



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 10:18 AM UTC

PDB ID : 6WD7 / pdb_00006wd7
EMDB ID : EMD-21626
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure II-D)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

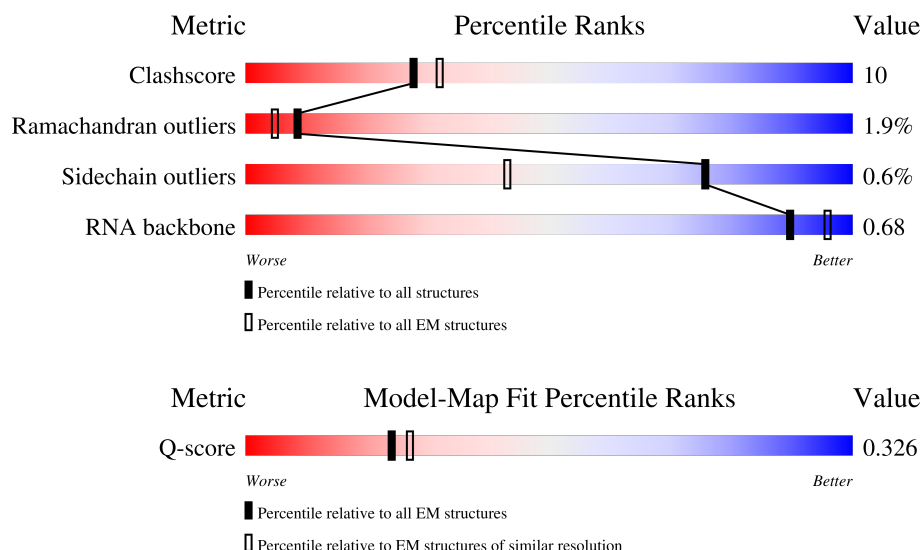
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.



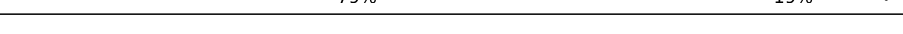
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	

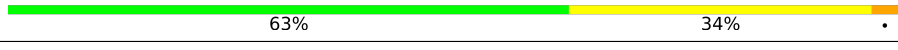
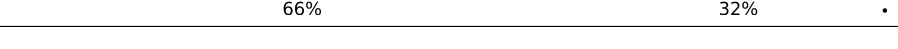
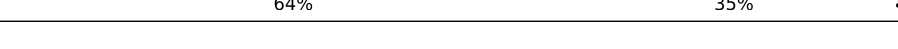
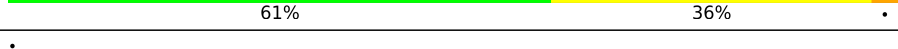
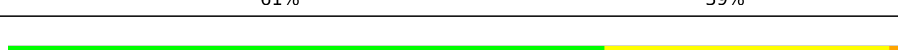
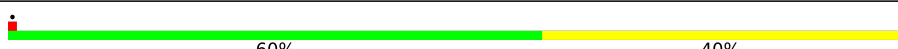
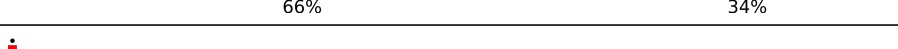
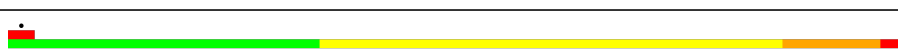
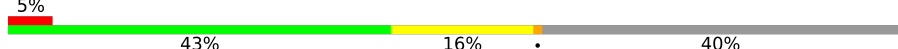
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
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	68%27%6%
55	5	77	70%26%
55	6	77	5% 68%32%
56	4	18	6% 72%28%
57	7	76	18% 54%36%9%
58	8	400	17% 12%9% 78%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 150887 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	75	Total	C	N	O	P	0	0
			1597	713	285	525	74		

- Molecule 58 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	89	Total	C	N	O	S	0	0
			698	450	121	123	4		

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).

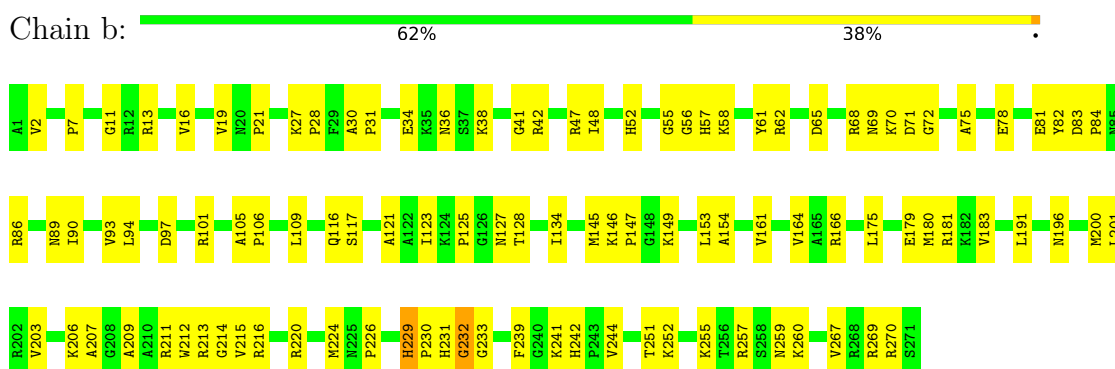


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
59	5	1	10	6	1	2	1	0

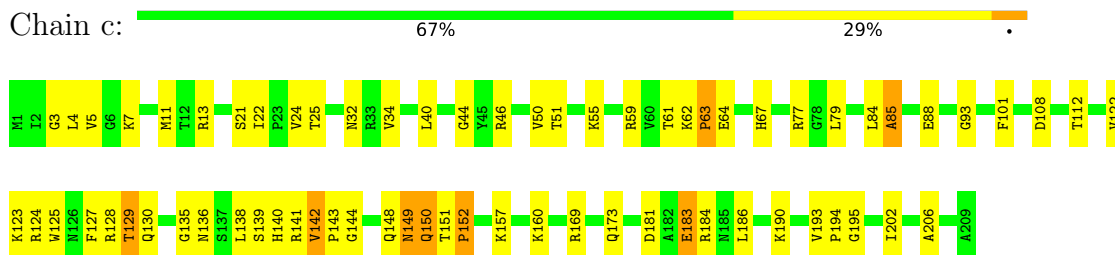
3 Residue-property plots

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.

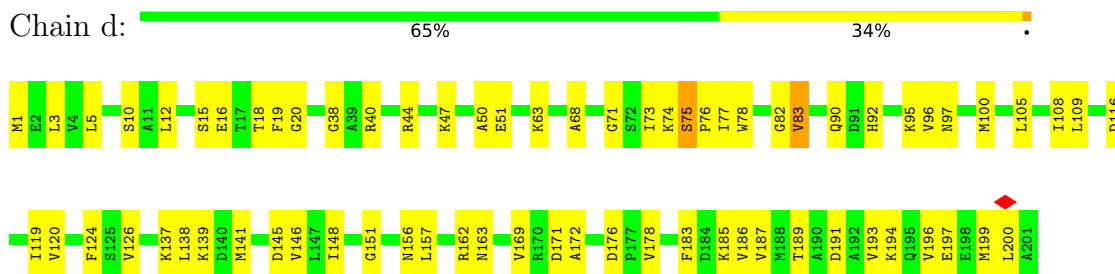
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

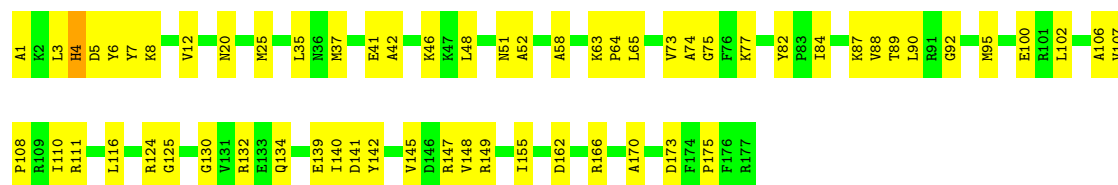


• Molecule 3: 50S ribosomal protein L4

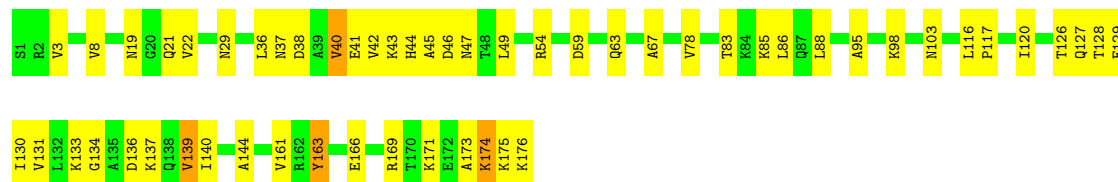


• Molecule 4: 50S ribosomal protein L5

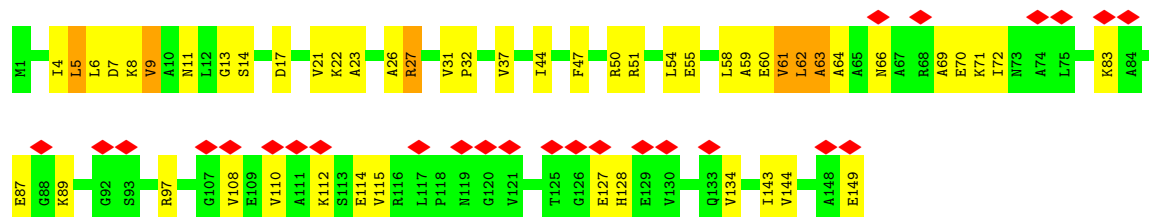




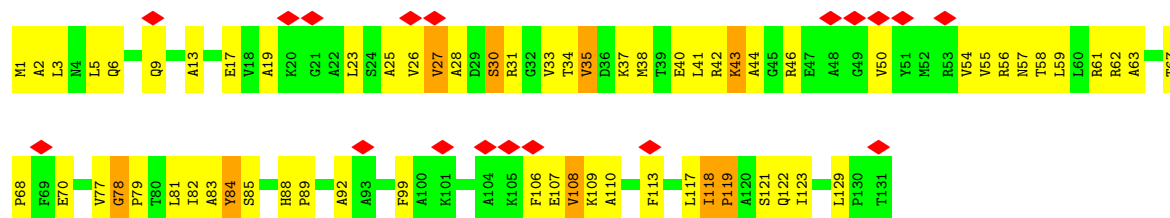
• Molecule 5: 50S ribosomal protein L6



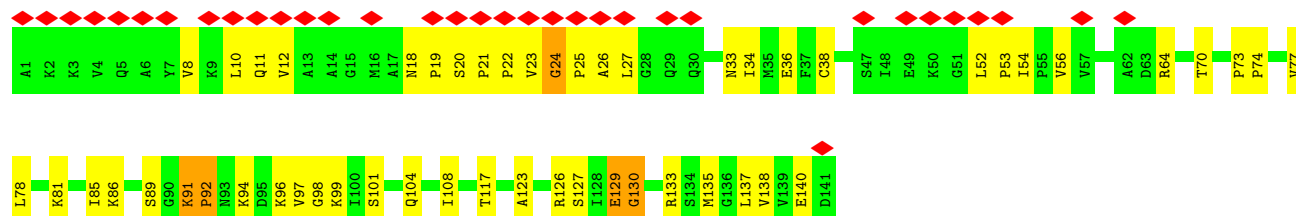
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10

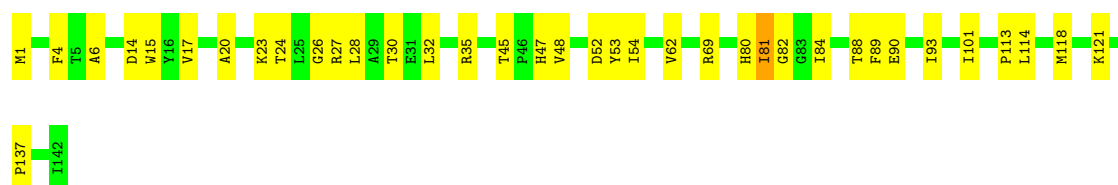


• Molecule 8: 50S ribosomal protein L11



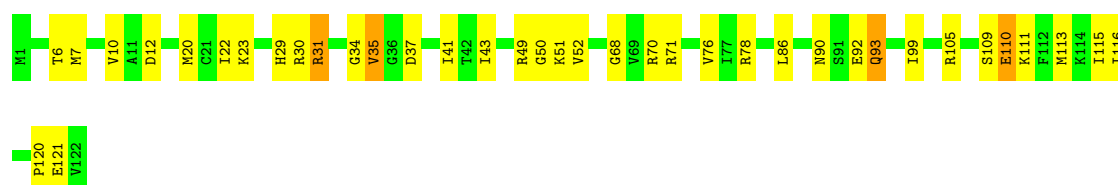
- Molecule 9: 50S ribosomal protein L13

Chain j:  74% 25% .



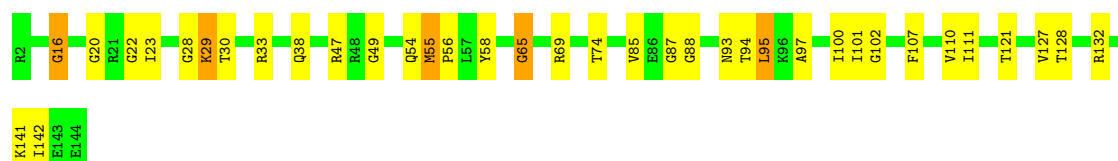
- Molecule 10: 50S ribosomal protein L14

Chain k:  69% 28% .



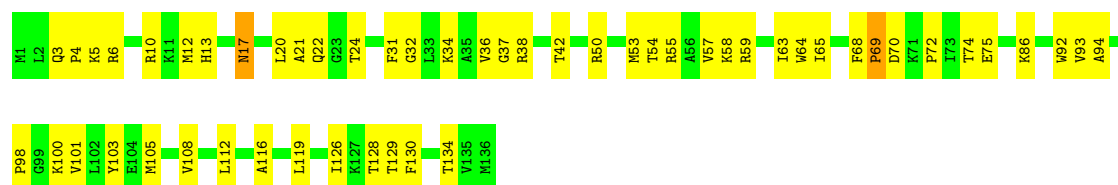
- Molecule 11: 50S ribosomal protein L15

Chain l:  74% 22% .



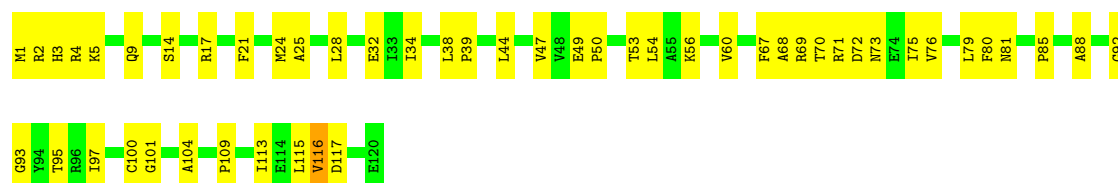
- Molecule 12: 50S ribosomal protein L16

Chain m:  61% 38% .



- Molecule 13: 50S ribosomal protein L17

Chain n:  58% 41% .



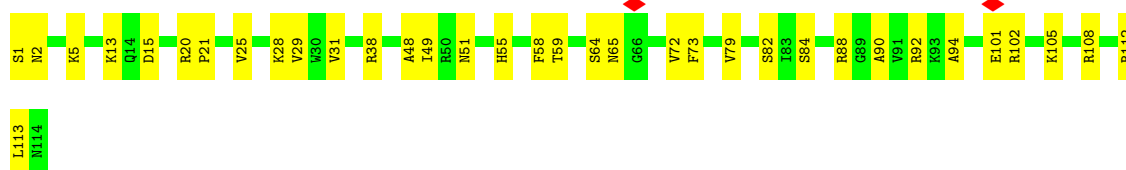
- Molecule 14: 50S ribosomal protein L18

Chain o:  73% 26%



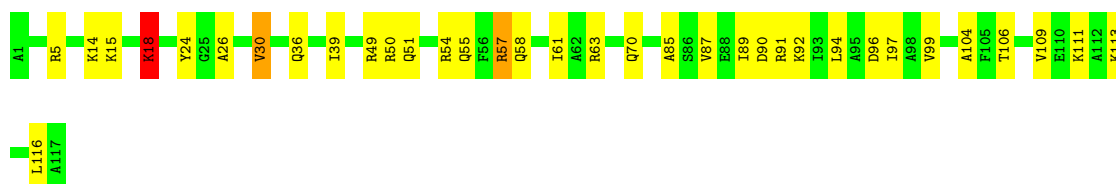
- Molecule 15: 50S ribosomal protein L19

Chain p:  69% 31%



- Molecule 16: 50S ribosomal protein L20

Chain q:  70% 27%



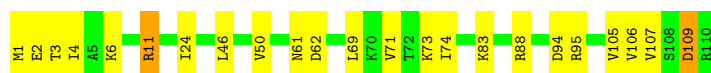
- Molecule 17: 50S ribosomal protein L21

Chain r:  71% 28%



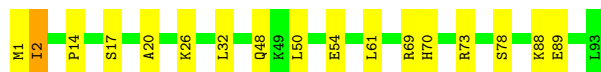
- Molecule 18: 50S ribosomal protein L22

Chain s:  79% 19%



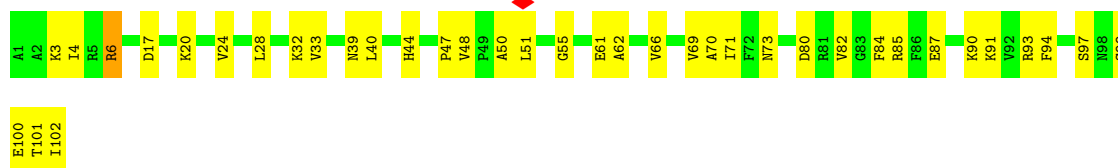
- Molecule 19: 50S ribosomal protein L23

Chain t:  82% 17%



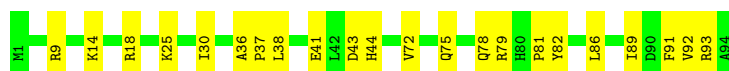
- Molecule 20: 50S ribosomal protein L24

Chain u:  63% 36%



- Molecule 21: 50S ribosomal protein L25

Chain v:  77% 23%



- Molecule 22: 50S ribosomal protein L27

Chain w:  77% 23%



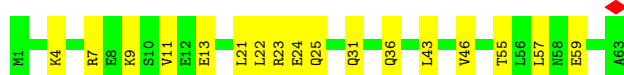
- Molecule 23: 50S ribosomal protein L28

Chain x:  69% 30%



- Molecule 24: 50S ribosomal protein L29

Chain y:  73% 27%



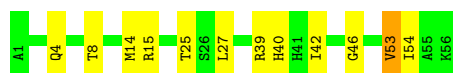
- Molecule 25: 50S ribosomal protein L30

Chain z:  69% 31%



- Molecule 26: 50S ribosomal protein L32

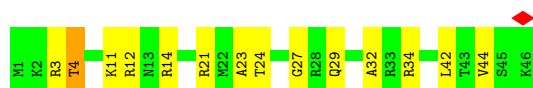
Chain B:  79% 20%



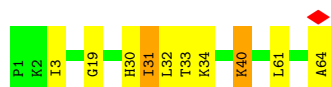
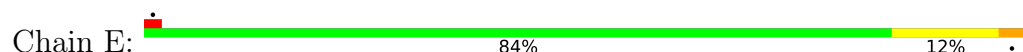
- Molecule 27: 50S ribosomal protein L33



- Molecule 28: 50S ribosomal protein L34



- Molecule 29: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L36

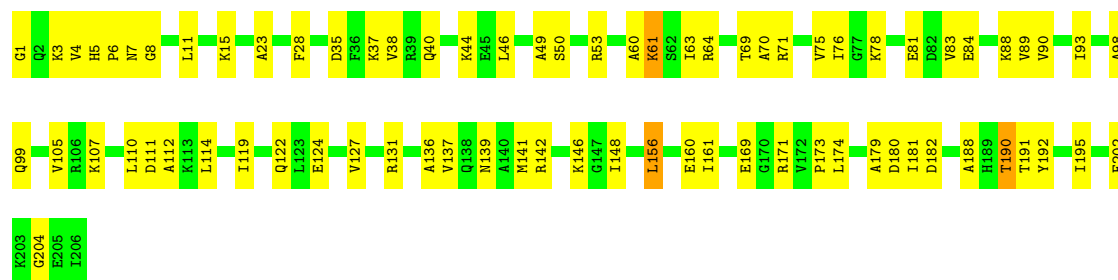


- Molecule 31: 30S ribosomal protein S2

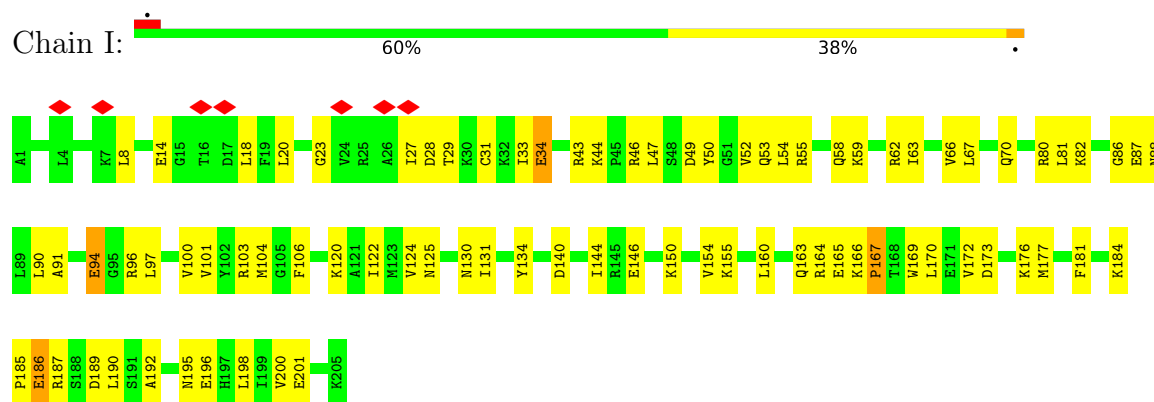


- Molecule 32: 30S ribosomal protein S3

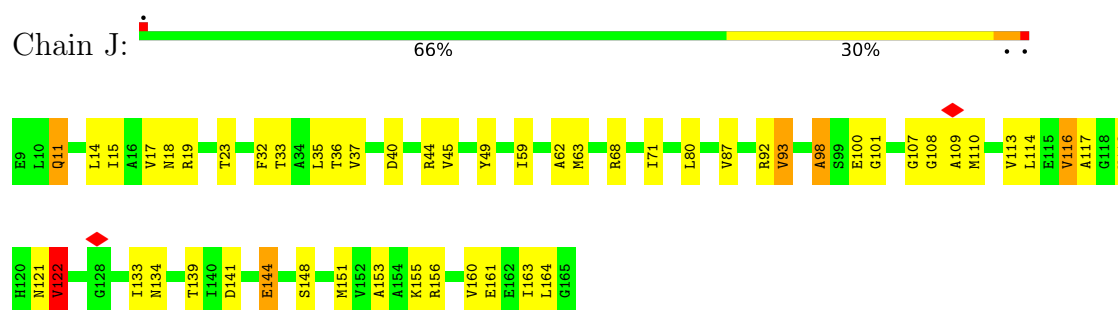




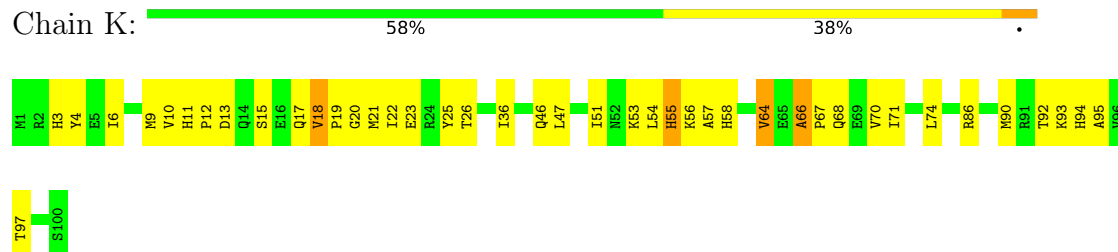
- Molecule 33: 30S ribosomal protein S4



- Molecule 34: 30S ribosomal protein S5

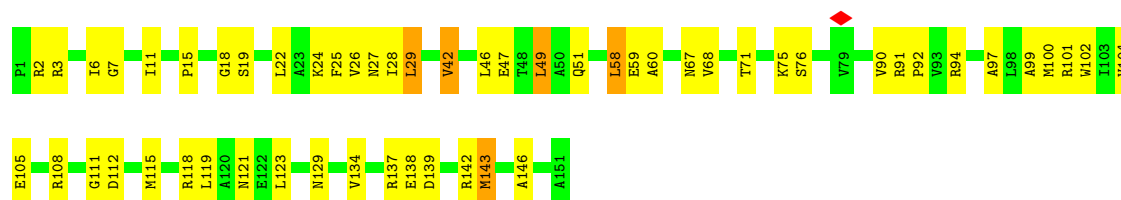


- Molecule 35: 30S ribosomal protein S6

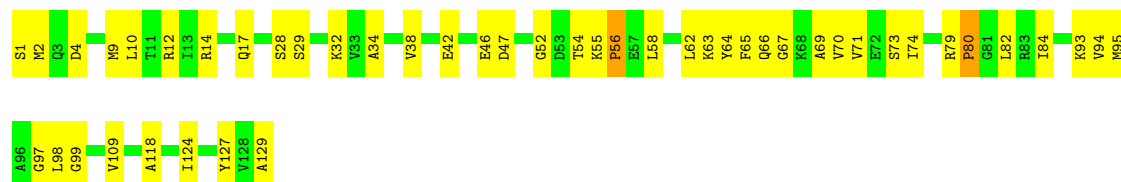


- Molecule 36: 30S ribosomal protein S7





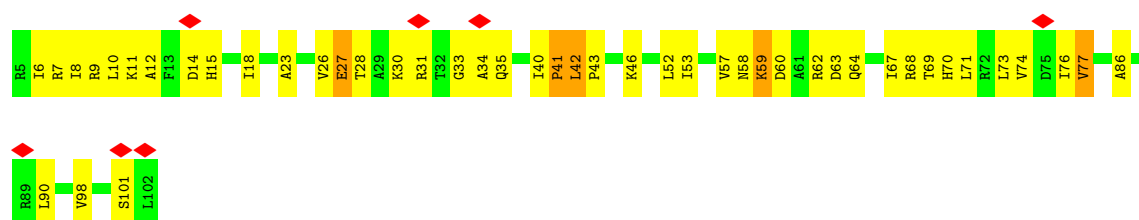
• Molecule 37: 30S ribosomal protein S8



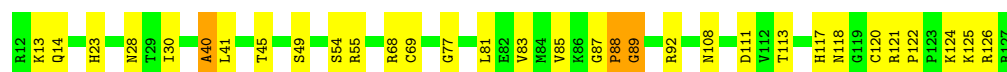
• Molecule 38: 30S ribosomal protein S9



• Molecule 39: 30S ribosomal protein S10

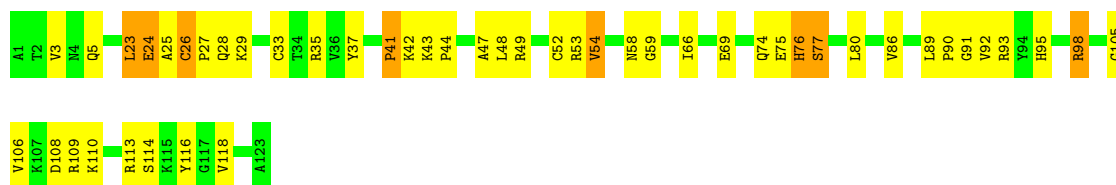


• Molecule 40: 30S ribosomal protein S11

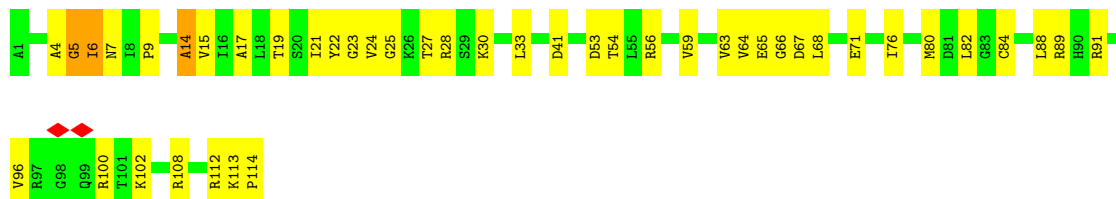


• Molecule 41: 30S ribosomal protein S12

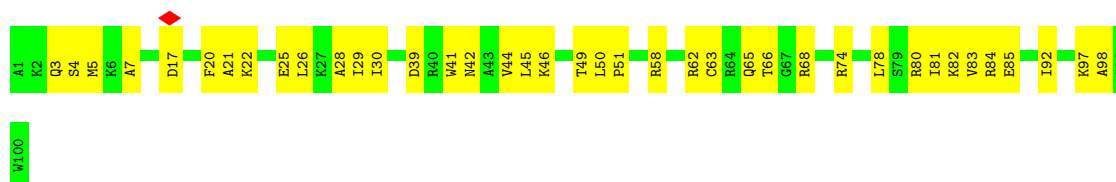




- Molecule 42: 30S ribosomal protein S13



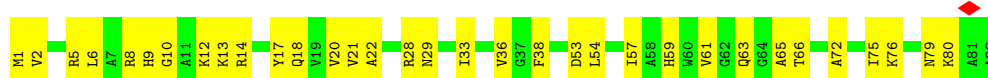
- Molecule 43: 30S ribosomal protein S14



- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16



- Molecule 46: 30S ribosomal protein S17



- Molecule 47: 30S ribosomal protein S18

Chain W:  72% 28%



- Molecule 48: 30S ribosomal protein S19

Chain X:  66% 34%



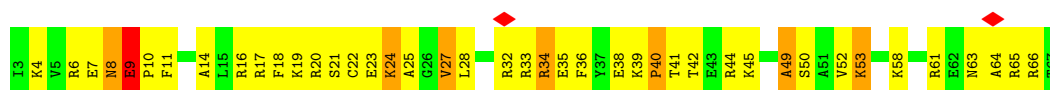
- Molecule 49: 30S ribosomal protein S20

Chain Y:  62% 36%



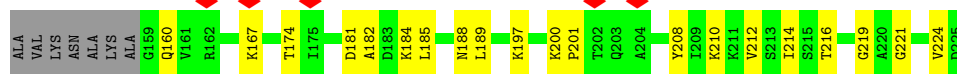
- Molecule 50: 30S ribosomal protein S21

Chain Z:  35% 52% 11%



- Molecule 51: 50S ribosomal protein L1

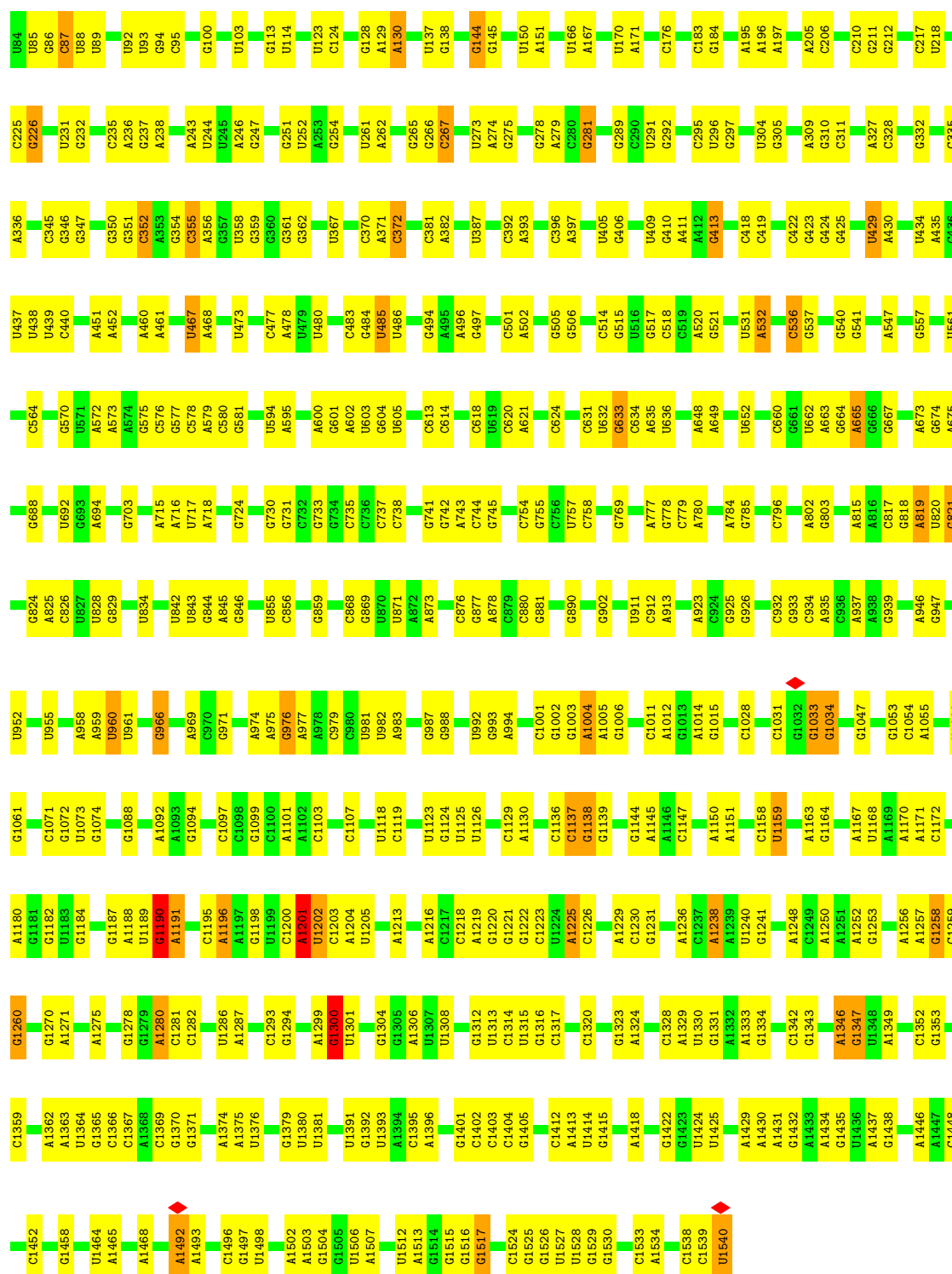
Chain a:  5% 43% 16% 40%



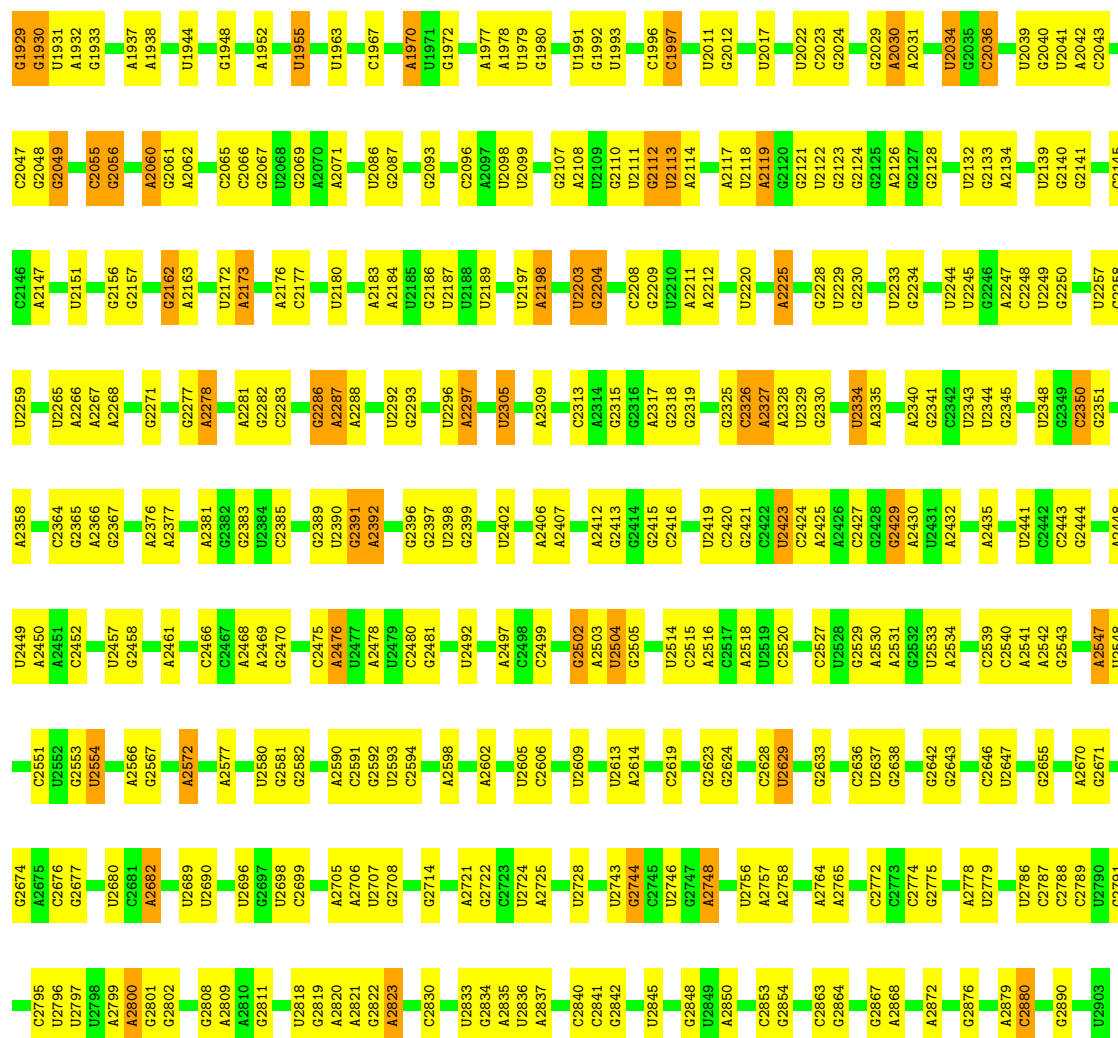
- Molecule 52: 16S ribosomal RNA

Chain 3:  63% 34%

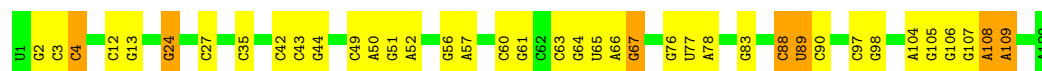








• Molecule 54: 5S ribosomal RNA



• Molecule 55: tRNA^{fMet}



• Molecule 55: tRNA^{fMet}



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	5468	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	17.817	Depositor
Minimum map value	-10.054	Depositor
Average map value	0.115	Depositor
Map value standard deviation	0.865	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	b	0.30	0/2122	0.93	6/2852 (0.2%)
2	c	0.29	0/1586	0.91	5/2134 (0.2%)
3	d	0.28	0/1571	0.85	3/2113 (0.1%)
4	e	0.31	0/1435	0.88	5/1926 (0.3%)
5	f	0.30	0/1343	0.94	4/1816 (0.2%)
6	g	0.32	0/1122	0.95	7/1515 (0.5%)
7	h	0.33	0/1002	1.09	11/1350 (0.8%)
8	i	0.35	0/1046	0.98	8/1410 (0.6%)
9	j	0.29	0/1152	0.87	0/1551
10	k	0.28	0/948	0.96	6/1268 (0.5%)
11	l	0.30	0/1054	0.96	3/1403 (0.2%)
12	m	0.31	0/1093	0.88	1/1460 (0.1%)
13	n	0.30	0/974	0.94	5/1301 (0.4%)
14	o	0.29	0/902	0.91	1/1209 (0.1%)
15	p	0.29	0/929	0.84	0/1242
16	q	0.30	0/960	0.96	5/1278 (0.4%)
17	r	0.29	0/829	0.91	4/1107 (0.4%)
18	s	0.28	0/864	0.88	0/1156
19	t	0.28	0/745	0.81	1/994 (0.1%)
20	u	0.30	0/788	0.89	1/1051 (0.1%)
21	v	0.29	0/766	0.90	1/1025 (0.1%)
22	w	0.29	0/582	0.87	2/769 (0.3%)
23	x	0.29	0/635	0.92	3/848 (0.4%)
24	y	0.28	0/510	0.92	1/677 (0.1%)
25	z	0.30	0/453	0.82	0/605
26	B	0.28	0/450	0.78	1/599 (0.2%)
27	C	0.33	0/417	0.92	1/554 (0.2%)
28	D	0.31	0/380	0.94	2/498 (0.4%)
29	E	0.30	0/513	0.83	1/676 (0.1%)
30	F	0.30	0/303	0.91	0/397
31	G	0.31	0/1788	0.91	5/2408 (0.2%)
32	H	0.30	0/1652	0.88	2/2225 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.93	7/2227 (0.3%)
34	J	0.31	0/1170	0.97	5/1573 (0.3%)
35	K	0.31	0/836	0.96	5/1128 (0.4%)
36	L	0.31	0/1196	0.92	4/1602 (0.2%)
37	M	0.29	0/989	0.98	3/1326 (0.2%)
38	N	0.31	0/1034	0.88	2/1375 (0.1%)
39	O	0.33	0/797	0.98	4/1077 (0.4%)
40	P	0.32	0/886	1.00	4/1195 (0.3%)
41	Q	0.30	0/969	1.04	9/1300 (0.7%)
42	R	0.32	0/893	0.91	2/1193 (0.2%)
43	S	0.30	0/817	0.84	0/1088
44	T	0.29	0/722	0.98	6/964 (0.6%)
45	U	0.31	0/659	0.85	0/884
46	V	0.30	0/658	0.91	3/881 (0.3%)
47	W	0.30	0/545	0.88	0/731
48	X	0.32	0/653	0.88	0/877
49	Y	0.30	0/671	1.00	5/888 (0.6%)
50	Z	0.33	0/551	1.08	4/728 (0.5%)
51	a	0.31	0/1034	0.83	3/1387 (0.2%)
52	3	0.40	0/36963	0.50	3/57662 (0.0%)
53	1	0.39	0/69796	0.50	1/108888 (0.0%)
54	2	0.40	0/2872	0.51	0/4479
55	5	0.40	0/1832	0.49	0/2855
55	6	0.40	0/1832	0.50	0/2855
56	4	0.40	0/436	0.50	0/679
57	7	0.40	0/1784	0.51	0/2780
58	8	0.34	0/713	0.85	0/960
All	All	0.37	0/163887	0.64	165/244999 (0.1%)

There are no bond length outliers.

All (165) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	l	95	LEU	N-CA-C	-9.25	100.57	112.23
7	h	117	LEU	N-CA-C	8.77	121.88	107.23
7	h	107	GLU	N-CA-C	-8.14	100.33	113.19
7	h	42	ARG	N-CA-C	-8.10	103.19	113.23
2	c	183	GLU	N-CA-C	7.81	121.31	111.24
7	h	106	PHE	N-CA-C	7.77	120.00	110.91
16	q	18	LYS	N-CA-C	-7.74	102.76	112.90
5	f	47	ASN	N-CA-C	-7.54	104.13	112.72
31	G	131	LYS	N-CA-C	7.47	120.13	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	u	100	GLU	N-CA-C	-7.34	98.57	109.81
6	g	61	VAL	N-CA-C	-7.32	103.11	113.07
7	h	43	LYS	N-CA-C	-7.21	103.46	111.82
27	C	30	PRO	N-CA-C	-7.10	104.62	114.98
35	K	66	ALA	N-CA-C	7.09	114.38	108.07
37	M	9	MET	N-CA-C	-7.07	103.66	111.36
41	Q	25	ALA	N-CA-C	7.05	121.21	112.47
21	v	44	HIS	N-CA-C	7.03	118.83	111.03
34	J	144	GLU	N-CA-C	-6.93	104.82	113.28
36	L	143	MET	N-CA-C	-6.93	104.63	113.23
40	P	117	HIS	N-CA-C	-6.91	102.03	110.88
37	M	67	GLY	N-CA-C	-6.87	104.16	113.37
41	Q	24	GLU	N-CA-C	6.87	120.64	111.30
35	K	68	GLN	N-CA-C	6.86	118.44	110.97
6	g	62	LEU	N-CA-C	-6.80	104.46	112.89
37	M	118	ALA	N-CA-C	-6.76	105.19	113.50
49	Y	5	SER	N-CA-C	-6.60	105.23	113.28
23	x	6	VAL	N-CA-C	6.58	116.69	110.30
41	Q	108	ASP	N-CA-C	6.57	118.60	110.91
39	O	59	LYS	N-CA-C	6.53	118.06	111.07
8	i	91	LYS	CA-C-N	6.51	127.97	119.84
8	i	91	LYS	C-N-CA	6.51	127.97	119.84
2	c	85	ALA	N-CA-C	6.50	118.24	110.44
38	N	105	ARG	N-CA-C	-6.47	104.07	112.23
50	Z	49	ALA	N-CA-C	-6.47	103.74	111.69
40	P	69	CYS	N-CA-C	-6.46	105.32	113.72
42	R	64	VAL	N-CA-C	6.46	118.46	109.29
31	G	130	LYS	N-CA-C	6.42	118.16	111.03
50	Z	53	LYS	N-CA-C	-6.40	103.82	111.69
41	Q	43	LYS	N-CA-C	6.39	123.93	109.81
35	K	90	MET	N-CA-C	6.37	119.59	109.65
49	Y	7	LYS	N-CA-C	-6.31	105.57	113.20
6	g	27	ARG	N-CA-C	6.29	118.22	111.36
10	k	43	ILE	N-CA-C	6.27	118.40	108.87
4	e	173	ASP	N-CA-C	6.25	119.80	111.30
5	f	163	TYR	N-CA-C	-6.25	102.12	110.55
8	i	129	GLU	N-CA-C	-6.23	104.60	111.82
36	L	29	LEU	N-CA-C	-6.22	105.84	113.50
4	e	4	HIS	N-CA-C	-6.17	104.63	111.36
52	3	1201	A	C2'-C3'-O3'	6.17	118.76	109.50
23	x	21	LEU	N-CA-C	6.15	120.04	111.74
13	n	25	ALA	N-CA-C	-6.14	104.67	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	x	57	VAL	N-CA-C	-6.11	103.73	112.35
17	r	36	ALA	N-CA-C	-6.09	104.49	112.41
2	c	129	THR	N-CA-C	6.08	119.99	110.32
52	3	1190	G	C2'-C3'-O3'	6.07	118.60	109.50
35	K	64	VAL	N-CA-C	6.01	117.14	108.48
3	d	73	ILE	N-CA-C	-6.00	106.89	112.83
1	b	105	ALA	N-CA-C	5.94	117.13	109.65
22	w	74	LYS	N-CA-C	5.91	117.67	109.15
36	L	58	LEU	N-CA-C	5.90	118.22	111.02
5	f	139	VAL	N-CA-C	5.90	116.64	110.62
34	J	117	ALA	N-CA-C	-5.90	104.80	112.23
1	b	69	ASN	N-CA-C	5.88	119.56	112.38
6	g	63	ALA	N-CA-C	-5.88	104.99	111.82
33	I	46	ARG	N-CA-C	-5.86	105.02	111.82
34	J	116	VAL	N-CA-C	-5.85	104.45	113.16
39	O	77	VAL	N-CA-C	5.84	120.22	112.04
16	q	85	ALA	N-CA-C	-5.84	105.47	113.30
31	G	162	VAL	N-CA-C	5.82	116.86	108.48
32	H	190	THR	N-CA-C	-5.78	101.28	109.96
44	T	51	SER	N-CA-C	-5.77	106.41	113.50
16	q	50	ARG	N-CA-C	-5.76	105.35	112.90
41	Q	26	CYS	CA-C-N	5.75	127.03	119.84
41	Q	26	CYS	C-N-CA	5.75	127.03	119.84
53	l	1020	A	C2'-C3'-O3'	5.75	118.13	109.50
7	h	58	THR	N-CA-C	5.74	121.01	113.20
40	P	83	VAL	N-CA-C	5.73	117.00	109.21
6	g	5	LEU	N-CA-C	5.73	118.89	110.59
7	h	35	VAL	N-CA-C	-5.63	104.77	113.16
33	I	94	GLU	N-CA-C	-5.63	106.42	113.28
5	f	40	VAL	N-CA-C	5.58	116.14	107.99
39	O	15	HIS	N-CA-C	5.56	117.42	111.36
14	o	3	LYS	N-CA-C	5.55	117.03	110.97
50	Z	42	THR	N-CA-C	5.55	117.13	111.14
1	b	123	ILE	N-CA-C	5.54	115.30	106.88
8	i	64	ARG	N-CA-C	5.54	119.86	113.38
7	h	84	TYR	N-CA-C	5.53	117.67	110.43
49	Y	15	LYS	N-CA-C	-5.51	105.82	112.54
2	c	150	GLN	N-CA-C	5.50	117.28	111.28
46	V	36	PHE	N-CA-C	5.46	117.62	109.59
22	w	52	ASP	N-CA-C	-5.46	106.21	112.92
4	e	170	ALA	N-CA-C	-5.45	105.42	111.36
34	J	122	VAL	N-CA-C	5.45	120.68	109.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	O	27	GLU	N-CA-C	-5.45	105.25	111.14
8	i	127	SER	N-CA-C	-5.44	106.14	112.89
33	I	146	GLU	N-CA-C	5.42	116.87	111.07
36	L	42	VAL	N-CA-C	5.42	116.15	110.62
12	m	17	ASN	N-CA-C	5.41	117.53	108.23
51	a	8	MET	N-CA-C	5.41	117.25	111.36
10	k	90	ASN	N-CA-C	5.40	116.85	111.07
46	V	69	THR	N-CA-C	-5.40	101.65	108.45
13	n	68	ALA	N-CA-C	-5.39	105.50	111.71
13	n	54	LEU	N-CA-C	-5.39	106.83	113.41
33	I	91	ALA	N-CA-C	-5.39	105.44	112.23
7	h	44	ALA	N-CA-C	-5.39	105.49	111.36
33	I	166	LYS	CA-C-N	5.38	126.56	119.84
33	I	166	LYS	C-N-CA	5.38	126.56	119.84
6	g	64	ALA	N-CA-C	-5.32	105.53	112.23
26	B	15	ARG	N-CA-C	-5.32	106.84	113.38
6	g	44	ILE	N-CA-C	-5.32	105.53	110.53
2	c	152	PRO	N-CA-C	-5.31	106.28	113.40
3	d	171	ASP	N-CA-C	-5.31	101.05	109.76
50	Z	9	GLU	N-CA-C	5.30	121.53	109.81
28	D	29	GLN	N-CA-C	-5.30	106.32	112.89
17	r	50	GLY	N-CA-C	-5.29	100.65	113.18
44	T	43	ALA	N-CA-C	-5.29	105.41	111.07
7	h	30	SER	N-CA-C	-5.27	106.44	112.92
4	e	134	GLN	N-CA-C	-5.27	106.53	113.17
10	k	71	ARG	N-CA-C	-5.26	103.44	110.07
10	k	35	VAL	N-CA-C	5.26	120.27	109.34
33	I	186	GLU	N-CA-C	-5.25	101.96	110.32
41	Q	54	VAL	N-CA-C	5.25	115.83	108.17
34	J	62	ALA	N-CA-C	5.24	116.99	111.28
1	b	229	HIS	CA-C-N	5.24	126.38	119.84
1	b	229	HIS	C-N-CA	5.24	126.38	119.84
41	Q	114	SER	N-CA-C	-5.23	105.47	111.07
35	K	18	VAL	N-CA-C	5.23	120.18	108.88
44	T	52	ARG	N-CA-C	-5.23	105.66	111.36
51	a	23	ILE	N-CA-C	5.22	115.37	110.30
13	n	67	PHE	N-CA-C	-5.22	107.29	113.97
52	3	1300	G	N9-C1'-C2'	5.22	119.83	112.00
4	e	149	ARG	N-CA-C	5.21	117.58	110.24
42	R	54	THR	N-CA-C	-5.21	105.78	111.82
8	i	24	GLY	CA-C-N	5.15	126.28	119.84
8	i	24	GLY	C-N-CA	5.15	126.28	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	l	55	MET	N-CA-C	-5.15	102.08	109.24
51	a	31	LYS	N-CA-C	-5.14	107.00	113.28
40	P	40	ALA	N-CA-C	5.14	117.16	110.43
44	T	32	THR	N-CA-C	-5.14	105.76	111.36
7	h	9	GLN	N-CA-C	-5.13	105.69	111.28
19	t	50	LEU	N-CA-C	5.13	118.69	112.23
38	N	92	SER	N-CA-C	-5.13	105.81	111.71
29	E	40	LYS	N-CA-C	5.12	116.55	111.07
44	T	49	HIS	N-CA-C	5.12	119.24	113.15
11	l	38	GLN	N-CA-C	5.11	116.54	111.07
10	k	50	GLY	N-CA-C	5.11	117.94	112.33
28	D	32	ALA	N-CA-C	-5.11	105.63	111.14
1	b	207	ALA	N-CA-C	-5.10	105.91	111.82
17	r	43	ASN	N-CA-C	-5.10	105.37	112.45
46	V	68	LYS	N-CA-C	-5.09	106.33	112.54
32	H	131	ARG	N-CA-C	5.08	118.25	111.75
8	i	130	GLY	N-CA-C	-5.06	106.59	113.37
49	Y	51	ASN	N-CA-C	-5.05	107.09	113.20
44	T	35	ILE	N-CA-C	5.05	115.28	110.53
41	Q	98	ARG	N-CA-C	-5.04	102.17	109.59
49	Y	47	GLN	N-CA-C	-5.04	105.97	111.82
16	q	57	ARG	N-CA-C	-5.04	105.86	111.36
3	d	116	ASP	N-CA-C	5.04	118.15	111.30
16	q	70	GLN	N-CA-C	-5.03	106.65	112.89
24	y	24	GLU	N-CA-C	5.01	117.12	111.11
17	r	69	GLY	N-CA-C	5.01	118.96	112.25
13	n	116	VAL	N-CA-C	5.01	119.76	109.34
10	k	34	GLY	N-CA-C	5.01	118.84	112.13
31	G	23	ASN	CA-C-N	5.00	126.09	119.84
31	G	23	ASN	C-N-CA	5.00	126.09	119.84

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	80	0
2	c	1565	0	1616	57	0
3	d	1552	0	1619	49	0
4	e	1411	0	1447	44	0
5	f	1323	0	1374	38	0
6	g	1111	0	1148	38	0
7	h	989	0	1025	53	0
8	i	1032	0	1088	40	0
9	j	1129	0	1162	41	0
10	k	939	0	1012	26	0
11	l	1045	0	1117	26	0
12	m	1074	0	1157	43	0
13	n	961	0	1000	30	0
14	o	892	0	923	20	0
15	p	917	0	965	32	0
16	q	947	0	1022	31	0
17	r	816	0	839	17	0
18	s	857	0	922	17	0
19	t	739	0	807	16	0
20	u	780	0	834	26	0
21	v	753	0	780	15	0
22	w	575	0	592	10	0
23	x	625	0	655	18	0
24	y	509	0	543	13	0
25	z	449	0	491	16	0
26	B	444	0	461	7	0
27	C	410	0	440	16	0
28	D	377	0	418	10	0
29	E	504	0	574	10	0
30	F	302	0	343	13	0
31	G	1757	0	1787	54	0
32	H	1625	0	1699	51	0
33	I	1643	0	1710	63	0
34	J	1157	0	1199	42	0
35	K	818	0	808	32	0
36	L	1182	0	1240	51	0
37	M	979	0	1034	33	0
38	N	1022	0	1070	46	0
39	O	787	0	828	44	0
40	P	870	0	878	28	0
41	Q	955	0	1019	30	0
42	R	884	0	944	32	0
43	S	805	0	847	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	T	714	0	737	19	0
45	U	649	0	666	27	0
46	V	649	0	691	31	0
47	W	536	0	552	14	0
48	X	638	0	665	22	0
49	Y	665	0	714	30	0
50	Z	545	0	579	41	0
51	a	1027	0	1092	35	0
52	3	33012	0	16618	420	0
53	1	62317	0	31346	693	0
54	2	2568	0	1303	41	0
55	5	1640	0	836	17	0
55	6	1640	0	837	19	0
56	4	388	0	196	2	0
57	7	1597	0	811	30	0
58	8	698	0	710	32	0
59	5	10	0	10	0	0
All	All	150887	0	101957	2451	0

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

All (2451) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:45:G:H5''	53:1:46:G:H5'	1.25	1.14
34:J:108:GLY:H	52:3:9:G:H4'	1.29	0.97
53:1:1906:G:H2'	53:1:1907:G:H5''	1.46	0.95
25:z:8:GLN:HG3	25:z:28:LEU:HD22	1.46	0.95
39:O:57:VAL:HG22	39:O:58:ASN:H	1.32	0.94
52:3:484:G:H4'	52:3:485:U:H5''	1.50	0.93
34:J:107:GLY:HA3	52:3:9:G:H5'	1.51	0.93
46:V:5:ARG:HH11	52:3:636:U:H5'	1.34	0.91
52:3:405:U:H3'	52:3:406:G:H5'	1.54	0.90
7:h:118:ILE:HB	7:h:119:PRO:HD3	1.55	0.88
53:1:821:A:H5''	53:1:822:G:H5''	1.54	0.88
31:G:23:ASN:HB3	31:G:26:MET:HE1	1.57	0.86
33:I:190:LEU:HD12	33:I:192:ALA:H	1.39	0.86
32:H:3:LYS:HE3	52:3:1191:A:H5''	1.54	0.86
53:1:1664:A:H61	53:1:1996:C:H42	1.24	0.86
2:c:142:VAL:HG22	2:c:143:PRO:HD2	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:122:GLN:HG3	7:h:123:ILE:H	1.39	0.85
53:1:542:C:H2'	53:1:543:G:H5''	1.59	0.84
55:5:75:C:H2'	55:5:76:A:H5''	1.57	0.84
53:1:1053:C:H2'	53:1:1054:A:H5''	1.59	0.84
12:m:12:MET:HA	53:1:910:A:H62	1.41	0.83
13:n:53:THR:HG21	53:1:2840:C:H5''	1.61	0.83
52:3:1496:C:H1'	52:3:1517:G:H22	1.43	0.83
34:J:119:VAL:HG12	34:J:121:ASN:H	1.44	0.83
42:R:25:GLY:H	52:3:1329:A:H5''	1.42	0.83
53:1:2277:G:H2'	53:1:2278:A:H5''	1.59	0.83
53:1:546:U:H2'	53:1:547:A:H4'	1.60	0.82
53:1:1645:G:H5''	53:1:1646:C:H5'	1.60	0.82
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.59	0.82
33:I:187:ARG:HH12	33:I:192:ALA:HA	1.45	0.82
7:h:33:VAL:HG12	53:1:1055:G:H5''	1.62	0.81
18:s:83:LYS:HE3	18:s:95:ARG:HD3	1.62	0.81
41:Q:26:CYS:SG	41:Q:29:LYS:HD3	2.20	0.81
13:n:95:THR:HB	13:n:113:ILE:HD11	1.61	0.81
6:g:97:ARG:HH21	53:1:2220:U:H5'	1.45	0.81
7:h:27:VAL:HG13	7:h:83:ALA:HB3	1.62	0.81
12:m:74:THR:HG21	12:m:86:LYS:HD2	1.62	0.81
52:3:1306:A:H61	52:3:1331:G:H1'	1.46	0.80
47:W:35:SER:HA	47:W:71:ASP:HB3	1.64	0.79
48:X:77:ARG:HH11	52:3:1222:G:H5''	1.48	0.79
36:L:3:ARG:HH21	52:3:932:C:H5''	1.46	0.79
36:L:142:ARG:HD2	55:6:41:C:H4'	1.64	0.79
51:a:4:LEU:H	51:a:4:LEU:HD12	1.46	0.79
28:D:11:LYS:HE3	53:1:686:U:H5''	1.64	0.78
9:j:4:PHE:HB3	16:q:63:ARG:HH12	1.48	0.78
41:Q:69:GLU:HG2	52:3:521:G:H4'	1.66	0.78
46:V:5:ARG:HD3	52:3:636:U:H5''	1.64	0.78
33:I:58:GLN:O	33:I:62:ARG:HG2	1.83	0.78
47:W:18:GLN:HG2	47:W:19:GLU:H	1.48	0.78
53:1:2286:G:H5''	53:1:2287:A:OP1	1.84	0.77
15:p:20:ARG:HB3	15:p:21:PRO:HD2	1.66	0.77
53:1:1077:A:H2'	53:1:1078:U:H5'	1.67	0.77
36:L:3:ARG:HH12	52:3:1092:A:H5'	1.49	0.77
39:O:40:ILE:HB	39:O:73:LEU:HB3	1.66	0.77
7:h:25:ALA:HB3	7:h:85:SER:HB3	1.67	0.77
28:D:12:ARG:HE	28:D:44:VAL:HG21	1.50	0.77
52:3:1158:C:H2'	52:3:1159:U:H4'	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:34:ILE:H	8:i:34:ILE:HD12	1.49	0.77
12:m:119:LEU:HD22	53:1:2468:A:H5'	1.64	0.77
51:a:174:THR:HB	53:1:2124:G:H5''	1.67	0.77
32:H:46:LEU:HB3	32:H:49:ALA:HB3	1.68	0.76
53:1:1020:A:H1'	53:1:1021:A:OP2	1.84	0.76
29:E:3:ILE:H	29:E:3:ILE:HD12	1.51	0.76
3:d:5:LEU:HD22	3:d:10:SER:HB3	1.68	0.76
35:K:10:VAL:HB	35:K:58:HIS:HB3	1.68	0.76
42:R:6:ILE:HG13	42:R:7:ASN:H	1.51	0.76
7:h:34:THR:O	7:h:37:LYS:HG3	1.86	0.75
24:y:43:LEU:HD22	53:1:61:C:H5''	1.68	0.75
53:1:1906:G:C2'	53:1:1907:G:H5''	2.15	0.75
57:7:7:A:H3'	57:7:8:U:H5''	1.68	0.75
27:C:37:LYS:HB2	27:C:48:TYR:HE2	1.51	0.75
47:W:72:ARG:HH22	50:Z:4:LYS:HB2	1.51	0.75
15:p:102:ARG:NH2	53:1:1754:A:H4'	2.01	0.75
55:6:34:C:H2'	55:6:34:C:O2	1.86	0.75
33:I:81:LEU:HD12	33:I:88:ASN:HB3	1.69	0.74
51:a:3:LYS:HG3	53:1:2107:G:H5''	1.70	0.74
54:2:3:C:H2'	54:2:4:C:H5''	1.67	0.73
14:o:51:ALA:HB3	14:o:78:VAL:HG12	1.69	0.73
33:I:120:LYS:HG2	33:I:130:ASN:HD21	1.53	0.73
52:3:1259:C:H3'	52:3:1260:G:H5''	1.69	0.73
7:h:30:SER:H	7:h:109:LYS:HZ1	1.34	0.73
8:i:98:GLY:H	8:i:137:LEU:HD22	1.53	0.73
42:R:89:ARG:HB2	42:R:96:VAL:HG12	1.69	0.73
9:j:114:LEU:HG	9:j:118:MET:HE1	1.70	0.73
42:R:102:LYS:HG3	52:3:1226:C:N4	2.03	0.73
53:1:2391:G:H4'	53:1:2392:A:OP1	1.89	0.73
4:e:42:ALA:HB3	4:e:84:ILE:HD12	1.69	0.73
12:m:69:PRO:HA	12:m:94:ALA:HB2	1.70	0.72
8:i:104:GLN:HE22	8:i:108:ILE:HD11	1.54	0.72
58:8:358:LYS:HE3	58:8:390:ALA:HB3	1.72	0.72
13:n:2:ARG:O	13:n:2:ARG:HD3	1.88	0.72
24:y:55:THR:O	24:y:59:GLU:HG2	1.89	0.72
52:3:327:A:O2'	52:3:328:C:H4'	1.89	0.72
43:S:58:ARG:HH12	52:3:979:C:H2'	1.53	0.72
53:1:275:C:H2'	53:1:276:U:H4'	1.71	0.72
52:3:1033:G:H2'	52:3:1034:G:H5''	1.72	0.71
5:f:86:LEU:HD11	5:f:144:ALA:HA	1.71	0.71
52:3:1200:C:H5''	52:3:1201:A:H3'	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:103:ARG:HB2	33:I:170:LEU:HD11	1.73	0.71
9:j:30:THR:HG21	53:1:1012:U:O4	1.91	0.71
20:u:47:PRO:HB3	20:u:55:GLY:H	1.54	0.71
29:E:31:ILE:HD11	53:1:2391:G:H5'	1.72	0.70
36:L:26:VAL:HG22	36:L:42:VAL:HG11	1.73	0.70
55:5:75:C:C2'	55:5:76:A:H5''	2.21	0.70
46:V:16:MET:HG3	46:V:19:SER:HB2	1.71	0.70
16:q:36:GLN:NE2	53:1:1252:G:H22	1.90	0.70
53:1:2114:A:H61	53:1:2117:A:H62	1.38	0.70
45:U:5:ARG:HH21	45:U:22:ALA:HB3	1.56	0.70
34:J:87:VAL:HA	34:J:92:ARG:HA	1.73	0.70
46:V:5:ARG:NH1	52:3:636:U:H5'	2.07	0.70
8:i:33:ASN:HB2	8:i:36:GLU:HG2	1.73	0.70
52:3:1306:A:N6	52:3:1331:G:H1'	2.07	0.70
32:H:112:ALA:HB2	32:H:182:ASP:HB3	1.74	0.69
35:K:25:TYR:HB3	35:K:74:LEU:HD11	1.74	0.69
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.73	0.69
53:1:2048:G:H2'	53:1:2049:G:H5''	1.73	0.69
35:K:36:ILE:HG23	35:K:64:VAL:HG22	1.73	0.69
53:1:917:A:H5''	53:1:2268:A:H61	1.56	0.69
38:N:68:GLY:HA2	52:3:1250:A:H5'	1.74	0.69
53:1:1807:G:H2'	53:1:1808:A:H5'	1.74	0.69
34:J:108:GLY:N	52:3:9:G:H4'	2.06	0.69
33:I:104:MET:HE2	33:I:170:LEU:HD12	1.73	0.69
33:I:66:VAL:HG12	33:I:67:LEU:H	1.58	0.69
48:X:52:ASN:HD21	48:X:55:GLN:HB2	1.58	0.69
53:1:2553:G:H3'	53:1:2554:U:H5''	1.74	0.69
9:j:81:ILE:HD11	53:1:2514:U:H4'	1.74	0.69
53:1:2277:G:C2'	53:1:2278:A:H5''	2.23	0.68
53:1:2296:U:H5''	53:1:2297:A:OP1	1.92	0.68
2:c:151:THR:HB	2:c:152:PRO:HD3	1.75	0.68
52:3:1506:U:O2'	52:3:1507:A:H5'	1.92	0.68
39:O:7:ARG:HB3	39:O:101:SER:HB3	1.73	0.68
52:3:769:G:H4'	52:3:1513:A:H4'	1.74	0.68
31:G:40:ILE:H	31:G:40:ILE:HD12	1.59	0.68
33:I:49:ASP:O	33:I:52:VAL:HG22	1.93	0.68
5:f:134:GLY:HA3	5:f:140:ILE:HG21	1.74	0.68
42:R:76:ILE:HG12	42:R:80:MET:HE2	1.75	0.68
2:c:46:ARG:HB2	2:c:84:LEU:HD12	1.75	0.68
3:d:47:LYS:O	3:d:83:VAL:HB	1.93	0.68
20:u:39:ASN:ND2	20:u:62:ALA:HB3	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:T:33:ALA:HA	44:T:36:ASN:HD21	1.59	0.68
39:O:67:ILE:HG13	39:O:67:ILE:O	1.94	0.68
47:W:38:ILE:H	47:W:38:ILE:HD12	1.57	0.68
57:7:25:C:H3'	57:7:26:A:H5''	1.76	0.68
53:1:2432:A:H1'	55:6:75:C:H4'	1.74	0.67
53:1:792:A:H3'	53:1:793:A:H5'	1.77	0.67
33:I:150:LYS:HE3	33:I:155:LYS:HD2	1.75	0.67
37:M:52:GLY:HA3	37:M:56:PRO:HA	1.76	0.67
53:1:1801:A:H5''	53:1:2203:U:H2'	1.74	0.67
37:M:28:SER:HB2	37:M:58:LEU:HB2	1.76	0.67
58:8:328:ARG:HB3	58:8:341:THR:HG22	1.76	0.67
3:d:137:LYS:HG2	3:d:141:MET:HE2	1.75	0.67
34:J:119:VAL:HG11	34:J:122:VAL:HG22	1.76	0.67
14:o:12:THR:HG23	53:1:2334:U:H4'	1.75	0.67
53:1:1105:U:H2'	53:1:1106:G:H5''	1.77	0.67
6:g:23:ALA:HB1	6:g:27:ARG:HH12	1.59	0.67
8:i:11:GLN:HE22	8:i:19:PRO:HG3	1.60	0.67
8:i:20:SER:HB2	8:i:21:PRO:HD3	1.77	0.67
6:g:58:LEU:O	6:g:61:VAL:HG22	1.93	0.67
31:G:104:LYS:HD2	52:3:1073:U:H4'	1.77	0.67
53:1:572:A:H61	53:1:2029:G:H21	1.42	0.67
53:1:161:A:H3'	53:1:162:U:H5''	1.77	0.66
53:1:1110:G:H2'	53:1:1111:A:H8	1.60	0.66
32:H:192:TYR:HA	52:3:532:A:H61	1.59	0.66
4:e:63:LYS:O	54:2:42:C:H1'	1.95	0.66
4:e:48:LEU:HA	4:e:51:ASN:HD22	1.60	0.66
8:i:10:LEU:HG	8:i:11:GLN:HG2	1.77	0.66
41:Q:109:ARG:HB2	41:Q:118:VAL:HG21	1.76	0.66
2:c:59:ARG:NH1	53:1:2830:C:H3'	2.11	0.66
36:L:101:ARG:HH12	52:3:939:G:H5'	1.61	0.66
50:Z:9:GLU:HB2	50:Z:10:PRO:HD3	1.78	0.66
51:a:5:THR:HG22	51:a:8:MET:HE2	1.76	0.66
14:o:25:ARG:HE	14:o:40:ILE:HD12	1.60	0.66
52:3:484:G:C4'	52:3:485:U:H5''	2.26	0.66
9:j:90:GLU:O	9:j:93:ILE:HG22	1.96	0.66
31:G:116:LEU:HG	31:G:140:LEU:HD13	1.78	0.66
53:1:821:A:H5''	53:1:822:G:C5'	2.25	0.66
53:1:1380:G:H1'	53:1:1569:A:H61	1.60	0.66
5:f:88:LEU:H	5:f:88:LEU:HD12	1.61	0.65
52:3:150:U:H3	52:3:171:A:H62	1.44	0.65
31:G:206:ILE:H	31:G:206:ILE:HD12	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:215:G:H4'	53:1:216:A:H4'	1.79	0.65
53:1:704:G:H2'	53:1:726:G:H22	1.61	0.65
53:1:1344:U:H3'	53:1:1345:C:H5'	1.77	0.65
38:N:33:SER:HB3	38:N:36:GLN:HG2	1.78	0.65
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.77	0.65
2:c:11:MET:HG2	2:c:25:THR:HG22	1.77	0.65
2:c:194:PRO:HA	53:1:2680:U:H5'	1.77	0.65
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.61	0.65
31:G:55:GLU:HA	31:G:58:LYS:HD2	1.77	0.65
2:c:173:GLN:NE2	53:1:2772:C:H5'	2.12	0.65
23:x:7:THR:HG21	23:x:9:LYS:HE2	1.77	0.65
25:z:29:ARG:HH12	53:1:930:G:H5''	1.62	0.65
51:a:4:LEU:HA	51:a:8:MET:HE3	1.77	0.65
53:1:1053:C:C2'	53:1:1054:A:H5''	2.26	0.65
4:e:92:GLY:O	4:e:95:MET:HG2	1.96	0.64
15:p:1:SER:N	53:1:2876:G:H5'	2.12	0.64
28:D:42:LEU:HD12	53:1:126:A:H61	1.61	0.64
8:i:96:LYS:HB3	8:i:99:LYS:HZ1	1.60	0.64
43:S:7:ALA:HB1	52:3:994:A:O2'	1.96	0.64
43:S:5:MET:HB2	43:S:62:ARG:HH12	1.60	0.64
45:U:36:VAL:HG12	45:U:53:ASP:HB3	1.79	0.64
43:S:80:ARG:O	43:S:83:VAL:HG12	1.96	0.64
14:o:38:GLN:OE1	14:o:50:ALA:HB2	1.98	0.64
15:p:88:ARG:HD2	15:p:112:ARG:HH21	1.63	0.64
36:L:139:ASP:O	36:L:143:MET:HG2	1.97	0.64
8:i:78:LEU:HD11	8:i:108:ILE:HG21	1.79	0.64
44:T:68:TYR:HB2	52:3:754:C:H4'	1.78	0.64
58:8:333:PHE:CZ	58:8:336:THR:HB	2.32	0.64
54:2:88:C:H5''	54:2:89:U:OP1	1.97	0.64
57:7:62:C:H2'	57:7:63:G:H5''	1.78	0.64
34:J:161:GLU:O	34:J:164:LEU:HG	1.98	0.64
58:8:334:ARG:HG3	58:8:335:THR:H	1.61	0.64
11:l:95:LEU:HD22	11:l:100:ILE:HD11	1.79	0.64
53:1:713:G:H21	53:1:718:A:H62	1.44	0.64
23:x:7:THR:HG23	23:x:9:LYS:HG3	1.79	0.63
34:J:80:LEU:HD23	34:J:122:VAL:HG11	1.80	0.63
7:h:38:MET:HG2	8:i:117:THR:HG21	1.78	0.63
31:G:150:ILE:HD12	31:G:150:ILE:H	1.64	0.63
32:H:3:LYS:CE	52:3:1191:A:H5''	2.27	0.63
2:c:150:GLN:NE2	53:1:574:A:H2	1.97	0.63
29:E:61:LEU:HD12	29:E:61:LEU:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1346:A:H2'	52:3:1347:G:H4'	1.79	0.63
49:Y:56:ILE:H	49:Y:56:ILE:HD12	1.62	0.63
2:c:13:ARG:HH11	15:p:55:HIS:HA	1.64	0.63
3:d:18:THR:HG23	3:d:19:PHE:HD1	1.64	0.63
7:h:118:ILE:CB	7:h:119:PRO:HD3	2.28	0.63
12:m:5:LYS:HB2	12:m:6:ARG:HH11	1.62	0.63
18:s:6:LYS:HG2	53:1:494:G:H4'	1.79	0.63
30:F:1:MET:HE2	30:F:36:ARG:HB3	1.80	0.63
40:P:126:ARG:HH12	52:3:796:C:H4'	1.63	0.63
48:X:2:ARG:HG2	52:3:1312:G:N7	2.14	0.63
53:1:310:A:C2'	53:1:311:A:H5''	2.28	0.63
19:t:88:LYS:HG2	19:t:89:GLU:H	1.64	0.63
32:H:171:ARG:HG2	32:H:173:PRO:HD3	1.80	0.63
1:b:134:ILE:HD11	1:b:191:LEU:HD21	1.81	0.63
12:m:5:LYS:C	12:m:6:ARG:HD3	2.23	0.63
13:n:24:MET:HE2	13:n:44:LEU:HD13	1.79	0.63
40:P:28:ASN:HD21	40:P:30:ILE:HB	1.64	0.63
17:r:80:ARG:NH1	53:1:571:U:H2'	2.13	0.63
29:E:61:LEU:HD13	29:E:64:ALA:HB3	1.81	0.63
51:a:64:VAL:HG22	51:a:160:GLN:HB2	1.80	0.63
3:d:71:GLY:N	53:1:674:G:H5''	2.14	0.62
38:N:89:TYR:HB3	38:N:93:LEU:HD12	1.80	0.62
2:c:46:ARG:HG3	2:c:84:LEU:HB2	1.82	0.62
24:y:21:LEU:HA	24:y:25:GLN:HB3	1.80	0.62
53:1:121:G:H4'	53:1:149:A:H5'	1.81	0.62
53:1:2423:U:O2'	53:1:2425:A:H2'	1.99	0.62
52:3:1201:A:H1'	52:3:1202:U:OP2	1.99	0.62
15:p:48:ALA:HB3	15:p:59:THR:HG22	1.82	0.62
48:X:17:LYS:HE3	48:X:30:LEU:HD21	1.81	0.62
49:Y:55:PRO:HG2	49:Y:56:ILE:HD12	1.80	0.62
19:t:48:GLN:HE22	19:t:54:GLU:HA	1.65	0.62
22:w:38:GLY:HA2	53:1:2330:G:H21	1.64	0.62
42:R:56:ARG:O	42:R:59:VAL:HG12	1.99	0.62
8:i:89:SER:HB2	8:i:92:PRO:HG3	1.82	0.62
36:L:142:ARG:CD	55:6:41:C:H4'	2.28	0.62
54:2:3:C:C2'	54:2:4:C:H5''	2.29	0.62
10:k:30:ARG:HG3	53:1:2674:G:H4'	1.82	0.62
28:D:24:THR:HG23	28:D:27:GLY:H	1.65	0.62
53:1:704:G:H2'	53:1:726:G:N2	2.15	0.62
53:1:2086:U:H2'	53:1:2087:G:C8	2.35	0.62
7:h:33:VAL:HA	53:1:1055:G:H4'	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:186:GLU:HB3	33:I:189:ASP:HB2	1.81	0.61
48:X:5:LYS:HG3	48:X:6:LYS:HG2	1.81	0.61
1:b:145:MET:SD	1:b:146:LYS:HG2	2.40	0.61
13:n:28:LEU:HD13	13:n:34:ILE:HG12	1.82	0.61
15:p:113:LEU:O	15:p:113:LEU:HD12	2.00	0.61
18:s:73:LYS:HB2	18:s:106:VAL:HB	1.82	0.61
32:H:50:SER:HB2	32:H:114:LEU:HD11	1.82	0.61
7:h:23:LEU:HD12	7:h:118:ILE:HD11	1.83	0.61
16:q:90:ASP:OD1	53:1:996:A:H4'	1.99	0.61
31:G:103:TRP:HA	31:G:106:VAL:HG12	1.82	0.61
49:Y:69:ASN:HB2	52:3:262:A:H4'	1.83	0.61
53:1:2048:G:C3'	53:1:2049:G:H5''	2.29	0.61
58:8:311:ILE:N	58:8:311:ILE:HD12	2.15	0.61
39:O:23:ALA:O	39:O:27:GLU:HG2	2.00	0.61
53:1:962:G:H21	53:1:2250:G:H1	1.46	0.61
53:1:2452:C:H42	53:1:2504:U:H3	1.48	0.61
5:f:175:LYS:HD2	5:f:176:LYS:HE3	1.83	0.61
9:j:6:ALA:H	9:j:45:THR:HG21	1.64	0.61
9:j:118:MET:HA	9:j:121:LYS:NZ	2.15	0.61
41:Q:35:ARG:HH21	41:Q:53:ARG:HG3	1.65	0.61
57:7:7:A:H3'	57:7:8:U:C5'	2.30	0.61
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.01	0.61
31:G:46:VAL:HG23	31:G:47:PRO:HD3	1.82	0.61
7:h:33:VAL:HG23	7:h:35:VAL:HG12	1.83	0.61
33:I:131:ILE:HG12	52:3:620:C:C2	2.35	0.61
52:3:1218:C:H2'	52:3:1219:A:C8	2.36	0.61
16:q:96:ASP:O	16:q:99:VAL:HG12	2.01	0.61
20:u:39:ASN:HD22	20:u:62:ALA:HB3	1.66	0.61
34:J:59:ILE:HG22	34:J:63:MET:HE1	1.82	0.61
42:R:65:GLU:HG2	42:R:66:GLY:H	1.66	0.61
53:1:615:U:H5''	53:1:616:A:OP2	2.01	0.61
57:7:45:U:H3'	57:7:46:G:H5''	1.82	0.61
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.82	0.60
14:o:26:LEU:HD13	14:o:39:VAL:HG22	1.83	0.60
41:Q:27:PRO:HB2	41:Q:28:GLN:OE1	2.00	0.60
52:3:211:G:H2'	52:3:212:G:H5'	1.82	0.60
11:l:93:ASN:O	11:l:94:THR:OG1	2.17	0.60
18:s:4:ILE:HG22	18:s:106:VAL:HG22	1.83	0.60
42:R:67:ASP:O	42:R:71:GLU:HG3	2.01	0.60
53:1:1872:A:H2'	53:1:1873:G:O4'	2.01	0.60
6:g:128:HIS:HB2	6:g:144:VAL:HG23	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:6:THR:HG23	53:1:1666:G:H4'	1.81	0.60
32:H:4:VAL:HG22	32:H:5:HIS:H	1.66	0.60
36:L:19:SER:HB2	36:L:22:LEU:HD13	1.83	0.60
17:r:78:ARG:HH12	53:1:990:A:H61	1.47	0.60
37:M:79:ARG:HG3	37:M:82:LEU:HB3	1.84	0.60
45:U:6:LEU:HD22	45:U:17:TYR:HB3	1.83	0.60
49:Y:43:LYS:HD2	49:Y:86:ALA:HB2	1.82	0.60
21:v:75:GLN:HB2	21:v:92:VAL:HG23	1.82	0.60
21:v:78:GLN:HE22	54:2:76:G:H1'	1.66	0.60
47:W:18:GLN:HG2	47:W:19:GLU:N	2.16	0.60
52:3:673:A:H2'	52:3:674:G:C8	2.37	0.60
15:p:29:VAL:HG13	15:p:79:VAL:HG22	1.82	0.60
52:3:1391:U:H2'	52:3:1392:G:C8	2.36	0.60
6:g:112:LYS:O	6:g:115:VAL:HG22	2.02	0.60
27:C:39:ASP:OD1	27:C:41:VAL:HG22	2.01	0.60
35:K:6:ILE:H	35:K:6:ILE:HD12	1.67	0.60
2:c:157:LYS:HA	53:1:2619:C:H5''	1.83	0.60
4:e:130:GLY:HA3	53:1:2305:U:H5''	1.82	0.60
4:e:140:ILE:HG13	4:e:142:TYR:H	1.65	0.60
40:P:118:ASN:HD22	52:3:717:U:H4'	1.67	0.60
50:Z:22:CYS:SG	50:Z:23:GLU:N	2.73	0.60
53:1:2048:G:C2'	53:1:2049:G:H5''	2.32	0.60
1:b:216:ARG:NH2	53:1:690:G:O3'	2.35	0.60
7:h:108:VAL:HG23	7:h:109:LYS:H	1.66	0.60
1:b:27:LYS:HD3	1:b:28:PRO:HD2	1.83	0.59
1:b:239:PHE:HB3	53:1:1903:G:OP1	2.00	0.59
39:O:57:VAL:HG22	39:O:58:ASN:N	2.12	0.59
53:1:2834:G:H2'	53:1:2879:A:H61	1.67	0.59
3:d:63:LYS:HD2	53:1:2444:G:OP2	2.02	0.59
11:l:22:GLY:HA2	53:1:811:U:H3'	1.84	0.59
23:x:13:THR:HG21	53:1:188:G:H5'	1.82	0.59
32:H:4:VAL:HG22	32:H:5:HIS:N	2.17	0.59
37:M:10:LEU:HD22	37:M:74:ILE:HD11	1.84	0.59
43:S:25:GLU:HA	43:S:28:ALA:HB3	1.84	0.59
50:Z:16:ARG:NH2	50:Z:19:LYS:HG2	2.17	0.59
53:1:528:A:N1	53:1:2042:A:H2'	2.17	0.59
14:o:108:ASP:HA	14:o:111:ARG:HD2	1.83	0.59
20:u:48:VAL:HG22	20:u:50:ALA:H	1.68	0.59
28:D:14:ARG:HD2	53:1:771:G:OP1	2.02	0.59
52:3:1512:U:H2'	52:3:1513:A:C8	2.37	0.59
53:1:2475:C:H42	53:1:2529:G:H22	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M:4:ASP:HB2	37:M:80:PRO:HG3	1.84	0.59
41:Q:66:ILE:HD12	41:Q:66:ILE:H	1.68	0.59
53:1:669:G:H2'	53:1:669:G:N3	2.18	0.59
53:1:796:C:H2'	53:1:797:G:C8	2.38	0.59
53:1:1133:A:H4'	53:1:1134:A:H5''	1.84	0.59
53:1:2432:A:H1'	55:6:75:C:C4'	2.32	0.59
4:e:107:VAL:HB	4:e:108:PRO:HD3	1.85	0.59
34:J:100:GLU:H	34:J:121:ASN:ND2	2.00	0.59
41:Q:74:GLN:HG2	41:Q:74:GLN:O	2.01	0.59
31:G:72:LYS:HG3	31:G:74:ALA:H	1.68	0.59
53:1:2128:G:H1'	53:1:2173:A:N3	2.18	0.59
1:b:19:VAL:HG12	1:b:21:PRO:HD3	1.84	0.59
53:1:1077:A:C2'	53:1:1078:U:H5'	2.32	0.59
53:1:1278:C:H2'	53:1:1279:G:H8	1.67	0.59
2:c:157:LYS:HG2	9:j:80:HIS:CE1	2.38	0.59
10:k:76:VAL:H	15:p:72:VAL:HG12	1.68	0.59
53:1:1186:G:H2'	53:1:1187:G:O4'	2.03	0.59
53:1:2287:A:O2'	53:1:2288:A:H2'	2.02	0.59
4:e:64:PRO:HA	4:e:88:VAL:HG22	1.85	0.58
8:i:101:SER:HA	8:i:140:GLU:O	2.03	0.58
14:o:49:VAL:HG22	14:o:85:LYS:HG3	1.85	0.58
24:y:43:LEU:HD22	53:1:61:C:C5'	2.32	0.58
38:N:105:ARG:O	38:N:105:ARG:HD3	2.03	0.58
43:S:17:ASP:C	43:S:22:LYS:HZ1	2.11	0.58
51:a:181:ASP:HB2	51:a:184:LYS:HE2	1.85	0.58
12:m:42:THR:HG22	12:m:93:VAL:HG12	1.86	0.58
22:w:27:VAL:HG21	22:w:78:ILE:HD13	1.84	0.58
42:R:25:GLY:N	52:3:1329:A:H5''	2.17	0.58
53:1:293:U:H2'	53:1:294:A:H5''	1.85	0.58
6:g:37:VAL:HG11	6:g:51:ARG:HH12	1.68	0.58
33:I:94:GLU:HG3	33:I:185:PRO:HG2	1.83	0.58
38:N:98:ARG:HA	38:N:103:VAL:HG11	1.85	0.58
38:N:119:LYS:HG3	52:3:1349:A:OP1	2.01	0.58
53:1:542:C:C2'	53:1:543:G:H5''	2.30	0.58
36:L:49:LEU:HD21	36:L:60:ALA:HB3	1.83	0.58
37:M:28:SER:HB3	37:M:56:PRO:HB2	1.83	0.58
42:R:88:LEU:HA	42:R:91:ARG:HE	1.68	0.58
43:S:92:ILE:H	43:S:92:ILE:HD12	1.67	0.58
52:3:29:U:O2'	52:3:30:U:H5'	2.03	0.58
52:3:65:A:H4'	52:3:66:A:H5''	1.86	0.58
52:3:1271:A:H5'	52:3:1314:C:H5''	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:940:G:H2'	53:1:941:A:H5''	1.85	0.58
3:d:47:LYS:HB3	3:d:51:GLU:HB2	1.85	0.58
4:e:41:GLU:HB2	4:e:48:LEU:HD23	1.84	0.58
38:N:4:GLN:HG3	38:N:21:LYS:HG2	1.85	0.58
53:1:1837:C:H2'	53:1:1899:A:H61	1.69	0.58
12:m:4:PRO:HG3	12:m:68:PHE:CE2	2.39	0.58
21:v:30:ILE:HD11	21:v:38:LEU:HB3	1.86	0.58
31:G:66:ILE:HA	31:G:159:ALA:HB3	1.86	0.58
33:I:8:LEU:HA	33:I:20:LEU:HD11	1.86	0.58
52:3:70:U:H5''	52:3:71:A:OP1	2.03	0.58
53:1:1105:U:C2'	53:1:1106:G:H5''	2.34	0.58
53:1:2427:C:H5''	53:1:2429:G:H5'	1.85	0.58
5:f:127:GLN:HG3	5:f:128:THR:HG23	1.85	0.58
27:C:32:LYS:HE3	27:C:50:GLU:H	1.69	0.58
33:I:167:PRO:HB2	33:I:170:LEU:HD21	1.86	0.58
52:3:291:U:H2'	52:3:292:G:H8	1.69	0.58
52:3:452:A:H61	52:3:480:U:H3	1.52	0.58
53:1:45:G:C5'	53:1:46:G:H5'	2.17	0.58
3:d:119:ILE:HB	3:d:187:VAL:HG12	1.86	0.58
3:d:194:LYS:O	3:d:197:GLU:HG3	2.03	0.58
34:J:153:ALA:HB2	34:J:163:ILE:HD13	1.86	0.58
39:O:53:ILE:HG22	52:3:1060:U:H5'	1.86	0.58
52:3:1005:A:H2'	52:3:1006:G:O4'	2.04	0.58
53:1:511:U:H2'	53:1:512:G:H5'	1.86	0.58
1:b:164:VAL:HG11	1:b:180:MET:HE1	1.86	0.57
2:c:59:ARG:HH11	53:1:2830:C:H3'	1.68	0.57
2:c:136:ASN:HD21	2:c:139:SER:C	2.11	0.57
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.85	0.57
27:C:37:LYS:HG2	53:1:2345:G:OP2	2.04	0.57
36:L:115:MET:HA	36:L:118:ARG:HE	1.69	0.57
46:V:13:SER:HB3	46:V:21:VAL:CG1	2.34	0.57
46:V:18:LYS:HZ2	46:V:49:ASN:H	1.51	0.57
55:5:6:G:O2'	55:5:7:G:H5'	2.03	0.57
57:7:6:G:H2'	57:7:7:A:H5''	1.86	0.57
36:L:24:LYS:HE2	52:3:1375:A:H5''	1.86	0.57
37:M:82:LEU:HG	37:M:84:ILE:HD11	1.84	0.57
49:Y:80:ALA:HA	49:Y:83:ASN:HD21	1.67	0.57
52:3:536:C:H2'	52:3:537:G:C8	2.39	0.57
53:1:2389:G:H5''	53:1:2390:U:O4'	2.04	0.57
53:1:2533:U:H2'	53:1:2534:A:O4'	2.04	0.57
4:e:3:LEU:HA	4:e:6:TYR:HB3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M:73:SER:H	37:M:129:ALA:HB3	1.69	0.57
53:1:729:G:H4'	53:1:763:G:H5'	1.85	0.57
53:1:1367:A:H2'	53:1:1368:G:H5'	1.85	0.57
53:1:1078:U:H5''	53:1:1079:C:H5''	1.87	0.57
53:1:2795:C:H2'	53:1:2796:U:O4'	2.04	0.57
53:1:310:A:O2'	53:1:311:A:H5''	2.05	0.57
53:1:1049:C:H41	53:1:1110:G:H21	1.52	0.57
18:s:2:GLU:HG3	18:s:4:ILE:HG23	1.86	0.57
23:x:61:LYS:HE3	53:1:372:G:OP2	2.05	0.57
50:Z:8:ASN:HB3	50:Z:9:GLU:OE1	2.04	0.57
7:h:1:MET:HE3	7:h:2:ALA:H	1.69	0.57
11:l:54:GLN:HE21	53:1:825:A:H1'	1.70	0.57
20:u:85:ARG:HD3	20:u:87:GLU:HG3	1.86	0.57
52:3:410:G:H2'	52:3:429:U:C4	2.39	0.57
52:3:1346:A:C2'	52:3:1347:G:H4'	2.34	0.57
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.85	0.57
11:l:23:ILE:HG13	17:r:82:HIS:CE1	2.40	0.57
13:n:92:GLY:O	53:1:2880:C:H1'	2.04	0.57
14:o:53:THR:HG21	14:o:65:THR:HB	1.87	0.57
16:q:94:LEU:O	16:q:97:ILE:HG22	2.04	0.57
32:H:141:MET:HE2	32:H:169:GLU:HG3	1.87	0.57
36:L:28:ILE:HD11	36:L:100:MET:HG2	1.86	0.57
51:a:26:ALA:HB1	51:a:214:ILE:HD11	1.87	0.57
53:1:1415:U:H2'	53:1:1416:G:H4'	1.86	0.57
7:h:27:VAL:CG1	7:h:83:ALA:HB3	2.35	0.57
8:i:96:LYS:HB3	8:i:99:LYS:NZ	2.19	0.57
10:k:99:ILE:HD13	10:k:115:ILE:HG23	1.85	0.57
43:S:3:GLN:OE1	52:3:1047:G:H5''	2.05	0.57
52:3:955:U:H3	52:3:1225:A:H61	1.53	0.57
53:1:503:A:H4'	53:1:505:A:H5''	1.86	0.57
53:1:581:C:H2'	53:1:582:A:C8	2.39	0.57
31:G:165:ALA:HB3	31:G:190:SER:HB2	1.87	0.57
42:R:53:ASP:HA	42:R:56:ARG:HH11	1.70	0.57
48:X:15:LEU:O	48:X:18:VAL:HG12	2.05	0.57
50:Z:34:ARG:HG3	50:Z:36:PHE:CE2	2.40	0.57
53:1:1026:G:H2'	53:1:1027:A:H8	1.69	0.57
53:1:1141:U:H4'	53:1:1142:A:O4'	2.05	0.57
57:7:62:C:C3'	57:7:63:G:H5''	2.34	0.57
1:b:233:GLY:HA3	53:1:2598:A:H5''	1.87	0.56
15:p:29:VAL:CG1	15:p:79:VAL:HG22	2.35	0.56
40:P:88:PRO:HG2	40:P:89:GLY:H	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:33:CYS:H	41:Q:54:VAL:HG23	1.70	0.56
53:1:577:G:OP1	53:1:2502:G:H2'	2.05	0.56
5:f:117:PRO:HD2	5:f:120:ILE:HG13	1.86	0.56
7:h:28:ALA:H	7:h:110:ALA:HA	1.68	0.56
9:j:88:THR:HG22	9:j:90:GLU:H	1.70	0.56
25:z:4:ILE:HD11	25:z:56:VAL:HG23	1.87	0.56
34:J:35:LEU:HD22	34:J:133:ILE:HD13	1.86	0.56
1:b:224:MET:HE2	53:1:782:A:C6	2.40	0.56
8:i:123:ALA:HB1	53:1:1081:U:H4'	1.86	0.56
13:n:73:ASN:HA	13:n:76:VAL:HG12	1.87	0.56
31:G:158:ASP:O	31:G:181:PRO:HG2	2.05	0.56
35:K:23:GLU:HA	35:K:26:THR:HG22	1.87	0.56
36:L:11:ILE:H	36:L:11:ILE:HD12	1.69	0.56
43:S:25:GLU:HB2	43:S:29:ILE:HG12	1.87	0.56
45:U:54:LEU:HB2	45:U:80:LYS:NZ	2.20	0.56
53:1:49:A:H5'	53:1:51:G:O4'	2.06	0.56
53:1:1900:A:H1'	53:1:1970:A:H2'	1.87	0.56
53:1:2682:A:H61	53:1:2728:U:H1'	1.70	0.56
54:2:3:C:C3'	54:2:4:C:H5''	2.36	0.56
7:h:55:VAL:HA	53:1:1084:A:H5''	1.87	0.56
9:j:24:THR:HB	9:j:27:ARG:HB2	1.86	0.56
13:n:53:THR:HA	13:n:56:LYS:HE2	1.86	0.56
20:u:90:LYS:NZ	53:1:101:A:H62	2.03	0.56
31:G:27:LYS:O	31:G:30:ILE:HG22	2.04	0.56
35:K:3:HIS:H	35:K:92:THR:HG22	1.70	0.56
43:S:39:ASP:HA	43:S:42:ASN:HD22	1.70	0.56
52:3:1219:A:H2'	52:3:1220:G:C8	2.40	0.56
53:1:1111:A:H2'	53:1:1111:A:N3	2.20	0.56
4:e:89:THR:HG23	54:2:43:C:O2	2.05	0.56
27:C:29:LYS:HE3	53:1:2286:G:H3'	1.86	0.56
28:D:11:LYS:CE	53:1:686:U:H5''	2.34	0.56
43:S:50:LEU:HD12	43:S:51:PRO:HD2	1.86	0.56
53:1:226:A:H2'	53:1:227:A:O4'	2.05	0.56
11:l:74:THR:HG22	11:l:107:PHE:HB2	1.87	0.56
18:s:6:LYS:CG	53:1:494:G:H4'	2.36	0.56
52:3:225:C:H2'	52:3:226:G:H5''	1.88	0.56
53:1:310:A:H2'	53:1:311:A:H5''	1.86	0.56
53:1:2229:U:H2'	53:1:2230:G:H8	1.70	0.56
53:1:2480:C:H2'	53:1:2481:G:O4'	2.06	0.56
1:b:180:MET:HB2	1:b:267:VAL:HB	1.87	0.56
15:p:25:VAL:HG23	15:p:84:SER:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:91:LYS:HE2	53:1:297:G:H5'	1.88	0.56
35:K:12:PRO:O	35:K:15:SER:HB3	2.05	0.56
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.71	0.56
1:b:149:LYS:HD3	53:1:2204:G:H4'	1.87	0.56
22:w:58:LYS:HE3	53:1:2366:A:H4'	1.87	0.56
31:G:180:ILE:HD12	31:G:181:PRO:HD2	1.88	0.56
42:R:6:ILE:HG13	42:R:7:ASN:N	2.19	0.56
50:Z:35:GLU:O	50:Z:36:PHE:HB2	2.04	0.56
8:i:27:LEU:HD23	8:i:27:LEU:H	1.71	0.56
15:p:28:LYS:HG2	15:p:82:SER:HB3	1.88	0.56
23:x:34:SER:HA	23:x:49:ARG:HA	1.87	0.56
53:1:991:C:H5'	53:1:1185:G:H2'	1.86	0.56
53:1:1674:G:H21	53:1:1677:A:H61	1.54	0.56
53:1:1810:A:H2'	53:1:1811:G:O4'	2.05	0.56
5:f:19:ASN:HB2	5:f:22:VAL:HB	1.88	0.56
48:X:28:LYS:HD3	48:X:28:LYS:H	1.71	0.56
53:1:2350:C:H2'	53:1:2351:G:O4'	2.06	0.56
57:7:45:U:H3'	57:7:46:G:C5'	2.36	0.56
6:g:5:LEU:HD22	6:g:13:GLY:HA2	1.89	0.55
7:h:67:THR:OG1	7:h:68:PRO:HD3	2.05	0.55
38:N:114:LYS:HE2	52:3:1187:G:H5'	1.89	0.55
49:Y:67:HIS:HB3	52:3:262:A:H5'	1.87	0.55
52:3:211:G:C2'	52:3:212:G:H5'	2.37	0.55
52:3:370:C:H2'	52:3:371:A:C8	2.41	0.55
55:5:75:C:C3'	55:5:76:A:H5''	2.36	0.55
57:7:18:G:N2	57:7:57:G:H2'	2.21	0.55
7:h:56:ARG:HB2	53:1:1084:A:O4'	2.07	0.55
23:x:30:PRO:HG2	23:x:32:LEU:HG	1.88	0.55
32:H:107:LYS:HD2	32:H:110:LEU:HD12	1.88	0.55
50:Z:44:ARG:HD2	50:Z:45:LYS:N	2.20	0.55
50:Z:50:SER:HA	50:Z:53:LYS:HB2	1.89	0.55
52:3:291:U:H2'	52:3:292:G:C8	2.41	0.55
53:1:1138:G:H2'	53:1:1139:G:O4'	2.07	0.55
53:1:2514:U:H2'	53:1:2515:C:C6	2.41	0.55
4:e:73:VAL:HG12	4:e:75:GLY:H	1.70	0.55
17:r:68:ARG:HH11	17:r:90:ARG:HB2	1.72	0.55
31:G:27:LYS:N	31:G:28:PRO:CD	2.69	0.55
52:3:346:G:C2'	52:3:347:G:H5'	2.36	0.55
52:3:1280:A:O2'	52:3:1281:C:H5'	2.06	0.55
53:1:2547:A:H2'	53:1:2548:U:C6	2.42	0.55
57:7:6:G:C3'	57:7:7:A:H5''	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:621:A:H2'	53:1:622:G:H5'	1.88	0.55
53:1:2756:U:H4'	53:1:2757:A:OP1	2.06	0.55
20:u:93:ARG:HB2	20:u:102:ILE:HD12	1.88	0.55
22:w:33:ILE:HG22	22:w:34:VAL:HG23	1.88	0.55
25:z:45:GLY:HA3	53:1:852:U:H5'	1.89	0.55
9:j:81:ILE:HG23	9:j:82:GLY:N	2.21	0.55
36:L:24:LYS:HA	36:L:27:ASN:HD22	1.69	0.55
53:1:1278:C:H2'	53:1:1279:G:C8	2.42	0.55
55:6:17:C:H5''	55:6:17(A):U:OP2	2.06	0.55
58:8:327:TYR:O	58:8:342:ILE:HG12	2.07	0.55
1:b:255:LYS:HZ2	53:1:1844:C:H4'	1.72	0.55
7:h:61:ARG:HB3	53:1:1046:A:H4'	1.89	0.55
20:u:73:ASN:HD22	20:u:80:ASP:HB2	1.72	0.55
32:H:1:GLY:H2	52:3:1060:U:H5	1.55	0.55
38:N:62:LEU:HB3	38:N:64:ILE:HD11	1.89	0.55
53:1:2277:G:C3'	53:1:2278:A:H5''	2.36	0.55
1:b:42:ARG:HE	53:1:691:C:H1'	1.70	0.55
2:c:51:THR:HB	2:c:79:LEU:HD23	1.89	0.55
3:d:68:ALA:HA	53:1:1255:U:C6	2.42	0.55
12:m:10:ARG:NH2	55:5:64:G:H4'	2.22	0.55
31:G:22:TRP:HZ2	52:3:829:G:H4'	1.72	0.55
31:G:138:ARG:HH12	52:3:1097:C:H5''	1.70	0.55
32:H:1:GLY:N	52:3:1060:U:H5	2.04	0.55
45:U:18:GLN:HA	45:U:38:PHE:HA	1.87	0.55
52:3:715:A:H2'	52:3:716:A:C8	2.41	0.55
53:1:1322:A:H61	53:1:1333:G:H21	1.53	0.55
1:b:116:GLN:HG3	1:b:121:ALA:HB2	1.88	0.55
1:b:220:ARG:HD2	53:1:1827:U:OP2	2.07	0.55
3:d:148:ILE:HB	3:d:169:VAL:HA	1.89	0.55
16:q:14:LYS:HE3	16:q:18:LYS:HZ2	1.72	0.55
31:G:79:VAL:HG12	31:G:90:PHE:HB2	1.89	0.55
31:G:217:ALA:HB1	31:G:221:ARG:HH12	1.72	0.55
32:H:64:ARG:HG3	32:H:99:GLN:O	2.06	0.55
35:K:3:HIS:HB2	35:K:92:THR:HA	1.88	0.55
35:K:17:GLN:O	35:K:17:GLN:HG2	2.06	0.55
58:8:329:PRO:O	58:8:339:THR:HG23	2.07	0.55
2:c:25:THR:HG21	2:c:193:VAL:HG22	1.88	0.54
7:h:118:ILE:HB	7:h:119:PRO:CD	2.32	0.54
42:R:22:TYR:CE1	52:3:1330:U:H4'	2.42	0.54
48:X:54:ARG:HG3	48:X:55:GLN:HG2	1.88	0.54
8:i:8:VAL:HG22	8:i:10:LEU:HD22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:92:PRO:HD2	53:1:1076:C:H1'	1.89	0.54
13:n:85:PRO:HA	13:n:88:ALA:HB2	1.90	0.54
31:G:66:ILE:N	31:G:66:ILE:HD12	2.22	0.54
15:p:102:ARG:HH21	53:1:1754:A:H4'	1.72	0.54
45:U:33:ILE:H	45:U:33:ILE:HD12	1.72	0.54
52:3:1346:A:H2'	52:3:1346:A:N3	2.22	0.54
52:3:1493:A:H4'	56:4:19:U:O2'	2.08	0.54
10:k:30:ARG:HH22	10:k:37:ASP:CG	2.15	0.54
10:k:109:SER:O	10:k:110:GLU:HG2	2.07	0.54
13:n:100:CYS:SG	13:n:101:GLY:N	2.81	0.54
32:H:174:LEU:HA	32:H:181:ILE:HD11	1.87	0.54
34:J:15:ILE:HD11	34:J:37:VAL:HG22	1.90	0.54
35:K:86:ARG:NH1	52:3:673:A:H4'	2.22	0.54
46:V:64:ARG:O	46:V:66:LEU:HD12	2.07	0.54
1:b:257:ARG:NH1	1:b:259:ASN:HD22	2.05	0.54
40:P:54:SER:OG	52:3:694:A:H5''	2.08	0.54
46:V:18:LYS:NZ	46:V:49:ASN:H	2.05	0.54
46:V:22:VAL:HG22	46:V:23:ALA:H	1.73	0.54
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.90	0.54
53:1:473:G:O2'	53:1:474:G:H5'	2.07	0.54
5:f:85:LYS:HG3	5:f:131:VAL:HG13	1.90	0.54
33:I:169:TRP:CG	33:I:185:PRO:HG3	2.42	0.54
34:J:14:LEU:HD11	34:J:17:VAL:HG23	1.89	0.54
40:P:124:LYS:HG2	50:Z:34:ARG:CZ	2.38	0.54
52:3:1219:A:H2'	52:3:1220:G:H8	1.73	0.54
53:1:613:A:H2'	53:1:613:A:N3	2.23	0.54
53:1:1373:A:H5'	53:1:2212:A:H1'	1.89	0.54
57:7:62:C:C2'	57:7:63:G:H5''	2.37	0.54
1:b:7:PRO:O	53:1:1695:G:H1'	2.07	0.54
12:m:57:VAL:HG12	12:m:112:LEU:HG	1.90	0.54
35:K:36:ILE:N	35:K:36:ILE:HD12	2.23	0.54
39:O:11:LYS:HZ2	39:O:71:LEU:HD13	1.73	0.54
50:Z:49:ALA:O	50:Z:53:LYS:HG3	2.08	0.54
53:1:1306:C:H41	53:1:1606:C:H2'	1.73	0.54
53:1:2112:G:H2'	53:1:2113:U:H5'	1.89	0.54
22:w:33:ILE:HD11	22:w:78:ILE:HD11	1.88	0.54
30:F:6:SER:OG	53:1:2466:C:H5''	2.07	0.54
31:G:150:ILE:HD12	31:G:150:ILE:N	2.23	0.54
33:I:27:ILE:HG13	33:I:29:THR:HG23	1.90	0.54
52:3:1402:C:H2'	52:3:1403:C:O4'	2.08	0.54
17:r:34:GLU:HG2	17:r:60:LYS:HG2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:2:VAL:HG23	45:U:65:ALA:HA	1.88	0.54
49:Y:8:LYS:HD2	52:3:103:U:OP2	2.07	0.54
49:Y:26:MET:O	49:Y:29:THR:HG22	2.08	0.54
52:3:784:A:H2'	52:3:785:G:C8	2.42	0.54
53:1:69:C:O2'	53:1:70:G:H5'	2.08	0.54
41:Q:113:ARG:HB2	41:Q:118:VAL:O	2.08	0.53
44:T:42:PHE:HE1	44:T:48:ASP:HB3	1.73	0.53
52:3:514:C:H2'	52:3:515:G:C8	2.44	0.53
53:1:479:A:H4'	53:1:480:A:H5'	1.90	0.53
53:1:1251:C:O2'	53:1:1252:G:H3'	2.08	0.53
53:1:1796:U:H2'	53:1:1797:G:H8	1.72	0.53
53:1:2286:G:H4'	53:1:2287:A:O5'	2.08	0.53
16:q:15:LYS:HA	16:q:18:LYS:HE2	1.88	0.53
16:q:51:GLN:NE2	16:q:55:GLN:HB2	2.23	0.53
35:K:18:VAL:HG12	35:K:19:PRO:HD3	1.88	0.53
40:P:49:SER:HA	40:P:68:ARG:HH11	1.73	0.53
53:1:807:U:H2'	53:1:808:G:C8	2.43	0.53
53:1:1285:A:H2'	53:1:1286:A:H5'	1.89	0.53
53:1:1874:C:H2'	53:1:1875:G:O4'	2.08	0.53
10:k:49:ARG:NH2	52:3:1422:G:H4'	2.23	0.53
12:m:34:LYS:HD3	21:v:81:PRO:O	2.08	0.53
15:p:112:ARG:O	15:p:113:LEU:HG	2.08	0.53
16:q:36:GLN:HE21	53:1:1252:G:H1	1.56	0.53
43:S:5:MET:CB	43:S:62:ARG:HH12	2.19	0.53
44:T:33:ALA:HA	44:T:36:ASN:ND2	2.23	0.53
53:1:340:A:H2'	53:1:341:C:O4'	2.08	0.53
53:1:2134:A:C6	53:1:2157:G:H4'	2.43	0.53
53:1:2743:U:C3'	53:1:2744:G:H5''	2.39	0.53
54:2:78:A:H62	54:2:98:G:H21	1.54	0.53
1:b:83:ASP:OD1	1:b:86:ARG:HD2	2.09	0.53
4:e:111:ARG:HD2	42:R:5:GLY:O	2.07	0.53
58:8:314:LYS:HE2	58:8:319:ARG:HA	1.90	0.53
1:b:47:ARG:HH21	53:1:774:G:H5''	1.74	0.53
3:d:50:ALA:HB2	53:1:801:G:C8	2.43	0.53
4:e:25:MET:HE3	54:2:57:A:N6	2.24	0.53
12:m:86:LYS:HE3	53:1:955:U:H5''	1.91	0.53
32:H:4:VAL:O	32:H:6:PRO:HD3	2.07	0.53
32:H:122:GLN:HG2	32:H:127:VAL:HG21	1.90	0.53
45:U:72:ALA:HA	45:U:75:ILE:HD12	1.90	0.53
51:a:51:ASP:OD2	51:a:54:LYS:HG3	2.09	0.53
52:3:346:G:H2'	52:3:347:G:H5'	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:794:A:H2'	53:1:795:C:C6	2.43	0.53
55:5:76:A:H5'	55:5:76:A:C8	2.43	0.53
11:l:16:GLY:HA2	53:1:662:G:H4'	1.91	0.53
49:Y:56:ILE:O	49:Y:60:GLN:NE2	2.41	0.53
52:3:620:C:H2'	52:3:621:A:O4'	2.09	0.53
53:1:974:G:H1'	53:1:975:A:C8	2.43	0.53
53:1:1854:A:N6	53:1:1888:G:H1'	2.24	0.53
53:1:1991:U:H2'	53:1:1992:G:H5''	1.91	0.53
52:3:70:U:H2'	52:3:94:G:O6	2.09	0.53
53:1:215:G:C4'	53:1:216:A:H4'	2.39	0.53
53:1:1856:U:H2'	53:1:1857:G:O4'	2.09	0.53
2:c:173:GLN:HE21	53:1:2772:C:H5'	1.73	0.53
10:k:41:ILE:HD11	10:k:86:LEU:HD22	1.89	0.53
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.90	0.53
25:z:40:THR:OG1	25:z:41:PRO:HD2	2.08	0.53
28:D:12:ARG:NE	28:D:44:VAL:HG21	2.21	0.53
52:3:225:C:C3'	52:3:226:G:H5''	2.39	0.53
52:3:784:A:H4'	53:1:1837:C:OP1	2.09	0.53
52:3:1220:G:H2'	52:3:1221:G:O4'	2.09	0.53
53:1:560:C:H2'	53:1:561:G:O4'	2.09	0.53
55:6:34:C:O2	55:6:34:C:C2'	2.57	0.53
15:p:51:ASN:O	53:1:2845:U:H5''	2.09	0.53
25:z:29:ARG:NE	53:1:1183:U:H5''	2.24	0.53
38:N:74:GLN:O	38:N:78:ILE:HG13	2.09	0.53
42:R:27:THR:HA	42:R:30:LYS:HE2	1.90	0.53
42:R:65:GLU:HG2	42:R:66:GLY:N	2.24	0.53
45:U:8:ARG:HB3	45:U:28:ARG:CZ	2.39	0.53
52:3:966:G:H2'	52:3:966:G:N3	2.23	0.53
52:3:1401:G:H2'	52:3:1402:C:O4'	2.09	0.53
55:6:26:G:H1	55:6:44:A:H61	1.56	0.53
4:e:77:LYS:HD3	4:e:77:LYS:N	2.24	0.53
42:R:100:ARG:HH21	42:R:102:LYS:HE2	1.73	0.53
52:3:828:U:H3	52:3:859:G:H1'	1.73	0.53
53:1:828:U:H2'	53:1:829:A:C8	2.44	0.53
57:7:58:A:H1'	57:7:60:U:C5	2.44	0.53
1:b:52:HIS:HA	1:b:216:ARG:HB3	1.92	0.52
1:b:89:ASN:OD1	1:b:196:ASN:ND2	2.41	0.52
3:d:15:SER:HB3	3:d:18:THR:HG22	1.91	0.52
5:f:36:LEU:HD23	5:f:37:ASN:N	2.23	0.52
7:h:31:ARG:NH2	53:1:1053:C:O2'	2.41	0.52
12:m:86:LYS:CE	53:1:955:U:H5''	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:77:A:H2'	52:3:78:A:H8	1.73	0.52
10:k:68:GLY:HA3	10:k:78:ARG:HG2	1.91	0.52
13:n:1:MET:SD	13:n:1:MET:N	2.82	0.52
32:H:35:ASP:O	32:H:38:VAL:HG12	2.09	0.52
32:H:60:ALA:O	32:H:61:LYS:HG3	2.09	0.52
36:L:42:VAL:O	36:L:46:LEU:HG	2.10	0.52
52:3:1014:A:H2'	52:3:1015:G:O4'	2.09	0.52
52:3:1352:C:H2'	52:3:1353:G:C8	2.44	0.52
4:e:5:ASP:HA	4:e:8:LYS:HD2	1.92	0.52
11:l:54:GLN:HE22	53:1:2358:A:H61	1.56	0.52
13:n:47:VAL:C	13:n:50:PRO:HD2	2.34	0.52
37:M:93:LYS:HD2	37:M:97:GLY:HA2	1.91	0.52
42:R:9:PRO:HG2	42:R:17:ALA:HB1	1.90	0.52
49:Y:49:ALA:O	49:Y:52:GLU:HB3	2.10	0.52
53:1:873:C:H2'	53:1:874:G:C8	2.44	0.52
57:7:25:C:C3'	57:7:26:A:H5''	2.38	0.52
57:7:58:A:H1'	57:7:60:U:H5	1.74	0.52
12:m:32:GLY:HA2	12:m:103:TYR:O	2.09	0.52
16:q:92:LYS:HE3	53:1:995:C:O2'	2.09	0.52
31:G:151:LYS:HG3	31:G:152:ASP:OD1	2.10	0.52
38:N:27:ILE:HG22	38:N:29:ILE:HD11	1.92	0.52
40:P:118:ASN:CG	52:3:718:A:H5'	2.33	0.52
46:V:43:LEU:HD11	46:V:72:TRP:CE2	2.44	0.52
52:3:70:U:H4'	52:3:71:A:H8	1.73	0.52
52:3:1033:G:C2'	52:3:1034:G:H5''	2.40	0.52
53:1:296:U:H2'	53:1:297:G:H8	1.74	0.52
53:1:1629:U:H2'	53:1:1630:A:C8	2.43	0.52
53:1:2628:C:H3'	53:1:2629:U:H5'	1.91	0.52
1:b:241:LYS:O	53:1:1902:C:H4'	2.09	0.52
5:f:88:LEU:HG	5:f:161:VAL:HG13	1.90	0.52
40:P:81:LEU:HD12	40:P:81:LEU:O	2.08	0.52
49:Y:67:HIS:CB	52:3:262:A:H5'	2.40	0.52
52:3:1429:A:H2'	52:3:1430:A:H8	1.75	0.52
46:V:67:SER:OG	46:V:68:LYS:N	2.42	0.52
47:W:38:ILE:HD12	47:W:38:ILE:N	2.24	0.52
53:1:554:U:H2'	53:1:555:G:O4'	2.09	0.52
53:1:796:C:H2'	53:1:797:G:H8	1.74	0.52
53:1:2834:G:O2'	53:1:2835:A:H5'	2.10	0.52
1:b:71:ASP:OD2	1:b:72:GLY:N	2.43	0.52
12:m:55:ARG:HA	12:m:59:ARG:HH11	1.74	0.52
16:q:36:GLN:HE21	53:1:1252:G:H22	1.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:P:118:ASN:ND2	52:3:717:U:H4'	2.25	0.52
41:Q:98:ARG:HB3	41:Q:105:GLY:HA2	1.91	0.52
50:Z:40:PRO:O	50:Z:44:ARG:HG3	2.09	0.52
52:3:1014:A:C2	52:3:1219:A:H1'	2.44	0.52
1:b:260:LYS:HD2	53:1:2228:G:P	2.49	0.52
17:r:2:TYR:CE1	17:r:42:ALA:HB3	2.45	0.52
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.90	0.52
1:b:153:LEU:HD13	1:b:175:LEU:HD21	1.92	0.52
2:c:150:GLN:NE2	53:1:574:A:C2	2.78	0.52
3:d:71:GLY:H	53:1:674:G:H5''	1.72	0.52
27:C:14:ALA:HB2	27:C:46:VAL:HG21	1.91	0.52
33:I:144:ILE:N	33:I:144:ILE:HD12	2.24	0.52
50:Z:23:GLU:CD	50:Z:27:VAL:HG13	2.34	0.52
51:a:42:VAL:HA	51:a:216:THR:HA	1.92	0.52
53:1:1053:C:C3'	53:1:1054:A:H5''	2.39	0.52
5:f:44:HIS:O	5:f:46:ASP:N	2.43	0.52
5:f:173:ALA:O	5:f:174:LYS:HG2	2.10	0.52
6:g:63:ALA:HA	6:g:66:ASN:HD22	1.74	0.52
11:l:94:THR:HA	11:l:97:ALA:HB3	1.91	0.52
12:m:13:HIS:HE1	53:1:2265:U:H4'	1.75	0.52
12:m:37:GLY:HA3	12:m:126:ILE:HD11	1.90	0.52
12:m:38:ARG:HG3	12:m:98:PRO:HD3	1.90	0.52
23:x:13:THR:CG2	53:1:188:G:H5'	2.39	0.52
26:B:27:LEU:HD12	26:B:27:LEU:O	2.09	0.52
30:F:7:VAL:HG22	30:F:38:GLY:HA3	1.91	0.52
47:W:59:LYS:HD3	52:3:735:C:H5'	1.92	0.52
51:a:28:ALA:HA	51:a:31:LYS:HD2	1.92	0.52
52:3:24:U:H2'	52:3:25:C:C6	2.45	0.52
53:1:296:U:H2'	53:1:297:G:C8	2.44	0.52
53:1:1765:U:H2'	53:1:1766:G:H8	1.74	0.52
53:1:2376:A:H2'	53:1:2377:A:O4'	2.10	0.52
53:1:2743:U:H3'	53:1:2744:G:H5''	1.90	0.52
4:e:37:MET:HE3	4:e:52:ALA:HB1	1.92	0.51
7:h:59:LEU:HB3	7:h:62:ARG:HB2	1.92	0.51
8:i:89:SER:HB3	8:i:135:MET:HA	1.92	0.51
16:q:87:VAL:HG12	16:q:89:ILE:H	1.75	0.51
33:I:8:LEU:HB3	52:3:430:A:OP1	2.10	0.51
38:N:104:THR:HG22	52:3:1180:A:OP1	2.10	0.51
44:T:44:GLU:O	44:T:45:HIS:HB2	2.09	0.51
33:I:150:LYS:HD3	33:I:177:MET:SD	2.50	0.51
46:V:22:VAL:HG22	46:V:23:ALA:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:632:U:H3'	52:3:633:G:H5'	1.91	0.51
52:3:960:U:O2'	52:3:1223:C:H4'	2.10	0.51
52:3:1170:A:H2'	52:3:1171:A:O4'	2.09	0.51
53:1:2030:A:N3	53:1:2499:C:H5''	2.25	0.51
9:j:53:TYR:CE1	9:j:121:LYS:HG2	2.46	0.51
12:m:105:MET:SD	12:m:108:VAL:HG21	2.50	0.51
13:n:47:VAL:O	13:n:50:PRO:HD2	2.11	0.51
37:M:14:ARG:HE	37:M:74:ILE:HG23	1.74	0.51
38:N:113:LYS:HE2	38:N:118:ARG:O	2.10	0.51
38:N:114:LYS:HG2	38:N:120:ALA:HA	1.91	0.51
42:R:63:VAL:HG22	42:R:68:LEU:HG	1.91	0.51
53:1:435:C:H2'	53:1:436:C:H5'	1.93	0.51
53:1:807:U:H2'	53:1:808:G:H8	1.76	0.51
15:p:59:THR:HA	15:p:72:VAL:HA	1.91	0.51
36:L:58:LEU:H	36:L:58:LEU:HD12	1.75	0.51
47:W:11:ARG:HD2	52:3:845:A:H4'	1.92	0.51
53:1:745:G:O2'	53:1:748:G:H1'	2.09	0.51
5:f:173:ALA:HB3	5:f:176:LYS:OXT	2.10	0.51
15:p:1:SER:H2	53:1:2876:G:H5'	1.75	0.51
15:p:90:ALA:HB2	15:p:112:ARG:HA	1.93	0.51
40:P:118:ASN:OD1	52:3:718:A:H5'	2.10	0.51
52:3:1391:U:H2'	52:3:1392:G:H8	1.75	0.51
52:3:1412:C:H2'	52:3:1413:A:C8	2.45	0.51
53:1:2011:U:H2'	53:1:2012:G:O4'	2.10	0.51
58:8:391:LYS:HG2	58:8:392:VAL:N	2.26	0.51
12:m:64:TRP:HE1	53:1:873:C:H4'	1.76	0.51
16:q:54:ARG:HG3	53:1:1155:A:OP1	2.11	0.51
36:L:68:VAL:HG13	36:L:99:ALA:HB1	1.93	0.51
38:N:32:ARG:HG3	38:N:36:GLN:HE21	1.76	0.51
54:2:106:G:H2'	54:2:107:G:O4'	2.11	0.51
58:8:311:ILE:HD12	58:8:311:ILE:H	1.75	0.51
4:e:35:LEU:HB2	4:e:88:VAL:HB	1.92	0.51
4:e:125:GLY:HA2	4:e:162:ASP:HA	1.92	0.51
8:i:126:ARG:HA	8:i:129:GLU:HG3	1.93	0.51
8:i:130:GLY:O	8:i:133:ARG:HG2	2.10	0.51
31:G:158:ASP:HA	31:G:180:ILE:HD11	1.93	0.51
39:O:42:LEU:HD23	39:O:71:LEU:HG	1.92	0.51
42:R:15:VAL:O	42:R:19:THR:HG23	2.11	0.51
48:X:69:LYS:HE2	52:3:1320:C:O4'	2.11	0.51
51:a:4:LEU:HB3	51:a:8:MET:HB2	1.92	0.51
53:1:2281:A:O2'	53:1:2282:G:H5'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2515:C:H2'	53:1:2516:A:H8	1.75	0.51
58:8:312:LEU:C	58:8:318:GLY:HA3	2.35	0.51
1:b:242:HIS:O	1:b:244:VAL:HG13	2.11	0.51
3:d:38:GLY:HA3	53:1:615:U:O2	2.10	0.51
6:g:4:ILE:HD11	6:g:47:PHE:CD2	2.46	0.51
31:G:153:MET:HG2	31:G:155:GLY:H	1.76	0.51
35:K:92:THR:OG1	35:K:93:LYS:N	2.38	0.51
38:N:32:ARG:HH12	52:3:1248:A:H4'	1.76	0.51
38:N:98:ARG:HD2	38:N:103:VAL:HG21	1.93	0.51
41:Q:48:LEU:HB2	52:3:520:A:OP1	2.11	0.51
50:Z:28:LEU:O	50:Z:32:ARG:HD2	2.11	0.51
52:3:1497:G:O2'	52:3:1498:U:H5'	2.11	0.51
53:1:100:U:H4'	53:1:101:A:C4	2.46	0.51
53:1:1775:U:H2'	53:1:1776:G:O4'	2.11	0.51
53:1:2233:U:H2'	53:1:2234:G:C8	2.46	0.51
53:1:2800:A:H3'	53:1:2801:G:H5'	1.91	0.51
1:b:16:VAL:HB	1:b:203:VAL:HG12	1.93	0.51
9:j:62:VAL:HG21	9:j:101:ILE:HD11	1.93	0.51
33:I:164:ARG:HG2	33:I:165:GLU:H	1.76	0.51
33:I:196:GLU:O	33:I:200:VAL:HG23	2.11	0.51
35:K:3:HIS:N	35:K:92:THR:HG22	2.26	0.51
43:S:20:PHE:O	43:S:21:ALA:HB3	2.11	0.51
46:V:48:GLU:O	46:V:49:ASN:C	2.53	0.51
52:3:634:C:H2'	52:3:635:A:H8	1.75	0.51
53:1:2636:C:H2'	53:1:2637:U:C6	2.46	0.51
54:2:56:G:H4'	54:2:57:A:H8	1.75	0.51
9:j:81:ILE:HD11	53:1:2514:U:C4'	2.40	0.51
10:k:31:ARG:HH22	53:1:2676:C:P	2.34	0.51
12:m:24:THR:HA	12:m:101:VAL:HG23	1.93	0.51
12:m:42:THR:HA	12:m:93:VAL:HA	1.93	0.51
18:s:88:ARG:HB2	18:s:94:ASP:OD2	2.11	0.51
44:T:65:LEU:HD23	52:3:754:C:O2'	2.11	0.51
52:3:1088:G:H21	52:3:1167:A:H61	1.59	0.51
52:3:1492:A:H2'	53:1:1913:A:H2	1.76	0.51
53:1:1854:A:H61	53:1:1888:G:H1'	1.75	0.51
53:1:2853:C:H2'	53:1:2854:G:C8	2.46	0.51
58:8:378:ARG:HD2	58:8:383:THR:HG22	1.93	0.51
16:q:97:ILE:HD11	16:q:104:ALA:HB3	1.93	0.50
19:t:14:PRO:HA	19:t:32:LEU:HB2	1.93	0.50
19:t:61:LEU:HD13	53:1:1341:G:H5'	1.93	0.50
26:B:4:GLN:O	53:1:2017:U:H4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C:12:SER:HA	27:C:48:TYR:HD1	1.76	0.50
27:C:41:VAL:HG23	27:C:42:VAL:HG13	1.92	0.50
49:Y:80:ALA:HA	49:Y:83:ASN:ND2	2.25	0.50
52:3:437:U:H2'	52:3:438:U:O4'	2.11	0.50
52:3:580:C:H2'	52:3:581:G:O4'	2.12	0.50
52:3:1258:G:H2'	52:3:1259:C:C6	2.46	0.50
53:1:1725:U:H3	53:1:1735:A:H61	1.59	0.50
54:2:56:G:H4'	54:2:57:A:C8	2.47	0.50
4:e:155:ILE:HD12	4:e:155:ILE:N	2.27	0.50
12:m:100:LYS:NZ	53:1:907:G:H4'	2.26	0.50
38:N:5:TYR:HB2	38:N:20:ILE:HG23	1.92	0.50
48:X:54:ARG:HB3	52:3:958:A:C2	2.45	0.50
52:3:828:U:N3	52:3:859:G:H1'	2.26	0.50
52:3:1238:A:H62	52:3:1301:U:H3	1.59	0.50
53:1:703:U:H2'	53:1:704:G:O4'	2.12	0.50
53:1:2412:A:H2'	53:1:2413:G:O4'	2.11	0.50
54:2:88:C:C5'	54:2:89:U:OP1	2.58	0.50
1:b:239:PHE:O	1:b:241:LYS:HG3	2.10	0.50
5:f:3:VAL:HG21	53:1:2748:A:H4'	1.94	0.50
5:f:59:ASP:O	5:f:63:GLN:HG2	2.10	0.50
9:j:47:HIS:ND1	9:j:48:VAL:HG23	2.26	0.50
35:K:54:LEU:HD23	35:K:55:HIS:N	2.26	0.50
38:N:98:ARG:HD2	38:N:103:VAL:HG11	1.92	0.50
53:1:532:A:H2'	53:1:532:A:N3	2.27	0.50
54:2:3:C:H3'	54:2:4:C:H5''	1.93	0.50
1:b:36:ASN:HB2	1:b:61:TYR:HB2	1.93	0.50
1:b:47:ARG:HD2	53:1:778:G:H5''	1.94	0.50
8:i:91:LYS:HE3	8:i:94:LYS:HD2	1.94	0.50
13:n:32:GLU:HA	13:n:115:LEU:HD12	1.93	0.50
18:s:24:ILE:HG22	18:s:71:VAL:HG21	1.93	0.50
23:x:54:GLY:O	23:x:58:ILE:HG12	2.12	0.50
36:L:101:ARG:HH22	52:3:939:G:H4'	1.74	0.50
38:N:10:ARG:HG3	38:N:105:ARG:HH21	1.76	0.50
53:1:1045:C:H5'	53:1:1046:A:H5''	1.92	0.50
53:1:2646:C:H2'	53:1:2647:U:O4'	2.12	0.50
58:8:342:ILE:HG13	58:8:342:ILE:O	2.10	0.50
2:c:64:GLU:HA	2:c:67:HIS:HB3	1.94	0.50
2:c:122:VAL:HG21	2:c:141:ARG:NH2	2.26	0.50
4:e:65:LEU:HD22	54:2:42:C:C5	2.46	0.50
45:U:14:ARG:HH12	52:3:618:C:H1'	1.77	0.50
46:V:71:SER:OG	52:3:235:C:H4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:166:U:H2'	52:3:167:A:C8	2.46	0.50
53:1:1179:G:N7	53:1:1180:U:H1'	2.27	0.50
53:1:1790:C:H2'	53:1:1791:A:C5	2.47	0.50
53:1:2039:U:H2'	53:1:2040:G:C8	2.47	0.50
5:f:21:GLN:HE21	5:f:38:ASP:HA	1.76	0.50
12:m:22:GLN:HB2	53:1:907:G:H5'	1.93	0.50
34:J:23:THR:HG21	52:3:1396:A:H2	1.77	0.50
38:N:68:GLY:HA2	52:3:1250:A:C5'	2.41	0.50
1:b:154:ALA:HB2	1:b:161:VAL:HG13	1.93	0.50
9:j:69:ARG:HA	9:j:89:PHE:HD2	1.77	0.50
10:k:6:THR:CG2	53:1:1666:G:H4'	2.42	0.50
10:k:51:LYS:HD3	10:k:52:VAL:HG13	1.93	0.50
10:k:105:ARG:O	10:k:105:ARG:HD2	2.11	0.50
33:I:131:ILE:HG21	52:3:620:C:H1'	1.93	0.50
42:R:108:ARG:NH1	52:3:1308:U:H5'	2.27	0.50
44:T:61:GLN:O	44:T:65:LEU:HG	2.12	0.50
51:a:4:LEU:H	51:a:4:LEU:CD1	2.22	0.50
52:3:335:C:H2'	52:3:336:A:C8	2.46	0.50
53:1:1827:U:O2'	53:1:1828:G:H5'	2.12	0.50
53:1:1996:C:O2	53:1:1997:C:H1'	2.11	0.50
7:h:27:VAL:HG12	7:h:83:ALA:O	2.12	0.50
14:o:51:ALA:HB3	14:o:78:VAL:CG1	2.39	0.50
38:N:115:VAL:HG21	39:O:62:ARG:HB2	1.94	0.50
40:P:125:LYS:C	50:Z:34:ARG:HH21	2.20	0.50
41:Q:74:GLN:O	41:Q:76:HIS:N	2.45	0.50
48:X:39:ILE:HD12	48:X:39:ILE:N	2.27	0.50
53:1:176:A:H3'	53:1:177:G:N2	2.26	0.50
53:1:1054:A:H61	53:1:1105:U:H3	1.60	0.50
53:1:2328:A:H2'	53:1:2329:U:C6	2.47	0.50
31:G:67:LEU:HD22	31:G:89:PHE:HB2	1.93	0.50
51:a:174:THR:HB	53:1:2124:G:C5'	2.38	0.50
52:3:1379:G:O2'	52:3:1380:U:H5'	2.12	0.50
1:b:255:LYS:NZ	53:1:1844:C:H4'	2.27	0.49
2:c:21:SER:C	2:c:22:ILE:HD12	2.37	0.49
12:m:50:ARG:HD3	12:m:65:ILE:HD11	1.93	0.49
12:m:64:TRP:NE1	53:1:873:C:H4'	2.27	0.49
45:U:54:LEU:HB2	45:U:80:LYS:HZ3	1.76	0.49
50:Z:23:GLU:OE1	50:Z:27:VAL:HG13	2.12	0.49
52:3:802:A:H2'	52:3:803:G:O4'	2.12	0.49
53:1:2248:C:H2'	53:1:2249:U:H5'	1.92	0.49
15:p:105:LYS:O	15:p:108:ARG:HG3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:1:MET:HG3	18:s:3:THR:HG23	1.94	0.49
33:I:33:ILE:O	33:I:34:GLU:HG2	2.11	0.49
3:d:97:ASN:HB2	3:d:100:MET:HG3	1.94	0.49
7:h:3:LEU:HD21	53:1:1043:C:H5''	1.94	0.49
41:Q:23:LEU:HD13	41:Q:58:ASN:HD22	1.75	0.49
53:1:112:U:H2'	53:1:113:U:H5'	1.94	0.49
53:1:2623:G:H2'	53:1:2624:G:H8	1.78	0.49
55:5:69:C:H2'	55:5:70:G:C8	2.47	0.49
1:b:86:ARG:NH2	53:1:1817:G:OP1	2.45	0.49
4:e:87:LYS:HD2	53:1:2313:C:H5''	1.93	0.49
12:m:5:LYS:O	12:m:6:ARG:HD3	2.12	0.49
41:Q:106:VAL:HB	41:Q:109:ARG:HD3	1.94	0.49
52:3:123:U:H5''	52:3:311:C:O2'	2.12	0.49
52:3:1418:A:H2	53:1:1948:G:H21	1.59	0.49
53:1:2048:G:H3'	53:1:2049:G:H5''	1.95	0.49
54:2:2:G:H2'	54:2:3:C:C6	2.47	0.49
10:k:120:PRO:HB2	10:k:121:GLU:OE2	2.12	0.49
45:U:12:LYS:O	45:U:13:LYS:HB2	2.12	0.49
49:Y:83:ASN:HA	49:Y:86:ALA:OXT	2.11	0.49
51:a:27:ILE:HG23	51:a:185:LEU:HD12	1.94	0.49
52:3:730:G:H2'	52:3:731:G:H5'	1.95	0.49
53:1:1432:G:H2'	53:1:1433:A:C8	2.47	0.49
53:1:2180:U:H4'	55:6:17(A):U:H5'	1.93	0.49
58:8:305:PHE:HA	58:8:393:LEU:HB2	1.92	0.49
1:b:48:ILE:HG23	1:b:48:ILE:O	2.11	0.49
40:P:120:CYS:HB2	52:3:778:G:H1'	1.94	0.49
42:R:24:VAL:HG23	42:R:28:ARG:HB3	1.94	0.49
46:V:42:LYS:HD2	52:3:278:G:OP2	2.13	0.49
52:3:868:C:H2'	52:3:869:G:O4'	2.13	0.49
53:1:2229:U:H2'	53:1:2230:G:C8	2.47	0.49
3:d:193:VAL:O	3:d:196:VAL:HG12	2.12	0.49
7:h:40:GLU:O	7:h:43:LYS:HB3	2.12	0.49
14:o:67:ASN:HA	54:2:50:A:OP2	2.13	0.49
19:t:73:ARG:NH1	53:1:64:A:N3	2.60	0.49
20:u:17:ASP:HB3	20:u:20:LYS:HD2	1.94	0.49
31:G:110:ILE:HG12	31:G:147:LEU:HD23	1.95	0.49
32:H:89:VAL:O	32:H:93:ILE:HG13	2.13	0.49
33:I:167:PRO:HB2	33:I:170:LEU:CD2	2.42	0.49
39:O:43:PRO:HA	52:3:1151:A:H5'	1.94	0.49
46:V:5:ARG:HH11	52:3:636:U:C5'	2.15	0.49
54:2:51:G:H2'	54:2:52:A:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:7:48:C:H5'	57:7:50:U:OP2	2.12	0.49
16:q:106:THR:O	16:q:109:VAL:HG12	2.12	0.49
39:O:10:LEU:HD23	39:O:10:LEU:H	1.78	0.49
40:P:14:GLN:HE22	40:P:77:GLY:HA3	1.78	0.49
44:T:24:THR:HG23	44:T:69:LEU:HD12	1.95	0.49
51:a:23:ILE:HG23	51:a:189:LEU:HD21	1.95	0.49
52:3:536:C:H2'	52:3:537:G:H8	1.77	0.49
52:3:744:C:H2'	52:3:745:G:C8	2.48	0.49
53:1:971:G:H2'	53:1:972:A:O4'	2.12	0.49
53:1:2247:A:H2'	53:1:2248:C:C6	2.48	0.49
13:n:21:PHE:HA	13:n:24:MET:HG2	1.95	0.49
20:u:6:ARG:O	20:u:24:VAL:HB	2.12	0.49
34:J:155:LYS:HB2	37:M:70:VAL:HG13	1.95	0.49
41:Q:109:ARG:C	41:Q:110:LYS:HD2	2.38	0.49
45:U:14:ARG:NH1	52:3:618:C:H1'	2.27	0.49
49:Y:53:MET:HA	49:Y:56:ILE:HD13	1.94	0.49
50:Z:18:PHE:HA	50:Z:21:SER:HB2	1.95	0.49
52:3:17:U:H2'	52:3:18:C:C6	2.48	0.49
52:3:231:U:H2'	52:3:232:G:H8	1.78	0.49
52:3:757:U:H2'	52:3:758:C:O4'	2.13	0.49
53:1:45:G:H5''	53:1:46:G:C5'	2.17	0.49
53:1:1918:A:H2	53:1:1919:A:H62	1.60	0.49
58:8:306:GLU:HB3	58:8:358:LYS:HE2	1.94	0.49
3:d:145:ASP:OD2	3:d:183:PHE:HA	2.13	0.49
31:G:102:ASN:ND2	31:G:105:THR:OG1	2.46	0.49
33:I:66:VAL:HG12	33:I:67:LEU:N	2.26	0.49
33:I:82:LYS:HD2	52:3:5:U:O4	2.13	0.49
36:L:138:GLU:HB3	36:L:142:ARG:NH1	2.27	0.49
43:S:26:LEU:HD11	43:S:46:LYS:HB3	1.94	0.49
53:1:582:A:H2'	53:1:583:G:C8	2.48	0.49
53:1:2605:U:H2'	53:1:2606:C:C6	2.48	0.49
53:1:2676:C:H2'	53:1:2677:G:H8	1.78	0.49
53:1:2698:U:H2'	53:1:2699:C:C6	2.48	0.49
58:8:313:SER:HB2	58:8:316:GLU:OE1	2.13	0.49
5:f:136:ASP:HB3	5:f:139:VAL:HG22	1.94	0.48
17:r:79:ARG:NH2	53:1:572:A:H5'	2.27	0.48
30:F:4:ARG:HB3	53:1:2466:C:OP1	2.13	0.48
39:O:6:ILE:H	39:O:6:ILE:HD12	1.78	0.48
51:a:221:GLY:N	53:1:2176:A:H5''	2.27	0.48
52:3:78:A:H2'	52:3:79:G:O4'	2.12	0.48
52:3:1464:U:H2'	52:3:1465:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:118:A:OP2	53:1:119:A:H5''	2.12	0.48
53:1:2065:C:H1'	53:1:2449:U:H3	1.78	0.48
53:1:2233:U:H2'	53:1:2234:G:H8	1.77	0.48
53:1:2577:A:H2'	53:1:2614:A:N6	2.28	0.48
6:g:4:ILE:HA	6:g:17:ASP:O	2.14	0.48
6:g:9:VAL:HG22	6:g:11:ASN:OD1	2.12	0.48
7:h:2:ALA:HB3	7:h:6:GLN:HB2	1.95	0.48
11:l:65:GLY:HA2	53:1:2415:G:H4'	1.93	0.48
12:m:17:ASN:O	54:2:90:C:H5'	2.12	0.48
21:v:9:ARG:HG2	21:v:41:GLU:HB2	1.95	0.48
32:H:179:ALA:HB1	32:H:202:PHE:HE1	1.78	0.48
36:L:15:PRO:HB2	38:N:44:ARG:NH1	2.28	0.48
39:O:53:ILE:HG22	52:3:1060:U:C5'	2.43	0.48
53:1:2530:A:H2'	53:1:2531:A:H5''	1.94	0.48
1:b:62:ARG:NE	1:b:84:PRO:HD2	2.28	0.48
1:b:215:VAL:HG12	1:b:216:ARG:N	2.28	0.48
5:f:116:LEU:HD22	5:f:120:ILE:HG21	1.94	0.48
6:g:89:LYS:HD3	6:g:89:LYS:HA	1.69	0.48
9:j:81:ILE:HD11	53:1:2514:U:H5''	1.95	0.48
30:F:22:VAL:HG22	30:F:24:ARG:HE	1.77	0.48
52:3:195:A:H2'	52:3:196:A:C8	2.48	0.48
52:3:784:A:H2'	52:3:785:G:H8	1.78	0.48
52:3:971:G:H1'	52:3:1365:G:O2'	2.14	0.48
53:1:78:U:H3	53:1:108:G:H1	1.60	0.48
53:1:1045:C:P	53:1:1047:G:H5'	2.53	0.48
53:1:1071:G:OP1	53:1:1071:G:H3'	2.13	0.48
53:1:2633:G:H5'	53:1:2811:G:O2'	2.13	0.48
4:e:102:LEU:HA	4:e:106:ALA:HB3	1.95	0.48
5:f:88:LEU:HD12	5:f:88:LEU:N	2.26	0.48
32:H:70:ALA:HA	32:H:105:VAL:HG22	1.96	0.48
40:P:124:LYS:HA	50:Z:34:ARG:HA	1.95	0.48
47:W:33:THR:OG1	47:W:34:GLU:N	2.46	0.48
53:1:694:U:H2'	53:1:695:G:H5''	1.95	0.48
9:j:113:PRO:HD2	53:1:558:U:P	2.53	0.48
10:k:92:GLU:O	10:k:93:GLN:C	2.57	0.48
19:t:2:ILE:H	19:t:2:ILE:HD12	1.79	0.48
32:H:119:ILE:HD11	32:H:136:ALA:HB2	1.95	0.48
32:H:156:LEU:HD12	32:H:156:LEU:O	2.14	0.48
33:I:173:ASP:OD2	33:I:176:LYS:HG2	2.14	0.48
33:I:198:LEU:HA	33:I:201:GLU:OE1	2.13	0.48
39:O:59:LYS:HZ2	39:O:62:ARG:HE	1.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:290:U:H2'	53:1:291:G:H8	1.79	0.48
53:1:1842:G:H1	53:1:1898:U:H3	1.62	0.48
2:c:169:ARG:HH12	2:c:202:ILE:HD12	1.77	0.48
3:d:76:PRO:HA	3:d:82:GLY:HA2	1.93	0.48
4:e:48:LEU:HA	4:e:51:ASN:ND2	2.28	0.48
18:s:11:ARG:N	18:s:11:ARG:HD2	2.29	0.48
20:u:91:LYS:HE2	53:1:297:G:C5'	2.43	0.48
31:G:40:ILE:HD12	31:G:40:ILE:N	2.28	0.48
32:H:180:ASP:HB3	32:H:204:GLY:H	1.78	0.48
34:J:71:ILE:HG23	34:J:144:GLU:OE1	2.14	0.48
34:J:110:MET:HE3	34:J:139:THR:HG21	1.95	0.48
36:L:25:PHE:HA	36:L:100:MET:HE3	1.95	0.48
37:M:80:PRO:HG2	52:3:878:A:H5'	1.96	0.48
39:O:6:ILE:HB	39:O:76:ILE:HG23	1.95	0.48
49:Y:56:ILE:HD12	49:Y:56:ILE:N	2.28	0.48
51:a:3:LYS:HD2	53:1:2108:A:P	2.53	0.48
53:1:441:U:O2'	53:1:442:G:H5'	2.14	0.48
53:1:1013:C:H2'	53:1:1014:A:H8	1.79	0.48
53:1:1434:A:H2'	53:1:1435:G:C8	2.48	0.48
54:2:66:A:H4'	54:2:67:G:C8	2.49	0.48
32:H:49:ALA:HB1	32:H:75:VAL:HG22	1.95	0.48
32:H:53:ARG:HH11	32:H:53:ARG:HG3	1.78	0.48
33:I:14:GLU:HG2	33:I:59:LYS:HG3	1.95	0.48
39:O:46:LYS:HE3	39:O:68:ARG:HE	1.77	0.48
43:S:30:ILE:O	43:S:30:ILE:HG13	2.13	0.48
49:Y:29:THR:O	49:Y:32:LYS:HG2	2.14	0.48
1:b:55:GLY:H	53:1:692:C:P	2.36	0.48
1:b:97:ASP:HB3	53:1:1490:A:N7	2.29	0.48
7:h:13:ALA:O	7:h:17:GLU:HG2	2.13	0.48
7:h:37:LYS:O	7:h:41:LEU:HB2	2.14	0.48
34:J:98:ALA:HB1	34:J:101:GLY:HA3	1.96	0.48
51:a:4:LEU:HD23	51:a:8:MET:HB3	1.96	0.48
51:a:7:ARG:O	51:a:11:ILE:HG13	2.13	0.48
52:3:56:U:H2'	52:3:57:G:C8	2.49	0.48
52:3:67:C:H2'	52:3:68:G:C8	2.48	0.48
52:3:501:C:H2'	52:3:502:A:C8	2.48	0.48
52:3:603:U:H2'	52:3:604:G:C8	2.48	0.48
52:3:1504:G:OP1	52:3:1507:A:H4'	2.13	0.48
53:1:2345:G:N3	53:1:2381:A:H2'	2.28	0.48
57:7:63:G:H21	58:8:380:GLY:HA3	1.78	0.48
2:c:5:VAL:H	2:c:32:ASN:HD21	1.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:54:LEU:HD12	6:g:55:GLU:N	2.29	0.48
13:n:32:GLU:OE1	13:n:117:ASP:HB2	2.14	0.48
15:p:29:VAL:HG13	15:p:79:VAL:O	2.14	0.48
17:r:49:ILE:HD12	17:r:52:PRO:HA	1.95	0.48
28:D:34:ARG:HD3	53:1:467:G:OP2	2.13	0.48
31:G:180:ILE:CD1	31:G:181:PRO:HD2	2.44	0.48
39:O:6:ILE:HD12	39:O:6:ILE:N	2.28	0.48
44:T:50:HIS:ND1	52:3:667:G:H4'	2.29	0.48
53:1:1083:U:H2'	53:1:1085:A:OP2	2.14	0.48
53:1:1102:C:H2'	53:1:1103:A:O4'	2.14	0.48
7:h:92:ALA:HB1	7:h:129:LEU:HD13	1.96	0.48
32:H:90:VAL:HA	32:H:93:ILE:HD12	1.95	0.48
33:I:18:LEU:O	33:I:18:LEU:HD23	2.14	0.48
37:M:79:ARG:HB2	52:3:878:A:OP1	2.14	0.48
41:Q:58:ASN:OD1	41:Q:59:GLY:N	2.45	0.48
52:3:77:A:H2'	52:3:78:A:C8	2.49	0.48
52:3:1270:G:H2'	52:3:1271:A:C8	2.49	0.48
53:1:254:G:C2'	53:1:255:A:H5''	2.44	0.48
53:1:631:A:H2'	53:1:632:A:O4'	2.14	0.48
53:1:1316:U:H2'	53:1:1317:G:C8	2.49	0.48
53:1:2743:U:H2'	53:1:2744:G:H5''	1.96	0.48
54:2:88:C:C4'	54:2:89:U:OP1	2.61	0.48
57:7:6:G:H3'	57:7:7:A:H5''	1.95	0.48
3:d:68:ALA:HA	53:1:1255:U:C5	2.49	0.47
7:h:77:VAL:HG13	7:h:78:GLY:N	2.28	0.47
10:k:109:SER:C	10:k:111:LYS:H	2.22	0.47
21:v:14:LYS:HE2	54:2:98:G:H22	1.78	0.47
25:z:8:GLN:CG	25:z:28:LEU:HD22	2.32	0.47
26:B:46:GLY:HA3	26:B:54:ILE:HG21	1.96	0.47
27:C:22:THR:HG22	27:C:23:THR:H	1.79	0.47
32:H:84:GLU:HG3	32:H:88:LYS:HE2	1.96	0.47
34:J:110:MET:O	34:J:113:VAL:HG22	2.14	0.47
38:N:6:TYR:CE2	52:3:1147:C:H4'	2.49	0.47
40:P:23:HIS:HB3	40:P:30:ILE:HG23	1.95	0.47
49:Y:4:LYS:O	49:Y:7:LYS:HG2	2.14	0.47
52:3:1259:C:H3'	52:3:1260:G:C5'	2.40	0.47
53:1:167:A:H2'	53:1:168:G:O4'	2.14	0.47
53:1:616:A:H2'	53:1:617:G:O4'	2.13	0.47
53:1:2248:C:C2'	53:1:2249:U:H5'	2.44	0.47
2:c:142:VAL:HG13	2:c:144:GLY:H	1.79	0.47
3:d:138:LEU:HD12	3:d:139:LYS:N	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:148:ILE:HG21	3:d:157:LEU:HD21	1.96	0.47
6:g:9:VAL:HG13	6:g:9:VAL:O	2.14	0.47
9:j:32:LEU:HD22	9:j:54:ILE:HD13	1.96	0.47
10:k:49:ARG:HH22	52:3:1422:G:H4'	1.79	0.47
11:l:54:GLN:HG2	53:1:825:A:O2'	2.14	0.47
12:m:74:THR:OG1	12:m:75:GLU:N	2.47	0.47
29:E:31:ILE:O	29:E:31:ILE:HG13	2.14	0.47
32:H:63:ILE:O	32:H:98:ALA:HA	2.14	0.47
33:I:54:LEU:HD23	33:I:55:ARG:HE	1.79	0.47
34:J:19:ARG:HB3	34:J:32:PHE:CE1	2.50	0.47
50:Z:17:ARG:HH22	52:3:1538:C:H2'	1.79	0.47
50:Z:49:ALA:O	50:Z:52:VAL:HG12	2.13	0.47
52:3:66:A:H61	52:3:103:U:H3	1.62	0.47
53:1:466:A:H2'	53:1:467:G:H5'	1.96	0.47
53:1:1067:A:H2'	53:1:1067:A:N3	2.29	0.47
53:1:1704:C:H2'	53:1:1705:A:C8	2.49	0.47
53:1:2637:U:H2'	53:1:2638:G:O4'	2.14	0.47
53:1:2676:C:H2'	53:1:2677:G:C8	2.49	0.47
53:1:2743:U:H2'	53:1:2744:G:C4'	2.44	0.47
53:1:2799:A:H2'	53:1:2800:A:H5'	1.97	0.47
10:k:92:GLU:HG3	10:k:93:GLN:H	1.80	0.47
11:l:30:THR:O	11:l:33:ARG:HG2	2.14	0.47
12:m:6:ARG:O	12:m:6:ARG:HG2	2.15	0.47
16:q:91:ARG:HD3	53:1:997:G:OP1	2.14	0.47
20:u:71:ILE:HD13	20:u:82:VAL:HG22	1.97	0.47
52:3:1429:A:H2'	52:3:1430:A:C8	2.49	0.47
53:1:596:U:H2'	53:1:597:G:C8	2.49	0.47
53:1:873:C:H2'	53:1:874:G:H8	1.79	0.47
53:1:2244:U:H2'	53:1:2245:U:O4'	2.14	0.47
53:1:2799:A:C2'	53:1:2800:A:H5'	2.44	0.47
54:2:108:A:H5'	54:2:109:A:O5'	2.14	0.47
1:b:179:GLU:OE2	1:b:269:ARG:HD2	2.14	0.47
2:c:34:VAL:HG23	2:c:93:GLY:H	1.79	0.47
9:j:32:LEU:HD22	9:j:54:ILE:HG21	1.96	0.47
22:w:63:VAL:HG22	22:w:64:LYS:N	2.29	0.47
27:C:9:LYS:O	27:C:51:ALA:HB3	2.14	0.47
43:S:46:LYS:HD2	43:S:49:THR:HG21	1.96	0.47
51:a:197:LYS:HA	51:a:200:LYS:NZ	2.30	0.47
52:3:1434:A:H2'	52:3:1435:G:O4'	2.15	0.47
52:3:1527:U:H2'	52:3:1528:U:C6	2.49	0.47
52:3:1534:A:H61	56:4:11:U:H3	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2183:A:H2'	53:1:2184:A:C8	2.49	0.47
53:1:2515:C:H2'	53:1:2516:A:C8	2.48	0.47
53:1:2580:U:H2'	53:1:2581:G:H5'	1.96	0.47
57:7:6:G:C2'	57:7:7:A:H5''	2.44	0.47
2:c:55:LYS:HD2	2:c:77:ARG:HA	1.96	0.47
2:c:128:ARG:NH1	2:c:129:THR:O	2.47	0.47
3:d:44:ARG:HD3	53:1:444:C:OP2	2.15	0.47
4:e:25:MET:HE3	54:2:57:A:H61	1.80	0.47
32:H:78:LYS:HB2	32:H:81:GLU:OE2	2.15	0.47
36:L:6:ILE:HG13	36:L:7:GLY:N	2.29	0.47
37:M:65:PHE:CD2	37:M:66:GLN:HG2	2.50	0.47
43:S:5:MET:HE2	52:3:982:U:H5''	1.94	0.47
46:V:17:GLU:C	46:V:19:SER:H	2.20	0.47
52:3:648:A:H2'	52:3:649:A:C8	2.48	0.47
52:3:1517:G:H1'	53:1:1919:A:O2'	2.14	0.47
53:1:1366:A:H2'	53:1:1367:A:O4'	2.15	0.47
53:1:2469:A:H2'	53:1:2470:G:O4'	2.14	0.47
53:1:2475:C:C2'	53:1:2476:A:H5'	2.44	0.47
5:f:173:ALA:O	5:f:175:LYS:N	2.47	0.47
9:j:80:HIS:CD2	53:1:2642:G:H5'	2.50	0.47
9:j:118:MET:HA	9:j:121:LYS:HZ3	1.78	0.47
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.95	0.47
38:N:64:ILE:HD12	38:N:64:ILE:N	2.30	0.47
46:V:15:LYS:O	52:3:275:G:H4'	2.15	0.47
53:1:639:U:H2'	53:1:640:C:C6	2.49	0.47
53:1:679:C:H2'	53:1:680:C:C6	2.49	0.47
53:1:1535:A:H3'	53:1:1536:C:H5'	1.97	0.47
2:c:130:GLN:NE2	2:c:139:SER:OG	2.47	0.47
5:f:8:VAL:HB	5:f:49:LEU:HB2	1.96	0.47
6:g:87:GLU:HG2	35:K:21:MET:HE3	1.96	0.47
9:j:20:ALA:HA	9:j:23:LYS:HG3	1.96	0.47
13:n:69:ARG:O	13:n:70:THR:OG1	2.24	0.47
20:u:90:LYS:HZ3	53:1:101:A:H62	1.61	0.47
24:y:31:GLN:HG2	24:y:36:GLN:HB2	1.97	0.47
25:z:52:PHE:CD2	54:2:83:G:H4'	2.50	0.47
28:D:21:ARG:C	28:D:23:ALA:H	2.23	0.47
30:F:20:ASP:HA	53:1:2757:A:OP2	2.14	0.47
31:G:44:LYS:C	31:G:47:PRO:HD2	2.40	0.47
31:G:96:LEU:HD13	52:3:1103:C:H5'	1.97	0.47
35:K:18:VAL:CG1	35:K:19:PRO:HD3	2.45	0.47
36:L:101:ARG:HH21	52:3:1376:U:H5'	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:118:ARG:HA	36:L:121:ASN:HD22	1.80	0.47
41:Q:86:VAL:HG12	41:Q:95:HIS:CE1	2.49	0.47
43:S:81:ILE:HG21	52:3:1202:U:N3	2.29	0.47
49:Y:25:SER:HB3	52:3:1458:G:H5''	1.97	0.47
51:a:185:LEU:HA	51:a:188:ASN:HD22	1.79	0.47
52:3:56:U:H2'	52:3:57:G:H8	1.79	0.47
52:3:355:C:H5'	52:3:355:C:H6	1.80	0.47
52:3:396:C:C3'	52:3:397:A:H5''	2.45	0.47
52:3:483:C:H2'	52:3:484:G:C8	2.50	0.47
52:3:665:A:O4'	52:3:733:G:H1'	2.15	0.47
52:3:912:C:O2'	52:3:913:A:H5'	2.15	0.47
52:3:1540:U:O2	52:3:1540:U:H3'	2.15	0.47
53:1:18:U:H2'	53:1:19:A:C8	2.49	0.47
53:1:326:G:H2'	53:1:327:G:H8	1.80	0.47
53:1:1509:A:H2'	53:1:1510:G:C8	2.49	0.47
53:1:2041:U:H2'	53:1:2042:A:C8	2.50	0.47
53:1:2128:G:H21	53:1:2173:A:H1'	1.80	0.47
53:1:2853:C:H2'	53:1:2854:G:H8	1.80	0.47
1:b:11:GLY:O	1:b:206:LYS:HG3	2.15	0.47
25:z:18:LYS:HE2	53:1:920:A:OP1	2.15	0.47
36:L:3:ARG:NH2	52:3:932:C:H5''	2.25	0.47
37:M:54:THR:HG23	37:M:55:LYS:HG3	1.97	0.47
43:S:44:VAL:HG13	43:S:45:LEU:HD22	1.96	0.47
53:1:596:U:H2'	53:1:597:G:H8	1.80	0.47
53:1:996:A:H2'	53:1:997:G:C8	2.49	0.47
53:1:1020:A:C1'	53:1:1021:A:OP2	2.58	0.47
53:1:1827:U:H2'	53:1:1828:G:O4'	2.14	0.47
53:1:2156:G:H2'	53:1:2157:G:H5'	1.97	0.47
3:d:124:PHE:HE1	3:d:141:MET:HE1	1.80	0.47
38:N:69:GLY:N	52:3:1250:A:H4'	2.29	0.47
39:O:18:ILE:HD12	39:O:70:HIS:HB2	1.97	0.47
41:Q:35:ARG:NH2	41:Q:53:ARG:HG3	2.30	0.47
46:V:5:ARG:HD3	52:3:636:U:C5'	2.39	0.47
53:1:1130:U:O2'	53:1:1131:G:OP1	2.28	0.47
53:1:2066:C:O2'	53:1:2067:G:H5'	2.15	0.47
53:1:2421:G:H2'	55:6:76:A:N6	2.29	0.47
55:6:28:C:H2'	55:6:29:G:C8	2.49	0.47
1:b:75:ALA:HB1	1:b:93:VAL:CG1	2.45	0.47
2:c:123:LYS:HZ2	53:1:2724:U:H5''	1.80	0.47
5:f:36:LEU:HD11	5:f:67:ALA:HB1	1.97	0.47
7:h:56:ARG:HB2	53:1:1084:A:C1'	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:148:SER:OG	34:J:151:MET:HG2	2.15	0.47
36:L:138:GLU:HB3	36:L:142:ARG:HH12	1.80	0.47
42:R:14:ALA:HB1	42:R:33:LEU:HD11	1.96	0.47
50:Z:58:LYS:HA	50:Z:61:ARG:HD2	1.96	0.47
52:3:664:G:H22	52:3:741:G:H1	1.62	0.47
53:1:482:A:H1'	53:1:498:G:N2	2.30	0.47
53:1:1268:A:H2'	53:1:1269:A:O4'	2.15	0.47
53:1:2343:U:O2'	53:1:2344:U:H5'	2.14	0.47
54:2:88:C:H4'	54:2:89:U:OP1	2.14	0.47
55:5:69:C:H2'	55:5:70:G:H8	1.80	0.47
55:6:59:A:H2'	55:6:60:U:H5'	1.97	0.47
1:b:127:ASN:HB2	1:b:191:LEU:HD12	1.97	0.46
3:d:12:LEU:HD12	3:d:120:VAL:HG11	1.96	0.46
6:g:5:LEU:HD12	6:g:5:LEU:N	2.30	0.46
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.96	0.46
9:j:84:ILE:HG23	9:j:84:ILE:O	2.15	0.46
16:q:24:TYR:HE1	53:1:17:G:H4'	1.79	0.46
44:T:44:GLU:HG3	44:T:45:HIS:CD2	2.49	0.46
49:Y:4:LYS:HG3	52:3:332:G:P	2.56	0.46
53:1:1412:U:H2'	53:1:1413:A:C8	2.50	0.46
1:b:47:ARG:HD3	53:1:773:U:HO2'	1.80	0.46
1:b:68:ARG:NE	1:b:128:THR:OG1	2.47	0.46
1:b:209:ALA:HA	1:b:212:TRP:NE1	2.30	0.46
2:c:124:ARG:NH1	2:c:125:TRP:HE1	2.12	0.46
9:j:47:HIS:CE1	9:j:48:VAL:HG23	2.50	0.46
12:m:68:PHE:CD1	12:m:69:PRO:HD2	2.51	0.46
16:q:5:ARG:HB2	53:1:584:C:OP2	2.15	0.46
26:B:14:MET:HG2	53:1:15:G:O2'	2.15	0.46
29:E:33:THR:HG23	53:1:2420:C:OP1	2.15	0.46
36:L:111:GLY:HA2	36:L:118:ARG:HH11	1.80	0.46
40:P:111:ASP:OD1	40:P:113:THR:HG23	2.14	0.46
51:a:212:VAL:HG13	51:a:224:VAL:HG23	1.97	0.46
53:1:1201:U:H2'	53:1:1202:G:H8	1.80	0.46
53:1:1773:A:H2'	53:1:1774:C:O4'	2.14	0.46
53:1:2364:C:H2'	53:1:2365:G:O4'	2.16	0.46
58:8:309:VAL:HG22	58:8:310:TYR:N	2.30	0.46
1:b:34:GLU:N	1:b:34:GLU:OE2	2.48	0.46
5:f:163:TYR:CD2	5:f:166:GLU:HB2	2.50	0.46
6:g:14:SER:HB2	6:g:17:ASP:OD2	2.15	0.46
12:m:36:VAL:HG13	21:v:82:TYR:CD2	2.50	0.46
13:n:72:ASP:OD2	13:n:75:ILE:HG13	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:58:GLN:HG3	53:1:1009:A:O4'	2.16	0.46
34:J:108:GLY:H	52:3:9:G:C4'	2.13	0.46
37:M:124:ILE:HD11	37:M:127:TYR:HE1	1.80	0.46
48:X:8:PRO:HB3	48:X:38:THR:HG21	1.96	0.46
52:3:70:U:H4'	52:3:71:A:C8	2.50	0.46
4:e:4:HIS:CD2	4:e:8:LYS:HE3	2.49	0.46
31:G:131:LYS:O	31:G:134:LEU:HB3	2.15	0.46
32:H:111:ASP:HB3	32:H:114:LEU:HB2	1.96	0.46
34:J:37:VAL:HG11	34:J:113:VAL:HG12	1.97	0.46
50:Z:9:GLU:HB2	50:Z:10:PRO:CD	2.44	0.46
53:1:690:G:H2'	53:1:691:C:C6	2.49	0.46
53:1:694:U:C3'	53:1:695:G:H5''	2.45	0.46
53:1:827:U:H4'	53:1:828:U:C5	2.51	0.46
58:8:298:THR:HG23	58:8:299:ILE:HG22	1.96	0.46
58:8:369:MET:HE1	58:8:392:VAL:HA	1.97	0.46
1:b:13:ARG:NH1	53:1:1977:A:H2	2.14	0.46
7:h:5:LEU:HG	7:h:6:GLN:HE21	1.80	0.46
16:q:30:VAL:HG21	53:1:580:U:H4'	1.98	0.46
21:v:18:ARG:HA	21:v:18:ARG:CZ	2.45	0.46
33:I:144:ILE:HD13	33:I:177:MET:HB3	1.98	0.46
33:I:150:LYS:HA	33:I:154:VAL:HB	1.96	0.46
36:L:94:ARG:HA	36:L:97:ALA:HB3	1.97	0.46
39:O:53:ILE:HD12	43:S:84:ARG:HD2	1.97	0.46
40:P:40:ALA:C	40:P:41:LEU:HD12	2.40	0.46
52:3:265:G:H2'	52:3:267:C:H5	1.81	0.46
52:3:393:A:H5'	52:3:483:C:O2'	2.15	0.46
53:1:370:G:H2'	53:1:423:A:N7	2.30	0.46
53:1:441:U:H2'	53:1:442:G:C8	2.51	0.46
53:1:635:C:H2'	53:1:636:G:C8	2.50	0.46
53:1:2642:G:H2'	53:1:2643:G:H8	1.80	0.46
57:7:62:C:H3'	57:7:63:G:H5''	1.96	0.46
11:l:101:ILE:HG13	11:l:102:GLY:H	1.81	0.46
30:F:31:PRO:CB	53:1:2527:C:H5''	2.46	0.46
32:H:160:GLU:OE2	52:3:1055:A:H4'	2.14	0.46
33:I:86:GLY:HA3	33:I:196:GLU:OE1	2.16	0.46
36:L:112:ASP:H	36:L:118:ARG:HD3	1.81	0.46
42:R:112:ARG:HD3	52:3:1229:A:OP2	2.16	0.46
42:R:112:ARG:HD3	52:3:1229:A:P	2.56	0.46
52:3:1432:G:H1'	52:3:1468:A:N6	2.30	0.46
53:1:63:A:H2'	53:1:64:A:H8	1.81	0.46
53:1:367:G:H2'	53:1:368:A:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2834:G:H2'	53:1:2879:A:N6	2.31	0.46
9:j:27:ARG:NH2	53:1:1142:A:H4'	2.28	0.46
14:o:71:ALA:HB1	14:o:106:LEU:HB2	1.98	0.46
15:p:101:GLU:CD	15:p:102:ARG:HG3	2.41	0.46
20:u:3:LYS:O	20:u:93:ARG:NH2	2.49	0.46
33:I:177:MET:HE2	33:I:177:MET:H	1.81	0.46
35:K:47:LEU:HD12	35:K:55:HIS:HA	1.98	0.46
43:S:74:ARG:HH21	52:3:1359:C:H6	1.63	0.46
48:X:47:THR:HA	48:X:60:PHE:HA	1.97	0.46
48:X:77:ARG:HG2	52:3:959:A:N6	2.30	0.46
52:3:92:U:H2'	52:3:93:U:O4'	2.15	0.46
53:1:225:C:H2'	53:1:226:A:O4'	2.15	0.46
53:1:1013:C:H2'	53:1:1014:A:C8	2.51	0.46
2:c:63:PRO:HG3	53:1:2787:C:H1'	1.98	0.46
15:p:88:ARG:HD2	15:p:112:ARG:NH2	2.30	0.46
17:r:14:VAL:HG21	17:r:98:ILE:HG13	1.98	0.46
41:Q:91:GLY:O	41:Q:93:ARG:NH1	2.49	0.46
49:Y:73:ARG:NH2	52:3:261:U:H5	2.14	0.46
52:3:820:U:H3'	52:3:821:G:C5'	2.46	0.46
52:3:1437:A:H2'	52:3:1438:G:H8	1.79	0.46
53:1:2098:U:H2'	53:1:2099:U:O4'	2.16	0.46
53:1:2297:A:N6	53:1:2319:G:H1'	2.31	0.46
53:1:2623:G:H2'	53:1:2624:G:C8	2.51	0.46
54:2:65:U:H3'	54:2:108:A:H61	1.81	0.46
58:8:336:THR:HG22	58:8:337:ASP:N	2.31	0.46
58:8:373:LEU:O	58:8:388:VAL:HG23	2.16	0.46
7:h:88:HIS:H	7:h:89:PRO:HD2	1.80	0.46
9:j:17:VAL:HG23	9:j:137:PRO:HB2	1.98	0.46
24:y:22:LEU:HG	24:y:23:ARG:HE	1.81	0.46
44:T:25:GLU:HG3	44:T:69:LEU:HD11	1.97	0.46
52:3:225:C:H3'	52:3:226:G:H5''	1.98	0.46
52:3:350:G:H2'	52:3:351:G:C8	2.51	0.46
52:3:381:C:H2'	52:3:382:A:O4'	2.15	0.46
52:3:422:C:H5'	52:3:423:G:C2	2.51	0.46
53:1:9:G:H21	53:1:2800:A:H61	1.64	0.46
58:8:313:SER:HA	58:8:319:ARG:O	2.15	0.46
58:8:369:MET:HE1	58:8:392:VAL:HG22	1.98	0.46
7:h:121:SER:OG	7:h:122:GLN:N	2.48	0.46
11:l:93:ASN:C	11:l:95:LEU:H	2.24	0.46
13:n:69:ARG:C	13:n:71:ARG:H	2.24	0.46
14:o:6:ALA:HA	14:o:9:ARG:HE	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C:47:ILE:N	27:C:47:ILE:HD12	2.31	0.46
30:F:3:VAL:HG12	30:F:36:ARG:HD3	1.97	0.46
44:T:55:LEU:HD21	53:1:715:A:C2	2.51	0.46
53:1:1300:G:H4'	53:1:1301:A:H5'	1.98	0.46
57:7:23:A:H2'	57:7:24:G:C8	2.51	0.46
1:b:226:PRO:HD3	1:b:233:GLY:H	1.79	0.45
4:e:58:ALA:O	4:e:139:GLU:HG2	2.17	0.45
21:v:36:ALA:HA	21:v:37:PRO:HD3	1.82	0.45
23:x:62:GLY:O	23:x:66:VAL:HG23	2.16	0.45
26:B:39:ARG:O	26:B:40:HIS:HB2	2.17	0.45
34:J:45:VAL:HG12	34:J:116:VAL:HG23	1.98	0.45
36:L:101:ARG:NH2	52:3:939:G:H4'	2.31	0.45
43:S:58:ARG:NH1	52:3:979:C:H2'	2.26	0.45
46:V:39:ARG:CZ	52:3:237:G:H4'	2.46	0.45
49:Y:26:MET:HA	49:Y:29:THR:HG22	1.98	0.45
52:3:59:A:H5''	52:3:387:U:H5''	1.98	0.45
52:3:1144:G:H2'	52:3:1145:A:C8	2.51	0.45
53:1:996:A:H2'	53:1:997:G:H8	1.79	0.45
1:b:81:GLU:HB2	1:b:90:ILE:HG13	1.98	0.45
3:d:176:ASP:OD2	3:d:178:VAL:HG12	2.16	0.45
8:i:23:VAL:HG12	8:i:26:ALA:HB3	1.98	0.45
12:m:20:LEU:HD23	12:m:21:ALA:N	2.31	0.45
32:H:23:ALA:HB3	32:H:28:PHE:CD1	2.51	0.45
39:O:8:ILE:HB	39:O:74:VAL:HB	1.98	0.45
41:Q:41:PRO:HG3	41:Q:49:ARG:HG3	1.98	0.45
45:U:9:HIS:CE1	45:U:29:ASN:HD22	2.33	0.45
49:Y:56:ILE:HA	49:Y:59:ARG:NH1	2.31	0.45
52:3:34:C:H2'	52:3:35:G:C8	2.51	0.45
52:3:1512:U:H2'	52:3:1513:A:H8	1.81	0.45
53:1:834:G:H1'	53:1:2358:A:N3	2.32	0.45
53:1:922:C:H2'	53:1:923:G:H8	1.81	0.45
53:1:1357:C:H2'	53:1:1358:G:O4'	2.16	0.45
1:b:78:GLU:OE2	1:b:94:LEU:HB2	2.16	0.45
2:c:122:VAL:HA	2:c:127:PHE:H	1.81	0.45
8:i:77:VAL:HG13	8:i:81:LYS:NZ	2.31	0.45
33:I:124:VAL:HG22	33:I:125:ASN:ND2	2.32	0.45
35:K:9:MET:HE1	35:K:86:ARG:HD2	1.98	0.45
37:M:34:ALA:HB1	37:M:109:VAL:HG21	1.99	0.45
39:O:73:LEU:CD2	52:3:1125:U:H1'	2.46	0.45
50:Z:7:GLU:HB3	50:Z:11:PHE:HB3	1.97	0.45
52:3:12:U:H2'	52:3:13:U:H5''	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:129:A:H1'	52:3:130:A:C8	2.51	0.45
53:1:1319:C:O2'	53:1:1320:C:H5'	2.16	0.45
53:1:1387:A:H2'	53:1:1388:G:C8	2.51	0.45
53:1:2841:C:H2'	53:1:2842:G:C8	2.50	0.45
58:8:334:ARG:HG3	58:8:335:THR:N	2.29	0.45
4:e:3:LEU:HG	4:e:100:GLU:OE2	2.16	0.45
5:f:169:ARG:HH22	5:f:171:LYS:HD2	1.81	0.45
7:h:99:PHE:HB2	7:h:113:PHE:HE1	1.81	0.45
10:k:7:MET:SD	10:k:20:MET:HB3	2.56	0.45
33:I:169:TRP:CD2	33:I:185:PRO:HG3	2.52	0.45
43:S:63:CYS:HB3	43:S:68:ARG:H	1.82	0.45
52:3:151:A:H62	52:3:170:U:H3	1.63	0.45
52:3:410:G:H2'	52:3:429:U:O4	2.17	0.45
52:3:604:G:H2'	52:3:605:U:O4'	2.17	0.45
52:3:981:U:H2'	52:3:982:U:C5	2.52	0.45
53:1:2808:G:H2'	53:1:2890:G:C6	2.51	0.45
8:i:12:VAL:HG22	53:1:1061:U:O2	2.16	0.45
9:j:81:ILE:HD11	53:1:2514:U:C5'	2.47	0.45
11:l:121:THR:HG23	11:l:141:LYS:HB3	1.98	0.45
15:p:72:VAL:HG22	15:p:73:PHE:H	1.82	0.45
20:u:4:ILE:HD12	20:u:4:ILE:N	2.31	0.45
22:w:14:ALA:HB1	53:1:2271:G:OP1	2.16	0.45
46:V:43:LEU:HD21	46:V:72:TRP:CG	2.51	0.45
48:X:27:LYS:HD3	48:X:28:LYS:HD3	1.98	0.45
52:3:225:C:C2'	52:3:226:G:H5''	2.46	0.45
52:3:460:A:H2'	52:3:461:A:C8	2.52	0.45
52:3:1369:C:H2'	52:3:1370:G:C8	2.51	0.45
53:1:414:C:H2'	53:1:415:A:C8	2.52	0.45
53:1:1234:U:H2'	53:1:1235:G:O4'	2.15	0.45
57:7:68:C:H2'	57:7:69:G:C8	2.50	0.45
1:b:251:THR:OG1	1:b:252:LYS:N	2.50	0.45
2:c:125:TRP:HB3	2:c:160:LYS:HD3	1.98	0.45
5:f:41:GLU:HA	5:f:54:ARG:NH2	2.31	0.45
8:i:73:PRO:HA	8:i:74:PRO:HD3	1.84	0.45
19:t:17:SER:H	19:t:20:ALA:HB3	1.82	0.45
21:v:72:VAL:HG12	21:v:93:ARG:HA	1.99	0.45
35:K:51:ILE:C	35:K:53:LYS:H	2.24	0.45
37:M:17:GLN:OE1	37:M:69:ALA:HB1	2.16	0.45
37:M:46:GLU:OE1	37:M:63:LYS:HD3	2.16	0.45
39:O:41:PRO:HG3	52:3:1150:A:C2	2.51	0.45
39:O:60:ASP:HA	39:O:62:ARG:NH1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:P:87:GLY:H	40:P:113:THR:HG22	1.82	0.45
52:3:297:G:H4'	52:3:557:G:H4'	1.98	0.45
53:1:869:G:H2'	53:1:870:U:O4'	2.16	0.45
53:1:1367:A:C2'	53:1:1368:G:H5'	2.45	0.45
53:1:1565:C:O2'	53:1:1566:A:H2'	2.17	0.45
53:1:2292:U:H2'	53:1:2293:G:C8	2.52	0.45
57:7:51:U:H2'	57:7:52:G:H8	1.81	0.45
6:g:8:LYS:O	6:g:9:VAL:C	2.59	0.45
7:h:26:VAL:HB	7:h:82:ILE:HD12	1.98	0.45
7:h:122:GLN:HG3	7:h:123:ILE:N	2.19	0.45
10:k:68:GLY:CA	10:k:78:ARG:HG2	2.46	0.45
30:F:36:ARG:O	30:F:37:GLN:O	2.35	0.45
34:J:156:ARG:HH12	34:J:163:ILE:HA	1.81	0.45
52:3:86:G:H4'	52:3:87:C:C5	2.51	0.45
52:3:144:G:H2'	52:3:145:G:O4'	2.17	0.45
52:3:235:C:H2'	52:3:236:A:H8	1.82	0.45
53:1:833:A:H2'	53:1:834:G:C8	2.52	0.45
53:1:1021:A:H3'	53:1:1021:A:N3	2.32	0.45
53:1:1266:G:N2	53:1:2012:G:H2'	2.32	0.45
53:1:2039:U:H2'	53:1:2040:G:H8	1.81	0.45
53:1:2047:C:H2'	53:1:2048:G:H8	1.82	0.45
53:1:2114:A:N6	53:1:2119:A:H61	2.14	0.45
1:b:257:ARG:HD3	53:1:1799:G:OP1	2.16	0.45
1:b:270:ARG:HG3	1:b:270:ARG:HH11	1.80	0.45
4:e:124:ARG:HG3	53:1:2315:G:O2'	2.17	0.45
5:f:137:LYS:HD3	53:1:2746:U:O3'	2.17	0.45
8:i:99:LYS:HD2	8:i:138:VAL:HB	1.99	0.45
10:k:22:ILE:HD12	53:1:1952:A:C2	2.52	0.45
22:w:71:LYS:HG2	22:w:73:ARG:HH21	1.82	0.45
37:M:1:SER:HB2	37:M:2:MET:SD	2.57	0.45
43:S:41:TRP:HZ3	48:X:7:GLY:HA3	1.81	0.45
52:3:1001:C:H2'	52:3:1002:G:H8	1.82	0.45
52:3:1299:A:H2'	52:3:1300:G:H4'	1.98	0.45
52:3:1366:C:H2'	52:3:1367:C:C6	2.52	0.45
53:1:738:G:O2'	53:1:739:A:H5'	2.16	0.45
53:1:828:U:H4'	53:1:831:G:N1	2.32	0.45
53:1:1758:U:C5	53:1:2696:U:H5'	2.52	0.45
58:8:378:ARG:HH11	58:8:378:ARG:HG3	1.80	0.45
5:f:29:ASN:HB2	5:f:78:VAL:HA	1.97	0.45
5:f:40:VAL:HG12	5:f:42:VAL:HG13	1.99	0.45
6:g:69:ALA:HB3	6:g:134:VAL:HB	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:19:ALA:HA	7:h:70:GLU:HG2	1.99	0.45
8:i:18:ASN:ND2	8:i:38:CYS:SG	2.90	0.45
9:j:4:PHE:O	16:q:63:ARG:NH2	2.50	0.45
10:k:113:MET:SD	10:k:116:ILE:HD11	2.56	0.45
19:t:26:LYS:C	19:t:26:LYS:HD3	2.41	0.45
34:J:92:ARG:O	34:J:93:VAL:C	2.60	0.45
37:M:54:THR:C	37:M:56:PRO:HD3	2.42	0.45
37:M:62:LEU:N	37:M:62:LEU:HD12	2.32	0.45
43:S:65:GLN:HB2	43:S:78:LEU:HD22	1.98	0.45
52:3:128:G:H2'	52:3:129:A:C8	2.51	0.45
52:3:352:C:H4'	52:3:354:G:OP1	2.17	0.45
52:3:424:G:H2'	52:3:425:G:H8	1.80	0.45
52:3:594:U:H2'	52:3:595:A:O4'	2.17	0.45
53:1:1326:U:H2'	53:1:1327:A:C8	2.52	0.45
53:1:2197:U:H1'	53:1:2198:A:C8	2.51	0.45
53:1:2801:G:H2'	53:1:2802:G:C8	2.52	0.45
54:2:66:A:H5''	54:2:67:G:OP1	2.17	0.45
9:j:113:PRO:HD2	53:1:558:U:OP2	2.17	0.45
16:q:54:ARG:HE	53:1:1155:A:H5''	1.81	0.45
21:v:30:ILE:HG22	21:v:91:PHE:HB2	1.99	0.45
25:z:8:GLN:HE21	25:z:54:VAL:HG12	1.82	0.45
47:W:44:THR:HG23	47:W:46:THR:HG23	1.99	0.45
49:Y:74:HIS:O	49:Y:78:LEU:HD13	2.16	0.45
52:3:744:C:H2'	52:3:745:G:H8	1.82	0.45
52:3:855:U:H2'	52:3:856:C:C6	2.51	0.45
53:1:311:A:H2	53:1:331:C:H3'	1.82	0.45
53:1:1023:U:O2'	53:1:1122:G:H5'	2.17	0.45
53:1:1026:G:H2'	53:1:1027:A:C8	2.50	0.45
53:1:1695:G:H3'	53:1:1695:G:N3	2.32	0.45
53:1:1720:U:H2'	53:1:1721:G:O4'	2.16	0.45
53:1:2398:U:H2'	53:1:2399:G:C8	2.52	0.45
55:5:47:U:H3'	55:5:48:C:C5'	2.47	0.45
5:f:98:LYS:NZ	5:f:103:ASN:HD22	2.15	0.44
10:k:23:LYS:NZ	53:1:2548:U:O2	2.49	0.44
15:p:13:LYS:HB2	15:p:15:ASP:OD1	2.18	0.44
15:p:94:ALA:HB2	53:1:2848:G:N7	2.32	0.44
20:u:87:GLU:OE1	20:u:101:THR:HG21	2.18	0.44
33:I:120:LYS:CE	52:3:439:U:H5''	2.47	0.44
33:I:172:VAL:HG22	33:I:173:ASP:N	2.32	0.44
35:K:46:GLN:HA	35:K:56:LYS:HA	2.00	0.44
35:K:66:ALA:HB1	35:K:67:PRO:HD2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:2:ARG:HB3	52:3:933:G:OP2	2.16	0.44
36:L:3:ARG:HH12	52:3:1092:A:C5'	2.23	0.44
39:O:9:ARG:HG2	39:O:71:LEU:HD11	1.98	0.44
40:P:124:LYS:NZ	52:3:1524:C:OP2	2.47	0.44
43:S:4:SER:CB	52:3:1216:A:H5''	2.47	0.44
52:3:273:U:O2'	52:3:274:A:H5'	2.17	0.44
52:3:779:C:H2'	52:3:780:A:O4'	2.18	0.44
53:1:917:A:H2'	53:1:918:A:O4'	2.17	0.44
53:1:1822:C:H2'	53:1:1823:G:H8	1.82	0.44
53:1:1930:G:O2'	53:1:1931:U:C5	2.70	0.44
53:1:2208:C:H2'	53:1:2209:G:C8	2.51	0.44
53:1:2318:G:H2'	53:1:2319:G:O4'	2.17	0.44
53:1:2818:U:H2'	53:1:2819:G:H8	1.81	0.44
54:2:51:G:O2'	54:2:52:A:H5'	2.17	0.44
55:6:63:G:H2'	55:6:64:G:C8	2.52	0.44
58:8:391:LYS:HG2	58:8:392:VAL:H	1.82	0.44
3:d:146:VAL:HA	3:d:185:LYS:O	2.17	0.44
6:g:83:LYS:HA	6:g:149:GLU:OXT	2.18	0.44
11:l:69:ARG:HB3	11:l:69:ARG:NH1	2.32	0.44
11:l:101:ILE:HG13	11:l:102:GLY:N	2.32	0.44
12:m:134:THR:OG1	21:v:79:ARG:NH1	2.51	0.44
13:n:2:ARG:HA	13:n:5:LYS:HD2	1.99	0.44
16:q:57:ARG:O	16:q:61:ILE:HG12	2.17	0.44
17:r:24:LYS:HA	17:r:94:THR:OG1	2.16	0.44
20:u:84:PHE:CE1	20:u:93:ARG:HG2	2.52	0.44
23:x:60:LYS:HE3	53:1:372:G:C4	2.52	0.44
24:y:9:LYS:NZ	24:y:11:VAL:HB	2.31	0.44
25:z:10:ARG:HB2	25:z:53:MET:HB2	1.97	0.44
31:G:67:LEU:HD12	31:G:91:VAL:HG23	1.99	0.44
32:H:171:ARG:HG3	52:3:1107:C:OP1	2.17	0.44
35:K:47:LEU:HD21	35:K:57:ALA:HB3	1.99	0.44
45:U:20:VAL:HG22	45:U:21:VAL:N	2.32	0.44
46:V:70:LYS:NZ	52:3:254:G:O3'	2.47	0.44
52:3:1252:A:H2'	52:3:1253:G:O4'	2.16	0.44
52:3:1315:U:H2'	52:3:1316:G:O4'	2.17	0.44
53:1:433:C:O2'	53:1:434:U:H5'	2.17	0.44
53:1:1697:G:H4'	53:1:1978:A:H5''	1.99	0.44
55:5:3:C:H2'	55:5:4:G:C8	2.53	0.44
2:c:108:ASP:OD2	2:c:206:ALA:HA	2.16	0.44
4:e:90:LEU:HD23	4:e:90:LEU:H	1.81	0.44
7:h:41:LEU:HD13	53:1:1083:U:O5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:59:LEU:HB3	7:h:62:ARG:CB	2.47	0.44
8:i:52:LEU:HD23	8:i:53:PRO:N	2.31	0.44
16:q:96:ASP:OD2	17:r:13:ARG:NE	2.47	0.44
16:q:113:LYS:HA	16:q:116:LEU:HB3	1.99	0.44
18:s:3:THR:OG1	18:s:107:VAL:O	2.34	0.44
22:w:7:ARG:N	22:w:7:ARG:HH11	2.16	0.44
24:y:13:GLU:OE1	24:y:57:LEU:HA	2.17	0.44
37:M:29:SER:HB2	37:M:32:LYS:HG3	1.99	0.44
41:Q:89:LEU:HA	41:Q:90:PRO:HD3	1.83	0.44
49:Y:31:ILE:O	49:Y:34:VAL:HG22	2.16	0.44
52:3:243:A:H4'	52:3:244:U:H3'	1.99	0.44
52:3:982:U:H4'	52:3:983:A:O5'	2.17	0.44
52:3:1137:C:H5'	52:3:1138:G:H5'	1.99	0.44
53:1:671:C:H2'	53:1:672:C:C6	2.52	0.44
53:1:2267:A:H5''	53:1:2268:A:H5'	1.98	0.44
54:2:97:C:H2'	54:2:98:G:O4'	2.17	0.44
1:b:231:HIS:HE1	53:1:1825:U:H4'	1.82	0.44
3:d:16:GLU:OE2	3:d:20:GLY:HA3	2.17	0.44
6:g:60:GLU:O	6:g:63:ALA:HB3	2.17	0.44
6:g:70:GLU:OE2	6:g:71:LYS:HE2	2.18	0.44
7:h:59:LEU:HG	7:h:61:ARG:H	1.81	0.44
8:i:99:LYS:HE3	8:i:138:VAL:HG23	1.99	0.44
12:m:55:ARG:HA	12:m:59:ARG:NH1	2.33	0.44
19:t:70:HIS:O	19:t:73:ARG:NH2	2.51	0.44
26:B:46:GLY:HA3	26:B:54:ILE:CG2	2.47	0.44
29:E:32:LEU:HB3	29:E:40:LYS:NZ	2.32	0.44
31:G:11:ALA:HB1	31:G:208:ALA:HA	1.99	0.44
33:I:87:GLU:O	33:I:90:LEU:HD23	2.17	0.44
33:I:169:TRP:CD1	33:I:185:PRO:HG3	2.52	0.44
36:L:71:THR:HA	36:L:90:VAL:HG22	2.00	0.44
39:O:42:LEU:HA	39:O:43:PRO:HD2	1.82	0.44
43:S:66:THR:OG1	52:3:1203:C:H5'	2.18	0.44
43:S:82:LYS:HA	43:S:85:GLU:HG3	1.99	0.44
45:U:13:LYS:HE3	52:3:392:C:H5'	2.00	0.44
45:U:57:ILE:HG22	45:U:61:VAL:HG13	1.98	0.44
46:V:18:LYS:HZ1	46:V:48:GLU:HA	1.82	0.44
53:1:2461:A:H1'	53:1:2492:U:N3	2.31	0.44
1:b:213:ARG:HH22	53:1:1566:A:H5'	1.82	0.44
6:g:51:ARG:HA	6:g:55:GLU:HB2	1.99	0.44
8:i:12:VAL:HG22	53:1:1061:U:C2	2.52	0.44
14:o:12:THR:HG23	53:1:2334:U:C4'	2.45	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:26:ALA:O	16:q:30:VAL:N	2.50	0.44
23:x:73:ARG:HB3	23:x:75:GLU:HG2	2.00	0.44
34:J:134:ASN:ND2	52:3:19:A:OP1	2.51	0.44
36:L:47:GLU:O	36:L:51:GLN:HG2	2.18	0.44
38:N:27:ILE:N	38:N:27:ILE:HD12	2.32	0.44
43:S:74:ARG:HH22	52:3:1359:C:H3'	1.82	0.44
52:3:631:C:H3'	52:3:632:U:H5'	1.99	0.44
52:3:824:G:H2'	52:3:825:A:H8	1.82	0.44
52:3:1002:G:H2'	52:3:1003:G:O4'	2.18	0.44
52:3:1088:G:N2	52:3:1167:A:H61	2.15	0.44
53:1:123:G:H2'	53:1:124:G:C8	2.53	0.44
53:1:2432:A:N3	55:6:75:C:H5'	2.32	0.44
1:b:57:HIS:HD1	1:b:58:LYS:N	2.16	0.44
4:e:7:TYR:O	4:e:12:VAL:HG23	2.17	0.44
6:g:8:LYS:O	6:g:13:GLY:HA3	2.17	0.44
6:g:59:ALA:O	6:g:62:LEU:HB2	2.18	0.44
8:i:23:VAL:CG1	8:i:26:ALA:HB3	2.47	0.44
31:G:33:ALA:HB2	31:G:38:HIS:HD2	1.83	0.44
31:G:217:ALA:HB1	31:G:221:ARG:NH1	2.33	0.44
36:L:146:ALA:O	40:P:55:ARG:NH2	2.42	0.44
37:M:80:PRO:HG2	52:3:878:A:C5'	2.48	0.44
52:3:295:C:H2'	52:3:296:U:O4'	2.18	0.44
52:3:361:G:H2'	52:3:362:G:O4'	2.18	0.44
52:3:1001:C:H2'	52:3:1002:G:C8	2.52	0.44
53:1:123:G:H2'	53:1:124:G:H8	1.82	0.44
53:1:621:A:C2'	53:1:622:G:H5'	2.48	0.44
53:1:1287:A:O2'	53:1:1288:G:H5'	2.18	0.44
53:1:1378:A:H1'	53:1:1379:U:C5	2.52	0.44
53:1:2329:U:H2'	53:1:2330:G:H8	1.81	0.44
53:1:2818:U:H2'	53:1:2819:G:C8	2.52	0.44
57:7:62:C:H2'	57:7:63:G:C5'	2.48	0.44
58:8:352:MET:HA	58:8:353:PRO:HD3	1.87	0.44
1:b:86:ARG:HG3	1:b:86:ARG:HH11	1.83	0.44
3:d:163:ASN:HB2	53:1:322:A:OP2	2.17	0.44
14:o:29:HIS:HB3	14:o:36:TYR:HB2	2.00	0.44
17:r:38:VAL:O	17:r:54:VAL:HG23	2.17	0.44
31:G:72:LYS:HB3	31:G:75:ALA:HB3	1.99	0.44
33:I:43:ARG:NH1	33:I:44:LYS:O	2.51	0.44
36:L:129:ASN:HB2	36:L:134:VAL:HG11	2.00	0.44
42:R:21:ILE:N	42:R:21:ILE:HD12	2.33	0.44
48:X:11:ASP:CG	48:X:14:LEU:HB2	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:501:C:H2'	52:3:502:A:H8	1.80	0.44
52:3:880:C:H2'	52:3:881:G:H8	1.83	0.44
52:3:1137:C:H4'	52:3:1138:G:N2	2.33	0.44
52:3:1163:A:H2'	52:3:1164:G:C8	2.53	0.44
52:3:1404:C:H2'	52:3:1405:G:C8	2.53	0.44
53:1:515:A:H2'	53:1:516:C:H5'	1.98	0.44
53:1:759:G:H2'	53:1:760:G:H8	1.83	0.44
1:b:2:VAL:HG21	1:b:201:LEU:HD13	2.00	0.44
3:d:1:MET:HG3	3:d:3:LEU:HD22	1.99	0.44
10:k:70:ARG:NH1	10:k:76:VAL:HB	2.32	0.44
24:y:4:LYS:HA	24:y:7:ARG:HH12	1.81	0.44
30:F:22:VAL:CG2	30:F:24:ARG:HE	2.30	0.44
32:H:137:VAL:HA	32:H:148:ILE:HD13	1.99	0.44
37:M:64:TYR:HD1	37:M:69:ALA:HA	1.82	0.44
45:U:33:ILE:HD12	45:U:33:ILE:N	2.33	0.44
46:V:17:GLU:CD	46:V:17:GLU:N	2.76	0.44
51:a:3:LYS:HD2	53:1:2107:G:H3'	2.00	0.44
52:3:67:C:H2'	52:3:68:G:H8	1.83	0.44
52:3:123:U:H2'	52:3:124:C:C6	2.53	0.44
52:3:309:A:H2'	52:3:310:G:H8	1.82	0.44
52:3:422:C:H5'	52:3:423:G:N3	2.33	0.44
53:1:1297:C:H2'	53:1:1298:C:C6	2.53	0.44
53:1:1563:U:H2'	53:1:1564:C:C6	2.52	0.44
53:1:1979:U:O2'	53:1:1980:G:H5'	2.18	0.44
53:1:2366:A:H2'	53:1:2367:G:O4'	2.18	0.44
53:1:2707:U:H2'	53:1:2708:G:H8	1.81	0.44
55:5:20:U:H3'	55:5:21:A:H5'	1.99	0.44
6:g:6:LEU:HD23	6:g:6:LEU:O	2.17	0.44
6:g:31:VAL:N	6:g:32:PRO:HD2	2.33	0.44
9:j:118:MET:HA	9:j:121:LYS:HZ1	1.83	0.44
15:p:31:VAL:HG12	15:p:38:ARG:O	2.18	0.44
18:s:69:LEU:HD12	18:s:109:ASP:HA	1.99	0.44
23:x:56:ARG:NH1	53:1:399:U:OP2	2.51	0.44
33:I:8:LEU:HD21	33:I:31:CYS:HB3	1.99	0.44
33:I:54:LEU:HD21	33:I:55:ARG:HH21	1.83	0.44
35:K:4:TYR:CE2	35:K:71:ILE:HG13	2.53	0.44
36:L:75:LYS:NZ	52:3:937:A:O3'	2.50	0.44
45:U:20:VAL:HG22	45:U:21:VAL:H	1.83	0.44
50:Z:23:GLU:O	50:Z:24:LYS:HG2	2.18	0.44
51:a:6:LYS:HG3	51:a:7:ARG:H	1.83	0.44
52:3:514:C:H2'	52:3:515:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:662:U:H2'	52:3:663:A:C8	2.53	0.44
52:3:730:G:C2'	52:3:731:G:H5'	2.48	0.44
53:1:729:G:H4'	53:1:763:G:C5'	2.47	0.44
53:1:1044:C:O3'	53:1:1047:G:H5'	2.18	0.44
2:c:46:ARG:NH2	2:c:88:GLU:O	2.51	0.43
2:c:50:VAL:HG22	2:c:51:THR:N	2.33	0.43
2:c:112:THR:O	2:c:195:GLY:HA2	2.18	0.43
4:e:116:LEU:CD1	4:e:175:PRO:HD2	2.48	0.43
4:e:145:VAL:HG22	4:e:147:ARG:H	1.83	0.43
12:m:3:GLN:HA	12:m:4:PRO:HD3	1.88	0.43
25:z:50:VAL:O	25:z:54:VAL:HG22	2.18	0.43
30:F:3:VAL:HG21	53:1:2539:C:H5'	2.00	0.43
31:G:169:HIS:HA	31:G:172:ILE:HD12	1.99	0.43
40:P:28:ASN:ND2	40:P:30:ILE:HB	2.31	0.43
50:Z:17:ARG:O	50:Z:20:ARG:HG2	2.18	0.43
51:a:5:THR:OG1	51:a:6:LYS:N	2.49	0.43
52:3:634:C:H2'	52:3:635:A:C8	2.53	0.43
52:3:1230:C:H5'	55:5:30:G:H5''	2.00	0.43
52:3:1496:C:H2'	52:3:1497:G:O4'	2.17	0.43
53:1:255:A:H2'	53:1:256:A:O4'	2.17	0.43
53:1:582:A:H2'	53:1:583:G:H8	1.82	0.43
53:1:942:G:H2'	53:1:943:A:O4'	2.17	0.43
53:1:1103:A:H2'	53:1:1103:A:N3	2.33	0.43
1:b:164:VAL:HG21	1:b:180:MET:HE1	2.00	0.43
13:n:79:LEU:O	13:n:80:PHE:HB2	2.19	0.43
19:t:78:SER:OG	53:1:58:G:H5'	2.18	0.43
30:F:11:CYS:HB3	30:F:14:CYS:SG	2.58	0.43
32:H:8:GLY:HA2	32:H:11:LEU:HG	2.00	0.43
32:H:71:ARG:O	32:H:75:VAL:HG23	2.18	0.43
33:I:80:ARG:HG2	52:3:613:C:OP1	2.17	0.43
38:N:61:ASP:C	38:N:62:LEU:HD22	2.43	0.43
42:R:102:LYS:NZ	52:3:952:U:H5	2.16	0.43
44:T:68:TYR:HB2	52:3:754:C:C4'	2.47	0.43
48:X:49:ALA:HA	48:X:58:PRO:HA	2.00	0.43
52:3:252:U:O2	52:3:252:U:H2'	2.18	0.43
52:3:824:G:H2'	52:3:825:A:C8	2.52	0.43
52:3:976:G:N2	52:3:1362:A:H2'	2.33	0.43
53:1:581:C:H2'	53:1:582:A:H8	1.82	0.43
53:1:1539:U:H2'	53:1:1540:G:H8	1.84	0.43
53:1:1683:U:H2'	53:1:1684:G:C8	2.54	0.43
53:1:1955:U:H2'	53:1:2551:C:O2'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2642:G:H2'	53:1:2643:G:C8	2.53	0.43
53:1:2836:U:H2'	53:1:2837:A:C8	2.52	0.43
1:b:134:ILE:H	1:b:166:ARG:HH12	1.66	0.43
2:c:24:VAL:HG12	2:c:190:LYS:HA	2.00	0.43
9:j:15:TRP:HB3	9:j:137:PRO:HB3	2.01	0.43
11:l:132:ARG:HG3	11:l:142:ILE:HD13	2.00	0.43
17:r:14:VAL:HG23	17:r:18:GLN:HE21	1.84	0.43
34:J:23:THR:HG21	52:3:1396:A:C2	2.53	0.43
36:L:91:ARG:HD3	36:L:92:PRO:HD2	1.99	0.43
45:U:75:ILE:HG23	45:U:80:LYS:HD3	2.00	0.43
52:3:273:U:C2'	52:3:274:A:H5'	2.48	0.43
52:3:674:G:H2'	52:3:675:A:C8	2.54	0.43
52:3:715:A:H2'	52:3:716:A:H8	1.82	0.43
53:1:20:C:H2'	53:1:21:A:C8	2.53	0.43
53:1:210:C:H2'	53:1:211:C:C6	2.53	0.43
53:1:727:A:O2'	53:1:728:G:H5'	2.18	0.43
53:1:1412:U:H2'	53:1:1413:A:H8	1.84	0.43
53:1:2060:A:O4'	53:1:2502:G:H1'	2.17	0.43
53:1:2126:A:H2'	53:1:2162:G:N2	2.32	0.43
54:2:3:C:H3'	54:2:4:C:C5'	2.49	0.43
3:d:95:LYS:NZ	53:1:607:U:H4'	2.32	0.43
31:G:206:ILE:HD12	31:G:206:ILE:N	2.30	0.43
33:I:52:VAL:HG23	33:I:53:GLN:NE2	2.32	0.43
38:N:123:ARG:HB2	52:3:1343:G:H4'	2.00	0.43
45:U:10:GLY:O	52:3:624:C:H4'	2.18	0.43
52:3:424:G:H2'	52:3:425:G:C8	2.52	0.43
52:3:601:G:H2'	52:3:602:A:C8	2.53	0.43
52:3:1071:C:H2'	52:3:1072:G:H8	1.83	0.43
52:3:1125:U:H2'	52:3:1126:U:H2'	1.99	0.43
53:1:1825:U:H2'	53:1:1826:G:C8	2.54	0.43
53:1:2139:U:H2'	53:1:2140:G:C8	2.54	0.43
1:b:209:ALA:HA	1:b:212:TRP:CE2	2.54	0.43
2:c:130:GLN:H	2:c:130:GLN:HG2	1.62	0.43
11:l:49:GLY:HA3	11:l:58:TYR:HE1	1.84	0.43
16:q:36:GLN:O	16:q:39:ILE:HG22	2.18	0.43
24:y:9:LYS:HZ2	24:y:11:VAL:HB	1.83	0.43
36:L:104:VAL:O	36:L:108:ARG:HG2	2.18	0.43
39:O:59:LYS:NZ	39:O:62:ARG:HE	2.16	0.43
42:R:23:GLY:O	52:3:1329:A:H4'	2.18	0.43
45:U:76:LYS:HZ3	52:3:473:U:H5''	1.83	0.43
49:Y:60:GLN:HG2	49:Y:65:LEU:HD23	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:64:ALA:O	50:Z:65:ARG:HB2	2.19	0.43
51:a:167:LYS:HE3	55:6:54:U:O2'	2.19	0.43
52:3:137:U:H2'	52:3:138:G:H8	1.83	0.43
52:3:876:C:H2'	52:3:877:G:H8	1.84	0.43
53:1:1073:A:H2'	53:1:1074:G:O4'	2.19	0.43
53:1:1370:C:H2'	53:1:1371:G:C8	2.54	0.43
53:1:1991:U:H2'	53:1:1992:G:C5'	2.48	0.43
53:1:2822:G:H2'	53:1:2823:A:H5''	2.00	0.43
57:7:16:U:H2'	57:7:17:C:H4'	2.01	0.43
2:c:157:LYS:HB3	9:j:80:HIS:HA	2.00	0.43
3:d:189:THR:HG22	3:d:191:ASP:H	1.82	0.43
15:p:15:ASP:OD1	15:p:15:ASP:N	2.52	0.43
31:G:138:ARG:HA	31:G:141:GLU:HB2	2.00	0.43
33:I:80:ARG:NH1	52:3:614:C:OP2	2.51	0.43
37:M:12:ARG:NH2	52:3:826:C:H5'	2.33	0.43
50:Z:66:ARG:NH2	52:3:1099:G:H4'	2.33	0.43
52:3:129:A:H1'	52:3:130:A:N7	2.33	0.43
52:3:405:U:C3'	52:3:406:G:H5'	2.38	0.43
53:1:1266:G:H22	53:1:2012:G:H2'	1.83	0.43
53:1:2055:C:H5'	53:1:2056:G:O5'	2.19	0.43
54:2:60:C:H2'	54:2:61:G:H8	1.83	0.43
57:7:26:A:H2'	57:7:27:G:O4'	2.18	0.43
1:b:41:GLY:HA3	1:b:48:ILE:HD12	2.01	0.43
3:d:162:ARG:NH1	53:1:321:U:H1'	2.34	0.43
20:u:28:LEU:HD12	20:u:32:LYS:HB2	2.00	0.43
21:v:25:LYS:HB3	21:v:41:GLU:OE1	2.18	0.43
23:x:7:THR:CG2	23:x:9:LYS:HG3	2.47	0.43
24:y:4:LYS:HG3	24:y:7:ARG:HH22	1.83	0.43
30:F:31:PRO:HB2	53:1:2527:C:H5''	2.00	0.43
34:J:14:LEU:HA	34:J:36:THR:HG22	1.99	0.43
34:J:18:ASN:O	34:J:33:THR:HG22	2.18	0.43
38:N:129:ARG:HH21	55:5:33:U:H3'	1.82	0.43
46:V:43:LEU:HD21	46:V:72:TRP:CD1	2.54	0.43
52:3:409:U:H2'	52:3:410:G:O4'	2.18	0.43
52:3:974:A:H5'	52:3:976:G:OP1	2.18	0.43
53:1:399:U:H2'	53:1:400:G:O4'	2.19	0.43
53:1:1167:C:H2'	53:1:1168:G:C8	2.54	0.43
53:1:1213:A:N6	53:1:1236:G:H1'	2.34	0.43
53:1:1219:U:H2'	53:1:1220:G:C8	2.54	0.43
53:1:1298:C:H2'	53:1:1299:G:O4'	2.18	0.43
53:1:1889:A:H2'	53:1:1890:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2047:C:H2'	53:1:2048:G:C8	2.53	0.43
53:1:2542:A:H4'	53:1:2543:G:H8	1.83	0.43
4:e:65:LEU:HD22	54:2:42:C:C4	2.54	0.43
11:l:47:ARG:HD3	53:1:195:A:H5''	2.00	0.43
23:x:39:VAL:HG12	23:x:44:ARG:O	2.18	0.43
28:D:3:ARG:HD2	28:D:4:THR:H	1.84	0.43
32:H:69:THR:OG1	32:H:70:ALA:N	2.52	0.43
33:I:90:LEU:HD12	33:I:190:LEU:HD21	2.00	0.43
33:I:101:VAL:HG22	33:I:106:PHE:HB2	2.01	0.43
33:I:140:ASP:OD1	33:I:181:PHE:HB3	2.18	0.43
48:X:17:LYS:HE3	48:X:30:LEU:CD2	2.49	0.43
49:Y:23:ARG:CZ	52:3:176:C:H5''	2.48	0.43
52:3:517:G:H2'	52:3:531:U:C5	2.53	0.43
52:3:987:G:H2'	52:3:988:G:C8	2.54	0.43
53:1:753:A:H2'	53:1:754:U:C6	2.53	0.43
53:1:1010:A:N3	53:1:1153:C:H1'	2.33	0.43
53:1:2443:C:O2'	53:1:2444:G:H5'	2.18	0.43
53:1:2724:U:H2'	53:1:2725:A:C8	2.53	0.43
53:1:2743:U:H2'	53:1:2744:G:C5'	2.49	0.43
57:7:52:G:H2'	57:7:53:G:C8	2.54	0.43
2:c:138:LEU:N	2:c:138:LEU:HD12	2.34	0.43
3:d:151:GLY:HA2	3:d:172:ALA:HB2	2.01	0.43
3:d:194:LYS:HA	3:d:194:LYS:HD2	1.84	0.43
7:h:122:GLN:CG	7:h:123:ILE:H	2.19	0.43
8:i:24:GLY:HA3	8:i:25:PRO:HD3	1.85	0.43
9:j:1:MET:SD	9:j:1:MET:N	2.85	0.43
12:m:54:THR:HG22	12:m:63:ILE:HD12	2.00	0.43
15:p:2:ASN:O	15:p:5:LYS:HB2	2.19	0.43
25:z:9:THR:HG23	25:z:10:ARG:HG2	2.00	0.43
34:J:68:ARG:HH11	34:J:68:ARG:HG3	1.84	0.43
39:O:64:GLN:HB3	43:S:98:ALA:HB3	2.01	0.43
48:X:77:ARG:NH1	52:3:1222:G:H5''	2.23	0.43
52:3:49:U:O2'	52:3:50:A:H2'	2.18	0.43
52:3:540:G:H2'	52:3:541:G:O4'	2.19	0.43
52:3:1201:A:C1'	52:3:1202:U:OP2	2.65	0.43
53:1:253:C:H2'	53:1:254:G:O4'	2.19	0.43
53:1:2024:G:OP2	53:1:2034:U:H4'	2.18	0.43
53:1:2055:C:H2'	53:1:2504:U:H5'	2.00	0.43
55:5:3:C:H2'	55:5:4:G:H8	1.84	0.43
2:c:135:GLY:HA2	53:1:743:A:OP1	2.19	0.43
3:d:47:LYS:HE2	53:1:451:U:H4'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:90:LEU:HG	4:e:95:MET:HA	2.01	0.43
7:h:35:VAL:HA	7:h:38:MET:HE3	2.01	0.43
13:n:3:HIS:O	13:n:4:ARG:HB2	2.18	0.43
14:o:68:LYS:HA	14:o:102:ARG:HG2	2.01	0.43
15:p:49:ILE:HD13	15:p:58:PHE:HB3	2.00	0.43
29:E:32:LEU:HD13	53:1:2419:U:OP2	2.19	0.43
33:I:96:ARG:O	33:I:100:VAL:HG23	2.19	0.43
34:J:107:GLY:HA2	52:3:8:A:H1'	2.00	0.43
34:J:113:VAL:HG23	34:J:114:LEU:HD12	2.00	0.43
34:J:164:LEU:C	34:J:164:LEU:HD12	2.44	0.43
37:M:17:GLN:HG3	37:M:71:VAL:HB	2.01	0.43
38:N:65:THR:HG21	52:3:1130:A:OP1	2.19	0.43
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.18	0.43
43:S:74:ARG:NH2	52:3:1359:C:H3'	2.34	0.43
52:3:51:A:H4'	52:3:52:C:H5''	2.00	0.43
52:3:505:G:H2'	52:3:506:G:C8	2.53	0.43
52:3:1293:C:H2'	52:3:1294:G:C8	2.54	0.43
53:1:1063:G:H1	53:1:1075:C:H42	1.65	0.43
53:1:2093:G:N7	53:1:2225:A:H2'	2.34	0.43
53:1:2123:G:H2'	53:1:2124:G:C8	2.54	0.43
53:1:2126:A:H2'	53:1:2162:G:C2	2.54	0.43
53:1:2317:A:H2'	53:1:2318:G:O4'	2.19	0.43
53:1:2457:U:O2'	53:1:2458:G:H5'	2.19	0.43
58:8:305:PHE:HA	58:8:393:LEU:HD23	2.01	0.43
2:c:40:LEU:HD23	2:c:44:GLY:C	2.44	0.42
4:e:166:ARG:NH1	4:e:166:ARG:HB2	2.34	0.42
7:h:46:ARG:HD2	7:h:46:ARG:C	2.42	0.42
9:j:81:ILE:HG23	9:j:82:GLY:H	1.83	0.42
16:q:91:ARG:HH11	53:1:997:G:H5''	1.84	0.42
31:G:212:TYR:O	31:G:216:VAL:HG23	2.18	0.42
36:L:58:LEU:HD12	36:L:58:LEU:N	2.34	0.42
37:M:94:VAL:HB	37:M:99:GLY:O	2.19	0.42
38:N:17:ARG:HB2	38:N:65:THR:OG1	2.18	0.42
52:3:205:A:H2'	52:3:206:C:O4'	2.19	0.42
52:3:396:C:H2'	52:3:397:A:H5''	2.00	0.42
52:3:1323:G:H2'	52:3:1324:A:C8	2.54	0.42
53:1:948:C:H2'	53:1:949:G:C8	2.53	0.42
53:1:1680:U:H2'	53:1:1681:G:H5'	2.01	0.42
53:1:1928:A:H2'	53:1:1929:G:O4'	2.19	0.42
1:b:47:ARG:HD3	53:1:773:U:O2'	2.19	0.42
6:g:21:VAL:HG22	6:g:22:LYS:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:44:HIS:HB2	53:1:482:A:H4'	2.01	0.42
21:v:86:LEU:HD23	21:v:89:ILE:HD11	2.01	0.42
32:H:40:GLN:O	32:H:44:LYS:HG2	2.19	0.42
32:H:139:ASN:O	32:H:142:ARG:HG2	2.18	0.42
45:U:59:HIS:O	45:U:63:GLN:HG2	2.18	0.42
46:V:60:ILE:CG2	46:V:72:TRP:HB3	2.49	0.42
47:W:18:GLN:CG	47:W:19:GLU:H	2.25	0.42
51:a:47:ASN:HB2	51:a:210:LYS:HB2	2.01	0.42
52:3:217:C:H2'	52:3:218:U:C6	2.53	0.42
52:3:946:A:H2'	52:3:947:G:H8	1.83	0.42
53:1:635:C:H2'	53:1:636:G:H8	1.84	0.42
53:1:1258:U:H2'	53:1:1259:G:C8	2.54	0.42
3:d:105:LEU:HA	3:d:108:ILE:HG22	2.00	0.42
4:e:102:LEU:O	4:e:106:ALA:HB3	2.19	0.42
7:h:57:ASN:O	7:h:63:ALA:HB2	2.19	0.42
39:O:30:LYS:HE3	39:O:35:GLN:H	1.83	0.42
41:Q:76:HIS:HB3	41:Q:77:SER:H	1.57	0.42
50:Z:36:PHE:C	50:Z:38:GLU:H	2.26	0.42
51:a:181:ASP:HB2	51:a:184:LYS:CE	2.49	0.42
52:3:477:C:H2'	52:3:478:A:C8	2.55	0.42
53:1:184:C:H4'	53:1:217:A:H2	1.85	0.42
53:1:326:G:H2'	53:1:327:G:C8	2.53	0.42
53:1:1528:A:H2'	53:1:1529:G:O4'	2.20	0.42
53:1:1542:U:H2'	53:1:1543:G:C8	2.54	0.42
53:1:2126:A:H2'	53:1:2162:G:N3	2.35	0.42
53:1:2836:U:H2'	53:1:2837:A:H8	1.84	0.42
3:d:108:ILE:HG23	3:d:109:LEU:HD22	2.02	0.42
7:h:61:ARG:HE	53:1:1046:A:P	2.42	0.42
7:h:118:ILE:CB	7:h:119:PRO:CD	2.95	0.42
11:l:111:ILE:HD11	53:1:636:G:C5	2.54	0.42
20:u:94:PHE:HD2	20:u:99:SER:HB2	1.83	0.42
22:w:55:LEU:HD12	22:w:76:ILE:HD12	2.00	0.42
39:O:35:GLN:O	39:O:77:VAL:HG22	2.19	0.42
41:Q:86:VAL:HG21	41:Q:92:VAL:HG13	2.02	0.42
44:T:86:LEU:N	44:T:86:LEU:HD23	2.34	0.42
52:3:418:C:H2'	52:3:419:C:C6	2.55	0.42
52:3:439:U:H2'	52:3:440:C:O4'	2.19	0.42
53:1:373:U:H2'	53:1:374:A:H8	1.84	0.42
53:1:572:A:H61	53:1:2029:G:N2	2.13	0.42
53:1:2208:C:H2'	53:1:2209:G:H8	1.84	0.42
53:1:2450:A:OP1	53:1:2497:A:H2'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:186:VAL:O	3:d:186:VAL:HG13	2.19	0.42
5:f:126:THR:HB	5:f:129:GLU:HB3	2.02	0.42
5:f:163:TYR:HB2	5:f:166:GLU:HB2	2.01	0.42
6:g:55:GLU:O	6:g:58:LEU:HG	2.20	0.42
11:l:127:VAL:HG22	11:l:128:THR:N	2.34	0.42
12:m:22:GLN:CB	53:1:907:G:H5'	2.49	0.42
14:o:92:PHE:HB2	14:o:117:PHE:CD2	2.54	0.42
27:C:30:PRO:HD2	27:C:31:GLU:OE2	2.20	0.42
32:H:3:LYS:HG2	52:3:1190:G:H3'	2.01	0.42
32:H:37:LYS:HA	32:H:40:GLN:HG3	2.02	0.42
36:L:75:LYS:HD2	36:L:76:SER:H	1.84	0.42
38:N:94:ARG:HA	38:N:97:LEU:HD12	2.00	0.42
45:U:76:LYS:NZ	52:3:473:U:H5''	2.34	0.42
50:Z:63:ASN:C	50:Z:65:ARG:HE	2.27	0.42
52:3:88:U:H2'	52:3:89:U:C6	2.55	0.42
52:3:304:U:O2'	52:3:305:G:H5'	2.20	0.42
52:3:600:A:H2'	52:3:601:G:C8	2.54	0.42
53:1:176:A:H3'	53:1:177:G:H21	1.85	0.42
53:1:1161:C:H2'	53:1:1162:G:C8	2.54	0.42
53:1:1386:C:H2'	53:1:1387:A:C8	2.55	0.42
53:1:1774:C:H4'	53:1:1979:U:O2	2.20	0.42
53:1:1880:U:H2'	53:1:1881:C:C6	2.55	0.42
2:c:142:VAL:CG2	2:c:143:PRO:HD2	2.40	0.42
2:c:184:ARG:HG3	2:c:186:LEU:HD23	2.01	0.42
3:d:47:LYS:CE	53:1:451:U:H4'	2.49	0.42
3:d:63:LYS:HD2	53:1:2444:G:P	2.60	0.42
4:e:46:LYS:HE3	4:e:82:TYR:OH	2.20	0.42
5:f:95:ALA:HB1	5:f:130:ILE:HG13	2.02	0.42
7:h:54:VAL:HA	7:h:84:TYR:O	2.20	0.42
12:m:31:PHE:HB3	12:m:130:PHE:HE1	1.85	0.42
15:p:72:VAL:HG22	15:p:73:PHE:N	2.34	0.42
16:q:49:ARG:HD2	53:1:993:G:OP1	2.20	0.42
19:t:2:ILE:HD12	19:t:2:ILE:N	2.34	0.42
19:t:61:LEU:N	19:t:61:LEU:HD23	2.33	0.42
20:u:40:LEU:HD23	20:u:61:GLU:OE1	2.19	0.42
33:l:120:LYS:HE3	52:3:439:U:H5''	2.00	0.42
37:M:38:VAL:O	37:M:42:GLU:HG2	2.19	0.42
39:O:6:ILE:HB	39:O:76:ILE:CG2	2.49	0.42
39:O:57:VAL:CG2	39:O:58:ASN:H	2.15	0.42
42:R:82:LEU:HD23	42:R:84:CYS:SG	2.59	0.42
42:R:113:LYS:HB2	42:R:114:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:23:GLU:O	50:Z:25:ALA:N	2.45	0.42
52:3:742:G:H2'	52:3:743:A:H8	1.85	0.42
53:1:471:A:H2'	53:1:472:A:O4'	2.20	0.42
53:1:1739:A:H2'	53:1:1740:G:O4'	2.20	0.42
53:1:1826:G:H2'	53:1:1827:U:C6	2.52	0.42
54:2:49:C:H2'	54:2:50:A:H8	1.85	0.42
55:5:37:A:H2'	55:5:38:A:O4'	2.20	0.42
55:6:63:G:H2'	55:6:64:G:H8	1.85	0.42
18:s:3:THR:HG22	18:s:62:ASP:OD2	2.19	0.42
18:s:74:ILE:HD13	18:s:105:VAL:HG22	2.00	0.42
24:y:43:LEU:O	24:y:46:VAL:HG12	2.20	0.42
25:z:51:SER:HA	25:z:54:VAL:HG22	2.01	0.42
32:H:53:ARG:HG3	32:H:53:ARG:NH1	2.34	0.42
32:H:76:ILE:HD12	32:H:83:VAL:HG21	2.02	0.42
34:J:40:ASP:OD1	34:J:44:ARG:N	2.52	0.42
37:M:1:SER:C	37:M:2:MET:SD	3.02	0.42
38:N:114:LYS:HG3	38:N:117:LEU:HD12	2.02	0.42
49:Y:23:ARG:NH2	52:3:176:C:H5''	2.34	0.42
52:3:79:G:O2'	52:3:80:A:H5'	2.19	0.42
52:3:1424:U:H2'	52:3:1425:U:O4'	2.19	0.42
53:1:329:G:O4'	53:1:477:A:H1'	2.19	0.42
53:1:677:A:O2'	53:1:2071:A:H5'	2.20	0.42
53:1:940:G:C3'	53:1:941:A:H5''	2.50	0.42
53:1:940:G:C2'	53:1:941:A:H5''	2.49	0.42
53:1:1201:U:H2'	53:1:1202:G:C8	2.55	0.42
53:1:1287:A:C2'	53:1:1288:G:H5'	2.50	0.42
1:b:56:GLY:HA3	1:b:214:GLY:HA2	2.02	0.42
1:b:57:HIS:ND1	1:b:58:LYS:N	2.68	0.42
3:d:40:ARG:HD2	53:1:443:A:C6	2.54	0.42
12:m:128:THR:OG1	12:m:129:THR:N	2.53	0.42
14:o:38:GLN:CD	14:o:50:ALA:HB2	2.44	0.42
17:r:78:ARG:NH1	53:1:990:A:H61	2.16	0.42
20:u:69:VAL:HG22	20:u:70:ALA:N	2.35	0.42
25:z:14:GLY:O	25:z:15:ARG:HD3	2.20	0.42
33:I:134:TYR:HE1	52:3:620:C:H5'	1.85	0.42
35:K:20:GLY:O	35:K:23:GLU:HG3	2.20	0.42
36:L:11:ILE:HD12	36:L:11:ILE:N	2.34	0.42
37:M:1:SER:O	37:M:2:MET:C	2.62	0.42
38:N:53:LEU:HD13	38:N:97:LEU:HD23	2.02	0.42
50:Z:17:ARG:NH2	52:3:1539:C:O4'	2.53	0.42
52:3:237:G:H2'	52:3:238:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:692:U:H2'	52:3:694:A:OP2	2.19	0.42
52:3:1312:G:H2'	52:3:1313:U:C6	2.55	0.42
53:1:774:G:O2'	53:1:775:G:H5''	2.20	0.42
53:1:2721:A:H2'	53:1:2722:G:O4'	2.19	0.42
2:c:183:GLU:OE2	2:c:184:ARG:HG2	2.20	0.42
5:f:42:VAL:C	5:f:43:LYS:HD3	2.44	0.42
8:i:10:LEU:N	8:i:10:LEU:HD23	2.35	0.42
8:i:86:LYS:HD3	8:i:86:LYS:HA	1.87	0.42
10:k:29:HIS:O	10:k:29:HIS:ND1	2.50	0.42
13:n:14:SER:HA	13:n:17:ARG:HB3	2.02	0.42
20:u:47:PRO:HB3	20:u:55:GLY:N	2.29	0.42
31:G:209:VAL:O	31:G:213:LEU:HG	2.20	0.42
34:J:100:GLU:H	34:J:121:ASN:HD21	1.66	0.42
36:L:22:LEU:O	36:L:26:VAL:HG23	2.20	0.42
36:L:68:VAL:C	36:L:137:ARG:HD3	2.45	0.42
38:N:20:ILE:HD11	38:N:60:LEU:HD22	2.01	0.42
42:R:27:THR:HG21	52:3:1328:C:H5''	2.02	0.42
53:1:606:U:H4'	53:1:658:U:O2'	2.20	0.42
53:1:672:C:O2'	53:1:673:C:H5'	2.19	0.42
53:1:1077:A:C3'	53:1:1078:U:H5'	2.49	0.42
53:1:2163:A:N3	53:1:2163:A:H2'	2.35	0.42
54:2:104:A:H2'	54:2:105:G:O4'	2.20	0.42
57:7:51:U:H2'	57:7:52:G:C8	2.55	0.42
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.48	0.42
9:j:28:LEU:HD23	9:j:28:LEU:O	2.20	0.42
13:n:9:GLN:HA	13:n:17:ARG:HH21	1.83	0.42
17:r:39:LEU:O	17:r:49:ILE:HG23	2.20	0.42
18:s:24:ILE:N	18:s:24:ILE:HD12	2.35	0.42
19:t:14:PRO:HA	19:t:32:LEU:CB	2.50	0.42
19:t:69:ARG:HA	19:t:73:ARG:O	2.20	0.42
33:I:160:LEU:HD12	33:I:163:GLN:OE1	2.19	0.42
33:I:195:ASN:ND2	33:I:198:LEU:HG	2.34	0.42
34:J:160:VAL:HG13	34:J:161:GLU:OE1	2.20	0.42
35:K:67:PRO:HG2	35:K:70:VAL:HG23	2.01	0.42
38:N:17:ARG:NH2	52:3:1129:C:H4'	2.35	0.42
39:O:52:LEU:HB2	43:S:80:ARG:HH11	1.85	0.42
52:3:1123:U:O2'	52:3:1124:G:H5'	2.19	0.42
53:1:76:C:H2'	53:1:77:G:H8	1.84	0.42
53:1:1827:U:C2'	53:1:1828:G:H5'	2.50	0.42
53:1:2590:A:H2'	53:1:2591:C:C6	2.55	0.42
53:1:2670:A:H2'	53:1:2671:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:65:ASP:CB	1:b:101:ARG:HD3	2.50	0.41
3:d:196:VAL:O	3:d:200:LEU:HD23	2.20	0.41
4:e:107:VAL:HA	4:e:110:ILE:HG13	2.02	0.41
6:g:50:ARG:O	6:g:54:LEU:HG	2.20	0.41
8:i:98:GLY:H	8:i:137:LEU:CD2	2.27	0.41
12:m:72:PRO:HD3	12:m:92:TRP:CZ3	2.56	0.41
18:s:46:LEU:O	18:s:50:VAL:HG23	2.19	0.41
27:C:38:PHE:CE2	53:1:2348:U:H1'	2.55	0.41
31:G:187:ASP:HB3	31:G:189:ASN:OD1	2.20	0.41
35:K:12:PRO:HG3	35:K:56:LYS:O	2.20	0.41
36:L:67:ASN:O	36:L:137:ARG:NE	2.53	0.41
39:O:63:ASP:OD2	43:S:97:LYS:HE2	2.20	0.41
43:S:92:ILE:HD12	43:S:92:ILE:N	2.34	0.41
51:a:219:GLY:O	53:1:2176:A:H5'	2.20	0.41
53:1:1153:C:H2'	53:1:1154:G:O4'	2.20	0.41
53:1:2114:A:N6	53:1:2117:A:H62	2.13	0.41
55:6:71:C:H2'	55:6:72:A:N9	2.35	0.41
57:7:26:A:H3'	57:7:27:G:H8	1.85	0.41
5:f:116:LEU:HA	5:f:117:PRO:HD3	1.88	0.41
7:h:23:LEU:HD23	7:h:23:LEU:C	2.45	0.41
13:n:49:GLU:OE2	13:n:93:GLY:HA2	2.20	0.41
16:q:36:GLN:NE2	53:1:564:C:H1'	2.35	0.41
19:t:1:MET:HB3	19:t:2:ILE:HD12	2.02	0.41
21:v:18:ARG:NH1	54:2:77:U:OP1	2.53	0.41
29:E:34:LYS:HD2	53:1:2391:G:OP2	2.20	0.41
32:H:146:LYS:HB2	32:H:202:PHE:CD2	2.56	0.41
39:O:14:ASP:O	39:O:18:ILE:HG13	2.19	0.41
50:Z:6:ARG:O	50:Z:7:GLU:HB2	2.21	0.41
52:3:9:G:H2'	52:3:10:A:C8	2.55	0.41
52:3:82:G:H2'	52:3:83:C:O4'	2.20	0.41
52:3:925:G:H1'	52:3:1502:A:C4	2.55	0.41
52:3:1004:A:H2'	52:3:1005:A:O4'	2.19	0.41
52:3:1060:U:H2'	52:3:1061:G:C8	2.55	0.41
52:3:1195:C:H5''	52:3:1196:A:OP2	2.20	0.41
52:3:1333:A:H2'	52:3:1334:G:O4'	2.20	0.41
53:1:158:U:H2'	53:1:159:G:O4'	2.19	0.41
53:1:267:C:H2'	53:1:268:C:C6	2.55	0.41
53:1:562:U:O4'	53:1:2036:C:H5'	2.20	0.41
53:1:974:G:N3	53:1:974:G:H2'	2.35	0.41
53:1:1417:C:H2'	53:1:1418:G:O4'	2.20	0.41
53:1:1420:A:H5'	53:1:1421:G:OP2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2475:C:H2'	53:1:2476:A:H5'	2.02	0.41
1:b:70:LYS:O	1:b:117:SER:OG	2.38	0.41
4:e:116:LEU:HD12	4:e:175:PRO:HD2	2.02	0.41
4:e:155:ILE:HD12	4:e:155:ILE:H	1.86	0.41
5:f:126:THR:HG22	5:f:128:THR:H	1.86	0.41
6:g:47:PHE:HA	6:g:51:ARG:HD2	2.02	0.41
7:h:118:ILE:HD13	7:h:118:ILE:HA	1.89	0.41
13:n:97:ILE:HD13	13:n:113:ILE:HD13	2.01	0.41
14:o:12:THR:HG21	53:1:2334:U:H5'	2.02	0.41
14:o:40:ILE:HG12	14:o:47:VAL:HG12	2.01	0.41
19:t:70:HIS:HB3	19:t:73:ARG:NH1	2.35	0.41
23:x:17:ARG:HB2	53:1:380:G:OP1	2.20	0.41
27:C:33:LEU:H	27:C:50:GLU:HG3	1.85	0.41
31:G:100:LEU:HD11	31:G:157:PRO:HG2	2.01	0.41
33:I:18:LEU:HD21	33:I:63:ILE:HA	2.02	0.41
35:K:3:HIS:HB3	35:K:95:ALA:HB2	2.02	0.41
36:L:142:ARG:NE	55:6:41:C:H4'	2.35	0.41
39:O:10:LEU:O	39:O:71:LEU:HD12	2.20	0.41
40:P:30:ILE:HG13	40:P:45:THR:HG22	2.02	0.41
40:P:122:PRO:HB2	50:Z:33:ARG:HA	2.02	0.41
41:Q:28:GLN:HB3	41:Q:80:LEU:HD11	2.01	0.41
41:Q:47:ALA:C	41:Q:48:LEU:HD12	2.46	0.41
43:S:4:SER:O	43:S:7:ALA:HB3	2.19	0.41
44:T:31:LEU:O	44:T:34:GLN:HB3	2.19	0.41
46:V:45:VAL:HG21	46:V:60:ILE:HD12	2.02	0.41
47:W:36:GLY:O	47:W:62:ARG:NH2	2.54	0.41
51:a:48:LEU:HD11	51:a:208:TYR:CE2	2.55	0.41
51:a:197:LYS:HA	51:a:200:LYS:HZ2	1.85	0.41
52:3:236:A:H2'	52:3:237:G:C8	2.55	0.41
52:3:946:A:H2'	52:3:947:G:C8	2.55	0.41
52:3:1256:A:O2'	52:3:1257:A:H5''	2.21	0.41
52:3:1414:U:H2'	52:3:1415:G:H8	1.85	0.41
52:3:1432:G:H1'	52:3:1468:A:H62	1.83	0.41
53:1:20:C:H2'	53:1:21:A:H8	1.86	0.41
53:1:230:G:O2'	53:1:231:A:H5'	2.20	0.41
53:1:535:G:H2'	53:1:536:G:H8	1.85	0.41
54:2:60:C:H2'	54:2:61:G:C8	2.56	0.41
55:5:51:C:H2'	55:5:52:G:C8	2.56	0.41
3:d:90:GLN:HE21	3:d:92:HIS:CE1	2.37	0.41
8:i:85:ILE:HG21	8:i:97:VAL:HG12	2.03	0.41
9:j:14:ASP:O	9:j:52:ASP:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:110:VAL:HB	11:l:127:VAL:HG23	2.03	0.41
31:G:5:MET:HA	31:G:8:MET:HE3	2.02	0.41
34:J:108:GLY:O	34:J:109:ALA:HB3	2.21	0.41
38:N:90:ASP:HB2	38:N:91:GLU:H	1.71	0.41
44:T:2:LEU:HD22	44:T:2:LEU:N	2.35	0.41
46:V:80:LYS:HD3	46:V:81:ALA:N	2.36	0.41
50:Z:41:THR:HG23	50:Z:44:ARG:NH2	2.35	0.41
51:a:4:LEU:HD12	51:a:4:LEU:N	2.24	0.41
52:3:1230:C:H2'	52:3:1231:G:H8	1.85	0.41
53:1:580:U:H2'	53:1:581:C:C6	2.55	0.41
53:1:594:U:H2'	53:1:595:C:C6	2.55	0.41
53:1:1111:A:O2'	53:1:1112:G:H4'	2.20	0.41
53:1:1507:C:H2'	53:1:1508:A:O4'	2.20	0.41
53:1:2266:A:H4'	53:1:2267:A:N3	2.35	0.41
53:1:2415:G:H2'	53:1:2416:C:C6	2.55	0.41
54:2:63:C:H2'	54:2:64:G:C8	2.56	0.41
1:b:38:LYS:NZ	1:b:55:GLY:O	2.54	0.41
1:b:200:MET:HG3	53:1:1820:U:C2	2.55	0.41
1:b:203:VAL:HG23	53:1:1792:G:C5'	2.50	0.41
2:c:3:GLY:C	2:c:4:LEU:HD12	2.46	0.41
3:d:199:MET:SD	53:1:616:A:O2'	2.79	0.41
6:g:26:ALA:O	6:g:31:VAL:HG23	2.20	0.41
6:g:143:ILE:HD12	6:g:143:ILE:N	2.35	0.41
8:i:52:LEU:O	8:i:54:ILE:HG12	2.21	0.41
23:x:17:ARG:HH11	23:x:21:LEU:HB3	1.85	0.41
39:O:18:ILE:HD13	39:O:70:HIS:O	2.21	0.41
39:O:69:THR:HG23	39:O:69:THR:O	2.20	0.41
47:W:48:ALA:HB2	52:3:834:U:OP1	2.20	0.41
48:X:33:TRP:O	48:X:35:ARG:HG3	2.20	0.41
52:3:742:G:H2'	52:3:743:A:C8	2.56	0.41
52:3:1118:U:H2'	52:3:1119:C:C6	2.55	0.41
52:3:1374:A:H2'	52:3:1375:A:O4'	2.21	0.41
53:1:46:G:H2'	53:1:47:C:C6	2.56	0.41
53:1:254:G:H2'	53:1:255:A:H5''	2.00	0.41
53:1:1373:A:C5'	53:1:2212:A:H1'	2.50	0.41
1:b:231:HIS:O	1:b:232:GLY:O	2.38	0.41
2:c:4:LEU:HD13	2:c:101:PHE:CE2	2.56	0.41
2:c:124:ARG:HG2	2:c:125:TRP:NE1	2.36	0.41
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.84	0.41
5:f:37:ASN:HD22	53:1:2758:A:H1'	1.85	0.41
6:g:21:VAL:HG22	6:g:22:LYS:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:60:VAL:HG13	53:1:1454:C:O2'	2.21	0.41
20:u:51:LEU:N	20:u:51:LEU:HD12	2.36	0.41
27:C:5:ARG:NH1	27:C:25:ASN:HB2	2.36	0.41
31:G:33:ALA:C	31:G:34:ARG:HD2	2.46	0.41
33:I:18:LEU:HG	33:I:63:ILE:HG12	2.02	0.41
37:M:74:ILE:HG23	37:M:74:ILE:O	2.19	0.41
37:M:94:VAL:HG12	37:M:95:MET:HG3	2.02	0.41
38:N:49:GLN:N	38:N:50:PRO:HD2	2.36	0.41
40:P:85:VAL:HG11	50:Z:16:ARG:HH12	1.86	0.41
52:3:113:G:H2'	52:3:114:U:C6	2.56	0.41
52:3:737:C:H2'	52:3:738:C:C6	2.56	0.41
52:3:1366:C:H2'	52:3:1367:C:H6	1.86	0.41
53:1:327:G:H2'	53:1:328:U:O4'	2.20	0.41
53:1:631:A:H1'	53:1:2415:G:O2'	2.21	0.41
53:1:1106:G:H2'	53:1:1107:G:O4'	2.20	0.41
53:1:1668:A:H61	53:1:1676:A:H61	1.67	0.41
53:1:1857:G:H1'	53:1:1885:A:N6	2.35	0.41
53:1:2176:A:H2'	53:1:2177:C:C6	2.55	0.41
53:1:2257:U:O2'	53:1:2258:C:H5'	2.21	0.41
53:1:2774:C:H2'	53:1:2775:G:O4'	2.21	0.41
53:1:2786:U:H2'	53:1:2787:C:C6	2.56	0.41
58:8:374:ARG:HH11	58:8:374:ARG:HA	1.85	0.41
2:c:140:HIS:CD2	53:1:1658:C:OP2	2.74	0.41
2:c:142:VAL:HG13	2:c:144:GLY:N	2.36	0.41
6:g:127:GLU:OE2	6:g:143:ILE:HG23	2.20	0.41
7:h:108:VAL:HG23	7:h:109:LYS:N	2.34	0.41
11:l:55:MET:HE3	53:1:2392:A:C2	2.55	0.41
14:o:11:ALA:O	14:o:15:ARG:HG2	2.21	0.41
15:p:102:ARG:NH2	53:1:1754:A:O3'	2.54	0.41
17:r:81:LYS:HD2	53:1:973:A:H5''	2.02	0.41
24:y:9:LYS:O	24:y:13:GLU:HG2	2.20	0.41
25:z:29:ARG:HD3	53:1:1183:U:O3'	2.21	0.41
31:G:36:LYS:HB2	31:G:36:LYS:HE3	1.86	0.41
31:G:44:LYS:O	31:G:47:PRO:HD2	2.21	0.41
31:G:48:MET:HE2	31:G:198:VAL:HG23	2.01	0.41
32:H:190:THR:O	32:H:192:TYR:N	2.53	0.41
35:K:3:HIS:H	35:K:92:THR:CG2	2.33	0.41
36:L:59:GLU:H	36:L:59:GLU:HG2	1.63	0.41
38:N:6:TYR:H	38:N:87:MET:HE2	1.84	0.41
39:O:40:ILE:HD12	39:O:73:LEU:HG	2.02	0.41
42:R:102:LYS:HG3	52:3:1226:C:C4	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:358:U:H2'	52:3:359:G:C8	2.55	0.41
52:3:578:C:H2'	52:3:579:A:C8	2.55	0.41
52:3:1188:A:H2'	52:3:1189:U:O4'	2.20	0.41
52:3:1236:A:H4'	52:3:1304:G:H4'	2.02	0.41
53:1:274:C:H2'	53:1:275:C:O4'	2.21	0.41
53:1:535:G:H2'	53:1:536:G:C8	2.56	0.41
53:1:720:U:H2'	53:1:721:A:C8	2.55	0.41
53:1:842:U:H2'	53:1:843:G:C8	2.56	0.41
53:1:1525:A:H2'	53:1:1526:C:O4'	2.21	0.41
53:1:1594:U:H2'	53:1:1595:C:C6	2.56	0.41
53:1:1765:U:H2'	53:1:1766:G:C8	2.53	0.41
53:1:2340:A:H2'	53:1:2341:G:H8	1.84	0.41
53:1:2396:G:H2'	53:1:2397:G:H8	1.86	0.41
9:j:35:ARG:HB2	9:j:54:ILE:HD11	2.02	0.41
23:x:11:PRO:HG2	53:1:1365:A:OP1	2.21	0.41
31:G:131:LYS:HE2	31:G:131:LYS:HB3	1.95	0.41
36:L:24:LYS:CE	52:3:1375:A:H5''	2.51	0.41
40:P:108:ASN:HB3	50:Z:6:ARG:CG	2.51	0.41
44:T:4:THR:HG21	52:3:660:C:OP1	2.20	0.41
48:X:38:THR:HG22	48:X:69:LYS:HG2	2.03	0.41
52:3:246:A:H62	52:3:281:G:N2	2.18	0.41
52:3:467:U:H5'	52:3:468:A:OP2	2.21	0.41
52:3:1204:A:H2'	52:3:1205:U:O4'	2.20	0.41
52:3:1525:G:H2'	52:3:1526:G:C8	2.56	0.41
53:1:323:C:H2'	53:1:1205:A:N1	2.35	0.41
53:1:750:A:H2'	53:1:751:A:H5''	2.02	0.41
53:1:1054:A:H2'	53:1:1055:G:C8	2.56	0.41
53:1:1526:C:H2'	53:1:1527:G:O4'	2.21	0.41
53:1:2326:C:O2'	53:1:2327:A:P	2.79	0.41
54:2:49:C:H2'	54:2:50:A:C8	2.55	0.41
54:2:65:U:H2'	54:2:66:A:H5'	2.01	0.41
1:b:82:TYR:HA	1:b:89:ASN:HD22	1.86	0.41
1:b:179:GLU:OE2	1:b:269:ARG:HA	2.21	0.41
1:b:181:ARG:NH1	1:b:183:VAL:HG22	2.35	0.41
1:b:229:HIS:HA	1:b:230:PRO:HD3	1.83	0.41
2:c:7:LYS:HE3	2:c:77:ARG:NH1	2.36	0.41
4:e:1:ALA:O	4:e:4:HIS:HB3	2.21	0.41
4:e:74:ALA:HB2	55:5:57:A:H5'	2.02	0.41
4:e:132:ARG:CZ	53:1:2305:U:H4'	2.50	0.41
8:i:56:VAL:HG22	8:i:70:THR:HA	2.03	0.41
18:s:61:ASN:HD21	53:1:495:G:H21	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:106:VAL:O	31:G:110:ILE:HG13	2.21	0.41
34:J:68:ARG:HG3	34:J:68:ARG:NH1	2.36	0.41
35:K:11:HIS:NE2	35:K:13:ASP:OD2	2.54	0.41
36:L:102:TRP:HA	36:L:105:GLU:HB3	2.03	0.41
38:N:59:LYS:HB3	38:N:60:LEU:HD12	2.02	0.41
39:O:12:ALA:HB3	39:O:18:ILE:CG1	2.51	0.41
41:Q:110:LYS:HD2	41:Q:110:LYS:N	2.36	0.41
44:T:7:THR:O	44:T:11:VAL:HG23	2.21	0.41
46:V:9:GLY:O	46:V:57:VAL:HA	2.21	0.41
46:V:30:HIS:HB3	46:V:35:LYS:H	1.85	0.41
47:W:12:PHE:C	47:W:14:ALA:H	2.29	0.41
49:Y:22:SER:OG	52:3:1458:G:H4'	2.21	0.41
50:Z:39:LYS:O	50:Z:40:PRO:C	2.62	0.41
50:Z:61:ARG:H	50:Z:61:ARG:HD3	1.85	0.41
52:3:64:G:H4'	52:3:65:A:H3'	2.03	0.41
52:3:166:U:H2'	52:3:167:A:H8	1.85	0.41
52:3:355:C:H2'	52:3:356:A:O4'	2.21	0.41
52:3:370:C:H2'	52:3:371:A:H8	1.84	0.41
52:3:434:U:H2'	52:3:435:A:C8	2.56	0.41
52:3:1011:C:H2'	52:3:1012:A:C8	2.55	0.41
52:3:1073:U:H2'	52:3:1074:G:C8	2.56	0.41
52:3:1171:A:H2'	52:3:1172:C:C6	2.56	0.41
53:1:548:G:H2'	53:1:549:G:O4'	2.21	0.41
53:1:598:U:H2'	53:1:599:A:C8	2.56	0.41
53:1:759:G:H2'	53:1:760:G:C8	2.55	0.41
53:1:1669:A:N3	53:1:1669:A:H2'	2.36	0.41
53:1:1932:A:H2'	53:1:1933:G:O4'	2.21	0.41
53:1:2141:G:H22	53:1:2151:U:H1'	1.86	0.41
53:1:2581:G:H4'	53:1:2582:G:C8	2.56	0.41
53:1:2591:C:H2'	53:1:2592:G:C8	2.56	0.41
57:7:52:G:H2'	57:7:53:G:H8	1.84	0.41
11:l:20:GLY:HA2	11:l:28:GLY:HA2	2.03	0.41
11:l:29:LYS:O	11:l:30:THR:OG1	2.26	0.41
20:u:33:VAL:HG13	20:u:66:VAL:HG22	2.02	0.41
33:I:55:ARG:HA	33:I:55:ARG:NE	2.36	0.41
33:I:66:VAL:HG12	33:I:70:GLN:HB3	2.03	0.41
33:I:97:LEU:HD21	33:I:122:ILE:HG12	2.03	0.41
38:N:34:LEU:HD23	38:N:34:LEU:C	2.45	0.41
40:P:108:ASN:HB3	50:Z:6:ARG:HG3	2.04	0.41
52:3:570:G:O2'	52:3:819:A:H2'	2.20	0.41
52:3:1011:C:H2'	52:3:1012:A:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:704:G:H1'	53:1:727:A:H61	1.86	0.41
53:1:1239:G:H2'	53:1:1240:U:O4'	2.20	0.41
53:1:1386:C:H2'	53:1:1387:A:H8	1.85	0.41
53:1:1498:C:H5'	53:1:1577:C:H5'	2.03	0.41
53:1:2398:U:H2'	53:1:2399:G:H8	1.86	0.41
53:1:2788:C:H2'	53:1:2789:C:C6	2.56	0.41
55:6:28:C:H2'	55:6:29:G:H8	1.86	0.41
1:b:203:VAL:HG23	53:1:1792:G:H5'	2.03	0.40
2:c:62:LYS:HB2	2:c:63:PRO:HD3	2.03	0.40
31:G:124:THR:O	31:G:128:LEU:HG	2.21	0.40
33:I:49:ASP:OD1	33:I:50:TYR:N	2.54	0.40
34:J:121:ASN:HB3	34:J:122:VAL:H	1.33	0.40
45:U:13:LYS:HD3	45:U:13:LYS:HA	1.93	0.40
49:Y:73:ARG:NH2	52:3:261:U:C5	2.89	0.40
51:a:27:ILE:HG21	51:a:182:ALA:HA	2.03	0.40
52:3:911:U:H2'	52:3:912:C:C6	2.56	0.40
52:3:1430:A:H2'	52:3:1431:A:O4'	2.21	0.40
52:3:1515:G:H2'	52:3:1516:G:C8	2.56	0.40
53:1:1751:U:H2'	53:1:1752:C:C6	2.56	0.40
53:1:2186:G:H2'	53:1:2187:U:O4'	2.21	0.40
1:b:203:VAL:O	1:b:203:VAL:HG13	2.22	0.40
1:b:211:ARG:HG3	53:1:764:A:O4'	2.21	0.40
9:j:69:ARG:HA	9:j:89:PHE:CD2	2.56	0.40
15:p:92:ARG:O	53:1:2848:G:H2'	2.20	0.40
27:C:9:LYS:HE3	27:C:9:LYS:HB2	1.89	0.40
32:H:84:GLU:O	32:H:88:LYS:HG2	2.21	0.40
32:H:188:ALA:HB3	32:H:195:ILE:HB	2.03	0.40
33:I:184:LYS:HA	33:I:185:PRO:HD3	1.84	0.40
34:J:11:GLN:OE1	34:J:116:VAL:HA	2.21	0.40
35:K:11:HIS:HA	35:K:12:PRO:HD3	1.96	0.40
35:K:18:VAL:O	35:K:22:ILE:HG13	2.22	0.40
41:Q:5:GLN:HE22	52:3:880:C:P	2.44	0.40
43:S:4:SER:HB2	52:3:1216:A:H5''	2.02	0.40
46:V:21:VAL:O	46:V:21:VAL:HG13	2.20	0.40
51:a:200:LYS:HA	51:a:201:PRO:HD3	1.87	0.40
52:3:413:G:H2'	52:3:413:G:N3	2.36	0.40
52:3:451:A:H4'	52:3:452:A:O4'	2.22	0.40
52:3:494:G:O2'	52:3:496:A:H1'	2.21	0.40
52:3:923:A:H61	52:3:1393:U:H3	1.69	0.40
53:1:259:G:H2'	53:1:260:G:C8	2.56	0.40
53:1:859:G:C2'	53:1:860:U:OP2	2.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1159:U:H2'	53:1:1160:G:H8	1.86	0.40
53:1:1437:C:H2'	53:1:1438:U:C6	2.56	0.40
53:1:1637:A:H5'	53:1:1760:C:O2'	2.21	0.40
3:d:74:LYS:O	3:d:75:SER:C	2.64	0.40
3:d:126:VAL:HG13	3:d:156:ASN:OD1	2.22	0.40
5:f:98:LYS:HZ2	5:f:103:ASN:HD22	1.69	0.40
7:h:50:VAL:HG22	7:h:50:VAL:O	2.22	0.40
12:m:69:PRO:O	12:m:70:ASP:OD2	2.39	0.40
23:x:3:VAL:HG13	23:x:9:LYS:O	2.22	0.40
29:E:30:HIS:O	29:E:31:ILE:O	2.39	0.40
36:L:115:MET:HB2	36:L:118:ARG:HH21	1.86	0.40
39:O:23:ALA:HA	39:O:26:VAL:HG22	2.03	0.40
41:Q:42:LYS:HG3	41:Q:44:PRO:HD2	2.02	0.40
45:U:1:MET:HE3	45:U:66:THR:HG21	2.02	0.40
52:3:40:C:H2'	52:3:41:G:C8	2.56	0.40
52:3:371:A:H2'	52:3:372:C:O4'	2.20	0.40
53:1:11:C:H3'	53:1:12:U:C5'	2.51	0.40
53:1:479:A:H1'	53:1:481:G:H5''	2.03	0.40
53:1:2705:A:H2'	53:1:2706:A:O4'	2.21	0.40
54:2:24:G:H21	54:2:27:C:N4	2.18	0.40
5:f:83:THR:HA	5:f:133:LYS:HA	2.04	0.40
6:g:50:ARG:HD2	6:g:50:ARG:C	2.46	0.40
32:H:7:ASN:HA	32:H:15:LYS:NZ	2.36	0.40
38:N:70:GLY:O	38:N:74:GLN:HG3	2.21	0.40
39:O:10:LEU:HB3	39:O:98:VAL:HG12	2.02	0.40
39:O:86:ALA:O	39:O:90:LEU:HD12	2.21	0.40
41:Q:52:CYS:HB3	41:Q:66:ILE:HD11	2.04	0.40
45:U:6:LEU:HD23	45:U:6:LEU:HA	1.92	0.40
49:Y:56:ILE:HG13	49:Y:59:ARG:HH12	1.87	0.40
52:3:987:G:H2'	52:3:988:G:H8	1.86	0.40
53:1:536:G:H2'	53:1:537:G:O4'	2.21	0.40
53:1:1130:U:O2'	53:1:1131:G:P	2.79	0.40
53:1:2724:U:H2'	53:1:2725:A:H8	1.86	0.40
53:1:2743:U:C2'	53:1:2744:G:H5''	2.51	0.40
2:c:61:THR:OG1	2:c:63:PRO:HD2	2.22	0.40
2:c:85:ALA:H	2:c:88:GLU:CD	2.30	0.40
3:d:95:LYS:HG2	3:d:96:VAL:N	2.37	0.40
6:g:110:VAL:HG23	6:g:114:GLU:HB3	2.03	0.40
10:k:10:VAL:HG12	10:k:12:ASP:H	1.86	0.40
12:m:53:MET:HG3	12:m:116:ALA:HB1	2.02	0.40
13:n:79:LEU:C	13:n:81:ASN:H	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:111:LYS:HG2	17:r:48:LYS:NZ	2.37	0.40
31:G:119:GLN:HE22	31:G:136:ARG:NH1	2.20	0.40
32:H:161:ILE:HG23	52:3:1196:A:C2	2.56	0.40
36:L:119:LEU:HD23	36:L:123:LEU:HD23	2.04	0.40
39:O:28:THR:HA	39:O:31:ARG:HH11	1.87	0.40
40:P:121:ARG:HG3	50:Z:35:GLU:HG3	2.03	0.40
44:T:4:THR:HG21	52:3:660:C:P	2.61	0.40
52:3:1342:C:H2'	52:3:1343:G:C8	2.57	0.40
53:1:2121:G:H2'	53:1:2122:U:O4'	2.20	0.40
53:1:2329:U:H2'	53:1:2330:G:C8	2.56	0.40
53:1:2540:C:H2'	53:1:2541:A:O4'	2.21	0.40
53:1:2593:U:H2'	53:1:2594:C:C6	2.56	0.40
53:1:2863:C:H2'	53:1:2864:G:C8	2.56	0.40
57:7:4:C:H2'	57:7:5:G:C8	2.56	0.40
58:8:334:ARG:HH21	58:8:335:THR:HG21	1.86	0.40
58:8:363:LEU:HD12	58:8:363:LEU:N	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	223 (83%)	43 (16%)	3 (1%)	11	43
2	c	207/209 (99%)	179 (86%)	26 (13%)	2 (1%)	12	45
3	d	199/201 (99%)	174 (87%)	23 (12%)	2 (1%)	12	45
4	e	175/177 (99%)	160 (91%)	14 (8%)	1 (1%)	21	55
5	f	174/176 (99%)	157 (90%)	15 (9%)	2 (1%)	11	43
6	g	147/149 (99%)	121 (82%)	25 (17%)	1 (1%)	18	53
7	h	129/131 (98%)	92 (71%)	30 (23%)	7 (5%)	1	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	i	139/141 (99%)	124 (89%)	14 (10%)	1 (1%)	18	53
9	j	140/142 (99%)	130 (93%)	9 (6%)	1 (1%)	18	53
10	k	120/122 (98%)	99 (82%)	17 (14%)	4 (3%)	3	24
11	l	141/143 (99%)	117 (83%)	17 (12%)	7 (5%)	1	18
12	m	134/136 (98%)	116 (87%)	16 (12%)	2 (2%)	8	37
13	n	118/120 (98%)	97 (82%)	18 (15%)	3 (2%)	4	29
14	o	114/116 (98%)	103 (90%)	10 (9%)	1 (1%)	14	47
15	p	112/114 (98%)	91 (81%)	20 (18%)	1 (1%)	14	47
16	q	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
17	r	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	6	32
18	s	108/110 (98%)	90 (83%)	17 (16%)	1 (1%)	14	47
19	t	91/93 (98%)	83 (91%)	8 (9%)	0	100	100
20	u	100/102 (98%)	85 (85%)	13 (13%)	2 (2%)	6	32
21	v	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	w	73/75 (97%)	68 (93%)	4 (6%)	1 (1%)	9	38
23	x	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
24	y	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
25	z	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
26	B	54/56 (96%)	45 (83%)	6 (11%)	3 (6%)	1	16
27	C	48/50 (96%)	45 (94%)	2 (4%)	1 (2%)	5	31
28	D	44/46 (96%)	38 (86%)	5 (11%)	1 (2%)	5	30
29	E	62/64 (97%)	54 (87%)	6 (10%)	2 (3%)	3	25
30	F	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	4	27
31	G	223/225 (99%)	204 (92%)	18 (8%)	1 (0%)	30	64
32	H	204/206 (99%)	188 (92%)	14 (7%)	2 (1%)	12	45
33	I	203/205 (99%)	179 (88%)	20 (10%)	4 (2%)	6	32
34	J	155/157 (99%)	133 (86%)	17 (11%)	5 (3%)	3	25
35	K	98/100 (98%)	75 (76%)	21 (21%)	2 (2%)	6	32
36	L	149/151 (99%)	131 (88%)	17 (11%)	1 (1%)	18	53
37	M	127/129 (98%)	113 (89%)	11 (9%)	3 (2%)	4	29
38	N	125/127 (98%)	100 (80%)	20 (16%)	5 (4%)	2	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	O	96/98 (98%)	79 (82%)	13 (14%)	4 (4%)	2	20
40	P	114/116 (98%)	92 (81%)	18 (16%)	4 (4%)	3	23
41	Q	121/123 (98%)	96 (79%)	19 (16%)	6 (5%)	1	18
42	R	112/114 (98%)	96 (86%)	11 (10%)	5 (4%)	2	19
43	S	98/100 (98%)	79 (81%)	19 (19%)	0	100	100
44	T	86/88 (98%)	79 (92%)	5 (6%)	2 (2%)	5	30
45	U	80/82 (98%)	69 (86%)	10 (12%)	1 (1%)	9	40
46	V	78/80 (98%)	61 (78%)	11 (14%)	6 (8%)	1	12
47	W	63/65 (97%)	55 (87%)	7 (11%)	1 (2%)	7	36
48	X	77/79 (98%)	64 (83%)	12 (16%)	1 (1%)	9	40
49	Y	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
50	Z	63/65 (97%)	44 (70%)	14 (22%)	5 (8%)	1	11
51	a	130/223 (58%)	119 (92%)	11 (8%)	0	100	100
58	8	85/400 (21%)	76 (89%)	7 (8%)	2 (2%)	4	29
All	All	6004/6512 (92%)	5191 (86%)	701 (12%)	112 (2%)	8	33

All (112) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
5	f	45	ALA
5	f	174	LYS
6	g	9	VAL
7	h	108	VAL
9	j	81	ILE
12	m	58	LYS
17	r	54	VAL
20	u	6	ARG
29	E	31	ILE
30	F	37	GLN
32	H	61	LYS
34	J	93	VAL
34	J	122	VAL
38	N	125	GLN
41	Q	75	GLU
42	R	4	ALA
46	V	17	GLU

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Mol	Chain	Res	Type
46	V	49	ASN
50	Z	14	ALA
58	8	334	ARG
10	k	110	GLU
11	l	87	GLY
13	n	104	ALA
32	H	191	THR
33	I	23	GLY
34	J	11	GLN
34	J	98	ALA
37	M	47	ASP
38	N	90	ASP
38	N	91	GLU
39	O	34	ALA
40	P	89	GLY
42	R	41	ASP
44	T	87	ARG
4	e	20	ASN
7	h	27	VAL
11	l	16	GLY
11	l	85	VAL
14	o	34	HIS
17	r	44	GLY
20	u	97	SER
22	w	80	ALA
26	B	25	THR
36	L	18	GLY
38	N	71	ILE
41	Q	23	LEU
44	T	2	LEU
45	U	79	ASN
46	V	15	LYS
50	Z	24	LYS
3	d	75	SER
7	h	79	PRO
7	h	118	ILE
10	k	93	GLN
11	l	29	LYS
11	l	65	GLY
11	l	88	GLY
15	p	64	SER
33	I	28	ASP

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Mol	Chain	Res	Type
33	I	47	LEU
35	K	55	HIS
35	K	94	HIS
38	N	8	THR
39	O	42	LEU
40	P	13	LYS
41	Q	76	HIS
42	R	14	ALA
48	X	34	SER
50	Z	8	ASN
50	Z	34	ARG
1	b	147	PRO
2	c	63	PRO
2	c	149	ASN
3	d	83	VAL
7	h	119	PRO
8	i	92	PRO
10	k	31	ARG
11	l	56	PRO
18	s	11	ARG
26	B	8	THR
27	C	15	GLY
31	G	24	PRO
33	I	167	PRO
39	O	41	PRO
40	P	92	ARG
41	Q	77	SER
46	V	70	LYS
47	W	13	THR
7	h	81	LEU
12	m	69	PRO
28	D	4	THR
34	J	49	TYR
37	M	56	PRO
40	P	88	PRO
42	R	5	GLY
50	Z	9	GLU
41	Q	41	PRO
42	R	6	ILE
10	k	35	VAL
39	O	33	GLY
41	Q	3	VAL

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Mol	Chain	Res	Type
46	V	31	PRO
46	V	32	ILE
1	b	125	PRO
7	h	78	GLY
13	n	109	PRO
29	E	19	GLY
13	n	116	VAL
26	B	53	VAL
37	M	80	PRO
58	8	353	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	72
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	146 (99%)	2 (1%)	59	71
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	75
7	h	100/100 (100%)	100 (100%)	0	100	100
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	103 (100%)	0	100	100
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	72
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	75
16	q	89/89 (100%)	87 (98%)	2 (2%)	45	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	r	84/84 (100%)	81 (96%)	3 (4%)	31	54
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	74
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%)	46 (98%)	1 (2%)	47	65
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	185 (100%)	1 (0%)	81	82
32	H	170/170 (100%)	168 (99%)	2 (1%)	63	72
33	I	172/172 (100%)	171 (99%)	1 (1%)	78	80
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	77
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	74
36	L	124/124 (100%)	122 (98%)	2 (2%)	55	69
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	75
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	86 (100%)	0	100	100
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	101 (98%)	2 (2%)	50	66
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%)	75 (99%)	1 (1%)	61	71
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	71
47	W	56/56 (100%)	56 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	75/332 (23%)	75 (100%)	0	100	100
All	All	4983/5304 (94%)	4952 (99%)	31 (1%)	76	80

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	c	142	VAL
2	c	181	ASP
4	e	141	ASP
4	e	148	VAL
6	g	7	ASP
14	o	67	ASN
15	p	65	ASN
16	q	18	LYS
16	q	30	VAL
17	r	11	GLN
17	r	22	LEU
17	r	54	VAL
18	s	109	ASP
19	t	2	ILE
21	v	43	ASP
26	B	53	VAL
31	G	38	HIS
32	H	124	GLU
32	H	156	LEU
33	I	34	GLU
34	J	141	ASP
35	K	97	THR
36	L	29	LEU
36	L	49	LEU
37	M	98	LEU
41	Q	24	GLU
41	Q	37	TYR
44	T	17	ASP
46	V	14	ASP
50	Z	27	VAL

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Mol	Chain	Res	Type
50	Z	40	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (119) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	52	HIS
1	b	116	GLN
1	b	127	ASN
1	b	142	ASN
1	b	196	ASN
1	b	225	ASN
1	b	259	ASN
2	c	49	GLN
2	c	130	GLN
2	c	136	ASN
2	c	150	GLN
3	d	9	GLN
3	d	90	GLN
3	d	92	HIS
3	d	97	ASN
3	d	136	GLN
3	d	165	HIS
5	f	21	GLN
5	f	103	ASN
5	f	127	GLN
6	g	33	GLN
6	g	66	ASN
7	h	6	GLN
8	i	5	GLN
8	i	11	GLN
8	i	18	ASN
8	i	30	GLN
8	i	42	ASN
8	i	104	GLN
9	j	58	ASN
9	j	76	HIS
9	j	128	ASN
11	l	38	GLN
11	l	54	GLN
12	m	97	GLN
13	n	9	GLN
13	n	16	HIS

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Mol	Chain	Res	Type
13	n	62	ASN
13	n	73	ASN
13	n	107	ASN
14	o	98	GLN
15	p	6	GLN
15	p	65	ASN
15	p	76	HIS
16	q	36	GLN
16	q	65	ASN
16	q	71	ASN
17	r	11	GLN
17	r	18	GLN
17	r	82	HIS
17	r	86	GLN
17	r	89	HIS
18	s	61	ASN
18	s	102	HIS
19	t	48	GLN
19	t	59	ASN
19	t	70	HIS
19	t	92	ASN
20	u	39	ASN
20	u	73	ASN
21	v	78	GLN
22	w	8	ASN
23	x	15	ASN
23	x	16	ASN
23	x	19	HIS
24	y	58	ASN
25	z	8	GLN
25	z	48	ASN
26	B	3	GLN
26	B	18	HIS
26	B	41	HIS
27	C	44	GLN
28	D	26	ASN
28	D	29	GLN
29	E	42	HIS
30	F	37	GLN
31	G	38	HIS
31	G	102	ASN
32	H	31	ASN

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Mol	Chain	Res	Type
32	H	68	HIS
33	I	115	GLN
33	I	130	ASN
33	I	151	GLN
33	I	195	ASN
34	J	82	HIS
34	J	121	ASN
34	J	134	ASN
35	K	3	HIS
35	K	63	ASN
36	L	27	ASN
36	L	121	ASN
36	L	147	ASN
37	M	15	ASN
37	M	37	ASN
37	M	66	GLN
38	N	4	GLN
38	N	36	GLN
39	O	58	ASN
40	P	14	GLN
40	P	27	ASN
40	P	37	GLN
40	P	39	ASN
40	P	118	ASN
41	Q	5	GLN
41	Q	45	ASN
41	Q	95	HIS
43	S	42	ASN
44	T	36	ASN
44	T	45	HIS
44	T	49	HIS
44	T	79	GLN
45	U	9	HIS
45	U	79	ASN
46	V	50	ASN
48	X	55	GLN
49	Y	60	GLN
49	Y	74	HIS
49	Y	83	ASN
51	a	188	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	136 (8%)	2 (0%)
53	1	2902/2903 (99%)	326 (11%)	7 (0%)
54	2	119/120 (99%)	10 (8%)	1 (0%)
55	5	76/77 (98%)	6 (7%)	0
55	6	76/77 (98%)	8 (10%)	0
56	4	17/18 (94%)	3 (17%)	0
57	7	74/76 (97%)	14 (18%)	0
All	All	4802/4810 (99%)	503 (10%)	10 (0%)

All (503) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A
52	3	71	A
52	3	85	U
52	3	87	C
52	3	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
52	3	267	C
52	3	279	A
52	3	281	G
52	3	289	G
52	3	345	C
52	3	352	C
52	3	355	C
52	3	367	U

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Mol	Chain	Res	Type
52	3	372	C
52	3	411	A
52	3	413	G
52	3	429	U
52	3	467	U
52	3	485	U
52	3	486	U
52	3	497	G
52	3	518	C
52	3	532	A
52	3	536	C
52	3	547	A
52	3	561	U
52	3	564	C
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	652	U
52	3	665	A
52	3	688	G
52	3	703	G
52	3	724	G
52	3	755	G
52	3	777	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	821	G
52	3	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

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Mol	Chain	Res	Type
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1053	G
52	3	1054	C
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1198	G
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1258	G
52	3	1260	G
52	3	1275	A
52	3	1278	G
52	3	1280	A

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Mol	Chain	Res	Type
52	3	1282	C
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1381	U
52	3	1395	C
52	3	1446	A
52	3	1448	C
52	3	1452	C
52	3	1492	A
52	3	1503	A
52	3	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	46	G
53	1	49	A
53	1	50	U
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A
53	1	75	G
53	1	119	A
53	1	120	U
53	1	138	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C

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Mol	Chain	Res	Type
53	1	181	A
53	1	196	A
53	1	216	A
53	1	221	A
53	1	222	A
53	1	228	C
53	1	229	C
53	1	248	G
53	1	249	C
53	1	255	A
53	1	265	A
53	1	266	G
53	1	276	U
53	1	278	A
53	1	281	C
53	1	294	A
53	1	301	G
53	1	311	A
53	1	323	C
53	1	324	A
53	1	329	G
53	1	330	A
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	424	G
53	1	451	U
53	1	455	C
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	531	C
53	1	532	A
53	1	543	G
53	1	545	U

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Mol	Chain	Res	Type
53	1	563	A
53	1	572	A
53	1	573	U
53	1	588	U
53	1	603	A
53	1	616	A
53	1	627	A
53	1	637	A
53	1	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	775	G
53	1	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	801	G
53	1	805	G
53	1	812	C
53	1	819	A
53	1	822	G
53	1	827	U
53	1	828	U
53	1	830	G
53	1	845	A
53	1	846	U
53	1	847	U
53	1	859	G
53	1	860	U
53	1	878	A
53	1	885	C
53	1	886	A
53	1	887	U
53	1	888	C

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Mol	Chain	Res	Type
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	983	A
53	1	995	C
53	1	996	A
53	1	1012	U
53	1	1013	C
53	1	1021	A
53	1	1022	G
53	1	1026	G
53	1	1033	U
53	1	1045	C
53	1	1046	A
53	1	1054	A
53	1	1060	U
53	1	1062	G
53	1	1066	U
53	1	1067	A
53	1	1070	A
53	1	1071	G
53	1	1079	C
53	1	1084	A
53	1	1088	A
53	1	1104	C
53	1	1106	G
53	1	1111	A
53	1	1131	G
53	1	1132	U
53	1	1133	A
53	1	1135	C
53	1	1143	A
53	1	1157	G
53	1	1173	U
53	1	1175	A
53	1	1177	G
53	1	1180	U

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Mol	Chain	Res	Type
53	1	1206	G
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	1275	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	1398	C
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1454	C
53	1	1461	C
53	1	1482	G
53	1	1490	A
53	1	1491	G
53	1	1493	C
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1535	A
53	1	1536	C
53	1	1537	G
53	1	1555	G
53	1	1559	U
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1585	C
53	1	1608	A

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Mol	Chain	Res	Type
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	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	1919	A
53	1	1929	G
53	1	1930	G
53	1	1937	A
53	1	1938	A
53	1	1944	U
53	1	1955	U
53	1	1963	U
53	1	1967	C
53	1	1970	A
53	1	1972	G
53	1	1993	U
53	1	1997	C
53	1	2022	U
53	1	2023	C
53	1	2030	A
53	1	2031	A
53	1	2034	U

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Mol	Chain	Res	Type
53	1	2036	C
53	1	2043	C
53	1	2049	G
53	1	2055	C
53	1	2056	G
53	1	2060	A
53	1	2061	G
53	1	2062	A
53	1	2069	G
53	1	2096	C
53	1	2110	G
53	1	2111	U
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2132	U
53	1	2133	G
53	1	2145	C
53	1	2147	A
53	1	2162	G
53	1	2172	U
53	1	2173	A
53	1	2189	U
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2211	A
53	1	2225	A
53	1	2259	U
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2297	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2335	A
53	1	2350	C
53	1	2383	G

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Mol	Chain	Res	Type
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2406	A
53	1	2407	A
53	1	2423	U
53	1	2424	C
53	1	2429	G
53	1	2430	A
53	1	2435	A
53	1	2441	U
53	1	2448	A
53	1	2476	A
53	1	2478	A
53	1	2502	G
53	1	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2520	C
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2609	U
53	1	2613	U
53	1	2629	U
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U
53	1	2714	G
53	1	2744	G
53	1	2748	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2797	U

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Mol	Chain	Res	Type
53	1	2800	A
53	1	2809	A
53	1	2820	A
53	1	2821	A
53	1	2823	A
53	1	2833	U
53	1	2850	A
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2880	C
54	2	4	C
54	2	12	C
54	2	13	G
54	2	24	G
54	2	35	C
54	2	44	G
54	2	67	G
54	2	89	U
54	2	108	A
54	2	109	A
55	5	9	G
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	61	C
55	6	6	G
55	6	16	C
55	6	18	G
55	6	19	G
55	6	20	U
55	6	47	U
55	6	48	C
55	6	61	C
56	4	12	A
56	4	13	A
56	4	16	A
57	7	8	U
57	7	9	A
57	7	10	G
57	7	18	G

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Mol	Chain	Res	Type
57	7	19	G
57	7	21	A
57	7	26	A
57	7	44	G
57	7	45	U
57	7	46	G
57	7	48	C
57	7	55	U
57	7	61	C
57	7	63	G

All (10) RNA pucker outliers are listed below:

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

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	FME	5	101	55	8,9,10	0.44	0	8,9,11	1.06	1 (12%)

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	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
59	5	101	FME	O-C-CA	-2.09	119.40	124.77

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

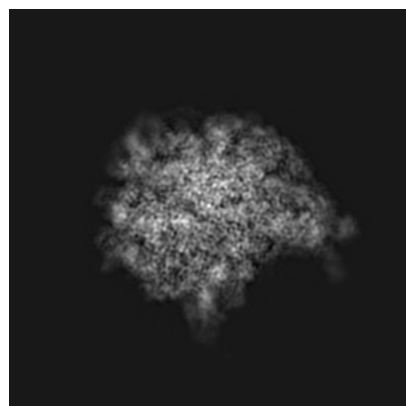
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21626. These allow visual inspection of the internal detail of the map and identification of artifacts.

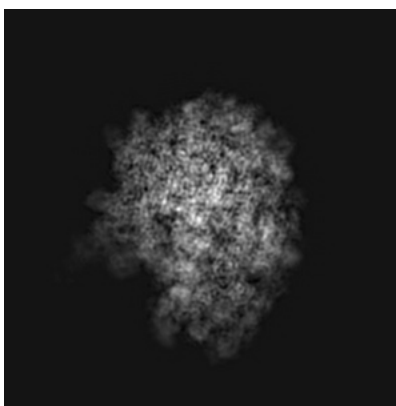
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

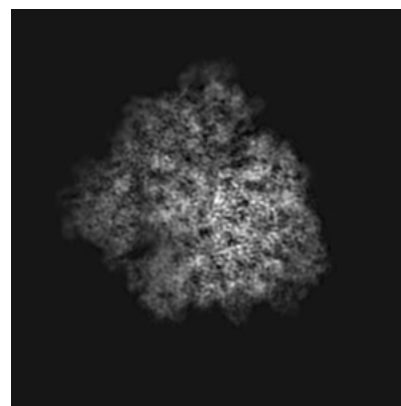
6.1.1 Primary map



X

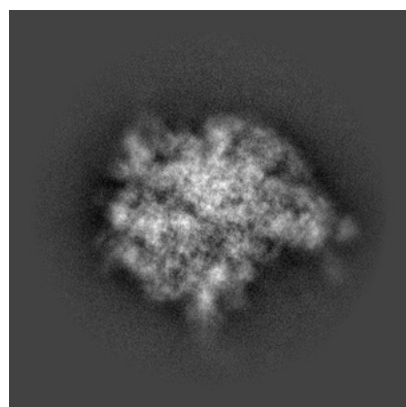


Y

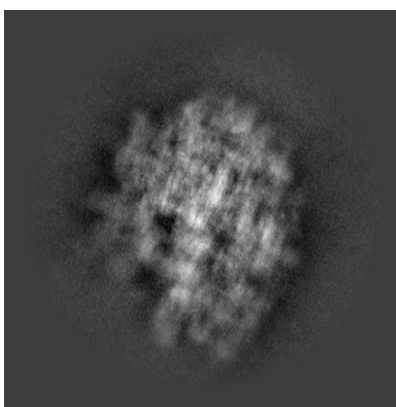


Z

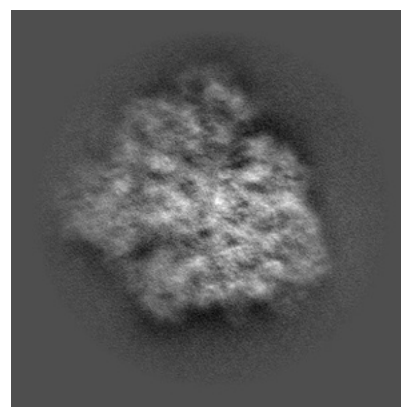
6.1.2 Raw map



X



Y

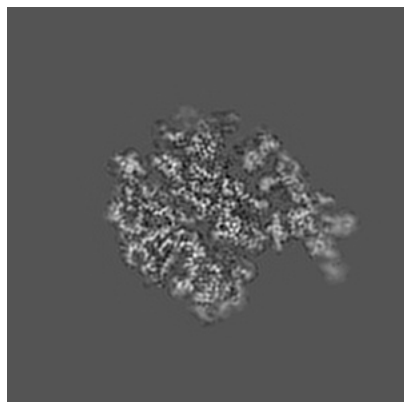


Z

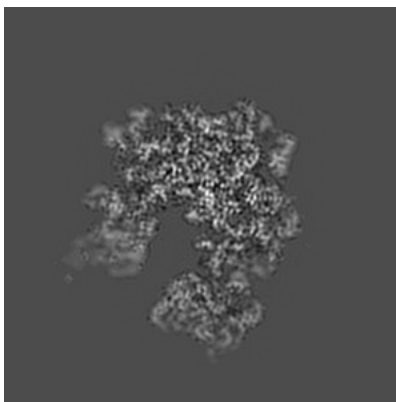
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

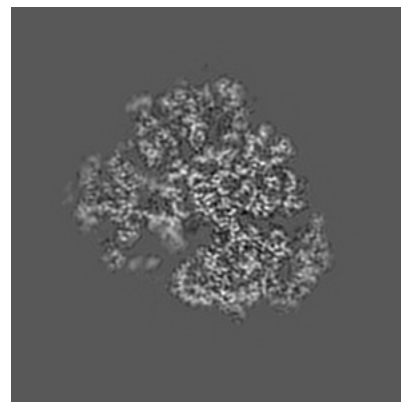
6.2.1 Primary map



X Index: 144

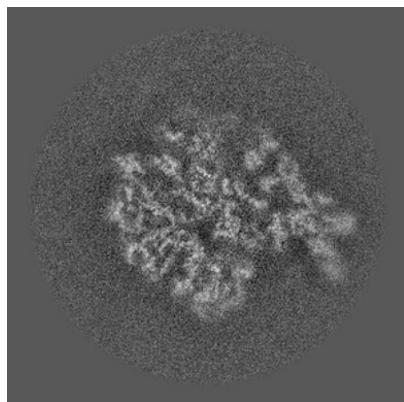


Y Index: 144

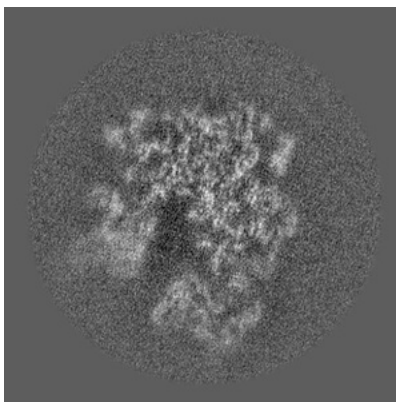


Z Index: 144

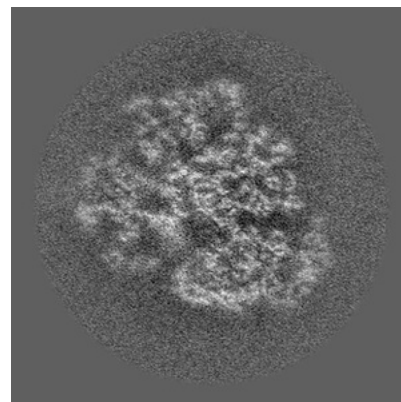
6.2.2 Raw map



X Index: 144



Y Index: 144

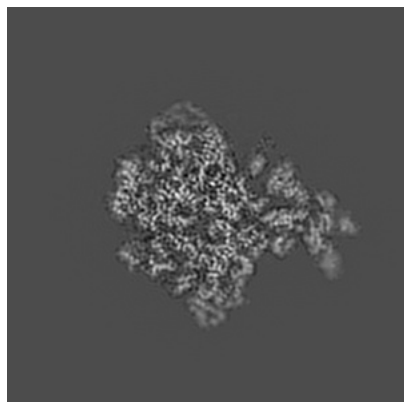


Z Index: 144

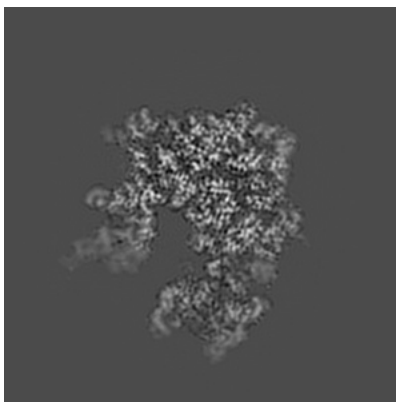
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

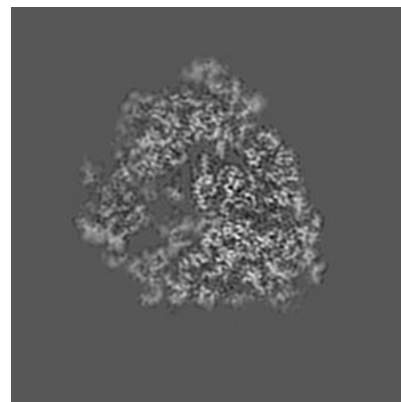
6.3.1 Primary map



X Index: 149

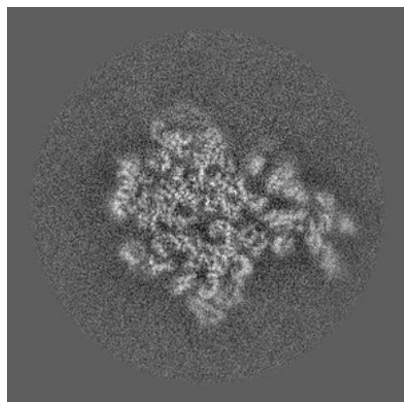


Y Index: 148

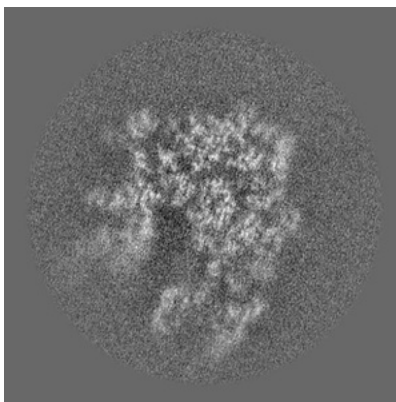


Z Index: 135

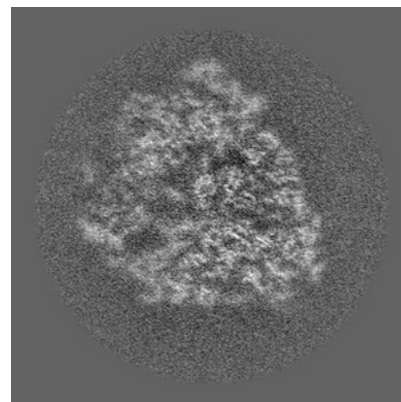
6.3.2 Raw map



X Index: 149



Y Index: 148

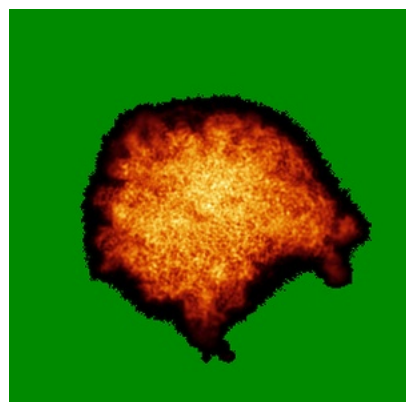


Z Index: 135

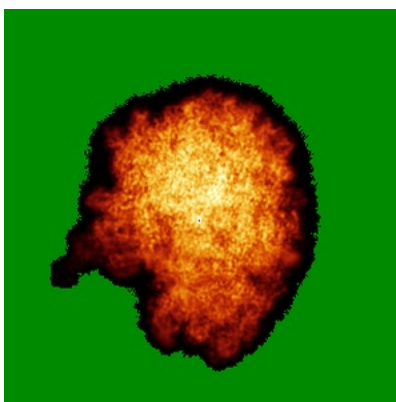
The images above show the largest variance slices of the map in three orthogonal directions.

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

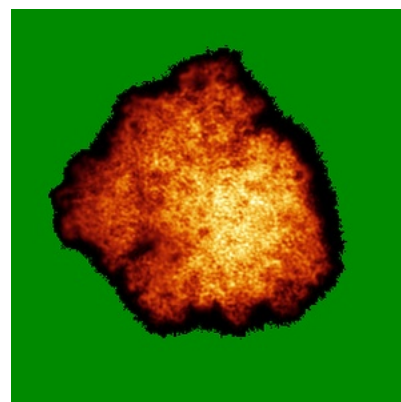
6.4.1 Primary map



X

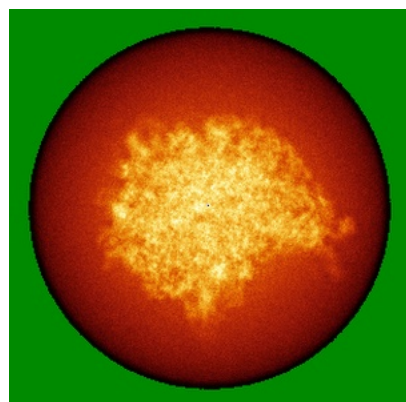


Y

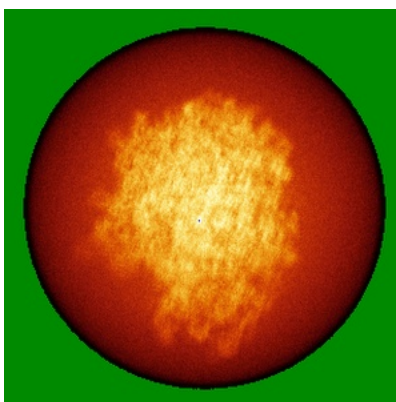


Z

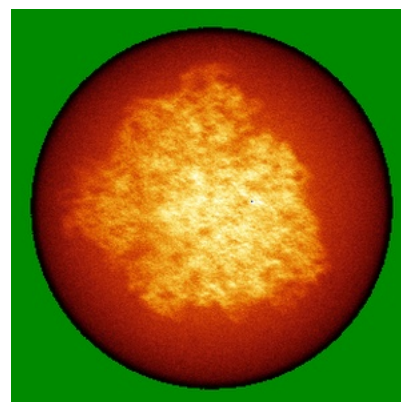
6.4.2 Raw map



X



Y



Z

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

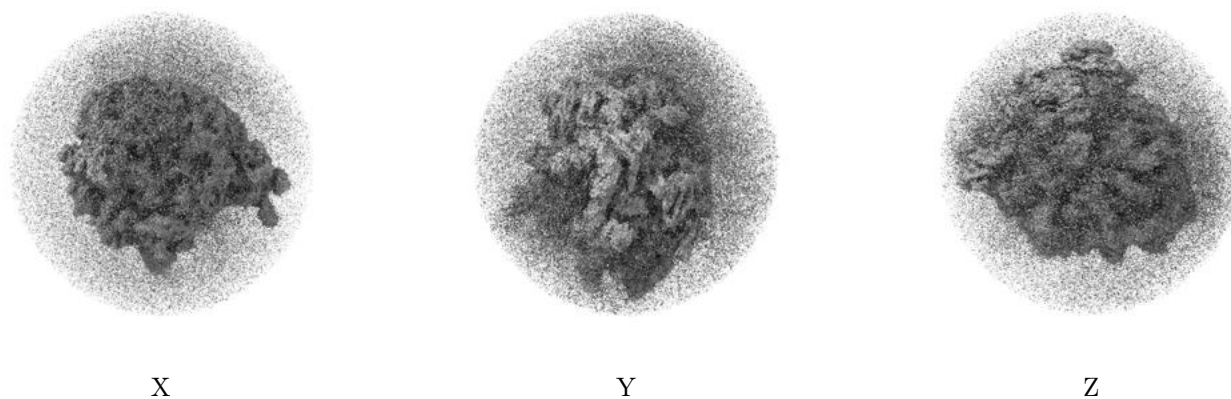
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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

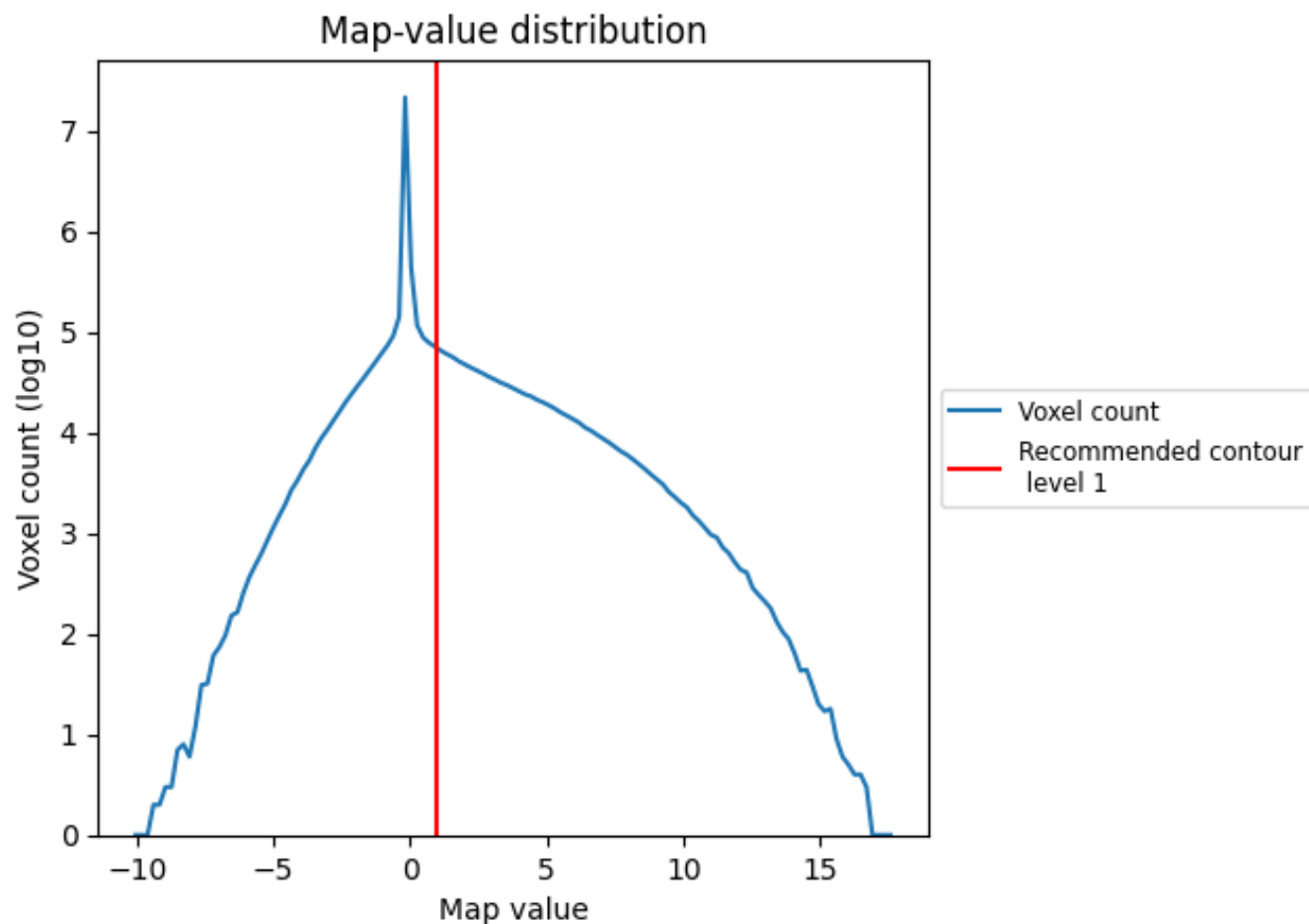
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

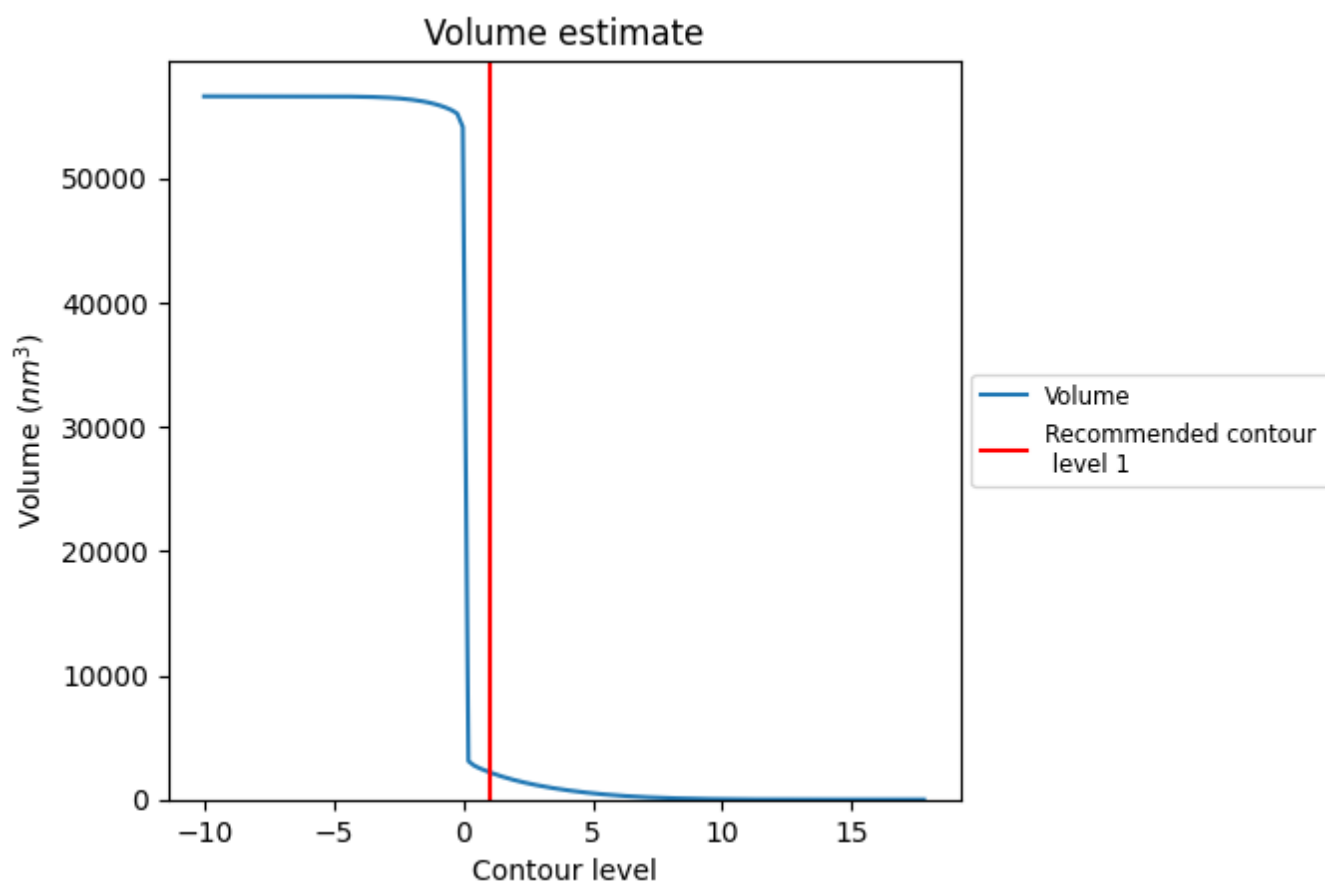
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

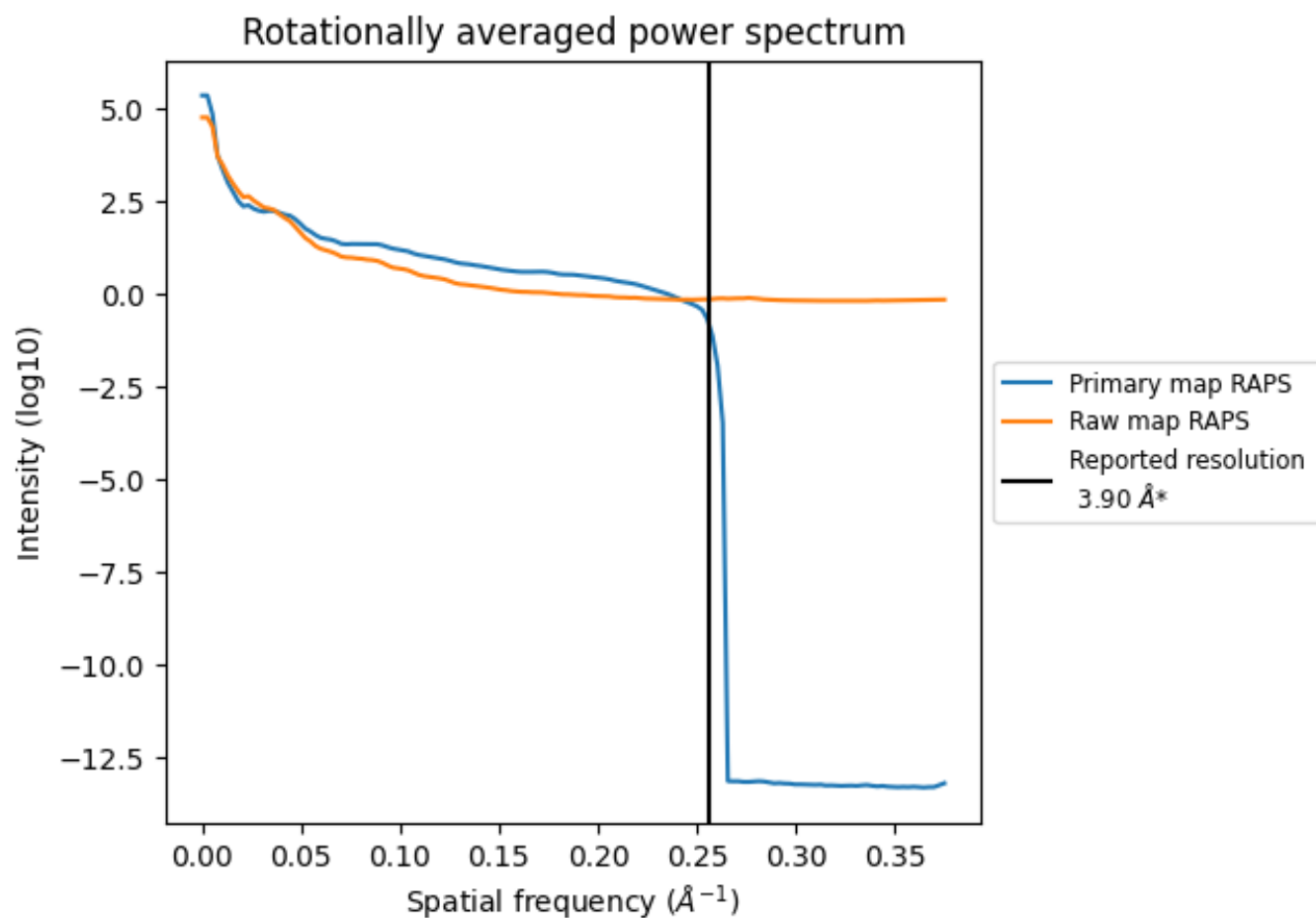
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2194 nm³; this corresponds to an approximate mass of 1982 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 ⓘ

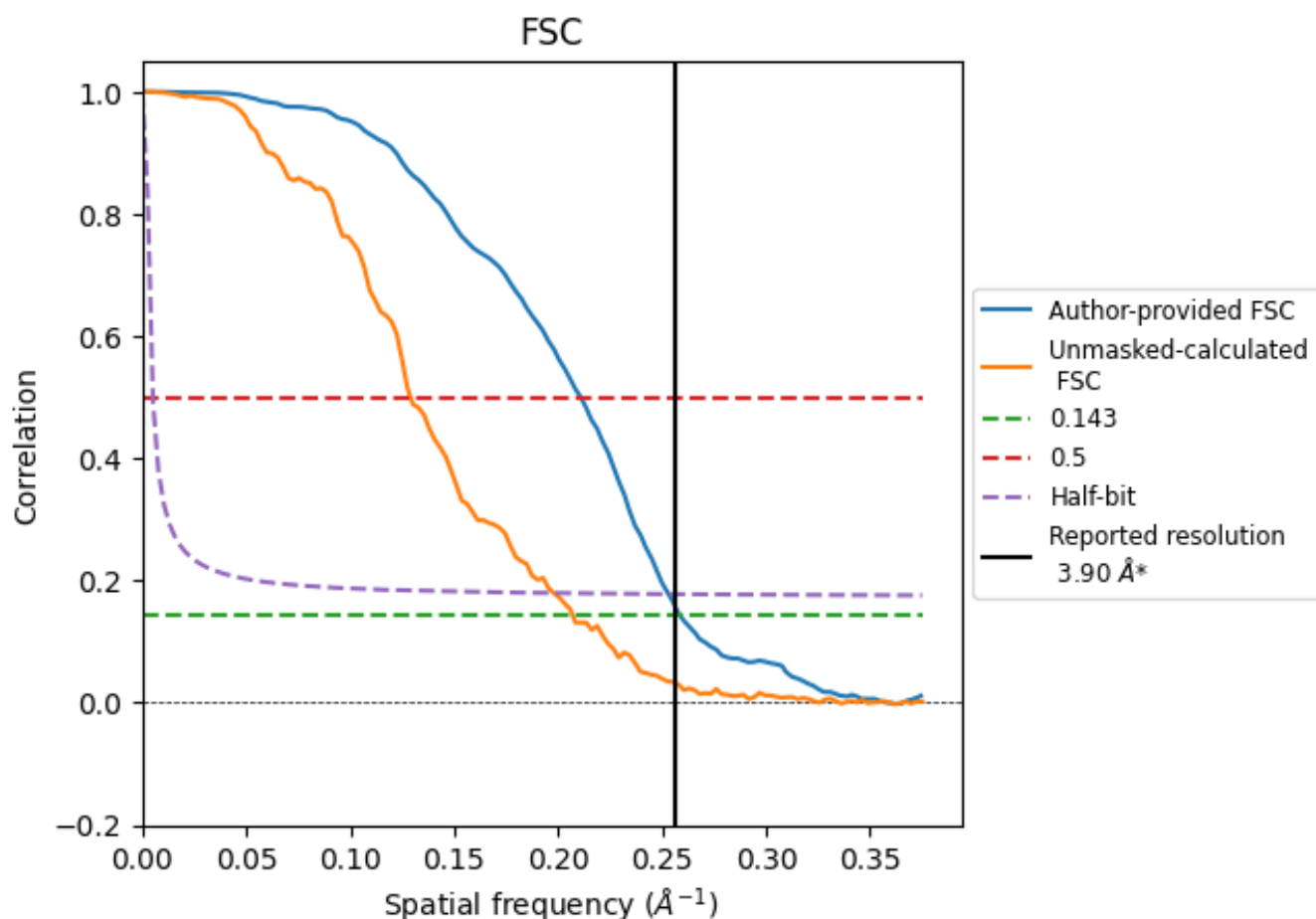


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

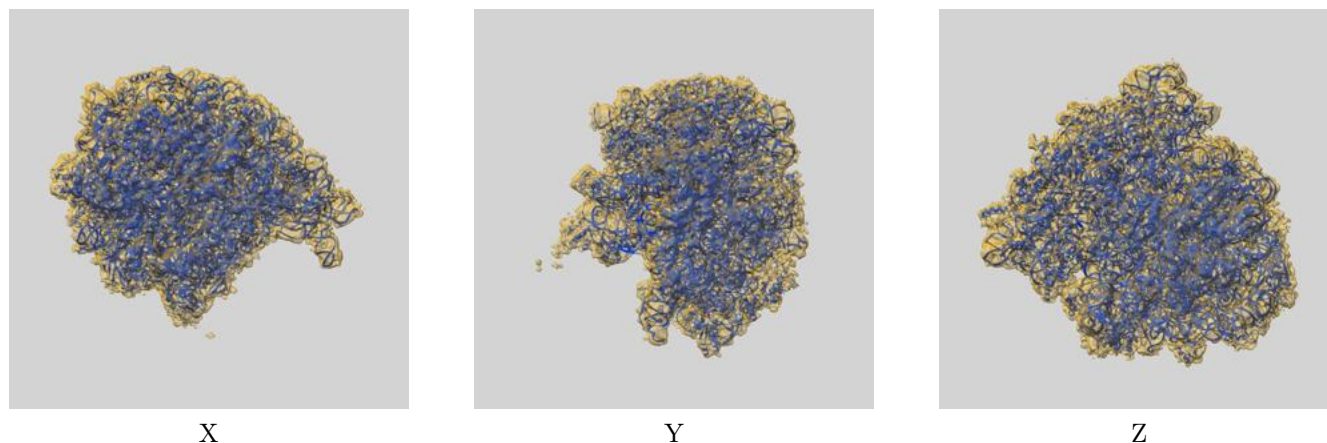
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.87	4.74	3.95
Unmasked-calculated*	4.83	7.75	5.05

*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 4.83 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

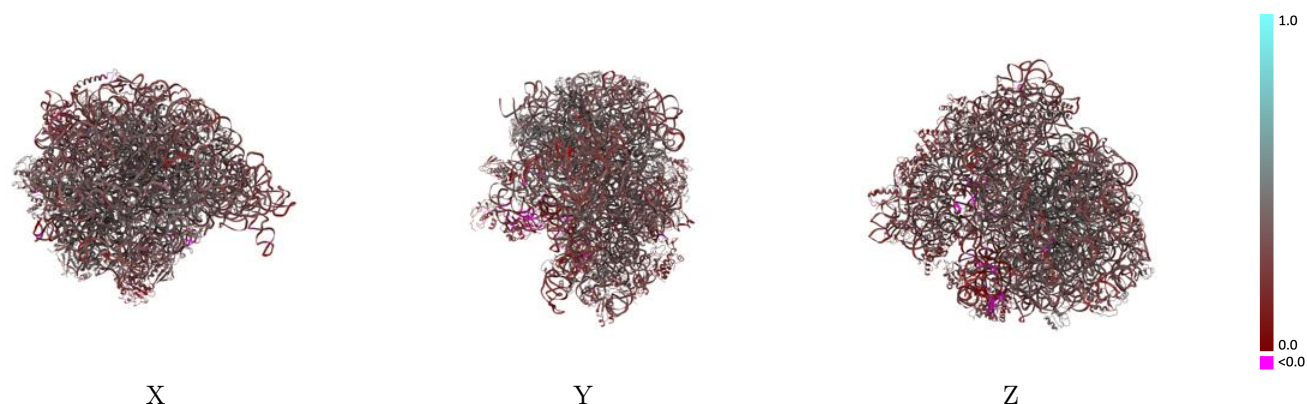
This section contains information regarding the fit between EMDB map EMD-21626 and PDB model 6WD7. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



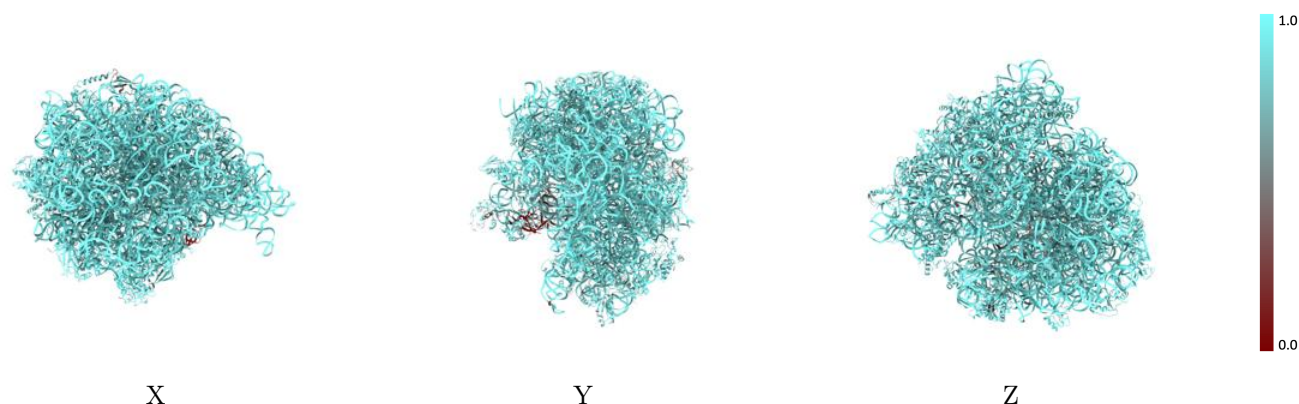
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



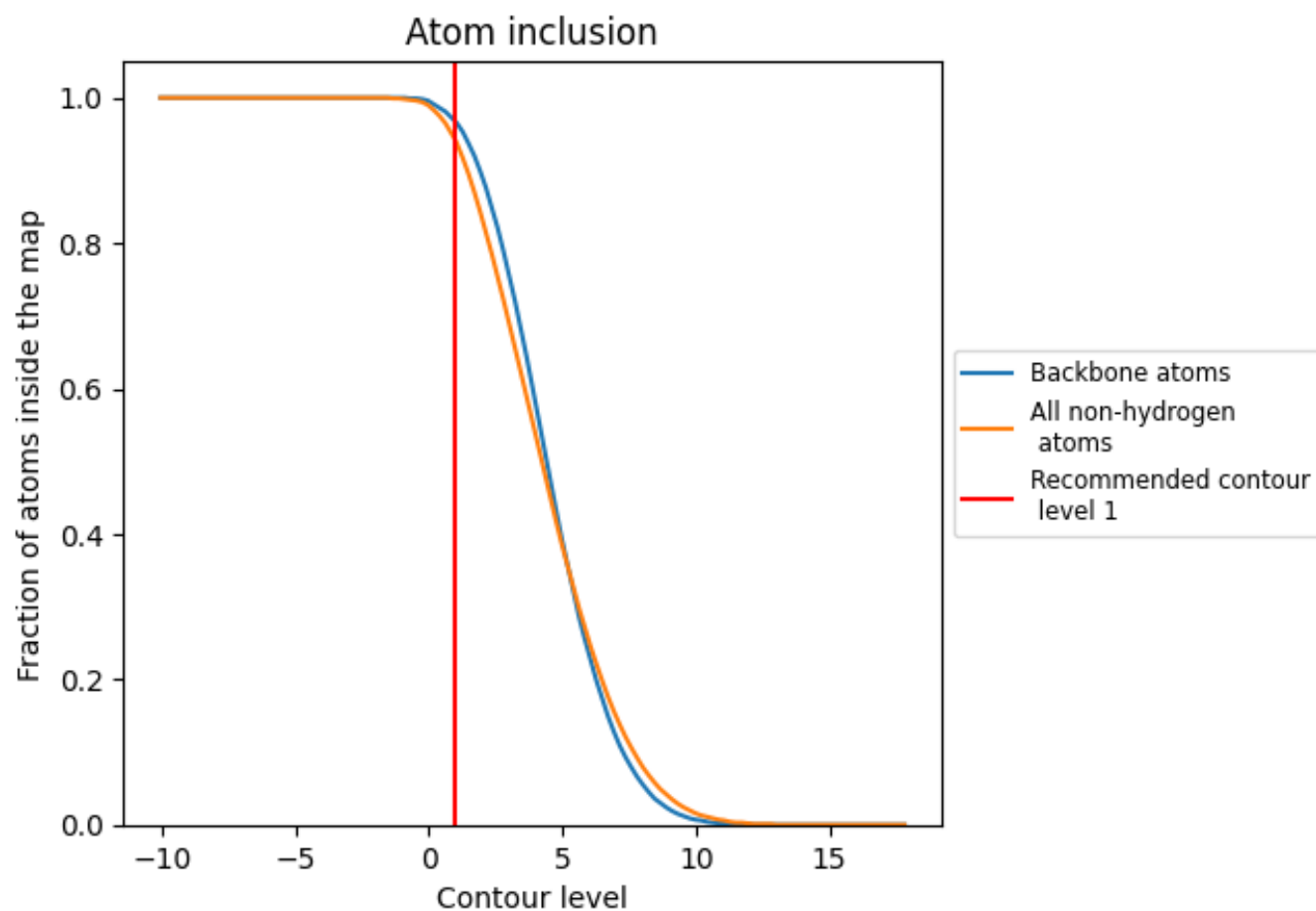
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 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	 0.9410	 0.3260
1	 0.9750	 0.3440
2	 0.9780	 0.3060
3	 0.9670	 0.3090
4	 0.8120	 0.1830
5	 0.9590	 0.2590
6	 0.7890	 0.1240
7	 0.6370	 0.1050
8	 0.2150	 0.1020
B	 0.9440	 0.4170
C	 0.7930	 0.3150
D	 0.9300	 0.4190
E	 0.9290	 0.4330
F	 0.8560	 0.3970
G	 0.8770	 0.2830
H	 0.8530	 0.3300
I	 0.8630	 0.2700
J	 0.9150	 0.3640
K	 0.9450	 0.3290
L	 0.9130	 0.3140
M	 0.8950	 0.3470
N	 0.8920	 0.3010
O	 0.7730	 0.2800
P	 0.9480	 0.3540
Q	 0.9100	 0.3850
R	 0.9070	 0.2900
S	 0.8630	 0.3040
T	 0.9270	 0.3420
U	 0.9120	 0.3520
V	 0.9380	 0.3700
W	 0.9220	 0.3280
X	 0.9500	 0.2890
Y	 0.9000	 0.3240
Z	 0.8360	 0.2640
a	 0.8050	 0.1260



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Chain	Atom inclusion	Q-score
b	 0.9440	 0.4210
c	 0.9440	 0.4130
d	 0.9250	 0.3700
e	 0.9530	 0.2960
f	 0.9520	 0.2950
g	 0.7310	 0.2430
h	 0.7510	 0.1520
i	 0.7190	 0.1520
j	 0.9360	 0.4030
k	 0.9160	 0.4220
l	 0.9490	 0.4120
m	 0.9130	 0.4090
n	 0.9370	 0.4060
o	 0.9300	 0.3300
p	 0.9350	 0.3930
q	 0.9280	 0.4020
r	 0.9460	 0.3980
s	 0.9030	 0.3960
t	 0.9220	 0.3810
u	 0.9380	 0.3500
v	 0.9420	 0.3550
w	 0.9270	 0.4240
x	 0.9370	 0.4160
y	 0.9460	 0.3010
z	 0.9220	 0.3530