.49
53:1:2161:C:H2'	53:1:2162:G:H5''	1.95	0.49
53:1:2322:A:H2'	53:1:2323:G:O4'	2.12	0.49
53:1:2845:U:H2'	53:1:2846:G:C8	2.48	0.49
55:5:18:G:H1	55:5:55:U:H6	1.61	0.49
1:b:245:THR:C	1:b:247:TRP:H	2.21	0.48
3:d:53:THR:OG1	53:1:452:G:H8	1.96	0.48
4:e:120:SER:OG	53:1:2304:G:H5'	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:64:TRP:HB2	12:m:104:GLU:HB2	1.95	0.48
14:o:49:VAL:HG11	14:o:81:ARG:HG3	1.95	0.48
44:T:71:ARG:HD2	44:T:71:ARG:C	2.38	0.48
52:3:613:C:H2'	52:3:614:C:C6	2.48	0.48
52:3:834:U:H2'	52:3:835:U:C6	2.48	0.48
53:1:1105:U:H2'	53:1:1106:G:H5''	1.95	0.48
53:1:1458:U:H4'	53:1:1459:G:C4	2.47	0.48
53:1:1564:C:H2'	53:1:1565:C:O4'	2.13	0.48
53:1:1751:U:H2'	53:1:1752:C:C6	2.48	0.48
53:1:2548:U:H2'	53:1:2549:G:O4'	2.12	0.48
4:e:46:LYS:NZ	4:e:83:PRO:HG2	2.29	0.48
9:j:84:ILE:HG23	9:j:84:ILE:O	2.13	0.48
16:q:89:ILE:HG12	17:r:39:LEU:HD23	1.95	0.48
28:D:30:VAL:O	28:D:34:ARG:HG2	2.14	0.48
31:G:22:TRP:HZ2	52:3:829:G:H4'	1.79	0.48
32:H:46:LEU:HB3	32:H:51:VAL:HG21	1.94	0.48
51:a:211:LYS:HD3	53:1:2178:C:OP1	2.12	0.48
52:3:77:A:H2'	52:3:78:A:C8	2.47	0.48
52:3:368:U:OP2	58:8:280:ARG:NE	2.45	0.48
53:1:20:C:H2'	53:1:21:A:C8	2.48	0.48
53:1:100:U:H4'	53:1:101:A:O4'	2.14	0.48
53:1:807:U:H2'	53:1:808:G:C8	2.48	0.48
53:1:1373:A:H5'	53:1:2212:A:H1'	1.93	0.48
53:1:1851:U:O2'	55:6:71:C:H4'	2.13	0.48
53:1:2082:A:H2'	53:1:2083:G:O4'	2.13	0.48
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.12	0.48
6:g:94:ILE:HD11	6:g:122:LEU:HD22	1.95	0.48
10:k:20:MET:SD	10:k:44:LYS:HD3	2.53	0.48
32:H:149:LYS:HG3	32:H:168:ARG:HB3	1.94	0.48
33:I:149:LYS:HG2	33:I:150:LYS:HG2	1.94	0.48
34:J:51:LYS:NZ	52:3:1081:A:OP2	2.47	0.48
36:L:46:LEU:HD21	36:L:57:GLU:HB3	1.95	0.48
50:Z:19:LYS:HB2	50:Z:24:LYS:HE2	1.94	0.48
52:3:865:A:H5'	52:3:1078:U:O4	2.12	0.48
52:3:1237:C:H4'	52:3:1334:G:N2	2.28	0.48
53:1:962:G:N2	53:1:2250:G:H1	2.10	0.48
53:1:1882:U:H2'	53:1:1883:U:C6	2.47	0.48
58:8:19:GLY:H	58:8:119:HIS:CD2	2.30	0.48
3:d:192:ALA:O	3:d:196:VAL:HG23	2.13	0.48
7:h:42:ARG:HH22	8:i:119:ALA:HB2	1.79	0.48
14:o:18:LEU:HD12	14:o:19:GLN:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:49:PRO:HA	20:u:53:GLN:HE21	1.77	0.48
21:v:6:ALA:HB1	21:v:40:ILE:HG21	1.94	0.48
36:L:142:ARG:CG	55:6:41:C:H4'	2.43	0.48
47:W:10:CYS:SG	47:W:11:ARG:N	2.85	0.48
52:3:1060:U:H2'	52:3:1061:G:C8	2.48	0.48
52:3:1218:C:H2'	52:3:1219:A:H8	1.77	0.48
53:1:688:U:H2'	53:1:689:A:H8	1.78	0.48
53:1:742:A:H2'	53:1:743:A:H8	1.78	0.48
53:1:948:C:H2'	53:1:949:G:H8	1.78	0.48
53:1:2863:C:H2'	53:1:2864:G:C8	2.48	0.48
2:c:46:ARG:NH2	2:c:88:GLU:O	2.46	0.48
4:e:72:SER:O	55:5:56:C:H4'	2.13	0.48
6:g:5:LEU:HD21	6:g:9:VAL:HG12	1.96	0.48
16:q:2:ARG:HD2	53:1:1248:G:C2	2.48	0.48
20:u:10:VAL:HG12	20:u:71:ILE:HA	1.96	0.48
28:D:37:LYS:HD2	28:D:39:ARG:HH21	1.78	0.48
35:K:52:ASN:O	35:K:53:LYS:HG2	2.13	0.48
36:L:24:LYS:HA	36:L:27:ASN:ND2	2.28	0.48
41:Q:43:LYS:HB3	41:Q:44:PRO:HD3	1.96	0.48
52:3:236:A:H2'	52:3:237:G:H8	1.77	0.48
52:3:312:C:H2'	52:3:313:A:C8	2.48	0.48
52:3:946:A:H2'	52:3:947:G:C8	2.47	0.48
52:3:1201:A:C1'	52:3:1202:U:OP2	2.58	0.48
53:1:974:G:C5'	53:1:1186:G:H21	2.25	0.48
53:1:2849:U:H1'	53:1:2866:U:O2	2.12	0.48
10:k:71:ARG:HH12	15:p:71:ARG:NH2	2.11	0.48
22:w:62:LYS:HG3	22:w:81:GLU:HB2	1.96	0.48
45:U:26:ASN:OD1	45:U:30:GLY:HA3	2.14	0.48
52:3:273:U:H2'	52:3:274:A:H5'	1.95	0.48
53:1:804:A:H2'	53:1:806:C:C4	2.49	0.48
53:1:1597:A:H5''	53:1:1598:A:H5'	1.95	0.48
53:1:2443:C:O2'	53:1:2444:G:H5'	2.14	0.48
5:f:15:ASP:HB3	5:f:17:LYS:NZ	2.29	0.48
7:h:4:ASN:HA	7:h:7:ASP:OD2	2.14	0.48
7:h:30:SER:HB3	7:h:109:LYS:HZ3	1.78	0.48
12:m:16:ARG:HG3	53:1:953:G:OP2	2.14	0.48
19:t:13:ALA:HB1	24:y:33:ALA:HB1	1.96	0.48
19:t:49:LYS:HB3	19:t:50:LEU:HD12	1.96	0.48
31:G:134:LEU:HD12	31:G:135:MET:N	2.29	0.48
44:T:3:SER:O	44:T:7:THR:HG23	2.13	0.48
53:1:96:C:H2'	53:1:97:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:974:G:N3	53:1:974:G:H2'	2.28	0.48
53:1:1772:A:H2'	53:1:1773:A:H5'	1.96	0.48
53:1:2898:U:H2'	53:1:2899:A:C8	2.48	0.48
54:2:60:C:H2'	54:2:61:G:C8	2.49	0.48
6:g:31:VAL:CG1	6:g:32:PRO:HD3	2.44	0.48
8:i:10:LEU:N	8:i:10:LEU:HD23	2.28	0.48
8:i:85:ILE:N	8:i:85:ILE:HD12	2.28	0.48
11:l:111:ILE:HD11	53:1:636:G:C6	2.48	0.48
14:o:31:THR:HG22	14:o:33:ARG:H	1.79	0.48
16:q:2:ARG:HA	53:1:1248:G:O2'	2.14	0.48
16:q:108:LEU:HD23	17:r:48:LYS:CE	2.44	0.48
31:G:22:TRP:CZ2	52:3:829:G:H4'	2.48	0.48
52:3:593:U:H2'	52:3:594:U:C6	2.47	0.48
52:3:1434:A:H2'	52:3:1435:G:O4'	2.14	0.48
53:1:955:U:H3	53:1:962:G:H1	1.62	0.48
53:1:1744:A:H3'	53:1:1745:A:H8	1.79	0.48
53:1:1928:A:H2'	53:1:1929:G:O4'	2.14	0.48
53:1:2163:A:C2'	53:1:2164:C:H5'	2.44	0.48
53:1:2180:U:H4'	55:6:17(A):U:O4'	2.14	0.48
53:1:2432:A:H1'	55:6:75:C:C4'	2.43	0.48
2:c:149:ASN:O	2:c:152:PRO:HD2	2.14	0.48
26:B:49:ARG:HG2	53:1:2884:U:C5	2.48	0.48
29:E:61:LEU:HD13	29:E:64:ALA:HB3	1.95	0.48
30:F:9:LYS:HG3	30:F:14:CYS:HB2	1.96	0.48
35:K:5:GLU:HB3	35:K:90:MET:HE3	1.96	0.48
39:O:10:LEU:HD23	39:O:10:LEU:H	1.78	0.48
52:3:194:C:O2'	52:3:195:A:H5'	2.14	0.48
52:3:1517:G:H2'	52:3:1518:A:H5'	1.96	0.48
53:1:175:G:H2'	53:1:176:A:C8	2.48	0.48
53:1:622:G:H2'	53:1:623:C:C6	2.49	0.48
53:1:1019:U:H3	53:1:1142:A:H62	1.60	0.48
53:1:1590:A:H2'	53:1:1591:A:H8	1.78	0.48
53:1:1709:U:H2'	53:1:1710:G:H8	1.79	0.48
2:c:8:LYS:HB2	2:c:201:LEU:HD11	1.96	0.48
7:h:110:ALA:HB3	7:h:113:PHE:CE2	2.49	0.48
12:m:57:VAL:O	12:m:60:GLN:NE2	2.47	0.48
13:n:63:ARG:HH12	53:1:1454:C:H5'	1.79	0.48
35:K:75:GLU:HA	35:K:78:PHE:CD2	2.48	0.48
36:L:139:ASP:O	36:L:143:MET:HG2	2.13	0.48
37:M:52:GLY:HA3	37:M:56:PRO:HA	1.95	0.48
39:O:50:THR:HG1	52:3:975:A:N6	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:35:TYR:O	49:Y:39:GLU:HG2	2.13	0.48
52:3:379:C:H2'	52:3:380:G:C8	2.49	0.48
52:3:401:C:H2'	52:3:402:G:H8	1.79	0.48
53:1:2556:C:H2'	53:1:2557:G:O4'	2.14	0.48
55:6:16:C:O2'	55:6:17:C:H5'	2.14	0.48
55:6:47:U:H3'	55:6:48:C:C5'	2.44	0.48
2:c:56:LYS:HZ2	53:1:2830:C:H5''	1.79	0.47
3:d:164:LEU:HB2	3:d:167:VAL:CG2	2.43	0.47
7:h:53:ARG:HH21	7:h:55:VAL:HG11	1.78	0.47
14:o:34:HIS:CE1	14:o:65:THR:HG21	2.49	0.47
14:o:76:LYS:O	14:o:80:GLU:HG3	2.13	0.47
34:J:22:LYS:NZ	52:3:1082:A:OP1	2.44	0.47
45:U:70:ARG:HG2	52:3:375:U:H5''	1.96	0.47
52:3:273:U:C2'	52:3:274:A:H5'	2.44	0.47
52:3:1256:A:H1'	52:3:1258:G:C4	2.49	0.47
53:1:2183:A:H2'	53:1:2184:A:C8	2.49	0.47
53:1:2370:G:H2'	53:1:2371:G:O4'	2.14	0.47
58:8:232:VAL:O	58:8:272:GLY:N	2.47	0.47
31:G:20:ARG:HD3	52:3:831:A:H5''	1.96	0.47
32:H:56:ILE:HG23	32:H:63:ILE:HD11	1.96	0.47
52:3:70:U:H4'	52:3:71:A:C8	2.48	0.47
52:3:245:U:O2'	52:3:246:A:H5'	2.14	0.47
52:3:1424:U:H2'	52:3:1425:U:O4'	2.14	0.47
53:1:1060:U:H4'	53:1:1061:U:C5'	2.44	0.47
53:1:1368:G:H2'	53:1:1369:G:C8	2.50	0.47
53:1:2832:U:O4	53:1:2884:U:H4'	2.15	0.47
1:b:43:ASN:HD21	1:b:45:ASN:HD22	1.60	0.47
12:m:42:THR:O	12:m:46:ILE:HG13	2.15	0.47
17:r:2:TYR:CE1	17:r:42:ALA:HB3	2.50	0.47
33:I:102:TYR:O	33:I:164:ARG:NH1	2.47	0.47
41:Q:32:VAL:CG2	41:Q:55:ARG:HB3	2.45	0.47
52:3:86:G:H4'	52:3:87:C:C5	2.50	0.47
52:3:1229:A:H2'	52:3:1230:C:C6	2.50	0.47
53:1:158:U:H2'	53:1:159:G:O4'	2.14	0.47
53:1:1475:G:O2'	53:1:1476:U:H6	1.97	0.47
53:1:1857:G:N2	53:1:1884:G:H2'	2.28	0.47
53:1:2358:A:H2'	53:1:2359:C:O4'	2.14	0.47
53:1:2376:A:H2'	53:1:2377:A:O4'	2.14	0.47
1:b:251:THR:OG1	1:b:252:LYS:N	2.43	0.47
2:c:172:VAL:HG13	2:c:175:LEU:HD11	1.97	0.47
4:e:65:LEU:HD22	54:2:42:C:C4	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:93:ASN:O	11:l:94:THR:OG1	2.28	0.47
14:o:34:HIS:NE2	14:o:65:THR:HG21	2.29	0.47
17:r:79:ARG:HD3	53:1:564:C:OP2	2.14	0.47
33:l:98:ASP:HA	33:l:101:VAL:HG12	1.96	0.47
36:l:67:ASN:ND2	36:l:126:ALA:O	2.48	0.47
36:l:146:ALA:CB	55:6:40:C:H4'	2.45	0.47
37:m:80:PRO:HG2	52:3:878:A:C5'	2.44	0.47
39:o:22:THR:O	39:o:25:ILE:HG22	2.14	0.47
48:x:40:PHE:H	48:x:43:MET:HE2	1.79	0.47
48:x:79:TYR:CZ	52:3:1226:C:H4'	2.49	0.47
51:a:175:ILE:HG21	51:a:189:LEU:HD23	1.95	0.47
52:3:51:A:H4'	52:3:52:C:H5''	1.96	0.47
53:1:1614:A:H2'	53:1:1615:C:H5'	1.96	0.47
53:1:2217:G:O2'	53:1:2218:G:H5'	2.15	0.47
58:8:12:HIS:HD2	58:8:273:GLU:HA	1.80	0.47
12:m:6:ARG:NH2	55:5:52:G:H5'	2.29	0.47
26:b:51:ARG:HD2	26:b:53:VAL:HG12	1.97	0.47
35:k:6:ILE:HD11	35:k:71:ILE:HD11	1.95	0.47
35:k:18:VAL:HG13	35:k:19:PRO:CD	2.44	0.47
46:v:44:HIS:CE1	52:3:276:G:H4'	2.50	0.47
49:y:74:HIS:O	49:y:78:LEU:HD23	2.14	0.47
52:3:64:G:H4'	52:3:65:A:H3'	1.95	0.47
52:3:257:G:H2'	52:3:258:G:H8	1.78	0.47
52:3:622:A:H2'	52:3:623:C:H5'	1.97	0.47
52:3:1429:A:H2'	52:3:1430:A:C8	2.50	0.47
52:3:1464:U:H2'	52:3:1465:A:H8	1.78	0.47
53:1:433:C:O2'	53:1:434:U:H5'	2.15	0.47
53:1:1111:A:H2'	53:1:1111:A:N3	2.30	0.47
53:1:1592:C:H2'	53:1:1593:A:H8	1.78	0.47
54:2:48:U:H2'	54:2:49:C:C6	2.50	0.47
6:g:30:LEU:HD13	6:g:35:LYS:HB3	1.97	0.47
6:g:40:THR:HB	6:g:43:ASN:ND2	2.29	0.47
11:l:27:LEU:O	11:l:27:LEU:HD23	2.13	0.47
12:m:123:LYS:NZ	53:1:2483:C:N3	2.62	0.47
18:s:103:ILE:H	18:s:103:ILE:HD12	1.80	0.47
31:g:23:ASN:OD1	31:g:25:LYS:HG2	2.14	0.47
33:l:115:GLN:NE2	52:3:406:G:N3	2.62	0.47
34:j:92:ARG:O	34:j:93:VAL:C	2.58	0.47
42:r:15:VAL:HG23	42:r:16:ILE:H	1.79	0.47
49:y:28:ARG:HH12	52:3:1437:A:H5''	1.79	0.47
51:a:181:ASP:OD2	51:a:184:LYS:HE2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:439:U:H2'	52:3:440:C:O4'	2.14	0.47
52:3:837:U:H2'	52:3:838:G:H8	1.79	0.47
52:3:1019:A:H2'	52:3:1020:G:O4'	2.15	0.47
52:3:1406:U:H2'	52:3:1407:C:O4'	2.15	0.47
53:1:331:C:H41	53:1:1210:G:H22	1.63	0.47
53:1:671:C:H2'	53:1:672:C:C6	2.50	0.47
53:1:1515:A:H2'	53:1:1516:G:H5'	1.96	0.47
53:1:2011:U:H2'	53:1:2012:G:O4'	2.13	0.47
53:1:2093:G:N7	53:1:2225:A:H2'	2.30	0.47
53:1:2469:A:H2'	53:1:2470:G:O4'	2.15	0.47
57:7:71:G:O2'	57:7:72:C:H5'	2.15	0.47
8:i:118:GLY:HA2	53:1:1082:U:H5'	1.97	0.47
11:l:79:LEU:HD12	11:l:112:LEU:HD12	1.95	0.47
20:u:42:LYS:HB2	53:1:499:U:H4'	1.95	0.47
23:x:6:VAL:HG23	23:x:7:THR:HG23	1.97	0.47
23:x:42:GLU:HB3	23:x:44:ARG:HG2	1.97	0.47
29:E:32:LEU:HD23	29:E:35:LYS:HD2	1.97	0.47
29:E:43:LEU:HD11	53:1:2362:C:P	2.55	0.47
32:H:86:LEU:HA	32:H:89:VAL:HG12	1.96	0.47
33:I:82:LYS:HG3	52:3:5:U:O4	2.15	0.47
33:I:83:GLY:H	52:3:5:U:H3	1.62	0.47
33:I:176:LYS:NZ	33:I:178:GLU:HB3	2.29	0.47
45:U:42:ILE:HD12	45:U:42:ILE:N	2.30	0.47
46:V:59:GLU:OE1	46:V:60:ILE:N	2.47	0.47
50:Z:9:GLU:HB2	50:Z:10:PRO:CD	2.44	0.47
51:a:183:ASP:O	51:a:187:GLU:HG3	2.13	0.47
52:3:950:U:H2'	52:3:951:G:H8	1.78	0.47
52:3:980:C:H2'	52:3:981:U:H5'	1.96	0.47
52:3:1351:U:H2'	52:3:1352:C:C6	2.49	0.47
52:3:1352:C:H2'	52:3:1353:G:H8	1.80	0.47
52:3:1469:C:H2'	52:3:1470:U:O4'	2.13	0.47
53:1:482:A:H1'	53:1:498:G:N2	2.30	0.47
53:1:807:U:H2'	53:1:808:G:H8	1.79	0.47
53:1:1229:C:H2'	53:1:1230:A:H8	1.80	0.47
53:1:1924:C:H2'	53:1:1925:C:C6	2.49	0.47
53:1:2141:G:H2'	53:1:2142:A:H8	1.80	0.47
53:1:2161:C:C2'	53:1:2162:G:H5''	2.45	0.47
53:1:2423:U:HO2'	53:1:2425:A:H2'	1.78	0.47
58:8:221:ILE:HB	58:8:224:ARG:HB2	1.96	0.47
1:b:62:ARG:HG3	1:b:62:ARG:HH11	1.79	0.47
7:h:74:ASP:O	7:h:77:VAL:HG22	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:18:ARG:HB3	10:k:45:GLU:CD	2.40	0.47
19:t:66:LYS:HE3	53:1:1312:U:O2'	2.14	0.47
33:I:33:ILE:HG23	33:I:34:GLU:HG3	1.97	0.47
37:M:46:GLU:O	37:M:61:THR:OG1	2.33	0.47
40:P:91:GLY:C	40:P:93:GLU:H	2.22	0.47
41:Q:57:THR:HG21	52:3:363:A:P	2.54	0.47
41:Q:91:GLY:HA2	52:3:911:U:OP1	2.14	0.47
44:T:56:LEU:O	44:T:59:VAL:HG12	2.15	0.47
52:3:743:A:H2'	52:3:744:C:C6	2.50	0.47
52:3:1251:A:H2'	52:3:1252:A:C8	2.50	0.47
52:3:1510:C:H2'	52:3:1511:G:C8	2.50	0.47
53:1:756:A:H2'	53:1:757:G:O4'	2.15	0.47
53:1:851:C:H2'	53:1:852:U:C6	2.49	0.47
55:6:73:A:H2'	55:6:74:C:H5'	1.97	0.47
58:8:325:LYS:HZ1	58:8:349:GLU:HA	1.80	0.47
5:f:163:TYR:HB2	5:f:166:GLU:HB2	1.97	0.47
8:i:33:ASN:ND2	8:i:35:MET:HB2	2.29	0.47
11:l:20:GLY:O	11:l:21:ARG:NH2	2.42	0.47
12:m:93:VAL:HG22	12:m:94:ALA:N	2.29	0.47
20:u:42:LYS:HB3	20:u:57:ILE:HD11	1.96	0.47
27:C:22:THR:OG1	27:C:23:THR:N	2.48	0.47
30:F:16:ILE:HG21	53:1:1032:A:O3'	2.15	0.47
52:3:166:U:H2'	52:3:167:A:H8	1.80	0.47
52:3:212:G:H2'	52:3:213:G:H8	1.79	0.47
52:3:893:C:H2'	52:3:894:G:C8	2.49	0.47
52:3:990:C:H2'	52:3:991:U:O4'	2.14	0.47
52:3:1005:A:H2'	52:3:1006:G:H5'	1.96	0.47
52:3:1033:G:H2'	52:3:1034:G:C5'	2.34	0.47
52:3:1054:C:H42	56:4:22:A:H2	1.63	0.47
52:3:1259:C:C3'	52:3:1260:G:H5''	2.30	0.47
53:1:26:G:O2'	53:1:27:G:H5'	2.15	0.47
53:1:596:U:H2'	53:1:597:G:C8	2.49	0.47
53:1:859:G:O2'	53:1:860:U:C6	2.67	0.47
53:1:1936:A:H3'	53:1:1937:A:H5'	1.97	0.47
53:1:2834:G:O2'	53:1:2835:A:H5'	2.15	0.47
4:e:3:LEU:HA	4:e:6:TYR:HB3	1.96	0.47
7:h:118:ILE:N	7:h:119:PRO:CD	2.77	0.47
17:r:35:PHE:HB2	17:r:59:ILE:HB	1.96	0.47
18:s:11:ARG:HH21	18:s:98:LYS:HD2	1.80	0.47
19:t:50:LEU:HD12	19:t:50:LEU:N	2.30	0.47
38:N:78:ILE:O	38:N:82:ILE:HG12	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:514:C:H2'	52:3:515:G:C8	2.49	0.47
53:1:1183:U:H2'	53:1:1184:U:C6	2.49	0.47
53:1:1229:C:H2'	53:1:1230:A:C8	2.50	0.47
53:1:1444:G:H2'	53:1:1445:G:C8	2.49	0.47
53:1:1794:A:H2'	53:1:1795:C:C6	2.49	0.47
53:1:2121:G:H2'	53:1:2122:U:O4'	2.14	0.47
58:8:256:CYS:SG	58:8:277:VAL:HG13	2.55	0.47
13:n:79:LEU:HD23	13:n:83:LEU:HB2	1.97	0.46
21:v:21:ARG:HA	21:v:25:LYS:O	2.16	0.46
30:F:4:ARG:HG3	30:F:4:ARG:HH11	1.80	0.46
31:G:160:LEU:CD2	31:G:162:VAL:HG22	2.46	0.46
33:I:112:GLU:HB3	52:3:408:A:H5'	1.98	0.46
33:I:131:ILE:HG21	52:3:620:C:O2	2.14	0.46
40:P:124:LYS:NZ	52:3:1524:C:OP2	2.40	0.46
47:W:59:LYS:HD3	52:3:734:G:O2'	2.14	0.46
53:1:406:G:H2'	53:1:407:G:C8	2.50	0.46
53:1:753:A:H2'	53:1:754:U:C6	2.50	0.46
3:d:148:ILE:HD13	3:d:187:VAL:HG21	1.96	0.46
3:d:148:ILE:HD13	3:d:187:VAL:CG2	2.46	0.46
7:h:35:VAL:HA	7:h:38:MET:HE3	1.96	0.46
9:j:85:LYS:HD2	53:1:2641:G:OP1	2.15	0.46
22:w:37:ARG:HA	22:w:37:ARG:HH11	1.80	0.46
29:E:22:LYS:HA	29:E:47:ALA:O	2.16	0.46
30:F:37:GLN:CG	30:F:38:GLY:N	2.76	0.46
37:M:9:MET:HG2	37:M:26:MET:SD	2.55	0.46
37:M:33:VAL:HG22	37:M:58:LEU:HD21	1.97	0.46
42:R:57:ASP:O	42:R:61:LYS:NZ	2.46	0.46
53:1:864:G:O2'	53:1:865:C:H5'	2.15	0.46
53:1:1051:G:H4'	53:1:2752:C:H1'	1.97	0.46
55:6:41:C:H2'	55:6:42:G:C8	2.50	0.46
1:b:229:HIS:CG	1:b:230:PRO:HD2	2.50	0.46
4:e:110:ILE:O	4:e:113:PHE:HB2	2.15	0.46
10:k:24:VAL:HG23	10:k:33:ALA:HB2	1.97	0.46
31:G:49:PHE:O	31:G:53:LEU:HD23	2.14	0.46
33:I:187:ARG:HH12	33:I:192:ALA:HA	1.80	0.46
37:M:5:PRO:HB2	37:M:32:LYS:HE3	1.97	0.46
40:P:124:LYS:HB2	50:Z:34:ARG:HH11	1.81	0.46
48:X:79:TYR:O	48:X:80:ARG:C	2.59	0.46
52:3:513:C:H2'	52:3:514:C:C6	2.50	0.46
52:3:920:U:H2'	52:3:921:U:C6	2.50	0.46
52:3:924:C:H2'	52:3:925:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1123:U:O2'	52:3:1124:G:H5'	2.16	0.46
53:1:481:G:H1'	53:1:506:G:N2	2.31	0.46
53:1:1499:C:H2'	53:1:1500:G:H8	1.80	0.46
58:8:17:THR:HG23	58:8:79:HIS:HE1	1.80	0.46
4:e:88:VAL:HA	54:2:42:C:O2	2.16	0.46
7:h:94:ARG:HH21	7:h:131:THR:HG22	1.80	0.46
10:k:58:LEU:N	10:k:58:LEU:HD23	2.31	0.46
11:l:128:THR:HG22	53:1:636:G:OP2	2.15	0.46
22:w:22:PHE:CD2	53:1:922:C:H1'	2.51	0.46
25:z:12:ALA:O	25:z:20:LYS:NZ	2.49	0.46
32:H:113:LYS:NZ	32:H:185:THR:O	2.48	0.46
36:L:83:THR:OG1	55:6:33:U:H4'	2.14	0.46
43:S:50:LEU:HD12	43:S:51:PRO:CD	2.42	0.46
48:X:54:ARG:HB3	52:3:958:A:C2	2.50	0.46
52:3:328:C:H5'	52:3:329:A:H5'	1.97	0.46
53:1:1055:G:H2'	53:1:1056:G:O4'	2.15	0.46
53:1:1087:G:N2	53:1:1103:A:H1'	2.30	0.46
53:1:2285:C:H2'	53:1:2286:G:H5'	1.97	0.46
55:5:16:C:O2'	55:5:17:C:H5'	2.16	0.46
55:6:34:C:O2	55:6:34:C:C2'	2.62	0.46
6:g:59:ALA:O	6:g:62:LEU:HG	2.15	0.46
6:g:115:VAL:HG13	6:g:132:PHE:HE1	1.81	0.46
10:k:76:VAL:HG12	15:p:72:VAL:HG12	1.97	0.46
27:C:36:LYS:HG2	27:C:47:ILE:HG23	1.96	0.46
30:F:11:CYS:HG	30:F:14:CYS:HG	1.64	0.46
31:G:27:LYS:HB3	31:G:28:PRO:HD3	1.96	0.46
43:S:4:SER:O	43:S:8:ARG:HG3	2.15	0.46
52:3:86:G:H4'	52:3:87:C:C6	2.50	0.46
52:3:350:G:H2'	52:3:351:G:C8	2.51	0.46
52:3:1064:G:H1'	52:3:1190:G:N2	2.30	0.46
53:1:537:G:H22	53:1:555:G:H2'	1.80	0.46
53:1:2317:A:H2'	53:1:2318:G:O4'	2.15	0.46
53:1:2364:C:H2'	53:1:2365:G:O4'	2.14	0.46
53:1:2492:U:H2'	53:1:2493:U:C6	2.51	0.46
7:h:59:LEU:HB3	7:h:62:ARG:CB	2.45	0.46
11:l:126:ARG:HH21	11:l:126:ARG:HB2	1.81	0.46
12:m:128:THR:OG1	12:m:129:THR:N	2.48	0.46
18:s:80:PRO:O	18:s:100:THR:HG22	2.15	0.46
27:C:46:VAL:HG12	27:C:47:ILE:N	2.29	0.46
31:G:20:ARG:HG3	52:3:831:A:H5'	1.98	0.46
31:G:207:ARG:O	31:G:211:LEU:HD23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M:29:SER:OG	37:M:32:LYS:HG2	2.15	0.46
39:O:18:ILE:HA	39:O:21:ALA:HB3	1.96	0.46
40:P:12:ARG:HD3	40:P:12:ARG:N	2.30	0.46
41:Q:43:LYS:HB3	41:Q:44:PRO:CD	2.46	0.46
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.98	0.46
44:T:61:GLN:O	44:T:65:LEU:HD23	2.16	0.46
52:3:1033:G:C3'	52:3:1034:G:H5''	2.46	0.46
52:3:1499:A:O2'	52:3:1520:C:H5'	2.16	0.46
53:1:937:C:H2'	53:1:938:G:H8	1.79	0.46
53:1:1001:A:H2'	53:1:1002:G:O4'	2.16	0.46
53:1:1817:G:N2	53:1:1818:U:H1'	2.31	0.46
53:1:2699:C:H2'	53:1:2700:A:H8	1.80	0.46
13:n:103:ARG:HB3	13:n:108:ALA:H	1.81	0.46
15:p:3:ILE:H	15:p:3:ILE:HD12	1.80	0.46
25:z:29:ARG:HH11	53:1:930:G:H5''	1.81	0.46
49:Y:31:ILE:HG22	49:Y:35:TYR:CE2	2.50	0.46
52:3:428:G:H4'	52:3:429:U:O5'	2.16	0.46
52:3:1346:A:C2'	52:3:1347:G:H4'	2.46	0.46
53:1:406:G:H2'	53:1:407:G:H8	1.79	0.46
53:1:996:A:H2'	53:1:997:G:H8	1.80	0.46
53:1:1524:G:H2'	53:1:1525:A:H8	1.81	0.46
53:1:2197:U:O2'	53:1:2198:A:H5''	2.16	0.46
53:1:2623:G:H2'	53:1:2624:G:C8	2.50	0.46
53:1:2639:A:H2'	53:1:2640:G:O4'	2.16	0.46
1:b:100:ARG:HH22	53:1:1500:G:H4'	1.81	0.46
7:h:88:HIS:HB2	7:h:89:PRO:CD	2.43	0.46
13:n:31:HIS:CD2	53:1:1279:G:H4'	2.51	0.46
31:G:209:VAL:O	31:G:213:LEU:HD13	2.15	0.46
34:J:40:ASP:OD1	34:J:44:ARG:N	2.48	0.46
35:K:36:ILE:HG23	35:K:64:VAL:HG12	1.96	0.46
36:L:111:GLY:HA2	36:L:118:ARG:CD	2.44	0.46
38:N:27:ILE:N	38:N:27:ILE:HD12	2.31	0.46
41:Q:109:ARG:HH22	41:Q:112:ALA:HB3	1.80	0.46
45:U:68:SER:OG	45:U:71:VAL:HG22	2.16	0.46
50:Z:17:ARG:HG3	50:Z:20:ARG:HD2	1.98	0.46
50:Z:32:ARG:HG3	50:Z:33:ARG:HG2	1.98	0.46
52:3:407:U:H2'	52:3:408:A:H8	1.80	0.46
52:3:1318:A:H2'	52:3:1319:A:H5'	1.98	0.46
52:3:1333:A:H2'	52:3:1334:G:O4'	2.14	0.46
53:1:2743:U:H2'	53:1:2744:G:C4'	2.46	0.46
54:2:65:U:H3'	54:2:108:A:N6	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:43:A:H2'	55:5:44:A:C8	2.50	0.46
4:e:74:ALA:HB2	55:5:57:A:H5'	1.96	0.46
8:i:18:ASN:HD21	8:i:35:MET:HE2	1.81	0.46
14:o:33:ARG:HG2	14:o:34:HIS:CD2	2.50	0.46
21:v:6:ALA:HB1	21:v:40:ILE:CG2	2.46	0.46
32:H:156:LEU:HD12	32:H:156:LEU:O	2.16	0.46
37:M:28:SER:OG	37:M:58:LEU:HG	2.16	0.46
40:P:52:ARG:NH2	40:P:56:LYS:HD3	2.31	0.46
41:Q:32:VAL:HA	41:Q:78:VAL:HG22	1.98	0.46
42:R:16:ILE:HD11	52:3:1302:C:OP2	2.16	0.46
42:R:90:HIS:CD2	42:R:96:VAL:HG21	2.51	0.46
44:T:13:GLU:HG2	44:T:83:ARG:NH2	2.29	0.46
52:3:220:G:O2'	52:3:221:C:H5'	2.16	0.46
52:3:422:C:H5'	52:3:423:G:N3	2.31	0.46
52:3:483:C:H2'	52:3:484:G:C8	2.50	0.46
53:1:325:G:H2'	53:1:326:G:C8	2.51	0.46
53:1:635:C:H2'	53:1:636:G:C8	2.51	0.46
53:1:1019:U:H3	53:1:1142:A:N6	2.14	0.46
53:1:1214:A:H2'	53:1:1215:G:O4'	2.16	0.46
53:1:2658:C:H2'	53:1:2659:G:O4'	2.15	0.46
57:7:76:A:O2'	60:7:101:PHE:C	2.58	0.46
1:b:71:ASP:OD2	1:b:188:ARG:NH2	2.49	0.46
1:b:95:TYR:CE2	1:b:101:ARG:HD2	2.46	0.46
3:d:1:MET:HB3	3:d:14:VAL:HG23	1.97	0.46
7:h:118:ILE:HG22	7:h:119:PRO:CD	2.45	0.46
8:i:76:ALA:O	8:i:79:LEU:HG	2.16	0.46
8:i:105:LEU:HA	8:i:108:ILE:HD11	1.98	0.46
16:q:57:ARG:NH1	53:1:1154:G:OP2	2.46	0.46
33:I:12:ARG:HD3	33:I:31:CYS:SG	2.55	0.46
37:M:11:THR:HG21	52:3:876:C:H1'	1.98	0.46
39:O:29:ALA:O	39:O:33:GLY:CA	2.64	0.46
39:O:32:THR:O	39:O:83:THR:OG1	2.31	0.46
52:3:321:A:O2'	52:3:322:C:H5'	2.15	0.46
52:3:529:G:H5'	52:3:533:A:N3	2.31	0.46
52:3:1106:G:H2'	52:3:1107:C:C6	2.51	0.46
52:3:1256:A:H1'	52:3:1258:G:C8	2.51	0.46
53:1:609:A:H2'	53:1:610:C:O4'	2.16	0.46
53:1:1023:U:H4'	53:1:1123:C:OP1	2.16	0.46
53:1:1605:C:H2'	53:1:1606:C:H5'	1.96	0.46
53:1:2693:G:O2'	53:1:2694:G:H5'	2.16	0.46
1:b:16:VAL:HB	1:b:203:VAL:HG12	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:4:LEU:HD23	2:c:32:ASN:HD22	1.80	0.45
3:d:149:ILE:HD13	3:d:170:ARG:HB2	1.98	0.45
4:e:150:GLY:C	4:e:151:LEU:HD12	2.41	0.45
6:g:81:ALA:HB1	6:g:149:GLU:HB2	1.98	0.45
11:l:126:ARG:HB2	11:l:126:ARG:NH2	2.31	0.45
24:y:37:LEU:HD23	24:y:37:LEU:C	2.41	0.45
35:K:11:HIS:CD2	35:K:12:PRO:HD2	2.51	0.45
43:S:52:ARG:HD2	52:3:1317:C:C4	2.51	0.45
53:1:275:C:H3'	53:1:276:U:H5''	1.98	0.45
53:1:677:A:O2'	53:1:2071:A:H5'	2.17	0.45
53:1:947:A:H2'	53:1:948:C:C6	2.51	0.45
53:1:2285:C:O2'	53:1:2287:A:H1'	2.15	0.45
55:5:44:A:H2'	55:5:45:G:O4'	2.17	0.45
55:5:47:U:H3'	55:5:48:C:C5'	2.46	0.45
57:7:76:A:H3'	58:8:263:ARG:HH11	1.80	0.45
58:8:261:MET:HG2	58:8:262:PHE:CD2	2.51	0.45
12:m:38:ARG:NH2	54:2:90:C:O3'	2.49	0.45
12:m:40:ARG:NH2	53:1:958:U:H5	2.13	0.45
29:E:57:VAL:HA	29:E:60:CYS:SG	2.55	0.45
30:F:6:SER:HB3	53:1:2466:C:H5''	1.97	0.45
32:H:171:ARG:HH21	32:H:202:PHE:HE2	1.63	0.45
35:K:3:HIS:HB2	35:K:92:THR:HA	1.98	0.45
36:L:35:LYS:O	36:L:39:GLU:HG3	2.16	0.45
40:P:92:ARG:NH2	40:P:111:ASP:OD2	2.50	0.45
53:1:729:G:H4'	53:1:763:G:H5'	1.98	0.45
53:1:1331:G:O2'	53:1:1332:G:H5''	2.17	0.45
53:1:1352:U:O2'	53:1:1353:A:H5'	2.16	0.45
60:7:101:PHE:HD1	58:8:229:THR:HG21	1.81	0.45
58:8:193:ALA:HA	58:8:196:LEU:HB2	1.97	0.45
1:b:224:MET:SD	1:b:229:HIS:HB2	2.57	0.45
3:d:79:ARG:NH2	53:1:448:U:O4'	2.44	0.45
5:f:85:LYS:HB2	5:f:164:ALA:HB2	1.99	0.45
6:g:118:PRO:HG2	6:g:130:VAL:HA	1.97	0.45
7:h:33:VAL:HG12	7:h:34:THR:N	2.30	0.45
34:J:129:SER:OG	52:3:20:U:OP2	2.32	0.45
36:L:55:LYS:HE3	36:L:59:GLU:OE2	2.17	0.45
36:L:67:ASN:HB3	36:L:129:ASN:HB3	1.98	0.45
36:L:69:ARG:HG3	36:L:95:ARG:HG2	1.99	0.45
37:M:72:GLU:HB2	37:M:129:ALA:OXT	2.17	0.45
49:Y:55:PRO:HA	52:3:193:C:O2'	2.16	0.45
52:3:684:U:H2'	52:3:685:G:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:952:U:H5'	52:3:972:C:N4	2.32	0.45
52:3:1158:C:H3'	52:3:1158:C:O2	2.17	0.45
53:1:192:C:H2'	53:1:193:U:H5'	1.98	0.45
53:1:2875:C:H2'	53:1:2876:G:C8	2.52	0.45
54:2:19:C:H2'	54:2:20:G:H8	1.81	0.45
54:2:56:G:H4'	54:2:57:A:H8	1.81	0.45
58:8:75:ARG:HH22	58:8:201:PRO:HA	1.81	0.45
58:8:103:ILE:HD11	58:8:196:LEU:HD21	1.99	0.45
1:b:207:ALA:HB2	53:1:1790:C:O2'	2.16	0.45
5:f:41:GLU:HA	5:f:54:ARG:HH21	1.81	0.45
5:f:128:THR:HG23	5:f:129:GLU:OE2	2.16	0.45
12:m:45:GLN:HG2	53:1:2485:G:H5'	1.99	0.45
26:B:54:ILE:HG23	26:B:56:LYS:HB3	1.97	0.45
33:I:80:ARG:HE	52:3:613:C:P	2.39	0.45
33:I:123:MET:HB2	33:I:128:VAL:HG22	1.98	0.45
39:O:72:ARG:NH2	52:3:1151:A:O2'	2.49	0.45
52:3:1282:C:H2'	52:3:1283:U:C6	2.51	0.45
53:1:873:C:H2'	53:1:874:G:C8	2.51	0.45
53:1:1550:C:H2'	53:1:1551:A:C8	2.52	0.45
53:1:1587:G:H2'	53:1:1588:G:H8	1.81	0.45
53:1:2314:A:H2'	53:1:2315:G:C8	2.50	0.45
53:1:2373:G:H2'	53:1:2374:C:C6	2.51	0.45
58:8:246:VAL:O	58:8:292:VAL:HG12	2.17	0.45
2:c:11:MET:O	53:1:2682:A:H5'	2.17	0.45
11:l:30:THR:O	11:l:32:GLY:N	2.50	0.45
12:m:30:SER:HA	12:m:133:LYS:HB2	1.99	0.45
35:K:47:LEU:HB3	47:W:65:SER:OG	2.15	0.45
51:a:38:PHE:CD1	53:1:2127:G:H4'	2.51	0.45
52:3:790:A:H5'	55:5:39:C:H5'	1.99	0.45
52:3:1484:C:H2'	52:3:1485:U:C6	2.51	0.45
53:1:749:A:H2'	53:1:750:A:H8	1.81	0.45
53:1:1772:A:C2'	53:1:1773:A:H5'	2.47	0.45
53:1:2297:A:H62	53:1:2319:G:H1'	1.80	0.45
53:1:2333:A:H5'	53:1:2335:A:H1'	1.98	0.45
54:2:78:A:H2'	54:2:79:G:O4'	2.16	0.45
58:8:212:LEU:HB3	58:8:234:ARG:HG2	1.98	0.45
3:d:68:ALA:HA	53:1:1255:U:C6	2.51	0.45
3:d:117:ARG:HH12	11:l:2:ARG:HG2	1.82	0.45
5:f:167:VAL:HB	5:f:169:ARG:HH12	1.81	0.45
7:h:31:ARG:HH21	7:h:107:GLU:HA	1.82	0.45
10:k:40:LYS:HZ3	10:k:89:ASN:ND2	2.13	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:51:LYS:HD3	10:k:95:ILE:HG22	1.98	0.45
13:n:39:PRO:HG2	53:1:1651:G:H4'	1.98	0.45
21:v:19:ARG:NH2	54:2:95:U:OP2	2.50	0.45
21:v:44:HIS:NE2	21:v:48:MET:SD	2.90	0.45
24:y:12:GLU:O	24:y:15:ASN:HB3	2.17	0.45
31:G:166:ASP:HB3	31:G:190:SER:HB2	1.99	0.45
35:K:51:ILE:O	35:K:52:ASN:HB2	2.17	0.45
41:Q:109:ARG:C	41:Q:110:LYS:HD2	2.41	0.45
52:3:162:A:H2'	52:3:163:C:O4'	2.16	0.45
52:3:1015:G:O2'	52:3:1016:A:H5'	2.17	0.45
53:1:1542:U:H2'	53:1:1543:G:O4'	2.17	0.45
53:1:1825:U:H2'	53:1:1826:G:H8	1.81	0.45
53:1:2318:G:H2'	53:1:2319:G:O4'	2.16	0.45
57:7:5:G:H2'	57:7:6:G:C8	2.51	0.45
6:g:11:ASN:HD22	6:g:12:LEU:HD22	1.82	0.45
7:h:3:LEU:HD23	7:h:3:LEU:N	2.31	0.45
8:i:133:ARG:NH1	53:1:1077:A:O2'	2.50	0.45
15:p:31:VAL:HG21	15:p:40:GLN:NE2	2.31	0.45
17:r:58:VAL:H	17:r:102:SER:HG	1.62	0.45
30:F:19:ARG:HG2	53:1:2756:U:H5''	1.98	0.45
34:J:86:GLY:O	34:J:138:ALA:HB1	2.16	0.45
36:L:119:LEU:HD23	36:L:123:LEU:HD23	1.99	0.45
38:N:45:MET:O	38:N:49:GLN:HG3	2.16	0.45
39:O:17:LEU:HD23	39:O:17:LEU:O	2.17	0.45
41:Q:77:SER:HB2	41:Q:102:ASP:HB3	1.98	0.45
45:U:48:GLU:HG3	45:U:49:GLY:H	1.82	0.45
51:a:6:LYS:HG3	51:a:7:ARG:H	1.82	0.45
52:3:514:C:H2'	52:3:515:G:H8	1.82	0.45
52:3:576:C:OP2	52:3:577:G:H5''	2.17	0.45
52:3:1005:A:C2'	52:3:1006:G:H5'	2.47	0.45
52:3:1202:U:H2'	52:3:1203:C:H5'	1.97	0.45
53:1:74:A:H4'	53:1:75:G:O5'	2.16	0.45
53:1:145:C:H2'	53:1:146:A:H8	1.82	0.45
53:1:1179:G:N7	53:1:1180:U:H1'	2.32	0.45
53:1:2609:U:O2'	53:1:2610:C:H5'	2.15	0.45
53:1:2785:C:O2'	53:1:2786:U:H5'	2.15	0.45
58:8:21:VAL:HG13	58:8:84:GLY:O	2.16	0.45
58:8:107:ALA:HB1	58:8:137:LYS:HD2	1.98	0.45
3:d:69:ARG:HG3	53:1:1255:U:H5	1.82	0.45
4:e:91:ARG:NH1	54:2:45:A:C4	2.85	0.45
9:j:72:LYS:NZ	53:1:1139:G:OP2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:70:ARG:HH22	10:k:74:GLY:HA2	1.80	0.45
24:y:58:ASN:ND2	53:1:111:A:O2'	2.43	0.45
26:B:4:GLN:O	53:1:2017:U:H4'	2.17	0.45
26:B:42:ILE:HG22	26:B:48:TYR:HB2	1.99	0.45
34:J:107:GLY:HA2	52:3:8:A:C1'	2.47	0.45
39:O:6:ILE:HB	39:O:76:ILE:CG2	2.41	0.45
43:S:5:MET:HE3	43:S:8:ARG:HB2	1.99	0.45
52:3:1173:U:H2'	52:3:1174:G:C8	2.52	0.45
53:1:255:A:H2'	53:1:256:A:O4'	2.17	0.45
53:1:1539:U:H2'	53:1:1540:G:H8	1.82	0.45
53:1:1565:C:O2'	53:1:1566:A:H2'	2.17	0.45
53:1:1918:A:H2	53:1:1919:A:H62	1.65	0.45
53:1:2190:G:H2'	53:1:2191:A:H8	1.82	0.45
53:1:2328:A:H2'	53:1:2329:U:C6	2.51	0.45
53:1:2818:U:H2'	53:1:2819:G:H8	1.81	0.45
53:1:2898:U:H2'	53:1:2899:A:H8	1.82	0.45
54:2:35:C:C2'	54:2:36:C:H5'	2.46	0.45
57:7:47:U:H2'	57:7:50:U:OP1	2.17	0.45
58:8:157:LEU:O	58:8:160:GLN:NE2	2.46	0.45
4:e:168:LEU:HD23	4:e:168:LEU:C	2.42	0.45
8:i:74:PRO:HG3	53:1:1060:U:OP2	2.17	0.45
24:y:2:LYS:HE2	53:1:77:G:C5'	2.47	0.45
32:H:37:LYS:HA	32:H:40:GLN:HG2	1.98	0.45
39:O:30:LYS:HG3	39:O:31:ARG:N	2.32	0.45
44:T:59:VAL:CG2	53:1:715:A:H5'	2.47	0.45
47:W:36:GLY:O	47:W:62:ARG:NH2	2.48	0.45
53:1:290:U:H2'	53:1:291:G:H8	1.82	0.45
53:1:395:U:H2'	53:1:396:G:H8	1.82	0.45
53:1:873:C:H2'	53:1:874:G:H8	1.82	0.45
53:1:1889:A:H2'	53:1:1890:A:C8	2.52	0.45
53:1:1994:C:O2'	53:1:1995:U:H5'	2.15	0.45
53:1:2747:G:O6	53:1:2755:C:H5''	2.17	0.45
57:7:36:A:O2'	57:7:37:A:H5'	2.17	0.45
10:k:40:LYS:NZ	10:k:89:ASN:ND2	2.64	0.45
29:E:34:LYS:HE2	29:E:34:LYS:HB3	1.79	0.45
39:O:59:LYS:NZ	52:3:973:G:OP1	2.38	0.45
52:3:89:U:H2'	52:3:90:C:O4'	2.17	0.45
52:3:272:C:H2'	52:3:273:U:C6	2.52	0.45
52:3:438:U:O2'	52:3:439:U:H6	1.99	0.45
52:3:521:G:O2'	52:3:522:C:H5'	2.17	0.45
52:3:556:C:H2'	52:3:557:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:981:U:H2'	52:3:982:U:C5	2.52	0.45
52:3:1171:A:H2'	52:3:1172:C:C6	2.52	0.45
53:1:458:G:O2'	53:1:459:U:C5	2.67	0.45
53:1:558:U:H2'	53:1:559:G:C8	2.52	0.45
53:1:1101:U:H2'	53:1:1102:C:H6	1.81	0.45
53:1:1355:G:H2'	53:1:1356:G:H8	1.82	0.45
3:d:111:GLU:HA	3:d:114:ARG:HE	1.82	0.44
8:i:16:MET:HE1	8:i:19:PRO:HA	1.97	0.44
16:q:50:ARG:O	16:q:54:ARG:HG3	2.17	0.44
16:q:80:ASN:OD1	53:1:1151:A:H4'	2.17	0.44
16:q:102:LYS:O	16:q:105:PHE:HB3	2.17	0.44
22:w:51:ARG:HB2	53:1:2365:G:P	2.58	0.44
22:w:51:ARG:NH2	53:1:2384:U:OP2	2.50	0.44
22:w:52:ASP:OD1	53:1:2386:A:O2'	2.34	0.44
30:F:3:VAL:HG11	53:1:2539:C:H5'	1.99	0.44
31:G:213:LEU:HA	31:G:216:VAL:HG12	1.98	0.44
35:K:15:SER:OG	35:K:16:GLU:OE1	2.34	0.44
52:3:824:G:H2'	52:3:825:A:C8	2.48	0.44
58:8:270:ARG:HD3	58:8:270:ARG:N	2.32	0.44
9:j:36:LEU:O	9:j:51:GLY:HA3	2.17	0.44
12:m:50:ARG:HA	12:m:53:MET:HE2	1.98	0.44
12:m:54:THR:HA	12:m:57:VAL:HG12	1.97	0.44
13:n:18:GLN:HE21	13:n:22:ARG:NH1	2.15	0.44
15:p:50:ARG:HB2	15:p:52:ARG:HH12	1.82	0.44
16:q:25:GLY:O	16:q:29:ARG:NH1	2.48	0.44
23:x:66:VAL:O	23:x:69:GLU:HB3	2.17	0.44
28:D:37:LYS:HG2	53:1:458:G:C8	2.52	0.44
40:P:121:ARG:O	52:3:779:C:H5'	2.17	0.44
41:Q:9:LYS:HD3	41:Q:10:PRO:O	2.17	0.44
43:S:26:LEU:HD13	43:S:47:LEU:HD13	2.00	0.44
47:W:11:ARG:HD2	52:3:845:A:O4'	2.16	0.44
49:Y:59:ARG:NH2	52:3:178:C:OP2	2.51	0.44
51:a:164:ARG:NH1	51:a:164:ARG:HB3	2.33	0.44
51:a:180:PHE:HB2	51:a:185:LEU:HG	1.99	0.44
52:3:1128:C:O2'	52:3:1129:C:H5'	2.17	0.44
52:3:1148:U:H2'	52:3:1149:C:O4'	2.17	0.44
52:3:1225:A:H2'	52:3:1225:A:N3	2.32	0.44
53:1:922:C:H2'	53:1:923:G:H8	1.82	0.44
53:1:1071:G:H1'	53:1:1089:A:C5	2.52	0.44
53:1:1348:C:H2'	53:1:1349:C:H5'	1.99	0.44
53:1:1435:G:H2'	53:1:1436:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1911:U:H2'	53:1:1918:A:N1	2.31	0.44
1:b:83:ASP:HB2	1:b:90:ILE:HD13	2.00	0.44
2:c:3:GLY:C	2:c:4:LEU:HD12	2.43	0.44
10:k:15:GLY:HA2	10:k:47:ILE:HD11	1.99	0.44
18:s:47:VAL:HG12	18:s:103:ILE:HG21	1.99	0.44
18:s:73:LYS:HB2	18:s:106:VAL:HB	1.98	0.44
19:t:61:LEU:N	19:t:61:LEU:HD23	2.33	0.44
29:E:37:THR:HG21	53:1:2348:U:OP2	2.18	0.44
31:G:129:THR:OG1	31:G:132:GLU:OE1	2.34	0.44
36:L:63:VAL:O	36:L:67:ASN:ND2	2.51	0.44
40:P:86:LYS:HE3	52:3:707:U:OP1	2.18	0.44
45:U:76:LYS:HA	45:U:80:LYS:HZ1	1.80	0.44
51:a:62:ALA:HA	51:a:162:ARG:HA	2.00	0.44
52:3:418:C:H2'	52:3:419:C:C6	2.52	0.44
52:3:1539:C:O2'	52:3:1540:U:H5'	2.17	0.44
53:1:141:G:H3'	53:1:142:A:O4'	2.17	0.44
53:1:248:G:N3	53:1:2431:U:H4'	2.32	0.44
53:1:1437:C:H2'	53:1:1438:U:C6	2.51	0.44
53:1:1526:C:H2'	53:1:1527:G:O4'	2.18	0.44
53:1:2197:U:H1'	53:1:2198:A:C8	2.52	0.44
58:8:318:GLY:HA2	58:8:384:VAL:HA	2.00	0.44
4:e:40:GLY:HA2	4:e:84:ILE:CD1	2.48	0.44
7:h:58:THR:HG23	53:1:1107:G:H5'	1.99	0.44
12:m:109:PRO:HD2	12:m:112:LEU:HD13	2.00	0.44
17:r:76:LYS:HB2	17:r:85:LYS:HB3	1.98	0.44
28:D:39:ARG:NH2	53:1:469:G:O6	2.50	0.44
31:G:91:VAL:HG11	31:G:99:MET:HE1	1.98	0.44
35:K:61:LEU:HD23	35:K:62:MET:N	2.32	0.44
38:N:68:GLY:HA2	52:3:1250:A:H4'	2.00	0.44
51:a:48:LEU:HD23	51:a:50:ILE:HD13	2.00	0.44
51:a:54:LYS:HD3	51:a:57:GLN:HE21	1.79	0.44
51:a:221:GLY:N	53:1:2176:A:H5''	2.33	0.44
52:3:211:G:H3'	52:3:211:G:N3	2.32	0.44
52:3:230:G:H2'	52:3:231:U:C6	2.52	0.44
52:3:1414:U:H2'	52:3:1415:G:H8	1.83	0.44
52:3:1473:G:O2'	52:3:1474:U:H5'	2.16	0.44
53:1:687:C:H6	53:1:687:C:H5'	1.83	0.44
53:1:737:C:O2'	53:1:738:G:H5'	2.17	0.44
53:1:940:G:H2'	53:1:941:A:H5''	1.98	0.44
53:1:990:A:H1'	53:1:1156:A:N3	2.32	0.44
55:6:17:C:H2'	55:6:17(A):U:H5	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:8:LYS:O	6:g:9:VAL:O	2.35	0.44
6:g:12:LEU:HG	6:g:13:GLY:H	1.82	0.44
6:g:31:VAL:HG13	6:g:32:PRO:CD	2.46	0.44
9:j:136:GLN:N	9:j:137:PRO:HD3	2.32	0.44
15:p:3:ILE:HD12	15:p:3:ILE:N	2.32	0.44
23:x:37:PHE:CZ	23:x:50:VAL:HG11	2.53	0.44
27:C:49:LYS:HD3	27:C:50:GLU:N	2.31	0.44
33:I:170:LEU:HD12	33:I:170:LEU:O	2.17	0.44
36:L:4:ARG:HH12	52:3:933:G:P	2.40	0.44
37:M:11:THR:HG22	37:M:14:ARG:HH12	1.81	0.44
45:U:33:ILE:N	45:U:33:ILE:HD12	2.32	0.44
52:3:767:A:H2'	52:3:768:A:C8	2.53	0.44
53:1:37:C:H4'	53:1:451:U:OP1	2.17	0.44
53:1:118:A:OP2	53:1:119:A:H5''	2.17	0.44
53:1:305:C:H2'	53:1:306:U:C6	2.52	0.44
53:1:548:G:H2'	53:1:549:G:O4'	2.17	0.44
53:1:1594:U:H2'	53:1:1595:C:C6	2.52	0.44
54:2:28:C:H2'	54:2:29:A:C8	2.52	0.44
1:b:221:GLY:H	53:1:1826:G:P	2.40	0.44
7:h:61:ARG:HD3	53:1:1045:C:O3'	2.18	0.44
9:j:72:LYS:HZ1	53:1:1139:G:P	2.40	0.44
10:k:38:ILE:N	10:k:38:ILE:HD12	2.32	0.44
23:x:56:ARG:HB3	53:1:372:G:N7	2.32	0.44
24:y:44:LYS:O	24:y:48:ARG:HG2	2.17	0.44
33:I:124:VAL:HG13	33:I:142:VAL:HG12	1.99	0.44
52:3:252:U:O2	52:3:252:U:H2'	2.17	0.44
52:3:751:U:H2'	52:3:752:G:H5'	2.00	0.44
52:3:1219:A:H2'	52:3:1220:G:H8	1.82	0.44
52:3:1413:A:H2	52:3:1487:G:H22	1.66	0.44
53:1:288:U:H2'	53:1:289:G:C8	2.52	0.44
53:1:543:G:H2'	53:1:544:C:O4'	2.18	0.44
53:1:759:G:H2'	53:1:760:G:H8	1.83	0.44
53:1:1275:A:N6	53:1:1296:G:H4'	2.33	0.44
53:1:1335:C:H2'	53:1:1336:A:C8	2.53	0.44
54:2:30:C:H2'	54:2:31:C:O4'	2.18	0.44
58:8:378:ARG:HA	58:8:383:THR:HA	1.99	0.44
3:d:126:VAL:HG13	3:d:156:ASN:OD1	2.17	0.44
14:o:7:ARG:HA	14:o:10:ARG:NH2	2.33	0.44
23:x:11:PRO:HG3	23:x:30:PRO:HD2	2.00	0.44
23:x:55:MET:HE1	53:1:2091:C:H4'	1.99	0.44
32:H:4:VAL:HB	52:3:1190:G:OP2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:173:PRO:HB2	32:H:176:THR:CG2	2.48	0.44
36:L:49:LEU:HD13	36:L:123:LEU:HB3	1.99	0.44
37:M:77:VAL:HG21	37:M:127:TYR:CD1	2.52	0.44
38:N:11:ARG:HA	38:N:105:ARG:HH12	1.83	0.44
38:N:112:ARG:HE	43:S:100:TRP:NE1	2.16	0.44
39:O:37:ARG:HH22	52:3:1125:U:C5'	2.27	0.44
40:P:120:CYS:HB3	52:3:778:G:O2'	2.18	0.44
42:R:48:SER:O	42:R:52:ILE:HG13	2.18	0.44
43:S:16:ALA:HA	43:S:54:SER:OG	2.18	0.44
46:V:74:LEU:HD23	46:V:75:VAL:N	2.31	0.44
50:Z:18:PHE:O	50:Z:21:SER:OG	2.29	0.44
52:3:556:C:H2'	52:3:557:G:H8	1.82	0.44
52:3:730:G:H2'	52:3:731:G:C5'	2.43	0.44
52:3:1283:U:O2'	52:3:1284:C:H5'	2.17	0.44
53:1:779:U:H2'	53:1:780:G:C8	2.53	0.44
53:1:2576:G:H3'	53:1:2576:G:N3	2.33	0.44
3:d:55:SER:OG	3:d:56:GLY:N	2.51	0.44
11:l:3:LEU:HD23	53:1:1203:U:H5'	1.99	0.44
13:n:33:ILE:HG23	13:n:33:ILE:O	2.17	0.44
13:n:47:VAL:O	13:n:51:LEU:HG	2.18	0.44
17:r:2:TYR:CZ	17:r:42:ALA:HB3	2.52	0.44
20:u:43:LYS:HD3	20:u:60:LYS:HD3	1.99	0.44
30:F:30:GLU:HG3	30:F:32:LYS:H	1.82	0.44
31:G:24:PRO:HB3	52:3:828:U:H2'	1.99	0.44
47:W:60:ARG:O	47:W:64:LEU:HG	2.17	0.44
48:X:79:TYR:CE1	52:3:1226:C:H4'	2.53	0.44
52:3:31:G:H5'	52:3:306:A:C2	2.53	0.44
52:3:1493:A:O2'	56:4:19:U:H1'	2.18	0.44
53:1:248:G:C4	53:1:2431:U:H4'	2.53	0.44
53:1:861:A:H2'	53:1:862:G:O4'	2.17	0.44
53:1:941:A:H2'	53:1:942:G:O4'	2.18	0.44
53:1:1313:U:H2'	53:1:1610:A:C2	2.53	0.44
53:1:2678:C:H2'	53:1:2679:A:H8	1.83	0.44
55:6:12:G:H2'	55:6:13:C:C6	2.53	0.44
58:8:229:THR:HG22	58:8:230:GLY:N	2.33	0.44
1:b:32:LEU:HD12	1:b:63:ILE:HG23	1.99	0.44
4:e:130:GLY:HA3	53:1:2305:U:H5''	1.99	0.44
10:k:41:ILE:HD11	10:k:86:LEU:HD22	2.00	0.44
14:o:29:HIS:HB3	14:o:36:TYR:HB2	2.00	0.44
22:w:42:HIS:HB2	22:w:75:PHE:CD1	2.53	0.44
23:x:4:CYS:HB2	23:x:32:LEU:HD21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:141:GLU:O	31:G:145:ASN:ND2	2.50	0.44
37:M:50:VAL:HG22	37:M:50:VAL:O	2.18	0.44
45:U:76:LYS:HE3	52:3:474:G:OP2	2.18	0.44
52:3:408:A:H2'	52:3:409:U:C6	2.53	0.44
52:3:559:A:H4'	52:3:560:A:H3'	1.99	0.44
52:3:1301:U:O2	52:3:1301:U:C2'	2.64	0.44
53:1:254:G:C2'	53:1:255:A:H5''	2.48	0.44
53:1:922:C:H2'	53:1:923:G:C8	2.53	0.44
53:1:1287:A:C2'	53:1:1288:G:H5'	2.48	0.44
53:1:1287:A:O2'	53:1:1288:G:H5'	2.18	0.44
53:1:1469:A:H2'	53:1:1470:A:C8	2.53	0.44
53:1:1506:U:H2'	53:1:1507:C:C6	2.52	0.44
53:1:1827:U:C2'	53:1:1828:G:H5'	2.48	0.44
53:1:2139:U:H2'	53:1:2140:G:C8	2.52	0.44
53:1:2573:C:OP1	53:1:2574:G:H5''	2.18	0.44
53:1:2743:U:H3'	53:1:2744:G:H5''	1.98	0.44
58:8:281:GLY:O	58:8:282:ILE:HD13	2.17	0.44
3:d:90:GLN:NE2	53:1:590:A:H5'	2.33	0.43
6:g:30:LEU:HA	6:g:35:LYS:HB2	1.99	0.43
7:h:43:LYS:O	7:h:46:ARG:HB3	2.18	0.43
9:j:76:HIS:NE2	53:1:2641:G:OP1	2.50	0.43
13:n:3:HIS:O	13:n:4:ARG:HB2	2.18	0.43
15:p:77:SER:O	15:p:80:VAL:HG22	2.18	0.43
15:p:103:THR:HG23	52:3:1432:G:OP1	2.18	0.43
19:t:77:ARG:HD3	19:t:77:ARG:HA	1.83	0.43
20:u:40:LEU:HD22	20:u:59:GLU:HB3	1.99	0.43
27:C:9:LYS:HB3	27:C:9:LYS:HE2	1.88	0.43
33:I:170:LEU:HD12	33:I:170:LEU:C	2.43	0.43
34:J:88:HIS:HB3	34:J:138:ALA:HB2	2.00	0.43
48:X:71:GLY:HA3	52:3:1320:C:O2	2.17	0.43
49:Y:2:ASN:ND2	52:3:351:G:OP1	2.51	0.43
50:Z:36:PHE:O	50:Z:37:TYR:HB2	2.18	0.43
52:3:428:G:O4'	52:3:430:A:C8	2.71	0.43
53:1:239:C:H2'	53:1:240:C:O4'	2.17	0.43
53:1:272:A:H2'	53:1:273:G:C8	2.53	0.43
53:1:1429:G:H2'	53:1:1430:G:H8	1.83	0.43
53:1:1524:G:H2'	53:1:1525:A:C8	2.53	0.43
53:1:1683:U:H2'	53:1:1684:G:H8	1.83	0.43
53:1:1823:G:O2'	53:1:1824:G:H5'	2.18	0.43
53:1:2810:A:H2'	53:1:2811:G:O4'	2.18	0.43
58:8:221:ILE:H	58:8:221:ILE:HD12	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:194:PRO:HA	53:1:2680:U:C5'	2.45	0.43
3:d:129:PRO:HA	3:d:160:ALA:HB2	1.99	0.43
13:n:83:LEU:HD22	13:n:83:LEU:N	2.33	0.43
16:q:33:VAL:HG21	53:1:2019:A:H4'	2.00	0.43
31:G:101:THR:O	52:3:1074:G:H4'	2.19	0.43
33:I:103:ARG:HD2	33:I:167:PRO:HG2	2.00	0.43
43:S:25:GLU:HA	43:S:28:ALA:HB3	2.00	0.43
44:T:23:SER:OG	44:T:26:VAL:HG23	2.17	0.43
51:a:46:VAL:HG22	51:a:212:VAL:HG23	2.00	0.43
52:3:539:A:H2'	52:3:540:G:H8	1.83	0.43
52:3:1238:A:C2'	52:3:1239:A:H5'	2.48	0.43
53:1:968:C:H2'	53:1:969:G:H8	1.83	0.43
53:1:1441:G:H2'	53:1:1442:U:C6	2.53	0.43
53:1:1796:U:H2'	53:1:1797:G:C8	2.48	0.43
53:1:2193:G:H2'	53:1:2194:U:C6	2.53	0.43
53:1:2360:G:H2'	53:1:2361:G:H5'	2.00	0.43
53:1:2678:C:H2'	53:1:2679:A:C8	2.53	0.43
55:6:3:C:H2'	55:6:4:G:C8	2.53	0.43
57:7:23:A:H2'	57:7:24:G:H8	1.83	0.43
1:b:242:HIS:HA	1:b:243:PRO:HD3	1.80	0.43
2:c:131:ASP:HA	53:1:1994:C:OP1	2.18	0.43
3:d:30:GLN:OE1	53:1:659:G:N2	2.51	0.43
7:h:87:GLU:CD	7:h:93:ALA:HB3	2.43	0.43
8:i:89:SER:O	8:i:91:LYS:N	2.51	0.43
9:j:40:HIS:ND1	9:j:41:LYS:HG3	2.34	0.43
10:k:23:LYS:HE3	53:1:2561:U:O2	2.18	0.43
11:l:79:LEU:HB3	11:l:116:VAL:CG1	2.48	0.43
12:m:17:ASN:HD22	12:m:95:LEU:HD22	1.83	0.43
16:q:2:ARG:HB2	53:1:1248:G:C5	2.54	0.43
18:s:65:ASP:OD2	18:s:68:ASP:HB2	2.19	0.43
23:x:6:VAL:HG11	23:x:58:ILE:HD11	1.99	0.43
30:F:19:ARG:NE	53:1:2756:U:OP2	2.51	0.43
32:H:112:ALA:HB1	32:H:199:VAL:HG13	2.00	0.43
33:I:117:VAL:HG12	33:I:130:ASN:O	2.18	0.43
33:I:149:LYS:C	33:I:150:LYS:HG2	2.43	0.43
35:K:44:ARG:NH1	35:K:44:ARG:HB3	2.33	0.43
42:R:89:ARG:HB2	42:R:96:VAL:HG22	2.00	0.43
52:3:32:A:H2'	52:3:33:A:C8	2.52	0.43
52:3:721:G:H4'	52:3:722:G:O4'	2.18	0.43
52:3:936:C:H2'	52:3:937:A:O4'	2.19	0.43
52:3:1510:C:H2'	52:3:1511:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:306:U:H2'	53:1:307:G:O4'	2.18	0.43
53:1:817:C:H2'	53:1:818:G:O4'	2.19	0.43
53:1:1680:U:C2'	53:1:1681:G:H5'	2.49	0.43
53:1:2290:G:H2'	53:1:2291:U:O4'	2.18	0.43
57:7:64:A:H1'	58:8:380:GLY:H	1.83	0.43
1:b:96:LYS:HB3	53:1:1490:A:H62	1.83	0.43
1:b:155:ARG:NH2	53:1:1818:U:H5	2.16	0.43
6:g:84:ALA:HB2	6:g:90:LEU:HD23	2.01	0.43
8:i:33:ASN:HB3	8:i:36:GLU:HG2	1.99	0.43
8:i:127:SER:HA	53:1:1080:A:H1'	2.00	0.43
11:l:86:GLU:O	11:l:88:GLY:N	2.50	0.43
12:m:41:LEU:O	12:m:94:ALA:N	2.50	0.43
37:M:49:LYS:O	37:M:58:LEU:HD23	2.18	0.43
38:N:64:ILE:HD12	38:N:64:ILE:N	2.34	0.43
38:N:98:ARG:NH2	52:3:1178:G:C8	2.87	0.43
42:R:15:VAL:HG23	42:R:16:ILE:N	2.34	0.43
45:U:40:ASN:HB3	45:U:43:ALA:HB2	1.99	0.43
46:V:16:MET:N	46:V:16:MET:SD	2.91	0.43
49:Y:3:ILE:HD12	49:Y:3:ILE:N	2.31	0.43
51:a:20:GLN:NE2	51:a:225:ASP:OD1	2.45	0.43
52:3:88:U:H2'	52:3:89:U:C6	2.54	0.43
52:3:184:G:C4'	52:3:224:U:H4'	2.48	0.43
52:3:1014:A:H2'	52:3:1015:G:O4'	2.19	0.43
52:3:1059:C:O2'	52:3:1060:U:H5'	2.18	0.43
52:3:1517:G:C2'	52:3:1518:A:H5'	2.48	0.43
53:1:222:A:H61	53:1:232:G:H1'	1.83	0.43
53:1:254:G:O2'	53:1:255:A:H5''	2.17	0.43
53:1:1429:G:H2'	53:1:1430:G:C8	2.54	0.43
53:1:1435:G:H2'	53:1:1436:G:C8	2.53	0.43
53:1:1601:G:C2'	53:1:1602:U:H5'	2.49	0.43
53:1:2141:G:H2'	53:1:2142:A:C8	2.53	0.43
53:1:2452:C:H42	53:1:2504:U:H3	1.66	0.43
53:1:2811:G:H2'	53:1:2812:G:C8	2.53	0.43
58:8:164:PRO:O	58:8:168:THR:HG23	2.19	0.43
3:d:95:LYS:NZ	53:1:607:U:H4'	2.34	0.43
7:h:58:THR:HA	7:h:63:ALA:HB3	1.99	0.43
9:j:131:ASN:OD1	9:j:131:ASN:N	2.51	0.43
17:r:55:ASP:OD2	17:r:55:ASP:N	2.50	0.43
32:H:67:ILE:HD12	32:H:67:ILE:N	2.33	0.43
40:P:24:ALA:HB1	40:P:89:GLY:HA3	2.01	0.43
45:U:20:VAL:HG22	45:U:21:VAL:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:35:G:H2'	52:3:36:C:C6	2.53	0.43
53:1:414:C:H5''	53:1:1879:C:O2'	2.18	0.43
53:1:1314:C:H42	53:1:1338:G:H1	1.66	0.43
53:1:1930:G:C2'	53:1:1931:U:OP2	2.67	0.43
53:1:2270:A:H2'	53:1:2271:G:O4'	2.18	0.43
53:1:2629:U:O2'	53:1:2630:G:H5''	2.18	0.43
55:5:62:C:H2'	55:5:63:G:C8	2.53	0.43
55:6:47:U:H3'	55:6:48:C:H5'	1.99	0.43
1:b:38:LYS:O	53:1:692:C:H4'	2.19	0.43
1:b:73:ILE:HG12	53:1:1490:A:C2	2.53	0.43
1:b:270:ARG:NH1	1:b:270:ARG:HB3	2.34	0.43
2:c:78:GLY:C	2:c:79:LEU:HD12	2.42	0.43
6:g:116:ARG:O	6:g:118:PRO:HD3	2.17	0.43
7:h:67:THR:N	7:h:68:PRO:CD	2.81	0.43
14:o:9:ARG:C	14:o:9:ARG:HD2	2.43	0.43
17:r:14:VAL:HG22	17:r:15:SER:N	2.34	0.43
17:r:14:VAL:HG23	17:r:18:GLN:HE21	1.83	0.43
18:s:24:ILE:HD13	18:s:36:LEU:HD21	2.00	0.43
18:s:88:ARG:HB2	18:s:92:ARG:O	2.18	0.43
22:w:12:SER:OG	53:1:2262:U:H5	2.01	0.43
28:D:15:SER:O	28:D:16:HIS:ND1	2.51	0.43
33:I:68:GLU:OE1	52:3:545:C:H5''	2.18	0.43
34:J:92:ARG:O	34:J:93:VAL:O	2.36	0.43
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.18	0.43
48:X:68:HIS:HB3	48:X:72:GLU:HG3	2.00	0.43
51:a:177:LYS:NZ	53:1:2125:G:H5'	2.33	0.43
52:3:665:A:O4'	52:3:733:G:H1'	2.18	0.43
52:3:731:G:C5'	52:3:766:A:H4'	2.48	0.43
52:3:1305:G:H22	52:3:1331:G:H2'	1.83	0.43
53:1:18:U:H2'	53:1:19:A:H8	1.83	0.43
53:1:167:A:H2'	53:1:168:G:O4'	2.17	0.43
53:1:207:A:H2'	53:1:208:C:O4'	2.18	0.43
53:1:331:C:H41	53:1:1210:G:N2	2.17	0.43
53:1:1394:U:H4'	53:1:1603:A:H4'	2.00	0.43
53:1:1509:A:H2'	53:1:1510:G:H8	1.83	0.43
53:1:1636:U:H2'	53:1:1637:A:H8	1.84	0.43
53:1:2190:G:H2'	53:1:2191:A:C8	2.53	0.43
54:2:19:C:H2'	54:2:20:G:C8	2.53	0.43
54:2:100:G:H2'	54:2:101:A:O4'	2.19	0.43
55:5:23:C:H2'	55:5:24:U:C6	2.53	0.43
1:b:174:ARG:HG3	1:b:180:MET:SD	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:16:ALA:HA	10:k:46:ALA:CB	2.48	0.43
11:l:79:LEU:HG	11:l:111:ILE:O	2.19	0.43
19:t:73:ARG:NH1	53:1:456:C:C5	2.86	0.43
28:D:12:ARG:NE	28:D:44:VAL:HG21	2.33	0.43
34:J:105:ILE:HG13	34:J:105:ILE:O	2.18	0.43
40:P:12:ARG:O	40:P:14:GLN:N	2.47	0.43
46:V:44:HIS:O	46:V:70:LYS:HA	2.18	0.43
49:Y:67:HIS:C	49:Y:69:ASN:H	2.26	0.43
52:3:359:G:H2'	52:3:360:G:O4'	2.18	0.43
53:1:464:U:H2'	53:1:465:G:O4'	2.19	0.43
53:1:968:C:H2'	53:1:969:G:C8	2.53	0.43
53:1:1181:U:H2'	53:1:1182:G:C8	2.53	0.43
53:1:1487:U:H2'	53:1:1488:C:C6	2.54	0.43
53:1:1952:A:N7	53:1:1953:A:C6	2.87	0.43
53:1:2808:G:H2'	53:1:2890:G:C6	2.54	0.43
2:c:24:VAL:HG22	2:c:25:THR:N	2.33	0.43
3:d:163:ASN:HB2	53:1:322:A:OP2	2.19	0.43
5:f:100:ASN:ND2	5:f:115:GLN:OE1	2.52	0.43
7:h:67:THR:OG1	7:h:68:PRO:HD3	2.19	0.43
9:j:5:THR:O	9:j:7:LYS:HD2	2.19	0.43
15:p:104:GLY:O	15:p:107:ALA:HB3	2.19	0.43
19:t:47:VAL:CG1	19:t:55:VAL:HG21	2.41	0.43
35:K:46:GLN:HG2	35:K:47:LEU:N	2.34	0.43
37:M:3:GLN:O	52:3:587:G:H4'	2.19	0.43
41:Q:49:ARG:HH21	52:3:522:C:H41	1.67	0.43
42:R:32:ILE:HG23	42:R:58:GLU:HG3	2.01	0.43
48:X:35:ARG:HA	48:X:70:LEU:HB2	2.00	0.43
52:3:354:G:O2'	52:3:355:C:H5'	2.19	0.43
52:3:1236:A:H2'	52:3:1237:C:O4'	2.19	0.43
53:1:191:A:H2'	53:1:192:C:C6	2.53	0.43
53:1:799:G:H5''	53:1:800:A:H2'	2.01	0.43
53:1:818:G:C2'	53:1:819:A:H5''	2.49	0.43
53:1:1070:A:H2'	53:1:1097:U:OP1	2.19	0.43
53:1:1089:A:H2	53:1:1090:A:H62	1.66	0.43
53:1:1152:C:H2'	53:1:1153:C:H6	1.83	0.43
53:1:1755:A:H2'	53:1:1756:G:H5'	2.01	0.43
53:1:2427:C:C5'	53:1:2429:G:H5'	2.46	0.43
53:1:2465:C:O2'	53:1:2466:C:H5'	2.19	0.43
53:1:2786:U:H2'	53:1:2787:C:C6	2.54	0.43
56:4:17:U:H2'	56:4:18:G:C8	2.54	0.43
57:7:5:G:H2'	57:7:6:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:226:THR:CG2	58:8:287:ILE:HD11	2.49	0.43
1:b:216:ARG:NH2	53:1:781:A:OP1	2.52	0.43
2:c:149:ASN:CG	2:c:150:GLN:H	2.27	0.43
4:e:39:VAL:HG13	4:e:40:GLY:N	2.34	0.43
4:e:69:ALA:HB3	4:e:82:TYR:H	1.84	0.43
5:f:93:TYR:OH	5:f:159:LYS:HE3	2.19	0.43
8:i:83:ALA:HA	8:i:100:ILE:HD11	1.99	0.43
10:k:40:LYS:HE3	10:k:57:VAL:CG1	2.42	0.43
10:k:48:PRO:HB3	52:3:1422:G:H4'	2.00	0.43
33:I:69:ARG:O	33:I:73:ASN:ND2	2.51	0.43
36:L:112:ASP:H	36:L:118:ARG:HD3	1.84	0.43
44:T:70:LYS:HE2	44:T:77:TYR:CZ	2.54	0.43
52:3:1487:G:O2'	52:3:1488:G:H5'	2.18	0.43
53:1:230:G:O2'	53:1:231:A:H5'	2.18	0.43
53:1:940:G:C3'	53:1:941:A:H5''	2.49	0.43
53:1:2446:G:H4'	53:1:2448:A:N7	2.34	0.43
53:1:2484:G:O2'	53:1:2485:G:H5'	2.19	0.43
53:1:2654:A:O3'	53:1:2655:G:H4'	2.18	0.43
53:1:2837:A:H2'	53:1:2838:G:H8	1.83	0.43
55:6:58:A:H1'	55:6:60:U:C5	2.54	0.43
57:7:72:C:O2'	57:7:73:A:H5'	2.18	0.43
58:8:68:VAL:HG23	58:8:79:HIS:HB3	2.01	0.43
58:8:153:GLU:O	58:8:157:LEU:HG	2.18	0.43
58:8:226:THR:HG23	58:8:284:ARG:HD2	2.01	0.43
1:b:204:LEU:HD12	53:1:1792:G:OP1	2.19	0.43
1:b:236:GLY:HA2	53:1:2590:A:OP2	2.19	0.43
5:f:175:LYS:C	5:f:176:LYS:HG3	2.43	0.43
9:j:140:LEU:HG	9:j:142:ILE:HG22	2.01	0.43
11:l:57:LEU:HG	29:E:13:PHE:HZ	1.84	0.43
21:v:80:HIS:CG	21:v:83:LYS:HB2	2.54	0.43
23:x:24:THR:HG21	53:1:2081:U:H4'	2.00	0.43
31:G:96:LEU:HD13	52:3:1103:C:H4'	2.01	0.43
41:Q:13:ARG:HH11	41:Q:14:LYS:N	2.12	0.43
42:R:76:ILE:HG13	42:R:77:LYS:N	2.34	0.43
51:a:38:PHE:HD1	53:1:2127:G:H4'	1.84	0.43
52:3:56:U:H2'	52:3:57:G:H8	1.84	0.43
52:3:571:U:O5'	52:3:571:U:H6	2.02	0.43
52:3:751:U:C2'	52:3:752:G:H5'	2.49	0.43
52:3:926:G:H22	56:4:15:A:H3'	1.84	0.43
53:1:327:G:H2'	53:1:328:U:O4'	2.19	0.43
53:1:871:U:H2'	53:1:872:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2737:G:H2'	53:1:2738:A:C8	2.54	0.43
1:b:62:ARG:HG3	1:b:62:ARG:NH1	2.34	0.42
1:b:106:PRO:HG2	1:b:109:LEU:HB2	2.00	0.42
5:f:128:THR:HG23	5:f:129:GLU:OE1	2.19	0.42
7:h:58:THR:HG21	7:h:82:ILE:H	1.84	0.42
7:h:87:GLU:OE2	7:h:95:LEU:HB2	2.18	0.42
11:l:23:ILE:HD12	11:l:23:ILE:H	1.83	0.42
11:l:55:MET:HE2	53:1:2392:A:C2	2.53	0.42
26:B:1:ALA:HB3	53:1:2612:C:O2'	2.19	0.42
33:I:38:GLY:HA2	52:3:427:U:OP1	2.19	0.42
39:O:37:ARG:HE	52:3:1124:G:H5''	1.84	0.42
51:a:29:LEU:O	51:a:29:LEU:HD23	2.19	0.42
52:3:162:A:H2'	52:3:163:C:H5'	2.01	0.42
54:2:66:A:H5''	54:2:67:G:OP1	2.19	0.42
57:7:68:C:H2'	57:7:69:G:C8	2.52	0.42
58:8:163:PHE:O	58:8:165:GLY:N	2.51	0.42
1:b:268:ARG:HH21	52:3:680:C:H4'	1.83	0.42
4:e:29:ARG:HG2	4:e:29:ARG:HH11	1.84	0.42
13:n:63:ARG:CZ	53:1:1454:C:H5'	2.49	0.42
29:E:12:ARG:NH1	53:1:2393:U:O2'	2.52	0.42
33:I:49:ASP:O	33:I:52:VAL:HG12	2.19	0.42
33:I:143:SER:OG	33:I:144:ILE:N	2.53	0.42
43:S:26:LEU:HD11	43:S:46:LYS:HG3	2.01	0.42
52:3:591:U:H2'	52:3:592:G:C8	2.54	0.42
52:3:1075:U:H2'	52:3:1076:U:C6	2.54	0.42
53:1:654:A:H3'	53:1:654:A:N3	2.34	0.42
53:1:983:A:N6	53:1:984:A:C2	2.87	0.42
53:1:1507:C:H2'	53:1:1508:A:C4'	2.49	0.42
53:1:2176:A:H2'	53:1:2177:C:C6	2.54	0.42
53:1:2875:C:H2'	53:1:2876:G:H8	1.84	0.42
58:8:176:LEU:HD12	58:8:179:LEU:HD12	2.01	0.42
2:c:173:GLN:HE21	53:1:2772:C:H5'	1.83	0.42
10:k:107:LEU:O	10:k:112:PHE:HB2	2.20	0.42
12:m:103:TYR:HB2	12:m:117:PHE:HE1	1.84	0.42
13:n:37:THR:OG1	13:n:40:LYS:HD2	2.19	0.42
30:F:9:LYS:HZ3	30:F:12:ARG:HA	1.84	0.42
32:H:37:LYS:H	32:H:37:LYS:HG2	1.64	0.42
33:I:9:LYS:HG2	33:I:12:ARG:HH21	1.84	0.42
33:I:138:PRO:HA	33:I:181:PHE:HD2	1.83	0.42
36:L:146:ALA:O	40:P:55:ARG:NH2	2.52	0.42
38:N:49:GLN:N	38:N:50:PRO:CD	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:15:LEU:HD13	43:S:53:ASP:HB3	2.02	0.42
43:S:58:ARG:NH1	52:3:979:C:O2	2.52	0.42
44:T:44:GLU:O	44:T:45:HIS:HB2	2.19	0.42
52:3:9:G:H2'	52:3:10:A:H8	1.84	0.42
52:3:82:G:H2'	52:3:83:C:H5'	1.99	0.42
52:3:302:G:N3	52:3:556:C:H4'	2.34	0.42
52:3:1005:A:H2'	52:3:1006:G:C5'	2.49	0.42
53:1:502:A:H2'	53:1:503:A:H5'	2.01	0.42
53:1:1079:C:H2'	53:1:1080:A:C8	2.54	0.42
53:1:1507:C:C2'	53:1:1508:A:H4'	2.50	0.42
53:1:2024:G:H2'	53:1:2025:C:O4'	2.19	0.42
53:1:2529:G:H5''	53:1:2530:A:H5''	2.01	0.42
58:8:211:PHE:CE2	58:8:293:LEU:HB3	2.55	0.42
1:b:75:ALA:N	1:b:115:ILE:O	2.52	0.42
3:d:90:GLN:OE1	53:1:590:A:H5''	2.19	0.42
4:e:45:ASP:OD2	4:e:45:ASP:N	2.52	0.42
9:j:40:HIS:HE1	9:j:41:LYS:HE3	1.85	0.42
15:p:52:ARG:HH21	53:1:2720:U:H5''	1.84	0.42
15:p:85:VAL:HG22	15:p:86:LYS:N	2.35	0.42
34:J:122:VAL:HG23	34:J:122:VAL:O	2.19	0.42
39:O:51:VAL:HG12	39:O:52:LEU:N	2.34	0.42
39:O:53:ILE:HG22	39:O:61:ALA:O	2.20	0.42
43:S:19:TYR:HB2	43:S:54:SER:OG	2.20	0.42
45:U:20:VAL:HG23	45:U:35:ARG:CA	2.48	0.42
52:3:128:G:O2'	52:3:129:A:H5'	2.20	0.42
52:3:477:C:H2'	52:3:478:A:C8	2.55	0.42
52:3:547:A:H4'	52:3:548:G:O5'	2.19	0.42
52:3:1329:A:O2'	52:3:1330:U:H5'	2.18	0.42
53:1:45:G:H5''	53:1:46:G:C4'	2.49	0.42
53:1:751:A:H2'	53:1:789:A:C2	2.55	0.42
53:1:1881:C:H2'	53:1:1882:U:O4'	2.20	0.42
53:1:1906:G:C3'	53:1:1907:G:H5''	2.49	0.42
53:1:2515:C:H2'	53:1:2516:A:H8	1.85	0.42
57:7:63:G:H21	58:8:380:GLY:CA	2.33	0.42
58:8:70:TYR:HE1	58:8:79:HIS:HB2	1.84	0.42
58:8:215:ILE:HD12	58:8:291:GLN:HB2	2.02	0.42
2:c:155:VAL:O	53:1:2619:C:H5'	2.19	0.42
5:f:21:GLN:HE21	5:f:36:LEU:HB2	1.85	0.42
8:i:21:PRO:HD2	8:i:22:PRO:HD3	2.02	0.42
8:i:74:PRO:O	8:i:77:VAL:HG12	2.19	0.42
8:i:79:LEU:HD12	8:i:80:LYS:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:22:GLN:NE2	53:1:864:G:OP2	2.53	0.42
20:u:45:GLN:NE2	20:u:54:PRO:HG3	2.35	0.42
23:x:4:CYS:SG	23:x:6:VAL:HG22	2.60	0.42
32:H:84:GLU:O	32:H:88:LYS:HG2	2.19	0.42
33:I:177:MET:HE2	33:I:177:MET:H	1.84	0.42
34:J:35:LEU:HD22	34:J:133:ILE:HD13	2.02	0.42
36:L:138:GLU:O	36:L:142:ARG:HD3	2.20	0.42
37:M:49:LYS:HD2	37:M:59:GLU:OE2	2.19	0.42
44:T:59:VAL:HG13	44:T:60:SER:N	2.33	0.42
47:W:24:ASP:OD1	47:W:24:ASP:N	2.52	0.42
51:a:164:ARG:HB3	51:a:164:ARG:HH11	1.85	0.42
52:3:229:U:H2'	52:3:230:G:C8	2.53	0.42
52:3:335:C:H2'	52:3:336:A:H8	1.82	0.42
52:3:1088:G:H21	52:3:1167:A:H61	1.67	0.42
52:3:1389:C:H2'	52:3:1390:U:C6	2.55	0.42
53:1:468:G:H2'	53:1:469:G:O4'	2.19	0.42
53:1:910:A:H1'	53:1:2264:C:O2'	2.19	0.42
53:1:2263:C:H2'	53:1:2264:C:C6	2.55	0.42
53:1:2849:U:H4'	53:1:2868:A:N1	2.34	0.42
7:h:118:ILE:CB	7:h:119:PRO:HD3	2.49	0.42
7:h:118:ILE:CG2	7:h:119:PRO:HD3	2.47	0.42
11:l:101:ILE:HB	11:l:105:ILE:HG13	2.01	0.42
13:n:36:THR:HG22	13:n:37:THR:H	1.85	0.42
14:o:81:ARG:HA	14:o:84:GLU:HG3	2.02	0.42
15:p:103:THR:OG1	15:p:104:GLY:N	2.53	0.42
16:q:3:VAL:HG22	53:1:1199:U:H1'	2.02	0.42
19:t:75:GLY:HA3	53:1:64:A:H4'	2.02	0.42
31:G:20:ARG:CG	52:3:831:A:H5'	2.50	0.42
34:J:22:LYS:HB3	34:J:29:ILE:HG22	2.00	0.42
35:K:51:ILE:HG23	35:K:86:ARG:HH21	1.85	0.42
36:L:83:THR:CB	55:6:33:U:H4'	2.50	0.42
37:M:49:LYS:HB2	37:M:59:GLU:HG2	2.01	0.42
38:N:66:VAL:HG22	38:N:67:LYS:N	2.34	0.42
38:N:95:SER:O	38:N:99:LYS:HG2	2.20	0.42
46:V:48:GLU:O	46:V:51:GLU:HG2	2.19	0.42
52:3:161:A:H2'	52:3:162:A:O4'	2.20	0.42
52:3:212:G:H2'	52:3:213:G:C8	2.55	0.42
52:3:225:C:H2'	52:3:226:G:C5'	2.46	0.42
52:3:538:G:H2'	52:3:539:A:C8	2.54	0.42
52:3:603:U:H2'	52:3:604:G:H8	1.84	0.42
52:3:1299:A:H2'	52:3:1300:G:H4'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:414:C:H2'	53:1:415:A:C8	2.54	0.42
53:1:419:U:H2'	53:1:420:C:C6	2.55	0.42
53:1:1133:A:H4'	53:1:1134:A:C5'	2.46	0.42
53:1:1140:C:C2'	53:1:1141:U:H5'	2.50	0.42
53:1:1695:G:H2'	53:1:1696:G:O4'	2.20	0.42
58:8:187:ALA:O	58:8:191:GLU:HG3	2.20	0.42
1:b:141:HIS:CE1	1:b:190:THR:HG22	2.55	0.42
7:h:80:THR:O	7:h:81:LEU:C	2.61	0.42
8:i:135:MET:HE1	53:1:1062:G:N3	2.34	0.42
9:j:81:ILE:HD11	53:1:2514:U:H5''	2.00	0.42
13:n:28:LEU:HD23	13:n:48:VAL:HG21	2.01	0.42
15:p:63:ILE:HG23	15:p:63:ILE:O	2.19	0.42
18:s:74:ILE:HG23	18:s:74:ILE:O	2.20	0.42
20:u:5:ARG:NH1	53:1:84:A:OP1	2.53	0.42
35:K:29:ILE:HG23	35:K:66:ALA:HB2	2.02	0.42
35:K:37:HIS:HB3	35:K:97:THR:HG22	2.01	0.42
43:S:92:ILE:HD12	43:S:93:PRO:CD	2.48	0.42
52:3:162:A:C2'	52:3:163:C:H5'	2.49	0.42
52:3:193:C:H2'	52:3:194:C:C6	2.54	0.42
52:3:354:G:C2'	52:3:355:C:H5'	2.48	0.42
52:3:748:G:H2'	52:3:749:A:C8	2.55	0.42
52:3:962:C:H2'	52:3:963:G:H8	1.84	0.42
53:1:149:A:H2'	53:1:150:U:C6	2.55	0.42
53:1:635:C:H2'	53:1:636:G:H8	1.84	0.42
53:1:741:U:H2'	53:1:742:A:H8	1.83	0.42
53:1:1152:C:H2'	53:1:1153:C:C6	2.55	0.42
53:1:1709:U:O2'	53:1:2859:G:H1'	2.20	0.42
53:1:2411:A:H2'	53:1:2412:A:C8	2.55	0.42
53:1:2818:U:H4'	53:1:2837:A:H4'	2.02	0.42
3:d:150:THR:OG1	3:d:151:GLY:N	2.52	0.42
4:e:66:ILE:N	54:2:41:G:H22	2.18	0.42
12:m:34:LYS:HB2	12:m:34:LYS:HE3	1.83	0.42
12:m:34:LYS:HE3	12:m:131:VAL:HG11	2.02	0.42
19:t:89:GLU:OE2	19:t:89:GLU:N	2.45	0.42
24:y:21:LEU:HD23	24:y:25:GLN:HG2	2.01	0.42
33:I:144:ILE:N	33:I:144:ILE:HD12	2.35	0.42
34:J:152:VAL:O	34:J:156:ARG:HB3	2.20	0.42
34:J:160:VAL:HA	34:J:163:ILE:HD11	2.01	0.42
35:K:18:VAL:HG11	35:K:58:HIS:CD2	2.55	0.42
38:N:59:LYS:C	38:N:60:LEU:HD12	2.45	0.42
39:O:40:ILE:HD12	39:O:40:ILE:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:26:ASN:OD1	45:U:27:ALA:N	2.53	0.42
48:X:52:ASN:HD21	48:X:55:GLN:HB2	1.85	0.42
52:3:597:G:H2'	52:3:598:U:H5'	2.01	0.42
52:3:599:C:H2'	52:3:600:A:C8	2.54	0.42
52:3:861:G:H2'	52:3:862:C:O4'	2.20	0.42
53:1:28:A:H1'	53:1:513:A:C2	2.54	0.42
53:1:182:A:O2'	53:1:183:C:H5'	2.20	0.42
53:1:420:C:O2'	53:1:421:C:H5'	2.19	0.42
53:1:656:G:H2'	53:1:657:U:O4'	2.20	0.42
53:1:825:A:H2'	53:1:826:U:C6	2.54	0.42
53:1:1412:U:H2'	53:1:1413:A:C8	2.55	0.42
53:1:1744:A:H3'	53:1:1745:A:C8	2.55	0.42
53:1:2078:C:H2'	53:1:2079:U:C6	2.55	0.42
53:1:2120:G:H2'	53:1:2121:G:C8	2.55	0.42
53:1:2733:A:O2'	53:1:2734:A:H5'	2.19	0.42
54:2:111:U:H2'	54:2:112:G:H8	1.85	0.42
2:c:56:LYS:HZ1	53:1:2830:C:H5''	1.82	0.42
4:e:131:VAL:HG23	4:e:151:LEU:H	1.84	0.42
7:h:55:VAL:HA	53:1:1084:A:H5''	2.01	0.42
8:i:34:ILE:HG23	8:i:35:MET:HE2	2.01	0.42
9:j:95:ARG:HG2	9:j:96:ARG:HG2	2.01	0.42
13:n:78:LYS:O	13:n:82:GLU:HB2	2.19	0.42
17:r:91:GLN:HE21	53:1:993:G:H1'	1.84	0.42
28:D:9:VAL:HG12	53:1:1309:G:OP1	2.20	0.42
30:F:37:GLN:O	30:F:38:GLY:C	2.62	0.42
33:I:25:ARG:HH12	33:I:30:LYS:HE3	1.85	0.42
33:I:128:VAL:HG21	33:I:145:ARG:HD3	2.02	0.42
38:N:32:ARG:HD3	38:N:36:GLN:HE21	1.85	0.42
41:Q:106:VAL:HG22	41:Q:116:TYR:HB3	2.01	0.42
52:3:411:A:N9	52:3:413:G:H1'	2.34	0.42
52:3:424:G:O2'	52:3:425:G:H5'	2.20	0.42
52:3:1126:U:O2	52:3:1280:A:H5'	2.19	0.42
52:3:1143:G:H2'	52:3:1144:G:C8	2.55	0.42
52:3:1404:C:H2'	52:3:1405:G:C8	2.55	0.42
52:3:1528:U:H4'	52:3:1529:G:H21	1.85	0.42
53:1:164:C:H2'	53:1:165:A:O4'	2.19	0.42
53:1:530:G:H4'	53:1:532:A:H62	1.85	0.42
53:1:687:C:H2'	53:1:688:U:H5'	2.02	0.42
53:1:969:G:H2'	53:1:970:U:C6	2.55	0.42
53:1:1019:U:H2'	53:1:1020:A:H8	1.83	0.42
53:1:1539:U:H2'	53:1:1540:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1773:A:C5	53:1:1829:A:H1'	2.54	0.42
53:1:2382:G:H5'	53:1:2383:G:O5'	2.20	0.42
53:1:2638:G:H1'	53:1:2778:A:H61	1.83	0.42
54:2:13:G:H21	54:2:16:G:H1'	1.84	0.42
57:7:23:A:H2'	57:7:24:G:C8	2.54	0.42
58:8:165:GLY:HA2	58:8:168:THR:HG23	2.01	0.42
3:d:44:ARG:NE	53:1:444:C:OP2	2.53	0.42
8:i:35:MET:O	8:i:39:LYS:HG2	2.20	0.42
23:x:17:ARG:HD3	23:x:17:ARG:HA	1.80	0.42
37:M:12:ARG:NH2	52:3:826:C:H5'	2.34	0.42
41:Q:9:LYS:HD3	41:Q:9:LYS:C	2.45	0.42
43:S:1:ALA:HA	52:3:1203:C:OP1	2.19	0.42
43:S:44:VAL:HG13	43:S:45:LEU:CD2	2.50	0.42
50:Z:17:ARG:HH11	50:Z:20:ARG:HD2	1.84	0.42
50:Z:25:ALA:HA	50:Z:28:LEU:HB2	2.01	0.42
53:1:987:C:H2'	53:1:988:A:O4'	2.20	0.42
53:1:1685:C:H2'	53:1:1686:C:C6	2.54	0.42
53:1:1833:C:H2'	53:1:1834:U:O4'	2.20	0.42
53:1:2529:G:OP2	53:1:2530:A:H8	2.03	0.42
53:1:2710:C:H2'	53:1:2711:A:H8	1.80	0.42
53:1:2863:C:H2'	53:1:2864:G:H8	1.84	0.42
58:8:70:TYR:CE1	58:8:79:HIS:HB2	2.55	0.42
1:b:48:ILE:HG23	1:b:48:ILE:O	2.20	0.41
1:b:176:ARG:HG2	53:1:1820:U:OP1	2.19	0.41
2:c:170:VAL:HG22	2:c:171:THR:H	1.85	0.41
3:d:118:LEU:HD23	3:d:118:LEU:C	2.45	0.41
6:g:47:PHE:HA	6:g:51:ARG:HD2	2.01	0.41
15:p:16:VAL:O	15:p:16:VAL:HG13	2.20	0.41
15:p:50:ARG:HG3	15:p:50:ARG:O	2.20	0.41
20:u:45:GLN:HE21	20:u:54:PRO:HG3	1.85	0.41
31:G:42:LEU:HD23	31:G:42:LEU:H	1.85	0.41
51:a:177:LYS:HD3	51:a:177:LYS:HA	1.87	0.41
51:a:211:LYS:HE2	51:a:211:LYS:HB3	1.88	0.41
52:3:202:G:H2'	52:3:203:G:C8	2.55	0.41
52:3:741:G:H2'	52:3:742:G:C8	2.55	0.41
52:3:922:G:H2'	52:3:923:A:O4'	2.20	0.41
52:3:1446:A:H2'	52:3:1447:A:O4'	2.20	0.41
53:1:395:U:H2'	53:1:396:G:C8	2.55	0.41
53:1:1028:A:H2'	53:1:1029:A:C8	2.54	0.41
53:1:1601:G:O2'	53:1:1602:U:H5'	2.20	0.41
53:1:2366:A:H2'	53:1:2367:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2843:G:O2'	53:1:2844:G:H5'	2.19	0.41
54:2:96:G:O2'	54:2:97:C:H5'	2.20	0.41
55:6:72:A:O2'	55:6:73:A:H5'	2.20	0.41
58:8:245:ILE:HD11	58:8:279:LEU:HD13	2.02	0.41
3:d:126:VAL:HG12	3:d:157:LEU:HD22	2.01	0.41
7:h:123:ILE:HG23	7:h:123:ILE:O	2.19	0.41
10:k:24:VAL:HG13	10:k:24:VAL:O	2.20	0.41
15:p:39:LEU:HD23	15:p:39:LEU:H	1.85	0.41
16:q:26:ALA:O	16:q:30:VAL:HG12	2.20	0.41
17:r:25:LEU:HD12	17:r:25:LEU:H	1.85	0.41
30:F:8:LYS:HE3	30:F:10:LEU:CD2	2.50	0.41
34:J:95:MET:HB3	34:J:124:ALA:HB2	2.02	0.41
38:N:6:TYR:CE2	52:3:1147:C:H4'	2.55	0.41
41:Q:69:GLU:HA	52:3:521:G:OP1	2.20	0.41
42:R:91:ARG:HH11	42:R:91:ARG:HB2	1.85	0.41
43:S:84:ARG:NH2	52:3:1059:C:O3'	2.52	0.41
48:X:54:ARG:HA	52:3:986:U:H1'	2.02	0.41
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.81	0.41
52:3:20:U:H2'	52:3:21:G:O4'	2.20	0.41
53:1:123:G:H5''	53:1:1375:U:O2'	2.19	0.41
53:1:325:G:H2'	53:1:326:G:H8	1.85	0.41
53:1:492:A:H2'	53:1:493:G:O4'	2.20	0.41
53:1:1078:U:H4'	53:1:1079:C:H5''	2.02	0.41
53:1:1378:A:H1'	53:1:1379:U:C5	2.55	0.41
53:1:1464:G:H2'	53:1:1465:G:C8	2.55	0.41
53:1:1971:U:H5'	53:1:1972:G:H5''	2.02	0.41
55:5:25:C:H2'	55:5:26:G:O4'	2.20	0.41
56:4:9:G:H2'	56:4:10:G:H8	1.85	0.41
57:7:1:G:O5'	58:8:289:ARG:NE	2.52	0.41
5:f:175:LYS:O	5:f:176:LYS:HG3	2.21	0.41
6:g:12:LEU:HD23	6:g:12:LEU:N	2.34	0.41
9:j:17:VAL:HG23	9:j:57:LEU:HD13	2.02	0.41
10:k:25:LEU:HD23	53:1:2562:U:H4'	2.02	0.41
10:k:102:PRO:HB3	10:k:121:GLU:OE1	2.19	0.41
11:l:38:GLN:CD	11:l:45:GLY:H	2.28	0.41
19:t:65:GLY:HA3	19:t:77:ARG:HB3	2.02	0.41
33:I:8:LEU:HD12	52:3:429:U:H3'	2.01	0.41
45:U:9:HIS:CD2	45:U:29:ASN:HD22	2.38	0.41
52:3:17:U:H2'	52:3:18:C:C6	2.56	0.41
52:3:68:G:H2'	52:3:69:G:O4'	2.19	0.41
52:3:152:A:H2'	52:3:153:C:H5'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:323:U:H2'	52:3:324:G:O4'	2.20	0.41
52:3:591:U:H2'	52:3:592:G:H8	1.85	0.41
52:3:1325:C:H2'	52:3:1326:U:C6	2.56	0.41
53:1:302:C:H2'	53:1:303:G:H8	1.85	0.41
53:1:326:G:H2'	53:1:327:G:C8	2.54	0.41
53:1:755:U:H2'	53:1:756:A:H8	1.84	0.41
53:1:854:C:H2'	53:1:855:G:C8	2.54	0.41
54:2:104:A:H2'	54:2:105:G:O4'	2.19	0.41
58:8:328:ARG:HH22	58:8:364:ILE:CG2	2.31	0.41
2:c:33:ARG:HA	2:c:95:SER:HA	2.02	0.41
14:o:12:THR:HG23	53:1:2334:U:H4'	2.02	0.41
14:o:30:ARG:NH1	14:o:102:ARG:HH11	2.11	0.41
15:p:50:ARG:HB2	15:p:52:ARG:NH1	2.35	0.41
16:q:21:LYS:HG2	53:1:19:A:H5''	2.03	0.41
28:D:31:LEU:HG	28:D:35:ARG:NH1	2.36	0.41
29:E:51:LYS:HE2	29:E:51:LYS:HB2	1.95	0.41
31:G:31:PHE:HB2	31:G:41:ASN:HA	2.02	0.41
32:H:176:THR:HG22	52:3:1111:A:N1	2.34	0.41
36:L:29:LEU:HD23	36:L:29:LEU:C	2.46	0.41
38:N:113:LYS:HE2	38:N:118:ARG:O	2.20	0.41
39:O:59:LYS:HG3	39:O:62:ARG:HH12	1.85	0.41
52:3:113:G:H4'	52:3:355:C:OP1	2.21	0.41
52:3:497:G:H2'	52:3:498:A:C8	2.55	0.41
52:3:1173:U:H2'	52:3:1174:G:H8	1.86	0.41
53:1:248:G:N7	53:1:250:G:N3	2.69	0.41
53:1:403:U:O3'	53:1:404:A:H4'	2.20	0.41
53:1:662:G:O2'	53:1:663:G:H5'	2.19	0.41
53:1:1086:A:H1'	53:1:1103:A:H61	1.85	0.41
53:1:1370:C:H2'	53:1:1371:G:O4'	2.20	0.41
53:1:1468:U:H2'	53:1:1522:A:H61	1.85	0.41
53:1:1666:G:H2'	53:1:1667:G:O4'	2.20	0.41
53:1:1709:U:H2'	53:1:1710:G:C8	2.55	0.41
53:1:2187:U:H2'	53:1:2188:U:C6	2.56	0.41
3:d:1:MET:N	3:d:14:VAL:O	2.48	0.41
7:h:59:LEU:HB3	7:h:62:ARG:HB3	2.03	0.41
19:t:63:VAL:C	19:t:64:LYS:HD2	2.45	0.41
28:D:26:ASN:OD1	53:1:682:G:H5'	2.20	0.41
36:L:78:ARG:NH2	36:L:81:GLY:O	2.53	0.41
45:U:5:ARG:HH22	45:U:26:ASN:HB3	1.86	0.41
50:Z:9:GLU:CB	50:Z:10:PRO:HD3	2.45	0.41
50:Z:33:ARG:HH11	50:Z:33:ARG:HG3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:54:LYS:HG2	51:a:56:ASP:OD1	2.19	0.41
53:1:1:G:H2'	53:1:2:G:C8	2.56	0.41
53:1:184:C:H4'	53:1:217:A:H2	1.84	0.41
53:1:435:C:C2'	53:1:436:C:H5'	2.51	0.41
53:1:441:U:H2'	53:1:442:G:C8	2.56	0.41
53:1:859:G:H1'	53:1:860:U:C5	2.47	0.41
53:1:1636:U:H2'	53:1:1637:A:C8	2.55	0.41
53:1:1677:A:H2'	53:1:1678:A:O4'	2.21	0.41
53:1:1788:C:H2'	53:1:1789:A:O4'	2.21	0.41
53:1:2215:C:H2'	53:1:2216:G:C8	2.55	0.41
53:1:2326:C:O2'	53:1:2327:A:OP1	2.38	0.41
53:1:2343:U:O2'	53:1:2344:U:H5'	2.20	0.41
53:1:2799:A:O2'	53:1:2800:A:H5'	2.20	0.41
55:5:31:G:O2'	55:5:32:C:H5'	2.21	0.41
5:f:17:LYS:HB2	5:f:24:THR:HB	2.01	0.41
6:g:72:ILE:HD12	6:g:108:VAL:HG13	2.02	0.41
7:h:7:ASP:O	7:h:11:ILE:HG12	2.20	0.41
13:n:13:ASN:OD1	13:n:13:ASN:N	2.49	0.41
13:n:18:GLN:HE21	13:n:22:ARG:HH12	1.69	0.41
34:J:152:VAL:HG11	37:M:98:LEU:HD13	2.01	0.41
36:L:85:GLN:NE2	55:6:32:C:H4'	2.35	0.41
36:L:142:ARG:CB	55:6:41:C:H4'	2.50	0.41
38:N:29:ILE:HG22	38:N:64:ILE:HB	2.03	0.41
41:Q:9:LYS:HA	41:Q:10:PRO:HD3	1.88	0.41
41:Q:40:THR:HA	41:Q:41:PRO:HD3	1.89	0.41
44:T:88:ARG:HG3	53:1:714:U:H5	1.86	0.41
52:3:24:U:H2'	52:3:25:C:C6	2.56	0.41
52:3:396:C:C3'	52:3:397:A:H5''	2.51	0.41
52:3:409:U:H2'	52:3:410:G:O4'	2.20	0.41
52:3:902:G:H2'	52:3:903:G:C8	2.55	0.41
52:3:1527:U:O2'	52:3:1528:U:H5'	2.21	0.41
53:1:112:U:H2'	53:1:113:U:H5'	2.03	0.41
53:1:937:C:H2'	53:1:938:G:C8	2.55	0.41
53:1:1105:U:C2'	53:1:1106:G:H5''	2.51	0.41
53:1:1170:C:H2'	53:1:1171:G:C8	2.55	0.41
53:1:2297:A:N1	53:1:2321:U:H5	2.17	0.41
53:1:2340:A:H2'	53:1:2341:G:H8	1.84	0.41
53:1:2441:U:O2'	53:1:2442:C:H5'	2.21	0.41
7:h:58:THR:CG2	53:1:1107:G:H5'	2.51	0.41
13:n:3:HIS:CD2	53:1:2820:A:H4'	2.55	0.41
21:v:26:PHE:HE1	21:v:44:HIS:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:w:39:THR:N	53:1:2331:G:H4'	2.34	0.41
22:w:52:ASP:OD1	53:1:2387:U:H5'	2.20	0.41
29:E:25:HIS:CE1	29:E:47:ALA:HB2	2.55	0.41
31:G:65:LYS:HE2	31:G:65:LYS:HB2	1.93	0.41
31:G:69:VAL:HG22	31:G:91:VAL:CG2	2.51	0.41
32:H:71:ARG:HG3	32:H:74:ILE:HG22	2.02	0.41
47:W:40:PRO:CB	52:3:720:C:H5''	2.36	0.41
48:X:54:ARG:HD3	52:3:958:A:C4	2.56	0.41
50:Z:13:VAL:HG13	50:Z:15:LEU:CG	2.48	0.41
51:a:175:ILE:HB	51:a:188:ASN:HB3	2.02	0.41
52:3:837:U:H2'	52:3:838:G:C8	2.54	0.41
52:3:1478:U:H2'	52:3:1479:C:C6	2.56	0.41
53:1:61:C:C2'	53:1:62:U:H5'	2.50	0.41
53:1:297:G:H2'	53:1:298:G:O4'	2.21	0.41
53:1:679:C:H2'	53:1:680:C:C6	2.56	0.41
53:1:1877:A:H2'	53:1:1878:G:O4'	2.21	0.41
53:1:2478:A:H2'	53:1:2479:U:O4'	2.20	0.41
53:1:2833:U:O2'	53:1:2834:G:H5'	2.21	0.41
58:8:224:ARG:HA	58:8:224:ARG:NH2	2.35	0.41
1:b:22:GLU:HB3	1:b:80:LEU:HD12	2.02	0.41
5:f:57:TYR:HB2	5:f:59:ASP:OD1	2.20	0.41
5:f:66:THR:HG23	53:1:2747:G:O2'	2.21	0.41
5:f:110:HIS:O	5:f:110:HIS:CG	2.73	0.41
15:p:6:GLN:O	15:p:10:GLU:OE2	2.39	0.41
15:p:88:ARG:HG3	15:p:112:ARG:HB3	2.03	0.41
19:t:61:LEU:HD21	19:t:82:LYS:HG3	2.02	0.41
20:u:31:GLY:O	20:u:66:VAL:HG23	2.21	0.41
26:B:8:THR:HG22	26:B:9:ARG:H	1.86	0.41
31:G:220:VAL:O	31:G:224:ARG:HG2	2.21	0.41
35:K:6:ILE:HG12	35:K:89:VAL:HG12	2.02	0.41
36:L:59:GLU:O	36:L:63:VAL:HG22	2.21	0.41
38:N:114:LYS:HB2	38:N:117:LEU:HD12	2.03	0.41
38:N:119:LYS:O	38:N:120:ALA:HB3	2.20	0.41
43:S:11:LYS:HZ1	43:S:15:LEU:CG	2.16	0.41
52:3:82:G:C2'	52:3:83:C:H5'	2.51	0.41
52:3:923:A:H61	52:3:1393:U:H3	1.67	0.41
52:3:1199:U:C2'	52:3:1200:C:H5'	2.49	0.41
52:3:1273:C:H2'	52:3:1274:A:O4'	2.21	0.41
53:1:341:C:H2'	53:1:342:A:H8	1.85	0.41
53:1:1528:A:H2'	53:1:1529:G:O4'	2.21	0.41
53:1:1538:G:O2'	53:1:1539:U:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1558:C:O4'	53:1:1560:G:C8	2.73	0.41
53:1:1801:A:H5''	53:1:2203:U:C2'	2.47	0.41
53:1:2361:G:O2'	53:1:2362:C:H5'	2.20	0.41
58:8:218:VAL:HG12	58:8:284:ARG:HE	1.86	0.41
2:c:100:LEU:HD13	2:c:100:LEU:HA	1.98	0.41
5:f:63:GLN:NE2	53:1:2757:A:H2	2.19	0.41
6:g:58:LEU:HA	6:g:61:VAL:HG22	2.01	0.41
7:h:59:LEU:HD22	7:h:62:ARG:NH2	2.35	0.41
9:j:96:ARG:NH2	53:1:2639:A:H4'	2.36	0.41
11:l:95:LEU:HD22	11:l:100:ILE:HD11	2.02	0.41
13:n:36:THR:HG22	13:n:37:THR:N	2.36	0.41
18:s:44:ALA:HA	18:s:47:VAL:HG22	2.02	0.41
21:v:36:ALA:HA	21:v:37:PRO:HD3	1.92	0.41
21:v:77:VAL:HG12	21:v:89:ILE:HG12	2.03	0.41
23:x:63:ILE:O	23:x:66:VAL:HG12	2.21	0.41
29:E:28:LEU:HD12	29:E:28:LEU:HA	1.94	0.41
31:G:9:LEU:O	31:G:14:HIS:HE1	2.04	0.41
33:I:184:LYS:HA	33:I:185:PRO:HD3	1.94	0.41
34:J:47:PHE:CZ	34:J:137:ARG:HG2	2.56	0.41
35:K:10:VAL:CG1	35:K:58:HIS:HB3	2.51	0.41
35:K:40:GLU:OE2	35:K:42:TRP:NE1	2.47	0.41
36:L:146:ALA:HB1	55:6:40:C:H4'	2.03	0.41
37:M:121:GLY:C	52:3:599:C:H4'	2.46	0.41
43:S:70:HIS:ND1	52:3:976:G:OP1	2.54	0.41
43:S:80:ARG:HG3	43:S:81:ILE:N	2.36	0.41
44:T:32:THR:HG22	44:T:36:ASN:ND2	2.36	0.41
46:V:68:LYS:HE2	52:3:267:C:OP2	2.20	0.41
51:a:212:VAL:HG13	51:a:212:VAL:O	2.20	0.41
52:3:138:G:H2'	52:3:139:A:C8	2.56	0.41
52:3:607:A:H2'	52:3:608:A:C8	2.56	0.41
52:3:1097:C:H2'	52:3:1098:C:C6	2.56	0.41
52:3:1409:C:H2'	52:3:1410:A:C8	2.56	0.41
53:1:828:U:H4'	53:1:831:G:C2	2.56	0.41
53:1:1308:A:H2'	53:1:1309:G:O4'	2.21	0.41
53:1:1827:U:H2'	53:1:1828:G:O4'	2.21	0.41
53:1:2070:A:H2'	53:1:2071:A:O4'	2.20	0.41
53:1:2092:U:C4'	53:1:2093:G:H5''	2.46	0.41
53:1:2273:A:H2'	53:1:2274:A:C8	2.56	0.41
53:1:2368:C:H2'	53:1:2369:A:C8	2.56	0.41
53:1:2417:C:H2'	53:1:2418:A:C8	2.55	0.41
53:1:2553:G:H3'	53:1:2554:U:C5'	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2665:A:O2'	53:1:2666:C:H5'	2.21	0.41
55:6:14:A:H2'	55:6:15:G:O4'	2.21	0.41
57:7:51:U:H2'	57:7:52:G:H8	1.86	0.41
58:8:14:ASN:HD21	58:8:231:ARG:HH21	1.68	0.41
58:8:171:VAL:HG11	58:8:192:LEU:HB2	2.03	0.41
58:8:216:GLU:OE1	58:8:230:GLY:HA2	2.20	0.41
58:8:220:SER:HB2	58:8:284:ARG:HD3	2.02	0.41
1:b:48:ILE:HG22	53:1:779:U:OP1	2.20	0.41
2:c:14:ILE:HG23	2:c:22:ILE:HB	2.03	0.41
6:g:117:LEU:HD12	6:g:117:LEU:N	2.36	0.41
8:i:123:ALA:HA	8:i:126:ARG:CZ	2.51	0.41
12:m:2:LEU:HD13	12:m:2:LEU:HA	1.93	0.41
17:r:49:ILE:O	17:r:49:ILE:HG13	2.20	0.41
20:u:33:VAL:HG22	20:u:34:ILE:N	2.36	0.41
24:y:2:LYS:HE2	53:1:77:G:C4'	2.49	0.41
25:z:5:LYS:HE3	25:z:5:LYS:HB3	1.99	0.41
33:I:12:ARG:HH22	52:3:428:G:H3'	1.85	0.41
35:K:47:LEU:HD22	47:W:65:SER:HB3	2.03	0.41
42:R:102:LYS:HD2	52:3:1226:C:N4	2.36	0.41
46:V:64:ARG:HA	46:V:65:PRO:HD3	1.95	0.41
52:3:246:A:H62	52:3:281:G:N2	2.19	0.41
52:3:600:A:H2'	52:3:601:G:C8	2.56	0.41
52:3:1062:U:H2'	52:3:1063:C:C6	2.56	0.41
53:1:249:C:H2'	53:1:2394:C:O2'	2.21	0.41
53:1:1805:A:H2'	53:1:1806:C:C6	2.56	0.41
53:1:1930:G:H2'	53:1:1931:U:OP2	2.21	0.41
53:1:2553:G:H1'	53:1:2582:G:H21	1.85	0.41
53:1:2569:G:O2'	53:1:2570:G:H5'	2.21	0.41
60:7:101:PHE:N	58:8:261:MET:HA	2.35	0.41
58:8:11:PRO:HD2	58:8:75:ARG:HA	2.03	0.41
6:g:125:THR:HG21	6:g:148:ALA:HB2	2.02	0.40
7:h:57:ASN:HB2	7:h:62:ARG:HD2	2.02	0.40
22:w:10:ARG:NH2	53:1:2279:G:N7	2.69	0.40
23:x:11:PRO:HB3	23:x:29:LEU:HD23	2.03	0.40
24:y:13:GLU:O	24:y:17:GLU:N	2.54	0.40
30:F:15:LYS:HE3	53:1:2753:A:H2	1.87	0.40
31:G:103:TRP:HD1	31:G:107:ARG:NH2	2.19	0.40
31:G:107:ARG:O	31:G:110:ILE:HG22	2.20	0.40
34:J:110:MET:CE	34:J:126:ALA:HB2	2.47	0.40
38:N:105:ARG:NE	52:3:1117:A:O3'	2.52	0.40
42:R:93:GLY:O	42:R:108:ARG:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:W:33:THR:HG22	47:W:37:LYS:O	2.22	0.40
52:3:853:C:O2'	52:3:854:U:H5'	2.21	0.40
52:3:1488:G:O2'	52:3:1489:G:H5'	2.20	0.40
53:1:751:A:H2'	53:1:789:A:H2	1.86	0.40
53:1:2553:G:H2'	53:1:2554:U:H4'	2.02	0.40
57:7:22:G:H2'	57:7:23:A:C8	2.56	0.40
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.52	0.40
8:i:89:SER:HB2	8:i:92:PRO:HG3	2.03	0.40
21:v:62:THR:HG22	21:v:69:GLU:HG2	2.02	0.40
21:v:82:TYR:O	21:v:83:LYS:HD3	2.21	0.40
24:y:2:LYS:HA	24:y:2:LYS:HD2	1.87	0.40
33:I:33:ILE:O	33:I:35:GLN:HG3	2.21	0.40
33:I:150:LYS:HE2	33:I:150:LYS:HB3	1.88	0.40
40:P:27:ASN:O	40:P:56:LYS:NZ	2.47	0.40
45:U:74:LEU:HD12	45:U:74:LEU:HA	1.93	0.40
46:V:4:ILE:HD12	46:V:4:ILE:N	2.35	0.40
46:V:59:GLU:HB3	46:V:76:ARG:O	2.20	0.40
48:X:16:LYS:HE3	48:X:16:LYS:HB3	1.95	0.40
52:3:45:G:H2'	52:3:46:G:C8	2.56	0.40
52:3:601:G:H2'	52:3:602:A:C8	2.56	0.40
52:3:608:A:H2'	52:3:609:A:O4'	2.21	0.40
52:3:629:A:H2'	52:3:630:A:O4'	2.20	0.40
53:1:176:A:O2'	53:1:177:G:H5'	2.21	0.40
53:1:741:U:H2'	53:1:742:A:C8	2.56	0.40
53:1:1077:A:C2'	53:1:1078:U:H5'	2.48	0.40
53:1:1169:A:O2'	53:1:1170:C:H5'	2.21	0.40
53:1:1771:C:H2'	53:1:1772:A:C8	2.56	0.40
53:1:1890:A:H2'	53:1:1891:G:O4'	2.21	0.40
53:1:2030:A:N3	53:1:2499:C:H5''	2.36	0.40
53:1:2186:G:H2'	53:1:2187:U:O4'	2.22	0.40
53:1:2227:A:H2'	53:1:2228:G:O4'	2.21	0.40
53:1:2464:G:O2'	53:1:2465:C:H5'	2.22	0.40
3:d:149:ILE:HG23	3:d:188:MET:SD	2.62	0.40
7:h:81:LEU:HB3	53:1:1107:G:O4'	2.21	0.40
14:o:62:LEU:HD12	14:o:62:LEU:C	2.46	0.40
19:t:13:ALA:HB1	24:y:33:ALA:CB	2.52	0.40
22:w:72:ASN:ND2	54:2:13:G:OP2	2.47	0.40
23:x:33:HIS:CE1	53:1:2228:G:N2	2.86	0.40
36:L:13:PRO:HA	36:L:20:GLU:HA	2.03	0.40
45:U:22:ALA:HB2	45:U:32:PHE:HB3	2.03	0.40
50:Z:28:LEU:C	50:Z:30:GLU:H	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:52:VAL:HA	50:Z:55:HIS:HB3	2.02	0.40
52:3:82:G:H2'	52:3:83:C:O4'	2.21	0.40
52:3:370:C:H2'	52:3:371:A:C8	2.56	0.40
52:3:1195:C:H2'	52:3:1197:A:O4'	2.21	0.40
52:3:1195:C:H5''	52:3:1196:A:OP2	2.21	0.40
53:1:607:U:O4	53:1:619:G:H2'	2.21	0.40
53:1:832:U:H2'	53:1:833:A:C8	2.57	0.40
53:1:1537:G:H3'	53:1:1537:G:N3	2.37	0.40
53:1:1843:C:H2'	53:1:1844:C:C6	2.57	0.40
53:1:1909:C:H2'	53:1:1910:G:C8	2.54	0.40
53:1:2070:A:O2'	53:1:2071:A:H5'	2.22	0.40
53:1:2495:G:O2'	53:1:2496:C:H5'	2.21	0.40
58:8:21:VAL:HA	61:8:501:GDP:O2B	2.20	0.40
7:h:122:GLN:N	7:h:122:GLN:CD	2.79	0.40
12:m:75:GLU:N	12:m:90:GLU:OE1	2.55	0.40
13:n:69:ARG:C	13:n:71:ARG:H	2.29	0.40
33:l:69:ARG:NH1	52:3:401:C:OP2	2.53	0.40
38:N:68:GLY:HA2	52:3:1250:A:H5'	2.04	0.40
38:N:117:LEU:HD21	38:N:123:ARG:HD3	2.02	0.40
49:Y:50:PHE:O	49:Y:53:MET:HG2	2.22	0.40
52:3:184:G:H4'	52:3:224:U:H4'	2.03	0.40
52:3:314:C:O2'	52:3:315:A:H5'	2.21	0.40
52:3:1202:U:C2'	52:3:1203:C:H5'	2.51	0.40
53:1:64:A:H2'	53:1:65:U:C6	2.57	0.40
53:1:374:A:H2'	53:1:375:G:O4'	2.21	0.40
53:1:1068:G:H2'	53:1:1069:A:H1'	2.03	0.40
53:1:2557:G:H2'	53:1:2558:C:C6	2.56	0.40
54:2:116:G:O2'	54:2:117:G:H5'	2.21	0.40
55:6:63:G:H2'	55:6:64:G:H8	1.85	0.40
1:b:119:VAL:HG12	1:b:130:PRO:HD2	2.02	0.40
10:k:58:LEU:HD23	10:k:58:LEU:H	1.86	0.40
10:k:76:VAL:HG22	10:k:77:ILE:N	2.36	0.40
10:k:105:ARG:O	10:k:108:ARG:NE	2.53	0.40
11:l:55:MET:HA	11:l:56:PRO:HD3	1.81	0.40
18:s:71:VAL:HG13	18:s:71:VAL:O	2.22	0.40
41:Q:31:GLY:C	41:Q:78:VAL:HG13	2.46	0.40
45:U:8:ARG:NH1	45:U:9:HIS:O	2.54	0.40
50:Z:50:SER:HA	50:Z:53:LYS:HD2	2.04	0.40
52:3:623:C:H2'	52:3:624:C:H6	1.87	0.40
53:1:553:G:H2'	53:1:554:U:O4'	2.22	0.40
53:1:581:C:H2'	53:1:582:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:984:A:H5''	53:1:985:C:OP2	2.21	0.40
53:1:1239:G:H2'	53:1:1240:U:O4'	2.21	0.40
53:1:1923:U:H2'	53:1:1924:C:C6	2.57	0.40
53:1:2194:U:H2'	53:1:2195:U:H6	1.87	0.40
54:2:88:C:H4'	54:2:89:U:OP1	2.20	0.40
55:5:17:C:H2'	55:5:17(A):U:C5	2.56	0.40
58:8:261:MET:HB2	58:8:275:VAL:HG12	2.04	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%)	238 (88%)	28 (10%)	3 (1%)	11	42
2	c	207/209 (99%)	184 (89%)	22 (11%)	1 (0%)	24	56
3	d	199/201 (99%)	182 (92%)	15 (8%)	2 (1%)	12	43
4	e	175/177 (99%)	156 (89%)	17 (10%)	2 (1%)	11	42
5	f	174/176 (99%)	162 (93%)	12 (7%)	0	100	100
6	g	147/149 (99%)	119 (81%)	25 (17%)	3 (2%)	6	32
7	h	129/131 (98%)	97 (75%)	26 (20%)	6 (5%)	2	18
8	i	139/141 (99%)	117 (84%)	17 (12%)	5 (4%)	2	23
9	j	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	9	37
10	k	120/122 (98%)	97 (81%)	18 (15%)	5 (4%)	2	20
11	l	141/143 (99%)	112 (79%)	24 (17%)	5 (4%)	3	24
12	m	134/136 (98%)	116 (87%)	15 (11%)	3 (2%)	5	31
13	n	118/120 (98%)	99 (84%)	18 (15%)	1 (1%)	16	48
14	o	114/116 (98%)	110 (96%)	3 (3%)	1 (1%)	14	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	p	112/114 (98%)	98 (88%)	13 (12%)	1 (1%)	14	45
16	q	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
17	r	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	6	32
18	s	108/110 (98%)	95 (88%)	10 (9%)	3 (3%)	4	27
19	t	91/93 (98%)	81 (89%)	9 (10%)	1 (1%)	11	42
20	u	100/102 (98%)	83 (83%)	15 (15%)	2 (2%)	6	32
21	v	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	w	73/75 (97%)	64 (88%)	8 (11%)	1 (1%)	9	37
23	x	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
24	y	61/63 (97%)	58 (95%)	2 (3%)	1 (2%)	7	35
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
26	B	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
27	C	48/50 (96%)	40 (83%)	7 (15%)	1 (2%)	5	31
28	D	44/46 (96%)	39 (89%)	4 (9%)	1 (2%)	5	30
29	E	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	35
30	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	27
31	G	223/225 (99%)	206 (92%)	17 (8%)	0	100	100
32	H	204/206 (99%)	194 (95%)	9 (4%)	1 (0%)	24	56
33	I	203/205 (99%)	174 (86%)	25 (12%)	4 (2%)	6	32
34	J	155/157 (99%)	125 (81%)	24 (16%)	6 (4%)	2	21
35	K	98/100 (98%)	76 (78%)	17 (17%)	5 (5%)	1	17
36	L	149/151 (99%)	131 (88%)	16 (11%)	2 (1%)	9	38
37	M	127/129 (98%)	115 (91%)	11 (9%)	1 (1%)	16	48
38	N	125/127 (98%)	102 (82%)	20 (16%)	3 (2%)	4	29
39	O	96/98 (98%)	77 (80%)	14 (15%)	5 (5%)	1	17
40	P	114/116 (98%)	88 (77%)	21 (18%)	5 (4%)	2	19
41	Q	121/123 (98%)	99 (82%)	17 (14%)	5 (4%)	2	20
42	R	112/114 (98%)	101 (90%)	7 (6%)	4 (4%)	2	23
43	S	98/100 (98%)	81 (83%)	17 (17%)	0	100	100
44	T	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	40
45	U	80/82 (98%)	72 (90%)	7 (9%)	1 (1%)	9	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	V	78/80 (98%)	66 (85%)	9 (12%)	3 (4%)	2	22
47	W	63/65 (97%)	57 (90%)	5 (8%)	1 (2%)	7	35
48	X	77/79 (98%)	68 (88%)	8 (10%)	1 (1%)	9	38
49	Y	83/85 (98%)	82 (99%)	1 (1%)	0	100	100
50	Z	63/65 (97%)	43 (68%)	17 (27%)	3 (5%)	2	17
51	a	130/223 (58%)	123 (95%)	6 (5%)	1 (1%)	16	48
58	8	340/400 (85%)	299 (88%)	38 (11%)	3 (1%)	14	45
All	All	6259/6512 (96%)	5480 (88%)	670 (11%)	109 (2%)	9	34

All (109) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	204	LEU
3	d	83	VAL
6	g	9	VAL
7	h	108	VAL
7	h	118	ILE
10	k	35	VAL
11	l	31	GLY
12	m	58	LYS
12	m	69	PRO
17	r	54	VAL
22	w	80	ALA
30	F	37	GLN
34	J	93	VAL
34	J	122	VAL
38	N	90	ASP
40	P	13	LYS
42	R	4	ALA
42	R	65	GLU
44	T	46	LYS
46	V	49	ASN
50	Z	8	ASN
50	Z	34	ARG
1	b	232	GLY
7	h	51	TYR
7	h	81	LEU
8	i	97	VAL
9	j	81	ILE
10	k	92	GLU

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Mol	Chain	Res	Type
10	k	93	GLN
11	l	65	GLY
11	l	87	GLY
12	m	59	ARG
15	p	104	GLY
20	u	51	LEU
24	y	24	GLU
29	E	31	ILE
32	H	156	LEU
33	I	23	GLY
33	I	34	GLU
39	O	89	ARG
40	P	89	GLY
41	Q	24	GLU
41	Q	27	PRO
50	Z	25	ALA
58	8	318	GLY
6	g	10	ALA
6	g	11	ASN
7	h	58	THR
8	i	11	GLN
13	n	107	ASN
27	C	6	GLU
33	I	167	PRO
34	J	50	GLY
34	J	99	SER
34	J	121	ASN
35	K	39	LEU
35	K	86	ARG
38	N	100	ALA
39	O	35	GLN
39	O	37	ARG
40	P	14	GLN
40	P	88	PRO
41	Q	35	ARG
41	Q	88	ASP
46	V	17	GLU
58	8	334	ARG
4	e	20	ASN
9	j	110	PRO
11	l	29	LYS
14	o	34	HIS

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Mol	Chain	Res	Type
18	s	3	THR
18	s	64	ALA
20	u	98	ASN
28	D	3	ARG
33	I	47	LEU
34	J	11	GLN
35	K	55	HIS
35	K	92	THR
37	M	47	ASP
39	O	42	LEU
40	P	92	ARG
41	Q	33	CYS
48	X	4	LEU
58	8	335	THR
1	b	246	PRO
2	c	113	SER
10	k	89	ASN
11	l	88	GLY
17	r	28	ALA
18	s	65	ASP
19	t	52	GLU
36	L	18	GLY
36	L	32	ASP
38	N	12	LYS
42	R	7	ASN
45	U	79	ASN
51	a	6	LYS
10	k	48	PRO
35	K	40	GLU
39	O	41	PRO
42	R	5	GLY
4	e	175	PRO
7	h	119	PRO
8	i	22	PRO
8	i	31	GLY
8	i	92	PRO
3	d	89	PRO
46	V	65	PRO
47	W	17	VAL

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%)	214 (99%)	2 (1%)	70	75
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	79
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	77
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100
7	h	100/100 (100%)	98 (98%)	2 (2%)	48	64
8	i	109/109 (100%)	108 (99%)	1 (1%)	70	75
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	103 (100%)	0	100	100
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	74
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	75
13	n	100/100 (100%)	99 (99%)	1 (1%)	68	74
14	o	86/86 (100%)	86 (100%)	0	100	100
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	73
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	72
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	71
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	46 (98%)	1 (2%)	47	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	C	45/45 (100%)	43 (96%)	2 (4%)	25	50
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	57
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	73
32	H	170/170 (100%)	170 (100%)	0	100	100
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	73
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	104 (100%)	0	100	100
38	N	105/105 (100%)	104 (99%)	1 (1%)	68	74
39	O	86/86 (100%)	86 (100%)	0	100	100
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	102 (99%)	1 (1%)	68	74
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	82 (99%)	1 (1%)	63	72
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	68
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%)	54 (98%)	1 (2%)	51	67
51	a	110/174 (63%)	110 (100%)	0	100	100
58	8	291/332 (88%)	289 (99%)	2 (1%)	76	77
All	All	5199/5304 (98%)	5171 (100%)	28 (0%)	78	80

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	156	SER
1	b	193	GLU

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Mol	Chain	Res	Type
2	c	180	VAL
3	d	133	LEU
4	e	90	LEU
7	h	118	ILE
7	h	119	PRO
8	i	138	VAL
11	l	116	VAL
12	m	118	LYS
13	n	60	VAL
16	q	58	GLN
17	r	54	VAL
21	v	78	GLN
26	B	8	THR
27	C	45	HIS
27	C	46	VAL
30	F	37	GLN
31	G	67	LEU
31	G	144	GLU
35	K	16	GLU
38	N	87	MET
41	Q	51	VAL
43	S	91	GLU
45	U	19	VAL
50	Z	10	PRO
58	8	196	LEU
58	8	293	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (128) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	24	HIS
1	b	45	ASN
1	b	57	HIS
1	b	116	GLN
1	b	127	ASN
1	b	133	ASN
2	c	32	ASN
2	c	42	ASN
2	c	149	ASN
3	d	41	GLN
3	d	62	GLN
3	d	97	ASN

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Mol	Chain	Res	Type
3	d	195	GLN
4	e	4	HIS
4	e	20	ASN
4	e	51	ASN
5	f	103	ASN
5	f	110	HIS
5	f	138	GLN
6	g	11	ASN
6	g	43	ASN
6	g	66	ASN
7	h	103	ASN
7	h	122	GLN
8	i	33	ASN
9	j	58	ASN
9	j	135	GLN
9	j	136	GLN
10	k	5	GLN
10	k	88	ASN
10	k	89	ASN
12	m	22	GLN
12	m	88	ASN
13	n	18	GLN
13	n	31	HIS
13	n	62	ASN
14	o	98	GLN
14	o	100	HIS
15	p	6	GLN
15	p	65	ASN
17	r	11	GLN
17	r	18	GLN
17	r	43	ASN
18	s	31	GLN
19	t	15	HIS
19	t	59	ASN
19	t	92	ASN
20	u	39	ASN
20	u	45	GLN
20	u	53	GLN
20	u	73	ASN
21	v	5	ASN
21	v	12	GLN
21	v	24	ASN

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Mol	Chain	Res	Type
21	v	87	GLN
22	w	46	ASN
22	w	53	HIS
23	x	5	GLN
23	x	33	HIS
24	y	27	ASN
24	y	39	GLN
24	y	41	HIS
24	y	58	ASN
25	z	19	HIS
26	B	3	GLN
26	B	5	ASN
27	C	18	HIS
29	E	42	HIS
31	G	18	GLN
31	G	92	ASN
31	G	119	GLN
31	G	145	ASN
31	G	169	HIS
31	G	176	ASN
32	H	31	ASN
32	H	184	ASN
32	H	189	HIS
33	I	35	GLN
33	I	53	GLN
33	I	73	ASN
33	I	88	ASN
33	I	99	ASN
33	I	195	ASN
33	I	197	HIS
34	J	18	ASN
34	J	72	ASN
34	J	131	ASN
35	K	3	HIS
35	K	11	HIS
35	K	68	GLN
36	L	27	ASN
36	L	67	ASN
36	L	121	ASN
36	L	129	ASN
38	N	4	GLN
38	N	49	GLN

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Mol	Chain	Res	Type
38	N	74	GLN
38	N	125	GLN
39	O	58	ASN
40	P	14	GLN
40	P	21	HIS
40	P	39	ASN
40	P	117	HIS
42	R	13	HIS
42	R	51	GLN
43	S	42	ASN
43	S	59	GLN
43	S	65	GLN
44	T	19	ASN
44	T	34	GLN
44	T	36	ASN
44	T	37	HIS
45	U	9	HIS
45	U	29	ASN
45	U	40	ASN
45	U	63	GLN
46	V	49	ASN
47	W	30	ASN
47	W	53	GLN
49	Y	19	HIS
49	Y	69	ASN
49	Y	81	GLN
51	a	188	ASN
58	8	12	HIS
58	8	14	ASN
58	8	20	HIS
58	8	119	HIS
58	8	330	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	136 (8%)	3 (0%)
53	1	2902/2903 (99%)	320 (11%)	10 (0%)
54	2	119/120 (99%)	9 (7%)	1 (0%)
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	8 (10%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	11 (14%)	1 (1%)
All	All	4803/4810 (99%)	493 (10%)	15 (0%)

All (493) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A
52	3	71	A
52	3	87	C
52	3	100	G
52	3	144	G
52	3	183	C
52	3	184	G
52	3	197	A
52	3	209	U
52	3	210	C
52	3	226	G
52	3	247	G
52	3	251	G
52	3	266	G
52	3	267	C
52	3	281	G
52	3	289	G
52	3	345	C
52	3	346	G
52	3	351	G
52	3	352	C
52	3	355	C
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	439	U

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Mol	Chain	Res	Type
52	3	467	U
52	3	479	U
52	3	485	U
52	3	486	U
52	3	496	A
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	642	A
52	3	665	A
52	3	688	G
52	3	703	G
52	3	724	G
52	3	755	G
52	3	777	A
52	3	794	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	873	A
52	3	890	G
52	3	902	G
52	3	926	G
52	3	934	C
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A

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Mol	Chain	Res	Type
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1030	U
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1053	G
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1146	A
52	3	1159	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1198	G
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1258	G
52	3	1260	G
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1282	C
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1320	C

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Mol	Chain	Res	Type
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1381	U
52	3	1395	C
52	3	1446	A
52	3	1448	C
52	3	1452	C
52	3	1492	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1533	C
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A
53	1	75	G
53	1	84	A
53	1	102	U
53	1	119	A
53	1	120	U
53	1	138	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	216	A
53	1	221	A
53	1	222	A

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Mol	Chain	Res	Type
53	1	229	C
53	1	248	G
53	1	249	C
53	1	255	A
53	1	265	A
53	1	266	G
53	1	276	U
53	1	278	A
53	1	281	C
53	1	294	A
53	1	301	G
53	1	311	A
53	1	323	C
53	1	329	G
53	1	330	A
53	1	353	C
53	1	361	G
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	405	U
53	1	406	G
53	1	411	G
53	1	422	A
53	1	424	G
53	1	451	U
53	1	455	C
53	1	457	A
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	531	C
53	1	532	A
53	1	542	C
53	1	543	G
53	1	545	U
53	1	563	A

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Mol	Chain	Res	Type
53	1	573	U
53	1	588	U
53	1	603	A
53	1	616	A
53	1	627	A
53	1	637	A
53	1	645	C
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	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	887	U
53	1	888	C
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G

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Mol	Chain	Res	Type
53	1	983	A
53	1	995	C
53	1	996	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	1046	A
53	1	1054	A
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	1143	A
53	1	1156	A
53	1	1175	A
53	1	1177	G
53	1	1180	U
53	1	1212	G
53	1	1250	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A
53	1	1301	A
53	1	1321	A
53	1	1329	U
53	1	1330	C
53	1	1332	G

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Mol	Chain	Res	Type
53	1	1345	C
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1395	A
53	1	1398	C
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1454	C
53	1	1458	U
53	1	1461	C
53	1	1476	U
53	1	1482	G
53	1	1490	A
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1533	C
53	1	1535	A
53	1	1536	C
53	1	1537	G
53	1	1555	G
53	1	1559	U
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1584	U
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	G
53	1	1699	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1738	G
53	1	1758	U
53	1	1764	C

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Mol	Chain	Res	Type
53	1	1773	A
53	1	1780	A
53	1	1800	C
53	1	1801	A
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1847	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	1931	U
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	1971	U
53	1	1972	G
53	1	1991	U
53	1	1993	U
53	1	1997	C
53	1	2022	U
53	1	2023	C
53	1	2030	A
53	1	2031	A
53	1	2036	C
53	1	2043	C
53	1	2055	C
53	1	2056	G
53	1	2060	A
53	1	2061	G
53	1	2062	A
53	1	2069	G
53	1	2072	C

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Mol	Chain	Res	Type
53	1	2093	G
53	1	2096	C
53	1	2110	G
53	1	2111	U
53	1	2112	G
53	1	2118	U
53	1	2119	A
53	1	2132	U
53	1	2133	G
53	1	2147	A
53	1	2162	G
53	1	2172	U
53	1	2173	A
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2212	A
53	1	2213	U
53	1	2225	A
53	1	2239	G
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	2406	A
53	1	2423	U
53	1	2424	C
53	1	2427	C
53	1	2429	G
53	1	2430	A
53	1	2435	A
53	1	2441	U

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Mol	Chain	Res	Type
53	1	2448	A
53	1	2476	A
53	1	2491	U
53	1	2498	C
53	1	2502	G
53	1	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2609	U
53	1	2613	U
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U
53	1	2714	G
53	1	2716	C
53	1	2744	G
53	1	2748	A
53	1	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
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2849	U
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2880	C

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Mol	Chain	Res	Type
53	1	2893	A
54	2	4	C
54	2	13	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	9	G
55	5	18	G
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	61	C
55	6	6	G
55	6	9	G
55	6	18	G
55	6	19	G
55	6	20	U
55	6	47	U
55	6	49	G
55	6	76	A
56	4	12	A
56	4	13	A
57	7	8	U
57	7	9	A
57	7	10	G
57	7	17	C
57	7	18	G
57	7	21	A
57	7	43	C
57	7	44	G
57	7	45	U
57	7	46	G
57	7	48	C

All (15) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
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Mol	Chain	Res	Type
52	3	438	U
52	3	1190	G
52	3	1201	A
53	1	421	C
53	1	490	C
53	1	859	G
53	1	1020	A
53	1	1130	U
53	1	1475	G
53	1	1930	G
53	1	2296	U
53	1	2326	C
53	1	2391	G
54	2	88	C
57	7	42	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](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	FME	5	101	55	8,9,10	0.49	0	8,9,11	0.90	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
61	GDP	8	501	-	29,30,30	1.34	2 (6%)	45,47,47	1.90	12 (26%)
60	PHE	7	101	57	10,11,12	0.68	0	8,13,15	0.26	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
59	FME	5	101	55	-	1/7/9/11	-
61	GDP	8	501	-	-	3/16/32/32	0/3/3/3
60	PHE	7	101	57	-	0/5/6/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PB-O1B	3.62	1.61	1.50
61	8	501	GDP	PA-O3A	2.39	1.62	1.59

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	C5-C4-N3	-5.65	119.41	128.39
61	8	501	GDP	C2-N3-C4	5.52	121.81	112.30
61	8	501	GDP	N9-C4-N3	4.28	134.51	125.95
61	8	501	GDP	C8-N7-C5	2.97	109.55	104.26
61	8	501	GDP	O4'-C4'-C3'	2.76	110.63	105.15
61	8	501	GDP	C2-N1-C6	-2.47	120.62	125.11
61	8	501	GDP	C6-C5-N7	2.37	134.60	130.29
61	8	501	GDP	O5'-PA-O1A	-2.34	99.65	108.94
61	8	501	GDP	C4-C5-N7	-2.23	107.14	110.67
61	8	501	GDP	O6-C6-C5	-2.18	120.77	126.53
61	8	501	GDP	C5-C6-N1	2.14	118.70	113.25
61	8	501	GDP	O2B-PB-O3A	2.12	111.75	104.64

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA
61	8	501	GDP	PA-O3A-PB-O2B

Continued on next page...

Continued from previous page...

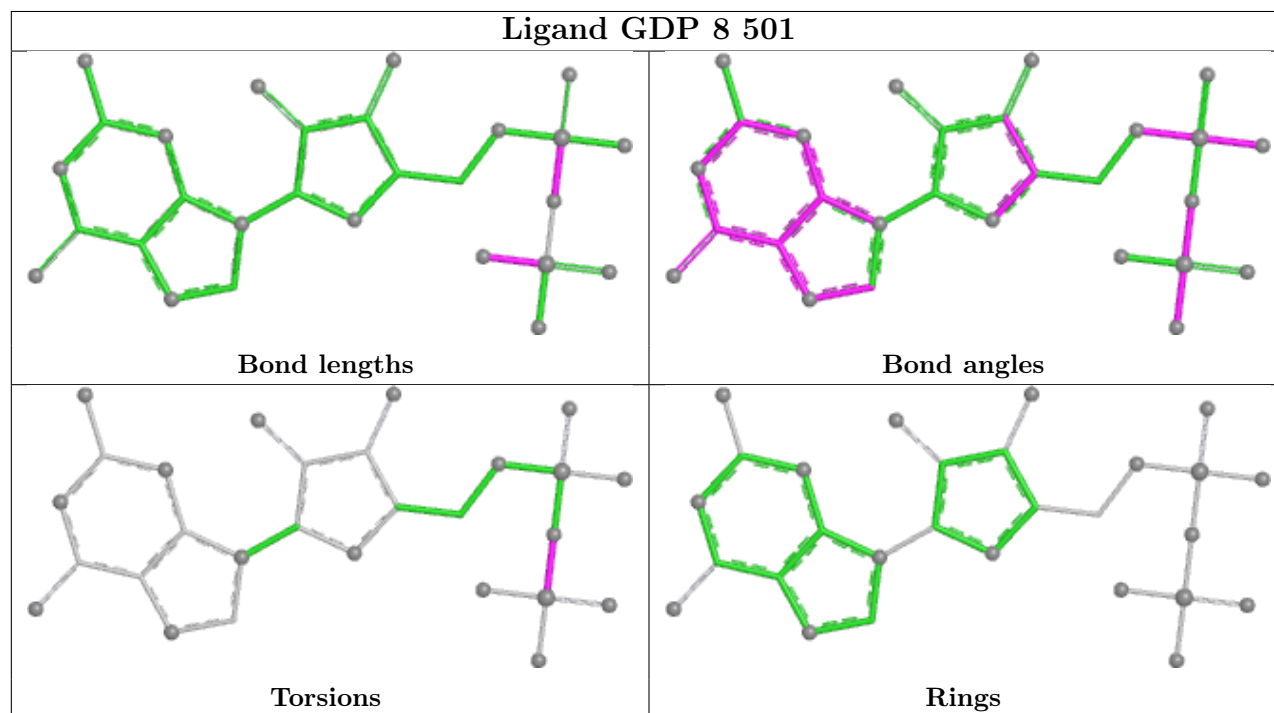
Mol	Chain	Res	Type	Atoms
61	8	501	GDP	PA-O3A-PB-O3B
61	8	501	GDP	PA-O3A-PB-O1B

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	8	501	GDP	1	0
60	7	101	PHE	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

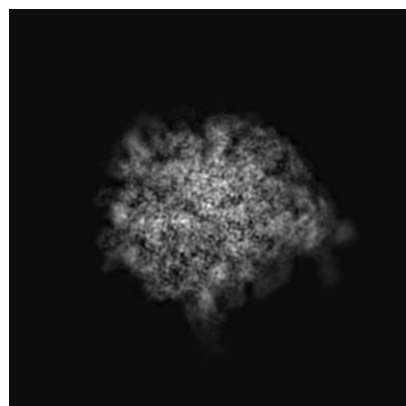
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21628. These allow visual inspection of the internal detail of the map and identification of artifacts.

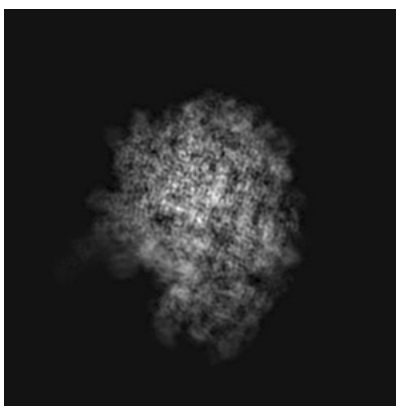
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

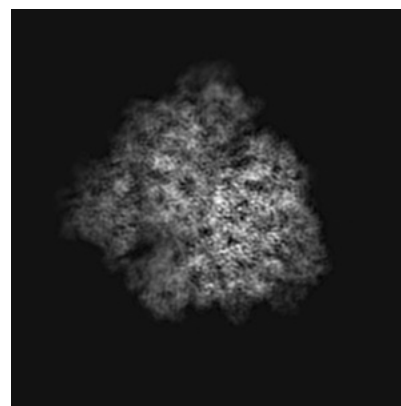
6.1.1 Primary map



X

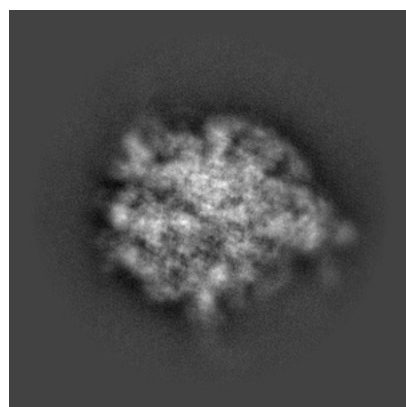


Y

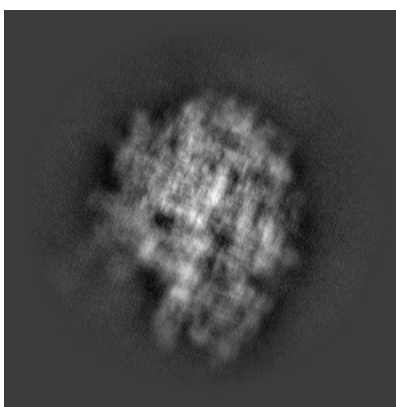


Z

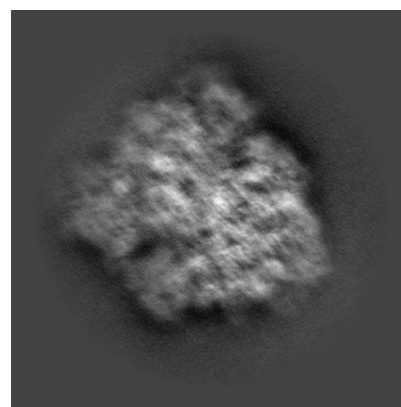
6.1.2 Raw map



X



Y

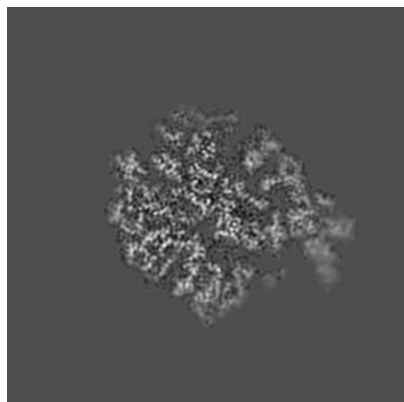


Z

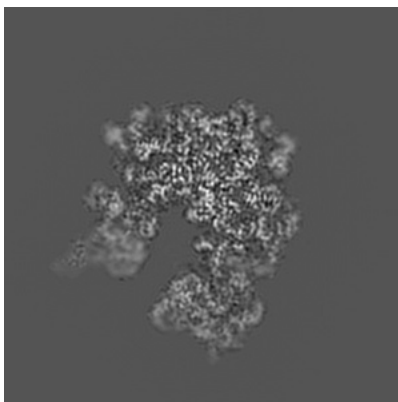
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

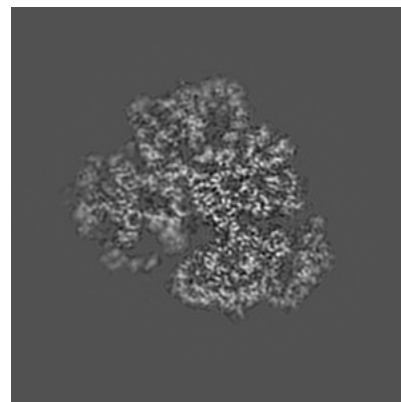
6.2.1 Primary map



X Index: 144

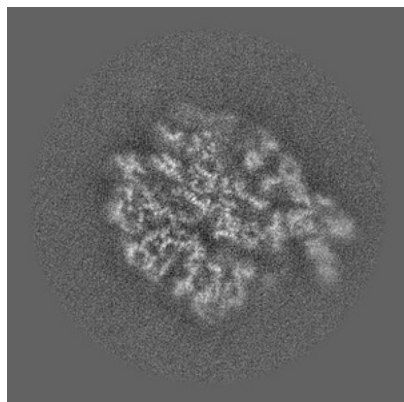


Y Index: 144

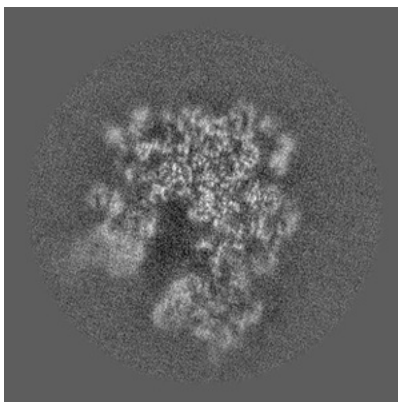


Z Index: 144

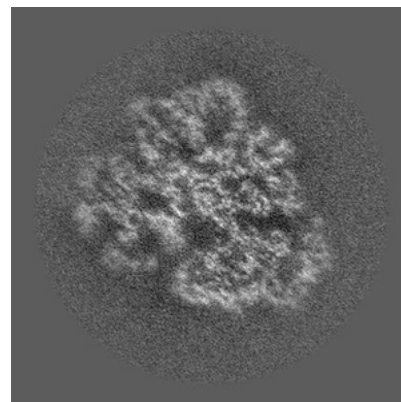
6.2.2 Raw map



X Index: 144



Y Index: 144

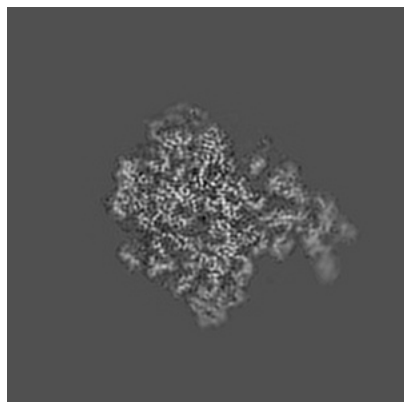


Z Index: 144

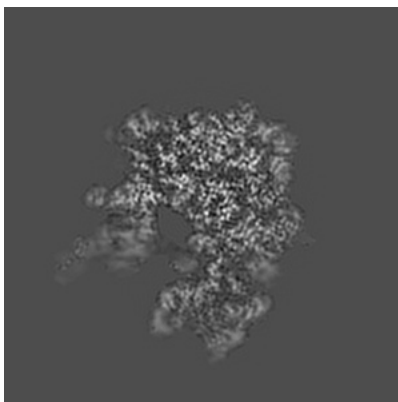
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

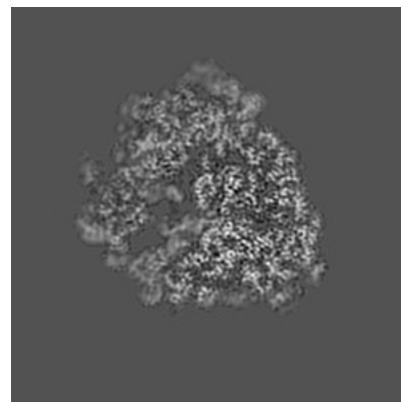
6.3.1 Primary map



X Index: 149

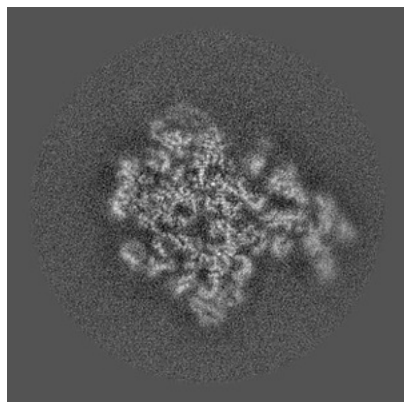


Y Index: 149

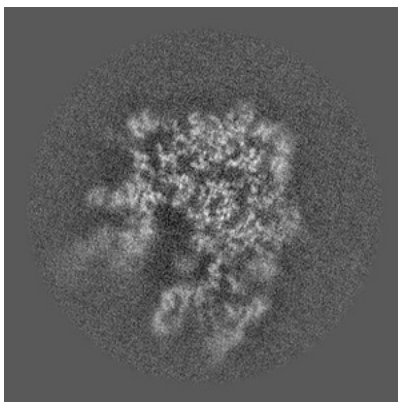


Z Index: 135

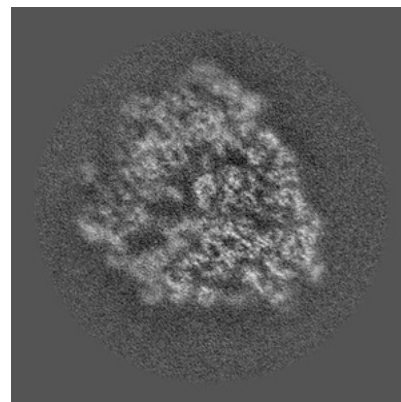
6.3.2 Raw map



X Index: 149



Y Index: 149

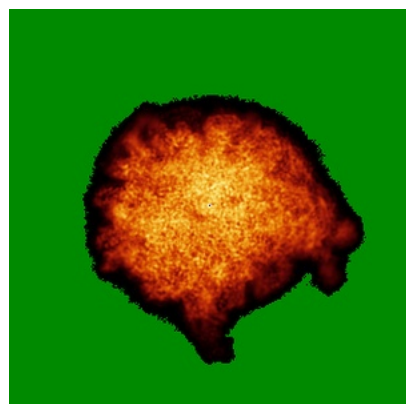


Z Index: 135

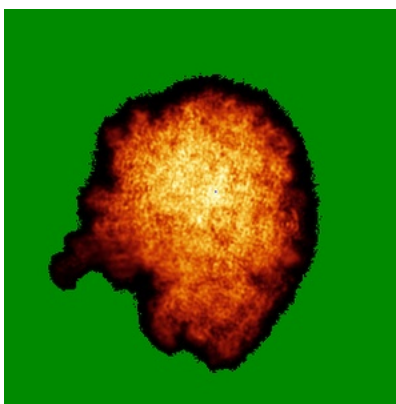
The images above show the largest variance slices of the map in three orthogonal directions.

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

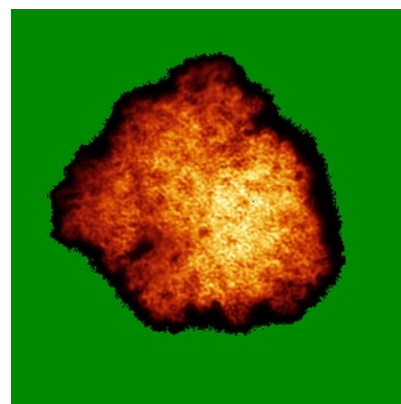
6.4.1 Primary map



X

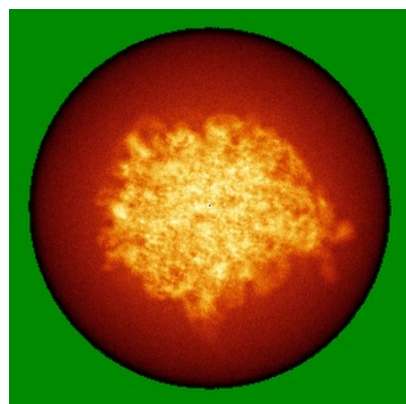


Y

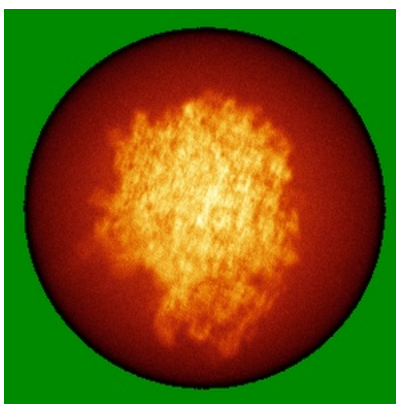


Z

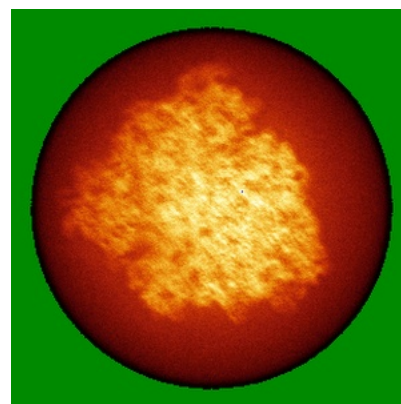
6.4.2 Raw map



X



Y

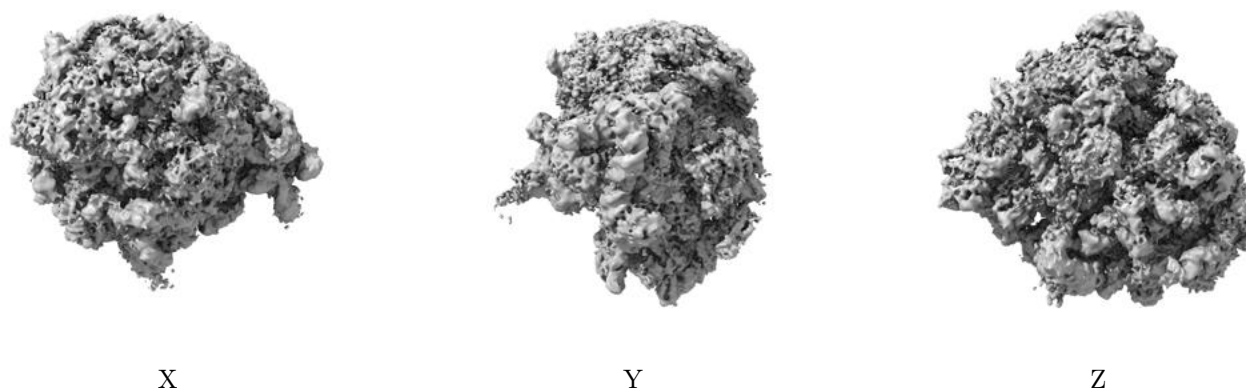


Z

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.

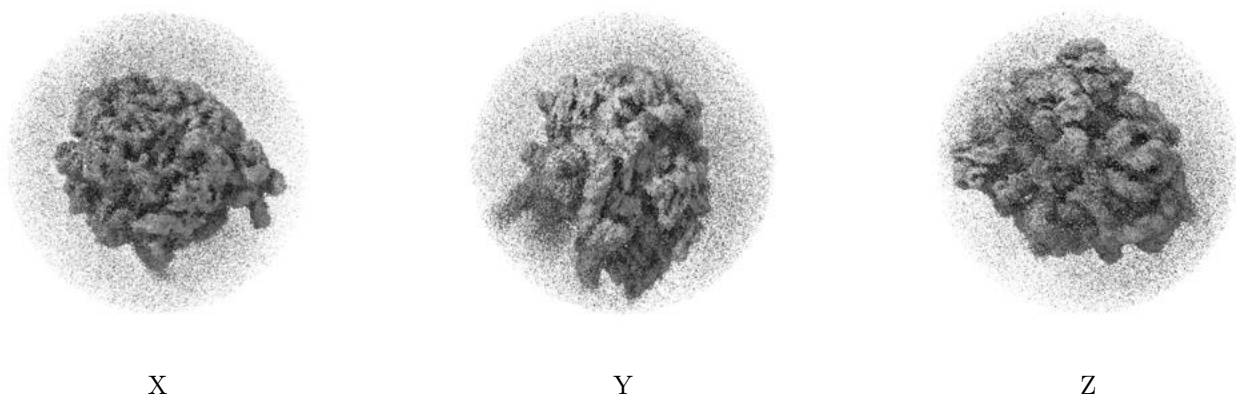
6.5 Orthogonal surface views [i](#)

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.

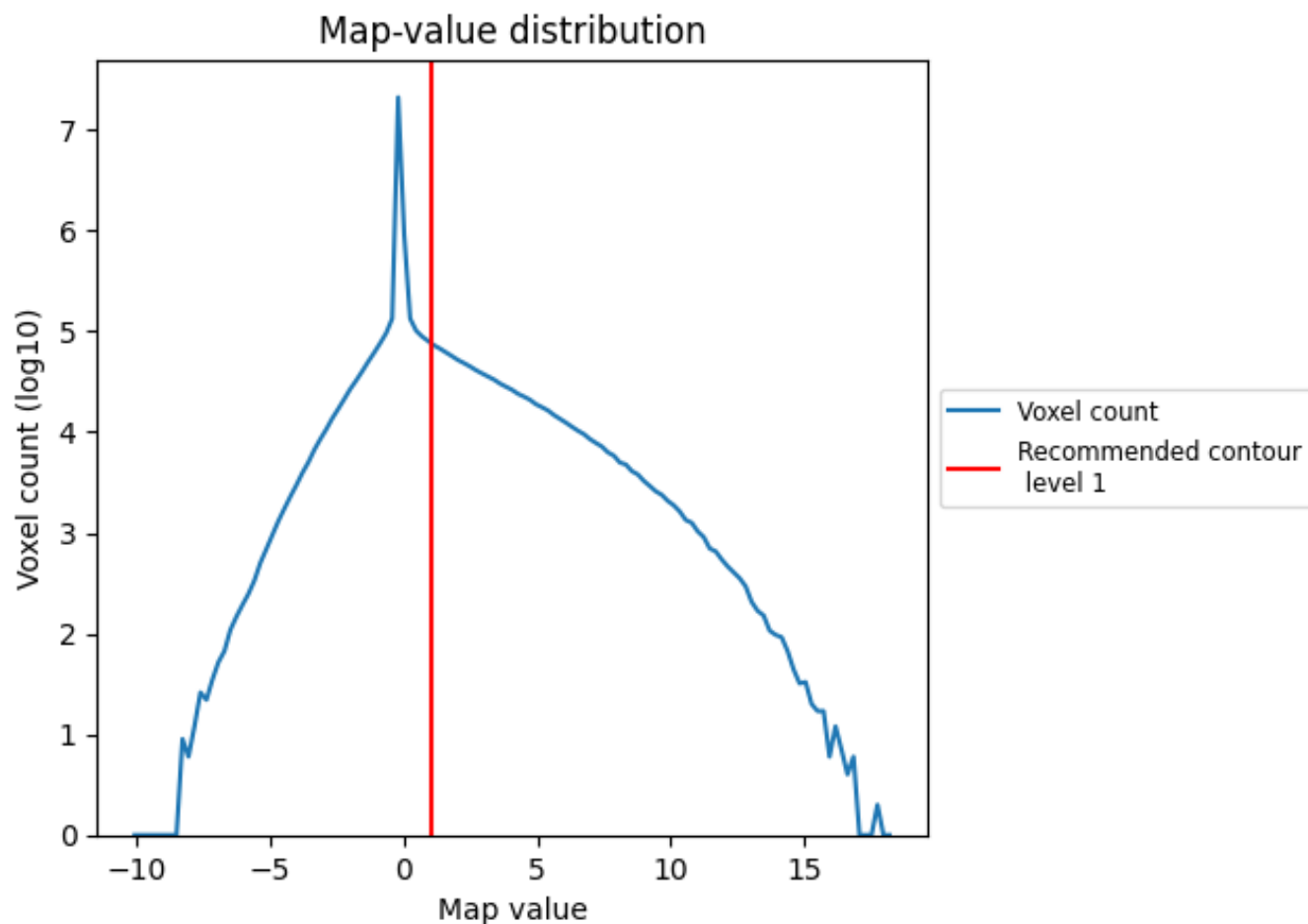
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

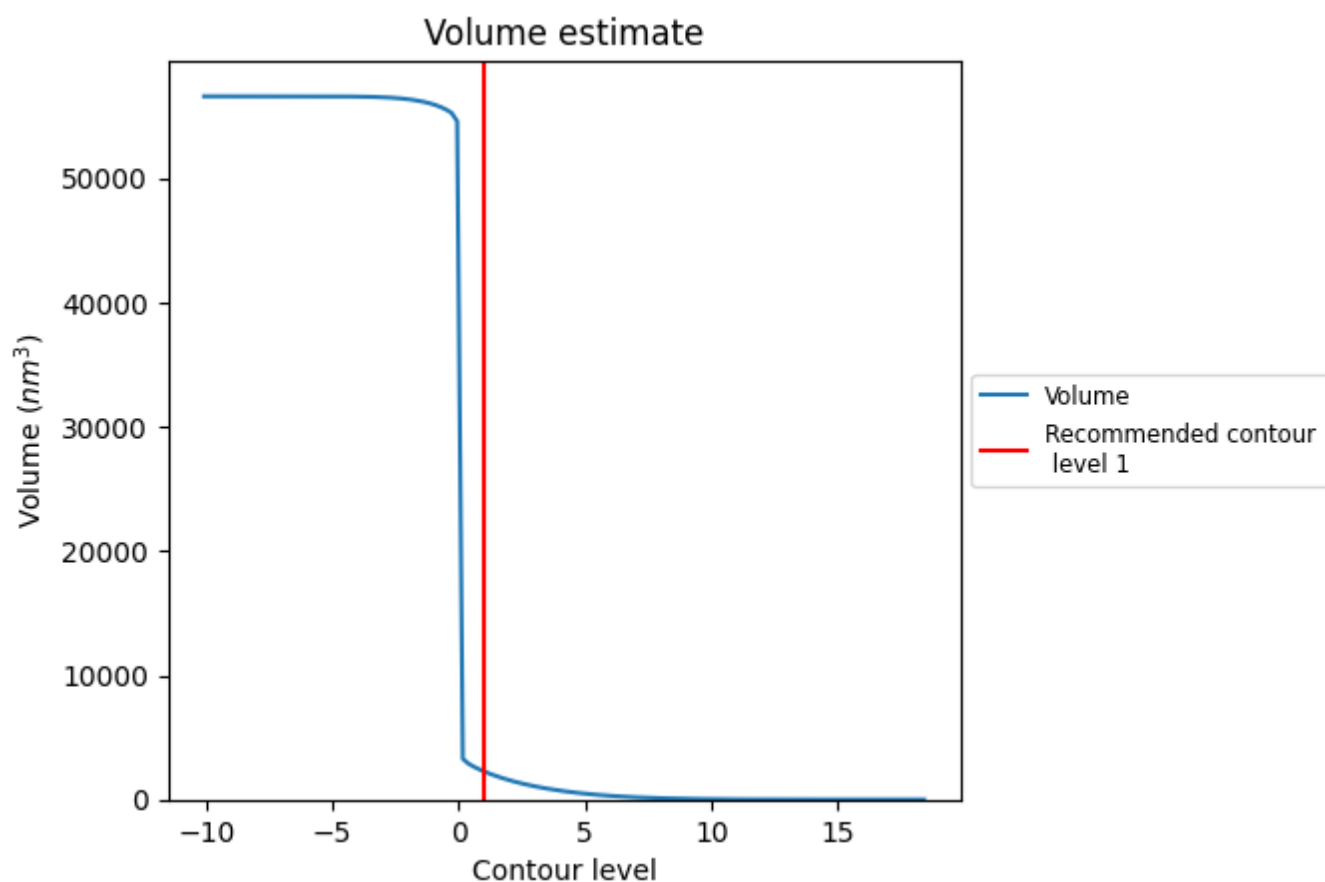
This section contains the results of statistical analysis of the map.

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.

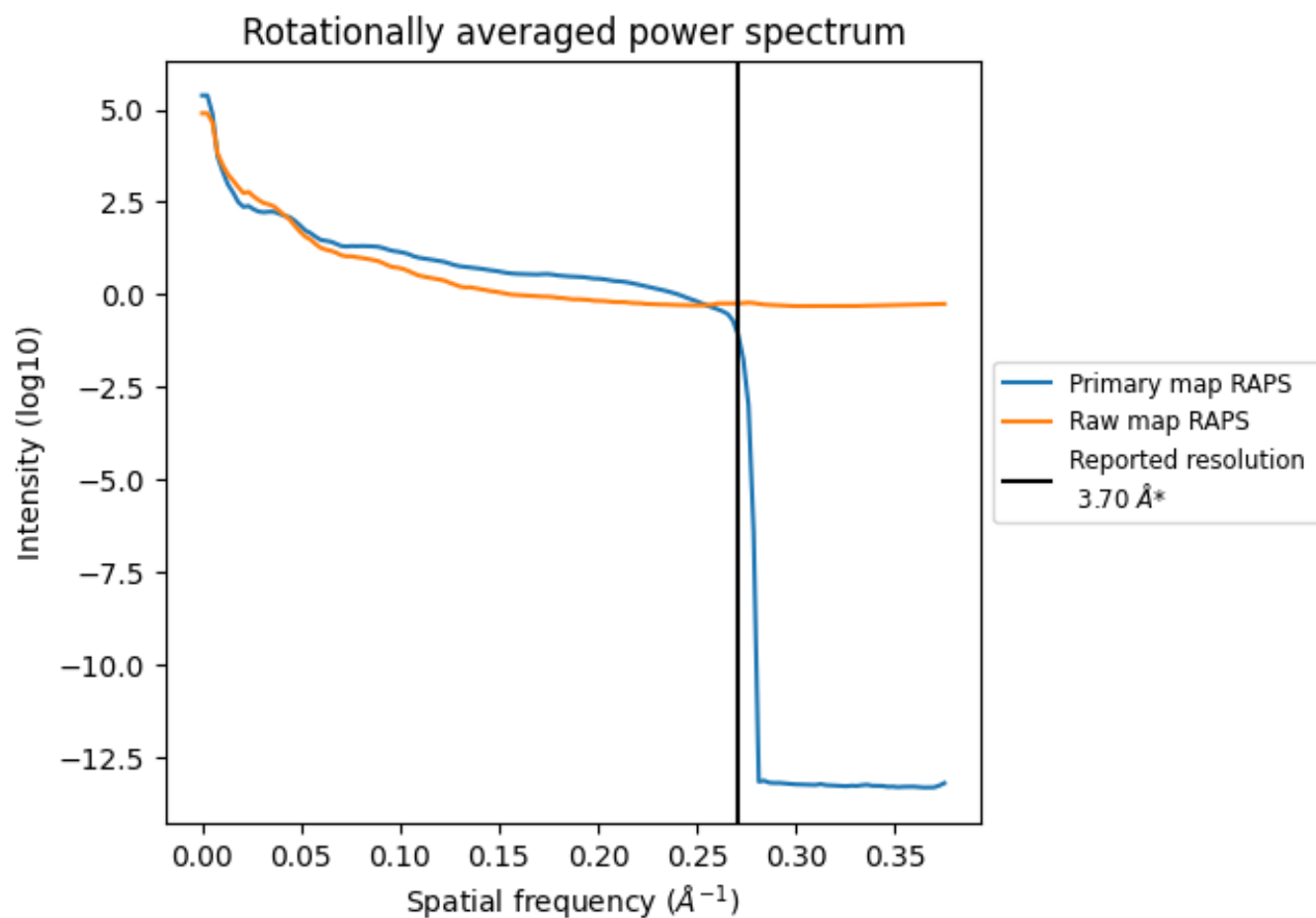
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2262 nm³; this corresponds to an approximate mass of 2043 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 ⓘ

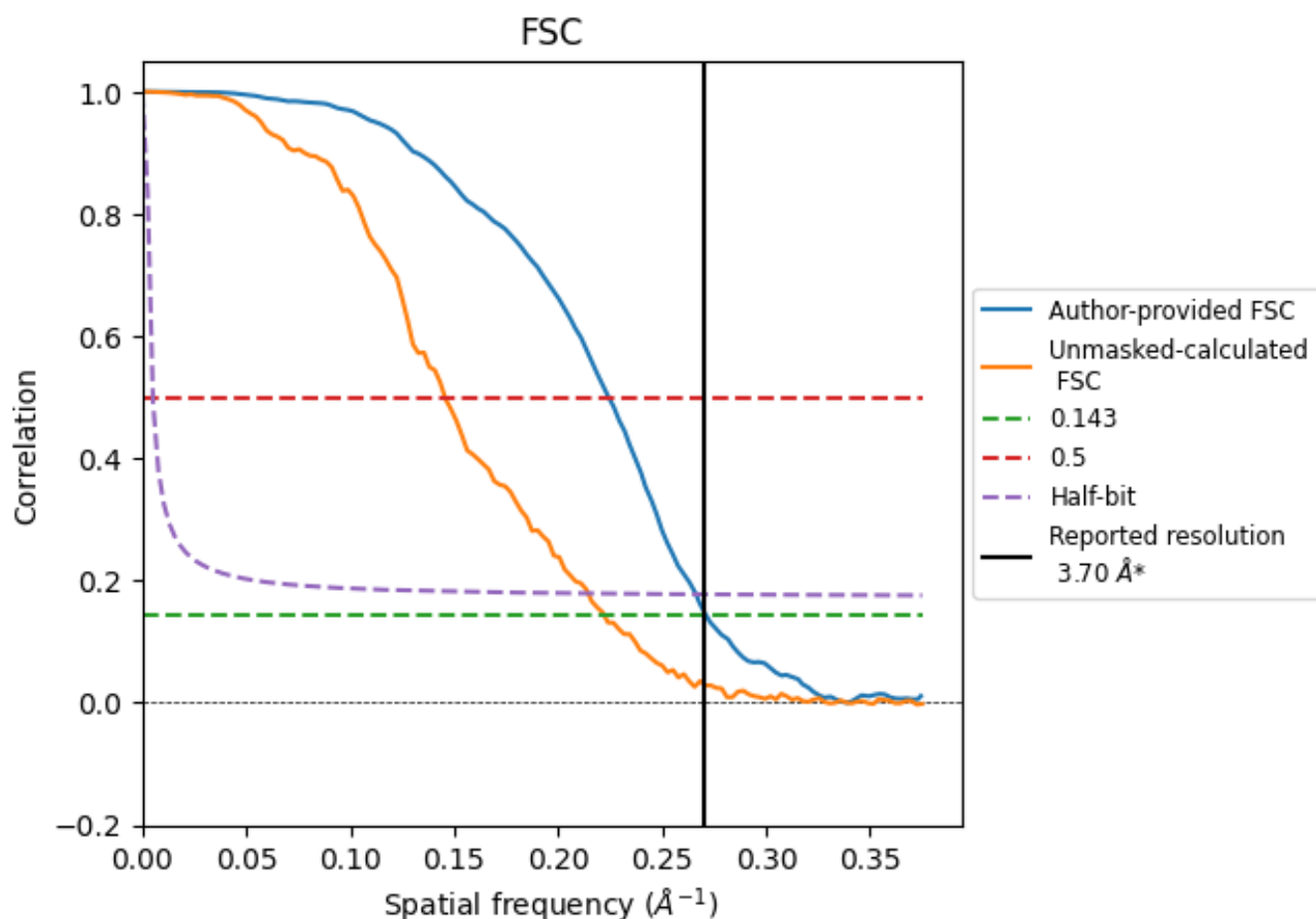


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

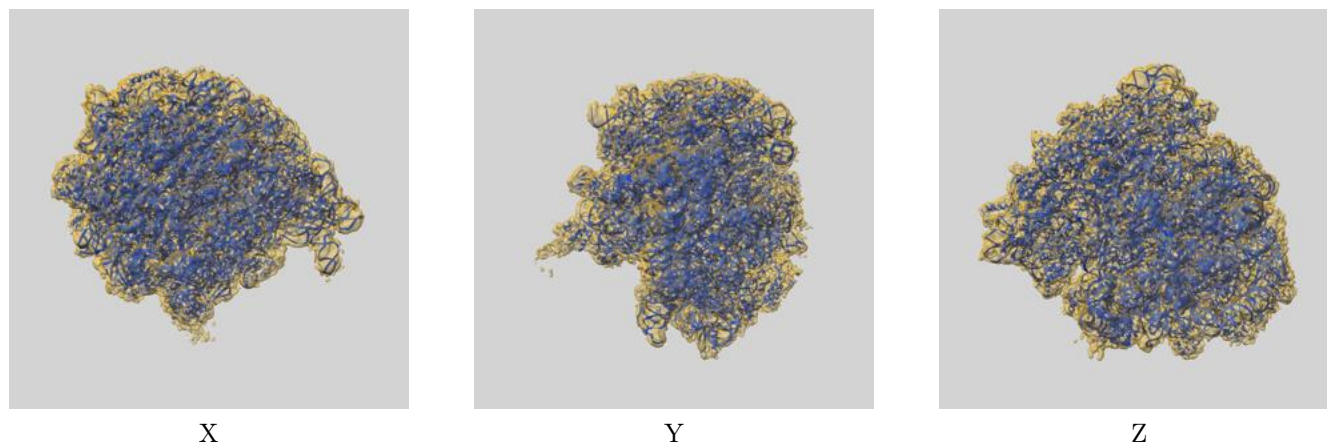
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.69	4.46	3.76
Unmasked-calculated*	4.50	6.87	4.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.50 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21628 and PDB model 6WD9. Per-residue inclusion information can be found in section [3](#) on page [17](#).

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](#)

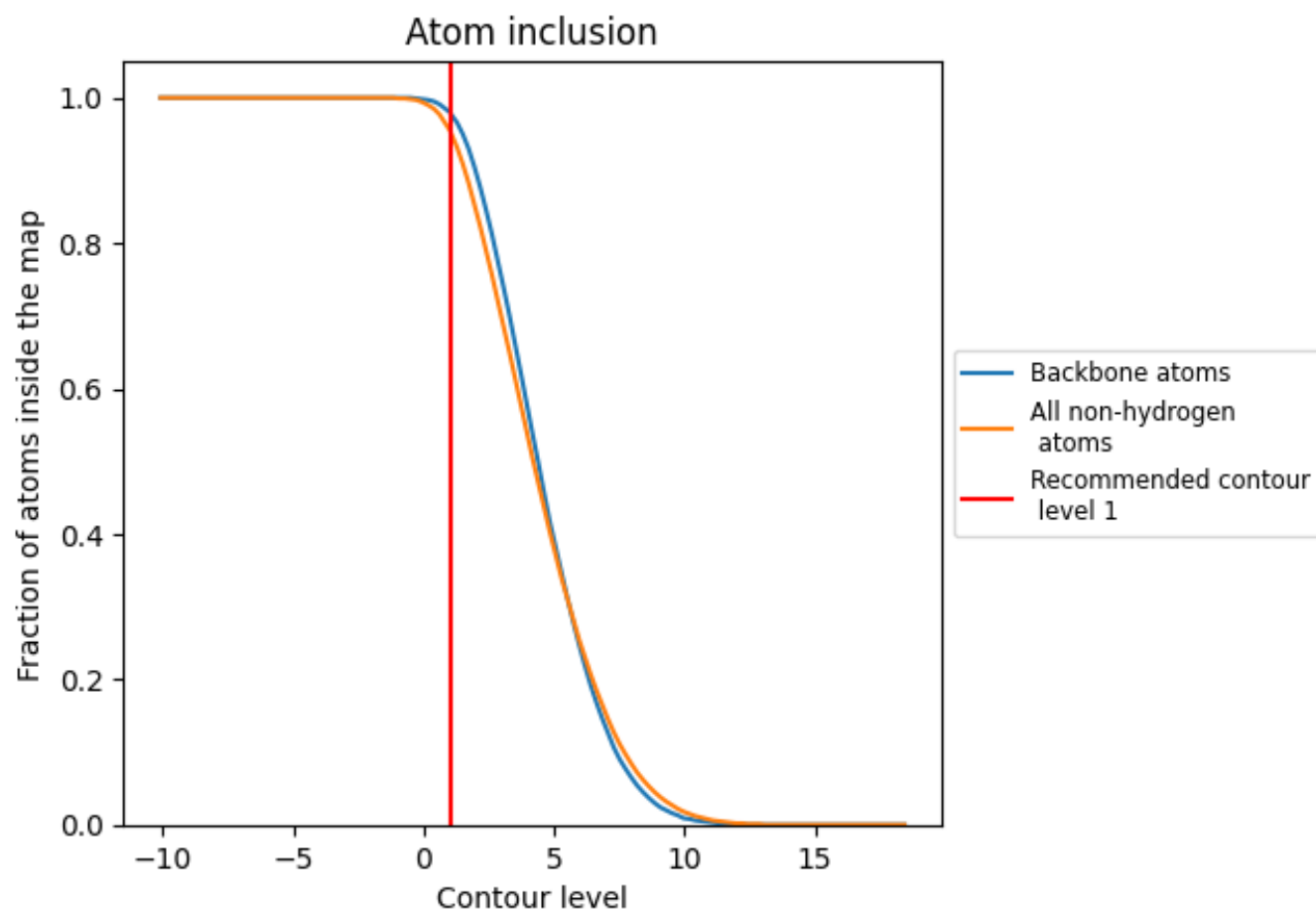


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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	 0.9550	 0.3440
1	 0.9810	 0.3690
2	 0.9810	 0.3220
3	 0.9780	 0.3250
4	 0.8990	 0.2650
5	 0.9690	 0.2720
6	 0.8140	 0.1420
7	 0.9640	 0.1980
8	 0.9450	 0.1980
B	 0.9440	 0.4080
C	 0.8010	 0.3280
D	 0.9320	 0.4600
E	 0.9210	 0.4520
F	 0.8250	 0.3660
G	 0.8770	 0.3100
H	 0.8650	 0.3350
I	 0.8190	 0.2570
J	 0.9230	 0.3780
K	 0.9470	 0.3620
L	 0.9350	 0.3110
M	 0.9180	 0.3820
N	 0.8890	 0.2990
O	 0.7900	 0.3020
P	 0.9410	 0.3800
Q	 0.9480	 0.3940
R	 0.9300	 0.2810
S	 0.8480	 0.3030
T	 0.9490	 0.3710
U	 0.9150	 0.3260
V	 0.9370	 0.3680
W	 0.9280	 0.3380
X	 0.9530	 0.3170
Y	 0.9060	 0.2760
Z	 0.8630	 0.3000
a	 0.8500	 0.1600



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Chain	Atom inclusion	Q-score
b	 0.9490	 0.4490
c	 0.9450	 0.4370
d	 0.9430	 0.3850
e	 0.9290	 0.2730
f	 0.9500	 0.3040
g	 0.7560	 0.2610
h	 0.7120	 0.1250
i	 0.7930	 0.1400
j	 0.9270	 0.4190
k	 0.9400	 0.4320
l	 0.9360	 0.4140
m	 0.9090	 0.4100
n	 0.9460	 0.4280
o	 0.9320	 0.3320
p	 0.9540	 0.4180
q	 0.9280	 0.4130
r	 0.9620	 0.4040
s	 0.9230	 0.4280
t	 0.9210	 0.3940
u	 0.9380	 0.3790
v	 0.9470	 0.3790
w	 0.9190	 0.4310
x	 0.9330	 0.4270
y	 0.9260	 0.3340
z	 0.9380	 0.3950