



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 06:01 AM UTC

PDB ID : 6WDA / pdb_00006wda
EMDB ID : EMD-21629
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure III-C)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.80 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

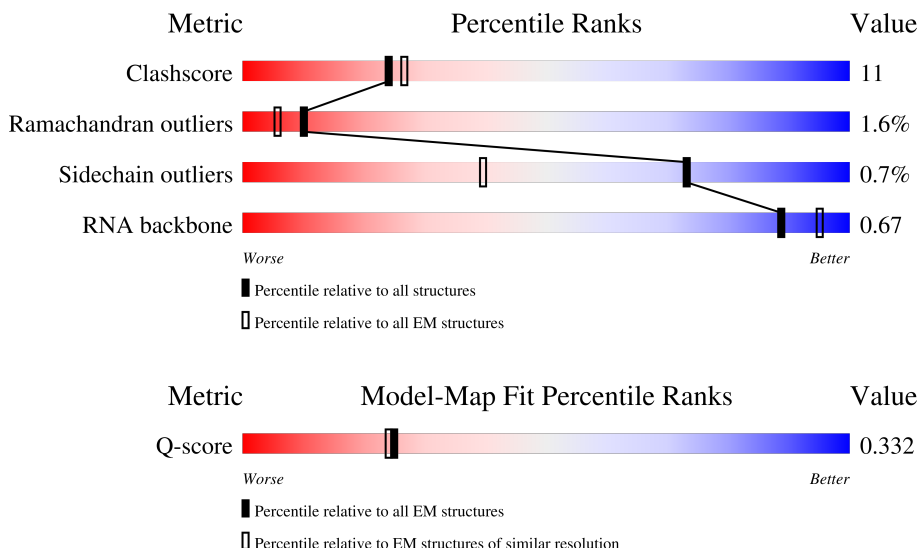
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.



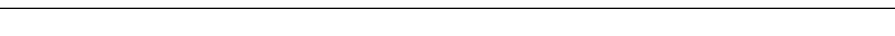
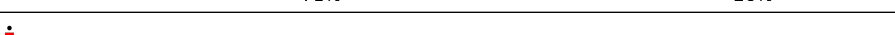
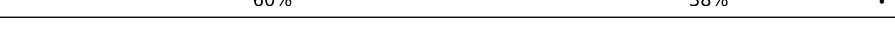
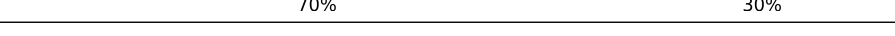
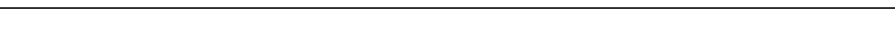
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	

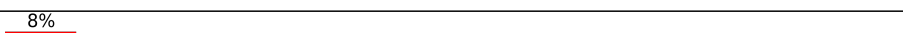
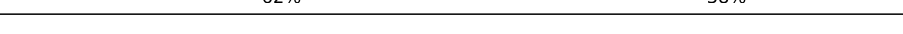
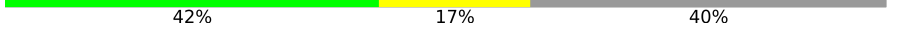
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
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	51%44%5%
55	5	77	64%32%.•
55	6	77	5% 55%39%6%
56	4	18	6% 61%39%
57	7	76	• 55%38%7%
58	8	400	20% 58%28%.13%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 152933 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1370526515

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

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

- Molecule 56 is a RNA chain called mRNA.

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

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

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

- Molecule 58 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	348	Total	C	N	O	S	0	0
			2683	1702	459	509	13		

There are 7 discrepancies between the modelled and reference sequences:

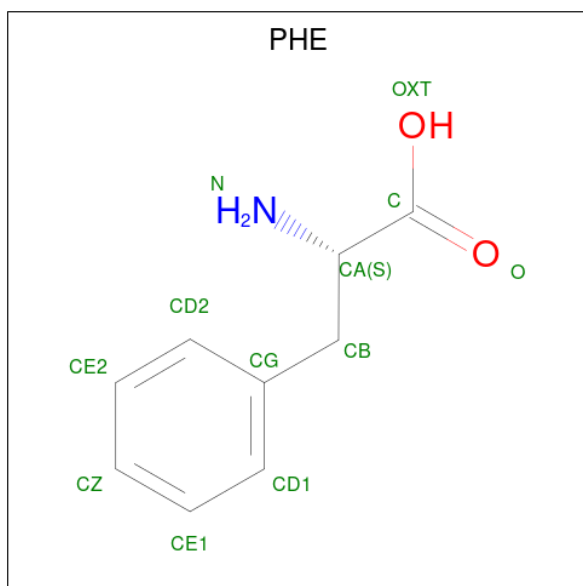
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag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

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



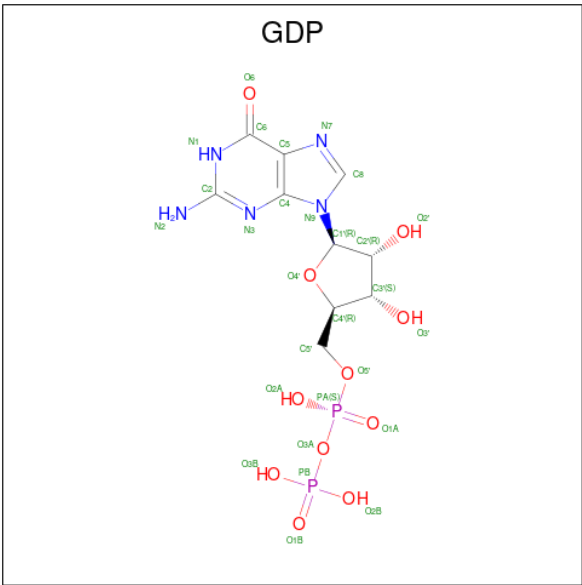
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

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

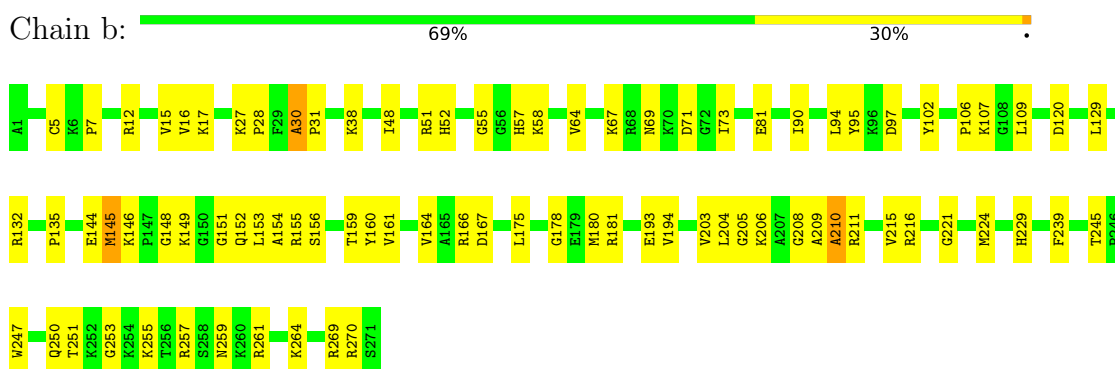


Mol	Chain	Residues	Atoms					AltConf
61	8	1	Total	C	N	O	P	0
			28	10	5	11	2	

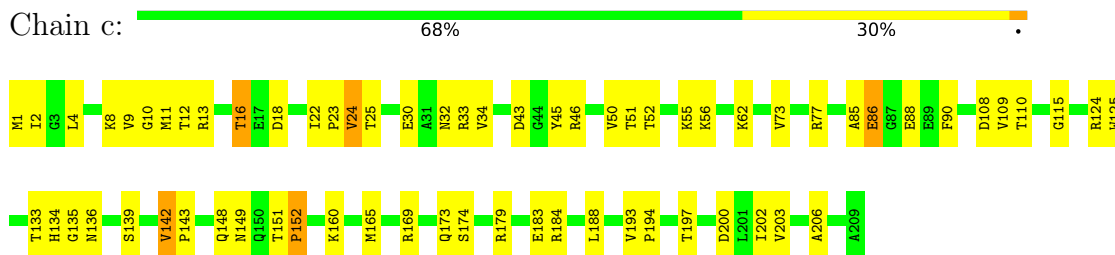
3 Residue-property plots

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.

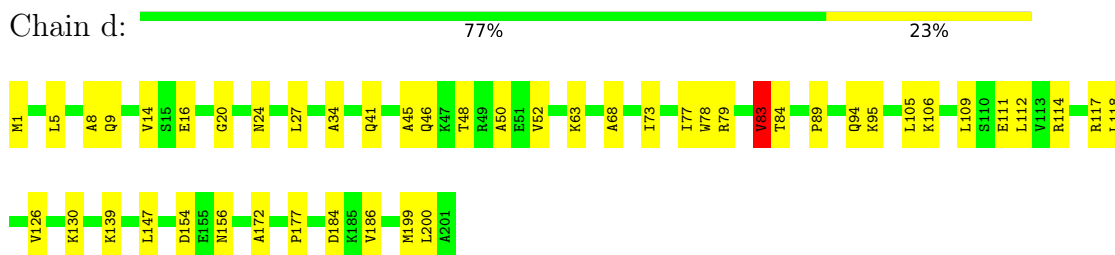
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

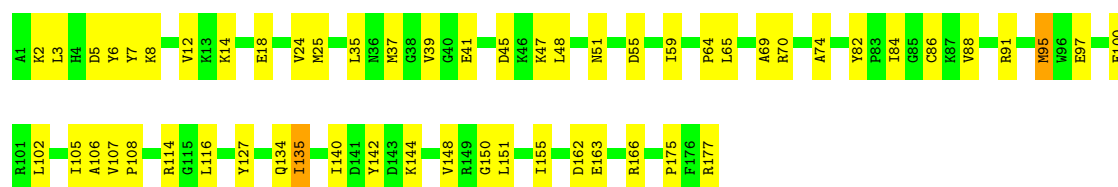


- Molecule 3: 50S ribosomal protein L4

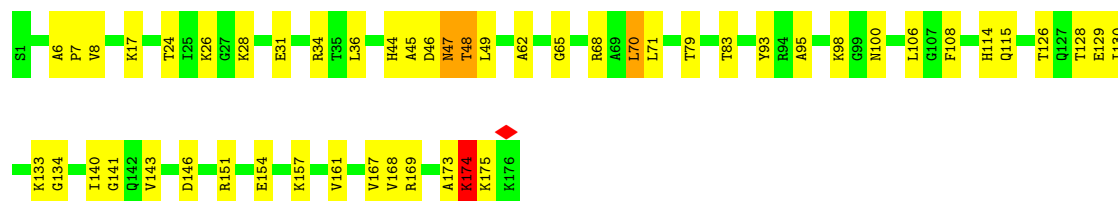


- Molecule 4: 50S ribosomal protein L5

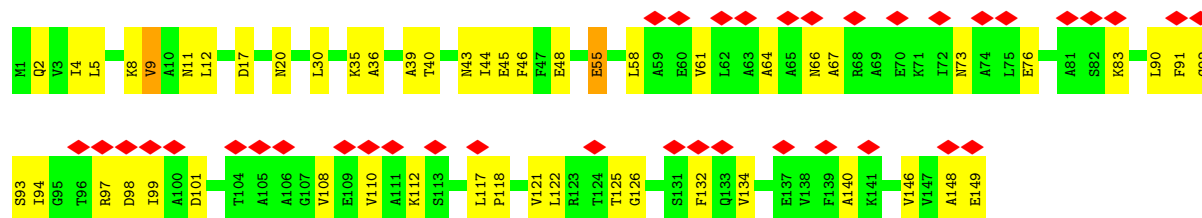




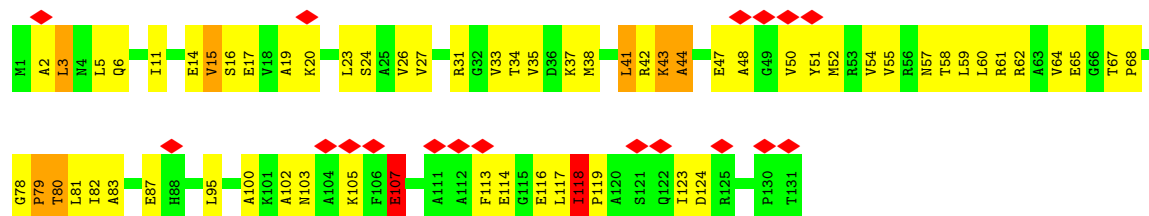
• Molecule 5: 50S ribosomal protein L6



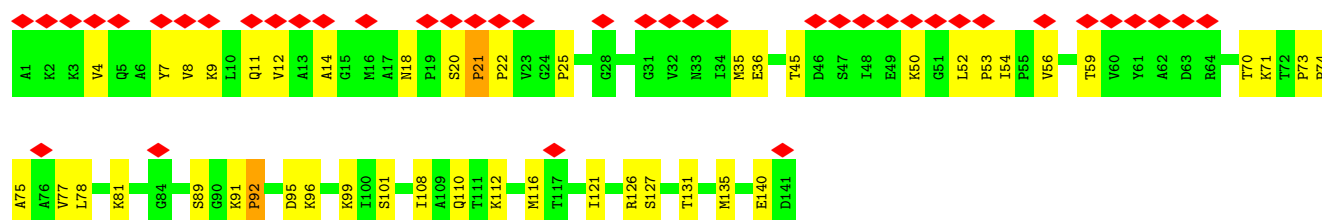
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10

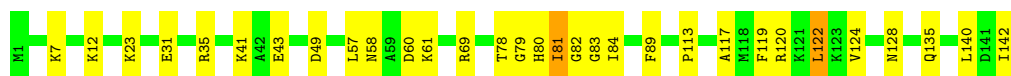


• Molecule 8: 50S ribosomal protein L11



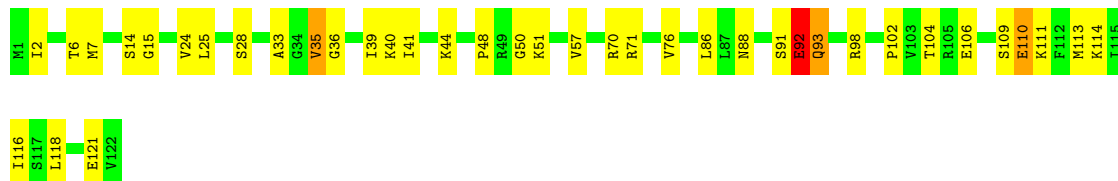
- Molecule 9: 50S ribosomal protein L13

Chain j:  78% 20%



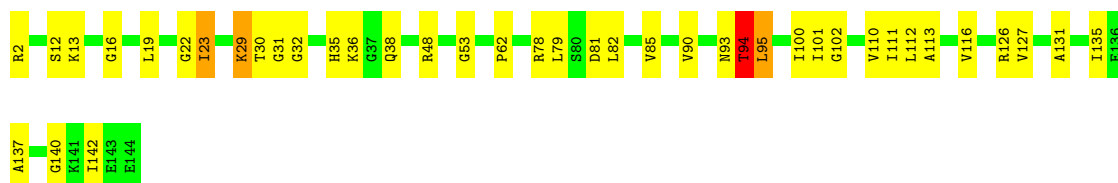
- Molecule 10: 50S ribosomal protein L14

Chain k:  68% 29%



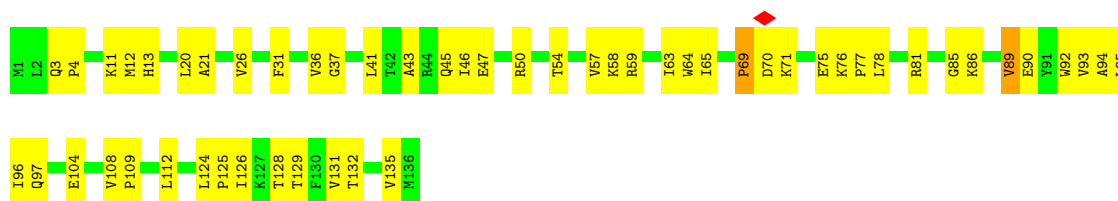
- Molecule 11: 50S ribosomal protein L15

Chain l:  71% 26%



- Molecule 12: 50S ribosomal protein L16

Chain m:  60% 38%



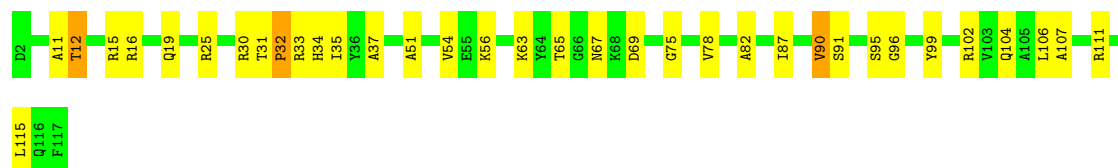
- Molecule 13: 50S ribosomal protein L17

Chain n:  70% 30%



- Molecule 14: 50S ribosomal protein L18

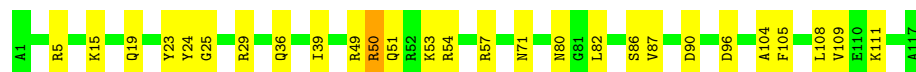
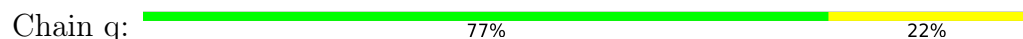
Chain o:  70% 28%



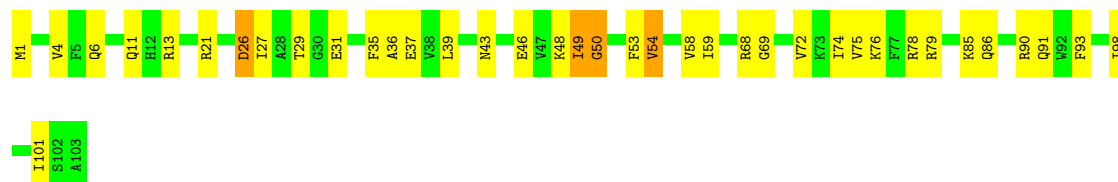
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20



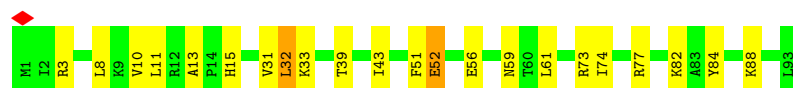
- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22

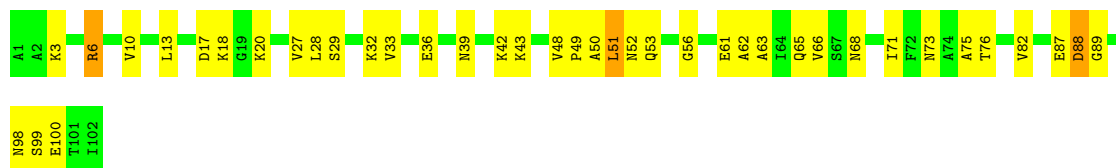


- Molecule 19: 50S ribosomal protein L23



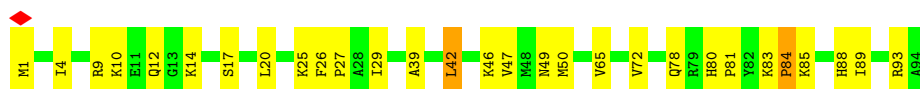
- Molecule 20: 50S ribosomal protein L24

Chain u:  61% 36%



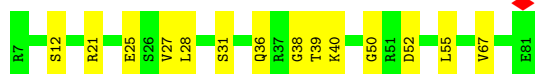
- Molecule 21: 50S ribosomal protein L25

Chain v:  69% 29%



- Molecule 22: 50S ribosomal protein L27

Chain w:  81% 19%



- Molecule 23: 50S ribosomal protein L28

Chain x:  75% 23%



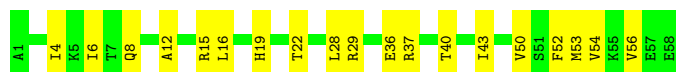
- Molecule 24: 50S ribosomal protein L29

Chain y:  75% 25%



- Molecule 25: 50S ribosomal protein L30

Chain z:  67% 33%

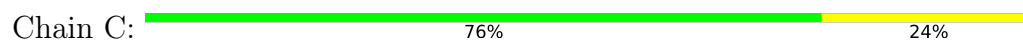


- Molecule 26: 50S ribosomal protein L32

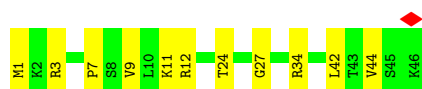
Chain B:  75% 25%



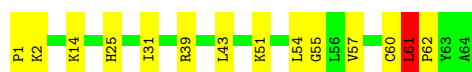
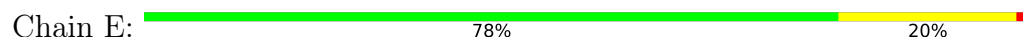
- Molecule 27: 50S ribosomal protein L33



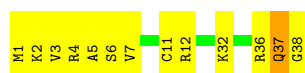
- Molecule 28: 50S ribosomal protein L34



- Molecule 29: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L36

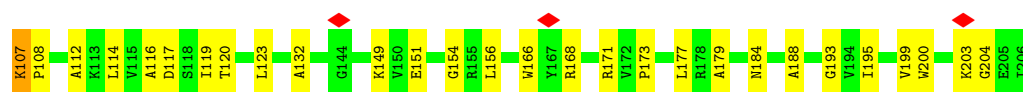


- Molecule 31: 30S ribosomal protein S2

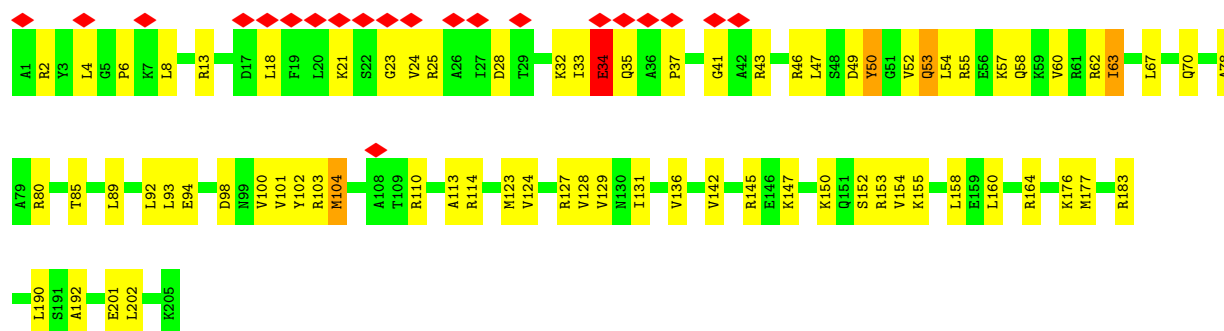


- Molecule 32: 30S ribosomal protein S3

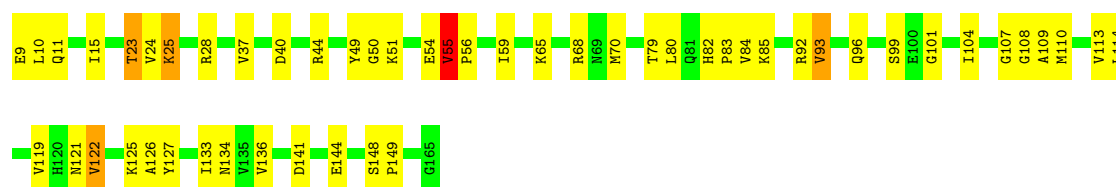




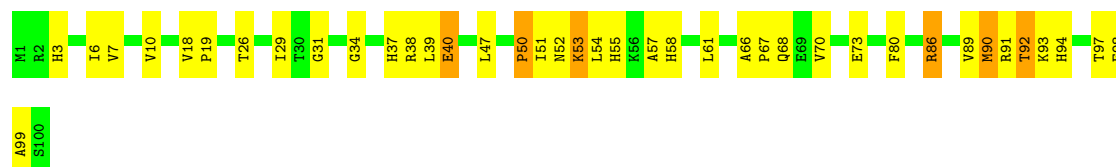
- Molecule 33: 30S ribosomal protein S4



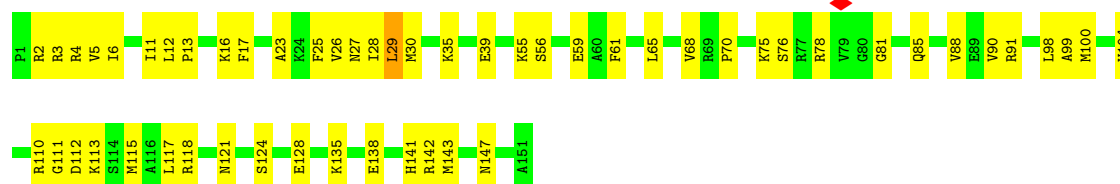
- Molecule 34: 30S ribosomal protein S5



- Molecule 35: 30S ribosomal protein S6



- Molecule 36: 30S ribosomal protein S7



- Molecule 37: 30S ribosomal protein S8

Chain M:  67% 32% .



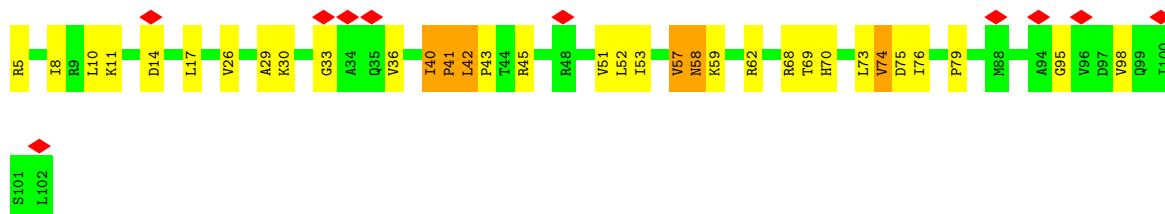
- Molecule 38: 30S ribosomal protein S9

Chain N:  62% 37% .



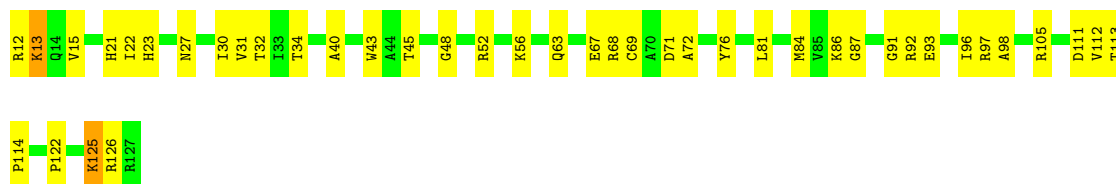
- Molecule 39: 30S ribosomal protein S10

Chain O:  10% 66% 28% 6% .



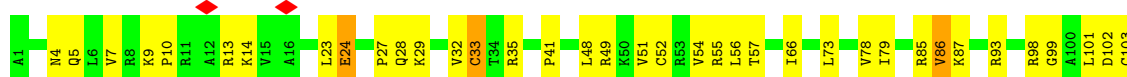
- Molecule 40: 30S ribosomal protein S11

Chain P:  64% 34% .



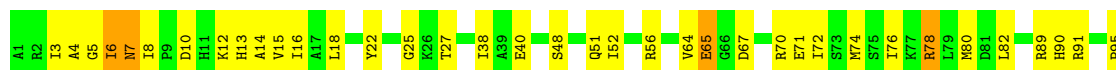
- Molecule 41: 30S ribosomal protein S12

Chain Q:  64% 33% .

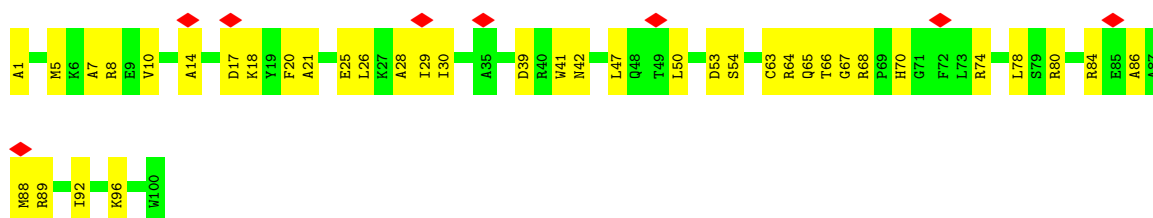




- Molecule 42: 30S ribosomal protein S13



- Molecule 43: 30S ribosomal protein S14



- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16

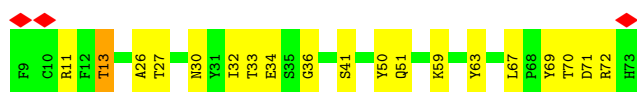


- Molecule 46: 30S ribosomal protein S17



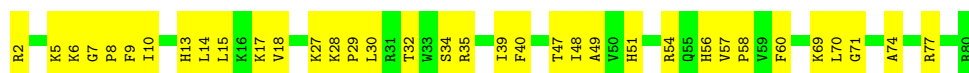
- Molecule 47: 30S ribosomal protein S18





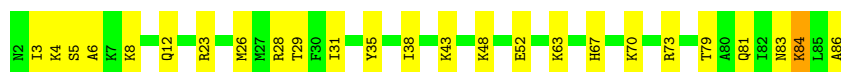
- Molecule 48: 30S ribosomal protein S19

Chain X:



- Molecule 49: 30S ribosomal protein S20

Chain Y:



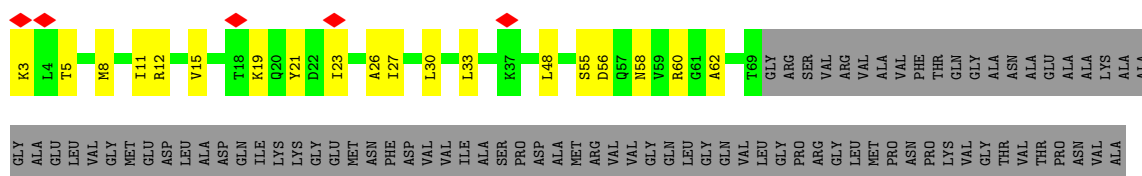
- Molecule 50: 30S ribosomal protein S21

Chain Z:



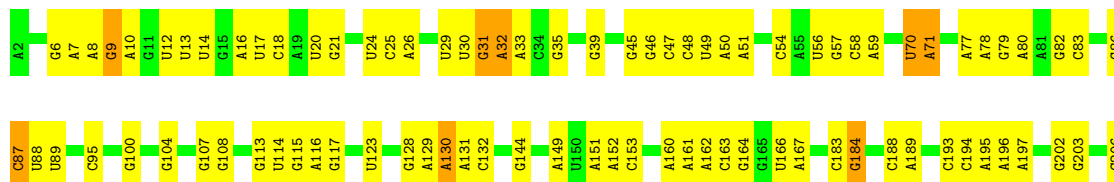
- Molecule 51: 50S ribosomal protein L1

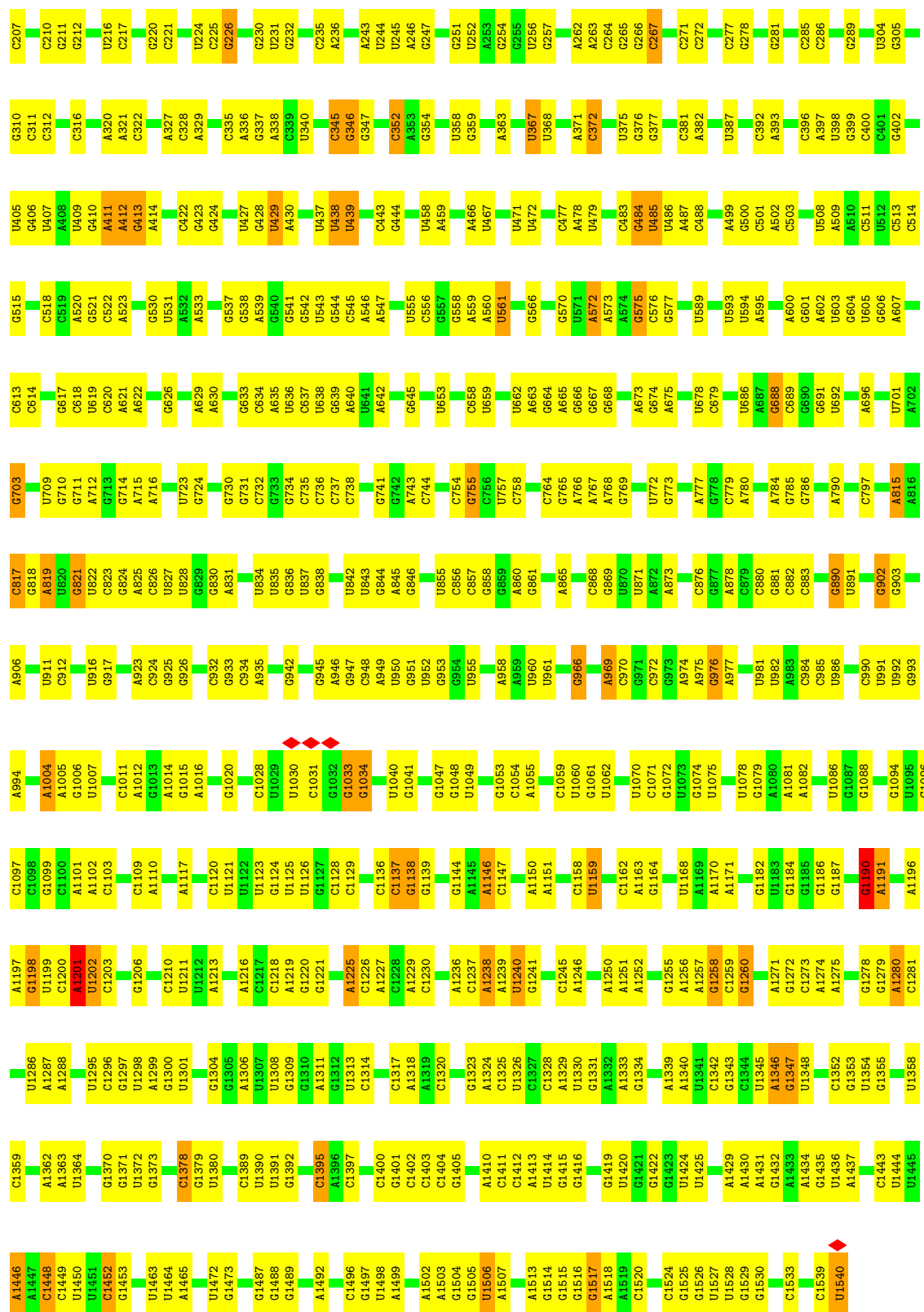
Chain a:



- Molecule 52: 16S ribosomal RNA

Chain 3:





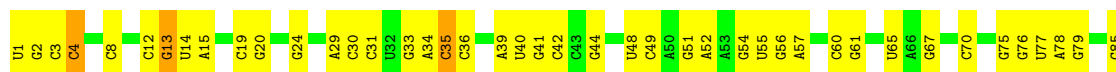
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G659	C660	G661	G662	A666	G669	C672	C679	C680	U686	C687	G690	C691	C692	A693	G694	G695	G696	G697	U703	G704	A705	U709	U615	A616	C617	G622	C623	A626	A627	G628	G629	U646	G630	C634	C635	G636	A637	U638	U639	C640	C645	U646	A653	C654	C655	U656	A655	G656	U657	U658
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	U2728	G2626	U2537		C2362	G2283	G2120	G2124	C2043	U1955	U1859		
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C2830	G2747	G2655	U2561	G2470	U2385	A2299	G2221	G2156	C2072	C1996	C1893	U1796	G1696
U2833	A2748			A2471	G2391	U2305	G2224	G2157		A1998	C1894	G1797	
G2834	C2752	C2658	A2566	G2472	A2392	A2309	A2225						
U2835	U2754	G2659	U2568	G2473	U2393	G2226	C2146						
U2836	C2755		G2569		C2394	A2311							
A2837	U2756	G2664	U2570	A2476	C2395	U2312	U2229						
G2838	U2757	U2671	U2571	U2477	G2396	C2313	G2230						
C2841	A2758		A2572	A2478	G2397	A2314							



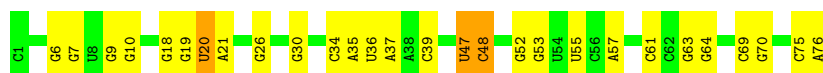
• Molecule 54: 5S ribosomal RNA

Chain 2: 51% 44% 5%



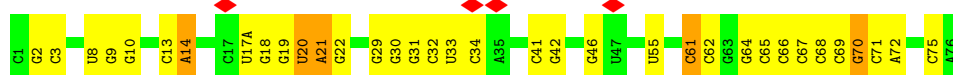
• Molecule 55: tRNA^{fMet}

Chain 5: 64% 32% .



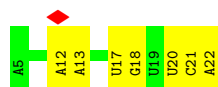
• Molecule 55: tRNA^{fMet}

Chain 6: 5% 55% 39% 6%



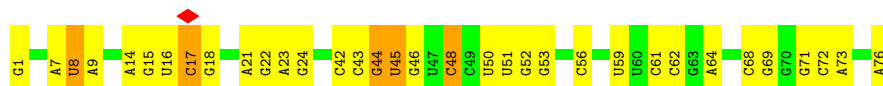
• Molecule 56: mRNA

Chain 4: 6% 61% 39%



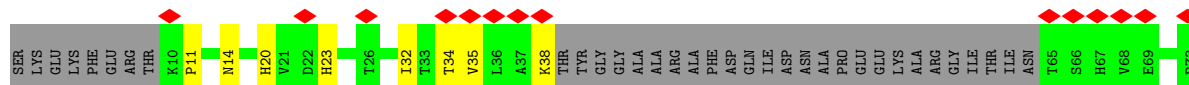
• Molecule 57: tRNA^{Phe}

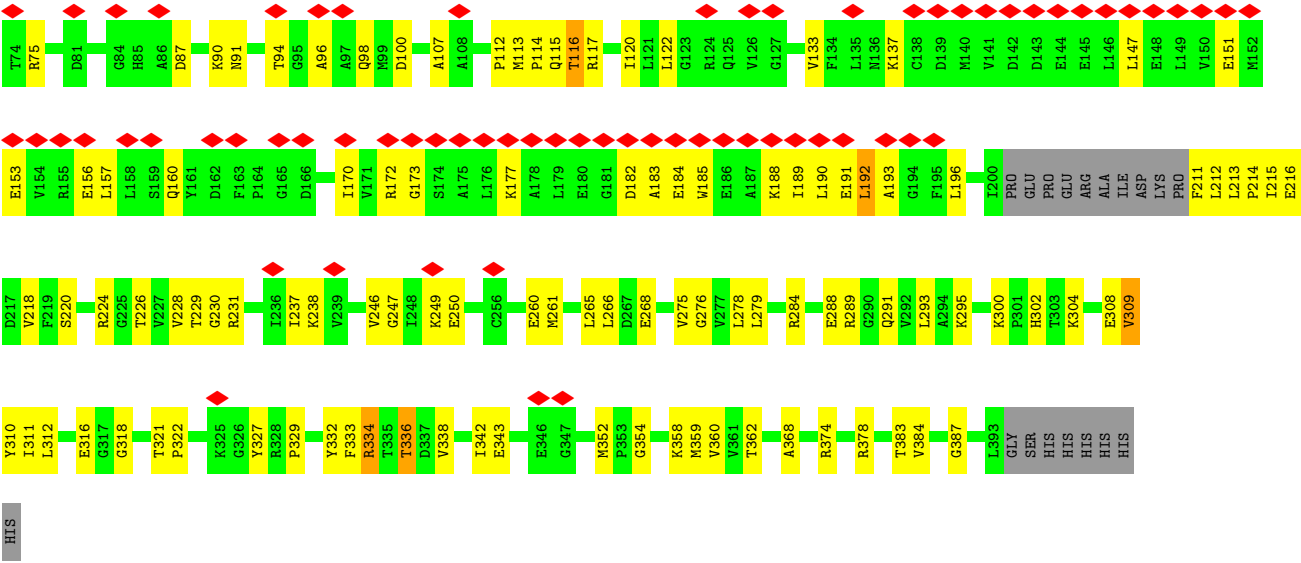
Chain 7: 55% 38% 7%



• Molecule 58: Elongation factor Tu

Chain 8: 20% 58% 28% 13%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	10215	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	17.183	Depositor
Minimum map value	-9.143	Depositor
Average map value	0.114	Depositor
Map value standard deviation	0.787	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	b	0.28	0/2122	0.93	5/2852 (0.2%)
2	c	0.30	0/1586	0.86	2/2134 (0.1%)
3	d	0.29	0/1571	0.92	3/2113 (0.1%)
4	e	0.31	0/1435	0.85	4/1926 (0.2%)
5	f	0.30	0/1343	0.89	5/1816 (0.3%)
6	g	0.32	0/1122	0.94	3/1515 (0.2%)
7	h	0.36	0/1002	1.01	6/1350 (0.4%)
8	i	0.35	0/1046	0.95	2/1410 (0.1%)
9	j	0.29	0/1152	0.90	4/1551 (0.3%)
10	k	0.28	0/948	0.88	0/1268
11	l	0.30	0/1054	0.92	4/1403 (0.3%)
12	m	0.29	0/1093	0.87	0/1460
13	n	0.29	0/974	0.89	2/1301 (0.2%)
14	o	0.28	0/902	0.89	1/1209 (0.1%)
15	p	0.29	0/929	0.79	1/1242 (0.1%)
16	q	0.29	0/960	0.87	1/1278 (0.1%)
17	r	0.29	0/829	0.92	3/1107 (0.3%)
18	s	0.28	0/864	0.92	2/1156 (0.2%)
19	t	0.28	0/745	0.84	0/994
20	u	0.29	0/788	0.90	3/1051 (0.3%)
21	v	0.28	0/766	0.82	0/1025
22	w	0.27	0/582	0.84	1/769 (0.1%)
23	x	0.29	0/635	0.84	2/848 (0.2%)
24	y	0.27	0/510	0.91	1/677 (0.1%)
25	z	0.29	0/453	0.87	1/605 (0.2%)
26	B	0.27	0/450	0.88	1/599 (0.2%)
27	C	0.33	0/417	0.84	0/554
28	D	0.31	0/380	0.91	1/498 (0.2%)
29	E	0.29	0/513	0.95	2/676 (0.3%)
30	F	0.32	0/303	0.88	1/397 (0.3%)
31	G	0.29	0/1788	0.86	2/2408 (0.1%)
32	H	0.32	0/1652	0.87	5/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.92	8/2227 (0.4%)
34	J	0.35	1/1170 (0.1%)	0.92	2/1573 (0.1%)
35	K	0.32	0/836	0.93	5/1128 (0.4%)
36	L	0.29	0/1196	0.95	3/1602 (0.2%)
37	M	0.29	0/989	0.87	3/1326 (0.2%)
38	N	0.31	0/1034	0.96	3/1375 (0.2%)
39	O	0.31	0/797	0.87	3/1077 (0.3%)
40	P	0.33	0/886	0.89	3/1195 (0.3%)
41	Q	0.32	0/969	0.98	5/1300 (0.4%)
42	R	0.31	0/893	0.96	5/1193 (0.4%)
43	S	0.29	0/817	0.89	1/1088 (0.1%)
44	T	0.29	0/722	0.97	5/964 (0.5%)
45	U	0.32	0/659	0.99	4/884 (0.5%)
46	V	0.30	0/658	0.88	1/881 (0.1%)
47	W	0.31	0/545	0.86	1/731 (0.1%)
48	X	0.32	0/653	0.87	0/877
49	Y	0.30	0/671	0.94	2/888 (0.2%)
50	Z	0.34	0/551	1.04	2/728 (0.3%)
51	a	0.30	0/1034	0.83	1/1387 (0.1%)
52	3	0.41	0/36963	0.47	2/57662 (0.0%)
53	1	0.40	0/69796	0.48	2/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.40	0/1832	0.46	0/2855
55	6	0.40	0/1832	0.49	0/2855
56	4	0.41	0/436	0.47	0/679
57	7	0.40	0/1809	0.47	0/2819
58	8	0.33	0/2730	0.89	10/3693 (0.3%)
All	All	0.38	1/165929 (0.0%)	0.62	139/247771 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	J	55	VAL	CA-CB	5.54	1.56	1.54

All (139) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	e	148	VAL	N-CA-C	-8.57	102.86	111.77
33	I	46	ARG	N-CA-C	-8.36	102.86	113.23
58	8	100	ASP	N-CA-C	-8.23	102.96	113.16
49	Y	84	LYS	N-CA-C	-8.08	102.45	111.82
20	u	89	GLY	N-CA-C	-7.90	104.86	114.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	h	117	LEU	N-CA-C	7.90	121.46	107.80
36	L	27	ASN	N-CA-C	7.66	119.71	111.36
26	B	53	VAL	N-CA-C	7.66	118.46	110.72
41	Q	114	SER	N-CA-C	-7.50	103.12	111.82
29	E	61	LEU	CA-C-N	7.47	126.74	118.97
29	E	61	LEU	C-N-CA	7.47	126.74	118.97
42	R	3	ILE	N-CA-C	7.35	118.52	110.21
49	Y	31	ILE	N-CA-C	-7.35	103.29	110.72
5	f	47	ASN	N-CA-C	-7.24	104.05	113.17
43	S	50	LEU	N-CA-C	-7.18	100.61	109.65
44	T	68	TYR	N-CA-C	-7.13	102.92	111.69
33	I	94	GLU	N-CA-C	-7.07	104.53	113.72
20	u	53	GLN	N-CA-C	7.05	119.80	109.30
36	L	143	MET	N-CA-C	-6.92	104.64	113.23
36	L	29	LEU	N-CA-C	-6.83	104.75	113.23
50	Z	7	GLU	N-CA-C	-6.82	102.26	111.54
17	r	50	GLY	N-CA-C	-6.78	97.12	113.18
7	h	43	LYS	N-CA-C	-6.70	104.05	111.82
4	e	150	GLY	N-CA-C	-6.64	104.82	112.79
13	n	68	ALA	N-CA-C	-6.58	104.14	111.71
1	b	71	ASP	N-CA-C	6.53	119.94	110.28
16	q	50	ARG	N-CA-C	-6.51	105.97	114.04
34	J	101	GLY	N-CA-C	-6.43	106.90	115.32
8	i	21	PRO	N-CA-C	6.40	118.51	110.70
13	n	67	PHE	N-CA-C	-6.36	105.66	113.41
45	U	47	GLU	N-CA-C	6.32	119.84	111.75
38	N	44	ARG	N-CA-C	6.29	117.93	111.14
45	U	77	GLU	N-CA-C	-6.27	105.45	113.23
58	8	91	ASN	N-CA-C	6.25	118.09	111.28
35	K	31	GLY	N-CA-C	-6.24	106.92	114.66
53	1	1130	U	C2'-C3'-O3'	6.23	118.84	109.50
5	f	141	GLY	N-CA-C	-6.20	105.06	113.37
32	H	5	HIS	CA-C-N	6.19	127.58	119.84
32	H	5	HIS	C-N-CA	6.19	127.58	119.84
18	s	35	ILE	N-CA-C	-6.16	105.05	111.58
39	O	74	VAL	N-CA-C	-6.13	106.78	111.62
9	j	119	PHE	N-CA-C	-6.11	105.98	113.50
44	T	27	GLN	N-CA-C	6.10	118.43	111.11
52	3	1190	G	C2'-C3'-O3'	6.08	118.62	109.50
42	R	96	VAL	N-CA-C	6.06	116.84	110.72
39	O	40	ILE	CA-C-N	6.05	127.40	119.84
39	O	40	ILE	C-N-CA	6.05	127.40	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	r	49	ILE	N-CA-C	6.03	116.61	108.17
58	8	120	ILE	N-CA-C	-6.03	103.85	112.35
58	8	116	THR	N-CA-C	-6.03	104.28	111.69
7	h	15	VAL	N-CA-C	-6.01	104.88	110.53
50	Z	30	GLU	N-CA-C	-6.00	105.53	114.64
40	P	97	ARG	N-CA-C	-5.92	104.91	111.36
33	I	104	MET	N-CA-C	-5.91	105.90	113.23
3	d	83	VAL	N-CA-C	5.90	121.60	109.34
23	x	6	VAL	N-CA-C	5.89	116.53	110.82
32	H	89	VAL	N-CA-C	5.89	116.62	110.62
44	T	43	ALA	N-CA-C	-5.88	106.06	113.18
2	c	152	PRO	N-CA-C	-5.88	105.53	113.40
32	H	107	LYS	CA-C-N	5.83	125.70	119.28
32	H	107	LYS	C-N-CA	5.83	125.70	119.28
1	b	210	ALA	N-CA-C	-5.76	106.80	113.88
33	I	176	LYS	N-CA-C	-5.74	106.04	113.16
17	r	29	THR	N-CA-C	5.73	117.52	111.28
14	o	12	THR	N-CA-C	5.72	119.07	111.75
46	V	69	THR	N-CA-C	-5.70	100.20	108.07
58	8	192	LEU	N-CA-C	-5.70	105.05	112.23
11	l	95	LEU	N-CA-C	-5.68	105.08	112.23
47	W	69	TYR	N-CA-C	-5.68	104.72	111.03
58	8	183	ALA	N-CA-C	5.62	117.41	111.28
42	R	78	ARG	N-CA-C	-5.62	105.24	111.36
1	b	145	MET	N-CA-C	-5.61	107.43	114.56
23	x	21	LEU	N-CA-C	5.61	119.43	111.92
33	I	50	TYR	N-CA-C	-5.58	105.35	111.82
6	g	55	GLU	N-CA-C	5.58	118.12	111.71
41	Q	9	LYS	CA-C-N	5.57	126.81	119.84
41	Q	9	LYS	C-N-CA	5.57	126.81	119.84
40	P	68	ARG	N-CA-C	-5.57	106.44	113.18
9	j	31	GLU	N-CA-C	-5.55	105.38	111.82
42	R	56	ARG	N-CA-C	-5.55	105.31	111.36
38	N	46	VAL	N-CA-C	5.54	118.82	111.17
3	d	73	ILE	N-CA-C	-5.52	106.45	112.80
33	I	53	GLN	N-CA-C	-5.51	105.35	111.36
24	y	24	GLU	N-CA-C	5.50	117.71	111.11
11	l	137	ALA	N-CA-C	-5.49	106.08	112.89
31	G	112	ARG	N-CA-C	-5.46	105.49	111.82
35	K	40	GLU	N-CA-C	5.45	122.41	110.80
40	P	69	CYS	N-CA-C	-5.45	106.79	113.50
44	T	52	ARG	N-CA-C	-5.44	105.37	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	8	191	GLU	N-CA-C	-5.44	106.15	112.89
42	R	64	VAL	N-CA-C	5.42	116.94	109.46
35	K	68	GLN	N-CA-C	5.40	118.08	111.82
5	f	174	LYS	N-CA-C	5.39	122.27	110.80
33	I	63	ILE	N-CA-C	5.38	115.59	110.53
9	j	43	GLU	N-CA-C	-5.38	105.15	112.26
58	8	309	VAL	N-CA-C	5.38	115.39	107.75
58	8	316	GLU	N-CA-C	-5.38	106.77	113.38
41	Q	86	VAL	N-CA-C	-5.37	107.49	112.43
30	F	5	ALA	N-CA-C	-5.36	105.39	112.94
7	h	41	LEU	N-CA-C	-5.36	106.25	112.89
38	N	92	SER	N-CA-C	-5.34	105.86	112.38
15	p	74	GLN	N-CA-C	-5.34	99.71	108.41
3	d	139	LYS	N-CA-C	-5.33	106.28	112.89
11	l	23	ILE	N-CA-C	-5.30	107.66	112.96
4	e	95	MET	N-CA-C	5.30	116.86	111.14
8	i	36	GLU	N-CA-C	-5.27	105.71	111.82
41	Q	56	LEU	N-CA-C	5.26	117.11	110.33
7	h	44	ALA	N-CA-C	-5.26	105.63	111.36
33	I	136	VAL	N-CA-C	5.24	115.76	108.84
6	g	64	ALA	N-CA-C	-5.24	106.39	112.89
35	K	73	GLU	N-CA-C	-5.24	105.65	111.36
25	z	12	ALA	N-CA-C	-5.23	104.19	110.88
6	g	67	ALA	N-CA-C	-5.22	105.65	112.23
11	l	113	ALA	N-CA-C	-5.22	106.82	114.39
34	J	134	ASN	N-CA-C	5.22	117.05	111.36
37	M	67	GLY	N-CA-C	-5.21	106.42	113.24
22	w	52	ASP	N-CA-C	-5.19	106.71	112.57
28	D	7	PRO	N-CA-C	5.19	119.35	111.15
1	b	178	GLY	N-CA-C	-5.17	107.65	114.95
5	f	168	VAL	N-CA-C	5.15	116.70	108.87
5	f	62	ALA	N-CA-C	-5.14	105.76	111.36
18	s	24	ILE	N-CA-C	5.13	114.87	106.72
35	K	90	MET	N-CA-C	5.12	117.20	109.41
31	G	120	SER	N-CA-C	-5.12	107.20	113.50
58	8	190	LEU	N-CA-C	-5.10	105.81	112.23
37	M	13	ILE	N-CA-C	-5.08	105.46	111.00
37	M	7	ALA	N-CA-C	-5.08	105.74	111.28
20	u	29	SER	N-CA-C	5.07	117.54	111.71
2	c	174	SER	N-CA-C	5.07	117.35	111.02
53	1	1020	A	C2'-C3'-O3'	5.06	117.09	109.50
1	b	30	ALA	N-CA-C	5.06	120.99	109.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	T	46	LYS	N-CA-C	5.05	121.55	110.80
7	h	42	ARG	N-CA-C	-5.05	106.97	113.23
51	a	56	ASP	N-CA-C	-5.05	107.09	113.20
45	U	27	ALA	N-CA-C	5.04	116.83	110.33
45	U	26	ASN	N-CA-C	5.04	114.79	108.45
52	3	1201	A	C2'-C3'-O3'	5.03	117.05	109.50
4	e	134	GLN	N-CA-C	-5.01	106.85	113.17
9	j	79	GLY	N-CA-C	-5.01	108.20	115.27

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	64	0
2	c	1565	0	1616	51	0
3	d	1552	0	1619	32	0
4	e	1411	0	1447	50	0
5	f	1323	0	1374	37	0
6	g	1111	0	1148	33	0
7	h	989	0	1025	56	0
8	i	1032	0	1088	30	0
9	j	1129	0	1162	23	0
10	k	939	0	1012	38	0
11	l	1045	0	1117	34	0
12	m	1074	0	1157	46	0
13	n	961	0	1000	26	0
14	o	892	0	923	28	0
15	p	917	0	965	34	0
16	q	947	0	1022	24	0
17	r	816	0	839	33	0
18	s	857	0	922	29	0
19	t	739	0	807	17	0
20	u	780	0	834	23	0
21	v	753	0	780	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	w	575	0	592	10	0
23	x	625	0	655	17	0
24	y	509	0	543	14	0
25	z	449	0	491	15	0
26	B	444	0	461	15	0
27	C	410	0	440	8	0
28	D	377	0	418	11	0
29	E	504	0	574	9	0
30	F	302	0	343	12	0
31	G	1757	0	1787	44	0
32	H	1625	0	1699	42	0
33	I	1643	0	1710	55	0
34	J	1157	0	1199	37	0
35	K	818	0	808	37	0
36	L	1182	0	1240	42	0
37	M	979	0	1034	34	0
38	N	1022	0	1070	42	0
39	O	787	0	828	32	0
40	P	870	0	878	34	0
41	Q	955	0	1019	37	0
42	R	884	0	944	40	0
43	S	805	0	847	29	0
44	T	714	0	737	15	0
45	U	649	0	666	31	0
46	V	649	0	691	23	0
47	W	536	0	552	14	0
48	X	638	0	665	29	0
49	Y	665	0	714	20	0
50	Z	545	0	579	28	0
51	a	1027	0	1092	31	0
52	3	33012	0	16618	575	0
53	1	62317	0	31346	896	0
54	2	2568	0	1303	55	0
55	5	1640	0	836	22	0
55	6	1640	0	837	25	0
56	4	388	0	196	5	0
57	7	1619	0	821	26	0
58	8	2683	0	2706	86	0
59	5	10	0	10	0	0
60	7	11	0	8	2	0
61	8	28	0	12	0	0
All	All	152933	0	103983	2784	0

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

All (2784) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:484:G:H4'	52:3:485:U:H5''	1.42	1.01
55:5:75:C:H2'	55:5:76:A:H5''	1.39	1.00
52:3:1259:C:H3'	52:3:1260:G:H5''	1.44	0.99
55:6:13:C:H2'	55:6:14:A:H5''	1.43	0.99
5:f:106:LEU:HD21	5:f:151:ARG:HB2	1.45	0.98
53:1:2277:G:H2'	53:1:2278:A:H5''	1.45	0.97
34:J:107:GLY:HA3	52:3:9:G:H5'	1.46	0.97
53:1:1906:G:H2'	53:1:1907:G:H5''	1.45	0.97
33:I:190:LEU:HD12	33:I:192:ALA:H	1.29	0.95
53:1:45:G:H5''	53:1:46:G:H5'	1.46	0.95
12:m:75:GLU:HG3	53:1:957:C:H5'	1.48	0.94
35:K:52:ASN:O	35:K:53:LYS:HG2	1.69	0.93
36:L:12:LEU:HD12	36:L:13:PRO:HD2	1.48	0.92
42:R:91:ARG:HH12	53:1:887:U:H5'	1.36	0.91
32:H:112:ALA:HB3	32:H:184:ASN:HD22	1.35	0.91
52:3:405:U:H3'	52:3:406:G:H5'	1.53	0.90
55:5:75:C:C2'	55:5:76:A:H5''	2.04	0.87
53:1:1051:G:H4'	53:1:2752:C:H1'	1.57	0.87
35:K:38:ARG:HH21	35:K:40:GLU:HB2	1.38	0.86
32:H:15:LYS:HD3	32:H:16:PRO:HD2	1.57	0.86
53:1:1053:C:H2'	53:1:1054:A:H5''	1.57	0.86
7:h:23:LEU:HD13	7:h:118:ILE:HG12	1.54	0.85
52:3:1033:G:H2'	52:3:1034:G:H5''	1.57	0.85
2:c:142:VAL:HG22	2:c:143:PRO:HD2	1.56	0.84
39:O:42:LEU:HD11	39:O:73:LEU:HG	1.59	0.84
5:f:34:ARG:HG2	5:f:70:LEU:HD21	1.59	0.84
5:f:174:LYS:HE3	53:1:2529:G:H4'	1.59	0.84
10:k:48:PRO:HG3	52:3:1422:G:H5'	1.56	0.84
53:1:1141:U:H4'	53:1:1142:A:O4'	1.77	0.84
7:h:61:ARG:HB3	53:1:1046:A:H4'	1.59	0.84
7:h:33:VAL:HG22	7:h:34:THR:H	1.42	0.84
31:G:45:THR:HG22	31:G:200:PRO:HB2	1.58	0.83
43:S:29:ILE:HG23	43:S:30:ILE:HD12	1.60	0.83
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.57	0.83
6:g:11:ASN:HD22	6:g:12:LEU:HD22	1.44	0.83
42:R:25:GLY:H	52:3:1329:A:H5''	1.44	0.82
42:R:91:ARG:NH1	53:1:887:U:H5'	1.93	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2502:G:H5'	53:1:2503:A:H5''	1.62	0.81
58:8:260:GLU:HG2	58:8:265:LEU:HA	1.62	0.81
52:3:1201:A:H1'	52:3:1202:U:OP2	1.81	0.81
36:L:30:MET:HE1	52:3:1373:G:H4'	1.63	0.81
52:3:59:A:H5''	52:3:387:U:H5''	1.63	0.81
43:S:70:HIS:HB3	52:3:974:A:H5'	1.63	0.80
7:h:57:ASN:HB2	7:h:62:ARG:HD2	1.63	0.80
45:U:36:VAL:HG12	45:U:53:ASP:HB3	1.64	0.80
1:b:208:GLY:HA2	1:b:211:ARG:HB2	1.63	0.80
8:i:25:PRO:HB2	53:1:1095:A:N6	1.95	0.80
16:q:111:LYS:HG2	17:r:48:LYS:HD2	1.62	0.80
53:1:1906:G:C2'	53:1:1907:G:H5''	2.12	0.80
12:m:12:MET:HA	53:1:910:A:H62	1.48	0.79
52:3:346:G:H2'	52:3:347:G:H5'	1.64	0.79
53:1:1020:A:H1'	53:1:1021:A:OP2	1.81	0.79
12:m:86:LYS:HE2	53:1:955:U:H5''	1.64	0.79
3:d:117:ARG:HH21	3:d:184:ASP:HA	1.45	0.78
52:3:327:A:O2'	52:3:328:C:H4'	1.83	0.78
39:O:57:VAL:HG12	39:O:58:ASN:H	1.48	0.78
52:3:1346:A:H2'	52:3:1347:G:H4'	1.62	0.78
1:b:145:MET:HE2	1:b:152:GLN:HG3	1.64	0.78
27:C:24:LYS:HZ1	27:C:29:LYS:HB2	1.49	0.78
54:2:3:C:H2'	54:2:4:C:H5''	1.66	0.77
13:n:103:ARG:NH1	53:1:1287:A:H5'	1.99	0.77
34:J:55:VAL:HG13	34:J:56:PRO:HD3	1.65	0.77
37:M:39:LEU:HD13	37:M:45:ILE:HD12	1.66	0.77
45:U:67:ILE:H	45:U:67:ILE:HD12	1.50	0.77
50:Z:9:GLU:HB3	50:Z:10:PRO:HD3	1.66	0.77
53:1:1645:G:H5''	53:1:1646:C:H5'	1.66	0.77
53:1:329:G:O4'	53:1:477:A:H1'	1.86	0.76
53:1:1801:A:H5''	53:1:2203:U:H2'	1.65	0.76
53:1:1796:U:H2'	53:1:1797:G:H8	1.49	0.76
53:1:2715:C:H2'	53:1:2716:C:H5''	1.67	0.76
50:Z:6:ARG:HG2	50:Z:8:ASN:HA	1.68	0.76
50:Z:40:PRO:O	50:Z:44:ARG:HB2	1.85	0.76
57:7:44:G:H1'	57:7:45:U:H2'	1.68	0.76
30:F:32:LYS:HE3	53:1:2478:A:H5'	1.68	0.76
51:a:23:ILE:H	51:a:23:ILE:HD12	1.50	0.75
52:3:1197:A:H2'	52:3:1198:G:H5''	1.67	0.75
53:1:275:C:H2'	53:1:276:U:H4'	1.66	0.75
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:z:8:GLN:HB2	25:z:28:LEU:HD13	1.67	0.75
52:3:664:G:H22	52:3:741:G:H1	1.33	0.75
53:1:1078:U:H4'	53:1:1079:C:H5''	1.68	0.74
12:m:41:LEU:HD23	12:m:96:ILE:HG13	1.69	0.74
12:m:124:LEU:HD12	12:m:125:PRO:HD2	1.69	0.74
41:Q:85:ARG:HB3	41:Q:93:ARG:HA	1.69	0.74
37:M:102:VAL:HG23	37:M:125:ILE:HB	1.69	0.74
52:3:769:G:H4'	52:3:1513:A:H4'	1.70	0.74
53:1:2391:G:H4'	53:1:2392:A:OP1	1.87	0.74
4:e:107:VAL:HG12	4:e:108:PRO:HD3	1.70	0.74
35:K:29:ILE:HG22	35:K:34:GLY:HA3	1.68	0.74
10:k:76:VAL:H	15:p:72:VAL:HG12	1.53	0.74
37:M:28:SER:HB2	37:M:56:PRO:HB2	1.69	0.73
53:1:1045:C:H5'	53:1:1046:A:H5''	1.70	0.73
42:R:105:ALA:HA	52:3:948:C:OP1	1.88	0.73
53:1:322:A:H5'	53:1:340:A:H1'	1.68	0.73
33:I:53:GLN:HE22	52:3:8:A:H61	1.37	0.73
44:T:68:TYR:HB2	52:3:754:C:H4'	1.70	0.73
53:1:1133:A:H4'	53:1:1134:A:H5''	1.69	0.73
58:8:216:GLU:HG2	58:8:230:GLY:HA2	1.71	0.73
2:c:151:THR:HB	2:c:152:PRO:HD3	1.71	0.73
37:M:21:LYS:HE3	52:3:827:U:H5''	1.69	0.73
2:c:135:GLY:HA2	53:1:743:A:OP1	1.89	0.72
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.69	0.72
38:N:33:SER:OG	38:N:36:GLN:HG2	1.89	0.72
53:1:572:A:H61	53:1:2029:G:H21	1.37	0.72
53:1:694:U:H2'	53:1:695:G:H5''	1.71	0.72
55:6:13:C:C2'	55:6:14:A:H5''	2.16	0.72
53:1:511:U:H2'	53:1:512:G:H5'	1.71	0.72
57:7:1:G:H5'	58:8:289:ARG:HE	1.53	0.72
28:D:11:LYS:HE3	53:1:686:U:H5''	1.69	0.72
53:1:1664:A:H61	53:1:1996:C:H42	1.38	0.72
19:t:8:LEU:HD13	24:y:21:LEU:HB3	1.72	0.72
53:1:2286:G:H5''	53:1:2287:A:OP1	1.89	0.72
8:i:7:TYR:HB3	8:i:59:THR:HA	1.71	0.72
41:Q:23:LEU:HD23	41:Q:29:LYS:NZ	2.04	0.72
49:Y:3:ILE:H	49:Y:3:ILE:HD12	1.53	0.72
45:U:52:LEU:HD11	45:U:74:LEU:HG	1.72	0.71
52:3:396:C:H2'	52:3:397:A:H5''	1.72	0.71
50:Z:65:ARG:HH11	52:3:1088:G:H4'	1.54	0.71
5:f:167:VAL:HG13	5:f:169:ARG:HH22	1.54	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:y:41:HIS:CD2	53:1:96:C:H4'	2.25	0.71
53:1:2277:G:C2'	53:1:2278:A:H5''	2.17	0.71
48:X:27:LYS:HG2	48:X:28:LYS:H	1.55	0.71
53:1:1077:A:H2'	53:1:1078:U:H5'	1.70	0.71
7:h:55:VAL:HA	53:1:1084:A:H4'	1.73	0.70
9:j:81:ILE:HG23	9:j:82:GLY:H	1.56	0.70
46:V:12:VAL:HG23	46:V:21:VAL:HG13	1.73	0.70
14:o:54:VAL:HG12	54:2:116:G:H4'	1.73	0.70
20:u:36:GLU:HA	20:u:61:GLU:HG2	1.72	0.70
36:L:70:PRO:HG3	36:L:98:LEU:HD11	1.72	0.70
53:1:1697:G:H4'	53:1:1978:A:H5''	1.73	0.70
4:e:84:ILE:HD11	53:1:2312:U:H5'	1.74	0.69
20:u:33:VAL:HG13	20:u:66:VAL:HG12	1.74	0.69
52:3:1200:C:H5''	52:3:1201:A:H3'	1.73	0.69
14:o:12:THR:HG23	53:1:2334:U:H4'	1.72	0.69
35:K:67:PRO:HG2	35:K:70:VAL:HG23	1.74	0.69
8:i:14:ALA:HB2	8:i:54:ILE:HG22	1.72	0.69
11:l:95:LEU:HD22	11:l:100:ILE:HD11	1.73	0.69
36:L:29:LEU:HD13	36:L:104:VAL:HG13	1.73	0.69
58:8:215:ILE:HD11	58:8:218:VAL:HG22	1.75	0.69
8:i:89:SER:HB2	8:i:92:PRO:HG3	1.75	0.69
15:p:61:ARG:HE	15:p:99:LEU:HG	1.58	0.69
42:R:25:GLY:N	52:3:1329:A:H5''	2.07	0.69
10:k:40:LYS:HD2	10:k:57:VAL:HG12	1.73	0.69
32:H:69:THR:HG21	32:H:75:VAL:HG21	1.74	0.69
52:3:31:G:H21	52:3:46:G:H5''	1.58	0.69
14:o:51:ALA:HB3	14:o:78:VAL:HG22	1.74	0.69
38:N:70:GLY:HA3	52:3:1371:G:O3'	1.93	0.69
38:N:98:ARG:HG3	38:N:103:VAL:HG21	1.73	0.69
53:1:310:A:C2'	53:1:311:A:H5''	2.23	0.69
53:1:2112:G:H2'	53:1:2113:U:H5'	1.75	0.69
58:8:249:LYS:HD3	58:8:250:GLU:N	2.08	0.69
34:J:108:GLY:H	52:3:9:G:H4'	1.58	0.69
52:3:1301:U:O2	52:3:1301:U:H2'	1.92	0.69
5:f:134:GLY:HA3	5:f:140:ILE:HG21	1.74	0.69
39:O:59:LYS:HG2	52:3:972:C:H4'	1.74	0.69
48:X:77:ARG:HH21	52:3:1225:A:H4'	1.56	0.69
53:1:2248:C:H2'	53:1:2249:U:H5'	1.73	0.69
10:k:98:ARG:HH21	52:3:340:U:H5''	1.58	0.68
45:U:46:LYS:NZ	52:3:617:G:H5''	2.08	0.68
52:3:70:U:H5''	52:3:71:A:OP1	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:45:G:H5''	53:1:46:G:C5'	2.23	0.68
40:P:87:GLY:H	40:P:113:THR:HG22	1.58	0.68
1:b:221:GLY:HA2	1:b:224:MET:HE3	1.75	0.68
5:f:34:ARG:HH22	53:1:2759:G:H1'	1.59	0.68
17:r:4:VAL:HG13	17:r:39:LEU:HB3	1.76	0.68
37:M:42:GLU:HG2	37:M:100:ILE:HD13	1.75	0.68
40:P:21:HIS:HA	40:P:84:MET:HB2	1.76	0.68
7:h:55:VAL:HA	53:1:1084:A:C4'	2.23	0.68
53:1:2423:U:O2'	53:1:2425:A:H2'	1.93	0.68
7:h:3:LEU:HD12	7:h:5:LEU:H	1.59	0.68
52:3:1236:A:H4'	52:3:1304:G:H4'	1.76	0.68
33:I:158:LEU:HD22	33:I:177:MET:HE2	1.76	0.67
52:3:26:A:H61	52:3:558:G:H1'	1.58	0.67
30:F:1:MET:HE2	30:F:36:ARG:HB3	1.77	0.67
34:J:54:GLU:HG3	34:J:56:PRO:HD2	1.76	0.67
34:J:80:LEU:HD13	34:J:122:VAL:HG11	1.77	0.67
4:e:135:ILE:H	4:e:135:ILE:HD12	1.59	0.67
54:2:3:C:C2'	54:2:4:C:H5''	2.24	0.67
32:H:56:ILE:HG23	32:H:63:ILE:HD11	1.76	0.67
36:L:3:ARG:HE	52:3:932:C:H5''	1.58	0.67
53:1:615:U:H5''	53:1:616:A:OP2	1.94	0.67
24:y:2:LYS:HE2	53:1:102:U:H1'	1.76	0.67
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.76	0.67
37:M:80:PRO:HG2	52:3:878:A:H5'	1.77	0.67
49:Y:35:TYR:O	49:Y:38:ILE:HG22	1.95	0.67
53:1:2086:U:H2'	53:1:2087:G:C8	2.29	0.67
1:b:16:VAL:HB	1:b:203:VAL:HG12	1.77	0.67
33:I:150:LYS:HE3	33:I:155:LYS:HD3	1.77	0.67
36:L:68:VAL:HG13	36:L:99:ALA:HB1	1.76	0.67
37:M:80:PRO:HG2	52:3:878:A:C5'	2.24	0.67
48:X:2:ARG:HH11	52:3:1311:A:H62	1.41	0.67
53:1:2800:A:H3'	53:1:2801:G:H5'	1.76	0.67
34:J:110:MET:HE2	34:J:126:ALA:HB2	1.75	0.67
40:P:125:LYS:HD2	52:3:797:C:OP1	1.94	0.67
15:p:38:ARG:HH22	15:p:40:GLN:HB3	1.60	0.67
1:b:145:MET:HE1	53:1:1800:C:H3'	1.77	0.67
47:W:11:ARG:HG3	52:3:845:A:H4'	1.77	0.67
53:1:1807:G:H2'	53:1:1808:A:H5'	1.77	0.67
58:8:309:VAL:HG11	58:8:359:MET:HE1	1.77	0.67
55:6:69:C:H2'	55:6:70:G:H5'	1.76	0.66
15:p:38:ARG:HD2	52:3:345:C:H5'	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:59:ILE:HG22	31:G:64:GLY:HA3	1.75	0.66
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.59	0.66
18:s:1:MET:HE1	18:s:63:GLY:HA3	1.76	0.66
52:3:730:G:H2'	52:3:731:G:H5'	1.77	0.66
52:3:1414:U:H2'	52:3:1415:G:H8	1.61	0.66
53:1:310:A:O2'	53:1:311:A:H5''	1.96	0.66
34:J:50:GLY:HA2	34:J:65:LYS:HE3	1.78	0.66
11:l:29:LYS:HE3	53:1:566:U:H5''	1.76	0.66
52:3:346:G:C2'	52:3:347:G:H5'	2.26	0.66
53:1:435:C:H2'	53:1:436:C:H5'	1.78	0.66
1:b:153:LEU:H	1:b:153:LEU:HD12	1.61	0.66
7:h:87:GLU:HB3	7:h:95:LEU:HD12	1.76	0.66
52:3:955:U:H3	52:3:1225:A:H61	1.43	0.66
58:8:246:VAL:HG11	58:8:368:ALA:HB2	1.78	0.66
38:N:8:THR:HG22	38:N:9:GLY:H	1.60	0.66
53:1:215:G:H4'	53:1:216:A:H4'	1.76	0.66
53:1:1300:G:H4'	53:1:1301:A:H5'	1.78	0.66
36:L:76:SER:HB3	55:6:33:U:OP1	1.95	0.66
42:R:71:GLU:HA	42:R:74:MET:HE2	1.77	0.66
51:a:211:LYS:HE2	51:a:213:SER:HB3	1.78	0.66
36:L:35:LYS:O	36:L:39:GLU:HG3	1.96	0.65
45:U:18:GLN:HA	45:U:38:PHE:HA	1.78	0.65
53:1:2553:G:H1'	53:1:2582:G:H21	1.61	0.65
54:2:3:C:C3'	54:2:4:C:H5''	2.26	0.65
58:8:177:LYS:HE3	58:8:185:TRP:CD1	2.31	0.65
53:1:962:G:H21	53:1:2250:G:H1	1.45	0.65
57:7:7:A:H3'	57:7:8:U:H5''	1.77	0.65
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.79	0.65
39:O:41:PRO:HG2	52:3:1150:A:C2	2.31	0.65
53:1:121:G:H4'	53:1:149:A:H5'	1.77	0.65
8:i:91:LYS:HB2	8:i:95:ASP:OD1	1.97	0.65
16:q:23:TYR:CD1	53:1:533:G:H5'	2.32	0.65
40:P:111:ASP:HB2	50:Z:19:LYS:HE3	1.77	0.65
8:i:25:PRO:HB2	53:1:1095:A:H61	1.61	0.65
18:s:41:LYS:HD3	53:1:2010:G:P	2.37	0.65
53:1:1394:U:H4'	53:1:1603:A:H4'	1.77	0.65
57:7:16:U:H2'	57:7:17:C:H4'	1.79	0.65
58:8:215:ILE:HG13	58:8:228:VAL:HG13	1.79	0.65
8:i:20:SER:HB2	8:i:21:PRO:HD3	1.79	0.65
50:Z:13:VAL:HG23	50:Z:15:LEU:HG	1.79	0.65
53:1:783:A:H2'	53:1:784:G:H4'	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:70:LYS:O	49:Y:73:ARG:HG2	1.96	0.64
53:1:542:C:H2'	53:1:543:G:H5''	1.79	0.64
28:D:11:LYS:CE	53:1:686:U:H5''	2.28	0.64
53:1:2553:G:H3'	53:1:2554:U:H5''	1.79	0.64
6:g:117:LEU:HD21	6:g:121:VAL:HA	1.79	0.64
50:Z:49:ALA:O	50:Z:53:LYS:HG3	1.98	0.64
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.80	0.64
23:x:17:ARG:HE	23:x:23:ALA:HB2	1.61	0.64
36:L:113:LYS:HB2	36:L:117:LEU:HD23	1.78	0.64
52:3:202:G:H21	52:3:466:A:H61	1.46	0.64
6:g:5:LEU:HD13	6:g:36:ALA:HB2	1.80	0.64
35:K:47:LEU:HD13	35:K:57:ALA:H	1.62	0.64
38:N:32:ARG:HD3	38:N:36:GLN:HE21	1.62	0.64
52:3:1137:C:H5'	52:3:1138:G:H5'	1.79	0.64
52:3:1259:C:H3'	52:3:1260:G:C5'	2.26	0.64
53:1:473:G:O2'	53:1:474:G:H5'	1.97	0.64
19:t:77:ARG:NE	53:1:63:A:H4'	2.12	0.64
6:g:132:PHE:HB2	6:g:140:ALA:HB3	1.79	0.64
36:L:142:ARG:HH11	55:6:42:G:H5''	1.62	0.64
49:Y:4:LYS:NZ	49:Y:6:ALA:HB3	2.13	0.64
28:D:12:ARG:NE	28:D:44:VAL:HG21	2.13	0.63
31:G:94:ARG:NE	52:3:1099:G:OP1	2.30	0.63
39:O:59:LYS:HE2	52:3:972:C:OP1	1.98	0.63
53:1:2296:U:H5''	53:1:2297:A:OP1	1.98	0.63
4:e:3:LEU:HA	4:e:6:TYR:HB3	1.80	0.63
17:r:68:ARG:HH11	17:r:90:ARG:HB2	1.61	0.63
52:3:501:C:H2'	52:3:502:A:H8	1.63	0.63
52:3:950:U:H2'	52:3:951:G:C8	2.33	0.63
35:K:29:ILE:HD12	35:K:29:ILE:H	1.62	0.63
52:3:1379:G:O2'	52:3:1380:U:H5'	1.98	0.63
53:1:1105:U:H2'	53:1:1106:G:H5''	1.79	0.63
4:e:105:ILE:C	4:e:108:PRO:HD2	2.22	0.63
10:k:102:PRO:HB3	10:k:121:GLU:HB2	1.80	0.63
38:N:111:GLU:OE2	52:3:1186:G:H4'	1.98	0.63
42:R:70:ARG:O	42:R:74:MET:HG3	1.98	0.63
49:Y:23:ARG:O	49:Y:26:MET:HG3	1.99	0.63
52:3:29:U:O2'	52:3:30:U:H5'	1.99	0.63
53:1:2285:C:O2'	53:1:2287:A:H1'	1.99	0.63
37:M:55:LYS:HE3	52:3:653:U:O2	1.98	0.63
46:V:74:LEU:HD23	46:V:75:VAL:N	2.14	0.63
52:3:1497:G:O2'	52:3:1498:U:H5'	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:103:ARG:HH21	33:I:164:ARG:HD3	1.62	0.63
38:N:94:ARG:HA	38:N:97:LEU:HB3	1.80	0.63
40:P:43:TRP:HZ2	52:3:686:U:H1'	1.63	0.63
52:3:26:A:N6	52:3:558:G:H1'	2.13	0.63
19:t:56:GLU:HG2	19:t:88:LYS:HG2	1.80	0.63
44:T:4:THR:HG23	52:3:659:U:H5''	1.80	0.63
2:c:149:ASN:HB3	53:1:2572:A:OP2	1.98	0.63
5:f:70:LEU:HD23	5:f:71:LEU:HD12	1.81	0.63
38:N:118:ARG:HD3	38:N:122:ARG:HG2	1.81	0.63
53:1:2134:A:N6	53:1:2157:G:H4'	2.13	0.62
53:1:2398:U:H2'	53:1:2399:G:H8	1.63	0.62
43:S:1:ALA:HA	52:3:1049:U:H5	1.65	0.62
52:3:1506:U:O2'	52:3:1507:A:H5'	1.98	0.62
1:b:106:PRO:HG2	1:b:109:LEU:HD22	1.82	0.62
38:N:125:GLN:NE2	52:3:942:G:H21	1.96	0.62
41:Q:73:LEU:HD21	41:Q:79:ILE:HG21	1.81	0.62
53:1:2432:A:H1'	55:6:75:C:H4'	1.82	0.62
2:c:142:VAL:CG2	2:c:143:PRO:HD2	2.28	0.62
33:I:8:LEU:HD11	33:I:21:LYS:HD2	1.80	0.62
38:N:125:GLN:HA	52:3:1342:C:O2'	2.00	0.62
52:3:1199:U:H2'	52:3:1200:C:H5'	1.82	0.62
53:1:713:G:H21	53:1:718:A:H62	1.47	0.62
53:1:766:U:H2'	53:1:767:U:C6	2.34	0.62
54:2:65:U:H3'	54:2:108:A:H61	1.63	0.62
1:b:160:TYR:HB3	1:b:193:GLU:HG2	1.81	0.62
25:z:4:ILE:HG23	25:z:6:ILE:HD11	1.81	0.62
52:3:1230:C:H5'	55:5:30:G:H5''	1.81	0.62
52:3:32:A:H2'	52:3:33:A:C8	2.34	0.62
52:3:715:A:H2'	52:3:716:A:C8	2.34	0.62
5:f:83:THR:HG22	5:f:133:LYS:HG2	1.80	0.62
35:K:10:VAL:HB	35:K:58:HIS:HB3	1.80	0.62
51:a:174:THR:OG1	53:1:2124:G:H4'	2.00	0.62
53:1:112:U:H2'	53:1:113:U:H5'	1.81	0.62
4:e:3:LEU:HD23	4:e:100:GLU:HG2	1.80	0.62
4:e:140:ILE:HG22	4:e:142:TYR:H	1.65	0.62
10:k:109:SER:O	10:k:110:GLU:HG3	2.00	0.62
58:8:261:MET:HG3	58:8:266:LEU:HD11	1.80	0.62
7:h:59:LEU:HG	7:h:61:ARG:H	1.63	0.62
42:R:22:TYR:HB3	42:R:65:GLU:HG3	1.82	0.62
53:1:1319:C:O2'	53:1:1320:C:H5'	2.00	0.61
53:1:1755:A:H2'	53:1:1756:G:H5'	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1856:U:H2'	53:1:1857:G:O4'	2.00	0.61
53:1:2398:U:H2'	53:1:2399:G:C8	2.35	0.61
5:f:95:ALA:HB1	5:f:130:ILE:HD11	1.81	0.61
33:I:150:LYS:HA	33:I:154:VAL:HB	1.81	0.61
34:J:55:VAL:HG13	34:J:56:PRO:CD	2.29	0.61
53:1:2163:A:H2'	53:1:2164:C:H5'	1.82	0.61
53:1:2197:U:O2'	53:1:2198:A:H5''	1.99	0.61
7:h:54:VAL:HG12	7:h:83:ALA:HB1	1.82	0.61
53:1:1825:U:H2'	53:1:1826:G:H8	1.65	0.61
54:2:3:C:H3'	54:2:4:C:H5''	1.82	0.61
10:k:70:ARG:HG2	10:k:76:VAL:HG12	1.83	0.61
10:k:92:GLU:CG	10:k:93:GLN:H	2.12	0.61
18:s:66:ILE:H	18:s:66:ILE:HD12	1.65	0.61
53:1:445:C:O2'	53:1:446:G:H5'	2.01	0.61
58:8:122:LEU:HD13	58:8:374:ARG:HG2	1.83	0.61
10:k:35:VAL:HG13	10:k:36:GLY:H	1.65	0.61
26:B:29:VAL:HG13	26:B:34:GLY:HA2	1.83	0.61
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.83	0.61
53:1:1186:G:H2'	53:1:1187:G:O4'	2.01	0.61
4:e:65:LEU:HD12	54:2:41:G:H21	1.66	0.61
12:m:75:GLU:HB3	12:m:90:GLU:CD	2.25	0.61
53:1:1183:U:H2'	53:1:1184:U:C6	2.35	0.61
9:j:7:LYS:HG2	53:1:538:A:H4'	1.83	0.61
52:3:130:A:O2'	52:3:264:C:H5'	2.01	0.61
52:3:411:A:H1'	52:3:413:G:H1'	1.82	0.61
52:3:946:A:H2'	52:3:947:G:H8	1.66	0.61
1:b:255:LYS:HD3	1:b:269:ARG:HH12	1.65	0.61
40:P:12:ARG:O	40:P:13:LYS:HG2	2.00	0.61
49:Y:23:ARG:HH22	49:Y:63:LYS:HG3	1.65	0.61
58:8:113:MET:H	58:8:116:THR:HB	1.66	0.61
1:b:255:LYS:HZ2	53:1:1844:C:H4'	1.64	0.61
10:k:92:GLU:HG3	10:k:93:GLN:H	1.64	0.61
16:q:24:TYR:HE2	53:1:2020:A:H4'	1.66	0.61
52:3:673:A:H2'	52:3:674:G:C8	2.36	0.61
41:Q:4:ASN:ND2	52:3:880:C:OP1	2.34	0.61
41:Q:33:CYS:HB2	41:Q:54:VAL:HG13	1.82	0.61
52:3:54:C:H2'	52:3:352:C:H41	1.65	0.61
52:3:572:A:H5''	52:3:917:G:H4'	1.83	0.61
53:1:2834:G:H2'	53:1:2879:A:H61	1.66	0.60
33:I:49:ASP:HA	33:I:52:VAL:HG22	1.82	0.60
37:M:11:THR:HG21	52:3:876:C:H1'	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:181:A:H1'	53:1:435:C:H5'	1.83	0.60
53:1:2715:C:C2'	53:1:2716:C:H5''	2.31	0.60
2:c:11:MET:HG3	2:c:25:THR:HG22	1.82	0.60
11:l:110:VAL:HB	11:l:127:VAL:HG13	1.83	0.60
33:I:190:LEU:HD12	33:I:192:ALA:N	2.10	0.60
52:3:1258:G:H2'	52:3:1259:C:C6	2.36	0.60
53:1:1874:C:H2'	53:1:1875:G:O4'	2.00	0.60
39:O:53:ILE:HG12	52:3:1060:U:H5''	1.82	0.60
19:t:61:LEU:HB3	53:1:1341:G:H4'	1.83	0.60
49:Y:4:LYS:HZ3	49:Y:6:ALA:HB3	1.66	0.60
53:1:225:C:H2'	53:1:226:A:O4'	2.02	0.60
53:1:1930:G:N2	53:1:1968:G:H2'	2.16	0.60
53:1:2799:A:H2'	53:1:2800:A:H5'	1.82	0.60
1:b:156:SER:O	1:b:194:VAL:HG21	2.02	0.60
42:R:67:ASP:HA	42:R:70:ARG:HH11	1.65	0.60
53:1:2432:A:H1'	55:6:75:C:C4'	2.32	0.60
58:8:216:GLU:O	58:8:289:ARG:NH1	2.34	0.60
58:8:343:GLU:HB2	58:8:360:VAL:HB	1.83	0.60
3:d:68:ALA:HA	53:1:1255:U:C6	2.36	0.60
12:m:12:MET:HA	53:1:910:A:N6	2.15	0.60
52:3:663:A:H5'	52:3:836:G:OP1	2.02	0.60
48:X:28:LYS:HE3	48:X:29:PRO:HD2	1.84	0.60
51:a:23:ILE:HG23	51:a:189:LEU:HD21	1.83	0.60
51:a:181:ASP:HB2	51:a:184:LYS:HD3	1.84	0.60
53:1:2248:C:C2'	53:1:2249:U:H5'	2.32	0.60
19:t:3:ARG:NH1	53:1:141:G:O6	2.34	0.59
20:u:17:ASP:HB3	20:u:20:LYS:HD2	1.84	0.59
50:Z:23:GLU:C	50:Z:25:ALA:H	2.10	0.59
51:a:3:LYS:HD2	53:1:2107:G:O3'	2.01	0.59
55:5:20:U:H3'	55:5:21:A:H5'	1.83	0.59
4:e:48:LEU:HA	4:e:51:ASN:HD22	1.67	0.59
28:D:24:THR:HG23	28:D:27:GLY:H	1.66	0.59
52:3:1005:A:H2'	52:3:1006:G:O4'	2.02	0.59
53:1:2298:A:H62	53:1:2318:G:H21	1.51	0.59
5:f:126:THR:HG22	5:f:128:THR:H	1.67	0.59
31:G:67:LEU:HD23	31:G:68:PHE:N	2.17	0.59
51:a:205:LYS:HE3	53:1:1860:G:O2'	2.02	0.59
57:7:50:U:H3	57:7:64:A:H61	1.50	0.59
11:l:101:ILE:HG13	11:l:102:GLY:N	2.16	0.59
22:w:21:ARG:HD2	22:w:25:GLU:OE2	2.01	0.59
52:3:1308:U:H2'	52:3:1309:G:C8	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:1:MET:H1	17:r:43:ASN:HA	1.68	0.59
43:S:5:MET:HE2	52:3:981:U:OP1	2.03	0.59
52:3:225:C:H2'	52:3:226:G:H5''	1.83	0.59
53:1:593:U:H2'	53:1:594:U:C6	2.37	0.59
53:1:694:U:C2'	53:1:695:G:H5''	2.33	0.59
53:1:2281:A:O2'	53:1:2282:G:H5'	2.02	0.59
3:d:46:GLN:HB3	3:d:83:VAL:HG21	1.85	0.59
41:Q:32:VAL:HB	41:Q:55:ARG:HB3	1.84	0.59
52:3:1033:G:C2'	52:3:1034:G:H5''	2.31	0.59
53:1:532:A:H2'	53:1:532:A:N3	2.17	0.59
53:1:1053:C:C2'	53:1:1054:A:H5''	2.30	0.59
53:1:2039:U:H2'	53:1:2040:G:C8	2.37	0.59
46:V:5:ARG:HD3	52:3:636:U:H5''	1.83	0.59
53:1:2628:C:H3'	53:1:2629:U:H5'	1.85	0.59
1:b:5:CYS:SG	1:b:17:LYS:NZ	2.72	0.59
4:e:107:VAL:CG1	4:e:108:PRO:HD3	2.32	0.59
18:s:93:ALA:HB2	53:1:1614:A:H2	1.67	0.59
32:H:12:GLY:HA3	43:S:96:LYS:HE2	1.83	0.59
35:K:6:ILE:N	35:K:6:ILE:HD12	2.17	0.59
52:3:925:G:H1	52:3:1391:U:H3	1.50	0.59
53:1:704:G:H2'	53:1:726:G:N2	2.18	0.59
53:1:974:G:H1'	53:1:975:A:C8	2.38	0.59
18:s:93:ALA:HB2	53:1:1614:A:C2	2.38	0.59
53:1:576:U:H2'	53:1:577:G:C8	2.38	0.59
53:1:1026:G:H2'	53:1:1027:A:H8	1.68	0.59
53:1:1078:U:C4'	53:1:1079:C:H5''	2.33	0.59
1:b:81:GLU:HB2	1:b:90:ILE:HG13	1.84	0.58
2:c:10:GLY:H	2:c:197:THR:HG23	1.68	0.58
5:f:68:ARG:HD3	5:f:68:ARG:C	2.27	0.58
53:1:1278:C:H2'	53:1:1279:G:H8	1.68	0.58
55:5:6:G:O2'	55:5:7:G:H5'	2.03	0.58
24:y:41:HIS:CG	53:1:96:C:H4'	2.38	0.58
33:I:80:ARG:HE	52:3:613:C:P	2.26	0.58
48:X:14:LEU:HD11	48:X:34:SER:HB2	1.84	0.58
52:3:1218:C:H2'	52:3:1219:A:C8	2.38	0.58
53:1:554:U:H2'	53:1:555:G:O4'	2.03	0.58
53:1:1936:A:H2	53:1:1943:U:H3	1.51	0.58
57:7:15:G:H2'	57:7:16:U:H5'	1.84	0.58
52:3:1342:C:H2'	52:3:1343:G:C8	2.38	0.58
58:8:261:MET:HG3	58:8:275:VAL:HG12	1.85	0.58
2:c:183:GLU:OE2	2:c:184:ARG:HG3	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:67:PRO:HG2	35:K:70:VAL:CG2	2.34	0.58
7:h:23:LEU:HD13	7:h:118:ILE:CG1	2.31	0.58
24:y:31:GLN:HG3	24:y:36:GLN:HB2	1.85	0.58
53:1:2297:A:N6	53:1:2319:G:H1'	2.18	0.58
53:1:2818:U:H2'	53:1:2819:G:H8	1.67	0.58
16:q:5:ARG:NH1	53:1:585:G:N7	2.52	0.58
33:I:4:LEU:HD23	52:3:406:G:H5''	1.85	0.58
52:3:128:G:O2'	52:3:129:A:H5'	2.03	0.58
57:7:7:A:H3'	57:7:8:U:C5'	2.33	0.58
14:o:37:ALA:HB3	14:o:78:VAL:HG21	1.86	0.58
53:1:1367:A:H2'	53:1:1368:G:H5'	1.85	0.58
53:1:2233:U:H2'	53:1:2234:G:C8	2.39	0.58
5:f:157:LYS:HD2	53:1:2658:C:O3'	2.02	0.58
53:1:278:A:H2'	53:1:278:A:N3	2.19	0.58
8:i:71:LYS:HZ1	8:i:116:MET:HE1	1.68	0.58
39:O:45:ARG:HB2	39:O:69:THR:HB	1.86	0.58
52:3:1306:A:N6	52:3:1331:G:H1'	2.19	0.58
53:1:2238:G:H2'	53:1:2238:G:N3	2.18	0.58
27:C:39:ASP:OD2	27:C:42:VAL:HG22	2.04	0.57
31:G:166:ASP:HB2	31:G:190:SER:HB2	1.85	0.57
1:b:239:PHE:HB3	53:1:1903:G:OP1	2.04	0.57
28:D:12:ARG:HE	28:D:44:VAL:HG21	1.66	0.57
39:O:52:LEU:HB2	43:S:80:ARG:HD2	1.85	0.57
47:W:70:THR:HG23	47:W:72:ARG:H	1.68	0.57
52:3:1256:A:H1'	52:3:1258:G:C4	2.39	0.57
53:1:917:A:H5''	53:1:2268:A:H61	1.68	0.57
53:1:1597:A:H5''	53:1:1598:A:H5'	1.85	0.57
15:p:92:ARG:HD3	53:1:1753:G:H5''	1.86	0.57
35:K:52:ASN:O	35:K:53:LYS:CG	2.49	0.57
36:L:28:ILE:HD11	36:L:104:VAL:HG21	1.85	0.57
17:r:76:LYS:HB2	17:r:85:LYS:HB3	1.87	0.57
20:u:73:ASN:HD22	20:u:76:THR:H	1.52	0.57
52:3:837:U:H2'	52:3:838:G:H8	1.70	0.57
52:3:1436:U:H2'	52:3:1437:A:H8	1.70	0.57
53:1:864:G:O2'	53:1:865:C:H5'	2.04	0.57
33:I:100:VAL:O	33:I:104:MET:HG2	2.05	0.57
41:Q:48:LEU:HB3	52:3:520:A:OP1	2.05	0.57
42:R:76:ILE:HG22	42:R:80:MET:HE2	1.86	0.57
2:c:24:VAL:HG11	2:c:188:LEU:HB3	1.86	0.57
3:d:63:LYS:HE3	53:1:2444:G:OP2	2.05	0.57
29:E:1:PRO:HD2	53:1:591:U:H1'	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:2:ILE:HD13	2:c:90:PHE:CE2	2.40	0.57
11:l:48:ARG:HE	53:1:666:A:H4'	1.69	0.57
39:O:5:ARG:HG2	39:O:79:PRO:HB3	1.87	0.57
53:1:222:A:H61	53:1:232:G:H1'	1.68	0.57
53:1:310:A:H2'	53:1:311:A:H5''	1.86	0.57
53:1:1909:C:H2'	53:1:1910:G:H8	1.70	0.57
57:7:53:G:H5'	58:8:321:THR:HB	1.87	0.57
7:h:31:ARG:O	7:h:31:ARG:HD2	2.05	0.57
12:m:109:PRO:HD2	12:m:112:LEU:HD13	1.87	0.57
17:r:39:LEU:O	17:r:49:ILE:HG23	2.05	0.57
36:L:3:ARG:NE	52:3:932:C:H5''	2.19	0.57
42:R:112:ARG:HD3	52:3:1229:A:OP2	2.04	0.57
52:3:405:U:C3'	52:3:406:G:H5'	2.31	0.57
53:1:729:G:H4'	53:1:763:G:C5'	2.35	0.57
53:1:745:G:O2'	53:1:748:G:H1'	2.05	0.57
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.87	0.57
14:o:30:ARG:HA	14:o:35:ILE:HG13	1.87	0.57
30:F:7:VAL:HG22	30:F:38:GLY:O	2.04	0.57
52:3:1345:U:H4'	52:3:1346:A:H8	1.69	0.57
43:S:41:TRP:HZ3	48:X:8:PRO:HD2	1.70	0.57
52:3:911:U:H2'	52:3:912:C:C6	2.40	0.57
53:1:996:A:H2'	53:1:997:G:H8	1.70	0.57
1:b:52:HIS:HA	1:b:216:ARG:HB3	1.85	0.56
32:H:106:ARG:N	32:H:106:ARG:HD2	2.20	0.56
32:H:120:THR:HA	32:H:123:LEU:HD12	1.86	0.56
34:J:23:THR:HA	34:J:28:ARG:HA	1.86	0.56
34:J:133:ILE:O	34:J:136:VAL:HG12	2.05	0.56
53:1:1965:C:H5''	53:1:1966:A:H2'	1.86	0.56
2:c:136:ASN:HD21	2:c:139:SER:C	2.13	0.56
12:m:85:GLY:HA2	53:1:2276:G:H5'	1.87	0.56
15:p:91:VAL:HG21	15:p:96:LEU:HD11	1.88	0.56
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.20	0.56
23:x:13:THR:HG21	53:1:188:G:H5'	1.87	0.56
39:O:10:LEU:HD23	39:O:10:LEU:H	1.70	0.56
53:1:703:U:H2'	53:1:704:G:O4'	2.05	0.56
53:1:2229:U:H2'	53:1:2230:G:H8	1.71	0.56
1:b:255:LYS:NZ	53:1:1844:C:H4'	2.20	0.56
3:d:68:ALA:HA	53:1:1255:U:C5	2.40	0.56
3:d:84:THR:HG21	53:1:672:C:H5''	1.87	0.56
11:l:111:ILE:HD11	53:1:636:G:C6	2.39	0.56
13:n:64:ARG:HG3	53:1:1454:C:O2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:p:104:GLY:HA3	52:3:1432:G:OP1	2.06	0.56
18:s:17:VAL:HB	18:s:76:VAL:HG11	1.86	0.56
18:s:20:VAL:HG21	18:s:43:ALA:HB3	1.87	0.56
36:L:13:PRO:HG2	38:N:45:MET:HE1	1.88	0.56
40:P:63:GLN:HG3	40:P:98:ALA:HB2	1.86	0.56
45:U:14:ARG:HH12	52:3:618:C:H1'	1.70	0.56
45:U:46:LYS:CD	52:3:617:G:H5''	2.36	0.56
51:a:11:ILE:HG23	51:a:33:LEU:HD22	1.88	0.56
52:3:410:G:H2'	52:3:429:U:C4	2.40	0.56
52:3:1306:A:H62	52:3:1331:G:H1'	1.70	0.56
53:1:598:U:H2'	53:1:599:A:C8	2.41	0.56
53:1:2799:A:C2'	53:1:2800:A:H5'	2.35	0.56
55:6:18:G:H22	55:6:55:U:H6	1.54	0.56
10:k:114:LYS:HE3	10:k:118:LEU:HD11	1.87	0.56
33:I:70:GLN:HG3	52:3:402:G:OP1	2.06	0.56
47:W:59:LYS:HD3	52:3:735:C:H5'	1.88	0.56
52:3:715:A:H2'	52:3:716:A:H8	1.71	0.56
53:1:1810:A:H2'	53:1:1811:G:O4'	2.05	0.56
1:b:156:SER:OG	53:1:1818:U:H5'	2.06	0.56
20:u:98:ASN:O	20:u:100:GLU:HG2	2.05	0.56
26:B:54:ILE:HG23	26:B:56:LYS:H	1.69	0.56
27:C:47:ILE:N	27:C:47:ILE:HD12	2.19	0.56
28:D:9:VAL:HG12	53:1:1309:G:OP1	2.05	0.56
8:i:45:THR:HG22	8:i:50:LYS:HG2	1.88	0.56
13:n:21:PHE:HA	13:n:24:MET:HG2	1.86	0.56
33:I:67:LEU:HD22	52:3:546:A:OP2	2.06	0.56
50:Z:53:LYS:O	50:Z:57:LYS:HG2	2.06	0.56
52:3:1071:C:H2'	52:3:1072:G:H8	1.71	0.56
53:1:2156:G:H2'	53:1:2157:G:H5'	1.87	0.56
7:h:33:VAL:HG22	7:h:34:THR:N	2.17	0.56
12:m:64:TRP:HE1	53:1:873:C:H4'	1.71	0.56
43:S:8:ARG:NH1	52:3:981:U:OP1	2.39	0.56
52:3:758:C:H4'	52:3:880:C:H4'	1.88	0.56
53:1:1509:A:H2'	53:1:1510:G:C8	2.41	0.56
58:8:32:ILE:HD11	58:8:196:LEU:HD11	1.86	0.56
1:b:210:ALA:O	1:b:215:VAL:HG22	2.05	0.56
35:K:3:HIS:O	35:K:92:THR:HG22	2.06	0.56
52:3:501:C:H2'	52:3:502:A:C8	2.41	0.56
52:3:1138:G:H3'	52:3:1138:G:N3	2.21	0.56
52:3:1354:U:H2'	52:3:1355:G:H8	1.71	0.56
53:1:2116:G:H1	53:1:2171:A:H61	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2267:A:H5''	53:1:2268:A:H5'	1.88	0.56
53:1:2457:U:O2'	53:1:2458:G:H5'	2.05	0.56
55:5:69:C:H2'	55:5:70:G:H8	1.71	0.56
52:3:304:U:O2'	52:3:305:G:H5'	2.06	0.56
52:3:1346:A:C2'	52:3:1347:G:H4'	2.35	0.56
53:1:45:G:C5'	53:1:46:G:H5'	2.29	0.56
53:1:2605:U:H2'	53:1:2606:C:C6	2.41	0.56
2:c:194:PRO:HA	53:1:2680:U:H5'	1.88	0.56
12:m:4:PRO:HG2	12:m:70:ASP:HA	1.88	0.56
13:n:8:ARG:HB2	13:n:43:GLU:HG3	1.87	0.56
35:K:51:ILE:C	35:K:53:LYS:H	2.14	0.56
35:K:92:THR:OG1	35:K:93:LYS:N	2.36	0.56
37:M:29:SER:OG	52:3:589:U:H5''	2.06	0.56
42:R:18:LEU:HD23	42:R:18:LEU:O	2.06	0.56
49:Y:67:HIS:ND1	52:3:262:A:H5'	2.21	0.56
55:5:76:A:H5'	55:5:76:A:C8	2.41	0.56
3:d:109:LEU:HD13	3:d:112:LEU:HD12	1.88	0.55
41:Q:52:CYS:HB3	41:Q:66:ILE:HD11	1.88	0.55
43:S:63:CYS:HB3	43:S:67:GLY:H	1.70	0.55
52:3:1346:A:H2'	52:3:1346:A:N3	2.21	0.55
53:1:222:A:N6	53:1:232:G:H1'	2.21	0.55
53:1:367:G:H2'	53:1:368:A:O4'	2.06	0.55
53:1:616:A:H2'	53:1:617:G:O4'	2.05	0.55
12:m:41:LEU:HD11	12:m:124:LEU:HD12	1.87	0.55
15:p:102:ARG:NH2	53:1:1755:A:H5'	2.21	0.55
18:s:84:ARG:HE	53:1:1323:C:H5''	1.72	0.55
51:a:55:SER:HA	51:a:58:ASN:ND2	2.21	0.55
53:1:2579:C:O2'	53:1:2580:U:H5'	2.06	0.55
7:h:31:ARG:HH22	7:h:107:GLU:HA	1.72	0.55
22:w:12:SER:OG	53:1:2262:U:H5	1.90	0.55
33:I:123:MET:HE2	33:I:145:ARG:HA	1.88	0.55
38:N:46:VAL:HA	38:N:49:GLN:HE21	1.70	0.55
1:b:148:GLY:HA3	53:1:2205:A:H5'	1.89	0.55
9:j:113:PRO:HD3	53:1:529:A:OP2	2.07	0.55
12:m:64:TRP:NE1	53:1:873:C:H4'	2.20	0.55
11:l:93:ASN:O	11:l:94:THR:HG22	2.06	0.55
15:p:7:LEU:O	15:p:7:LEU:HD23	2.07	0.55
52:3:225:C:C3'	52:3:226:G:H5''	2.37	0.55
2:c:12:THR:HG22	2:c:13:ARG:H	1.71	0.55
15:p:31:VAL:HG21	15:p:40:GLN:HE21	1.71	0.55
31:G:110:ILE:O	31:G:114:LYS:HG2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:249:C:H2'	53:1:2394:C:O2'	2.05	0.55
53:1:445:C:C2'	53:1:446:G:H5'	2.37	0.55
53:1:502:A:H2'	53:1:503:A:H5'	1.87	0.55
53:1:1906:G:C3'	53:1:1907:G:H5''	2.37	0.55
58:8:333:PHE:O	58:8:334:ARG:HG2	2.07	0.55
22:w:36:GLN:NE2	22:w:39:THR:HA	2.21	0.55
45:U:38:PHE:CZ	52:3:626:G:H4'	2.41	0.55
53:1:750:A:H2'	53:1:751:A:H5''	1.88	0.55
53:1:1930:G:H22	53:1:1968:G:H2'	1.72	0.55
11:l:38:GLN:HG3	53:1:805:G:H5''	1.88	0.55
12:m:31:PHE:HE2	12:m:108:VAL:O	1.90	0.55
25:z:50:VAL:O	25:z:54:VAL:HG22	2.07	0.55
32:H:112:ALA:HB1	32:H:199:VAL:HG13	1.89	0.55
48:X:9:PHE:CD2	52:3:1318:A:H4'	2.41	0.55
52:3:337:G:H2'	52:3:338:A:C8	2.42	0.55
53:1:2318:G:H2'	53:1:2319:G:O4'	2.07	0.55
10:k:104:THR:HG22	10:k:106:GLU:H	1.72	0.55
36:L:56:SER:OG	36:L:59:GLU:HG2	2.07	0.55
51:a:15:VAL:HG21	51:a:220:ALA:HB3	1.88	0.55
53:1:2314:A:H2'	53:1:2315:G:C8	2.41	0.55
31:G:150:ILE:N	31:G:150:ILE:HD12	2.21	0.55
40:P:63:GLN:O	40:P:67:GLU:HG3	2.06	0.55
44:T:45:HIS:O	44:T:47:LYS:N	2.40	0.55
50:Z:34:ARG:HD2	50:Z:36:PHE:HE1	1.72	0.55
52:3:946:A:H2'	52:3:947:G:C8	2.42	0.55
53:1:2241:A:H2'	53:1:2242:G:C8	2.41	0.55
7:h:118:ILE:HB	7:h:119:PRO:HD3	1.89	0.54
37:M:3:GLN:HE22	52:3:755:G:H21	1.54	0.54
48:X:77:ARG:NH2	52:3:1225:A:H4'	2.22	0.54
18:s:74:ILE:HG23	18:s:74:ILE:O	2.07	0.54
41:Q:78:VAL:O	41:Q:102:ASP:HB2	2.08	0.54
52:3:70:U:H4'	52:3:71:A:H8	1.72	0.54
52:3:243:A:H4'	52:3:244:U:H3'	1.89	0.54
52:3:1527:U:O2'	52:3:1528:U:H5'	2.07	0.54
53:1:948:C:H2'	53:1:949:G:C8	2.42	0.54
4:e:97:GLU:OE1	4:e:97:GLU:N	2.40	0.54
13:n:99:LYS:H	13:n:99:LYS:HD2	1.71	0.54
39:O:73:LEU:HD12	52:3:1125:U:H1'	1.89	0.54
41:Q:23:LEU:HD23	41:Q:29:LYS:HZ1	1.72	0.54
52:3:320:A:H2'	52:3:321:A:C8	2.43	0.54
52:3:1402:C:H2'	52:3:1403:C:O4'	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:690:G:O2'	53:1:691:C:H5'	2.08	0.54
53:1:704:G:H2'	53:1:726:G:H22	1.71	0.54
53:1:828:U:H4'	53:1:831:G:N1	2.22	0.54
53:1:2156:G:C2'	53:1:2157:G:H5'	2.38	0.54
53:1:2208:C:H2'	53:1:2209:G:C8	2.42	0.54
58:8:182:ASP:OD2	58:8:184:GLU:HG2	2.08	0.54
2:c:34:VAL:HG22	2:c:50:VAL:HG12	1.89	0.54
4:e:65:LEU:HD22	54:2:42:C:C5	2.42	0.54
15:p:77:SER:O	15:p:80:VAL:HG22	2.07	0.54
18:s:96:ILE:HG22	53:1:2013:A:H4'	1.89	0.54
34:J:51:LYS:HE3	52:3:1081:A:OP2	2.08	0.54
52:3:335:C:H2'	52:3:336:A:C8	2.42	0.54
52:3:1158:C:H2'	52:3:1159:U:H4'	1.89	0.54
53:1:1077:A:C2'	53:1:1078:U:H5'	2.37	0.54
54:2:13:G:N7	54:2:70:C:H4'	2.22	0.54
1:b:7:PRO:O	53:1:1695:G:H1'	2.06	0.54
19:t:73:ARG:NH1	53:1:456:C:N4	2.56	0.54
33:I:131:ILE:HD13	52:3:620:C:N3	2.22	0.54
43:S:84:ARG:HH22	52:3:1059:C:H4'	1.71	0.54
46:V:12:VAL:HG23	46:V:13:SER:H	1.73	0.54
51:a:211:LYS:NZ	53:1:2177:C:H5''	2.22	0.54
53:1:729:G:H4'	53:1:763:G:H5'	1.88	0.54
54:2:29:A:H2'	54:2:30:C:C6	2.43	0.54
12:m:75:GLU:HB3	12:m:90:GLU:OE1	2.08	0.54
34:J:15:ILE:HD11	34:J:37:VAL:HG22	1.89	0.54
44:T:88:ARG:HG3	53:1:714:U:H5	1.73	0.54
53:1:1105:U:C2'	53:1:1106:G:H5''	2.38	0.54
1:b:67:LYS:HB3	1:b:69:ASN:OD1	2.08	0.54
35:K:18:VAL:HG12	35:K:19:PRO:HD3	1.90	0.54
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.88	0.54
48:X:13:HIS:CE1	48:X:14:LEU:HG	2.43	0.54
49:Y:8:LYS:NZ	52:3:104:G:N7	2.51	0.54
42:R:12:LYS:HD3	42:R:16:ILE:HG22	1.89	0.54
46:V:16:MET:HB2	46:V:19:SER:HB2	1.90	0.54
52:3:113:G:H1'	52:3:354:G:H5''	1.89	0.54
53:1:2646:C:H2'	53:1:2647:U:O4'	2.08	0.54
53:1:2756:U:H4'	53:1:2757:A:OP1	2.08	0.54
54:2:2:G:H2'	54:2:3:C:C6	2.43	0.54
3:d:126:VAL:HG13	3:d:156:ASN:OD1	2.07	0.54
6:g:108:VAL:HG12	6:g:110:VAL:HG13	1.90	0.54
32:H:35:ASP:O	32:H:38:VAL:HG12	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:27:ILE:HB	38:N:34:LEU:HD22	1.90	0.54
38:N:46:VAL:HA	38:N:49:GLN:NE2	2.23	0.54
48:X:2:ARG:NH1	52:3:1311:A:H62	2.03	0.54
52:3:1463:U:H2'	52:3:1464:U:C6	2.43	0.54
53:1:565:C:H2'	53:1:566:U:C6	2.42	0.54
53:1:2183:A:H2'	53:1:2184:A:C8	2.42	0.54
53:1:2492:U:H2'	53:1:2493:U:C6	2.43	0.54
58:8:231:ARG:HH11	58:8:231:ARG:HG2	1.73	0.54
18:s:41:LYS:HZ1	26:B:21:LEU:HD11	1.73	0.54
22:w:55:LEU:HD22	22:w:55:LEU:N	2.23	0.54
26:B:14:MET:HE3	53:1:2045:C:H5''	1.90	0.54
37:M:36:ALA:HA	37:M:39:LEU:HD12	1.90	0.54
46:V:18:LYS:HA	46:V:49:ASN:HA	1.90	0.54
52:3:24:U:H2'	52:3:25:C:C6	2.43	0.54
52:3:1333:A:H2'	52:3:1334:G:O4'	2.09	0.54
58:8:173:GLY:HA2	58:8:185:TRP:CZ3	2.43	0.54
52:3:575:G:O2'	52:3:821:G:H5'	2.07	0.53
53:1:20:C:H2'	53:1:21:A:C8	2.43	0.53
53:1:796:C:H2'	53:1:797:G:C8	2.44	0.53
53:1:1662:U:H2'	53:1:1663:G:O4'	2.08	0.53
55:6:71:C:H2'	55:6:72:A:C8	2.43	0.53
9:j:69:ARG:HD3	9:j:89:PHE:HD2	1.73	0.53
21:v:14:LYS:HB2	54:2:98:G:H1	1.74	0.53
40:P:126:ARG:O	50:Z:34:ARG:NH2	2.41	0.53
52:3:570:G:O2'	52:3:819:A:H2'	2.07	0.53
52:3:594:U:H3	52:3:645:G:H1	1.55	0.53
53:1:211:C:H2'	53:1:212:G:C8	2.42	0.53
53:1:2715:C:C3'	53:1:2716:C:H5''	2.38	0.53
10:k:28:SER:OG	53:1:2566:A:N1	2.40	0.53
17:r:49:ILE:HG22	17:r:54:VAL:HG22	1.90	0.53
48:X:5:LYS:HB3	52:3:1313:U:OP2	2.09	0.53
53:1:69:C:O2'	53:1:70:G:H5'	2.08	0.53
53:1:2537:U:H2'	53:1:2538:C:C6	2.43	0.53
12:m:69:PRO:HA	12:m:94:ALA:HB2	1.89	0.53
27:C:4:ILE:N	27:C:4:ILE:HD12	2.23	0.53
31:G:131:LYS:HE3	52:3:1158:C:O2'	2.08	0.53
52:3:235:C:H2'	52:3:236:A:C8	2.44	0.53
53:1:1911:U:H2'	53:1:1918:A:N1	2.24	0.53
53:1:2257:U:O2'	53:1:2258:C:H5'	2.09	0.53
55:5:75:C:C3'	55:5:76:A:H5''	2.39	0.53
42:R:113:LYS:H	42:R:114:PRO:HD2	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:3:ILE:HD12	49:Y:3:ILE:N	2.24	0.53
53:1:2743:U:H2'	53:1:2744:G:C4'	2.39	0.53
53:1:2743:U:H2'	53:1:2744:G:H5''	1.90	0.53
53:1:2818:U:H4'	53:1:2837:A:H4'	1.90	0.53
54:2:3:C:H3'	54:2:4:C:C5'	2.39	0.53
7:h:59:LEU:HB3	7:h:62:ARG:HB2	1.91	0.53
15:p:14:GLN:OE1	15:p:14:GLN:N	2.42	0.53
15:p:105:LYS:O	15:p:108:ARG:HG2	2.08	0.53
31:G:195:VAL:HB	31:G:198:VAL:HG12	1.90	0.53
49:Y:48:LYS:O	49:Y:52:GLU:HG3	2.07	0.53
53:1:2461:A:H1'	53:1:2492:U:C2	2.44	0.53
54:2:78:A:H2'	54:2:79:G:O4'	2.09	0.53
13:n:47:VAL:C	13:n:50:PRO:HD2	2.33	0.53
20:u:42:LYS:NZ	53:1:499:U:H5''	2.24	0.53
37:M:80:PRO:HG2	52:3:878:A:H5''	1.90	0.53
40:P:34:THR:HG22	40:P:40:ALA:HA	1.91	0.53
51:a:30:LEU:HD21	51:a:185:LEU:HD13	1.90	0.53
52:3:244:U:O4	52:3:906:A:H1'	2.08	0.53
52:3:1016:A:H4'	52:3:1218:C:H4'	1.91	0.53
52:3:1352:C:H2'	52:3:1353:G:C8	2.44	0.53
53:1:1083:U:H2'	53:1:1085:A:OP2	2.08	0.53
55:5:69:C:H2'	55:5:70:G:C8	2.44	0.53
57:7:51:U:H2'	57:7:52:G:H8	1.74	0.53
1:b:27:LYS:HG2	1:b:28:PRO:HD2	1.91	0.53
30:F:3:VAL:HG13	30:F:36:ARG:HD3	1.90	0.53
52:3:667:G:H2'	52:3:668:G:C8	2.44	0.53
52:3:1120:C:H2'	52:3:1121:U:C6	2.44	0.53
53:1:11:C:H3'	53:1:12:U:H5''	1.91	0.53
53:1:1447:C:H2'	53:1:1448:G:H8	1.72	0.53
53:1:1720:U:H2'	53:1:1721:G:O4'	2.09	0.53
53:1:2623:G:H2'	53:1:2624:G:H8	1.73	0.53
58:8:212:LEU:HD23	58:8:213:LEU:N	2.24	0.53
4:e:25:MET:CE	54:2:54:G:H21	2.22	0.53
29:E:2:LYS:HB2	53:1:242:G:C8	2.44	0.53
32:H:8:GLY:HA2	32:H:11:LEU:HG	1.89	0.53
40:P:52:ARG:HD2	40:P:56:LYS:HD2	1.91	0.53
52:3:458:U:H2'	52:3:459:A:C8	2.44	0.53
52:3:477:C:H2'	52:3:478:A:C8	2.43	0.53
52:3:1436:U:H2'	52:3:1437:A:C8	2.43	0.53
53:1:20:C:H2'	53:1:21:A:H8	1.73	0.53
53:1:2104:C:H2'	53:1:2105:U:C6	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:133:THR:OG1	2:c:134:HIS:N	2.39	0.53
7:h:58:THR:HG21	7:h:82:ILE:H	1.74	0.53
10:k:113:MET:SD	10:k:116:ILE:HD11	2.49	0.53
38:N:68:GLY:HA2	52:3:1250:A:H4'	1.91	0.53
53:1:458:G:O2'	53:1:459:U:H5	1.92	0.53
53:1:979:A:H2'	53:1:982:C:H42	1.74	0.53
53:1:2328:A:H2'	53:1:2329:U:C6	2.44	0.53
53:1:2795:C:H2'	53:1:2796:U:O4'	2.09	0.53
55:6:21:A:N6	55:6:46:G:H2'	2.23	0.53
2:c:4:LEU:HD22	2:c:32:ASN:HD22	1.74	0.52
6:g:58:LEU:O	6:g:61:VAL:HG12	2.10	0.52
7:h:64:VAL:O	7:h:67:THR:HG22	2.09	0.52
12:m:47:GLU:O	12:m:50:ARG:HB3	2.09	0.52
37:M:65:PHE:CD2	37:M:66:GLN:HG2	2.44	0.52
41:Q:99:GLY:N	41:Q:103:CYS:O	2.40	0.52
52:3:730:G:C2'	52:3:731:G:H5'	2.39	0.52
53:1:1825:U:H2'	53:1:1826:G:C8	2.43	0.52
53:1:2024:G:OP2	53:1:2034:U:H4'	2.08	0.52
23:x:73:ARG:HD2	23:x:75:GLU:OE1	2.08	0.52
52:3:1070:U:H2'	52:3:1071:C:H6	1.75	0.52
53:1:161:A:H3'	53:1:162:U:H5''	1.91	0.52
15:p:28:LYS:HD2	15:p:82:SER:OG	2.09	0.52
23:x:13:THR:CG2	53:1:188:G:H5'	2.39	0.52
52:3:17:U:H2'	52:3:18:C:C6	2.44	0.52
52:3:410:G:H2'	52:3:429:U:O4	2.09	0.52
52:3:1170:A:H2'	52:3:1171:A:O4'	2.09	0.52
53:1:467:G:O2'	53:1:468:G:H5'	2.09	0.52
6:g:40:THR:H	6:g:43:ASN:HD22	1.56	0.52
24:y:52:ARG:HG3	53:1:77:G:H5'	1.91	0.52
52:3:132:C:H5'	52:3:262:A:O2'	2.09	0.52
52:3:764:C:H2'	52:3:765:G:O4'	2.09	0.52
53:1:1344:U:H3'	53:1:1345:C:H5'	1.91	0.52
53:1:2472:G:H2'	53:1:2475:C:H42	1.74	0.52
53:1:2788:C:H2'	53:1:2789:C:C6	2.44	0.52
3:d:106:LYS:HG3	3:d:200:LEU:HD23	1.92	0.52
32:H:84:GLU:O	32:H:88:LYS:HG2	2.10	0.52
38:N:62:LEU:HD12	38:N:62:LEU:N	2.25	0.52
53:1:275:C:H2'	53:1:276:U:C4'	2.39	0.52
53:1:1437:C:H2'	53:1:1438:U:C6	2.45	0.52
53:1:1882:U:H2'	53:1:1883:U:C6	2.45	0.52
53:1:2233:U:H2'	53:1:2234:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2417:C:H2'	53:1:2418:A:H8	1.74	0.52
54:2:48:U:H2'	54:2:49:C:C6	2.43	0.52
7:h:26:VAL:HB	7:h:82:ILE:HG23	1.92	0.52
14:o:63:LYS:NZ	54:2:51:G:H5'	2.23	0.52
33:I:129:VAL:HG22	52:3:619:U:O2'	2.10	0.52
37:M:45:ILE:HD13	37:M:60:LEU:HD22	1.91	0.52
38:N:79:ARG:O	38:N:82:ILE:HG22	2.10	0.52
53:1:2229:U:H2'	53:1:2230:G:C8	2.44	0.52
8:i:78:LEU:HD23	8:i:81:LYS:HE3	1.92	0.52
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.91	0.52
16:q:23:TYR:CE1	53:1:533:G:H5'	2.45	0.52
17:r:74:ILE:H	17:r:74:ILE:HD12	1.74	0.52
38:N:27:ILE:N	38:N:27:ILE:HD12	2.24	0.52
39:O:43:PRO:HA	52:3:1151:A:H5'	1.91	0.52
46:V:30:HIS:HD2	46:V:33:TYR:H	1.58	0.52
52:3:107:G:H2'	52:3:108:G:O4'	2.09	0.52
52:3:860:A:H2'	52:3:861:G:O4'	2.10	0.52
53:1:2350:C:H2'	53:1:2351:G:O4'	2.09	0.52
58:8:309:VAL:HG22	58:8:310:TYR:N	2.24	0.52
26:B:11:LYS:HE3	53:1:2616:C:H5''	1.90	0.52
52:3:252:U:O2	52:3:252:U:H2'	2.08	0.52
52:3:662:U:H2'	52:3:663:A:C8	2.44	0.52
9:j:117:ALA:HA	9:j:120:ARG:HH21	1.73	0.52
18:s:42:LYS:HD3	53:1:2010:G:H4'	1.92	0.52
31:G:166:ASP:OD1	31:G:189:ASN:ND2	2.43	0.52
32:H:35:ASP:O	32:H:39:ARG:HG2	2.10	0.52
52:3:78:A:H2'	52:3:79:G:O4'	2.09	0.52
52:3:231:U:H2'	52:3:232:G:H8	1.74	0.52
52:3:994:A:C8	52:3:1216:A:H4'	2.44	0.52
53:1:581:C:H2'	53:1:582:A:H8	1.75	0.52
53:1:967:U:H2'	53:1:968:C:C6	2.45	0.52
53:1:1258:U:H2'	53:1:1259:G:H8	1.74	0.52
53:1:1775:U:H2'	53:1:1776:G:O4'	2.10	0.52
53:1:1801:A:H5''	53:1:2203:U:C2'	2.38	0.52
54:2:30:C:H2'	54:2:31:C:O4'	2.10	0.52
10:k:6:THR:HG23	53:1:1666:G:H4'	1.92	0.52
21:v:4:ILE:HD13	21:v:47:VAL:HG22	1.90	0.52
24:y:5:GLU:O	24:y:56:LEU:HD21	2.10	0.52
25:z:40:THR:HG23	25:z:43:ILE:H	1.73	0.52
33:I:57:LYS:O	33:I:60:VAL:HG12	2.10	0.52
36:L:16:LYS:HG2	36:L:17:PHE:HD1	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:55:LYS:HE3	36:L:59:GLU:OE2	2.10	0.52
53:1:679:C:H2'	53:1:680:C:C6	2.45	0.52
53:1:742:A:H2'	53:1:743:A:C8	2.45	0.52
53:1:1893:C:H2'	53:1:1894:C:H5'	1.92	0.52
53:1:1918:A:H2	53:1:1919:A:H62	1.57	0.52
53:1:2704:C:H2'	53:1:2705:A:O4'	2.10	0.52
53:1:2724:U:H2'	53:1:2725:A:C8	2.44	0.52
15:p:112:ARG:C	15:p:113:LEU:HD23	2.34	0.51
30:F:37:GLN:OE1	53:1:1125:G:H5'	2.10	0.51
38:N:50:PRO:HG3	38:N:82:ILE:HG21	1.92	0.51
39:O:36:VAL:HG13	39:O:76:ILE:HG12	1.92	0.51
43:S:74:ARG:NH2	52:3:1359:C:OP2	2.43	0.51
48:X:10:ILE:HD13	48:X:40:PHE:CE2	2.45	0.51
52:3:86:G:H4'	52:3:87:C:C5	2.45	0.51
52:3:152:A:H2'	52:3:153:C:H5'	1.92	0.51
53:1:2287:A:O2'	53:1:2288:A:H2'	2.10	0.51
31:G:59:ILE:HA	31:G:62:ARG:HE	1.76	0.51
39:O:40:ILE:HB	39:O:73:LEU:HB2	1.91	0.51
52:3:674:G:H2'	52:3:675:A:C8	2.45	0.51
52:3:779:C:H2'	52:3:780:A:O4'	2.09	0.51
52:3:824:G:H2'	52:3:825:A:H8	1.75	0.51
52:3:1210:C:C2'	52:3:1211:U:H5'	2.40	0.51
53:1:828:U:H2'	53:1:829:A:C8	2.45	0.51
53:1:1258:U:H2'	53:1:1259:G:C8	2.46	0.51
53:1:1796:U:H2'	53:1:1797:G:C8	2.38	0.51
4:e:3:LEU:C	4:e:3:LEU:HD12	2.36	0.51
31:G:27:LYS:N	31:G:28:PRO:CD	2.73	0.51
52:3:605:U:H2'	52:3:606:G:C8	2.45	0.51
52:3:757:U:H2'	52:3:758:C:O4'	2.09	0.51
52:3:1070:U:H2'	52:3:1071:C:C6	2.46	0.51
2:c:16:THR:HG23	2:c:18:ASP:OD1	2.11	0.51
34:J:40:ASP:OD1	34:J:44:ARG:HB2	2.10	0.51
35:K:6:ILE:HG13	35:K:89:VAL:HG12	1.92	0.51
38:N:70:GLY:O	38:N:74:GLN:HG3	2.10	0.51
39:O:29:ALA:O	39:O:33:GLY:HA3	2.10	0.51
40:P:112:VAL:HG22	40:P:112:VAL:O	2.11	0.51
41:Q:109:ARG:HB2	41:Q:118:VAL:HG11	1.93	0.51
52:3:1163:A:H2'	52:3:1164:G:C8	2.45	0.51
53:1:940:G:C3'	53:1:941:A:H5''	2.41	0.51
55:6:65:C:H2'	55:6:66:C:C6	2.46	0.51
58:8:288:GLU:H	58:8:291:GLN:NE2	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:74:ALA:HB2	55:5:57:A:H5'	1.91	0.51
18:s:7:HIS:HB3	18:s:103:ILE:HG13	1.90	0.51
52:3:396:C:C2'	52:3:397:A:H5''	2.39	0.51
52:3:815:A:H5''	52:3:817:C:N4	2.26	0.51
52:3:1323:G:H2'	52:3:1324:A:C8	2.46	0.51
52:3:1325:C:O2'	52:3:1326:U:H5'	2.11	0.51
53:1:639:U:H2'	53:1:640:C:C6	2.46	0.51
7:h:33:VAL:HG13	7:h:35:VAL:H	1.74	0.51
17:r:35:PHE:HB2	17:r:59:ILE:HB	1.91	0.51
31:G:96:LEU:O	31:G:99:MET:HG3	2.10	0.51
46:V:69:THR:HG22	52:3:254:G:OP1	2.11	0.51
53:1:1447:C:H2'	53:1:1448:G:C8	2.46	0.51
53:1:1695:G:H2'	53:1:1696:G:O4'	2.11	0.51
53:1:1827:U:O2'	53:1:1828:G:H5'	2.11	0.51
53:1:1979:U:O2'	53:1:1980:G:H5'	2.10	0.51
58:8:246:VAL:HG12	58:8:247:GLY:H	1.75	0.51
6:g:8:LYS:O	6:g:9:VAL:C	2.53	0.51
9:j:81:ILE:HG23	9:j:82:GLY:N	2.22	0.51
23:x:15:ASN:ND2	53:1:381:G:H5''	2.26	0.51
23:x:18:SER:OG	53:1:2080:A:H5'	2.10	0.51
24:y:31:GLN:HG2	24:y:37:LEU:HB2	1.93	0.51
37:M:12:ARG:NH2	52:3:826:C:H5'	2.26	0.51
42:R:91:ARG:HD2	53:1:888:C:C5	2.46	0.51
48:X:69:LYS:HD2	52:3:1320:C:H5'	1.91	0.51
52:3:335:C:H2'	52:3:336:A:H8	1.75	0.51
53:1:2798:U:H4'	53:1:2799:A:C4	2.46	0.51
7:h:102:ALA:HA	7:h:105:LYS:HG3	1.92	0.51
9:j:80:HIS:CD2	53:1:2642:G:H5'	2.46	0.51
12:m:36:VAL:HG21	12:m:129:THR:HG23	1.92	0.51
19:t:13:ALA:O	19:t:33:LYS:N	2.39	0.51
20:u:27:VAL:HG12	20:u:33:VAL:HG12	1.92	0.51
47:W:41:SER:HB2	47:W:51:GLN:HE21	1.74	0.51
52:3:1354:U:H2'	52:3:1355:G:C8	2.45	0.51
52:3:1413:A:H2	52:3:1487:G:H22	1.57	0.51
53:1:2834:G:O2'	53:1:2835:A:H5'	2.11	0.51
57:7:14:A:H2'	57:7:15:G:O4'	2.11	0.51
11:l:23:ILE:HD12	11:l:23:ILE:N	2.26	0.51
32:H:168:ARG:HD2	32:H:168:ARG:C	2.36	0.51
32:H:193:GLY:HA2	52:3:1206:G:O4'	2.11	0.51
33:I:102:TYR:O	33:I:164:ARG:NH1	2.42	0.51
41:Q:28:GLN:O	41:Q:29:LYS:HD2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:7:ALA:O	43:S:10:VAL:HG22	2.11	0.51
52:3:737:C:H2'	52:3:738:C:C6	2.46	0.51
53:1:255:A:H2'	53:1:256:A:O4'	2.11	0.51
53:1:1506:U:H2'	53:1:1507:C:C6	2.46	0.51
53:1:2066:C:O2'	53:1:2067:G:H5'	2.10	0.51
53:1:2266:A:H4'	53:1:2267:A:N3	2.26	0.51
53:1:2514:U:H2'	53:1:2515:C:C6	2.46	0.51
53:1:2818:U:H4'	53:1:2837:A:C4'	2.41	0.51
5:f:65:GLY:HA3	53:1:2748:A:O2'	2.11	0.51
35:K:86:ARG:HH22	52:3:673:A:H4'	1.75	0.51
40:P:71:ASP:O	40:P:72:ALA:HB3	2.11	0.51
42:R:15:VAL:HG23	42:R:40:GLU:HB2	1.93	0.51
45:U:31:ARG:HB2	52:3:310:G:H5''	1.93	0.51
52:3:637:C:H2'	52:3:638:U:C6	2.46	0.51
52:3:855:U:H2'	52:3:856:C:C6	2.46	0.51
52:3:1060:U:H2'	52:3:1061:G:H8	1.76	0.51
53:1:694:U:C3'	53:1:695:G:H5''	2.40	0.51
53:1:2327:A:H2'	53:1:2328:A:C8	2.46	0.51
53:1:2743:U:C3'	53:1:2744:G:H5''	2.41	0.51
5:f:93:TYR:CE1	5:f:106:LEU:HD12	2.45	0.50
10:k:76:VAL:HG22	15:p:72:VAL:HG12	1.94	0.50
17:r:98:ILE:HD11	17:r:101:ILE:HD11	1.91	0.50
29:E:57:VAL:HA	29:E:60:CYS:SG	2.51	0.50
48:X:39:ILE:HD12	48:X:39:ILE:N	2.26	0.50
50:Z:9:GLU:HB3	50:Z:10:PRO:CD	2.38	0.50
51:a:5:THR:OG1	51:a:8:MET:HE3	2.11	0.50
52:3:1060:U:H3	52:3:1197:A:H61	1.58	0.50
53:1:18:U:H2'	53:1:19:A:C8	2.47	0.50
53:1:290:U:H2'	53:1:291:G:C8	2.45	0.50
53:1:2743:U:H2'	53:1:2744:G:C5'	2.41	0.50
2:c:88:GLU:OE1	2:c:88:GLU:N	2.44	0.50
11:l:101:ILE:HG13	11:l:102:GLY:H	1.74	0.50
20:u:48:VAL:HG12	20:u:52:ASN:HB3	1.93	0.50
40:P:86:LYS:NZ	40:P:114:PRO:HD3	2.26	0.50
41:Q:109:ARG:HG3	41:Q:118:VAL:HG21	1.93	0.50
48:X:49:ALA:HB1	48:X:56:HIS:HB3	1.94	0.50
52:3:399:G:H2'	52:3:400:C:C6	2.46	0.50
52:3:422:C:H5'	52:3:423:G:C2	2.46	0.50
52:3:691:G:H2'	52:3:692:U:C6	2.46	0.50
53:1:26:G:O2'	53:1:27:G:H5'	2.12	0.50
53:1:37:C:H4'	53:1:451:U:OP1	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:211:C:H2'	53:1:212:G:H8	1.76	0.50
53:1:669:G:H2'	53:1:669:G:N3	2.26	0.50
53:1:1175:A:H5'	53:1:1176:U:O4'	2.11	0.50
53:1:2244:U:H2'	53:1:2245:U:O4'	2.11	0.50
53:1:2815:C:H2'	53:1:2816:G:H8	1.76	0.50
57:7:51:U:H2'	57:7:52:G:C8	2.46	0.50
58:8:11:PRO:HD2	58:8:75:ARG:HA	1.94	0.50
7:h:67:THR:N	7:h:68:PRO:CD	2.75	0.50
26:B:1:ALA:H3	53:1:2056:G:N2	2.09	0.50
38:N:53:LEU:O	38:N:53:LEU:HD23	2.12	0.50
41:Q:113:ARG:HB2	41:Q:118:VAL:O	2.11	0.50
42:R:13:HIS:HB2	42:R:16:ILE:HD13	1.93	0.50
42:R:16:ILE:HD12	42:R:16:ILE:N	2.25	0.50
52:3:1230:C:C5'	55:5:30:G:H5''	2.42	0.50
52:3:1514:G:O2'	52:3:1515:G:H5'	2.11	0.50
53:1:598:U:H2'	53:1:599:A:H8	1.75	0.50
53:1:738:G:O2'	53:1:739:A:H5'	2.10	0.50
53:1:2220:U:H2'	53:1:2221:G:H8	1.75	0.50
1:b:55:GLY:H	53:1:692:C:P	2.34	0.50
13:n:79:LEU:O	13:n:80:PHE:HB2	2.10	0.50
32:H:4:VAL:O	32:H:6:PRO:HD3	2.11	0.50
37:M:9:MET:O	37:M:13:ILE:HG13	2.10	0.50
46:V:10:ARG:NH1	46:V:11:VAL:O	2.45	0.50
50:Z:6:ARG:C	50:Z:8:ASN:N	2.65	0.50
52:3:225:C:C2'	52:3:226:G:H5''	2.42	0.50
52:3:950:U:H2'	52:3:951:G:H8	1.74	0.50
53:1:2699:C:H2'	53:1:2700:A:C8	2.46	0.50
54:2:106:G:H2'	54:2:107:G:O4'	2.12	0.50
9:j:135:GLN:HE22	53:1:7:G:H1'	1.76	0.50
18:s:41:LYS:HD3	53:1:2010:G:OP1	2.11	0.50
29:E:60:CYS:C	29:E:62:PRO:HD3	2.36	0.50
29:E:61:LEU:HD12	29:E:61:LEU:O	2.11	0.50
32:H:5:HIS:HB2	43:S:88:MET:HE3	1.93	0.50
36:L:16:LYS:HG2	36:L:17:PHE:CD1	2.47	0.50
40:P:111:ASP:HB3	50:Z:3:ILE:HG23	1.92	0.50
44:T:88:ARG:HG3	53:1:714:U:C5	2.46	0.50
53:1:1071:G:OP1	53:1:1071:G:H3'	2.11	0.50
53:1:2144:G:H1'	53:1:2147:A:H61	1.77	0.50
58:8:229:THR:HA	58:8:276:GLY:HA2	1.93	0.50
1:b:144:GLU:HG2	1:b:151:GLY:N	2.27	0.50
12:m:93:VAL:HG22	12:m:94:ALA:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:63:ARG:NH2	53:1:1454:C:H5'	2.26	0.50
18:s:41:LYS:NZ	26:B:21:LEU:HD11	2.26	0.50
38:N:74:GLN:O	38:N:78:ILE:HG13	2.12	0.50
41:Q:24:GLU:OE2	41:Q:24:GLU:N	2.44	0.50
52:3:601:G:H2'	52:3:602:A:C8	2.47	0.50
53:1:1231:U:H2'	53:1:1232:G:H8	1.77	0.50
53:1:1268:A:H2'	53:1:1269:A:O4'	2.12	0.50
53:1:1563:U:H2'	53:1:1564:C:C6	2.47	0.50
7:h:11:ILE:O	7:h:15:VAL:HG23	2.11	0.50
16:q:86:SER:OG	17:r:50:GLY:O	2.29	0.50
31:G:96:LEU:HD13	52:3:1103:C:H4'	1.93	0.50
32:H:116:ALA:O	32:H:119:ILE:HG22	2.12	0.50
34:J:141:ASP:HA	34:J:144:GLU:HB2	1.92	0.50
42:R:102:LYS:HE2	52:3:952:U:O4	2.12	0.50
52:3:1162:C:H2'	52:3:1163:A:C8	2.47	0.50
53:1:634:C:H2'	53:1:635:C:C6	2.46	0.50
53:1:1434:A:H2'	53:1:1435:G:C8	2.46	0.50
54:2:65:U:H3'	54:2:108:A:N6	2.27	0.50
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.94	0.50
3:d:79:ARG:HH21	53:1:448:U:C4'	2.25	0.50
8:i:110:GLN:HG3	8:i:121:ILE:HD13	1.94	0.50
24:y:31:GLN:HG2	24:y:37:LEU:N	2.26	0.50
33:I:32:LYS:HB3	33:I:35:GLN:HE21	1.76	0.50
34:J:125:LYS:HG2	34:J:127:TYR:CZ	2.46	0.50
35:K:86:ARG:NH2	52:3:673:A:H4'	2.26	0.50
47:W:71:ASP:C	47:W:72:ARG:HD2	2.37	0.50
52:3:423:G:H2'	52:3:424:G:H5'	1.94	0.50
53:1:2849:U:H4'	53:1:2868:A:C2	2.46	0.50
55:6:68:C:H2'	55:6:69:C:C4'	2.42	0.50
1:b:155:ARG:CZ	53:1:1818:U:H5	2.25	0.50
2:c:13:ARG:HG2	15:p:55:HIS:HE1	1.77	0.50
4:e:24:VAL:HG13	4:e:25:MET:HE2	1.94	0.50
13:n:99:LYS:O	26:B:42:ILE:HG23	2.11	0.50
16:q:111:LYS:HG2	17:r:48:LYS:CD	2.39	0.50
17:r:31:GLU:N	17:r:31:GLU:OE1	2.45	0.50
33:I:124:VAL:HA	33:I:142:VAL:HA	1.94	0.50
33:I:153:ARG:HH12	52:3:406:G:H21	1.60	0.50
38:N:22:PRO:HA	38:N:60:LEU:HD13	1.94	0.50
38:N:59:LYS:C	38:N:60:LEU:HD22	2.37	0.50
38:N:107:ALA:HB2	52:3:1117:A:H4'	1.92	0.50
45:U:36:VAL:CG1	45:U:53:ASP:HB3	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:521:G:O2'	52:3:522:C:H5'	2.12	0.50
52:3:966:G:C2	55:5:34:C:H5'	2.47	0.50
53:1:49:A:H5'	53:1:51:G:O4'	2.12	0.50
53:1:215:G:C4'	53:1:216:A:H4'	2.41	0.50
53:1:2266:A:H4'	53:1:2267:A:C2	2.47	0.50
58:8:112:PRO:HD2	58:8:153:GLU:OE2	2.12	0.50
2:c:77:ARG:NH2	2:c:200:ASP:OD2	2.45	0.49
3:d:117:ARG:HH12	11:l:2:ARG:HG2	1.76	0.49
7:h:48:ALA:HB3	7:h:51:TYR:CE1	2.47	0.49
11:l:38:GLN:HE21	53:1:805:G:H5''	1.77	0.49
11:l:79:LEU:HB3	11:l:116:VAL:HG23	1.94	0.49
25:z:52:PHE:HE2	25:z:53:MET:HE3	1.77	0.49
40:P:87:GLY:N	40:P:113:THR:HG22	2.26	0.49
43:S:25:GLU:HA	43:S:28:ALA:HB3	1.94	0.49
52:3:88:U:H2'	52:3:89:U:C6	2.47	0.49
53:1:740:C:H5'	53:1:1784:A:O2'	2.11	0.49
53:1:2286:G:H4'	53:1:2287:A:O5'	2.12	0.49
55:5:47:U:H3'	55:5:48:C:C5'	2.42	0.49
6:g:94:ILE:HD11	6:g:122:LEU:HD22	1.93	0.49
9:j:122:LEU:HD21	9:j:124:VAL:HG13	1.93	0.49
14:o:90:VAL:HG12	14:o:91:SER:H	1.77	0.49
15:p:88:ARG:HH11	15:p:112:ARG:HH11	1.60	0.49
37:M:10:LEU:HD12	37:M:74:ILE:HG12	1.93	0.49
39:O:68:ARG:HB3	39:O:70:HIS:CE1	2.47	0.49
47:W:59:LYS:HD3	52:3:734:G:O2'	2.12	0.49
52:3:321:A:O2'	52:3:322:C:H5'	2.12	0.49
53:1:825:A:H2'	53:1:826:U:O4'	2.12	0.49
53:1:2737:G:H2'	53:1:2738:A:C8	2.47	0.49
58:8:193:ALA:HA	58:8:196:LEU:HD12	1.94	0.49
1:b:135:PRO:HG2	35:K:80:PHE:HD1	1.76	0.49
6:g:40:THR:OG1	6:g:43:ASN:ND2	2.46	0.49
41:Q:49:ARG:HH22	52:3:522:C:H41	1.59	0.49
52:3:667:G:H2'	52:3:668:G:H8	1.77	0.49
53:1:2236:U:H2'	53:1:2237:G:O4'	2.12	0.49
58:8:213:LEU:HD23	58:8:293:LEU:HD13	1.92	0.49
4:e:37:MET:HE3	4:e:151:LEU:HB3	1.93	0.49
10:k:14:SER:OG	10:k:86:LEU:HD12	2.12	0.49
17:r:36:ALA:HA	17:r:58:VAL:HA	1.94	0.49
36:L:30:MET:CE	52:3:1373:G:H4'	2.39	0.49
44:T:21:THR:HA	44:T:26:VAL:HG11	1.93	0.49
46:V:16:MET:HG3	46:V:19:SER:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:214:G:H2'	53:1:215:G:C8	2.47	0.49
2:c:24:VAL:HG12	2:c:25:THR:H	1.77	0.49
18:s:7:HIS:HD2	18:s:103:ILE:HD11	1.76	0.49
25:z:4:ILE:HD11	25:z:56:VAL:HG21	1.95	0.49
49:Y:79:THR:O	49:Y:83:ASN:ND2	2.45	0.49
52:3:1202:U:H2'	52:3:1203:C:O4'	2.13	0.49
52:3:1308:U:H2'	52:3:1309:G:H8	1.78	0.49
53:1:1549:A:H2'	53:1:1550:C:C6	2.47	0.49
53:1:1550:C:H2'	53:1:1551:A:H8	1.76	0.49
53:1:2533:U:H2'	53:1:2534:A:O4'	2.12	0.49
53:1:2655:G:H2'	53:1:2664:G:N1	2.28	0.49
3:d:154:ASP:OD1	3:d:154:ASP:N	2.46	0.49
4:e:140:ILE:N	4:e:140:ILE:HD12	2.27	0.49
12:m:37:GLY:HA3	12:m:126:ILE:HB	1.94	0.49
51:a:62:ALA:HB1	51:a:160:GLN:NE2	2.27	0.49
52:3:1096:C:H2'	52:3:1097:C:C6	2.48	0.49
52:3:1163:A:H2'	52:3:1164:G:H8	1.78	0.49
53:1:581:C:H2'	53:1:582:A:C8	2.48	0.49
53:1:996:A:H2'	53:1:997:G:C8	2.48	0.49
53:1:2360:G:H2'	53:1:2361:G:H5'	1.95	0.49
53:1:2366:A:H2'	53:1:2367:G:O4'	2.12	0.49
53:1:2376:A:H2'	53:1:2377:A:O4'	2.13	0.49
53:1:2818:U:H2'	53:1:2819:G:C8	2.46	0.49
1:b:224:MET:SD	1:b:229:HIS:HB2	2.52	0.49
11:l:82:LEU:HD23	11:l:82:LEU:O	2.11	0.49
14:o:82:ALA:HB1	14:o:87:ILE:HD11	1.95	0.49
20:u:39:ASN:HD22	20:u:62:ALA:HB3	1.78	0.49
35:K:3:HIS:N	35:K:92:THR:HG22	2.28	0.49
39:O:41:PRO:HG2	52:3:1150:A:H2	1.75	0.49
43:S:20:PHE:O	43:S:21:ALA:HB3	2.13	0.49
51:a:166:ASP:HB3	53:1:2122:U:H4'	1.94	0.49
52:3:163:C:H2'	52:3:164:G:O4'	2.12	0.49
52:3:443:C:H2'	52:3:444:G:C8	2.47	0.49
53:1:277:G:H4'	53:1:278:A:N7	2.27	0.49
53:1:2086:U:H2'	53:1:2087:G:H8	1.76	0.49
53:1:2163:A:C2'	53:1:2164:C:H5'	2.43	0.49
53:1:2747:G:O6	53:1:2755:C:H5''	2.13	0.49
57:7:61:C:H2'	57:7:62:C:C6	2.48	0.49
36:L:85:GLN:HB2	36:L:147:ASN:ND2	2.28	0.49
37:M:9:MET:HB2	37:M:26:MET:HE1	1.94	0.49
45:U:22:ALA:HB2	45:U:32:PHE:CB	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1288:A:O2'	52:3:1353:G:H5'	2.12	0.49
53:1:1001:A:H2'	53:1:1002:G:O4'	2.13	0.49
53:1:1872:A:H2'	53:1:1873:G:O4'	2.13	0.49
2:c:109:VAL:HG22	2:c:203:VAL:HG12	1.95	0.49
4:e:45:ASP:HB3	4:e:48:LEU:HB2	1.95	0.49
6:g:90:LEU:HG	6:g:92:GLY:H	1.77	0.49
7:h:14:GLU:HA	7:h:17:GLU:HB3	1.95	0.49
7:h:27:VAL:HB	7:h:83:ALA:HB3	1.94	0.49
13:n:103:ARG:HH11	53:1:1287:A:H5'	1.74	0.49
31:G:59:ILE:HG12	31:G:62:ARG:HH21	1.77	0.49
31:G:103:TRP:CD1	31:G:107:ARG:HH21	2.31	0.49
37:M:44:PHE:HE2	37:M:100:ILE:HD11	1.77	0.49
40:P:86:LYS:HB2	40:P:112:VAL:HG13	1.93	0.49
43:S:14:ALA:O	43:S:17:ASP:OD1	2.31	0.49
51:a:27:ILE:HD12	51:a:182:ALA:HB1	1.95	0.49
52:3:674:G:H2'	52:3:675:A:H8	1.78	0.49
53:1:150:U:H2'	53:1:151:C:C6	2.47	0.49
53:1:1285:A:H2'	53:1:1286:A:H5'	1.95	0.49
53:1:1752:C:H2'	53:1:1753:G:C8	2.48	0.49
5:f:48:THR:HG22	5:f:49:LEU:H	1.78	0.49
7:h:24:SER:O	7:h:116:GLU:HB2	2.13	0.49
7:h:80:THR:HA	53:1:1107:G:O2'	2.13	0.49
15:p:101:GLU:N	15:p:101:GLU:OE2	2.46	0.49
25:z:29:ARG:NE	53:1:1183:U:H5'	2.28	0.49
34:J:79:THR:OG1	34:J:80:LEU:N	2.46	0.49
38:N:17:ARG:NH2	52:3:1129:C:H4'	2.28	0.49
52:3:1412:C:H2'	52:3:1413:A:C8	2.47	0.49
53:1:948:C:H2'	53:1:949:G:H8	1.78	0.49
53:1:1149:G:H2'	53:1:1150:C:C6	2.48	0.49
53:1:2139:U:H2'	53:1:2140:G:C8	2.48	0.49
54:2:30:C:H2'	54:2:31:C:H5'	1.95	0.49
2:c:108:ASP:OD2	2:c:206:ALA:HA	2.13	0.48
14:o:63:LYS:HZ1	54:2:51:G:H5'	1.78	0.48
14:o:107:ALA:O	14:o:111:ARG:HG3	2.13	0.48
25:z:6:ILE:HD12	25:z:6:ILE:N	2.28	0.48
31:G:210:THR:HA	31:G:213:LEU:HG	1.95	0.48
32:H:156:LEU:HD12	32:H:156:LEU:O	2.13	0.48
32:H:171:ARG:HG2	32:H:173:PRO:HD3	1.95	0.48
39:O:59:LYS:HG2	52:3:972:C:O5'	2.12	0.48
52:3:162:A:H2'	52:3:163:C:O4'	2.13	0.48
52:3:352:C:H4'	52:3:354:G:OP1	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:605:U:H2'	52:3:606:G:H8	1.77	0.48
53:1:288:U:H2'	53:1:289:G:C8	2.48	0.48
53:1:2888:C:H2'	53:1:2889:C:H6	1.77	0.48
58:8:117:ARG:HB2	58:8:157:LEU:HD11	1.95	0.48
2:c:85:ALA:O	2:c:86:GLU:HG3	2.14	0.48
6:g:98:ASP:O	6:g:101:ASP:OD2	2.31	0.48
20:u:18:LYS:HD3	53:1:310:A:OP1	2.13	0.48
20:u:65:GLN:HB2	20:u:68:ASN:OD1	2.12	0.48
41:Q:33:CYS:HA	41:Q:54:VAL:HA	1.94	0.48
41:Q:49:ARG:NH2	52:3:522:C:H41	2.11	0.48
43:S:68:ARG:HH12	52:3:974:A:P	2.36	0.48
53:1:1747:U:H2'	53:1:1748:C:C6	2.48	0.48
54:2:104:A:H2'	54:2:105:G:O4'	2.14	0.48
55:6:66:C:H2'	55:6:67:C:O4'	2.14	0.48
7:h:67:THR:HG22	7:h:68:PRO:HD3	1.94	0.48
17:r:75:VAL:HG22	17:r:86:GLN:OE1	2.13	0.48
18:s:3:THR:HG21	18:s:58:ALA:HB2	1.94	0.48
33:I:123:MET:HG2	33:I:128:VAL:HG22	1.96	0.48
34:J:96:GLN:NE2	52:3:7:A:N6	2.61	0.48
50:Z:61:ARG:HD2	50:Z:61:ARG:C	2.37	0.48
52:3:225:C:H3'	52:3:226:G:H5''	1.96	0.48
52:3:604:G:H2'	52:3:605:U:O4'	2.13	0.48
52:3:1273:C:H2'	52:3:1274:A:O4'	2.12	0.48
52:3:1448:C:H2'	52:3:1449:C:C6	2.49	0.48
53:1:2743:U:H3'	53:1:2744:G:H5''	1.94	0.48
58:8:279:LEU:HD12	58:8:279:LEU:N	2.29	0.48
6:g:55:GLU:O	6:g:58:LEU:HG	2.13	0.48
10:k:88:ASN:N	10:k:92:GLU:O	2.45	0.48
23:x:18:SER:OG	23:x:19:HIS:N	2.46	0.48
33:I:145:ARG:CZ	33:I:147:LYS:HE2	2.44	0.48
39:O:52:LEU:HD23	39:O:62:ARG:HG2	1.94	0.48
52:3:1342:C:H2'	52:3:1343:G:H8	1.77	0.48
53:1:572:A:H61	53:1:2029:G:N2	2.09	0.48
53:1:647:G:H21	53:1:2351:G:H5'	1.78	0.48
53:1:827:U:H4'	53:1:828:U:C5	2.48	0.48
54:2:30:C:C2'	54:2:31:C:H5'	2.43	0.48
57:7:68:C:H2'	57:7:69:G:H8	1.77	0.48
8:i:127:SER:HA	53:1:1080:A:H1'	1.96	0.48
16:q:71:ASN:OD1	16:q:109:VAL:HG21	2.12	0.48
19:t:15:HIS:H	19:t:32:LEU:HA	1.78	0.48
36:L:11:ILE:HD12	36:L:11:ILE:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:14:ARG:NH1	52:3:618:C:H1'	2.29	0.48
50:Z:33:ARG:HG3	50:Z:34:ARG:HG2	1.94	0.48
51:a:19:LYS:NZ	51:a:21:TYR:HA	2.29	0.48
53:1:527:C:H4'	53:1:528:A:O4'	2.13	0.48
53:1:580:U:H2'	53:1:581:C:C6	2.49	0.48
53:1:2053:G:O2'	53:1:2054:A:H5'	2.13	0.48
53:1:2637:U:H2'	53:1:2638:G:O4'	2.13	0.48
4:e:70:ARG:HD2	53:1:2298:A:OP1	2.14	0.48
5:f:174:LYS:HB3	53:1:2529:G:H5'	1.95	0.48
6:g:45:GLU:HA	6:g:48:GLU:HG2	1.96	0.48
13:n:73:ASN:HB3	53:1:1453:A:N6	2.28	0.48
20:u:87:GLU:O	20:u:88:ASP:HB2	2.14	0.48
52:3:1255:G:H2'	52:3:1279:G:H1	1.78	0.48
52:3:1526:G:H2'	52:3:1527:U:C6	2.49	0.48
53:1:832:U:H2'	53:1:833:A:C8	2.48	0.48
53:1:937:C:H2'	53:1:938:G:H8	1.79	0.48
53:1:1023:U:O2'	53:1:1122:G:H5'	2.13	0.48
53:1:1356:G:H2'	53:1:1357:C:C6	2.49	0.48
53:1:1404:C:O2'	53:1:1405:U:H5'	2.13	0.48
53:1:1507:C:H2'	53:1:1508:A:O4'	2.14	0.48
55:6:61:C:O2'	55:6:62:C:H5'	2.13	0.48
58:8:133:VAL:O	58:8:170:ILE:HA	2.13	0.48
58:8:311:ILE:HB	58:8:354:GLY:H	1.77	0.48
9:j:12:LYS:O	9:j:41:LYS:NZ	2.46	0.48
10:k:98:ARG:NH2	52:3:340:U:H5''	2.27	0.48
36:L:135:LYS:O	36:L:138:GLU:HG3	2.13	0.48
37:M:79:ARG:HB2	52:3:878:A:OP1	2.14	0.48
39:O:26:VAL:O	39:O:30:LYS:HG2	2.14	0.48
42:R:103:THR:HG23	42:R:104:ASN:H	1.79	0.48
52:3:57:G:H2'	52:3:58:C:C6	2.48	0.48
53:1:874:G:H2'	53:1:875:G:H8	1.79	0.48
5:f:167:VAL:HG22	5:f:169:ARG:HH12	1.78	0.48
10:k:2:ILE:HB	10:k:33:ALA:HB3	1.95	0.48
33:I:92:LEU:HD12	33:I:93:LEU:N	2.28	0.48
33:I:131:ILE:HD13	52:3:620:C:C2	2.49	0.48
44:T:4:THR:CG2	52:3:659:U:H5''	2.44	0.48
52:3:16:A:O2'	52:3:17:U:H5'	2.13	0.48
52:3:77:A:H2'	52:3:78:A:C8	2.48	0.48
52:3:151:A:H2'	52:3:152:A:O4'	2.14	0.48
53:1:691:C:H2'	53:1:692:C:C6	2.49	0.48
53:1:1213:A:N6	53:1:1236:G:H1'	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2875:C:H2'	53:1:2876:G:C8	2.49	0.48
58:8:172:ARG:O	58:8:172:ARG:HD2	2.14	0.48
3:d:16:GLU:OE2	3:d:20:GLY:HA3	2.13	0.48
17:r:1:MET:N	17:r:43:ASN:HA	2.27	0.48
19:t:51:PHE:C	19:t:52:GLU:HG2	2.39	0.48
33:I:6:PRO:HG3	52:3:430:A:H4'	1.96	0.48
45:U:5:ARG:HD3	52:3:377:G:OP1	2.13	0.48
50:Z:17:ARG:NH2	52:3:1539:C:O4'	2.46	0.48
53:1:596:U:H2'	53:1:597:G:H8	1.79	0.48
53:1:1110:G:H2'	53:1:1111:A:H8	1.78	0.48
53:1:2698:U:H2'	53:1:2699:C:C6	2.49	0.48
58:8:322:PRO:HB3	58:8:352:MET:HA	1.96	0.48
1:b:206:LYS:HD3	53:1:729:G:OP2	2.13	0.48
1:b:269:ARG:HG2	1:b:270:ARG:N	2.28	0.48
2:c:46:ARG:NH2	2:c:88:GLU:O	2.47	0.48
34:J:107:GLY:HA2	52:3:8:A:H1'	1.94	0.48
48:X:32:THR:HG21	48:X:70:LEU:HD21	1.96	0.48
51:a:62:ALA:HB1	51:a:160:GLN:HE22	1.78	0.48
52:3:114:U:O2'	52:3:115:G:H5'	2.14	0.48
52:3:412:A:C2	52:3:414:A:H1'	2.49	0.48
52:3:1015:G:O2'	52:3:1016:A:H5'	2.13	0.48
52:3:1516:G:H2'	52:3:1518:A:OP2	2.13	0.48
53:1:807:U:H2'	53:1:808:G:H8	1.78	0.48
53:1:1067:A:H1'	57:7:56:C:H1'	1.96	0.48
53:1:1278:C:H2'	53:1:1279:G:C8	2.48	0.48
53:1:2491:U:H2'	53:1:2492:U:H5'	1.96	0.48
7:h:55:VAL:HA	53:1:1084:A:C5'	2.43	0.47
7:h:55:VAL:HA	53:1:1084:A:H5''	1.96	0.47
32:H:119:ILE:HD11	32:H:132:ALA:HB1	1.96	0.47
33:I:80:ARG:HB2	52:3:613:C:OP1	2.14	0.47
33:I:127:ARG:HE	52:3:619:U:H4'	1.79	0.47
36:L:110:ARG:HH22	36:L:121:ASN:HB3	1.78	0.47
52:3:79:G:O2'	52:3:80:A:H5'	2.13	0.47
52:3:865:A:H5'	52:3:1078:U:O4	2.14	0.47
53:1:1806:C:H2'	53:1:1807:G:O4'	2.14	0.47
53:1:1858:A:H1'	53:1:1885:A:C2	2.49	0.47
53:1:1919:A:H2'	53:1:1920:C:H5'	1.95	0.47
53:1:2220:U:H2'	53:1:2221:G:C8	2.49	0.47
53:1:2257:U:H2'	53:1:2258:C:C6	2.48	0.47
53:1:2671:G:H2'	53:1:2672:U:C6	2.49	0.47
1:b:203:VAL:HG23	53:1:1792:G:H5'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:9:LYS:NZ	53:1:1070:A:N3	2.61	0.47
10:k:7:MET:HE1	10:k:44:LYS:HG3	1.95	0.47
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.94	0.47
39:O:53:ILE:HD11	52:3:1060:U:OP1	2.12	0.47
40:P:43:TRP:CZ3	40:P:45:THR:HG23	2.49	0.47
43:S:1:ALA:HA	52:3:1049:U:C5	2.48	0.47
52:3:211:G:C2'	52:3:212:G:H5'	2.44	0.47
52:3:471:U:H2'	52:3:472:U:C6	2.48	0.47
53:1:302:C:H2'	53:1:303:G:H8	1.79	0.47
53:1:310:A:O2'	53:1:311:A:H2'	2.14	0.47
53:1:796:C:H2'	53:1:797:G:H8	1.78	0.47
53:1:808:G:H2'	53:1:809:G:H8	1.80	0.47
53:1:937:C:H2'	53:1:938:G:C8	2.49	0.47
53:1:1045:C:P	53:1:1047:G:H5'	2.55	0.47
53:1:2811:G:H2'	53:1:2812:G:C8	2.49	0.47
54:2:55:U:H2'	54:2:56:G:C8	2.48	0.47
1:b:5:CYS:SG	1:b:12:ARG:NH1	2.86	0.47
4:e:35:LEU:HB2	4:e:88:VAL:HB	1.95	0.47
19:t:31:VAL:HG12	19:t:84:TYR:HA	1.95	0.47
32:H:35:ASP:OD1	32:H:56:ILE:HG21	2.15	0.47
42:R:16:ILE:HD12	42:R:16:ILE:H	1.80	0.47
52:3:45:G:H2'	52:3:46:G:C8	2.49	0.47
52:3:1059:C:O2'	52:3:1060:U:H5'	2.14	0.47
53:1:1594:U:H2'	53:1:1595:C:C6	2.49	0.47
53:1:1837:C:H2'	53:1:1899:A:H61	1.79	0.47
1:b:245:THR:C	1:b:247:TRP:H	2.22	0.47
3:d:111:GLU:OE2	3:d:114:ARG:NH2	2.48	0.47
5:f:36:LEU:HD21	5:f:70:LEU:HD22	1.96	0.47
6:g:126:GLY:H	6:g:146:VAL:HB	1.80	0.47
15:p:102:ARG:HH22	53:1:1755:A:H5'	1.80	0.47
29:E:54:LEU:HD12	29:E:55:GLY:N	2.29	0.47
31:G:49:PHE:O	31:G:53:LEU:HD23	2.14	0.47
33:I:43:ARG:NH2	52:3:511:C:OP2	2.48	0.47
36:L:85:GLN:HB2	36:L:147:ASN:HD22	1.77	0.47
46:V:42:LYS:HD2	52:3:277:C:OP1	2.14	0.47
52:3:271:C:H2'	52:3:272:C:C6	2.50	0.47
52:3:1464:U:H2'	52:3:1465:A:C8	2.49	0.47
53:1:164:C:H2'	53:1:165:A:H5'	1.95	0.47
53:1:576:U:H2'	53:1:577:G:H8	1.78	0.47
53:1:1138:G:H2'	53:1:1139:G:O4'	2.13	0.47
53:1:1283:G:H1'	53:1:1329:U:O2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1652:A:H2'	53:1:1653:G:O4'	2.12	0.47
58:8:327:TYR:CZ	58:8:329:PRO:HB3	2.49	0.47
3:d:24:ASN:ND2	3:d:27:LEU:HB2	2.30	0.47
18:s:57:ASN:O	18:s:61:ASN:HB2	2.14	0.47
20:u:48:VAL:HG22	20:u:49:PRO:HD2	1.96	0.47
23:x:6:VAL:HA	23:x:70:LEU:HD21	1.97	0.47
25:z:19:HIS:O	25:z:22:THR:HG22	2.14	0.47
33:l:6:PRO:HA	52:3:430:A:P	2.54	0.47
40:P:12:ARG:HH11	40:P:12:ARG:HA	1.78	0.47
42:R:91:ARG:HH12	53:1:887:U:P	2.38	0.47
52:3:600:A:H2'	52:3:601:G:C8	2.49	0.47
53:1:248:G:N3	53:1:2431:U:H4'	2.30	0.47
53:1:905:A:O2'	53:1:906:U:H5'	2.14	0.47
53:1:1015:U:H2'	53:1:1016:G:C8	2.50	0.47
53:1:1700:A:H2'	53:1:1701:A:H5'	1.96	0.47
58:8:288:GLU:HG3	58:8:289:ARG:N	2.29	0.47
58:8:308:GLU:HA	58:8:358:LYS:HA	1.97	0.47
2:c:43:ASP:HB3	2:c:45:TYR:CE1	2.49	0.47
3:d:5:LEU:HB2	3:d:9:GLN:H	1.78	0.47
9:j:113:PRO:HD2	53:1:558:U:OP2	2.14	0.47
31:G:186:VAL:HG21	31:G:192:PRO:HB3	1.96	0.47
32:H:13:ILE:HG12	32:H:177:LEU:HD21	1.95	0.47
34:J:96:GLN:NE2	52:3:7:A:H62	2.13	0.47
36:L:4:ARG:HB3	36:L:6:ILE:HG23	1.96	0.47
52:3:231:U:H2'	52:3:232:G:C8	2.49	0.47
52:3:458:U:H2'	52:3:459:A:H8	1.79	0.47
53:1:184:C:H2'	53:1:185:G:C8	2.50	0.47
53:1:832:U:H2'	53:1:833:A:H8	1.80	0.47
53:1:1079:C:H2'	53:1:1080:A:C8	2.49	0.47
53:1:2417:C:H2'	53:1:2418:A:C8	2.49	0.47
53:1:2834:G:H2'	53:1:2879:A:N6	2.27	0.47
58:8:34:THR:O	58:8:38:LYS:HG2	2.14	0.47
58:8:309:VAL:HG22	58:8:310:TYR:H	1.79	0.47
1:b:120:ASP:HB3	6:g:91:PHE:CE1	2.50	0.47
2:c:124:ARG:HG3	2:c:165:MET:HG3	1.96	0.47
3:d:50:ALA:HB2	53:1:801:G:C8	2.49	0.47
3:d:147:LEU:HB3	3:d:186:VAL:HG22	1.96	0.47
13:n:99:LYS:HD2	13:n:99:LYS:N	2.30	0.47
17:r:6:GLN:HG2	17:r:11:GLN:CD	2.40	0.47
23:x:11:PRO:HG3	23:x:30:PRO:HD2	1.96	0.47
27:C:10:LEU:HD23	27:C:50:GLU:HA	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:9:ILE:HG23	32:H:10:ARG:HG3	1.96	0.47
33:I:4:LEU:HD21	52:3:405:U:C5	2.50	0.47
40:P:23:HIS:HB3	40:P:30:ILE:HG23	1.97	0.47
42:R:14:ALA:HB3	42:R:40:GLU:HA	1.95	0.47
42:R:113:LYS:N	42:R:114:PRO:HD2	2.30	0.47
46:V:14:ASP:OD1	46:V:20:ILE:HD11	2.14	0.47
47:W:32:ILE:HG21	47:W:67:LEU:HD21	1.97	0.47
48:X:54:ARG:HB3	52:3:958:A:C2	2.50	0.47
51:a:26:ALA:HB1	51:a:214:ILE:HD11	1.95	0.47
52:3:129:A:H1'	52:3:130:A:C8	2.50	0.47
52:3:784:A:H2'	52:3:785:G:C8	2.50	0.47
52:3:1339:A:H2'	52:3:1340:A:O4'	2.15	0.47
52:3:1540:U:O2	52:3:1540:U:H3'	2.15	0.47
53:1:226:A:H2'	53:1:227:A:O4'	2.15	0.47
53:1:319:G:H2'	53:1:320:A:O4'	2.14	0.47
53:1:657:U:H2'	53:1:658:U:C6	2.50	0.47
53:1:807:U:H2'	53:1:808:G:C8	2.50	0.47
53:1:1073:A:H2'	53:1:1074:G:O4'	2.14	0.47
53:1:1827:U:H2'	53:1:1828:G:O4'	2.15	0.47
53:1:2364:C:H2'	53:1:2365:G:O4'	2.14	0.47
53:1:2849:U:H4'	53:1:2868:A:N1	2.29	0.47
2:c:110:THR:HB	2:c:202:ILE:HB	1.96	0.47
3:d:5:LEU:HD12	3:d:8:ALA:HB3	1.96	0.47
14:o:11:ALA:HB2	14:o:96:GLY:N	2.30	0.47
16:q:36:GLN:O	16:q:39:ILE:HG22	2.14	0.47
34:J:108:GLY:N	52:3:9:G:H4'	2.28	0.47
41:Q:57:THR:HG21	52:3:363:A:P	2.54	0.47
43:S:18:LYS:HE3	52:3:1007:U:OP1	2.15	0.47
52:3:393:A:H5'	52:3:483:C:O2'	2.15	0.47
52:3:701:U:H5''	52:3:703:G:H1'	1.97	0.47
53:1:466:A:H2'	53:1:467:G:H5'	1.97	0.47
53:1:610:C:H2'	53:1:611:C:C6	2.49	0.47
53:1:1297:C:OP1	53:1:2710:C:H4'	2.15	0.47
53:1:2126:A:H2'	53:1:2162:G:N2	2.29	0.47
5:f:167:VAL:HG13	5:f:169:ARG:NH2	2.27	0.47
6:g:11:ASN:ND2	6:g:12:LEU:HD22	2.21	0.47
12:m:131:VAL:HG22	12:m:132:THR:H	1.80	0.47
19:t:39:THR:O	19:t:43:ILE:HG13	2.15	0.47
22:w:39:THR:H	53:1:2331:G:H4'	1.80	0.47
30:F:4:ARG:HB3	53:1:2466:C:OP1	2.15	0.47
32:H:106:ARG:HD2	32:H:106:ARG:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:18:C:H1'	52:3:1079:G:H21	1.80	0.47
52:3:678:U:H2'	52:3:679:C:C6	2.50	0.47
52:3:1060:U:H2'	52:3:1061:G:C8	2.49	0.47
53:1:874:G:H2'	53:1:875:G:C8	2.50	0.47
53:1:877:A:H1'	53:1:900:A:H61	1.79	0.47
53:1:1660:G:O2'	53:1:1661:G:H5'	2.14	0.47
53:1:2170:A:H2'	53:1:2171:A:O4'	2.15	0.47
53:1:2340:A:H2'	53:1:2341:G:H8	1.80	0.47
53:1:2463:C:H2'	53:1:2464:G:H8	1.80	0.47
54:2:56:G:H4'	54:2:57:A:H8	1.80	0.47
58:8:216:GLU:HG2	58:8:230:GLY:CA	2.42	0.47
1:b:94:LEU:HD21	53:1:1501:G:H4'	1.97	0.47
1:b:203:VAL:HG23	53:1:1792:G:C5'	2.45	0.47
1:b:204:LEU:HB3	1:b:209:ALA:HB3	1.97	0.47
3:d:1:MET:O	3:d:14:VAL:HG22	2.15	0.47
7:h:19:ALA:HB3	7:h:20:LYS:NZ	2.30	0.47
7:h:67:THR:CG2	7:h:68:PRO:HD3	2.45	0.47
7:h:78:GLY:N	7:h:79:PRO:HD2	2.29	0.47
16:q:96:ASP:CG	17:r:13:ARG:HE	2.23	0.47
21:v:29:ILE:HG13	54:2:75:G:H1'	1.95	0.47
32:H:2:GLN:HB3	52:3:1190:G:O2'	2.15	0.47
36:L:78:ARG:NH2	36:L:81:GLY:O	2.47	0.47
40:P:22:ILE:HG12	40:P:31:VAL:HG13	1.96	0.47
48:X:35:ARG:HH21	48:X:74:ALA:HB3	1.80	0.47
49:Y:43:LYS:HD2	49:Y:86:ALA:HB2	1.96	0.47
52:3:538:G:H2'	52:3:539:A:C8	2.50	0.47
52:3:766:A:H2'	52:3:767:A:O4'	2.14	0.47
52:3:1070:U:O2'	52:3:1071:C:H5'	2.15	0.47
52:3:1191:A:H2'	52:3:1191:A:N3	2.29	0.47
52:3:1329:A:O2'	52:3:1330:U:H5'	2.15	0.47
52:3:1391:U:H2'	52:3:1392:G:C8	2.50	0.47
53:1:12:U:O2	53:1:2626:C:H4'	2.16	0.47
53:1:112:U:C2'	53:1:113:U:H5'	2.45	0.47
53:1:289:G:H2'	53:1:290:U:C6	2.50	0.47
53:1:969:G:H2'	53:1:970:U:C6	2.50	0.47
53:1:1443:U:H2'	53:1:1444:G:H8	1.80	0.47
53:1:1794:A:H2'	53:1:1795:C:C6	2.50	0.47
53:1:2190:G:H2'	53:1:2191:A:H8	1.80	0.47
55:5:36:U:H2'	55:5:37:A:H8	1.80	0.47
56:4:17:U:H2'	56:4:18:G:C8	2.50	0.47
58:8:238:LYS:HE2	58:8:268:GLU:OE1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:71:VAL:HG13	18:s:71:VAL:O	2.14	0.46
32:H:39:ARG:NH1	32:H:54:ILE:HG13	2.30	0.46
35:K:18:VAL:CG1	35:K:19:PRO:HD3	2.45	0.46
37:M:85:TYR:CE1	37:M:123:GLU:HB2	2.49	0.46
51:a:183:ASP:OD2	51:a:184:LYS:HD2	2.15	0.46
52:3:235:C:H2'	52:3:236:A:H8	1.80	0.46
53:1:394:C:H2'	53:1:395:U:O4'	2.15	0.46
53:1:542:C:H2'	53:1:543:G:C5'	2.43	0.46
53:1:705:A:C2	53:1:727:A:H1'	2.50	0.46
53:1:1420:A:H5'	53:1:1421:G:OP2	2.16	0.46
55:6:41:C:H2'	55:6:42:G:H8	1.80	0.46
1:b:160:TYR:CB	1:b:193:GLU:HG2	2.44	0.46
2:c:8:LYS:HD2	2:c:193:VAL:HG23	1.97	0.46
4:e:5:ASP:HA	4:e:8:LYS:HD2	1.97	0.46
4:e:25:MET:HB3	54:2:57:A:C5	2.51	0.46
11:l:135:ILE:HG22	11:l:140:GLY:HA3	1.97	0.46
12:m:11:LYS:HD2	12:m:86:LYS:HG2	1.96	0.46
17:r:6:GLN:HG2	17:r:11:GLN:OE1	2.15	0.46
32:H:21:TRP:HB3	32:H:58:ARG:H	1.79	0.46
32:H:188:ALA:HB3	32:H:195:ILE:HB	1.97	0.46
34:J:82:HIS:HB2	34:J:83:PRO:HD2	1.97	0.46
52:3:1004:A:H2'	52:3:1005:A:O4'	2.15	0.46
52:3:1014:A:C2	52:3:1219:A:H1'	2.49	0.46
53:1:406:G:H2'	53:1:407:G:H8	1.80	0.46
53:1:741:U:H2'	53:1:742:A:C8	2.51	0.46
53:1:744:U:H5''	53:1:1658:C:H5''	1.97	0.46
53:1:1190:G:H2'	53:1:1191:G:H8	1.80	0.46
53:1:1316:U:H2'	53:1:1317:G:C8	2.51	0.46
53:1:1900:A:O4'	53:1:1970:A:H5''	2.16	0.46
53:1:2329:U:H2'	53:1:2330:G:H8	1.80	0.46
53:1:2472:G:H2'	53:1:2529:G:N2	2.31	0.46
54:2:14:U:O2	54:2:107:G:H4'	2.15	0.46
55:6:69:C:C2'	55:6:70:G:H5'	2.44	0.46
57:7:48:C:H5'	57:7:50:U:OP2	2.15	0.46
58:8:211:PHE:HB3	58:8:295:LYS:HB2	1.97	0.46
58:8:220:SER:HB3	58:8:284:ARG:HD2	1.97	0.46
58:8:332:TYR:CG	58:8:378:ARG:HD3	2.50	0.46
1:b:270:ARG:NH1	1:b:270:ARG:HB3	2.31	0.46
7:h:43:LYS:HZ3	7:h:95:LEU:HD22	1.79	0.46
11:l:16:GLY:HA2	53:1:662:G:O3'	2.15	0.46
11:l:35:HIS:HB3	11:l:36:LYS:H	1.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:148:SER:HB2	34:J:149:PRO:HD2	1.97	0.46
35:K:66:ALA:HB1	35:K:67:PRO:HD2	1.98	0.46
36:L:115:MET:HE2	52:3:1240:U:C2	2.50	0.46
48:X:10:ILE:HD13	48:X:40:PHE:CZ	2.50	0.46
49:Y:28:ARG:NH1	52:3:1437:A:OP1	2.47	0.46
53:1:542:C:C2'	53:1:543:G:H5''	2.45	0.46
53:1:2093:G:N7	53:1:2225:A:H2'	2.30	0.46
4:e:144:LYS:N	4:e:144:LYS:HD2	2.30	0.46
7:h:31:ARG:HD2	7:h:31:ARG:C	2.40	0.46
16:q:80:ASN:HB2	53:1:1151:A:O2'	2.15	0.46
32:H:18:ASN:O	32:H:55:VAL:HG13	2.16	0.46
35:K:50:PRO:HG3	35:K:55:HIS:NE2	2.30	0.46
35:K:86:ARG:HD3	47:W:63:TYR:O	2.16	0.46
38:N:118:ARG:HB2	38:N:122:ARG:HB3	1.97	0.46
39:O:8:ILE:HD12	39:O:8:ILE:N	2.31	0.46
53:1:2623:G:H2'	53:1:2624:G:C8	2.50	0.46
58:8:342:ILE:HD12	58:8:359:MET:HG3	1.97	0.46
1:b:52:HIS:HD2	53:1:1824:G:OP2	1.98	0.46
1:b:106:PRO:CG	1:b:109:LEU:HD22	2.45	0.46
5:f:100:ASN:ND2	5:f:115:GLN:OE1	2.48	0.46
8:i:126:ARG:HG3	53:1:1080:A:O2'	2.15	0.46
9:j:57:LEU:O	9:j:58:ASN:HB2	2.15	0.46
15:p:38:ARG:NH2	15:p:40:GLN:HB3	2.29	0.46
22:w:67:VAL:HG22	22:w:67:VAL:O	2.15	0.46
34:J:104:ILE:HD11	34:J:119:VAL:O	2.15	0.46
48:X:15:LEU:O	48:X:18:VAL:HG12	2.15	0.46
48:X:47:THR:HG22	48:X:60:PHE:HD1	1.81	0.46
52:3:1450:U:H2'	52:3:1452:C:O4'	2.16	0.46
53:1:49:A:C5'	53:1:51:G:H5'	2.46	0.46
53:1:435:C:C2'	53:1:436:C:H5'	2.42	0.46
53:1:744:U:H2'	53:1:745:G:O4'	2.15	0.46
57:7:48:C:H2'	57:7:59:U:H5'	1.98	0.46
58:8:237:ILE:HD12	58:8:237:ILE:N	2.30	0.46
58:8:308:GLU:HG2	58:8:309:VAL:H	1.80	0.46
1:b:73:ILE:HG12	53:1:1490:A:C6	2.51	0.46
4:e:69:ALA:HB3	4:e:82:TYR:H	1.81	0.46
5:f:151:ARG:HB3	5:f:161:VAL:HG12	1.97	0.46
11:l:29:LYS:O	11:l:30:THR:OG1	2.23	0.46
24:y:9:LYS:HG3	24:y:11:VAL:HG22	1.97	0.46
27:C:5:ARG:NH1	27:C:25:ASN:HB2	2.31	0.46
52:3:969:A:H2'	52:3:970:C:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:74:A:H4'	53:1:75:G:O5'	2.15	0.46
53:1:890:C:H2'	53:1:891:G:H5'	1.98	0.46
53:1:1441:G:H2'	53:1:1442:U:C6	2.51	0.46
53:1:1509:A:H2'	53:1:1510:G:H8	1.81	0.46
53:1:2463:C:H2'	53:1:2464:G:C8	2.51	0.46
53:1:2710:C:H2'	53:1:2711:A:C8	2.50	0.46
2:c:142:VAL:HG22	2:c:143:PRO:CD	2.38	0.46
7:h:33:VAL:HG23	53:1:1055:G:O3'	2.15	0.46
7:h:37:LYS:O	7:h:41:LEU:HB2	2.15	0.46
10:k:76:VAL:HG22	15:p:72:VAL:CG1	2.46	0.46
14:o:12:THR:HA	14:o:15:ARG:HB2	1.97	0.46
17:r:74:ILE:HD12	17:r:74:ILE:N	2.30	0.46
34:J:28:ARG:NH2	52:3:1397:C:OP2	2.48	0.46
40:P:122:PRO:HG2	50:Z:35:GLU:HB3	1.97	0.46
42:R:38:ILE:HD12	42:R:51:GLN:OE1	2.15	0.46
42:R:89:ARG:HH21	42:R:95:PRO:HG2	1.81	0.46
52:3:166:U:H2'	52:3:167:A:C8	2.50	0.46
52:3:265:G:H2'	52:3:267:C:H5	1.81	0.46
52:3:285:C:H2'	52:3:286:C:C6	2.51	0.46
52:3:1415:G:H2'	52:3:1416:G:H8	1.81	0.46
53:1:974:G:N3	53:1:974:G:H2'	2.30	0.46
53:1:995:C:H6	53:1:995:C:H5'	1.80	0.46
53:1:1086:A:H3'	53:1:1086:A:N3	2.31	0.46
53:1:1111:A:O2'	53:1:1112:G:H4'	2.15	0.46
53:1:1367:A:C2'	53:1:1368:G:H5'	2.46	0.46
53:1:1571:A:H2'	53:1:1572:A:C8	2.51	0.46
53:1:2190:G:H2'	53:1:2191:A:C8	2.51	0.46
53:1:2475:C:H2'	53:1:2476:A:H5'	1.98	0.46
53:1:2515:C:H2'	53:1:2516:A:H8	1.79	0.46
53:1:2802:G:H2'	53:1:2803:G:C8	2.51	0.46
57:7:76:A:O2'	60:7:101:PHE:C	2.58	0.46
5:f:17:LYS:HB2	5:f:24:THR:CG2	2.45	0.46
7:h:50:VAL:HG22	7:h:50:VAL:O	2.15	0.46
10:k:35:VAL:HG13	10:k:36:GLY:N	2.30	0.46
20:u:6:ARG:N	53:1:85:G:OP1	2.47	0.46
24:y:54:LYS:HD3	53:1:72:U:H5'	1.97	0.46
36:L:90:VAL:HG22	36:L:91:ARG:N	2.31	0.46
52:3:882:C:O2'	52:3:883:C:H5'	2.15	0.46
53:1:2193:G:H2'	53:1:2194:U:C6	2.51	0.46
53:1:2591:C:H2'	53:1:2592:G:C8	2.51	0.46
54:2:35:C:H2'	54:2:36:C:H5'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:13:ASN:ND2	13:n:14:SER:H	2.14	0.46
21:v:80:HIS:HB3	21:v:83:LYS:O	2.15	0.46
23:x:13:THR:HG22	23:x:27:ARG:HG3	1.97	0.46
24:y:9:LYS:O	24:y:13:GLU:HG2	2.15	0.46
34:J:82:HIS:CE1	37:M:95:MET:HE2	2.51	0.46
36:L:5:VAL:HG13	52:3:1378:C:OP2	2.15	0.46
38:N:113:LYS:HE2	38:N:118:ARG:O	2.15	0.46
42:R:109:LYS:HD3	52:3:1227:A:OP2	2.15	0.46
45:U:20:VAL:HG22	45:U:35:ARG:HB3	1.97	0.46
45:U:48:GLU:CD	45:U:49:GLY:H	2.23	0.46
52:3:1128:C:O2'	52:3:1129:C:H5'	2.16	0.46
52:3:1218:C:H2'	52:3:1219:A:H8	1.79	0.46
53:1:406:G:H2'	53:1:407:G:C8	2.51	0.46
53:1:595:C:H2'	53:1:596:U:C6	2.51	0.46
53:1:687:C:H6	53:1:687:C:H5'	1.81	0.46
53:1:1396:U:H5''	53:1:1397:U:OP2	2.16	0.46
53:1:1434:A:H2'	53:1:1435:G:H8	1.80	0.46
53:1:2036:C:H2'	53:1:2037:A:C8	2.51	0.46
53:1:2073:C:O2'	53:1:2074:U:H5'	2.16	0.46
55:6:31:G:H2'	55:6:32:C:H5'	1.98	0.46
58:8:336:THR:CG2	58:8:338:VAL:HG23	2.46	0.46
1:b:132:ARG:HA	1:b:166:ARG:HD2	1.97	0.46
12:m:54:THR:HG22	12:m:63:ILE:HD12	1.97	0.46
30:F:11:CYS:SG	30:F:12:ARG:N	2.89	0.46
31:G:140:LEU:HG	31:G:144:GLU:OE2	2.16	0.46
45:U:58:ALA:O	45:U:61:VAL:HG22	2.15	0.46
52:3:49:U:O2'	52:3:50:A:H2'	2.16	0.46
52:3:149:A:H1'	52:3:1446:A:C2	2.51	0.46
52:3:216:U:H2'	52:3:217:C:C6	2.51	0.46
52:3:1391:U:H2'	52:3:1392:G:H8	1.81	0.46
53:1:655:A:H4'	53:1:656:G:H5'	1.98	0.46
53:1:862:G:H2'	53:1:863:A:O4'	2.15	0.46
53:1:941:A:H2'	53:1:942:G:O4'	2.16	0.46
53:1:1370:C:H2'	53:1:1371:G:O4'	2.16	0.46
53:1:2120:G:H2'	53:1:2121:G:C8	2.51	0.46
53:1:2343:U:H2'	53:1:2344:U:C6	2.51	0.46
55:6:68:C:H2'	55:6:69:C:H4'	1.98	0.46
1:b:48:ILE:HD11	1:b:51:ARG:HA	1.97	0.45
4:e:102:LEU:O	4:e:106:ALA:HB3	2.15	0.45
5:f:28:LYS:HG2	5:f:79:THR:HA	1.99	0.45
8:i:56:VAL:HG22	8:i:70:THR:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:v:26:PHE:HE2	21:v:89:ILE:HG13	1.80	0.45
43:S:39:ASP:HA	43:S:42:ASN:HD22	1.81	0.45
46:V:42:LYS:HE3	52:3:278:G:OP2	2.16	0.45
52:3:594:U:H2'	52:3:595:A:O4'	2.16	0.45
52:3:1210:C:H2'	52:3:1211:U:H5'	1.97	0.45
53:1:189:G:H2'	53:1:205:G:N2	2.31	0.45
53:1:833:A:H2'	53:1:834:G:C8	2.51	0.45
53:1:2252:G:O2'	53:1:2253:G:H5'	2.16	0.45
53:1:2581:G:H2'	53:1:2581:G:N3	2.31	0.45
53:1:2650:U:H2'	53:1:2651:C:C6	2.50	0.45
53:1:2860:A:H2'	53:1:2861:U:H5'	1.98	0.45
55:5:36:U:H2'	55:5:37:A:C8	2.51	0.45
1:b:95:TYR:HB2	1:b:97:ASP:OD1	2.16	0.45
12:m:45:GLN:NE2	53:1:2485:G:H5''	2.30	0.45
14:o:75:GLY:HA2	14:o:106:LEU:HG	1.97	0.45
17:r:68:ARG:HB2	17:r:90:ARG:HH21	1.81	0.45
33:I:190:LEU:CD1	33:I:192:ALA:H	2.16	0.45
39:O:57:VAL:HG12	39:O:58:ASN:N	2.25	0.45
49:Y:26:MET:O	49:Y:29:THR:HG22	2.16	0.45
50:Z:6:ARG:O	50:Z:7:GLU:C	2.58	0.45
52:3:184:G:H4'	52:3:224:U:H4'	1.97	0.45
52:3:541:G:H2'	52:3:542:G:C8	2.50	0.45
52:3:1301:U:O2	52:3:1301:U:C2'	2.63	0.45
53:1:96:C:H2'	53:1:97:C:C6	2.51	0.45
53:1:414:C:H2'	53:1:415:A:C8	2.52	0.45
53:1:817:C:H2'	53:1:818:G:O4'	2.15	0.45
53:1:1555:G:H5'	53:1:1555:G:H8	1.81	0.45
53:1:1565:C:O2'	53:1:1566:A:H2'	2.17	0.45
53:1:2130:U:H5'	53:1:2159:G:N2	2.31	0.45
53:1:2317:A:H2'	53:1:2318:G:O4'	2.17	0.45
53:1:2875:C:H2'	53:1:2876:G:H8	1.80	0.45
1:b:156:SER:O	1:b:159:THR:HG22	2.17	0.45
2:c:115:GLY:HA3	53:1:2822:G:P	2.57	0.45
5:f:26:LYS:HB2	5:f:31:GLU:HG2	1.98	0.45
5:f:173:ALA:O	5:f:175:LYS:N	2.41	0.45
7:h:33:VAL:CG1	7:h:35:VAL:HG12	2.46	0.45
7:h:60:LEU:O	7:h:64:VAL:HB	2.16	0.45
15:p:43:GLU:CD	15:p:43:GLU:H	2.24	0.45
17:r:49:ILE:CG2	17:r:54:VAL:HG22	2.46	0.45
37:M:12:ARG:CZ	52:3:826:C:H5'	2.47	0.45
37:M:112:ASP:O	37:M:116:ARG:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:86:ALA:HA	43:S:89:ARG:HH11	1.81	0.45
45:U:31:ARG:HB2	52:3:310:G:C5'	2.46	0.45
46:V:42:LYS:HE2	52:3:277:C:H5''	1.98	0.45
51:a:5:THR:HB	53:1:2130:U:OP2	2.16	0.45
52:3:58:C:O2'	52:3:59:A:H5'	2.17	0.45
52:3:202:G:H2'	52:3:203:G:C8	2.52	0.45
52:3:1443:C:H2'	52:3:1444:U:O4'	2.15	0.45
52:3:1453:G:H3'	52:3:1453:G:N3	2.32	0.45
53:1:18:U:H2'	53:1:19:A:H8	1.82	0.45
53:1:940:G:H2'	53:1:941:A:H5''	1.98	0.45
53:1:1301:A:H2'	53:1:1301:A:N3	2.31	0.45
53:1:2029:G:O6	53:1:2032:G:H5''	2.16	0.45
53:1:2296:U:H4'	53:1:2297:A:O5'	2.16	0.45
53:1:2467:C:H2'	53:1:2468:A:O4'	2.16	0.45
58:8:14:ASN:ND2	58:8:98:GLN:OE1	2.48	0.45
12:m:13:HIS:O	12:m:71:LYS:NZ	2.49	0.45
12:m:78:LEU:HD11	53:1:2459:A:C2	2.51	0.45
16:q:82:LEU:HB3	16:q:87:VAL:HB	1.99	0.45
22:w:40:LYS:NZ	53:1:858:G:OP1	2.47	0.45
35:K:3:HIS:CD2	35:K:94:HIS:HA	2.51	0.45
35:K:29:ILE:HD12	35:K:29:ILE:N	2.30	0.45
39:O:8:ILE:HB	39:O:74:VAL:HB	1.97	0.45
40:P:93:GLU:O	40:P:96:ILE:HG12	2.16	0.45
51:a:48:LEU:HD11	51:a:208:TYR:CE2	2.52	0.45
52:3:123:U:OP1	52:3:312:C:H5'	2.16	0.45
52:3:621:A:H2'	52:3:622:A:C8	2.51	0.45
52:3:990:C:H2'	52:3:991:U:O4'	2.16	0.45
52:3:1190:G:H8	52:3:1190:G:O5'	1.98	0.45
53:1:1298:C:H2'	53:1:1299:G:O4'	2.17	0.45
53:1:1469:A:H2'	53:1:1470:A:C8	2.52	0.45
53:1:1539:U:H2'	53:1:1540:G:H8	1.81	0.45
53:1:1611:C:H6	53:1:1611:C:H5'	1.82	0.45
53:1:2208:C:H2'	53:1:2209:G:H8	1.80	0.45
3:d:105:LEU:HD21	3:d:177:PRO:HG3	1.97	0.45
12:m:86:LYS:CE	53:1:955:U:H5''	2.40	0.45
19:t:73:ARG:N	19:t:73:ARG:HD2	2.31	0.45
31:G:24:PRO:HB3	52:3:828:U:H2'	1.97	0.45
31:G:46:VAL:HG13	31:G:47:PRO:HD3	1.99	0.45
33:I:50:TYR:CE2	52:3:508:U:H4'	2.52	0.45
33:I:150:LYS:HB2	33:I:155:LYS:HG2	1.98	0.45
37:M:32:LYS:O	37:M:35:ILE:HG22	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:17:TYR:O	45:U:39:PHE:N	2.44	0.45
48:X:35:ARG:O	48:X:71:GLY:N	2.50	0.45
52:3:12:U:H2'	52:3:13:U:H5''	1.98	0.45
52:3:1245:C:H2'	52:3:1246:A:H8	1.80	0.45
53:1:942:G:H2'	53:1:943:A:O4'	2.16	0.45
53:1:1387:A:H5'	53:1:1469:A:H1'	1.98	0.45
53:1:1477:A:H2'	53:1:1478:G:O4'	2.17	0.45
53:1:2197:U:H1'	53:1:2198:A:C8	2.51	0.45
53:1:2286:G:H4'	53:1:2287:A:O4'	2.16	0.45
53:1:2297:A:H62	53:1:2319:G:H1'	1.81	0.45
57:7:76:A:HO2'	60:7:101:PHE:C	2.24	0.45
58:8:216:GLU:CG	58:8:230:GLY:HA2	2.44	0.45
1:b:264:LYS:HD2	53:1:2224:G:OP1	2.17	0.45
13:n:22:ARG:HG3	13:n:70:THR:HA	1.98	0.45
40:P:105:ARG:HA	40:P:105:ARG:HD2	1.79	0.45
50:Z:23:GLU:C	50:Z:25:ALA:N	2.75	0.45
51:a:211:LYS:HZ2	53:1:2177:C:H5''	1.80	0.45
52:3:629:A:H2'	52:3:630:A:O4'	2.16	0.45
53:1:340:A:H2'	53:1:341:C:O4'	2.16	0.45
53:1:912:C:O2'	53:1:913:U:H5'	2.16	0.45
53:1:940:G:H3'	53:1:941:A:H5''	1.98	0.45
53:1:1102:C:H2'	53:1:1103:A:O4'	2.17	0.45
53:1:2810:A:H2'	53:1:2811:G:O4'	2.16	0.45
54:2:114:C:H2'	54:2:115:A:C8	2.52	0.45
9:j:78:THR:OG1	9:j:83:GLY:HA3	2.17	0.45
10:k:92:GLU:CG	10:k:93:GLN:N	2.78	0.45
12:m:3:GLN:HE21	12:m:92:TRP:NE1	2.15	0.45
19:t:61:LEU:HD21	19:t:82:LYS:HE3	1.98	0.45
33:I:58:GLN:HG3	33:I:62:ARG:HE	1.82	0.45
45:U:16:PHE:HE1	45:U:40:ASN:HB2	1.81	0.45
52:3:123:U:H5''	52:3:311:C:O2'	2.17	0.45
52:3:772:U:H2'	52:3:773:G:C8	2.52	0.45
52:3:1237:C:H4'	52:3:1334:G:N2	2.31	0.45
53:1:2224:G:H4'	53:1:2226:C:C2	2.51	0.45
58:8:309:VAL:CG1	58:8:359:MET:HE1	2.45	0.45
1:b:146:LYS:HB2	1:b:149:LYS:HG2	1.99	0.45
2:c:194:PRO:HA	53:1:2680:U:C5'	2.47	0.45
4:e:7:TYR:O	4:e:12:VAL:HG23	2.17	0.45
4:e:114:ARG:HG2	4:e:114:ARG:HH21	1.82	0.45
4:e:177:ARG:OXT	4:e:177:ARG:HD2	2.17	0.45
12:m:21:ALA:HB2	12:m:97:GLN:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:t:59:ASN:HB2	19:t:84:TYR:HB2	1.98	0.45
40:P:91:GLY:C	40:P:93:GLU:H	2.22	0.45
41:Q:117:GLY:HA2	52:3:35:G:O2'	2.17	0.45
42:R:89:ARG:NH2	42:R:95:PRO:HG2	2.31	0.45
46:V:48:GLU:O	46:V:49:ASN:C	2.59	0.45
52:3:514:C:H2'	52:3:515:G:H8	1.82	0.45
52:3:1201:A:C1'	52:3:1202:U:OP2	2.58	0.45
53:1:871:U:H2'	53:1:872:U:C6	2.52	0.45
53:1:1709:U:H2'	53:1:1710:G:H8	1.81	0.45
2:c:173:GLN:NE2	53:1:2771:C:HO2'	2.15	0.45
9:j:23:LYS:HZ1	9:j:142:ILE:HG13	1.82	0.45
14:o:106:LEU:O	14:o:106:LEU:HD23	2.17	0.45
16:q:105:PHE:HA	16:q:108:LEU:HD12	1.98	0.45
31:G:40:ILE:N	31:G:40:ILE:HD12	2.32	0.45
35:K:26:THR:HA	35:K:29:ILE:HD13	1.99	0.45
44:T:34:GLN:O	44:T:37:HIS:HB3	2.17	0.45
52:3:405:U:H3'	52:3:406:G:C5'	2.37	0.45
52:3:483:C:H2'	52:3:484:G:C8	2.51	0.45
52:3:514:C:H2'	52:3:515:G:C8	2.52	0.45
52:3:1054:C:H4'	52:3:1055:A:H5''	1.99	0.45
53:1:12:U:H2'	53:1:13:A:H5'	1.97	0.45
53:1:151:C:H2'	53:1:152:A:H8	1.82	0.45
53:1:503:A:H4'	53:1:505:A:H5''	1.99	0.45
53:1:1279:G:H2'	53:1:1280:G:H8	1.82	0.45
53:1:1542:U:H2'	53:1:1543:G:O4'	2.17	0.45
58:8:304:LYS:NZ	58:8:362:THR:HB	2.32	0.45
3:d:34:ALA:HA	3:d:94:GLN:HE21	1.82	0.45
7:h:16:SER:O	7:h:20:LYS:HG2	2.17	0.45
7:h:41:LEU:HD13	53:1:1083:U:H4'	1.98	0.45
7:h:118:ILE:HD13	7:h:118:ILE:HA	1.91	0.45
11:l:142:ILE:HD12	11:l:142:ILE:N	2.32	0.45
14:o:31:THR:HG22	14:o:32:PRO:HD2	1.99	0.45
16:q:80:ASN:CG	53:1:1151:A:H4'	2.42	0.45
16:q:111:LYS:CG	17:r:48:LYS:HD2	2.39	0.45
17:r:37:GLU:HB3	17:r:53:PHE:CE1	2.52	0.45
20:u:43:LYS:HG3	53:1:480:A:O3'	2.17	0.45
25:z:36:GLU:O	25:z:37:ARG:NH1	2.50	0.45
36:L:61:PHE:O	36:L:65:LEU:HG	2.17	0.45
38:N:122:ARG:NH1	38:N:123:ARG:O	2.50	0.45
39:O:59:LYS:CG	52:3:972:C:H4'	2.43	0.45
44:T:21:THR:HG21	52:3:658:C:H1'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1123:U:O2'	52:3:1124:G:H5'	2.16	0.45
52:3:1197:A:C2'	52:3:1198:G:H5''	2.42	0.45
53:1:589:U:H2'	53:1:590:A:C8	2.52	0.45
53:1:742:A:H2'	53:1:743:A:H8	1.82	0.45
53:1:1087:G:N2	53:1:1103:A:H1'	2.32	0.45
53:1:2322:A:H2'	53:1:2323:G:O4'	2.17	0.45
53:1:2804:U:H2'	53:1:2805:C:C6	2.52	0.45
58:8:107:ALA:HB1	58:8:137:LYS:HD2	1.97	0.45
1:b:12:ARG:O	1:b:15:VAL:HG22	2.17	0.44
1:b:164:VAL:HG21	1:b:180:MET:HE3	1.99	0.44
4:e:2:LYS:HB3	4:e:100:GLU:OE2	2.16	0.44
9:j:23:LYS:NZ	9:j:142:ILE:HG13	2.31	0.44
23:x:27:ARG:NH2	53:1:1365:A:OP1	2.51	0.44
31:G:4:SER:O	31:G:7:ASP:OD1	2.35	0.44
35:K:90:MET:HA	52:3:737:C:OP1	2.18	0.44
44:T:44:GLU:C	44:T:46:LYS:H	2.25	0.44
52:3:256:U:H2'	52:3:257:G:C8	2.52	0.44
52:3:890:G:O2'	52:3:891:U:C6	2.71	0.44
52:3:1347:G:O2'	52:3:1348:U:C5	2.70	0.44
53:1:1909:C:H2'	53:1:1910:G:C8	2.50	0.44
53:1:2098:U:H2'	53:1:2099:U:O4'	2.17	0.44
53:1:2370:G:H2'	53:1:2371:G:C8	2.52	0.44
53:1:2800:A:H3'	53:1:2801:G:C5'	2.46	0.44
58:8:378:ARG:HG2	58:8:383:THR:HA	1.99	0.44
8:i:108:ILE:HG22	8:i:112:LYS:NZ	2.32	0.44
26:B:1:ALA:N	53:1:2056:G:N2	2.66	0.44
42:R:90:HIS:CE1	42:R:96:VAL:HG21	2.52	0.44
48:X:30:LEU:HD13	48:X:48:ILE:HG22	1.98	0.44
49:Y:81:GLN:O	49:Y:84:LYS:HB3	2.17	0.44
52:3:193:C:H2'	52:3:194:C:C6	2.52	0.44
52:3:709:U:H2'	52:3:710:G:C8	2.52	0.44
52:3:784:A:H2'	52:3:785:G:H8	1.82	0.44
52:3:1424:U:H2'	52:3:1425:U:O4'	2.16	0.44
52:3:1502:A:C8	52:3:1505:G:N2	2.85	0.44
53:1:635:C:H2'	53:1:636:G:C8	2.53	0.44
53:1:660:C:H2'	53:1:661:A:C8	2.52	0.44
53:1:1629:U:H2'	53:1:1630:A:C8	2.52	0.44
53:1:2293:G:H2'	53:1:2294:G:H8	1.82	0.44
53:1:2297:A:N1	53:1:2321:U:H5	2.14	0.44
53:1:2480:C:H2'	53:1:2481:G:O4'	2.17	0.44
18:s:97:LEU:HD12	18:s:97:LEU:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:t:10:VAL:HG13	19:t:11:LEU:N	2.31	0.44
20:u:32:LYS:HB3	20:u:63:ALA:HB1	1.99	0.44
52:3:437:U:O2'	52:3:438:U:H5'	2.17	0.44
52:3:714:G:H2'	52:3:715:A:C8	2.53	0.44
52:3:985:C:H2'	52:3:986:U:C6	2.52	0.44
53:1:162:U:C2'	53:1:163:C:H5'	2.47	0.44
53:1:481:G:H1'	53:1:506:G:N2	2.32	0.44
53:1:818:G:O2'	53:1:819:A:H5''	2.18	0.44
53:1:1213:A:H62	53:1:1236:G:H1'	1.80	0.44
55:6:41:C:H2'	55:6:42:G:C8	2.53	0.44
3:d:5:LEU:HB2	3:d:9:GLN:N	2.33	0.44
7:h:44:ALA:HB2	7:h:52:MET:HE3	1.99	0.44
10:k:14:SER:O	10:k:51:LYS:HG3	2.18	0.44
13:n:98:LEU:HD21	26:B:42:ILE:HG21	2.00	0.44
22:w:38:GLY:HA2	53:1:2330:G:H21	1.82	0.44
31:G:20:ARG:HB2	52:3:831:A:H5'	1.99	0.44
31:G:102:ASN:O	31:G:106:VAL:HG23	2.18	0.44
33:I:58:GLN:O	33:I:62:ARG:HG2	2.17	0.44
48:X:29:PRO:HA	48:X:48:ILE:HA	1.98	0.44
49:Y:3:ILE:H	49:Y:3:ILE:CD1	2.28	0.44
52:3:443:C:H2'	52:3:444:G:H8	1.83	0.44
52:3:560:A:H5'	52:3:566:G:N2	2.33	0.44
53:1:65:U:H2'	53:1:66:C:C6	2.53	0.44
53:1:784:G:HO2'	53:1:785:G:H8	1.66	0.44
53:1:1564:C:H2'	53:1:1565:C:O4'	2.17	0.44
53:1:1726:C:H2'	53:1:1727:C:C6	2.53	0.44
53:1:2678:C:H2'	53:1:2679:A:C8	2.52	0.44
55:5:10:G:C2	55:5:26:G:H1'	2.52	0.44
1:b:145:MET:O	1:b:146:LYS:HD3	2.18	0.44
6:g:5:LEU:HB2	6:g:17:ASP:H	1.81	0.44
8:i:12:VAL:HG12	53:1:1061:U:C2	2.53	0.44
20:u:3:LYS:HD3	20:u:82:VAL:HB	2.00	0.44
33:I:18:LEU:HB3	33:I:63:ILE:HG12	1.99	0.44
33:I:37:PRO:HD2	33:I:41:GLY:HA3	2.00	0.44
36:L:138:GLU:HA	36:L:141:HIS:HB2	1.99	0.44
38:N:117:LEU:HD22	38:N:123:ARG:HD2	1.98	0.44
45:U:22:ALA:HB2	45:U:32:PHE:HB3	1.98	0.44
52:3:487:A:H2'	52:3:488:C:O4'	2.18	0.44
52:3:537:G:H2'	52:3:538:G:C8	2.52	0.44
52:3:1488:G:H2'	52:3:1489:G:H8	1.82	0.44
53:1:1550:C:H2'	53:1:1551:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2008:C:H2'	53:1:2009:A:H8	1.83	0.44
53:1:2898:U:H2'	53:1:2899:A:C8	2.53	0.44
3:d:172:ALA:O	3:d:199:MET:HE1	2.17	0.44
6:g:66:ASN:ND2	6:g:134:VAL:O	2.50	0.44
6:g:97:ARG:HH11	6:g:112:LYS:HD3	1.82	0.44
16:q:51:GLN:HE22	16:q:54:ARG:HD2	1.82	0.44
31:G:102:ASN:HD22	52:3:1102:A:H2	1.66	0.44
32:H:114:LEU:O	32:H:117:ASP:OD2	2.36	0.44
38:N:18:VAL:HG13	38:N:64:ILE:HG12	1.99	0.44
42:R:48:SER:O	42:R:52:ILE:HG13	2.18	0.44
46:V:5:ARG:HH11	52:3:636:U:H5'	1.82	0.44
52:3:1472:U:H2'	52:3:1473:G:C8	2.53	0.44
53:1:290:U:H2'	53:1:291:G:H8	1.81	0.44
53:1:859:G:C2'	53:1:860:U:OP2	2.65	0.44
53:1:1440:U:H2'	53:1:1441:G:C8	2.52	0.44
53:1:2415:G:H2'	53:1:2416:C:C6	2.53	0.44
55:6:13:C:C3'	55:6:14:A:H5''	2.47	0.44
58:8:177:LYS:HE3	58:8:185:TRP:NE1	2.32	0.44
58:8:261:MET:CG	58:8:266:LEU:HD11	2.47	0.44
8:i:8:VAL:HG22	53:1:1098:A:H4'	1.99	0.44
40:P:27:ASN:O	40:P:56:LYS:NZ	2.51	0.44
52:3:20:U:H2'	52:3:21:G:O4'	2.17	0.44
52:3:230:G:O2'	52:3:231:U:H5'	2.17	0.44
52:3:428:G:O4'	52:3:430:A:C8	2.71	0.44
52:3:1395:C:H6	52:3:1395:C:H5'	1.82	0.44
52:3:1496:C:H1'	52:3:1517:G:H22	1.83	0.44
53:1:1140:C:O2'	53:1:1141:U:H5'	2.18	0.44
53:1:1745:A:O2'	53:1:1746:A:H5'	2.18	0.44
53:1:2101:A:H2'	53:1:2102:G:H8	1.83	0.44
53:1:2841:C:H2'	53:1:2842:G:C8	2.52	0.44
23:x:6:VAL:HG13	23:x:7:THR:N	2.32	0.44
31:G:46:VAL:HG22	31:G:50:ASN:HD21	1.83	0.44
36:L:113:LYS:HE2	36:L:113:LYS:HA	2.00	0.44
52:3:211:G:H2'	52:3:212:G:H5'	1.99	0.44
52:3:538:G:H2'	52:3:539:A:H8	1.82	0.44
53:1:696:G:O2'	53:1:697:G:H5'	2.18	0.44
53:1:1316:U:H2'	53:1:1317:G:H8	1.82	0.44
53:1:1675:C:H2'	53:1:1676:A:O4'	2.18	0.44
53:1:1704:C:H2'	53:1:1705:A:C8	2.53	0.44
53:1:2195:U:H2'	53:1:2196:C:C6	2.53	0.44
53:1:2569:G:O2'	53:1:2570:G:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2743:U:C2'	53:1:2744:G:H5''	2.48	0.44
54:2:1:U:H2'	54:2:2:G:C8	2.52	0.44
54:2:2:G:H2'	54:2:3:C:H6	1.83	0.44
54:2:88:C:H4'	54:2:89:U:OP1	2.17	0.44
54:2:88:C:H5''	54:2:89:U:OP1	2.18	0.44
1:b:257:ARG:HD3	53:1:1799:G:OP1	2.18	0.44
2:c:77:ARG:HH21	2:c:77:ARG:HG3	1.82	0.44
4:e:41:GLU:OE2	53:1:2311:A:N6	2.51	0.44
4:e:140:ILE:HD12	4:e:140:ILE:H	1.83	0.44
6:g:4:ILE:HB	6:g:39:ALA:HB2	1.99	0.44
11:l:62:PRO:HA	53:1:2393:U:O3'	2.18	0.44
12:m:124:LEU:CD1	12:m:125:PRO:HD2	2.42	0.44
14:o:33:ARG:O	14:o:34:HIS:HB2	2.18	0.44
15:p:46:VAL:HA	15:p:59:THR:O	2.18	0.44
16:q:57:ARG:NH1	53:1:1154:G:OP2	2.51	0.44
21:v:29:ILE:HD13	21:v:39:ALA:HA	2.00	0.44
21:v:72:VAL:HG12	21:v:93:ARG:HA	2.00	0.44
33:I:23:GLY:HA3	52:3:409:U:OP1	2.18	0.44
33:I:101:VAL:HG13	33:I:113:ALA:HB1	1.98	0.44
35:K:18:VAL:N	35:K:19:PRO:CD	2.81	0.44
52:3:56:U:H2'	52:3:57:G:H8	1.83	0.44
52:3:423:G:C2'	52:3:424:G:H5'	2.47	0.44
52:3:731:G:O2'	52:3:732:C:H5'	2.18	0.44
52:3:981:U:H2'	52:3:982:U:C5	2.53	0.44
52:3:1245:C:H2'	52:3:1246:A:C8	2.53	0.44
53:1:854:C:H2'	53:1:855:G:H8	1.82	0.44
53:1:1111:A:H2'	53:1:1111:A:N3	2.31	0.44
53:1:1279:G:H2'	53:1:1280:G:C8	2.53	0.44
53:1:1528:A:H2'	53:1:1529:G:O4'	2.17	0.44
53:1:1709:U:H2'	53:1:1710:G:C8	2.53	0.44
53:1:1725:U:H2'	53:1:1726:C:C6	2.52	0.44
53:1:2011:U:H2'	53:1:2012:G:O4'	2.17	0.44
53:1:2185:U:H2'	53:1:2186:G:C8	2.51	0.44
53:1:2217:G:O2'	53:1:2218:G:H5'	2.18	0.44
53:1:2679:A:O2'	53:1:2680:U:H5'	2.17	0.44
54:2:85:G:H2'	54:2:86:G:H8	1.83	0.44
55:5:20:U:C3'	55:5:21:A:H5'	2.45	0.44
36:L:23:ALA:O	36:L:26:VAL:HG22	2.18	0.43
39:O:10:LEU:C	39:O:11:LYS:HD3	2.43	0.43
47:W:11:ARG:HD2	52:3:845:A:H1'	1.99	0.43
47:W:27:THR:HA	47:W:30:ASN:ND2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:73:ARG:HH22	52:3:263:A:P	2.41	0.43
50:Z:23:GLU:O	50:Z:25:ALA:N	2.50	0.43
51:a:171:ILE:HD12	51:a:171:ILE:N	2.33	0.43
52:3:371:A:H2'	52:3:372:C:O4'	2.18	0.43
52:3:438:U:HO2'	52:3:439:U:H6	1.65	0.43
52:3:634:C:H2'	52:3:635:A:H8	1.84	0.43
53:1:1181:U:H2'	53:1:1182:G:C8	2.53	0.43
53:1:1421:G:H1'	53:1:1494:A:H61	1.83	0.43
53:1:1525:A:H2'	53:1:1526:C:O4'	2.19	0.43
53:1:1666:G:O2'	53:1:1667:G:H5'	2.18	0.43
53:1:2329:U:H2'	53:1:2330:G:C8	2.53	0.43
2:c:62:LYS:HD3	53:1:2810:A:H4'	2.00	0.43
2:c:173:GLN:NE2	53:1:2771:C:O2'	2.50	0.43
10:k:41:ILE:HD11	10:k:86:LEU:HD22	1.99	0.43
11:l:38:GLN:HB3	53:1:832:U:H5'	2.00	0.43
12:m:65:ILE:N	12:m:65:ILE:HD12	2.33	0.43
13:n:7:GLY:HA3	53:1:2690:U:H3	1.82	0.43
14:o:99:TYR:CZ	14:o:104:GLN:HG3	2.53	0.43
15:p:23:ASP:HB3	15:p:85:VAL:HG13	2.00	0.43
15:p:53:GLY:O	15:p:76:HIS:NE2	2.51	0.43
17:r:26:ASP:O	17:r:27:ILE:HD13	2.17	0.43
17:r:72:VAL:O	17:r:74:ILE:HD12	2.19	0.43
21:v:12:GLN:HG2	54:2:76:G:OP1	2.18	0.43
21:v:42:LEU:HD13	21:v:47:VAL:HG21	1.99	0.43
23:x:60:LYS:NZ	53:1:371:A:N3	2.60	0.43
28:D:1:MET:HE2	28:D:3:ARG:HD2	2.00	0.43
40:P:91:GLY:O	40:P:93:GLU:N	2.43	0.43
41:Q:101:LEU:HD23	41:Q:101:LEU:H	1.82	0.43
45:U:27:ALA:HB3	45:U:30:GLY:HA3	1.99	0.43
46:V:67:SER:HB2	46:V:69:THR:O	2.18	0.43
49:Y:8:LYS:HE2	49:Y:12:GLN:OE1	2.18	0.43
52:3:381:C:H2'	52:3:382:A:O4'	2.17	0.43
52:3:530:G:H3'	52:3:531:U:H5''	1.99	0.43
52:3:711:G:O2'	52:3:712:A:H5'	2.18	0.43
52:3:868:C:H2'	52:3:869:G:O4'	2.18	0.43
53:1:492:A:H2'	53:1:493:G:O4'	2.18	0.43
53:1:863:A:H2'	53:1:864:G:C8	2.53	0.43
53:1:1078:U:C5'	53:1:1079:C:H5''	2.48	0.43
53:1:1183:U:H2'	53:1:1184:U:H6	1.80	0.43
53:1:2082:A:H2'	53:1:2083:G:O4'	2.18	0.43
53:1:2291:U:H2'	53:1:2292:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2774:C:H2'	53:1:2775:G:O4'	2.17	0.43
54:2:56:G:H4'	54:2:57:A:C8	2.53	0.43
57:7:48:C:H5'	57:7:50:U:P	2.58	0.43
58:8:192:LEU:O	58:8:196:LEU:HG	2.17	0.43
4:e:14:LYS:O	4:e:18:GLU:HG3	2.17	0.43
4:e:91:ARG:HA	4:e:95:MET:SD	2.59	0.43
5:f:157:LYS:HD2	53:1:2659:G:P	2.59	0.43
6:g:11:ASN:ND2	53:1:2095:A:OP1	2.51	0.43
12:m:20:LEU:HD23	21:v:81:PRO:HG2	2.00	0.43
28:D:44:VAL:HG13	28:D:44:VAL:O	2.18	0.43
31:G:103:TRP:HD1	31:G:107:ARG:HH21	1.64	0.43
31:G:119:GLN:HB3	31:G:124:THR:OG1	2.19	0.43
32:H:104:GLU:OE2	32:H:106:ARG:NE	2.51	0.43
34:J:113:VAL:HG13	34:J:114:LEU:CD1	2.48	0.43
35:K:86:ARG:NH1	52:3:673:A:H4'	2.33	0.43
36:L:13:PRO:HG2	38:N:45:MET:CE	2.48	0.43
36:L:25:PHE:HA	36:L:100:MET:CE	2.48	0.43
41:Q:99:GLY:HA3	41:Q:117:GLY:HA3	1.99	0.43
43:S:29:ILE:CG2	43:S:30:ILE:HD12	2.38	0.43
43:S:65:GLN:HE21	43:S:78:LEU:HD22	1.82	0.43
44:T:23:SER:HB3	44:T:26:VAL:HG23	2.00	0.43
45:U:71:VAL:O	45:U:75:ILE:HG13	2.19	0.43
46:V:42:LYS:O	46:V:42:LYS:HG3	2.18	0.43
52:3:184:G:C4'	52:3:224:U:H4'	2.48	0.43
52:3:398:U:H2'	52:3:399:G:H8	1.82	0.43
52:3:1086:U:H3	52:3:1099:G:H1	1.66	0.43
52:3:1404:C:H2'	52:3:1405:G:H8	1.84	0.43
53:1:158:U:H2'	53:1:159:G:O4'	2.18	0.43
53:1:2678:C:H2'	53:1:2679:A:H8	1.83	0.43
53:1:2798:U:H4'	53:1:2799:A:N3	2.33	0.43
55:6:21:A:H61	55:6:46:G:H2'	1.82	0.43
1:b:106:PRO:HA	1:b:194:VAL:HA	2.00	0.43
3:d:41:GLN:HE21	53:1:442:G:C4'	2.31	0.43
6:g:40:THR:O	6:g:44:ILE:HG13	2.19	0.43
7:h:62:ARG:O	7:h:65:GLU:HB3	2.18	0.43
8:i:18:ASN:ND2	8:i:35:MET:SD	2.91	0.43
9:j:84:ILE:HG23	9:j:84:ILE:O	2.18	0.43
12:m:26:VAL:HG13	12:m:104:GLU:HG2	1.99	0.43
16:q:15:LYS:O	16:q:19:GLN:HG3	2.17	0.43
21:v:17:SER:O	21:v:20:LEU:HG	2.19	0.43
23:x:27:ARG:HH21	23:x:29:LEU:HD21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:E:39:ARG:O	29:E:43:LEU:HD23	2.19	0.43
38:N:10:ARG:O	38:N:105:ARG:NH2	2.51	0.43
41:Q:13:ARG:NH1	41:Q:14:LYS:H	2.15	0.43
41:Q:27:PRO:HB2	41:Q:28:GLN:CD	2.44	0.43
45:U:46:LYS:HZ3	52:3:617:G:H5''	1.81	0.43
46:V:42:LYS:HE3	52:3:278:G:P	2.59	0.43
49:Y:70:LYS:HG3	49:Y:73:ARG:HE	1.84	0.43
51:a:12:ARG:HH12	53:1:2175:C:H5''	1.83	0.43
52:3:129:A:H1'	52:3:130:A:N7	2.34	0.43
52:3:225:C:H2'	52:3:226:G:C5'	2.47	0.43
52:3:601:G:H2'	52:3:602:A:H8	1.83	0.43
53:1:741:U:H2'	53:1:742:A:H8	1.82	0.43
53:1:1020:A:C1'	53:1:1021:A:OP2	2.59	0.43
53:1:1127:A:H2'	53:1:1128:G:H5''	2.00	0.43
53:1:1790:C:H2'	53:1:1791:A:C5	2.53	0.43
53:1:1947:C:H2'	53:1:1948:G:H8	1.82	0.43
53:1:2008:C:H2'	53:1:2009:A:C8	2.53	0.43
54:2:51:G:H2'	54:2:52:A:O4'	2.19	0.43
1:b:181:ARG:NH1	53:1:1800:C:OP2	2.51	0.43
2:c:22:ILE:HA	2:c:23:PRO:HD3	1.80	0.43
4:e:127:TYR:HB3	4:e:155:ILE:HB	1.99	0.43
7:h:54:VAL:C	53:1:1084:A:H5''	2.43	0.43
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.48	0.43
8:i:52:LEU:HA	8:i:53:PRO:HD3	1.91	0.43
10:k:24:VAL:HG12	10:k:39:ILE:HG22	2.01	0.43
21:v:20:LEU:HD11	21:v:27:PRO:HD3	1.99	0.43
27:C:12:SER:HB3	27:C:48:TYR:CE1	2.53	0.43
31:G:182:VAL:HG12	31:G:195:VAL:HG13	1.98	0.43
32:H:10:ARG:NE	32:H:179:ALA:O	2.43	0.43
33:I:98:ASP:OD1	33:I:98:ASP:N	2.52	0.43
33:I:202:LEU:O	33:I:202:LEU:HD23	2.18	0.43
34:J:84:VAL:HG22	34:J:85:LYS:N	2.34	0.43
41:Q:109:ARG:NH1	52:3:537:G:O3'	2.46	0.43
45:U:6:LEU:HG	45:U:71:VAL:HG22	2.00	0.43
47:W:11:ARG:NE	52:3:845:A:O4'	2.52	0.43
53:1:729:G:H4'	53:1:763:G:O5'	2.19	0.43
53:1:2508:G:H1	53:1:2580:U:H3	1.66	0.43
2:c:125:TRP:CG	2:c:160:LYS:HB3	2.52	0.43
3:d:95:LYS:NZ	53:1:607:U:H4'	2.33	0.43
4:e:25:MET:HE3	54:2:54:G:H21	1.83	0.43
20:u:48:VAL:HG12	20:u:52:ASN:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:w:27:VAL:HG22	22:w:28:LEU:O	2.18	0.43
25:z:4:ILE:HD11	25:z:56:VAL:CG2	2.48	0.43
30:F:2:LYS:HG3	30:F:4:ARG:CZ	2.49	0.43
30:F:2:LYS:HB3	30:F:4:ARG:HG3	2.00	0.43
32:H:46:LEU:HD22	32:H:46:LEU:N	2.34	0.43
34:J:9:GLU:HG2	34:J:10:LEU:HD22	1.98	0.43
44:T:71:ARG:NH2	52:3:754:C:OP1	2.52	0.43
44:T:78:THR:HA	44:T:81:ILE:HG12	2.01	0.43
46:V:38:LYS:HD2	46:V:38:LYS:O	2.19	0.43
52:3:358:U:H2'	52:3:359:G:C8	2.54	0.43
52:3:555:U:H2'	52:3:556:C:C6	2.54	0.43
52:3:1434:A:H2'	52:3:1435:G:O4'	2.18	0.43
53:1:1739:A:H2'	53:1:1740:G:O4'	2.19	0.43
53:1:2293:G:H2'	53:1:2294:G:C8	2.54	0.43
53:1:2345:G:H5'	53:1:2347:C:O4'	2.19	0.43
54:2:30:C:H2'	54:2:31:C:C5'	2.48	0.43
2:c:33:ARG:HH21	2:c:73:VAL:HB	1.83	0.43
2:c:133:THR:HG23	2:c:134:HIS:HD2	1.83	0.43
4:e:107:VAL:N	4:e:108:PRO:CD	2.81	0.43
6:g:83:LYS:HA	6:g:149:GLU:OXT	2.18	0.43
7:h:118:ILE:CB	7:h:119:PRO:HD3	2.49	0.43
9:j:35:ARG:NH1	9:j:140:LEU:HD11	2.33	0.43
10:k:15:GLY:HA3	10:k:50:GLY:HA3	2.01	0.43
11:l:78:ARG:CZ	53:1:626:A:H2'	2.49	0.43
14:o:65:THR:HG23	14:o:65:THR:O	2.19	0.43
34:J:113:VAL:HG13	34:J:114:LEU:HD12	2.00	0.43
38:N:117:LEU:HD22	38:N:123:ARG:CD	2.49	0.43
42:R:10:ASP:H	42:R:12:LYS:NZ	2.16	0.43
52:3:107:G:O2'	52:3:108:G:H5'	2.19	0.43
52:3:396:C:C3'	52:3:397:A:H5''	2.49	0.43
52:3:406:G:H2'	52:3:407:U:C6	2.53	0.43
52:3:1251:A:H2'	52:3:1252:A:O4'	2.19	0.43
53:1:96:C:H2'	53:1:97:C:H6	1.83	0.43
53:1:720:U:H2'	53:1:721:A:C8	2.54	0.43
53:1:1373:A:H5'	53:1:2212:A:H1'	2.00	0.43
53:1:1991:U:H2'	53:1:1992:G:H5''	2.01	0.43
53:1:2196:C:O2'	53:1:2197:U:H5'	2.18	0.43
53:1:2809:A:H2'	53:1:2810:A:C8	2.54	0.43
4:e:114:ARG:HG2	4:e:114:ARG:NH2	2.34	0.43
15:p:92:ARG:HD3	53:1:1753:G:C5'	2.48	0.43
27:C:4:ILE:HB	53:1:2284:A:OP1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:86:ARG:HH12	52:3:673:A:H4'	1.84	0.43
45:U:78:VAL:O	45:U:79:ASN:O	2.37	0.43
48:X:17:LYS:HG2	48:X:30:LEU:HD23	2.00	0.43
52:3:131:A:H2'	52:3:132:C:C6	2.54	0.43
52:3:195:A:H2'	52:3:196:A:C8	2.54	0.43
53:1:131:A:H2'	53:1:132:G:C8	2.54	0.43
53:1:404:A:H1'	53:1:406:G:C4	2.53	0.43
53:1:464:U:H2'	53:1:465:G:O4'	2.18	0.43
53:1:1068:G:H2'	53:1:1069:A:O4'	2.18	0.43
53:1:1526:C:H2'	53:1:1527:G:O4'	2.19	0.43
53:1:2786:U:H2'	53:1:2787:C:C6	2.54	0.43
58:8:87:ASP:HA	58:8:90:LYS:HD2	2.00	0.43
1:b:259:ASN:C	1:b:261:ARG:H	2.26	0.43
4:e:163:GLU:HA	4:e:166:ARG:NH1	2.34	0.43
7:h:80:THR:O	7:h:82:ILE:HG13	2.19	0.43
18:s:82:MET:HE3	18:s:98:LYS:HB3	2.01	0.43
20:u:10:VAL:HG12	20:u:71:ILE:HA	2.01	0.43
21:v:20:LEU:HD12	21:v:25:LYS:O	2.18	0.43
21:v:46:LYS:HA	21:v:49:ASN:HD22	1.83	0.43
31:G:88:GLN:HE22	31:G:224:ARG:HH22	1.67	0.43
38:N:59:LYS:HG3	38:N:60:LEU:CD2	2.48	0.43
40:P:81:LEU:C	40:P:81:LEU:HD12	2.43	0.43
42:R:100:ARG:NH1	52:3:950:U:H3'	2.34	0.43
52:3:9:G:O2'	52:3:10:A:H5'	2.19	0.43
52:3:696:A:H1'	52:3:786:G:O2'	2.19	0.43
52:3:857:C:H2'	52:3:858:G:O4'	2.18	0.43
52:3:1120:C:H2'	52:3:1121:U:H6	1.84	0.43
52:3:1419:G:O2'	52:3:1420:U:H5'	2.19	0.43
52:3:1498:U:C4	56:4:17:U:H5''	2.54	0.43
52:3:1499:A:H1'	52:3:1520:C:O5'	2.18	0.43
53:1:1326:U:H2'	53:1:1327:A:H8	1.84	0.43
53:1:2096:C:H2'	53:1:2097:A:H8	1.83	0.43
53:1:2180:U:H4'	55:6:17(A):U:H5'	2.00	0.43
53:1:2579:C:H2'	53:1:2580:U:O4'	2.18	0.43
54:2:91:C:H2'	54:2:92:C:C6	2.53	0.43
55:5:34:C:H2'	55:5:35:A:H8	1.83	0.43
16:q:104:ALA:HA	17:r:46:GLU:HG2	2.01	0.43
17:r:21:ARG:HG3	17:r:93:PHE:HD2	1.84	0.43
31:G:76:SER:O	31:G:80:LYS:HG2	2.17	0.43
31:G:177:ASN:ND2	52:3:1075:U:OP1	2.52	0.43
37:M:107:LYS:HE2	37:M:107:LYS:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:104:ASN:ND2	52:3:949:A:N7	2.67	0.43
43:S:64:ARG:NH1	43:S:64:ARG:O	2.51	0.43
52:3:376:G:O2'	52:3:377:G:H5'	2.18	0.43
52:3:593:U:H2'	52:3:594:U:C6	2.53	0.43
52:3:834:U:H2'	52:3:835:U:C6	2.54	0.43
52:3:1397:C:H42	56:4:22:A:H2'	1.84	0.43
52:3:1524:C:H2'	52:3:1525:G:C8	2.53	0.43
53:1:441:U:H2'	53:1:442:G:C8	2.54	0.43
53:1:579:G:H4'	53:1:2018:G:H5''	2.01	0.43
53:1:1333:G:H2'	53:1:1334:G:H8	1.83	0.43
53:1:2004:G:H2'	53:1:2005:A:O4'	2.19	0.43
53:1:2121:G:H2'	53:1:2122:U:O4'	2.19	0.43
53:1:2699:C:H2'	53:1:2700:A:H8	1.82	0.43
53:1:2707:U:H2'	53:1:2708:G:H8	1.84	0.43
53:1:2739:U:O2'	53:1:2740:A:H5'	2.18	0.43
5:f:8:VAL:HB	5:f:49:LEU:HD12	2.00	0.42
12:m:89:VAL:HG13	12:m:89:VAL:O	2.18	0.42
20:u:13:LEU:O	20:u:18:LYS:HG2	2.19	0.42
29:E:51:LYS:O	29:E:54:LEU:HG	2.19	0.42
33:I:33:ILE:HG13	33:I:34:GLU:OE2	2.19	0.42
51:a:198:LYS:HA	51:a:198:LYS:HD3	1.85	0.42
52:3:114:U:H2'	52:3:115:G:C8	2.54	0.42
52:3:976:G:N2	52:3:1362:A:H2'	2.34	0.42
53:1:521:U:H2'	53:1:522:A:H8	1.84	0.42
53:1:1883:U:H2'	53:1:1884:G:O4'	2.19	0.42
8:i:131:THR:O	8:i:135:MET:HG2	2.19	0.42
11:l:81:ASP:OD1	11:l:81:ASP:N	2.52	0.42
16:q:25:GLY:O	16:q:29:ARG:NH1	2.52	0.42
18:s:3:THR:HB	18:s:107:VAL:HG23	2.01	0.42
21:v:78:GLN:HB2	21:v:88:HIS:O	2.19	0.42
33:I:2:ARG:HD2	33:I:114:ARG:HD3	2.01	0.42
33:I:24:VAL:HA	33:I:160:LEU:HD11	2.02	0.42
34:J:56:PRO:HA	34:J:59:ILE:HG12	2.00	0.42
41:Q:41:PRO:HG3	41:Q:49:ARG:HG2	2.01	0.42
51:a:12:ARG:NH1	53:1:2175:C:OP1	2.52	0.42
52:3:1400:C:H5'	56:4:18:G:C6	2.54	0.42
52:3:1429:A:H2'	52:3:1430:A:H8	1.84	0.42
53:1:184:C:H2'	53:1:185:G:H8	1.83	0.42
53:1:297:G:H2'	53:1:298:G:O4'	2.19	0.42
53:1:1783:A:H5'	53:1:2608:G:H4'	2.01	0.42
57:7:72:C:O2'	57:7:73:A:H5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:81:ARG:NH1	53:1:2496:C:OP2	2.52	0.42
12:m:131:VAL:HG22	12:m:132:THR:N	2.34	0.42
14:o:25:ARG:NH1	54:2:8:C:O2'	2.52	0.42
26:B:4:GLN:HB2	53:1:2054:A:C2	2.54	0.42
32:H:21:TRP:HA	39:O:95:GLY:HA2	2.00	0.42
34:J:108:GLY:O	34:J:109:ALA:HB3	2.19	0.42
35:K:37:HIS:O	35:K:97:THR:HG22	2.20	0.42
50:Z:35:GLU:O	50:Z:37:TYR:N	2.45	0.42
52:3:392:C:H2'	52:3:393:A:C8	2.55	0.42
52:3:398:U:H2'	52:3:399:G:C8	2.54	0.42
52:3:1219:A:H2'	52:3:1220:G:C8	2.54	0.42
52:3:1415:G:H2'	52:3:1416:G:C8	2.53	0.42
52:3:1497:G:H2'	52:3:1498:U:O2	2.19	0.42
53:1:179:C:O2'	53:1:180:G:H5'	2.20	0.42
53:1:302:C:H2'	53:1:303:G:C8	2.54	0.42
53:1:783:A:N3	53:1:785:G:H1'	2.35	0.42
53:1:1089:A:H2	53:1:1090:A:H62	1.67	0.42
53:1:1398:C:H2'	53:1:1399:C:C6	2.54	0.42
53:1:1443:U:H2'	53:1:1444:G:C8	2.54	0.42
53:1:1822:C:H2'	53:1:1823:G:H8	1.83	0.42
53:1:2194:U:H2'	53:1:2195:U:C6	2.54	0.42
58:8:312:LEU:O	58:8:318:GLY:HA3	2.19	0.42
3:d:45:ALA:HB2	3:d:89:PRO:HD3	2.00	0.42
4:e:39:VAL:HG21	4:e:48:LEU:HG	2.02	0.42
4:e:45:ASP:OD2	4:e:47:LYS:HG2	2.20	0.42
11:l:79:LEU:HD22	11:l:116:VAL:HG21	2.01	0.42
23:x:16:ASN:HD22	53:1:2081:U:H5''	1.84	0.42
26:B:16:ARG:HA	26:B:19:ASP:OD2	2.19	0.42
32:H:203:LYS:HG3	32:H:204:GLY:H	1.84	0.42
33:I:54:LEU:HD22	52:3:509:A:H4'	2.00	0.42
36:L:113:LYS:HB3	52:3:1297:G:N2	2.35	0.42
53:1:727:A:O2'	53:1:728:G:H5'	2.20	0.42
53:1:799:G:H5''	53:1:800:A:H2'	2.00	0.42
53:1:877:A:H1'	53:1:900:A:N6	2.34	0.42
53:1:968:C:H2'	53:1:969:G:C8	2.55	0.42
53:1:1572:A:O2'	53:1:1573:G:H5'	2.19	0.42
53:1:2361:G:O2'	53:1:2362:C:H5'	2.20	0.42
55:5:52:G:O2'	55:5:53:G:H5'	2.20	0.42
58:8:170:ILE:HG23	58:8:170:ILE:O	2.18	0.42
1:b:15:VAL:HG12	1:b:205:GLY:HA3	2.02	0.42
3:d:24:ASN:HD22	3:d:27:LEU:HB2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:25:MET:HB3	54:2:57:A:C6	2.55	0.42
5:f:143:VAL:O	5:f:146:ASP:OD1	2.37	0.42
21:v:9:ARG:C	21:v:10:LYS:HD2	2.44	0.42
30:F:3:VAL:HG21	53:1:2539:C:H5'	2.01	0.42
33:I:201:GLU:O	52:3:8:A:N6	2.52	0.42
34:J:92:ARG:O	34:J:93:VAL:C	2.61	0.42
35:K:98:GLU:HB3	35:K:99:ALA:H	1.67	0.42
40:P:43:TRP:CZ2	52:3:686:U:H1'	2.50	0.42
40:P:48:GLY:HA2	52:3:688:G:H5'	2.01	0.42
41:Q:13:ARG:HH11	41:Q:14:LYS:H	1.66	0.42
42:R:27:THR:HG21	52:3:1328:C:H5''	2.00	0.42
52:3:758:C:H4'	52:3:880:C:C4'	2.48	0.42
52:3:822:U:H2'	52:3:823:C:C6	2.55	0.42
52:3:1040:U:H2'	52:3:1041:G:C8	2.55	0.42
52:3:1186:G:H2'	52:3:1187:G:C8	2.55	0.42
53:1:118:A:H2'	53:1:120:U:O4	2.18	0.42
53:1:1889:A:H2'	53:1:1890:A:C8	2.55	0.42
53:1:2543:G:H2'	53:1:2544:G:C8	2.54	0.42
54:2:39:A:H2'	54:2:40:U:C6	2.53	0.42
54:2:76:G:O2'	54:2:77:U:H5'	2.20	0.42
58:8:216:GLU:HG2	58:8:229:THR:O	2.19	0.42
4:e:2:LYS:O	4:e:5:ASP:OD2	2.37	0.42
7:h:102:ALA:HA	7:h:105:LYS:HE3	2.01	0.42
11:l:126:ARG:HH21	11:l:126:ARG:HB2	1.85	0.42
18:s:29:VAL:HG23	18:s:69:LEU:O	2.19	0.42
23:x:71:ARG:HG2	23:x:71:ARG:HH11	1.84	0.42
43:S:26:LEU:HA	43:S:30:ILE:HD13	2.01	0.42
45:U:40:ASN:ND2	45:U:43:ALA:HB2	2.35	0.42
45:U:67:ILE:HD12	45:U:67:ILE:N	2.27	0.42
52:3:161:A:H2'	52:3:162:A:O4'	2.19	0.42
52:3:499:A:N3	52:3:500:G:H1'	2.34	0.42
52:3:1170:A:H2'	52:3:1171:A:H5'	2.02	0.42
53:1:546:U:H2'	53:1:547:A:H4'	2.02	0.42
53:1:594:U:H2'	53:1:595:C:C6	2.54	0.42
53:1:1019:U:H3	53:1:1142:A:H62	1.66	0.42
53:1:1300:G:H4'	53:1:1301:A:C5'	2.48	0.42
53:1:1910:G:O2'	53:1:1911:U:H5'	2.19	0.42
53:1:2074:U:O2'	53:1:2597:G:H1'	2.19	0.42
53:1:2475:C:C2'	53:1:2476:A:H5'	2.49	0.42
53:1:2478:A:H2'	53:1:2479:U:O4'	2.18	0.42
53:1:2732:G:O2'	53:1:2733:A:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2888:C:H2'	53:1:2889:C:C6	2.54	0.42
54:2:35:C:C2'	54:2:36:C:H5'	2.50	0.42
57:7:71:G:O2'	57:7:72:C:H5'	2.18	0.42
4:e:162:ASP:OD2	4:e:163:GLU:N	2.53	0.42
7:h:2:ALA:HB3	7:h:6:GLN:NE2	2.34	0.42
7:h:100:ALA:O	7:h:103:ASN:ND2	2.53	0.42
14:o:32:PRO:HD2	54:2:29:A:OP2	2.20	0.42
16:q:90:ASP:OD2	53:1:996:A:H4'	2.20	0.42
32:H:100:ILE:HD12	32:H:100:ILE:N	2.34	0.42
33:I:63:ILE:O	33:I:110:ARG:HD2	2.20	0.42
35:K:51:ILE:O	35:K:52:ASN:HB2	2.20	0.42
50:Z:23:GLU:O	50:Z:24:LYS:HG2	2.20	0.42
50:Z:34:ARG:HD2	50:Z:36:PHE:CE1	2.54	0.42
52:3:20:U:O2'	52:3:21:G:H5'	2.20	0.42
52:3:1256:A:O2'	52:3:1257:A:H5''	2.19	0.42
52:3:1504:G:OP1	52:3:1507:A:H4'	2.19	0.42
53:1:139:U:H5'	53:1:140:C:OP1	2.18	0.42
53:1:973:A:H5'	53:1:1188:U:H1'	2.00	0.42
53:1:976:G:H5'	53:1:1156:A:N6	2.33	0.42
53:1:1066:U:H2'	53:1:1068:G:OP2	2.20	0.42
53:1:1866:A:H2'	53:1:1867:G:O4'	2.18	0.42
53:1:2030:A:N3	53:1:2499:C:H5''	2.35	0.42
53:1:2443:C:H2'	53:1:2444:G:C8	2.55	0.42
58:8:94:THR:HG23	58:8:96:ALA:H	1.84	0.42
58:8:374:ARG:HD2	58:8:387:GLY:O	2.20	0.42
2:c:202:ILE:HD12	2:c:202:ILE:N	2.35	0.42
5:f:106:LEU:HB3	5:f:108:PHE:CE2	2.55	0.42
5:f:114:HIS:NE2	5:f:146:ASP:OD2	2.52	0.42
6:g:30:LEU:HA	6:g:35:LYS:HB2	2.02	0.42
9:j:58:ASN:HD21	9:j:128:ASN:HB2	1.85	0.42
11:l:79:LEU:HB3	11:l:116:VAL:CG2	2.48	0.42
12:m:65:ILE:HD12	12:m:65:ILE:H	1.85	0.42
12:m:135:VAL:O	12:m:135:VAL:HG13	2.20	0.42
17:r:79:ARG:NH2	53:1:572:A:H5'	2.35	0.42
19:t:74:ILE:H	19:t:74:ILE:HG12	1.65	0.42
20:u:28:LEU:HB3	20:u:32:LYS:HB2	2.02	0.42
20:u:50:ALA:O	20:u:51:LEU:HG	2.20	0.42
25:z:15:ARG:HA	25:z:15:ARG:HD3	1.86	0.42
31:G:131:LYS:O	31:G:135:MET:HG2	2.19	0.42
34:J:24:VAL:O	34:J:25:LYS:C	2.63	0.42
43:S:47:LEU:HD12	43:S:47:LEU:HA	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:53:ASP:HB3	43:S:54:SER:H	1.74	0.42
48:X:5:LYS:HE2	48:X:6:LYS:HE3	2.01	0.42
52:3:220:G:O2'	52:3:221:C:H5'	2.20	0.42
52:3:560:A:H4'	52:3:561:U:H5'	2.00	0.42
52:3:1372:U:H2'	52:3:1373:G:O4'	2.20	0.42
53:1:45:G:H5''	53:1:46:G:C4'	2.50	0.42
53:1:160:A:H2'	53:1:161:A:C8	2.55	0.42
53:1:511:U:C2'	53:1:512:G:H5'	2.46	0.42
53:1:861:A:H2'	53:1:862:G:O4'	2.20	0.42
53:1:885:C:H2'	53:1:886:A:H8	1.85	0.42
53:1:2047:C:H2'	53:1:2048:G:H8	1.84	0.42
53:1:2529:G:OP2	53:1:2530:A:H5''	2.20	0.42
53:1:2685:G:H2'	53:1:2686:G:C8	2.55	0.42
57:7:76:A:H62	58:8:224:ARG:HG3	1.84	0.42
58:8:172:ARG:HD2	58:8:188:LYS:HE2	2.02	0.42
1:b:154:ALA:HB2	1:b:161:VAL:HG23	2.02	0.42
1:b:167:ASP:OD1	1:b:167:ASP:N	2.52	0.42
2:c:9:VAL:HG13	2:c:9:VAL:O	2.20	0.42
5:f:46:ASP:HB3	5:f:47:ASN:H	1.67	0.42
6:g:73:ASN:CG	6:g:76:GLU:H	2.28	0.42
12:m:71:LYS:HD3	12:m:95:LEU:HD13	2.02	0.42
14:o:69:ASP:OD2	14:o:69:ASP:N	2.53	0.42
31:G:34:ARG:HB2	31:G:39:ILE:HD11	2.01	0.42
31:G:46:VAL:O	31:G:50:ASN:ND2	2.52	0.42
33:I:150:LYS:HE3	33:I:155:LYS:CD	2.48	0.42
39:O:40:ILE:HA	39:O:41:PRO:HD3	1.93	0.42
50:Z:64:ALA:C	50:Z:66:ARG:H	2.28	0.42
50:Z:65:ARG:NH1	52:3:1088:G:H4'	2.27	0.42
51:a:170:ILE:C	51:a:171:ILE:HD12	2.44	0.42
52:3:1238:A:C2'	52:3:1239:A:H5'	2.50	0.42
53:1:635:C:H2'	53:1:636:G:H8	1.84	0.42
53:1:2617:U:H2'	53:1:2618:G:O4'	2.19	0.42
57:7:14:A:C2'	57:7:15:G:H5'	2.49	0.42
58:8:20:HIS:HB3	58:8:23:HIS:CD2	2.55	0.42
58:8:293:LEU:HD23	58:8:293:LEU:C	2.45	0.42
58:8:300:LYS:HE3	58:8:302:HIS:NE2	2.34	0.42
11:l:53:GLY:HA3	53:1:826:U:O2'	2.20	0.42
18:s:73:LYS:HB3	18:s:73:LYS:HE2	1.86	0.42
32:H:154:GLY:HA3	32:H:195:ILE:HG12	2.02	0.42
34:J:108:GLY:H	52:3:9:G:C4'	2.30	0.42
37:M:45:ILE:HG21	37:M:60:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:51:VAL:HG22	41:Q:52:CYS:N	2.35	0.42
42:R:6:ILE:HG13	42:R:7:ASN:N	2.35	0.42
45:U:79:ASN:HB2	45:U:82:ALA:OXT	2.19	0.42
52:3:206:C:H2'	52:3:207:C:O4'	2.20	0.42
52:3:328:C:H5'	52:3:329:A:H5'	2.02	0.42
52:3:1280:A:O2'	52:3:1281:C:H5'	2.20	0.42
53:1:167:A:H2'	53:1:168:G:O4'	2.19	0.42
53:1:216:A:H2'	53:1:217:A:O4'	2.20	0.42
53:1:560:C:H2'	53:1:561:G:O4'	2.19	0.42
53:1:765:C:H2'	53:1:766:U:C6	2.55	0.42
53:1:857:G:H2'	53:1:858:G:O4'	2.19	0.42
53:1:1188:U:O2'	53:1:1189:A:H5'	2.20	0.42
53:1:1833:C:H2'	53:1:1834:U:O4'	2.18	0.42
53:1:1923:U:H2'	53:1:1924:C:C6	2.54	0.42
53:1:2396:G:O2'	53:1:2397:G:H5'	2.20	0.42
53:1:2404:U:H2'	53:1:2405:G:O4'	2.19	0.42
53:1:2553:G:C3'	53:1:2554:U:H5''	2.48	0.42
53:1:2707:U:H2'	53:1:2708:G:C8	2.55	0.42
53:1:2837:A:H2'	53:1:2838:G:H8	1.83	0.42
55:6:68:C:H2'	55:6:69:C:O4'	2.20	0.42
58:8:214:PRO:HD2	58:8:231:ARG:O	2.19	0.42
1:b:129:LEU:N	1:b:129:LEU:HD23	2.35	0.41
8:i:4:VAL:HA	8:i:7:TYR:CZ	2.55	0.41
8:i:75:ALA:HA	8:i:78:LEU:HD12	2.02	0.41
10:k:71:ARG:NH1	15:p:71:ARG:HH22	2.18	0.41
10:k:92:GLU:O	10:k:93:GLN:C	2.63	0.41
11:l:19:LEU:HD12	11:l:19:LEU:N	2.35	0.41
11:l:30:THR:O	11:l:32:GLY:N	2.52	0.41
11:l:112:LEU:O	11:l:112:LEU:HD23	2.20	0.41
12:m:64:TRP:CD1	53:1:873:C:H4'	2.55	0.41
14:o:11:ALA:HB2	14:o:95:SER:C	2.45	0.41
21:v:1:MET:HE1	21:v:50:MET:SD	2.60	0.41
29:E:25:HIS:HB3	29:E:43:LEU:HD13	2.01	0.41
33:I:80:ARG:NH2	52:3:614:C:OP2	2.50	0.41
37:M:3:GLN:HE22	52:3:755:G:N2	2.16	0.41
37:M:26:MET:HE2	37:M:32:LYS:HD3	2.02	0.41
42:R:6:ILE:HG13	42:R:7:ASN:H	1.84	0.41
43:S:92:ILE:HD12	43:S:92:ILE:N	2.35	0.41
45:U:39:PHE:HE1	45:U:50:THR:HG22	1.85	0.41
52:3:188:C:H2'	52:3:189:A:O4'	2.20	0.41
52:3:1011:C:H2'	52:3:1012:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2498:C:O2'	53:1:2499:C:H5'	2.20	0.41
54:2:19:C:H2'	54:2:20:G:C8	2.55	0.41
58:8:157:LEU:HA	58:8:160:GLN:HE21	1.84	0.41
8:i:101:SER:HA	8:i:140:GLU:O	2.20	0.41
13:n:28:LEU:HD23	13:n:48:VAL:HG21	2.01	0.41
13:n:63:ARG:HH21	53:1:1454:C:H4'	1.85	0.41
17:r:46:GLU:OE2	17:r:46:GLU:N	2.52	0.41
18:s:29:VAL:HG21	18:s:69:LEU:HD23	2.02	0.41
19:t:73:ARG:HH11	53:1:456:C:N4	2.17	0.41
28:D:34:ARG:NH2	53:1:466:A:OP1	2.53	0.41
33:I:13:ARG:O	33:I:55:ARG:NH1	2.53	0.41
39:O:10:LEU:HB3	39:O:98:VAL:HG23	2.02	0.41
39:O:58:ASN:ND2	52:3:969:A:OP2	2.53	0.41
40:P:45:THR:HB	52:3:689:C:OP1	2.21	0.41
44:T:28:VAL:CG2	44:T:80:LEU:HD21	2.50	0.41
52:3:502:A:O2'	52:3:503:C:H5'	2.21	0.41
52:3:634:C:H2'	52:3:635:A:C8	2.55	0.41
52:3:1251:A:O2'	52:3:1370:G:H5'	2.20	0.41
52:3:1271:A:H2'	52:3:1272:G:C8	2.55	0.41
52:3:1488:G:H2'	52:3:1489:G:C8	2.56	0.41
53:1:572:A:H5''	53:1:573:U:OP2	2.20	0.41
53:1:808:G:H2'	53:1:809:G:C8	2.55	0.41
53:1:2281:A:C2'	53:1:2282:G:H5'	2.50	0.41
53:1:2339:C:H2'	53:1:2340:A:C8	2.55	0.41
55:5:63:G:H2'	55:5:64:G:H8	1.84	0.41
58:8:122:LEU:HD13	58:8:374:ARG:CG	2.50	0.41
25:z:16:LEU:HB2	25:z:19:HIS:CD2	2.55	0.41
26:B:1:ALA:H3	53:1:2056:G:H21	1.67	0.41
26:B:8:THR:HG21	53:1:2021:C:P	2.61	0.41
37:M:94:VAL:HB	37:M:99:GLY:C	2.46	0.41
51:a:60:ARG:HB3	51:a:164:ARG:HG3	2.02	0.41
52:3:13:U:O2'	52:3:14:U:H5'	2.20	0.41
52:3:116:A:H2'	52:3:117:G:O4'	2.20	0.41
52:3:160:A:H61	52:3:347:G:N2	2.19	0.41
52:3:558:G:H2'	52:3:559:A:C2	2.54	0.41
52:3:952:U:H2'	52:3:953:G:H8	1.84	0.41
52:3:1430:A:H2'	52:3:1431:A:O4'	2.20	0.41
53:1:750:A:H5''	53:1:1615:C:N4	2.35	0.41
53:1:1066:U:H3'	53:1:1067:A:C5'	2.50	0.41
53:1:2103:C:H2'	53:1:2104:C:C6	2.55	0.41
53:1:2760:C:O2'	53:1:2761:A:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:60:C:H2'	54:2:61:G:H8	1.85	0.41
4:e:65:LEU:CD1	54:2:41:G:H21	2.31	0.41
6:g:125:THR:HG21	6:g:148:ALA:HB2	2.02	0.41
7:h:124:ASP:OD1	7:h:124:ASP:N	2.54	0.41
10:k:40:LYS:NZ	53:1:2561:U:O3'	2.51	0.41
12:m:93:VAL:HG22	12:m:94:ALA:N	2.34	0.41
18:s:85:ILE:HD12	18:s:85:ILE:N	2.35	0.41
25:z:29:ARG:CZ	53:1:1183:U:H4'	2.51	0.41
33:I:89:LEU:O	33:I:92:LEU:HG	2.21	0.41
37:M:25:THR:OG1	37:M:57:GLU:OE1	2.37	0.41
48:X:51:HIS:HB2	48:X:56:HIS:CE1	2.56	0.41
50:Z:16:ARG:O	50:Z:20:ARG:NH1	2.54	0.41
52:3:790:A:H5'	55:5:39:C:H5'	2.02	0.41
52:3:1144:G:H21	52:3:1146:A:H62	1.67	0.41
52:3:1202:U:C2'	52:3:1203:C:H5'	2.50	0.41
52:3:1304:G:H21	52:3:1333:A:H62	1.67	0.41
52:3:1472:U:H2'	52:3:1473:G:H8	1.85	0.41
52:3:1499:A:O2'	52:3:1520:C:H5'	2.20	0.41
53:1:189:G:H2'	53:1:205:G:H22	1.85	0.41
53:1:1066:U:H3'	53:1:1067:A:H5''	2.02	0.41
53:1:1590:A:H2'	53:1:1591:A:C8	2.56	0.41
53:1:1683:U:H2'	53:1:1684:G:C8	2.55	0.41
53:1:2087:G:H2'	53:1:2088:A:H8	1.85	0.41
53:1:2180:U:H2'	53:1:2181:U:O4'	2.20	0.41
53:1:2266:A:H4'	53:1:2267:A:C4	2.55	0.41
54:2:12:C:H1'	54:2:15:A:C2	2.55	0.41
55:6:29:G:H2'	55:6:30:G:O4'	2.21	0.41
1:b:216:ARG:NH2	53:1:691:C:H5''	2.35	0.41
6:g:2:GLN:O	6:g:39:ALA:HB3	2.21	0.41
6:g:20:ASN:OD1	6:g:20:ASN:N	2.53	0.41
10:k:76:VAL:H	15:p:72:VAL:CG1	2.27	0.41
13:n:60:VAL:HG22	53:1:1454:C:O2'	2.21	0.41
16:q:49:ARG:O	16:q:53:LYS:NZ	2.46	0.41
17:r:69:GLY:N	17:r:91:GLN:O	2.48	0.41
21:v:83:LYS:HA	21:v:84:PRO:HD3	1.94	0.41
22:w:27:VAL:HG23	22:w:31:SER:HB2	2.02	0.41
23:x:6:VAL:HG13	23:x:7:THR:H	1.86	0.41
24:y:41:HIS:CE1	53:1:96:C:H4'	2.55	0.41
30:F:6:SER:HB3	53:1:2466:C:H5''	2.01	0.41
32:H:107:LYS:HA	32:H:108:PRO:HD2	1.90	0.41
35:K:7:VAL:CG1	35:K:61:LEU:HD13	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:123:ARG:HB2	52:3:1343:G:H4'	2.02	0.41
39:O:17:LEU:HD23	39:O:17:LEU:O	2.21	0.41
41:Q:4:ASN:O	41:Q:7:VAL:HG12	2.20	0.41
41:Q:57:THR:HG21	52:3:363:A:OP1	2.19	0.41
52:3:245:U:O2'	52:3:246:A:H5'	2.20	0.41
52:3:916:U:O2'	52:3:917:G:H5'	2.20	0.41
52:3:984:C:H42	52:3:1221:G:H1	1.68	0.41
52:3:1014:A:H2'	52:3:1015:G:O4'	2.20	0.41
52:3:1170:A:C2'	52:3:1171:A:H5'	2.51	0.41
52:3:1225:A:H2'	52:3:1225:A:N3	2.36	0.41
52:3:1271:A:H2'	52:3:1272:G:H8	1.85	0.41
53:1:256:A:O2'	53:1:257:C:H5'	2.21	0.41
53:1:440:C:H2'	53:1:441:U:C6	2.56	0.41
53:1:854:C:H2'	53:1:855:G:C8	2.56	0.41
53:1:1476:U:H3	53:1:1515:A:H62	1.69	0.41
53:1:2047:C:H2'	53:1:2048:G:C8	2.56	0.41
53:1:2609:U:O2'	53:1:2610:C:H5'	2.19	0.41
56:4:20:U:H2'	56:4:21:C:C6	2.56	0.41
58:8:20:HIS:ND1	58:8:115:GLN:HB2	2.35	0.41
4:e:55:ASP:O	4:e:59:ILE:HG13	2.21	0.41
4:e:102:LEU:HA	4:e:106:ALA:HB3	2.02	0.41
5:f:126:THR:HB	5:f:129:GLU:HB3	2.02	0.41
6:g:43:ASN:HA	6:g:46:PHE:CD2	2.56	0.41
8:i:96:LYS:HB3	8:i:99:LYS:NZ	2.35	0.41
9:j:113:PRO:HD2	53:1:558:U:P	2.60	0.41
10:k:35:VAL:HG21	10:k:106:GLU:HB2	2.02	0.41
11:l:90:VAL:HG13	11:l:95:LEU:HD21	2.03	0.41
15:p:95:LYS:HG3	53:1:2718:G:O3'	2.20	0.41
31:G:186:VAL:HG22	31:G:187:ASP:O	2.21	0.41
32:H:151:GLU:HG2	32:H:166:TRP:HB3	2.02	0.41
33:I:78:ALA:HB1	33:I:85:THR:HB	2.01	0.41
34:J:126:ALA:HB3	52:3:9:G:OP1	2.21	0.41
35:K:3:HIS:HB2	35:K:92:THR:HB	2.02	0.41
42:R:8:ILE:HG22	42:R:8:ILE:O	2.21	0.41
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.86	0.41
52:3:545:C:H2'	52:3:546:A:C8	2.56	0.41
52:3:1198:G:H2'	52:3:1199:U:C6	2.56	0.41
52:3:1295:U:H2'	52:3:1296:C:C6	2.55	0.41
53:1:208:C:H2'	53:1:209:C:C6	2.55	0.41
53:1:441:U:O2'	53:1:442:G:H5'	2.21	0.41
53:1:1182:G:H2'	53:1:1183:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1197:G:H2'	53:1:1198:U:C6	2.56	0.41
53:1:2027:G:O2'	53:1:2028:U:H5'	2.20	0.41
53:1:2469:A:H2'	53:1:2470:G:O4'	2.19	0.41
53:1:2834:G:O6	53:1:2879:A:H2'	2.21	0.41
1:b:57:HIS:ND1	1:b:58:LYS:N	2.68	0.41
3:d:130:LYS:HA	53:1:321:U:OP2	2.21	0.41
9:j:135:GLN:NE2	53:1:7:G:H1'	2.36	0.41
12:m:43:ALA:O	12:m:46:ILE:HG12	2.21	0.41
12:m:76:LYS:HA	12:m:77:PRO:HD3	1.98	0.41
14:o:30:ARG:HH11	14:o:102:ARG:NH1	2.19	0.41
15:p:30:TRP:CE3	15:p:37:LYS:HG2	2.55	0.41
15:p:33:GLU:HB2	15:p:36:LYS:HB2	2.02	0.41
18:s:77:ASP:OD2	18:s:77:ASP:N	2.52	0.41
28:D:12:ARG:CZ	28:D:44:VAL:HG21	2.51	0.41
34:J:68:ARG:NH2	52:3:1074:G:OP1	2.54	0.41
36:L:124:SER:O	36:L:128:GLU:HG2	2.19	0.41
38:N:49:GLN:N	38:N:50:PRO:HD2	2.35	0.41
40:P:32:THR:HG23	40:P:43:TRP:HB3	2.03	0.41
47:W:13:THR:HG23	47:W:50:TYR:CZ	2.56	0.41
52:3:1137:C:H4'	52:3:1138:G:C2	2.56	0.41
52:3:1389:C:H2'	52:3:1390:U:C6	2.56	0.41
53:1:886:A:H1'	53:1:889:C:H41	1.85	0.41
53:1:2584:U:H2'	53:1:2585:U:C6	2.55	0.41
55:5:55:U:H2'	55:5:57:A:OP2	2.21	0.41
58:8:215:ILE:HG22	58:8:291:GLN:O	2.21	0.41
58:8:333:PHE:C	58:8:334:ARG:HG2	2.44	0.41
2:c:23:PRO:HG2	53:1:2728:U:O2'	2.20	0.41
17:r:78:ARG:HH12	53:1:990:A:N6	2.18	0.41
36:L:28:ILE:CD1	36:L:104:VAL:HG21	2.50	0.41
36:L:135:LYS:HD2	36:L:135:LYS:HA	1.92	0.41
45:U:46:LYS:HZ2	52:3:617:G:H5''	1.81	0.41
45:U:76:LYS:O	45:U:79:ASN:ND2	2.53	0.41
47:W:32:ILE:HD12	47:W:36:GLY:HA2	2.02	0.41
52:3:427:U:H4'	52:3:541:G:H5''	2.02	0.41
52:3:606:G:H5''	52:3:607:A:H5'	2.02	0.41
52:3:902:G:H2'	52:3:903:G:C8	2.56	0.41
53:1:1106:G:H2'	53:1:1107:G:O4'	2.20	0.41
53:1:1239:G:H2'	53:1:1240:U:O4'	2.21	0.41
53:1:2321:U:H5''	53:1:2322:A:OP2	2.20	0.41
57:7:23:A:H2'	57:7:24:G:C8	2.55	0.41
1:b:64:VAL:HG23	1:b:102:TYR:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:30:GLU:HB3	2:c:52:THR:OG1	2.21	0.41
2:c:55:LYS:HD2	2:c:77:ARG:HA	2.03	0.41
2:c:56:LYS:HD2	53:1:2830:C:H5''	2.02	0.41
3:d:48:THR:O	3:d:52:VAL:HG23	2.21	0.41
4:e:64:PRO:HB2	4:e:86:CYS:SG	2.61	0.41
5:f:6:ALA:HA	5:f:7:PRO:HD3	1.88	0.41
5:f:167:VAL:CG2	5:f:169:ARG:HH12	2.34	0.41
7:h:47:GLU:OE1	7:h:95:LEU:HD11	2.21	0.41
7:h:114:GLU:HA	7:h:123:ILE:HD13	2.03	0.41
8:i:73:PRO:HA	8:i:74:PRO:HD3	1.87	0.41
8:i:74:PRO:O	8:i:77:VAL:HG12	2.20	0.41
9:j:49:ASP:OD1	9:j:49:ASP:N	2.54	0.41
10:k:28:SER:OG	53:1:2566:A:N6	2.53	0.41
10:k:91:SER:O	10:k:92:GLU:C	2.63	0.41
12:m:57:VAL:O	12:m:59:ARG:N	2.54	0.41
13:n:9:GLN:NE2	53:1:2002:G:OP2	2.54	0.41
14:o:12:THR:CG2	53:1:2334:U:H4'	2.48	0.41
14:o:67:ASN:OD1	14:o:67:ASN:N	2.54	0.41
14:o:90:VAL:HG21	14:o:115:LEU:HG	2.02	0.41
15:p:50:ARG:HE	15:p:52:ARG:CZ	2.33	0.41
18:s:41:LYS:HE3	53:1:2009:A:H5''	2.03	0.41
21:v:83:LYS:O	21:v:85:LYS:N	2.54	0.41
24:y:16:THR:O	24:y:20:ASN:ND2	2.54	0.41
30:F:12:ARG:NH1	53:1:1091:G:H1'	2.36	0.41
31:G:22:TRP:HE1	52:3:830:G:C5'	2.33	0.41
32:H:2:GLN:HG2	52:3:1062:U:O4	2.20	0.41
35:K:93:LYS:HA	35:K:93:LYS:HD2	1.82	0.41
36:L:75:LYS:HE3	36:L:88:VAL:HG11	2.02	0.41
37:M:9:MET:CB	37:M:26:MET:HE1	2.51	0.41
41:Q:78:VAL:HG13	41:Q:101:LEU:HD11	2.01	0.41
41:Q:86:VAL:HB	52:3:523:A:C6	2.56	0.41
41:Q:111:GLN:OE1	52:3:539:A:OP2	2.39	0.41
41:Q:114:SER:OG	52:3:501:C:O3'	2.37	0.41
42:R:100:ARG:NH1	52:3:951:G:OP2	2.54	0.41
52:3:367:U:O2'	52:3:368:U:H4'	2.21	0.41
52:3:368:U:C2	58:8:224:ARG:NH2	2.89	0.41
52:3:603:U:H2'	52:3:604:G:C8	2.55	0.41
52:3:736:C:H2'	52:3:737:C:C6	2.55	0.41
52:3:911:U:H2'	52:3:912:C:H6	1.83	0.41
52:3:1109:C:H2'	52:3:1110:A:O4'	2.21	0.41
52:3:1125:U:H2'	52:3:1126:U:H2'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1225:A:H5'	52:3:1226:C:OP2	2.20	0.41
53:1:133:U:H2'	53:1:134:G:H8	1.85	0.41
53:1:172:A:H2'	53:1:173:A:H8	1.86	0.41
53:1:365:U:H2'	53:1:366:C:C6	2.55	0.41
53:1:457:A:H5'	53:1:459:U:H1'	2.02	0.41
53:1:596:U:H2'	53:1:597:G:C8	2.55	0.41
53:1:1035:U:H2'	53:1:1036:G:H8	1.86	0.41
53:1:1417:C:H2'	53:1:1418:G:O4'	2.21	0.41
53:1:1423:G:H2'	53:1:1424:G:H8	1.85	0.41
53:1:1657:U:H2'	53:1:1658:C:C6	2.56	0.41
53:1:1669:A:O3'	53:1:2549:G:H5'	2.21	0.41
53:1:1836:C:O2'	53:1:1837:C:H5'	2.21	0.41
53:1:1935:G:H1'	53:1:1964:G:N2	2.35	0.41
53:1:1971:U:H5'	53:1:1972:G:H5''	2.02	0.41
53:1:2119:A:N6	53:1:2169:A:H61	2.19	0.41
53:1:2122:U:H2'	53:1:2123:G:O4'	2.21	0.41
53:1:2195:U:H2'	53:1:2196:C:H6	1.85	0.41
53:1:2412:A:H2'	53:1:2413:G:O4'	2.20	0.41
53:1:2419:U:H2'	53:1:2420:C:C6	2.55	0.41
53:1:2577:A:H2'	53:1:2614:A:N6	2.36	0.41
32:H:149:LYS:O	32:H:200:TRP:HE3	2.03	0.41
38:N:29:ILE:HG22	38:N:64:ILE:HB	2.02	0.41
46:V:64:ARG:HA	46:V:65:PRO:HD3	1.98	0.41
52:3:31:G:H22	52:3:47:C:H5''	1.85	0.41
52:3:542:G:O2'	52:3:543:U:H5'	2.21	0.41
52:3:976:G:C8	52:3:1358:U:H2'	2.55	0.41
52:3:1186:G:H2'	52:3:1187:G:H8	1.86	0.41
52:3:1298:U:H4'	52:3:1299:A:O4'	2.21	0.41
52:3:1401:G:H2'	52:3:1402:C:O4'	2.21	0.41
53:1:565:C:H4'	53:1:1253:A:N6	2.36	0.41
53:1:1023:U:H4'	53:1:1123:C:OP1	2.21	0.41
53:1:1900:A:H1'	53:1:1970:A:H2'	2.02	0.41
58:8:226:THR:O	58:8:278:LEU:HD12	2.21	0.41
1:b:250:GLN:NE2	1:b:251:THR:O	2.46	0.40
8:i:9:LYS:HE2	53:1:1061:U:P	2.61	0.40
13:n:51:LEU:HD22	13:n:70:THR:HG21	2.03	0.40
16:q:50:ARG:HH11	16:q:50:ARG:HG3	1.86	0.40
17:r:26:ASP:N	17:r:26:ASP:OD1	2.54	0.40
28:D:42:LEU:N	28:D:42:LEU:HD12	2.36	0.40
32:H:41:TYR:CZ	32:H:89:VAL:HG21	2.56	0.40
34:J:44:ARG:NH2	34:J:70:MET:SD	2.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M:52:GLY:HA3	37:M:56:PRO:HA	2.02	0.40
46:V:5:ARG:HD3	52:3:636:U:C5'	2.48	0.40
52:3:743:A:H2'	52:3:744:C:C6	2.56	0.40
52:3:1390:U:H2'	52:3:1391:U:C6	2.56	0.40
52:3:1414:U:H2'	52:3:1415:G:C8	2.47	0.40
53:1:123:G:H4'	53:1:1376:C:O5'	2.21	0.40
53:1:709:U:H3	53:1:722:A:H61	1.70	0.40
53:1:2489:U:H2'	53:1:2490:G:O4'	2.22	0.40
53:1:2548:U:H2'	53:1:2549:G:O4'	2.20	0.40
53:1:2747:G:H1	53:1:2754:U:H2'	1.86	0.40
53:1:2811:G:H2'	53:1:2812:G:H8	1.85	0.40
57:7:22:G:H2'	57:7:23:A:C8	2.57	0.40
58:8:153:GLU:O	58:8:156:GLU:HG3	2.21	0.40
58:8:308:GLU:HG2	58:8:309:VAL:N	2.36	0.40
3:d:118:LEU:C	3:d:118:LEU:HD23	2.46	0.40
4:e:88:VAL:HA	54:2:42:C:O2	2.21	0.40
5:f:44:HIS:O	5:f:46:ASP:N	2.54	0.40
6:g:97:ARG:HD3	6:g:112:LYS:HD3	2.02	0.40
9:j:23:LYS:HB3	9:j:23:LYS:HE3	1.88	0.40
10:k:25:LEU:HD12	10:k:25:LEU:H	1.86	0.40
10:k:92:GLU:O	10:k:93:GLN:O	2.39	0.40
10:k:111:LYS:HE2	10:k:111:LYS:HB3	1.84	0.40
31:G:160:LEU:HD21	31:G:175:ALA:HB2	2.04	0.40
33:I:25:ARG:HD3	33:I:28:ASP:HA	2.03	0.40
38:N:35:GLU:O	38:N:40:ARG:HG2	2.22	0.40
42:R:78:ARG:O	42:R:82:LEU:HB2	2.21	0.40
52:3:82:G:H2'	52:3:83:C:H5'	2.02	0.40
52:3:202:G:H2'	52:3:203:G:H8	1.86	0.40
52:3:541:G:H2'	52:3:542:G:H8	1.85	0.40
52:3:639:G:O2'	52:3:640:A:H5'	2.21	0.40
52:3:662:U:H2'	52:3:663:A:H8	1.85	0.40
52:3:923:A:H2'	52:3:924:C:C6	2.56	0.40
52:3:945:G:H2'	52:3:945:G:N3	2.36	0.40
53:1:737:C:H2'	53:1:738:G:O4'	2.21	0.40
53:1:813:U:H2'	53:1:814:C:C6	2.56	0.40
53:1:934:U:H2'	53:1:935:C:C6	2.56	0.40
53:1:1387:A:H2'	53:1:1388:G:C8	2.56	0.40
53:1:1403:A:O2'	53:1:1404:C:H5'	2.22	0.40
53:1:1423:G:H2'	53:1:1424:G:C8	2.57	0.40
53:1:2655:G:H2'	53:1:2664:G:H1	1.86	0.40
54:2:33:G:H2'	54:2:34:A:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:41:G:H3'	54:2:41:G:N3	2.36	0.40
58:8:20:HIS:HB3	58:8:23:HIS:NE2	2.36	0.40
58:8:35:VAL:HG21	58:8:189:ILE:HG22	2.03	0.40
58:8:318:GLY:HA2	58:8:384:VAL:HA	2.03	0.40
2:c:1:MET:HB2	2:c:2:ILE:H	1.67	0.40
2:c:169:ARG:NH2	53:1:2773:C:OP1	2.54	0.40
5:f:98:LYS:HE2	5:f:98:LYS:HB2	1.98	0.40
7:h:35:VAL:HA	7:h:38:MET:HE3	2.02	0.40
14:o:16:ARG:NH1	14:o:19:GLN:OE1	2.48	0.40
31:G:119:GLN:OE1	31:G:136:ARG:NH1	2.55	0.40
38:N:17:ARG:HH11	52:3:1147:C:H1'	1.87	0.40
46:V:38:LYS:HD2	46:V:38:LYS:C	2.46	0.40
47:W:33:THR:OG1	47:W:34:GLU:N	2.54	0.40
51:a:23:ILE:HD12	51:a:23:ILE:N	2.28	0.40
52:3:131:A:H4'	52:3:263:A:H4'	2.03	0.40
52:3:193:C:H2'	52:3:194:C:H6	1.86	0.40
52:3:1271:A:H5'	52:3:1314:C:H5''	2.02	0.40
52:3:1410:A:H2'	52:3:1411:C:C6	2.56	0.40
53:1:317:G:H2'	53:1:318:C:O4'	2.20	0.40
53:1:1049:C:H2'	53:1:1050:A:H8	1.85	0.40
53:1:1999:C:H5''	53:1:2723:C:O2'	2.22	0.40
53:1:2121:G:O2'	53:1:2122:U:H5'	2.21	0.40
53:1:2340:A:H2'	53:1:2341:G:C8	2.56	0.40
53:1:2515:C:H2'	53:1:2516:A:C8	2.56	0.40
53:1:2638:G:H22	53:1:2775:G:H2'	1.86	0.40
6:g:99:ILE:N	6:g:99:ILE:HD12	2.36	0.40
9:j:60:ASP:OD2	9:j:61:LYS:HE3	2.21	0.40
11:l:22:GLY:HA2	53:1:811:U:H3'	2.03	0.40
12:m:47:GLU:HG2	12:m:50:ARG:HH11	1.85	0.40
12:m:128:THR:OG1	12:m:129:THR:N	2.54	0.40
14:o:90:VAL:HG12	14:o:91:SER:N	2.37	0.40
15:p:28:LYS:HA	15:p:41:ALA:HA	2.03	0.40
16:q:51:GLN:NE2	16:q:54:ARG:HD2	2.37	0.40
35:K:91:ARG:HG3	35:K:92:THR:H	1.87	0.40
36:L:29:LEU:HD11	36:L:115:MET:HE1	2.02	0.40
40:P:15:VAL:HG12	40:P:76:TYR:HB3	2.03	0.40
40:P:86:LYS:HZ3	40:P:114:PRO:HD3	1.84	0.40
51:a:175:ILE:HB	51:a:188:ASN:HB3	2.03	0.40
52:3:375:U:H2'	52:3:376:G:H8	1.87	0.40
52:3:513:C:H2'	52:3:514:C:C6	2.57	0.40
52:3:543:U:H2'	52:3:544:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1047:G:O2'	52:3:1048:G:H5'	2.22	0.40
52:3:1404:C:H2'	52:3:1405:G:C8	2.56	0.40
53:1:374:A:H2'	53:1:375:G:O4'	2.21	0.40
53:1:941:A:O2'	53:1:1190:G:H4'	2.21	0.40
53:1:1357:C:H2'	53:1:1358:G:O4'	2.22	0.40
53:1:2427:C:H5''	53:1:2429:G:H5'	2.03	0.40
58:8:113:MET:HE3	58:8:114:PRO:HD2	2.04	0.40
1:b:132:ARG:NH2	6:g:93:SER:OG	2.53	0.40
2:c:33:ARG:O	2:c:51:THR:HG22	2.20	0.40
4:e:116:LEU:HD13	4:e:175:PRO:HD2	2.03	0.40
5:f:154:GLU:OE2	5:f:157:LYS:HB2	2.22	0.40
11:l:12:SER:O	11:l:13:LYS:HD3	2.21	0.40
11:l:131:ALA:O	11:l:135:ILE:HG13	2.22	0.40
13:n:36:THR:OG1	13:n:37:THR:N	2.54	0.40
13:n:113:ILE:O	13:n:113:ILE:HG23	2.21	0.40
21:v:65:VAL:HG13	21:v:65:VAL:O	2.21	0.40
25:z:52:PHE:CE2	25:z:53:MET:HE3	2.55	0.40
31:G:109:SER:O	31:G:112:ARG:HB3	2.21	0.40
31:G:182:VAL:CG1	31:G:195:VAL:HG13	2.52	0.40
31:G:209:VAL:HA	31:G:212:TYR:CD2	2.56	0.40
36:L:2:ARG:HB3	52:3:933:G:OP2	2.22	0.40
39:O:51:VAL:HG22	39:O:52:LEU:N	2.37	0.40
41:Q:5:GLN:NE2	52:3:881:G:OP2	2.50	0.40
42:R:71:GLU:OE2	42:R:72:ILE:HG13	2.22	0.40
43:S:65:GLN:HG3	43:S:66:THR:HG23	2.03	0.40
44:T:75:ALA:O	44:T:78:THR:HG22	2.22	0.40
48:X:35:ARG:NH1	52:3:1221:G:H5''	2.37	0.40
50:Z:17:ARG:HA	50:Z:20:ARG:HH11	1.87	0.40
52:3:767:A:H2'	52:3:768:A:O4'	2.21	0.40
52:3:1081:A:O2'	52:3:1082:A:H5'	2.21	0.40
53:1:622:G:H2'	53:1:623:C:C6	2.56	0.40
53:1:630:G:H4'	53:1:640:C:O2'	2.21	0.40
53:1:779:U:H2'	53:1:780:G:O4'	2.21	0.40
53:1:1356:G:H2'	53:1:1357:C:H6	1.87	0.40
53:1:2112:G:C2	55:6:20:U:H5'	2.57	0.40
53:1:2323:G:O2'	53:1:2324:U:H5'	2.21	0.40
53:1:2539:C:O2'	53:1:2540:C:H5'	2.22	0.40
53:1:2841:C:H2'	53:1:2842:G:H8	1.87	0.40
57:7:68:C:H2'	57:7:69:G:C8	2.55	0.40
58:8:147:LEU:O	58:8:151:GLU:HG2	2.22	0.40
58:8:172:ARG:CD	58:8:188:LYS:HE2	2.51	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%)	233 (87%)	32 (12%)	4 (2%)	8	36
2	c	207/209 (99%)	186 (90%)	20 (10%)	1 (0%)	24	57
3	d	199/201 (99%)	184 (92%)	14 (7%)	1 (0%)	24	57
4	e	175/177 (99%)	155 (89%)	20 (11%)	0	100	100
5	f	174/176 (99%)	149 (86%)	23 (13%)	2 (1%)	11	41
6	g	147/149 (99%)	130 (88%)	15 (10%)	2 (1%)	9	37
7	h	129/131 (98%)	96 (74%)	27 (21%)	6 (5%)	2	18
8	i	139/141 (99%)	126 (91%)	11 (8%)	2 (1%)	9	37
9	j	140/142 (99%)	128 (91%)	11 (8%)	1 (1%)	18	51
10	k	120/122 (98%)	93 (78%)	23 (19%)	4 (3%)	3	24
11	l	141/143 (99%)	109 (77%)	28 (20%)	4 (3%)	4	26
12	m	134/136 (98%)	117 (87%)	15 (11%)	2 (2%)	8	36
13	n	118/120 (98%)	103 (87%)	12 (10%)	3 (2%)	4	28
14	o	114/116 (98%)	104 (91%)	10 (9%)	0	100	100
15	p	112/114 (98%)	98 (88%)	12 (11%)	2 (2%)	6	33
16	q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
17	r	101/103 (98%)	83 (82%)	16 (16%)	2 (2%)	6	32
18	s	108/110 (98%)	100 (93%)	7 (6%)	1 (1%)	14	45
19	t	91/93 (98%)	82 (90%)	8 (9%)	1 (1%)	11	41
20	u	100/102 (98%)	82 (82%)	13 (13%)	5 (5%)	1	17
21	v	92/94 (98%)	83 (90%)	8 (9%)	1 (1%)	11	41
22	w	73/75 (97%)	66 (90%)	6 (8%)	1 (1%)	9	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	x	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
24	y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
25	z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
26	B	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
27	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
28	D	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
29	E	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	35
30	F	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	26
31	G	223/225 (99%)	208 (93%)	14 (6%)	1 (0%)	30	62
32	H	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
33	I	203/205 (99%)	180 (89%)	20 (10%)	3 (2%)	8	36
34	J	155/157 (99%)	126 (81%)	21 (14%)	8 (5%)	1	17
35	K	98/100 (98%)	77 (79%)	16 (16%)	5 (5%)	1	17
36	L	149/151 (99%)	136 (91%)	13 (9%)	0	100	100
37	M	127/129 (98%)	114 (90%)	13 (10%)	0	100	100
38	N	125/127 (98%)	101 (81%)	22 (18%)	2 (2%)	7	35
39	O	96/98 (98%)	80 (83%)	12 (12%)	4 (4%)	2	19
40	P	114/116 (98%)	95 (83%)	16 (14%)	3 (3%)	4	27
41	Q	121/123 (98%)	91 (75%)	25 (21%)	5 (4%)	2	20
42	R	112/114 (98%)	97 (87%)	10 (9%)	5 (4%)	2	18
43	S	98/100 (98%)	81 (83%)	17 (17%)	0	100	100
44	T	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	40
45	U	80/82 (98%)	70 (88%)	9 (11%)	1 (1%)	9	38
46	V	78/80 (98%)	62 (80%)	15 (19%)	1 (1%)	9	38
47	W	63/65 (97%)	55 (87%)	6 (10%)	2 (3%)	3	24
48	X	77/79 (98%)	72 (94%)	4 (5%)	1 (1%)	9	38
49	Y	83/85 (98%)	78 (94%)	4 (5%)	1 (1%)	10	40
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	8
51	a	130/223 (58%)	122 (94%)	7 (5%)	1 (1%)	16	48
58	8	342/400 (86%)	321 (94%)	20 (6%)	1 (0%)	36	67
All	All	6261/6512 (96%)	5500 (88%)	663 (11%)	98 (2%)	10	35

All (98) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
5	f	45	ALA
5	f	174	LYS
7	h	80	THR
10	k	92	GLU
11	l	31	GLY
12	m	58	LYS
13	n	71	ARG
15	p	18	SER
17	r	54	VAL
30	F	37	GLN
34	J	25	LYS
34	J	93	VAL
34	J	122	VAL
35	K	53	LYS
35	K	54	LEU
38	N	90	ASP
41	Q	33	CYS
44	T	46	LYS
45	U	79	ASN
50	Z	8	ASN
50	Z	25	ALA
7	h	113	PHE
8	i	11	GLN
10	k	110	GLU
11	l	85	VAL
19	t	52	GLU
20	u	51	LEU
20	u	88	ASP
20	u	99	SER
29	E	31	ILE
34	J	121	ASN
38	N	106	ASP
40	P	125	LYS
41	Q	24	GLU
42	R	4	ALA
42	R	7	ASN
46	V	17	GLU
50	Z	24	LYS
50	Z	36	PHE
58	8	334	ARG
1	b	107	LYS

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Mol	Chain	Res	Type
2	c	86	GLU
7	h	81	LEU
7	h	107	GLU
7	h	118	ILE
10	k	35	VAL
11	l	29	LYS
12	m	69	PRO
13	n	2	ARG
17	r	26	ASP
18	s	65	ASP
33	I	34	GLU
33	I	47	LEU
34	J	23	THR
35	K	86	ARG
35	K	92	THR
40	P	92	ARG
41	Q	35	ARG
41	Q	87	LYS
47	W	13	THR
49	Y	5	SER
1	b	38	LYS
1	b	175	LEU
13	n	32	GLU
20	u	6	ARG
39	O	41	PRO
39	O	75	ASP
40	P	13	LYS
42	R	65	GLU
6	g	9	VAL
15	p	94	ALA
33	I	152	SER
34	J	11	GLN
34	J	49	TYR
34	J	99	SER
39	O	42	LEU
39	O	58	ASN
47	W	26	ALA
50	Z	14	ALA
51	a	208	TYR
6	g	118	PRO
9	j	81	ILE
10	k	93	GLN

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Mol	Chain	Res	Type
11	l	94	THR
31	G	19	THR
50	Z	66	ARG
20	u	56	GLY
21	v	84	PRO
41	Q	10	PRO
22	w	50	GLY
42	R	5	GLY
48	X	7	GLY
1	b	253	GLY
7	h	79	PRO
8	i	92	PRO
35	K	50	PRO
42	R	6	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	161 (98%)	3 (2%)	51	67
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	77
5	f	137/137 (100%)	135 (98%)	2 (2%)	57	69
6	g	114/114 (100%)	114 (100%)	0	100	100
7	h	100/100 (100%)	97 (97%)	3 (3%)	36	57
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	74
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	74
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	74
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	74
13	n	100/100 (100%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	o	86/86 (100%)	83 (96%)	3 (4%)	32	54
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	73
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	71
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	71
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	49 (96%)	2 (4%)	28	52
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	73
32	H	170/170 (100%)	170 (100%)	0	100	100
33	I	172/172 (100%)	170 (99%)	2 (1%)	63	72
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%)	123 (99%)	1 (1%)	73	76
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	74
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	63
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	83 (100%)	0	100	100
44	T	76/76 (100%)	76 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	U	65/65 (100%)	63 (97%)	2 (3%)	35	57
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	53 (96%)	2 (4%)	31	54
51	a	110/174 (63%)	110 (100%)	0	100	100
58	8	290/332 (87%)	289 (100%)	1 (0%)	86	84
All	All	5198/5304 (98%)	5162 (99%)	36 (1%)	73	77

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	c	16	THR
2	c	24	VAL
2	c	142	VAL
4	e	135	ILE
5	f	48	THR
5	f	70	LEU
7	h	3	LEU
7	h	107	GLU
7	h	118	ILE
9	j	122	LEU
10	k	92	GLU
11	l	94	THR
12	m	89	VAL
14	o	32	PRO
14	o	56	LYS
14	o	90	VAL
18	s	103	ILE
19	t	32	LEU
21	v	42	LEU
29	E	14	LYS
29	E	61	LEU
31	G	144	GLU
31	G	150	ILE
33	I	34	GLU
33	I	183	ARG
34	J	55	VAL

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Mol	Chain	Res	Type
35	K	39	LEU
36	L	112	ASP
37	M	50	VAL
39	O	14	ASP
39	O	57	VAL
45	U	36	VAL
45	U	77	GLU
50	Z	13	VAL
50	Z	40	PRO
58	8	336	THR

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

Mol	Chain	Res	Type
1	b	20	ASN
1	b	52	HIS
1	b	85	ASN
1	b	133	ASN
1	b	196	ASN
1	b	199	HIS
1	b	225	ASN
1	b	238	ASN
1	b	242	HIS
2	c	32	ASN
2	c	49	GLN
2	c	130	GLN
2	c	134	HIS
2	c	148	GLN
2	c	173	GLN
3	d	9	GLN
3	d	30	GLN
3	d	41	GLN
3	d	90	GLN
3	d	97	ASN
4	e	36	ASN
4	e	51	ASN
5	f	72	ASN
5	f	100	ASN
5	f	115	GLN
6	g	11	ASN
6	g	43	ASN
7	h	9	GLN

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Mol	Chain	Res	Type
8	i	5	GLN
9	j	58	ASN
9	j	135	GLN
10	k	5	GLN
11	l	38	GLN
12	m	3	GLN
12	m	45	GLN
12	m	88	ASN
12	m	97	GLN
13	n	3	HIS
13	n	9	GLN
13	n	13	ASN
13	n	62	ASN
14	o	38	GLN
14	o	100	HIS
15	p	40	GLN
18	s	7	HIS
20	u	39	ASN
20	u	44	HIS
20	u	52	ASN
20	u	65	GLN
20	u	73	ASN
21	v	12	GLN
21	v	49	ASN
22	w	8	ASN
22	w	53	HIS
23	x	15	ASN
23	x	16	ASN
24	y	20	ASN
24	y	41	HIS
25	z	8	GLN
25	z	19	HIS
26	B	3	GLN
26	B	4	GLN
31	G	38	HIS
31	G	50	ASN
31	G	177	ASN
32	H	7	ASN
32	H	18	ASN
32	H	99	GLN
32	H	139	ASN
32	H	184	ASN

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Mol	Chain	Res	Type
33	I	35	GLN
33	I	40	HIS
33	I	53	GLN
33	I	88	ASN
33	I	163	GLN
33	I	197	HIS
34	J	11	GLN
34	J	81	GLN
34	J	96	GLN
35	K	37	HIS
36	L	141	HIS
37	M	3	GLN
37	M	37	ASN
38	N	36	GLN
38	N	109	GLN
38	N	125	GLN
40	P	37	GLN
40	P	118	ASN
41	Q	4	ASN
41	Q	74	GLN
42	R	7	ASN
43	S	3	GLN
43	S	42	ASN
43	S	65	GLN
44	T	36	ASN
44	T	41	HIS
45	U	26	ASN
45	U	29	ASN
45	U	40	ASN
45	U	79	ASN
46	V	8	GLN
46	V	30	HIS
47	W	18	GLN
47	W	30	ASN
47	W	51	GLN
48	X	51	HIS
49	Y	54	GLN
49	Y	83	ASN
51	a	58	ASN
51	a	67	HIS
51	a	160	GLN
51	a	165	ASN

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Mol	Chain	Res	Type
58	8	14	ASN
58	8	98	GLN
58	8	115	GLN
58	8	160	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	139 (9%)	4 (0%)
53	1	2902/2903 (99%)	323 (11%)	9 (0%)
54	2	119/120 (99%)	10 (8%)	1 (0%)
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	14 (18%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	10 (13%)	1 (1%)
All	All	4803/4810 (99%)	505 (10%)	15 (0%)

All (505) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A
52	3	71	A
52	3	87	C
52	3	95	C
52	3	100	G
52	3	130	A
52	3	144	G
52	3	183	C
52	3	184	G
52	3	197	A
52	3	210	C
52	3	226	G
52	3	247	G
52	3	251	G
52	3	266	G

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Mol	Chain	Res	Type
52	3	267	C
52	3	281	G
52	3	289	G
52	3	316	C
52	3	345	C
52	3	346	G
52	3	352	C
52	3	367	U
52	3	372	C
52	3	411	A
52	3	412	A
52	3	413	G
52	3	429	U
52	3	439	U
52	3	467	U
52	3	479	U
52	3	484	G
52	3	485	U
52	3	486	U
52	3	518	C
52	3	533	A
52	3	547	A
52	3	561	U
52	3	572	A
52	3	573	A
52	3	575	G
52	3	576	C
52	3	577	G
52	3	633	G
52	3	642	A
52	3	665	A
52	3	666	G
52	3	688	G
52	3	703	G
52	3	723	U
52	3	724	G
52	3	755	G
52	3	777	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A

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Mol	Chain	Res	Type
52	3	821	G
52	3	842	U
52	3	843	U
52	3	844	G
52	3	846	G
52	3	871	U
52	3	873	A
52	3	890	G
52	3	902	G
52	3	926	G
52	3	934	C
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1020	G
52	3	1028	C
52	3	1030	U
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1053	G
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1146	A
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A

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Mol	Chain	Res	Type
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	1364	U
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	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1533	C
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A

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Mol	Chain	Res	Type
53	1	75	G
53	1	102	U
53	1	119	A
53	1	120	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	199	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	281	C
53	1	294	A
53	1	301	G
53	1	311	A
53	1	312	G
53	1	323	C
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	422	A
53	1	424	G
53	1	451	U

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Mol	Chain	Res	Type
53	1	457	A
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	530	G
53	1	531	C
53	1	532	A
53	1	542	C
53	1	543	G
53	1	563	A
53	1	573	U
53	1	588	U
53	1	603	A
53	1	616	A
53	1	627	A
53	1	628	G
53	1	637	A
53	1	645	C
53	1	646	U
53	1	654	A
53	1	669	G
53	1	686	U
53	1	687	C
53	1	695	G
53	1	730	A
53	1	747	C
53	1	748	G
53	1	752	A
53	1	764	A
53	1	771	G
53	1	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	805	G
53	1	812	C
53	1	819	A
53	1	827	U
53	1	828	U

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Mol	Chain	Res	Type
53	1	830	G
53	1	845	A
53	1	846	U
53	1	847	U
53	1	859	G
53	1	878	A
53	1	887	U
53	1	888	C
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	983	A
53	1	995	C
53	1	1012	U
53	1	1013	C
53	1	1021	A
53	1	1022	G
53	1	1026	G
53	1	1033	U
53	1	1045	C
53	1	1046	A
53	1	1047	G
53	1	1054	A
53	1	1060	U
53	1	1062	G
53	1	1066	U
53	1	1070	A
53	1	1071	G
53	1	1079	C
53	1	1084	A
53	1	1088	A
53	1	1090	A
53	1	1104	C
53	1	1106	G
53	1	1111	A
53	1	1131	G
53	1	1132	U

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Mol	Chain	Res	Type
53	1	1133	A
53	1	1135	C
53	1	1143	A
53	1	1174	U
53	1	1175	A
53	1	1176	U
53	1	1177	G
53	1	1180	U
53	1	1211	C
53	1	1212	G
53	1	1250	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A
53	1	1301	A
53	1	1321	A
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1395	A
53	1	1398	C
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1461	C
53	1	1476	U
53	1	1482	G
53	1	1490	A
53	1	1491	G
53	1	1504	A
53	1	1515	A
53	1	1524	G
53	1	1535	A
53	1	1536	C
53	1	1537	G

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Mol	Chain	Res	Type
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	1654	A
53	1	1674	G
53	1	1699	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1800	C
53	1	1801	A
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	1914	C
53	1	1919	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

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Mol	Chain	Res	Type
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	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	2110	G
53	1	2111	U
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2132	U
53	1	2133	G
53	1	2145	C
53	1	2147	A
53	1	2162	G
53	1	2172	U
53	1	2173	A
53	1	2189	U
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2211	A
53	1	2213	U
53	1	2225	A
53	1	2238	G
53	1	2239	G
53	1	2278	A

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Mol	Chain	Res	Type
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	2335	A
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2406	A
53	1	2423	U
53	1	2424	C
53	1	2429	G
53	1	2430	A
53	1	2435	A
53	1	2441	U
53	1	2448	A
53	1	2476	A
53	1	2498	C
53	1	2502	G
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2603	G
53	1	2609	U
53	1	2613	U
53	1	2646	C
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U

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Mol	Chain	Res	Type
53	1	2714	G
53	1	2716	C
53	1	2744	G
53	1	2748	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2794	C
53	1	2797	U
53	1	2800	A
53	1	2809	A
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2849	U
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2880	C
54	2	4	C
54	2	13	G
54	2	24	G
54	2	35	C
54	2	44	G
54	2	67	G
54	2	89	U
54	2	90	C
54	2	108	A
54	2	109	A
55	5	9	G
55	5	18	G
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	61	C
55	6	2	G
55	6	3	C
55	6	8	U
55	6	9	G

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Mol	Chain	Res	Type
55	6	10	G
55	6	14	A
55	6	19	G
55	6	20	U
55	6	21	A
55	6	22	G
55	6	34	C
55	6	61	C
55	6	64	G
55	6	70	G
56	4	12	A
56	4	13	A
57	7	8	U
57	7	9	A
57	7	17	C
57	7	18	G
57	7	21	A
57	7	43	C
57	7	44	G
57	7	45	U
57	7	46	G
57	7	48	C

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	70	U
52	3	438	U
52	3	1190	G
52	3	1201	A
53	1	421	C
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
54	2	88	C
57	7	42	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	FME	5	101	55	8,9,10	0.50	0	8,9,11	0.88	0
60	PHE	7	101	57	10,11,12	0.69	0	8,13,15	0.24	0
61	GDP	8	501	-	29,30,30	1.40	5 (17%)	45,47,47	1.93	13 (28%)

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	-	0/5/6/8	0/1/1/1
61	GDP	8	501	-	-	4/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PB-O1B	3.06	1.60	1.50
61	8	501	GDP	PA-O1A	2.75	1.60	1.50
61	8	501	GDP	PB-O3B	-2.54	1.45	1.54
61	8	501	GDP	O4'-C1'	2.45	1.47	1.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PA-O3A	-2.08	1.57	1.59

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	C2-N3-C4	5.58	121.91	112.30
61	8	501	GDP	C5-C4-N3	-5.01	120.42	128.39
61	8	501	GDP	N9-C4-N3	3.54	133.03	125.95
61	8	501	GDP	O4'-C4'-C3'	3.24	111.58	105.15
61	8	501	GDP	C6-C5-N7	3.08	135.89	130.29
61	8	501	GDP	C8-N7-C5	2.74	109.14	104.26
61	8	501	GDP	C4-C5-N7	-2.30	107.03	110.67
61	8	501	GDP	C2-N1-C6	-2.25	121.03	125.11
61	8	501	GDP	C5-C6-N1	2.24	118.96	113.25
61	8	501	GDP	O2A-PA-O1A	2.20	122.67	112.44
61	8	501	GDP	O4'-C4'-C5'	2.16	116.24	109.33
61	8	501	GDP	C3'-C2'-C1'	2.05	105.35	101.46
61	8	501	GDP	O6-C6-C5	-2.04	121.16	126.53

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA
61	8	501	GDP	PA-O3A-PB-O3B
61	8	501	GDP	O4'-C4'-C5'-O5'
61	8	501	GDP	C3'-C4'-C5'-O5'
61	8	501	GDP	C5'-O5'-PA-O1A

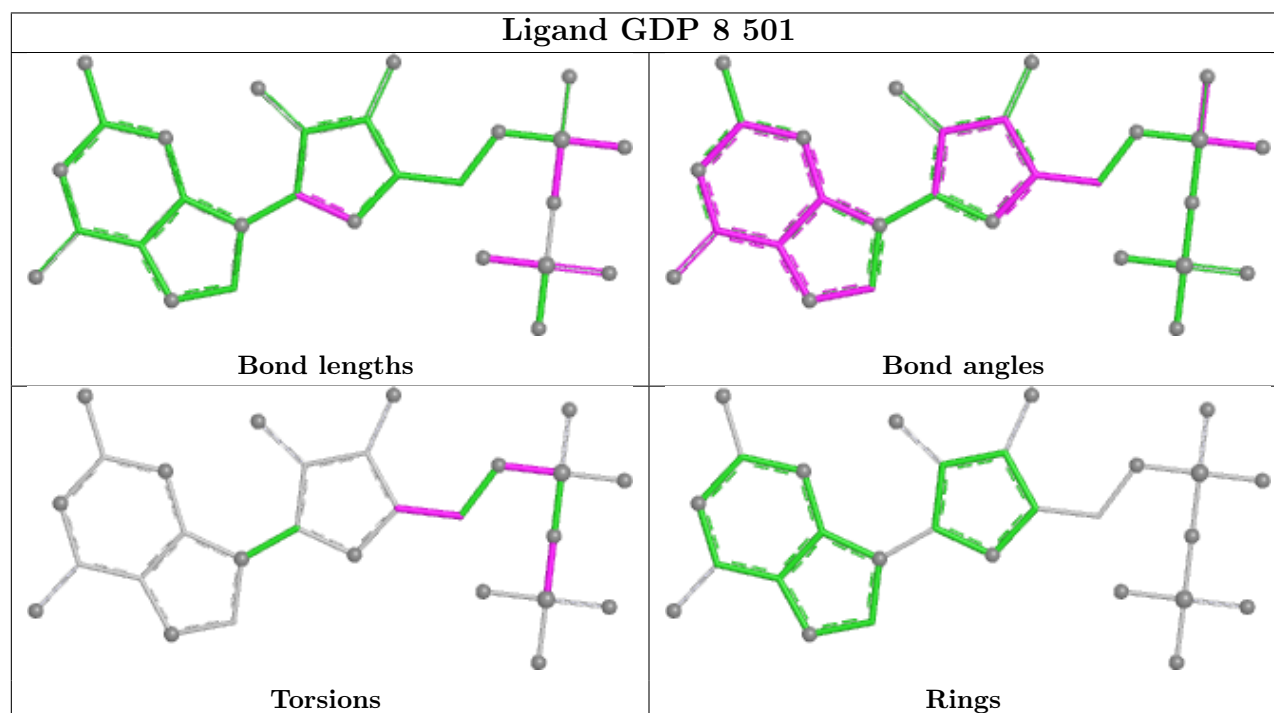
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	101	PHE	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

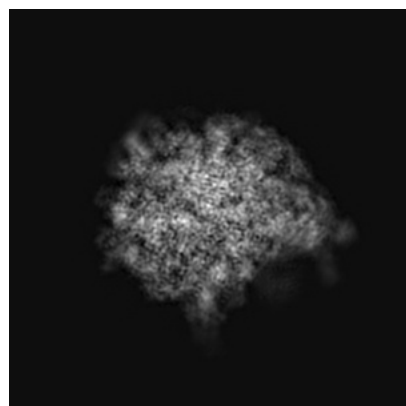
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21629. These allow visual inspection of the internal detail of the map and identification of artifacts.

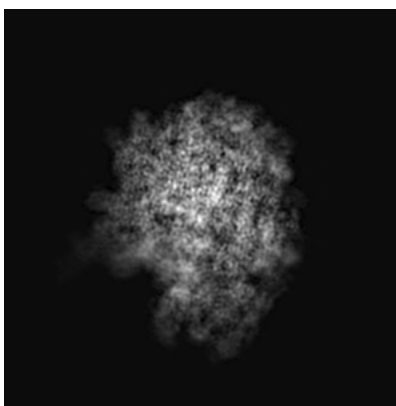
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

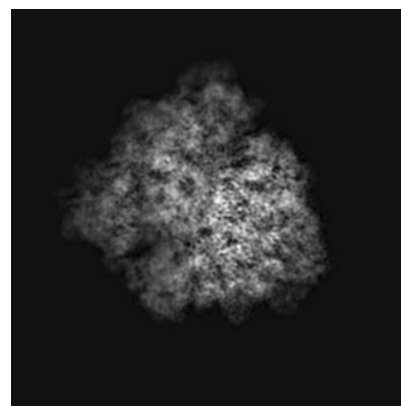
6.1.1 Primary map



X

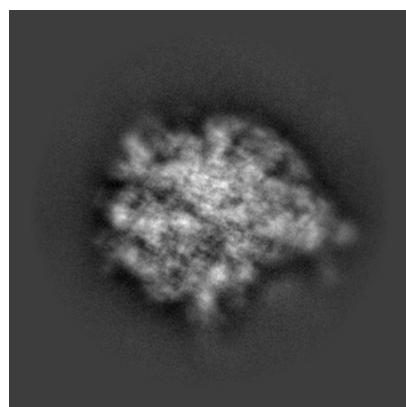


Y

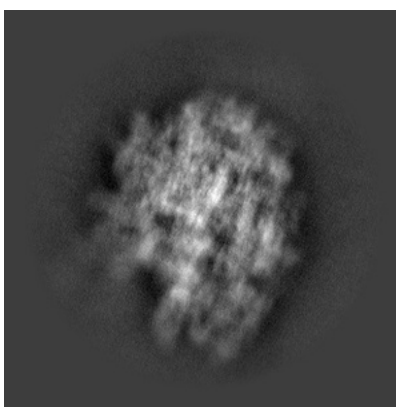


Z

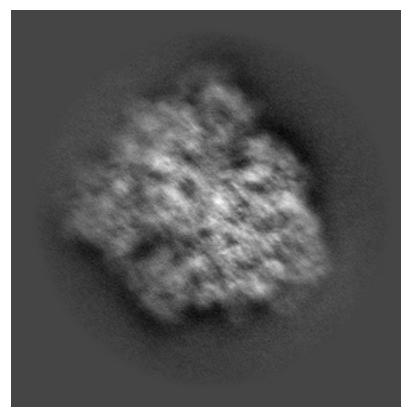
6.1.2 Raw map



X



Y

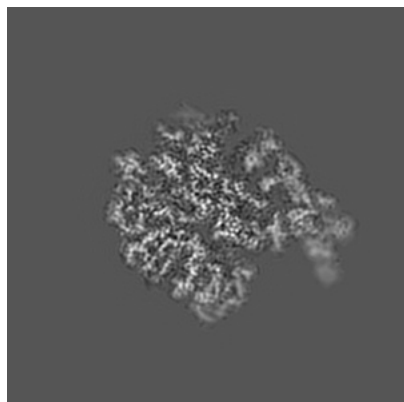


Z

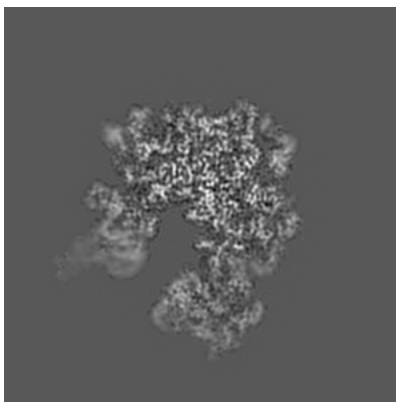
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

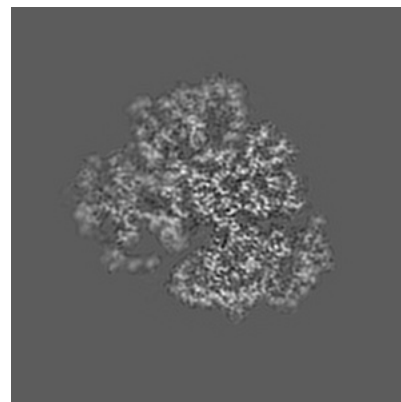
6.2.1 Primary map



X Index: 144

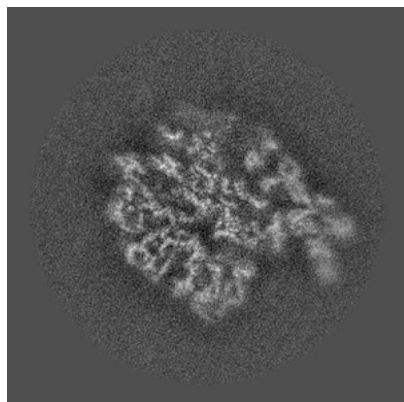


Y Index: 144

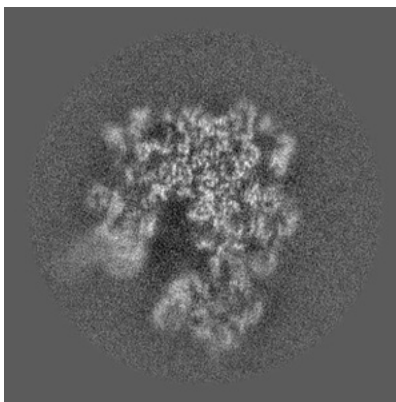


Z Index: 144

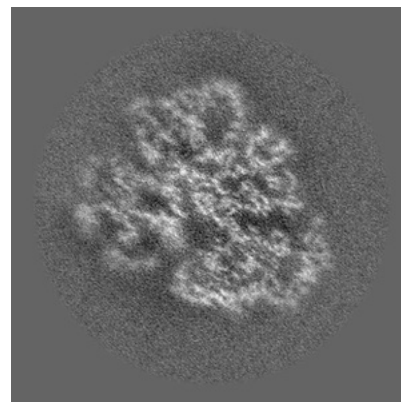
6.2.2 Raw map



X Index: 144



Y Index: 144

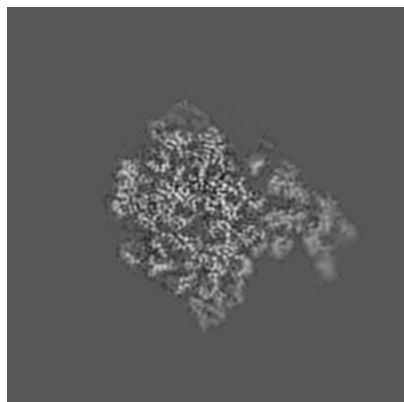


Z Index: 144

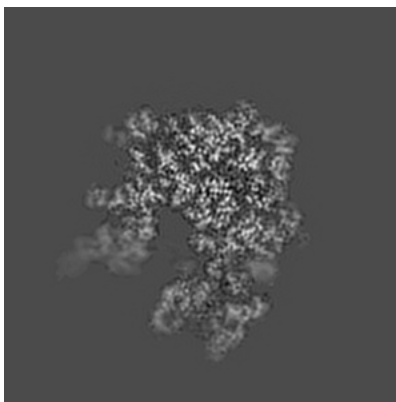
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

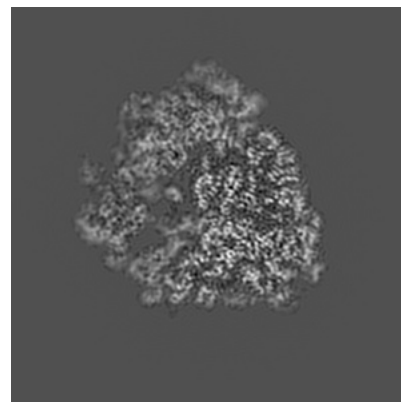
6.3.1 Primary map



X Index: 149

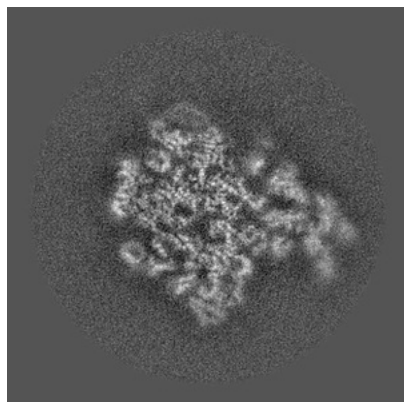


Y Index: 148

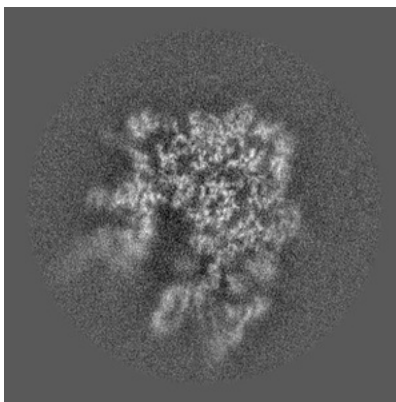


Z Index: 135

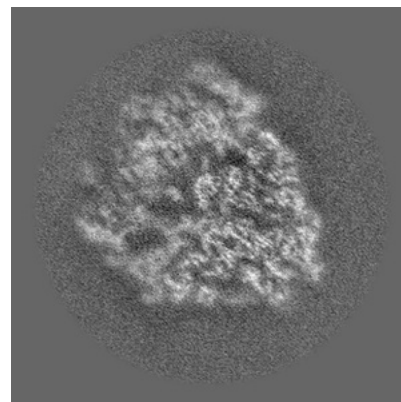
6.3.2 Raw map



X Index: 149



Y Index: 149

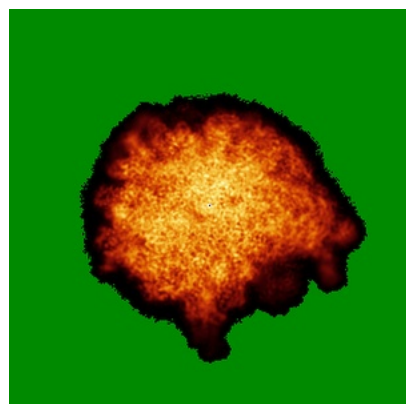


Z Index: 135

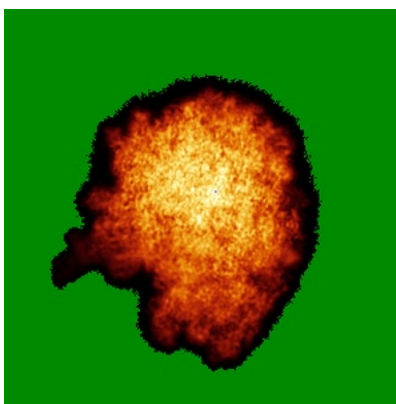
The images above show the largest variance slices of the map in three orthogonal directions.

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

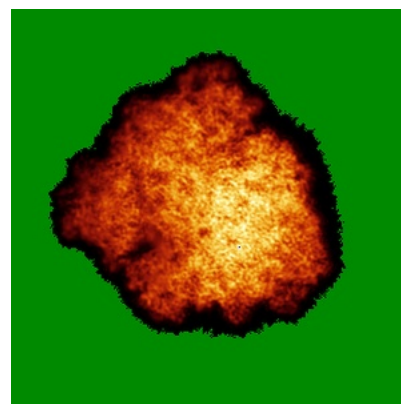
6.4.1 Primary map



X

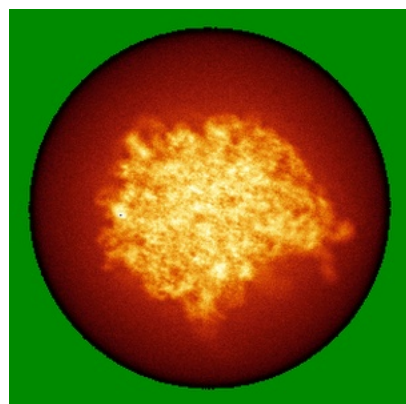


Y

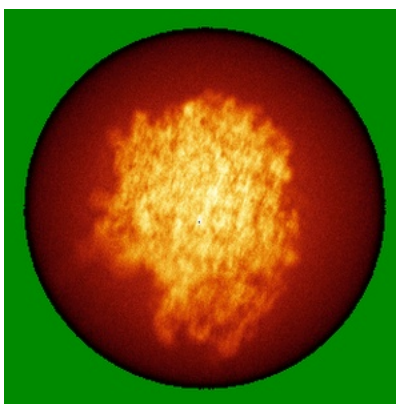


Z

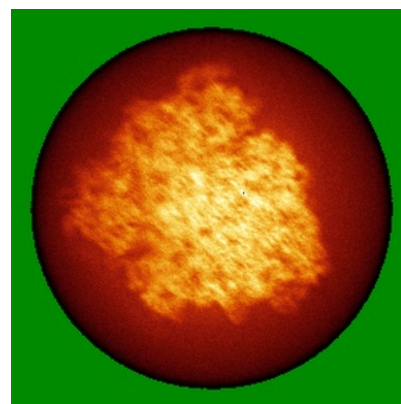
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



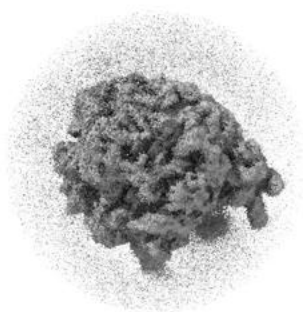
Y



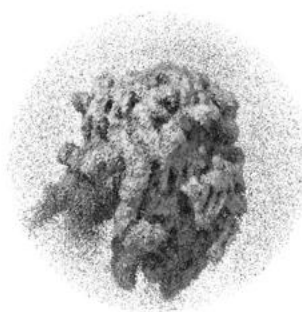
Z

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

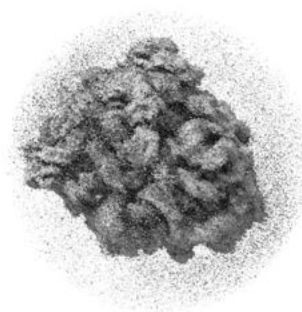
6.5.2 Raw map



X



Y



Z

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.

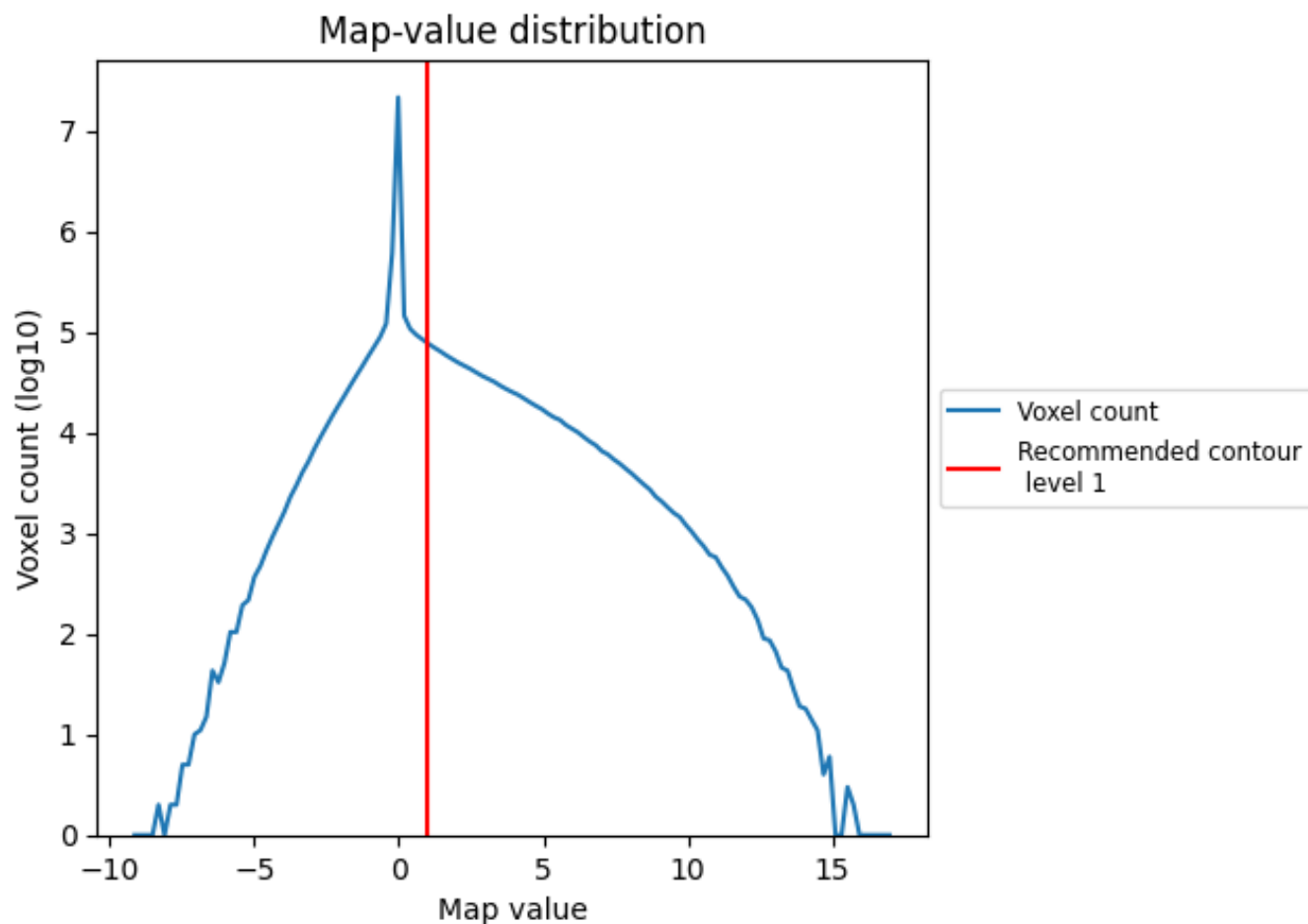
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

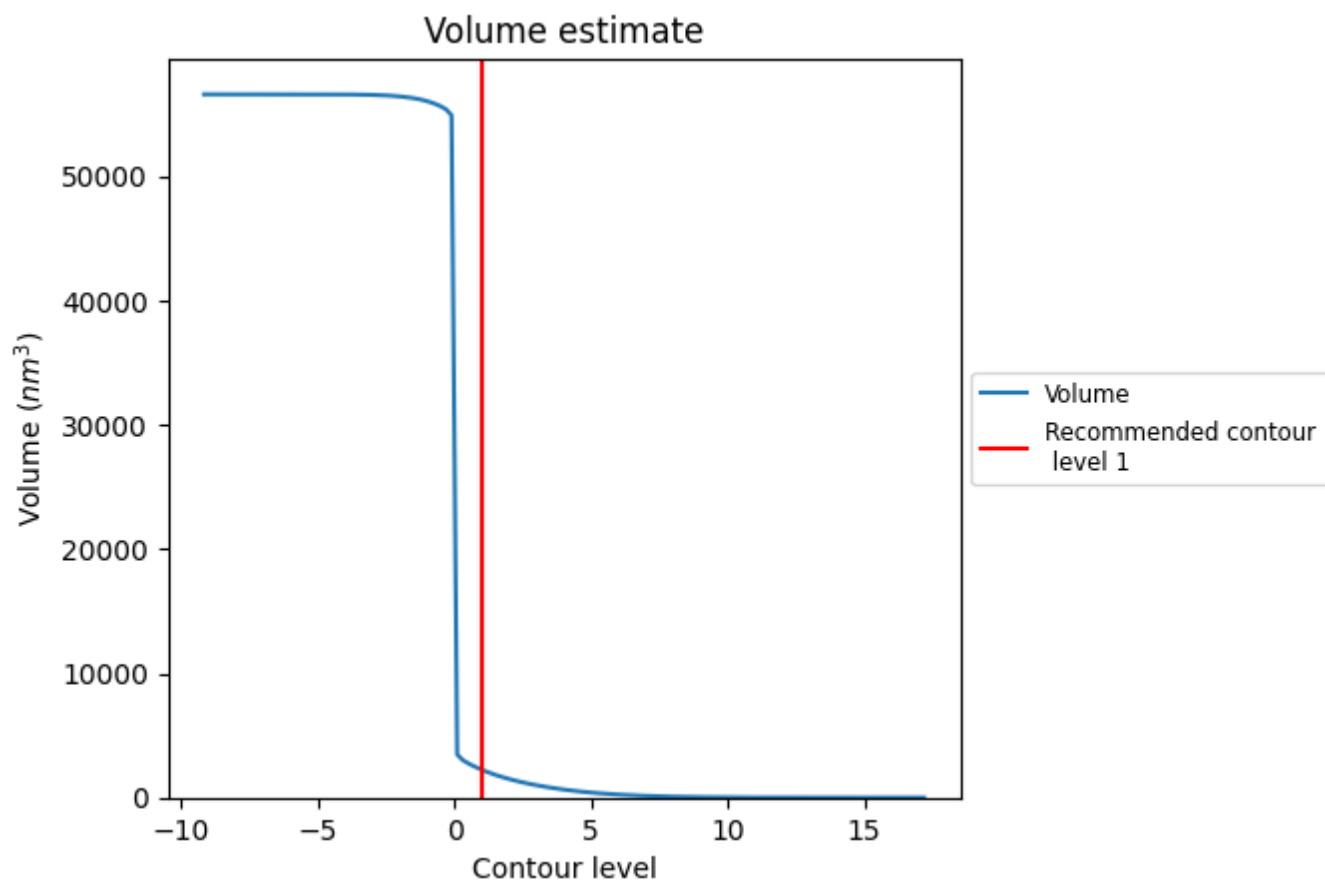
This section contains the results of statistical analysis of the map.

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.

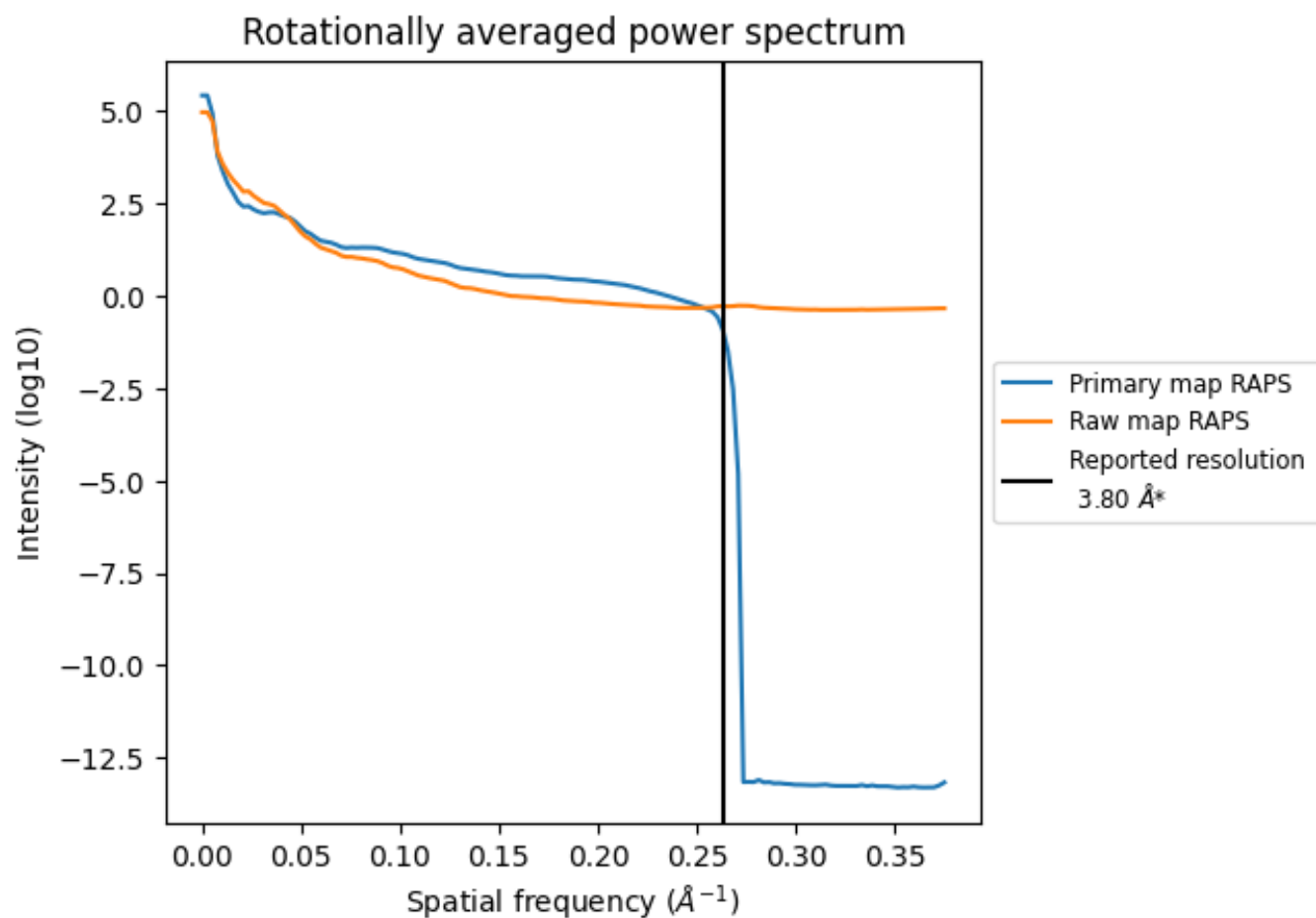
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2247 nm^3 ; this corresponds to an approximate mass of 2030 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 ⓘ

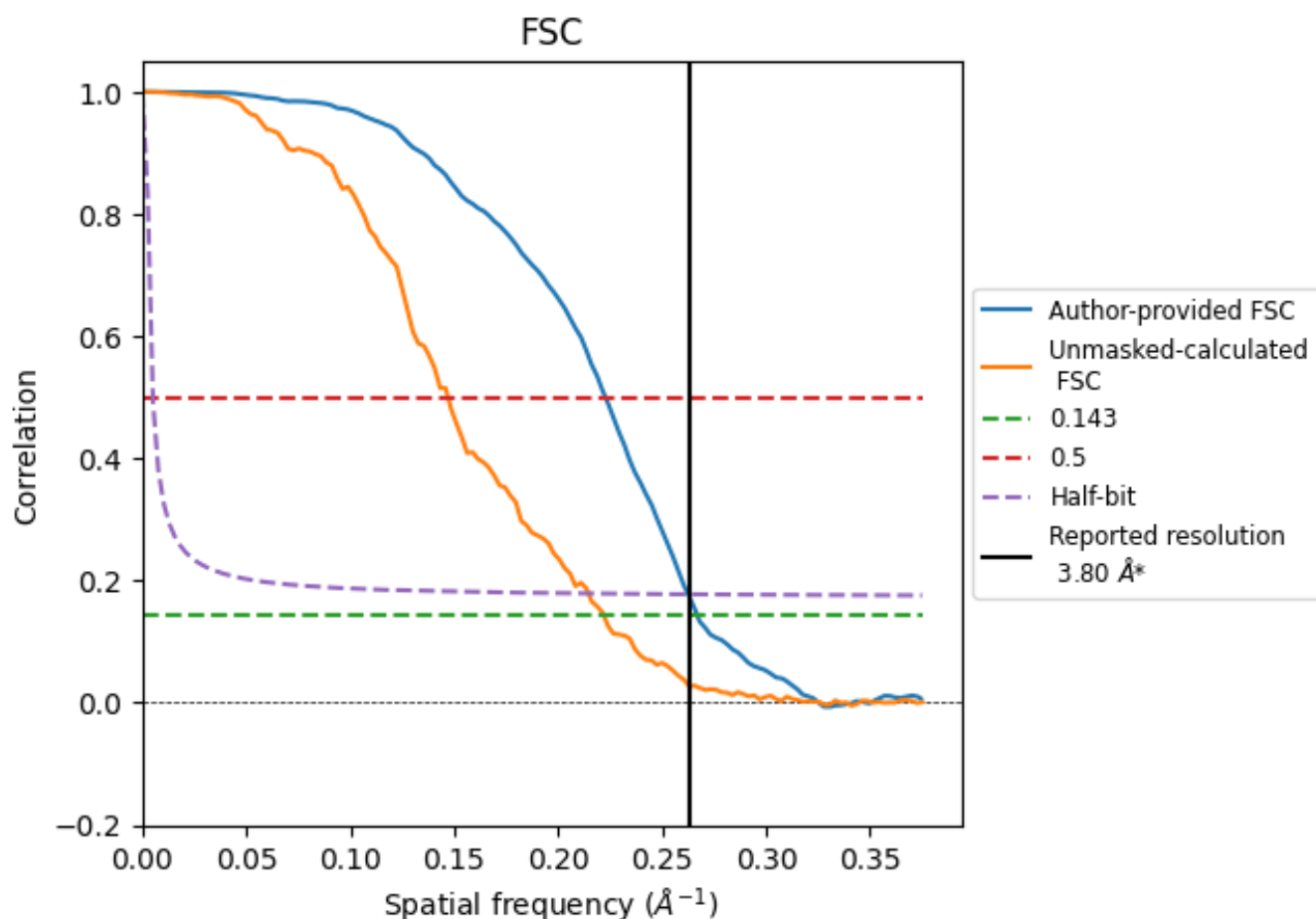


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

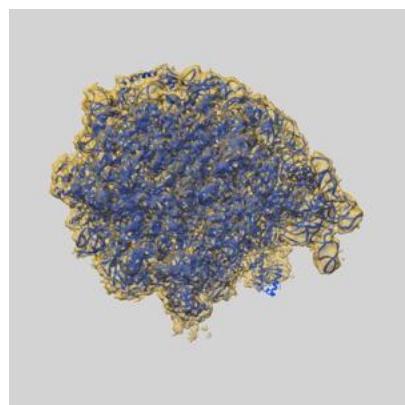
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.75	4.49	3.81
Unmasked-calculated*	4.50	6.80	4.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.50 differs from the reported value 3.8 by more than 10 %

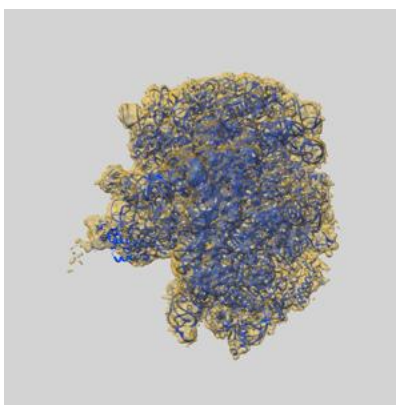
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21629 and PDB model 6WDA. Per-residue inclusion information can be found in section [3](#) on page [17](#).

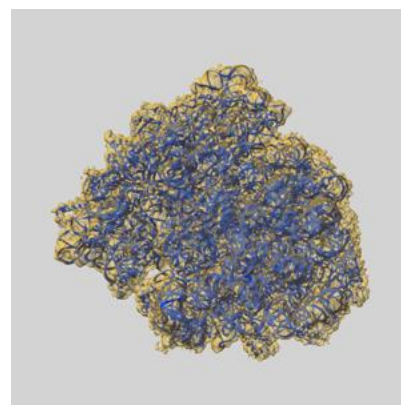
9.1 Map-model overlay [i](#)



X



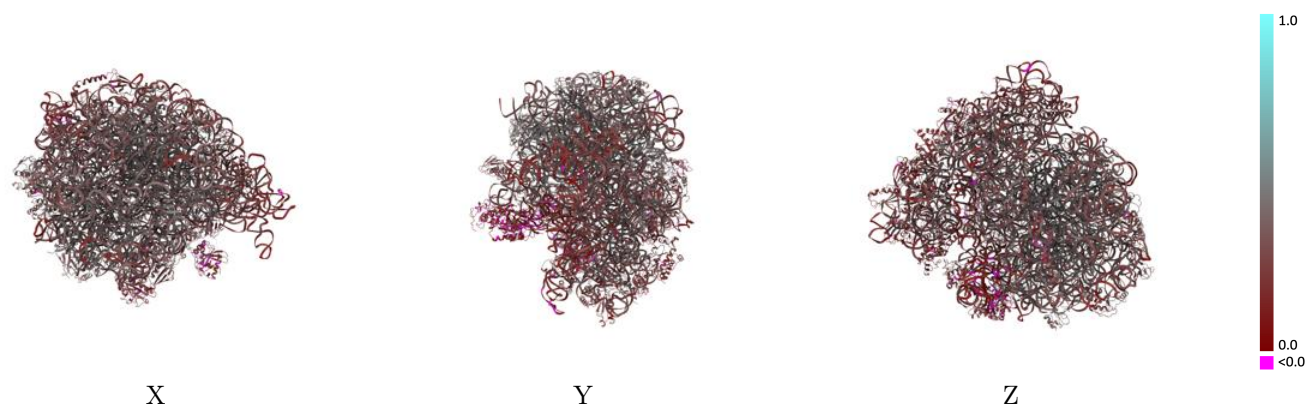
Y



Z

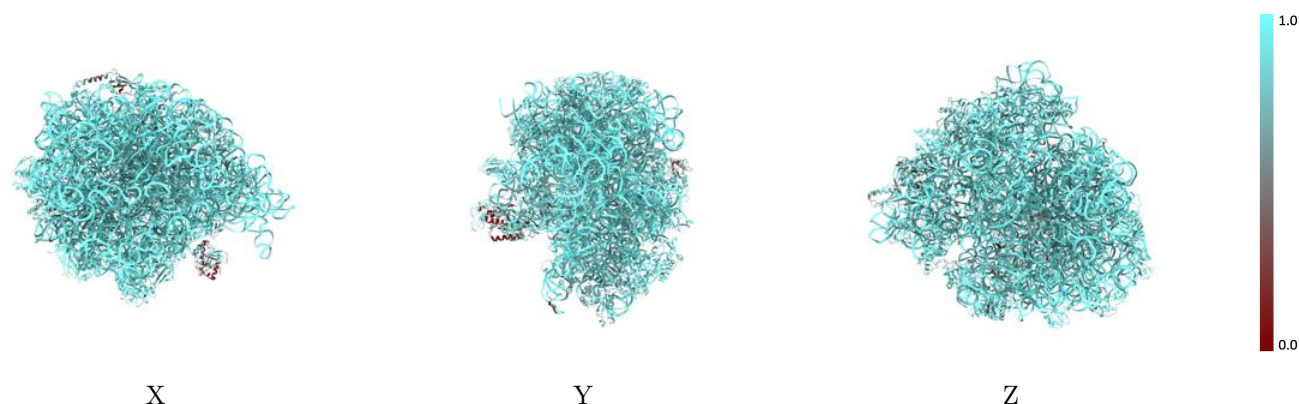
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



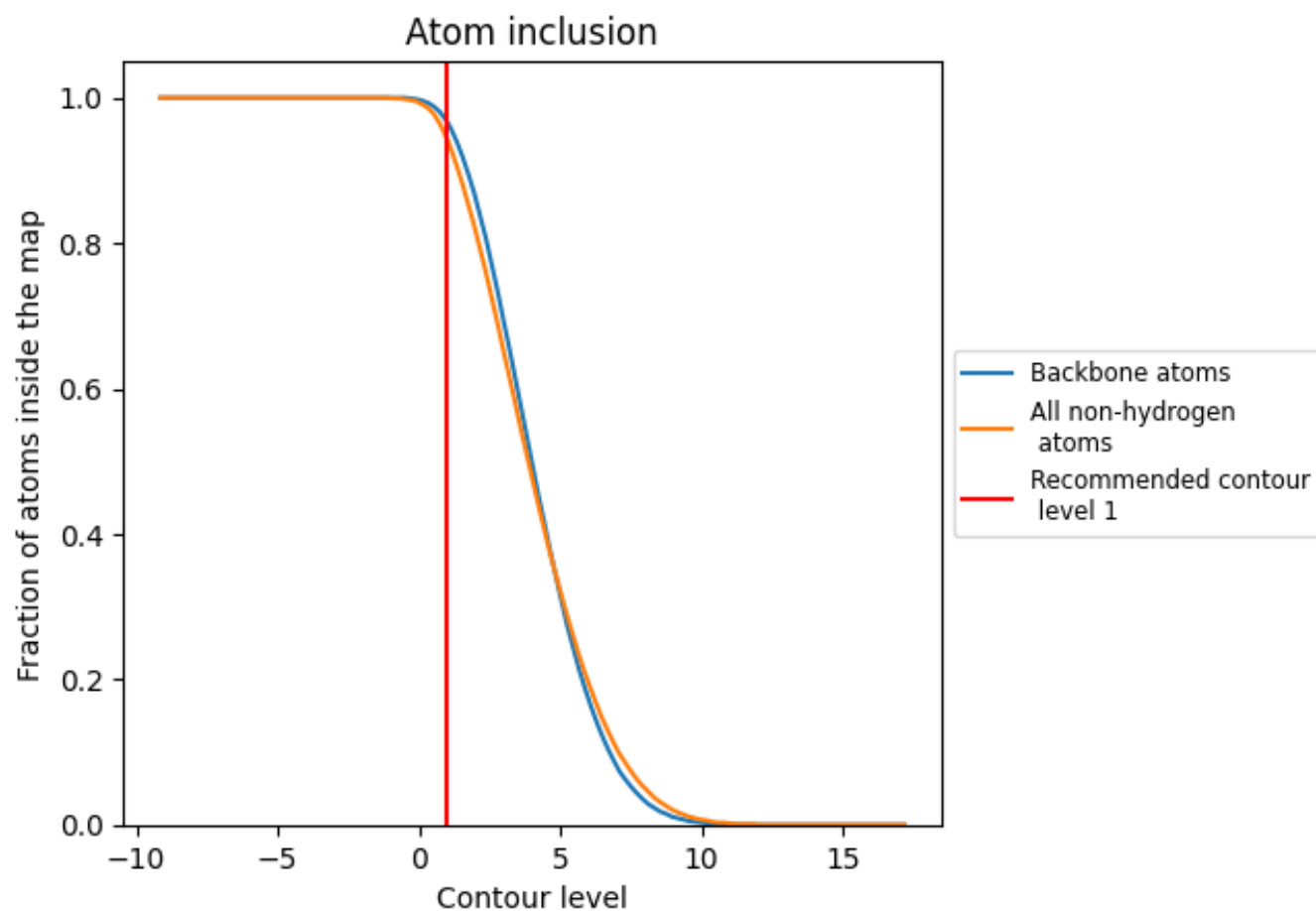
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.3320
1	 0.9810	 0.3610
2	 0.9820	 0.3160
3	 0.9750	 0.3080
4	 0.8790	 0.2360
5	 0.9690	 0.2890
6	 0.8190	 0.1350
7	 0.9280	 0.1450
8	 0.6980	 0.1460
B	 0.9390	 0.4060
C	 0.8280	 0.3600
D	 0.9270	 0.4330
E	 0.9180	 0.4380
F	 0.8250	 0.3670
G	 0.8690	 0.2920
H	 0.7740	 0.3050
I	 0.7720	 0.2170
J	 0.9150	 0.3650
K	 0.9320	 0.3550
L	 0.8990	 0.2690
M	 0.9250	 0.3560
N	 0.8620	 0.2830
O	 0.7180	 0.2840
P	 0.9270	 0.3480
Q	 0.9220	 0.3460
R	 0.9140	 0.2810
S	 0.7540	 0.2790
T	 0.9450	 0.3520
U	 0.8910	 0.3040
V	 0.9080	 0.3270
W	 0.8950	 0.3250
X	 0.9490	 0.2800
Y	 0.9340	 0.2880
Z	 0.8570	 0.2900
a	 0.7850	 0.1230



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Chain	Atom inclusion	Q-score
b	 0.9470	 0.4420
c	 0.9360	 0.4280
d	 0.9340	 0.3790
e	 0.9290	 0.2790
f	 0.9410	 0.3010
g	 0.6510	 0.2480
h	 0.7510	 0.1410
i	 0.6430	 0.1390
j	 0.9470	 0.4230
k	 0.9290	 0.4250
l	 0.9320	 0.4050
m	 0.9120	 0.4070
n	 0.9350	 0.4160
o	 0.9260	 0.3340
p	 0.9580	 0.4100
q	 0.9290	 0.4120
r	 0.9460	 0.3960
s	 0.9190	 0.4190
t	 0.9320	 0.4010
u	 0.9310	 0.3580
v	 0.9400	 0.3800
w	 0.9210	 0.4180
x	 0.9330	 0.4270
y	 0.9230	 0.3270
z	 0.9450	 0.4130