



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 05:46 AM UTC

PDB ID : 6WD5 / pdb_00006wd5
EMDB ID : EMD-21624
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure II-C1)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

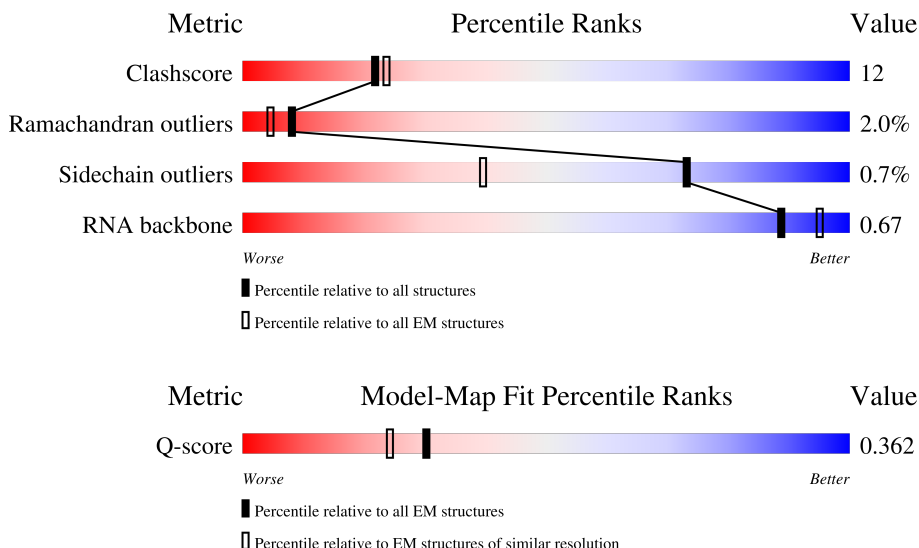
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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.



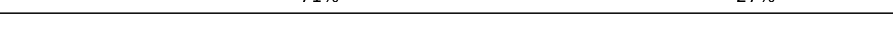
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	

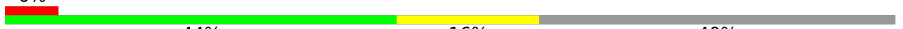
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	e	177	 66% 33% .
5	f	176	 69% 30% .
6	g	149	 7% 62% 36% .
7	h	131	 10% 52% 40% 6% .
8	i	141	 23% 58% 38% . .
9	j	142	 77% 20% .
10	k	122	 60% 39% .
11	l	143	 69% 28% .
12	m	136	 66% 30% . .
13	n	120	 60% 38% . .
14	o	116	 67% 29% .
15	p	114	 58% 41% .
16	q	117	 74% 25% .
17	r	103	 71% 27% . .
18	s	110	 75% 25% .
19	t	93	 71% 27% .
20	u	102	 66% 32% .
21	v	94	 68% 30% . .
22	w	75	 73% 27% .
23	x	77	 68% 31% .
24	y	63	 67% 30% .
25	z	58	 78% 22% .
26	B	56	 57% 41% .
27	C	50	 74% 24% .
28	D	46	 65% 30% . .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	E	64	 66% 33% .
30	F	38	 66% 32% .
31	G	225	 69% 29% .
32	H	206	 12% 67% 31% .
33	I	205	 64% 35% .
34	J	157	 59% 39% ..
35	K	100	 45% 51% .
36	L	151	 66% 32% .
37	M	129	 59% 40% .
38	N	127	 52% 45% .
39	O	98	 15% 62% 33% . .
40	P	116	 60% 34% . .
41	Q	123	 61% 33% 6% .
42	R	114	 62% 34% .
43	S	100	 9% 56% 42% .
44	T	88	 70% 30%
45	U	82	 65% 35%
46	V	80	 61% 35% .
47	W	65	 57% 43%
48	X	79	 63% 34% .
49	Y	85	 72% 27% .
50	Z	65	 43% 45% 9% .
51	a	223	 6% 44% 16% 40%
52	3	1539	 55% 41% .
53	1	2903	 56% 38% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	2	120	56%38%7%
55	5	77	70%29%
55	6	77	61%38%
56	4	18	6%56%44%
57	7	76	58%33%9%
58	8	400	22%58%35%6%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 153135 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

- Molecule 56 is a RNA chain called mRNA.

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

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

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

- Molecule 58 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	375	Total	C	N	O	S	0	0
			2885	1826	496	550	13		

There are 7 discrepancies between the modelled and reference sequences:

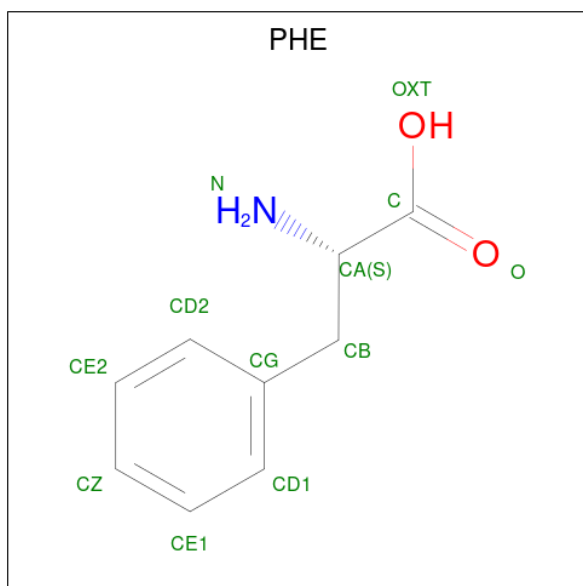
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag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

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



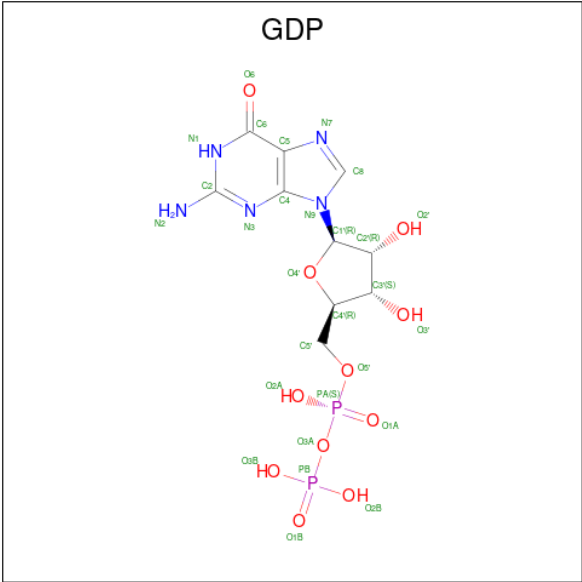
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

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



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

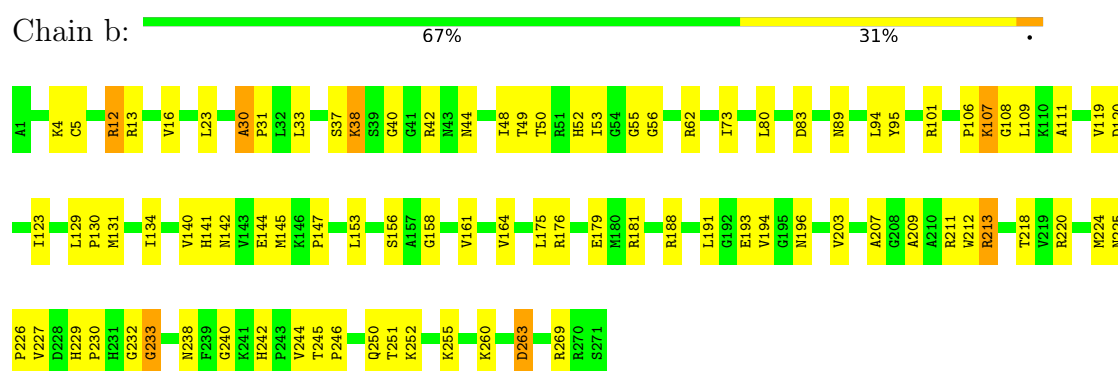
- Molecule 61 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



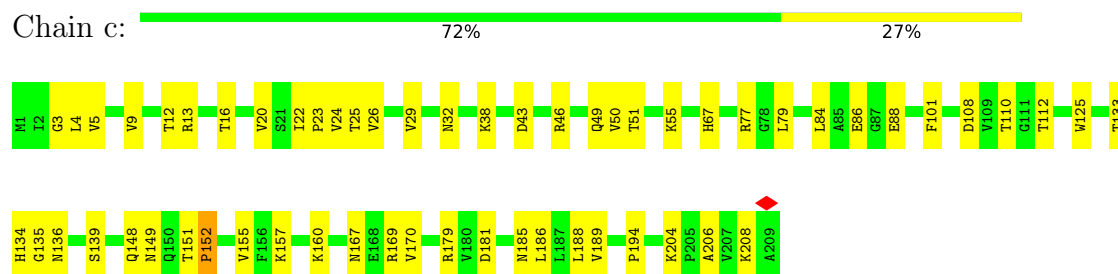
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

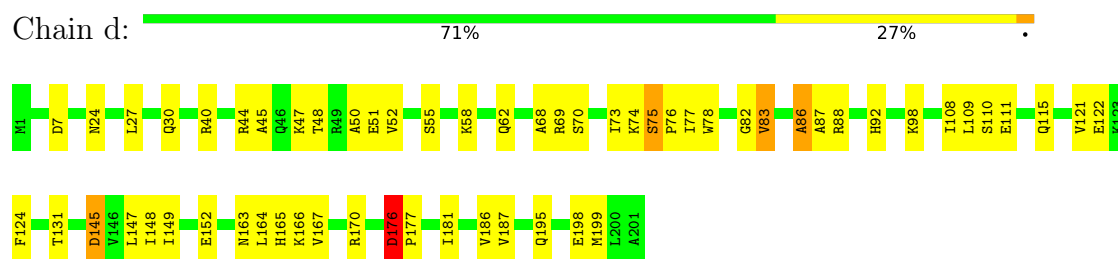
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

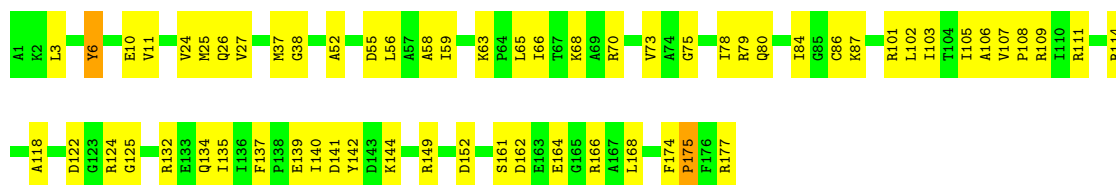


• Molecule 3: 50S ribosomal protein L4



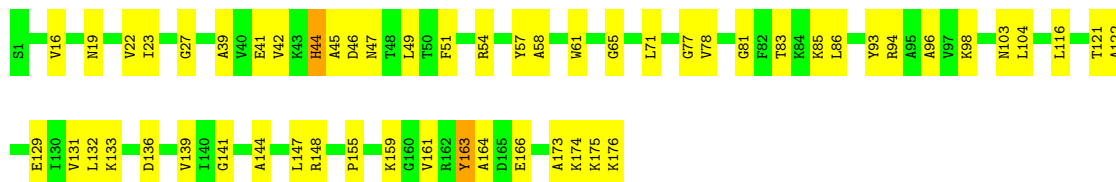
• Molecule 4: 50S ribosomal protein L5





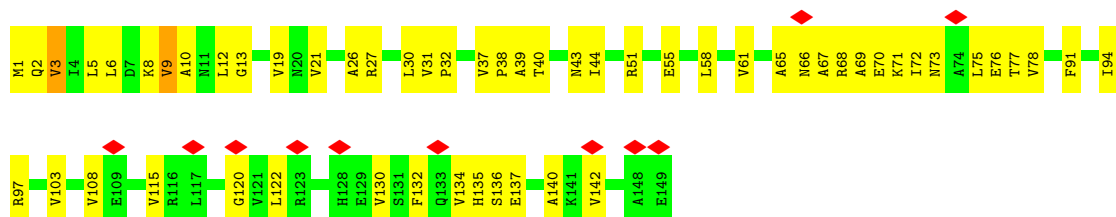
• Molecule 5: 50S ribosomal protein L6

Chain f: 69% 30% .



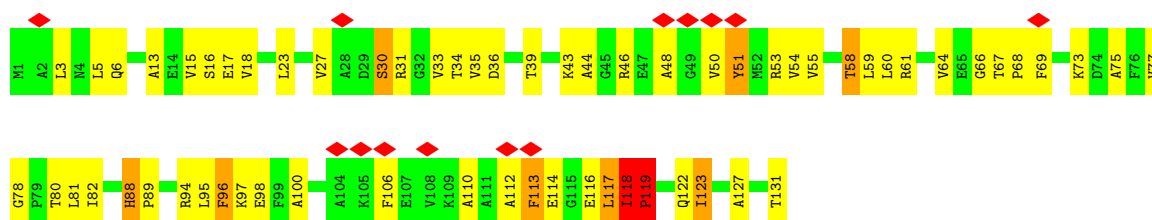
• Molecule 6: 50S ribosomal protein L9

Chain g: 7% 62% 36% .



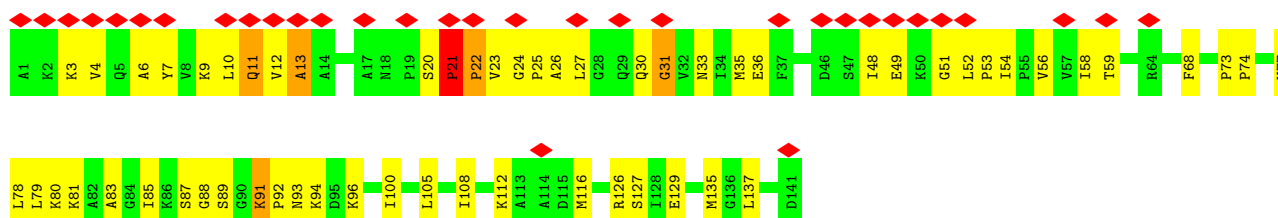
• Molecule 7: 50S ribosomal protein L10

Chain h: 10% 52% 40% 6% .



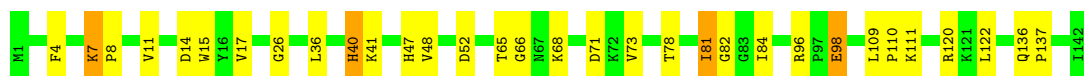
• Molecule 8: 50S ribosomal protein L11

Chain i: 23% 58% 38% . .



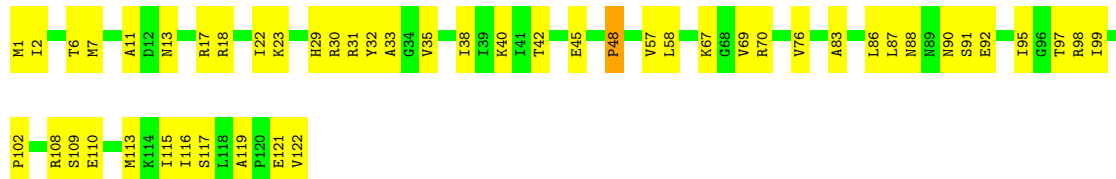
- Molecule 9: 50S ribosomal protein L13

Chain j:  77% 20% .



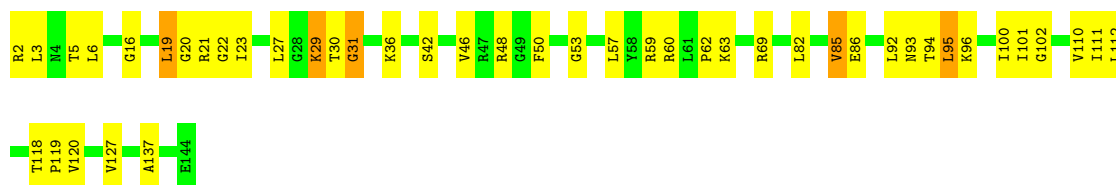
- Molecule 10: 50S ribosomal protein L14

Chain k:  60% 39% .



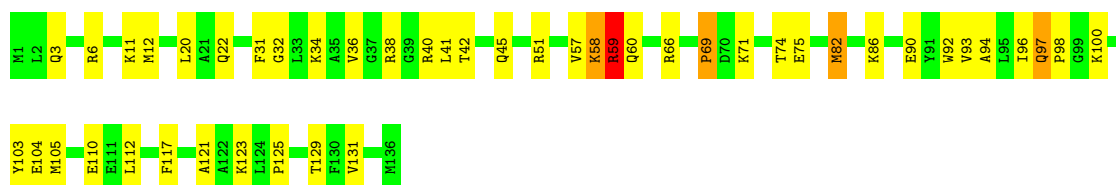
- Molecule 11: 50S ribosomal protein L15

Chain l:  69% 28% .



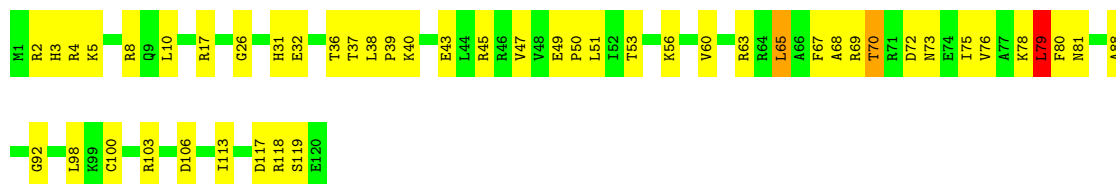
- Molecule 12: 50S ribosomal protein L16

Chain m:  66% 30% . .



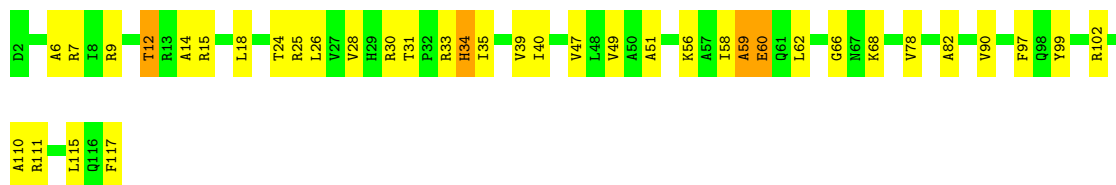
- Molecule 13: 50S ribosomal protein L17

Chain n:  60% 38% . .



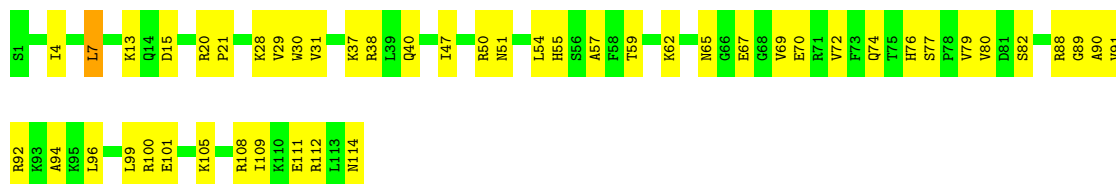
- Molecule 14: 50S ribosomal protein L18

Chain o:  67% 29% .



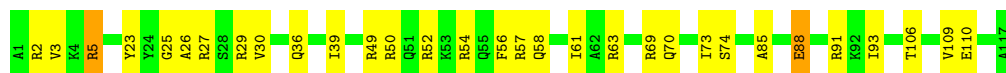
- Molecule 15: 50S ribosomal protein L19

Chain p:  58% 41% .



- Molecule 16: 50S ribosomal protein L20

Chain q:  74% 25% .



- Molecule 17: 50S ribosomal protein L21

Chain r:  71% 27% ..



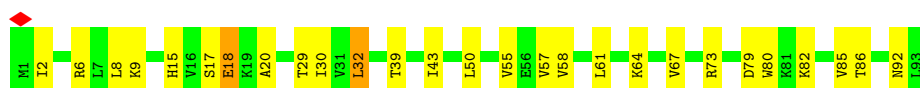
- Molecule 18: 50S ribosomal protein L22

Chain s:  75% 25%



- Molecule 19: 50S ribosomal protein L23

Chain t:  71% 27% .



- Molecule 20: 50S ribosomal protein L24

Chain u:  66% 32% .



- Molecule 21: 50S ribosomal protein L25

Chain v:  68% 30% ..



- Molecule 22: 50S ribosomal protein L27

Chain w:  73% 27%



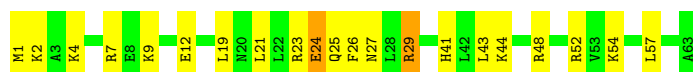
- Molecule 23: 50S ribosomal protein L28

Chain x:  68% 31% .



- Molecule 24: 50S ribosomal protein L29

Chain y:  67% 30% .



- Molecule 25: 50S ribosomal protein L30

Chain z:  78% 22%

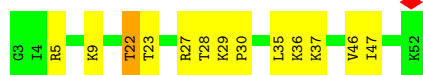
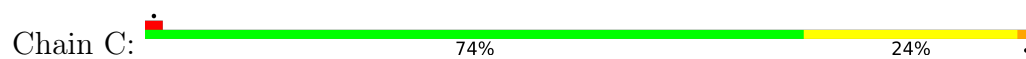


- Molecule 26: 50S ribosomal protein L32

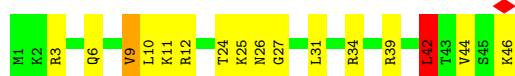
Chain B:  57% 41% .



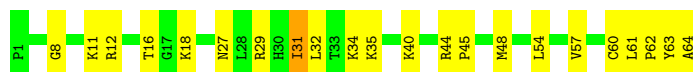
- Molecule 27: 50S ribosomal protein L33



- Molecule 28: 50S ribosomal protein L34



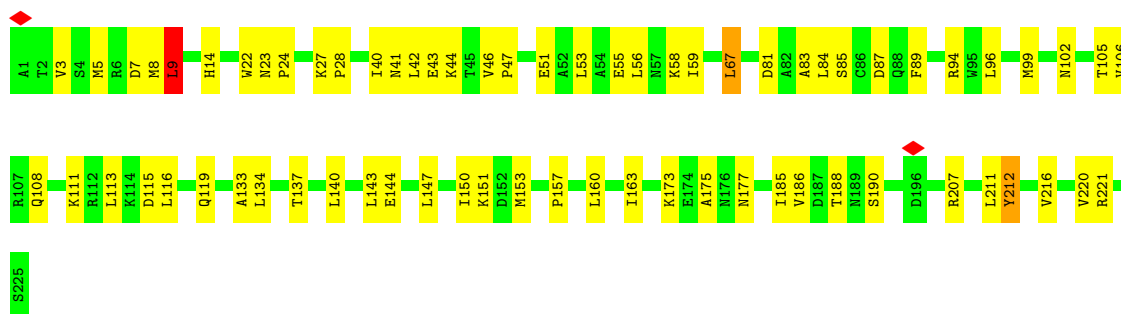
- Molecule 29: 50S ribosomal protein L35



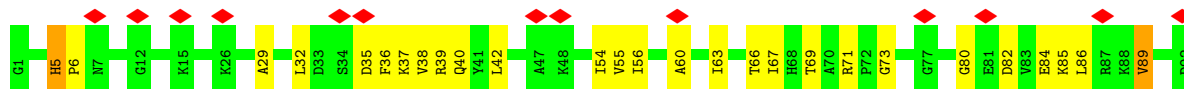
- Molecule 30: 50S ribosomal protein L36



- Molecule 31: 30S ribosomal protein S2

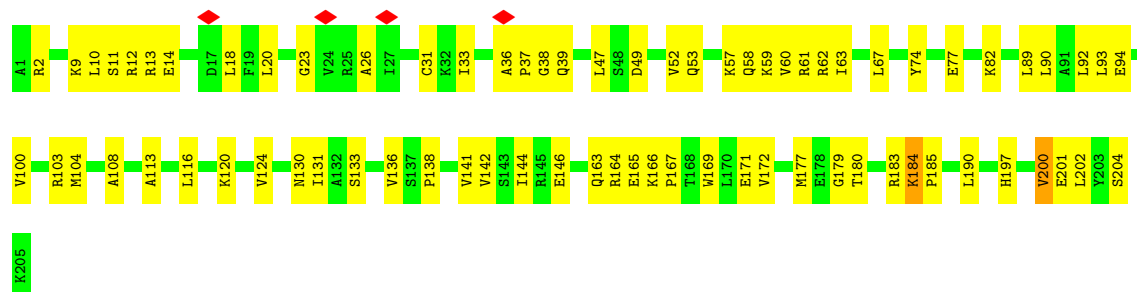


- Molecule 32: 30S ribosomal protein S3

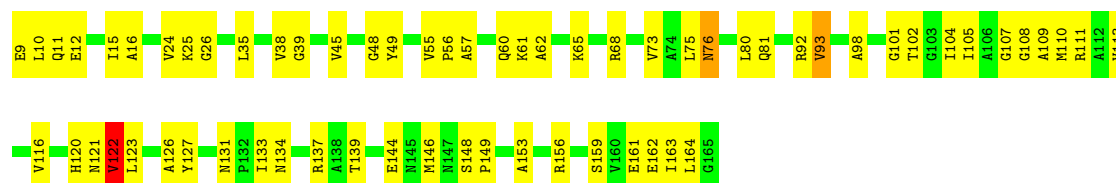




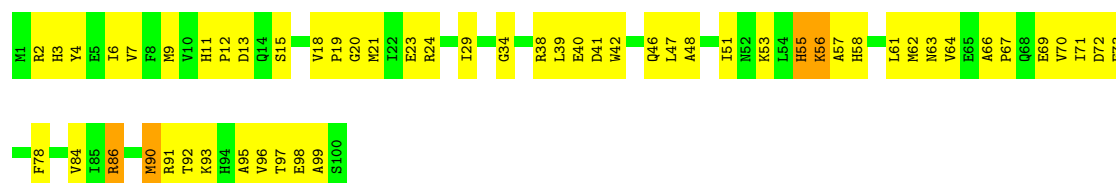
• Molecule 33: 30S ribosomal protein S4



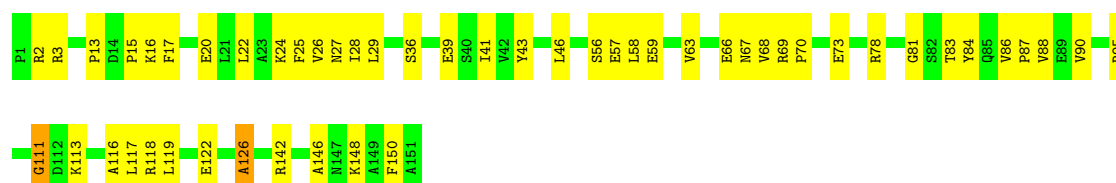
• Molecule 34: 30S ribosomal protein S5



• Molecule 35: 30S ribosomal protein S6



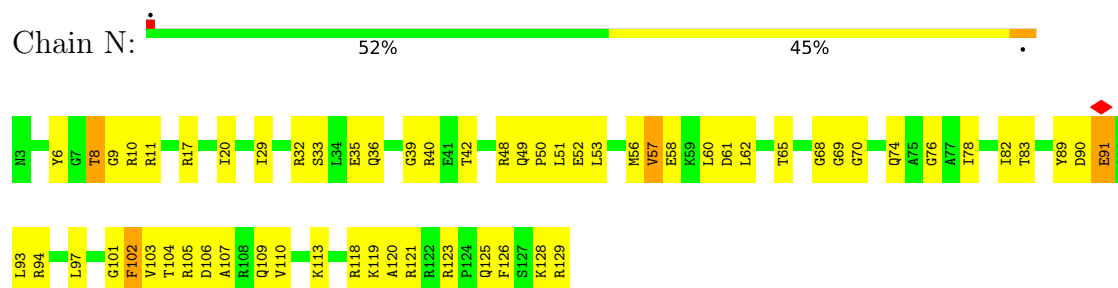
• Molecule 36: 30S ribosomal protein S7



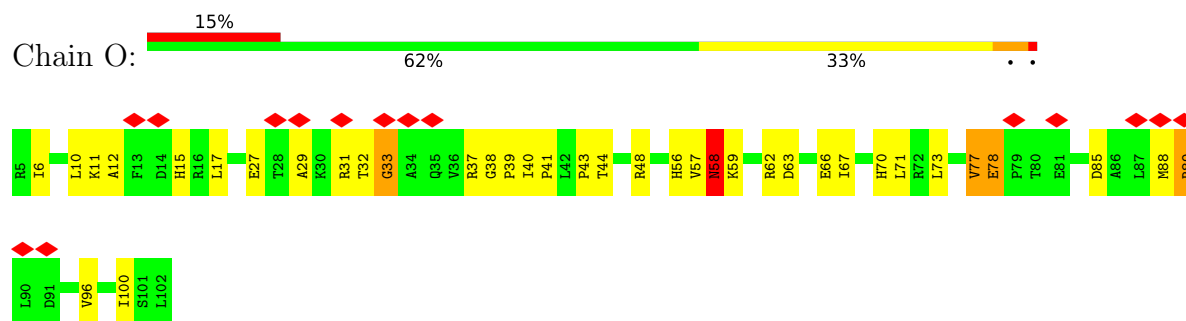
- Molecule 37: 30S ribosomal protein S8



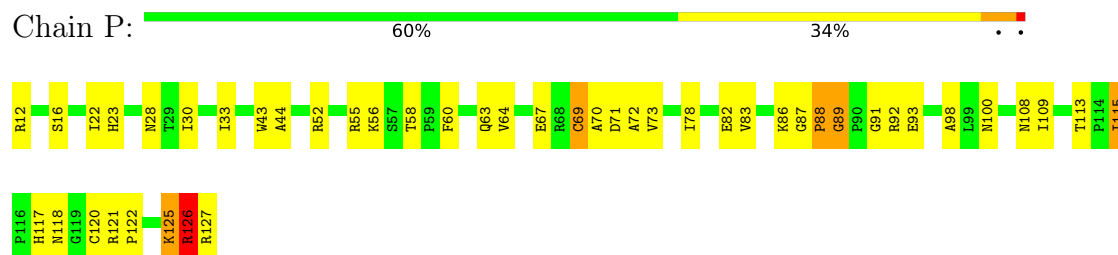
- Molecule 38: 30S ribosomal protein S9



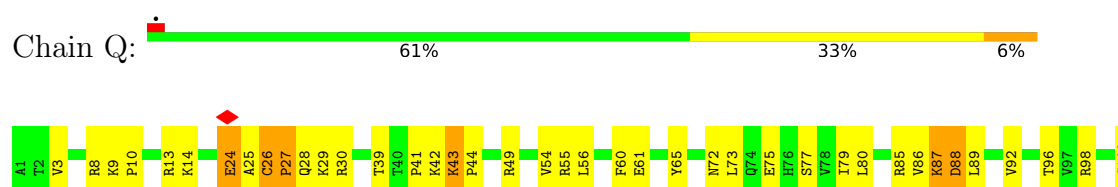
- Molecule 39: 30S ribosomal protein S10



- Molecule 40: 30S ribosomal protein S11



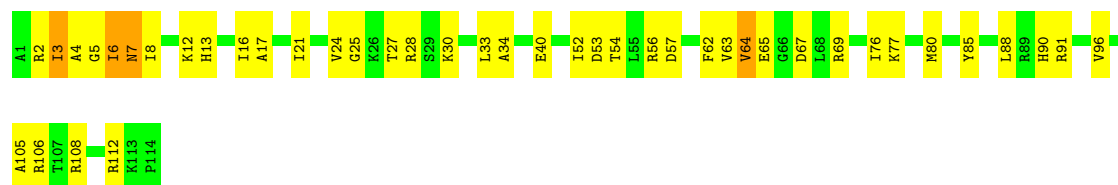
- Molecule 41: 30S ribosomal protein S12





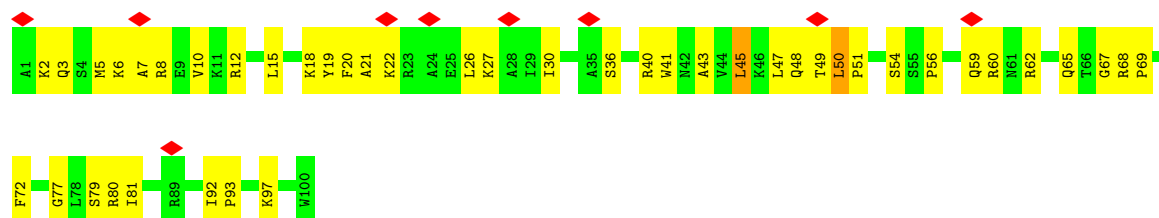
- Molecule 42: 30S ribosomal protein S13

Chain R: 62% 34%



- Molecule 43: 30S ribosomal protein S14

Chain S: 9% 56% 42%



- Molecule 44: 30S ribosomal protein S15

Chain T: 70% 30%



- Molecule 45: 30S ribosomal protein S16

Chain U: 65% 35%



- Molecule 46: 30S ribosomal protein S17

Chain V: 61% 35%



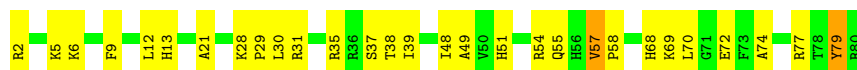
- Molecule 47: 30S ribosomal protein S18

Chain W: 57% 43%



- Molecule 48: 30S ribosomal protein S19

Chain X: 63% 34% .



- Molecule 49: 30S ribosomal protein S20

Chain Y: 72% 27% .



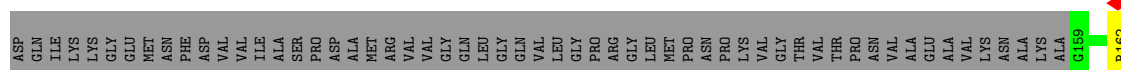
- Molecule 50: 30S ribosomal protein S21

Chain Z: 43% 45% 9% .



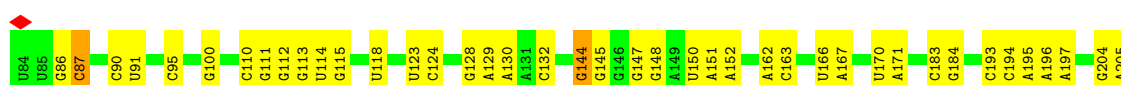
- Molecule 51: 50S ribosomal protein L1

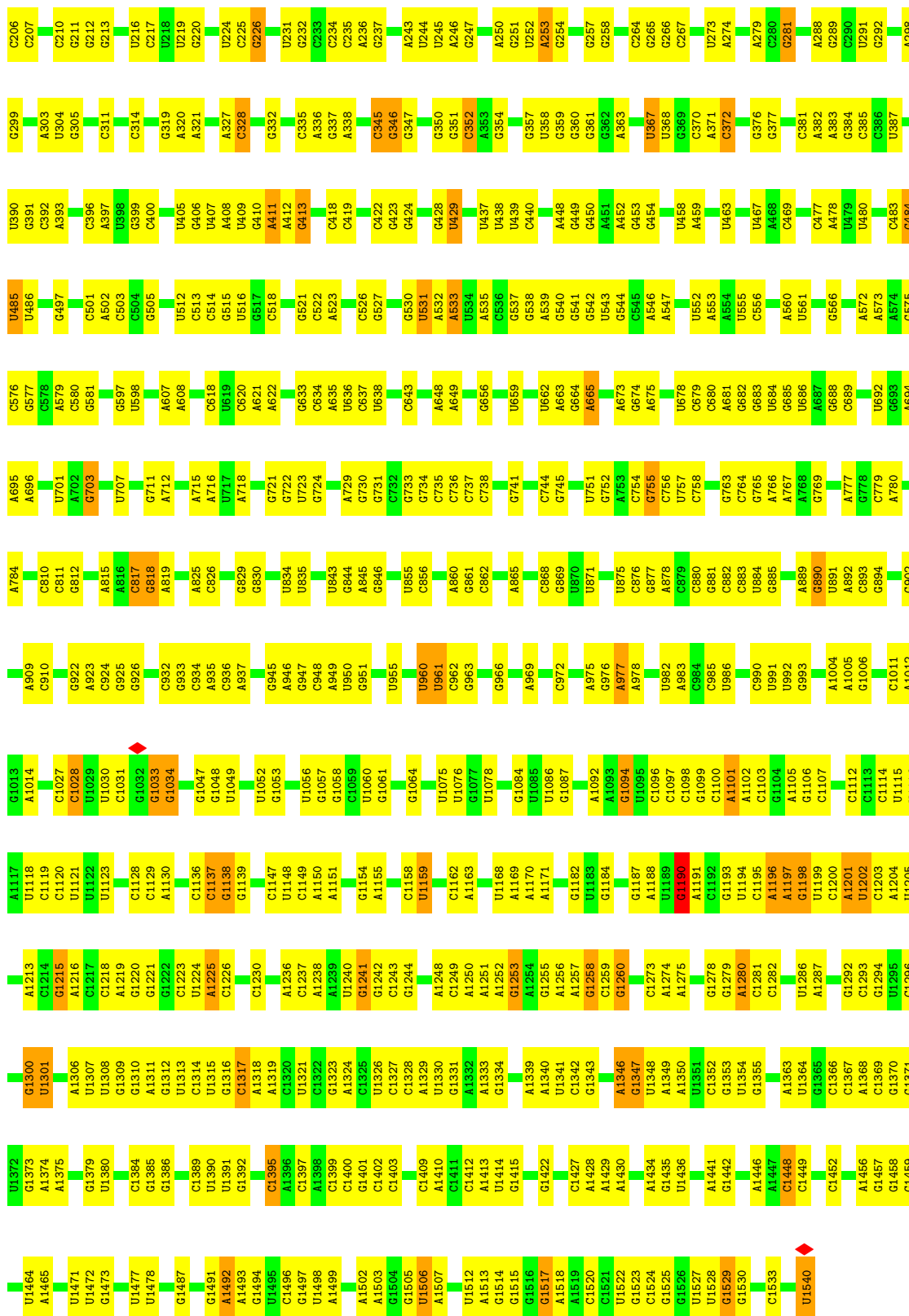
Chain a: 6% 44% 16% 40%



- Molecule 52: 16S ribosomal RNA

Chain 3: 55% 41% .





• Molecule 53: 23S ribosomal RNA

Chain 1: 56% 38% 5%

C1357	G1250	G1138	G1059	U970	C885	A782	G697	A616	G533	U441	A310	C210	U112	G1
A1358	C1251	G1139	U1060	G971	U871	A783	U703	G617	U534	G442	A311	C211	U113	A10
G1359	A1252	C1140	U1061	A972	U872	G784	U704	A621	G535	A443	A312	G214	A118	C11
G1360	U1254	A1141	G973	G974	C873	G785	A705	G622	G536	C444	G319	G215	A119	U12
G1361	U1255	A1142	G975	G976	C874	A786	G708	A627	G537	G445	A320	A216	U120	U18
A1365	G1256	G1149	U1066	G977	C875	C796	U709	G628	C542	U451	U321	A221	G121	A19
A1366	U1257	C1150	G1067	G978	C876	G797	U710	G629	G543	A457	A322	A222	U139	C20
G1367	G1258	G1151	U1068	G979	C877	G798	U711	A633	C544	G458	C323	G225	C140	A21
G1368	U1259	A1143	A1069	A979	C878	G799	U712	G634	U545	A459	A324	G226	G141	C22
A1373	C1153	C1153	G1070	C982	C879	A800	A715	C635	U546	A460	A325	A227	C142	G23
A1374	G1154	A1155	G1071	A983	A886	G801	A716	C636	U547	A461	A326	G228	C143	G24
A1375	A1269	A1156	G1072	A984	U887	A802	C717	G637	G548	G467	A327	G229	A144	U25
U1378	G1270	G1157	U1073	G989	C888	A803	A718	A638	G549	G468	C341	G230	C145	G26
U1379	A1271	C1158	G1074	A990	U889	G804	A719	G639	U554	A473	C342	A231	C146	G27
A1383	U1272	G1159	U1075	C993	C890	G805	C720	C640	G555	G474	C343	G232	C147	U34
A1384	A1273	A1160	C1076	G994	U891	C806	G721	C641	U556	A475	C344	G233	U148	G35
A1385	U1274	G1161	U1077	C995	C892	U892	A722	C642	U557	G476	C345	G234	A149	G36
A1386	A1275	G1162	C1078	A996	A899	G893	C723	C643	U558	A477	C346	G235	U150	C37
A1387	C1278	A1175	U1083	G997	U900	C894	U724	U646	U559	A478	C347	G236	C151	A38
U1394	G1279	G1176	A1084	A1001	C907	C895	G725	C650	U560	A479	C348	G237	U152	G39
U1395	A1285	U1177	U1085	G1002	C908	G896	G726	C651	U561	A480	C349	G238	U153	G43
C1398	A1286	C1178	A1086	G1007	A909	U897	A727	G652	U562	A481	C350	G239	U154	G44
G1401	U1180	G1179	G1087	C1008	A910	C898	G728	A654	C564	A482	C351	G240	A155	G45
U1402	U1181	U1180	U1088	G1009	A911	C899	G729	A655	U565	A483	C352	G241	U156	G46
U1412	C1295	G1182	A1090	A1010	C912	G900	A730	A656	U566	A484	C353	G242	C157	G47
A1413	U1296	U1183	G1091	G1011	U913	U891	C731	G657	C567	A485	C354	G243	U158	G48
G1416	C1297	U1184	C1092	U1012	A914	C892	G732	U658	U568	A486	C355	G244	U159	G49
C1417	U1185	G1186	G1093	C1013	A915	C893	G733	G659	A574	A487	C356	G245	U160	G50
A1419	C1298	U1187	U1094	A1014	A916	C894	A742	C660	U575	A488	C357	G246	U161	G51
A1420	G1299	G1188	A1098	U1015	G926	U895	A743	A661	U576	A489	C358	G247	U162	C61
A1434	U1300	G1189	U1016	G1016	G927	U896	A744	A662	U577	G495	C359	G248	U163	U62
G1435	C1306	U1190	U1017	A1019	U932	U897	G745	A663	U580	U499	C360	G249	U174	A64
C1437	G1309	U1191	C1102	A1020	C935	U898	C746	A670	C581	A502	C361	G250	G175	U65
U1438	U1203	U1200	A1103	A1021	A936	U899	G747	C671	U582	A503	C362	G251	G176	C68
A1439	U1204	U1201	C1104	G1022	C937	C900	G748	C672	U583	A504	C363	G252	G177	A71
U1440	C1319	U1202	G1105	U1023	C938	U901	A752	G673	C584	A505	C364	G253	G180	G75
G1441	C1320	A1205	G1106	G1024	G939	U902	C758	A674	U585	U405	C365	G254	A181	A74
U1442	U1206	G1206	U1107	G1025	A941	C903	G759	A675	U586	G406	C366	G255	G182	G75
C1447	A1326	U1207	G1108	U1033	C942	U904	A760	A676	U587	G411	C367	G256	G183	A78
G1448	A1327	G1212	A1111	A1039	C943	U905	A761	A677	U588	C414	C368	G257	A191	A83
G1449	U1321	A1213	G1112	A1040	C944	U906	G762	C680	U589	A415	C369	G258	C192	A84
C1451	A1336	G1214	U1113	G1041	C945	U907	A763	C681	U590	U416	C370	G259	U193	C86
C1454	G1331	U1224	G1114	G1042	G946	U908	A764	C682	C595	U417	C371	G260	G194	U102
G1450	C1332	G1225	G1115	G1043	C947	U909	C765	A685	U596	U418	C372	G261	A195	A103
A1459	U1335	U1231	U1119	C1045	C948	U910	U766	U686	U597	U419	C373	G262	A196	A104
C1461	A1336	G1232	C1123	A1046	C949	U911	U767	C687	U598	C420	C374	G263	U197	C106
A1469	G1341	U1236	U1130	G1047	C950	U912	U768	U687	C599	G424	C375	G264	C198	A107
U1470	C1342	A1287	G1131	A1054	C951	U913	G769	A688	U603	A528	C376	G265	U200	C108
	U1344	G1238	U1132	G1055	C952	U914	G770	C689	A609	A529	C377	G266	U201	G109
	C1345	U1248	A1133	G1056	C953	U915	G771	C690	C610	G530	C378	G267	C202	
	A1469	U1249	A1134	G1057	C954	U916	G772	A691	C611	C531	C379	G268	C203	
			C1135	U1058	C955	U917	G773	C692	C612	A532	C380	G269	C204	
					C956	U918	G774	A693	C613		C381	G270	C205	
					C957	U919	G775	C694	C614		C382	G271	C206	
					C958	U920	G776	A695	C615		C383	G272	C207	
					C959	U921	G777	C696	C616		C384	G273	C208	
					C960	U922	G778	C697	C617		C385	G274	C209	
					C961	U923	G779	C698	C618		C386	G275	C210	
					C962	U924	G780	C699	C619		C387	G276	C211	
					C963	U925	G781	C700	C620		C388	G277	C212	
					C964	U926	G782	C701	C621		C389	G278	C213	
					C965	U927	G783	C702	C622		C390	G279	C214	
					C966	U928	G784	C703	C623		C391	G280	C215	
					C967	U929	G785	C704	C624		C392	G281	C216	
					C968	U930	G786	C705	C625		C393	G282	C217	
					C969	U931	G787	C706	C626		C394	G283	C218	
					C970	U932	G788	C707	C627		C395	G284	C219	
					C971	U933	G789	C708	C628		C396	G285	C220	
					C972	U934	G790	C709	C629		C397	G286	C221	
					C973	U935	G791	C710	C630		C398	G287	C222	
					C974	U936	G792	C711	C631		C399	G288	C223	
					C975	U937	G793	C712	C632		C400	G289	C224	
					C976	U938	G794	C713	C633		C401	G290	C225	
					C977	U939	G795	C714	C634		C402	G291	C226	
					C978	U940	G796	C715	C635		C403	G292	C227	
					C979	U941	G797	C716	C636		C404	G293	C228	
					C980	U942	G798	C717	C637		C405	G294	C229	
					C981	U943	G799	C718	C638		C406	G295	C230	
					C982	U944	G800	C719	C639		C407	G296	C231	
					C983	U945	G801	C720	C640		C408	G297	C232	
					C984	U946	G802	C721	C641		C409	G298	C233	
					C985	U947	G803	C722	C642		C410	G299	C234	
					C986	U948	G804	C723	C643		C411	G300	C235	
					C987	U949	G805	C724	C644		C412	G301	C236	
					C988	U950	G806	C725	C645		C413	G302	C237	
					C989	U951	G807	C726	C646		C414	G303	C238	
					C990	U952	G808	C727	C647		C415	G304	C239	
					C991	U953	G809	C728	C648		C416	G305	C240	
					C992	U954	G810	C729	C649		C417	G306	C241	
					C993	U955	G811	C730	C650		C418	G307	C242	
					C994	U956	G812	C731	C651		C419	G308	C243	
					C995	U957	G813	C732	C652		C420	G309	C244	
					C996	U958	G814	C733	C653		C421	G310	C245	
					C997	U959	G815	C734	C654		C422	G311	C246	
					C998	U960	G816	C735	C655		C423	G312	C247	
					C999	U961	G817	C736	C656		C424	G313	C248	
					C1000	U962	G818	C737	C657		C425	G314	C249	
					C1001	U963	G819	C738	C658		C426	G315	C250	
					C1002	U964	G820	C739	C659		C427	G316	C251	
					C1003	U965	G821	C740	C660		C428	G317	C252	
					C1004	U966	G822	C741	C661		C429	G318	C253	
					C1005	U967	G823	C742	C662		C430	G319	C254	
					C1006	U968	G824	C743	C663		C431	G320	C255	
					C1007	U969	G825	C744	C664		C432	G321	C256	
					C1008	U970	G826	C745	C665		C433	G322	C257	
					C1009	U971	G827	C746	C666		C434	G323	C258	
					C1010	U972	G828	C747	C667		C435	G324	C259	
					C1011	U973	G829	C748	C668		C436	G325	C260	

A2820	U2724	G2623	C2527	C2442	U2285	U2180	G2087	U1991	A1900	C1806	U1709	C1592	U1474	
A2821	A2725	G2624	U2528	C2443	A2266	U2181	A2088	G1992	A1901	G1807	G1710	A1593	G1475	
G2825	U2728	G2625	G2529	G2444	A2267	U2182	C2089	U1993	G1902	A1808	G1715	U1594	U1476	
A2826	G2731	G2627	A2530	U2448	A2268	A2183	G2093	C1996	G1903	A1809	G1720	C1595	G1482	
A2829	G2732	G2628	G2532	A2449	U2272	A2184	C2096	C1997	G1904	G1811	U1720	A1603	A1490	
G2830	A2733	G2630	U2533	C2452	A2273	U2187	U2104	C1999	G1905	G1816	G1721	C1606	C1498	
G2831	G2742	G2631	U2537	U2457	G2277	U2188	U2105	G2010	G1906	G1817	U1726	C1607	C1499	
U2832	U2632	G2632	G2538	G2458	A2278	U2189	U2106	U2011	G1907	G1818	C1725	A1608	G1500	
G2834	U2743	G2633	G2539	U2459	G2279	G2190	G2107	G2012	G1908	G1819	U1729	A1609	G1501	
A2835	G2744	G2634	C2539	C2462	G2280	G2193	G2110	A2013	G1909	U1820	C1730	A1610	U1506	
U2836	G2747	G2635	U2544	C2463	G2282	U2194	G2111	A2014	G1910	G1823	U1736	C1611	C1507	
C2840	A2748	G2636	G2547	C2467	C2283	U2195	G2112	A2015	G1911	G1824	U1737	A1614	C1508	
C2841	U2749	G2637	A2548	U2468	G2286	U2196	G2113	A2020	G1912	G1825	G1738	C1615	A1509	
G2842	A2750	G2641	G2549	G2469	A2287	U2197	U2114	G2021	G1913	U1827	U1747	A1616	G1510	
U2845	G2751	C2646	G2550	G2470	A2288	A2199	G2115	U2022	G1914	G1828	A1739	C1625	G1524	
U2846	C2755	U2647	G2557	G2475	A2289	C2200	G2116	C2023	G1915	G1829	A1746	C1626	A1515	
G2848	U2756	G2653	G2563	A2476	U2292	U2203	G2117	G2029	G1916	G1830	U1747	A1627	G1528	
A2849	A2757	U2554	U2554	G2476	G2293	G2204	U2118	A2030	G1917	G1831	C1748	G1628	G1529	
U2850	G2758	C2651	G2556	C2480	U2296	U2205	U2119	A2031	G1918	G1832	U1629	A1630	A1524	
C2853	G2759	G2652	C2557	G2481	A2297	G2206	G2120	G2032	G1919	G1833	U1758	A1637	A1528	
G2854	C2762	U2656	G2567	A2482	A2298	U2207	U2122	C2036	G1920	G1834	A1759	C1637	G1529	
U2855	G2763	A2657	U2561	C2483	U2302	U2210	G2123	U2039	G1921	G1837	C1760	A1535	A1535	
G2859	U2764	G2658	U2562	G2484	G2303	A2211	A2126	A2040	G1922	U1851	C1761	C1536	C1536	
A2860	A2765	G2659	G2563	G2485	G2304	U2212	G2127	G2041	G1923	G1856	G1763	C1537	G1537	
U2861	G2766	A2660	G2566	G2486	U2305	U2213	G2128	U2042	G1924	U1857	C1764	G1642	G1538	
G2862	C2772	G2661	G2567	G2487	U2306	U2220	C2129	C2043	G1925	G1858	U1765	G1645	G1539	
C2863	C2773	U2662	U2568	G2488	A2309	G2221	G2132	C2045	G1926	G1859	G1766	C1646	U1540	
G2864	G2774	A2663	A2572	U2489	U2312	G2222	G2133	C2046	G1927	G1860	A1773	U1647	A1549	
U2867	G2775	G2664	G2573	G2490	C2313	A2225	U2139	U2055	G1928	G1861	C1774	U1648	C1550	
A2868	U2776	G2674	G2574	U2491	G2318	G2226	G2140	C2056	G1929	G1866	U1775	G1649	A1551	
G2869	A2778	C2678	U2580	C2498	U2319	U2230	U2147	U2060	G1930	G1867	G1776	A1650	A1554	
C2870	U2779	A2679	G2581	C2499	G2321	U2231	G2141	C2056	G1931	U1871	U1779	C1658	G1554	
A2872	G2784	U2680	U2584	G2502	G2322	U2232	U2151	A2061	G1932	A1872	A1781	U1662	U1559	
U2873	C2785	G2681	U2585	A2503	A2326	G2233	G2156	A2062	G1933	C1873	U1784	G1663	G1560	
A2874	U2786	C2682	G2586	G2504	U2329	A2241	G2157	C2063	G1934	G1874	A1785	A1664	U1563	
C2875	G2787	G2683	U2588	G2505	G2330	G2242	G2157	C2064	G1935	A1876	C1786	C1665	C1564	
U2876	U2788	C2684	G2589	G2506	G2331	U2243	G2157	C2065	G1936	G1877	A1787	G1666	C1565	
G2877	A2789	U2685	A2590	G2507	C2332	U2244	G2157	C2066	G1937	G1878	C1788	A1566	A1566	
C2878	U2790	G2686	G2591	G2508	C2333	U2245	G2157	C2067	G1938	G1879	A1789	A1669	A1569	
U2879	G2791	A2687	U2592	G2509	U2334	U2246	A2163	U2068	A1970	C1880	C1790	C1670	A1570	
G2880	C2792	U2688	A2593	G2510	A2335	U2247	U2166	G2069	U1971	C1881	A1791	G1674	A1571	
U2881	U2793	G2689	G2594	G2511	U2336	C2248	G2166	A2070	G1972	U1882	C1795	C1685	A1572	
C2882	G2794	U2690	U2595	G2512	A2337	U2249	A2170	A2071	A1977	U1883	U1796	C1686	G1581	
G2883	U2795	G2691	G2596	A2513	U2338	U2250	G2171	C2072	A1978	G1884	G1797	C1687	U1584	
U2884	U2796	A2700	U2605	G2514	C2339	U2251	A2172	C2073	U1979	A1885	U1798	G1697	C1585	
C2885	G2797	G2701	C2606	G2515	A2340	U2252	G2173	U2074	G1980	A1890	G1799	C1704	A1586	
G2886	U2798	U2702	G2607	G2516	C2341	U2253	A2173	U2075	U1981	G1891	C1800	A1587	G1587	
C2887	A2799	G2703	U2608	G2517	C2342	U2254	A2174	A2080	U1982	A1899	A1801	A1705		
U2888	U2800	G2704	G2609	G2518	C2343	U2255	A2175	A2081						
A2889	G2801	U2705	U2610	G2519	C2344	U2256	A2176	U2086						
G2890	U2802	A2706	G2611	G2520	U2345	U2257	A2177							
U2891	C2803	G2707	C2612	G2521	U2346	U2258	A2178							
C2892	U2804	U2708	G2613	U2522	C2347	U2259	A2179							
G2893	A2805	G2709	G2614	G2523	C2348	U2260	A2180							
U2894	U2806	U2710	U2615	U2524	U2349	U2261	A2181							
C2895	G2807	A2711	G2616	G2525	U2350	U2262	A2182							
G2896	U2808	G2712	C2617	U2526	U2351	U2263	A2183							
A2897	C2809	U2713	U2618	G2527	U2352	U2264	A2184							
U2898	U2810	G2714	G2619	G2528	U2353	U2265	A2185							
C2899	A2811	U2715	U2619	U2529	U2354	U2266	A2186							
G2900	G2812	A2716	G2620	G2530	U2355	U2267	A2187							
U2901	U2813	U2717	C2621	U2531	U2356	U2268	A2188							
C2902	A2814	G2718	U2622	G2532	U2357	U2269	A2189							
G2903	U2815	U2719	G2623	U2533	U2358	U2270	A2190							
U2904	C2816	A2720	U2624	G2534	U2359	U2271	A2191							
C2905	U2817	U2721	G2625	U2535	U2360	U2272	A2192							
G2906	A2818	G2722	C2626	G2536	U2361	U2273	A2193							
U2907	U2819	U2723	U2627	U2537	U2362	U2274	A2194							
C2908	G2820	A2724	G2628	U2538	U2363	U2275	A2195							
G2909	U2821	U2725	G2629	G2539	U2364	U2276	A2196							
U2910	C2822	G2726	U2630	U2540	U2365	U2277	A2197							
C2911	A2823	U2727	G2631	G2541	U2366	U2278	A2198							
G2912	U2824	A2728	G2632	U2542	U2367	U2279	A2199							
U2913	G2825	U2729	U2633	G2543	U2368	U2280	A2200							
C2914	A2826	G2730	G2634	U2544	U2369	U2281	A2201							
G2915	U2827	U2731	G2635	G2545	U2370	U2282	A2202							
U2916	C2828	A2732	U2636	U2546	U2371	U2283	A2203							
C2917	G2829	U2733	G2637	G2547	U2372	U2284	A2204							
G2918	U2830	G2734	U2638	U2548	U2373	U2285	A2205							
U2919	A2831	A2735	G2639	G2549	U2374	U2286	A2206							
C2920	G2832	U2736	U2639	U2550	U2375	U2287	A2207							
G2921	U2833	G2737	G2640	G2551	U2376	U2288	A2208							
U2922	A2834	A2738	U2641	U2552	U2377	U2289	A2209							
C2923	G2835	U2739	G2642	G2553	U2378	U2290	A2210							
G2924	U2836	G2740	U2643	U2554	U2379	U2291	A2211							
U2925	A2837	A2741	G2644	G2555	U2380	U2292	A2212							
C2926	G2838	U2742	U2645	U2556	U2381	U2293	A2213							
G2927	U2839	G2743	G2646	G2557	U2382	U2294	A2214							
U2928	A2840	A2744	U2647	U2558	U2383	U2295	A2215							
C2929	G2841	U2745	G2648	G2559	U2384	U2296	A2216							
G2930	U2842	G2746	U2649	U2560	U2385	U2297	A2217							
U2931	A2843	A2747	G2650	G2561	U2386	U2298	A2218							
C2932	G2844	U2748	U2651	U2562	U2387	U2299	A2219							
G2933	U2845	G2749	G2652	G2563	U2388	U2300	A2220							
U2934	A2846	A2750	U2653	U2564	U2389	U2301	A2221							
C2935	G2847	U2751	G2654	G2565	U2390	U2302	A2222							
G2936	U2848	G2752	U2655	U2566	U2391	U2303	A2223							
U2937	A2849	A2753	G2656	G2567	U2392	U2304	A2224							
C2938	G2850	U2754	U2657	U2568	U2393	U2305	A2225							
G2939	U2851	G2755	G2658	G2569	U2394	U2306	A2226							
U2940	A2852	A2756	U2659	U2570	U2395	U2307	A2227							
C2941	G2853	U2757	G2659	G2571	U2396	U2308	A2228							
G2942														

- Molecule 54: 5S ribosomal RNA

Chain 2: 



- Molecule 55: tRNA^{fMet}

Chain 5: 



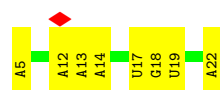
- Molecule 55: tRNA^{fMet}

Chain 6: 



- Molecule 56: mRNA

Chain 4: 



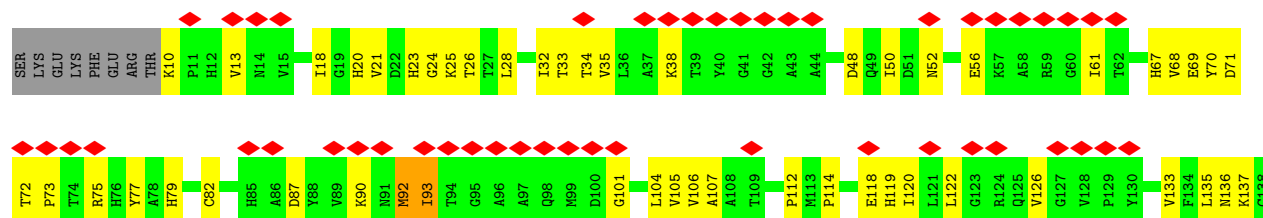
- Molecule 57: tRNA^{Phe}

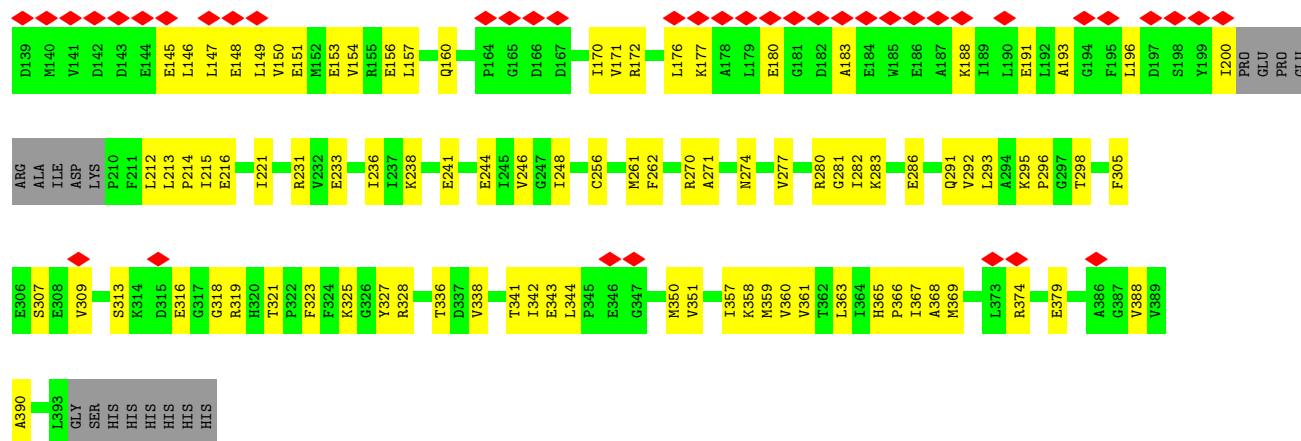
Chain 7: 



- Molecule 58: Elongation factor Tu

Chain 8: 





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	7840	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	18.517	Depositor
Minimum map value	-9.717	Depositor
Average map value	0.113	Depositor
Map value standard deviation	0.863	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	b	0.29	0/2122	0.96	8/2852 (0.3%)
2	c	0.29	0/1586	0.86	1/2134 (0.0%)
3	d	0.28	0/1571	0.87	6/2113 (0.3%)
4	e	0.31	0/1435	0.89	5/1926 (0.3%)
5	f	0.30	0/1343	0.87	4/1816 (0.2%)
6	g	0.31	0/1122	0.94	5/1515 (0.3%)
7	h	0.33	0/1002	1.01	10/1350 (0.7%)
8	i	0.36	0/1046	0.99	6/1410 (0.4%)
9	j	0.30	0/1152	0.94	4/1551 (0.3%)
10	k	0.28	0/948	0.89	3/1268 (0.2%)
11	l	0.30	0/1054	0.98	5/1403 (0.4%)
12	m	0.29	0/1093	0.88	3/1460 (0.2%)
13	n	0.29	0/974	0.96	6/1301 (0.5%)
14	o	0.28	0/902	0.86	2/1209 (0.2%)
15	p	0.29	0/929	0.82	1/1242 (0.1%)
16	q	0.28	0/960	0.97	4/1278 (0.3%)
17	r	0.29	0/829	0.93	3/1107 (0.3%)
18	s	0.29	0/864	0.92	1/1156 (0.1%)
19	t	0.27	0/745	0.88	2/994 (0.2%)
20	u	0.29	0/788	0.88	2/1051 (0.2%)
21	v	0.28	0/766	0.90	2/1025 (0.2%)
22	w	0.29	0/582	0.90	4/769 (0.5%)
23	x	0.28	0/635	0.90	1/848 (0.1%)
24	y	0.28	0/510	0.94	2/677 (0.3%)
25	z	0.30	0/453	0.81	0/605
26	B	0.27	0/450	0.85	1/599 (0.2%)
27	C	0.31	0/417	0.89	2/554 (0.4%)
28	D	0.33	0/380	0.92	0/498
29	E	0.30	0/513	0.94	1/676 (0.1%)
30	F	0.31	0/303	0.88	0/397
31	G	0.29	0/1788	0.90	4/2408 (0.2%)
32	H	0.33	0/1652	0.93	7/2225 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.29	0/1665	0.94	10/2227 (0.4%)
34	J	0.35	0/1170	0.97	5/1573 (0.3%)
35	K	0.32	0/836	0.87	2/1128 (0.2%)
36	L	0.29	0/1196	0.92	4/1602 (0.2%)
37	M	0.29	0/989	0.88	2/1326 (0.2%)
38	N	0.31	0/1034	0.91	0/1375
39	O	0.35	0/797	0.92	3/1077 (0.3%)
40	P	0.30	0/886	0.96	5/1195 (0.4%)
41	Q	0.32	0/969	1.07	10/1300 (0.8%)
42	R	0.30	0/893	0.90	1/1193 (0.1%)
43	S	0.30	0/817	0.93	3/1088 (0.3%)
44	T	0.28	0/722	0.86	2/964 (0.2%)
45	U	0.31	0/659	0.84	0/884
46	V	0.29	0/658	0.92	3/881 (0.3%)
47	W	0.31	0/545	0.94	2/731 (0.3%)
48	X	0.32	0/653	0.94	3/877 (0.3%)
49	Y	0.28	0/671	0.93	1/888 (0.1%)
50	Z	0.33	0/551	1.08	6/728 (0.8%)
51	a	0.31	0/1034	0.80	0/1387
52	3	0.41	0/36963	0.47	3/57662 (0.0%)
53	1	0.40	0/69796	0.48	5/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.40	0/1832	0.45	0/2855
55	6	0.41	0/1832	0.46	0/2855
56	4	0.40	0/436	0.47	0/679
57	7	0.40	0/1809	0.48	0/2819
58	8	0.31	0/2937	0.89	6/3975 (0.2%)
All	All	0.37	0/166136	0.63	181/248053 (0.1%)

There are no bond length outliers.

All (181) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R	3	ILE	N-CA-C	9.16	122.18	109.45
17	r	50	GLY	N-CA-C	-8.87	101.76	112.49
44	T	43	ALA	N-CA-C	-8.80	101.61	111.82
33	I	200	VAL	N-CA-C	8.71	119.51	110.36
9	j	120	ARG	N-CA-C	-8.39	102.48	112.89
3	d	110	SER	N-CA-C	-7.96	103.02	112.89
34	J	120	HIS	N-CA-C	-7.95	100.67	110.61
36	L	126	ALA	N-CA-C	-7.94	103.72	113.41
41	Q	114	SER	N-CA-C	-7.78	102.88	111.36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	q	49	ARG	N-CA-C	-7.74	103.83	113.28
23	x	6	VAL	N-CA-C	7.71	117.78	110.30
4	e	137	PHE	CA-C-N	7.67	128.37	119.47
4	e	137	PHE	C-N-CA	7.67	128.37	119.47
50	Z	17	ARG	N-CA-C	-7.65	103.97	113.38
1	b	213	ARG	N-CA-C	-7.64	101.83	112.45
48	X	57	VAL	N-CA-C	7.63	115.19	108.63
32	H	5	HIS	CA-C-N	7.57	129.30	119.84
32	H	5	HIS	C-N-CA	7.57	129.30	119.84
11	l	95	LEU	N-CA-C	-7.45	102.85	112.23
18	s	20	VAL	N-CA-C	-7.43	105.88	111.90
41	Q	54	VAL	N-CA-C	7.41	118.96	108.36
32	H	129	PHE	N-CA-C	7.29	118.87	111.07
9	j	7	LYS	CA-C-N	7.21	128.86	119.84
9	j	7	LYS	C-N-CA	7.21	128.86	119.84
11	l	59	ARG	N-CA-C	-7.13	105.76	114.75
29	E	63	TYR	N-CA-C	7.12	119.94	111.33
5	f	47	ASN	N-CA-C	-7.09	104.78	113.50
27	C	27	ARG	N-CA-C	6.98	119.49	111.11
17	r	36	ALA	N-CA-C	-6.90	103.97	112.88
22	w	40	LYS	N-CA-C	-6.86	104.78	113.01
7	h	117	LEU	N-CA-C	6.86	120.33	109.50
12	m	110	GLU	N-CA-C	6.85	119.33	111.11
39	O	77	VAL	N-CA-C	6.77	119.51	111.05
3	d	115	GLN	N-CA-C	-6.73	104.69	113.17
46	V	75	VAL	N-CA-C	-6.68	105.20	111.48
20	u	96	LYS	N-CA-C	-6.67	100.59	110.46
49	Y	84	LYS	N-CA-C	-6.66	104.10	111.36
35	K	56	LYS	N-CA-C	6.55	118.58	110.91
21	v	21	ARG	N-CA-C	-6.55	104.55	112.54
37	M	67	GLY	N-CA-C	-6.53	107.21	115.31
13	n	68	ALA	N-CA-C	-6.52	104.18	111.28
43	S	49	THR	N-CA-C	-6.50	104.28	111.82
31	G	212	TYR	N-CA-C	-6.47	103.74	111.69
53	l	1130	U	C2'-C3'-O3'	6.43	119.15	109.50
47	W	51	GLN	N-CA-C	-6.39	104.39	111.36
33	I	163	GLN	N-CA-C	-6.38	103.94	112.94
7	h	43	LYS	N-CA-C	-6.37	104.43	111.82
48	X	9	PHE	N-CA-C	6.35	119.44	110.23
1	b	12	ARG	N-CA-C	-6.33	104.81	113.30
32	H	107	LYS	CA-C-N	6.33	126.54	119.32
32	H	107	LYS	C-N-CA	6.33	126.54	119.32

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	I	146	GLU	N-CA-C	6.29	118.14	111.28
16	q	85	ALA	N-CA-C	-6.24	105.31	113.17
58	8	92	MET	N-CA-C	6.23	118.15	111.36
22	w	52	ASP	N-CA-C	-6.22	104.86	112.88
8	i	21	PRO	N-CA-C	6.21	118.28	110.70
7	h	106	PHE	N-CA-C	6.19	118.16	110.91
13	n	79	LEU	N-CA-C	-6.19	100.83	110.42
14	o	59	ALA	N-CA-C	6.17	117.68	111.07
13	n	119	SER	N-CA-C	-6.16	104.93	112.88
7	h	44	ALA	N-CA-C	-6.14	104.49	112.23
43	S	45	LEU	N-CA-C	-6.14	105.70	113.43
33	I	184	LYS	CA-C-N	6.13	126.10	119.78
33	I	184	LYS	C-N-CA	6.13	126.10	119.78
7	h	30	SER	N-CA-C	-6.13	105.75	113.72
40	P	126	ARG	N-CA-C	6.10	123.80	110.80
10	k	32	TYR	N-CA-C	6.10	119.77	109.76
44	T	67	ASP	N-CA-C	-6.09	104.72	111.36
40	P	125	LYS	N-CA-C	6.07	123.73	110.80
6	g	44	ILE	N-CA-C	-6.03	104.63	110.72
24	y	27	ASN	N-CA-C	6.02	117.54	110.97
35	K	90	MET	N-CA-C	5.98	116.33	108.07
1	b	30	ALA	N-CA-C	5.98	121.66	113.77
41	Q	26	CYS	CA-C-N	5.98	127.31	119.84
41	Q	26	CYS	C-N-CA	5.98	127.31	119.84
20	u	5	ARG	N-CA-C	5.97	118.28	109.69
6	g	3	VAL	N-CA-C	5.94	117.08	109.30
4	e	6	TYR	N-CA-C	-5.90	104.93	111.36
50	Z	55	HIS	N-CA-C	-5.89	104.45	111.69
19	t	92	ASN	N-CA-C	-5.89	107.91	114.62
33	I	166	LYS	CA-C-N	5.88	127.19	119.84
33	I	166	LYS	C-N-CA	5.88	127.19	119.84
40	P	69	CYS	N-CA-C	-5.86	105.96	113.23
50	Z	8	ASN	N-CA-C	5.79	123.12	110.80
4	e	10	GLU	N-CA-C	5.78	117.44	111.03
1	b	164	VAL	N-CA-C	5.74	116.39	110.82
11	l	19	LEU	N-CA-C	5.74	118.57	109.96
8	i	127	SER	N-CA-C	-5.72	105.18	111.82
52	3	1190	G	C2'-C3'-O3'	5.71	118.06	109.50
13	n	67	PHE	N-CA-C	-5.71	106.86	113.88
7	h	100	ALA	N-CA-C	-5.69	105.22	111.82
19	t	18	GLU	N-CA-C	-5.69	105.15	111.36
13	n	78	LYS	N-CA-C	-5.69	106.17	113.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	8	191	GLU	N-CA-C	-5.66	105.09	112.23
37	M	118	ALA	N-CA-C	-5.66	105.88	112.89
5	f	44	HIS	N-CA-C	-5.66	104.54	112.12
47	W	17	VAL	N-CA-C	5.64	121.08	109.34
58	8	93	ILE	N-CA-C	5.64	115.83	110.53
40	P	100	ASN	N-CA-C	-5.63	106.24	113.23
43	S	50	LEU	N-CA-C	-5.63	102.94	109.93
16	q	70	GLN	N-CA-C	-5.60	106.29	113.01
13	n	65	LEU	N-CA-C	-5.57	106.32	113.23
3	d	176	ASP	CA-C-N	5.56	125.66	119.32
3	d	176	ASP	C-N-CA	5.56	125.66	119.32
53	1	1020	A	C2'-C3'-O3'	5.55	117.83	109.50
32	H	89	VAL	N-CA-C	5.53	116.26	110.62
7	h	50	VAL	N-CA-C	5.52	117.01	111.00
21	v	22	ALA	N-CA-C	-5.51	106.56	113.28
17	r	43	ASN	N-CA-C	-5.50	104.75	112.12
39	O	78	GLU	N-CA-C	5.46	117.07	108.55
3	d	73	ILE	N-CA-C	-5.46	104.92	112.50
10	k	17	ARG	N-CA-C	-5.45	108.40	114.62
7	h	96	PHE	N-CA-C	-5.45	105.42	111.36
7	h	75	ALA	N-CA-C	5.44	117.21	111.28
46	V	81	ALA	N-CA-C	5.44	117.35	110.33
33	I	204	SER	N-CA-C	-5.43	105.52	111.82
50	Z	42	THR	N-CA-C	5.43	117.01	111.14
41	Q	115	LYS	N-CA-C	-5.43	102.48	110.52
40	P	70	ALA	N-CA-C	-5.42	105.93	112.54
34	J	144	GLU	N-CA-C	-5.40	105.42	112.23
52	3	1300	G	N9-C1'-C2'	5.40	120.10	112.00
41	Q	96	THR	N-CA-C	-5.39	101.20	109.76
41	Q	43	LYS	N-CA-C	5.38	121.70	109.81
31	G	85	SER	N-CA-C	-5.38	105.45	112.23
36	L	84	TYR	N-CA-C	5.37	118.07	110.50
39	O	58	ASN	N-CA-C	-5.36	99.39	110.80
1	b	225	ASN	CA-C-N	5.35	126.53	119.84
1	b	225	ASN	C-N-CA	5.35	126.53	119.84
36	L	90	VAL	N-CA-C	5.33	116.89	109.80
16	q	88	GLU	N-CA-C	5.33	118.59	112.57
12	m	59	ARG	N-CA-C	5.32	122.14	110.80
12	m	82	MET	N-CA-C	5.31	117.18	110.33
34	J	101	GLY	N-CA-C	-5.31	107.01	115.66
33	I	31	CYS	N-CA-C	-5.27	106.36	114.16
6	g	67	ALA	N-CA-C	-5.26	105.72	111.82

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	l	92	LEU	N-CA-C	-5.24	105.74	111.82
2	c	152	PRO	N-CA-C	-5.24	106.39	113.40
5	f	163	TYR	N-CA-C	-5.23	102.01	110.32
41	Q	88	ASP	N-CA-C	-5.22	108.17	114.75
50	Z	54	ARG	N-CA-C	-5.20	106.44	112.89
27	C	30	PRO	N-CA-C	-5.20	109.27	114.68
32	H	112	ALA	N-CA-C	5.20	117.69	111.71
53	1	669	G	N9-C1'-C2'	5.20	119.79	112.00
58	8	183	ALA	N-CA-C	5.19	118.39	111.75
11	l	137	ALA	N-CA-C	-5.19	105.69	112.23
24	y	29	ARG	N-CA-C	-5.19	105.71	111.36
8	i	91	LYS	CA-C-N	5.19	126.32	119.84
8	i	91	LYS	C-N-CA	5.19	126.32	119.84
46	V	15	LYS	N-CA-C	5.18	118.01	108.58
6	g	120	GLY	N-CA-C	5.17	120.52	111.78
1	b	207	ALA	N-CA-C	-5.16	105.73	112.23
26	B	53	VAL	N-CA-C	5.14	117.52	111.09
58	8	28	LEU	N-CA-C	-5.14	105.75	112.23
31	G	9	LEU	N-CA-C	-5.14	106.52	112.89
34	J	76	ASN	N-CA-C	5.13	117.30	107.75
34	J	122	VAL	N-CA-C	5.13	120.02	109.34
8	i	73	PRO	CA-C-N	5.13	125.13	119.90
8	i	73	PRO	C-N-CA	5.13	125.13	119.90
48	X	79	TYR	N-CA-C	5.12	116.93	108.13
1	b	245	THR	N-CA-C	-5.10	103.53	110.36
50	Z	21	SER	N-CA-C	-5.09	106.92	113.23
58	8	292	VAL	N-CA-C	5.09	115.98	108.45
10	k	117	SER	N-CA-C	-5.08	105.83	112.23
9	j	40	HIS	N-CA-C	-5.07	105.88	113.89
7	h	77	VAL	N-CA-C	-5.07	106.50	111.77
33	I	11	SER	N-CA-C	-5.07	105.85	112.23
22	w	69	GLY	CA-C-N	5.06	124.37	118.85
22	w	69	GLY	C-N-CA	5.06	124.37	118.85
3	d	62	GLN	N-CA-C	-5.06	106.28	112.90
53	1	1818	U	N1-C1'-C2'	5.06	119.59	112.00
5	f	141	GLY	N-CA-C	-5.06	106.30	112.77
41	Q	9	LYS	CA-C-N	5.05	126.15	119.84
41	Q	9	LYS	C-N-CA	5.05	126.15	119.84
15	p	7	LEU	N-CA-C	-5.05	106.95	113.01
31	G	7	ASP	N-CA-C	-5.05	105.87	112.23
52	3	1301	U	N1-C1'-C2'	5.05	119.57	112.00
6	g	10	ALA	N-CA-C	5.03	117.28	108.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	o	12	THR	N-CA-C	5.02	118.18	111.75
53	l	372	G	N9-C1'-C2'	5.02	119.53	112.00
36	L	29	LEU	N-CA-C	-5.02	105.52	111.69
4	e	11	VAL	N-CA-C	5.01	115.73	110.62

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	59	0
2	c	1565	0	1616	44	0
3	d	1552	0	1619	47	0
4	e	1411	0	1447	46	0
5	f	1323	0	1374	36	0
6	g	1111	0	1148	39	0
7	h	989	0	1025	55	0
8	i	1032	0	1088	56	0
9	j	1129	0	1162	28	0
10	k	939	0	1012	39	0
11	l	1045	0	1117	34	0
12	m	1074	0	1157	36	0
13	n	961	0	1000	39	0
14	o	892	0	923	25	0
15	p	917	0	965	36	0
16	q	947	0	1022	32	0
17	r	816	0	839	28	0
18	s	857	0	922	19	0
19	t	739	0	807	28	0
20	u	780	0	834	27	0
21	v	753	0	780	22	0
22	w	575	0	592	17	0
23	x	625	0	655	20	0
24	y	509	0	543	19	0
25	z	449	0	491	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	B	444	0	461	24	0
27	C	410	0	440	8	0
28	D	377	0	418	15	0
29	E	504	0	574	17	0
30	F	302	0	343	13	0
31	G	1757	0	1787	53	0
32	H	1625	0	1699	49	0
33	I	1643	0	1710	56	0
34	J	1157	0	1199	49	0
35	K	818	0	808	45	0
36	L	1182	0	1240	38	0
37	M	979	0	1034	40	0
38	N	1022	0	1070	52	0
39	O	787	0	828	33	0
40	P	870	0	878	35	0
41	Q	955	0	1019	30	0
42	R	884	0	944	37	0
43	S	805	0	847	45	0
44	T	714	0	737	18	0
45	U	649	0	666	24	0
46	V	649	0	691	30	0
47	W	536	0	552	18	0
48	X	638	0	665	26	0
49	Y	665	0	714	22	0
50	Z	545	0	579	39	0
51	a	1027	0	1092	21	0
52	3	33012	0	16618	599	0
53	1	62317	0	31346	936	0
54	2	2568	0	1303	51	0
55	5	1640	0	836	17	0
55	6	1640	0	837	20	0
56	4	388	0	196	6	0
57	7	1619	0	821	31	0
58	8	2885	0	2900	99	0
59	5	10	0	10	1	0
60	7	11	0	8	2	0
61	8	28	0	12	2	0
All	All	153135	0	104177	2993	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (2993) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1906:G:H2'	53:1:1907:G:H5''	1.39	1.05
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.36	1.05
34:J:107:GLY:HA3	52:3:9:G:H5'	1.39	1.03
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.21	1.03
52:3:1197:A:H2'	52:3:1198:G:H5''	1.41	0.99
53:1:45:G:H5''	53:1:46:G:H5'	1.43	0.98
53:1:2277:G:H2'	53:1:2278:A:H5''	1.46	0.96
53:1:1053:C:H2'	53:1:1054:A:H5''	1.46	0.95
43:S:2:LYS:NZ	52:3:983:A:H5'	1.82	0.93
52:3:1259:C:H3'	52:3:1260:G:H5''	1.48	0.93
52:3:405:U:H3'	52:3:406:G:H5'	1.47	0.93
53:1:1645:G:H5''	53:1:1646:C:H5'	1.51	0.92
48:X:35:ARG:HH21	48:X:74:ALA:HB3	1.33	0.92
43:S:81:ILE:HG21	52:3:1202:U:H3	1.35	0.91
38:N:20:ILE:HD11	38:N:60:LEU:HD22	1.51	0.90
7:h:61:ARG:HB3	53:1:1046:A:H4'	1.52	0.90
57:7:7:A:H3'	57:7:8:U:H5''	1.54	0.89
13:n:53:THR:HG21	53:1:2840:C:H5''	1.54	0.88
57:7:6:G:H3'	57:7:7:A:H5''	1.57	0.86
50:Z:9:GLU:HB3	50:Z:10:PRO:HD3	1.56	0.86
57:7:25:C:H3'	57:7:26:A:H5''	1.58	0.86
38:N:11:ARG:HD2	38:N:76:GLY:HA3	1.59	0.85
25:z:12:ALA:HB2	25:z:53:MET:HE1	1.59	0.84
52:3:484:G:H4'	52:3:485:U:H5''	1.60	0.84
8:i:93:ASN:HD22	53:1:1077:A:H4'	1.39	0.84
44:T:71:ARG:HH22	52:3:754:C:H5'	1.43	0.83
53:1:1906:G:C2'	53:1:1907:G:H5''	2.07	0.83
43:S:26:LEU:HD11	43:S:47:LEU:HD13	1.59	0.82
40:P:23:HIS:HB3	40:P:30:ILE:HG23	1.61	0.82
53:1:1020:A:H1'	53:1:1021:A:OP2	1.80	0.82
8:i:12:VAL:HG22	8:i:13:ALA:H	1.45	0.81
12:m:12:MET:HA	53:1:910:A:H62	1.43	0.81
4:e:84:ILE:HD11	53:1:2312:U:H5'	1.61	0.81
43:S:2:LYS:HZ1	52:3:983:A:H5'	1.42	0.81
7:h:3:LEU:HD12	7:h:5:LEU:H	1.46	0.80
37:M:45:ILE:HD13	37:M:60:LEU:HD23	1.64	0.79
52:3:1201:A:H1'	52:3:1202:U:OP2	1.83	0.79
8:i:25:PRO:HG2	57:7:55:U:H3'	1.63	0.78
53:1:1077:A:H2'	53:1:1078:U:H5'	1.64	0.78
53:1:1326:U:H2'	53:1:1327:A:H8	1.47	0.78
13:n:26:GLY:HA2	13:n:75:ILE:HD12	1.66	0.78
46:V:5:ARG:HD3	52:3:636:U:H5'	1.65	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1141:U:H4'	53:1:1142:A:O4'	1.83	0.78
54:2:13:G:H21	54:2:16:G:H1'	1.49	0.78
28:D:12:ARG:HE	28:D:44:VAL:HG21	1.48	0.78
43:S:48:GLN:HB2	48:X:12:LEU:HD23	1.66	0.77
13:n:39:PRO:HG2	53:1:1651:G:H4'	1.66	0.77
52:3:1197:A:C2'	52:3:1198:G:H5''	2.14	0.77
46:V:5:ARG:HH11	52:3:636:U:H5'	1.48	0.77
43:S:81:ILE:HG21	52:3:1202:U:N3	1.98	0.77
58:8:215:ILE:HD12	58:8:291:GLN:HB2	1.66	0.77
39:O:40:ILE:HB	39:O:73:LEU:HB3	1.66	0.76
55:5:76:A:H5'	55:5:76:A:C8	2.20	0.76
53:1:814:C:H1'	53:1:1225:G:H21	1.50	0.76
13:n:72:ASP:HB3	13:n:75:ILE:HG22	1.67	0.76
28:D:24:THR:HG23	28:D:27:GLY:H	1.51	0.76
52:3:327:A:O2'	52:3:328:C:H4'	1.84	0.76
6:g:94:ILE:HD11	6:g:122:LEU:HD13	1.68	0.75
35:K:9:MET:HE1	35:K:86:ARG:HD2	1.69	0.75
53:1:2286:G:H5''	53:1:2287:A:OP1	1.86	0.75
1:b:153:LEU:HD13	1:b:175:LEU:HD21	1.65	0.75
37:M:10:LEU:HG	37:M:74:ILE:HD11	1.68	0.75
7:h:33:VAL:HG12	53:1:1055:G:H5''	1.68	0.75
53:1:1306:C:H41	53:1:1606:C:H2'	1.52	0.75
13:n:103:ARG:HH11	53:1:1287:A:H5'	1.49	0.75
53:1:1807:G:H2'	53:1:1808:A:H5'	1.69	0.74
9:j:17:VAL:HG23	9:j:137:PRO:HB2	1.69	0.74
46:V:5:ARG:HD3	52:3:636:U:C5'	2.17	0.74
10:k:35:VAL:HG21	10:k:69:VAL:HB	1.68	0.74
53:1:275:C:H2'	53:1:276:U:H4'	1.69	0.74
40:P:63:GLN:HG3	40:P:98:ALA:HB2	1.69	0.74
8:i:48:ILE:HG22	8:i:49:GLU:HG3	1.68	0.74
33:I:33:ILE:H	33:I:33:ILE:HD12	1.52	0.74
53:1:1900:A:H1'	53:1:1970:A:H2'	1.68	0.74
7:h:73:LYS:HB3	7:h:117:LEU:HD21	1.70	0.74
57:7:6:G:C3'	57:7:7:A:H5''	2.17	0.74
22:w:39:THR:H	53:1:2331:G:H4'	1.52	0.73
54:2:66:A:H5''	54:2:67:G:OP1	1.88	0.73
46:V:5:ARG:HH11	52:3:636:U:C5'	2.00	0.73
58:8:214:PRO:HD3	58:8:233:GLU:HG2	1.71	0.73
11:l:96:LYS:HG3	11:l:101:ILE:HD11	1.69	0.73
42:R:64:VAL:HG12	42:R:65:GLU:H	1.53	0.73
53:1:694:U:H2'	53:1:695:G:H5''	1.70	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:85:ARG:HD3	20:u:87:GLU:HG3	1.69	0.73
18:s:17:VAL:HB	18:s:76:VAL:HG11	1.69	0.72
43:S:18:LYS:O	43:S:22:LYS:HE2	1.89	0.72
49:Y:30:PHE:HB3	49:Y:53:MET:HG2	1.70	0.72
53:1:1105:U:H2'	53:1:1106:G:H5''	1.70	0.72
53:1:181:A:H1'	53:1:435:C:H5'	1.70	0.72
30:F:1:MET:HE2	30:F:36:ARG:HB2	1.70	0.72
52:3:151:A:H62	52:3:170:U:H3	1.37	0.72
5:f:41:GLU:HA	5:f:54:ARG:HH21	1.55	0.72
53:1:2248:C:H2'	53:1:2249:U:H5'	1.71	0.72
53:1:528:A:N1	53:1:2042:A:H2'	2.05	0.72
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.70	0.71
33:I:9:LYS:HG2	33:I:12:ARG:HH21	1.53	0.71
58:8:156:GLU:HG2	58:8:160:GLN:HE21	1.54	0.71
8:i:93:ASN:ND2	53:1:1077:A:H4'	2.05	0.71
58:8:336:THR:HG22	58:8:338:VAL:HG23	1.73	0.71
12:m:75:GLU:HB2	12:m:90:GLU:HG3	1.73	0.71
13:n:56:LYS:HE3	13:n:88:ALA:HA	1.73	0.71
30:F:3:VAL:HG21	53:1:2539:C:H5'	1.71	0.71
32:H:82:ASP:HA	32:H:85:LYS:HE3	1.71	0.71
33:I:23:GLY:HA3	52:3:409:U:OP1	1.91	0.71
14:o:110:ALA:HB1	14:o:115:LEU:HD12	1.72	0.71
17:r:1:MET:H1	17:r:43:ASN:HA	1.56	0.70
22:w:36:GLN:HE22	22:w:39:THR:HA	1.56	0.70
50:Z:48:LYS:HG2	52:3:723:U:H6	1.56	0.70
53:1:995:C:H6	53:1:995:C:H5'	1.54	0.70
12:m:97:GLN:H	12:m:97:GLN:CD	1.99	0.70
53:1:546:U:H2'	53:1:547:A:H4'	1.72	0.70
53:1:2277:G:C2'	53:1:2278:A:H5''	2.21	0.70
54:2:3:C:H2'	54:2:4:C:H5''	1.73	0.70
40:P:88:PRO:HG2	40:P:89:GLY:H	1.55	0.70
15:p:7:LEU:O	15:p:7:LEU:HD23	1.91	0.70
34:J:80:LEU:HD13	34:J:122:VAL:HG11	1.74	0.70
35:K:29:ILE:HG22	35:K:34:GLY:HA3	1.74	0.70
50:Z:44:ARG:NH1	52:3:723:U:H5'	2.06	0.70
53:1:2286:G:H4'	53:1:2287:A:O4'	1.90	0.70
53:1:2553:G:H3'	53:1:2554:U:H5''	1.73	0.70
12:m:69:PRO:HA	12:m:94:ALA:HB2	1.72	0.70
13:n:69:ARG:O	13:n:70:THR:HG22	1.92	0.69
44:T:82:GLU:OE2	44:T:83:ARG:HG3	1.92	0.69
10:k:121:GLU:HG2	10:k:122:VAL:HG23	1.73	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:215:G:H4'	53:1:216:A:H4'	1.74	0.69
53:1:729:G:H4'	53:1:763:G:H5'	1.75	0.69
26:B:30:ASP:HB3	26:B:34:GLY:H	1.57	0.69
32:H:198:LYS:HE3	52:3:1058:G:OP1	1.92	0.69
17:r:1:MET:N	17:r:43:ASN:HA	2.07	0.69
19:t:2:ILE:HD11	53:1:144:A:H4'	1.74	0.69
38:N:109:GLN:HE22	52:3:1116:U:H4'	1.56	0.69
44:T:71:ARG:NH2	52:3:754:C:H5'	2.06	0.69
50:Z:34:ARG:HB3	50:Z:36:PHE:CE2	2.27	0.69
52:3:29:U:O2'	52:3:30:U:H5'	1.92	0.69
53:1:542:C:H2'	53:1:543:G:H5''	1.74	0.69
37:M:102:VAL:HG23	37:M:125:ILE:HB	1.74	0.69
40:P:28:ASN:ND2	40:P:56:LYS:HD2	2.08	0.69
33:I:169:TRP:CD1	33:I:185:PRO:HG3	2.28	0.69
41:Q:13:ARG:HE	41:Q:14:LYS:H	1.39	0.69
52:3:960:U:H4'	52:3:961:U:O5'	1.93	0.69
10:k:2:ILE:HG23	10:k:6:THR:HG21	1.74	0.69
52:3:1492:A:H2'	53:1:1913:A:H2	1.57	0.69
53:1:195:A:H2'	53:1:198:C:N4	2.07	0.69
53:1:310:A:C2'	53:1:311:A:H5''	2.22	0.68
53:1:2682:A:H61	53:1:2728:U:H1'	1.57	0.68
53:1:1053:C:C2'	53:1:1054:A:H5''	2.20	0.68
33:I:190:LEU:HD12	33:I:190:LEU:O	1.93	0.68
54:2:3:C:C3'	54:2:4:C:H5''	2.24	0.68
15:p:38:ARG:CZ	52:3:345:C:H5'	2.23	0.68
49:Y:80:ALA:HA	49:Y:83:ASN:HD21	1.58	0.68
58:8:33:THR:HA	58:8:70:TYR:HB3	1.75	0.68
15:p:91:VAL:HG21	15:p:96:LEU:HD21	1.75	0.68
53:1:668:A:H2'	53:1:670:A:H62	1.58	0.68
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.74	0.68
55:5:75:C:C3'	55:5:76:A:H5''	2.23	0.68
53:1:1078:U:H5''	53:1:1079:C:H5''	1.74	0.68
58:8:151:GLU:HG3	58:8:172:ARG:HH21	1.59	0.68
11:l:60:ARG:O	53:1:2393:U:H5'	1.94	0.68
33:I:82:LYS:HD2	52:3:5:U:C4	2.29	0.68
54:2:3:C:H3'	54:2:4:C:H5''	1.76	0.68
10:k:1:MET:HE3	10:k:67:LYS:HG2	1.76	0.68
15:p:112:ARG:HG2	15:p:114:ASN:HD22	1.58	0.68
53:1:2698:U:H2'	53:1:2699:C:C6	2.29	0.68
53:1:1437:C:H2'	53:1:1438:U:C6	2.28	0.67
52:3:112:G:H21	52:3:354:G:H5'	1.59	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:44:ARG:HH12	53:1:1248:G:P	2.17	0.67
5:f:51:PHE:HE1	5:f:71:LEU:HD12	1.58	0.67
5:f:136:ASP:HB3	5:f:139:VAL:HG12	1.75	0.67
19:t:6:ARG:HA	19:t:9:LYS:NZ	2.09	0.67
52:3:225:C:H2'	52:3:226:G:H5''	1.76	0.67
53:1:2156:G:H2'	53:1:2157:G:H5'	1.76	0.67
8:i:79:LEU:HD13	8:i:137:LEU:HD11	1.76	0.67
53:1:2514:U:H2'	53:1:2515:C:C6	2.30	0.67
53:1:2296:U:H5''	53:1:2297:A:OP1	1.95	0.67
4:e:107:VAL:CG1	4:e:108:PRO:HD3	2.24	0.67
26:B:46:GLY:HA3	26:B:54:ILE:HG21	1.77	0.67
52:3:1429:A:H2'	52:3:1430:A:H8	1.58	0.67
37:M:28:SER:HB2	37:M:58:LEU:HB2	1.77	0.67
29:E:31:ILE:HD11	53:1:2391:G:H5'	1.76	0.66
21:v:30:ILE:HG12	21:v:91:PHE:HB2	1.77	0.66
34:J:24:VAL:HG22	34:J:25:LYS:H	1.60	0.66
53:1:2561:U:H2'	53:1:2562:U:H5''	1.76	0.66
31:G:96:LEU:HD23	52:3:1103:C:H4'	1.78	0.66
16:q:56:PHE:HE2	53:1:536:G:H4'	1.60	0.66
53:1:1213:A:H62	53:1:1236:G:H1'	1.61	0.66
48:X:5:LYS:HG3	48:X:6:LYS:HG2	1.77	0.66
18:s:17:VAL:HG11	18:s:103:ILE:HD12	1.77	0.66
19:t:6:ARG:HA	19:t:9:LYS:HZ3	1.60	0.66
53:1:49:A:H5'	53:1:51:G:O4'	1.96	0.66
52:3:396:C:H2'	52:3:397:A:H5''	1.76	0.66
18:s:82:MET:HG3	18:s:98:LYS:HB2	1.78	0.66
33:I:197:HIS:O	33:I:200:VAL:HG12	1.96	0.66
35:K:2:ARG:NH1	35:K:91:ARG:HH12	1.94	0.66
53:1:503:A:H4'	53:1:505:A:H5''	1.78	0.66
20:u:48:VAL:HG12	20:u:50:ALA:H	1.61	0.66
50:Z:44:ARG:HD3	52:3:723:U:P	2.35	0.66
52:3:946:A:H2'	52:3:947:G:C8	2.31	0.66
33:I:131:ILE:H	33:I:131:ILE:HD12	1.60	0.65
36:L:118:ARG:O	36:L:122:GLU:HG2	1.95	0.65
39:O:85:ASP:HA	39:O:88:MET:HE2	1.77	0.65
5:f:19:ASN:HB3	5:f:22:VAL:HG13	1.79	0.65
53:1:1979:U:O2'	53:1:1980:G:H5'	1.97	0.65
58:8:281:GLY:C	58:8:282:ILE:HD12	2.21	0.65
10:k:108:ARG:HG3	10:k:113:MET:HE1	1.78	0.65
40:P:118:ASN:CG	52:3:718:A:H5'	2.20	0.65
7:h:97:LYS:HD3	7:h:127:ALA:HA	1.78	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:27:G:N2	53:1:512:G:H1'	2.11	0.65
14:o:40:ILE:HG12	14:o:47:VAL:HG12	1.79	0.65
19:t:2:ILE:HD11	53:1:144:A:C5'	2.27	0.65
48:X:28:LYS:HG2	48:X:29:PRO:HD2	1.79	0.65
57:7:7:A:H3'	57:7:8:U:C5'	2.26	0.65
2:c:9:VAL:HB	2:c:26:VAL:HG23	1.77	0.65
8:i:79:LEU:HD21	8:i:135:MET:HG3	1.79	0.65
35:K:4:TYR:O	35:K:63:ASN:HA	1.97	0.65
52:3:1137:C:H5'	52:3:1138:G:H5'	1.78	0.65
28:D:26:ASN:OD1	53:1:682:G:H5'	1.97	0.65
52:3:769:G:H4'	52:3:1513:A:H4'	1.78	0.65
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.79	0.65
53:1:310:A:H2'	53:1:311:A:H5''	1.76	0.65
6:g:97:ARG:HH22	53:1:2220:U:H4'	1.62	0.65
20:u:50:ALA:O	20:u:51:LEU:HG	1.97	0.65
30:F:12:ARG:HH12	53:1:1102:C:H4'	1.62	0.64
53:1:974:G:H1'	53:1:975:A:C8	2.32	0.64
7:h:33:VAL:HG23	7:h:35:VAL:H	1.63	0.64
16:q:56:PHE:CE2	53:1:536:G:H4'	2.33	0.64
52:3:70:U:H5''	52:3:71:A:OP1	1.96	0.64
53:1:2208:C:H2'	53:1:2209:G:C8	2.32	0.64
29:E:8:GLY:O	29:E:12:ARG:NH2	2.29	0.64
35:K:86:ARG:HH12	52:3:673:A:H4'	1.63	0.64
52:3:1414:U:H2'	52:3:1415:G:H8	1.63	0.64
53:1:828:U:H2'	53:1:829:A:C8	2.33	0.64
42:R:25:GLY:H	52:3:1329:A:H5''	1.61	0.64
53:1:1068:G:H2'	53:1:1069:A:O4'	1.97	0.64
53:1:2298:A:H62	53:1:2318:G:H21	1.46	0.64
6:g:26:ALA:HA	6:g:30:LEU:HB2	1.79	0.64
23:x:15:ASN:HD21	23:x:23:ALA:HB1	1.62	0.64
32:H:55:VAL:HB	32:H:66:THR:HB	1.79	0.64
2:c:136:ASN:HD21	2:c:139:SER:HB3	1.63	0.64
13:n:73:ASN:HA	13:n:76:VAL:HG12	1.77	0.64
13:n:103:ARG:NH1	53:1:1287:A:H5'	2.13	0.64
37:M:94:VAL:HG12	37:M:95:MET:HG2	1.80	0.64
49:Y:26:MET:HB3	52:3:1458:G:H5'	1.79	0.64
53:1:704:G:H2'	53:1:726:G:H22	1.62	0.64
53:1:2248:C:C2'	53:1:2249:U:H5'	2.28	0.64
14:o:31:THR:H	14:o:35:ILE:HG22	1.63	0.64
20:u:94:PHE:HD2	20:u:99:SER:HG	1.44	0.64
31:G:115:ASP:O	31:G:119:GLN:HG2	1.97	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:133:MET:SD	32:H:134:LYS:HG2	2.38	0.64
52:3:1524:C:H2'	52:3:1525:G:C8	2.32	0.64
53:1:704:G:H2'	53:1:726:G:N2	2.13	0.64
53:1:1664:A:H61	53:1:1996:C:H42	1.46	0.64
32:H:109:GLU:HB2	32:H:143:LEU:HD21	1.79	0.63
27:C:35:LEU:HD22	27:C:37:LYS:HG3	1.80	0.63
52:3:501:C:H2'	52:3:502:A:H8	1.62	0.63
54:2:3:C:C2'	54:2:4:C:H5''	2.28	0.63
8:i:23:VAL:HG12	8:i:26:ALA:HB3	1.79	0.63
8:i:23:VAL:CG1	8:i:26:ALA:HB3	2.28	0.63
28:D:25:LYS:HD2	53:1:1367:A:O2'	1.98	0.63
33:I:120:LYS:HE2	33:I:130:ASN:HD21	1.64	0.63
37:M:6:ILE:HD12	37:M:6:ILE:H	1.62	0.63
53:1:118:A:H5'	53:1:119:A:H8	1.64	0.63
7:h:53:ARG:HG2	7:h:55:VAL:HG13	1.80	0.63
2:c:151:THR:HB	2:c:152:PRO:HD3	1.80	0.63
4:e:107:VAL:HG12	4:e:108:PRO:HD3	1.80	0.63
27:C:35:LEU:HD23	27:C:36:LYS:N	2.13	0.63
53:1:677:A:O2'	53:1:2071:A:H5'	1.98	0.63
55:5:16:C:O2'	55:5:17:C:H5'	1.99	0.63
58:8:34:THR:O	58:8:38:LYS:HG2	1.98	0.63
6:g:73:ASN:ND2	6:g:76:GLU:HA	2.14	0.63
22:w:74:LYS:HE2	53:1:857:G:H5''	1.80	0.63
55:6:54:U:H3	55:6:58:A:H62	1.44	0.63
58:8:50:ILE:HG12	58:8:68:VAL:HG11	1.80	0.63
46:V:64:ARG:HD2	52:3:264:C:H4'	1.80	0.63
53:1:558:U:H2'	53:1:559:G:H8	1.64	0.63
5:f:155:PRO:HG3	53:1:2530:A:N6	2.14	0.62
31:G:22:TRP:HE1	52:3:830:G:H5'	1.62	0.62
52:3:715:A:H2'	52:3:716:A:H8	1.64	0.62
53:1:807:U:H2'	53:1:808:G:H8	1.63	0.62
55:5:75:C:H3'	55:5:76:A:H5''	1.81	0.62
32:H:35:ASP:O	32:H:38:VAL:HG12	1.99	0.62
52:3:1413:A:H2	52:3:1487:G:H22	1.46	0.62
53:1:1105:U:C2'	53:1:1106:G:H5''	2.29	0.62
3:d:145:ASP:HA	3:d:166:LYS:HG2	1.80	0.62
8:i:20:SER:OG	8:i:21:PRO:HD3	1.99	0.62
37:M:88:LYS:O	37:M:91:LEU:HD23	1.99	0.62
55:6:36:U:H2'	55:6:37:A:H5'	1.81	0.62
5:f:132:LEU:HD12	5:f:132:LEU:O	1.99	0.62
53:1:1019:U:H3	53:1:1142:A:H62	1.46	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:105:ILE:HG13	34:J:123:LEU:HA	1.81	0.62
52:3:715:A:H2'	52:3:716:A:C8	2.35	0.62
52:3:1412:C:H2'	52:3:1413:A:C8	2.34	0.62
7:h:60:LEU:HD12	7:h:61:ARG:HG2	1.81	0.62
52:3:683:G:H1	52:3:707:U:H3	1.48	0.62
53:1:2391:G:H4'	53:1:2392:A:OP1	1.98	0.62
24:y:41:HIS:CD2	53:1:96:C:H4'	2.35	0.62
35:K:21:MET:HA	35:K:24:ARG:HD3	1.82	0.62
41:Q:113:ARG:HE	41:Q:120:ARG:HA	1.64	0.62
4:e:161:SER:OG	4:e:164:GLU:HG3	2.00	0.62
31:G:186:VAL:HG13	31:G:190:SER:HB2	1.80	0.62
45:U:5:ARG:HB2	52:3:376:G:H5''	1.81	0.62
10:k:18:ARG:HB3	10:k:45:GLU:HB3	1.81	0.62
12:m:36:VAL:HG12	21:v:82:TYR:HB2	1.82	0.62
27:C:35:LEU:HD23	27:C:36:LYS:H	1.64	0.62
31:G:47:PRO:O	31:G:51:GLU:HG3	1.99	0.62
43:S:3:GLN:HE21	52:3:1048:G:P	2.22	0.62
53:1:1796:U:H2'	53:1:1797:G:H8	1.65	0.62
4:e:68:LYS:NZ	54:2:41:G:O6	2.33	0.62
7:h:88:HIS:H	7:h:89:PRO:HD2	1.64	0.62
13:n:60:VAL:HG22	53:1:1454:C:O2'	2.00	0.62
50:Z:50:SER:HA	50:Z:53:LYS:HE3	1.81	0.62
29:E:61:LEU:HD12	29:E:61:LEU:O	1.99	0.61
52:3:880:C:H2'	52:3:881:G:H8	1.65	0.61
53:1:633:A:H1'	53:1:2403:C:H4'	1.82	0.61
53:1:1810:A:H2'	53:1:1811:G:O4'	2.00	0.61
1:b:156:SER:HB2	53:1:1818:U:H5'	1.82	0.61
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.80	0.61
15:p:77:SER:O	15:p:80:VAL:HG22	2.01	0.61
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.81	0.61
14:o:56:LYS:NZ	54:2:116:G:O3'	2.34	0.61
34:J:108:GLY:H	52:3:9:G:H4'	1.65	0.61
35:K:92:THR:OG1	35:K:93:LYS:N	2.33	0.61
42:R:76:ILE:HG12	42:R:80:MET:HE2	1.83	0.61
49:Y:54:GLN:N	49:Y:55:PRO:HD2	2.16	0.61
52:3:1033:G:H2'	52:3:1034:G:H5''	1.82	0.61
53:1:414:C:H2'	53:1:415:A:C8	2.36	0.61
7:h:54:VAL:C	53:1:1084:A:H5''	2.26	0.61
7:h:112:ALA:O	7:h:114:GLU:N	2.33	0.61
9:j:8:PRO:O	9:j:11:VAL:HG22	2.00	0.61
9:j:136:GLN:N	9:j:137:PRO:HD3	2.14	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:6:THR:HG23	53:1:1666:G:H4'	1.83	0.61
37:M:94:VAL:HB	37:M:99:GLY:O	2.01	0.61
52:3:418:C:H2'	52:3:419:C:C6	2.36	0.61
2:c:194:PRO:HA	53:1:2680:U:H5'	1.82	0.61
8:i:11:GLN:HE21	8:i:54:ILE:HG23	1.66	0.61
53:1:717:C:H2'	53:1:718:A:H5'	1.82	0.61
17:r:91:GLN:HE22	53:1:1162:G:H21	1.49	0.61
32:H:162:ALA:HB2	52:3:1056:U:H4'	1.83	0.61
47:W:70:THR:HG22	47:W:73:HIS:NE2	2.15	0.61
52:3:304:U:O2'	52:3:305:G:H5'	2.00	0.61
53:1:1078:U:C5'	53:1:1079:C:H5''	2.31	0.61
1:b:251:THR:HG23	1:b:252:LYS:HG2	1.81	0.61
31:G:94:ARG:NH1	52:3:1101:A:OP2	2.33	0.61
32:H:152:VAL:HG22	32:H:165:GLU:O	2.01	0.61
52:3:946:A:H2'	52:3:947:G:H8	1.65	0.61
53:1:796:C:H2'	53:1:797:G:H8	1.66	0.61
9:j:7:LYS:HE3	53:1:538:A:H5''	1.82	0.61
13:n:51:LEU:HD21	13:n:69:ARG:HG3	1.82	0.61
15:p:92:ARG:O	53:1:2848:G:H2'	2.01	0.61
52:3:352:C:H4'	52:3:354:G:OP1	2.01	0.61
53:1:1251:C:O2'	53:1:1252:G:H3'	2.00	0.61
57:7:62:C:C3'	57:7:63:G:H5''	2.31	0.61
58:8:107:ALA:HB1	58:8:137:LYS:HD2	1.82	0.61
17:r:65:ALA:HB3	17:r:95:ASP:HB2	1.81	0.61
41:Q:72:ASN:HD21	41:Q:104:SER:HB3	1.66	0.61
8:i:10:LEU:N	8:i:10:LEU:HD23	2.15	0.60
33:I:131:ILE:HG22	33:I:133:SER:H	1.66	0.60
52:3:50:A:H4'	52:3:51:A:H5'	1.83	0.60
58:8:156:GLU:HG2	58:8:160:GLN:NE2	2.16	0.60
9:j:81:ILE:HG23	9:j:82:GLY:H	1.66	0.60
43:S:81:ILE:H	43:S:81:ILE:HD12	1.66	0.60
8:i:126:ARG:HA	8:i:129:GLU:HG3	1.83	0.60
21:v:21:ARG:HH12	21:v:87:GLN:HB3	1.65	0.60
53:1:1133:A:H4'	53:1:1134:A:H5''	1.84	0.60
53:1:1319:C:O2'	53:1:1320:C:H5'	2.01	0.60
58:8:343:GLU:HB2	58:8:360:VAL:HB	1.83	0.60
32:H:69:THR:HG22	32:H:71:ARG:H	1.66	0.60
35:K:3:HIS:O	35:K:92:THR:HG22	2.00	0.60
35:K:18:VAL:HG21	35:K:58:HIS:CD2	2.36	0.60
53:1:615:U:H5''	53:1:616:A:OP2	2.00	0.60
53:1:2544:G:H1'	53:1:2646:C:H5'	1.84	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:64:VAL:HG21	7:h:78:GLY:HA2	1.84	0.60
16:q:36:GLN:O	16:q:39:ILE:HG22	2.02	0.60
33:I:57:LYS:HD3	33:I:202:LEU:HD23	1.83	0.60
51:a:181:ASP:HB2	51:a:184:LYS:HD3	1.83	0.60
58:8:13:VAL:HG23	58:8:75:ARG:HE	1.66	0.60
58:8:309:VAL:HG21	58:8:359:MET:HE2	1.84	0.60
1:b:16:VAL:HB	1:b:203:VAL:HG22	1.83	0.60
22:w:36:GLN:NE2	22:w:39:THR:HA	2.16	0.60
31:G:55:GLU:HA	31:G:58:LYS:HD2	1.83	0.60
35:K:18:VAL:HB	35:K:19:PRO:HD3	1.82	0.60
39:O:41:PRO:HG3	52:3:1150:A:N3	2.17	0.60
52:3:1352:C:H2'	52:3:1353:G:C8	2.36	0.60
53:1:45:G:H5''	53:1:46:G:C5'	2.26	0.60
53:1:2297:A:N6	53:1:2319:G:H1'	2.17	0.60
53:1:2743:U:H2'	53:1:2744:G:H5''	1.82	0.60
5:f:159:LYS:HE2	53:1:2658:C:H5'	1.84	0.60
33:I:36:ALA:N	33:I:37:PRO:HD3	2.16	0.60
42:R:85:TYR:CZ	52:3:1321:U:H4'	2.37	0.60
52:3:673:A:H2'	52:3:674:G:C8	2.37	0.60
53:1:445:C:O2'	53:1:446:G:H5'	2.02	0.60
54:2:2:G:H2'	54:2:3:C:C6	2.37	0.60
58:8:93:ILE:H	58:8:93:ILE:HD12	1.67	0.60
10:k:29:HIS:HE1	10:k:31:ARG:HH22	1.50	0.60
37:M:5:PRO:HG2	37:M:6:ILE:HD12	1.84	0.60
38:N:65:THR:HG21	52:3:1130:A:OP1	2.02	0.60
52:3:245:U:O2'	52:3:246:A:H5'	2.02	0.60
52:3:335:C:H2'	52:3:336:A:H8	1.67	0.60
52:3:335:C:H2'	52:3:336:A:C8	2.37	0.60
53:1:687:C:H6	53:1:687:C:H5'	1.66	0.60
53:1:2537:U:H2'	53:1:2538:C:C6	2.37	0.60
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.84	0.60
12:m:41:LEU:HG	12:m:96:ILE:HG13	1.83	0.60
14:o:49:VAL:HG21	14:o:82:ALA:HA	1.82	0.60
34:J:9:GLU:C	34:J:10:LEU:HD22	2.26	0.60
37:M:9:MET:HG3	37:M:26:MET:SD	2.42	0.60
15:p:90:ALA:HB2	15:p:112:ARG:HB2	1.84	0.60
37:M:126:CYS:SG	37:M:127:TYR:N	2.74	0.60
42:R:16:ILE:H	42:R:16:ILE:HD12	1.66	0.60
50:Z:66:ARG:HG3	52:3:1099:G:O4'	2.02	0.60
52:3:162:A:H2'	52:3:163:C:H5'	1.83	0.60
53:1:1874:C:H2'	53:1:1875:G:O4'	2.02	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1186:G:H2'	53:1:1187:G:O4'	2.02	0.59
54:2:60:C:H2'	54:2:61:G:H8	1.67	0.59
1:b:120:ASP:HB3	6:g:91:PHE:HE1	1.65	0.59
4:e:66:ILE:N	4:e:66:ILE:HD12	2.17	0.59
32:H:120:THR:HG23	32:H:188:ALA:HB2	1.83	0.59
52:3:357:G:OP1	52:3:367:U:H5''	2.02	0.59
53:1:766:U:H2'	53:1:767:U:C6	2.37	0.59
53:1:1367:A:H2'	53:1:1368:G:H5'	1.83	0.59
4:e:65:LEU:HD22	54:2:42:C:C4	2.37	0.59
46:V:8:GLN:NE2	46:V:59:GLU:OE2	2.35	0.59
52:3:79:G:O2'	52:3:80:A:H5'	2.01	0.59
2:c:88:GLU:OE1	2:c:88:GLU:N	2.35	0.59
28:D:12:ARG:NE	28:D:44:VAL:HG21	2.18	0.59
51:a:175:ILE:HB	51:a:188:ASN:HB3	1.84	0.59
52:3:423:G:H2'	52:3:424:G:H5'	1.84	0.59
52:3:730:G:H2'	52:3:731:G:H5'	1.84	0.59
52:3:1084:G:H5'	52:3:1102:A:OP2	2.02	0.59
53:1:917:A:H5''	53:1:2268:A:H61	1.67	0.59
53:1:1213:A:N6	53:1:1236:G:H1'	2.17	0.59
15:p:105:LYS:O	15:p:108:ARG:HG2	2.03	0.59
53:1:2628:C:H3'	53:1:2629:U:H5'	1.82	0.59
5:f:85:LYS:HG3	5:f:164:ALA:HB3	1.85	0.59
10:k:31:ARG:HG3	10:k:31:ARG:HH11	1.67	0.59
30:F:31:PRO:HB3	53:1:2527:C:H5''	1.84	0.59
52:3:399:G:H2'	52:3:400:C:C6	2.38	0.59
52:3:950:U:H2'	52:3:951:G:H8	1.66	0.59
53:1:796:C:H2'	53:1:797:G:C8	2.38	0.59
53:1:1078:U:H4'	53:1:1079:C:H5''	1.83	0.59
53:1:2139:U:H2'	53:1:2140:G:C8	2.37	0.59
55:6:16:C:O2'	55:6:17:C:H5'	2.02	0.59
3:d:47:LYS:O	3:d:83:VAL:HB	2.03	0.59
19:t:2:ILE:HD11	53:1:144:A:H5''	1.83	0.59
31:G:53:LEU:HD23	31:G:56:LEU:HD12	1.84	0.59
53:1:694:U:C2'	53:1:695:G:H5''	2.31	0.59
24:y:2:LYS:HD2	53:1:78:U:OP2	2.02	0.59
29:E:16:THR:HG21	29:E:48:MET:HE1	1.84	0.59
31:G:46:VAL:HG13	31:G:47:PRO:HD3	1.83	0.59
40:P:43:TRP:CZ2	52:3:686:U:H1'	2.38	0.59
49:Y:67:HIS:O	49:Y:68:LYS:HG3	2.02	0.59
52:3:224:U:H2'	52:3:225:C:C6	2.38	0.59
20:u:56:GLY:N	53:1:483:A:O2'	2.36	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:142:ARG:HG3	55:6:41:C:H4'	1.85	0.59
41:Q:119:LYS:HD2	52:3:36:C:H5''	1.84	0.59
46:V:5:ARG:NH1	52:3:636:U:H5'	2.18	0.59
50:Z:23:GLU:C	50:Z:25:ALA:H	2.11	0.59
52:3:1409:C:H2'	52:3:1410:A:C8	2.37	0.59
17:r:4:VAL:HG13	17:r:39:LEU:HB2	1.84	0.58
33:I:9:LYS:HE3	52:3:428:G:H5''	1.85	0.58
34:J:107:GLY:HA2	52:3:8:A:H1'	1.85	0.58
38:N:105:ARG:HH11	38:N:107:ALA:HA	1.67	0.58
40:P:122:PRO:HG2	50:Z:35:GLU:HG3	1.85	0.58
45:U:28:ARG:HH22	52:3:390:U:H4'	1.68	0.58
23:x:6:VAL:HG13	23:x:7:THR:H	1.68	0.58
35:K:38:ARG:HH21	35:K:40:GLU:HB2	1.68	0.58
35:K:63:ASN:HD21	35:K:95:ALA:HB1	1.67	0.58
39:O:88:MET:O	39:O:89:ARG:HG2	2.02	0.58
51:a:60:ARG:HG2	51:a:164:ARG:HG3	1.84	0.58
52:3:150:U:H3	52:3:171:A:H62	1.51	0.58
52:3:410:G:H2'	52:3:429:U:O4	2.03	0.58
53:1:1071:G:OP1	53:1:1071:G:H3'	2.02	0.58
53:1:1476:U:H3	53:1:1515:A:H62	1.51	0.58
53:1:2281:A:O2'	53:1:2282:G:H5'	2.02	0.58
50:Z:34:ARG:HB3	50:Z:36:PHE:CZ	2.39	0.58
53:1:2452:C:H42	53:1:2504:U:H3	1.50	0.58
8:i:11:GLN:NE2	8:i:54:ILE:HG23	2.19	0.58
8:i:94:LYS:NZ	53:1:1076:C:H4'	2.18	0.58
12:m:45:GLN:HE21	53:1:2485:G:H5''	1.69	0.58
21:v:72:VAL:HG12	21:v:93:ARG:HA	1.86	0.58
36:L:36:SER:HA	38:N:42:THR:HG21	1.84	0.58
39:O:6:ILE:H	39:O:6:ILE:HD12	1.68	0.58
50:Z:9:GLU:HB3	50:Z:10:PRO:CD	2.31	0.58
52:3:225:C:C3'	52:3:226:G:H5''	2.33	0.58
53:1:161:A:H3'	53:1:162:U:H5''	1.86	0.58
53:1:2286:G:H4'	53:1:2287:A:O5'	2.01	0.58
53:1:2561:U:H2'	53:1:2562:U:C5'	2.33	0.58
53:1:2646:C:H2'	53:1:2647:U:O4'	2.03	0.58
4:e:114:ARG:HG3	4:e:177:ARG:HD3	1.85	0.58
10:k:30:ARG:HD2	53:1:2674:G:H4'	1.85	0.58
19:t:80:TRP:HZ3	19:t:82:LYS:HB3	1.69	0.58
38:N:121:ARG:HG3	52:3:1348:U:H4'	1.84	0.58
39:O:44:THR:HG21	39:O:70:HIS:HD2	1.67	0.58
49:Y:25:SER:OG	52:3:1458:G:H5''	2.03	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:6:ARG:C	50:Z:8:ASN:H	2.11	0.58
2:c:110:THR:HG21	2:c:169:ARG:HH11	1.68	0.58
52:3:1094:G:N3	52:3:1094:G:H2'	2.18	0.58
52:3:1306:A:N6	52:3:1331:G:H1'	2.19	0.58
53:1:310:A:O2'	53:1:311:A:H5''	2.04	0.58
57:7:58:A:H1'	57:7:60:U:H5	1.68	0.58
4:e:65:LEU:HD22	54:2:42:C:C5	2.38	0.58
4:e:70:ARG:HD2	53:1:2298:A:OP1	2.03	0.58
10:k:38:ILE:N	10:k:38:ILE:HD12	2.19	0.58
38:N:57:VAL:HG23	38:N:58:GLU:H	1.69	0.58
38:N:74:GLN:O	38:N:78:ILE:HG12	2.04	0.58
42:R:12:LYS:HD2	42:R:17:ALA:HA	1.85	0.58
52:3:1527:U:H2'	52:3:1528:U:C6	2.39	0.58
53:1:2287:A:O2'	53:1:2288:A:H2'	2.03	0.58
53:1:2512:C:H2'	53:1:2513:A:O4'	2.03	0.58
57:7:62:C:H3'	57:7:63:G:H5''	1.85	0.58
8:i:94:LYS:HZ2	53:1:1076:C:H4'	1.67	0.58
12:m:34:LYS:HE3	12:m:131:VAL:HG11	1.86	0.58
13:n:98:LEU:HD21	26:B:53:VAL:HG11	1.86	0.58
53:1:20:C:H2'	53:1:21:A:C8	2.38	0.58
2:c:46:ARG:HB2	2:c:84:LEU:HD12	1.85	0.58
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.85	0.58
30:F:36:ARG:O	30:F:37:GLN:HB2	2.02	0.58
39:O:11:LYS:HG2	39:O:71:LEU:HG	1.84	0.58
40:P:43:TRP:HZ2	52:3:686:U:H1'	1.68	0.58
42:R:52:ILE:O	42:R:56:ARG:HG3	2.04	0.58
43:S:12:ARG:HB3	43:S:59:GLN:HE22	1.68	0.58
52:3:1200:C:H5''	52:3:1201:A:H3'	1.85	0.58
53:1:546:U:H2'	53:1:547:A:C4'	2.34	0.58
53:1:2112:G:H2'	53:1:2113:U:H5'	1.85	0.58
53:1:2800:A:H3'	53:1:2801:G:H5'	1.86	0.58
37:M:31:LEU:HD22	52:3:643:C:H5''	1.86	0.58
53:1:1611:C:H6	53:1:1611:C:H5'	1.68	0.58
53:1:2233:U:H2'	53:1:2234:G:C8	2.39	0.58
20:u:39:ASN:HD21	20:u:64:ILE:HB	1.69	0.57
32:H:106:ARG:HD3	32:H:106:ARG:H	1.69	0.57
51:a:55:SER:HA	51:a:58:ASN:ND2	2.18	0.57
52:3:1391:U:H2'	52:3:1392:G:C8	2.39	0.57
53:1:1111:A:H2'	53:1:1111:A:N3	2.19	0.57
53:1:1434:A:H2'	53:1:1435:G:C8	2.39	0.57
8:i:74:PRO:HB2	8:i:77:VAL:HG22	1.85	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:62:PRO:HB2	29:E:29:ARG:HH11	1.69	0.57
21:v:20:LEU:HD11	21:v:41:GLU:OE2	2.02	0.57
52:3:950:U:H2'	52:3:951:G:C8	2.39	0.57
58:8:305:PHE:HE1	58:8:363:LEU:HD22	1.68	0.57
4:e:87:LYS:HD2	53:1:2313:C:H5''	1.85	0.57
15:p:74:GLN:HB2	15:p:77:SER:HB2	1.86	0.57
29:E:27:ASN:HB3	29:E:35:LYS:HE2	1.86	0.57
32:H:171:ARG:HG2	32:H:173:PRO:HD3	1.86	0.57
33:I:58:GLN:O	33:I:62:ARG:HD3	2.04	0.57
43:S:15:LEU:HD12	43:S:18:LYS:HB3	1.86	0.57
47:W:35:SER:HA	47:W:71:ASP:HB3	1.86	0.57
48:X:77:ARG:HD2	52:3:1225:A:H1'	1.86	0.57
50:Z:48:LYS:HG2	52:3:723:U:C6	2.39	0.57
52:3:406:G:O2'	52:3:407:U:H5'	2.05	0.57
53:1:1539:U:H2'	53:1:1540:G:H8	1.68	0.57
3:d:98:LYS:HE3	53:1:617:G:P	2.43	0.57
31:G:113:LEU:HD13	31:G:143:LEU:HD23	1.86	0.57
32:H:135:ARG:HA	32:H:138:GLN:HE21	1.70	0.57
34:J:24:VAL:HG13	34:J:26:GLY:H	1.69	0.57
38:N:104:THR:HG22	38:N:106:ASP:H	1.68	0.57
41:Q:26:CYS:SG	41:Q:29:LYS:HD3	2.44	0.57
53:1:523:C:H2'	53:1:524:G:H8	1.68	0.57
53:1:1909:C:H2'	53:1:1910:G:H8	1.69	0.57
53:1:2063:C:O4'	59:5:101:FME:HG3	2.04	0.57
53:1:2086:U:H2'	53:1:2087:G:C8	2.38	0.57
1:b:242:HIS:O	1:b:244:VAL:HG13	2.04	0.57
8:i:80:LYS:HG2	8:i:85:ILE:O	2.05	0.57
52:3:1397:C:H42	56:4:22:A:H3'	1.69	0.57
53:1:1981:A:H5''	53:1:1982:U:OP2	2.05	0.57
1:b:145:MET:SD	1:b:181:ARG:NH2	2.78	0.57
8:i:9:LYS:HD3	53:1:1061:U:H5''	1.86	0.57
20:u:32:LYS:NZ	53:1:478:A:H4'	2.20	0.57
28:D:26:ASN:CG	53:1:682:G:H5'	2.30	0.57
35:K:15:SER:O	35:K:18:VAL:HG23	2.05	0.57
52:3:1005:A:H2'	52:3:1006:G:O4'	2.05	0.57
53:1:1801:A:H5''	53:1:2203:U:H2'	1.86	0.57
53:1:2233:U:H2'	53:1:2234:G:H8	1.69	0.57
4:e:73:VAL:HG22	4:e:75:GLY:H	1.69	0.57
6:g:75:LEU:HB3	6:g:77:THR:HG22	1.85	0.57
10:k:7:MET:HB3	10:k:18:ARG:HD2	1.86	0.57
52:3:1256:A:H1'	52:3:1258:G:N9	2.19	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:639:U:H2'	53:1:640:C:C6	2.39	0.57
53:1:912:C:O2'	53:1:913:U:H5'	2.03	0.57
53:1:1326:U:H2'	53:1:1327:A:C8	2.34	0.57
53:1:1786:A:H1'	53:1:1938:A:N6	2.19	0.57
35:K:86:ARG:NH1	52:3:673:A:H4'	2.20	0.57
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.05	0.57
53:1:1373:A:H5'	53:1:2212:A:H1'	1.87	0.57
53:1:1507:C:H2'	53:1:1508:A:H4'	1.87	0.57
15:p:20:ARG:HB3	15:p:21:PRO:HD2	1.87	0.57
19:t:2:ILE:CD1	53:1:144:A:H4'	2.34	0.57
38:N:119:LYS:HD2	52:3:1350:A:OP2	2.04	0.57
49:Y:67:HIS:HE1	52:3:132:C:H4'	1.70	0.57
52:3:130:A:O2'	52:3:264:C:H5'	2.05	0.57
52:3:1395:C:H5''	52:3:1402:C:H4'	1.85	0.57
53:1:367:G:H2'	53:1:368:A:O4'	2.05	0.57
1:b:209:ALA:HA	1:b:212:TRP:NE1	2.19	0.56
5:f:173:ALA:HB3	5:f:176:LYS:OXT	2.03	0.56
24:y:24:GLU:HG2	24:y:25:GLN:N	2.20	0.56
52:3:891:U:O2'	52:3:892:A:H5'	2.05	0.56
52:3:955:U:H3	52:3:1225:A:H61	1.52	0.56
53:1:112:U:H2'	53:1:113:U:H5'	1.87	0.56
53:1:2788:C:H2'	53:1:2789:C:C6	2.40	0.56
8:i:24:GLY:O	8:i:27:LEU:HD23	2.05	0.56
11:l:101:ILE:HG13	11:l:102:GLY:H	1.71	0.56
52:3:736:C:H2'	52:3:737:C:C6	2.40	0.56
52:3:817:C:H4'	52:3:818:G:H5''	1.86	0.56
53:1:445:C:C2'	53:1:446:G:H5'	2.36	0.56
53:1:713:G:H21	53:1:718:A:H62	1.53	0.56
53:1:2163:A:N3	53:1:2163:A:H2'	2.19	0.56
53:1:2799:A:C2'	53:1:2800:A:H5'	2.35	0.56
56:4:17:U:H2'	56:4:18:G:C8	2.40	0.56
3:d:108:ILE:O	3:d:111:GLU:HB3	2.04	0.56
10:k:29:HIS:CE1	10:k:31:ARG:HH22	2.22	0.56
34:J:92:ARG:HB2	34:J:127:TYR:HB2	1.88	0.56
38:N:109:GLN:NE2	52:3:1116:U:H4'	2.20	0.56
43:S:19:TYR:HB3	43:S:50:LEU:HD11	1.88	0.56
52:3:501:C:H2'	52:3:502:A:C8	2.39	0.56
53:1:2156:G:C2'	53:1:2157:G:H5'	2.34	0.56
53:1:2467:C:H2'	53:1:2468:A:O4'	2.05	0.56
53:1:2743:U:C3'	53:1:2744:G:H5''	2.36	0.56
57:7:62:C:H2'	57:7:63:G:H5''	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:216:U:H2'	52:3:217:C:C6	2.40	0.56
53:1:669:G:H2'	53:1:669:G:N3	2.20	0.56
31:G:116:LEU:HG	31:G:140:LEU:HD13	1.88	0.56
35:K:66:ALA:HB1	35:K:67:PRO:HD2	1.87	0.56
41:Q:85:ARG:NH1	41:Q:92:VAL:O	2.38	0.56
52:3:1414:U:H2'	52:3:1415:G:C8	2.40	0.56
52:3:1497:G:O2'	52:3:1498:U:H5'	2.06	0.56
53:1:2732:G:O2'	53:1:2733:A:H5'	2.04	0.56
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.86	0.56
22:w:73:ARG:HH22	53:1:2333:A:P	2.28	0.56
43:S:80:ARG:HG3	43:S:81:ILE:HD12	1.86	0.56
53:1:582:A:H2'	53:1:583:G:C8	2.40	0.56
53:1:2515:C:H2'	53:1:2516:A:C8	2.41	0.56
20:u:39:ASN:HB3	20:u:62:ALA:HB3	1.87	0.56
32:H:178:ARG:HH21	52:3:1112:C:H4'	1.70	0.56
34:J:76:ASN:HB2	34:J:81:GLN:HE22	1.70	0.56
35:K:29:ILE:HD13	35:K:64:VAL:HG11	1.88	0.56
35:K:67:PRO:HG2	35:K:70:VAL:HG23	1.88	0.56
38:N:105:ARG:O	38:N:105:ARG:HD3	2.06	0.56
43:S:68:ARG:HD2	52:3:1202:U:H1'	1.86	0.56
53:1:2066:C:O2'	53:1:2067:G:H5'	2.06	0.56
5:f:27:GLY:HA3	5:f:78:VAL:HB	1.88	0.56
29:E:32:LEU:HB3	29:E:40:LYS:NZ	2.20	0.56
31:G:160:LEU:HD22	31:G:175:ALA:HB2	1.87	0.56
41:Q:109:ARG:HH11	52:3:537:G:H5''	1.71	0.56
52:3:78:A:H2'	52:3:79:G:O4'	2.05	0.56
52:3:1301:U:O2	52:3:1301:U:H2'	2.05	0.56
53:1:193:U:H2'	53:1:194:G:H8	1.71	0.56
53:1:1657:U:H2'	53:1:1658:C:C6	2.41	0.56
54:2:48:U:H2'	54:2:49:C:C6	2.41	0.56
58:8:171:VAL:HG13	58:8:188:LYS:HE3	1.87	0.56
7:h:67:THR:HG23	7:h:68:PRO:HD3	1.88	0.56
8:i:135:MET:HE1	53:1:1062:G:N3	2.21	0.56
11:l:93:ASN:C	11:l:95:LEU:H	2.13	0.56
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.88	0.56
30:F:23:ILE:HD12	30:F:23:ILE:N	2.21	0.56
33:I:67:LEU:HB3	52:3:546:A:OP2	2.05	0.56
49:Y:80:ALA:HA	49:Y:83:ASN:ND2	2.20	0.56
51:a:195:ALA:O	51:a:198:LYS:HG3	2.06	0.56
52:3:225:C:C2'	52:3:226:G:H5''	2.36	0.56
50:Z:32:ARG:HG3	50:Z:33:ARG:HG2	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:737:C:H2'	52:3:738:C:C6	2.41	0.56
52:3:1323:G:H2'	52:3:1324:A:C8	2.41	0.56
53:1:2588:G:H2'	53:1:2589:A:H5'	1.88	0.56
53:1:2134:A:C6	53:1:2157:G:H4'	2.41	0.55
3:d:40:ARG:HD3	3:d:92:HIS:HB2	1.88	0.55
7:h:46:ARG:HH21	7:h:95:LEU:HD21	1.71	0.55
18:s:4:ILE:HG22	18:s:106:VAL:HG22	1.88	0.55
32:H:107:LYS:HD3	32:H:143:LEU:HD13	1.86	0.55
42:R:88:LEU:HA	42:R:91:ARG:HE	1.71	0.55
53:1:433:C:O2'	53:1:434:U:H5'	2.05	0.55
53:1:532:A:H2'	53:1:532:A:N3	2.21	0.55
3:d:163:ASN:HB2	53:1:322:A:OP2	2.05	0.55
36:L:57:GLU:HG3	36:L:58:LEU:H	1.71	0.55
33:I:82:LYS:HD2	52:3:5:U:O4	2.06	0.55
34:J:61:LYS:HE2	34:J:65:LYS:HZ1	1.71	0.55
47:W:36:GLY:O	47:W:62:ARG:NH2	2.39	0.55
52:3:1086:U:H2'	52:3:1087:G:H8	1.71	0.55
53:1:2257:U:H2'	53:1:2258:C:C6	2.42	0.55
2:c:4:LEU:HD23	2:c:29:VAL:HG21	1.88	0.55
21:v:20:LEU:H	21:v:20:LEU:HD23	1.69	0.55
35:K:3:HIS:HB2	35:K:92:THR:HA	1.88	0.55
46:V:59:GLU:HB3	46:V:75:VAL:HB	1.88	0.55
48:X:79:TYR:CE1	52:3:1226:C:H4'	2.42	0.55
53:1:581:C:H2'	53:1:582:A:C8	2.41	0.55
4:e:58:ALA:HB1	4:e:139:GLU:HG3	1.89	0.55
12:m:75:GLU:CD	53:1:957:C:H5'	2.32	0.55
14:o:51:ALA:HB3	14:o:78:VAL:HG22	1.87	0.55
19:t:55:VAL:HG23	19:t:86:THR:O	2.07	0.55
26:B:46:GLY:HA3	26:B:54:ILE:CG2	2.36	0.55
34:J:15:ILE:HG22	34:J:35:LEU:O	2.06	0.55
35:K:48:ALA:H	47:W:65:SER:HG	1.54	0.55
36:L:78:ARG:HB3	36:L:83:THR:HG23	1.88	0.55
36:L:87:PRO:HG3	36:L:148:LYS:HA	1.89	0.55
40:P:82:GLU:HG2	40:P:108:ASN:OD1	2.07	0.55
41:Q:39:THR:HG21	41:Q:89:LEU:HD21	1.88	0.55
52:3:1346:A:H2'	52:3:1346:A:N3	2.22	0.55
53:1:696:G:O2'	53:1:697:G:H5'	2.07	0.55
53:1:2443:C:H2'	53:1:2444:G:H8	1.71	0.55
53:1:2584:U:H2'	53:1:2585:U:C6	2.42	0.55
57:7:68:C:H2'	57:7:69:G:C8	2.41	0.55
1:b:260:LYS:HA	1:b:263:ASP:OD1	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:4:LEU:HD13	2:c:101:PHE:CE2	2.41	0.55
5:f:173:ALA:O	5:f:174:LYS:HG2	2.06	0.55
13:n:2:ARG:HA	13:n:5:LYS:HE2	1.89	0.55
13:n:10:LEU:HD11	13:n:43:GLU:OE1	2.06	0.55
15:p:89:GLY:HA2	15:p:111:GLU:HA	1.87	0.55
34:J:123:LEU:HD12	34:J:123:LEU:O	2.07	0.55
34:J:156:ARG:HD3	37:M:42:GLU:HG3	1.88	0.55
52:3:784:A:H4'	53:1:1837:C:OP1	2.05	0.55
52:3:1379:G:O2'	52:3:1380:U:H5'	2.05	0.55
53:1:2475:C:H2'	53:1:2476:A:H5'	1.87	0.55
53:1:2724:U:H2'	53:1:2725:A:C8	2.40	0.55
55:6:9:G:H5'	55:6:46:G:H1'	1.87	0.55
2:c:5:VAL:H	2:c:32:ASN:HD21	1.53	0.55
20:u:3:LYS:O	20:u:93:ARG:NH2	2.39	0.55
24:y:41:HIS:CE1	53:1:96:C:H4'	2.41	0.55
42:R:28:ARG:HH21	42:R:62:PHE:HB2	1.72	0.55
52:3:983:A:H1'	52:3:1049:U:O2	2.07	0.55
52:3:1369:C:H2'	52:3:1370:G:C8	2.41	0.55
53:1:119:A:H4'	53:1:120:U:H5'	1.89	0.55
53:1:1806:C:H2'	53:1:1807:G:O4'	2.06	0.55
3:d:181:ILE:HD13	11:l:6:LEU:HD11	1.89	0.55
4:e:26:GLN:NE2	54:2:57:A:H4'	2.22	0.55
6:g:130:VAL:HG23	6:g:142:VAL:HG13	1.89	0.55
9:j:4:PHE:HB3	16:q:63:ARG:HH12	1.72	0.55
15:p:38:ARG:NH2	52:3:345:C:H5'	2.22	0.55
18:s:57:ASN:HD21	53:1:495:G:C1'	2.20	0.55
32:H:80:GLY:O	32:H:84:GLU:HG2	2.07	0.55
37:M:63:LYS:HG3	37:M:70:VAL:HG21	1.88	0.55
45:U:75:ILE:O	45:U:78:VAL:HG12	2.07	0.55
53:1:940:G:H2'	53:1:941:A:H5''	1.89	0.55
53:1:1509:A:H2'	53:1:1510:G:C8	2.42	0.55
53:1:2238:G:H2'	53:1:2238:G:N3	2.22	0.55
54:2:63:C:H2'	54:2:64:G:C8	2.42	0.55
2:c:157:LYS:HE2	53:1:2619:C:OP1	2.07	0.55
52:3:948:C:H2'	52:3:949:A:H8	1.71	0.55
53:1:834:G:H1'	53:1:2358:A:N3	2.22	0.55
53:1:1830:C:H2'	53:1:1831:G:H8	1.72	0.55
53:1:2088:A:H2'	53:1:2089:C:C6	2.42	0.55
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.88	0.54
4:e:79:ARG:NH2	55:5:19:G:H1	2.05	0.54
18:s:88:ARG:HG3	18:s:94:ASP:OD2	2.06	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:77:A:H2'	52:3:78:A:C8	2.41	0.54
52:3:360:G:O2'	52:3:361:G:H5'	2.06	0.54
7:h:48:ALA:HB3	7:h:51:TYR:CE2	2.42	0.54
19:t:8:LEU:HD13	24:y:21:LEU:HB3	1.89	0.54
29:E:18:LYS:HG3	53:1:651:G:H5'	1.89	0.54
52:3:252:U:O2	52:3:252:U:H2'	2.06	0.54
53:1:2029:G:O6	53:1:2032:G:H5''	2.07	0.54
58:8:336:THR:CG2	58:8:338:VAL:HG23	2.37	0.54
15:p:30:TRP:CZ3	15:p:37:LYS:HG2	2.43	0.54
26:B:1:ALA:H3	53:1:2056:G:N2	2.04	0.54
48:X:68:HIS:HB3	48:X:72:GLU:HG3	1.89	0.54
53:1:2533:U:H2'	53:1:2534:A:O4'	2.08	0.54
7:h:67:THR:CG2	7:h:68:PRO:HD3	2.37	0.54
9:j:7:LYS:HG2	53:1:538:A:H4'	1.89	0.54
34:J:134:ASN:ND2	52:3:19:A:OP1	2.40	0.54
52:3:1258:G:H2'	52:3:1259:C:C6	2.42	0.54
53:1:476:G:H4'	53:1:502:A:H61	1.73	0.54
4:e:73:VAL:HG12	4:e:78:ILE:HD11	1.90	0.54
10:k:31:ARG:HG3	10:k:31:ARG:NH1	2.23	0.54
13:n:47:VAL:C	13:n:50:PRO:HD2	2.33	0.54
23:x:33:HIS:HE1	53:1:2200:C:H4'	1.72	0.54
23:x:58:ILE:HA	23:x:66:VAL:HG21	1.90	0.54
27:C:22:THR:HG21	53:1:2286:G:H1	1.72	0.54
48:X:21:ALA:HB2	48:X:30:LEU:HD21	1.89	0.54
53:1:353:C:H2'	53:1:354:A:H8	1.73	0.54
57:7:51:U:H2'	57:7:52:G:H8	1.71	0.54
58:8:133:VAL:HB	58:8:170:ILE:HG12	1.88	0.54
45:U:5:ARG:HD2	52:3:376:G:H4'	1.89	0.54
51:a:215:SER:HB3	51:a:221:GLY:HA2	1.90	0.54
52:3:1128:C:O2'	52:3:1129:C:H5'	2.07	0.54
53:1:2561:U:H2'	53:1:2562:U:C4'	2.37	0.54
3:d:147:LEU:HB3	3:d:186:VAL:HG12	1.90	0.54
17:r:79:ARG:HD2	53:1:564:C:OP2	2.07	0.54
23:x:15:ASN:ND2	23:x:23:ALA:HB1	2.23	0.54
33:I:108:ALA:O	33:I:164:ARG:NH2	2.41	0.54
35:K:41:ASP:OD2	35:K:58:HIS:NE2	2.41	0.54
35:K:72:ASP:OD1	35:K:73:GLU:N	2.41	0.54
42:R:13:HIS:HB2	42:R:16:ILE:HD13	1.88	0.54
48:X:54:ARG:HG3	48:X:55:GLN:HG2	1.89	0.54
52:3:211:G:H2'	52:3:212:G:H5'	1.88	0.54
52:3:537:G:H2'	52:3:538:G:C8	2.43	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1162:C:H2'	52:3:1163:A:C8	2.42	0.54
55:5:75:C:H2'	55:5:76:A:H5''	1.89	0.54
58:8:283:LYS:HB2	58:8:286:GLU:HG3	1.89	0.54
5:f:96:ALA:HB3	5:f:103:ASN:HB3	1.90	0.54
11:l:110:VAL:HB	11:l:127:VAL:HG13	1.90	0.54
17:r:49:ILE:HG22	17:r:54:VAL:N	2.22	0.54
25:z:30:ARG:HD2	53:1:1158:C:H5''	1.89	0.54
35:K:12:PRO:O	35:K:15:SER:OG	2.24	0.54
37:M:72:GLU:HB3	37:M:129:ALA:HB3	1.89	0.54
46:V:37:ILE:N	46:V:37:ILE:HD12	2.23	0.54
51:a:4:LEU:HD12	51:a:8:MET:HG3	1.89	0.54
52:3:1352:C:H2'	52:3:1353:G:H8	1.73	0.54
53:1:593:U:H2'	53:1:594:U:C6	2.43	0.54
53:1:2093:G:N7	53:1:2225:A:H2'	2.22	0.54
2:c:24:VAL:HG21	2:c:188:LEU:HB3	1.90	0.54
12:m:3:GLN:HE21	12:m:92:TRP:HE1	1.55	0.54
31:G:5:MET:HA	31:G:8:MET:HE2	1.88	0.54
52:3:521:G:O2'	52:3:522:C:H5'	2.08	0.54
53:1:2071:A:H2'	53:1:2072:C:C6	2.43	0.54
53:1:2183:A:H2'	53:1:2184:A:C8	2.43	0.54
53:1:2547:A:H2'	53:1:2548:U:C6	2.43	0.54
6:g:58:LEU:O	6:g:61:VAL:HG22	2.08	0.54
31:G:41:ASN:HD22	31:G:44:LYS:HB2	1.73	0.54
34:J:55:VAL:HG12	34:J:56:PRO:HD3	1.88	0.54
36:L:146:ALA:HB1	55:6:40:C:H4'	1.89	0.54
53:1:215:G:C4'	53:1:216:A:H4'	2.37	0.54
35:K:20:GLY:O	35:K:23:GLU:HG3	2.08	0.53
39:O:27:GLU:HG3	39:O:31:ARG:HH21	1.72	0.53
39:O:67:ILE:HG13	39:O:67:ILE:O	2.08	0.53
44:T:4:THR:HG23	52:3:659:U:H5''	1.88	0.53
52:3:360:G:OP2	58:8:283:LYS:HE2	2.08	0.53
52:3:422:C:H4'	52:3:423:G:H5''	1.90	0.53
53:1:1181:U:H2'	53:1:1182:G:C8	2.43	0.53
55:5:6:G:O2'	55:5:7:G:H5'	2.08	0.53
55:6:71:C:H2'	55:6:72:A:C8	2.42	0.53
58:8:93:ILE:HD12	58:8:93:ILE:N	2.22	0.53
3:d:176:ASP:N	3:d:176:ASP:OD1	2.41	0.53
10:k:102:PRO:HB3	10:k:121:GLU:HB3	1.89	0.53
15:p:13:LYS:NZ	15:p:80:VAL:HG23	2.23	0.53
31:G:89:PHE:HB3	31:G:150:ILE:HG22	1.89	0.53
52:3:70:U:H4'	52:3:71:A:H8	1.72	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:278:A:H2'	53:1:278:A:N3	2.24	0.53
53:1:1067:A:H2'	53:1:1067:A:N3	2.24	0.53
53:1:1078:U:C4'	53:1:1079:C:H5''	2.37	0.53
53:1:2196:C:O2'	53:1:2197:U:H5'	2.08	0.53
53:1:2705:A:H2'	53:1:2706:A:O4'	2.08	0.53
53:1:2834:G:O2'	53:1:2835:A:H5'	2.08	0.53
54:2:19:C:H2'	54:2:20:G:C8	2.43	0.53
17:r:55:ASP:OD1	17:r:56:GLY:N	2.38	0.53
21:v:18:ARG:HA	21:v:21:ARG:HD2	1.90	0.53
34:J:39:GLY:HA3	34:J:116:VAL:HB	1.90	0.53
49:Y:67:HIS:CE1	52:3:132:C:H4'	2.44	0.53
53:1:729:G:H4'	53:1:763:G:C5'	2.38	0.53
18:s:57:ASN:OD1	53:1:495:G:H1'	2.09	0.53
22:w:36:GLN:OE1	22:w:41:PHE:HB2	2.09	0.53
35:K:69:GLU:O	35:K:72:ASP:OD1	2.25	0.53
53:1:288:U:H2'	53:1:289:G:C8	2.43	0.53
53:1:473:G:O2'	53:1:474:G:H5'	2.09	0.53
54:2:3:C:H3'	54:2:4:C:C5'	2.37	0.53
1:b:48:ILE:HG23	1:b:48:ILE:O	2.09	0.53
32:H:156:LEU:HD12	32:H:156:LEU:O	2.08	0.53
39:O:6:ILE:HD12	39:O:6:ILE:N	2.24	0.53
39:O:77:VAL:HG23	39:O:78:GLU:HG2	1.90	0.53
40:P:16:SER:O	40:P:78:ILE:HD12	2.09	0.53
41:Q:13:ARG:HE	41:Q:14:LYS:N	2.06	0.53
47:W:11:ARG:HB3	52:3:845:A:O2'	2.09	0.53
52:3:337:G:H2'	52:3:338:A:C8	2.44	0.53
52:3:390:U:H2'	52:3:391:G:H8	1.72	0.53
53:1:657:U:H2'	53:1:658:U:C6	2.43	0.53
53:1:1344:U:H3'	53:1:1345:C:H5'	1.90	0.53
53:1:1900:A:O4'	53:1:1970:A:H5''	2.09	0.53
58:8:246:VAL:HG11	58:8:368:ALA:HB2	1.89	0.53
6:g:5:LEU:HD22	6:g:13:GLY:HA3	1.90	0.53
17:r:49:ILE:HG22	17:r:54:VAL:H	1.72	0.53
22:w:74:LYS:CE	53:1:857:G:H5''	2.38	0.53
26:B:51:ARG:HD2	26:B:53:VAL:HG22	1.91	0.53
39:O:100:ILE:HD12	39:O:100:ILE:N	2.23	0.53
52:3:56:U:H2'	52:3:57:G:H8	1.73	0.53
53:1:1020:A:C1'	53:1:1021:A:OP2	2.52	0.53
53:1:2073:C:O2'	53:1:2074:U:H5'	2.09	0.53
58:8:13:VAL:HG23	58:8:75:ARG:NE	2.23	0.53
3:d:45:ALA:HB3	53:1:38:A:H4'	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:68:ALA:HA	53:1:1255:U:C6	2.44	0.53
12:m:12:MET:SD	12:m:71:LYS:HG3	2.48	0.53
34:J:131:ASN:HD22	52:3:19:A:P	2.32	0.53
46:V:48:GLU:O	46:V:49:ASN:C	2.51	0.53
52:3:1218:C:H2'	52:3:1219:A:H8	1.72	0.53
53:1:226:A:H2'	53:1:227:A:O4'	2.08	0.53
53:1:970:U:H2'	53:1:971:G:H8	1.72	0.53
3:d:76:PRO:HA	3:d:82:GLY:HA2	1.91	0.53
13:n:98:LEU:HD21	26:B:53:VAL:CG1	2.37	0.53
18:s:53:SER:O	18:s:57:ASN:HB2	2.09	0.53
39:O:44:THR:HG22	39:O:70:HIS:HA	1.90	0.53
52:3:537:G:H2'	52:3:538:G:H8	1.74	0.53
53:1:1720:U:H2'	53:1:1721:G:O4'	2.09	0.53
53:1:2128:G:H1'	53:1:2173:A:N3	2.24	0.53
53:1:2636:C:H2'	53:1:2637:U:C6	2.44	0.53
3:d:131:THR:HG23	53:1:321:U:H5''	1.90	0.53
28:D:9:VAL:HG12	53:1:1309:G:OP1	2.09	0.53
36:L:86:VAL:HG12	36:L:150:PHE:HB3	1.90	0.53
39:O:12:ALA:HB2	39:O:96:VAL:HG23	1.91	0.53
40:P:44:ALA:HB3	40:P:69:CYS:HB2	1.91	0.53
41:Q:49:ARG:NH2	52:3:522:C:H41	2.07	0.53
42:R:25:GLY:N	52:3:1329:A:H5''	2.24	0.53
42:R:28:ARG:NH2	42:R:62:PHE:HB2	2.24	0.53
47:W:52:ARG:HB3	47:W:56:ARG:HH22	1.74	0.53
52:3:291:U:H2'	52:3:292:G:H8	1.73	0.53
53:1:616:A:H2'	53:1:617:G:O4'	2.09	0.53
53:1:807:U:H2'	53:1:808:G:C8	2.42	0.53
53:1:2176:A:H2'	53:1:2177:C:C6	2.43	0.53
53:1:2629:U:O2'	53:1:2630:G:H5''	2.09	0.53
1:b:13:ARG:NH1	53:1:1977:A:H2	2.06	0.53
3:d:164:LEU:HD22	3:d:167:VAL:HG21	1.90	0.53
10:k:70:ARG:HG2	10:k:76:VAL:HG22	1.90	0.53
13:n:37:THR:HG22	13:n:40:LYS:HD2	1.90	0.53
20:u:42:LYS:HD2	53:1:499:U:H5''	1.90	0.53
24:y:43:LEU:HD23	53:1:61:C:H5''	1.90	0.53
37:M:60:LEU:HD12	37:M:60:LEU:N	2.23	0.53
40:P:12:ARG:HD3	40:P:12:ARG:N	2.23	0.53
40:P:118:ASN:OD1	52:3:718:A:H5'	2.09	0.53
41:Q:27:PRO:HB2	41:Q:28:GLN:OE1	2.08	0.53
46:V:5:ARG:HH11	52:3:636:U:C4'	2.21	0.53
52:3:437:U:O2'	52:3:438:U:H5'	2.09	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1259:C:H3'	52:3:1260:G:C5'	2.32	0.53
53:1:466:A:H2'	53:1:467:G:H5'	1.91	0.53
53:1:1911:U:H2'	53:1:1918:A:N1	2.23	0.53
1:b:5:CYS:SG	1:b:12:ARG:NH2	2.82	0.52
40:P:33:ILE:HD12	40:P:73:VAL:HG11	1.91	0.52
52:3:664:G:H22	52:3:741:G:H1	1.55	0.52
52:3:1052:U:H2'	52:3:1200:C:H41	1.74	0.52
52:3:1540:U:O2	52:3:1540:U:H3'	2.08	0.52
53:1:200:U:H2'	53:1:201:C:H5'	1.91	0.52
53:1:2111:U:H5'	53:1:2112:G:OP2	2.09	0.52
5:f:77:GLY:HA2	5:f:81:GLY:HA2	1.90	0.52
5:f:86:LEU:HD11	5:f:144:ALA:HA	1.91	0.52
8:i:93:ASN:HD22	53:1:1077:A:C4'	2.13	0.52
8:i:96:LYS:HE2	8:i:96:LYS:HA	1.91	0.52
21:v:76:ASP:H	21:v:90:ASP:HB2	1.73	0.52
52:3:219:U:H2'	52:3:220:G:H8	1.74	0.52
52:3:1259:C:C3'	52:3:1260:G:H5''	2.30	0.52
53:1:2065:C:H1'	53:1:2449:U:H3	1.74	0.52
54:2:60:C:H2'	54:2:61:G:C8	2.44	0.52
31:G:5:MET:O	31:G:9:LEU:HD12	2.09	0.52
34:J:107:GLY:CA	52:3:9:G:H5'	2.26	0.52
43:S:56:PRO:HA	43:S:59:GLN:HG2	1.91	0.52
48:X:77:ARG:HD2	52:3:1225:A:O2'	2.09	0.52
52:3:1435:G:H2'	52:3:1436:U:C6	2.44	0.52
53:1:758:C:O2	53:1:758:C:H2'	2.09	0.52
53:1:948:C:H2'	53:1:949:G:H8	1.73	0.52
55:5:75:C:C2'	55:5:76:A:H5''	2.40	0.52
58:8:367:ILE:HG13	58:8:368:ALA:N	2.24	0.52
5:f:16:VAL:HG21	5:f:49:LEU:HD21	1.91	0.52
5:f:93:TYR:C	5:f:94:ARG:HD2	2.33	0.52
10:k:1:MET:CE	10:k:67:LYS:HE2	2.39	0.52
34:J:92:ARG:O	34:J:93:VAL:C	2.52	0.52
34:J:161:GLU:O	34:J:164:LEU:HG	2.10	0.52
35:K:86:ARG:HD3	47:W:63:TYR:O	2.10	0.52
39:O:43:PRO:HA	52:3:1151:A:H5'	1.91	0.52
46:V:80:LYS:HG2	46:V:81:ALA:H	1.73	0.52
52:3:579:A:H2'	52:3:580:C:C6	2.45	0.52
52:3:763:G:H2'	52:3:764:C:C6	2.44	0.52
52:3:1308:U:H2'	52:3:1309:G:C8	2.43	0.52
13:n:47:VAL:O	13:n:50:PRO:HD2	2.09	0.52
18:s:17:VAL:HG12	18:s:76:VAL:HG21	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:113:LYS:N	32:H:184:ASN:HD22	2.07	0.52
53:1:158:U:H2'	53:1:159:G:O4'	2.10	0.52
7:h:23:LEU:HD21	7:h:96:PHE:HB2	1.90	0.52
22:w:32:ILE:HG22	53:1:2354:C:O2'	2.10	0.52
39:O:57:VAL:O	39:O:58:ASN:HB2	2.09	0.52
52:3:1506:U:O2'	52:3:1507:A:H5'	2.08	0.52
53:1:255:A:H2'	53:1:256:A:O4'	2.09	0.52
53:1:548:G:H2'	53:1:549:G:O4'	2.08	0.52
53:1:1506:U:H2'	53:1:1507:C:C6	2.45	0.52
57:7:25:C:C3'	57:7:26:A:H5''	2.34	0.52
19:t:61:LEU:HD21	19:t:82:LYS:HG3	1.90	0.52
26:B:24:VAL:HG13	26:B:25:THR:H	1.74	0.52
33:I:138:PRO:HB3	33:I:183:ARG:HA	1.92	0.52
36:L:27:ASN:ND2	52:3:1374:A:OP1	2.38	0.52
52:3:665:A:O4'	52:3:733:G:H1'	2.09	0.52
52:3:1251:A:H2'	52:3:1252:A:C8	2.45	0.52
53:1:554:U:H2'	53:1:555:G:O4'	2.10	0.52
53:1:1268:A:H2'	53:1:1269:A:O4'	2.08	0.52
53:1:1278:C:H2'	53:1:1279:G:H8	1.75	0.52
53:1:1300:G:H4'	53:1:1301:A:C5'	2.40	0.52
53:1:1827:U:H2'	53:1:1828:G:O4'	2.09	0.52
53:1:2360:G:H2'	53:1:2361:G:H5'	1.92	0.52
53:1:2538:C:H2'	53:1:2539:C:C6	2.45	0.52
53:1:2588:G:C2'	53:1:2589:A:H5'	2.39	0.52
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.92	0.52
1:b:119:VAL:HG12	1:b:130:PRO:HD2	1.91	0.52
5:f:163:TYR:HB2	5:f:166:GLU:HB2	1.91	0.52
10:k:113:MET:SD	10:k:116:ILE:HD11	2.50	0.52
13:n:72:ASP:HB3	13:n:75:ILE:CG2	2.39	0.52
36:L:56:SER:HB3	36:L:59:GLU:HG2	1.91	0.52
42:R:6:ILE:HG23	42:R:7:ASN:H	1.75	0.52
48:X:38:THR:HG22	48:X:69:LYS:HG2	1.91	0.52
52:3:890:G:O2'	52:3:891:U:H6	1.93	0.52
53:1:1077:A:C2'	53:1:1078:U:H5'	2.38	0.52
53:1:2244:U:H2'	53:1:2245:U:O4'	2.09	0.52
3:d:69:ARG:HD3	53:1:674:G:H1'	1.92	0.52
7:h:34:THR:HG21	53:1:1057:A:H1'	1.92	0.52
17:r:51:VAL:HG12	17:r:52:PRO:HD2	1.91	0.52
20:u:3:LYS:HB3	20:u:4:ILE:HD12	1.91	0.52
32:H:171:ARG:HG3	52:3:1107:C:P	2.50	0.52
51:a:169:GLY:C	51:a:170:ILE:HD12	2.35	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1736:U:H2'	53:1:1737:G:O4'	2.09	0.52
3:d:45:ALA:CB	53:1:38:A:H4'	2.39	0.52
8:i:30:GLN:HG2	8:i:31:GLY:H	1.75	0.52
25:z:6:ILE:HD12	25:z:6:ILE:N	2.25	0.52
31:G:67:LEU:HD23	31:G:157:PRO:HB3	1.92	0.52
52:3:358:U:H2'	52:3:359:G:H8	1.75	0.52
52:3:405:U:C3'	52:3:406:G:H5'	2.30	0.52
52:3:1342:C:H2'	52:3:1343:G:H8	1.74	0.52
52:3:1399:C:H4'	52:3:1400:C:H3'	1.92	0.52
53:1:2515:C:H2'	53:1:2516:A:H8	1.74	0.52
53:1:2679:A:O2'	53:1:2680:U:H5'	2.09	0.52
55:6:36:U:C2'	55:6:37:A:H5'	2.38	0.52
57:7:9:A:O2'	57:7:46:G:H4'	2.10	0.52
21:v:19:ARG:NH2	54:2:95:U:OP2	2.42	0.51
26:B:1:ALA:H3	53:1:2056:G:H21	1.57	0.51
34:J:24:VAL:HG22	34:J:25:LYS:N	2.25	0.51
46:V:26:ARG:NE	46:V:28:VAL:HB	2.25	0.51
52:3:195:A:H2'	52:3:196:A:C8	2.44	0.51
52:3:211:G:C2'	52:3:212:G:H5'	2.39	0.51
52:3:1323:G:H2'	52:3:1324:A:H8	1.73	0.51
53:1:1300:G:H4'	53:1:1301:A:H5'	1.92	0.51
54:2:65:U:H3'	54:2:108:A:N6	2.26	0.51
58:8:114:PRO:O	58:8:118:GLU:HG2	2.10	0.51
14:o:56:LYS:HB3	14:o:60:GLU:OE2	2.10	0.51
19:t:2:ILE:HD11	53:1:144:A:C4'	2.40	0.51
28:D:34:ARG:HH11	28:D:39:ARG:HD2	1.74	0.51
38:N:29:ILE:N	38:N:29:ILE:HD12	2.25	0.51
52:3:321:A:H2	52:3:332:G:H22	1.59	0.51
52:3:358:U:H2'	52:3:359:G:C8	2.45	0.51
52:3:1429:A:H2'	52:3:1430:A:C8	2.43	0.51
54:2:63:C:H2'	54:2:64:G:H8	1.74	0.51
52:3:422:C:H5'	52:3:423:G:C4	2.46	0.51
52:3:621:A:H2'	52:3:622:A:C8	2.45	0.51
53:1:208:C:H2'	53:1:209:C:C6	2.45	0.51
53:1:2475:C:C2'	53:1:2476:A:H5'	2.40	0.51
55:5:76:A:H5'	55:5:76:A:H8	1.71	0.51
57:7:16:U:H1'	57:7:60:U:H1'	1.92	0.51
9:j:78:THR:HB	53:1:2641:G:H5''	1.92	0.51
14:o:56:LYS:HA	14:o:59:ALA:HB3	1.93	0.51
31:G:22:TRP:HE1	52:3:830:G:C5'	2.22	0.51
53:1:69:C:O2'	53:1:70:G:H5'	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2480:C:H2'	53:1:2481:G:O4'	2.11	0.51
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.11	0.51
16:q:25:GLY:O	16:q:29:ARG:NH1	2.43	0.51
21:v:20:LEU:HA	21:v:23:ALA:HB3	1.92	0.51
36:L:78:ARG:HB3	36:L:83:THR:HA	1.93	0.51
38:N:49:GLN:N	38:N:50:PRO:HD2	2.25	0.51
43:S:60:ARG:HH22	52:3:977:A:P	2.33	0.51
46:V:5:ARG:HD3	52:3:636:U:H5''	1.92	0.51
52:3:711:G:O2'	52:3:712:A:H5'	2.09	0.51
52:3:1409:C:H2'	52:3:1410:A:H8	1.75	0.51
52:3:1493:A:H5''	52:3:1494:G:OP1	2.11	0.51
53:1:441:U:O2'	53:1:442:G:H5'	2.11	0.51
53:1:1833:C:H2'	53:1:1834:U:O4'	2.10	0.51
53:1:1906:G:C3'	53:1:1907:G:H5''	2.41	0.51
1:b:62:ARG:HH12	1:b:83:ASP:HA	1.75	0.51
4:e:25:MET:HE3	54:2:57:A:N1	2.26	0.51
13:n:49:GLU:HB2	13:n:50:PRO:HD3	1.92	0.51
13:n:103:ARG:HD2	13:n:106:ASP:OD1	2.11	0.51
28:D:12:ARG:HE	28:D:44:VAL:CG2	2.20	0.51
37:M:65:PHE:CD2	37:M:66:GLN:HG2	2.45	0.51
38:N:10:ARG:HD2	52:3:1118:U:OP1	2.10	0.51
48:X:2:ARG:HG2	52:3:1312:G:N7	2.25	0.51
52:3:1318:A:H2'	52:3:1319:A:H5'	1.93	0.51
53:1:225:C:H2'	53:1:226:A:O4'	2.11	0.51
53:1:329:G:O4'	53:1:477:A:H1'	2.10	0.51
53:1:2799:A:H2'	53:1:2800:A:H5'	1.93	0.51
55:6:41:C:H2'	55:6:42:G:C8	2.46	0.51
7:h:118:ILE:HG22	7:h:119:PRO:CD	2.41	0.51
15:p:88:ARG:HH11	15:p:112:ARG:HE	1.58	0.51
15:p:101:GLU:N	15:p:101:GLU:OE2	2.44	0.51
16:q:106:THR:O	16:q:109:VAL:HG12	2.10	0.51
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.92	0.51
22:w:66:GLU:HB3	22:w:68:LYS:HG3	1.92	0.51
44:T:86:LEU:HD23	44:T:86:LEU:H	1.75	0.51
53:1:745:G:O2'	53:1:748:G:H1'	2.11	0.51
58:8:295:LYS:HD2	58:8:298:THR:HG23	1.93	0.51
1:b:95:TYR:HE2	1:b:101:ARG:HD2	1.76	0.51
7:h:88:HIS:N	7:h:89:PRO:HD2	2.25	0.51
13:n:45:ARG:O	13:n:49:GLU:HG3	2.11	0.51
24:y:19:LEU:O	24:y:23:ARG:HB2	2.11	0.51
25:z:50:VAL:O	25:z:54:VAL:HG22	2.11	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:580:C:H2'	52:3:581:G:O4'	2.10	0.51
53:1:580:U:H2'	53:1:581:C:C6	2.46	0.51
53:1:703:U:H2'	53:1:704:G:O4'	2.11	0.51
53:1:1073:A:H2'	53:1:1074:G:O4'	2.11	0.51
58:8:69:GLU:HG2	58:8:77:TYR:O	2.11	0.51
58:8:82:CYS:HB3	58:8:87:ASP:HB3	1.93	0.51
58:8:120:ILE:HD12	58:8:157:LEU:HD23	1.92	0.51
8:i:13:ALA:HA	8:i:53:PRO:HA	1.93	0.51
31:G:81:ASP:HA	31:G:84:LEU:HG	1.92	0.51
33:I:38:GLY:HA2	52:3:542:G:H5'	1.92	0.51
37:M:75:GLN:HG3	37:M:127:TYR:HB2	1.91	0.51
40:P:91:GLY:C	40:P:93:GLU:H	2.19	0.51
41:Q:41:PRO:HG3	41:Q:49:ARG:HD3	1.93	0.51
43:S:27:LYS:HE2	52:3:1317:C:OP2	2.11	0.51
52:3:880:C:H2'	52:3:881:G:C8	2.46	0.51
53:1:523:C:H2'	53:1:524:G:C8	2.46	0.51
53:1:1103:A:H2'	53:1:1103:A:N3	2.25	0.51
53:1:1441:G:H2'	53:1:1442:U:C6	2.46	0.51
4:e:66:ILE:HD12	4:e:66:ILE:H	1.75	0.51
7:h:116:GLU:O	7:h:117:LEU:HD23	2.11	0.51
26:B:47:TYR:CZ	26:B:52:LYS:HD3	2.46	0.51
45:U:28:ARG:HH12	52:3:390:U:H4'	1.76	0.51
46:V:16:MET:HE1	46:V:21:VAL:HG12	1.93	0.51
46:V:18:LYS:HE2	46:V:49:ASN:H	1.76	0.51
52:3:123:U:H5''	52:3:311:C:O2'	2.11	0.51
52:3:945:G:H2'	52:3:945:G:N3	2.24	0.51
52:3:1251:A:O2'	52:3:1370:G:H5'	2.11	0.51
52:3:1354:U:H2'	52:3:1355:G:H8	1.75	0.51
53:1:174:U:H2'	53:1:175:G:C8	2.46	0.51
53:1:948:C:H2'	53:1:949:G:C8	2.46	0.51
4:e:24:VAL:O	4:e:27:VAL:HG22	2.10	0.50
7:h:55:VAL:HA	53:1:1084:A:H4'	1.91	0.50
21:v:77:VAL:HG12	21:v:89:ILE:HG12	1.93	0.50
34:J:75:LEU:HD23	34:J:75:LEU:H	1.76	0.50
40:P:126:ARG:O	50:Z:34:ARG:NH2	2.43	0.50
52:3:458:U:H2'	52:3:459:A:C8	2.46	0.50
52:3:539:A:H2'	52:3:540:G:C8	2.46	0.50
52:3:868:C:H2'	52:3:869:G:O4'	2.10	0.50
52:3:1220:G:H2'	52:3:1221:G:C8	2.45	0.50
53:1:239:C:H2'	53:1:240:C:O4'	2.11	0.50
53:1:353:C:H2'	53:1:354:A:C8	2.46	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1285:A:H2'	53:1:1286:A:H5'	1.93	0.50
53:1:1951:U:H2'	53:1:1953:A:OP2	2.11	0.50
53:1:2743:U:C2'	53:1:2744:G:H5''	2.41	0.50
6:g:19:VAL:HG23	6:g:21:VAL:HG13	1.92	0.50
25:z:35:VAL:HG22	25:z:36:GLU:H	1.77	0.50
29:E:54:LEU:O	29:E:57:VAL:HG22	2.11	0.50
37:M:37:ASN:O	37:M:41:GLU:HG2	2.11	0.50
49:Y:70:LYS:HA	49:Y:73:ARG:HH12	1.76	0.50
53:1:705:A:C2	53:1:727:A:H1'	2.46	0.50
53:1:2266:A:H4'	53:1:2267:A:N3	2.26	0.50
53:1:2749:A:OP2	53:1:2751:G:H5''	2.12	0.50
1:b:129:LEU:N	1:b:129:LEU:HD23	2.27	0.50
2:c:155:VAL:HG21	53:1:2618:G:H21	1.76	0.50
21:v:56:PHE:CE1	21:v:61:LEU:HD21	2.47	0.50
37:M:28:SER:OG	37:M:29:SER:N	2.44	0.50
41:Q:109:ARG:NH1	52:3:537:G:H5''	2.26	0.50
42:R:16:ILE:HD12	42:R:16:ILE:N	2.25	0.50
49:Y:70:LYS:HA	49:Y:73:ARG:NH1	2.26	0.50
53:1:74:A:H4'	53:1:75:G:O5'	2.11	0.50
53:1:1857:G:N2	53:1:1884:G:H2'	2.25	0.50
53:1:1956:U:H2'	53:1:1957:C:H5'	1.93	0.50
53:1:2469:A:H2'	53:1:2470:G:O4'	2.10	0.50
58:8:133:VAL:HG11	58:8:154:VAL:HG11	1.93	0.50
1:b:226:PRO:HD3	1:b:233:GLY:N	2.27	0.50
2:c:135:GLY:HA2	53:1:743:A:OP1	2.11	0.50
7:h:64:VAL:O	7:h:67:THR:HG22	2.11	0.50
8:i:105:LEU:HD23	8:i:108:ILE:HD12	1.93	0.50
10:k:58:LEU:HD11	10:k:86:LEU:HD23	1.93	0.50
15:p:108:ARG:C	15:p:109:ILE:HD12	2.37	0.50
20:u:4:ILE:HD12	20:u:4:ILE:N	2.27	0.50
34:J:61:LYS:HE2	34:J:65:LYS:NZ	2.26	0.50
43:S:8:ARG:O	43:S:12:ARG:HG3	2.12	0.50
45:U:35:ARG:HG3	45:U:35:ARG:O	2.10	0.50
52:3:45:G:H2'	52:3:46:G:H8	1.76	0.50
52:3:922:G:H2'	52:3:923:A:C8	2.47	0.50
53:1:386:G:H3'	53:1:387:U:C5'	2.42	0.50
53:1:1909:C:H2'	53:1:1910:G:C8	2.46	0.50
53:1:2039:U:H2'	53:1:2040:G:C8	2.46	0.50
53:1:2699:C:H2'	53:1:2700:A:H8	1.76	0.50
2:c:3:GLY:HA3	2:c:204:LYS:HA	1.92	0.50
12:m:66:ARG:NH1	12:m:104:GLU:OE2	2.43	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:68:ARG:HH11	17:r:90:ARG:HB2	1.76	0.50
35:K:6:ILE:HB	35:K:62:MET:HB2	1.92	0.50
35:K:91:ARG:HG3	35:K:92:THR:H	1.77	0.50
40:P:126:ARG:NH2	52:3:692:U:H5''	2.27	0.50
43:S:41:TRP:O	43:S:45:LEU:HG	2.12	0.50
52:3:1524:C:H2'	52:3:1525:G:H8	1.74	0.50
53:1:570:G:H2'	53:1:2030:A:N7	2.27	0.50
53:1:694:U:OP1	53:1:1569:A:H1'	2.12	0.50
53:1:722:A:H2'	53:1:723:C:C6	2.47	0.50
53:1:1759:A:C2	53:1:2697:G:H1'	2.47	0.50
53:1:1856:U:H2'	53:1:1857:G:O4'	2.11	0.50
53:1:2257:U:O2'	53:1:2258:C:H5'	2.11	0.50
2:c:3:GLY:C	2:c:4:LEU:HD12	2.35	0.50
7:h:31:ARG:NH1	53:1:1054:A:O3'	2.44	0.50
24:y:41:HIS:NE2	53:1:96:C:H4'	2.26	0.50
52:3:372:C:N4	52:3:387:U:H2'	2.26	0.50
52:3:1464:U:H2'	52:3:1465:A:C8	2.45	0.50
52:3:1496:C:H2'	52:3:1497:G:O4'	2.12	0.50
1:b:220:ARG:HD2	53:1:1827:U:OP2	2.12	0.50
4:e:37:MET:HE1	4:e:55:ASP:HB2	1.93	0.50
6:g:12:LEU:HD12	6:g:13:GLY:N	2.27	0.50
7:h:118:ILE:CG2	7:h:119:PRO:HD3	2.42	0.50
9:j:68:LYS:HD3	53:1:1022:G:N7	2.26	0.50
11:l:23:ILE:HG23	17:r:82:HIS:CD2	2.46	0.50
19:t:15:HIS:H	19:t:32:LEU:HA	1.77	0.50
26:B:12:ARG:NH2	53:1:517:C:OP1	2.44	0.50
33:I:12:ARG:HD2	33:I:36:ALA:HB3	1.94	0.50
43:S:30:ILE:CG2	43:S:43:ALA:HB2	2.42	0.50
52:3:77:A:H2'	52:3:78:A:H8	1.76	0.50
52:3:413:G:N2	52:3:428:G:H1'	2.26	0.50
53:1:833:A:H2'	53:1:834:G:C8	2.47	0.50
53:1:974:G:N3	53:1:974:G:H2'	2.27	0.50
53:1:2514:U:H2'	53:1:2515:C:H6	1.76	0.50
54:2:56:G:H4'	54:2:57:A:H8	1.76	0.50
4:e:132:ARG:NH2	53:1:2305:U:O2'	2.45	0.50
10:k:97:THR:OG1	10:k:98:ARG:N	2.45	0.50
26:B:49:ARG:HG2	53:1:2884:U:C6	2.46	0.50
37:M:6:ILE:O	37:M:10:LEU:HD13	2.11	0.50
52:3:1528:U:H4'	52:3:1529:G:H21	1.75	0.50
53:1:1366:A:H2'	53:1:1367:A:O4'	2.11	0.50
16:q:88:GLU:OE1	17:r:52:PRO:HB3	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:108:GLN:HA	31:G:111:LYS:HD3	1.94	0.50
32:H:67:ILE:HD12	32:H:67:ILE:N	2.26	0.50
32:H:115:VAL:HG21	32:H:201:ILE:HD11	1.93	0.50
37:M:4:ASP:HB2	37:M:80:PRO:HG3	1.94	0.50
48:X:30:LEU:H	48:X:30:LEU:HD12	1.77	0.50
48:X:79:TYR:CZ	52:3:1226:C:H4'	2.47	0.50
52:3:889:A:H5'	52:3:891:U:H1'	1.94	0.50
52:3:1106:G:O2'	52:3:1107:C:H5'	2.12	0.50
52:3:1195:C:H2'	52:3:1197:A:O4'	2.11	0.50
53:1:214:G:H2'	53:1:215:G:C8	2.47	0.50
53:1:760:G:H2'	53:1:761:A:O4'	2.11	0.50
53:1:2756:U:H4'	53:1:2757:A:OP1	2.12	0.50
58:8:56:GLU:HA	58:8:262:PHE:HZ	1.77	0.50
4:e:70:ARG:O	4:e:80:GLN:NE2	2.40	0.49
7:h:59:LEU:HG	53:1:1107:G:OP1	2.12	0.49
8:i:89:SER:HB3	8:i:135:MET:C	2.37	0.49
13:n:79:LEU:O	13:n:80:PHE:HB2	2.12	0.49
21:v:6:ALA:HB3	21:v:65:VAL:HG22	1.94	0.49
28:D:31:LEU:HD22	28:D:42:LEU:HD21	1.92	0.49
33:I:18:LEU:HD22	33:I:63:ILE:HD11	1.94	0.49
38:N:129:ARG:HE	55:5:35:A:P	2.35	0.49
46:V:18:LYS:HE2	46:V:49:ASN:N	2.27	0.49
52:3:1273:C:H2'	52:3:1274:A:O4'	2.12	0.49
52:3:1340:A:O2'	52:3:1341:U:H5'	2.12	0.49
53:1:720:U:H2'	53:1:721:A:C8	2.47	0.49
1:b:12:ARG:HG2	53:1:729:G:OP1	2.12	0.49
19:t:57:VAL:HG22	19:t:58:VAL:H	1.75	0.49
53:1:742:A:H2'	53:1:743:A:C8	2.47	0.49
53:1:1001:A:H2'	53:1:1002:G:O4'	2.12	0.49
53:1:1045:C:P	53:1:1047:G:H5'	2.52	0.49
53:1:2489:U:O2'	53:1:2490:G:H5'	2.12	0.49
53:1:2795:C:H2'	53:1:2796:U:O4'	2.11	0.49
57:7:68:C:H2'	57:7:69:G:H8	1.77	0.49
58:8:21:VAL:HG12	58:8:25:LYS:HZ3	1.76	0.49
9:j:14:ASP:OD2	9:j:15:TRP:N	2.44	0.49
9:j:14:ASP:N	9:j:52:ASP:OD1	2.45	0.49
34:J:133:ILE:O	34:J:137:ARG:HG3	2.12	0.49
36:L:2:ARG:HB3	52:3:933:G:OP2	2.12	0.49
40:P:91:GLY:O	40:P:93:GLU:N	2.41	0.49
52:3:1255:G:H2'	52:3:1279:G:H1	1.77	0.49
53:1:493:G:O2'	53:1:494:G:H5'	2.11	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:995:C:H5'	53:1:995:C:C6	2.43	0.49
53:1:1295:C:H2'	53:1:1296:G:H8	1.75	0.49
53:1:1507:C:H2'	53:1:1508:A:C4'	2.41	0.49
53:1:2589:A:H2'	53:1:2590:A:C8	2.48	0.49
53:1:2849:U:H4'	53:1:2868:A:C2	2.47	0.49
1:b:226:PRO:HD3	1:b:233:GLY:H	1.76	0.49
3:d:195:GLN:O	3:d:199:MET:HG2	2.12	0.49
14:o:33:ARG:NH2	54:2:52:A:N7	2.61	0.49
20:u:94:PHE:HD2	20:u:99:SER:OG	1.94	0.49
31:G:185:ILE:HD13	31:G:212:TYR:CD2	2.47	0.49
44:T:50:HIS:O	44:T:53:ARG:HB3	2.12	0.49
50:Z:19:LYS:HB2	50:Z:24:LYS:HE2	1.95	0.49
52:3:463:U:H3	52:3:469:C:H42	1.59	0.49
52:3:1491:G:N2	52:3:1492:A:H62	2.10	0.49
53:1:704:G:H1'	53:1:727:A:N6	2.27	0.49
53:1:1775:U:C2'	53:1:1776:G:H5'	2.42	0.49
53:1:2538:C:H2'	53:1:2539:C:H6	1.76	0.49
5:f:83:THR:HG22	5:f:133:LYS:HG2	1.94	0.49
16:q:57:ARG:O	16:q:61:ILE:HG13	2.12	0.49
19:t:57:VAL:HG22	19:t:58:VAL:N	2.28	0.49
33:I:47:LEU:HG	33:I:52:VAL:HG12	1.94	0.49
33:I:142:VAL:HG22	33:I:179:GLY:O	2.12	0.49
40:P:55:ARG:NH2	55:6:40:C:H5'	2.26	0.49
52:3:7:A:H4'	52:3:298:A:OP1	2.12	0.49
52:3:370:C:H2'	52:3:371:A:C8	2.47	0.49
52:3:381:C:H2'	52:3:382:A:O4'	2.13	0.49
52:3:695:A:H2'	52:3:696:A:C8	2.48	0.49
52:3:1342:C:H2'	52:3:1343:G:C8	2.47	0.49
53:1:859:G:O2'	53:1:860:U:C6	2.65	0.49
53:1:968:C:H2'	53:1:969:G:C8	2.47	0.49
53:1:1860:G:H2'	53:1:1861:G:H8	1.76	0.49
53:1:2272:U:H5''	53:1:2273:A:OP1	2.13	0.49
3:d:98:LYS:HE3	53:1:617:G:OP1	2.12	0.49
4:e:140:ILE:HG13	4:e:142:TYR:H	1.77	0.49
8:i:9:LYS:CD	53:1:1061:U:H5''	2.42	0.49
11:l:19:LEU:HB2	53:1:587:C:O2'	2.11	0.49
52:3:147:G:H2'	52:3:148:G:C8	2.47	0.49
53:1:528:A:C2	53:1:2042:A:H2'	2.48	0.49
53:1:580:U:H2'	53:1:581:C:H6	1.77	0.49
53:1:596:U:H2'	53:1:597:G:C8	2.47	0.49
55:5:62:C:H2'	55:5:63:G:C8	2.48	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:224:MET:SD	1:b:229:HIS:HB2	2.53	0.49
7:h:95:LEU:HD23	7:h:98:GLU:HG3	1.93	0.49
7:h:123:ILE:HG23	7:h:123:ILE:O	2.13	0.49
10:k:86:LEU:H	10:k:86:LEU:HD12	1.77	0.49
11:l:69:ARG:HH11	11:l:69:ARG:HG3	1.78	0.49
29:E:61:LEU:HD13	29:E:64:ALA:HB3	1.94	0.49
32:H:106:ARG:O	32:H:108:PRO:HD3	2.13	0.49
36:L:41:ILE:HG23	36:L:116:ALA:HB2	1.95	0.49
43:S:6:LYS:HE2	43:S:67:GLY:HA3	1.92	0.49
52:3:680:C:H2'	52:3:681:A:C8	2.48	0.49
52:3:1060:U:H3	52:3:1197:A:H61	1.61	0.49
53:1:542:C:C2'	53:1:543:G:H5''	2.40	0.49
53:1:858:G:H5'	53:1:859:G:OP2	2.12	0.49
53:1:1763:G:H2'	53:1:1764:C:H4'	1.95	0.49
53:1:1917:U:O2'	53:1:1918:A:H5'	2.12	0.49
53:1:2526:G:H2'	53:1:2527:C:C6	2.48	0.49
58:8:72:THR:HG22	58:8:73:PRO:HD2	1.95	0.49
39:O:48:ARG:HA	39:O:66:GLU:HA	1.95	0.49
41:Q:8:ARG:NH1	41:Q:8:ARG:HB2	2.27	0.49
52:3:410:G:H2'	52:3:429:U:C4	2.47	0.49
53:1:690:G:O2'	53:1:691:C:H5'	2.13	0.49
53:1:1641:A:H2'	53:1:1642:G:O4'	2.12	0.49
57:7:76:A:HO2'	60:7:101:PHE:C	2.21	0.49
11:l:19:LEU:HD22	11:l:19:LEU:N	2.28	0.49
11:l:62:PRO:HA	53:1:2393:U:O3'	2.13	0.49
45:U:75:ILE:HG23	45:U:80:LYS:HE3	1.95	0.49
52:3:49:U:O2'	52:3:50:A:H2'	2.13	0.49
52:3:162:A:C2'	52:3:163:C:H5'	2.43	0.49
52:3:225:C:H3'	52:3:226:G:H5''	1.95	0.49
52:3:370:C:H2'	52:3:371:A:H8	1.78	0.49
52:3:1202:U:C2'	52:3:1203:C:H5'	2.42	0.49
53:1:1295:C:H2'	53:1:1296:G:C8	2.48	0.49
53:1:1357:C:H2'	53:1:1358:G:O4'	2.12	0.49
55:6:67:C:H2'	55:6:68:C:C6	2.48	0.49
12:m:58:LYS:O	12:m:60:GLN:HG2	2.13	0.49
34:J:110:MET:CE	34:J:126:ALA:HB2	2.43	0.49
34:J:133:ILE:HD11	52:3:18:C:H5''	1.93	0.49
36:L:25:PHE:HZ	36:L:119:LEU:HD11	1.78	0.49
37:M:6:ILE:HD12	37:M:6:ILE:N	2.27	0.49
37:M:80:PRO:HG2	52:3:878:A:C5'	2.42	0.49
40:P:52:ARG:NH1	52:3:689:C:OP2	2.46	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:105:ALA:HA	52:3:948:C:OP1	2.13	0.49
52:3:448:A:H3'	52:3:449:G:C8	2.48	0.49
52:3:758:C:H4'	52:3:880:C:H4'	1.95	0.49
52:3:1280:A:O2'	52:3:1281:C:H5'	2.13	0.49
53:1:1775:U:H2'	53:1:1776:G:H5'	1.95	0.49
53:1:2853:C:H2'	53:1:2854:G:C8	2.47	0.49
36:L:16:LYS:HD2	36:L:17:PHE:HD1	1.78	0.48
52:3:346:G:H2'	52:3:347:G:H5'	1.94	0.48
52:3:860:A:H2'	52:3:861:G:O4'	2.13	0.48
52:3:876:C:H2'	52:3:877:G:H8	1.78	0.48
52:3:1252:A:H2'	52:3:1253:G:O4'	2.13	0.48
53:1:1365:A:N3	53:1:1365:A:H2'	2.28	0.48
55:6:6:G:O2'	55:6:7:G:H5'	2.13	0.48
58:8:261:MET:HG2	58:8:262:PHE:HD2	1.77	0.48
3:d:83:VAL:HG12	3:d:86:ALA:HA	1.94	0.48
4:e:3:LEU:HA	4:e:6:TYR:HB3	1.95	0.48
7:h:15:VAL:HA	7:h:18:VAL:HG12	1.94	0.48
27:C:5:ARG:HG2	27:C:23:THR:HB	1.95	0.48
31:G:27:LYS:N	31:G:28:PRO:CD	2.76	0.48
32:H:71:ARG:HH12	32:H:73:GLY:H	1.60	0.48
36:L:22:LEU:O	36:L:26:VAL:HG23	2.13	0.48
52:3:423:G:C2'	52:3:424:G:H5'	2.43	0.48
52:3:555:U:H2'	52:3:556:C:C6	2.48	0.48
52:3:1346:A:O2'	52:3:1347:G:H4'	2.13	0.48
53:1:1779:U:H5	53:1:1784:A:N7	2.10	0.48
53:1:2561:U:C2'	53:1:2562:U:H5''	2.43	0.48
58:8:244:GLU:OE1	58:8:296:PRO:HA	2.13	0.48
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.94	0.48
26:B:24:VAL:HG13	26:B:25:THR:N	2.28	0.48
50:Z:44:ARG:HD2	50:Z:44:ARG:C	2.38	0.48
52:3:371:A:H2'	52:3:372:C:O4'	2.14	0.48
52:3:1098:C:H2'	52:3:1099:G:O4'	2.13	0.48
53:1:435:C:H2'	53:1:436:C:H5'	1.93	0.48
53:1:859:G:H1'	53:1:860:U:H5	1.77	0.48
53:1:864:G:O2'	53:1:865:C:H5'	2.13	0.48
53:1:1287:A:C2	53:1:1649:G:H4'	2.48	0.48
53:1:1554:U:H3'	53:1:1555:G:H5'	1.94	0.48
53:1:1697:G:H4'	53:1:1978:A:H5''	1.96	0.48
12:m:42:THR:HA	12:m:93:VAL:HA	1.95	0.48
12:m:57:VAL:HG12	12:m:112:LEU:HG	1.95	0.48
13:n:36:THR:OG1	13:n:37:THR:N	2.46	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:3:VAL:HG12	30:F:37:GLN:CD	2.39	0.48
32:H:106:ARG:HD3	32:H:106:ARG:N	2.28	0.48
33:I:18:LEU:HB2	33:I:20:LEU:HD23	1.96	0.48
36:L:24:LYS:HE2	52:3:1375:A:H5''	1.94	0.48
52:3:865:A:H5'	52:3:1078:U:O4	2.14	0.48
52:3:1220:G:H2'	52:3:1221:G:H8	1.77	0.48
53:1:1140:C:C2'	53:1:1141:U:H5'	2.43	0.48
53:1:1670:C:O5'	53:1:1670:C:H6	1.97	0.48
53:1:1900:A:C1'	53:1:1970:A:H2'	2.40	0.48
55:5:18:G:H1	55:5:55:U:H6	1.60	0.48
1:b:4:LYS:HA	1:b:16:VAL:HG22	1.94	0.48
1:b:179:GLU:OE2	1:b:269:ARG:HA	2.13	0.48
1:b:193:GLU:HG2	1:b:194:VAL:N	2.29	0.48
6:g:27:ARG:HH22	23:x:59:ASP:HB2	1.78	0.48
8:i:91:LYS:HE3	8:i:94:LYS:HE3	1.94	0.48
10:k:13:ASN:ND2	10:k:98:ARG:HB3	2.28	0.48
36:L:69:ARG:HG2	36:L:95:ARG:HG2	1.94	0.48
41:Q:28:GLN:HB3	41:Q:80:LEU:HG	1.94	0.48
42:R:65:GLU:OE2	42:R:69:ARG:NE	2.44	0.48
45:U:14:ARG:HH12	52:3:618:C:H1'	1.78	0.48
52:3:1011:C:H2'	52:3:1012:A:H8	1.78	0.48
53:1:2126:A:H2'	53:1:2162:G:H21	1.79	0.48
53:1:2180:U:H2'	53:1:2181:U:O4'	2.13	0.48
54:2:97:C:H2'	54:2:98:G:O4'	2.13	0.48
1:b:227:VAL:HG11	53:1:784:G:C2	2.48	0.48
11:l:93:ASN:O	11:l:94:THR:OG1	2.22	0.48
47:W:32:ILE:HD13	47:W:67:LEU:HD21	1.94	0.48
53:1:2339:C:H2'	53:1:2340:A:C8	2.48	0.48
53:1:2743:U:H3'	53:1:2744:G:H5''	1.95	0.48
57:7:76:A:H5'	58:8:221:ILE:HD11	1.95	0.48
2:c:38:LYS:HB3	2:c:43:ASP:OD2	2.13	0.48
6:g:97:ARG:NH2	53:1:2220:U:H4'	2.26	0.48
7:h:13:ALA:O	7:h:17:GLU:OE1	2.31	0.48
7:h:54:VAL:O	7:h:54:VAL:HG22	2.14	0.48
18:s:94:ASP:OD1	53:1:2014:A:H4'	2.14	0.48
19:t:73:ARG:HE	53:1:65:U:H1'	1.79	0.48
31:G:140:LEU:O	31:G:144:GLU:HG3	2.13	0.48
49:Y:19:HIS:O	49:Y:23:ARG:HG2	2.14	0.48
52:3:225:C:H2'	52:3:226:G:C5'	2.43	0.48
53:1:107:G:H2'	53:1:108:G:H8	1.79	0.48
53:1:118:A:H5'	53:1:119:A:C8	2.46	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:676:A:H62	53:1:802:A:H61	1.60	0.48
53:1:704:G:H1'	53:1:727:A:H61	1.78	0.48
53:1:1664:A:H2'	53:1:1664:A:N3	2.29	0.48
53:1:1790:C:H2'	53:1:1791:A:C5	2.47	0.48
53:1:1833:C:O2'	53:1:1834:U:H5'	2.13	0.48
53:1:2011:U:H2'	53:1:2012:G:O4'	2.14	0.48
53:1:2329:U:H2'	53:1:2330:G:C8	2.49	0.48
53:1:2660:A:H2'	53:1:2661:G:O4'	2.13	0.48
53:1:2869:G:H2'	53:1:2870:C:C6	2.49	0.48
54:2:95:U:H2'	54:2:96:G:C8	2.49	0.48
57:7:62:C:C2'	57:7:63:G:H5''	2.42	0.48
4:e:26:GLN:HE21	54:2:57:A:H4'	1.77	0.48
9:j:109:LEU:O	9:j:111:LYS:HD2	2.14	0.48
17:r:39:LEU:O	17:r:49:ILE:HG23	2.13	0.48
19:t:6:ARG:HD2	19:t:9:LYS:NZ	2.29	0.48
24:y:26:PHE:HD1	24:y:29:ARG:HH11	1.61	0.48
36:L:73:GLU:OE2	36:L:88:VAL:HG23	2.14	0.48
46:V:5:ARG:HH11	52:3:636:U:H4'	1.78	0.48
53:1:1858:A:H1'	53:1:1885:A:C2	2.49	0.48
53:1:2121:G:H2'	53:1:2122:U:O4'	2.12	0.48
53:1:2172:U:OP1	53:1:2173:A:H5'	2.13	0.48
2:c:108:ASP:OD2	2:c:206:ALA:HA	2.13	0.48
3:d:55:SER:HB2	53:1:797:G:OP1	2.14	0.48
4:e:141:ASP:H	4:e:144:LYS:NZ	2.11	0.48
5:f:65:GLY:HA3	53:1:2748:A:O2'	2.14	0.48
8:i:12:VAL:O	8:i:13:ALA:C	2.55	0.48
11:l:20:GLY:O	11:l:21:ARG:NH2	2.40	0.48
18:s:57:ASN:HD21	53:1:495:G:C4'	2.25	0.48
23:x:71:ARG:NH1	23:x:77:TYR:OH	2.47	0.48
34:J:153:ALA:HB2	34:J:163:ILE:HD11	1.95	0.48
34:J:161:GLU:OE1	34:J:164:LEU:HD21	2.14	0.48
38:N:69:GLY:N	52:3:1250:A:H4'	2.29	0.48
49:Y:4:LYS:HG3	49:Y:6:ALA:H	1.78	0.48
52:3:439:U:H2'	52:3:440:C:O4'	2.13	0.48
52:3:477:C:H2'	52:3:478:A:C8	2.49	0.48
52:3:597:G:H2'	52:3:598:U:H5'	1.95	0.48
52:3:1075:U:H4'	52:3:1101:A:N6	2.29	0.48
52:3:1148:U:H2'	52:3:1149:C:O4'	2.14	0.48
53:1:598:U:H2'	53:1:599:A:H8	1.78	0.48
53:1:634:C:H2'	53:1:635:C:C6	2.49	0.48
53:1:1704:C:H2'	53:1:1705:A:C8	2.49	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2070:A:H2'	53:1:2071:A:O4'	2.14	0.48
53:1:2391:G:H2'	53:1:2424:C:H41	1.79	0.48
55:6:9:G:H1'	55:6:45:G:H2'	1.96	0.48
57:7:26:A:H61	57:7:45:U:H3	1.61	0.48
2:c:133:THR:HG23	2:c:134:HIS:CD2	2.49	0.48
6:g:132:PHE:HB2	6:g:140:ALA:HB3	1.95	0.48
32:H:37:LYS:HA	32:H:40:GLN:OE1	2.14	0.48
33:I:77:GLU:OE1	33:I:92:LEU:HD22	2.14	0.48
33:I:131:ILE:HG21	52:3:620:C:O2	2.13	0.48
34:J:159:SER:OG	34:J:162:GLU:HG2	2.13	0.48
38:N:8:THR:OG1	38:N:9:GLY:N	2.46	0.48
52:3:235:C:H2'	52:3:236:A:H8	1.78	0.48
52:3:502:A:H2'	52:3:503:C:O4'	2.14	0.48
52:3:1056:U:H2'	52:3:1057:G:H8	1.79	0.48
53:1:581:C:H2'	53:1:582:A:H8	1.78	0.48
53:1:1335:C:H2'	53:1:1336:A:C8	2.49	0.48
53:1:2041:U:H2'	53:1:2042:A:C8	2.49	0.48
53:1:2340:A:H2'	53:1:2341:G:H8	1.79	0.48
58:8:92:MET:HB3	58:8:126:VAL:HG11	1.95	0.48
1:b:33:LEU:HD11	1:b:62:ARG:HD3	1.94	0.47
1:b:252:LYS:HZ3	53:1:1901:A:H4'	1.79	0.47
2:c:29:VAL:O	2:c:185:ASN:HB3	2.13	0.47
2:c:46:ARG:NH2	2:c:88:GLU:O	2.47	0.47
7:h:112:ALA:O	7:h:113:PHE:C	2.57	0.47
10:k:11:ALA:HB2	10:k:83:ALA:HB1	1.95	0.47
21:v:25:LYS:HG2	21:v:43:ASP:HA	1.97	0.47
21:v:83:LYS:HD3	53:1:1119:U:OP1	2.14	0.47
22:w:23:GLY:HA2	22:w:63:VAL:HB	1.96	0.47
34:J:55:VAL:CG1	34:J:56:PRO:HD3	2.44	0.47
35:K:96:VAL:HG12	35:K:97:THR:H	1.79	0.47
46:V:54:ILE:H	46:V:81:ALA:HB2	1.79	0.47
51:a:62:ALA:HB2	51:a:162:ARG:HG2	1.96	0.47
52:3:24:U:H2'	52:3:25:C:C6	2.48	0.47
52:3:243:A:H4'	52:3:244:U:H3'	1.95	0.47
52:3:452:A:H61	52:3:480:U:H3	1.62	0.47
52:3:664:G:N2	52:3:741:G:H1	2.12	0.47
53:1:214:G:O2'	53:1:215:G:H5'	2.14	0.47
53:1:2170:A:H2'	53:1:2171:A:O4'	2.14	0.47
53:1:2193:G:H2'	53:1:2194:U:C6	2.50	0.47
53:1:2567:G:H2'	53:1:2568:U:C6	2.49	0.47
1:b:44:ASN:ND2	53:1:1812:U:H1'	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:1:MET:HE1	10:k:67:LYS:HE2	1.96	0.47
12:m:11:LYS:HD2	12:m:86:LYS:HG2	1.95	0.47
16:q:23:TYR:CD1	53:1:533:G:H5'	2.48	0.47
34:J:65:LYS:HA	34:J:68:ARG:NH1	2.29	0.47
36:L:113:LYS:HB2	36:L:117:LEU:HD23	1.96	0.47
37:M:8:ASP:O	37:M:12:ARG:HG3	2.14	0.47
45:U:37:GLY:HA3	45:U:51:ARG:O	2.14	0.47
49:Y:28:ARG:O	49:Y:32:LYS:HG2	2.14	0.47
52:3:257:G:H2'	52:3:258:G:H8	1.79	0.47
52:3:291:U:H2'	52:3:292:G:C8	2.49	0.47
53:1:562:U:O4'	53:1:2036:C:H5'	2.14	0.47
53:1:694:U:C3'	53:1:695:G:H5''	2.44	0.47
53:1:1901:A:O2'	53:1:1902:C:H5'	2.13	0.47
53:1:2055:C:H2'	53:1:2504:U:H5'	1.95	0.47
53:1:2230:G:H2'	53:1:2231:U:C6	2.49	0.47
57:7:25:C:H2'	57:7:26:A:H4'	1.96	0.47
57:7:76:A:O2'	60:7:101:PHE:C	2.58	0.47
4:e:59:ILE:O	4:e:101:ARG:NH1	2.47	0.47
9:j:65:THR:OG1	9:j:66:GLY:N	2.47	0.47
9:j:122:LEU:HD23	9:j:122:LEU:C	2.38	0.47
23:x:6:VAL:HG13	23:x:7:THR:N	2.29	0.47
28:D:11:LYS:HE2	53:1:686:U:OP1	2.14	0.47
40:P:83:VAL:HB	40:P:109:ILE:HG23	1.96	0.47
42:R:6:ILE:HG23	42:R:7:ASN:N	2.29	0.47
42:R:90:HIS:CE1	42:R:96:VAL:HG21	2.49	0.47
43:S:20:PHE:O	43:S:21:ALA:HB3	2.14	0.47
52:3:346:G:C2'	52:3:347:G:H5'	2.44	0.47
52:3:924:C:H2'	52:3:925:G:C8	2.49	0.47
53:1:395:U:H2'	53:1:396:G:C8	2.49	0.47
53:1:1140:C:H2'	53:1:1141:U:H5'	1.96	0.47
53:1:2832:U:H1'	53:1:2834:G:C2	2.49	0.47
53:1:2841:C:H2'	53:1:2842:G:C8	2.49	0.47
8:i:126:ARG:HA	8:i:129:GLU:CG	2.44	0.47
9:j:36:LEU:HD11	9:j:122:LEU:HD12	1.96	0.47
12:m:12:MET:HA	53:1:910:A:N6	2.23	0.47
22:w:14:ALA:HB2	53:1:2272:U:OP2	2.15	0.47
26:B:24:VAL:HG22	26:B:26:SER:H	1.79	0.47
31:G:207:ARG:O	31:G:211:LEU:HD23	2.13	0.47
39:O:63:ASP:OD1	43:S:97:LYS:HE3	2.14	0.47
41:Q:42:LYS:HG3	41:Q:44:PRO:HD2	1.96	0.47
46:V:3:LYS:NZ	52:3:637:C:H5''	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:W:40:PRO:HG2	47:W:43:ILE:HG12	1.96	0.47
52:3:368:U:OP2	58:8:280:ARG:NE	2.47	0.47
52:3:1114:C:H2'	52:3:1115:U:C6	2.49	0.47
52:3:1256:A:H1'	52:3:1258:G:C4	2.48	0.47
52:3:1427:C:H2'	52:3:1428:A:C8	2.49	0.47
53:1:210:C:H2'	53:1:211:C:C6	2.49	0.47
53:1:1298:C:H2'	53:1:1299:G:O4'	2.14	0.47
53:1:2398:U:H2'	53:1:2399:G:C8	2.50	0.47
58:8:323:PHE:CE2	58:8:344:LEU:HD21	2.50	0.47
7:h:54:VAL:O	53:1:1084:A:H5''	2.15	0.47
8:i:3:LYS:HG3	8:i:4:VAL:H	1.79	0.47
35:K:7:VAL:HG12	35:K:61:LEU:HG	1.96	0.47
38:N:110:VAL:HG21	52:3:1370:G:P	2.54	0.47
41:Q:56:LEU:HD12	41:Q:60:PHE:HB2	1.96	0.47
41:Q:88:ASP:HB2	52:3:523:A:N1	2.30	0.47
52:3:219:U:H2'	52:3:220:G:C8	2.50	0.47
52:3:390:U:H2'	52:3:391:G:C8	2.49	0.47
52:3:1540:U:H3	56:4:5:A:H2	1.62	0.47
53:1:621:A:H2'	53:1:622:G:H5'	1.96	0.47
53:1:1637:A:H5'	53:1:1760:C:O2'	2.14	0.47
53:1:2043:C:H1'	53:1:2779:U:O4	2.14	0.47
53:1:2267:A:H5''	53:1:2268:A:H5'	1.97	0.47
54:2:1:U:H2'	54:2:2:G:C8	2.49	0.47
1:b:158:GLY:HA3	53:1:1820:U:C4	2.50	0.47
2:c:55:LYS:HG3	2:c:77:ARG:HA	1.95	0.47
28:D:10:LEU:HD23	53:1:770:G:H5''	1.96	0.47
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.96	0.47
39:O:40:ILE:H	39:O:40:ILE:HD12	1.79	0.47
50:Z:66:ARG:NH2	52:3:1099:G:H4'	2.06	0.47
52:3:1033:G:H2'	52:3:1034:G:C5'	2.45	0.47
53:1:1592:C:H2'	53:1:1593:A:C8	2.49	0.47
53:1:1851:U:O2'	55:6:71:C:H4'	2.15	0.47
53:1:2126:A:H2'	53:1:2162:G:N2	2.29	0.47
53:1:2277:G:H2'	53:1:2278:A:C5'	2.33	0.47
53:1:2786:U:H2'	53:1:2787:C:C6	2.49	0.47
58:8:177:LYS:HA	58:8:180:GLU:OE1	2.14	0.47
2:c:170:VAL:HG21	53:1:2679:A:H4'	1.97	0.47
3:d:164:LEU:HB2	3:d:167:VAL:HB	1.97	0.47
4:e:63:LYS:O	54:2:42:C:O2'	2.29	0.47
6:g:40:THR:HB	6:g:43:ASN:HB2	1.96	0.47
9:j:47:HIS:CE1	9:j:48:VAL:HG23	2.48	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:84:ILE:HG23	9:j:84:ILE:O	2.14	0.47
10:k:48:PRO:HB3	52:3:1422:G:C5'	2.44	0.47
13:n:118:ARG:HH12	26:B:55:ALA:HB3	1.79	0.47
19:t:50:LEU:HD23	24:y:26:PHE:CE2	2.50	0.47
21:v:20:LEU:HD11	21:v:41:GLU:CD	2.40	0.47
25:z:11:SER:OG	53:1:989:G:OP2	2.28	0.47
26:B:2:VAL:HG12	53:1:2015:A:C2	2.50	0.47
28:D:34:ARG:NH2	53:1:466:A:OP1	2.47	0.47
33:I:144:ILE:N	33:I:144:ILE:HD12	2.29	0.47
36:L:25:PHE:HD1	36:L:28:ILE:HD11	1.79	0.47
38:N:68:GLY:HA2	52:3:1250:A:H4'	1.96	0.47
38:N:113:LYS:HE2	38:N:118:ARG:O	2.14	0.47
38:N:126:PHE:O	52:3:1342:C:H4'	2.14	0.47
39:O:57:VAL:O	39:O:58:ASN:CB	2.62	0.47
45:U:28:ARG:NH2	52:3:390:U:H4'	2.30	0.47
50:Z:66:ARG:HD2	52:3:1099:G:H4'	1.96	0.47
52:3:113:G:H2'	52:3:114:U:C6	2.50	0.47
52:3:1241:G:H2'	52:3:1242:G:H8	1.79	0.47
52:3:1316:G:H2'	52:3:1317:C:H5''	1.97	0.47
53:1:1023:U:H4'	53:1:1123:C:OP1	2.15	0.47
53:1:2208:C:H2'	53:1:2209:G:H8	1.79	0.47
54:2:88:C:H5''	54:2:89:U:OP1	2.14	0.47
58:8:48:ASP:O	58:8:52:ASN:ND2	2.48	0.47
10:k:99:ILE:HD13	10:k:115:ILE:HG23	1.97	0.47
37:M:24:VAL:HG23	37:M:60:LEU:HD13	1.97	0.47
43:S:68:ARG:NH1	43:S:79:SER:OG	2.48	0.47
48:X:69:LYS:H	48:X:72:GLU:HG3	1.78	0.47
52:3:721:G:H4'	52:3:722:G:O4'	2.15	0.47
52:3:948:C:H2'	52:3:949:A:C8	2.49	0.47
52:3:1096:C:H2'	52:3:1097:C:C6	2.49	0.47
53:1:680:C:H2'	53:1:681:G:C8	2.49	0.47
53:1:845:A:N7	53:1:847:U:H1'	2.30	0.47
53:1:1161:C:H2'	53:1:1162:G:H8	1.79	0.47
53:1:1709:U:H2'	53:1:1710:G:C8	2.50	0.47
53:1:1947:C:H2'	53:1:1948:G:C8	2.49	0.47
53:1:2443:C:H2'	53:1:2444:G:C8	2.48	0.47
56:4:17:U:O2'	56:4:18:G:H5'	2.14	0.47
7:h:58:THR:HG21	7:h:82:ILE:H	1.79	0.47
9:j:4:PHE:HB3	16:q:63:ARG:NH1	2.30	0.47
9:j:4:PHE:O	16:q:63:ARG:NH2	2.35	0.47
11:l:101:ILE:HG13	11:l:102:GLY:N	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:61:ASP:OD2	38:N:61:ASP:N	2.46	0.47
50:Z:44:ARG:HD3	52:3:723:U:OP2	2.15	0.47
53:1:370:G:H2'	53:1:423:A:N7	2.30	0.47
53:1:519:U:H2'	53:1:520:G:H8	1.80	0.47
53:1:1149:G:H2'	53:1:1150:C:C6	2.50	0.47
53:1:1438:U:O2'	53:1:1439:A:H5'	2.15	0.47
53:1:1918:A:H2	53:1:1919:A:H62	1.62	0.47
4:e:152:ASP:OD1	4:e:152:ASP:N	2.47	0.47
6:g:3:VAL:HG13	6:g:37:VAL:O	2.15	0.47
6:g:31:VAL:N	6:g:32:PRO:HD2	2.30	0.47
33:I:104:MET:SD	33:I:172:VAL:HG22	2.55	0.47
38:N:32:ARG:HD3	38:N:36:GLN:HE21	1.79	0.47
38:N:60:LEU:HD12	38:N:60:LEU:O	2.14	0.47
52:3:1170:A:H2'	52:3:1171:A:O4'	2.14	0.47
53:1:1045:C:OP1	53:1:1047:G:H5'	2.15	0.47
53:1:1092:C:H2'	53:1:1093:G:O4'	2.14	0.47
53:1:2529:G:OP2	53:1:2530:A:H5''	2.15	0.47
53:1:2605:U:H2'	53:1:2606:C:C6	2.50	0.47
5:f:44:HIS:O	5:f:46:ASP:N	2.48	0.46
7:h:55:VAL:HA	53:1:1084:A:C4'	2.45	0.46
7:h:55:VAL:HA	53:1:1084:A:H5''	1.97	0.46
7:h:94:ARG:HD3	7:h:131:THR:HG22	1.96	0.46
11:l:3:LEU:HD23	53:1:1203:U:H5'	1.97	0.46
12:m:40:ARG:NH1	53:1:958:U:OP1	2.48	0.46
19:t:6:ARG:HD2	19:t:9:LYS:HZ3	1.80	0.46
31:G:5:MET:SD	31:G:5:MET:N	2.89	0.46
33:I:9:LYS:HE3	52:3:428:G:C5'	2.44	0.46
36:L:24:LYS:CE	52:3:1375:A:H5''	2.45	0.46
52:3:86:G:H4'	52:3:87:C:C5	2.50	0.46
52:3:350:G:H2'	52:3:351:G:C8	2.50	0.46
52:3:422:C:H5'	52:3:423:G:N3	2.30	0.46
52:3:1064:G:H1'	52:3:1190:G:N2	2.30	0.46
52:3:1236:A:H2'	52:3:1237:C:C6	2.50	0.46
53:1:720:U:H2'	53:1:721:A:H8	1.80	0.46
53:1:2241:A:H2'	53:1:2242:G:C8	2.50	0.46
53:1:2834:G:H2'	53:1:2879:A:H61	1.79	0.46
58:8:342:ILE:HD12	58:8:361:VAL:HG22	1.96	0.46
4:e:38:GLY:HA3	53:1:2312:U:O2	2.15	0.46
4:e:134:GLN:NE2	4:e:149:ARG:HB3	2.30	0.46
17:r:91:GLN:HE22	53:1:1162:G:N2	2.13	0.46
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.30	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:y:44:LYS:HE3	24:y:48:ARG:HH22	1.79	0.46
31:G:3:VAL:O	31:G:8:MET:HE1	2.15	0.46
31:G:83:ALA:O	31:G:87:ASP:N	2.48	0.46
32:H:107:LYS:HD2	32:H:110:LEU:HD11	1.97	0.46
33:I:184:LYS:HA	33:I:185:PRO:HD3	1.79	0.46
39:O:10:LEU:HD23	39:O:10:LEU:H	1.79	0.46
52:3:20:U:H2'	52:3:21:G:O4'	2.14	0.46
52:3:204:G:H2'	52:3:205:A:C8	2.50	0.46
52:3:986:U:H3	52:3:1219:A:H61	1.64	0.46
53:1:251:A:H2'	53:1:252:G:O4'	2.16	0.46
53:1:654:A:H3'	53:1:654:A:N3	2.31	0.46
53:1:680:C:H2'	53:1:681:G:H8	1.79	0.46
53:1:743:A:O2'	53:1:744:U:H5'	2.15	0.46
53:1:1765:U:H2'	53:1:1766:G:H8	1.80	0.46
53:1:2318:G:H2'	53:1:2319:G:O4'	2.16	0.46
58:8:236:ILE:HD13	58:8:271:ALA:H	1.80	0.46
58:8:282:ILE:HG23	58:8:286:GLU:OE2	2.16	0.46
2:c:25:THR:HG23	2:c:189:VAL:HG23	1.97	0.46
4:e:111:ARG:HG2	4:e:111:ARG:HH21	1.80	0.46
5:f:148:ARG:HA	5:f:161:VAL:HG13	1.97	0.46
16:q:52:ARG:O	16:q:56:PHE:HB2	2.16	0.46
25:z:23:LEU:HD21	25:z:53:MET:HE2	1.97	0.46
31:G:46:VAL:N	31:G:47:PRO:HD2	2.30	0.46
40:P:120:CYS:SG	40:P:121:ARG:N	2.88	0.46
42:R:77:LYS:HE2	42:R:80:MET:HE3	1.98	0.46
48:X:37:SER:O	48:X:70:LEU:HD23	2.15	0.46
52:3:264:C:H2'	52:3:265:G:O4'	2.16	0.46
52:3:1120:C:H2'	52:3:1121:U:C6	2.50	0.46
52:3:1368:A:O2'	52:3:1369:C:H5'	2.15	0.46
53:1:1011:G:H1'	53:1:1013:C:O4'	2.15	0.46
53:1:1386:C:H2'	53:1:1387:A:C8	2.50	0.46
53:1:2122:U:H2'	53:1:2123:G:O4'	2.15	0.46
53:1:2128:G:H2'	53:1:2129:C:H5'	1.98	0.46
53:1:2650:U:H2'	53:1:2651:C:C6	2.51	0.46
54:2:95:U:H2'	54:2:96:G:H8	1.80	0.46
1:b:55:GLY:H	53:1:692:C:P	2.38	0.46
2:c:208:LYS:NZ	53:1:2731:G:O3'	2.48	0.46
3:d:152:GLU:N	3:d:152:GLU:OE2	2.48	0.46
5:f:61:TRP:O	5:f:65:GLY:N	2.48	0.46
8:i:94:LYS:NZ	53:1:1076:C:O2'	2.48	0.46
15:p:96:LEU:HB3	15:p:99:LEU:HD23	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B:10:SER:O	26:B:14:MET:HG3	2.16	0.46
30:F:36:ARG:O	30:F:37:GLN:CB	2.63	0.46
31:G:14:HIS:HB3	31:G:42:LEU:HD21	1.98	0.46
41:Q:65:TYR:OH	52:3:522:C:OP2	2.32	0.46
45:U:42:ILE:O	45:U:42:ILE:HG13	2.14	0.46
52:3:1168:U:H5'	52:3:1169:A:OP2	2.14	0.46
52:3:1434:A:H2'	52:3:1435:G:O4'	2.16	0.46
53:1:576:U:H2'	53:1:577:G:C8	2.50	0.46
53:1:2189:U:H2'	53:1:2190:G:H8	1.79	0.46
53:1:2860:A:H2'	53:1:2861:U:H5'	1.96	0.46
11:l:82:LEU:HG	11:l:120:VAL:HG11	1.96	0.46
13:n:31:HIS:O	13:n:32:GLU:HB3	2.15	0.46
16:q:93:ILE:HD12	17:r:13:ARG:HB2	1.97	0.46
31:G:220:VAL:HG23	31:G:221:ARG:H	1.81	0.46
36:L:68:VAL:O	36:L:70:PRO:HD3	2.15	0.46
39:O:17:LEU:HD23	39:O:17:LEU:C	2.41	0.46
48:X:35:ARG:NH2	48:X:74:ALA:HB3	2.14	0.46
51:a:38:PHE:CD1	53:1:2127:G:H4'	2.50	0.46
52:3:423:G:H2'	52:3:424:G:C5'	2.45	0.46
52:3:890:G:O2'	52:3:891:U:C6	2.67	0.46
52:3:1412:C:H2'	52:3:1413:A:H8	1.81	0.46
52:3:1512:U:H2'	52:3:1513:A:C8	2.49	0.46
53:1:1936:A:H2	53:1:1943:U:H3	1.62	0.46
53:1:2292:U:H2'	53:1:2293:G:C8	2.50	0.46
53:1:2699:C:H2'	53:1:2700:A:C8	2.50	0.46
53:1:2743:U:H2'	53:1:2744:G:C5'	2.45	0.46
58:8:213:LEU:HD23	58:8:293:LEU:HD22	1.98	0.46
58:8:313:SER:HB2	58:8:316:GLU:CD	2.40	0.46
2:c:208:LYS:NZ	53:1:2732:G:H5'	2.30	0.46
3:d:47:LYS:HE2	53:1:451:U:H4'	1.97	0.46
6:g:78:VAL:HG21	6:g:103:VAL:HG22	1.97	0.46
8:i:77:VAL:HA	8:i:80:LYS:HB2	1.97	0.46
18:s:9:HIS:CE1	18:s:80:PRO:HG2	2.51	0.46
26:B:1:ALA:N	53:1:2056:G:N2	2.63	0.46
35:K:46:GLN:HA	35:K:56:LYS:HA	1.98	0.46
48:X:30:LEU:HD13	48:X:48:ILE:HG22	1.97	0.46
52:3:483:C:H2'	52:3:484:G:C8	2.51	0.46
52:3:662:U:H2'	52:3:663:A:C8	2.51	0.46
52:3:665:A:C1'	52:3:733:G:H1'	2.45	0.46
53:1:817:C:H2'	53:1:818:G:O4'	2.16	0.46
53:1:1947:C:H2'	53:1:1948:G:H8	1.81	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2731:G:H2'	53:1:2732:G:C8	2.50	0.46
53:1:2773:C:H2'	53:1:2774:C:C6	2.51	0.46
53:1:2786:U:O2'	53:1:2787:C:H5'	2.15	0.46
54:2:118:C:H2'	54:2:119:A:C8	2.51	0.46
58:8:93:ILE:HD11	58:8:122:LEU:HD22	1.98	0.46
1:b:229:HIS:ND1	1:b:230:PRO:HD2	2.30	0.46
4:e:101:ARG:HG3	4:e:105:ILE:HD11	1.98	0.46
9:j:71:ASP:O	9:j:73:VAL:HG23	2.16	0.46
10:k:48:PRO:HB3	52:3:1422:G:H5'	1.98	0.46
12:m:20:LEU:HD23	21:v:81:PRO:HG2	1.98	0.46
13:n:106:ASP:OD1	13:n:106:ASP:N	2.49	0.46
19:t:39:THR:O	19:t:43:ILE:HG13	2.16	0.46
26:B:45:ASP:OD1	26:B:52:LYS:NZ	2.48	0.46
32:H:171:ARG:HB2	52:3:1106:G:H5''	1.97	0.46
35:K:51:ILE:C	35:K:53:LYS:H	2.23	0.46
44:T:73:ASP:OD2	44:T:76:ARG:HG3	2.15	0.46
47:W:11:ARG:HG3	52:3:845:A:H4'	1.98	0.46
50:Z:6:ARG:HG2	50:Z:8:ASN:H	1.80	0.46
52:3:52:C:H2'	52:3:53:A:C8	2.50	0.46
52:3:407:U:H2'	52:3:408:A:C8	2.51	0.46
52:3:449:G:H2'	52:3:450:G:C8	2.51	0.46
52:3:1441:A:H2'	52:3:1442:G:H5'	1.96	0.46
53:1:145:C:H2'	53:1:146:A:C8	2.50	0.46
53:1:708:G:O2'	53:1:709:U:H5'	2.16	0.46
53:1:1709:U:O2'	53:1:2859:G:H1'	2.16	0.46
53:1:1725:U:H2'	53:1:1726:C:C6	2.50	0.46
53:1:1773:A:C2'	53:1:1774:C:H5'	2.46	0.46
53:1:2487:G:H2'	53:1:2488:G:H8	1.80	0.46
55:5:50:U:H2'	55:5:51:C:C6	2.50	0.46
55:6:26:G:H1	55:6:44:A:H61	1.62	0.46
3:d:149:ILE:HG13	3:d:170:ARG:O	2.16	0.46
16:q:3:VAL:HG21	53:1:1249:U:H4'	1.97	0.46
17:r:49:ILE:HD12	17:r:52:PRO:HA	1.98	0.46
21:v:80:HIS:HB3	21:v:83:LYS:O	2.16	0.46
43:S:72:PHE:HE1	43:S:77:GLY:HA2	1.80	0.46
50:Z:11:PHE:O	50:Z:13:VAL:N	2.48	0.46
52:3:206:C:H2'	52:3:207:C:O4'	2.15	0.46
52:3:513:C:H2'	52:3:514:C:C6	2.51	0.46
52:3:1158:C:H2'	52:3:1159:U:H4'	1.97	0.46
52:3:1201:A:C1'	52:3:1202:U:OP2	2.61	0.46
53:1:230:G:O2'	53:1:231:A:H5'	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:534:U:H2'	53:1:535:G:C8	2.51	0.46
53:1:582:A:H2'	53:1:583:G:H8	1.80	0.46
53:1:878:A:H3'	53:1:879:G:H8	1.79	0.46
53:1:996:A:H2'	53:1:997:G:H8	1.81	0.46
53:1:1059:G:H3'	53:1:1060:U:H2'	1.97	0.46
53:1:1447:C:H2'	53:1:1448:G:H8	1.80	0.46
1:b:176:ARG:HG2	53:1:1819:A:H3'	1.98	0.46
7:h:36:ASP:HA	7:h:39:THR:HG22	1.98	0.46
7:h:118:ILE:CB	7:h:119:PRO:HD3	2.45	0.46
11:l:42:SER:OG	53:1:672:C:H5	1.99	0.46
28:D:3:ARG:O	28:D:6:GLN:NE2	2.49	0.46
44:T:57:ARG:HG2	44:T:57:ARG:HH11	1.80	0.46
50:Z:22:CYS:O	50:Z:23:GLU:HG3	2.16	0.46
52:3:422:C:H5''	52:3:423:G:O5'	2.16	0.46
52:3:1326:U:H2'	52:3:1327:C:C6	2.51	0.46
53:1:2389:G:H5''	53:1:2390:U:O4'	2.16	0.46
55:6:17:C:H2'	55:6:17(A):U:H5	1.81	0.46
1:b:130:PRO:HD3	1:b:188:ARG:NH1	2.31	0.46
3:d:48:THR:HG22	3:d:86:ALA:HB3	1.98	0.46
3:d:58:LYS:NZ	3:d:70:SER:O	2.49	0.46
8:i:10:LEU:HD23	8:i:10:LEU:H	1.79	0.46
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.45	0.46
25:z:6:ILE:HB	25:z:35:VAL:HG12	1.98	0.46
32:H:183:TYR:OH	32:H:198:LYS:HD3	2.15	0.46
33:I:57:LYS:O	33:I:60:VAL:HG12	2.16	0.46
52:3:64:G:H4'	52:3:65:A:H3'	1.97	0.46
52:3:1075:U:H2'	52:3:1076:U:C6	2.51	0.46
53:1:419:U:H2'	53:1:420:C:C6	2.50	0.46
53:1:2520:C:O2'	53:1:2521:C:H5'	2.16	0.46
53:1:2742:G:H1	53:1:2762:C:H42	1.63	0.46
54:2:30:C:H2'	54:2:31:C:O4'	2.16	0.46
5:f:174:LYS:HE2	53:1:2531:A:OP1	2.16	0.45
8:i:112:LYS:O	8:i:116:MET:N	2.48	0.45
14:o:18:LEU:HD23	14:o:25:ARG:HB3	1.97	0.45
24:y:2:LYS:HB3	24:y:52:ARG:HD3	1.99	0.45
30:F:2:LYS:HB2	30:F:35:GLN:HB3	1.99	0.45
46:V:20:ILE:O	46:V:45:VAL:HG12	2.16	0.45
52:3:166:U:H2'	52:3:167:A:C8	2.50	0.45
52:3:1202:U:H2'	52:3:1203:C:O4'	2.16	0.45
53:1:322:A:H5'	53:1:340:A:H1'	1.96	0.45
53:1:2819:G:H2'	53:1:2821:A:N7	2.31	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:56:G:H4'	54:2:57:A:C8	2.50	0.45
1:b:251:THR:OG1	1:b:252:LYS:N	2.48	0.45
23:x:56:ARG:NH2	53:1:372:G:O6	2.49	0.45
35:K:47:LEU:HD21	35:K:57:ALA:HB3	1.98	0.45
38:N:61:ASP:C	38:N:62:LEU:HD12	2.40	0.45
40:P:28:ASN:HD21	40:P:56:LYS:HD2	1.80	0.45
40:P:88:PRO:CG	40:P:89:GLY:H	2.26	0.45
45:U:51:ARG:C	45:U:52:LEU:HD12	2.41	0.45
46:V:10:ARG:NH1	46:V:55:GLY:HA2	2.31	0.45
52:3:810:C:O2'	52:3:811:C:H5'	2.16	0.45
52:3:1401:G:H2'	52:3:1402:C:O4'	2.16	0.45
53:1:340:A:H2'	53:1:341:C:O4'	2.16	0.45
53:1:576:U:H2'	53:1:577:G:H8	1.81	0.45
53:1:910:A:H1'	53:1:2264:C:O2'	2.16	0.45
53:1:935:C:H2'	53:1:936:A:H8	1.81	0.45
53:1:1297:C:OP1	53:1:2710:C:H4'	2.16	0.45
54:2:51:G:H2'	54:2:52:A:O4'	2.17	0.45
54:2:51:G:O2'	54:2:52:A:H5'	2.16	0.45
55:6:59:A:H2'	55:6:60:U:H5'	1.98	0.45
2:c:16:THR:OG1	2:c:20:VAL:O	2.31	0.45
9:j:81:ILE:HG12	53:1:2515:C:OP1	2.15	0.45
17:r:38:VAL:O	17:r:53:PHE:HA	2.17	0.45
19:t:17:SER:H	19:t:20:ALA:HB3	1.82	0.45
36:L:16:LYS:HE3	36:L:43:TYR:CE1	2.52	0.45
43:S:5:MET:HE1	52:3:982:U:P	2.57	0.45
52:3:82:G:H2'	52:3:83:C:O4'	2.17	0.45
52:3:193:C:H2'	52:3:194:C:C6	2.51	0.45
52:3:985:C:H2'	52:3:986:U:C6	2.52	0.45
52:3:1225:A:H2'	52:3:1225:A:N3	2.31	0.45
53:1:543:G:H2'	53:1:544:C:O4'	2.17	0.45
53:1:1386:C:H2'	53:1:1387:A:H8	1.81	0.45
53:1:1450:G:O2'	53:1:1451:C:H5'	2.17	0.45
53:1:2106:U:H2'	53:1:2107:G:C8	2.52	0.45
53:1:2345:G:N3	53:1:2381:A:H2'	2.31	0.45
1:b:220:ARG:NH2	53:1:1788:C:OP1	2.50	0.45
2:c:49:GLN:OE1	2:c:67:HIS:NE2	2.47	0.45
12:m:82:MET:HE3	53:1:960:A:H61	1.81	0.45
13:n:63:ARG:NH1	53:1:1454:C:H5'	2.30	0.45
13:n:63:ARG:NH1	53:1:1454:C:O5'	2.50	0.45
14:o:12:THR:HA	14:o:15:ARG:HB2	1.98	0.45
19:t:17:SER:OG	19:t:18:GLU:N	2.50	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:29:ALA:O	32:H:32:LEU:HG	2.16	0.45
37:M:9:MET:HE1	37:M:35:ILE:HG23	1.99	0.45
41:Q:98:ARG:HD2	41:Q:103:CYS:SG	2.56	0.45
42:R:33:LEU:HD22	42:R:40:GLU:HG3	1.99	0.45
48:X:49:ALA:HA	48:X:58:PRO:HA	1.99	0.45
52:3:337:G:H2'	52:3:338:A:H8	1.82	0.45
52:3:1293:C:H2'	52:3:1294:G:C8	2.52	0.45
53:1:558:U:H2'	53:1:559:G:C8	2.47	0.45
53:1:968:C:H2'	53:1:969:G:H8	1.80	0.45
53:1:1093:G:H21	53:1:1098:A:H62	1.65	0.45
53:1:2432:A:H1'	55:6:75:C:O4'	2.16	0.45
53:1:2830:C:O2'	53:1:2831:G:H5'	2.17	0.45
58:8:56:GLU:OE2	58:8:67:HIS:NE2	2.49	0.45
58:8:156:GLU:O	58:8:160:GLN:HG3	2.15	0.45
58:8:319:ARG:NH2	58:8:321:THR:OG1	2.49	0.45
3:d:30:GLN:HE22	53:1:660:C:H4'	1.81	0.45
9:j:81:ILE:HG23	9:j:82:GLY:N	2.31	0.45
21:v:17:SER:OG	21:v:21:ARG:NE	2.46	0.45
23:x:5:GLN:O	23:x:73:ARG:NH2	2.50	0.45
33:I:89:LEU:O	33:I:93:LEU:HG	2.17	0.45
34:J:159:SER:OG	34:J:162:GLU:OE2	2.34	0.45
38:N:113:LYS:HA	38:N:120:ALA:HB2	1.98	0.45
41:Q:115:LYS:O	41:Q:116:TYR:HB2	2.17	0.45
42:R:64:VAL:HG12	42:R:65:GLU:N	2.25	0.45
43:S:15:LEU:HG	43:S:54:SER:HB2	1.98	0.45
48:X:51:HIS:ND1	48:X:55:GLN:O	2.49	0.45
49:Y:54:GLN:N	49:Y:55:PRO:CD	2.79	0.45
52:3:32:A:H2'	52:3:33:A:C8	2.51	0.45
52:3:730:G:C2'	52:3:731:G:H5'	2.45	0.45
53:1:1021:A:H3'	53:1:1021:A:N3	2.31	0.45
53:1:1563:U:H2'	53:1:1564:C:C6	2.52	0.45
53:1:1565:C:O2'	53:1:1566:A:H2'	2.17	0.45
53:1:2682:A:N6	53:1:2728:U:H1'	2.29	0.45
54:2:14:U:O2	54:2:107:G:H4'	2.16	0.45
4:e:109:ARG:NH1	4:e:135:ILE:O	2.50	0.45
5:f:121:THR:O	5:f:133:LYS:N	2.49	0.45
6:g:51:ARG:HA	6:g:55:GLU:HB2	1.98	0.45
8:i:12:VAL:HG22	8:i:13:ALA:N	2.22	0.45
22:w:22:PHE:N	22:w:25:GLU:OE1	2.49	0.45
32:H:36:PHE:O	32:H:39:ARG:HB2	2.16	0.45
39:O:40:ILE:HD12	39:O:40:ILE:N	2.30	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:32:A:H2'	52:3:33:A:H8	1.81	0.45
52:3:1199:U:H2'	52:3:1200:C:H5'	1.97	0.45
53:1:64:A:H2'	53:1:65:U:C6	2.51	0.45
53:1:2343:U:O2'	53:1:2344:U:H5'	2.16	0.45
53:1:2376:A:H2'	53:1:2377:A:O4'	2.16	0.45
53:1:2818:U:H2'	53:1:2819:G:H8	1.81	0.45
55:5:69:C:H2'	55:5:70:G:H8	1.82	0.45
57:7:62:C:H2'	57:7:63:G:C5'	2.47	0.45
6:g:115:VAL:HG13	6:g:132:PHE:HE1	1.80	0.45
10:k:23:LYS:NZ	53:1:2548:U:O2	2.46	0.45
14:o:6:ALA:O	14:o:9:ARG:HG3	2.16	0.45
14:o:7:ARG:HD2	14:o:97:PHE:CZ	2.51	0.45
31:G:96:LEU:O	31:G:99:MET:HG3	2.15	0.45
34:J:80:LEU:HD13	34:J:122:VAL:CG1	2.45	0.45
52:3:90:C:H2'	52:3:91:U:C5	2.52	0.45
52:3:110:C:H2'	52:3:111:G:O4'	2.17	0.45
52:3:411:A:C4	52:3:413:G:H1'	2.52	0.45
52:3:1329:A:O2'	52:3:1330:U:H5'	2.17	0.45
53:1:174:U:H2'	53:1:175:G:H8	1.81	0.45
53:1:827:U:H4'	53:1:828:U:C5	2.52	0.45
53:1:1412:U:H2'	53:1:1413:A:C8	2.52	0.45
53:1:1876:A:H2'	53:1:1877:A:O4'	2.17	0.45
53:1:2104:C:H2'	53:1:2105:U:C6	2.52	0.45
53:1:2114:A:H61	53:1:2117:A:H62	1.63	0.45
56:4:13:A:O2'	56:4:14:A:H5'	2.17	0.45
57:7:14:A:H2'	57:7:15:G:O4'	2.16	0.45
58:8:307:SER:HA	58:8:390:ALA:H	1.82	0.45
58:8:327:TYR:OH	58:8:379:GLU:HG3	2.16	0.45
1:b:131:MET:HG2	1:b:134:ILE:HD12	1.99	0.45
3:d:74:LYS:O	3:d:75:SER:C	2.59	0.45
15:p:54:LEU:HA	15:p:76:HIS:HD2	1.81	0.45
31:G:41:ASN:ND2	31:G:44:LYS:HB2	2.31	0.45
38:N:78:ILE:O	38:N:82:ILE:HG13	2.17	0.45
39:O:56:HIS:CG	39:O:57:VAL:H	2.35	0.45
43:S:68:ARG:NE	52:3:1202:U:H1'	2.32	0.45
53:1:27:G:H22	53:1:512:G:H1'	1.80	0.45
53:1:151:C:H2'	53:1:152:A:H8	1.81	0.45
53:1:193:U:H2'	53:1:194:G:C8	2.52	0.45
53:1:799:G:H5''	53:1:800:A:H2'	1.98	0.45
53:1:937:C:H2'	53:1:938:G:H8	1.81	0.45
53:1:1341:G:C2	53:1:1398:C:H4'	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:20:HIS:HB3	58:8:23:HIS:CE1	2.52	0.45
7:h:112:ALA:C	7:h:114:GLU:N	2.74	0.45
12:m:34:LYS:CE	12:m:131:VAL:HG11	2.47	0.45
14:o:40:ILE:HA	14:o:47:VAL:HA	1.97	0.45
16:q:3:VAL:HG12	53:1:1199:U:O4'	2.17	0.45
32:H:86:LEU:HA	32:H:89:VAL:HG12	1.99	0.45
38:N:119:LYS:HG3	52:3:1349:A:OP1	2.17	0.45
41:Q:85:ARG:HH21	41:Q:87:LYS:HA	1.81	0.45
49:Y:55:PRO:HB3	52:3:193:C:O3'	2.16	0.45
53:1:874:G:H2'	53:1:875:G:H8	1.82	0.45
53:1:1628:G:H21	53:1:2699:C:H5'	1.82	0.45
53:1:2141:G:H1	53:1:2151:U:H1'	1.82	0.45
53:1:2197:U:H1'	53:1:2198:A:C8	2.52	0.45
53:1:2366:A:H2'	53:1:2367:G:O4'	2.17	0.45
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.81	0.45
12:m:51:ARG:NH1	53:1:2483:C:O2'	2.49	0.45
14:o:28:VAL:HG13	14:o:28:VAL:O	2.17	0.45
16:q:52:ARG:NH1	53:1:995:C:OP1	2.50	0.45
30:F:11:CYS:HB3	30:F:33:HIS:HE1	1.82	0.45
33:I:100:VAL:HG21	33:I:136:VAL:HG21	2.00	0.45
36:L:13:PRO:HB3	36:L:20:GLU:CD	2.41	0.45
43:S:62:ARG:HD2	43:S:69:PRO:HD3	1.99	0.45
46:V:77:VAL:O	46:V:77:VAL:HG13	2.17	0.45
50:Z:22:CYS:C	50:Z:23:GLU:HG3	2.41	0.45
52:3:114:U:O2'	52:3:115:G:H5'	2.16	0.45
52:3:1471:U:O2'	52:3:1472:U:H5'	2.17	0.45
53:1:828:U:H4'	53:1:831:G:N1	2.32	0.45
53:1:1083:U:H2'	53:1:1085:A:OP2	2.16	0.45
53:1:1181:U:H2'	53:1:1182:G:H8	1.82	0.45
53:1:1571:A:H2'	53:1:1572:A:C8	2.52	0.45
53:1:1830:C:H2'	53:1:1831:G:C8	2.52	0.45
53:1:1918:A:H2	53:1:1919:A:N6	2.15	0.45
53:1:2286:G:C4'	53:1:2287:A:O4'	2.62	0.45
53:1:2853:C:H2'	53:1:2854:G:H8	1.81	0.45
58:8:216:GLU:OE1	58:8:216:GLU:N	2.51	0.45
1:b:140:VAL:HG12	1:b:141:HIS:H	1.82	0.44
20:u:32:LYS:HZ1	53:1:478:A:H4'	1.82	0.44
24:y:54:LYS:O	24:y:57:LEU:HB3	2.17	0.44
27:C:46:VAL:HG12	27:C:47:ILE:N	2.32	0.44
31:G:105:THR:O	31:G:108:GLN:HB2	2.17	0.44
32:H:36:PHE:CE2	43:S:65:GLN:HG2	2.51	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:142:ARG:HA	36:L:142:ARG:HD3	1.85	0.44
37:M:91:LEU:O	37:M:116:ARG:NH2	2.46	0.44
40:P:115:ILE:HD11	52:3:718:A:N3	2.33	0.44
43:S:68:ARG:CD	52:3:1202:U:H1'	2.46	0.44
45:U:36:VAL:HG13	45:U:36:VAL:O	2.18	0.44
45:U:61:VAL:HG21	45:U:67:ILE:HD11	1.98	0.44
50:Z:11:PHE:C	50:Z:13:VAL:H	2.25	0.44
52:3:543:U:H2'	52:3:544:G:H8	1.83	0.44
53:1:18:U:H2'	53:1:19:A:C8	2.52	0.44
53:1:937:C:H2'	53:1:938:G:C8	2.52	0.44
53:1:1278:C:H2'	53:1:1279:G:C8	2.52	0.44
53:1:2863:C:H2'	53:1:2864:G:C8	2.52	0.44
6:g:26:ALA:HA	6:g:30:LEU:HD12	1.99	0.44
7:h:66:GLY:HA2	7:h:69:PHE:CD2	2.53	0.44
8:i:83:ALA:HB2	8:i:100:ILE:HD11	1.98	0.44
31:G:102:ASN:O	31:G:106:VAL:HG23	2.17	0.44
33:I:82:LYS:HD2	52:3:5:U:C5	2.53	0.44
41:Q:73:LEU:HD11	41:Q:79:ILE:HG21	1.97	0.44
44:T:62:ARG:HH22	53:1:715:A:H4'	1.82	0.44
51:a:170:ILE:HD12	51:a:170:ILE:N	2.33	0.44
53:1:151:C:H2'	53:1:152:A:C8	2.52	0.44
53:1:660:C:H2'	53:1:661:A:C8	2.52	0.44
53:1:818:G:O2'	53:1:819:A:H5''	2.17	0.44
53:1:1780:A:O2'	53:1:1781:U:H2'	2.18	0.44
53:1:2039:U:H2'	53:1:2040:G:H8	1.81	0.44
57:7:47:U:H2'	57:7:50:U:OP1	2.17	0.44
1:b:123:ILE:HG23	1:b:191:LEU:HD21	1.99	0.44
5:f:175:LYS:HD2	5:f:175:LYS:HA	1.71	0.44
7:h:30:SER:O	7:h:31:ARG:HD2	2.18	0.44
9:j:110:PRO:HB3	53:1:1007:C:O3'	2.16	0.44
10:k:2:ILE:HB	10:k:33:ALA:HB3	1.98	0.44
16:q:23:TYR:CE1	53:1:533:G:H5'	2.53	0.44
23:x:50:VAL:HG22	23:x:51:SER:N	2.32	0.44
25:z:5:LYS:C	25:z:6:ILE:HD12	2.43	0.44
25:z:52:PHE:CD2	54:2:83:G:H4'	2.53	0.44
32:H:168:ARG:NH2	52:3:1106:G:H1'	2.33	0.44
43:S:30:ILE:HG22	43:S:40:ARG:HA	2.00	0.44
45:U:75:ILE:CG2	45:U:80:LYS:HE3	2.47	0.44
52:3:1366:C:H2'	52:3:1367:C:C6	2.52	0.44
52:3:1472:U:H2'	52:3:1473:G:C8	2.53	0.44
53:1:415:A:H2'	53:1:416:U:C6	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:609:A:H2'	53:1:610:C:O4'	2.18	0.44
53:1:776:G:H22	53:1:2072:C:H5'	1.82	0.44
53:1:871:U:H2'	53:1:872:U:C6	2.52	0.44
53:1:1101:U:H2'	53:1:1102:C:C6	2.52	0.44
53:1:1936:A:H3'	53:1:1937:A:H5'	2.00	0.44
53:1:2556:C:H2'	53:1:2557:G:O4'	2.17	0.44
53:1:2888:C:H2'	53:1:2889:C:H6	1.82	0.44
54:2:106:G:H2'	54:2:107:G:O4'	2.18	0.44
58:8:238:LYS:HG2	58:8:241:GLU:OE2	2.17	0.44
58:8:238:LYS:N	58:8:241:GLU:OE2	2.47	0.44
3:d:48:THR:HG22	3:d:86:ALA:CB	2.47	0.44
3:d:176:ASP:HA	3:d:177:PRO:HD3	1.84	0.44
5:f:93:TYR:O	5:f:94:ARG:HD2	2.18	0.44
8:i:7:TYR:HB3	8:i:59:THR:HA	1.98	0.44
14:o:24:THR:HG23	14:o:90:VAL:HA	2.00	0.44
15:p:54:LEU:HD12	15:p:76:HIS:HB2	1.99	0.44
16:q:5:ARG:NH1	53:1:585:G:N7	2.65	0.44
31:G:102:ASN:OD1	31:G:105:THR:HG22	2.17	0.44
33:I:113:ALA:O	33:I:116:LEU:HG	2.17	0.44
39:O:29:ALA:O	39:O:33:GLY:HA3	2.18	0.44
41:Q:86:VAL:HG23	41:Q:88:ASP:H	1.81	0.44
52:3:648:A:H2'	52:3:649:A:C8	2.53	0.44
52:3:1517:G:H2'	52:3:1518:A:H5'	1.99	0.44
53:1:26:G:O2'	53:1:27:G:H5'	2.17	0.44
53:1:435:C:C2'	53:1:436:C:H5'	2.48	0.44
53:1:1102:C:H2'	53:1:1103:A:O4'	2.18	0.44
53:1:1474:U:H2'	53:1:1475:G:O4'	2.17	0.44
58:8:61:ILE:HD12	58:8:61:ILE:N	2.33	0.44
58:8:193:ALA:HA	58:8:196:LEU:HD12	2.00	0.44
2:c:22:ILE:HA	2:c:23:PRO:HD3	1.84	0.44
2:c:125:TRP:CD1	2:c:160:LYS:HB3	2.52	0.44
3:d:44:ARG:HD2	53:1:444:C:OP2	2.17	0.44
3:d:55:SER:O	3:d:74:LYS:HE3	2.17	0.44
7:h:48:ALA:HB3	7:h:51:TYR:HE2	1.83	0.44
13:n:79:LEU:C	13:n:81:ASN:H	2.25	0.44
17:r:10:LYS:HE2	53:1:994:C:O2'	2.17	0.44
20:u:34:ILE:HG12	20:u:63:ALA:HB2	2.00	0.44
36:L:15:PRO:HG2	36:L:39:GLU:OE2	2.18	0.44
37:M:80:PRO:HG2	52:3:878:A:H5''	2.00	0.44
38:N:6:TYR:CE2	52:3:1147:C:H4'	2.53	0.44
42:R:24:VAL:HA	52:3:1329:A:H5''	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:W:31:TYR:O	47:W:39:VAL:HG22	2.17	0.44
50:Z:39:LYS:HA	50:Z:42:THR:HB	1.99	0.44
52:3:552:U:H2'	52:3:553:A:H8	1.83	0.44
52:3:634:C:H2'	52:3:635:A:H8	1.83	0.44
52:3:882:C:O2'	52:3:883:C:H5'	2.18	0.44
53:1:1054:A:H2'	53:1:1055:G:C8	2.52	0.44
53:1:1110:G:H2'	53:1:1111:A:H8	1.83	0.44
53:1:1287:A:O2'	53:1:1288:G:H5'	2.17	0.44
53:1:1417:C:H2'	53:1:1418:G:O4'	2.17	0.44
53:1:1669:A:O3'	53:1:2549:G:H5'	2.17	0.44
53:1:1890:A:H2'	53:1:1891:G:O4'	2.18	0.44
53:1:1977:A:H2'	53:1:1978:A:O4'	2.17	0.44
53:1:2360:G:C2'	53:1:2361:G:H5'	2.48	0.44
53:1:2561:U:H2'	53:1:2562:U:O4'	2.18	0.44
2:c:50:VAL:HG22	2:c:51:THR:N	2.33	0.44
5:f:175:LYS:O	5:f:176:LYS:HG3	2.17	0.44
7:h:122:GLN:CD	7:h:122:GLN:N	2.76	0.44
10:k:48:PRO:HB3	52:3:1422:G:H4'	2.00	0.44
11:l:85:VAL:O	11:l:86:GLU:HG2	2.17	0.44
27:C:28:THR:HG23	27:C:29:LYS:HG3	1.98	0.44
29:E:32:LEU:HB3	29:E:40:LYS:HZ1	1.82	0.44
31:G:41:ASN:HD21	31:G:43:GLU:CD	2.26	0.44
42:R:85:TYR:CE1	52:3:1321:U:H4'	2.53	0.44
52:3:876:C:H2'	52:3:877:G:C8	2.52	0.44
52:3:962:C:H2'	52:3:963:G:H8	1.83	0.44
52:3:1011:C:H2'	52:3:1012:A:C8	2.52	0.44
52:3:1033:G:C2'	52:3:1034:G:H5''	2.47	0.44
52:3:1243:C:H2'	52:3:1244:G:H8	1.82	0.44
53:1:717:C:C2'	53:1:718:A:H5'	2.46	0.44
53:1:1086:A:H3'	53:1:1086:A:N3	2.33	0.44
53:1:1111:A:O2'	53:1:1112:G:H4'	2.18	0.44
53:1:1114:C:H2'	53:1:1115:G:C8	2.53	0.44
53:1:2786:U:H2'	53:1:2787:C:H6	1.82	0.44
58:8:24:GLY:HA3	58:8:136:ASN:ND2	2.33	0.44
58:8:176:LEU:HD12	58:8:177:LYS:HD2	1.99	0.44
2:c:29:VAL:O	2:c:29:VAL:HG13	2.17	0.44
2:c:49:GLN:CD	2:c:79:LEU:HD13	2.43	0.44
8:i:78:LEU:HA	8:i:81:LYS:HE3	2.00	0.44
10:k:40:LYS:HE3	53:1:2561:U:O3'	2.17	0.44
13:n:8:ARG:N	13:n:43:GLU:OE2	2.50	0.44
32:H:56:ILE:HG23	32:H:63:ILE:HD11	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:69:THR:HG22	32:H:71:ARG:N	2.31	0.44
33:I:53:GLN:OE1	33:I:201:GLU:HG2	2.18	0.44
33:I:131:ILE:HD12	33:I:131:ILE:N	2.29	0.44
34:J:104:ILE:O	34:J:111:ARG:NH1	2.47	0.44
35:K:78:PHE:CD1	35:K:84:VAL:HG11	2.52	0.44
37:M:104:SER:HB2	37:M:125:ILE:HD11	2.00	0.44
43:S:68:ARG:HE	52:3:1202:U:C1'	2.30	0.44
51:a:197:LYS:O	51:a:200:LYS:HG2	2.18	0.44
52:3:597:G:C2'	52:3:598:U:H5'	2.47	0.44
52:3:1086:U:H2'	52:3:1087:G:C8	2.51	0.44
52:3:1456:A:H2'	52:3:1457:G:O4'	2.17	0.44
53:1:49:A:H5'	53:1:51:G:H5'	2.00	0.44
53:1:121:G:H4'	53:1:149:A:H5'	2.00	0.44
53:1:414:C:H2'	53:1:415:A:H8	1.82	0.44
53:1:1999:C:H5''	53:1:2723:C:O2'	2.17	0.44
4:e:102:LEU:O	4:e:106:ALA:HB3	2.18	0.44
15:p:51:ASN:O	53:1:2845:U:H5''	2.18	0.44
17:r:91:GLN:HE21	53:1:993:G:H1'	1.83	0.44
20:u:47:PRO:HG3	53:1:484:C:OP1	2.17	0.44
26:B:8:THR:OG1	26:B:9:ARG:N	2.50	0.44
31:G:14:HIS:HA	31:G:40:ILE:HB	2.00	0.44
32:H:39:ARG:NH1	32:H:54:ILE:HB	2.33	0.44
34:J:57:ALA:O	34:J:60:GLN:NE2	2.51	0.44
34:J:153:ALA:HB2	34:J:163:ILE:CD1	2.48	0.44
36:L:41:ILE:HD11	52:3:1240:U:O4'	2.17	0.44
37:M:14:ARG:HD2	52:3:875:U:O2'	2.18	0.44
42:R:3:ILE:HG12	42:R:7:ASN:HD22	1.83	0.44
42:R:27:THR:HG21	52:3:1328:C:OP1	2.18	0.44
49:Y:2:ASN:ND2	52:3:351:G:OP1	2.51	0.44
52:3:1060:U:H2'	52:3:1061:G:H8	1.82	0.44
52:3:1193:G:O2'	52:3:1194:U:H5'	2.18	0.44
52:3:1218:C:H2'	52:3:1219:A:C8	2.51	0.44
52:3:1293:C:H2'	52:3:1294:G:H8	1.82	0.44
52:3:1402:C:H2'	52:3:1403:C:O4'	2.17	0.44
53:1:146:A:H2'	53:1:147:C:C6	2.52	0.44
53:1:208:C:H2'	53:1:209:C:H6	1.82	0.44
53:1:1101:U:H2'	53:1:1102:C:H6	1.82	0.44
53:1:1231:U:H2'	53:1:1232:G:H8	1.83	0.44
53:1:2187:U:H2'	53:1:2188:U:C6	2.53	0.44
58:8:145:GLU:O	58:8:148:GLU:HG3	2.18	0.44
58:8:196:LEU:O	58:8:200:ILE:HB	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:144:GLU:OE2	1:b:188:ARG:HB2	2.18	0.44
2:c:13:ARG:HH11	15:p:55:HIS:HA	1.83	0.44
22:w:36:GLN:NE2	22:w:38:GLY:O	2.51	0.44
40:P:58:THR:HG22	40:P:60:PHE:H	1.82	0.44
52:3:681:A:H2'	52:3:682:G:C8	2.53	0.44
52:3:757:U:H2'	52:3:758:C:O4'	2.17	0.44
52:3:936:C:H2'	52:3:937:A:O4'	2.18	0.44
52:3:990:C:H2'	52:3:991:U:O4'	2.18	0.44
52:3:1472:U:H2'	52:3:1473:G:H8	1.83	0.44
53:1:250:G:C6	53:1:251:A:C6	3.05	0.44
53:1:2638:G:N2	53:1:2775:G:H2'	2.33	0.44
53:1:2772:C:H2'	53:1:2773:C:C6	2.52	0.44
58:8:87:ASP:HA	58:8:90:LYS:HE3	2.00	0.44
58:8:256:CYS:SG	58:8:277:VAL:HG13	2.58	0.44
2:c:9:VAL:HB	2:c:26:VAL:CG2	2.46	0.43
7:h:114:GLU:HA	7:h:123:ILE:HA	1.98	0.43
38:N:33:SER:H	38:N:36:GLN:CD	2.26	0.43
38:N:57:VAL:HG23	38:N:58:GLU:N	2.33	0.43
42:R:33:LEU:HD12	42:R:34:ALA:N	2.32	0.43
49:Y:55:PRO:CB	52:3:194:C:H5'	2.48	0.43
52:3:52:C:H2'	52:3:53:A:H8	1.83	0.43
52:3:205:A:H2'	52:3:206:C:O4'	2.18	0.43
52:3:1243:C:H2'	52:3:1244:G:C8	2.53	0.43
53:1:139:U:H5'	53:1:140:C:OP1	2.18	0.43
53:1:1335:C:H2'	53:1:1336:A:H8	1.82	0.43
53:1:1747:U:H2'	53:1:1748:C:C6	2.53	0.43
53:1:2475:C:H42	53:1:2529:G:H22	1.65	0.43
58:8:367:ILE:HG23	58:8:369:MET:HG2	2.00	0.43
13:n:17:ARG:HH21	13:n:17:ARG:HB2	1.83	0.43
14:o:58:ILE:O	14:o:62:LEU:HG	2.18	0.43
16:q:69:ARG:NH1	53:1:1012:U:OP2	2.51	0.43
18:s:109:ASP:OD1	18:s:109:ASP:N	2.49	0.43
19:t:30:ILE:HG23	19:t:85:VAL:HB	2.00	0.43
30:F:3:VAL:O	30:F:37:GLN:NE2	2.51	0.43
45:U:39:PHE:CE2	45:U:41:PRO:HB3	2.53	0.43
51:a:209:ILE:O	51:a:210:LYS:C	2.61	0.43
52:3:86:G:H4'	52:3:87:C:C6	2.53	0.43
52:3:212:G:O2'	52:3:213:G:H5'	2.18	0.43
52:3:399:G:H2'	52:3:400:C:H6	1.83	0.43
52:3:516:U:H3	52:3:533:A:H62	1.65	0.43
52:3:530:G:H3'	52:3:531:U:C5'	2.48	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:26:G:H1'	53:1:514:A:N6	2.32	0.43
53:1:49:A:C5'	53:1:51:G:H5'	2.48	0.43
53:1:359:G:H2'	53:1:360:U:O4'	2.18	0.43
53:1:1378:A:H1'	53:1:1379:U:C5	2.52	0.43
53:1:1417:C:H4'	53:1:1587:G:H21	1.83	0.43
53:1:1550:C:H2'	53:1:1551:A:C8	2.52	0.43
58:8:26:THR:HG23	58:8:50:ILE:HG22	1.99	0.43
58:8:112:PRO:HG2	58:8:153:GLU:HB3	2.00	0.43
1:b:141:HIS:HD2	1:b:142:ASN:HB2	1.82	0.43
8:i:33:ASN:O	8:i:36:GLU:HG2	2.19	0.43
11:l:36:LYS:HE2	53:1:808:G:OP2	2.18	0.43
22:w:39:THR:C	22:w:41:PHE:N	2.75	0.43
31:G:28:PRO:O	31:G:44:LYS:NZ	2.50	0.43
32:H:100:ILE:HD12	32:H:100:ILE:N	2.33	0.43
39:O:39:PRO:HD2	52:3:1123:U:H4'	1.99	0.43
42:R:76:ILE:HG23	42:R:77:LYS:N	2.33	0.43
45:U:48:GLU:HG3	45:U:49:GLY:H	1.83	0.43
52:3:1162:C:H2'	52:3:1163:A:H8	1.83	0.43
53:1:196:A:N3	53:1:196:A:H2'	2.33	0.43
53:1:935:C:H2'	53:1:936:A:C8	2.53	0.43
53:1:1401:G:H2'	53:1:1402:U:O4'	2.18	0.43
53:1:1935:G:H1'	53:1:1964:G:N2	2.32	0.43
53:1:1965:C:H5''	53:1:1966:A:H2'	1.99	0.43
53:1:2282:G:H4'	53:1:2389:G:O2'	2.18	0.43
53:1:2784:U:H2'	53:1:2785:C:C6	2.53	0.43
58:8:71:ASP:OD2	58:8:71:ASP:N	2.49	0.43
58:8:282:ILE:HG23	58:8:286:GLU:HB2	2.00	0.43
4:e:141:ASP:H	4:e:144:LYS:HZ3	1.66	0.43
8:i:52:LEU:HA	8:i:53:PRO:HD3	1.89	0.43
12:m:22:GLN:HG2	53:1:864:G:OP2	2.18	0.43
13:n:92:GLY:O	53:1:2880:C:H1'	2.18	0.43
29:E:31:ILE:O	29:E:31:ILE:HG13	2.18	0.43
31:G:41:ASN:HD21	31:G:43:GLU:HG3	1.84	0.43
33:I:39:GLN:HB2	52:3:541:G:O2'	2.18	0.43
38:N:53:LEU:HD12	38:N:53:LEU:N	2.33	0.43
52:3:463:U:H3	52:3:469:C:N4	2.16	0.43
52:3:1119:C:H2'	52:3:1120:C:C6	2.53	0.43
52:3:1458:G:H2'	52:3:1459:G:H8	1.83	0.43
53:1:519:U:H2'	53:1:520:G:C8	2.54	0.43
53:1:970:U:H2'	53:1:971:G:C8	2.52	0.43
53:1:1287:A:C2'	53:1:1288:G:H5'	2.48	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2589:A:H2'	53:1:2590:A:H8	1.82	0.43
53:1:2863:C:H2'	53:1:2864:G:H8	1.83	0.43
54:2:108:A:H5'	54:2:109:A:O5'	2.19	0.43
57:7:39:U:H2'	57:7:40:C:C6	2.54	0.43
58:8:357:ILE:HG12	58:8:358:LYS:H	1.84	0.43
2:c:12:THR:HB	15:p:4:ILE:HD11	2.01	0.43
4:e:56:LEU:HD12	4:e:86:CYS:SG	2.58	0.43
8:i:10:LEU:N	8:i:10:LEU:CD2	2.82	0.43
15:p:109:ILE:HD12	15:p:109:ILE:N	2.33	0.43
16:q:91:ARG:HG3	16:q:91:ARG:NH1	2.33	0.43
23:x:60:LYS:HD3	53:1:372:G:C8	2.53	0.43
27:C:9:LYS:N	27:C:9:LYS:HD3	2.33	0.43
35:K:51:ILE:HG23	35:K:86:ARG:HH21	1.84	0.43
38:N:33:SER:H	38:N:36:GLN:HG2	1.83	0.43
45:U:1:MET:HE3	45:U:2:VAL:H	1.83	0.43
52:3:128:G:O2'	52:3:129:A:H5'	2.18	0.43
52:3:194:C:O2'	52:3:195:A:H5'	2.18	0.43
52:3:861:G:H2'	52:3:862:C:O4'	2.17	0.43
52:3:1053:G:O6	52:3:1200:C:H5'	2.17	0.43
53:1:275:C:H3'	53:1:276:U:H5''	2.01	0.43
53:1:441:U:H2'	53:1:442:G:C8	2.54	0.43
53:1:560:C:H2'	53:1:561:G:O4'	2.18	0.43
53:1:714:U:H2'	53:1:716:A:N7	2.34	0.43
53:1:1669:A:H5''	53:1:2550:G:OP1	2.18	0.43
53:1:1881:C:H2'	53:1:1882:U:O4'	2.18	0.43
53:1:1912:A:H62	53:1:1917:U:H3	1.65	0.43
53:1:2328:A:H2'	53:1:2329:U:C6	2.53	0.43
53:1:2665:A:O2'	53:1:2666:C:H5'	2.19	0.43
53:1:2758:A:H2'	53:1:2759:G:O4'	2.18	0.43
58:8:213:LEU:HA	58:8:214:PRO:HD3	1.84	0.43
1:b:42:ARG:HD3	1:b:48:ILE:HA	2.00	0.43
1:b:107:LYS:N	1:b:193:GLU:O	2.49	0.43
12:m:41:LEU:HD22	12:m:125:PRO:HD2	1.99	0.43
33:I:14:GLU:HG2	33:I:59:LYS:HE2	2.01	0.43
52:3:1517:G:C2'	52:3:1518:A:H5'	2.49	0.43
53:1:178:G:O2'	53:1:179:C:H5'	2.19	0.43
53:1:685:A:H5''	53:1:788:A:H62	1.84	0.43
53:1:857:G:H2'	53:1:858:G:O4'	2.19	0.43
53:1:1161:C:H2'	53:1:1162:G:C8	2.52	0.43
53:1:2431:U:H2'	53:1:2433:A:OP2	2.19	0.43
54:2:28:C:H2'	54:2:29:A:C8	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:209:ALA:O	1:b:213:ARG:HG2	2.19	0.43
3:d:165:HIS:HE1	53:1:1205:A:H2'	1.84	0.43
3:d:195:GLN:HA	3:d:198:GLU:OE2	2.18	0.43
6:g:2:GLN:O	6:g:39:ALA:HB2	2.19	0.43
17:r:38:VAL:HG12	17:r:59:ILE:HG13	2.01	0.43
36:L:3:ARG:NH1	52:3:932:C:H5''	2.33	0.43
38:N:113:LYS:HG2	52:3:1368:A:OP2	2.19	0.43
45:U:47:GLU:CD	45:U:47:GLU:H	2.26	0.43
51:a:163:TYR:HB2	51:a:171:ILE:HD11	2.00	0.43
52:3:396:C:C2'	52:3:397:A:H5''	2.44	0.43
52:3:756:C:H2'	52:3:757:U:O4'	2.18	0.43
52:3:766:A:H2'	52:3:767:A:O4'	2.19	0.43
53:1:191:A:H2'	53:1:192:C:C6	2.54	0.43
53:1:594:U:H2'	53:1:595:C:C6	2.54	0.43
53:1:655:A:H4'	53:1:656:G:H5'	2.00	0.43
53:1:1367:A:C2'	53:1:1368:G:H5'	2.49	0.43
53:1:1609:A:H1'	53:1:1616:A:O4'	2.19	0.43
53:1:2333:A:H5'	53:1:2335:A:H1'	2.01	0.43
53:1:2747:G:O6	53:1:2755:C:H5''	2.19	0.43
58:8:231:ARG:HA	58:8:274:ASN:HA	2.01	0.43
3:d:7:ASP:HB2	3:d:122:GLU:OE2	2.19	0.43
8:i:23:VAL:HG13	8:i:26:ALA:HB3	2.01	0.43
8:i:25:PRO:HG2	57:7:55:U:C3'	2.42	0.43
8:i:33:ASN:ND2	8:i:35:MET:HB2	2.33	0.43
12:m:66:ARG:O	12:m:100:LYS:NZ	2.52	0.43
15:p:47:ILE:HG13	15:p:59:THR:HG23	2.00	0.43
17:r:51:VAL:CG1	17:r:52:PRO:HD2	2.48	0.43
23:x:13:THR:CG2	53:1:188:G:H5'	2.49	0.43
31:G:163:ILE:HG13	31:G:185:ILE:HD12	2.01	0.43
32:H:38:VAL:O	32:H:42:LEU:HD23	2.18	0.43
38:N:17:ARG:HB2	38:N:65:THR:OG1	2.18	0.43
52:3:680:C:H2'	52:3:681:A:H8	1.82	0.43
52:3:1448:C:H2'	52:3:1449:C:C6	2.53	0.43
53:1:925:A:H2'	53:1:926:G:C8	2.54	0.43
53:1:1866:A:H2'	53:1:1867:G:O4'	2.19	0.43
53:1:2364:C:H2'	53:1:2365:G:O4'	2.17	0.43
53:1:2398:U:H2'	53:1:2399:G:H8	1.83	0.43
53:1:2626:C:O2'	53:1:2627:G:H5'	2.19	0.43
55:5:16:C:HO2'	55:5:17:C:H5'	1.84	0.43
1:b:23:LEU:HA	1:b:80:LEU:O	2.19	0.43
1:b:73:ILE:HG12	53:1:1490:A:C6	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:140:VAL:HG12	1:b:141:HIS:N	2.34	0.43
5:f:23:ILE:HD11	5:f:42:VAL:HG11	2.00	0.43
6:g:72:ILE:HB	6:g:108:VAL:HG22	2.00	0.43
8:i:78:LEU:HD13	8:i:112:LYS:HE3	2.00	0.43
10:k:87:LEU:HB3	10:k:92:GLU:O	2.18	0.43
12:m:58:LYS:HE3	12:m:59:ARG:HG2	2.01	0.43
15:p:50:ARG:HD3	15:p:57:ALA:HB3	2.01	0.43
17:r:87:GLN:HG3	53:1:1224:U:O2'	2.19	0.43
20:u:5:ARG:NH1	53:1:84:A:OP1	2.52	0.43
26:B:5:ASN:ND2	53:1:2020:A:H62	2.17	0.43
33:I:59:LYS:O	33:I:63:ILE:HG13	2.19	0.43
35:K:46:GLN:HA	35:K:56:LYS:HG2	2.00	0.43
39:O:15:HIS:HB3	39:O:70:HIS:CE1	2.53	0.43
46:V:42:LYS:C	46:V:43:LEU:HD12	2.43	0.43
48:X:13:HIS:HB2	52:3:1014:A:H5''	2.01	0.43
52:3:24:U:H2'	52:3:25:C:H6	1.84	0.43
52:3:1346:A:C2'	52:3:1347:G:H4'	2.48	0.43
52:3:1347:G:O2'	52:3:1348:U:H5	2.02	0.43
53:1:1015:U:H2'	53:1:1016:G:C8	2.53	0.43
53:1:1273:U:H5''	53:1:1646:C:N4	2.34	0.43
54:2:19:C:H2'	54:2:20:G:H8	1.84	0.43
55:5:62:C:H2'	55:5:63:G:H8	1.82	0.43
58:8:283:LYS:H	58:8:286:GLU:CD	2.27	0.43
1:b:250:GLN:NE2	1:b:251:THR:O	2.47	0.43
8:i:87:SER:OG	8:i:88:GLY:N	2.51	0.43
33:I:171:GLU:HB3	33:I:180:THR:HG23	2.01	0.43
34:J:15:ILE:HG23	34:J:16:ALA:N	2.33	0.43
38:N:94:ARG:HG2	38:N:97:LEU:HD12	2.00	0.43
42:R:30:LYS:HA	42:R:33:LEU:HG	2.00	0.43
45:U:12:LYS:O	45:U:13:LYS:HB2	2.19	0.43
49:Y:4:LYS:HE3	52:3:61:G:P	2.58	0.43
51:a:22:ASP:HB3	51:a:25:GLU:HG3	2.01	0.43
52:3:674:G:H2'	52:3:675:A:H8	1.84	0.43
52:3:1105:A:H2'	52:3:1106:G:H8	1.84	0.43
52:3:1347:G:O2'	52:3:1348:U:C5	2.72	0.43
52:3:1397:C:N4	56:4:22:A:H3'	2.34	0.43
53:1:43:G:H2'	53:1:44:A:O4'	2.19	0.43
53:1:1041:G:O2'	53:1:1042:G:H5'	2.19	0.43
53:1:1055:G:H2'	53:1:1056:G:O4'	2.19	0.43
53:1:1979:U:C2'	53:1:1980:G:H5'	2.49	0.43
53:1:2248:C:H2'	53:1:2249:U:C5'	2.46	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:147:LEU:O	58:8:150:VAL:HG12	2.19	0.43
58:8:323:PHE:CE1	58:8:351:VAL:HB	2.54	0.43
6:g:70:GLU:OE2	6:g:71:LYS:HG2	2.19	0.42
7:h:3:LEU:HG	7:h:6:GLN:OE1	2.19	0.42
11:l:95:LEU:HD22	11:l:100:ILE:HD11	2.00	0.42
14:o:12:THR:HG23	53:1:2334:U:H4'	2.00	0.42
16:q:50:ARG:HG2	53:1:1156:A:C8	2.54	0.42
19:t:64:LYS:HA	19:t:79:ASP:OD2	2.19	0.42
29:E:18:LYS:HB3	29:E:18:LYS:HE2	1.82	0.42
37:M:51:GLU:O	37:M:57:GLU:N	2.51	0.42
42:R:13:HIS:NE2	52:3:1296:C:H5'	2.33	0.42
43:S:48:GLN:NE2	52:3:1317:C:O2'	2.52	0.42
46:V:13:SER:O	46:V:21:VAL:HG12	2.19	0.42
48:X:30:LEU:HD12	48:X:30:LEU:N	2.34	0.42
52:3:236:A:H2'	52:3:237:G:H8	1.84	0.42
52:3:1056:U:H2'	52:3:1057:G:C8	2.54	0.42
53:1:490:C:O2'	53:1:491:G:P	2.77	0.42
53:1:821:A:H2'	53:1:946:C:O4'	2.19	0.42
53:1:874:G:H2'	53:1:875:G:C8	2.54	0.42
53:1:1190:G:H2'	53:1:1191:G:H8	1.84	0.42
53:1:1629:U:H2'	53:1:1630:A:C8	2.54	0.42
53:1:1823:G:O2'	53:1:1824:G:H5'	2.18	0.42
53:1:1860:G:H2'	53:1:1861:G:C8	2.53	0.42
53:1:2172:U:OP1	53:1:2173:A:H8	2.02	0.42
53:1:2522:U:C2'	53:1:2523:G:H5'	2.49	0.42
53:1:2655:G:O2'	53:1:2656:U:H5	2.02	0.42
54:2:5:U:H2'	54:2:6:G:H8	1.84	0.42
58:8:248:ILE:HA	58:8:366:PRO:O	2.18	0.42
4:e:122:ASP:OD2	4:e:124:ARG:HB2	2.19	0.42
7:h:55:VAL:HA	53:1:1084:A:C5'	2.49	0.42
12:m:31:PHE:HB2	12:m:105:MET:SD	2.58	0.42
15:p:28:LYS:HD2	15:p:82:SER:HB2	2.01	0.42
24:y:41:HIS:CG	53:1:96:C:H4'	2.53	0.42
31:G:94:ARG:HD3	52:3:1100:C:OP2	2.19	0.42
31:G:134:LEU:HD23	31:G:134:LEU:O	2.19	0.42
33:I:49:ASP:O	33:I:52:VAL:HG22	2.19	0.42
33:I:58:GLN:OE1	33:I:58:GLN:HA	2.19	0.42
34:J:12:GLU:HA	34:J:38:VAL:HG12	2.01	0.42
37:M:14:ARG:NH2	37:M:74:ILE:O	2.51	0.42
44:T:27:GLN:NE2	52:3:656:G:O2'	2.52	0.42
47:W:20:ILE:HG21	47:W:54:LEU:HD12	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:253:A:H2'	52:3:254:G:C8	2.54	0.42
52:3:1347:G:H22	52:3:1373:G:H3'	1.83	0.42
52:3:1522:U:H2'	52:3:1523:G:C8	2.54	0.42
53:1:167:A:H2'	53:1:168:G:O4'	2.19	0.42
53:1:1360:G:H2'	53:1:1361:G:H5'	2.01	0.42
53:1:1594:U:H2'	53:1:1595:C:C6	2.54	0.42
53:1:1956:U:C2'	53:1:1957:C:H5'	2.49	0.42
53:1:2522:U:H2'	53:1:2523:G:H5'	2.00	0.42
53:1:2638:G:H22	53:1:2775:G:H2'	1.83	0.42
58:8:10:LYS:HZ1	58:8:236:ILE:HG12	1.84	0.42
58:8:24:GLY:HA3	58:8:136:ASN:HD22	1.84	0.42
6:g:12:LEU:HD13	6:g:19:VAL:HG21	2.01	0.42
16:q:54:ARG:HH12	53:1:977:G:H5''	1.83	0.42
23:x:18:SER:HB2	53:1:2080:A:H5'	2.02	0.42
42:R:63:VAL:HG23	42:R:67:ASP:HB2	2.01	0.42
50:Z:49:ALA:O	50:Z:53:LYS:HG2	2.20	0.42
50:Z:50:SER:O	50:Z:54:ARG:HG3	2.19	0.42
52:3:231:U:H2'	52:3:232:G:H8	1.83	0.42
52:3:1333:A:H2'	52:3:1334:G:O4'	2.20	0.42
52:3:1384:C:H2'	52:3:1385:G:C8	2.54	0.42
52:3:1389:C:H2'	52:3:1390:U:C6	2.54	0.42
53:1:106:C:H2'	53:1:107:G:C8	2.54	0.42
53:1:1086:A:H4'	53:1:1103:A:N1	2.34	0.42
58:8:328:ARG:HB3	58:8:341:THR:HA	2.01	0.42
2:c:25:THR:CG2	2:c:189:VAL:HG23	2.50	0.42
9:j:40:HIS:CE1	9:j:41:LYS:HG3	2.54	0.42
11:l:63:LYS:HE3	29:E:11:LYS:HD2	2.00	0.42
12:m:38:ARG:NH1	12:m:98:PRO:HD3	2.34	0.42
15:p:94:ALA:HB2	53:1:2848:G:C8	2.55	0.42
16:q:26:ALA:O	16:q:30:VAL:HG22	2.18	0.42
17:r:7:SER:OG	17:r:22:LEU:HD22	2.19	0.42
31:G:89:PHE:CZ	31:G:153:MET:HA	2.55	0.42
34:J:45:VAL:HG12	34:J:116:VAL:HG23	2.01	0.42
36:L:67:ASN:ND2	36:L:126:ALA:O	2.51	0.42
49:Y:10:ALA:O	49:Y:14:GLU:HG2	2.18	0.42
52:3:279:A:H4'	52:3:281:G:C8	2.54	0.42
52:3:512:U:H2'	52:3:513:C:C6	2.55	0.42
52:3:674:G:H2'	52:3:675:A:C8	2.55	0.42
52:3:1014:A:C2	52:3:1219:A:H1'	2.54	0.42
52:3:1187:G:O2'	52:3:1188:A:H5'	2.19	0.42
52:3:1464:U:H2'	52:3:1465:A:H8	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1184:U:O2'	53:1:1185:G:H5'	2.19	0.42
53:1:1258:U:H2'	53:1:1259:G:H8	1.84	0.42
53:1:2427:C:H5''	53:1:2429:G:H5'	2.00	0.42
53:1:2516:A:O2'	53:1:2517:C:H5'	2.19	0.42
53:1:2773:C:H2'	53:1:2774:C:H6	1.83	0.42
58:8:104:LEU:HG	58:8:106:VAL:HG23	2.01	0.42
2:c:110:THR:HG21	2:c:169:ARG:NH1	2.32	0.42
4:e:103:ILE:HG21	4:e:174:PHE:HE1	1.84	0.42
4:e:107:VAL:HG21	4:e:175:PRO:HG2	2.01	0.42
5:f:175:LYS:C	5:f:176:LYS:HG3	2.44	0.42
6:g:3:VAL:HG13	6:g:37:VAL:C	2.44	0.42
10:k:42:THR:HG22	10:k:57:VAL:HG22	2.02	0.42
11:l:2:ARG:HD2	11:l:5:THR:OG1	2.19	0.42
15:p:13:LYS:HZ1	15:p:80:VAL:HG23	1.84	0.42
23:x:16:ASN:HB3	23:x:24:THR:OG1	2.20	0.42
32:H:112:ALA:HB3	32:H:184:ASN:ND2	2.34	0.42
33:I:2:ARG:HH12	52:3:406:G:H4'	1.83	0.42
34:J:113:VAL:HG11	34:J:139:THR:HG21	2.01	0.42
34:J:121:ASN:HB3	34:J:122:VAL:H	1.43	0.42
35:K:12:PRO:HG3	35:K:56:LYS:O	2.20	0.42
38:N:48:ARG:O	38:N:52:GLU:HG2	2.19	0.42
39:O:88:MET:HG3	39:O:89:ARG:HD3	2.01	0.42
42:R:2:ARG:HA	42:R:7:ASN:O	2.19	0.42
43:S:2:LYS:HB3	43:S:2:LYS:HE2	1.85	0.42
44:T:61:GLN:O	44:T:65:LEU:HG	2.19	0.42
50:Z:11:PHE:HB2	50:Z:15:LEU:HD12	2.01	0.42
50:Z:39:LYS:O	50:Z:40:PRO:C	2.58	0.42
51:a:221:GLY:N	53:1:2176:A:H5''	2.35	0.42
52:3:34:C:H2'	52:3:35:G:H8	1.83	0.42
52:3:1248:A:O2'	52:3:1249:C:H5'	2.19	0.42
53:1:492:A:H2'	53:1:493:G:O4'	2.19	0.42
53:1:621:A:C2'	53:1:622:G:H5'	2.49	0.42
53:1:1528:A:H2'	53:1:1529:G:O4'	2.19	0.42
53:1:1882:U:H2'	53:1:1883:U:C6	2.53	0.42
53:1:2041:U:H2'	53:1:2042:A:H8	1.84	0.42
53:1:2114:A:H2'	53:1:2114:A:N3	2.35	0.42
53:1:2498:C:O2'	53:1:2499:C:H5'	2.20	0.42
53:1:2508:G:H1	53:1:2580:U:H3	1.68	0.42
53:1:2825:G:H2'	53:1:2826:A:H5'	2.02	0.42
54:2:37:C:H42	54:2:49:C:H1'	1.84	0.42
58:8:32:ILE:HA	58:8:35:VAL:HG12	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:89:ASN:ND2	1:b:196:ASN:ND2	2.67	0.42
1:b:94:LEU:HD11	53:1:1501:G:H4'	2.00	0.42
3:d:24:ASN:ND2	3:d:27:LEU:HB2	2.34	0.42
6:g:31:VAL:CG1	6:g:32:PRO:HD3	2.49	0.42
7:h:67:THR:N	7:h:68:PRO:CD	2.83	0.42
9:j:78:THR:CB	53:1:2641:G:H5''	2.49	0.42
12:m:97:GLN:CD	12:m:97:GLN:N	2.75	0.42
23:x:2:ARG:HD3	23:x:29:LEU:HD22	2.02	0.42
32:H:128:MET:HB2	32:H:131:ARG:HD2	2.02	0.42
32:H:162:ALA:HB3	52:3:1056:U:H5'	2.02	0.42
36:L:46:LEU:HD11	36:L:57:GLU:HA	2.01	0.42
36:L:78:ARG:NH2	36:L:81:GLY:O	2.52	0.42
38:N:123:ARG:HB2	52:3:1343:G:H4'	2.01	0.42
39:O:38:GLY:O	39:O:40:ILE:HD12	2.19	0.42
45:U:1:MET:HE2	45:U:66:THR:HG22	2.01	0.42
50:Z:19:LYS:HB3	50:Z:24:LYS:HG3	2.02	0.42
53:1:302:C:H2'	53:1:303:G:H8	1.83	0.42
53:1:466:A:C2'	53:1:467:G:H5'	2.50	0.42
53:1:1138:G:H2'	53:1:1139:G:O4'	2.20	0.42
53:1:1330:C:O2'	53:1:1331:G:H5'	2.20	0.42
53:1:1447:C:H2'	53:1:1448:G:C8	2.55	0.42
54:2:100:G:H2'	54:2:101:A:O4'	2.20	0.42
7:h:27:VAL:HG13	7:h:110:ALA:HA	2.02	0.42
10:k:109:SER:O	10:k:110:GLU:HB2	2.20	0.42
31:G:220:VAL:HG23	31:G:221:ARG:N	2.34	0.42
33:I:144:ILE:HD13	33:I:177:MET:HB3	2.02	0.42
34:J:108:GLY:O	34:J:109:ALA:HB3	2.19	0.42
35:K:42:TRP:CD1	35:K:61:LEU:HD13	2.55	0.42
37:M:80:PRO:HG2	52:3:878:A:H5'	2.01	0.42
40:P:71:ASP:O	40:P:72:ALA:HB3	2.18	0.42
43:S:30:ILE:HG22	43:S:30:ILE:O	2.20	0.42
46:V:80:LYS:HG2	46:V:81:ALA:N	2.35	0.42
50:Z:58:LYS:O	50:Z:61:ARG:HD2	2.20	0.42
52:3:35:G:H2'	52:3:36:C:C6	2.55	0.42
52:3:621:A:H2'	52:3:622:A:H8	1.83	0.42
52:3:834:U:H2'	52:3:835:U:C6	2.55	0.42
52:3:1339:A:H2'	52:3:1340:A:H5'	2.02	0.42
53:1:162:U:O2'	53:1:163:C:H5'	2.20	0.42
53:1:1930:G:O2'	53:1:1931:U:C5	2.72	0.42
53:1:2086:U:H2'	53:1:2087:G:H8	1.83	0.42
53:1:2581:G:H2'	53:1:2581:G:N3	2.33	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2841:C:H2'	53:1:2842:G:H8	1.83	0.42
3:d:45:ALA:HA	3:d:87:ALA:O	2.19	0.42
6:g:37:VAL:HA	6:g:38:PRO:HD3	1.93	0.42
8:i:11:GLN:HG2	8:i:54:ILE:O	2.19	0.42
12:m:74:THR:OG1	12:m:75:GLU:N	2.53	0.42
13:n:103:ARG:HH11	53:1:1287:A:C5'	2.24	0.42
16:q:58:GLN:HA	16:q:61:ILE:HD12	2.01	0.42
20:u:48:VAL:O	20:u:53:GLN:HB3	2.20	0.42
22:w:10:ARG:NH2	53:1:2279:G:N7	2.68	0.42
31:G:212:TYR:O	31:G:216:VAL:HG23	2.19	0.42
33:I:90:LEU:O	33:I:94:GLU:HG2	2.20	0.42
42:R:106:ARG:NE	42:R:112:ARG:HG2	2.35	0.42
52:3:34:C:H2'	52:3:35:G:C8	2.55	0.42
52:3:144:G:O2'	52:3:145:G:H5'	2.19	0.42
52:3:298:A:H2'	52:3:299:G:O4'	2.20	0.42
52:3:382:A:O2'	52:3:383:A:H5'	2.20	0.42
52:3:384:G:H2'	52:3:385:C:C6	2.55	0.42
52:3:744:C:H2'	52:3:745:G:C8	2.55	0.42
53:1:767:U:H2'	53:1:768:G:H8	1.85	0.42
53:1:876:C:H2'	53:1:877:A:O4'	2.19	0.42
53:1:2350:C:H2'	53:1:2351:G:O4'	2.20	0.42
53:1:2422:C:O2'	53:1:2423:U:H5'	2.19	0.42
5:f:39:ALA:HA	5:f:57:TYR:CD2	2.55	0.42
15:p:70:GLU:OE2	15:p:100:ARG:NH1	2.53	0.42
34:J:108:GLY:N	52:3:9:G:H4'	2.31	0.42
37:M:84:ILE:CG2	37:M:124:ILE:HD11	2.50	0.42
38:N:68:GLY:HA2	52:3:1250:A:C4'	2.50	0.42
40:P:64:VAL:O	40:P:67:GLU:HG3	2.19	0.42
52:3:40:C:H2'	52:3:41:G:H8	1.85	0.42
52:3:50:A:N6	52:3:361:G:H4'	2.34	0.42
52:3:250:A:H4'	52:3:252:U:C6	2.55	0.42
53:1:940:G:C3'	53:1:941:A:H5''	2.50	0.42
53:1:971:G:H2'	53:1:972:A:O4'	2.20	0.42
53:1:1068:G:H2'	53:1:1069:A:C1'	2.49	0.42
53:1:1507:C:C2'	53:1:1508:A:H4'	2.50	0.42
53:1:1877:A:H2'	53:1:1878:G:O4'	2.20	0.42
53:1:2489:U:C2'	53:1:2490:G:H5'	2.49	0.42
53:1:2678:C:H2'	53:1:2679:A:C8	2.55	0.42
57:7:62:C:H2'	57:7:63:G:C4'	2.49	0.42
1:b:49:THR:OG1	1:b:50:THR:N	2.53	0.42
3:d:48:THR:O	3:d:52:VAL:HG23	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:136:SER:HB2	6:g:137:GLU:OE1	2.20	0.42
8:i:24:GLY:HA3	8:i:25:PRO:HD3	1.87	0.42
14:o:30:ARG:HH22	54:2:48:U:P	2.42	0.42
14:o:68:LYS:HA	14:o:102:ARG:HG2	2.02	0.42
19:t:29:THR:HG22	19:t:86:THR:HA	2.02	0.42
21:v:1:MET:SD	21:v:1:MET:N	2.85	0.42
23:x:13:THR:HG21	53:1:188:G:H5'	2.01	0.42
26:B:6:LYS:O	26:B:6:LYS:HG3	2.20	0.42
26:B:14:MET:SD	53:1:2045:C:H5''	2.60	0.42
29:E:44:ARG:N	29:E:45:PRO:HD2	2.34	0.42
34:J:104:ILE:O	34:J:104:ILE:HG13	2.19	0.42
34:J:110:MET:HA	34:J:113:VAL:HG12	2.01	0.42
41:Q:30:ARG:HB2	52:3:363:A:OP2	2.20	0.42
44:T:87:ARG:O	44:T:88:ARG:C	2.62	0.42
45:U:38:PHE:CE1	45:U:51:ARG:HB2	2.55	0.42
46:V:64:ARG:HA	46:V:65:PRO:HD3	1.95	0.42
50:Z:13:VAL:HG13	50:Z:15:LEU:HG	2.01	0.42
50:Z:23:GLU:C	50:Z:25:ALA:N	2.77	0.42
50:Z:64:ALA:C	50:Z:66:ARG:H	2.28	0.42
51:a:7:ARG:HB3	53:1:2129:C:OP1	2.18	0.42
52:3:79:G:H2'	52:3:80:A:O4'	2.20	0.42
52:3:319:G:O2'	52:3:320:A:H5'	2.20	0.42
52:3:648:A:H2'	52:3:649:A:H8	1.85	0.42
52:3:684:U:H2'	52:3:685:G:O4'	2.20	0.42
52:3:1315:U:H2'	52:3:1316:G:O4'	2.20	0.42
52:3:1492:A:H2'	53:1:1913:A:C2	2.46	0.42
53:1:106:C:H2'	53:1:107:G:H8	1.85	0.42
53:1:687:C:H5'	53:1:687:C:C6	2.50	0.42
53:1:963:U:O2'	53:1:964:C:H5'	2.19	0.42
53:1:1273:U:H4'	53:1:1275:A:OP1	2.19	0.42
53:1:1685:C:H2'	53:1:1686:C:C6	2.55	0.42
53:1:1746:A:H2'	53:1:1747:U:C6	2.55	0.42
53:1:2115:G:H4'	53:1:2166:U:O2	2.20	0.42
58:8:374:ARG:NE	58:8:388:VAL:HB	2.35	0.42
1:b:38:LYS:H	1:b:38:LYS:HG3	1.67	0.41
3:d:48:THR:C	3:d:50:ALA:H	2.27	0.41
6:g:6:LEU:HD23	6:g:6:LEU:O	2.19	0.41
7:h:118:ILE:N	7:h:119:PRO:CD	2.82	0.41
8:i:51:GLY:C	8:i:52:LEU:HD12	2.46	0.41
9:j:96:ARG:NH1	9:j:98:GLU:OE1	2.53	0.41
14:o:66:GLY:O	14:o:102:ARG:NH2	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:v:20:LEU:C	21:v:23:ALA:H	2.27	0.41
35:K:18:VAL:HG21	35:K:58:HIS:HD2	1.84	0.41
35:K:98:GLU:HB3	35:K:99:ALA:H	1.66	0.41
36:L:3:ARG:NH2	52:3:932:C:H5''	2.35	0.41
37:M:3:GLN:HE22	52:3:755:G:N2	2.18	0.41
37:M:54:THR:HG23	37:M:55:LYS:HG2	2.01	0.41
42:R:21:ILE:N	42:R:21:ILE:HD12	2.35	0.41
42:R:53:ASP:HA	42:R:56:ARG:HH11	1.85	0.41
44:T:66:LEU:HD21	44:T:80:LEU:HD23	2.01	0.41
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.81	0.41
51:a:5:THR:OG1	51:a:6:LYS:N	2.53	0.41
52:3:82:G:C2'	52:3:83:C:H5'	2.50	0.41
52:3:729:A:O2'	52:3:730:G:H5'	2.19	0.41
53:1:20:C:H2'	53:1:21:A:H8	1.81	0.41
53:1:45:G:C5'	53:1:46:G:H5'	2.31	0.41
53:1:2462:C:H2'	53:1:2463:C:C6	2.55	0.41
58:8:146:LEU:HD13	58:8:149:LEU:HD12	2.01	0.41
6:g:31:VAL:N	6:g:32:PRO:CD	2.83	0.41
7:h:66:GLY:HA2	7:h:69:PHE:CE2	2.54	0.41
13:n:3:HIS:O	13:n:4:ARG:HB2	2.20	0.41
18:s:87:PRO:HB3	53:1:1614:A:C6	2.56	0.41
19:t:8:LEU:HD13	24:y:21:LEU:CB	2.50	0.41
19:t:61:LEU:CD2	19:t:82:LYS:HG3	2.50	0.41
22:w:13:GLU:HG3	53:1:2261:C:OP2	2.20	0.41
30:F:12:ARG:HH22	53:1:1102:C:H1'	1.84	0.41
32:H:93:ILE:N	32:H:93:ILE:HD12	2.35	0.41
33:I:38:GLY:HA2	52:3:542:G:C5'	2.49	0.41
34:J:48:GLY:O	34:J:62:ALA:HB1	2.20	0.41
34:J:73:VAL:HG13	34:J:146:MET:HE1	2.02	0.41
39:O:58:ASN:HD22	39:O:58:ASN:HA	1.58	0.41
41:Q:43:LYS:HB3	41:Q:44:PRO:HD3	2.02	0.41
42:R:108:ARG:HD3	52:3:1307:U:O2'	2.20	0.41
43:S:47:LEU:HD21	52:3:1317:C:H4'	2.01	0.41
48:X:5:LYS:HE3	52:3:1313:U:OP1	2.20	0.41
52:3:376:G:O2'	52:3:377:G:H5'	2.20	0.41
52:3:855:U:H2'	52:3:856:C:C6	2.54	0.41
52:3:1477:U:H2'	52:3:1478:U:C6	2.55	0.41
53:1:36:G:O2'	53:1:37:C:H5'	2.19	0.41
53:1:598:U:H2'	53:1:599:A:C8	2.55	0.41
53:1:723:C:H2'	53:1:724:U:O4'	2.19	0.41
53:1:898:C:H2'	53:1:899:A:O4'	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:907:G:O2'	53:1:908:C:H5'	2.19	0.41
53:1:1967:C:H2'	53:1:1968:G:H5'	2.00	0.41
58:8:18:ILE:HB	58:8:119:HIS:CD2	2.54	0.41
58:8:25:LYS:N	61:8:501:GDP:O1A	2.53	0.41
4:e:107:VAL:HG13	4:e:108:PRO:HD3	1.99	0.41
6:g:43:ASN:OD1	6:g:51:ARG:NH1	2.53	0.41
17:r:53:PHE:O	17:r:54:VAL:C	2.62	0.41
20:u:12:VAL:HA	20:u:69:VAL:HG12	2.02	0.41
20:u:16:LYS:HE3	20:u:16:LYS:HB3	1.89	0.41
20:u:46:LYS:HE3	20:u:46:LYS:HB2	1.92	0.41
31:G:173:LYS:O	31:G:177:ASN:ND2	2.53	0.41
32:H:116:ALA:O	32:H:119:ILE:HG22	2.20	0.41
33:I:141:VAL:HA	33:I:180:THR:HA	2.01	0.41
37:M:5:PRO:HB2	37:M:32:LYS:HE2	2.03	0.41
42:R:54:THR:O	42:R:57:ASP:OD1	2.38	0.41
46:V:56:ASP:N	46:V:56:ASP:OD1	2.54	0.41
47:W:70:THR:HG22	47:W:73:HIS:CE1	2.55	0.41
48:X:39:ILE:HG12	48:X:70:LEU:HD22	2.01	0.41
52:3:392:C:H2'	52:3:393:A:H8	1.86	0.41
52:3:526:C:H2'	52:3:527:G:H4'	2.02	0.41
52:3:681:A:H2'	52:3:682:G:H8	1.85	0.41
53:1:414:C:H5''	53:1:1879:C:O2'	2.20	0.41
53:1:1469:A:H2'	53:1:1470:A:C8	2.56	0.41
53:1:1721:G:H1'	53:1:1739:A:H61	1.86	0.41
53:1:2443:C:O2'	53:1:2444:G:H5'	2.20	0.41
53:1:2619:C:O2'	53:1:2620:C:H5'	2.20	0.41
53:1:2888:C:H2'	53:1:2889:C:C6	2.55	0.41
54:2:88:C:H4'	54:2:89:U:OP1	2.19	0.41
57:7:52:G:H2'	57:7:53:G:H8	1.85	0.41
58:8:212:LEU:O	58:8:233:GLU:HB2	2.20	0.41
58:8:325:LYS:HD3	58:8:344:LEU:HD12	2.02	0.41
7:h:16:SER:OG	7:h:17:GLU:OE1	2.38	0.41
11:l:46:VAL:HG11	11:l:50:PHE:CD2	2.55	0.41
11:l:57:LEU:HD12	11:l:57:LEU:HA	1.94	0.41
15:p:77:SER:OG	15:p:79:VAL:HG22	2.19	0.41
16:q:88:GLU:H	17:r:49:ILE:HD11	1.85	0.41
28:D:46:LYS:HE3	28:D:46:LYS:HB3	1.94	0.41
31:G:113:LEU:HD23	31:G:151:LYS:HD3	2.01	0.41
32:H:133:MET:SD	32:H:134:LYS:N	2.93	0.41
32:H:150:VAL:HG12	32:H:199:VAL:HG12	2.02	0.41
43:S:92:ILE:HA	43:S:93:PRO:HD3	1.89	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:118:U:O4	52:3:288:A:H2'	2.19	0.41
52:3:1310:G:H2'	52:3:1311:A:C8	2.55	0.41
52:3:1353:G:O2'	52:3:1354:U:H5'	2.20	0.41
53:1:23:G:H2'	53:1:24:G:H8	1.85	0.41
53:1:1394:U:H4'	53:1:1603:A:H4'	2.02	0.41
53:1:2372:U:H2'	53:1:2373:G:H8	1.85	0.41
53:1:2743:U:H2'	53:1:2744:G:C4'	2.50	0.41
55:6:41:C:H2'	55:6:42:G:H8	1.83	0.41
3:d:83:VAL:CG1	3:d:86:ALA:HA	2.51	0.41
4:e:125:GLY:HA2	4:e:162:ASP:HA	2.03	0.41
5:f:85:LYS:CG	5:f:164:ALA:HB3	2.50	0.41
5:f:104:LEU:HD11	5:f:147:LEU:HD22	2.02	0.41
11:l:27:LEU:O	11:l:31:GLY:HA2	2.21	0.41
15:p:31:VAL:HG21	15:p:40:GLN:HE21	1.85	0.41
20:u:32:LYS:HZ2	53:1:478:A:H4'	1.86	0.41
23:x:58:ILE:HG12	23:x:66:VAL:HG11	2.03	0.41
31:G:147:LEU:HD13	31:G:150:ILE:HD11	2.02	0.41
33:I:10:LEU:O	33:I:13:ARG:HB3	2.21	0.41
33:I:169:TRP:CG	33:I:185:PRO:HG3	2.53	0.41
44:T:47:LYS:O	44:T:49:HIS:N	2.54	0.41
51:a:11:ILE:HG23	51:a:33:LEU:HD22	2.01	0.41
51:a:196:LEU:HB2	51:a:208:TYR:HE2	1.85	0.41
52:3:30:U:H3	52:3:553:A:H61	1.68	0.41
52:3:62:U:H2'	52:3:63:C:C6	2.55	0.41
52:3:505:G:P	52:3:535:A:H5'	2.60	0.41
52:3:751:U:C2'	52:3:752:G:H5'	2.50	0.41
52:3:909:A:H2'	52:3:910:C:O4'	2.21	0.41
52:3:1195:C:H5''	52:3:1196:A:OP2	2.20	0.41
52:3:1314:C:H2'	52:3:1315:U:C6	2.56	0.41
53:1:195:A:H2'	53:1:198:C:H41	1.83	0.41
53:1:253:C:H2'	53:1:254:G:O4'	2.20	0.41
53:1:262:A:H2'	53:1:263:G:O4'	2.20	0.41
53:1:838:C:H2'	53:1:839:U:C6	2.55	0.41
53:1:1499:C:H2'	53:1:1500:G:H8	1.86	0.41
53:1:1592:C:H2'	53:1:1593:A:H8	1.86	0.41
53:1:1827:U:O2'	53:1:1828:G:H5'	2.19	0.41
1:b:40:GLY:HA2	1:b:53:ILE:HG22	2.02	0.41
1:b:52:HIS:CE1	1:b:218:THR:HG23	2.55	0.41
3:d:124:PHE:CE2	3:d:148:ILE:HD12	2.55	0.41
3:d:148:ILE:HD13	3:d:187:VAL:CG2	2.51	0.41
5:f:122:ALA:HA	5:f:132:LEU:HA	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:129:GLU:OE1	5:f:131:VAL:HG23	2.21	0.41
7:h:118:ILE:HD13	7:h:118:ILE:HA	1.84	0.41
8:i:58:ILE:HG23	8:i:58:ILE:O	2.20	0.41
12:m:32:GLY:HA2	12:m:103:TYR:O	2.20	0.41
19:t:50:LEU:HD12	19:t:50:LEU:N	2.36	0.41
21:v:29:ILE:HD12	21:v:39:ALA:HA	2.02	0.41
31:G:133:ALA:O	31:G:137:THR:N	2.52	0.41
33:I:74:TYR:CD1	33:I:92:LEU:HD21	2.56	0.41
35:K:6:ILE:HD11	35:K:71:ILE:HD11	2.02	0.41
36:L:142:ARG:CG	55:6:41:C:H4'	2.47	0.41
39:O:57:VAL:HG23	52:3:972:C:H1'	2.02	0.41
43:S:3:GLN:HG3	52:3:1048:G:OP1	2.20	0.41
46:V:66:LEU:C	52:3:265:G:H4'	2.45	0.41
52:3:54:C:H2'	52:3:352:C:H41	1.84	0.41
52:3:123:U:H2'	52:3:124:C:C6	2.56	0.41
52:3:273:U:C2'	52:3:274:A:H5'	2.50	0.41
52:3:692:U:H2'	52:3:694:A:OP2	2.20	0.41
53:1:513:A:H2	53:1:582:A:H4'	1.85	0.41
53:1:979:A:H2'	53:1:982:C:H42	1.86	0.41
53:1:1799:G:H4'	53:1:1800:C:H6	1.85	0.41
54:2:28:C:H2'	54:2:29:A:H8	1.85	0.41
57:7:76:A:C5'	58:8:221:ILE:HD11	2.51	0.41
4:e:52:ALA:HA	4:e:55:ASP:OD2	2.20	0.41
14:o:111:ARG:NH2	14:o:117:PHE:OXT	2.54	0.41
18:s:71:VAL:HG23	18:s:71:VAL:O	2.20	0.41
30:F:19:ARG:HD2	30:F:24:ARG:HD2	2.02	0.41
35:K:3:HIS:HB2	35:K:92:THR:CA	2.49	0.41
35:K:90:MET:HE1	47:W:60:ARG:NH1	2.34	0.41
40:P:86:LYS:HE3	52:3:707:U:OP1	2.20	0.41
43:S:7:ALA:O	43:S:10:VAL:HG12	2.20	0.41
44:T:46:LYS:HE2	44:T:46:LYS:HB2	1.91	0.41
48:X:31:ARG:HA	48:X:49:ALA:HB3	2.03	0.41
52:3:234:C:H2'	52:3:235:C:C6	2.56	0.41
52:3:273:U:O2'	52:3:274:A:H5'	2.21	0.41
52:3:763:G:H2'	52:3:764:C:H6	1.84	0.41
52:3:829:G:O2'	52:3:830:G:H5'	2.20	0.41
52:3:1330:U:H2'	52:3:1331:G:O4'	2.20	0.41
52:3:1354:U:H2'	52:3:1355:G:C8	2.55	0.41
53:1:103:A:H2'	53:1:104:A:O4'	2.20	0.41
53:1:629:G:H5''	53:1:650:C:O2'	2.21	0.41
53:1:779:U:H2'	53:1:780:G:C8	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:872:U:H2'	53:1:873:C:C6	2.56	0.41
53:1:1795:C:H2'	53:1:1796:U:O4'	2.21	0.41
53:1:1799:G:H4'	53:1:1800:C:C6	2.56	0.41
53:1:2266:A:H4'	53:1:2267:A:C4	2.56	0.41
53:1:2317:A:H2'	53:1:2318:G:O4'	2.20	0.41
58:8:25:LYS:HA	58:8:105:VAL:HG21	2.02	0.41
2:c:208:LYS:HZ1	53:1:2732:G:H5'	1.86	0.41
4:e:168:LEU:HD23	4:e:168:LEU:C	2.46	0.41
5:f:98:LYS:NZ	5:f:103:ASN:HB2	2.35	0.41
6:g:69:ALA:O	6:g:72:ILE:HG12	2.20	0.41
7:h:81:LEU:HD13	53:1:1107:G:O4'	2.21	0.41
11:l:111:ILE:HG22	11:l:112:LEU:N	2.36	0.41
12:m:117:PHE:O	12:m:121:ALA:HB2	2.21	0.41
12:m:123:LYS:NZ	53:1:2483:C:N3	2.68	0.41
13:n:63:ARG:CZ	53:1:1454:C:H5'	2.51	0.41
15:p:62:LYS:O	15:p:69:VAL:HG12	2.20	0.41
15:p:67:GLU:H	15:p:67:GLU:HG3	1.75	0.41
17:r:54:VAL:HB	17:r:55:ASP:H	1.69	0.41
18:s:93:ALA:HB2	53:1:1614:A:C2	2.56	0.41
31:G:23:ASN:HA	31:G:24:PRO:HD3	1.90	0.41
42:R:2:ARG:HD2	42:R:8:ILE:HG12	2.03	0.41
47:W:32:ILE:HG22	47:W:38:ILE:HA	2.03	0.41
49:Y:79:THR:O	49:Y:83:ASN:ND2	2.54	0.41
51:a:15:VAL:HG11	51:a:222:VAL:HG22	2.03	0.41
52:3:51:A:H61	52:3:314:C:H1'	1.86	0.41
52:3:1204:A:H2'	52:3:1205:U:O4'	2.21	0.41
53:1:1010:A:N3	53:1:1153:C:H1'	2.36	0.41
53:1:1872:A:H2'	53:1:1873:G:O4'	2.20	0.41
53:1:2224:G:H4'	53:1:2226:C:C2	2.56	0.41
53:1:2572:A:OP1	53:1:2574:G:H4'	2.21	0.41
58:8:18:ILE:HG13	58:8:104:LEU:HA	2.03	0.41
58:8:236:ILE:HD12	58:8:270:ARG:HB2	2.02	0.41
1:b:213:ARG:CZ	53:1:1566:A:H5'	2.50	0.41
2:c:181:ASP:HB3	2:c:186:LEU:HB2	2.02	0.41
3:d:51:GLU:OE2	3:d:88:ARG:NH1	2.53	0.41
4:e:56:LEU:HD23	4:e:56:LEU:HA	1.92	0.41
8:i:56:VAL:HG21	8:i:68:PHE:HB2	2.02	0.41
9:j:8:PRO:HG3	9:j:48:VAL:HG13	2.03	0.41
11:l:48:ARG:HD2	29:E:60:CYS:HA	2.02	0.41
11:l:93:ASN:C	11:l:95:LEU:N	2.79	0.41
12:m:34:LYS:HE3	12:m:131:VAL:HG21	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:o:26:LEU:HD13	14:o:39:VAL:HG22	2.02	0.41
16:q:27:ARG:HH22	53:1:532:A:H5'	1.85	0.41
16:q:73:ILE:HG12	16:q:74:SER:H	1.86	0.41
16:q:91:ARG:HG3	16:q:91:ARG:HH11	1.86	0.41
16:q:91:ARG:HH12	53:1:997:G:H5''	1.86	0.41
18:s:72:THR:OG1	18:s:73:LYS:N	2.54	0.41
18:s:82:MET:HB2	18:s:84:ARG:HH22	1.85	0.41
23:x:76:LYS:HD3	23:x:76:LYS:HA	1.90	0.41
25:z:29:ARG:NH2	25:z:29:ARG:HG2	2.35	0.41
29:E:34:LYS:HB3	29:E:34:LYS:HE2	1.90	0.41
31:G:55:GLU:O	31:G:59:ILE:HG13	2.21	0.41
31:G:96:LEU:CD2	52:3:1103:C:H4'	2.49	0.41
33:I:67:LEU:HB3	52:3:546:A:P	2.61	0.41
34:J:148:SER:OG	34:J:149:PRO:HD2	2.21	0.41
36:L:13:PRO:HB3	36:L:20:GLU:OE1	2.20	0.41
38:N:101:GLY:C	38:N:103:VAL:H	2.28	0.41
38:N:119:LYS:O	38:N:120:ALA:HB3	2.20	0.41
40:P:127:ARG:HG3	50:Z:34:ARG:HH22	1.86	0.41
41:Q:55:ARG:NH2	41:Q:61:GLU:OE1	2.53	0.41
43:S:3:GLN:NE2	52:3:1047:G:H5''	2.36	0.41
44:T:84:LEU:HB2	44:T:86:LEU:HD22	2.01	0.41
45:U:20:VAL:HG13	45:U:34:GLU:O	2.21	0.41
46:V:46:HIS:HB2	46:V:70:LYS:HE2	2.02	0.41
47:W:24:ASP:OD1	47:W:24:ASP:N	2.50	0.41
49:Y:66:ILE:HG22	49:Y:67:HIS:N	2.36	0.41
52:3:56:U:H2'	52:3:57:G:C8	2.56	0.41
52:3:303:A:H2'	52:3:304:U:O4'	2.20	0.41
52:3:458:U:H2'	52:3:459:A:H8	1.85	0.41
52:3:515:G:O2'	52:3:516:U:H5'	2.21	0.41
52:3:620:C:H2'	52:3:621:A:O4'	2.20	0.41
52:3:678:U:O2'	52:3:679:C:H5'	2.21	0.41
52:3:765:G:H3'	52:3:812:G:H22	1.85	0.41
52:3:825:A:H2'	52:3:826:C:C6	2.56	0.41
52:3:893:C:H2'	52:3:894:G:C8	2.56	0.41
52:3:977:A:H2'	52:3:978:A:H5''	2.02	0.41
52:3:1060:U:H2'	52:3:1061:G:C8	2.55	0.41
53:1:259:G:O2'	53:1:260:G:H5'	2.20	0.41
53:1:296:U:H2'	53:1:297:G:H8	1.86	0.41
53:1:467:G:O2'	53:1:468:G:H5'	2.21	0.41
53:1:732:C:H2'	53:1:733:G:O4'	2.20	0.41
53:1:860:U:O2'	53:1:861:A:H5'	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1903:G:H2'	53:1:1904:G:H8	1.85	0.41
53:1:2197:U:O2'	53:1:2198:A:H5''	2.21	0.41
53:1:2327:A:H2'	53:1:2328:A:C8	2.56	0.41
53:1:2457:U:O2'	53:1:2458:G:H5'	2.21	0.41
53:1:2555:U:H2'	53:1:2556:C:H5'	2.03	0.41
58:8:137:LYS:HG2	61:8:501:GDP:C6	2.56	0.41
58:8:248:ILE:HB	58:8:365:HIS:HB3	2.03	0.41
6:g:3:VAL:HG22	6:g:38:PRO:HA	2.02	0.41
6:g:8:LYS:O	6:g:9:VAL:C	2.64	0.41
6:g:66:ASN:HD22	6:g:135:HIS:HB2	1.86	0.41
10:k:76:VAL:H	15:p:72:VAL:CG1	2.34	0.41
11:l:29:LYS:O	11:l:30:THR:OG1	2.30	0.41
12:m:11:LYS:HD2	12:m:86:LYS:CG	2.51	0.41
14:o:31:THR:OG1	14:o:34:HIS:O	2.39	0.41
15:p:29:VAL:HG22	15:p:30:TRP:N	2.36	0.41
20:u:39:ASN:N	20:u:61:GLU:OE2	2.53	0.41
20:u:57:ILE:HG13	20:u:57:ILE:O	2.20	0.41
22:w:39:THR:C	22:w:41:PHE:H	2.29	0.41
24:y:4:LYS:HA	24:y:7:ARG:HH12	1.86	0.41
31:G:56:LEU:HD13	31:G:216:VAL:HG13	2.03	0.41
32:H:123:LEU:HA	32:H:127:VAL:HG12	2.02	0.41
33:I:103:ARG:HA	33:I:103:ARG:HD3	1.88	0.41
33:I:124:VAL:HG13	33:I:142:VAL:HG12	2.02	0.41
35:K:29:ILE:HG21	35:K:64:VAL:HG21	2.02	0.41
36:L:63:VAL:O	36:L:66:GLU:HG2	2.21	0.41
38:N:40:ARG:CZ	52:3:1292:G:H5'	2.51	0.41
41:Q:113:ARG:NH2	52:3:501:C:OP1	2.54	0.41
47:W:59:LYS:HD3	52:3:734:G:O2'	2.21	0.41
50:Z:11:PHE:CG	50:Z:12:ASP:N	2.89	0.41
52:3:45:G:H2'	52:3:46:G:C8	2.56	0.41
52:3:1033:G:C3'	52:3:1034:G:H5''	2.51	0.41
52:3:1215:G:O2'	52:3:1216:A:H5'	2.21	0.41
53:1:854:C:O2'	53:1:855:G:H5'	2.21	0.41
53:1:1971:U:H5'	53:1:1972:G:H5''	2.03	0.41
53:1:2476:A:H2	53:1:2481:G:H1	1.68	0.41
53:1:2682:A:O2'	53:1:2683:C:H5'	2.21	0.41
58:8:101:GLY:HA3	58:8:200:ILE:HD13	2.03	0.41
11:l:53:GLY:HA3	53:1:826:U:O2'	2.21	0.40
16:q:57:ARG:NH1	53:1:1154:G:OP2	2.54	0.40
16:q:109:VAL:HG13	16:q:110:GLU:N	2.36	0.40
17:r:85:LYS:HB2	17:r:85:LYS:HE3	1.83	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:171:ARG:HG3	52:3:1106:G:O3'	2.21	0.40
35:K:11:HIS:HB3	35:K:13:ASP:OD1	2.21	0.40
38:N:89:TYR:HB3	38:N:93:LEU:HD12	2.02	0.40
38:N:109:GLN:OE1	52:3:1116:U:H4'	2.21	0.40
40:P:88:PRO:HG2	40:P:89:GLY:N	2.30	0.40
40:P:117:HIS:O	40:P:118:ASN:HB2	2.21	0.40
41:Q:24:GLU:O	41:Q:25:ALA:HB3	2.21	0.40
43:S:12:ARG:HD3	43:S:59:GLN:OE1	2.21	0.40
44:T:66:LEU:HD23	44:T:66:LEU:HA	1.83	0.40
52:3:82:G:H2'	52:3:83:C:H5'	2.04	0.40
52:3:607:A:H2'	52:3:608:A:H8	1.85	0.40
52:3:637:C:H2'	52:3:638:U:C6	2.56	0.40
52:3:779:C:H2'	52:3:780:A:O4'	2.21	0.40
52:3:884:U:H4'	52:3:885:G:H5''	2.02	0.40
52:3:1027:C:H2'	52:3:1028:C:OP1	2.20	0.40
52:3:1223:C:OP2	52:3:1224:U:H2'	2.21	0.40
52:3:1514:G:O2'	52:3:1515:G:H5'	2.21	0.40
53:1:69:C:H2'	53:1:70:G:C8	2.56	0.40
53:1:112:U:C2'	53:1:113:U:H5'	2.52	0.40
53:1:395:U:H2'	53:1:396:G:H8	1.86	0.40
53:1:588:U:H2'	53:1:589:U:C6	2.57	0.40
53:1:2302:U:H2'	53:1:2303:G:C8	2.56	0.40
53:1:2623:G:H2'	53:1:2624:G:H8	1.86	0.40
58:8:122:LEU:O	58:8:126:VAL:HG22	2.21	0.40
1:b:211:ARG:HD2	1:b:211:ARG:HA	1.97	0.40
5:f:116:LEU:HD11	5:f:122:ALA:HB3	2.03	0.40
6:g:65:ALA:O	6:g:68:ARG:HB3	2.21	0.40
10:k:116:ILE:HA	10:k:119:ALA:HB2	2.03	0.40
11:l:118:THR:HA	11:l:119:PRO:HD3	1.88	0.40
12:m:34:LYS:O	12:m:129:THR:HG22	2.21	0.40
13:n:63:ARG:NH1	53:1:1454:C:C5'	2.83	0.40
14:o:14:ALA:O	14:o:18:LEU:HD13	2.22	0.40
20:u:1:ALA:N	53:1:83:A:OP1	2.47	0.40
36:L:3:ARG:CZ	52:3:1092:A:H5''	2.51	0.40
43:S:26:LEU:HA	43:S:30:ILE:HD13	2.03	0.40
43:S:36:SER:HA	43:S:40:ARG:HD3	2.03	0.40
47:W:59:LYS:HD3	52:3:735:C:H5'	2.03	0.40
50:Z:39:LYS:O	50:Z:43:GLU:N	2.44	0.40
52:3:453:G:H2'	52:3:454:G:O4'	2.21	0.40
52:3:552:U:H2'	52:3:553:A:C8	2.55	0.40
52:3:1138:G:H3'	52:3:1138:G:N3	2.35	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1499:A:O2'	52:3:1520:C:H5'	2.20	0.40
53:1:154:U:H2'	53:1:155:A:C8	2.57	0.40
53:1:969:G:H2'	53:1:970:U:C6	2.57	0.40
53:1:1258:U:H2'	53:1:1259:G:C8	2.56	0.40
53:1:1549:A:H2'	53:1:1550:C:C6	2.56	0.40
53:1:2487:G:H2'	53:1:2488:G:C8	2.56	0.40
53:1:2632:A:O2'	53:1:2633:G:H5'	2.20	0.40
53:1:2829:A:H2'	53:1:2830:C:C6	2.56	0.40
54:2:48:U:H2'	54:2:49:C:H6	1.86	0.40
54:2:69:G:H2'	54:2:70:C:O4'	2.21	0.40
58:8:68:VAL:HG23	58:8:79:HIS:HB3	2.03	0.40
1:b:62:ARG:NH1	1:b:83:ASP:HA	2.36	0.40
3:d:109:LEU:HD23	3:d:109:LEU:HA	1.90	0.40
6:g:1:MET:HB3	6:g:3:VAL:HG23	2.03	0.40
10:k:22:ILE:HG13	10:k:23:LYS:N	2.36	0.40
16:q:2:ARG:HD2	53:1:1248:G:C2	2.56	0.40
23:x:1:SER:O	23:x:49:ARG:NH1	2.54	0.40
24:y:2:LYS:NZ	53:1:102:U:H1'	2.35	0.40
24:y:9:LYS:HG3	24:y:12:GLU:H	1.87	0.40
32:H:179:ALA:HB1	32:H:202:PHE:HE1	1.86	0.40
33:I:61:ARG:HH21	33:I:67:LEU:HA	1.87	0.40
33:I:164:ARG:HB3	33:I:165:GLU:H	1.70	0.40
38:N:33:SER:N	38:N:36:GLN:HG2	2.36	0.40
40:P:23:HIS:HB3	40:P:30:ILE:CG2	2.41	0.40
45:U:28:ARG:NH1	52:3:390:U:H4'	2.35	0.40
52:3:151:A:H2'	52:3:152:A:O4'	2.22	0.40
52:3:560:A:H5'	52:3:566:G:N2	2.36	0.40
52:3:924:C:H2'	52:3:925:G:H8	1.86	0.40
52:3:1230:C:H5'	55:5:30:G:H5''	2.03	0.40
53:1:319:G:H2'	53:1:320:A:O4'	2.22	0.40
53:1:783:A:H2'	53:1:784:G:H5'	2.03	0.40
53:1:947:A:H2'	53:1:948:C:C6	2.57	0.40
53:1:1760:C:H2'	53:1:1761:C:H5'	2.03	0.40
53:1:1837:C:H2'	53:1:1899:A:H61	1.87	0.40
54:2:13:G:N2	54:2:16:G:H1'	2.28	0.40
58:8:350:MET:SD	58:8:350:MET:O	2.79	0.40
1:b:140:VAL:O	1:b:161:VAL:HG22	2.21	0.40
3:d:121:VAL:HG21	3:d:124:PHE:HB2	2.03	0.40
4:e:118:ALA:HB1	4:e:166:ARG:HE	1.85	0.40
10:k:88:ASN:O	10:k:91:SER:O	2.38	0.40
11:l:30:THR:HG22	53:1:810:U:O4	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:t:61:LEU:HB3	53:1:1341:G:H5'	2.04	0.40
20:u:49:PRO:HA	20:u:53:GLN:NE2	2.37	0.40
24:y:1:MET:HA	24:y:4:LYS:HE2	2.04	0.40
35:K:42:TRP:HE1	35:K:61:LEU:HD22	1.86	0.40
37:M:26:MET:HA	37:M:27:PRO:HD3	1.96	0.40
37:M:82:LEU:O	37:M:82:LEU:HD23	2.21	0.40
38:N:51:LEU:HB3	38:N:56:MET:HB3	2.03	0.40
39:O:59:LYS:O	39:O:62:ARG:HD2	2.22	0.40
40:P:22:ILE:N	40:P:22:ILE:HD12	2.36	0.40
40:P:87:GLY:H	40:P:113:THR:HG23	1.86	0.40
43:S:15:LEU:CD1	43:S:18:LYS:HD3	2.52	0.40
44:T:64:LYS:HD3	52:3:755:G:OP2	2.21	0.40
52:3:1154:G:H2'	52:3:1155:A:C8	2.56	0.40
52:3:1385:G:H2'	52:3:1386:G:H8	1.86	0.40
53:1:290:U:H2'	53:1:291:G:H8	1.86	0.40
53:1:1039:A:O2'	53:1:1040:A:H5'	2.21	0.40
53:1:1199:U:H2'	53:1:1200:C:C6	2.55	0.40
53:1:1662:U:H2'	53:1:1663:G:O4'	2.22	0.40
53:1:1883:U:H2'	53:1:1884:G:O4'	2.20	0.40
53:1:2298:A:H62	53:1:2318:G:N2	2.16	0.40
53:1:2410:G:H2'	53:1:2411:A:O4'	2.22	0.40
53:1:2553:G:H2'	53:1:2554:U:H4'	2.03	0.40
58:8:157:LEU:HD12	58:8:157:LEU:HA	1.96	0.40
2:c:112:THR:HG23	2:c:167:ASN:O	2.22	0.40
6:g:66:ASN:ND2	6:g:134:VAL:O	2.55	0.40
8:i:21:PRO:HD2	8:i:22:PRO:HD3	2.03	0.40
10:k:90:ASN:OD1	10:k:91:SER:N	2.51	0.40
11:l:22:GLY:HA2	53:1:811:U:H3'	2.03	0.40
25:z:29:ARG:HG2	25:z:29:ARG:HH21	1.86	0.40
32:H:5:HIS:HA	32:H:6:PRO:HD3	1.75	0.40
39:O:32:THR:HG23	39:O:32:THR:O	2.22	0.40
52:3:701:U:H5''	52:3:703:G:H1'	2.04	0.40
52:3:1502:A:C8	52:3:1505:G:N2	2.90	0.40
53:1:63:A:H2'	53:1:64:A:C8	2.56	0.40
53:1:365:U:H2'	53:1:366:C:C6	2.56	0.40
53:1:833:A:H2'	53:1:834:G:H8	1.87	0.40
53:1:1183:U:H2'	53:1:1184:U:C6	2.57	0.40
53:1:1625:C:H2'	53:1:1626:A:O4'	2.21	0.40
53:1:2391:G:O2'	53:1:2392:A:O5'	2.33	0.40
57:7:6:G:H3'	57:7:7:A:C5'	2.40	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%)	220 (82%)	37 (14%)	12 (4%)	2	17
2	c	207/209 (99%)	183 (88%)	23 (11%)	1 (0%)	24	57
3	d	199/201 (99%)	169 (85%)	27 (14%)	3 (2%)	8	37
4	e	175/177 (99%)	155 (89%)	19 (11%)	1 (1%)	21	54
5	f	174/176 (99%)	156 (90%)	16 (9%)	2 (1%)	11	43
6	g	147/149 (99%)	130 (88%)	16 (11%)	1 (1%)	18	51
7	h	129/131 (98%)	100 (78%)	21 (16%)	8 (6%)	1	12
8	i	139/141 (99%)	121 (87%)	11 (8%)	7 (5%)	1	16
9	j	140/142 (99%)	132 (94%)	7 (5%)	1 (1%)	18	51
10	k	120/122 (98%)	105 (88%)	14 (12%)	1 (1%)	16	49
11	l	141/143 (99%)	118 (84%)	19 (14%)	4 (3%)	4	26
12	m	134/136 (98%)	113 (84%)	17 (13%)	4 (3%)	3	25
13	n	118/120 (98%)	97 (82%)	20 (17%)	1 (1%)	16	49
14	o	114/116 (98%)	106 (93%)	6 (5%)	2 (2%)	6	34
15	p	112/114 (98%)	93 (83%)	18 (16%)	1 (1%)	14	46
16	q	115/117 (98%)	109 (95%)	5 (4%)	1 (1%)	14	46
17	r	101/103 (98%)	83 (82%)	15 (15%)	3 (3%)	3	25
18	s	108/110 (98%)	92 (85%)	11 (10%)	5 (5%)	2	17
19	t	91/93 (98%)	79 (87%)	12 (13%)	0	100	100
20	u	100/102 (98%)	87 (87%)	9 (9%)	4 (4%)	2	20
21	v	92/94 (98%)	84 (91%)	7 (8%)	1 (1%)	11	43
22	w	73/75 (97%)	63 (86%)	10 (14%)	0	100	100
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	58 (95%)	2 (3%)	1 (2%)	7	36
25	z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	47 (87%)	7 (13%)	0	100	100
27	C	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
28	D	44/46 (96%)	36 (82%)	7 (16%)	1 (2%)	5	30
29	E	62/64 (97%)	54 (87%)	6 (10%)	2 (3%)	3	24
30	F	36/38 (95%)	28 (78%)	7 (19%)	1 (3%)	4	26
31	G	223/225 (99%)	203 (91%)	19 (8%)	1 (0%)	30	61
32	H	204/206 (99%)	185 (91%)	18 (9%)	1 (0%)	24	57
33	I	203/205 (99%)	171 (84%)	30 (15%)	2 (1%)	12	45
34	J	155/157 (99%)	124 (80%)	25 (16%)	6 (4%)	2	20
35	K	98/100 (98%)	77 (79%)	18 (18%)	3 (3%)	3	25
36	L	149/151 (99%)	128 (86%)	20 (13%)	1 (1%)	18	51
37	M	127/129 (98%)	113 (89%)	12 (9%)	2 (2%)	7	36
38	N	125/127 (98%)	99 (79%)	19 (15%)	7 (6%)	1	14
39	O	96/98 (98%)	78 (81%)	15 (16%)	3 (3%)	3	25
40	P	114/116 (98%)	95 (83%)	14 (12%)	5 (4%)	2	18
41	Q	121/123 (98%)	95 (78%)	20 (16%)	6 (5%)	1	16
42	R	112/114 (98%)	97 (87%)	11 (10%)	4 (4%)	2	22
43	S	98/100 (98%)	78 (80%)	19 (19%)	1 (1%)	12	45
44	T	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	41
45	U	80/82 (98%)	67 (84%)	12 (15%)	1 (1%)	9	39
46	V	78/80 (98%)	65 (83%)	12 (15%)	1 (1%)	9	39
47	W	63/65 (97%)	56 (89%)	5 (8%)	2 (3%)	3	24
48	X	77/79 (98%)	68 (88%)	9 (12%)	0	100	100
49	Y	83/85 (98%)	76 (92%)	6 (7%)	1 (1%)	10	41
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	6
51	a	130/223 (58%)	124 (95%)	5 (4%)	1 (1%)	16	49
58	8	371/400 (93%)	333 (90%)	37 (10%)	1 (0%)	36	65
All	All	6290/6512 (97%)	5438 (86%)	728 (12%)	124 (2%)	8	32

All (124) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	56	GLY

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	c	86	GLU
5	f	45	ALA
6	g	9	VAL
7	h	113	PHE
7	h	118	ILE
9	j	81	ILE
11	l	31	GLY
12	m	58	LYS
12	m	59	ARG
17	r	54	VAL
24	y	24	GLU
29	E	31	ILE
30	F	37	GLN
34	J	49	TYR
34	J	93	VAL
34	J	122	VAL
38	N	90	ASP
38	N	91	GLU
39	O	58	ASN
40	P	89	GLY
40	P	125	LYS
46	V	49	ASN
47	W	13	THR
50	Z	8	ASN
50	Z	34	ARG
51	a	210	LYS
1	b	38	LYS
1	b	232	GLY
7	h	51	TYR
7	h	80	THR
7	h	123	ILE
8	i	6	ALA
11	l	16	GLY
11	l	29	LYS
11	l	85	VAL
17	r	23	GLU
18	s	3	THR
18	s	63	GLY
35	K	39	LEU
38	N	125	GLN
41	Q	77	SER
42	R	6	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
42	R	7	ASN
44	T	48	ASP
45	U	79	ASN
50	Z	12	ASP
50	Z	25	ALA
58	8	318	GLY
1	b	111	ALA
3	d	86	ALA
7	h	58	THR
8	i	31	GLY
12	m	69	PRO
18	s	11	ARG
20	u	97	SER
28	D	42	LEU
29	E	62	PRO
36	L	111	GLY
38	N	57	VAL
38	N	102	PHE
38	N	128	LYS
40	P	92	ARG
41	Q	75	GLU
49	Y	68	LYS
50	Z	9	GLU
1	b	107	LYS
1	b	255	LYS
8	i	11	GLN
8	i	13	ALA
12	m	6	ARG
14	o	99	TYR
15	p	15	ASP
18	s	67	ASP
32	H	60	ALA
35	K	55	HIS
35	K	86	ARG
37	M	72	GLU
39	O	37	ARG
40	P	126	ARG
41	Q	24	GLU
41	Q	27	PRO
42	R	4	ALA
42	R	5	GLY
47	W	18	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	b	37	SER
3	d	75	SER
5	f	58	ALA
8	i	22	PRO
8	i	92	PRO
14	o	34	HIS
16	q	5	ARG
18	s	65	ASP
20	u	6	ARG
20	u	51	LEU
20	u	98	ASN
31	G	188	THR
33	I	26	ALA
33	I	167	PRO
34	J	11	GLN
34	J	98	ALA
34	J	102	THR
38	N	8	THR
1	b	147	PRO
7	h	119	PRO
10	k	48	PRO
1	b	233	GLY
1	b	240	GLY
3	d	83	VAL
4	e	175	PRO
8	i	21	PRO
41	Q	3	VAL
1	b	108	GLY
7	h	88	HIS
13	n	113	ILE
17	r	44	GLY
40	P	88	PRO
50	Z	10	PRO
21	v	81	PRO
41	Q	10	PRO
43	S	51	PRO
1	b	246	PRO
37	M	56	PRO
39	O	33	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	214 (99%)	2 (1%)	70	76
2	c	164/164 (100%)	164 (100%)	0	100	100
3	d	165/165 (100%)	163 (99%)	2 (1%)	63	73
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100
7	h	100/100 (100%)	98 (98%)	2 (2%)	48	66
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	76
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	75
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	76
13	n	100/100 (100%)	96 (96%)	4 (4%)	28	54
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	73
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	75
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	73
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	74
19	t	80/80 (100%)	78 (98%)	2 (2%)	42	63
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	72
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	68
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	C	45/45 (100%)	44 (98%)	1 (2%)	45	65
28	D	38/38 (100%)	36 (95%)	2 (5%)	20	48
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	33 (97%)	1 (3%)	37	60
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	74
32	H	170/170 (100%)	170 (100%)	0	100	100
33	I	172/172 (100%)	172 (100%)	0	100	100
34	J	119/119 (100%)	119 (100%)	0	100	100
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	74
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	104 (100%)	0	100	100
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	64
40	P	89/89 (100%)	88 (99%)	1 (1%)	65	74
41	Q	103/103 (100%)	102 (99%)	1 (1%)	68	75
42	R	92/92 (100%)	91 (99%)	1 (1%)	65	74
43	S	83/83 (100%)	83 (100%)	0	100	100
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	70
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	55 (98%)	1 (2%)	51	68
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%)	52 (94%)	3 (6%)	19	47
51	a	110/174 (63%)	110 (100%)	0	100	100
58	8	309/332 (93%)	308 (100%)	1 (0%)	86	83
All	All	5217/5304 (98%)	5178 (99%)	39 (1%)	73	78

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	238	ASN
1	b	263	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	d	145	ASP
3	d	176	ASP
7	h	118	ILE
7	h	119	PRO
9	j	98	GLU
10	k	95	ILE
12	m	97	GLN
13	n	65	LEU
13	n	70	THR
13	n	79	LEU
13	n	117	ASP
14	o	60	GLU
15	p	65	ASN
17	r	54	VAL
18	s	77	ASP
19	t	32	LEU
19	t	67	VAL
21	v	81	PRO
22	w	34	VAL
27	C	22	THR
28	D	9	VAL
28	D	42	LEU
30	F	37	GLN
31	G	9	LEU
31	G	67	LEU
35	K	55	HIS
39	O	58	ASN
39	O	89	ARG
40	P	115	ILE
41	Q	87	LYS
42	R	64	VAL
45	U	19	VAL
47	W	19	GLU
50	Z	10	PRO
50	Z	28	LEU
50	Z	31	VAL
58	8	135	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (136) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	14	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	b	52	HIS
1	b	59	GLN
1	b	85	ASN
1	b	89	ASN
1	b	141	HIS
1	b	196	ASN
1	b	199	HIS
2	c	32	ASN
2	c	94	GLN
2	c	164	GLN
2	c	167	ASN
3	d	30	GLN
3	d	41	GLN
3	d	90	GLN
3	d	94	GLN
3	d	97	ASN
3	d	136	GLN
3	d	156	ASN
3	d	165	HIS
4	e	51	ASN
5	f	103	ASN
5	f	114	HIS
5	f	142	GLN
6	g	2	GLN
6	g	66	ASN
6	g	128	HIS
7	h	122	GLN
8	i	11	GLN
8	i	33	ASN
8	i	42	ASN
8	i	93	ASN
9	j	40	HIS
9	j	58	ASN
9	j	128	ASN
9	j	135	GLN
10	k	3	GLN
10	k	13	ASN
10	k	82	ASN
10	k	89	ASN
11	l	99	ASN
12	m	3	GLN
12	m	13	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	n	18	GLN
13	n	62	ASN
15	p	40	GLN
15	p	76	HIS
15	p	114	ASN
16	q	71	ASN
16	q	80	ASN
17	r	6	GLN
17	r	82	HIS
17	r	91	GLN
18	s	7	HIS
18	s	9	HIS
18	s	31	GLN
19	t	15	HIS
19	t	59	ASN
20	u	39	ASN
20	u	53	GLN
20	u	73	ASN
21	v	5	ASN
21	v	49	ASN
21	v	75	GLN
21	v	78	GLN
22	w	8	ASN
22	w	72	ASN
23	x	16	ASN
23	x	31	ASN
23	x	33	HIS
24	y	20	ASN
25	z	48	ASN
26	B	5	ASN
27	C	18	HIS
27	C	45	HIS
29	E	27	ASN
30	F	37	GLN
31	G	41	ASN
31	G	57	ASN
31	G	145	ASN
31	G	176	ASN
31	G	177	ASN
32	H	31	ASN
32	H	101	ASN
32	H	138	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	H	139	ASN
32	H	184	ASN
33	I	35	GLN
33	I	39	GLN
33	I	70	GLN
33	I	88	ASN
33	I	125	ASN
33	I	130	ASN
33	I	151	GLN
33	I	197	HIS
34	J	72	ASN
34	J	81	GLN
34	J	121	ASN
34	J	147	ASN
35	K	17	GLN
35	K	55	HIS
36	L	147	ASN
37	M	3	GLN
37	M	66	GLN
38	N	31	GLN
38	N	36	GLN
38	N	80	HIS
38	N	125	GLN
39	O	58	ASN
40	P	21	HIS
40	P	37	GLN
41	Q	4	ASN
41	Q	5	GLN
41	Q	72	ASN
41	Q	74	GLN
41	Q	95	HIS
42	R	7	ASN
42	R	99	GLN
43	S	3	GLN
43	S	48	GLN
44	T	27	GLN
44	T	49	HIS
45	U	63	GLN
46	V	8	GLN
47	W	30	ASN
48	X	55	GLN
49	Y	67	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	Y	81	GLN
49	Y	83	ASN
51	a	47	ASN
58	8	12	HIS
58	8	98	GLN
58	8	125	GLN
58	8	160	GLN
58	8	291	GLN
58	8	302	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	135 (8%)	4 (0%)
53	1	2902/2903 (99%)	321 (11%)	8 (0%)
54	2	119/120 (99%)	10 (8%)	2 (1%)
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	7 (9%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	13 (17%)	0
All	All	4803/4810 (99%)	495 (10%)	14 (0%)

All (495) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	7	A
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	87	C
52	3	95	C
52	3	100	G
52	3	144	G
52	3	183	C
52	3	184	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	3	197	A
52	3	210	C
52	3	226	G
52	3	247	G
52	3	251	G
52	3	253	A
52	3	266	G
52	3	267	C
52	3	281	G
52	3	289	G
52	3	328	C
52	3	345	C
52	3	346	G
52	3	352	C
52	3	367	U
52	3	372	C
52	3	411	A
52	3	412	A
52	3	413	G
52	3	429	U
52	3	467	U
52	3	484	G
52	3	485	U
52	3	486	U
52	3	497	G
52	3	518	C
52	3	531	U
52	3	532	A
52	3	533	A
52	3	547	A
52	3	561	U
52	3	572	A
52	3	573	A
52	3	575	G
52	3	576	C
52	3	577	G
52	3	633	G
52	3	665	A
52	3	688	G
52	3	703	G
52	3	724	G
52	3	755	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	3	777	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	843	U
52	3	844	G
52	3	846	G
52	3	871	U
52	3	890	G
52	3	902	G
52	3	926	G
52	3	934	C
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1030	U
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1159	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1197	A
52	3	1198	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1215	G
52	3	1225	A
52	3	1238	A
52	3	1241	G
52	3	1253	G
52	3	1257	A
52	3	1258	G
52	3	1260	G
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1282	C
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1395	C
52	3	1446	A
52	3	1448	C
52	3	1452	C
52	3	1492	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1533	C
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	49	A
53	1	51	G
53	1	63	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	71	A
53	1	74	A
53	1	75	G
53	1	84	A
53	1	118	A
53	1	120	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	216	A
53	1	221	A
53	1	222	A
53	1	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	361	G
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	424	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	451	U
53	1	457	A
53	1	458	G
53	1	480	A
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	531	C
53	1	532	A
53	1	543	G
53	1	545	U
53	1	563	A
53	1	573	U
53	1	575	A
53	1	588	U
53	1	603	A
53	1	616	A
53	1	627	A
53	1	637	A
53	1	645	C
53	1	646	U
53	1	654	A
53	1	669	G
53	1	686	U
53	1	687	C
53	1	695	G
53	1	730	A
53	1	747	C
53	1	752	A
53	1	764	A
53	1	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	805	G
53	1	812	C
53	1	819	A
53	1	822	G
53	1	827	U
53	1	828	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	830	G
53	1	845	A
53	1	846	U
53	1	847	U
53	1	860	U
53	1	878	A
53	1	886	A
53	1	887	U
53	1	888	C
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	983	A
53	1	995	C
53	1	996	A
53	1	1012	U
53	1	1013	C
53	1	1021	A
53	1	1022	G
53	1	1026	G
53	1	1033	U
53	1	1046	A
53	1	1047	G
53	1	1054	A
53	1	1060	U
53	1	1062	G
53	1	1066	U
53	1	1070	A
53	1	1071	G
53	1	1079	C
53	1	1084	A
53	1	1088	A
53	1	1090	A
53	1	1104	C
53	1	1106	G
53	1	1111	A
53	1	1131	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	1132	U
53	1	1133	A
53	1	1135	C
53	1	1143	A
53	1	1175	A
53	1	1177	G
53	1	1178	C
53	1	1180	U
53	1	1206	G
53	1	1212	G
53	1	1238	G
53	1	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	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1352	U
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	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	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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	1559	U
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1584	U
53	1	1585	C
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1800	C
53	1	1801	A
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	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	1971	U
53	1	1972	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	1991	U
53	1	1993	U
53	1	1997	C
53	1	2022	U
53	1	2023	C
53	1	2030	A
53	1	2031	A
53	1	2036	C
53	1	2043	C
53	1	2052	A
53	1	2055	C
53	1	2056	G
53	1	2060	A
53	1	2061	G
53	1	2062	A
53	1	2069	G
53	1	2072	C
53	1	2096	C
53	1	2110	G
53	1	2111	U
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2132	U
53	1	2133	G
53	1	2147	A
53	1	2162	G
53	1	2171	A
53	1	2172	U
53	1	2173	A
53	1	2189	U
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2211	A
53	1	2213	U
53	1	2225	A
53	1	2238	G
53	1	2278	A
53	1	2283	C
53	1	2287	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	2297	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2406	A
53	1	2423	U
53	1	2427	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	2491	U
53	1	2498	C
53	1	2502	G
53	1	2503	A
53	1	2505	G
53	1	2518	A
53	1	2529	G
53	1	2547	A
53	1	2554	U
53	1	2562	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2609	U
53	1	2613	U
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U
53	1	2714	G
53	1	2744	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	2748	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2794	C
53	1	2797	U
53	1	2800	A
53	1	2809	A
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2849	U
53	1	2850	A
53	1	2867	G
53	1	2872	A
53	1	2880	C
53	1	2884	U
53	1	2893	A
54	2	4	C
54	2	13	G
54	2	24	G
54	2	35	C
54	2	44	G
54	2	67	G
54	2	89	U
54	2	90	C
54	2	108	A
54	2	109	A
55	5	8	U
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	18	G
55	6	19	G
55	6	20	U
55	6	47	U

Continued on next page...

Continued from previous page...

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

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	70	U
52	3	960	U
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	2296	U
53	1	2326	C
53	1	2391	G
54	2	66	A
54	2	88	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
60	PHE	7	101	57	10,11,12	0.67	0	8,13,15	0.28	0
59	FME	5	101	55	8,9,10	0.45	0	8,9,11	1.05	0
61	GDP	8	501	-	29,30,30	1.04	1 (3%)	45,47,47	1.92	13 (28%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	PHE	7	101	57	-	1/5/6/8	0/1/1/1
59	FME	5	101	55	-	2/7/9/11	-
61	GDP	8	501	-	-	5/16/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PB-O3B	2.03	1.62	1.54

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	C2-N3-C4	5.49	121.76	112.30
61	8	501	GDP	C5-C4-N3	-5.41	119.78	128.39
61	8	501	GDP	N9-C4-N3	4.09	134.13	125.95

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	O4'-C4'-C3'	3.18	111.46	105.15
61	8	501	GDP	C8-N7-C5	2.91	109.44	104.26
61	8	501	GDP	O3B-PB-O2B	2.90	118.66	107.80
61	8	501	GDP	C2-N1-C6	-2.41	120.74	125.11
61	8	501	GDP	C6-C5-N7	2.40	134.66	130.29
61	8	501	GDP	C4-C5-N7	-2.20	107.18	110.67
61	8	501	GDP	O6-C6-C5	-2.19	120.75	126.53
61	8	501	GDP	C5-C6-N1	2.09	118.57	113.25
61	8	501	GDP	C3'-C2'-C1'	2.09	105.41	101.46
61	8	501	GDP	O2A-PA-O1A	2.05	121.98	112.44

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA
60	7	101	PHE	O-C-CA-CB
61	8	501	GDP	C5'-O5'-PA-O3A
61	8	501	GDP	O4'-C4'-C5'-O5'
61	8	501	GDP	C3'-C4'-C5'-O5'
61	8	501	GDP	PA-O3A-PB-O3B
59	5	101	FME	CB-CA-N-CN
61	8	501	GDP	PA-O3A-PB-O1B

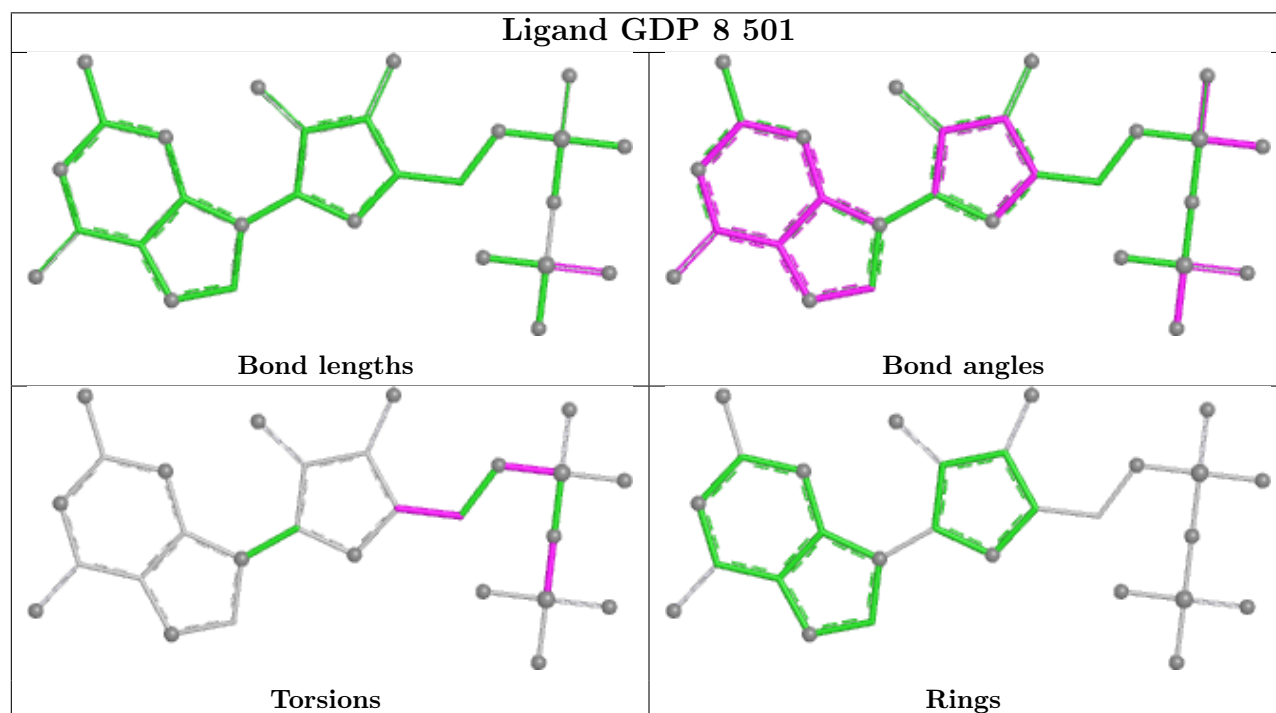
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	101	PHE	2	0
59	5	101	FME	1	0
61	8	501	GDP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

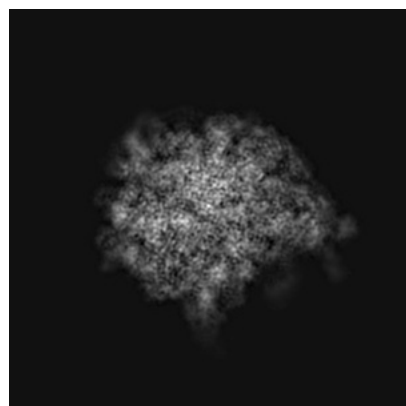
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21624. These allow visual inspection of the internal detail of the map and identification of artifacts.

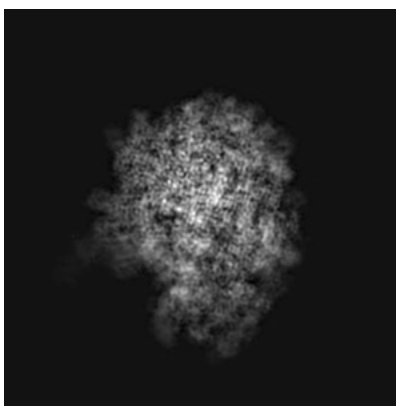
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

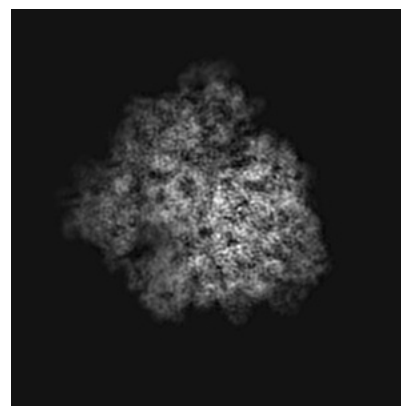
6.1.1 Primary map



X

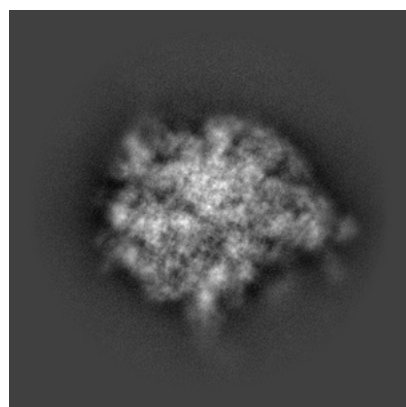


Y

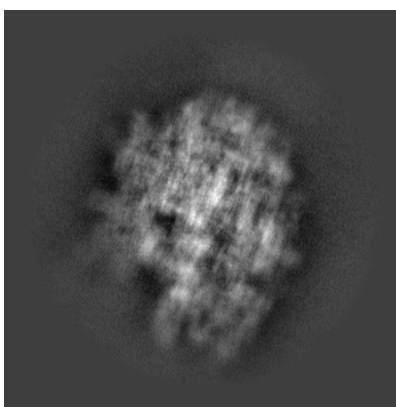


Z

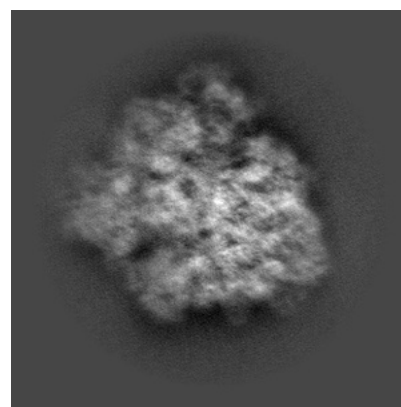
6.1.2 Raw map



X



Y

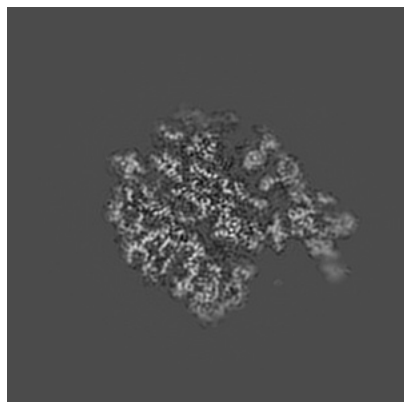


Z

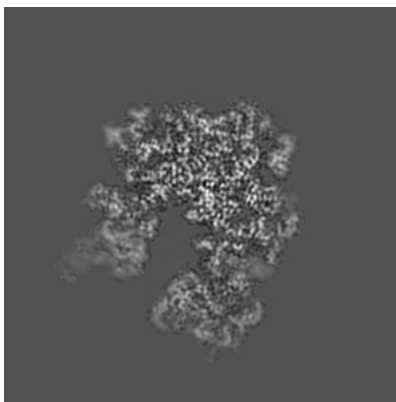
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

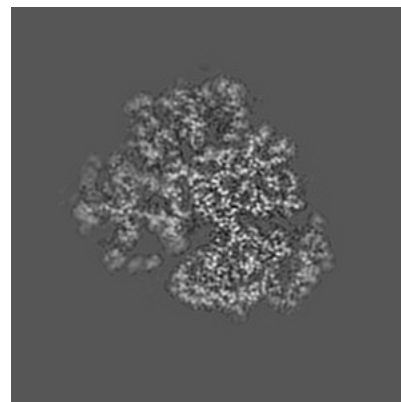
6.2.1 Primary map



X Index: 144

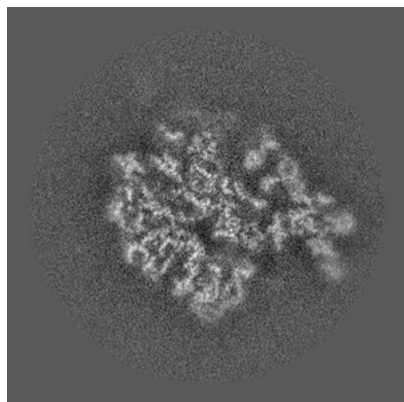


Y Index: 144

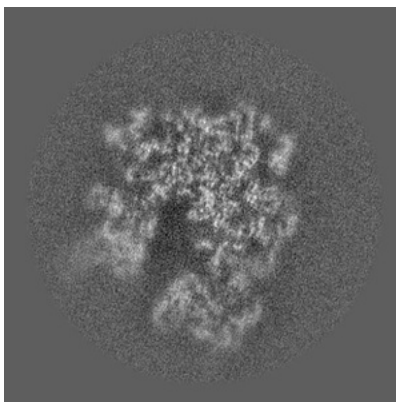


Z Index: 144

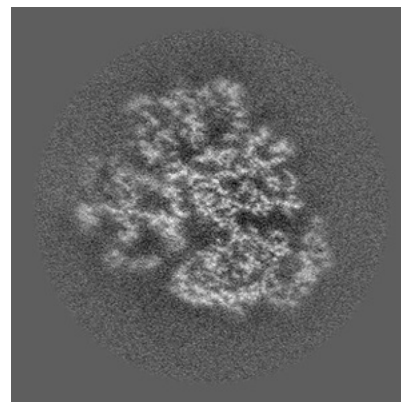
6.2.2 Raw map



X Index: 144



Y Index: 144

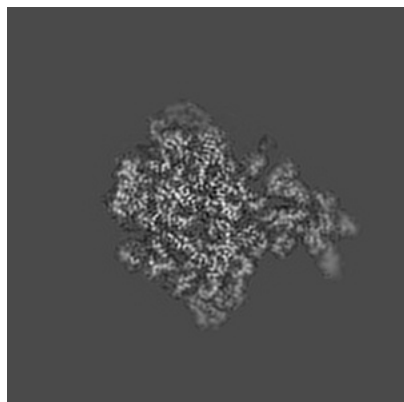


Z Index: 144

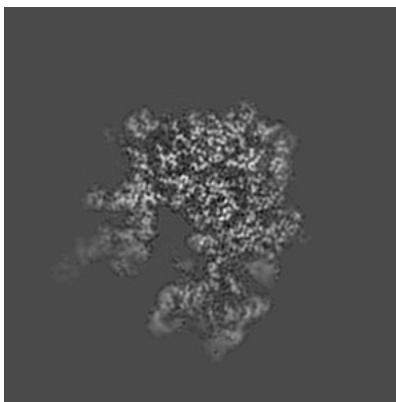
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

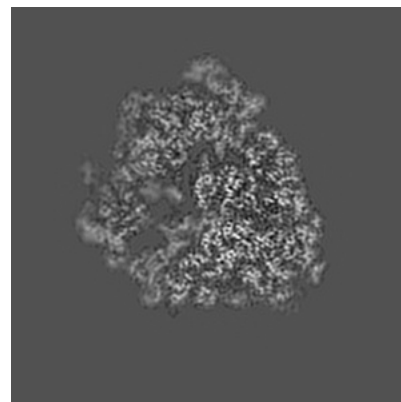
6.3.1 Primary map



X Index: 149

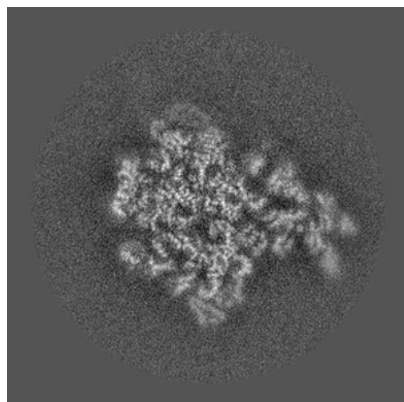


Y Index: 149

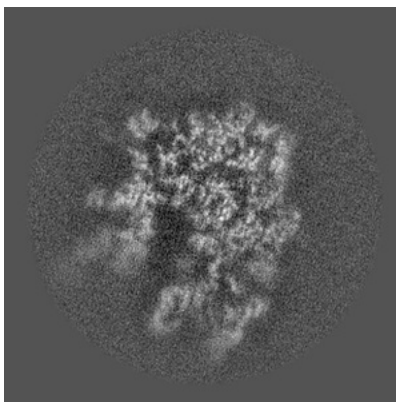


Z Index: 135

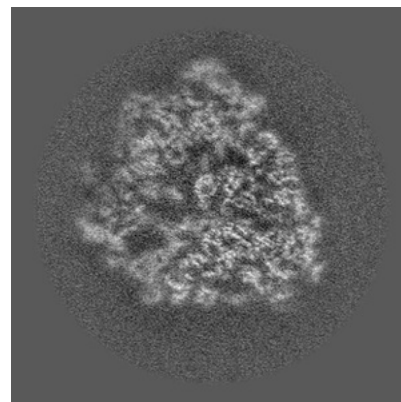
6.3.2 Raw map



X Index: 149



Y Index: 149

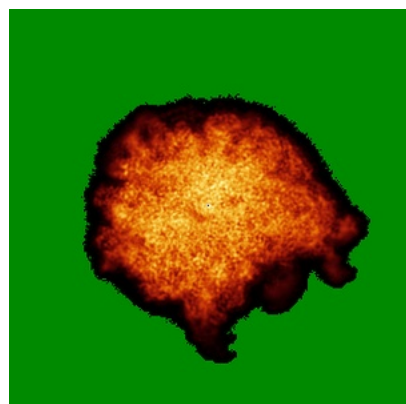


Z Index: 135

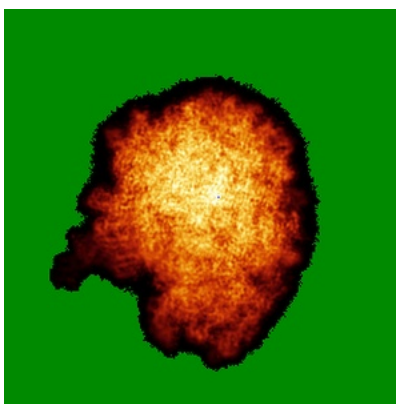
The images above show the largest variance slices of the map in three orthogonal directions.

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

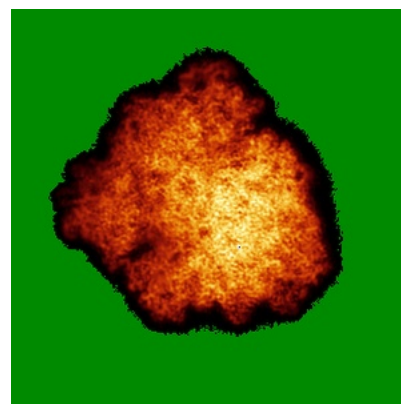
6.4.1 Primary map



X

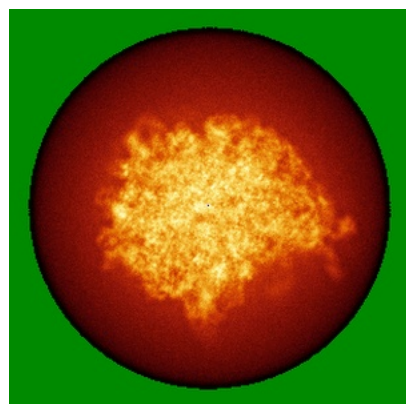


Y

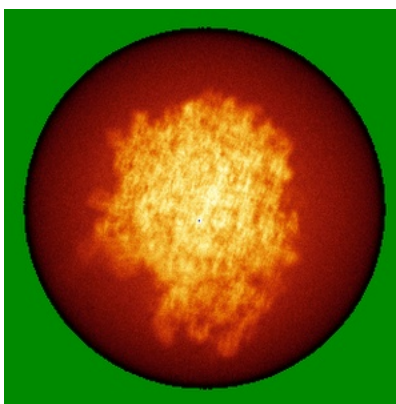


Z

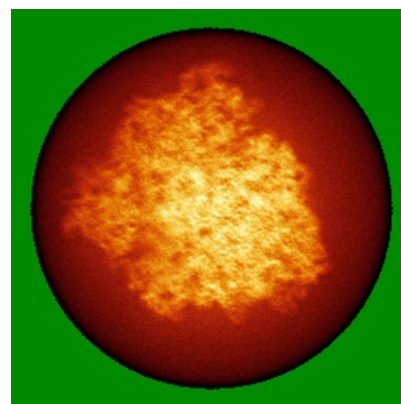
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

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

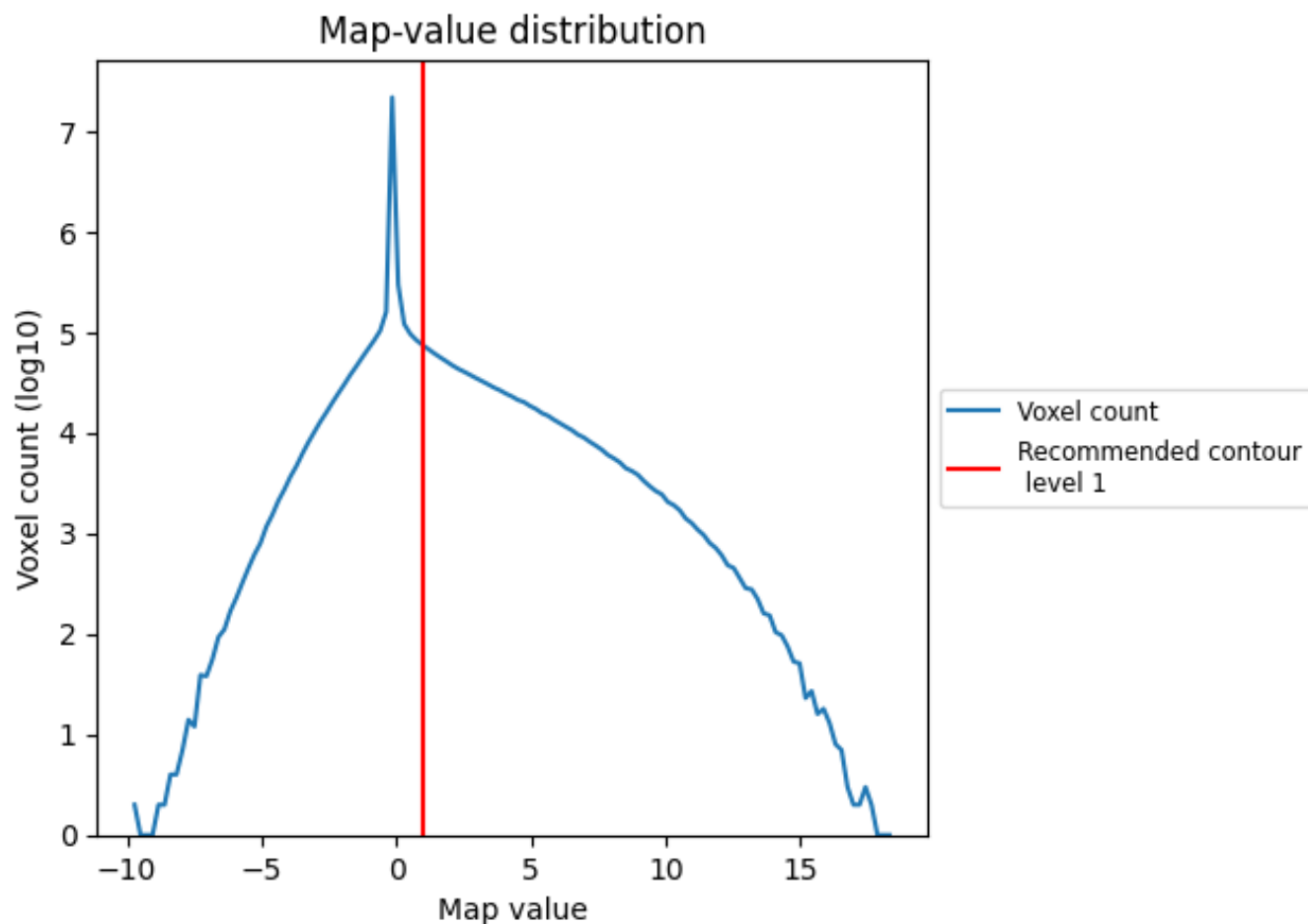
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

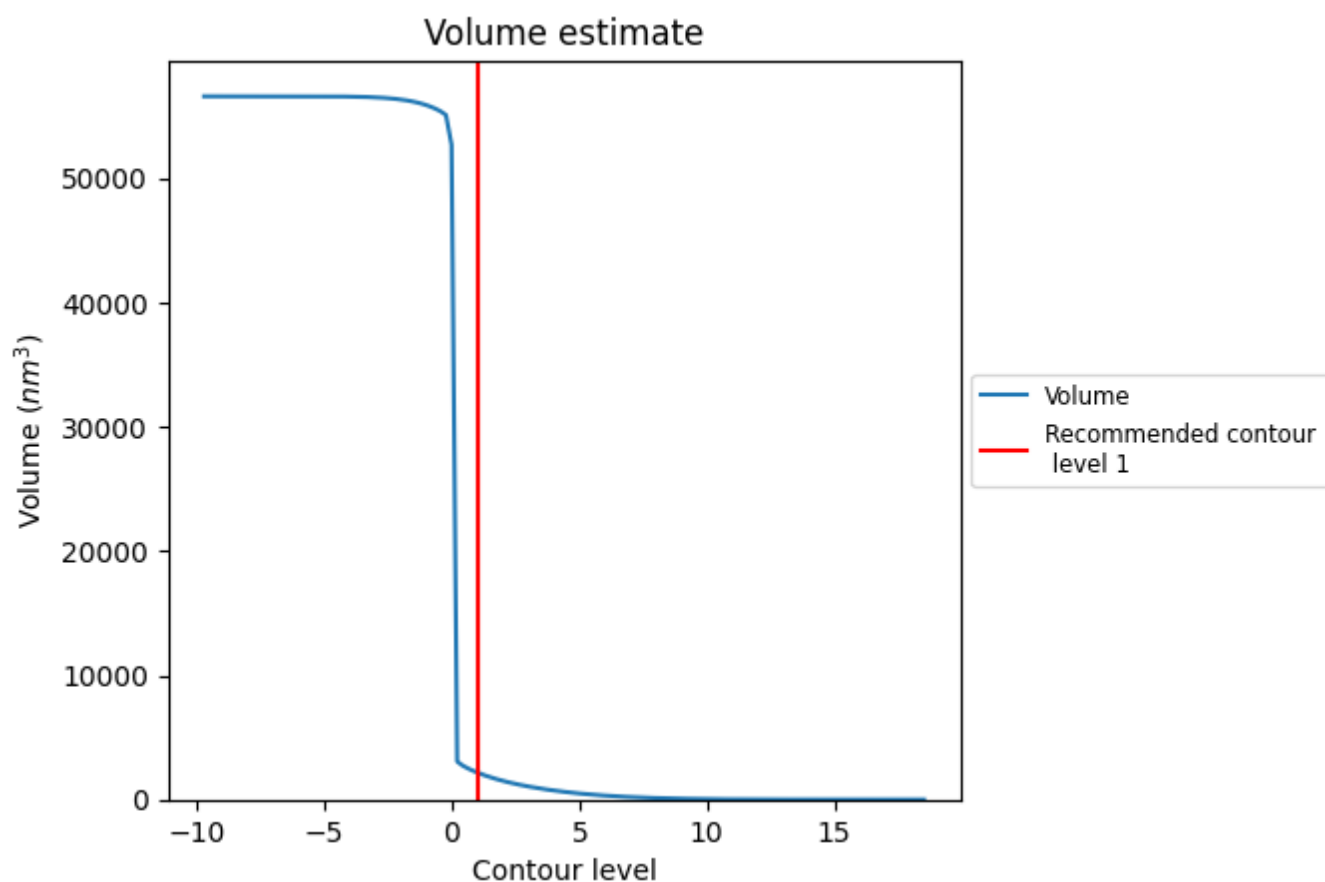
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

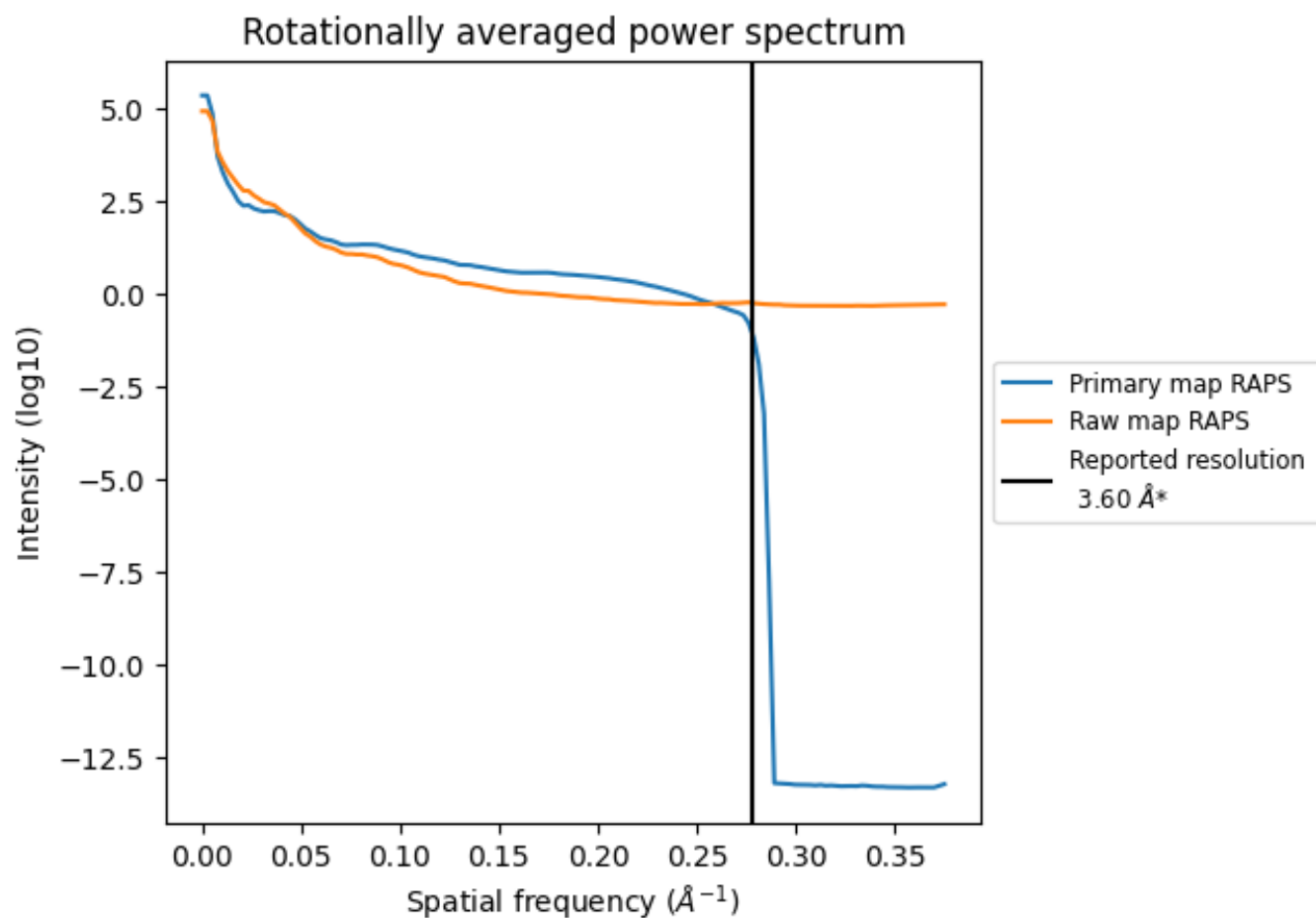
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2173 nm³; this corresponds to an approximate mass of 1963 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 ⓘ

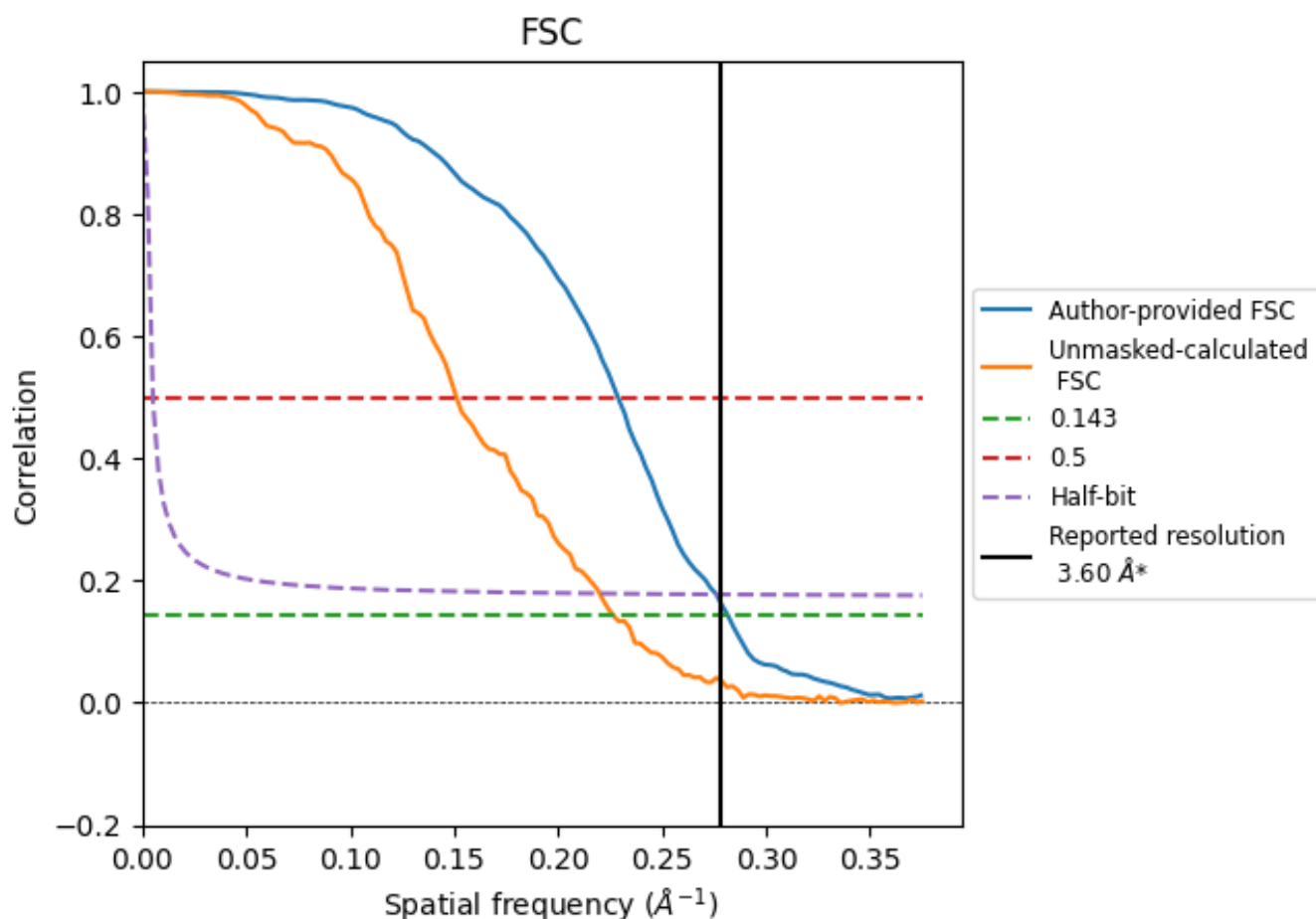


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

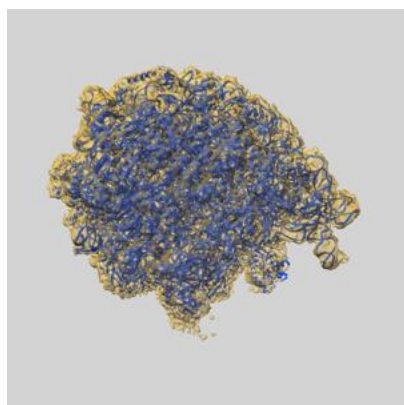
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.55	4.37	3.62
Unmasked-calculated*	4.42	6.62	4.55

*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 4.42 differs from the reported value 3.6 by more than 10 %

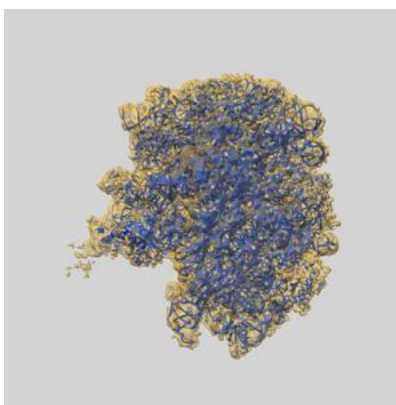
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21624 and PDB model 6WD5. Per-residue inclusion information can be found in section [3](#) on page [17](#).

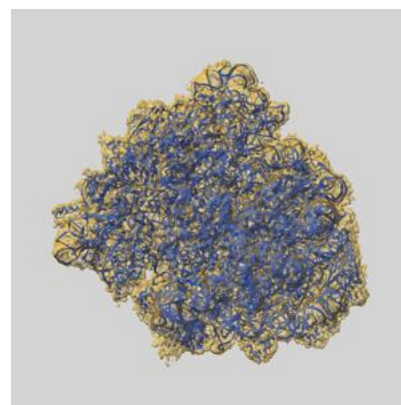
9.1 Map-model overlay [i](#)



X



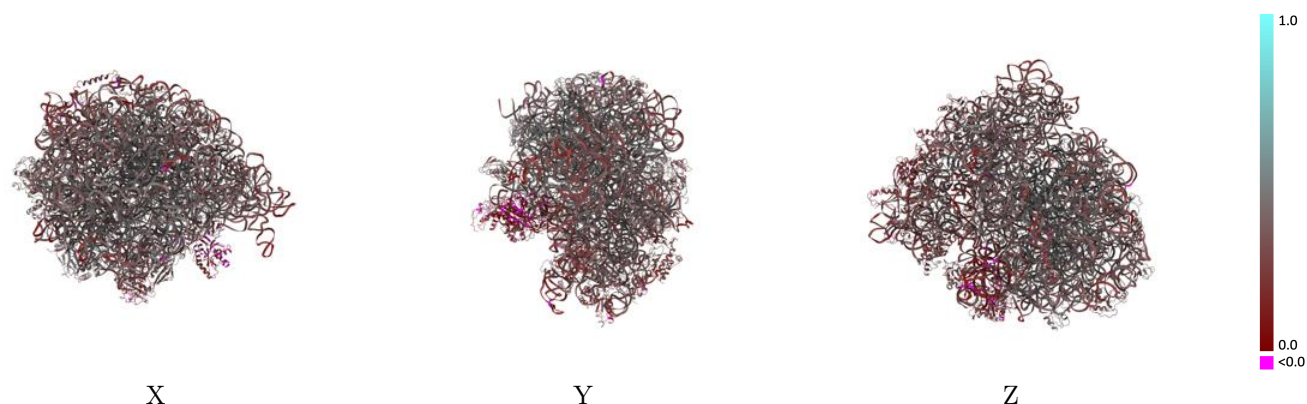
Y



Z

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

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

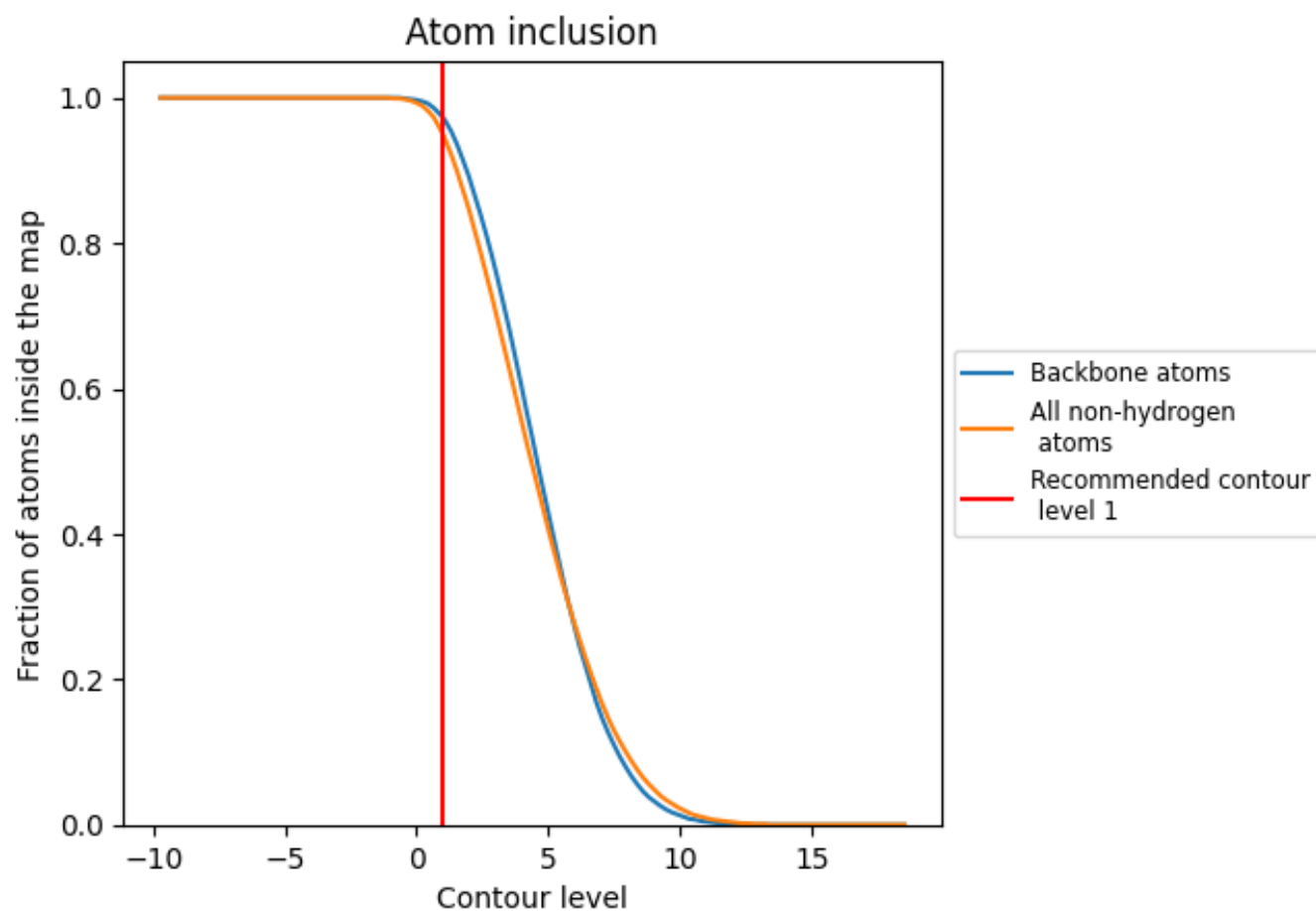


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9500	 0.3620
1	 0.9840	 0.3860
2	 0.9880	 0.3360
3	 0.9780	 0.3500
4	 0.8810	 0.2410
5	 0.9690	 0.3150
6	 0.8380	 0.1570
7	 0.9420	 0.1960
8	 0.6960	 0.1670
B	 0.9530	 0.4520
C	 0.8680	 0.3840
D	 0.9440	 0.4550
E	 0.9390	 0.4680
F	 0.8970	 0.4250
G	 0.8830	 0.3120
H	 0.6920	 0.3020
I	 0.8770	 0.3180
J	 0.9190	 0.4010
K	 0.9460	 0.3640
L	 0.9370	 0.3240
M	 0.9210	 0.4100
N	 0.8880	 0.3040
O	 0.6610	 0.2650
P	 0.9470	 0.3960
Q	 0.9080	 0.4110
R	 0.9330	 0.3190
S	 0.7440	 0.2990
T	 0.9570	 0.3820
U	 0.9030	 0.4000
V	 0.9340	 0.3730
W	 0.9400	 0.3570
X	 0.9630	 0.3050
Y	 0.9030	 0.3630
Z	 0.8690	 0.2970
a	 0.8160	 0.1700



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
b	 0.9530	 0.4560
c	 0.9400	 0.4510
d	 0.9380	 0.4020
e	 0.9300	 0.3280
f	 0.9540	 0.3560
g	 0.7770	 0.2720
h	 0.7880	 0.1540
i	 0.7220	 0.1840
j	 0.9440	 0.4430
k	 0.9350	 0.4520
l	 0.9510	 0.4380
m	 0.9260	 0.4360
n	 0.9360	 0.4370
o	 0.9590	 0.3640
p	 0.9380	 0.4390
q	 0.9420	 0.4400
r	 0.9610	 0.4350
s	 0.9510	 0.4410
t	 0.9310	 0.4010
u	 0.9360	 0.3860
v	 0.9570	 0.4050
w	 0.9460	 0.4560
x	 0.9470	 0.4340
y	 0.9360	 0.3380
z	 0.9500	 0.4310