



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:29 PM UTC

PDB ID : 6WD4 / pdb_00006wd4
EMDB ID : EMD-21623
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure II-B2)
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

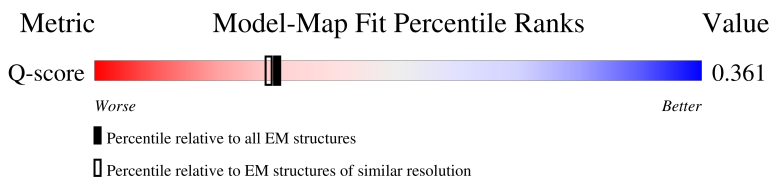
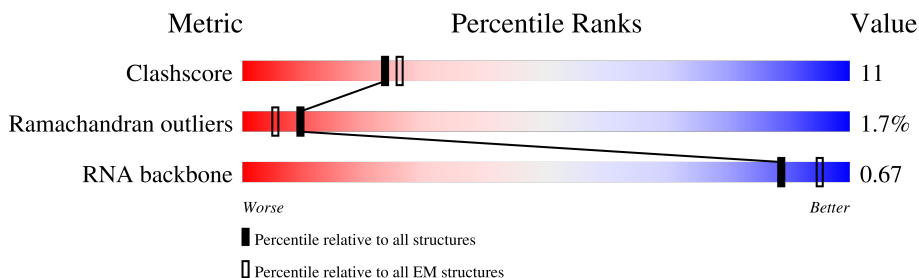
1 Overall quality at a glance

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.



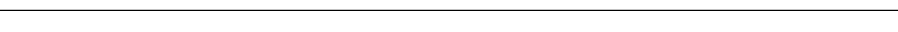
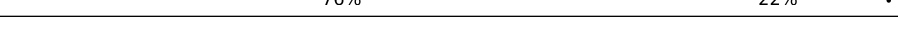
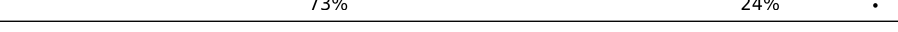
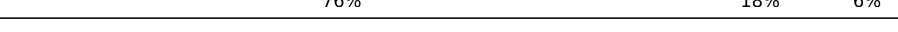
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	
2	c	209	
3	d	201	
4	e	177	

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Mol	Chain	Length	Quality of chain
5	f	176	 76% 23% .
6	g	149	 7% 74% 25% .
7	h	131	 12% 53% 42% 5% .
8	i	141	 21% 61% 36% .
9	j	142	 76% 23% .
10	k	122	 60% 37% .
11	l	143	 76% 22% .
12	m	136	 68% 31% .
13	n	120	 73% 24% .
14	o	116	 69% 30% .
15	p	114	 60% 40% .
16	q	117	 78% 22% .
17	r	103	 79% 19% .
18	s	110	 75% 24% .
19	t	93	 63% 35% .
20	u	102	 76% 18% 6% .
21	v	94	 71% 27% .
22	w	75	 69% 31% .
23	x	77	 71% 27% .
24	y	63	 76% 24% .
25	z	58	 76% 24% .
26	B	56	 68% 30% .
27	C	50	 64% 36% .
28	D	46	 67% 33% .
29	E	64	 66% 33% .

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Mol	Chain	Length	Quality of chain
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	
54	2	120	

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Mol	Chain	Length	Quality of chain
55	5	77	73%21%6%
55	6	77	47%51%
56	4	18	50%44%6%
57	7	76	58%29%13%
58	8	400	9%62%28%8%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 153083 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	variant	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	366	Total	C	N	O	S	0	0
			2833	1796	485	539	13		

There are 7 discrepancies between the modelled and reference sequences:

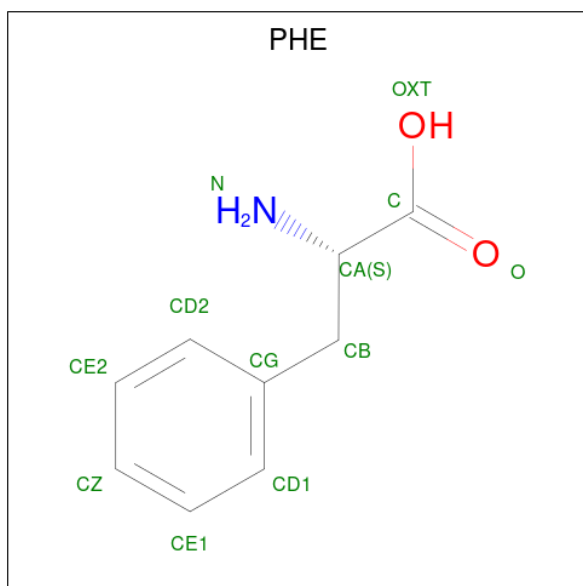
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag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

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



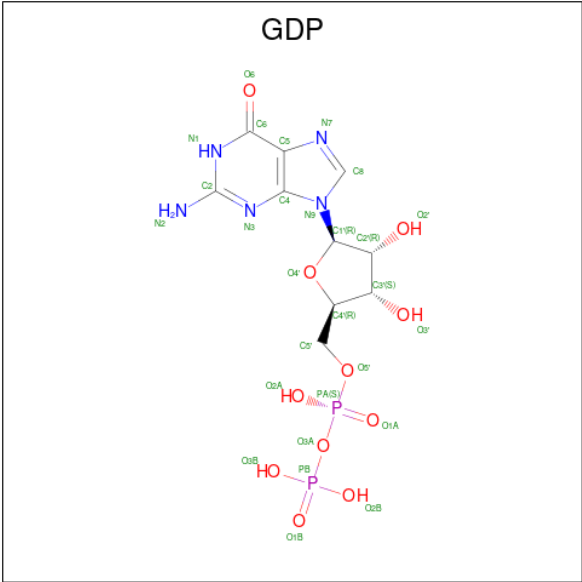
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

- 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: $C_{10}H_{15}N_5O_{11}P_2$).

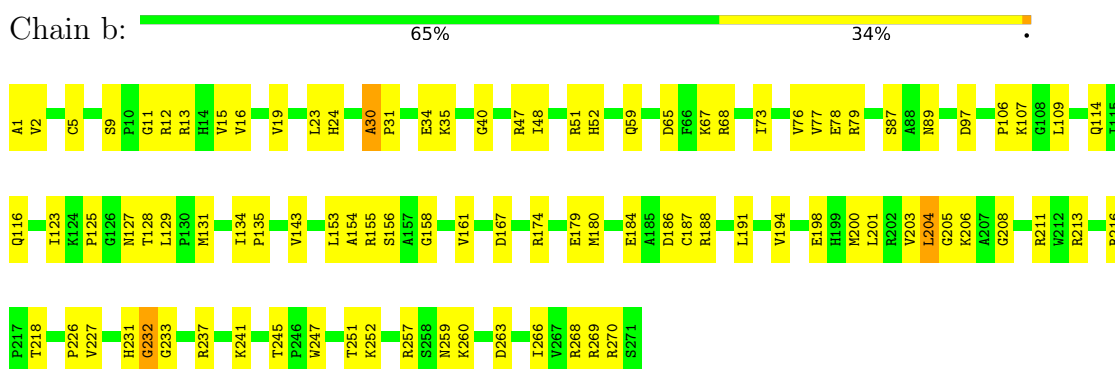


Mol	Chain	Residues	Atoms					AltConf
61	8	1	Total	C	N	O	P	0
			28	10	5	11	2	

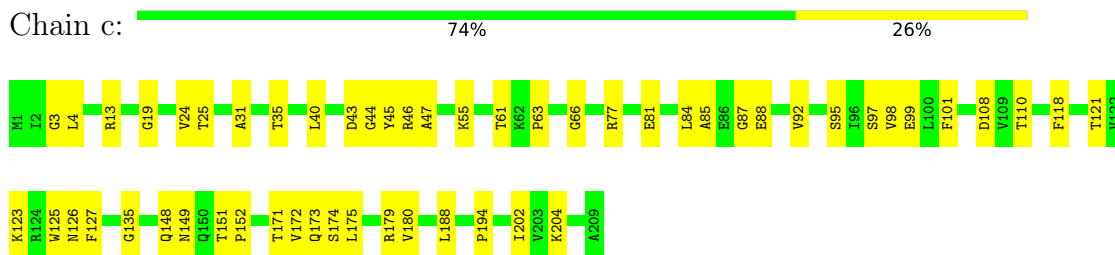
3 Residue-property plots

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.

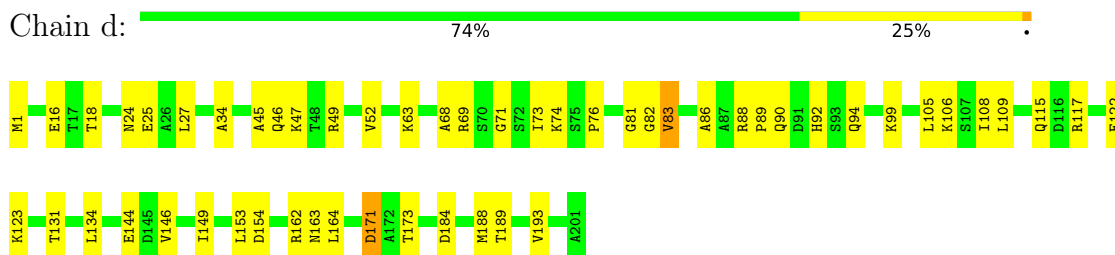
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3



- Molecule 3: 50S ribosomal protein L4



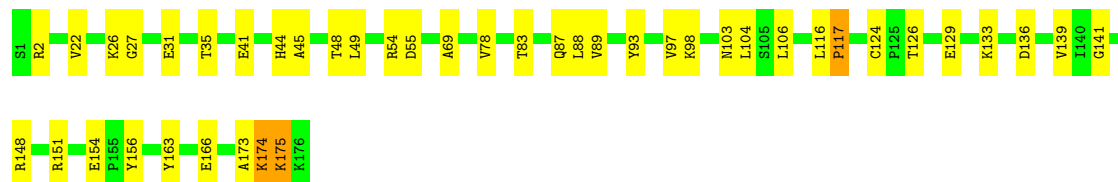
- Molecule 4: 50S ribosomal protein L5





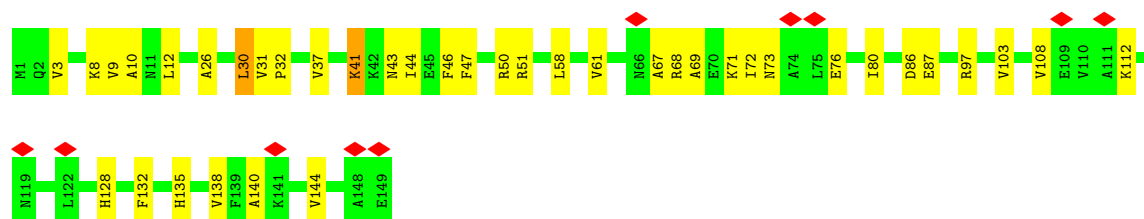
• Molecule 5: 50S ribosomal protein L6

Chain f: 76% 23% .



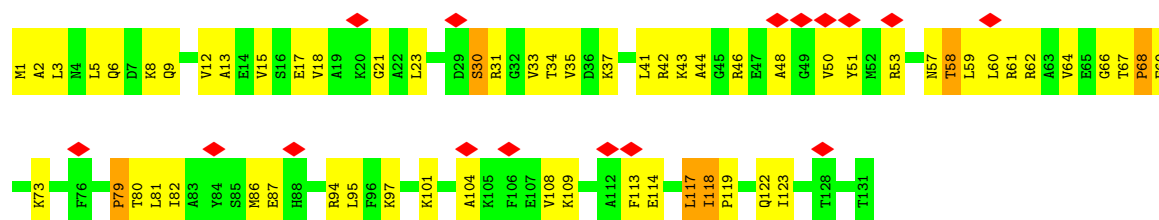
• Molecule 6: 50S ribosomal protein L9

Chain g: 7% 74% 25% .



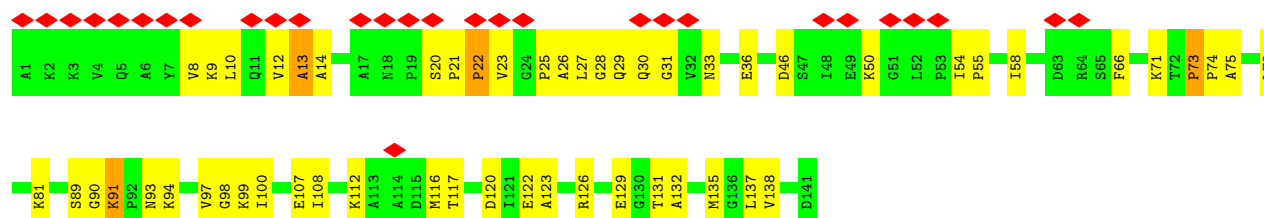
• Molecule 7: 50S ribosomal protein L10

Chain h: 12% 53% 42% 5% .

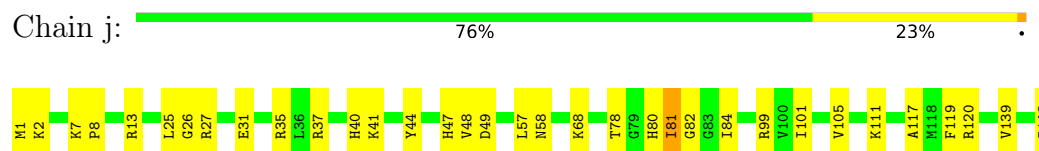


• Molecule 8: 50S ribosomal protein L11

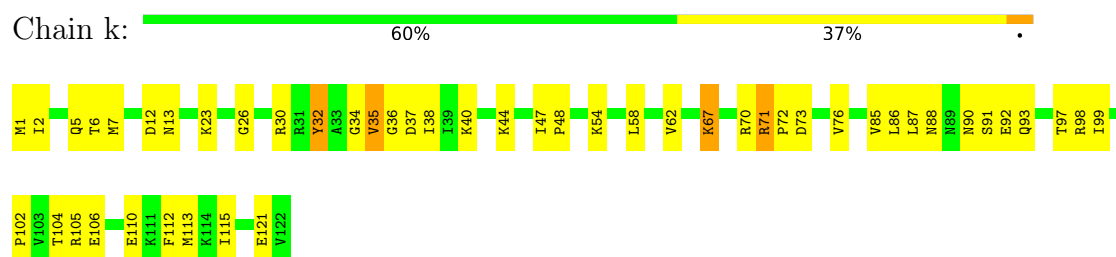
Chain i: 21% 61% 36% .



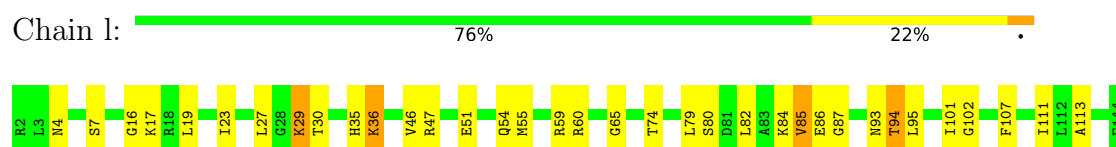
- Molecule 9: 50S ribosomal protein L13



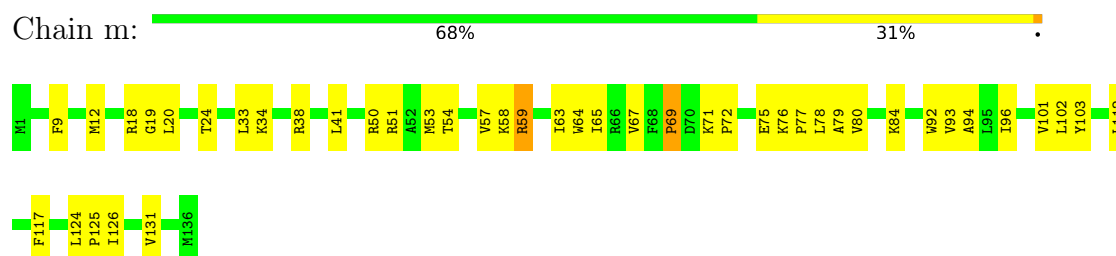
- Molecule 10: 50S ribosomal protein L14



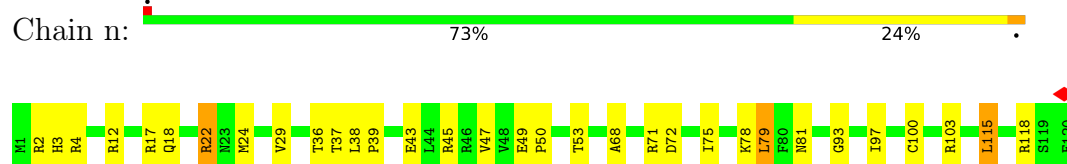
- Molecule 11: 50S ribosomal protein L15



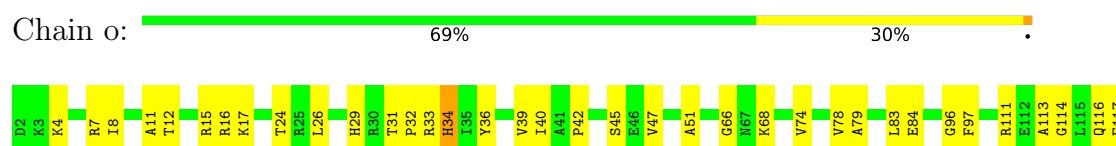
- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18



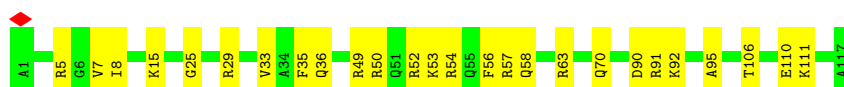
- Molecule 15: 50S ribosomal protein L19

Chain p:  60% 40%



- Molecule 16: 50S ribosomal protein L20

Chain q:  78% 22%



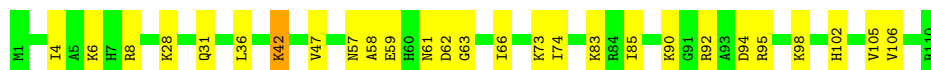
- Molecule 17: 50S ribosomal protein L21

Chain r:  79% 19%



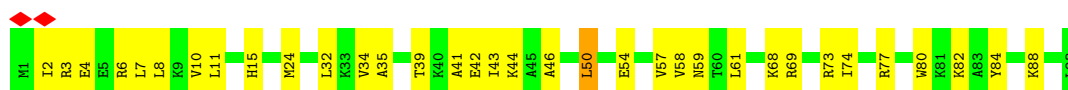
- Molecule 18: 50S ribosomal protein L22

Chain s:  75% 24%



- Molecule 19: 50S ribosomal protein L23

Chain t:  63% 35%



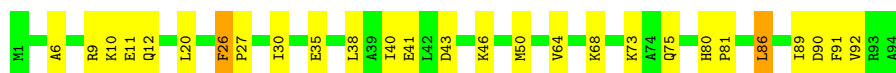
- Molecule 20: 50S ribosomal protein L24

Chain u:  76% 18% 6%



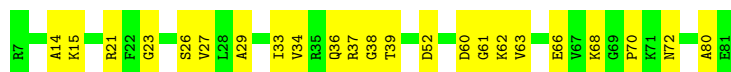
- Molecule 21: 50S ribosomal protein L25

Chain v:  71% 27%



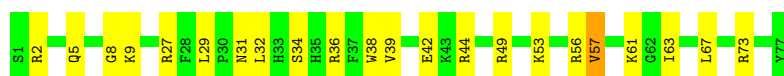
- Molecule 22: 50S ribosomal protein L27

Chain w: 69% 31%



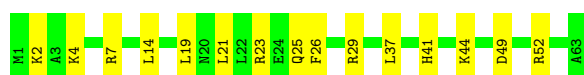
- Molecule 23: 50S ribosomal protein L28

Chain x: 71% 27%



- Molecule 24: 50S ribosomal protein L29

Chain y: 76% 24%



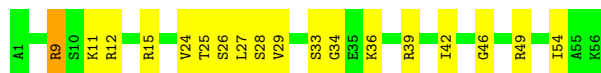
- Molecule 25: 50S ribosomal protein L30

Chain z: 76% 24%



- Molecule 26: 50S ribosomal protein L32

Chain B: 68% 30%



- Molecule 27: 50S ribosomal protein L33

Chain C: 64% 36%



- Molecule 28: 50S ribosomal protein L34

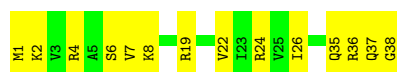
Chain D: 67% 33%



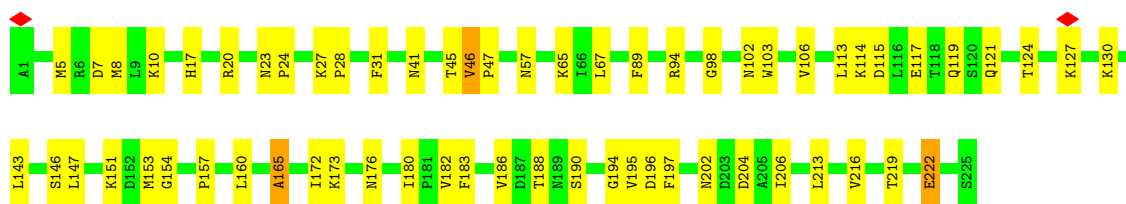
- Molecule 29: 50S ribosomal protein L35



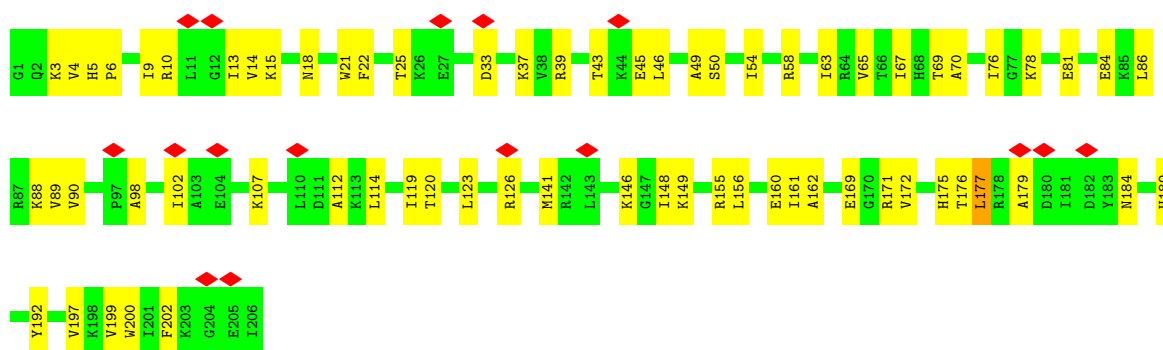
- Molecule 30: 50S ribosomal protein L36



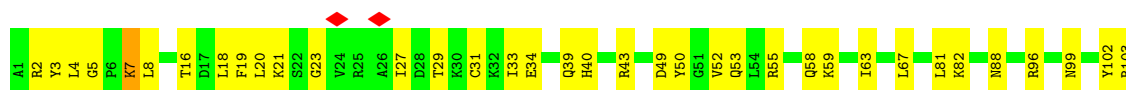
- Molecule 31: 30S ribosomal protein S2



- Molecule 32: 30S ribosomal protein S3



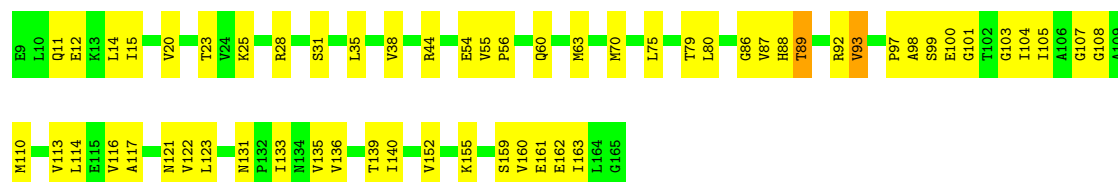
- Molecule 33: 30S ribosomal protein S4





- Molecule 34: 30S ribosomal protein S5

Chain J: 63% 36%



- Molecule 35: 30S ribosomal protein S6

Chain K: 49% 48%



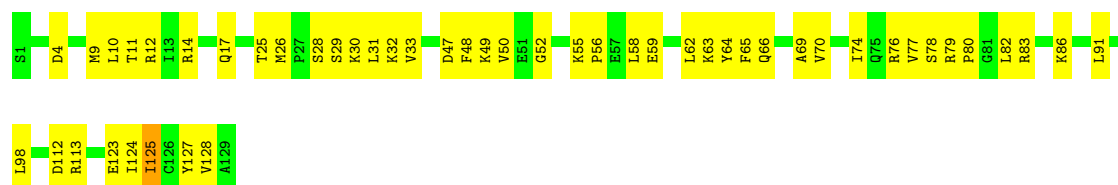
- Molecule 36: 30S ribosomal protein S7

Chain L: 70% 29%



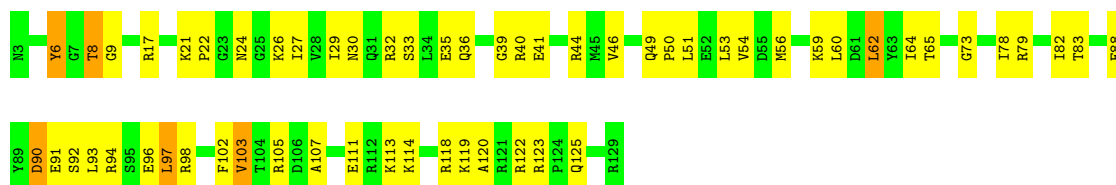
- Molecule 37: 30S ribosomal protein S8

Chain M: 62% 37%

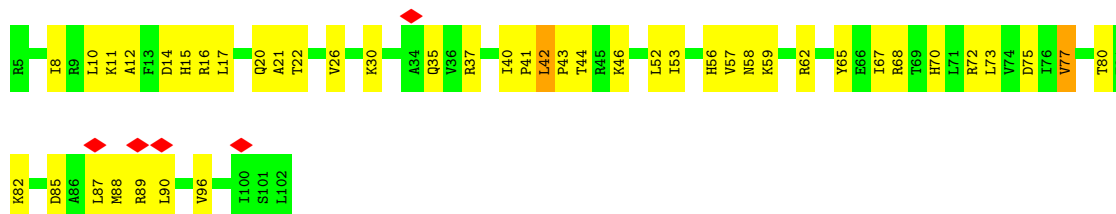


- Molecule 38: 30S ribosomal protein S9

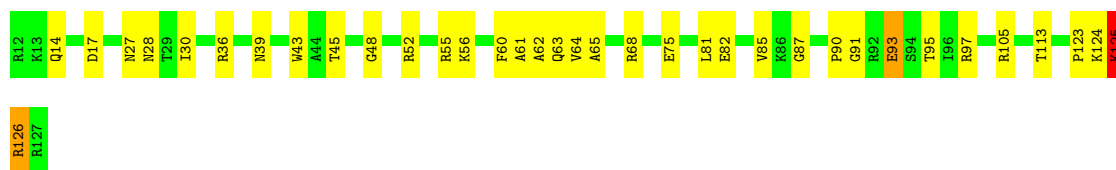
Chain N: 54% 41% 5%



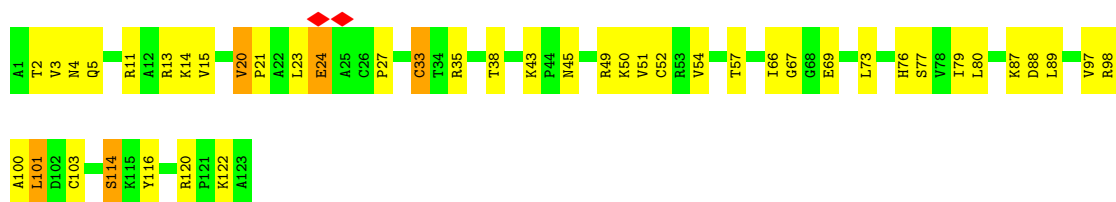
- Molecule 39: 30S ribosomal protein S10



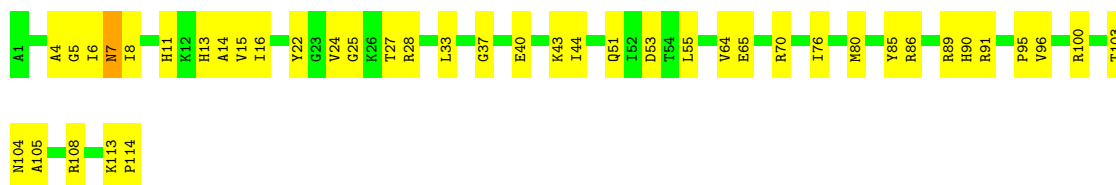
- Molecule 40: 30S ribosomal protein S11



- Molecule 41: 30S ribosomal protein S12

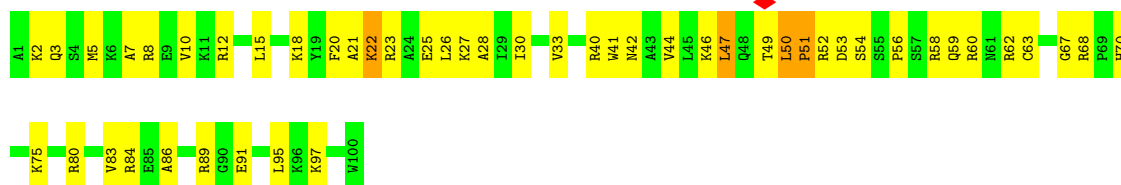


- Molecule 42: 30S ribosomal protein S13



- Molecule 43: 30S ribosomal protein S14

Chain S:  51% 45%



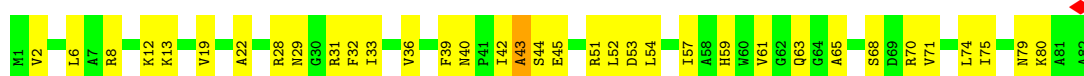
- Molecule 44: 30S ribosomal protein S15

Chain T:  81% 18%



- Molecule 45: 30S ribosomal protein S16

Chain U:  57% 41%



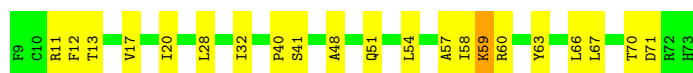
- Molecule 46: 30S ribosomal protein S17

Chain V:  60% 38%



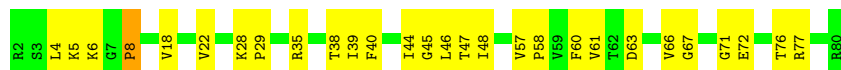
- Molecule 47: 30S ribosomal protein S18

Chain W:  68% 31%



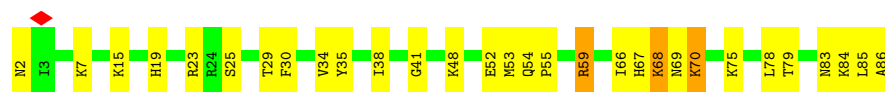
- Molecule 48: 30S ribosomal protein S19

Chain X:  65% 34%



- Molecule 49: 30S ribosomal protein S20

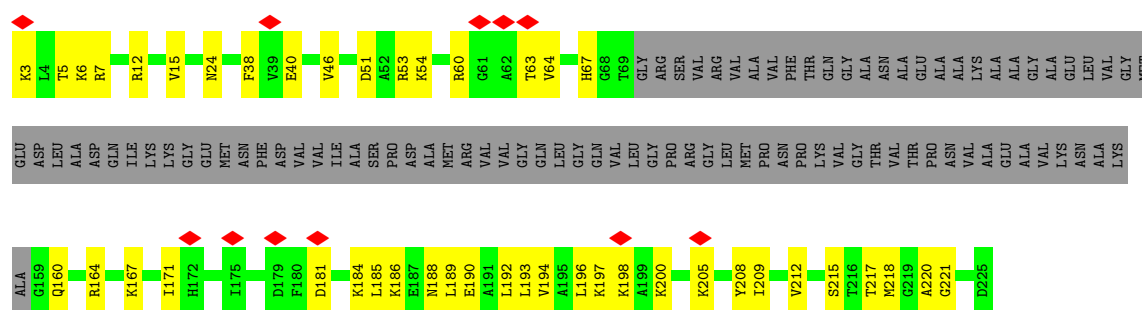
Chain Y:  65% 32%



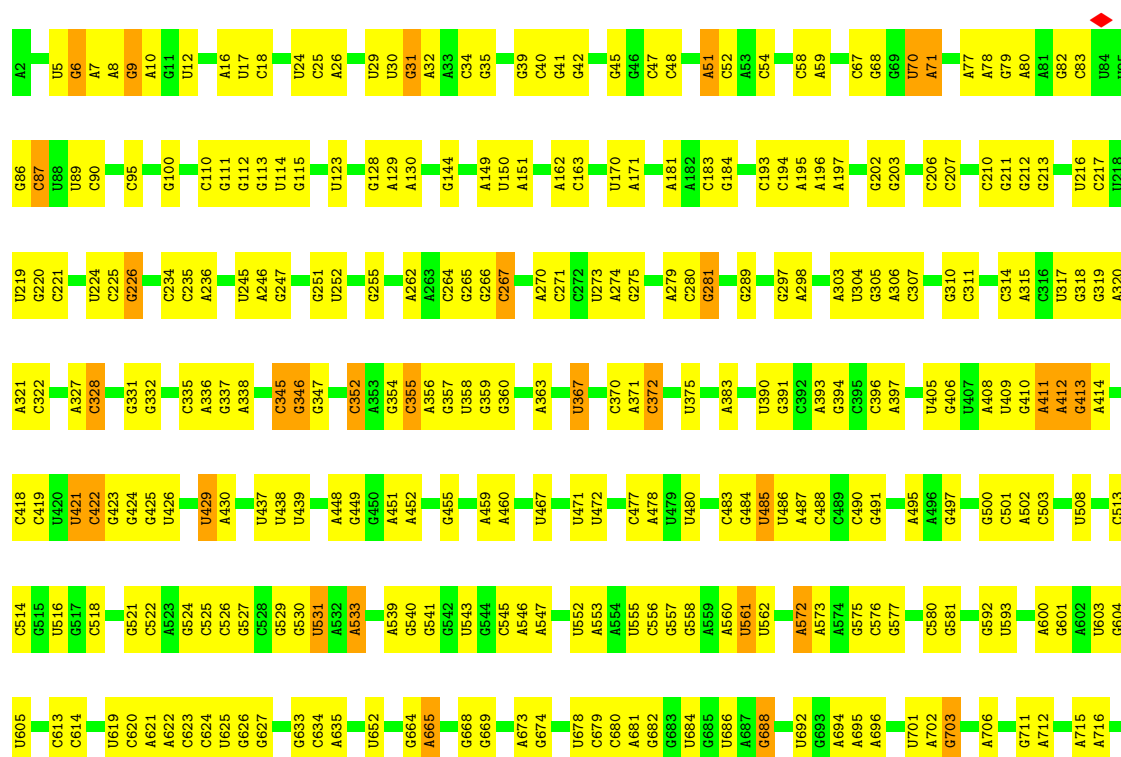
- Molecule 50: 30S ribosomal protein S21

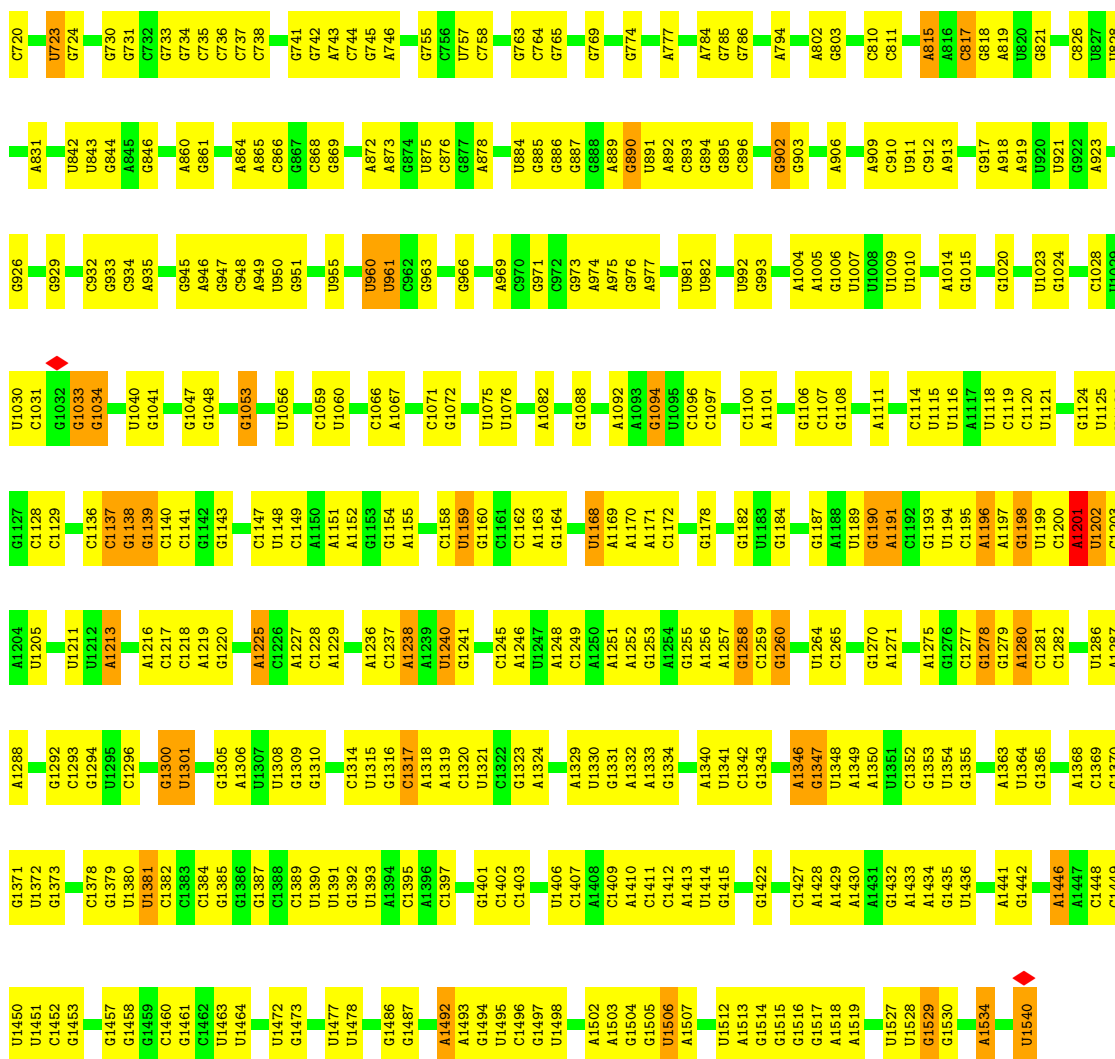


- Molecule 51: 50S ribosomal protein L1



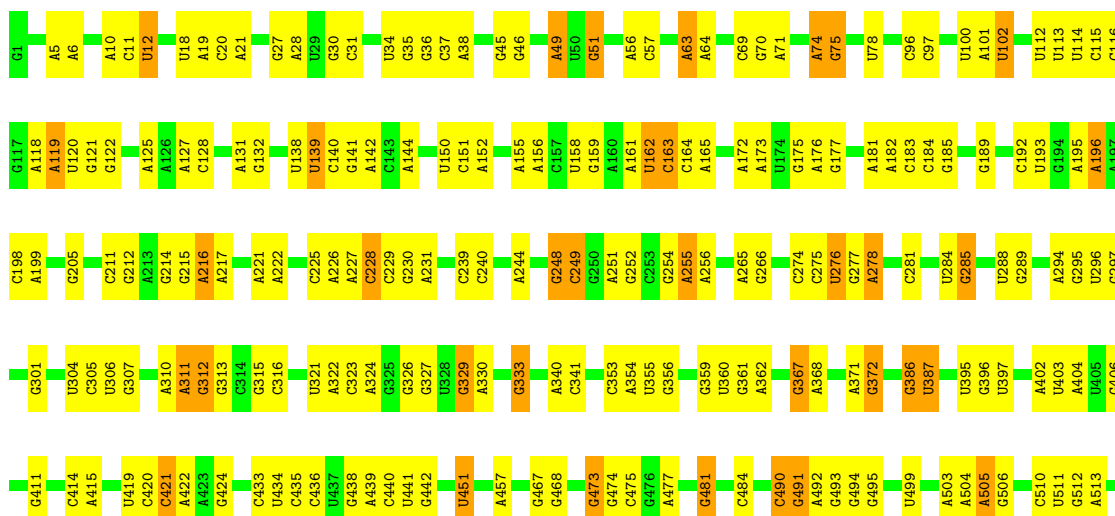
- Molecule 52: 16S ribosomal RNA





• Molecule 53: 23S ribosomal RNA

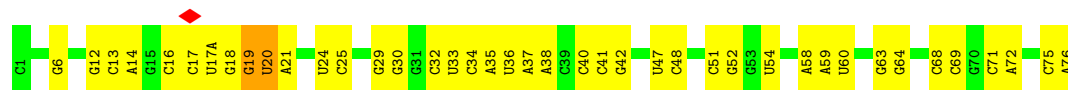
Chain 1: 57% 38% 5%



C1925	A1810	G1696	U1584	C1480	G1369	A1268	G1149	U1061	A975	U872	G785	G695	G597	C516
G1929	G1811	G1697	C1585	U1481	C1370	A1269	G1150	G1062	A983	C873	A792	G696	U598	C517
G1930	C1816	A1701	A1586	G1482	U1372	G1270	A1151	U1066	A984	C876	A793	G700	U599	G518
U1931	G1817	G1702	G1587	U1371	U1372	A1271	C1152	A1067	G989	A877	G796	U702	C601	G519
G1932	U1818	U1709	U1594	G1491	A1373	A1272	C1153	G1068	G990	A878	G797	U703	A602	G520
G1933	U1827	G1710	C1595	A1495	C1376	A1275	G1154	G1069	C992	C885	G805	U704	A603	C523
C1934	G1828	G1715	A1596	U1496	G1377	A1276	A1155	A1077	C993	A886	G806	A705	U607	G524
G1935	U1829	G1716	A1597	G1501	U1379	C1277	A1156	A1078	C994	A887	C807	A706	C610	A528
A1936	C1830	G1717	U1598	U1502	A1383	C1278	G1170	U1076	C995	C890	U807	C717	C611	A529
A1937	G1831	U1720	G1601	A1503	A1384	G1279	G1171	A1077	C996	G891	G808	C718	G612	G530
A1938	C1832	G1721	A1602	U1504	A1385	G1280	G1172	C1079	A997	C892	G809	C719	A613	C531
U1943	C1833	G1722	A1603	U1505	C1386	A1285	A1176	U1083	G997	A896	U810	U720	A614	A532
U1944	U1834	C1726	A1608	C1507	A1387	A1286	U1176	A1084	A1000	C897	U811	A721	C615	G533
C1947	G1837	C1727	C1611	A1508	G1388	A1287	G1177	U1085	A1001	C898	C812	A722	U534	U534
G1948	U1838	U1729	C1612	G1510	G1389	G1288	G1178	A1086	C1007	C899	U813	C723	A616	G535
U1955	U1851	C1730	G1613	A1515	U1394	C1297	U1180	G1087	A1008	A899	C814	U724	G617	C542
U1956	U1856	C1732	A1616	G1524	A1395	C1298	U1181	A1088	A1009	G907	C816	C726	C619	G543
C1957	G1857	G1738	C1625	C1526	U1409	C1299	U1182	A1089	U1012	A909	C817	A727	G620	G544
C1958	U1858	U1739	A1626	G1527	G1410	G1300	U1183	A1090	U1013	A910	C818	C728	U545	U545
G1959	U1859	C1740	A1626	A1528	G1416	A1301	G1185	G1091	A1014	A911	C819	C729	A627	G548
U1963	G1860	U1746	A1637	G1529	C1417	G1310	G1186	C1092	U1015	C912	C822	A730	G636	G549
G1964	U1861	U1747	U1637	U1535	G1418	G1311	G1187	G1093	G1016	U913	G738	A739	A637	U554
C1965	A1866	A1754	G1642	C1536	A1419	U1316	U1198	C1103	U1019	U826	U827	A738	G638	U555
A1966	G1867	G1754	G1643	G1537	A1420	G1317	G1206	C1104	A1020	U828	A742	A743	C640	G558
C1967	U1871	U1758	C1644	C1538	G1423	U1318	G1207	G1106	A1021	A829	A744	U745	C645	G559
A1970	A1872	A1759	G1645	U1539	G1424	C1319	G1212	G1107	G1022	G830	U746	U746	U646	A563
U1971	A1873	C1764	C1646	G1540	U1424	C1320	G1219	C1108	U1023	G831	U747	U747	A654	U567
G1972	G1874	U1765	U1647	C1541	A1427	U1329	U1219	C1109	G1026	C935	U748	C747	A654	U568
G1973	G1875	U1766	U1648	G1542	C1428	G1330	G1220	C1110	A1028	A833	A749	A750	U657	U569
A1976	A1876	A1773	G1663	G1543	A1433	G1331	G1225	C1111	A1029	C936	U751	A751	G659	G570
U1979	U1877	C1774	A1664	A1549	A1434	G1332	A1226	U1113	U1033	C940	A752	A752	C660	U571
G1980	G1878	U1775	A1665	C1560	G1435	G1337	G1227	C1114	U1033	A941	U753	U753	A661	A572
A1981	G1884	G1776	G1666	G1555	U1436	G1338	G1227	G1115	G1036	G942	U754	U754	G662	U573
U1982	A1885	U1779	G1667	G1556	C1437	G1339	U1231	G1116	U1036	U846	U755	U755	G663	A574
U1991	C1893	A1780	A1668	C1560	A1438	G1341	G1232	U1119	A1039	U847	A756	G760	A670	A575
G1992	C1894	G1785	G1669	C1561	A1439	A1342	G1238	C946	A1040	C851	U757	G763	C671	U576
U1993	A1900	A1784	A1672	U1562	C1447	G1343	G1238	A947	G1041	U852	C672	A764	C672	G577
C1996	A1901	U1785	G1673	C1563	G1448	U1344	C1243	C948	G1042	C853	C673	C765	C673	U580
G1997	G1902	A1786	G1674	C1564	U1448	C1345	C1243	G949	C1043	C854	C674	U766	G674	C581
C2008	G1903	C1795	A1677	C1565	C1454	U1352	G1250	G856	C1044	G855	A677	U767	A677	A592
A2009	G1904	U1796	U1680	C1566	G1455	C1357	C1251	C957	C1045	G856	A678	G771	A678	G583
G2010	C1905	G1797	G1681	G1567	C1461	G1358	A1252	C961	A1046	G857	G682	G776	G682	C584
U2011	G1906	U1798	G1682	C1568	C1462	A1359	A1253	U967	G1053	C858	U686	G777	A586	G585
G2012	C1907	C1799	U1683	A1570	C1463	G1360	U1254	U968	A1054	U860	A861	G778	C587	U586
A2013	A2013	C1800	G1684	C1571	G1464	G1361	C1256	G969	G1055	A862	U687	U779	C588	U588
A2014	A1913	A1801	G1684	A1572	U1475	C1362	C1257	U970	G1056	G863	U688	G780	U688	C589
A2019	U1917	C1806	A1690	U1578	U1476	A1365	U1258	G971	A1057	C864	U689	A781	U689	U593
U2022	A1918	G1807	C1691	G1581	A1477	A1366	G1259	G972	A1058	C865	C691	A782	C691	U594
C2023	C1924	A1808	G1695	G1581	G1479	A1367	G1260	A973	U1059	A783	U694	A784	U694	U596

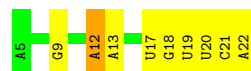
- Molecule 55: tRNA^{fMet}

Chain 6:  47% 51%



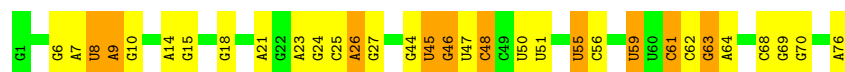
- Molecule 56: mRNA

Chain 4:  50% 44% 6%



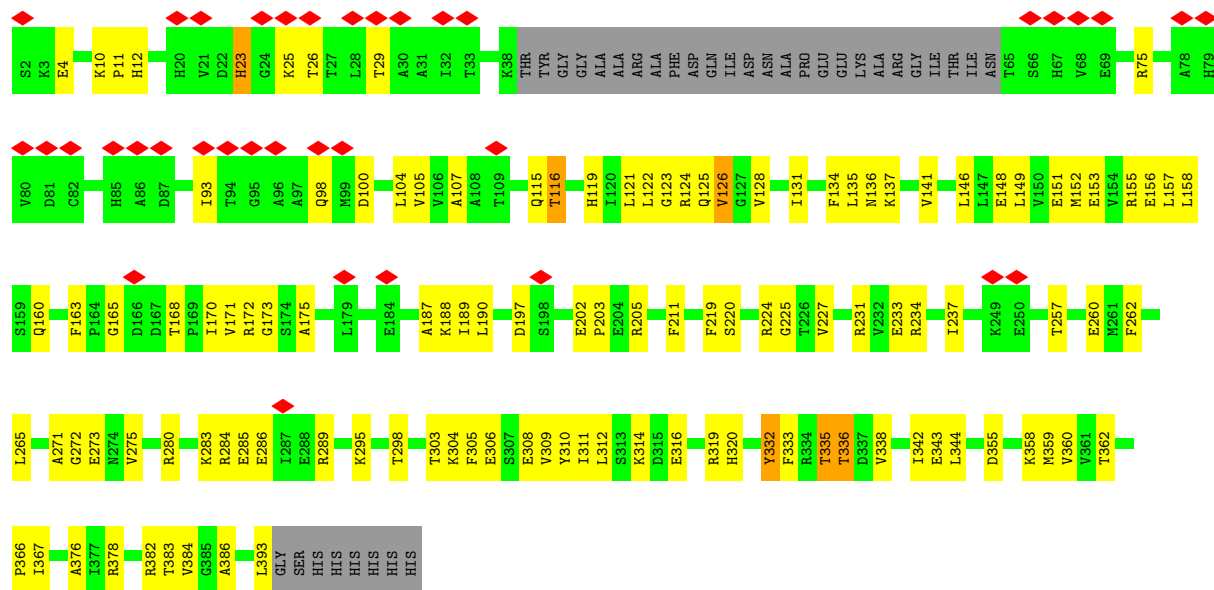
- Molecule 57: tRNA^{Phe}

Chain 7:  58% 29% 13%



- Molecule 58: Elongation factor Tu

Chain 8:  9% 62% 28% 8%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6805	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	18.305	Depositor
Minimum map value	-10.599	Depositor
Average map value	0.113	Depositor
Map value standard deviation	0.860	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: GDP, FME

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	b	0.30	0/2122	0.94	8/2852 (0.3%)
2	c	0.29	0/1586	0.84	1/2134 (0.0%)
3	d	0.28	0/1571	0.86	4/2113 (0.2%)
4	e	0.30	0/1435	0.90	4/1926 (0.2%)
5	f	0.30	0/1343	0.84	1/1816 (0.1%)
6	g	0.32	0/1122	0.93	4/1515 (0.3%)
7	h	0.33	0/1002	1.07	7/1350 (0.5%)
8	i	0.36	0/1046	0.98	7/1410 (0.5%)
9	j	0.29	0/1152	0.84	2/1551 (0.1%)
10	k	0.28	0/948	0.92	4/1268 (0.3%)
11	l	0.30	0/1054	0.96	2/1403 (0.1%)
12	m	0.29	0/1093	0.81	0/1460
13	n	0.30	0/974	0.93	6/1301 (0.5%)
14	o	0.30	0/902	0.87	2/1209 (0.2%)
15	p	0.28	0/929	0.83	1/1242 (0.1%)
16	q	0.28	0/960	0.89	3/1278 (0.2%)
17	r	0.29	0/829	0.88	2/1107 (0.2%)
18	s	0.27	0/864	0.89	1/1156 (0.1%)
19	t	0.27	0/745	0.86	1/994 (0.1%)
20	u	0.29	0/788	0.90	2/1051 (0.2%)
21	v	0.30	0/766	0.91	4/1025 (0.4%)
22	w	0.28	0/582	0.90	2/769 (0.3%)
23	x	0.28	0/635	0.82	2/848 (0.2%)
24	y	0.28	0/510	0.86	2/677 (0.3%)
25	z	0.30	0/453	0.77	1/605 (0.2%)
26	B	0.29	0/450	0.84	1/599 (0.2%)
27	C	0.31	0/417	0.82	1/554 (0.2%)
28	D	0.31	0/380	0.91	1/498 (0.2%)
29	E	0.29	0/513	0.89	3/676 (0.4%)
30	F	0.32	0/303	0.88	0/397
31	G	0.30	0/1788	0.91	6/2408 (0.2%)
32	H	0.32	0/1652	0.92	6/2225 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.29	0/1665	0.85	4/2227 (0.2%)
34	J	0.31	0/1170	1.00	8/1573 (0.5%)
35	K	0.32	0/836	0.97	1/1128 (0.1%)
36	L	0.30	0/1196	0.93	2/1602 (0.1%)
37	M	0.30	0/989	0.90	1/1326 (0.1%)
38	N	0.31	0/1034	0.94	6/1375 (0.4%)
39	O	0.33	0/797	0.93	4/1077 (0.4%)
40	P	0.33	0/886	0.97	3/1195 (0.3%)
41	Q	0.30	0/969	1.01	3/1300 (0.2%)
42	R	0.30	0/893	0.86	0/1193
43	S	0.29	0/817	0.89	4/1088 (0.4%)
44	T	0.28	0/722	0.89	1/964 (0.1%)
45	U	0.31	0/659	0.89	0/884
46	V	0.30	0/658	0.92	1/881 (0.1%)
47	W	0.33	0/545	0.97	3/731 (0.4%)
48	X	0.31	0/653	0.86	2/877 (0.2%)
49	Y	0.29	0/671	0.93	4/888 (0.5%)
50	Z	0.34	0/551	1.02	5/728 (0.7%)
51	a	0.31	0/1034	0.77	0/1387
52	3	0.41	0/36963	0.47	4/57662 (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	0.45	0/2855
55	6	0.41	0/1832	0.47	0/2855
56	4	0.41	0/436	0.47	0/679
57	7	0.40	0/1809	0.49	0/2819
58	8	0.32	0/2885	0.89	8/3902 (0.2%)
All	All	0.37	0/166084	0.62	157/247980 (0.1%)

There are no bond length outliers.

All (157) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	8	336	THR	N-CA-C	9.46	122.04	110.41
41	Q	20	VAL	N-CA-C	9.00	118.32	107.61
7	h	43	LYS	N-CA-C	-8.34	101.73	112.23
41	Q	114	SER	N-CA-C	-8.23	102.28	111.82
7	h	117	LEU	N-CA-C	8.21	122.96	109.24
16	q	49	ARG	N-CA-C	-8.11	102.95	112.92
44	T	43	ALA	N-CA-C	-8.03	102.75	112.54
43	S	49	THR	N-CA-C	-7.60	103.00	111.82
6	g	30	LEU	N-CA-C	7.26	119.08	111.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	h	50	VAL	N-CA-C	7.25	118.05	111.81
43	S	22	LYS	N-CA-C	-7.19	104.37	113.43
2	c	173	GLN	N-CA-C	7.03	121.04	110.14
11	l	95	LEU	N-CA-C	-6.72	103.76	112.23
53	l	1130	U	C2'-C3'-O3'	6.63	119.44	109.50
22	w	52	ASP	N-CA-C	-6.62	104.33	112.88
35	K	78	PHE	N-CA-C	-6.62	105.73	113.88
10	k	67	LYS	N-CA-C	-6.60	104.17	111.82
58	8	285	GLU	N-CA-C	6.55	119.78	110.68
28	D	29	GLN	N-CA-C	-6.51	104.03	112.23
1	b	9	SER	N-CA-C	6.49	114.06	108.22
9	j	119	PHE	N-CA-C	-6.46	105.40	113.28
50	Z	42	THR	N-CA-C	6.46	118.12	111.14
21	v	80	HIS	N-CA-C	-6.44	99.89	109.42
3	d	171	ASP	N-CA-C	-6.42	100.47	110.42
6	g	10	ALA	N-CA-C	6.40	119.56	109.39
34	J	101	GLY	N-CA-C	-6.37	105.59	115.73
41	Q	43	LYS	N-CA-C	6.37	121.15	112.55
7	h	44	ALA	N-CA-C	-6.34	104.24	112.23
4	e	143	ASP	N-CA-C	6.33	118.99	111.71
20	u	96	LYS	N-CA-C	-6.32	101.11	110.46
49	Y	7	LYS	N-CA-C	-6.28	105.37	113.16
3	d	73	ILE	N-CA-C	-6.27	106.62	112.83
43	S	47	LEU	N-CA-C	-6.24	105.63	113.18
32	H	177	LEU	N-CA-C	6.19	119.93	112.38
10	k	32	TYR	N-CA-C	6.19	120.16	110.32
38	N	103	VAL	N-CA-C	-6.16	104.63	113.07
58	8	116	THR	N-CA-C	-6.15	104.66	111.36
39	O	21	ALA	N-CA-C	-6.11	104.53	112.23
50	Z	58	LYS	N-CA-C	-6.10	104.71	111.36
34	J	116	VAL	N-CA-C	-6.09	106.80	112.83
1	b	131	MET	N-CA-C	6.08	120.42	113.19
34	J	140	ILE	N-CA-C	6.06	116.24	110.42
39	O	77	VAL	N-CA-C	6.05	116.23	110.42
40	P	125	LYS	N-CA-C	6.04	123.67	110.80
49	Y	84	LYS	N-CA-C	-6.03	104.27	111.69
4	e	11	VAL	N-CA-C	6.00	116.18	110.42
31	G	23	ASN	CA-C-N	5.99	125.69	119.82
31	G	23	ASN	C-N-CA	5.99	125.69	119.82
6	g	3	VAL	N-CA-C	5.96	117.11	109.30
33	I	166	LYS	CA-C-N	5.96	127.29	119.84
33	I	166	LYS	C-N-CA	5.96	127.29	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	G	46	VAL	N-CA-C	5.95	121.23	112.61
3	d	146	VAL	N-CA-C	5.92	117.96	108.85
38	N	97	LEU	N-CA-C	-5.88	105.20	112.90
7	h	12	VAL	N-CA-C	-5.83	104.83	110.72
38	N	62	LEU	N-CA-C	5.82	118.21	108.96
7	h	104	ALA	N-CA-C	-5.78	105.99	113.16
49	Y	59	ARG	N-CA-C	-5.76	105.75	112.89
37	M	125	ILE	N-CA-C	5.75	115.87	110.30
36	L	67	ASN	N-CA-C	-5.71	105.64	113.30
20	u	82	VAL	N-CA-C	5.71	117.82	108.97
32	H	107	LYS	CA-C-N	5.71	125.38	119.56
32	H	107	LYS	C-N-CA	5.71	125.38	119.56
7	h	30	SER	N-CA-C	-5.63	106.41	113.28
13	n	115	LEU	N-CA-C	-5.63	101.31	110.20
53	l	1020	A	C2'-C3'-O3'	5.62	117.94	109.50
5	f	141	GLY	N-CA-C	-5.62	105.58	112.77
8	i	27	LEU	N-CA-C	-5.61	106.21	113.16
19	t	50	LEU	N-CA-C	5.60	117.46	111.36
49	Y	70	LYS	N-CA-C	-5.60	105.26	111.36
29	E	63	TYR	N-CA-C	5.59	117.84	111.02
40	P	65	ALA	N-CA-C	-5.58	105.20	112.23
34	J	161	GLU	N-CA-C	5.55	117.02	110.97
31	G	222	GLU	N-CA-C	-5.54	105.25	112.23
38	N	90	ASP	N-CA-C	5.54	122.60	110.80
36	L	58	LEU	N-CA-C	5.53	117.31	111.28
31	G	165	ALA	N-CA-C	5.52	118.06	111.71
11	l	59	ARG	N-CA-C	-5.52	107.80	114.75
39	O	85	ASP	N-CA-C	-5.51	106.60	113.38
16	q	70	GLN	N-CA-C	-5.51	105.29	112.23
52	3	1201	A	C2'-C3'-O3'	5.50	117.75	109.50
40	P	93	GLU	N-CA-C	-5.49	107.84	114.75
47	W	11	ARG	N-CA-C	5.48	116.59	108.86
25	z	3	THR	N-CA-C	5.48	117.15	110.41
22	w	38	GLY	N-CA-C	-5.47	104.78	112.60
8	i	97	VAL	N-CA-C	5.44	115.53	110.42
46	V	45	VAL	N-CA-C	5.44	115.78	108.17
50	Z	37	TYR	N-CA-C	-5.43	107.03	113.38
13	n	79	LEU	N-CA-C	-5.42	102.49	110.52
34	J	117	ALA	N-CA-C	-5.42	105.03	111.69
8	i	28	GLY	N-CA-C	-5.41	107.22	115.66
29	E	61	LEU	CA-C-N	5.41	126.60	119.84
29	E	61	LEU	C-N-CA	5.41	126.60	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	i	73	PRO	CA-C-N	5.40	125.33	119.76
8	i	73	PRO	C-N-CA	5.40	125.33	119.76
17	r	49	ILE	N-CA-C	5.40	116.26	108.48
58	8	100	ASP	N-CA-C	-5.39	106.83	113.41
14	o	68	LYS	N-CA-C	5.39	116.84	110.97
50	Z	31	VAL	N-CA-C	-5.38	107.50	112.83
23	x	57	VAL	N-CA-C	-5.38	105.29	110.72
47	W	66	LEU	N-CA-C	-5.38	107.26	113.88
39	O	44	THR	N-CA-C	5.38	118.03	109.96
33	I	7	LYS	N-CA-C	5.38	118.94	112.38
13	n	2	ARG	N-CA-C	5.36	118.73	111.17
4	e	48	LEU	N-CA-C	-5.35	105.61	111.82
1	b	40	GLY	N-CA-C	-5.33	107.91	115.43
9	j	139	VAL	N-CA-C	5.33	115.97	109.30
32	H	5	HIS	CA-C-N	5.33	125.14	119.28
32	H	5	HIS	C-N-CA	5.33	125.14	119.28
32	H	76	ILE	N-CA-C	-5.32	107.64	112.96
1	b	13	ARG	N-CA-C	5.32	116.76	111.07
16	q	57	ARG	N-CA-C	-5.31	105.66	111.82
23	x	8	GLY	N-CA-C	-5.31	107.46	115.32
34	J	122	VAL	N-CA-C	5.31	120.38	109.34
52	3	1300	G	N9-C1'-C2'	5.30	119.95	112.00
3	d	115	GLN	N-CA-C	-5.29	105.67	113.61
38	N	6	TYR	N-CA-C	5.28	118.06	109.24
6	g	67	ALA	N-CA-C	-5.28	105.70	111.82
13	n	43	GLU	N-CA-C	-5.28	107.22	113.97
8	i	91	LYS	CA-C-N	5.27	126.42	119.84
8	i	91	LYS	C-N-CA	5.27	126.42	119.84
58	8	23	HIS	N-CA-C	-5.27	107.52	114.31
52	3	1301	U	N1-C1'-C2'	5.25	119.88	112.00
21	v	86	LEU	N-CA-C	5.25	117.11	110.33
1	b	30	ALA	N-CA-C	5.25	121.40	109.81
34	J	88	HIS	N-CA-C	5.21	115.93	107.23
33	I	102	TYR	N-CA-C	-5.19	105.70	111.36
1	b	134	ILE	CA-C-N	5.19	125.18	119.89
1	b	134	ILE	C-N-CA	5.19	125.18	119.89
58	8	126	VAL	N-CA-C	-5.18	105.77	113.39
15	p	15	ASP	N-CA-C	5.17	117.62	109.39
17	r	14	VAL	N-CA-C	5.17	116.73	108.87
4	e	142	TYR	N-CA-C	5.17	117.32	111.11
26	B	9	ARG	N-CA-C	-5.17	105.72	112.23
24	y	44	LYS	N-CA-C	5.14	116.57	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	3	1190	G	C2'-C3'-O3'	5.14	117.21	109.50
43	S	50	LEU	N-CA-C	-5.13	103.19	109.65
14	o	84	GLU	N-CA-C	-5.13	105.77	112.23
48	X	40	PHE	CA-C-N	5.12	125.16	119.32
48	X	40	PHE	C-N-CA	5.12	125.16	119.32
50	Z	9	GLU	N-CA-C	5.12	121.12	109.81
31	G	57	ASN	N-CA-C	-5.12	106.55	112.89
21	v	26	PHE	CA-C-N	5.11	124.87	119.76
21	v	26	PHE	C-N-CA	5.11	124.87	119.76
1	b	87	SER	N-CA-C	-5.10	107.11	113.38
10	k	71	ARG	CA-C-N	5.09	126.20	119.84
10	k	71	ARG	C-N-CA	5.09	126.20	119.84
38	N	88	GLU	N-CA-C	-5.09	106.33	112.54
13	n	68	ALA	N-CA-C	-5.08	105.75	111.28
58	8	189	ILE	N-CA-C	-5.05	105.48	112.50
58	8	332	TYR	N-CA-C	5.05	117.57	107.62
18	s	42	LYS	N-CA-C	-5.04	105.97	111.82
13	n	22	ARG	N-CA-C	-5.04	105.25	111.40
24	y	14	LEU	N-CA-C	-5.04	105.97	111.82
27	C	41	VAL	N-CA-C	5.02	115.79	110.72
34	J	103	GLY	N-CA-C	5.01	118.89	112.18
47	W	59	LYS	N-CA-C	5.00	116.42	111.07

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	76	0
2	c	1565	0	1616	39	0
3	d	1552	0	1619	43	0
4	e	1411	0	1447	42	0
5	f	1323	0	1374	30	0
6	g	1111	0	1148	25	0
7	h	989	0	1025	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	i	1032	0	1088	50	0
9	j	1129	0	1162	34	0
10	k	939	0	1012	42	0
11	l	1045	0	1117	25	0
12	m	1074	0	1157	38	0
13	n	961	0	1000	21	0
14	o	892	0	923	23	0
15	p	917	0	965	43	0
16	q	947	0	1022	21	0
17	r	816	0	839	14	0
18	s	857	0	922	20	0
19	t	739	0	807	31	0
20	u	780	0	834	16	0
21	v	753	0	780	18	0
22	w	575	0	592	13	0
23	x	625	0	655	17	0
24	y	509	0	543	16	0
25	z	449	0	491	9	0
26	B	444	0	461	15	0
27	C	410	0	440	13	0
28	D	377	0	418	15	0
29	E	504	0	574	14	0
30	F	302	0	343	16	0
31	G	1757	0	1787	38	0
32	H	1625	0	1699	51	0
33	I	1643	0	1710	63	0
34	J	1157	0	1199	42	0
35	K	818	0	808	42	0
36	L	1182	0	1240	35	0
37	M	979	0	1034	37	0
38	N	1022	0	1070	46	0
39	O	787	0	828	37	0
40	P	870	0	878	31	0
41	Q	955	0	1019	29	0
42	R	884	0	944	44	0
43	S	805	0	847	44	0
44	T	714	0	737	12	0
45	U	649	0	666	33	0
46	V	649	0	691	25	0
47	W	536	0	552	11	0
48	X	638	0	665	22	0
49	Y	665	0	714	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	Z	545	0	579	36	0
51	a	1027	0	1092	38	0
52	3	33012	0	16618	538	0
53	1	62317	0	31346	903	0
54	2	2568	0	1303	56	0
55	5	1640	0	836	17	0
55	6	1640	0	837	31	0
56	4	388	0	196	9	0
57	7	1619	0	821	38	0
58	8	2833	0	2857	79	0
59	5	10	0	10	0	0
60	7	11	0	8	2	0
61	8	28	0	12	0	0
All	All	153083	0	104134	2821	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 (2821) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1906:G:H2'	53:1:1907:G:H5''	1.42	0.98
53:1:2277:G:H2'	53:1:2278:A:H5''	1.43	0.98
52:3:225:C:H2'	52:3:226:G:H5''	1.46	0.97
53:1:45:G:H5''	53:1:46:G:H5'	1.46	0.97
52:3:1259:C:H3'	52:3:1260:G:H5''	1.45	0.96
34:J:35:LEU:HD22	34:J:133:ILE:HD13	1.46	0.96
12:m:12:MET:HA	53:1:910:A:H62	1.33	0.93
52:3:405:U:H3'	52:3:406:G:H5'	1.51	0.93
57:7:7:A:H3'	57:7:8:U:H5''	1.52	0.93
39:O:57:VAL:HG22	39:O:58:ASN:H	1.33	0.92
53:1:1300:G:H4'	53:1:1301:A:H5''	1.52	0.90
4:e:84:ILE:HD11	53:1:2312:U:H5'	1.50	0.90
24:y:4:LYS:NZ	53:1:102:U:H3	1.70	0.90
46:V:45:VAL:HG21	46:V:60:ILE:HD13	1.54	0.89
10:k:48:PRO:HG3	52:3:1422:G:H5'	1.57	0.86
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.55	0.86
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.56	0.85
42:R:44:ILE:H	42:R:44:ILE:HD12	1.39	0.85
7:h:123:ILE:H	7:h:123:ILE:HD12	1.41	0.85
34:J:107:GLY:HA3	52:3:9:G:H5'	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:105:ILE:HD11	34:J:123:LEU:HD23	1.58	0.84
53:1:1645:G:H5''	53:1:1646:C:H5'	1.58	0.84
53:1:1053:C:H2'	53:1:1054:A:H5''	1.60	0.82
53:1:1141:U:H4'	53:1:1142:A:O4'	1.80	0.81
53:1:1906:G:C2'	53:1:1907:G:H5''	2.10	0.81
16:q:8:ILE:HD11	53:1:1198:U:H4'	1.63	0.81
52:3:327:A:O2'	52:3:328:C:H4'	1.79	0.81
53:1:1807:G:H2'	53:1:1808:A:H5'	1.63	0.81
38:N:53:LEU:HD23	38:N:54:VAL:HG13	1.63	0.80
52:3:484:G:H4'	52:3:485:U:H5''	1.61	0.80
53:1:215:G:H4'	53:1:216:A:H4'	1.61	0.80
39:O:46:LYS:HZ3	39:O:68:ARG:HG2	1.47	0.80
57:7:62:C:H2'	57:7:63:G:H5''	1.61	0.79
7:h:59:LEU:HD23	7:h:61:ARG:H	1.47	0.79
45:U:31:ARG:HB3	52:3:310:G:H5''	1.65	0.79
53:1:1020:A:H1'	53:1:1021:A:OP2	1.82	0.79
23:x:2:ARG:HG2	23:x:32:LEU:HD12	1.65	0.79
53:1:1077:A:H2'	53:1:1078:U:H5'	1.64	0.79
16:q:7:VAL:HG23	16:q:8:ILE:HD12	1.65	0.79
19:t:54:GLU:HB3	19:t:88:LYS:HD2	1.66	0.78
2:c:151:THR:HB	2:c:152:PRO:HD3	1.66	0.77
52:3:396:C:H2'	52:3:397:A:H5''	1.65	0.77
18:s:36:LEU:HD21	18:s:47:VAL:HG13	1.64	0.77
54:2:3:C:H2'	54:2:4:C:H5''	1.65	0.77
52:3:225:C:C2'	52:3:226:G:H5''	2.13	0.77
58:8:104:LEU:HD11	58:8:116:THR:HG23	1.67	0.76
8:i:9:LYS:HD3	53:1:1061:U:H5''	1.66	0.76
10:k:35:VAL:HG23	10:k:36:GLY:H	1.50	0.76
1:b:156:SER:O	1:b:194:VAL:HG21	1.85	0.76
35:K:67:PRO:HG2	35:K:70:VAL:HG23	1.66	0.76
53:1:2715:C:H2'	53:1:2716:C:H5''	1.66	0.76
53:1:310:A:H2'	53:1:311:A:H5''	1.66	0.76
53:1:2277:G:C2'	53:1:2278:A:H5''	2.15	0.76
57:7:25:C:H3'	57:7:26:A:H5''	1.67	0.76
53:1:2296:U:H5''	53:1:2297:A:OP1	1.86	0.75
35:K:3:HIS:O	35:K:92:THR:HG22	1.86	0.75
7:h:60:LEU:HD11	53:1:1047:G:O6	1.86	0.75
15:p:38:ARG:NE	52:3:345:C:H5'	2.02	0.75
52:3:1306:A:N6	52:3:1331:G:H1'	2.01	0.75
53:1:2800:A:H3'	53:1:2801:G:H5'	1.68	0.75
22:w:33:ILE:HG22	22:w:34:VAL:HG23	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:55:VAL:HG23	34:J:56:PRO:HD3	1.70	0.74
53:1:275:C:H2'	53:1:276:U:H4'	1.69	0.74
6:g:37:VAL:HG21	6:g:51:ARG:HH12	1.53	0.73
28:D:26:ASN:CG	53:1:682:G:H5'	2.12	0.73
48:X:48:ILE:H	48:X:48:ILE:HD12	1.53	0.73
52:3:1137:C:H5'	52:3:1138:G:H5'	1.69	0.73
52:3:1201:A:H1'	52:3:1202:U:OP2	1.88	0.73
58:8:312:LEU:HD23	58:8:316:GLU:HG2	1.70	0.73
39:O:37:ARG:HH21	39:O:77:VAL:HG21	1.52	0.73
58:8:303:THR:HG22	58:8:366:PRO:HB3	1.70	0.73
24:y:4:LYS:HZ2	53:1:102:U:H3	0.83	0.73
31:G:206:ILE:H	31:G:206:ILE:HD12	1.52	0.73
53:1:503:A:H4'	53:1:505:A:H5''	1.70	0.73
53:1:310:A:C2'	53:1:311:A:H5''	2.18	0.73
35:K:12:PRO:O	35:K:15:SER:HB3	1.89	0.72
57:7:7:A:H3'	57:7:8:U:C5'	2.19	0.72
4:e:26:GLN:NE2	54:2:57:A:H4'	2.04	0.72
53:1:615:U:H5''	53:1:616:A:OP2	1.90	0.72
4:e:107:VAL:HB	4:e:108:PRO:HD3	1.72	0.72
53:1:1300:G:C4'	53:1:1301:A:H5''	2.19	0.72
50:Z:44:ARG:HH11	52:3:723:U:H5'	1.55	0.72
53:1:580:U:H2'	53:1:581:C:C6	2.25	0.72
52:3:1256:A:H1'	52:3:1258:G:C4	2.25	0.72
14:o:40:ILE:HG12	14:o:47:VAL:HG12	1.71	0.72
2:c:47:ALA:HB1	2:c:81:GLU:OE2	1.89	0.71
37:M:11:THR:HG21	52:3:876:C:H1'	1.72	0.71
57:7:6:G:H3'	57:7:7:A:H5''	1.70	0.71
36:L:12:LEU:HD12	36:L:13:PRO:HD2	1.71	0.71
24:y:2:LYS:HD2	53:1:78:U:OP2	1.91	0.71
51:a:15:VAL:HG11	51:a:220:ALA:HB3	1.71	0.71
1:b:155:ARG:NH1	53:1:1818:U:H5	1.89	0.70
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.71	0.70
53:1:2048:G:H2'	53:1:2049:G:H5''	1.73	0.70
39:O:88:MET:SD	39:O:89:ARG:HG3	2.32	0.70
8:i:12:VAL:HG12	8:i:13:ALA:H	1.57	0.70
35:K:96:VAL:HG22	35:K:97:THR:H	1.55	0.70
28:D:12:ARG:HE	28:D:44:VAL:HG21	1.56	0.70
53:1:1078:U:H4'	53:1:1079:C:H5''	1.74	0.69
52:3:1280:A:O2'	52:3:1281:C:H5'	1.92	0.69
5:f:173:ALA:O	5:f:174:LYS:HG3	1.91	0.69
50:Z:34:ARG:HB3	50:Z:36:PHE:CE2	2.28	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.74	0.69
41:Q:4:ASN:HB2	46:V:35:LYS:HZ3	1.55	0.69
52:3:1200:C:H5''	52:3:1201:A:H3'	1.74	0.69
28:D:34:ARG:HD3	53:1:467:G:OP2	1.93	0.69
51:a:205:LYS:HD3	53:1:1860:G:H4'	1.74	0.69
53:1:2553:G:H3'	53:1:2554:U:H5''	1.74	0.69
53:1:2114:A:H61	53:1:2117:A:H62	1.41	0.69
57:7:6:G:C3'	57:7:7:A:H5''	2.21	0.69
39:O:53:ILE:HG12	52:3:1060:U:H5''	1.74	0.69
8:i:91:LYS:HB3	8:i:94:LYS:HE2	1.75	0.69
38:N:123:ARG:HB2	52:3:1343:G:H4'	1.75	0.69
52:3:1197:A:H2'	52:3:1198:G:H5''	1.74	0.69
34:J:14:LEU:HD23	34:J:15:ILE:N	2.08	0.68
47:W:40:PRO:HB3	52:3:720:C:H5''	1.74	0.68
52:3:279:A:H5'	52:3:281:G:H5'	1.74	0.68
53:1:2286:G:H5''	53:1:2287:A:OP1	1.92	0.68
4:e:130:GLY:HA3	53:1:2305:U:H5''	1.76	0.68
33:I:150:LYS:HE2	33:I:177:MET:SD	2.32	0.68
52:3:29:U:O2'	52:3:30:U:H5'	1.94	0.68
53:1:807:U:H2'	53:1:808:G:H8	1.58	0.68
54:2:3:C:C2'	54:2:4:C:H5''	2.22	0.68
42:R:100:ARG:HB3	42:R:100:ARG:HH11	1.57	0.68
52:3:946:A:H2'	52:3:947:G:H8	1.59	0.68
53:1:18:U:H2'	53:1:19:A:C8	2.28	0.68
58:8:310:TYR:HB3	58:8:386:ALA:HB3	1.75	0.68
31:G:27:LYS:HB3	31:G:28:PRO:HD3	1.76	0.68
51:a:40:GLU:HB3	51:a:217:THR:HG22	1.76	0.68
54:2:3:C:C3'	54:2:4:C:H5''	2.24	0.68
31:G:130:LYS:CE	52:3:1160:G:H5'	2.24	0.68
39:O:42:LEU:HD22	39:O:73:LEU:HD11	1.76	0.68
33:I:33:ILE:H	33:I:33:ILE:HD12	1.58	0.68
11:l:46:VAL:HG12	11:l:47:ARG:H	1.58	0.68
20:u:42:LYS:HD2	53:1:499:U:C5'	2.24	0.68
45:U:36:VAL:HG23	45:U:53:ASP:HB3	1.76	0.68
55:5:75:C:H2'	55:5:76:A:H5''	1.74	0.68
32:H:160:GLU:HG3	32:H:161:ILE:HG12	1.76	0.67
36:L:69:ARG:HH21	36:L:95:ARG:HD2	1.60	0.67
39:O:40:ILE:HB	39:O:73:LEU:HB2	1.76	0.67
7:h:118:ILE:HG22	7:h:119:PRO:CD	2.22	0.67
31:G:113:LEU:O	31:G:117:GLU:HG3	1.95	0.67
42:R:15:VAL:HG23	42:R:16:ILE:HG13	1.74	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:88:C:H5''	54:2:89:U:OP1	1.94	0.67
50:Z:44:ARG:NH1	52:3:723:U:H5'	2.09	0.67
9:j:78:THR:HG22	53:1:2641:G:H5''	1.76	0.67
12:m:41:LEU:HD13	12:m:96:ILE:HG13	1.75	0.67
38:N:105:ARG:O	38:N:105:ARG:HD3	1.94	0.67
1:b:260:LYS:HA	1:b:263:ASP:OD2	1.94	0.67
4:e:91:ARG:HA	4:e:95:MET:HB2	1.75	0.67
34:J:152:VAL:HA	34:J:155:LYS:HG2	1.76	0.67
35:K:20:GLY:O	35:K:23:GLU:HG3	1.95	0.67
36:L:78:ARG:HH11	52:3:1382:C:H4'	1.59	0.67
53:1:677:A:O2'	53:1:2071:A:H5'	1.95	0.67
60:7:101:PHE:HB3	58:8:262:PHE:CE1	2.30	0.67
7:h:61:ARG:HB3	53:1:1046:A:H4'	1.76	0.67
53:1:1664:A:H61	53:1:1996:C:H42	1.43	0.67
58:8:283:LYS:HB3	58:8:286:GLU:OE1	1.95	0.66
8:i:25:PRO:HD2	57:7:56:C:H5''	1.77	0.66
12:m:69:PRO:HA	12:m:94:ALA:HB2	1.76	0.66
45:U:75:ILE:HG23	45:U:80:LYS:HD3	1.75	0.66
51:a:46:VAL:HB	51:a:171:ILE:HG22	1.77	0.66
6:g:46:PHE:HB3	6:g:50:ARG:HH21	1.60	0.66
28:D:14:ARG:HD2	53:1:771:G:OP1	1.95	0.66
40:P:60:PHE:O	40:P:63:GLN:HG2	1.95	0.66
1:b:48:ILE:HD11	1:b:51:ARG:HA	1.77	0.66
53:1:1796:U:H2'	53:1:1797:G:H8	1.60	0.66
3:d:153:LEU:HD23	3:d:153:LEU:H	1.60	0.66
29:E:61:LEU:HD12	29:E:61:LEU:O	1.95	0.66
31:G:117:GLU:O	31:G:121:GLN:HG2	1.95	0.66
52:3:960:U:H4'	52:3:961:U:O5'	1.95	0.66
53:1:2715:C:C2'	53:1:2716:C:H5''	2.26	0.66
57:7:62:C:C2'	57:7:63:G:H5''	2.25	0.66
47:W:41:SER:HB3	47:W:51:GLN:HE21	1.60	0.66
58:8:107:ALA:HB1	58:8:137:LYS:HD2	1.78	0.66
2:c:149:ASN:HB3	53:1:2572:A:OP2	1.95	0.66
6:g:135:HIS:HB3	6:g:138:VAL:HB	1.78	0.66
50:Z:40:PRO:O	50:Z:44:ARG:HG2	1.96	0.65
53:1:2756:U:H1'	53:1:2757:A:H5''	1.77	0.65
5:f:97:VAL:HG23	5:f:124:CYS:SG	2.36	0.65
24:y:41:HIS:CD2	53:1:96:C:H4'	2.31	0.65
35:K:92:THR:OG1	35:K:93:LYS:N	2.26	0.65
53:1:558:U:H2'	53:1:559:G:H8	1.61	0.65
53:1:2267:A:H5''	53:1:2268:A:H5'	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:1:MET:HE3	7:h:2:ALA:H	1.60	0.65
12:m:125:PRO:HG2	12:m:126:ILE:HD12	1.79	0.65
42:R:76:ILE:HG22	42:R:80:MET:HE2	1.78	0.65
33:I:23:GLY:HA3	52:3:409:U:OP1	1.96	0.65
33:I:131:ILE:HG12	52:3:620:C:C2	2.32	0.65
23:x:2:ARG:HH12	23:x:29:LEU:HD13	1.61	0.65
35:K:9:MET:HE1	35:K:86:ARG:HD2	1.79	0.65
43:S:70:HIS:HB3	52:3:974:A:H5'	1.77	0.65
48:X:39:ILE:HB	48:X:66:VAL:HA	1.78	0.65
7:h:33:VAL:HG12	7:h:34:THR:H	1.62	0.65
39:O:57:VAL:HG22	39:O:58:ASN:N	2.09	0.65
45:U:70:ARG:HH12	52:3:451:A:H5'	1.62	0.65
53:1:2715:C:C3'	53:1:2716:C:H5''	2.26	0.65
10:k:76:VAL:H	15:p:72:VAL:HG12	1.62	0.65
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.78	0.64
36:L:110:ARG:HH22	36:L:121:ASN:HB3	1.62	0.64
33:I:18:LEU:HB3	33:I:63:ILE:HG12	1.80	0.64
52:3:1259:C:C3'	52:3:1260:G:H5''	2.23	0.64
54:2:3:C:H3'	54:2:4:C:H5''	1.80	0.64
49:Y:41:GLY:HA2	49:Y:85:LEU:HD21	1.78	0.64
5:f:41:GLU:HA	5:f:54:ARG:HH21	1.62	0.64
14:o:51:ALA:HB3	14:o:78:VAL:HG22	1.80	0.64
19:t:10:VAL:HG23	19:t:11:LEU:HD12	1.79	0.64
32:H:67:ILE:HB	32:H:102:ILE:HG13	1.80	0.64
7:h:57:ASN:HB2	7:h:62:ARG:HD2	1.80	0.64
38:N:59:LYS:C	38:N:60:LEU:HD22	2.23	0.64
43:S:5:MET:HE1	52:3:982:U:H3'	1.80	0.64
43:S:40:ARG:HH12	48:X:6:LYS:HZ2	1.46	0.64
53:1:1083:U:H2'	53:1:1085:A:OP2	1.98	0.64
7:h:46:ARG:HH21	7:h:95:LEU:HD21	1.62	0.64
10:k:76:VAL:HG22	15:p:72:VAL:HG12	1.79	0.64
10:k:99:ILE:HD13	10:k:115:ILE:HG23	1.79	0.64
52:3:1413:A:H2	52:3:1487:G:H22	1.44	0.64
18:s:98:LYS:HD2	53:1:2012:G:OP1	1.98	0.64
31:G:46:VAL:HG23	31:G:47:PRO:HD3	1.79	0.64
42:R:22:TYR:HD2	42:R:65:GLU:HG3	1.61	0.64
53:1:814:C:H1'	53:1:1225:G:H21	1.63	0.64
1:b:227:VAL:HG11	53:1:784:G:C6	2.32	0.64
52:3:405:U:C3'	52:3:406:G:H5'	2.27	0.64
53:1:2423:U:O2'	53:1:2425:A:H2'	1.98	0.64
58:8:309:VAL:HG11	58:8:359:MET:HE1	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:4:ASN:O	53:1:1243:C:H1'	1.98	0.63
42:R:100:ARG:HB3	42:R:100:ARG:NH1	2.12	0.63
18:s:85:ILE:HD12	18:s:85:ILE:N	2.13	0.63
4:e:102:LEU:O	4:e:106:ALA:HB3	1.97	0.63
28:D:13:ASN:O	53:1:125:A:H4'	1.98	0.63
42:R:89:ARG:HB2	42:R:96:VAL:HG12	1.79	0.63
53:1:528:A:N1	53:1:2042:A:H2'	2.13	0.63
8:i:55:PRO:HD3	8:i:74:PRO:HD3	1.81	0.63
32:H:112:ALA:HB3	32:H:184:ASN:HD22	1.64	0.63
32:H:146:LYS:HB2	32:H:202:PHE:HD2	1.63	0.63
53:1:1697:G:H4'	53:1:1978:A:H5''	1.79	0.63
15:p:28:LYS:HD3	15:p:82:SER:OG	1.98	0.63
35:K:6:ILE:HB	35:K:62:MET:HB2	1.80	0.63
58:8:93:ILE:HD11	58:8:122:LEU:HD13	1.80	0.63
9:j:40:HIS:CE1	9:j:41:LYS:HG3	2.33	0.63
10:k:1:MET:HA	10:k:32:TYR:HB3	1.81	0.63
52:3:769:G:H4'	52:3:1513:A:H4'	1.81	0.63
20:u:42:LYS:HD2	53:1:499:U:H5''	1.79	0.63
52:3:235:C:H2'	52:3:236:A:H8	1.63	0.63
53:1:796:C:H2'	53:1:797:G:H8	1.64	0.63
53:1:2048:G:C3'	53:1:2049:G:H5''	2.28	0.63
1:b:73:ILE:HG12	53:1:1490:A:N6	2.14	0.62
31:G:130:LYS:HE3	52:3:1160:G:H5'	1.81	0.62
33:I:50:TYR:CD2	52:3:508:U:H4'	2.34	0.62
40:P:30:ILE:HD11	52:3:706:A:H4'	1.81	0.62
52:3:1255:G:H2'	52:3:1279:G:H1	1.63	0.62
54:2:66:A:H5''	54:2:67:G:OP1	1.99	0.62
4:e:65:LEU:HD22	54:2:42:C:C4	2.34	0.62
34:J:80:LEU:HB2	34:J:97:PRO:HG3	1.81	0.62
36:L:115:MET:HA	36:L:118:ARG:HD2	1.80	0.62
38:N:114:LYS:NZ	52:3:1187:G:H5'	2.13	0.62
53:1:2055:C:H2'	53:1:2504:U:H5'	1.80	0.62
53:1:1367:A:H2'	53:1:1368:G:H5'	1.81	0.62
36:L:87:PRO:HG3	36:L:148:LYS:HA	1.80	0.62
4:e:65:LEU:HD12	54:2:41:G:N2	2.14	0.62
52:3:889:A:H5'	52:3:891:U:H1'	1.81	0.62
52:3:1441:A:H2'	52:3:1442:G:H5'	1.81	0.62
18:s:4:ILE:HG22	18:s:106:VAL:HG12	1.81	0.62
42:R:114:PRO:HG2	52:3:1228:C:C5'	2.30	0.62
1:b:226:PRO:HD3	1:b:233:GLY:CA	2.29	0.62
14:o:26:LEU:HD13	14:o:39:VAL:HG22	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1071:G:OP1	53:1:1071:G:H3'	1.99	0.62
58:8:257:THR:HG21	58:8:280:ARG:HE	1.64	0.62
8:i:9:LYS:HZ1	53:1:1060:U:H5''	1.63	0.62
52:3:501:C:H2'	52:3:502:A:C8	2.35	0.62
52:3:1513:A:H2'	52:3:1514:G:C8	2.35	0.62
2:c:13:ARG:HH11	15:p:55:HIS:HA	1.63	0.62
11:l:111:ILE:HD11	53:1:636:G:H2'	1.80	0.62
46:V:18:LYS:HG2	46:V:49:ASN:HA	1.81	0.62
53:1:45:G:H5''	53:1:46:G:C5'	2.27	0.62
31:G:115:ASP:O	31:G:119:GLN:HG2	1.99	0.61
38:N:114:LYS:HZ3	52:3:1187:G:H5'	1.64	0.61
3:d:71:GLY:N	53:1:674:G:H5''	2.15	0.61
33:I:176:LYS:HZ3	33:I:178:GLU:HB3	1.65	0.61
50:Z:65:ARG:HD3	52:3:1088:G:H4'	1.81	0.61
52:3:673:A:H2'	52:3:674:G:C8	2.35	0.61
53:1:1300:G:H4'	53:1:1301:A:C5'	2.26	0.61
11:l:17:LYS:HE3	11:l:27:LEU:HD11	1.82	0.61
15:p:113:LEU:O	15:p:113:LEU:HD12	2.00	0.61
21:v:30:ILE:HD12	21:v:91:PHE:O	2.01	0.61
53:1:2818:U:H2'	53:1:2819:G:H8	1.64	0.61
12:m:75:GLU:HG2	53:1:957:C:H5'	1.82	0.61
52:3:946:A:H2'	52:3:947:G:C8	2.34	0.61
53:1:1827:U:H2'	53:1:1828:G:O4'	1.99	0.61
53:1:2180:U:H4'	55:6:17(A):U:H5'	1.81	0.61
53:1:1674:G:H21	53:1:1677:A:H61	1.46	0.61
11:l:101:ILE:HG13	11:l:102:GLY:N	2.15	0.61
27:C:28:THR:HG23	27:C:29:LYS:HG2	1.81	0.61
38:N:119:LYS:HD2	52:3:1350:A:OP2	2.00	0.61
39:O:59:LYS:HE3	39:O:62:ARG:NH2	2.15	0.61
52:3:396:C:C2'	52:3:397:A:H5''	2.29	0.61
52:3:1352:C:H2'	52:3:1353:G:H8	1.66	0.61
10:k:87:LEU:HD22	10:k:92:GLU:O	2.01	0.61
32:H:54:ILE:HD11	32:H:65:VAL:HB	1.82	0.61
46:V:14:ASP:OD1	46:V:20:ILE:HG22	2.01	0.61
3:d:34:ALA:HA	3:d:94:GLN:HE21	1.66	0.61
52:3:950:U:H2'	52:3:951:G:H8	1.66	0.61
26:B:28:SER:OG	26:B:39:ARG:HD3	2.01	0.61
11:l:101:ILE:HG13	11:l:102:GLY:H	1.66	0.60
12:m:78:LEU:HD23	12:m:79:ALA:N	2.16	0.60
34:J:93:VAL:HG21	34:J:110:MET:HE1	1.81	0.60
53:1:995:C:H6	53:1:995:C:H5'	1.64	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1077:A:C2'	53:1:1078:U:H5'	2.30	0.60
53:1:1856:U:H2'	53:1:1857:G:O4'	2.00	0.60
53:1:2350:C:H2'	53:1:2351:G:O4'	2.00	0.60
58:8:342:ILE:HG23	58:8:359:MET:HG3	1.83	0.60
4:e:77:LYS:HE3	55:5:19:G:H21	1.65	0.60
11:l:93:ASN:O	11:l:94:THR:HG22	2.01	0.60
43:S:12:ARG:HH21	43:S:58:ARG:HH21	1.47	0.60
52:3:695:A:H2'	52:3:696:A:C8	2.37	0.60
52:3:1352:C:H2'	52:3:1353:G:C8	2.36	0.60
53:1:215:G:C4'	53:1:216:A:H4'	2.29	0.60
2:c:77:ARG:HD2	2:c:77:ARG:O	2.02	0.60
21:v:86:LEU:HD23	21:v:89:ILE:HD11	1.83	0.60
24:y:19:LEU:HB3	24:y:23:ARG:HH12	1.65	0.60
28:D:11:LYS:HE3	53:1:686:U:H5''	1.83	0.60
33:I:3:TYR:C	33:I:4:LEU:HD23	2.27	0.60
33:I:8:LEU:HB3	52:3:430:A:OP1	2.01	0.60
40:P:93:GLU:HG3	40:P:97:ARG:NH1	2.16	0.60
41:Q:120:ARG:CZ	52:3:500:G:H5'	2.31	0.60
43:S:23:ARG:HH12	43:S:25:GLU:HB2	1.65	0.60
17:r:78:ARG:HH12	53:1:974:G:H4'	1.66	0.60
50:Z:25:ALA:HB1	56:4:9:G:H5'	1.83	0.60
35:K:66:ALA:HB1	35:K:67:PRO:HD2	1.82	0.60
43:S:21:ALA:HB3	43:S:22:LYS:HZ2	1.67	0.60
52:3:1316:G:H2'	52:3:1317:C:H5''	1.83	0.60
53:1:704:G:H2'	53:1:726:G:N2	2.16	0.60
53:1:1434:A:H2'	53:1:1435:G:C8	2.36	0.60
10:k:88:ASN:HB2	10:k:91:SER:O	2.01	0.60
38:N:114:LYS:HG2	38:N:120:ALA:HA	1.83	0.60
41:Q:73:LEU:HD21	41:Q:79:ILE:HG21	1.82	0.60
42:R:22:TYR:CD2	42:R:65:GLU:HG3	2.35	0.60
42:R:114:PRO:HG2	52:3:1228:C:H5'	1.84	0.60
52:3:70:U:H5''	52:3:71:A:OP1	2.00	0.60
53:1:2834:G:H2'	53:1:2879:A:H61	1.66	0.60
6:g:58:LEU:O	6:g:61:VAL:HG12	2.02	0.60
50:Z:8:ASN:HB3	50:Z:9:GLU:OE1	2.02	0.60
53:1:2229:U:H2'	53:1:2230:G:H8	1.66	0.60
33:I:2:ARG:HE	33:I:114:ARG:HD3	1.66	0.60
53:1:49:A:H5'	53:1:51:G:O4'	2.02	0.60
53:1:2156:G:H2'	53:1:2157:G:H5'	1.82	0.60
53:1:807:U:H2'	53:1:808:G:C8	2.34	0.60
36:L:101:ARG:NH1	36:L:101:ARG:HB2	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:715:A:H2'	52:3:716:A:C8	2.36	0.60
53:1:859:G:HO2'	53:1:860:U:H6	1.48	0.60
53:1:2605:U:H2'	53:1:2606:C:C6	2.37	0.60
37:M:14:ARG:HD2	52:3:875:U:O2'	2.01	0.59
52:3:1005:A:H2'	52:3:1006:G:O4'	2.02	0.59
52:3:1301:U:O2	52:3:1301:U:H2'	2.02	0.59
53:1:1476:U:H3	53:1:1515:A:H62	1.50	0.59
58:8:308:GLU:HG2	58:8:358:LYS:HG2	1.83	0.59
32:H:177:LEU:HD12	32:H:177:LEU:H	1.67	0.59
34:J:133:ILE:O	34:J:136:VAL:HG12	2.02	0.59
52:3:665:A:C1'	52:3:733:G:H1'	2.32	0.59
53:1:523:C:H2'	53:1:524:G:H8	1.67	0.59
55:6:54:U:H3	55:6:58:A:H62	1.48	0.59
58:8:141:VAL:HG11	58:8:146:LEU:HD11	1.83	0.59
23:x:2:ARG:NH1	23:x:29:LEU:HD13	2.16	0.59
33:I:18:LEU:HD22	33:I:63:ILE:HD11	1.84	0.59
37:M:80:PRO:HG2	52:3:878:A:H5''	1.84	0.59
53:1:2086:U:H2'	53:1:2087:G:C8	2.37	0.59
11:l:74:THR:HG22	11:l:107:PHE:HB2	1.84	0.59
37:M:12:ARG:CZ	52:3:826:C:H5'	2.33	0.59
53:1:542:C:H2'	53:1:543:G:H5''	1.85	0.59
53:1:2281:A:O2'	53:1:2282:G:H5'	2.02	0.59
55:6:16:C:O2'	55:6:17:C:H5'	2.03	0.59
52:3:1066:C:C2'	52:3:1067:A:H5'	2.33	0.59
52:3:1318:A:H2'	52:3:1319:A:H5'	1.84	0.59
53:1:2834:G:H2'	53:1:2879:A:N6	2.18	0.59
5:f:104:LEU:HB3	5:f:106:LEU:HD13	1.84	0.59
36:L:16:LYS:HG2	36:L:17:PHE:HD1	1.68	0.59
52:3:1412:C:H2'	52:3:1413:A:C8	2.36	0.59
53:1:2512:C:H2'	53:1:2513:A:O4'	2.01	0.59
8:i:98:GLY:O	8:i:99:LYS:HE2	2.03	0.59
10:k:76:VAL:HG22	15:p:72:VAL:CG1	2.32	0.59
13:n:29:VAL:HG21	13:n:75:ILE:HG23	1.84	0.59
53:1:2048:G:C2'	53:1:2049:G:H5''	2.32	0.59
7:h:31:ARG:HD3	7:h:109:LYS:HB3	1.85	0.59
8:i:10:LEU:N	8:i:10:LEU:HD23	2.17	0.59
34:J:60:GLN:HA	34:J:63:MET:HE3	1.84	0.59
5:f:98:LYS:NZ	5:f:103:ASN:HB2	2.18	0.59
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.85	0.59
19:t:54:GLU:CB	19:t:88:LYS:HD2	2.32	0.59
52:3:225:C:C3'	52:3:226:G:H5''	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:110:THR:HB	2:c:202:ILE:HB	1.84	0.59
2:c:123:LYS:HZ1	53:1:2724:U:H5''	1.67	0.59
42:R:14:ALA:HB1	42:R:33:LEU:HD21	1.84	0.59
42:R:103:THR:HG21	52:3:951:G:O6	2.03	0.59
37:M:14:ARG:O	37:M:17:GLN:NE2	2.34	0.58
53:1:2170:A:H2'	53:1:2171:A:O4'	2.03	0.58
1:b:206:LYS:HD3	53:1:729:G:OP2	2.03	0.58
2:c:135:GLY:HA2	53:1:743:A:OP1	2.03	0.58
34:J:75:LEU:HD23	34:J:75:LEU:H	1.68	0.58
52:3:1429:A:H2'	52:3:1430:A:H8	1.68	0.58
53:1:1019:U:H3	53:1:1142:A:H62	1.51	0.58
53:1:1434:A:H2'	53:1:1435:G:H8	1.68	0.58
54:2:56:G:H4'	54:2:57:A:H8	1.68	0.58
11:l:29:LYS:HZ1	53:1:567:U:P	2.25	0.58
52:3:24:U:H2'	52:3:25:C:C6	2.39	0.58
52:3:1516:G:H2'	52:3:1518:A:OP2	2.03	0.58
53:1:1067:A:H2'	53:1:1067:A:N3	2.18	0.58
53:1:1611:C:H6	53:1:1611:C:H5'	1.69	0.58
53:1:2286:G:H4'	53:1:2287:A:O5'	2.02	0.58
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.83	0.58
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.68	0.58
19:t:6:ARG:NH2	53:1:144:A:H5'	2.18	0.58
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.85	0.58
9:j:40:HIS:HE1	9:j:41:LYS:HE3	1.69	0.58
53:1:974:G:H1'	53:1:975:A:C8	2.39	0.58
57:7:68:C:H2'	57:7:69:G:C8	2.37	0.58
5:f:154:GLU:OE2	5:f:156:TYR:HB2	2.03	0.58
27:C:5:ARG:HE	27:C:23:THR:HG23	1.68	0.58
33:I:82:LYS:HD2	52:3:5:U:O4	2.03	0.58
53:1:414:C:H2'	53:1:415:A:C8	2.39	0.58
53:1:2849:U:H3	53:1:2867:G:H5''	1.69	0.58
4:e:73:VAL:HG12	4:e:75:GLY:H	1.69	0.58
8:i:89:SER:HB3	8:i:135:MET:C	2.29	0.58
36:L:3:ARG:CZ	52:3:1092:A:H5''	2.34	0.58
41:Q:51:VAL:HG22	41:Q:52:CYS:H	1.68	0.58
43:S:3:GLN:OE1	52:3:1047:G:H5''	2.04	0.58
52:3:162:A:H2'	52:3:163:C:H5'	1.85	0.58
53:1:161:A:H3'	53:1:162:U:H5''	1.84	0.58
53:1:1045:C:H5'	53:1:1046:A:H5''	1.86	0.58
53:1:1319:C:O2'	53:1:1320:C:H5'	2.04	0.58
54:2:2:G:H2'	54:2:3:C:C6	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:31:VAL:N	6:g:32:PRO:HD2	2.18	0.58
7:h:21:GLY:HA3	7:h:86:MET:HE2	1.86	0.58
32:H:175:HIS:ND1	52:3:1108:G:H5'	2.19	0.58
52:3:521:G:O2'	52:3:522:C:H5'	2.04	0.58
53:1:69:C:O2'	53:1:70:G:H5'	2.04	0.58
53:1:1874:C:H2'	53:1:1875:G:O4'	2.03	0.58
31:G:7:ASP:HA	31:G:10:LYS:HD3	1.85	0.58
51:a:51:ASP:OD2	51:a:54:LYS:HG3	2.04	0.58
52:3:1513:A:H2'	52:3:1514:G:H8	1.67	0.58
53:1:225:C:H2'	53:1:226:A:O4'	2.04	0.58
53:1:511:U:H2'	53:1:512:G:H5'	1.84	0.58
53:1:2238:G:H2'	53:1:2238:G:N3	2.19	0.58
58:8:233:GLU:OE2	58:8:234:ARG:HG3	2.04	0.58
2:c:43:ASP:HB3	2:c:45:TYR:CE1	2.39	0.57
39:O:52:LEU:HB2	43:S:80:ARG:HD2	1.85	0.57
52:3:715:A:H2'	52:3:716:A:H8	1.69	0.57
54:2:95:U:H2'	54:2:96:G:C8	2.38	0.57
55:6:71:C:H2'	55:6:72:A:C8	2.39	0.57
28:D:11:LYS:CE	53:1:686:U:H5''	2.34	0.57
32:H:67:ILE:H	32:H:67:ILE:HD12	1.69	0.57
42:R:64:VAL:HG12	42:R:65:GLU:H	1.68	0.57
52:3:335:C:H2'	52:3:336:A:H8	1.69	0.57
27:C:33:LEU:HD21	53:1:2286:G:N7	2.18	0.57
31:G:31:PHE:HB2	31:G:41:ASN:HA	1.85	0.57
33:I:8:LEU:HD21	33:I:31:CYS:HB3	1.86	0.57
37:M:55:LYS:HD2	52:3:652:U:O2'	2.03	0.57
52:3:212:G:H2'	52:3:213:G:H8	1.70	0.57
52:3:572:A:H5''	52:3:917:G:H4'	1.85	0.57
53:1:720:U:H2'	53:1:721:A:C8	2.39	0.57
53:1:2795:C:H2'	53:1:2796:U:O4'	2.03	0.57
7:h:60:LEU:HD12	7:h:61:ARG:HG3	1.87	0.57
52:3:112:G:H21	52:3:354:G:H5'	1.69	0.57
1:b:226:PRO:HD3	1:b:233:GLY:N	2.19	0.57
31:G:65:LYS:NZ	31:G:154:GLY:O	2.38	0.57
37:M:48:PHE:HB2	37:M:58:LEU:HD11	1.86	0.57
52:3:352:C:H4'	52:3:354:G:OP1	2.04	0.57
52:3:1066:C:H2'	52:3:1067:A:H5'	1.87	0.57
53:1:1053:C:C2'	53:1:1054:A:H5''	2.34	0.57
53:1:1251:C:O2'	53:1:1252:G:H3'	2.05	0.57
53:1:2139:U:H2'	53:1:2140:G:C8	2.40	0.57
16:q:106:THR:O	16:q:110:GLU:HG3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:3:LYS:HE3	52:3:1191:A:H5''	1.86	0.57
33:I:96:ARG:HH22	33:I:114:ARG:HH12	1.52	0.57
46:V:16:MET:HG3	46:V:19:SER:OG	2.04	0.57
51:a:60:ARG:HB3	51:a:164:ARG:HG3	1.85	0.57
52:3:78:A:H2'	52:3:79:G:O4'	2.05	0.57
53:1:2128:G:H1'	53:1:2173:A:N3	2.19	0.57
53:1:2208:C:H2'	53:1:2209:G:C8	2.39	0.57
8:i:12:VAL:O	8:i:13:ALA:C	2.47	0.57
22:w:61:GLY:HA3	22:w:80:ALA:HA	1.86	0.57
43:S:63:CYS:HB3	43:S:67:GLY:H	1.69	0.57
57:7:62:C:C3'	57:7:63:G:H5''	2.35	0.57
48:X:35:ARG:HH12	48:X:76:THR:HG22	1.69	0.57
49:Y:34:VAL:HG21	49:Y:78:LEU:HD21	1.87	0.57
52:3:410:G:H2'	52:3:429:U:C4	2.38	0.57
52:3:1340:A:O2'	52:3:1341:U:H5'	2.04	0.57
52:3:1506:U:O2'	52:3:1507:A:H5'	2.04	0.57
53:1:593:U:H2'	53:1:594:U:C6	2.40	0.57
53:1:2047:C:H2'	53:1:2048:G:H8	1.69	0.57
57:7:25:C:C3'	57:7:26:A:H5''	2.35	0.57
3:d:134:LEU:HD23	3:d:164:LEU:HD22	1.87	0.57
52:3:1389:C:H2'	52:3:1390:U:C6	2.39	0.57
53:1:1495:A:H2	53:1:1578:U:H1'	1.70	0.57
53:1:1965:C:H5''	53:1:1966:A:H2'	1.86	0.57
53:1:2646:C:H2'	53:1:2647:U:O4'	2.04	0.57
34:J:98:ALA:HB2	34:J:123:LEU:HG	1.86	0.57
51:a:12:ARG:HH11	53:1:2175:C:H5''	1.69	0.57
52:3:501:C:H2'	52:3:502:A:H8	1.70	0.57
53:1:2391:G:H5'	53:1:2392:A:OP1	2.05	0.57
53:1:2462:C:H2'	53:1:2463:C:C6	2.40	0.57
57:7:76:A:H4'	58:8:219:PHE:CD2	2.40	0.57
2:c:98:VAL:HG22	2:c:180:VAL:HG13	1.87	0.56
9:j:27:ARG:NH1	53:1:1140:C:O3'	2.38	0.56
26:B:46:GLY:HA3	26:B:54:ILE:HG22	1.87	0.56
33:I:49:ASP:O	33:I:52:VAL:HG22	2.05	0.56
39:O:16:ARG:NH1	52:3:1152:A:O3'	2.38	0.56
45:U:70:ARG:HD3	52:3:375:U:OP1	2.05	0.56
52:3:701:U:H4'	52:3:703:G:H1'	1.87	0.56
53:1:1447:C:H2'	53:1:1448:G:H8	1.70	0.56
53:1:2134:A:N6	53:1:2157:G:H4'	2.20	0.56
28:D:24:THR:HG23	28:D:27:GLY:H	1.70	0.56
39:O:37:ARG:HG3	52:3:1124:G:H5''	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:7:26:A:H2'	57:7:27:G:O4'	2.05	0.56
58:8:220:SER:HB3	58:8:284:ARG:HD3	1.87	0.56
3:d:105:LEU:HA	3:d:108:ILE:HG22	1.86	0.56
8:i:78:LEU:HD13	8:i:112:LYS:HD3	1.86	0.56
33:I:55:ARG:NH2	33:I:58:GLN:HG3	2.20	0.56
48:X:66:VAL:HG23	48:X:67:GLY:H	1.70	0.56
50:Z:9:GLU:HB2	50:Z:10:PRO:HD3	1.87	0.56
52:3:79:G:O2'	52:3:80:A:H5'	2.05	0.56
52:3:211:G:H2'	52:3:212:G:H5'	1.87	0.56
52:3:357:G:OP1	52:3:367:U:H5''	2.05	0.56
53:1:2743:U:H2'	53:1:2744:G:H5''	1.86	0.56
38:N:21:LYS:HD2	38:N:22:PRO:HD2	1.86	0.56
53:1:473:G:O2'	53:1:474:G:H5'	2.06	0.56
54:2:35:C:H2'	54:2:36:C:H5'	1.87	0.56
55:5:75:C:C2'	55:5:76:A:H5''	2.36	0.56
58:8:314:LYS:HE3	58:8:320:HIS:HA	1.87	0.56
3:d:99:LYS:NZ	53:1:601:C:H4'	2.20	0.56
5:f:27:GLY:HA3	5:f:78:VAL:HB	1.86	0.56
15:p:28:LYS:HD3	15:p:82:SER:HG	1.70	0.56
31:G:5:MET:HA	31:G:8:MET:HE2	1.88	0.56
52:3:730:G:H2'	52:3:731:G:H5'	1.87	0.56
52:3:1379:G:O2'	52:3:1380:U:H5'	2.06	0.56
53:1:1186:G:H2'	53:1:1187:G:O4'	2.06	0.56
53:1:2799:A:H2'	53:1:2800:A:H5'	1.86	0.56
2:c:66:GLY:HA3	53:1:2786:U:O2'	2.06	0.56
14:o:24:THR:HG22	14:o:42:PRO:HD3	1.87	0.56
26:B:24:VAL:HG22	26:B:26:SER:H	1.70	0.56
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.88	0.56
8:i:116:MET:HE3	8:i:117:THR:H	1.71	0.56
14:o:12:THR:HA	14:o:15:ARG:HB2	1.88	0.56
52:3:335:C:H2'	52:3:336:A:C8	2.40	0.56
53:1:239:C:H2'	53:1:240:C:O4'	2.04	0.56
53:1:967:U:H2'	53:1:968:C:C6	2.40	0.56
53:1:1133:A:H4'	53:1:1134:A:H5''	1.88	0.56
53:1:2609:U:H5'	53:1:2610:C:OP2	2.06	0.56
8:i:46:ASP:OD1	8:i:50:LYS:HD3	2.05	0.56
8:i:116:MET:HE1	53:1:1058:U:O2	2.05	0.56
52:3:1259:C:H3'	52:3:1260:G:C5'	2.30	0.56
53:1:576:U:H2'	53:1:577:G:C8	2.41	0.56
53:1:2514:U:H2'	53:1:2515:C:C6	2.41	0.56
12:m:77:PRO:O	12:m:80:VAL:HG22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:E:6:VAL:HG23	29:E:9:ALA:HB3	1.88	0.56
32:H:18:ASN:HD21	43:S:89:ARG:HH21	1.52	0.56
43:S:25:GLU:HA	43:S:28:ALA:HB3	1.88	0.56
53:1:613:A:H2'	53:1:613:A:N3	2.18	0.56
53:1:796:C:H2'	53:1:797:G:C8	2.40	0.56
23:x:42:GLU:HB3	23:x:44:ARG:HG2	1.87	0.56
33:I:120:LYS:HG2	33:I:130:ASN:OD1	2.06	0.56
48:X:35:ARG:HE	48:X:71:GLY:HA3	1.71	0.56
52:3:1305:G:H22	52:3:1331:G:H2'	1.70	0.56
58:8:289:ARG:NH2	58:8:335:THR:O	2.39	0.56
21:v:46:LYS:O	21:v:50:MET:HG2	2.06	0.55
52:3:17:U:H2'	52:3:18:C:C6	2.41	0.55
52:3:252:U:O2	52:3:252:U:H2'	2.05	0.55
52:3:1409:C:H2'	52:3:1410:A:C8	2.41	0.55
57:7:48:C:H2'	57:7:59:U:H4'	1.88	0.55
19:t:34:VAL:HG22	19:t:35:ALA:H	1.71	0.55
33:I:143:SER:C	33:I:144:ILE:HD12	2.31	0.55
37:M:29:SER:HB3	37:M:32:LYS:HG2	1.86	0.55
53:1:598:U:H2'	53:1:599:A:C8	2.41	0.55
14:o:16:ARG:O	14:o:16:ARG:HD2	2.07	0.55
24:y:4:LYS:NZ	53:1:102:U:N3	2.41	0.55
46:V:18:LYS:HD2	52:3:255:G:H4'	1.87	0.55
52:3:1306:A:H61	52:3:1331:G:H1'	1.71	0.55
52:3:1346:A:H2'	52:3:1347:G:H4'	1.89	0.55
53:1:402:A:H2'	53:1:403:U:H5'	1.88	0.55
53:1:441:U:O2'	53:1:442:G:H5'	2.06	0.55
53:1:558:U:H2'	53:1:559:G:C8	2.41	0.55
53:1:1036:G:H1	53:1:1119:U:H3	1.55	0.55
1:b:12:ARG:HG2	53:1:729:G:OP1	2.05	0.55
1:b:135:PRO:HG2	35:K:80:PHE:HD1	1.71	0.55
7:h:79:PRO:HA	53:1:1108:U:OP1	2.06	0.55
35:K:69:GLU:O	35:K:72:ASP:OD2	2.25	0.55
42:R:114:PRO:HG3	52:3:1227:A:O2'	2.06	0.55
53:1:2724:U:H2'	53:1:2725:A:C8	2.40	0.55
58:8:205:ARG:HB3	58:8:271:ALA:HB3	1.88	0.55
4:e:101:ARG:HG3	4:e:105:ILE:HD11	1.89	0.55
7:h:118:ILE:CG2	7:h:119:PRO:HD3	2.33	0.55
16:q:58:GLN:HG3	53:1:1009:A:O4'	2.07	0.55
25:z:18:LYS:HE2	53:1:920:A:OP1	2.06	0.55
53:1:532:A:H2'	53:1:532:A:N3	2.20	0.55
53:1:1539:U:H2'	53:1:1540:G:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:108:ILE:HG23	3:d:109:LEU:HD22	1.88	0.55
20:u:47:PRO:HG3	53:1:484:C:OP1	2.07	0.55
36:L:114:SER:O	36:L:118:ARG:HG3	2.05	0.55
52:3:1163:A:H2'	52:3:1164:G:C8	2.42	0.55
55:6:36:U:H2'	55:6:37:A:O4'	2.07	0.55
2:c:172:VAL:HG13	2:c:175:LEU:HD11	1.89	0.55
10:k:48:PRO:CG	52:3:1422:G:H5'	2.34	0.55
11:l:79:LEU:H	11:l:113:ALA:HB3	1.72	0.55
15:p:105:LYS:O	15:p:108:ARG:HG2	2.07	0.55
22:w:36:GLN:NE2	22:w:39:THR:HA	2.22	0.55
36:L:76:SER:OG	55:6:32:C:H4'	2.07	0.55
52:3:224:U:H2'	52:3:225:C:C6	2.41	0.55
52:3:626:G:H2'	52:3:627:G:C8	2.42	0.55
53:1:435:C:H2'	53:1:436:C:H5'	1.88	0.55
53:1:481:G:H1'	53:1:506:G:N2	2.21	0.55
53:1:2799:A:C2'	53:1:2800:A:H5'	2.36	0.55
32:H:189:HIS:HD2	52:3:1205:U:H4'	1.72	0.55
35:K:52:ASN:O	35:K:53:LYS:HG2	2.06	0.55
52:3:202:G:H2'	52:3:203:G:C8	2.42	0.55
53:1:1447:C:H2'	53:1:1448:G:C8	2.42	0.55
53:1:2287:A:O2'	53:1:2288:A:H2'	2.06	0.55
1:b:67:LYS:HZ1	53:1:2205:A:H4'	1.72	0.55
3:d:149:ILE:HG23	3:d:188:MET:HA	1.89	0.55
19:t:32:LEU:N	19:t:32:LEU:HD23	2.22	0.55
49:Y:35:TYR:O	49:Y:38:ILE:HG22	2.07	0.55
53:1:720:U:H2'	53:1:721:A:H8	1.71	0.55
53:1:745:G:O2'	53:1:748:G:H1'	2.07	0.55
54:2:13:G:N7	54:2:70:C:H4'	2.22	0.55
54:2:19:C:H2'	54:2:20:G:C8	2.41	0.55
2:c:123:LYS:NZ	53:1:2724:U:H5''	2.21	0.55
32:H:171:ARG:HG2	52:3:1106:G:H5''	1.88	0.55
35:K:18:VAL:CG1	35:K:19:PRO:HD3	2.37	0.55
42:R:89:ARG:NH2	42:R:95:PRO:HG2	2.22	0.55
58:8:136:ASN:HD21	58:8:175:ALA:HB2	1.72	0.55
4:e:37:MET:HE3	4:e:52:ALA:HB1	1.88	0.54
5:f:174:LYS:HB3	53:1:2529:G:H5'	1.87	0.54
8:i:90:GLY:O	8:i:91:LYS:HD2	2.07	0.54
9:j:37:ARG:HH21	53:1:1007:C:H5''	1.70	0.54
19:t:54:GLU:HB2	19:t:88:LYS:HB2	1.87	0.54
33:I:27:ILE:HG13	33:I:29:THR:HG23	1.88	0.54
52:3:1347:G:O2'	52:3:1348:U:H5	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1497:G:O2'	52:3:1498:U:H5'	2.07	0.54
53:1:189:G:H2'	53:1:205:G:N2	2.23	0.54
53:1:687:C:H6	53:1:687:C:H5'	1.71	0.54
10:k:47:ILE:HG12	10:k:48:PRO:HD2	1.89	0.54
10:k:71:ARG:CZ	15:p:71:ARG:HH21	2.21	0.54
16:q:5:ARG:NH1	53:1:585:G:N7	2.55	0.54
19:t:43:ILE:HD12	19:t:46:ALA:HB3	1.89	0.54
19:t:80:TRP:HZ3	19:t:82:LYS:HB3	1.72	0.54
53:1:704:G:H2'	53:1:726:G:H22	1.71	0.54
53:1:2248:C:C2'	53:1:2249:U:H5'	2.36	0.54
1:b:24:HIS:CD2	1:b:79:ARG:HH11	2.24	0.54
15:p:22:GLY:H	15:p:46:VAL:HG13	1.72	0.54
15:p:58:PHE:CE1	15:p:73:PHE:HB2	2.42	0.54
19:t:69:ARG:HB2	19:t:74:ILE:HG22	1.89	0.54
34:J:108:GLY:H	52:3:9:G:H4'	1.71	0.54
38:N:6:TYR:OH	38:N:8:THR:HG22	2.08	0.54
40:P:91:GLY:C	40:P:93:GLU:H	2.16	0.54
51:a:205:LYS:CD	53:1:1860:G:H4'	2.36	0.54
52:3:711:G:O2'	52:3:712:A:H5'	2.07	0.54
53:1:1026:G:H2'	53:1:1027:A:H8	1.72	0.54
53:1:2698:U:H2'	53:1:2699:C:C6	2.43	0.54
53:1:2798:U:H4'	53:1:2799:A:C4	2.42	0.54
8:i:9:LYS:NZ	53:1:1060:U:H5''	2.22	0.54
15:p:101:GLU:OE1	15:p:101:GLU:N	2.40	0.54
37:M:31:LEU:HD23	37:M:31:LEU:O	2.08	0.54
52:3:1218:C:H2'	52:3:1219:A:C8	2.41	0.54
53:1:414:C:H2'	53:1:415:A:H8	1.72	0.54
55:5:20:U:H3'	55:5:21:A:H5'	1.89	0.54
58:8:23:HIS:O	58:8:136:ASN:ND2	2.41	0.54
52:3:211:G:C2'	52:3:212:G:H5'	2.36	0.54
52:3:634:C:H2'	52:3:635:A:H8	1.72	0.54
53:1:1827:U:O2'	53:1:1828:G:H5'	2.07	0.54
1:b:143:VAL:HB	1:b:153:LEU:HB2	1.88	0.54
15:p:104:GLY:HA3	52:3:1432:G:OP1	2.07	0.54
22:w:15:LYS:HB3	22:w:37:ARG:HH21	1.71	0.54
52:3:70:U:H4'	52:3:71:A:H8	1.71	0.54
53:1:554:U:H2'	53:1:555:G:O4'	2.07	0.54
53:1:2185:U:H2'	53:1:2186:G:C8	2.43	0.54
53:1:2515:C:H2'	53:1:2516:A:H8	1.72	0.54
55:5:6:G:O2'	55:5:7:G:H5'	2.07	0.54
9:j:120:ARG:NE	53:1:2780:G:OP2	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:25:SER:OG	52:3:1458:G:H5''	2.07	0.54
51:a:7:ARG:HD3	53:1:2129:C:P	2.48	0.54
51:a:38:PHE:CD1	53:1:2127:G:H4'	2.43	0.54
53:1:1417:C:H4'	53:1:1587:G:H21	1.72	0.54
53:1:1509:A:H2'	53:1:1510:G:C8	2.43	0.54
53:1:2756:U:H4'	53:1:2757:A:OP1	2.08	0.54
1:b:204:LEU:HD21	1:b:213:ARG:HE	1.73	0.54
15:p:38:ARG:CZ	52:3:345:C:H5'	2.38	0.54
15:p:96:LEU:HB3	15:p:99:LEU:HD13	1.89	0.54
24:y:21:LEU:HA	24:y:25:GLN:HB3	1.89	0.54
29:E:18:LYS:HE2	53:1:654:A:H61	1.73	0.54
32:H:119:ILE:O	32:H:123:LEU:HG	2.06	0.54
52:3:1256:A:H1'	52:3:1258:G:N9	2.23	0.54
53:1:151:C:H2'	53:1:152:A:H8	1.73	0.54
53:1:2404:U:H2'	53:1:2405:G:O4'	2.08	0.54
2:c:55:LYS:NZ	53:1:2830:C:OP1	2.41	0.54
11:l:79:LEU:HD23	11:l:82:LEU:HD13	1.90	0.54
12:m:20:LEU:HD23	21:v:81:PRO:HG2	1.90	0.54
40:P:125:LYS:HE2	40:P:126:ARG:HB2	1.88	0.54
46:V:26:ARG:CZ	46:V:39:ARG:HB2	2.37	0.54
52:3:235:C:H2'	52:3:236:A:C8	2.42	0.54
52:3:245:U:O2'	52:3:246:A:H5'	2.07	0.54
52:3:354:G:H2'	52:3:355:C:H5'	1.90	0.54
53:1:433:C:O2'	53:1:434:U:H5'	2.08	0.54
53:1:1278:C:H2'	53:1:1279:G:H8	1.73	0.54
53:1:1386:C:H2'	53:1:1387:A:C8	2.43	0.54
53:1:2093:G:N7	53:1:2225:A:H2'	2.23	0.54
11:l:30:THR:HG22	53:1:810:U:O4	2.08	0.54
12:m:54:THR:HG22	12:m:63:ILE:HD12	1.90	0.54
18:s:94:ASP:OD2	53:1:2014:A:H5'	2.08	0.54
30:F:2:LYS:HB2	30:F:35:GLN:HB3	1.89	0.54
38:N:33:SER:H	38:N:36:GLN:HE21	1.54	0.54
42:R:64:VAL:HG12	42:R:65:GLU:N	2.23	0.54
42:R:113:LYS:HG3	42:R:114:PRO:HD3	1.90	0.54
43:S:80:ARG:O	43:S:83:VAL:HG12	2.08	0.54
46:V:39:ARG:CZ	52:3:280:C:H1'	2.37	0.54
48:X:77:ARG:HD2	52:3:960:U:H5	1.72	0.54
52:3:1033:G:H2'	52:3:1034:G:H5''	1.90	0.54
1:b:241:LYS:O	53:1:1902:C:H4'	2.07	0.53
2:c:125:TRP:O	2:c:126:ASN:HB2	2.08	0.53
8:i:58:ILE:HD11	8:i:66:PHE:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:t:15:HIS:H	19:t:32:LEU:HA	1.72	0.53
32:H:146:LYS:HB2	32:H:202:PHE:CD2	2.43	0.53
40:P:28:ASN:ND2	40:P:56:LYS:HD3	2.24	0.53
54:2:12:C:H1'	54:2:15:A:C2	2.43	0.53
3:d:18:THR:HA	3:d:106:LYS:HE3	1.90	0.53
8:i:93:ASN:OD1	53:1:1077:A:H4'	2.08	0.53
38:N:17:ARG:HH22	52:3:1129:C:H4'	1.73	0.53
50:Z:28:LEU:HD12	50:Z:29:ALA:N	2.23	0.53
53:1:703:U:H2'	53:1:704:G:O4'	2.08	0.53
1:b:257:ARG:HH22	1:b:266:ILE:HD12	1.74	0.53
8:i:131:THR:HG22	53:1:1060:U:O4	2.09	0.53
12:m:12:MET:HA	53:1:910:A:N6	2.14	0.53
14:o:114:GLY:O	14:o:116:GLN:NE2	2.41	0.53
44:T:32:THR:HG21	44:T:84:LEU:HD21	1.89	0.53
52:3:891:U:O2'	52:3:892:A:H5'	2.08	0.53
52:3:1168:U:H5''	52:3:1169:A:OP2	2.08	0.53
53:1:189:G:H2'	53:1:205:G:H22	1.72	0.53
53:1:669:G:H2'	53:1:669:G:N3	2.22	0.53
12:m:50:ARG:NH2	12:m:54:THR:HG21	2.24	0.53
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.90	0.53
14:o:11:ALA:HB2	14:o:96:GLY:N	2.23	0.53
43:S:26:LEU:HD23	43:S:47:LEU:HD13	1.91	0.53
43:S:97:LYS:HE2	52:3:1189:U:OP1	2.09	0.53
52:3:273:U:O2'	52:3:274:A:H5'	2.08	0.53
53:1:1258:U:H2'	53:1:1259:G:C8	2.44	0.53
53:1:1481:U:H2'	53:1:1482:G:H4'	1.90	0.53
53:1:2029:G:O6	53:1:2032:G:H5''	2.08	0.53
53:1:2156:G:C2'	53:1:2157:G:H5'	2.38	0.53
1:b:226:PRO:HD3	1:b:233:GLY:HA2	1.89	0.53
7:h:15:VAL:HA	7:h:18:VAL:HG12	1.91	0.53
7:h:37:LYS:HG2	7:h:41:LEU:HD12	1.89	0.53
7:h:114:GLU:HA	7:h:123:ILE:HG13	1.91	0.53
32:H:126:ARG:H	32:H:126:ARG:HD3	1.74	0.53
36:L:63:VAL:O	36:L:67:ASN:ND2	2.42	0.53
37:M:77:VAL:HG11	37:M:127:TYR:CE2	2.43	0.53
52:3:1497:G:C2'	52:3:1498:U:H5'	2.38	0.53
57:7:68:C:H2'	57:7:69:G:H8	1.73	0.53
13:n:3:HIS:O	13:n:4:ARG:HB2	2.08	0.53
24:y:2:LYS:NZ	53:1:102:U:H1'	2.24	0.53
37:M:63:LYS:HD2	37:M:70:VAL:HG21	1.90	0.53
45:U:22:ALA:HB2	45:U:32:PHE:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:194:VAL:O	51:a:198:LYS:HG2	2.08	0.53
53:1:1454:C:H2'	53:1:1455:G:H8	1.74	0.53
53:1:2208:C:H2'	53:1:2209:G:H8	1.73	0.53
53:1:2257:U:O2'	53:1:2258:C:H5'	2.08	0.53
53:1:2452:C:H42	53:1:2504:U:H3	1.57	0.53
58:8:104:LEU:HB2	58:8:131:ILE:HD11	1.91	0.53
1:b:226:PRO:HD3	1:b:233:GLY:H	1.74	0.53
8:i:30:GLN:CD	8:i:31:GLY:H	2.17	0.53
37:M:17:GLN:HB3	37:M:62:LEU:HD21	1.89	0.53
51:a:185:LEU:HA	51:a:188:ASN:HD22	1.73	0.53
52:3:1094:G:N3	52:3:1094:G:H2'	2.23	0.53
52:3:1137:C:H4'	52:3:1138:G:N2	2.23	0.53
52:3:1219:A:H2'	52:3:1220:G:C8	2.44	0.53
5:f:69:ALA:HB1	53:1:2747:G:H5''	1.90	0.53
5:f:88:LEU:HD23	5:f:93:TYR:HB3	1.91	0.53
7:h:23:LEU:O	7:h:86:MET:HE3	2.09	0.53
32:H:162:ALA:HB2	52:3:1056:U:H4'	1.89	0.53
49:Y:29:THR:HG21	52:3:1457:G:H5''	1.90	0.53
50:Z:5:VAL:HG22	50:Z:7:GLU:HG2	1.89	0.53
51:a:53:ARG:HH22	51:a:167:LYS:HB3	1.74	0.53
53:1:1669:A:O3'	53:1:2549:G:H5'	2.09	0.53
53:1:2668:G:H2'	53:1:2669:G:H8	1.74	0.53
53:1:2715:C:H3'	53:1:2716:C:H5''	1.90	0.53
8:i:9:LYS:HZ3	53:1:1060:U:H3'	1.72	0.53
39:O:65:TYR:HB3	43:S:95:LEU:HD11	1.91	0.53
40:P:14:GLN:NE2	40:P:75:GLU:O	2.41	0.53
52:3:513:C:H2'	52:3:514:C:C6	2.44	0.53
52:3:757:U:H2'	52:3:758:C:O4'	2.09	0.53
53:1:1078:U:C5'	53:1:1079:C:H5''	2.39	0.53
53:1:1979:U:O2'	53:1:1980:G:H5'	2.09	0.53
53:1:2818:U:H4'	53:1:2837:A:H4'	1.91	0.53
4:e:127:TYR:HB3	4:e:155:ILE:HB	1.89	0.53
40:P:81:LEU:HD12	40:P:81:LEU:O	2.09	0.53
50:Z:34:ARG:HB3	50:Z:36:PHE:HE2	1.73	0.53
52:3:195:A:H2'	52:3:196:A:C8	2.43	0.53
52:3:483:C:H2'	52:3:484:G:C8	2.44	0.53
52:3:1346:A:H2'	52:3:1346:A:N3	2.23	0.53
53:1:513:A:H2	53:1:582:A:H4'	1.73	0.53
53:1:1786:A:H1'	53:1:1938:A:N6	2.24	0.53
53:1:1932:A:H2'	53:1:1933:G:O4'	2.09	0.53
53:1:1936:A:H2	53:1:1943:U:H3	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:77:LYS:CE	55:5:19:G:H21	2.22	0.52
7:h:34:THR:O	7:h:37:LYS:HB3	2.09	0.52
32:H:148:ILE:HG23	32:H:169:GLU:HB3	1.91	0.52
35:K:86:ARG:HD3	47:W:63:TYR:O	2.09	0.52
36:L:56:SER:OG	36:L:59:GLU:HG2	2.08	0.52
43:S:63:CYS:HB3	43:S:68:ARG:H	1.74	0.52
48:X:8:PRO:HB3	48:X:38:THR:HG21	1.91	0.52
52:3:202:G:H2'	52:3:203:G:H8	1.73	0.52
52:3:371:A:H2'	52:3:372:C:O4'	2.10	0.52
52:3:912:C:O2'	52:3:913:A:H5'	2.09	0.52
52:3:1251:A:H2'	52:3:1252:A:C8	2.45	0.52
52:3:1391:U:H2'	52:3:1392:G:C8	2.43	0.52
53:1:968:C:H2'	53:1:969:G:C8	2.44	0.52
53:1:2196:C:O2'	53:1:2197:U:H5'	2.08	0.52
53:1:2427:C:H5''	53:1:2429:G:H5'	1.90	0.52
55:5:75:C:C3'	55:5:76:A:H5''	2.39	0.52
6:g:26:ALA:HA	6:g:30:LEU:HB2	1.91	0.52
13:n:36:THR:OG1	13:n:37:THR:N	2.42	0.52
24:y:4:LYS:NZ	53:1:102:U:C2	2.77	0.52
26:B:12:ARG:NH2	53:1:517:C:OP1	2.42	0.52
52:3:77:A:H2'	52:3:78:A:C8	2.44	0.52
53:1:826:U:H5''	53:1:2429:G:P	2.49	0.52
53:1:912:C:O2'	53:1:913:U:H5'	2.09	0.52
53:1:940:G:C3'	53:1:941:A:H5''	2.39	0.52
53:1:1055:G:H2'	53:1:1056:G:O4'	2.09	0.52
3:d:49:ARG:O	3:d:74:LYS:HD3	2.10	0.52
10:k:70:ARG:HG2	10:k:76:VAL:HG12	1.90	0.52
12:m:33:LEU:HD13	12:m:117:PHE:HB3	1.91	0.52
12:m:94:ALA:O	12:m:96:ILE:HG12	2.08	0.52
26:B:49:ARG:HG2	53:1:2884:U:C6	2.44	0.52
46:V:78:VAL:O	46:V:79:GLU:HG2	2.09	0.52
52:3:314:C:O2'	52:3:315:A:H5'	2.09	0.52
53:1:195:A:H2'	53:1:198:C:N4	2.24	0.52
53:1:278:A:H2'	53:1:278:A:N3	2.25	0.52
53:1:353:C:H2'	53:1:354:A:H8	1.74	0.52
53:1:395:U:H2'	53:1:396:G:H8	1.74	0.52
53:1:971:G:H2'	53:1:972:A:O4'	2.08	0.52
53:1:2389:G:H5''	53:1:2390:U:O4'	2.10	0.52
58:8:203:PRO:HG2	58:8:205:ARG:HE	1.75	0.52
3:d:52:VAL:HG21	3:d:81:GLY:HA2	1.92	0.52
4:e:106:ALA:O	4:e:110:ILE:HG13	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:136:ASP:OD2	5:f:139:VAL:HG23	2.09	0.52
31:G:114:LYS:NZ	31:G:151:LYS:O	2.43	0.52
31:G:165:ALA:HB1	31:G:172:ILE:HD11	1.90	0.52
33:I:176:LYS:NZ	33:I:178:GLU:HB3	2.24	0.52
35:K:51:ILE:HG23	35:K:86:ARG:HH21	1.75	0.52
36:L:113:LYS:HB2	36:L:117:LEU:HD13	1.90	0.52
36:L:128:GLU:HG3	36:L:130:LYS:HG2	1.92	0.52
37:M:4:ASP:OD2	37:M:76:ARG:NE	2.40	0.52
52:3:26:A:N6	52:3:558:G:H1'	2.25	0.52
52:3:355:C:H5'	52:3:355:C:H6	1.75	0.52
52:3:1237:C:OP1	52:3:1238:A:H1'	2.10	0.52
52:3:1504:G:H4'	52:3:1505:G:O4'	2.09	0.52
53:1:467:G:O2'	53:1:468:G:H5'	2.10	0.52
53:1:2360:G:H2'	53:1:2361:G:H5'	1.91	0.52
53:1:2818:U:H2'	53:1:2819:G:C8	2.43	0.52
54:2:101:A:H2'	54:2:102:G:O4'	2.09	0.52
58:8:382:ARG:HH11	58:8:382:ARG:HG3	1.74	0.52
5:f:98:LYS:HZ1	5:f:103:ASN:HB2	1.73	0.52
9:j:99:ARG:NH1	53:1:2780:G:O6	2.42	0.52
21:v:6:ALA:HB1	21:v:40:ILE:HG23	1.92	0.52
41:Q:33:CYS:H	41:Q:54:VAL:HG23	1.74	0.52
45:U:22:ALA:HB2	45:U:32:PHE:CB	2.40	0.52
50:Z:40:PRO:O	50:Z:44:ARG:CG	2.57	0.52
51:a:64:VAL:HG23	51:a:160:GLN:HE21	1.74	0.52
53:1:523:C:H2'	53:1:524:G:C8	2.44	0.52
53:1:694:U:OP1	53:1:1569:A:H1'	2.10	0.52
50:Z:16:ARG:HE	50:Z:24:LYS:NZ	2.08	0.52
3:d:131:THR:HG23	53:1:321:U:H5''	1.92	0.52
32:H:86:LEU:HA	32:H:89:VAL:HG22	1.91	0.52
33:I:195:ASN:ND2	33:I:198:LEU:HD13	2.24	0.52
34:J:55:VAL:CG2	34:J:56:PRO:HD3	2.39	0.52
36:L:110:ARG:NH2	36:L:121:ASN:HB3	2.25	0.52
52:3:784:A:H2'	52:3:785:G:C8	2.45	0.52
53:1:2248:C:H2'	53:1:2249:U:H5'	1.90	0.52
1:b:203:VAL:O	1:b:205:GLY:N	2.43	0.52
4:e:84:ILE:HD11	53:1:2312:U:C5'	2.33	0.52
4:e:111:ARG:NH2	4:e:112:ASP:HB3	2.24	0.52
31:G:130:LYS:HE2	52:3:1160:G:H5'	1.90	0.52
38:N:111:GLU:HG2	52:3:1348:U:OP1	2.10	0.52
52:3:1472:U:H2'	52:3:1473:G:C8	2.45	0.52
53:1:322:A:H5'	53:1:340:A:H1'	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2048:G:H3'	53:1:2049:G:H5''	1.92	0.52
53:1:2185:U:H2'	53:1:2186:G:H8	1.73	0.52
8:i:9:LYS:NZ	53:1:1060:U:H3'	2.24	0.52
33:I:18:LEU:HB2	33:I:20:LEU:HG	1.90	0.52
44:T:66:LEU:HD23	44:T:87:ARG:HH21	1.75	0.52
52:3:736:C:H2'	52:3:737:C:C6	2.45	0.52
52:3:884:U:H4'	52:3:885:G:H5''	1.91	0.52
53:1:395:U:H2'	53:1:396:G:C8	2.44	0.52
3:d:149:ILE:HG21	3:d:188:MET:HG2	1.90	0.52
8:i:12:VAL:HG12	8:i:13:ALA:N	2.24	0.52
13:n:47:VAL:C	13:n:50:PRO:HD2	2.35	0.52
19:t:4:GLU:HA	19:t:7:LEU:HB2	1.92	0.52
35:K:64:VAL:HG22	35:K:65:GLU:N	2.24	0.52
35:K:67:PRO:HG2	35:K:70:VAL:CG2	2.37	0.52
37:M:28:SER:HB2	37:M:56:PRO:HB2	1.92	0.52
37:M:49:LYS:O	37:M:58:LEU:HD12	2.09	0.52
38:N:40:ARG:HH22	52:3:1292:G:H5''	1.75	0.52
48:X:5:LYS:HZ3	48:X:6:LYS:HG2	1.75	0.52
52:3:31:G:H21	52:3:47:C:H5''	1.74	0.52
52:3:216:U:H2'	52:3:217:C:C6	2.45	0.52
52:3:418:C:H2'	52:3:419:C:C6	2.45	0.52
52:3:502:A:H2'	52:3:503:C:O4'	2.10	0.52
52:3:1071:C:H2'	52:3:1072:G:H8	1.75	0.52
52:3:1384:C:H2'	52:3:1385:G:C8	2.44	0.52
53:1:353:C:H2'	53:1:354:A:C8	2.45	0.52
53:1:419:U:H2'	53:1:420:C:C6	2.44	0.52
58:8:10:LYS:HB3	58:8:75:ARG:HA	1.90	0.52
7:h:94:ARG:HD2	7:h:97:LYS:HD2	1.92	0.51
32:H:25:THR:HA	43:S:75:LYS:HE3	1.91	0.51
43:S:3:GLN:HG3	52:3:1048:G:OP1	2.11	0.51
53:1:1028:A:H2'	53:1:1029:A:C8	2.45	0.51
53:1:1285:A:H2'	53:1:1286:A:H5'	1.92	0.51
53:1:1810:A:H2'	53:1:1811:G:O4'	2.09	0.51
53:1:1906:G:C3'	53:1:1907:G:H5''	2.40	0.51
53:1:2229:U:H2'	53:1:2230:G:C8	2.45	0.51
53:1:2537:U:H2'	53:1:2538:C:C6	2.45	0.51
54:2:3:C:H3'	54:2:4:C:C5'	2.40	0.51
12:m:41:LEU:HD21	12:m:124:LEU:HD21	1.92	0.51
42:R:44:ILE:HD12	42:R:44:ILE:N	2.16	0.51
48:X:28:LYS:HB3	48:X:29:PRO:HD2	1.91	0.51
53:1:1078:U:C4'	53:1:1079:C:H5''	2.38	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:7:23:A:H2'	57:7:24:G:C8	2.45	0.51
2:c:3:GLY:C	2:c:4:LEU:HD12	2.36	0.51
7:h:6:GLN:O	7:h:9:GLN:HG2	2.10	0.51
40:P:30:ILE:HD11	52:3:706:A:C4'	2.39	0.51
41:Q:69:GLU:OE1	52:3:521:G:H4'	2.11	0.51
52:3:409:U:H2'	52:3:410:G:O4'	2.10	0.51
54:2:104:A:H2'	54:2:105:G:O4'	2.10	0.51
58:8:343:GLU:HB2	58:8:360:VAL:HB	1.92	0.51
1:b:257:ARG:HE	1:b:259:ASN:HB2	1.75	0.51
9:j:78:THR:CG2	53:1:2641:G:H5''	2.39	0.51
19:t:73:ARG:H	19:t:73:ARG:HD2	1.76	0.51
23:x:31:ASN:HD21	53:1:2090:A:H2	1.57	0.51
29:E:4:LYS:NZ	53:1:254:G:N7	2.58	0.51
33:I:40:HIS:CD2	33:I:43:ARG:HE	2.29	0.51
37:M:82:LEU:O	37:M:82:LEU:HD23	2.11	0.51
38:N:98:ARG:NH2	52:3:1178:G:N7	2.58	0.51
52:3:1527:U:H2'	52:3:1528:U:C6	2.46	0.51
53:1:729:G:H4'	53:1:763:G:H5'	1.93	0.51
53:1:940:G:H3'	53:1:941:A:H5''	1.92	0.51
53:1:1701:A:H2'	53:1:1702:G:H5'	1.91	0.51
53:1:2328:A:H2'	53:1:2329:U:C6	2.45	0.51
31:G:98:GLY:O	31:G:102:ASN:HB3	2.10	0.51
33:I:167:PRO:HB2	33:I:170:LEU:CD2	2.40	0.51
35:K:38:ARG:HD3	35:K:97:THR:HA	1.92	0.51
45:U:39:PHE:CD1	45:U:74:LEU:HD11	2.46	0.51
48:X:77:ARG:HH21	52:3:1225:A:H4'	1.75	0.51
52:3:59:A:H3'	52:3:331:G:H22	1.74	0.51
53:1:1103:A:H2'	53:1:1103:A:N3	2.25	0.51
53:1:1900:A:H1'	53:1:1970:A:H2'	1.93	0.51
53:1:2019:A:H2	53:1:2035:G:H22	1.57	0.51
53:1:2423:U:H5'	53:1:2424:C:C5'	2.41	0.51
53:1:2432:A:H1'	55:6:75:C:C4'	2.40	0.51
54:2:87:U:H5''	54:2:88:C:OP2	2.10	0.51
14:o:111:ARG:NH2	14:o:117:PHE:OXT	2.44	0.51
33:I:33:ILE:HG22	33:I:34:GLU:HG2	1.92	0.51
42:R:11:HIS:HA	42:R:43:LYS:HG2	1.93	0.51
52:3:948:C:H2'	52:3:949:A:H8	1.75	0.51
53:1:828:U:H4'	53:1:831:G:C2	2.46	0.51
53:1:2469:A:H2'	53:1:2470:G:O4'	2.11	0.51
1:b:257:ARG:HH11	1:b:269:ARG:HH12	1.59	0.51
18:s:83:LYS:HG2	18:s:95:ARG:HE	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:173:LYS:HE3	52:3:1076:U:OP1	2.11	0.51
35:K:96:VAL:HG22	35:K:97:THR:N	2.25	0.51
37:M:98:LEU:HD23	37:M:98:LEU:H	1.75	0.51
40:P:17:ASP:OD2	40:P:36:ARG:NE	2.44	0.51
52:3:1414:U:H2'	52:3:1415:G:H8	1.75	0.51
53:1:2220:U:H2'	53:1:2221:G:H8	1.75	0.51
9:j:40:HIS:ND1	9:j:41:LYS:HG3	2.26	0.51
12:m:125:PRO:HG2	12:m:126:ILE:CD1	2.40	0.51
45:U:39:PHE:CG	45:U:74:LEU:HD11	2.46	0.51
46:V:15:LYS:HG3	52:3:275:G:H5'	1.93	0.51
50:Z:25:ALA:HB1	56:4:9:G:C5'	2.41	0.51
53:1:227:A:O2'	53:1:228:C:H4'	2.11	0.51
53:1:543:G:H2'	53:1:544:C:O4'	2.10	0.51
53:1:2070:A:H2'	53:1:2071:A:O4'	2.11	0.51
53:1:2638:G:H1'	53:1:2778:A:H61	1.74	0.51
1:b:216:ARG:NH2	53:1:781:A:OP1	2.44	0.51
17:r:15:SER:O	17:r:18:GLN:HG2	2.10	0.51
32:H:46:LEU:HB3	32:H:49:ALA:HB3	1.93	0.51
40:P:52:ARG:NH1	40:P:56:LYS:HZ1	2.09	0.51
42:R:90:HIS:CD2	42:R:96:VAL:HG11	2.46	0.51
52:3:560:A:H4'	52:3:561:U:H5'	1.93	0.51
53:1:1060:U:H4'	53:1:1061:U:H5'	1.92	0.51
53:1:1105:U:H2'	53:1:1106:G:H5''	1.92	0.51
53:1:1506:U:H2'	53:1:1507:C:C6	2.46	0.51
53:1:2039:U:H2'	53:1:2040:G:C8	2.46	0.51
53:1:2266:A:H4'	53:1:2267:A:N3	2.26	0.51
54:2:65:U:H3'	54:2:108:A:N6	2.26	0.51
8:i:74:PRO:HG3	53:1:1060:U:OP2	2.11	0.51
24:y:4:LYS:NZ	53:1:102:U:O2	2.44	0.51
27:C:8:ILE:HD12	27:C:50:GLU:HG3	1.93	0.51
30:F:4:ARG:HG3	53:1:2466:C:OP1	2.11	0.51
44:T:42:PHE:CE2	44:T:55:LEU:HD22	2.46	0.51
52:3:358:U:H2'	52:3:359:G:C8	2.45	0.51
52:3:604:G:H2'	52:3:605:U:O4'	2.11	0.51
58:8:231:ARG:HH11	58:8:272:GLY:HA2	1.76	0.51
10:k:6:THR:HG23	53:1:1666:G:H4'	1.92	0.50
19:t:2:ILE:HD11	53:1:144:A:H4'	1.93	0.50
38:N:92:SER:OG	38:N:93:LEU:HD12	2.10	0.50
52:3:1333:A:H2'	52:3:1334:G:O4'	2.11	0.50
53:1:329:G:O4'	53:1:477:A:H1'	2.11	0.50
53:1:864:G:O2'	53:1:865:C:H5'	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2339:C:H2'	53:1:2340:A:H8	1.75	0.50
53:1:2543:G:H2'	53:1:2544:G:C8	2.46	0.50
54:2:100:G:H2'	54:2:101:A:O4'	2.11	0.50
58:8:115:GLN:HE21	58:8:119:HIS:HE1	1.58	0.50
8:i:120:ASP:OD2	8:i:122:GLU:HB2	2.12	0.50
9:j:81:ILE:HG23	9:j:82:GLY:N	2.27	0.50
52:3:622:A:H2'	52:3:623:C:H5'	1.93	0.50
52:3:1493:A:H5''	52:3:1494:G:OP1	2.12	0.50
53:1:1857:G:H1'	53:1:1885:A:N6	2.26	0.50
12:m:53:MET:HE1	12:m:103:TYR:CG	2.46	0.50
43:S:21:ALA:HB3	43:S:22:LYS:NZ	2.26	0.50
53:1:340:A:H2'	53:1:341:C:O4'	2.10	0.50
53:1:705:A:C2	53:1:727:A:H1'	2.46	0.50
54:2:95:U:H2'	54:2:96:G:H8	1.76	0.50
1:b:73:ILE:HG12	53:1:1490:A:C6	2.46	0.50
33:I:16:THR:HG21	33:I:59:LYS:HE3	1.94	0.50
34:J:25:LYS:NZ	52:3:1387:G:OP1	2.33	0.50
40:P:87:GLY:H	40:P:113:THR:HG22	1.76	0.50
52:3:955:U:H3	52:3:1225:A:H61	1.58	0.50
16:q:7:VAL:CG2	16:q:8:ILE:HD12	2.39	0.50
34:J:86:GLY:HA3	34:J:93:VAL:HG13	1.93	0.50
35:K:50:PRO:HG3	35:K:55:HIS:CE1	2.46	0.50
52:3:86:G:H4'	52:3:87:C:C5	2.47	0.50
52:3:487:A:H2'	52:3:488:C:O4'	2.11	0.50
52:3:950:U:H2'	52:3:951:G:C8	2.44	0.50
52:3:1170:A:H2'	52:3:1171:A:O4'	2.11	0.50
53:1:304:U:H2'	53:1:305:C:C6	2.47	0.50
1:b:78:GLU:HG2	1:b:79:ARG:HG3	1.94	0.50
1:b:227:VAL:HG12	53:1:2073:C:C5'	2.41	0.50
3:d:46:GLN:O	3:d:86:ALA:HB1	2.12	0.50
6:g:37:VAL:CG1	6:g:43:ASN:HD22	2.25	0.50
9:j:117:ALA:HA	9:j:120:ARG:HD2	1.94	0.50
11:l:36:LYS:HD2	53:1:568:U:OP1	2.12	0.50
14:o:79:ALA:HB3	14:o:113:ALA:HB3	1.93	0.50
15:p:52:ARG:HH22	53:1:2720:U:H5''	1.76	0.50
22:w:72:ASN:HD21	54:2:13:G:P	2.34	0.50
26:B:29:VAL:HG22	26:B:36:LYS:HE2	1.93	0.50
40:P:39:ASN:HD22	52:3:684:U:H4'	1.77	0.50
52:3:1106:G:O2'	52:3:1107:C:H5'	2.11	0.50
53:1:639:U:H2'	53:1:640:C:C6	2.47	0.50
53:1:2443:C:O2'	53:1:2444:G:H5'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:333:PHE:CZ	58:8:367:ILE:HD13	2.46	0.50
2:c:174:SER:HB2	53:1:2731:G:OP1	2.12	0.50
4:e:3:LEU:HA	4:e:6:TYR:HB3	1.94	0.50
19:t:68:LYS:HG3	19:t:77:ARG:NH2	2.26	0.50
34:J:98:ALA:O	34:J:100:GLU:N	2.44	0.50
35:K:22:ILE:O	35:K:26:THR:HG23	2.12	0.50
52:3:358:U:H2'	52:3:359:G:H8	1.76	0.50
52:3:1308:U:H2'	52:3:1309:G:C8	2.46	0.50
53:1:155:A:H2'	53:1:156:A:C8	2.47	0.50
53:1:876:C:H2'	53:1:877:A:O4'	2.12	0.50
53:1:1086:A:H1'	53:1:1103:A:H61	1.77	0.50
53:1:2679:A:O2'	53:1:2680:U:H5'	2.12	0.50
1:b:227:VAL:HG12	53:1:2073:C:H5''	1.92	0.50
2:c:121:THR:HB	2:c:127:PHE:CD2	2.46	0.50
19:t:80:TRP:CZ3	19:t:82:LYS:HB3	2.47	0.50
30:F:1:MET:N	53:1:2526:G:N3	2.59	0.50
33:I:129:VAL:HG22	52:3:619:U:O2'	2.12	0.50
35:K:51:ILE:C	35:K:53:LYS:H	2.20	0.50
42:R:33:LEU:O	42:R:37:GLY:N	2.43	0.50
46:V:6:THR:C	46:V:7:LEU:HD22	2.36	0.50
53:1:275:C:H2'	53:1:276:U:C4'	2.41	0.50
53:1:1935:G:H1'	53:1:1964:G:N2	2.26	0.50
54:2:60:C:H2'	54:2:61:G:C8	2.47	0.50
58:8:333:PHE:HZ	58:8:367:ILE:HD13	1.76	0.50
2:c:4:LEU:HD13	2:c:101:PHE:CE2	2.47	0.50
3:d:88:ARG:O	3:d:90:GLN:N	2.45	0.50
21:v:35:GLU:OE1	21:v:35:GLU:N	2.44	0.50
21:v:75:GLN:HB2	21:v:92:VAL:HG13	1.94	0.50
38:N:40:ARG:NH2	52:3:1292:G:H5''	2.27	0.50
46:V:22:VAL:HG22	46:V:23:ALA:N	2.26	0.50
52:3:149:A:H1'	52:3:1446:A:H2	1.77	0.50
52:3:664:G:H22	52:3:741:G:H1	1.59	0.50
52:3:1129:C:H42	52:3:1143:G:H1	1.59	0.50
52:3:1346:A:C2'	52:3:1347:G:H4'	2.42	0.50
53:1:5:A:H2'	53:1:6:A:C8	2.47	0.50
53:1:2070:A:O2'	53:1:2071:A:H5'	2.12	0.50
53:1:2692:G:H2'	53:1:2693:G:H8	1.77	0.50
7:h:33:VAL:HB	7:h:35:VAL:HG12	1.92	0.49
12:m:9:PHE:CZ	53:1:911:A:H2'	2.47	0.49
20:u:50:ALA:O	20:u:51:LEU:HG	2.12	0.49
27:C:9:LYS:HG3	27:C:19:PHE:CD2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:50:SER:HB2	32:H:114:LEU:HD11	1.93	0.49
43:S:18:LYS:HD2	52:3:1007:U:OP1	2.12	0.49
43:S:27:LYS:NZ	52:3:1316:G:H3'	2.27	0.49
52:3:337:G:H2'	52:3:338:A:C8	2.47	0.49
53:1:278:A:C2	53:1:362:A:H1'	2.47	0.49
53:1:1138:G:H2'	53:1:1139:G:O4'	2.12	0.49
53:1:1507:C:H2'	53:1:1508:A:C4'	2.42	0.49
58:8:305:PHE:HA	58:8:393:LEU:H	1.76	0.49
8:i:23:VAL:HG13	8:i:26:ALA:HB3	1.92	0.49
30:F:1:MET:HE1	30:F:36:ARG:HG2	1.94	0.49
33:I:159:GLU:N	33:I:159:GLU:OE2	2.44	0.49
35:K:68:GLN:NE2	52:3:738:C:OP1	2.44	0.49
37:M:65:PHE:CD2	37:M:66:GLN:HG2	2.46	0.49
38:N:30:ASN:O	38:N:32:ARG:NH1	2.45	0.49
50:Z:39:LYS:O	50:Z:43:GLU:N	2.41	0.49
50:Z:58:LYS:O	50:Z:61:ARG:HD2	2.11	0.49
52:3:1125:U:H2'	52:3:1126:U:H2'	1.95	0.49
53:1:1373:A:H5'	53:1:2212:A:H1'	1.94	0.49
53:1:2298:A:H2'	53:1:2299:U:O4'	2.12	0.49
54:2:63:C:H2'	54:2:64:G:C8	2.47	0.49
57:7:25:C:H2'	57:7:26:A:C4'	2.41	0.49
58:8:11:PRO:HB3	58:8:202:GLU:HG3	1.94	0.49
4:e:111:ARG:O	4:e:112:ASP:OD2	2.30	0.49
8:i:23:VAL:CG1	8:i:26:ALA:HB3	2.42	0.49
9:j:44:TYR:O	16:q:63:ARG:NE	2.43	0.49
10:k:12:ASP:OD2	10:k:85:VAL:HG13	2.13	0.49
19:t:39:THR:OG1	19:t:42:GLU:HG2	2.12	0.49
23:x:36:ARG:NH2	53:1:2199:A:OP1	2.45	0.49
33:I:146:GLU:HA	33:I:149:LYS:HE2	1.94	0.49
38:N:22:PRO:HA	38:N:60:LEU:HD13	1.92	0.49
40:P:27:ASN:O	40:P:56:LYS:HG2	2.11	0.49
52:3:130:A:O2'	52:3:264:C:H5'	2.12	0.49
52:3:634:C:H2'	52:3:635:A:C8	2.47	0.49
53:1:367:G:H2'	53:1:368:A:O4'	2.12	0.49
53:1:1564:C:H2'	53:1:1565:C:O4'	2.11	0.49
53:1:2467:C:H2'	53:1:2468:A:O4'	2.11	0.49
54:2:106:G:H2'	54:2:107:G:O4'	2.13	0.49
58:8:153:GLU:O	58:8:156:GLU:HG3	2.12	0.49
14:o:33:ARG:HG2	14:o:34:HIS:HD2	1.78	0.49
19:t:73:ARG:HD2	19:t:73:ARG:N	2.27	0.49
41:Q:87:LYS:HE2	52:3:526:C:OP2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:176:A:O2'	53:1:177:G:H5'	2.12	0.49
53:1:1278:C:H2'	53:1:1279:G:C8	2.47	0.49
53:1:1858:A:H1'	53:1:1885:A:C2	2.47	0.49
53:1:2111:U:H5'	53:1:2112:G:OP2	2.11	0.49
53:1:2286:G:H4'	53:1:2287:A:O4'	2.11	0.49
53:1:2443:C:H2'	53:1:2444:G:C8	2.48	0.49
3:d:163:ASN:HB2	53:1:322:A:OP2	2.11	0.49
7:h:41:LEU:HD13	53:1:1083:U:O5'	2.13	0.49
11:l:51:GLU:O	11:l:54:GLN:HB3	2.12	0.49
18:s:59:GLU:HB3	18:s:66:ILE:HD11	1.93	0.49
31:G:41:ASN:O	31:G:45:THR:HG23	2.12	0.49
32:H:141:MET:HE2	32:H:169:GLU:HG3	1.94	0.49
42:R:113:LYS:HD2	42:R:114:PRO:N	2.27	0.49
47:W:32:ILE:HD13	47:W:67:LEU:HD13	1.93	0.49
52:3:572:A:H4'	52:3:917:G:H5'	1.94	0.49
53:1:542:C:C2'	53:1:543:G:H5''	2.43	0.49
53:1:1015:U:H2'	53:1:1016:G:C8	2.47	0.49
53:1:1183:U:H2'	53:1:1184:U:C6	2.47	0.49
53:1:1775:U:H2'	53:1:1776:G:H5'	1.93	0.49
53:1:2398:U:H2'	53:1:2399:G:C8	2.47	0.49
55:6:16:C:H4'	55:6:60:U:O2	2.11	0.49
6:g:47:PHE:HA	6:g:51:ARG:HB2	1.95	0.49
6:g:80:ILE:HD12	6:g:80:ILE:N	2.28	0.49
44:T:25:GLU:OE2	44:T:69:LEU:HD11	2.13	0.49
50:Z:39:LYS:HA	50:Z:42:THR:HB	1.94	0.49
50:Z:41:THR:O	50:Z:44:ARG:HG3	2.12	0.49
52:3:1429:A:H2'	52:3:1430:A:C8	2.47	0.49
53:1:1437:C:H2'	53:1:1438:U:C6	2.47	0.49
53:1:1563:U:H2'	53:1:1564:C:C6	2.48	0.49
2:c:19:GLY:HA2	15:p:78:PRO:HB2	1.95	0.49
2:c:66:GLY:HA3	53:1:2787:C:H5'	1.95	0.49
5:f:26:LYS:HB2	5:f:31:GLU:OE1	2.13	0.49
15:p:64:SER:OG	15:p:65:ASN:N	2.46	0.49
23:x:9:LYS:HG2	53:1:396:G:OP1	2.13	0.49
32:H:67:ILE:HD12	32:H:67:ILE:N	2.27	0.49
34:J:107:GLY:HA2	52:3:8:A:H1'	1.94	0.49
38:N:33:SER:HB3	38:N:36:GLN:HG2	1.94	0.49
52:3:680:C:H2'	52:3:681:A:C8	2.48	0.49
52:3:1397:C:H42	56:4:22:A:H3'	1.78	0.49
52:3:1512:U:H2'	52:3:1513:A:H8	1.78	0.49
53:1:948:C:H2'	53:1:949:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1078:U:H5''	53:1:1079:C:H5''	1.94	0.49
53:1:1775:U:C2'	53:1:1776:G:H5'	2.42	0.49
55:6:34:C:O2	55:6:34:C:H3'	2.12	0.49
1:b:179:GLU:OE2	1:b:270:ARG:N	2.45	0.49
8:i:98:GLY:C	8:i:99:LYS:HE2	2.37	0.49
9:j:111:LYS:H	9:j:111:LYS:HD2	1.78	0.49
12:m:34:LYS:HE3	12:m:131:VAL:HG11	1.95	0.49
15:p:102:ARG:HD3	15:p:106:ALA:HB1	1.94	0.49
22:w:14:ALA:HB2	53:1:2272:U:OP2	2.12	0.49
42:R:44:ILE:H	42:R:44:ILE:CD1	2.16	0.49
51:a:215:SER:HB2	51:a:221:GLY:HA2	1.95	0.49
53:1:274:C:H2'	53:1:275:C:O4'	2.13	0.49
53:1:2441:U:H2'	53:1:2442:C:H6	1.77	0.49
1:b:16:VAL:HB	1:b:203:VAL:HG22	1.95	0.49
1:b:73:ILE:HG23	53:1:1490:A:H62	1.78	0.49
3:d:68:ALA:HA	53:1:1255:U:C6	2.48	0.49
6:g:69:ALA:HA	6:g:72:ILE:HG13	1.93	0.49
10:k:1:MET:SD	10:k:67:LYS:HG2	2.52	0.49
11:l:19:LEU:HB2	53:1:587:C:O2'	2.12	0.49
38:N:27:ILE:HG23	38:N:62:LEU:HB2	1.95	0.49
46:V:78:VAL:HB	46:V:79:GLU:OE1	2.13	0.49
50:Z:20:ARG:HA	50:Z:24:LYS:HB2	1.94	0.49
51:a:200:LYS:HE2	51:a:208:TYR:CB	2.43	0.49
52:3:1330:U:H2'	52:3:1331:G:O4'	2.13	0.49
53:1:833:A:H2'	53:1:834:G:C8	2.48	0.49
53:1:2345:G:H5'	53:1:2347:C:O4'	2.12	0.49
53:1:2443:C:H2'	53:1:2444:G:H8	1.78	0.49
53:1:2693:G:O2'	53:1:2694:G:H5'	2.13	0.49
2:c:118:PHE:HB2	53:1:2823:A:OP1	2.13	0.49
14:o:29:HIS:HB3	14:o:36:TYR:HB2	1.95	0.49
30:F:37:GLN:HE21	53:1:1125:G:H4'	1.77	0.49
32:H:155:ARG:HD3	32:H:192:TYR:O	2.13	0.49
33:I:173:ASP:OD2	33:I:176:LYS:HG2	2.11	0.49
35:K:51:ILE:O	35:K:52:ASN:CG	2.56	0.49
52:3:304:U:O2'	52:3:305:G:H5'	2.13	0.49
52:3:1258:G:H2'	52:3:1259:C:C6	2.47	0.49
52:3:1502:A:C8	52:3:1505:G:N2	2.81	0.49
58:8:93:ILE:HG13	58:8:332:TYR:CD2	2.48	0.49
4:e:111:ARG:HH22	4:e:112:ASP:HB3	1.78	0.48
9:j:81:ILE:HG23	9:j:82:GLY:H	1.78	0.48
20:u:13:LEU:HD21	20:u:70:ALA:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:42:LYS:HD2	53:1:499:U:H5'	1.95	0.48
33:I:50:TYR:CE2	52:3:508:U:H4'	2.48	0.48
35:K:86:ARG:NH1	52:3:673:A:H4'	2.28	0.48
41:Q:38:THR:HG22	41:Q:50:LYS:HD3	1.95	0.48
45:U:57:ILE:O	45:U:61:VAL:HG23	2.13	0.48
46:V:8:GLN:NE2	46:V:59:GLU:OE1	2.45	0.48
52:3:692:U:H2'	52:3:694:A:OP2	2.13	0.48
53:1:150:U:H2'	53:1:151:C:C6	2.47	0.48
53:1:1111:A:O2'	53:1:1112:G:H4'	2.13	0.48
53:1:1956:U:H2'	53:1:1957:C:H5'	1.94	0.48
54:2:2:G:H2'	54:2:3:C:H6	1.78	0.48
54:2:60:C:H2'	54:2:61:G:H8	1.76	0.48
12:m:71:LYS:HB3	12:m:93:VAL:O	2.13	0.48
16:q:25:GLY:O	16:q:29:ARG:NH1	2.46	0.48
25:z:5:LYS:HB2	25:z:57:GLU:HB2	1.95	0.48
26:B:9:ARG:NH1	53:1:516:C:OP1	2.46	0.48
36:L:22:LEU:O	36:L:22:LEU:HD23	2.13	0.48
40:P:82:GLU:N	40:P:82:GLU:OE1	2.46	0.48
45:U:51:ARG:C	45:U:52:LEU:HD12	2.38	0.48
52:3:77:A:H2'	52:3:78:A:H8	1.77	0.48
52:3:422:C:H4'	52:3:423:G:H5''	1.94	0.48
52:3:1197:A:C2'	52:3:1198:G:H5''	2.42	0.48
53:1:1287:A:H3'	53:1:1288:G:N2	2.28	0.48
53:1:2047:C:H2'	53:1:2048:G:C8	2.48	0.48
55:5:47:U:H3'	55:5:48:C:C5'	2.42	0.48
55:6:12:G:H2'	55:6:13:C:C6	2.48	0.48
7:h:64:VAL:O	7:h:68:PRO:HD3	2.12	0.48
12:m:125:PRO:C	12:m:126:ILE:HD12	2.38	0.48
33:I:59:LYS:HE2	33:I:194:ILE:HG22	1.95	0.48
50:Z:5:VAL:O	50:Z:5:VAL:HG13	2.13	0.48
52:3:552:U:H2'	52:3:553:A:H8	1.77	0.48
52:3:981:U:H2'	52:3:982:U:C5	2.47	0.48
53:1:402:A:C2'	53:1:403:U:H5'	2.43	0.48
53:1:2515:C:H2'	53:1:2516:A:C8	2.47	0.48
1:b:167:ASP:OD1	1:b:167:ASP:N	2.45	0.48
4:e:125:GLY:HA2	4:e:162:ASP:HA	1.95	0.48
15:p:92:ARG:O	53:1:2848:G:H2'	2.14	0.48
34:J:93:VAL:HG21	34:J:110:MET:CE	2.43	0.48
35:K:68:GLN:O	35:K:71:ILE:HG22	2.12	0.48
38:N:46:VAL:HG12	38:N:79:ARG:HD3	1.96	0.48
52:3:1225:A:H2'	52:3:1225:A:N3	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:779:U:H2'	53:1:780:G:C8	2.47	0.48
53:1:1594:U:H2'	53:1:1595:C:C6	2.48	0.48
53:1:1720:U:H2'	53:1:1721:G:O4'	2.13	0.48
53:1:2277:G:C3'	53:1:2278:A:H5''	2.44	0.48
10:k:1:MET:SD	10:k:67:LYS:HE2	2.53	0.48
14:o:31:THR:O	14:o:32:PRO:C	2.57	0.48
33:I:201:GLU:OE2	34:J:104:ILE:N	2.46	0.48
36:L:101:ARG:HB2	36:L:101:ARG:HH11	1.78	0.48
37:M:9:MET:HG3	37:M:26:MET:SD	2.52	0.48
51:a:181:ASP:HB3	51:a:184:LYS:HG3	1.95	0.48
53:1:1947:C:H2'	53:1:1948:G:H8	1.77	0.48
53:1:2553:G:H2'	53:1:2554:U:H4'	1.95	0.48
53:1:2707:U:H2'	53:1:2708:G:H8	1.78	0.48
6:g:8:LYS:O	6:g:9:VAL:C	2.56	0.48
6:g:12:LEU:C	6:g:12:LEU:HD12	2.39	0.48
34:J:108:GLY:H	52:3:9:G:C5'	2.25	0.48
36:L:2:ARG:HB3	52:3:933:G:OP2	2.14	0.48
52:3:540:G:H2'	52:3:541:G:H8	1.78	0.48
53:1:20:C:H2'	53:1:21:A:C8	2.49	0.48
53:1:435:C:C2'	53:1:436:C:H5'	2.44	0.48
53:1:948:C:H2'	53:1:949:G:C8	2.49	0.48
53:1:1373:A:C5'	53:1:2212:A:H1'	2.43	0.48
53:1:2183:A:H2'	53:1:2184:A:C8	2.49	0.48
1:b:123:ILE:HG23	1:b:191:LEU:HD13	1.95	0.48
15:p:105:LYS:HD3	52:3:1433:A:OP1	2.12	0.48
23:x:34:SER:HA	23:x:49:ARG:HA	1.96	0.48
34:J:55:VAL:HG23	34:J:56:PRO:CD	2.42	0.48
39:O:56:HIS:CE1	52:3:963:G:H21	2.31	0.48
41:Q:122:LYS:HD3	41:Q:122:LYS:N	2.29	0.48
47:W:59:LYS:HD3	52:3:735:C:H5'	1.96	0.48
52:3:16:A:O2'	52:3:17:U:H5'	2.14	0.48
52:3:396:C:C3'	52:3:397:A:H5''	2.43	0.48
52:3:411:A:C4	52:3:413:G:H1'	2.49	0.48
52:3:1228:C:H2'	52:3:1229:A:H8	1.79	0.48
53:1:1153:C:H2'	53:1:1154:G:O4'	2.13	0.48
53:1:2066:C:O2'	53:1:2067:G:H5'	2.14	0.48
53:1:2655:G:O2'	53:1:2656:U:H5	1.97	0.48
57:7:9:A:O2'	57:7:46:G:H4'	2.13	0.48
3:d:68:ALA:HA	53:1:1255:U:C5	2.48	0.48
8:i:132:ALA:HB1	8:i:137:LEU:HB2	1.94	0.48
9:j:35:ARG:HD3	9:j:40:HIS:CD2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:51:ARG:HH12	53:1:2483:C:H4'	1.79	0.48
23:x:61:LYS:HE3	53:1:372:G:OP2	2.13	0.48
34:J:44:ARG:NH2	34:J:70:MET:SD	2.87	0.48
52:3:555:U:H2'	52:3:556:C:C6	2.49	0.48
52:3:1071:C:H2'	52:3:1072:G:C8	2.49	0.48
52:3:1277:C:H2'	52:3:1278:G:H5''	1.96	0.48
52:3:1354:U:H2'	52:3:1355:G:H8	1.78	0.48
52:3:1453:G:H3'	52:3:1453:G:N3	2.29	0.48
53:1:63:A:H2'	53:1:64:A:C8	2.49	0.48
53:1:192:C:H2'	53:1:193:U:H5'	1.96	0.48
53:1:255:A:H2'	53:1:256:A:O4'	2.13	0.48
53:1:1023:U:H4'	53:1:1123:C:OP1	2.13	0.48
53:1:1893:C:H2'	53:1:1894:C:H5'	1.96	0.48
53:1:2039:U:H2'	53:1:2040:G:H8	1.78	0.48
53:1:2853:C:H2'	53:1:2854:G:H8	1.79	0.48
1:b:174:ARG:HA	1:b:179:GLU:O	2.14	0.48
1:b:180:MET:HB2	1:b:268:ARG:HB3	1.96	0.48
7:h:42:ARG:NE	7:h:42:ARG:HA	2.28	0.48
10:k:26:GLY:O	10:k:30:ARG:NH1	2.46	0.48
13:n:49:GLU:HB2	13:n:50:PRO:HD3	1.95	0.48
32:H:6:PRO:HG2	32:H:200:TRP:HE1	1.79	0.48
36:L:3:ARG:CZ	52:3:932:C:H5''	2.44	0.48
40:P:30:ILE:HG22	40:P:45:THR:HB	1.96	0.48
43:S:3:GLN:CD	52:3:1047:G:H5''	2.39	0.48
50:Z:54:ARG:HA	50:Z:57:LYS:HE3	1.96	0.48
52:3:860:A:H2'	52:3:861:G:O4'	2.14	0.48
52:3:945:G:H2'	52:3:945:G:N3	2.28	0.48
52:3:1427:C:H2'	52:3:1428:A:C8	2.49	0.48
53:1:814:C:H1'	53:1:1225:G:N2	2.29	0.48
53:1:1105:U:C2'	53:1:1106:G:H5''	2.44	0.48
53:1:1709:U:H2'	53:1:1710:G:C8	2.49	0.48
53:1:2376:A:H2'	53:1:2377:A:O4'	2.14	0.48
54:2:30:C:H2'	54:2:31:C:O4'	2.13	0.48
58:8:378:ARG:HG2	58:8:383:THR:HA	1.95	0.48
1:b:158:GLY:H	1:b:194:VAL:HG23	1.79	0.48
9:j:2:LYS:HA	53:1:995:C:N3	2.29	0.48
32:H:22:PHE:CE2	39:O:11:LYS:HG3	2.49	0.48
35:K:3:HIS:HB2	35:K:92:THR:HB	1.96	0.48
43:S:20:PHE:O	43:S:21:ALA:HB3	2.14	0.48
52:3:297:G:H4'	52:3:557:G:H4'	1.95	0.48
52:3:621:A:H2'	52:3:622:A:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:194:PRO:HA	53:1:2680:U:H5'	1.96	0.47
3:d:24:ASN:ND2	3:d:27:LEU:HB2	2.29	0.47
12:m:58:LYS:O	12:m:59:ARG:HG2	2.14	0.47
18:s:94:ASP:CG	53:1:2014:A:H5'	2.39	0.47
32:H:84:GLU:OE2	32:H:88:LYS:HD3	2.14	0.47
38:N:17:ARG:HH12	52:3:1129:C:H4'	1.79	0.47
39:O:57:VAL:CG2	39:O:58:ASN:H	2.14	0.47
39:O:87:LEU:HD12	39:O:88:MET:N	2.30	0.47
40:P:39:ASN:ND2	52:3:684:U:H4'	2.29	0.47
46:V:26:ARG:NH1	46:V:39:ARG:HB2	2.29	0.47
52:3:150:U:H3	52:3:171:A:H62	1.62	0.47
52:3:220:G:O2'	52:3:221:C:H5'	2.14	0.47
52:3:1096:C:H2'	52:3:1097:C:C6	2.49	0.47
52:3:1288:A:O2'	52:3:1353:G:H5'	2.14	0.47
53:1:211:C:H2'	53:1:212:G:C8	2.49	0.47
53:1:1152:C:H2'	53:1:1153:C:C6	2.49	0.47
53:1:1344:U:H3'	53:1:1345:C:H5'	1.96	0.47
53:1:2161:C:H2'	53:1:2162:G:H5'	1.96	0.47
53:1:2163:A:H2'	53:1:2164:C:H5'	1.95	0.47
53:1:2345:G:N3	53:1:2381:A:H2'	2.29	0.47
58:8:149:LEU:O	58:8:153:GLU:HG3	2.13	0.47
5:f:83:THR:OG1	5:f:133:LYS:HG2	2.14	0.47
6:g:128:HIS:HB2	6:g:144:VAL:HB	1.95	0.47
8:i:126:ARG:O	8:i:129:GLU:HG3	2.14	0.47
9:j:25:LEU:HB3	53:1:1140:C:OP1	2.13	0.47
17:r:74:ILE:HD13	53:1:992:C:H4'	1.96	0.47
32:H:126:ARG:HD3	32:H:126:ARG:N	2.29	0.47
33:I:202:LEU:HD23	33:I:202:LEU:C	2.39	0.47
45:U:70:ARG:HH11	52:3:452:A:H1'	1.80	0.47
51:a:193:LEU:O	51:a:196:LEU:HG	2.13	0.47
51:a:220:ALA:HA	53:1:2176:A:C5'	2.45	0.47
53:1:440:C:H2'	53:1:441:U:C6	2.49	0.47
53:1:1539:U:H2'	53:1:1540:G:C8	2.49	0.47
57:7:76:A:H4'	58:8:219:PHE:CE2	2.49	0.47
58:8:283:LYS:HB3	58:8:286:GLU:CD	2.39	0.47
1:b:129:LEU:N	1:b:129:LEU:HD23	2.27	0.47
7:h:67:THR:HB	7:h:68:PRO:HD3	1.96	0.47
12:m:65:ILE:HG12	12:m:103:TYR:HE1	1.79	0.47
20:u:33:VAL:HG13	20:u:66:VAL:HG22	1.96	0.47
30:F:1:MET:HE1	30:F:36:ARG:HB3	1.96	0.47
34:J:12:GLU:HB3	34:J:38:VAL:HG12	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:6:TYR:CZ	38:N:8:THR:HG22	2.50	0.47
38:N:113:LYS:HG3	38:N:119:LYS:HA	1.95	0.47
40:P:62:ALA:HB1	40:P:95:THR:HB	1.94	0.47
53:1:616:A:H2'	53:1:617:G:O4'	2.15	0.47
53:1:974:G:N3	53:1:974:G:H2'	2.29	0.47
53:1:1316:U:H2'	53:1:1317:G:C8	2.50	0.47
54:2:14:U:O2	54:2:107:G:H4'	2.14	0.47
22:w:26:SER:HA	22:w:62:LYS:HA	1.96	0.47
27:C:25:ASN:HD22	53:1:2285:C:P	2.38	0.47
31:G:219:THR:O	31:G:222:GLU:HG2	2.14	0.47
33:I:202:LEU:HD23	33:I:202:LEU:O	2.14	0.47
52:3:1075:U:H2'	52:3:1076:U:C6	2.49	0.47
53:1:607:U:O4	53:1:619:G:H2'	2.15	0.47
54:2:48:U:H2'	54:2:49:C:C6	2.50	0.47
3:d:122:GLU:HG2	3:d:123:LYS:N	2.29	0.47
9:j:13:ARG:NH1	9:j:49:ASP:O	2.47	0.47
10:k:58:LEU:HD11	10:k:86:LEU:HD22	1.96	0.47
12:m:51:ARG:NH1	53:1:2483:C:O2'	2.47	0.47
15:p:27:VAL:HG12	15:p:83:ILE:HA	1.94	0.47
19:t:61:LEU:HB3	53:1:1341:G:H4'	1.96	0.47
32:H:161:ILE:HD12	52:3:1196:A:C2	2.49	0.47
48:X:44:ILE:HD13	48:X:63:ASP:HA	1.96	0.47
51:a:197:LYS:O	51:a:200:LYS:HG3	2.14	0.47
52:3:82:G:H2'	52:3:83:C:O4'	2.14	0.47
52:3:1347:G:O2'	52:3:1348:U:C5	2.68	0.47
53:1:1019:U:H3	53:1:1142:A:N6	2.12	0.47
53:1:1625:C:H2'	53:1:1626:A:O4'	2.14	0.47
53:1:1683:U:H2'	53:1:1684:G:C8	2.49	0.47
53:1:2243:U:H2'	53:1:2244:U:C6	2.49	0.47
53:1:2704:C:H2'	53:1:2705:A:O4'	2.14	0.47
1:b:1:ALA:HB3	1:b:19:VAL:HB	1.97	0.47
1:b:77:VAL:HG21	1:b:109:LEU:HD11	1.97	0.47
4:e:177:ARG:OXT	4:e:177:ARG:HD2	2.14	0.47
7:h:48:ALA:HB3	7:h:51:TYR:HE2	1.78	0.47
29:E:7:ARG:NH2	53:1:244:A:OP2	2.47	0.47
34:J:54:GLU:HB3	34:J:56:PRO:HD2	1.95	0.47
37:M:80:PRO:HG2	52:3:878:A:C5'	2.44	0.47
39:O:8:ILE:HD12	39:O:8:ILE:N	2.30	0.47
39:O:15:HIS:HB3	39:O:70:HIS:CD2	2.50	0.47
52:3:31:G:H5'	52:3:306:A:C2	2.49	0.47
52:3:1009:U:O2'	52:3:1010:U:H5'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1349:A:H2'	52:3:1350:A:O4'	2.15	0.47
53:1:834:G:H1'	53:1:2358:A:N3	2.29	0.47
53:1:1298:C:H2'	53:1:1299:G:O4'	2.15	0.47
53:1:2221:G:O2'	53:1:2222:C:H5'	2.15	0.47
53:1:2412:A:H2'	53:1:2413:G:O4'	2.14	0.47
1:b:251:THR:OG1	1:b:252:LYS:N	2.45	0.47
9:j:27:ARG:NH2	53:1:1142:A:H4'	2.29	0.47
15:p:13:LYS:HG2	15:p:76:HIS:ND1	2.30	0.47
19:t:61:LEU:C	19:t:61:LEU:HD12	2.39	0.47
32:H:6:PRO:O	32:H:10:ARG:NH1	2.48	0.47
35:K:11:HIS:O	35:K:15:SER:N	2.48	0.47
35:K:29:ILE:HD12	35:K:36:ILE:HB	1.97	0.47
37:M:10:LEU:HD22	37:M:74:ILE:HD12	1.97	0.47
37:M:112:ASP:N	37:M:112:ASP:OD1	2.47	0.47
38:N:49:GLN:N	38:N:50:PRO:HD2	2.30	0.47
42:R:104:ASN:O	42:R:105:ALA:HB3	2.15	0.47
42:R:114:PRO:HG2	52:3:1228:C:H5''	1.95	0.47
43:S:50:LEU:HD21	43:S:54:SER:OG	2.14	0.47
50:Z:33:ARG:HG3	50:Z:34:ARG:HG2	1.97	0.47
51:a:200:LYS:HE2	51:a:208:TYR:HB2	1.97	0.47
52:3:451:A:H4'	52:3:452:A:O4'	2.15	0.47
52:3:802:A:H2'	52:3:803:G:O4'	2.15	0.47
52:3:1211:U:H4'	52:3:1213:A:N3	2.30	0.47
52:3:1252:A:H2'	52:3:1253:G:O4'	2.15	0.47
52:3:1402:C:H2'	52:3:1403:C:O4'	2.14	0.47
53:1:198:C:O2'	53:1:199:A:H5'	2.14	0.47
53:1:288:U:H2'	53:1:289:G:C8	2.49	0.47
53:1:580:U:H2'	53:1:581:C:H6	1.78	0.47
53:1:937:C:H2'	53:1:938:G:H8	1.80	0.47
53:1:1367:A:C2'	53:1:1368:G:H5'	2.43	0.47
53:1:1642:G:O2'	53:1:1643:G:H5'	2.14	0.47
53:1:1866:A:H2'	53:1:1867:G:O4'	2.15	0.47
53:1:1876:A:H2'	53:1:1877:A:O4'	2.15	0.47
53:1:2380:C:H2'	53:1:2381:A:C8	2.49	0.47
53:1:2457:U:O2'	53:1:2458:G:H5'	2.15	0.47
54:2:97:C:H2'	54:2:98:G:O4'	2.13	0.47
55:6:20:U:H5'	55:6:21:A:OP2	2.14	0.47
1:b:47:ARG:NH2	53:1:777:G:O2'	2.48	0.47
5:f:148:ARG:NE	5:f:166:GLU:OE1	2.48	0.47
13:n:93:GLY:HA3	53:1:2880:C:O2	2.15	0.47
39:O:59:LYS:HE3	39:O:62:ARG:HH21	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:84:ARG:NH2	52:3:1059:C:O3'	2.48	0.47
52:3:346:G:H2'	52:3:347:G:H5'	1.96	0.47
52:3:540:G:H2'	52:3:541:G:C8	2.50	0.47
52:3:923:A:H61	52:3:1393:U:H3	1.63	0.47
53:1:942:G:H2'	53:1:943:A:O4'	2.15	0.47
53:1:1045:C:P	53:1:1047:G:H5'	2.55	0.47
53:1:1830:C:H2'	53:1:1831:G:H8	1.80	0.47
53:1:1924:C:H2'	53:1:1925:C:C6	2.50	0.47
54:2:35:C:C2'	54:2:36:C:H5'	2.44	0.47
55:6:41:C:H2'	55:6:42:G:C8	2.50	0.47
2:c:46:ARG:HB2	2:c:84:LEU:HD12	1.97	0.47
7:h:34:THR:HG21	53:1:1057:A:H1'	1.96	0.47
8:i:100:ILE:N	8:i:100:ILE:HD12	2.30	0.47
32:H:33:ASP:O	32:H:37:LYS:HG2	2.15	0.47
33:I:169:TRP:CD1	33:I:170:LEU:HD22	2.50	0.47
41:Q:52:CYS:HB3	41:Q:66:ILE:HD11	1.97	0.47
43:S:30:ILE:O	43:S:30:ILE:HG13	2.15	0.47
52:3:918:A:H2'	52:3:919:A:O4'	2.15	0.47
52:3:1060:U:H3	52:3:1197:A:H61	1.62	0.47
52:3:1148:U:H2'	52:3:1149:C:O4'	2.15	0.47
52:3:1293:C:H2'	52:3:1294:G:H8	1.80	0.47
53:1:118:A:OP2	53:1:119:A:H5''	2.15	0.47
53:1:827:U:H4'	53:1:828:U:C5	2.50	0.47
39:O:43:PRO:HA	52:3:1151:A:H5'	1.97	0.47
43:S:7:ALA:O	43:S:10:VAL:HG12	2.15	0.47
49:Y:67:HIS:O	49:Y:69:ASN:N	2.42	0.47
52:3:921:U:H5''	52:3:1082:A:H5'	1.96	0.47
52:3:1162:C:H2'	52:3:1163:A:C8	2.50	0.47
52:3:1498:U:H4'	52:3:1519:A:H2	1.79	0.47
53:1:1394:U:H4'	53:1:1603:A:H4'	1.96	0.47
53:1:1905:C:O2'	53:1:1929:G:H1'	2.15	0.47
53:1:2637:U:H2'	53:1:2638:G:O4'	2.15	0.47
4:e:65:LEU:HD22	54:2:42:C:C5	2.51	0.46
10:k:7:MET:HB2	53:1:1667:G:OP1	2.15	0.46
12:m:9:PHE:HZ	53:1:911:A:H2'	1.79	0.46
17:r:49:ILE:HG22	17:r:54:VAL:HA	1.97	0.46
27:C:7:LYS:HA	27:C:23:THR:HA	1.95	0.46
38:N:6:TYR:CE2	52:3:1147:C:H4'	2.51	0.46
40:P:61:ALA:O	40:P:64:VAL:HG12	2.13	0.46
41:Q:49:ARG:HB2	41:Q:89:LEU:HD21	1.97	0.46
52:3:1195:C:H5''	52:3:1196:A:OP2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1507:C:C2'	53:1:1508:A:H4'	2.44	0.46
53:1:2339:C:H2'	53:1:2340:A:C8	2.49	0.46
53:1:2480:C:H2'	53:1:2481:G:O4'	2.15	0.46
54:2:78:A:H2'	54:2:79:G:O4'	2.15	0.46
56:4:17:U:O2'	56:4:18:G:H5'	2.15	0.46
1:b:208:GLY:HA2	1:b:211:ARG:HB3	1.96	0.46
2:c:121:THR:HB	2:c:127:PHE:HD2	1.79	0.46
3:d:144:GLU:N	3:d:144:GLU:OE2	2.49	0.46
7:h:73:LYS:HG3	7:h:117:LEU:HD21	1.96	0.46
13:n:50:PRO:O	13:n:53:THR:HB	2.16	0.46
38:N:39:GLY:O	38:N:44:ARG:HD3	2.15	0.46
39:O:26:VAL:O	39:O:30:LYS:HG2	2.15	0.46
43:S:5:MET:HB3	43:S:62:ARG:HH12	1.80	0.46
49:Y:55:PRO:HB3	52:3:193:C:O3'	2.15	0.46
52:3:58:C:O2'	52:3:59:A:H5'	2.15	0.46
52:3:471:U:H2'	52:3:472:U:C6	2.51	0.46
52:3:947:G:H4'	52:3:1332:A:H2	1.80	0.46
53:1:28:A:H1'	53:1:513:A:C2	2.50	0.46
53:1:828:U:H2'	53:1:829:A:C8	2.49	0.46
53:1:1507:C:H2'	53:1:1508:A:H4'	1.97	0.46
54:2:1:U:H2'	54:2:2:G:C8	2.50	0.46
57:7:45:U:H3'	57:7:46:G:C5'	2.45	0.46
11:l:60:ARG:HH21	53:1:2360:G:H1'	1.81	0.46
15:p:23:ASP:HB3	15:p:85:VAL:HG23	1.98	0.46
18:s:28:LYS:HE2	18:s:31:GLN:OE1	2.15	0.46
19:t:3:ARG:O	19:t:7:LEU:HD23	2.15	0.46
33:I:128:VAL:HG11	33:I:145:ARG:NH2	2.30	0.46
35:K:18:VAL:HG12	35:K:19:PRO:HD3	1.97	0.46
37:M:78:SER:HB2	37:M:124:ILE:O	2.15	0.46
41:Q:49:ARG:HG2	41:Q:49:ARG:HH11	1.79	0.46
52:3:865:A:H2'	52:3:866:C:C6	2.51	0.46
52:3:1368:A:O2'	52:3:1369:C:H5'	2.16	0.46
52:3:1433:A:H2'	52:3:1434:A:O4'	2.14	0.46
52:3:1477:U:H2'	52:3:1478:U:C6	2.49	0.46
53:1:11:C:H2'	53:1:12:U:H5''	1.97	0.46
53:1:596:U:H2'	53:1:597:G:H8	1.81	0.46
53:1:1287:A:C2'	53:1:1288:G:H5'	2.45	0.46
53:1:1316:U:H2'	53:1:1317:G:H8	1.80	0.46
53:1:2114:A:H2'	53:1:2114:A:N3	2.31	0.46
53:1:2713:U:H3'	53:1:2714:G:H5''	1.98	0.46
58:8:125:GLN:HB3	58:8:376:ALA:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:2:VAL:HG13	1:b:16:VAL:HG11	1.97	0.46
2:c:172:VAL:CG1	2:c:175:LEU:HD11	2.46	0.46
3:d:18:THR:HG23	3:d:106:LYS:HG2	1.98	0.46
5:f:126:THR:HB	5:f:129:GLU:HB3	1.98	0.46
7:h:67:THR:N	7:h:68:PRO:CD	2.78	0.46
24:y:37:LEU:HD23	24:y:37:LEU:C	2.40	0.46
31:G:186:VAL:HG23	31:G:190:SER:HB2	1.98	0.46
32:H:4:VAL:HG21	32:H:9:ILE:HD11	1.97	0.46
41:Q:79:ILE:HG22	41:Q:103:CYS:HB2	1.97	0.46
43:S:12:ARG:HE	43:S:58:ARG:HE	1.62	0.46
52:3:162:A:C2'	52:3:163:C:H5'	2.45	0.46
52:3:502:A:H61	52:3:543:U:H3	1.62	0.46
52:3:1293:C:H2'	52:3:1294:G:C8	2.50	0.46
53:1:475:C:H4'	53:1:510:C:H5'	1.97	0.46
53:1:1020:A:C1'	53:1:1021:A:OP2	2.58	0.46
53:1:2333:A:H5'	53:1:2335:A:H1'	1.98	0.46
57:7:6:G:H2'	57:7:7:A:H5''	1.98	0.46
4:e:73:VAL:HG21	53:1:2310:C:O2'	2.16	0.46
5:f:48:THR:OG1	5:f:49:LEU:N	2.48	0.46
10:k:102:PRO:HB3	10:k:121:GLU:HB2	1.98	0.46
10:k:121:GLU:HG3	15:p:65:ASN:HD21	1.81	0.46
13:n:45:ARG:HD3	13:n:97:ILE:HD11	1.96	0.46
30:F:7:VAL:HG22	30:F:38:GLY:HA3	1.96	0.46
40:P:85:VAL:HG11	50:Z:16:ARG:HH22	1.79	0.46
44:T:55:LEU:O	44:T:59:VAL:HG23	2.15	0.46
44:T:58:MET:HA	44:T:61:GLN:HB3	1.96	0.46
52:3:331:G:OP1	52:3:332:G:H5''	2.16	0.46
52:3:1540:U:O2	52:3:1540:U:H3'	2.15	0.46
53:1:74:A:H4'	53:1:75:G:O5'	2.15	0.46
53:1:1000:A:H2'	53:1:1001:A:C8	2.50	0.46
53:1:1140:C:O2'	53:1:1141:U:H5'	2.16	0.46
53:1:1279:G:H2'	53:1:1280:G:C8	2.50	0.46
53:1:2489:U:O2'	53:1:2490:G:H5'	2.16	0.46
54:2:63:C:H2'	54:2:64:G:H8	1.81	0.46
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.98	0.46
8:i:8:VAL:HG22	8:i:9:LYS:H	1.80	0.46
13:n:45:ARG:O	13:n:49:GLU:HG3	2.15	0.46
13:n:47:VAL:O	13:n:50:PRO:HD2	2.14	0.46
29:E:6:VAL:HG21	29:E:60:CYS:HB2	1.97	0.46
33:I:162:GLU:HB2	33:I:163:GLN:NE2	2.30	0.46
35:K:15:SER:OG	35:K:58:HIS:ND1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:65:LEU:O	36:L:69:ARG:HG3	2.15	0.46
52:3:524:G:H2'	52:3:525:C:C6	2.50	0.46
52:3:948:C:H5'	52:3:1306:A:O2'	2.15	0.46
52:3:1323:G:H2'	52:3:1324:A:C8	2.50	0.46
53:1:573:U:O2'	53:1:574:A:H3'	2.16	0.46
53:1:742:A:H2'	53:1:743:A:C8	2.51	0.46
53:1:1114:C:H2'	53:1:1115:G:C8	2.50	0.46
53:1:1149:G:H2'	53:1:1150:C:C6	2.51	0.46
53:1:1231:U:H2'	53:1:1232:G:H8	1.81	0.46
53:1:2547:A:H2'	53:1:2548:U:C6	2.50	0.46
53:1:2860:A:H2'	53:1:2861:U:H5'	1.97	0.46
21:v:75:GLN:HB3	21:v:90:ASP:O	2.16	0.46
38:N:113:LYS:HD2	38:N:118:ARG:O	2.14	0.46
45:U:54:LEU:HA	45:U:57:ILE:HD12	1.98	0.46
51:a:186:LYS:O	51:a:189:LEU:HD23	2.15	0.46
52:3:1472:U:H2'	52:3:1473:G:H8	1.81	0.46
53:1:968:C:H2'	53:1:969:G:H8	1.80	0.46
53:1:1833:C:H2'	53:1:1834:U:O4'	2.16	0.46
55:5:52:G:H2'	55:5:53:G:C8	2.51	0.46
57:7:47:U:H2'	57:7:50:U:OP1	2.16	0.46
57:7:62:C:H2'	57:7:63:G:C5'	2.39	0.46
58:8:260:GLU:HG2	58:8:265:LEU:HD22	1.97	0.46
3:d:154:ASP:OD1	3:d:154:ASP:N	2.49	0.46
4:e:1:ALA:HB1	4:e:4:HIS:HB3	1.98	0.46
12:m:126:ILE:HD12	12:m:126:ILE:N	2.31	0.46
18:s:8:ARG:HE	18:s:102:HIS:HE1	1.63	0.46
18:s:74:ILE:HB	18:s:105:VAL:HG23	1.97	0.46
28:D:22:MET:HE2	28:D:31:LEU:HD22	1.97	0.46
36:L:21:LEU:O	36:L:21:LEU:HD23	2.16	0.46
46:V:5:ARG:NH2	52:3:635:A:O3'	2.48	0.46
46:V:10:ARG:NE	46:V:55:GLY:HA2	2.31	0.46
52:3:744:C:H2'	52:3:745:G:C8	2.50	0.46
52:3:911:U:H2'	52:3:912:C:C6	2.51	0.46
52:3:1140:C:H2'	52:3:1141:C:C6	2.51	0.46
53:1:738:G:O2'	53:1:739:A:H5'	2.16	0.46
53:1:1680:U:C2'	53:1:1681:G:H5'	2.46	0.46
53:1:1872:A:H2'	53:1:1873:G:O4'	2.15	0.46
53:1:2134:A:C6	53:1:2157:G:H4'	2.50	0.46
53:1:2241:A:H2'	53:1:2242:G:C8	2.51	0.46
53:1:2590:A:O2'	53:1:2591:C:H5'	2.16	0.46
55:6:63:G:H2'	55:6:64:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:171:ASP:C	3:d:173:THR:H	2.24	0.46
29:E:21:PHE:O	29:E:49:VAL:HG23	2.16	0.46
32:H:86:LEU:O	32:H:90:VAL:HG22	2.16	0.46
32:H:119:ILE:HD11	32:H:197:VAL:HG11	1.98	0.46
33:I:33:ILE:HD12	33:I:33:ILE:N	2.30	0.46
45:U:8:ARG:O	45:U:28:ARG:NH1	2.49	0.46
46:V:10:ARG:HE	46:V:55:GLY:HA2	1.81	0.46
46:V:60:ILE:HG23	46:V:73:THR:O	2.16	0.46
52:3:815:A:H5''	52:3:817:C:N4	2.31	0.46
52:3:869:G:H4'	52:3:872:A:C8	2.51	0.46
53:1:151:C:H2'	53:1:152:A:C8	2.50	0.46
53:1:729:G:H4'	53:1:763:G:C5'	2.45	0.46
53:1:937:C:H2'	53:1:938:G:C8	2.51	0.46
53:1:1857:G:N2	53:1:1884:G:H2'	2.31	0.46
53:1:2190:G:H2'	53:1:2191:A:C8	2.51	0.46
7:h:61:ARG:HD2	53:1:1047:G:N7	2.31	0.46
10:k:36:GLY:HA2	10:k:62:VAL:O	2.16	0.46
14:o:4:LYS:O	14:o:8:ILE:HG13	2.16	0.46
14:o:33:ARG:HB2	54:2:52:A:H62	1.79	0.46
18:s:57:ASN:OD1	18:s:61:ASN:ND2	2.49	0.46
18:s:58:ALA:O	18:s:62:ASP:OD1	2.34	0.46
29:E:41:ARG:NH2	53:1:2350:C:H5	2.14	0.46
34:J:159:SER:OG	34:J:162:GLU:HG3	2.15	0.46
42:R:91:ARG:NH1	53:1:887:U:OP1	2.47	0.46
52:3:45:G:H5''	52:3:307:C:O2'	2.15	0.46
52:3:234:C:H2'	52:3:235:C:C6	2.51	0.46
52:3:383:A:H4'	52:3:455:G:H5'	1.97	0.46
52:3:405:U:H3'	52:3:406:G:C5'	2.33	0.46
53:1:112:U:H2'	53:1:113:U:H5'	1.97	0.46
53:1:1170:C:H2'	53:1:1171:G:C8	2.51	0.46
53:1:1672:A:C2	53:1:2582:G:H5'	2.51	0.46
53:1:2626:C:O2'	53:1:2627:G:H5'	2.16	0.46
57:7:6:G:C2'	57:7:7:A:H5''	2.46	0.46
4:e:141:ASP:H	4:e:144:LYS:NZ	2.14	0.45
5:f:87:GLN:HG2	5:f:89:VAL:HG23	1.97	0.45
6:g:103:VAL:HG22	6:g:108:VAL:HB	1.98	0.45
8:i:14:ALA:HB2	8:i:54:ILE:HG22	1.99	0.45
10:k:71:ARG:NH2	15:p:71:ARG:HH21	2.14	0.45
32:H:45:GLU:OE2	32:H:86:LEU:HD21	2.16	0.45
36:L:142:ARG:HD3	55:6:41:C:H5''	1.98	0.45
45:U:44:SER:OG	45:U:45:GLU:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:68:SER:OG	45:U:71:VAL:HG22	2.16	0.45
47:W:48:ALA:O	47:W:51:GLN:HB3	2.15	0.45
52:3:810:C:H2'	52:3:811:C:O4'	2.16	0.45
52:3:893:C:H2'	52:3:894:G:C8	2.51	0.45
53:1:1463:C:H2'	53:1:1464:G:C8	2.51	0.45
53:1:2122:U:H2'	53:1:2123:G:O4'	2.16	0.45
53:1:2189:U:H2'	53:1:2190:G:H8	1.80	0.45
53:1:2244:U:H2'	53:1:2245:U:O4'	2.16	0.45
53:1:2801:G:H2'	53:1:2802:G:C8	2.51	0.45
53:1:2819:G:H2'	53:1:2821:A:N7	2.31	0.45
54:2:22:U:H2'	54:2:23:G:C8	2.51	0.45
9:j:101:ILE:O	9:j:105:VAL:HG23	2.17	0.45
26:B:27:LEU:HD23	26:B:27:LEU:H	1.81	0.45
27:C:35:LEU:HD11	53:1:2286:G:C2	2.51	0.45
49:Y:2:ASN:HB3	52:3:332:G:OP2	2.16	0.45
52:3:70:U:H4'	52:3:71:A:C8	2.51	0.45
52:3:129:A:H1'	52:3:130:A:C8	2.51	0.45
52:3:360:G:OP2	58:8:283:LYS:HD2	2.16	0.45
52:3:681:A:H2'	52:3:682:G:C8	2.51	0.45
52:3:1435:G:H2'	52:3:1436:U:C6	2.50	0.45
53:1:582:A:H2'	53:1:583:G:C8	2.52	0.45
53:1:813:U:H2'	53:1:814:C:C6	2.50	0.45
53:1:1958:C:H2'	53:1:1959:G:H8	1.81	0.45
54:2:30:C:H2'	54:2:31:C:H5'	1.98	0.45
55:5:47:U:H3'	55:5:48:C:H5'	1.99	0.45
10:k:44:LYS:O	10:k:54:LYS:HD3	2.16	0.45
11:l:23:ILE:HD12	11:l:23:ILE:N	2.31	0.45
11:l:35:HIS:O	11:l:36:LYS:C	2.60	0.45
12:m:72:PRO:HB3	12:m:92:TRP:CZ3	2.51	0.45
30:F:6:SER:O	30:F:8:LYS:NZ	2.48	0.45
31:G:113:LEU:HB2	31:G:143:LEU:HD23	1.99	0.45
32:H:176:THR:HA	52:3:1111:A:H61	1.82	0.45
42:R:51:GLN:O	42:R:55:LEU:HD23	2.16	0.45
52:3:67:C:H2'	52:3:68:G:C8	2.51	0.45
52:3:355:C:H2'	52:3:356:A:O4'	2.16	0.45
52:3:477:C:H2'	52:3:478:A:C8	2.51	0.45
52:3:516:U:H3	52:3:533:A:H62	1.65	0.45
53:1:310:A:O2'	53:1:311:A:H2'	2.16	0.45
53:1:610:C:H2'	53:1:611:C:C6	2.51	0.45
53:1:766:U:H2'	53:1:767:U:C6	2.51	0.45
53:1:1683:U:H2'	53:1:1684:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1806:C:H2'	53:1:1807:G:O4'	2.17	0.45
58:8:98:GLN:HG2	58:8:231:ARG:HB2	1.97	0.45
8:i:25:PRO:HG2	57:7:55:U:H3'	1.97	0.45
15:p:91:VAL:HG21	15:p:96:LEU:HD11	1.98	0.45
30:F:7:VAL:C	30:F:8:LYS:HD3	2.42	0.45
33:I:81:LEU:HD13	33:I:88:ASN:HD22	1.82	0.45
39:O:12:ALA:HB2	39:O:96:VAL:HG12	1.99	0.45
41:Q:51:VAL:HG22	41:Q:52:CYS:N	2.31	0.45
42:R:113:LYS:N	42:R:114:PRO:HD2	2.32	0.45
47:W:28:LEU:HD12	47:W:58:ILE:HD13	1.98	0.45
49:Y:30:PHE:HB3	49:Y:53:MET:HB3	1.98	0.45
51:a:24:ASN:HA	51:a:186:LYS:HZ1	1.81	0.45
52:3:1346:A:O2'	52:3:1347:G:H4'	2.17	0.45
52:3:1498:U:C4	56:4:17:U:H5''	2.52	0.45
53:1:2581:G:H2'	53:1:2581:G:N3	2.31	0.45
53:1:2619:C:O2'	53:1:2620:C:H5'	2.16	0.45
53:1:2841:C:H2'	53:1:2842:G:C8	2.52	0.45
58:8:306:GLU:HA	58:8:360:VAL:HA	1.99	0.45
4:e:30:VAL:HA	4:e:157:THR:HG22	1.99	0.45
7:h:58:THR:HG21	7:h:82:ILE:H	1.80	0.45
8:i:9:LYS:NZ	53:1:1061:U:OP1	2.48	0.45
9:j:47:HIS:CE1	9:j:48:VAL:HG23	2.52	0.45
32:H:4:VAL:O	32:H:6:PRO:HD3	2.17	0.45
32:H:78:LYS:O	32:H:81:GLU:HG2	2.17	0.45
33:I:2:ARG:HH22	33:I:111:ALA:HB1	1.82	0.45
35:K:98:GLU:HB3	35:K:99:ALA:H	1.52	0.45
45:U:70:ARG:NH1	52:3:452:A:H1'	2.31	0.45
53:1:182:A:O2'	53:1:183:C:H5'	2.17	0.45
53:1:2724:U:H2'	53:1:2725:A:H8	1.80	0.45
54:2:30:C:C2'	54:2:31:C:H5'	2.46	0.45
55:6:32:C:H2'	55:6:33:U:C6	2.51	0.45
34:J:160:VAL:HA	34:J:163:ILE:HD11	1.98	0.45
36:L:64:ALA:HA	36:L:127:ALA:HA	1.99	0.45
36:L:102:TRP:CD1	36:L:136:LYS:HG2	2.51	0.45
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.99	0.45
50:Z:39:LYS:O	50:Z:40:PRO:C	2.59	0.45
53:1:310:A:O2'	53:1:311:A:H5''	2.16	0.45
53:1:956:G:H2'	53:1:957:C:H2'	1.97	0.45
53:1:1873:G:O2'	53:1:1874:C:H5'	2.17	0.45
53:1:2073:C:O2'	53:1:2074:U:H5'	2.17	0.45
53:1:2233:U:H2'	53:1:2234:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2293:G:H2'	53:1:2294:G:H8	1.82	0.45
53:1:2830:C:O2'	53:1:2831:G:H5'	2.16	0.45
57:7:76:A:O2'	60:7:101:PHE:C	2.59	0.45
58:8:134:PHE:HD1	58:8:171:VAL:HG13	1.81	0.45
4:e:33:ILE:O	4:e:90:LEU:HD23	2.17	0.45
15:p:95:LYS:HG3	53:1:2718:G:O3'	2.16	0.45
18:s:94:ASP:OD1	53:1:2014:A:H5'	2.17	0.45
19:t:34:VAL:HG22	19:t:35:ALA:N	2.31	0.45
33:I:55:ARG:HA	33:I:55:ARG:NE	2.31	0.45
37:M:62:LEU:HD23	37:M:64:TYR:OH	2.16	0.45
37:M:76:ARG:NH1	37:M:125:ILE:HG23	2.31	0.45
45:U:33:ILE:N	45:U:33:ILE:HD12	2.31	0.45
49:Y:83:ASN:HA	49:Y:86:ALA:HB3	1.99	0.45
52:3:539:A:H2'	52:3:540:G:C8	2.51	0.45
52:3:909:A:H2'	52:3:910:C:O4'	2.16	0.45
52:3:1401:G:H2'	52:3:1402:C:O4'	2.16	0.45
53:1:598:U:H2'	53:1:599:A:H8	1.81	0.45
53:1:1041:G:O2'	53:1:1042:G:H5'	2.17	0.45
53:1:2636:C:H2'	53:1:2637:U:C6	2.52	0.45
55:6:13:C:O2'	55:6:14:A:H5'	2.16	0.45
55:6:41:C:H2'	55:6:42:G:H8	1.82	0.45
56:4:20:U:H2'	56:4:21:C:C6	2.52	0.45
2:c:40:LEU:HA	2:c:44:GLY:H	1.81	0.45
5:f:44:HIS:CG	5:f:45:ALA:H	2.35	0.45
7:h:122:GLN:HB2	7:h:123:ILE:HD12	1.98	0.45
12:m:57:VAL:HA	12:m:112:LEU:HD21	1.99	0.45
25:z:40:THR:OG1	25:z:41:PRO:HD2	2.17	0.45
30:F:1:MET:SD	30:F:36:ARG:HG2	2.57	0.45
31:G:213:LEU:HA	31:G:216:VAL:HG22	1.99	0.45
35:K:29:ILE:HG21	35:K:64:VAL:HG21	1.99	0.45
39:O:53:ILE:HG23	52:3:1060:U:H4'	1.97	0.45
52:3:613:C:H2'	52:3:614:C:C6	2.52	0.45
52:3:1118:U:H2'	52:3:1119:C:C6	2.52	0.45
53:1:818:G:O2'	53:1:819:A:H5''	2.17	0.45
53:1:1361:G:H2'	53:1:1362:C:C6	2.52	0.45
53:1:2685:G:H2'	53:1:2686:G:H8	1.82	0.45
54:2:64:G:H2'	54:2:65:U:C6	2.51	0.45
58:8:124:ARG:HD3	58:8:163:PHE:CZ	2.51	0.45
7:h:57:ASN:C	7:h:59:LEU:H	2.25	0.45
13:n:79:LEU:C	13:n:81:ASN:H	2.24	0.45
31:G:103:TRP:HA	31:G:106:VAL:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:146:SER:C	31:G:147:LEU:HD12	2.42	0.45
35:K:13:ASP:OD1	35:K:13:ASP:N	2.50	0.45
38:N:51:LEU:HD11	38:N:62:LEU:HD11	1.99	0.45
42:R:8:ILE:O	42:R:8:ILE:HG22	2.16	0.45
52:3:151:A:H62	52:3:170:U:H3	1.65	0.45
52:3:206:C:H2'	52:3:207:C:O4'	2.17	0.45
52:3:412:A:C2	52:3:414:A:H1'	2.52	0.45
52:3:737:C:H2'	52:3:738:C:C6	2.52	0.45
52:3:1248:A:O2'	52:3:1249:C:H5'	2.17	0.45
52:3:1504:G:OP1	52:3:1507:A:H4'	2.17	0.45
53:1:172:A:H2'	53:1:173:A:C8	2.52	0.45
53:1:581:C:H2'	53:1:582:A:H8	1.82	0.45
53:1:1139:G:O2'	53:1:1140:C:H5'	2.17	0.45
53:1:1795:C:H2'	53:1:1796:U:C6	2.51	0.45
53:1:1860:G:H2'	53:1:1861:G:H8	1.82	0.45
53:1:2533:U:H2'	53:1:2534:A:O4'	2.17	0.45
57:7:61:C:H2'	57:7:62:C:C6	2.52	0.45
1:b:68:ARG:NH1	1:b:128:THR:OG1	2.50	0.45
1:b:180:MET:HB2	1:b:268:ARG:H	1.82	0.45
5:f:136:ASP:HB3	5:f:139:VAL:HB	1.99	0.45
7:h:5:LEU:HD23	7:h:5:LEU:H	1.82	0.45
7:h:33:VAL:HG12	7:h:34:THR:N	2.29	0.45
7:h:97:LYS:O	7:h:101:LYS:HG2	2.17	0.45
16:q:90:ASP:OD1	16:q:92:LYS:HB3	2.17	0.45
17:r:65:ALA:HB3	17:r:95:ASP:HB2	1.99	0.45
31:G:183:PHE:HA	31:G:197:PHE:HB2	1.99	0.45
44:T:4:THR:HG23	44:T:5:GLU:CD	2.42	0.45
49:Y:79:THR:O	49:Y:83:ASN:ND2	2.50	0.45
52:3:321:A:H2'	52:3:322:C:C6	2.52	0.45
52:3:545:C:H2'	52:3:546:A:C8	2.51	0.45
52:3:1171:A:H2'	52:3:1172:C:C6	2.51	0.45
52:3:1236:A:H2'	52:3:1237:C:O4'	2.17	0.45
52:3:1512:U:H2'	52:3:1513:A:C8	2.51	0.45
53:1:121:G:H2'	53:1:122:G:H8	1.82	0.45
53:1:2843:G:O2'	53:1:2844:G:H5'	2.17	0.45
3:d:83:VAL:CG1	3:d:86:ALA:HA	2.48	0.44
5:f:106:LEU:O	5:f:151:ARG:NH2	2.44	0.44
10:k:30:ARG:NE	53:1:2674:G:H4'	2.32	0.44
25:z:11:SER:OG	53:1:989:G:OP2	2.31	0.44
28:D:24:THR:OG1	28:D:25:LYS:N	2.48	0.44
34:J:79:THR:OG1	34:J:80:LEU:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:9:MET:HA	35:K:58:HIS:O	2.17	0.44
36:L:31:VAL:HG11	36:L:108:ARG:HH22	1.82	0.44
39:O:14:ASP:HB3	39:O:17:LEU:HB2	1.98	0.44
41:Q:67:GLY:O	41:Q:98:ARG:NH1	2.47	0.44
45:U:2:VAL:HG23	45:U:65:ALA:HA	1.99	0.44
49:Y:19:HIS:O	49:Y:23:ARG:HG2	2.17	0.44
52:3:346:G:C2'	52:3:347:G:H5'	2.47	0.44
52:3:452:A:H61	52:3:480:U:H3	1.65	0.44
52:3:1318:A:C2'	52:3:1319:A:H5'	2.46	0.44
53:1:27:G:N2	53:1:512:G:H1'	2.32	0.44
53:1:251:A:H2'	53:1:252:G:O4'	2.17	0.44
53:1:765:C:H2'	53:1:766:U:C6	2.53	0.44
53:1:1140:C:C2'	53:1:1141:U:H5'	2.47	0.44
53:1:1601:G:C2'	53:1:1602:U:H5'	2.47	0.44
53:1:2008:C:H2'	53:1:2009:A:H8	1.82	0.44
53:1:2112:G:H1'	55:6:19:G:O2'	2.17	0.44
53:1:2372:U:H2'	53:1:2373:G:H8	1.82	0.44
58:8:237:ILE:HD11	58:8:275:VAL:HG21	1.99	0.44
58:8:343:GLU:HG3	58:8:362:THR:HG23	1.98	0.44
4:e:135:ILE:O	4:e:135:ILE:HG13	2.17	0.44
8:i:78:LEU:HA	8:i:81:LYS:HE3	1.98	0.44
9:j:101:ILE:N	9:j:101:ILE:HD12	2.32	0.44
17:r:17:GLY:H	17:r:98:ILE:HB	1.82	0.44
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.32	0.44
21:v:12:GLN:NE2	54:2:75:G:OP1	2.51	0.44
28:D:12:ARG:NE	28:D:44:VAL:HG21	2.28	0.44
37:M:50:VAL:HG22	37:M:50:VAL:O	2.17	0.44
37:M:83:ARG:HD2	37:M:123:GLU:OE1	2.16	0.44
45:U:36:VAL:HG13	45:U:36:VAL:O	2.17	0.44
46:V:26:ARG:HD3	46:V:26:ARG:H	1.82	0.44
52:3:745:G:O2'	52:3:746:A:H5'	2.18	0.44
52:3:784:A:H2'	52:3:785:G:H8	1.82	0.44
53:1:511:U:C2'	53:1:512:G:H5'	2.48	0.44
53:1:1092:C:H2'	53:1:1093:G:O4'	2.16	0.44
53:1:2220:U:H2'	53:1:2221:G:C8	2.53	0.44
53:1:2739:U:O2'	53:1:2740:A:H5'	2.17	0.44
2:c:88:GLU:N	2:c:88:GLU:OE2	2.51	0.44
7:h:81:LEU:O	7:h:81:LEU:HD23	2.18	0.44
9:j:84:ILE:HG23	9:j:84:ILE:O	2.16	0.44
10:k:6:THR:CG2	53:1:1666:G:H4'	2.48	0.44
12:m:19:GLY:O	12:m:38:ARG:NH1	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:t:41:ALA:O	19:t:44:LYS:HB3	2.18	0.44
21:v:26:PHE:HE2	21:v:89:ILE:HG13	1.82	0.44
26:B:9:ARG:HD2	26:B:9:ARG:N	2.32	0.44
39:O:40:ILE:HD12	52:3:1124:G:H4'	1.98	0.44
41:Q:114:SER:OG	52:3:501:C:O3'	2.35	0.44
52:3:1410:A:H2'	52:3:1411:C:C6	2.52	0.44
52:3:1441:A:C2'	52:3:1442:G:H5'	2.46	0.44
52:3:1496:C:H2'	52:3:1497:G:O4'	2.17	0.44
52:3:1497:G:H2'	52:3:1498:U:H5'	1.99	0.44
53:1:164:C:H2'	53:1:165:A:O4'	2.17	0.44
53:1:743:A:O2'	53:1:744:U:H5'	2.18	0.44
53:1:1370:C:H2'	53:1:1371:G:O4'	2.17	0.44
53:1:2024:G:OP2	53:1:2034:U:H4'	2.17	0.44
53:1:2285:C:O2'	53:1:2287:A:H1'	2.17	0.44
53:1:2343:U:O2'	53:1:2344:U:H5'	2.17	0.44
58:8:344:LEU:HA	58:8:359:MET:HB2	2.00	0.44
1:b:65:ASP:OD2	1:b:68:ARG:HD2	2.17	0.44
3:d:1:MET:HB2	3:d:16:GLU:HA	1.99	0.44
33:I:39:GLN:HA	52:3:426:U:H4'	1.99	0.44
36:L:146:ALA:O	40:P:55:ARG:NH2	2.48	0.44
38:N:56:MET:N	38:N:56:MET:SD	2.90	0.44
38:N:73:GLY:N	52:3:1372:U:OP1	2.50	0.44
41:Q:23:LEU:O	41:Q:24:GLU:C	2.60	0.44
52:3:9:G:H2'	52:3:10:A:C8	2.52	0.44
52:3:265:G:H2'	52:3:267:C:H5	1.82	0.44
52:3:868:C:H2'	52:3:869:G:O4'	2.17	0.44
53:1:481:G:H1'	53:1:506:G:H21	1.81	0.44
53:1:677:A:HO2'	53:1:2071:A:H5'	1.82	0.44
53:1:766:U:H2'	53:1:767:U:H6	1.82	0.44
53:1:871:U:H2'	53:1:872:U:C6	2.52	0.44
53:1:1258:U:H2'	53:1:1259:G:H8	1.80	0.44
53:1:1542:U:H2'	53:1:1543:G:C8	2.52	0.44
53:1:1571:A:H2'	53:1:1572:A:C8	2.53	0.44
53:1:1877:A:H2'	53:1:1878:G:C8	2.52	0.44
53:1:2172:U:OP1	53:1:2173:A:H8	2.01	0.44
53:1:2655:G:HO2'	53:1:2656:U:H5	1.65	0.44
53:1:2661:G:H2'	53:1:2662:A:O4'	2.18	0.44
57:7:45:U:H3'	57:7:46:G:H5''	2.00	0.44
1:b:198:GLU:HB3	1:b:201:LEU:HD12	1.99	0.44
3:d:71:GLY:H	53:1:674:G:H5''	1.82	0.44
7:h:61:ARG:HD2	53:1:1047:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:20:SER:HB2	8:i:21:PRO:HD3	1.99	0.44
8:i:33:ASN:HB3	8:i:36:GLU:HG2	1.98	0.44
9:j:47:HIS:ND1	9:j:48:VAL:HG23	2.32	0.44
31:G:24:PRO:HB3	52:3:828:U:H2'	1.98	0.44
34:J:23:THR:HA	34:J:28:ARG:HA	1.98	0.44
39:O:59:LYS:HD3	52:3:973:G:OP1	2.17	0.44
49:Y:48:LYS:NZ	49:Y:52:GLU:OE2	2.49	0.44
49:Y:66:ILE:HD12	49:Y:70:LYS:HD2	2.00	0.44
52:3:1251:A:O2'	52:3:1370:G:H5'	2.18	0.44
53:1:131:A:H2'	53:1:132:G:C8	2.52	0.44
53:1:1112:G:H2'	53:1:1113:U:C6	2.53	0.44
55:6:24:U:H2'	55:6:25:C:C6	2.52	0.44
58:8:135:LEU:HB2	58:8:172:ARG:HD3	1.99	0.44
4:e:111:ARG:NH2	42:R:65:GLU:OE2	2.51	0.44
15:p:28:LYS:HB3	15:p:39:LEU:HD11	2.00	0.44
15:p:51:ASN:O	53:1:2845:U:H5''	2.18	0.44
34:J:87:VAL:HG13	34:J:92:ARG:HD2	2.00	0.44
35:K:53:LYS:HA	35:K:53:LYS:HE2	1.99	0.44
48:X:46:LEU:O	48:X:61:VAL:HG12	2.18	0.44
49:Y:67:HIS:O	49:Y:68:LYS:HG3	2.18	0.44
52:3:110:C:H2'	52:3:111:G:O4'	2.17	0.44
52:3:603:U:H2'	52:3:604:G:C8	2.52	0.44
52:3:742:G:O2'	52:3:743:A:H5'	2.18	0.44
52:3:971:G:H1'	52:3:1365:G:O2'	2.16	0.44
53:1:196:A:N3	53:1:196:A:H2'	2.33	0.44
53:1:859:G:H1'	53:1:860:U:H5	1.82	0.44
53:1:1021:A:H3'	53:1:1021:A:N3	2.32	0.44
53:1:1297:C:OP1	53:1:2710:C:H4'	2.17	0.44
53:1:2123:G:H2'	53:1:2124:G:C8	2.53	0.44
53:1:2623:G:H2'	53:1:2624:G:H8	1.83	0.44
10:k:23:LYS:HB3	10:k:40:LYS:HB3	1.99	0.44
12:m:50:ARG:HH22	12:m:54:THR:HG21	1.81	0.44
16:q:63:ARG:HB2	16:q:95:ALA:HB1	2.00	0.44
34:J:105:ILE:CD1	34:J:123:LEU:HD23	2.38	0.44
34:J:131:ASN:O	34:J:135:VAL:HG22	2.16	0.44
37:M:74:ILE:HG22	37:M:128:VAL:HG22	1.99	0.44
43:S:53:ASP:HA	43:S:58:ARG:HD3	1.99	0.44
43:S:68:ARG:HH12	43:S:70:HIS:HB2	1.83	0.44
45:U:51:ARG:NH1	52:3:626:G:O2'	2.48	0.44
52:3:552:U:H2'	52:3:553:A:C8	2.53	0.44
52:3:1115:U:H2'	52:3:1116:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1308:U:H2'	52:3:1309:G:H8	1.82	0.44
52:3:1347:G:N2	52:3:1373:G:H2'	2.32	0.44
53:1:1538:G:O2'	53:1:1539:U:H5'	2.18	0.44
6:g:97:ARG:HG2	6:g:112:LYS:HD2	1.98	0.44
7:h:53:ARG:HB3	53:1:1084:A:OP1	2.18	0.44
7:h:86:MET:HG3	7:h:87:GLU:H	1.81	0.44
11:l:16:GLY:HA2	53:1:662:G:O3'	2.18	0.44
15:p:110:LYS:HG3	15:p:111:GLU:O	2.18	0.44
16:q:15:LYS:HB3	16:q:15:LYS:HE2	1.90	0.44
16:q:33:VAL:O	16:q:36:GLN:HG2	2.18	0.44
18:s:73:LYS:O	18:s:106:VAL:HG22	2.18	0.44
21:v:73:LYS:HB2	21:v:92:VAL:HG23	1.99	0.44
27:C:8:ILE:HD13	27:C:24:LYS:HG2	2.00	0.44
37:M:25:THR:HA	37:M:59:GLU:HA	2.00	0.44
43:S:27:LYS:HZ1	52:3:1316:G:H8	1.62	0.44
43:S:50:LEU:HD23	43:S:51:PRO:O	2.17	0.44
44:T:47:LYS:HA	44:T:47:LYS:HE2	2.00	0.44
45:U:59:HIS:O	45:U:63:GLN:HG2	2.17	0.44
52:3:354:G:H2'	52:3:355:C:C5'	2.48	0.44
53:1:596:U:H2'	53:1:597:G:C8	2.52	0.44
53:1:671:C:H2'	53:1:672:C:C6	2.52	0.44
53:1:2553:G:H2'	53:1:2554:U:C4'	2.47	0.44
53:1:2639:A:H2'	53:1:2640:G:O4'	2.18	0.44
1:b:179:GLU:OE1	1:b:270:ARG:HB2	2.18	0.44
2:c:97:SER:HB3	2:c:99:GLU:OE1	2.18	0.44
3:d:117:ARG:HH21	3:d:184:ASP:HA	1.81	0.44
4:e:23:SER:HB3	4:e:26:GLN:HB2	1.99	0.44
4:e:76:PHE:CE1	53:1:2308:G:C6	3.06	0.44
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.48	0.44
20:u:94:PHE:HD2	20:u:99:SER:HB2	1.82	0.44
32:H:21:TRP:HB3	32:H:58:ARG:H	1.82	0.44
33:I:130:ASN:HD22	52:3:619:U:H3	1.66	0.44
36:L:81:GLY:HA2	56:4:12:A:H4'	2.00	0.44
38:N:24:ASN:HB3	38:N:26:LYS:HG2	1.99	0.44
39:O:80:THR:HG22	39:O:82:LYS:HG2	2.00	0.44
40:P:55:ARG:NH1	55:6:40:C:H5'	2.32	0.44
40:P:125:LYS:O	50:Z:34:ARG:NH1	2.51	0.44
42:R:13:HIS:NE2	52:3:1296:C:H5'	2.33	0.44
42:R:24:VAL:HA	52:3:1329:A:H5''	2.00	0.44
45:U:42:ILE:O	45:U:42:ILE:HG13	2.18	0.44
52:3:421:U:O2'	52:3:422:C:P	2.76	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:490:C:H2'	52:3:491:G:H8	1.83	0.44
52:3:917:G:H2'	52:3:918:A:C8	2.53	0.44
53:1:1917:U:O2'	53:1:1918:A:H5'	2.17	0.44
53:1:2231:U:H2'	53:1:2232:C:C6	2.53	0.44
53:1:2398:U:H2'	53:1:2399:G:H8	1.83	0.44
53:1:2818:U:O2'	53:1:2837:A:H5'	2.18	0.44
1:b:155:ARG:CZ	53:1:1818:U:H5	2.30	0.43
6:g:31:VAL:N	6:g:32:PRO:CD	2.80	0.43
13:n:18:GLN:HE21	13:n:22:ARG:NH1	2.16	0.43
13:n:115:LEU:HD12	13:n:115:LEU:O	2.18	0.43
16:q:35:PHE:HZ	17:r:84:ARG:NH2	2.16	0.43
27:C:20:TYR:CE1	27:C:37:LYS:HD3	2.52	0.43
40:P:124:LYS:O	50:Z:34:ARG:NH1	2.46	0.43
43:S:23:ARG:NH1	43:S:25:GLU:OE1	2.51	0.43
45:U:28:ARG:HH11	45:U:29:ASN:HD21	1.65	0.43
51:a:7:ARG:HD3	53:1:2129:C:OP2	2.18	0.43
53:1:277:G:H4'	53:1:278:A:N7	2.33	0.43
53:1:1310:G:H2'	53:1:1311:G:H5'	2.00	0.43
53:1:2115:G:H4'	53:1:2166:U:O2	2.17	0.43
53:1:2364:C:H2'	53:1:2365:G:O4'	2.18	0.43
1:b:116:GLN:H	1:b:127:ASN:ND2	2.16	0.43
16:q:15:LYS:NZ	53:1:1227:G:OP2	2.50	0.43
20:u:97:SER:O	20:u:98:ASN:HB3	2.18	0.43
36:L:45:ALA:O	36:L:49:LEU:HG	2.18	0.43
37:M:12:ARG:NH2	52:3:826:C:H5'	2.33	0.43
38:N:53:LEU:HD21	38:N:96:GLU:OE2	2.19	0.43
38:N:119:LYS:HG3	52:3:1349:A:OP1	2.17	0.43
45:U:40:ASN:CG	45:U:43:ALA:HB2	2.43	0.43
52:3:437:U:H2'	52:3:438:U:O4'	2.18	0.43
52:3:1154:G:H2'	52:3:1155:A:C8	2.53	0.43
53:1:56:A:H2'	53:1:57:C:O4'	2.18	0.43
53:1:138:U:H5'	53:1:139:U:OP2	2.18	0.43
53:1:214:G:H2'	53:1:215:G:C8	2.53	0.43
53:1:1279:G:H2'	53:1:1280:G:H8	1.83	0.43
53:1:2101:A:H2'	53:1:2102:G:H8	1.83	0.43
53:1:2692:G:H2'	53:1:2693:G:C8	2.53	0.43
53:1:2853:C:H2'	53:1:2854:G:C8	2.53	0.43
7:h:113:PHE:O	7:h:123:ILE:HG23	2.19	0.43
32:H:149:LYS:HB2	32:H:172:VAL:HG11	2.00	0.43
38:N:8:THR:OG1	38:N:9:GLY:N	2.40	0.43
47:W:70:THR:OG1	47:W:71:ASP:N	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:317:U:H2'	52:3:318:G:C8	2.53	0.43
52:3:1494:G:O2'	52:3:1495:U:H5'	2.19	0.43
53:1:326:G:H2'	53:1:327:G:H8	1.83	0.43
53:1:542:C:H2'	53:1:543:G:C5'	2.47	0.43
53:1:1433:A:H2'	53:1:1434:A:C8	2.53	0.43
53:1:2475:C:H2'	53:1:2476:A:H5'	2.00	0.43
55:6:29:G:H2'	55:6:30:G:C8	2.53	0.43
58:8:123:GLY:O	58:8:126:VAL:HG12	2.18	0.43
1:b:12:ARG:HG2	53:1:729:G:P	2.59	0.43
10:k:92:GLU:O	10:k:93:GLN:C	2.61	0.43
15:p:16:VAL:O	15:p:16:VAL:HG13	2.18	0.43
24:y:4:LYS:O	24:y:7:ARG:NH1	2.52	0.43
25:z:12:ALA:HB2	25:z:53:MET:HE1	2.00	0.43
31:G:202:ASN:HD21	31:G:204:ASP:HB2	1.83	0.43
47:W:20:ILE:HG21	47:W:54:LEU:HD12	2.00	0.43
52:3:678:U:O2'	52:3:679:C:H5'	2.18	0.43
52:3:695:A:H5'	55:6:38:A:H4'	1.99	0.43
53:1:296:U:H2'	53:1:297:G:H8	1.83	0.43
53:1:704:G:H1'	53:1:727:A:H61	1.83	0.43
53:1:854:C:O2'	53:1:855:G:H5'	2.18	0.43
53:1:983:A:N6	53:1:984:A:C2	2.86	0.43
55:6:37:A:O2'	55:6:38:A:H5'	2.18	0.43
1:b:15:VAL:HG22	1:b:205:GLY:HA3	2.00	0.43
1:b:200:MET:HE1	52:3:774:G:OP1	2.17	0.43
7:h:13:ALA:O	7:h:17:GLU:HG2	2.19	0.43
27:C:32:LYS:NZ	27:C:50:GLU:HB3	2.34	0.43
29:E:38:LYS:HE2	53:1:2351:G:O6	2.18	0.43
33:I:191:SER:O	33:I:192:ALA:HB3	2.18	0.43
40:P:55:ARG:HH12	55:6:40:C:H5'	1.84	0.43
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.99	0.43
51:a:24:ASN:HA	51:a:186:LYS:NZ	2.33	0.43
52:3:41:G:H2'	52:3:42:G:H8	1.84	0.43
53:1:248:G:O5'	53:1:249:C:H5'	2.18	0.43
53:1:288:U:H2'	53:1:289:G:H8	1.83	0.43
53:1:492:A:H2'	53:1:493:G:O4'	2.19	0.43
53:1:696:G:H1	53:1:766:U:H3	1.67	0.43
53:1:1695:G:H2'	53:1:1696:G:O4'	2.18	0.43
53:1:2516:A:O2'	53:1:2517:C:H5'	2.18	0.43
53:1:2564:A:OP1	53:1:2648:G:H4'	2.18	0.43
58:8:311:ILE:HB	58:8:355:ASP:H	1.84	0.43
1:b:216:ARG:NH1	53:1:691:C:OP1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:67:THR:H	7:h:68:PRO:CD	2.32	0.43
13:n:72:ASP:HB2	13:n:75:ILE:HG12	2.00	0.43
14:o:31:THR:CG2	14:o:32:PRO:HD2	2.49	0.43
23:x:63:ILE:O	23:x:67:LEU:HD23	2.17	0.43
30:F:24:ARG:HA	30:F:36:ARG:HA	2.00	0.43
32:H:14:VAL:HG13	32:H:15:LYS:HG2	2.00	0.43
41:Q:2:THR:HB	41:Q:5:GLN:NE2	2.32	0.43
43:S:8:ARG:HD2	43:S:12:ARG:HH12	1.83	0.43
50:Z:23:GLU:C	50:Z:25:ALA:H	2.26	0.43
51:a:184:LYS:O	51:a:188:ASN:ND2	2.52	0.43
52:3:459:A:H2'	52:3:460:A:C8	2.54	0.43
52:3:764:C:H2'	52:3:765:G:O4'	2.19	0.43
52:3:929:G:H5''	52:3:1534:A:O2'	2.18	0.43
52:3:1371:G:H2'	52:3:1372:U:C6	2.53	0.43
52:3:1492:A:H2'	53:1:1913:A:C2	2.54	0.43
53:1:100:U:H4'	53:1:101:A:C4	2.54	0.43
53:1:863:A:H2'	53:1:864:G:C8	2.53	0.43
53:1:1068:G:H2'	53:1:1069:A:O4'	2.19	0.43
53:1:1423:G:H2'	53:1:1424:G:H8	1.84	0.43
53:1:1565:C:O2'	53:1:1566:A:H2'	2.18	0.43
1:b:73:ILE:HD13	1:b:97:ASP:OD2	2.18	0.43
2:c:85:ALA:O	2:c:87:GLY:N	2.51	0.43
4:e:103:ILE:HG13	4:e:104:THR:HG23	1.99	0.43
5:f:116:LEU:HA	5:f:117:PRO:HD3	1.90	0.43
11:l:80:SER:O	11:l:84:LYS:NZ	2.51	0.43
12:m:64:TRP:HE1	53:1:873:C:H4'	1.83	0.43
13:n:12:ARG:O	13:n:17:ARG:NH2	2.52	0.43
16:q:52:ARG:HG3	16:q:56:PHE:CD2	2.53	0.43
43:S:15:LEU:O	43:S:15:LEU:HD23	2.17	0.43
51:a:12:ARG:NH1	53:1:2175:C:H5''	2.32	0.43
52:3:51:A:H4'	52:3:52:C:H5''	2.01	0.43
53:1:127:A:H5''	53:1:128:C:O4'	2.19	0.43
53:1:359:G:H2'	53:1:360:U:O4'	2.19	0.43
53:1:420:C:O2'	53:1:421:C:H5'	2.18	0.43
53:1:1028:A:N6	53:1:1125:G:H2'	2.33	0.43
53:1:2233:U:H2'	53:1:2234:G:H8	1.83	0.43
53:1:2572:A:OP1	53:1:2574:G:H4'	2.19	0.43
58:8:336:THR:HB	58:8:338:VAL:HG13	2.00	0.43
1:b:48:ILE:HG23	1:b:48:ILE:O	2.19	0.43
2:c:35:THR:O	2:c:92:VAL:HG13	2.19	0.43
5:f:2:ARG:NH1	53:1:1113:U:H5'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:66:GLY:HA2	7:h:69:PHE:CE1	2.53	0.43
7:h:118:ILE:N	7:h:119:PRO:CD	2.81	0.43
15:p:31:VAL:HG13	15:p:31:VAL:O	2.19	0.43
30:F:19:ARG:HA	53:1:2756:U:H5''	1.99	0.43
31:G:195:VAL:HG12	31:G:197:PHE:H	1.83	0.43
39:O:56:HIS:HE1	52:3:963:G:H21	1.65	0.43
52:3:40:C:O2'	52:3:41:G:H5'	2.18	0.43
52:3:113:G:H2'	52:3:114:U:C6	2.52	0.43
52:3:886:G:H2'	52:3:887:G:C8	2.54	0.43
53:1:118:A:OP2	53:1:119:A:H2'	2.18	0.43
53:1:172:A:H2'	53:1:173:A:H8	1.83	0.43
53:1:576:U:H2'	53:1:577:G:H8	1.82	0.43
53:1:851:C:H2'	53:1:852:U:C6	2.54	0.43
53:1:1360:G:H2'	53:1:1361:G:H5'	2.01	0.43
53:1:1851:U:O2'	55:6:71:C:H4'	2.19	0.43
53:1:1903:G:H2'	53:1:1904:G:H8	1.84	0.43
53:1:2812:G:O2'	53:1:2813:A:H5'	2.18	0.43
57:7:14:A:H2'	57:7:15:G:O4'	2.19	0.43
58:8:148:GLU:O	58:8:152:MET:HG2	2.18	0.43
58:8:158:LEU:HD13	58:8:168:THR:HG21	2.01	0.43
58:8:233:GLU:CD	58:8:234:ARG:HG3	2.44	0.43
58:8:295:LYS:HB3	58:8:298:THR:HG21	2.01	0.43
58:8:304:LYS:HE2	58:8:360:VAL:HG11	2.00	0.43
1:b:59:GLN:HA	53:1:1568:G:H5'	2.01	0.43
1:b:68:ARG:O	1:b:188:ARG:NH1	2.51	0.43
8:i:99:LYS:HZ3	8:i:138:VAL:HB	1.83	0.43
10:k:5:GLN:HG3	53:1:1669:A:O4'	2.17	0.43
10:k:35:VAL:HG23	10:k:36:GLY:N	2.27	0.43
14:o:45:SER:O	54:2:112:G:N2	2.52	0.43
22:w:70:PRO:HB3	54:2:12:C:N4	2.33	0.43
24:y:7:ARG:HD3	24:y:7:ARG:H	1.84	0.43
30:F:7:VAL:H	30:F:38:GLY:HA3	1.84	0.43
32:H:69:THR:OG1	32:H:70:ALA:N	2.52	0.43
33:I:151:GLN:N	33:I:151:GLN:OE1	2.52	0.43
34:J:100:GLU:HA	34:J:121:ASN:ND2	2.34	0.43
39:O:89:ARG:HH11	39:O:90:LEU:HD21	1.84	0.43
40:P:43:TRP:HZ2	52:3:686:U:H1'	1.84	0.43
43:S:60:ARG:HD2	43:S:60:ARG:HA	1.82	0.43
43:S:89:ARG:NE	43:S:89:ARG:O	2.52	0.43
47:W:59:LYS:HD3	52:3:734:G:O2'	2.19	0.43
48:X:77:ARG:NH2	52:3:1225:A:H4'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1202:U:H2'	52:3:1203:C:O4'	2.19	0.43
52:3:1245:C:H2'	52:3:1246:A:C8	2.54	0.43
53:1:230:G:O2'	53:1:231:A:H5'	2.19	0.43
53:1:441:U:H2'	53:1:442:G:C8	2.54	0.43
53:1:570:G:H2'	53:1:2030:A:N7	2.34	0.43
53:1:704:G:H1'	53:1:727:A:N6	2.34	0.43
53:1:808:G:H2'	53:1:809:G:H8	1.84	0.43
53:1:996:A:H2'	53:1:997:G:H8	1.84	0.43
53:1:1040:A:H2'	53:1:1041:G:H8	1.83	0.43
53:1:1562:U:H2'	53:1:1563:U:O4'	2.19	0.43
53:1:2685:G:H2'	53:1:2686:G:C8	2.53	0.43
53:1:2743:U:H2'	53:1:2744:G:O4'	2.18	0.43
58:8:173:GLY:HA2	58:8:188:LYS:HE3	2.01	0.43
13:n:17:ARG:HH21	13:n:17:ARG:HB2	1.84	0.43
16:q:91:ARG:HG3	16:q:91:ARG:HH11	1.84	0.43
20:u:14:THR:OG1	20:u:15:GLY:N	2.52	0.43
25:z:15:ARG:HE	25:z:52:PHE:HE2	1.67	0.43
32:H:63:ILE:HD11	32:H:98:ALA:HB2	2.01	0.43
41:Q:20:VAL:HA	41:Q:21:PRO:HD3	1.80	0.43
41:Q:57:THR:HG21	52:3:363:A:OP2	2.18	0.43
42:R:104:ASN:HB3	42:R:105:ALA:H	1.66	0.43
45:U:36:VAL:CG2	45:U:53:ASP:HB3	2.45	0.43
48:X:45:GLY:HA2	48:X:60:PHE:HE1	1.84	0.43
52:3:149:A:H1'	52:3:1446:A:C2	2.54	0.43
52:3:219:U:H2'	52:3:220:G:C8	2.54	0.43
52:3:1414:U:H2'	52:3:1415:G:C8	2.54	0.43
53:1:36:G:O2'	53:1:37:C:H5'	2.19	0.43
53:1:284:U:H2'	53:1:285:G:C8	2.54	0.43
53:1:438:G:H2'	53:1:439:A:C8	2.54	0.43
53:1:490:C:H4'	53:1:491:G:OP2	2.18	0.43
53:1:723:C:H2'	53:1:724:U:C6	2.54	0.43
53:1:935:C:H2'	53:1:936:A:C8	2.54	0.43
53:1:935:C:H2'	53:1:936:A:H8	1.83	0.43
53:1:2008:C:H2'	53:1:2009:A:C8	2.53	0.43
53:1:2446:G:H2'	53:1:2447:G:H5''	2.01	0.43
53:1:2475:C:C2'	53:1:2476:A:H5'	2.48	0.43
56:4:21:C:H2'	56:4:22:A:O4'	2.18	0.43
8:i:8:VAL:HG22	8:i:9:LYS:N	2.33	0.42
8:i:99:LYS:C	8:i:100:ILE:HD12	2.44	0.42
11:l:29:LYS:O	11:l:30:THR:OG1	2.34	0.42
15:p:74:GLN:HB2	15:p:77:SER:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:w:23:GLY:HA2	22:w:63:VAL:HG23	2.01	0.42
22:w:66:GLU:HB3	22:w:68:LYS:HG3	2.00	0.42
31:G:176:ASN:ND2	31:G:194:GLY:O	2.52	0.42
33:I:21:LYS:HE3	52:3:430:A:P	2.59	0.42
40:P:48:GLY:HA2	52:3:688:G:O5'	2.19	0.42
42:R:85:TYR:CE2	52:3:1321:U:H5''	2.54	0.42
43:S:33:VAL:O	43:S:33:VAL:HG22	2.19	0.42
52:3:89:U:H2'	52:3:90:C:O4'	2.19	0.42
52:3:624:C:H2'	52:3:625:U:O4'	2.19	0.42
52:3:1449:C:H2'	52:3:1450:U:O4'	2.19	0.42
53:1:1111:A:H2'	53:1:1111:A:N3	2.34	0.42
53:1:2343:U:H2'	53:1:2344:U:C6	2.54	0.42
53:1:2371:G:O2'	53:1:2372:U:H5'	2.18	0.42
53:1:2641:G:H2'	53:1:2642:G:H8	1.83	0.42
58:8:12:HIS:HD2	58:8:273:GLU:HA	1.84	0.42
58:8:26:THR:O	58:8:29:THR:OG1	2.37	0.42
3:d:49:ARG:NH2	53:1:673:C:OP1	2.52	0.42
4:e:32:LYS:HG2	4:e:156:THR:OG1	2.19	0.42
5:f:22:VAL:HG22	5:f:35:THR:HG22	2.01	0.42
9:j:78:THR:HG22	53:1:2641:G:OP1	2.19	0.42
10:k:38:ILE:HD11	10:k:112:PHE:HZ	1.83	0.42
13:n:103:ARG:HH11	53:1:1287:A:H5'	1.84	0.42
20:u:27:VAL:HA	20:u:33:VAL:HA	2.01	0.42
28:D:24:THR:HG23	28:D:27:GLY:N	2.34	0.42
29:E:44:ARG:N	29:E:45:PRO:HD2	2.33	0.42
31:G:20:ARG:HD2	52:3:831:A:C5'	2.49	0.42
31:G:182:VAL:HG13	31:G:196:ASP:H	1.83	0.42
34:J:110:MET:HE3	34:J:139:THR:HG22	2.01	0.42
36:L:23:ALA:O	36:L:26:VAL:HG12	2.19	0.42
37:M:86:LYS:HB2	37:M:91:LEU:HD23	2.02	0.42
41:Q:100:ALA:O	41:Q:101:LEU:C	2.61	0.42
47:W:57:ALA:HA	47:W:60:ARG:NH1	2.33	0.42
51:a:221:GLY:N	53:1:2176:A:H5''	2.34	0.42
52:3:626:G:H2'	52:3:627:G:H8	1.84	0.42
52:3:784:A:H4'	53:1:1837:C:OP1	2.20	0.42
52:3:1014:A:H2'	52:3:1015:G:O4'	2.19	0.42
52:3:1137:C:H4'	52:3:1138:G:H21	1.83	0.42
52:3:1163:A:H2'	52:3:1164:G:H8	1.84	0.42
52:3:1391:U:H2'	52:3:1392:G:H8	1.83	0.42
53:1:355:U:H2'	53:1:356:G:H8	1.83	0.42
53:1:438:G:H2'	53:1:439:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:6:51:C:H2'	55:6:52:G:C8	2.55	0.42
55:6:59:A:H2'	55:6:60:U:H5'	2.01	0.42
1:b:76:VAL:HG22	1:b:114:GLN:NE2	2.35	0.42
6:g:8:LYS:HD2	6:g:8:LYS:C	2.45	0.42
6:g:41:LYS:HD2	6:g:44:ILE:HD12	2.01	0.42
19:t:59:ASN:O	19:t:84:TYR:N	2.50	0.42
23:x:9:LYS:HD3	53:1:397:U:OP2	2.18	0.42
30:F:26:ILE:O	30:F:26:ILE:HG23	2.20	0.42
35:K:18:VAL:O	35:K:22:ILE:HG13	2.19	0.42
42:R:25:GLY:H	52:3:1329:A:H5''	1.83	0.42
52:3:1195:C:H2'	52:3:1197:A:O4'	2.19	0.42
53:1:2366:A:H2'	53:1:2367:G:O4'	2.18	0.42
53:1:2564:A:C2	53:1:2647:U:H4'	2.54	0.42
53:1:2756:U:C1'	53:1:2757:A:H5''	2.49	0.42
55:5:35:A:H2'	55:5:36:U:C6	2.55	0.42
58:8:309:VAL:HG22	58:8:310:TYR:N	2.34	0.42
4:e:90:LEU:HD23	4:e:90:LEU:H	1.84	0.42
6:g:68:ARG:HD2	6:g:68:ARG:C	2.44	0.42
9:j:68:LYS:HD3	53:1:1022:G:N7	2.34	0.42
12:m:67:VAL:HG11	12:m:102:LEU:HD23	1.99	0.42
17:r:68:ARG:NH1	17:r:90:ARG:O	2.52	0.42
31:G:124:THR:HA	31:G:127:LYS:HZ3	1.84	0.42
33:I:18:LEU:O	33:I:19:PHE:HB2	2.18	0.42
37:M:79:ARG:HB2	52:3:878:A:OP1	2.18	0.42
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.84	0.42
50:Z:49:ALA:HA	52:3:723:U:O4	2.17	0.42
50:Z:54:ARG:HA	50:Z:57:LYS:HG2	2.01	0.42
52:3:370:C:H2'	52:3:371:A:C8	2.55	0.42
52:3:1033:G:C3'	52:3:1034:G:H5''	2.48	0.42
52:3:1463:U:H2'	52:3:1464:U:C6	2.55	0.42
53:1:184:C:H2'	53:1:185:G:H8	1.85	0.42
53:1:657:U:H2'	53:1:658:U:C6	2.55	0.42
53:1:828:U:H4'	53:1:831:G:N1	2.34	0.42
53:1:940:G:H2'	53:1:941:A:H5''	2.01	0.42
53:1:1666:G:H2'	53:1:1667:G:O4'	2.20	0.42
53:1:1779:U:H5	53:1:1784:A:N7	2.17	0.42
53:1:2742:G:O2'	53:1:2743:U:H5'	2.19	0.42
53:1:2786:U:H2'	53:1:2787:C:C6	2.54	0.42
58:8:187:ALA:O	58:8:190:LEU:HB2	2.19	0.42
58:8:224:ARG:HA	58:8:224:ARG:HD2	1.94	0.42
12:m:84:LYS:NZ	53:1:2250:G:OP1	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:o:83:LEU:HD11	14:o:114:GLY:HA3	2.01	0.42
15:p:79:VAL:HG13	15:p:80:VAL:HG13	2.01	0.42
18:s:57:ASN:OD1	53:1:495:G:H1'	2.19	0.42
18:s:85:ILE:N	18:s:85:ILE:CD1	2.82	0.42
21:v:10:LYS:HG3	21:v:11:GLU:HG3	2.01	0.42
21:v:64:VAL:O	21:v:64:VAL:HG13	2.19	0.42
24:y:41:HIS:CG	53:1:96:C:H4'	2.54	0.42
26:B:46:GLY:HA3	26:B:54:ILE:CG2	2.49	0.42
33:I:123:MET:HB2	33:I:128:VAL:HG12	2.01	0.42
33:I:160:LEU:HG	33:I:164:ARG:HH21	1.84	0.42
34:J:108:GLY:H	52:3:9:G:C4'	2.33	0.42
35:K:54:LEU:HD23	35:K:55:HIS:N	2.35	0.42
36:L:16:LYS:HG2	36:L:17:PHE:CD1	2.52	0.42
36:L:77:ARG:HG3	52:3:1381:U:H3	1.85	0.42
39:O:67:ILE:HG13	39:O:67:ILE:O	2.20	0.42
42:R:27:THR:OG1	42:R:28:ARG:N	2.52	0.42
42:R:53:ASP:OD1	42:R:53:ASP:N	2.51	0.42
52:3:128:G:O2'	52:3:129:A:H5'	2.19	0.42
52:3:212:G:H2'	52:3:213:G:C8	2.54	0.42
52:3:390:U:H2'	52:3:391:G:H8	1.85	0.42
52:3:1515:G:O2'	52:3:1516:G:H5'	2.20	0.42
53:1:211:C:H2'	53:1:212:G:H8	1.85	0.42
53:1:907:G:O2'	53:1:908:C:H5'	2.19	0.42
53:1:992:C:H2'	53:1:993:G:H8	1.83	0.42
53:1:1219:U:H2'	53:1:1220:G:C8	2.55	0.42
53:1:1417:C:H2'	53:1:1418:G:O4'	2.19	0.42
53:1:2155:U:H2'	53:1:2156:G:H5'	2.00	0.42
53:1:2391:G:H1'	53:1:2429:G:N2	2.34	0.42
53:1:2579:C:O2'	53:1:2580:U:H5'	2.19	0.42
53:1:2898:U:H2'	53:1:2899:A:C8	2.54	0.42
58:8:25:LYS:HZ3	58:8:105:VAL:HB	1.84	0.42
1:b:23:LEU:HD21	1:b:89:ASN:OD1	2.20	0.42
5:f:163:TYR:HB2	5:f:166:GLU:HB2	2.00	0.42
7:h:123:ILE:HD12	7:h:123:ILE:N	2.22	0.42
14:o:74:VAL:O	14:o:78:VAL:HG23	2.19	0.42
15:p:52:ARG:NH2	53:1:2720:U:OP1	2.52	0.42
17:r:74:ILE:CD1	53:1:992:C:H4'	2.50	0.42
32:H:39:ARG:NH1	32:H:54:ILE:HG23	2.34	0.42
42:R:40:GLU:N	42:R:40:GLU:OE2	2.53	0.42
44:T:61:GLN:NE2	44:T:65:LEU:HD13	2.34	0.42
48:X:72:GLU:OE2	52:3:1320:C:H4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:5:THR:OG1	51:a:6:LYS:N	2.52	0.42
51:a:46:VAL:HG13	51:a:212:VAL:HG22	2.00	0.42
52:3:9:G:H2'	52:3:10:A:H8	1.84	0.42
52:3:408:A:H2'	52:3:409:U:C6	2.55	0.42
52:3:592:G:H2'	52:3:593:U:O4'	2.20	0.42
52:3:1158:C:H2'	52:3:1159:U:H4'	2.01	0.42
52:3:1193:G:O2'	52:3:1194:U:H5'	2.19	0.42
53:1:581:C:H2'	53:1:582:A:C8	2.54	0.42
53:1:750:A:H2'	53:1:751:A:H5''	2.02	0.42
53:1:1764:C:O2'	53:1:1765:U:H5'	2.19	0.42
53:1:2800:A:C2	53:1:2895:G:H1'	2.55	0.42
57:7:15:G:H22	57:7:48:C:H42	1.66	0.42
1:b:34:GLU:OE2	1:b:35:LYS:N	2.53	0.42
16:q:5:ARG:CD	53:1:1250:G:H5''	2.50	0.42
21:v:20:LEU:HD11	21:v:27:PRO:HD3	2.02	0.42
23:x:5:GLN:O	23:x:73:ARG:NH2	2.52	0.42
26:B:33:SER:OG	26:B:34:GLY:N	2.53	0.42
33:I:96:ARG:HH22	33:I:114:ARG:NH1	2.17	0.42
41:Q:80:LEU:HB3	41:Q:97:VAL:HB	2.01	0.42
45:U:33:ILE:HD12	45:U:33:ILE:H	1.85	0.42
49:Y:54:GLN:HB3	49:Y:55:PRO:CD	2.50	0.42
50:Z:16:ARG:HE	50:Z:24:LYS:HZ1	1.66	0.42
52:3:1053:G:O6	52:3:1199:U:H2'	2.19	0.42
53:1:214:G:O2'	53:1:215:G:H5'	2.19	0.42
53:1:312:G:H2'	53:1:313:G:H8	1.85	0.42
53:1:386:G:H3'	53:1:387:U:C5'	2.50	0.42
53:1:595:C:H2'	53:1:596:U:C6	2.55	0.42
53:1:700:G:H2'	53:1:701:G:C8	2.54	0.42
53:1:1055:G:H1	53:1:1104:C:H42	1.66	0.42
53:1:1373:A:H4'	53:1:2212:A:H1'	2.00	0.42
53:1:1663:G:H1	53:1:1997:C:H42	1.68	0.42
53:1:2283:C:H2'	53:1:2284:A:O4'	2.20	0.42
53:1:2399:G:H2'	53:1:2400:G:H8	1.85	0.42
53:1:2573:C:OP1	53:1:2574:G:H5''	2.20	0.42
57:7:69:G:O2'	57:7:70:G:H5'	2.18	0.42
58:8:155:ARG:NH1	58:8:165:GLY:O	2.52	0.42
3:d:69:ARG:HD3	53:1:674:G:H1'	2.02	0.42
7:h:30:SER:O	53:1:1054:A:H4'	2.20	0.42
10:k:104:THR:HG22	10:k:105:ARG:N	2.35	0.42
18:s:90:LYS:HB2	18:s:92:ARG:NH1	2.34	0.42
20:u:40:LEU:HD12	20:u:61:GLU:OE2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:v:9:ARG:HG2	21:v:41:GLU:HB2	2.00	0.42
21:v:30:ILE:HG23	21:v:38:LEU:HB3	2.01	0.42
24:y:26:PHE:HA	24:y:29:ARG:NH2	2.35	0.42
27:C:26:LYS:HD2	27:C:26:LYS:C	2.44	0.42
31:G:67:LEU:HD23	31:G:157:PRO:HB3	2.02	0.42
34:J:20:VAL:HG23	34:J:31:SER:OG	2.20	0.42
38:N:78:ILE:HG22	38:N:82:ILE:HG13	2.02	0.42
38:N:94:ARG:HA	38:N:97:LEU:HB3	2.02	0.42
51:a:197:LYS:HD3	51:a:209:ILE:HG13	2.02	0.42
52:3:319:G:H2'	52:3:320:A:C8	2.55	0.42
52:3:370:C:H2'	52:3:371:A:H8	1.85	0.42
52:3:1128:C:O2'	52:3:1129:C:H5'	2.20	0.42
52:3:1342:C:H2'	52:3:1343:G:H8	1.84	0.42
52:3:1460:C:H2'	52:3:1461:G:H8	1.83	0.42
53:1:162:U:C2'	53:1:163:C:H5'	2.49	0.42
53:1:387:U:H5'	53:1:387:U:H6	1.85	0.42
53:1:1110:G:H2'	53:1:1111:A:H8	1.83	0.42
53:1:1287:A:C2	53:1:1649:G:H4'	2.54	0.42
53:1:1664:A:H2'	53:1:1664:A:N3	2.35	0.42
53:1:1779:U:OP1	53:1:1780:A:H5'	2.19	0.42
53:1:1817:G:C2	53:1:1818:U:H1'	2.55	0.42
53:1:1860:G:H2'	53:1:1861:G:C8	2.53	0.42
53:1:2146:C:H4'	53:1:2147:A:C5	2.54	0.42
53:1:2195:U:O2'	53:1:2196:C:H5'	2.20	0.42
53:1:2421:G:H2'	55:6:76:A:N6	2.34	0.42
55:5:61:C:H2'	55:5:62:C:C6	2.54	0.42
1:b:47:ARG:NH1	53:1:778:G:H5'	2.35	0.42
2:c:61:THR:HB	2:c:63:PRO:HD2	2.02	0.42
4:e:112:ASP:OD2	4:e:112:ASP:C	2.63	0.42
6:g:32:PRO:HA	23:x:38:TRP:CD1	2.55	0.42
8:i:75:ALA:HB2	8:i:112:LYS:HE3	2.02	0.42
9:j:31:GLU:HG3	9:j:142:ILE:HG12	2.02	0.42
11:l:85:VAL:O	11:l:86:GLU:HG2	2.20	0.42
14:o:17:LYS:NZ	53:1:2379:G:O2'	2.52	0.42
15:p:46:VAL:HA	15:p:59:THR:O	2.19	0.42
16:q:53:LYS:HE3	53:1:995:C:OP2	2.19	0.42
17:r:53:PHE:O	17:r:54:VAL:C	2.63	0.42
19:t:2:ILE:CD1	53:1:144:A:H4'	2.49	0.42
25:z:52:PHE:CG	54:2:83:G:H4'	2.55	0.42
32:H:54:ILE:HG23	32:H:54:ILE:O	2.19	0.42
42:R:86:ARG:HH22	52:3:1310:G:P	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:45:LYS:NZ	52:3:723:U:C1'	2.83	0.42
52:3:1528:U:H4'	52:3:1529:G:H21	1.84	0.42
53:1:839:U:H2'	53:1:840:C:C6	2.55	0.42
53:1:2041:U:H2'	53:1:2042:A:C8	2.55	0.42
57:7:25:C:H2'	57:7:26:A:H4'	2.01	0.42
58:8:152:MET:HE1	58:8:155:ARG:HE	1.85	0.42
1:b:184:GLU:HB3	1:b:187:CYS:SG	2.59	0.42
1:b:227:VAL:HG11	53:1:784:G:O6	2.20	0.42
1:b:231:HIS:O	1:b:232:GLY:O	2.36	0.42
3:d:90:GLN:HE21	3:d:92:HIS:CE1	2.38	0.42
3:d:94:GLN:HB2	53:1:660:C:OP1	2.19	0.42
3:d:149:ILE:CG2	3:d:188:MET:HG2	2.50	0.42
4:e:137:PHE:HA	4:e:138:PRO:HD3	1.91	0.42
22:w:14:ALA:HB1	53:1:2271:G:OP1	2.20	0.42
30:F:22:VAL:HG11	30:F:36:ARG:NH2	2.35	0.42
33:I:123:MET:O	33:I:143:SER:N	2.47	0.42
36:L:104:VAL:O	36:L:108:ARG:HG2	2.20	0.42
41:Q:98:ARG:NE	41:Q:103:CYS:SG	2.92	0.42
43:S:86:ALA:HB1	43:S:91:GLU:HB2	2.01	0.42
49:Y:55:PRO:O	49:Y:59:ARG:NH1	2.53	0.42
52:3:902:G:H2'	52:3:903:G:H8	1.85	0.42
52:3:1120:C:H2'	52:3:1121:U:C6	2.55	0.42
53:1:861:A:H2'	53:1:862:G:O4'	2.19	0.42
53:1:1039:A:H2	53:1:1116:G:H22	1.67	0.42
53:1:1759:A:C2	53:1:2697:G:H1'	2.53	0.42
53:1:2559:C:H2'	53:1:2560:A:H8	1.85	0.42
54:2:19:C:H2'	54:2:20:G:H8	1.83	0.42
54:2:108:A:H5'	54:2:109:A:O5'	2.20	0.42
55:5:43:A:H2'	55:5:44:A:C8	2.55	0.42
3:d:162:ARG:NH1	53:1:340:A:O2'	2.52	0.41
5:f:173:ALA:O	5:f:175:LYS:N	2.50	0.41
6:g:86:ASP:O	6:g:87:GLU:HG2	2.20	0.41
8:i:123:ALA:HA	8:i:126:ARG:NE	2.34	0.41
10:k:2:ILE:HG23	10:k:6:THR:HG21	2.01	0.41
14:o:31:THR:HG22	14:o:32:PRO:HD2	2.02	0.41
15:p:63:ILE:HA	15:p:68:GLY:HA2	2.02	0.41
20:u:6:ARG:O	20:u:24:VAL:HB	2.20	0.41
22:w:21:ARG:HD2	22:w:27:VAL:HG12	2.01	0.41
23:x:39:VAL:HG12	23:x:42:GLU:H	1.85	0.41
38:N:29:ILE:HA	38:N:64:ILE:O	2.20	0.41
40:P:93:GLU:HG3	40:P:97:ARG:HH11	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:12:LYS:O	45:U:13:LYS:HB2	2.19	0.41
49:Y:67:HIS:HB3	52:3:262:A:H5'	2.01	0.41
52:3:114:U:O2'	52:3:115:G:H5'	2.19	0.41
52:3:1114:C:H2'	52:3:1115:U:O4'	2.19	0.41
52:3:1202:U:C2'	52:3:1203:C:H5'	2.50	0.41
53:1:296:U:H2'	53:1:297:G:C8	2.54	0.41
53:1:2246:G:H2'	53:1:2247:A:C8	2.54	0.41
53:1:2272:U:H5''	53:1:2273:A:OP1	2.19	0.41
53:1:2327:A:H2'	53:1:2328:A:C8	2.55	0.41
58:8:75:ARG:NH2	58:8:197:ASP:O	2.52	0.41
3:d:25:GLU:OE2	11:l:7:SER:OG	2.38	0.41
3:d:76:PRO:HA	3:d:82:GLY:HA2	2.02	0.41
4:e:119:LYS:HA	4:e:119:LYS:HD3	1.90	0.41
5:f:154:GLU:HG2	5:f:156:TYR:H	1.85	0.41
6:g:71:LYS:HD3	6:g:71:LYS:HA	1.86	0.41
6:g:132:PHE:HB2	6:g:140:ALA:HB3	2.01	0.41
8:i:73:PRO:HA	8:i:74:PRO:HD3	1.83	0.41
15:p:102:ARG:NH2	53:1:1754:A:O2'	2.53	0.41
16:q:50:ARG:O	16:q:54:ARG:HG3	2.20	0.41
28:D:41:ARG:HD3	28:D:41:ARG:HA	1.78	0.41
32:H:112:ALA:HB1	32:H:199:VAL:HG13	2.03	0.41
33:I:184:LYS:HA	33:I:185:PRO:HD3	1.94	0.41
34:J:113:VAL:HG13	34:J:114:LEU:HD13	2.02	0.41
38:N:98:ARG:NH1	38:N:103:VAL:HG21	2.35	0.41
39:O:10:LEU:HD23	39:O:72:ARG:O	2.19	0.41
45:U:6:LEU:HD23	45:U:19:VAL:HA	2.02	0.41
49:Y:54:GLN:HB3	49:Y:55:PRO:HD3	2.01	0.41
51:a:218:MET:HE1	53:1:2128:G:H4'	2.02	0.41
52:3:530:G:H3'	52:3:531:U:C5'	2.50	0.41
52:3:668:G:H2'	52:3:669:G:H8	1.84	0.41
53:1:1287:A:O2'	53:1:1288:G:H5'	2.20	0.41
53:1:1463:C:H2'	53:1:1464:G:H8	1.85	0.41
53:1:1637:A:H5'	53:1:1760:C:O2'	2.19	0.41
53:1:2800:A:H3'	53:1:2801:G:C5'	2.43	0.41
58:8:157:LEU:O	58:8:160:GLN:HG3	2.20	0.41
1:b:52:HIS:CE1	1:b:218:THR:HG23	2.56	0.41
1:b:203:VAL:O	1:b:204:LEU:C	2.63	0.41
2:c:24:VAL:HG22	2:c:25:THR:N	2.34	0.41
3:d:99:LYS:HZ1	53:1:601:C:H4'	1.82	0.41
7:h:13:ALA:HB1	7:h:53:ARG:HH22	1.85	0.41
11:l:19:LEU:HD22	11:l:19:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:75:GLU:HA	53:1:957:C:OP2	2.20	0.41
25:z:35:VAL:HG22	25:z:37:ARG:NH1	2.36	0.41
31:G:160:LEU:HD23	31:G:180:ILE:HG21	2.03	0.41
40:P:48:GLY:O	40:P:68:ARG:NH1	2.53	0.41
41:Q:45:ASN:ND2	52:3:529:G:O6	2.53	0.41
42:R:6:ILE:HG23	42:R:7:ASN:N	2.35	0.41
45:U:28:ARG:NH1	45:U:29:ASN:HD21	2.19	0.41
50:Z:35:GLU:O	50:Z:36:PHE:HB2	2.20	0.41
52:3:270:A:H2'	52:3:271:C:C6	2.55	0.41
52:3:1139:G:H5''	52:3:1140:C:H5	1.84	0.41
53:1:30:G:H2'	53:1:31:C:C6	2.55	0.41
53:1:1376:C:H2'	53:1:1377:G:O4'	2.21	0.41
53:1:1709:U:O2'	53:1:2859:G:H1'	2.20	0.41
53:1:2103:C:H2'	53:1:2104:C:C6	2.54	0.41
53:1:2360:G:C2'	53:1:2361:G:H5'	2.51	0.41
53:1:2498:C:O2'	53:1:2499:C:H5'	2.20	0.41
58:8:121:LEU:HD23	58:8:121:LEU:C	2.45	0.41
58:8:289:ARG:HH12	58:8:336:THR:HA	1.85	0.41
3:d:189:THR:O	3:d:193:VAL:HG23	2.20	0.41
14:o:7:ARG:HD2	14:o:97:PHE:CZ	2.55	0.41
14:o:33:ARG:HB2	54:2:52:A:N6	2.35	0.41
15:p:105:LYS:O	15:p:108:ARG:NH2	2.49	0.41
18:s:6:LYS:HG2	53:1:494:G:H4'	2.03	0.41
19:t:50:LEU:N	19:t:50:LEU:HD22	2.33	0.41
20:u:27:VAL:HG12	20:u:33:VAL:HG12	2.02	0.41
32:H:120:THR:HA	32:H:123:LEU:HD12	2.03	0.41
33:I:123:MET:HA	33:I:128:VAL:HA	2.02	0.41
37:M:30:LYS:O	37:M:33:VAL:HG12	2.21	0.41
37:M:77:VAL:HG11	37:M:127:TYR:CD2	2.55	0.41
38:N:41:GLU:O	38:N:44:ARG:NE	2.53	0.41
52:3:422:C:H5''	52:3:423:G:O5'	2.20	0.41
52:3:423:G:C2'	52:3:424:G:H5'	2.50	0.41
52:3:424:G:O2'	52:3:425:G:H5'	2.19	0.41
52:3:785:G:O2'	52:3:786:G:H5'	2.20	0.41
52:3:1202:U:H2'	52:3:1203:C:H5'	2.02	0.41
52:3:1228:C:H2'	52:3:1229:A:C8	2.55	0.41
53:1:2293:G:H2'	53:1:2294:G:C8	2.54	0.41
57:7:76:A:N3	58:8:227:VAL:HG11	2.36	0.41
5:f:55:ASP:OD2	5:f:55:ASP:N	2.53	0.41
7:h:3:LEU:HD13	53:1:1044:C:OP2	2.19	0.41
9:j:57:LEU:O	9:j:58:ASN:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:80:HIS:O	9:j:81:ILE:C	2.62	0.41
25:z:14:GLY:O	25:z:15:ARG:NH1	2.49	0.41
29:E:28:LEU:C	29:E:28:LEU:HD23	2.46	0.41
33:I:141:VAL:HA	33:I:180:THR:HA	2.01	0.41
43:S:42:ASN:C	43:S:46:LYS:HZ2	2.28	0.41
46:V:62:GLU:H	46:V:62:GLU:CD	2.29	0.41
48:X:18:VAL:O	48:X:22:VAL:HG23	2.20	0.41
52:3:34:C:H2'	52:3:35:G:C8	2.54	0.41
52:3:1216:A:H2'	52:3:1217:C:C6	2.55	0.41
52:3:1301:U:O2	52:3:1301:U:C2'	2.67	0.41
52:3:1406:U:C2'	52:3:1407:C:H5'	2.51	0.41
53:1:1181:U:H2'	53:1:1182:G:C8	2.55	0.41
53:1:1427:A:H4'	53:1:1428:C:O4'	2.20	0.41
53:1:2462:C:H2'	53:1:2463:C:H6	1.86	0.41
53:1:2772:C:H2'	53:1:2773:C:C6	2.55	0.41
55:5:50:U:H2'	55:5:51:C:C6	2.56	0.41
57:7:46:G:O2'	57:7:47:U:H5''	2.19	0.41
57:7:50:U:H3	57:7:64:A:H61	1.68	0.41
58:8:151:GLU:HG3	58:8:170:ILE:HG21	2.03	0.41
3:d:47:LYS:HE3	53:1:451:U:H4'	2.02	0.41
5:f:173:ALA:C	5:f:175:LYS:H	2.29	0.41
12:m:69:PRO:HB3	12:m:92:TRP:O	2.21	0.41
13:n:38:LEU:HB3	13:n:39:PRO:HD3	2.03	0.41
15:p:77:SER:HA	15:p:78:PRO:HD3	1.92	0.41
23:x:27:ARG:NH1	53:1:1808:A:C6	2.88	0.41
31:G:89:PHE:CZ	31:G:153:MET:HA	2.56	0.41
39:O:22:THR:O	39:O:26:VAL:HG13	2.21	0.41
41:Q:33:CYS:N	41:Q:54:VAL:HG23	2.34	0.41
44:T:32:THR:OG1	44:T:84:LEU:HD21	2.21	0.41
44:T:32:THR:CG2	44:T:84:LEU:HD21	2.51	0.41
46:V:19:SER:HB3	46:V:70:LYS:NZ	2.35	0.41
48:X:45:GLY:H	48:X:61:VAL:HG13	1.85	0.41
52:3:181:A:H61	52:3:194:C:H2'	1.84	0.41
52:3:303:A:H2'	52:3:304:U:O4'	2.21	0.41
52:3:600:A:H2'	52:3:601:G:C8	2.56	0.41
53:1:315:G:H2'	53:1:316:C:O4'	2.20	0.41
53:1:1300:G:C3'	53:1:1301:A:H5''	2.50	0.41
53:1:1409:U:H2'	53:1:1410:G:C8	2.55	0.41
53:1:1746:A:H2'	53:1:1747:U:C6	2.56	0.41
54:2:44:G:H1'	54:2:47:C:H42	1.86	0.41
58:8:211:PHE:H	58:8:295:LYS:HD3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:319:ARG:HD3	58:8:384:VAL:HG11	2.02	0.41
2:c:110:THR:HG23	2:c:171:THR:HG22	2.03	0.41
2:c:123:LYS:HZ1	53:1:2724:U:C5'	2.33	0.41
8:i:25:PRO:HB2	57:7:56:C:OP2	2.21	0.41
8:i:107:GLU:HG3	8:i:108:ILE:HG13	2.02	0.41
9:j:7:LYS:HA	9:j:8:PRO:HD3	1.91	0.41
31:G:94:ARG:NH2	52:3:1100:C:H3'	2.36	0.41
31:G:165:ALA:HB3	31:G:190:SER:HB3	2.03	0.41
32:H:179:ALA:HB1	32:H:202:PHE:HE1	1.85	0.41
34:J:89:THR:HG23	52:3:864:A:H5''	2.03	0.41
37:M:64:TYR:HD1	37:M:69:ALA:HA	1.86	0.41
38:N:118:ARG:HH22	38:N:122:ARG:HE	1.69	0.41
44:T:86:LEU:N	44:T:86:LEU:HD23	2.36	0.41
45:U:22:ALA:HA	45:U:33:ILE:CD1	2.51	0.41
45:U:22:ALA:HA	45:U:33:ILE:HD12	2.03	0.41
50:Z:17:ARG:HA	50:Z:20:ARG:HH11	1.86	0.41
51:a:63:THR:HG21	51:a:192:LEU:HD23	2.03	0.41
52:3:79:G:H2'	52:3:80:A:O4'	2.21	0.41
52:3:438:U:O2'	52:3:439:U:H6	2.04	0.41
53:1:857:G:H2'	53:1:858:G:O4'	2.20	0.41
53:1:859:G:O2'	53:1:860:U:C6	2.70	0.41
53:1:1357:C:H2'	53:1:1358:G:O4'	2.21	0.41
53:1:1549:A:H2'	53:1:1550:C:C6	2.55	0.41
53:1:2538:C:H2'	53:1:2539:C:C6	2.56	0.41
53:1:2662:A:H2'	53:1:2663:G:O4'	2.21	0.41
55:5:51:C:H2'	55:5:52:G:H8	1.86	0.41
3:d:47:LYS:CE	53:1:451:U:H4'	2.51	0.41
3:d:63:LYS:HB3	3:d:63:LYS:HE3	1.84	0.41
4:e:140:ILE:HD11	4:e:145:VAL:HG11	2.03	0.41
10:k:110:GLU:HA	10:k:113:MET:HE2	2.02	0.41
19:t:24:MET:O	19:t:24:MET:HE3	2.20	0.41
33:I:127:ARG:HH21	52:3:619:U:H4'	1.85	0.41
50:Z:9:GLU:HB2	50:Z:10:PRO:CD	2.50	0.41
51:a:64:VAL:HG13	51:a:64:VAL:O	2.21	0.41
52:3:5:U:H4'	52:3:6:G:C4	2.55	0.41
52:3:7:A:H5'	52:3:298:A:H5'	2.03	0.41
52:3:54:C:H2'	52:3:352:C:H41	1.86	0.41
52:3:358:U:H4'	58:8:225:GLY:N	2.36	0.41
52:3:580:C:H2'	52:3:581:G:O4'	2.21	0.41
52:3:730:G:C2'	52:3:731:G:H5'	2.49	0.41
52:3:763:G:H2'	52:3:764:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1245:C:H2'	52:3:1246:A:H8	1.86	0.41
53:1:115:C:O2'	53:1:116:C:H5'	2.21	0.41
53:1:548:G:H2'	53:1:549:G:O4'	2.20	0.41
53:1:687:C:H2'	53:1:688:U:O4'	2.20	0.41
53:1:1089:A:H2	53:1:1090:A:H62	1.69	0.41
58:8:148:GLU:O	58:8:151:GLU:HB3	2.20	0.41
1:b:158:GLY:N	1:b:194:VAL:HG23	2.36	0.41
2:c:108:ASP:OD1	2:c:204:LYS:HG3	2.21	0.41
3:d:83:VAL:HG11	3:d:86:ALA:HA	2.03	0.41
4:e:70:ARG:C	4:e:80:GLN:HE22	2.29	0.41
4:e:114:ARG:HH11	42:R:70:ARG:HD2	1.85	0.41
6:g:73:ASN:HD22	6:g:76:GLU:HA	1.85	0.41
8:i:55:PRO:HG2	8:i:71:LYS:HB2	2.03	0.41
12:m:76:LYS:H	53:1:957:C:P	2.44	0.41
16:q:111:LYS:HG2	17:r:48:LYS:NZ	2.36	0.41
17:r:57:GLY:HA2	17:r:102:SER:HB3	2.03	0.41
19:t:57:VAL:HG22	19:t:58:VAL:N	2.35	0.41
21:v:68:LYS:H	21:v:68:LYS:HD2	1.85	0.41
23:x:56:ARG:NH1	53:1:372:G:N7	2.68	0.41
26:B:24:VAL:HG13	26:B:25:THR:N	2.36	0.41
27:C:5:ARG:NH1	53:1:2285:C:OP2	2.51	0.41
30:F:37:GLN:O	30:F:37:GLN:HG2	2.21	0.41
31:G:17:HIS:H	31:G:188:THR:HG21	1.85	0.41
32:H:13:ILE:HG13	32:H:14:VAL:HG12	2.02	0.41
32:H:39:ARG:O	32:H:43:THR:HG23	2.21	0.41
33:I:53:GLN:NE2	33:I:198:LEU:HG	2.36	0.41
33:I:67:LEU:HB3	52:3:546:A:OP2	2.21	0.41
33:I:143:SER:OG	33:I:144:ILE:N	2.54	0.41
33:I:197:HIS:O	33:I:201:GLU:HG3	2.21	0.41
35:K:46:GLN:HG2	35:K:47:LEU:O	2.21	0.41
35:K:91:ARG:HE	35:K:92:THR:HG23	1.85	0.41
36:L:114:SER:OG	52:3:1240:U:OP2	2.38	0.41
37:M:52:GLY:HA3	37:M:56:PRO:HA	2.02	0.41
42:R:113:LYS:N	42:R:114:PRO:CD	2.84	0.41
43:S:52:ARG:CD	52:3:1317:C:N3	2.84	0.41
45:U:39:PHE:HE2	45:U:70:ARG:HH21	1.69	0.41
49:Y:67:HIS:C	49:Y:69:ASN:H	2.29	0.41
49:Y:75:LYS:O	49:Y:79:THR:N	2.53	0.41
50:Z:31:VAL:HG12	50:Z:31:VAL:O	2.21	0.41
51:a:3:LYS:HD2	53:1:2108:A:OP1	2.21	0.41
52:3:31:G:N2	52:3:47:C:H5''	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:246:A:H62	52:3:281:G:N2	2.19	0.41
52:3:895:G:H2'	52:3:896:C:C6	2.55	0.41
52:3:1023:U:H2'	52:3:1024:G:C8	2.56	0.41
52:3:1040:U:H2'	52:3:1041:G:C8	2.56	0.41
52:3:1271:A:H5'	52:3:1314:C:H5''	2.02	0.41
53:1:63:A:H2'	53:1:64:A:H8	1.86	0.41
53:1:158:U:H2'	53:1:159:G:O4'	2.21	0.41
53:1:175:G:H2'	53:1:176:A:C8	2.56	0.41
53:1:872:U:H2'	53:1:873:C:C6	2.56	0.41
53:1:910:A:H2'	53:1:911:A:C8	2.56	0.41
53:1:934:U:H6	53:1:934:U:O5'	2.04	0.41
53:1:1026:G:H2'	53:1:1027:A:C8	2.54	0.41
53:1:1438:U:O2'	53:1:1439:A:H5'	2.21	0.41
53:1:1526:C:H2'	53:1:1527:G:O4'	2.21	0.41
53:1:1859:U:H2'	53:1:1860:G:H8	1.86	0.41
53:1:1980:G:O2'	53:1:1982:U:OP2	2.38	0.41
53:1:2093:G:O6	53:1:2225:A:H5''	2.20	0.41
53:1:2217:G:O2'	53:1:2218:G:H5'	2.21	0.41
53:1:2292:U:H2'	53:1:2293:G:C8	2.56	0.41
55:5:62:C:H2'	55:5:63:G:C8	2.56	0.41
55:6:68:C:H2'	55:6:69:C:C6	2.56	0.41
4:e:111:ARG:HG2	4:e:111:ARG:HH21	1.85	0.41
7:h:8:LYS:HE2	7:h:8:LYS:HA	2.03	0.41
9:j:35:ARG:HA	9:j:40:HIS:CD2	2.55	0.41
17:r:24:LYS:HA	17:r:94:THR:OG1	2.20	0.41
21:v:43:ASP:HB3	21:v:46:LYS:HB2	2.02	0.41
24:y:49:ASP:HA	24:y:52:ARG:NH2	2.36	0.41
26:B:15:ARG:NH1	53:1:1264:A:OP1	2.54	0.41
39:O:42:LEU:HD11	52:3:1280:A:C5'	2.51	0.41
39:O:46:LYS:NZ	39:O:68:ARG:HG2	2.27	0.41
41:Q:11:ARG:HB3	52:3:562:U:O2'	2.20	0.41
43:S:41:TRP:O	43:S:44:VAL:HG22	2.21	0.41
49:Y:15:LYS:HB2	49:Y:15:LYS:HE3	1.86	0.41
51:a:67:HIS:HB2	51:a:188:ASN:HD21	1.85	0.41
52:3:123:U:H5''	52:3:311:C:O2'	2.21	0.41
52:3:219:U:H2'	52:3:220:G:H8	1.86	0.41
52:3:410:G:H2'	52:3:429:U:O4	2.21	0.41
52:3:423:G:H2'	52:3:424:G:H5'	2.02	0.41
52:3:448:A:H3'	52:3:449:G:C8	2.56	0.41
52:3:890:G:H2'	52:3:906:A:N6	2.36	0.41
53:1:306:U:H2'	53:1:307:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:816:C:H2'	53:1:817:C:C6	2.55	0.41
53:1:1337:G:H2'	53:1:1338:G:H8	1.86	0.41
53:1:1501:G:O2'	53:1:1502:A:H5'	2.21	0.41
53:1:1690:A:H2'	53:1:1691:C:O4'	2.21	0.41
54:2:3:C:C3'	54:2:4:C:C5'	2.96	0.41
54:2:105:G:O2'	54:2:106:G:H5'	2.21	0.41
55:5:51:C:H2'	55:5:52:G:C8	2.55	0.41
1:b:154:ALA:HB2	1:b:161:VAL:HG23	2.03	0.40
10:k:34:GLY:O	10:k:35:VAL:C	2.64	0.40
10:k:35:VAL:HB	10:k:106:GLU:OE1	2.21	0.40
11:l:55:MET:HE3	53:1:2392:A:C2	2.57	0.40
34:J:108:GLY:C	34:J:110:MET:H	2.29	0.40
41:Q:76:HIS:O	41:Q:77:SER:C	2.63	0.40
43:S:56:PRO:HA	43:S:59:GLN:HG2	2.03	0.40
48:X:5:LYS:HG3	48:X:6:LYS:HG2	2.04	0.40
48:X:47:THR:HA	48:X:60:PHE:HA	2.02	0.40
53:1:155:A:H2'	53:1:156:A:H8	1.86	0.40
53:1:700:G:H2'	53:1:701:G:H8	1.86	0.40
53:1:1343:G:H1'	53:1:1597:A:C4	2.56	0.40
53:1:1478:G:O2'	53:1:1479:G:H5'	2.21	0.40
1:b:184:GLU:HG3	1:b:186:ASP:H	1.86	0.40
1:b:245:THR:C	1:b:247:TRP:H	2.29	0.40
2:c:31:ALA:HB1	2:c:95:SER:HB3	2.03	0.40
5:f:174:LYS:O	5:f:175:LYS:HB2	2.21	0.40
10:k:13:ASN:HD21	10:k:98:ARG:H	1.69	0.40
10:k:76:VAL:H	15:p:72:VAL:CG1	2.30	0.40
10:k:97:THR:OG1	10:k:98:ARG:N	2.53	0.40
13:n:24:MET:HE3	53:1:1277:G:O2'	2.20	0.40
19:t:8:LEU:HD21	19:t:50:LEU:HD11	2.02	0.40
22:w:29:ALA:N	22:w:60:ASP:OD1	2.54	0.40
23:x:53:LYS:O	23:x:57:VAL:HG23	2.21	0.40
29:E:24:LYS:HD2	29:E:46:LYS:HE3	2.03	0.40
32:H:14:VAL:HG13	32:H:15:LYS:N	2.37	0.40
33:I:144:ILE:HD12	33:I:144:ILE:N	2.37	0.40
36:L:16:LYS:HZ2	36:L:17:PHE:HE1	1.68	0.40
37:M:113:ARG:HD2	37:M:113:ARG:O	2.22	0.40
38:N:17:ARG:HB2	38:N:65:THR:OG1	2.22	0.40
46:V:29:LYS:HB2	46:V:36:PHE:CE1	2.56	0.40
46:V:80:LYS:HG2	46:V:81:ALA:H	1.84	0.40
48:X:76:THR:OG1	48:X:77:ARG:N	2.55	0.40
51:a:7:ARG:HB3	53:1:2129:C:OP1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:12:U:H4'	52:3:526:C:H4'	2.02	0.40
52:3:1370:G:H2'	52:3:1371:G:H8	1.86	0.40
52:3:1486:G:H2'	52:3:1487:G:O4'	2.22	0.40
53:1:96:C:H2'	53:1:97:C:C6	2.57	0.40
53:1:792:A:H3'	53:1:793:A:H5'	2.03	0.40
53:1:890:C:H2'	53:1:891:G:H5'	2.02	0.40
53:1:898:C:H2'	53:1:899:A:O4'	2.21	0.40
58:8:128:VAL:O	58:8:128:VAL:HG13	2.20	0.40
3:d:45:ALA:HB2	53:1:38:A:H4'	2.02	0.40
7:h:66:GLY:HA2	7:h:69:PHE:HE1	1.86	0.40
20:u:82:VAL:HG12	20:u:83:GLY:N	2.37	0.40
33:I:5:GLY:O	33:I:7:LYS:N	2.54	0.40
34:J:92:ARG:O	34:J:93:VAL:C	2.64	0.40
34:J:160:VAL:HA	34:J:163:ILE:CD1	2.51	0.40
39:O:22:THR:O	39:O:26:VAL:HG22	2.21	0.40
46:V:21:VAL:O	46:V:21:VAL:HG13	2.21	0.40
52:3:393:A:O2'	52:3:394:G:H5'	2.20	0.40
52:3:1138:G:H3'	52:3:1138:G:N3	2.37	0.40
52:3:1270:G:H2'	52:3:1271:A:H8	1.85	0.40
52:3:1315:U:H2'	52:3:1316:G:O4'	2.22	0.40
53:1:519:U:H2'	53:1:520:G:H8	1.87	0.40
53:1:1060:U:H4'	53:1:1061:U:C5'	2.50	0.40
53:1:1268:A:H2'	53:1:1269:A:O4'	2.20	0.40
53:1:1388:G:H2'	53:1:1389:G:C8	2.56	0.40
53:1:1528:A:H2'	53:1:1529:G:H5'	2.02	0.40
53:1:2538:C:H2'	53:1:2539:C:H6	1.85	0.40
1:b:5:CYS:SG	1:b:12:ARG:NH2	2.94	0.40
1:b:206:LYS:HB3	53:1:729:G:N7	2.37	0.40
10:k:90:ASN:OD1	10:k:91:SER:N	2.54	0.40
12:m:18:ARG:HH12	54:2:80:U:P	2.45	0.40
19:t:32:LEU:HD23	19:t:32:LEU:H	1.86	0.40
29:E:8:GLY:O	29:E:12:ARG:NH2	2.53	0.40
33:I:99:ASN:O	33:I:103:ARG:HG2	2.20	0.40
34:J:152:VAL:HG23	34:J:163:ILE:HD12	2.04	0.40
35:K:81:ASN:HB3	35:K:84:VAL:HG22	2.04	0.40
39:O:17:LEU:HD23	39:O:20:GLN:HE21	1.86	0.40
40:P:105:ARG:HD2	40:P:105:ARG:HA	1.71	0.40
41:Q:13:ARG:HD3	41:Q:14:LYS:H	1.86	0.40
51:a:190:GLU:HA	51:a:193:LEU:HG	2.02	0.40
52:3:701:U:C4'	52:3:703:G:H1'	2.50	0.40
52:3:1033:G:C2'	52:3:1034:G:H5''	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1264:U:H2'	52:3:1265:C:C6	2.56	0.40
52:3:1514:G:O2'	52:3:1515:G:H5'	2.21	0.40
53:1:163:C:H2'	53:1:164:C:O4'	2.21	0.40
53:1:295:G:O2'	53:1:296:U:H5'	2.22	0.40
53:1:534:U:H2'	53:1:535:G:H8	1.87	0.40
53:1:717:C:H2'	53:1:718:A:H5'	2.02	0.40
53:1:783:A:H2'	53:1:784:G:H5'	2.04	0.40
53:1:859:G:C2'	53:1:860:U:OP2	2.70	0.40
53:1:1386:C:H2'	53:1:1387:A:H8	1.86	0.40
53:1:1388:G:H2'	53:1:1389:G:H8	1.87	0.40
53:1:1680:U:H2'	53:1:1681:G:H5'	2.02	0.40
53:1:1726:C:H2'	53:1:1727:C:C6	2.56	0.40
53:1:1859:U:H2'	53:1:1860:G:C8	2.56	0.40
53:1:2224:G:H4'	53:1:2226:C:C2	2.56	0.40
53:1:2417:C:H2'	53:1:2418:A:H8	1.86	0.40
53:1:2441:U:H2'	53:1:2442:C:C6	2.57	0.40
54:2:3:C:H42	54:2:117:G:H1	1.69	0.40
55:6:59:A:C2'	55:6:60:U:H5'	2.52	0.40
57:7:76:A:C4	58:8:227:VAL:HG11	2.56	0.40
1:b:11:GLY:O	1:b:206:LYS:HG2	2.21	0.40
1:b:106:PRO:HD2	1:b:109:LEU:HD22	2.03	0.40
1:b:179:GLU:HG3	53:1:1799:G:N7	2.36	0.40
8:i:25:PRO:O	8:i:29:GLN:HG3	2.22	0.40
9:j:1:MET:SD	9:j:1:MET:N	2.85	0.40
10:k:37:ASP:OD1	10:k:38:ILE:N	2.50	0.40
12:m:24:THR:HA	12:m:101:VAL:HG23	2.04	0.40
13:n:29:VAL:O	13:n:78:LYS:HD3	2.22	0.40
16:q:50:ARG:HG2	53:1:1156:A:C8	2.56	0.40
17:r:77:PHE:O	17:r:78:ARG:HD2	2.21	0.40
19:t:6:ARG:CZ	53:1:144:A:H5'	2.50	0.40
26:B:11:LYS:HD3	26:B:11:LYS:HA	1.95	0.40
28:D:3:ARG:HD2	53:1:1613:G:O2'	2.21	0.40
28:D:26:ASN:ND2	53:1:682:G:H5'	2.35	0.40
29:E:56:LEU:HD23	29:E:56:LEU:C	2.47	0.40
35:K:50:PRO:HG3	35:K:55:HIS:HE1	1.86	0.40
40:P:43:TRP:CZ2	52:3:686:U:H1'	2.56	0.40
42:R:103:THR:OG1	42:R:104:ASN:N	2.55	0.40
42:R:108:ARG:HA	42:R:108:ARG:HD2	1.84	0.40
50:Z:36:PHE:C	50:Z:38:GLU:N	2.79	0.40
52:3:886:G:H2'	52:3:887:G:H8	1.86	0.40
52:3:1384:C:H2'	52:3:1385:G:H8	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:184:C:H4'	53:1:217:A:C2	2.56	0.40
53:1:244:A:H1'	53:1:255:A:N6	2.36	0.40
53:1:333:G:N3	53:1:333:G:H2'	2.37	0.40
53:1:619:G:H3'	53:1:620:G:H21	1.86	0.40
53:1:759:G:H2'	53:1:760:G:H8	1.87	0.40
53:1:2707:U:H2'	53:1:2708:G:C8	2.55	0.40
53:1:2709:G:H2'	53:1:2710:C:C6	2.56	0.40
53:1:2743:U:C3'	53:1:2744:G:H5''	2.51	0.40
54:2:88:C:C5'	54:2:89:U:OP1	2.67	0.40
55:6:35:A:H2'	55:6:36:U:C6	2.57	0.40
56:4:21:C:O2'	56:4:22:A:H5'	2.21	0.40
57:7:50:U:H2'	57:7:51:U:C6	2.56	0.40
58:8:295:LYS:HE2	58:8:298:THR:HG21	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	236/271 (87%)	208 (88%)	23 (10%)	5 (2%)	5	31
2	c	76/209 (36%)	66 (87%)	10 (13%)	0	100	100
3	d	183/201 (91%)	153 (84%)	28 (15%)	2 (1%)	11	42
4	e	175/177 (99%)	154 (88%)	19 (11%)	2 (1%)	11	42
5	f	116/176 (66%)	105 (90%)	8 (7%)	3 (3%)	4	28
6	g	101/149 (68%)	90 (89%)	10 (10%)	1 (1%)	12	43
7	h	129/131 (98%)	95 (74%)	28 (22%)	6 (5%)	2	18
8	i	139/141 (99%)	122 (88%)	15 (11%)	2 (1%)	9	37
9	j	140/142 (99%)	127 (91%)	12 (9%)	1 (1%)	18	50
10	k	120/122 (98%)	103 (86%)	14 (12%)	3 (2%)	4	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	l	141/143 (99%)	119 (84%)	16 (11%)	6 (4%)	2	19
12	m	134/136 (98%)	113 (84%)	19 (14%)	2 (2%)	8	36
13	n	118/120 (98%)	97 (82%)	19 (16%)	2 (2%)	7	34
14	o	114/116 (98%)	99 (87%)	13 (11%)	2 (2%)	6	34
15	p	112/114 (98%)	92 (82%)	20 (18%)	0	100	100
16	q	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
17	r	101/103 (98%)	85 (84%)	14 (14%)	2 (2%)	6	32
18	s	108/110 (98%)	92 (85%)	15 (14%)	1 (1%)	14	45
19	t	91/93 (98%)	83 (91%)	8 (9%)	0	100	100
20	u	100/102 (98%)	85 (85%)	10 (10%)	5 (5%)	1	17
21	v	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
22	w	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
25	z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
26	B	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
27	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
28	D	44/46 (96%)	36 (82%)	8 (18%)	0	100	100
29	E	62/64 (97%)	53 (86%)	7 (11%)	2 (3%)	3	25
30	F	36/38 (95%)	28 (78%)	8 (22%)	0	100	100
31	G	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
32	H	204/206 (99%)	187 (92%)	16 (8%)	1 (0%)	24	56
33	I	203/205 (99%)	172 (85%)	31 (15%)	0	100	100
34	J	155/157 (99%)	126 (81%)	25 (16%)	4 (3%)	4	28
35	K	98/100 (98%)	79 (81%)	12 (12%)	7 (7%)	1	12
36	L	149/151 (99%)	133 (89%)	16 (11%)	0	100	100
37	M	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	48
38	N	125/127 (98%)	101 (81%)	20 (16%)	4 (3%)	3	25
39	O	96/98 (98%)	82 (85%)	10 (10%)	4 (4%)	2	20
40	P	114/116 (98%)	89 (78%)	21 (18%)	4 (4%)	3	24
41	Q	121/123 (98%)	95 (78%)	18 (15%)	8 (7%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	R	112/114 (98%)	96 (86%)	13 (12%)	3 (3%)	4	27
43	S	98/100 (98%)	81 (83%)	15 (15%)	2 (2%)	6	32
44	T	86/88 (98%)	78 (91%)	7 (8%)	1 (1%)	10	40
45	U	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	29
46	V	78/80 (98%)	64 (82%)	12 (15%)	2 (3%)	4	28
47	W	63/65 (97%)	58 (92%)	2 (3%)	3 (5%)	2	17
48	X	77/79 (98%)	65 (84%)	10 (13%)	2 (3%)	4	28
49	Y	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	40
50	Z	63/65 (97%)	45 (71%)	12 (19%)	6 (10%)	0	7
51	a	130/223 (58%)	126 (97%)	4 (3%)	0	100	100
58	8	362/400 (90%)	329 (91%)	31 (9%)	2 (1%)	21	52
All	All	5997/6512 (92%)	5210 (87%)	683 (11%)	104 (2%)	9	34

All (104) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	204	LEU
1	b	232	GLY
7	h	108	VAL
7	h	118	ILE
9	j	81	ILE
10	k	35	VAL
17	r	54	VAL
34	J	93	VAL
34	J	99	SER
38	N	8	THR
38	N	90	ASP
40	P	125	LYS
41	Q	101	LEU
46	V	49	ASN
49	Y	68	LYS
3	d	83	VAL
5	f	174	LYS
5	f	175	LYS
6	g	41	LYS
7	h	80	THR
11	l	36	LYS
11	l	87	GLY

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Mol	Chain	Res	Type
13	n	71	ARG
13	n	118	ARG
18	s	63	GLY
20	u	6	ARG
29	E	31	ILE
29	E	62	PRO
35	K	40	GLU
35	K	92	THR
37	M	47	ASP
38	N	125	GLN
39	O	35	GLN
41	Q	3	VAL
41	Q	24	GLU
42	R	4	ALA
42	R	5	GLY
42	R	7	ASN
44	T	87	ARG
46	V	17	GLU
4	e	20	ASN
5	f	117	PRO
7	h	58	THR
8	i	13	ALA
10	k	73	ASP
11	l	94	THR
12	m	59	ARG
32	H	156	LEU
34	J	11	GLN
35	K	86	ARG
35	K	94	HIS
38	N	107	ALA
39	O	41	PRO
40	P	126	ARG
41	Q	88	ASP
43	S	2	LYS
45	U	43	ALA
48	X	4	LEU
50	Z	34	ARG
50	Z	62	GLU
58	8	335	THR
1	b	125	PRO
1	b	237	ARG
4	e	175	PRO

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Mol	Chain	Res	Type
7	h	79	PRO
11	l	29	LYS
20	u	47	PRO
20	u	51	LEU
20	u	98	ASN
34	J	89	THR
35	K	39	LEU
35	K	52	ASN
35	K	56	LYS
40	P	90	PRO
41	Q	27	PRO
41	Q	33	CYS
41	Q	35	ARG
45	U	79	ASN
50	Z	24	LYS
50	Z	25	ALA
58	8	4	GLU
1	b	107	LYS
7	h	68	PRO
8	i	22	PRO
12	m	69	PRO
14	o	34	HIS
17	r	52	PRO
39	O	42	LEU
39	O	75	ASP
43	S	51	PRO
47	W	12	PHE
47	W	13	THR
50	Z	9	GLU
10	k	72	PRO
11	l	85	VAL
20	u	97	SER
50	Z	8	ASN
11	l	65	GLY
47	W	17	VAL
48	X	8	PRO
14	o	66	GLY
40	P	123	PRO
41	Q	15	VAL
3	d	89	PRO

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	143 (9%)	5 (0%)
53	1	2902/2903 (99%)	330 (11%)	12 (0%)
54	2	119/120 (99%)	9 (7%)	1 (0%)
55	5	76/77 (98%)	6 (7%)	0
55	6	76/77 (98%)	6 (7%)	0
56	4	17/18 (94%)	3 (17%)	0
57	7	75/76 (98%)	14 (18%)	0
All	All	4803/4810 (99%)	511 (10%)	18 (0%)

All (511) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A
52	3	71	A
52	3	87	C
52	3	95	C
52	3	100	G
52	3	144	G
52	3	183	C
52	3	184	G
52	3	197	A
52	3	210	C
52	3	226	G
52	3	247	G
52	3	251	G
52	3	266	G
52	3	267	C
52	3	281	G
52	3	289	G
52	3	328	C

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Mol	Chain	Res	Type
52	3	345	C
52	3	346	G
52	3	352	C
52	3	355	C
52	3	367	U
52	3	372	C
52	3	411	A
52	3	412	A
52	3	413	G
52	3	422	C
52	3	429	U
52	3	467	U
52	3	485	U
52	3	486	U
52	3	495	A
52	3	497	G
52	3	518	C
52	3	527	G
52	3	531	U
52	3	533	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	665	A
52	3	688	G
52	3	702	A
52	3	703	G
52	3	723	U
52	3	724	G
52	3	755	G
52	3	777	A
52	3	794	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	821	G

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Mol	Chain	Res	Type
52	3	842	U
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
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1020	G
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	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1198	G
52	3	1201	A
52	3	1202	U

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Mol	Chain	Res	Type
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1257	A
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	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1378	C
52	3	1381	U
52	3	1395	C
52	3	1446	A
52	3	1448	C
52	3	1451	U
52	3	1452	C
52	3	1492	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1534	A
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	49	A
53	1	51	G
53	1	63	A

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Mol	Chain	Res	Type
53	1	71	A
53	1	74	A
53	1	75	G
53	1	102	U
53	1	114	U
53	1	119	A
53	1	120	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	216	A
53	1	221	A
53	1	222	A
53	1	228	C
53	1	229	C
53	1	248	G
53	1	249	C
53	1	255	A
53	1	265	A
53	1	266	G
53	1	276	U
53	1	278	A
53	1	281	C
53	1	285	G
53	1	294	A
53	1	301	G
53	1	311	A
53	1	312	G
53	1	323	C
53	1	324	A
53	1	329	G
53	1	330	A
53	1	333	G
53	1	361	G
53	1	367	G
53	1	371	A
53	1	372	G

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Mol	Chain	Res	Type
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	422	A
53	1	424	G
53	1	451	U
53	1	457	A
53	1	473	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	543	G
53	1	545	U
53	1	563	A
53	1	572	A
53	1	573	U
53	1	574	A
53	1	575	A
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	776	G
53	1	782	A
53	1	784	G
53	1	785	G

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Mol	Chain	Res	Type
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	885	C
53	1	886	A
53	1	887	U
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
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	1045	C
53	1	1046	A
53	1	1047	G
53	1	1054	A
53	1	1060	U
53	1	1062	G
53	1	1066	U
53	1	1070	A
53	1	1071	G
53	1	1079	C

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Mol	Chain	Res	Type
53	1	1084	A
53	1	1088	A
53	1	1090	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	1178	C
53	1	1180	U
53	1	1206	G
53	1	1212	G
53	1	1238	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A
53	1	1275	A
53	1	1301	A
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1352	U
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1395	A
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1454	C
53	1	1461	C
53	1	1476	U

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Mol	Chain	Res	Type
53	1	1482	G
53	1	1490	A
53	1	1491	G
53	1	1515	A
53	1	1524	G
53	1	1535	A
53	1	1536	C
53	1	1537	G
53	1	1555	G
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1584	U
53	1	1585	C
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1732	C
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1800	C
53	1	1801	A
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	1929	G
53	1	1930	G
53	1	1937	A

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Mol	Chain	Res	Type
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	2043	C
53	1	2049	G
53	1	2055	C
53	1	2056	G
53	1	2060	A
53	1	2061	G
53	1	2062	A
53	1	2069	G
53	1	2096	C
53	1	2110	G
53	1	2111	U
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2132	U
53	1	2133	G
53	1	2145	C
53	1	2147	A
53	1	2162	G
53	1	2172	U
53	1	2173	A
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2211	A
53	1	2212	A

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Mol	Chain	Res	Type
53	1	2225	A
53	1	2259	U
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2297	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2406	A
53	1	2423	U
53	1	2424	C
53	1	2429	G
53	1	2430	A
53	1	2435	A
53	1	2441	U
53	1	2448	A
53	1	2476	A
53	1	2498	C
53	1	2502	G
53	1	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2520	C
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2603	G
53	1	2609	U
53	1	2613	U
53	1	2655	G

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Mol	Chain	Res	Type
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	2757	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2794	C
53	1	2797	U
53	1	2800	A
53	1	2809	A
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2849	U
53	1	2850	A
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2879	A
53	1	2880	C
53	1	2883	A
53	1	2884	U
53	1	2893	A
54	2	4	C
54	2	13	G
54	2	24	G
54	2	35	C
54	2	44	G
54	2	67	G
54	2	89	U
54	2	108	A
54	2	109	A
55	5	9	G
55	5	19	G
55	5	20	U
55	5	47	U

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Mol	Chain	Res	Type
55	5	48	C
55	5	61	C
55	6	6	G
55	6	18	G
55	6	19	G
55	6	20	U
55	6	47	U
55	6	48	C
56	4	12	A
56	4	13	A
56	4	19	U
57	7	8	U
57	7	9	A
57	7	10	G
57	7	18	G
57	7	21	A
57	7	26	A
57	7	44	G
57	7	45	U
57	7	46	G
57	7	48	C
57	7	55	U
57	7	59	U
57	7	61	C
57	7	63	G

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	70	U
52	3	421	U
52	3	960	U
52	3	1190	G
52	3	1201	A
53	1	372	G
53	1	421	C
53	1	490	C
53	1	859	G
53	1	1020	A
53	1	1130	U
53	1	1475	G
53	1	2286	G

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Mol	Chain	Res	Type
53	1	2296	U
53	1	2326	C
53	1	2391	G
53	1	2756	U
54	2	88	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
61	GDP	8	501	-	29,30,30	1.44	4 (13%)	45,47,47	1.95	14 (31%)
60	PHE	7	101	57	10,11,12	0.73	0	8,13,15	0.25	0
59	FME	5	101	55	8,9,10	0.48	0	8,9,11	0.82	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
61	GDP	8	501	-	-	5/16/32/32	0/3/3/3
60	PHE	7	101	57	-	0/5/6/8	0/1/1/1
59	FME	5	101	55	-	1/7/9/11	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PB-O1B	3.97	1.62	1.50
61	8	501	GDP	O4'-C1'	2.31	1.47	1.42
61	8	501	GDP	PA-O3A	2.19	1.61	1.59
61	8	501	GDP	PB-O3B	2.01	1.62	1.54

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	C5-C4-N3	-5.65	119.39	128.39
61	8	501	GDP	C2-N3-C4	5.51	121.78	112.30
61	8	501	GDP	N9-C4-N3	4.04	134.03	125.95
61	8	501	GDP	C8-N7-C5	3.01	109.63	104.26
61	8	501	GDP	C2-N1-C6	-2.69	120.23	125.11
61	8	501	GDP	O5'-PA-O1A	-2.55	98.83	108.94
61	8	501	GDP	O4'-C4'-C3'	2.49	110.10	105.15
61	8	501	GDP	O6-C6-C5	-2.40	120.21	126.53
61	8	501	GDP	C5-C6-N1	2.15	118.72	113.25
61	8	501	GDP	C2'-C1'-N9	-2.14	107.29	113.25
61	8	501	GDP	O2A-PA-O1A	2.13	122.34	112.44
61	8	501	GDP	C4-C5-N7	-2.12	107.31	110.67
61	8	501	GDP	C6-C5-N7	2.11	134.12	130.29
61	8	501	GDP	O2B-PB-O3A	2.01	111.39	104.64

There are no chirality outliers.

All (6) torsion outliers are listed below:

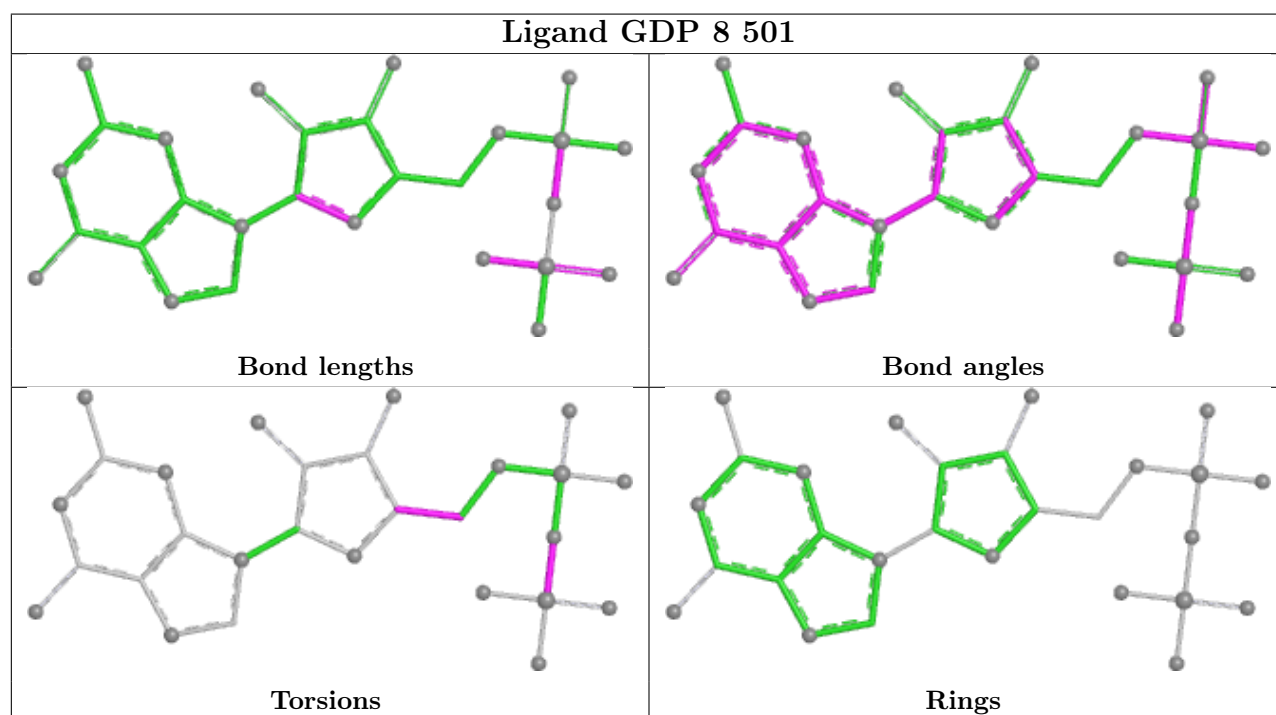
Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA
61	8	501	GDP	PA-O3A-PB-O2B
61	8	501	GDP	PA-O3A-PB-O3B
61	8	501	GDP	O4'-C4'-C5'-O5'
61	8	501	GDP	C3'-C4'-C5'-O5'
61	8	501	GDP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	101	PHE	2	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

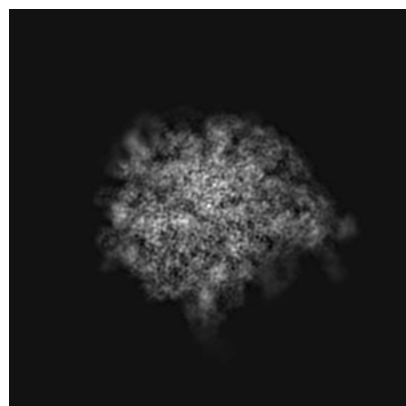
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21623. These allow visual inspection of the internal detail of the map and identification of artifacts.

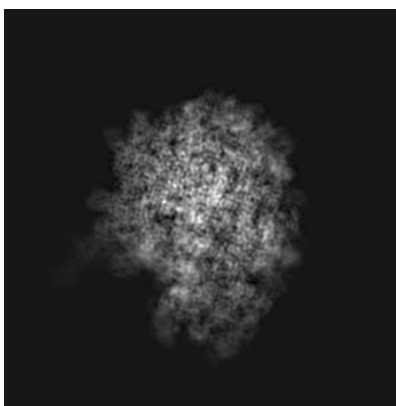
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

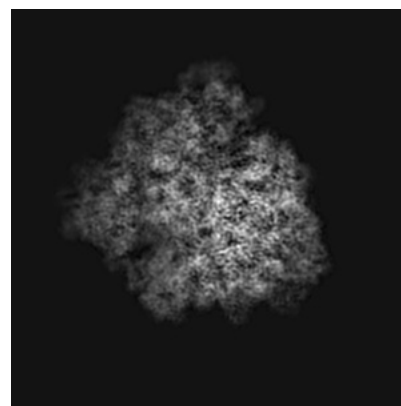
6.1.1 Primary map



X

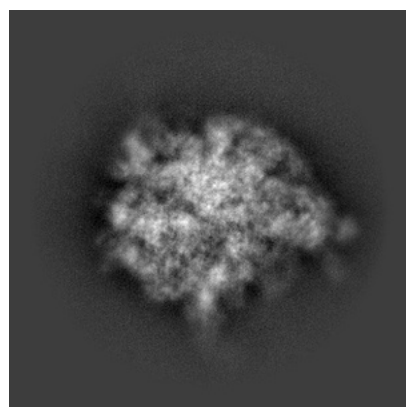


Y

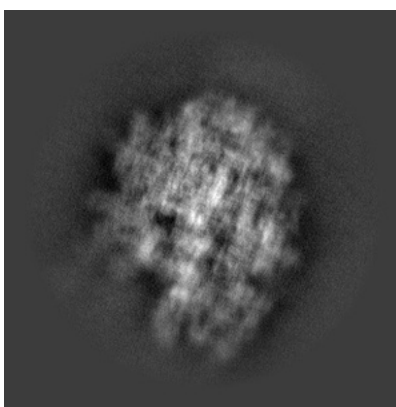


Z

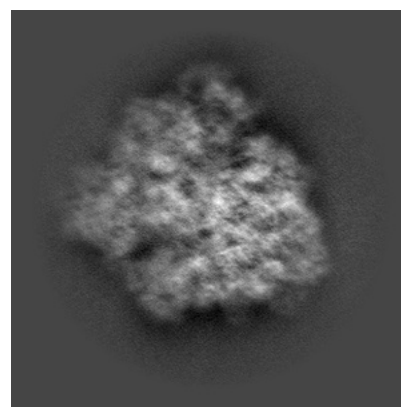
6.1.2 Raw map



X



Y

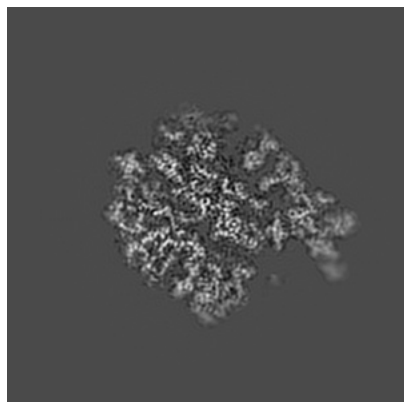


Z

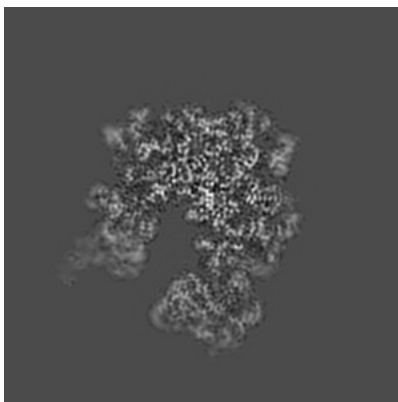
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

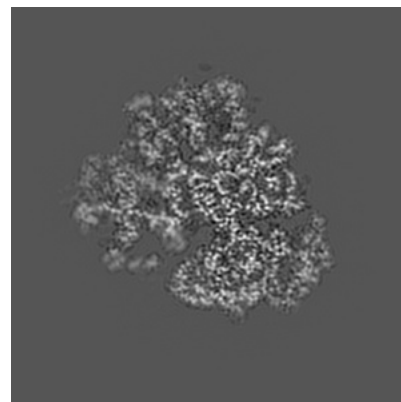
6.2.1 Primary map



X Index: 144

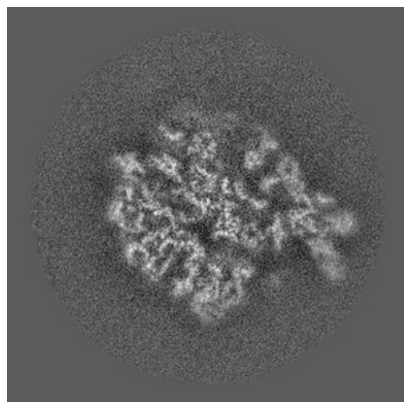


Y Index: 144

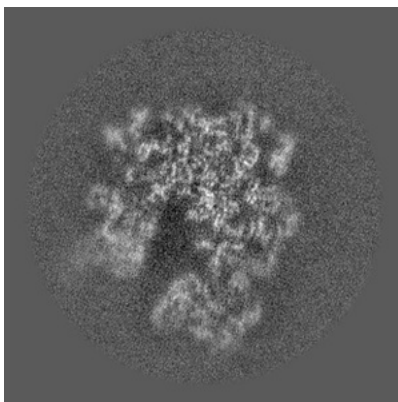


Z Index: 144

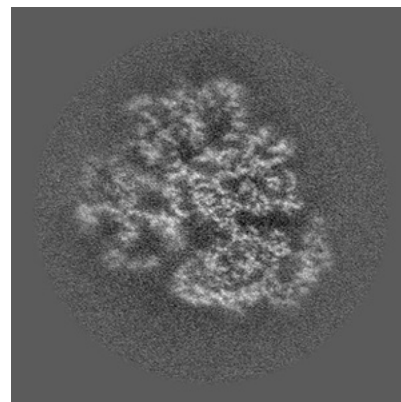
6.2.2 Raw map



X Index: 144



Y Index: 144

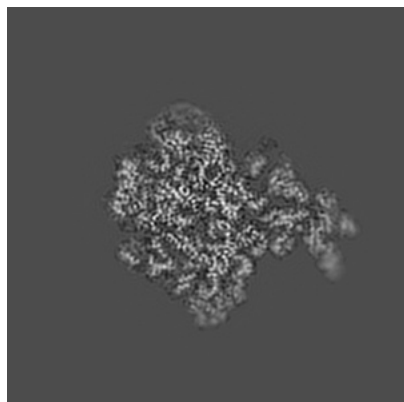


Z Index: 144

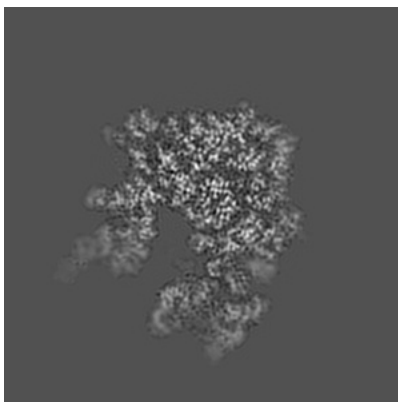
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

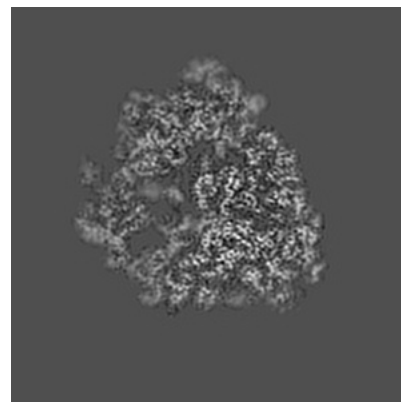
6.3.1 Primary map



X Index: 149

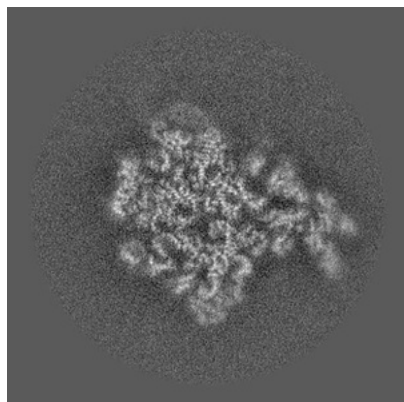


Y Index: 148

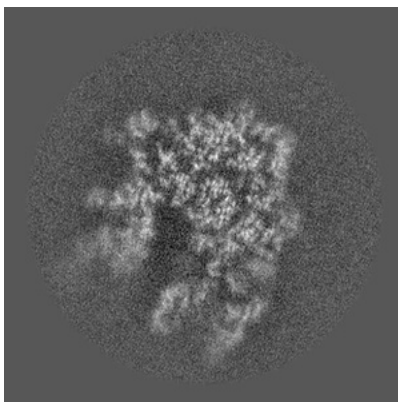


Z Index: 135

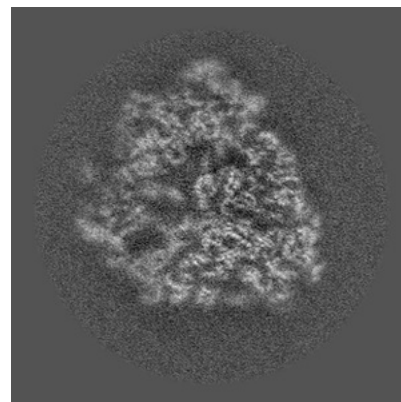
6.3.2 Raw map



X Index: 149



Y Index: 148

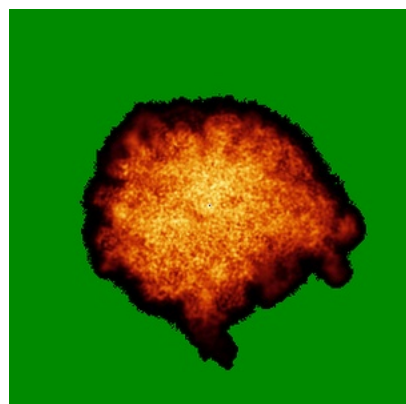


Z Index: 135

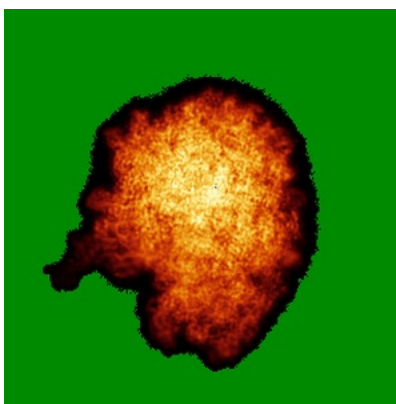
The images above show the largest variance slices of the map in three orthogonal directions.

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

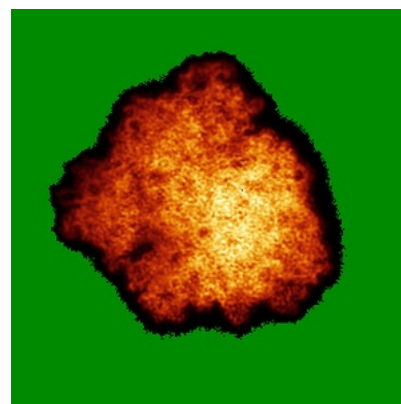
6.4.1 Primary map



X

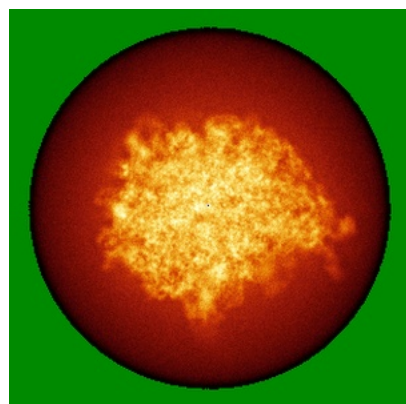


Y

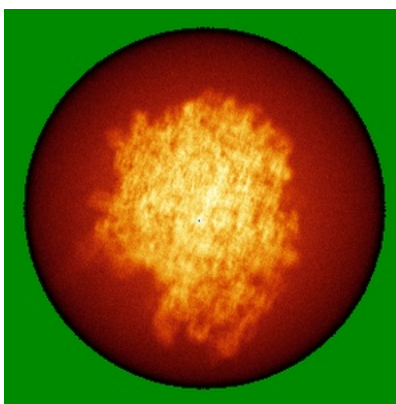


Z

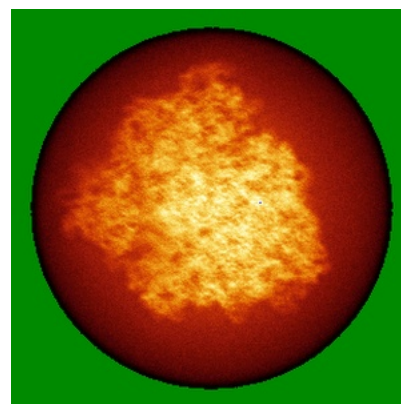
6.4.2 Raw map



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



X



Y



Z

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.

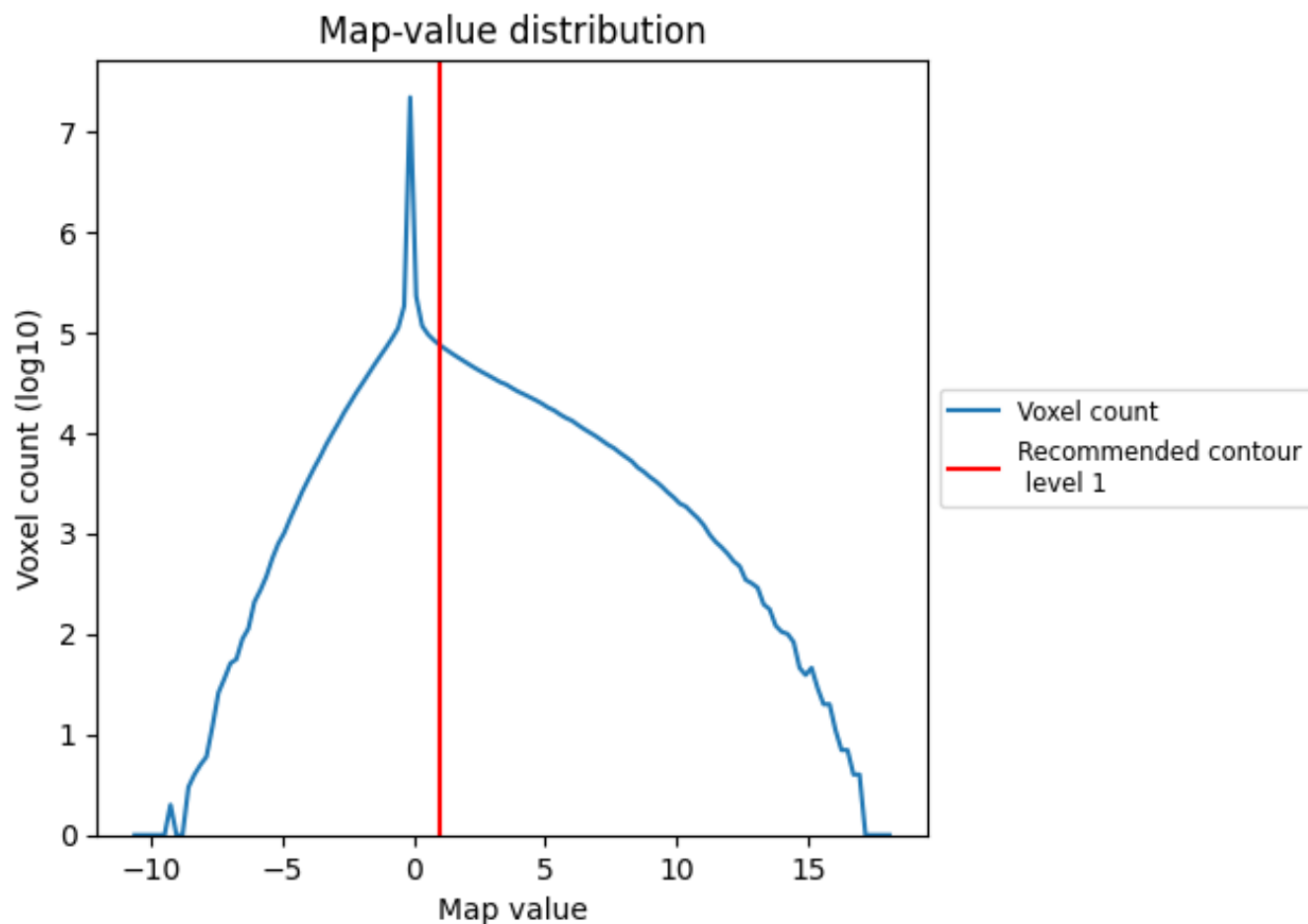
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

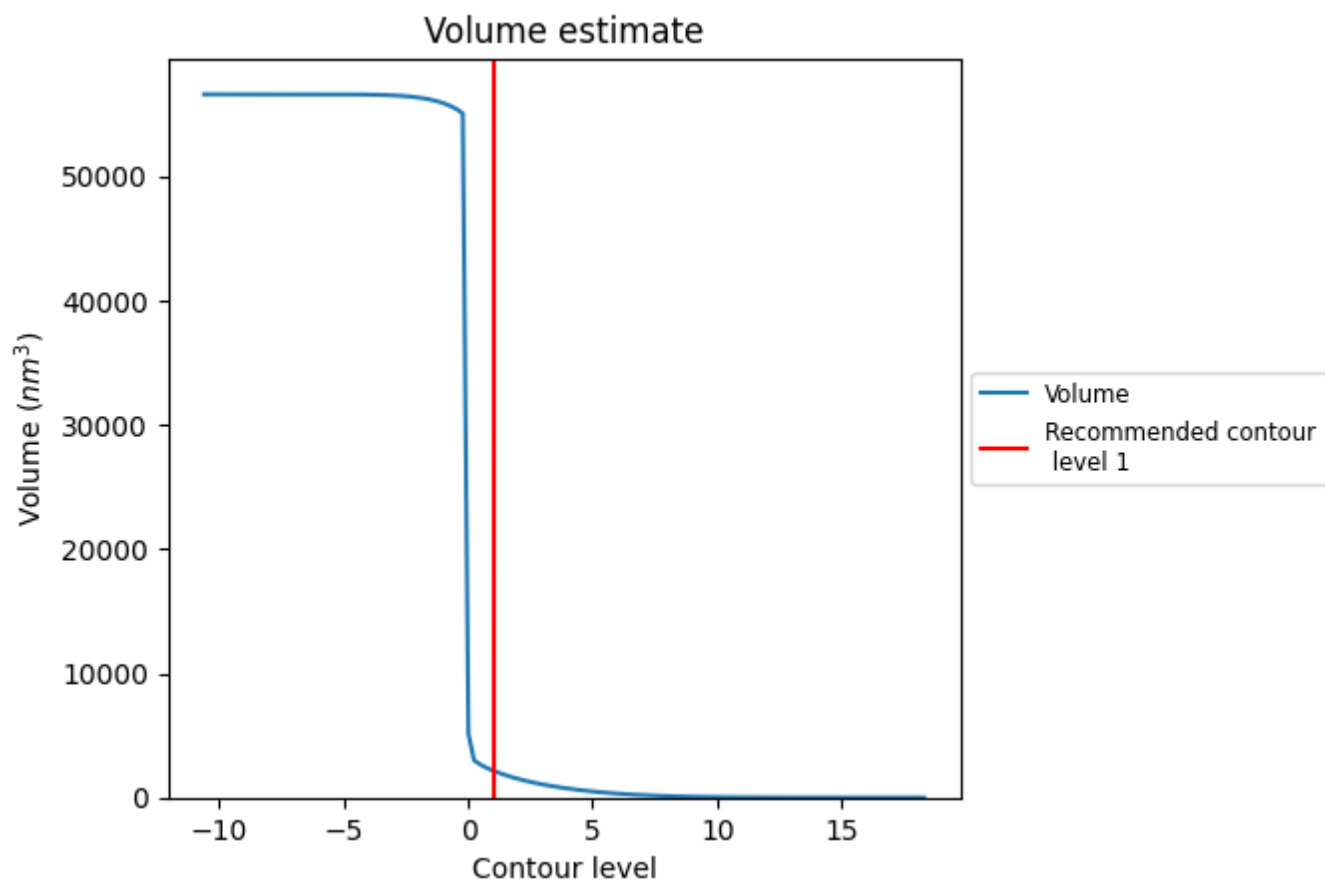
This section contains the results of statistical analysis of the map.

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.

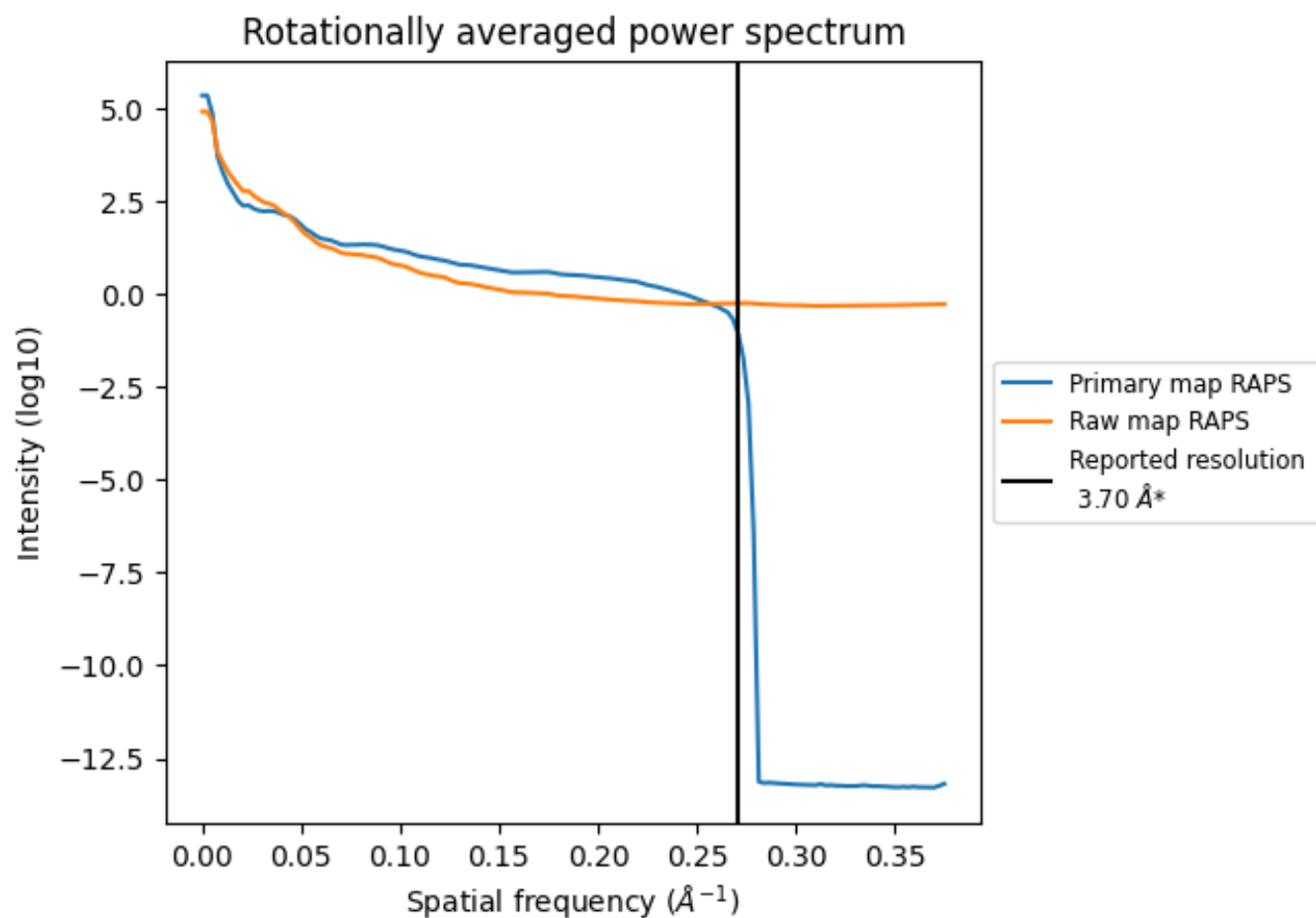
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2174 nm³; this corresponds to an approximate mass of 1964 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 ⓘ

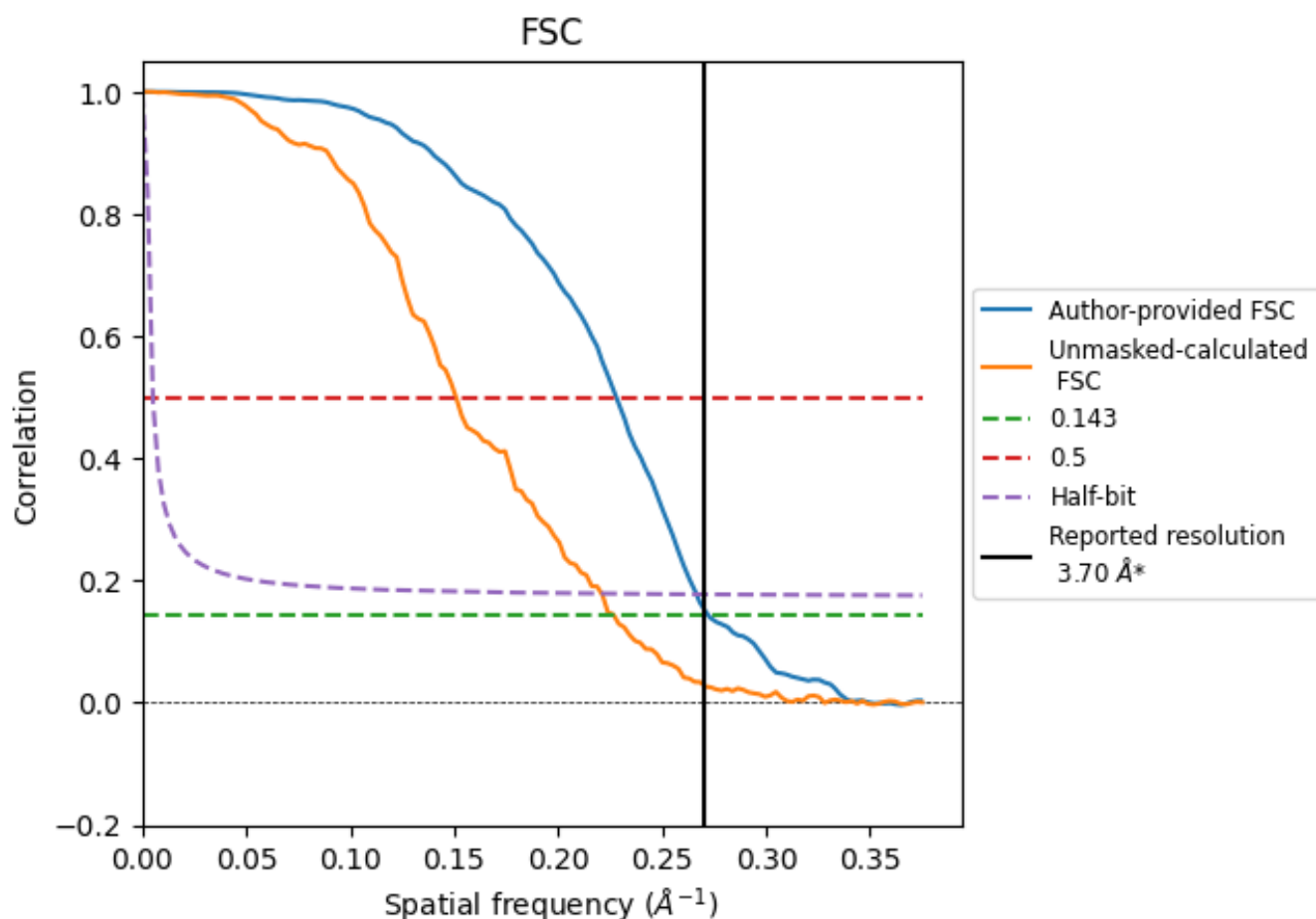


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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	3.67	4.39	3.75
Unmasked-calculated*	4.41	6.63	4.53

*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 4.41 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-21623 and PDB model 6WD4. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)

This section was not generated.

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

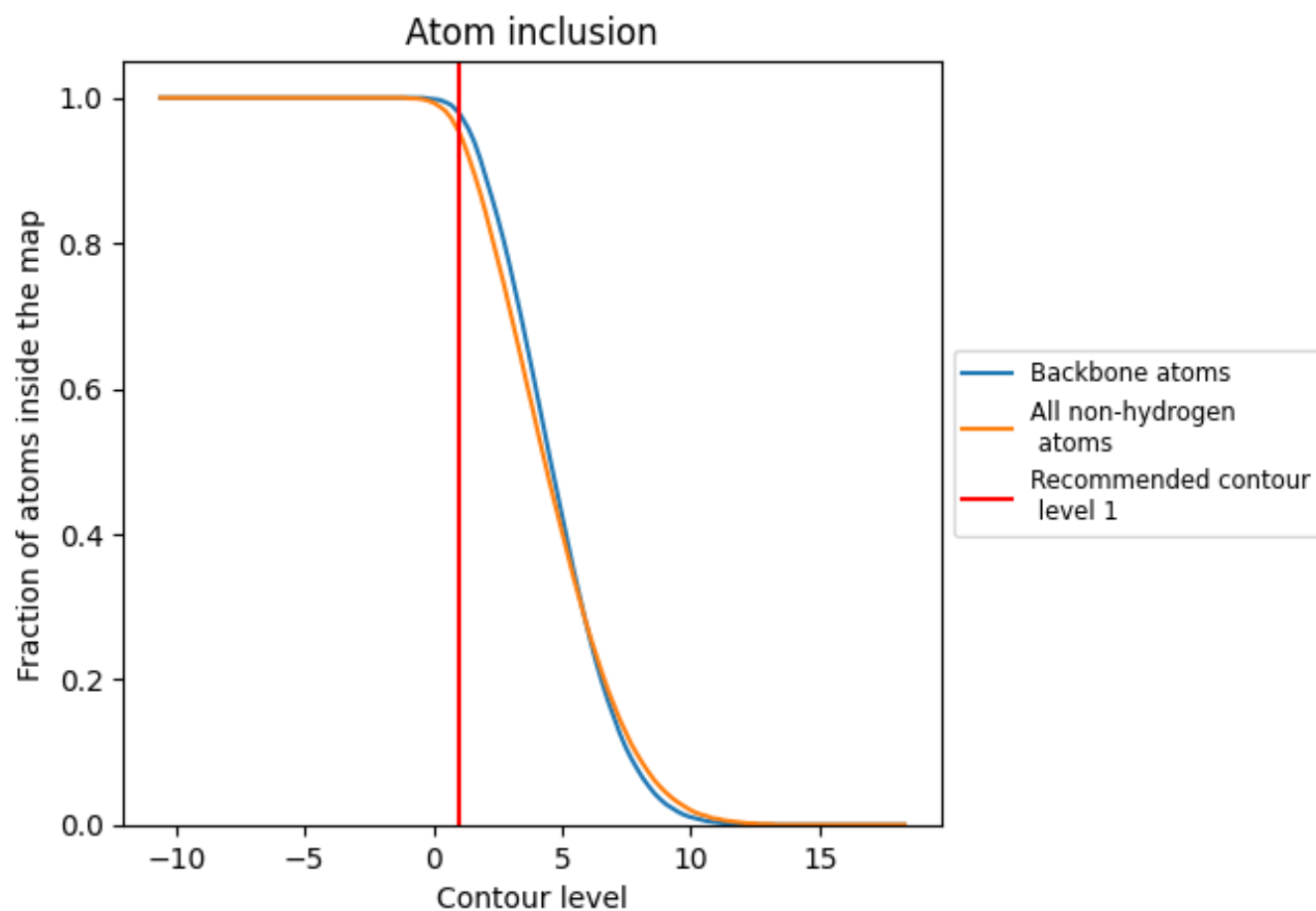


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% 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	 0.9530	 0.3610
1	 0.9830	 0.3810
2	 0.9860	 0.3380
3	 0.9770	 0.3510
4	 0.8840	 0.2510
5	 0.9580	 0.3000
6	 0.8320	 0.1500
7	 0.9140	 0.1910
8	 0.8080	 0.1840
B	 0.9530	 0.4320
C	 0.8430	 0.3760
D	 0.9210	 0.4480
E	 0.9510	 0.4640
F	 0.8660	 0.4320
G	 0.8920	 0.3130
H	 0.7620	 0.3170
I	 0.8830	 0.3220
J	 0.9180	 0.3810
K	 0.9540	 0.3680
L	 0.9320	 0.3500
M	 0.9080	 0.3810
N	 0.9100	 0.3220
O	 0.7350	 0.2790
P	 0.9500	 0.3820
Q	 0.9050	 0.4120
R	 0.9350	 0.3450
S	 0.8220	 0.3330
T	 0.9510	 0.3770
U	 0.9120	 0.3880
V	 0.9160	 0.3960
W	 0.9400	 0.3680
X	 0.9570	 0.3300
Y	 0.9000	 0.3500
Z	 0.8650	 0.3070
a	 0.8340	 0.1500



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Chain	Atom inclusion	Q-score
b	 0.9540	 0.4520
c	 0.9450	 0.4470
d	 0.9420	 0.4060
e	 0.9260	 0.3360
f	 0.9660	 0.3690
g	 0.7930	 0.2920
h	 0.7840	 0.1630
i	 0.7250	 0.1970
j	 0.9510	 0.4400
k	 0.9310	 0.4460
l	 0.9600	 0.4240
m	 0.9250	 0.4470
n	 0.9500	 0.4360
o	 0.9460	 0.3720
p	 0.9360	 0.4320
q	 0.9280	 0.4250
r	 0.9510	 0.4130
s	 0.9210	 0.4300
t	 0.9270	 0.4040
u	 0.9300	 0.3860
v	 0.9470	 0.3920
w	 0.9450	 0.4570
x	 0.9600	 0.4310
y	 0.9300	 0.3350
z	 0.9340	 0.4310