



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 08:19 AM UTC

PDB ID : 8YDJ / pdb_00008ydj
EMDB ID : EMD-39173
Title : E.coli transcription translation coupling complex in TTC-P containing mRNA with 39-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and viomycin
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.
Deposited on : 2024-02-20
Resolution : 5.10 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

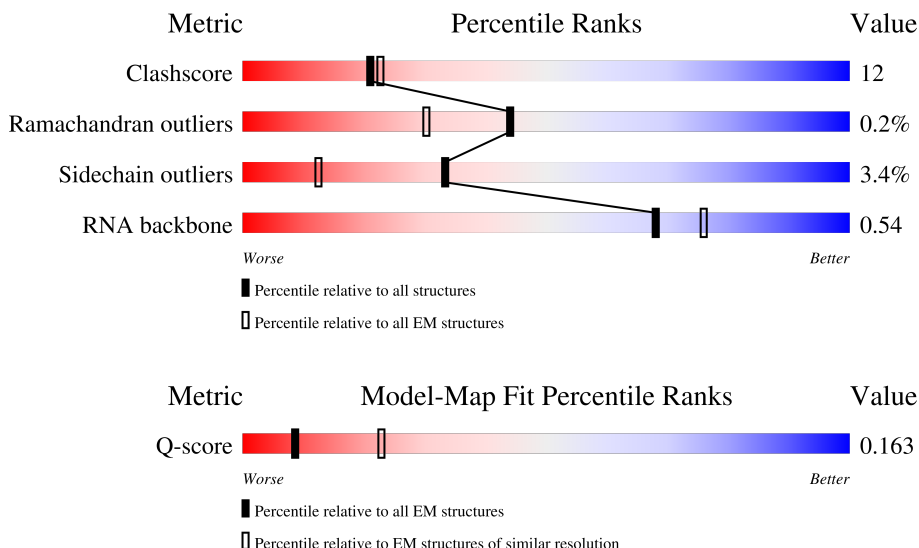
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.10 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.



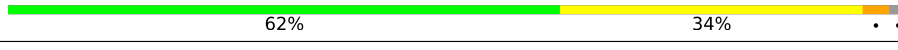
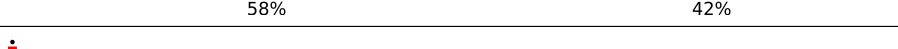
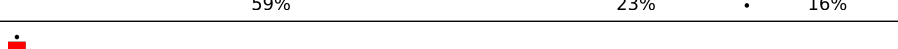
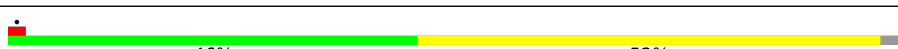
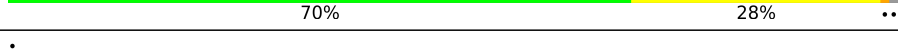
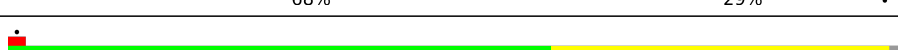
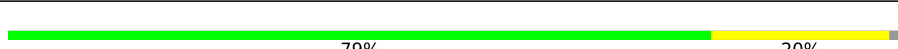
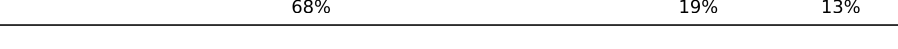
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	844 (4.60 - 5.60)

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	

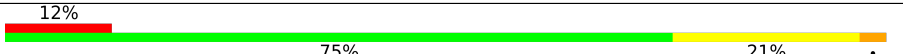
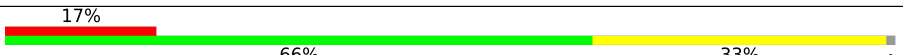
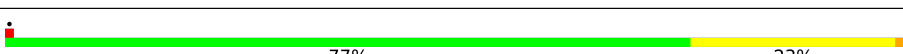
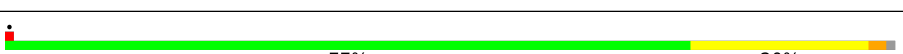
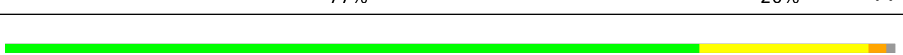
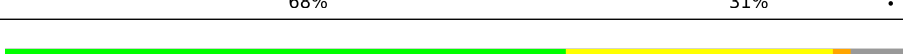
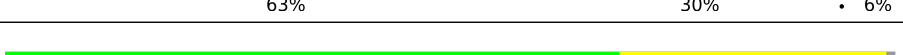
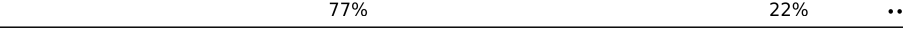
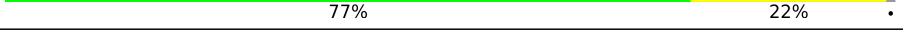
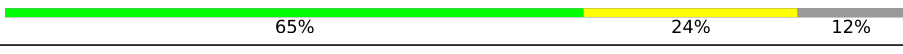
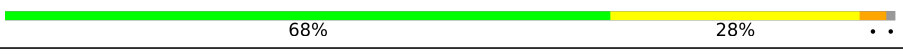
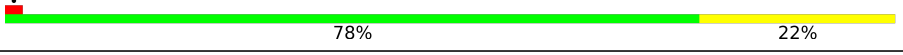
Continued on next page...

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	

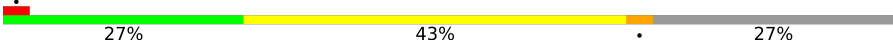
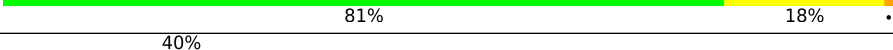
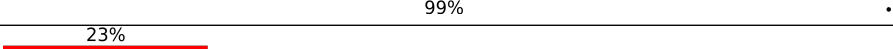
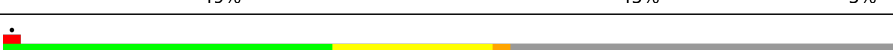
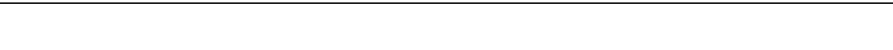
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	d	201	
30	e	179	
31	f	177	
32	g	149	
33	i	142	
34	j	142	
35	k	123	
36	l	144	
37	m	136	
38	n	127	
39	o	117	
40	p	115	
41	q	118	
42	r	103	
43	s	110	
44	t	100	
45	u	104	
46	v	94	
47	w	85	
48	x	78	
49	y	63	
50	z	59	
51	1	2904	
52	2	120	
53	3	1542	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	4	56	
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

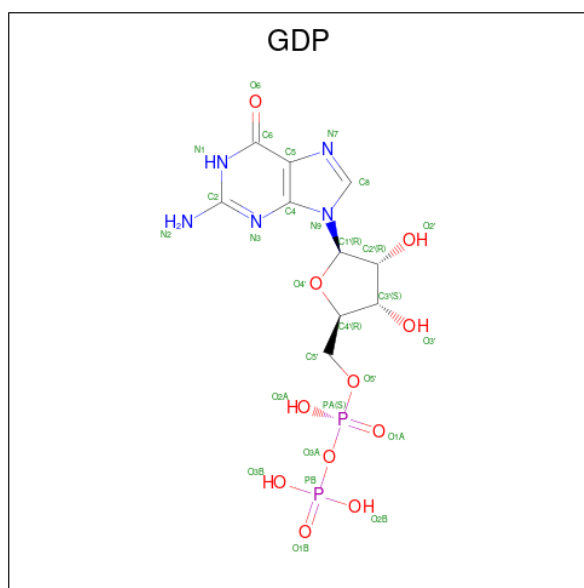
- Molecule 67 is a protein (with D amino acids) called Viomycin.

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).

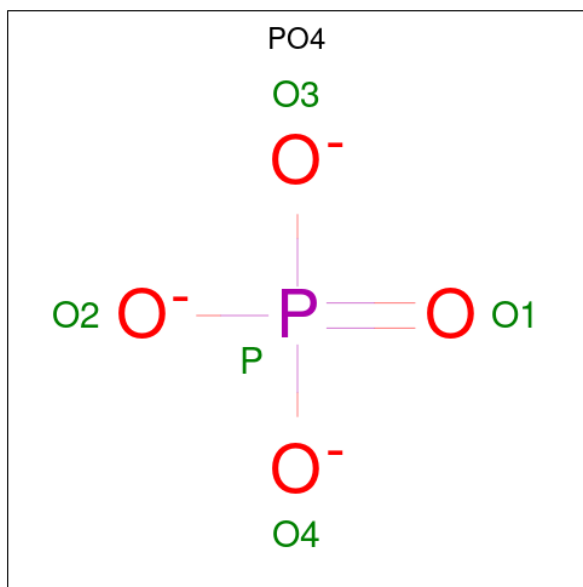
Mol	Chain	Residues	Atoms		AltConf
68	B1	1	Total	Mg	0
			1	1	

- 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).

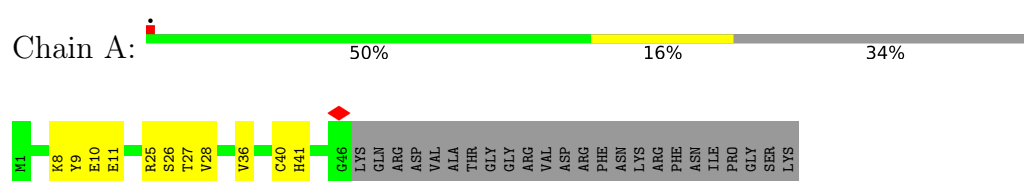


Mol	Chain	Residues	Atoms			AltConf
			Total	O	P	
70	0	1	5	4	1	0

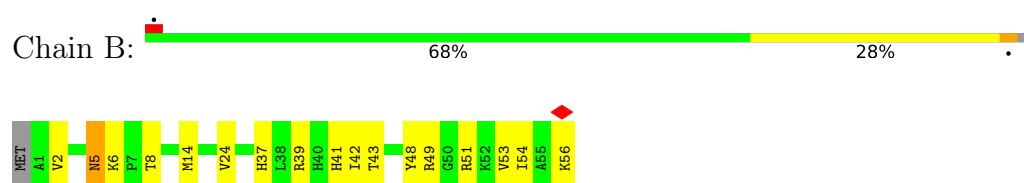
3 Residue-property plots

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.

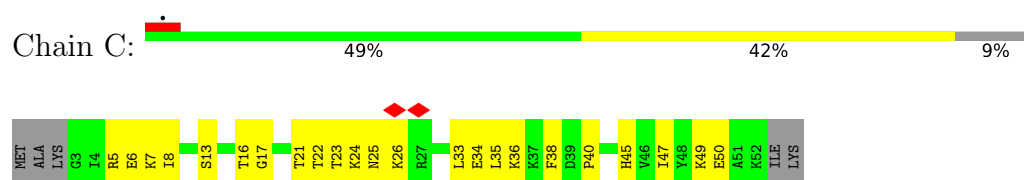
• Molecule 1: 50S ribosomal protein L31



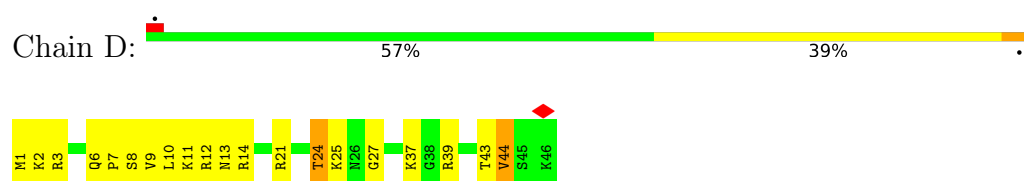
• Molecule 2: 50S ribosomal protein L32



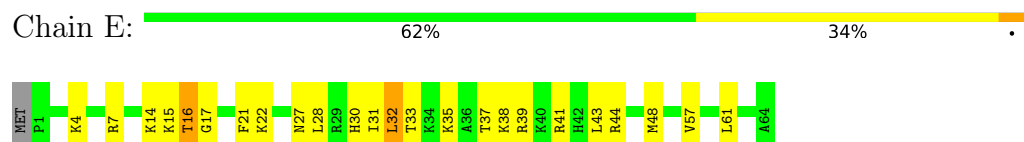
• Molecule 3: 50S ribosomal protein L33



• Molecule 4: 50S ribosomal protein L34

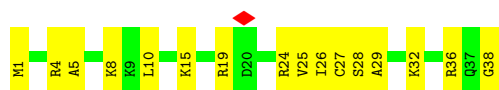


• Molecule 5: 50S ribosomal protein L35



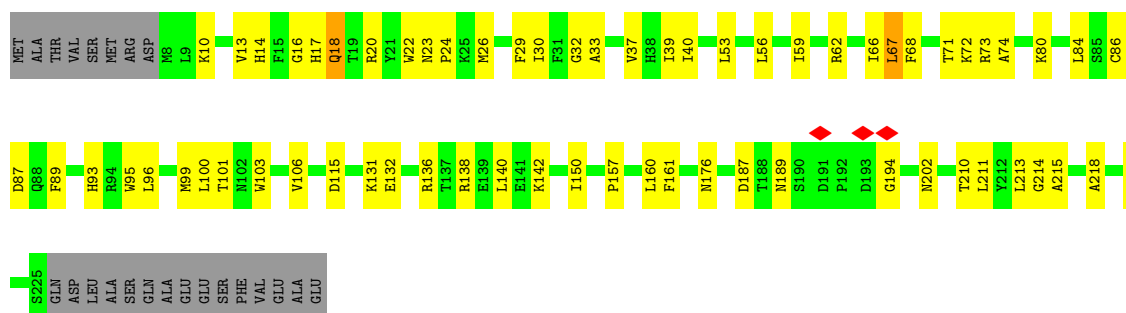
- Molecule 6: 50S ribosomal protein L36

Chain F:  58% 42%



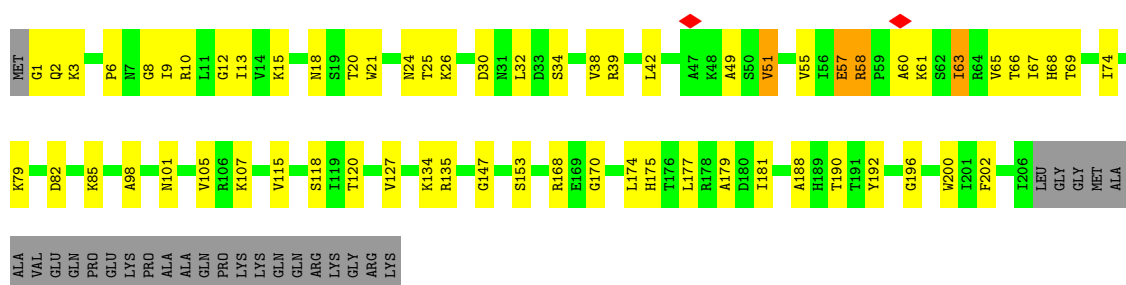
- Molecule 7: 30S ribosomal protein S2

Chain G:  63% 26% 10%



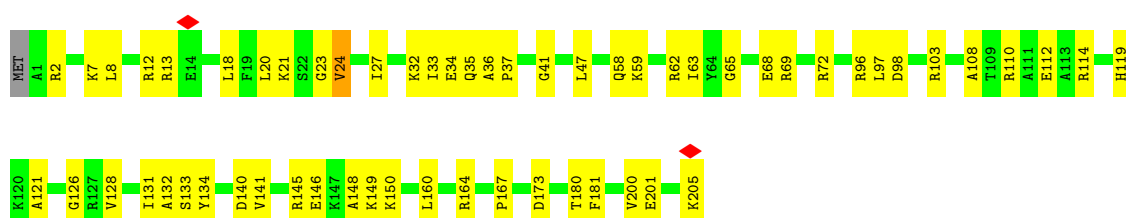
- Molecule 8: 30S ribosomal protein S3

Chain H:  61% 26% 12%



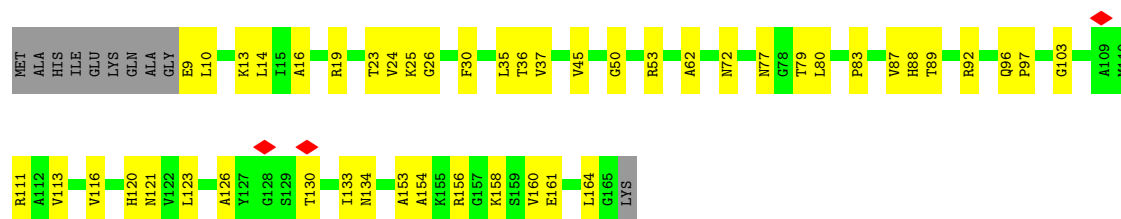
- Molecule 9: 30S ribosomal protein S4

Chain I:  71% 28%

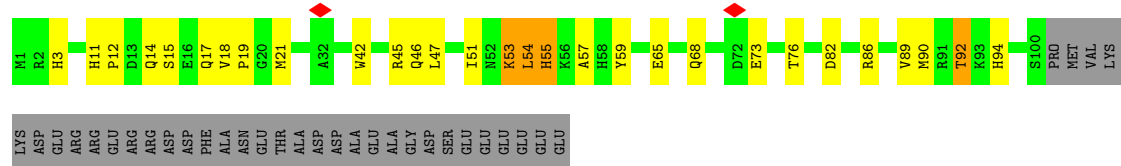


- Molecule 10: 30S ribosomal protein S5

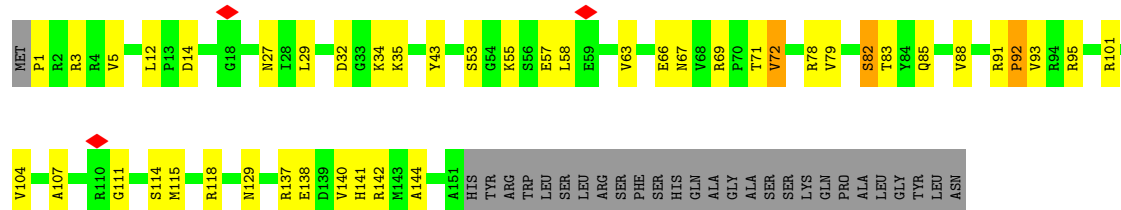
Chain J:  66% 28% 6%



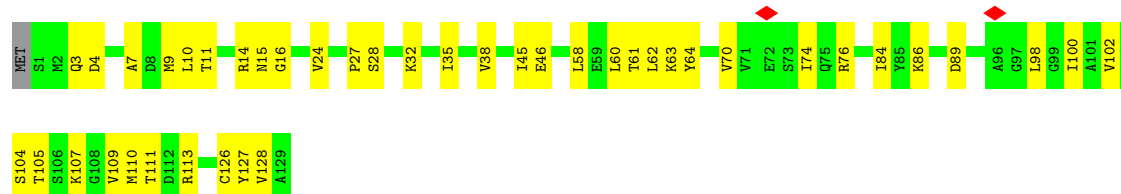
- Molecule 11: 30S ribosomal protein S6, fully modified isoform



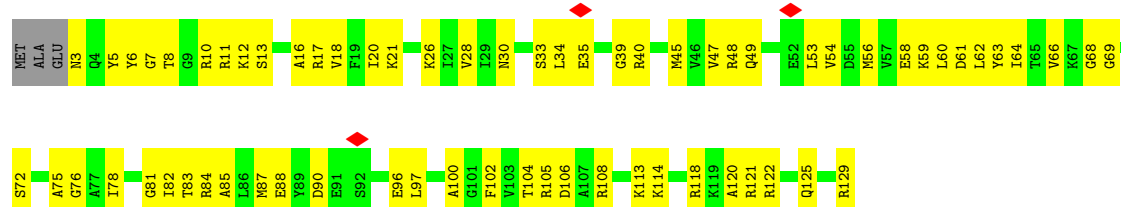
- Molecule 12: 30S ribosomal protein S7



- Molecule 13: 30S ribosomal protein S8

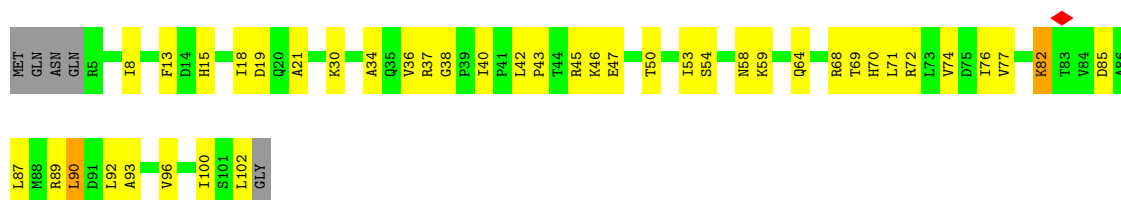


- Molecule 14: 30S ribosomal protein S9



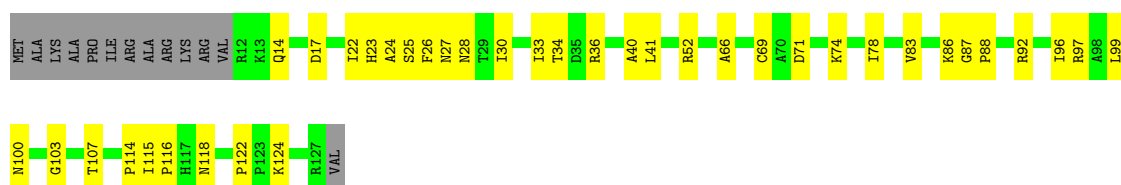
- Molecule 15: 30S ribosomal protein S10

Chain O: 



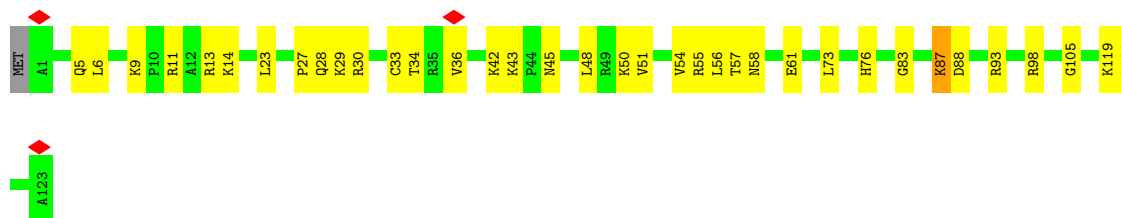
- Molecule 16: 30S ribosomal protein S11

Chain P: 



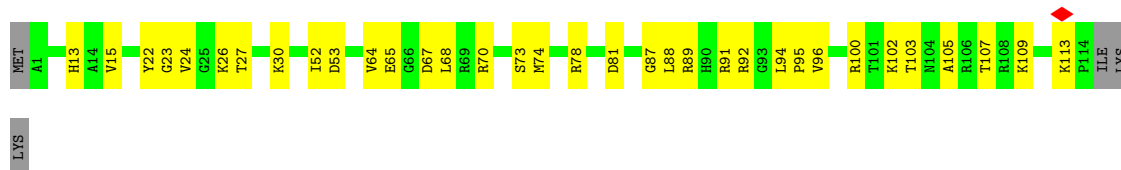
- Molecule 17: 30S ribosomal protein S12

Chain Q: 



- Molecule 18: 30S ribosomal protein S13

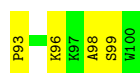
Chain R: 



- Molecule 19: 30S ribosomal protein S14

Chain S: 





- Molecule 20: 30S ribosomal protein S15

Chain T: 79% 20% .



- Molecule 21: 30S ribosomal protein S16

Chain U: 72% 28%



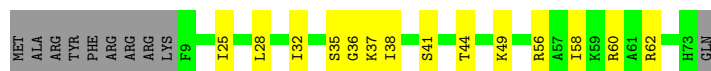
- Molecule 22: 30S ribosomal protein S17

Chain V: 67% 29% 5%



- Molecule 23: 30S ribosomal protein S18

Chain W: 68% 19% 13%



- Molecule 24: 30S ribosomal protein S19

Chain X: 65% 21% 14%



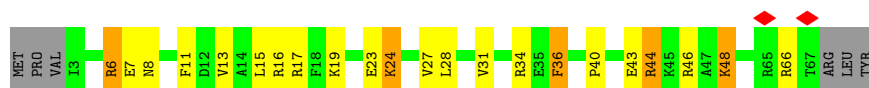
- Molecule 25: 30S ribosomal protein S20

Chain Y: 64% 33%



- Molecule 26: 30S ribosomal protein S21

Chain Z: 61% 24% 7% 8%



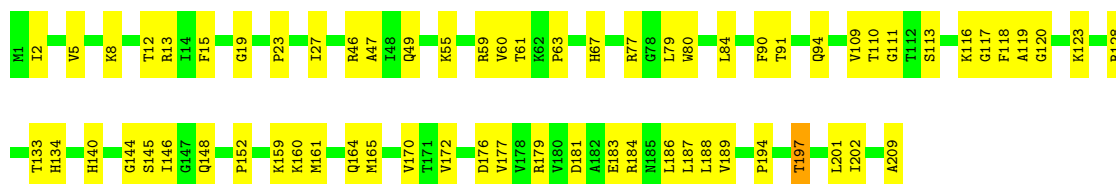
- Molecule 27: 50S ribosomal protein L2

Chain b: 70% 29%



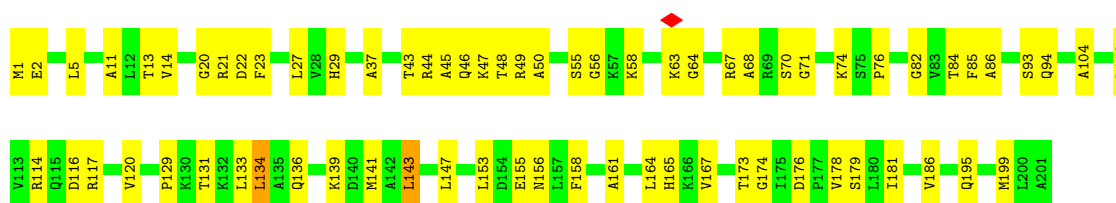
- Molecule 28: 50S ribosomal protein L3

Chain c: 68% 31%



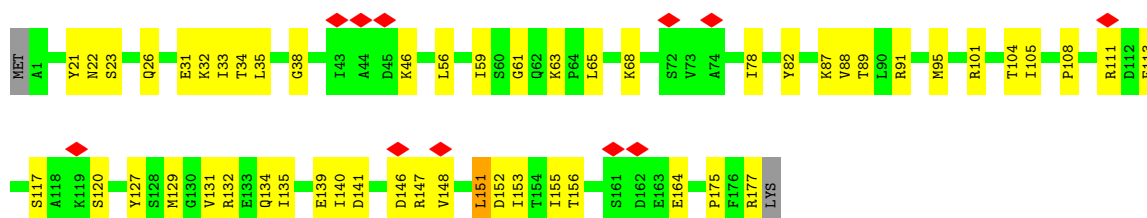
- Molecule 29: 50S ribosomal protein L4

Chain d: 65% 34%



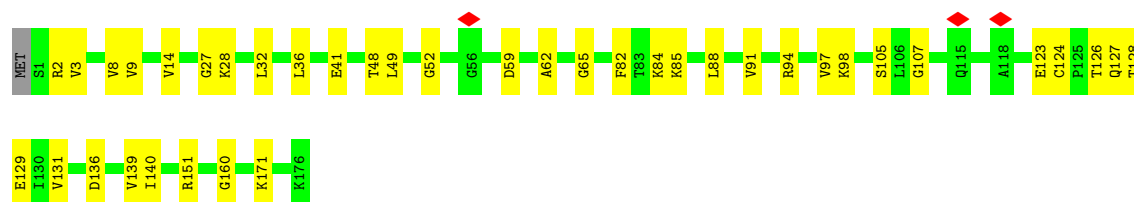
- Molecule 30: 50S ribosomal protein L5

Chain e: 6% 70% 28%



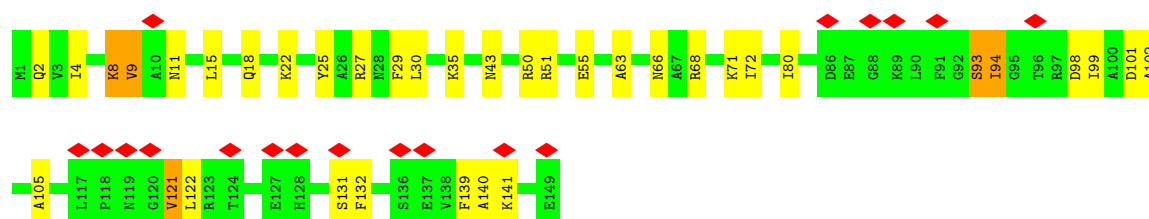
- Molecule 31: 50S ribosomal protein L6

Chain f: 



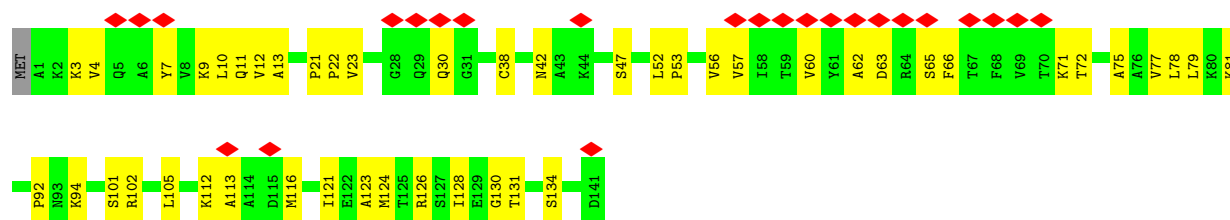
- Molecule 32: 50S ribosomal protein L9

Chain g: 



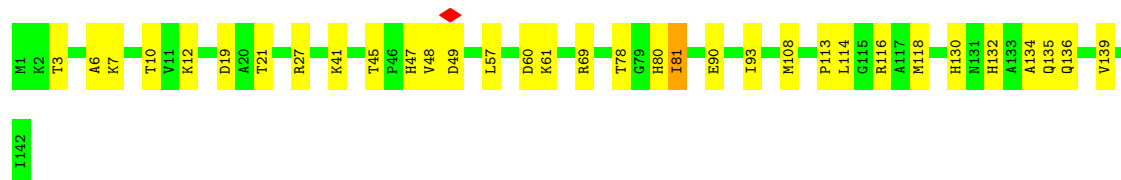
- Molecule 33: 50S ribosomal protein L11

Chain i: 



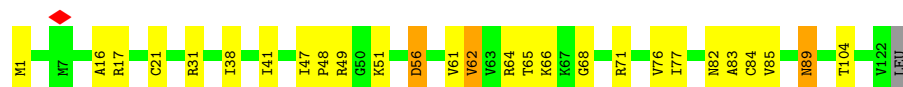
- Molecule 34: 50S ribosomal protein L13

Chain j: 

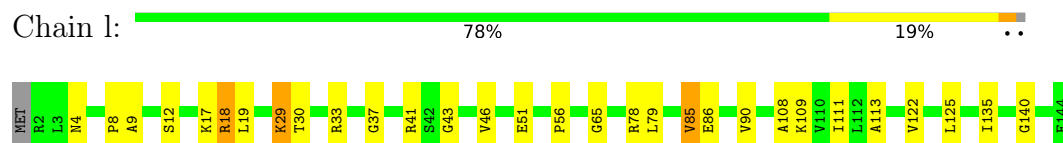


- Molecule 35: 50S ribosomal protein L14

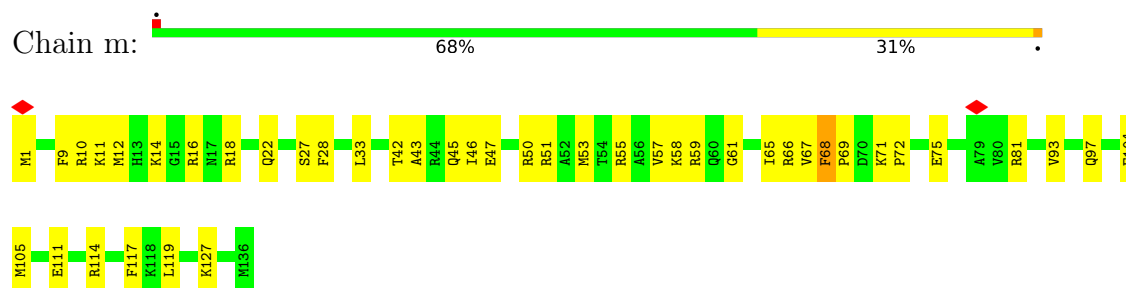
Chain k: 



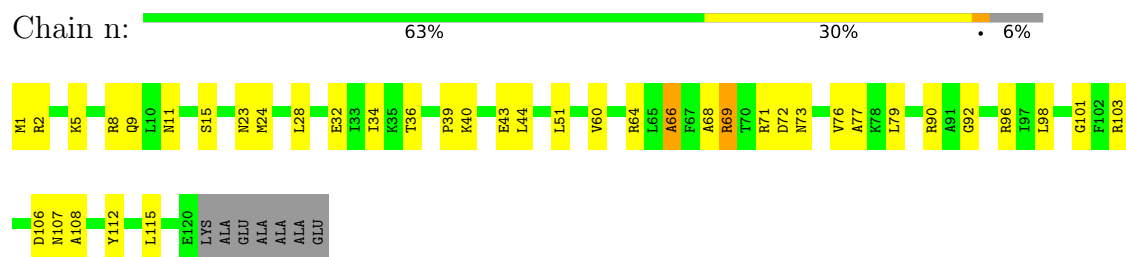
- Molecule 36: 50S ribosomal protein L15



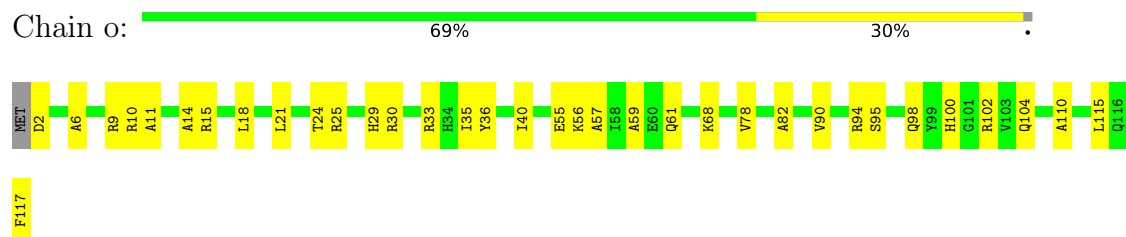
• Molecule 37: 50S ribosomal protein L16



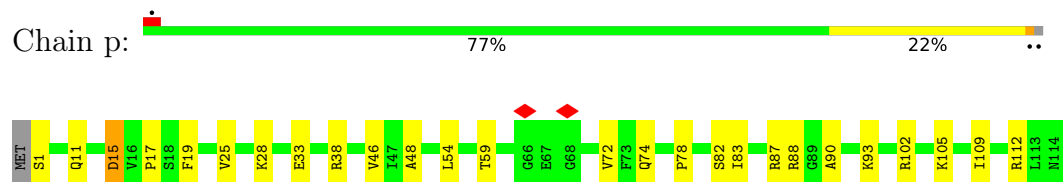
• Molecule 38: 50S ribosomal protein L17



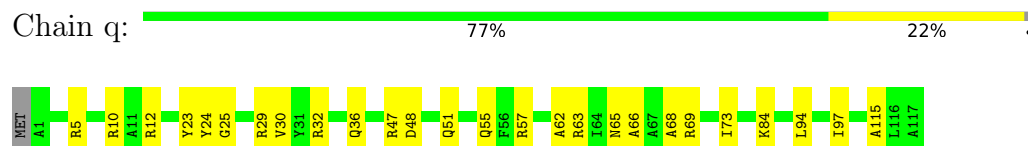
• Molecule 39: 50S ribosomal protein L18



• Molecule 40: 50S ribosomal protein L19



• Molecule 41: 50S ribosomal protein L20



- Molecule 42: 50S ribosomal protein L21

Chain r:  71% 29%



- Molecule 43: 50S ribosomal protein L22

Chain s:  72% 27% .



- Molecule 44: 50S ribosomal protein L23

Chain t:  64% 28% . 7%



- Molecule 45: 50S ribosomal protein L24

Chain u:  74% 23% ..



- Molecule 46: 50S ribosomal protein L25

Chain v:  79% 21%



- Molecule 47: 50S ribosomal protein L27

Chain w:  65% 24% 12%

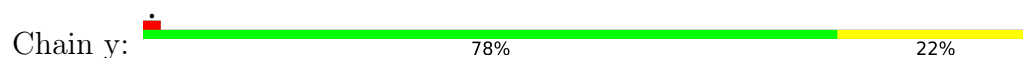


- Molecule 48: 50S ribosomal protein L28

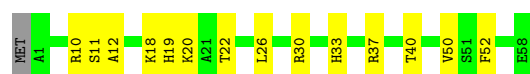
Chain x:  68% 28% ..



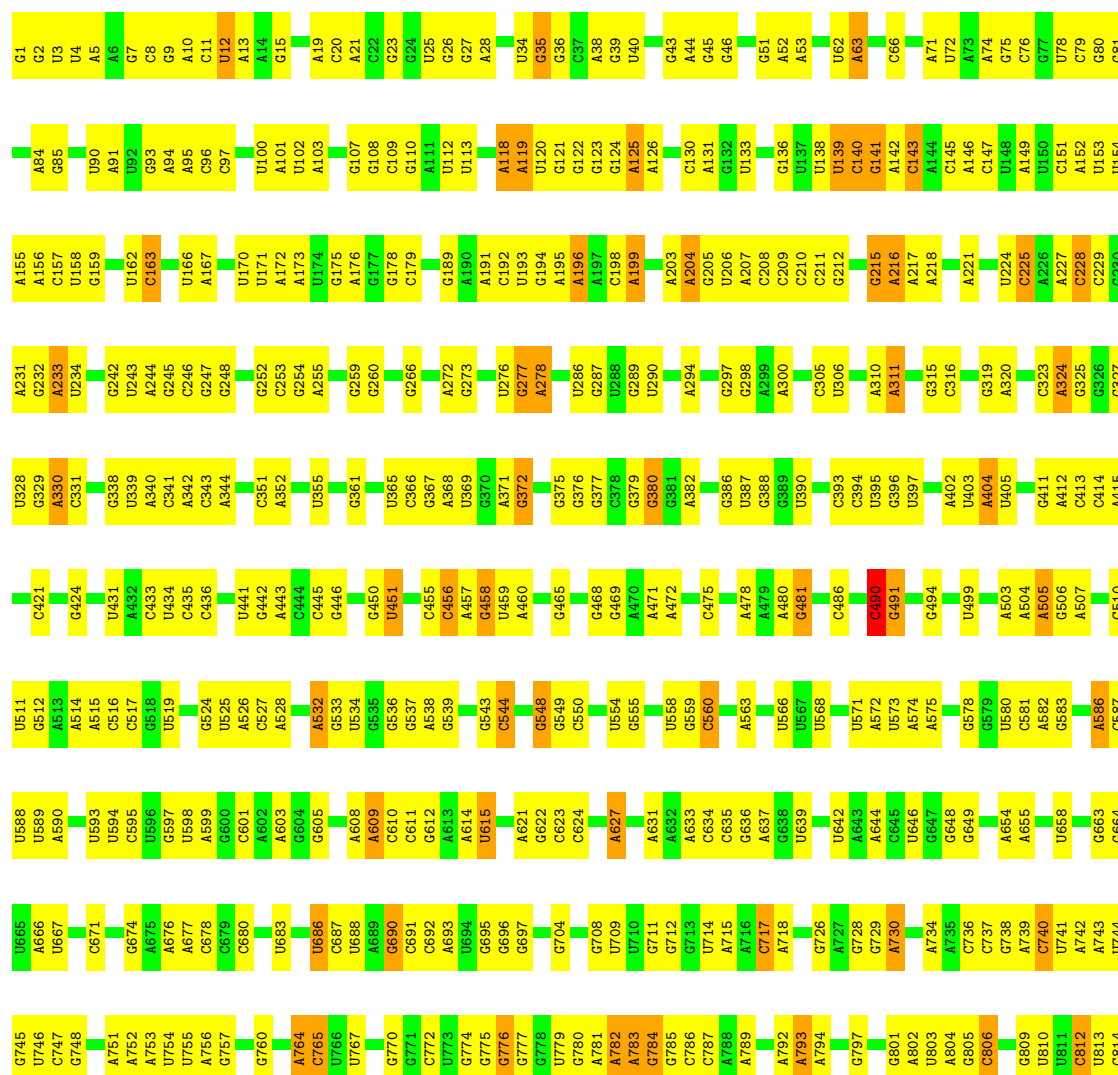
- Molecule 49: 50S ribosomal protein L29



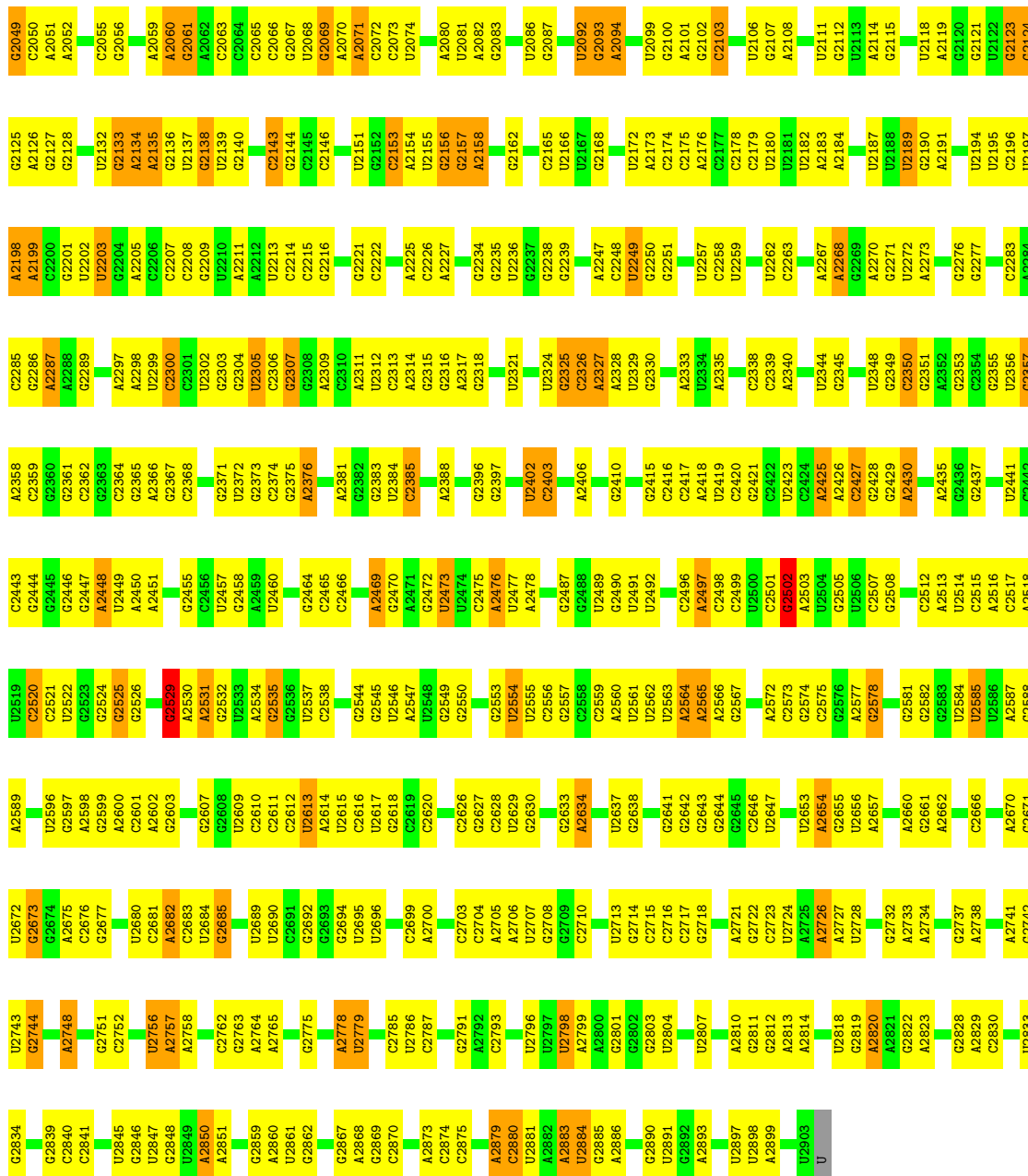
- Molecule 50: 50S ribosomal protein L30



- Molecule 51: 23S rRNA



G1972	G1973	G1974	G1975	G1976	A1977	A1978	G1979	A1980	C1889	C1893	C1894	A1900	A1901	C1902	G1903	G1904	C1905	A1912	A1913	C1914	G1995	U1917	A1918	U1997	A1998	G1999	C2000	U2007	C2008	A2009	G2010	A2013	A2020	C2021	U2022	G2023	G2024	U2025	U1841	C1842	C1843	U1844	U1951	A1952	A1953	C2033	A2034	U1955	U1956	C2036	G2037	C1962	U1963	C1964	C1965	A1966	C1967	A1970	U1971				
C1795	U1796	G1797	U1798	G1799	C1800	A1801	A1802	A1803	C1804	A1805	C1806	G1807	A1808	A1809	A1810	A1811	A1815	C1816	G1817	U1818	A1819	U1820	A1821	C1822	G1823	U1824	U1825	U1826	U1827	U1828	U1829	U1830	U1831	U1832	U1833	C1836	C1837	U1838	U1839	U1840	U1841	C1842	C1843	C1844	U1853	A1854	U1855	U1856	G1857	A1858	G1863	U1864	G1867	C1868	G1869	C1870							
U1716	A1717	G1718	G1719	C1730	G1642	G1643	G1644	G1645	G1646	U1647	U1648	U1742	G1743	A1650	A1651	A1652	A1653	A1654	C1655	C1656	U1657	G1658	G1659	G1660	G1661	G1662	G1663	A1664	G1665	G1666	G1667	G1674	C1675	A1676	A1677	A1678	A1679	U1680	G1681	C1686	A1608	G1687	C1694	G1695	G1696	A1697	A1698	G1699	U1700	A1701	G1707	G1710	A1711	G1715									
A1635	C1638	C1639	A1640	A1641	G1642	G1643	G1644	G1645	G1646	U1647	U1648	U1649	G1650	A1650	G1651	A1652	G1653	A1654	C1655	C1656	U1657	G1658	G1659	G1660	G1661	G1662	G1663	A1664	G1665	G1666	G1667	G1674	C1675	A1676	A1677	A1678	A1679	U1680	G1681	C1686	A1608	G1687	C1694	G1695	G1696	A1697	A1698	G1699	U1700	A1701	G1707	G1710	A1711	G1715									
A1549	C1550	A1551	G1555	C1558	U1559	C1564	C1565	A1566	U1567	C1568	A1569	A1570	G1571	A1572	C1573	C1574	A1580	G1581	C1582	G1587	G1588	A1591	C1592	A1593	U1594	C1595	A1596	A1597	U1598	U1599	C1600	A1603	C1607	A1608	A1609	A1614	C1615	A1616	C1617	A1618	G1619	U1620	U1621	C1625	A1626	A1630	G1631																
A1453	C1454	C1455	G1456	U1457	A1458	A1459	A1460	U1461	U1462	U1463	U1464	U1465	U1466	U1467	U1468	U1469	U1470	U1471	U1472	U1473	U1474	U1475	U1476	U1477	U1478	U1479	U1480	U1481	U1482	U1483	U1484	U1485	U1486	A1490	A1504	A1505	U1506	C1507	A1508	A1509	U1510	G1511	C1512	A1515	C1518	G1521	A1522	U1523	G1524	A1528	U1529	U1534	A1535	A1536	A1537	A1538	U1539	U1540	U1541	U1542	U1545	U1546	A1548
G1368	G1369	C1370	G1371	U1372	A1373	G1374	A1378	U1379	G1380	A1383	A1387	G1388	G1389	U1390	U1391	U1394	A1395	U1396	U1397	A1403	C1404	U1409	G1410	U1411	U1412	U1413	U1414	U1415	G1416	C1417	G1418	A1419	A1420	G1424	G1425	C1428	G1429	G1432	A1433	A1434	A1439	U1440	G1444	U1445	C1446	G1447	G1448																
A1287	C1288	G1289	U1294	C1297	G1300	A1301	A1302	A1303	A1304	C1305	G1306	A1307	A1308	U1309	G1310	G1311	U1312	U1313	C1319	C1320	A1321	A1322	U1325	U1326	A1327	C1330	G1332	G1333	G1334	G1337	G1338	A1342	G1343	U1352	A1353	G1354	G1355	A1356	C1357	G1360	C1361	C1362	C1363	G1364	A1365	A1366	A1367																
G1193	C1196	G1197	U1198	U1203	A1204	A1205	G1206	U1209	G1210	C1211	G1212	G1216	U1219	G1220	G1225	A1226	G1229	A1230	G1236	A1246	A1247	G1248	U1249	G1250	C1251	G1252	A1253	A1254	U1255	G1256	C1257	U1258	G1259	A1262	A1265	G1266	U1267	A1268	A1269	C1270	A1271	A1272	A1275	A1276	G1277	C1278	G1279																
C1122	C1123	G1124	G1125	A1126	C1127	G1128	A1129	U1130	G1131	U1132	A1133	A1134	C1135	G1136	G1137	U1138	C1140	U1141	A1142	A1143	A1144	C1145	C1146	A1147	U1148	C1153	A1154	A1155	A1156	G1157	C1158	C1161	G1162	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	C1177	G1178	G1179	U1180	U1181	U1182	U1183	U1184	G1185	G1186	G1187	G1191	G1192									
A1050	C1051	C1052	G1053	A1054	G1055	G1056	A1057	U1058	G1059	U1060	A1061	C1062	G1063	C1064	U1065	U1066	A1067	G1068	C1069	A1070	G1071	C1072	A1073	U1077	A1078	U1081	U1082	U1083	A1084	A1085	A1086	G1087	A1088	G1093	U1094	A1095	A1096	U1097	C1102	A1103	C1104	U1105	G1106	G1107	G1110	A1111	G1114	G1115	U1119	G1120	C1121												
G971	A972	A973	G974	A975	G976	A980	A981	C982	A983	A984	C985	C986	C987	A988	A989	C990	A990	A991	C994	C995	A996	U999	A1000	C1005	C1006	U1012	C1013	A927	A928	U929	A1020	A1021	G1022	U1023	G1024	G1025	G1026	A1027	A1028	A1029	C1030	U1033	G1036	G1037	G1038	A1039	A1040	G1041	G1042	C1043	C1044	C1045	A1046	C1047									
U884	C885	A886	U887	C888	C889	C890	G891	U895	U896	A897	C898	A899	G831	A900	C901	A833	C902	A910	A911	C912	U913	G916	A917	A918	G923	G924	U927	A928	U929	A933	C937	G938	C939	G940	A941	C944	A945	C946	C947	G948	G949	G952	C953	G954	U955	G956	C957	U958	A959	A960	C961												
C817	G818	A819	A820	A821	G822	C823	U824	A825	U826	U827	U828	A829	G830	U831	U832	A833	G834	C837	C838	U839	C840	G841	U842	G843	A844	A845	U846	U847	C848	A849	U850	C851	U852	G857	C858	C859	U860	A861	G862	A863	G864	C865	A866	G869	U870	U871	U872	A877	A878	C879	G880	G881	G882	G883									



• Molecule 52: 5S rRNA

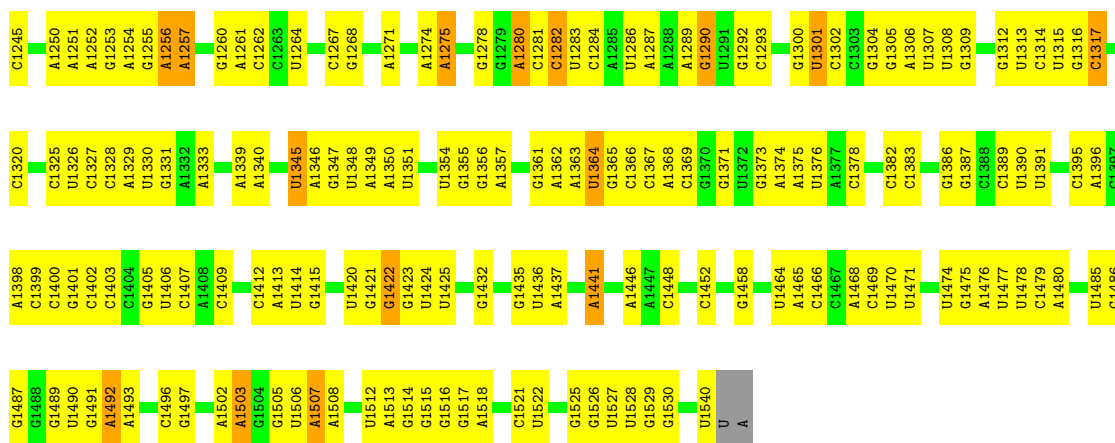
Chain 2: 52% 38% 10%



• Molecule 53: 16S rRNA

Chain 3: 45% 48% 6%

A1169	A1093	A1014	C934	G846	G766	A673	C580	A509	C422	G351	A270	U180	A71	A
A1170	G1094	G1015	A935	U850	U757	A674	G581	A510	G423	C352	C271	A181	G79	A2
A1171	U1095	A1016	C936	G851	C768	A675	U593	C511	G424	A353	C272	A182	A80	A3
A1172	C1096	U1017	A937	G851	G761	A676	U594	U512	G425	G354	U273	G183	A81	G6
A1173	C1097	G1018	A938	U855	U762	U677	A595	C513	U426	C355	G276	G184	G82	A7
G1174	C1098	A1019	C939	G856	G763	U678	A596	C514	G428	G357	A279	C193	C83	A8
A1179	G1109	A1022	C940	C857	G763	C679	U597	C515	U429	U388	C280	C194	U84	A9
A1180	A1101	U1023	G945	G858	A768	U684	U598	U516	A430	C359	G281	A197	U85	A10
G1181	A1102	G1024	A946	C859	C769	G685	A600	C517	A431	G362	C284	G204	C90	G15
G1182	C1103	U1025	C947	A860	C770	G685	A601	C518	A432	A363	C285	A205	U91	A16
U1183	G1104	G1026	G950	C861	C771	G690	G602	C519	A433	A363	C285	G204	U92	C18
G1184	A1105	C1027	U950	C862	U772	G691	A602	A520	U434	A363	C285	A205	U93	A19
A1187	C1107	G1028	C951	U863	G773	G691	A607	C528	A436	A366	G289	G206	U94	U20
A1188	A1108	U1029	G952	A864	A777	U701	A608	G529	C436	U367	C290	C207	G86	G11
G1189	C1109	G1030	U953	A865	C778	A702	G703	U531	U437	G369	U291	U208	C87	
C1190	A1110	G1032	U955	C866	C779	G703	C613	A532	U438	A369	U296	C210	C95	G22
G1193	A1111	G1033	U956	C867	A782	A706	C620	A533	C440	C372	C297	G211	G100	C23
U1194	A1117	G1034	U957	A872	A782	U707	C621	U534	G445	A373	A298	G212	U24	U24
C1195	U1118	A1035	U958	A873	A782	U707	A621	A535	G445	A374	A298	G213	G107	C25
A1196	C1119	A1042	U959	G874	A792	G710	C623	C536	A448	U375	G299	G213	U108	A26
A1197	U1120	G1043	U960	U875	G710	G710	C624	G537	A452	G376	A300	G219	A109	G27
G1198	C1121	A1043	U961	C876	G713	G714	U625	G538	G453	G377	G302	U218	C110	A28
U1199	U1122	G1047	C962	A877	G714	G715	G626	A539	G454	C379	A303	G220	G111	
C1200	U1123	U1048	G963	A878	A715	G715	G627	A540	G455	G380	A304	C221	G112	A32
A1201	G1124	G1049	U965	G881	C803	A718	C628	A541	G456	G381	C308	U224	U114	A33
C1210	U1125	G1050	U966	C882	U804	C719	C631	C545	A457	G385	A309	C225	G128	C34
U1211	C1126	G966	C967	U876	C805	C720	U632	A546	U458	C386	A310	A228	U129	C35
A1212	G1127	U967	C968	U884	C806	G721	U633	A547	A459	U387	G310	U229	C36	C36
U1213	C1128	G1053	U969	C885	A807	G722	U634	A548	A460	G388	A461	U230	U37	U37
G1214	U1129	C1054	C970	G886	C812	U723	U635	U552	A461	G389	C315	G230	G38	G38
C1215	G1134	G1057	G971	A889	A814	G724	A636	A553	G462	G391	C316	G232	C40	C40
A1216	U1135	C1058	C972	C894	A815	G725	U637	A554	G463	G392	U317	G134	G41	G41
G1217	C1136	G1059	G973	G895	A816	A728	U638	U555	U467	C392	U317	G135	G42	G42
C1218	U1137	U1060	A974	C895	C817	A728	U639	C556	A468	A393	U323	C235	G46	G46
A1219	G1138	G1061	A975	G895	C818	G731	U640	C557	A478	A397	G324	A236	C47	C47
G1220	U1139	U1062	G976	A900	A819	C732	A642	C558	U479	A397	A325	G240	C48	C48
C1221	C1140	G1063	A977	A901	U820	G733	C643	A560	U490	C401	G326	G241	U49	U49
A1225	U1147	U1064	C980	G903	G821	G734	U644	U561	C492	G402	A327	A246	A50	A50
C1226	C1148	C1069	U981	U904	C826	G735	U644	U562	C493	A405	C328	G246	A51	A51
A1229	U1149	U1070	U982	A907	U827	C736	G650	A563	G484	U405	U323	G247	G144	G144
C1230	A1150	C1071	U992	A908	U827	C737	C651	C564	U485	G406	G332	A250	G145	C54
G1231	U1151	G1072	G993	A909	C738	C739	U652	U565	U486	U407	U333	G251	G148	A55
U1232	C1152	U1073	A994	C910	C739	C739	U653	C566	A408	U408	C334	G252	U56	U56
G1233	G1153	G1074	C994	C910	C832	C832	U657	C569	C493	G410	C335	U253	G57	G57
C1234	U1154	U1075	U995	A913	U835	G742	U657	C570	A493	G410	C337	G254	C58	C58
U1235	A1155	G1077	C1001	A917	U836	A743	C658	G571	G494	C413	A338	A262	A59	A59
A1236	U1156	U1078	U1004	G917	U837	A743	U659	U571	G497	G414	A338	A262	A60	A60
C1237	C1157	G1079	A1005	G917	U837	A743	U659	U571	G497	G414	A338	A262	G61	G61
A1238	U1158	U1080	U1006	A923	C840	A749	C661	A572	A498	A415	U343	A263	A160	A160
U1239	G1159	G1081	U1007	C924	C841	C750	C661	A574	A498	G416	A344	C264	A161	A161
U1240	C1160	G1082	U1008	G925	U842	C751	A665	C575	C501	G417	G347	G265	A162	A162
G1241	U1161	U1091	A1012	G927	U843	G752	G666	C576	A502	C418	G348	G266	C163	C163
C1242	C1162	U1092	G1013	G927	U844	G752	G667	C577	G505	C419	G349	C267	A174	A174
A1244	U1168	A1092	G1013	A845	A845	G755	C669	A579	G506	U421	G350	C269	C175	C175



• Molecule 54: mRNA



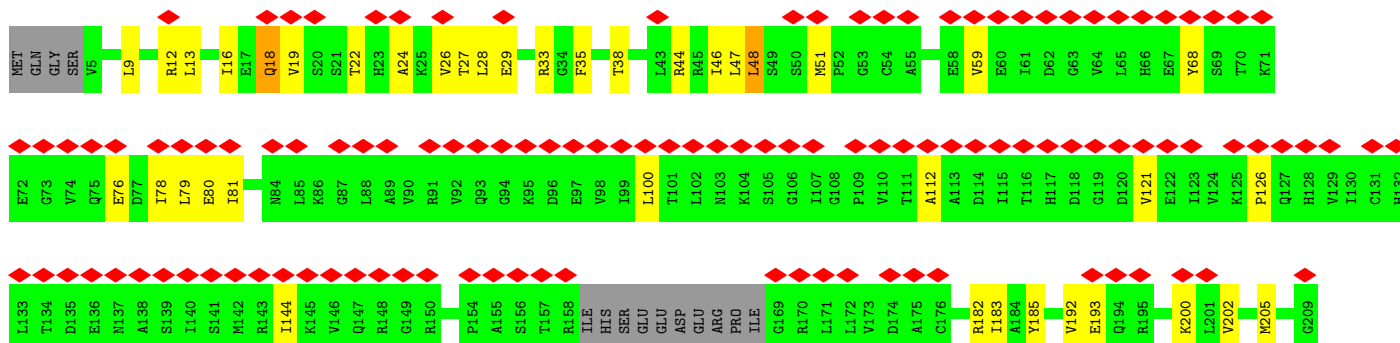
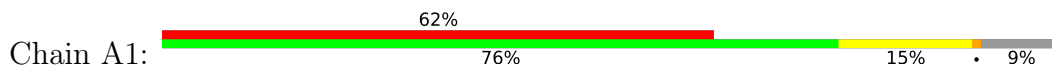
• Molecule 55: template DNA strand

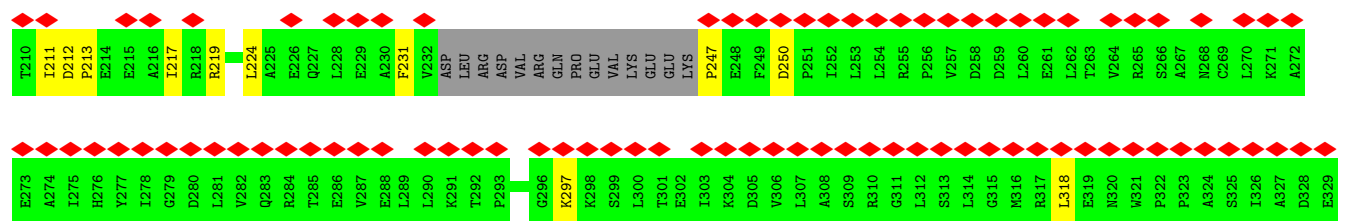


• Molecule 56: non-template DNA strand

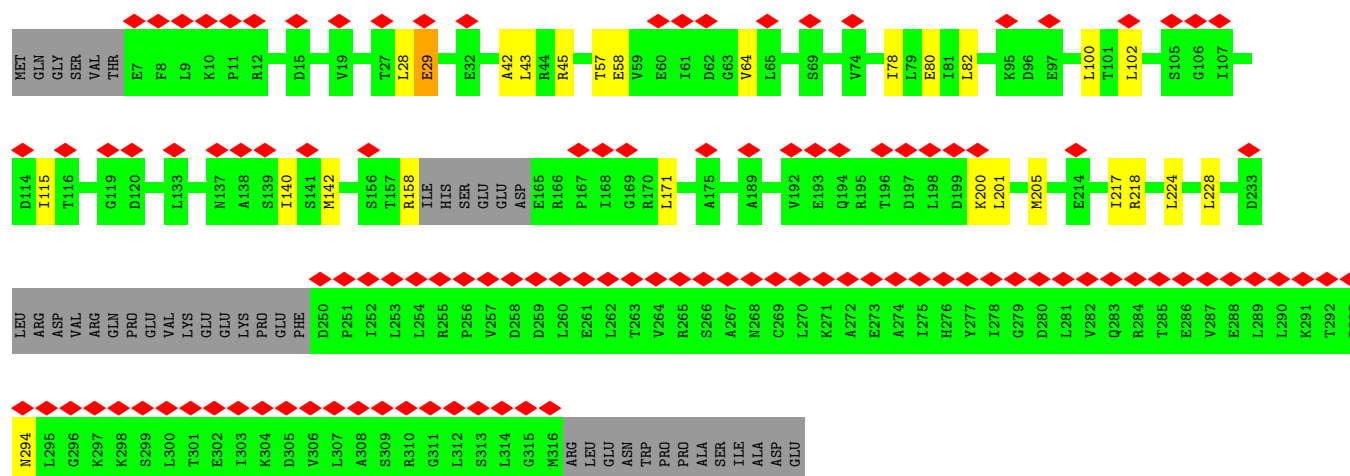
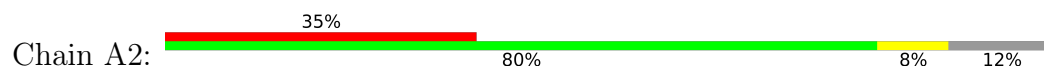


• Molecule 57: DNA-directed RNA polymerase subunit alpha

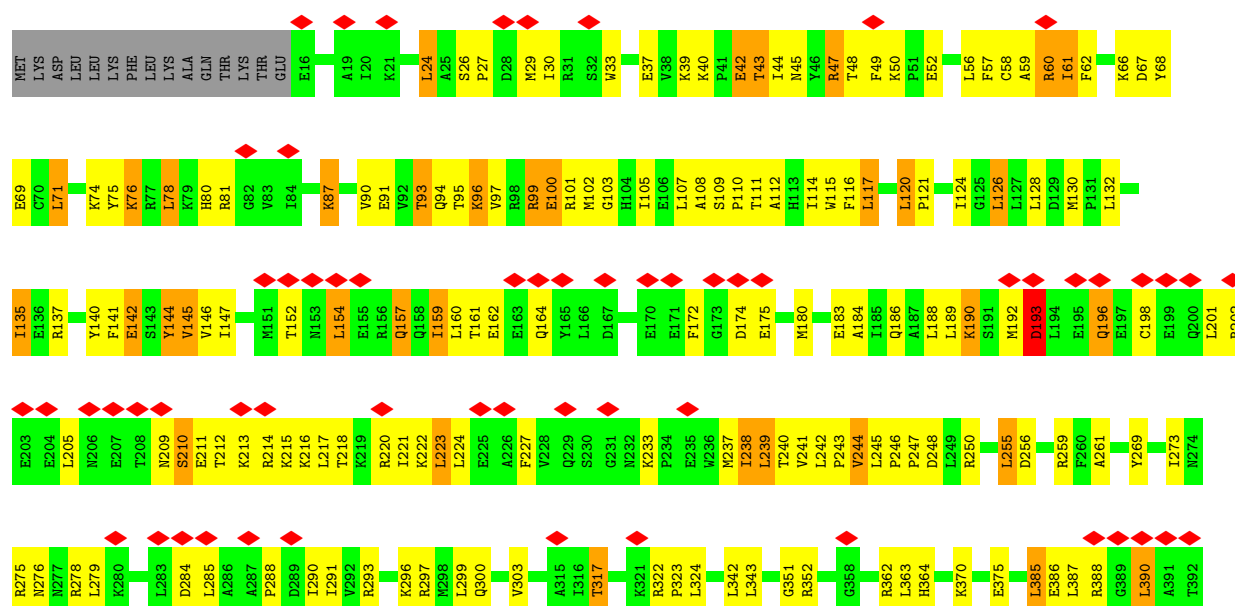


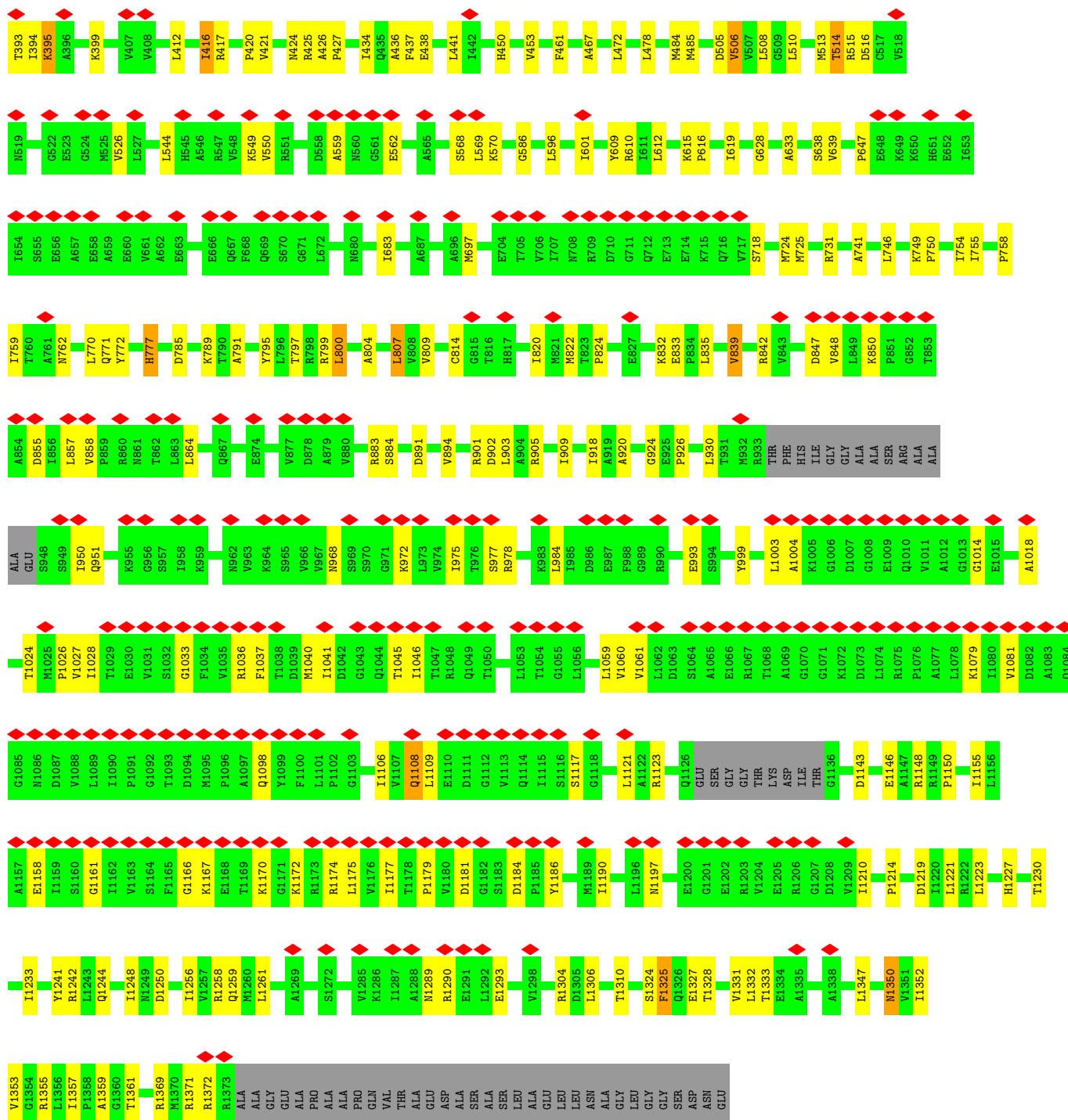


• Molecule 57: DNA-directed RNA polymerase subunit alpha

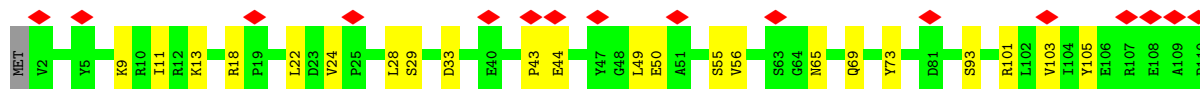
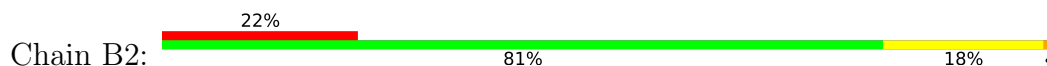


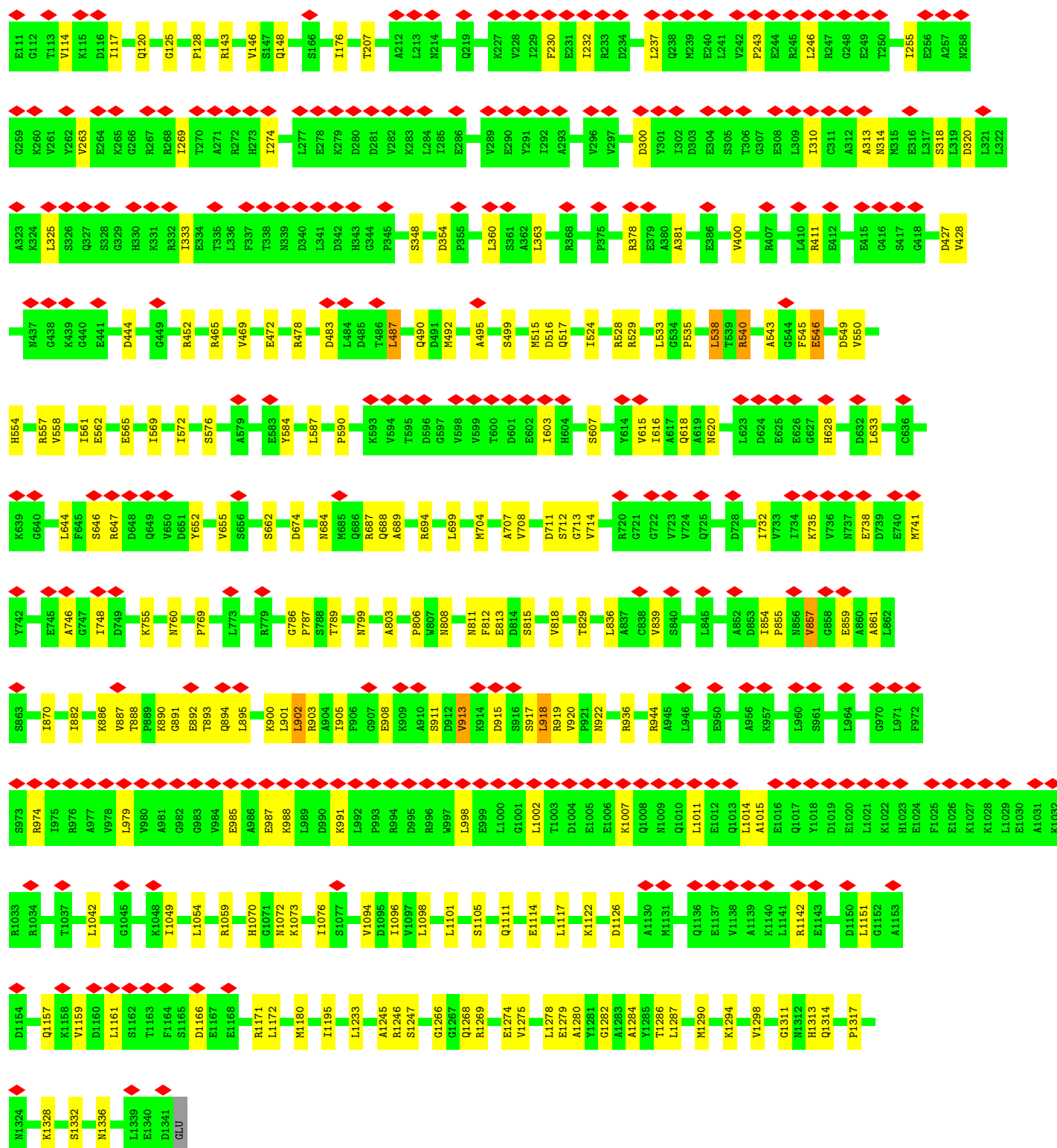
• Molecule 58: DNA-directed RNA polymerase subunit beta'



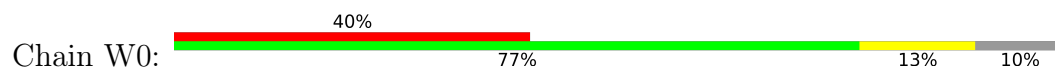


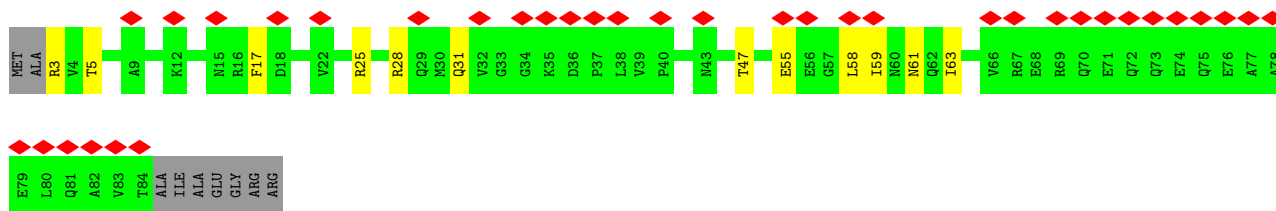
• Molecule 59: DNA-directed RNA polymerase subunit beta



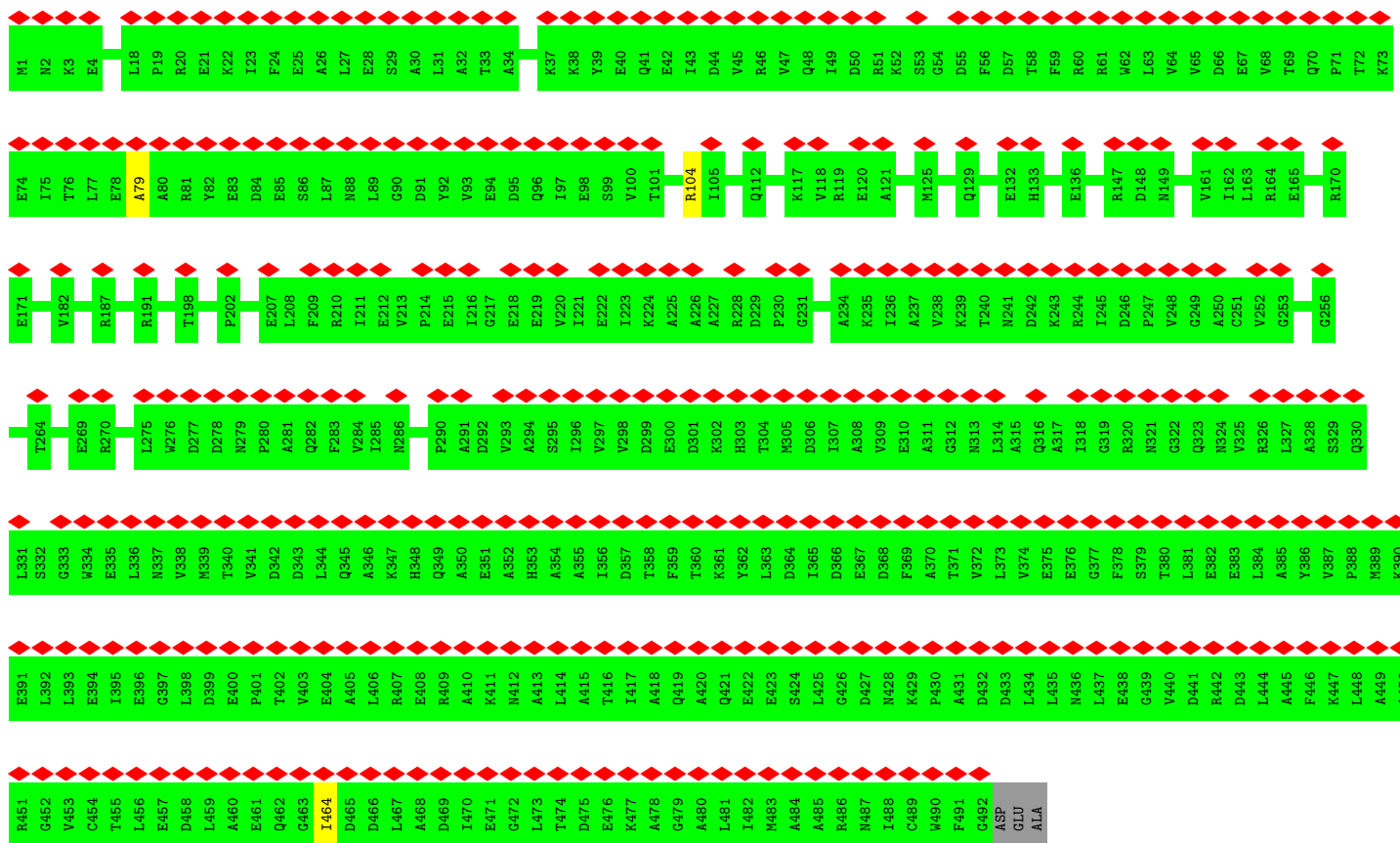
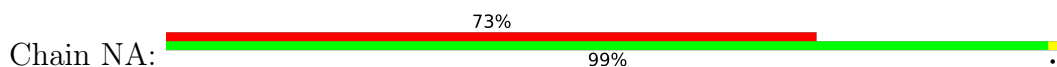


• Molecule 60: DNA-directed RNA polymerase subunit omega

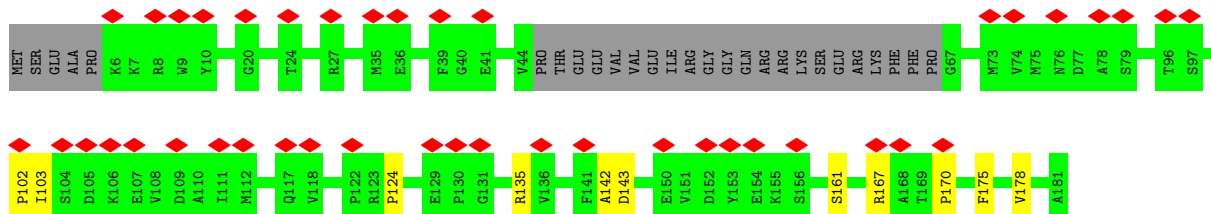
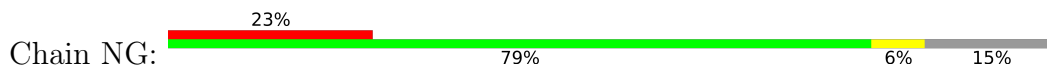




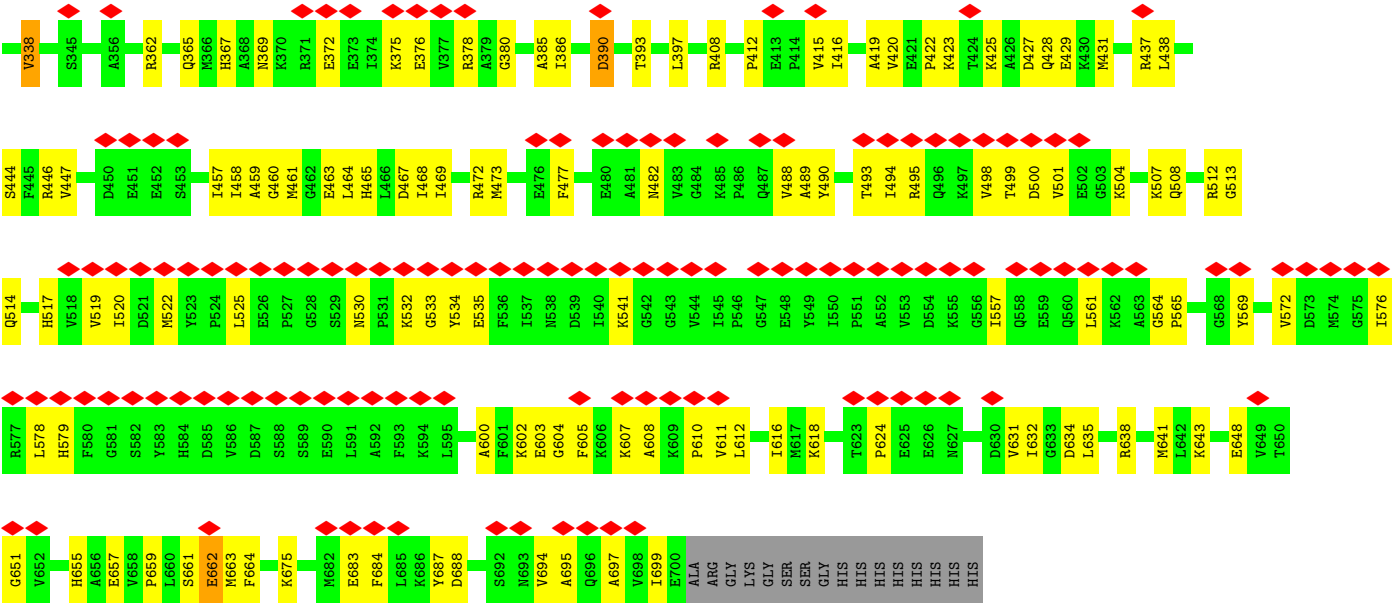
• Molecule 61: Transcription termination/antitermination protein NusA



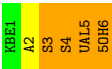
• Molecule 62: Transcription termination/antitermination protein NusG



• Molecule 63: tRNA(Phe)



● Molecule 67: Viomycin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	513759	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	0.156	Depositor
Minimum map value	-0.064	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.011	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, DPP, UAL, PO4, GDP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.25	0/362	0.73	0/485
2	B	0.37	0/450	0.80	2/599 (0.3%)
3	C	0.32	0/416	0.61	0/554
4	D	0.48	0/380	0.95	0/498
5	E	0.47	0/513	0.80	0/676
6	F	0.41	0/303	0.79	0/397
7	G	0.39	0/1735	0.83	0/2338
8	H	0.41	0/1651	0.80	0/2225
9	I	0.28	0/1665	0.76	1/2227 (0.0%)
10	J	0.46	0/1169	0.80	0/1573
11	K	0.42	0/835	0.86	0/1128
12	L	0.42	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	0.42	0/885	0.76	0/1195
17	Q	0.43	0/969	0.81	0/1300
18	R	0.29	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	0.30	0/659	0.64	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	0.64	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	0.30	0/1434	0.66	0/1926
31	f	0.29	0/1343	0.61	0/1816
32	g	0.34	0/1122	0.77	3/1515 (0.2%)

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	0.40	0/1093	0.81	2/1460 (0.1%)
38	n	0.54	1/973 (0.1%)	0.88	0/1301
39	o	0.32	0/902	0.68	0/1209
40	p	0.39	0/929	0.72	2/1242 (0.2%)
41	q	0.43	0/960	0.72	0/1278
42	r	0.38	0/829	0.79	1/1107 (0.1%)
43	s	0.52	0/864	0.83	0/1156
44	t	0.48	0/744	0.81	1/994 (0.1%)
45	u	0.33	0/787	0.74	2/1051 (0.2%)
46	v	0.36	0/766	0.66	0/1025
47	w	0.40	0/582	0.80	2/769 (0.3%)
48	x	0.62	0/635	1.16	5/848 (0.6%)
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	17/108888 (0.0%)
52	2	0.60	0/2872	0.55	1/4479 (0.0%)
53	3	0.60	0/36963	0.57	5/57662 (0.0%)
54	4	0.60	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	0.55	0/2106	0.81	0/2868
57	A2	0.49	0/2048	0.76	0/2786
58	B1	0.56	4/10510 (0.0%)	0.75	8/14196 (0.1%)
59	B2	0.46	0/10714	0.67	0/14459
60	W0	0.31	0/652	0.63	0/879
61	NA	0.76	0/2431	1.22	0/3385
62	NG	1.15	0/756	1.05	0/1048
63	5	0.59	0/1812	0.90	3/2823 (0.1%)
64	6	0.60	0/1832	0.59	0/2855
65	a	0.50	0/1020	0.81	0/1370
66	0	0.39	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	73/289390 (0.0%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	h	3	SER	CA-C	-6.76	1.38	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	h	4	SER	CA-C	-6.29	1.39	1.52
38	n	66	ALA	CA-C	-5.91	1.44	1.52
58	B1	1350	ASN	CG-ND2	-5.26	1.22	1.33
58	B1	777	HIS	ND1-CE1	5.12	1.37	1.32
58	B1	1108	GLN	CD-OE1	5.09	1.33	1.23
58	B1	424	ASN	CG-ND2	-5.08	1.22	1.33
36	l	18	ARG	CA-CB	-5.01	1.44	1.52

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	92	PRO	N-CA-C	-10.52	98.42	113.47
51	1	1020	A	C2'-C3'-O3'	7.36	120.54	109.50
48	x	11	PRO	N-CA-C	-7.32	99.55	111.77
51	1	2425	A	O3'-P-O5'	-6.93	93.61	104.00
12	L	82	SER	N-CA-C	6.88	116.41	108.49
58	B1	450	HIS	CB-CG-CD2	-6.57	122.67	131.20
48	x	30	PRO	N-CA-C	6.51	125.87	112.47
36	l	29	LYS	CA-C-N	6.46	133.87	121.54
36	l	29	LYS	C-N-CA	6.46	133.87	121.54
58	B1	61	ILE	CA-C-N	-6.39	113.97	121.64
58	B1	61	ILE	C-N-CA	-6.39	113.97	121.64
51	1	2428	G	O3'-P-O5'	-6.39	94.42	104.00
58	B1	777	HIS	CB-CG-CD2	-6.34	122.95	131.20
45	u	45	GLN	CA-C-N	6.33	129.48	120.49
45	u	45	GLN	C-N-CA	6.33	129.48	120.49
51	1	490	C	N1-C1'-C2'	6.33	121.50	112.00
9	I	24	VAL	N-CA-C	-6.28	107.74	113.71
32	g	8	LYS	CA-C-N	6.27	133.25	121.97
32	g	8	LYS	C-N-CA	6.27	133.25	121.97
53	3	1301	U	N1-C1'-C2'	6.25	121.37	112.00
48	x	71	ARG	N-CA-C	-6.20	105.71	113.28
48	x	67	LEU	N-CA-C	-6.09	104.56	111.14
66	0	367	HIS	CA-C-N	6.06	133.11	121.54
66	0	367	HIS	C-N-CA	6.06	133.11	121.54
19	S	21	ALA	N-CA-C	-6.05	107.72	114.62
32	g	121	VAL	N-CA-C	-5.92	106.64	111.91
63	5	39	U	C3'-C2'-O2'	5.87	119.51	110.70
51	1	1816	C	N1-C1'-C2'	5.77	120.66	112.00
2	B	5	ASN	CA-C-N	5.74	129.03	120.83
2	B	5	ASN	C-N-CA	5.74	129.03	120.83
26	Z	17	ARG	N-CA-C	-5.73	104.84	113.89

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	x	54	GLY	N-CA-C	5.72	120.73	113.24
58	B1	450	HIS	CB-CG-ND1	5.70	131.25	122.70
33	i	62	ALA	N-CA-C	5.58	117.05	110.97
51	1	1343	G	N9-C1'-C2'	5.58	120.36	112.00
29	d	74	LYS	CA-C-N	5.49	128.68	120.83
29	d	74	LYS	C-N-CA	5.49	128.68	120.83
51	1	2502	G	O3'-P-O5'	5.46	112.19	104.00
37	m	57	VAL	CA-C-N	5.46	131.96	121.54
37	m	57	VAL	C-N-CA	5.46	131.96	121.54
58	B1	777	HIS	CB-CG-ND1	5.44	130.86	122.70
42	r	51	VAL	N-CA-C	-5.43	97.14	108.88
53	3	130	A	N9-C1'-C2'	5.42	120.14	112.00
51	1	1106	G	C2'-C3'-O3'	5.42	121.83	113.70
55	8	7	DC	C2'-C3'-O3'	-5.41	103.39	111.50
53	3	813	U	N1-C1'-C2'	5.39	120.09	112.00
25	Y	53	MET	CA-C-N	5.33	127.61	120.58
25	Y	53	MET	C-N-CA	5.33	127.61	120.58
29	d	20	GLY	N-CA-C	-5.31	107.47	114.95
58	B1	27	PRO	N-CA-C	-5.27	106.17	113.81
35	k	89	ASN	N-CA-C	5.24	117.41	111.02
51	1	2529	G	N9-C1'-C2'	5.22	119.83	112.00
63	5	39	U	C4'-C3'-O3'	5.22	120.83	113.00
51	1	858	G	C4'-C3'-O3'	5.21	120.82	113.00
66	0	664	PHE	CA-CB-CG	5.21	119.01	113.80
51	1	1211	C	N1-C1'-C2'	5.21	119.81	112.00
52	2	66	A	N9-C1'-C2'	5.20	119.80	112.00
44	t	65	GLY	N-CA-C	5.19	117.43	111.36
47	w	15	LYS	CA-C-N	5.16	129.74	122.46
47	w	15	LYS	C-N-CA	5.16	129.74	122.46
51	1	1924	C	N1-C1'-C2'	5.16	119.74	112.00
50	z	40	THR	N-CA-C	-5.14	101.19	109.58
63	5	74	C	C4'-C3'-O3'	-5.14	105.29	113.00
53	3	722	G	N9-C1'-C2'	5.12	119.68	112.00
58	B1	61	ILE	CA-C-O	-5.10	115.64	120.95
51	1	278	A	N9-C1'-C2'	5.09	119.63	112.00
53	3	1043	G	N9-C1'-C2'	5.05	119.57	112.00
51	1	1087	G	N9-C1'-C2'	5.04	119.55	112.00
51	1	1508	A	N9-C1'-C2'	5.03	119.54	112.00
51	1	2071	A	N9-C1'-C2'	5.03	119.54	112.00
40	p	15	ASP	CA-C-N	5.01	131.41	122.13
40	p	15	ASP	C-N-CA	5.01	131.41	122.13
51	1	933	A	N9-C1'-C2'	5.01	119.52	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	355	0	353	10	0
2	B	444	0	461	14	0
3	C	409	0	440	18	0
4	D	377	0	418	18	0
5	E	504	0	574	18	0
6	F	302	0	341	15	0
7	G	1704	0	1732	45	0
8	H	1624	0	1699	47	0
9	I	1643	0	1710	44	0
10	J	1156	0	1199	39	0
11	K	817	0	808	22	0
12	L	1181	0	1240	47	0
13	M	979	0	1034	30	0
14	N	1022	0	1070	54	0
15	O	786	0	828	34	0
16	P	869	0	878	28	0
17	Q	955	0	1019	34	0
18	R	883	0	944	26	0
19	S	805	0	847	33	0
20	T	714	0	737	16	0
21	U	649	0	666	21	0
22	V	648	0	691	17	0
23	W	535	0	552	14	0
24	X	637	0	665	16	0
25	Y	665	0	714	21	0
26	Z	544	0	579	17	0
27	b	2082	0	2157	68	0
28	c	1565	0	1616	53	0
29	d	1552	0	1619	51	0
30	e	1410	0	1447	43	0
31	f	1323	0	1374	31	0
32	g	1111	0	1148	29	0
33	i	1032	0	1088	38	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	j	1129	0	1162	34	0
35	k	938	0	1012	21	0
36	l	1045	0	1117	28	0
37	m	1074	0	1157	31	0
38	n	960	0	1000	34	0
39	o	892	0	923	21	0
40	p	917	0	965	22	0
41	q	947	0	1022	22	0
42	r	816	0	839	22	0
43	s	857	0	922	20	0
44	t	738	0	807	15	0
45	u	779	0	834	20	0
46	v	753	0	780	13	0
47	w	575	0	592	19	0
48	x	625	0	655	22	0
49	y	509	0	543	9	0
50	z	449	0	491	10	0
51	1	62317	0	31346	1354	0
52	2	2568	0	1303	56	0
53	3	33012	0	16618	731	0
54	4	627	0	313	6	0
55	8	539	0	305	28	0
56	9	417	0	224	1	0
57	A1	2088	0	1895	26	0
57	A2	2029	0	1864	19	0
58	B1	10353	0	10548	312	0
59	B2	10546	0	10550	162	0
60	W0	650	0	658	10	0
61	NA	2432	0	1171	5	0
62	NG	758	0	334	8	0
63	5	1622	0	821	33	0
64	6	1640	0	837	28	0
65	a	1013	0	1081	33	0
66	0	5399	0	5363	154	0
67	h	48	0	40	5	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	3754	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 (3754) 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	1.11	1.14
53:3:112:G:H21	53:3:354:G:H5'	1.16	1.11
50:z:37:ARG:HH12	51:1:929:U:H5'	1.12	1.10
51:1:2061:G:H2'	51:1:2501:C:O2'	1.52	1.09
51:1:1060:U:H4'	51:1:1061:U:H5'	1.32	1.06
9:I:131:ILE:HG21	53:3:620:C:H1'	1.40	1.03
51:1:1796:U:H2'	51:1:1797:G:H8	1.18	1.03
51:1:45:G:H5''	51:1:46:G:H5'	1.34	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
51:1:1645:G:H5''	51:1:1646:C:H5'	1.44	0.98
51:1:2324:U:H3'	51:1:2325:G:H5''	1.45	0.98
58:B1:352:ARG:HD2	59:B2:1268:GLN:NE2	1.79	0.98
51:1:572:A:H61	51:1:2029:G:H21	1.04	0.98
51:1:2672:U:H2'	51:1:2673:G:H5''	1.43	0.97
51:1:1597:A:H5''	51:1:1598:A:H5'	1.45	0.97
52:2:118:C:H2'	52:2:119:A:H4'	1.46	0.96
57:A1:247:PRO:HA	57:A1:318:LEU:HA	1.48	0.96
52:2:90:C:H2'	52:2:91:C:H5''	1.44	0.95
10:J:120:HIS:ND1	10:J:121:ASN:ND2	2.14	0.95
58:B1:68:TYR:O	58:B1:75:TYR:CE2	2.20	0.95
7:G:16:GLY:HA2	7:G:39:ILE:HA	1.49	0.95
51:1:413:C:H42	51:1:2410:G:H1	1.14	0.94
51:1:828:U:H2'	51:1:829:A:C8	2.02	0.94
42:r:79:ARG:HH22	51:1:572:A:H5'	1.33	0.94
38:n:39:PRO:HG3	51:1:1651:G:H5'	1.49	0.93
43:s:59:GLU:HA	43:s:64:ALA:HA	1.50	0.93
23:W:38:ILE:HD11	53:3:720:C:H1'	1.52	0.92
53:3:1156:G:H1'	53:3:1179:A:H61	1.32	0.92
51:1:2068:U:H3	51:1:2430:A:H62	1.15	0.92
53:3:674:G:H2'	53:3:675:A:C8	2.05	0.91
53:3:674:G:H2'	53:3:675:A:H8	1.34	0.91
53:3:91:U:H2'	53:3:92:U:H5''	1.53	0.91
58:B1:202:ARG:HG2	58:B1:202:ARG:HH11	1.35	0.90
53:3:409:U:H3	53:3:433:G:H1	1.12	0.90
54:4:56:G:H21	58:B1:427:PRO:HD3	1.34	0.90
51:1:1558:C:H4'	51:1:1559:U:H5''	1.51	0.90
53:3:1218:C:H2'	53:3:1219:A:C8	2.06	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2653:U:H3'	51:1:2654:A:H5''	1.52	0.89
29:d:68:ALA:HA	51:1:1255:U:C5	2.08	0.89
12:L:92:PRO:HA	12:L:95:ARG:NE	1.88	0.88
51:1:1796:U:H2'	51:1:1797:G:C8	2.08	0.88
58:B1:68:TYR:C	58:B1:75:TYR:HE2	1.80	0.88
50:z:37:ARG:NH1	51:1:929:U:H5'	1.89	0.88
51:1:435:C:H2'	51:1:436:C:H5'	1.56	0.88
51:1:1473:G:H1	51:1:1518:C:H42	1.21	0.88
58:B1:317:THR:HA	58:B1:323:PRO:HA	1.55	0.88
52:2:78:A:H62	52:2:98:G:H21	1.17	0.87
53:3:1395:C:HO2'	53:3:1396:A:H8	0.87	0.87
53:3:1422:G:H22	53:3:1478:U:H3	1.22	0.87
63:5:9:A:H2'	63:5:11:C:H41	1.38	0.87
12:L:91:ARG:HB3	12:L:93:VAL:HG12	1.54	0.87
58:B1:68:TYR:O	58:B1:75:TYR:HE2	1.58	0.87
7:G:131:LYS:HD2	53:3:1158:C:H4'	1.57	0.87
14:N:68:GLY:HA2	53:3:1250:A:H5'	1.55	0.86
42:r:79:ARG:NH2	51:1:572:A:H5'	1.91	0.86
52:2:3:C:H2'	52:2:4:C:H5''	1.55	0.86
51:1:2128:G:OP1	65:a:38:PHE:CE1	2.29	0.85
51:1:2443:C:H2'	51:1:2444:G:H8	1.42	0.85
59:B2:855:PRO:HB3	61:NA:104:ARG:CB	2.07	0.85
58:B1:633:ALA:HB2	59:B2:808:ASN:H	1.41	0.85
53:3:1218:C:H2'	53:3:1219:A:H8	1.41	0.85
12:L:27:ASN:HD22	53:3:1374:A:H4'	1.42	0.84
34:j:116:ARG:NH2	51:1:528:A:H5''	1.92	0.84
51:1:1783:A:C6	51:1:2587:A:C2	2.66	0.84
51:1:2822:G:H2'	51:1:2823:A:H5''	1.58	0.84
19:S:70:HIS:HB2	53:3:974:A:H5'	1.59	0.84
37:m:12:MET:HA	51:1:910:A:H62	1.41	0.84
51:1:1783:A:N1	51:1:2587:A:C4	2.46	0.84
58:B1:68:TYR:HB3	58:B1:75:TYR:OH	1.76	0.84
53:3:835:U:H2'	53:3:836:G:H5''	1.60	0.83
53:3:3:A:H5'	53:3:613:C:H4'	1.58	0.83
58:B1:770:LEU:HD13	59:B2:618:GLN:HG3	1.61	0.83
53:3:1424:U:H3	53:3:1476:A:H61	1.26	0.83
23:W:37:LYS:HB3	53:3:719:C:H1'	1.60	0.83
66:0:40:ILE:HG23	66:0:198:GLN:OE1	1.79	0.83
51:1:554:U:H2'	51:1:555:G:O4'	1.79	0.83
51:1:2262:U:H2'	51:1:2263:C:C6	2.13	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)
51:1:1433:A:H2'	51:1:1434:A:O4'	1.79	0.82
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
53:3:1512:U:H2'	53:3:1513:A:C8	2.14	0.82
58:B1:141:PHE:HE2	58:B1:296:LYS:HB2	1.44	0.82
51:1:1937:A:O2'	51:1:1938:A:H5'	1.78	0.82
51:1:1680:U:H2'	51:1:1681:G:H5'	1.60	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	0.81
55:8:1:DC:H5''	58:B1:210:SER:OG	1.80	0.81
53:3:555:U:H2'	53:3:556:C:C6	2.15	0.81
51:1:695:G:H1	51:1:767:U:H3	1.26	0.80
58:B1:111:THR:HG23	58:B1:300:GLN:OE1	1.81	0.80
51:1:1064:C:H3'	51:1:1065:U:H5''	1.62	0.80
26:Z:7:GLU:HB2	26:Z:11:PHE:HB3	1.63	0.80
51:1:2402:U:C2'	51:1:2403:C:H5''	2.11	0.80
53:3:769:G:H4'	53:3:1513:A:H4'	1.63	0.79
51:1:2128:G:OP1	65:a:38:PHE:CD1	2.34	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
53:3:1073:U:H3	53:3:1102:A:H61	1.29	0.79
58:B1:144:TYR:HE1	58:B1:162:GLU:OE2	1.64	0.79
58:B1:186:GLN:HG3	58:B1:238:ILE:HG13	1.65	0.79
51:1:1791:A:C2'	51:1:1792:G:H5'	2.13	0.79
58:B1:37:GLU:O	58:B1:61:ILE:HD11	1.81	0.79
66:0:498:VAL:HG11	66:0:522:MET:HE3	1.65	0.78
51:1:784:G:H5'	51:1:785:G:OP1	1.84	0.78
51:1:2402:U:H2'	51:1:2403:C:H5''	1.64	0.78
53:3:1422:G:N2	53:3:1478:U:H3	1.80	0.78
51:1:1783:A:C6	51:1:2587:A:N3	2.51	0.78
51:1:1052:C:H42	51:1:1107:G:H1	1.30	0.78
51:1:2124:G:O2'	65:a:41:SER:HB3	1.83	0.78
51:1:2524:G:H2'	51:1:2525:G:H5''	1.66	0.78
53:3:153:C:H3'	53:3:154:U:H5''	1.66	0.78
51:1:2036:C:H2'	51:1:2037:A:C8	2.18	0.78
52:2:65:U:H3'	52:2:108:A:H61	1.49	0.78
51:1:1661:G:H2'	51:1:1662:U:H6	1.49	0.77
8:H:175:HIS:ND1	53:3:1108:G:H5'	2.00	0.77
51:1:208:C:H2'	51:1:209:C:H6	1.49	0.77
51:1:20:C:H2'	51:1:21:A:C8	2.19	0.77
51:1:1853:A:H2'	51:1:1854:A:C8	2.19	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2259:U:C4	51:1:2427:C:N4	2.52	0.77
55:8:15:DC:H1'	58:B1:426:ALA:HB1	1.67	0.77
51:1:52:A:H2'	51:1:53:A:C8	2.20	0.76
51:1:1126:A:H4'	51:1:1127:A:H5''	1.67	0.76
51:1:2443:C:H2'	51:1:2444:G:C8	2.20	0.76
51:1:324:A:H62	51:1:338:G:H21	1.32	0.76
28:c:148:GLN:O	51:1:2052:A:H4'	1.86	0.76
55:8:13:DT:H72	58:B1:791:ALA:HB2	1.67	0.76
58:B1:202:ARG:HG2	58:B1:202:ARG:NH1	2.00	0.76
66:0:40:ILE:CG2	66:0:198:GLN:OE1	2.33	0.76
51:1:2672:U:C2'	51:1:2673:G:H5''	2.16	0.76
51:1:687:C:H2'	51:1:688:U:H5'	1.66	0.76
51:1:1287:A:C2	51:1:1649:G:H4'	2.20	0.76
22:V:68:LYS:HB3	53:3:267:C:OP1	1.85	0.76
51:1:1020:A:H1'	51:1:1021:A:OP2	1.86	0.76
51:1:1935:G:H1'	51:1:1964:G:N2	2.00	0.76
53:3:1356:G:H2'	53:3:1357:A:H8	1.51	0.75
53:3:768:A:OP1	53:3:804:U:H4'	1.86	0.75
8:H:127:VAL:HG23	54:4:14:U:H4'	1.67	0.75
53:3:1330:U:H2'	53:3:1331:G:O4'	1.86	0.75
33:i:10:LEU:HD11	51:1:1070:A:H2	1.51	0.75
51:1:2124:G:O2'	65:a:41:SER:CB	2.34	0.75
51:1:2375:G:H2'	51:1:2376:A:H5''	1.69	0.75
53:3:57:G:H2'	53:3:58:C:C6	2.21	0.75
53:3:3:A:C5'	53:3:613:C:H4'	2.17	0.75
53:3:193:C:H2'	53:3:194:C:C6	2.21	0.75
51:1:1783:A:C2	51:1:2587:A:C5	2.75	0.74
53:3:850:U:H2'	53:3:851:G:H5''	1.69	0.74
53:3:1412:C:H2'	53:3:1413:A:C8	2.22	0.74
66:0:490:TYR:HA	66:0:612:LEU:HD13	1.69	0.74
30:e:34:THR:HG21	51:1:2314:A:H5'	1.69	0.74
51:1:633:A:H2'	51:1:634:C:O4'	1.87	0.74
51:1:1718:G:H2'	51:1:1719:G:H8	1.52	0.74
51:1:581:C:H2'	51:1:582:A:C8	2.23	0.74
53:3:354:G:H2'	53:3:355:C:C6	2.23	0.74
12:L:71:THR:HG23	12:L:72:VAL:HG12	1.68	0.74
53:3:212:G:H2'	53:3:213:G:H8	1.53	0.74
53:3:1236:A:H4'	53:3:1304:G:H4'	1.69	0.74
51:1:208:C:H2'	51:1:209:C:C6	2.23	0.74
51:1:917:A:H5''	51:1:2268:A:H61	1.53	0.74
47:w:28:LEU:HD22	51:1:2353:G:H4'	1.68	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2221:G:H2'	51:1:2222:C:C6	2.23	0.74
51:1:2743:U:H2'	51:1:2744:G:O4'	1.87	0.74
53:3:153:C:C3'	53:3:154:U:H5''	2.18	0.74
53:3:884:U:H4'	53:3:885:G:H5''	1.70	0.74
10:J:25:LYS:NZ	53:3:923:A:H5''	2.03	0.73
58:B1:157:GLN:OE1	58:B1:157:GLN:HA	1.88	0.73
53:3:279:A:H5''	53:3:281:G:H5'	1.69	0.73
51:1:1019:U:H3	51:1:1142:A:H62	1.36	0.73
51:1:1528:A:H2'	51:1:1529:G:H5'	1.69	0.73
51:1:1161:C:H2'	51:1:1162:G:C8	2.23	0.73
51:1:2859:G:H2'	51:1:2860:A:C8	2.22	0.73
58:B1:110:PRO:HG2	58:B1:183:GLU:HG3	1.68	0.73
58:B1:1143:ASP:OD1	58:B1:1148:ARG:NH1	2.21	0.73
51:1:2030:A:N3	51:1:2499:C:H5''	2.04	0.73
15:O:45:ARG:HB3	15:O:69:THR:HB	1.71	0.73
51:1:1940:U:H1'	51:1:1942:C:N4	2.04	0.73
52:2:87:U:H5''	52:2:88:C:C5	2.23	0.73
53:3:1306:A:H61	53:3:1331:G:H1'	1.54	0.73
58:B1:105:ILE:HD12	58:B1:242:LEU:HD22	1.71	0.73
58:B1:107:LEU:HD11	58:B1:242:LEU:HB2	1.70	0.73
51:1:1265:A:H61	51:1:2013:A:H5''	1.53	0.73
55:8:3:DC:H2'	55:8:4:DT:H72	1.69	0.73
30:e:65:LEU:HD22	52:2:42:C:C4	2.24	0.72
9:I:23:GLY:HA3	53:3:408:A:H4'	1.71	0.72
46:v:9:ARG:HB3	46:v:41:GLU:HB2	1.71	0.72
51:1:1310:G:H2'	51:1:1311:G:H5'	1.71	0.72
51:1:1868:C:H2'	51:1:1869:G:H5'	1.70	0.72
53:3:175:C:H2'	53:3:176:C:C6	2.24	0.72
36:l:79:LEU:HD12	36:l:113:ALA:H	1.52	0.72
53:3:1424:U:H2'	53:3:1425:U:C6	2.24	0.72
66:0:499:THR:HG23	66:0:500:ASP:H	1.53	0.72
21:U:5:ARG:HB2	53:3:376:G:H5''	1.72	0.72
53:3:1028:C:H3'	53:3:1029:U:H5''	1.70	0.72
58:B1:210:SER:HB3	58:B1:213:LYS:HB2	1.71	0.72
58:B1:211:GLU:HG2	58:B1:215:LYS:HE3	1.70	0.72
51:1:2562:U:H3	51:1:2566:A:H62	1.35	0.72
58:B1:220:ARG:HG2	58:B1:220:ARG:HH11	1.55	0.72
12:L:27:ASN:ND2	53:3:1374:A:H4'	2.05	0.72
34:j:116:ARG:HH22	51:1:528:A:H5''	1.53	0.72
51:1:2629:U:O2'	51:1:2630:G:H5''	1.90	0.72
53:3:1073:U:H2'	53:3:1074:G:C8	2.24	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:3:DC:C2'	55:8:4:DT:H72	2.19	0.72
48:x:2:ARG:HG2	48:x:32:LEU:HD12	1.73	0.71
51:1:777:G:N7	51:1:793:A:H2	1.87	0.71
51:1:2036:C:H2'	51:1:2037:A:H8	1.55	0.71
12:L:92:PRO:CA	12:L:95:ARG:HE	1.97	0.71
51:1:1791:A:H2'	51:1:1792:G:H5'	1.70	0.71
51:1:2125:G:H5'	65:a:39:VAL:O	1.89	0.71
51:1:2733:A:H2'	51:1:2734:A:C8	2.25	0.71
53:3:419:C:H2'	53:3:420:U:O4'	1.90	0.71
53:3:840:C:H2'	53:3:841:C:H5''	1.70	0.71
53:3:1507:A:H2'	53:3:1508:A:O4'	1.89	0.71
51:1:1064:C:H3'	51:1:1065:U:C5'	2.20	0.71
51:1:2086:U:H2'	51:1:2087:G:C8	2.25	0.71
53:3:1435:G:H2'	53:3:1436:U:C6	2.26	0.71
51:1:96:C:H2'	51:1:97:C:H6	1.54	0.71
51:1:435:C:C2'	51:1:436:C:H5'	2.21	0.71
51:1:952:G:H2'	51:1:953:G:H5''	1.71	0.71
51:1:2818:U:H2'	51:1:2819:G:H8	1.55	0.71
53:3:1374:A:H2'	53:3:1375:A:H8	1.56	0.71
58:B1:68:TYR:C	58:B1:75:TYR:CE2	2.65	0.71
51:1:2491:U:H2'	51:1:2492:U:H5'	1.71	0.71
12:L:92:PRO:HA	12:L:95:ARG:HG3	1.71	0.71
53:3:1412:C:H2'	53:3:1413:A:H8	1.56	0.71
58:B1:142:GLU:HG3	58:B1:142:GLU:O	1.89	0.71
59:B2:854:ILE:HG21	59:B2:917:SER:HB3	1.71	0.71
6:F:4:ARG:HB2	51:1:2466:C:OP1	1.89	0.71
51:1:1161:C:H2'	51:1:1162:G:H8	1.55	0.71
51:1:1170:C:H2'	51:1:1171:G:H8	1.54	0.71
53:3:1243:C:H2'	53:3:1244:G:C8	2.26	0.71
53:3:1395:C:H4'	53:3:1402:C:H4'	1.73	0.70
12:L:91:ARG:O	12:L:95:ARG:HG2	1.91	0.70
51:1:52:A:H2'	51:1:53:A:H8	1.56	0.70
51:1:1447:C:H2'	51:1:1448:G:H8	1.56	0.70
53:3:501:C:H2'	53:3:502:A:H8	1.57	0.70
53:3:939:G:H2'	53:3:940:C:C6	2.26	0.70
53:3:946:A:H2'	53:3:947:G:H8	1.56	0.70
51:1:100:U:H4'	51:1:101:A:O4'	1.91	0.70
52:2:90:C:C2'	52:2:91:C:H5''	2.20	0.70
53:3:979:C:H2'	53:3:980:C:H5'	1.73	0.70
57:A2:294:ASN:HA	61:NA:464:ILE:H	1.57	0.70
64:6:26:G:H2'	64:6:27:U:H5''	1.73	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:77:ARG:NH1	53:3:1225:A:H4'	2.07	0.70
36:l:17:LYS:HB2	51:1:663:G:H5''	1.74	0.70
48:x:60:LYS:HD3	51:1:372:G:H5''	1.73	0.70
51:1:1739:A:H2'	51:1:1740:G:O4'	1.92	0.70
51:1:2818:U:H2'	51:1:2819:G:C8	2.27	0.70
51:1:2859:G:H2'	51:1:2860:A:H8	1.54	0.70
66:0:695:ALA:HA	66:0:699:ILE:HB	1.74	0.70
38:n:66:ALA:HA	38:n:69:ARG:HD2	1.72	0.70
51:1:677:A:H2'	51:1:678:C:H6	1.57	0.70
51:1:2514:U:H2'	51:1:2515:C:C6	2.27	0.70
53:3:86:G:H4'	53:3:87:C:C4	2.26	0.70
51:1:2030:A:C2	51:1:2499:C:H5''	2.27	0.69
59:B2:65:ASN:HB3	59:B2:105:TYR:HB2	1.73	0.69
57:A1:297:LYS:CB	61:NA:79:ALA:HB1	2.22	0.69
38:n:1:MET:HE3	51:1:2723:C:H4'	1.74	0.69
53:3:673:A:H2'	53:3:674:G:C8	2.26	0.69
58:B1:128:LEU:HD11	58:B1:189:LEU:HG	1.73	0.69
27:b:6:LYS:NZ	51:1:1695:G:H5'	2.08	0.69
51:1:1270:C:H5''	51:1:1271:G:C5'	2.21	0.69
67:h:6:5OH:N	67:h:6:5OH:HS	2.07	0.69
12:L:92:PRO:O	12:L:95:ARG:HG3	1.93	0.69
29:d:165:HIS:HB2	51:1:1205:A:C6	2.27	0.69
51:1:1077:A:H2'	51:1:1078:U:H5'	1.74	0.69
51:1:1935:G:H1'	51:1:1964:G:C2	2.28	0.69
53:3:960:U:H4'	53:3:961:U:H5''	1.74	0.69
14:N:17:ARG:CZ	53:3:1129:C:H4'	2.22	0.69
17:Q:23:LEU:HD12	17:Q:29:LYS:HG2	1.75	0.69
51:1:2446:G:H2'	51:1:2501:C:H5	1.57	0.69
53:3:520:A:H62	53:3:529:G:H21	1.38	0.69
63:5:47:U:H4'	63:5:48:C:H5'	1.75	0.69
64:6:56:C:H2'	64:6:57:A:H8	1.58	0.69
51:1:2061:G:H2'	51:1:2501:C:HO2'	1.55	0.69
53:3:70:U:H5''	53:3:71:A:OP1	1.92	0.69
58:B1:93:THR:HB	58:B1:97:VAL:HG21	1.73	0.69
64:6:69:C:H2'	64:6:70:G:H8	1.55	0.69
66:0:29:ARG:HH21	66:0:272:ASN:HD21	1.40	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
8:H:34:SER:HB3	8:H:58:ARG:HH12	1.57	0.69
51:1:740:C:H6	51:1:740:C:H5'	1.58	0.69
51:1:2553:G:H3'	51:1:2554:U:H5''	1.75	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1421:G:H2'	53:3:1422:G:H4'	1.74	0.68
14:N:10:ARG:HH22	53:3:1148:U:H5''	1.59	0.68
67:h:4:SER:O	67:h:5:UAL:N1	2.26	0.68
51:1:1697:G:H3'	51:1:1698:A:H5''	1.76	0.68
51:1:687:C:C2'	51:1:688:U:H5'	2.23	0.68
51:1:1979:U:H2'	51:1:1980:G:H5'	1.75	0.68
53:3:501:C:H2'	53:3:502:A:C8	2.29	0.68
58:B1:243:PRO:HG2	59:B2:1332:SER:O	1.93	0.68
58:B1:832:LYS:C	58:B1:1242:ARG:HH12	2.01	0.68
31:f:91:VAL:HG21	51:1:2657:A:O3'	1.93	0.68
51:1:1607:C:H4'	51:1:1608:A:C5'	2.19	0.68
51:1:2450:A:O2'	51:1:2451:A:H5'	1.93	0.68
51:1:2656:U:H5''	66:0:146:ARG:CZ	2.24	0.68
53:3:900:A:H2'	53:3:901:A:C8	2.29	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
53:3:478:A:H2'	53:3:479:U:H4'	1.76	0.68
51:1:1219:U:H2'	51:1:1220:G:C8	2.29	0.68
51:1:1801:A:H5''	51:1:2203:U:H2'	1.75	0.68
51:1:2628:C:H3'	51:1:2629:U:H5'	1.75	0.68
14:N:121:ARG:HG3	53:3:1348:U:H4'	1.75	0.68
28:c:181:ASP:HB2	28:c:186:LEU:H	1.59	0.68
58:B1:141:PHE:CD2	58:B1:293:ARG:O	2.47	0.68
51:1:781:A:H2'	51:1:1777:U:O2'	1.93	0.68
17:Q:13:ARG:HH21	53:3:303:A:H5'	1.60	0.67
51:1:869:G:H2'	51:1:870:U:O4'	1.93	0.67
58:B1:39:LYS:O	58:B1:273:ILE:CG2	2.41	0.67
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE22	1.55	0.67
12:L:35:LYS:HB2	53:3:1373:G:H4'	1.76	0.67
51:1:2464:G:H2'	51:1:2465:C:C6	2.29	0.67
27:b:73:ILE:HG12	51:1:1490:A:C2	2.29	0.67
51:1:1024:G:H3'	51:1:1025:G:H5''	1.75	0.67
51:1:1697:G:H5''	51:1:1698:A:H5''	1.77	0.67
53:3:747:A:H3'	53:3:748:G:H5''	1.75	0.67
53:3:1346:A:H61	53:3:1374:A:H3'	1.57	0.67
55:8:3:DC:C6	55:8:4:DT:H72	2.29	0.67
55:8:23:DC:H2''	55:8:24:DC:C5	2.30	0.67
18:R:102:LYS:HG2	53:3:1226:C:C5	2.29	0.67
38:n:71:ARG:HH21	51:1:2708:G:H1'	1.59	0.67
58:B1:1355:ARG:NH1	58:B1:1369:ARG:HH12	1.92	0.67
36:l:111:ILE:HD12	51:1:627:A:N7	2.09	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:84:A:H4'	51:1:85:G:O5'	1.94	0.67
58:B1:161:THR:HG22	58:B1:164:GLN:HB2	1.75	0.67
64:6:69:C:H2'	64:6:70:G:C8	2.30	0.67
66:0:501:VAL:HG12	66:0:607:LYS:HZ1	1.60	0.67
29:d:27:LEU:HD22	29:d:104:ALA:HB2	1.75	0.67
51:1:1755:A:H2'	51:1:1756:G:H5'	1.76	0.67
18:R:113:LYS:HZ3	64:6:44:A:H4'	1.58	0.67
38:n:2:ARG:HD2	51:1:2822:G:O6	1.95	0.67
51:1:848:C:H2'	51:1:849:A:H8	1.59	0.66
51:1:1139:G:O2'	51:1:1140:C:H5'	1.96	0.66
51:1:1783:A:C2	51:1:2587:A:C4	2.83	0.66
51:1:2415:G:H2'	51:1:2416:C:C6	2.29	0.66
53:3:1007:U:H3	53:3:1022:A:H61	1.43	0.66
53:3:1172:C:H2'	53:3:1173:U:O4'	1.95	0.66
51:1:2086:U:H2'	51:1:2087:G:H8	1.59	0.66
53:3:924:C:H2'	53:3:925:G:H8	1.60	0.66
55:8:13:DT:OP2	58:B1:791:ALA:HB1	1.95	0.66
58:B1:108:ALA:HB3	58:B1:279:LEU:HD22	1.77	0.66
66:0:103:MET:HG3	66:0:129:GLN:HB3	1.77	0.66
39:o:68:LYS:HG2	52:2:50:A:OP1	1.94	0.66
51:1:1799:G:H4'	51:1:1800:C:O5'	1.95	0.66
51:1:2633:G:H2'	51:1:2634:A:H5''	1.77	0.66
53:3:1356:G:H2'	53:3:1357:A:C8	2.30	0.66
58:B1:108:ALA:CB	58:B1:279:LEU:HD22	2.25	0.66
48:x:27:ARG:NH2	51:1:1365:A:OP1	2.29	0.66
64:6:12:G:H2'	64:6:13:C:O4'	1.95	0.66
4:D:8:SER:HA	51:1:1309:G:H5''	1.78	0.66
38:n:96:ARG:HA	51:1:2881:U:O2'	1.95	0.66
51:1:849:A:H2'	51:1:850:U:C6	2.30	0.66
51:1:1824:G:O2'	51:1:1825:U:H5'	1.96	0.66
53:3:113:G:H2'	53:3:114:U:C6	2.31	0.66
58:B1:117:LEU:HD12	58:B1:117:LEU:O	1.94	0.66
10:J:25:LYS:HE2	53:3:923:A:OP1	1.96	0.66
51:1:621:A:H2'	51:1:622:G:O4'	1.95	0.66
51:1:1509:A:H2'	51:1:1510:G:C8	2.31	0.66
51:1:1661:G:H2'	51:1:1662:U:C6	2.29	0.66
29:d:176:ASP:HB2	29:d:179:SER:HB3	1.77	0.66
51:1:395:U:H2'	51:1:396:G:C8	2.31	0.66
51:1:1528:A:C2'	51:1:1529:G:H5'	2.26	0.66
51:1:1680:U:C2'	51:1:1681:G:H5'	2.26	0.66
53:3:1026:G:H1	53:3:1035:A:H61	1.43	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:193:ASP:HB3	58:B1:196:GLN:HB2	1.78	0.66
51:1:1268:A:H2'	51:1:1269:A:C8	2.31	0.66
58:B1:978:ARG:HG2	58:B1:1197:ASN:HD21	1.60	0.66
58:B1:984:LEU:HB3	58:B1:993:GLU:HB2	1.77	0.66
58:B1:1037:PHE:HB3	58:B1:1040:MET:HB2	1.78	0.66
10:J:53:ARG:NH1	53:3:1071:C:H5'	2.12	0.65
53:3:955:U:H3	53:3:1225:A:H61	1.42	0.65
53:3:1125:U:H2'	53:3:1126:U:H2'	1.78	0.65
53:3:153:C:H2'	53:3:154:U:O4'	1.96	0.65
53:3:660:C:H2'	53:3:661:G:O4'	1.95	0.65
58:B1:461:PHE:HD2	59:B2:813:GLU:HB2	1.62	0.65
51:1:2008:C:H2'	51:1:2009:A:H8	1.61	0.65
53:3:1173:U:H2'	53:3:1174:G:H8	1.62	0.65
58:B1:141:PHE:HD2	58:B1:293:ARG:O	1.79	0.65
35:k:76:VAL:H	40:p:72:VAL:HG12	1.62	0.65
51:1:1170:C:H2'	51:1:1171:G:C8	2.32	0.65
51:1:2029:G:O6	51:1:2032:G:H5''	1.97	0.65
11:K:42:TRP:HB2	11:K:59:TYR:HB2	1.78	0.65
51:1:1718:G:H2'	51:1:1719:G:C8	2.30	0.65
51:1:2047:C:H2'	51:1:2048:G:C8	2.32	0.65
52:2:3:C:C2'	52:2:4:C:H5''	2.25	0.65
52:2:13:G:H2'	52:2:14:U:H5''	1.78	0.65
53:3:835:U:C2'	53:3:836:G:H5''	2.27	0.65
58:B1:975:ILE:HG22	58:B1:977:SER:H	1.62	0.65
3:C:5:ARG:NH1	51:1:2285:C:C5	2.65	0.65
51:1:2048:G:H2'	51:1:2049:G:H5''	1.79	0.65
51:1:203:A:H3'	51:1:204:A:H5''	1.79	0.65
51:1:581:C:H2'	51:1:582:A:H8	1.60	0.65
53:3:211:G:H2'	53:3:212:G:O4'	1.96	0.65
22:V:60:ILE:HG22	22:V:74:LEU:HA	1.78	0.65
51:1:195:A:H3'	51:1:196:A:H4'	1.78	0.65
53:3:738:C:H2'	53:3:739:C:H6	1.62	0.65
66:0:17:ALA:HB2	66:0:112:VAL:HG23	1.79	0.65
31:f:94:ARG:H	31:f:105:SER:HB3	1.62	0.64
47:w:40:LYS:NZ	51:1:2330:G:O2'	2.30	0.64
51:1:748:G:O6	51:1:751:A:H4'	1.97	0.64
51:1:1278:C:H2'	51:1:1279:G:H8	1.62	0.64
51:1:1474:U:H2'	51:1:1475:G:H5'	1.79	0.64
51:1:2704:C:H2'	51:1:2705:A:O4'	1.97	0.64
53:3:246:A:H62	53:3:281:G:N2	1.95	0.64
13:M:111:THR:HG22	13:M:113:ARG:H	1.62	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:i:112:LYS:NZ	33:i:124:MET:SD	2.69	0.64
51:1:1127:A:H2'	51:1:1128:G:H5''	1.80	0.64
51:1:1447:C:H2'	51:1:1448:G:C8	2.31	0.64
58:B1:68:TYR:HB3	58:B1:75:TYR:CE2	2.32	0.64
17:Q:33:CYS:H	17:Q:54:VAL:HG13	1.60	0.64
30:e:104:THR:HG23	30:e:105:ILE:HG13	1.79	0.64
32:g:94:ILE:HG12	32:g:122:LEU:HB2	1.78	0.64
51:1:2215:C:H2'	51:1:2216:G:C8	2.31	0.64
53:3:1306:A:N6	53:3:1331:G:H1'	2.12	0.64
53:3:1366:C:H2'	53:3:1367:C:C6	2.32	0.64
53:3:1436:U:H2'	53:3:1437:A:H8	1.62	0.64
59:B2:314:ASN:HD21	59:B2:348:SER:HA	1.62	0.64
17:Q:98:ARG:HB3	17:Q:105:GLY:HA2	1.79	0.64
23:W:41:SER:HA	23:W:44:THR:HG22	1.80	0.64
31:f:82:PHE:HB2	31:f:140:ILE:HG12	1.79	0.64
51:1:2267:A:H3'	51:1:2267:A:N3	2.13	0.64
51:1:2329:U:H2'	51:1:2330:G:C8	2.32	0.64
58:B1:111:THR:CG2	58:B1:300:GLN:CD	2.66	0.64
4:D:7:PRO:HA	51:1:686:U:O2	1.96	0.64
53:3:952:U:H2'	53:3:953:G:C8	2.32	0.64
53:3:966:G:C2	64:6:34:C:H5'	2.33	0.64
66:0:501:VAL:HG11	66:0:604:GLY:HA2	1.78	0.64
22:V:47:ASP:HB3	22:V:74:LEU:HB3	1.78	0.64
55:8:3:DC:C2'	55:8:4:DT:C7	2.75	0.64
27:b:155:ARG:NH1	51:1:1818:U:H5	1.96	0.64
51:1:2464:G:H2'	51:1:2465:C:H6	1.63	0.64
2:B:8:THR:HB	51:1:2020:A:H5'	1.79	0.64
4:D:14:ARG:HG2	51:1:125:A:H5'	1.80	0.64
17:Q:27:PRO:HB3	53:3:552:U:O2	1.98	0.64
32:g:4:ILE:HA	32:g:18:GLN:HE22	1.63	0.64
58:B1:918:ILE:HG22	59:B2:1280:ALA:HB1	1.79	0.64
66:0:624:PRO:HA	66:0:651:GLY:HA2	1.80	0.64
44:t:37:ASP:OD1	44:t:37:ASP:N	2.29	0.64
15:O:46:LYS:HE3	53:3:1253:G:OP1	1.98	0.64
51:1:20:C:H2'	51:1:21:A:H8	1.60	0.64
25:Y:54:GLN:HE22	53:3:193:C:C1'	2.11	0.63
53:3:56:U:O2	66:0:362:ARG:NH1	2.30	0.63
53:3:600:A:H61	53:3:638:U:H3	1.47	0.63
53:3:1148:U:H2'	53:3:1149:C:O4'	1.98	0.63
53:3:1156:G:H21	53:3:1179:A:H2	1.44	0.63
53:3:1474:U:H2'	53:3:1475:G:O4'	1.98	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:6:61:C:O2'	65:a:53:ARG:HD2	1.97	0.63
4:D:21:ARG:NH1	51:1:465:G:O3'	2.32	0.63
48:x:60:LYS:CD	51:1:372:G:H5''	2.28	0.63
51:1:96:C:H2'	51:1:97:C:C6	2.33	0.63
51:1:246:C:H2'	51:1:247:G:H5'	1.80	0.63
58:B1:128:LEU:HA	58:B1:192:MET:HE1	1.81	0.63
58:B1:162:GLU:HA	58:B1:162:GLU:OE1	1.97	0.63
48:x:1:SER:HB2	51:1:1366:A:OP2	1.99	0.63
51:1:1597:A:H5''	51:1:1598:A:C5'	2.24	0.63
53:3:1243:C:H2'	53:3:1244:G:H8	1.63	0.63
53:3:1345:U:H4'	53:3:1346:A:H5'	1.80	0.63
64:6:26:G:H3'	64:6:27:U:H5''	1.80	0.63
47:w:19:VAL:HG13	47:w:34:VAL:HG22	1.80	0.63
51:1:764:A:O2'	51:1:765:C:H5'	1.98	0.63
51:1:1297:C:OP1	51:1:2710:C:H4'	1.97	0.63
51:1:2123:G:H8	51:1:2125:G:H21	1.44	0.63
53:3:67:C:H2'	53:3:68:G:H8	1.64	0.63
58:B1:1357:ILE:HD11	59:B2:1287:LEU:HD13	1.81	0.63
51:1:2898:U:H2'	51:1:2899:A:C8	2.34	0.63
15:O:59:LYS:HE3	53:3:972:C:H5'	1.81	0.63
34:j:78:THR:HB	51:1:2641:G:H5''	1.81	0.63
51:1:746:U:H1'	51:1:748:G:H21	1.61	0.63
51:1:2066:C:O2'	51:1:2067:G:H5'	1.99	0.63
53:3:492:C:H2'	53:3:493:A:C8	2.34	0.63
14:N:17:ARG:NH2	53:3:1129:C:H4'	2.13	0.63
51:1:340:A:H2'	51:1:341:C:H5'	1.81	0.63
51:1:1063:G:H3'	51:1:1064:C:H6	1.63	0.63
52:2:13:G:N7	52:2:70:C:H4'	2.14	0.63
53:3:1007:U:H2'	53:3:1008:U:C6	2.34	0.63
21:U:34:GLU:OE1	21:U:60:TRP:NE1	2.30	0.63
42:r:41:ILE:HB	42:r:47:VAL:HB	1.80	0.63
58:B1:245:LEU:HG	58:B1:246:PRO:HD2	1.80	0.63
66:0:94:ASP:HB2	66:0:465:HIS:HB2	1.81	0.63
32:g:4:ILE:HD11	32:g:43:ASN:HB3	1.80	0.63
51:1:315:G:H2'	51:1:316:C:C6	2.33	0.63
51:1:948:C:H2'	51:1:949:G:H8	1.64	0.63
53:3:34:C:H2'	53:3:35:G:C8	2.33	0.63
58:B1:1355:ARG:NH1	58:B1:1369:ARG:NH1	2.47	0.63
64:6:54:U:H3	64:6:58:A:H8	1.47	0.63
14:N:105:ARG:HD2	53:3:1117:A:O2'	1.99	0.62
19:S:75:LYS:NZ	53:3:1357:A:H5''	2.14	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:158:U:H2'	51:1:159:G:O4'	1.97	0.62
51:1:1783:A:C5	51:1:2587:A:C2	2.87	0.62
53:3:946:A:H2'	53:3:947:G:C8	2.34	0.62
66:0:490:TYR:HA	66:0:612:LEU:CD1	2.29	0.62
6:F:1:MET:HG3	51:1:2742:G:H5'	1.79	0.62
14:N:68:GLY:HA2	53:3:1250:A:C5'	2.27	0.62
27:b:49:THR:OG1	27:b:50:THR:N	2.31	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
8:H:10:ARG:HH12	8:H:181:ILE:H	1.46	0.62
12:L:1:PRO:HD2	12:L:5:VAL:HA	1.82	0.62
12:L:92:PRO:CA	12:L:95:ARG:HG3	2.28	0.62
16:P:17:ASP:HB2	16:P:36:ARG:HH22	1.65	0.62
30:e:35:LEU:HB3	30:e:151:LEU:HD11	1.81	0.62
59:B2:120:GLN:NE2	59:B2:490:GLN:OE1	2.32	0.62
23:W:38:ILE:CD1	53:3:720:C:H1'	2.27	0.62
41:q:12:ARG:NH1	51:1:1251:C:H5''	2.15	0.62
43:s:25:ARG:HH22	51:1:519:U:H5''	1.64	0.62
51:1:1173:U:H2'	51:1:1177:G:H1	1.64	0.62
51:1:1736:U:H2'	51:1:1737:G:O4'	1.99	0.62
51:1:2384:U:O2'	51:1:2385:C:H5'	1.98	0.62
9:I:8:LEU:HD23	9:I:21:LYS:HE2	1.82	0.62
51:1:481:G:H1'	51:1:506:G:N2	2.14	0.62
51:1:948:C:H2'	51:1:949:G:C8	2.34	0.62
51:1:1395:A:H4'	51:1:1397:U:C5	2.35	0.62
53:3:91:U:C2'	53:3:92:U:H5''	2.27	0.62
53:3:668:G:H1	53:3:738:C:H42	1.47	0.62
58:B1:100:GLU:HA	59:B2:1328:LYS:HE2	1.82	0.62
58:B1:395:LYS:HZ2	58:B1:399:LYS:CD	2.12	0.62
14:N:12:LYS:H	14:N:105:ARG:HH22	1.45	0.62
22:V:19:SER:OG	22:V:20:ILE:N	2.33	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:NE2	2.63	0.62
58:B1:201:LEU:HB2	58:B1:221:ILE:HD13	1.80	0.62
51:1:66:C:H1'	51:1:456:C:O2	2.00	0.62
51:1:1867:G:H1	51:1:1874:C:H42	1.48	0.62
51:1:2810:A:H62	51:1:2890:G:H21	1.46	0.62
55:8:1:DC:H2''	55:8:2:DC:C5	2.35	0.62
63:5:32:U:H2'	63:5:33:U:C2	2.34	0.62
51:1:2512:C:H2'	51:1:2513:A:O4'	2.00	0.62
51:1:2656:U:H5''	66:0:146:ARG:NH1	2.14	0.62
52:2:90:C:H2'	52:2:91:C:C5'	2.24	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:119:HIS:CD2	53:3:438:U:H4'	2.35	0.62
51:1:848:C:H2'	51:1:849:A:C8	2.35	0.62
51:1:1675:C:H2'	51:1:1676:A:O4'	2.00	0.62
51:1:1901:A:H2'	51:1:1902:C:C6	2.35	0.62
53:3:939:G:H2'	53:3:940:C:H6	1.63	0.62
53:3:1110:A:H2'	53:3:1111:A:C8	2.35	0.62
53:3:1347:G:N2	53:3:1373:G:H2'	2.15	0.62
58:B1:395:LYS:NZ	58:B1:399:LYS:HD3	2.15	0.62
58:B1:770:LEU:HD13	59:B2:618:GLN:CG	2.30	0.62
7:G:67:LEU:HD12	7:G:160:LEU:HD12	1.82	0.62
51:1:812:C:H5''	51:1:1250:G:O2'	2.00	0.62
51:1:1746:A:H2'	51:1:1747:U:C6	2.34	0.62
37:m:58:LYS:O	37:m:59:ARG:NH2	2.32	0.61
51:1:2121:G:H1'	65:a:167:LYS:HB2	1.82	0.61
57:A1:211:ILE:HG12	57:A1:219:ARG:HH12	1.65	0.61
7:G:89:PHE:HB3	7:G:150:ILE:HD12	1.81	0.61
13:M:28:SER:HB2	13:M:58:LEU:HB2	1.82	0.61
53:3:737:C:H2'	53:3:738:C:C6	2.34	0.61
30:e:38:GLY:HA3	51:1:2312:U:O2	2.00	0.61
34:j:113:PRO:HG3	51:1:528:A:H5'	1.81	0.61
45:u:87:GLU:HG2	45:u:92:VAL:HG11	1.81	0.61
51:1:1740:G:H2'	51:1:1741:C:H6	1.66	0.61
51:1:2286:G:H4'	51:1:2287:A:O4'	2.00	0.61
51:1:2885:G:H2'	51:1:2886:A:O4'	2.00	0.61
53:3:1084:G:H5'	53:3:1102:A:OP2	2.00	0.61
55:8:3:DC:H2'	55:8:4:DT:C7	2.30	0.61
55:8:13:DT:C7	58:B1:791:ALA:HB2	2.29	0.61
8:H:21:TRP:CD1	8:H:58:ARG:H	2.18	0.61
51:1:1063:G:H5''	51:1:1064:C:H5	1.64	0.61
53:3:358:U:H2'	53:3:359:G:H8	1.64	0.61
53:3:452:A:H61	53:3:480:U:H3	1.49	0.61
6:F:27:CYS:SG	6:F:28:SER:N	2.71	0.61
7:G:32:GLY:HA2	7:G:39:ILE:H	1.65	0.61
17:Q:55:ARG:HA	17:Q:61:GLU:HA	1.83	0.61
19:S:23:ARG:HH11	19:S:26:LEU:HB3	1.65	0.61
34:j:113:PRO:HD2	51:1:558:U:OP1	2.00	0.61
51:1:1361:G:H2'	51:1:1362:C:C6	2.35	0.61
30:e:132:ARG:O	30:e:132:ARG:NH2	2.34	0.61
51:1:1270:C:H5''	51:1:1271:G:H5''	1.79	0.61
51:1:2082:A:C2	51:1:2083:G:H1'	2.35	0.61
53:3:657:U:H2'	53:3:658:C:C6	2.35	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:11:C:H2'	51:1:12:U:H5''	1.83	0.61
57:A1:38:THR:HB	57:A2:45:ARG:HD3	1.82	0.61
59:B2:1282:GLY:HA3	60:W0:17:PHE:HE1	1.63	0.61
18:R:81:ASP:OD1	30:e:111:ARG:NH2	2.34	0.61
42:r:63:VAL:HG12	42:r:96:VAL:HG12	1.83	0.61
48:x:4:CYS:HB3	48:x:9:LYS:H	1.65	0.61
51:1:368:A:O2'	51:1:369:U:H5'	2.00	0.61
51:1:1078:U:H4'	51:1:1088:A:H2	1.65	0.61
53:3:924:C:H2'	53:3:925:G:C8	2.34	0.61
58:B1:144:TYR:CE1	58:B1:162:GLU:OE2	2.51	0.61
58:B1:1161:GLY:HA3	58:B1:1179:PRO:HA	1.83	0.61
51:1:2327:A:H2'	51:1:2328:A:C8	2.35	0.61
53:3:367:U:H3	53:3:393:A:H2	1.47	0.61
46:v:17:SER:HB3	46:v:27:PRO:HG3	1.83	0.61
46:v:72:VAL:HG13	46:v:93:ARG:HA	1.82	0.61
51:1:572:A:N6	51:1:2029:G:H21	1.88	0.61
58:B1:68:TYR:HB3	58:B1:75:TYR:CZ	2.35	0.61
63:5:39:U:H2'	63:5:40:C:C6	2.36	0.61
51:1:677:A:H2'	51:1:678:C:C6	2.34	0.60
51:1:1053:C:H2'	51:1:1054:A:H5'	1.83	0.60
53:3:715:A:H5''	53:3:805:C:O2'	2.00	0.60
59:B2:55:SER:OG	59:B2:465:ARG:NH1	2.33	0.60
59:B2:855:PRO:CB	61:NA:104:ARG:CB	2.78	0.60
65:a:216:THR:H	65:a:220:ALA:HB3	1.66	0.60
15:O:50:THR:HG22	15:O:64:GLN:HG3	1.83	0.60
29:d:64:GLY:O	51:1:2059:A:H4'	2.01	0.60
51:1:139:U:H2'	51:1:140:C:H5	1.65	0.60
51:1:611:C:H2'	51:1:612:G:O4'	2.01	0.60
51:1:1064:C:H2'	51:1:1065:U:C6	2.37	0.60
51:1:1369:G:H21	51:1:1810:A:H2	1.48	0.60
52:2:30:C:H2'	52:2:31:C:O4'	2.01	0.60
64:6:26:G:C2'	64:6:27:U:H5''	2.31	0.60
66:0:321:ALA:HB2	66:0:397:LEU:HD21	1.82	0.60
42:r:81:LYS:HD3	51:1:973:A:H5''	1.83	0.60
51:1:729:G:H2'	51:1:1775:U:O2	2.01	0.60
51:1:2699:C:H2'	51:1:2700:A:H8	1.66	0.60
59:B2:528:ARG:NH2	59:B2:576:SER:O	2.30	0.60
21:U:2:VAL:HB	53:3:229:U:H4'	1.83	0.60
22:V:10:ARG:NH1	22:V:11:VAL:O	2.33	0.60
40:p:90:ALA:HB2	40:p:112:ARG:HA	1.81	0.60
51:1:971:G:H2'	51:1:972:A:O4'	2.01	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1374:A:H2'	53:3:1375:A:C8	2.37	0.60
58:B1:395:LYS:HZ2	58:B1:399:LYS:HD3	1.67	0.60
51:1:1818:U:H4'	51:1:1821:A:H1'	1.83	0.60
53:3:454:G:H2'	53:3:455:G:C8	2.37	0.60
57:A1:112:ALA:HB3	57:A1:126:PRO:HA	1.83	0.60
27:b:201:LEU:HD22	53:3:773:G:H5''	1.82	0.60
37:m:14:LYS:NZ	51:1:955:U:OP2	2.35	0.60
29:d:155:GLU:HA	29:d:158:PHE:HB3	1.82	0.60
51:1:1308:A:H61	51:1:1608:A:H61	1.49	0.60
51:1:2048:G:C3'	51:1:2049:G:H5''	2.31	0.60
51:1:2208:C:H2'	51:1:2209:G:C8	2.37	0.60
51:1:2324:U:C3'	51:1:2325:G:H5''	2.26	0.60
58:B1:951:GLN:NE2	58:B1:1014:GLY:O	2.35	0.60
10:J:96:GLN:HG2	53:3:7:A:C6	2.36	0.60
18:R:95:PRO:HG2	18:R:105:ALA:HB1	1.83	0.60
32:g:51:ARG:HA	32:g:55:GLU:HB2	1.84	0.60
51:1:1674:G:H21	51:1:1677:A:H61	1.49	0.60
51:1:2743:U:H3'	51:1:2744:G:H5''	1.83	0.60
53:3:314:C:H2'	53:3:315:A:C8	2.37	0.60
55:8:11:DC:H2'	55:8:12:DG:C8	2.37	0.60
36:l:108:ALA:HB3	36:l:125:LEU:HD11	1.83	0.60
51:1:1081:U:H3'	51:1:1081:U:O2	2.02	0.60
53:3:979:C:C2'	53:3:980:C:H5'	2.32	0.60
48:x:31:ASN:ND2	48:x:52:ALA:CB	2.65	0.60
51:1:192:C:H2'	51:1:193:U:H5'	1.84	0.60
51:1:468:G:H2'	51:1:469:G:H5'	1.83	0.60
51:1:729:G:H5''	51:1:730:A:H5''	1.83	0.60
51:1:1278:C:H2'	51:1:1279:G:C8	2.37	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
7:G:73:ARG:HH22	7:G:93:HIS:HA	1.67	0.59
51:1:445:C:C2'	51:1:446:G:H5'	2.32	0.59
51:1:1484:U:H2'	51:1:1485:U:C6	2.36	0.59
51:1:1889:A:H2'	51:1:1890:A:C8	2.37	0.59
51:1:2898:U:H2'	51:1:2899:A:H8	1.67	0.59
53:3:747:A:C3'	53:3:748:G:H5''	2.32	0.59
59:B2:891:GLY:HA3	59:B2:913:VAL:HB	1.84	0.59
59:B2:1072:ASN:ND2	59:B2:1111:GLN:OE1	2.35	0.59
17:Q:13:ARG:NH1	17:Q:14:LYS:O	2.35	0.59
19:S:12:ARG:NH1	19:S:58:ARG:O	2.35	0.59
43:s:42:LYS:HE3	51:1:2010:G:H4'	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:w:56:PHE:CE2	51:1:2365:G:H4'	2.37	0.59
51:1:589:U:H2'	51:1:590:A:C8	2.36	0.59
51:1:2521:C:O2'	51:1:2522:U:H5'	2.02	0.59
7:G:99:MET:HA	7:G:106:VAL:HG21	1.84	0.59
9:I:121:ALA:HA	9:I:145:ARG:HB2	1.83	0.59
27:b:48:ILE:HG22	51:1:779:U:P	2.43	0.59
51:1:1993:U:H2'	51:1:1994:C:H6	1.67	0.59
51:1:2653:U:C3'	51:1:2654:A:H5''	2.30	0.59
53:3:128:G:H2'	53:3:129:A:C8	2.37	0.59
53:3:419:C:H5''	53:3:513:C:H1'	1.83	0.59
53:3:1280:A:O2'	53:3:1281:C:H5'	2.02	0.59
45:u:40:LEU:HD12	45:u:59:GLU:HB3	1.84	0.59
51:1:35:G:H1	51:1:445:C:H42	1.50	0.59
51:1:635:C:O2'	51:1:639:U:H5''	2.02	0.59
51:1:911:A:H5'	51:1:912:C:H5''	1.84	0.59
51:1:2443:C:O2'	51:1:2444:G:H5'	2.02	0.59
51:1:2537:U:H2'	51:1:2538:C:C6	2.37	0.59
53:3:207:C:H3'	53:3:208:U:H5''	1.84	0.59
10:J:25:LYS:HB2	53:3:923:A:OP1	2.02	0.59
18:R:26:LYS:O	18:R:30:LYS:NZ	2.36	0.59
22:V:61:ARG:NH1	22:V:73:THR:OG1	2.36	0.59
36:l:79:LEU:HB2	36:l:113:ALA:HB3	1.83	0.59
41:q:12:ARG:HH12	51:1:1251:C:H5''	1.68	0.59
51:1:729:G:H5''	51:1:730:A:C5'	2.33	0.59
51:1:1062:G:H5'	51:1:1071:G:H5'	1.85	0.59
53:3:253:A:H2'	53:3:254:G:O4'	2.03	0.59
58:B1:154:LEU:HD21	58:B1:160:LEU:HD21	1.83	0.59
58:B1:370:LYS:HG2	58:B1:441:LEU:HD23	1.84	0.59
58:B1:926:PRO:HG2	58:B1:1248:ILE:HD11	1.84	0.59
17:Q:48:LEU:HB2	53:3:520:A:OP1	2.02	0.59
51:1:881:G:N2	51:1:897:C:N3	2.50	0.59
51:1:952:G:C2'	51:1:953:G:H5''	2.32	0.59
51:1:1638:C:H4'	51:1:2710:C:O2	2.02	0.59
53:3:235:C:H2'	53:3:236:A:C8	2.38	0.59
53:3:570:G:O2'	53:3:819:A:H2'	2.03	0.59
58:B1:97:VAL:HG11	58:B1:101:ARG:NH2	2.18	0.59
58:B1:223:LEU:HG	58:B1:223:LEU:O	2.00	0.59
58:B1:633:ALA:HA	59:B2:806:PRO:O	2.01	0.59
27:b:116:GLN:O	27:b:127:ASN:ND2	2.35	0.59
51:1:1063:G:H3'	51:1:1064:C:C6	2.37	0.59
53:3:1421:G:H3'	53:3:1422:G:C5'	2.33	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:275:ARG:NH1	58:B1:278:ARG:NH1	2.51	0.59
64:6:55:U:H2'	64:6:56:C:H6	1.68	0.59
19:S:17:ASP:O	19:S:22:LYS:NZ	2.35	0.59
21:U:5:ARG:HD3	53:3:376:G:H4'	1.85	0.59
29:d:21:ARG:NH2	29:d:22:ASP:OD1	2.35	0.59
51:1:1802:A:H2'	51:1:1803:A:C8	2.38	0.59
51:1:2306:C:H2'	51:1:2307:G:C8	2.38	0.59
53:3:337:G:H2'	53:3:338:A:C8	2.38	0.59
53:3:448:A:H62	53:3:486:U:H3	1.48	0.59
53:3:579:A:H5'	53:3:728:A:H1'	1.85	0.59
53:3:1512:U:H2'	53:3:1513:A:H8	1.66	0.59
51:1:1982:U:H2'	51:1:1983:G:H8	1.68	0.59
51:1:2189:U:H2'	51:1:2190:G:C8	2.37	0.59
53:3:34:C:H2'	53:3:35:G:H8	1.68	0.59
58:B1:342:LEU:HD23	58:B1:1352:ILE:HG23	1.83	0.59
40:p:1:SER:OG	51:1:2875:C:H4'	2.03	0.59
51:1:704:G:H1'	51:1:726:G:H22	1.68	0.59
51:1:1065:U:O4	51:1:1069:A:H5''	2.03	0.59
51:1:2446:G:H2'	51:1:2501:C:C5	2.38	0.59
53:3:738:C:H2'	53:3:739:C:C6	2.38	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
58:B1:438:GLU:HG3	58:B1:485:MET:HE1	1.85	0.59
58:B1:725:MET:SD	59:B2:1101:LEU:HD23	2.42	0.59
59:B2:918:LEU:O	59:B2:918:LEU:HD23	2.02	0.59
9:I:8:LEU:HD21	53:3:429:U:O5'	2.03	0.58
53:3:677:U:H3	53:3:713:G:H1	1.51	0.58
58:B1:201:LEU:HD11	58:B1:220:ARG:HH11	1.67	0.58
6:F:19:ARG:NE	51:1:2756:U:OP2	2.36	0.58
7:G:142:LYS:HE2	53:3:1098:C:OP1	2.03	0.58
28:c:46:ARG:HG2	28:c:84:LEU:HD12	1.85	0.58
50:z:12:ALA:O	50:z:20:LYS:NZ	2.36	0.58
51:1:1444:G:H2'	51:1:1445:G:C8	2.37	0.58
51:1:1770:G:H4'	51:1:1938:A:OP1	2.03	0.58
51:1:2032:G:OP2	51:1:2455:G:H5'	2.03	0.58
53:3:41:G:H2'	53:3:42:G:H8	1.69	0.58
53:3:59:A:H5''	53:3:387:U:H5''	1.84	0.58
53:3:1005:A:H2'	53:3:1006:G:H5'	1.85	0.58
55:8:7:DC:H2''	55:8:8:DT:H71	1.84	0.58
58:B1:514:THR:HG21	58:B1:596:LEU:HD12	1.84	0.58
58:B1:638:SER:OG	58:B1:639:VAL:N	2.36	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:69:GLN:HE21	59:B2:101:ARG:HD2	1.67	0.58
5:E:21:PHE:HE2	5:E:61:LEU:HD23	1.68	0.58
7:G:103:TRP:HA	7:G:106:VAL:HB	1.86	0.58
28:c:118:PHE:HD2	51:1:1654:A:H2	1.52	0.58
29:d:55:SER:OG	29:d:56:GLY:N	2.36	0.58
43:s:25:ARG:NH2	51:1:519:U:H5''	2.18	0.58
51:1:1000:A:H62	51:1:1154:G:H2'	1.68	0.58
51:1:1836:C:O2'	51:1:1837:C:H5'	2.03	0.58
53:3:850:U:C2'	53:3:851:G:H5''	2.33	0.58
58:B1:99:ARG:NH1	58:B1:99:ARG:HG3	2.17	0.58
58:B1:615:LYS:HG2	60:W0:5:THR:HG21	1.85	0.58
63:5:29:G:H5'	66:0:513:GLY:HA3	1.85	0.58
3:C:7:LYS:HA	3:C:23:THR:HA	1.84	0.58
9:I:68:GLU:HB3	53:3:546:A:OP2	2.04	0.58
28:c:194:PRO:HA	51:1:2680:U:H5'	1.85	0.58
45:u:42:LYS:HG3	51:1:499:U:H4'	1.85	0.58
51:1:166:U:H2'	51:1:167:A:C8	2.38	0.58
51:1:952:G:C3'	51:1:953:G:H5''	2.33	0.58
58:B1:241:VAL:O	58:B1:241:VAL:HG12	2.04	0.58
64:6:6:G:O2'	64:6:7:G:H5'	2.03	0.58
15:O:40:ILE:CD1	53:3:1124:G:H4'	2.34	0.58
51:1:36:G:H4'	51:1:451:U:C2	2.38	0.58
51:1:572:A:H61	51:1:2029:G:N2	1.88	0.58
51:1:1319:C:O2'	51:1:1320:C:H5'	2.02	0.58
53:3:885:G:H2'	53:3:886:G:C8	2.39	0.58
53:3:1521:C:H2'	53:3:1522:U:C6	2.37	0.58
58:B1:412:LEU:HD22	58:B1:441:LEU:HD21	1.84	0.58
9:I:12:ARG:HH21	9:I:35:GLN:H	1.50	0.58
13:M:38:VAL:HG11	13:M:110:MET:HA	1.83	0.58
25:Y:73:ARG:O	25:Y:77:ASN:ND2	2.35	0.58
29:d:164:LEU:HB2	29:d:167:VAL:HG22	1.84	0.58
35:k:16:ALA:O	35:k:17:ARG:NH1	2.36	0.58
51:1:1197:G:H2'	51:1:1198:U:H6	1.67	0.58
51:1:1806:C:H2'	51:1:1807:G:O4'	2.04	0.58
52:2:24:G:H4'	52:2:25:U:C5	2.38	0.58
64:6:14:A:H2'	64:6:15:G:H5'	1.85	0.58
66:0:223:ILE:HB	66:0:243:LEU:HD22	1.86	0.58
12:L:137:ARG:NH1	12:L:138:GLU:OE2	2.36	0.58
51:1:414:C:H2'	51:1:415:A:C8	2.39	0.58
53:3:742:G:H2'	53:3:743:A:C8	2.38	0.58
51:1:1197:G:H2'	51:1:1198:U:C6	2.39	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1924:C:H3'	51:1:1925:C:C6	2.38	0.58
53:3:308:C:H2'	53:3:309:A:H8	1.69	0.58
64:6:4:G:H2'	64:6:5:G:O4'	2.03	0.58
9:I:58:GLN:HB3	9:I:62:ARG:HH21	1.68	0.58
20:T:13:GLU:OE1	20:T:83:ARG:NH2	2.36	0.58
28:c:128:ARG:NH2	51:1:2512:C:OP2	2.37	0.58
51:1:12:U:O2	51:1:12:U:H2'	2.02	0.58
51:1:1787:A:C2	51:1:1788:C:C6	2.91	0.58
51:1:2333:A:H5'	51:1:2335:A:H1'	1.85	0.58
27:b:221:GLY:HA2	27:b:224:MET:HE3	1.85	0.58
40:p:11:GLN:HB2	40:p:54:LEU:HD11	1.85	0.58
47:w:51:ARG:NH2	51:1:2384:U:OP2	2.37	0.58
51:1:62:U:O2'	51:1:63:A:H5'	2.04	0.58
51:1:1565:C:H2'	51:1:1567:G:N7	2.18	0.58
51:1:2123:G:O6	51:1:2174:C:N4	2.37	0.58
51:1:2196:C:H2'	51:1:2197:U:C6	2.39	0.58
53:3:180:U:H2'	53:3:181:A:O4'	2.03	0.58
7:G:176:ASN:ND2	7:G:194:GLY:O	2.33	0.57
32:g:139:PHE:O	32:g:141:LYS:NZ	2.37	0.57
51:1:1270:C:H5''	51:1:1271:G:H5'	1.84	0.57
53:3:41:G:H2'	53:3:42:G:C8	2.38	0.57
53:3:626:G:H2'	53:3:627:G:C8	2.39	0.57
53:3:1195:C:H2'	53:3:1197:A:O4'	2.04	0.57
57:A2:82:LEU:HD11	57:A2:171:LEU:HD23	1.86	0.57
58:B1:42:GLU:HB3	58:B1:52:GLU:HG3	1.86	0.57
59:B2:1142:ARG:NH1	59:B2:1161:LEU:O	2.36	0.57
65:a:26:ALA:HA	65:a:29:LEU:HB3	1.85	0.57
8:H:105:VAL:HG22	8:H:107:LYS:H	1.69	0.57
23:W:56:ARG:NH1	53:3:735:C:OP1	2.37	0.57
32:g:15:LEU:HG	32:g:51:ARG:HH22	1.69	0.57
42:r:79:ARG:NH1	51:1:572:A:OP2	2.37	0.57
51:1:1843:C:H2'	51:1:1844:C:C6	2.38	0.57
53:3:16:A:O2'	53:3:17:U:H5'	2.03	0.57
53:3:721:G:H4'	53:3:722:G:O4'	2.04	0.57
59:B2:707:ALA:O	59:B2:711:ASP:HB2	2.03	0.57
10:J:87:VAL:HG13	10:J:92:ARG:HG3	1.86	0.57
14:N:69:GLY:N	53:3:1250:A:H4'	2.20	0.57
27:b:140:VAL:O	27:b:161:VAL:N	2.35	0.57
40:p:33:GLU:OE1	40:p:38:ARG:NH1	2.37	0.57
51:1:1368:G:H2'	51:1:1369:G:H8	1.68	0.57
53:3:408:A:H61	53:3:434:U:H3	1.52	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1069:C:O2'	53:3:1192:C:H1'	2.03	0.57
58:B1:1046:ILE:HD12	58:B1:1059:LEU:HB3	1.86	0.57
17:Q:119:LYS:HD3	53:3:36:C:H5''	1.86	0.57
59:B2:1122:LYS:NZ	59:B2:1126:ASP:OD1	2.38	0.57
5:E:4:LYS:HD3	51:1:242:G:C8	2.38	0.57
8:H:18:ASN:HD21	8:H:39:ARG:HH12	1.51	0.57
37:m:66:ARG:NH1	37:m:104:GLU:OE2	2.37	0.57
38:n:92:GLY:HA3	51:1:2839:G:H21	1.69	0.57
51:1:211:C:H2'	51:1:212:G:C8	2.40	0.57
51:1:2675:A:H2'	51:1:2676:C:C6	2.39	0.57
58:B1:161:THR:HG23	58:B1:164:GLN:H	1.68	0.57
58:B1:741:ALA:O	58:B1:762:ASN:ND2	2.38	0.57
3:C:5:ARG:HG3	3:C:25:ASN:HA	1.86	0.57
10:J:36:THR:OG1	10:J:37:VAL:N	2.38	0.57
44:t:38:ALA:O	44:t:81:LYS:NZ	2.37	0.57
51:1:1941:C:H2'	51:1:1942:C:O4'	2.04	0.57
51:1:2475:C:N4	51:1:2529:G:H22	2.03	0.57
53:3:19:A:H1'	53:3:864:A:N3	2.19	0.57
53:3:279:A:H5''	53:3:281:G:C5'	2.34	0.57
53:3:1004:A:H5'	53:3:1024:G:H1	1.70	0.57
58:B1:99:ARG:CG	58:B1:99:ARG:HH11	2.18	0.57
58:B1:750:PRO:CB	59:B2:549:ASP:OD2	2.45	0.57
58:B1:1361:THR:HB	59:B2:1284:ALA:HB3	1.86	0.57
15:O:13:PHE:O	15:O:70:HIS:ND1	2.36	0.57
29:d:76:PRO:CA	29:d:82:GLY:HA3	2.35	0.57
51:1:1069:A:H2'	51:1:1073:A:N7	2.20	0.57
51:1:1697:G:C5'	51:1:1698:A:H5''	2.35	0.57
53:3:539:A:H2'	53:3:540:G:C8	2.40	0.57
58:B1:160:LEU:HD22	58:B1:164:GLN:HB3	1.86	0.57
66:0:616:ILE:HG13	66:0:688:ASP:HB2	1.87	0.57
7:G:138:ARG:HH21	7:G:142:LYS:HG2	1.69	0.57
16:P:71:ASP:HA	16:P:74:LYS:HG3	1.86	0.57
16:P:116:PRO:HA	53:3:675:A:H2	1.70	0.57
30:e:31:GLU:OE1	30:e:32:LYS:NZ	2.37	0.57
51:1:1332:G:N7	51:1:1609:A:H2'	2.18	0.57
53:3:651:C:H2'	53:3:652:U:O4'	2.04	0.57
53:3:1271:A:H5'	53:3:1314:C:C5'	2.34	0.57
53:3:1399:C:N3	53:3:1502:A:N1	2.53	0.57
66:0:31:LEU:HD21	66:0:68:THR:HG21	1.87	0.57
2:B:5:ASN:ND2	51:1:2020:A:N7	2.52	0.57
16:P:33:ILE:HG22	16:P:41:LEU:HD12	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:601:C:O2	51:1:605:G:H4'	2.05	0.57
51:1:2554:U:H2'	51:1:2555:U:C6	2.40	0.57
53:3:1016:A:H4'	53:3:1218:C:H4'	1.86	0.57
51:1:78:U:H2'	51:1:79:C:C6	2.40	0.57
51:1:1120:G:H2'	51:1:1121:C:O4'	2.05	0.57
51:1:1177:G:H2'	51:1:1178:C:H5''	1.86	0.57
51:1:1791:A:H2'	51:1:1792:G:C5'	2.34	0.57
51:1:1933:G:O2'	51:1:1974:C:H4'	2.04	0.57
66:0:168:PRO:HG2	66:0:218:TRP:HE1	1.70	0.57
5:E:27:ASN:O	5:E:35:LYS:NZ	2.38	0.56
8:H:60:ALA:HB3	62:NG:167:ARG:HA	1.86	0.56
10:J:120:HIS:CE1	10:J:121:ASN:ND2	2.73	0.56
20:T:19:ASN:HB2	53:3:750:C:O4'	2.04	0.56
51:1:324:A:H62	51:1:338:G:N2	2.00	0.56
51:1:2420:C:O2'	51:1:2421:G:H5'	2.05	0.56
51:1:2743:U:C3'	51:1:2744:G:H5''	2.35	0.56
58:B1:37:GLU:O	58:B1:61:ILE:CD1	2.52	0.56
20:T:60:SER:HB2	53:3:581:G:H5'	1.86	0.56
40:p:88:ARG:HD3	40:p:112:ARG:HD3	1.86	0.56
51:1:2396:G:O2'	51:1:2397:G:H5'	2.05	0.56
53:3:302:G:H2'	53:3:303:A:C8	2.41	0.56
53:3:882:C:O2'	53:3:883:C:H5'	2.04	0.56
2:B:49:ARG:O	2:B:51:ARG:NH2	2.37	0.56
11:K:90:MET:SD	23:W:60:ARG:NH1	2.78	0.56
13:M:24:VAL:HG13	13:M:62:LEU:HD11	1.87	0.56
13:M:27:PRO:O	13:M:32:LYS:NZ	2.38	0.56
25:Y:13:SER:O	25:Y:17:ARG:N	2.38	0.56
31:f:59:ASP:OD1	31:f:59:ASP:N	2.36	0.56
34:j:45:THR:OG1	41:q:63:ARG:NH2	2.37	0.56
39:o:2:ASP:N	52:2:59:A:HO2'	2.03	0.56
46:v:21:ARG:HH22	52:2:77:U:H5'	1.70	0.56
47:w:52:ASP:OD2	51:1:2364:C:H5'	2.05	0.56
51:1:28:A:O2'	51:1:583:G:H5'	2.05	0.56
51:1:849:A:H2'	51:1:850:U:H6	1.68	0.56
51:1:1774:C:H4'	51:1:1979:U:O2	2.05	0.56
51:1:1827:U:C2'	51:1:1828:G:H5'	2.35	0.56
51:1:2208:C:H2'	51:1:2209:G:H8	1.70	0.56
51:1:2692:G:H1'	51:1:2847:U:H1'	1.87	0.56
53:3:24:U:H2'	53:3:25:C:C6	2.40	0.56
53:3:428:G:H4'	53:3:429:U:H4'	1.86	0.56
53:3:885:G:H2'	53:3:886:G:H8	1.69	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1513:A:H2'	53:3:1514:G:C8	2.40	0.56
57:A2:28:LEU:HB2	57:A2:201:LEU:HB3	1.85	0.56
58:B1:102:MET:HG2	58:B1:246:PRO:HG3	1.87	0.56
58:B1:247:PRO:HA	58:B1:250:ARG:HG3	1.87	0.56
59:B2:818:VAL:HG22	59:B2:1096:ILE:HG12	1.87	0.56
65:a:26:ALA:HB1	65:a:30:LEU:HB2	1.87	0.56
66:0:438:LEU:HD22	66:0:469:ILE:HD11	1.88	0.56
4:D:12:ARG:HD2	4:D:44:VAL:HG11	1.88	0.56
9:I:65:GLY:O	9:I:96:ARG:NH1	2.39	0.56
14:N:5:TYR:HB2	14:N:20:ILE:HD11	1.86	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
27:b:158:GLY:HA3	51:1:1820:U:C4	2.40	0.56
45:u:32:LYS:HE3	51:1:478:A:H4'	1.87	0.56
47:w:20:LYS:HD2	51:1:2355:G:H4'	1.86	0.56
47:w:33:ILE:HG22	47:w:34:VAL:HG23	1.88	0.56
51:1:379:G:H2'	51:1:380:G:O4'	2.05	0.56
51:1:1370:C:H2'	51:1:1371:G:O4'	2.04	0.56
51:1:2637:U:H2'	51:1:2638:G:O4'	2.04	0.56
53:3:416:G:H2'	53:3:417:G:H8	1.70	0.56
53:3:1093:A:C2'	53:3:1094:G:H5'	2.36	0.56
58:B1:130:MET:HE2	58:B1:135:ILE:HG12	1.87	0.56
65:a:19:LYS:NZ	65:a:20:GLN:O	2.38	0.56
66:0:493:THR:O	66:0:610:PRO:HA	2.06	0.56
13:M:15:ASN:HB3	53:3:827:U:H4'	1.86	0.56
46:v:72:VAL:HA	46:v:94:ALA:H	1.71	0.56
51:1:1114:C:H2'	51:1:1115:G:C8	2.41	0.56
51:1:2050:C:C2'	51:1:2051:A:H5'	2.32	0.56
52:2:4:C:H2'	52:2:5:U:C6	2.41	0.56
53:3:936:C:H2'	53:3:937:A:O4'	2.04	0.56
58:B1:198:CYS:HA	58:B1:221:ILE:HD11	1.86	0.56
3:C:8:ILE:HB	3:C:24:LYS:HB2	1.88	0.56
8:H:32:LEU:HD13	19:S:92:ILE:HD11	1.88	0.56
14:N:47:VAL:HG23	14:N:48:ARG:HG3	1.88	0.56
30:e:113:PHE:HZ	30:e:175:PRO:HB3	1.71	0.56
44:t:55:VAL:O	44:t:88:LYS:NZ	2.37	0.56
47:w:35:ARG:HH21	51:1:2355:G:H1'	1.69	0.56
51:1:959:A:H1'	51:1:2457:U:O2'	2.06	0.56
51:1:2430:A:N3	51:1:2430:A:H2'	2.20	0.56
51:1:2584:U:H2'	51:1:2585:U:H2'	1.87	0.56
53:3:416:G:H2'	53:3:417:G:C8	2.41	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1513:A:H2'	53:3:1514:G:H8	1.70	0.56
53:3:1525:G:O2'	53:3:1526:G:H5'	2.06	0.56
12:L:91:ARG:CB	12:L:93:VAL:HG12	2.32	0.56
18:R:113:LYS:NZ	64:6:44:A:H4'	2.20	0.56
33:i:53:PRO:HD2	33:i:77:VAL:HG21	1.87	0.56
33:i:123:ALA:HB1	51:1:1081:U:H4'	1.87	0.56
51:1:259:G:O2'	51:1:260:G:H5'	2.06	0.56
51:1:1310:G:C2'	51:1:1311:G:H5'	2.34	0.56
51:1:1868:C:H2'	51:1:1869:G:C5'	2.35	0.56
51:1:2317:A:H2'	51:1:2318:G:O4'	2.06	0.56
53:3:212:G:H2'	53:3:213:G:C8	2.38	0.56
53:3:1395:C:O2'	53:3:1396:A:H8	1.70	0.56
59:B2:13:LYS:HB2	59:B2:1180:MET:HE2	1.87	0.56
63:5:38:A:C8	63:5:39:U:H1'	2.40	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:82:ASP:HA	8:H:85:LYS:HD2	1.86	0.56
27:b:17:LYS:HD3	51:1:1565:C:OP1	2.05	0.56
28:c:109:VAL:HG23	28:c:172:VAL:HG13	1.88	0.56
40:p:15:ASP:N	40:p:15:ASP:OD1	2.39	0.56
51:1:1783:A:N1	51:1:2587:A:H2'	2.21	0.56
66:0:11:ARG:NH2	66:0:283:ILE:O	2.39	0.56
21:U:1:MET:HB2	53:3:135:C:N3	2.21	0.56
26:Z:48:LYS:HB3	53:3:723:U:C5	2.41	0.56
33:i:3:LYS:HD3	51:1:1055:G:O5'	2.06	0.56
34:j:60:ASP:HA	34:j:93:ILE:HD11	1.88	0.56
50:z:10:ARG:NH2	50:z:52:PHE:O	2.39	0.56
51:1:27:G:N2	51:1:512:G:H1'	2.20	0.56
51:1:923:G:O2'	51:1:924:G:H5'	2.06	0.56
51:1:1186:G:N2	51:1:1187:G:H1'	2.20	0.56
51:1:1801:A:H5''	51:1:2203:U:C2'	2.35	0.56
51:1:2529:G:H5'	51:1:2530:A:H5''	1.87	0.56
58:B1:144:TYR:HE1	58:B1:162:GLU:CD	2.14	0.56
66:0:323:LYS:HB2	66:0:335:PHE:HB2	1.88	0.56
4:D:8:SER:OG	4:D:9:VAL:N	2.38	0.56
8:H:20:THR:HA	19:S:93:PRO:HB3	1.88	0.56
8:H:120:THR:HG23	8:H:188:ALA:HB2	1.87	0.56
13:M:74:ILE:HG22	13:M:128:VAL:HA	1.87	0.56
35:k:65:THR:HA	35:k:82:ASN:HA	1.88	0.56
51:1:683:U:H3	51:1:794:A:H61	1.53	0.56
51:1:1141:U:H4'	51:1:1142:A:O4'	2.05	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1740:G:H2'	51:1:1741:C:C6	2.41	0.56
51:1:2041:U:H2'	51:1:2042:A:C8	2.40	0.56
53:3:301:G:H2'	53:3:302:G:C8	2.41	0.56
57:A1:29:GLU:HB3	57:A1:200:LYS:HG3	1.88	0.56
58:B1:510:LEU:HD22	58:B1:601:ILE:HD12	1.86	0.56
14:N:11:ARG:NH1	14:N:106:ASP:O	2.39	0.55
25:Y:2:ASN:O	25:Y:7:LYS:NZ	2.38	0.55
26:Z:66:ARG:NH1	53:3:1098:C:O2'	2.38	0.55
28:c:63:PRO:O	28:c:67:HIS:N	2.39	0.55
51:1:2524:G:C2'	51:1:2525:G:H5''	2.34	0.55
51:1:2726:A:O2'	51:1:2727:A:H5'	2.06	0.55
52:2:105:G:H2'	52:2:106:G:H8	1.71	0.55
53:3:560:A:H5'	53:3:566:G:N2	2.21	0.55
53:3:971:G:OP1	53:3:971:G:H3'	2.07	0.55
66:0:322:PHE:HB3	66:0:323:LYS:HD2	1.86	0.55
10:J:120:HIS:CE1	10:J:121:ASN:HD21	2.23	0.55
15:O:42:LEU:HD22	15:O:71:LEU:HB2	1.88	0.55
29:d:2:GLU:HB2	29:d:11:ALA:HB1	1.87	0.55
30:e:32:LYS:HB3	30:e:91:ARG:HE	1.71	0.55
30:e:56:LEU:HG	30:e:59:ILE:HD12	1.89	0.55
45:u:32:LYS:HB3	45:u:63:ALA:HB1	1.87	0.55
51:1:782:A:H4'	51:1:783:A:H5'	1.88	0.55
51:1:1923:U:H2'	51:1:1924:C:H6	1.70	0.55
53:3:1244:G:H2'	53:3:1245:C:C6	2.40	0.55
53:3:1257:A:H3'	53:3:1257:A:N3	2.21	0.55
53:3:1401:G:H2'	53:3:1402:C:O4'	2.06	0.55
14:N:83:THR:HG21	14:N:102:PHE:HB3	1.88	0.55
28:c:119:ALA:O	51:1:1655:A:H4'	2.06	0.55
30:e:46:LYS:NZ	30:e:82:TYR:OH	2.40	0.55
51:1:310:A:C2'	51:1:311:A:H5''	2.37	0.55
51:1:1257:C:O5'	51:1:1257:C:H6	1.90	0.55
51:1:2207:C:O2'	51:1:2208:C:H5'	2.07	0.55
51:1:2299:U:H2'	51:1:2300:C:C6	2.42	0.55
51:1:2496:C:C2'	51:1:2497:A:H5'	2.36	0.55
51:1:2508:G:C6	51:1:2582:G:O6	2.59	0.55
51:1:2563:U:H2'	51:1:2564:A:H5''	1.88	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
7:G:59:ILE:HG12	7:G:62:ARG:HH21	1.71	0.55
17:Q:50:LYS:NZ	17:Q:51:VAL:O	2.39	0.55
21:U:5:ARG:NH2	21:U:23:ASP:O	2.40	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:d:112:LEU:HD22	29:d:117:ARG:HB3	1.88	0.55
40:p:87:ARG:NH2	40:p:109:ILE:O	2.36	0.55
41:q:68:ALA:HB1	41:q:73:ILE:HG13	1.87	0.55
51:1:36:G:H4'	51:1:451:U:N3	2.21	0.55
51:1:687:C:H2'	51:1:688:U:C5'	2.36	0.55
52:2:4:C:H6	52:2:4:C:H5'	1.71	0.55
58:B1:804:ALA:HA	58:B1:1259:GLN:HG3	1.88	0.55
58:B1:833:GLU:HB2	58:B1:1242:ARG:NH1	2.22	0.55
7:G:101:THR:HG22	53:3:1074:G:H4'	1.88	0.55
11:K:89:VAL:HG23	53:3:737:C:H5'	1.89	0.55
19:S:75:LYS:HZ3	53:3:1357:A:H5''	1.70	0.55
51:1:146:A:H2'	51:1:147:C:C6	2.41	0.55
51:1:490:C:H5'	51:1:491:G:OP2	2.06	0.55
51:1:881:G:H2'	51:1:882:G:H8	1.71	0.55
51:1:2796:U:H3	51:1:2799:A:H61	1.52	0.55
53:3:459:A:H2'	53:3:460:A:C8	2.42	0.55
53:3:684:U:H2'	53:3:685:G:O4'	2.06	0.55
58:B1:508:LEU:HD22	59:B2:1101:LEU:HD21	1.88	0.55
66:0:225:SER:O	66:0:255:ARG:NH1	2.39	0.55
5:E:43:LEU:HD11	51:1:2362:C:P	2.46	0.55
8:H:21:TRP:HD1	8:H:57:GLU:HA	1.71	0.55
9:I:96:ARG:NH2	9:I:98:ASP:OD2	2.39	0.55
10:J:25:LYS:HG3	53:3:923:A:H5'	1.87	0.55
13:M:14:ARG:NH1	13:M:74:ILE:O	2.39	0.55
22:V:64:ARG:HB2	53:3:130:A:H8	1.71	0.55
38:n:11:ASN:N	51:1:1653:G:O6	2.37	0.55
51:1:155:A:H2'	51:1:156:A:H8	1.71	0.55
51:1:1697:G:C3'	51:1:1698:A:H5''	2.36	0.55
53:3:596:A:H2'	53:3:597:G:O4'	2.07	0.55
59:B2:839:VAL:HG12	59:B2:1049:ILE:HG12	1.87	0.55
4:D:37:LYS:NZ	51:1:468:G:OP2	2.34	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
13:M:84:ILE:HD11	13:M:86:LYS:HG2	1.89	0.55
27:b:140:VAL:HG12	27:b:191:LEU:HA	1.89	0.55
41:q:24:TYR:OH	51:1:2020:A:O3'	2.25	0.55
51:1:1255:U:OP1	51:1:1256:G:H5''	2.06	0.55
53:3:46:G:H2'	53:3:366:A:H62	1.72	0.55
53:3:1127:G:H2'	53:3:1128:C:C6	2.41	0.55
58:B1:39:LYS:O	58:B1:273:ILE:HG21	2.06	0.55
58:B1:759:ILE:HG23	58:B1:771:GLN:HB3	1.89	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:0:427:ASP:O	66:0:431:MET:N	2.39	0.55
3:C:21:THR:HG21	51:1:2419:U:H5''	1.89	0.55
12:L:32:ASP:HA	53:3:1350:A:O2'	2.06	0.55
51:1:1791:A:O2'	51:1:1792:G:H5'	2.07	0.55
51:1:1827:U:H2'	51:1:1828:G:H5'	1.88	0.55
51:1:2682:A:H61	51:1:2728:U:H1'	1.72	0.55
58:B1:1166:GLY:HA3	58:B1:1174:ARG:HB2	1.88	0.55
65:a:189:LEU:HA	65:a:192:LEU:HG	1.88	0.55
66:0:694:VAL:HA	66:0:697:ALA:HB3	1.87	0.55
3:C:36:LYS:NZ	3:C:45:HIS:O	2.38	0.55
28:c:110:THR:OG1	28:c:111:GLY:N	2.38	0.55
36:l:29:LYS:HG2	51:1:566:U:OP1	2.07	0.55
41:q:5:ARG:NH2	51:1:1251:C:OP2	2.40	0.55
51:1:171:U:H2'	51:1:172:A:C8	2.42	0.55
51:1:2008:C:H2'	51:1:2009:A:C8	2.42	0.55
53:3:1091:U:H2'	53:3:1093:A:OP2	2.07	0.55
53:3:1213:A:O2'	53:3:1214:C:H2'	2.06	0.55
66:0:103:MET:HB3	66:0:135:VAL:HG21	1.89	0.55
66:0:564:GLY:HA3	66:0:569:TYR:H	1.71	0.55
5:E:22:LYS:HZ1	51:1:631:A:H5''	1.72	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
31:f:3:VAL:HG11	31:f:65:GLY:HA2	1.89	0.55
38:n:64:ARG:O	38:n:68:ALA:N	2.40	0.55
51:1:207:A:H2'	51:1:208:C:O4'	2.07	0.55
51:1:305:C:H2'	51:1:306:U:C6	2.42	0.55
51:1:1191:G:H2'	51:1:1192:G:H8	1.71	0.55
51:1:1343:G:H1'	51:1:1597:A:C4	2.42	0.55
53:3:1096:C:H2'	53:3:1097:C:C6	2.41	0.55
53:3:1390:U:H2'	53:3:1391:U:C6	2.42	0.55
66:0:192:ASN:HB3	66:0:203:GLU:HB2	1.87	0.55
1:A:28:VAL:HG23	30:e:139:GLU:HA	1.88	0.54
6:F:10:LEU:HD21	51:1:2477:U:C5	2.42	0.54
10:J:16:ALA:HB3	10:J:35:LEU:H	1.71	0.54
16:P:122:PRO:HG2	26:Z:34:ARG:HA	1.89	0.54
28:c:118:PHE:HD2	51:1:1654:A:C2	2.24	0.54
51:1:286:U:H2'	51:1:287:G:H8	1.73	0.54
51:1:486:C:H42	51:1:494:G:H1	1.56	0.54
51:1:1614:A:H2'	51:1:1615:C:H5'	1.89	0.54
51:1:1809:A:H2'	51:1:1810:A:C8	2.42	0.54
51:1:2048:G:C2'	51:1:2049:G:H5''	2.37	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1348:U:H2'	53:3:1349:A:H5'	1.87	0.54
58:B1:58:CYS:SG	58:B1:59:ALA:N	2.80	0.54
58:B1:1155:ILE:HG13	58:B1:1210:ILE:HB	1.89	0.54
66:0:488:VAL:HG11	66:0:661:SER:HA	1.88	0.54
27:b:206:LYS:HE3	27:b:209:ALA:HB2	1.89	0.54
29:d:147:LEU:HB3	29:d:186:VAL:HG12	1.88	0.54
30:e:120:SER:HA	51:1:2303:G:H4'	1.89	0.54
30:e:127:TYR:HB3	30:e:155:ILE:HG13	1.89	0.54
33:i:38:CYS:O	33:i:42:ASN:ND2	2.40	0.54
34:j:6:ALA:HB3	34:j:48:VAL:HG11	1.89	0.54
44:t:14:PRO:HA	44:t:32:LEU:HA	1.90	0.54
48:x:2:ARG:HG2	48:x:32:LEU:CD1	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
51:1:1063:G:OP2	51:1:1070:A:H4'	2.06	0.54
51:1:1403:A:H2'	51:1:1404:C:C6	2.42	0.54
53:3:350:G:O2'	53:3:351:G:H5'	2.08	0.54
53:3:874:G:H2'	53:3:875:U:C6	2.42	0.54
53:3:1325:C:H2'	53:3:1326:U:C6	2.42	0.54
65:a:194:VAL:HA	65:a:197:LYS:HB2	1.89	0.54
8:H:26:LYS:HE3	53:3:1256:A:H3'	1.89	0.54
9:I:205:LYS:HE2	53:3:8:A:C6	2.42	0.54
13:M:9:MET:HB2	13:M:32:LYS:HE2	1.87	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
25:Y:14:GLU:O	25:Y:18:LYS:NZ	2.41	0.54
33:i:11:GLN:HB2	33:i:56:VAL:HG22	1.88	0.54
37:m:1:MET:HE1	63:5:63:G:H21	1.72	0.54
38:n:2:ARG:NH1	51:1:2820:A:OP2	2.41	0.54
51:1:310:A:H2'	51:1:311:A:H5''	1.90	0.54
51:1:605:G:H21	51:1:658:U:H5'	1.73	0.54
51:1:2128:G:H5'	65:a:218:MET:HE1	1.89	0.54
53:3:1042:A:H2'	53:3:1043:G:C4'	2.37	0.54
53:3:1105:A:H2'	53:3:1106:G:C8	2.42	0.54
58:B1:799:ARG:HG2	58:B1:1325:PHE:HZ	1.72	0.54
59:B2:29:SER:O	59:B2:33:ASP:HB2	2.07	0.54
10:J:153:ALA:HB1	10:J:160:VAL:HA	1.90	0.54
15:O:43:PRO:HA	53:3:1151:A:H5'	1.89	0.54
19:S:9:GLU:HA	19:S:12:ARG:HB2	1.89	0.54
27:b:204:LEU:HD21	27:b:213:ARG:HH21	1.72	0.54
39:o:33:ARG:HD3	52:2:52:A:N7	2.22	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:65:GLN:OE1	51:1:328:U:H4'	2.07	0.54
51:1:2813:A:H2'	51:1:2814:A:C8	2.42	0.54
53:3:866:C:C4	53:3:867:G:H1'	2.42	0.54
53:3:1042:A:H2'	53:3:1043:G:O4'	2.08	0.54
53:3:1347:G:H22	53:3:1373:G:H2'	1.72	0.54
57:A2:100:LEU:HD23	57:A2:115:ILE:HG21	1.89	0.54
63:5:31:A:H5'	63:5:33:U:O4	2.07	0.54
3:C:40:PRO:HG3	51:1:2348:U:H4'	1.89	0.54
11:K:46:GLN:NE2	11:K:47:LEU:O	2.39	0.54
27:b:257:ARG:HD3	51:1:1799:G:OP1	2.07	0.54
38:n:98:LEU:HB2	38:n:112:TYR:HB2	1.88	0.54
51:1:614:A:H5'	51:1:615:U:OP1	2.06	0.54
51:1:1192:G:O2'	51:1:1193:G:H5'	2.08	0.54
51:1:1652:A:H2'	51:1:1653:G:O4'	2.07	0.54
53:3:539:A:H2'	53:3:540:G:H8	1.72	0.54
59:B2:633:LEU:HD13	59:B2:644:LEU:HD23	1.89	0.54
59:B2:684:ASN:OD1	59:B2:687:ARG:NH2	2.41	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
66:0:393:THR:OG1	66:0:408:ARG:NH1	2.40	0.54
12:L:91:ARG:NE	12:L:91:ARG:HA	2.22	0.54
17:Q:120:ARG:HG2	53:3:37:U:H5'	1.89	0.54
51:1:1905:C:H2'	51:1:1930:G:C8	2.42	0.54
53:3:1414:U:H2'	53:3:1415:G:C8	2.43	0.54
66:0:416:ILE:N	66:0:460:GLY:O	2.40	0.54
9:I:141:VAL:HA	9:I:180:THR:HA	1.88	0.54
12:L:111:GLY:HA2	12:L:118:ARG:HG2	1.88	0.54
21:U:1:MET:SD	21:U:24:SER:OG	2.64	0.54
29:d:70:SER:C	51:1:674:G:H5'	2.33	0.54
42:r:76:LYS:NZ	42:r:85:LYS:O	2.40	0.54
51:1:471:A:H2'	51:1:472:A:O4'	2.08	0.54
51:1:1126:A:H4'	51:1:1127:A:C5'	2.38	0.54
66:0:171:LEU:HB2	66:0:183:VAL:HB	1.88	0.54
23:W:49:LYS:HB2	53:3:835:U:OP1	2.08	0.54
27:b:208:GLY:HA2	27:b:211:ARG:HB3	1.89	0.54
53:3:162:A:H2'	53:3:163:C:H5'	1.88	0.54
53:3:1399:C:H4'	53:3:1400:C:H3'	1.88	0.54
59:B2:811:ASN:HA	59:B2:815:SER:HB2	1.90	0.54
66:0:92:HIS:HD2	66:0:464:LEU:HD21	1.71	0.54
6:F:5:ALA:HB3	51:1:2466:C:H5'	1.88	0.54
51:1:121:G:H4'	51:1:149:A:H5'	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:142:A:H2'	51:1:143:C:C6	2.42	0.54
52:2:78:A:H62	52:2:98:G:N2	1.97	0.54
53:3:36:C:H2'	53:3:37:U:H6	1.73	0.54
53:3:1234:C:H1'	53:3:1364:U:O2	2.08	0.54
58:B1:785:ASP:O	58:B1:789:LYS:HB2	2.08	0.54
63:5:40:C:H2'	63:5:41:C:C6	2.42	0.54
5:E:48:MET:SD	5:E:48:MET:N	2.79	0.54
13:M:105:THR:HG22	13:M:107:LYS:H	1.73	0.54
24:X:4:LEU:HG	24:X:6:LYS:H	1.72	0.54
27:b:106:PRO:HG2	27:b:109:LEU:HB2	1.90	0.54
31:f:2:ARG:HG2	51:1:2751:G:C4	2.43	0.54
51:1:1319:C:H2'	51:1:1320:C:H6	1.73	0.54
51:1:1433:A:H2'	51:1:1434:A:C1'	2.38	0.54
51:1:1936:A:H2	51:1:1943:U:H3	1.50	0.54
51:1:2375:G:C2'	51:1:2376:A:H5''	2.38	0.54
58:B1:746:LEU:HG	58:B1:758:PRO:HG3	1.90	0.54
66:0:632:ILE:HA	66:0:635:LEU:HB3	1.89	0.54
8:H:58:ARG:HA	8:H:63:ILE:HA	1.90	0.53
14:N:45:MET:HE3	14:N:49:GLN:HA	1.90	0.53
14:N:104:THR:HG22	53:3:1180:A:OP1	2.08	0.53
32:g:29:PHE:HB2	51:1:2198:A:C2	2.43	0.53
39:o:15:ARG:NH2	39:o:95:SER:OG	2.39	0.53
51:1:772:C:H5''	51:1:1356:G:H5'	1.90	0.53
51:1:851:C:H2'	51:1:852:U:C6	2.42	0.53
51:1:1889:A:H2'	51:1:1890:A:H8	1.73	0.53
53:3:1013:G:N2	53:3:1015:G:H3'	2.23	0.53
53:3:1402:C:H2'	53:3:1403:C:O4'	2.08	0.53
58:B1:99:ARG:HG3	58:B1:99:ARG:HH11	1.73	0.53
59:B2:360:LEU:HD13	59:B2:378:ARG:HH11	1.72	0.53
16:P:124:LYS:HA	26:Z:34:ARG:HE	1.73	0.53
41:q:48:ASP:HA	41:q:51:GLN:HB3	1.89	0.53
51:1:737:C:H2'	51:1:738:G:H8	1.72	0.53
51:1:2092:U:C5	51:1:2199:A:H2	2.26	0.53
51:1:2155:U:OP1	51:1:2157:G:N2	2.41	0.53
53:3:20:U:H2'	53:3:21:G:O4'	2.08	0.53
53:3:401:C:H2'	53:3:402:G:H8	1.73	0.53
53:3:563:A:H4'	53:3:566:G:O2'	2.09	0.53
53:3:1420:U:H3	53:3:1480:A:H2	1.54	0.53
58:B1:145:VAL:HG23	58:B1:159:ILE:HG22	1.89	0.53
58:B1:1175:LEU:HD22	58:B1:1190:ILE:HD11	1.88	0.53
59:B2:103:VAL:HB	59:B2:114:VAL:HG11	1.89	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:10:LYS:HG2	7:G:211:LEU:HD21	1.89	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
8:H:190:THR:HG23	8:H:192:TYR:H	1.73	0.53
14:N:97:LEU:O	14:N:102:PHE:N	2.39	0.53
51:1:1127:A:C2'	51:1:1128:G:H5''	2.37	0.53
51:1:1550:C:H2'	51:1:1551:A:H8	1.73	0.53
51:1:1659:G:H2'	51:1:1660:G:O4'	2.08	0.53
51:1:1760:C:H2'	51:1:1761:C:H5'	1.91	0.53
51:1:1836:C:C2'	51:1:1837:C:H5'	2.37	0.53
53:3:1084:G:HO2'	53:3:1103:C:H5	1.56	0.53
57:A1:47:LEU:HD23	57:A1:51:MET:HG3	1.89	0.53
59:B2:243:PRO:HB2	59:B2:274:ILE:HG23	1.90	0.53
22:V:49:ASN:ND2	22:V:51:GLU:OE2	2.42	0.53
28:c:15:PHE:HB3	40:p:78:PRO:HD3	1.89	0.53
29:d:68:ALA:HA	51:1:1255:U:C6	2.42	0.53
29:d:141:MET:HB2	29:d:143:LEU:HD11	1.90	0.53
52:2:102:G:H2'	52:2:103:U:O4'	2.08	0.53
53:3:951:G:H2'	53:3:952:U:C6	2.43	0.53
53:3:1093:A:C6	53:3:1095:U:H1'	2.43	0.53
53:3:1271:A:C5'	53:3:1314:C:H5''	2.38	0.53
57:A2:29:GLU:HG3	57:A2:200:LYS:HG3	1.88	0.53
58:B1:39:LYS:O	58:B1:273:ILE:HG23	2.08	0.53
58:B1:209:ASN:HA	58:B1:214:ARG:HH21	1.74	0.53
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE21	1.68	0.53
58:B1:800:LEU:HB3	58:B1:920:ALA:HB1	1.89	0.53
59:B2:628:HIS:HB3	59:B2:647:ARG:HH21	1.74	0.53
65:a:11:ILE:HG13	65:a:219:GLY:HA3	1.91	0.53
7:G:68:PHE:HA	7:G:161:PHE:HB3	1.90	0.53
9:I:13:ARG:NH2	9:I:37:PRO:O	2.42	0.53
28:c:146:ILE:O	28:c:159:LYS:NZ	2.41	0.53
38:n:8:ARG:NH2	38:n:43:GLU:OE1	2.42	0.53
38:n:60:VAL:HG12	38:n:64:ARG:HH22	1.73	0.53
46:v:73:LYS:O	46:v:92:VAL:N	2.41	0.53
51:1:155:A:H2'	51:1:156:A:C8	2.44	0.53
51:1:231:A:H2'	51:1:232:G:O4'	2.08	0.53
51:1:351:C:H2'	51:1:352:A:C8	2.44	0.53
51:1:2516:A:O2'	51:1:2517:C:H5'	2.08	0.53
51:1:2638:G:H1	51:1:2775:G:H2'	1.74	0.53
53:3:952:U:H2'	53:3:953:G:H8	1.73	0.53
58:B1:30:ILE:HG21	58:B1:241:VAL:O	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:78:LEU:O	58:B1:78:LEU:HD13	2.08	0.53
66:0:415:VAL:H	66:0:461:MET:HA	1.73	0.53
10:J:53:ARG:CZ	53:3:1071:C:H5'	2.39	0.53
10:J:154:ALA:O	10:J:158:LYS:NZ	2.41	0.53
11:K:11:HIS:ND1	11:K:14:GLN:OE1	2.41	0.53
29:d:133:LEU:O	29:d:136:GLN:NE2	2.40	0.53
33:i:9:LYS:HD2	51:1:1059:G:OP2	2.07	0.53
37:m:27:SER:OG	37:m:66:ARG:NH1	2.42	0.53
43:s:40:ASN:OD1	43:s:40:ASN:N	2.40	0.53
49:y:21:LEU:HA	49:y:25:GLN:HB3	1.90	0.53
51:1:533:G:H1	51:1:560:C:H42	1.56	0.53
51:1:2124:G:N1	51:1:2175:C:O2	2.42	0.53
53:3:337:G:H2'	53:3:338:A:H8	1.74	0.53
53:3:737:C:H2'	53:3:738:C:H6	1.74	0.53
53:3:1077:G:N2	53:3:1079:G:H3'	2.23	0.53
53:3:1507:A:H61	53:3:1528:U:H3	1.56	0.53
4:D:11:LYS:HE2	51:1:770:G:OP2	2.09	0.53
4:D:13:ASN:HB3	51:1:125:A:C4'	2.39	0.53
28:c:23:PRO:HB3	51:1:2682:A:C2	2.43	0.53
37:m:127:LYS:HE2	51:1:1030:C:OP2	2.08	0.53
38:n:103:ARG:HB3	38:n:108:ALA:H	1.74	0.53
51:1:1352:U:O2'	51:1:1353:A:H5'	2.08	0.53
51:1:2048:G:H3'	51:1:2049:G:H5''	1.91	0.53
51:1:2125:G:H5'	65:a:39:VAL:C	2.34	0.53
51:1:2373:G:H2'	51:1:2374:C:C6	2.43	0.53
53:3:36:C:H2'	53:3:37:U:C6	2.44	0.53
57:A2:28:LEU:HD22	57:A2:201:LEU:HD23	1.90	0.53
58:B1:770:LEU:CD1	59:B2:618:GLN:HG3	2.37	0.53
63:5:38:A:H2'	63:5:39:U:H4'	1.91	0.53
65:a:63:THR:HG21	65:a:195:ALA:HB1	1.90	0.53
66:0:501:VAL:CG1	66:0:607:LYS:HZ1	2.21	0.53
66:0:641:MET:HB3	66:0:657:GLU:HB2	1.90	0.53
6:F:24:ARG:HE	6:F:36:ARG:HG3	1.73	0.53
12:L:53:SER:HB2	12:L:55:LYS:HE3	1.91	0.53
13:M:9:MET:HE1	13:M:35:ILE:HD13	1.91	0.53
14:N:11:ARG:HH11	14:N:105:ARG:HH12	1.57	0.53
22:V:46:HIS:HB2	22:V:70:LYS:HD3	1.91	0.53
28:c:144:GLY:HA2	51:1:2578:G:H1'	1.91	0.53
36:l:29:LYS:HE3	51:1:566:U:H5''	1.90	0.53
51:1:534:U:H3	51:1:559:G:H1	1.55	0.53
51:1:1065:U:H3'	51:1:1066:U:H5''	1.91	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2276:G:O2'	51:1:2277:G:H5'	2.09	0.53
51:1:2699:C:H2'	51:1:2700:A:C8	2.44	0.53
52:2:24:G:H4'	52:2:25:U:H5	1.73	0.53
53:3:601:G:H2'	53:3:602:A:C8	2.44	0.53
58:B1:814:CYS:SG	58:B1:883:ARG:NH2	2.81	0.53
66:0:327:ASP:O	66:0:437:ARG:NH2	2.42	0.53
12:L:63:VAL:HA	12:L:66:GLU:HG2	1.91	0.53
16:P:99:LEU:O	16:P:103:GLY:N	2.38	0.53
25:Y:14:GLU:OE2	25:Y:18:LYS:NZ	2.41	0.53
36:l:29:LYS:HA	51:1:810:U:C5	2.44	0.53
39:o:29:HIS:HB3	39:o:36:TYR:HD2	1.74	0.53
39:o:30:ARG:HG3	39:o:102:ARG:HD2	1.89	0.53
51:1:838:C:H2'	51:1:839:U:C6	2.44	0.53
51:1:859:G:N2	51:1:916:G:H2'	2.23	0.53
51:1:937:C:H2'	51:1:938:G:C8	2.43	0.53
51:1:1357:C:H42	51:1:1374:G:H1	1.57	0.53
51:1:2694:G:H2'	51:1:2695:U:O4'	2.09	0.53
53:3:690:G:H2'	53:3:691:G:O4'	2.08	0.53
57:A1:16:ILE:HG23	57:A1:26:VAL:HG22	1.91	0.53
58:B1:111:THR:HG22	58:B1:300:GLN:NE2	2.23	0.53
58:B1:832:LYS:HB3	58:B1:1242:ARG:NH1	2.24	0.53
59:B2:1070:HIS:NE2	59:B2:1114:GLU:OE1	2.36	0.53
59:B2:1142:ARG:NH2	59:B2:1166:ASP:OD1	2.38	0.53
13:M:32:LYS:HA	13:M:35:ILE:HD12	1.90	0.53
17:Q:6:LEU:HD21	17:Q:11:ARG:HH21	1.73	0.53
19:S:8:ARG:HB2	19:S:62:ARG:HH12	1.74	0.53
29:d:45:ALA:HB3	51:1:38:A:H4'	1.91	0.53
30:e:33:ILE:HD12	30:e:155:ILE:HG22	1.90	0.53
38:n:39:PRO:CG	51:1:1651:G:H5'	2.33	0.53
43:s:4:ILE:HG23	43:s:106:VAL:HG22	1.91	0.53
51:1:1592:C:H2'	51:1:1593:A:C8	2.44	0.53
51:1:1656:C:H2'	51:1:1657:U:C6	2.44	0.53
51:1:1674:G:N2	51:1:1677:A:H61	2.07	0.53
51:1:1783:A:C6	51:1:2587:A:C4	2.96	0.53
52:2:33:G:H2'	52:2:34:A:O4'	2.09	0.53
53:3:1169:A:H2'	53:3:1170:A:O4'	2.09	0.53
66:0:217:GLU:O	66:0:220:GLN:NE2	2.41	0.53
8:H:18:ASN:HA	8:H:55:VAL:HG22	1.91	0.52
32:g:2:GLN:HB3	32:g:18:GLN:HB3	1.91	0.52
51:1:351:C:H2'	51:1:352:A:H8	1.73	0.52
51:1:1303:G:H2'	51:1:1304:A:H8	1.74	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:722:G:H1	53:3:733:G:H1	1.56	0.52
53:3:1421:G:H3'	53:3:1422:G:H5''	1.90	0.52
57:A2:140:ILE:HD12	57:A2:142:MET:HE3	1.91	0.52
58:B1:205:LEU:HG	58:B1:217:LEU:HB3	1.90	0.52
58:B1:975:ILE:HD11	58:B1:1003:LEU:HD11	1.91	0.52
66:0:136:PRO:HG2	66:0:287:PRO:HG3	1.90	0.52
7:G:210:THR:HA	7:G:213:LEU:HB2	1.90	0.52
33:i:101:SER:OG	33:i:102:ARG:N	2.42	0.52
40:p:19:PHE:HE2	40:p:46:VAL:HG21	1.74	0.52
51:1:1536:C:H4'	51:1:1537:G:C2	2.44	0.52
51:1:1655:A:H2'	51:1:1656:C:H5'	1.91	0.52
53:3:884:U:OP2	53:3:884:U:H6	1.92	0.52
53:3:1274:A:C2'	53:3:1275:A:H5''	2.40	0.52
58:B1:112:ALA:HA	58:B1:238:ILE:HA	1.91	0.52
66:0:107:ASP:OD1	66:0:107:ASP:N	2.40	0.52
66:0:334:THR:OG1	66:0:385:ALA:N	2.40	0.52
66:0:446:ARG:HH11	66:0:447:VAL:H	1.54	0.52
66:0:520:ILE:HB	66:0:576:ILE:HD11	1.90	0.52
12:L:14:ASP:OD1	12:L:43:TYR:OH	2.24	0.52
25:Y:76:ALA:O	25:Y:79:THR:OG1	2.27	0.52
29:d:1:MET:N	29:d:14:VAL:O	2.35	0.52
33:i:92:PRO:HB3	33:i:134:SER:HA	1.89	0.52
42:r:77:PHE:HD1	42:r:84:ARG:HB3	1.73	0.52
49:y:44:LYS:HE2	49:y:48:ARG:HG3	1.91	0.52
51:1:133:U:H3	51:1:146:A:H61	1.57	0.52
51:1:532:A:H2'	51:1:532:A:N3	2.24	0.52
51:1:2345:G:N3	51:1:2381:A:H2'	2.24	0.52
51:1:2402:U:O2'	51:1:2403:C:H5''	2.09	0.52
57:A2:43:LEU:HD13	57:A2:217:ILE:HD11	1.90	0.52
58:B1:215:LYS:HA	58:B1:218:THR:HG22	1.92	0.52
66:0:53:MET:O	66:0:57:GLN:NE2	2.43	0.52
7:G:67:LEU:HD11	7:G:157:PRO:HG3	1.91	0.52
16:P:87:GLY:O	16:P:92:ARG:NH1	2.43	0.52
18:R:89:ARG:NH2	18:R:95:PRO:O	2.34	0.52
22:V:11:VAL:HG23	22:V:55:GLY:H	1.74	0.52
29:d:63:LYS:HE3	51:1:2060:A:H3'	1.91	0.52
32:g:25:TYR:HB2	51:1:2093:G:O3'	2.08	0.52
51:1:803:U:O2'	51:1:804:A:H5'	2.10	0.52
51:1:1635:A:H2	51:1:1761:C:O2'	1.92	0.52
53:3:153:C:H2'	53:3:154:U:C4'	2.39	0.52
53:3:369:G:H22	53:3:393:A:H1'	1.75	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:437:U:H2'	53:3:438:U:H5'	1.91	0.52
53:3:1479:C:H2'	53:3:1480:A:O4'	2.09	0.52
57:A1:100:LEU:HD21	57:A1:121:VAL:HG11	1.90	0.52
58:B1:68:TYR:CA	58:B1:75:TYR:HE2	2.22	0.52
15:O:15:HIS:CD2	53:3:1152:A:H5'	2.44	0.52
20:T:2:LEU:HD11	20:T:30:LEU:HD11	1.90	0.52
25:Y:67:HIS:HD2	25:Y:69:ASN:HB2	1.73	0.52
27:b:36:ASN:HB3	27:b:38:LYS:HG2	1.91	0.52
35:k:64:ARG:O	35:k:83:ALA:N	2.42	0.52
36:l:85:VAL:HG22	36:l:86:GLU:HG2	1.92	0.52
38:n:32:GLU:HG2	38:n:115:LEU:HD13	1.92	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
51:1:1229:C:H2'	51:1:1230:A:H8	1.74	0.52
53:3:1366:C:H2'	53:3:1367:C:H6	1.72	0.52
66:0:541:LYS:NZ	66:0:579:HIS:O	2.41	0.52
13:M:16:GLY:O	13:M:64:TYR:OH	2.28	0.52
32:g:2:GLN:NE2	32:g:18:GLN:O	2.40	0.52
34:j:135:GLN:HE22	51:1:7:G:H1'	1.75	0.52
51:1:413:C:N4	51:1:2410:G:H1	1.96	0.52
51:1:1864:U:H5''	51:1:2410:G:O2'	2.10	0.52
53:3:224:U:H2'	53:3:225:C:C6	2.44	0.52
53:3:977:A:H2'	53:3:977:A:N3	2.25	0.52
53:3:1064:G:O3'	53:3:1065:U:H4'	2.09	0.52
5:E:38:LYS:HG3	5:E:41:ARG:HH22	1.74	0.52
8:H:181:ILE:HD11	8:H:200:TRP:HB3	1.91	0.52
11:K:47:LEU:HD21	11:K:55:HIS:HA	1.92	0.52
12:L:12:LEU:HD13	53:3:1374:A:OP1	2.09	0.52
16:P:17:ASP:N	16:P:17:ASP:OD1	2.42	0.52
27:b:7:PRO:HB3	27:b:13:ARG:HA	1.92	0.52
32:g:50:ARG:O	32:g:55:GLU:N	2.38	0.52
42:r:29:THR:HA	42:r:63:VAL:HG23	1.92	0.52
51:1:1841:U:H2'	51:1:1842:G:H8	1.73	0.52
51:1:2415:G:H2'	51:1:2416:C:H6	1.75	0.52
53:3:67:C:H2'	53:3:68:G:C8	2.44	0.52
53:3:148:G:H1	53:3:174:A:H61	1.58	0.52
53:3:1239:A:H5''	53:3:1240:U:C5	2.44	0.52
58:B1:144:TYR:CE1	58:B1:162:GLU:CD	2.88	0.52
58:B1:850:LYS:HB2	58:B1:857:LEU:HB2	1.91	0.52
14:N:122:ARG:NH1	53:3:1350:A:OP1	2.43	0.52
19:S:82:LYS:HA	19:S:85:GLU:HB2	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:g:94:ILE:HD12	32:g:99:ILE:HD13	1.91	0.52
34:j:49:ASP:N	34:j:49:ASP:OD1	2.39	0.52
36:l:9:ALA:HB3	36:l:12:SER:HB3	1.91	0.52
51:1:1903:G:C2	51:1:1904:G:C8	2.98	0.52
52:2:30:C:C2'	52:2:31:C:H5'	2.40	0.52
53:3:358:U:H2'	53:3:359:G:C8	2.44	0.52
53:3:1406:U:H2'	53:3:1407:C:O4'	2.10	0.52
57:A1:205:MET:HE3	57:A1:213:PRO:HB3	1.91	0.52
66:0:192:ASN:ND2	66:0:203:GLU:OE1	2.43	0.52
12:L:92:PRO:HA	12:L:95:ARG:CG	2.38	0.52
14:N:64:ILE:HG21	14:N:78:ILE:HG13	1.91	0.52
27:b:6:LYS:HZ1	51:1:1695:G:H5'	1.74	0.52
31:f:151:ARG:HG3	31:f:160:GLY:HA2	1.92	0.52
51:1:25:U:H2'	51:1:26:G:O4'	2.10	0.52
51:1:1332:G:N3	51:1:1332:G:H5'	2.25	0.52
51:1:1333:G:H2'	51:1:1334:G:H8	1.75	0.52
51:1:2061:G:H8	51:1:2501:C:H4'	1.73	0.52
51:1:2272:U:H5''	51:1:2273:A:OP1	2.10	0.52
51:1:2660:A:OP1	66:0:675:LYS:HD2	2.10	0.52
53:3:299:G:N2	53:3:565:U:H3	2.06	0.52
59:B2:246:LEU:HB3	59:B2:269:ILE:HD13	1.91	0.52
65:a:183:ASP:OD1	65:a:183:ASP:N	2.43	0.52
66:0:223:ILE:HG13	66:0:237:TYR:HE1	1.73	0.52
66:0:499:THR:HG23	66:0:500:ASP:N	2.23	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
19:S:7:ALA:HB1	53:3:994:A:O2'	2.09	0.52
30:e:23:SER:HB3	30:e:26:GLN:HB2	1.92	0.52
41:q:57:ARG:NH2	51:1:1154:G:OP2	2.43	0.52
51:1:376:G:H2'	51:1:377:G:H8	1.74	0.52
51:1:543:G:H3'	51:1:544:C:H5''	1.92	0.52
51:1:2082:A:H2'	51:1:2083:G:O4'	2.10	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
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
53:3:1105:A:H2'	53:3:1106:G:H8	1.75	0.52
62:NG:161:SER:HA	62:NG:170:PRO:HA	1.92	0.52
13:M:11:THR:OG1	53:3:876:C:H1'	2.10	0.51
14:N:33:SER:OG	14:N:34:LEU:N	2.43	0.51
14:N:35:GLU:HA	14:N:39:GLY:HA3	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:28:GLN:HB2	53:3:363:A:H1'	1.92	0.51
35:k:21:CYS:HA	35:k:41:ILE:HA	1.92	0.51
38:n:64:ARG:HD3	51:1:2706:A:O2'	2.10	0.51
41:q:23:TYR:HD1	51:1:533:G:H5'	1.75	0.51
51:1:1361:G:H2'	51:1:1362:C:H6	1.74	0.51
51:1:1470:A:H61	51:1:1521:G:H1'	1.75	0.51
51:1:1951:U:C2	51:1:1953:A:OP2	2.63	0.51
51:1:1954:G:H1	51:1:1986:C:H5''	1.75	0.51
53:3:1073:U:H2'	53:3:1074:G:H8	1.69	0.51
53:3:1225:A:H2'	53:3:1225:A:N3	2.25	0.51
53:3:1496:C:H2'	53:3:1497:G:O4'	2.10	0.51
58:B1:633:ALA:HB2	59:B2:808:ASN:N	2.19	0.51
59:B2:974:ARG:HD2	59:B2:1014:LEU:HD21	1.92	0.51
9:I:18:LEU:HB3	9:I:20:LEU:HD22	1.91	0.51
9:I:146:GLU:HA	9:I:149:LYS:HE2	1.92	0.51
11:K:82:ASP:OD1	11:K:82:ASP:N	2.38	0.51
17:Q:45:ASN:OD1	17:Q:45:ASN:N	2.43	0.51
27:b:231:HIS:ND1	51:1:1826:G:OP1	2.38	0.51
30:e:117:SER:HB3	30:e:177:ARG:HH21	1.76	0.51
51:1:12:U:H2'	51:1:13:A:H5'	1.91	0.51
51:1:745:G:H2'	51:1:746:U:O4'	2.09	0.51
51:1:1024:G:H3'	51:1:1025:G:C5'	2.37	0.51
51:1:1268:A:H2'	51:1:1269:A:H8	1.74	0.51
51:1:1599:U:H2'	51:1:1600:C:H6	1.75	0.51
53:3:174:A:C2'	53:3:175:C:H5'	2.41	0.51
53:3:218:U:H2'	53:3:219:U:O4'	2.09	0.51
66:0:473:MET:HA	66:0:477:PHE:HB2	1.91	0.51
21:U:55:ASP:OD1	21:U:55:ASP:N	2.41	0.51
27:b:31:PRO:HG2	27:b:32:LEU:HD12	1.92	0.51
28:c:161:MET:HE1	51:1:2050:C:H1'	1.91	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
51:1:1409:U:H2'	51:1:1410:G:C8	2.46	0.51
51:1:1889:A:H2'	51:1:1890:A:O4'	2.10	0.51
53:3:731:G:O2'	53:3:732:C:H5'	2.10	0.51
66:0:530:ASN:ND2	66:0:535:GLU:OE1	2.42	0.51
2:B:54:ILE:HG13	2:B:56:LYS:H	1.76	0.51
29:d:67:ARG:O	51:1:1255:U:H5	1.94	0.51
51:1:838:C:H2'	51:1:839:U:H6	1.75	0.51
51:1:2656:U:H2'	51:1:2657:A:H8	1.75	0.51
53:3:1485:U:O2'	53:3:1486:G:H5'	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:99:ARG:HA	58:B1:248:ASP:HB2	1.92	0.51
8:H:9:ILE:HG13	8:H:177:LEU:HD21	1.91	0.51
30:e:32:LYS:O	30:e:156:THR:OG1	2.27	0.51
31:f:126:THR:OG1	31:f:127:GLN:N	2.44	0.51
33:i:4:VAL:HB	51:1:1055:G:OP2	2.10	0.51
39:o:110:ALA:HB1	39:o:115:LEU:HD12	1.92	0.51
44:t:61:LEU:HD21	44:t:82:LYS:HD2	1.92	0.51
51:1:44:A:H2'	51:1:45:G:H5'	1.93	0.51
51:1:243:U:O2'	51:1:244:A:H5'	2.11	0.51
51:1:2022:U:O2'	51:1:2617:U:H5'	2.10	0.51
51:1:2372:U:H2'	51:1:2373:G:C8	2.46	0.51
51:1:2417:C:H2'	51:1:2418:A:H8	1.76	0.51
58:B1:390:LEU:N	58:B1:390:LEU:CD1	2.73	0.51
65:a:165:ASN:HD22	65:a:169:GLY:HA2	1.75	0.51
1:A:26:SER:OG	30:e:139:GLU:OE2	2.28	0.51
24:X:35:ARG:HB2	53:3:1320:C:N4	2.25	0.51
34:j:69:ARG:NH1	34:j:90:GLU:OE2	2.38	0.51
51:1:203:A:H3'	51:1:204:A:C5'	2.39	0.51
51:1:1082:U:H3	51:1:1086:A:H2	1.56	0.51
51:1:2850:A:H2'	51:1:2851:A:O4'	2.11	0.51
53:3:49:U:O2'	53:3:50:A:H2'	2.10	0.51
53:3:410:G:H21	53:3:432:A:H62	1.57	0.51
53:3:515:G:O2'	53:3:516:U:H5'	2.10	0.51
66:0:603:GLU:O	66:0:607:LYS:NZ	2.41	0.51
11:K:68:GLN:NE2	53:3:738:C:O3'	2.44	0.51
51:1:178:G:O2'	51:1:179:C:H5'	2.10	0.51
51:1:526:A:N6	51:1:2626:C:H4'	2.25	0.51
51:1:755:U:H2'	51:1:756:A:H8	1.75	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
51:1:1505:A:H2'	51:1:1506:U:O4'	2.10	0.51
51:1:2248:C:H3'	51:1:2249:U:C6	2.46	0.51
51:1:2656:U:H5''	66:0:146:ARG:NH2	2.25	0.51
53:3:955:U:H2'	53:3:956:U:H6	1.74	0.51
53:3:1230:C:H5'	64:6:30:G:H5''	1.93	0.51
53:3:1271:A:H4'	53:3:1314:C:OP1	2.10	0.51
59:B2:125:GLY:HA2	59:B2:499:SER:HB2	1.92	0.51
59:B2:255:ILE:HB	59:B2:263:VAL:HB	1.92	0.51
66:0:17:ALA:H	66:0:23:LYS:HZ1	1.59	0.51
15:O:59:LYS:HE3	53:3:972:C:C5'	2.41	0.51
19:S:78:LEU:HD13	19:S:82:LYS:HB3	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:27:VAL:HG22	26:Z:31:VAL:HB	1.93	0.51
29:d:58:LYS:HE2	51:1:676:A:OP1	2.11	0.51
32:g:8:LYS:NZ	32:g:11:ASN:O	2.44	0.51
51:1:1710:G:H2'	51:1:1711:A:H8	1.74	0.51
51:1:1767:G:O5'	51:1:1767:G:H8	1.93	0.51
51:1:2489:U:H2'	51:1:2490:G:O4'	2.11	0.51
53:3:894:G:H2'	53:3:895:G:H8	1.75	0.51
66:0:295:ILE:HG13	66:0:309:ARG:HB2	1.91	0.51
51:1:1473:G:H1	51:1:1518:C:N4	2.00	0.51
51:1:1937:A:C2'	51:1:1938:A:H5'	2.41	0.51
51:1:2545:G:H2'	51:1:2546:U:O4'	2.11	0.51
53:3:265:G:H2'	53:3:267:C:H5	1.75	0.51
53:3:379:C:H2'	53:3:380:G:O4'	2.10	0.51
53:3:1400:C:N4	64:6:34:C:H1'	2.25	0.51
53:3:1421:G:C2'	53:3:1422:G:H4'	2.40	0.51
58:B1:505:ASP:OD2	59:B2:812:PHE:HA	2.11	0.51
58:B1:902:ASP:HB3	58:B1:905:ARG:HB2	1.93	0.51
58:B1:1179:PRO:HD2	58:B1:1184:ASP:HA	1.93	0.51
11:K:92:THR:OG1	11:K:94:HIS:O	2.29	0.51
32:g:131:SER:OG	32:g:140:ALA:O	2.28	0.51
36:l:51:GLU:HG3	36:l:56:PRO:HB3	1.93	0.51
42:r:61:ALA:HB1	42:r:96:VAL:HB	1.92	0.51
51:1:216:A:O2'	51:1:217:A:H5'	2.11	0.51
51:1:801:G:H3'	51:1:802:A:H5'	1.92	0.51
51:1:1597:A:H4'	51:1:1598:A:H8	1.76	0.51
53:3:574:A:N3	53:3:883:C:H1'	2.25	0.51
53:3:1251:A:H2'	53:3:1252:A:C8	2.46	0.51
53:3:1516:G:H2'	53:3:1518:A:OP2	2.10	0.51
58:B1:412:LEU:HD23	58:B1:416:ILE:HG13	1.92	0.51
59:B2:524:ILE:HG21	59:B2:708:VAL:HG13	1.92	0.51
4:D:3:ARG:O	4:D:6:GLN:NE2	2.40	0.50
9:I:24:VAL:HG12	53:3:409:U:H5''	1.93	0.50
9:I:160:LEU:HD21	9:I:164:ARG:HH21	1.75	0.50
11:K:17:GLN:O	11:K:21:MET:N	2.44	0.50
14:N:118:ARG:NH2	53:3:1366:C:OP1	2.44	0.50
18:R:89:ARG:HB3	18:R:96:VAL:HG22	1.93	0.50
28:c:27:ILE:HD11	28:c:187:LEU:HD23	1.93	0.50
28:c:177:VAL:HA	28:c:189:VAL:HA	1.93	0.50
33:i:113:ALA:HB2	33:i:121:ILE:HD11	1.94	0.50
39:o:100:HIS:O	39:o:104:GLN:NE2	2.43	0.50
40:p:93:LYS:HE2	51:1:1754:A:OP1	2.11	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:14:GLY:HA3	48:x:28:PHE:HE1	1.76	0.50
51:1:286:U:H2'	51:1:287:G:C8	2.46	0.50
51:1:402:A:H2'	51:1:403:U:O4'	2.12	0.50
51:1:1439:A:H2'	51:1:1440:U:H5'	1.93	0.50
51:1:1794:A:H1'	51:1:1900:A:C2	2.46	0.50
51:1:2616:C:H2'	51:1:2617:U:H6	1.76	0.50
53:3:284:C:O2'	53:3:285:C:H5'	2.11	0.50
53:3:793:U:O2	53:3:1516:G:H4'	2.11	0.50
53:3:1271:A:H5'	53:3:1314:C:H5''	1.91	0.50
59:B2:714:VAL:HB	59:B2:787:PRO:HD2	1.92	0.50
8:H:67:ILE:N	8:H:101:ASN:O	2.42	0.50
15:O:37:ARG:HG2	15:O:77:VAL:HB	1.93	0.50
16:P:22:ILE:HD13	16:P:83:VAL:HG13	1.92	0.50
51:1:548:G:H2'	51:1:549:G:O4'	2.10	0.50
51:1:558:U:H2'	51:1:559:G:C8	2.46	0.50
51:1:622:G:O2'	51:1:623:C:H5'	2.10	0.50
51:1:871:U:H2'	51:1:872:U:C6	2.47	0.50
51:1:1187:G:O5'	51:1:1187:G:H8	1.93	0.50
51:1:1394:U:H4'	51:1:1603:A:H4'	1.92	0.50
51:1:1917:U:O2'	51:1:1918:A:H5'	2.11	0.50
51:1:1963:U:C2'	51:1:1964:G:H5''	2.41	0.50
51:1:1977:A:H2'	51:1:1978:A:O4'	2.12	0.50
51:1:2372:U:H2'	51:1:2373:G:H8	1.77	0.50
51:1:2549:G:H2'	51:1:2550:G:H8	1.76	0.50
53:3:135:C:H2'	53:3:136:C:H5'	1.92	0.50
53:3:138:G:H2'	53:3:139:A:C8	2.46	0.50
53:3:993:G:N3	53:3:993:G:H2'	2.25	0.50
66:0:141:VAL:HB	66:0:266:CYS:HA	1.92	0.50
66:0:490:TYR:HB2	66:0:569:TYR:CD1	2.46	0.50
66:0:659:PRO:HB2	66:0:662:GLU:HB2	1.93	0.50
12:L:92:PRO:C	12:L:95:ARG:HG3	2.36	0.50
15:O:8:ILE:HB	15:O:74:VAL:HB	1.91	0.50
34:j:108:MET:HB3	51:1:1006:C:O2'	2.11	0.50
41:q:24:TYR:N	51:1:533:G:OP1	2.38	0.50
51:1:216:A:H2'	51:1:217:A:O4'	2.11	0.50
51:1:990:A:N6	51:1:1186:G:H1'	2.27	0.50
51:1:1934:C:H2'	51:1:1935:G:O4'	2.12	0.50
52:2:88:C:H4'	52:2:90:C:N3	2.27	0.50
53:3:678:U:H2'	53:3:679:C:O4'	2.11	0.50
53:3:903:G:H2'	53:3:904:U:O4'	2.11	0.50
58:B1:437:PHE:HZ	58:B1:453:VAL:HG11	1.76	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:0:194:ASN:OD1	66:0:200:VAL:N	2.44	0.50
7:G:53:LEU:HD11	7:G:215:ALA:HB1	1.93	0.50
14:N:62:LEU:HD12	14:N:64:ILE:HD11	1.92	0.50
15:O:47:GLU:HG3	53:3:1254:A:OP1	2.12	0.50
25:Y:10:ALA:O	25:Y:13:SER:OG	2.28	0.50
25:Y:54:GLN:HE22	53:3:193:C:H1'	1.75	0.50
26:Z:16:ARG:HG3	26:Z:19:LYS:HB2	1.94	0.50
40:p:102:ARG:HH22	51:1:1755:A:P	2.34	0.50
43:s:47:VAL:O	43:s:51:LEU:N	2.39	0.50
51:1:1390:U:O2'	51:1:1391:U:H5'	2.11	0.50
51:1:1937:A:C3'	51:1:1938:A:H5'	2.41	0.50
51:1:2259:U:C5	51:1:2427:C:N4	2.80	0.50
52:2:29:A:H2'	52:2:30:C:O4'	2.11	0.50
53:3:62:U:H2'	53:3:63:C:C6	2.46	0.50
53:3:554:A:H2'	53:3:555:U:H5'	1.93	0.50
53:3:599:C:H2'	53:3:600:A:H8	1.77	0.50
55:8:13:DT:OP2	58:B1:791:ALA:CB	2.59	0.50
66:0:70:ALA:HB3	66:0:84:ILE:HB	1.94	0.50
66:0:446:ARG:O	66:0:459:ALA:N	2.38	0.50
51:1:598:U:H2'	51:1:599:A:H8	1.76	0.50
51:1:1783:A:N6	51:1:2587:A:N3	2.59	0.50
53:3:207:C:C3'	53:3:208:U:H5''	2.40	0.50
53:3:953:G:H2'	53:3:954:G:O4'	2.12	0.50
53:3:1515:G:H2'	53:3:1516:G:C8	2.46	0.50
58:B1:375:GLU:HG2	59:B2:1245:ALA:O	2.10	0.50
59:B2:400:VAL:HG21	59:B2:452:ARG:HE	1.76	0.50
8:H:8:GLY:O	19:S:96:LYS:NZ	2.42	0.50
8:H:38:VAL:O	8:H:42:LEU:N	2.43	0.50
10:J:25:LYS:HZ1	53:3:923:A:H5''	1.75	0.50
29:d:195:GLN:HE22	29:d:199:MET:HE2	1.77	0.50
48:x:57:VAL:O	48:x:61:LYS:NZ	2.44	0.50
51:1:198:C:O2'	51:1:199:A:H5'	2.12	0.50
51:1:403:U:O3'	51:1:404:A:H4'	2.11	0.50
51:1:1700:A:H2'	51:1:1701:A:H5'	1.93	0.50
51:1:2262:U:H2'	51:1:2263:C:H6	1.72	0.50
51:1:2297:A:N1	51:1:2321:U:H5	2.09	0.50
51:1:2339:C:H2'	51:1:2340:A:C8	2.45	0.50
51:1:2358:A:H2'	51:1:2359:C:O4'	2.11	0.50
53:3:570:G:H2'	53:3:571:U:O4'	2.11	0.50
58:B1:124:ILE:HG23	58:B1:128:LEU:HD12	1.94	0.50
59:B2:9:LYS:HG2	59:B2:1171:ARG:HH12	1.77	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:93:SER:HA	59:B2:128:PRO:HA	1.92	0.50
59:B2:400:VAL:HG11	59:B2:452:ARG:HD2	1.94	0.50
60:W0:3:ARG:NH1	60:W0:55:GLU:OE2	2.40	0.50
5:E:35:LYS:HE2	5:E:39:ARG:HE	1.76	0.50
9:I:131:ILE:HD12	53:3:620:C:C2	2.47	0.50
30:e:129:MET:HG3	30:e:153:ILE:HB	1.94	0.50
33:i:9:LYS:HZ3	51:1:1059:G:H5'	1.77	0.50
35:k:1:MET:HE1	51:1:1664:A:H2	1.77	0.50
41:q:62:ALA:O	41:q:66:ALA:N	2.43	0.50
51:1:108:G:O2'	51:1:109:C:H5'	2.11	0.50
51:1:704:G:H1'	51:1:726:G:N2	2.27	0.50
51:1:866:A:H61	51:1:913:U:H1'	1.76	0.50
51:1:1040:A:H2'	51:1:1041:G:C8	2.47	0.50
51:1:1686:C:H2'	51:1:1687:G:O4'	2.12	0.50
53:3:162:A:C2'	53:3:163:C:H5'	2.42	0.50
53:3:454:G:H2'	53:3:455:G:H8	1.77	0.50
53:3:559:A:H4'	53:3:560:A:H3'	1.94	0.50
53:3:812:G:OP1	53:3:903:G:H1'	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:B1:201:LEU:HD12	58:B1:224:LEU:HD12	1.92	0.50
58:B1:683:ILE:HD12	58:B1:754:ILE:HG21	1.93	0.50
67:h:6:5OH:N	67:h:6:5OH:CS	2.75	0.50
42:r:10:LYS:HE2	51:1:994:C:O2'	2.11	0.50
42:r:80:ARG:HD3	51:1:566:U:C5	2.47	0.50
51:1:123:G:H2'	51:1:124:G:H8	1.77	0.50
51:1:737:C:H2'	51:1:738:G:C8	2.47	0.50
51:1:1424:G:H2'	51:1:1425:G:O4'	2.12	0.50
51:1:1867:G:H1	51:1:1874:C:N4	2.08	0.50
51:1:2549:G:H2'	51:1:2550:G:C8	2.47	0.50
52:2:53:A:C2	52:2:54:G:H1'	2.47	0.50
53:3:302:G:H2'	53:3:303:A:H8	1.75	0.50
53:3:439:U:H2'	53:3:440:C:O4'	2.12	0.50
53:3:1231:G:H2'	53:3:1232:U:C6	2.47	0.50
58:B1:421:VAL:O	58:B1:436:ALA:HA	2.12	0.50
58:B1:1167:LYS:HZ2	58:B1:1170:LYS:HB2	1.77	0.50
58:B1:1361:THR:OG1	59:B2:1282:GLY:O	2.28	0.50
59:B2:786:GLY:N	59:B2:789:THR:OG1	2.41	0.50
1:A:8:LYS:O	1:A:27:THR:OG1	2.28	0.50
9:I:96:ARG:NE	9:I:132:ALA:O	2.44	0.50
10:J:37:VAL:HG11	10:J:113:VAL:HA	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:3:ASN:N	14:N:88:GLU:OE1	2.45	0.50
14:N:26:LYS:HG2	14:N:61:ASP:HB2	1.93	0.50
15:O:19:ASP:OD1	15:O:19:ASP:N	2.45	0.50
24:X:76:THR:HG21	53:3:1221:G:H4'	1.94	0.50
25:Y:4:LYS:HB3	25:Y:6:ALA:H	1.76	0.50
27:b:24:HIS:CD2	27:b:79:ARG:HH21	2.29	0.50
40:p:102:ARG:NH2	51:1:1755:A:H5'	2.26	0.50
47:w:10:ARG:HD2	51:1:2258:C:OP1	2.12	0.50
51:1:227:A:O2'	51:1:228:C:H4'	2.11	0.50
51:1:1550:C:H2'	51:1:1551:A:C8	2.46	0.50
51:1:1810:A:H2'	51:1:1811:G:O4'	2.12	0.50
51:1:1984:G:H2'	51:1:1985:C:C6	2.47	0.50
53:3:269:C:H2'	53:3:270:A:H8	1.76	0.50
53:3:650:G:H2'	53:3:651:C:C6	2.47	0.50
53:3:1327:C:O2'	53:3:1328:C:H5'	2.12	0.50
59:B2:18:ARG:HE	59:B2:620:ASN:HA	1.77	0.50
22:V:4:ILE:HD11	22:V:61:ARG:HD3	1.94	0.49
23:W:49:LYS:NZ	53:3:836:G:OP1	2.45	0.49
28:c:160:LYS:HD2	51:1:2513:A:OP1	2.12	0.49
35:k:71:ARG:HG3	35:k:77:ILE:HD11	1.92	0.49
37:m:12:MET:H	37:m:72:PRO:HG2	1.77	0.49
41:q:10:ARG:NH1	51:1:1216:G:H5''	2.25	0.49
42:r:76:LYS:HZ1	42:r:85:LYS:HE2	1.77	0.49
45:u:73:ASN:HD22	45:u:76:THR:H	1.60	0.49
51:1:233:A:H2'	51:1:234:U:H5'	1.92	0.49
51:1:341:C:H2'	51:1:342:A:C8	2.46	0.49
51:1:1042:G:H2'	51:1:1043:C:C6	2.46	0.49
51:1:1289:C:O2'	51:1:1330:C:H4'	2.12	0.49
52:2:87:U:H5''	52:2:88:C:H5	1.74	0.49
53:3:7:A:O2'	53:3:8:A:H5'	2.12	0.49
53:3:162:A:C2	53:3:348:G:H4'	2.47	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
53:3:1351:U:H3	53:3:1371:G:H1	1.59	0.49
65:a:46:VAL:HG11	65:a:196:LEU:HD13	1.94	0.49
66:0:92:HIS:CD2	66:0:464:LEU:HD21	2.47	0.49
7:G:71:THR:OG1	7:G:72:LYS:N	2.45	0.49
10:J:79:THR:OG1	10:J:80:LEU:N	2.44	0.49
20:T:27:GLN:HE21	20:T:31:LEU:HG	1.77	0.49
20:T:88:ARG:HH22	51:1:715:A:H5''	1.76	0.49
38:n:107:ASN:HD22	51:1:2009:A:H4'	1.74	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:t:34:VAL:HG11	44:t:43:ILE:HD13	1.93	0.49
46:v:58:SER:OG	46:v:59:GLU:OE1	2.31	0.49
48:x:2:ARG:CG	48:x:32:LEU:HD12	2.41	0.49
51:1:306:U:H3	51:1:310:A:H62	1.61	0.49
51:1:375:G:C2'	51:1:376:G:H5'	2.42	0.49
51:1:475:C:H4'	51:1:510:C:H5'	1.93	0.49
51:1:664:G:O2'	51:1:940:G:H5''	2.12	0.49
51:1:839:U:H2'	51:1:840:C:C6	2.47	0.49
53:3:128:G:H2'	53:3:129:A:H8	1.76	0.49
53:3:579:A:H2'	53:3:580:C:C6	2.48	0.49
53:3:945:G:H2'	53:3:945:G:N3	2.27	0.49
53:3:1382:C:H3'	53:3:1382:C:O2	2.13	0.49
58:B1:972:LYS:HD2	58:B1:1004:ALA:HA	1.93	0.49
66:0:390:ASP:OD1	66:0:390:ASP:N	2.44	0.49
9:I:32:LYS:HB3	53:3:429:U:OP2	2.12	0.49
12:L:107:ALA:HB1	12:L:115:MET:HE1	1.94	0.49
14:N:108:ARG:HB3	53:3:1347:G:C8	2.47	0.49
17:Q:33:CYS:HA	17:Q:54:VAL:HG22	1.94	0.49
19:S:9:GLU:HA	19:S:12:ARG:HE	1.76	0.49
21:U:5:ARG:NH1	21:U:26:ASN:O	2.43	0.49
28:c:12:THR:OG1	28:c:13:ARG:N	2.45	0.49
32:g:80:ILE:HG13	32:g:102:ALA:HB1	1.94	0.49
47:w:52:ASP:HB2	47:w:54:THR:HG23	1.94	0.49
51:1:458:G:N2	51:1:469:G:H2'	2.27	0.49
51:1:2040:G:H2'	51:1:2041:U:O4'	2.12	0.49
53:3:184:G:H4'	53:3:224:U:O3'	2.12	0.49
53:3:803:G:H2'	53:3:804:U:C6	2.47	0.49
59:B2:533:LEU:HD13	59:B2:540:ARG:HH21	1.77	0.49
64:6:26:G:H3'	64:6:27:U:C5'	2.42	0.49
64:6:61:C:HO2'	65:a:53:ARG:HD2	1.76	0.49
66:0:365:GLN:N	66:0:372:GLU:O	2.38	0.49
66:0:419:ALA:HA	66:0:457:ILE:HA	1.93	0.49
11:K:73:GLU:O	11:K:76:THR:OG1	2.31	0.49
12:L:34:LYS:HE2	53:3:1290:G:H4'	1.95	0.49
15:O:54:SER:O	19:S:80:ARG:NH2	2.44	0.49
18:R:24:VAL:HA	53:3:1329:A:H5''	1.94	0.49
33:i:9:LYS:HD3	51:1:1060:U:OP2	2.13	0.49
33:i:30:GLN:HG3	33:i:60:VAL:HG11	1.93	0.49
41:q:10:ARG:HH11	51:1:1216:G:H5''	1.78	0.49
41:q:65:ASN:HD21	41:q:69:ARG:HH11	1.61	0.49
44:t:58:VAL:HG22	44:t:85:VAL:HG22	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1952:A:H2'	51:1:1953:A:O4'	2.13	0.49
51:1:2416:C:H2'	51:1:2417:C:C6	2.47	0.49
53:3:770:C:O2'	53:3:771:G:H5'	2.12	0.49
59:B2:232:ILE:HG12	59:B2:237:LEU:HG	1.94	0.49
59:B2:857:VAL:HG13	59:B2:919:ARG:HH21	1.78	0.49
66:0:128:ARG:HA	66:0:131:ASN:HD22	1.77	0.49
14:N:72:SER:O	14:N:76:GLY:N	2.45	0.49
30:e:65:LEU:HD22	52:2:42:C:C5	2.47	0.49
31:f:2:ARG:HD3	51:1:2751:G:OP2	2.12	0.49
37:m:18:ARG:O	37:m:97:GLN:NE2	2.46	0.49
43:s:10:ALA:N	43:s:101:SER:O	2.43	0.49
43:s:16:LYS:HE3	51:1:1266:G:N7	2.27	0.49
51:1:90:U:H1'	51:1:456:C:H42	1.77	0.49
51:1:1130:U:H5	51:1:2026:U:P	2.35	0.49
51:1:1219:U:H2'	51:1:1220:G:H8	1.78	0.49
51:1:1366:A:H2'	51:1:1367:A:O4'	2.11	0.49
52:2:49:C:H2'	52:2:50:A:C8	2.48	0.49
53:3:17:U:H2'	53:3:18:C:C6	2.48	0.49
53:3:153:C:C2'	53:3:154:U:H5''	2.43	0.49
57:A1:100:LEU:HB2	57:A1:144:ILE:HG23	1.95	0.49
59:B2:529:ARG:HH11	59:B2:572:ILE:HG22	1.77	0.49
4:D:13:ASN:HB3	51:1:125:A:H4'	1.93	0.49
17:Q:76:HIS:O	66:0:425:LYS:NZ	2.45	0.49
19:S:1:ALA:N	19:S:66:THR:O	2.45	0.49
43:s:42:LYS:HB2	51:1:2010:G:H5''	1.94	0.49
51:1:376:G:H2'	51:1:377:G:C8	2.47	0.49
51:1:1620:G:O2'	51:1:1621:U:H5'	2.13	0.49
51:1:1657:U:H2'	51:1:1658:C:C6	2.48	0.49
51:1:1963:U:H2'	51:1:1964:G:H5''	1.93	0.49
53:3:636:U:H2'	53:3:637:C:C6	2.47	0.49
53:3:1049:U:H4'	53:3:1050:G:H5''	1.94	0.49
27:b:155:ARG:CZ	51:1:1818:U:H5	2.26	0.49
33:i:10:LEU:HD11	51:1:1070:A:C2	2.41	0.49
35:k:65:THR:OG1	35:k:66:LYS:N	2.44	0.49
36:l:65:GLY:HA2	51:1:631:A:O2'	2.12	0.49
40:p:28:LYS:HD3	40:p:82:SER:HB3	1.93	0.49
42:r:8:GLY:HA3	42:r:23:GLU:HG3	1.93	0.49
46:v:13:GLY:N	52:2:76:G:OP1	2.39	0.49
50:z:30:ARG:HG2	50:z:33:HIS:HB2	1.94	0.49
51:1:594:U:H2'	51:1:595:C:H6	1.77	0.49
51:1:739:A:H8	51:1:739:A:O5'	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
51:1:1528:A:H2'	51:1:1529:G:C5'	2.40	0.49
51:1:2716:C:O2'	51:1:2717:C:H5'	2.13	0.49
53:3:23:C:H2'	53:3:24:U:C6	2.48	0.49
53:3:666:G:H5'	53:3:725:G:N2	2.27	0.49
53:3:1253:G:H2'	53:3:1254:A:H8	1.78	0.49
54:4:1:A:H2'	54:4:2:U:H6	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
66:0:169:LEU:HD11	66:0:186:VAL:HG13	1.95	0.49
6:F:1:MET:CG	51:1:2742:G:H5'	2.43	0.49
9:I:7:LYS:HB3	9:I:20:LEU:HG	1.94	0.49
14:N:87:MET:HA	14:N:90:ASP:HB3	1.94	0.49
35:k:89:ASN:N	35:k:89:ASN:OD1	2.45	0.49
37:m:53:MET:HE3	37:m:119:LEU:HB3	1.94	0.49
47:w:65:PHE:CD2	51:1:857:G:H5'	2.48	0.49
51:1:1378:A:H1'	51:1:1379:U:C5	2.48	0.49
51:1:1581:G:H2'	51:1:1582:C:O4'	2.12	0.49
51:1:1999:C:O2'	51:1:2000:C:H5'	2.12	0.49
51:1:2194:U:H2'	51:1:2195:U:H6	1.77	0.49
53:3:25:C:H2'	53:3:26:A:H8	1.77	0.49
53:3:174:A:H2'	53:3:175:C:H5'	1.95	0.49
53:3:865:A:H8	53:3:865:A:O5'	1.96	0.49
53:3:955:U:H2'	53:3:956:U:C6	2.48	0.49
53:3:1339:A:H2'	53:3:1340:A:O4'	2.12	0.49
53:3:1354:U:H2'	53:3:1355:G:H8	1.78	0.49
58:B1:102:MET:HG2	58:B1:246:PRO:HD3	1.95	0.49
58:B1:749:LYS:HB3	58:B1:755:ILE:HD11	1.94	0.49
58:B1:1371:ARG:HE	58:B1:1372:ARG:NH1	2.10	0.49
66:0:530:ASN:ND2	66:0:532:LYS:O	2.45	0.49
7:G:187:ASP:OD1	7:G:187:ASP:N	2.42	0.49
14:N:8:THR:H	14:N:84:ARG:HB2	1.78	0.49
19:S:19:TYR:HB3	19:S:23:ARG:HH21	1.77	0.49
36:l:46:VAL:HG21	51:1:832:U:H4'	1.94	0.49
48:x:7:THR:HG23	48:x:9:LYS:HG3	1.95	0.49
51:1:445:C:H2'	51:1:446:G:H5'	1.94	0.49
51:1:1893:C:H2'	51:1:1894:C:O4'	2.13	0.49
51:1:2314:A:H2'	51:1:2315:G:C8	2.48	0.49
51:1:2638:G:H1'	51:1:2778:A:H61	1.78	0.49
55:8:14:DC:H2'	55:8:15:DC:C6	2.48	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:A1:18:GLN:HA	57:A1:24:ALA:HA	1.94	0.49
66:0:105:VAL:HG23	66:0:106:LEU:HD12	1.93	0.49
66:0:631:VAL:O	66:0:635:LEU:N	2.42	0.49
3:C:35:LEU:CD2	51:1:2286:G:H22	2.26	0.49
35:k:65:THR:HG23	35:k:68:GLY:H	1.78	0.49
51:1:1807:G:H2'	51:1:1808:A:H5'	1.95	0.49
51:1:2531:A:H2'	51:1:2532:G:H5'	1.95	0.49
53:3:505:G:H2'	53:3:506:G:C8	2.47	0.49
53:3:513:C:H2'	53:3:514:C:O4'	2.13	0.49
7:G:210:THR:O	7:G:214:GLY:N	2.40	0.48
8:H:6:PRO:O	8:H:10:ARG:NE	2.41	0.48
26:Z:6:ARG:HD2	26:Z:6:ARG:HA	1.61	0.48
34:j:47:HIS:CG	51:1:536:G:H21	2.31	0.48
51:1:153:U:O2'	51:1:154:U:H5'	2.13	0.48
51:1:319:G:H2'	51:1:320:A:O4'	2.13	0.48
51:1:2235:G:H2'	51:1:2236:U:O4'	2.12	0.48
51:1:2247:A:H2'	51:1:2248:C:O4'	2.13	0.48
53:3:1012:A:H5'	53:3:1012:A:H8	1.77	0.48
59:B2:554:HIS:HD2	59:B2:558:VAL:HB	1.77	0.48
59:B2:565:GLU:HA	59:B2:569:ILE:HG12	1.95	0.48
66:0:565:PRO:HD3	66:0:602:LYS:HZ2	1.77	0.48
9:I:12:ARG:HG3	9:I:37:PRO:HG3	1.94	0.48
25:Y:34:VAL:HG22	25:Y:49:ALA:HB1	1.95	0.48
27:b:59:GLN:NE2	51:1:1567:G:OP1	2.46	0.48
28:c:133:THR:OG1	28:c:134:HIS:N	2.38	0.48
37:m:28:PHE:N	37:m:104:GLU:OE1	2.44	0.48
42:r:4:VAL:HG22	42:r:13:ARG:HA	1.95	0.48
43:s:72:THR:OG1	43:s:73:LYS:N	2.45	0.48
51:1:881:G:H1	51:1:895:U:H3	1.61	0.48
51:1:1225:G:O2'	51:1:1226:A:H5'	2.13	0.48
51:1:1595:C:H2'	51:1:1596:A:C8	2.48	0.48
51:1:2364:C:H2'	51:1:2365:G:O4'	2.13	0.48
51:1:2807:U:H3	51:1:2891:U:H3	1.61	0.48
58:B1:220:ARG:HH11	58:B1:220:ARG:CG	2.26	0.48
66:0:145:ASP:OD1	66:0:273:LYS:NZ	2.45	0.48
22:V:56:ASP:HB3	22:V:80:LYS:HA	1.94	0.48
24:X:76:THR:HG21	53:3:1221:G:O2'	2.13	0.48
25:Y:16:ALA:O	25:Y:20:ASN:N	2.45	0.48
27:b:146:LYS:HB2	27:b:149:LYS:HB2	1.94	0.48
29:d:2:GLU:HA	29:d:13:THR:HA	1.96	0.48
33:i:75:ALA:HA	33:i:78:LEU:HB2	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:175:G:H2'	51:1:176:A:C8	2.49	0.48
51:1:210:C:H2'	51:1:211:C:C6	2.48	0.48
51:1:387:U:H4'	51:1:388:G:O4'	2.14	0.48
51:1:445:C:O2	51:1:450:G:H1'	2.14	0.48
51:1:532:A:N1	51:1:2020:A:H1'	2.28	0.48
51:1:1005:C:H2'	51:1:1006:C:H6	1.77	0.48
51:1:1178:C:H2'	51:1:1179:G:C8	2.48	0.48
51:1:1755:A:C2'	51:1:1756:G:H5'	2.40	0.48
51:1:2786:U:H2'	51:1:2787:C:C6	2.48	0.48
51:1:2803:G:H2'	51:1:2804:U:C6	2.48	0.48
51:1:2810:A:H62	51:1:2890:G:N2	2.11	0.48
53:3:423:G:C2	53:3:424:G:H1'	2.48	0.48
53:3:792:A:H4'	53:3:793:U:H5''	1.95	0.48
58:B1:103:GLY:H	58:B1:244:VAL:HG22	1.79	0.48
7:G:100:LEU:HD11	7:G:160:LEU:HD13	1.95	0.48
9:I:59:LYS:O	9:I:63:ILE:N	2.44	0.48
23:W:32:ILE:HD12	23:W:36:GLY:HA2	1.95	0.48
30:e:21:TYR:OH	30:e:164:GLU:OE1	2.31	0.48
31:f:91:VAL:CG2	51:1:2657:A:H4'	2.43	0.48
51:1:93:G:O2'	51:1:94:A:H5'	2.13	0.48
51:1:189:G:N2	51:1:206:U:C5	2.82	0.48
51:1:1658:C:O5'	51:1:1658:C:H6	1.95	0.48
51:1:2298:A:H2'	51:1:2299:U:O4'	2.13	0.48
52:2:45:A:H2'	52:2:46:A:O4'	2.13	0.48
53:3:153:C:H2'	53:3:154:U:H5''	1.95	0.48
53:3:714:G:H2'	53:3:715:A:C8	2.48	0.48
57:A1:182:ARG:O	57:A1:205:MET:HA	2.14	0.48
58:B1:115:TRP:O	58:B1:1333:THR:HG21	2.13	0.48
58:B1:141:PHE:HE2	58:B1:296:LYS:CB	2.22	0.48
58:B1:201:LEU:HD11	58:B1:220:ARG:HG2	1.95	0.48
58:B1:275:ARG:HH12	58:B1:278:ARG:NH1	2.09	0.48
58:B1:550:VAL:O	58:B1:569:LEU:HA	2.13	0.48
59:B2:363:LEU:HB3	59:B2:381:ALA:HB1	1.96	0.48
65:a:43:ASP:OD1	65:a:174:THR:OG1	2.32	0.48
29:d:112:LEU:O	29:d:117:ARG:N	2.43	0.48
31:f:8:VAL:O	31:f:49:LEU:N	2.43	0.48
36:l:41:ARG:HG2	51:1:806:C:H41	1.78	0.48
37:m:61:GLY:HA3	37:m:105:MET:HE1	1.95	0.48
38:n:68:ALA:HA	51:1:2707:U:O2'	2.13	0.48
51:1:999:U:H5''	51:1:1154:G:O6	2.13	0.48
51:1:1343:G:N3	51:1:1343:G:H2'	2.28	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2556:C:H2'	51:1:2557:G:H5'	1.96	0.48
53:3:83:C:O2'	53:3:84:U:H3'	2.13	0.48
64:6:36:U:H2'	64:6:37:A:C8	2.48	0.48
1:A:36:VAL:HG13	1:A:40:CYS:HB3	1.94	0.48
3:C:16:THR:OG1	3:C:17:GLY:N	2.44	0.48
27:b:48:ILE:HG22	51:1:779:U:OP2	2.13	0.48
28:c:59:ARG:O	28:c:59:ARG:NH2	2.37	0.48
51:1:157:C:H2'	51:1:158:U:O4'	2.13	0.48
51:1:441:U:H2'	51:1:442:G:C8	2.49	0.48
51:1:459:U:H2'	51:1:460:A:O4'	2.13	0.48
51:1:821:A:H5''	51:1:822:G:C8	2.49	0.48
51:1:1333:G:H2'	51:1:1334:G:C8	2.49	0.48
51:1:2834:G:H2'	51:1:2879:A:N6	2.29	0.48
53:3:193:C:H2'	53:3:194:C:C5	2.49	0.48
53:3:701:U:O4'	53:3:703:G:H1'	2.14	0.48
53:3:1251:A:H2'	53:3:1252:A:H8	1.79	0.48
4:D:24:THR:HG23	4:D:27:GLY:H	1.78	0.48
9:I:12:ARG:NH1	9:I:36:ALA:O	2.46	0.48
9:I:37:PRO:HD2	9:I:41:GLY:HA3	1.96	0.48
17:Q:36:VAL:HG13	17:Q:73:LEU:HD11	1.96	0.48
21:U:8:ARG:NH1	53:3:391:G:H5''	2.29	0.48
37:m:65:ILE:HG22	37:m:67:VAL:H	1.78	0.48
41:q:84:LYS:HB3	41:q:115:ALA:HB1	1.94	0.48
51:1:166:U:H2'	51:1:167:A:H8	1.78	0.48
51:1:340:A:C2'	51:1:341:C:H5'	2.43	0.48
51:1:443:A:H2	51:1:1246:A:H1'	1.78	0.48
51:1:2884:U:O2	51:1:2884:U:H3'	2.14	0.48
53:3:483:C:C3'	53:3:484:G:H5'	2.44	0.48
53:3:1308:U:H2'	53:3:1309:G:C8	2.49	0.48
59:B2:207:THR:OG1	59:B2:354:ASP:OD2	2.32	0.48
1:A:26:SER:OG	1:A:27:THR:N	2.47	0.48
15:O:15:HIS:HA	15:O:18:ILE:HG22	1.96	0.48
28:c:8:LYS:HB2	28:c:201:LEU:HD11	1.96	0.48
29:d:23:PHE:H	29:d:114:ARG:HH22	1.60	0.48
35:k:48:PRO:HB3	53:3:1422:G:OP1	2.13	0.48
37:m:22:GLN:NE2	51:1:864:G:OP1	2.47	0.48
37:m:22:GLN:HE21	51:1:864:G:P	2.36	0.48
51:1:1036:G:H1	51:1:1119:U:H3	1.60	0.48
51:1:1258:U:H2'	51:1:1259:G:C8	2.48	0.48
51:1:2600:A:H2'	51:1:2601:C:C6	2.48	0.48
53:3:129:A:O2'	53:3:130:A:H5''	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1349:A:H2'	53:3:1350:A:O4'	2.13	0.48
55:8:3:DC:H2''	55:8:4:DT:C7	2.42	0.48
58:B1:108:ALA:HB1	58:B1:279:LEU:HD22	1.96	0.48
58:B1:395:LYS:NZ	58:B1:399:LYS:CD	2.74	0.48
58:B1:833:GLU:N	58:B1:1242:ARG:HH12	2.12	0.48
62:NG:161:SER:CA	62:NG:170:PRO:HA	2.43	0.48
12:L:78:ARG:NH1	12:L:82:SER:O	2.46	0.48
16:P:83:VAL:HG11	16:P:96:ILE:HG12	1.95	0.48
28:c:134:HIS:CD2	51:1:1675:C:H42	2.32	0.48
30:e:132:ARG:NH1	30:e:148:VAL:O	2.46	0.48
36:l:43:GLY:N	51:1:671:C:OP1	2.47	0.48
38:n:34:ILE:HA	51:1:1279:G:OP1	2.13	0.48
51:1:404:A:H2	51:1:421:C:N3	2.11	0.48
51:1:858:G:H5'	51:1:859:G:OP2	2.14	0.48
51:1:1182:G:H2'	51:1:1183:U:C6	2.48	0.48
51:1:2828:G:O2'	51:1:2829:A:H5'	2.13	0.48
53:3:27:G:H2'	53:3:28:A:C8	2.49	0.48
58:B1:202:ARG:HH11	58:B1:202:ARG:CG	2.14	0.48
58:B1:1036:ARG:HE	58:B1:1081:VAL:HG11	1.79	0.48
58:B1:1221:LEU:HD22	58:B1:1306:LEU:HB2	1.96	0.48
66:0:157:GLN:HE22	66:0:161:ARG:HE	1.61	0.48
66:0:319:ALA:HB3	66:0:397:LEU:HB2	1.96	0.48
66:0:330:VAL:HG11	66:0:386:ILE:HD11	1.96	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
37:m:43:ALA:HB2	37:m:69:PRO:HG3	1.96	0.48
45:u:5:ARG:HH11	51:1:84:A:H5''	1.77	0.48
51:1:80:G:H2'	51:1:81:G:C8	2.49	0.48
51:1:511:U:H2'	51:1:512:G:H5'	1.95	0.48
51:1:1810:A:C2'	51:1:1811:G:H5'	2.44	0.48
53:3:92:U:H2'	53:3:93:U:H5'	1.96	0.48
53:3:230:G:O2'	53:3:231:U:H5'	2.14	0.48
53:3:483:C:H3'	53:3:484:G:H5'	1.94	0.48
53:3:1465:A:H2'	53:3:1466:C:C6	2.48	0.48
58:B1:29:MET:HG2	59:B2:1336:ASN:ND2	2.29	0.48
66:0:99:VAL:HG11	66:0:126:VAL:HG12	1.95	0.48
66:0:501:VAL:HG11	66:0:604:GLY:CA	2.43	0.48
66:0:530:ASN:HD22	66:0:532:LYS:HB2	1.79	0.48
27:b:15:VAL:HB	27:b:205:GLY:HA3	1.95	0.47
29:d:67:ARG:NH2	51:1:1257:C:H5''	2.29	0.47
33:i:65:SER:OG	33:i:66:PHE:N	2.46	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:j:118:MET:HB2	34:j:118:MET:HE3	1.75	0.47
49:y:43:LEU:HD21	49:y:47:ARG:HH11	1.79	0.47
51:1:367:G:H2'	51:1:368:A:O4'	2.14	0.47
51:1:1993:U:H2'	51:1:1994:C:O4'	2.14	0.47
51:1:2143:C:H3'	51:1:2144:G:C8	2.49	0.47
51:1:2276:G:C2'	51:1:2277:G:H5'	2.44	0.47
51:1:2588:G:C6	51:1:2607:G:C2	3.02	0.47
52:2:3:C:C3'	52:2:4:C:H5''	2.42	0.47
53:3:751:U:C2'	53:3:752:G:H5'	2.44	0.47
58:B1:145:VAL:HG12	58:B1:184:ALA:HB1	1.94	0.47
58:B1:255:LEU:HD23	58:B1:261:ALA:HB2	1.95	0.47
59:B2:411:ARG:NH2	59:B2:427:ASP:OD2	2.44	0.47
66:0:422:PRO:HG3	66:0:428:GLN:HB2	1.96	0.47
1:A:8:LYS:NZ	1:A:10:GLU:OE1	2.45	0.47
3:C:5:ARG:NH2	3:C:23:THR:O	2.48	0.47
7:G:53:LEU:HA	7:G:56:LEU:HB2	1.96	0.47
12:L:91:ARG:HG2	12:L:91:ARG:HH11	1.78	0.47
20:T:74:VAL:HA	20:T:77:TYR:HB3	1.96	0.47
24:X:39:ILE:HD11	24:X:70:LEU:HD23	1.96	0.47
29:d:178:VAL:HA	29:d:181:ILE:HG22	1.95	0.47
37:m:111:GLU:HA	37:m:114:ARG:HB3	1.96	0.47
51:1:118:A:H5'	51:1:119:A:H8	1.79	0.47
51:1:145:C:H2'	51:1:146:A:C8	2.49	0.47
51:1:1306:C:O2'	51:1:1307:A:H5'	2.13	0.47
51:1:1580:A:H2'	51:1:1581:G:O4'	2.14	0.47
51:1:2257:U:O2'	51:1:2258:C:H5'	2.14	0.47
51:1:2367:G:O2'	51:1:2368:C:H5'	2.14	0.47
55:8:14:DC:H2'	55:8:15:DC:H6	1.79	0.47
7:G:72:LYS:HZ2	7:G:74:ALA:HB3	1.78	0.47
10:J:83:PRO:HD3	10:J:97:PRO:HG3	1.96	0.47
34:j:116:ARG:HH22	51:1:528:A:H8	1.60	0.47
36:l:30:THR:O	36:l:33:ARG:N	2.46	0.47
38:n:40:LYS:O	38:n:44:LEU:N	2.48	0.47
51:1:1710:G:H2'	51:1:1711:A:C8	2.49	0.47
51:1:1810:A:H2'	51:1:1811:G:H5'	1.96	0.47
51:1:2654:A:H8	51:1:2654:A:OP1	1.97	0.47
53:3:211:G:H3'	53:3:211:G:N3	2.29	0.47
53:3:563:A:H5'	53:3:566:G:C2	2.48	0.47
53:3:840:C:C2'	53:3:841:C:H5''	2.41	0.47
53:3:1414:U:H2'	53:3:1415:G:H8	1.79	0.47
53:3:1478:U:H2'	53:3:1479:C:C6	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1493:A:N7	67:h:6:5OH:NQ	2.61	0.47
58:B1:1150:PRO:HG3	58:B1:1214:PRO:HB2	1.97	0.47
59:B2:562:GLU:OE1	59:B2:662:SER:OG	2.28	0.47
66:0:463:GLU:O	66:0:467:ASP:N	2.42	0.47
2:B:37:HIS:HB3	2:B:43:THR:HG22	1.97	0.47
7:G:18:GLN:NE2	7:G:189:ASN:HB3	2.30	0.47
10:J:24:VAL:HG13	10:J:26:GLY:H	1.79	0.47
10:J:87:VAL:HA	10:J:92:ARG:HA	1.96	0.47
11:K:86:ARG:NH2	53:3:673:A:O3'	2.48	0.47
17:Q:87:LYS:HE3	17:Q:87:LYS:HB3	1.69	0.47
31:f:107:GLY:O	51:1:2666:C:N4	2.47	0.47
34:j:7:LYS:HE2	51:1:539:G:H5'	1.95	0.47
51:1:139:U:H2'	51:1:140:C:C5	2.49	0.47
51:1:524:G:O2'	51:1:525:U:H5'	2.14	0.47
51:1:833:A:H2'	51:1:834:G:H8	1.78	0.47
51:1:937:C:H2'	51:1:938:G:H8	1.78	0.47
51:1:1414:C:H42	51:1:1588:G:H1	1.62	0.47
51:1:2475:C:H2'	51:1:2476:A:H5'	1.97	0.47
53:3:316:C:H2'	53:3:317:U:H6	1.79	0.47
53:3:631:C:H5''	53:3:632:U:O4'	2.15	0.47
53:3:1015:G:H2'	53:3:1016:A:O4'	2.14	0.47
57:A2:102:LEU:HD12	57:A2:115:ILE:HG12	1.96	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
58:B1:1146:GLU:OE2	58:B1:1310:THR:HG22	2.14	0.47
59:B2:1286:THR:O	59:B2:1290:MET:HB2	2.14	0.47
9:I:140:ASP:O	9:I:181:PHE:N	2.46	0.47
10:J:23:THR:HG21	53:3:15:G:N3	2.29	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	2.50	0.47
48:x:4:CYS:SG	48:x:5:GLN:N	2.86	0.47
51:1:341:C:H2'	51:1:342:A:H8	1.79	0.47
51:1:739:A:H1'	51:1:740:C:H5	1.79	0.47
51:1:1463:C:H2'	51:1:1464:G:C8	2.48	0.47
51:1:1856:U:H2'	51:1:1857:G:O4'	2.15	0.47
51:1:1914:C:N4	53:3:1409:C:O3'	2.47	0.47
51:1:2316:G:O2'	51:1:2317:A:H5'	2.14	0.47
53:3:1435:G:H1	53:3:1466:C:H42	1.63	0.47
58:B1:1261:LEU:HD12	58:B1:1304:ARG:HH21	1.79	0.47
2:B:2:VAL:O	51:1:2615:U:C4	2.67	0.47
8:H:32:LEU:HD21	19:S:78:LEU:HD11	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:51:VAL:HA	8:H:69:THR:HA	1.97	0.47
13:M:63:LYS:HG2	13:M:70:VAL:HG21	1.95	0.47
18:R:23:GLY:HA2	18:R:68:LEU:HD13	1.97	0.47
18:R:27:THR:HG22	53:3:1328:C:H5''	1.97	0.47
19:S:12:ARG:HH22	19:S:60:ARG:H	1.61	0.47
51:1:215:G:O3'	51:1:216:A:H4'	2.15	0.47
51:1:696:G:O2'	51:1:697:G:H5'	2.15	0.47
51:1:1103:A:H2'	51:1:1103:A:N3	2.29	0.47
51:1:2450:A:OP1	51:1:2497:A:O2'	2.31	0.47
51:1:2537:U:H2'	51:1:2538:C:H6	1.78	0.47
51:1:2721:A:H2'	51:1:2722:G:O4'	2.14	0.47
51:1:2813:A:H2'	51:1:2814:A:H8	1.78	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
53:3:1436:U:H2'	53:3:1437:A:C8	2.45	0.47
53:3:1465:A:H2'	53:3:1466:C:H6	1.80	0.47
58:B1:1347:LEU:HG	58:B1:1357:ILE:HG23	1.96	0.47
66:0:22:GLY:N	69:0:801:GDP:O1B	2.47	0.47
7:G:66:ILE:HD11	7:G:161:PHE:HB2	1.96	0.47
17:Q:58:ASN:OD1	17:Q:58:ASN:N	2.46	0.47
30:e:22:ASN:ND2	30:e:26:GLN:OE1	2.48	0.47
30:e:31:GLU:HG2	30:e:32:LYS:H	1.80	0.47
32:g:93:SER:HB3	32:g:121:VAL:HG12	1.97	0.47
33:i:7:TYR:CE1	51:1:1058:U:H5'	2.49	0.47
34:j:60:ASP:OD1	34:j:60:ASP:N	2.41	0.47
44:t:89:GLU:OE1	44:t:91:GLN:NE2	2.48	0.47
51:1:593:U:H2'	51:1:594:U:C6	2.49	0.47
51:1:744:U:H5''	51:1:1658:C:H5''	1.96	0.47
51:1:820:A:O2'	51:1:821:A:H5'	2.15	0.47
51:1:1095:A:C8	66:0:632:ILE:HD11	2.50	0.47
51:1:1153:C:H2'	51:1:1154:G:O4'	2.15	0.47
52:2:51:G:N3	52:2:52:A:H1'	2.30	0.47
53:3:325:A:H2'	53:3:326:G:O4'	2.15	0.47
53:3:554:A:C2'	53:3:555:U:H5'	2.43	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
53:3:1424:U:H3	53:3:1476:A:N6	2.05	0.47
58:B1:842:ARG:HH22	58:B1:1250:ASP:HB2	1.80	0.47
58:B1:968:ASN:HA	58:B1:1117:SER:HB2	1.96	0.47
59:B2:400:VAL:HG22	59:B2:584:TYR:HB3	1.96	0.47
59:B2:517:GLN:HB3	59:B2:760:ASN:H	1.79	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:689:ALA:HB2	59:B2:1233:LEU:HD23	1.97	0.47
59:B2:1314:GLN:HB2	60:W0:28:ARG:HH12	1.79	0.47
63:5:50:U:H2'	63:5:51:U:C6	2.49	0.47
64:6:62:C:H5'	65:a:53:ARG:CZ	2.45	0.47
66:0:369:ASN:OD1	66:0:369:ASN:N	2.48	0.47
7:G:132:GLU:OE2	7:G:136:ARG:NE	2.47	0.47
13:M:4:ASP:OD2	13:M:76:ARG:NH2	2.47	0.47
13:M:89:ASP:OD1	13:M:89:ASP:N	2.37	0.47
15:O:21:ALA:HB2	15:O:93:ALA:HB2	1.97	0.47
27:b:240:GLY:HA2	51:1:2597:G:H5''	1.97	0.47
31:f:85:LYS:HE2	31:f:129:GLU:HB3	1.97	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
46:v:21:ARG:HH12	52:2:77:U:H5''	1.80	0.47
47:w:45:ALA:N	47:w:77:SER:OG	2.42	0.47
47:w:56:PHE:HE2	51:1:2365:G:H5'	1.80	0.47
51:1:1018:U:H2'	51:1:1019:U:O4'	2.13	0.47
51:1:1572:A:O2'	51:1:1573:G:H5'	2.15	0.47
52:2:30:C:H2'	52:2:31:C:H5'	1.95	0.47
53:3:1268:G:H21	53:3:1327:C:H1'	1.79	0.47
53:3:1441:A:N3	53:3:1441:A:H2'	2.30	0.47
53:3:1486:G:H2'	53:3:1487:G:O4'	2.15	0.47
59:B2:732:ILE:HD11	59:B2:769:PRO:HB3	1.95	0.47
59:B2:1311:GLY:O	60:W0:31:GLN:NE2	2.47	0.47
15:O:64:GLN:HB3	19:S:98:ALA:HB3	1.96	0.47
33:i:79:LEU:HD22	33:i:131:THR:HG23	1.97	0.47
48:x:1:SER:HG	51:1:1365:A:H5'	1.80	0.47
51:1:1595:C:H2'	51:1:1596:A:H8	1.79	0.47
51:1:1900:A:H5'	51:1:1970:A:H5'	1.96	0.47
51:1:2248:C:C2'	51:1:2249:U:H5'	2.44	0.47
51:1:2515:C:O2'	51:1:2516:A:H5'	2.15	0.47
52:2:116:G:O2'	52:2:117:G:H5'	2.15	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
58:B1:1167:LYS:NZ	58:B1:1170:LYS:HB2	2.30	0.47
59:B2:1314:GLN:HA	60:W0:28:ARG:HH22	1.80	0.47
62:NG:142:ALA:O	62:NG:143:ASP:CB	2.63	0.47
66:0:420:VAL:HB	66:0:458:ILE:HD11	1.97	0.47
16:P:23:HIS:HB3	16:P:30:ILE:HG23	1.96	0.47
51:1:1196:C:O2'	51:1:1197:G:H5'	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1388:G:H2'	51:1:1389:G:C8	2.50	0.47
51:1:1414:C:H2'	51:1:1415:U:H5'	1.95	0.47
51:1:1858:A:N6	51:1:1884:G:O2'	2.48	0.47
51:1:2153:C:H3'	51:1:2154:A:H8	1.78	0.47
51:1:2521:C:H42	51:1:2544:G:H1	1.62	0.47
51:1:2682:A:O2'	51:1:2683:C:H5'	2.14	0.47
53:3:344:A:OP1	66:0:38:HIS:NE2	2.48	0.47
53:3:835:U:C3'	53:3:836:G:H5''	2.45	0.47
53:3:859:G:O2'	53:3:860:A:H5'	2.15	0.47
53:3:1161:C:H2'	53:3:1162:C:H6	1.78	0.47
58:B1:198:CYS:HA	58:B1:221:ILE:CD1	2.45	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
63:5:29:G:H3'	63:5:30:G:C8	2.50	0.47
66:0:24:THR:HG21	66:0:62:THR:HG21	1.97	0.47
66:0:498:VAL:HG22	66:0:499:THR:H	1.79	0.47
3:C:6:GLU:HG2	3:C:26:LYS:HD3	1.96	0.46
24:X:32:THR:O	24:X:56:HIS:NE2	2.45	0.46
25:Y:22:SER:HB2	53:3:1458:G:H4'	1.98	0.46
33:i:47:SER:O	33:i:47:SER:OG	2.31	0.46
51:1:680:C:H42	51:1:797:G:H1	1.63	0.46
51:1:1209:U:H2'	51:1:1210:G:H21	1.80	0.46
51:1:1321:A:C2	51:1:1322:A:H1'	2.50	0.46
51:1:1470:A:N6	51:1:1521:G:H1'	2.31	0.46
51:1:1663:G:O2'	51:1:1664:A:H8	1.98	0.46
51:1:1924:C:H3'	51:1:1925:C:C5	2.49	0.46
51:1:1933:G:H2'	51:1:1934:C:H6	1.80	0.46
53:3:556:C:H2'	53:3:557:G:O4'	2.15	0.46
53:3:1084:G:O2'	53:3:1103:C:H5	1.98	0.46
53:3:1093:A:H2'	53:3:1094:G:H5'	1.95	0.46
53:3:1274:A:H2'	53:3:1275:A:H5''	1.96	0.46
54:4:1:A:H2'	54:4:2:U:C6	2.50	0.46
58:B1:395:LYS:HE3	58:B1:395:LYS:HB3	1.45	0.46
66:0:136:PRO:HB3	66:0:256:VAL:HG12	1.97	0.46
66:0:376:GLU:OE1	66:0:378:ARG:NE	2.48	0.46
66:0:494:ILE:HG21	66:0:605:PHE:CD1	2.50	0.46
3:C:8:ILE:HD11	3:C:50:GLU:HB2	1.96	0.46
8:H:2:GLN:NE2	53:3:1062:U:O4	2.48	0.46
13:M:102:VAL:HB	13:M:126:CYS:HB3	1.96	0.46
28:c:49:GLN:HE21	28:c:79:LEU:HB3	1.79	0.46
28:c:119:ALA:C	51:1:1655:A:H4'	2.40	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:i:9:LYS:HZ2	51:1:1059:G:P	2.38	0.46
42:r:80:ARG:HD3	51:1:566:U:H5	1.80	0.46
43:s:82:MET:HE1	51:1:1322:A:H4'	1.97	0.46
51:1:1444:G:H2'	51:1:1445:G:H8	1.76	0.46
51:1:1485:U:H2'	51:1:1486:U:C6	2.50	0.46
51:1:1826:G:H2'	51:1:1827:U:C6	2.50	0.46
51:1:2080:A:C6	51:1:2081:U:C4	3.04	0.46
51:1:2134:A:C5	51:1:2157:G:H4'	2.51	0.46
51:1:2861:U:O2'	51:1:2862:G:H5'	2.15	0.46
53:3:1000:A:H2'	53:3:1001:C:O4'	2.15	0.46
58:B1:809:VAL:HG21	58:B1:909:ILE:HG12	1.95	0.46
58:B1:1027:VAL:HB	58:B1:1121:LEU:HB2	1.96	0.46
58:B1:1357:ILE:HD13	59:B2:1279:GLU:HG2	1.97	0.46
5:E:7:ARG:NH2	51:1:245:G:N7	2.63	0.46
6:F:15:LYS:N	6:F:26:ILE:O	2.41	0.46
7:G:33:ALA:N	7:G:37:VAL:O	2.46	0.46
8:H:30:ASP:OD1	8:H:30:ASP:N	2.47	0.46
14:N:56:MET:HB2	14:N:60:LEU:HB2	1.97	0.46
25:Y:79:THR:HA	25:Y:82:ILE:HB	1.97	0.46
29:d:22:ASP:OD1	29:d:22:ASP:N	2.48	0.46
29:d:173:THR:OG1	29:d:174:GLY:N	2.48	0.46
31:f:98:LYS:HD2	31:f:98:LYS:HA	1.79	0.46
51:1:233:A:H5'	51:1:233:A:C8	2.51	0.46
51:1:786:C:O2'	51:1:787:C:H5'	2.16	0.46
51:1:1136:G:H2'	51:1:1137:G:H8	1.80	0.46
51:1:1842:G:O2'	51:1:1843:C:H5'	2.15	0.46
51:1:2491:U:C2'	51:1:2492:U:H5'	2.42	0.46
53:3:528:C:H4'	53:3:535:A:C6	2.51	0.46
53:3:857:C:H2'	53:3:858:G:O4'	2.14	0.46
58:B1:109:SER:HB2	58:B1:296:LYS:HG2	1.98	0.46
59:B2:148:GLN:NE2	59:B2:535:PRO:O	2.40	0.46
63:5:26:A:H61	63:5:44:G:H22	1.64	0.46
2:B:14:MET:HG2	51:1:15:G:O2'	2.16	0.46
7:G:17:HIS:CE1	7:G:187:ASP:HB2	2.50	0.46
8:H:49:ALA:O	8:H:69:THR:OG1	2.34	0.46
8:H:147:GLY:HA2	8:H:170:GLY:HA3	1.97	0.46
31:f:88:LEU:O	31:f:128:THR:OG1	2.33	0.46
36:l:37:GLY:O	36:l:41:ARG:NH2	2.44	0.46
43:s:82:MET:HB2	43:s:98:LYS:HB2	1.97	0.46
51:1:441:U:H2'	51:1:442:G:H8	1.81	0.46
51:1:1639:C:H2'	51:1:1640:A:H5'	1.98	0.46

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	0.46
51:1:2135:A:H8	51:1:2156:G:H21	1.64	0.46
51:1:2646:C:H2'	51:1:2647:U:O4'	2.16	0.46
53:3:980:C:H2'	53:3:981:U:O4'	2.15	0.46
58:B1:772:TYR:HE2	59:B2:561:ILE:HG21	1.81	0.46
59:B2:28:LEU:HD21	59:B2:524:ILE:HG13	1.98	0.46
59:B2:1002:LEU:HD21	59:B2:1007:LYS:HB2	1.98	0.46
63:5:8:U:H2'	63:5:13:C:N4	2.30	0.46
5:E:32:LEU:HD12	5:E:32:LEU:HA	1.73	0.46
8:H:39:ARG:HA	8:H:42:LEU:HB3	1.97	0.46
27:b:120:ASP:N	27:b:120:ASP:OD1	2.49	0.46
27:b:210:ALA:HA	27:b:213:ARG:HG3	1.96	0.46
27:b:250:GLN:HB3	27:b:254:LYS:HD2	1.96	0.46
29:d:47:LYS:HG2	51:1:451:U:OP2	2.15	0.46
32:g:30:LEU:HA	32:g:35:LYS:HE3	1.97	0.46
35:k:31:ARG:HH12	51:1:2676:C:P	2.39	0.46
45:u:8:ASP:O	45:u:23:LYS:NZ	2.45	0.46
46:v:7:GLU:HG3	46:v:41:GLU:HB3	1.97	0.46
51:1:2845:U:H2'	51:1:2846:G:C8	2.50	0.46
53:3:951:G:H2'	53:3:952:U:H6	1.79	0.46
55:8:20:DA:H4'	59:B2:143:ARG:NH1	2.31	0.46
58:B1:352:ARG:HB2	59:B2:1268:GLN:NE2	2.30	0.46
9:I:103:ARG:HD2	9:I:167:PRO:HG3	1.97	0.46
12:L:101:ARG:HH22	53:3:940:C:P	2.37	0.46
14:N:30:ASN:N	14:N:64:ILE:O	2.48	0.46
14:N:40:ARG:NE	53:3:1292:G:H5''	2.31	0.46
14:N:72:SER:HA	14:N:75:ALA:HB3	1.98	0.46
27:b:155:ARG:NH1	51:1:1818:U:C5	2.81	0.46
28:c:55:LYS:HG3	28:c:77:ARG:HB3	1.97	0.46
51:1:175:G:H2'	51:1:176:A:H8	1.81	0.46
51:1:365:U:H2'	51:1:366:C:O4'	2.16	0.46
51:1:690:G:H2'	51:1:691:C:H5'	1.98	0.46
51:1:704:G:N3	51:1:726:G:C2	2.84	0.46
51:1:866:A:H61	51:1:913:U:C1'	2.28	0.46
51:1:1569:A:H2'	51:1:1570:A:C8	2.51	0.46
51:1:1868:C:C2'	51:1:1869:G:H5'	2.42	0.46
51:1:2259:U:C6	51:1:2427:C:C5	3.04	0.46
51:1:2531:A:C2'	51:1:2532:G:H5'	2.45	0.46
53:3:460:A:H2'	53:3:461:A:C8	2.51	0.46
53:3:1018:G:O2'	53:3:1019:A:H5'	2.16	0.46
59:B2:318:SER:OG	59:B2:320:ASP:OD1	2.31	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:91:ARG:HG2	12:L:91:ARG:NH1	2.30	0.46
17:Q:34:THR:HG22	17:Q:76:HIS:CD2	2.51	0.46
17:Q:83:GLY:H	53:3:552:U:H4'	1.80	0.46
31:f:136:ASP:HB3	31:f:139:VAL:HG12	1.97	0.46
51:1:233:A:H5'	51:1:233:A:H8	1.81	0.46
51:1:433:C:O2'	51:1:434:U:H5'	2.15	0.46
51:1:717:C:H2'	51:1:718:A:H5'	1.98	0.46
51:1:845:A:N3	51:1:845:A:H3'	2.31	0.46
51:1:1085:A:H2'	51:1:1086:A:N7	2.30	0.46
51:1:1313:U:O2	51:1:1313:U:C2'	2.64	0.46
51:1:1587:G:H2'	51:1:1588:G:C8	2.50	0.46
51:1:1642:G:O2'	51:1:1643:G:H5'	2.15	0.46
51:1:2785:C:H2'	51:1:2786:U:C6	2.51	0.46
53:3:138:G:H2'	53:3:139:A:H8	1.79	0.46
53:3:1260:G:H4'	53:3:1284:C:H5'	1.98	0.46
57:A2:64:VAL:HG11	57:A2:78:ILE:HG21	1.97	0.46
58:B1:209:ASN:HA	58:B1:214:ARG:NH2	2.30	0.46
3:C:35:LEU:HD21	51:1:2286:G:H22	1.81	0.46
5:E:57:VAL:O	5:E:61:LEU:N	2.41	0.46
13:M:104:SER:OG	53:3:642:A:N3	2.48	0.46
14:N:96:GLU:O	14:N:100:ALA:N	2.41	0.46
16:P:97:ARG:HA	16:P:100:ASN:HD22	1.81	0.46
25:Y:60:GLN:HA	25:Y:63:LYS:HD2	1.98	0.46
29:d:49:ARG:NH1	51:1:674:G:OP2	2.48	0.46
51:1:1086:A:H1'	51:1:1103:A:H2	1.81	0.46
51:1:1695:G:H2'	51:1:1696:G:O4'	2.15	0.46
51:1:1841:U:H2'	51:1:1842:G:C8	2.51	0.46
53:3:37:U:H2'	53:3:38:G:H5'	1.98	0.46
53:3:250:A:O4'	53:3:252:U:H1'	2.15	0.46
53:3:556:C:O2'	53:3:557:G:H5'	2.16	0.46
53:3:1069:C:H4'	53:3:1192:C:O2	2.16	0.46
58:B1:220:ARG:HG2	58:B1:220:ARG:NH1	2.26	0.46
58:B1:375:GLU:HB3	59:B2:1245:ALA:HB3	1.97	0.46
59:B2:735:LYS:HA	59:B2:748:ILE:HG22	1.97	0.46
1:A:9:TYR:HE1	30:e:61:GLY:H	1.63	0.46
8:H:10:ARG:HA	8:H:13:ILE:HD11	1.97	0.46
12:L:79:VAL:O	12:L:79:VAL:HG12	2.16	0.46
14:N:16:ALA:HA	14:N:66:VAL:HA	1.98	0.46
17:Q:11:ARG:NH1	53:3:563:A:H2	2.13	0.46
20:T:50:HIS:ND1	53:3:667:G:H4'	2.31	0.46
34:j:7:LYS:HG2	34:j:10:THR:HG23	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:o:6:ALA:HA	39:o:9:ARG:HE	1.81	0.46
49:y:10:SER:HA	49:y:13:GLU:HB3	1.98	0.46
51:1:44:A:C2'	51:1:45:G:H5'	2.45	0.46
51:1:1661:G:O2'	51:1:1662:U:H5'	2.16	0.46
51:1:2695:U:H2'	51:1:2696:U:C6	2.51	0.46
53:3:478:A:H2'	53:3:479:U:C4'	2.46	0.46
53:3:1104:G:H2'	53:3:1105:A:O4'	2.16	0.46
57:A2:80:GLU:HG3	59:B2:694:ARG:HH22	1.81	0.46
65:a:193:LEU:O	65:a:197:LYS:N	2.42	0.46
10:J:161:GLU:HA	10:J:164:LEU:HD12	1.98	0.46
12:L:66:GLU:HA	12:L:69:ARG:HG3	1.96	0.46
15:O:36:VAL:HG22	15:O:38:GLY:H	1.80	0.46
27:b:71:ASP:HB3	27:b:118:GLY:HA2	1.98	0.46
51:1:742:A:O2'	51:1:743:A:H5'	2.15	0.46
51:1:824:U:H2'	51:1:825:A:O4'	2.15	0.46
51:1:940:G:H2'	51:1:941:A:H5''	1.97	0.46
51:1:1177:G:C2'	51:1:1178:C:H5''	2.45	0.46
51:1:1790:C:H2'	51:1:1791:A:C5	2.51	0.46
51:1:2190:G:H2'	51:1:2191:A:O4'	2.16	0.46
51:1:2741:A:H61	51:1:2763:G:H1'	1.80	0.46
53:3:10:A:H2'	53:3:11:G:C8	2.51	0.46
53:3:545:C:O2'	53:3:546:A:H5'	2.14	0.46
53:3:569:C:H4'	53:3:574:A:N7	2.31	0.46
53:3:1448:C:O2	53:3:1448:C:H2'	2.15	0.46
57:A1:35:PHE:HA	57:A1:38:THR:HG22	1.97	0.46
57:A1:59:VAL:HG22	57:A1:144:ILE:HA	1.97	0.46
58:B1:484:MET:CE	59:B2:1278:LEU:HD21	2.46	0.46
58:B1:1060:VAL:HG13	58:B1:1106:ILE:HG12	1.96	0.46
59:B2:902:LEU:HD11	59:B2:908:GLU:HB3	1.97	0.46
66:0:533:GLY:HA3	66:0:572:VAL:HG22	1.97	0.46
4:D:1:MET:HE3	4:D:3:ARG:HH21	1.80	0.45
7:G:115:ASP:OD1	7:G:115:ASP:N	2.42	0.45
13:M:46:GLU:O	13:M:61:THR:OG1	2.28	0.45
16:P:115:ILE:HD12	16:P:116:PRO:HD2	1.98	0.45
18:R:53:ASP:OD1	18:R:53:ASP:N	2.48	0.45
20:T:38:LEU:HD23	20:T:55:LEU:HD12	1.98	0.45
21:U:4:ILE:HD13	21:U:21:VAL:HA	1.98	0.45
29:d:131:THR:HA	29:d:134:LEU:HB3	1.98	0.45
48:x:16:ASN:HB2	48:x:24:THR:HB	1.97	0.45
51:1:107:G:H2'	51:1:108:G:C8	2.51	0.45
51:1:141:G:C8	51:1:142:A:H1'	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2680:U:O2'	51:1:2681:C:H5'	2.17	0.45
53:3:113:G:O2'	53:3:353:A:H4'	2.16	0.45
53:3:271:C:H2'	53:3:272:C:C6	2.51	0.45
53:3:323:U:H3	53:3:327:A:H62	1.64	0.45
53:3:684:U:H3	53:3:706:A:H61	1.63	0.45
53:3:994:A:H3'	53:3:994:A:OP2	2.15	0.45
53:3:1121:U:H2'	53:3:1122:U:C6	2.51	0.45
58:B1:105:ILE:HD12	58:B1:242:LEU:CD2	2.44	0.45
58:B1:506:VAL:HG23	58:B1:628:GLY:HA3	1.98	0.45
59:B2:103:VAL:HG12	59:B2:117:ILE:HG22	1.97	0.45
59:B2:230:PHE:HB2	59:B2:333:ILE:HB	1.97	0.45
63:5:6:G:H2'	63:5:7:A:C8	2.51	0.45
63:5:70:G:H2'	63:5:71:G:C8	2.51	0.45
5:E:7:ARG:NH1	51:1:243:U:OP2	2.49	0.45
15:O:15:HIS:CG	53:3:1152:A:H5'	2.51	0.45
16:P:71:ASP:OD1	16:P:71:ASP:N	2.43	0.45
22:V:21:VAL:HG22	22:V:44:HIS:HA	1.98	0.45
23:W:37:LYS:HE2	23:W:37:LYS:HB2	1.73	0.45
27:b:86:ARG:HB3	27:b:88:ALA:H	1.80	0.45
27:b:155:ARG:CZ	51:1:1818:U:C5	2.99	0.45
32:g:68:ARG:O	32:g:72:ILE:N	2.48	0.45
35:k:61:VAL:O	35:k:85:VAL:N	2.47	0.45
40:p:74:GLN:NE2	51:1:2683:C:O2'	2.49	0.45
51:1:2101:A:H2'	51:1:2102:G:C8	2.50	0.45
53:3:334:C:H2'	53:3:335:C:O4'	2.16	0.45
53:3:1198:G:H2'	53:3:1199:U:C6	2.51	0.45
57:A1:185:TYR:HA	57:A1:202:VAL:O	2.16	0.45
58:B1:1227:HIS:HA	58:B1:1230:THR:HG22	1.99	0.45
60:W0:25:ARG:NH1	60:W0:61:ASN:OD1	2.49	0.45
66:0:15:ILE:O	66:0:89:THR:OG1	2.35	0.45
66:0:520:ILE:HD12	66:0:576:ILE:HD11	1.99	0.45
6:F:28:SER:OG	6:F:29:ALA:N	2.50	0.45
10:J:88:HIS:HB3	10:J:134:ASN:HD21	1.81	0.45
10:J:156:ARG:NH1	13:M:98:LEU:O	2.49	0.45
11:K:18:VAL:HG13	11:K:19:PRO:HD3	1.97	0.45
28:c:61:THR:HB	28:c:63:PRO:HD2	1.96	0.45
42:r:49:ILE:HG22	42:r:54:VAL:HG22	1.98	0.45
48:x:57:VAL:HG12	48:x:61:LYS:HZ3	1.81	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
51:1:2751:G:O2'	51:1:2752:C:H5'	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:131:A:H2'	53:3:132:C:C6	2.51	0.45
53:3:433:G:H2'	53:3:434:U:C6	2.51	0.45
53:3:607:A:H2'	53:3:608:A:O4'	2.17	0.45
53:3:1289:A:H2'	53:3:1290:G:H5'	1.98	0.45
53:3:1316:G:H2'	53:3:1317:C:H5''	1.99	0.45
58:B1:128:LEU:HD21	58:B1:188:LEU:HB3	1.97	0.45
58:B1:141:PHE:CE2	58:B1:296:LYS:CB	2.94	0.45
58:B1:201:LEU:CD1	58:B1:224:LEU:HD12	2.47	0.45
58:B1:385:LEU:HD23	58:B1:390:LEU:HB2	1.97	0.45
58:B1:1219:ASP:O	58:B1:1223:LEU:HB2	2.15	0.45
12:L:140:VAL:O	12:L:144:ALA:N	2.46	0.45
15:O:47:GLU:OE2	15:O:69:THR:OG1	2.29	0.45
19:S:23:ARG:HH12	19:S:27:LYS:HB3	1.82	0.45
32:g:94:ILE:HD12	32:g:99:ILE:HG21	1.98	0.45
34:j:19:ASP:OD2	34:j:21:THR:OG1	2.29	0.45
36:l:18:ARG:NE	51:1:1249:U:C5	2.79	0.45
51:1:393:C:H2'	51:1:394:C:H6	1.81	0.45
51:1:514:A:N3	51:1:581:C:O2'	2.45	0.45
51:1:817:C:O2'	51:1:839:U:H5''	2.16	0.45
51:1:912:C:O2'	51:1:913:U:H5'	2.15	0.45
51:1:2123:G:N3	51:1:2176:A:N6	2.65	0.45
51:1:2226:C:H2'	51:1:2227:A:O4'	2.17	0.45
51:1:2457:U:O2'	51:1:2458:G:H5'	2.15	0.45
51:1:2643:G:O2'	51:1:2644:G:H5'	2.16	0.45
53:3:280:C:H5''	53:3:281:G:OP2	2.17	0.45
53:3:782:A:O3'	53:3:1515:G:H4'	2.16	0.45
55:8:13:DT:C6	58:B1:791:ALA:HA	2.51	0.45
58:B1:75:TYR:CD2	58:B1:75:TYR:O	2.70	0.45
58:B1:213:LYS:HA	58:B1:213:LYS:HE3	1.99	0.45
15:O:59:LYS:HD3	53:3:972:C:O3'	2.17	0.45
24:X:71:GLY:HA3	53:3:1320:C:C2	2.51	0.45
27:b:6:LYS:HD2	27:b:7:PRO:HD2	1.99	0.45
28:c:194:PRO:HA	51:1:2680:U:C5'	2.46	0.45
31:f:28:LYS:HE3	31:f:28:LYS:HB2	1.86	0.45
31:f:88:LEU:HB3	31:f:128:THR:HA	1.97	0.45
40:p:48:ALA:N	40:p:59:THR:OG1	2.50	0.45
45:u:5:ARG:NH1	51:1:84:A:H5''	2.31	0.45
51:1:753:A:H2'	51:1:754:U:C6	2.52	0.45
51:1:1979:U:O5'	51:1:1979:U:H6	1.99	0.45
51:1:2041:U:H2'	51:1:2042:A:H8	1.81	0.45
51:1:2599:G:H2'	51:1:2600:A:H8	1.80	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:2:30:C:H2'	52:2:31:C:C5'	2.47	0.45
53:3:962:C:H1'	53:3:1201:A:C6	2.51	0.45
56:9:12:DC:H3'	58:B1:47:ARG:HH12	1.82	0.45
58:B1:43:THR:HG22	58:B1:57:PHE:HE1	1.80	0.45
58:B1:1158:GLU:HA	58:B1:1223:LEU:HD21	1.99	0.45
59:B2:557:ARG:NH2	59:B2:607:SER:O	2.50	0.45
63:5:27:G:H1	63:5:43:C:H42	1.64	0.45
66:0:171:LEU:HD11	66:0:218:TRP:HD1	1.82	0.45
66:0:618:LYS:N	66:0:683:GLU:O	2.49	0.45
15:O:36:VAL:HA	15:O:76:ILE:HA	1.97	0.45
16:P:114:PRO:O	26:Z:28:LEU:HD21	2.17	0.45
31:f:91:VAL:HG21	51:1:2657:A:H4'	1.97	0.45
31:f:94:ARG:HA	31:f:127:GLN:HB2	1.99	0.45
33:i:126:ARG:O	33:i:130:GLY:N	2.50	0.45
40:p:28:LYS:HB2	40:p:82:SER:H	1.81	0.45
51:1:1337:G:O2'	51:1:1338:G:H5'	2.17	0.45
53:3:520:A:H62	53:3:529:G:N2	2.11	0.45
53:3:1096:C:H2'	53:3:1097:C:H6	1.80	0.45
2:B:49:ARG:NH2	51:1:2884:U:H1'	2.32	0.45
8:H:58:ARG:HB3	8:H:63:ILE:HB	1.98	0.45
11:K:12:PRO:O	11:K:15:SER:OG	2.32	0.45
15:O:85:ASP:OD2	58:B1:87:LYS:NZ	2.50	0.45
18:R:107:THR:HG21	53:3:1307:U:H4'	1.99	0.45
19:S:2:LYS:HG2	19:S:4:SER:H	1.81	0.45
30:e:35:LEU:HD22	30:e:151:LEU:HD21	1.99	0.45
30:e:91:ARG:HA	30:e:95:MET:HG2	1.99	0.45
33:i:52:LEU:HD13	33:i:77:VAL:HG13	1.97	0.45
34:j:57:LEU:HD11	34:j:130:HIS:HD2	1.82	0.45
45:u:65:GLN:CD	51:1:328:U:H4'	2.42	0.45
51:1:224:U:H2'	51:1:225:C:O4'	2.17	0.45
51:1:623:C:H2'	51:1:624:C:C6	2.52	0.45
51:1:1024:G:O5'	51:1:1025:G:H5''	2.16	0.45
51:1:1044:C:O5'	51:1:1044:C:H6	2.00	0.45
51:1:1087:G:H1	51:1:1102:C:H42	1.64	0.45
51:1:1954:G:H21	51:1:1956:U:H3	1.65	0.45
52:2:6:G:O2'	52:2:7:G:H5'	2.17	0.45
53:3:144:G:H2'	53:3:145:G:O4'	2.16	0.45
53:3:1147:C:H2'	53:3:1148:U:C6	2.52	0.45
57:A1:231:PHE:O	57:A2:218:ARG:NH1	2.49	0.45
58:B1:375:GLU:O	59:B2:1247:SER:HB3	2.16	0.45
63:5:22:G:H2'	63:5:23:A:C8	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
66:0:320:LEU:HD12	66:0:320:LEU:HA	1.85	0.45
1:A:41:HIS:HD2	30:e:108:PRO:HA	1.81	0.45
9:I:145:ARG:HB3	9:I:148:ALA:HB3	1.99	0.45
11:K:45:ARG:N	11:K:57:ALA:O	2.44	0.45
12:L:57:GLU:HG3	12:L:58:LEU:HD12	1.99	0.45
14:N:28:VAL:HG13	14:N:63:TYR:HA	1.99	0.45
19:S:61:ASN:HB3	19:S:72:PHE:CE2	2.52	0.45
29:d:43:THR:O	51:1:38:A:H1'	2.17	0.45
42:r:38:VAL:HG21	42:r:57:GLY:HA3	1.97	0.45
43:s:25:ARG:NE	43:s:74:ILE:O	2.45	0.45
43:s:72:THR:OG1	43:s:73:LYS:NZ	2.42	0.45
45:u:88:ASP:OD1	45:u:88:ASP:N	2.47	0.45
51:1:708:G:O2'	51:1:709:U:H5'	2.17	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
51:1:960:A:H5''	51:1:961:C:OP1	2.17	0.45
51:1:1300:G:N7	51:1:1626:A:H2'	2.32	0.45
51:1:1432:G:H2'	51:1:1433:A:C8	2.52	0.45
51:1:1565:C:O2'	51:1:1566:A:H2'	2.16	0.45
51:1:1786:A:O2'	51:1:1787:A:H5'	2.17	0.45
51:1:1792:G:H1	51:1:1827:U:H3	1.65	0.45
51:1:2099:U:H2'	51:1:2100:G:C8	2.51	0.45
51:1:2560:A:O2'	51:1:2561:U:H5'	2.17	0.45
51:1:2869:G:H2'	51:1:2870:C:O4'	2.16	0.45
53:3:347:G:H2'	53:3:348:G:O4'	2.17	0.45
53:3:384:G:H2'	53:3:385:C:C6	2.52	0.45
53:3:437:U:C2'	53:3:438:U:H5'	2.46	0.45
53:3:771:G:H2'	53:3:772:U:C6	2.51	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	1.65	0.45
53:3:1255:G:H1	53:3:1282:C:H42	1.64	0.45
58:B1:343:LEU:HD11	58:B1:1324:SER:HB3	1.97	0.45
58:B1:388:ARG:HG2	58:B1:388:ARG:NH1	2.32	0.45
63:5:8:U:H2'	63:5:13:C:H41	1.81	0.45
8:H:153:SER:O	8:H:196:GLY:N	2.50	0.45
9:I:96:ARG:HG2	9:I:133:SER:HA	1.99	0.45
20:T:19:ASN:O	53:3:750:C:H1'	2.16	0.45
27:b:212:TRP:NE1	51:1:1566:A:O4'	2.50	0.45
29:d:134:LEU:HD11	29:d:161:ALA:HB2	1.99	0.45
31:f:41:GLU:N	31:f:52:GLY:O	2.49	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:g:98:ASP:O	32:g:102:ALA:N	2.49	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
35:k:62:VAL:HA	35:k:84:CYS:HA	1.99	0.45
36:l:135:ILE:HG23	36:l:140:GLY:HA3	1.99	0.45
39:o:94:ARG:NH2	39:o:98:GLN:OE1	2.50	0.45
51:1:927:A:H2'	51:1:928:A:O4'	2.17	0.45
51:1:1573:G:H2'	51:1:1574:C:O4'	2.17	0.45
51:1:2127:G:H2'	51:1:2128:G:C8	2.52	0.45
51:1:2194:U:H2'	51:1:2195:U:C6	2.52	0.45
51:1:2757:A:H2'	51:1:2757:A:N3	2.32	0.45
53:3:768:A:C2	53:3:1512:U:H4'	2.52	0.45
53:3:1098:C:H2'	53:3:1099:G:O4'	2.17	0.45
57:A1:68:TYR:HE1	57:A1:79:LEU:HD13	1.82	0.45
58:B1:352:ARG:CD	59:B2:1268:GLN:NE2	2.67	0.45
58:B1:515:ARG:NH2	58:B1:718:SER:O	2.48	0.45
58:B1:847:ASP:N	58:B1:847:ASP:OD1	2.49	0.45
59:B2:176:ILE:HD11	59:B2:428:VAL:HG21	1.98	0.45
62:NG:135:ARG:O	62:NG:178:VAL:HA	2.16	0.45
65:a:211:LYS:HE2	65:a:211:LYS:HB2	1.58	0.45
66:0:618:LYS:H	66:0:684:PHE:HA	1.82	0.45
66:0:643:LYS:HE3	66:0:655:HIS:HB3	1.99	0.45
2:B:6:LYS:HZ3	51:1:1262:A:H2	1.64	0.45
10:J:72:ASN:OD1	10:J:72:ASN:N	2.50	0.45
14:N:113:LYS:NZ	53:3:1368:A:OP2	2.39	0.45
17:Q:57:THR:HG21	53:3:362:G:H5''	1.99	0.45
29:d:37:ALA:HB1	29:d:94:GLN:H	1.82	0.45
43:s:13:SER:OG	43:s:14:ALA:N	2.50	0.45
51:1:191:A:H2'	51:1:192:C:H6	1.81	0.45
51:1:586:A:N1	51:1:809:G:O2'	2.45	0.45
51:1:598:U:H2'	51:1:599:A:C8	2.52	0.45
51:1:885:C:H2'	51:1:891:G:H22	1.83	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
51:1:1429:G:C2	51:1:1568:G:C2	3.05	0.45
51:1:2737:G:H2'	51:1:2738:A:C8	2.52	0.45
53:3:757:U:H2'	53:3:758:C:H5'	1.99	0.45
53:3:962:C:H1'	53:3:1201:A:N1	2.32	0.45
53:3:973:G:H2'	53:3:974:A:C8	2.52	0.45
57:A2:294:ASN:HA	61:NA:464:ILE:N	2.28	0.45
58:B1:115:TRP:HB3	58:B1:1333:THR:CG2	2.46	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:0:75:MET:HG3	66:0:279:LEU:HD11	1.99	0.45
5:E:15:LYS:HA	5:E:21:PHE:HA	1.99	0.44
11:K:11:HIS:HB3	11:K:14:GLN:HB2	1.99	0.44
24:X:46:LEU:HD12	24:X:48:ILE:HD11	1.99	0.44
27:b:57:HIS:CE1	51:1:1567:G:H4'	2.52	0.44
30:e:35:LEU:HB2	30:e:88:VAL:HG12	1.98	0.44
35:k:56:ASP:N	35:k:56:ASP:OD1	2.49	0.44
40:p:105:LYS:HG2	53:3:1464:U:OP1	2.17	0.44
51:1:91:A:H8	51:1:91:A:OP1	1.99	0.44
51:1:162:U:H6	51:1:163:C:H5	1.64	0.44
51:1:252:G:H2'	51:1:253:C:H6	1.81	0.44
51:1:397:U:O5'	51:1:397:U:H6	2.00	0.44
51:1:776:G:C8	51:1:793:A:C2	3.05	0.44
51:1:864:G:H2'	51:1:865:C:O4'	2.16	0.44
51:1:1276:A:H61	51:1:1294:U:H3	1.65	0.44
51:1:1614:A:C2'	51:1:1615:C:H5'	2.46	0.44
53:3:806:C:H2'	53:3:807:A:C8	2.52	0.44
53:3:1361:G:H2'	53:3:1362:A:O4'	2.16	0.44
58:B1:850:LYS:HB3	58:B1:855:ASP:HB2	1.99	0.44
62:NG:161:SER:CB	62:NG:170:PRO:HA	2.47	0.44
63:5:49:C:H2'	63:5:50:U:C6	2.52	0.44
63:5:69:G:H2'	63:5:70:G:C8	2.52	0.44
66:0:97:ILE:HD13	66:0:412:PRO:HG3	2.00	0.44
66:0:498:VAL:CG1	66:0:522:MET:HE3	2.43	0.44
3:C:45:HIS:ND1	51:1:2372:U:H4'	2.32	0.44
9:I:47:LEU:HD22	53:3:510:A:OP1	2.17	0.44
17:Q:120:ARG:HG2	53:3:37:U:C5'	2.46	0.44
21:U:26:ASN:HD21	21:U:31:ARG:N	2.15	0.44
25:Y:4:LYS:NZ	53:3:332:G:P	2.91	0.44
27:b:73:ILE:HG12	51:1:1490:A:H2	1.79	0.44
27:b:84:PRO:HG3	51:1:1568:G:OP1	2.16	0.44
30:e:134:GLN:NE2	30:e:147:ARG:O	2.41	0.44
37:m:27:SER:H	37:m:104:GLU:CD	2.24	0.44
39:o:10:ARG:HE	39:o:10:ARG:HB2	1.61	0.44
40:p:25:VAL:HG21	40:p:83:ILE:HG22	1.99	0.44
49:y:38:GLN:O	51:1:95:A:H4'	2.16	0.44
50:z:37:ARG:NH1	51:1:928:A:O2'	2.50	0.44
51:1:468:G:C2'	51:1:469:G:H5'	2.46	0.44
51:1:740:C:H5'	51:1:740:C:C6	2.46	0.44
51:1:777:G:N7	51:1:793:A:C2	2.78	0.44
51:1:1697:G:H3'	51:1:1698:A:C5'	2.45	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1954:G:N2	51:1:1956:U:H3	2.15	0.44
51:1:2066:C:H2'	51:1:2067:G:H8	1.81	0.44
53:3:622:A:H2'	53:3:623:C:H5'	1.99	0.44
58:B1:213:LYS:HE3	58:B1:213:LYS:CA	2.47	0.44
58:B1:434:ILE:HD11	59:B2:1274:GLU:HG3	2.00	0.44
58:B1:472:LEU:CD1	59:B2:1294:LYS:HG2	2.47	0.44
58:B1:478:LEU:HD21	60:W0:47:THR:HG23	1.99	0.44
66:0:73:SER:O	66:0:73:SER:OG	2.29	0.44
10:J:50:GLY:HA3	10:J:62:ALA:HB2	1.99	0.44
11:K:53:LYS:HD3	11:K:53:LYS:HA	1.75	0.44
16:P:52:ARG:HA	16:P:52:ARG:HD3	1.85	0.44
17:Q:11:ARG:HH11	53:3:563:A:H2	1.64	0.44
18:R:94:LEU:HD12	18:R:95:PRO:HD2	2.00	0.44
23:W:35:SER:OG	23:W:37:LYS:NZ	2.37	0.44
38:n:73:ASN:O	38:n:77:ALA:N	2.50	0.44
45:u:7:ASP:OD1	45:u:7:ASP:N	2.46	0.44
48:x:31:ASN:ND2	48:x:52:ALA:HB3	2.32	0.44
51:1:1130:U:C5	51:1:2025:C:H5''	2.53	0.44
51:1:1545:A:H2'	51:1:1546:G:O4'	2.17	0.44
51:1:2069:G:H2'	51:1:2070:A:H8	1.82	0.44
51:1:2073:C:O5'	51:1:2073:C:H6	1.99	0.44
51:1:2102:G:H1	51:1:2187:U:H3	1.65	0.44
52:2:16:G:N2	52:2:69:G:H1'	2.31	0.44
53:3:20:U:O2'	53:3:21:G:H5'	2.17	0.44
53:3:925:G:H1'	53:3:1502:A:C4	2.53	0.44
55:8:1:DC:H2''	55:8:2:DC:C6	2.51	0.44
58:B1:395:LYS:NZ	58:B1:399:LYS:HE2	2.32	0.44
58:B1:1357:ILE:HG22	58:B1:1359:ALA:H	1.82	0.44
66:0:173:ILE:HD13	66:0:173:ILE:HA	1.90	0.44
66:0:600:ALA:HA	66:0:603:GLU:HB2	1.98	0.44
8:H:63:ILE:HG23	8:H:98:ALA:HA	1.99	0.44
12:L:91:ARG:O	12:L:92:PRO:C	2.59	0.44
14:N:6:TYR:OH	53:3:1148:U:H5'	2.16	0.44
22:V:64:ARG:CB	53:3:130:A:H8	2.31	0.44
27:b:106:PRO:HD2	27:b:109:LEU:HD22	1.99	0.44
29:d:153:LEU:HD11	29:d:158:PHE:HB2	1.98	0.44
34:j:81:ILE:HG21	51:1:2514:U:H4'	1.99	0.44
39:o:18:LEU:HD23	39:o:21:LEU:HD12	1.99	0.44
51:1:368:A:C2'	51:1:369:U:H5'	2.47	0.44
51:1:878:A:H3'	51:1:879:G:H8	1.82	0.44
51:1:2007:U:O5'	51:1:2007:U:H6	2.01	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2723:C:H2'	51:1:2724:U:O4'	2.17	0.44
52:2:118:C:C2'	52:2:119:A:H4'	2.33	0.44
53:3:563:A:H2'	53:3:563:A:N3	2.32	0.44
53:3:971:G:H4'	53:3:972:C:H5''	2.00	0.44
53:3:1312:G:H2'	53:3:1313:U:C6	2.52	0.44
58:B1:62:PHE:CD1	58:B1:62:PHE:N	2.85	0.44
58:B1:161:THR:H	58:B1:164:GLN:HB2	1.82	0.44
59:B2:11:ILE:HG22	59:B2:1172:LEU:HD11	1.99	0.44
59:B2:546:GLU:H	59:B2:546:GLU:HG3	1.53	0.44
66:0:11:ARG:HG3	66:0:283:ILE:HA	1.99	0.44
66:0:119:VAL:HG21	66:0:162:LEU:HD11	1.99	0.44
7:G:20:ARG:HD2	53:3:831:A:H5''	1.98	0.44
15:O:70:HIS:HD2	15:O:72:ARG:HH22	1.64	0.44
37:m:42:THR:N	37:m:45:GLN:OE1	2.40	0.44
50:z:19:HIS:CD2	50:z:50:VAL:HG12	2.52	0.44
51:1:754:U:O5'	51:1:754:U:H6	2.01	0.44
51:1:1147:A:O2'	51:1:1148:U:H5'	2.17	0.44
51:1:1656:C:H2'	51:1:1657:U:H6	1.82	0.44
51:1:1747:U:H2'	51:1:1748:C:C6	2.52	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	2.52	0.44
53:3:946:A:H4'	53:3:1333:A:O2'	2.17	0.44
53:3:994:A:H61	53:3:1047:G:C4'	2.30	0.44
57:A1:212:ASP:OD1	57:A1:212:ASP:N	2.48	0.44
58:B1:67:ASP:OD1	58:B1:67:ASP:O	2.35	0.44
58:B1:770:LEU:HD13	59:B2:618:GLN:CD	2.42	0.44
58:B1:800:LEU:HD12	58:B1:800:LEU:HA	1.79	0.44
58:B1:1033:GLY:HA3	58:B1:1081:VAL:O	2.18	0.44
58:B1:1108:GLN:HG3	58:B1:1109:LEU:HD12	1.99	0.44
59:B2:24:VAL:HG11	59:B2:704:MET:HE1	1.99	0.44
59:B2:1246:ARG:HH11	59:B2:1266:GLY:HA2	1.82	0.44
64:6:70:G:H2'	64:6:71:C:C6	2.52	0.44
66:0:13:ILE:HG22	66:0:86:ILE:HA	1.98	0.44
12:L:34:LYS:NZ	53:3:1289:A:C2	2.86	0.44
12:L:114:SER:O	12:L:118:ARG:N	2.38	0.44
14:N:129:ARG:NH1	64:6:32:C:OP2	2.50	0.44
32:g:27:ARG:NH2	48:x:55:MET:HB3	2.32	0.44
37:m:81:ARG:NH1	51:1:2251:G:OP1	2.51	0.44
51:1:233:A:C2'	51:1:234:U:H5'	2.48	0.44
51:1:324:A:N6	51:1:338:G:H21	2.10	0.44
51:1:388:G:H2'	51:1:390:U:H5	1.81	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1057:A:H5''	51:1:1058:U:O2	2.17	0.44
51:1:2524:G:C3'	51:1:2525:G:H5''	2.48	0.44
53:3:253:A:O4'	53:3:276:G:H1'	2.18	0.44
53:3:272:C:H2'	53:3:273:U:H6	1.83	0.44
53:3:369:G:N2	53:3:393:A:H1'	2.33	0.44
53:3:596:A:H61	53:3:644:U:H3	1.66	0.44
53:3:777:A:C2	53:3:778:G:H1'	2.52	0.44
58:B1:33:TRP:HZ2	59:B2:1336:ASN:OD1	2.00	0.44
58:B1:245:LEU:CG	58:B1:246:PRO:HD2	2.47	0.44
58:B1:926:PRO:HB2	58:B1:1241:TYR:HE1	1.82	0.44
12:L:67:ASN:HB3	12:L:129:ASN:HD21	1.83	0.44
17:Q:48:LEU:HD12	17:Q:48:LEU:HA	1.85	0.44
19:S:55:SER:OG	19:S:57:SER:OG	2.30	0.44
28:c:2:ILE:HG12	28:c:90:PHE:HZ	1.82	0.44
28:c:120:GLY:H	28:c:123:LYS:HB2	1.82	0.44
30:e:135:ILE:HA	30:e:140:ILE:HD11	1.99	0.44
31:f:62:ALA:HA	51:1:2748:A:O2'	2.18	0.44
33:i:94:LYS:HD3	33:i:94:LYS:HA	1.72	0.44
39:o:90:VAL:HG23	39:o:117:PHE:HB3	2.00	0.44
41:q:25:GLY:O	41:q:29:ARG:NH1	2.50	0.44
41:q:51:GLN:O	41:q:55:GLN:N	2.48	0.44
47:w:58:LYS:HD3	51:1:2366:A:H4'	1.99	0.44
51:1:146:A:H2'	51:1:147:C:H6	1.81	0.44
51:1:435:C:H2'	51:1:436:C:C5'	2.37	0.44
51:1:514:A:O2'	51:1:515:A:H5'	2.17	0.44
51:1:755:U:H2'	51:1:756:A:C8	2.52	0.44
51:1:1541:C:H2'	51:1:1542:U:O4'	2.18	0.44
51:1:1913:A:H61	53:3:1493:A:H2'	1.83	0.44
51:1:2073:C:O2'	51:1:2074:U:H5'	2.17	0.44
51:1:2125:G:C5'	65:a:39:VAL:HG22	2.47	0.44
51:1:2845:U:H2'	51:1:2846:G:H8	1.83	0.44
53:3:505:G:C6	53:3:535:A:C2	3.05	0.44
53:3:570:G:H5'	53:3:820:U:O4'	2.18	0.44
53:3:894:G:H2'	53:3:895:G:C8	2.53	0.44
53:3:1508:A:H61	53:3:1527:U:H3	1.66	0.44
58:B1:288:PRO:HG2	58:B1:291:ILE:HG13	2.00	0.44
59:B2:674:ASP:OD2	59:B2:1070:HIS:ND1	2.50	0.44
65:a:203:GLN:HG2	65:a:205:LYS:H	1.82	0.44
8:H:68:HIS:HE2	8:H:105:VAL:HB	1.81	0.44
11:K:47:LEU:HD21	11:K:54:LEU:O	2.17	0.44
14:N:45:MET:HA	14:N:48:ARG:HH21	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:25:SER:OG	16:P:28:ASN:N	2.48	0.44
18:R:70:ARG:O	18:R:73:SER:OG	2.36	0.44
28:c:197:THR:HG23	51:1:2820:A:C6	2.52	0.44
29:d:5:LEU:HG	29:d:120:VAL:HG13	2.00	0.44
34:j:80:HIS:CD2	51:1:2642:G:H5'	2.53	0.44
39:o:55:GLU:OE2	52:2:116:G:H5''	2.17	0.44
47:w:56:PHE:HE1	47:w:58:LYS:HE2	1.83	0.44
51:1:298:G:C2	51:1:339:U:H5	2.36	0.44
51:1:537:G:H22	51:1:555:G:H2'	1.83	0.44
51:1:728:G:H3'	51:1:729:G:H5'	2.00	0.44
51:1:974:G:O2'	51:1:989:G:N2	2.51	0.44
51:1:974:G:C6	51:1:1186:G:C6	3.06	0.44
51:1:1308:A:N6	51:1:1608:A:H61	2.16	0.44
51:1:2270:A:H2'	51:1:2271:G:O4'	2.18	0.44
53:3:152:A:H2'	53:3:153:C:H5'	1.99	0.44
53:3:240:G:H2'	53:3:241:G:C8	2.53	0.44
53:3:1134:G:H1	53:3:1140:C:H42	1.66	0.44
53:3:1475:G:C2	53:3:1476:A:H1'	2.52	0.44
58:B1:76:LYS:NZ	58:B1:76:LYS:HB3	2.32	0.44
58:B1:804:ALA:HB2	58:B1:1256:ILE:CD1	2.48	0.44
59:B2:557:ARG:HB3	59:B2:587:LEU:HD13	2.00	0.44
66:0:338:VAL:HG13	66:0:380:GLY:H	1.83	0.44
66:0:499:THR:CG2	66:0:500:ASP:H	2.23	0.44
66:0:607:LYS:HE2	66:0:607:LYS:HB2	1.83	0.44
5:E:44:ARG:NH2	51:1:2349:G:OP1	2.48	0.44
15:O:68:ARG:HD3	15:O:68:ARG:HA	1.68	0.44
27:b:227:VAL:HG11	51:1:784:G:C2	2.52	0.44
34:j:41:LYS:HB2	34:j:41:LYS:HE3	1.86	0.44
34:j:134:ALA:HB1	51:1:2898:U:O2	2.17	0.44
37:m:16:ARG:HD3	37:m:16:ARG:HA	1.90	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
51:1:152:A:H2'	51:1:153:U:C6	2.53	0.44
51:1:578:G:H21	51:1:1252:G:N2	2.16	0.44
51:1:1086:A:H3'	51:1:1086:A:N3	2.33	0.44
51:1:1093:G:H22	51:1:1097:U:H3'	1.82	0.44
51:1:1368:G:H2'	51:1:1369:G:C8	2.51	0.44
51:1:2703:C:H2'	51:1:2704:C:H6	1.82	0.44
53:3:37:U:C2'	53:3:38:G:H5'	2.48	0.44
53:3:68:G:H2'	53:3:69:G:O4'	2.17	0.44
53:3:182:A:N1	53:3:224:U:H5'	2.33	0.44

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	0.44
59:B2:811:ASN:ND2	59:B2:1098:LEU:O	2.51	0.44
3:C:33:LEU:HD21	51:1:2286:G:C5	2.53	0.43
6:F:1:MET:N	51:1:2526:G:H1'	2.32	0.43
10:J:158:LYS:HD3	10:J:158:LYS:HA	1.73	0.43
11:K:3:HIS:ND1	11:K:65:GLU:HB2	2.33	0.43
13:M:45:ILE:HG12	13:M:60:LEU:HD23	2.00	0.43
14:N:47:VAL:HG12	14:N:78:ILE:HG21	2.00	0.43
21:U:13:LYS:CD	53:3:392:C:H5'	2.48	0.43
26:Z:66:ARG:O	53:3:1088:G:O2'	2.36	0.43
34:j:12:LYS:HA	34:j:12:LYS:HD2	1.78	0.43
34:j:93:ILE:HD12	34:j:93:ILE:HA	1.72	0.43
42:r:1:MET:N	42:r:42:ALA:O	2.42	0.43
45:u:27:VAL:HA	45:u:33:VAL:HG13	1.99	0.43
51:1:138:U:H3'	51:1:139:U:H5'	1.99	0.43
51:1:2599:G:H2'	51:1:2600:A:C8	2.53	0.43
53:3:563:A:H5'	53:3:566:G:N2	2.33	0.43
53:3:635:A:H2'	53:3:636:U:C6	2.53	0.43
53:3:675:A:C2	53:3:676:A:H1'	2.52	0.43
53:3:1042:A:H2'	53:3:1043:G:H4'	2.00	0.43
53:3:1057:G:H2'	53:3:1058:G:O4'	2.18	0.43
58:B1:111:THR:HG21	58:B1:303:VAL:HB	2.00	0.43
59:B2:646:SER:OG	59:B2:647:ARG:N	2.51	0.43
59:B2:829:THR:HG23	59:B2:1059:ARG:HG2	2.00	0.43
63:5:17:C:H6	63:5:17:C:H2'	1.69	0.43
7:G:23:ASN:HA	7:G:24:PRO:HD3	1.85	0.43
9:I:33:ILE:HG23	9:I:34:GLU:HG2	1.99	0.43
9:I:200:VAL:HG11	10:J:103:GLY:HA2	2.00	0.43
14:N:53:LEU:HD12	14:N:54:VAL:HG13	2.00	0.43
14:N:125:GLN:HG3	53:3:1232:U:H5''	1.99	0.43
20:T:60:SER:HB2	53:3:581:G:C5'	2.48	0.43
26:Z:24:LYS:HA	26:Z:24:LYS:HD3	1.80	0.43
27:b:209:ALA:HA	27:b:212:TRP:CE2	2.54	0.43
28:c:5:VAL:HG22	28:c:202:ILE:HG12	2.00	0.43
29:d:129:PRO:HG3	29:d:156:ASN:HA	2.00	0.43
41:q:32:ARG:HB2	51:1:581:C:OP1	2.18	0.43
51:1:252:G:H2'	51:1:253:C:C6	2.53	0.43
51:1:861:A:H2'	51:1:862:G:O4'	2.18	0.43
51:1:1028:A:C2	51:1:2487:G:H1'	2.52	0.43
51:1:1943:U:OP1	51:1:1943:U:C6	2.71	0.43
51:1:2183:A:H2'	51:1:2184:A:C8	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2248:C:H3'	51:1:2249:U:H6	1.82	0.43
52:2:115:A:H2'	52:2:116:G:C8	2.53	0.43
57:A1:78:ILE:HA	57:A1:81:ILE:HG22	2.00	0.43
58:B1:126:LEU:H	58:B1:126:LEU:HG	1.67	0.43
58:B1:128:LEU:CD2	58:B1:188:LEU:HB3	2.47	0.43
58:B1:978:ARG:HD3	58:B1:999:TYR:H	1.83	0.43
63:5:63:G:H2'	63:5:64:A:C8	2.53	0.43
66:0:498:VAL:HG22	66:0:499:THR:N	2.33	0.43
7:G:33:ALA:HB3	7:G:37:VAL:HB	1.99	0.43
16:P:118:ASN:OD1	53:3:718:A:H5'	2.18	0.43
20:T:80:LEU:O	20:T:84:LEU:N	2.42	0.43
38:n:36:THR:HG22	51:1:1278:C:OP1	2.18	0.43
48:x:9:LYS:HB3	48:x:30:PRO:CB	2.48	0.43
51:1:812:C:H1'	51:1:1250:G:C2	2.53	0.43
51:1:1020:A:C1'	51:1:1021:A:OP2	2.61	0.43
51:1:1191:G:H2'	51:1:1192:G:C8	2.51	0.43
51:1:1744:A:H3'	51:1:1745:A:H8	1.83	0.43
51:1:2065:C:H2'	51:1:2066:C:C6	2.53	0.43
51:1:2102:G:H2'	51:1:2103:C:O4'	2.18	0.43
51:1:2762:C:H2'	51:1:2763:G:H5'	2.00	0.43
53:3:599:C:H2'	53:3:600:A:C8	2.53	0.43
53:3:964:A:H2'	53:3:965:U:H5'	2.00	0.43
53:3:969:A:H2'	53:3:970:C:O4'	2.18	0.43
53:3:1252:A:H2'	53:3:1253:G:O4'	2.19	0.43
53:3:1489:G:H2'	53:3:1490:U:C6	2.53	0.43
55:8:3:DC:N1	55:8:4:DT:H72	2.34	0.43
55:8:16:DT:H2'	55:8:17:DC:C6	2.52	0.43
58:B1:58:CYS:SG	58:B1:60:ARG:HG2	2.58	0.43
58:B1:824:PRO:HD3	58:B1:835:LEU:HD12	2.00	0.43
58:B1:1079:LYS:HD3	58:B1:1098:GLN:HB3	1.99	0.43
59:B2:300:ASP:OD1	59:B2:313:ALA:N	2.52	0.43
59:B2:998:LEU:HG	59:B2:1011:LEU:HB3	1.99	0.43
66:0:73:SER:HB2	66:0:81:PRO:HG3	2.00	0.43
66:0:112:VAL:HG12	66:0:140:PHE:HB3	2.00	0.43
66:0:159:LYS:HG3	66:0:166:PRO:HD2	2.00	0.43
66:0:423:LYS:HA	66:0:482:ASN:HD21	1.82	0.43
8:H:66:THR:HA	8:H:101:ASN:HB2	1.99	0.43
10:J:123:LEU:HD22	53:3:7:A:H2'	1.99	0.43
12:L:82:SER:HB3	12:L:83:THR:H	1.60	0.43
23:W:58:ILE:O	23:W:62:ARG:N	2.49	0.43
24:X:38:THR:HG23	24:X:69:LYS:HD3	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:d:136:GLN:HA	29:d:139:LYS:HB2	1.99	0.43
31:f:9:VAL:HA	31:f:48:THR:HA	2.01	0.43
33:i:128:ILE:HA	33:i:131:THR:HG22	2.00	0.43
37:m:68:PHE:CE2	51:1:871:U:H5''	2.53	0.43
37:m:71:LYS:HD3	37:m:72:PRO:HD2	2.00	0.43
51:1:824:U:H1'	51:1:2358:A:N7	2.34	0.43
51:1:1135:C:O2	51:1:1135:C:H2'	2.18	0.43
51:1:1177:G:H2'	51:1:1178:C:C5'	2.48	0.43
51:1:1412:U:H2'	51:1:1413:A:O4'	2.18	0.43
51:1:2259:U:C2	51:1:2427:C:C4	3.06	0.43
51:1:2564:A:C2	51:1:2647:U:H4'	2.54	0.43
51:1:2638:G:H22	51:1:2775:G:H2'	1.83	0.43
53:3:296:U:H2'	53:3:297:G:O4'	2.19	0.43
53:3:1095:U:OP1	53:3:1108:G:N2	2.52	0.43
53:3:1233:G:O2'	53:3:1365:G:H5''	2.18	0.43
53:3:1382:C:H2'	53:3:1383:C:C5	2.54	0.43
55:8:12:DG:OP1	58:B1:795:TYR:CE1	2.71	0.43
58:B1:375:GLU:HB3	59:B2:1245:ALA:CB	2.48	0.43
58:B1:568:SER:HB3	58:B1:570:LYS:NZ	2.34	0.43
58:B1:1026:PRO:HB2	58:B1:1028:ILE:HG23	2.00	0.43
63:5:13:C:H42	63:5:46:G:N2	2.16	0.43
66:0:634:ASP:O	66:0:638:ARG:NH1	2.52	0.43
7:G:136:ARG:O	7:G:140:LEU:N	2.47	0.43
16:P:25:SER:HG	16:P:28:ASN:N	2.16	0.43
31:f:85:LYS:HE3	31:f:131:VAL:HG22	2.00	0.43
31:f:171:LYS:NZ	51:1:2529:G:OP2	2.40	0.43
34:j:130:HIS:HB2	34:j:132:HIS:HD2	1.84	0.43
36:l:37:GLY:H	36:l:41:ARG:HH22	1.66	0.43
38:n:107:ASN:HD22	51:1:2009:A:C4'	2.31	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
51:1:330:A:H8	51:1:1210:G:C5	2.36	0.43
51:1:395:U:H2'	51:1:396:G:H8	1.80	0.43
51:1:728:G:O2'	51:1:730:A:H8	2.01	0.43
51:1:1428:C:C5	51:1:1569:A:H5''	2.53	0.43
51:1:1630:A:H2'	51:1:1631:G:H5'	2.00	0.43
51:1:2553:G:C3'	51:1:2554:U:H5''	2.47	0.43
51:1:2556:C:H2'	51:1:2557:G:C5'	2.48	0.43
53:3:160:A:H2'	53:3:161:A:O4'	2.19	0.43
53:3:973:G:H2'	53:3:974:A:H8	1.84	0.43
53:3:1242:G:H4'	53:3:1304:G:OP1	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:96:LYS:NZ	59:B2:1298:VAL:HG11	2.34	0.43
59:B2:538:LEU:HD13	59:B2:543:ALA:HB2	2.00	0.43
63:5:37:A:H2'	63:5:38:A:C8	2.53	0.43
11:K:89:VAL:HG23	53:3:737:C:C4'	2.49	0.43
14:N:58:GLU:HG2	14:N:59:LYS:HG3	2.01	0.43
29:d:131:THR:HG21	51:1:320:A:H2'	1.99	0.43
35:k:49:ARG:HH22	53:3:1423:G:H5'	1.84	0.43
35:k:51:LYS:HD3	35:k:51:LYS:HA	1.75	0.43
40:p:59:THR:HG22	40:p:72:VAL:HG23	2.00	0.43
45:u:48:VAL:HA	45:u:49:PRO:HD3	1.92	0.43
51:1:597:G:H2'	51:1:598:U:O4'	2.18	0.43
51:1:608:A:H2'	51:1:609:A:O4'	2.18	0.43
51:1:648:G:H2'	51:1:649:G:H8	1.82	0.43
51:1:984:A:P	51:1:985:C:H5	2.41	0.43
51:1:1056:G:H1'	51:1:1103:A:N6	2.33	0.43
51:1:1313:U:O2	51:1:1313:U:H2'	2.19	0.43
51:1:1675:C:O2'	51:1:1676:A:H5'	2.19	0.43
51:1:2581:G:N1	51:1:2610:C:O2'	2.52	0.43
53:3:640:A:H2'	53:3:641:U:H5'	2.01	0.43
53:3:723:U:O2	53:3:855:U:H4'	2.17	0.43
53:3:1236:A:H2'	53:3:1237:C:O4'	2.19	0.43
53:3:1515:G:H2'	53:3:1516:G:H8	1.82	0.43
57:A1:192:VAL:HG12	57:A1:193:GLU:H	1.82	0.43
6:F:38:GLY:OXT	51:1:1124:G:H1'	2.19	0.43
7:G:22:TRP:HA	7:G:189:ASN:HA	2.01	0.43
9:I:69:ARG:HH11	9:I:72:ARG:HH22	1.67	0.43
10:J:25:LYS:HG3	53:3:923:A:C5'	2.49	0.43
12:L:29:LEU:HD23	12:L:104:VAL:HG23	2.01	0.43
12:L:138:GLU:HA	12:L:141:HIS:HB2	1.99	0.43
14:N:18:VAL:HG21	14:N:81:GLY:HA3	2.01	0.43
16:P:24:ALA:N	16:P:86:LYS:O	2.39	0.43
16:P:25:SER:HG	16:P:28:ASN:H	1.64	0.43
28:c:176:ASP:OD1	28:c:176:ASP:N	2.37	0.43
32:g:71:LYS:HD3	32:g:71:LYS:HA	1.66	0.43
36:l:29:LYS:HA	36:l:29:LYS:HD2	1.71	0.43
51:1:74:A:H2'	51:1:74:A:N3	2.33	0.43
51:1:960:A:O3'	51:1:961:C:H3'	2.18	0.43
51:1:1123:C:O2'	51:1:1124:G:H5'	2.18	0.43
51:1:1931:U:H2'	51:1:1932:A:C8	2.54	0.43
51:1:1962:C:H1'	51:1:1963:U:C5	2.53	0.43
51:1:2598:A:N7	51:1:2599:G:H1'	2.34	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2672:U:C3'	51:1:2673:G:H5''	2.48	0.43
52:2:4:C:H6	52:2:4:C:C5'	2.31	0.43
53:3:304:U:O2'	53:3:305:G:H5'	2.19	0.43
53:3:633:G:H2'	53:3:634:C:C6	2.54	0.43
53:3:1158:C:H2'	53:3:1159:U:H4'	2.01	0.43
55:8:15:DC:H5'	59:B2:1269:ARG:HD3	2.00	0.43
58:B1:731:ARG:HB3	59:B2:1105:SER:HB2	2.00	0.43
59:B2:712:SER:OG	59:B2:713:GLY:N	2.49	0.43
60:W0:58:LEU:HD12	60:W0:59:ILE:HG12	2.00	0.43
65:a:48:LEU:HB3	65:a:50:ILE:HG23	2.01	0.43
4:D:10:LEU:HD13	51:1:125:A:C2	2.54	0.43
8:H:3:LYS:HA	8:H:3:LYS:HD3	1.95	0.43
9:I:110:ARG:O	9:I:114:ARG:N	2.52	0.43
33:i:3:LYS:HB3	51:1:1055:G:O5'	2.19	0.43
36:l:29:LYS:HA	51:1:810:U:H5	1.81	0.43
37:m:46:ILE:O	37:m:50:ARG:N	2.45	0.43
38:n:72:ASP:O	38:n:76:VAL:HG23	2.19	0.43
43:s:84:ARG:NH1	51:1:1322:A:O2'	2.51	0.43
44:t:17:SER:OG	44:t:20:ALA:N	2.48	0.43
51:1:1064:C:H5''	51:1:1065:U:C5	2.54	0.43
51:1:1592:C:H2'	51:1:1593:A:H8	1.83	0.43
51:1:1771:C:H2'	51:1:1772:A:O4'	2.19	0.43
51:1:1815:A:O4'	51:1:1817:G:H1'	2.18	0.43
51:1:1823:G:C6	51:1:1824:G:C6	3.06	0.43
51:1:2626:C:O2'	51:1:2627:G:H5'	2.19	0.43
51:1:2633:G:C2'	51:1:2634:A:H5''	2.47	0.43
53:3:927:G:H4'	53:3:1503:A:N7	2.33	0.43
53:3:1014:A:C2	53:3:1219:A:H1'	2.54	0.43
58:B1:1046:ILE:HG22	58:B1:1061:VAL:HA	2.00	0.43
59:B2:515:MET:HE2	59:B2:515:MET:HB3	1.82	0.43
59:B2:1313:HIS:CD2	60:W0:31:GLN:HE22	2.37	0.43
5:E:28:LEU:HD12	5:E:32:LEU:HD11	2.01	0.43
9:I:173:ASP:OD1	9:I:173:ASP:N	2.44	0.43
14:N:7:GLY:HA3	14:N:85:ALA:HB2	2.00	0.43
31:f:140:ILE:HD12	31:f:140:ILE:HA	1.91	0.43
33:i:12:VAL:HG12	33:i:13:ALA:H	1.83	0.43
37:m:9:PHE:HB3	37:m:10:ARG:H	1.67	0.43
39:o:57:ALA:O	39:o:61:GLN:NE2	2.52	0.43
42:r:34:GLU:HB2	42:r:58:VAL:HB	1.99	0.43
51:1:170:U:H2'	51:1:171:U:C6	2.53	0.43
51:1:1716:U:C2'	51:1:1717:A:H5'	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1803:A:C2	51:1:1823:G:H1'	2.53	0.43
51:1:1983:G:C2	51:1:1984:G:C8	3.07	0.43
51:1:2101:A:H2'	51:1:2102:G:H8	1.84	0.43
51:1:2234:G:O2'	51:1:2235:G:H5'	2.19	0.43
51:1:2267:A:H5''	51:1:2268:A:H5'	2.01	0.43
51:1:2311:A:H3'	51:1:2312:U:C6	2.54	0.43
53:3:439:U:O2'	53:3:440:C:H5'	2.19	0.43
53:3:865:A:H5'	53:3:1078:U:O4	2.19	0.43
53:3:1061:G:H2'	53:3:1062:U:O4'	2.19	0.43
58:B1:362:ARG:HB2	58:B1:364:HIS:HD2	1.83	0.43
58:B1:388:ARG:HG2	58:B1:388:ARG:HH11	1.84	0.43
58:B1:515:ARG:HH12	58:B1:724:MET:HG2	1.84	0.43
59:B2:487:LEU:HD22	59:B2:487:LEU:HA	1.77	0.43
65:a:193:LEU:HG	65:a:197:LYS:HG3	2.00	0.43
8:H:1:GLY:HA2	53:3:1060:U:C5	2.54	0.43
8:H:174:LEU:HB3	53:3:1108:G:OP1	2.19	0.43
17:Q:5:GLN:NE2	53:3:881:G:N7	2.67	0.43
17:Q:43:LYS:HG3	53:3:1492:A:H4'	2.00	0.43
19:S:92:ILE:HD13	19:S:92:ILE:HA	1.84	0.43
20:T:27:GLN:O	20:T:27:GLN:NE2	2.52	0.43
29:d:93:SER:O	29:d:93:SER:OG	2.32	0.43
33:i:105:LEU:HD13	33:i:128:ILE:HG23	2.01	0.43
38:n:9:GLN:HB2	51:1:1653:G:C6	2.54	0.43
44:t:29:THR:HG22	44:t:86:THR:HA	2.01	0.43
50:z:11:SER:OG	51:1:988:A:H5''	2.18	0.43
51:1:533:G:H5''	51:1:533:G:H8	1.83	0.43
51:1:786:C:H2'	51:1:787:C:H6	1.83	0.43
51:1:1037:G:O2'	51:1:1038:G:H5'	2.18	0.43
51:1:1984:G:H2'	51:1:1985:C:H6	1.82	0.43
51:1:2489:U:O2'	51:1:2490:G:H5'	2.18	0.43
51:1:2556:C:C2'	51:1:2557:G:H5'	2.48	0.43
51:1:2617:U:H2'	51:1:2618:G:H5'	2.01	0.43
53:3:301:G:H2'	53:3:302:G:H8	1.83	0.43
53:3:778:G:H2'	53:3:779:C:O4'	2.19	0.43
53:3:1364:U:O2'	53:3:1365:G:H5'	2.19	0.43
58:B1:45:ASN:HD22	58:B1:48:THR:H	1.65	0.43
58:B1:609:TYR:HD2	58:B1:610:ARG:NH1	2.17	0.43
58:B1:1024:THR:HG23	58:B1:1123:ARG:HA	2.00	0.43
59:B2:125:GLY:H	59:B2:495:ALA:HB1	1.84	0.43
66:0:129:GLN:HG3	66:0:132:LYS:HE2	2.00	0.43
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)
9:I:119:HIS:HA	53:3:439:U:H5''	2.01	0.42
18:R:78:ARG:HD3	24:X:64:GLU:HG2	2.01	0.42
26:Z:44:ARG:HD3	26:Z:44:ARG:HA	1.77	0.42
29:d:46:GLN:HE21	29:d:86:ALA:HA	1.84	0.42
30:e:88:VAL:HA	52:2:42:C:O2	2.19	0.42
32:g:22:LYS:HD3	32:g:22:LYS:HA	1.86	0.42
41:q:47:ARG:NH2	51:1:560:C:O2'	2.52	0.42
51:1:172:A:H2'	51:1:173:A:C8	2.54	0.42
51:1:343:C:C2'	51:1:344:A:H5'	2.49	0.42
51:1:571:U:C4	51:1:575:A:C5	3.07	0.42
51:1:666:A:H2'	51:1:667:U:C6	2.54	0.42
51:1:793:A:OP2	51:1:793:A:H8	2.01	0.42
51:1:1050:A:O2'	51:1:2752:C:H1'	2.19	0.42
51:1:1794:A:O2'	51:1:1795:C:H5'	2.18	0.42
51:1:1801:A:C8	51:1:1801:A:H5'	2.54	0.42
51:1:1998:A:H4'	51:1:2724:U:O2'	2.19	0.42
51:1:2326:C:O2'	51:1:2327:A:OP1	2.31	0.42
51:1:2475:C:H42	51:1:2529:G:H22	1.66	0.42
53:3:405:U:O2	53:3:498:A:H2'	2.19	0.42
53:3:1229:A:H2'	53:3:1230:C:C6	2.54	0.42
53:3:1423:G:H1	53:3:1477:U:H3	1.65	0.42
58:B1:586:GLY:HA3	58:B1:612:LEU:HD11	2.01	0.42
58:B1:894:VAL:HG22	58:B1:1258:ARG:HH11	1.83	0.42
59:B2:1275:VAL:HG13	59:B2:1287:LEU:HD11	2.01	0.42
63:5:35:A:H1'	63:5:36:A:OP1	2.19	0.42
17:Q:50:LYS:HA	17:Q:50:LYS:HD2	1.86	0.42
27:b:204:LEU:O	27:b:206:LYS:N	2.48	0.42
30:e:131:VAL:N	30:e:152:ASP:OD1	2.49	0.42
32:g:63:ALA:HA	32:g:66:ASN:HD22	1.84	0.42
36:l:18:ARG:NE	51:1:1249:U:C4	2.88	0.42
39:o:35:ILE:HD13	39:o:35:ILE:HA	1.95	0.42
46:v:88:HIS:CE1	52:2:75:G:H21	2.37	0.42
51:1:481:G:H2'	51:1:507:A:N1	2.34	0.42
51:1:690:G:C2'	51:1:691:C:H5'	2.49	0.42
51:1:742:A:H2'	51:1:743:A:O4'	2.19	0.42
51:1:820:A:H5'	51:1:837:C:O2'	2.19	0.42
51:1:878:A:H3'	51:1:879:G:C8	2.54	0.42
51:1:1060:U:OP2	51:1:1060:U:H3'	2.19	0.42
51:1:1177:G:C3'	51:1:1178:C:H5''	2.49	0.42
51:1:1388:G:H2'	51:1:1389:G:H8	1.84	0.42
51:1:1404:C:O5'	51:1:1404:C:H6	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1794:A:H1'	51:1:1900:A:N3	2.34	0.42
51:1:2897:U:H2'	51:1:2898:U:C6	2.54	0.42
58:B1:68:TYR:O	58:B1:75:TYR:CD2	2.70	0.42
58:B1:107:LEU:HA	58:B1:276:ASN:ND2	2.33	0.42
58:B1:820:ILE:HG12	58:B1:884:SER:HB2	2.01	0.42
59:B2:1157:GLN:HG3	59:B2:1159:VAL:HG13	2.00	0.42
8:H:79:LYS:HE2	8:H:79:LYS:HB2	1.95	0.42
13:M:15:ASN:HB3	53:3:827:U:C4'	2.48	0.42
14:N:113:LYS:HA	14:N:120:ALA:HB2	2.01	0.42
21:U:38:PHE:HZ	21:U:48:GLU:HG3	1.84	0.42
28:c:183:GLU:OE2	28:c:184:ARG:NE	2.53	0.42
31:f:84:LYS:HD2	31:f:84:LYS:HA	1.78	0.42
37:m:33:LEU:HD12	37:m:117:PHE:HB3	2.00	0.42
38:n:51:LEU:HD23	38:n:79:LEU:HD11	2.02	0.42
43:s:29:VAL:HG21	43:s:55:ILE:HG21	2.01	0.42
51:1:441:U:O2'	51:1:442:G:H5'	2.19	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
51:1:784:G:N7	51:1:792:A:C5	2.87	0.42
51:1:809:G:O4'	51:1:1254:A:H1'	2.19	0.42
51:1:862:G:H2'	51:1:863:A:O4'	2.18	0.42
51:1:981:A:H1'	51:1:2037:A:H1'	2.00	0.42
51:1:1363:C:O2'	51:1:1809:A:H1'	2.20	0.42
51:1:1797:G:C4	51:1:1798:U:C6	3.07	0.42
51:1:2061:G:C8	51:1:2501:C:H4'	2.53	0.42
51:1:2338:C:H6	51:1:2338:C:O5'	2.01	0.42
53:3:7:A:H5'	53:3:298:A:O4'	2.19	0.42
53:3:1195:C:O5'	53:3:1195:C:H6	2.01	0.42
58:B1:242:LEU:C	58:B1:242:LEU:HD23	2.44	0.42
58:B1:385:LEU:CD2	58:B1:390:LEU:HB2	2.50	0.42
58:B1:797:THR:HG22	58:B1:924:GLY:HA3	2.01	0.42
2:B:24:VAL:H	43:s:35:ILE:HD11	1.84	0.42
13:M:86:LYS:HD2	13:M:86:LYS:HA	1.73	0.42
16:P:14:GLN:H	16:P:14:GLN:HG3	1.69	0.42
18:R:13:HIS:HB3	18:R:15:VAL:HG12	2.00	0.42
18:R:22:TYR:HD2	18:R:65:GLU:HA	1.84	0.42
27:b:73:ILE:HA	27:b:74:PRO:HD3	1.90	0.42
27:b:148:GLY:O	51:1:2205:A:H5'	2.20	0.42
27:b:218:THR:HG22	51:1:1790:C:OP1	2.19	0.42
28:c:140:HIS:NE2	51:1:1658:C:OP1	2.52	0.42
28:c:152:PRO:HA	51:1:1130:U:O2	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:l:90:VAL:HG22	36:l:122:VAL:HA	2.02	0.42
38:n:73:ASN:HB3	51:1:1453:A:C8	2.54	0.42
49:y:9:LYS:HD3	49:y:10:SER:H	1.84	0.42
51:1:1:G:H2'	51:1:2:G:C8	2.55	0.42
51:1:832:U:C5	51:1:944:C:N4	2.87	0.42
51:1:1183:U:O2'	51:1:1184:U:H5'	2.19	0.42
51:1:1797:G:N2	51:1:1798:U:H1'	2.34	0.42
51:1:2656:U:H2'	51:1:2657:A:C8	2.55	0.42
51:1:2670:A:H2'	51:1:2671:G:C8	2.55	0.42
53:3:112:G:N2	53:3:354:G:H5'	2.02	0.42
53:3:228:A:H2'	53:3:229:U:O4'	2.20	0.42
53:3:1210:C:H2'	53:3:1211:U:H5'	2.00	0.42
58:B1:141:PHE:CD2	58:B1:297:ARG:HB2	2.54	0.42
59:B2:616:ILE:HG13	59:B2:652:TYR:HB2	2.01	0.42
63:5:34:G:H5'	63:5:35:A:C8	2.55	0.42
66:0:375:LYS:HE2	66:0:375:LYS:HB2	1.89	0.42
66:0:498:VAL:HG11	66:0:522:MET:CE	2.43	0.42
2:B:41:HIS:HD2	38:n:101:GLY:HA2	1.84	0.42
8:H:168:ARG:NH1	53:3:1106:G:O2'	2.53	0.42
18:R:105:ALA:HB3	18:R:109:LYS:HE3	2.02	0.42
44:t:1:MET:HG3	51:1:136:G:H21	1.84	0.42
44:t:7:LEU:HD23	44:t:7:LEU:HA	1.89	0.42
47:w:37:ARG:HA	47:w:37:ARG:HD3	1.69	0.42
49:y:1:MET:HA	49:y:4:LYS:HE2	2.01	0.42
51:1:19:A:H2'	51:1:20:C:C6	2.54	0.42
51:1:39:G:H2'	51:1:40:U:C6	2.54	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
51:1:2061:G:C2'	51:1:2501:C:HO2'	2.27	0.42
51:1:2138:G:N1	51:1:2154:A:O2'	2.47	0.42
51:1:2350:C:H2'	51:1:2351:G:O4'	2.19	0.42
51:1:2469:A:H2'	51:1:2470:G:O4'	2.20	0.42
51:1:2520:C:H1'	51:1:2565:A:O2'	2.19	0.42
51:1:2654:A:H1'	51:1:2656:U:C6	2.54	0.42
53:3:182:A:H2'	53:3:183:C:H5''	2.01	0.42
53:3:250:A:H4'	53:3:251:G:O5'	2.19	0.42
53:3:540:G:H2'	53:3:541:G:O4'	2.20	0.42
53:3:1271:A:H5'	53:3:1314:C:H5'	2.01	0.42
53:3:1292:G:H2'	53:3:1293:C:C6	2.55	0.42
53:3:1405:G:H21	53:3:1518:A:H8	1.66	0.42
58:B1:111:THR:CG2	58:B1:300:GLN:HA	2.48	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:839:VAL:HG12	58:B1:864:LEU:HD12	2.02	0.42
59:B2:469:VAL:HA	59:B2:472:GLU:HG2	2.01	0.42
59:B2:741:MET:HE3	59:B2:974:ARG:HH12	1.84	0.42
66:O:493:THR:OG1	66:O:525:LEU:CD1	2.68	0.42
7:G:96:LEU:HD23	7:G:96:LEU:HA	1.93	0.42
10:J:126:ALA:H	53:3:9:G:P	2.43	0.42
11:K:47:LEU:CD2	11:K:55:HIS:HA	2.49	0.42
13:M:10:LEU:HD13	13:M:74:ILE:HG13	2.00	0.42
15:O:90:LEU:HD13	15:O:90:LEU:HA	1.79	0.42
21:U:5:ARG:NH2	53:3:377:G:H5''	2.35	0.42
23:W:25:ILE:HA	23:W:28:LEU:HD12	2.01	0.42
25:Y:4:LYS:HE2	53:3:332:G:OP1	2.20	0.42
27:b:144:GLU:HA	27:b:151:GLY:HA2	2.00	0.42
28:c:161:MET:CE	51:1:2050:C:H1'	2.49	0.42
35:k:38:ILE:HG22	35:k:61:VAL:HG22	2.01	0.42
37:m:55:ARG:HA	37:m:58:LYS:HA	2.02	0.42
45:u:14:THR:OG1	45:u:15:GLY:N	2.51	0.42
46:v:44:HIS:CE1	46:v:86:LEU:H	2.37	0.42
46:v:76:ASP:H	46:v:90:ASP:HB3	1.85	0.42
51:1:8:C:H2'	51:1:9:G:O4'	2.20	0.42
51:1:76:C:H42	51:1:110:G:H1	1.68	0.42
51:1:974:G:C8	51:1:989:G:C2	3.07	0.42
51:1:1145:C:H2'	51:1:1146:C:C6	2.54	0.42
51:1:1321:A:H3'	51:1:1322:A:H8	1.84	0.42
51:1:1741:C:C2'	51:1:1742:U:H5'	2.50	0.42
51:1:2472:G:H5''	51:1:2473:U:OP2	2.20	0.42
53:3:58:C:H2'	53:3:59:A:H5'	2.01	0.42
58:B1:24:LEU:HD21	58:B1:116:PHE:CE2	2.54	0.42
58:B1:647:PRO:HG3	58:B1:697:MET:HB3	2.01	0.42
58:B1:1350:ASN:HA	58:B1:1353:VAL:HG12	2.01	0.42
59:B2:524:ILE:HD12	59:B2:712:SER:HB2	2.02	0.42
62:NG:135:ARG:O	62:NG:178:VAL:CA	2.68	0.42
17:Q:56:LEU:HD13	17:Q:56:LEU:HA	1.91	0.42
21:U:12:LYS:HB3	53:3:392:C:OP2	2.20	0.42
27:b:17:LYS:HB3	27:b:17:LYS:HE3	1.80	0.42
28:c:118:PHE:CD2	51:1:1654:A:H2	2.35	0.42
28:c:118:PHE:O	51:1:1655:A:H5'	2.18	0.42
29:d:85:PHE:CG	51:1:588:U:H1'	2.54	0.42
34:j:116:ARG:HH21	51:1:528:A:H5''	1.81	0.42
51:1:503:A:H4'	51:1:505:A:H5''	2.02	0.42
51:1:2060:A:O2'	51:1:2061:G:OP2	2.35	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2114:A:C5	51:1:2115:G:H1'	2.55	0.42
51:1:2521:C:C2'	51:1:2522:U:H5'	2.50	0.42
52:2:79:G:H2'	52:2:80:U:O4'	2.19	0.42
53:3:269:C:H2'	53:3:270:A:C8	2.55	0.42
53:3:971:G:N7	53:3:1233:G:H1'	2.34	0.42
53:3:1194:U:H2'	53:3:1195:C:C6	2.54	0.42
53:3:1199:U:H2'	53:3:1200:C:H5'	2.01	0.42
58:B1:71:LEU:HD23	58:B1:71:LEU:HA	1.75	0.42
58:B1:244:VAL:HA	58:B1:269:TYR:OH	2.19	0.42
63:5:9:A:H1'	63:5:45:U:H2'	2.01	0.42
66:0:324:ILE:HA	66:0:334:THR:HA	2.01	0.42
8:H:12:GLY:N	8:H:15:LYS:O	2.35	0.42
9:I:12:ARG:NH2	9:I:36:ALA:H	2.17	0.42
24:X:32:THR:OG1	24:X:33:TRP:N	2.53	0.42
30:e:32:LYS:H	30:e:32:LYS:HG2	1.68	0.42
32:g:50:ARG:H	32:g:50:ARG:HG2	1.55	0.42
34:j:136:GLN:NE2	51:1:2899:A:H5'	2.34	0.42
38:n:106:ASP:OD2	51:1:1287:A:C5	2.72	0.42
51:1:45:G:C5'	51:1:46:G:H5'	2.25	0.42
51:1:72:U:C4	51:1:112:U:H4'	2.55	0.42
51:1:516:C:H2'	51:1:517:C:H5'	2.02	0.42
51:1:736:C:H42	51:1:760:G:H1	1.67	0.42
51:1:813:U:H2'	51:1:814:C:C6	2.54	0.42
51:1:1086:A:C1'	51:1:1103:A:H2	2.33	0.42
51:1:1310:G:C3'	51:1:1311:G:H5'	2.50	0.42
51:1:1379:U:H2'	51:1:1380:G:H5'	2.01	0.42
51:1:2114:A:N6	51:1:2119:A:H61	2.18	0.42
51:1:2577:A:H2'	51:1:2614:A:N6	2.33	0.42
53:3:492:C:H2'	53:3:493:A:H8	1.83	0.42
53:3:668:G:H2'	53:3:669:G:C8	2.55	0.42
53:3:1032:G:H21	53:3:1033:G:H4'	1.85	0.42
53:3:1119:C:O2'	53:3:1120:C:H5'	2.20	0.42
53:3:1173:U:H2'	53:3:1174:G:C8	2.48	0.42
58:B1:201:LEU:HD11	58:B1:220:ARG:NH1	2.32	0.42
58:B1:434:ILE:HD11	59:B2:1274:GLU:CG	2.49	0.42
58:B1:950:ILE:HB	58:B1:1018:ALA:HB3	2.01	0.42
66:0:281:ALA:O	66:0:285:TYR:N	2.53	0.42
4:D:13:ASN:HB3	51:1:125:A:O4'	2.20	0.42
7:G:53:LEU:HD23	7:G:56:LEU:HD12	2.00	0.42
7:G:218:ALA:HA	7:G:221:ARG:HE	1.85	0.42
13:M:7:ALA:HA	13:M:10:LEU:HB2	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:21:LYS:HZ1	14:N:63:TYR:H	1.68	0.42
20:T:3:SER:OG	20:T:4:THR:N	2.52	0.42
22:V:16:MET:HE2	22:V:16:MET:HB3	1.84	0.42
27:b:131:MET:HE3	27:b:131:MET:HB2	1.84	0.42
29:d:29:HIS:CE1	36:l:8:PRO:HB3	2.55	0.42
29:d:85:PHE:CE2	51:1:587:C:H5'	2.54	0.42
31:f:97:VAL:HG12	31:f:124:CYS:HB2	2.02	0.42
38:n:90:ARG:NH2	51:1:2880:C:O2'	2.48	0.42
51:1:191:A:N3	51:1:192:C:C6	2.88	0.42
51:1:382:A:C2	51:1:393:C:N3	2.88	0.42
51:1:445:C:O2'	51:1:446:G:H5'	2.20	0.42
51:1:2133:G:H8	51:1:2158:A:C2	2.38	0.42
51:1:2139:U:H2'	51:1:2140:G:C8	2.54	0.42
51:1:2402:U:H2'	51:1:2403:C:C5'	2.42	0.42
51:1:2733:A:H2'	51:1:2734:A:H8	1.81	0.42
51:1:2873:A:O2'	51:1:2874:C:H5'	2.20	0.42
53:3:1264:U:H3	53:3:1271:A:H61	1.67	0.42
53:3:1386:G:O2'	53:3:1387:G:H5'	2.20	0.42
58:B1:137:ARG:HA	58:B1:142:GLU:HG2	2.02	0.42
58:B1:201:LEU:CB	58:B1:221:ILE:HD13	2.47	0.42
63:5:4:C:H2'	63:5:5:G:C8	2.55	0.42
65:a:42:VAL:HG13	65:a:175:ILE:HG13	2.02	0.42
67:h:2:DPP:NG	67:h:3:SER:N	2.65	0.42
1:A:26:SER:HB2	30:e:101:ARG:HH11	1.84	0.42
12:L:35:LYS:HD3	53:3:1373:G:H5''	2.01	0.42
27:b:107:LYS:N	27:b:193:GLU:O	2.49	0.42
28:c:59:ARG:HA	28:c:59:ARG:HD2	1.85	0.42
32:g:101:ASP:O	32:g:105:ALA:N	2.46	0.42
45:u:96:LYS:HE2	51:1:300:A:P	2.60	0.42
51:1:877:A:O2'	51:1:900:A:N6	2.53	0.42
51:1:917:A:H5''	51:1:2268:A:N6	2.30	0.42
51:1:1373:A:H2'	51:1:1374:G:O4'	2.20	0.42
51:1:1854:A:H2'	51:1:1855:U:H5'	2.02	0.42
51:1:2448:A:H3'	51:1:2449:U:H2'	2.01	0.42
51:1:2544:G:H2'	51:1:2545:G:C8	2.55	0.42
52:2:53:A:H2'	52:2:54:G:O4'	2.20	0.42
53:3:111:G:O2'	53:3:389:A:H1'	2.20	0.42
53:3:316:C:H2'	53:3:317:U:C6	2.55	0.42
53:3:678:U:H2'	53:3:679:C:C6	2.55	0.42
53:3:1368:A:O2'	53:3:1369:C:H5'	2.19	0.42
53:3:1469:C:C2'	53:3:1470:U:H5'	2.50	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:144:TYR:CE1	58:B1:162:GLU:OE1	2.73	0.42
58:B1:246:PRO:HA	58:B1:247:PRO:HD3	1.96	0.42
58:B1:1289:ASN:O	58:B1:1293:GLU:HB2	2.20	0.42
66:0:520:ILE:HG22	66:0:578:LEU:HA	2.02	0.42
5:E:7:ARG:NH1	51:1:254:G:H22	2.18	0.41
11:K:89:VAL:HG23	53:3:737:C:C5'	2.48	0.41
17:Q:9:LYS:HE2	17:Q:9:LYS:HB2	1.85	0.41
18:R:100:ARG:HG2	53:3:950:U:C5	2.55	0.41
21:U:31:ARG:HB2	53:3:310:G:H5''	2.00	0.41
27:b:27:LYS:NZ	51:1:1428:C:OP2	2.44	0.41
27:b:219:VAL:HG21	51:1:782:A:N7	2.35	0.41
28:c:19:GLY:HA2	40:p:78:PRO:HD2	2.02	0.41
28:c:116:LYS:HB2	28:c:165:MET:HB3	2.02	0.41
28:c:117:GLY:H	28:c:164:GLN:HE22	1.69	0.41
37:m:42:THR:HA	37:m:93:VAL:HA	2.02	0.41
41:q:30:VAL:HG11	51:1:580:U:H4'	2.02	0.41
51:1:272:A:H2'	51:1:273:G:C8	2.54	0.41
51:1:538:A:H2'	51:1:539:G:O4'	2.20	0.41
51:1:842:U:H2'	51:1:843:G:O4'	2.19	0.41
51:1:1024:G:P	51:1:1025:G:H3'	2.60	0.41
51:1:1512:C:O5'	51:1:1512:C:H6	2.03	0.41
51:1:1564:C:C4	51:1:1565:C:C4	3.08	0.41
51:1:2081:U:H2'	51:1:2082:A:H8	1.85	0.41
51:1:2588:G:C2'	51:1:2589:A:H5'	2.50	0.41
51:1:2596:U:H2'	51:1:2597:G:O4'	2.19	0.41
51:1:2840:C:H2'	51:1:2841:C:C6	2.55	0.41
53:3:627:G:H2'	53:3:628:G:C8	2.54	0.41
53:3:1153:G:H2'	53:3:1154:G:O4'	2.20	0.41
58:B1:559:ALA:HB3	58:B1:562:GLU:HB3	2.01	0.41
7:G:56:LEU:HD23	7:G:56:LEU:HA	1.93	0.41
8:H:24:ASN:OD1	8:H:25:THR:N	2.53	0.41
14:N:13:SER:HG	53:3:1251:A:H5'	1.81	0.41
15:O:40:ILE:HD11	53:3:1124:G:H4'	2.01	0.41
33:i:123:ALA:CB	51:1:1081:U:H4'	2.50	0.41
35:k:62:VAL:H	35:k:62:VAL:HG12	1.65	0.41
39:o:11:ALA:HB1	39:o:14:ALA:HB3	2.01	0.41
50:z:18:LYS:HE2	50:z:18:LYS:HB3	1.89	0.41
51:1:4:U:H2'	51:1:5:A:O4'	2.20	0.41
51:1:52:A:C5	51:1:118:A:C2	3.08	0.41
51:1:324:A:H2'	51:1:325:G:H5'	2.01	0.41
51:1:481:G:H1'	51:1:506:G:H22	1.82	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:711:G:H2'	51:1:712:G:O4'	2.21	0.41
51:1:958:U:C2'	52:2:89:U:H1'	2.47	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
51:1:2139:U:H2'	51:1:2140:G:H8	1.85	0.41
51:1:2302:U:H2'	51:1:2303:G:C8	2.55	0.41
53:3:264:C:H2'	53:3:265:G:O4'	2.19	0.41
53:3:762:U:H2'	53:3:763:G:C8	2.55	0.41
53:3:866:C:N3	53:3:867:G:H1'	2.36	0.41
53:3:909:A:H2'	53:3:910:C:O4'	2.20	0.41
53:3:938:A:H1'	53:3:1376:U:O2'	2.20	0.41
53:3:1007:U:H2'	53:3:1008:U:C5	2.54	0.41
53:3:1422:G:N2	53:3:1479:C:N4	2.68	0.41
58:B1:390:LEU:H	58:B1:390:LEU:HD13	1.85	0.41
59:B2:50:GLU:HG2	59:B2:73:TYR:HE1	1.85	0.41
59:B2:590:PRO:HB2	59:B2:655:VAL:HG21	2.01	0.41
66:0:493:THR:OG1	66:0:525:LEU:HD11	2.20	0.41
3:C:38:PHE:HD1	3:C:45:HIS:HD2	1.68	0.41
7:G:23:ASN:H	7:G:189:ASN:HA	1.86	0.41
9:I:149:LYS:HG2	9:I:150:LYS:HG2	2.02	0.41
13:M:4:ASP:HB3	13:M:7:ALA:HB3	2.02	0.41
28:c:91:THR:H	28:c:94:GLN:HE21	1.66	0.41
38:n:24:MET:O	38:n:28:LEU:N	2.54	0.41
44:t:36:LYS:NZ	44:t:79:ASP:OD1	2.38	0.41
51:1:43:G:O2'	51:1:44:A:H5'	2.20	0.41
51:1:194:G:H2'	51:1:195:A:O4'	2.19	0.41
51:1:1158:C:O5'	51:1:1158:C:H6	2.02	0.41
51:1:1387:A:H2'	51:1:1388:G:C8	2.55	0.41
51:1:1591:A:H2'	51:1:1592:C:C6	2.55	0.41
51:1:1639:C:C2'	51:1:1640:A:H5'	2.51	0.41
51:1:1680:U:H2'	51:1:1681:G:C5'	2.40	0.41
51:1:2553:G:H2'	51:1:2554:U:C4'	2.49	0.41
51:1:2556:C:H2'	51:1:2557:G:O4'	2.19	0.41
51:1:2676:C:O5'	51:1:2676:C:H6	2.03	0.41
53:3:1093:A:O2'	53:3:1094:G:H5'	2.20	0.41
57:A1:76:GLU:HB3	57:A1:80:GLU:HB3	2.01	0.41
58:B1:279:LEU:HD13	58:B1:299:LEU:HD13	2.02	0.41
59:B2:22:LEU:HB3	59:B2:655:VAL:HG11	2.01	0.41
66:0:64:THR:HG23	66:0:472:ARG:HH22	1.86	0.41
4:D:24:THR:OG1	4:D:25:LYS:N	2.53	0.41
5:E:16:THR:OG1	5:E:17:GLY:N	2.52	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:34:THR:HA	16:P:40:ALA:HA	2.03	0.41
18:R:64:VAL:H	18:R:67:ASP:HB3	1.85	0.41
19:S:52:ARG:HD3	53:3:1317:C:N3	2.35	0.41
21:U:50:THR:HB	21:U:78:VAL:HB	2.02	0.41
27:b:145:MET:SD	51:1:1800:C:H5'	2.61	0.41
27:b:170:TYR:HB3	27:b:182:LYS:HB3	2.02	0.41
34:j:114:LEU:O	34:j:118:MET:N	2.54	0.41
39:o:24:THR:HB	39:o:90:VAL:HG12	2.02	0.41
48:x:57:VAL:HG13	51:1:372:G:H5'	2.02	0.41
51:1:734:A:O2'	51:1:1635:A:H4'	2.21	0.41
51:1:1054:A:H2'	51:1:1055:G:C8	2.55	0.41
51:1:1509:A:H2'	51:1:1510:G:H8	1.82	0.41
51:1:1972:G:H2'	51:1:1973:G:H8	1.85	0.41
53:3:79:G:H2'	53:3:80:A:H5'	2.03	0.41
53:3:224:U:H2'	53:3:225:C:C5	2.55	0.41
53:3:426:U:H2'	53:3:427:U:C6	2.54	0.41
53:3:520:A:N6	53:3:529:G:H21	2.13	0.41
58:B1:190:LYS:HB2	58:B1:190:LYS:HE3	1.41	0.41
58:B1:513:MET:HG3	58:B1:544:LEU:HD11	2.01	0.41
66:0:444:SER:O	66:0:444:SER:OG	2.31	0.41
66:0:494:ILE:HB	66:0:608:ALA:HB1	2.03	0.41
1:A:11:GLU:HG2	1:A:25:ARG:HG2	2.02	0.41
6:F:8:LYS:HD2	6:F:8:LYS:HA	1.80	0.41
6:F:32:LYS:HD2	51:1:2478:A:OP1	2.20	0.41
10:J:37:VAL:HG21	10:J:113:VAL:HG13	2.02	0.41
15:O:45:ARG:NH1	15:O:47:GLU:OE1	2.53	0.41
17:Q:42:LYS:HA	17:Q:42:LYS:HD2	1.79	0.41
23:W:62:ARG:NH1	53:3:718:A:N6	2.69	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
34:j:61:LYS:HE2	34:j:61:LYS:HB2	1.88	0.41
35:k:1:MET:HE3	51:1:1665:A:H1'	2.02	0.41
36:l:78:ARG:HE	36:l:111:ILE:HD11	1.86	0.41
51:1:1625:C:H2'	51:1:1626:A:O4'	2.20	0.41
51:1:1716:U:O2'	51:1:1717:A:H5'	2.19	0.41
51:1:1741:C:H2'	51:1:1742:U:H5'	2.01	0.41
51:1:1900:A:H5'	51:1:1970:A:C5'	2.50	0.41
51:1:2049:G:N2	51:1:2620:C:C2	2.89	0.41
51:1:2073:C:O2	51:1:2437:G:C2	2.73	0.41
51:1:2575:C:O5'	51:1:2575:C:H6	2.03	0.41
53:3:458:U:H2'	53:3:459:A:C8	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:850:U:O5'	53:3:850:U:H6	2.03	0.41
53:3:957:U:H2'	53:3:959:A:OP2	2.21	0.41
53:3:1389:C:H2'	53:3:1390:U:O4'	2.21	0.41
54:4:55:G:H5'	59:B2:688:GLN:HE22	1.85	0.41
59:B2:310:ILE:HG21	59:B2:325:LEU:HB3	2.02	0.41
59:B2:699:LEU:HG	59:B2:799:ASN:HD22	1.85	0.41
59:B2:870:ILE:HB	59:B2:944:ARG:HD3	2.02	0.41
62:NG:175:PHE:O	62:NG:178:VAL:O	2.38	0.41
66:0:495:ARG:HG3	66:0:495:ARG:NH1	2.36	0.41
66:0:520:ILE:HD13	66:0:557:ILE:HD11	2.01	0.41
2:B:53:VAL:HG23	2:B:54:ILE:HG23	2.02	0.41
15:O:46:LYS:HB3	53:3:1253:G:OP1	2.21	0.41
19:S:99:SER:HG	53:3:1187:G:H21	1.69	0.41
28:c:209:ALA:OXT	51:1:2733:A:C2	2.74	0.41
47:w:56:PHE:HE2	51:1:2365:G:C5'	2.34	0.41
51:1:140:C:C6	51:1:141:G:H4'	2.55	0.41
51:1:2305:U:H2'	51:1:2306:C:H5'	2.02	0.41
51:1:2643:G:H2'	51:1:2644:G:O4'	2.20	0.41
52:2:78:A:H2'	52:2:79:G:O4'	2.20	0.41
53:3:130:A:N3	53:3:130:A:H2'	2.36	0.41
53:3:1005:A:C2'	53:3:1006:G:H5'	2.49	0.41
53:3:1315:U:H2'	53:3:1316:G:O4'	2.21	0.41
53:3:1490:U:H2'	53:3:1491:G:O4'	2.19	0.41
58:B1:59:ALA:HB1	58:B1:90:VAL:HG23	2.01	0.41
58:B1:102:MET:HG2	58:B1:246:PRO:CG	2.49	0.41
58:B1:616:PRO:HA	58:B1:619:ILE:HG22	2.02	0.41
59:B2:444:ASP:N	59:B2:444:ASP:OD1	2.51	0.41
59:B2:478:ARG:HD2	59:B2:492:MET:HA	2.02	0.41
66:0:83:ARG:HE	66:0:83:ARG:HB2	1.75	0.41
66:0:446:ARG:HB3	66:0:459:ALA:HB3	2.02	0.41
2:B:39:ARG:CZ	51:1:2884:U:H3	2.34	0.41
15:O:53:ILE:HD12	19:S:84:ARG:HD2	2.03	0.41
16:P:86:LYS:HG3	16:P:114:PRO:HD3	2.02	0.41
21:U:71:VAL:HA	21:U:74:LEU:HB2	2.02	0.41
25:Y:78:LEU:HA	25:Y:78:LEU:HD13	1.85	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
31:f:32:LEU:HD23	31:f:32:LEU:HA	1.86	0.41
36:l:4:ASN:OD1	51:1:1203:U:O2	2.39	0.41
51:1:151:C:H5''	51:1:1360:G:OP1	2.21	0.41
51:1:1354:A:H2'	51:1:1355:G:O4'	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2356:U:H3'	51:1:2357:G:H5''	2.03	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
53:3:862:C:O2'	53:3:863:U:H5'	2.20	0.41
53:3:946:A:H4'	53:3:1333:A:HO2'	1.85	0.41
53:3:1305:G:H22	53:3:1331:G:H2'	1.86	0.41
57:A1:205:MET:HE1	57:A1:217:ILE:HG13	2.02	0.41
58:B1:68:TYR:HB3	58:B1:75:TYR:HE2	1.81	0.41
59:B2:861:ALA:HB1	59:B2:882:ILE:HD13	2.02	0.41
66:0:18:HIS:ND1	66:0:120:GLN:HB3	2.36	0.41
66:0:468:ILE:O	66:0:472:ARG:N	2.51	0.41
3:C:13:SER:OG	3:C:47:ILE:O	2.27	0.41
12:L:3:ARG:HE	12:L:3:ARG:HB3	1.68	0.41
15:O:30:LYS:HA	15:O:34:ALA:HA	2.02	0.41
16:P:25:SER:HA	16:P:88:PRO:HD2	2.02	0.41
18:R:88:LEU:HD21	18:R:92:ARG:HE	1.86	0.41
26:Z:27:VAL:O	26:Z:31:VAL:N	2.53	0.41
29:d:50:ALA:HB2	51:1:801:G:C8	2.55	0.41
30:e:63:LYS:O	52:2:42:C:H1'	2.21	0.41
48:x:31:ASN:ND2	48:x:52:ALA:HB2	2.34	0.41
50:z:18:LYS:O	50:z:22:THR:OG1	2.31	0.41
51:1:413:C:H2'	51:1:414:C:C6	2.56	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
51:1:1609:A:H5'	51:1:1609:A:C8	2.55	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
51:1:2259:U:H1'	51:1:2427:C:H2'	2.02	0.41
51:1:2638:G:H1'	51:1:2778:A:N6	2.34	0.41
53:3:153:C:H2'	53:3:154:U:C5'	2.51	0.41
53:3:794:A:O2'	53:3:795:C:H5'	2.20	0.41
53:3:1327:C:H2'	53:3:1328:C:H6	1.84	0.41
57:A2:42:ALA:HB1	57:A2:224:LEU:HD11	2.03	0.41
58:B1:144:TYR:N	58:B1:144:TYR:CD1	2.88	0.41
58:B1:848:VAL:HB	58:B1:858:VAL:HG22	2.02	0.41
59:B2:746:ALA:O	59:B2:974:ARG:NH2	2.45	0.41
63:5:32:U:H3'	63:5:33:U:C6	2.55	0.41
66:0:268:SER:N	66:0:273:LYS:O	2.44	0.41
5:E:14:LYS:HD3	5:E:14:LYS:HA	1.84	0.41
7:G:17:HIS:HB2	7:G:202:ASN:HD22	1.86	0.41
9:I:201:GLU:OE1	10:J:111:ARG:NH1	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:13:LYS:NZ	10:J:14:LEU:O	2.53	0.41
13:M:3:GLN:HE21	53:3:878:A:H1'	1.86	0.41
16:P:26:PHE:O	16:P:27:ASN:ND2	2.54	0.41
19:S:1:ALA:HB1	53:3:1049:U:C4	2.56	0.41
25:Y:21:ALA:HA	25:Y:24:ARG:HD3	2.02	0.41
27:b:7:PRO:HB3	27:b:13:ARG:HG3	2.03	0.41
27:b:121:ALA:HA	27:b:129:LEU:HD13	2.02	0.41
27:b:152:GLN:HG2	51:1:1818:U:C4	2.55	0.41
28:c:55:LYS:HE3	28:c:60:VAL:HG22	2.03	0.41
28:c:113:SER:HB3	28:c:194:PRO:HB3	2.03	0.41
29:d:45:ALA:CB	51:1:38:A:H4'	2.50	0.41
31:f:123:GLU:HB2	31:f:131:VAL:HB	2.03	0.41
33:i:52:LEU:HD21	33:i:81:LYS:HB2	2.03	0.41
34:j:27:ARG:NH2	51:1:1142:A:H4'	2.35	0.41
45:u:73:ASN:ND2	45:u:76:THR:H	2.19	0.41
45:u:84:PHE:HB2	51:1:297:G:O3'	2.21	0.41
51:1:549:G:H2'	51:1:550:C:C6	2.56	0.41
51:1:740:C:O2'	51:1:741:U:H5'	2.21	0.41
51:1:1047:G:N2	51:1:1110:G:H2'	2.36	0.41
51:1:1177:G:H3'	51:1:1178:C:H5''	2.02	0.41
51:1:1229:C:H2'	51:1:1230:A:C8	2.53	0.41
51:1:1698:A:N7	51:1:1700:A:C8	2.89	0.41
51:1:1823:G:C6	51:1:1824:G:C5	3.09	0.41
51:1:1853:A:H2'	51:1:1854:A:H8	1.82	0.41
51:1:1917:U:O5'	51:1:1917:U:O2	2.39	0.41
51:1:2070:A:C2	51:1:2071:A:C4	3.08	0.41
51:1:2498:C:O2'	51:1:2499:C:H5'	2.20	0.41
51:1:2534:A:C2	51:1:2535:G:H1'	2.56	0.41
51:1:2559:C:H2'	51:1:2560:A:H8	1.86	0.41
51:1:2611:C:H2'	51:1:2612:C:H6	1.85	0.41
51:1:2830:C:O2	51:1:2883:A:H2	2.03	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
53:3:270:A:H2'	53:3:271:C:O4'	2.20	0.41
53:3:520:A:H61	53:3:533:A:H61	1.67	0.41
55:8:2:DC:C6	55:8:2:DC:H5'	2.56	0.41
57:A2:57:THR:HG23	57:A2:158:ARG:HH21	1.86	0.41
58:B1:71:LEU:HB2	58:B1:90:VAL:HG11	2.03	0.41
58:B1:108:ALA:HB2	58:B1:276:ASN:OD1	2.21	0.41
58:B1:390:LEU:N	58:B1:390:LEU:HD13	2.35	0.41
58:B1:820:ILE:HD11	58:B1:822:MET:HE2	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1177:ILE:HD12	58:B1:1186:TYR:HE2	1.85	0.41
59:B2:738:GLU:HA	59:B2:741:MET:HE2	2.03	0.41
59:B2:755:LYS:HA	59:B2:755:LYS:HD2	1.86	0.41
59:B2:987:GLU:HG2	59:B2:991:LYS:HE3	2.03	0.41
59:B2:998:LEU:HD21	59:B2:1015:ALA:HB2	2.02	0.41
64:6:33:U:H2'	64:6:35:A:OP2	2.21	0.41
65:a:167:LYS:HE2	65:a:167:LYS:HB3	1.52	0.41
66:0:161:ARG:HD2	66:0:162:LEU:HD23	2.02	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
9:I:108:ALA:N	9:I:112:GLU:OE2	2.43	0.41
21:U:60:TRP:HB3	21:U:65:ALA:HB2	2.03	0.41
24:X:46:LEU:HB3	24:X:48:ILE:HG12	2.03	0.41
27:b:153:LEU:HA	51:1:1799:G:N2	2.35	0.41
30:e:78:ILE:HD11	30:e:82:TYR:HB3	2.03	0.41
31:f:14:VAL:HG12	31:f:27:GLY:HA2	2.01	0.41
32:g:132:PHE:HB2	32:g:140:ALA:HB3	2.03	0.41
35:k:47:ILE:HA	35:k:47:ILE:HD13	1.85	0.41
48:x:1:SER:OG	51:1:1365:A:H5'	2.20	0.41
49:y:31:GLN:HB3	49:y:37:LEU:HD12	2.02	0.41
51:1:121:G:H2'	51:1:122:G:H8	1.86	0.41
51:1:289:G:H2'	51:1:290:U:O4'	2.20	0.41
51:1:692:C:H2'	51:1:693:A:H8	1.86	0.41
51:1:1146:C:O2'	51:1:1147:A:H5'	2.21	0.41
51:1:1597:A:C5'	51:1:1598:A:H5'	2.32	0.41
51:1:1679:A:H4'	51:1:1990:C:H4'	2.03	0.41
51:1:2063:C:O2	51:1:2450:A:N1	2.54	0.41
51:1:2140:G:H1	51:1:2151:U:H3	1.68	0.41
51:1:2656:U:OP1	66:0:146:ARG:NH2	2.52	0.41
51:1:2798:U:H4'	51:1:2799:A:C6	2.56	0.41
51:1:2811:G:O2'	51:1:2812:G:H5'	2.21	0.41
53:3:461:A:H2'	53:3:462:G:C8	2.56	0.41
53:3:1346:A:N1	53:3:1374:A:H5''	2.35	0.41
53:3:1468:A:H2'	53:3:1469:C:O4'	2.21	0.41
58:B1:140:TYR:HD1	58:B1:140:TYR:HA	1.79	0.41
58:B1:243:PRO:HG2	59:B2:1332:SER:C	2.44	0.41
58:B1:472:LEU:HD11	59:B2:1294:LYS:HG2	2.02	0.41
58:B1:777:HIS:CD2	59:B2:550:VAL:HG13	2.56	0.41
59:B2:22:LEU:HD22	59:B2:603:ILE:HG21	2.02	0.41
59:B2:936:ARG:HB2	59:B2:1042:LEU:HD12	2.03	0.41
63:5:23:A:H2'	63:5:24:G:C8	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:0:489:ALA:HB3	66:0:687:TYR:HE1	1.85	0.41
6:F:10:LEU:HD21	51:1:2477:U:H5	1.82	0.40
7:G:95:TRP:HZ3	7:G:99:MET:HE2	1.85	0.40
9:I:97:LEU:HG	9:I:134:TYR:HB3	2.04	0.40
10:J:83:PRO:HB3	10:J:97:PRO:HD3	2.02	0.40
12:L:34:LYS:CE	53:3:1290:G:H4'	2.51	0.40
14:N:21:LYS:HE2	14:N:21:LYS:HB2	1.85	0.40
15:O:58:ASN:HD21	53:3:1061:G:H4'	1.85	0.40
19:S:4:SER:OG	53:3:1216:A:H5''	2.21	0.40
22:V:46:HIS:CG	22:V:66:LEU:HD22	2.56	0.40
24:X:20:LYS:O	24:X:24:SER:OG	2.38	0.40
27:b:139:THR:OG1	27:b:162:GLN:OE1	2.30	0.40
30:e:68:LYS:HD3	30:e:68:LYS:HA	1.86	0.40
37:m:47:GLU:O	37:m:51:ARG:N	2.48	0.40
38:n:5:LYS:NZ	51:1:2000:C:OP1	2.48	0.40
41:q:94:LEU:HA	41:q:97:ILE:HG22	2.03	0.40
44:t:49:LYS:HD2	44:t:49:LYS:HA	1.75	0.40
45:u:67:SER:HB2	51:1:327:G:H21	1.85	0.40
49:y:31:GLN:HG2	49:y:37:LEU:HB2	2.04	0.40
51:1:272:A:H2'	51:1:273:G:H8	1.86	0.40
51:1:986:C:H6	51:1:986:C:O5'	2.04	0.40
51:1:1063:G:OP2	51:1:1070:A:C4'	2.69	0.40
51:1:1642:G:H2'	51:1:1643:G:O4'	2.21	0.40
51:1:1801:A:H5'	51:1:1801:A:H8	1.86	0.40
51:1:2136:G:N1	51:1:2137:U:O2	2.54	0.40
53:3:204:G:H2'	53:3:205:A:C8	2.55	0.40
53:3:456:A:H2'	53:3:457:G:C8	2.56	0.40
53:3:883:C:H2'	53:3:884:U:C6	2.56	0.40
57:A1:224:LEU:HD23	57:A2:228:LEU:HD21	2.03	0.40
58:B1:515:ARG:HG2	58:B1:516:ASP:H	1.85	0.40
58:B1:930:LEU:HA	58:B1:1244:GLN:HG3	2.02	0.40
59:B2:1072:ASN:OD1	59:B2:1072:ASN:N	2.52	0.40
2:B:42:ILE:HG22	2:B:48:TYR:HB2	2.03	0.40
10:J:25:LYS:HZ3	53:3:923:A:H5''	1.81	0.40
18:R:52:ILE:HD12	18:R:52:ILE:HA	1.96	0.40
18:R:70:ARG:NE	30:e:141:ASP:O	2.53	0.40
26:Z:36:PHE:CE1	26:Z:40:PRO:HD3	2.57	0.40
27:b:247:TRP:CE2	51:1:1805:A:H5''	2.57	0.40
30:e:146:ASP:OD1	30:e:146:ASP:N	2.52	0.40
51:1:527:C:OP2	51:1:2779:U:N3	2.51	0.40
51:1:1169:A:H2'	51:1:1170:C:O4'	2.22	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2313:C:H2'	51:1:2314:A:C8	2.56	0.40
51:1:2741:A:N6	51:1:2763:G:H1'	2.37	0.40
53:3:354:G:H2'	53:3:355:C:H6	1.77	0.40
53:3:374:A:H2'	53:3:375:U:C6	2.55	0.40
53:3:706:A:H2'	53:3:707:U:H5'	2.04	0.40
53:3:795:C:C5	53:3:796:C:C5	3.09	0.40
55:8:14:DC:C2	55:8:15:DC:C5	3.09	0.40
58:B1:211:GLU:CG	58:B1:215:LYS:HE3	2.44	0.40
58:B1:239:LEU:N	58:B1:239:LEU:HD23	2.36	0.40
63:5:17:C:H2'	63:5:18:G:C8	2.56	0.40
64:6:62:C:H5'	65:a:53:ARG:NE	2.36	0.40
66:0:169:LEU:HD12	66:0:185:LEU:HB3	2.01	0.40
4:D:1:MET:SD	4:D:2:LYS:N	2.95	0.40
9:I:21:LYS:HD2	9:I:21:LYS:HA	1.77	0.40
12:L:138:GLU:O	12:L:142:ARG:N	2.52	0.40
14:N:82:ILE:HA	14:N:85:ALA:HB3	2.03	0.40
16:P:66:ALA:HA	16:P:69:CYS:HB3	2.04	0.40
17:Q:30:ARG:NH1	66:0:429:GLU:OE2	2.54	0.40
26:Z:66:ARG:HB2	53:3:1088:G:H1'	2.03	0.40
27:b:145:MET:HE3	27:b:153:LEU:HD11	2.02	0.40
27:b:255:LYS:HD3	51:1:1844:C:H5''	2.02	0.40
30:e:65:LEU:N	30:e:87:LYS:O	2.53	0.40
33:i:63:ASP:OD1	33:i:63:ASP:N	2.53	0.40
39:o:25:ARG:HG3	39:o:40:ILE:HB	2.03	0.40
40:p:17:PRO:HD2	40:p:83:ILE:HB	2.04	0.40
41:q:36:GLN:OE1	51:1:1252:G:N2	2.38	0.40
51:1:324:A:C2'	51:1:325:G:H5'	2.51	0.40
51:1:571:U:C5	51:1:575:A:C6	3.10	0.40
51:1:954:G:C6	51:1:955:U:C2	3.10	0.40
51:1:1054:A:H2	51:1:1105:U:H3	1.69	0.40
51:1:1255:U:H3	51:1:2060:A:H8	1.65	0.40
51:1:1810:A:H2'	51:1:1811:G:C5'	2.51	0.40
51:1:2201:G:H2'	51:1:2202:U:O4'	2.21	0.40
53:3:220:G:O2'	53:3:221:C:H5'	2.21	0.40
53:3:262:A:H2'	53:3:263:A:C8	2.55	0.40
53:3:407:U:H3	53:3:435:A:H61	1.69	0.40
53:3:413:G:N3	53:3:413:G:H2'	2.36	0.40
53:3:866:C:C2	53:3:867:G:H1'	2.57	0.40
53:3:994:A:H61	53:3:1047:G:H4'	1.85	0.40
53:3:1028:C:H3'	53:3:1029:U:C5'	2.45	0.40
53:3:1034:G:H2'	53:3:1035:A:H8	1.86	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:A1:44:ARG:HA	57:A1:183:ILE:HD12	2.03	0.40
57:A2:205:MET:HE2	57:A2:205:MET:HB3	2.00	0.40
58:B1:351:GLY:O	58:B1:467:ALA:HA	2.21	0.40
58:B1:1041:ILE:N	58:B1:1045:THR:OG1	2.53	0.40
59:B2:886:LYS:HE2	59:B2:918:LEU:HD13	2.03	0.40
65:a:54:LYS:NZ	65:a:56:ASP:OD1	2.53	0.40
66:0:187:LYS:HE2	66:0:189:LYS:HB2	2.02	0.40
3:C:34:GLU:OE1	3:C:49:LYS:NZ	2.51	0.40
12:L:115:MET:HA	12:L:118:ARG:HB2	2.04	0.40
13:M:126:CYS:SG	13:M:127:TYR:N	2.93	0.40
15:O:82:LYS:HD2	15:O:82:LYS:HA	1.53	0.40
18:R:74:MET:HE2	18:R:74:MET:HB3	1.84	0.40
24:X:77:ARG:HH11	53:3:1225:A:H4'	1.83	0.40
25:Y:27:MET:H	25:Y:27:MET:HG3	1.74	0.40
27:b:4:LYS:HA	27:b:16:VAL:HG22	2.03	0.40
27:b:77:VAL:HB	27:b:112:GLY:H	1.86	0.40
28:c:179:ARG:HB3	28:c:188:LEU:HB2	2.03	0.40
29:d:71:GLY:N	51:1:674:G:H5''	2.37	0.40
33:i:10:LEU:HG	33:i:23:VAL:HG13	2.03	0.40
33:i:21:PRO:HB2	33:i:22:PRO:HD3	2.03	0.40
34:j:81:ILE:H	34:j:81:ILE:HG13	1.47	0.40
42:r:78:ARG:HH22	51:1:975:A:H4'	1.86	0.40
51:1:191:A:H2'	51:1:192:C:C6	2.56	0.40
51:1:838:C:C2	51:1:941:A:C6	3.09	0.40
51:1:1444:G:H2'	51:1:1445:G:O4'	2.21	0.40
51:1:1607:C:C4'	51:1:1608:A:C5'	2.97	0.40
51:1:2153:C:H3'	51:1:2154:A:C8	2.56	0.40
53:3:240:G:H2'	53:3:241:G:H8	1.87	0.40
53:3:410:G:H2'	53:3:429:U:O4	2.21	0.40
59:B2:741:MET:SD	59:B2:974:ARG:NH2	2.93	0.40
59:B2:803:ALA:HB2	59:B2:1094:VAL:HG21	2.03	0.40
64:6:25:C:H2'	64:6:26:G:H8	1.85	0.40
8:H:68:HIS:NE2	8:H:105:VAL:HB	2.37	0.40
8:H:115:VAL:O	8:H:118:SER:OG	2.36	0.40
9:I:2:ARG:HD3	53:3:405:U:OP2	2.22	0.40
14:N:6:TYR:CZ	53:3:1147:C:H4'	2.56	0.40
20:T:27:GLN:O	20:T:31:LEU:N	2.47	0.40
32:g:9:VAL:HG12	32:g:11:ASN:H	1.85	0.40
33:i:71:LYS:HD3	33:i:116:MET:HE2	2.03	0.40
33:i:81:LYS:HE2	33:i:81:LYS:HB3	1.94	0.40
37:m:11:LYS:O	51:1:910:A:N6	2.54	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:m:75:GLU:CD	51:1:957:C:H5'	2.47	0.40
38:n:23:ASN:HD21	51:1:1294:U:H1'	1.87	0.40
39:o:78:VAL:O	39:o:82:ALA:N	2.55	0.40
47:w:11:ASP:OD1	47:w:12:SER:N	2.54	0.40
51:1:1468:U:H2'	51:1:1522:A:H61	1.87	0.40
51:1:1666:G:N7	51:1:1667:G:C6	2.89	0.40
51:1:1831:G:C2	51:1:1975:G:C2	3.10	0.40
51:1:2684:U:C4	51:1:2685:G:N7	2.90	0.40
53:3:231:U:O2'	53:3:232:G:H5'	2.21	0.40
53:3:408:A:N6	53:3:434:U:H3	2.18	0.40
53:3:537:G:H2'	53:3:538:G:C8	2.57	0.40
53:3:581:G:N2	53:3:761:G:C6	2.89	0.40
53:3:1283:U:O2'	53:3:1284:C:H5'	2.22	0.40
54:4:56:G:OP1	59:B2:1073:LYS:NZ	2.35	0.40
57:A2:57:THR:HG22	57:A2:58:GLU:HG3	2.04	0.40
58:B1:26:SER:HB3	58:B1:29:MET:H	1.86	0.40
58:B1:56:LEU:HD12	58:B1:56:LEU:HA	1.84	0.40
58:B1:210:SER:HB3	58:B1:213:LYS:CB	2.48	0.40
58:B1:807:LEU:HD21	58:B1:894:VAL:HG21	2.04	0.40
59:B2:979:LEU:HD11	59:B2:1011:LEU:HD11	2.03	0.40
66:0:23:LYS:HD2	66:0:90:PRO:HA	2.03	0.40
66:0:32:PHE:HA	66:0:37:ASN:HB2	2.03	0.40
66:0:122:GLN:O	66:0:125:THR:OG1	2.36	0.40
66:0:648:GLU:N	66:0:651:GLY:O	2.48	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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	36
6	F	36/38 (95%)	29 (81%)	7 (19%)	0	100	100
7	G	216/241 (90%)	182 (84%)	34 (16%)	0	100	100
8	H	204/233 (88%)	187 (92%)	17 (8%)	0	100	100
9	I	203/206 (98%)	171 (84%)	31 (15%)	1 (0%)	24	63
10	J	155/167 (93%)	129 (83%)	26 (17%)	0	100	100
11	K	98/135 (73%)	81 (83%)	17 (17%)	0	100	100
12	L	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
13	M	127/130 (98%)	110 (87%)	17 (13%)	0	100	100
14	N	125/130 (96%)	110 (88%)	15 (12%)	0	100	100
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	53
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%)	124 (84%)	23 (16%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	89 (88%)	12 (12%)	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%)	83 (83%)	17 (17%)	0	100	100
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%)	66 (88%)	9 (12%)	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%)	275 (93%)	19 (6%)	1 (0%)	36	72
57	A2	282/329 (86%)	272 (96%)	10 (4%)	0	100	100
58	B1	1329/1407 (94%)	1206 (91%)	119 (9%)	4 (0%)	36	72
59	B2	1338/1342 (100%)	1208 (90%)	126 (9%)	4 (0%)	36	72
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	475 (97%)	15 (3%)	0	100	100
62	NG	150/181 (83%)	136 (91%)	11 (7%)	3 (2%)	6	30
65	a	128/234 (55%)	107 (84%)	21 (16%)	0	100	100
66	0	695/716 (97%)	618 (89%)	72 (10%)	5 (1%)	18	55
67	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	10486/11185 (94%)	9335 (89%)	1131 (11%)	20 (0%)	44	78

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	B1	121	PRO
62	NG	124	PRO
59	B2	43	PRO
59	B2	911	SER
62	NG	102	PRO
66	0	199	GLY
66	0	298	ILE
66	0	299	LEU
17	Q	87	LYS
58	B1	43	THR
58	B1	193	ASP
59	B2	888	THR
66	0	196	ALA
5	E	16	THR
58	B1	1325	PHE
57	A1	250	ASP
62	NG	103	ILE
9	I	126	GLY
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	32
5	E	51/52 (98%)	46 (90%)	5 (10%)	7	24
6	F	34/34 (100%)	33 (97%)	1 (3%)	37	58
7	G	180/199 (90%)	172 (96%)	8 (4%)	25	46
8	H	170/190 (90%)	162 (95%)	8 (5%)	23	45
9	I	172/173 (99%)	170 (99%)	2 (1%)	63	74

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	119/126 (94%)	112 (94%)	7 (6%)	18	39
11	K	87/116 (75%)	82 (94%)	5 (6%)	18	40
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	26
16	P	89/99 (90%)	87 (98%)	2 (2%)	45	64
17	Q	103/104 (99%)	101 (98%)	2 (2%)	50	66
18	R	92/96 (96%)	91 (99%)	1 (1%)	65	74
19	S	83/84 (99%)	82 (99%)	1 (1%)	63	74
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
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	11
27	b	216/218 (99%)	212 (98%)	4 (2%)	50	66
28	c	164/164 (100%)	163 (99%)	1 (1%)	78	82
29	d	165/165 (100%)	160 (97%)	5 (3%)	36	57
30	e	148/150 (99%)	146 (99%)	2 (1%)	59	72
31	f	137/138 (99%)	136 (99%)	1 (1%)	76	80
32	g	114/114 (100%)	111 (97%)	3 (3%)	40	61
33	i	109/110 (99%)	108 (99%)	1 (1%)	70	77
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	66
37	m	109/109 (100%)	108 (99%)	1 (1%)	70	77
38	n	100/103 (97%)	98 (98%)	2 (2%)	48	66
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	99 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	q	89/90 (99%)	89 (100%)	0	100	100
42	r	84/84 (100%)	84 (100%)	0	100	100
43	s	93/93 (100%)	86 (92%)	7 (8%)	12	32
44	t	80/84 (95%)	77 (96%)	3 (4%)	29	50
45	u	83/85 (98%)	82 (99%)	1 (1%)	63	74
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	73
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	39
57	A2	186/286 (65%)	185 (100%)	1 (0%)	81	82
58	B1	1110/1168 (95%)	1018 (92%)	92 (8%)	10	30
59	B2	1150/1157 (99%)	1118 (97%)	32 (3%)	38	59
60	W0	70/75 (93%)	69 (99%)	1 (1%)	59	72
65	a	109/181 (60%)	98 (90%)	11 (10%)	7	23
66	o	574/588 (98%)	554 (96%)	20 (4%)	32	53
67	h	2/2 (100%)	2 (100%)	0	100	100
All	All	8120/8683 (94%)	7841 (97%)	279 (3%)	33	54

All (279) 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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	27	ILE
9	I	128	VAL
10	J	9	GLU
10	J	10	LEU
10	J	45	VAL
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	78	ILE
16	P	107	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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	151	LEU
31	f	36	LEU
32	g	9	VAL
32	g	93	SER
32	g	94	ILE
33	i	72	THR
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
43	s	22	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
43	s	65	ASP
43	s	67	ASP
43	s	74	ILE
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
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
58	B1	255	LEU
58	B1	256	ASP
58	B1	259	ARG
58	B1	284	ASP
58	B1	285	LEU
58	B1	290	ILE
58	B1	317	THR
58	B1	322	ARG
58	B1	324	LEU
58	B1	363	LEU
58	B1	385	LEU
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	892	GLU
59	B2	893	THR
59	B2	894	GLN
59	B2	895	LEU
59	B2	900	LYS
59	B2	901	LEU
59	B2	902	LEU
59	B2	903	ARG
59	B2	905	ILE
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
66	0	301	ASP
66	0	303	LYS
66	0	338	VAL
66	0	390	ASP
66	0	504	LYS
66	0	507	LYS
66	0	508	GLN
66	0	512	ARG
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 (145) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	J	131	ASN
10	J	147	ASN
11	K	52	ASN
11	K	55	HIS
11	K	94	HIS
12	L	8	GLN
12	L	27	ASN
12	L	96	ASN
12	L	129	ASN
13	M	3	GLN
13	M	15	ASN
13	M	20	ASN
14	N	3	ASN
16	P	27	ASN
16	P	80	ASN
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	24	HIS
27	b	85	ASN
27	b	250	GLN
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
33	i	18	ASN
33	i	42	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
45	u	45	GLN
45	u	68	ASN
45	u	73	ASN
46	v	24	ASN
46	v	78	GLN
46	v	88	HIS
48	x	31	ASN
49	y	41	HIS
57	A1	66	HIS
57	A1	84	ASN
57	A1	117	HIS
57	A1	128	HIS
57	A1	227	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
57	A2	23	HIS
57	A2	227	GLN
58	B1	45	ASN
58	B1	364	HIS
58	B1	424	ASN
58	B1	469	HIS
58	B1	805	GLN
58	B1	865	HIS
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	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

5.3.3 RNA

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	440 (15%)	6 (0%)
52	2	119/120 (99%)	18 (15%)	0
53	3	1538/1542 (99%)	193 (12%)	1 (0%)
54	4	28/56 (50%)	17 (60%)	4 (14%)
63	5	75/76 (98%)	45 (60%)	10 (13%)
64	6	76/77 (98%)	14 (18%)	0
All	All	4738/4775 (99%)	727 (15%)	21 (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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	225	C
51	1	228	C
51	1	229	C
51	1	233	A
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	560	C
51	1	563	A
51	1	568	U
51	1	573	U
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	858	G
51	1	859	G
51	1	865	C
51	1	878	A
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	1065	U
51	1	1066	U
51	1	1068	G
51	1	1069	A
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	1313	U
51	1	1321	A
51	1	1325	U
51	1	1326	U
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	1707	G
51	1	1715	G
51	1	1730	C
51	1	1738	G
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	1997	C
51	1	2022	U
51	1	2023	C
51	1	2031	A
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	2173	A
51	1	2178	C
51	1	2179	C
51	1	2180	U
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	2425	A
51	1	2426	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	2427	C
51	1	2429	G
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	1	2685	G
51	1	2689	U
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	2	88	C
52	2	89	U
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	3	280	C
53	3	281	G
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	3	573	A
53	3	575	G
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	3	960	U
53	3	961	U
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	3	1261	A
53	3	1262	C
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	8	U
54	4	9	U
54	4	10	C
54	4	11	U
54	4	12	U
54	4	14	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	4	15	U
54	4	16	U
54	4	17	U
54	4	18	U
54	4	19	U
54	4	20	U
54	4	48	G
54	4	49	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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
63	5	56	C
63	5	57	G
63	5	58	A
63	5	59	U
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 (21) RNA pucker outliers are listed below:

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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
63	5	32	U
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	0.52	0	1,5,7	0.06	0
67	5OH	h	6	67	7,12,13	0.75	0	4,16,18	1.34	1 (25%)
67	UAL	h	5	67	6,8,9	2.34	2 (33%)	4,9,11	1.86	1 (25%)
67	KBE	h	1	67	8,8,9	0.59	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	5OH	h	6	67	-	0/2/18/20	0/1/1/1
67	UAL	h	5	67	-	0/3/7/9	-
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	-4.88	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	-3.28	121.28	125.39
67	h	6	5OH	CR-CB-CA	-2.39	110.07	112.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
67	h	2	DPP	1	0
67	h	6	5OH	3	0
67	h	5	UAL	1	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	$\# Z > 2$
70	PO4	0	802	-	4,4,4	1.01	0	6,6,6	0.51	0
69	GDP	0	801	-	29,30,30	1.17	3 (10%)	45,47,47	1.88	8 (17%)

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	2.81	1.46	1.38
69	0	801	GDP	C6-N1	-2.65	1.33	1.38
69	0	801	GDP	C4-N9	-2.03	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	-5.99	118.85	128.39
69	0	801	GDP	C2-N3-C4	5.05	120.99	112.30
69	0	801	GDP	N9-C4-N3	4.48	134.90	125.95
69	0	801	GDP	C6-C5-N7	3.62	136.88	130.29
69	0	801	GDP	C4-C5-N7	-2.77	106.28	110.67
69	0	801	GDP	C2'-C1'-N9	-2.11	107.39	113.25
69	0	801	GDP	O6-C6-C5	-2.11	120.97	126.53
69	0	801	GDP	C5-C6-N1	2.04	118.45	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

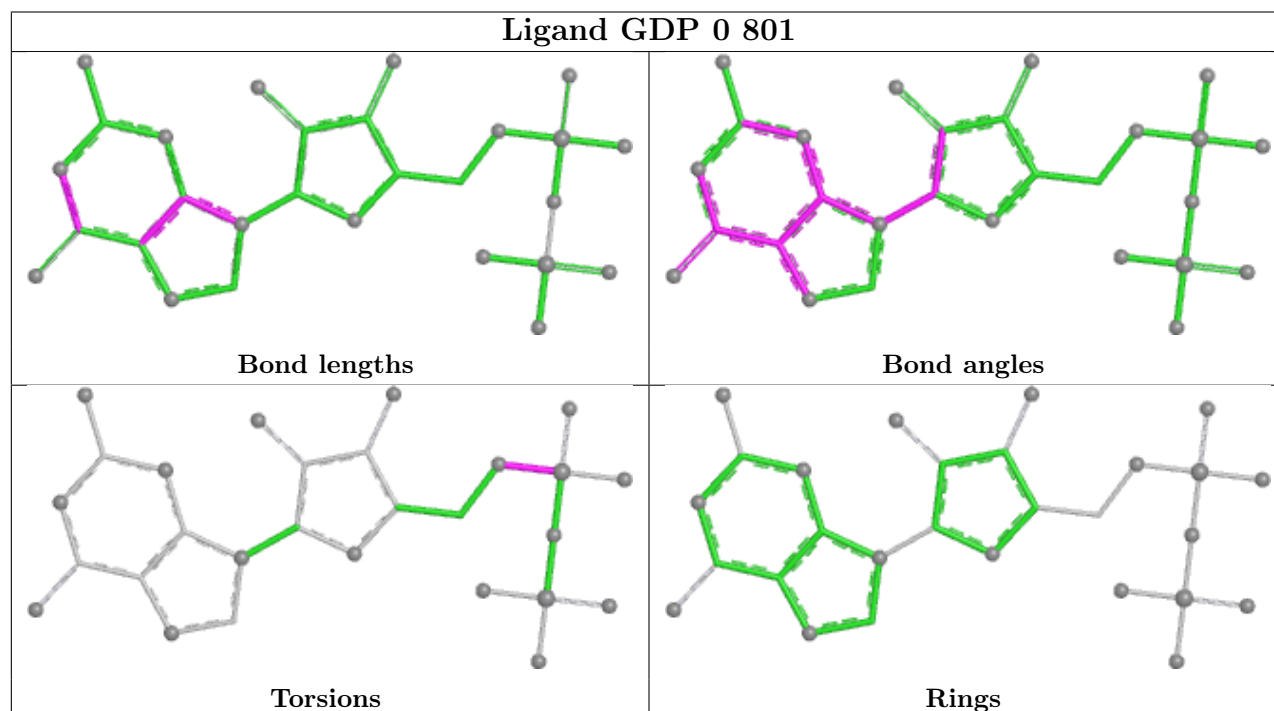
There are no ring outliers.

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.

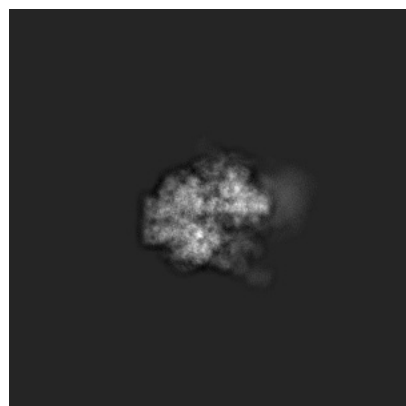
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39173. These allow visual inspection of the internal detail of the map and identification of artifacts.

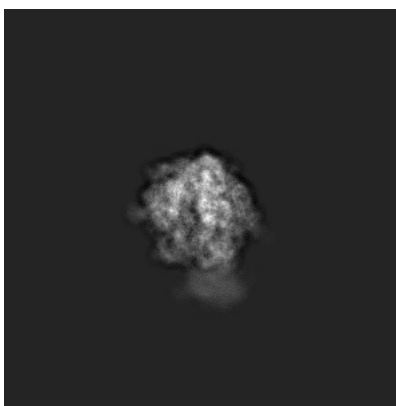
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

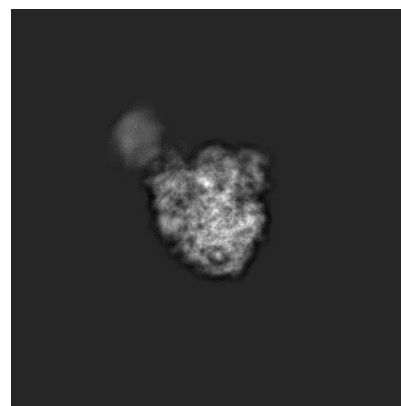
6.1.1 Primary map



X

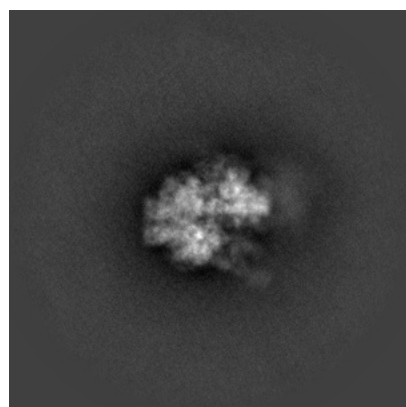


Y

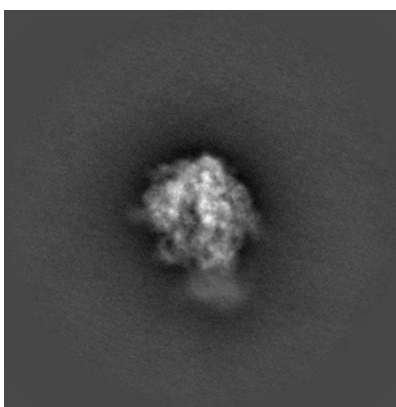


Z

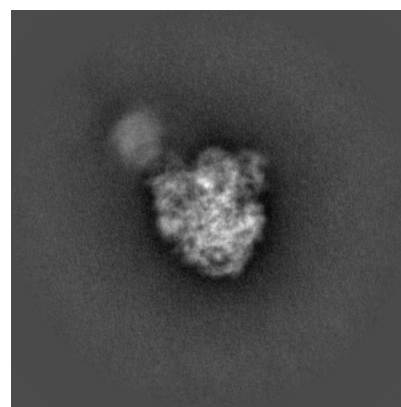
6.1.2 Raw map



X



Y

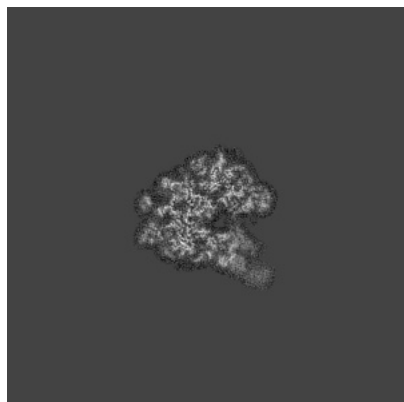


Z

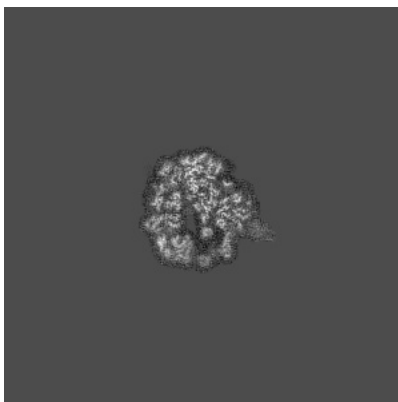
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

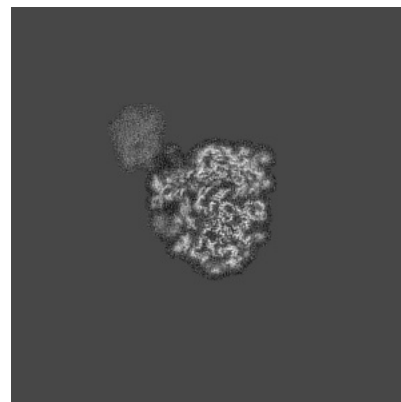
6.2.1 Primary map



X Index: 240

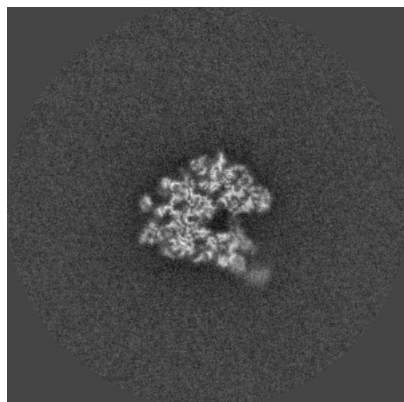


Y Index: 240

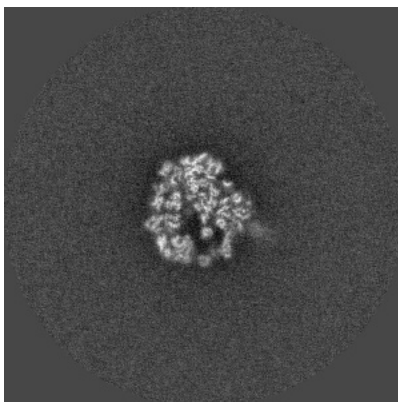


Z Index: 240

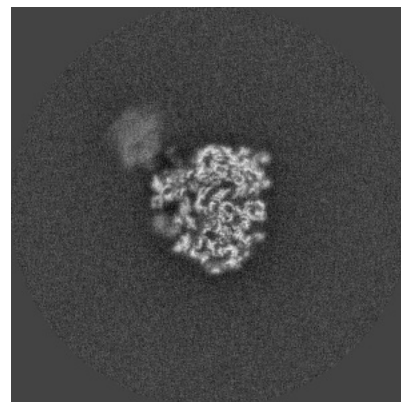
6.2.2 Raw map



X Index: 240



Y Index: 240

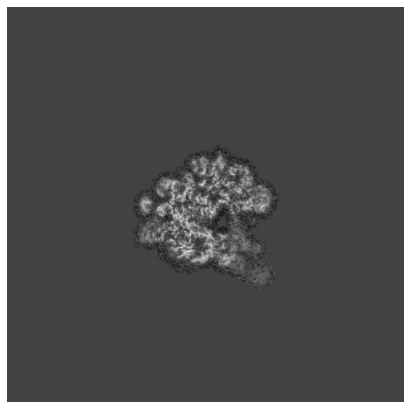


Z Index: 240

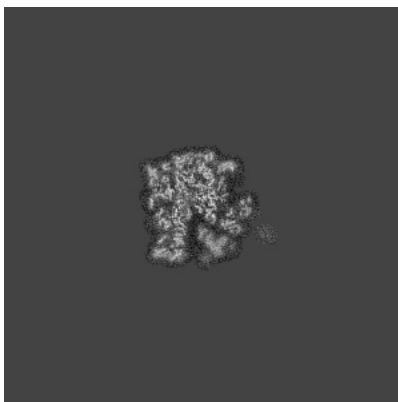
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

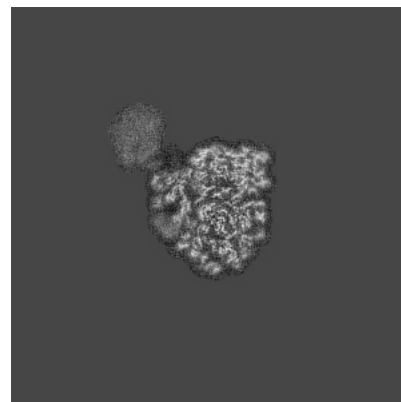
6.3.1 Primary map



X Index: 243

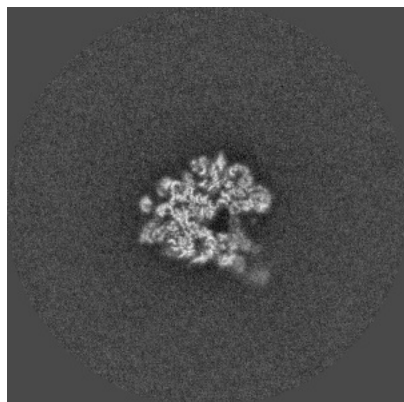


Y Index: 228

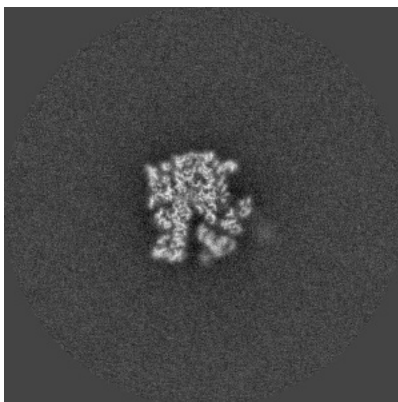


Z Index: 243

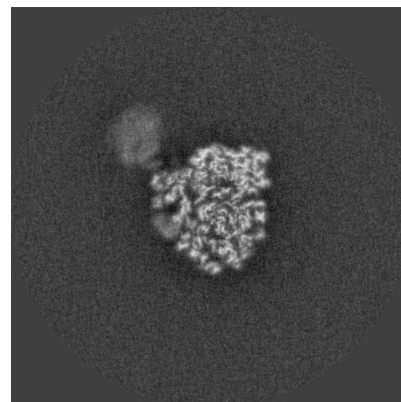
6.3.2 Raw map



X Index: 242



Y Index: 227

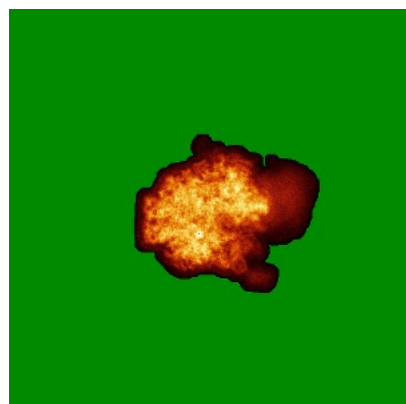


Z Index: 243

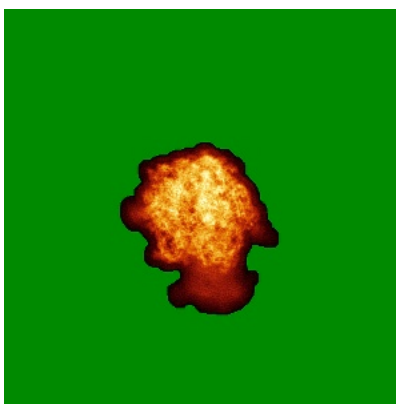
The images above show the largest variance slices of the map in three orthogonal directions.

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

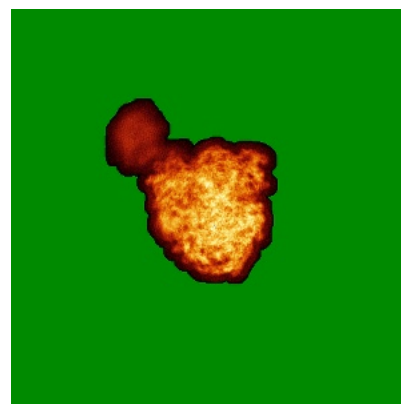
6.4.1 Primary map



X

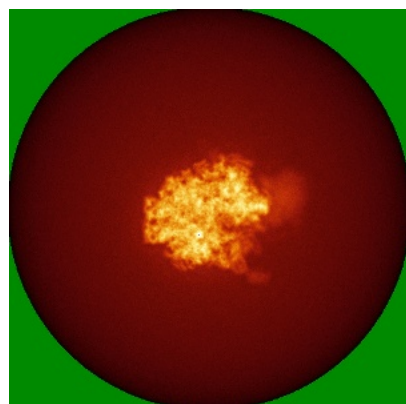


Y

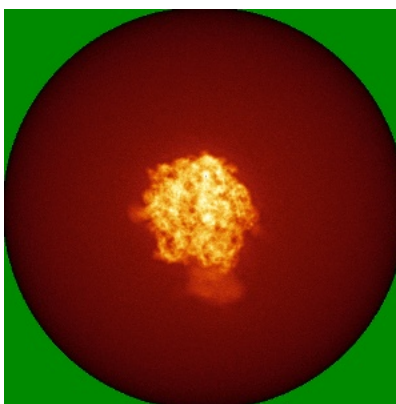


Z

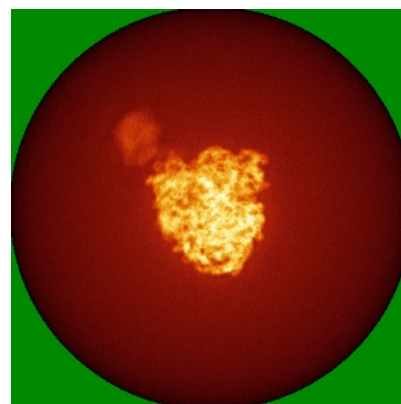
6.4.2 Raw map



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.

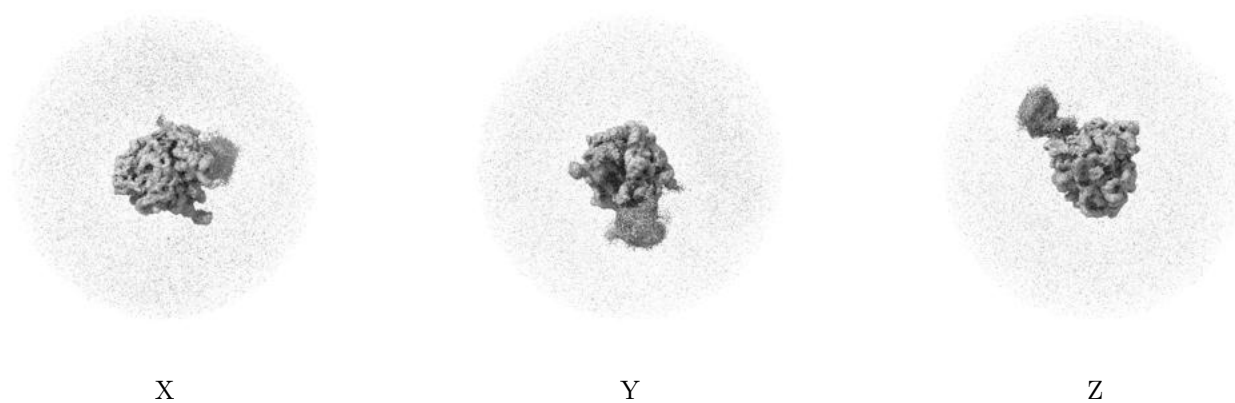
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.011. 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.

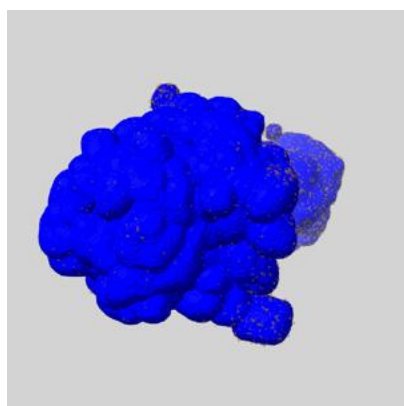
6.6 Mask visualisation [i](#)

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

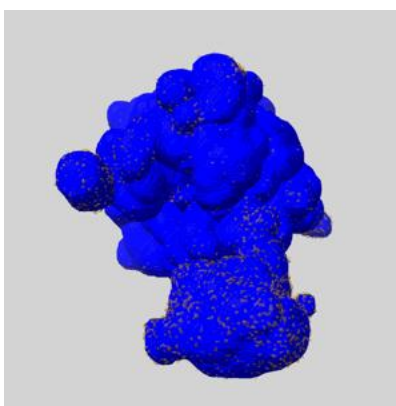
A mask typically either:

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

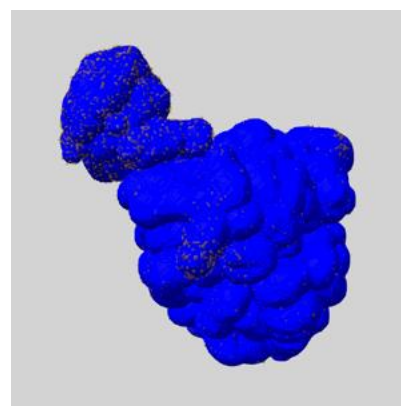
6.6.1 emd_39173_msk_1.map [i](#)



X



Y

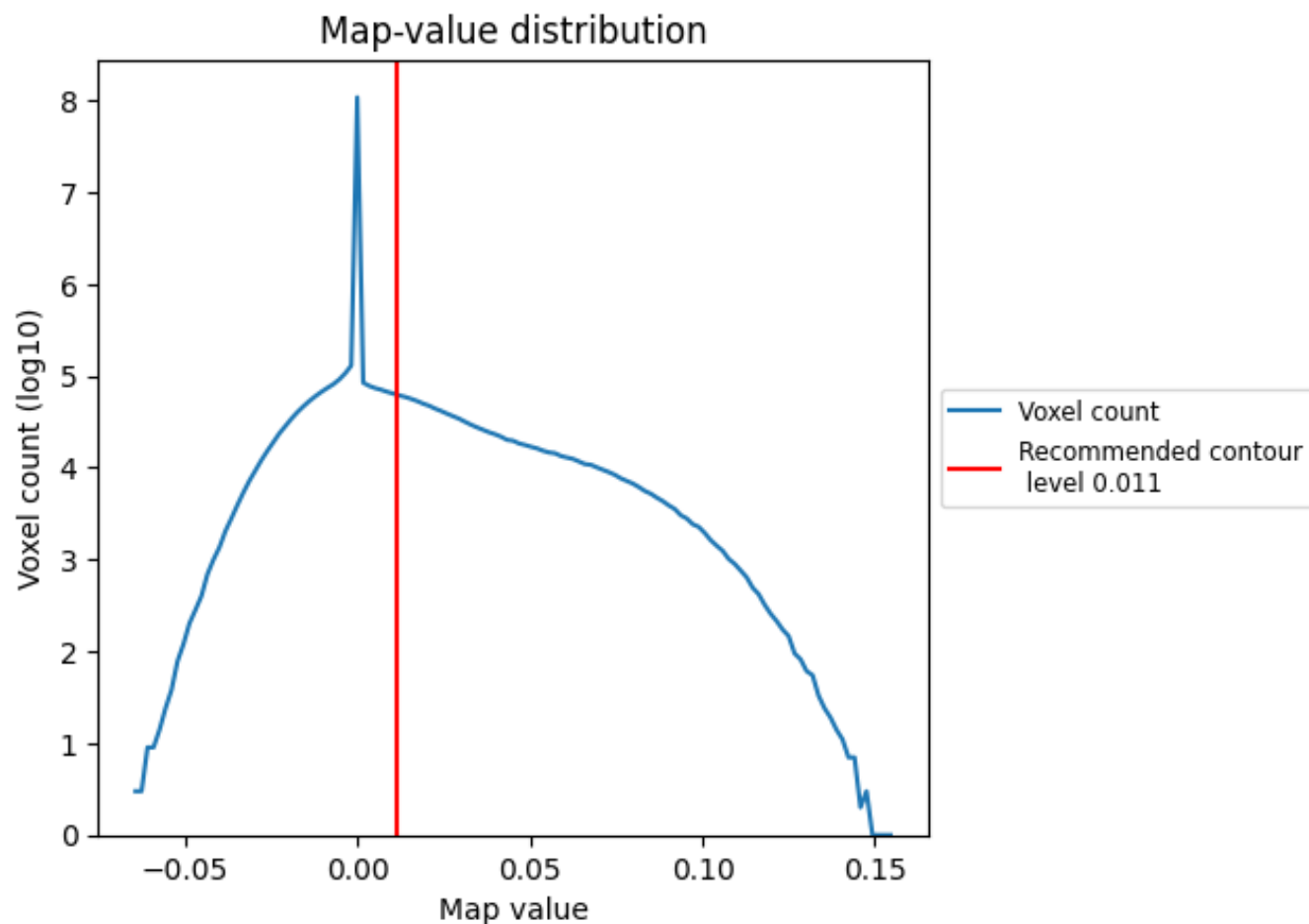


Z

7 Map analysis [i](#)

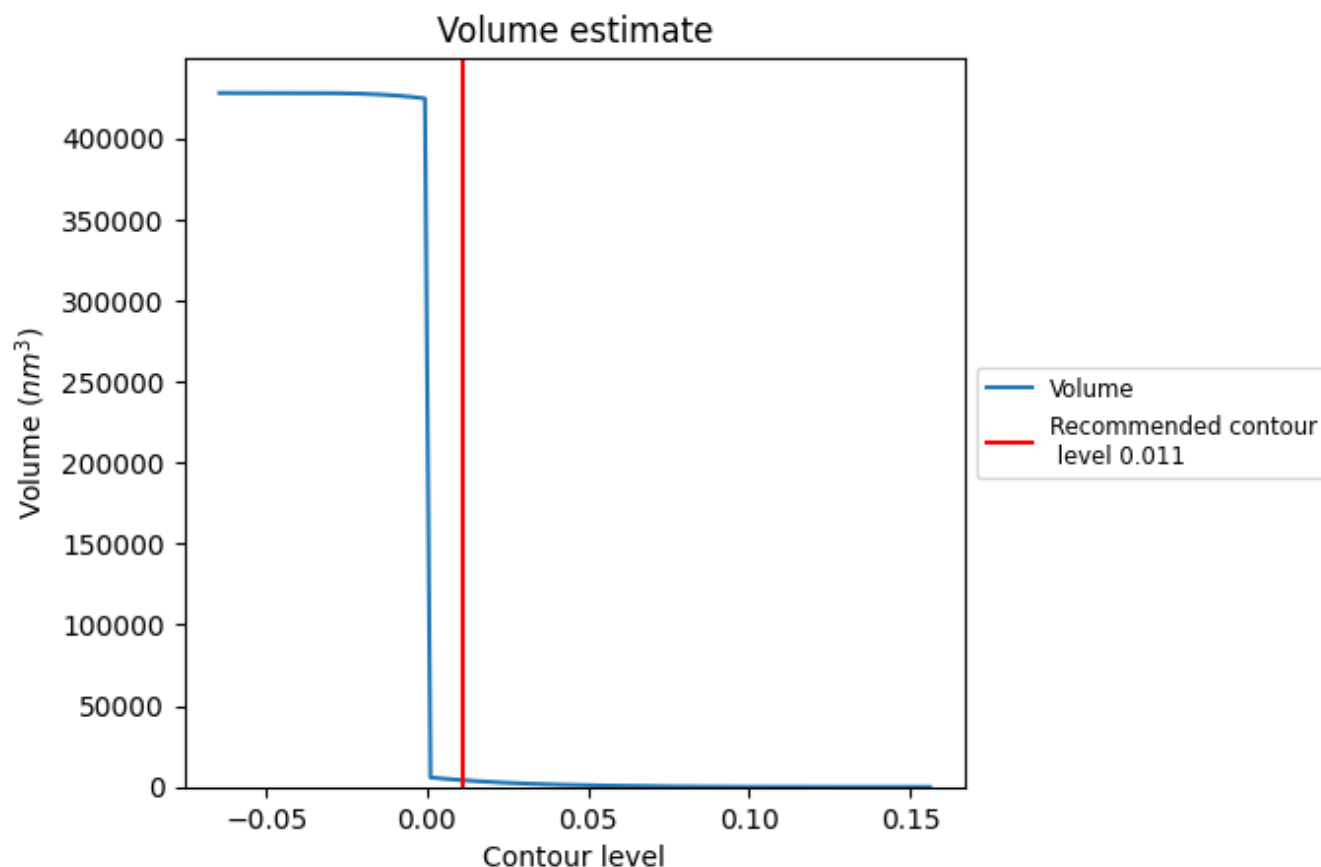
This section contains the results of statistical analysis of the map.

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.

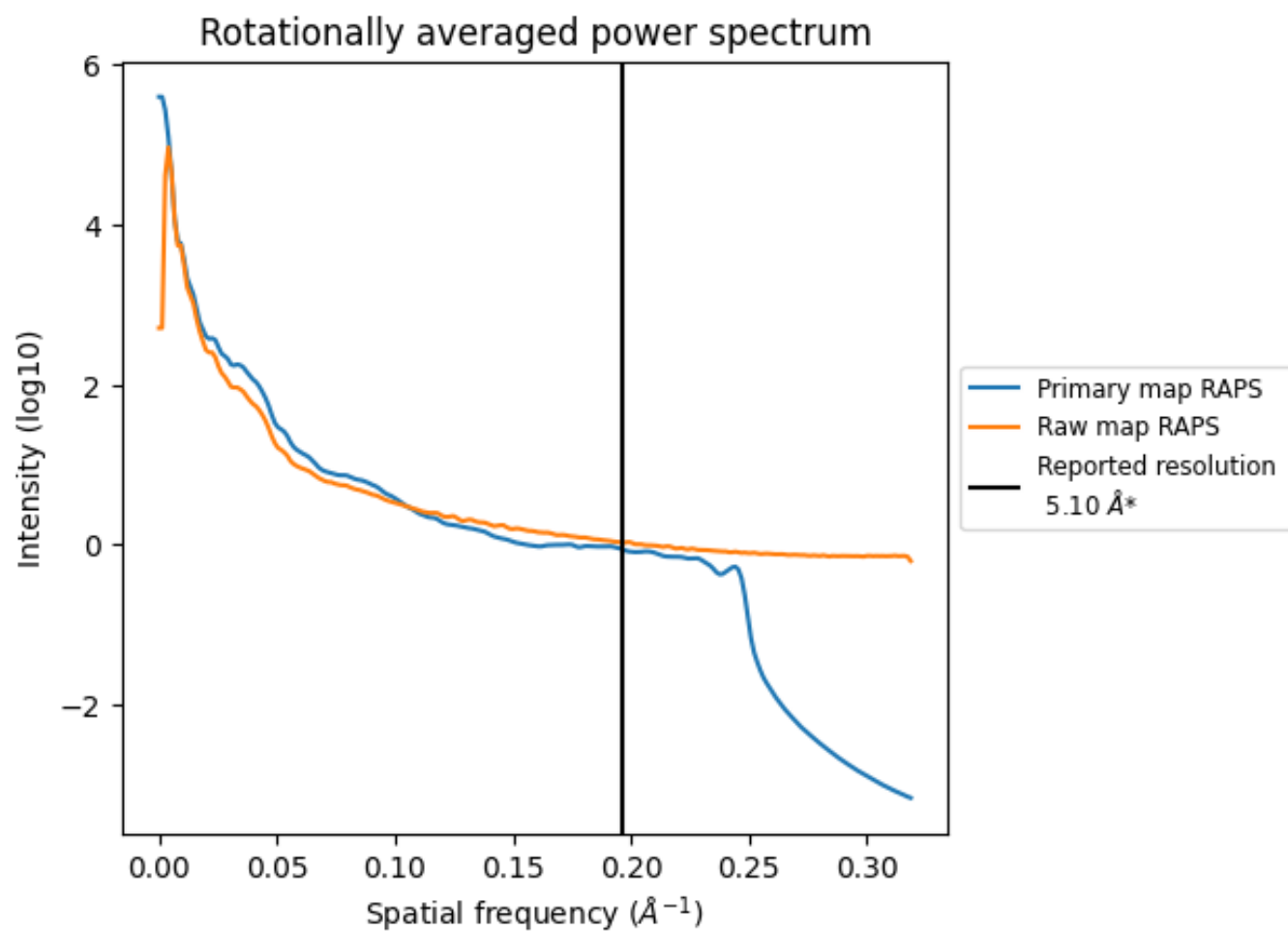
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4189 nm³; this corresponds to an approximate mass of 3784 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

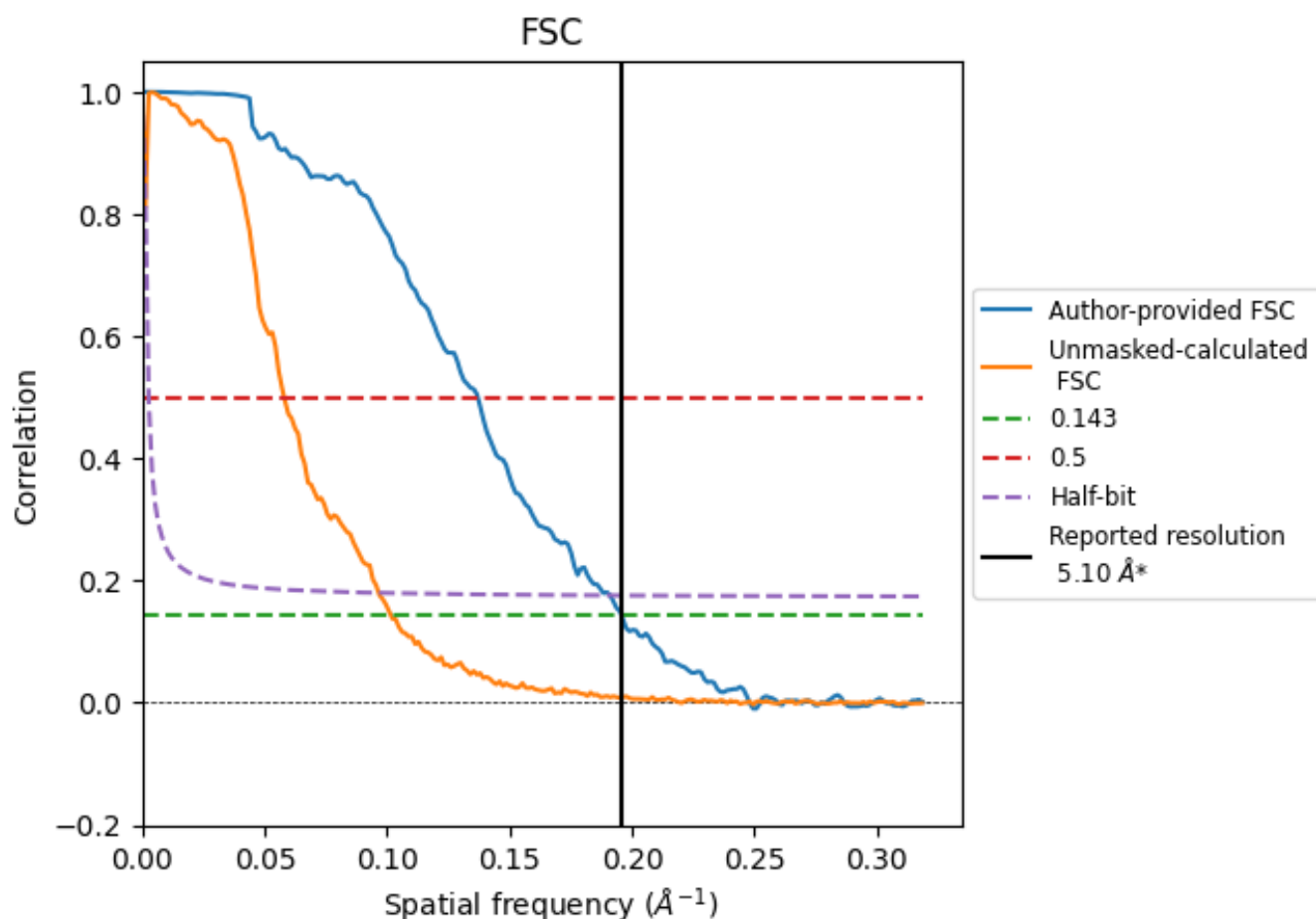


*Reported resolution corresponds to spatial frequency of 0.196 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.196 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

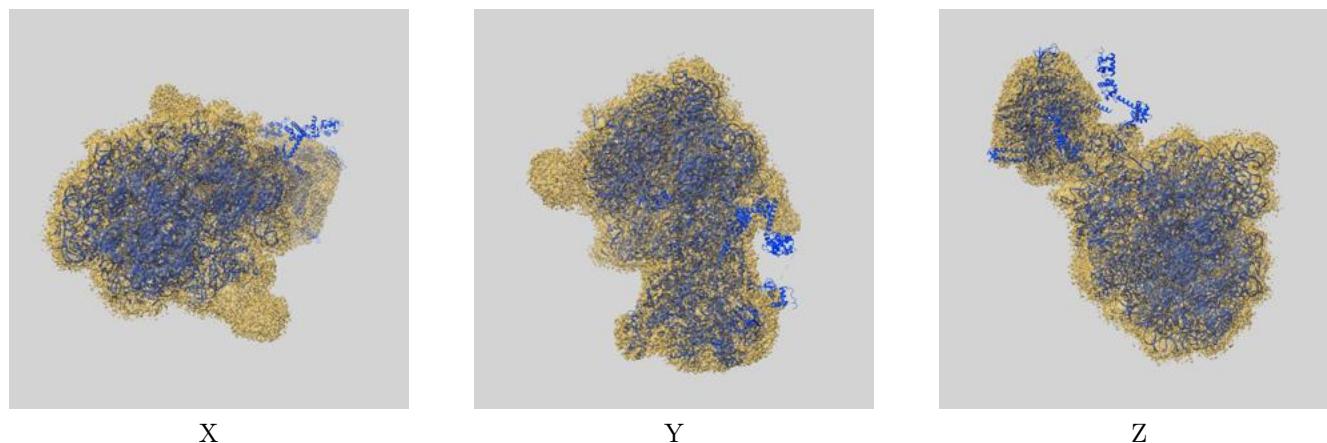
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.10	-	-
Author-provided FSC curve	5.11	7.30	5.23
Unmasked-calculated*	9.84	17.27	714.29

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.84 differs from the reported value 5.1 by more than 10 %

9 Map-model fit [i](#)

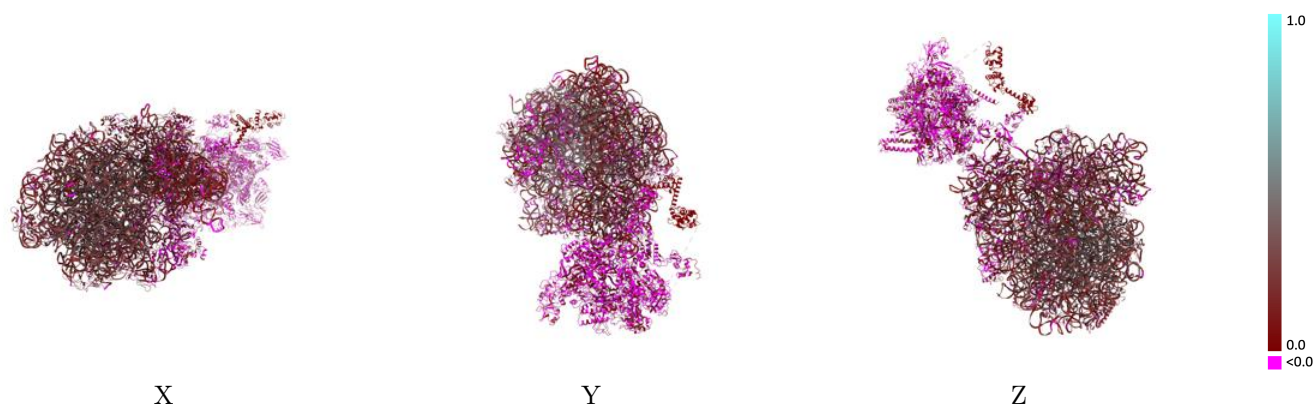
This section contains information regarding the fit between EMDB map EMD-39173 and PDB model 8YDJ. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



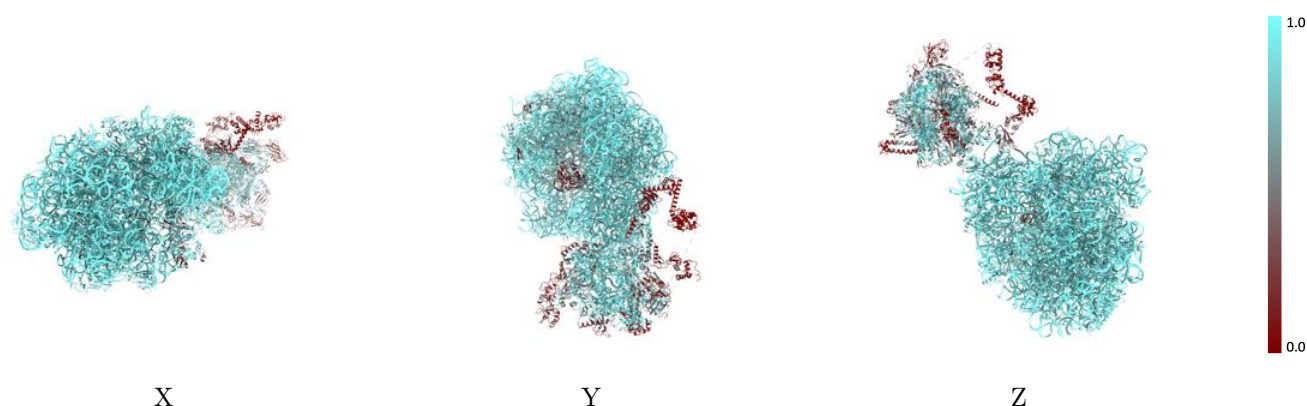
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



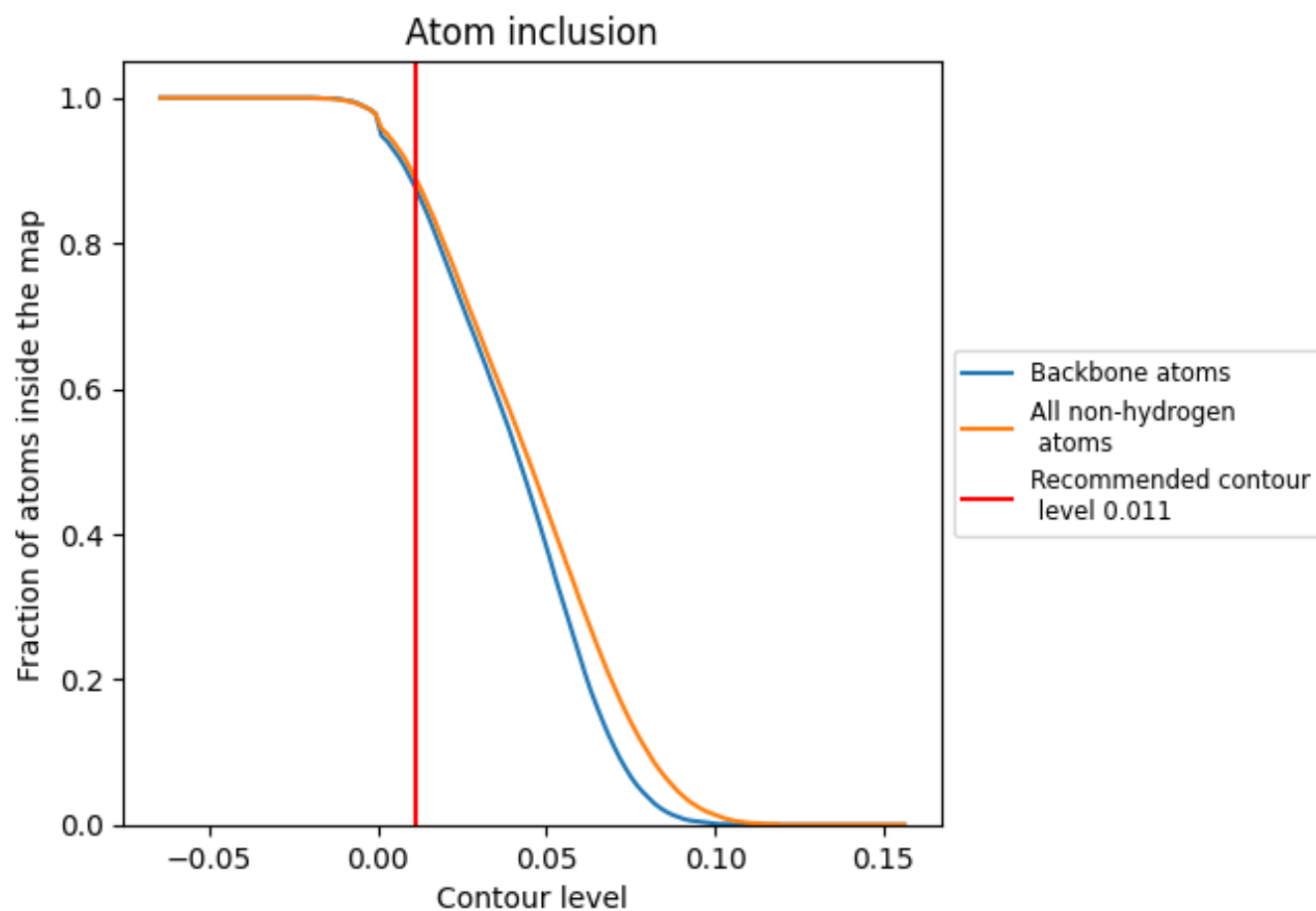
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).

9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 89% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.1630
0	 0.6170	 0.0440
1	 0.9880	 0.2460
2	 0.9790	 0.1390
3	 0.9820	 0.1930
4	 0.8500	 0.0680
5	 0.4280	 0.0410
6	 0.9630	 0.1960
8	 0.8200	 0.0220
9	 0.9040	 0.0500
A	 0.9090	 0.0620
A1	 0.3200	 -0.0120
A2	 0.5590	 -0.0060
B	 0.9390	 0.2500
B1	 0.6730	 -0.0000
B2	 0.6840	 0.0120
C	 0.8780	 0.1010
D	 0.9320	 0.2970
E	 0.9180	 0.1920
F	 0.9310	 0.1730
G	 0.9120	 0.1110
H	 0.9000	 0.1300
I	 0.9330	 0.1280
J	 0.8870	 0.1270
K	 0.9260	 0.1350
L	 0.8950	 0.1080
M	 0.9040	 0.1100
N	 0.9070	 0.1000
NA	 0.2630	 0.0010
NG	 0.6940	 0.0110
O	 0.9030	 0.0950
P	 0.9420	 0.1640
Q	 0.8600	 0.1700
R	 0.9110	 0.1240
S	 0.9130	 0.1000



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
T	 0.9330	 0.1470
U	 0.9390	 0.1010
V	 0.9110	 0.0880
W	 0.9300	 0.1570
W0	 0.4950	 0.0110
X	 0.9400	 0.1370
Y	 0.9260	 0.1060
Z	 0.8320	 0.1120
a	 0.9280	 0.0560
b	 0.9220	 0.2740
c	 0.9500	 0.2320
d	 0.9390	 0.1670
e	 0.8860	 0.0790
f	 0.9180	 0.1040
g	 0.7470	 0.0830
h	 1.0000	 0.2940
i	 0.7790	 0.0160
j	 0.9410	 0.2390
k	 0.8860	 0.2540
l	 0.9250	 0.1730
m	 0.8740	 0.1600
n	 0.9610	 0.2530
o	 0.9550	 0.0450
p	 0.9210	 0.2120
q	 0.9580	 0.2380
r	 0.9520	 0.1800
s	 0.9270	 0.2590
t	 0.9210	 0.1640
u	 0.9530	 0.1540
v	 0.9390	 0.1100
w	 0.9270	 0.1120
x	 0.9370	 0.2230
y	 0.9360	 0.1350
z	 0.9200	 0.1250