



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:24 PM UTC

PDB ID : 8Y5O / pdb_00008y5o
EMDB ID : EMD-38944
Title : E.coli transcription translation coupling complex in TTC-B state 3 (subclass1) containing mRNA with 30-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and viomycin
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.
Deposited on : 2024-01-31
Resolution : 4.20 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

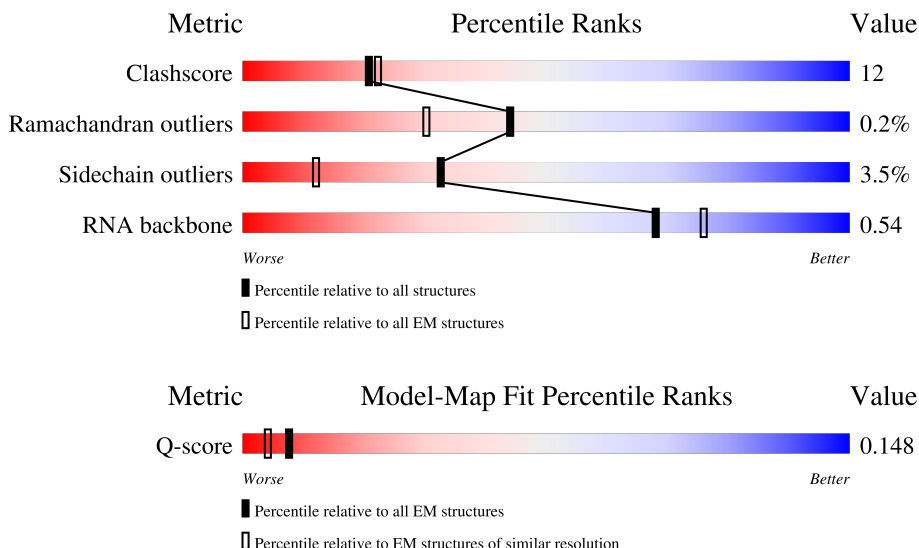
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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.



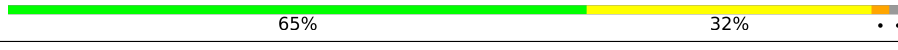
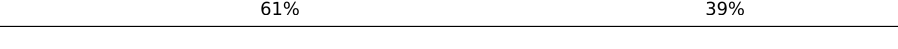
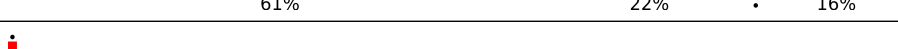
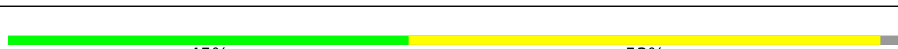
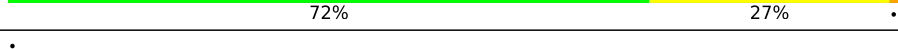
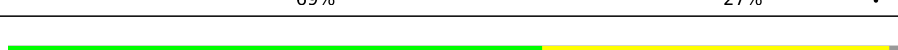
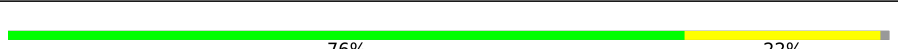
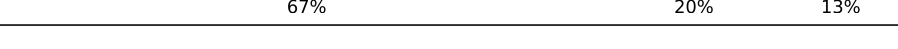
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	A	70	
2	B	57	
3	C	55	

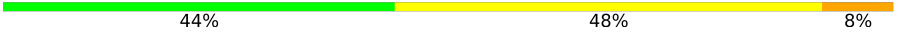
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	46	
5	E	65	
6	F	38	
7	G	241	
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	
27	b	273	
28	c	209	

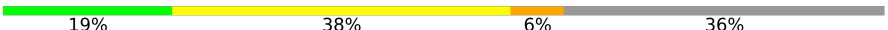
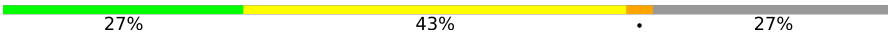
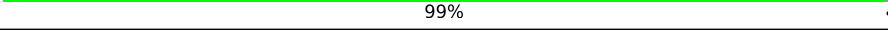
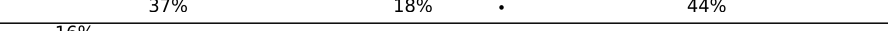
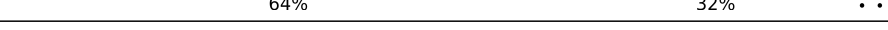
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	d	201	 66% 33% .
30	e	179	 72% 27% ..
31	f	177	 78% 21% .
32	g	149	 9% 69% 27% ..
33	i	142	 8% 68% 31% .
34	j	142	 79% 20% .
35	k	123	 76% 21% ..
36	l	144	 76% 21% ..
37	m	136	 71% 28% .
38	n	127	 63% 30% . 6%
39	o	117	 71% 28% .
40	p	115	 77% 23% .
41	q	118	 77% 22% .
42	r	103	 70% 30%
43	s	110	 72% 28%
44	t	100	 64% 28% . 7%
45	u	104	 71% 26% ..
46	v	94	 78% 22%
47	w	85	 64% 25% 12%
48	x	78	 68% 29% ..
49	y	63	 78% 22%
50	z	59	 75% 24% .
51	1	2904	 44% 48% 8%
52	2	120	 50% 40% 10%
53	3	1542	 45% 48% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	4	47	
55	8	37	
56	9	37	
57	A1	329	
57	A2	329	
58	B1	1407	
59	B2	1342	
60	W0	91	
61	NA	495	
62	NG	181	
63	5	76	
64	6	77	
65	a	234	
66	0	716	
67	h	6	

2 Entry composition

There are 70 unique types of molecules in this entry. The entry contains 183377 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 L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	46	Total	C	N	O	S	0	0
			355	221	62	66	6		

- Molecule 2 is a protein called 50S ribosomal protein L32.

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

- Molecule 3 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 4 is a protein called 50S ribosomal protein L34.

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

- Molecule 5 is a protein called 50S ribosomal protein L35.

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

- Molecule 6 is a protein called 50S ribosomal protein L36.

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

- Molecule 7 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 8 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 9 is a protein called 30S ribosomal protein S4.

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

- Molecule 10 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 11 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 12 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 13 is a protein called 30S ribosomal protein S8.

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

- Molecule 14 is a protein called 30S ribosomal protein S9.

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

- Molecule 15 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 16 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 17 is a protein called 30S ribosomal protein S12.

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

- Molecule 18 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 19 is a protein called 30S ribosomal protein S14.

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

- Molecule 20 is a protein called 30S ribosomal protein S15.

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

- Molecule 21 is a protein called 30S ribosomal protein S16.

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

- Molecule 22 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 23 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 24 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 25 is a protein called 30S ribosomal protein S20.

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

- Molecule 26 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 28 is a protein called 50S ribosomal protein L3.

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

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

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

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	u	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

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

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

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

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

- Molecule 51 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1929590828

- Molecule 52 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	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	U	conflict	GB NR_103249

- Molecule 53 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	30	Total	C	N	O	P	0	0
			627	280	92	225	30		

- Molecule 55 is a DNA chain called templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	27	Total	C	N	O	P	0	0
			539	257	88	167	27		

- Molecule 56 is a DNA chain called non-templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	9	20	Total	C	N	O	P	0	0
			417	195	84	118	20		

- Molecule 57 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A1	301	Total	C	N	O	S	0	0
			2088	1293	380	409	6		
57	A2	288	Total	C	N	O	S	0	0
			2029	1257	366	400	6		

- Molecule 58 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	B1	1335	Total	C	N	O	S	0	0
			10353	6509	1842	1955	47		

- Molecule 59 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B2	1340	Total	C	N	O	S	0	0
			10546	6616	1839	2048	43		

- Molecule 60 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	W0	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 61 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	NA	492	Total	C	N	O	0	0
			2432	1448	492	492		

- Molecule 62 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	NG	154	Total	C	N	O	0	0
			758	450	154	154		

- Molecule 63 is a RNA chain called tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
63	5	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 64 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
64	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 65 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	a	132	Total	C	N	O	S	0	0
			1013	638	183	190	2		

- Molecule 66 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	0	697	Total	C	N	O	S	0	0
			5399	3403	929	1042	25		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	705	GLY	-	expression tag	UNP P0A6M8
0	706	SER	-	expression tag	UNP P0A6M8
0	707	SER	-	expression tag	UNP P0A6M8
0	708	GLY	-	expression tag	UNP P0A6M8
0	709	HIS	-	expression tag	UNP P0A6M8
0	710	HIS	-	expression tag	UNP P0A6M8
0	711	HIS	-	expression tag	UNP P0A6M8
0	712	HIS	-	expression tag	UNP P0A6M8
0	713	HIS	-	expression tag	UNP P0A6M8
0	714	HIS	-	expression tag	UNP P0A6M8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
0	715	HIS	-	expression tag	UNP P0A6M8
0	716	HIS	-	expression tag	UNP P0A6M8

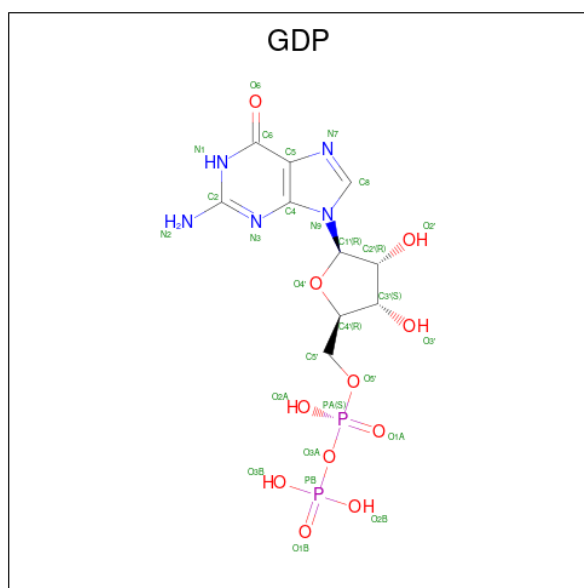
- Molecule 67 is a protein (with D amino acids) called Viomycin.

Mol	Chain	Residues	Atoms				AltConf	Trace
67	h	6	Total	C	N	O	0	0
			48	25	13	10		

- Molecule 68 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

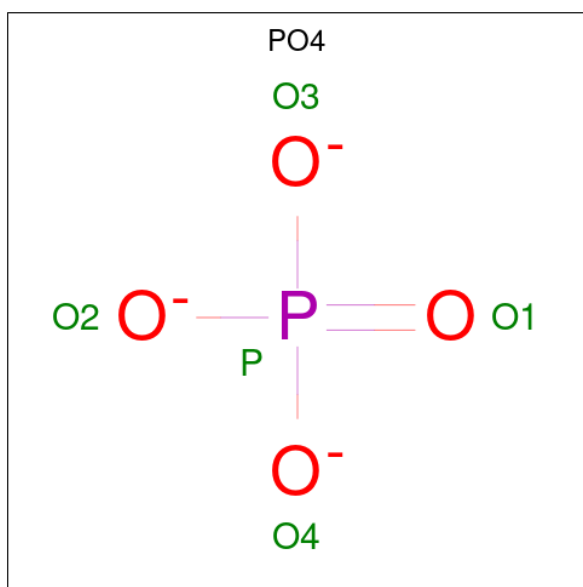
Mol	Chain	Residues	Atoms		AltConf
68	B1	1	Total	Mg	0
			1	1	

- Molecule 69 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
69	0	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 70 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).

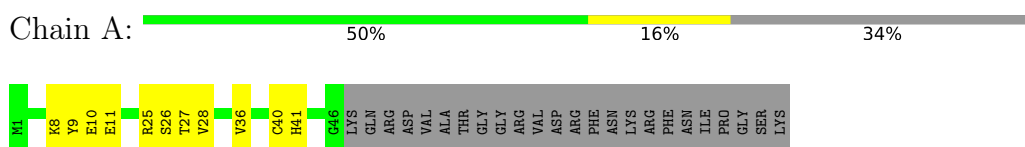


Mol	Chain	Residues	Atoms			AltConf
			Total	O	P	
70	0	1	5	4	1	0

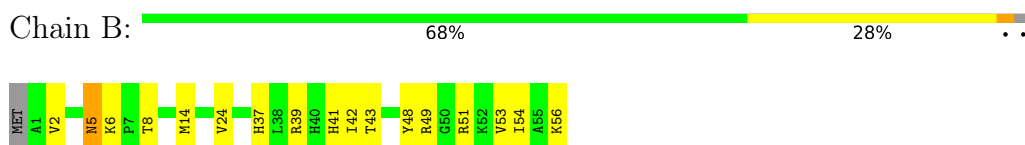
3 Residue-property plots

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

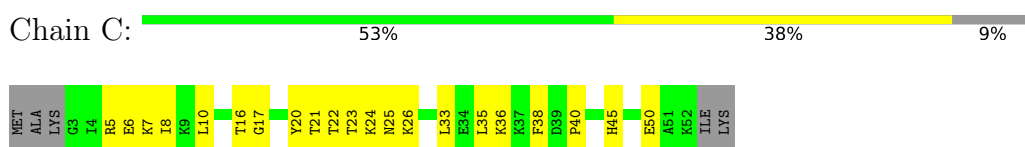
• Molecule 1: 50S ribosomal protein L31



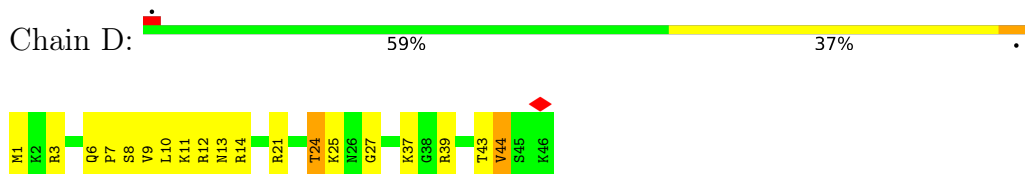
• Molecule 2: 50S ribosomal protein L32



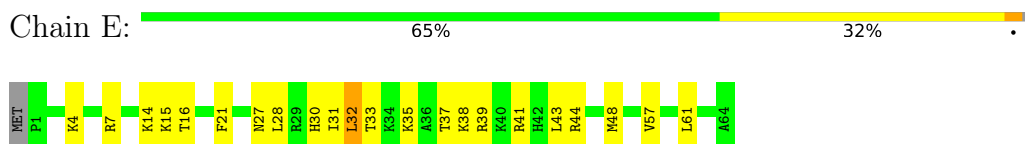
• Molecule 3: 50S ribosomal protein L33



• Molecule 4: 50S ribosomal protein L34

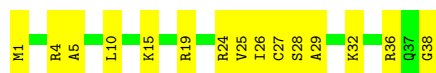


• Molecule 5: 50S ribosomal protein L35



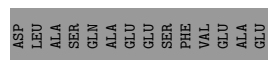
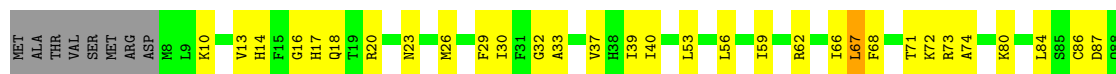
• Molecule 6: 50S ribosomal protein L36

Chain F:  61% 39%



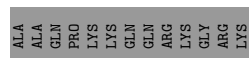
• Molecule 7: 30S ribosomal protein S2

Chain G:  64% 26% 10%



• Molecule 8: 30S ribosomal protein S3

Chain H:  63% 24% 12%



• Molecule 9: 30S ribosomal protein S4

Chain I:  71% 27% 2%



• Molecule 10: 30S ribosomal protein S5

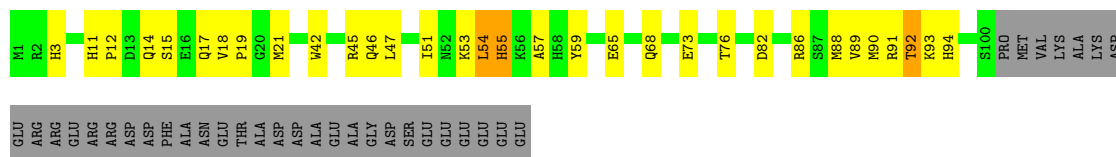
Chain J:  66% 28% 6%





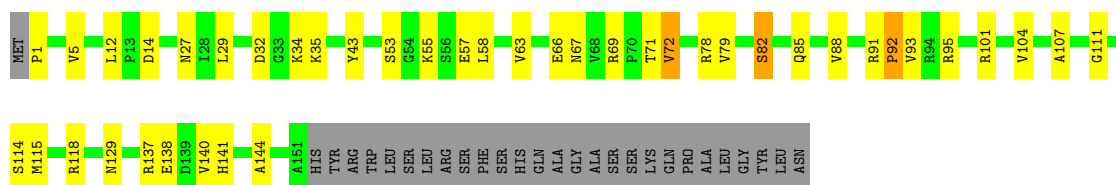
- Molecule 11: 30S ribosomal protein S6, fully modified isoform

Chain K: 50% 21% 26%



- Molecule 12: 30S ribosomal protein S7

Chain L: 61% 22% 16%



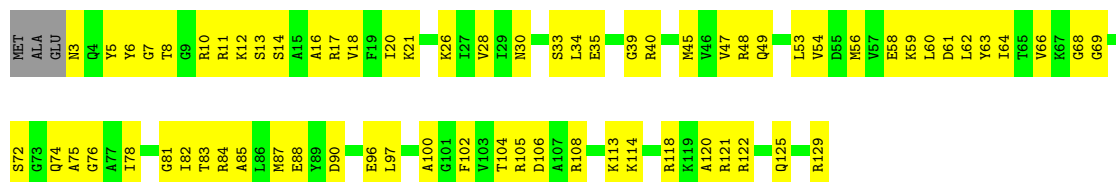
- Molecule 13: 30S ribosomal protein S8

Chain M: 66% 33% 1%



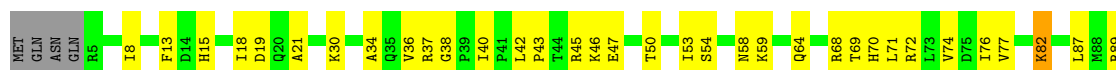
- Molecule 14: 30S ribosomal protein S9

Chain N: 45% 53% 2%



- Molecule 15: 30S ribosomal protein S10

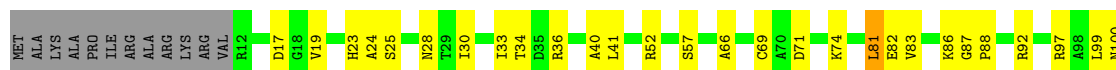
Chain O: 56% 38% 5%





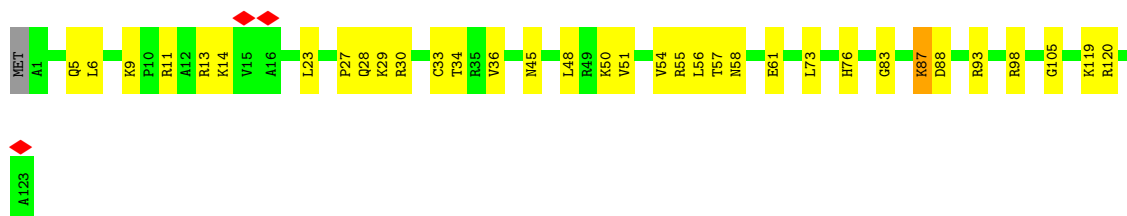
- Molecule 16: 30S ribosomal protein S11

Chain P: 61% 28% 10%



- Molecule 17: 30S ribosomal protein S12

Chain Q: 72% 27% 1%



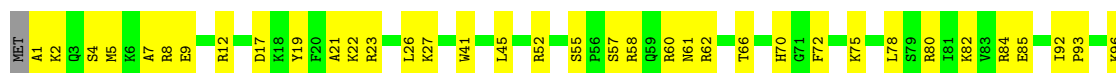
- Molecule 18: 30S ribosomal protein S13

Chain R: 69% 27% 4%



- Molecule 19: 30S ribosomal protein S14

Chain S: 60% 39% 1%



- Molecule 20: 30S ribosomal protein S15

Chain T: 76% 22% 2%



- Molecule 21: 30S ribosomal protein S16

Chain U:  72% 28%



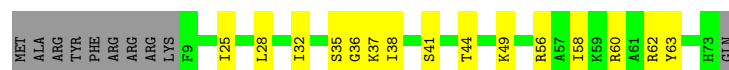
- Molecule 22: 30S ribosomal protein S17

Chain V:  67% 29% 5%



- Molecule 23: 30S ribosomal protein S18

Chain W:  67% 20% 13%



- Molecule 24: 30S ribosomal protein S19

Chain X:  64% 22% 14%



- Molecule 25: 30S ribosomal protein S20

Chain Y:  64% 33% 3%



- Molecule 26: 30S ribosomal protein S21

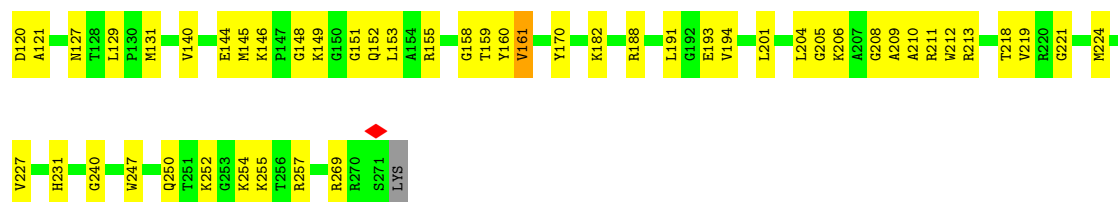
Chain Z:  61% 25% 6% 8%



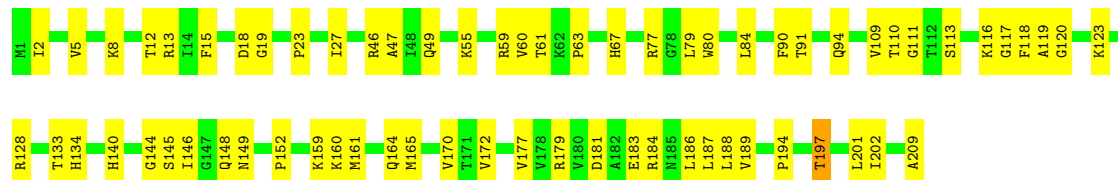
- Molecule 27: 50S ribosomal protein L2

Chain b:  70% 29% 1%

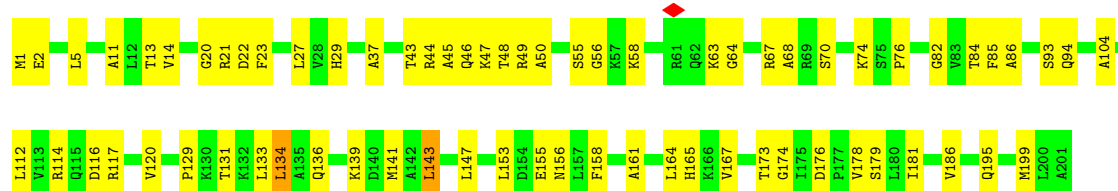




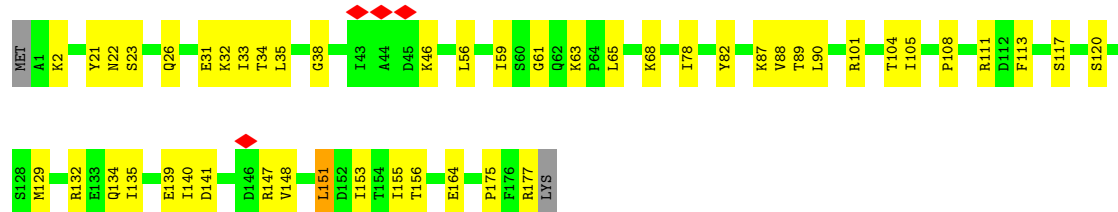
• Molecule 28: 50S ribosomal protein L3



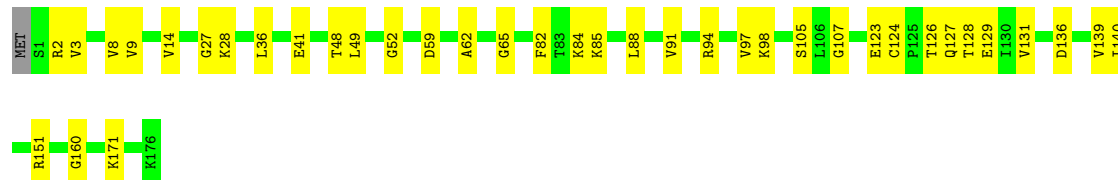
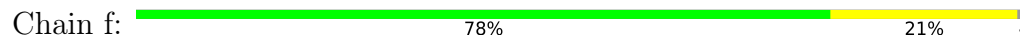
• Molecule 29: 50S ribosomal protein L4



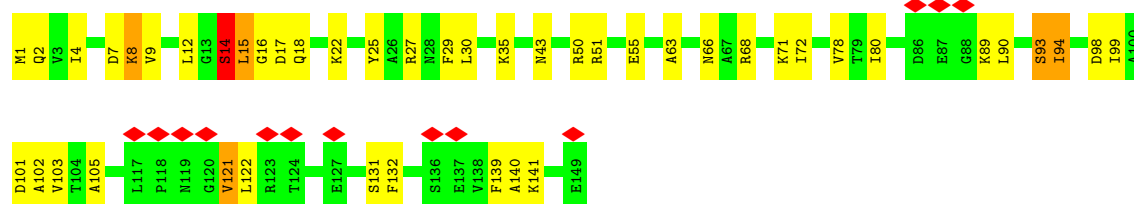
• Molecule 30: 50S ribosomal protein L5



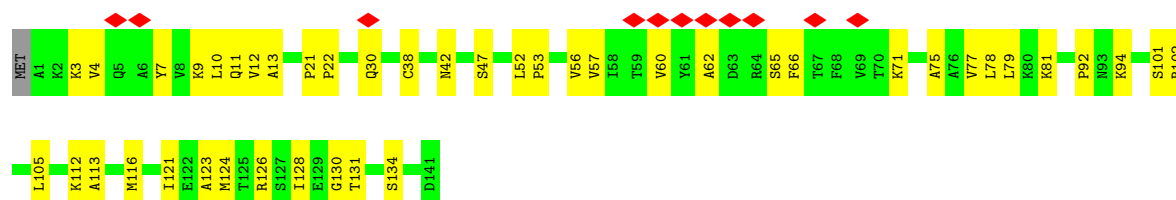
• Molecule 31: 50S ribosomal protein L6



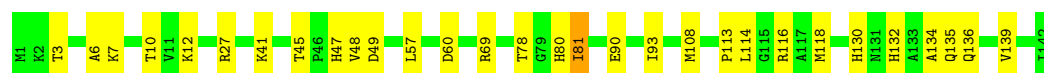
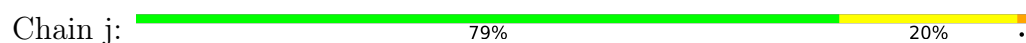
• Molecule 32: 50S ribosomal protein L9



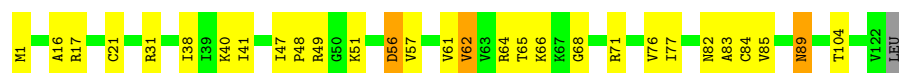
- Molecule 33: 50S ribosomal protein L11



- Molecule 34: 50S ribosomal protein L13



- Molecule 35: 50S ribosomal protein L14



- Molecule 36: 50S ribosomal protein L15



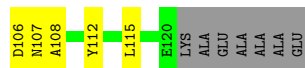
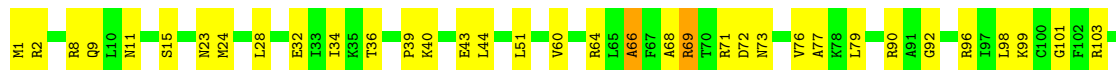
- Molecule 37: 50S ribosomal protein L16





- Molecule 38: 50S ribosomal protein L17

Chain n: 63% 30% 6%



- Molecule 39: 50S ribosomal protein L18

Chain o: 71% 28%



- Molecule 40: 50S ribosomal protein L19

Chain p: 77% 23%



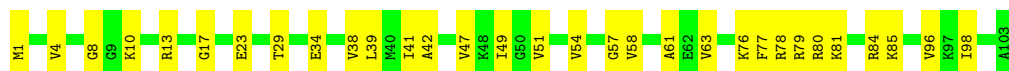
- Molecule 41: 50S ribosomal protein L20

Chain q: 77% 22%



- Molecule 42: 50S ribosomal protein L21

Chain r: 70% 30%

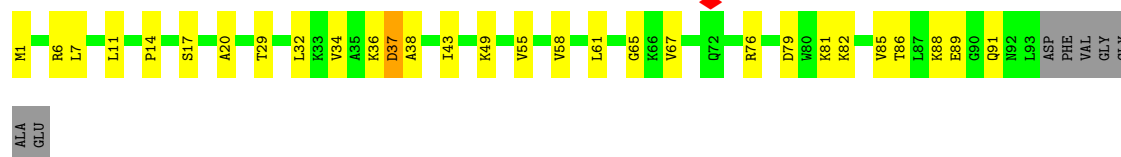


- Molecule 43: 50S ribosomal protein L22

Chain s: 72% 28%



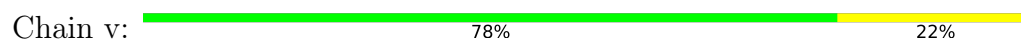
- Molecule 44: 50S ribosomal protein L23



- Molecule 45: 50S ribosomal protein L24



- Molecule 46: 50S ribosomal protein L25



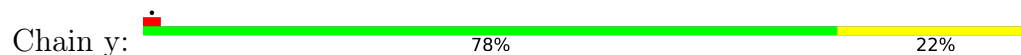
- Molecule 47: 50S ribosomal protein L27



- Molecule 48: 50S ribosomal protein L28



- Molecule 49: 50S ribosomal protein L29

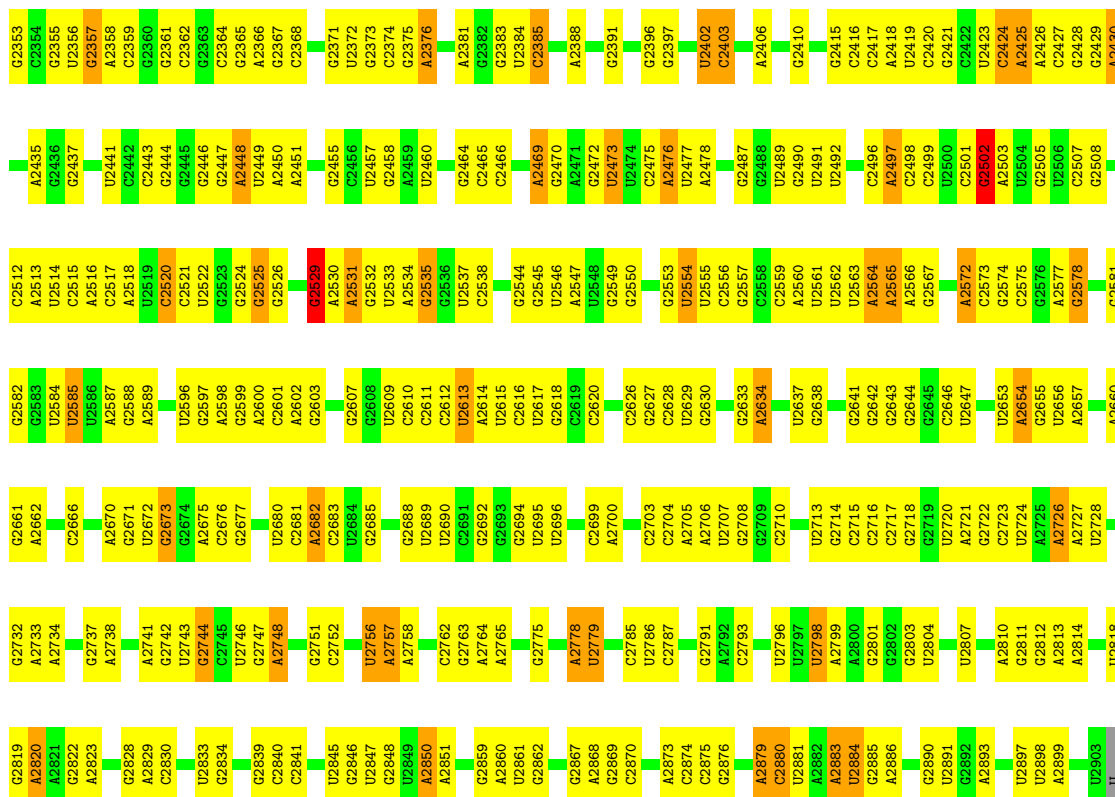


- Molecule 50: 50S ribosomal protein L30



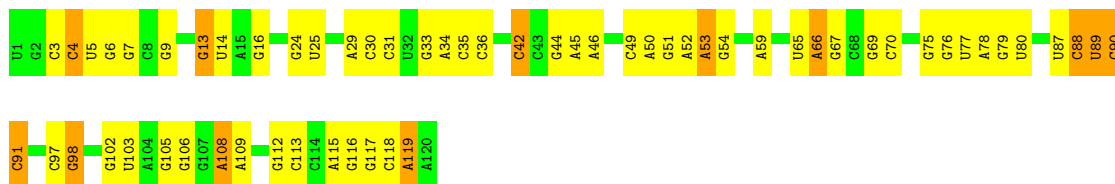


G2276	G2277	C2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249	G2250	G2251	G2255	G2256	U2257	G2258	U2262	G2263	A2264	A2267	A2268	G2269	U2270	G2271	G2272	G2273	C2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	A2297	A2298	G2299	G2300	C2301	A2211	A2212	G2213	G2214	G2215	G2216	G2221	G2222	A2225	G2226	A2227	A2228	G2230	G2234	G2235	U2236	G2237	G2238	G2239	A2247	G2248	U2249
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------



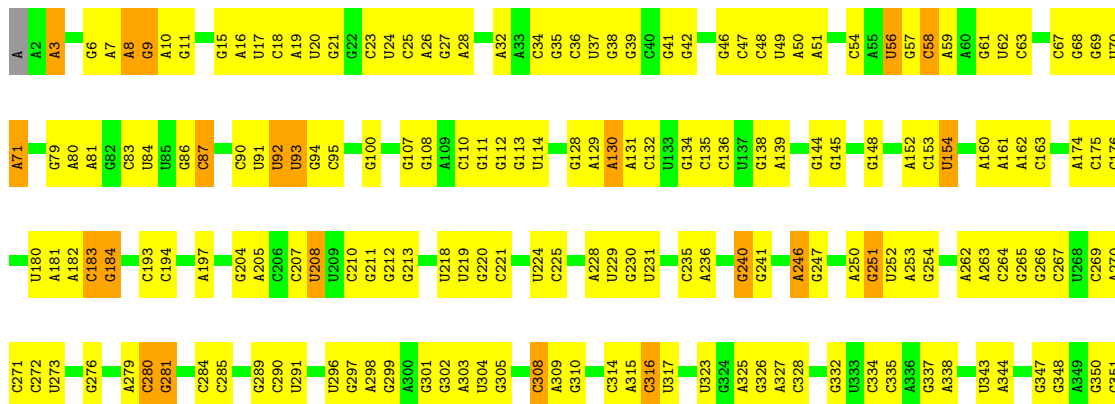
• Molecule 52: 5S rRNA

Chain 2: 50% 40% 10%



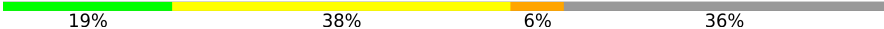
• Molecule 53: 16S rRNA

Chain 3: 45% 48% 6%



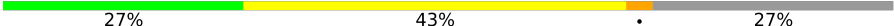
U1490	C1400	U1326	U1173	C1097	G1018		G858	U768	A596	U512	G424	C352
G1491	G1401	C1327	G1174	C1098	A1019	G944	G859	G769	G597	C513	G425	A353
A1492	C1402	G1253		G1099		G945	A860	G770	U598	G514	U426	G354
A1493	C1403	A1254	A1179	C1100	A1022	A946	G861	G771	G599	G515	U427	C355
G1494	C1404	G1255	A1180	A1102	U1023	G947	G862	G772	A600	G516	G428	A356
U1495	G1405	G1331	G1181	C1103	G1024	U950	U863	G773	G601	U517	U429	G357
C1496	U1406	A1257	G1182	C1104	U1025	U951	A864		A602	C518	U358	U358
G1497	C1407		U1183	G1105	G1026	A865	A866			C519	A431	G359
A1502	A1408		G1184	A1105	G1027	U952	G866		A607	A520	A432	
A1503	C1409		G1185	C1106	U1028	U953	G867		A608	G528	G433	G362
G1504	C1412		G1186	G1107	U1029	G954				G529	U434	A363
G1505	A1413		A1187	C1108	U1030	U955	A872		C613	G530	U437	A366
U1506	U1414		A1110	A1111	G1031	U956	A873		G620	U531	U438	U867
A1507	G1415		U1112		U1032	A958	G874		A621	A532	U439	U868
A1508			U1113		G1033	A959	C876		A622	A533	C440	G369
U1512	U1420		A1114		A1035	U960	A877		G623	U534	G445	C372
A1513	G1421		U1115		A1042	U961	A878		U625	A535		
G1514	G1422		C1119		G1043	G962			G626	A539	A448	G376
G1515	U1424		C1120		G1044	A964	G881		G627	G540	G377	G377
G1516	U1425		U1122		U1047	U965	C883		G628	G541	G452	G378
G1517			U1123		G1048	G966	U884				G453	C379
A1518	G1432		A1201		C1049	C967	U885		C631	C546	G454	G380
			U1204		U1050	A968	G886		U632	A546	G455	
			G1125		G1051	A969			G633	A547		G384
			U1126		G1052	C970	A889		C634			C385
			C1127		C1054	G971			U552		U458	C386
			C1129		G1057	G972	G894		A635		A459	C387
			U1134		C1058	C973	G895		U636		A460	U387
			U1135		C1059	A974	A900		U638		A461	G388
			C1136		U1060	A975	A901		G639		G462	U389
			C1137		G1061	G976	A902		C556		U467	G391
			G1138		U1062	A977	G902		U641		A468	C392
			G1139		C1063	G978	G903		A642		G478	A393
			C1140		U1064	C979	U904		G643		A479	
					G1065	C980	U905		U644		U480	A397
					U1065	U981	A906					
						C990	A907		G650			C400
						U991	A908		C651		C483	C401
						U992	A909		U652		G484	G402
						G993	C910		U653		U485	
						A994	A913				U486	U405
						A1000			U657		G492	G406
						C1001	G917		C658		A493	U409
						A1004	A923		U659		G494	G410
						A1005	C924		G661		G497	G413
						G1006	G925		A665		A414	A414
						U1007	G926		G667		A415	A415
						U1008	G927		G668		G416	G416
						A1012	C934		G669		G417	G417
						G1013	A935		A673		G505	C418
						A1014	C936		G674		G506	C419
						G1015	A937		A675		U421	U420
						U1016	A938		U676		A509	A509
						C1096	C940		U677		A510	C422
											C511	G423

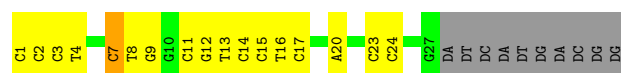
• Molecule 54: mRNA

Chain 4: 



- Molecule 55: template DNA strand

Chain 8: 



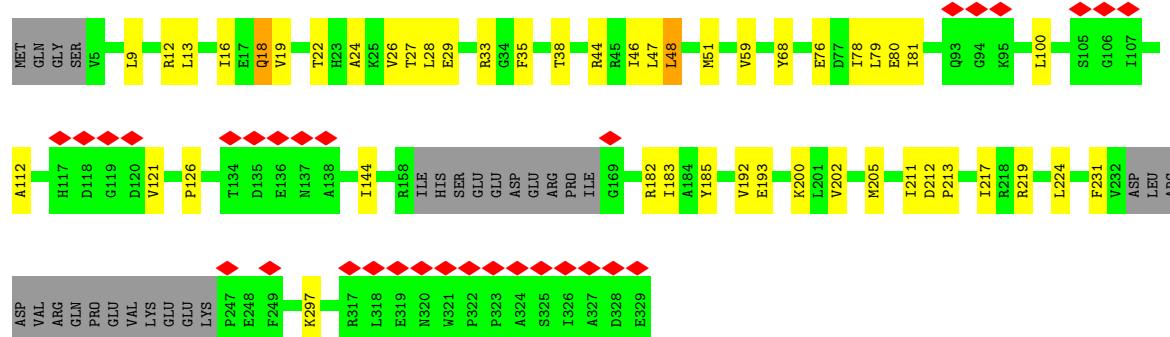
- Molecule 56: non-template DNA strand

Chain 9: 



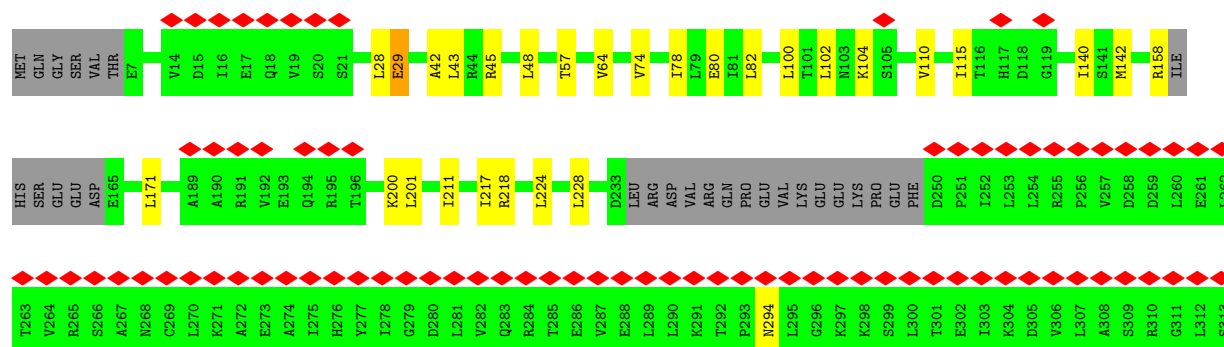
- Molecule 57: DNA-directed RNA polymerase subunit alpha

Chain A1: 



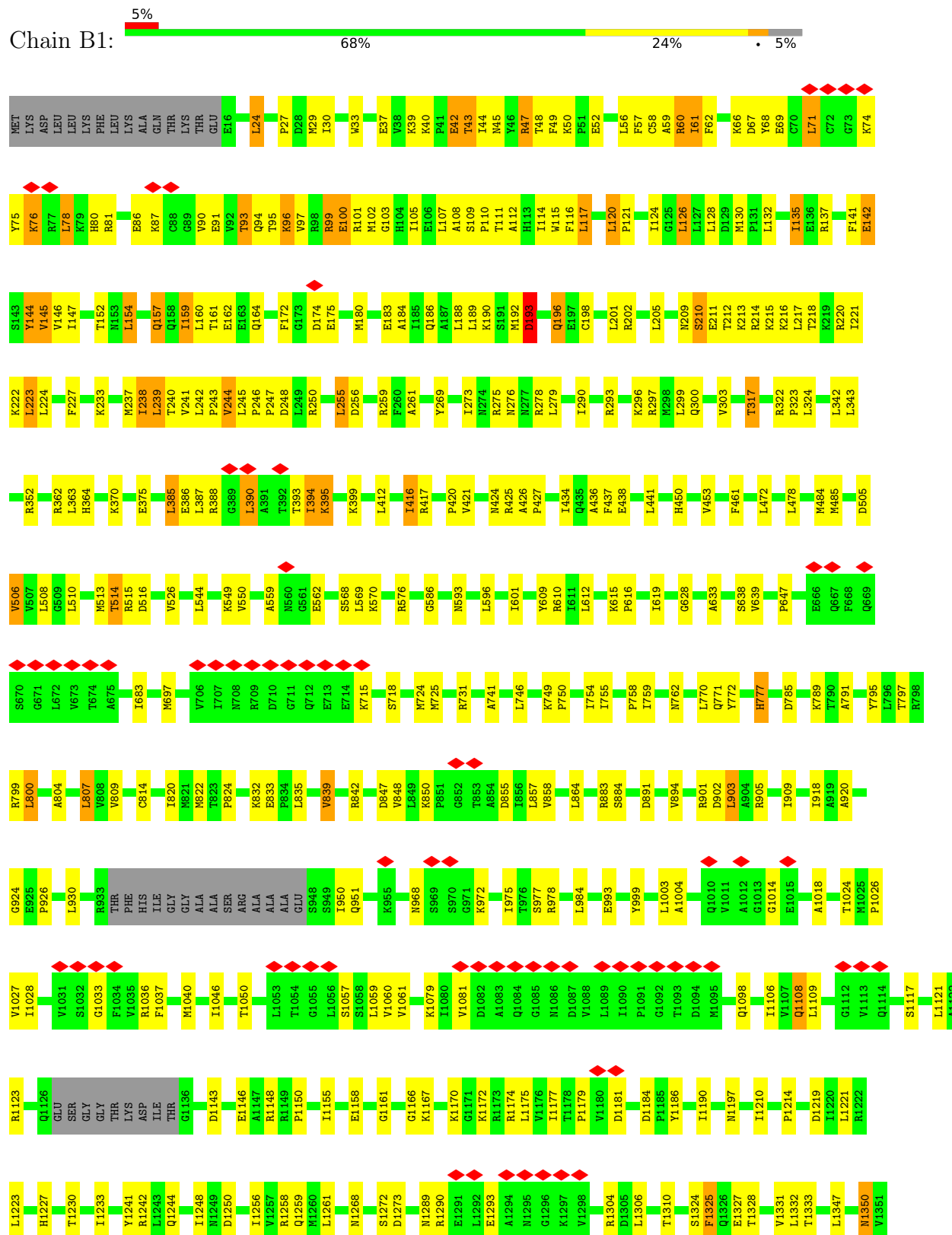
- Molecule 57: DNA-directed RNA polymerase subunit alpha

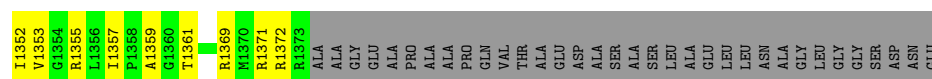
Chain A2: 



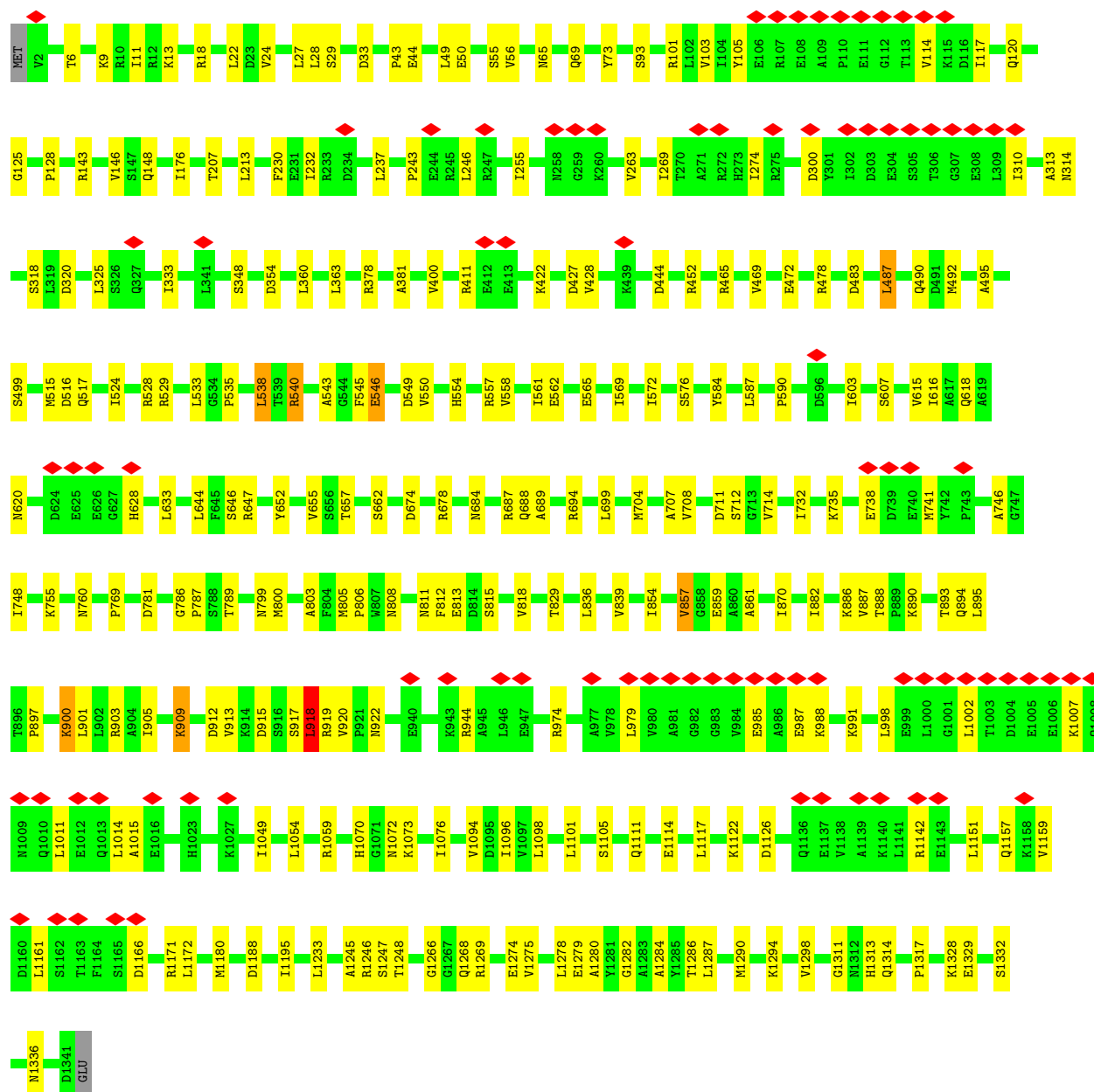
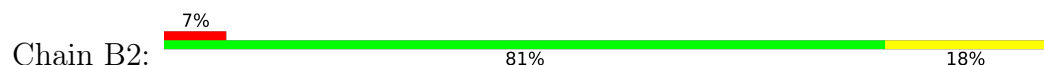
PRO
ALA
SER
ILE
ALA
ASP
GLU

• Molecule 58: DNA-directed RNA polymerase subunit beta'

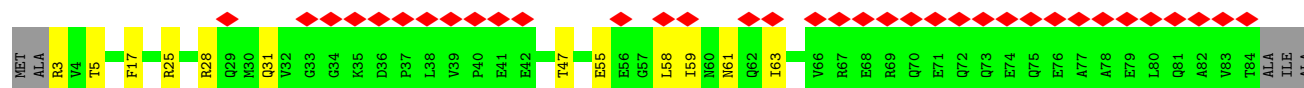
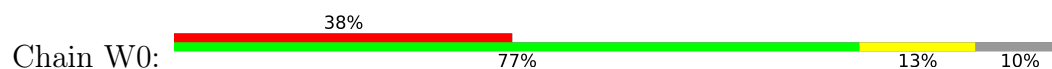




• Molecule 59: DNA-directed RNA polymerase subunit beta

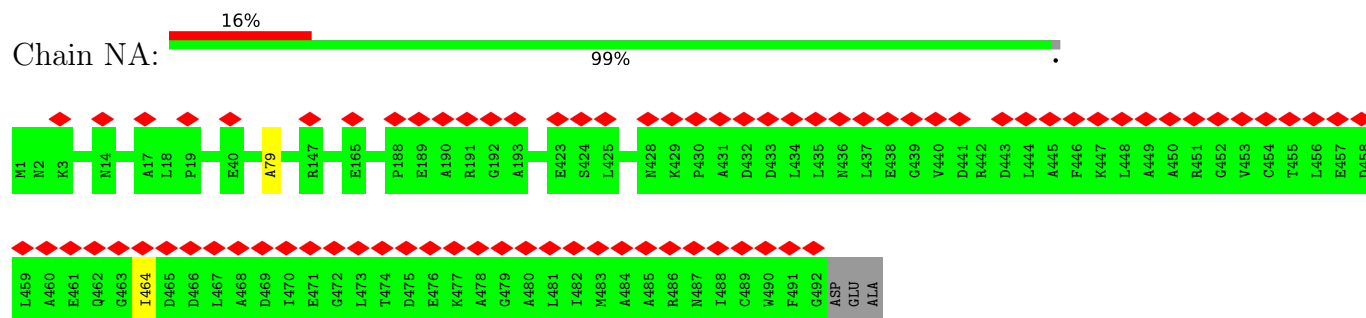


• Molecule 60: DNA-directed RNA polymerase subunit omega

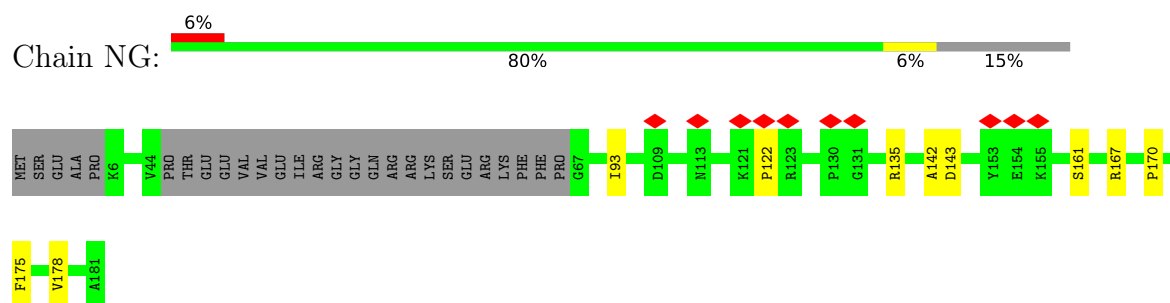


GLU
GLY
ARG
ARG

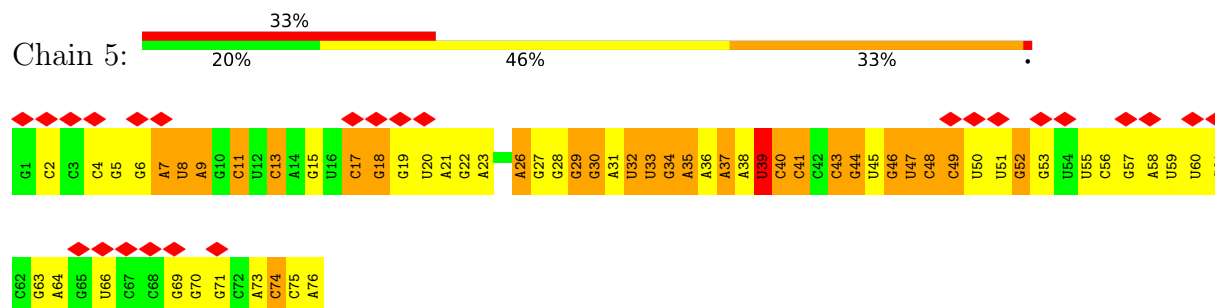
- Molecule 61: Transcription termination/antitermination protein NusA



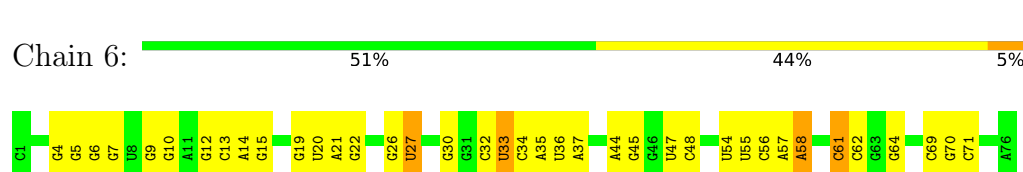
- Molecule 62: Transcription termination/antitermination protein NusG



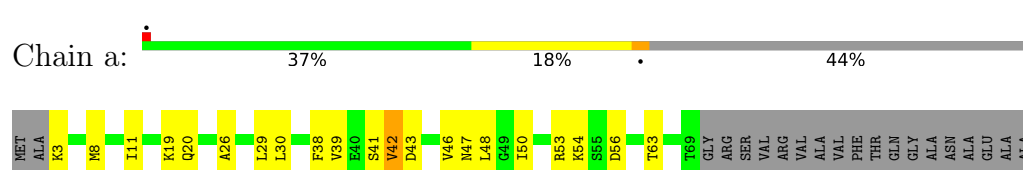
- Molecule 63: tRNA(Phe)

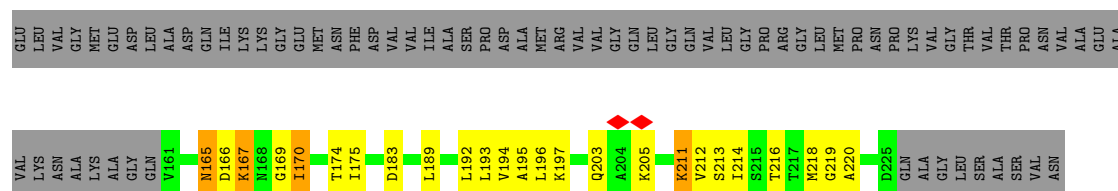


- Molecule 64: tRNA(fMet)



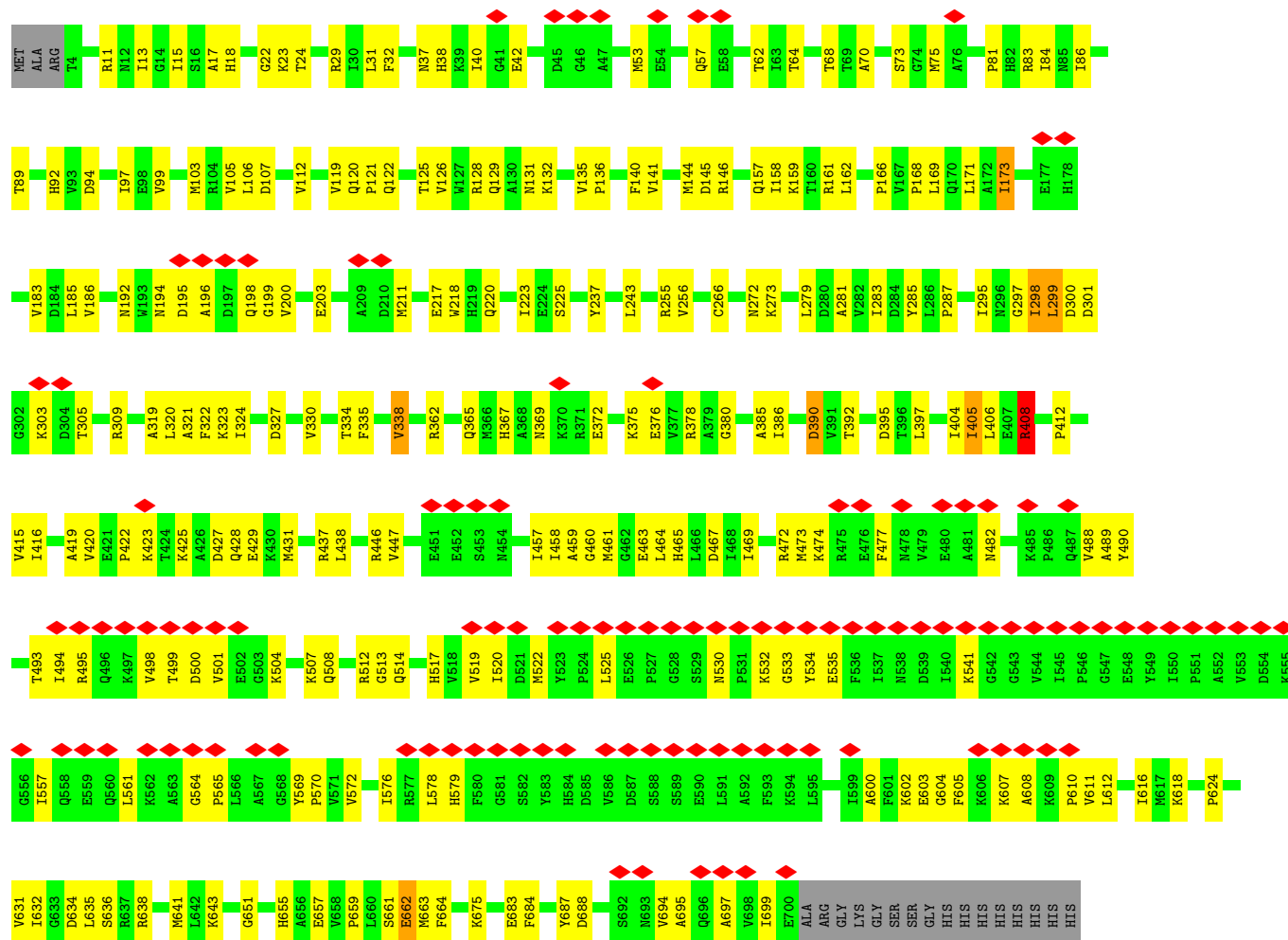
- Molecule 65: Large ribosomal subunit protein uL1





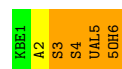
• Molecule 66: Elongation factor G

Chain 0:



• Molecule 67: Viomycin

Chain h:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35620	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.082	Depositor
Minimum map value	-0.031	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.006	Depositor
Map size ($\text{\AA}$)	753.60004, 753.60004, 753.60004	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.57, 1.57, 1.57	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5OH, MG, KBE, GDP, UAL, PO4, DPP

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	A	0.25	0/362	0.73	0/485
2	B	0.37	0/450	0.80	2/599 (0.3%)
3	C	0.31	0/416	0.61	0/554
4	D	0.48	0/380	0.95	0/498
5	E	0.46	0/513	0.80	0/676
6	F	0.40	0/303	0.79	0/397
7	G	0.41	0/1735	0.83	0/2338
8	H	0.41	0/1651	0.80	0/2225
9	I	0.31	0/1665	0.77	1/2227 (0.0%)
10	J	0.47	0/1169	0.81	0/1573
11	K	0.44	0/835	0.87	0/1128
12	L	0.41	0/1195	0.82	2/1602 (0.1%)
13	M	0.31	0/989	0.75	0/1326
14	N	0.29	0/1034	0.74	0/1375
15	O	0.56	0/796	0.81	0/1077
16	P	0.47	0/885	0.78	0/1195
17	Q	0.42	0/969	0.80	0/1300
18	R	0.28	0/892	0.68	0/1193
19	S	0.28	0/817	0.68	1/1088 (0.1%)
20	T	0.37	0/722	0.74	0/964
21	U	0.29	0/659	0.63	0/884
22	V	0.33	0/657	0.72	0/881
23	W	0.28	0/544	0.69	0/731
24	X	0.28	0/652	0.65	0/877
25	Y	0.26	0/671	0.64	2/888 (0.2%)
26	Z	0.56	0/550	1.09	1/728 (0.1%)
27	b	0.49	0/2121	0.82	0/2852
28	c	0.45	0/1586	0.77	0/2134
29	d	0.40	0/1571	0.80	3/2113 (0.1%)
30	e	0.32	0/1434	0.66	0/1926
31	f	0.29	0/1343	0.61	0/1816
32	g	0.41	0/1122	0.73	1/1515 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.39	0/1046	0.80	1/1410 (0.1%)
34	j	0.46	0/1152	0.72	0/1551
35	k	0.42	0/947	0.91	1/1268 (0.1%)
36	l	0.41	1/1054 (0.1%)	0.80	2/1403 (0.1%)
37	m	0.39	0/1093	0.81	2/1460 (0.1%)
38	n	0.54	1/973 (0.1%)	0.87	0/1301
39	o	0.32	0/902	0.68	0/1209
40	p	0.39	0/929	0.72	0/1242
41	q	0.43	0/960	0.72	0/1278
42	r	0.42	0/829	0.79	0/1107
43	s	0.52	0/864	0.83	0/1156
44	t	0.48	0/744	0.81	1/994 (0.1%)
45	u	0.38	0/787	0.75	2/1051 (0.2%)
46	v	0.35	0/766	0.66	0/1025
47	w	0.40	0/582	0.80	2/769 (0.3%)
48	x	0.64	0/635	1.13	4/848 (0.5%)
49	y	0.28	0/510	0.71	0/677
50	z	0.36	0/453	0.76	1/605 (0.2%)
51	1	0.59	0/69796	0.60	12/108888 (0.0%)
52	2	0.60	0/2872	0.55	1/4479 (0.0%)
53	3	0.60	0/36963	0.57	4/57662 (0.0%)
54	4	0.61	0/695	0.77	0/1076
55	8	0.56	0/599	0.70	1/919 (0.1%)
56	9	0.49	0/468	0.53	0/719
57	A1	0.56	0/2106	0.81	0/2868
57	A2	0.49	0/2048	0.76	0/2786
58	B1	0.56	4/10510 (0.0%)	0.74	8/14196 (0.1%)
59	B2	0.45	0/10714	0.66	0/14459
60	W0	0.30	0/652	0.61	0/879
61	NA	0.76	0/2431	1.22	0/3385
62	NG	1.16	0/756	1.03	0/1048
63	5	0.59	0/1812	0.90	3/2823 (0.1%)
64	6	0.59	0/1832	0.59	0/2855
65	a	0.49	0/1020	0.81	0/1370
66	0	0.40	0/5501	0.72	3/7446 (0.0%)
67	h	3.21	2/11 (18.2%)	0.75	0/13
All	All	0.54	8/196700 (0.0%)	0.67	61/289390 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
66	0	0	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	h	3	SER	CA-C	-6.73	1.38	1.52
67	h	4	SER	CA-C	-6.31	1.39	1.52
38	n	66	ALA	CA-C	-5.95	1.44	1.52
58	B1	1350	ASN	CG-ND2	-5.26	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.16	1.33	1.23
58	B1	424	ASN	CG-ND2	-5.10	1.22	1.33
36	l	18	ARG	CA-CB	-5.05	1.44	1.52
58	B1	1268	ASN	CG-OD1	5.02	1.33	1.23

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	92	PRO	N-CA-C	-10.48	98.48	113.47
51	1	1020	A	C2'-C3'-O3'	7.36	120.54	109.50
48	x	11	PRO	N-CA-C	-7.35	99.50	111.77
12	L	82	SER	N-CA-C	6.91	116.43	108.49
58	B1	450	HIS	CB-CG-CD2	-6.57	122.66	131.20
36	l	29	LYS	CA-C-N	6.48	133.91	121.54
36	l	29	LYS	C-N-CA	6.48	133.91	121.54
58	B1	61	ILE	CA-C-N	-6.41	113.95	121.64
58	B1	61	ILE	C-N-CA	-6.41	113.95	121.64
58	B1	777	HIS	CB-CG-CD2	-6.34	122.96	131.20
45	u	45	GLN	CA-C-N	6.31	129.44	120.49
45	u	45	GLN	C-N-CA	6.31	129.44	120.49
9	I	24	VAL	N-CA-C	-6.29	107.73	113.71
48	x	71	ARG	N-CA-C	-6.21	105.70	113.28
48	x	67	LEU	N-CA-C	-6.09	104.56	111.14
66	0	367	HIS	CA-C-N	6.05	133.10	121.54
66	0	367	HIS	C-N-CA	6.05	133.10	121.54
63	5	39	U	C3'-C2'-O2'	5.86	119.49	110.70
32	g	121	VAL	N-CA-C	-5.85	106.71	111.91
48	x	54	GLY	N-CA-C	5.74	120.75	113.24
2	B	5	ASN	CA-C-N	5.72	129.01	120.83
2	B	5	ASN	C-N-CA	5.72	129.01	120.83
26	Z	17	ARG	N-CA-C	-5.71	104.86	113.89
58	B1	450	HIS	CB-CG-ND1	5.67	131.20	122.70
19	S	21	ALA	N-CA-C	-5.57	107.73	114.75
51	1	1343	G	N9-C1'-C2'	5.56	120.34	112.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	i	62	ALA	N-CA-C	5.55	117.02	110.97
37	m	57	VAL	CA-C-N	5.47	131.99	121.54
37	m	57	VAL	C-N-CA	5.47	131.99	121.54
29	d	74	LYS	CA-C-N	5.44	128.61	120.83
29	d	74	LYS	C-N-CA	5.44	128.61	120.83
51	1	2502	G	O3'-P-O5'	5.44	112.16	104.00
53	3	813	U	N1-C1'-C2'	5.42	120.14	112.00
53	3	130	A	N9-C1'-C2'	5.42	120.13	112.00
58	B1	777	HIS	CB-CG-ND1	5.42	130.82	122.70
55	8	7	DC	C2'-C3'-O3'	-5.40	103.40	111.50
29	d	20	GLY	N-CA-C	-5.30	107.48	114.95
35	k	89	ASN	N-CA-C	5.28	117.46	111.02
25	Y	53	MET	CA-C-N	5.26	127.53	120.58
25	Y	53	MET	C-N-CA	5.26	127.53	120.58
58	B1	27	PRO	N-CA-C	-5.24	106.22	113.81
63	5	39	U	C4'-C3'-O3'	5.23	120.85	113.00
51	1	2529	G	N9-C1'-C2'	5.23	119.84	112.00
52	2	66	A	N9-C1'-C2'	5.22	119.83	112.00
51	1	858	G	C4'-C3'-O3'	5.19	120.79	113.00
51	1	1924	C	N1-C1'-C2'	5.19	119.78	112.00
66	0	664	PHE	CA-CB-CG	5.19	118.99	113.80
51	1	1211	C	N1-C1'-C2'	5.17	119.75	112.00
58	B1	61	ILE	CA-C-O	-5.14	115.61	120.95
47	w	15	LYS	CA-C-N	5.13	129.69	122.46
47	w	15	LYS	C-N-CA	5.13	129.69	122.46
50	z	40	THR	N-CA-C	-5.12	101.23	109.58
44	t	65	GLY	N-CA-C	5.12	117.35	111.36
53	3	1043	G	N9-C1'-C2'	5.12	119.68	112.00
51	1	278	A	N9-C1'-C2'	5.10	119.64	112.00
63	5	74	C	C4'-C3'-O3'	-5.09	105.36	113.00
53	3	722	G	N9-C1'-C2'	5.07	119.60	112.00
51	1	1087	G	N9-C1'-C2'	5.06	119.59	112.00
51	1	1508	A	N9-C1'-C2'	5.04	119.56	112.00
51	1	933	A	N9-C1'-C2'	5.02	119.54	112.00
51	1	2071	A	N9-C1'-C2'	5.00	119.50	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
66	0	408	ARG	Sidechain

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	A	355	0	353	10	0
2	B	444	0	461	14	0
3	C	409	0	440	17	0
4	D	377	0	418	17	0
5	E	504	0	574	16	0
6	F	302	0	341	14	0
7	G	1704	0	1732	41	0
8	H	1624	0	1699	43	0
9	I	1643	0	1710	47	0
10	J	1156	0	1199	38	0
11	K	817	0	808	23	0
12	L	1181	0	1240	44	0
13	M	979	0	1034	32	0
14	N	1022	0	1070	56	0
15	O	786	0	828	32	0
16	P	869	0	878	27	0
17	Q	955	0	1019	34	0
18	R	883	0	944	23	0
19	S	805	0	847	33	0
20	T	714	0	737	18	0
21	U	649	0	666	21	0
22	V	648	0	691	17	0
23	W	535	0	552	15	0
24	X	637	0	665	17	0
25	Y	665	0	714	21	0
26	Z	544	0	579	16	0
27	b	2082	0	2157	73	0
28	c	1565	0	1616	57	0
29	d	1552	0	1619	50	0
30	e	1410	0	1447	40	0
31	f	1323	0	1374	30	0
32	g	1111	0	1148	33	0
33	i	1032	0	1088	34	0
34	j	1129	0	1162	31	0
35	k	938	0	1012	21	0
36	l	1045	0	1117	30	0
37	m	1074	0	1157	29	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	n	960	0	1000	34	0
39	o	892	0	923	21	0
40	p	917	0	965	23	0
41	q	947	0	1022	23	0
42	r	816	0	839	24	0
43	s	857	0	922	19	0
44	t	738	0	807	15	0
45	u	779	0	834	23	0
46	v	753	0	780	14	0
47	w	575	0	592	21	0
48	x	625	0	655	23	0
49	y	509	0	543	9	0
50	z	449	0	491	10	0
51	1	62317	0	31346	1363	0
52	2	2568	0	1303	59	0
53	3	33012	0	16618	723	0
54	4	627	0	313	8	0
55	8	539	0	305	28	0
56	9	417	0	224	1	0
57	A1	2088	0	1895	27	0
57	A2	2029	0	1864	20	0
58	B1	10353	0	10548	321	0
59	B2	10546	0	10550	171	0
60	W0	650	0	658	10	0
61	NA	2432	0	1171	3	0
62	NG	758	0	334	9	0
63	5	1622	0	821	31	0
64	6	1640	0	837	24	0
65	a	1013	0	1081	35	0
66	0	5399	0	5363	154	0
67	h	48	0	40	6	0
68	B1	1	0	0	0	0
69	0	28	0	12	1	0
70	0	5	0	0	0	0
All	All	183377	0	132752	3780	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 (3780) 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)
12:L:92:PRO:HA	12:L:95:ARG:HE	1.12	1.13
51:1:1060:U:H4'	51:1:1061:U:H5'	1.32	1.10
53:3:112:G:H21	53:3:354:G:H5'	1.16	1.10
51:1:2061:G:H2'	51:1:2501:C:O2'	1.52	1.08
50:z:37:ARG:HH12	51:1:929:U:H5'	1.12	1.07
9:I:131:ILE:HG21	53:3:620:C:H1'	1.40	1.04
51:1:45:G:H5''	51:1:46:G:H5'	1.34	1.03
51:1:1796:U:H2'	51:1:1797:G:H8	1.18	1.02
51:1:1607:C:H4'	51:1:1608:A:H5'	1.40	1.02
51:1:1104:C:H2'	51:1:1105:U:H4'	1.38	1.01
58:B1:750:PRO:HB3	59:B2:549:ASP:OD2	1.60	1.01
58:B1:111:THR:HG23	58:B1:300:GLN:CD	1.86	0.99
51:1:572:A:H61	51:1:2029:G:H21	1.04	0.99
51:1:2324:U:H3'	51:1:2325:G:H5''	1.45	0.99
51:1:1645:G:H5''	51:1:1646:C:H5'	1.45	0.98
58:B1:352:ARG:HD2	59:B2:1268:GLN:NE2	1.79	0.97
10:J:120:HIS:ND1	10:J:121:ASN:ND2	2.14	0.96
51:1:2672:U:H2'	51:1:2673:G:H5''	1.43	0.96
52:2:90:C:H2'	52:2:91:C:H5''	1.44	0.95
51:1:413:C:H42	51:1:2410:G:H1	1.15	0.95
51:1:1597:A:H5''	51:1:1598:A:H5'	1.45	0.95
7:G:16:GLY:HA2	7:G:39:ILE:HA	1.49	0.95
38:n:39:PRO:HG3	51:1:1651:G:H5'	1.49	0.94
52:2:118:C:H2'	52:2:119:A:H4'	1.46	0.94
58:B1:68:TYR:O	58:B1:75:TYR:CE2	2.20	0.94
43:s:59:GLU:HA	43:s:64:ALA:HA	1.50	0.94
53:3:1156:G:H1'	53:3:1179:A:H61	1.32	0.94
42:r:79:ARG:HH22	51:1:572:A:H5'	1.33	0.93
51:1:828:U:H2'	51:1:829:A:C8	2.02	0.93
54:4:47:G:H21	58:B1:427:PRO:HD3	1.34	0.92
58:B1:202:ARG:HG2	58:B1:202:ARG:HH11	1.35	0.92
23:W:38:ILE:HD11	53:3:720:C:H1'	1.52	0.92
53:3:674:G:H2'	53:3:675:A:C8	2.05	0.92
51:1:1558:C:H4'	51:1:1559:U:H5''	1.51	0.91
53:3:91:U:H2'	53:3:92:U:H5''	1.53	0.90
51:1:2068:U:H3	51:1:2430:A:H62	1.15	0.90
51:1:2653:U:H3'	51:1:2654:A:H5''	1.52	0.90
53:3:409:U:H3	53:3:433:G:H1	1.12	0.90
59:B2:854:ILE:HG21	59:B2:917:SER:HB3	1.54	0.90
53:3:674:G:H2'	53:3:675:A:H8	1.34	0.90
53:3:1218:C:H2'	53:3:1219:A:C8	2.06	0.89
52:2:78:A:H62	52:2:98:G:H21	1.17	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:92:PRO:HA	12:L:95:ARG:NE	1.88	0.89
12:L:91:ARG:HB3	12:L:93:VAL:HG12	1.54	0.88
29:d:68:ALA:HA	51:1:1255:U:C5	2.08	0.88
53:3:1422:G:H22	53:3:1478:U:H3	1.22	0.88
50:z:37:ARG:NH1	51:1:929:U:H5'	1.89	0.88
58:B1:68:TYR:C	58:B1:75:TYR:HE2	1.80	0.88
51:1:1473:G:H1	51:1:1518:C:H42	1.21	0.88
51:1:1796:U:H2'	51:1:1797:G:C8	2.08	0.87
52:2:3:C:H2'	52:2:4:C:H5''	1.55	0.87
58:B1:317:THR:HA	58:B1:323:PRO:HA	1.55	0.87
51:1:435:C:H2'	51:1:436:C:H5'	1.56	0.87
63:5:9:A:H2'	63:5:11:C:H41	1.38	0.86
7:G:131:LYS:HD2	53:3:1158:C:H4'	1.57	0.86
51:1:2128:G:OP1	65:a:38:PHE:CE1	2.29	0.86
58:B1:68:TYR:O	58:B1:75:TYR:HE2	1.58	0.86
51:1:2822:G:H2'	51:1:2823:A:H5''	1.58	0.85
53:3:1218:C:H2'	53:3:1219:A:H8	1.41	0.85
14:N:68:GLY:HA2	53:3:1250:A:H5'	1.55	0.85
58:B1:633:ALA:HB2	59:B2:808:ASN:H	1.41	0.85
42:r:79:ARG:NH2	51:1:572:A:H5'	1.91	0.85
53:3:1395:C:HO2'	53:3:1396:A:H8	0.87	0.85
51:1:2443:C:H2'	51:1:2444:G:H8	1.42	0.85
51:1:1783:A:C6	51:1:2587:A:C2	2.66	0.84
19:S:70:HIS:HB2	53:3:974:A:H5'	1.59	0.84
53:3:3:A:H5'	53:3:613:C:H4'	1.58	0.84
37:m:12:MET:HA	51:1:910:A:H62	1.41	0.84
58:B1:68:TYR:HB3	58:B1:75:TYR:OH	1.76	0.84
51:1:1783:A:N1	51:1:2587:A:C4	2.46	0.84
51:1:2262:U:H2'	51:1:2263:C:C6	2.13	0.84
53:3:835:U:H2'	53:3:836:G:H5''	1.60	0.84
12:L:27:ASN:HD22	53:3:1374:A:H4'	1.42	0.83
34:j:116:ARG:NH2	51:1:528:A:H5''	1.91	0.83
53:3:1424:U:H3	53:3:1476:A:H61	1.26	0.83
58:B1:770:LEU:HD13	59:B2:618:GLN:HG3	1.61	0.83
66:0:40:ILE:HG23	66:0:198:GLN:OE1	1.79	0.83
51:1:1937:A:O2'	51:1:1938:A:H5'	1.78	0.83
23:W:37:LYS:HB3	53:3:719:C:H1'	1.60	0.82
53:3:1512:U:H2'	53:3:1513:A:C8	2.14	0.82
51:1:554:U:H2'	51:1:555:G:O4'	1.79	0.82
51:1:695:G:H1	51:1:767:U:H3	1.26	0.82
53:3:572:A:H5''	53:3:917:G:H4'	1.59	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2050:C:H2'	51:1:2051:A:H5'	1.62	0.82
14:N:13:SER:OG	53:3:1251:A:H5'	1.80	0.82
53:3:555:U:H2'	53:3:556:C:C6	2.15	0.81
55:8:1:DC:H5''	58:B1:210:SER:OG	1.80	0.81
58:B1:141:PHE:HE2	58:B1:296:LYS:HB2	1.44	0.81
26:Z:7:GLU:HB2	26:Z:11:PHE:HB3	1.63	0.81
51:1:1433:A:H2'	51:1:1434:A:O4'	1.79	0.81
58:B1:141:PHE:CE2	58:B1:296:LYS:HB2	2.15	0.81
27:b:55:GLY:HA2	51:1:692:C:OP1	1.81	0.80
51:1:1064:C:H3'	51:1:1065:U:H5''	1.63	0.80
51:1:1680:U:H2'	51:1:1681:G:H5'	1.60	0.80
51:1:2128:G:OP1	65:a:38:PHE:CD1	2.35	0.80
58:B1:111:THR:HG23	58:B1:300:GLN:OE1	1.81	0.80
58:B1:37:GLU:O	58:B1:61:ILE:HD11	1.81	0.80
51:1:2402:U:C2'	51:1:2403:C:H5''	2.11	0.79
29:d:76:PRO:HA	29:d:82:GLY:HA3	1.62	0.79
53:3:952:U:H4'	53:3:964:A:H61	1.47	0.79
58:B1:144:TYR:HE1	58:B1:162:GLU:OE2	1.64	0.79
66:0:498:VAL:HG11	66:0:522:MET:HE3	1.65	0.79
51:1:2036:C:H2'	51:1:2037:A:C8	2.18	0.78
53:3:769:G:H4'	53:3:1513:A:H4'	1.63	0.78
51:1:1052:C:H42	51:1:1107:G:H1	1.30	0.78
51:1:2402:U:H2'	51:1:2403:C:H5''	1.64	0.78
51:1:1791:A:C2'	51:1:1792:G:H5'	2.13	0.78
58:B1:186:GLN:HG3	58:B1:238:ILE:HG13	1.65	0.78
51:1:1783:A:C6	51:1:2587:A:N3	2.51	0.78
52:2:65:U:H3'	52:2:108:A:H61	1.49	0.78
51:1:784:G:H5'	51:1:785:G:OP1	1.84	0.78
51:1:1661:G:H2'	51:1:1662:U:H6	1.49	0.78
53:3:1073:U:H3	53:3:1102:A:H61	1.29	0.78
8:H:175:HIS:ND1	53:3:1108:G:H5'	2.00	0.77
51:1:2124:G:O2'	65:a:41:SER:HB3	1.83	0.77
53:3:1422:G:N2	53:3:1478:U:H3	1.80	0.77
51:1:208:C:H2'	51:1:209:C:H6	1.49	0.77
51:1:2524:G:H2'	51:1:2525:G:H5''	1.65	0.77
51:1:52:A:H2'	51:1:53:A:C8	2.20	0.77
51:1:1287:A:C2	51:1:1649:G:H4'	2.20	0.77
51:1:1853:A:H2'	51:1:1854:A:C8	2.19	0.77
53:3:153:C:H3'	53:3:154:U:H5''	1.66	0.77
51:1:20:C:H2'	51:1:21:A:C8	2.19	0.77
22:V:68:LYS:HB3	53:3:267:C:OP1	1.85	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:c:148:GLN:O	51:1:2052:A:H4'	1.86	0.76
55:8:13:DT:H72	58:B1:791:ALA:HB2	1.66	0.76
51:1:687:C:H2'	51:1:688:U:H5'	1.66	0.76
58:B1:202:ARG:HG2	58:B1:202:ARG:NH1	1.99	0.76
51:1:2443:C:H2'	51:1:2444:G:C8	2.20	0.76
66:0:40:ILE:CG2	66:0:198:GLN:OE1	2.33	0.76
53:3:1356:G:H2'	53:3:1357:A:H8	1.51	0.76
51:1:2672:U:C2'	51:1:2673:G:H5''	2.16	0.76
53:3:57:G:H2'	53:3:58:C:C6	2.21	0.75
51:1:1935:G:H1'	51:1:1964:G:N2	2.00	0.75
51:1:2124:G:O2'	65:a:41:SER:CB	2.34	0.75
53:3:768:A:OP1	53:3:804:U:H4'	1.86	0.75
53:3:193:C:H2'	53:3:194:C:C6	2.21	0.75
51:1:324:A:H62	51:1:338:G:H21	1.32	0.75
58:B1:110:PRO:HG2	58:B1:183:GLU:HG3	1.68	0.75
51:1:1020:A:H1'	51:1:1021:A:OP2	1.86	0.75
55:8:15:DC:H1'	58:B1:426:ALA:HB1	1.67	0.75
51:1:1126:A:H4'	51:1:1127:A:H5''	1.67	0.75
51:1:1783:A:C2	51:1:2587:A:C5	2.75	0.75
66:0:490:TYR:HA	66:0:612:LEU:HD13	1.69	0.75
51:1:1718:G:H2'	51:1:1719:G:H8	1.52	0.75
53:3:850:U:H2'	53:3:851:G:H5''	1.69	0.75
8:H:127:VAL:HG23	54:4:14:U:H4'	1.67	0.74
9:I:18:LEU:HB3	9:I:20:LEU:HD22	1.68	0.74
51:1:633:A:H2'	51:1:634:C:O4'	1.88	0.74
51:1:2375:G:H2'	51:1:2376:A:H5''	1.69	0.74
53:3:1330:U:H2'	53:3:1331:G:O4'	1.86	0.74
53:3:212:G:H2'	53:3:213:G:H8	1.53	0.74
51:1:1019:U:H3	51:1:1142:A:H62	1.36	0.74
53:3:3:A:C5'	53:3:613:C:H4'	2.17	0.74
53:3:354:G:H2'	53:3:355:C:C6	2.23	0.74
53:3:1236:A:H4'	53:3:1304:G:H4'	1.69	0.74
51:1:581:C:H2'	51:1:582:A:C8	2.23	0.74
51:1:208:C:H2'	51:1:209:C:C6	2.23	0.74
51:1:2221:G:H2'	51:1:2222:C:C6	2.23	0.74
33:i:10:LEU:HD11	51:1:1070:A:H2	1.51	0.74
51:1:917:A:H5''	51:1:2268:A:H61	1.53	0.74
10:J:25:LYS:NZ	53:3:923:A:H5''	2.03	0.74
30:e:34:THR:HG21	51:1:2314:A:H5'	1.69	0.74
53:3:1412:C:H2'	53:3:1413:A:C8	2.22	0.74
12:L:71:THR:HG23	12:L:72:VAL:HG12	1.68	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2859:G:H2'	51:1:2860:A:C8	2.22	0.73
58:B1:1143:ASP:OD1	58:B1:1148:ARG:NH1	2.21	0.73
47:w:28:LEU:HD22	51:1:2353:G:H4'	1.68	0.73
53:3:175:C:H2'	53:3:176:C:C6	2.24	0.73
58:B1:211:GLU:HG2	58:B1:215:LYS:HE3	1.70	0.73
15:O:45:ARG:HB3	15:O:69:THR:HB	1.71	0.73
51:1:1161:C:H2'	51:1:1162:G:C8	2.23	0.73
51:1:1310:G:H2'	51:1:1311:G:H5'	1.71	0.73
51:1:1528:A:H2'	51:1:1529:G:H5'	1.69	0.73
51:1:1940:U:H1'	51:1:1942:C:N4	2.04	0.73
53:3:884:U:H4'	53:3:885:G:H5''	1.70	0.73
55:8:3:DC:H2'	55:8:4:DT:H72	1.69	0.73
51:1:2743:U:H2'	51:1:2744:G:O4'	1.87	0.73
51:1:1265:A:H61	51:1:2013:A:H5''	1.53	0.73
51:1:2030:A:N3	51:1:2499:C:H5''	2.04	0.73
58:B1:210:SER:HB3	58:B1:213:LYS:HB2	1.71	0.73
66:0:499:THR:HG23	66:0:500:ASP:H	1.53	0.73
53:3:279:A:H5''	53:3:281:G:H5'	1.69	0.72
53:3:1073:U:H2'	53:3:1074:G:C8	2.24	0.72
58:B1:220:ARG:HG2	58:B1:220:ARG:HH11	1.55	0.72
9:I:23:GLY:HA3	53:3:408:A:H4'	1.71	0.72
52:2:87:U:H5''	52:2:88:C:C5	2.23	0.72
53:3:840:C:H2'	53:3:841:C:H5''	1.70	0.72
53:3:1028:C:H3'	53:3:1029:U:H5''	1.71	0.72
53:3:1306:A:H61	53:3:1331:G:H1'	1.54	0.72
55:8:3:DC:C2'	55:8:4:DT:H72	2.19	0.72
58:B1:107:LEU:HD11	58:B1:242:LEU:HB2	1.70	0.72
51:1:96:C:H2'	51:1:97:C:H6	1.54	0.72
30:e:65:LEU:HD22	52:2:42:C:C4	2.24	0.72
46:v:9:ARG:HB3	46:v:41:GLU:HB2	1.71	0.72
53:3:153:C:C3'	53:3:154:U:H5''	2.18	0.72
53:3:1424:U:H2'	53:3:1425:U:C6	2.24	0.72
53:3:1507:A:H2'	53:3:1508:A:O4'	1.89	0.72
12:L:92:PRO:HA	12:L:95:ARG:HG3	1.71	0.72
51:1:777:G:N7	51:1:793:A:H2	1.88	0.72
51:1:952:G:H2'	51:1:953:G:H5''	1.71	0.72
51:1:2562:U:H3	51:1:2566:A:H62	1.35	0.72
51:1:1170:C:H2'	51:1:1171:G:H8	1.54	0.72
51:1:1868:C:H2'	51:1:1869:G:H5'	1.70	0.72
58:B1:105:ILE:HD12	58:B1:242:LEU:HD22	1.71	0.72
12:L:27:ASN:ND2	53:3:1374:A:H4'	2.05	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:5:ARG:HB2	53:3:376:G:H5''	1.72	0.72
51:1:2818:U:H2'	51:1:2819:G:H8	1.55	0.72
6:F:4:ARG:HB2	51:1:2466:C:OP1	1.89	0.71
58:B1:157:GLN:OE1	58:B1:157:GLN:HA	1.88	0.71
51:1:2036:C:H2'	51:1:2037:A:H8	1.55	0.71
51:1:2629:U:O2'	51:1:2630:G:H5''	1.90	0.71
36:l:79:LEU:HD12	36:l:113:ALA:H	1.52	0.71
48:x:2:ARG:HG2	48:x:32:LEU:HD12	1.73	0.71
51:1:2733:A:H2'	51:1:2734:A:C8	2.25	0.71
52:2:90:C:C2'	52:2:91:C:H5''	2.20	0.71
51:1:435:C:C2'	51:1:436:C:H5'	2.21	0.71
51:1:1064:C:H3'	51:1:1065:U:C5'	2.20	0.71
53:3:419:C:H2'	53:3:420:U:O4'	1.90	0.71
51:1:2125:G:H5'	65:a:39:VAL:O	1.89	0.71
53:3:1243:C:H2'	53:3:1244:G:C8	2.26	0.71
53:3:1435:G:H2'	53:3:1436:U:C6	2.26	0.71
53:3:946:A:H2'	53:3:947:G:H8	1.56	0.71
34:j:116:ARG:HH22	51:1:528:A:H5''	1.53	0.71
51:1:2086:U:H2'	51:1:2087:G:C8	2.25	0.71
53:3:1395:C:H4'	53:3:1402:C:H4'	1.73	0.71
9:I:19:PHE:C	9:I:21:LYS:H	1.98	0.71
51:1:2491:U:H2'	51:1:2492:U:H5'	1.71	0.71
53:3:979:C:H2'	53:3:980:C:H5'	1.73	0.71
53:3:1374:A:H2'	53:3:1375:A:H8	1.56	0.71
51:1:52:A:H2'	51:1:53:A:H8	1.56	0.71
51:1:1161:C:H2'	51:1:1162:G:H8	1.55	0.71
51:1:2061:G:H2'	51:1:2501:C:HO2'	1.54	0.71
48:x:60:LYS:HD3	51:1:372:G:H5''	1.73	0.70
51:1:1447:C:H2'	51:1:1448:G:H8	1.56	0.70
51:1:1791:A:H2'	51:1:1792:G:H5'	1.71	0.70
53:3:86:G:H4'	53:3:87:C:C4	2.26	0.70
51:1:2514:U:H2'	51:1:2515:C:C6	2.27	0.70
53:3:501:C:H2'	53:3:502:A:H8	1.57	0.70
32:g:14:SER:HB3	32:g:17:ASP:HB2	1.74	0.70
53:3:673:A:H2'	53:3:674:G:C8	2.26	0.70
58:B1:93:THR:HB	58:B1:97:VAL:HG21	1.73	0.70
58:B1:142:GLU:HG3	58:B1:142:GLU:O	1.89	0.70
64:6:69:C:H2'	64:6:70:G:H8	1.55	0.70
38:n:1:MET:HE3	51:1:2723:C:H4'	1.74	0.70
51:1:1270:C:H5''	51:1:1271:G:C5'	2.21	0.70
59:B2:65:ASN:HB3	59:B2:105:TYR:HB2	1.73	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:A2:294:ASN:HA	61:NA:464:ILE:H	1.57	0.70
12:L:92:PRO:CA	12:L:95:ARG:HE	1.97	0.70
51:1:100:U:H4'	51:1:101:A:O4'	1.91	0.70
51:1:677:A:H2'	51:1:678:C:H6	1.57	0.70
53:3:939:G:H2'	53:3:940:C:C6	2.26	0.70
36:l:17:LYS:HB2	51:1:663:G:H5''	1.74	0.70
51:1:2030:A:C2	51:1:2499:C:H5''	2.27	0.70
66:0:695:ALA:HA	66:0:699:ILE:HB	1.74	0.70
12:L:91:ARG:O	12:L:95:ARG:HG2	1.91	0.70
51:1:1607:C:H4'	51:1:1608:A:C5'	2.19	0.69
51:1:2446:G:H2'	51:1:2501:C:H5	1.57	0.69
24:X:77:ARG:NH1	53:3:1225:A:H4'	2.07	0.69
38:n:66:ALA:HA	38:n:69:ARG:HD2	1.72	0.69
58:B1:128:LEU:HD11	58:B1:189:LEU:HG	1.73	0.69
64:6:26:G:H2'	64:6:27:U:H5''	1.73	0.69
29:d:165:HIS:HB2	51:1:1205:A:C6	2.27	0.69
51:1:1739:A:H2'	51:1:1740:G:O4'	1.92	0.69
53:3:1412:C:H2'	53:3:1413:A:H8	1.56	0.69
53:3:1421:G:H2'	53:3:1422:G:H4'	1.74	0.69
27:b:6:LYS:NZ	51:1:1695:G:H5'	2.08	0.69
57:A1:297:LYS:CB	61:NA:79:ALA:HB1	2.22	0.69
51:1:958:U:H2'	52:2:89:U:H1'	1.75	0.69
51:1:2502:G:H5''	51:1:2503:A:H5''	1.74	0.69
53:3:520:A:H62	53:3:529:G:H21	1.38	0.69
53:3:960:U:H4'	53:3:961:U:H5''	1.74	0.69
63:5:47:U:H4'	63:5:48:C:H5'	1.75	0.69
66:0:29:ARG:HH21	66:0:272:ASN:HD21	1.40	0.69
51:1:2818:U:H2'	51:1:2819:G:C8	2.27	0.69
64:6:56:C:H2'	64:6:57:A:H8	1.58	0.69
67:h:6:5OH:N	67:h:6:5OH:HS	2.07	0.69
51:1:2628:C:H3'	51:1:2629:U:H5'	1.75	0.69
51:1:2859:G:H2'	51:1:2860:A:H8	1.54	0.69
58:B1:161:THR:HG22	58:B1:164:GLN:HB2	1.75	0.69
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE22	1.55	0.69
14:N:17:ARG:CZ	53:3:1129:C:H4'	2.22	0.69
51:1:740:C:H6	51:1:740:C:H5'	1.58	0.69
51:1:2450:A:O2'	51:1:2451:A:H5'	1.93	0.69
58:B1:243:PRO:HG2	59:B2:1332:SER:O	1.93	0.69
14:N:121:ARG:HG3	53:3:1348:U:H4'	1.75	0.68
31:f:91:VAL:HG21	51:1:2657:A:O3'	1.93	0.68
51:1:1935:G:H1'	51:1:1964:G:C2	2.28	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:23:LEU:HD12	17:Q:29:LYS:HG2	1.75	0.68
26:Z:48:LYS:HB3	53:3:723:U:H5	1.58	0.68
51:1:1481:U:H3	51:1:1510:G:H1	1.42	0.68
58:B1:832:LYS:C	58:B1:1242:ARG:HH12	2.01	0.68
8:H:34:SER:HB3	8:H:58:ARG:HH12	1.57	0.68
12:L:92:PRO:O	12:L:95:ARG:HG3	1.93	0.68
51:1:1697:G:H3'	51:1:1698:A:H5''	1.76	0.68
51:1:2553:G:H3'	51:1:2554:U:H5''	1.75	0.68
53:3:70:U:H5''	53:3:71:A:OP1	1.92	0.68
53:3:900:A:H2'	53:3:901:A:C8	2.29	0.68
51:1:1024:G:H3'	51:1:1025:G:H5''	1.75	0.68
28:c:181:ASP:HB2	28:c:186:LEU:H	1.59	0.68
51:1:1077:A:H2'	51:1:1078:U:H5'	1.74	0.68
51:1:2464:G:H2'	51:1:2465:C:C6	2.29	0.68
58:B1:39:LYS:O	58:B1:273:ILE:CG2	2.41	0.68
58:B1:68:TYR:C	58:B1:75:TYR:CE2	2.65	0.68
51:1:781:A:H2'	51:1:1777:U:O2'	1.93	0.68
53:3:1346:A:H61	53:3:1374:A:H3'	1.57	0.68
55:8:3:DC:C6	55:8:4:DT:H72	2.29	0.68
67:h:4:SER:O	67:h:5:UAL:N1	2.26	0.68
53:3:478:A:H2'	53:3:479:U:H4'	1.76	0.68
51:1:2656:U:H5''	66:0:146:ARG:CZ	2.24	0.68
12:L:35:LYS:HB2	53:3:1373:G:H4'	1.76	0.68
14:N:10:ARG:HH22	53:3:1148:U:H5''	1.59	0.68
51:1:869:G:H2'	51:1:870:U:O4'	1.93	0.68
53:3:501:C:H2'	53:3:502:A:C8	2.29	0.68
27:b:73:ILE:HG12	51:1:1490:A:C2	2.29	0.67
51:1:687:C:C2'	51:1:688:U:H5'	2.23	0.67
51:1:1219:U:H2'	51:1:1220:G:C8	2.29	0.67
17:Q:13:ARG:HH21	53:3:303:A:H5'	1.59	0.67
51:1:1979:U:H2'	51:1:1980:G:H5'	1.75	0.67
58:B1:984:LEU:HB3	58:B1:993:GLU:HB2	1.77	0.67
51:1:1801:A:H5''	51:1:2203:U:H2'	1.75	0.67
53:3:747:A:H3'	53:3:748:G:H5''	1.75	0.67
58:B1:117:LEU:HD12	58:B1:117:LEU:O	1.94	0.67
58:B1:141:PHE:CD2	58:B1:293:ARG:O	2.47	0.67
58:B1:1355:ARG:NH1	58:B1:1369:ARG:HH12	1.93	0.67
36:l:111:ILE:HD12	51:1:627:A:N7	2.09	0.67
51:1:84:A:H4'	51:1:85:G:O5'	1.94	0.67
66:0:501:VAL:HG12	66:0:607:LYS:HZ1	1.60	0.67
51:1:848:C:H2'	51:1:849:A:H8	1.59	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1697:G:H5''	51:1:1698:A:H5''	1.77	0.67
51:1:2633:G:H2'	51:1:2634:A:H5''	1.77	0.67
51:1:1783:A:C2	51:1:2587:A:C4	2.83	0.67
51:1:1799:G:H4'	51:1:1800:C:O5'	1.95	0.67
55:8:23:DC:H2''	55:8:24:DC:C5	2.30	0.67
51:1:1139:G:O2'	51:1:1140:C:H5'	1.95	0.67
18:R:102:LYS:HG2	53:3:1226:C:C5	2.29	0.67
29:d:27:LEU:HD22	29:d:104:ALA:HB2	1.75	0.67
53:3:955:U:H3	53:3:1225:A:H61	1.42	0.67
53:3:1007:U:H3	53:3:1022:A:H61	1.43	0.67
53:3:1026:G:H1	53:3:1035:A:H61	1.43	0.67
64:6:69:C:H2'	64:6:70:G:C8	2.29	0.67
66:0:103:MET:HG3	66:0:129:GLN:HB3	1.77	0.67
51:1:849:A:H2'	51:1:850:U:C6	2.30	0.66
51:1:1661:G:H2'	51:1:1662:U:C6	2.29	0.66
38:n:71:ARG:HH21	51:1:2708:G:H1'	1.59	0.66
38:n:96:ARG:HA	51:1:2881:U:O2'	1.95	0.66
51:1:621:A:H2'	51:1:622:G:O4'	1.95	0.66
53:3:924:C:H2'	53:3:925:G:H8	1.60	0.66
39:o:68:LYS:HG2	52:2:50:A:OP1	1.94	0.66
51:1:395:U:H2'	51:1:396:G:C8	2.31	0.66
51:1:1824:G:O2'	51:1:1825:U:H5'	1.96	0.66
51:1:2086:U:H2'	51:1:2087:G:H8	1.59	0.66
51:1:2415:G:H2'	51:1:2416:C:C6	2.30	0.66
53:3:1356:G:H2'	53:3:1357:A:C8	2.30	0.66
53:3:113:G:H2'	53:3:114:U:C6	2.31	0.66
11:K:42:TRP:HB2	11:K:59:TYR:HB2	1.77	0.66
29:d:176:ASP:HB2	29:d:179:SER:HB3	1.77	0.66
51:1:1680:U:C2'	51:1:1681:G:H5'	2.26	0.66
52:2:3:C:C2'	52:2:4:C:H5''	2.25	0.66
64:6:12:G:H2'	64:6:13:C:O4'	1.95	0.66
10:J:25:LYS:HE2	53:3:923:A:OP1	1.96	0.66
17:Q:33:CYS:H	17:Q:54:VAL:HG13	1.60	0.66
51:1:1718:G:H2'	51:1:1719:G:C8	2.30	0.66
53:3:1172:C:H2'	53:3:1173:U:O4'	1.95	0.66
4:D:8:SER:HA	51:1:1309:G:H5''	1.78	0.66
48:x:27:ARG:NH2	51:1:1365:A:OP1	2.29	0.66
51:1:1528:A:C2'	51:1:1529:G:H5'	2.26	0.66
53:3:211:G:H2'	53:3:212:G:O4'	1.96	0.66
58:B1:108:ALA:CB	58:B1:279:LEU:HD22	2.25	0.66
38:n:2:ARG:HD2	51:1:2822:G:O6	1.95	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:978:ARG:HG2	58:B1:1197:ASN:HD21	1.60	0.66
22:V:60:ILE:HG22	22:V:74:LEU:HA	1.78	0.65
51:1:1755:A:H2'	51:1:1756:G:H5'	1.76	0.65
53:3:660:C:H2'	53:3:661:G:O4'	1.96	0.65
58:B1:461:PHE:HD2	59:B2:813:GLU:HB2	1.61	0.65
53:3:835:U:C2'	53:3:836:G:H5''	2.26	0.65
10:J:53:ARG:NH1	53:3:1071:C:H5'	2.12	0.65
35:k:76:VAL:H	40:p:72:VAL:HG12	1.61	0.65
53:3:153:C:H2'	53:3:154:U:O4'	1.96	0.65
53:3:1125:U:H2'	53:3:1126:U:H2'	1.78	0.65
4:D:7:PRO:HA	51:1:686:U:O2	1.96	0.65
53:3:738:C:H2'	53:3:739:C:H6	1.62	0.65
51:1:1509:A:H2'	51:1:1510:G:C8	2.31	0.65
55:8:13:DT:OP2	58:B1:791:ALA:HB1	1.95	0.65
58:B1:108:ALA:HB3	58:B1:279:LEU:HD22	1.77	0.65
17:Q:98:ARG:HB3	17:Q:105:GLY:HA2	1.79	0.65
22:V:47:ASP:HB3	22:V:74:LEU:HB3	1.78	0.65
51:1:203:A:H3'	51:1:204:A:H5''	1.79	0.65
51:1:2008:C:H2'	51:1:2009:A:H8	1.61	0.65
66:0:17:ALA:HB2	66:0:112:VAL:HG23	1.79	0.65
3:C:5:ARG:NH1	51:1:2285:C:C5	2.65	0.65
51:1:195:A:H3'	51:1:196:A:H4'	1.78	0.65
51:1:1268:A:H2'	51:1:1269:A:C8	2.31	0.65
51:1:2029:G:O6	51:1:2032:G:H5''	1.97	0.65
51:1:2048:G:H2'	51:1:2049:G:H5''	1.79	0.65
51:1:2329:U:H2'	51:1:2330:G:C8	2.32	0.65
53:3:1173:U:H2'	53:3:1174:G:H8	1.61	0.65
58:B1:1037:PHE:HB3	58:B1:1040:MET:HB2	1.78	0.65
51:1:748:G:O6	51:1:751:A:H4'	1.97	0.65
13:M:111:THR:HG22	13:M:113:ARG:H	1.62	0.65
31:f:82:PHE:HB2	31:f:140:ILE:HG12	1.79	0.65
51:1:20:C:H2'	51:1:21:A:H8	1.60	0.65
59:B2:314:ASN:HD21	59:B2:348:SER:HA	1.62	0.65
59:B2:528:ARG:NH2	59:B2:576:SER:O	2.30	0.65
30:e:104:THR:HG23	30:e:105:ILE:HG13	1.80	0.64
47:w:40:LYS:NZ	51:1:2330:G:O2'	2.30	0.64
51:1:1170:C:H2'	51:1:1171:G:C8	2.32	0.64
52:2:13:G:H2'	52:2:14:U:H5''	1.78	0.64
53:3:1366:C:H2'	53:3:1367:C:C6	2.32	0.64
55:8:3:DC:C2'	55:8:4:DT:C7	2.75	0.64
58:B1:975:ILE:HG22	58:B1:977:SER:H	1.62	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:g:94:ILE:HG12	32:g:122:LEU:HB2	1.78	0.64
51:1:2047:C:H2'	51:1:2048:G:C8	2.32	0.64
58:B1:68:TYR:HB3	58:B1:75:TYR:CE2	2.32	0.64
10:J:25:LYS:HZ1	53:3:923:A:H5''	1.61	0.64
23:W:41:SER:HA	23:W:44:THR:HG22	1.80	0.64
51:1:246:C:H2'	51:1:247:G:H5'	1.79	0.64
51:1:581:C:H2'	51:1:582:A:H8	1.60	0.64
51:1:1127:A:H2'	51:1:1128:G:H5''	1.80	0.64
51:1:1278:C:H2'	51:1:1279:G:H8	1.62	0.64
51:1:2704:C:H2'	51:1:2705:A:O4'	1.97	0.64
53:3:1156:G:H21	53:3:1179:A:H2	1.44	0.64
66:0:501:VAL:HG11	66:0:604:GLY:HA2	1.78	0.64
58:B1:162:GLU:HA	58:B1:162:GLU:OE1	1.97	0.64
31:f:94:ARG:H	31:f:105:SER:HB3	1.62	0.64
53:3:246:A:H62	53:3:281:G:N2	1.95	0.64
53:3:1436:U:H2'	53:3:1437:A:H8	1.62	0.64
51:1:1297:C:OP1	51:1:2710:C:H4'	1.97	0.64
51:1:1447:C:H2'	51:1:1448:G:C8	2.31	0.64
51:1:1474:U:H2'	51:1:1475:G:H5'	1.79	0.64
51:1:2267:A:H3'	51:1:2267:A:N3	2.13	0.64
53:3:56:U:O2	66:0:362:ARG:NH1	2.30	0.64
53:3:1345:U:H4'	53:3:1346:A:H5'	1.80	0.64
58:B1:918:ILE:HG22	59:B2:1280:ALA:HB1	1.79	0.64
59:B2:1282:GLY:HA3	60:W0:17:PHE:HE1	1.63	0.64
27:b:155:ARG:NH1	51:1:1818:U:H5	1.96	0.64
51:1:746:U:H1'	51:1:748:G:H21	1.61	0.64
53:3:1306:A:N6	53:3:1331:G:H1'	2.12	0.64
2:B:8:THR:HB	51:1:2020:A:H5'	1.80	0.64
17:Q:27:PRO:HB3	53:3:552:U:O2	1.98	0.64
64:6:26:G:H3'	64:6:27:U:H5''	1.80	0.64
15:O:46:LYS:HE3	53:3:1253:G:OP1	1.98	0.64
32:g:4:ILE:HA	32:g:18:GLN:HE22	1.63	0.64
51:1:2123:G:H8	51:1:2125:G:H21	1.44	0.64
51:1:2215:C:H2'	51:1:2216:G:C8	2.31	0.64
53:3:1148:U:H2'	53:3:1149:C:O4'	1.98	0.64
53:3:1474:U:H2'	53:3:1475:G:O4'	1.98	0.64
58:B1:193:ASP:HB3	58:B1:196:GLN:HB2	1.78	0.64
4:D:14:ARG:HG2	51:1:125:A:H5'	1.80	0.63
51:1:158:U:H2'	51:1:159:G:O4'	1.97	0.63
66:0:624:PRO:HA	66:0:651:GLY:HA2	1.80	0.63
4:D:21:ARG:NH1	51:1:465:G:O3'	2.32	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:1:SER:HB2	51:1:1366:A:OP2	1.99	0.63
53:3:1243:C:H2'	53:3:1244:G:H8	1.63	0.63
25:Y:54:GLN:HE22	53:3:193:C:C1'	2.11	0.63
59:B2:120:GLN:NE2	59:B2:490:GLN:OE1	2.32	0.63
64:6:54:U:H3	64:6:58:A:H8	1.47	0.63
27:b:49:THR:OG1	27:b:50:THR:N	2.31	0.63
44:t:37:ASP:OD1	44:t:37:ASP:N	2.29	0.63
53:3:952:U:H2'	53:3:953:G:C8	2.32	0.63
58:B1:245:LEU:HG	58:B1:246:PRO:HD2	1.80	0.63
64:6:61:C:O2'	65:a:53:ARG:HD2	1.97	0.63
14:N:68:GLY:HA2	53:3:1250:A:C5'	2.27	0.63
33:i:112:LYS:NZ	33:i:124:MET:SD	2.69	0.63
53:3:966:G:C2	64:6:34:C:H5'	2.33	0.63
58:B1:128:LEU:HA	58:B1:192:MET:HE1	1.81	0.63
58:B1:201:LEU:HB2	58:B1:221:ILE:HD13	1.80	0.63
58:B1:1355:ARG:NH1	58:B1:1369:ARG:NH1	2.47	0.63
58:B1:1357:ILE:HD11	59:B2:1287:LEU:HD13	1.81	0.63
8:H:10:ARG:HH12	8:H:181:ILE:H	1.45	0.63
32:g:4:ILE:HD11	32:g:43:ASN:HB3	1.80	0.63
51:1:340:A:H2'	51:1:341:C:H5'	1.81	0.63
51:1:764:A:O2'	51:1:765:C:H5'	1.99	0.63
6:F:1:MET:HG3	51:1:2742:G:H5'	1.79	0.63
12:L:92:PRO:CA	12:L:95:ARG:HG3	2.28	0.63
14:N:105:ARG:HD2	53:3:1117:A:O2'	1.99	0.63
21:U:34:GLU:OE1	21:U:60:TRP:NE1	2.30	0.63
51:1:96:C:H2'	51:1:97:C:C6	2.33	0.63
51:1:2810:A:H62	51:1:2890:G:H21	1.46	0.63
53:3:600:A:H61	53:3:638:U:H3	1.46	0.63
14:N:17:ARG:NH2	53:3:1129:C:H4'	2.13	0.63
15:O:59:LYS:HE3	53:3:972:C:H5'	1.81	0.63
42:r:41:ILE:HB	42:r:47:VAL:HB	1.80	0.63
51:1:2066:C:O2'	51:1:2067:G:H5'	1.99	0.63
51:1:2656:U:H5''	66:0:146:ARG:NH1	2.14	0.63
53:3:91:U:C2'	53:3:92:U:H5''	2.27	0.63
53:3:492:C:H2'	53:3:493:A:C8	2.34	0.63
53:3:1007:U:H2'	53:3:1008:U:C6	2.34	0.63
51:1:948:C:H2'	51:1:949:G:H8	1.64	0.63
51:1:1063:G:H3'	51:1:1064:C:H6	1.63	0.63
51:1:1736:U:H2'	51:1:1737:G:O4'	1.99	0.63
51:1:2464:G:H2'	51:1:2465:C:H6	1.63	0.63
52:2:13:G:N7	52:2:70:C:H4'	2.14	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:27:CYS:SG	6:F:28:SER:N	2.71	0.62
51:1:1270:C:H5''	51:1:1271:G:H5''	1.79	0.62
51:1:2339:C:H2'	51:1:2340:A:H8	1.64	0.62
64:6:26:G:C3'	64:6:27:U:H5''	2.29	0.62
66:0:94:ASP:HB2	66:0:465:HIS:HB2	1.81	0.62
7:G:32:GLY:HA2	7:G:39:ILE:H	1.64	0.62
23:W:38:ILE:CD1	53:3:720:C:H1'	2.27	0.62
51:1:948:C:H2'	51:1:949:G:C8	2.34	0.62
58:B1:141:PHE:HD2	58:B1:293:ARG:O	1.79	0.62
66:0:490:TYR:HA	66:0:612:LEU:CD1	2.29	0.62
30:e:35:LEU:HB3	30:e:151:LEU:HD11	1.81	0.62
45:u:87:GLU:HG2	45:u:92:VAL:HG11	1.81	0.62
48:x:60:LYS:CD	51:1:372:G:H5''	2.28	0.62
51:1:481:G:H1'	51:1:506:G:N2	2.14	0.62
51:1:1173:U:H2'	51:1:1177:G:H1	1.64	0.62
51:1:1901:A:H2'	51:1:1902:C:C6	2.35	0.62
53:3:67:C:H2'	53:3:68:G:H8	1.64	0.62
53:3:946:A:H2'	53:3:947:G:C8	2.34	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:CD	2.66	0.62
9:I:19:PHE:C	9:I:21:LYS:N	2.56	0.62
34:j:113:PRO:HG3	51:1:528:A:H5'	1.81	0.62
51:1:315:G:H2'	51:1:316:C:C6	2.33	0.62
51:1:1675:C:H2'	51:1:1676:A:O4'	2.00	0.62
34:j:78:THR:HB	51:1:2641:G:H5''	1.81	0.62
41:q:12:ARG:NH1	51:1:1251:C:H5''	2.15	0.62
51:1:66:C:H1'	51:1:456:C:O2	1.99	0.62
51:1:1783:A:C5	51:1:2587:A:C2	2.87	0.62
51:1:2898:U:H2'	51:1:2899:A:C8	2.33	0.62
53:3:668:G:H1	53:3:738:C:H42	1.47	0.62
7:G:67:LEU:HD12	7:G:160:LEU:HD12	1.82	0.62
7:G:89:PHE:HB3	7:G:150:ILE:HD12	1.81	0.62
19:S:75:LYS:NZ	53:3:1357:A:H5''	2.14	0.62
47:w:19:VAL:HG13	47:w:34:VAL:HG22	1.81	0.62
51:1:1395:A:H4'	51:1:1397:U:C5	2.35	0.62
51:1:1597:A:H5''	51:1:1598:A:C5'	2.24	0.62
51:1:1867:G:H1	51:1:1874:C:H42	1.48	0.62
51:1:2384:U:O2'	51:1:2385:C:H5'	1.98	0.62
53:3:34:C:H2'	53:3:35:G:C8	2.33	0.62
53:3:367:U:H3	53:3:393:A:H2	1.47	0.62
53:3:1347:G:N2	53:3:1373:G:H2'	2.15	0.62
8:H:21:TRP:CD1	8:H:58:ARG:H	2.18	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:8:LEU:HD23	9:I:21:LYS:HE2	1.82	0.62
14:N:12:LYS:H	14:N:105:ARG:HH22	1.45	0.62
16:P:17:ASP:HB2	16:P:36:ARG:HH22	1.64	0.62
53:3:939:G:H2'	53:3:940:C:H6	1.63	0.62
53:3:1084:G:H5'	53:3:1102:A:OP2	2.00	0.62
58:B1:395:LYS:NZ	58:B1:399:LYS:HD3	2.15	0.62
51:1:812:C:H5''	51:1:1250:G:O2'	2.00	0.62
55:8:1:DC:H2''	55:8:2:DC:C5	2.35	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:NE2	2.63	0.62
58:B1:144:TYR:CE1	58:B1:162:GLU:OE2	2.51	0.62
30:e:38:GLY:HA3	51:1:2312:U:O2	2.00	0.62
51:1:677:A:H2'	51:1:678:C:C6	2.34	0.62
51:1:848:C:H2'	51:1:849:A:C8	2.35	0.62
51:1:2082:A:C2	51:1:2083:G:H1'	2.35	0.62
51:1:2121:G:H1'	65:a:167:LYS:HB2	1.82	0.62
55:8:3:DC:H2'	55:8:4:DT:C7	2.30	0.62
12:L:1:PRO:HD2	12:L:5:VAL:HA	1.82	0.61
51:1:572:A:N6	51:1:2029:G:H21	1.88	0.61
51:1:1078:U:H4'	51:1:1088:A:H2	1.65	0.61
51:1:1746:A:H2'	51:1:1747:U:C6	2.34	0.61
53:3:737:C:H2'	53:3:738:C:C6	2.34	0.61
9:I:119:HIS:CD2	53:3:438:U:H4'	2.35	0.61
17:Q:55:ARG:HA	17:Q:61:GLU:HA	1.83	0.61
51:1:368:A:O2'	51:1:369:U:H5'	2.00	0.61
51:1:2286:G:H4'	51:1:2287:A:O4'	2.00	0.61
55:8:13:DT:C7	58:B1:791:ALA:HB2	2.29	0.61
42:r:63:VAL:HG12	42:r:96:VAL:HG12	1.83	0.61
43:s:25:ARG:HH22	51:1:519:U:H5''	1.64	0.61
46:v:72:VAL:HG13	46:v:93:ARG:HA	1.82	0.61
51:1:2512:C:H2'	51:1:2513:A:O4'	2.00	0.61
53:3:657:U:H2'	53:3:658:C:C6	2.36	0.61
58:B1:342:LEU:HD23	58:B1:1352:ILE:HG23	1.83	0.61
30:e:132:ARG:O	30:e:132:ARG:NH2	2.34	0.61
51:1:729:G:H2'	51:1:1775:U:O2	2.00	0.61
51:1:1740:G:H2'	51:1:1741:C:H6	1.66	0.61
51:1:2653:U:C3'	51:1:2654:A:H5''	2.29	0.61
53:3:452:A:H61	53:3:480:U:H3	1.49	0.61
53:3:924:C:H2'	53:3:925:G:C8	2.34	0.61
58:B1:395:LYS:HZ2	58:B1:399:LYS:CD	2.13	0.61
58:B1:770:LEU:HD13	59:B2:618:GLN:CG	2.30	0.61
42:r:81:LYS:HD3	51:1:973:A:H5''	1.83	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:v:17:SER:HB3	46:v:27:PRO:HG3	1.83	0.61
58:B1:633:ALA:HA	59:B2:806:PRO:O	2.01	0.61
51:1:1063:G:H5''	51:1:1064:C:H5	1.64	0.61
51:1:1361:G:H2'	51:1:1362:C:C6	2.35	0.61
51:1:2885:G:H2'	51:1:2886:A:O4'	2.00	0.61
53:3:1110:A:H2'	53:3:1111:A:C8	2.35	0.61
57:A1:112:ALA:HB3	57:A1:126:PRO:HA	1.83	0.61
57:A1:211:ILE:HG12	57:A1:219:ARG:HH12	1.65	0.61
58:B1:1161:GLY:HA3	58:B1:1179:PRO:HA	1.82	0.61
19:S:23:ARG:HH11	19:S:26:LEU:HB3	1.65	0.61
51:1:468:G:H2'	51:1:469:G:H5'	1.83	0.61
51:1:1053:C:H2'	51:1:1054:A:H5'	1.83	0.61
53:3:358:U:H2'	53:3:359:G:H8	1.64	0.61
53:3:715:A:H5''	53:3:805:C:O2'	2.00	0.61
40:p:90:ALA:HB2	40:p:112:ARG:HA	1.81	0.61
51:1:11:C:H2'	51:1:12:U:H5''	1.83	0.61
51:1:139:U:H2'	51:1:140:C:H5	1.65	0.61
58:B1:68:TYR:HB3	58:B1:75:TYR:CZ	2.35	0.61
59:B2:55:SER:OG	59:B2:465:ARG:NH1	2.33	0.61
29:d:155:GLU:HA	29:d:158:PHE:HB3	1.82	0.60
48:x:4:CYS:HB3	48:x:9:LYS:H	1.65	0.60
52:2:30:C:H2'	52:2:31:C:O4'	2.01	0.60
58:B1:154:LEU:HD21	58:B1:160:LEU:HD21	1.83	0.60
13:M:28:SER:HB2	13:M:58:LEU:HB2	1.82	0.60
18:R:81:ASP:OD1	30:e:111:ARG:NH2	2.34	0.60
51:1:971:G:H2'	51:1:972:A:O4'	2.01	0.60
51:1:2699:C:H2'	51:1:2700:A:H8	1.66	0.60
66:0:321:ALA:HB2	66:0:397:LEU:HD21	1.82	0.60
22:V:10:ARG:NH1	22:V:11:VAL:O	2.33	0.60
53:3:979:C:C2'	53:3:980:C:H5'	2.32	0.60
63:5:39:U:H2'	63:5:40:C:C6	2.36	0.60
36:l:79:LEU:HB2	36:l:113:ALA:HB3	1.83	0.60
37:m:14:LYS:NZ	51:1:955:U:OP2	2.35	0.60
51:1:589:U:H2'	51:1:590:A:C8	2.37	0.60
51:1:1818:U:H4'	51:1:1821:A:H1'	1.83	0.60
51:1:2327:A:H2'	51:1:2328:A:C8	2.35	0.60
55:8:11:DC:H2'	55:8:12:DG:C8	2.37	0.60
51:1:1484:U:H2'	51:1:1485:U:C6	2.36	0.60
51:1:2208:C:H2'	51:1:2209:G:C8	2.37	0.60
52:2:90:C:H2'	52:2:91:C:C5'	2.24	0.60
53:3:314:C:H2'	53:3:315:A:C8	2.37	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:A1:38:THR:HB	57:A2:45:ARG:HD3	1.82	0.60
58:B1:100:GLU:HA	59:B2:1328:LYS:HE2	1.82	0.60
58:B1:201:LEU:HD11	58:B1:220:ARG:HH11	1.67	0.60
27:b:201:LEU:HD22	53:3:773:G:H5''	1.82	0.60
34:j:113:PRO:HD2	51:1:558:U:OP1	2.00	0.60
51:1:1308:A:H61	51:1:1608:A:H61	1.49	0.60
53:3:454:G:H2'	53:3:455:G:C8	2.37	0.60
29:d:64:GLY:O	51:1:2059:A:H4'	2.01	0.60
51:1:445:C:C2'	51:1:446:G:H5'	2.32	0.60
51:1:729:G:H5''	51:1:730:A:H5''	1.83	0.60
51:1:1064:C:H2'	51:1:1065:U:C6	2.37	0.60
51:1:2048:G:C3'	51:1:2049:G:H5''	2.31	0.60
51:1:2898:U:H2'	51:1:2899:A:H8	1.67	0.60
17:Q:48:LEU:HB2	53:3:520:A:OP1	2.02	0.60
21:U:2:VAL:HB	53:3:229:U:H4'	1.83	0.60
43:s:42:LYS:HE3	51:1:2010:G:H4'	1.84	0.60
51:1:1278:C:H2'	51:1:1279:G:C8	2.37	0.60
52:2:78:A:H62	52:2:98:G:N2	1.97	0.60
53:3:1512:U:H2'	53:3:1513:A:H8	1.67	0.60
15:O:50:THR:HG22	15:O:64:GLN:HG3	1.83	0.60
37:m:58:LYS:O	37:m:59:ARG:NH2	2.32	0.60
51:1:572:A:H61	51:1:2029:G:N2	1.88	0.60
51:1:1369:G:H21	51:1:1810:A:H2	1.48	0.60
51:1:2303:G:O2'	51:1:2304:G:H5'	2.02	0.60
51:1:2356:U:H2'	51:1:2357:G:O4'	2.01	0.60
51:1:2443:C:O2'	51:1:2444:G:H5'	2.02	0.60
51:1:2537:U:H2'	51:1:2538:C:C6	2.37	0.60
53:3:747:A:C3'	53:3:748:G:H5''	2.32	0.60
58:B1:725:MET:SD	59:B2:1101:LEU:HD23	2.42	0.60
58:B1:951:GLN:NE2	58:B1:1014:GLY:O	2.35	0.60
59:B2:69:GLN:HE21	59:B2:101:ARG:HD2	1.67	0.60
64:6:26:G:C2'	64:6:27:U:H5''	2.31	0.60
19:S:12:ARG:NH1	19:S:58:ARG:O	2.35	0.60
36:l:108:ALA:HB3	36:l:125:LEU:HD11	1.83	0.60
51:1:611:C:H2'	51:1:612:G:O4'	2.01	0.60
51:1:635:C:O2'	51:1:639:U:H5''	2.02	0.60
51:1:1674:G:H21	51:1:1677:A:H61	1.49	0.60
51:1:2189:U:H2'	51:1:2190:G:C8	2.37	0.60
51:1:2743:U:H3'	51:1:2744:G:H5''	1.83	0.60
58:B1:223:LEU:HG	58:B1:223:LEU:O	2.00	0.60
65:a:216:THR:H	65:a:220:ALA:HB3	1.67	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:g:51:ARG:HA	32:g:55:GLU:HB2	1.84	0.59
51:1:192:C:H2'	51:1:193:U:H5'	1.84	0.59
53:3:419:C:H5''	53:3:513:C:H1'	1.83	0.59
59:B2:918:LEU:O	59:B2:918:LEU:HD23	2.02	0.59
29:d:21:ARG:NH2	29:d:22:ASP:OD1	2.35	0.59
51:1:12:U:O2	51:1:12:U:H2'	2.02	0.59
51:1:2521:C:O2'	51:1:2522:U:H5'	2.02	0.59
53:3:1374:A:H2'	53:3:1375:A:C8	2.37	0.59
53:3:1521:C:H2'	53:3:1522:U:C6	2.37	0.59
9:I:121:ALA:HA	9:I:145:ARG:HB2	1.83	0.59
51:1:35:G:H1	51:1:445:C:H42	1.50	0.59
51:1:729:G:H5''	51:1:730:A:C5'	2.33	0.59
51:1:911:A:H5'	51:1:912:C:H5''	1.84	0.59
53:3:579:A:H5'	53:3:728:A:H1'	1.85	0.59
58:B1:99:ARG:NH1	58:B1:99:ARG:HG3	2.17	0.59
58:B1:438:GLU:HG3	58:B1:485:MET:HE1	1.85	0.59
59:B2:1072:ASN:ND2	59:B2:1111:GLN:OE1	2.35	0.59
10:J:96:GLN:HG2	53:3:7:A:C6	2.36	0.59
22:V:61:ARG:NH1	22:V:73:THR:OG1	2.36	0.59
47:w:56:PHE:CE2	51:1:2365:G:H4'	2.37	0.59
51:1:1081:U:H3'	51:1:1081:U:O2	2.02	0.59
51:1:1889:A:H2'	51:1:1890:A:C8	2.38	0.59
51:1:1982:U:H2'	51:1:1983:G:H8	1.68	0.59
53:3:836:G:H2'	53:3:837:U:O4'	2.02	0.59
55:8:9:DG:H4'	58:B1:120:LEU:HG	1.84	0.59
18:R:26:LYS:O	18:R:30:LYS:NZ	2.36	0.59
51:1:1802:A:H2'	51:1:1803:A:C8	2.38	0.59
53:3:128:G:H2'	53:3:129:A:C8	2.37	0.59
27:b:48:ILE:HG22	51:1:779:U:P	2.43	0.59
51:1:1444:G:H2'	51:1:1445:G:C8	2.37	0.59
58:B1:275:ARG:NH1	58:B1:278:ARG:NH1	2.51	0.59
58:B1:750:PRO:CB	59:B2:549:ASP:OD2	2.45	0.59
59:B2:1142:ARG:NH1	59:B2:1161:LEU:O	2.36	0.59
63:5:29:G:H5'	66:0:513:GLY:HA3	1.84	0.59
7:G:73:ARG:HH22	7:G:93:HIS:HA	1.67	0.59
7:G:142:LYS:HE2	53:3:1098:C:OP1	2.03	0.59
10:J:25:LYS:HB2	53:3:923:A:OP1	2.02	0.59
21:U:5:ARG:HD3	53:3:376:G:H4'	1.85	0.59
51:1:1924:C:H3'	51:1:1925:C:C6	2.38	0.59
53:3:34:C:H2'	53:3:35:G:H8	1.68	0.59
58:B1:514:THR:HG21	58:B1:596:LEU:HD12	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:q:12:ARG:HH12	51:1:1251:C:H5''	1.68	0.59
45:u:40:LEU:HD12	45:u:59:GLU:HB3	1.84	0.59
51:1:704:G:H1'	51:1:726:G:H22	1.68	0.59
51:1:881:G:N2	51:1:897:C:N3	2.50	0.59
51:1:1638:C:H4'	51:1:2710:C:O2	2.02	0.59
51:1:2032:G:OP2	51:1:2455:G:H5'	2.03	0.59
53:3:738:C:H2'	53:3:739:C:C6	2.38	0.59
18:R:95:PRO:HG2	18:R:105:ALA:HB1	1.83	0.59
29:d:55:SER:OG	29:d:56:GLY:N	2.36	0.59
40:p:1:SER:OG	51:1:2875:C:H4'	2.03	0.59
53:3:207:C:H3'	53:3:208:U:H5''	1.83	0.59
53:3:337:G:H2'	53:3:338:A:C8	2.38	0.59
58:B1:97:VAL:HG11	58:B1:101:ARG:NH2	2.18	0.59
27:b:116:GLN:O	27:b:127:ASN:ND2	2.35	0.59
28:c:46:ARG:HG2	28:c:84:LEU:HD12	1.85	0.59
28:c:194:PRO:HA	51:1:2680:U:H5'	1.85	0.59
51:1:1000:A:H62	51:1:1154:G:H2'	1.68	0.59
53:3:253:A:H2'	53:3:254:G:O4'	2.03	0.59
53:3:742:G:H2'	53:3:743:A:C8	2.38	0.59
58:B1:638:SER:OG	58:B1:639:VAL:N	2.36	0.59
64:6:55:U:H2'	64:6:56:C:H6	1.68	0.59
7:G:103:TRP:HA	7:G:106:VAL:HB	1.85	0.58
29:d:164:LEU:HB2	29:d:167:VAL:HG22	1.84	0.58
51:1:1836:C:O2'	51:1:1837:C:H5'	2.03	0.58
51:1:2333:A:H5'	51:1:2335:A:H1'	1.85	0.58
53:3:59:A:H5''	53:3:387:U:H5''	1.84	0.58
5:E:4:LYS:HD3	51:1:242:G:C8	2.38	0.58
9:I:68:GLU:HB3	53:3:546:A:OP2	2.03	0.58
13:M:38:VAL:HG11	13:M:110:MET:HA	1.83	0.58
17:Q:13:ARG:NH1	17:Q:14:LYS:O	2.35	0.58
50:z:12:ALA:O	50:z:20:LYS:NZ	2.36	0.58
51:1:166:U:H2'	51:1:167:A:C8	2.38	0.58
51:1:952:G:C2'	51:1:953:G:H5''	2.32	0.58
51:1:1063:G:H3'	51:1:1064:C:C6	2.37	0.58
51:1:1319:C:O2'	51:1:1320:C:H5'	2.02	0.58
51:1:2324:U:C3'	51:1:2325:G:H5''	2.26	0.58
51:1:2446:G:H2'	51:1:2501:C:C5	2.38	0.58
53:3:885:G:H2'	53:3:886:G:C8	2.39	0.58
35:k:16:ALA:O	35:k:17:ARG:NH1	2.36	0.58
51:1:1065:U:O4	51:1:1069:A:H5''	2.03	0.58
51:1:1806:C:H2'	51:1:1807:G:O4'	2.04	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:721:G:H4'	53:3:722:G:O4'	2.03	0.58
53:3:1280:A:O2'	53:3:1281:C:H5'	2.02	0.58
58:B1:161:THR:HG23	58:B1:164:GLN:H	1.68	0.58
58:B1:412:LEU:HD22	58:B1:441:LEU:HD21	1.84	0.58
59:B2:707:ALA:O	59:B2:711:ASP:HB2	2.03	0.58
64:6:6:G:O2'	64:6:7:G:H5'	2.04	0.58
64:6:14:A:H2'	64:6:15:G:H5'	1.85	0.58
7:G:99:MET:HA	7:G:106:VAL:HG21	1.84	0.58
7:G:176:ASN:ND2	7:G:194:GLY:O	2.33	0.58
28:c:118:PHE:HD2	51:1:1654:A:H2	1.52	0.58
43:s:25:ARG:NH2	51:1:519:U:H5''	2.19	0.58
51:1:1062:G:H5'	51:1:1071:G:H5'	1.85	0.58
51:1:1993:U:H2'	51:1:1994:C:H6	1.67	0.58
53:3:235:C:H2'	53:3:236:A:C8	2.38	0.58
53:3:570:G:O2'	53:3:819:A:H2'	2.03	0.58
53:3:677:U:H3	53:3:713:G:H1	1.51	0.58
15:O:40:ILE:CD1	53:3:1124:G:H4'	2.34	0.58
19:S:17:ASP:O	19:S:22:LYS:NZ	2.35	0.58
40:p:11:GLN:HB2	40:p:54:LEU:HD11	1.84	0.58
51:1:1368:G:H2'	51:1:1369:G:H8	1.68	0.58
53:3:41:G:H2'	53:3:42:G:H8	1.69	0.58
53:3:1195:C:H2'	53:3:1197:A:O4'	2.04	0.58
55:8:7:DC:H2''	55:8:8:DT:H71	1.84	0.58
57:A2:28:LEU:HB2	57:A2:201:LEU:HB3	1.86	0.58
58:B1:926:PRO:HG2	58:B1:1248:ILE:HD11	1.84	0.58
9:I:8:LEU:HD21	53:3:429:U:O5'	2.03	0.58
51:1:1197:G:H2'	51:1:1198:U:H6	1.67	0.58
53:3:16:A:O2'	53:3:17:U:H5'	2.03	0.58
53:3:41:G:H2'	53:3:42:G:C8	2.38	0.58
53:3:448:A:H62	53:3:486:U:H3	1.48	0.58
58:B1:370:LYS:HG2	58:B1:441:LEU:HD23	1.84	0.58
3:C:7:LYS:HA	3:C:23:THR:HA	1.85	0.58
9:I:12:ARG:HH21	9:I:35:GLN:H	1.50	0.58
9:I:58:GLN:HB3	9:I:62:ARG:HH21	1.68	0.58
25:Y:73:ARG:O	25:Y:77:ASN:ND2	2.36	0.58
51:1:952:G:C3'	51:1:953:G:H5''	2.33	0.58
51:1:1270:C:H5''	51:1:1271:G:H5'	1.84	0.58
51:1:2306:C:H2'	51:1:2307:G:C8	2.38	0.58
53:3:1069:C:O2'	53:3:1192:C:H1'	2.03	0.58
53:3:1421:G:H3'	53:3:1422:G:C5'	2.33	0.58
58:B1:615:LYS:HG2	60:W0:5:THR:HG21	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:a:26:ALA:HA	65:a:29:LEU:HB3	1.85	0.58
51:1:1332:G:N7	51:1:1609:A:H2'	2.18	0.58
51:1:1787:A:C2	51:1:1788:C:C6	2.91	0.58
51:1:1941:C:H2'	51:1:1942:C:O4'	2.04	0.58
64:6:4:G:H2'	64:6:5:G:O4'	2.03	0.58
8:H:18:ASN:HD21	8:H:39:ARG:HH12	1.51	0.58
40:p:33:GLU:OE1	40:p:38:ARG:NH1	2.37	0.58
51:1:414:C:H2'	51:1:415:A:C8	2.39	0.58
53:3:180:U:H2'	53:3:181:A:O4'	2.03	0.58
53:3:626:G:H2'	53:3:627:G:C8	2.39	0.58
53:3:850:U:C2'	53:3:851:G:H5''	2.33	0.58
5:E:21:PHE:HE2	5:E:61:LEU:HD23	1.68	0.58
10:J:87:VAL:HG13	10:J:92:ARG:HG3	1.86	0.58
23:W:56:ARG:NH1	53:3:735:C:OP1	2.37	0.58
51:1:36:G:H4'	51:1:451:U:C2	2.38	0.58
51:1:1197:G:H2'	51:1:1198:U:C6	2.39	0.58
51:1:2123:G:O6	51:1:2174:C:N4	2.37	0.58
53:3:1005:A:H2'	53:3:1006:G:H5'	1.85	0.58
6:F:19:ARG:NE	51:1:2756:U:OP2	2.36	0.57
12:L:137:ARG:NH1	12:L:138:GLU:OE2	2.36	0.57
51:1:1565:C:H2'	51:1:1567:G:N7	2.18	0.57
51:1:2196:C:H2'	51:1:2197:U:C6	2.39	0.57
51:1:2675:A:H2'	51:1:2676:C:C6	2.39	0.57
4:D:37:LYS:NZ	51:1:468:G:OP2	2.34	0.57
8:H:105:VAL:HG22	8:H:107:LYS:H	1.69	0.57
14:N:69:GLY:N	53:3:1250:A:H4'	2.20	0.57
16:P:33:ILE:HG22	16:P:41:LEU:HD12	1.86	0.57
32:g:15:LEU:HG	32:g:51:ARG:HH22	1.69	0.57
34:j:45:THR:OG1	41:q:63:ARG:NH2	2.37	0.57
42:r:79:ARG:NH1	51:1:572:A:OP2	2.37	0.57
51:1:1177:G:H2'	51:1:1178:C:H5''	1.86	0.57
51:1:1770:G:H4'	51:1:1938:A:OP1	2.04	0.57
51:1:1843:C:H2'	51:1:1844:C:C6	2.38	0.57
15:O:13:PHE:O	15:O:70:HIS:ND1	2.36	0.57
53:3:308:C:H2'	53:3:309:A:H8	1.69	0.57
2:B:49:ARG:O	2:B:51:ARG:NH2	2.37	0.57
14:N:5:TYR:HB2	14:N:20:ILE:HD11	1.86	0.57
20:T:13:GLU:OE1	20:T:83:ARG:NH2	2.36	0.57
20:T:60:SER:HB2	53:3:581:G:H5'	1.86	0.57
28:c:18:ASP:OD1	28:c:18:ASP:N	2.37	0.57
45:u:42:LYS:HG3	51:1:499:U:H4'	1.85	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:324:A:H62	51:1:338:G:N2	2.00	0.57
52:2:24:G:H4'	52:2:25:U:C5	2.38	0.57
2:B:5:ASN:ND2	51:1:2020:A:N7	2.52	0.57
28:c:110:THR:OG1	28:c:111:GLY:N	2.38	0.57
29:d:76:PRO:CA	29:d:82:GLY:HA3	2.35	0.57
58:B1:395:LYS:HZ2	58:B1:399:LYS:HD3	1.68	0.57
66:0:168:PRO:HG2	66:0:218:TRP:HE1	1.70	0.57
44:t:38:ALA:O	44:t:81:LYS:NZ	2.37	0.57
51:1:1697:G:C5'	51:1:1698:A:H5''	2.35	0.57
51:1:2050:C:C2'	51:1:2051:A:H5'	2.33	0.57
51:1:2524:G:C2'	51:1:2525:G:H5''	2.34	0.57
53:3:19:A:H1'	53:3:864:A:N3	2.19	0.57
53:3:1271:A:H5'	53:3:1314:C:C5'	2.35	0.57
58:B1:198:CYS:HA	58:B1:221:ILE:HD11	1.86	0.57
66:0:223:ILE:HB	66:0:243:LEU:HD22	1.85	0.57
8:H:60:ALA:HB3	62:NG:167:ARG:HA	1.86	0.57
11:K:82:ASP:OD1	11:K:82:ASP:N	2.38	0.57
12:L:91:ARG:CB	12:L:93:VAL:HG12	2.32	0.57
19:S:75:LYS:HZ3	53:3:1357:A:H5''	1.66	0.57
20:T:19:ASN:HB2	53:3:750:C:O4'	2.04	0.57
28:c:128:ARG:NH2	51:1:2512:C:OP2	2.37	0.57
37:m:66:ARG:NH1	37:m:104:GLU:OE2	2.37	0.57
51:1:62:U:O2'	51:1:63:A:H5'	2.04	0.57
53:3:651:C:H2'	53:3:652:U:O4'	2.04	0.57
53:3:885:G:H2'	53:3:886:G:H8	1.69	0.57
59:B2:818:VAL:HG22	59:B2:1096:ILE:HG12	1.87	0.57
11:K:90:MET:SD	23:W:60:ARG:NH1	2.78	0.57
27:b:221:GLY:HA2	27:b:224:MET:HE3	1.85	0.57
46:v:21:ARG:HH22	52:2:77:U:H5'	1.70	0.57
51:1:78:U:H2'	51:1:79:C:C6	2.40	0.57
51:1:1310:G:C2'	51:1:1311:G:H5'	2.34	0.57
53:3:279:A:H5''	53:3:281:G:C5'	2.34	0.57
53:3:1493:A:N7	67:h:6:5OH:NQ	2.52	0.57
13:M:15:ASN:HB3	53:3:827:U:H4'	1.86	0.57
32:g:139:PHE:O	32:g:141:LYS:NZ	2.37	0.57
38:n:92:GLY:HA3	51:1:2839:G:H21	1.69	0.57
47:w:20:LYS:HD2	51:1:2355:G:H4'	1.85	0.57
51:1:601:C:O2	51:1:605:G:H4'	2.05	0.57
51:1:1069:A:H2'	51:1:1073:A:N7	2.20	0.57
51:1:1791:A:H2'	51:1:1792:G:C5'	2.34	0.57
51:1:2475:C:N4	51:1:2529:G:H22	2.03	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1046:ILE:HD12	58:B1:1059:LEU:HB3	1.86	0.57
66:0:322:PHE:HB3	66:0:323:LYS:HD2	1.86	0.57
47:w:51:ARG:NH2	51:1:2384:U:OP2	2.37	0.57
51:1:27:G:N2	51:1:512:G:H1'	2.20	0.57
51:1:2420:C:O2'	51:1:2421:G:H5'	2.05	0.57
53:3:416:G:H2'	53:3:417:G:H8	1.70	0.57
53:3:539:A:H2'	53:3:540:G:C8	2.40	0.57
53:3:1004:A:H5'	53:3:1024:G:H1	1.70	0.57
53:3:1399:C:N3	53:3:1502:A:N1	2.53	0.57
53:3:1513:A:H2'	53:3:1514:G:C8	2.40	0.57
58:B1:99:ARG:CG	58:B1:99:ARG:HH11	2.17	0.57
58:B1:241:VAL:O	58:B1:241:VAL:HG12	2.04	0.57
59:B2:1122:LYS:NZ	59:B2:1126:ASP:OD1	2.38	0.57
17:Q:119:LYS:HD3	53:3:36:C:H5''	1.86	0.56
30:e:31:GLU:OE1	30:e:32:LYS:NZ	2.37	0.56
31:f:59:ASP:OD1	31:f:59:ASP:N	2.37	0.56
51:1:211:C:H2'	51:1:212:G:C8	2.40	0.56
51:1:2554:U:H2'	51:1:2555:U:C6	2.40	0.56
51:1:2743:U:C3'	51:1:2744:G:H5''	2.35	0.56
53:3:302:G:H2'	53:3:303:A:C8	2.40	0.56
58:B1:510:LEU:HD22	58:B1:601:ILE:HD12	1.86	0.56
4:D:12:ARG:HD2	4:D:44:VAL:HG11	1.88	0.56
29:d:2:GLU:HB2	29:d:11:ALA:HB1	1.87	0.56
51:1:28:A:O2'	51:1:583:G:H5'	2.05	0.56
51:1:1370:C:H2'	51:1:1371:G:O4'	2.04	0.56
51:1:2208:C:H2'	51:1:2209:G:H8	1.70	0.56
51:1:2396:G:O2'	51:1:2397:G:H5'	2.05	0.56
51:1:2529:G:H5'	51:1:2530:A:H5''	1.87	0.56
51:1:2637:U:H2'	51:1:2638:G:O4'	2.04	0.56
53:3:1016:A:H4'	53:3:1218:C:H4'	1.86	0.56
58:B1:102:MET:HG2	58:B1:246:PRO:HG3	1.87	0.56
58:B1:160:LEU:HD22	58:B1:164:GLN:HB3	1.86	0.56
58:B1:1166:GLY:HA3	58:B1:1174:ARG:HB2	1.88	0.56
3:C:5:ARG:HG3	3:C:25:ASN:HA	1.86	0.56
5:E:27:ASN:O	5:E:35:LYS:NZ	2.38	0.56
7:G:138:ARG:HH21	7:G:142:LYS:HG2	1.69	0.56
10:J:120:HIS:CE1	10:J:121:ASN:ND2	2.73	0.56
16:P:71:ASP:HA	16:P:74:LYS:HG3	1.87	0.56
18:R:87:GLY:O	18:R:91:ARG:NH2	2.39	0.56
19:S:5:MET:O	19:S:62:ARG:NH1	2.38	0.56
25:Y:2:ASN:O	25:Y:7:LYS:NZ	2.39	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:17:LYS:HD3	51:1:1565:C:OP1	2.05	0.56
33:i:123:ALA:HB1	51:1:1081:U:H4'	1.87	0.56
40:p:87:ARG:NH2	40:p:109:ILE:O	2.36	0.56
51:1:259:G:O2'	51:1:260:G:H5'	2.05	0.56
51:1:1801:A:H5''	51:1:2203:U:C2'	2.35	0.56
51:1:1923:U:H2'	51:1:1924:C:H6	1.70	0.56
51:1:2692:G:H1'	51:1:2847:U:H1'	1.87	0.56
52:2:4:C:H2'	52:2:5:U:C6	2.41	0.56
53:3:408:A:H61	53:3:434:U:H3	1.52	0.56
53:3:936:C:H2'	53:3:937:A:O4'	2.04	0.56
57:A2:82:LEU:HD11	57:A2:171:LEU:HD23	1.86	0.56
58:B1:130:MET:HE2	58:B1:135:ILE:HG12	1.87	0.56
58:B1:741:ALA:O	58:B1:762:ASN:ND2	2.38	0.56
63:5:38:A:C8	63:5:39:U:H1'	2.40	0.56
66:0:31:LEU:HD21	66:0:68:THR:HG21	1.87	0.56
66:0:438:LEU:HD22	66:0:469:ILE:HD11	1.88	0.56
66:0:446:ARG:O	66:0:459:ALA:N	2.38	0.56
66:0:616:ILE:HG13	66:0:688:ASP:HB2	1.87	0.56
3:C:8:ILE:HB	3:C:24:LYS:HB2	1.88	0.56
16:P:116:PRO:HA	53:3:675:A:H2	1.70	0.56
18:R:113:LYS:NZ	64:6:44:A:H4'	2.20	0.56
45:u:32:LYS:HE3	51:1:478:A:H4'	1.87	0.56
51:1:379:G:H2'	51:1:380:G:O4'	2.05	0.56
51:1:1774:C:H4'	51:1:1979:U:O2	2.05	0.56
58:B1:1361:THR:HB	59:B2:1284:ALA:HB3	1.85	0.56
3:C:36:LYS:NZ	3:C:45:HIS:O	2.38	0.56
10:J:120:HIS:CE1	10:J:121:ASN:HD21	2.23	0.56
34:j:60:ASP:HA	34:j:93:ILE:HD11	1.88	0.56
45:u:32:LYS:HB3	45:u:63:ALA:HB1	1.87	0.56
51:1:1114:C:H2'	51:1:1115:G:C8	2.41	0.56
51:1:1141:U:H4'	51:1:1142:A:O4'	2.05	0.56
51:1:1740:G:H2'	51:1:1741:C:C6	2.41	0.56
51:1:2796:U:H3	51:1:2799:A:H61	1.52	0.56
53:3:428:G:H4'	53:3:429:U:H4'	1.86	0.56
53:3:1257:A:H3'	53:3:1257:A:N3	2.21	0.56
22:V:19:SER:OG	22:V:20:ILE:N	2.33	0.56
25:Y:13:SER:O	25:Y:17:ARG:N	2.38	0.56
28:c:109:VAL:HG23	28:c:172:VAL:HG13	1.88	0.56
30:e:113:PHE:HZ	30:e:175:PRO:HB3	1.71	0.56
33:i:3:LYS:HD3	51:1:1055:G:O5'	2.06	0.56
40:p:88:ARG:HD3	40:p:112:ARG:HD3	1.86	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:w:35:ARG:HH21	51:1:2355:G:H1'	1.69	0.56
51:1:36:G:H4'	51:1:451:U:N3	2.21	0.56
51:1:683:U:H3	51:1:794:A:H61	1.53	0.56
53:3:212:G:H2'	53:3:213:G:C8	2.38	0.56
53:3:1513:A:H2'	53:3:1514:G:H8	1.71	0.56
57:A1:29:GLU:HB3	57:A1:200:LYS:HG3	1.88	0.56
7:G:23:ASN:ND2	7:G:191:ASP:HB3	2.21	0.56
13:M:27:PRO:O	13:M:32:LYS:NZ	2.38	0.56
27:b:158:GLY:HA3	51:1:1820:U:C4	2.40	0.56
29:d:112:LEU:HD22	29:d:117:ARG:HB3	1.88	0.56
51:1:687:C:H2'	51:1:688:U:C5'	2.36	0.56
51:1:1120:G:H2'	51:1:1121:C:O4'	2.05	0.56
51:1:2041:U:H2'	51:1:2042:A:C8	2.40	0.56
51:1:2317:A:H2'	51:1:2318:G:O4'	2.06	0.56
51:1:2430:A:N3	51:1:2430:A:H2'	2.20	0.56
52:2:105:G:H2'	52:2:106:G:H8	1.71	0.56
53:3:24:U:H2'	53:3:25:C:C6	2.40	0.56
53:3:416:G:H2'	53:3:417:G:C8	2.41	0.56
8:H:32:LEU:HD13	19:S:92:ILE:HD11	1.88	0.56
9:I:65:GLY:O	9:I:96:ARG:NH1	2.39	0.56
10:J:25:LYS:HG3	53:3:923:A:H5'	1.87	0.56
14:N:47:VAL:HG23	14:N:48:ARG:HG3	1.88	0.56
47:w:52:ASP:OD2	51:1:2364:C:H5'	2.05	0.56
51:1:959:A:H1'	51:1:2457:U:O2'	2.06	0.56
53:3:882:C:O2'	53:3:883:C:H5'	2.05	0.56
58:B1:42:GLU:HB3	58:B1:52:GLU:HG3	1.86	0.56
59:B2:13:LYS:HB2	59:B2:1180:MET:HE2	1.86	0.56
66:0:493:THR:O	66:0:610:PRO:HA	2.06	0.56
1:A:28:VAL:HG23	30:e:139:GLU:HA	1.88	0.56
7:G:30:ILE:HG22	7:G:40:ILE:HA	1.88	0.56
8:H:49:ALA:HA	8:H:74:ILE:HD11	1.88	0.56
8:H:120:THR:HG23	8:H:188:ALA:HB2	1.87	0.56
14:N:83:THR:HG21	14:N:102:PHE:HB3	1.88	0.56
28:c:63:PRO:O	28:c:67:HIS:N	2.39	0.56
51:1:1933:G:O2'	51:1:1974:C:H4'	2.04	0.56
53:3:1401:G:H2'	53:3:1402:C:O4'	2.06	0.56
58:B1:37:GLU:O	58:B1:61:ILE:CD1	2.52	0.56
58:B1:804:ALA:HA	58:B1:1259:GLN:HG3	1.88	0.56
59:B2:1142:ARG:NH2	59:B2:1166:ASP:OD1	2.38	0.56
8:H:82:ASP:HA	8:H:85:LYS:HD2	1.86	0.56
11:K:89:VAL:HG23	53:3:737:C:H5'	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:50:LYS:NZ	17:Q:51:VAL:O	2.39	0.56
28:c:119:ALA:O	51:1:1655:A:H4'	2.06	0.56
46:v:72:VAL:HA	46:v:94:ALA:H	1.71	0.56
47:w:33:ILE:HG22	47:w:34:VAL:HG23	1.88	0.56
51:1:1186:G:N2	51:1:1187:G:H1'	2.20	0.56
51:1:1827:U:C2'	51:1:1828:G:H5'	2.35	0.56
51:1:2508:G:C6	51:1:2582:G:O6	2.59	0.56
52:2:4:C:H6	52:2:4:C:H5'	1.71	0.56
53:3:301:G:H2'	53:3:302:G:C8	2.41	0.56
53:3:684:U:H2'	53:3:685:G:O4'	2.06	0.56
66:0:564:GLY:HA3	66:0:569:TYR:H	1.71	0.56
26:Z:48:LYS:HB3	53:3:723:U:C5	2.41	0.55
27:b:140:VAL:O	27:b:161:VAL:N	2.35	0.55
41:q:68:ALA:HB1	41:q:73:ILE:HG13	1.87	0.55
51:1:1255:U:OP1	51:1:1256:G:H5''	2.06	0.55
51:1:2584:U:H2'	51:1:2585:U:H2'	1.87	0.55
53:3:1093:A:C2'	53:3:1094:G:H5'	2.36	0.55
59:B2:839:VAL:HG12	59:B2:1049:ILE:HG12	1.87	0.55
7:G:101:THR:HG22	53:3:1074:G:H4'	1.88	0.55
13:M:24:VAL:HG13	13:M:62:LEU:HD11	1.87	0.55
13:M:74:ILE:HG22	13:M:128:VAL:HA	1.87	0.55
51:1:146:A:H2'	51:1:147:C:C6	2.42	0.55
51:1:1827:U:H2'	51:1:1828:G:H5'	1.88	0.55
51:1:2563:U:H2'	51:1:2564:A:H5''	1.88	0.55
58:B1:1175:LEU:HD22	58:B1:1190:ILE:HD11	1.88	0.55
8:H:20:THR:HA	19:S:93:PRO:HB3	1.88	0.55
14:N:11:ARG:NH1	14:N:106:ASP:O	2.39	0.55
35:k:65:THR:HA	35:k:82:ASN:HA	1.88	0.55
51:1:155:A:H2'	51:1:156:A:H8	1.71	0.55
51:1:881:G:H2'	51:1:882:G:H8	1.71	0.55
51:1:2207:C:O2'	51:1:2208:C:H5'	2.07	0.55
53:3:560:A:H5'	53:3:566:G:N2	2.21	0.55
53:3:1127:G:H2'	53:3:1128:C:C6	2.41	0.55
53:3:1244:G:H2'	53:3:1245:C:C6	2.40	0.55
58:B1:247:PRO:HA	58:B1:250:ARG:HG3	1.87	0.55
66:0:11:ARG:NH2	66:0:283:ILE:O	2.39	0.55
66:0:192:ASN:HB3	66:0:203:GLU:HB2	1.87	0.55
5:E:43:LEU:HD11	51:1:2362:C:P	2.46	0.55
10:J:16:ALA:HB3	10:J:35:LEU:H	1.71	0.55
10:J:19:ARG:HG2	10:J:30:PHE:HB3	1.89	0.55
12:L:91:ARG:O	12:L:95:ARG:CG	2.55	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:111:GLY:HA2	12:L:118:ARG:HG2	1.88	0.55
28:c:118:PHE:HD2	51:1:1654:A:C2	2.24	0.55
33:i:53:PRO:HD2	33:i:77:VAL:HG21	1.87	0.55
50:z:10:ARG:NH2	50:z:52:PHE:O	2.39	0.55
51:1:310:A:C2'	51:1:311:A:H5''	2.37	0.55
51:1:923:G:O2'	51:1:924:G:H5'	2.06	0.55
51:1:1191:G:H2'	51:1:1192:G:H8	1.71	0.55
51:1:2299:U:H2'	51:1:2300:C:C6	2.42	0.55
53:3:971:G:OP1	53:3:971:G:H3'	2.07	0.55
53:3:1525:G:O2'	53:3:1526:G:H5'	2.06	0.55
58:B1:508:LEU:HD22	59:B2:1101:LEU:HD21	1.88	0.55
65:a:26:ALA:HB1	65:a:30:LEU:HB2	1.87	0.55
66:0:225:SER:O	66:0:255:ARG:NH1	2.39	0.55
66:0:323:LYS:HB2	66:0:335:PHE:HB2	1.88	0.55
13:M:14:ARG:NH1	13:M:74:ILE:O	2.39	0.55
15:O:42:LEU:HD22	15:O:71:LEU:HB2	1.88	0.55
21:U:1:MET:HB2	53:3:135:C:N3	2.21	0.55
22:V:64:ARG:HB2	53:3:130:A:H8	1.70	0.55
38:n:64:ARG:O	38:n:68:ALA:N	2.40	0.55
40:p:15:ASP:N	40:p:15:ASP:OD1	2.39	0.55
66:0:694:VAL:HA	66:0:697:ALA:HB3	1.87	0.55
4:D:8:SER:OG	4:D:9:VAL:N	2.38	0.55
6:F:5:ALA:HB3	51:1:2466:C:H5'	1.88	0.55
12:L:32:ASP:HA	53:3:1350:A:O2'	2.06	0.55
27:b:257:ARG:HD3	51:1:1799:G:OP1	2.07	0.55
51:1:1868:C:H2'	51:1:1869:G:C5'	2.35	0.55
53:3:539:A:H2'	53:3:540:G:H8	1.72	0.55
66:0:501:VAL:CG1	66:0:607:LYS:HZ1	2.19	0.55
13:M:84:ILE:HD11	13:M:86:LYS:HG2	1.89	0.55
21:U:5:ARG:NH2	21:U:23:ASP:O	2.40	0.55
27:b:204:LEU:HD21	27:b:213:ARG:HH21	1.72	0.55
30:e:46:LYS:NZ	30:e:82:TYR:OH	2.40	0.55
30:e:56:LEU:HG	30:e:59:ILE:HD12	1.89	0.55
32:g:14:SER:O	32:g:15:LEU:C	2.50	0.55
51:1:782:A:H4'	51:1:783:A:H5'	1.87	0.55
51:1:1063:G:OP2	51:1:1070:A:H4'	2.06	0.55
51:1:1403:A:H2'	51:1:1404:C:C6	2.42	0.55
51:1:2682:A:H61	51:1:2728:U:H1'	1.72	0.55
53:3:46:G:H2'	53:3:366:A:H62	1.72	0.55
53:3:357:G:OP1	53:3:367:U:H5''	2.06	0.55
53:3:593:U:H2'	53:3:594:U:C6	2.41	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:596:A:H2'	53:3:597:G:O4'	2.07	0.55
53:3:1348:U:H2'	53:3:1349:A:H5'	1.87	0.55
58:B1:833:GLU:HB2	58:B1:1242:ARG:NH1	2.22	0.55
65:a:189:LEU:HA	65:a:192:LEU:HG	1.88	0.55
66:0:427:ASP:O	66:0:431:MET:N	2.39	0.55
66:0:488:VAL:HG11	66:0:661:SER:HA	1.87	0.55
3:C:40:PRO:HG3	51:1:2348:U:H4'	1.88	0.55
7:G:59:ILE:HG12	7:G:62:ARG:HH21	1.71	0.55
13:M:9:MET:HB2	13:M:32:LYS:HE2	1.88	0.55
29:d:147:LEU:HB3	29:d:186:VAL:HG12	1.88	0.55
51:1:286:U:H2'	51:1:287:G:H8	1.72	0.55
51:1:1257:C:O5'	51:1:1257:C:H6	1.90	0.55
51:1:1783:A:N1	51:1:2587:A:H2'	2.21	0.55
59:B2:103:VAL:HB	59:B2:114:VAL:HG11	1.89	0.55
59:B2:917:SER:O	59:B2:919:ARG:HG3	2.07	0.55
3:C:21:THR:HG21	51:1:2419:U:H5''	1.89	0.55
33:i:11:GLN:HB2	33:i:56:VAL:HG22	1.88	0.55
39:o:33:ARG:HD3	52:2:52:A:N7	2.22	0.55
51:1:305:C:H2'	51:1:306:U:C6	2.42	0.55
51:1:1343:G:H1'	51:1:1597:A:C4	2.42	0.55
51:1:2008:C:H2'	51:1:2009:A:C8	2.42	0.55
51:1:2048:G:C2'	51:1:2049:G:H5''	2.37	0.55
51:1:2726:A:O2'	51:1:2727:A:H5'	2.06	0.55
53:3:459:A:H2'	53:3:460:A:C8	2.42	0.55
53:3:1096:C:H2'	53:3:1097:C:C6	2.41	0.55
58:B1:39:LYS:O	58:B1:273:ILE:HG21	2.06	0.55
58:B1:58:CYS:SG	58:B1:59:ALA:N	2.80	0.55
58:B1:800:LEU:HB3	58:B1:920:ALA:HB1	1.89	0.55
59:B2:360:LEU:HD13	59:B2:378:ARG:HH11	1.72	0.55
63:5:40:C:H2'	63:5:41:C:C6	2.41	0.55
9:I:141:VAL:HA	9:I:180:THR:HA	1.88	0.55
26:Z:13:VAL:HG13	26:Z:15:LEU:HG	1.89	0.55
29:d:44:ARG:HH12	51:1:1248:G:P	2.30	0.55
34:j:6:ALA:HB3	34:j:48:VAL:HG11	1.89	0.55
36:l:29:LYS:HG2	51:1:566:U:OP1	2.07	0.55
51:1:310:A:H2'	51:1:311:A:H5''	1.90	0.55
51:1:849:A:H2'	51:1:850:U:H6	1.68	0.55
58:B1:144:TYR:HE1	58:B1:162:GLU:CD	2.14	0.55
66:0:92:HIS:HD2	66:0:464:LEU:HD21	1.71	0.55
66:0:103:MET:HB3	66:0:135:VAL:HG21	1.89	0.55
31:f:3:VAL:HG11	31:f:65:GLY:HA2	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:171:U:H2'	51:1:172:A:C8	2.42	0.54
51:1:614:A:H5'	51:1:615:U:OP1	2.06	0.54
53:3:874:G:H2'	53:3:875:U:C6	2.42	0.54
53:3:1042:A:H2'	53:3:1043:G:C4'	2.38	0.54
53:3:1390:U:H2'	53:3:1391:U:C6	2.42	0.54
58:B1:1155:ILE:HG13	58:B1:1210:ILE:HB	1.89	0.54
66:0:171:LEU:HB2	66:0:183:VAL:HB	1.88	0.54
6:F:10:LEU:HD21	51:1:2477:U:C5	2.42	0.54
15:O:43:PRO:HA	53:3:1151:A:H5'	1.89	0.54
33:i:38:CYS:O	33:i:42:ASN:ND2	2.40	0.54
41:q:5:ARG:NH2	51:1:1251:C:OP2	2.40	0.54
42:r:76:LYS:NZ	42:r:85:LYS:O	2.40	0.54
48:x:2:ARG:HG2	48:x:32:LEU:CD1	2.37	0.54
51:1:486:C:H42	51:1:494:G:H1	1.56	0.54
51:1:605:G:H21	51:1:658:U:H5'	1.72	0.54
51:1:1024:G:H3'	51:1:1025:G:C5'	2.37	0.54
51:1:1652:A:H2'	51:1:1653:G:O4'	2.07	0.54
51:1:1697:G:C3'	51:1:1698:A:H5''	2.36	0.54
51:1:2128:G:H5'	65:a:218:MET:HE1	1.89	0.54
53:3:866:C:C4	53:3:867:G:H1'	2.41	0.54
53:3:1213:A:O2'	53:3:1214:C:H2'	2.06	0.54
53:3:1347:G:H22	53:3:1373:G:H2'	1.72	0.54
53:3:1414:U:H2'	53:3:1415:G:C8	2.43	0.54
57:A2:100:LEU:HD23	57:A2:115:ILE:HG21	1.89	0.54
59:B2:811:ASN:HA	59:B2:815:SER:HB2	1.90	0.54
59:B2:985:GLU:HB3	59:B2:988:LYS:HB2	1.88	0.54
59:B2:1117:LEU:HD12	59:B2:1195:ILE:HG12	1.90	0.54
10:J:153:ALA:HB1	10:J:160:VAL:HA	1.90	0.54
12:L:91:ARG:NE	12:L:91:ARG:HA	2.22	0.54
16:P:99:LEU:O	16:P:103:GLY:N	2.38	0.54
26:Z:66:ARG:NH1	53:3:1098:C:O2'	2.38	0.54
37:m:1:MET:HE1	63:5:63:G:H21	1.72	0.54
44:t:14:PRO:HA	44:t:32:LEU:HA	1.89	0.54
51:1:471:A:H2'	51:1:472:A:O4'	2.08	0.54
53:3:1073:U:H2'	53:3:1074:G:H8	1.69	0.54
65:a:19:LYS:NZ	65:a:20:GLN:O	2.38	0.54
8:H:21:TRP:HD1	8:H:57:GLU:HA	1.71	0.54
8:H:26:LYS:HE3	53:3:1256:A:H3'	1.89	0.54
30:e:127:TYR:HB3	30:e:155:ILE:HG13	1.89	0.54
38:n:2:ARG:NH1	51:1:2820:A:OP2	2.40	0.54
39:o:15:ARG:NH2	39:o:95:SER:OG	2.39	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:121:G:H4'	51:1:149:A:H5'	1.89	0.54
51:1:2813:A:H2'	51:1:2814:A:C8	2.42	0.54
53:3:350:G:O2'	53:3:351:G:H5'	2.08	0.54
53:3:1042:A:H2'	53:3:1043:G:O4'	2.08	0.54
57:A2:29:GLU:HG3	57:A2:200:LYS:HG3	1.88	0.54
59:B2:684:ASN:OD1	59:B2:687:ARG:NH2	2.41	0.54
66:0:416:ILE:N	66:0:460:GLY:O	2.40	0.54
9:I:96:ARG:NH2	9:I:98:ASP:OD2	2.39	0.54
16:P:122:PRO:HG2	26:Z:34:ARG:HA	1.89	0.54
27:b:6:LYS:HZ1	51:1:1695:G:H5'	1.71	0.54
27:b:140:VAL:HG12	27:b:191:LEU:HA	1.89	0.54
38:n:11:ASN:N	51:1:1653:G:O6	2.37	0.54
51:1:130:C:H2'	51:1:131:A:O4'	2.07	0.54
51:1:1040:A:H2'	51:1:1041:G:H8	1.72	0.54
51:1:1836:C:C2'	51:1:1837:C:H5'	2.37	0.54
51:1:2496:C:C2'	51:1:2497:A:H5'	2.36	0.54
53:3:1105:A:H2'	53:3:1106:G:C8	2.43	0.54
58:B1:799:ARG:HG2	58:B1:1325:PHE:HZ	1.72	0.54
28:c:146:ILE:O	28:c:159:LYS:NZ	2.41	0.54
51:1:1936:A:H2	51:1:1943:U:H3	1.51	0.54
53:3:1091:U:H2'	53:3:1093:A:OP2	2.07	0.54
9:I:205:LYS:HE2	53:3:8:A:C6	2.42	0.54
17:Q:23:LEU:HB2	17:Q:29:LYS:HD3	1.90	0.54
21:U:16:PHE:CE2	53:3:625:U:H5''	2.42	0.54
27:b:206:LYS:HE3	27:b:209:ALA:HB2	1.89	0.54
39:o:2:ASP:N	52:2:59:A:HO2'	2.05	0.54
45:u:65:GLN:OE1	51:1:328:U:H4'	2.07	0.54
51:1:142:A:H2'	51:1:143:C:C6	2.42	0.54
51:1:1192:G:O2'	51:1:1193:G:H5'	2.08	0.54
51:1:1889:A:H2'	51:1:1890:A:H8	1.73	0.54
51:1:2373:G:H2'	51:1:2374:C:C6	2.43	0.54
53:3:1399:C:H4'	53:3:1400:C:H3'	1.88	0.54
58:B1:99:ARG:HG3	58:B1:99:ARG:HH11	1.73	0.54
11:K:11:HIS:ND1	11:K:14:GLN:OE1	2.41	0.54
14:N:104:THR:HG22	53:3:1180:A:OP1	2.08	0.54
27:b:106:PRO:HG2	27:b:109:LEU:HB2	1.90	0.54
29:d:141:MET:HB2	29:d:143:LEU:HD11	1.90	0.54
33:i:9:LYS:HD2	51:1:1059:G:OP2	2.07	0.54
38:n:98:LEU:HB2	38:n:112:TYR:HB2	1.88	0.54
51:1:207:A:H2'	51:1:208:C:O4'	2.07	0.54
51:1:1659:G:H2'	51:1:1660:G:O4'	2.08	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1809:A:H2'	51:1:1810:A:C8	2.42	0.54
58:B1:205:LEU:HG	58:B1:217:LEU:HB3	1.90	0.54
58:B1:785:ASP:O	58:B1:789:LYS:HB2	2.08	0.54
66:0:334:THR:OG1	66:0:385:ALA:N	2.40	0.54
66:0:446:ARG:HH11	66:0:447:VAL:H	1.54	0.54
29:d:70:SER:C	51:1:674:G:H5''	2.33	0.54
51:1:534:U:H3	51:1:559:G:H1	1.55	0.54
51:1:1614:A:H2'	51:1:1615:C:H5'	1.90	0.54
51:1:1783:A:C6	51:1:2587:A:C4	2.96	0.54
51:1:2155:U:OP1	51:1:2157:G:N2	2.41	0.54
53:3:401:C:H2'	53:3:402:G:H8	1.73	0.54
53:3:1013:G:N2	53:3:1015:G:H3'	2.23	0.54
57:A1:47:LEU:HD23	57:A1:51:MET:HG3	1.89	0.54
58:B1:30:ILE:HG21	58:B1:241:VAL:O	2.08	0.54
58:B1:111:THR:HG22	58:B1:300:GLN:NE2	2.23	0.54
7:G:10:LYS:HG2	7:G:211:LEU:HD21	1.89	0.54
19:S:9:GLU:HA	19:S:12:ARG:HB2	1.89	0.54
23:W:49:LYS:HB2	53:3:835:U:OP1	2.08	0.54
25:Y:14:GLU:O	25:Y:18:LYS:NZ	2.41	0.54
32:g:29:PHE:HB2	51:1:2198:A:C2	2.43	0.54
51:1:851:C:H2'	51:1:852:U:C6	2.43	0.54
51:1:1126:A:H4'	51:1:1127:A:C5'	2.38	0.54
51:1:1791:A:O2'	51:1:1792:G:H5'	2.07	0.54
53:3:951:G:H2'	53:3:952:U:C6	2.43	0.54
53:3:1093:A:C6	53:3:1095:U:H1'	2.43	0.54
57:A2:43:LEU:HD13	57:A2:217:ILE:HD11	1.90	0.54
58:B1:814:CYS:SG	58:B1:883:ARG:NH2	2.81	0.54
59:B2:29:SER:O	59:B2:33:ASP:HB2	2.08	0.54
66:0:641:MET:HB3	66:0:657:GLU:HB2	1.90	0.54
8:H:58:ARG:HA	8:H:63:ILE:HA	1.90	0.53
11:K:46:GLN:NE2	11:K:47:LEU:O	2.39	0.53
25:Y:14:GLU:OE2	25:Y:18:LYS:NZ	2.41	0.53
27:b:208:GLY:HA2	27:b:211:ARG:HB3	1.89	0.53
38:n:60:VAL:HG12	38:n:64:ARG:HH22	1.73	0.53
51:1:2516:A:O2'	51:1:2517:C:H5'	2.08	0.53
53:3:20:U:H2'	53:3:21:G:O4'	2.08	0.53
53:3:1234:C:H1'	53:3:1364:U:O2	2.08	0.53
53:3:1271:A:C5'	53:3:1314:C:H5''	2.39	0.53
53:3:1325:C:H2'	53:3:1326:U:C6	2.42	0.53
53:3:1507:A:H61	53:3:1528:U:H3	1.56	0.53
66:0:632:ILE:HA	66:0:635:LEU:HB3	1.89	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:162:A:H2'	53:3:163:C:H5'	1.89	0.53
53:3:1084:G:HO2'	53:3:1103:C:H5	1.57	0.53
53:3:1421:G:H3'	53:3:1422:G:H5''	1.90	0.53
58:B1:78:LEU:O	58:B1:78:LEU:HD13	2.09	0.53
58:B1:759:ILE:HG23	58:B1:771:GLN:HB3	1.89	0.53
6:F:24:ARG:HE	6:F:36:ARG:HG3	1.73	0.53
8:H:190:THR:HG23	8:H:192:TYR:H	1.73	0.53
12:L:53:SER:HB2	12:L:55:LYS:HE3	1.90	0.53
22:V:49:ASN:ND2	22:V:51:GLU:OE2	2.42	0.53
38:n:39:PRO:CG	51:1:1651:G:H5'	2.33	0.53
51:1:937:C:H2'	51:1:938:G:C8	2.43	0.53
51:1:1127:A:C2'	51:1:1128:G:H5''	2.37	0.53
51:1:1319:C:H2'	51:1:1320:C:H6	1.73	0.53
51:1:1905:C:H2'	51:1:1930:G:C8	2.42	0.53
51:1:2092:U:C5	51:1:2199:A:H2	2.26	0.53
53:3:690:G:H2'	53:3:691:G:O4'	2.08	0.53
53:3:952:U:H2'	53:3:953:G:H8	1.74	0.53
53:3:1420:U:H3	53:3:1480:A:H2	1.54	0.53
57:A1:205:MET:HE3	57:A1:213:PRO:HB3	1.91	0.53
58:B1:209:ASN:HA	58:B1:214:ARG:HH21	1.73	0.53
7:G:20:ARG:HD2	53:3:831:A:C5'	2.39	0.53
8:H:179:ALA:HB1	8:H:202:PHE:HE1	1.73	0.53
13:M:105:THR:HG22	13:M:107:LYS:H	1.73	0.53
30:e:120:SER:HA	51:1:2303:G:H4'	1.89	0.53
37:m:127:LYS:HE2	51:1:1030:C:OP2	2.08	0.53
39:o:30:ARG:HG3	39:o:102:ARG:HD2	1.89	0.53
51:1:1550:C:H2'	51:1:1551:A:H8	1.73	0.53
51:1:2125:G:H5'	65:a:39:VAL:C	2.33	0.53
53:3:36:C:H2'	53:3:37:U:H6	1.73	0.53
53:3:1402:C:H2'	53:3:1403:C:O4'	2.08	0.53
58:B1:145:VAL:HG23	58:B1:159:ILE:HG22	1.89	0.53
58:B1:1167:LYS:HZ2	58:B1:1170:LYS:HB2	1.73	0.53
59:B2:633:LEU:HD13	59:B2:644:LEU:HD23	1.89	0.53
66:0:327:ASP:O	66:0:437:ARG:NH2	2.42	0.53
7:G:68:PHE:HA	7:G:161:PHE:HB3	1.90	0.53
16:P:124:LYS:HA	26:Z:34:ARG:HE	1.73	0.53
24:X:4:LEU:HG	24:X:6:LYS:H	1.72	0.53
32:g:2:GLN:NE2	32:g:18:GLN:O	2.40	0.53
51:1:859:G:N2	51:1:916:G:H2'	2.23	0.53
51:1:2276:G:O2'	51:1:2277:G:H5'	2.09	0.53
53:3:1366:C:H2'	53:3:1367:C:H6	1.72	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:a:11:ILE:HG13	65:a:219:GLY:HA3	1.91	0.53
4:D:11:LYS:HE2	51:1:770:G:OP2	2.09	0.53
13:M:32:LYS:HA	13:M:35:ILE:HD12	1.90	0.53
32:g:25:TYR:HB2	51:1:2093:G:O3'	2.07	0.53
49:y:21:LEU:HA	49:y:25:GLN:HB3	1.90	0.53
51:1:772:C:H5''	51:1:1356:G:H5'	1.90	0.53
51:1:1760:C:H2'	51:1:1761:C:H5'	1.91	0.53
51:1:2048:G:H3'	51:1:2049:G:H5''	1.91	0.53
57:A2:28:LEU:HD22	57:A2:201:LEU:HD23	1.90	0.53
29:d:63:LYS:HE3	51:1:2060:A:H3'	1.91	0.53
51:1:231:A:H2'	51:1:232:G:O4'	2.08	0.53
51:1:737:C:H2'	51:1:738:G:H8	1.72	0.53
51:1:1352:U:O2'	51:1:1353:A:H5'	2.08	0.53
53:3:337:G:H2'	53:3:338:A:H8	1.74	0.53
58:B1:111:THR:HG23	58:B1:300:GLN:NE2	2.24	0.53
14:N:97:LEU:O	14:N:102:PHE:N	2.39	0.53
28:c:144:GLY:HA2	51:1:2578:G:H1'	1.91	0.53
45:u:47:PRO:HB2	45:u:53:GLN:HB3	1.91	0.53
51:1:838:C:H2'	51:1:839:U:C6	2.44	0.53
51:1:1303:G:H2'	51:1:1304:A:H8	1.74	0.53
51:1:2638:G:H1	51:1:2775:G:H2'	1.74	0.53
51:1:2699:C:H2'	51:1:2700:A:C8	2.44	0.53
57:A1:16:ILE:HG23	57:A1:26:VAL:HG22	1.91	0.53
58:B1:746:LEU:HG	58:B1:758:PRO:HG3	1.90	0.53
58:B1:770:LEU:CD1	59:B2:618:GLN:HG3	2.37	0.53
65:a:194:VAL:HA	65:a:197:LYS:HB2	1.89	0.53
66:0:136:PRO:HG2	66:0:287:PRO:HG3	1.90	0.53
66:0:223:ILE:HG13	66:0:237:TYR:HE1	1.73	0.53
4:D:13:ASN:HB3	51:1:125:A:C4'	2.39	0.53
10:J:53:ARG:CZ	53:3:1071:C:H5'	2.39	0.53
12:L:12:LEU:HD13	53:3:1374:A:OP1	2.09	0.53
13:M:9:MET:HE1	13:M:35:ILE:HD13	1.91	0.53
14:N:45:MET:HE3	14:N:49:GLN:HA	1.90	0.53
29:d:68:ALA:HA	51:1:1255:U:C6	2.42	0.53
33:i:92:PRO:HB3	33:i:134:SER:HA	1.89	0.53
46:v:73:LYS:O	46:v:92:VAL:N	2.41	0.53
51:1:133:U:H3	51:1:146:A:H61	1.57	0.53
51:1:351:C:H2'	51:1:352:A:H8	1.73	0.53
51:1:351:C:H2'	51:1:352:A:C8	2.44	0.53
51:1:1065:U:H3'	51:1:1066:U:H5''	1.91	0.53
51:1:1433:A:H2'	51:1:1434:A:C1'	2.38	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:112:G:N2	53:3:354:G:H5'	2.02	0.53
53:3:601:G:H2'	53:3:602:A:C8	2.44	0.53
58:B1:850:LYS:HB2	58:B1:857:LEU:HB2	1.91	0.53
60:W0:3:ARG:NH1	60:W0:55:GLU:OE2	2.40	0.53
7:G:210:THR:HA	7:G:213:LEU:HB2	1.90	0.53
12:L:63:VAL:HA	12:L:66:GLU:HG2	1.91	0.53
12:L:92:PRO:HA	12:L:95:ARG:CG	2.37	0.53
29:d:45:ALA:HB3	51:1:38:A:H4'	1.91	0.53
40:p:19:PHE:HE2	40:p:46:VAL:HG21	1.74	0.53
41:q:48:ASP:HA	41:q:51:GLN:HB3	1.89	0.53
43:s:4:ILE:HG23	43:s:106:VAL:HG22	1.91	0.53
51:1:533:G:H1	51:1:560:C:H42	1.56	0.53
51:1:1229:C:H2'	51:1:1230:A:H8	1.74	0.53
51:1:1592:C:H2'	51:1:1593:A:C8	2.44	0.53
52:2:33:G:H2'	52:2:34:A:O4'	2.09	0.53
53:3:224:U:H2'	53:3:225:C:C6	2.44	0.53
53:3:563:A:H4'	53:3:566:G:O2'	2.09	0.53
66:0:415:VAL:H	66:0:461:MET:HA	1.73	0.53
8:H:18:ASN:HA	8:H:55:VAL:HG22	1.91	0.52
9:I:13:ARG:NH2	9:I:37:PRO:O	2.42	0.52
17:Q:6:LEU:HD21	17:Q:11:ARG:HH21	1.73	0.52
19:S:8:ARG:HB2	19:S:62:ARG:HH12	1.74	0.52
20:T:2:LEU:HD11	20:T:30:LEU:HD11	1.90	0.52
31:f:2:ARG:HG2	51:1:2751:G:C4	2.43	0.52
32:g:2:GLN:HB3	32:g:18:GLN:HB3	1.91	0.52
33:i:101:SER:OG	33:i:102:ARG:N	2.42	0.52
36:l:29:LYS:HA	51:1:810:U:C5	2.44	0.52
36:l:29:LYS:HE3	51:1:566:U:H5''	1.90	0.52
38:n:8:ARG:NH2	38:n:43:GLU:OE1	2.42	0.52
51:1:2124:G:N1	51:1:2175:C:O2	2.42	0.52
53:3:299:G:N2	53:3:565:U:H3	2.06	0.52
53:3:737:C:H2'	53:3:738:C:H6	1.74	0.52
53:3:1064:G:O3'	53:3:1065:U:H4'	2.09	0.52
53:3:1077:G:N2	53:3:1079:G:H3'	2.24	0.52
14:N:64:ILE:HG21	14:N:78:ILE:HG13	1.91	0.52
17:Q:120:ARG:HG2	53:3:37:U:H5'	1.89	0.52
27:b:231:HIS:ND1	51:1:1826:G:OP1	2.38	0.52
28:c:23:PRO:HB3	51:1:2682:A:C2	2.43	0.52
30:e:33:ILE:HD12	30:e:155:ILE:HG22	1.90	0.52
35:k:64:ARG:O	35:k:83:ALA:N	2.42	0.52
42:r:77:PHE:HD1	42:r:84:ARG:HB3	1.73	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1361:G:H2'	51:1:1362:C:H6	1.74	0.52
51:1:1656:C:H2'	51:1:1657:U:C6	2.44	0.52
57:A1:100:LEU:HD21	57:A1:121:VAL:HG11	1.90	0.52
57:A2:140:ILE:HD12	57:A2:142:MET:HE3	1.91	0.52
59:B2:243:PRO:HB2	59:B2:274:ILE:HG23	1.90	0.52
7:G:67:LEU:HD11	7:G:157:PRO:HG3	1.91	0.52
22:V:11:VAL:HG23	22:V:55:GLY:H	1.74	0.52
22:V:46:HIS:HB2	22:V:70:LYS:HD3	1.91	0.52
28:c:15:PHE:HB3	40:p:78:PRO:HD3	1.89	0.52
36:l:85:VAL:HG22	36:l:86:GLU:HG2	1.92	0.52
37:m:27:SER:OG	37:m:66:ARG:NH1	2.42	0.52
49:y:44:LYS:HE2	49:y:48:ARG:HG3	1.91	0.52
51:1:1082:U:H3	51:1:1086:A:H2	1.56	0.52
51:1:1635:A:H2	51:1:1761:C:O2'	1.92	0.52
51:1:2694:G:H2'	51:1:2695:U:O4'	2.09	0.52
52:2:30:C:C2'	52:2:31:C:H5'	2.40	0.52
52:2:102:G:H2'	52:2:103:U:O4'	2.08	0.52
53:3:36:C:H2'	53:3:37:U:C6	2.44	0.52
53:3:722:G:H1	53:3:733:G:H1	1.56	0.52
58:B1:112:ALA:HA	58:B1:238:ILE:HA	1.91	0.52
63:5:38:A:H2'	63:5:39:U:H4'	1.91	0.52
66:0:530:ASN:ND2	66:0:535:GLU:OE1	2.42	0.52
5:E:48:MET:SD	5:E:48:MET:N	2.79	0.52
19:S:82:LYS:HA	19:S:85:GLU:HB2	1.92	0.52
48:x:30:PRO:HG2	48:x:32:LEU:HG	1.91	0.52
51:1:413:C:N4	51:1:2410:G:H1	1.96	0.52
51:1:2345:G:N3	51:1:2381:A:H2'	2.24	0.52
53:3:67:C:H2'	53:3:68:G:C8	2.44	0.52
53:3:369:G:H22	53:3:393:A:H1'	1.75	0.52
53:3:1406:U:H2'	53:3:1407:C:O4'	2.10	0.52
58:B1:201:LEU:HD12	58:B1:224:LEU:HD12	1.92	0.52
66:0:520:ILE:HB	66:0:576:ILE:HD11	1.90	0.52
8:H:181:ILE:HD11	8:H:200:TRP:HB3	1.92	0.52
16:P:87:GLY:O	16:P:92:ARG:NH1	2.43	0.52
38:n:32:GLU:HG2	38:n:115:LEU:HD13	1.92	0.52
38:n:103:ARG:HB3	38:n:108:ALA:H	1.74	0.52
42:r:29:THR:HA	42:r:63:VAL:HG23	1.91	0.52
51:1:803:U:O2'	51:1:804:A:H5'	2.09	0.52
51:1:1841:U:H2'	51:1:1842:G:H8	1.73	0.52
53:3:153:C:H2'	53:3:154:U:C4'	2.39	0.52
53:3:358:U:H2'	53:3:359:G:C8	2.44	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1169:A:H2'	53:3:1170:A:O4'	2.09	0.52
53:3:1479:C:H2'	53:3:1480:A:O4'	2.09	0.52
66:0:541:LYS:NZ	66:0:579:HIS:O	2.41	0.52
10:J:36:THR:OG1	10:J:37:VAL:N	2.38	0.52
15:O:15:HIS:CD2	53:3:1152:A:H5'	2.44	0.52
18:R:89:ARG:NH2	18:R:95:PRO:O	2.34	0.52
25:Y:67:HIS:HD2	25:Y:69:ASN:HB2	1.73	0.52
35:k:21:CYS:HA	35:k:41:ILE:HA	1.92	0.52
51:1:155:A:H2'	51:1:156:A:C8	2.44	0.52
51:1:1674:G:N2	51:1:1677:A:H61	2.06	0.52
51:1:2507:C:H6	51:1:2507:C:O5'	1.93	0.52
51:1:2577:A:H2'	51:1:2614:A:H61	1.75	0.52
11:K:47:LEU:HD21	11:K:55:HIS:HA	1.92	0.52
14:N:11:ARG:HH11	14:N:105:ARG:HH12	1.57	0.52
27:b:7:PRO:HB3	27:b:13:ARG:HA	1.92	0.52
28:c:161:MET:HE1	51:1:2050:C:H1'	1.91	0.52
30:e:23:SER:HB3	30:e:26:GLN:HB2	1.92	0.52
42:r:49:ILE:HG22	42:r:54:VAL:HG22	1.91	0.52
51:1:25:U:H2'	51:1:26:G:O4'	2.10	0.52
51:1:203:A:H3'	51:1:204:A:C5'	2.39	0.52
51:1:1357:C:H42	51:1:1374:G:H1	1.57	0.52
51:1:1864:U:H5''	51:1:2410:G:O2'	2.10	0.52
51:1:1903:G:C2	51:1:1904:G:C8	2.98	0.52
51:1:2061:G:H8	51:1:2501:C:H4'	1.73	0.52
53:3:1274:A:C2'	53:3:1275:A:H5''	2.40	0.52
58:B1:390:LEU:N	58:B1:390:LEU:CD1	2.73	0.52
58:B1:633:ALA:HB2	59:B2:808:ASN:N	2.19	0.52
58:B1:832:LYS:HB3	58:B1:1242:ARG:NH1	2.24	0.52
10:J:133:ILE:HD11	53:3:1079:G:H5'	1.92	0.52
14:N:114:LYS:HE3	53:3:1188:A:P	2.49	0.52
27:b:36:ASN:HB3	27:b:38:LYS:HG2	1.91	0.52
29:d:133:LEU:O	29:d:136:GLN:NE2	2.40	0.52
34:j:135:GLN:HE22	51:1:7:G:H1'	1.75	0.52
39:o:29:HIS:HB3	39:o:36:TYR:HD2	1.74	0.52
51:1:745:G:H2'	51:1:746:U:O4'	2.09	0.52
51:1:1655:A:H2'	51:1:1656:C:H5'	1.91	0.52
51:1:1767:G:O5'	51:1:1767:G:H8	1.93	0.52
53:3:19:A:H1'	53:3:864:A:C2	2.45	0.52
53:3:90:C:H2'	53:3:91:U:C6	2.45	0.52
58:B1:68:TYR:CA	58:B1:75:TYR:HE2	2.22	0.52
58:B1:144:TYR:CE1	58:B1:162:GLU:CD	2.88	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:975:ILE:HD11	58:B1:1003:LEU:HD11	1.91	0.52
59:B2:246:LEU:HB3	59:B2:269:ILE:HD13	1.91	0.52
59:B2:628:HIS:HB3	59:B2:647:ARG:HH21	1.74	0.52
62:NG:161:SER:HA	62:NG:170:PRO:HA	1.92	0.52
65:a:63:THR:HG21	65:a:195:ALA:HB1	1.90	0.52
66:0:53:MET:O	66:0:57:GLN:NE2	2.42	0.52
14:N:122:ARG:NH1	53:3:1350:A:OP1	2.43	0.52
16:P:17:ASP:N	16:P:17:ASP:OD1	2.42	0.52
39:o:110:ALA:HB1	39:o:115:LEU:HD12	1.92	0.52
41:q:57:ARG:NH2	51:1:1154:G:OP2	2.43	0.52
51:1:2402:U:O2'	51:1:2403:C:H5''	2.09	0.52
53:3:174:A:C2'	53:3:175:C:H5'	2.40	0.52
53:3:265:G:H2'	53:3:267:C:H5	1.75	0.52
53:3:977:A:H2'	53:3:977:A:N3	2.25	0.52
65:a:183:ASP:OD1	65:a:183:ASP:N	2.43	0.52
66:0:217:GLU:O	66:0:220:GLN:NE2	2.41	0.52
66:0:473:MET:HA	66:0:477:PHE:HB2	1.91	0.52
17:Q:28:GLN:HB2	53:3:363:A:H1'	1.92	0.52
17:Q:45:ASN:OD1	17:Q:45:ASN:N	2.44	0.52
21:U:55:ASP:OD1	21:U:55:ASP:N	2.41	0.52
30:e:32:LYS:O	30:e:156:THR:OG1	2.27	0.52
32:g:94:ILE:HD12	32:g:99:ILE:HD13	1.91	0.52
51:1:277:G:H4'	51:1:278:A:C8	2.44	0.52
51:1:958:U:H2'	52:2:89:U:C1'	2.39	0.52
51:1:1505:A:H2'	51:1:1506:U:O4'	2.10	0.52
51:1:1954:G:H1	51:1:1986:C:H5''	1.75	0.52
51:1:2022:U:O2'	51:1:2617:U:H5'	2.10	0.52
53:3:1496:C:H2'	53:3:1497:G:O4'	2.10	0.52
58:B1:39:LYS:O	58:B1:273:ILE:HG23	2.08	0.52
8:H:9:ILE:HG13	8:H:177:LEU:HD21	1.91	0.51
12:L:114:SER:O	12:L:118:ARG:N	2.38	0.51
19:S:7:ALA:HB1	53:3:994:A:O2'	2.09	0.51
51:1:755:U:H2'	51:1:756:A:H8	1.75	0.51
51:1:1187:G:O5'	51:1:1187:G:H8	1.93	0.51
51:1:1409:U:H2'	51:1:1410:G:C8	2.46	0.51
53:3:148:G:H1	53:3:174:A:H61	1.58	0.51
53:3:410:G:H21	53:3:432:A:H62	1.57	0.51
53:3:731:G:O2'	53:3:732:C:H5'	2.10	0.51
53:3:1225:A:H2'	53:3:1225:A:N3	2.25	0.51
58:B1:375:GLU:HG2	59:B2:1245:ALA:O	2.10	0.51
66:0:297:GLY:HA2	66:0:405:ILE:HD13	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:38:VAL:O	8:H:42:LEU:N	2.43	0.51
28:c:59:ARG:O	28:c:59:ARG:NH2	2.37	0.51
28:c:133:THR:OG1	28:c:134:HIS:N	2.38	0.51
36:l:9:ALA:HB3	36:l:12:SER:HB3	1.91	0.51
51:1:526:A:N6	51:1:2626:C:H4'	2.25	0.51
51:1:1394:U:H4'	51:1:1603:A:H4'	1.92	0.51
51:1:1755:A:C2'	51:1:1756:G:H5'	2.40	0.51
51:1:2272:U:H5''	51:1:2273:A:OP1	2.10	0.51
53:3:437:U:H2'	53:3:438:U:H5'	1.91	0.51
53:3:1485:U:O2'	53:3:1486:G:H5'	2.10	0.51
59:B2:974:ARG:HD2	59:B2:1014:LEU:HD21	1.92	0.51
66:0:295:ILE:HG13	66:0:309:ARG:HB2	1.91	0.51
30:e:117:SER:HB3	30:e:177:ARG:HH21	1.76	0.51
34:j:69:ARG:NH1	34:j:90:GLU:OE2	2.38	0.51
42:r:61:ALA:HB1	42:r:96:VAL:HB	1.92	0.51
51:1:532:A:H2'	51:1:532:A:N3	2.24	0.51
51:1:1332:G:N3	51:1:1332:G:H5'	2.25	0.51
51:1:1333:G:H2'	51:1:1334:G:H8	1.75	0.51
51:1:1536:C:H4'	51:1:1537:G:C2	2.44	0.51
51:1:1889:A:H2'	51:1:1890:A:O4'	2.10	0.51
51:1:2660:A:OP1	66:0:675:LYS:HD2	2.10	0.51
53:3:135:C:H2'	53:3:136:C:H5'	1.92	0.51
53:3:574:A:N3	53:3:883:C:H1'	2.25	0.51
53:3:1271:A:H5'	53:3:1314:C:H5''	1.91	0.51
59:B2:524:ILE:HG21	59:B2:708:VAL:HG13	1.92	0.51
2:B:54:ILE:HG13	2:B:56:LYS:H	1.76	0.51
5:E:38:LYS:HG3	5:E:41:ARG:HH22	1.75	0.51
9:I:24:VAL:HG12	53:3:409:U:H5''	1.92	0.51
9:I:160:LEU:HD21	9:I:164:ARG:HH21	1.75	0.51
24:X:35:ARG:HB2	53:3:1320:C:N4	2.25	0.51
51:1:622:G:O2'	51:1:623:C:H5'	2.10	0.51
51:1:1710:G:H2'	51:1:1711:A:H8	1.74	0.51
51:1:2248:C:H3'	51:1:2249:U:C6	2.46	0.51
53:3:49:U:O2'	53:3:50:A:H2'	2.10	0.51
53:3:207:C:C3'	53:3:208:U:H5''	2.40	0.51
53:3:218:U:H2'	53:3:219:U:O4'	2.09	0.51
53:3:884:U:OP2	53:3:884:U:H6	1.92	0.51
53:3:955:U:H2'	53:3:956:U:H6	1.74	0.51
53:3:1251:A:H2'	53:3:1252:A:C8	2.46	0.51
58:B1:99:ARG:HA	58:B1:248:ASP:HB2	1.92	0.51
59:B2:1070:HIS:NE2	59:B2:1114:GLU:OE1	2.36	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:154:ALA:O	10:J:158:LYS:NZ	2.41	0.51
21:U:1:MET:SD	21:U:24:SER:OG	2.64	0.51
32:g:131:SER:OG	32:g:140:ALA:O	2.28	0.51
43:s:40:ASN:OD1	43:s:40:ASN:N	2.40	0.51
51:1:178:G:O2'	51:1:179:C:H5'	2.10	0.51
53:3:302:G:H2'	53:3:303:A:H8	1.74	0.51
53:3:515:G:O2'	53:3:516:U:H5'	2.10	0.51
53:3:1239:A:H5''	53:3:1240:U:C5	2.44	0.51
58:B1:1179:PRO:HD2	58:B1:1184:ASP:HA	1.93	0.51
59:B2:125:GLY:HA2	59:B2:499:SER:HB2	1.92	0.51
59:B2:714:VAL:HB	59:B2:787:PRO:HD2	1.92	0.51
66:0:107:ASP:OD1	66:0:107:ASP:N	2.40	0.51
8:H:67:ILE:N	8:H:101:ASN:O	2.42	0.51
14:N:35:GLU:HA	14:N:39:GLY:HA3	1.92	0.51
38:n:64:ARG:HD3	51:1:2706:A:O2'	2.10	0.51
40:p:93:LYS:HE2	51:1:1754:A:OP1	2.11	0.51
40:p:102:ARG:HH22	51:1:1755:A:P	2.34	0.51
41:q:23:TYR:HD1	51:1:533:G:H5'	1.75	0.51
41:q:24:TYR:OH	51:1:2020:A:O3'	2.25	0.51
51:1:548:G:H2'	51:1:549:G:O4'	2.10	0.51
51:1:1951:U:C2	51:1:1953:A:OP2	2.63	0.51
51:1:2082:A:H2'	51:1:2083:G:O4'	2.10	0.51
51:1:2489:U:H2'	51:1:2490:G:O4'	2.11	0.51
58:B1:290:ILE:HG21	62:NG:93:ILE:O	2.09	0.51
58:B1:902:ASP:HB3	58:B1:905:ARG:HB2	1.93	0.51
66:0:192:ASN:ND2	66:0:203:GLU:OE1	2.43	0.51
1:A:26:SER:OG	30:e:139:GLU:OE2	2.28	0.51
27:b:31:PRO:HG2	27:b:32:LEU:HD12	1.92	0.51
51:1:12:U:H2'	51:1:13:A:H5'	1.91	0.51
51:1:216:A:O2'	51:1:217:A:H5'	2.11	0.51
51:1:1210:G:P	51:1:1212:G:H5'	2.51	0.51
51:1:1410:G:O2'	51:1:1411:U:H5'	2.10	0.51
51:1:1470:A:H61	51:1:1521:G:H1'	1.75	0.51
51:1:2656:U:H2'	51:1:2657:A:H8	1.75	0.51
53:3:379:C:H2'	53:3:380:G:O4'	2.10	0.51
7:G:187:ASP:OD1	7:G:187:ASP:N	2.42	0.51
32:g:22:LYS:HB2	51:1:2094:A:OP1	2.11	0.51
51:1:3:U:H2'	51:1:4:U:C6	2.45	0.51
51:1:44:A:H2'	51:1:45:G:H5'	1.93	0.51
51:1:216:A:H2'	51:1:217:A:O4'	2.11	0.51
51:1:243:U:O2'	51:1:244:A:H5'	2.11	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1268:A:H2'	51:1:1269:A:H8	1.74	0.51
51:1:1550:C:H2'	51:1:1551:A:C8	2.46	0.51
51:1:2616:C:H2'	51:1:2617:U:H6	1.76	0.51
53:3:894:G:H2'	53:3:895:G:H8	1.75	0.51
28:c:177:VAL:HA	28:c:189:VAL:HA	1.93	0.51
29:d:67:ARG:O	51:1:1255:U:H5	1.94	0.51
33:i:4:VAL:HB	51:1:1055:G:OP2	2.10	0.51
39:o:100:HIS:O	39:o:104:GLN:NE2	2.43	0.51
51:1:233:A:H2'	51:1:234:U:H5'	1.92	0.51
51:1:286:U:H2'	51:1:287:G:C8	2.46	0.51
51:1:376:G:H2'	51:1:377:G:H8	1.74	0.51
51:1:1963:U:C2'	51:1:1964:G:H5''	2.41	0.51
51:1:2372:U:H2'	51:1:2373:G:C8	2.46	0.51
51:1:2415:G:H2'	51:1:2416:C:H6	1.75	0.51
52:2:24:G:H4'	52:2:25:U:H5	1.73	0.51
52:2:29:A:H2'	52:2:30:C:O4'	2.11	0.51
53:3:1351:U:H3	53:3:1371:G:H1	1.58	0.51
66:0:194:ASN:OD1	66:0:200:VAL:N	2.44	0.51
13:M:11:THR:OG1	53:3:876:C:H1'	2.10	0.51
13:M:16:GLY:O	13:M:64:TYR:OH	2.28	0.51
14:N:33:SER:OG	14:N:34:LEU:N	2.43	0.51
15:O:8:ILE:HB	15:O:74:VAL:HB	1.91	0.51
15:O:59:LYS:HE3	53:3:972:C:C5'	2.41	0.51
31:f:126:THR:OG1	31:f:127:GLN:N	2.44	0.51
36:l:51:GLU:HG3	36:l:56:PRO:HB3	1.93	0.51
51:1:866:A:H61	51:1:913:U:H1'	1.76	0.51
51:1:1473:G:H1	51:1:1518:C:N4	2.00	0.51
51:1:1599:U:H2'	51:1:1600:C:H6	1.75	0.51
51:1:1917:U:O2'	51:1:1918:A:H5'	2.11	0.51
51:1:2545:G:H2'	51:1:2546:U:O4'	2.11	0.51
53:3:554:A:H2'	53:3:555:U:H5'	1.93	0.51
53:3:678:U:H2'	53:3:679:C:O4'	2.11	0.51
53:3:1105:A:H2'	53:3:1106:G:H8	1.75	0.51
53:3:1421:G:C2'	53:3:1422:G:H4'	2.40	0.51
1:A:8:LYS:O	1:A:27:THR:OG1	2.28	0.50
7:G:53:LEU:HD11	7:G:215:ALA:HB1	1.93	0.50
11:K:92:THR:OG1	11:K:94:HIS:O	2.29	0.50
28:c:27:ILE:HD11	28:c:187:LEU:HD23	1.93	0.50
29:d:1:MET:N	29:d:14:VAL:O	2.35	0.50
31:f:151:ARG:HG3	31:f:160:GLY:HA2	1.92	0.50
33:i:113:ALA:HB2	33:i:121:ILE:HD11	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:403:U:O3'	51:1:404:A:H4'	2.11	0.50
51:1:543:G:H3'	51:1:544:C:H5''	1.92	0.50
51:1:558:U:H2'	51:1:559:G:C8	2.46	0.50
51:1:1794:A:H1'	51:1:1900:A:C2	2.46	0.50
51:1:1977:A:H2'	51:1:1978:A:O4'	2.12	0.50
51:1:2358:A:H2'	51:1:2359:C:O4'	2.11	0.50
51:1:2656:U:H5''	66:0:146:ARG:NH2	2.25	0.50
51:1:2850:A:H2'	51:1:2851:A:O4'	2.10	0.50
53:3:993:G:N3	53:3:993:G:H2'	2.25	0.50
54:4:47:G:OP1	59:B2:1073:LYS:NZ	2.35	0.50
58:B1:275:ARG:HH12	58:B1:278:ARG:NH1	2.09	0.50
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE21	1.68	0.50
58:B1:412:LEU:HD23	58:B1:416:ILE:HG13	1.92	0.50
59:B2:786:GLY:N	59:B2:789:THR:OG1	2.41	0.50
9:I:146:GLU:HA	9:I:149:LYS:HE2	1.91	0.50
18:R:89:ARG:HB3	18:R:96:VAL:HG22	1.93	0.50
29:d:58:LYS:HE2	51:1:676:A:OP1	2.11	0.50
35:k:71:ARG:HG3	35:k:77:ILE:HD11	1.92	0.50
38:n:107:ASN:HD22	51:1:2009:A:H4'	1.75	0.50
44:t:55:VAL:O	44:t:88:LYS:NZ	2.37	0.50
51:1:1783:A:N6	51:1:2587:A:N3	2.59	0.50
51:1:2372:U:H2'	51:1:2373:G:H8	1.77	0.50
53:3:945:G:H2'	53:3:945:G:N3	2.27	0.50
53:3:1400:C:N4	64:6:34:C:H1'	2.26	0.50
55:8:13:DT:OP2	58:B1:791:ALA:CB	2.59	0.50
66:0:499:THR:HG23	66:0:500:ASP:N	2.23	0.50
19:S:78:LEU:HD13	19:S:82:LYS:HB3	1.92	0.50
48:x:14:GLY:HA3	48:x:28:PHE:HE1	1.76	0.50
48:x:57:VAL:O	48:x:61:LYS:NZ	2.44	0.50
51:1:402:A:H2'	51:1:403:U:O4'	2.12	0.50
51:1:1042:G:H2'	51:1:1043:C:C6	2.46	0.50
51:1:1439:A:H2'	51:1:1440:U:H5'	1.94	0.50
51:1:1597:A:H4'	51:1:1598:A:H8	1.76	0.50
51:1:1810:A:H2'	51:1:1811:G:O4'	2.12	0.50
51:1:2549:G:H2'	51:1:2550:G:H8	1.76	0.50
53:3:793:U:O2	53:3:1516:G:H4'	2.11	0.50
53:3:1230:C:H5'	64:6:30:G:H5''	1.93	0.50
53:3:1516:G:H2'	53:3:1518:A:OP2	2.10	0.50
58:B1:215:LYS:HA	58:B1:218:THR:HG22	1.92	0.50
58:B1:683:ILE:HD12	58:B1:754:ILE:HG21	1.93	0.50
59:B2:400:VAL:HG21	59:B2:452:ARG:HE	1.76	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:0:70:ALA:HB3	66:0:84:ILE:HB	1.94	0.50
26:Z:16:ARG:HG3	26:Z:19:LYS:HB2	1.93	0.50
44:t:61:LEU:HD21	44:t:82:LYS:HD2	1.92	0.50
51:1:375:G:C2'	51:1:376:G:H5'	2.42	0.50
51:1:838:C:H2'	51:1:839:U:H6	1.75	0.50
51:1:839:U:H2'	51:1:840:C:C6	2.47	0.50
51:1:990:A:N6	51:1:1186:G:H1'	2.27	0.50
51:1:1040:A:H2'	51:1:1041:G:C8	2.47	0.50
53:3:162:A:C2'	53:3:163:C:H5'	2.42	0.50
53:3:1271:A:H4'	53:3:1314:C:OP1	2.11	0.50
58:B1:421:VAL:O	58:B1:436:ALA:HA	2.12	0.50
66:0:490:TYR:HB2	66:0:569:TYR:CD1	2.46	0.50
9:I:173:ASP:OD1	9:I:173:ASP:N	2.44	0.50
29:d:195:GLN:HE22	29:d:199:MET:HE2	1.77	0.50
33:i:30:GLN:HG3	33:i:60:VAL:HG11	1.93	0.50
53:3:284:C:O2'	53:3:285:C:H5'	2.11	0.50
53:3:559:A:H4'	53:3:560:A:H3'	1.94	0.50
53:3:599:C:H2'	53:3:600:A:H8	1.77	0.50
58:B1:395:LYS:NZ	58:B1:399:LYS:CD	2.74	0.50
66:0:105:VAL:HG23	66:0:106:LEU:HD12	1.93	0.50
66:0:419:ALA:HA	66:0:457:ILE:HA	1.93	0.50
11:K:68:GLN:NE2	53:3:738:C:O3'	2.44	0.50
25:Y:4:LYS:HB3	25:Y:6:ALA:H	1.76	0.50
31:f:171:LYS:NZ	51:1:2529:G:OP2	2.40	0.50
40:p:28:LYS:HD3	40:p:82:SER:HB3	1.93	0.50
41:q:10:ARG:NH1	51:1:1216:G:H5''	2.25	0.50
43:s:42:LYS:HB2	51:1:2010:G:H5''	1.94	0.50
51:1:704:G:H1'	51:1:726:G:N2	2.27	0.50
51:1:801:G:H3'	51:1:802:A:H5'	1.92	0.50
51:1:871:U:H2'	51:1:872:U:C6	2.47	0.50
51:1:2297:A:N1	51:1:2321:U:H5	2.09	0.50
51:1:2417:C:H2'	51:1:2418:A:H8	1.76	0.50
53:3:650:G:H2'	53:3:651:C:C6	2.47	0.50
53:3:953:G:H2'	53:3:954:G:O4'	2.12	0.50
53:3:1017:U:H2'	53:3:1018:G:O4'	2.11	0.50
53:3:1267:C:H2'	53:3:1268:G:O4'	2.11	0.50
58:B1:505:ASP:OD2	59:B2:812:PHE:HA	2.11	0.50
58:B1:972:LYS:HD2	58:B1:1004:ALA:HA	1.93	0.50
58:B1:1371:ARG:HE	58:B1:1372:ARG:NH1	2.10	0.50
59:B2:93:SER:HA	59:B2:128:PRO:HA	1.92	0.50
7:G:210:THR:O	7:G:214:GLY:N	2.40	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:96:ARG:NE	9:I:132:ALA:O	2.44	0.50
12:L:14:ASP:OD1	12:L:43:TYR:OH	2.24	0.50
12:L:92:PRO:C	12:L:95:ARG:HG3	2.36	0.50
12:L:107:ALA:HB1	12:L:115:MET:HE1	1.94	0.50
14:N:26:LYS:HG2	14:N:61:ASP:HB2	1.93	0.50
14:N:118:ARG:NH2	53:3:1366:C:OP1	2.44	0.50
15:O:37:ARG:HG2	15:O:77:VAL:HB	1.93	0.50
17:Q:33:CYS:HA	17:Q:54:VAL:HG22	1.94	0.50
28:c:160:LYS:HD2	51:1:2513:A:OP1	2.12	0.50
30:e:129:MET:HG3	30:e:153:ILE:HB	1.94	0.50
34:j:60:ASP:OD1	34:j:60:ASP:N	2.42	0.50
42:r:76:LYS:HZ1	42:r:85:LYS:HE2	1.76	0.50
45:u:73:ASN:HD22	45:u:76:THR:H	1.60	0.50
51:1:1390:U:O2'	51:1:1391:U:H5'	2.11	0.50
51:1:1581:G:H2'	51:1:1582:C:O4'	2.12	0.50
51:1:1867:G:H1	51:1:1874:C:N4	2.08	0.50
51:1:1937:A:C2'	51:1:1938:A:H5'	2.41	0.50
52:2:88:C:H4'	52:2:90:C:N3	2.27	0.50
53:3:903:G:H2'	53:3:904:U:O4'	2.11	0.50
59:B2:18:ARG:HE	59:B2:620:ASN:HA	1.77	0.50
59:B2:255:ILE:HB	59:B2:263:VAL:HB	1.92	0.50
66:0:141:VAL:HB	66:0:266:CYS:HA	1.92	0.50
10:J:37:VAL:HG11	10:J:113:VAL:HA	1.93	0.50
24:X:76:THR:HG21	53:3:1221:G:H4'	1.94	0.50
27:b:24:HIS:CD2	27:b:79:ARG:HH21	2.29	0.50
28:c:12:THR:OG1	28:c:13:ARG:N	2.45	0.50
40:p:102:ARG:NH2	51:1:1755:A:H5'	2.26	0.50
42:r:8:GLY:HA3	42:r:23:GLU:HG3	1.94	0.50
42:r:39:LEU:O	42:r:49:ILE:HG12	2.12	0.50
43:s:16:LYS:HE3	51:1:1266:G:N7	2.27	0.50
47:w:52:ASP:HB2	47:w:54:THR:HG23	1.94	0.50
51:1:198:C:O2'	51:1:199:A:H5'	2.12	0.50
51:1:598:U:H2'	51:1:599:A:H8	1.76	0.50
51:1:2375:G:C2'	51:1:2376:A:H5''	2.38	0.50
51:1:2416:C:H2'	51:1:2417:C:C6	2.47	0.50
53:3:128:G:H2'	53:3:129:A:H8	1.76	0.50
53:3:636:U:H2'	53:3:637:C:C6	2.47	0.50
53:3:812:G:OP1	53:3:903:G:H1'	2.12	0.50
53:3:1327:C:O2'	53:3:1328:C:H5'	2.12	0.50
58:B1:437:PHE:HZ	58:B1:453:VAL:HG11	1.76	0.50
4:D:13:ASN:HB3	51:1:125:A:H4'	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:18:LEU:HD21	9:I:63:ILE:HA	1.92	0.50
21:U:5:ARG:NH1	21:U:26:ASN:O	2.43	0.50
30:e:65:LEU:HD22	52:2:42:C:C5	2.47	0.50
31:f:2:ARG:HD3	51:1:2751:G:OP2	2.12	0.50
34:j:108:MET:HB3	51:1:1006:C:O2'	2.11	0.50
42:r:80:ARG:HD3	51:1:566:U:C5	2.47	0.50
51:1:737:C:H2'	51:1:738:G:C8	2.47	0.50
51:1:1934:C:H2'	51:1:1935:G:O4'	2.12	0.50
52:2:87:U:H5''	52:2:88:C:H5	1.74	0.50
53:3:439:U:H2'	53:3:440:C:O4'	2.12	0.50
53:3:1012:A:H5'	53:3:1012:A:H8	1.77	0.50
53:3:1049:U:H4'	53:3:1050:G:H5''	1.94	0.50
59:B2:400:VAL:HG11	59:B2:452:ARG:HD2	1.93	0.50
59:B2:411:ARG:NH2	59:B2:427:ASP:OD2	2.44	0.50
41:q:10:ARG:HH11	51:1:1216:G:H5''	1.77	0.49
51:1:45:G:C5'	51:1:46:G:H5'	2.25	0.49
51:1:594:U:H2'	51:1:595:C:H6	1.77	0.49
53:3:62:U:H2'	53:3:63:C:C6	2.46	0.49
53:3:184:G:H4'	53:3:224:U:O3'	2.12	0.49
58:B1:749:LYS:HB3	58:B1:755:ILE:HD11	1.93	0.49
66:0:73:SER:O	66:0:73:SER:OG	2.29	0.49
66:0:169:LEU:HD11	66:0:186:VAL:HG13	1.94	0.49
67:h:6:5OH:N	67:h:6:5OH:CS	2.75	0.49
5:E:35:LYS:HE2	5:E:39:ARG:HE	1.76	0.49
7:G:71:THR:OG1	7:G:72:LYS:N	2.45	0.49
11:K:17:GLN:O	11:K:21:MET:N	2.44	0.49
14:N:3:ASN:N	14:N:88:GLU:OE1	2.45	0.49
15:O:54:SER:O	19:S:80:ARG:NH2	2.44	0.49
22:V:4:ILE:HD11	22:V:61:ARG:HD3	1.94	0.49
26:Z:27:VAL:HG22	26:Z:31:VAL:HB	1.93	0.49
33:i:9:LYS:HD3	51:1:1060:U:OP2	2.13	0.49
43:s:10:ALA:N	43:s:101:SER:O	2.43	0.49
46:v:58:SER:OG	46:v:59:GLU:OE1	2.30	0.49
51:1:123:G:H2'	51:1:124:G:H8	1.77	0.49
51:1:376:G:H2'	51:1:377:G:C8	2.47	0.49
51:1:1686:C:H2'	51:1:1687:G:O4'	2.12	0.49
51:1:2040:G:H2'	51:1:2041:U:O4'	2.12	0.49
53:3:25:C:H2'	53:3:26:A:H8	1.77	0.49
53:3:162:A:C2	53:3:348:G:H4'	2.47	0.49
53:3:505:G:H2'	53:3:506:G:C8	2.47	0.49
53:3:579:A:H2'	53:3:580:C:C6	2.48	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1339:A:H2'	53:3:1340:A:O4'	2.12	0.49
55:8:3:DC:H2''	55:8:4:DT:C7	2.42	0.49
66:0:603:GLU:O	66:0:607:LYS:NZ	2.41	0.49
66:0:631:VAL:O	66:0:635:LEU:N	2.42	0.49
9:I:131:ILE:HD12	53:3:620:C:C2	2.47	0.49
13:M:89:ASP:OD1	13:M:89:ASP:N	2.37	0.49
14:N:62:LEU:HD12	14:N:64:ILE:HD11	1.92	0.49
14:N:108:ARG:HB3	53:3:1347:G:C8	2.47	0.49
15:O:47:GLU:HG3	53:3:1254:A:OP1	2.12	0.49
19:S:9:GLU:HA	19:S:12:ARG:HE	1.76	0.49
20:T:27:GLN:HE21	20:T:31:LEU:HG	1.77	0.49
41:q:62:ALA:O	41:q:66:ALA:N	2.43	0.49
48:x:2:ARG:CG	48:x:32:LEU:HD12	2.41	0.49
51:1:475:C:H4'	51:1:510:C:H5'	1.93	0.49
51:1:739:A:H8	51:1:739:A:O5'	1.95	0.49
51:1:864:G:O5'	51:1:864:G:H8	1.95	0.49
51:1:1326:U:H2'	51:1:1327:A:H8	1.78	0.49
51:1:1424:G:H2'	51:1:1425:G:O4'	2.12	0.49
51:1:1952:A:H2'	51:1:1953:A:O4'	2.12	0.49
51:1:1984:G:H2'	51:1:1985:C:C6	2.47	0.49
51:1:2549:G:H2'	51:1:2550:G:C8	2.47	0.49
52:2:53:A:C2	52:2:54:G:H1'	2.47	0.49
53:3:7:A:O2'	53:3:8:A:H5'	2.12	0.49
53:3:138:G:H2'	53:3:139:A:C8	2.46	0.49
53:3:803:G:H2'	53:3:804:U:C6	2.47	0.49
53:3:1515:G:H2'	53:3:1516:G:C8	2.46	0.49
59:B2:9:LYS:HG2	59:B2:1171:ARG:HH12	1.77	0.49
9:I:59:LYS:O	9:I:63:ILE:N	2.44	0.49
18:R:24:VAL:HA	53:3:1329:A:H5''	1.94	0.49
35:k:1:MET:HE1	51:1:1664:A:H2	1.77	0.49
42:r:10:LYS:HE2	51:1:994:C:O2'	2.12	0.49
44:t:58:VAL:HG22	44:t:85:VAL:HG22	1.94	0.49
51:1:227:A:O2'	51:1:228:C:H4'	2.12	0.49
51:1:1366:A:H2'	51:1:1367:A:O4'	2.12	0.49
51:1:1620:G:O2'	51:1:1621:U:H5'	2.13	0.49
53:3:570:G:H2'	53:3:571:U:O4'	2.11	0.49
53:3:860:A:H2'	53:3:861:G:O4'	2.13	0.49
53:3:967:C:H2'	53:3:968:A:N7	2.26	0.49
54:4:1:A:H2'	54:4:2:U:H6	1.78	0.49
65:a:46:VAL:HG11	65:a:196:LEU:HD13	1.94	0.49
66:0:128:ARG:HA	66:0:131:ASN:HD22	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:16:THR:OG1	3:C:17:GLY:N	2.44	0.49
9:I:12:ARG:HG3	9:I:37:PRO:HG3	1.94	0.49
14:N:72:SER:O	14:N:76:GLY:N	2.45	0.49
33:i:10:LEU:HD11	51:1:1070:A:C2	2.41	0.49
37:m:18:ARG:O	37:m:97:GLN:NE2	2.46	0.49
47:w:10:ARG:HD2	51:1:2258:C:OP1	2.12	0.49
51:1:341:C:H2'	51:1:342:A:C8	2.46	0.49
51:1:1700:A:H2'	51:1:1701:A:H5'	1.93	0.49
52:2:49:C:H2'	52:2:50:A:C8	2.48	0.49
53:3:23:C:H2'	53:3:24:U:C6	2.48	0.49
53:3:174:A:H2'	53:3:175:C:H5'	1.94	0.49
53:3:666:G:H5'	53:3:725:G:N2	2.27	0.49
53:3:1231:G:H2'	53:3:1232:U:C6	2.47	0.49
53:3:1382:C:H3'	53:3:1382:C:O2	2.13	0.49
66:0:92:HIS:CD2	66:0:464:LEU:HD21	2.47	0.49
1:A:36:VAL:HG13	1:A:40:CYS:HB3	1.94	0.49
10:J:79:THR:OG1	10:J:80:LEU:N	2.44	0.49
36:l:46:VAL:HG21	51:1:832:U:H4'	1.94	0.49
36:l:65:GLY:HA2	51:1:631:A:O2'	2.12	0.49
37:m:12:MET:H	37:m:72:PRO:HG2	1.77	0.49
41:q:65:ASN:HD21	41:q:69:ARG:HH11	1.61	0.49
48:x:7:THR:HG23	48:x:9:LYS:HG3	1.95	0.49
51:1:90:U:H1'	51:1:456:C:H42	1.77	0.49
51:1:108:G:O2'	51:1:109:C:H5'	2.11	0.49
51:1:210:C:H2'	51:1:211:C:C6	2.48	0.49
51:1:306:U:H3	51:1:310:A:H62	1.61	0.49
51:1:1289:C:O2'	51:1:1330:C:H4'	2.12	0.49
51:1:1963:U:H2'	51:1:1964:G:H5''	1.93	0.49
51:1:2235:G:H2'	51:1:2236:U:O4'	2.12	0.49
53:3:269:C:H2'	53:3:270:A:H8	1.77	0.49
59:B2:232:ILE:HG12	59:B2:237:LEU:HG	1.94	0.49
59:B2:529:ARG:HH11	59:B2:572:ILE:HG22	1.77	0.49
59:B2:533:LEU:HD13	59:B2:540:ARG:HH21	1.77	0.49
66:0:530:ASN:ND2	66:0:532:LYS:O	2.45	0.49
6:F:1:MET:CG	51:1:2742:G:H5'	2.43	0.49
12:L:34:LYS:HE2	53:3:1290:G:H4'	1.95	0.49
19:S:1:ALA:N	19:S:66:THR:O	2.45	0.49
20:T:88:ARG:HH22	51:1:715:A:H5''	1.76	0.49
43:s:72:THR:OG1	43:s:73:LYS:N	2.45	0.49
48:x:1:SER:HG	51:1:1365:A:H5'	1.77	0.49
51:1:458:G:N2	51:1:469:G:H2'	2.27	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1378:A:H1'	51:1:1379:U:C5	2.48	0.49
51:1:1937:A:C3'	51:1:1938:A:H5'	2.41	0.49
51:1:2194:U:H2'	51:1:2195:U:H6	1.77	0.49
51:1:2638:G:H1'	51:1:2778:A:H61	1.78	0.49
51:1:2807:U:H3	51:1:2891:U:H3	1.61	0.49
59:B2:857:VAL:HG13	59:B2:919:ARG:HH21	1.78	0.49
66:0:659:PRO:HB2	66:0:662:GLU:HB2	1.93	0.49
3:C:35:LEU:CD2	51:1:2286:G:H22	2.26	0.49
14:N:87:MET:HA	14:N:90:ASP:HB3	1.94	0.49
31:f:91:VAL:CG2	51:1:2657:A:H4'	2.43	0.49
35:k:65:THR:HG23	35:k:68:GLY:H	1.78	0.49
38:n:68:ALA:HA	51:1:2707:U:O2'	2.13	0.49
44:t:34:VAL:HG11	44:t:43:ILE:HD13	1.93	0.49
51:1:664:G:O2'	51:1:940:G:H5''	2.12	0.49
51:1:1130:U:H5	51:1:2026:U:P	2.35	0.49
51:1:1528:A:H2'	51:1:1529:G:C5'	2.40	0.49
51:1:1658:C:O5'	51:1:1658:C:H6	1.95	0.49
51:1:2716:C:O2'	51:1:2717:C:H5'	2.13	0.49
53:3:153:C:C2'	53:3:154:U:H5''	2.43	0.49
53:3:423:G:C2	53:3:424:G:H1'	2.48	0.49
53:3:955:U:H2'	53:3:956:U:C6	2.48	0.49
58:B1:145:VAL:HG12	58:B1:184:ALA:HB1	1.94	0.49
58:B1:255:LEU:HD23	58:B1:261:ALA:HB2	1.95	0.49
58:B1:550:VAL:O	58:B1:569:LEU:HA	2.13	0.49
59:B2:554:HIS:HD2	59:B2:558:VAL:HB	1.77	0.49
14:N:8:THR:H	14:N:84:ARG:HB2	1.78	0.49
17:Q:58:ASN:OD1	17:Q:58:ASN:N	2.46	0.49
23:W:49:LYS:NZ	53:3:836:G:OP1	2.45	0.49
25:Y:54:GLN:HE22	53:3:193:C:H1'	1.75	0.49
30:e:132:ARG:NH1	30:e:148:VAL:O	2.45	0.49
32:g:50:ARG:O	32:g:55:GLU:N	2.38	0.49
32:g:80:ILE:HG13	32:g:102:ALA:HB1	1.94	0.49
37:m:61:GLY:HA3	37:m:105:MET:HE1	1.95	0.49
45:u:5:ARG:HH11	51:1:84:A:H5''	1.77	0.49
47:w:65:PHE:CD2	51:1:857:G:H5'	2.48	0.49
51:1:1005:C:H2'	51:1:1006:C:H6	1.77	0.49
51:1:1036:G:H1	51:1:1119:U:H3	1.60	0.49
51:1:1595:C:H2'	51:1:1596:A:C8	2.48	0.49
51:1:2262:U:H2'	51:1:2263:C:H6	1.71	0.49
51:1:2786:U:H2'	51:1:2787:C:C6	2.48	0.49
53:3:454:G:H2'	53:3:455:G:H8	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1354:U:H2'	53:3:1355:G:H8	1.78	0.49
59:B2:836:LEU:HD13	59:B2:1054:LEU:HD13	1.95	0.49
63:5:51:U:H2'	63:5:52:G:C8	2.48	0.49
31:f:8:VAL:O	31:f:49:LEU:N	2.43	0.49
51:1:157:C:H2'	51:1:158:U:O4'	2.13	0.49
51:1:2247:A:H2'	51:1:2248:C:O4'	2.13	0.49
51:1:2803:G:H2'	51:1:2804:U:C6	2.48	0.49
53:3:17:U:H2'	53:3:18:C:C6	2.48	0.49
53:3:1253:G:H2'	53:3:1254:A:H8	1.78	0.49
9:I:32:LYS:HB3	53:3:429:U:OP2	2.12	0.48
27:b:48:ILE:HG22	51:1:779:U:OP2	2.13	0.48
27:b:155:ARG:CZ	51:1:1818:U:H5	2.26	0.48
29:d:2:GLU:HA	29:d:13:THR:HA	1.95	0.48
30:e:21:TYR:OH	30:e:164:GLU:OE1	2.31	0.48
34:j:47:HIS:CG	51:1:536:G:H21	2.31	0.48
51:1:937:C:H2'	51:1:938:G:H8	1.78	0.48
51:1:1178:C:H2'	51:1:1179:G:C8	2.48	0.48
51:1:2600:A:H2'	51:1:2601:C:C6	2.48	0.48
52:2:3:C:C3'	52:2:4:C:H5''	2.42	0.48
53:3:513:C:H2'	53:3:514:C:O4'	2.13	0.48
53:3:1349:A:H2'	53:3:1350:A:O4'	2.13	0.48
7:G:100:LEU:HD11	7:G:160:LEU:HD13	1.95	0.48
9:I:12:ARG:NH1	9:I:36:ALA:O	2.46	0.48
11:K:91:ARG:O	11:K:93:LYS:NZ	2.39	0.48
12:L:78:ARG:NH1	12:L:82:SER:O	2.46	0.48
33:i:75:ALA:HA	33:i:78:LEU:HB2	1.95	0.48
41:q:24:TYR:N	51:1:533:G:OP1	2.38	0.48
51:1:1893:C:H2'	51:1:1894:C:O4'	2.13	0.48
51:1:1999:C:O2'	51:1:2000:C:H5'	2.12	0.48
51:1:2339:C:H2'	51:1:2340:A:C8	2.45	0.48
51:1:2364:C:H2'	51:1:2365:G:O4'	2.13	0.48
53:3:83:C:O2'	53:3:84:U:H3'	2.13	0.48
53:3:1424:U:H3	53:3:1476:A:N6	2.05	0.48
57:A1:100:LEU:HB2	57:A1:144:ILE:HG23	1.95	0.48
58:B1:124:ILE:HG23	58:B1:128:LEU:HD12	1.94	0.48
41:q:84:LYS:HB3	41:q:115:ALA:HB1	1.94	0.48
42:r:4:VAL:HG22	42:r:13:ARG:HA	1.95	0.48
51:1:387:U:H4'	51:1:388:G:O4'	2.14	0.48
51:1:532:A:N1	51:1:2020:A:H1'	2.27	0.48
51:1:1807:G:H2'	51:1:1808:A:H5'	1.95	0.48
51:1:1810:A:H2'	51:1:1811:G:H5'	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:363:LEU:HB3	59:B2:381:ALA:HB1	1.96	0.48
66:0:390:ASP:OD1	66:0:390:ASP:N	2.44	0.48
66:0:501:VAL:HG11	66:0:604:GLY:CA	2.43	0.48
15:O:15:HIS:HA	15:O:18:ILE:HG22	1.95	0.48
17:Q:36:VAL:HG13	17:Q:73:LEU:HD11	1.96	0.48
17:Q:76:HIS:O	66:0:425:LYS:NZ	2.45	0.48
19:S:19:TYR:HB3	19:S:23:ARG:HH21	1.77	0.48
19:S:96:LYS:HZ3	19:S:97:LYS:H	1.61	0.48
27:b:59:GLN:NE2	51:1:1567:G:OP1	2.46	0.48
37:m:28:PHE:N	37:m:104:GLU:OE1	2.44	0.48
51:1:153:U:O2'	51:1:154:U:H5'	2.13	0.48
51:1:445:C:O2	51:1:450:G:H1'	2.14	0.48
51:1:999:U:H5''	51:1:1154:G:O6	2.13	0.48
51:1:1182:G:H2'	51:1:1183:U:C6	2.48	0.48
51:1:1219:U:H2'	51:1:1220:G:H8	1.78	0.48
51:1:2810:A:H62	51:1:2890:G:N2	2.11	0.48
51:1:2834:G:H2'	51:1:2879:A:N6	2.29	0.48
57:A1:182:ARG:O	57:A1:205:MET:HA	2.14	0.48
64:6:26:G:H3'	64:6:27:U:C5'	2.42	0.48
64:6:36:U:H2'	64:6:37:A:C8	2.48	0.48
5:E:32:LEU:HD12	5:E:32:LEU:HA	1.73	0.48
14:N:113:LYS:NZ	53:3:1368:A:OP2	2.39	0.48
27:b:146:LYS:HB2	27:b:149:LYS:HB2	1.94	0.48
44:t:36:LYS:NZ	44:t:79:ASP:OD1	2.38	0.48
51:1:445:C:H2'	51:1:446:G:H5'	1.94	0.48
51:1:459:U:H2'	51:1:460:A:O4'	2.13	0.48
51:1:1657:U:H2'	51:1:1658:C:C6	2.48	0.48
51:1:2556:C:H2'	51:1:2557:G:H5'	1.96	0.48
53:3:701:U:O4'	53:3:703:G:H1'	2.14	0.48
53:3:1414:U:H2'	53:3:1415:G:H8	1.79	0.48
56:9:12:DC:H3'	58:B1:47:ARG:HH12	1.78	0.48
58:B1:102:MET:HG2	58:B1:246:PRO:HD3	1.95	0.48
65:a:43:ASP:OD1	65:a:174:THR:OG1	2.32	0.48
66:0:157:GLN:HE22	66:0:161:ARG:HE	1.61	0.48
1:A:26:SER:OG	1:A:27:THR:N	2.47	0.48
24:X:32:THR:O	24:X:56:HIS:NE2	2.45	0.48
24:X:76:THR:HG21	53:3:1221:G:O2'	2.13	0.48
37:m:53:MET:HE3	37:m:119:LEU:HB3	1.94	0.48
45:u:48:VAL:HG22	45:u:50:ALA:H	1.79	0.48
51:1:175:G:H2'	51:1:176:A:C8	2.49	0.48
51:1:404:A:H2	51:1:421:C:N3	2.11	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:511:U:H2'	51:1:512:G:H5'	1.95	0.48
51:1:821:A:H5''	51:1:822:G:C8	2.49	0.48
51:1:1258:U:H2'	51:1:1259:G:C8	2.48	0.48
53:3:483:C:H3'	53:3:484:G:H5'	1.94	0.48
53:3:714:G:H2'	53:3:715:A:C8	2.48	0.48
53:3:770:C:O2'	53:3:771:G:H5'	2.12	0.48
58:B1:220:ARG:HG2	58:B1:220:ARG:NH1	2.25	0.48
59:B2:1314:GLN:HB2	60:W0:28:ARG:HH12	1.79	0.48
66:0:530:ASN:HD22	66:0:532:LYS:HB2	1.79	0.48
4:D:3:ARG:O	4:D:6:GLN:NE2	2.40	0.48
9:I:7:LYS:HB3	9:I:20:LEU:HG	1.95	0.48
29:d:23:PHE:H	29:d:114:ARG:HH22	1.61	0.48
29:d:67:ARG:NH2	51:1:1257:C:H5''	2.29	0.48
34:j:7:LYS:HE2	51:1:539:G:H5'	1.95	0.48
35:k:48:PRO:HB3	53:3:1422:G:OP1	2.13	0.48
40:p:1:SER:N	51:1:2876:G:OP1	2.44	0.48
50:z:30:ARG:HG2	50:z:33:HIS:HB2	1.94	0.48
51:1:93:G:O2'	51:1:94:A:H5'	2.12	0.48
51:1:441:U:H2'	51:1:442:G:C8	2.49	0.48
51:1:1225:G:O2'	51:1:1226:A:H5'	2.13	0.48
51:1:2314:A:H2'	51:1:2315:G:C8	2.48	0.48
53:3:554:A:C2'	53:3:555:U:H5'	2.44	0.48
53:3:1251:A:H2'	53:3:1252:A:H8	1.79	0.48
53:3:1308:U:H2'	53:3:1309:G:C8	2.49	0.48
53:3:1490:U:H2'	53:3:1491:G:O4'	2.14	0.48
58:B1:99:ARG:NH1	58:B1:99:ARG:CG	2.76	0.48
37:m:65:ILE:HG22	37:m:67:VAL:H	1.79	0.48
37:m:111:GLU:HA	37:m:114:ARG:HB3	1.96	0.48
48:x:4:CYS:SG	48:x:5:GLN:N	2.87	0.48
51:1:1018:U:H2'	51:1:1019:U:O4'	2.13	0.48
51:1:2654:A:H8	51:1:2654:A:OP1	1.97	0.48
53:3:483:C:C3'	53:3:484:G:H5'	2.44	0.48
53:3:865:A:H8	53:3:865:A:O5'	1.96	0.48
57:A1:18:GLN:HA	57:A1:24:ALA:HA	1.94	0.48
59:B2:207:THR:OG1	59:B2:354:ASP:OD2	2.32	0.48
66:0:99:VAL:HG11	66:0:126:VAL:HG12	1.95	0.48
20:T:19:ASN:HB2	53:3:750:C:C4'	2.43	0.48
22:V:11:VAL:HA	22:V:22:VAL:HA	1.95	0.48
23:W:32:ILE:HD12	23:W:36:GLY:HA2	1.95	0.48
28:c:8:LYS:HB2	28:c:201:LEU:HD11	1.96	0.48
28:c:134:HIS:CD2	51:1:1675:C:H42	2.32	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:k:65:THR:OG1	35:k:66:LYS:N	2.44	0.48
51:1:80:G:H2'	51:1:81:G:C8	2.49	0.48
51:1:166:U:H2'	51:1:167:A:H8	1.78	0.48
51:1:319:G:H2'	51:1:320:A:O4'	2.13	0.48
51:1:443:A:H2	51:1:1246:A:H1'	1.78	0.48
51:1:1103:A:H2'	51:1:1103:A:N3	2.29	0.48
51:1:1710:G:H2'	51:1:1711:A:C8	2.49	0.48
51:1:2298:A:H2'	51:1:2299:U:O4'	2.13	0.48
51:1:2828:G:O2'	51:1:2829:A:H5'	2.13	0.48
53:3:193:C:H2'	53:3:194:C:C5	2.48	0.48
58:B1:103:GLY:H	58:B1:244:VAL:HG22	1.79	0.48
58:B1:833:GLU:N	58:B1:1242:ARG:HH12	2.12	0.48
58:B1:1261:LEU:HD12	58:B1:1304:ARG:HH21	1.78	0.48
59:B2:732:ILE:HD11	59:B2:769:PRO:HB3	1.95	0.48
10:J:87:VAL:HA	10:J:92:ARG:HA	1.96	0.48
19:S:12:ARG:HH22	19:S:60:ARG:H	1.61	0.48
21:U:8:ARG:NH1	53:3:391:G:H5''	2.29	0.48
22:V:56:ASP:HB3	22:V:80:LYS:HA	1.94	0.48
45:u:8:ASP:O	45:u:23:LYS:NZ	2.45	0.48
51:1:189:G:N2	51:1:206:U:C5	2.82	0.48
51:1:1343:G:N3	51:1:1343:G:H2'	2.28	0.48
51:1:1414:C:H2'	51:1:1415:U:H5'	1.95	0.48
51:1:1463:C:H2'	51:1:1464:G:C8	2.48	0.48
51:1:1993:U:H2'	51:1:1994:C:O4'	2.14	0.48
51:1:2276:G:C2'	51:1:2277:G:H5'	2.44	0.48
51:1:2531:A:H2'	51:1:2532:G:H5'	1.95	0.48
52:2:45:A:H2'	52:2:46:A:O4'	2.13	0.48
53:3:27:G:H2'	53:3:28:A:C8	2.49	0.48
53:3:316:C:H2'	53:3:317:U:H6	1.79	0.48
57:A2:102:LEU:HD12	57:A2:115:ILE:HG12	1.96	0.48
59:B2:565:GLU:HA	59:B2:569:ILE:HG12	1.95	0.48
62:NG:161:SER:CA	62:NG:170:PRO:HA	2.43	0.48
9:I:37:PRO:HD2	9:I:41:GLY:HA3	1.96	0.47
10:J:23:THR:HG21	53:3:15:G:N3	2.29	0.47
10:J:24:VAL:HG13	10:J:26:GLY:H	1.79	0.47
33:i:9:LYS:HZ3	51:1:1059:G:H5'	1.79	0.47
37:m:22:GLN:HE21	51:1:864:G:P	2.36	0.47
38:n:34:ILE:HA	51:1:1279:G:OP1	2.13	0.47
51:1:1414:C:H42	51:1:1588:G:H1	1.62	0.47
51:1:2367:G:O2'	51:1:2368:C:H5'	2.14	0.47
51:1:2521:C:H42	51:1:2544:G:H1	1.61	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:129:A:O2'	53:3:130:A:H5''	2.13	0.47
53:3:563:A:H5'	53:3:566:G:C2	2.49	0.47
53:3:1274:A:H2'	53:3:1275:A:H5''	1.96	0.47
58:B1:809:VAL:HG21	58:B1:909:ILE:HG12	1.95	0.47
59:B2:1286:THR:O	59:B2:1290:MET:HB2	2.14	0.47
66:0:330:VAL:HG11	66:0:386:ILE:HD11	1.96	0.47
66:0:498:VAL:HG22	66:0:499:THR:H	1.79	0.47
3:C:5:ARG:NH2	3:C:23:THR:O	2.48	0.47
4:D:24:THR:HG23	4:D:27:GLY:H	1.78	0.47
20:T:74:VAL:HA	20:T:77:TYR:HB3	1.96	0.47
25:Y:34:VAL:HG22	25:Y:49:ALA:HB1	1.95	0.47
27:b:15:VAL:HB	27:b:205:GLY:HA3	1.95	0.47
36:l:41:ARG:HG2	51:1:806:C:H41	1.78	0.47
49:y:43:LEU:HD21	49:y:47:ARG:HH11	1.79	0.47
51:1:881:G:H1	51:1:895:U:H3	1.61	0.47
51:1:1924:C:H3'	51:1:1925:C:C5	2.49	0.47
51:1:2884:U:O2	51:1:2884:U:H3'	2.14	0.47
53:3:92:U:H2'	53:3:93:U:H5'	1.96	0.47
53:3:792:A:H4'	53:3:793:U:H5''	1.95	0.47
53:3:1015:G:H2'	53:3:1016:A:O4'	2.14	0.47
58:B1:968:ASN:HA	58:B1:1117:SER:HB2	1.96	0.47
58:B1:1150:PRO:HG3	58:B1:1214:PRO:HB2	1.97	0.47
66:0:22:GLY:N	69:0:801:GDP:O1B	2.48	0.47
66:0:422:PRO:HG3	66:0:428:GLN:HB2	1.96	0.47
34:j:49:ASP:N	34:j:49:ASP:OD1	2.39	0.47
34:j:116:ARG:HH22	51:1:528:A:H8	1.60	0.47
35:k:89:ASN:OD1	35:k:89:ASN:N	2.45	0.47
37:m:22:GLN:NE2	51:1:864:G:OP1	2.47	0.47
51:1:367:G:H2'	51:1:368:A:O4'	2.14	0.47
51:1:1095:A:C8	66:0:632:ILE:HD11	2.50	0.47
51:1:1680:U:H2'	51:1:1681:G:C5'	2.40	0.47
51:1:1810:A:C2'	51:1:1811:G:H5'	2.44	0.47
51:1:2143:C:H3'	51:1:2144:G:C8	2.50	0.47
51:1:2257:U:O2'	51:1:2258:C:H5'	2.14	0.47
51:1:2515:C:O2'	51:1:2516:A:H5'	2.15	0.47
51:1:2588:G:C6	51:1:2607:G:C2	3.02	0.47
51:1:2721:A:H2'	51:1:2722:G:O4'	2.14	0.47
53:3:153:C:H2'	53:3:154:U:H5''	1.95	0.47
53:3:840:C:C2'	53:3:841:C:H5''	2.41	0.47
53:3:1465:A:H2'	53:3:1466:C:C6	2.48	0.47
58:B1:115:TRP:O	58:B1:1333:THR:HG21	2.13	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:0:319:ALA:HB3	66:0:397:LEU:HB2	1.96	0.47
5:E:57:VAL:O	5:E:61:LEU:N	2.41	0.47
8:H:30:ASP:OD1	8:H:30:ASP:N	2.47	0.47
12:L:91:ARG:HG2	12:L:91:ARG:HH11	1.78	0.47
29:d:112:LEU:O	29:d:117:ARG:N	2.43	0.47
29:d:178:VAL:HA	29:d:181:ILE:HG22	1.95	0.47
30:e:31:GLU:HG2	30:e:32:LYS:H	1.80	0.47
32:g:71:LYS:HD3	32:g:71:LYS:HA	1.66	0.47
33:i:65:SER:OG	33:i:66:PHE:N	2.46	0.47
36:l:37:GLY:O	36:l:41:ARG:NH2	2.44	0.47
36:l:43:GLY:N	51:1:671:C:OP1	2.47	0.47
47:w:45:ALA:N	47:w:77:SER:OG	2.42	0.47
51:1:118:A:H5'	51:1:119:A:H8	1.79	0.47
51:1:514:A:N3	51:1:581:C:O2'	2.45	0.47
51:1:739:A:H1'	51:1:740:C:H5	1.79	0.47
51:1:833:A:H2'	51:1:834:G:H8	1.78	0.47
51:1:858:G:H5'	51:1:859:G:OP2	2.14	0.47
51:1:1265:A:N6	51:1:2013:A:H5''	2.27	0.47
52:2:30:C:H2'	52:2:31:C:H5'	1.95	0.47
53:3:631:C:H5''	53:3:632:U:O4'	2.15	0.47
53:3:1000:A:H2'	53:3:1001:C:O4'	2.15	0.47
53:3:1268:G:H21	53:3:1327:C:H1'	1.79	0.47
55:8:14:DC:H2'	55:8:15:DC:C6	2.48	0.47
55:8:14:DC:H2'	55:8:15:DC:H6	1.79	0.47
58:B1:29:MET:HG2	59:B2:1336:ASN:ND2	2.29	0.47
58:B1:395:LYS:HE3	58:B1:395:LYS:HB3	1.45	0.47
58:B1:1027:VAL:HB	58:B1:1121:LEU:HB2	1.95	0.47
58:B1:1146:GLU:OE2	58:B1:1310:THR:HG22	2.14	0.47
59:B2:1311:GLY:O	60:W0:31:GLN:NE2	2.47	0.47
3:C:8:ILE:HD11	3:C:50:GLU:HB2	1.96	0.47
11:K:86:ARG:NH2	53:3:673:A:O3'	2.48	0.47
13:M:4:ASP:OD2	13:M:76:ARG:NH2	2.47	0.47
18:R:27:THR:HG22	53:3:1328:C:H5''	1.96	0.47
33:i:9:LYS:HZ2	51:1:1059:G:P	2.37	0.47
36:l:30:THR:O	36:l:33:ARG:N	2.46	0.47
36:l:42:SER:O	36:l:42:SER:OG	2.32	0.47
51:1:215:G:O3'	51:1:216:A:H4'	2.15	0.47
51:1:593:U:H2'	51:1:594:U:C6	2.49	0.47
51:1:1085:A:H2'	51:1:1086:A:N7	2.30	0.47
51:1:1900:A:H5'	51:1:1970:A:H5'	1.96	0.47
51:1:2316:G:O2'	51:1:2317:A:H5'	2.13	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2813:A:H2'	51:1:2814:A:H8	1.78	0.47
53:3:230:G:O2'	53:3:231:U:H5'	2.14	0.47
53:3:1093:A:H2'	53:3:1094:G:H5'	1.95	0.47
58:B1:375:GLU:HB3	59:B2:1245:ALA:HB3	1.97	0.47
59:B2:517:GLN:HB3	59:B2:760:ASN:H	1.79	0.47
2:B:2:VAL:O	51:1:2615:U:C4	2.67	0.47
3:C:6:GLU:HG2	3:C:26:LYS:HD3	1.96	0.47
24:X:39:ILE:HD11	24:X:70:LEU:HD23	1.96	0.47
27:b:240:GLY:HA2	51:1:2597:G:H5''	1.97	0.47
43:s:47:VAL:O	43:s:51:LEU:N	2.39	0.47
50:z:18:LYS:O	50:z:22:THR:OG1	2.31	0.47
51:1:145:C:H2'	51:1:146:A:C8	2.49	0.47
51:1:744:U:H5''	51:1:1658:C:H5''	1.96	0.47
51:1:1153:C:H2'	51:1:1154:G:O4'	2.15	0.47
51:1:2475:C:H2'	51:1:2476:A:H5'	1.97	0.47
53:3:1161:C:H2'	53:3:1162:C:H6	1.78	0.47
58:B1:352:ARG:HB2	59:B2:1268:GLN:NE2	2.30	0.47
58:B1:526:VAL:HG12	58:B1:549:LYS:HB2	1.96	0.47
58:B1:891:ASP:OD2	58:B1:1290:ARG:NH2	2.47	0.47
1:A:8:LYS:NZ	1:A:10:GLU:OE1	2.45	0.47
2:B:37:HIS:HB3	2:B:43:THR:HG22	1.97	0.47
7:G:66:ILE:HD11	7:G:161:PHE:HB2	1.96	0.47
8:H:32:LEU:HD21	19:S:78:LEU:HD11	1.97	0.47
8:H:147:GLY:HA2	8:H:170:GLY:HA3	1.97	0.47
10:J:83:PRO:HD3	10:J:97:PRO:HG3	1.96	0.47
13:M:63:LYS:HG2	13:M:70:VAL:HG21	1.95	0.47
15:O:64:GLN:HB3	19:S:98:ALA:HB3	1.96	0.47
18:R:23:GLY:HA2	18:R:68:LEU:HD13	1.97	0.47
19:S:41:TRP:HZ2	24:X:10:ILE:HG22	1.79	0.47
27:b:158:GLY:HA3	51:1:1820:U:C5	2.49	0.47
31:f:107:GLY:O	51:1:2666:C:N4	2.47	0.47
34:j:47:HIS:CD2	51:1:536:G:H21	2.32	0.47
36:l:109:LYS:HB3	51:1:636:G:O6	2.15	0.47
44:t:67:VAL:HG12	44:t:76:ARG:HA	1.96	0.47
44:t:89:GLU:OE1	44:t:91:GLN:NE2	2.48	0.47
46:v:13:GLY:N	52:2:76:G:OP1	2.40	0.47
46:v:21:ARG:HH12	52:2:77:U:H5''	1.80	0.47
47:w:56:PHE:HE2	51:1:2365:G:H5'	1.80	0.47
51:1:1209:U:H2'	51:1:1210:G:H21	1.80	0.47
51:1:1333:G:H2'	51:1:1334:G:C8	2.49	0.47
51:1:1587:G:H2'	51:1:1588:G:C8	2.50	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1943:U:OP1	51:1:1943:U:H6	1.98	0.47
51:1:2682:A:O2'	51:1:2683:C:H5'	2.15	0.47
53:3:253:A:H4'	53:3:276:G:O2'	2.15	0.47
53:3:343:U:O2'	53:3:344:A:H2'	2.14	0.47
53:3:344:A:OP1	66:0:38:HIS:NE2	2.48	0.47
53:3:751:U:C2'	53:3:752:G:H5'	2.44	0.47
53:3:1059:C:H2'	53:3:1060:U:C6	2.49	0.47
53:3:1161:C:H2'	53:3:1162:C:C6	2.50	0.47
53:3:1170:A:H2'	53:3:1171:A:H5'	1.97	0.47
53:3:1382:C:H2'	53:3:1383:C:C6	2.50	0.47
53:3:1435:G:H1	53:3:1466:C:H42	1.62	0.47
53:3:1441:A:N3	53:3:1441:A:H2'	2.30	0.47
53:3:1465:A:H2'	53:3:1466:C:H6	1.80	0.47
53:3:1478:U:H2'	53:3:1479:C:C6	2.49	0.47
53:3:1486:G:H2'	53:3:1487:G:O4'	2.15	0.47
58:B1:128:LEU:HD21	58:B1:188:LEU:HB3	1.97	0.47
58:B1:201:LEU:HD11	58:B1:220:ARG:HG2	1.95	0.47
58:B1:395:LYS:NZ	58:B1:399:LYS:CE	2.78	0.47
58:B1:420:PRO:HA	58:B1:437:PHE:O	2.15	0.47
59:B2:900:LYS:HB3	59:B2:900:LYS:HE3	1.66	0.47
62:NG:142:ALA:O	62:NG:143:ASP:CB	2.63	0.47
63:5:50:U:H2'	63:5:51:U:C6	2.49	0.47
66:0:24:THR:HG21	66:0:62:THR:HG21	1.97	0.47
66:0:494:ILE:HG21	66:0:605:PHE:CD1	2.50	0.47
7:G:17:HIS:CE1	7:G:187:ASP:HB2	2.50	0.47
7:G:53:LEU:HA	7:G:56:LEU:HB2	1.97	0.47
36:l:18:ARG:NE	51:1:1249:U:C5	2.79	0.47
42:r:80:ARG:HD3	51:1:566:U:H5	1.80	0.47
51:1:524:G:O2'	51:1:525:U:H5'	2.14	0.47
51:1:680:C:H42	51:1:797:G:H1	1.63	0.47
51:1:696:G:O2'	51:1:697:G:H5'	2.15	0.47
51:1:1580:A:H2'	51:1:1581:G:O4'	2.14	0.47
51:1:1856:U:H2'	51:1:1857:G:O4'	2.15	0.47
51:1:1868:C:C2'	51:1:1869:G:H5'	2.42	0.47
58:B1:842:ARG:HH22	58:B1:1250:ASP:HB2	1.80	0.47
66:0:420:VAL:HB	66:0:458:ILE:HD11	1.97	0.47
66:0:463:GLU:O	66:0:467:ASP:N	2.42	0.47
15:O:21:ALA:HB2	15:O:93:ALA:HB2	1.97	0.47
28:c:55:LYS:HG3	28:c:77:ARG:HB3	1.97	0.47
30:e:22:ASN:ND2	30:e:26:GLN:OE1	2.48	0.47
32:g:93:SER:HB3	32:g:121:VAL:HG12	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:m:43:ALA:HB2	37:m:69:PRO:HG3	1.96	0.47
51:1:1306:C:O2'	51:1:1307:A:H5'	2.13	0.47
51:1:1444:G:H2'	51:1:1445:G:H8	1.76	0.47
51:1:1663:G:O2'	51:1:1664:A:H8	1.98	0.47
51:1:2248:C:C2'	51:1:2249:U:H5'	2.44	0.47
53:3:138:G:H2'	53:3:139:A:H8	1.79	0.47
58:B1:1347:LEU:HG	58:B1:1357:ILE:HG23	1.96	0.47
64:6:62:C:H5'	65:a:53:ARG:CZ	2.45	0.47
31:f:84:LYS:HA	31:f:84:LYS:HD2	1.78	0.47
32:g:68:ARG:O	32:g:72:ILE:N	2.47	0.47
51:1:233:A:H5'	51:1:233:A:C8	2.51	0.47
51:1:940:G:H2'	51:1:941:A:H5''	1.97	0.47
51:1:1595:C:H2'	51:1:1596:A:H8	1.79	0.47
51:1:1639:C:H2'	51:1:1640:A:H5'	1.97	0.47
51:1:2153:C:H3'	51:1:2154:A:H8	1.79	0.47
53:3:1448:C:O2	53:3:1448:C:H2'	2.15	0.47
58:B1:772:TYR:HE2	59:B2:561:ILE:HG21	1.80	0.47
5:E:7:ARG:NH2	51:1:245:G:N7	2.63	0.46
8:H:39:ARG:HA	8:H:42:LEU:HB3	1.97	0.46
13:M:102:VAL:HB	13:M:126:CYS:HB3	1.96	0.46
28:c:119:ALA:C	51:1:1655:A:H4'	2.40	0.46
35:k:31:ARG:HH12	51:1:2676:C:P	2.38	0.46
51:1:341:C:H2'	51:1:342:A:H8	1.79	0.46
51:1:1136:G:H2'	51:1:1137:G:H8	1.80	0.46
51:1:2531:A:C2'	51:1:2532:G:H5'	2.45	0.46
53:3:325:A:H2'	53:3:326:G:O4'	2.14	0.46
58:B1:1167:LYS:NZ	58:B1:1170:LYS:HB2	2.30	0.46
58:B1:1221:LEU:HD22	58:B1:1306:LEU:HB2	1.96	0.46
59:B2:400:VAL:HG22	59:B2:584:TYR:HB3	1.96	0.46
63:5:29:G:H3'	63:5:30:G:C8	2.50	0.46
65:a:193:LEU:O	65:a:197:LYS:N	2.42	0.46
12:L:66:GLU:HA	12:L:69:ARG:HG3	1.96	0.46
16:P:23:HIS:HB3	16:P:30:ILE:HG23	1.96	0.46
17:Q:83:GLY:H	53:3:552:U:H4'	1.80	0.46
19:S:55:SER:OG	19:S:57:SER:OG	2.30	0.46
25:Y:16:ALA:O	25:Y:20:ASN:N	2.45	0.46
25:Y:22:SER:HB2	53:3:1458:G:H4'	1.98	0.46
33:i:79:LEU:HD22	33:i:131:THR:HG23	1.97	0.46
48:x:16:ASN:HB2	48:x:24:THR:HB	1.97	0.46
51:1:742:A:O2'	51:1:743:A:H5'	2.15	0.46
51:1:1826:G:H2'	51:1:1827:U:C6	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1933:G:H2'	51:1:1934:C:H6	1.80	0.46
51:1:2080:A:C6	51:1:2081:U:C4	3.04	0.46
51:1:2491:U:C2'	51:1:2492:U:H5'	2.42	0.46
51:1:2845:U:H2'	51:1:2846:G:C8	2.50	0.46
53:3:835:U:C3'	53:3:836:G:H5''	2.45	0.46
53:3:859:G:O2'	53:3:860:A:H5'	2.15	0.46
58:B1:209:ASN:HA	58:B1:214:ARG:NH2	2.30	0.46
25:Y:76:ALA:O	25:Y:79:THR:OG1	2.27	0.46
25:Y:79:THR:HA	25:Y:82:ILE:HB	1.98	0.46
27:b:86:ARG:HB3	27:b:88:ALA:H	1.80	0.46
27:b:210:ALA:HA	27:b:213:ARG:HG3	1.96	0.46
31:f:85:LYS:HE2	31:f:129:GLU:HB3	1.97	0.46
51:1:139:U:H2'	51:1:140:C:C5	2.49	0.46
51:1:1388:G:H2'	51:1:1389:G:C8	2.51	0.46
51:1:2741:A:H61	51:1:2763:G:H1'	1.80	0.46
53:3:545:C:O2'	53:3:546:A:H5'	2.14	0.46
54:4:1:A:H2'	54:4:2:U:C6	2.50	0.46
58:B1:86:GLU:H	58:B1:86:GLU:HG3	1.64	0.46
58:B1:1060:VAL:HG13	58:B1:1106:ILE:HG12	1.96	0.46
58:B1:1357:ILE:HD13	59:B2:1279:GLU:HG2	1.97	0.46
63:5:8:U:H2'	63:5:13:C:N4	2.30	0.46
63:5:26:A:H61	63:5:44:G:H22	1.64	0.46
12:L:101:ARG:HH22	53:3:940:C:P	2.37	0.46
15:O:19:ASP:OD1	15:O:19:ASP:N	2.45	0.46
17:Q:11:ARG:NH1	53:3:563:A:H2	2.14	0.46
29:d:173:THR:OG1	29:d:174:GLY:N	2.48	0.46
31:f:88:LEU:O	31:f:128:THR:OG1	2.32	0.46
33:i:7:TYR:CE1	51:1:1058:U:H5'	2.50	0.46
33:i:47:SER:O	33:i:47:SER:OG	2.31	0.46
46:v:7:GLU:HG3	46:v:41:GLU:HB3	1.97	0.46
51:1:786:C:O2'	51:1:787:C:H5'	2.16	0.46
51:1:1572:A:O2'	51:1:1573:G:H5'	2.15	0.46
51:1:1790:C:H2'	51:1:1791:A:C5	2.51	0.46
51:1:2135:A:H8	51:1:2156:G:H21	1.64	0.46
51:1:2537:U:H2'	51:1:2538:C:H6	1.78	0.46
51:1:2861:U:O2'	51:1:2862:G:H5'	2.15	0.46
52:2:51:G:N3	52:2:52:A:H1'	2.30	0.46
52:2:116:G:O2'	52:2:117:G:H5'	2.15	0.46
52:2:118:C:C2'	52:2:119:A:H4'	2.33	0.46
53:3:250:A:O4'	53:3:252:U:H1'	2.15	0.46
53:3:520:A:H62	53:3:529:G:N2	2.11	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:857:C:H2'	53:3:858:G:O4'	2.14	0.46
57:A1:59:VAL:HG22	57:A1:144:ILE:HA	1.97	0.46
58:B1:198:CYS:HA	58:B1:221:ILE:CD1	2.45	0.46
59:B2:1002:LEU:HD21	59:B2:1007:LYS:HB2	1.98	0.46
66:0:136:PRO:HB3	66:0:256:VAL:HG12	1.97	0.46
2:B:14:MET:HG2	51:1:15:G:O2'	2.16	0.46
8:H:2:GLN:NE2	53:3:1062:U:O4	2.48	0.46
11:K:18:VAL:HG13	11:K:19:PRO:HD3	1.97	0.46
12:L:91:ARG:HG2	12:L:91:ARG:NH1	2.30	0.46
14:N:40:ARG:NE	53:3:1292:G:H5''	2.31	0.46
45:u:88:ASP:OD1	45:u:88:ASP:N	2.47	0.46
51:1:141:G:C8	51:1:142:A:H1'	2.51	0.46
51:1:175:G:H2'	51:1:176:A:H8	1.81	0.46
51:1:820:A:O2'	51:1:821:A:H5'	2.15	0.46
51:1:824:U:H2'	51:1:825:A:O4'	2.15	0.46
51:1:1321:A:C2	51:1:1322:A:H1'	2.50	0.46
51:1:1842:G:O2'	51:1:1843:C:H5'	2.15	0.46
51:1:2134:A:C5	51:1:2157:G:H4'	2.51	0.46
51:1:2450:A:OP1	51:1:2497:A:O2'	2.31	0.46
53:3:1084:G:O2'	53:3:1103:C:H5	1.98	0.46
57:A1:35:PHE:HA	57:A1:38:THR:HG22	1.97	0.46
58:B1:43:THR:HG22	58:B1:57:PHE:HE1	1.80	0.46
58:B1:109:SER:HB2	58:B1:296:LYS:HG2	1.98	0.46
58:B1:141:PHE:CE2	58:B1:296:LYS:CB	2.94	0.46
58:B1:1361:THR:OG1	59:B2:1282:GLY:O	2.28	0.46
59:B2:230:PHE:HB2	59:B2:333:ILE:HB	1.97	0.46
66:0:376:GLU:OE1	66:0:378:ARG:NE	2.48	0.46
66:0:474:LYS:HD3	66:0:474:LYS:HA	1.72	0.46
8:H:51:VAL:HA	8:H:69:THR:HA	1.97	0.46
9:I:103:ARG:HD2	9:I:167:PRO:HG3	1.97	0.46
10:J:158:LYS:HD3	10:J:158:LYS:HA	1.73	0.46
15:O:36:VAL:HA	15:O:76:ILE:HA	1.97	0.46
27:b:250:GLN:HB3	27:b:254:LYS:HD2	1.96	0.46
51:1:365:U:H2'	51:1:366:C:O4'	2.16	0.46
51:1:433:C:O2'	51:1:434:U:H5'	2.15	0.46
51:1:912:C:O2'	51:1:913:U:H5'	2.15	0.46
51:1:1196:C:O2'	51:1:1197:G:H5'	2.16	0.46
51:1:1470:A:N6	51:1:1521:G:H1'	2.30	0.46
51:1:1485:U:H2'	51:1:1486:U:C6	2.50	0.46
51:1:1569:A:H2'	51:1:1570:A:C8	2.51	0.46
51:1:1614:A:C2'	51:1:1615:C:H5'	2.46	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1642:G:O2'	51:1:1643:G:H5'	2.15	0.46
53:3:211:G:H3'	53:3:211:G:N3	2.29	0.46
53:3:556:C:O2'	53:3:557:G:H5'	2.16	0.46
53:3:994:A:H3'	53:3:994:A:OP2	2.15	0.46
59:B2:103:VAL:HG12	59:B2:117:ILE:HG22	1.97	0.46
59:B2:1314:GLN:HA	60:W0:28:ARG:HH22	1.80	0.46
66:0:369:ASN:OD1	66:0:369:ASN:N	2.48	0.46
8:H:49:ALA:O	8:H:69:THR:OG1	2.33	0.46
9:I:140:ASP:O	9:I:181:PHE:N	2.46	0.46
20:T:50:HIS:ND1	53:3:667:G:H4'	2.31	0.46
27:b:6:LYS:HD2	27:b:7:PRO:HD2	1.98	0.46
27:b:71:ASP:HB3	27:b:118:GLY:HA2	1.98	0.46
29:d:49:ARG:NH1	51:1:674:G:OP2	2.48	0.46
31:f:136:ASP:HB3	31:f:139:VAL:HG12	1.97	0.46
32:g:14:SER:O	32:g:16:GLY:N	2.49	0.46
43:s:82:MET:HE1	51:1:1322:A:H4'	1.97	0.46
51:1:340:A:C2'	51:1:341:C:H5'	2.43	0.46
51:1:704:G:N3	51:1:726:G:C2	2.84	0.46
51:1:1313:U:O2	51:1:1313:U:C2'	2.64	0.46
51:1:1661:G:O2'	51:1:1662:U:H5'	2.16	0.46
51:1:2751:G:O2'	51:1:2752:C:H5'	2.16	0.46
53:3:10:A:H2'	53:3:11:G:C8	2.51	0.46
53:3:528:C:H4'	53:3:535:A:C6	2.51	0.46
53:3:1018:G:O2'	53:3:1019:A:H5'	2.16	0.46
55:8:13:DT:C6	58:B1:791:ALA:HA	2.51	0.46
14:N:72:SER:HA	14:N:75:ALA:HB3	1.98	0.46
16:P:25:SER:HG	16:P:28:ASN:H	1.62	0.46
25:Y:60:GLN:HA	25:Y:63:LYS:HD2	1.98	0.46
28:c:49:GLN:HE21	28:c:79:LEU:HB3	1.79	0.46
29:d:47:LYS:HG2	51:1:451:U:OP2	2.15	0.46
34:j:7:LYS:HG2	34:j:10:THR:HG23	1.97	0.46
39:o:6:ALA:HA	39:o:9:ARG:HE	1.81	0.46
45:u:48:VAL:O	45:u:53:GLN:HG3	2.16	0.46
51:1:393:C:H2'	51:1:394:C:H6	1.81	0.46
51:1:441:U:H2'	51:1:442:G:H8	1.81	0.46
51:1:690:G:H2'	51:1:691:C:H5'	1.98	0.46
53:3:980:C:H2'	53:3:981:U:O4'	2.15	0.46
53:3:1260:G:H4'	53:3:1284:C:H5'	1.98	0.46
63:5:8:U:H2'	63:5:13:C:H41	1.81	0.46
3:C:35:LEU:HD21	51:1:2286:G:H22	1.81	0.46
4:D:1:MET:HE3	4:D:3:ARG:HH21	1.80	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:132:GLU:OE2	7:G:136:ARG:NE	2.47	0.46
12:L:79:VAL:O	12:L:79:VAL:HG12	2.16	0.46
14:N:96:GLU:O	14:N:100:ALA:N	2.41	0.46
15:O:36:VAL:HG22	15:O:38:GLY:H	1.80	0.46
16:P:115:ILE:HD12	16:P:116:PRO:HD2	1.98	0.46
31:f:91:VAL:HG21	51:1:2657:A:H4'	1.97	0.46
43:s:82:MET:HB2	43:s:98:LYS:HB2	1.97	0.46
49:y:10:SER:HA	49:y:13:GLU:HB3	1.98	0.46
51:1:107:G:H2'	51:1:108:G:C8	2.51	0.46
51:1:1858:A:N6	51:1:1884:G:O2'	2.48	0.46
51:1:2695:U:H2'	51:1:2696:U:C6	2.51	0.46
53:3:113:G:O2'	53:3:353:A:H4'	2.16	0.46
53:3:131:A:H2'	53:3:132:C:C6	2.51	0.46
53:3:962:C:H1'	53:3:1201:A:C6	2.51	0.46
55:8:1:DC:H2''	55:8:2:DC:C6	2.51	0.46
57:A1:185:TYR:HA	57:A1:202:VAL:O	2.16	0.46
57:A2:80:GLU:HG3	59:B2:694:ARG:HH22	1.81	0.46
59:B2:28:LEU:HD21	59:B2:524:ILE:HG13	1.98	0.46
59:B2:176:ILE:HD11	59:B2:428:VAL:HG21	1.98	0.46
63:5:70:G:H2'	63:5:71:G:C8	2.51	0.46
8:H:10:ARG:HA	8:H:13:ILE:HD11	1.97	0.46
10:J:156:ARG:NH1	13:M:98:LEU:O	2.49	0.46
16:P:97:ARG:HA	16:P:100:ASN:HD22	1.81	0.46
32:g:30:LEU:HA	32:g:35:LYS:HE3	1.96	0.46
48:x:57:VAL:HG12	48:x:61:LYS:HZ1	1.80	0.46
51:1:388:G:H2'	51:1:390:U:H5	1.81	0.46
51:1:1695:G:H2'	51:1:1696:G:O4'	2.15	0.46
51:1:2099:U:H2'	51:1:2100:G:C8	2.51	0.46
51:1:2643:G:O2'	51:1:2644:G:H5'	2.16	0.46
53:3:144:G:H2'	53:3:145:G:O4'	2.16	0.46
53:3:951:G:H2'	53:3:952:U:H6	1.79	0.46
53:3:973:G:H2'	53:3:974:A:C8	2.51	0.46
53:3:1121:U:H2'	53:3:1122:U:C6	2.51	0.46
53:3:1361:G:H2'	53:3:1362:A:O4'	2.16	0.46
54:4:39:G:H2'	54:4:40:G:C8	2.51	0.46
58:B1:1036:ARG:HE	58:B1:1081:VAL:HG11	1.79	0.46
59:B2:689:ALA:HB2	59:B2:1233:LEU:HD23	1.97	0.46
1:A:9:TYR:HE1	30:e:61:GLY:H	1.63	0.45
6:F:15:LYS:N	6:F:26:ILE:O	2.40	0.45
14:N:30:ASN:N	14:N:64:ILE:O	2.48	0.45
15:O:47:GLU:OE2	15:O:69:THR:OG1	2.30	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:4:ILE:HD13	21:U:21:VAL:HA	1.99	0.45
27:b:107:LYS:N	27:b:193:GLU:O	2.49	0.45
27:b:155:ARG:CZ	51:1:1818:U:C5	2.99	0.45
31:f:98:LYS:HD2	31:f:98:LYS:HA	1.78	0.45
32:g:94:ILE:HD12	32:g:99:ILE:HG21	1.98	0.45
51:1:468:G:C2'	51:1:469:G:H5'	2.46	0.45
51:1:845:A:N3	51:1:845:A:H3'	2.31	0.45
51:1:864:G:H2'	51:1:865:C:O4'	2.16	0.45
51:1:2869:G:H2'	51:1:2870:C:O4'	2.16	0.45
53:3:271:C:H2'	53:3:272:C:C6	2.51	0.45
53:3:1069:C:H4'	53:3:1192:C:O2	2.16	0.45
53:3:1289:A:H2'	53:3:1290:G:H5'	1.98	0.45
55:8:20:DA:H4'	59:B2:143:ARG:NH1	2.31	0.45
58:B1:484:MET:CE	59:B2:1278:LEU:HD21	2.46	0.45
66:0:15:ILE:O	66:0:89:THR:OG1	2.35	0.45
66:0:17:ALA:H	66:0:23:LYS:HZ3	1.63	0.45
66:0:533:GLY:HA3	66:0:572:VAL:HG22	1.97	0.45
66:0:618:LYS:N	66:0:683:GLU:O	2.49	0.45
31:f:94:ARG:HA	31:f:127:GLN:HB2	1.99	0.45
33:i:52:LEU:HD13	33:i:77:VAL:HG13	1.97	0.45
43:s:25:ARG:NE	43:s:74:ILE:O	2.46	0.45
45:u:5:ARG:NH1	51:1:84:A:H5''	2.31	0.45
51:1:2101:A:H2'	51:1:2102:G:C8	2.50	0.45
51:1:2646:C:H2'	51:1:2647:U:O4'	2.16	0.45
52:2:30:C:H2'	52:2:31:C:C5'	2.47	0.45
53:3:460:A:H2'	53:3:461:A:C8	2.51	0.45
53:3:684:U:H3	53:3:706:A:H61	1.63	0.45
58:B1:506:VAL:HG23	58:B1:628:GLY:HA3	1.99	0.45
58:B1:1219:ASP:O	58:B1:1223:LEU:HB2	2.15	0.45
13:M:86:LYS:HD2	13:M:86:LYS:HA	1.73	0.45
14:N:56:MET:HB2	14:N:60:LEU:HB2	1.97	0.45
17:Q:34:THR:HG22	17:Q:76:HIS:CD2	2.51	0.45
22:V:21:VAL:HG22	22:V:44:HIS:HA	1.98	0.45
29:d:22:ASP:OD1	29:d:22:ASP:N	2.48	0.45
31:f:88:LEU:HB3	31:f:128:THR:HA	1.97	0.45
48:x:30:PRO:O	48:x:31:ASN:C	2.59	0.45
51:1:191:A:H2'	51:1:192:C:H6	1.81	0.45
51:1:1177:G:C2'	51:1:1178:C:H5''	2.45	0.45
51:1:2680:U:O2'	51:1:2681:C:H5'	2.17	0.45
53:3:37:U:H2'	53:3:38:G:H5'	1.97	0.45
53:3:437:U:C2'	53:3:438:U:H5'	2.46	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1104:G:H2'	53:3:1105:A:O4'	2.16	0.45
59:B2:318:SER:OG	59:B2:320:ASP:OD1	2.31	0.45
62:NG:135:ARG:O	62:NG:178:VAL:HA	2.16	0.45
66:0:520:ILE:HD12	66:0:576:ILE:HD11	1.99	0.45
10:J:161:GLU:HA	10:J:164:LEU:HD12	1.98	0.45
15:O:59:LYS:HD3	53:3:972:C:O3'	2.17	0.45
16:P:24:ALA:N	16:P:86:LYS:O	2.39	0.45
29:d:43:THR:O	51:1:38:A:H1'	2.17	0.45
34:j:57:LEU:HD11	34:j:130:HIS:HD2	1.82	0.45
51:1:233:A:H5'	51:1:233:A:H8	1.81	0.45
51:1:717:C:H2'	51:1:718:A:H5'	1.98	0.45
51:1:817:C:O2'	51:1:839:U:H5''	2.16	0.45
53:3:280:C:H5''	53:3:281:G:OP2	2.17	0.45
53:3:323:U:H3	53:3:327:A:H62	1.64	0.45
53:3:556:C:H2'	53:3:557:G:O4'	2.15	0.45
53:3:946:A:H4'	53:3:1333:A:HO2'	1.82	0.45
53:3:1316:G:H2'	53:3:1317:C:H5''	1.99	0.45
57:A1:231:PHE:O	57:A2:218:ARG:NH1	2.50	0.45
58:B1:847:ASP:N	58:B1:847:ASP:OD1	2.49	0.45
63:5:27:G:H1	63:5:43:C:H42	1.64	0.45
15:O:15:HIS:CG	53:3:1152:A:H5'	2.51	0.45
20:T:80:LEU:O	20:T:84:LEU:N	2.42	0.45
24:X:46:LEU:HD12	24:X:48:ILE:HD11	1.99	0.45
28:c:61:THR:HB	28:c:63:PRO:HD2	1.96	0.45
29:d:153:LEU:HD11	29:d:158:PHE:HB2	1.98	0.45
35:k:56:ASP:N	35:k:56:ASP:OD1	2.49	0.45
37:m:27:SER:H	37:m:104:GLU:CD	2.24	0.45
42:r:38:VAL:HG21	42:r:57:GLY:HA3	1.97	0.45
51:1:642:U:H2'	51:1:644:A:OP2	2.16	0.45
51:1:1069:A:H2'	51:1:1073:A:C5	2.51	0.45
51:1:1086:A:H1'	51:1:1103:A:H2	1.81	0.45
51:1:1573:G:H2'	51:1:1574:C:O4'	2.17	0.45
51:1:1792:G:H1	51:1:1827:U:H3	1.65	0.45
51:1:1841:U:H2'	51:1:1842:G:C8	2.51	0.45
51:1:1954:G:H21	51:1:1956:U:H3	1.65	0.45
51:1:2190:G:H2'	51:1:2191:A:O4'	2.16	0.45
52:2:16:G:N2	52:2:69:G:H1'	2.31	0.45
58:B1:115:TRP:HB3	58:B1:1333:THR:CG2	2.46	0.45
58:B1:213:LYS:HA	58:B1:213:LYS:HE3	1.99	0.45
59:B2:24:VAL:HG11	59:B2:704:MET:HE1	1.98	0.45
59:B2:735:LYS:HA	59:B2:748:ILE:HG22	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:5:6:G:H2'	63:5:7:A:C8	2.51	0.45
66:0:171:LEU:HD11	66:0:218:TRP:HD1	1.82	0.45
66:0:600:ALA:HA	66:0:603:GLU:HB2	1.98	0.45
2:B:49:ARG:NH2	51:1:2884:U:H1'	2.32	0.45
16:P:114:PRO:O	26:Z:28:LEU:HD21	2.17	0.45
20:T:38:LEU:HD23	20:T:55:LEU:HD12	1.98	0.45
24:X:71:GLY:HA3	53:3:1320:C:C2	2.51	0.45
25:Y:10:ALA:O	25:Y:13:SER:OG	2.28	0.45
51:1:91:A:H8	51:1:91:A:OP1	1.99	0.45
51:1:252:G:H2'	51:1:253:C:H6	1.81	0.45
51:1:1028:A:N6	51:1:1125:G:H2'	2.31	0.45
51:1:1094:U:H2'	51:1:1096:A:OP2	2.17	0.45
51:1:1337:G:O2'	51:1:1338:G:H5'	2.17	0.45
51:1:2123:G:N3	51:1:2176:A:N6	2.65	0.45
51:1:2457:U:O2'	51:1:2458:G:H5'	2.15	0.45
51:1:2785:C:H2'	51:1:2786:U:C6	2.51	0.45
53:3:607:A:H2'	53:3:608:A:O4'	2.17	0.45
53:3:792:A:H4'	53:3:793:U:C5'	2.47	0.45
53:3:962:C:H42	53:3:973:G:H1	1.64	0.45
53:3:1436:U:H2'	53:3:1437:A:C8	2.45	0.45
66:0:392:THR:OG1	66:0:395:ASP:OD2	2.31	0.45
5:E:7:ARG:NH1	51:1:243:U:OP2	2.50	0.45
8:H:63:ILE:HG23	8:H:98:ALA:HA	1.99	0.45
10:J:88:HIS:HB3	10:J:134:ASN:HD21	1.81	0.45
17:Q:120:ARG:HG2	53:3:37:U:C5'	2.46	0.45
39:o:94:ARG:NH2	39:o:98:GLN:OE1	2.50	0.45
50:z:19:HIS:CD2	50:z:50:VAL:HG12	2.52	0.45
50:z:37:ARG:NH1	51:1:928:A:O2'	2.50	0.45
51:1:44:A:C2'	51:1:45:G:H5'	2.45	0.45
51:1:708:G:O2'	51:1:709:U:H5'	2.17	0.45
51:1:1786:A:O2'	51:1:1787:A:H5'	2.17	0.45
51:1:2183:A:H2'	51:1:2184:A:C8	2.52	0.45
53:3:384:G:H2'	53:3:385:C:C6	2.52	0.45
53:3:478:A:H2'	53:3:479:U:C4'	2.46	0.45
53:3:771:G:H2'	53:3:772:U:C6	2.51	0.45
58:B1:71:LEU:HD23	58:B1:71:LEU:HA	1.75	0.45
58:B1:201:LEU:CB	58:B1:221:ILE:HD13	2.47	0.45
58:B1:213:LYS:HE3	58:B1:213:LYS:CA	2.47	0.45
59:B2:674:ASP:OD2	59:B2:1070:HIS:ND1	2.50	0.45
59:B2:909:LYS:HD3	59:B2:909:LYS:HA	1.63	0.45
63:5:49:C:H2'	63:5:50:U:C6	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:0:144:MET:HG2	66:0:266:CYS:HB2	1.99	0.45
7:G:115:ASP:OD1	7:G:115:ASP:N	2.42	0.45
16:P:25:SER:HG	16:P:28:ASN:N	2.14	0.45
27:b:73:ILE:HG12	51:1:1490:A:H2	1.79	0.45
29:d:37:ALA:HB1	29:d:94:GLN:H	1.82	0.45
29:d:131:THR:HA	29:d:134:LEU:HB3	1.98	0.45
30:e:35:LEU:HD22	30:e:151:LEU:HD21	1.99	0.45
38:n:73:ASN:O	38:n:77:ALA:N	2.50	0.45
40:p:28:LYS:HB2	40:p:82:SER:H	1.81	0.45
51:1:162:U:H6	51:1:163:C:H5	1.65	0.45
51:1:776:G:C8	51:1:793:A:C2	3.05	0.45
51:1:866:A:H61	51:1:913:U:C1'	2.28	0.45
51:1:918:A:H4'	52:2:97:C:O2	2.16	0.45
51:1:952:G:H3'	51:1:953:G:H5''	1.98	0.45
51:1:1954:G:N2	51:1:1956:U:H3	2.15	0.45
51:1:1979:U:O5'	51:1:1979:U:H6	1.99	0.45
51:1:2226:C:H2'	51:1:2227:A:O4'	2.17	0.45
58:B1:76:LYS:NZ	58:B1:76:LYS:HB3	2.32	0.45
58:B1:201:LEU:CD1	58:B1:224:LEU:HD12	2.46	0.45
58:B1:770:LEU:HD13	59:B2:618:GLN:CD	2.42	0.45
63:5:31:A:H5'	63:5:33:U:O4	2.16	0.45
66:0:565:PRO:HD3	66:0:602:LYS:HZ2	1.81	0.45
66:0:643:LYS:HE3	66:0:655:HIS:HB3	1.99	0.45
1:A:41:HIS:HD2	30:e:108:PRO:HA	1.82	0.45
12:L:140:VAL:O	12:L:144:ALA:N	2.46	0.45
14:N:28:VAL:HG13	14:N:63:TYR:HA	1.99	0.45
16:P:105:ARG:HD2	16:P:105:ARG:HA	1.84	0.45
17:Q:11:ARG:HH11	53:3:563:A:H2	1.64	0.45
18:R:107:THR:HG21	53:3:1307:U:H4'	1.99	0.45
27:b:84:PRO:HG3	51:1:1568:G:OP1	2.16	0.45
32:g:98:ASP:O	32:g:102:ALA:N	2.49	0.45
44:t:17:SER:OG	44:t:20:ALA:N	2.48	0.45
49:y:38:GLN:O	51:1:95:A:H4'	2.16	0.45
51:1:878:A:H3'	51:1:879:G:H8	1.82	0.45
51:1:927:A:H2'	51:1:928:A:O4'	2.17	0.45
51:1:2073:C:O5'	51:1:2073:C:H6	1.99	0.45
51:1:2125:G:C5'	65:a:39:VAL:HG22	2.47	0.45
51:1:2127:G:H2'	51:1:2128:G:C8	2.52	0.45
51:1:2599:G:H2'	51:1:2600:A:H8	1.80	0.45
53:3:20:U:O2'	53:3:21:G:H5'	2.17	0.45
53:3:757:U:H2'	53:3:758:C:H5'	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:782:A:O3'	53:3:1515:G:H4'	2.16	0.45
53:3:1096:C:H2'	53:3:1097:C:H6	1.80	0.45
53:3:1147:C:H2'	53:3:1148:U:C6	2.52	0.45
53:3:1173:U:H2'	53:3:1174:G:C8	2.48	0.45
53:3:1198:G:H2'	53:3:1199:U:C6	2.51	0.45
59:B2:546:GLU:H	59:B2:546:GLU:HG3	1.53	0.45
59:B2:562:GLU:OE1	59:B2:662:SER:OG	2.28	0.45
66:0:11:ARG:HG3	66:0:283:ILE:HA	1.99	0.45
7:G:20:ARG:HD2	53:3:831:A:H5''	1.98	0.45
9:I:47:LEU:HD22	53:3:510:A:OP1	2.17	0.45
11:K:11:HIS:HB3	11:K:14:GLN:HB2	1.99	0.45
13:M:104:SER:OG	53:3:642:A:N3	2.48	0.45
14:N:16:ALA:HA	14:N:66:VAL:HA	1.98	0.45
16:P:71:ASP:OD1	16:P:71:ASP:N	2.43	0.45
17:Q:57:THR:HG21	53:3:362:G:H5''	1.99	0.45
19:S:23:ARG:HH12	19:S:27:LYS:HB3	1.82	0.45
20:T:19:ASN:O	53:3:750:C:H1'	2.16	0.45
28:c:2:ILE:HG12	28:c:90:PHE:HZ	1.82	0.45
30:e:35:LEU:HB2	30:e:88:VAL:HG12	1.98	0.45
33:i:9:LYS:HA	33:i:57:VAL:HA	1.99	0.45
33:i:52:LEU:HD11	33:i:81:LYS:HD3	1.99	0.45
33:i:94:LYS:HD3	33:i:94:LYS:HA	1.73	0.45
40:p:48:ALA:N	40:p:59:THR:OG1	2.50	0.45
42:r:49:ILE:O	42:r:49:ILE:HG13	2.17	0.45
51:1:224:U:H2'	51:1:225:C:O4'	2.17	0.45
51:1:598:U:H2'	51:1:599:A:C8	2.52	0.45
51:1:1429:G:C2	51:1:1568:G:C2	3.05	0.45
51:1:1541:C:H2'	51:1:1542:U:O4'	2.17	0.45
53:3:334:C:H2'	53:3:335:C:O4'	2.16	0.45
53:3:433:G:H2'	53:3:434:U:C6	2.51	0.45
53:3:925:G:H1'	53:3:1502:A:C4	2.52	0.45
53:3:962:C:H1'	53:3:1201:A:N1	2.32	0.45
53:3:1098:C:H2'	53:3:1099:G:O4'	2.17	0.45
57:A2:64:VAL:HG11	57:A2:78:ILE:HG21	1.97	0.45
58:B1:375:GLU:O	59:B2:1247:SER:HB3	2.16	0.45
58:B1:1158:GLU:HA	58:B1:1223:LEU:HD21	1.99	0.45
63:5:32:U:H2'	63:5:33:U:C2	2.52	0.45
66:0:145:ASP:OD1	66:0:273:LYS:NZ	2.45	0.45
5:E:15:LYS:HA	5:E:21:PHE:HA	1.99	0.44
6:F:28:SER:OG	6:F:29:ALA:N	2.50	0.44
7:G:33:ALA:HB3	7:G:37:VAL:HB	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:153:SER:O	8:H:196:GLY:N	2.50	0.44
12:L:57:GLU:HG3	12:L:58:LEU:HD12	1.99	0.44
19:S:2:LYS:HG2	19:S:4:SER:H	1.81	0.44
27:b:212:TRP:NE1	51:1:1566:A:O4'	2.50	0.44
31:f:41:GLU:N	31:f:52:GLY:O	2.49	0.44
33:i:126:ARG:O	33:i:130:GLY:N	2.50	0.44
39:o:18:LEU:HD23	39:o:21:LEU:HD12	1.99	0.44
40:p:74:GLN:NE2	51:1:2683:C:O2'	2.49	0.44
40:p:105:LYS:HG2	53:3:1464:U:OP1	2.17	0.44
41:q:25:GLY:O	41:q:29:ARG:NH1	2.50	0.44
51:1:753:A:H2'	51:1:754:U:C6	2.52	0.44
51:1:1093:G:H22	51:1:1097:U:H3'	1.82	0.44
51:1:1276:A:H61	51:1:1294:U:H3	1.64	0.44
51:1:1300:G:N7	51:1:1626:A:H2'	2.32	0.44
51:1:1656:C:H2'	51:1:1657:U:H6	1.82	0.44
53:3:768:A:C2	53:3:1512:U:H4'	2.52	0.44
53:3:946:A:H4'	53:3:1333:A:O2'	2.17	0.44
53:3:1255:G:H1	53:3:1282:C:H42	1.64	0.44
62:NG:161:SER:CB	62:NG:170:PRO:HA	2.47	0.44
63:5:22:G:H2'	63:5:23:A:C8	2.51	0.44
64:6:70:G:H2'	64:6:71:C:C6	2.52	0.44
3:C:45:HIS:ND1	51:1:2372:U:H4'	2.32	0.44
8:H:58:ARG:HB3	8:H:63:ILE:HB	1.98	0.44
10:J:72:ASN:OD1	10:J:72:ASN:N	2.50	0.44
19:S:61:ASN:HB3	19:S:72:PHE:CE2	2.52	0.44
22:V:64:ARG:CB	53:3:130:A:H8	2.31	0.44
28:c:194:PRO:HA	51:1:2680:U:C5'	2.46	0.44
34:j:118:MET:HE3	34:j:118:MET:HB2	1.76	0.44
51:1:623:C:H2'	51:1:624:C:C6	2.52	0.44
51:1:1024:G:O5'	51:1:1025:G:H5''	2.16	0.44
51:1:1130:U:C5	51:1:2025:C:H5''	2.52	0.44
51:1:2560:A:O2'	51:1:2561:U:H5'	2.17	0.44
53:3:152:A:H2'	53:3:153:C:H5'	1.99	0.44
53:3:675:A:C2	53:3:676:A:H1'	2.52	0.44
58:B1:343:LEU:HD11	58:B1:1324:SER:HB3	1.98	0.44
58:B1:385:LEU:HD23	58:B1:390:LEU:HB2	1.98	0.44
58:B1:472:LEU:CD1	59:B2:1294:LYS:HG2	2.47	0.44
59:B2:1246:ARG:HH11	59:B2:1266:GLY:HA2	1.82	0.44
60:W0:25:ARG:NH1	60:W0:61:ASN:OD1	2.49	0.44
63:5:69:G:H2'	63:5:70:G:C8	2.52	0.44
66:0:13:ILE:HG22	66:0:86:ILE:HA	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:0:618:LYS:H	66:0:684:PHE:HA	1.82	0.44
11:K:47:LEU:HD21	11:K:54:LEU:O	2.17	0.44
14:N:6:TYR:OH	53:3:1148:U:H5'	2.16	0.44
15:O:70:HIS:HD2	15:O:72:ARG:HH22	1.64	0.44
25:Y:4:LYS:NZ	53:3:332:G:P	2.91	0.44
34:j:134:ALA:HB1	51:1:2898:U:O2	2.17	0.44
36:l:135:ILE:HG23	36:l:140:GLY:HA3	1.99	0.44
45:u:65:GLN:CD	51:1:328:U:H4'	2.42	0.44
51:1:146:A:H2'	51:1:147:C:H6	1.81	0.44
51:1:2061:G:C2'	51:1:2501:C:HO2'	2.25	0.44
52:2:6:G:O2'	52:2:7:G:H5'	2.17	0.44
53:3:347:G:H2'	53:3:348:G:O4'	2.17	0.44
53:3:569:C:H4'	53:3:574:A:N7	2.31	0.44
53:3:806:C:H2'	53:3:807:A:C8	2.52	0.44
58:B1:804:ALA:HB2	58:B1:1256:ILE:CD1	2.47	0.44
58:B1:1227:HIS:HA	58:B1:1230:THR:HG22	1.99	0.44
9:I:96:ARG:HG2	9:I:133:SER:HA	1.99	0.44
23:W:37:LYS:HE2	23:W:37:LYS:HB2	1.73	0.44
26:Z:44:ARG:HD3	26:Z:44:ARG:HA	1.77	0.44
27:b:227:VAL:HG11	51:1:784:G:C2	2.52	0.44
29:d:5:LEU:HG	29:d:120:VAL:HG13	2.00	0.44
38:n:40:LYS:O	38:n:44:LEU:N	2.48	0.44
45:u:27:VAL:HA	45:u:33:VAL:HG13	1.99	0.44
51:1:138:U:H3'	51:1:139:U:H5'	1.99	0.44
51:1:233:A:C2'	51:1:234:U:H5'	2.48	0.44
51:1:397:U:O5'	51:1:397:U:H6	2.00	0.44
51:1:974:G:O2'	51:1:989:G:N2	2.51	0.44
51:1:1147:A:O2'	51:1:1148:U:H5'	2.17	0.44
51:1:1432:G:H2'	51:1:1433:A:C8	2.52	0.44
51:1:2007:U:O5'	51:1:2007:U:H6	2.01	0.44
51:1:2073:C:O2'	51:1:2074:U:H5'	2.17	0.44
51:1:2102:G:H2'	51:1:2103:C:O4'	2.18	0.44
53:3:969:A:H2'	53:3:970:C:O4'	2.18	0.44
55:8:16:DT:H2'	55:8:17:DC:C6	2.52	0.44
58:B1:67:ASP:OD1	58:B1:67:ASP:O	2.35	0.44
58:B1:395:LYS:NZ	58:B1:399:LYS:HE2	2.32	0.44
58:B1:434:ILE:HD11	59:B2:1274:GLU:HG3	2.00	0.44
66:0:97:ILE:HD13	66:0:412:PRO:HG3	2.00	0.44
7:G:136:ARG:O	7:G:140:LEU:N	2.47	0.44
12:L:67:ASN:HB3	12:L:129:ASN:HD21	1.83	0.44
16:P:19:VAL:HG13	16:P:82:GLU:HB3	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:94:LEU:HD12	18:R:95:PRO:HD2	2.00	0.44
21:U:26:ASN:HD21	21:U:31:ARG:N	2.15	0.44
27:b:155:ARG:NH1	51:1:1818:U:C5	2.81	0.44
51:1:754:U:O5'	51:1:754:U:H6	2.01	0.44
51:1:885:C:H2'	51:1:891:G:H22	1.83	0.44
51:1:1020:A:C1'	51:1:1021:A:OP2	2.61	0.44
51:1:1565:C:O2'	51:1:1566:A:H2'	2.16	0.44
51:1:2270:A:H2'	51:1:2271:G:O4'	2.18	0.44
51:1:2737:G:H2'	51:1:2738:A:C8	2.52	0.44
51:1:2757:A:H2'	51:1:2757:A:N3	2.32	0.44
53:3:68:G:H2'	53:3:69:G:O4'	2.17	0.44
53:3:563:A:H5'	53:3:566:G:N2	2.33	0.44
53:3:563:A:H2'	53:3:563:A:N3	2.32	0.44
53:3:723:U:O2	53:3:855:U:H4'	2.18	0.44
58:B1:33:TRP:HZ2	59:B2:1336:ASN:OD1	2.00	0.44
58:B1:75:TYR:CD2	58:B1:75:TYR:O	2.70	0.44
58:B1:128:LEU:CD2	58:B1:188:LEU:HB3	2.47	0.44
58:B1:245:LEU:CG	58:B1:246:PRO:HD2	2.48	0.44
58:B1:926:PRO:HB2	58:B1:1241:TYR:HE1	1.82	0.44
58:B1:1079:LYS:HD3	58:B1:1098:GLN:HB3	1.99	0.44
6:F:1:MET:N	51:1:2526:G:H1'	2.32	0.44
9:I:145:ARG:HB3	9:I:148:ALA:HB3	1.99	0.44
11:K:3:HIS:ND1	11:K:65:GLU:HB2	2.33	0.44
17:Q:50:LYS:HA	17:Q:50:LYS:HD2	1.86	0.44
23:W:58:ILE:O	23:W:62:ARG:N	2.49	0.44
35:k:62:VAL:HA	35:k:84:CYS:HA	2.00	0.44
37:m:81:ARG:NH1	51:1:2251:G:OP1	2.51	0.44
39:o:90:VAL:HG23	39:o:117:PHE:HB3	2.00	0.44
41:q:32:ARG:HB2	51:1:581:C:OP1	2.18	0.44
41:q:51:GLN:O	41:q:55:GLN:N	2.48	0.44
43:s:13:SER:OG	43:s:14:ALA:N	2.50	0.44
47:w:56:PHE:HE1	47:w:58:LYS:HE2	1.83	0.44
51:1:514:A:O2'	51:1:515:A:H5'	2.17	0.44
51:1:648:G:H2'	51:1:649:G:H8	1.82	0.44
51:1:960:A:H5''	51:1:961:C:OP1	2.17	0.44
51:1:1028:A:C2	51:1:2487:G:H1'	2.52	0.44
51:1:1087:G:H1	51:1:1102:C:H42	1.64	0.44
51:1:2194:U:H2'	51:1:2195:U:C6	2.52	0.44
53:3:240:G:H2'	53:3:241:G:C8	2.53	0.44
53:3:272:C:H2'	53:3:273:U:H6	1.83	0.44
53:3:1494:G:H2'	53:3:1495:U:C6	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:903:LEU:HD12	58:B1:903:LEU:HA	1.81	0.44
58:B1:1108:GLN:HG3	58:B1:1109:LEU:HD12	1.99	0.44
66:0:305:THR:O	66:0:305:THR:OG1	2.33	0.44
66:0:338:VAL:HG13	66:0:380:GLY:H	1.83	0.44
8:H:68:HIS:HE2	8:H:105:VAL:HB	1.81	0.44
10:J:50:GLY:HA3	10:J:62:ALA:HB2	2.00	0.44
16:P:57:SER:O	16:P:57:SER:OG	2.34	0.44
31:f:62:ALA:HA	51:1:2748:A:O2'	2.18	0.44
40:p:25:VAL:HG21	40:p:83:ILE:HG22	1.99	0.44
51:1:861:A:H2'	51:1:862:G:O4'	2.18	0.44
51:1:1177:G:H2'	51:1:1178:C:C5'	2.48	0.44
51:1:1744:A:H3'	51:1:1745:A:H8	1.83	0.44
51:1:2066:C:H2'	51:1:2067:G:H8	1.81	0.44
51:1:2762:C:H2'	51:1:2763:G:H5'	2.00	0.44
53:3:182:A:N1	53:3:224:U:H5'	2.33	0.44
53:3:505:G:C6	53:3:535:A:C2	3.05	0.44
53:3:622:A:H2'	53:3:623:C:H5'	1.99	0.44
53:3:894:G:H2'	53:3:895:G:C8	2.53	0.44
53:3:994:A:H61	53:3:1047:G:C4'	2.30	0.44
53:3:1312:G:H2'	53:3:1313:U:C6	2.52	0.44
57:A1:68:TYR:HE1	57:A1:79:LEU:HD13	1.82	0.44
58:B1:108:ALA:HB1	58:B1:279:LEU:HD22	1.96	0.44
58:B1:388:ARG:HG2	58:B1:388:ARG:NH1	2.32	0.44
58:B1:731:ARG:HB3	59:B2:1105:SER:HB2	2.00	0.44
58:B1:1026:PRO:HB2	58:B1:1028:ILE:HG23	2.00	0.44
58:B1:1033:GLY:HA3	58:B1:1081:VAL:O	2.18	0.44
59:B2:829:THR:HG23	59:B2:1059:ARG:HG2	2.00	0.44
66:0:119:VAL:HG21	66:0:162:LEU:HD11	2.00	0.44
14:N:125:GLN:HG3	53:3:1232:U:H5''	1.99	0.44
26:Z:6:ARG:HA	26:Z:6:ARG:HD2	1.61	0.44
28:c:5:VAL:HG22	28:c:202:ILE:HG12	2.00	0.44
28:c:197:THR:HG23	51:1:2820:A:C6	2.52	0.44
29:d:136:GLN:HA	29:d:139:LYS:HB2	1.99	0.44
30:e:135:ILE:HA	30:e:140:ILE:HD11	1.99	0.44
35:k:61:VAL:O	35:k:85:VAL:N	2.47	0.44
36:l:29:LYS:HA	51:1:810:U:H5	1.81	0.44
37:m:68:PHE:CE2	51:1:871:U:H5''	2.53	0.44
37:m:71:LYS:HD3	37:m:72:PRO:HD2	2.00	0.44
45:u:14:THR:OG1	45:u:15:GLY:N	2.51	0.44
51:1:368:A:C2'	51:1:369:U:H5'	2.47	0.44
51:1:728:G:O2'	51:1:730:A:H8	2.01	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:740:C:H5'	51:1:740:C:C6	2.46	0.44
51:1:1056:G:H1'	51:1:1103:A:N6	2.33	0.44
51:1:1630:A:H2'	51:1:1631:G:H5'	2.00	0.44
51:1:1747:U:H2'	51:1:1748:C:C6	2.52	0.44
51:1:1783:A:N1	51:1:2587:A:N3	2.63	0.44
51:1:2069:G:H2'	51:1:2070:A:H8	1.82	0.44
51:1:2326:C:O2'	51:1:2327:A:OP1	2.32	0.44
51:1:2703:C:H2'	51:1:2704:C:H6	1.82	0.44
52:2:115:A:H2'	52:2:116:G:C8	2.53	0.44
53:3:253:A:O4'	53:3:276:G:H1'	2.18	0.44
53:3:369:G:N2	53:3:393:A:H1'	2.33	0.44
53:3:599:C:H2'	53:3:600:A:C8	2.53	0.44
53:3:964:A:H2'	53:3:965:U:H5'	2.00	0.44
57:A1:192:VAL:HG12	57:A1:193:GLU:H	1.83	0.44
58:B1:352:ARG:CD	59:B2:1268:GLN:NE2	2.67	0.44
63:5:13:C:H42	63:5:46:G:N2	2.16	0.44
8:H:6:PRO:O	8:H:10:ARG:NE	2.41	0.44
14:N:47:VAL:HG12	14:N:78:ILE:HG21	2.00	0.44
27:b:57:HIS:CE1	51:1:1567:G:H4'	2.52	0.44
28:c:94:GLN:H	28:c:94:GLN:HG3	1.59	0.44
42:r:17:GLY:H	42:r:98:ILE:HB	1.83	0.44
51:1:118:A:H5'	51:1:119:A:C8	2.53	0.44
51:1:298:G:C2	51:1:339:U:H5	2.35	0.44
51:1:1044:C:O5'	51:1:1044:C:H6	2.00	0.44
51:1:1086:A:H3'	51:1:1086:A:N3	2.33	0.44
53:3:290:C:H2'	53:3:291:U:O4'	2.18	0.44
53:3:865:A:H2'	53:3:866:C:C6	2.53	0.44
53:3:1475:G:C2	53:3:1476:A:H1'	2.52	0.44
53:3:1508:A:H61	53:3:1527:U:H3	1.66	0.44
58:B1:62:PHE:N	58:B1:62:PHE:CD1	2.85	0.44
58:B1:107:LEU:HA	58:B1:276:ASN:ND2	2.33	0.44
58:B1:111:THR:CG2	58:B1:300:GLN:HA	2.48	0.44
58:B1:141:PHE:HE2	58:B1:296:LYS:CB	2.22	0.44
58:B1:375:GLU:HB3	59:B2:1245:ALA:CB	2.48	0.44
63:5:34:G:H5'	63:5:35:A:C8	2.52	0.44
63:5:63:G:H2'	63:5:64:A:C8	2.53	0.44
66:0:173:ILE:HD13	66:0:173:ILE:HA	1.90	0.44
3:C:33:LEU:HD21	51:1:2286:G:C5	2.53	0.43
11:K:73:GLU:O	11:K:76:THR:OG1	2.31	0.43
13:M:45:ILE:HG12	13:M:60:LEU:HD23	2.00	0.43
21:U:13:LYS:CD	53:3:392:C:H5'	2.48	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:p:59:THR:HG22	40:p:72:VAL:HG23	2.00	0.43
51:1:862:G:H2'	51:1:863:A:O4'	2.18	0.43
51:1:1308:A:N6	51:1:1608:A:H61	2.16	0.43
51:1:2065:C:H2'	51:1:2066:C:C6	2.53	0.43
51:1:2524:G:C3'	51:1:2525:G:H5''	2.48	0.43
51:1:2599:G:H2'	51:1:2600:A:C8	2.53	0.43
53:3:570:G:H5'	53:3:820:U:O4'	2.17	0.43
53:3:1242:G:H4'	53:3:1304:G:OP1	2.18	0.43
58:B1:58:CYS:SG	58:B1:60:ARG:HG2	2.59	0.43
58:B1:68:TYR:O	58:B1:75:TYR:CD2	2.70	0.43
58:B1:68:TYR:HB3	58:B1:75:TYR:HE2	1.81	0.43
58:B1:800:LEU:HD12	58:B1:800:LEU:HA	1.79	0.43
58:B1:850:LYS:HB3	58:B1:855:ASP:HB2	2.00	0.43
59:B2:515:MET:HE2	59:B2:515:MET:HB3	1.82	0.43
65:a:203:GLN:HG2	65:a:205:LYS:H	1.83	0.43
66:0:122:GLN:O	66:0:125:THR:OG1	2.36	0.43
7:G:23:ASN:H	7:G:189:ASN:HA	1.82	0.43
9:I:33:ILE:HG23	9:I:34:GLU:HG2	1.99	0.43
12:L:34:LYS:NZ	53:3:1289:A:C2	2.86	0.43
14:N:45:MET:HA	14:N:48:ARG:HH21	1.83	0.43
14:N:129:ARG:NH1	64:6:32:C:OP2	2.49	0.43
26:Z:24:LYS:HD3	26:Z:24:LYS:HA	1.80	0.43
27:b:106:PRO:HD2	27:b:109:LEU:HD22	1.99	0.43
33:i:128:ILE:HA	33:i:131:THR:HG22	2.01	0.43
34:j:81:ILE:HG21	51:1:2514:U:H4'	1.99	0.43
34:j:116:ARG:HH21	51:1:528:A:H5''	1.81	0.43
39:o:55:GLU:OE2	52:2:116:G:H5''	2.17	0.43
51:1:330:A:H8	51:1:1210:G:C5	2.36	0.43
51:1:537:G:H22	51:1:555:G:H2'	1.83	0.43
51:1:608:A:H2'	51:1:609:A:O4'	2.18	0.43
51:1:1697:G:H3'	51:1:1698:A:C5'	2.45	0.43
51:1:2102:G:H1	51:1:2187:U:H3	1.65	0.43
51:1:2723:C:H2'	51:1:2724:U:O4'	2.17	0.43
53:3:160:A:H2'	53:3:161:A:O4'	2.19	0.43
53:3:296:U:H2'	53:3:297:G:O4'	2.19	0.43
55:8:12:DG:OP1	58:B1:795:TYR:CE1	2.71	0.43
57:A1:78:ILE:HA	57:A1:81:ILE:HG22	2.00	0.43
58:B1:478:LEU:HD21	60:W0:47:THR:HG23	1.99	0.43
58:B1:824:PRO:HD3	58:B1:835:LEU:HD12	2.00	0.43
58:B1:978:ARG:HD3	58:B1:999:TYR:H	1.83	0.43
59:B2:557:ARG:HB3	59:B2:587:LEU:HD13	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:646:SER:OG	59:B2:647:ARG:N	2.51	0.43
63:5:37:A:H2'	63:5:38:A:C8	2.53	0.43
66:0:73:SER:HB2	66:0:81:PRO:HG3	2.00	0.43
66:0:75:MET:HG3	66:0:279:LEU:HD11	1.99	0.43
66:0:423:LYS:HA	66:0:482:ASN:HD21	1.83	0.43
27:b:120:ASP:OD1	27:b:120:ASP:N	2.49	0.43
35:k:40:LYS:HZ2	35:k:57:VAL:HG12	1.84	0.43
38:n:36:THR:HG22	51:1:1278:C:OP1	2.18	0.43
39:o:56:LYS:HA	39:o:59:ALA:HB3	2.01	0.43
43:s:36:LEU:HD23	43:s:48:LYS:HB2	2.01	0.43
43:s:84:ARG:NH1	51:1:1322:A:O2'	2.51	0.43
47:w:58:LYS:HD3	51:1:2366:A:H4'	1.99	0.43
48:x:17:ARG:HA	48:x:17:ARG:HD3	1.72	0.43
51:1:74:A:H2'	51:1:74:A:N3	2.33	0.43
51:1:152:A:H2'	51:1:153:U:C6	2.53	0.43
51:1:578:G:H21	51:1:1252:G:N2	2.16	0.43
51:1:755:U:H2'	51:1:756:A:C8	2.52	0.43
51:1:974:G:C6	51:1:1186:G:C6	3.06	0.43
51:1:1368:G:H2'	51:1:1369:G:C8	2.51	0.43
51:1:1545:A:H2'	51:1:1546:G:O4'	2.17	0.43
51:1:2061:G:C8	51:1:2501:C:H4'	2.53	0.43
51:1:2267:A:H5''	51:1:2268:A:H5'	2.01	0.43
52:2:4:C:H6	52:2:4:C:C5'	2.31	0.43
53:3:1134:G:H1	53:3:1140:C:H42	1.66	0.43
53:3:1195:C:O5'	53:3:1195:C:H6	2.01	0.43
59:B2:811:ASN:ND2	59:B2:1098:LEU:O	2.51	0.43
66:0:365:GLN:N	66:0:372:GLU:O	2.38	0.43
12:L:91:ARG:O	12:L:92:PRO:C	2.59	0.43
15:O:68:ARG:HD3	15:O:68:ARG:HA	1.68	0.43
16:P:118:ASN:OD1	53:3:718:A:H5'	2.18	0.43
31:f:28:LYS:HE3	31:f:28:LYS:HB2	1.86	0.43
38:n:72:ASP:O	38:n:76:VAL:HG23	2.19	0.43
38:n:99:LYS:HE3	38:n:99:LYS:HB3	1.72	0.43
51:1:170:U:H2'	51:1:171:U:C6	2.53	0.43
51:1:793:A:OP2	51:1:793:A:H8	2.01	0.43
51:1:1037:G:O2'	51:1:1038:G:H5'	2.18	0.43
51:1:1404:C:O5'	51:1:1404:C:H6	2.01	0.43
51:1:1815:A:O4'	51:1:1817:G:H1'	2.18	0.43
51:1:2338:C:H6	51:1:2338:C:O5'	2.01	0.43
53:3:971:G:H4'	53:3:972:C:H5''	1.99	0.43
53:3:1057:G:H2'	53:3:1058:G:O4'	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:3:DC:N1	55:8:4:DT:H72	2.34	0.43
58:B1:45:ASN:HD22	58:B1:48:THR:H	1.65	0.43
58:B1:894:VAL:HG22	58:B1:1258:ARG:HH11	1.83	0.43
59:B2:487:LEU:HD22	59:B2:487:LEU:HA	1.77	0.43
59:B2:1157:GLN:HG3	59:B2:1159:VAL:HG13	2.00	0.43
28:c:120:GLY:H	28:c:123:LYS:HB2	1.82	0.43
29:d:134:LEU:HD11	29:d:161:ALA:HB2	1.99	0.43
32:g:27:ARG:NH2	48:x:55:MET:HB3	2.32	0.43
34:j:80:HIS:CD2	51:1:2642:G:H5'	2.53	0.43
35:k:49:ARG:HH22	53:3:1423:G:H5'	1.84	0.43
37:m:46:ILE:O	37:m:50:ARG:N	2.45	0.43
51:1:1123:C:O2'	51:1:1124:G:H5'	2.18	0.43
51:1:1794:A:O2'	51:1:1795:C:H5'	2.18	0.43
51:1:2556:C:H2'	51:1:2557:G:C5'	2.48	0.43
51:1:2638:G:H22	51:1:2775:G:H2'	1.83	0.43
51:1:2672:U:C3'	51:1:2673:G:H5''	2.48	0.43
51:1:2845:U:H2'	51:1:2846:G:H8	1.83	0.43
53:3:1095:U:OP1	53:3:1108:G:N2	2.52	0.43
53:3:1252:A:H2'	53:3:1253:G:O4'	2.18	0.43
58:B1:111:THR:HG21	58:B1:303:VAL:HB	2.00	0.43
58:B1:161:THR:H	58:B1:164:GLN:HB2	1.82	0.43
58:B1:1046:ILE:HG22	58:B1:1061:VAL:HA	2.00	0.43
58:B1:1357:ILE:HG22	58:B1:1359:ALA:H	1.82	0.43
59:B2:538:LEU:HD13	59:B2:543:ALA:HB2	2.01	0.43
59:B2:557:ARG:NH2	59:B2:607:SER:O	2.50	0.43
65:a:193:LEU:HG	65:a:197:LYS:HG3	2.00	0.43
66:0:112:VAL:HG12	66:0:140:PHE:HB3	2.00	0.43
8:H:66:THR:HA	8:H:101:ASN:HB2	1.99	0.43
9:I:69:ARG:HH11	9:I:72:ARG:HH22	1.67	0.43
11:K:45:ARG:N	11:K:57:ALA:O	2.45	0.43
17:Q:5:GLN:NE2	53:3:881:G:N7	2.67	0.43
24:X:38:THR:HG23	24:X:69:LYS:HD3	1.99	0.43
26:Z:66:ARG:O	53:3:1088:G:O2'	2.36	0.43
34:j:130:HIS:HB2	34:j:132:HIS:HD2	1.84	0.43
38:n:90:ARG:NH2	51:1:2880:C:O2'	2.48	0.43
39:o:57:ALA:O	39:o:61:GLN:NE2	2.52	0.43
51:1:812:C:H1'	51:1:1250:G:C2	2.53	0.43
51:1:984:A:P	51:1:985:C:H5	2.41	0.43
51:1:1057:A:H5''	51:1:1058:U:O2	2.18	0.43
51:1:1064:C:H5''	51:1:1065:U:C5	2.54	0.43
51:1:1428:C:C5	51:1:1569:A:H5''	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1716:U:C2'	51:1:1717:A:H5'	2.49	0.43
51:1:1771:C:H2'	51:1:1772:A:O4'	2.19	0.43
53:3:1014:A:C2	53:3:1219:A:H1'	2.54	0.43
53:3:1042:A:H2'	53:3:1043:G:H4'	2.00	0.43
53:3:1158:C:H2'	53:3:1159:U:H4'	2.01	0.43
53:3:1364:U:O2'	53:3:1365:G:H5'	2.19	0.43
53:3:1382:C:H2'	53:3:1383:C:C5	2.54	0.43
53:3:1515:G:H2'	53:3:1516:G:H8	1.82	0.43
58:B1:568:SER:HB3	58:B1:570:LYS:NZ	2.34	0.43
59:B2:1275:VAL:HG13	59:B2:1287:LEU:HD11	2.01	0.43
11:K:89:VAL:HG23	53:3:737:C:C4'	2.49	0.43
12:L:29:LEU:HD23	12:L:104:VAL:HG23	2.01	0.43
17:Q:87:LYS:HB3	17:Q:87:LYS:HE3	1.69	0.43
20:T:60:SER:HB2	53:3:581:G:C5'	2.48	0.43
26:Z:53:LYS:HB2	26:Z:53:LYS:HE2	1.90	0.43
27:b:209:ALA:HA	27:b:212:TRP:CE2	2.54	0.43
28:c:118:PHE:O	51:1:1655:A:H5'	2.18	0.43
29:d:129:PRO:HG3	29:d:156:ASN:HA	2.00	0.43
31:f:9:VAL:HA	31:f:48:THR:HA	2.00	0.43
35:k:51:LYS:HD3	35:k:51:LYS:HA	1.75	0.43
50:z:11:SER:OG	51:1:988:A:H5''	2.18	0.43
51:1:252:G:H2'	51:1:253:C:C6	2.53	0.43
51:1:481:G:H2'	51:1:507:A:N1	2.34	0.43
51:1:571:U:C4	51:1:575:A:C5	3.07	0.43
51:1:742:A:H2'	51:1:743:A:O4'	2.19	0.43
51:1:878:A:H3'	51:1:879:G:C8	2.54	0.43
51:1:974:G:C8	51:1:989:G:C2	3.07	0.43
51:1:1412:U:H2'	51:1:1413:A:O4'	2.18	0.43
51:1:1823:G:C6	51:1:1824:G:C6	3.06	0.43
51:1:1984:G:H2'	51:1:1985:C:H6	1.82	0.43
51:1:2101:A:H2'	51:1:2102:G:H8	1.84	0.43
51:1:2577:A:H2'	51:1:2614:A:N6	2.33	0.43
53:3:640:A:H2'	53:3:641:U:H5'	2.01	0.43
53:3:1489:G:H2'	53:3:1490:U:C6	2.53	0.43
58:B1:388:ARG:HG2	58:B1:388:ARG:HH11	1.84	0.43
58:B1:950:ILE:HB	58:B1:1018:ALA:HB3	2.01	0.43
60:W0:58:LEU:HD12	60:W0:59:ILE:HG12	2.00	0.43
66:0:68:THR:N	66:0:86:ILE:O	2.46	0.43
66:0:634:ASP:O	66:0:638:ARG:NH1	2.52	0.43
8:H:1:GLY:HA2	53:3:1060:U:C5	2.54	0.43
10:J:25:LYS:HG3	53:3:923:A:C5'	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:89:VAL:HG23	53:3:737:C:C5'	2.48	0.43
14:N:7:GLY:HA3	14:N:85:ALA:HB2	2.00	0.43
14:N:58:GLU:HG2	14:N:59:LYS:HG3	2.00	0.43
29:d:131:THR:HG21	51:1:320:A:H2'	2.00	0.43
30:e:134:GLN:NE2	30:e:147:ARG:O	2.41	0.43
38:n:9:GLN:HB2	51:1:1653:G:C6	2.54	0.43
42:r:34:GLU:HB2	42:r:58:VAL:HB	1.99	0.43
51:1:666:A:H2'	51:1:667:U:C6	2.54	0.43
51:1:728:G:H3'	51:1:729:G:H5'	2.00	0.43
51:1:784:G:N7	51:1:792:A:C5	2.87	0.43
51:1:824:U:H1'	51:1:2358:A:N7	2.34	0.43
51:1:960:A:O3'	51:1:961:C:H3'	2.18	0.43
51:1:1794:A:H1'	51:1:1900:A:N3	2.34	0.43
51:1:1803:A:C2	51:1:1823:G:H1'	2.53	0.43
51:1:1931:U:H2'	51:1:1932:A:C8	2.54	0.43
51:1:1998:A:H4'	51:1:2724:U:O2'	2.19	0.43
51:1:2489:U:O2'	51:1:2490:G:H5'	2.18	0.43
53:3:777:A:C2	53:3:778:G:H1'	2.53	0.43
55:8:15:DC:H5'	59:B2:1269:ARG:HD3	2.00	0.43
65:a:48:LEU:HB3	65:a:50:ILE:HG23	2.01	0.43
66:0:159:LYS:HG3	66:0:166:PRO:HD2	2.00	0.43
14:N:18:VAL:HG21	14:N:81:GLY:HA3	2.01	0.43
17:Q:48:LEU:HD12	17:Q:48:LEU:HA	1.85	0.43
18:R:13:HIS:HB3	18:R:15:VAL:HG12	2.00	0.43
23:W:35:SER:OG	23:W:37:LYS:NZ	2.37	0.43
27:b:252:LYS:HD3	27:b:252:LYS:HA	1.80	0.43
28:c:118:PHE:CD2	51:1:1654:A:H2	2.35	0.43
32:g:8:LYS:HA	32:g:8:LYS:HD2	1.72	0.43
44:t:1:MET:HG3	51:1:136:G:H21	1.84	0.43
46:v:88:HIS:CE1	52:2:75:G:H21	2.36	0.43
51:1:597:G:H2'	51:1:598:U:O4'	2.18	0.43
51:1:786:C:H2'	51:1:787:C:H6	1.83	0.43
51:1:832:U:C5	51:1:944:C:N4	2.87	0.43
51:1:1313:U:O2	51:1:1313:U:H2'	2.19	0.43
51:1:1797:G:C4	51:1:1798:U:C6	3.07	0.43
51:1:1914:C:N4	53:3:1409:C:O3'	2.52	0.43
51:1:2234:G:O2'	51:1:2235:G:H5'	2.19	0.43
51:1:2248:C:H3'	51:1:2249:U:H6	1.81	0.43
51:1:2617:U:H2'	51:1:2618:G:H5'	2.01	0.43
51:1:2626:C:O2'	51:1:2627:G:H5'	2.19	0.43
53:3:304:U:O2'	53:3:305:G:H5'	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:439:U:O2'	53:3:440:C:H5'	2.19	0.43
53:3:596:A:H61	53:3:644:U:H3	1.66	0.43
53:3:635:A:H2'	53:3:636:U:C6	2.53	0.43
53:3:1233:G:O2'	53:3:1365:G:H5''	2.18	0.43
58:B1:434:ILE:HD11	59:B2:1274:GLU:CG	2.49	0.43
59:B2:800:MET:HB2	59:B2:800:MET:HE3	1.69	0.43
66:0:498:VAL:HG22	66:0:499:THR:N	2.33	0.43
9:I:200:VAL:HG11	10:J:103:GLY:HA2	2.00	0.43
10:J:123:LEU:HD22	53:3:7:A:H2'	2.00	0.43
18:R:78:ARG:HD3	24:X:64:GLU:HG2	2.01	0.43
30:e:88:VAL:HA	52:2:42:C:O2	2.19	0.43
32:g:63:ALA:HA	32:g:66:ASN:HD22	1.84	0.43
34:j:93:ILE:HD12	34:j:93:ILE:HA	1.72	0.43
37:m:33:LEU:HD12	37:m:117:PHE:HB3	2.00	0.43
38:n:73:ASN:HB3	51:1:1453:A:C8	2.54	0.43
38:n:107:ASN:HD22	51:1:2009:A:C4'	2.31	0.43
39:o:40:ILE:HD13	39:o:40:ILE:HA	1.92	0.43
51:1:194:G:H2'	51:1:195:A:O4'	2.19	0.43
51:1:272:A:H2'	51:1:273:G:C8	2.54	0.43
51:1:1675:C:O2'	51:1:1676:A:H5'	2.19	0.43
51:1:1943:U:OP1	51:1:1943:U:C6	2.71	0.43
51:1:1962:C:H1'	51:1:1963:U:C5	2.53	0.43
51:1:2564:A:C2	51:1:2647:U:H4'	2.54	0.43
53:3:37:U:C2'	53:3:38:G:H5'	2.48	0.43
53:3:1210:C:H2'	53:3:1211:U:H5'	2.00	0.43
53:3:1236:A:H2'	53:3:1237:C:O4'	2.19	0.43
58:B1:141:PHE:CD2	58:B1:297:ARG:HB2	2.54	0.43
58:B1:201:LEU:HD11	58:B1:220:ARG:NH1	2.32	0.43
59:B2:998:LEU:HG	59:B2:1011:LEU:HB3	1.99	0.43
59:B2:1313:HIS:CD2	60:W0:31:GLN:HE22	2.37	0.43
66:0:129:GLN:HG3	66:0:132:LYS:HE2	2.00	0.43
67:h:2:DPP:NG	67:h:3:SER:N	2.65	0.43
13:M:10:LEU:HD13	13:M:74:ILE:HG13	2.00	0.42
14:N:11:ARG:O	14:N:14:SER:OG	2.32	0.42
27:b:17:LYS:HE3	27:b:17:LYS:HB3	1.80	0.42
33:i:105:LEU:HD13	33:i:128:ILE:HG23	2.01	0.42
34:j:136:GLN:NE2	51:1:2899:A:H5'	2.34	0.42
36:l:37:GLY:H	36:l:41:ARG:HH22	1.66	0.42
44:t:29:THR:HG22	44:t:86:THR:HA	2.01	0.42
47:w:56:PHE:HB2	47:w:57:ALA:H	1.73	0.42
50:z:18:LYS:HE2	50:z:18:LYS:HB3	1.89	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:690:G:C2'	51:1:691:C:H5'	2.49	0.42
51:1:1060:U:OP2	51:1:1060:U:H3'	2.19	0.42
51:1:1321:A:H3'	51:1:1322:A:H8	1.84	0.42
51:1:2311:A:H3'	51:1:2312:U:C6	2.54	0.42
51:1:2598:A:N7	51:1:2599:G:H1'	2.34	0.42
53:3:405:U:O2	53:3:498:A:H2'	2.19	0.42
53:3:633:G:H2'	53:3:634:C:C6	2.54	0.42
53:3:778:G:H2'	53:3:779:C:O4'	2.19	0.42
53:3:1423:G:H1	53:3:1477:U:H3	1.65	0.42
58:B1:515:ARG:NH2	58:B1:718:SER:O	2.48	0.42
58:B1:559:ALA:HB3	58:B1:562:GLU:HB3	2.01	0.42
59:B2:11:ILE:HG22	59:B2:1172:LEU:HD11	1.99	0.42
59:B2:1278:LEU:HD23	59:B2:1278:LEU:HA	1.86	0.42
63:5:9:A:H1'	63:5:45:U:H2'	2.01	0.42
7:G:72:LYS:HZ2	7:G:74:ALA:HB3	1.83	0.42
9:I:12:ARG:NH2	9:I:36:ALA:H	2.17	0.42
9:I:110:ARG:O	9:I:114:ARG:N	2.52	0.42
9:I:119:HIS:HA	53:3:439:U:H5''	2.01	0.42
11:K:12:PRO:O	11:K:15:SER:OG	2.32	0.42
13:M:15:ASN:HB3	53:3:827:U:C4'	2.48	0.42
23:W:25:ILE:HA	23:W:28:LEU:HD12	2.01	0.42
28:c:183:GLU:OE2	28:c:184:ARG:NE	2.53	0.42
36:l:18:ARG:NE	51:1:1249:U:C4	2.88	0.42
43:s:29:VAL:HG21	43:s:55:ILE:HG21	2.01	0.42
48:x:31:ASN:CG	51:1:2230:G:H1'	2.44	0.42
51:1:441:U:O2'	51:1:442:G:H5'	2.19	0.42
51:1:533:G:H5''	51:1:533:G:H8	1.83	0.42
51:1:1135:C:O2	51:1:1135:C:H2'	2.18	0.42
51:1:1177:G:C3'	51:1:1178:C:H5''	2.49	0.42
51:1:1801:A:C8	51:1:1801:A:H5'	2.54	0.42
51:1:2556:C:H2'	51:1:2557:G:O4'	2.19	0.42
51:1:2656:U:H2'	51:1:2657:A:C8	2.55	0.42
53:3:250:A:H4'	53:3:251:G:O5'	2.19	0.42
58:B1:24:LEU:HD21	58:B1:116:PHE:CE2	2.54	0.42
58:B1:243:PRO:HG2	59:B2:1332:SER:C	2.44	0.42
58:B1:586:GLY:HA3	58:B1:612:LEU:HD11	2.01	0.42
59:B2:22:LEU:HB3	59:B2:655:VAL:HG11	2.01	0.42
59:B2:300:ASP:OD1	59:B2:313:ALA:N	2.51	0.42
4:D:10:LEU:HD13	51:1:125:A:C2	2.54	0.42
6:F:38:GLY:OXT	51:1:1124:G:H1'	2.19	0.42
14:N:68:GLY:O	14:N:74:GLN:NE2	2.37	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:22:TYR:HD2	18:R:65:GLU:HA	1.84	0.42
18:R:77:LYS:HB2	18:R:77:LYS:HE3	1.88	0.42
24:X:44:ILE:HD12	24:X:44:ILE:HA	1.92	0.42
27:b:204:LEU:O	27:b:206:LYS:N	2.48	0.42
27:b:204:LEU:HD23	27:b:204:LEU:HA	1.90	0.42
29:d:93:SER:O	29:d:93:SER:OG	2.32	0.42
33:i:12:VAL:HG12	33:i:13:ALA:H	1.83	0.42
39:o:10:ARG:HE	39:o:10:ARG:HB2	1.61	0.42
51:1:343:C:C2'	51:1:344:A:H5'	2.49	0.42
51:1:1363:C:O2'	51:1:1809:A:H1'	2.20	0.42
51:1:2133:G:H8	51:1:2158:A:C2	2.38	0.42
52:2:79:G:H2'	52:2:80:U:O4'	2.19	0.42
54:4:38:U:H6	54:4:38:U:H2'	1.68	0.42
58:B1:59:ALA:HB1	58:B1:90:VAL:HG23	2.01	0.42
58:B1:242:LEU:C	58:B1:242:LEU:HD23	2.44	0.42
58:B1:279:LEU:HD13	58:B1:299:LEU:HD13	2.02	0.42
58:B1:385:LEU:CD2	58:B1:390:LEU:HB2	2.50	0.42
58:B1:820:ILE:HG12	58:B1:884:SER:HB2	2.01	0.42
58:B1:1024:THR:HG23	58:B1:1123:ARG:HA	2.00	0.42
59:B2:125:GLY:H	59:B2:495:ALA:HB1	1.84	0.42
59:B2:861:ALA:HB1	59:B2:882:ILE:HD13	2.02	0.42
59:B2:895:LEU:HD23	59:B2:895:LEU:HA	1.87	0.42
66:0:493:THR:OG1	66:0:525:LEU:CD1	2.68	0.42
2:B:41:HIS:HD2	38:n:101:GLY:HA2	1.84	0.42
5:E:28:LEU:HD12	5:E:32:LEU:HD11	2.01	0.42
7:G:53:LEU:HD23	7:G:56:LEU:HD12	2.01	0.42
14:N:113:LYS:HA	14:N:120:ALA:HB2	2.01	0.42
18:R:70:ARG:O	18:R:73:SER:OG	2.36	0.42
21:U:31:ARG:HB2	53:3:310:G:H5'	2.00	0.42
25:Y:4:LYS:HE2	53:3:332:G:OP1	2.20	0.42
27:b:73:ILE:HA	27:b:74:PRO:HD3	1.90	0.42
36:l:90:VAL:HG22	36:l:122:VAL:HA	2.02	0.42
51:1:139:G:H2'	51:1:40:U:C6	2.54	0.42
51:1:1145:C:H2'	51:1:1146:C:C6	2.54	0.42
51:1:1191:G:H2'	51:1:1192:G:C8	2.51	0.42
51:1:1741:C:H2'	51:1:1742:U:H5'	2.01	0.42
51:1:1797:G:N2	51:1:1798:U:H1'	2.34	0.42
51:1:2060:A:O2'	51:1:2061:G:OP2	2.35	0.42
53:3:264:C:H2'	53:3:265:G:O4'	2.19	0.42
53:3:316:C:H2'	53:3:317:U:C6	2.55	0.42
53:3:865:A:H5'	53:3:1078:U:O4	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:973:G:H2'	53:3:974:A:H8	1.84	0.42
53:3:1061:G:H2'	53:3:1062:U:O4'	2.19	0.42
53:3:1119:C:O2'	53:3:1120:C:H5'	2.20	0.42
53:3:1194:U:H2'	53:3:1195:C:C6	2.54	0.42
53:3:1271:A:H5'	53:3:1314:C:H5'	2.01	0.42
53:3:1305:G:HO2'	53:3:1306:A:H8	1.62	0.42
57:A1:76:GLU:HB3	57:A1:80:GLU:HB3	2.01	0.42
57:A1:212:ASP:OD1	57:A1:212:ASP:N	2.48	0.42
58:B1:96:LYS:NZ	59:B2:1298:VAL:HG11	2.34	0.42
59:B2:616:ILE:HG13	59:B2:652:TYR:HB2	2.01	0.42
59:B2:1072:ASN:OD1	59:B2:1072:ASN:N	2.52	0.42
8:H:168:ARG:NH1	53:3:1106:G:O2'	2.53	0.42
8:H:174:LEU:HB3	53:3:1108:G:OP1	2.19	0.42
12:L:138:GLU:HA	12:L:141:HIS:HB2	2.00	0.42
14:N:53:LEU:HD12	14:N:54:VAL:HG13	2.00	0.42
27:b:218:THR:HG22	51:1:1790:C:OP1	2.19	0.42
27:b:219:VAL:HG21	51:1:782:A:N7	2.35	0.42
28:c:140:HIS:NE2	51:1:1658:C:OP1	2.52	0.42
28:c:161:MET:CE	51:1:2050:C:H1'	2.49	0.42
31:f:85:LYS:HE3	31:f:131:VAL:HG22	2.01	0.42
38:n:106:ASP:OD2	51:1:1287:A:C5	2.72	0.42
41:q:47:ARG:NH2	51:1:560:C:O2'	2.52	0.42
51:1:481:G:H1'	51:1:506:G:H22	1.82	0.42
51:1:842:U:H2'	51:1:843:G:O4'	2.19	0.42
51:1:1373:A:H2'	51:1:1374:G:O4'	2.20	0.42
51:1:2391:G:O6	51:1:2425:A:H5''	2.20	0.42
51:1:2575:C:O5'	51:1:2575:C:H6	2.03	0.42
51:1:2581:G:N1	51:1:2610:C:O2'	2.52	0.42
51:1:2596:U:H2'	51:1:2597:G:O4'	2.19	0.42
53:3:927:G:H4'	53:3:1503:A:N7	2.33	0.42
53:3:1199:U:H2'	53:3:1200:C:H5'	2.01	0.42
53:3:1469:C:C2'	53:3:1470:U:H5'	2.50	0.42
55:8:2:DC:H6	55:8:2:DC:H2'	1.74	0.42
58:B1:102:MET:HG2	58:B1:246:PRO:CG	2.49	0.42
58:B1:362:ARG:HB2	58:B1:364:HIS:HD2	1.83	0.42
66:0:211:MET:HE2	66:0:211:MET:HB3	1.63	0.42
66:0:607:LYS:HE2	66:0:607:LYS:HB2	1.84	0.42
2:B:24:VAL:H	43:s:35:ILE:HD11	1.84	0.42
4:D:13:ASN:HB3	51:1:125:A:O4'	2.20	0.42
5:E:44:ARG:NH2	51:1:2349:G:OP1	2.48	0.42
7:G:26:MET:HG3	7:G:29:PHE:HB2	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:47:LEU:CD2	11:K:55:HIS:HA	2.49	0.42
14:N:13:SER:HG	53:3:1251:A:H5'	1.81	0.42
16:P:81:LEU:HD11	16:P:99:LEU:HD13	2.01	0.42
24:X:32:THR:OG1	24:X:33:TRP:N	2.53	0.42
27:b:144:GLU:HA	27:b:151:GLY:HA2	2.01	0.42
27:b:148:GLY:O	51:1:2205:A:H5'	2.20	0.42
46:v:44:HIS:CE1	46:v:86:LEU:H	2.37	0.42
49:y:1:MET:HA	49:y:4:LYS:HE2	2.01	0.42
51:1:76:C:H42	51:1:110:G:H1	1.68	0.42
51:1:516:C:H2'	51:1:517:C:H5'	2.02	0.42
51:1:809:G:O4'	51:1:1254:A:H1'	2.19	0.42
51:1:828:U:H2'	51:1:829:A:N7	2.30	0.42
51:1:1854:A:H2'	51:1:1855:U:H5'	2.02	0.42
51:1:1983:G:C2	51:1:1984:G:C8	3.07	0.42
51:1:2350:C:H2'	51:1:2351:G:O4'	2.19	0.42
51:1:2521:C:C2'	51:1:2522:U:H5'	2.50	0.42
51:1:2553:G:C3'	51:1:2554:U:H5''	2.47	0.42
51:1:2654:A:H1'	51:1:2656:U:C6	2.54	0.42
51:1:2670:A:H2'	51:1:2671:G:C8	2.55	0.42
53:3:7:A:H5'	53:3:298:A:O4'	2.19	0.42
53:3:540:G:H2'	53:3:541:G:O4'	2.20	0.42
58:B1:120:LEU:HD22	58:B1:120:LEU:HA	1.77	0.42
58:B1:238:ILE:H	58:B1:238:ILE:HG12	1.72	0.42
59:B2:755:LYS:HD2	59:B2:755:LYS:HA	1.86	0.42
10:J:126:ALA:H	53:3:9:G:P	2.43	0.42
19:S:52:ARG:HD3	53:3:1317:C:N3	2.34	0.42
20:T:3:SER:OG	20:T:4:THR:N	2.53	0.42
21:U:71:VAL:HA	21:U:74:LEU:HB2	2.02	0.42
22:V:29:LYS:HE2	22:V:29:LYS:HB3	1.83	0.42
31:f:14:VAL:HG12	31:f:27:GLY:HA2	2.01	0.42
35:k:47:ILE:HD13	35:k:47:ILE:HA	1.85	0.42
37:m:55:ARG:HA	37:m:58:LYS:HA	2.02	0.42
51:1:172:A:H2'	51:1:173:A:C8	2.54	0.42
51:1:382:A:C2	51:1:393:C:N3	2.88	0.42
51:1:820:A:H5'	51:1:837:C:O2'	2.19	0.42
51:1:981:A:H1'	51:1:2037:A:H1'	2.00	0.42
51:1:1229:C:H2'	51:1:1230:A:C8	2.53	0.42
51:1:2177:C:O2	65:a:170:ILE:HG12	2.19	0.42
51:1:2556:C:C2'	51:1:2557:G:H5'	2.48	0.42
51:1:2897:U:H2'	51:1:2898:U:C6	2.54	0.42
53:3:182:A:H2'	53:3:183:C:H5''	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:301:G:H2'	53:3:302:G:H8	1.83	0.42
53:3:627:G:H2'	53:3:628:G:C8	2.54	0.42
58:B1:144:TYR:CE1	58:B1:162:GLU:OE1	2.73	0.42
58:B1:211:GLU:CG	58:B1:215:LYS:HE3	2.44	0.42
58:B1:394:ILE:O	58:B1:394:ILE:HG13	2.19	0.42
58:B1:609:TYR:HD2	58:B1:610:ARG:NH1	2.17	0.42
58:B1:839:VAL:HG12	58:B1:864:LEU:HD12	2.02	0.42
59:B2:148:GLN:NE2	59:B2:535:PRO:O	2.40	0.42
59:B2:444:ASP:OD1	59:B2:444:ASP:N	2.51	0.42
9:I:57:LYS:NZ	9:I:68:GLU:OE1	2.43	0.42
18:R:64:VAL:H	18:R:67:ASP:HB3	1.85	0.42
18:R:105:ALA:HB3	18:R:109:LYS:HE3	2.02	0.42
20:T:27:GLN:O	20:T:27:GLN:NE2	2.51	0.42
21:U:5:ARG:NH2	53:3:377:G:H5''	2.35	0.42
21:U:50:THR:HB	21:U:78:VAL:HB	2.02	0.42
28:c:59:ARG:HA	28:c:59:ARG:HD2	1.85	0.42
28:c:152:PRO:HA	51:1:1130:U:O2	2.20	0.42
29:d:85:PHE:CG	51:1:588:U:H1'	2.55	0.42
38:n:51:LEU:HD23	38:n:79:LEU:HD11	2.02	0.42
39:o:11:ALA:HB1	39:o:14:ALA:HB3	2.01	0.42
42:r:1:MET:N	42:r:42:ALA:O	2.42	0.42
44:t:49:LYS:HD2	44:t:49:LYS:HA	1.75	0.42
46:v:76:ASP:H	46:v:90:ASP:HB3	1.85	0.42
49:y:9:LYS:HD3	49:y:10:SER:H	1.84	0.42
51:1:503:A:H4'	51:1:505:A:H5''	2.01	0.42
51:1:736:C:H42	51:1:760:G:H1	1.66	0.42
51:1:813:U:H2'	51:1:814:C:C6	2.54	0.42
51:1:1387:A:H2'	51:1:1388:G:C8	2.55	0.42
51:1:2114:A:N6	51:1:2119:A:H61	2.18	0.42
51:1:2391:G:H1	51:1:2424:C:H3'	1.85	0.42
51:1:2475:C:H42	51:1:2529:G:H22	1.66	0.42
51:1:2544:G:H2'	51:1:2545:G:C8	2.55	0.42
53:3:1229:A:H2'	53:3:1230:C:C6	2.54	0.42
53:3:1368:A:O2'	53:3:1369:C:H5'	2.19	0.42
53:3:1405:G:H21	53:3:1518:A:H8	1.67	0.42
58:B1:930:LEU:HA	58:B1:1244:GLN:HG3	2.02	0.42
59:B2:50:GLU:HG2	59:B2:73:TYR:HE1	1.85	0.42
59:B2:741:MET:SD	59:B2:974:ARG:NH2	2.93	0.42
65:a:46:VAL:O	65:a:170:ILE:HA	2.20	0.42
66:0:281:ALA:O	66:0:285:TYR:N	2.53	0.42
66:0:493:THR:OG1	66:0:525:LEU:HD11	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:56:LEU:HD23	7:G:56:LEU:HA	1.93	0.42
8:H:12:GLY:N	8:H:15:LYS:O	2.35	0.42
15:O:40:ILE:HD11	53:3:1124:G:H4'	2.02	0.42
16:P:52:ARG:HA	16:P:52:ARG:HD3	1.85	0.42
20:T:84:LEU:HD12	20:T:84:LEU:HA	1.93	0.42
29:d:50:ALA:HB2	51:1:801:G:C8	2.55	0.42
33:i:3:LYS:HB3	51:1:1055:G:O5'	2.19	0.42
35:k:38:ILE:HG22	35:k:61:VAL:HG22	2.01	0.42
51:1:8:C:H2'	51:1:9:G:O4'	2.20	0.42
51:1:445:C:O2'	51:1:446:G:H5'	2.20	0.42
51:1:751:A:H62	51:1:789:A:H62	1.67	0.42
51:1:780:G:H21	51:1:783:A:H62	1.67	0.42
51:1:877:A:O2'	51:1:900:A:N6	2.53	0.42
51:1:1050:A:O2'	51:1:2752:C:H1'	2.19	0.42
51:1:1512:C:O5'	51:1:1512:C:H6	2.03	0.42
51:1:1564:C:C4	51:1:1565:C:C4	3.08	0.42
51:1:1913:A:N1	53:3:1493:A:H2'	2.35	0.42
51:1:1972:G:H2'	51:1:1973:G:H8	1.85	0.42
51:1:2305:U:H2'	51:1:2306:C:H5'	2.01	0.42
51:1:2472:G:H5''	51:1:2473:U:OP2	2.20	0.42
51:1:2498:C:O2'	51:1:2499:C:H5'	2.20	0.42
51:1:2873:A:O2'	51:1:2874:C:H5'	2.20	0.42
53:3:58:C:H2'	53:3:59:A:H5'	2.01	0.42
53:3:269:C:H2'	53:3:270:A:C8	2.55	0.42
53:3:1005:A:C2'	53:3:1006:G:H5'	2.49	0.42
53:3:1153:G:H2'	53:3:1154:G:O4'	2.20	0.42
57:A2:48:LEU:HD23	57:A2:48:LEU:HA	1.86	0.42
58:B1:506:VAL:H	58:B1:506:VAL:HG12	1.59	0.42
59:B2:524:ILE:HD12	59:B2:712:SER:HB2	2.02	0.42
59:B2:741:MET:HE3	59:B2:974:ARG:HH12	1.85	0.42
66:0:520:ILE:HG22	66:0:578:LEU:HA	2.02	0.42
6:F:10:LEU:HD21	51:1:2477:U:H5	1.82	0.42
9:I:19:PHE:HD1	9:I:19:PHE:HA	1.58	0.42
16:P:34:THR:HA	16:P:40:ALA:HA	2.02	0.42
18:R:100:ARG:HG2	53:3:950:U:C5	2.55	0.42
21:U:38:PHE:HZ	21:U:48:GLU:HG3	1.84	0.42
27:b:170:TYR:HB3	27:b:182:LYS:HB3	2.02	0.42
29:d:46:GLN:HE21	29:d:86:ALA:HA	1.84	0.42
51:1:52:A:C5	51:1:118:A:C2	3.08	0.42
51:1:458:G:H21	51:1:469:G:H2'	1.84	0.42
51:1:976:G:H5'	51:1:1156:A:N6	2.35	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1379:U:H2'	51:1:1380:G:H5'	2.02	0.42
51:1:1592:C:H2'	51:1:1593:A:H8	1.83	0.42
51:1:1716:U:O2'	51:1:1717:A:H5'	2.20	0.42
51:1:1741:C:C2'	51:1:1742:U:H5'	2.50	0.42
51:1:2469:A:H2'	51:1:2470:G:O4'	2.20	0.42
53:3:1007:U:H2'	53:3:1008:U:C5	2.54	0.42
53:3:1327:C:H2'	53:3:1328:C:H6	1.84	0.42
57:A2:294:ASN:HA	61:NA:464:ILE:N	2.28	0.42
58:B1:244:VAL:HA	58:B1:269:TYR:OH	2.19	0.42
66:0:169:LEU:HD12	66:0:185:LEU:HB3	2.01	0.42
3:C:38:PHE:HD1	3:C:45:HIS:HD2	1.68	0.41
7:G:95:TRP:HZ3	7:G:99:MET:HE2	1.85	0.41
8:H:113:LYS:HA	8:H:113:LYS:HD2	1.88	0.41
9:I:155:LYS:HA	9:I:155:LYS:HD2	1.86	0.41
15:O:30:LYS:HA	15:O:34:ALA:HA	2.02	0.41
28:c:47:ALA:HA	28:c:84:LEU:HG	2.01	0.41
28:c:80:TRP:CD1	28:c:202:ILE:HD11	2.55	0.41
28:c:116:LYS:HB2	28:c:165:MET:HB3	2.02	0.41
29:d:85:PHE:CE2	51:1:587:C:H5'	2.54	0.41
34:j:41:LYS:HB2	34:j:41:LYS:HE3	1.86	0.41
37:m:42:THR:N	37:m:45:GLN:OE1	2.40	0.41
39:o:35:ILE:HD13	39:o:35:ILE:HA	1.95	0.41
51:1:2553:G:H2'	51:1:2554:U:C4'	2.49	0.41
51:1:2633:G:C2'	51:1:2634:A:H5''	2.47	0.41
53:3:668:G:H2'	53:3:669:G:C8	2.55	0.41
58:B1:126:LEU:H	58:B1:126:LEU:HG	1.67	0.41
58:B1:616:PRO:HA	58:B1:619:ILE:HG22	2.02	0.41
58:B1:647:PRO:HG3	58:B1:697:MET:HB3	2.01	0.41
59:B2:22:LEU:HD22	59:B2:603:ILE:HG21	2.02	0.41
59:B2:478:ARG:HD2	59:B2:492:MET:HA	2.02	0.41
59:B2:590:PRO:HB2	59:B2:655:VAL:HG21	2.01	0.41
62:NG:135:ARG:O	62:NG:178:VAL:CA	2.68	0.41
63:5:34:G:H5'	63:5:35:A:N7	2.35	0.41
65:a:42:VAL:HG13	65:a:175:ILE:HG13	2.02	0.41
66:0:499:THR:CG2	66:0:500:ASP:H	2.23	0.41
8:H:24:ASN:OD1	8:H:25:THR:N	2.53	0.41
9:I:201:GLU:OE1	10:J:111:ARG:NH1	2.53	0.41
10:J:13:LYS:NZ	10:J:14:LEU:O	2.53	0.41
23:W:62:ARG:NH1	53:3:718:A:N6	2.69	0.41
29:d:29:HIS:CE1	36:l:8:PRO:HB3	2.55	0.41
51:1:19:A:H2'	51:1:20:C:C6	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:43:G:O2'	51:1:44:A:H5'	2.20	0.41
51:1:140:C:C6	51:1:141:G:H4'	2.55	0.41
51:1:191:A:N3	51:1:192:C:C6	2.88	0.41
51:1:527:C:OP2	51:1:2779:U:N3	2.51	0.41
51:1:538:A:H2'	51:1:539:G:O4'	2.20	0.41
51:1:1625:C:H2'	51:1:1626:A:O4'	2.20	0.41
51:1:2114:A:C5	51:1:2115:G:H1'	2.55	0.41
51:1:2638:G:H1'	51:1:2778:A:N6	2.34	0.41
51:1:2733:A:H2'	51:1:2734:A:H8	1.81	0.41
53:3:224:U:H2'	53:3:225:C:C5	2.56	0.41
53:3:228:A:H2'	53:3:229:U:O4'	2.20	0.41
53:3:426:U:H2'	53:3:427:U:C6	2.54	0.41
53:3:850:U:O5'	53:3:850:U:H6	2.03	0.41
53:3:866:C:N3	53:3:867:G:H1'	2.35	0.41
53:3:1292:G:H2'	53:3:1293:C:C6	2.55	0.41
53:3:1386:G:O2'	53:3:1387:G:H5'	2.20	0.41
53:3:1422:G:N2	53:3:1479:C:N4	2.69	0.41
58:B1:144:TYR:N	58:B1:144:TYR:CD1	2.88	0.41
58:B1:390:LEU:N	58:B1:390:LEU:HD13	2.35	0.41
58:B1:515:ARG:HH12	58:B1:724:MET:HG2	1.84	0.41
58:B1:1289:ASN:O	58:B1:1293:GLU:HB2	2.20	0.41
65:a:54:LYS:NZ	65:a:56:ASP:OD1	2.53	0.41
1:A:11:GLU:HG2	1:A:25:ARG:HG2	2.02	0.41
2:B:53:VAL:HG23	2:B:54:ILE:HG23	2.03	0.41
7:G:218:ALA:HA	7:G:221:ARG:HE	1.85	0.41
9:I:149:LYS:HG2	9:I:150:LYS:HG2	2.02	0.41
13:M:7:ALA:HA	13:M:10:LEU:HB2	2.02	0.41
15:O:58:ASN:HD21	53:3:1061:G:H4'	1.85	0.41
16:P:86:LYS:HG3	16:P:114:PRO:HD3	2.02	0.41
24:X:77:ARG:HH11	53:3:1225:A:H4'	1.83	0.41
25:Y:15:LYS:HE2	25:Y:15:LYS:HB3	1.92	0.41
45:u:67:SER:HB2	51:1:327:G:H21	1.85	0.41
51:1:72:U:C4	51:1:112:U:H4'	2.55	0.41
51:1:711:G:H2'	51:1:712:G:O4'	2.21	0.41
51:1:1054:A:H2'	51:1:1055:G:C8	2.55	0.41
51:1:1086:A:C1'	51:1:1103:A:H2	2.33	0.41
51:1:1158:C:O5'	51:1:1158:C:H6	2.02	0.41
51:1:1183:U:O2'	51:1:1184:U:H5'	2.20	0.41
51:1:1388:G:H2'	51:1:1389:G:H8	1.84	0.41
51:1:1591:A:H2'	51:1:1592:C:C6	2.55	0.41
51:1:2139:U:H2'	51:1:2140:G:C8	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2402:U:H2'	51:1:2403:C:C5'	2.42	0.41
51:1:2448:A:H3'	51:1:2449:U:H2'	2.02	0.41
51:1:2676:C:O5'	51:1:2676:C:H6	2.03	0.41
51:1:2840:C:H2'	51:1:2841:C:C6	2.56	0.41
52:2:53:A:H2'	52:2:54:G:O4'	2.20	0.41
53:3:458:U:H2'	53:3:459:A:C8	2.55	0.41
53:3:957:U:H2'	53:3:959:A:OP2	2.21	0.41
53:3:971:G:N7	53:3:1233:G:H1'	2.34	0.41
57:A1:211:ILE:HD12	57:A1:211:ILE:HA	1.92	0.41
58:B1:239:LEU:N	58:B1:239:LEU:HD23	2.36	0.41
58:B1:515:ARG:HG2	58:B1:516:ASP:H	1.85	0.41
58:B1:797:THR:HG22	58:B1:924:GLY:HA3	2.01	0.41
63:5:4:C:H2'	63:5:5:G:C8	2.55	0.41
63:5:17:C:H6	63:5:17:C:H2'	1.69	0.41
66:0:324:ILE:HA	66:0:334:THR:HA	2.01	0.41
66:0:495:ARG:HG3	66:0:495:ARG:NH1	2.36	0.41
6:F:32:LYS:HD2	51:1:2478:A:OP1	2.20	0.41
12:L:35:LYS:HD3	53:3:1373:G:H5''	2.01	0.41
28:c:145:SER:HB3	51:1:2578:G:N7	2.35	0.41
28:c:170:VAL:HG13	28:c:194:PRO:HG3	2.01	0.41
28:c:209:ALA:OXT	51:1:2733:A:C2	2.74	0.41
30:e:2:LYS:O	30:e:2:LYS:NZ	2.49	0.41
32:g:101:ASP:O	32:g:105:ALA:N	2.46	0.41
45:u:96:LYS:HE2	51:1:300:A:P	2.60	0.41
47:w:56:PHE:HE2	51:1:2365:G:C5'	2.34	0.41
51:1:151:C:H5''	51:1:1360:G:OP1	2.21	0.41
51:1:1024:G:P	51:1:1025:G:H3'	2.60	0.41
51:1:1609:A:H5'	51:1:1609:A:C8	2.55	0.41
51:1:1639:C:C2'	51:1:1640:A:H5'	2.51	0.41
51:1:1974:C:H2'	51:1:1975:G:C8	2.55	0.41
51:1:2013:A:H61	51:1:2613:U:H3	1.68	0.41
51:1:2520:C:H1'	51:1:2565:A:O2'	2.19	0.41
53:3:461:A:H2'	53:3:462:G:C8	2.56	0.41
53:3:678:U:H2'	53:3:679:C:C6	2.55	0.41
53:3:762:U:H2'	53:3:763:G:C8	2.55	0.41
53:3:909:A:H2'	53:3:910:C:O4'	2.20	0.41
53:3:1032:G:H21	53:3:1033:G:H4'	1.85	0.41
53:3:1315:U:H2'	53:3:1316:G:O4'	2.21	0.41
55:8:14:DC:C2	55:8:15:DC:C5	3.09	0.41
58:B1:246:PRO:HA	58:B1:247:PRO:HD3	1.96	0.41
59:B2:870:ILE:HB	59:B2:944:ARG:HD3	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:a:41:SER:OG	65:a:43:ASP:OD2	2.32	0.41
65:a:165:ASN:HD22	65:a:169:GLY:HA2	1.85	0.41
66:0:64:THR:HG23	66:0:472:ARG:HH22	1.86	0.41
5:E:7:ARG:NH1	51:1:254:G:H22	2.18	0.41
14:N:21:LYS:HZ1	14:N:63:TYR:H	1.67	0.41
17:Q:9:LYS:HE2	17:Q:9:LYS:HB2	1.85	0.41
18:R:88:LEU:HD21	18:R:92:ARG:HE	1.86	0.41
28:c:117:GLY:H	28:c:164:GLN:HE22	1.68	0.41
30:e:63:LYS:O	52:2:42:C:H1'	2.21	0.41
30:e:65:LEU:N	30:e:87:LYS:O	2.53	0.41
34:j:114:LEU:O	34:j:118:MET:N	2.54	0.41
37:m:42:THR:HA	37:m:93:VAL:HA	2.02	0.41
38:n:24:MET:O	38:n:28:LEU:N	2.54	0.41
51:1:272:A:H2'	51:1:273:G:H8	1.86	0.41
51:1:2140:G:H1	51:1:2151:U:H3	1.69	0.41
51:1:2611:C:H2'	51:1:2612:C:H6	1.85	0.41
53:3:68:G:C2	53:3:69:G:H1'	2.55	0.41
53:3:107:G:H2'	53:3:108:G:O4'	2.20	0.41
53:3:111:G:O2'	53:3:389:A:H1'	2.20	0.41
53:3:938:A:H1'	53:3:1376:U:O2'	2.20	0.41
58:B1:111:THR:HG23	58:B1:300:GLN:HA	2.03	0.41
58:B1:137:ARG:HA	58:B1:142:GLU:HG2	2.02	0.41
58:B1:1350:ASN:HA	58:B1:1353:VAL:HG12	2.02	0.41
59:B2:310:ILE:HG21	59:B2:325:LEU:HB3	2.03	0.41
59:B2:469:VAL:HA	59:B2:472:GLU:HG2	2.02	0.41
62:NG:175:PHE:O	62:NG:178:VAL:O	2.38	0.41
65:a:211:LYS:HB2	65:a:211:LYS:HE2	1.57	0.41
13:M:3:GLN:HE21	53:3:878:A:H1'	1.86	0.41
17:Q:23:LEU:HA	17:Q:23:LEU:HD23	1.82	0.41
24:X:20:LYS:O	24:X:24:SER:OG	2.38	0.41
36:l:4:ASN:OD1	51:1:1203:U:O2	2.39	0.41
37:m:62:LYS:HD2	37:m:62:LYS:HA	1.91	0.41
48:x:9:LYS:HB3	48:x:30:PRO:HB3	2.03	0.41
51:1:1:G:H2'	51:1:2:G:C8	2.55	0.41
51:1:324:A:H2'	51:1:325:G:H5'	2.01	0.41
51:1:692:C:H2'	51:1:693:A:H8	1.86	0.41
51:1:1853:A:H2'	51:1:1854:A:H8	1.82	0.41
51:1:2139:U:H2'	51:1:2140:G:H8	1.84	0.41
51:1:2302:U:H2'	51:1:2303:G:C8	2.56	0.41
51:1:2688:G:N1	51:1:2720:U:OP2	2.40	0.41
53:3:262:A:H2'	53:3:263:A:C8	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:520:A:H61	53:3:533:A:H61	1.67	0.41
53:3:862:C:O2'	53:3:863:U:H5'	2.20	0.41
57:A1:205:MET:HE1	57:A1:217:ILE:HG13	2.02	0.41
58:B1:105:ILE:HD12	58:B1:242:LEU:CD2	2.44	0.41
58:B1:144:TYR:OH	58:B1:162:GLU:OE1	2.34	0.41
59:B2:897:PRO:HA	59:B2:900:LYS:HD2	2.02	0.41
66:0:18:HIS:ND1	66:0:120:GLN:HB3	2.36	0.41
66:0:446:ARG:HB3	66:0:459:ALA:HB3	2.01	0.41
1:A:26:SER:HB2	30:e:101:ARG:HH11	1.84	0.41
2:B:6:LYS:NZ	51:1:1262:A:C2	2.89	0.41
12:L:55:LYS:H	12:L:55:LYS:HG2	1.76	0.41
19:S:99:SER:HG	53:3:1187:G:H21	1.69	0.41
34:j:27:ARG:NH2	51:1:1142:A:H4'	2.36	0.41
36:l:78:ARG:HE	36:l:111:ILE:HD11	1.86	0.41
48:x:57:VAL:HG13	51:1:372:G:H5'	2.03	0.41
51:1:734:A:O2'	51:1:1635:A:H4'	2.21	0.41
51:1:1063:G:OP2	51:1:1070:A:C4'	2.69	0.41
51:1:1310:G:C3'	51:1:1311:G:H5'	2.50	0.41
51:1:1354:A:H2'	51:1:1355:G:O4'	2.20	0.41
51:1:1932:A:H62	51:1:1968:G:H21	1.68	0.41
51:1:2049:G:N2	51:1:2620:C:C2	2.89	0.41
51:1:2063:C:O2	51:1:2450:A:N1	2.54	0.41
51:1:2073:C:O2	51:1:2437:G:C2	2.74	0.41
51:1:2559:C:H2'	51:1:2560:A:H8	1.86	0.41
51:1:2588:G:C2'	51:1:2589:A:H5'	2.50	0.41
53:3:79:G:H2'	53:3:80:A:H5'	2.02	0.41
53:3:1264:U:H3	53:3:1271:A:H61	1.67	0.41
58:B1:71:LEU:HB2	58:B1:90:VAL:HG11	2.03	0.41
58:B1:472:LEU:HD11	59:B2:1294:LYS:HG2	2.03	0.41
58:B1:576:ARG:HD3	58:B1:593:ASN:HA	2.03	0.41
58:B1:1272:SER:OG	58:B1:1273:ASP:N	2.53	0.41
59:B2:6:THR:OG1	59:B2:781:ASP:OD1	2.33	0.41
59:B2:699:LEU:HG	59:B2:799:ASN:HD22	1.85	0.41
59:B2:805:MET:HE3	59:B2:805:MET:HB2	1.86	0.41
66:0:408:ARG:HD2	66:0:408:ARG:HA	1.36	0.41
66:0:520:ILE:HD13	66:0:557:ILE:HD11	2.01	0.41
66:0:569:TYR:HA	66:0:570:PRO:HD3	1.93	0.41
13:M:46:GLU:O	13:M:61:THR:OG1	2.28	0.41
26:Z:27:VAL:O	26:Z:31:VAL:N	2.54	0.41
27:b:240:GLY:CA	51:1:2597:G:H5''	2.51	0.41
29:d:45:ALA:CB	51:1:38:A:H4'	2.50	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:l:29:LYS:HA	36:l:29:LYS:HD2	1.71	0.41
37:m:82:MET:HE2	37:m:82:MET:HB2	1.80	0.41
39:o:24:THR:HB	39:o:90:VAL:HG12	2.02	0.41
51:1:395:U:H2'	51:1:396:G:H8	1.80	0.41
51:1:549:G:H2'	51:1:550:C:C6	2.56	0.41
51:1:838:C:C2	51:1:941:A:C6	3.09	0.41
51:1:986:C:O5'	51:1:986:C:H6	2.04	0.41
51:1:1444:G:H2'	51:1:1445:G:O4'	2.21	0.41
51:1:1752:C:O2'	51:1:1753:G:H5'	2.21	0.41
51:1:1863:G:H2'	51:1:1864:U:C6	2.56	0.41
51:1:1900:A:H5'	51:1:1970:A:C5'	2.50	0.41
51:1:2201:G:H2'	51:1:2202:U:O4'	2.21	0.41
51:1:2534:A:C2	51:1:2535:G:H1'	2.56	0.41
53:3:26:A:H61	53:3:558:G:H1'	1.86	0.41
53:3:562:U:H4'	53:3:563:A:O5'	2.20	0.41
54:4:46:G:H5'	59:B2:688:GLN:HE22	1.85	0.41
58:B1:513:MET:HG3	58:B1:544:LEU:HD11	2.01	0.41
66:0:494:ILE:HB	66:0:608:ALA:HB1	2.03	0.41
66:0:632:ILE:O	66:0:636:SER:OG	2.36	0.41
2:B:39:ARG:CZ	51:1:2884:U:H3	2.34	0.41
11:K:88:MET:HB2	23:W:63:TYR:HE2	1.86	0.41
14:N:6:TYR:CZ	53:3:1147:C:H4'	2.56	0.41
15:O:46:LYS:HB3	53:3:1253:G:OP1	2.21	0.41
15:O:82:LYS:HD2	15:O:82:LYS:HA	1.53	0.41
16:P:25:SER:HA	16:P:88:PRO:HD2	2.02	0.41
19:S:96:LYS:HA	19:S:96:LYS:HD2	1.79	0.41
21:U:12:LYS:HB3	53:3:392:C:OP2	2.20	0.41
22:V:46:HIS:CG	22:V:66:LEU:HD22	2.56	0.41
27:b:71:ASP:OD2	27:b:188:ARG:NH2	2.46	0.41
27:b:145:MET:HE3	27:b:153:LEU:HD11	2.02	0.41
27:b:145:MET:SD	51:1:1800:C:H5''	2.61	0.41
27:b:153:LEU:HA	51:1:1799:G:N2	2.35	0.41
28:c:55:LYS:HE3	28:c:60:VAL:HG22	2.03	0.41
28:c:91:THR:H	28:c:94:GLN:HE21	1.66	0.41
28:c:113:SER:HB3	28:c:194:PRO:HB3	2.03	0.41
28:c:123:LYS:HB3	28:c:123:LYS:HE3	1.94	0.41
31:f:97:VAL:HG12	31:f:124:CYS:HB2	2.02	0.41
31:f:123:GLU:HB2	31:f:131:VAL:HB	2.03	0.41
33:i:123:ALA:CB	51:1:1081:U:H4'	2.50	0.41
36:l:2:ARG:O	36:l:5:THR:OG1	2.36	0.41
37:m:11:LYS:O	51:1:910:A:N6	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:84:PHE:HB2	51:1:297:G:O3'	2.21	0.41
47:w:37:ARG:HA	47:w:37:ARG:HD3	1.68	0.41
49:y:31:GLN:HB3	49:y:37:LEU:HD12	2.02	0.41
51:1:4:U:H2'	51:1:5:A:O4'	2.20	0.41
51:1:226:A:H2'	51:1:227:A:O4'	2.21	0.41
51:1:413:C:H2'	51:1:414:C:C6	2.56	0.41
51:1:435:C:H2'	51:1:436:C:C5'	2.37	0.41
51:1:958:U:C2'	52:2:89:U:H1'	2.47	0.41
51:1:1054:A:H2	51:1:1105:U:H3	1.69	0.41
51:1:1698:A:N7	51:1:1700:A:C8	2.89	0.41
51:1:1700:A:C2'	51:1:1701:A:H5'	2.50	0.41
51:1:1787:A:H2'	51:1:1787:A:N3	2.36	0.41
51:1:1801:A:H5'	51:1:1801:A:H8	1.86	0.41
51:1:1810:A:H2'	51:1:1811:G:C5'	2.51	0.41
51:1:1823:G:C6	51:1:1824:G:C5	3.09	0.41
51:1:2081:U:H2'	51:1:2082:A:H8	1.85	0.41
53:3:153:C:H2'	53:3:154:U:C5'	2.51	0.41
53:3:204:G:H2'	53:3:205:A:C8	2.55	0.41
53:3:795:C:C5	53:3:796:C:C5	3.09	0.41
53:3:1346:A:N1	53:3:1374:A:H5''	2.35	0.41
53:3:1389:C:H2'	53:3:1390:U:O4'	2.21	0.41
57:A1:44:ARG:HA	57:A1:183:ILE:HD12	2.03	0.41
57:A1:224:LEU:HD23	57:A2:228:LEU:HD21	2.03	0.41
57:A2:57:THR:HG23	57:A2:158:ARG:HH21	1.86	0.41
58:B1:848:VAL:HB	58:B1:858:VAL:HG22	2.02	0.41
59:B2:213:LEU:HD13	59:B2:422:LYS:HG2	2.03	0.41
59:B2:746:ALA:O	59:B2:974:ARG:NH2	2.45	0.41
59:B2:979:LEU:HD11	59:B2:1011:LEU:HD11	2.03	0.41
59:B2:998:LEU:HD21	59:B2:1015:ALA:HB2	2.02	0.41
66:0:375:LYS:HE2	66:0:375:LYS:HB2	1.90	0.41
66:0:534:TYR:HB2	66:0:561:LEU:HD11	2.03	0.41
4:D:39:ARG:CZ	51:1:469:G:O6	2.69	0.41
10:J:83:PRO:HB3	10:J:97:PRO:HD3	2.02	0.41
15:O:45:ARG:NH1	15:O:47:GLU:OE1	2.53	0.41
21:U:60:TRP:HB3	21:U:65:ALA:HB2	2.03	0.41
27:b:7:PRO:HB3	27:b:13:ARG:HG3	2.03	0.41
27:b:255:LYS:HD3	51:1:1844:C:H5''	2.02	0.41
28:c:19:GLY:HA2	40:p:78:PRO:HD2	2.02	0.41
28:c:179:ARG:HB3	28:c:188:LEU:HB2	2.03	0.41
30:e:32:LYS:H	30:e:32:LYS:HG2	1.68	0.41
41:q:30:VAL:HG11	51:1:580:U:H4'	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:42:LYS:HE2	45:u:42:LYS:HB3	1.90	0.41
45:u:73:ASN:ND2	45:u:76:THR:H	2.19	0.41
46:v:78:GLN:HB3	46:v:88:HIS:HB3	2.03	0.41
51:1:121:G:H2'	51:1:122:G:H8	1.86	0.41
51:1:375:G:H2'	51:1:376:G:H5'	2.03	0.41
51:1:740:C:O2'	51:1:741:U:H5'	2.21	0.41
51:1:772:C:H5''	51:1:1356:G:C5'	2.50	0.41
51:1:940:G:C3'	51:1:941:A:H5''	2.51	0.41
51:1:1146:C:O2'	51:1:1147:A:H5'	2.21	0.41
51:1:1679:A:H4'	51:1:1990:C:H4'	2.03	0.41
51:1:2136:G:N1	51:1:2137:U:O2	2.54	0.41
52:2:78:A:H2'	52:2:79:G:O4'	2.20	0.41
52:2:102:G:H2'	52:2:103:U:C1'	2.51	0.41
53:3:240:G:H2'	53:3:241:G:H8	1.86	0.41
58:B1:1050:THR:HG23	58:B1:1057:SER:HB3	2.03	0.41
59:B2:27:LEU:O	59:B2:528:ARG:NH1	2.43	0.41
66:0:320:LEU:HD12	66:0:320:LEU:HA	1.86	0.41
7:G:17:HIS:HB2	7:G:202:ASN:HD22	1.86	0.40
14:N:82:ILE:HA	14:N:85:ALA:HB3	2.03	0.40
15:O:53:ILE:HD12	19:S:84:ARG:HD2	2.03	0.40
27:b:77:VAL:HB	27:b:112:GLY:H	1.86	0.40
27:b:116:GLN:NE2	27:b:120:ASP:OD2	2.54	0.40
27:b:152:GLN:HG2	51:1:1818:U:C4	2.55	0.40
30:e:68:LYS:HD3	30:e:68:LYS:HA	1.86	0.40
35:k:1:MET:HE3	51:1:1665:A:H1'	2.02	0.40
41:q:14:LYS:HA	41:q:14:LYS:HD3	1.88	0.40
41:q:94:LEU:HA	41:q:97:ILE:HG22	2.03	0.40
44:t:7:LEU:HD23	44:t:7:LEU:HA	1.89	0.40
45:u:48:VAL:HG13	45:u:50:ALA:O	2.22	0.40
51:1:677:A:C6	51:1:802:A:C6	3.09	0.40
51:1:777:G:N7	51:1:793:A:C2	2.78	0.40
51:1:1340:U:H4'	51:1:1394:U:O2'	2.22	0.40
51:1:1831:G:C2	51:1:1975:G:C2	3.10	0.40
51:1:2041:U:H2'	51:1:2042:A:H8	1.81	0.40
51:1:2070:A:C2	51:1:2071:A:C4	3.08	0.40
51:1:2255:G:H2'	51:1:2256:G:C8	2.56	0.40
51:1:2313:C:H2'	51:1:2314:A:C8	2.56	0.40
53:3:408:A:N6	53:3:434:U:H3	2.18	0.40
53:3:883:C:H2'	53:3:884:U:C6	2.56	0.40
53:3:1093:A:O2'	53:3:1094:G:H5'	2.20	0.40
53:3:1283:U:O2'	53:3:1284:C:H5'	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1536:C:H2'	53:3:1537:U:C6	2.56	0.40
58:B1:108:ALA:HB2	58:B1:276:ASN:OD1	2.21	0.40
58:B1:1223:LEU:HA	58:B1:1223:LEU:HD23	1.89	0.40
2:B:42:ILE:HG22	2:B:48:TYR:HB2	2.03	0.40
4:D:24:THR:OG1	4:D:25:LYS:N	2.53	0.40
13:M:4:ASP:HB3	13:M:7:ALA:HB3	2.02	0.40
13:M:110:MET:HE2	13:M:110:MET:HB3	1.84	0.40
16:P:66:ALA:HA	16:P:69:CYS:HB3	2.04	0.40
17:Q:56:LEU:HD13	17:Q:56:LEU:HA	1.90	0.40
17:Q:56:LEU:HB3	17:Q:57:THR:H	1.81	0.40
24:X:46:LEU:HB3	24:X:48:ILE:HG12	2.03	0.40
27:b:121:ALA:HA	27:b:129:LEU:HD13	2.02	0.40
27:b:131:MET:HE3	27:b:131:MET:HB2	1.84	0.40
27:b:247:TRP:CE2	51:1:1805:A:H5''	2.57	0.40
27:b:269:ARG:HA	27:b:269:ARG:HD2	1.84	0.40
28:c:209:ALA:OXT	51:1:2733:A:N3	2.54	0.40
32:g:89:LYS:HD2	32:g:89:LYS:HA	1.83	0.40
32:g:132:PHE:HB2	32:g:140:ALA:HB3	2.03	0.40
33:i:71:LYS:HD3	33:i:116:MET:HE2	2.03	0.40
39:o:25:ARG:HG3	39:o:40:ILE:HB	2.03	0.40
41:q:23:TYR:HD1	51:1:533:G:C5'	2.35	0.40
48:x:1:SER:OG	51:1:1365:A:H5'	2.20	0.40
51:1:43:G:H2'	51:1:44:A:O4'	2.22	0.40
51:1:2140:G:H2'	51:1:2141:G:C8	2.56	0.40
51:1:2356:U:H3'	51:1:2357:G:H5''	2.03	0.40
51:1:2656:U:OP1	66:0:146:ARG:NH2	2.52	0.40
51:1:2746:U:H2'	51:1:2747:G:O4'	2.21	0.40
51:1:2830:C:O2	51:1:2883:A:H2	2.03	0.40
53:3:79:G:C2'	53:3:80:A:H5'	2.51	0.40
53:3:270:A:H2'	53:3:271:C:O4'	2.20	0.40
53:3:392:C:H2'	53:3:393:A:O4'	2.21	0.40
53:3:794:A:O2'	53:3:795:C:H5'	2.20	0.40
57:A2:42:ALA:HB1	57:A2:224:LEU:HD11	2.03	0.40
57:A2:211:ILE:HD13	57:A2:211:ILE:HA	1.99	0.40
58:B1:390:LEU:HD13	58:B1:390:LEU:H	1.85	0.40
58:B1:777:HIS:CD2	59:B2:550:VAL:HG13	2.56	0.40
59:B2:738:GLU:HA	59:B2:741:MET:HE2	2.03	0.40
59:B2:803:ALA:HB2	59:B2:1094:VAL:HG21	2.03	0.40
59:B2:886:LYS:HE2	59:B2:918:LEU:HD13	2.03	0.40
66:0:158:ILE:HG23	66:0:162:LEU:HB2	2.03	0.40
67:h:5:UAL:C	67:h:6:5OH:HS	2.52	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:126:CYS:SG	13:M:127:TYR:N	2.94	0.40
18:R:70:ARG:NE	30:e:141:ASP:O	2.53	0.40
19:S:1:ALA:HB1	53:3:1049:U:C4	2.56	0.40
27:b:110:LYS:HD2	27:b:110:LYS:HA	1.90	0.40
27:b:159:THR:OG1	27:b:160:TYR:N	2.54	0.40
28:c:149:ASN:ND2	51:1:2572:A:C8	2.90	0.40
32:g:1:MET:HE3	32:g:1:MET:HB3	1.90	0.40
34:j:12:LYS:HD2	34:j:12:LYS:HA	1.78	0.40
38:n:23:ASN:HD21	51:1:1294:U:H1'	1.87	0.40
40:p:17:PRO:HD2	40:p:83:ILE:HB	2.03	0.40
47:w:58:LYS:HB2	47:w:58:LYS:HE3	1.76	0.40
51:1:1169:A:H2'	51:1:1170:C:O4'	2.22	0.40
51:1:1601:G:O2'	51:1:1602:U:H5'	2.22	0.40
51:1:1666:G:N7	51:1:1667:G:C6	2.89	0.40
51:1:1955:U:H6	51:1:1955:U:H5'	1.86	0.40
51:1:1967:C:H2'	51:1:1968:G:O4'	2.22	0.40
51:1:2643:G:H2'	51:1:2644:G:O4'	2.20	0.40
51:1:2741:A:N6	51:1:2763:G:H1'	2.37	0.40
51:1:2811:G:O2'	51:1:2812:G:H5'	2.21	0.40
53:3:220:G:O2'	53:3:221:C:H5'	2.21	0.40
53:3:492:C:H2'	53:3:493:A:H8	1.83	0.40
53:3:990:C:H2'	53:3:991:U:O4'	2.21	0.40
59:B2:987:GLU:HG2	59:B2:991:LYS:HE3	2.03	0.40
64:6:33:U:H2'	64:6:35:A:OP2	2.21	0.40
65:a:167:LYS:HE2	65:a:167:LYS:HB3	1.52	0.40
66:0:32:PHE:HA	66:0:37:ASN:HB2	2.03	0.40
66:0:489:ALA:HB3	66:0:687:TYR:HE1	1.85	0.40
3:C:10:LEU:HB2	3:C:20:TYR:HB2	2.03	0.40
9:I:49:ASP:OD1	9:I:49:ASP:N	2.55	0.40
12:L:34:LYS:CE	53:3:1290:G:H4'	2.51	0.40
13:M:26:MET:HB3	13:M:58:LEU:HB3	2.04	0.40
14:N:21:LYS:HE2	14:N:21:LYS:HB2	1.85	0.40
19:S:4:SER:OG	53:3:1216:A:H5''	2.21	0.40
20:T:47:LYS:HA	20:T:47:LYS:HD3	1.94	0.40
25:Y:30:PHE:O	25:Y:34:VAL:N	2.52	0.40
32:g:78:VAL:HG21	32:g:103:VAL:HG23	2.04	0.40
33:i:21:PRO:HB2	33:i:22:PRO:HD3	2.03	0.40
42:r:78:ARG:HH22	51:1:975:A:H4'	1.87	0.40
47:w:11:ASP:OD1	47:w:12:SER:N	2.54	0.40
49:y:31:GLN:HG2	49:y:37:LEU:HB2	2.03	0.40
51:1:191:A:H2'	51:1:192:C:C6	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:375:G:O2'	51:1:376:G:H5'	2.21	0.40
51:1:1468:U:H2'	51:1:1522:A:H61	1.86	0.40
51:1:2108:A:OP1	65:a:3:LYS:HB3	2.22	0.40
51:1:2356:U:C3'	51:1:2357:G:H5''	2.52	0.40
52:2:112:G:H2'	52:2:113:C:C6	2.56	0.40
53:3:409:U:H2'	53:3:410:G:O4'	2.22	0.40
53:3:866:C:C2	53:3:867:G:H1'	2.56	0.40
53:3:904:U:H2'	53:3:905:U:C6	2.56	0.40
53:3:944:G:N1	53:3:1338:G:OP2	2.50	0.40
57:A1:79:LEU:HD11	58:B1:526:VAL:HG21	2.04	0.40
57:A2:104:LYS:HG2	57:A2:110:VAL:HG22	2.03	0.40
58:B1:109:SER:CB	58:B1:296:LYS:HG2	2.51	0.40
58:B1:245:LEU:HD13	59:B2:1329:GLU:HA	2.04	0.40
59:B2:657:THR:HG21	59:B2:1188:ASP:HB2	2.03	0.40
59:B2:678:ARG:HD3	59:B2:678:ARG:HA	1.84	0.40
63:5:17:C:H2'	63:5:18:G:C8	2.56	0.40
66:0:83:ARG:HE	66:0:83:ARG:HB2	1.75	0.40
5:E:14:LYS:HA	5:E:14:LYS:HD3	1.84	0.40
10:J:37:VAL:HG21	10:J:113:VAL:HG13	2.02	0.40
17:Q:30:ARG:NH1	66:0:429:GLU:OE2	2.54	0.40
20:T:3:SER:OG	20:T:5:GLU:OE1	2.33	0.40
25:Y:21:ALA:HA	25:Y:24:ARG:HD3	2.02	0.40
30:e:78:ILE:HD11	30:e:82:TYR:HB3	2.03	0.40
31:f:97:VAL:HG11	31:f:123:GLU:HA	2.04	0.40
32:g:90:LEU:HD11	32:g:93:SER:HA	2.02	0.40
51:1:126:A:C6	51:1:127:A:C2	3.10	0.40
51:1:277:G:H2'	51:1:361:G:O6	2.21	0.40
51:1:289:G:H2'	51:1:290:U:O4'	2.20	0.40
51:1:324:A:C2'	51:1:325:G:H5'	2.51	0.40
51:1:1028:A:H2'	51:1:1029:A:C8	2.56	0.40
51:1:1642:G:H2'	51:1:1643:G:O4'	2.21	0.40
51:1:2153:C:H3'	51:1:2154:A:C8	2.56	0.40
51:1:2247:A:H2'	51:1:2248:C:H6	1.86	0.40
51:1:2533:U:H2'	51:1:2534:A:O4'	2.21	0.40
51:1:2798:U:H4'	51:1:2799:A:C6	2.56	0.40
52:2:4:C:H2'	52:2:5:U:H6	1.83	0.40
53:3:42:G:H1	53:3:400:C:H42	1.70	0.40
53:3:130:A:N3	53:3:130:A:H2'	2.36	0.40
53:3:962:C:H1'	53:3:1201:A:N6	2.36	0.40
53:3:1221:G:O2'	53:3:1222:G:H5'	2.22	0.40
53:3:1305:G:H22	53:3:1331:G:H2'	1.86	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:A1:48:LEU:HD12	57:A1:48:LEU:HA	1.79	0.40
58:B1:56:LEU:HD12	58:B1:56:LEU:HA	1.84	0.40
58:B1:715:LYS:HE2	58:B1:715:LYS:HB3	1.93	0.40
58:B1:807:LEU:HD21	58:B1:894:VAL:HG21	2.04	0.40
58:B1:820:ILE:HD11	58:B1:822:MET:HE2	2.02	0.40
58:B1:1177:ILE:HD12	58:B1:1186:TYR:HE2	1.85	0.40
59:B2:1247:SER:OG	59:B2:1248:THR:N	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	44/70 (63%)	38 (86%)	6 (14%)	0	100	100
2	B	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
3	C	48/55 (87%)	37 (77%)	11 (23%)	0	100	100
4	D	44/46 (96%)	35 (80%)	9 (20%)	0	100	100
5	E	62/65 (95%)	48 (77%)	13 (21%)	1 (2%)	7	37
6	F	36/38 (95%)	29 (81%)	7 (19%)	0	100	100
7	G	216/241 (90%)	181 (84%)	35 (16%)	0	100	100
8	H	204/233 (88%)	187 (92%)	17 (8%)	0	100	100
9	I	203/206 (98%)	169 (83%)	33 (16%)	1 (0%)	24	62
10	J	155/167 (93%)	129 (83%)	26 (17%)	0	100	100
11	K	98/135 (73%)	79 (81%)	19 (19%)	0	100	100
12	L	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
13	M	127/130 (98%)	111 (87%)	16 (13%)	0	100	100
14	N	125/130 (96%)	110 (88%)	15 (12%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	O	96/103 (93%)	82 (85%)	14 (15%)	0	100	100
16	P	114/129 (88%)	104 (91%)	10 (9%)	0	100	100
17	Q	121/124 (98%)	97 (80%)	23 (19%)	1 (1%)	16	52
18	R	112/118 (95%)	99 (88%)	13 (12%)	0	100	100
19	S	98/101 (97%)	86 (88%)	12 (12%)	0	100	100
20	T	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	9 (12%)	0	100	100
23	W	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
24	X	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
25	Y	83/87 (95%)	77 (93%)	6 (7%)	0	100	100
26	Z	63/71 (89%)	47 (75%)	16 (25%)	0	100	100
27	b	269/273 (98%)	227 (84%)	42 (16%)	0	100	100
28	c	207/209 (99%)	177 (86%)	30 (14%)	0	100	100
29	d	199/201 (99%)	182 (92%)	17 (8%)	0	100	100
30	e	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
31	f	174/177 (98%)	157 (90%)	17 (10%)	0	100	100
32	g	147/149 (99%)	125 (85%)	20 (14%)	2 (1%)	9	39
33	i	139/142 (98%)	124 (89%)	15 (11%)	0	100	100
34	j	140/142 (99%)	120 (86%)	20 (14%)	0	100	100
35	k	120/123 (98%)	98 (82%)	22 (18%)	0	100	100
36	l	141/144 (98%)	117 (83%)	24 (17%)	0	100	100
37	m	134/136 (98%)	116 (87%)	18 (13%)	0	100	100
38	n	118/127 (93%)	104 (88%)	14 (12%)	0	100	100
39	o	114/117 (97%)	103 (90%)	11 (10%)	0	100	100
40	p	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
41	q	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
42	r	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
43	s	108/110 (98%)	92 (85%)	16 (15%)	0	100	100
44	t	91/100 (91%)	77 (85%)	14 (15%)	0	100	100
45	u	100/104 (96%)	82 (82%)	18 (18%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	v	92/94 (98%)	79 (86%)	13 (14%)	0	100	100
47	w	73/85 (86%)	63 (86%)	10 (14%)	0	100	100
48	x	75/78 (96%)	65 (87%)	10 (13%)	0	100	100
49	y	61/63 (97%)	61 (100%)	0	0	100	100
50	z	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
57	A1	295/329 (90%)	273 (92%)	22 (8%)	0	100	100
57	A2	282/329 (86%)	271 (96%)	11 (4%)	0	100	100
58	B1	1329/1407 (94%)	1207 (91%)	118 (9%)	4 (0%)	36	71
59	B2	1338/1342 (100%)	1205 (90%)	129 (10%)	4 (0%)	36	71
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	476 (97%)	14 (3%)	0	100	100
62	NG	150/181 (83%)	137 (91%)	12 (8%)	1 (1%)	18	54
65	a	128/234 (55%)	105 (82%)	23 (18%)	0	100	100
66	0	695/716 (97%)	617 (89%)	73 (10%)	5 (1%)	18	54
67	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	10486/11185 (94%)	9322 (89%)	1145 (11%)	19 (0%)	44	77

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	g	15	LEU
58	B1	121	PRO
32	g	14	SER
59	B2	43	PRO
59	B2	918	LEU
62	NG	122	PRO
66	0	199	GLY
59	B2	888	THR
66	0	298	ILE
66	0	299	LEU
17	Q	87	LYS
58	B1	43	THR
58	B1	193	ASP
66	0	196	ALA
58	B1	1325	PHE
5	E	16	THR
9	I	126	GLY

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
59	B2	1317	PRO
66	0	121	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	42/62 (68%)	42 (100%)	0	100	100
2	B	47/48 (98%)	47 (100%)	0	100	100
3	C	45/49 (92%)	44 (98%)	1 (2%)	45	64
4	D	38/38 (100%)	35 (92%)	3 (8%)	11	33
5	E	51/52 (98%)	46 (90%)	5 (10%)	7	25
6	F	34/34 (100%)	33 (97%)	1 (3%)	37	58
7	G	180/199 (90%)	172 (96%)	8 (4%)	25	48
8	H	170/190 (90%)	162 (95%)	8 (5%)	23	46
9	I	172/173 (99%)	168 (98%)	4 (2%)	44	64
10	J	119/126 (94%)	113 (95%)	6 (5%)	22	44
11	K	87/116 (75%)	82 (94%)	5 (6%)	18	42
12	L	124/147 (84%)	121 (98%)	3 (2%)	43	63
13	M	104/105 (99%)	102 (98%)	2 (2%)	50	66
14	N	105/107 (98%)	105 (100%)	0	100	100
15	O	86/90 (96%)	78 (91%)	8 (9%)	8	27
16	P	89/99 (90%)	86 (97%)	3 (3%)	32	55
17	Q	103/104 (99%)	101 (98%)	2 (2%)	50	66
18	R	92/96 (96%)	91 (99%)	1 (1%)	65	73
19	S	83/84 (99%)	82 (99%)	1 (1%)	63	73
20	T	76/77 (99%)	76 (100%)	0	100	100
21	U	65/65 (100%)	65 (100%)	0	100	100
22	V	74/78 (95%)	74 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	56/65 (86%)	56 (100%)	0	100	100
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	65 (100%)	0	100	100
26	Z	55/61 (90%)	46 (84%)	9 (16%)	2	13
27	b	216/218 (99%)	212 (98%)	4 (2%)	50	66
28	c	164/164 (100%)	163 (99%)	1 (1%)	78	80
29	d	165/165 (100%)	160 (97%)	5 (3%)	36	57
30	e	148/150 (99%)	145 (98%)	3 (2%)	48	65
31	f	137/138 (99%)	136 (99%)	1 (1%)	76	78
32	g	114/114 (100%)	107 (94%)	7 (6%)	17	40
33	i	109/110 (99%)	109 (100%)	0	100	100
34	j	116/116 (100%)	113 (97%)	3 (3%)	40	61
35	k	103/104 (99%)	100 (97%)	3 (3%)	37	58
36	l	102/103 (99%)	100 (98%)	2 (2%)	48	65
37	m	109/109 (100%)	108 (99%)	1 (1%)	70	75
38	n	100/103 (97%)	98 (98%)	2 (2%)	48	65
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	99 (100%)	0	100	100
41	q	89/90 (99%)	89 (100%)	0	100	100
42	r	84/84 (100%)	83 (99%)	1 (1%)	63	73
43	s	93/93 (100%)	87 (94%)	6 (6%)	15	38
44	t	80/84 (95%)	77 (96%)	3 (4%)	29	51
45	u	83/85 (98%)	80 (96%)	3 (4%)	31	52
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	71
47	w	57/63 (90%)	57 (100%)	0	100	100
48	x	67/68 (98%)	65 (97%)	2 (3%)	36	57
49	y	55/55 (100%)	55 (100%)	0	100	100
50	z	48/49 (98%)	47 (98%)	1 (2%)	47	65
57	A1	185/286 (65%)	174 (94%)	11 (6%)	18	41
57	A2	186/286 (65%)	184 (99%)	2 (1%)	65	73
58	B1	1110/1168 (95%)	1021 (92%)	89 (8%)	11	32

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	B2	1150/1157 (99%)	1119 (97%)	31 (3%)	39	60
60	W0	70/75 (93%)	69 (99%)	1 (1%)	59	70
65	a	109/181 (60%)	98 (90%)	11 (10%)	7	24
66	0	574/588 (98%)	550 (96%)	24 (4%)	26	49
67	h	2/2 (100%)	2 (100%)	0	100	100
All	All	8120/8683 (94%)	7832 (96%)	288 (4%)	32	53

All (288) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	22	THR
4	D	24	THR
4	D	43	THR
4	D	44	VAL
5	E	30	HIS
5	E	31	ILE
5	E	32	LEU
5	E	33	THR
5	E	37	THR
6	F	25	VAL
7	G	13	VAL
7	G	14	HIS
7	G	18	GLN
7	G	67	LEU
7	G	80	LYS
7	G	84	LEU
7	G	86	CYS
7	G	87	ASP
8	H	51	VAL
8	H	57	GLU
8	H	58	ARG
8	H	61	LYS
8	H	63	ILE
8	H	65	VAL
8	H	134	LYS
8	H	135	ARG
9	I	18	LEU
9	I	19	PHE
9	I	27	ILE
9	I	128	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	J	9	GLU
10	J	10	LEU
10	J	77	ASN
10	J	89	THR
10	J	116	VAL
10	J	130	THR
11	K	51	ILE
11	K	53	LYS
11	K	54	LEU
11	K	55	HIS
11	K	92	THR
12	L	72	VAL
12	L	85	GLN
12	L	88	VAL
13	M	100	ILE
13	M	109	VAL
15	O	82	LYS
15	O	87	LEU
15	O	89	ARG
15	O	90	LEU
15	O	92	LEU
15	O	96	VAL
15	O	100	ILE
15	O	102	LEU
16	P	81	LEU
16	P	83	VAL
16	P	107	THR
17	Q	88	ASP
17	Q	93	ARG
18	R	103	THR
19	S	45	LEU
26	Z	6	ARG
26	Z	8	ASN
26	Z	23	GLU
26	Z	24	LYS
26	Z	36	PHE
26	Z	43	GLU
26	Z	44	ARG
26	Z	46	ARG
26	Z	48	LYS
27	b	15	VAL
27	b	64	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	b	161	VAL
27	b	194	VAL
28	c	197	THR
29	d	48	THR
29	d	84	THR
29	d	116	ASP
29	d	134	LEU
29	d	143	LEU
30	e	89	THR
30	e	90	LEU
30	e	151	LEU
31	f	36	LEU
32	g	7	ASP
32	g	8	LYS
32	g	9	VAL
32	g	12	LEU
32	g	14	SER
32	g	93	SER
32	g	94	ILE
34	j	3	THR
34	j	81	ILE
34	j	139	VAL
35	k	56	ASP
35	k	62	VAL
35	k	104	THR
36	l	19	LEU
36	l	85	VAL
37	m	68	PHE
38	n	15	SER
38	n	69	ARG
42	r	51	VAL
43	s	22	ASP
43	s	65	ASP
43	s	67	ASP
43	s	76	VAL
43	s	92	ARG
43	s	97	LEU
44	t	6	ARG
44	t	11	LEU
44	t	37	ASP
45	u	27	VAL
45	u	51	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
45	u	52	ASN
46	v	65	VAL
48	x	6	VAL
48	x	57	VAL
50	z	26	LEU
57	A1	9	LEU
57	A1	12	ARG
57	A1	13	LEU
57	A1	18	GLN
57	A1	19	VAL
57	A1	22	THR
57	A1	27	THR
57	A1	28	LEU
57	A1	33	ARG
57	A1	46	ILE
57	A1	48	LEU
57	A2	29	GLU
57	A2	74	VAL
58	B1	24	LEU
58	B1	40	LYS
58	B1	42	GLU
58	B1	44	ILE
58	B1	47	ARG
58	B1	49	PHE
58	B1	50	LYS
58	B1	60	ARG
58	B1	66	LYS
58	B1	69	GLU
58	B1	71	LEU
58	B1	74	LYS
58	B1	76	LYS
58	B1	78	LEU
58	B1	80	HIS
58	B1	81	ARG
58	B1	87	LYS
58	B1	91	GLU
58	B1	93	THR
58	B1	94	GLN
58	B1	95	THR
58	B1	96	LYS
58	B1	99	ARG
58	B1	100	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
58	B1	114	ILE
58	B1	117	LEU
58	B1	120	LEU
58	B1	126	LEU
58	B1	132	LEU
58	B1	135	ILE
58	B1	142	GLU
58	B1	144	TYR
58	B1	145	VAL
58	B1	146	VAL
58	B1	147	ILE
58	B1	152	THR
58	B1	154	LEU
58	B1	157	GLN
58	B1	159	ILE
58	B1	172	PHE
58	B1	174	ASP
58	B1	175	GLU
58	B1	180	MET
58	B1	190	LYS
58	B1	193	ASP
58	B1	196	GLN
58	B1	210	SER
58	B1	212	THR
58	B1	216	LYS
58	B1	222	LYS
58	B1	223	LEU
58	B1	227	PHE
58	B1	233	LYS
58	B1	237	MET
58	B1	238	ILE
58	B1	239	LEU
58	B1	240	THR
58	B1	244	VAL
58	B1	255	LEU
58	B1	256	ASP
58	B1	259	ARG
58	B1	317	THR
58	B1	322	ARG
58	B1	324	LEU
58	B1	363	LEU
58	B1	385	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
58	B1	386	GLU
58	B1	387	LEU
58	B1	390	LEU
58	B1	393	THR
58	B1	394	ILE
58	B1	395	LYS
58	B1	416	ILE
58	B1	417	ARG
58	B1	425	ARG
58	B1	506	VAL
58	B1	514	THR
58	B1	800	LEU
58	B1	807	LEU
58	B1	839	VAL
58	B1	901	ARG
58	B1	903	LEU
58	B1	1172	LYS
58	B1	1181	ASP
58	B1	1233	ILE
58	B1	1327	GLU
58	B1	1328	THR
58	B1	1331	VAL
58	B1	1332	LEU
59	B2	44	GLU
59	B2	49	LEU
59	B2	56	VAL
59	B2	146	VAL
59	B2	483	ASP
59	B2	487	LEU
59	B2	516	ASP
59	B2	538	LEU
59	B2	540	ARG
59	B2	545	PHE
59	B2	546	GLU
59	B2	615	VAL
59	B2	857	VAL
59	B2	859	GLU
59	B2	887	VAL
59	B2	890	LYS
59	B2	893	THR
59	B2	894	GLN
59	B2	900	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
59	B2	901	LEU
59	B2	903	ARG
59	B2	905	ILE
59	B2	909	LYS
59	B2	912	ASP
59	B2	913	VAL
59	B2	915	ASP
59	B2	918	LEU
59	B2	920	VAL
59	B2	922	ASN
59	B2	1076	ILE
59	B2	1151	LEU
60	W0	63	ILE
65	a	8	MET
65	a	42	VAL
65	a	47	ASN
65	a	165	ASN
65	a	166	ASP
65	a	167	LYS
65	a	170	ILE
65	a	211	LYS
65	a	212	VAL
65	a	213	SER
65	a	214	ILE
66	0	42	GLU
66	0	173	ILE
66	0	195	ASP
66	0	298	ILE
66	0	299	LEU
66	0	300	ASP
66	0	301	ASP
66	0	303	LYS
66	0	338	VAL
66	0	390	ASP
66	0	404	ILE
66	0	405	ILE
66	0	406	LEU
66	0	408	ARG
66	0	504	LYS
66	0	507	LYS
66	0	508	GLN
66	0	512	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
66	0	514	GLN
66	0	517	HIS
66	0	519	VAL
66	0	611	VAL
66	0	662	GLU
66	0	663	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (150) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
3	C	45	HIS
5	E	30	HIS
7	G	18	GLN
7	G	57	ASN
7	G	93	HIS
7	G	102	ASN
7	G	119	GLN
7	G	169	HIS
7	G	202	ASN
8	H	7	ASN
8	H	18	ASN
8	H	139	ASN
8	H	184	ASN
9	I	35	GLN
9	I	53	GLN
9	I	58	GLN
9	I	73	ASN
9	I	125	ASN
9	I	130	ASN
9	I	135	GLN
9	I	195	ASN
9	I	197	HIS
10	J	69	ASN
10	J	121	ASN
10	J	147	ASN
11	K	52	ASN
11	K	94	HIS
12	L	8	GLN
12	L	27	ASN
12	L	96	ASN
13	M	3	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	M	15	ASN
13	M	20	ASN
14	N	3	ASN
16	P	21	HIS
16	P	27	ASN
17	Q	28	GLN
17	Q	72	ASN
17	Q	76	HIS
17	Q	111	GLN
18	R	90	HIS
19	S	48	GLN
19	S	59	GLN
20	T	45	HIS
21	U	26	ASN
21	U	29	ASN
21	U	40	ASN
21	U	79	ASN
22	V	46	HIS
23	W	53	GLN
25	Y	74	HIS
25	Y	81	GLN
25	Y	83	ASN
26	Z	55	HIS
27	b	14	HIS
27	b	24	HIS
27	b	85	ASN
27	b	142	ASN
28	c	32	ASN
28	c	49	GLN
28	c	67	HIS
28	c	136	ASN
28	c	148	GLN
28	c	164	GLN
28	c	185	ASN
29	d	62	GLN
29	d	195	GLN
30	e	22	ASN
31	f	63	GLN
32	g	18	GLN
32	g	33	GLN
32	g	66	ASN
32	g	135	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
33	i	18	ASN
34	j	80	HIS
34	j	128	ASN
34	j	130	HIS
34	j	135	GLN
35	k	9	ASN
36	l	93	ASN
37	m	22	GLN
38	n	9	GLN
38	n	23	ASN
38	n	107	ASN
39	o	38	GLN
39	o	104	GLN
39	o	116	GLN
40	p	74	GLN
41	q	65	ASN
41	q	70	GLN
43	s	31	GLN
43	s	60	HIS
44	t	59	ASN
44	t	92	ASN
45	u	45	GLN
45	u	53	GLN
45	u	68	ASN
45	u	73	ASN
46	v	24	ASN
46	v	78	GLN
46	v	88	HIS
49	y	41	HIS
57	A1	66	HIS
57	A1	84	ASN
57	A1	117	HIS
57	A1	128	HIS
57	A1	227	GLN
57	A2	147	GLN
57	A2	227	GLN
58	B1	45	ASN
58	B1	196	GLN
58	B1	364	HIS
58	B1	424	ASN
58	B1	469	HIS
58	B1	771	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
58	B1	805	GLN
58	B1	865	HIS
58	B1	1195	GLN
58	B1	1238	GLN
58	B1	1259	GLN
59	B2	69	GLN
59	B2	314	ASN
59	B2	330	HIS
59	B2	343	HIS
59	B2	518	ASN
59	B2	554	HIS
59	B2	688	GLN
59	B2	762	ASN
59	B2	808	ASN
59	B2	1237	HIS
59	B2	1268	GLN
59	B2	1313	HIS
60	W0	7	GLN
60	W0	31	GLN
60	W0	62	GLN
65	a	24	ASN
66	0	85	ASN
66	0	92	HIS
66	0	157	GLN
66	0	170	GLN
66	0	259	ASN
66	0	272	ASN
66	0	276	GLN
66	0	351	ASN
66	0	455	GLN
66	0	487	GLN
66	0	514	GLN
66	0	530	ASN
66	0	584	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	442 (15%)	8 (0%)
52	2	119/120 (99%)	18 (15%)	0
53	3	1538/1542 (99%)	193 (12%)	1 (0%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
54	4	29/47 (61%)	15 (51%)	5 (17%)
63	5	75/76 (98%)	45 (60%)	11 (14%)
64	6	76/77 (98%)	14 (18%)	0
All	All	4739/4766 (99%)	727 (15%)	25 (0%)

All (727) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A
51	1	12	U
51	1	23	G
51	1	34	U
51	1	35	G
51	1	51	G
51	1	63	A
51	1	71	A
51	1	75	G
51	1	102	U
51	1	103	A
51	1	113	U
51	1	118	A
51	1	119	A
51	1	120	U
51	1	125	A
51	1	126	A
51	1	139	U
51	1	140	C
51	1	141	G
51	1	143	C
51	1	163	C
51	1	196	A
51	1	199	A
51	1	204	A
51	1	205	G
51	1	215	G
51	1	216	A
51	1	218	A
51	1	221	A
51	1	225	C
51	1	228	C
51	1	229	C
51	1	233	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	248	G
51	1	255	A
51	1	266	G
51	1	276	U
51	1	277	G
51	1	294	A
51	1	311	A
51	1	323	C
51	1	324	A
51	1	329	G
51	1	330	A
51	1	331	C
51	1	355	U
51	1	361	G
51	1	371	A
51	1	372	G
51	1	380	G
51	1	386	G
51	1	404	A
51	1	405	U
51	1	411	G
51	1	412	A
51	1	424	G
51	1	431	U
51	1	451	U
51	1	455	C
51	1	456	C
51	1	457	A
51	1	458	G
51	1	480	A
51	1	481	G
51	1	490	C
51	1	491	G
51	1	504	A
51	1	505	A
51	1	532	A
51	1	544	C
51	1	548	G
51	1	560	C
51	1	563	A
51	1	568	U
51	1	573	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	574	A
51	1	586	A
51	1	603	A
51	1	609	A
51	1	610	C
51	1	615	U
51	1	627	A
51	1	637	A
51	1	646	U
51	1	654	A
51	1	655	A
51	1	686	U
51	1	690	G
51	1	714	U
51	1	717	C
51	1	730	A
51	1	740	C
51	1	747	C
51	1	752	A
51	1	757	G
51	1	764	A
51	1	765	C
51	1	774	G
51	1	775	G
51	1	776	G
51	1	782	A
51	1	783	A
51	1	784	G
51	1	793	A
51	1	805	G
51	1	806	C
51	1	812	C
51	1	819	A
51	1	827	U
51	1	829	A
51	1	830	G
51	1	845	A
51	1	846	U
51	1	858	G
51	1	859	G
51	1	865	C
51	1	878	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	883	G
51	1	887	U
51	1	890	C
51	1	896	A
51	1	897	C
51	1	898	C
51	1	902	C
51	1	910	A
51	1	941	A
51	1	945	A
51	1	946	C
51	1	953	G
51	1	961	C
51	1	974	G
51	1	980	A
51	1	982	C
51	1	983	A
51	1	989	G
51	1	995	C
51	1	996	A
51	1	1005	C
51	1	1012	U
51	1	1013	C
51	1	1021	A
51	1	1022	G
51	1	1025	G
51	1	1026	G
51	1	1033	U
51	1	1045	C
51	1	1046	A
51	1	1054	A
51	1	1055	G
51	1	1056	G
51	1	1057	A
51	1	1058	U
51	1	1059	G
51	1	1060	U
51	1	1062	G
51	1	1065	U
51	1	1066	U
51	1	1068	G
51	1	1069	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	1070	A
51	1	1071	G
51	1	1073	A
51	1	1078	U
51	1	1081	U
51	1	1084	A
51	1	1088	A
51	1	1104	C
51	1	1105	U
51	1	1106	G
51	1	1107	G
51	1	1111	A
51	1	1130	U
51	1	1132	U
51	1	1133	A
51	1	1134	A
51	1	1135	C
51	1	1143	A
51	1	1155	A
51	1	1172	C
51	1	1173	U
51	1	1175	A
51	1	1178	C
51	1	1180	U
51	1	1206	G
51	1	1212	G
51	1	1225	G
51	1	1236	G
51	1	1248	G
51	1	1253	A
51	1	1256	G
51	1	1271	G
51	1	1272	A
51	1	1275	A
51	1	1287	A
51	1	1300	G
51	1	1301	A
51	1	1312	U
51	1	1313	U
51	1	1321	A
51	1	1325	U
51	1	1326	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	1342	A
51	1	1365	A
51	1	1378	A
51	1	1379	U
51	1	1383	A
51	1	1397	U
51	1	1416	G
51	1	1417	C
51	1	1419	A
51	1	1420	A
51	1	1428	C
51	1	1453	A
51	1	1461	C
51	1	1478	G
51	1	1482	G
51	1	1490	A
51	1	1504	A
51	1	1515	A
51	1	1524	G
51	1	1534	U
51	1	1535	A
51	1	1537	G
51	1	1548	A
51	1	1555	G
51	1	1559	U
51	1	1566	A
51	1	1569	A
51	1	1608	A
51	1	1609	A
51	1	1616	A
51	1	1617	C
51	1	1618	A
51	1	1647	U
51	1	1648	U
51	1	1654	A
51	1	1674	G
51	1	1694	C
51	1	1698	A
51	1	1707	G
51	1	1715	G
51	1	1730	C
51	1	1738	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	1758	U
51	1	1764	C
51	1	1773	A
51	1	1780	A
51	1	1781	U
51	1	1784	A
51	1	1800	C
51	1	1801	A
51	1	1802	A
51	1	1808	A
51	1	1816	C
51	1	1827	U
51	1	1829	A
51	1	1833	C
51	1	1869	G
51	1	1870	C
51	1	1901	A
51	1	1902	C
51	1	1912	A
51	1	1913	A
51	1	1914	C
51	1	1930	G
51	1	1936	A
51	1	1937	A
51	1	1938	A
51	1	1939	U
51	1	1955	U
51	1	1963	U
51	1	1964	G
51	1	1966	A
51	1	1967	C
51	1	1970	A
51	1	1971	U
51	1	1972	G
51	1	1991	U
51	1	1992	G
51	1	1993	U
51	1	1996	C
51	1	1997	C
51	1	2022	U
51	1	2023	C
51	1	2031	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	2034	U
51	1	2043	C
51	1	2049	G
51	1	2055	C
51	1	2056	G
51	1	2060	A
51	1	2061	G
51	1	2069	G
51	1	2072	C
51	1	2092	U
51	1	2093	G
51	1	2094	A
51	1	2103	C
51	1	2106	U
51	1	2107	G
51	1	2108	A
51	1	2111	U
51	1	2112	G
51	1	2118	U
51	1	2123	G
51	1	2124	G
51	1	2126	A
51	1	2132	U
51	1	2133	G
51	1	2134	A
51	1	2135	A
51	1	2138	G
51	1	2143	C
51	1	2146	C
51	1	2153	C
51	1	2156	G
51	1	2157	G
51	1	2158	A
51	1	2162	G
51	1	2165	C
51	1	2166	U
51	1	2168	G
51	1	2172	U
51	1	2173	A
51	1	2178	C
51	1	2179	C
51	1	2180	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	2182	U
51	1	2189	U
51	1	2198	A
51	1	2199	A
51	1	2203	U
51	1	2211	A
51	1	2213	U
51	1	2214	C
51	1	2225	A
51	1	2238	G
51	1	2239	G
51	1	2249	U
51	1	2250	G
51	1	2268	A
51	1	2283	C
51	1	2287	A
51	1	2289	G
51	1	2300	C
51	1	2305	U
51	1	2307	G
51	1	2309	A
51	1	2325	G
51	1	2327	A
51	1	2344	U
51	1	2350	C
51	1	2357	G
51	1	2361	G
51	1	2371	G
51	1	2376	A
51	1	2383	G
51	1	2385	C
51	1	2388	A
51	1	2402	U
51	1	2403	C
51	1	2406	A
51	1	2423	U
51	1	2424	C
51	1	2425	A
51	1	2426	A
51	1	2427	C
51	1	2428	G
51	1	2429	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	2430	A
51	1	2435	A
51	1	2441	U
51	1	2447	G
51	1	2448	A
51	1	2460	U
51	1	2469	A
51	1	2473	U
51	1	2476	A
51	1	2497	A
51	1	2502	G
51	1	2505	G
51	1	2518	A
51	1	2520	C
51	1	2525	G
51	1	2529	G
51	1	2531	A
51	1	2535	G
51	1	2547	A
51	1	2554	U
51	1	2564	A
51	1	2565	A
51	1	2567	G
51	1	2572	A
51	1	2573	C
51	1	2574	G
51	1	2578	G
51	1	2585	U
51	1	2602	A
51	1	2603	G
51	1	2609	U
51	1	2613	U
51	1	2634	A
51	1	2654	A
51	1	2655	G
51	1	2661	G
51	1	2662	A
51	1	2673	G
51	1	2677	G
51	1	2682	A
51	1	2685	G
51	1	2689	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	2690	U
51	1	2713	U
51	1	2714	G
51	1	2715	C
51	1	2718	G
51	1	2726	A
51	1	2732	G
51	1	2744	G
51	1	2748	A
51	1	2757	A
51	1	2758	A
51	1	2764	A
51	1	2765	A
51	1	2778	A
51	1	2779	U
51	1	2791	G
51	1	2793	C
51	1	2798	U
51	1	2801	G
51	1	2820	A
51	1	2833	U
51	1	2848	G
51	1	2850	A
51	1	2867	G
51	1	2868	A
51	1	2879	A
51	1	2880	C
51	1	2883	A
51	1	2884	U
51	1	2893	A
52	2	4	C
52	2	9	G
52	2	13	G
52	2	35	C
52	2	36	C
52	2	42	C
52	2	44	G
52	2	53	A
52	2	66	A
52	2	67	G
52	2	88	C
52	2	89	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	2	90	C
52	2	91	C
52	2	98	G
52	2	108	A
52	2	109	A
52	2	119	A
53	3	3	A
53	3	6	G
53	3	8	A
53	3	9	G
53	3	32	A
53	3	39	G
53	3	47	C
53	3	48	C
53	3	51	A
53	3	54	C
53	3	56	U
53	3	58	C
53	3	61	G
53	3	71	A
53	3	81	A
53	3	87	C
53	3	92	U
53	3	93	U
53	3	94	G
53	3	95	C
53	3	100	G
53	3	110	C
53	3	134	G
53	3	154	U
53	3	183	C
53	3	184	G
53	3	197	A
53	3	208	U
53	3	210	C
53	3	240	G
53	3	246	A
53	3	247	G
53	3	251	G
53	3	266	G
53	3	280	C
53	3	281	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	3	289	G
53	3	308	C
53	3	316	C
53	3	328	C
53	3	352	C
53	3	354	G
53	3	367	U
53	3	369	G
53	3	372	C
53	3	397	A
53	3	406	G
53	3	408	A
53	3	413	G
53	3	414	A
53	3	422	C
53	3	429	U
53	3	430	A
53	3	439	U
53	3	445	G
53	3	448	A
53	3	462	G
53	3	467	U
53	3	468	A
53	3	479	U
53	3	486	U
53	3	494	G
53	3	497	G
53	3	509	A
53	3	510	A
53	3	511	C
53	3	512	U
53	3	518	C
53	3	531	U
53	3	532	A
53	3	533	A
53	3	547	A
53	3	555	U
53	3	559	A
53	3	566	G
53	3	572	A
53	3	573	A
53	3	575	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	3	576	C
53	3	577	G
53	3	596	A
53	3	633	G
53	3	642	A
53	3	653	U
53	3	665	A
53	3	675	A
53	3	702	A
53	3	703	G
53	3	710	G
53	3	713	G
53	3	721	G
53	3	748	G
53	3	755	G
53	3	777	A
53	3	793	U
53	3	794	A
53	3	815	A
53	3	817	C
53	3	818	G
53	3	819	A
53	3	821	G
53	3	826	C
53	3	832	G
53	3	836	G
53	3	841	C
53	3	843	U
53	3	844	G
53	3	846	G
53	3	851	G
53	3	872	A
53	3	884	U
53	3	889	A
53	3	902	G
53	3	907	A
53	3	913	A
53	3	934	C
53	3	935	A
53	3	938	A
53	3	960	U
53	3	961	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	3	966	G
53	3	968	A
53	3	969	A
53	3	971	G
53	3	974	A
53	3	975	A
53	3	976	G
53	3	977	A
53	3	992	U
53	3	993	G
53	3	994	A
53	3	1004	A
53	3	1012	A
53	3	1029	U
53	3	1031	C
53	3	1033	G
53	3	1053	G
53	3	1054	C
53	3	1064	G
53	3	1077	G
53	3	1094	G
53	3	1095	U
53	3	1101	A
53	3	1136	C
53	3	1137	C
53	3	1138	G
53	3	1139	G
53	3	1159	U
53	3	1168	U
53	3	1182	G
53	3	1184	G
53	3	1196	A
53	3	1212	U
53	3	1213	A
53	3	1225	A
53	3	1226	C
53	3	1238	A
53	3	1241	G
53	3	1256	A
53	3	1257	A
53	3	1261	A
53	3	1262	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	3	1275	A
53	3	1278	G
53	3	1280	A
53	3	1282	C
53	3	1286	U
53	3	1287	A
53	3	1290	G
53	3	1300	G
53	3	1301	U
53	3	1302	C
53	3	1317	C
53	3	1345	U
53	3	1363	A
53	3	1364	U
53	3	1378	C
53	3	1398	A
53	3	1422	G
53	3	1432	G
53	3	1441	A
53	3	1446	A
53	3	1452	C
53	3	1471	U
53	3	1492	A
53	3	1503	A
53	3	1505	G
53	3	1506	U
53	3	1507	A
53	3	1517	G
53	3	1529	G
53	3	1530	G
53	3	1540	U
54	4	4	U
54	4	6	U
54	4	7	C
54	4	9	U
54	4	10	C
54	4	11	U
54	4	12	U
54	4	14	U
54	4	15	U
54	4	16	U
54	4	17	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	4	18	U
54	4	19	U
54	4	20	U
54	4	39	G
63	5	2	C
63	5	7	A
63	5	8	U
63	5	9	A
63	5	11	C
63	5	13	C
63	5	15	G
63	5	17	C
63	5	18	G
63	5	19	G
63	5	20	U
63	5	21	A
63	5	26	A
63	5	28	G
63	5	29	G
63	5	30	G
63	5	32	U
63	5	33	U
63	5	34	G
63	5	35	A
63	5	36	A
63	5	37	A
63	5	39	U
63	5	40	C
63	5	41	C
63	5	43	C
63	5	44	G
63	5	46	G
63	5	47	U
63	5	48	C
63	5	49	C
63	5	52	G
63	5	53	G
63	5	55	U
63	5	56	C
63	5	57	G
63	5	58	A
63	5	59	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
63	5	60	U
63	5	61	C
63	5	66	U
63	5	73	A
63	5	74	C
63	5	75	C
63	5	76	A
64	6	9	G
64	6	10	G
64	6	19	G
64	6	20	U
64	6	21	A
64	6	22	G
64	6	27	U
64	6	33	U
64	6	45	G
64	6	47	U
64	6	48	C
64	6	58	A
64	6	61	C
64	6	64	G

All (25) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	490	C
51	1	858	G
51	1	1020	A
51	1	1106	G
51	1	1801	A
51	1	2326	C
51	1	2426	A
51	1	2756	U
53	3	413	G
54	4	10	C
54	4	11	U
54	4	18	U
54	4	19	U
54	4	38	U
63	5	7	A
63	5	29	G
63	5	32	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
63	5	34	G
63	5	35	A
63	5	39	U
63	5	48	C
63	5	57	G
63	5	60	U
63	5	73	A
63	5	75	C

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
67	DPP	h	2	67	4,5,6	0.50	0	1,5,7	0.06	0
67	UAL	h	5	67	6,8,9	2.34	2 (33%)	4,9,11	1.89	1 (25%)
67	5OH	h	6	67	7,12,13	0.77	0	4,16,18	1.32	1 (25%)
67	KBE	h	1	67	8,8,9	0.60	0	6,8,10	1.19	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
67	DPP	h	2	67	-	0/2/4/6	-
67	UAL	h	5	67	-	0/3/7/9	-
67	5OH	h	6	67	-	0/2/18/20	0/1/1/1
67	KBE	h	1	67	-	0/7/7/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	h	5	UAL	C1-N1	-4.87	1.32	1.40
67	h	5	UAL	C-CA	-2.82	1.40	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	h	5	UAL	O-C-CA	-3.33	121.21	125.39
67	h	6	5OH	CR-CB-CA	-2.37	110.09	112.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
67	h	2	DPP	1	0
67	h	5	UAL	2	0
67	h	6	5OH	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
69	GDP	0	801	-	29,30,30	1.17	3 (10%)	45,47,47	1.88	8 (17%)
70	PO4	0	802	-	4,4,4	1.00	0	6,6,6	0.50	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
69	GDP	0	801	-	-	2/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
69	0	801	GDP	C5-C4	2.79	1.46	1.38
69	0	801	GDP	C6-N1	-2.58	1.34	1.38
69	0	801	GDP	C4-N9	-2.01	1.32	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	0	801	GDP	C5-C4-N3	-6.00	118.84	128.39
69	0	801	GDP	C2-N3-C4	5.07	121.02	112.30
69	0	801	GDP	N9-C4-N3	4.48	134.91	125.95
69	0	801	GDP	C6-C5-N7	3.61	136.85	130.29
69	0	801	GDP	C4-C5-N7	-2.77	106.28	110.67
69	0	801	GDP	C2'-C1'-N9	-2.11	107.36	113.25
69	0	801	GDP	O6-C6-C5	-2.09	121.00	126.53
69	0	801	GDP	C5-C6-N1	2.03	118.43	113.25

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
69	0	801	GDP	C5'-O5'-PA-O3A
69	0	801	GDP	C5'-O5'-PA-O1A

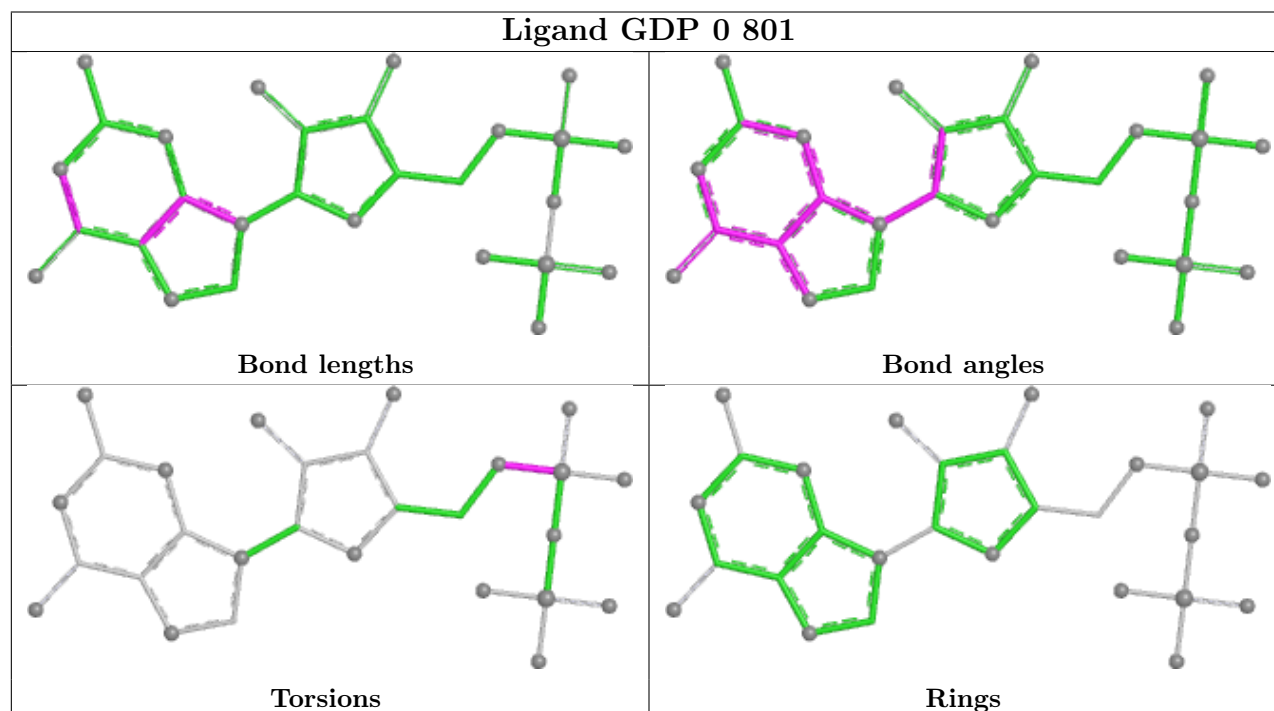
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
69	0	801	GDP	1	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.

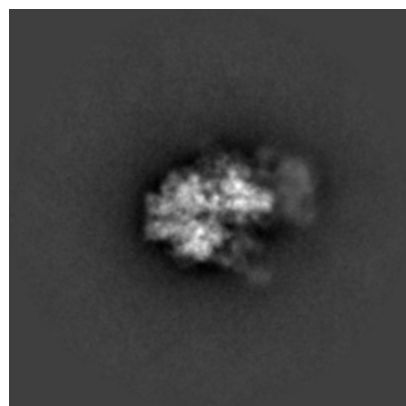
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38944. These allow visual inspection of the internal detail of the map and identification of artifacts.

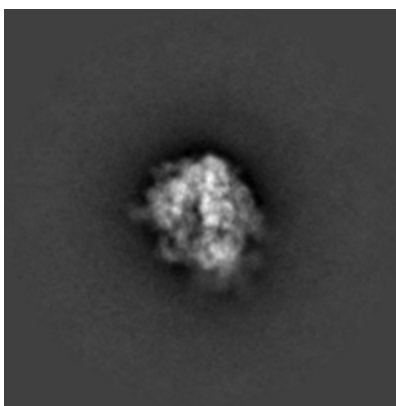
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

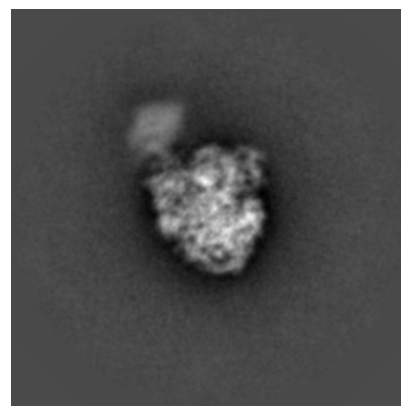
6.1.1 Primary map



X

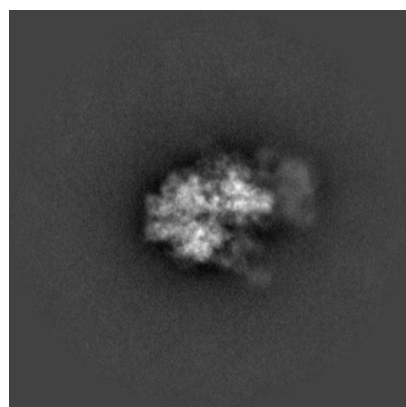


Y

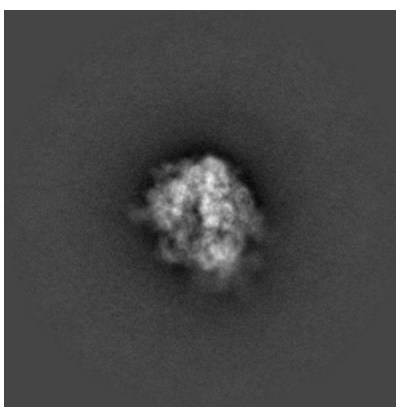


Z

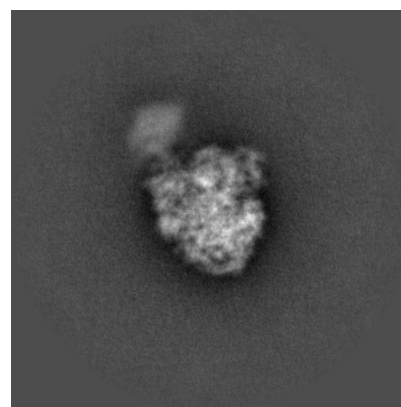
6.1.2 Raw map



X



Y

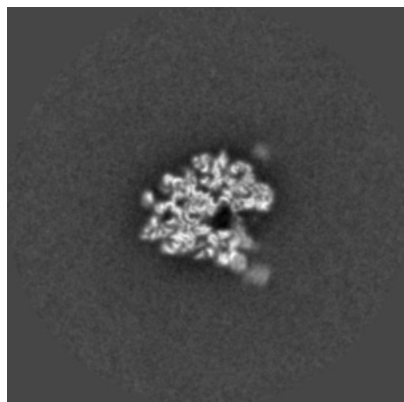


Z

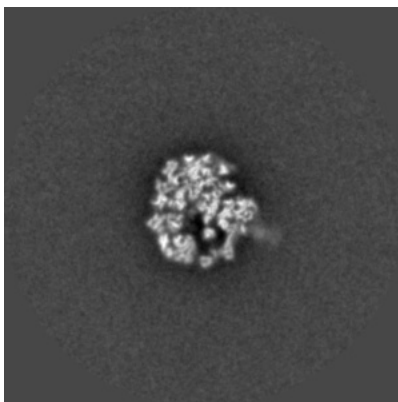
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

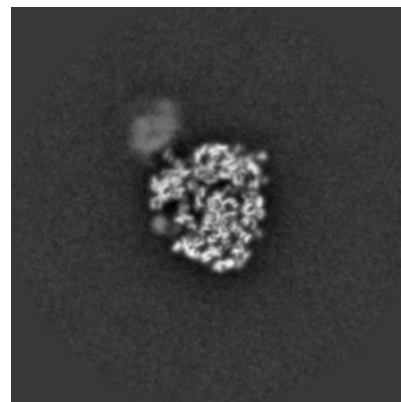
6.2.1 Primary map



X Index: 240

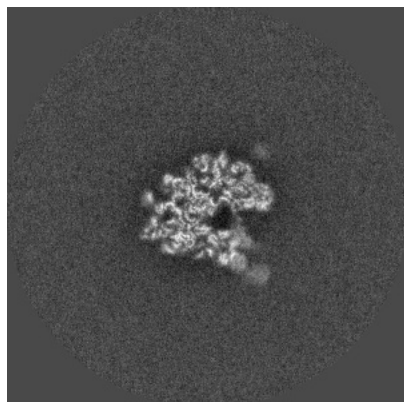


Y Index: 240

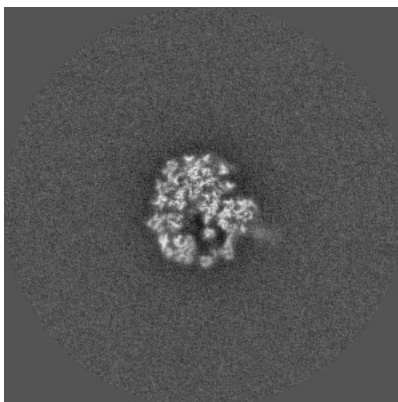


Z Index: 240

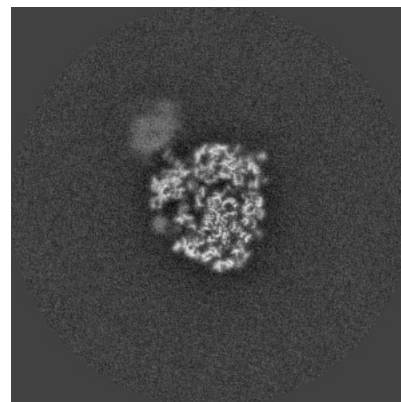
6.2.2 Raw map



X Index: 240



Y Index: 240

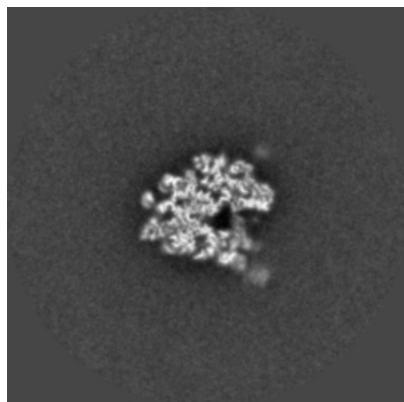


Z Index: 240

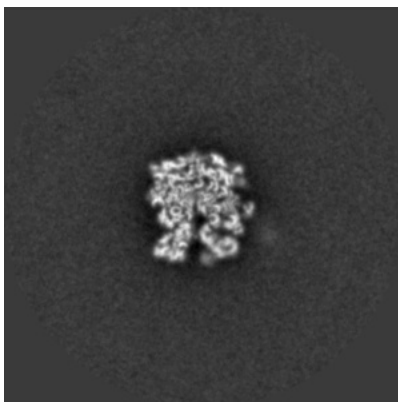
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

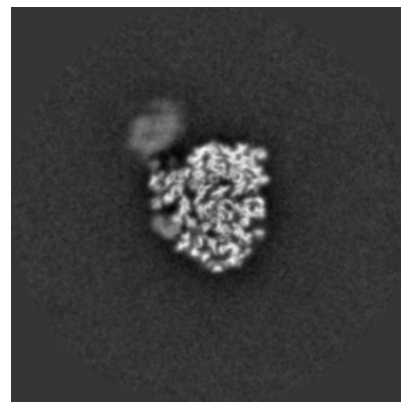
6.3.1 Primary map



X Index: 242

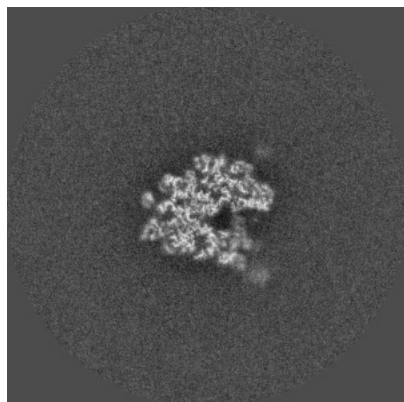


Y Index: 225

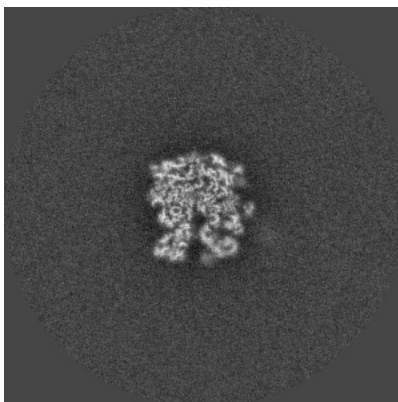


Z Index: 245

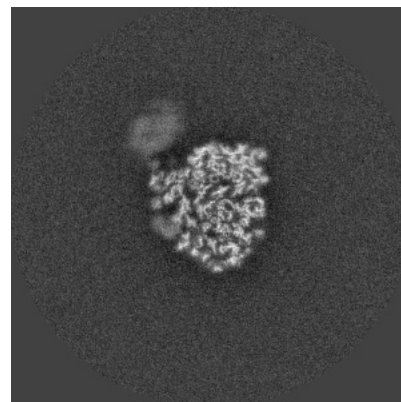
6.3.2 Raw map



X Index: 242



Y Index: 225



Z Index: 245

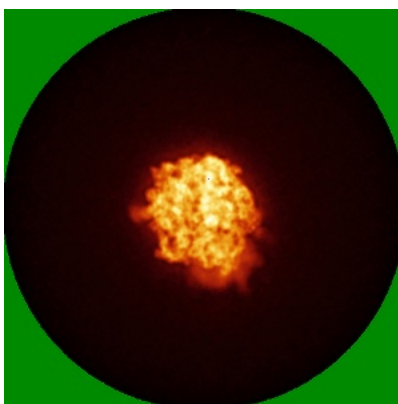
The images above show the largest variance slices of the map in three orthogonal directions.

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

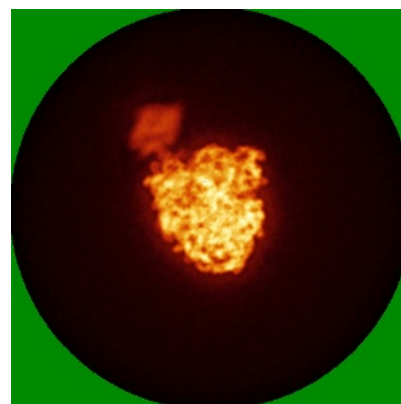
6.4.1 Primary map



X

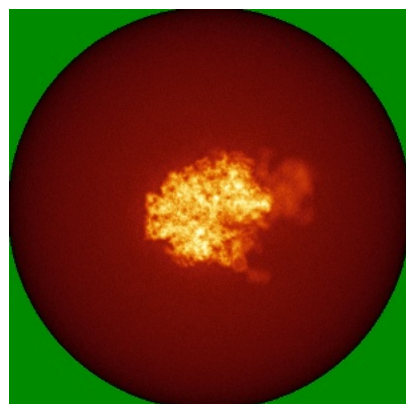


Y

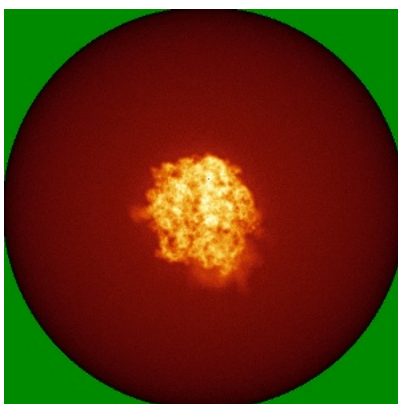


Z

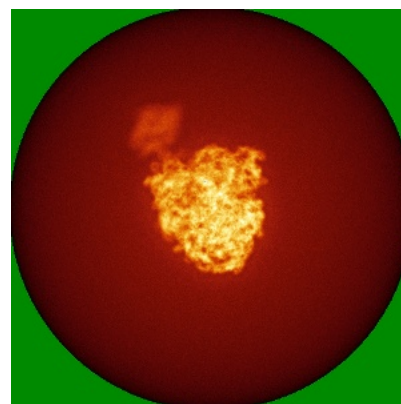
6.4.2 Raw map



X



Y



Z

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

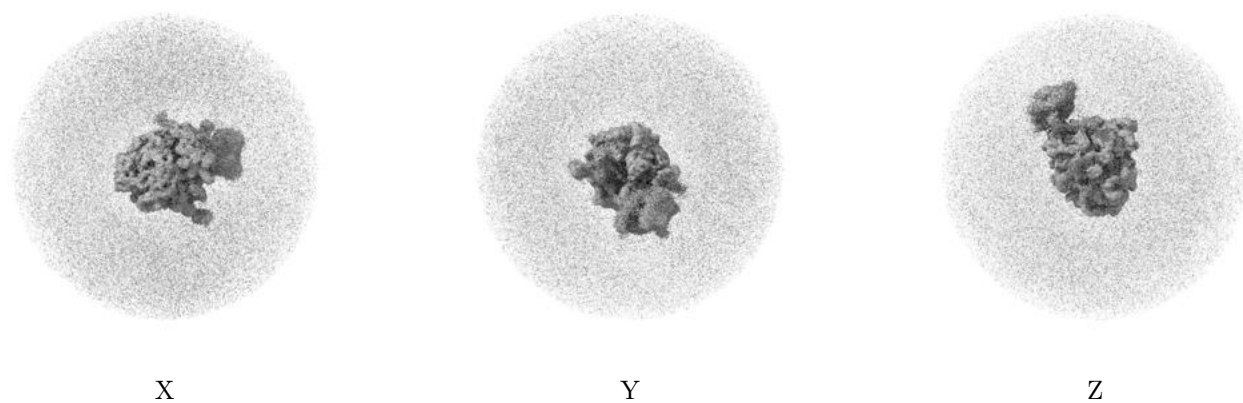
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

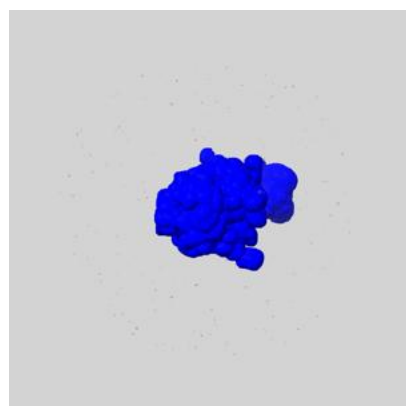
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

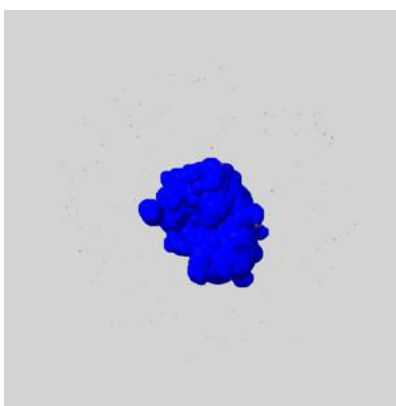
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

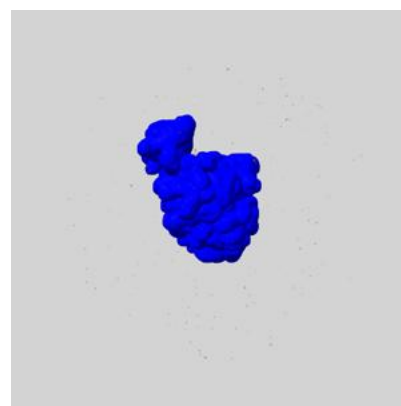
6.6.1 emd_38944_msk_1.map [i](#)



X



Y

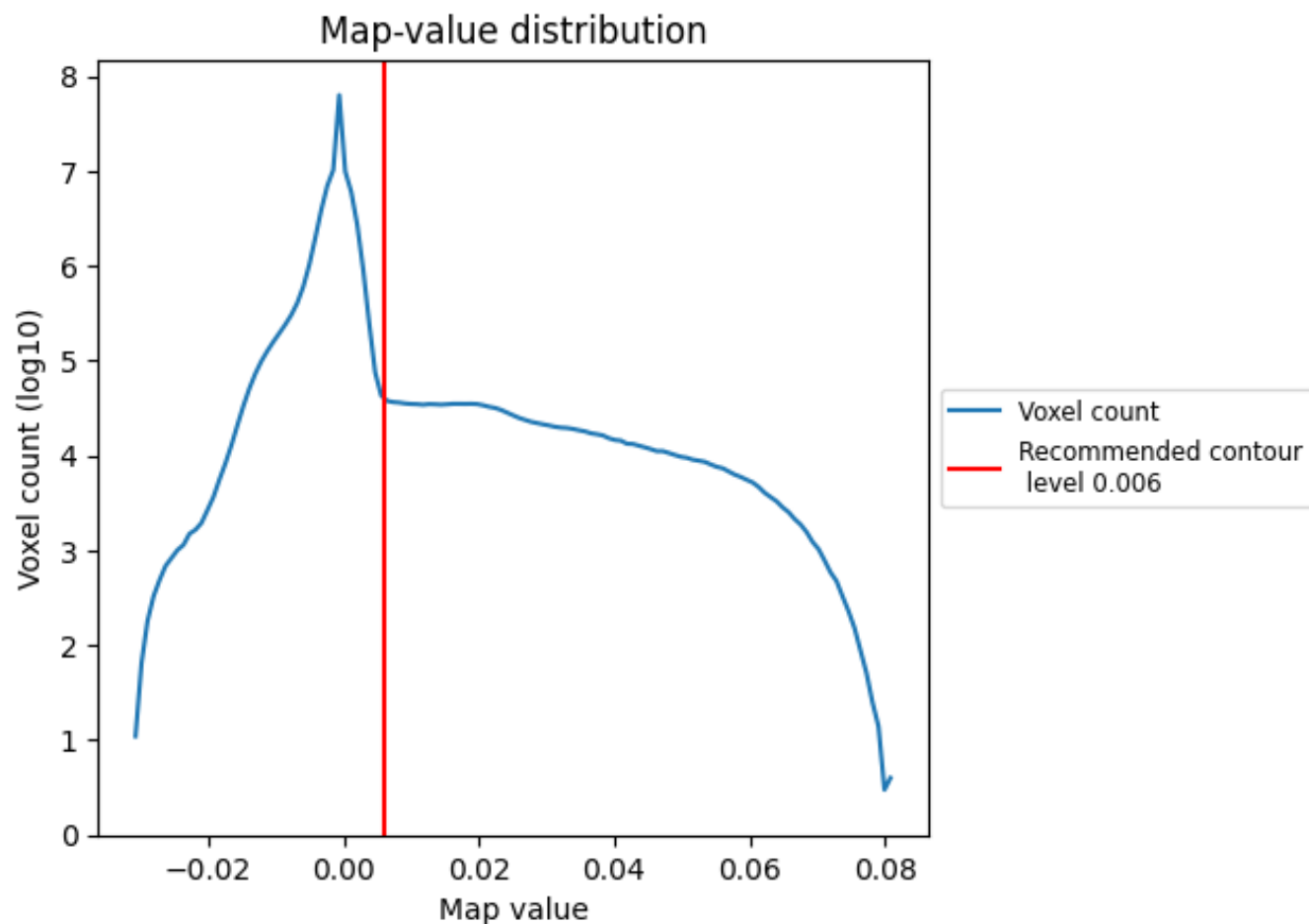


Z

7 Map analysis [i](#)

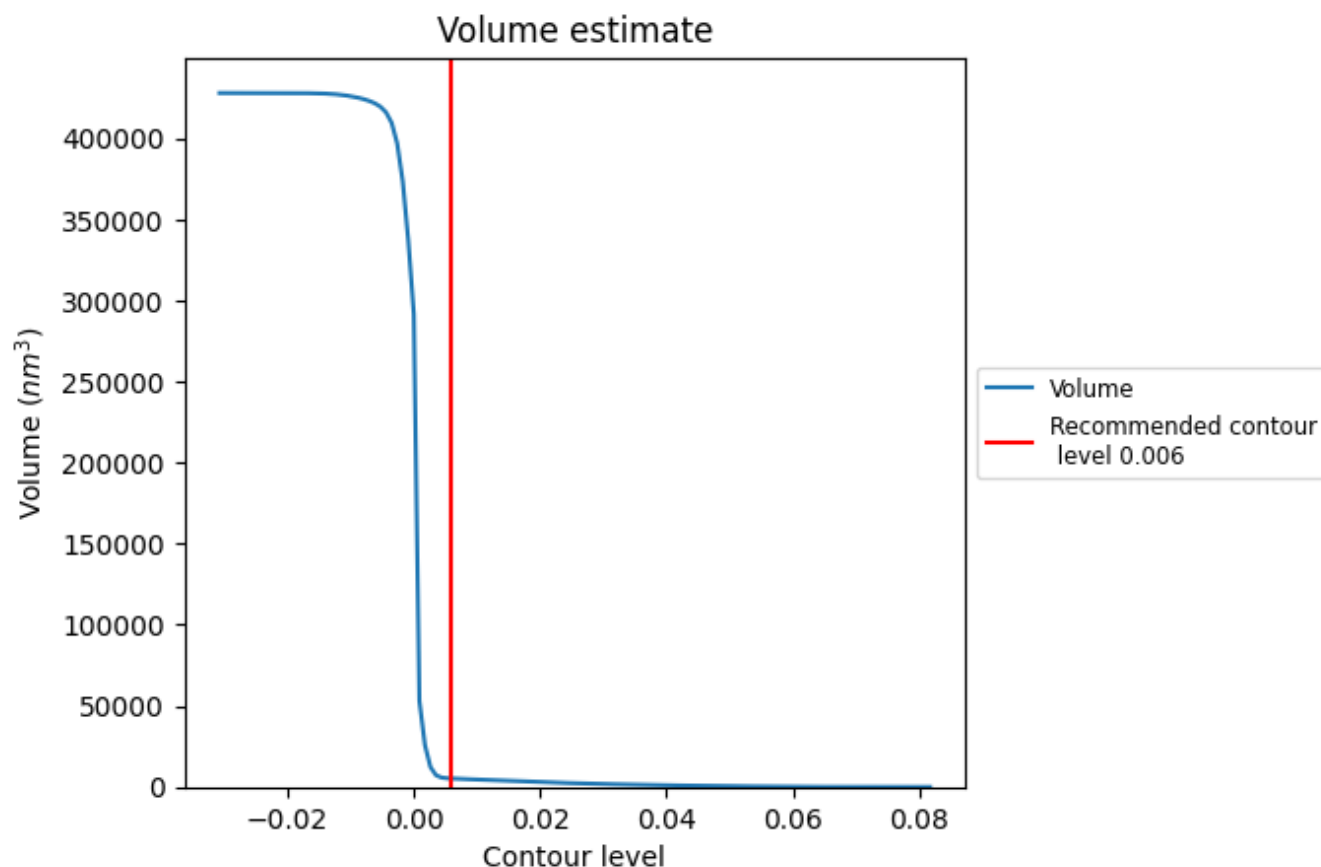
This section contains the results of statistical analysis of the map.

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.

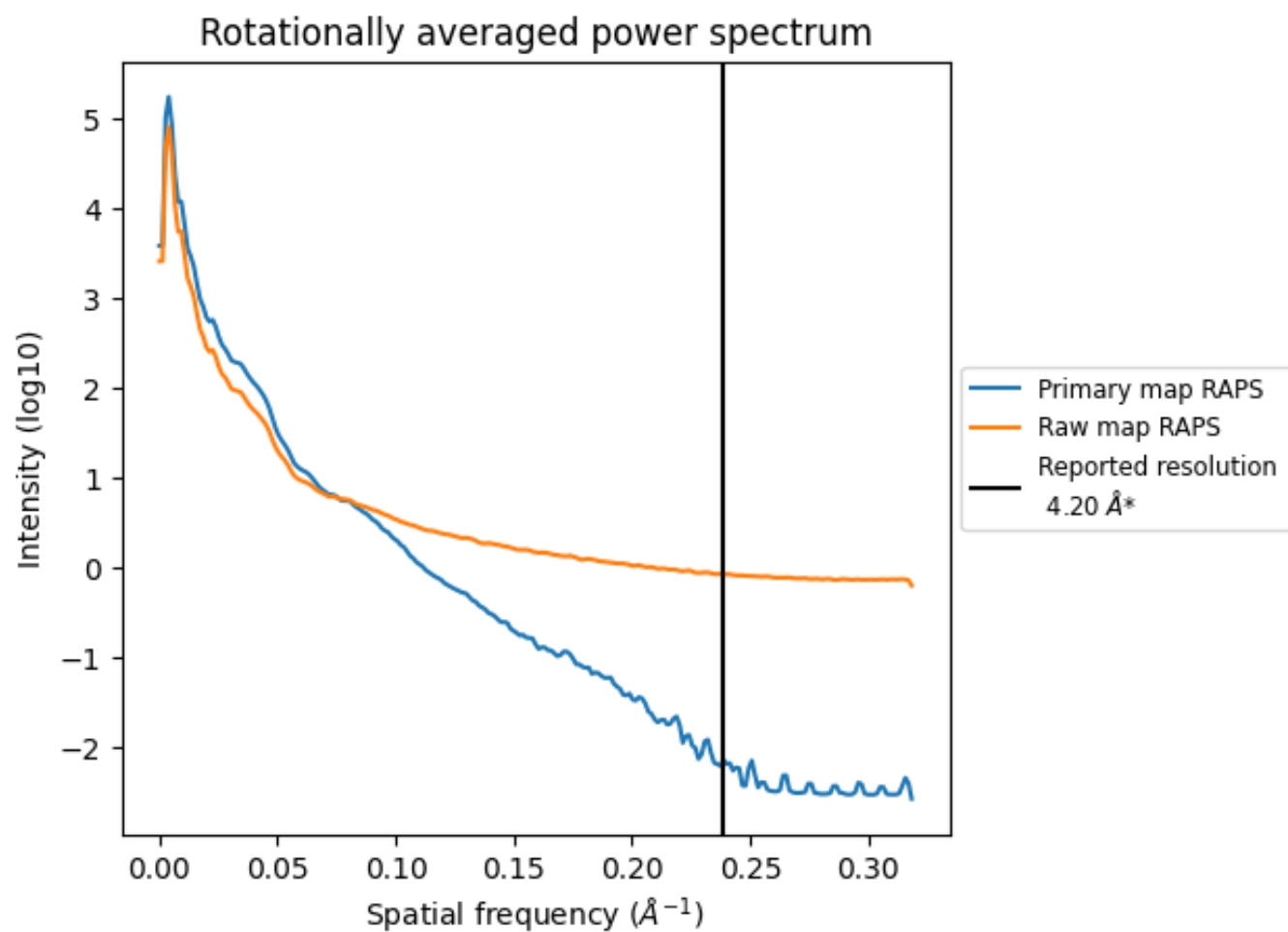
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5225 nm³; this corresponds to an approximate mass of 4720 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 [i](#)

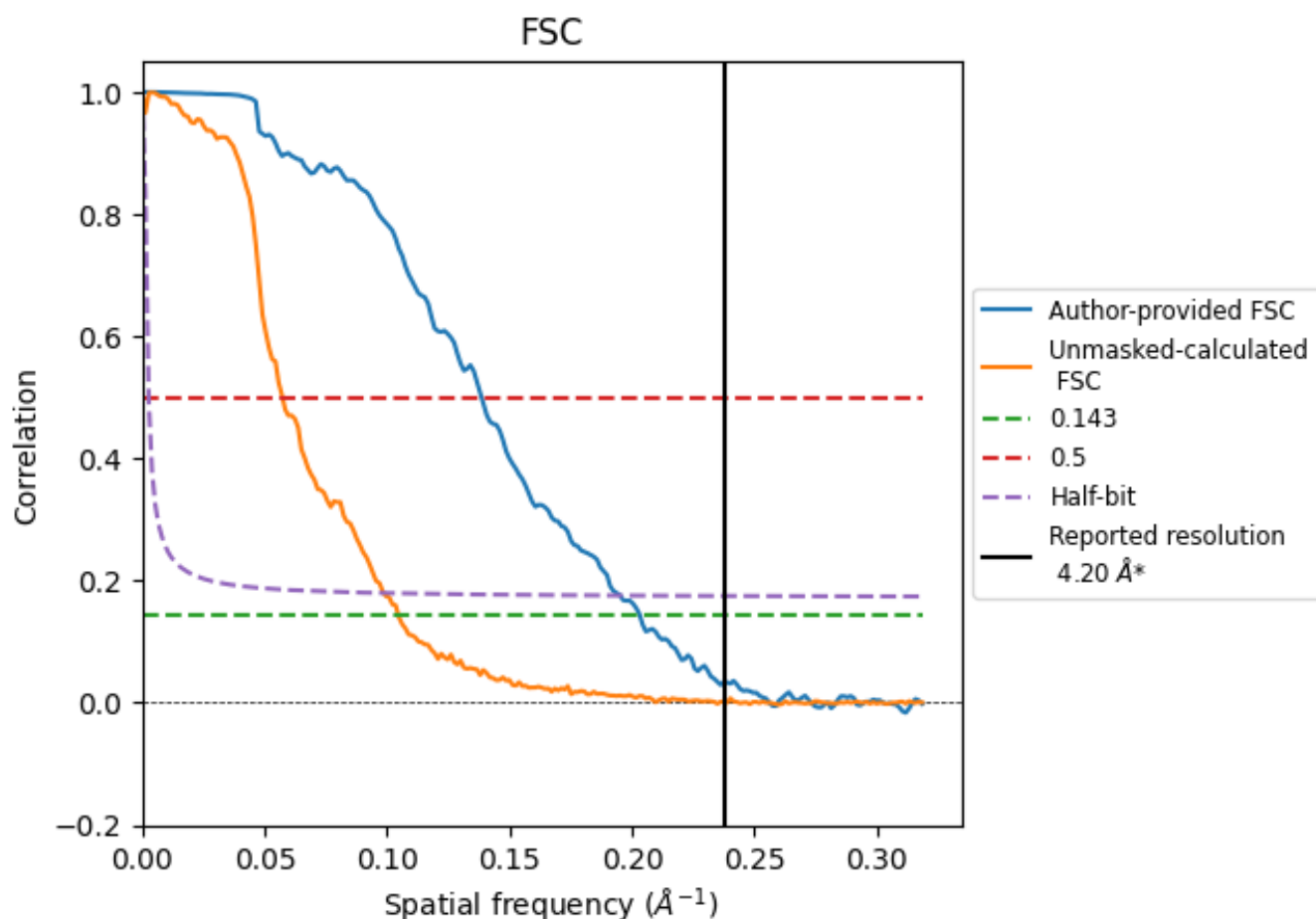


*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.92	7.22	5.12
Unmasked-calculated*	9.56	17.48	10.13

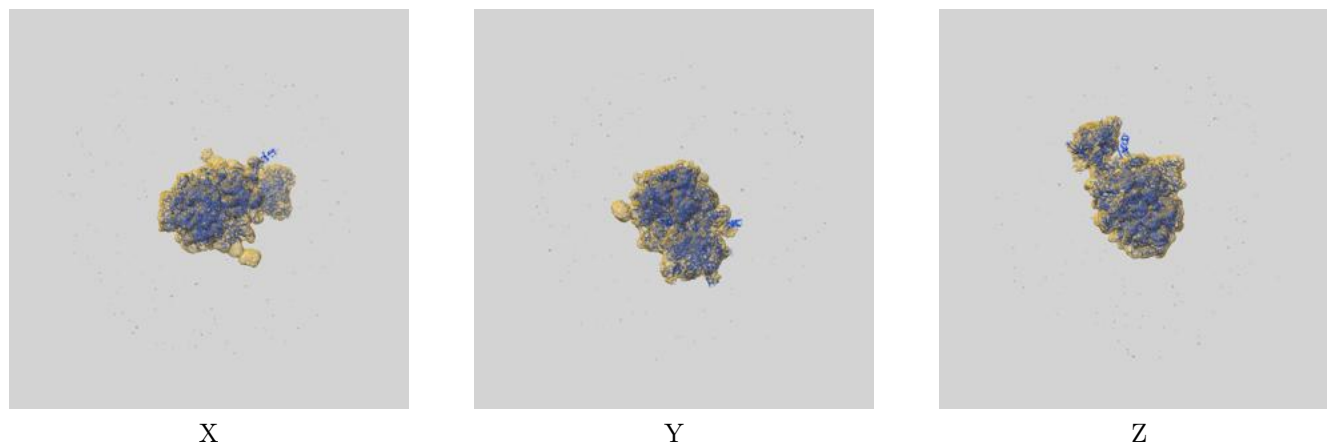
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.92 differs from the reported value 4.2 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.56 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38944 and PDB model 8Y5O. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



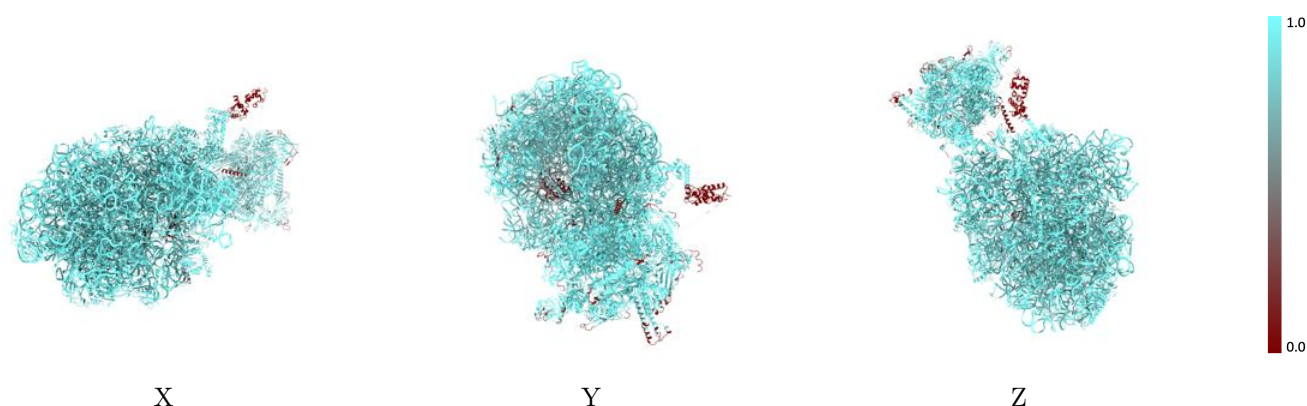
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



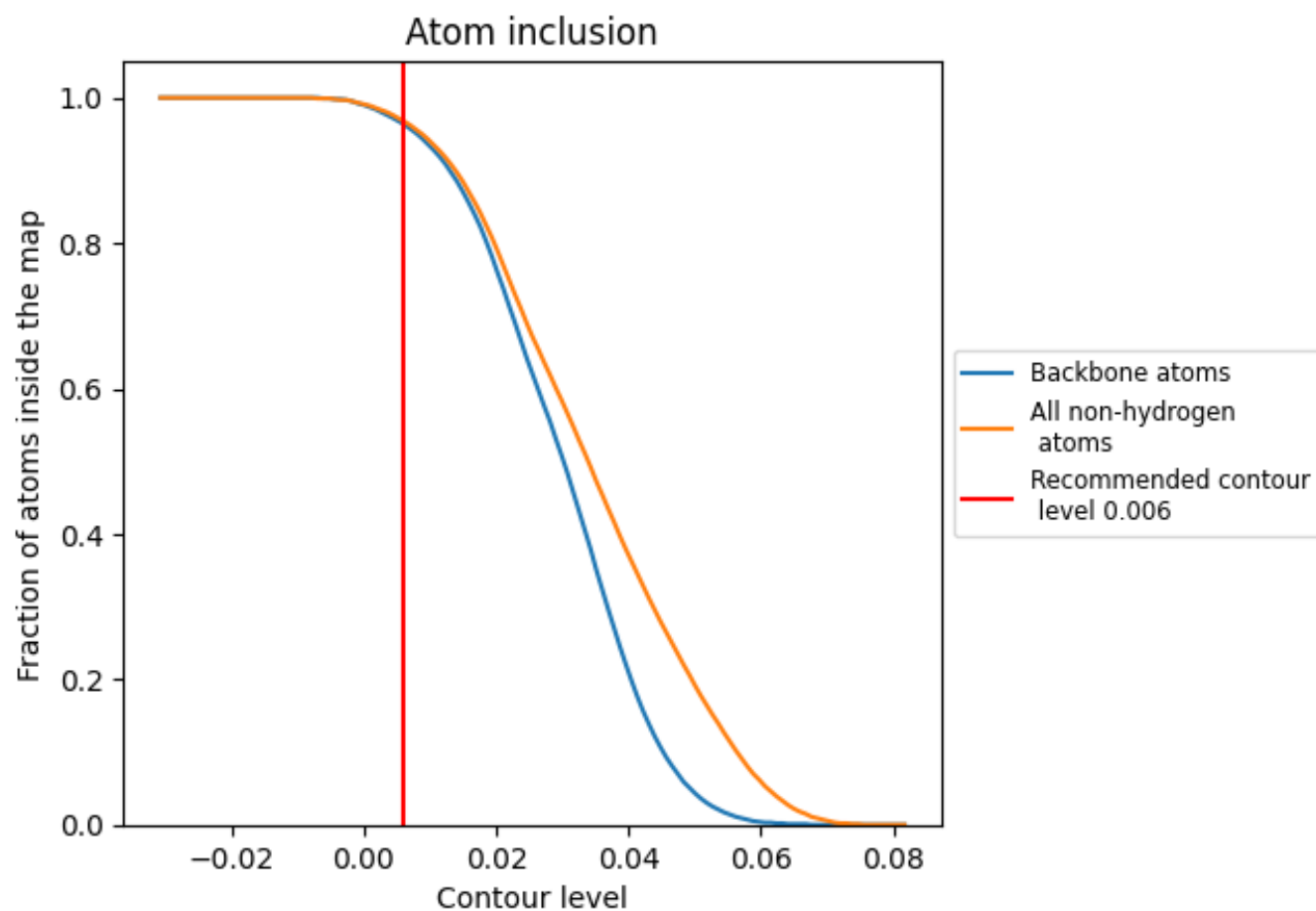
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 97% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9680	 0.1480
0	 0.7960	 0.0940
1	 0.9980	 0.1980
2	 1.0000	 0.1570
3	 0.9990	 0.1790
4	 0.9680	 0.1100
5	 0.6240	 0.0980
6	 0.9930	 0.1720
8	 1.0000	 0.0200
9	 1.0000	 0.0670
A	 0.9970	 0.1130
A1	 0.8930	 0.0340
A2	 0.7520	 0.0430
B	 0.9860	 0.1430
B1	 0.9350	 0.0230
B2	 0.9170	 0.0360
C	 0.9550	 0.1350
D	 0.9750	 0.1360
E	 0.9980	 0.1230
F	 0.9930	 0.1030
G	 0.9800	 0.1360
H	 0.9880	 0.1440
I	 0.9920	 0.1270
J	 0.9900	 0.1410
K	 0.9850	 0.1510
L	 0.9730	 0.1380
M	 0.9760	 0.1110
N	 0.9810	 0.1040
NA	 0.8340	 0.1340
NG	 0.9350	 0.0530
O	 0.9950	 0.1140
P	 0.9870	 0.1500
Q	 0.9450	 0.1460
R	 0.9740	 0.1410
S	 0.9970	 0.1150



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
T	 0.9960	 0.1360
U	 1.0000	 0.1100
V	 0.9890	 0.1100
W	 0.9980	 0.1440
W0	 0.5380	 0.0170
X	 1.0000	 0.1160
Y	 0.9790	 0.1170
Z	 0.9340	 0.1470
a	 0.9770	 0.0990
b	 0.9810	 0.1670
c	 0.9940	 0.1550
d	 0.9890	 0.1430
e	 0.9500	 0.1060
f	 0.9880	 0.1370
g	 0.8680	 0.1230
h	 1.0000	 0.1790
i	 0.8950	 0.0460
j	 0.9940	 0.1560
k	 0.9580	 0.1810
l	 0.9940	 0.1200
m	 0.9630	 0.1320
n	 0.9990	 0.1550
o	 1.0000	 0.0960
p	 0.9930	 0.1790
q	 0.9970	 0.1290
r	 0.9940	 0.1370
s	 0.9880	 0.1620
t	 0.9850	 0.1470
u	 0.9840	 0.1410
v	 0.9920	 0.1410
w	 0.9890	 0.1050
x	 0.9970	 0.1580
y	 0.9900	 0.1450
z	 0.9820	 0.1480