



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 12:19 PM UTC

PDB ID : 6WD6 / pdb_00006wd6
EMDB ID : EMD-21625
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure II-C2)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

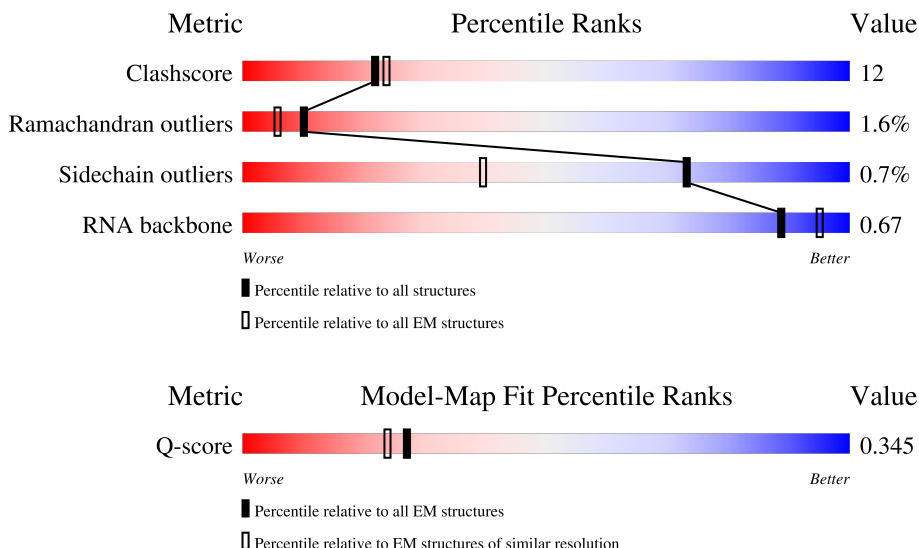
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

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



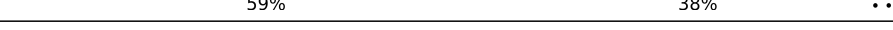
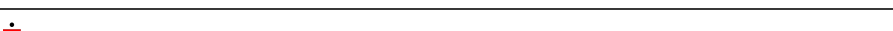
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

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

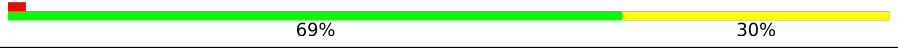
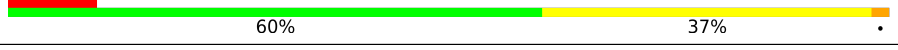
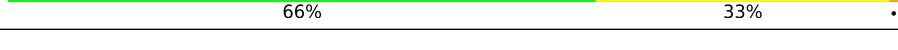
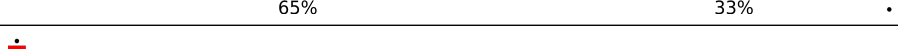
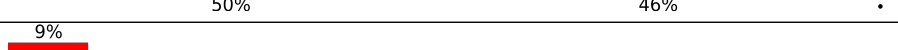
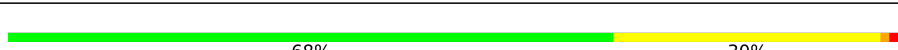
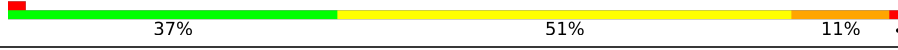
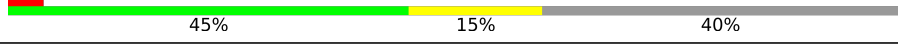
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56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

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

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Mol	Chain	Length	Quality of chain
54	2	120	50% 42% 8%
55	5	77	68% 26% 6%
55	6	77	53% 44%
56	4	18	50% 50%
57	7	76	53% 37% 11%
58	8	400	28% 60% 32% 7%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 153103 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	0
			917	574	179	163	1		

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

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

- 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	0
			816	516	153	145	2		

- 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	0
			857	532	166	156	3		

- 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	0
			739	466	139	132	2		

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

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

- 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 802133627

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

- Molecule 56 is a RNA chain called mRNA.

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

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

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

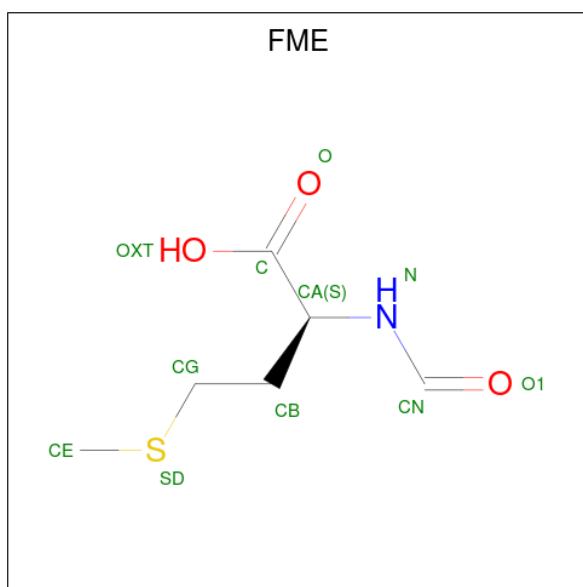
- Molecule 58 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	371	Total	C	N	O	S	0	0
			2853	1804	490	546	13		

There are 7 discrepancies between the modelled and reference sequences:

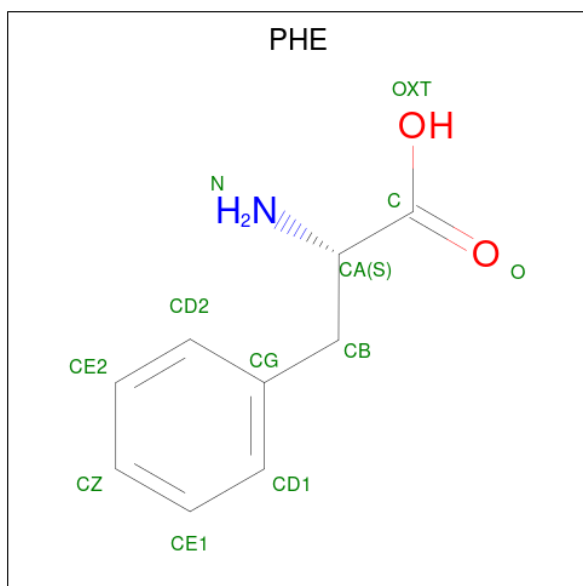
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag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

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



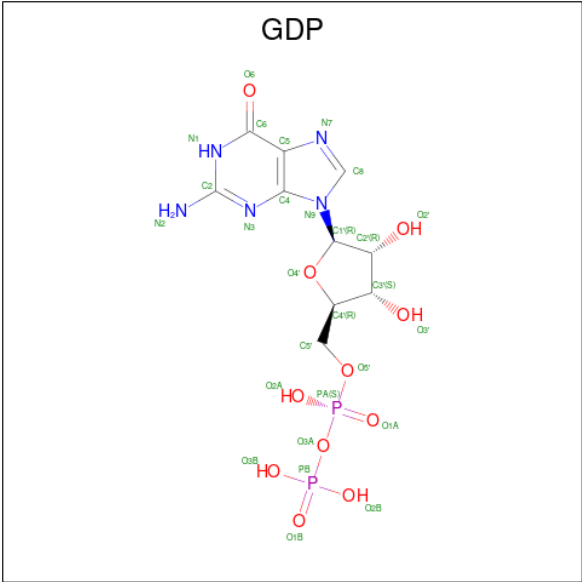
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

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

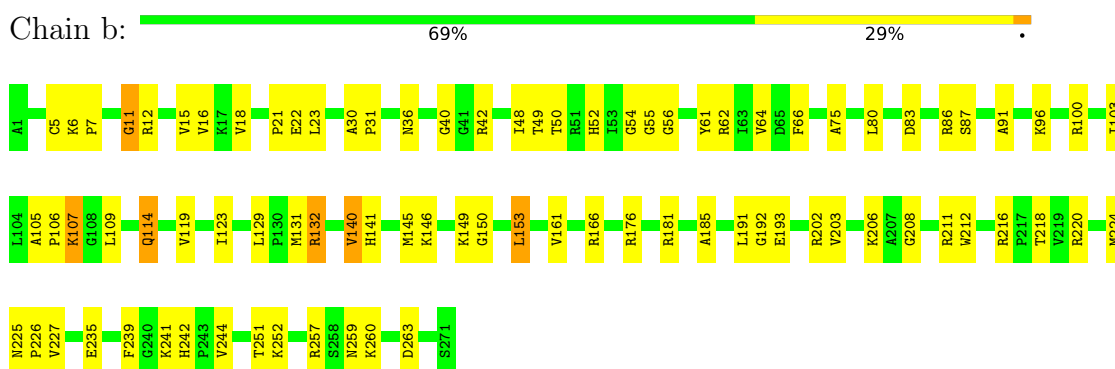


Mol	Chain	Residues	Atoms					AltConf
61	8	1	Total	C	N	O	P	0
			28	10	5	11	2	

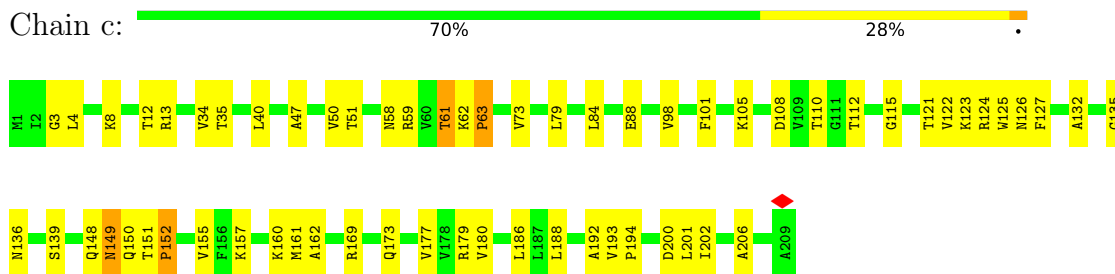
3 Residue-property plots

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.

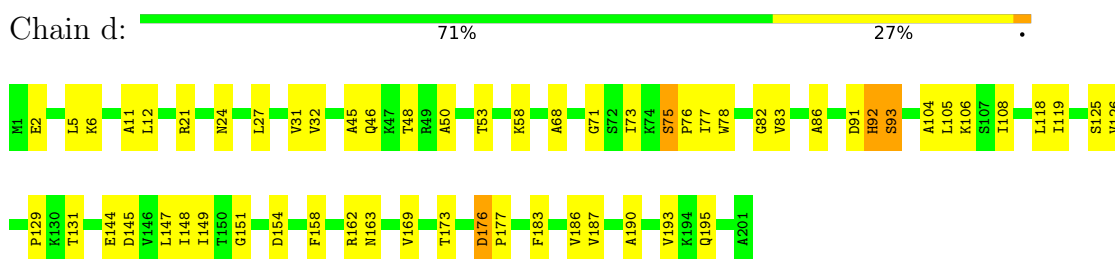
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

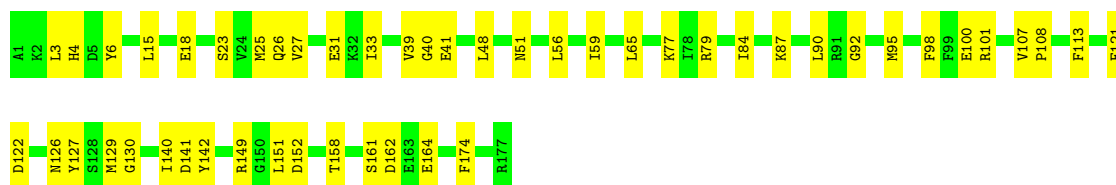


• Molecule 3: 50S ribosomal protein L4



• Molecule 4: 50S ribosomal protein L5





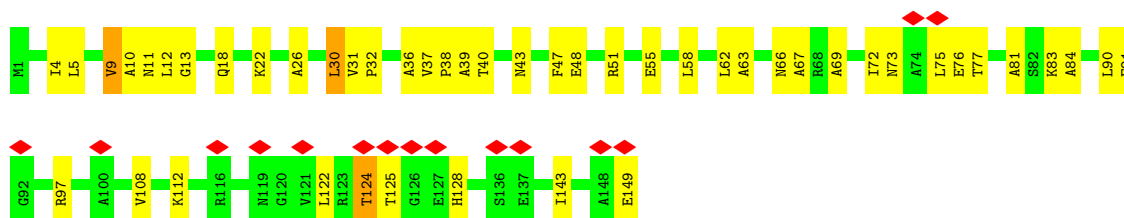
• Molecule 5: 50S ribosomal protein L6

Chain f: 79% 19% .



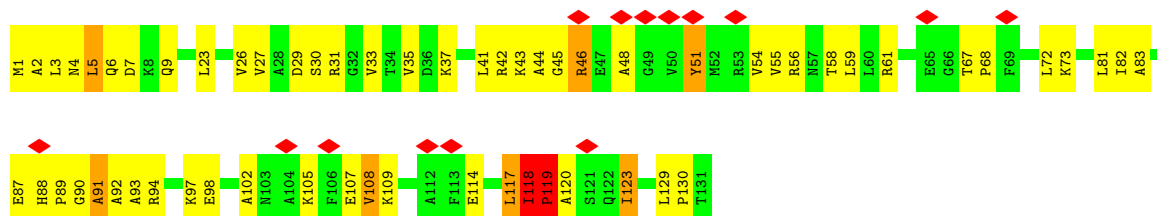
• Molecule 6: 50S ribosomal protein L9

Chain g: 10% 68% 30% .



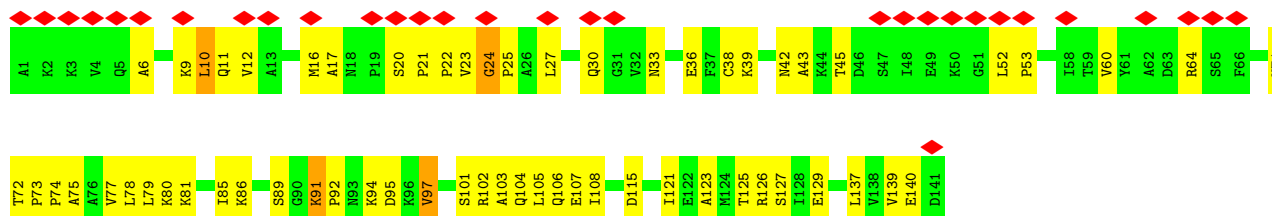
• Molecule 7: 50S ribosomal protein L10

Chain h: 11% 53% 40% 5% .



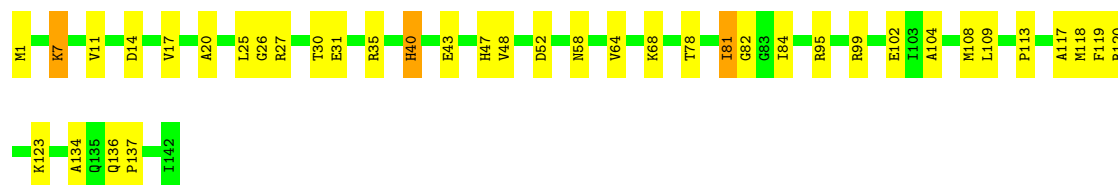
• Molecule 8: 50S ribosomal protein L11

Chain i: 22% 56% 41% .

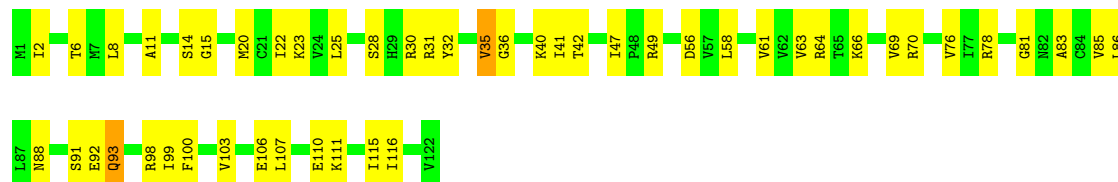


• Molecule 9: 50S ribosomal protein L13

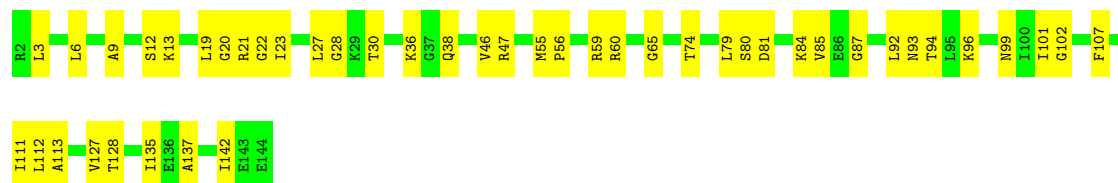
Chain j: 73% 25% .



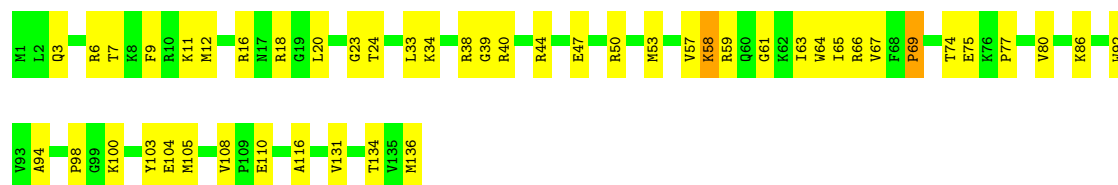
• Molecule 10: 50S ribosomal protein L14



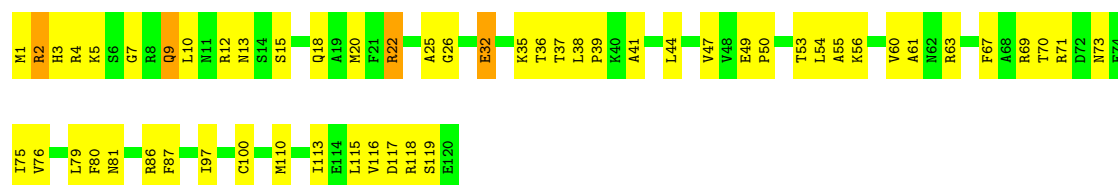
• Molecule 11: 50S ribosomal protein L15



• Molecule 12: 50S ribosomal protein L16

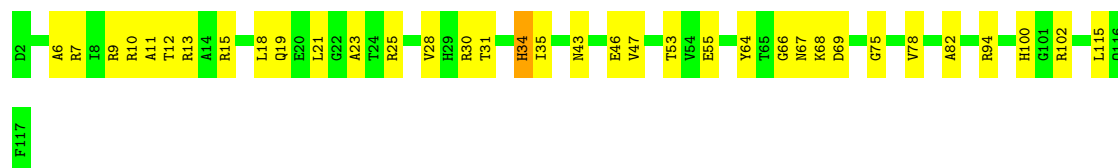


• Molecule 13: 50S ribosomal protein L17



• Molecule 14: 50S ribosomal protein L18





- Molecule 15: 50S ribosomal protein L19

Chain p: 67% 32%



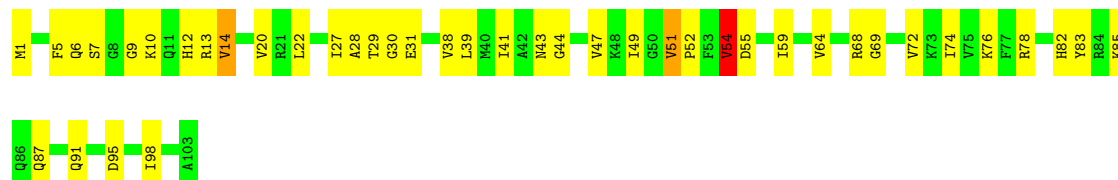
- Molecule 16: 50S ribosomal protein L20

Chain q: 81% 18%



- Molecule 17: 50S ribosomal protein L21

Chain r: 59% 38%



- Molecule 18: 50S ribosomal protein L22

Chain s: 66% 33%



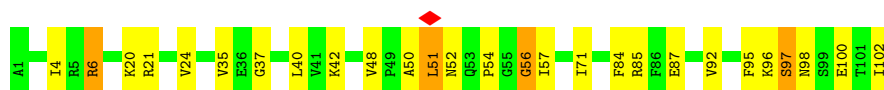
- Molecule 19: 50S ribosomal protein L23

Chain t: 73% 25%



- Molecule 20: 50S ribosomal protein L24

Chain u:  74% 23%



- Molecule 21: 50S ribosomal protein L25

Chain v:  76% 24%



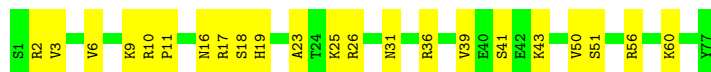
- Molecule 22: 50S ribosomal protein L27

Chain w:  76% 24%



- Molecule 23: 50S ribosomal protein L28

Chain x:  71% 29%



- Molecule 24: 50S ribosomal protein L29

Chain y:  67% 33%



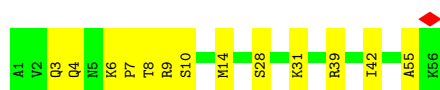
- Molecule 25: 50S ribosomal protein L30

Chain z:  74% 26%

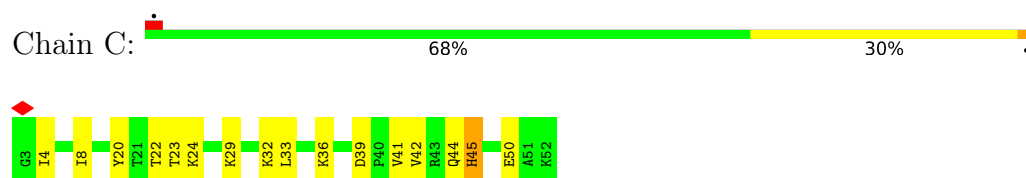


- Molecule 26: 50S ribosomal protein L32

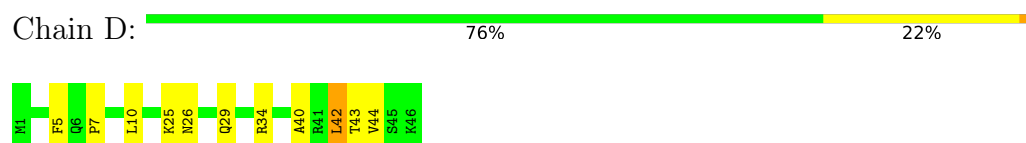
Chain B:  77% 23%



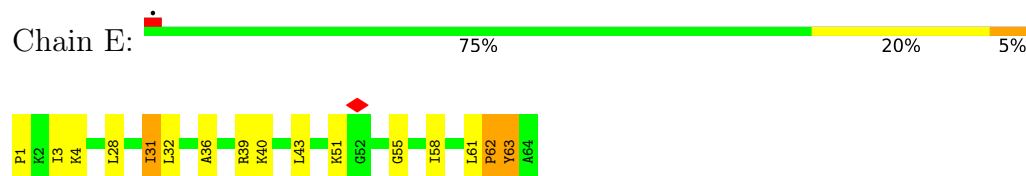
- Molecule 27: 50S ribosomal protein L33



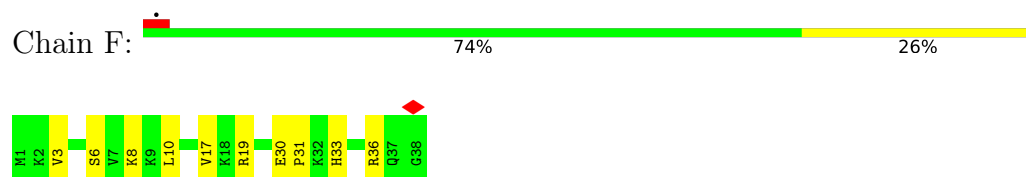
- Molecule 28: 50S ribosomal protein L34



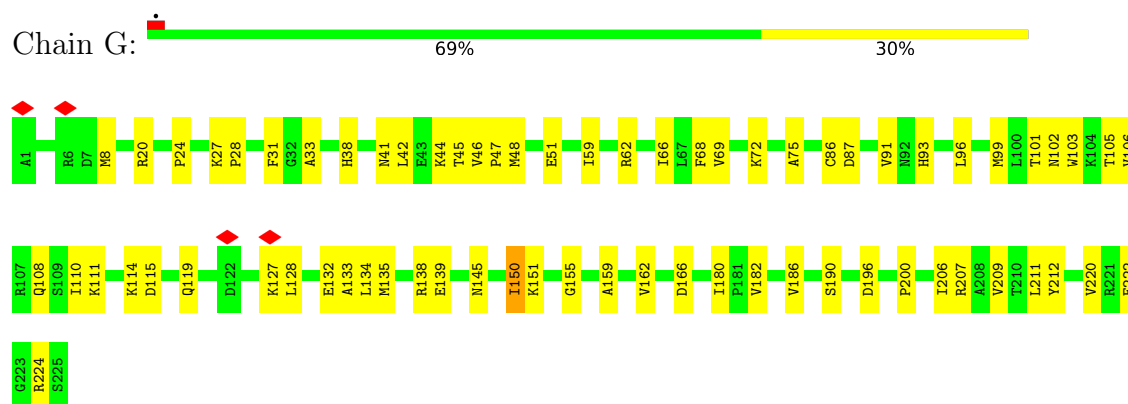
- Molecule 29: 50S ribosomal protein L35



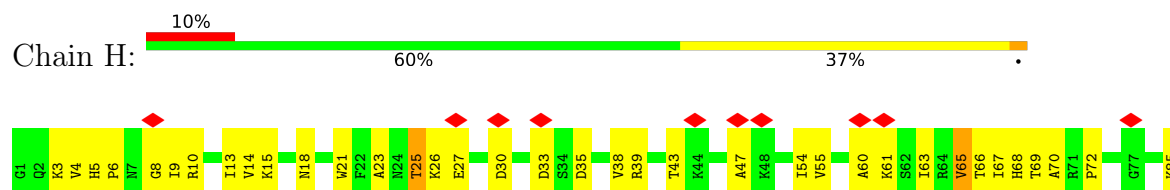
- Molecule 30: 50S ribosomal protein L36

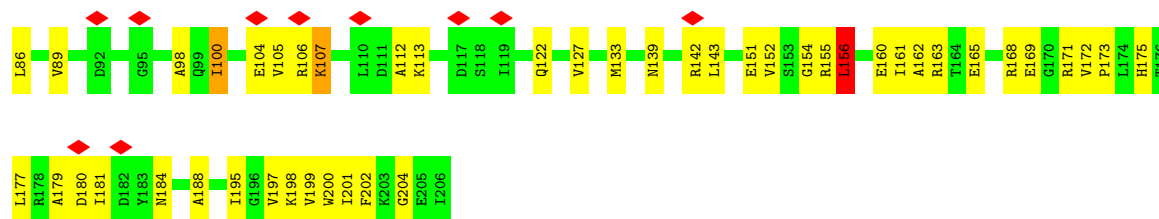


- Molecule 31: 30S ribosomal protein S2



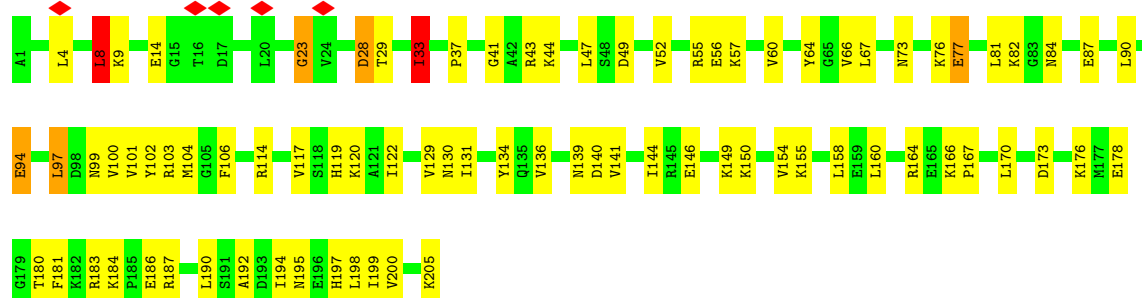
- Molecule 32: 30S ribosomal protein S3





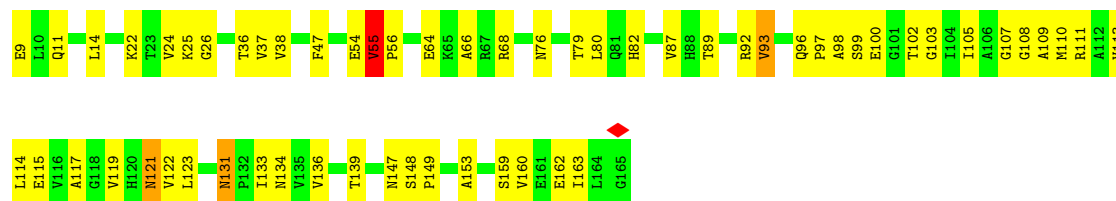
- Molecule 33: 30S ribosomal protein S4

Chain I: 60% 37% ..



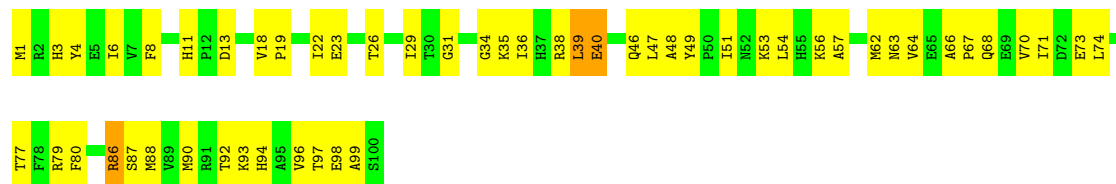
- Molecule 34: 30S ribosomal protein S5

Chain J: 62% 35% ..



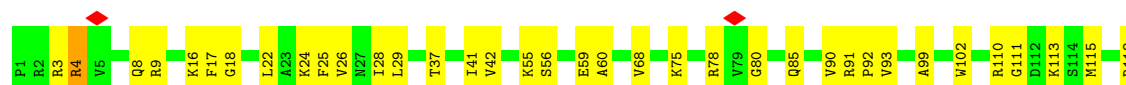
- Molecule 35: 30S ribosomal protein S6

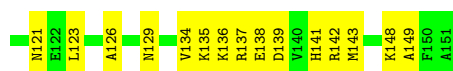
Chain K: 47% 50% .



- Molecule 36: 30S ribosomal protein S7

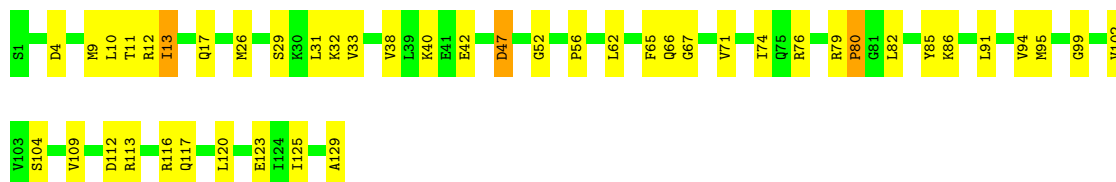
Chain L: 66% 33% .





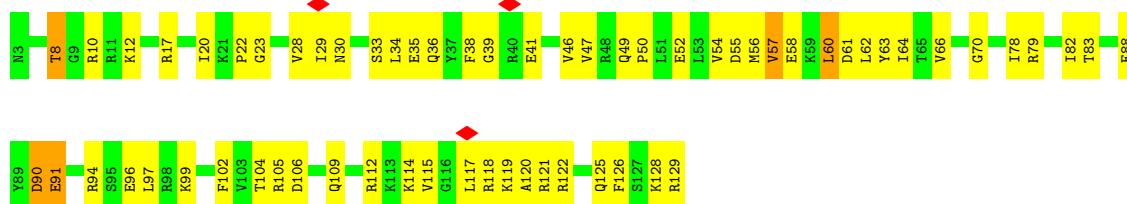
- Molecule 37: 30S ribosomal protein S8

Chain M: 65% 33%



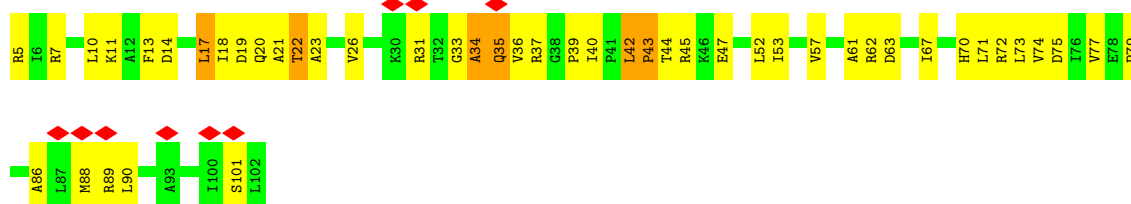
- Molecule 38: 30S ribosomal protein S9

Chain N: 50% 46%



- Molecule 39: 30S ribosomal protein S10

Chain O: 9% 52% 42% 6%



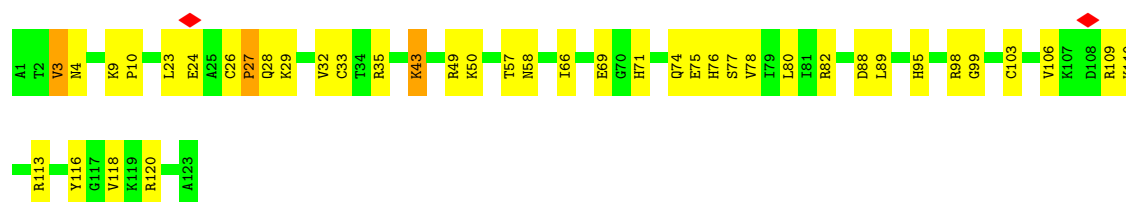
- Molecule 40: 30S ribosomal protein S11

Chain P: 55% 42%



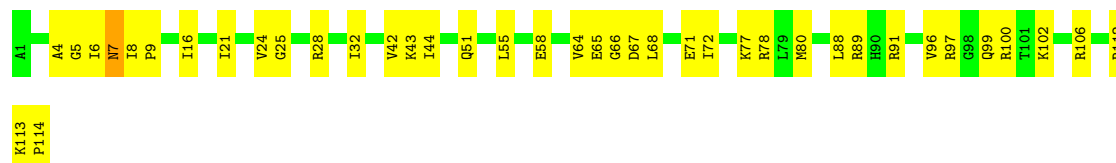
- Molecule 41: 30S ribosomal protein S12

Chain Q: 67% 31%



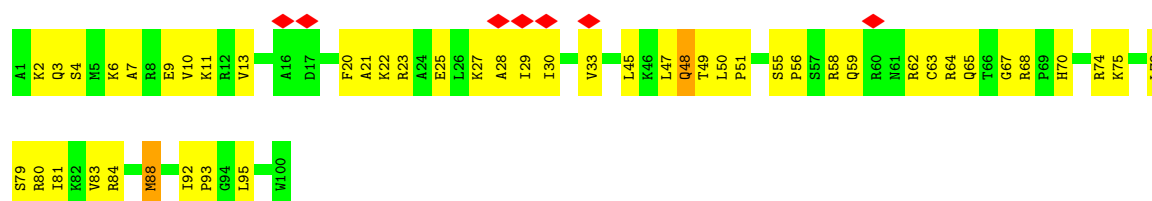
- Molecule 42: 30S ribosomal protein S13

Chain R: 65% 34% .



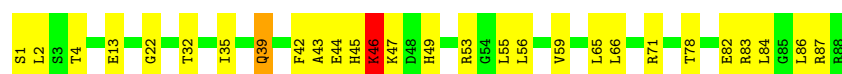
- Molecule 43: 30S ribosomal protein S14

Chain S: 7% 52% 46% .



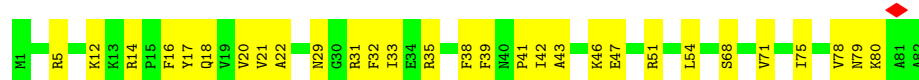
- Molecule 44: 30S ribosomal protein S15

Chain T: 68% 30% ..



- Molecule 45: 30S ribosomal protein S16

Chain U: 65% 35%

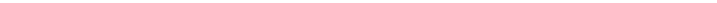


- Molecule 46: 30S ribosomal protein S17

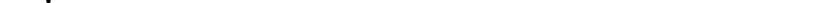
Chain V: 56% 41% .

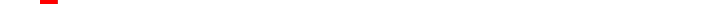


- Molecule 47: 30S ribosomal protein S18

- Chain X:  73% 27%

Category	Count
R2	10
S3	10
L4	10
K5	10
F9	10
L14	10
K17	10
V18	10
K28	10
P29	10
L30	10
R35	10
R36	10
I39	10
I48	10
V57	10
P58	10
T62	10
M65	10
H68	10
F73	10
A74	10
P75	10
R80	10

- Chain Y:  75% 25%

- Chain Z:  37% 51% 11%

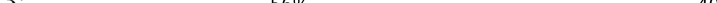
I3	K4	V5	R6	E7	N8	E9	P10	F11	D12	V13	A14	L15	R16	R17	F18	K19	R20	S21	C22	E23	K24	A25	L28	V31	R34	E35	F36	V37	F38	K39	P40	T41	T42	F43	E44	K45	R46	A47	K48	A49	K53	A56	K57	K58	L59	A60	R61	A64	R65	R66	T67
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- Chain a:

 K3
  L4
  T5
  K6
  R7
  M8
  V15
  A26
  F38
  D43
  V44
  M47
  D51
  A52
  R53
  K54
  V59
  T63
  G68
  T69
 GLY
 ARG
 SER
 VAL
 ARG
 VAL
 VAL
 ALA
 VAL
 VAL
 PHE
 THR
 GLN
 GLY
 ALA
 ALA
 ASN
 ALA
 ALA
 GLU
 ALA
 ALA
 LYS
 GLY
 GLY
 GLU
 LEU
 VAL
 GLY
 MET
 GLU
 ASP

ALA	ASP	GLN	ILE	LYS	LYS	GLY	GLU	MET	ASN	PHE	ASP	VAL	VAL	ALA	ALA	ARG	VAL	VAL	GLY	GLN	LEU	GLY	GLN	VAL	LEU	GLY	PRO	PRO	GLY	LEU	MET	ASN	ASN	PRO	PRO	LYS	VAL	THR	THR	PRO	ASN	VAL	ALA	GLU	ALA	VAL	LYS	ALA	ALA	LYS	ALA	ALA	Cys9
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------

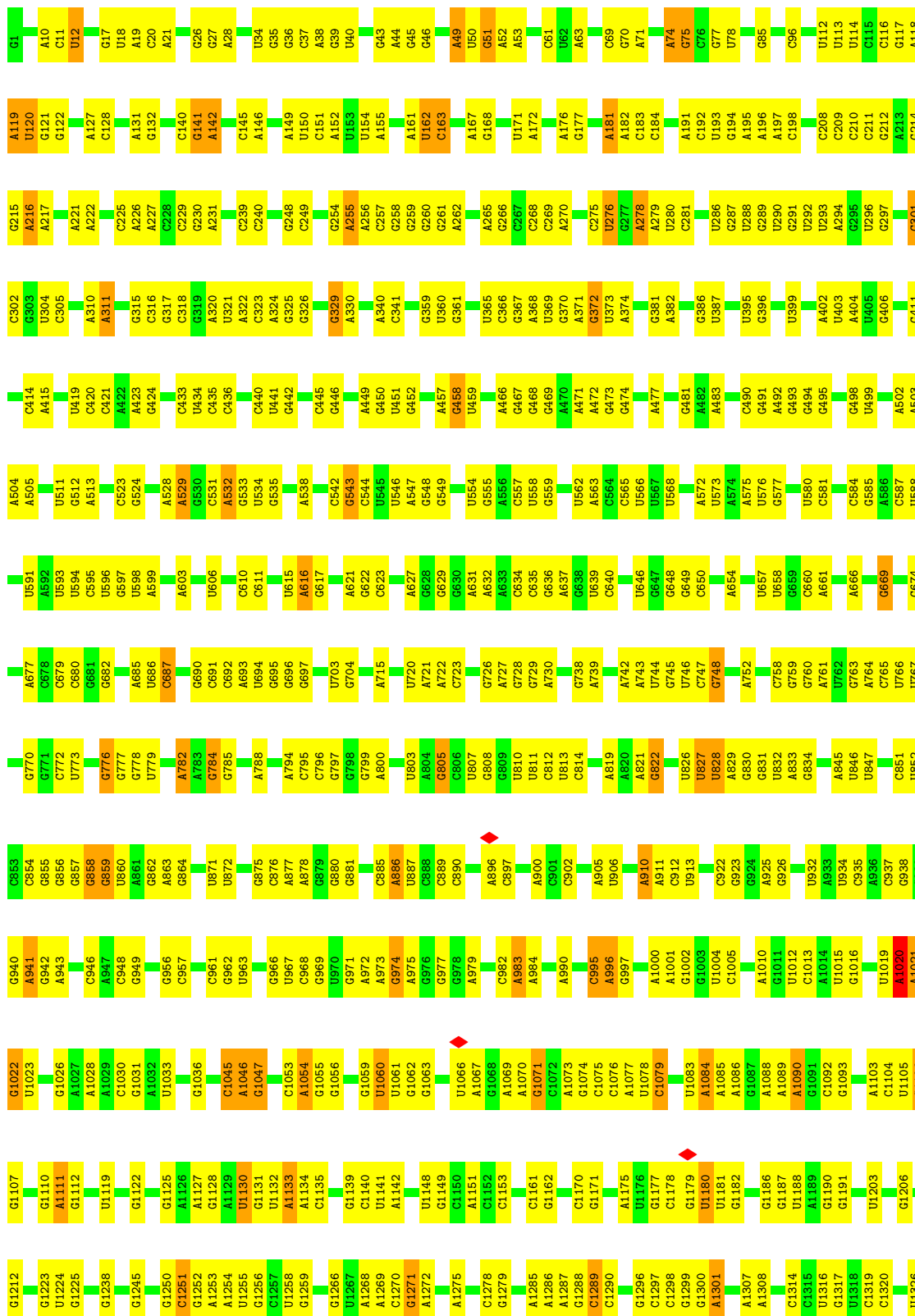
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N165	9
D166	8
K167	7
N168	6
G169	5
I170	4
T174	3
K177	2
D181	1
K184	1
L185	1
N188	1
L189	1
L192	1
L193	1
L196	1
K205	10
G206	9
K210	10
I214	8
G219	7
V222	6
D225	5

- Chain 3:  56% 40% .

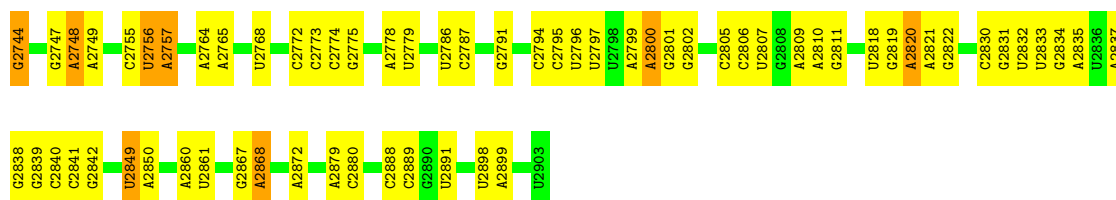
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G1461	G1371	G1300	U1205	U1008	G1006	A912	C817	A716	A621	A523	G410	U323	G212	U84
U1464	A1374	A1301	A1213	U1118	U1009	A918	C818	A717	C624	C525	A412	A327	G213	U85
A1465	A1375	G1304	A1216	C1119	C1011	A919	U820	C719	U625	C526	G413	A328	U216	C87
A1468	C1378	A1305	G1217	U1120	A1012	U920	C821	C720	C628	G530	C418	A329	C217	C90
G1475	G1379	G1306	C1218	U1122	G1013	A921	A825	C721	A629	U531	C419	G332	U218	U91
A1476	U1380	G1310	A1219	G1123	A1014	G922	C826	C722	G628	A532	U421	C335	U219	U92
U1477	U1381	G1311	G1220	U1125	G1015	A923	U827	C723	A632	A533	G422	A336	G220	U93
U1478	C1382	A1312	G1221	U1126	C924	G925	U828	C724	G633	A534	C423	G337	U224	G84
U1391	U1391	U1313	G1222	G1127	A1019	G926	C829	A728	C633	G537	G424	A338	C225	C95
G1392	G1392	C1314	A1225	C1128	G1020	G933	U830	A729	U636	G538	G425	C339	G226	G100
U1485	U1393	G1315	C1226	C1129	U1023	G934	U834	C730	A640	A539	C426	C345	A101	A101
G1486	G1394	G1316	A1227	U1130	G1024	A935	U835	C731	U641	G540	G428	C346	U229	G112
G1487	C1395	C1317	C1228	G1137	U1030	C936	C836	C732	A642	G541	U429	C347	G230	G113
A1488	A1318	A1318	A1229	G1138	C1028	A937	U843	C733	G645	G542	A430	G348	U231	U114
A1489	A1319	A1319	C1230	G1139	U1031	A938	U844	C734	G646	U543	U437	A349	G232	G123
A1490	C1320	C1320	G1231	U1140	G1032	G939	U845	C735	U653	A547	U438	G351	C235	U123
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G1496	G1324	A1324	C1237	A1150	G1034	A946	C857	C737	U659	A552	G449	A353	G237	C132
A1497	A1238	A1238	A1238	C1158	U1038	G947	U858	C742	U662	A553	G450	C354	A243	G144
U1498	C1239	C1239	A1239	U1159	C1039	U950	C859	A743	U663	A554	A451	C355	U244	G145
A1502	U1240	U1240	G1241	C1160	U1040	A951	U865	C744	A663	U555	U452	C356	U245	G146
A1503	G1242	G1242	A1243	C1161	U1041	U952	C866	C745	G664	A556	U453	C357	G246	G147
G1504	C1243	A1332	G1244	U1162	U1042	U953	C867	C746	A665	A557	U454	C372	G247	G148
U1505	G1244	G1333	G1244	G1164	U1043	G954	C868	C747	C671	A558	U455	G376	G251	A149
U1506	G1334	G1334	A1251	U1165	U1052	U955	U869	C748	U672	A559	A460	G377	U252	U150
A1507	G1334	G1334	A1252	U1166	U1053	U956	C870	C749	U673	U561	A461	A381	G255	A152
U1512	A1339	A1339	G1253	A1169	C1054	U960	U872	C754	U674	A563	U464	A382	U261	A161
A1513	U1340	U1340	A1254	A1170	U1055	U961	C876	C755	A675	A564	U465	C371	A262	A162
G1514	G1341	G1341	G1255	A1171	U1060	G966	C877	C756	A676	U571	U466	C372	G266	C163
G1515	G1342	G1342	A1256	G1174	U1061	A969	U878	C757	U677	A572	U467	G376	C267	U166
G1516	G1343	G1343	A1257	G1175	U1071	C970	C879	C758	U678	A573	C477	G377	A279	A167
U1517	A1344	A1344	G1258	G1176	C1072	G971	U884	C759	C680	A574	A478	A381	C285	A171
A1518	U1345	U1345	C1259	U1182	U1073	G971	U885	C760	U684	C576	C483	A382	C286	C183
U1519	A1346	A1346	G1260	G1184	G1074	G971	U886	C761	U685	C577	C484	A382	G289	C193
G1524	U1347	U1347	G1260	G1184	G1074	G971	U887	C762	U686	C578	U485	A382	C290	C194
G1525	U1348	U1348	C1273	G1187	U1075	A974	U888	C763	U687	C579	U486	A382	G281	A195
G1526	A1349	A1349	A1274	U1188	U1076	A975	U889	C764	U688	A579	U487	A382	C285	A196
U1527	G1350	G1350	A1275	U1189	U1077	G976	U890	C765	U689	C580	U488	A382	C286	A197
U1528	C1351	C1351	G1278	G1190	A1081	A977	U891	C766	U690	C581	U489	A382	C287	G202
G1529	U1352	U1352	G1279	A1191	A1082	A978	U892	C767	U691	C582	U490	A382	C288	G203
G1530	G1353	G1353	A1280	C1192	U1083	A983	U893	C768	U692	C583	U491	A382	C289	G204
U1533	U1444	G1355	C1281	G1193	A1092	C984	U894	C769	U693	C584	U492	A382	C290	A205
A1534	U1445	G1356	A1282	U1194	A1093	C985	U895	C770	U694	C585	U493	A382	C291	C206
U1537	A1446	A1357	U1286	C1195	G1094	U986	U896	C771	U695	C586	U494	A382	C292	C207
U1540	G1448	C1359	A1287	A1196	C1095	U987	U897	C772	U696	C587	U495	A382	C293	
	C1449	A1288	A1288	G1197	C1096	U988	U898	C773	U697	C588	U496	A382	C294	
		A1363	A1289	A1198	C1097	G993	U899	C774	U698	C589	U497	A382	C295	
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	G1458	A1368	G1297	A1201	C1100	U996	U902	C777	U701	C592	U501	A382	C298	
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							U905	C780	U704	C595	U504	A382	C301	
							U906	C781	U705	C596	U505	A382	C302	
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							U908	C783	U707	C598	U507	A382	C304	
							U909	C784	U708	C599	U508	A382	C305	
							U910	C785	U709	C600	U509	A382	C306	
							U911	C786	U710	C601	U510	A382	C307	
							U912	C787	U711	C602	U511	A382	C308	
							U913	C788	U712	C603	U512	A382	C309	
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							U915	C790	U714	C605	U514	A382	C311	
							U916	C791	U715	C606	U515	A382	C312	
							U917	C792	U716	C607	U516	A382	C313	
							U918	C793	U717	C608	U517	A382	C314	
							U919	C794	U718	C609	U518	A382	C315	
							U920	C795	U719	C610	U519	A382	C316	
							U921	C796	U720	C611	U520	A382	C317	
							U922	C797	U721	C612	U521	A382	C318	
							U923	C798	U722	C613	U522	A382	C319	
							U924	C799	U723	C614	U523	A382	C320	
							U925	C800	U724	C615	U524	A382	C321	
							U926	C801	U725	C616	U525	A382	C322	
							U927	C802	U726	C617	U526	A382	C323	
							U928	C803	U727	C618	U527	A382	C324	
							U929	C804	U728	C619	U528	A382	C325	
							U930	C805	U729	C620	U529	A382	C326	
							U931	C806	U730	C621	U530	A382	C327	
							U932	C807	U731	C622	U531	A382	C328	
							U933	C808	U732	C623	U532	A382	C329	
							U934	C809	U733	C624	U533	A382	C330	
							U935	C810	U734	C625	U534	A382	C331	
							U936	C811	U735	C626	U535	A382	C332	
							U937	C812	U736	C627	U536	A382	C333	
							U938	C813	U737	C628	U537	A382	C334	
							U939	C814	U738	C629	U538	A382	C335	
							U940	C815	U739	C630	U539	A382	C336	
							U941	C816	U740	C631	U540	A382	C337	
							U942	C817	U741	C632	U541	A382	C338	
							U943	C818	U742	C633	U542	A382	C339	
							U944	C819	U743	C634	U543	A382	C340	
							U945	C820	U744	C635	U544	A382	C341	
							U946	C821	U745	C636	U545	A382	C342	
							U947	C822	U746	C637	U546	A382	C343	
							U948	C823	U747	C638	U547	A382	C344	
							U949	C824	U748	C639	U548	A382	C345	
							U950	C825	U749	C640	U549	A382	C346	
							U951	C826	U750	C641	U550	A382	C347	
							U952	C827	U751	C642	U551	A382	C348	
							U953	C828	U752	C643	U552	A382	C349	
							U954	C829	U753	C644	U553	A382	C350	
							U955	C830	U754	C645	U554	A382	C351	
							U956	C831	U755	C646	U			

● Molecule 53: 23S ribosomal RNA

Chain 1: 

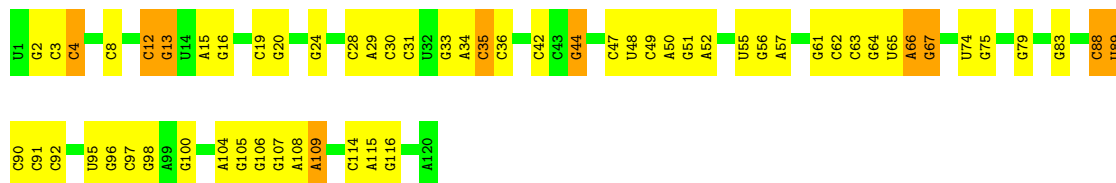


G2641	G2553	G2462	G2350	G2289	A2184	A2101	G2024	U1923	G1828	G1738	A1608	G1528	G1416	A1327
G2646	U2555	C2463	G2351	A2270	U2189	G2102	C2025	C1924	A1829	G1739	A1609	A1528	C1417	A1328
U2647	C2556	A2469	G2361	G2271	G2106	U2106	U2026	C1925	C1833	G1740	C1611	G1529	A1418	U1329
G2648	G2557	G2470	G2362	A2277	C2362	C2107	U2028	C1926	C1837	G1741	A1616	A1533	A1419	U1330
G2655	U2561	C2475	G2363	G2278	U2195	U2109	G2030	G1930	U1841	C1748	C1625	A1534	A1420	G1331
G2671	U2562	A2476	G2365	A2281	C2196	G2110	A2031	U1931	U1842		A1626	G1535	G1421	G1332
U2672	U2563	U2477	G2366	G2282	C2197	G2111	G2032	G1932	G1848	G1753	U1629	C1536	G1424	A1336
G2673	A2564	A2478	G2367	C2283	A2198	G2112	U2034	G1933	G1849	A1754	A1630	A1537	G1425	U1341
G2674	G2565	U2479	G2376	A2284	A2199	U2113	G2035	A1936	U1853	U1758	A1637	G1538	G1429	U1344
A2675	G2566	C2480	A2377	C2285	C2200	A2114	G2036	A1937	A1854	C1760		G1539	G1430	G1345
C2676	C2567	G2481	A2378	A2287	U2203	A2117	U2039	A1938	A1855	G1761		G1540	A1431	U1346
G2677	A2572	G2484	G2379	A2288	G2204	U2118	G2040	U1943	U1856	C1764	G1645	U1539	G1435	
C2678	C2573	A2489	C2380	A2289	A2119	A2118	U2041	U1944	U1857		G1646	G1540	G1436	
A2679	G2574	U2490	A2381	U2291	G2120	G2121	U2042	U1946	U1858	G1771	U1647	C1541	G1441	U1351
U2680	U2579	G2491	G2382	U2292	G2121	G2122	C2043	C1947	U1859	A1772	U1648	G1542	U1442	A1352
C2681	C2580	U2491	U2383	G2293	U2122	G2123			U1860	A1773	G1649	G1543	U1443	A1353
A2682	U2581	C2498	G2384	C2294	G2123	G2124	C2047	U1955	G1861		U1651	A1544	G1444	A1354
G2686	G2582	C2499	U2385	G2295	G2125	G2126	G2048	U1956	G1871	U1775		G1545	G1445	C1357
U2687	U2583	U2296	A2391	A2297	A2126	A2127	G2049	C1957	A1872	G1776		G1546	C1446	G1358
G2688	G2584	A2298	A2392	U2298	G2128	G2129	A2052	U1963	A1873	U1779	G1661	A1549	G1447	C1363
U2689	U2585	U2299	U2393	U2299	G2130	C2129	C2055	G1964	G1874	A1780	G1662	C1550	G1448	G1364
U2690	G2590	U2305	U2403	U2305	U2131	U2132	G2056	C1965	C1875	A1784	U1664	G1555	C1454	A1365
U2696	A2590	U2309	U2404	A2309	U2131	U2132	G2061	C1966	U1881	A1785	U1666	G1559	U1468	A1366
G2697	C2591	U2310	U2405	C2310	U2132	G2133	A2062	C1967	U1882	A1786		G1560	G1469	A1367
U2698	G2592	A2311	A2406	A2311	G2134	A2134	A2062	U1970	U1883		U1669	G1560	U1469	G1368
C2699	U2599	G2315	G2415	G2315	U2139	U2140	C2066	U1971	G1888	G1796	C1670	U1563	C1461	C1370
G2704	A2602	G2316	G2416	A2316	G2140	G2141	G2067	U1979	G1889	G1797	U1671	C1564	U1470	G1371
A2706	U2505	G2318	G2418	G2318	C2145	C2146	U2068	G1980	U1890	G1797	G1681	C1565	A1376	U1372
C2710	C2606	G2319	U2229	G2319	C2147	C2148	A2070	G1989	A1890	G1797	U1680	G1567	U1475	A1373
G2714	U2609	A2322	U2233	A2322	C2153	C2154	A2071	C1990	C1893	C1800	G1682	A1569	U1476	C1376
C2715	C2610	G2323	G2234	G2323	A2154	U2155	C2072	U1991	C1894	A1801	U1683	A1570	A1378	G1377
C2717	U2613	U2324	G2234	G2324	C2155	U2156	C2073	G1992	C1894	A1802	G1674	A1571	G1482	U1379
G2718	U2614	G2325	U2238	G2325	G2156	G2157	U2074	U1993	A1900	G1807	U1684	A1572	U1486	A1383
U2719	U2615	C2326	G2238	G2326	C2157	G2157	U2075	C1996	A1901	G1808	G1695	U1578	U1487	
G2729	A2531	A2327	U2244	A2327	G2162	G2162	C2078	C1997	C1902	A1809		A1579	C1386	C1387
U2720	U2532	A2328	U2245	A2328	A2163	A2163	U2079	A1998	G1903	A1810	A1700	G1581	A1490	A1387
U2728	G2533	U2329	G2246	G2329	C2164	C2164	A2080	C1999	G1904	A1811	A1701	U1584	U1494	U1394
G2730	A2534	G2331	C2248	G2331	U2170	U2170	U2086	C2000	C1905	G1811	G1704	C1585	A1495	A1395
C2731	U2537	U2334	U2249	U2334	A2171	A2171	G2087	C2008	G1907	C1816	A1705	C1586	C1498	C1398
G2732	C2538	G2339	G2250	G2339	U2172	U2172	A2088	A2009	C1908	G1817		G1587	G1499	C1404
A2733	G2543	A2340	C2258	G2340	A2173	A2173	C2089	G2010	G1909	U1818	G1715	U1593	U1500	U1405
G2737	U2544	U2343	C2258	U2343	C2176	C2176	G2093	G2011	G1910	A1819	U1720	A1594	G1501	G1510
U2738	G2545	U2344	C2263	U2344	A2177	A2177	C2096	A2013	A1913	G1822	G1721	U1594	U1506	U1409
U2739	U2546	G2345	A2266	G2345	C2178	C2178	A2097	U2017	U1917	G1823	C1727	G1601	C1507	U1411
A2740	A2547	G2346	A2267	G2346	C2179	C2179	U2099	U2022	A1918	U1825	C1728	A1603	A1508	U1412
G2741	U2548	U2348	U2267	U2348	C2179	C2179	G2100		A1919	U1826	U1729	U1603	A1509	A1413
U2743	G2549	G2349	A2268	G2349	A2183	A2183			C1920	C1730			G1510	



• Molecule 54: 5S ribosomal RNA

Chain 2: 50% 42% 8%



• Molecule 55: tRNAfMet

Chain 5: 68% 26% 6%



• Molecule 55: tRNAfMet

Chain 6: 53% 44% 3%



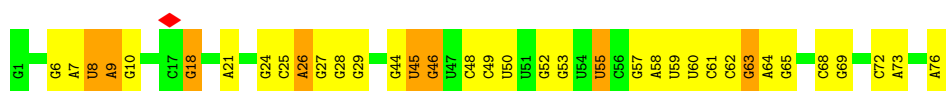
• Molecule 56: mRNA

Chain 4: 50% 50%



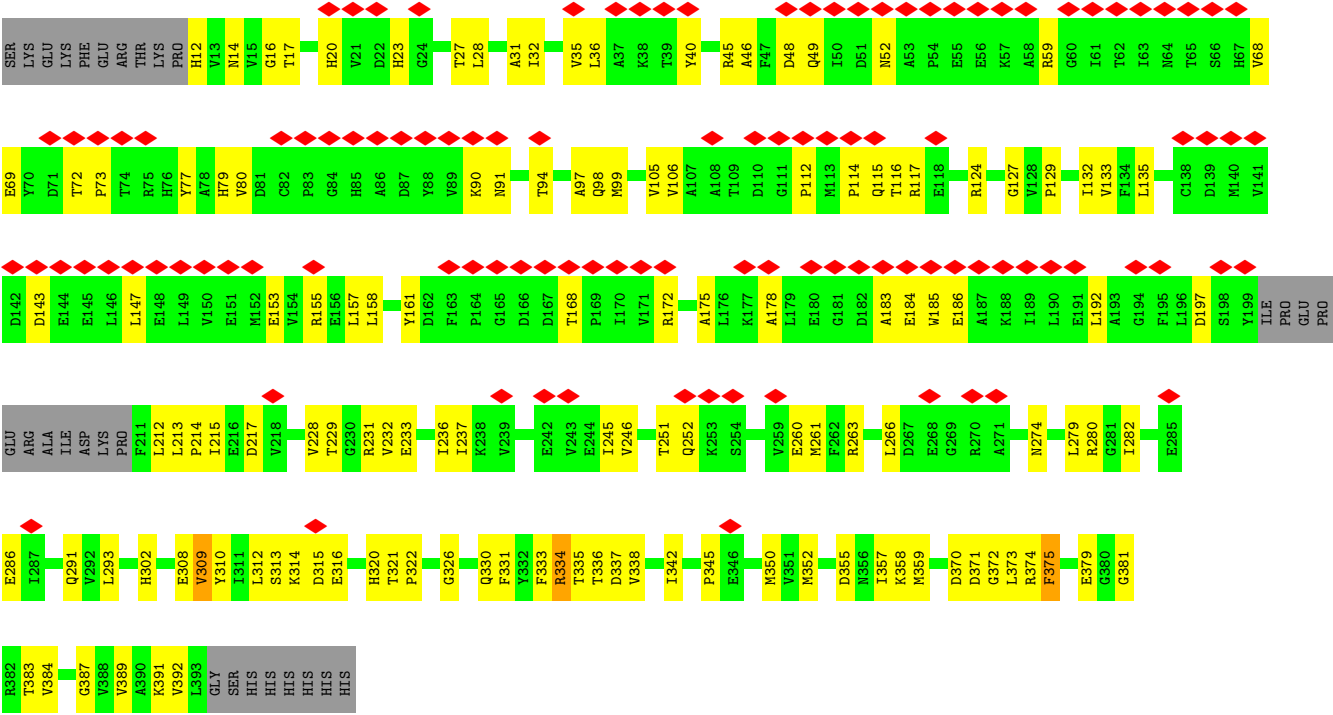
• Molecule 57: tRNA^{Phe}

Chain 7: 53% 37% 11%



• Molecule 58: Elongation factor Tu

Chain 8: 28% 60% 32% 7%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6311	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	16.931	Depositor
Minimum map value	-9.315	Depositor
Average map value	0.111	Depositor
Map value standard deviation	0.831	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	0.93	4/2852 (0.1%)
2	c	0.29	0/1586	0.85	4/2134 (0.2%)
3	d	0.29	0/1571	0.92	6/2113 (0.3%)
4	e	0.30	0/1435	0.83	1/1926 (0.1%)
5	f	0.31	0/1343	0.89	2/1816 (0.1%)
6	g	0.32	0/1122	1.02	7/1515 (0.5%)
7	h	0.34	0/1002	1.05	9/1350 (0.7%)
8	i	0.37	0/1046	1.05	7/1410 (0.5%)
9	j	0.29	0/1152	0.87	4/1551 (0.3%)
10	k	0.29	0/948	0.95	2/1268 (0.2%)
11	l	0.29	0/1054	0.94	3/1403 (0.2%)
12	m	0.29	0/1093	0.87	2/1460 (0.1%)
13	n	0.29	0/974	0.98	8/1301 (0.6%)
14	o	0.28	0/902	0.86	2/1209 (0.2%)
15	p	0.28	0/929	0.81	1/1242 (0.1%)
16	q	0.29	0/960	0.92	6/1278 (0.5%)
17	r	0.30	0/829	0.87	3/1107 (0.3%)
18	s	0.28	0/864	0.83	1/1156 (0.1%)
19	t	0.28	0/745	0.86	3/994 (0.3%)
20	u	0.28	0/788	0.86	0/1051
21	v	0.28	0/766	0.90	1/1025 (0.1%)
22	w	0.29	0/582	0.88	1/769 (0.1%)
23	x	0.28	0/635	0.88	2/848 (0.2%)
24	y	0.27	0/510	0.90	3/677 (0.4%)
25	z	0.30	0/453	0.76	0/605
26	B	0.28	0/450	0.84	1/599 (0.2%)
27	C	0.34	0/417	0.90	0/554
28	D	0.31	0/380	0.95	0/498
29	E	0.30	0/513	0.85	1/676 (0.1%)
30	F	0.32	0/303	0.87	1/397 (0.3%)
31	G	0.30	0/1788	0.87	5/2408 (0.2%)
32	H	0.32	0/1652	0.90	5/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.93	10/2227 (0.4%)
34	J	0.31	0/1170	0.92	5/1573 (0.3%)
35	K	0.32	0/836	0.96	4/1128 (0.4%)
36	L	0.29	0/1196	0.90	1/1602 (0.1%)
37	M	0.29	0/989	0.93	2/1326 (0.2%)
38	N	0.31	0/1034	0.89	1/1375 (0.1%)
39	O	0.33	0/797	0.91	3/1077 (0.3%)
40	P	0.32	0/886	0.98	5/1195 (0.4%)
41	Q	0.32	0/969	0.96	2/1300 (0.2%)
42	R	0.31	0/893	0.92	4/1193 (0.3%)
43	S	0.31	0/817	0.90	2/1088 (0.2%)
44	T	0.28	0/722	0.93	4/964 (0.4%)
45	U	0.30	0/659	0.89	2/884 (0.2%)
46	V	0.30	0/658	0.93	2/881 (0.2%)
47	W	0.31	0/545	0.90	3/731 (0.4%)
48	X	0.31	0/653	0.84	0/877
49	Y	0.29	0/671	0.92	2/888 (0.2%)
50	Z	0.34	0/551	1.03	4/728 (0.5%)
51	a	0.30	0/1034	0.77	0/1387
52	3	0.41	0/36963	0.47	3/57662 (0.0%)
53	1	0.40	0/69796	0.48	1/108888 (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	0.46	0/2855
56	4	0.40	0/436	0.46	0/679
57	7	0.40	0/1809	0.48	0/2819
58	8	0.32	0/2903	0.91	7/3928 (0.2%)
All	All	0.37	0/166102	0.62	162/248006 (0.1%)

There are no bond length outliers.

All (162) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	S	49	THR	N-CA-C	-8.94	101.63	112.54
7	h	43	LYS	N-CA-C	-8.56	101.44	112.23
3	d	73	ILE	N-CA-C	-8.28	104.96	112.90
6	g	11	ASN	N-CA-C	7.97	120.67	111.11
33	I	176	LYS	N-CA-C	-7.73	102.94	113.30
47	W	69	TYR	N-CA-C	-7.55	102.74	110.97
46	V	51	GLU	N-CA-C	7.48	121.51	112.38
50	Z	44	ARG	N-CA-C	-7.44	102.10	112.45
7	h	117	LEU	N-CA-C	7.35	121.52	109.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	M	67	GLY	N-CA-C	-7.25	103.74	113.24
33	I	9	LYS	N-CA-C	-7.19	103.98	112.89
50	Z	42	THR	N-CA-C	7.07	118.64	111.07
8	i	97	VAL	N-CA-C	6.92	116.93	110.42
5	f	47	ASN	N-CA-C	-6.88	104.00	112.88
44	T	49	HIS	N-CA-C	6.86	118.84	111.36
44	T	39	GLN	N-CA-C	-6.77	103.98	111.36
49	Y	84	LYS	N-CA-C	-6.72	103.76	112.23
13	n	119	SER	N-CA-C	-6.71	104.22	112.88
7	h	42	ARG	N-CA-C	-6.70	105.10	113.28
11	l	92	LEU	N-CA-C	-6.68	104.08	111.36
8	i	91	LYS	CA-C-N	6.59	126.10	119.24
8	i	91	LYS	C-N-CA	6.59	126.10	119.24
7	h	55	VAL	N-CA-C	6.58	117.53	109.30
22	w	52	ASP	N-CA-C	-6.57	104.41	112.88
58	8	326	GLY	N-CA-C	-6.52	106.05	114.85
17	r	51	VAL	CA-C-N	-6.51	113.56	120.66
17	r	51	VAL	C-N-CA	-6.51	113.56	120.66
2	c	150	GLN	N-CA-C	6.50	118.36	111.28
13	n	67	PHE	N-CA-C	-6.47	105.52	113.41
7	h	5	LEU	N-CA-C	-6.46	104.08	112.23
19	t	50	LEU	N-CA-C	6.46	118.32	111.28
3	d	176	ASP	CA-C-N	6.46	125.96	119.24
3	d	176	ASP	C-N-CA	6.46	125.96	119.24
7	h	30	SER	N-CA-C	-6.38	105.07	112.92
30	F	36	ARG	N-CA-C	6.37	116.86	108.07
44	T	43	ALA	N-CA-C	-6.27	104.52	111.36
31	G	133	ALA	N-CA-C	-6.27	105.12	112.89
6	g	10	ALA	N-CA-C	6.26	124.13	110.80
58	8	309	VAL	N-CA-C	6.18	118.07	109.29
13	n	54	LEU	N-CA-C	-6.15	105.58	114.12
15	p	75	THR	N-CA-C	6.14	117.64	111.07
35	K	40	GLU	N-CA-C	6.14	119.24	110.10
29	E	63	TYR	N-CA-C	6.11	118.02	111.36
1	b	87	SER	N-CA-C	-6.09	105.84	113.28
45	U	54	LEU	N-CA-C	6.09	118.42	111.11
33	I	166	LYS	CA-C-N	6.07	127.42	119.84
33	I	166	LYS	C-N-CA	6.07	127.42	119.84
40	P	125	LYS	N-CA-C	6.05	117.70	110.19
41	Q	43	LYS	N-CA-C	6.02	123.11	109.81
50	Z	21	SER	N-CA-C	-6.01	105.99	113.38
35	K	39	LEU	N-CA-C	-5.99	104.82	113.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	3	1190	G	C2'-C3'-O3'	5.98	118.46	109.50
19	t	72	GLN	N-CA-C	-5.97	105.74	114.39
7	h	44	ALA	N-CA-C	-5.96	104.72	112.23
9	j	7	LYS	CA-C-N	5.93	127.25	119.84
9	j	7	LYS	C-N-CA	5.93	127.25	119.84
10	k	111	LYS	N-CA-C	-5.92	106.06	113.28
23	x	25	LYS	N-CA-C	5.91	118.09	108.63
35	K	31	GLY	N-CA-C	-5.90	105.46	113.37
16	q	91	ARG	N-CA-C	5.86	118.42	111.33
47	W	17	VAL	N-CA-C	5.85	116.97	109.30
12	m	110	GLU	N-CA-C	5.83	118.14	111.02
53	1	1020	A	C2'-C3'-O3'	5.79	118.18	109.50
34	J	121	ASN	N-CA-C	5.74	120.11	112.30
6	g	30	LEU	N-CA-C	5.72	117.59	111.36
31	G	139	GLU	N-CA-C	-5.69	105.83	112.89
32	H	100	ILE	N-CA-C	5.69	117.19	108.71
10	k	32	TYR	N-CA-C	5.68	119.22	110.42
35	K	68	GLN	N-CA-C	5.68	119.31	112.38
52	3	1300	G	N9-C1'-C2'	5.65	120.48	112.00
2	c	132	ALA	N-CA-C	-5.65	106.38	113.72
13	n	56	LYS	N-CA-C	-5.65	105.20	111.36
11	l	113	ALA	N-CA-C	-5.63	106.09	114.64
3	d	75	SER	CA-C-N	5.62	125.24	119.56
3	d	75	SER	C-N-CA	5.62	125.24	119.56
21	v	80	HIS	N-CA-C	-5.61	102.97	109.93
31	G	222	GLU	N-CA-C	-5.60	105.18	112.23
33	I	146	GLU	N-CA-C	5.60	117.06	111.07
24	y	14	LEU	N-CA-C	-5.59	105.34	111.82
41	Q	88	ASP	N-CA-C	-5.57	107.48	114.56
11	l	137	ALA	N-CA-C	-5.57	105.98	112.89
46	V	68	LYS	N-CA-C	-5.57	105.30	111.71
1	b	114	GLN	N-CA-C	5.57	118.56	109.59
42	R	89	ARG	N-CA-C	-5.56	105.14	111.14
26	B	31	LYS	N-CA-C	5.55	117.01	111.07
13	n	2	ARG	N-CA-C	5.54	118.84	111.30
19	t	78	SER	N-CA-C	5.54	118.05	110.24
49	Y	36	ALA	N-CA-C	-5.53	105.33	111.36
17	r	14	VAL	N-CA-C	5.53	115.85	108.11
16	q	24	TYR	N-CA-C	5.51	118.43	110.28
33	I	33	ILE	N-CA-C	5.50	116.05	110.05
1	b	11	GLY	N-CA-C	-5.50	107.42	115.72
32	H	107	LYS	CA-C-N	5.49	125.01	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	H	107	LYS	C-N-CA	5.49	125.01	119.19
58	8	133	VAL	N-CA-C	5.46	116.10	108.89
3	d	148	ILE	N-CA-C	5.44	115.41	108.12
7	h	45	GLY	N-CA-C	-5.44	107.58	114.16
40	P	97	ARG	N-CA-C	-5.44	105.51	111.82
33	I	77	GLU	N-CA-C	-5.41	105.42	112.23
47	W	63	TYR	N-CA-C	-5.41	106.19	112.89
39	O	21	ALA	N-CA-C	-5.41	105.55	111.82
8	i	27	LEU	N-CA-C	-5.39	106.71	113.72
39	O	20	GLN	N-CA-C	-5.39	106.54	113.23
52	3	1201	A	C2'-C3'-O3'	5.38	117.57	109.50
37	M	31	LEU	N-CA-C	5.38	116.83	110.97
1	b	132	ARG	N-CA-C	-5.37	106.04	112.59
16	q	70	GLN	N-CA-C	-5.37	105.47	112.23
7	h	46	ARG	N-CA-C	-5.35	105.49	112.23
50	Z	56	ALA	N-CA-C	-5.35	105.62	111.82
40	P	100	ASN	N-CA-C	-5.33	105.51	112.23
31	G	180	ILE	CA-C-N	5.33	125.34	119.90
31	G	180	ILE	C-N-CA	5.33	125.34	119.90
18	s	28	LYS	N-CA-C	-5.33	101.96	109.96
34	J	55	VAL	N-CA-C	5.32	119.33	112.67
24	y	27	ASN	N-CA-C	5.31	116.87	111.14
13	n	9	GLN	N-CA-C	5.29	116.72	111.07
42	R	102	LYS	N-CA-C	5.28	117.03	111.28
33	I	8	LEU	N-CA-C	-5.27	106.36	114.16
38	N	88	GLU	N-CA-C	-5.26	106.12	112.54
58	8	192	LEU	N-CA-C	-5.25	105.64	111.36
16	q	18	LYS	N-CA-C	-5.24	106.91	113.72
45	U	29	ASN	N-CA-C	-5.23	106.21	112.59
2	c	61	THR	N-CA-C	5.20	118.16	110.46
13	n	22	ARG	N-CA-C	-5.20	105.53	111.14
14	o	82	ALA	N-CA-C	-5.19	105.69	112.23
34	J	117	ALA	N-CA-C	-5.19	105.69	112.23
14	o	12	THR	N-CA-C	5.18	117.60	111.33
2	c	152	PRO	N-CA-C	-5.18	106.46	113.40
43	S	48	GLN	N-CA-C	-5.17	107.14	113.50
16	q	31	TYR	N-CA-C	5.17	116.60	111.07
5	f	44	HIS	N-CA-C	-5.17	105.05	112.13
13	n	25	ALA	N-CA-C	-5.17	105.73	111.36
8	i	43	ALA	N-CA-C	-5.16	106.94	113.18
42	R	78	ARG	N-CA-C	-5.16	105.73	111.36
23	x	6	VAL	N-CA-C	5.15	115.26	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R	96	VAL	N-CA-C	5.15	116.23	111.81
6	g	39	ALA	N-CA-C	5.14	117.57	109.39
58	8	178	ALA	N-CA-C	-5.14	106.96	113.18
24	y	20	ASN	N-CA-C	-5.13	106.18	112.90
33	I	94	GLU	N-CA-C	-5.12	106.72	113.17
39	O	22	THR	N-CA-C	-5.11	105.79	112.23
58	8	183	ALA	N-CA-C	5.10	117.57	111.71
6	g	67	ALA	N-CA-C	-5.09	105.91	111.82
8	i	129	GLU	N-CA-C	-5.09	105.92	111.82
16	q	88	GLU	N-CA-C	5.09	119.17	112.25
4	e	4	HIS	N-CA-C	-5.08	105.82	111.36
6	g	62	LEU	N-CA-C	-5.08	106.59	112.89
6	g	48	GLU	N-CA-C	5.07	118.93	112.34
32	H	65	VAL	N-CA-C	5.06	115.25	108.17
9	j	31	GLU	N-CA-C	-5.06	105.95	111.82
34	J	131	ASN	CA-C-N	5.05	126.15	119.84
34	J	131	ASN	C-N-CA	5.05	126.15	119.84
9	j	40	HIS	N-CA-C	-5.04	106.98	114.64
32	H	25	THR	N-CA-C	5.04	118.20	111.75
8	i	10	LEU	N-CA-C	5.03	114.28	108.49
33	I	23	GLY	N-CA-C	5.03	120.29	111.78
36	L	4	ARG	N-CA-C	5.03	117.76	110.42
40	P	121	ARG	CA-C-N	5.03	123.28	119.66
40	P	121	ARG	C-N-CA	5.03	123.28	119.66
12	m	24	THR	N-CA-C	-5.01	107.16	114.12
44	T	46	LYS	N-CA-C	5.00	121.46	110.80
58	8	337	ASP	N-CA-C	-5.00	105.48	112.03

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	75	0
2	c	1565	0	1616	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	d	1552	0	1619	39	0
4	e	1411	0	1447	38	0
5	f	1323	0	1374	24	0
6	g	1111	0	1148	31	0
7	h	989	0	1025	63	0
8	i	1032	0	1088	46	0
9	j	1129	0	1162	41	0
10	k	939	0	1012	43	0
11	l	1045	0	1117	36	0
12	m	1074	0	1157	33	0
13	n	961	0	1000	41	0
14	o	892	0	923	31	0
15	p	917	0	965	34	0
16	q	947	0	1022	15	0
17	r	816	0	839	34	0
18	s	857	0	922	25	0
19	t	739	0	807	21	0
20	u	780	0	834	20	0
21	v	753	0	780	18	0
22	w	575	0	592	14	0
23	x	625	0	655	17	0
24	y	509	0	543	18	0
25	z	449	0	491	10	0
26	B	444	0	461	10	0
27	C	410	0	440	18	0
28	D	377	0	418	10	0
29	E	504	0	574	16	0
30	F	302	0	343	8	0
31	G	1757	0	1787	47	0
32	H	1625	0	1699	76	0
33	I	1643	0	1710	63	0
34	J	1157	0	1199	44	0
35	K	818	0	808	37	0
36	L	1182	0	1240	54	0
37	M	979	0	1034	36	0
38	N	1022	0	1070	57	0
39	O	787	0	828	41	0
40	P	870	0	878	43	0
41	Q	955	0	1019	32	0
42	R	884	0	944	31	0
43	S	805	0	847	48	0
44	T	714	0	737	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	U	649	0	666	25	0
46	V	649	0	691	31	0
47	W	536	0	552	23	0
48	X	638	0	665	19	0
49	Y	665	0	714	19	0
50	Z	545	0	579	46	0
51	a	1027	0	1092	27	0
52	3	33012	0	16618	576	0
53	1	62317	0	31346	968	0
54	2	2568	0	1303	63	0
55	5	1640	0	836	20	0
55	6	1640	0	837	29	0
56	4	388	0	196	7	0
57	7	1619	0	821	35	0
58	8	2853	0	2860	92	0
59	5	10	0	10	0	0
60	7	11	0	8	3	0
61	8	28	0	12	0	0
All	All	153103	0	104137	2978	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 12.

All (2978) 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)
31:G:186:VAL:HG13	31:G:190:SER:HB2	1.44	0.97
53:1:45:G:H5''	53:1:46:G:H5'	1.46	0.97
58:8:98:GLN:HG2	58:8:387:GLY:O	1.65	0.96
24:y:43:LEU:HD23	53:1:61:C:H5''	1.49	0.94
33:I:190:LEU:HD12	33:I:192:ALA:H	1.30	0.94
52:3:835:U:H2'	52:3:836:G:H5''	1.46	0.94
53:1:2048:G:H2'	53:1:2049:G:H5''	1.48	0.93
38:N:20:ILE:HD11	38:N:60:LEU:HD22	1.52	0.92
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.48	0.92
53:1:1645:G:H5''	53:1:1646:C:H5'	1.52	0.91
52:3:1259:C:H3'	52:3:1260:G:H5''	1.53	0.91
50:Z:40:PRO:O	50:Z:44:ARG:HG2	1.70	0.91
57:7:7:A:H3'	57:7:8:U:H5''	1.52	0.91
7:h:26:VAL:HG23	7:h:82:ILE:HG23	1.51	0.91
43:S:2:LYS:NZ	52:3:983:A:H5'	1.85	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1053:C:H2'	53:1:1054:A:H5''	1.52	0.89
43:S:23:ARG:HH22	52:3:1008:U:H5''	1.36	0.89
7:h:59:LEU:HD23	7:h:61:ARG:H	1.36	0.88
1:b:6:LYS:NZ	53:1:1695:G:H5'	1.89	0.88
52:3:769:G:H4'	52:3:1513:A:H4'	1.55	0.88
53:1:2277:G:H2'	53:1:2278:A:H5''	1.53	0.88
54:2:13:G:H21	54:2:16:G:H1'	1.37	0.88
50:Z:9:GLU:HB3	50:Z:10:PRO:HD3	1.56	0.88
1:b:6:LYS:HZ1	53:1:1695:G:H5'	1.38	0.88
54:2:65:U:H3'	54:2:108:A:H61	1.38	0.87
34:J:54:GLU:HG3	34:J:56:PRO:HD2	1.57	0.87
53:1:2432:A:H1'	55:6:75:C:H4'	1.57	0.86
7:h:61:ARG:HG3	53:1:1046:A:H4'	1.58	0.86
52:3:664:G:H22	52:3:741:G:H1	1.23	0.86
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.57	0.86
52:3:1033:G:H2'	52:3:1034:G:H5''	1.57	0.86
19:t:10:VAL:HG23	19:t:11:LEU:HD12	1.58	0.86
53:1:1020:A:H1'	53:1:1021:A:OP2	1.76	0.85
38:N:17:ARG:HH12	52:3:1129:C:H4'	1.40	0.84
52:3:327:A:O2'	52:3:328:C:H4'	1.78	0.84
58:8:45:ARG:HH12	58:8:68:VAL:HG13	1.43	0.83
55:5:75:C:H2'	55:5:76:A:H5''	1.58	0.83
38:N:114:LYS:NZ	52:3:1187:G:H5'	1.92	0.83
36:L:3:ARG:HH12	52:3:1092:A:H5'	1.42	0.83
53:1:2048:G:C2'	53:1:2049:G:H5''	2.09	0.82
33:I:33:ILE:H	33:I:33:ILE:HD12	1.45	0.82
53:1:1664:A:H61	53:1:1996:C:H42	1.27	0.82
46:V:18:LYS:HD2	52:3:255:G:H4'	1.62	0.82
53:1:1141:U:H4'	53:1:1142:A:O4'	1.79	0.81
13:n:53:THR:HG21	53:1:2840:C:H5''	1.62	0.81
53:1:1906:G:H2'	53:1:1907:G:H5''	1.62	0.81
52:3:1200:C:H5''	52:3:1201:A:H3'	1.62	0.81
53:1:2682:A:H61	53:1:2728:U:H1'	1.45	0.81
46:V:5:ARG:HD3	52:3:636:U:H5''	1.63	0.81
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.61	0.80
43:S:50:LEU:HD12	43:S:51:PRO:HD2	1.63	0.80
53:1:1105:U:H2'	53:1:1106:G:H5''	1.62	0.80
47:W:59:LYS:HD3	52:3:735:C:H5'	1.63	0.80
52:3:1137:C:H5'	52:3:1138:G:H5'	1.62	0.80
34:J:107:GLY:HA3	52:3:9:G:H5'	1.63	0.80
52:3:484:G:H4'	52:3:485:U:H5''	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:78:ARG:HH11	52:3:1382:C:H4'	1.47	0.79
53:1:1801:A:H5''	53:1:2203:U:H2'	1.64	0.79
1:b:16:VAL:HB	1:b:203:VAL:HG12	1.65	0.79
1:b:12:ARG:HH21	53:1:728:G:H5'	1.49	0.78
38:N:128:LYS:HD2	52:3:966:G:H21	1.46	0.78
57:7:25:C:H3'	57:7:26:A:H5''	1.66	0.78
53:1:1133:A:H4'	53:1:1134:A:H5''	1.65	0.78
53:1:1077:A:H2'	53:1:1078:U:H5'	1.65	0.78
37:M:38:VAL:O	37:M:42:GLU:HG2	1.84	0.78
1:b:5:CYS:HB3	1:b:15:VAL:HG23	1.65	0.77
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.66	0.77
32:H:160:GLU:HG3	32:H:161:ILE:HG12	1.67	0.77
39:O:40:ILE:HB	39:O:73:LEU:HB3	1.67	0.77
41:Q:3:VAL:HG13	46:V:35:LYS:HD2	1.66	0.77
41:Q:110:LYS:HD2	52:3:539:A:OP1	1.85	0.77
53:1:2286:G:H5''	53:1:2287:A:OP1	1.84	0.77
43:S:2:LYS:HZ2	52:3:983:A:H5'	1.45	0.77
7:h:56:ARG:HB2	53:1:1084:A:H1'	1.67	0.77
18:s:36:LEU:HD21	18:s:47:VAL:HG13	1.66	0.76
47:W:40:PRO:HB3	52:3:720:C:H5''	1.68	0.76
58:8:14:ASN:HD21	58:8:80:VAL:HG13	1.49	0.76
12:m:75:GLU:OE2	53:1:957:C:H5'	1.86	0.76
38:N:114:LYS:HZ3	52:3:1187:G:H5'	1.47	0.76
17:r:14:VAL:HG21	17:r:98:ILE:HG13	1.68	0.76
38:N:114:LYS:HG2	38:N:120:ALA:HA	1.67	0.75
8:i:25:PRO:HG2	57:7:55:U:H3'	1.67	0.75
9:j:7:LYS:HG2	53:1:538:A:H4'	1.69	0.75
31:G:45:THR:HG22	31:G:200:PRO:HB2	1.67	0.75
1:b:106:PRO:HG2	1:b:109:LEU:HB2	1.67	0.75
12:m:53:MET:HG3	12:m:116:ALA:HB1	1.69	0.75
53:1:1796:U:H2'	53:1:1797:G:H8	1.50	0.75
31:G:206:ILE:H	31:G:206:ILE:HD12	1.50	0.75
37:M:12:ARG:NH2	52:3:826:C:H5'	2.02	0.75
39:O:7:ARG:HB3	39:O:101:SER:HB3	1.68	0.75
58:8:245:ILE:HD11	58:8:291:GLN:HB3	1.69	0.75
38:N:104:THR:HG22	38:N:106:ASP:H	1.51	0.75
46:V:30:HIS:HD2	46:V:33:TYR:H	1.34	0.75
43:S:3:GLN:HG3	43:S:6:LYS:HE2	1.69	0.75
53:1:2391:G:H4'	53:1:2392:A:OP1	1.86	0.74
36:L:91:ARG:HG2	36:L:92:PRO:HD2	1.69	0.74
52:3:835:U:C2'	52:3:836:G:H5''	2.17	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:3:C:H2'	54:2:4:C:H5''	1.70	0.74
58:8:333:PHE:HB3	58:8:375:PHE:HB3	1.70	0.74
36:L:3:ARG:HH22	52:3:1092:A:H5''	1.51	0.74
48:X:30:LEU:H	48:X:30:LEU:HD12	1.53	0.74
53:1:310:A:H2'	53:1:311:A:H5''	1.70	0.74
36:L:91:ARG:HD2	36:L:93:VAL:H	1.53	0.74
52:3:701:U:H4'	52:3:703:G:H1'	1.70	0.74
53:1:2553:G:H3'	53:1:2554:U:H5''	1.68	0.73
52:3:1429:A:H2'	52:3:1430:A:H8	1.53	0.73
31:G:132:GLU:HA	31:G:135:MET:HG2	1.70	0.73
45:U:20:VAL:HG22	45:U:21:VAL:H	1.53	0.73
4:e:79:ARG:NH1	55:5:19:G:H1	1.86	0.73
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.70	0.72
17:r:78:ARG:HH12	53:1:990:A:H61	1.37	0.72
33:I:73:ASN:HA	33:I:76:LYS:HE2	1.72	0.72
32:H:3:LYS:HE3	52:3:1191:A:H5''	1.71	0.72
53:1:1807:G:H2'	53:1:1808:A:H5'	1.71	0.72
53:1:1476:U:H3	53:1:1515:A:H62	1.38	0.72
53:1:2296:U:H5''	53:1:2297:A:OP1	1.89	0.72
39:O:88:MET:O	39:O:89:ARG:HG3	1.89	0.72
39:O:53:ILE:HG23	43:S:84:ARG:HD2	1.71	0.72
58:8:45:ARG:NH1	58:8:68:VAL:HG13	2.04	0.72
52:3:1201:A:H1'	52:3:1202:U:OP2	1.90	0.71
53:1:2048:G:C3'	53:1:2049:G:H5''	2.20	0.71
53:1:2277:G:C2'	53:1:2278:A:H5''	2.20	0.71
55:5:75:C:C2'	55:5:76:A:H5''	2.20	0.71
36:L:3:ARG:HH12	52:3:1092:A:C5'	2.03	0.71
53:1:215:G:H4'	53:1:216:A:H4'	1.71	0.71
8:i:74:PRO:HB2	8:i:77:VAL:HG22	1.73	0.71
35:K:96:VAL:HG12	35:K:97:THR:H	1.56	0.71
15:p:90:ALA:HB2	15:p:112:ARG:HG3	1.72	0.71
53:1:1019:U:H3	53:1:1142:A:H62	1.36	0.71
15:p:29:VAL:HG23	15:p:79:VAL:HG22	1.73	0.71
29:E:36:ALA:HB3	29:E:39:ARG:HG2	1.73	0.71
53:1:2248:C:H2'	53:1:2249:U:H5'	1.70	0.71
54:2:3:C:C3'	54:2:4:C:H5''	2.20	0.71
9:j:109:LEU:HD22	9:j:118:MET:HE2	1.73	0.70
52:3:1236:A:H4'	52:3:1304:G:H4'	1.73	0.70
53:1:704:G:H2'	53:1:726:G:N2	2.07	0.70
53:1:974:G:H1'	53:1:975:A:C8	2.26	0.70
6:g:40:THR:HB	6:g:43:ASN:HD22	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C:44:GLN:HG2	27:C:45:HIS:N	2.05	0.70
53:1:2628:C:H3'	53:1:2629:U:H5'	1.72	0.70
7:h:114:GLU:HA	7:h:123:ILE:HG12	1.72	0.70
53:1:1278:C:H2'	53:1:1279:G:H8	1.57	0.70
39:O:11:LYS:HE2	39:O:71:LEU:HD11	1.74	0.70
52:3:405:U:H3'	52:3:406:G:H5'	1.72	0.70
38:N:29:ILE:HG13	38:N:30:ASN:OD1	1.91	0.69
22:w:39:THR:H	53:1:2331:G:H4'	1.57	0.69
40:P:92:ARG:HD3	50:Z:24:LYS:NZ	2.07	0.69
47:W:11:ARG:HD2	52:3:845:A:H1'	1.74	0.69
35:K:3:HIS:O	35:K:92:THR:HG22	1.92	0.69
41:Q:27:PRO:HG3	52:3:553:A:H1'	1.75	0.69
39:O:42:LEU:HD11	39:O:73:LEU:HB2	1.74	0.69
53:1:310:A:C2'	53:1:311:A:H5''	2.23	0.69
8:i:52:LEU:HD12	8:i:53:PRO:HD2	1.73	0.69
8:i:71:LYS:HD2	8:i:72:THR:H	1.57	0.69
54:2:3:C:H3'	54:2:4:C:H5''	1.73	0.69
54:2:66:A:H5''	54:2:67:G:OP1	1.92	0.69
55:6:54:U:H3	55:6:58:A:H62	1.40	0.69
33:I:103:ARG:HH12	33:I:164:ARG:HD3	1.58	0.69
32:H:35:ASP:O	32:H:38:VAL:HG12	1.93	0.69
53:1:1105:U:C2'	53:1:1106:G:H5''	2.23	0.69
32:H:63:ILE:HG13	32:H:98:ALA:HB2	1.74	0.68
53:1:1270:C:H5''	53:1:1271:G:H5''	1.75	0.68
42:R:113:LYS:HG3	42:R:114:PRO:HD3	1.75	0.68
57:7:65:G:H4'	58:8:330:GLN:HG2	1.76	0.68
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.74	0.68
53:1:275:C:H2'	53:1:276:U:H4'	1.76	0.68
40:P:23:HIS:HB3	40:P:30:ILE:HG23	1.76	0.68
41:Q:82:ARG:HG2	41:Q:95:HIS:HB2	1.74	0.68
45:U:75:ILE:O	45:U:78:VAL:HG12	1.94	0.68
3:d:190:ALA:O	3:d:193:VAL:HG12	1.93	0.68
24:y:2:LYS:HD2	53:1:78:U:OP2	1.93	0.68
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.75	0.68
53:1:2423:U:O2'	53:1:2425:A:H2'	1.94	0.68
54:2:3:C:C2'	54:2:4:C:H5''	2.24	0.68
2:c:35:THR:HG22	2:c:73:VAL:HG21	1.74	0.68
37:M:10:LEU:HD22	37:M:74:ILE:HD11	1.75	0.68
41:Q:69:GLU:HG2	52:3:521:G:H4'	1.75	0.68
53:1:2266:A:H4'	53:1:2267:A:C2	2.28	0.68
6:g:12:LEU:HD12	6:g:13:GLY:N	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:42:ASN:HA	8:i:45:THR:HG22	1.75	0.67
17:r:49:ILE:HB	17:r:51:VAL:O	1.94	0.67
52:3:29:U:O2'	52:3:30:U:H5'	1.93	0.67
58:8:345:PRO:HD3	58:8:359:MET:HA	1.74	0.67
52:3:1379:G:O2'	52:3:1380:U:H5'	1.93	0.67
53:1:528:A:N1	53:1:2042:A:H2'	2.09	0.67
42:R:9:PRO:HG2	42:R:44:ILE:HG13	1.74	0.67
53:1:2345:G:H21	53:1:2381:A:H3'	1.59	0.67
49:Y:32:LYS:HE2	52:3:1439:G:OP1	1.95	0.67
11:l:19:LEU:HB2	53:1:587:C:O2'	1.95	0.67
38:N:17:ARG:HH22	52:3:1129:C:H5''	1.60	0.67
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.75	0.67
13:n:26:GLY:HA2	13:n:75:ILE:HD12	1.76	0.67
35:K:6:ILE:H	35:K:6:ILE:HD12	1.60	0.67
3:d:76:PRO:HA	3:d:82:GLY:HA2	1.77	0.67
29:E:28:LEU:HD22	29:E:43:LEU:HB2	1.77	0.67
10:k:35:VAL:HG13	10:k:36:GLY:H	1.60	0.67
14:o:10:ARG:HH21	53:1:2294:G:H5''	1.59	0.67
52:3:1412:C:H2'	52:3:1413:A:C8	2.30	0.67
12:m:12:MET:HA	53:1:910:A:H62	1.59	0.66
34:J:105:ILE:HB	34:J:123:LEU:HD23	1.76	0.66
53:1:2800:A:H3'	53:1:2801:G:H5'	1.77	0.66
1:b:227:VAL:HG21	53:1:784:G:C6	2.30	0.66
33:I:4:LEU:HD23	52:3:406:G:H5''	1.77	0.66
36:L:149:ALA:HB1	40:P:58:THR:HG21	1.78	0.66
42:R:6:ILE:HG23	42:R:7:ASN:H	1.61	0.66
32:H:151:GLU:HB3	32:H:198:LYS:HB2	1.78	0.66
33:I:195:ASN:HD21	33:I:197:HIS:HB3	1.60	0.66
34:J:133:ILE:HD11	52:3:18:C:H5''	1.78	0.66
57:7:7:A:H3'	57:7:8:U:C5'	2.25	0.66
27:C:8:ILE:HB	27:C:50:GLU:OE1	1.96	0.66
52:3:112:G:H21	52:3:354:G:H5'	1.61	0.66
53:1:807:U:H2'	53:1:808:G:H8	1.59	0.66
7:h:88:HIS:HB2	7:h:89:PRO:HD3	1.77	0.66
33:I:131:ILE:HG12	52:3:620:C:C2	2.31	0.66
36:L:4:ARG:H	36:L:4:ARG:HD3	1.61	0.66
38:N:115:VAL:HG21	39:O:62:ARG:HB2	1.78	0.66
53:1:1909:C:H2'	53:1:1910:G:H8	1.61	0.66
15:p:52:ARG:HH21	53:1:2720:U:H5''	1.61	0.66
2:c:151:THR:OG1	2:c:152:PRO:HD3	1.96	0.66
53:1:799:G:H5''	53:1:800:A:H2'	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:20:SER:HB3	8:i:21:PRO:HD3	1.78	0.66
21:v:72:VAL:HG12	21:v:93:ARG:HA	1.78	0.66
34:J:24:VAL:HG22	34:J:25:LYS:H	1.60	0.66
57:7:6:G:C3'	57:7:7:A:H5''	2.25	0.66
58:8:215:ILE:HD11	58:8:293:LEU:HD23	1.77	0.66
29:E:51:LYS:HE3	53:1:937:C:OP2	1.96	0.65
8:i:9:LYS:HD2	53:1:1061:U:H5''	1.78	0.65
35:K:67:PRO:HG2	35:K:70:VAL:HG23	1.78	0.65
1:b:6:LYS:HG2	1:b:7:PRO:HD2	1.77	0.65
8:i:85:ILE:HD12	8:i:97:VAL:HG12	1.78	0.65
48:X:5:LYS:HD2	52:3:1313:U:OP1	1.96	0.65
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.78	0.65
32:H:26:LYS:NZ	52:3:1256:A:H5''	2.12	0.65
52:3:225:C:H2'	52:3:226:G:H5''	1.79	0.65
57:7:25:C:H2'	57:7:26:A:H4'	1.78	0.65
4:e:107:VAL:CG1	4:e:108:PRO:HD3	2.27	0.65
48:X:2:ARG:HG2	52:3:1312:G:N7	2.11	0.65
52:3:1497:G:O2'	52:3:1498:U:H5'	1.97	0.65
8:i:16:MET:HE3	8:i:17:ALA:H	1.61	0.65
53:1:2799:A:H2'	53:1:2800:A:H5'	1.78	0.65
27:C:4:ILE:H	27:C:4:ILE:HD12	1.60	0.65
52:3:396:C:H2'	52:3:397:A:H5''	1.77	0.65
52:3:1197:A:H2'	52:3:1198:G:H5''	1.79	0.65
10:k:99:ILE:HD13	10:k:115:ILE:HG23	1.78	0.65
39:O:11:LYS:HB3	39:O:71:LEU:HD13	1.79	0.65
43:S:80:ARG:O	43:S:83:VAL:HG22	1.97	0.65
19:t:9:LYS:HZ1	24:y:21:LEU:HD22	1.62	0.65
45:U:31:ARG:HB2	52:3:310:G:H5''	1.78	0.65
49:Y:67:HIS:HE1	52:3:132:C:H4'	1.61	0.65
29:E:31:ILE:HD11	53:1:2391:G:H5'	1.78	0.65
42:R:25:GLY:H	52:3:1329:A:H5''	1.62	0.65
53:1:2818:U:H2'	53:1:2819:G:H8	1.61	0.65
14:o:100:HIS:HD2	54:2:48:U:H4'	1.62	0.64
33:I:120:LYS:HG2	33:I:130:ASN:OD1	1.97	0.64
42:R:114:PRO:HG2	52:3:1228:C:H5''	1.77	0.64
52:3:1369:C:H2'	52:3:1370:G:C8	2.32	0.64
53:1:2698:U:H2'	53:1:2699:C:C6	2.32	0.64
34:J:55:VAL:HG23	34:J:56:PRO:HD3	1.79	0.64
34:J:153:ALA:HB2	34:J:163:ILE:HD13	1.79	0.64
57:7:6:G:H3'	57:7:7:A:H5''	1.79	0.64
7:h:23:LEU:HD13	7:h:118:ILE:HG13	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:29:ASP:HB2	7:h:56:ARG:HH22	1.61	0.64
54:2:88:C:H5''	54:2:89:U:OP1	1.98	0.64
35:K:8:PHE:HB3	35:K:87:SER:HB2	1.79	0.64
51:a:15:VAL:HG11	51:a:222:VAL:HG22	1.77	0.64
53:1:1903:G:H2'	53:1:1904:G:C8	2.33	0.64
32:H:163:ARG:HG3	32:H:165:GLU:OE2	1.96	0.64
53:1:1270:C:H5''	53:1:1271:G:C5'	2.28	0.64
53:1:2047:C:H2'	53:1:2048:G:H8	1.63	0.64
57:7:62:C:H2'	57:7:63:G:H5''	1.77	0.64
1:b:146:LYS:HB2	1:b:149:LYS:HB2	1.79	0.64
1:b:227:VAL:HG21	53:1:784:G:C5	2.32	0.64
39:O:17:LEU:HD12	39:O:17:LEU:C	2.23	0.64
53:1:49:A:H5'	53:1:51:G:O4'	1.98	0.64
25:z:52:PHE:CD2	54:2:83:G:H4'	2.32	0.64
52:3:1346:A:O2'	52:3:1347:G:H4'	1.97	0.64
53:1:2605:U:H2'	53:1:2606:C:C6	2.32	0.64
46:V:63:CYS:SG	46:V:64:ARG:N	2.71	0.64
2:c:59:ARG:HH11	53:1:2830:C:H3'	1.62	0.64
25:z:46:MET:HA	53:1:851:C:H4'	1.80	0.64
51:a:38:PHE:CD1	53:1:2127:G:H4'	2.33	0.64
53:1:1936:A:H2	53:1:1943:U:H3	1.46	0.64
57:7:62:C:C3'	57:7:63:G:H5''	2.27	0.64
31:G:150:ILE:N	31:G:150:ILE:HD12	2.13	0.64
37:M:102:VAL:HG23	37:M:125:ILE:HB	1.79	0.64
51:a:3:LYS:HD2	53:1:2108:A:P	2.38	0.64
53:1:821:A:H5''	53:1:822:G:H5''	1.78	0.64
55:6:17:C:H2'	55:6:17(A):U:H5	1.62	0.64
58:8:117:ARG:HG2	58:8:157:LEU:HD21	1.79	0.64
8:i:89:SER:HB2	8:i:92:PRO:HG3	1.81	0.63
37:M:79:ARG:HB2	52:3:878:A:OP1	1.98	0.63
36:L:142:ARG:HB3	55:6:41:C:H4'	1.81	0.63
52:3:715:A:H2'	52:3:716:A:C8	2.33	0.63
54:2:65:U:H3'	54:2:108:A:N6	2.10	0.63
40:P:63:GLN:HG3	40:P:98:ALA:HB2	1.80	0.63
43:S:2:LYS:HZ1	52:3:983:A:H5'	1.60	0.63
19:t:54:GLU:HB2	19:t:88:LYS:HB2	1.81	0.63
29:E:3:ILE:HD12	53:1:666:A:H1'	1.80	0.63
7:h:23:LEU:HD13	7:h:118:ILE:CG1	2.29	0.63
19:t:61:LEU:HB3	53:1:1341:G:H5'	1.81	0.63
43:S:23:ARG:NH2	52:3:1008:U:H5''	2.12	0.63
53:1:546:U:H2'	53:1:547:A:H4'	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:183:ARG:HH12	33:I:186:GLU:HB2	1.61	0.63
58:8:312:LEU:HD23	58:8:312:LEU:H	1.63	0.63
1:b:5:CYS:SG	1:b:12:ARG:HD2	2.38	0.63
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.81	0.63
16:q:96:ASP:OD2	17:r:13:ARG:NE	2.32	0.63
51:a:181:ASP:HB3	51:a:184:LYS:HD3	1.81	0.63
53:1:996:A:H2'	53:1:997:G:H8	1.64	0.63
6:g:124:THR:HG22	6:g:125:THR:H	1.63	0.62
2:c:40:LEU:H	2:c:40:LEU:HD12	1.63	0.62
13:n:63:ARG:NE	53:1:1454:C:H5'	2.15	0.62
16:q:23:TYR:CD1	53:1:533:G:H5'	2.33	0.62
53:1:1872:A:H2'	53:1:1873:G:O4'	1.99	0.62
54:2:56:G:H4'	54:2:57:A:H8	1.64	0.62
52:3:1259:C:C3'	52:3:1260:G:H5''	2.29	0.62
53:1:2233:U:H2'	53:1:2234:G:H8	1.63	0.62
4:e:79:ARG:HH11	55:5:19:G:H1	1.47	0.62
7:h:4:ASN:HA	7:h:7:ASP:HB2	1.79	0.62
14:o:15:ARG:HH22	54:2:8:C:H5''	1.64	0.62
15:p:92:ARG:HD3	53:1:1753:G:OP1	1.99	0.62
39:O:40:ILE:HD11	52:3:1124:G:C4'	2.29	0.62
53:1:2834:G:H2'	53:1:2879:A:H61	1.65	0.62
43:S:68:ARG:HD2	52:3:1202:U:H1'	1.81	0.62
58:8:98:GLN:HE21	58:8:387:GLY:C	2.07	0.62
10:k:92:GLU:O	10:k:93:GLN:C	2.42	0.62
38:N:54:VAL:HG22	38:N:55:ASP:H	1.64	0.62
40:P:125:LYS:HE3	52:3:797:C:OP1	2.00	0.62
52:3:744:C:H2'	52:3:745:G:H8	1.64	0.62
53:1:1053:C:C2'	53:1:1054:A:H5''	2.28	0.62
1:b:18:VAL:HB	1:b:202:ARG:HH21	1.65	0.62
52:3:225:C:C3'	52:3:226:G:H5''	2.30	0.62
6:g:112:LYS:HE3	53:1:2220:U:OP1	2.00	0.62
36:L:25:PHE:O	36:L:28:ILE:HG22	2.00	0.62
50:Z:9:GLU:HB3	50:Z:10:PRO:CD	2.30	0.62
52:3:78:A:H2'	52:3:79:G:O4'	2.00	0.62
53:1:2248:C:C2'	53:1:2249:U:H5'	2.30	0.62
14:o:10:ARG:HD3	53:1:2295:C:OP2	2.00	0.61
46:V:78:VAL:HG12	46:V:79:GLU:HG2	1.81	0.61
50:Z:34:ARG:HB3	50:Z:36:PHE:CZ	2.35	0.61
53:1:2345:G:N3	53:1:2381:A:H2'	2.15	0.61
8:i:107:GLU:OE2	8:i:108:ILE:HG23	1.99	0.61
11:l:19:LEU:HD13	11:l:27:LEU:HD13	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:p:93:LYS:HE3	53:1:1754:A:OP1	2.00	0.61
36:L:4:ARG:HH12	52:3:933:G:P	2.23	0.61
52:3:1033:G:C2'	52:3:1034:G:H5''	2.28	0.61
52:3:1512:U:H2'	52:3:1513:A:C8	2.35	0.61
53:1:2114:A:H61	53:1:2117:A:H62	1.47	0.61
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.66	0.61
53:1:2512:C:H2'	53:1:2513:A:O4'	2.00	0.61
31:G:66:ILE:HA	31:G:159:ALA:HB3	1.81	0.61
33:I:82:LYS:HD3	52:3:5:U:O4	2.00	0.61
50:Z:46:ARG:HE	52:3:1533:C:H41	1.48	0.61
52:3:715:A:H2'	52:3:716:A:H8	1.64	0.61
52:3:1060:U:H2'	52:3:1061:G:H8	1.66	0.61
53:1:615:U:H5''	53:1:616:A:OP2	2.01	0.61
4:e:48:LEU:HA	4:e:51:ASN:HD22	1.65	0.61
23:x:17:ARG:HE	23:x:23:ALA:HB2	1.66	0.61
41:Q:57:THR:HG21	52:3:363:A:OP2	2.01	0.61
45:U:20:VAL:HG22	45:U:21:VAL:N	2.15	0.61
52:3:1352:C:H2'	52:3:1353:G:C8	2.35	0.61
53:1:45:G:H5''	53:1:46:G:C5'	2.25	0.61
53:1:2469:A:H2'	53:1:2470:G:O4'	2.00	0.61
53:1:745:G:O2'	53:1:748:G:H1'	2.01	0.61
53:1:807:U:H2'	53:1:808:G:C8	2.35	0.61
53:1:1906:G:C2'	53:1:1907:G:H5''	2.30	0.61
10:k:35:VAL:HG21	10:k:106:GLU:HB2	1.83	0.61
37:M:65:PHE:CD2	37:M:66:GLN:HG2	2.36	0.61
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.83	0.61
53:1:1965:C:H5''	53:1:1966:A:H2'	1.82	0.61
13:n:47:VAL:O	13:n:50:PRO:HD2	1.99	0.61
33:I:149:LYS:HG2	33:I:150:LYS:HG2	1.83	0.61
36:L:139:ASP:O	36:L:143:MET:HG2	2.01	0.61
9:j:81:ILE:HG23	9:j:82:GLY:H	1.65	0.61
53:1:2462:C:H2'	53:1:2463:C:C6	2.35	0.61
19:t:51:PHE:O	19:t:52:GLU:HG2	2.01	0.61
43:S:7:ALA:O	43:S:10:VAL:HG12	2.00	0.61
53:1:184:C:H4'	53:1:217:A:H2	1.66	0.61
6:g:84:ALA:HA	6:g:91:PHE:H	1.66	0.60
53:1:704:G:H2'	53:1:726:G:H22	1.64	0.60
11:l:22:GLY:HA2	53:1:811:U:H3'	1.82	0.60
36:L:75:LYS:HZ3	52:3:938:A:H5'	1.66	0.60
37:M:9:MET:HG3	37:M:26:MET:HE1	1.82	0.60
52:3:946:A:H2'	52:3:947:G:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:973:A:H5'	53:1:1188:U:H1'	1.83	0.60
34:J:24:VAL:HG13	34:J:26:GLY:H	1.67	0.60
44:T:13:GLU:O	44:T:83:ARG:NH2	2.35	0.60
53:1:69:C:O2'	53:1:70:G:H5'	2.02	0.60
53:1:1278:C:H2'	53:1:1279:G:C8	2.36	0.60
53:1:2086:U:H2'	53:1:2087:G:C8	2.35	0.60
14:o:6:ALA:O	14:o:9:ARG:HG3	2.01	0.60
31:G:69:VAL:HB	31:G:162:VAL:HG22	1.83	0.60
33:I:104:MET:HE2	33:I:170:LEU:HD22	1.83	0.60
51:a:185:LEU:HA	51:a:188:ASN:HD22	1.65	0.60
53:1:1268:A:H2'	53:1:1269:A:O4'	2.02	0.60
2:c:12:THR:HG22	2:c:13:ARG:H	1.66	0.60
7:h:37:LYS:HZ3	53:1:1085:A:N6	2.00	0.60
34:J:160:VAL:O	34:J:163:ILE:HG12	1.99	0.60
37:M:11:THR:HG21	52:3:876:C:H1'	1.83	0.60
53:1:1319:C:O2'	53:1:1320:C:H5'	2.02	0.60
33:I:139:ASN:HA	33:I:181:PHE:O	2.01	0.60
48:X:14:LEU:O	48:X:18:VAL:HG23	2.01	0.60
53:1:1186:G:H2'	53:1:1187:G:O4'	2.02	0.60
53:1:2055:C:H2'	53:1:2504:U:H5'	1.83	0.60
10:k:41:ILE:HD11	10:k:86:LEU:HD21	1.84	0.60
52:3:211:G:H2'	52:3:212:G:H5'	1.84	0.60
53:1:2066:C:O2'	53:1:2067:G:H5'	2.02	0.60
1:b:75:ALA:O	1:b:114:GLN:HG3	2.01	0.60
6:g:84:ALA:HB1	6:g:90:LEU:HA	1.84	0.60
29:E:61:LEU:HD12	29:E:61:LEU:O	2.02	0.60
35:K:92:THR:OG1	35:K:93:LYS:N	2.35	0.60
38:N:33:SER:OG	38:N:36:GLN:HG2	2.02	0.60
39:O:53:ILE:HD11	39:O:63:ASP:HB2	1.82	0.60
58:8:16:GLY:HA3	58:8:99:MET:HE2	1.84	0.60
43:S:79:SER:O	43:S:83:VAL:HG13	2.02	0.60
52:3:736:C:H2'	52:3:737:C:C6	2.36	0.60
53:1:1386:C:H2'	53:1:1387:A:C8	2.37	0.60
53:1:2475:C:H2'	53:1:2476:A:H5'	1.83	0.60
53:1:2743:U:C3'	53:1:2744:G:H5''	2.32	0.60
13:n:49:GLU:OE1	53:1:2839:G:H4'	2.01	0.59
22:w:33:ILE:HD11	22:w:78:ILE:HD11	1.83	0.59
35:K:29:ILE:HG22	35:K:34:GLY:HA3	1.84	0.59
52:3:235:C:H2'	52:3:236:A:H8	1.66	0.59
52:3:744:C:H2'	52:3:745:G:C8	2.37	0.59
53:1:2139:U:H2'	53:1:2140:G:C8	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:63:ARG:CZ	53:1:1454:C:H5'	2.32	0.59
31:G:134:LEU:HG	31:G:138:ARG:HH21	1.67	0.59
52:3:235:C:H2'	52:3:236:A:C8	2.37	0.59
4:e:3:LEU:HA	4:e:6:TYR:HB3	1.84	0.59
8:i:10:LEU:N	8:i:10:LEU:HD23	2.18	0.59
27:C:29:LYS:HE3	53:1:2286:G:H3'	1.83	0.59
35:K:18:VAL:HG12	35:K:19:PRO:HD3	1.82	0.59
37:M:95:MET:HE3	37:M:129:ALA:HB1	1.85	0.59
52:3:1202:U:H2'	52:3:1203:C:H5'	1.85	0.59
6:g:97:ARG:NH2	53:1:2220:U:H4'	2.17	0.59
7:h:59:LEU:HD21	53:1:1047:G:N7	2.17	0.59
32:H:55:VAL:HB	32:H:66:THR:HB	1.84	0.59
18:s:88:ARG:HH12	53:1:2013:A:H2	1.49	0.59
36:L:8:GLN:HG2	36:L:9:ARG:O	2.01	0.59
39:O:14:ASP:HB2	39:O:17:LEU:HD23	1.85	0.59
4:e:107:VAL:HG12	4:e:108:PRO:HD3	1.85	0.59
24:y:19:LEU:O	24:y:23:ARG:HB2	2.01	0.59
31:G:103:TRP:HE1	31:G:155:GLY:HA2	1.67	0.59
34:J:100:GLU:HA	34:J:121:ASN:HD22	1.67	0.59
53:1:2039:U:H2'	53:1:2040:G:C8	2.38	0.59
53:1:2799:A:C2'	53:1:2800:A:H5'	2.32	0.59
2:c:51:THR:HB	2:c:79:LEU:HD23	1.85	0.59
32:H:30:ASP:HA	43:S:64:ARG:HH12	1.67	0.59
35:K:46:GLN:HA	35:K:56:LYS:HG2	1.85	0.59
53:1:2515:C:H2'	53:1:2516:A:H8	1.67	0.59
27:C:29:LYS:HE2	53:1:2286:G:OP1	2.03	0.59
36:L:80:GLY:HA3	56:4:11:U:O2'	2.03	0.59
51:a:193:LEU:O	51:a:196:LEU:HG	2.02	0.59
53:1:580:U:H2'	53:1:581:C:C6	2.38	0.59
53:1:1344:U:H3'	53:1:1345:C:H5'	1.84	0.59
12:m:20:LEU:HD11	21:v:81:PRO:HG2	1.83	0.59
32:H:26:LYS:HE3	52:3:1256:A:H5''	1.85	0.59
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.84	0.59
52:3:1400:C:H5'	56:4:18:G:C6	2.38	0.59
58:8:46:ALA:HB3	58:8:49:GLN:OE1	2.02	0.59
2:c:34:VAL:HG22	2:c:50:VAL:HG12	1.85	0.58
4:e:92:GLY:O	4:e:95:MET:HG2	2.03	0.58
35:K:73:GLU:O	35:K:77:THR:HG23	2.03	0.58
38:N:126:PHE:O	52:3:1342:C:H4'	2.03	0.58
47:W:59:LYS:HD3	52:3:734:G:O2'	2.02	0.58
58:8:35:VAL:HG11	58:8:186:GLU:OE2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:91:LYS:N	8:i:92:PRO:HD3	2.16	0.58
31:G:101:THR:HB	52:3:1074:G:H4'	1.85	0.58
53:1:119:A:H4'	53:1:120:U:H5'	1.85	0.58
53:1:226:A:H2'	53:1:227:A:O4'	2.03	0.58
55:5:6:G:O2'	55:5:7:G:H5'	2.01	0.58
55:5:75:C:C3'	55:5:76:A:H5''	2.33	0.58
39:O:40:ILE:HD11	52:3:1124:G:H4'	1.85	0.58
41:Q:74:GLN:O	41:Q:76:HIS:N	2.37	0.58
52:3:835:U:H2'	52:3:836:G:C5'	2.29	0.58
53:1:1367:A:H2'	53:1:1368:G:H5'	1.84	0.58
53:1:2267:A:H5''	53:1:2268:A:H5'	1.85	0.58
1:b:42:ARG:HH12	53:1:690:G:H21	1.50	0.58
13:n:87:PHE:HE1	13:n:116:VAL:HG23	1.68	0.58
39:O:23:ALA:HA	39:O:26:VAL:HG22	1.84	0.58
49:Y:67:HIS:CE1	52:3:132:C:H4'	2.38	0.58
52:3:1158:C:H2'	52:3:1159:U:H4'	1.84	0.58
53:1:1251:C:O2'	53:1:1252:G:H3'	2.03	0.58
41:Q:49:ARG:HD2	41:Q:89:LEU:HD21	1.85	0.58
53:1:2220:U:H2'	53:1:2221:G:H8	1.68	0.58
9:j:26:GLY:HA3	53:1:1140:C:C5'	2.31	0.58
32:H:107:LYS:HG2	32:H:143:LEU:HD11	1.85	0.58
52:3:673:A:H2'	52:3:674:G:C8	2.39	0.58
52:3:1255:G:H2'	52:3:1279:G:H1	1.68	0.58
53:1:2163:A:H2'	53:1:2164:C:H5'	1.85	0.58
7:h:102:ALA:HA	7:h:105:LYS:HE3	1.86	0.58
22:w:21:ARG:HE	22:w:27:VAL:HG12	1.68	0.58
32:H:107:LYS:HE3	32:H:143:LEU:CD2	2.33	0.58
50:Z:64:ALA:O	50:Z:65:ARG:HG2	2.02	0.58
53:1:1111:A:H2'	53:1:1111:A:N3	2.17	0.58
53:1:1979:U:O2'	53:1:1980:G:H5'	2.04	0.58
34:J:114:LEU:O	34:J:119:VAL:HG22	2.03	0.58
34:J:131:ASN:HD22	52:3:19:A:P	2.27	0.58
37:M:80:PRO:HG2	52:3:878:A:C5'	2.34	0.58
52:3:428:G:H4'	52:3:429:U:O5'	2.04	0.58
53:1:1326:U:H2'	53:1:1327:A:H8	1.69	0.58
52:3:1256:A:H1'	52:3:1258:G:C4	2.38	0.58
58:8:231:ARG:HA	58:8:274:ASN:HA	1.86	0.58
52:3:539:A:H2'	52:3:540:G:C8	2.39	0.58
53:1:45:G:C5'	53:1:46:G:H5'	2.28	0.58
53:1:1790:C:H2'	53:1:1791:A:C5	2.39	0.58
53:1:1903:G:H2'	53:1:1904:G:H8	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2183:A:H2'	53:1:2184:A:C8	2.38	0.58
9:j:113:PRO:HD2	53:1:558:U:P	2.44	0.57
18:s:86:MET:HE3	18:s:87:PRO:HD2	1.87	0.57
50:Z:40:PRO:O	50:Z:44:ARG:CG	2.49	0.57
7:h:108:VAL:HG23	7:h:109:LYS:H	1.69	0.57
31:G:24:PRO:HB3	52:3:828:U:H2'	1.85	0.57
52:3:1429:A:H2'	52:3:1430:A:C8	2.35	0.57
53:1:1854:A:H61	53:1:1888:G:H1'	1.70	0.57
57:7:6:G:H2'	57:7:7:A:H5''	1.86	0.57
2:c:148:GLN:O	53:1:2052:A:H4'	2.05	0.57
36:L:75:LYS:NZ	52:3:938:A:H5'	2.18	0.57
49:Y:20:ASN:ND2	52:3:323:U:H5''	2.20	0.57
52:3:418:C:H2'	52:3:419:C:C6	2.40	0.57
52:3:483:C:H2'	52:3:484:G:C8	2.39	0.57
53:1:2747:G:O6	53:1:2755:C:H5''	2.04	0.57
58:8:336:THR:HB	58:8:338:VAL:HG23	1.86	0.57
6:g:55:GLU:O	6:g:58:LEU:HG	2.05	0.57
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.86	0.57
52:3:825:A:H2'	52:3:826:C:C6	2.39	0.57
52:3:955:U:H3	52:3:1225:A:H61	1.51	0.57
53:1:657:U:H2'	53:1:658:U:C6	2.39	0.57
53:1:796:C:H2'	53:1:797:G:C8	2.39	0.57
53:1:1386:C:H2'	53:1:1387:A:H8	1.69	0.57
56:4:20:U:H2'	56:4:21:C:C6	2.40	0.57
52:3:82:G:H2'	52:3:83:C:H5'	1.87	0.57
53:1:1077:A:C2'	53:1:1078:U:H5'	2.32	0.57
32:H:171:ARG:HG3	52:3:1107:C:P	2.45	0.57
38:N:57:VAL:HG23	38:N:58:GLU:H	1.69	0.57
52:3:784:A:H4'	53:1:1837:C:OP1	2.04	0.57
53:1:20:C:H2'	53:1:21:A:H8	1.70	0.57
53:1:1535:A:H3'	53:1:1536:C:H5'	1.87	0.57
57:7:62:C:C2'	57:7:63:G:H5''	2.34	0.57
1:b:12:ARG:HH21	53:1:728:G:C5'	2.18	0.57
31:G:66:ILE:N	31:G:66:ILE:HD12	2.20	0.57
50:Z:28:LEU:HA	50:Z:31:VAL:HG12	1.85	0.57
53:1:2281:A:O2'	53:1:2282:G:H5'	2.04	0.57
3:d:176:ASP:N	3:d:176:ASP:OD1	2.37	0.57
5:f:44:HIS:O	5:f:46:ASP:N	2.37	0.57
7:h:94:ARG:O	7:h:98:GLU:HG2	2.04	0.57
9:j:117:ALA:HA	9:j:120:ARG:HH21	1.70	0.57
24:y:31:GLN:HE21	24:y:37:LEU:HA	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:139:ASN:HA	32:H:142:ARG:HG2	1.86	0.57
53:1:1509:A:H2'	53:1:1510:G:C8	2.39	0.57
54:2:35:C:C2'	54:2:36:C:H5'	2.35	0.57
1:b:12:ARG:NH2	53:1:728:G:H5'	2.18	0.57
6:g:73:ASN:ND2	6:g:76:GLU:HG2	2.20	0.57
32:H:43:THR:O	32:H:47:ALA:HB2	2.04	0.57
46:V:5:ARG:HH11	52:3:636:U:H5'	1.69	0.57
52:3:521:G:O2'	52:3:522:C:H5'	2.05	0.57
52:3:946:A:H2'	52:3:947:G:C8	2.40	0.57
53:1:466:A:H2'	53:1:467:G:H5'	1.87	0.57
53:1:2849:U:H4'	53:1:2868:A:C2	2.40	0.57
57:7:26:A:H61	57:7:45:U:H3	1.51	0.57
2:c:149:ASN:O	2:c:152:PRO:HD2	2.05	0.56
6:g:4:ILE:HD13	6:g:18:GLN:HG3	1.86	0.56
11:l:93:ASN:HA	11:l:96:LYS:HE2	1.87	0.56
31:G:48:MET:HE3	31:G:200:PRO:HD3	1.85	0.56
32:H:106:ARG:N	32:H:106:ARG:HD2	2.20	0.56
50:Z:6:ARG:C	50:Z:8:ASN:H	2.11	0.56
50:Z:18:PHE:O	50:Z:21:SER:HB3	2.03	0.56
52:3:1391:U:H2'	52:3:1392:G:C8	2.39	0.56
53:1:1856:U:H2'	53:1:1857:G:O4'	2.05	0.56
33:I:117:VAL:HG23	33:I:122:ILE:HG21	1.87	0.56
40:P:30:ILE:HG13	40:P:45:THR:HG22	1.87	0.56
40:P:58:THR:HG22	40:P:60:PHE:H	1.70	0.56
52:3:1128:C:O2'	52:3:1129:C:H5'	2.06	0.56
53:1:161:A:H3'	53:1:162:U:H5''	1.86	0.56
53:1:367:G:H2'	53:1:368:A:O4'	2.06	0.56
1:b:42:ARG:N	1:b:42:ARG:HD2	2.20	0.56
3:d:58:LYS:HG2	3:d:71:GLY:HA2	1.86	0.56
4:e:65:LEU:HD22	54:2:42:C:C4	2.40	0.56
8:i:23:VAL:HG23	8:i:24:GLY:H	1.70	0.56
8:i:102:ARG:HG2	8:i:139:VAL:HG22	1.86	0.56
18:s:3:THR:HG21	18:s:58:ALA:HB2	1.87	0.56
31:G:48:MET:O	31:G:51:GLU:HG2	2.05	0.56
32:H:26:LYS:CE	52:3:1256:A:H5''	2.35	0.56
50:Z:49:ALA:HA	52:3:723:U:O4	2.04	0.56
52:3:225:C:H3'	52:3:226:G:H5''	1.87	0.56
53:1:796:C:H2'	53:1:797:G:H8	1.70	0.56
53:1:1810:A:H2'	53:1:1811:G:O4'	2.04	0.56
53:1:2041:U:H2'	53:1:2042:A:C8	2.41	0.56
53:1:2475:C:C2'	53:1:2476:A:H5'	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:203:VAL:HG23	53:1:1792:G:H5''	1.87	0.56
36:L:24:LYS:HE2	52:3:1375:A:H5''	1.87	0.56
53:1:2039:U:H2'	53:1:2040:G:H8	1.68	0.56
53:1:2743:U:H3'	53:1:2744:G:H5''	1.86	0.56
54:2:19:C:H2'	54:2:20:G:C8	2.40	0.56
18:s:6:LYS:HG2	53:1:494:G:H4'	1.87	0.56
52:3:410:G:H2'	52:3:429:U:C4	2.41	0.56
52:3:1162:C:H2'	52:3:1163:A:C8	2.39	0.56
36:L:3:ARG:NH1	52:3:1092:A:H5'	2.17	0.56
52:3:70:U:H4'	52:3:71:A:H8	1.70	0.56
52:3:1432:G:H1'	52:3:1468:A:H62	1.70	0.56
53:1:1373:A:C5'	53:1:2212:A:H1'	2.35	0.56
53:1:2537:U:H2'	53:1:2538:C:C6	2.41	0.56
57:7:62:C:H3'	57:7:63:G:H5''	1.86	0.56
52:3:211:G:C2'	52:3:212:G:H5'	2.35	0.56
53:1:1578:U:H2'	53:1:1579:A:H8	1.70	0.56
53:1:2047:C:H2'	53:1:2048:G:C8	2.41	0.56
53:1:2238:G:H2'	53:1:2238:G:N3	2.21	0.56
55:6:6:G:O2'	55:6:7:G:H5'	2.06	0.56
5:f:79:THR:HG23	5:f:80:GLU:CD	2.31	0.56
7:h:118:ILE:HG22	7:h:119:PRO:CD	2.36	0.56
11:l:74:THR:HG22	11:l:107:PHE:HB2	1.87	0.56
18:s:29:VAL:HG22	18:s:55:ILE:HD11	1.87	0.56
36:L:78:ARG:HD3	52:3:1382:C:H5'	1.87	0.56
51:a:53:ARG:HB3	55:6:62:C:H4'	1.86	0.56
52:3:225:C:C2'	52:3:226:G:H5''	2.36	0.56
52:3:1395:C:H6	52:3:1395:C:H5'	1.71	0.56
2:c:62:LYS:HB2	2:c:63:PRO:HD3	1.87	0.56
36:L:90:VAL:HG22	36:L:91:ARG:H	1.71	0.56
36:L:90:VAL:HG22	36:L:91:ARG:N	2.20	0.56
41:Q:43:LYS:HE2	52:3:1492:A:O5'	2.05	0.56
46:V:74:LEU:HD23	46:V:75:VAL:N	2.21	0.56
1:b:208:GLY:HA2	1:b:211:ARG:HB2	1.88	0.56
3:d:163:ASN:HB2	53:1:322:A:OP2	2.05	0.56
25:z:45:GLY:HA3	53:1:852:U:H5'	1.88	0.56
35:K:79:ARG:HH22	52:3:671:G:H4'	1.70	0.56
40:P:118:ASN:OD1	52:3:718:A:H5'	2.06	0.56
47:W:21:ASP:OD2	47:W:23:LYS:HB2	2.06	0.56
49:Y:23:ARG:O	49:Y:26:MET:HG3	2.06	0.56
53:1:2795:C:H2'	53:1:2796:U:O4'	2.06	0.56
58:8:59:ARG:HD2	58:8:383:THR:HG23	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:4:VAL:HB	52:3:1190:G:OP2	2.05	0.55
32:H:107:LYS:HE3	32:H:143:LEU:HD21	1.87	0.55
42:R:65:GLU:HG2	42:R:66:GLY:N	2.21	0.55
52:3:304:U:O2'	52:3:305:G:H5'	2.05	0.55
53:1:2328:A:H2'	53:1:2329:U:C6	2.41	0.55
58:8:27:THR:HG23	58:8:175:ALA:HB3	1.88	0.55
1:b:203:VAL:HG23	53:1:1792:G:C5'	2.36	0.55
13:n:13:ASN:ND2	13:n:15:SER:HB3	2.21	0.55
28:D:26:ASN:CG	53:1:682:G:H5'	2.32	0.55
35:K:48:ALA:H	47:W:65:SER:HG	1.55	0.55
53:1:395:U:H2'	53:1:396:G:C8	2.41	0.55
53:1:677:A:O2'	53:1:2071:A:H5'	2.06	0.55
53:1:1889:A:H2'	53:1:1890:A:C8	2.41	0.55
58:8:132:ILE:N	58:8:132:ILE:HD12	2.20	0.55
1:b:48:ILE:HG23	1:b:48:ILE:O	2.06	0.55
33:I:141:VAL:HG12	33:I:180:THR:HG22	1.87	0.55
52:3:70:U:H5''	52:3:71:A:OP1	2.06	0.55
52:3:868:C:H2'	52:3:869:G:O4'	2.05	0.55
9:j:64:VAL:HB	9:j:68:LYS:HE3	1.88	0.55
42:R:68:LEU:HA	42:R:71:GLU:HB2	1.87	0.55
53:1:2297:A:N6	53:1:2319:G:H1'	2.22	0.55
3:d:24:ASN:HD22	3:d:27:LEU:HB2	1.71	0.55
14:o:64:TYR:HB3	14:o:67:ASN:ND2	2.21	0.55
32:H:180:ASP:C	32:H:181:ILE:HD12	2.31	0.55
53:1:598:U:H2'	53:1:599:A:H8	1.71	0.55
53:1:814:C:H1'	53:1:1225:G:H21	1.71	0.55
53:1:1827:U:O2'	53:1:1828:G:H5'	2.07	0.55
2:c:149:ASN:HD22	53:1:2572:A:H2'	1.72	0.55
4:e:161:SER:OG	4:e:164:GLU:HG3	2.07	0.55
32:H:13:ILE:HG23	32:H:14:VAL:HG13	1.89	0.55
37:M:29:SER:O	37:M:33:VAL:HG23	2.06	0.55
43:S:55:SER:HB3	43:S:58:ARG:HD3	1.89	0.55
50:Z:40:PRO:HA	50:Z:44:ARG:NH1	2.22	0.55
52:3:372:C:N4	52:3:387:U:H2'	2.22	0.55
53:1:1078:U:H5''	53:1:1079:C:H5''	1.89	0.55
53:1:1469:A:H2'	53:1:1470:A:C8	2.41	0.55
53:1:2533:U:H2'	53:1:2534:A:O4'	2.07	0.55
54:2:44:G:H1'	54:2:47:C:H42	1.72	0.55
11:l:36:LYS:HD2	53:1:807:U:OP2	2.06	0.55
40:P:111:ASP:OD1	40:P:113:THR:HG23	2.07	0.55
43:S:2:LYS:HZ2	52:3:983:A:C5'	2.18	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1170:A:H2'	52:3:1171:A:O4'	2.07	0.55
15:p:101:GLU:OE2	15:p:102:ARG:HG3	2.07	0.55
19:t:28:ASN:ND2	19:t:87:LEU:HB2	2.21	0.55
34:J:89:THR:HG23	34:J:134:ASN:ND2	2.22	0.55
36:L:3:ARG:NH2	52:3:1092:A:H5''	2.22	0.55
52:3:236:A:H2'	52:3:237:G:H8	1.72	0.55
53:1:131:A:H2'	53:1:132:G:C8	2.42	0.55
53:1:1854:A:N6	53:1:1888:G:H1'	2.21	0.55
15:p:83:ILE:HD12	15:p:83:ILE:N	2.21	0.55
37:M:85:TYR:CE1	37:M:123:GLU:HB2	2.42	0.55
37:M:112:ASP:O	37:M:116:ARG:HG3	2.07	0.55
39:O:47:GLU:HB2	39:O:67:ILE:HB	1.89	0.55
41:Q:99:GLY:HA2	41:Q:103:CYS:O	2.06	0.55
44:T:65:LEU:HD23	52:3:754:C:O2'	2.07	0.55
53:1:2743:U:H2'	53:1:2744:G:H5''	1.88	0.55
53:1:2834:G:O2'	53:1:2835:A:H5'	2.06	0.55
4:e:56:LEU:HD23	4:e:59:ILE:HD12	1.88	0.55
20:u:50:ALA:O	20:u:51:LEU:HG	2.07	0.55
24:y:43:LEU:HD23	53:1:61:C:C5'	2.29	0.55
50:Z:66:ARG:HD2	52:3:1099:G:H4'	1.88	0.55
51:a:166:ASP:OD2	51:a:168:ASN:HB2	2.06	0.55
52:3:1219:A:H2'	52:3:1220:G:C8	2.42	0.55
53:1:1417:C:H4'	53:1:1587:G:H21	1.72	0.55
25:z:5:LYS:HB2	25:z:57:GLU:HG3	1.88	0.54
52:3:202:G:H21	52:3:466:A:H61	1.55	0.54
52:3:1512:U:H2'	52:3:1513:A:H8	1.72	0.54
53:1:2110:G:H22	53:1:2179:C:H42	1.56	0.54
54:2:48:U:H2'	54:2:49:C:C6	2.42	0.54
17:r:38:VAL:HG11	17:r:59:ILE:HG13	1.88	0.54
32:H:65:VAL:HB	32:H:100:ILE:HG12	1.88	0.54
40:P:115:ILE:HD12	40:P:116:PRO:HD2	1.88	0.54
53:1:286:U:H2'	53:1:287:G:C8	2.42	0.54
53:1:2339:C:H2'	53:1:2340:A:C8	2.41	0.54
53:1:2676:C:H2'	53:1:2677:G:C8	2.43	0.54
58:8:312:LEU:HD12	58:8:316:GLU:HG3	1.88	0.54
4:e:3:LEU:HD13	4:e:100:GLU:HG2	1.88	0.54
7:h:1:MET:HE3	7:h:2:ALA:H	1.71	0.54
7:h:87:GLU:OE1	7:h:93:ALA:HB3	2.06	0.54
29:E:36:ALA:HB3	29:E:39:ARG:CG	2.37	0.54
40:P:88:PRO:HG2	40:P:89:GLY:H	1.73	0.54
42:R:113:LYS:CG	42:R:114:PRO:HD3	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:T:4:THR:HG23	52:3:659:U:H5''	1.88	0.54
52:3:663:A:H5'	52:3:836:G:OP1	2.07	0.54
52:3:834:U:H2'	52:3:835:U:C6	2.43	0.54
52:3:1402:C:H2'	52:3:1403:C:O4'	2.07	0.54
53:1:278:A:H2'	53:1:278:A:N3	2.22	0.54
53:1:554:U:H2'	53:1:555:G:O4'	2.06	0.54
53:1:598:U:H2'	53:1:599:A:C8	2.42	0.54
53:1:2196:C:O2'	53:1:2197:U:H5'	2.07	0.54
53:1:2837:A:H2'	53:1:2838:G:H8	1.72	0.54
58:8:17:THR:HG23	58:8:79:HIS:CE1	2.42	0.54
1:b:52:HIS:HA	1:b:216:ARG:HB3	1.89	0.54
7:h:27:VAL:HG12	7:h:83:ALA:HB3	1.89	0.54
29:E:31:ILE:O	29:E:31:ILE:HG13	2.07	0.54
35:K:29:ILE:HG21	35:K:64:VAL:HG21	1.89	0.54
35:K:51:ILE:C	35:K:53:LYS:H	2.15	0.54
38:N:17:ARG:NH2	52:3:1129:C:H5''	2.23	0.54
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.08	0.54
53:1:729:G:H4'	53:1:763:G:H5'	1.89	0.54
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.73	0.54
11:l:93:ASN:O	11:l:94:THR:OG1	2.23	0.54
11:l:135:ILE:HD12	11:l:142:ILE:HD11	1.89	0.54
40:P:44:ALA:HB3	40:P:69:CYS:HB2	1.87	0.54
52:3:24:U:H2'	52:3:25:C:C6	2.43	0.54
52:3:335:C:H2'	52:3:336:A:C8	2.42	0.54
58:8:314:LYS:HB2	58:8:320:HIS:HB3	1.90	0.54
31:G:72:LYS:HB3	31:G:75:ALA:HB3	1.90	0.54
32:H:60:ALA:O	32:H:61:LYS:HG3	2.08	0.54
53:1:728:G:H3'	53:1:729:G:H5'	1.90	0.54
53:1:1796:U:H2'	53:1:1797:G:C8	2.37	0.54
9:j:136:GLN:N	9:j:137:PRO:HD3	2.23	0.54
14:o:10:ARG:NH2	53:1:2294:G:H5''	2.22	0.54
14:o:94:ARG:CZ	53:1:2293:G:H5''	2.38	0.54
17:r:41:ILE:HB	17:r:47:VAL:HB	1.90	0.54
33:I:49:ASP:O	33:I:52:VAL:HG22	2.08	0.54
34:J:80:LEU:HD13	34:J:122:VAL:HG11	1.90	0.54
35:K:3:HIS:HB2	35:K:92:THR:HB	1.90	0.54
36:L:4:ARG:HD3	36:L:4:ARG:N	2.22	0.54
52:3:1477:U:H2'	52:3:1478:U:C6	2.43	0.54
52:3:1516:G:H2'	52:3:1518:A:OP2	2.07	0.54
53:1:1495:A:H2	53:1:1578:U:H1'	1.73	0.54
53:1:2257:U:O2'	53:1:2258:C:H5'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:130:GLY:HA3	53:1:2305:U:H5''	1.90	0.54
7:h:48:ALA:HB3	7:h:51:TYR:CE1	2.43	0.54
7:h:54:VAL:O	53:1:1084:A:H5''	2.08	0.54
38:N:12:LYS:HA	38:N:109:GLN:HE22	1.73	0.54
39:O:22:THR:O	39:O:26:VAL:HG13	2.08	0.54
39:O:34:ALA:HB1	39:O:35:GLN:NE2	2.23	0.54
41:Q:109:ARG:NH1	52:3:537:G:H5''	2.23	0.54
53:1:1779:U:H5	53:1:1784:A:N7	2.06	0.54
53:1:2233:U:H2'	53:1:2234:G:C8	2.41	0.54
14:o:47:VAL:CG2	54:2:114:C:H4'	2.38	0.54
32:H:33:ASP:OD2	43:S:64:ARG:HD3	2.08	0.54
36:L:16:LYS:HG2	36:L:17:PHE:CD1	2.42	0.54
38:N:112:ARG:O	38:N:114:LYS:HD2	2.07	0.54
53:1:669:G:H2'	53:1:669:G:N3	2.23	0.54
53:1:2030:A:H4'	53:1:2031:A:C8	2.42	0.54
3:d:118:LEU:HD12	3:d:186:VAL:HG13	1.90	0.54
8:i:89:SER:OG	53:1:1063:G:H1'	2.07	0.54
34:J:55:VAL:HG23	34:J:56:PRO:CD	2.37	0.54
53:1:473:G:O2'	53:1:474:G:H5'	2.07	0.54
53:1:532:A:H2'	53:1:532:A:N3	2.22	0.54
53:1:2339:C:H2'	53:1:2340:A:H8	1.73	0.54
54:2:35:C:H2'	54:2:36:C:H5'	1.90	0.54
1:b:36:ASN:HB2	1:b:61:TYR:HB2	1.89	0.53
24:y:43:LEU:CD2	53:1:61:C:H5''	2.33	0.53
33:I:197:HIS:O	33:I:200:VAL:HG12	2.08	0.53
43:S:7:ALA:O	43:S:11:LYS:HG2	2.08	0.53
52:3:352:C:H4'	52:3:354:G:OP1	2.08	0.53
53:1:580:U:H2'	53:1:581:C:H6	1.73	0.53
53:1:1609:A:H1'	53:1:1616:A:O4'	2.08	0.53
53:1:2286:G:H4'	53:1:2287:A:O4'	2.08	0.53
12:m:77:PRO:O	12:m:80:VAL:HG12	2.07	0.53
21:v:19:ARG:NH2	54:2:95:U:OP2	2.41	0.53
22:w:22:PHE:CD2	53:1:922:C:H1'	2.43	0.53
33:I:144:ILE:N	33:I:144:ILE:HD12	2.22	0.53
36:L:138:GLU:O	36:L:142:ARG:HG3	2.07	0.53
49:Y:28:ARG:NH2	52:3:1437:A:H5''	2.24	0.53
52:3:701:U:C4'	52:3:703:G:H1'	2.38	0.53
53:1:2170:A:H2'	53:1:2171:A:O4'	2.09	0.53
53:1:2443:C:O2'	53:1:2444:G:H5'	2.08	0.53
54:2:95:U:H2'	54:2:96:G:H8	1.72	0.53
55:6:17:C:H2'	55:6:17(A):U:C5	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:144:GLU:HG2	3:d:145:ASP:N	2.23	0.53
10:k:25:LEU:CD1	53:1:2562:U:H4'	2.39	0.53
18:s:72:THR:HG23	18:s:73:LYS:H	1.72	0.53
31:G:93:HIS:CD2	31:G:145:ASN:HB3	2.43	0.53
52:3:757:U:H2'	52:3:758:C:O4'	2.08	0.53
53:1:1036:G:H1	53:1:1119:U:H3	1.56	0.53
53:1:2366:A:H2'	53:1:2367:G:O4'	2.08	0.53
54:2:66:A:H4'	54:2:67:G:C8	2.43	0.53
55:6:35:A:H2'	55:6:36:U:C5	2.43	0.53
41:Q:99:GLY:N	41:Q:103:CYS:SG	2.81	0.53
45:U:20:VAL:HG23	45:U:35:ARG:HA	1.91	0.53
50:Z:17:ARG:HA	50:Z:20:ARG:HH11	1.74	0.53
52:3:909:A:H2'	52:3:910:C:O4'	2.07	0.53
53:1:2008:C:H2'	53:1:2009:A:H8	1.73	0.53
53:1:2287:A:O2'	53:1:2288:A:H2'	2.08	0.53
1:b:153:LEU:H	1:b:153:LEU:HD12	1.73	0.53
7:h:27:VAL:CG1	7:h:83:ALA:HB3	2.39	0.53
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.90	0.53
9:j:27:ARG:NH2	53:1:1142:A:H4'	2.23	0.53
14:o:18:LEU:HD12	14:o:19:GLN:N	2.23	0.53
27:C:36:LYS:O	53:1:2344:U:H3'	2.08	0.53
32:H:3:LYS:CE	52:3:1191:A:H5''	2.37	0.53
36:L:148:LYS:HG2	36:L:148:LYS:O	2.08	0.53
46:V:13:SER:HB3	46:V:21:VAL:CG1	2.38	0.53
52:3:530:G:H3'	52:3:531:U:C5'	2.39	0.53
53:1:279:A:H2'	53:1:280:U:H5'	1.89	0.53
13:n:2:ARG:HA	13:n:5:LYS:HD2	1.89	0.53
32:H:152:VAL:HG12	32:H:197:VAL:HG22	1.91	0.53
34:J:107:GLY:HA2	52:3:8:A:H1'	1.89	0.53
52:3:1506:U:O2'	52:3:1507:A:H5'	2.08	0.53
53:1:365:U:H2'	53:1:366:C:C6	2.43	0.53
53:1:660:C:H2'	53:1:661:A:C8	2.43	0.53
53:1:765:C:H2'	53:1:766:U:C6	2.44	0.53
53:1:1300:G:H4'	53:1:1301:A:H5'	1.91	0.53
1:b:140:VAL:O	1:b:161:VAL:HG22	2.08	0.53
53:1:435:C:H2'	53:1:436:C:H5'	1.90	0.53
2:c:3:GLY:C	2:c:4:LEU:HD12	2.33	0.53
27:C:20:TYR:OH	53:1:2348:U:H5'	2.09	0.53
34:J:159:SER:OG	34:J:162:GLU:HB3	2.09	0.53
42:R:114:PRO:HG2	52:3:1228:C:C5'	2.37	0.53
52:3:368:U:OP2	58:8:280:ARG:NE	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1549:A:H2'	53:1:1550:C:C6	2.44	0.53
53:1:2011:U:H2'	53:1:2012:G:O4'	2.08	0.53
53:1:2581:G:H2'	53:1:2581:G:N3	2.23	0.53
3:d:131:THR:HG23	53:1:321:U:H5''	1.90	0.53
9:j:102:GLU:HG3	9:j:119:PHE:CZ	2.44	0.53
9:j:113:PRO:HD2	53:1:558:U:OP2	2.09	0.53
11:l:101:ILE:HG13	11:l:102:GLY:N	2.23	0.53
32:H:179:ALA:HB1	32:H:202:PHE:HE1	1.72	0.53
37:M:12:ARG:HH21	52:3:826:C:H5'	1.73	0.53
41:Q:50:LYS:HD2	41:Q:50:LYS:N	2.23	0.53
53:1:703:U:H2'	53:1:704:G:O4'	2.09	0.53
55:5:76:A:H5'	55:5:76:A:C8	2.44	0.53
1:b:224:MET:HE2	53:1:782:A:C6	2.43	0.53
7:h:59:LEU:HD23	7:h:61:ARG:N	2.15	0.53
37:M:80:PRO:HG2	52:3:878:A:H5''	1.91	0.53
52:3:82:G:C2'	52:3:83:C:H5'	2.39	0.53
52:3:335:C:H2'	52:3:336:A:H8	1.74	0.53
52:3:1537:U:H3	56:4:8:A:H61	1.55	0.53
53:1:1045:C:OP1	53:1:1047:G:H5'	2.08	0.53
53:1:2609:U:H5'	53:1:2610:C:OP2	2.09	0.53
3:d:21:ARG:HH21	3:d:106:LYS:HE2	1.74	0.52
17:r:10:LYS:HD3	53:1:996:A:OP2	2.10	0.52
27:C:8:ILE:HG21	27:C:24:LYS:HE2	1.91	0.52
31:G:102:ASN:HD21	52:3:1074:G:H1'	1.73	0.52
33:I:101:VAL:HG13	33:I:106:PHE:HB2	1.90	0.52
33:I:155:LYS:O	33:I:158:LEU:HG	2.09	0.52
35:K:66:ALA:HB1	35:K:67:PRO:HD2	1.91	0.52
52:3:966:G:C2	55:5:34:C:H5'	2.45	0.52
52:3:1448:C:H2'	52:3:1449:C:C6	2.44	0.52
53:1:660:C:H2'	53:1:661:A:H8	1.74	0.52
53:1:1909:C:H2'	53:1:1910:G:C8	2.42	0.52
53:1:2572:A:OP1	53:1:2574:G:H4'	2.09	0.52
39:O:71:LEU:O	39:O:72:ARG:NH1	2.40	0.52
42:R:88:LEU:HA	42:R:91:ARG:HB2	1.92	0.52
43:S:68:ARG:NH1	43:S:70:HIS:O	2.42	0.52
52:3:1081:A:H2'	52:3:1082:A:H8	1.74	0.52
52:3:1202:U:C2'	52:3:1203:C:H5'	2.39	0.52
52:3:1540:U:O2	52:3:1540:U:H3'	2.09	0.52
53:1:181:A:H1'	53:1:435:C:H5'	1.90	0.52
53:1:2544:G:H2'	53:1:2545:G:H8	1.74	0.52
4:e:84:ILE:HD11	53:1:2311:A:C2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C:41:VAL:HG23	27:C:42:VAL:H	1.74	0.52
32:H:156:LEU:H	32:H:195:ILE:HD11	1.74	0.52
32:H:201:ILE:HD12	32:H:201:ILE:N	2.24	0.52
33:I:195:ASN:ND2	33:I:197:HIS:HB3	2.24	0.52
34:J:108:GLY:O	34:J:109:ALA:HB3	2.09	0.52
53:1:2443:C:H2'	53:1:2444:G:H8	1.74	0.52
3:d:71:GLY:N	53:1:674:G:H5''	2.23	0.52
3:d:163:ASN:HD21	53:1:322:A:H2'	1.75	0.52
12:m:11:LYS:HD3	12:m:86:LYS:HG2	1.91	0.52
28:D:10:LEU:HD23	53:1:770:G:H5''	1.91	0.52
31:G:96:LEU:HB2	31:G:99:MET:HE2	1.91	0.52
50:Z:66:ARG:HD2	52:3:1099:G:H5'	1.92	0.52
52:3:1346:A:H2'	52:3:1346:A:N3	2.24	0.52
53:1:948:C:H2'	53:1:949:G:C8	2.45	0.52
58:8:135:LEU:HD12	58:8:172:ARG:HE	1.74	0.52
2:c:194:PRO:HA	53:1:2680:U:H5'	1.89	0.52
12:m:67:VAL:HG12	12:m:100:LYS:HE2	1.91	0.52
19:t:61:LEU:HB3	53:1:1341:G:C5'	2.40	0.52
43:S:92:ILE:H	43:S:92:ILE:HD12	1.75	0.52
52:3:50:A:H4'	52:3:51:A:H5'	1.91	0.52
52:3:413:G:N2	52:3:428:G:H1'	2.24	0.52
52:3:1001:C:H2'	52:3:1002:G:C8	2.44	0.52
52:3:1280:A:O2'	52:3:1281:C:H5'	2.10	0.52
53:1:414:C:H2'	53:1:415:A:C8	2.45	0.52
53:1:1494:A:H2	53:1:1579:A:H1'	1.74	0.52
52:3:764:C:H2'	52:3:765:G:O4'	2.09	0.52
53:1:441:U:O2'	53:1:442:G:H5'	2.09	0.52
53:1:1669:A:H2'	53:1:1670:C:H5'	1.91	0.52
53:1:2156:G:C2'	53:1:2157:G:H5'	2.40	0.52
54:2:49:C:H2'	54:2:50:A:H8	1.74	0.52
58:8:17:THR:HG23	58:8:79:HIS:HE1	1.75	0.52
1:b:64:VAL:HG13	1:b:103:ILE:HA	1.91	0.52
1:b:119:VAL:HB	6:g:91:PHE:CE1	2.45	0.52
10:k:63:VAL:HG23	10:k:64:ARG:HG3	1.91	0.52
11:l:23:ILE:HG13	17:r:82:HIS:CE1	2.45	0.52
13:n:12:ARG:CZ	13:n:20:MET:HE1	2.40	0.52
22:w:39:THR:H	53:1:2331:G:C4'	2.22	0.52
24:y:41:HIS:CE1	53:1:96:C:H4'	2.44	0.52
33:I:129:VAL:HG22	52:3:619:U:O2'	2.09	0.52
51:a:177:LYS:NZ	53:1:2125:G:H5'	2.25	0.52
52:3:802:A:H2'	52:3:803:G:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:325:G:H2'	53:1:326:G:C8	2.45	0.52
53:1:325:G:H2'	53:1:326:G:H8	1.75	0.52
53:1:1956:U:H2'	53:1:1957:C:H5'	1.92	0.52
53:1:2679:A:O2'	53:1:2680:U:H5'	2.09	0.52
54:2:95:U:H2'	54:2:96:G:C8	2.44	0.52
56:4:17:U:O2'	56:4:18:G:H5'	2.10	0.52
7:h:117:LEU:HD23	7:h:120:ALA:HA	1.91	0.52
9:j:78:THR:HG22	53:1:2641:G:H5''	1.92	0.52
9:j:113:PRO:HB2	53:1:557:C:H5''	1.90	0.52
10:k:31:ARG:H	10:k:31:ARG:HD3	1.73	0.52
10:k:88:ASN:HB3	10:k:91:SER:O	2.09	0.52
20:u:42:LYS:HD2	53:1:499:U:H5''	1.92	0.52
22:w:13:GLU:OE2	22:w:16:ARG:NH1	2.42	0.52
28:D:34:ARG:HD3	53:1:467:G:OP2	2.10	0.52
33:I:67:LEU:HG	52:3:546:A:OP1	2.09	0.52
35:K:53:LYS:HD2	35:K:54:LEU:O	2.10	0.52
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.90	0.52
40:P:112:VAL:O	40:P:112:VAL:HG12	2.09	0.52
47:W:40:PRO:HG2	47:W:43:ILE:HG12	1.92	0.52
50:Z:46:ARG:HE	52:3:1533:C:N4	2.07	0.52
52:3:79:G:O2'	52:3:80:A:H5'	2.10	0.52
53:1:502:A:H2'	53:1:503:A:H5'	1.90	0.52
4:e:51:ASN:HB3	4:e:149:ARG:HH22	1.75	0.52
39:O:31:ARG:HD2	39:O:31:ARG:O	2.10	0.52
41:Q:26:CYS:SG	41:Q:29:LYS:HD3	2.49	0.52
41:Q:74:GLN:O	41:Q:74:GLN:HG2	2.10	0.52
42:R:6:ILE:HG23	42:R:7:ASN:N	2.24	0.52
49:Y:26:MET:HB3	52:3:1458:G:H5'	1.92	0.52
53:1:359:G:H2'	53:1:360:U:O4'	2.09	0.52
53:1:1071:G:OP1	53:1:1071:G:H3'	2.10	0.52
53:1:2156:G:H2'	53:1:2157:G:H5'	1.92	0.52
3:d:147:LEU:HD13	3:d:183:PHE:CE2	2.45	0.52
6:g:63:ALA:HA	6:g:66:ASN:HD22	1.73	0.52
7:h:73:LYS:O	7:h:73:LYS:HD3	2.09	0.52
10:k:76:VAL:H	15:p:72:VAL:HG12	1.75	0.52
17:r:51:VAL:CG2	17:r:52:PRO:HD2	2.40	0.52
19:t:68:LYS:NZ	53:1:1336:A:OP2	2.42	0.52
40:P:92:ARG:HD3	50:Z:24:LYS:HZ1	1.75	0.52
47:W:72:ARG:HH12	50:Z:4:LYS:HD3	1.74	0.52
53:1:288:U:H2'	53:1:289:G:C8	2.45	0.52
53:1:621:A:H2'	53:1:622:G:H5'	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:694:U:OP1	53:1:1569:A:H1'	2.10	0.52
53:1:2029:G:O6	53:1:2032:G:H5''	2.10	0.52
53:1:2818:U:H2'	53:1:2819:G:C8	2.44	0.52
1:b:100:ARG:HH22	53:1:1501:G:C5'	2.22	0.51
1:b:242:HIS:O	1:b:244:VAL:HG13	2.11	0.51
8:i:105:LEU:HD23	8:i:108:ILE:HD11	1.92	0.51
13:n:39:PRO:HG2	53:1:1651:G:H4'	1.91	0.51
32:H:86:LEU:HA	32:H:89:VAL:HG22	1.91	0.51
45:U:68:SER:HB3	45:U:71:VAL:HG23	1.91	0.51
51:a:189:LEU:O	51:a:192:LEU:HG	2.10	0.51
52:3:252:U:O2	52:3:252:U:H2'	2.10	0.51
52:3:1052:U:H2'	52:3:1200:C:H41	1.74	0.51
53:1:523:C:H2'	53:1:524:G:H8	1.75	0.51
53:1:585:G:H21	53:1:1254:A:H62	1.57	0.51
53:1:833:A:H2'	53:1:834:G:C8	2.44	0.51
53:1:877:A:H1'	53:1:900:A:N6	2.25	0.51
53:1:1307:A:H2'	53:1:1308:A:H5'	1.92	0.51
58:8:72:THR:HG22	58:8:73:PRO:HD2	1.91	0.51
16:q:5:ARG:HG3	53:1:584:C:OP2	2.11	0.51
25:z:50:VAL:O	25:z:54:VAL:HG22	2.11	0.51
31:G:105:THR:O	31:G:108:GLN:HB2	2.10	0.51
40:P:126:ARG:NH2	52:3:796:C:H4'	2.24	0.51
43:S:88:MET:N	43:S:88:MET:SD	2.83	0.51
45:U:5:ARG:HB2	52:3:376:G:H5''	1.92	0.51
52:3:360:G:O2'	52:3:361:G:H5'	2.10	0.51
53:1:214:G:H2'	53:1:215:G:C8	2.45	0.51
53:1:594:U:H2'	53:1:595:C:C6	2.45	0.51
53:1:1858:A:H1'	53:1:1885:A:C2	2.45	0.51
53:1:2291:U:H2'	53:1:2292:U:C6	2.46	0.51
1:b:216:ARG:NH1	53:1:691:C:OP1	2.43	0.51
2:c:4:LEU:HD13	2:c:101:PHE:CE2	2.46	0.51
4:e:98:PHE:HD1	4:e:101:ARG:HH11	1.57	0.51
10:k:23:LYS:HB3	10:k:40:LYS:HB3	1.93	0.51
12:m:134:THR:HG21	21:v:79:ARG:HH12	1.75	0.51
13:n:118:ARG:HH12	26:B:55:ALA:HB3	1.76	0.51
31:G:220:VAL:O	31:G:224:ARG:HG2	2.11	0.51
34:J:24:VAL:HG22	34:J:25:LYS:N	2.23	0.51
35:K:49:TYR:OH	35:K:86:ARG:NH1	2.42	0.51
52:3:16:A:O2'	52:3:17:U:H5'	2.10	0.51
52:3:784:A:H2'	52:3:785:G:C8	2.45	0.51
52:3:1201:A:Cl'	52:3:1202:U:OP2	2.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1289:C:H2'	53:1:1290:C:C6	2.45	0.51
53:1:2786:U:O2'	53:1:2787:C:H5'	2.11	0.51
58:8:45:ARG:HH22	58:8:69:GLU:H	1.57	0.51
32:H:168:ARG:HD2	32:H:169:GLU:N	2.26	0.51
38:N:61:ASP:C	38:N:62:LEU:HD22	2.36	0.51
53:1:191:A:H2'	53:1:192:C:C6	2.45	0.51
53:1:458:G:O2'	53:1:459:U:H5	1.92	0.51
54:2:63:C:H2'	54:2:64:G:H8	1.75	0.51
7:h:90:GLY:O	7:h:91:ALA:C	2.54	0.51
36:L:85:GLN:OE1	55:6:32:C:H4'	2.10	0.51
52:3:1391:U:H2'	52:3:1392:G:H8	1.74	0.51
53:1:2194:U:H2'	53:1:2195:U:C6	2.46	0.51
53:1:2515:C:H2'	53:1:2516:A:C8	2.44	0.51
7:h:72:LEU:HD23	7:h:72:LEU:H	1.75	0.51
8:i:52:LEU:HD21	8:i:73:PRO:HG3	1.93	0.51
9:j:104:ALA:O	9:j:108:MET:HE3	2.11	0.51
15:p:102:ARG:NH2	53:1:1754:A:O3'	2.44	0.51
38:N:105:ARG:O	38:N:105:ARG:HD3	2.10	0.51
53:1:192:C:H2'	53:1:193:U:H5'	1.92	0.51
53:1:2073:C:O2'	53:1:2074:U:H5'	2.11	0.51
53:1:2114:A:H2'	53:1:2114:A:N3	2.26	0.51
58:8:20:HIS:CD2	58:8:115:GLN:HB2	2.45	0.51
7:h:48:ALA:HB3	7:h:51:TYR:HE1	1.75	0.51
7:h:118:ILE:CG2	7:h:119:PRO:HD3	2.41	0.51
13:n:26:GLY:HA2	13:n:75:ILE:CD1	2.41	0.51
19:t:34:VAL:HG22	19:t:35:ALA:H	1.75	0.51
23:x:17:ARG:NE	23:x:23:ALA:HB2	2.25	0.51
36:L:68:VAL:HG23	36:L:99:ALA:HB1	1.92	0.51
38:N:29:ILE:HD11	38:N:66:VAL:HG12	1.93	0.51
38:N:34:LEU:HD23	38:N:34:LEU:C	2.36	0.51
52:3:1409:C:H2'	52:3:1410:A:C8	2.46	0.51
53:1:685:A:H5''	53:1:788:A:H62	1.76	0.51
53:1:1285:A:H2'	53:1:1286:A:H5'	1.93	0.51
53:1:2514:U:H2'	53:1:2515:C:C6	2.46	0.51
57:7:6:G:C2'	57:7:7:A:H5''	2.40	0.51
57:7:25:C:H2'	57:7:26:A:C4'	2.39	0.51
1:b:91:ALA:HB2	1:b:105:ALA:HB2	1.93	0.51
4:e:56:LEU:HD21	4:e:151:LEU:HD22	1.93	0.51
8:i:102:ARG:HG2	8:i:139:VAL:CG2	2.40	0.51
10:k:30:ARG:HG3	53:1:2674:G:H4'	1.92	0.51
20:u:52:ASN:OD1	20:u:54:PRO:HD3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:P:92:ARG:HD3	50:Z:24:LYS:HZ3	1.75	0.51
48:X:9:PHE:CD2	52:3:1318:A:H4'	2.45	0.51
52:3:370:C:H2'	52:3:371:A:C8	2.45	0.51
52:3:552:U:H2'	52:3:553:A:C8	2.46	0.51
52:3:950:U:H2'	52:3:951:G:C8	2.46	0.51
53:1:948:C:H2'	53:1:949:G:H8	1.75	0.51
53:1:2163:A:C2'	53:1:2164:C:H5'	2.41	0.51
53:1:2756:U:H4'	53:1:2757:A:OP1	2.11	0.51
60:7:101:PHE:HD1	58:8:229:THR:HG21	1.76	0.51
58:8:45:ARG:NH2	58:8:233:GLU:O	2.43	0.51
1:b:260:LYS:HA	1:b:263:ASP:OD2	2.10	0.51
13:n:69:ARG:O	13:n:70:THR:OG1	2.25	0.51
31:G:207:ARG:O	31:G:211:LEU:HD23	2.11	0.51
32:H:63:ILE:CG1	32:H:98:ALA:HB2	2.41	0.51
44:T:71:ARG:NH2	52:3:754:C:OP1	2.44	0.51
52:3:1414:U:H2'	52:3:1415:G:H8	1.74	0.51
53:1:225:C:H2'	53:1:226:A:O4'	2.11	0.51
53:1:704:G:H1'	53:1:727:A:H61	1.74	0.51
53:1:813:U:H2'	53:1:814:C:C6	2.46	0.51
53:1:1181:U:H2'	53:1:1182:G:C8	2.46	0.51
53:1:1545:A:H2'	53:1:1546:G:O4'	2.10	0.51
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.93	0.51
9:j:1:MET:HE1	17:r:20:VAL:HG13	1.92	0.51
11:l:65:GLY:HA2	53:1:2415:G:H4'	1.92	0.51
36:L:37:THR:O	36:L:41:ILE:HG13	2.11	0.51
52:3:328:C:H5'	52:3:329:A:H5'	1.93	0.51
52:3:354:G:H2'	52:3:355:C:H5'	1.92	0.51
53:1:20:C:H2'	53:1:21:A:C8	2.45	0.51
53:1:940:G:H2'	53:1:941:A:H5''	1.92	0.51
53:1:1067:A:H2'	53:1:1067:A:N3	2.26	0.51
53:1:1373:A:H4'	53:1:2212:A:H1'	1.92	0.51
53:1:2350:C:H2'	53:1:2351:G:O4'	2.11	0.51
53:1:2404:U:H2'	53:1:2405:G:O4'	2.10	0.51
53:1:2860:A:H2'	53:1:2861:U:H5'	1.92	0.51
58:8:237:ILE:HD12	58:8:237:ILE:N	2.26	0.51
58:8:260:GLU:OE2	58:8:263:ARG:HA	2.11	0.51
5:f:173:ALA:O	5:f:175:LYS:N	2.38	0.50
7:h:41:LEU:HD13	53:1:1083:U:O5'	2.10	0.50
11:l:30:THR:HG22	53:1:810:U:O4	2.10	0.50
27:C:44:GLN:O	27:C:45:HIS:HB2	2.09	0.50
31:G:27:LYS:N	31:G:28:PRO:CD	2.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:55:ARG:HA	33:I:55:ARG:NE	2.25	0.50
34:J:92:ARG:O	34:J:93:VAL:C	2.54	0.50
39:O:71:LEU:O	39:O:72:ARG:HG2	2.11	0.50
51:a:206:GLY:H	53:1:1861:G:P	2.34	0.50
53:1:118:A:OP2	53:1:119:A:H5''	2.11	0.50
53:1:395:U:H2'	53:1:396:G:H8	1.75	0.50
53:1:616:A:H2'	53:1:617:G:O4'	2.10	0.50
53:1:1111:A:O2'	53:1:1112:G:H4'	2.11	0.50
53:1:2277:G:C3'	53:1:2278:A:H5''	2.40	0.50
4:e:65:LEU:HD22	54:2:42:C:C5	2.45	0.50
23:x:18:SER:OG	53:1:2080:A:H5'	2.12	0.50
52:3:371:A:H2'	52:3:372:C:O4'	2.11	0.50
52:3:1436:U:H2'	52:3:1437:A:C8	2.46	0.50
53:1:1827:U:C2'	53:1:1828:G:H5'	2.42	0.50
58:8:14:ASN:HB3	58:8:372:GLY:HA3	1.92	0.50
58:8:214:PRO:HG3	58:8:334:ARG:HH12	1.77	0.50
2:c:88:GLU:OE1	2:c:88:GLU:N	2.44	0.50
2:c:173:GLN:NE2	53:1:2772:C:H5'	2.26	0.50
5:f:90:GLY:HA3	5:f:93:TYR:CE2	2.47	0.50
33:I:100:VAL:HG21	33:I:136:VAL:HG21	1.92	0.50
47:W:48:ALA:HB2	52:3:834:U:OP1	2.12	0.50
50:Z:23:GLU:C	50:Z:25:ALA:H	2.18	0.50
52:3:730:G:H2'	52:3:731:G:H5'	1.93	0.50
52:3:1315:U:H2'	52:3:1316:G:O4'	2.12	0.50
53:1:1103:A:H2'	53:1:1103:A:N3	2.25	0.50
53:1:2208:C:H2'	53:1:2209:G:C8	2.46	0.50
53:1:2266:A:H4'	53:1:2267:A:N3	2.26	0.50
53:1:2646:C:H2'	53:1:2647:U:O4'	2.09	0.50
58:8:322:PRO:HB3	58:8:352:MET:HA	1.94	0.50
12:m:23:GLY:HA3	12:m:66:ARG:HH22	1.76	0.50
24:y:47:ARG:O	24:y:50:VAL:HG22	2.12	0.50
34:J:76:ASN:HB3	34:J:79:THR:HG23	1.93	0.50
41:Q:4:ASN:HB2	46:V:35:LYS:NZ	2.26	0.50
46:V:30:HIS:HB3	46:V:34:GLY:H	1.76	0.50
51:a:174:THR:HB	53:1:2124:G:H5''	1.92	0.50
52:3:555:U:H2'	52:3:556:C:C6	2.47	0.50
53:1:471:A:H2'	53:1:472:A:O4'	2.11	0.50
53:1:2112:G:H2'	53:1:2113:U:H5'	1.93	0.50
58:8:155:ARG:HH12	58:8:168:THR:HB	1.75	0.50
1:b:56:GLY:HA2	1:b:212:TRP:HA	1.93	0.50
6:g:30:LEU:HB3	6:g:36:ALA:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:72:THR:HG23	8:i:73:PRO:HD2	1.93	0.50
11:l:55:MET:HE3	53:1:2392:A:C2	2.46	0.50
32:H:122:GLN:HE21	32:H:127:VAL:HG11	1.77	0.50
33:I:23:GLY:HA3	52:3:409:U:OP1	2.11	0.50
39:O:61:ALA:HB2	52:3:1061:G:H5'	1.93	0.50
41:Q:120:ARG:HG3	41:Q:120:ARG:HH11	1.76	0.50
48:X:17:LYS:HG2	48:X:30:LEU:HD23	1.92	0.50
52:3:530:G:H3'	52:3:531:U:H5''	1.94	0.50
52:3:1441:A:H2'	52:3:1442:G:H5'	1.94	0.50
53:1:523:C:H2'	53:1:524:G:C8	2.47	0.50
53:1:1444:G:H2'	53:1:1445:G:H8	1.77	0.50
53:1:1447:C:H2'	53:1:1448:G:H8	1.76	0.50
53:1:2423:U:H5'	53:1:2424:C:C5'	2.42	0.50
53:1:2888:C:H2'	53:1:2889:C:C6	2.47	0.50
55:6:63:G:H2'	55:6:64:G:H8	1.77	0.50
58:8:379:GLU:HB3	58:8:384:VAL:HG21	1.94	0.50
2:c:161:MET:HG2	2:c:162:ALA:H	1.76	0.50
11:l:111:ILE:HD11	53:1:636:G:H2'	1.94	0.50
15:p:28:LYS:HD3	15:p:39:LEU:HD21	1.94	0.50
16:q:92:LYS:HE3	53:1:995:C:O2'	2.12	0.50
31:G:128:LEU:HB3	31:G:132:GLU:HG3	1.94	0.50
47:W:48:ALA:O	47:W:51:GLN:HB3	2.11	0.50
52:3:405:U:C3'	52:3:406:G:H5'	2.39	0.50
52:3:477:C:H2'	52:3:478:A:C8	2.47	0.50
52:3:912:C:O2'	52:3:913:A:H5'	2.11	0.50
52:3:1401:G:H2'	52:3:1402:C:O4'	2.11	0.50
53:1:690:G:O2'	53:1:691:C:H5'	2.11	0.50
53:1:1779:U:OP2	53:1:1784:A:N6	2.40	0.50
57:7:53:G:H5''	58:8:321:THR:OG1	2.11	0.50
32:H:6:PRO:HG2	32:H:200:TRP:HE1	1.76	0.50
38:N:49:GLN:N	38:N:50:PRO:HD2	2.27	0.50
41:Q:32:VAL:HA	41:Q:78:VAL:HG12	1.93	0.50
50:Z:22:CYS:SG	50:Z:23:GLU:N	2.84	0.50
52:3:945:G:H2'	52:3:945:G:N3	2.27	0.50
52:3:1236:A:H2'	52:3:1237:C:C6	2.47	0.50
52:3:1306:A:H62	52:3:1331:G:H1'	1.76	0.50
53:1:729:G:H4'	53:1:763:G:C5'	2.41	0.50
53:1:1307:A:C2'	53:1:1308:A:H5'	2.42	0.50
53:1:1758:U:C5	53:1:2696:U:H5'	2.47	0.50
54:2:2:G:H2'	54:2:3:C:C6	2.46	0.50
54:2:97:C:H2'	54:2:98:G:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:106:G:H2'	54:2:107:G:O4'	2.11	0.50
58:8:371:ASP:OD1	58:8:392:VAL:HG23	2.11	0.50
2:c:112:THR:HA	2:c:169:ARG:HA	1.92	0.50
3:d:125:SER:OG	3:d:126:VAL:N	2.45	0.50
15:p:10:GLU:HG3	15:p:11:GLN:NE2	2.27	0.50
31:G:46:VAL:N	31:G:47:PRO:HD2	2.27	0.50
32:H:161:ILE:HD11	52:3:1196:A:C2	2.46	0.50
34:J:96:GLN:HB2	34:J:123:LEU:HB2	1.94	0.50
35:K:86:ARG:HD3	47:W:63:TYR:O	2.12	0.50
53:1:827:U:H4'	53:1:828:U:C5	2.46	0.50
53:1:1300:G:H4'	53:1:1301:A:C5'	2.42	0.50
57:7:28:G:H2'	57:7:29:G:H8	1.75	0.50
35:K:67:PRO:HG2	35:K:70:VAL:CG2	2.40	0.50
44:T:32:THR:HG21	44:T:84:LEU:HD11	1.94	0.50
47:W:29:LYS:O	47:W:29:LYS:HD3	2.12	0.50
52:3:552:U:H2'	52:3:553:A:H8	1.77	0.50
52:3:758:C:H4'	52:3:880:C:H4'	1.94	0.50
52:3:835:U:C3'	52:3:836:G:H5''	2.41	0.50
52:3:1038:C:H2'	52:3:1039:G:H8	1.77	0.50
52:3:1218:C:H2'	52:3:1219:A:C8	2.47	0.50
53:1:215:G:C4'	53:1:216:A:H4'	2.40	0.50
53:1:863:A:H4'	54:2:100:G:N2	2.27	0.50
55:6:71:C:H2'	55:6:72:A:C8	2.46	0.50
2:c:155:VAL:HG21	53:1:2618:G:H21	1.76	0.49
3:d:158:PHE:HA	3:d:169:VAL:HG21	1.93	0.49
5:f:132:LEU:HD23	5:f:132:LEU:H	1.76	0.49
7:h:73:LYS:CB	7:h:117:LEU:HD21	2.42	0.49
8:i:91:LYS:HG2	8:i:94:LYS:HE2	1.93	0.49
15:p:24:THR:HB	15:p:87:ARG:HB2	1.93	0.49
38:N:56:MET:N	38:N:56:MET:SD	2.81	0.49
39:O:52:LEU:HD23	39:O:62:ARG:HD3	1.94	0.49
42:R:77:LYS:HA	42:R:80:MET:HE3	1.92	0.49
45:U:33:ILE:N	45:U:33:ILE:HD12	2.27	0.49
52:3:890:G:H2'	52:3:906:A:N6	2.26	0.49
52:3:983:A:H1'	52:3:1049:U:O2	2.12	0.49
52:3:1475:G:H2'	52:3:1476:A:H8	1.77	0.49
52:3:1527:U:H2'	52:3:1528:U:C6	2.46	0.49
53:1:851:C:H2'	53:1:852:U:C6	2.47	0.49
53:1:1287:A:C2	53:1:1649:G:H4'	2.47	0.49
53:1:1704:C:H2'	53:1:1705:A:C8	2.47	0.49
53:1:2228:G:H2'	53:1:2229:U:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2589:A:H2'	53:1:2590:A:H8	1.77	0.49
53:1:2888:C:H2'	53:1:2889:C:H6	1.75	0.49
58:8:35:VAL:HG11	58:8:186:GLU:CD	2.37	0.49
2:c:135:GLY:HA2	53:1:743:A:OP1	2.12	0.49
7:h:59:LEU:HD21	53:1:1047:G:C8	2.47	0.49
9:j:47:HIS:CE1	9:j:48:VAL:HG23	2.47	0.49
38:N:119:LYS:HB3	52:3:1349:A:OP1	2.11	0.49
44:T:45:HIS:O	44:T:47:LYS:N	2.44	0.49
49:Y:10:ALA:O	49:Y:14:GLU:HG2	2.12	0.49
52:3:1464:U:H2'	52:3:1465:A:C8	2.47	0.49
53:1:18:U:H2'	53:1:19:A:C8	2.48	0.49
53:1:1601:G:C2'	53:1:1602:U:H5'	2.42	0.49
53:1:1773:A:H2'	53:1:1774:C:O4'	2.11	0.49
53:1:2774:C:H2'	53:1:2775:G:O4'	2.12	0.49
4:e:122:ASP:OD1	4:e:126:ASN:N	2.46	0.49
7:h:3:LEU:HG	7:h:5:LEU:H	1.77	0.49
9:j:95:ARG:HH22	53:1:2768:U:H4'	1.77	0.49
47:W:40:PRO:CB	52:3:720:C:H5''	2.41	0.49
52:3:56:U:H2'	52:3:57:G:C8	2.48	0.49
52:3:1060:U:H2'	52:3:1061:G:C8	2.46	0.49
52:3:1251:A:O2'	52:3:1370:G:H5'	2.12	0.49
53:1:1720:U:H2'	53:1:1721:G:O4'	2.12	0.49
54:2:3:C:H3'	54:2:4:C:C5'	2.41	0.49
19:t:64:LYS:HA	19:t:79:ASP:OD2	2.12	0.49
33:I:160:LEU:HD22	33:I:164:ARG:HH21	1.77	0.49
37:M:80:PRO:HG2	52:3:878:A:H5'	1.94	0.49
49:Y:73:ARG:CZ	52:3:261:U:H5	2.25	0.49
50:Z:17:ARG:HA	50:Z:20:ARG:HG2	1.94	0.49
52:3:571:U:H2'	52:3:572:A:H5''	1.94	0.49
52:3:1138:G:H3'	52:3:1138:G:N3	2.27	0.49
53:1:208:C:H2'	53:1:209:C:H6	1.77	0.49
53:1:548:G:H2'	53:1:549:G:O4'	2.12	0.49
53:1:2432:A:N3	55:6:75:C:H5'	2.28	0.49
2:c:108:ASP:OD2	2:c:206:ALA:HA	2.12	0.49
6:g:31:VAL:HG12	6:g:32:PRO:HD3	1.93	0.49
18:s:67:ASP:OD1	18:s:67:ASP:N	2.45	0.49
32:H:200:TRP:C	32:H:201:ILE:HD12	2.38	0.49
42:R:8:ILE:HG22	42:R:8:ILE:O	2.12	0.49
42:R:112:ARG:HD3	52:3:1229:A:OP2	2.12	0.49
52:3:1301:U:O2	52:3:1301:U:H2'	2.10	0.49
52:3:1410:A:H2'	52:3:1411:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1258:U:H2'	53:1:1259:G:C8	2.48	0.49
4:e:130:GLY:HA2	4:e:152:ASP:HA	1.93	0.49
38:N:114:LYS:CE	52:3:1187:G:H5'	2.42	0.49
39:O:37:ARG:HH21	39:O:77:VAL:HG11	1.77	0.49
45:U:31:ARG:NH1	52:3:311:C:OP1	2.45	0.49
50:Z:66:ARG:HG3	52:3:1099:G:O4'	2.13	0.49
52:3:1005:A:H2'	52:3:1006:G:O4'	2.13	0.49
53:1:1161:C:H2'	53:1:1162:G:H8	1.76	0.49
53:1:2676:C:H2'	53:1:2677:G:H8	1.76	0.49
58:8:309:VAL:HG12	58:8:387:GLY:HA3	1.95	0.49
52:3:113:G:H2'	52:3:114:U:C6	2.48	0.49
52:3:337:G:H2'	52:3:338:A:C8	2.47	0.49
53:1:36:G:O2'	53:1:37:C:H5'	2.13	0.49
53:1:742:A:H2'	53:1:743:A:C8	2.48	0.49
58:8:98:GLN:OE1	58:8:373:LEU:O	2.30	0.49
4:e:31:GLU:OE2	4:e:158:THR:HG23	2.13	0.49
6:g:75:LEU:HG	6:g:77:THR:H	1.78	0.49
8:i:12:VAL:HG22	53:1:1061:U:O2	2.13	0.49
20:u:85:ARG:HG3	20:u:92:VAL:HG23	1.93	0.49
27:C:33:LEU:HD21	53:1:2286:G:C6	2.48	0.49
32:H:4:VAL:HG22	32:H:5:HIS:N	2.27	0.49
32:H:168:ARG:HD2	32:H:168:ARG:C	2.37	0.49
40:P:85:VAL:HG21	50:Z:16:ARG:HH22	1.76	0.49
42:R:64:VAL:HB	42:R:65:GLU:OE2	2.13	0.49
42:R:97:ARG:HB2	42:R:99:GLN:HE22	1.77	0.49
43:S:2:LYS:HZ3	52:3:982:U:H5''	1.78	0.49
43:S:30:ILE:HG22	43:S:30:ILE:O	2.12	0.49
52:3:243:A:H4'	52:3:244:U:H3'	1.93	0.49
52:3:1353:G:O2'	52:3:1354:U:H5'	2.12	0.49
53:1:1775:U:H2'	53:1:1776:G:O4'	2.11	0.49
53:1:2224:G:H4'	53:1:2226:C:C2	2.47	0.49
2:c:47:ALA:HA	2:c:84:LEU:HG	1.95	0.49
17:r:51:VAL:HG22	17:r:52:PRO:HD2	1.94	0.49
26:B:10:SER:O	26:B:14:MET:HG3	2.12	0.49
35:K:22:ILE:HG23	35:K:62:MET:HE3	1.94	0.49
49:Y:4:LYS:HB2	49:Y:7:LYS:HE3	1.95	0.49
50:Z:20:ARG:HA	50:Z:24:LYS:HB2	1.94	0.49
53:1:52:A:H2'	53:1:53:A:C8	2.47	0.49
53:1:794:A:H2'	53:1:795:C:C6	2.47	0.49
53:1:974:G:N3	53:1:974:G:H2'	2.28	0.49
53:1:2093:G:N7	53:1:2225:A:H2'	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2756:U:H1'	53:1:2757:A:H5''	1.94	0.49
55:6:62:C:H2'	55:6:63:G:C8	2.48	0.49
58:8:245:ILE:HD13	58:8:293:LEU:HD22	1.95	0.49
4:e:79:ARG:NH1	55:5:19:G:N1	2.58	0.49
5:f:175:LYS:HG3	5:f:176:LYS:N	2.28	0.49
35:K:47:LEU:HD21	35:K:57:ALA:HB3	1.94	0.49
38:N:78:ILE:O	38:N:82:ILE:HG13	2.12	0.49
47:W:72:ARG:HH22	50:Z:4:LYS:HD3	1.77	0.49
52:3:123:U:H5''	52:3:311:C:O2'	2.12	0.49
53:1:889:C:H2'	53:1:890:C:O4'	2.13	0.49
53:1:996:A:H2'	53:1:997:G:C8	2.45	0.49
54:2:49:C:H2'	54:2:50:A:C8	2.48	0.49
55:6:63:G:H2'	55:6:64:G:C8	2.48	0.49
57:7:64:A:H4'	58:8:381:GLY:HA3	1.93	0.49
2:c:13:ARG:HH11	15:p:55:HIS:HA	1.78	0.48
5:f:21:GLN:HE21	5:f:36:LEU:HB2	1.78	0.48
10:k:107:LEU:HD23	10:k:107:LEU:O	2.13	0.48
12:m:44:ARG:HD2	53:1:2484:G:OP1	2.13	0.48
18:s:48:LYS:O	18:s:52:GLU:HG2	2.13	0.48
22:w:22:PHE:HD2	53:1:922:C:H1'	1.78	0.48
27:C:39:ASP:OD1	27:C:41:VAL:HG22	2.13	0.48
32:H:171:ARG:HG2	32:H:173:PRO:HD3	1.94	0.48
34:J:113:VAL:HG13	34:J:114:LEU:HD12	1.95	0.48
37:M:40:LYS:HZ2	37:M:47:ASP:H	1.61	0.48
43:S:56:PRO:HA	43:S:59:GLN:HG2	1.93	0.48
44:T:1:SER:OG	44:T:2:LEU:N	2.46	0.48
52:3:370:C:H2'	52:3:371:A:H8	1.77	0.48
52:3:396:C:C2'	52:3:397:A:H5''	2.43	0.48
52:3:405:U:H3'	52:3:406:G:C5'	2.42	0.48
52:3:1023:U:H2'	52:3:1024:G:C8	2.47	0.48
52:3:1298:U:H4'	52:3:1299:A:O4'	2.13	0.48
53:1:1092:C:H2'	53:1:1093:G:O4'	2.13	0.48
53:1:1881:C:H2'	53:1:1882:U:O4'	2.14	0.48
5:f:26:LYS:HG3	5:f:31:GLU:HG3	1.96	0.48
10:k:11:ALA:HB2	10:k:83:ALA:HB1	1.95	0.48
11:l:80:SER:O	11:l:84:LYS:NZ	2.46	0.48
12:m:38:ARG:HG2	12:m:98:PRO:HD3	1.95	0.48
20:u:97:SER:O	20:u:98:ASN:HB3	2.13	0.48
27:C:22:THR:OG1	27:C:23:THR:N	2.46	0.48
27:C:32:LYS:HB3	27:C:50:GLU:HB3	1.94	0.48
33:I:100:VAL:O	33:I:104:MET:HG2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M:13:ILE:HG13	37:M:62:LEU:HD11	1.95	0.48
43:S:9:GLU:HB2	43:S:62:ARG:HH21	1.78	0.48
43:S:10:VAL:O	43:S:13:VAL:HG12	2.13	0.48
53:1:766:U:H2'	53:1:767:U:C6	2.49	0.48
1:b:96:LYS:HB3	53:1:1490:A:H62	1.78	0.48
1:b:129:LEU:N	1:b:129:LEU:HD23	2.28	0.48
19:t:67:VAL:HG22	19:t:76:ARG:HG2	1.95	0.48
30:F:10:LEU:HD23	30:F:33:HIS:NE2	2.28	0.48
30:F:17:VAL:HG12	30:F:19:ARG:HG3	1.96	0.48
32:H:155:ARG:HD3	52:3:1055:A:O2'	2.12	0.48
33:I:173:ASP:HB3	33:I:178:GLU:H	1.78	0.48
34:J:148:SER:HB2	34:J:149:PRO:HD2	1.94	0.48
38:N:28:VAL:HG13	38:N:63:TYR:HA	1.96	0.48
38:N:54:VAL:HG22	38:N:55:ASP:N	2.28	0.48
47:W:47:ARG:HB2	47:W:50:TYR:HD2	1.78	0.48
52:3:30:U:H3	52:3:553:A:H61	1.61	0.48
52:3:1441:A:C2'	52:3:1442:G:H5'	2.44	0.48
53:1:877:A:H1'	53:1:900:A:H61	1.77	0.48
53:1:979:A:H2'	53:1:982:C:H42	1.78	0.48
53:1:1020:A:C1'	53:1:1021:A:OP2	2.54	0.48
53:1:1367:A:C2'	53:1:1368:G:H5'	2.43	0.48
58:8:91:ASN:OD1	58:8:97:ALA:HB3	2.14	0.48
3:d:68:ALA:HA	53:1:1255:U:C6	2.48	0.48
4:e:33:ILE:O	4:e:90:LEU:HD23	2.13	0.48
9:j:102:GLU:HG3	9:j:119:PHE:HZ	1.78	0.48
12:m:3:GLN:HE21	12:m:92:TRP:HE1	1.60	0.48
15:p:9:GLN:HA	15:p:12:MET:HE3	1.95	0.48
15:p:52:ARG:NH2	53:1:2720:U:H5''	2.26	0.48
15:p:105:LYS:HD3	52:3:1433:A:OP1	2.13	0.48
36:L:4:ARG:H	36:L:4:ARG:CD	2.25	0.48
38:N:114:LYS:HE2	52:3:1187:G:H5''	1.95	0.48
42:R:16:ILE:HD12	42:R:16:ILE:N	2.29	0.48
53:1:558:U:H2'	53:1:559:G:C8	2.48	0.48
53:1:2121:G:H2'	53:1:2122:U:O4'	2.12	0.48
58:8:217:ASP:HB3	58:8:229:THR:HB	1.95	0.48
7:h:97:LYS:HE3	7:h:129:LEU:HD22	1.96	0.48
13:n:18:GLN:HE21	13:n:22:ARG:HH12	1.62	0.48
17:r:69:GLY:N	17:r:91:GLN:O	2.44	0.48
38:N:38:PHE:HA	38:N:41:GLU:OE2	2.13	0.48
41:Q:23:LEU:HD22	41:Q:58:ASN:HD22	1.78	0.48
47:W:36:GLY:O	47:W:62:ARG:NH2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:4:LYS:HG3	52:3:332:G:OP1	2.14	0.48
52:3:26:A:N6	52:3:558:G:H1'	2.29	0.48
52:3:162:A:H2'	52:3:163:C:H5'	1.95	0.48
52:3:501:C:H2'	52:3:502:A:C8	2.48	0.48
53:1:176:A:O2'	53:1:177:G:H5'	2.13	0.48
53:1:971:G:H2'	53:1:972:A:O4'	2.13	0.48
53:1:1447:C:H2'	53:1:1448:G:C8	2.49	0.48
53:1:1786:A:H1'	53:1:1938:A:N6	2.29	0.48
53:1:1874:C:H2'	53:1:1875:G:O4'	2.13	0.48
53:1:2343:U:O2'	53:1:2344:U:H5'	2.14	0.48
53:1:2637:U:H2'	53:1:2638:G:O4'	2.12	0.48
3:d:129:PRO:O	53:1:321:U:H5'	2.14	0.48
5:f:27:GLY:HA3	5:f:78:VAL:HB	1.96	0.48
7:h:33:VAL:HG12	53:1:1055:G:H5''	1.95	0.48
7:h:94:ARG:HD2	7:h:97:LYS:HD2	1.94	0.48
17:r:1:MET:N	17:r:43:ASN:HA	2.27	0.48
52:3:1448:C:H2'	52:3:1449:C:H6	1.78	0.48
53:1:1001:A:H2'	53:1:1002:G:O4'	2.13	0.48
53:1:1357:C:H2'	53:1:1358:G:O4'	2.14	0.48
53:1:2074:U:H2'	53:1:2075:U:C6	2.49	0.48
53:1:2220:U:H2'	53:1:2221:G:C8	2.48	0.48
53:1:2421:G:H2'	55:6:76:A:N6	2.28	0.48
54:2:63:C:H2'	54:2:64:G:C8	2.49	0.48
5:f:1:SER:OG	5:f:2:ARG:N	2.45	0.48
9:j:35:ARG:HA	9:j:40:HIS:CD2	2.49	0.48
12:m:3:GLN:HE21	12:m:92:TRP:NE1	2.11	0.48
12:m:39:GLY:C	12:m:40:ARG:HD3	2.39	0.48
13:n:86:ARG:NH2	13:n:117:ASP:OD2	2.47	0.48
15:p:105:LYS:O	15:p:108:ARG:HG2	2.14	0.48
18:s:44:ALA:HA	18:s:47:VAL:HG12	1.96	0.48
32:H:68:HIS:HE2	32:H:105:VAL:HB	1.78	0.48
32:H:113:LYS:HG3	32:H:184:ASN:OD1	2.14	0.48
33:I:14:GLU:OE2	33:I:55:ARG:HD3	2.13	0.48
33:I:56:GLU:OE1	33:I:195:ASN:HB3	2.13	0.48
38:N:64:ILE:HG21	38:N:78:ILE:HD12	1.96	0.48
53:1:1023:U:O2'	53:1:1122:G:H5'	2.14	0.48
53:1:1353:A:H2'	53:1:1354:A:C8	2.49	0.48
53:1:1424:G:H2'	53:1:1425:G:O4'	2.14	0.48
53:1:2376:A:H2'	53:1:2377:A:O4'	2.14	0.48
53:1:2478:A:H2'	53:1:2479:U:O4'	2.14	0.48
10:k:66:LYS:CG	10:k:81:GLY:H	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:64:TRP:HB2	12:m:104:GLU:HB2	1.96	0.48
23:x:56:ARG:NH1	53:1:399:U:H5''	2.28	0.48
25:z:30:ARG:HD3	25:z:30:ARG:H	1.77	0.48
31:G:182:VAL:HB	31:G:196:ASP:H	1.79	0.48
33:I:49:ASP:OD2	33:I:49:ASP:N	2.46	0.48
34:J:87:VAL:HG22	34:J:92:ARG:HB3	1.95	0.48
37:M:10:LEU:HD12	37:M:76:ARG:HB2	1.95	0.48
38:N:94:ARG:HA	38:N:97:LEU:HD12	1.94	0.48
38:N:96:GLU:HA	38:N:99:LYS:NZ	2.29	0.48
41:Q:106:VAL:HB	41:Q:109:ARG:HG3	1.95	0.48
51:a:205:LYS:HD3	53:1:1860:G:O2'	2.14	0.48
52:3:224:U:H2'	52:3:225:C:C6	2.49	0.48
52:3:1432:G:H1'	52:3:1468:A:N6	2.28	0.48
53:1:127:A:H5''	53:1:128:C:O4'	2.14	0.48
53:1:2743:U:C2'	53:1:2744:G:H5''	2.44	0.48
5:f:37:ASN:HD22	5:f:39:ALA:HB3	1.79	0.48
8:i:10:LEU:HD23	8:i:10:LEU:H	1.78	0.48
16:q:113:LYS:HA	16:q:116:LEU:HD12	1.94	0.48
20:u:4:ILE:HD13	20:u:71:ILE:HG22	1.95	0.48
23:x:39:VAL:HG22	23:x:41:SER:H	1.78	0.48
36:L:115:MET:HG3	36:L:118:ARG:HH21	1.78	0.48
38:N:129:ARG:HE	55:5:35:A:P	2.36	0.48
50:Z:66:ARG:HD2	52:3:1099:G:C5'	2.44	0.48
53:1:1563:U:H2'	53:1:1564:C:C6	2.49	0.48
53:1:1857:G:H1'	53:1:1885:A:N6	2.29	0.48
54:2:55:U:H2'	54:2:56:G:C8	2.49	0.48
1:b:49:THR:OG1	1:b:50:THR:N	2.46	0.48
1:b:107:LYS:HB2	1:b:193:GLU:HG2	1.96	0.48
2:c:121:THR:HB	2:c:127:PHE:CD2	2.49	0.48
7:h:67:THR:HB	7:h:68:PRO:HD3	1.96	0.48
10:k:25:LEU:HD11	53:1:2562:U:C5'	2.44	0.48
11:l:101:ILE:HG13	11:l:102:GLY:H	1.78	0.48
13:n:60:VAL:HG13	13:n:61:ALA:N	2.29	0.48
20:u:95:PHE:HB2	20:u:100:GLU:H	1.79	0.48
26:B:4:GLN:O	53:1:2017:U:H4'	2.13	0.48
29:E:32:LEU:HB3	29:E:40:LYS:HE3	1.96	0.48
31:G:66:ILE:HD12	31:G:66:ILE:H	1.79	0.48
32:H:69:THR:OG1	32:H:70:ALA:N	2.47	0.48
32:H:175:HIS:ND1	52:3:1108:G:H5'	2.29	0.48
53:1:441:U:H2'	53:1:442:G:C8	2.48	0.48
53:1:1330:C:H2'	53:1:1331:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:100:ARG:HH22	53:1:1501:G:H5''	1.78	0.47
3:d:48:THR:C	3:d:50:ALA:H	2.22	0.47
3:d:154:ASP:OD1	3:d:154:ASP:N	2.47	0.47
4:e:39:VAL:HG22	4:e:41:GLU:H	1.78	0.47
10:k:49:ARG:HH22	52:3:1422:G:H4'	1.79	0.47
11:l:46:VAL:HG22	11:l:47:ARG:N	2.29	0.47
12:m:134:THR:HG21	21:v:79:ARG:NH1	2.29	0.47
29:E:62:PRO:HG2	29:E:63:TYR:H	1.79	0.47
30:F:10:LEU:HD23	30:F:33:HIS:CD2	2.48	0.47
31:G:166:ASP:HB3	31:G:190:SER:HA	1.95	0.47
32:H:8:GLY:HA3	43:S:88:MET:HE3	1.96	0.47
33:I:120:LYS:HE2	33:I:130:ASN:HD21	1.78	0.47
36:L:111:GLY:HA2	36:L:118:ARG:CD	2.43	0.47
37:M:10:LEU:HD22	37:M:74:ILE:CD1	2.43	0.47
52:3:889:A:H5'	52:3:891:U:H1'	1.96	0.47
53:1:195:A:H2'	53:1:198:C:H41	1.79	0.47
53:1:542:C:H2'	53:1:543:G:H5''	1.96	0.47
53:1:886:A:H1'	53:1:889:C:H41	1.79	0.47
53:1:2678:C:H2'	53:1:2679:A:C8	2.49	0.47
53:1:2898:U:H2'	53:1:2899:A:C8	2.49	0.47
1:b:6:LYS:HZ3	53:1:1695:G:C4'	2.27	0.47
2:c:4:LEU:HD13	2:c:101:PHE:CZ	2.48	0.47
7:h:26:VAL:HG22	7:h:27:VAL:N	2.29	0.47
8:i:74:PRO:HA	53:1:1060:U:OP1	2.13	0.47
22:w:39:THR:N	53:1:2331:G:H4'	2.28	0.47
26:B:8:THR:OG1	26:B:9:ARG:N	2.47	0.47
43:S:20:PHE:O	43:S:21:ALA:HB3	2.13	0.47
46:V:5:ARG:HH11	52:3:636:U:C5'	2.27	0.47
46:V:16:MET:HG3	46:V:19:SER:O	2.14	0.47
53:1:925:A:H2'	53:1:926:G:C8	2.49	0.47
53:1:1073:A:H2'	53:1:1074:G:O4'	2.14	0.47
53:1:1570:A:H2'	53:1:1571:A:C8	2.49	0.47
53:1:1900:A:H1'	53:1:1970:A:H2'	1.97	0.47
53:1:2475:C:H42	53:1:2529:G:H22	1.61	0.47
57:7:18:G:N2	57:7:57:G:H2'	2.29	0.47
9:j:120:ARG:O	9:j:123:LYS:NZ	2.48	0.47
16:q:54:ARG:HH12	53:1:977:G:H5''	1.80	0.47
20:u:20:LYS:C	20:u:21:ARG:HD3	2.40	0.47
32:H:180:ASP:HB3	32:H:204:GLY:HA3	1.95	0.47
34:J:103:GLY:O	34:J:105:ILE:HD12	2.14	0.47
37:M:94:VAL:HB	37:M:99:GLY:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:3:VAL:CG1	46:V:35:LYS:HD2	2.42	0.47
43:S:22:LYS:HD2	43:S:23:ARG:HG3	1.96	0.47
43:S:29:ILE:HG13	43:S:30:ILE:HD12	1.96	0.47
52:3:541:G:H2'	52:3:542:G:C8	2.49	0.47
52:3:952:U:H2'	52:3:953:G:H8	1.79	0.47
52:3:1148:U:H2'	52:3:1149:C:O4'	2.14	0.47
52:3:1513:A:H2'	52:3:1514:G:C8	2.50	0.47
53:1:1841:U:H2'	53:1:1842:G:H8	1.78	0.47
53:1:2636:C:H2'	53:1:2637:U:C6	2.50	0.47
53:1:2716:C:O2'	53:1:2717:C:H5'	2.15	0.47
8:i:30:GLN:HG2	8:i:60:VAL:HG11	1.96	0.47
10:k:6:THR:HG23	53:1:1666:G:H4'	1.95	0.47
10:k:25:LEU:HD12	53:1:2562:U:H4'	1.97	0.47
12:m:33:LEU:HD23	12:m:103:TYR:HD2	1.79	0.47
19:t:15:HIS:H	19:t:32:LEU:HA	1.79	0.47
32:H:152:VAL:HG23	32:H:165:GLU:HB2	1.96	0.47
39:O:88:MET:HE3	39:O:89:ARG:H	1.79	0.47
40:P:91:GLY:C	40:P:93:GLU:H	2.23	0.47
43:S:25:GLU:HA	43:S:28:ALA:HB3	1.96	0.47
52:3:813:U:H5''	52:3:904:U:OP1	2.15	0.47
53:1:433:C:O2'	53:1:434:U:H5'	2.15	0.47
53:1:629:G:H5''	53:1:650:C:O2'	2.14	0.47
53:1:631:A:H2'	53:1:632:A:O4'	2.14	0.47
53:1:720:U:H2'	53:1:721:A:C8	2.49	0.47
53:1:1625:C:H2'	53:1:1626:A:O4'	2.15	0.47
9:j:84:ILE:HG23	9:j:84:ILE:O	2.14	0.47
11:l:13:LYS:HE3	53:1:1245:G:OP1	2.14	0.47
13:n:35:LYS:HZ3	13:n:110:MET:HE3	1.80	0.47
28:D:43:THR:HG22	28:D:44:VAL:H	1.80	0.47
30:F:17:VAL:CG1	30:F:19:ARG:HG3	2.45	0.47
31:G:102:ASN:O	31:G:106:VAL:HG23	2.14	0.47
35:K:79:ARG:NH2	52:3:671:G:H4'	2.29	0.47
37:M:17:GLN:HE21	37:M:71:VAL:H	1.62	0.47
39:O:36:VAL:HG21	39:O:74:VAL:HG12	1.96	0.47
52:3:665:A:C1'	52:3:733:G:H1'	2.44	0.47
53:1:1161:C:H2'	53:1:1162:G:C8	2.50	0.47
53:1:1853:A:H2'	53:1:1854:A:C8	2.50	0.47
58:8:331:PHE:HZ	58:8:342:ILE:HD11	1.80	0.47
58:8:370:ASP:HB2	58:8:373:LEU:HG	1.96	0.47
1:b:131:MET:O	1:b:166:ARG:NH2	2.47	0.47
12:m:47:GLU:OE2	12:m:50:ARG:NH1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:24:TYR:HE1	53:1:17:G:H4'	1.79	0.47
32:H:9:ILE:HG23	32:H:10:ARG:HG3	1.97	0.47
34:J:64:GLU:HB3	34:J:68:ARG:HH22	1.79	0.47
34:J:113:VAL:HG11	34:J:139:THR:HG21	1.96	0.47
40:P:43:TRP:NE1	52:3:705:G:H1	2.12	0.47
42:R:106:ARG:HB3	52:3:947:G:OP1	2.15	0.47
52:3:563:A:H61	52:3:884:U:H3	1.62	0.47
53:1:766:U:H2'	53:1:767:U:H6	1.78	0.47
53:1:968:C:H2'	53:1:969:G:H8	1.80	0.47
53:1:1028:A:N6	53:1:1125:G:H2'	2.30	0.47
54:2:66:A:N1	54:2:107:G:H2'	2.28	0.47
1:b:100:ARG:HH12	53:1:1501:G:H5'	1.80	0.47
1:b:176:ARG:HG2	53:1:1819:A:H3'	1.96	0.47
1:b:235:GLU:HG2	53:1:2599:G:C8	2.48	0.47
6:g:73:ASN:O	6:g:76:GLU:HG3	2.14	0.47
7:h:3:LEU:HD11	7:h:5:LEU:HD13	1.97	0.47
7:h:37:LYS:HZ3	53:1:1085:A:H61	1.60	0.47
7:h:46:ARG:HD2	7:h:46:ARG:O	2.15	0.47
11:l:13:LYS:HZ2	53:1:661:A:H4'	1.79	0.47
11:l:127:VAL:HG11	11:l:142:ILE:HD13	1.97	0.47
18:s:83:LYS:HE3	18:s:95:ARG:HD2	1.95	0.47
18:s:85:ILE:HD11	18:s:93:ALA:HB1	1.95	0.47
25:z:23:LEU:HD21	25:z:53:MET:CE	2.44	0.47
28:D:34:ARG:HH12	53:1:466:A:P	2.38	0.47
31:G:68:PHE:O	31:G:91:VAL:HG22	2.13	0.47
32:H:26:LYS:HZ2	52:3:1256:A:H5''	1.79	0.47
39:O:13:PHE:CD2	43:S:93:PRO:HB2	2.50	0.47
40:P:124:LYS:HD2	40:P:124:LYS:C	2.39	0.47
43:S:74:ARG:NH2	52:3:1359:C:H3'	2.30	0.47
44:T:42:PHE:CE2	44:T:55:LEU:HD22	2.50	0.47
46:V:59:GLU:HB2	46:V:75:VAL:HB	1.96	0.47
50:Z:11:PHE:C	50:Z:13:VAL:H	2.23	0.47
52:3:45:G:H5''	52:3:307:C:O2'	2.15	0.47
52:3:236:A:H2'	52:3:237:G:C8	2.48	0.47
52:3:410:G:H2'	52:3:429:U:O4	2.14	0.47
52:3:742:G:O2'	52:3:743:A:H5'	2.14	0.47
53:1:131:A:H2'	53:1:132:G:H8	1.79	0.47
53:1:467:G:O2'	53:1:468:G:H5'	2.15	0.47
53:1:1083:U:H2'	53:1:1085:A:OP2	2.15	0.47
53:1:1662:U:O2'	53:1:1663:G:H5'	2.15	0.47
53:1:1889:A:H2'	53:1:1890:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1932:A:H2'	53:1:1933:G:O4'	2.15	0.47
53:1:2837:A:H2'	53:1:2838:G:C8	2.49	0.47
58:8:31:ALA:O	58:8:35:VAL:HG22	2.15	0.47
58:8:68:VAL:O	58:8:79:HIS:N	2.48	0.47
58:8:68:VAL:HB	58:8:79:HIS:HB3	1.97	0.47
58:8:127:GLY:O	58:8:129:PRO:HD3	2.14	0.47
24:y:39:GLN:HB3	24:y:41:HIS:CE1	2.50	0.47
32:H:161:ILE:HD11	52:3:1196:A:H2	1.79	0.47
35:K:36:ILE:HA	35:K:64:VAL:HG23	1.96	0.47
50:Z:49:ALA:HB1	50:Z:53:LYS:NZ	2.29	0.47
52:3:1497:G:C2'	52:3:1498:U:H5'	2.44	0.47
53:1:329:G:O4'	53:1:477:A:H1'	2.15	0.47
53:1:1015:U:H2'	53:1:1016:G:C8	2.49	0.47
53:1:1316:U:H2'	53:1:1317:G:C8	2.49	0.47
53:1:1506:U:H2'	53:1:1507:C:C6	2.50	0.47
4:e:121:PHE:HB3	4:e:162:ASP:OD1	2.15	0.47
5:f:88:LEU:HD21	5:f:104:LEU:HD22	1.97	0.47
11:l:81:ASP:OD1	11:l:81:ASP:N	2.46	0.47
13:n:73:ASN:O	13:n:76:VAL:HG12	2.14	0.47
14:o:25:ARG:NH1	54:2:8:C:O2'	2.48	0.47
52:3:86:G:H4'	52:3:87:C:C6	2.50	0.47
52:3:516:U:H3	52:3:533:A:H62	1.62	0.47
52:3:594:U:H3	52:3:645:G:H1	1.63	0.47
52:3:876:C:H2'	52:3:877:G:H8	1.79	0.47
52:3:1193:G:O2'	52:3:1194:U:H5'	2.15	0.47
53:1:208:C:H2'	53:1:209:C:C6	2.49	0.47
53:1:210:C:H2'	53:1:211:C:C6	2.50	0.47
53:1:257:C:H2'	53:1:258:G:O4'	2.15	0.47
53:1:304:U:H2'	53:1:305:C:C6	2.50	0.47
53:1:622:G:H2'	53:1:623:C:C6	2.50	0.47
53:1:856:G:H2'	53:1:857:G:C8	2.50	0.47
53:1:910:A:H2'	53:1:911:A:C8	2.50	0.47
53:1:1373:A:H5'	53:1:2212:A:H1'	1.96	0.47
53:1:1825:U:H2'	53:1:1826:G:C8	2.50	0.47
53:1:2810:A:H2'	53:1:2811:G:O4'	2.14	0.47
55:5:4:G:H2'	55:5:5:G:C8	2.50	0.47
55:6:59:A:H2'	55:6:60:U:H5'	1.97	0.47
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.15	0.47
7:h:114:GLU:CA	7:h:123:ILE:HG12	2.43	0.47
8:i:80:LYS:HB3	8:i:86:LYS:HD3	1.97	0.47
13:n:3:HIS:O	13:n:4:ARG:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:72:VAL:O	17:r:74:ILE:HD12	2.15	0.47
36:L:56:SER:HB3	36:L:59:GLU:HG2	1.96	0.47
37:M:13:ILE:HD11	37:M:71:VAL:HG21	1.97	0.47
40:P:71:ASP:O	40:P:72:ALA:HB3	2.15	0.47
45:U:16:PHE:HE2	45:U:18:GLN:HG3	1.80	0.47
45:U:22:ALA:HB2	45:U:32:PHE:HB3	1.97	0.47
52:3:337:G:H2'	52:3:338:A:H8	1.80	0.47
52:3:721:G:H4'	52:3:722:G:O4'	2.14	0.47
53:1:121:G:H4'	53:1:149:A:H5'	1.97	0.47
53:1:286:U:H2'	53:1:287:G:H8	1.79	0.47
53:1:794:A:H2'	53:1:795:C:H6	1.80	0.47
53:1:937:C:H2'	53:1:938:G:H8	1.79	0.47
53:1:966:G:H1'	53:1:2267:A:H62	1.80	0.47
53:1:2834:G:H2'	53:1:2879:A:N6	2.27	0.47
58:8:184:GLU:HG3	58:8:185:TRP:CD1	2.50	0.47
4:e:127:TYR:HE2	4:e:129:MET:HE2	1.79	0.46
6:g:22:LYS:HD3	53:1:2093:G:OP2	2.15	0.46
9:j:43:GLU:N	9:j:43:GLU:OE1	2.48	0.46
12:m:63:ILE:HD12	12:m:63:ILE:N	2.30	0.46
22:w:26:SER:HB3	22:w:62:LYS:HE2	1.96	0.46
34:J:89:THR:O	34:J:134:ASN:ND2	2.47	0.46
42:R:24:VAL:HG23	42:R:28:ARG:HB3	1.96	0.46
51:a:6:LYS:HD2	53:1:2130:U:H5	1.80	0.46
51:a:7:ARG:HB3	53:1:2129:C:OP1	2.15	0.46
52:3:161:A:H2'	52:3:162:A:O4'	2.14	0.46
52:3:1413:A:H2	52:3:1487:G:H22	1.61	0.46
52:3:1441:A:H62	52:3:1461:G:H21	1.61	0.46
53:1:457:A:H5'	53:1:459:U:H1'	1.96	0.46
53:1:863:A:O2'	53:1:864:G:H5'	2.15	0.46
53:1:1571:A:H2'	53:1:1572:A:C8	2.50	0.46
53:1:2270:A:H2'	53:1:2271:G:O4'	2.15	0.46
53:1:2841:C:H2'	53:1:2842:G:C8	2.50	0.46
57:7:25:C:C3'	57:7:26:A:H5''	2.41	0.46
58:8:302:HIS:CE1	58:8:392:VAL:HG11	2.50	0.46
13:n:60:VAL:HG13	13:n:61:ALA:H	1.80	0.46
37:M:4:ASP:HB2	37:M:80:PRO:HG3	1.96	0.46
50:Z:58:LYS:HE2	50:Z:58:LYS:HA	1.98	0.46
53:1:547:A:H3'	53:1:547:A:N3	2.30	0.46
53:1:1287:A:C2'	53:1:1288:G:H5'	2.45	0.46
53:1:2111:U:H3	53:1:2147:A:H1'	1.79	0.46
54:2:28:C:H2'	54:2:29:A:C8	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:7:9:A:O2'	57:7:46:G:H4'	2.14	0.46
2:c:122:VAL:O	2:c:126:ASN:HA	2.15	0.46
3:d:173:THR:OG1	53:1:616:A:H1'	2.15	0.46
5:f:28:LYS:HG2	5:f:79:THR:HA	1.97	0.46
10:k:56:ASP:HB3	10:k:58:LEU:HD22	1.98	0.46
16:q:23:TYR:CE1	53:1:533:G:H5'	2.50	0.46
20:u:42:LYS:HB3	20:u:57:ILE:HG22	1.96	0.46
21:v:29:ILE:HD11	21:v:37:PRO:HB3	1.97	0.46
23:x:16:ASN:HB2	23:x:26:ARG:HB3	1.97	0.46
23:x:36:ARG:HB3	53:1:2200:C:OP1	2.16	0.46
27:C:44:GLN:CG	27:C:45:HIS:N	2.76	0.46
33:I:114:ARG:HA	33:I:117:VAL:HG12	1.96	0.46
44:T:56:LEU:HA	44:T:59:VAL:HG12	1.97	0.46
46:V:6:THR:C	46:V:7:LEU:HD22	2.39	0.46
46:V:18:LYS:HG2	46:V:18:LYS:O	2.16	0.46
46:V:59:GLU:HG3	46:V:76:ARG:CZ	2.45	0.46
52:3:56:U:H2'	52:3:57:G:H8	1.80	0.46
52:3:628:G:H2'	52:3:629:A:C8	2.50	0.46
52:3:884:U:H4'	52:3:885:G:H5''	1.96	0.46
53:1:2364:C:H2'	53:1:2365:G:O4'	2.14	0.46
53:1:2380:C:H2'	53:1:2381:A:C8	2.51	0.46
55:5:69:C:H2'	55:5:70:G:C8	2.50	0.46
10:k:78:ARG:HH21	15:p:100:ARG:HH12	1.64	0.46
12:m:105:MET:HE1	12:m:116:ALA:HB3	1.98	0.46
18:s:109:ASP:OD1	18:s:109:ASP:N	2.49	0.46
19:t:69:ARG:HD2	19:t:72:GLN:HA	1.96	0.46
31:G:33:ALA:HA	31:G:38:HIS:HA	1.97	0.46
37:M:29:SER:OG	37:M:32:LYS:HG2	2.15	0.46
38:N:22:PRO:HA	38:N:60:LEU:HB3	1.98	0.46
46:V:67:SER:OG	46:V:68:LYS:N	2.48	0.46
49:Y:24:ARG:O	49:Y:28:ARG:HG3	2.16	0.46
51:a:5:THR:OG1	51:a:8:MET:HE3	2.15	0.46
52:3:604:G:H2'	52:3:605:U:O4'	2.16	0.46
53:1:290:U:H2'	53:1:291:G:H8	1.80	0.46
53:1:419:U:H2'	53:1:420:C:C6	2.49	0.46
53:1:687:C:H6	53:1:687:C:H5'	1.80	0.46
53:1:1542:U:H2'	53:1:1543:G:O4'	2.15	0.46
53:1:2329:U:H2'	53:1:2330:G:C8	2.50	0.46
53:1:2698:U:H2'	53:1:2699:C:H6	1.79	0.46
53:1:2773:C:H2'	53:1:2774:C:C6	2.51	0.46
53:1:2805:C:H2'	53:1:2806:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:30:C:H2'	54:2:31:C:O4'	2.15	0.46
58:8:147:LEU:HG	58:8:172:ARG:NH1	2.31	0.46
1:b:6:LYS:HZ3	53:1:1695:G:H5'	1.76	0.46
1:b:48:ILE:HG22	53:1:779:U:OP1	2.15	0.46
10:k:98:ARG:NH1	52:3:339:C:OP2	2.49	0.46
11:l:56:PRO:HD2	11:l:59:ARG:HB2	1.98	0.46
12:m:66:ARG:HD3	12:m:104:GLU:OE2	2.15	0.46
14:o:21:LEU:HD11	14:o:23:ALA:HB2	1.97	0.46
32:H:112:ALA:HB1	32:H:199:VAL:HG23	1.98	0.46
38:N:114:LYS:HE2	52:3:1187:G:C5'	2.46	0.46
43:S:65:GLN:HG3	43:S:78:LEU:HG	1.97	0.46
49:Y:28:ARG:HD3	52:3:1438:G:OP1	2.15	0.46
52:3:865:A:H5'	52:3:1078:U:O4	2.15	0.46
52:3:1356:G:H2'	52:3:1357:A:C8	2.51	0.46
53:1:934:U:H2'	53:1:935:C:C6	2.51	0.46
4:e:41:GLU:HB2	4:e:48:LEU:HD23	1.98	0.46
4:e:107:VAL:HG22	4:e:113:PHE:CE1	2.50	0.46
8:i:6:ALA:HB3	8:i:60:VAL:HB	1.97	0.46
33:I:195:ASN:ND2	33:I:198:LEU:HD23	2.31	0.46
34:J:87:VAL:HA	34:J:92:ARG:HA	1.98	0.46
39:O:36:VAL:HG22	39:O:37:ARG:N	2.30	0.46
46:V:43:LEU:HD11	46:V:72:TRP:CE2	2.50	0.46
49:Y:54:GLN:N	49:Y:55:PRO:HD2	2.31	0.46
52:3:77:A:H2'	52:3:78:A:H8	1.81	0.46
52:3:407:U:H2'	52:3:408:A:H8	1.81	0.46
52:3:1339:A:H2'	52:3:1340:A:H5'	1.98	0.46
53:1:433:C:H2'	53:1:434:U:C6	2.50	0.46
55:5:20:U:H3'	55:5:21:A:H5'	1.97	0.46
58:8:155:ARG:NH2	58:8:158:LEU:HD22	2.30	0.46
1:b:12:ARG:HD3	1:b:15:VAL:HG21	1.98	0.46
7:h:41:LEU:HD22	53:1:1083:U:OP1	2.16	0.46
14:o:15:ARG:HH21	14:o:25:ARG:HE	1.64	0.46
14:o:34:HIS:HA	14:o:53:THR:OG1	2.16	0.46
17:r:28:ALA:HB3	17:r:31:GLU:HB2	1.96	0.46
20:u:37:GLY:H	20:u:40:LEU:HD21	1.81	0.46
22:w:25:GLU:HG3	53:1:923:G:H4'	1.97	0.46
35:K:1:MET:HE1	35:K:35:LYS:HG2	1.98	0.46
35:K:3:HIS:CD2	35:K:94:HIS:HA	2.51	0.46
40:P:120:CYS:SG	52:3:677:U:H1'	2.55	0.46
44:T:53:ARG:HD2	52:3:728:A:C6	2.51	0.46
51:a:3:LYS:HD2	53:1:2108:A:OP1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:47:ASN:ND2	53:1:2177:C:O2'	2.49	0.46
52:3:57:G:H2'	52:3:58:C:O4'	2.16	0.46
52:3:711:G:H2'	52:3:712:A:H8	1.80	0.46
52:3:1118:U:H2'	52:3:1119:C:C6	2.51	0.46
52:3:1225:A:H2'	52:3:1225:A:N3	2.31	0.46
53:1:449:A:H2'	53:1:450:G:O4'	2.16	0.46
53:1:744:U:H2'	53:1:745:G:O4'	2.14	0.46
53:1:759:G:H2'	53:1:760:G:H8	1.80	0.46
53:1:814:C:H1'	53:1:1225:G:N2	2.29	0.46
53:1:828:U:H2'	53:1:829:A:C8	2.50	0.46
53:1:859:G:H5'	53:1:2268:A:O2'	2.16	0.46
53:1:1822:C:H2'	53:1:1823:G:H8	1.81	0.46
53:1:1989:G:H2'	53:1:1990:C:O4'	2.16	0.46
53:1:2380:C:H2'	53:1:2381:A:H8	1.81	0.46
57:7:26:A:H2'	57:7:27:G:O4'	2.16	0.46
7:h:56:ARG:NE	7:h:83:ALA:HB2	2.31	0.46
11:l:60:ARG:O	53:1:2393:U:H5'	2.16	0.46
14:o:31:THR:HG21	54:2:28:C:OP1	2.16	0.46
14:o:35:ILE:HG12	14:o:66:GLY:HA2	1.97	0.46
40:P:118:ASN:ND2	52:3:718:A:H5'	2.29	0.46
47:W:61:ALA:HB1	47:W:67:LEU:HD23	1.97	0.46
48:X:62:THR:OG1	48:X:65:MET:SD	2.72	0.46
52:3:748:G:H2'	52:3:749:A:H8	1.81	0.46
52:3:769:G:H4'	52:3:1513:A:C4'	2.38	0.46
52:3:1259:C:H3'	52:3:1260:G:C5'	2.36	0.46
53:1:296:U:H2'	53:1:297:G:H8	1.80	0.46
53:1:1000:A:H2'	53:1:1001:A:C8	2.51	0.46
57:7:76:A:O2'	60:7:101:PHE:C	2.58	0.46
1:b:123:ILE:HG13	35:K:80:PHE:CE1	2.51	0.46
5:f:38:ASP:OD1	5:f:38:ASP:N	2.49	0.46
9:j:109:LEU:HD13	9:j:118:MET:HG3	1.98	0.46
10:k:22:ILE:HD13	10:k:42:THR:OG1	2.16	0.46
20:u:56:GLY:N	53:1:483:A:O2'	2.49	0.46
25:z:40:THR:OG1	25:z:41:PRO:HD2	2.15	0.46
38:N:23:GLY:H	38:N:60:LEU:HA	1.80	0.46
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.81	0.46
52:3:166:U:H2'	52:3:167:A:C8	2.51	0.46
52:3:1458:G:H2'	52:3:1459:G:H8	1.81	0.46
52:3:1524:C:H2'	52:3:1525:G:C8	2.51	0.46
53:1:1394:U:H4'	53:1:1603:A:H4'	1.97	0.46
3:d:105:LEU:HA	3:d:108:ILE:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:174:LYS:HB3	53:1:2529:G:H5'	1.98	0.46
13:n:100:CYS:SG	26:B:42:ILE:HD11	2.55	0.46
27:C:44:GLN:O	27:C:45:HIS:CB	2.64	0.46
32:H:23:ALA:HB1	32:H:27:GLU:HG2	1.98	0.46
32:H:25:THR:HG22	43:S:75:LYS:HE3	1.98	0.46
32:H:39:ARG:HG2	32:H:54:ILE:HD11	1.97	0.46
33:I:8:LEU:HB2	52:3:430:A:OP1	2.15	0.46
39:O:43:PRO:HD3	52:3:1150:A:O2'	2.16	0.46
39:O:44:THR:HG22	39:O:70:HIS:HA	1.97	0.46
43:S:27:LYS:HB3	43:S:47:LEU:HD11	1.98	0.46
50:Z:16:ARG:HB2	50:Z:19:LYS:HD3	1.97	0.46
52:3:70:U:H4'	52:3:71:A:C8	2.50	0.46
52:3:82:G:H2'	52:3:83:C:C5'	2.45	0.46
52:3:216:U:H2'	52:3:217:C:C6	2.51	0.46
52:3:514:C:H2'	52:3:515:G:H8	1.81	0.46
52:3:985:C:H2'	52:3:986:U:C6	2.50	0.46
52:3:1001:C:H2'	52:3:1002:G:H8	1.80	0.46
52:3:1096:C:H2'	52:3:1097:C:C6	2.50	0.46
53:1:39:G:H2'	53:1:40:U:C6	2.51	0.46
53:1:151:C:H2'	53:1:152:A:C8	2.52	0.46
53:1:195:A:H2'	53:1:198:C:N4	2.30	0.46
53:1:859:G:O2'	53:1:860:U:C5	2.68	0.46
53:1:1848:A:H2'	53:1:1849:G:O4'	2.16	0.46
54:2:30:C:H1'	54:2:57:A:H61	1.80	0.46
58:8:310:TYR:HA	58:8:355:ASP:O	2.17	0.46
2:c:8:LYS:HB2	2:c:201:LEU:HD11	1.98	0.45
2:c:8:LYS:HB2	2:c:201:LEU:CD1	2.46	0.45
7:h:33:VAL:O	7:h:37:LYS:HG2	2.16	0.45
33:I:119:HIS:HB3	52:3:438:U:H4'	1.98	0.45
52:3:969:A:H2'	52:3:970:C:O4'	2.15	0.45
53:1:150:U:H2'	53:1:151:C:C6	2.51	0.45
53:1:738:G:O2'	53:1:739:A:H5'	2.16	0.45
58:8:98:GLN:CD	58:8:389:VAL:HG23	2.42	0.45
12:m:136:MET:HE2	21:v:57:TYR:HB3	1.98	0.45
23:x:18:SER:OG	23:x:19:HIS:N	2.50	0.45
35:K:88:MET:HE3	35:K:90:MET:SD	2.57	0.45
36:L:110:ARG:HH12	36:L:121:ASN:HD22	1.64	0.45
43:S:81:ILE:HG21	52:3:1202:U:N3	2.31	0.45
49:Y:20:ASN:HD22	52:3:323:U:H5''	1.79	0.45
49:Y:67:HIS:CB	52:3:262:A:H5'	2.46	0.45
51:a:206:GLY:CA	53:1:1860:G:H5''	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:225:C:H2'	52:3:226:G:C5'	2.45	0.45
52:3:974:A:H5'	52:3:976:G:OP1	2.15	0.45
52:3:1484:C:H2'	52:3:1485:U:C6	2.51	0.45
53:1:239:C:H2'	53:1:240:C:O4'	2.16	0.45
53:1:776:G:H22	53:1:2072:C:H5'	1.81	0.45
53:1:1019:U:H3	53:1:1142:A:N6	2.11	0.45
53:1:1330:C:H2'	53:1:1331:G:H8	1.81	0.45
53:1:1363:C:H2'	53:1:1364:G:C8	2.51	0.45
53:1:1841:U:H2'	53:1:1842:G:C8	2.50	0.45
53:1:2098:U:H2'	53:1:2099:U:O4'	2.16	0.45
53:1:2285:C:O2'	53:1:2287:A:H1'	2.16	0.45
53:1:2737:G:H2'	53:1:2738:A:C8	2.51	0.45
54:2:108:A:H5'	54:2:109:A:O5'	2.16	0.45
58:8:308:GLU:HA	58:8:358:LYS:HA	1.97	0.45
1:b:220:ARG:HD2	53:1:1827:U:OP2	2.16	0.45
7:h:88:HIS:HB2	7:h:89:PRO:CD	2.44	0.45
8:i:23:VAL:HG23	8:i:24:GLY:N	2.31	0.45
13:n:4:ARG:HA	53:1:2820:A:OP1	2.15	0.45
36:L:137:ARG:HH11	36:L:141:HIS:HD1	1.65	0.45
42:R:32:ILE:HG23	42:R:58:GLU:HG2	1.98	0.45
43:S:95:LEU:C	43:S:95:LEU:HD23	2.41	0.45
52:3:411:A:N9	52:3:413:G:H1'	2.32	0.45
52:3:1163:A:H2'	52:3:1164:G:C8	2.51	0.45
53:1:270:A:C2	53:1:369:U:H4'	2.52	0.45
53:1:1906:G:C3'	53:1:1907:G:H5''	2.47	0.45
53:1:2348:U:H2'	53:1:2349:G:C8	2.51	0.45
53:1:2807:U:H3	53:1:2891:U:H3	1.64	0.45
54:2:12:C:H1'	54:2:15:A:C2	2.51	0.45
54:2:56:G:H4'	54:2:57:A:C8	2.49	0.45
1:b:132:ARG:HB3	1:b:185:ALA:HB1	1.97	0.45
1:b:220:ARG:HG3	53:1:1789:A:OP1	2.17	0.45
1:b:251:THR:OG1	1:b:252:LYS:N	2.49	0.45
2:c:127:PHE:HZ	2:c:160:LYS:HB2	1.81	0.45
3:d:144:GLU:OE1	3:d:144:GLU:N	2.49	0.45
10:k:35:VAL:HG13	10:k:36:GLY:N	2.27	0.45
17:r:76:LYS:HB2	17:r:85:LYS:HB2	1.98	0.45
28:D:40:ALA:O	28:D:42:LEU:N	2.47	0.45
33:I:170:LEU:C	33:I:170:LEU:HD12	2.41	0.45
38:N:28:VAL:HG13	38:N:63:TYR:HD1	1.82	0.45
47:W:11:ARG:CD	52:3:845:A:H1'	2.45	0.45
48:X:39:ILE:HD12	48:X:68:HIS:O	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:346:G:C2'	52:3:347:G:H5'	2.47	0.45
52:3:1333:A:H2'	52:3:1334:G:O4'	2.15	0.45
52:3:1475:G:H2'	52:3:1476:A:C8	2.51	0.45
53:1:593:U:H2'	53:1:594:U:C6	2.52	0.45
53:1:1363:C:H2'	53:1:1364:G:H8	1.81	0.45
10:k:28:SER:HB2	53:1:2566:A:N1	2.32	0.45
13:n:115:LEU:O	13:n:117:ASP:N	2.49	0.45
14:o:11:ALA:O	14:o:15:ARG:HG3	2.16	0.45
21:v:64:VAL:HA	21:v:69:GLU:HA	1.98	0.45
26:B:28:SER:OG	26:B:39:ARG:HD3	2.17	0.45
28:D:25:LYS:HD2	28:D:29:GLN:NE2	2.32	0.45
29:E:36:ALA:HB3	29:E:39:ARG:HD3	1.97	0.45
33:I:140:ASP:H	33:I:181:PHE:HB3	1.82	0.45
39:O:10:LEU:HD23	39:O:10:LEU:H	1.81	0.45
40:P:87:GLY:O	40:P:92:ARG:NH1	2.50	0.45
42:R:100:ARG:HD2	52:3:950:U:OP2	2.16	0.45
48:X:35:ARG:HH21	48:X:74:ALA:HB3	1.80	0.45
50:Z:7:GLU:HB2	50:Z:11:PHE:HB3	1.98	0.45
52:3:212:G:O2'	52:3:213:G:H5'	2.16	0.45
52:3:603:U:H2'	52:3:604:G:H8	1.82	0.45
52:3:857:C:H2'	52:3:858:G:O4'	2.16	0.45
53:1:857:G:H2'	53:1:858:G:O4'	2.15	0.45
53:1:1680:U:H2'	53:1:1681:G:H5'	1.97	0.45
53:1:1680:U:C2'	53:1:1681:G:H5'	2.47	0.45
53:1:1747:U:H2'	53:1:1748:C:C6	2.52	0.45
53:1:2462:C:H2'	53:1:2463:C:H6	1.82	0.45
58:8:77:TYR:OH	58:8:197:ASP:HA	2.17	0.45
6:g:26:ALA:HA	6:g:30:LEU:HB2	1.98	0.45
10:k:66:LYS:HG2	10:k:81:GLY:H	1.82	0.45
14:o:68:LYS:HE3	54:2:49:C:H4'	1.97	0.45
15:p:25:VAL:HG21	15:p:83:ILE:HG22	1.99	0.45
31:G:209:VAL:HA	31:G:212:TYR:CD2	2.51	0.45
32:H:10:ARG:NH1	32:H:177:LEU:HA	2.31	0.45
32:H:21:TRP:H	43:S:93:PRO:HG2	1.82	0.45
50:Z:58:LYS:O	50:Z:61:ARG:HD2	2.17	0.45
52:3:784:A:H2'	52:3:785:G:H8	1.81	0.45
52:3:794:A:O2'	52:3:795:C:H5'	2.16	0.45
52:3:1498:U:C4	56:4:17:U:H5''	2.51	0.45
53:1:259:G:O2'	53:1:260:G:H5'	2.17	0.45
53:1:340:A:H2'	53:1:341:C:O4'	2.16	0.45
53:1:1444:G:H2'	53:1:1445:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2070:A:O2'	53:1:2071:A:H5'	2.17	0.45
9:j:81:ILE:HG23	9:j:82:GLY:N	2.31	0.45
14:o:7:ARG:HA	14:o:10:ARG:HE	1.81	0.45
16:q:25:GLY:O	16:q:29:ARG:NH1	2.50	0.45
21:v:37:PRO:HG2	54:2:74:U:H1'	1.98	0.45
23:x:3:VAL:HG13	23:x:9:LYS:O	2.17	0.45
52:3:41:G:H2'	52:3:42:G:H8	1.81	0.45
52:3:314:C:O2'	52:3:315:A:H5'	2.17	0.45
52:3:1174:G:H2'	52:3:1175:G:C8	2.52	0.45
52:3:1494:G:O2'	52:3:1495:U:H5'	2.17	0.45
53:1:315:G:H2'	53:1:316:C:O4'	2.17	0.45
53:1:2361:G:O2'	53:1:2362:C:H5'	2.16	0.45
58:8:246:VAL:HA	58:8:251:THR:HG22	1.99	0.45
1:b:6:LYS:NZ	53:1:1695:G:C5'	2.71	0.45
1:b:66:PHE:HB3	1:b:150:GLY:O	2.16	0.45
2:c:193:VAL:O	53:1:2680:U:H4'	2.17	0.45
3:d:68:ALA:HA	53:1:1255:U:C5	2.52	0.45
15:p:28:LYS:HG2	15:p:82:SER:OG	2.17	0.45
17:r:78:ARG:HH12	53:1:990:A:N6	2.08	0.45
29:E:1:PRO:HG2	53:1:591:U:O2	2.17	0.45
34:J:133:ILE:O	34:J:136:VAL:HG22	2.17	0.45
37:M:113:ARG:O	37:M:117:GLN:HG2	2.16	0.45
47:W:31:TYR:CG	47:W:54:LEU:HD11	2.52	0.45
49:Y:25:SER:OG	52:3:1458:G:H5''	2.17	0.45
52:3:421:U:O2'	52:3:422:C:P	2.74	0.45
52:3:710:G:H2'	52:3:711:G:C8	2.52	0.45
52:3:923:A:H61	52:3:1393:U:H3	1.64	0.45
52:3:1323:G:H2'	52:3:1324:A:C8	2.52	0.45
53:1:211:C:H2'	53:1:212:G:H8	1.80	0.45
53:1:621:A:C2'	53:1:622:G:H5'	2.47	0.45
53:1:1404:C:O2'	53:1:1405:U:H5'	2.17	0.45
53:1:2048:G:H3'	53:1:2049:G:H5''	1.95	0.45
4:e:77:LYS:HD3	4:e:77:LYS:N	2.32	0.45
9:j:68:LYS:HD3	53:1:1022:G:N7	2.32	0.45
23:x:17:ARG:CD	23:x:23:ALA:HB2	2.47	0.45
33:I:43:ARG:HD2	33:I:44:LYS:O	2.16	0.45
39:O:5:ARG:HG2	39:O:79:PRO:HD3	1.97	0.45
40:P:118:ASN:HD21	52:3:718:A:H5'	1.81	0.45
52:3:26:A:H61	52:3:558:G:H1'	1.82	0.45
52:3:49:U:O2'	52:3:50:A:H2'	2.17	0.45
52:3:147:G:H2'	52:3:148:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:355:C:O4'	52:3:388:G:H1'	2.17	0.45
52:3:423:G:H2'	52:3:424:G:H5'	1.99	0.45
52:3:424:G:H2'	52:3:425:G:C8	2.52	0.45
52:3:711:G:O2'	52:3:712:A:H5'	2.17	0.45
53:1:420:C:O2'	53:1:421:C:H5'	2.17	0.45
53:1:912:C:O2'	53:1:913:U:H5'	2.17	0.45
53:1:1917:U:O2'	53:1:1918:A:H5'	2.17	0.45
53:1:2207:C:H2'	53:1:2208:C:C6	2.52	0.45
53:1:2544:G:H2'	53:1:2545:G:C8	2.51	0.45
58:8:245:ILE:HG23	58:8:252:GLN:H	1.82	0.45
5:f:1:SER:HB3	53:1:2749:A:H5''	1.99	0.45
7:h:56:ARG:NH2	7:h:83:ALA:HB2	2.32	0.45
9:j:78:THR:CG2	53:1:2641:G:H5''	2.47	0.45
21:v:88:HIS:HE1	21:v:90:ASP:OD1	2.00	0.45
31:G:150:ILE:HD12	31:G:150:ILE:H	1.82	0.45
32:H:133:MET:SD	32:H:133:MET:C	3.00	0.45
33:I:77:GLU:O	33:I:81:LEU:HD13	2.16	0.45
33:I:84:ASN:HB3	33:I:87:GLU:HB2	1.99	0.45
33:I:183:ARG:HD2	33:I:184:LYS:O	2.17	0.45
37:M:9:MET:HG3	37:M:26:MET:CE	2.47	0.45
45:U:39:PHE:CE2	45:U:41:PRO:HB3	2.51	0.45
52:3:1358:U:H3	52:3:1363:A:H61	1.65	0.45
52:3:1438:G:O2'	52:3:1439:G:H5'	2.17	0.45
53:1:296:U:H2'	53:1:297:G:C8	2.52	0.45
53:1:381:G:H2'	53:1:382:A:H8	1.82	0.45
53:1:511:U:H2'	53:1:512:G:H5'	1.99	0.45
53:1:828:U:H4'	53:1:831:G:N1	2.32	0.45
53:1:1179:G:C5	53:1:1180:U:H1'	2.52	0.45
58:8:36:LEU:O	58:8:40:TYR:HB2	2.17	0.45
58:8:213:LEU:HD13	58:8:232:VAL:HG22	1.99	0.45
2:c:157:LYS:HE2	53:1:2619:C:OP1	2.17	0.44
3:d:151:GLY:HA2	3:d:195:GLN:OE1	2.17	0.44
8:i:38:CYS:O	8:i:42:ASN:ND2	2.50	0.44
8:i:78:LEU:O	8:i:81:LYS:HG3	2.17	0.44
8:i:103:ALA:O	8:i:106:GLN:HG3	2.16	0.44
20:u:21:ARG:HD3	20:u:21:ARG:N	2.32	0.44
21:v:29:ILE:HD11	21:v:37:PRO:CB	2.47	0.44
29:E:55:GLY:O	29:E:58:ILE:HG22	2.17	0.44
32:H:85:LYS:HG3	32:H:86:LEU:HD22	1.99	0.44
38:N:90:ASP:HB2	38:N:91:GLU:H	1.65	0.44
38:N:114:LYS:CE	52:3:1187:G:C5'	2.94	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:P:27:ASN:O	40:P:56:LYS:HG2	2.17	0.44
48:X:9:PHE:CE1	52:3:1318:A:H5'	2.52	0.44
52:3:367:U:H5'	58:8:280:ARG:HD2	1.98	0.44
52:3:502:A:H2'	52:3:503:C:O4'	2.16	0.44
52:3:502:A:O2'	52:3:503:C:H5'	2.16	0.44
52:3:603:U:H2'	52:3:604:G:C8	2.52	0.44
52:3:1305:G:H22	52:3:1331:G:H2'	1.82	0.44
53:1:261:G:H2'	53:1:262:A:C8	2.52	0.44
53:1:288:U:H2'	53:1:289:G:H8	1.82	0.44
53:1:301:G:H1'	53:1:302:C:C6	2.52	0.44
53:1:1946:U:H2'	53:1:1947:C:C6	2.52	0.44
53:1:2193:G:H2'	53:1:2194:U:C6	2.51	0.44
53:1:2543:G:H2'	53:1:2544:G:C8	2.52	0.44
57:7:62:C:H2'	57:7:63:G:C5'	2.47	0.44
1:b:52:HIS:HD2	53:1:1824:G:OP2	2.01	0.44
11:l:20:GLY:O	11:l:21:ARG:NH2	2.40	0.44
20:u:42:LYS:HD2	53:1:499:U:C5'	2.47	0.44
21:v:83:LYS:HA	21:v:84:PRO:HD3	1.82	0.44
38:N:60:LEU:HD12	38:N:60:LEU:O	2.16	0.44
41:Q:109:ARG:HB2	41:Q:118:VAL:HG11	1.99	0.44
45:U:42:ILE:O	45:U:42:ILE:HG12	2.18	0.44
52:3:17:U:H2'	52:3:18:C:C6	2.52	0.44
52:3:285:C:H2'	52:3:286:C:C6	2.51	0.44
53:1:2322:A:H2'	53:1:2323:G:O4'	2.17	0.44
14:o:66:GLY:O	14:o:102:ARG:NH2	2.51	0.44
19:t:34:VAL:HG22	19:t:35:ALA:N	2.32	0.44
31:G:44:LYS:C	31:G:47:PRO:HD2	2.43	0.44
34:J:82:HIS:NE2	34:J:147:ASN:OD1	2.50	0.44
38:N:41:GLU:OE2	38:N:41:GLU:N	2.50	0.44
39:O:17:LEU:HD12	39:O:18:ILE:N	2.32	0.44
40:P:35:ASP:OD1	40:P:39:ASN:N	2.51	0.44
40:P:93:GLU:CD	40:P:96:ILE:HD11	2.41	0.44
41:Q:28:GLN:HG2	41:Q:80:LEU:HD21	1.98	0.44
41:Q:74:GLN:OE1	41:Q:74:GLN:N	2.50	0.44
52:3:407:U:H2'	52:3:408:A:C8	2.53	0.44
52:3:512:U:H2'	52:3:513:C:C6	2.52	0.44
52:3:513:C:H2'	52:3:514:C:C6	2.53	0.44
52:3:1019:A:H2'	52:3:1020:G:O4'	2.17	0.44
52:3:1227:A:H2'	52:3:1228:C:H5'	1.98	0.44
53:1:255:A:H2'	53:1:256:A:O4'	2.16	0.44
53:1:1923:U:H2'	53:1:1924:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2106:U:H2'	53:1:2107:G:C8	2.53	0.44
53:1:2128:G:H21	53:1:2173:A:H1'	1.81	0.44
53:1:2323:G:O2'	53:1:2324:U:H5'	2.18	0.44
53:1:2459:A:H2'	53:1:2459:A:N3	2.32	0.44
5:f:48:THR:HG22	5:f:49:LEU:H	1.82	0.44
7:h:56:ARG:HB2	53:1:1084:A:C1'	2.43	0.44
11:l:99:ASN:ND2	53:1:621:A:OP2	2.51	0.44
18:s:57:ASN:OD1	53:1:495:G:H1'	2.18	0.44
19:t:61:LEU:HD13	53:1:1340:U:H2'	2.00	0.44
32:H:172:VAL:N	52:3:1107:C:OP1	2.50	0.44
33:I:33:ILE:H	33:I:33:ILE:CD1	2.16	0.44
33:I:97:LEU:HD12	33:I:134:TYR:HB3	1.99	0.44
48:X:36:ARG:HB3	52:3:1320:C:N4	2.32	0.44
50:Z:39:LYS:O	50:Z:40:PRO:C	2.59	0.44
52:3:579:A:H2'	52:3:580:C:C6	2.53	0.44
52:3:580:C:H2'	52:3:581:G:O4'	2.18	0.44
52:3:1005:A:H2'	52:3:1006:G:H5'	1.98	0.44
53:1:1486:U:H2'	53:1:1487:U:C6	2.53	0.44
53:1:2343:U:H2'	53:1:2344:U:C6	2.52	0.44
54:2:104:A:H2'	54:2:105:G:O4'	2.17	0.44
58:8:106:VAL:HG22	58:8:116:THR:HG21	1.99	0.44
10:k:58:LEU:HD23	10:k:58:LEU:H	1.83	0.44
10:k:70:ARG:HA	10:k:76:VAL:HG12	1.98	0.44
10:k:103:VAL:HG21	10:k:116:ILE:HG22	1.98	0.44
13:n:117:ASP:CG	13:n:118:ARG:H	2.25	0.44
15:p:28:LYS:HD2	15:p:81:ASP:HB3	1.98	0.44
20:u:48:VAL:HG22	20:u:50:ALA:H	1.82	0.44
32:H:14:VAL:HG23	32:H:15:LYS:H	1.82	0.44
32:H:181:ILE:HD12	32:H:181:ILE:N	2.33	0.44
33:I:57:LYS:O	33:I:60:VAL:HG12	2.18	0.44
34:J:38:VAL:HG22	34:J:66:ALA:HB1	1.99	0.44
36:L:22:LEU:O	36:L:26:VAL:HG23	2.17	0.44
40:P:118:ASN:CG	52:3:718:A:H5'	2.42	0.44
45:U:68:SER:HB3	45:U:71:VAL:CG2	2.48	0.44
50:Z:64:ALA:C	50:Z:66:ARG:H	2.26	0.44
52:3:77:A:H2'	52:3:78:A:C8	2.53	0.44
52:3:279:A:H4'	52:3:281:G:C8	2.53	0.44
52:3:748:G:H2'	52:3:749:A:C8	2.53	0.44
52:3:1081:A:H2'	52:3:1082:A:C8	2.50	0.44
53:1:542:C:H2'	53:1:543:G:C5'	2.47	0.44
53:1:679:C:H2'	53:1:680:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:889:C:O2'	53:1:890:C:H5'	2.17	0.44
53:1:1524:G:H2'	53:1:1525:A:H8	1.83	0.44
53:1:2293:G:H2'	53:1:2294:G:C8	2.52	0.44
53:1:2298:A:H2'	53:1:2299:U:O4'	2.17	0.44
53:1:2686:G:H2'	53:1:2687:U:C6	2.52	0.44
53:1:2705:A:H2'	53:1:2706:A:O4'	2.18	0.44
58:8:90:LYS:NZ	58:8:94:THR:HG21	2.33	0.44
58:8:279:LEU:HD23	58:8:282:ILE:HD13	2.00	0.44
16:q:15:LYS:HB3	16:q:15:LYS:HE2	1.86	0.44
17:r:6:GLN:HE21	17:r:9:GLY:H	1.64	0.44
24:y:19:LEU:O	24:y:23:ARG:NE	2.50	0.44
33:I:37:PRO:HD2	33:I:41:GLY:HA3	2.00	0.44
33:I:187:ARG:NH2	33:I:194:ILE:O	2.50	0.44
39:O:52:LEU:HD23	39:O:62:ARG:CD	2.47	0.44
44:T:86:LEU:HD12	44:T:87:ARG:HB2	1.99	0.44
46:V:49:ASN:O	46:V:50:ASN:HB3	2.17	0.44
48:X:30:LEU:H	48:X:30:LEU:CD1	2.28	0.44
52:3:483:C:H2'	52:3:484:G:N7	2.33	0.44
52:3:1188:A:H2'	52:3:1189:U:O4'	2.18	0.44
53:1:230:G:O2'	53:1:231:A:H5'	2.18	0.44
53:1:368:A:H2'	53:1:369:U:H5'	1.98	0.44
53:1:859:G:O2'	53:1:860:U:H5	2.00	0.44
53:1:1030:C:H2'	53:1:1031:G:H8	1.83	0.44
53:1:1429:G:H2'	53:1:1430:G:H8	1.82	0.44
53:1:2801:G:H2'	53:1:2802:G:C8	2.52	0.44
53:1:2830:C:O2'	53:1:2831:G:H5'	2.17	0.44
54:2:61:G:H2'	54:2:62:C:C6	2.53	0.44
5:f:41:GLU:HA	5:f:54:ARG:HE	1.82	0.44
9:j:113:PRO:CB	53:1:557:C:H5''	2.47	0.44
12:m:58:LYS:HB3	12:m:59:ARG:H	1.67	0.44
40:P:49:SER:HA	40:P:68:ARG:HH11	1.82	0.44
40:P:122:PRO:HG2	50:Z:35:GLU:HB3	2.00	0.44
42:R:42:VAL:HG22	42:R:43:LYS:O	2.17	0.44
52:3:81:A:H61	52:3:86:G:H21	1.66	0.44
52:3:193:C:H2'	52:3:194:C:C6	2.53	0.44
52:3:206:C:H2'	52:3:207:C:O4'	2.17	0.44
52:3:524:G:H2'	52:3:525:C:C6	2.52	0.44
53:1:211:C:H2'	53:1:212:G:C8	2.53	0.44
53:1:468:G:H2'	53:1:469:G:O4'	2.18	0.44
53:1:562:U:O4'	53:1:2036:C:H5'	2.18	0.44
53:1:1378:A:HI1'	53:1:1379:U:C5	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2238:G:N3	53:1:2238:G:C2'	2.80	0.44
55:5:47:U:H3'	55:5:48:C:C5'	2.48	0.44
57:7:58:A:H1'	57:7:60:U:H5	1.82	0.44
3:d:53:THR:OG1	53:1:452:G:H8	2.01	0.44
12:m:61:GLY:HA3	12:m:108:VAL:HG13	2.00	0.44
12:m:74:THR:OG1	12:m:75:GLU:N	2.51	0.44
14:o:55:GLU:HG2	54:2:116:G:O5'	2.18	0.44
18:s:17:VAL:HG11	18:s:103:ILE:HG12	2.00	0.44
18:s:62:ASP:HB3	18:s:63:GLY:H	1.67	0.44
24:y:9:LYS:NZ	24:y:11:VAL:HB	2.33	0.44
37:M:82:LEU:O	37:M:82:LEU:HD23	2.18	0.44
37:M:86:LYS:HB2	37:M:91:LEU:HD23	1.99	0.44
41:Q:71:HIS:HA	41:Q:98:ARG:NH2	2.32	0.44
52:3:514:C:H2'	52:3:515:G:C8	2.53	0.44
52:3:900:A:H2'	52:3:901:A:C8	2.53	0.44
52:3:971:G:H1'	52:3:1365:G:O2'	2.18	0.44
53:1:162:U:C2'	53:1:163:C:H5'	2.48	0.44
53:1:268:C:H2'	53:1:269:C:C6	2.53	0.44
53:1:596:U:H2'	53:1:597:G:H8	1.83	0.44
53:1:1110:G:H2'	53:1:1111:A:H8	1.81	0.44
53:1:1458:U:H4'	53:1:1459:G:O4'	2.18	0.44
53:1:2318:G:H2'	53:1:2319:G:O4'	2.17	0.44
53:1:2348:U:H2'	53:1:2349:G:H8	1.82	0.44
53:1:2579:C:O2'	53:1:2580:U:H5'	2.17	0.44
53:1:2584:U:H2'	53:1:2585:U:C6	2.53	0.44
58:8:215:ILE:HD12	58:8:228:VAL:HG11	2.00	0.44
8:i:101:SER:HB2	8:i:104:GLN:HG3	2.00	0.44
8:i:127:SER:OG	53:1:1059:G:N2	2.51	0.44
10:k:2:ILE:HG21	10:k:8:LEU:HD11	2.00	0.44
14:o:18:LEU:HB2	14:o:23:ALA:HB3	1.99	0.44
21:v:34:LYS:HD2	21:v:35:GLU:N	2.33	0.44
35:K:71:ILE:N	35:K:71:ILE:HD12	2.33	0.44
40:P:85:VAL:HG23	40:P:111:ASP:OD1	2.18	0.44
43:S:47:LEU:O	43:S:50:LEU:HB3	2.18	0.44
48:X:62:THR:HG23	48:X:65:MET:HE1	1.99	0.44
48:X:73:PHE:C	48:X:75:PRO:HD3	2.42	0.44
53:1:116:C:H2'	53:1:117:G:O4'	2.17	0.44
53:1:145:C:H2'	53:1:146:A:C8	2.52	0.44
53:1:440:C:H2'	53:1:441:U:C6	2.52	0.44
53:1:1500:G:H2'	53:1:1501:G:H8	1.83	0.44
53:1:2462:C:H1'	53:1:2491:U:O4	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:286:GLU:N	58:8:286:GLU:OE2	2.51	0.44
3:d:31:VAL:HG21	3:d:104:ALA:HB2	2.00	0.43
6:g:26:ALA:O	6:g:31:VAL:HG12	2.18	0.43
9:j:113:PRO:HD3	53:1:529:A:OP2	2.18	0.43
10:k:31:ARG:HD3	10:k:31:ARG:N	2.32	0.43
21:v:12:GLN:NE2	54:2:75:G:OP1	2.46	0.43
23:x:17:ARG:HD3	23:x:23:ALA:HB2	2.00	0.43
34:J:79:THR:OG1	34:J:97:PRO:O	2.35	0.43
34:J:103:GLY:H	34:J:121:ASN:CG	2.26	0.43
36:L:135:LYS:HA	36:L:138:GLU:HG2	2.00	0.43
40:P:55:ARG:HH22	55:6:39:C:H4'	1.82	0.43
52:3:448:A:H3'	52:3:449:G:C8	2.53	0.43
53:1:171:U:H2'	53:1:172:A:C8	2.53	0.43
53:1:543:G:H2'	53:1:544:C:O4'	2.18	0.43
53:1:942:G:H2'	53:1:943:A:O4'	2.18	0.43
53:1:1270:C:H5''	53:1:1271:G:H5'	2.00	0.43
53:1:2805:C:H2'	53:1:2806:C:H6	1.83	0.43
7:h:3:LEU:HD23	7:h:3:LEU:H	1.82	0.43
11:l:36:LYS:HE2	53:1:568:U:OP1	2.18	0.43
13:n:2:ARG:HA	13:n:5:LYS:CD	2.48	0.43
23:x:60:LYS:HD2	53:1:372:G:O4'	2.18	0.43
31:G:111:LYS:HA	31:G:114:LYS:HG2	2.00	0.43
31:G:150:ILE:O	31:G:150:ILE:HG22	2.17	0.43
36:L:29:LEU:C	36:L:29:LEU:HD12	2.43	0.43
40:P:71:ASP:HA	40:P:74:LYS:HE3	1.99	0.43
47:W:66:LEU:C	47:W:67:LEU:HD22	2.44	0.43
50:Z:39:LYS:N	50:Z:40:PRO:CD	2.81	0.43
52:3:1328:C:H2'	52:3:1329:A:H8	1.83	0.43
52:3:1458:G:H2'	52:3:1459:G:C8	2.53	0.43
53:1:154:U:H2'	53:1:155:A:C8	2.53	0.43
53:1:1181:U:H2'	53:1:1182:G:H8	1.83	0.43
53:1:1376:C:H2'	53:1:1377:G:O4'	2.18	0.43
53:1:1771:C:H2'	53:1:1772:A:C8	2.53	0.43
53:1:2008:C:H2'	53:1:2009:A:C8	2.51	0.43
53:1:2041:U:H2'	53:1:2042:A:H8	1.81	0.43
55:5:69:C:H2'	55:5:70:G:H8	1.83	0.43
57:7:68:C:H2'	57:7:69:G:C8	2.54	0.43
58:8:342:ILE:HG23	58:8:359:MET:HG3	1.99	0.43
1:b:21:PRO:HG2	1:b:22:GLU:OE2	2.18	0.43
6:g:5:LEU:HD22	6:g:9:VAL:HG21	2.00	0.43
9:j:30:THR:HG21	53:1:1005:C:O2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:66:LYS:HD3	53:1:1666:G:OP1	2.17	0.43
17:r:83:TYR:CZ	53:1:1187:G:H5''	2.54	0.43
42:R:25:GLY:N	52:3:1329:A:H5''	2.31	0.43
42:R:72:ILE:HD12	52:3:1309:G:H1'	1.99	0.43
42:R:113:LYS:CD	42:R:114:PRO:HD3	2.49	0.43
44:T:55:LEU:HD21	53:1:715:A:C2	2.53	0.43
52:3:32:A:H2'	52:3:33:A:C8	2.53	0.43
52:3:204:G:H2'	52:3:205:A:C8	2.52	0.43
52:3:423:G:C2'	52:3:424:G:H5'	2.48	0.43
52:3:605:U:H2'	52:3:606:G:C8	2.53	0.43
52:3:1464:U:H2'	52:3:1465:A:H8	1.84	0.43
53:1:576:U:H2'	53:1:577:G:C8	2.53	0.43
53:1:1078:U:C5'	53:1:1079:C:H5''	2.48	0.43
53:1:1130:U:C2	53:1:2025:C:H5''	2.53	0.43
53:1:1326:U:H5'	53:1:2011:U:H1'	2.00	0.43
53:1:1352:U:O2'	53:1:1353:A:H5'	2.19	0.43
53:1:1629:U:H2'	53:1:1630:A:C8	2.53	0.43
53:1:1893:C:H2'	53:1:1894:C:H5'	1.98	0.43
1:b:11:GLY:O	1:b:206:LYS:HG2	2.18	0.43
1:b:40:GLY:HA2	1:b:54:GLY:HA2	2.00	0.43
3:d:45:ALA:HB3	53:1:38:A:C5'	2.47	0.43
9:j:25:LEU:HB3	53:1:1140:C:OP1	2.17	0.43
11:l:46:VAL:HG22	11:l:47:ARG:H	1.84	0.43
12:m:7:THR:OG1	12:m:9:PHE:O	2.37	0.43
13:n:32:GLU:N	13:n:32:GLU:OE2	2.51	0.43
17:r:74:ILE:HD12	17:r:74:ILE:N	2.33	0.43
17:r:87:GLN:HG2	53:1:1224:U:O2'	2.19	0.43
23:x:56:ARG:HH12	53:1:399:U:H5''	1.83	0.43
31:G:33:ALA:HB2	31:G:38:HIS:CE1	2.54	0.43
33:I:8:LEU:HD13	52:3:429:U:H3'	2.01	0.43
36:L:8:GLN:HG2	36:L:9:ARG:N	2.33	0.43
50:Z:66:ARG:HD2	52:3:1099:G:C4'	2.48	0.43
52:3:150:U:H3	52:3:171:A:H62	1.65	0.43
52:3:424:G:H2'	52:3:425:G:H8	1.83	0.43
52:3:1120:C:H2'	52:3:1121:U:C6	2.53	0.43
53:1:118:A:OP2	53:1:119:A:H2'	2.18	0.43
53:1:1326:U:H2'	53:1:1327:A:C8	2.51	0.43
53:1:1509:A:H2'	53:1:1510:G:H8	1.81	0.43
53:1:2730:C:H2'	53:1:2731:G:H8	1.83	0.43
58:8:212:LEU:HD12	58:8:212:LEU:HA	1.92	0.43
8:i:75:ALA:O	8:i:79:LEU:HG	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:123:ALA:HA	8:i:126:ARG:NH1	2.34	0.43
10:k:41:ILE:HD11	10:k:86:LEU:CD2	2.48	0.43
17:r:29:THR:HG23	17:r:30:GLY:H	1.83	0.43
33:I:102:TYR:O	33:I:164:ARG:NH1	2.51	0.43
42:R:67:ASP:O	42:R:71:GLU:N	2.50	0.43
43:S:3:GLN:HA	43:S:6:LYS:HE2	2.01	0.43
45:U:39:PHE:CZ	45:U:41:PRO:HB3	2.53	0.43
48:X:30:LEU:HD12	48:X:30:LEU:N	2.28	0.43
52:3:1318:A:H2'	52:3:1319:A:H5'	2.01	0.43
53:1:141:G:H3'	53:1:142:A:O4'	2.18	0.43
53:1:2215:C:H2'	53:1:2216:G:C8	2.54	0.43
53:1:2216:G:H2'	53:1:2217:G:C8	2.53	0.43
53:1:2293:G:H2'	53:1:2294:G:H8	1.84	0.43
58:8:236:ILE:HD12	58:8:236:ILE:N	2.32	0.43
1:b:52:HIS:CG	1:b:218:THR:HG22	2.53	0.43
2:c:124:ARG:HD3	2:c:125:TRP:NE1	2.33	0.43
10:k:6:THR:O	10:k:20:MET:HA	2.19	0.43
11:l:127:VAL:HG22	11:l:128:THR:H	1.83	0.43
16:q:5:ARG:HG3	53:1:584:C:P	2.59	0.43
18:s:4:ILE:HG22	18:s:106:VAL:HG22	2.00	0.43
19:t:32:LEU:N	19:t:32:LEU:HD23	2.33	0.43
20:u:95:PHE:CZ	20:u:102:ILE:HG12	2.54	0.43
31:G:59:ILE:HD13	31:G:62:ARG:HE	1.83	0.43
33:I:150:LYS:HA	33:I:154:VAL:CG1	2.48	0.43
34:J:37:VAL:HG12	34:J:47:PHE:HB3	1.99	0.43
39:O:53:ILE:HG13	39:O:63:ASP:OD2	2.19	0.43
46:V:30:HIS:HA	46:V:31:PRO:HD3	1.85	0.43
53:1:445:C:O2'	53:1:446:G:H5'	2.18	0.43
53:1:458:G:O2'	53:1:459:U:C5	2.70	0.43
53:1:596:U:H2'	53:1:597:G:C8	2.53	0.43
53:1:905:A:O2'	53:1:906:U:H5'	2.18	0.43
53:1:1133:A:H4'	53:1:1134:A:C5'	2.43	0.43
53:1:1825:U:H2'	53:1:1826:G:H8	1.84	0.43
53:1:1826:G:H2'	53:1:1827:U:C6	2.53	0.43
53:1:2498:C:O2'	53:1:2499:C:H5'	2.18	0.43
53:1:2704:C:H2'	53:1:2705:A:O4'	2.17	0.43
57:7:6:G:H3'	57:7:7:A:C5'	2.48	0.43
57:7:68:C:H2'	57:7:69:G:H8	1.83	0.43
1:b:140:VAL:HG12	1:b:141:HIS:H	1.84	0.43
2:c:110:THR:HB	2:c:202:ILE:HB	2.01	0.43
2:c:179:ARG:H	2:c:188:LEU:HB2	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:25:MET:HB3	54:2:57:A:C4	2.52	0.43
6:g:77:THR:HG22	6:g:143:ILE:HB	1.99	0.43
13:n:63:ARG:NE	53:1:1454:C:C5'	2.82	0.43
14:o:47:VAL:HG21	54:2:114:C:H4'	2.00	0.43
22:w:8:ASN:HD21	53:1:2278:A:H5'	1.83	0.43
26:B:3:GLN:HA	53:1:2615:U:C2	2.54	0.43
32:H:188:ALA:HB3	32:H:195:ILE:HB	2.01	0.43
35:K:74:LEU:O	35:K:77:THR:OG1	2.31	0.43
36:L:85:GLN:CD	55:6:32:C:H4'	2.43	0.43
37:M:52:GLY:HA3	37:M:56:PRO:HA	1.99	0.43
38:N:114:LYS:HD2	38:N:114:LYS:N	2.34	0.43
40:P:51:PHE:CE2	40:P:64:VAL:HG21	2.54	0.43
46:V:45:VAL:HG22	46:V:46:HIS:N	2.34	0.43
52:3:327:A:HO2'	52:3:328:C:H4'	1.79	0.43
52:3:1243:C:H2'	52:3:1244:G:C8	2.54	0.43
52:3:1273:C:H2'	52:3:1274:A:O4'	2.18	0.43
53:1:832:U:H2'	53:1:833:A:C8	2.53	0.43
53:1:1148:U:H2'	53:1:1149:G:C8	2.54	0.43
53:1:2134:A:N6	53:1:2157:G:H4'	2.33	0.43
53:1:2443:C:H2'	53:1:2444:G:C8	2.51	0.43
1:b:225:ASN:HA	1:b:226:PRO:HD3	1.87	0.43
7:h:92:ALA:HB3	7:h:130:PRO:HD2	2.00	0.43
11:l:79:LEU:HD12	11:l:112:LEU:HA	2.01	0.43
32:H:72:PRO:HD3	32:H:104:GLU:OE1	2.19	0.43
37:M:104:SER:HA	37:M:109:VAL:HG12	1.99	0.43
39:O:39:PRO:HD2	52:3:1123:U:H4'	1.99	0.43
45:U:12:LYS:HD3	52:3:44:A:OP2	2.18	0.43
52:3:86:G:H4'	52:3:87:C:C5	2.54	0.43
52:3:1149:C:O2'	52:3:1150:A:H5'	2.19	0.43
52:3:1202:U:H2'	52:3:1203:C:C5'	2.48	0.43
52:3:1252:A:H2'	52:3:1253:G:O4'	2.18	0.43
52:3:1502:A:C8	52:3:1505:G:N2	2.85	0.43
53:1:466:A:C2'	53:1:467:G:H5'	2.48	0.43
53:1:876:C:H2'	53:1:877:A:O4'	2.19	0.43
53:1:940:G:C3'	53:1:941:A:H5''	2.49	0.43
53:1:1060:U:H4'	53:1:1061:U:O5'	2.19	0.43
53:1:1287:A:H2'	53:1:1288:G:H5'	2.01	0.43
53:1:1500:G:H2'	53:1:1501:G:C8	2.53	0.43
53:1:2292:U:H2'	53:1:2293:G:C8	2.53	0.43
53:1:2730:C:H2'	53:1:2731:G:C8	2.54	0.43
54:2:19:C:H2'	54:2:20:G:H8	1.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:6:7:G:H2'	55:6:49:G:OP2	2.18	0.43
58:8:143:ASP:O	58:8:147:LEU:HD13	2.19	0.43
58:8:375:PHE:C	58:8:375:PHE:CD2	2.97	0.43
7:h:37:LYS:NZ	53:1:1085:A:H61	2.16	0.43
13:n:7:GLY:HA3	53:1:2690:U:H3	1.84	0.43
22:w:36:GLN:OE1	22:w:40:LYS:N	2.51	0.43
36:L:137:ARG:NH1	36:L:141:HIS:HD1	2.16	0.43
43:S:45:LEU:HA	43:S:48:GLN:OE1	2.19	0.43
46:V:18:LYS:CD	52:3:255:G:H4'	2.43	0.43
52:3:152:A:H2'	52:3:153:C:H5'	2.00	0.43
52:3:381:C:H2'	52:3:382:A:O4'	2.19	0.43
52:3:662:U:H2'	52:3:663:A:C8	2.53	0.43
52:3:1288:A:O2'	52:3:1353:G:H5'	2.19	0.43
52:3:1374:A:H2'	52:3:1375:A:C8	2.54	0.43
53:1:167:A:H2'	53:1:168:G:O4'	2.18	0.43
53:1:317:G:H2'	53:1:318:C:O4'	2.18	0.43
53:1:368:A:C2'	53:1:369:U:H5'	2.49	0.43
53:1:704:G:H1'	53:1:727:A:N6	2.33	0.43
53:1:1010:A:N3	53:1:1153:C:H1'	2.34	0.43
53:1:1601:G:O2'	53:1:1602:U:H5'	2.19	0.43
55:6:37:A:H2'	55:6:38:A:O4'	2.18	0.43
8:i:33:ASN:OD1	8:i:64:ARG:NH2	2.52	0.43
10:k:11:ALA:O	10:k:100:PHE:N	2.51	0.43
11:l:13:LYS:NZ	53:1:661:A:H4'	2.34	0.43
15:p:59:THR:HG22	15:p:72:VAL:HG23	2.00	0.43
16:q:80:ASN:HB2	53:1:1151:A:O2'	2.19	0.43
24:y:28:LEU:HD22	24:y:42:LEU:HB3	2.01	0.43
31:G:46:VAL:HG12	31:G:47:PRO:HD3	2.01	0.43
38:N:8:THR:HG21	38:N:10:ARG:NH2	2.33	0.43
52:3:9:G:H2'	52:3:10:A:H8	1.83	0.43
52:3:684:U:H3	52:3:706:A:H61	1.67	0.43
53:1:197:A:H2'	53:1:198:C:O4'	2.18	0.43
53:1:498:G:H2'	53:1:499:U:C6	2.54	0.43
53:1:729:G:O2'	53:1:763:G:H4'	2.19	0.43
53:1:2024:G:OP2	53:1:2034:U:H4'	2.18	0.43
53:1:2480:C:H2'	53:1:2481:G:O4'	2.19	0.43
53:1:2589:A:H2'	53:1:2590:A:C8	2.54	0.43
4:e:141:ASP:O	4:e:142:TYR:HB3	2.18	0.42
5:f:29:ASN:HB2	5:f:78:VAL:HA	2.01	0.42
10:k:14:SER:OG	10:k:86:LEU:HD12	2.19	0.42
18:s:17:VAL:HG12	18:s:76:VAL:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:x:2:ARG:HB2	53:1:1365:A:OP2	2.19	0.42
30:F:3:VAL:O	30:F:3:VAL:HG12	2.19	0.42
32:H:4:VAL:O	32:H:6:PRO:HD3	2.19	0.42
38:N:129:ARG:HG3	38:N:129:ARG:NH1	2.35	0.42
45:U:38:PHE:CE1	45:U:51:ARG:HB2	2.54	0.42
46:V:56:ASP:N	46:V:56:ASP:OD1	2.52	0.42
51:a:59:VAL:HB	51:a:165:ASN:HB3	2.01	0.42
52:3:219:U:H2'	52:3:220:G:H8	1.84	0.42
53:1:968:C:H2'	53:1:969:G:C8	2.53	0.42
53:1:1409:U:H2'	53:1:1410:G:H8	1.83	0.42
53:1:2247:A:O2'	53:1:2248:C:H5'	2.19	0.42
53:1:2671:G:H2'	53:1:2672:U:C6	2.54	0.42
53:1:2741:A:H2'	53:1:2742:G:O4'	2.19	0.42
55:5:27:U:H2'	55:5:28:C:C6	2.54	0.42
55:5:66:C:H2'	55:5:67:C:C6	2.54	0.42
58:8:98:GLN:HG3	58:8:374:ARG:HA	2.00	0.42
1:b:23:LEU:HA	1:b:80:LEU:O	2.18	0.42
1:b:86:ARG:HD3	53:1:1817:G:H5''	2.00	0.42
4:e:23:SER:HB3	4:e:26:GLN:HE21	1.82	0.42
8:i:10:LEU:N	8:i:10:LEU:CD2	2.81	0.42
12:m:57:VAL:O	12:m:58:LYS:O	2.37	0.42
14:o:13:ARG:HD2	14:o:13:ARG:HA	1.83	0.42
34:J:14:LEU:HA	34:J:36:THR:HG22	2.00	0.42
37:M:12:ARG:CZ	52:3:826:C:H5'	2.48	0.42
40:P:15:VAL:HG13	40:P:78:ILE:HD11	2.01	0.42
43:S:4:SER:HB3	52:3:1216:A:H5''	2.01	0.42
44:T:66:LEU:HD23	44:T:66:LEU:HA	1.86	0.42
52:3:3:A:H1'	52:3:613:C:H1'	2.01	0.42
52:3:194:C:O2'	52:3:195:A:H5'	2.19	0.42
52:3:355:C:H2'	52:3:356:A:O4'	2.19	0.42
52:3:1053:G:O6	52:3:1199:U:H2'	2.18	0.42
52:3:1293:C:H2'	52:3:1294:G:C8	2.54	0.42
53:1:759:G:H2'	53:1:760:G:C8	2.54	0.42
53:1:1351:C:H2'	53:1:1352:U:C6	2.54	0.42
53:1:1956:U:C2'	53:1:1957:C:H5'	2.49	0.42
53:1:2508:G:H2'	53:1:2509:G:H8	1.84	0.42
53:1:2623:G:H2'	53:1:2624:G:H8	1.84	0.42
55:5:42:G:H2'	55:5:43:A:C8	2.55	0.42
58:8:355:ASP:HB3	58:8:357:ILE:HG12	2.01	0.42
3:d:176:ASP:HA	3:d:177:PRO:HD3	1.85	0.42
7:h:118:ILE:N	7:h:119:PRO:CD	2.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:24:GLY:HA3	8:i:25:PRO:HD3	1.91	0.42
12:m:50:ARG:HD3	12:m:65:ILE:HD11	2.01	0.42
14:o:100:HIS:CD2	54:2:48:U:H4'	2.49	0.42
15:p:31:VAL:HG22	15:p:38:ARG:O	2.20	0.42
17:r:10:LYS:HD2	17:r:12:HIS:CE1	2.53	0.42
20:u:96:LYS:O	20:u:97:SER:C	2.61	0.42
36:L:3:ARG:NH1	52:3:1092:A:C5'	2.79	0.42
36:L:55:LYS:HE3	36:L:59:GLU:OE2	2.19	0.42
47:W:59:LYS:CD	52:3:735:C:H5'	2.42	0.42
50:Z:40:PRO:HA	50:Z:44:ARG:HH12	1.84	0.42
52:3:67:C:H2'	52:3:68:G:C8	2.54	0.42
52:3:458:U:H2'	52:3:459:A:C8	2.54	0.42
52:3:518:C:H5'	52:3:530:G:C4'	2.49	0.42
52:3:939:G:N3	52:3:1375:A:H2	2.18	0.42
52:3:1125:U:H2'	52:3:1126:U:H2'	2.02	0.42
52:3:1162:C:H2'	52:3:1163:A:H8	1.84	0.42
52:3:1204:A:H2'	52:3:1205:U:O4'	2.19	0.42
53:1:493:G:O2'	53:1:494:G:H5'	2.19	0.42
53:1:1417:C:H2'	53:1:1418:G:O4'	2.20	0.42
53:1:1441:G:H2'	53:1:1442:U:C6	2.54	0.42
53:1:1727:C:H2'	53:1:1728:C:O4'	2.19	0.42
58:8:12:HIS:HB3	58:8:370:ASP:HB3	2.01	0.42
1:b:62:ARG:HB2	1:b:83:ASP:OD2	2.18	0.42
2:c:59:ARG:NH1	53:1:2830:C:H3'	2.32	0.42
7:h:58:THR:HG23	53:1:1107:G:H5''	2.02	0.42
12:m:16:ARG:HB2	12:m:18:ARG:HH11	1.85	0.42
15:p:43:GLU:N	15:p:43:GLU:OE2	2.53	0.42
16:q:30:VAL:HG13	16:q:33:VAL:HB	2.01	0.42
17:r:64:VAL:HB	17:r:95:ASP:HB2	2.01	0.42
19:t:9:LYS:HZ1	24:y:21:LEU:HD13	1.84	0.42
29:E:36:ALA:HB3	29:E:39:ARG:CD	2.49	0.42
36:L:55:LYS:HB2	36:L:60:ALA:HB2	2.00	0.42
39:O:23:ALA:HA	39:O:26:VAL:CG2	2.50	0.42
44:T:35:ILE:O	44:T:39:GLN:HG2	2.20	0.42
46:V:43:LEU:HD23	46:V:44:HIS:N	2.34	0.42
52:3:950:U:H2'	52:3:951:G:H8	1.84	0.42
53:1:193:U:O3'	53:1:803:U:H4'	2.20	0.42
53:1:275:C:H3'	53:1:276:U:H5''	2.01	0.42
53:1:777:G:O2'	53:1:778:G:H5'	2.19	0.42
53:1:863:A:H4'	54:2:100:G:H21	1.82	0.42
53:1:1420:A:H5'	53:1:1421:G:OP2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2078:C:O2'	53:1:2079:U:H5'	2.20	0.42
53:1:2088:A:H2'	53:1:2089:C:C6	2.55	0.42
53:1:2315:G:H2'	53:1:2316:G:C8	2.54	0.42
53:1:2432:A:H1'	55:6:75:C:C4'	2.39	0.42
53:1:2547:A:H61	53:1:2561:U:H3	1.67	0.42
53:1:2556:C:H2'	53:1:2557:G:O4'	2.19	0.42
54:2:3:C:C3'	54:2:4:C:C5'	2.96	0.42
57:7:52:G:H2'	57:7:53:G:H8	1.84	0.42
58:8:48:ASP:OD2	58:8:52:ASN:ND2	2.52	0.42
58:8:112:PRO:HG2	58:8:153:GLU:HB3	2.02	0.42
5:f:156:TYR:CZ	53:1:2531:A:H4'	2.54	0.42
6:g:84:ALA:CB	6:g:90:LEU:HA	2.47	0.42
7:h:118:ILE:HD13	7:h:118:ILE:HA	1.89	0.42
16:q:36:GLN:O	16:q:40:LYS:HG2	2.20	0.42
17:r:5:PHE:HB3	17:r:59:ILE:HD12	2.02	0.42
25:z:37:ARG:HA	25:z:37:ARG:HD3	1.92	0.42
27:C:4:ILE:HD12	27:C:4:ILE:N	2.30	0.42
32:H:60:ALA:C	32:H:61:LYS:HG3	2.44	0.42
32:H:156:LEU:HD12	32:H:156:LEU:O	2.20	0.42
32:H:173:PRO:HA	52:3:1108:G:OP2	2.19	0.42
34:J:9:GLU:OE1	34:J:9:GLU:N	2.52	0.42
45:U:14:ARG:HH22	52:3:618:C:C1'	2.32	0.42
47:W:31:TYR:O	47:W:39:VAL:HG22	2.19	0.42
52:3:640:A:O2'	52:3:641:U:H5'	2.19	0.42
52:3:1310:G:O2'	52:3:1311:A:H5'	2.19	0.42
52:3:1434:A:H2'	52:3:1435:G:O4'	2.18	0.42
53:1:2146:C:H4'	53:1:2147:A:C5	2.55	0.42
53:1:2406:A:H5'	53:1:2407:A:OP1	2.19	0.42
53:1:2732:G:O2'	53:1:2733:A:H5'	2.19	0.42
2:c:192:ALA:HB1	53:1:2680:U:H1'	2.01	0.42
6:g:122:LEU:HD11	6:g:128:HIS:CG	2.55	0.42
7:h:31:ARG:HH21	7:h:107:GLU:HA	1.85	0.42
10:k:6:THR:HG23	53:1:1666:G:O3'	2.19	0.42
18:s:41:LYS:CD	53:1:2009:A:H5''	2.49	0.42
19:t:80:TRP:CZ3	19:t:82:LYS:HB3	2.54	0.42
21:v:56:PHE:CE1	21:v:61:LEU:HD13	2.55	0.42
29:E:51:LYS:HD2	53:1:937:C:OP1	2.20	0.42
31:G:8:MET:SD	31:G:42:LEU:HD12	2.60	0.42
32:H:39:ARG:HA	32:H:54:ILE:HD11	2.02	0.42
33:I:47:LEU:HD23	33:I:47:LEU:O	2.20	0.42
34:J:22:LYS:NZ	52:3:921:U:H4'	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:113:LYS:NZ	52:3:1297:G:O2'	2.49	0.42
42:R:28:ARG:O	42:R:32:ILE:HG12	2.19	0.42
46:V:16:MET:HG3	46:V:19:SER:C	2.45	0.42
52:3:924:C:H2'	52:3:925:G:C8	2.54	0.42
52:3:1514:G:O2'	52:3:1515:G:H5'	2.19	0.42
53:1:192:C:C2'	53:1:193:U:H5'	2.50	0.42
53:1:826:U:H5''	53:1:2429:G:P	2.59	0.42
53:1:1578:U:H2'	53:1:1579:A:C8	2.54	0.42
53:1:1919:A:H2'	53:1:1920:C:H5'	2.02	0.42
53:1:2687:U:H2'	53:1:2688:G:O4'	2.18	0.42
55:6:62:C:H2'	55:6:63:G:H8	1.84	0.42
8:i:36:GLU:HA	8:i:39:LYS:HD2	2.00	0.42
43:S:92:ILE:HD12	43:S:92:ILE:N	2.34	0.42
46:V:5:ARG:HD3	52:3:636:U:C5'	2.43	0.42
52:3:12:U:H4'	52:3:526:C:H4'	2.02	0.42
52:3:245:U:O2'	52:3:246:A:H5'	2.20	0.42
52:3:1329:A:O2'	52:3:1330:U:H5'	2.19	0.42
52:3:1443:C:H2'	52:3:1444:U:O4'	2.20	0.42
52:3:1453:G:H3'	52:3:1453:G:N3	2.34	0.42
53:1:74:A:H4'	53:1:75:G:O5'	2.19	0.42
53:1:648:G:H2'	53:1:649:G:H8	1.85	0.42
53:1:1266:G:H22	53:1:2012:G:H2'	1.85	0.42
53:1:2120:G:H2'	53:1:2121:G:C8	2.55	0.42
53:1:2153:C:H2'	53:1:2154:A:C8	2.55	0.42
53:1:2860:A:C2'	53:1:2861:U:H5'	2.50	0.42
57:7:52:G:H2'	57:7:53:G:C8	2.53	0.42
58:8:266:LEU:O	58:8:266:LEU:HD23	2.19	0.42
2:c:98:VAL:HG22	2:c:98:VAL:O	2.19	0.42
4:e:65:LEU:N	4:e:87:LYS:O	2.53	0.42
6:g:31:VAL:CG1	6:g:32:PRO:HD3	2.49	0.42
7:h:33:VAL:HG23	7:h:35:VAL:H	1.85	0.42
9:j:17:VAL:HG13	9:j:137:PRO:HB2	2.01	0.42
9:j:109:LEU:HD22	9:j:118:MET:CE	2.46	0.42
9:j:134:ALA:HB1	53:1:2898:U:O2	2.20	0.42
13:n:36:THR:OG1	13:n:37:THR:N	2.53	0.42
14:o:43:ASN:ND2	14:o:46:GLU:OE1	2.52	0.42
14:o:115:LEU:HD12	14:o:115:LEU:HA	1.89	0.42
28:D:34:ARG:NH1	53:1:466:A:OP1	2.53	0.42
35:K:4:TYR:CD2	35:K:71:ILE:HG12	2.55	0.42
38:N:121:ARG:HB3	52:3:1344:C:H5''	2.02	0.42
52:3:399:G:H2'	52:3:400:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1254:A:H2'	52:3:1255:G:C8	2.55	0.42
53:1:1637:A:H5'	53:1:1760:C:O2'	2.20	0.42
53:1:1669:A:O3'	53:1:2549:G:H5'	2.20	0.42
53:1:2591:C:H2'	53:1:2592:G:C8	2.54	0.42
55:6:18:G:H1'	55:6:60:U:H3	1.85	0.42
2:c:136:ASN:HD21	2:c:139:SER:C	2.28	0.42
7:h:118:ILE:CB	7:h:119:PRO:HD3	2.49	0.42
13:n:69:ARG:C	13:n:71:ARG:H	2.28	0.42
25:z:8:GLN:HB2	25:z:28:LEU:HD13	2.01	0.42
31:G:20:ARG:HA	52:3:830:G:H4'	2.02	0.42
33:I:120:LYS:HE2	33:I:130:ASN:ND2	2.35	0.42
34:J:24:VAL:HG13	34:J:26:GLY:N	2.31	0.42
37:M:29:SER:OG	37:M:32:LYS:HE3	2.18	0.42
38:N:114:LYS:HB2	38:N:117:LEU:HD12	2.01	0.42
45:U:46:LYS:HB2	45:U:47:GLU:OE1	2.19	0.42
47:W:24:ASP:OD2	47:W:27:THR:OG1	2.38	0.42
52:3:279:A:H4'	52:3:281:G:N7	2.34	0.42
52:3:600:A:H2'	52:3:601:G:C8	2.55	0.42
52:3:711:G:H2'	52:3:712:A:C8	2.55	0.42
53:1:320:A:H4'	53:1:322:A:N7	2.35	0.42
53:1:758:C:O2	53:1:758:C:H2'	2.20	0.42
53:1:862:G:H2'	53:1:863:A:O4'	2.20	0.42
53:1:1366:A:H2'	53:1:1367:A:O4'	2.19	0.42
53:1:1430:G:H2'	53:1:1431:A:O4'	2.20	0.42
53:1:1539:U:H2'	53:1:1540:G:H8	1.83	0.42
53:1:1683:U:H2'	53:1:1684:G:C8	2.54	0.42
53:1:1999:C:H2'	53:1:2000:C:C6	2.55	0.42
60:7:101:PHE:N	58:8:261:MET:HA	2.34	0.42
4:e:90:LEU:HD23	4:e:90:LEU:H	1.85	0.42
5:f:108:PHE:HB3	5:f:110:HIS:CE1	2.55	0.42
6:g:47:PHE:HA	6:g:51:ARG:HB2	2.02	0.42
11:l:19:LEU:HD22	11:l:19:LEU:N	2.34	0.42
14:o:15:ARG:NH2	54:2:8:C:H5''	2.34	0.42
16:q:26:ALA:HB1	16:q:30:VAL:CG1	2.50	0.42
24:y:2:LYS:HD3	53:1:77:G:OP1	2.19	0.42
28:D:5:PHE:O	28:D:7:PRO:HD3	2.19	0.42
29:E:4:LYS:NZ	53:1:254:G:N7	2.68	0.42
30:F:6:SER:HB2	30:F:8:LYS:HZ2	1.85	0.42
32:H:122:GLN:HG3	32:H:127:VAL:HG21	2.01	0.42
33:I:190:LEU:HD12	33:I:192:ALA:N	2.14	0.42
37:M:9:MET:HG3	37:M:26:MET:SD	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:49:GLN:HE21	38:N:79:ARG:HD3	1.85	0.42
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	2.02	0.42
46:V:37:ILE:HD12	46:V:39:ARG:HE	1.84	0.42
52:3:1330:U:H2'	52:3:1331:G:O4'	2.20	0.42
52:3:1432:G:O2'	52:3:1468:A:N6	2.53	0.42
53:1:28:A:H1'	53:1:513:A:C2	2.55	0.42
53:1:121:G:H2'	53:1:122:G:H8	1.85	0.42
53:1:151:C:H2'	53:1:152:A:H8	1.85	0.42
53:1:171:U:H2'	53:1:172:A:H8	1.84	0.42
53:1:370:G:H2'	53:1:423:A:N7	2.34	0.42
53:1:871:U:H2'	53:1:872:U:C6	2.55	0.42
53:1:1004:U:H3	53:1:1151:A:H61	1.68	0.42
53:1:1170:C:H2'	53:1:1171:G:C8	2.55	0.42
53:1:2030:A:N3	53:1:2499:C:H5''	2.35	0.42
2:c:115:GLY:HA3	53:1:2822:G:P	2.60	0.41
24:y:1:MET:HA	24:y:4:LYS:HB2	2.02	0.41
40:P:88:PRO:HB3	50:Z:28:LEU:HD23	2.02	0.41
43:S:29:ILE:HG13	43:S:30:ILE:CD1	2.49	0.41
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.79	0.41
52:3:539:A:H2'	52:3:540:G:H8	1.83	0.41
52:3:1033:G:C3'	52:3:1034:G:H5''	2.49	0.41
52:3:1101:A:H4'	52:3:1102:A:O5'	2.20	0.41
52:3:1342:C:H2'	52:3:1343:G:C8	2.55	0.41
53:1:43:G:H2'	53:1:44:A:O4'	2.20	0.41
53:1:162:U:O2'	53:1:163:C:H5'	2.20	0.41
53:1:937:C:H2'	53:1:938:G:C8	2.55	0.41
53:1:1089:A:H2	53:1:1090:A:H62	1.67	0.41
53:1:1106:G:H2'	53:1:1107:G:O4'	2.20	0.41
53:1:1593:A:H2'	53:1:1594:U:C6	2.55	0.41
53:1:2415:G:H2'	53:1:2416:C:C6	2.55	0.41
57:7:24:G:H2'	57:7:25:C:C6	2.55	0.41
57:7:72:C:H2'	57:7:73:A:O4'	2.20	0.41
1:b:257:ARG:NH1	1:b:259:ASN:ND2	2.68	0.41
2:c:123:LYS:HE2	13:n:1:MET:HE1	2.01	0.41
3:d:32:VAL:HG21	11:l:6:LEU:HD13	2.02	0.41
3:d:162:ARG:NH1	53:1:321:U:H1'	2.35	0.41
18:s:72:THR:HG23	18:s:73:LYS:N	2.35	0.41
20:u:6:ARG:N	53:1:85:G:OP1	2.46	0.41
27:C:41:VAL:HG23	27:C:42:VAL:N	2.34	0.41
28:D:34:ARG:HA	28:D:34:ARG:HD2	1.84	0.41
31:G:110:ILE:HD12	31:G:151:LYS:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:104:MET:HE1	33:I:170:LEU:HB2	2.01	0.41
40:P:126:ARG:HH21	52:3:796:C:H4'	1.84	0.41
45:U:17:TYR:O	45:U:39:PHE:N	2.50	0.41
49:Y:70:LYS:HA	49:Y:73:ARG:NH1	2.35	0.41
52:3:389:A:H2'	52:3:390:U:H5'	2.01	0.41
52:3:620:C:H2'	52:3:621:A:O4'	2.20	0.41
52:3:1038:C:H2'	52:3:1039:G:C8	2.53	0.41
52:3:1195:C:H5''	52:3:1196:A:OP2	2.21	0.41
52:3:1221:G:H2'	52:3:1222:G:C8	2.54	0.41
53:1:26:G:O2'	53:1:27:G:H5'	2.20	0.41
53:1:546:U:H2'	53:1:547:A:C4'	2.49	0.41
53:1:1045:C:P	53:1:1047:G:H5'	2.60	0.41
53:1:1565:C:O2'	53:1:1566:A:H2'	2.19	0.41
53:1:2511:U:O2'	53:1:2512:C:H5'	2.20	0.41
54:2:33:G:H2'	54:2:34:A:O4'	2.19	0.41
58:8:124:ARG:HD2	58:8:161:TYR:HB3	2.03	0.41
1:b:263:ASP:OD1	1:b:263:ASP:N	2.53	0.41
3:d:92:HIS:O	3:d:93:SER:C	2.62	0.41
5:f:173:ALA:C	5:f:175:LYS:H	2.27	0.41
6:g:83:LYS:HD2	6:g:91:PHE:CD2	2.55	0.41
9:j:7:LYS:O	9:j:11:VAL:HG23	2.21	0.41
17:r:7:SER:CB	17:r:22:LEU:HD22	2.51	0.41
17:r:7:SER:HB2	17:r:22:LEU:HD22	2.01	0.41
17:r:51:VAL:HG22	17:r:52:PRO:CD	2.50	0.41
18:s:90:LYS:HD2	18:s:92:ARG:HH22	1.85	0.41
20:u:84:PHE:HB2	53:1:297:G:H5''	2.01	0.41
21:v:14:LYS:NZ	54:2:79:G:N7	2.67	0.41
35:K:11:HIS:NE2	35:K:13:ASP:OD2	2.48	0.41
36:L:102:TRP:CD1	36:L:136:LYS:HG2	2.55	0.41
37:M:40:LYS:NZ	37:M:47:ASP:H	2.18	0.41
41:Q:9:LYS:HA	41:Q:10:PRO:HD3	1.80	0.41
51:a:170:ILE:HD12	51:a:170:ILE:N	2.36	0.41
52:3:464:U:H2'	52:3:466:A:OP2	2.20	0.41
52:3:501:C:H2'	52:3:502:A:H8	1.85	0.41
52:3:887:G:H2'	52:3:888:G:O4'	2.20	0.41
53:1:983:A:N6	53:1:984:A:C2	2.89	0.41
53:1:1857:G:N2	53:1:1884:G:H2'	2.35	0.41
53:1:1924:C:H2'	53:1:1925:C:C6	2.54	0.41
53:1:2297:A:H62	53:1:2319:G:H1'	1.85	0.41
54:2:91:C:H2'	54:2:92:C:C6	2.56	0.41
58:8:322:PRO:HB3	58:8:352:MET:CA	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:191:LEU:HD23	1:b:192:GLY:N	2.36	0.41
2:c:105:LYS:HA	2:c:177:VAL:HG12	2.02	0.41
3:d:45:ALA:HB3	53:1:38:A:H5'	2.03	0.41
4:e:15:LEU:HD23	4:e:27:VAL:HG23	2.01	0.41
7:h:56:ARG:CZ	7:h:83:ALA:HB2	2.50	0.41
7:h:108:VAL:HG23	7:h:109:LYS:N	2.34	0.41
8:i:121:ILE:O	8:i:125:THR:HG23	2.21	0.41
14:o:69:ASP:OD1	14:o:69:ASP:N	2.52	0.41
17:r:68:ARG:NH2	53:1:1223:G:OP1	2.53	0.41
19:t:50:LEU:N	19:t:50:LEU:HD22	2.35	0.41
20:u:24:VAL:HA	20:u:35:VAL:HG22	2.03	0.41
23:x:50:VAL:HG12	23:x:51:SER:O	2.20	0.41
37:M:120:LEU:N	37:M:120:LEU:HD23	2.35	0.41
38:N:118:ARG:HB3	38:N:122:ARG:HB3	2.02	0.41
40:P:91:GLY:O	40:P:93:GLU:N	2.52	0.41
46:V:6:THR:HG21	46:V:59:GLU:HB3	2.01	0.41
46:V:74:LEU:HD23	46:V:75:VAL:C	2.45	0.41
51:a:43:ASP:HA	51:a:174:THR:HA	2.02	0.41
51:a:51:ASP:OD2	51:a:54:LYS:HG2	2.20	0.41
52:3:231:U:H2'	52:3:232:G:H8	1.85	0.41
52:3:437:U:H2'	52:3:438:U:O4'	2.20	0.41
52:3:460:A:H2'	52:3:461:A:C8	2.56	0.41
52:3:820:U:H3'	52:3:821:G:C5'	2.51	0.41
53:1:194:G:H2'	53:1:195:A:O4'	2.21	0.41
53:1:634:C:H2'	53:1:635:C:C6	2.56	0.41
53:1:696:G:O2'	53:1:697:G:H5'	2.21	0.41
53:1:967:U:H2'	53:1:968:C:C6	2.55	0.41
53:1:1345:C:H2'	53:1:1346:G:H8	1.85	0.41
53:1:1700:A:H2'	53:1:1701:A:H5'	2.02	0.41
53:1:2555:U:H2'	53:1:2556:C:H5'	2.03	0.41
57:7:27:G:O2'	57:7:28:G:H5'	2.21	0.41
5:f:65:GLY:HA3	53:1:2748:A:O2'	2.20	0.41
11:l:9:ALA:HB3	11:l:12:SER:HB3	2.02	0.41
14:o:30:ARG:HH22	54:2:48:U:P	2.43	0.41
15:p:111:GLU:OE1	15:p:111:GLU:N	2.53	0.41
17:r:49:ILE:CG2	17:r:54:VAL:HG22	2.51	0.41
18:s:17:VAL:HB	18:s:76:VAL:HG11	2.01	0.41
22:w:7:ARG:N	22:w:7:ARG:HD3	2.36	0.41
33:I:94:GLU:HA	33:I:99:ASN:HD22	1.85	0.41
35:K:98:GLU:HB3	35:K:99:ALA:H	1.69	0.41
40:P:19:VAL:HG22	40:P:82:GLU:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:170:ILE:HG12	53:1:2177:C:O2'	2.20	0.41
52:3:645:G:H2'	52:3:646:G:H8	1.85	0.41
52:3:1011:C:H2'	52:3:1012:A:H8	1.86	0.41
53:1:1054:A:H2'	53:1:1055:G:C8	2.55	0.41
53:1:1055:G:H2'	53:1:1056:G:O4'	2.20	0.41
53:1:1298:C:H2'	53:1:1299:G:O4'	2.21	0.41
53:1:2027:G:H2'	53:1:2028:U:C6	2.55	0.41
53:1:2244:U:H2'	53:1:2245:U:O4'	2.21	0.41
53:1:2564:A:OP1	53:1:2648:G:H4'	2.21	0.41
3:d:46:GLN:HB2	3:d:86:ALA:HB1	2.01	0.41
8:i:95:ASP:O	8:i:95:ASP:OD2	2.39	0.41
9:j:99:ARG:HA	9:j:102:GLU:HB3	2.02	0.41
12:m:75:GLU:CD	53:1:957:C:OP1	2.64	0.41
13:n:79:LEU:O	13:n:80:PHE:HB2	2.21	0.41
15:p:95:LYS:HE2	53:1:2719:G:OP1	2.21	0.41
17:r:39:LEU:HD12	17:r:39:LEU:N	2.36	0.41
17:r:54:VAL:HG12	17:r:55:ASP:OD1	2.20	0.41
19:t:9:LYS:NZ	24:y:21:LEU:HD13	2.35	0.41
19:t:51:PHE:C	19:t:52:GLU:HG2	2.45	0.41
38:N:119:LYS:O	38:N:120:ALA:HB3	2.20	0.41
42:R:16:ILE:HD12	42:R:16:ILE:H	1.85	0.41
44:T:78:THR:O	44:T:82:GLU:HG2	2.21	0.41
50:Z:48:LYS:HB2	52:3:723:U:OP1	2.21	0.41
51:a:44:VAL:HG12	51:a:214:ILE:HG22	2.03	0.41
52:3:542:G:O2'	52:3:543:U:H5'	2.21	0.41
52:3:624:C:H2'	52:3:625:U:O4'	2.21	0.41
52:3:674:G:H2'	52:3:675:A:C8	2.55	0.41
52:3:679:C:H2'	52:3:680:C:C6	2.56	0.41
52:3:918:A:H2'	52:3:919:A:O4'	2.20	0.41
52:3:1126:U:H1'	52:3:1281:C:O4'	2.20	0.41
53:1:854:C:O2'	53:1:855:G:H5'	2.20	0.41
53:1:1139:G:H2'	53:1:1140:C:C6	2.55	0.41
53:1:2128:G:H2'	53:1:2129:C:O4'	2.20	0.41
53:1:2743:U:H2'	53:1:2744:G:C5'	2.50	0.41
54:2:114:C:H2'	54:2:115:A:C8	2.55	0.41
58:8:313:SER:OG	58:8:315:ASP:OD1	2.38	0.41
58:8:391:LYS:HG3	58:8:392:VAL:N	2.36	0.41
4:e:15:LEU:HD12	4:e:18:GLU:HB3	2.03	0.41
4:e:39:VAL:HG13	4:e:40:GLY:N	2.35	0.41
9:j:47:HIS:ND1	9:j:48:VAL:HG23	2.35	0.41
10:k:15:GLY:O	10:k:47:ILE:HG12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:p:25:VAL:HG22	15:p:26:GLU:N	2.36	0.41
31:G:96:LEU:H	31:G:99:MET:HE2	1.85	0.41
38:N:129:ARG:NH2	55:5:34:C:H5''	2.34	0.41
41:Q:50:LYS:HD2	41:Q:50:LYS:H	1.85	0.41
45:U:14:ARG:HA	45:U:14:ARG:HD3	1.92	0.41
48:X:30:LEU:HB2	48:X:48:ILE:HG22	2.02	0.41
52:3:367:U:H4'	58:8:280:ARG:CZ	2.51	0.41
52:3:406:G:H2'	52:3:407:U:C6	2.55	0.41
52:3:1014:A:H2'	52:3:1015:G:O4'	2.20	0.41
52:3:1346:A:C2'	52:3:1347:G:H4'	2.50	0.41
53:1:11:C:H2'	53:1:12:U:H5''	2.03	0.41
53:1:279:A:C2'	53:1:280:U:H5'	2.49	0.41
53:1:1190:G:H2'	53:1:1191:G:H8	1.86	0.41
53:1:1275:A:N6	53:1:1296:G:H4'	2.36	0.41
53:1:1524:G:H2'	53:1:1525:A:C8	2.56	0.41
53:1:2101:A:H2'	53:1:2102:G:H8	1.86	0.41
53:1:2223:G:H2'	53:1:2224:G:H5'	2.03	0.41
53:1:2263:C:H4'	53:1:2329:U:H4'	2.03	0.41
53:1:2316:G:O2'	53:1:2317:A:H5'	2.19	0.41
55:6:35:A:H2'	55:6:36:U:C6	2.56	0.41
58:8:322:PRO:HG2	58:8:350:MET:HE3	2.03	0.41
2:c:186:LEU:HD13	15:p:7:LEU:HD11	2.01	0.41
5:f:28:LYS:HG3	5:f:29:ASN:ND2	2.36	0.41
8:i:79:LEU:HD13	8:i:137:LEU:HD12	2.02	0.41
8:i:80:LYS:HD2	8:i:86:LYS:HA	2.03	0.41
8:i:101:SER:HA	8:i:140:GLU:O	2.20	0.41
14:o:75:GLY:O	14:o:78:VAL:HG12	2.20	0.41
21:v:34:LYS:HD2	21:v:34:LYS:C	2.46	0.41
32:H:3:LYS:HZ1	52:3:1191:A:H5''	1.86	0.41
32:H:171:ARG:HG3	52:3:1107:C:OP1	2.20	0.41
40:P:32:THR:HG23	40:P:43:TRP:HB3	2.02	0.41
40:P:88:PRO:HD3	50:Z:28:LEU:HD21	2.01	0.41
40:P:115:ILE:HG23	40:P:115:ILE:O	2.20	0.41
41:Q:27:PRO:HB2	41:Q:28:GLN:OE1	2.20	0.41
44:T:22:GLY:HA3	52:3:750:C:O2	2.21	0.41
52:3:195:A:H2'	52:3:196:A:C8	2.55	0.41
52:3:1349:A:H2'	52:3:1350:A:O4'	2.20	0.41
52:3:1524:C:H2'	52:3:1525:G:H8	1.86	0.41
53:1:534:U:H2'	53:1:535:G:C8	2.55	0.41
53:1:542:C:C2'	53:1:543:G:H5''	2.51	0.41
53:1:606:U:H4'	53:1:658:U:O2'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:610:C:H2'	53:1:611:C:C6	2.56	0.41
53:1:1661:G:O2'	53:1:1662:U:H5'	2.20	0.41
53:1:2217:G:O2'	53:1:2218:G:H5'	2.21	0.41
53:1:2245:U:H5''	53:1:2246:G:H5'	2.03	0.41
53:1:2457:U:O2'	53:1:2458:G:H5'	2.21	0.41
1:b:203:VAL:HG23	53:1:1792:G:H5'	2.03	0.41
1:b:239:PHE:O	1:b:241:LYS:HG3	2.21	0.41
3:d:2:GLU:HB3	3:d:11:ALA:HB1	2.03	0.41
3:d:6:LYS:HD2	3:d:119:ILE:HD12	2.03	0.41
3:d:91:ASP:OD2	3:d:91:ASP:N	2.54	0.41
4:e:107:VAL:HG13	4:e:108:PRO:HD3	2.00	0.41
6:g:69:ALA:O	6:g:72:ILE:HG12	2.21	0.41
10:k:25:LEU:HD11	53:1:2562:U:H4'	2.02	0.41
10:k:58:LEU:HD23	10:k:58:LEU:N	2.35	0.41
10:k:78:ARG:O	15:p:70:GLU:HB3	2.21	0.41
13:n:79:LEU:C	13:n:81:ASN:H	2.29	0.41
15:p:49:ILE:HG13	15:p:49:ILE:O	2.20	0.41
15:p:90:ALA:N	15:p:110:LYS:O	2.53	0.41
15:p:92:ARG:O	15:p:93:LYS:HG3	2.21	0.41
17:r:83:TYR:HE1	17:r:85:LYS:HE3	1.85	0.41
18:s:8:ARG:HD3	53:1:494:G:OP1	2.21	0.41
23:x:43:LYS:HD2	23:x:43:LYS:N	2.36	0.41
26:B:6:LYS:HA	26:B:7:PRO:HD3	1.83	0.41
30:F:30:GLU:HA	30:F:31:PRO:HD3	1.95	0.41
32:H:67:ILE:H	32:H:67:ILE:HD12	1.85	0.41
33:I:28:ASP:O	33:I:29:THR:OG1	2.36	0.41
33:I:43:ARG:NH1	33:I:44:LYS:O	2.54	0.41
34:J:98:ALA:HB3	34:J:122:VAL:HA	2.01	0.41
34:J:110:MET:N	34:J:110:MET:SD	2.94	0.41
36:L:3:ARG:HH12	52:3:1092:A:P	2.44	0.41
36:L:123:LEU:HA	36:L:126:ALA:HB3	2.03	0.41
39:O:11:LYS:HE2	39:O:71:LEU:CD1	2.46	0.41
39:O:19:ASP:OD1	39:O:19:ASP:N	2.54	0.41
39:O:45:ARG:HA	39:O:45:ARG:HD2	1.92	0.41
39:O:61:ALA:HB2	52:3:1061:G:C5'	2.50	0.41
39:O:86:ALA:O	39:O:90:LEU:HD12	2.21	0.41
41:Q:66:ILE:HD12	41:Q:66:ILE:H	1.86	0.41
41:Q:82:ARG:CG	41:Q:95:HIS:HB2	2.48	0.41
48:X:36:ARG:NH1	52:3:1318:A:H1'	2.36	0.41
49:Y:83:ASN:HA	49:Y:86:ALA:HB3	2.03	0.41
51:a:43:ASP:HB3	53:1:2124:G:H4'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:219:GLY:O	53:1:2176:A:H5'	2.21	0.41
52:3:1316:G:H2'	52:3:1317:C:H5''	2.03	0.41
52:3:1348:U:O2'	52:3:1349:A:H5'	2.21	0.41
52:3:1368:A:O2'	52:3:1369:C:H5'	2.20	0.41
53:1:184:C:H4'	53:1:217:A:C2	2.51	0.41
53:1:292:U:H2'	53:1:293:U:C6	2.56	0.41
53:1:692:C:H2'	53:1:693:A:H8	1.85	0.41
53:1:722:A:H2'	53:1:723:C:C6	2.56	0.41
53:1:1075:C:H5	53:1:1076:C:C5	2.39	0.41
53:1:1316:U:H2'	53:1:1317:G:H8	1.84	0.41
53:1:1370:C:H2'	53:1:1371:G:O4'	2.20	0.41
53:1:1435:G:O2'	53:1:1436:G:H5'	2.20	0.41
53:1:1528:A:H2'	53:1:1529:G:O4'	2.21	0.41
53:1:1924:C:O2'	53:1:1925:C:H5'	2.21	0.41
53:1:2197:U:H1'	53:1:2198:A:C8	2.56	0.41
53:1:2377:A:H2'	53:1:2378:A:C8	2.56	0.41
53:1:2740:A:H2'	53:1:2741:A:C8	2.56	0.41
55:6:21:A:O2'	55:6:22:G:C8	2.74	0.41
58:8:14:ASN:CB	58:8:372:GLY:HA3	2.51	0.41
58:8:32:ILE:O	58:8:36:LEU:HB2	2.20	0.41
1:b:55:GLY:H	53:1:692:C:P	2.44	0.41
1:b:203:VAL:HG13	1:b:203:VAL:O	2.21	0.41
6:g:31:VAL:N	6:g:32:PRO:HD2	2.35	0.41
6:g:37:VAL:HA	6:g:38:PRO:HD3	1.97	0.41
7:h:6:GLN:O	7:h:9:GLN:HB3	2.21	0.41
10:k:66:LYS:HG3	10:k:81:GLY:O	2.21	0.41
17:r:27:ILE:HG22	17:r:31:GLU:HB3	2.03	0.41
33:I:119:HIS:CG	52:3:438:U:H4'	2.57	0.41
36:L:75:LYS:NZ	52:3:937:A:O3'	2.54	0.41
36:L:142:ARG:CB	55:6:41:C:H4'	2.50	0.41
42:R:51:GLN:O	42:R:55:LEU:HG	2.21	0.41
52:3:34:C:H2'	52:3:35:G:H8	1.86	0.41
52:3:144:G:O2'	52:3:145:G:H5'	2.20	0.41
52:3:817:C:H4'	52:3:818:G:H5''	2.03	0.41
53:1:112:U:H2'	53:1:113:U:H5'	2.02	0.41
53:1:402:A:H2'	53:1:403:U:H5'	2.03	0.41
53:1:772:C:O2'	53:1:773:U:H5'	2.21	0.41
53:1:962:G:O2'	53:1:963:U:H5'	2.21	0.41
2:c:61:THR:HB	53:1:2811:G:OP1	2.21	0.40
6:g:81:ALA:HB1	6:g:149:GLU:HB2	2.03	0.40
7:h:61:ARG:HG3	53:1:1046:A:C4'	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:3:LEU:HD23	53:1:1203:U:H5'	2.02	0.40
12:m:69:PRO:HA	12:m:94:ALA:HB2	2.03	0.40
15:p:28:LYS:CD	15:p:81:ASP:HB3	2.51	0.40
26:B:3:GLN:OE1	26:B:6:LYS:HA	2.21	0.40
31:G:115:ASP:O	31:G:119:GLN:HG3	2.21	0.40
32:H:18:ASN:O	32:H:55:VAL:HA	2.21	0.40
32:H:63:ILE:HG13	32:H:98:ALA:CB	2.44	0.40
36:L:26:VAL:HG22	36:L:42:VAL:HG21	2.03	0.40
42:R:21:ILE:N	42:R:21:ILE:HD12	2.36	0.40
50:Z:25:ALA:HB3	56:4:9:G:H5'	2.02	0.40
52:3:149:A:H1'	52:3:1446:A:C2	2.56	0.40
52:3:229:U:H2'	52:3:230:G:C8	2.56	0.40
52:3:355:C:H5'	52:3:355:C:H6	1.86	0.40
52:3:1251:A:H2'	52:3:1252:A:C8	2.55	0.40
53:1:373:U:H2'	53:1:374:A:H8	1.86	0.40
53:1:639:U:H2'	53:1:640:C:C6	2.56	0.40
53:1:692:C:H2'	53:1:693:A:C8	2.56	0.40
53:1:1086:A:H3'	53:1:1086:A:N3	2.36	0.40
53:1:1086:A:H1'	53:1:1103:A:H61	1.85	0.40
53:1:1412:U:H2'	53:1:1413:A:C8	2.56	0.40
53:1:2832:U:H1'	53:1:2834:G:C2	2.57	0.40
1:b:181:ARG:NH2	53:1:1800:C:OP2	2.54	0.40
8:i:52:LEU:HD12	8:i:53:PRO:CD	2.47	0.40
9:j:7:LYS:HG2	53:1:538:A:C4'	2.46	0.40
9:j:20:ALA:HB3	9:j:58:ASN:O	2.21	0.40
12:m:34:LYS:HD2	12:m:131:VAL:HG21	2.03	0.40
13:n:55:ALA:HA	13:n:80:PHE:CE1	2.56	0.40
30:F:31:PRO:HB3	53:1:2527:C:H5''	2.02	0.40
31:G:127:LYS:HE3	31:G:127:LYS:HB2	1.94	0.40
33:I:205:LYS:HB3	52:3:8:A:C5	2.56	0.40
34:J:111:ARG:O	34:J:115:GLU:HG2	2.20	0.40
35:K:18:VAL:N	35:K:19:PRO:CD	2.84	0.40
35:K:79:ARG:NH2	52:3:671:G:O2'	2.55	0.40
38:N:46:VAL:HA	38:N:49:GLN:HG2	2.02	0.40
43:S:63:CYS:HB3	43:S:67:GLY:H	1.86	0.40
45:U:12:LYS:NZ	52:3:43:C:OP2	2.54	0.40
48:X:28:LYS:C	48:X:28:LYS:HD2	2.46	0.40
52:3:1094:G:N3	52:3:1094:G:H2'	2.36	0.40
52:3:1352:C:H2'	52:3:1353:G:H8	1.82	0.40
53:1:182:A:O2'	53:1:183:C:H5'	2.21	0.40
53:1:875:G:H1	53:1:902:C:H42	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1127:A:H2'	53:1:1128:G:H5''	2.02	0.40
53:1:1672:A:C2	53:1:2582:G:H5'	2.56	0.40
53:1:1739:A:H2'	53:1:1740:G:O4'	2.21	0.40
53:1:1936:A:H3'	53:1:1937:A:H5'	2.03	0.40
53:1:2489:U:O2'	53:1:2490:G:H5'	2.21	0.40
1:b:145:MET:HE2	1:b:181:ARG:NH2	2.37	0.40
7:h:82:ILE:HD12	7:h:82:ILE:N	2.36	0.40
12:m:86:LYS:HD3	53:1:956:G:OP1	2.22	0.40
13:n:9:GLN:O	13:n:10:LEU:HB2	2.21	0.40
13:n:13:ASN:HD21	13:n:15:SER:HB3	1.85	0.40
13:n:41:ALA:HB1	13:n:97:ILE:HD12	2.03	0.40
23:x:10:ARG:HG3	23:x:11:PRO:HD2	2.03	0.40
34:J:87:VAL:HG22	34:J:92:ARG:CB	2.52	0.40
41:Q:113:ARG:NH2	52:3:501:C:OP1	2.54	0.40
42:R:21:ILE:HD12	42:R:21:ILE:H	1.87	0.40
43:S:27:LYS:HE2	52:3:1317:C:OP2	2.21	0.40
43:S:80:ARG:HA	43:S:83:VAL:HG22	2.03	0.40
44:T:32:THR:OG1	44:T:84:LEU:HD21	2.21	0.40
44:T:44:GLU:C	44:T:46:LYS:H	2.29	0.40
45:U:20:VAL:CG2	45:U:21:VAL:H	2.29	0.40
45:U:33:ILE:HD12	45:U:33:ILE:H	1.86	0.40
50:Z:17:ARG:HA	50:Z:20:ARG:NH1	2.34	0.40
52:3:92:U:H2'	52:3:93:U:H5'	2.04	0.40
52:3:451:A:H4'	52:3:452:A:O4'	2.21	0.40
52:3:707:U:H2'	52:3:708:C:C6	2.57	0.40
53:1:37:C:O2'	53:1:38:A:H5'	2.21	0.40
53:1:381:G:H2'	53:1:382:A:C8	2.57	0.40
53:1:746:U:H5''	53:1:748:G:O4'	2.21	0.40
53:1:821:A:C5'	53:1:822:G:H5''	2.49	0.40
53:1:941:A:H2'	53:1:942:G:O4'	2.21	0.40
53:1:962:G:H21	53:1:2250:G:H1	1.69	0.40
53:1:1609:A:H1'	53:1:1616:A:C1'	2.51	0.40
54:2:51:G:H2'	54:2:52:A:O4'	2.22	0.40
55:5:18:G:H1	55:5:55:U:H6	1.68	0.40
55:6:40:C:H2'	55:6:41:C:C6	2.57	0.40
57:7:49:C:H2'	57:7:50:U:C6	2.56	0.40
3:d:119:ILE:HB	3:d:187:VAL:HG12	2.03	0.40
11:l:20:GLY:HA2	11:l:28:GLY:HA2	2.04	0.40
21:v:26:PHE:HE2	21:v:89:ILE:HG13	1.85	0.40
31:G:86:CYS:O	31:G:87:ASP:OD2	2.39	0.40
33:I:56:GLU:HG2	33:I:199:ILE:HD11	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:64:TYR:HB3	33:I:66:VAL:HG23	2.02	0.40
33:I:90:LEU:N	33:I:90:LEU:HD22	2.36	0.40
35:K:38:ARG:NH2	35:K:40:GLU:OE1	2.51	0.40
36:L:78:ARG:NH1	52:3:1382:C:H4'	2.26	0.40
36:L:129:ASN:HB2	36:L:134:VAL:HG21	2.03	0.40
52:3:560:A:H4'	52:3:561:U:H5'	2.03	0.40
52:3:691:G:O2'	52:3:797:C:H4'	2.22	0.40
52:3:710:G:H2'	52:3:711:G:H8	1.85	0.40
52:3:865:A:H2'	52:3:866:C:O4'	2.21	0.40
52:3:869:G:H4'	52:3:872:A:C8	2.57	0.40
52:3:1005:A:H2'	52:3:1006:G:C5'	2.51	0.40
52:3:1005:A:C2'	52:3:1006:G:H5'	2.52	0.40
52:3:1071:C:H2'	52:3:1072:G:H8	1.85	0.40
52:3:1230:C:O2'	52:3:1231:G:H5'	2.21	0.40
53:1:492:A:H2'	53:1:493:G:O4'	2.22	0.40
53:1:543:G:H8	53:1:543:G:H5'	1.86	0.40
53:1:760:G:H2'	53:1:761:A:O4'	2.20	0.40
53:1:2266:A:H4'	53:1:2267:A:C4	2.56	0.40
53:1:2508:G:H2'	53:1:2509:G:C8	2.57	0.40
53:1:2617:U:H2'	53:1:2618:G:O4'	2.21	0.40
53:1:2639:A:H2'	53:1:2640:G:O4'	2.22	0.40
55:6:13:C:O2'	55:6:14:A:H5'	2.22	0.40
55:6:28:C:H2'	55:6:29:G:C8	2.56	0.40
58:8:28:LEU:HD23	58:8:105:VAL:HG22	2.04	0.40
3:d:5:LEU:HD11	3:d:12:LEU:HD23	2.02	0.40
4:e:140:ILE:N	4:e:140:ILE:HD12	2.37	0.40
9:j:14:ASP:O	9:j:52:ASP:HB3	2.21	0.40
10:k:61:VAL:HG13	10:k:85:VAL:HB	2.02	0.40
11:l:38:GLN:HG3	53:1:805:G:C4'	2.51	0.40
15:p:38:ARG:CZ	52:3:345:C:H5'	2.52	0.40
18:s:36:LEU:HG	18:s:48:LYS:HB2	2.03	0.40
20:u:85:ARG:NH2	20:u:87:GLU:OE1	2.53	0.40
22:w:42:HIS:CD2	22:w:73:ARG:HD3	2.57	0.40
24:y:9:LYS:HZ2	24:y:11:VAL:HB	1.86	0.40
31:G:31:PHE:HB2	31:G:41:ASN:HA	2.03	0.40
31:G:45:THR:C	31:G:47:PRO:HD2	2.46	0.40
32:H:33:ASP:HB2	43:S:64:ARG:HD3	2.03	0.40
32:H:154:GLY:O	32:H:162:ALA:HA	2.22	0.40
35:K:23:GLU:HA	35:K:26:THR:HG22	2.04	0.40
38:N:47:VAL:HG12	38:N:78:ILE:HB	2.03	0.40
45:U:80:LYS:H	45:U:80:LYS:HG2	1.71	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:9:G:H2'	52:3:10:A:C8	2.56	0.40
52:3:58:C:O2'	52:3:59:A:H5'	2.22	0.40
52:3:68:G:H22	52:3:101:A:H2	1.69	0.40
52:3:90:C:H2'	52:3:91:U:C5	2.57	0.40
52:3:349:A:O2'	52:3:350:G:H5'	2.21	0.40
52:3:763:G:H2'	52:3:764:C:C6	2.56	0.40
53:1:565:C:O2'	53:1:566:U:H5'	2.21	0.40
53:1:880:G:H2'	53:1:881:G:H8	1.87	0.40
53:1:1297:C:OP1	53:1:2710:C:H4'	2.21	0.40
53:1:1566:A:O2'	53:1:1567:G:H5'	2.22	0.40
53:1:2286:G:C5'	53:1:2287:A:O4'	2.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	236 (88%)	32 (12%)	1 (0%)	30	60
2	c	207/209 (99%)	180 (87%)	24 (12%)	3 (1%)	9	37
3	d	199/201 (99%)	174 (87%)	21 (11%)	4 (2%)	6	32
4	e	175/177 (99%)	158 (90%)	17 (10%)	0	100	100
5	f	174/176 (99%)	159 (91%)	12 (7%)	3 (2%)	7	34
6	g	147/149 (99%)	130 (88%)	16 (11%)	1 (1%)	18	50
7	h	129/131 (98%)	94 (73%)	28 (22%)	7 (5%)	1	16
8	i	139/141 (99%)	120 (86%)	17 (12%)	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
11	l	141/143 (99%)	116 (82%)	23 (16%)	2 (1%)	9	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	m	134/136 (98%)	122 (91%)	9 (7%)	3 (2%)	5	31
13	n	118/120 (98%)	99 (84%)	18 (15%)	1 (1%)	16	48
14	o	114/116 (98%)	103 (90%)	10 (9%)	1 (1%)	14	45
15	p	112/114 (98%)	96 (86%)	16 (14%)	0	100	100
16	q	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
17	r	101/103 (98%)	84 (83%)	15 (15%)	2 (2%)	6	32
18	s	108/110 (98%)	94 (87%)	13 (12%)	1 (1%)	14	45
19	t	91/93 (98%)	81 (89%)	10 (11%)	0	100	100
20	u	100/102 (98%)	84 (84%)	12 (12%)	4 (4%)	2	21
21	v	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	w	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
23	x	75/77 (97%)	68 (91%)	6 (8%)	1 (1%)	9	38
24	y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	35
25	z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
26	B	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
27	C	48/50 (96%)	41 (85%)	6 (12%)	1 (2%)	5	31
28	D	44/46 (96%)	36 (82%)	7 (16%)	1 (2%)	5	30
29	E	62/64 (97%)	53 (86%)	7 (11%)	2 (3%)	3	25
30	F	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
31	G	223/225 (99%)	205 (92%)	18 (8%)	0	100	100
32	H	204/206 (99%)	189 (93%)	14 (7%)	1 (0%)	24	56
33	I	203/205 (99%)	173 (85%)	28 (14%)	2 (1%)	12	43
34	J	155/157 (99%)	129 (83%)	22 (14%)	4 (3%)	4	28
35	K	98/100 (98%)	77 (79%)	19 (19%)	2 (2%)	6	32
36	L	149/151 (99%)	135 (91%)	13 (9%)	1 (1%)	18	50
37	M	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	7	35
38	N	125/127 (98%)	99 (79%)	21 (17%)	5 (4%)	2	21
39	O	96/98 (98%)	74 (77%)	16 (17%)	6 (6%)	1	14
40	P	114/116 (98%)	93 (82%)	16 (14%)	5 (4%)	2	19
41	Q	121/123 (98%)	99 (82%)	15 (12%)	7 (6%)	1	15
42	R	112/114 (98%)	95 (85%)	14 (12%)	3 (3%)	4	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	S	98/100 (98%)	83 (85%)	14 (14%)	1 (1%)	12	43
44	T	86/88 (98%)	76 (88%)	9 (10%)	1 (1%)	10	40
45	U	80/82 (98%)	72 (90%)	6 (8%)	2 (2%)	4	29
46	V	78/80 (98%)	64 (82%)	12 (15%)	2 (3%)	4	28
47	W	63/65 (97%)	57 (90%)	6 (10%)	0	100	100
48	X	77/79 (98%)	60 (78%)	16 (21%)	1 (1%)	9	38
49	Y	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
50	Z	63/65 (97%)	41 (65%)	15 (24%)	7 (11%)	0	5
51	a	130/223 (58%)	130 (100%)	0	0	100	100
58	8	367/400 (92%)	344 (94%)	20 (5%)	3 (1%)	16	48
All	All	6286/6512 (96%)	5490 (87%)	696 (11%)	100 (2%)	10	35

All (100) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
5	f	45	ALA
5	f	174	LYS
6	g	9	VAL
7	h	108	VAL
7	h	118	ILE
9	j	81	ILE
12	m	58	LYS
17	r	54	VAL
24	y	24	GLU
27	C	45	HIS
28	D	42	LEU
29	E	31	ILE
38	N	90	ASP
41	Q	24	GLU
41	Q	75	GLU
42	R	4	ALA
44	T	46	LYS
46	V	17	GLU
46	V	50	ASN
3	d	93	SER
7	h	81	LEU
10	k	35	VAL

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Mol	Chain	Res	Type
10	k	110	GLU
11	l	85	VAL
12	m	69	PRO
20	u	51	LEU
20	u	97	SER
34	J	93	VAL
34	J	99	SER
35	K	86	ARG
36	L	18	GLY
38	N	91	GLU
39	O	35	GLN
41	Q	35	ARG
41	Q	77	SER
42	R	7	ASN
50	Z	14	ALA
50	Z	25	ALA
58	8	335	THR
5	f	175	LYS
7	h	91	ALA
12	m	6	ARG
18	s	3	THR
20	u	6	ARG
32	H	156	LEU
34	J	11	GLN
38	N	8	THR
38	N	57	VAL
38	N	125	GLN
39	O	43	PRO
40	P	92	ARG
41	Q	27	PRO
50	Z	9	GLU
1	b	107	LYS
2	c	149	ASN
8	i	11	GLN
11	l	87	GLY
13	n	32	GLU
14	o	34	HIS
20	u	56	GLY
23	x	31	ASN
33	I	167	PRO
37	M	47	ASP
39	O	34	ALA

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Mol	Chain	Res	Type
39	O	75	ASP
40	P	89	GLY
45	U	43	ALA
45	U	79	ASN
48	X	4	LEU
50	Z	65	ARG
50	Z	66	ARG
58	8	334	ARG
7	h	51	TYR
7	h	119	PRO
10	k	93	GLN
33	I	28	ASP
35	K	63	ASN
40	P	13	LYS
41	Q	33	CYS
2	c	58	ASN
3	d	92	HIS
34	J	102	THR
37	M	80	PRO
50	Z	12	ASP
58	8	114	PRO
3	d	75	SER
29	E	62	PRO
39	O	57	VAL
2	c	63	PRO
7	h	123	ILE
17	r	44	GLY
41	Q	3	VAL
39	O	33	GLY
40	P	90	PRO
50	Z	10	PRO
8	i	24	GLY
40	P	38	GLY
42	R	5	GLY
43	S	33	VAL

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	214 (99%)	2 (1%)	70	75
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	72
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	79
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	77
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	77
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	75
7	h	100/100 (100%)	98 (98%)	2 (2%)	48	64
8	i	109/109 (100%)	108 (99%)	1 (1%)	70	75
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	74
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	72
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	74
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	72
18	s	93/93 (100%)	91 (98%)	2 (2%)	45	63
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	78 (100%)	0	100	100
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	185 (100%)	1 (0%)	81	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	79
33	I	172/172 (100%)	169 (98%)	3 (2%)	53	67
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	76
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	73
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	74
38	N	105/105 (100%)	103 (98%)	2 (2%)	50	65
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	62
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	82 (99%)	1 (1%)	63	72
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	64 (98%)	1 (2%)	57	68
50	Z	55/55 (100%)	51 (93%)	4 (7%)	13	40
51	a	110/174 (63%)	110 (100%)	0	100	100
58	8	304/332 (92%)	302 (99%)	2 (1%)	76	77
All	All	5212/5304 (98%)	5175 (99%)	37 (1%)	73	77

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	140	VAL
1	b	153	LEU
2	c	180	VAL
2	c	200	ASP
3	d	149	ILE
4	e	174	PHE
5	f	35	THR
6	g	124	THR
7	h	118	ILE

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Mol	Chain	Res	Type
7	h	119	PRO
8	i	115	ASP
10	k	69	VAL
14	o	28	VAL
15	p	83	ILE
17	r	54	VAL
18	s	71	VAL
18	s	77	ASP
31	G	150	ILE
32	H	156	LEU
33	I	8	LEU
33	I	33	ILE
33	I	97	LEU
34	J	55	VAL
35	K	39	LEU
37	M	13	ILE
38	N	52	GLU
38	N	60	LEU
39	O	17	LEU
39	O	42	LEU
43	S	88	MET
49	Y	39	GLU
50	Z	10	PRO
50	Z	37	TYR
50	Z	40	PRO
50	Z	59	LEU
58	8	23	HIS
58	8	375	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (118) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	14	HIS
1	b	45	ASN
1	b	52	HIS
1	b	69	ASN
1	b	85	ASN
1	b	89	ASN
1	b	242	HIS
1	b	259	ASN
2	c	58	ASN
2	c	136	ASN

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Mol	Chain	Res	Type
2	c	149	ASN
2	c	164	GLN
3	d	24	ASN
3	d	30	GLN
3	d	41	GLN
3	d	97	ASN
3	d	115	GLN
3	d	163	ASN
4	e	26	GLN
5	f	21	GLN
5	f	29	ASN
5	f	37	ASN
5	f	44	HIS
5	f	100	ASN
5	f	110	HIS
6	g	11	ASN
6	g	28	ASN
6	g	43	ASN
6	g	66	ASN
6	g	119	ASN
8	i	11	GLN
8	i	110	GLN
9	j	40	HIS
9	j	58	ASN
9	j	80	HIS
9	j	135	GLN
10	k	5	GLN
10	k	9	ASN
11	l	99	ASN
11	l	104	GLN
12	m	3	GLN
12	m	45	GLN
13	n	18	GLN
13	n	62	ASN
13	n	81	ASN
14	o	19	GLN
14	o	38	GLN
14	o	100	HIS
14	o	104	GLN
15	p	6	GLN
15	p	9	GLN
15	p	11	GLN

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Mol	Chain	Res	Type
15	p	76	HIS
16	q	65	ASN
17	r	6	GLN
17	r	12	HIS
18	s	60	HIS
19	t	70	HIS
20	u	98	ASN
21	v	24	ASN
21	v	78	GLN
21	v	88	HIS
22	w	8	ASN
24	y	27	ASN
24	y	31	GLN
24	y	58	ASN
29	E	27	ASN
31	G	23	ASN
31	G	145	ASN
31	G	176	ASN
32	H	5	HIS
32	H	122	GLN
32	H	138	GLN
32	H	139	ASN
33	I	40	HIS
33	I	88	ASN
33	I	130	ASN
33	I	151	GLN
33	I	195	ASN
34	J	81	GLN
34	J	134	ASN
36	L	67	ASN
36	L	121	ASN
37	M	3	GLN
37	M	15	ASN
37	M	66	GLN
38	N	31	GLN
38	N	49	GLN
38	N	109	GLN
39	O	15	HIS
39	O	35	GLN
40	P	37	GLN
41	Q	5	GLN
41	Q	45	ASN

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Mol	Chain	Res	Type
43	S	42	ASN
43	S	65	GLN
44	T	34	GLN
45	U	29	ASN
45	U	40	ASN
46	V	30	HIS
46	V	49	ASN
49	Y	2	ASN
49	Y	20	ASN
49	Y	51	ASN
49	Y	60	GLN
49	Y	67	HIS
49	Y	69	ASN
51	a	47	ASN
51	a	188	ASN
58	8	14	ASN
58	8	52	ASN
58	8	79	HIS
58	8	85	HIS
58	8	98	GLN
58	8	115	GLN
58	8	160	GLN
58	8	291	GLN
58	8	365	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	133 (8%)	4 (0%)
53	1	2902/2903 (99%)	324 (11%)	9 (0%)
54	2	119/120 (99%)	10 (8%)	2 (1%)
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	7 (9%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	14 (18%)	0
All	All	4803/4810 (99%)	497 (10%)	15 (0%)

All (497) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G

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Mol	Chain	Res	Type
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	50	A
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	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	497	G
52	3	518	C
52	3	531	U
52	3	532	A

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Mol	Chain	Res	Type
52	3	547	A
52	3	561	U
52	3	572	A
52	3	573	A
52	3	575	G
52	3	576	C
52	3	577	G
52	3	633	G
52	3	642	A
52	3	653	U
52	3	665	A
52	3	688	G
52	3	703	G
52	3	724	G
52	3	755	G
52	3	777	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	821	G
52	3	836	G
52	3	843	U
52	3	844	G
52	3	846	G
52	3	890	G
52	3	902	G
52	3	926	G
52	3	934	C
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1030	U

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Mol	Chain	Res	Type
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1094	G
52	3	1101	A
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1198	G
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1258	G
52	3	1260	G
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1378	C
52	3	1395	C
52	3	1446	A
52	3	1448	C
52	3	1452	C
52	3	1492	A
52	3	1494	G
52	3	1503	A

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Mol	Chain	Res	Type
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	50	U
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A
53	1	75	G
53	1	114	U
53	1	119	A
53	1	120	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	216	A
53	1	221	A
53	1	222	A
53	1	229	C
53	1	248	G
53	1	249	C
53	1	255	A
53	1	265	A
53	1	266	G
53	1	276	U
53	1	278	A
53	1	281	C
53	1	294	A
53	1	301	G
53	1	311	A

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Mol	Chain	Res	Type
53	1	323	C
53	1	324	A
53	1	329	G
53	1	330	A
53	1	361	G
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	424	G
53	1	451	U
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	531	C
53	1	532	A
53	1	543	G
53	1	563	A
53	1	572	A
53	1	573	U
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	646	U
53	1	654	A
53	1	669	G
53	1	686	U
53	1	687	C
53	1	695	G
53	1	730	A
53	1	747	C
53	1	748	G
53	1	752	A

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Mol	Chain	Res	Type
53	1	764	A
53	1	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	805	G
53	1	812	C
53	1	819	A
53	1	822	G
53	1	827	U
53	1	828	U
53	1	830	G
53	1	845	A
53	1	846	U
53	1	847	U
53	1	858	G
53	1	859	G
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

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Mol	Chain	Res	Type
53	1	1060	U
53	1	1062	G
53	1	1066	U
53	1	1069	A
53	1	1070	A
53	1	1071	G
53	1	1079	C
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	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	1250	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A
53	1	1289	C
53	1	1301	A
53	1	1314	C
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1395	A

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Mol	Chain	Res	Type
53	1	1398	C
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1454	C
53	1	1461	C
53	1	1476	U
53	1	1482	G
53	1	1490	A
53	1	1491	G
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1533	C
53	1	1535	A
53	1	1536	C
53	1	1537	G
53	1	1555	G
53	1	1559	U
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1584	U
53	1	1585	C
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1800	C
53	1	1801	A
53	1	1802	A
53	1	1808	A

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Mol	Chain	Res	Type
53	1	1816	C
53	1	1829	A
53	1	1833	C
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	1929	G
53	1	1930	G
53	1	1937	A
53	1	1938	A
53	1	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	2072	C
53	1	2096	C
53	1	2098	U
53	1	2110	G
53	1	2111	U
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A

Continued on next page...

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Mol	Chain	Res	Type
53	1	2132	U
53	1	2133	G
53	1	2145	C
53	1	2147	A
53	1	2162	G
53	1	2171	A
53	1	2172	U
53	1	2173	A
53	1	2189	U
53	1	2198	A
53	1	2204	G
53	1	2213	U
53	1	2225	A
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	2407	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

Continued on next page...

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Mol	Chain	Res	Type
53	1	2518	A
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2609	U
53	1	2613	U
53	1	2646	C
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U
53	1	2714	G
53	1	2744	G
53	1	2748	A
53	1	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	2880	C
54	2	4	C
54	2	12	C
54	2	13	G
54	2	24	G
54	2	35	C
54	2	44	G

Continued on next page...

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Mol	Chain	Res	Type
54	2	67	G
54	2	89	U
54	2	90	C
54	2	109	A
55	5	9	G
55	5	18	G
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	61	C
55	6	6	G
55	6	18	G
55	6	19	G
55	6	20	U
55	6	47	U
55	6	48	C
55	6	61	C
56	4	12	A
56	4	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 (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	70	U
52	3	421	U
52	3	1190	G
52	3	1201	A

Continued on next page...

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Mol	Chain	Res	Type
53	1	490	C
53	1	1020	A
53	1	1130	U
53	1	1475	G
53	1	2286	G
53	1	2296	U
53	1	2326	C
53	1	2391	G
53	1	2756	U
54	2	66	A
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	$\# Z > 2$
59	FME	5	101	55	8,9,10	0.49	0	8,9,11	1.11	1 (12%)
60	PHE	7	101	57	10,11,12	0.71	0	8,13,15	0.23	0
61	GDP	8	501	-	29,30,30	1.43	3 (10%)	45,47,47	2.15	15 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	FME	5	101	55	-	1/7/9/11	-
60	PHE	7	101	57	-	1/5/6/8	0/1/1/1
61	GDP	8	501	-	-	4/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PA-O3A	3.70	1.63	1.59
61	8	501	GDP	PA-O1A	3.23	1.62	1.50
61	8	501	GDP	PB-O2B	2.28	1.63	1.54

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	C2-N3-C4	5.59	121.92	112.30
61	8	501	GDP	C5-C4-N3	-5.53	119.58	128.39
61	8	501	GDP	O3B-PB-O1B	4.34	127.73	110.83
61	8	501	GDP	N9-C4-N3	4.03	134.02	125.95
61	8	501	GDP	O3B-PB-O2B	-3.92	93.09	107.80
61	8	501	GDP	O3B-PB-O3A	-3.21	93.89	104.64
61	8	501	GDP	C8-N7-C5	2.98	109.58	104.26
61	8	501	GDP	O4'-C4'-C3'	2.65	110.42	105.15
61	8	501	GDP	O2B-PB-O1B	2.65	121.15	110.83
61	8	501	GDP	C6-C5-N7	2.65	135.10	130.29
61	8	501	GDP	C2-N1-C6	-2.44	120.69	125.11
61	8	501	GDP	C4-C5-N7	-2.35	106.95	110.67
59	5	101	FME	O-C-CA	-2.21	119.09	124.77
61	8	501	GDP	O6-C6-C5	-2.20	120.72	126.53
61	8	501	GDP	C5-C6-N1	2.18	118.80	113.25
61	8	501	GDP	O2A-PA-O5'	-2.07	98.17	107.57

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
60	7	101	PHE	O-C-CA-CB
61	8	501	GDP	PA-O3A-PB-O2B
61	8	501	GDP	O4'-C4'-C5'-O5'
61	8	501	GDP	C3'-C4'-C5'-O5'

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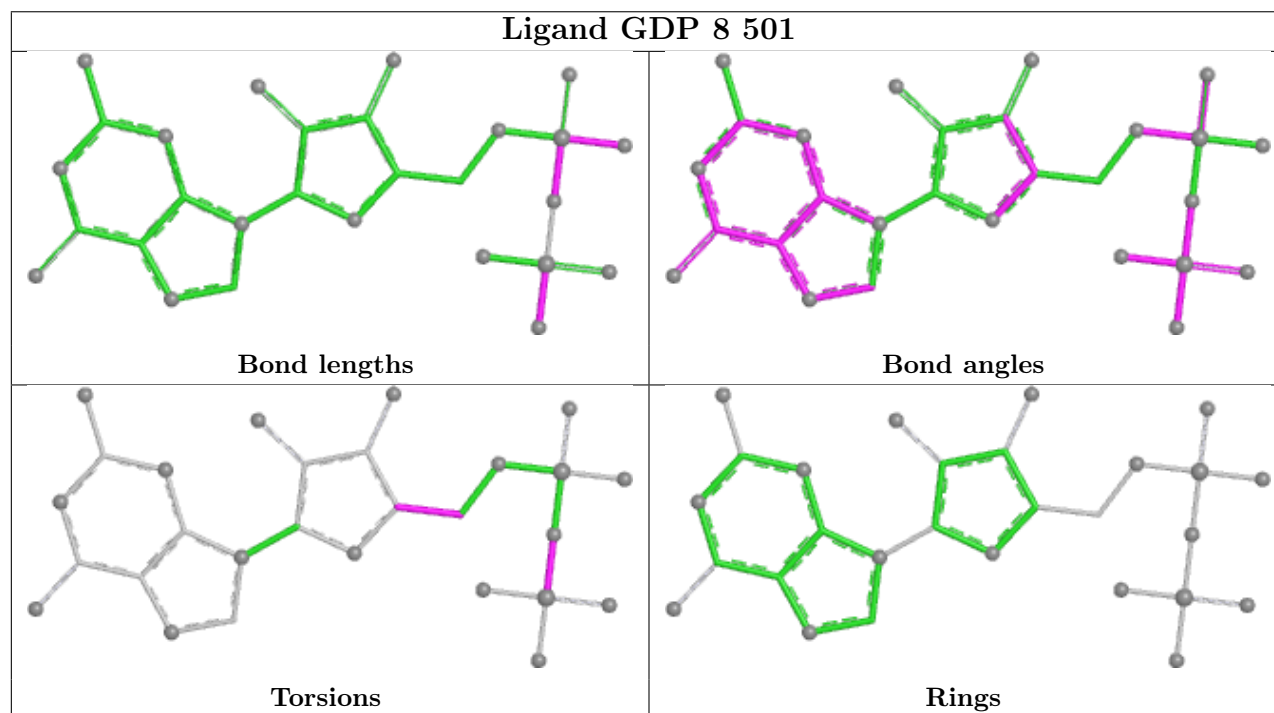
Mol	Chain	Res	Type	Atoms
61	8	501	GDP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	101	PHE	3	0

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

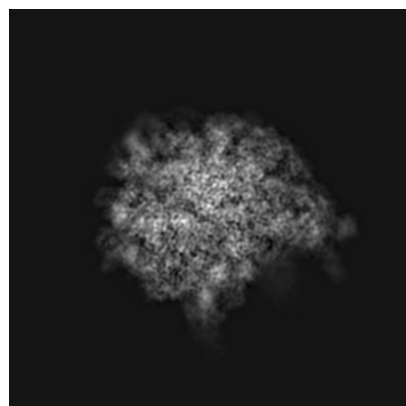
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21625. These allow visual inspection of the internal detail of the map and identification of artifacts.

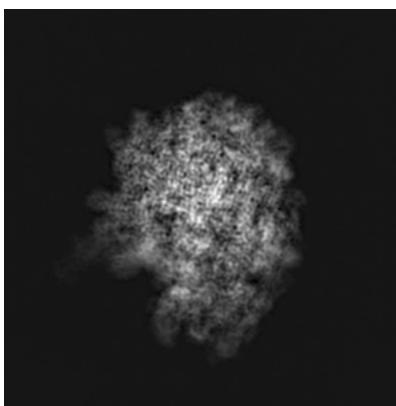
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

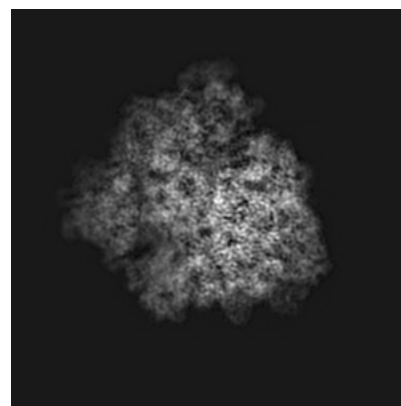
6.1.1 Primary map



X

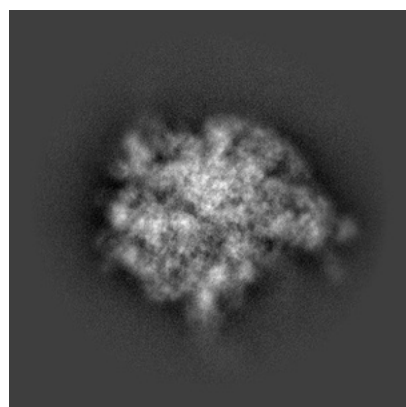


Y

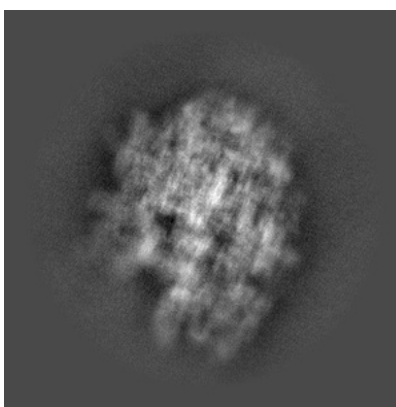


Z

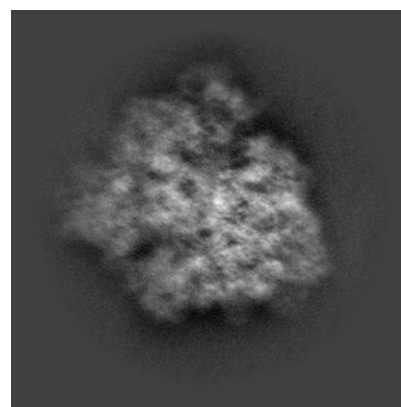
6.1.2 Raw map



X



Y

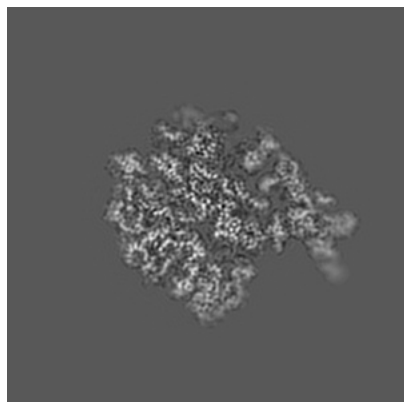


Z

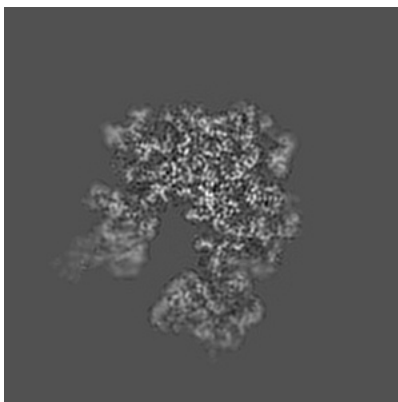
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

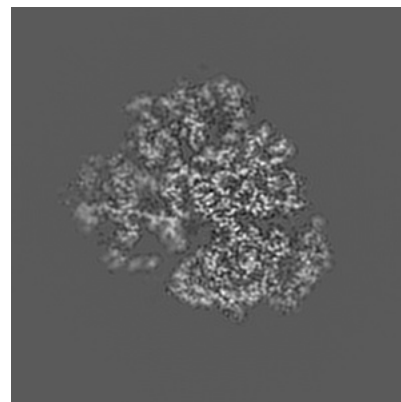
6.2.1 Primary map



X Index: 144

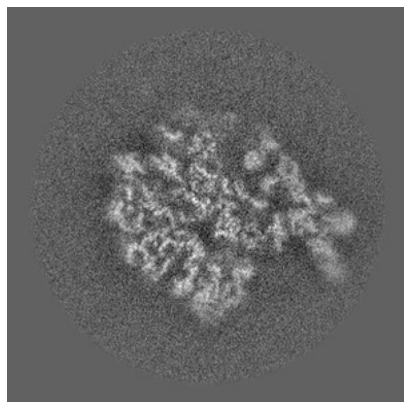


Y Index: 144

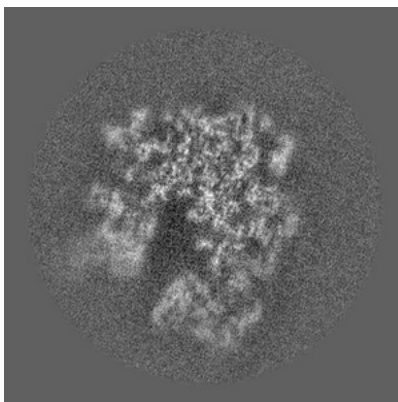


Z Index: 144

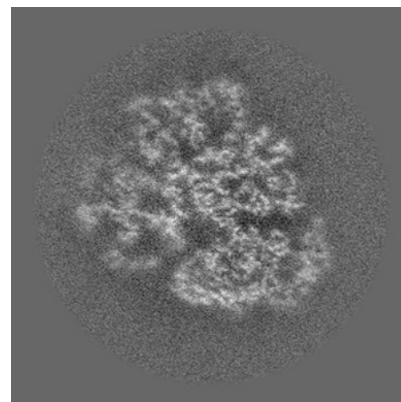
6.2.2 Raw map



X Index: 144



Y Index: 144

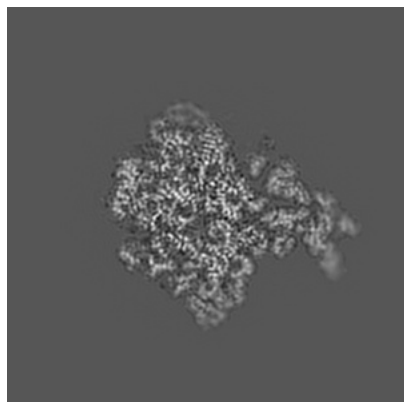


Z Index: 144

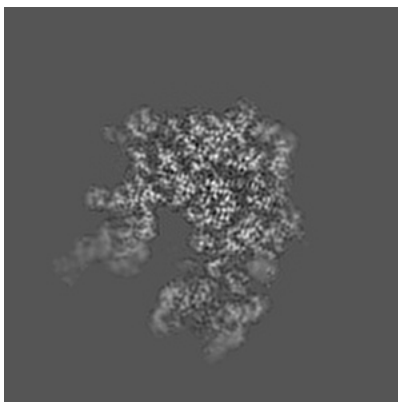
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

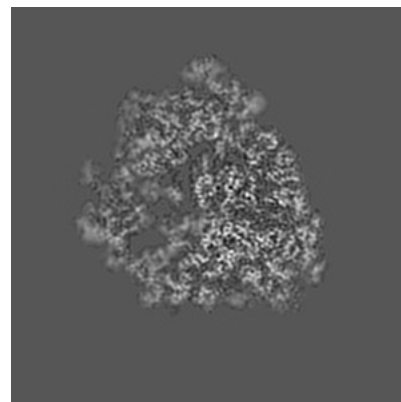
6.3.1 Primary map



X Index: 149

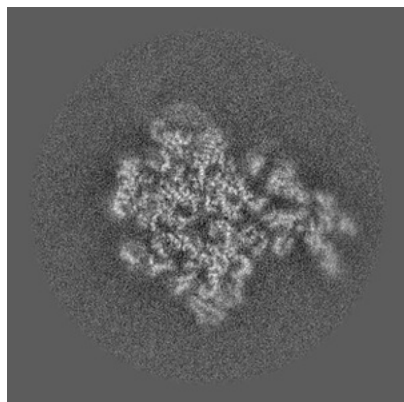


Y Index: 148

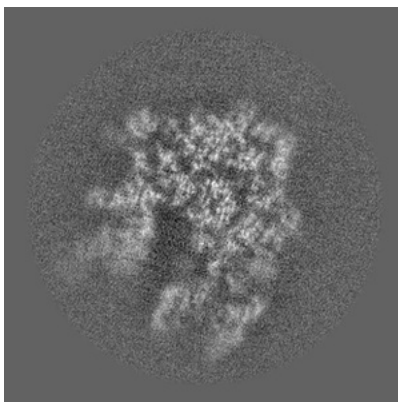


Z Index: 135

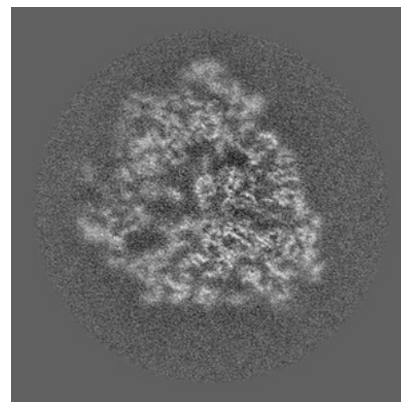
6.3.2 Raw map



X Index: 149



Y Index: 148

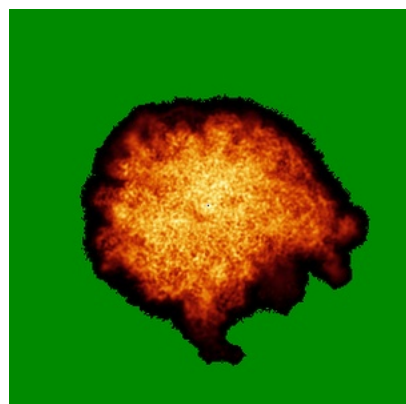


Z Index: 135

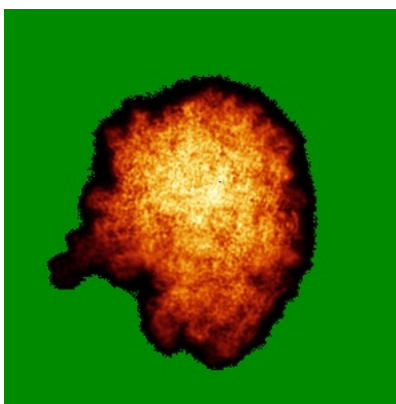
The images above show the largest variance slices of the map in three orthogonal directions.

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

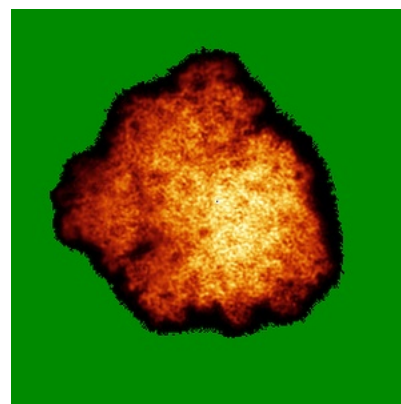
6.4.1 Primary map



X

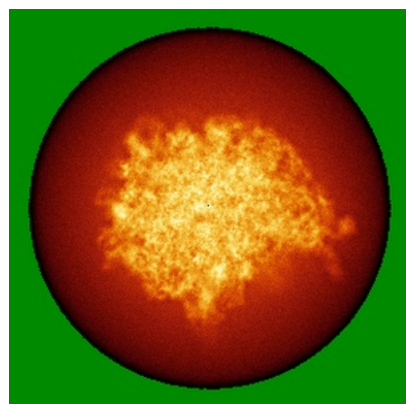


Y

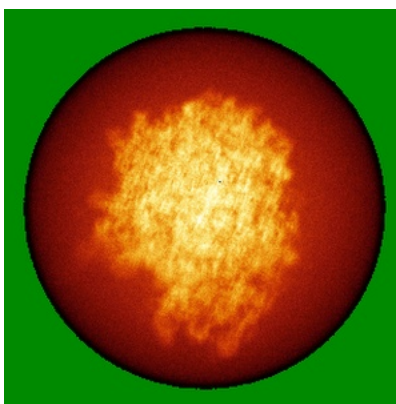


Z

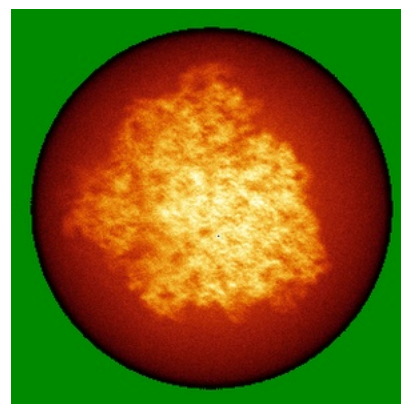
6.4.2 Raw map



X



Y

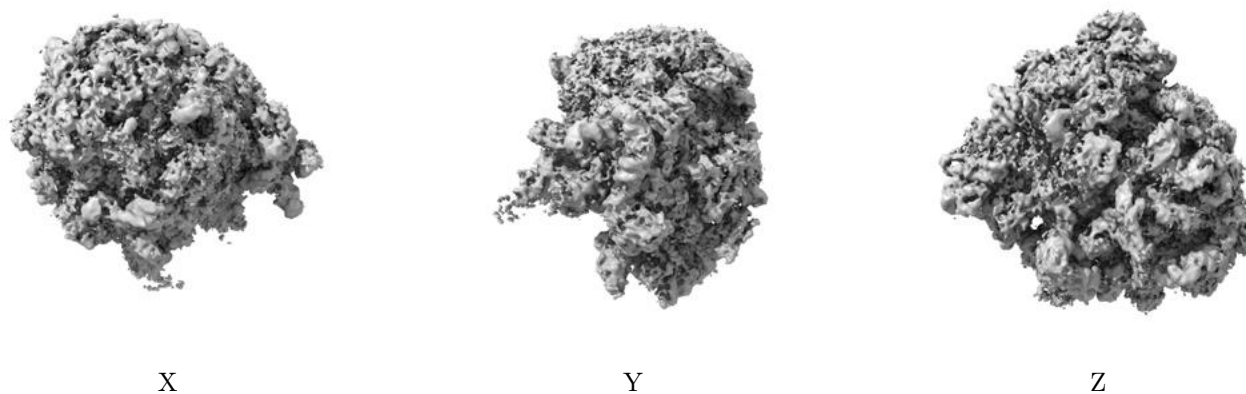


Z

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.

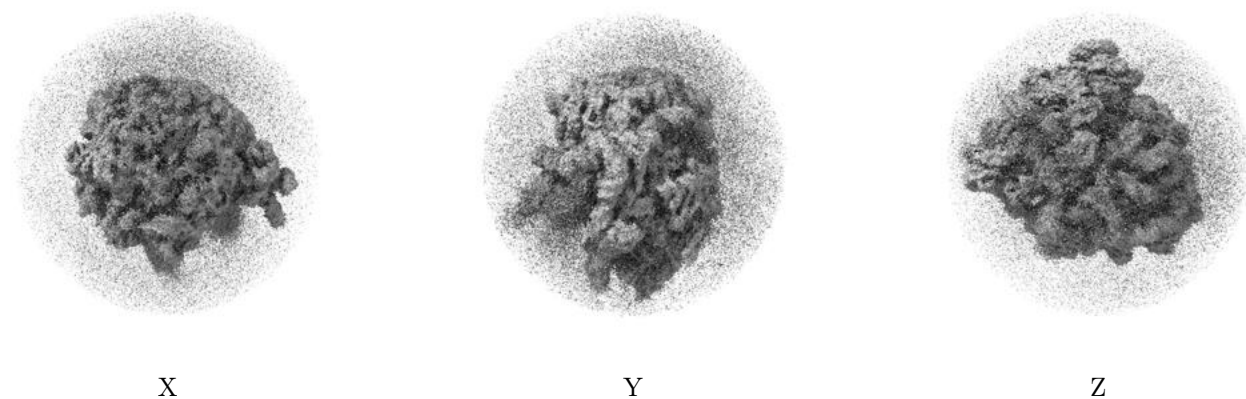
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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

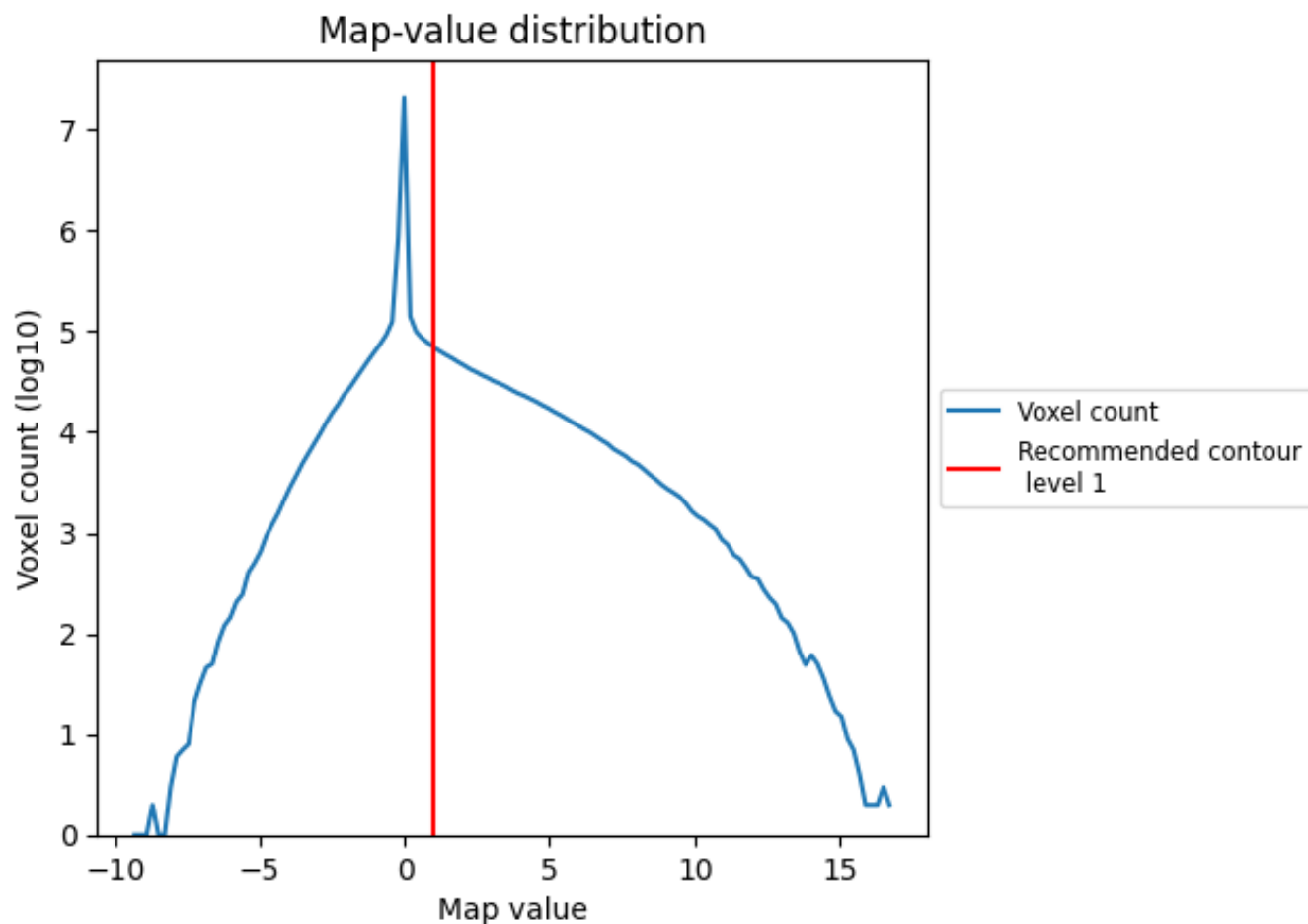
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

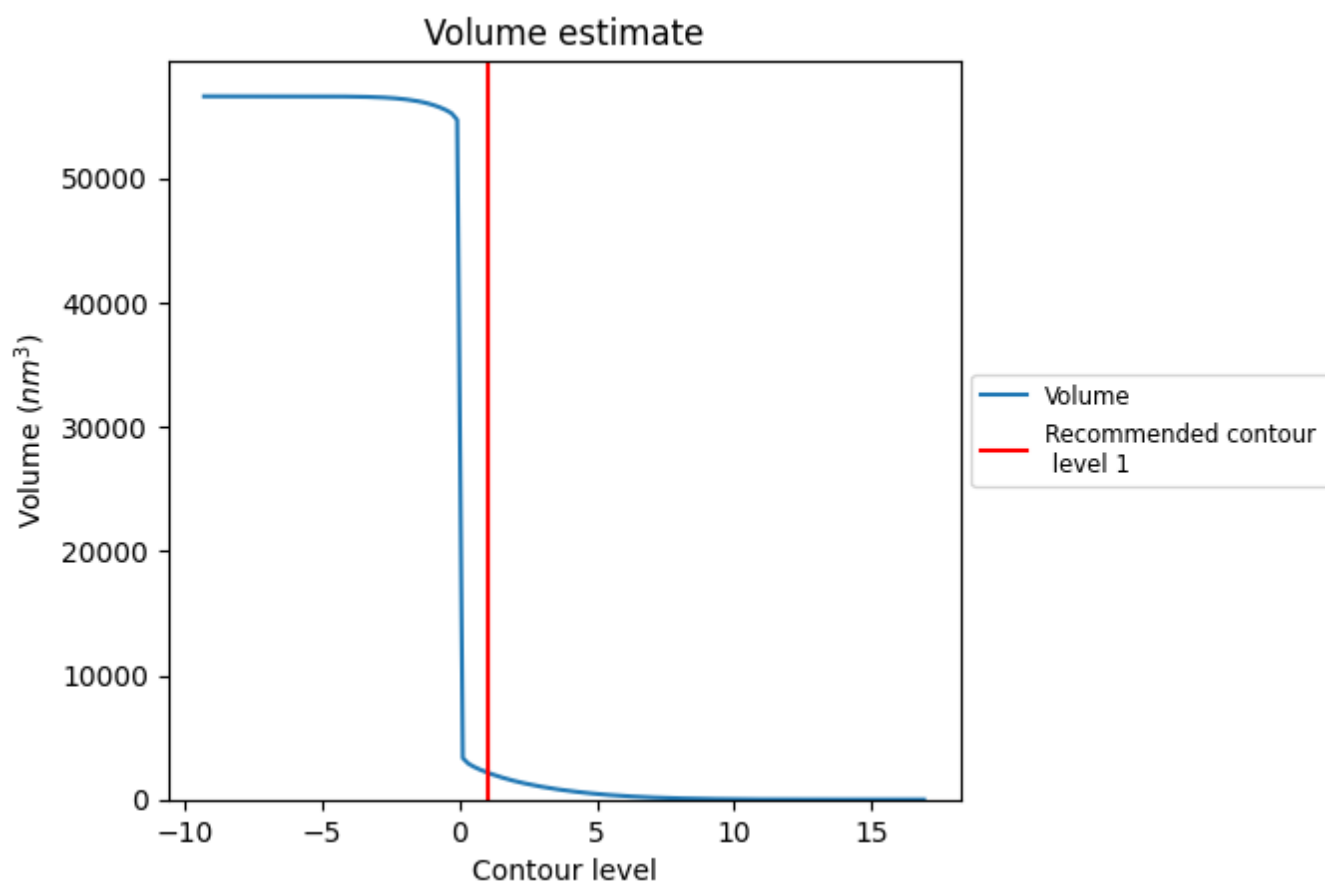
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

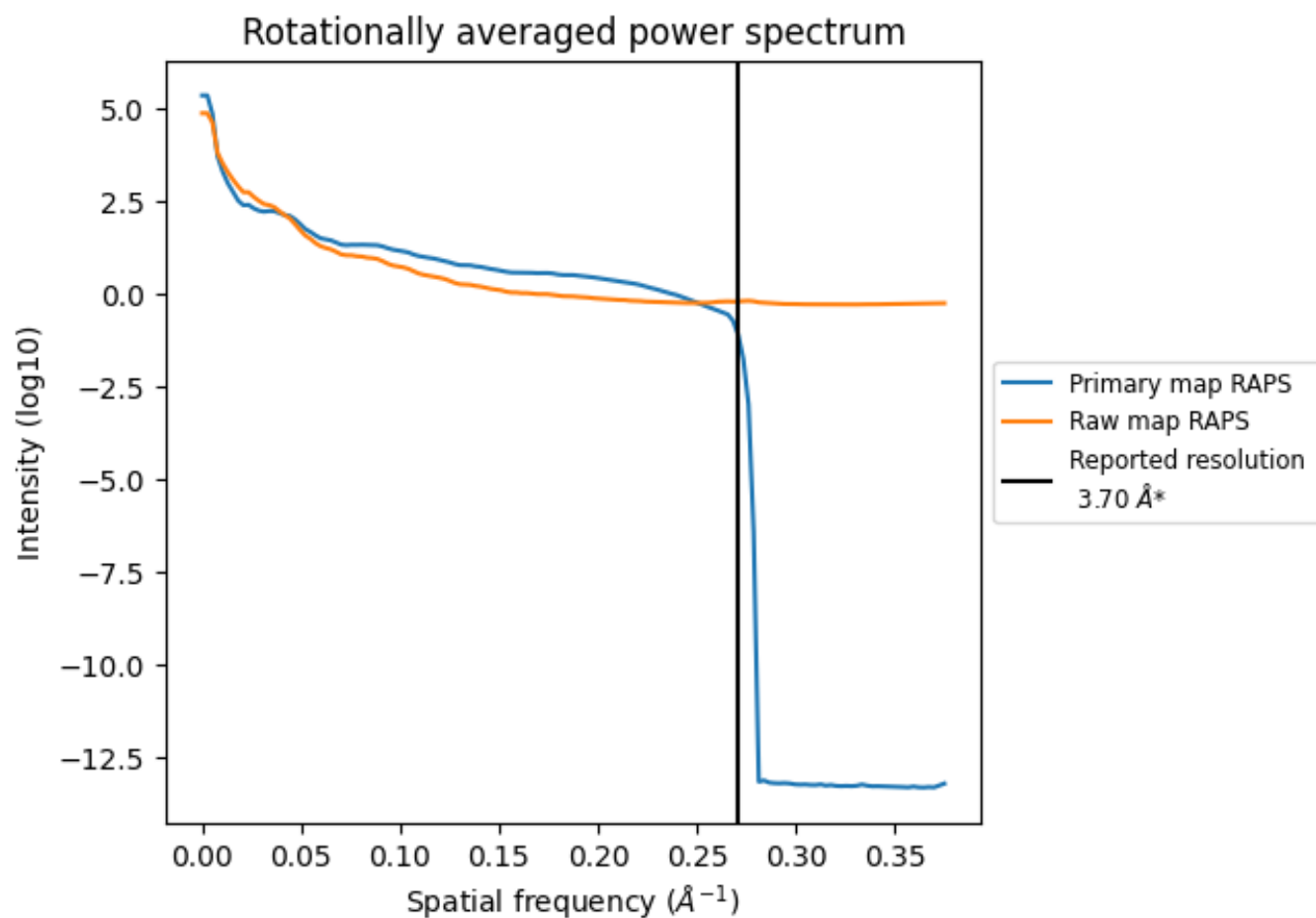
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2183 nm³; this corresponds to an approximate mass of 1972 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 ⓘ

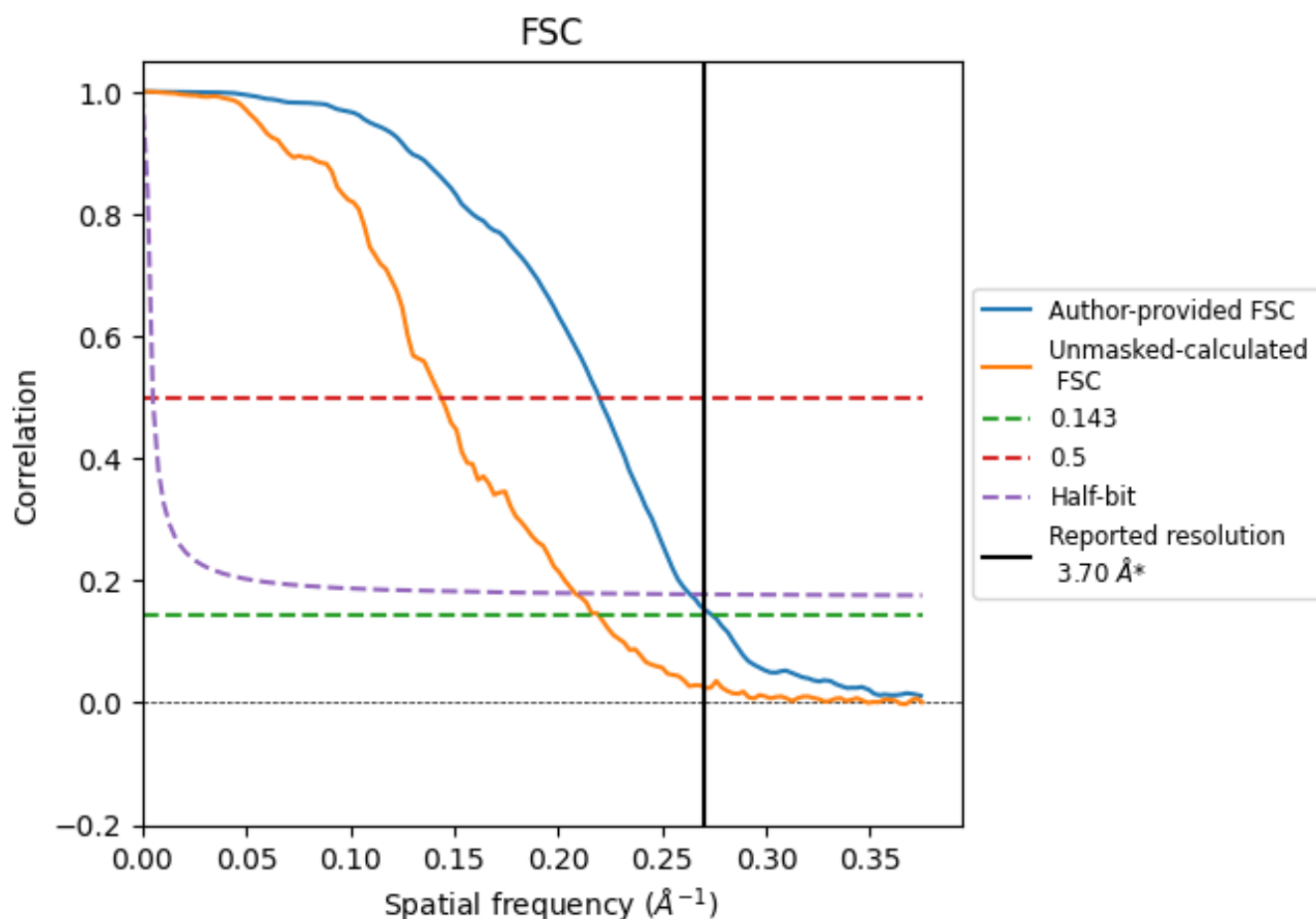


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

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](#)

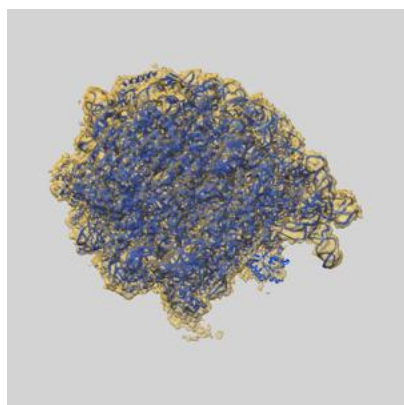
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.65	4.55	3.80
Unmasked-calculated*	4.56	6.96	4.80

*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 4.56 differs from the reported value 3.7 by more than 10 %

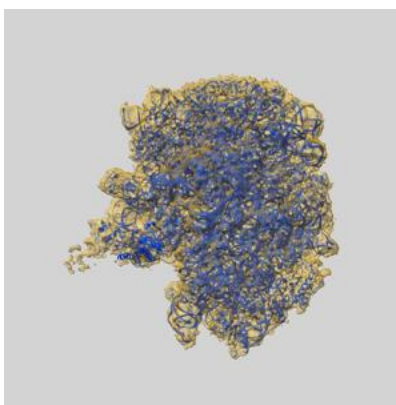
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21625 and PDB model 6WD6. Per-residue inclusion information can be found in section [3](#) on page [17](#).

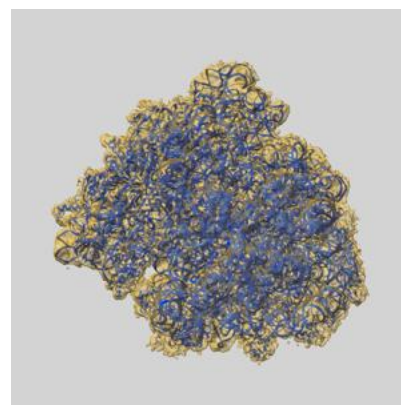
9.1 Map-model overlay [i](#)



X



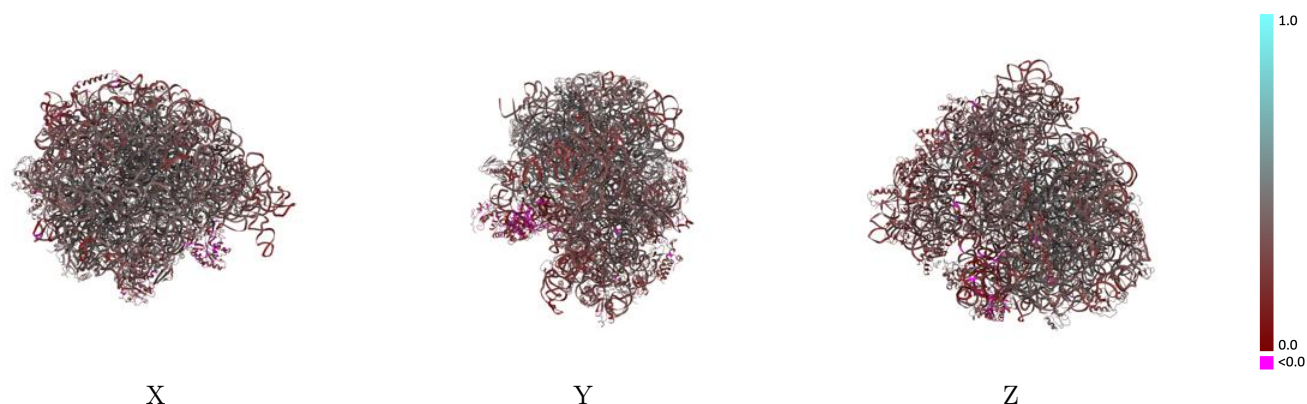
Y



Z

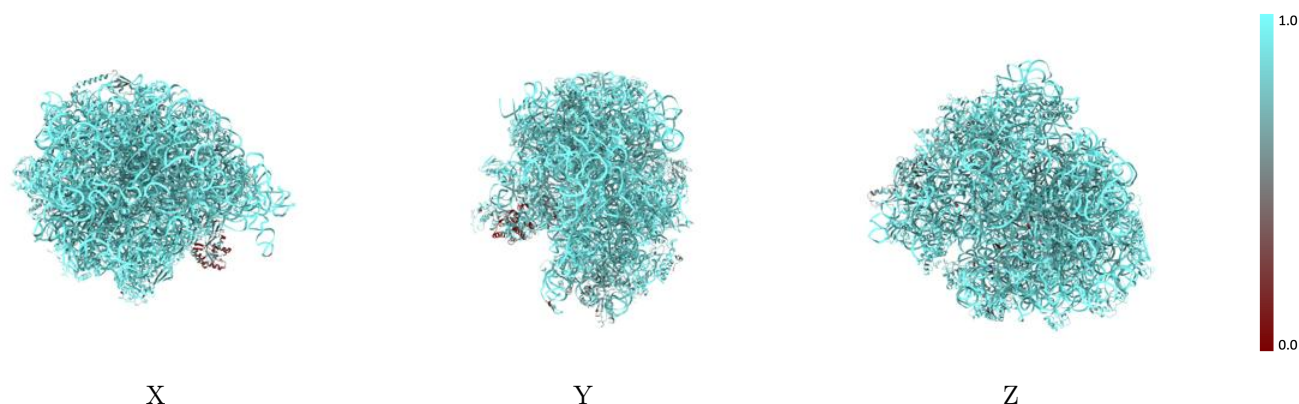
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



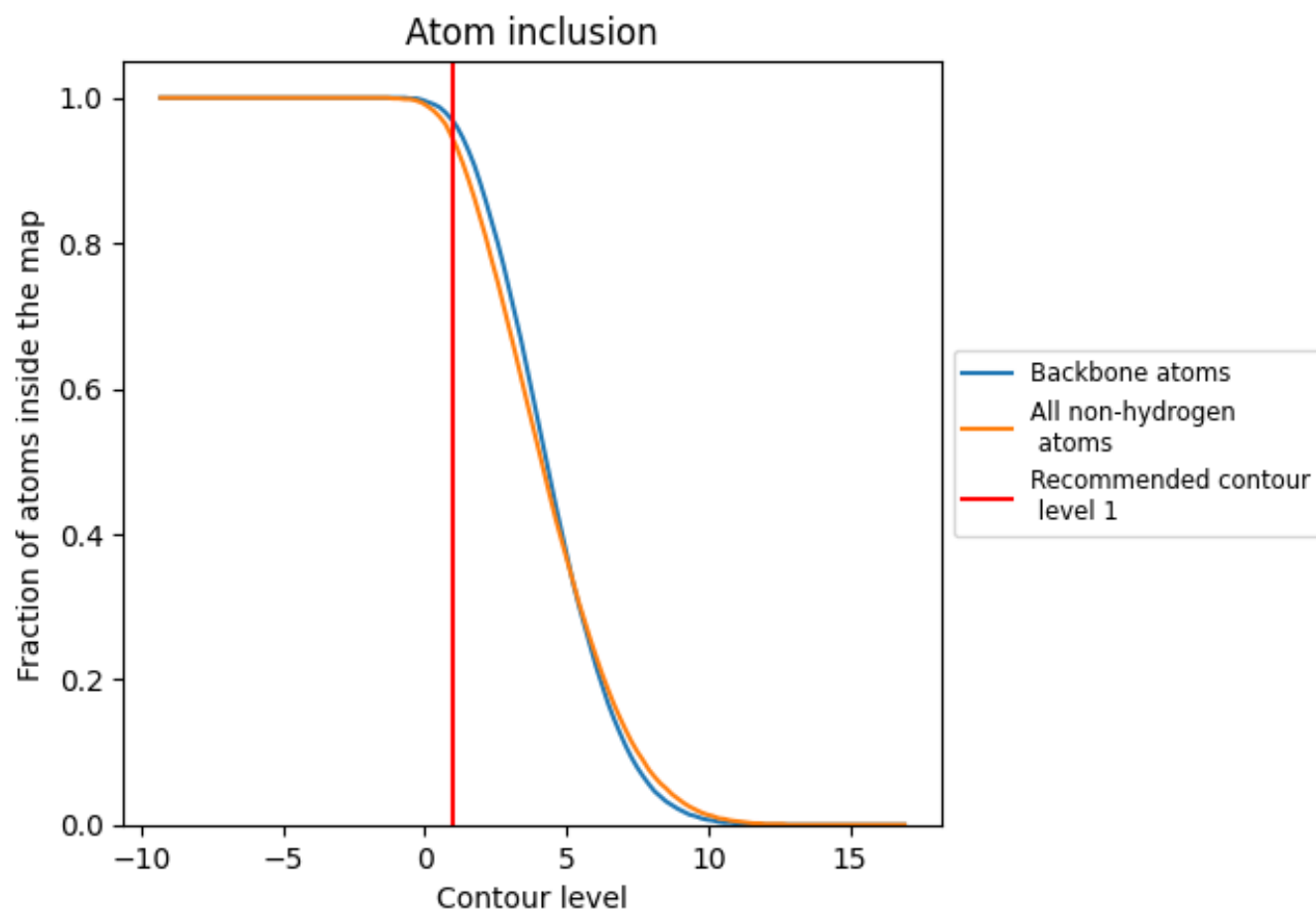
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% 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	 0.9430	 0.3450
1	 0.9820	 0.3710
2	 0.9830	 0.3330
3	 0.9740	 0.3330
4	 0.8840	 0.2180
5	 0.9640	 0.2920
6	 0.8310	 0.1480
7	 0.9040	 0.1590
8	 0.6280	 0.1350
B	 0.9350	 0.4230
C	 0.8480	 0.3640
D	 0.9070	 0.4310
E	 0.9250	 0.4420
F	 0.8360	 0.3810
G	 0.8570	 0.3060
H	 0.7050	 0.2990
I	 0.8580	 0.2940
J	 0.9120	 0.3690
K	 0.9450	 0.3380
L	 0.9070	 0.2980
M	 0.9160	 0.3650
N	 0.8650	 0.2790
O	 0.6800	 0.2750
P	 0.9470	 0.3800
Q	 0.9090	 0.3920
R	 0.9060	 0.2870
S	 0.7380	 0.2750
T	 0.9350	 0.3690
U	 0.8840	 0.3670
V	 0.9130	 0.3710
W	 0.9150	 0.3430
X	 0.9530	 0.2710
Y	 0.8690	 0.3290
Z	 0.8360	 0.2720
a	 0.8090	 0.1420



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Chain	Atom inclusion	Q-score
b	 0.9480	 0.4470
c	 0.9430	 0.4320
d	 0.9330	 0.3870
e	 0.9290	 0.3030
f	 0.9540	 0.3330
g	 0.7820	 0.2630
h	 0.7710	 0.1500
i	 0.7100	 0.1490
j	 0.9390	 0.4230
k	 0.9120	 0.4410
l	 0.9470	 0.4190
m	 0.9250	 0.4190
n	 0.9310	 0.4220
o	 0.9260	 0.3360
p	 0.9360	 0.4190
q	 0.9380	 0.4210
r	 0.9570	 0.4110
s	 0.9070	 0.4250
t	 0.9460	 0.4130
u	 0.9280	 0.3580
v	 0.9570	 0.3880
w	 0.9280	 0.4320
x	 0.9380	 0.4250
y	 0.9150	 0.3060
z	 0.9290	 0.4060