



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 11:34 PM UTC

PDB ID : 8P8W / pdb_00008p8w
EMDB ID : EMD-17145
Title : Mycoplasma pneumoniae di-ribosome in chloramphenicol-treated cells (following 70S)
Authors : Schacherl, M.; Xue, L.; Spahn, C.M.T.; Mahamid, J.
Deposited on : 2023-06-02
Resolution : 8.70 Å (reported)
Based on initial models : 7OOC, 7OOD

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

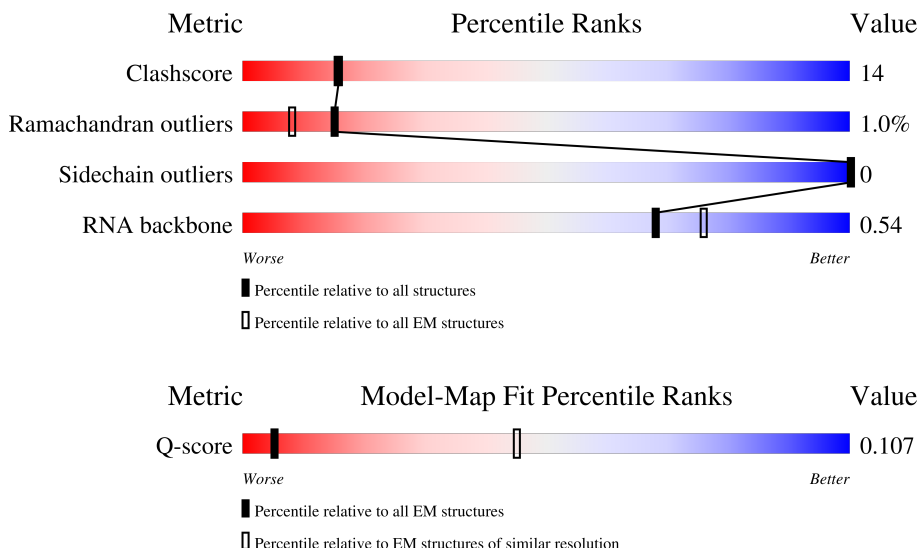
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.70 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	282 (8.20 - 9.20)

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	0	48	
2	1	59	
3	2	37	

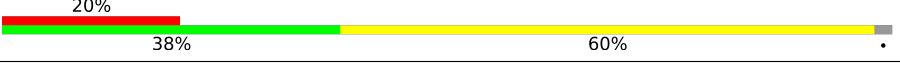
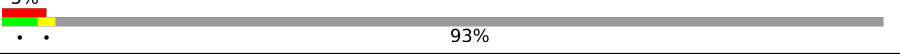
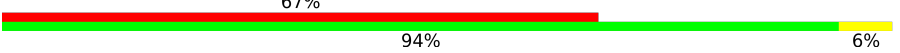
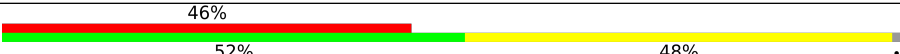
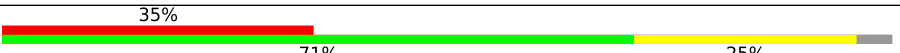
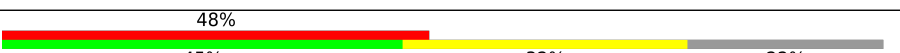
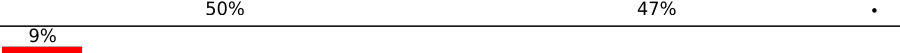
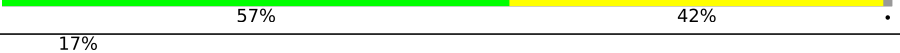
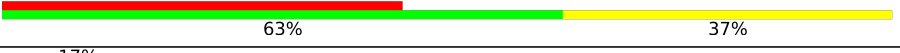
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	3	2907	
5	4	108	
6	5	1520	
7	6	76	
8	7	75	
9	A	294	
10	B	273	
11	C	205	
11	U	205	
12	D	219	
13	E	215	
14	F	155	
15	G	142	
16	H	132	
17	I	108	
18	J	121	
19	K	139	
20	L	124	
21	M	61	
22	N	86	
23	O	94	
24	P	85	
25	Q	104	
26	R	87	
27	S	87	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
28	T	60	
29	X	444	
30	Y	29	
31	Z	36	
32	a	287	
33	b	287	
34	c	212	
35	d	180	
36	e	184	
37	f	149	
38	g	161	
39	h	137	
40	i	146	
41	j	122	
42	k	151	
43	l	139	
44	m	124	
45	n	116	
46	o	119	
47	p	127	
48	q	100	
49	r	159	
50	s	237	
51	t	111	
52	u	104	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
53	v	65	25% 49% 48% • •
54	w	111	50% 75% 24% •
55	x	97	61% 54% 37% • 8%
56	y	57	19% 53% 44% • •
57	z	53	40% 68% 26% 6%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 151559 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 L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	2893	Total	C	N	O	P	0	0
			61995	27704	11293	20105	2893		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	108	Total	C	N	O	P	0	0
			2305	1030	415	752	108		

- Molecule 6 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	1507	Total	C	N	O	P	0	0
			32258	14420	5847	10484	1507		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	1003	A	G	conflict	GB 26117688

- Molecule 7 is a RNA chain called tRNA-Ala (E-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	76	Total	C	N	O	P	0	0
			1620	723	287	534	76		

- Molecule 8 is a RNA chain called tRNA-Asp (P-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	75	Total	C	N	O	P	0	0
			1599	712	279	533	75		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	17	G	-	insertion	GB 26117688
7	55	C	U	conflict	GB 26117688

- Molecule 9 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	268	Total	C	N	O	S	0	0
			2152	1368	379	396	9		

- Molecule 10 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	225	Total	C	N	O	S	0	0
			1773	1121	328	319	5		

- Molecule 11 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	204	Total	C	N	O	S	0	0
			1669	1057	316	292	4		
11	U	204	Total	C	N	O	S	0	0
			1669	1057	316	292	4		

- Molecule 12 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	173	Total	C	N	O	S	0	0
			1346	846	265	232	3		

- Molecule 13 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 14 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	155	Total	C	N	O	S	0	0
			1254	790	240	217	7		

- Molecule 15 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	142	Total	C	N	O	S	0	0
			1118	728	194	193	3		

- Molecule 16 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	129	Total	C	N	O	S	0	0
			1040	661	195	183	1		

- Molecule 17 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	104	Total	C	N	O	S	0	0
			832	536	147	148	1		

- Molecule 18 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 19 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	135	Total	C	N	O	S	0	0
			1071	677	212	180	2		

- Molecule 20 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	121	Total	C	N	O	S	0	0
			975	609	197	169			

- Molecule 21 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 22 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	86	Total	C	N	O	S	0	0
			697	441	131	124	1		

- Molecule 23 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	87	Total	C	N	O	S	0	0
			705	453	130	118	4		

- Molecule 24 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	85	Total	C	N	O	S	0	0
			693	436	138	118	1		

- Molecule 25 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	78	Total	C	N	O	S	0	0
			651	417	129	100	5		

- Molecule 26 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	86	Total	C	N	O	S	0	0
			700	444	132	122	2		

- Molecule 27 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	79	Total	C	N	O		0	0
			643	391	138	114			

- Molecule 28 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	59	Total	C	N	O	S	0	0
			519	326	111	80	2		

- Molecule 29 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	30	Total	C	N	O	S	0	0
			242	155	43	43	1		

- Molecule 30 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	29	Total	C	N	O	P	0	0
			623	280	120	194	29		

- Molecule 31 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	Z	36	Total	C	N	O	0	0
			187	112	37	38		

- Molecule 32 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 33 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	231	Total	C	N	O	S	0	0
			1778	1129	320	322	7		

- Molecule 34 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	211	Total	C	N	O	S	0	0
			1654	1053	299	299	3		

- Molecule 35 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	179	Total	C	N	O	S	0	0
			1416	910	251	251	4		

- Molecule 36 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	176	Total	C	N	O		0	0
			1396	899	247	250			

- Molecule 37 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	149	Total	C	N	O	S	0	0
			1210	780	212	215	3		

- Molecule 38 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	125	Total	C	N	O	S	0	0
			951	606	165	177	3		

- Molecule 39 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 40 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 41 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 42 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	150	Total	C	N	O	S	0	0
			1170	741	228	200	1		

- Molecule 43 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 44 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 45 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	116	Total	C	N	O	S	0	0
			918	573	181	162	2		

- Molecule 46 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	118	Total	C	N	O	S	0	0
			966	609	186	170	1		

- Molecule 47 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	118	Total	C	N	O	S	0	0
			981	624	194	161	2		

- Molecule 48 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 49 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	142	Total	C	N	O	S	0	0
			1091	677	212	195	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	95	Total	C	N	O	S	0	0
			740	486	125	128	1		

- Molecule 51 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	111	Total	C	N	O	S	0	0
			871	550	166	152	3		

- Molecule 52 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	101	Total	C	N	O	S	0	0
			786	498	148	139	1		

- Molecule 53 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	64	Total	C	N	O	S	0	0
			520	320	109	90	1		

- Molecule 54 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	w	110	Total	C	N	O	0	0
			906	576	168	162		

- Molecule 55 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	x	89	Total	C	N	O	S	0	0
			708	449	124	131	4		

- Molecule 56 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

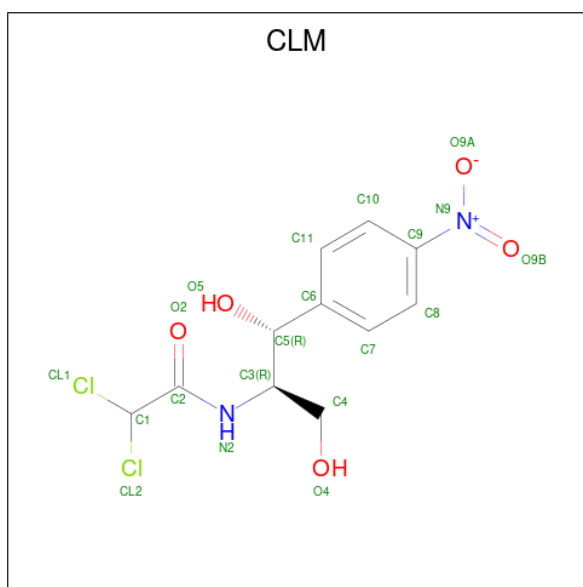
- Molecule 57 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	2	1	Total	Zn	0
			1	1	
58	M	1	Total	Zn	0
			1	1	
58	Q	1	Total	Zn	0
			1	1	
58	x	1	Total	Zn	0
			1	1	
58	y	1	Total	Zn	0
			1	1	
58	z	1	Total	Zn	0
			1	1	

- Molecule 59 is CHLORAMPHENICOL (CCD ID: CLM) (formula: $C_{11}H_{12}Cl_2N_2O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
59	3	1	Total	C	Cl	N	O	0
			20	11	2	2	5	

- Molecule 60 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
60	3	1	Total	K	0
			1	1	

- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
61	3	206	Total	Mg	0
			206	206	
61	4	1	Total	Mg	0
			1	1	
61	5	90	Total	Mg	0
			90	90	
61	6	1	Total	Mg	0
			1	1	
61	K	1	Total	Mg	0
			1	1	
61	P	1	Total	Mg	0
			1	1	
61	Y	1	Total	Mg	0
			1	1	

Continued on next page...

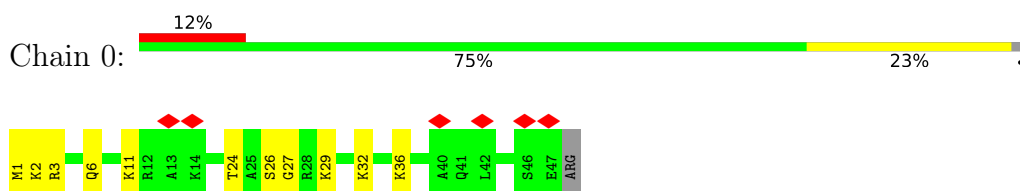
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
61	b	2	Total 2	Mg 2	0
61	i	1	Total 1	Mg 1	0
61	k	2	Total 2	Mg 2	0
61	y	2	Total 2	Mg 2	0

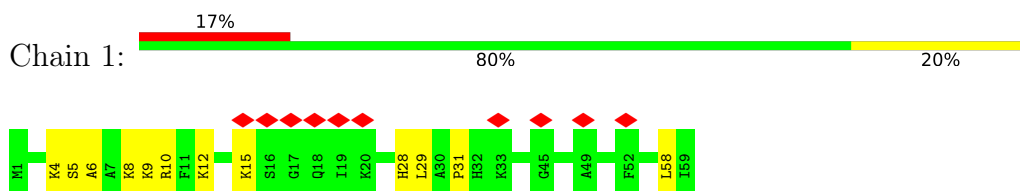
3 Residue-property plots

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.

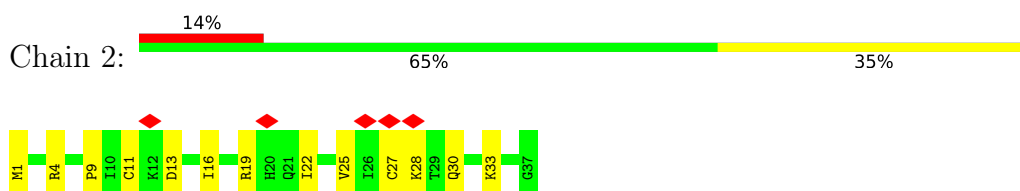
- Molecule 1: 50S ribosomal protein L34



- Molecule 2: 50S ribosomal protein L35

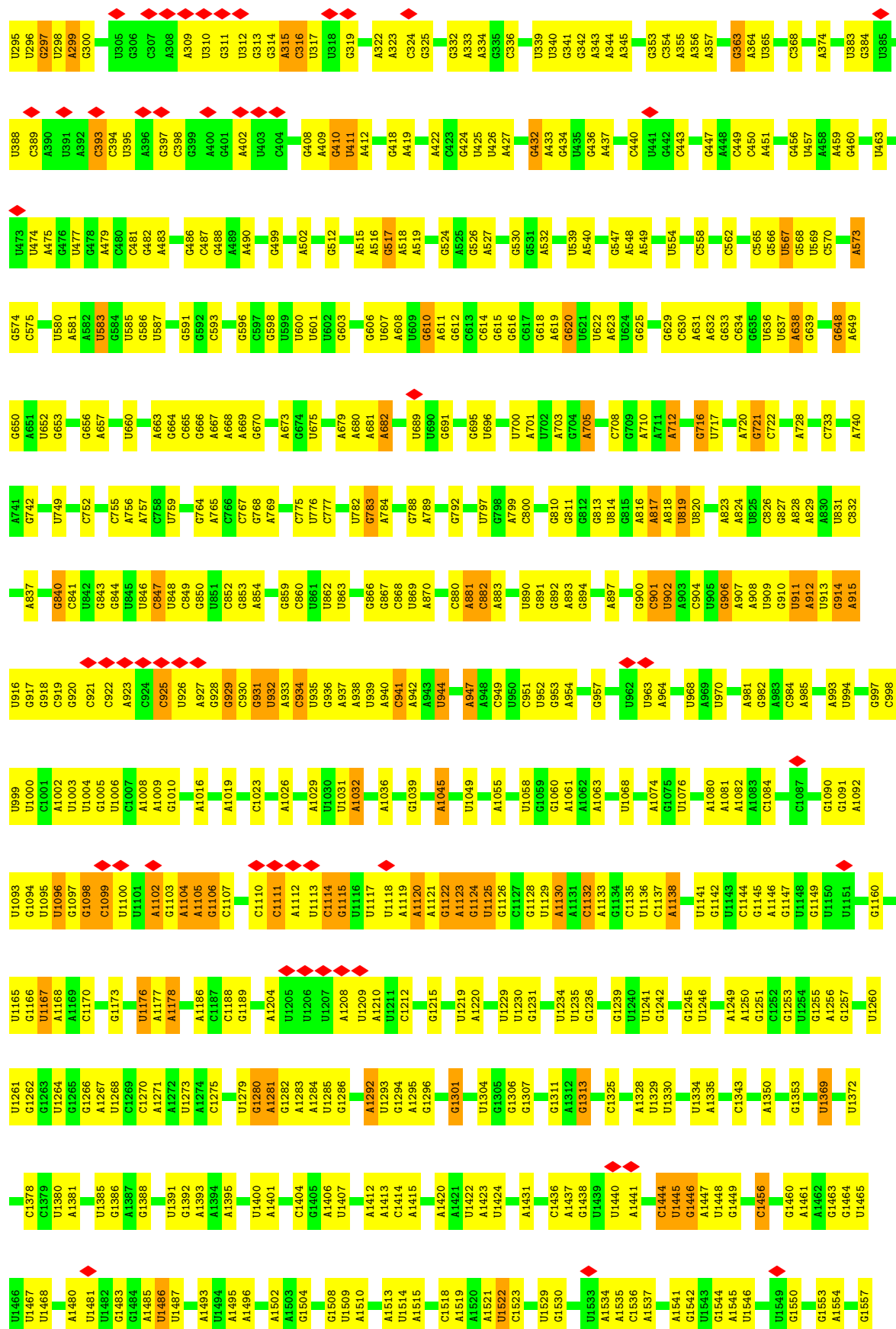


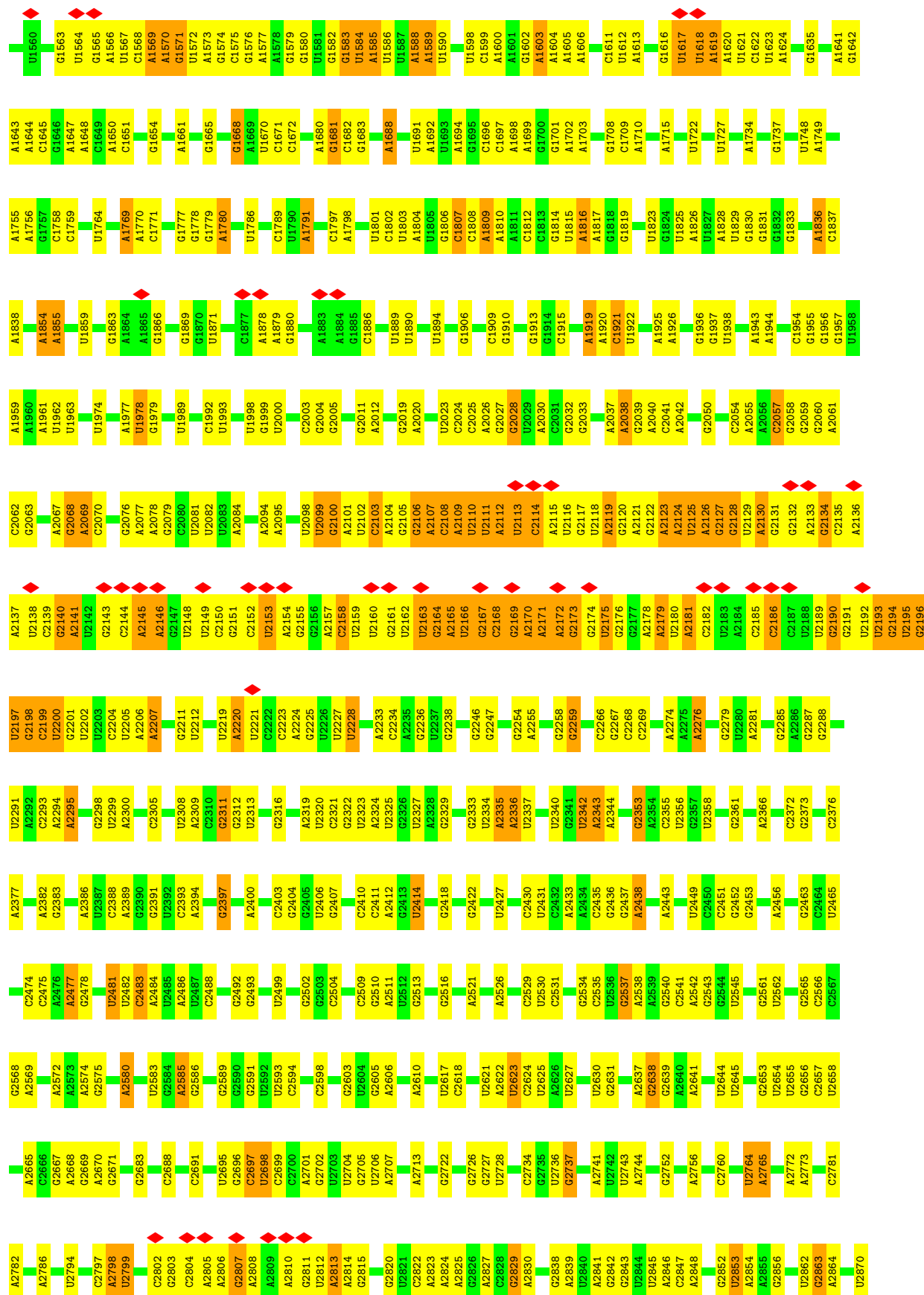
- Molecule 3: 50S ribosomal protein L36

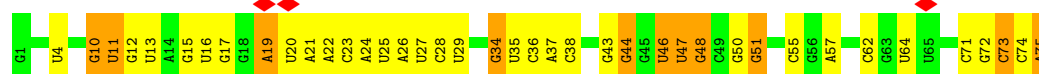
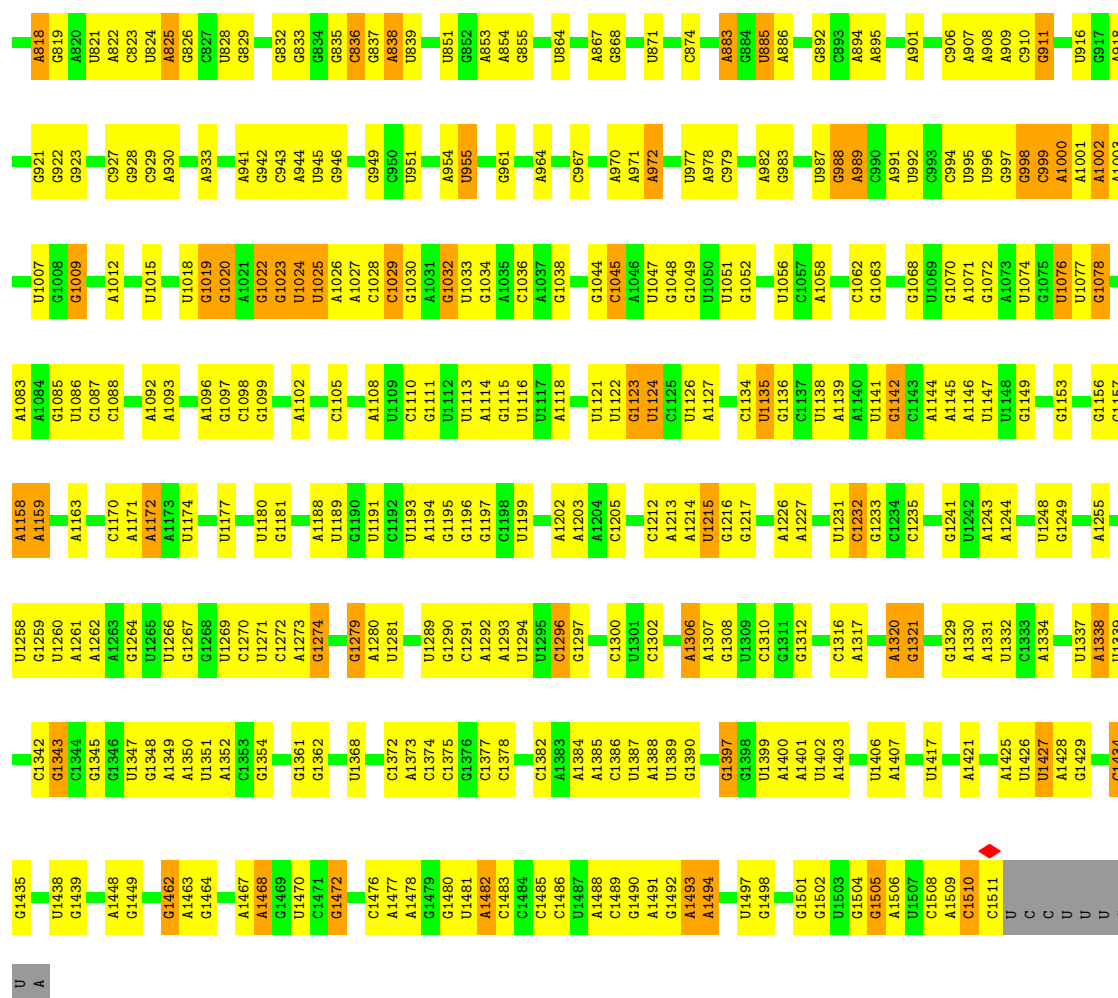


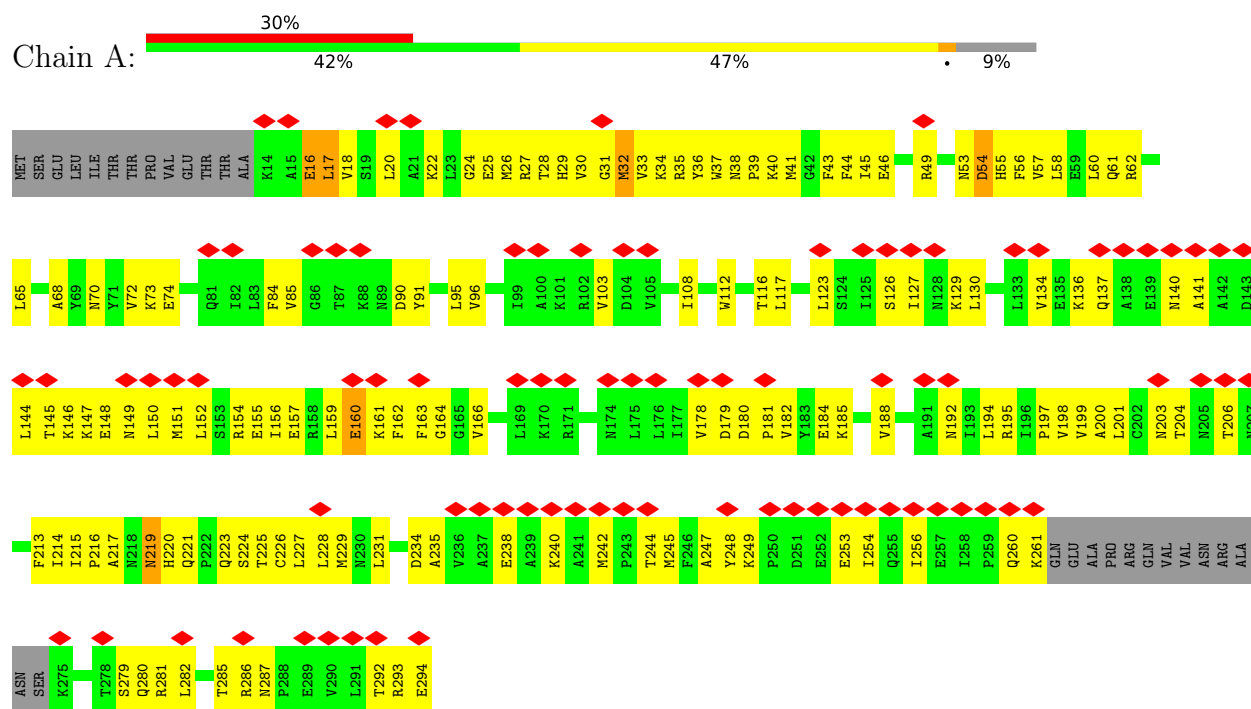
- Molecule 4: 23S ribosomal RNA



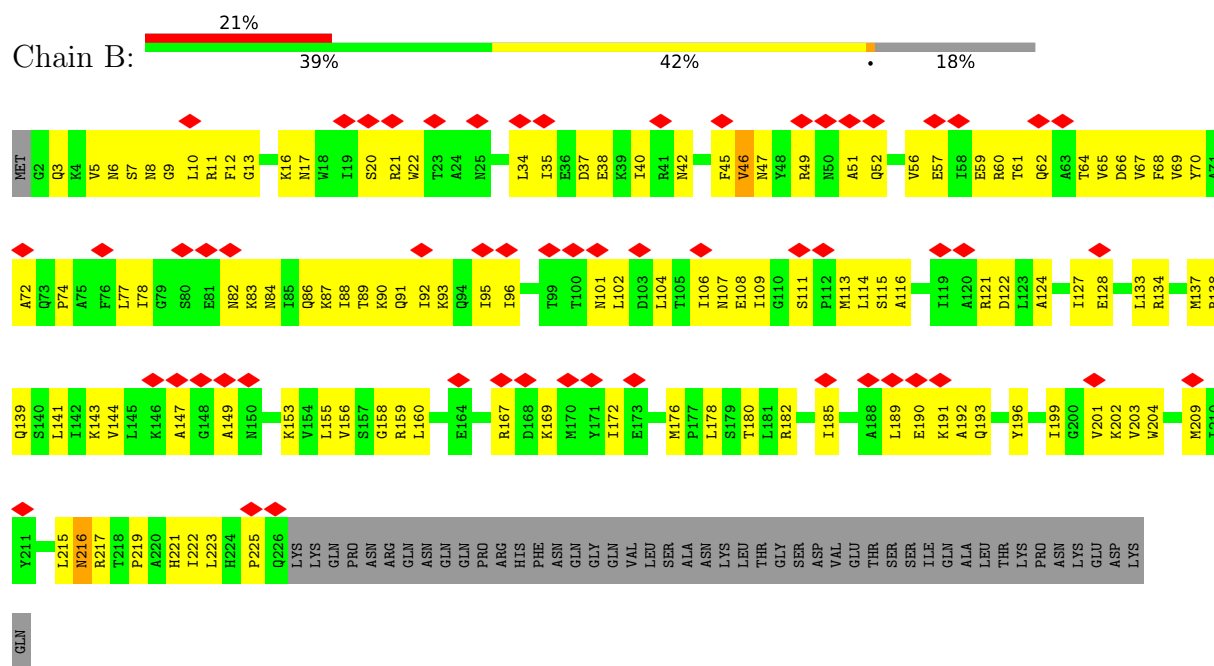




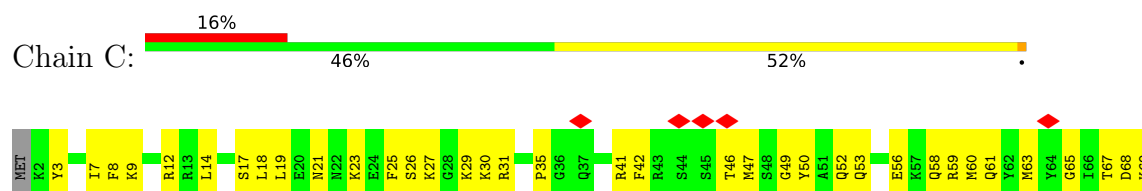


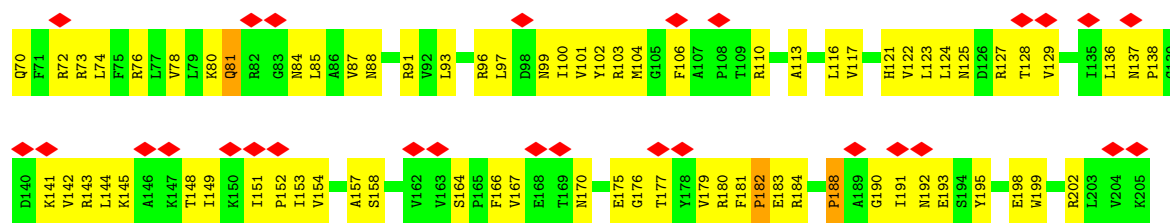


• Molecule 10: 30S ribosomal protein S3

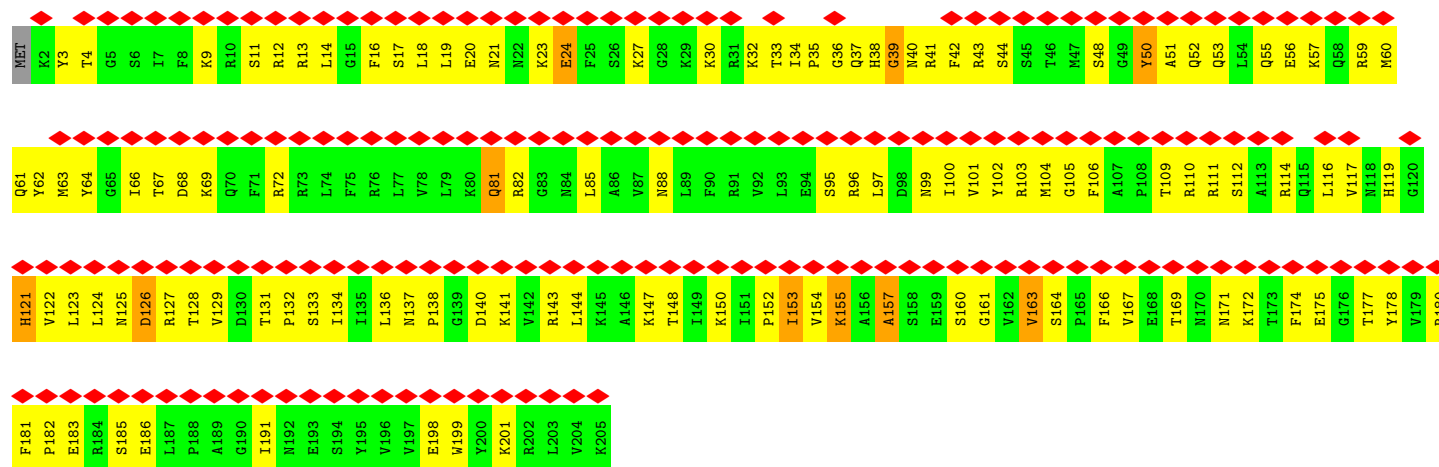


• Molecule 11: 30S ribosomal protein S4

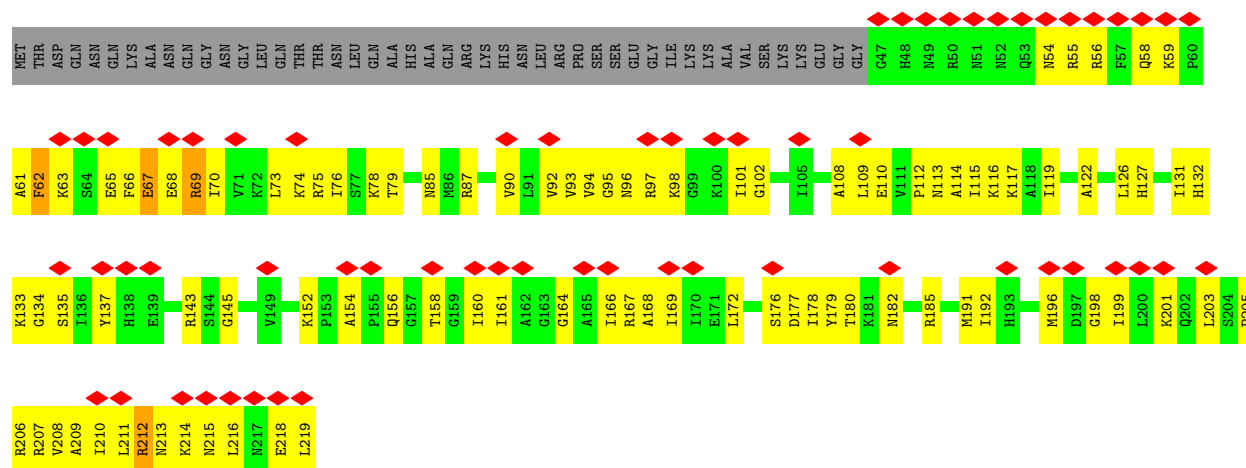




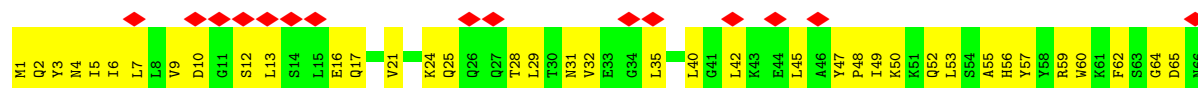
• Molecule 11: 30S ribosomal protein S4

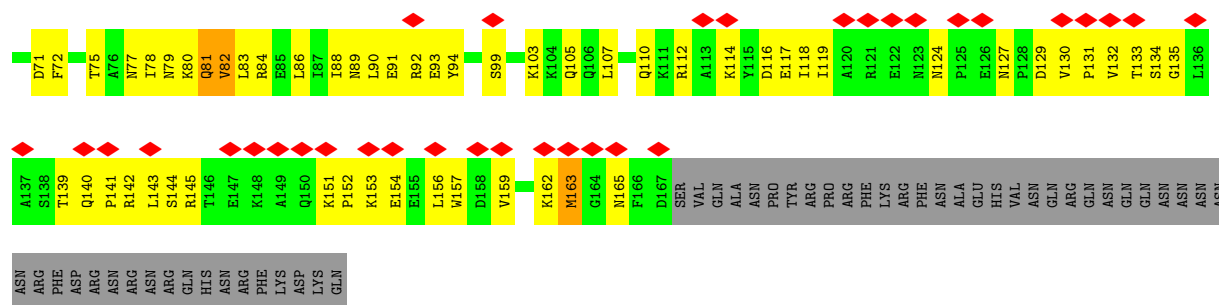


• Molecule 12: 30S ribosomal protein S5

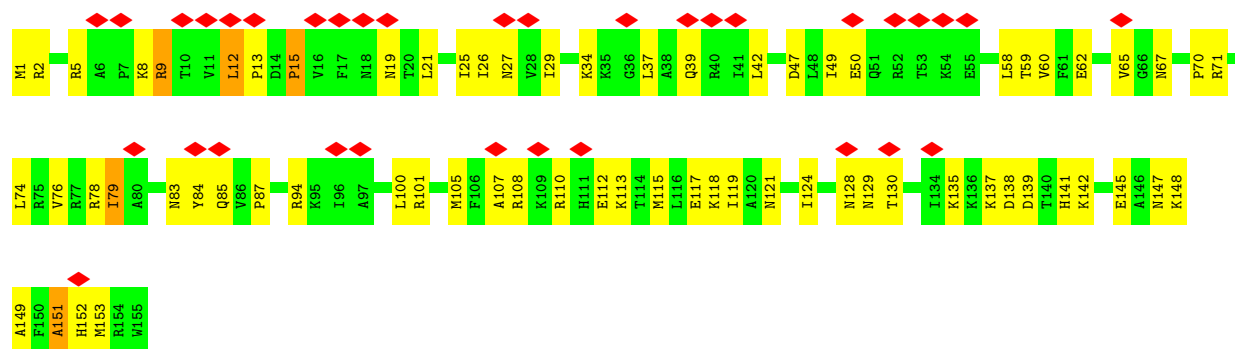


• Molecule 13: 30S ribosomal protein S6

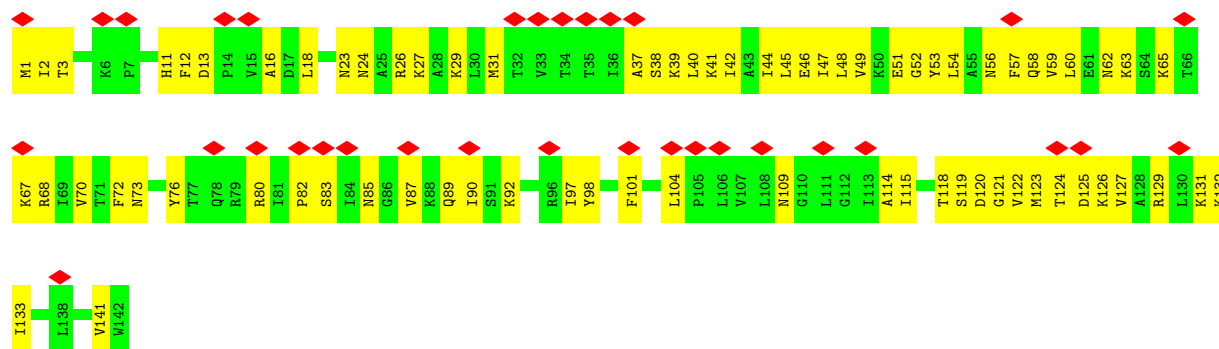




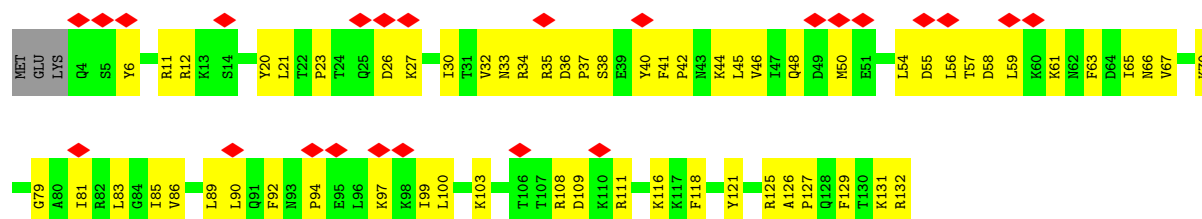
• Molecule 14: 30S ribosomal protein S7



• Molecule 15: 30S ribosomal protein S8



• Molecule 16: 30S ribosomal protein S9



Chain I:

Chain J:

Sequence logo for Chain J. The y-axis represents frequency in bits (0.00 to 0.25). The x-axis shows positions 1 to 221. A bar chart at the top indicates the overall composition: 16% red, 56% green, 38% yellow, and 6% grey.

Position	Amino Acid	Frequency (bits)
1	ALA	0.00
2	LYS	0.00
3	LYS	0.00
4	LYS	0.00
5	LYS	0.00
6	ILE	0.00
7	H8	0.00
8	V9	0.00
9	S10	0.00
10	S11	0.00
11	G12	0.00
12	I13	0.00
13	I14	0.00
14	H15	0.00
15	V16	0.00
16	S17	0.00
17	N21	0.00
18	N22	0.00
19	T23	0.00
20	I24	0.00
21	V25	0.00
22	D29	0.00
23	P30	0.00
24	N33	0.00
25	Y34	0.00
26	L35	0.00
27	S40	0.00
28	M43	0.00
29	K51	0.00
30	Y54	0.00
31	S55	0.00
32	F58	0.00
33	A59	0.00
34	A60	0.00
35	D61	0.00
36	K65	0.00
37	T66	0.00
38	E69	0.00
39	M70	0.00
40	G71	0.00
41	H72	0.00
42	A73	0.00
43	T74	0.00
44	V75	0.00
45	K76	0.00
46	L77	0.00
47	F78	0.00
48	V79	0.00
49	K80	0.00
50	R84	0.00
51	G85	0.00
52	K86	0.00
53	D87	0.00
54	L90	0.00
55	R91	0.00
56	S92	0.00
57	F93	0.00
58	A94	0.00
59	N95	0.00
60	A96	0.00
61	G97	0.00
62	L98	0.00
63	S99	0.00
64	I100	0.00
65	T101	0.00
66	E102	0.00
67	I103	0.00
68	M104	0.00
69	E105	0.00
70	K106	0.00
71	H111	0.00
72	K115	0.00
73	P116	0.00
74	R119	0.00
75	P120	0.00
76	R121	0.00

Chain K:

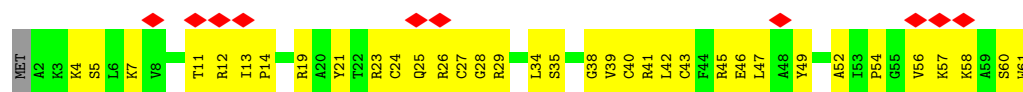
Chain L:

23% 65% 33%

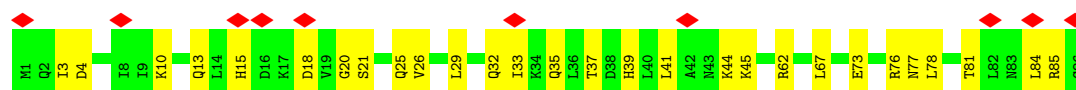
MET A2 R3 G6 I7 D8 K13 R14 A18 L19 T20 Y21 G26 L27 S28 R29 S30 Q31 A32 I33 Q36 A37 N38 I39 K43 D47 L48 T49 E50 E51 E52 F53 V54 A55 V59 A60 S61 A62 Y63 K64 L65 E66 G67 D68 L69 R70 R71 E72 I73 A74 L75 V76

I77 K78 H79 E82 I83 K93 Q100 R101 T104 A117 N118 K119 I121 E122 SER LYS

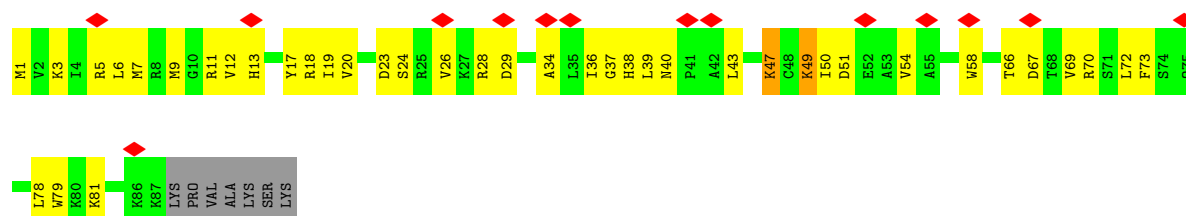
Chain M:



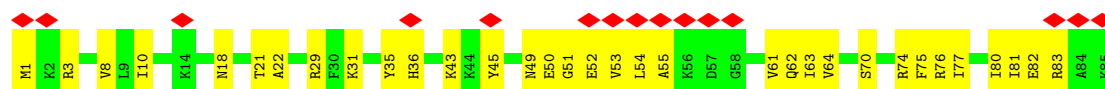
- Molecule 22: 30S ribosomal protein S15



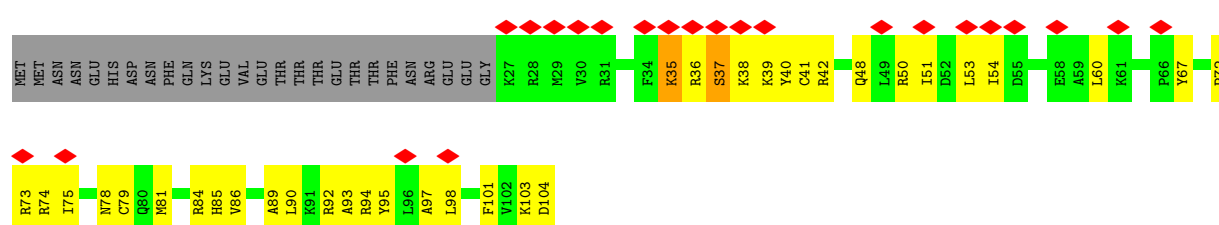
- Molecule 23: 30S ribosomal protein S16



- Molecule 24: 30S ribosomal protein S17

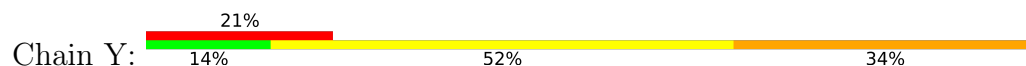


- Molecule 25: 30S ribosomal protein S18



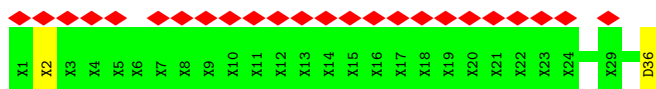
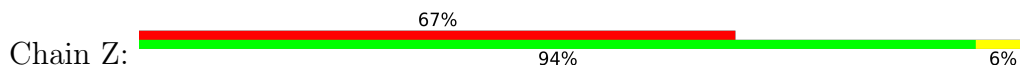
- Molecule 26: 30S ribosomal protein S19



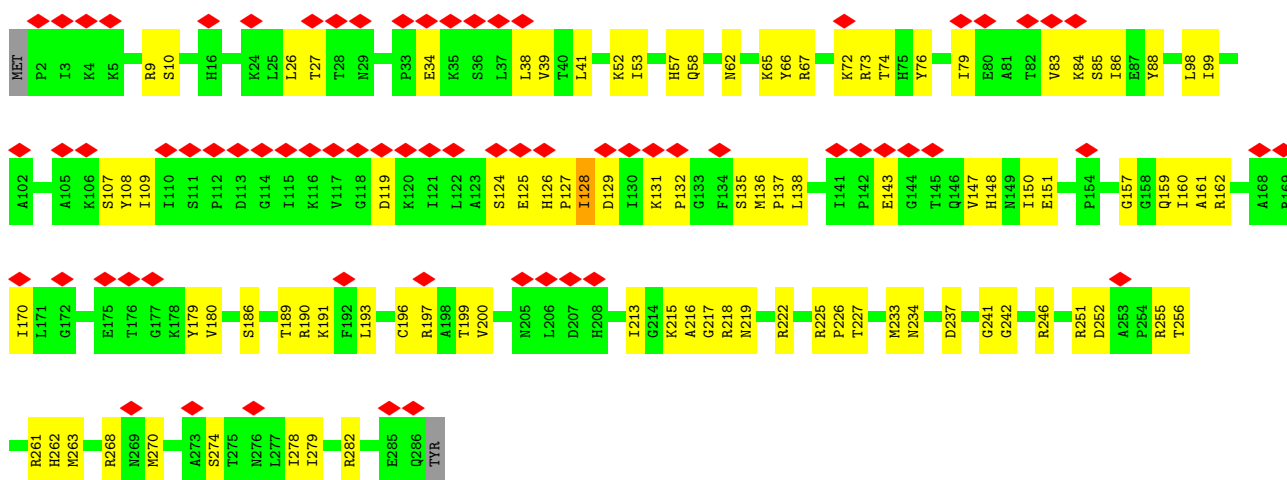




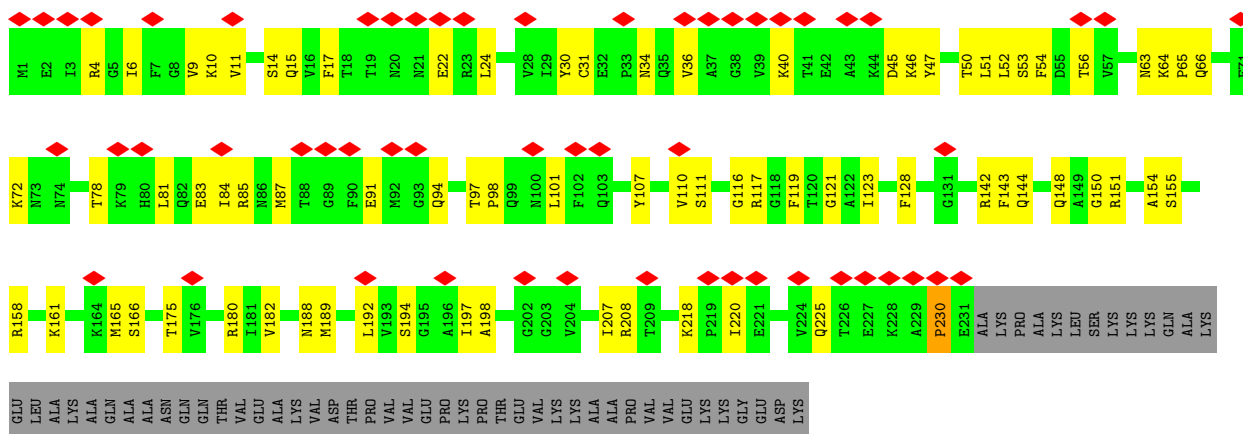
- Molecule 31: Nascent chain



- Molecule 32: 50S ribosomal protein L2

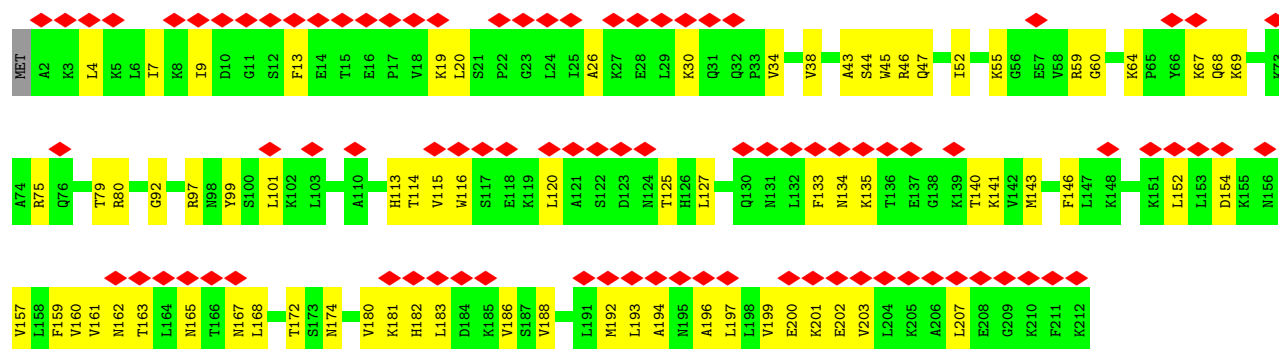


- Molecule 33: 50S ribosomal protein L3

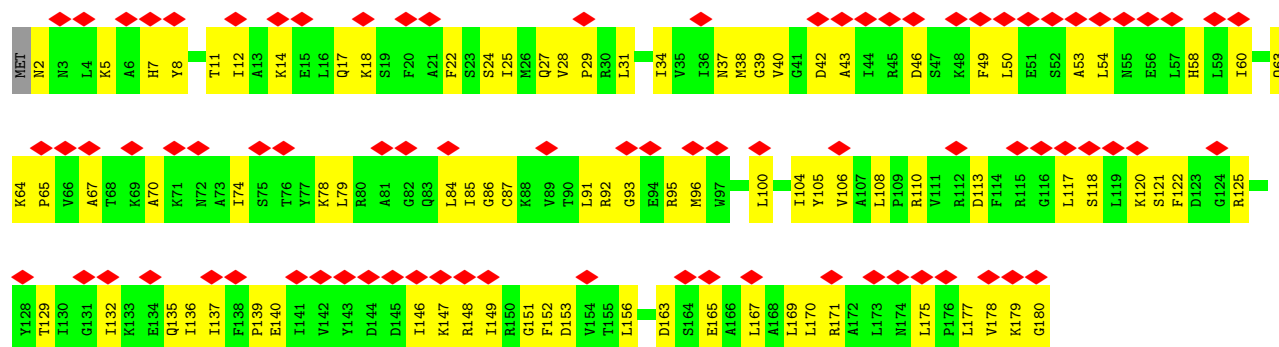


- Molecule 34: 50S ribosomal protein L4

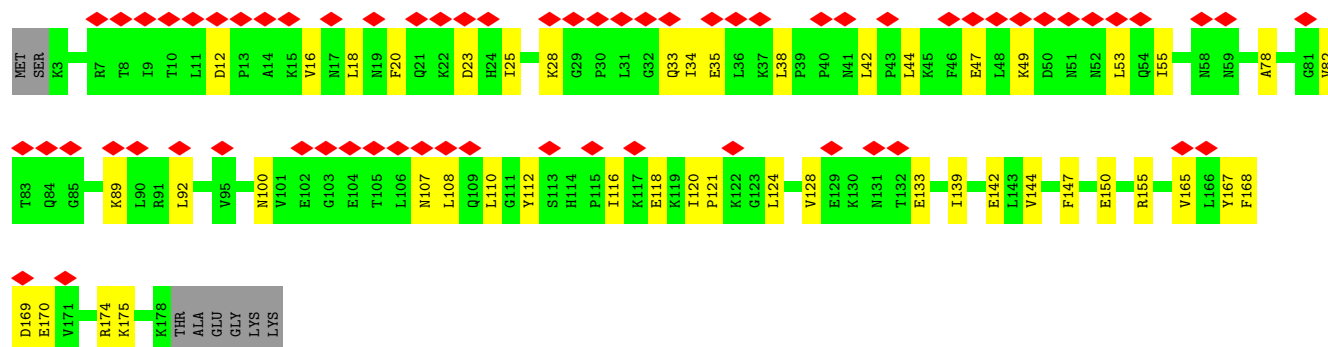




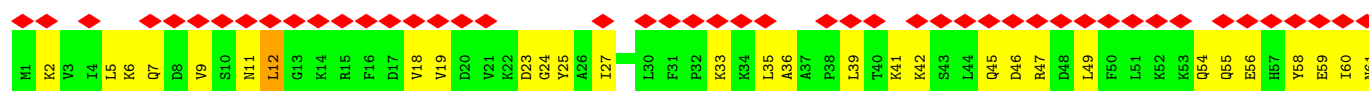
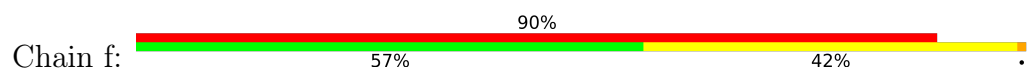
• Molecule 35: 50S ribosomal protein L5

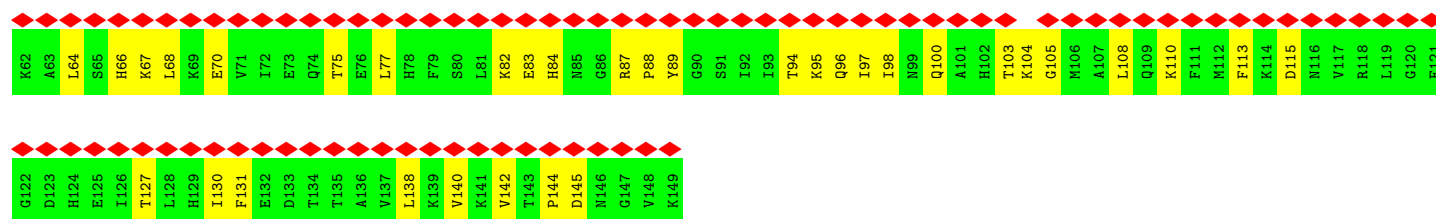


• Molecule 36: 50S ribosomal protein L6

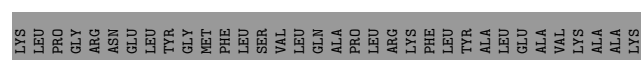


• Molecule 37: 50S ribosomal protein L9

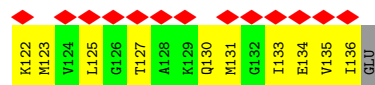
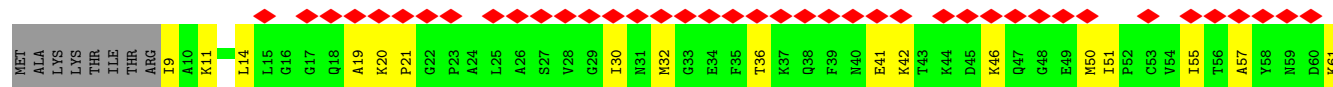
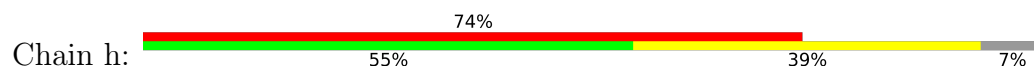




• Molecule 38: 50S ribosomal protein L10



• Molecule 39: 50S ribosomal protein L11

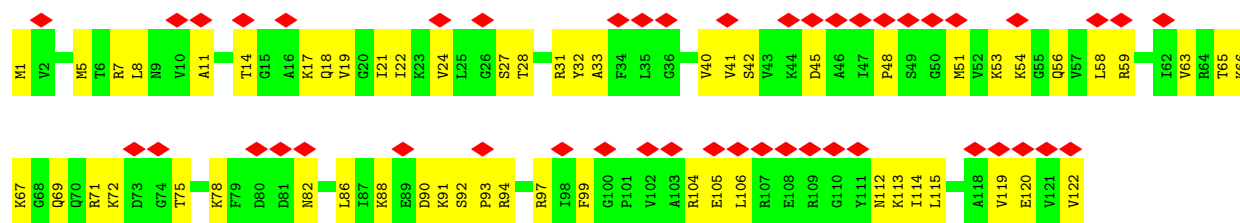


• Molecule 40: 50S ribosomal protein L13

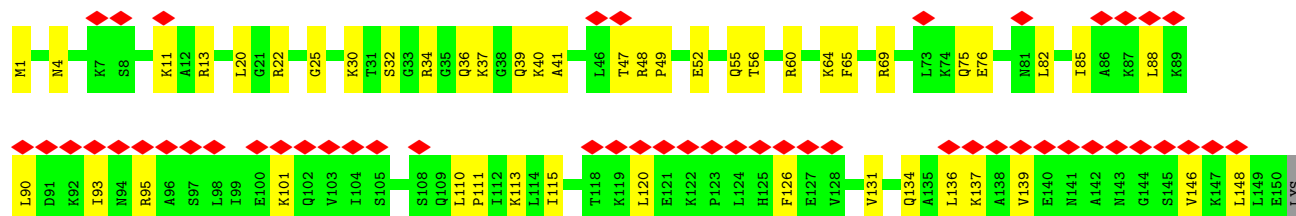


• Molecule 41: 50S ribosomal protein L14

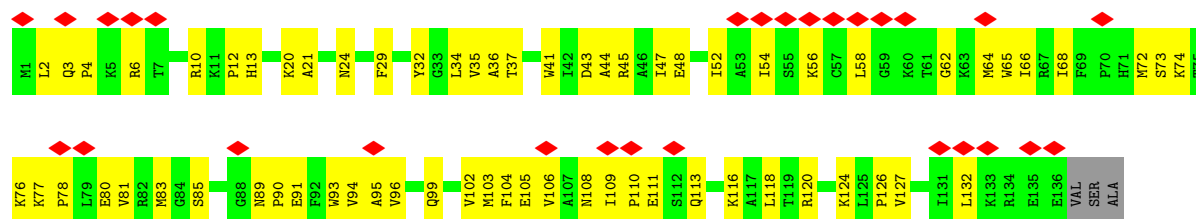




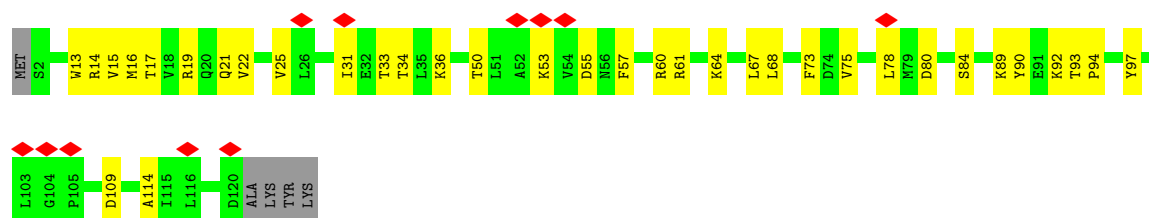
• Molecule 42: 50S ribosomal protein L15



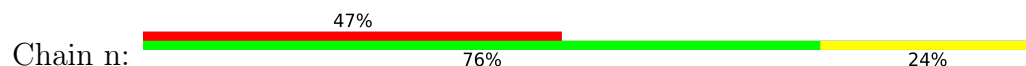
• Molecule 43: 50S ribosomal protein L16

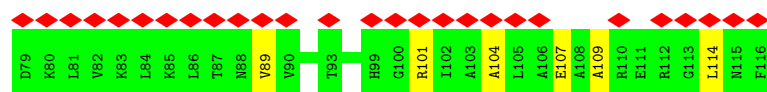


• Molecule 44: 50S ribosomal protein L17

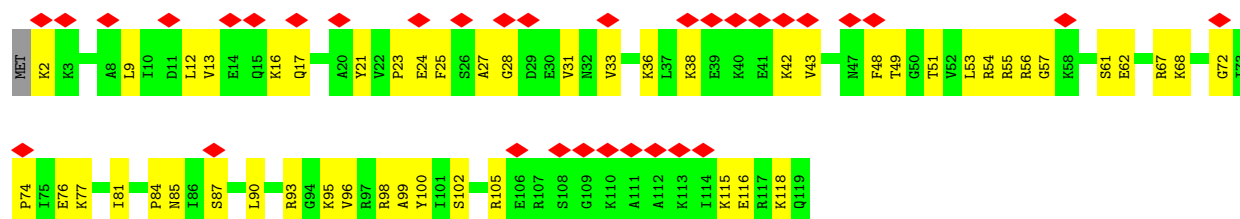


• Molecule 45: 50S ribosomal protein L18

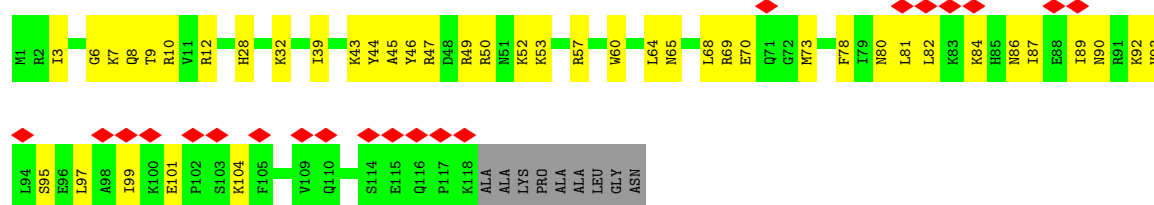




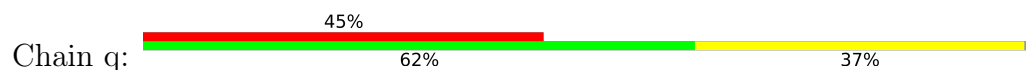
• Molecule 46: 50S ribosomal protein L19



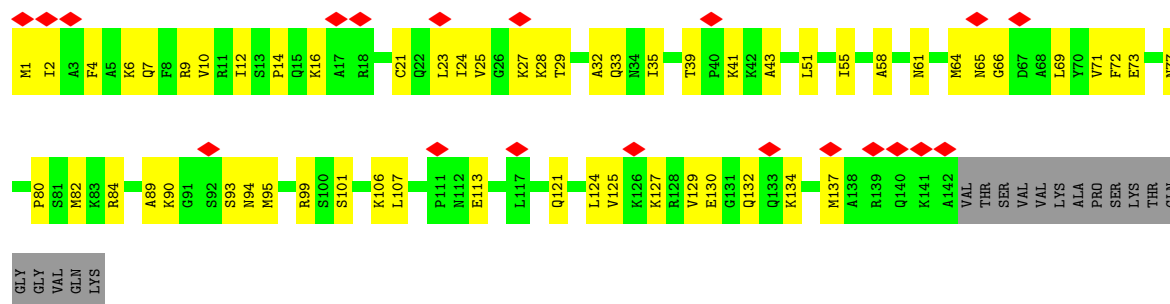
• Molecule 47: 50S ribosomal protein L20



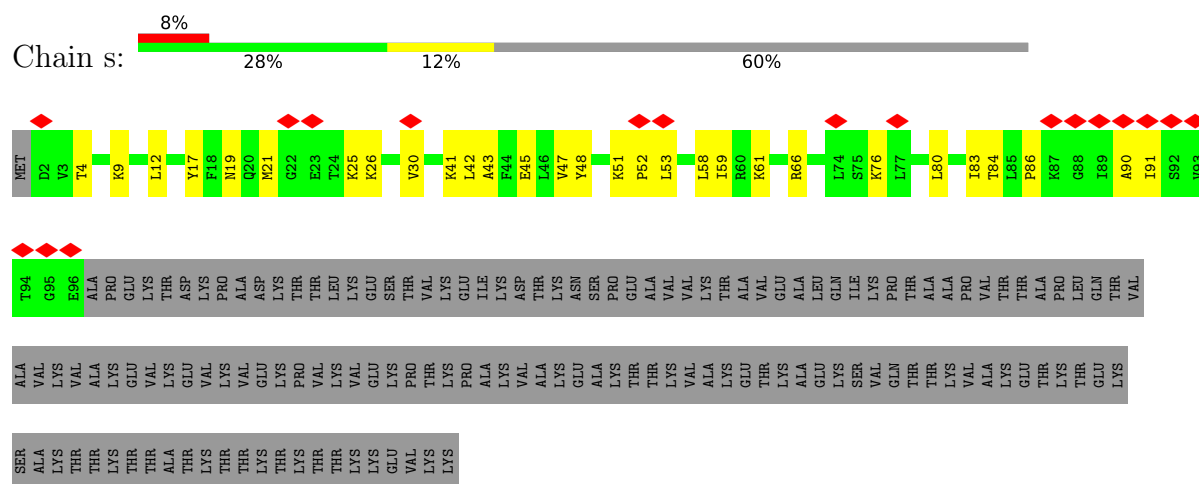
• Molecule 48: 50S ribosomal protein L21



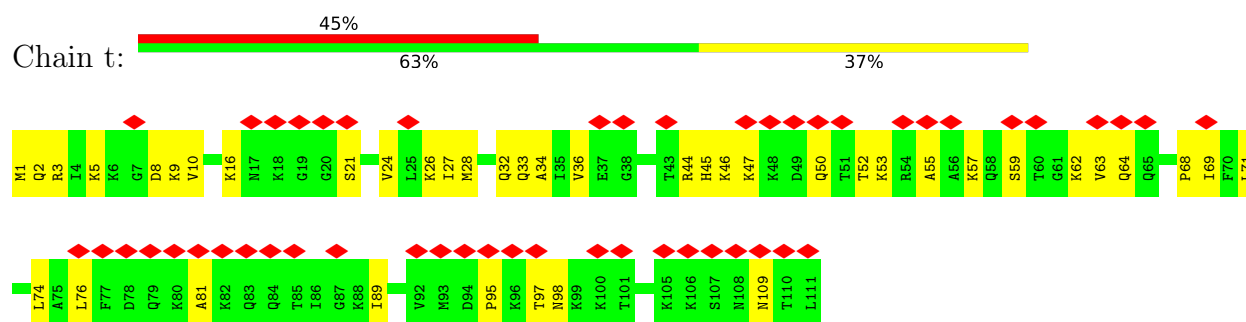
• Molecule 49: 50S ribosomal protein L22



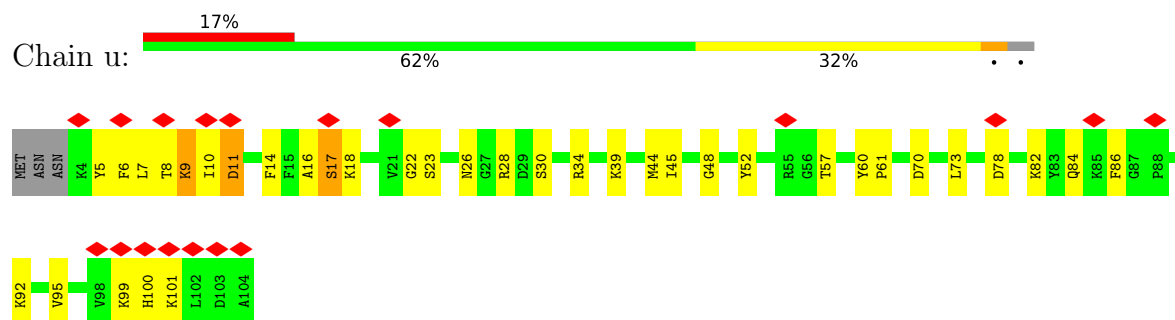
- Molecule 50: 50S ribosomal protein L23



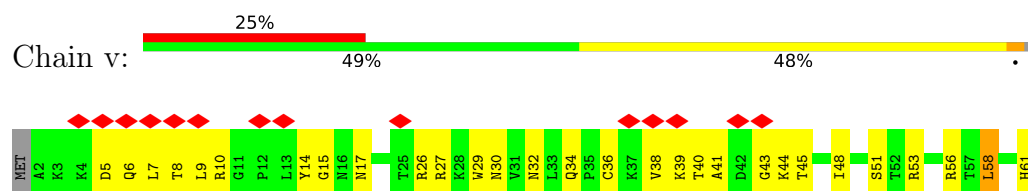
- Molecule 51: 50S ribosomal protein L24



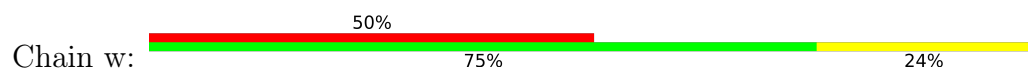
- Molecule 52: 50S ribosomal protein L27

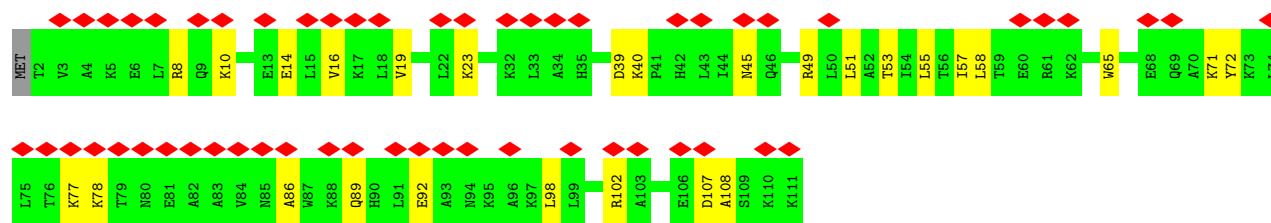


- Molecule 53: 50S ribosomal protein L28

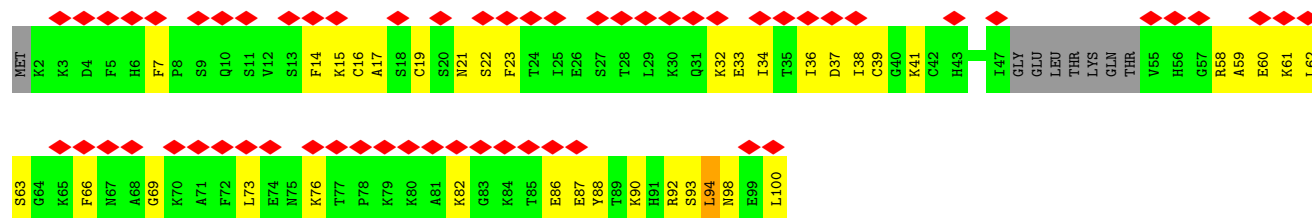


- Molecule 54: 50S ribosomal protein L29

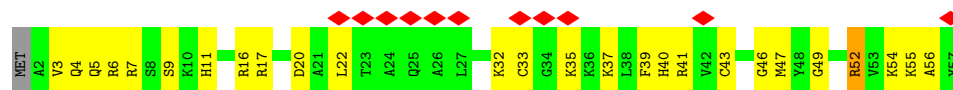




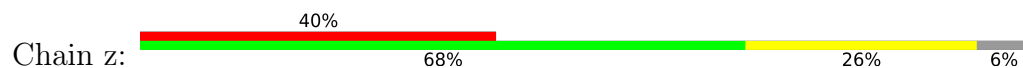
• Molecule 55: 50S ribosomal protein L31



• Molecule 56: 50S ribosomal protein L32



• Molecule 57: 50S ribosomal protein L33 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	963	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF estimation and 3D CTF correction are done in Warp	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	137	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3250	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	5.477	Depositor
Minimum map value	-2.425	Depositor
Average map value	0.022	Depositor
Map value standard deviation	0.237	Depositor
Recommended contour level	1.2	Depositor
Map size (Å)	793.6, 793.6, 793.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.1, 3.1, 3.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: K, 5MC, 7MG, 1MG, OMG, B8T, MG, ZN, 2MA, CLM, MA6

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	0	0.14	0/383	0.42	0/504
2	1	0.10	0/484	0.30	0/637
3	2	0.17	0/306	0.54	0/401
4	3	0.10	1/69363 (0.0%)	0.24	1/108161 (0.0%)
5	4	0.08	0/2578	0.20	0/4016
6	5	0.11	0/35992	0.23	1/56111 (0.0%)
7	6	0.16	0/1810	0.47	1/2817 (0.0%)
8	7	0.23	1/1785 (0.1%)	0.31	0/2779
9	A	0.22	0/2186	0.66	2/2952 (0.1%)
10	B	0.18	0/1800	0.53	0/2433
11	C	0.25	0/1700	0.71	0/2278
11	U	0.27	0/1700	0.82	0/2278
12	D	0.23	0/1365	0.61	0/1827
13	E	0.23	0/1384	0.68	0/1867
14	F	0.21	0/1274	0.62	0/1710
15	G	0.22	0/1134	0.62	1/1527 (0.1%)
16	H	0.20	0/1056	0.55	1/1409 (0.1%)
17	I	0.24	0/843	0.64	0/1132
18	J	0.16	0/844	0.48	0/1136
19	K	0.18	0/1089	0.52	0/1461
20	L	0.20	0/986	0.50	0/1321
21	M	0.24	0/483	0.54	0/643
22	N	0.17	0/703	0.50	0/936
23	O	0.24	0/718	0.72	0/962
24	P	0.14	0/702	0.44	0/934
25	Q	0.19	0/663	0.59	0/883
26	R	0.19	0/716	0.56	1/958 (0.1%)
27	S	0.13	0/645	0.38	0/857
28	T	0.23	0/524	0.68	0/685
29	X	0.18	0/245	0.65	0/325
30	Y	0.19	0/699	0.48	0/1087
31	Z	0.89	0/26	1.70	0/33

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	a	0.14	0/2267	0.44	0/3044
33	b	0.21	0/1812	0.55	0/2436
34	c	0.14	0/1681	0.46	0/2257
35	d	0.18	0/1437	0.50	0/1931
36	e	0.17	0/1420	0.47	0/1912
37	f	0.19	0/1233	0.53	0/1653
38	g	0.18	0/960	0.47	0/1284
39	h	0.16	0/968	0.46	0/1298
40	i	0.17	0/1186	0.46	0/1592
41	j	0.19	0/953	0.56	0/1275
42	k	0.15	0/1187	0.50	0/1581
43	l	0.21	0/1104	0.55	0/1481
44	m	0.15	0/973	0.42	0/1309
45	n	0.13	0/927	0.41	0/1239
46	o	0.19	0/976	0.53	0/1296
47	p	0.14	0/996	0.43	0/1325
48	q	0.21	0/828	0.55	0/1111
49	r	0.18	0/1100	0.59	0/1471
50	s	0.12	0/752	0.39	0/1015
51	t	0.23	0/878	0.65	2/1165 (0.2%)
52	u	0.15	0/798	0.52	0/1063
53	v	0.23	0/526	0.69	1/703 (0.1%)
54	w	0.11	0/916	0.34	0/1222
55	x	0.21	0/722	0.76	2/959 (0.2%)
56	y	0.19	0/457	0.62	1/601 (0.2%)
57	z	0.16	0/412	0.48	0/547
All	All	0.14	2/163655 (0.0%)	0.36	14/243830 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	U	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	7	72	G	O3'-P	-6.41	1.51	1.61
4	3	783	1MG	O3'-P	5.29	1.61	1.56

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	5	1434	C	P-O3'-C3'	-8.27	107.79	120.20
55	x	94	LEU	CA-C-N	7.24	135.37	121.54
55	x	94	LEU	C-N-CA	7.24	135.37	121.54
51	t	95	PRO	CA-N-CD	-6.39	103.05	112.00
26	R	76	PRO	CA-N-CD	-6.21	103.30	112.00
9	A	32	MET	CB-CG-SD	-5.97	94.78	112.70
53	v	58	LEU	CA-CB-CG	5.55	135.72	116.30
56	y	52	ARG	CA-CB-CG	5.47	125.05	114.10
51	t	95	PRO	CB-CG-CD	-5.46	88.63	106.10
15	G	52	GLY	N-CA-C	5.43	126.04	113.18
4	3	393	C	O3'-P-O5'	5.27	111.91	104.00
9	A	160	GLU	N-CA-CB	5.18	117.91	110.20
7	6	46	G	C2'-C3'-O3'	5.16	117.24	109.50
16	H	94	PRO	N-CA-C	5.14	123.05	112.47

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	U	121	HIS	Peptide
11	U	153	ILE	Peptide

5.2 Too-close contacts [i](#)

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	0	380	0	429	10	0
2	1	477	0	530	10	0
3	2	304	0	348	11	0
4	3	61995	0	31115	937	0
5	4	2305	0	1164	23	0
6	5	32258	0	16205	508	0
7	6	1620	0	818	26	0
8	7	1599	0	805	24	0
9	A	2152	0	2222	125	0
10	B	1773	0	1841	107	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	C	1669	0	1729	116	0
11	U	1669	0	1729	140	0
12	D	1346	0	1433	107	0
13	E	1362	0	1377	88	0
14	F	1254	0	1320	66	0
15	G	1118	0	1238	87	0
16	H	1040	0	1107	59	0
17	I	832	0	918	84	0
18	J	829	0	855	41	0
19	K	1071	0	1165	64	0
20	L	975	0	1043	37	0
21	M	474	0	505	42	0
22	N	697	0	758	22	0
23	O	705	0	755	50	0
24	P	693	0	753	27	0
25	Q	651	0	700	38	0
26	R	700	0	709	42	0
27	S	643	0	694	26	0
28	T	519	0	578	40	0
29	X	242	0	263	8	0
30	Y	623	0	315	25	0
31	Z	187	0	68	2	0
32	a	2225	0	2301	83	0
33	b	1778	0	1821	76	0
34	c	1654	0	1744	61	0
35	d	1416	0	1500	74	0
36	e	1396	0	1481	37	0
37	f	1210	0	1259	56	0
38	g	951	0	1001	42	0
39	h	959	0	1039	41	0
40	i	1164	0	1192	38	0
41	j	944	0	1019	61	0
42	k	1170	0	1274	44	0
43	l	1079	0	1134	68	0
44	m	958	0	1011	29	0
45	n	918	0	979	22	0
46	o	966	0	1042	55	0
47	p	981	0	1062	46	0
48	q	811	0	858	33	0
49	r	1091	0	1178	46	0
50	s	740	0	819	23	0
51	t	871	0	972	35	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	u	786	0	823	31	0
53	v	520	0	565	46	0
54	w	906	0	981	15	0
55	x	708	0	710	40	0
56	y	452	0	471	32	0
57	z	408	0	436	11	0
58	2	1	0	0	0	0
58	M	1	0	0	0	0
58	Q	1	0	0	0	0
58	x	1	0	0	0	0
58	y	1	0	0	0	0
58	z	1	0	0	0	0
59	3	20	0	11	1	0
60	3	1	0	0	0	0
61	3	206	0	0	0	0
61	4	1	0	0	0	0
61	5	90	0	0	0	0
61	6	1	0	0	0	0
61	K	1	0	0	0	0
61	P	1	0	0	0	0
61	Y	1	0	0	0	0
61	b	2	0	0	0	0
61	i	1	0	0	0	0
61	k	2	0	0	0	0
61	y	2	0	0	0	0
All	All	151559	0	104172	3524	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 14.

All (3524) 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:D:211:LEU:HD21	15:G:83:SER:OG	1.53	1.05
22:N:21:SER:O	22:N:25:GLN:NE2	1.91	1.04
11:C:193:GLU:HG3	11:C:195:TYR:HD1	1.23	1.03
12:D:212:ARG:NH1	15:G:53:TYR:CE1	2.29	1.01
12:D:212:ARG:NH1	15:G:53:TYR:CD1	2.31	0.99
4:3:2698:U:H5'	44:m:14:ARG:HH22	1.28	0.98
33:b:84:ILE:HB	33:b:87:MET:HE3	1.46	0.97
49:r:9:ARG:NH1	49:r:80:PRO:O	1.98	0.96

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:211:LEU:CD2	15:G:83:SER:OG	2.14	0.95
4:3:2580:A:H2'	33:b:151:ARG:HH12	1.31	0.94
29:X:37:ASN:H	29:X:45:LYS:HD3	1.34	0.93
49:r:12:ILE:HG12	49:r:43:ALA:HB2	1.49	0.92
14:F:115:MET:HA	14:F:118:LYS:HB2	1.52	0.91
6:5:594:A:N3	24:P:29:ARG:NH2	2.19	0.90
10:B:219:PRO:HB3	10:B:222:ILE:HB	1.52	0.90
4:3:271:G:H5'	11:U:37:GLN:HE21	1.33	0.90
11:C:179:VAL:HG12	11:C:180:ARG:H	1.37	0.90
11:C:193:GLU:HG3	11:C:195:TYR:CD1	2.07	0.90
12:D:212:ARG:HH21	15:G:51:GLU:C	1.78	0.89
12:D:212:ARG:HG3	12:D:214:LYS:HD3	1.55	0.88
43:l:20:LYS:HD3	43:l:21:ALA:H	1.38	0.88
10:B:153:LYS:HB2	10:B:176:MET:HE1	1.56	0.87
9:A:203:ASN:HB2	9:A:219:ASN:HD22	1.40	0.87
11:U:103:ARG:NH2	11:U:164:SER:O	2.08	0.87
30:Y:30:G:H3'	30:Y:31:A:H5''	1.55	0.87
12:D:198:GLY:HA2	12:D:201:LYS:HE2	1.56	0.87
6:5:1501:G:H3'	28:T:37:ARG:HH22	1.38	0.86
42:k:75:GLN:NE2	42:k:76:GLU:O	2.08	0.86
4:3:2144:C:H2'	4:3:2145:A:H8	1.39	0.86
6:5:1038:G:H4'	21:M:4:LYS:HE2	1.55	0.85
9:A:214:ILE:HG22	9:A:216:PRO:HD3	1.58	0.85
15:G:37:ALA:HB3	15:G:68:ARG:HG3	1.58	0.85
17:I:9:TYR:HB3	17:I:12:LEU:HD21	1.58	0.85
53:v:17:ASN:HB2	53:v:27:ARG:HD2	1.58	0.85
4:3:1600:A:O4'	32:a:222:ARG:NH2	2.09	0.85
6:5:1320:A:N1	14:F:9:ARG:NH2	2.24	0.85
12:D:212:ARG:NE	15:G:51:GLU:O	2.10	0.85
43:l:35:VAL:HG11	43:l:132:LEU:HD12	1.59	0.85
6:5:1197:G:H4'	26:R:78:ARG:HH21	1.40	0.84
11:U:14:LEU:HA	53:v:63:ARG:NH1	1.90	0.84
13:E:94:TYR:HB3	25:Q:85:HIS:CD2	2.13	0.84
48:q:19:THR:HG22	48:q:93:LYS:HB2	1.58	0.84
12:D:214:LYS:NZ	15:G:51:GLU:O	2.11	0.83
29:X:29:LYS:HG3	29:X:30:GLN:H	1.43	0.83
37:f:100:GLN:HA	37:f:103:THR:HG22	1.59	0.82
33:b:50:THR:HB	33:b:87:MET:HG3	1.61	0.82
13:E:1:MET:HE2	13:E:91:GLU:HG2	1.61	0.82
33:b:188:ASN:HD21	46:o:12:LEU:HD13	1.44	0.81
7:6:49:G:H1	7:6:65:U:H3	1.28	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:o:67:ARG:NH1	46:o:76:GLU:OE2	2.12	0.81
4:3:434:G:OP2	53:v:53:ARG:NH1	2.13	0.81
56:y:17:ARG:NH1	56:y:20:ASP:OD2	2.13	0.81
56:y:47:MET:HE1	56:y:52:ARG:HD2	1.60	0.81
4:3:1702:A:H5''	41:j:5:MET:HE1	1.60	0.80
6:5:369:A:O2'	6:5:448:A:N7	2.12	0.80
51:t:3:ARG:HH22	51:t:74:LEU:HB2	1.47	0.80
16:H:20:TYR:HB2	16:H:66:ASN:HB3	1.63	0.80
12:D:211:LEU:HD21	15:G:83:SER:HG	1.47	0.80
14:F:67:ASN:HD21	14:F:129:ASN:HB2	1.47	0.80
4:3:192:U:H5''	53:v:14:TYR:HD2	1.47	0.79
9:A:199:VAL:HG12	9:A:213:PHE:HB2	1.64	0.79
19:K:7:LEU:HD11	19:K:12:ARG:HG2	1.62	0.79
9:A:32:MET:HE2	9:A:281:ARG:HB2	1.63	0.79
13:E:29:LEU:HG	13:E:35:LEU:HD21	1.65	0.79
4:3:47:G:H5''	4:3:48:G:H5'	1.64	0.79
43:l:20:LYS:HA	43:l:99:GLN:HE21	1.47	0.79
46:o:21:TYR:HD2	46:o:23:PRO:HD3	1.48	0.79
15:G:44:ILE:HG22	15:G:122:VAL:HG11	1.65	0.79
25:Q:81:MET:O	25:Q:85:HIS:ND1	2.12	0.79
6:5:1174:U:O2'	17:I:62:HIS:NE2	2.16	0.79
51:t:3:ARG:NH2	51:t:71:LEU:O	2.16	0.79
4:3:2583:U:OP1	33:b:151:ARG:NH2	2.16	0.79
4:3:1293:U:O2	56:y:7:ARG:NH1	2.15	0.78
13:E:4:ASN:OD1	13:E:59:ARG:NH1	2.16	0.78
6:5:871:U:H5''	15:G:92:LYS:HD2	1.63	0.78
6:5:506:U:H5''	11:C:50:TYR:CZ	2.18	0.78
7:6:46:G:O2'	7:6:47:U:H5'	1.84	0.78
33:b:111:SER:OG	33:b:208:ARG:NH1	2.17	0.78
9:A:34:LYS:O	9:A:37:TRP:HD1	1.66	0.78
43:l:110:PRO:O	43:l:113:GLN:NE2	2.17	0.78
11:U:117:VAL:HG22	11:U:122:VAL:HG21	1.66	0.77
16:H:54:LEU:HD11	16:H:85:ILE:HG21	1.66	0.77
6:5:335:C:OP2	41:j:97:ARG:NH1	2.16	0.77
11:C:149:ILE:HA	11:C:154:VAL:HG21	1.66	0.77
4:3:2238:G:H5''	53:v:30:ASN:HD22	1.49	0.77
6:5:1350:A:OP2	14:F:9:ARG:NH1	2.17	0.77
4:3:1803:U:H3	4:3:1830:G:H1	1.32	0.77
4:3:1921:C:N4	6:5:1384:A:O2'	2.17	0.77
11:U:126:ASP:OD2	34:c:163:THR:OG1	2.02	0.77
8:7:10:G:H1	8:7:25:U:H3	1.29	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:293:ARG:NE	28:T:50:GLN:OE1	2.18	0.76
12:D:203:LEU:HD21	15:G:85:ASN:HD21	1.50	0.76
35:d:148:ARG:HE	35:d:149:ILE:H	1.31	0.76
37:f:100:GLN:OE1	37:f:110:LYS:NZ	2.17	0.76
4:3:1094:G:OP1	39:h:68:LYS:NZ	2.17	0.76
13:E:151:LYS:HD2	13:E:152:PRO:HD2	1.67	0.76
32:a:126:HIS:HB3	32:a:127:PRO:HD2	1.67	0.76
6:5:507:A:OP1	11:C:50:TYR:OH	2.03	0.76
17:I:59:ARG:NH1	17:I:60:SER:OG	2.19	0.76
41:j:93:PRO:HG3	41:j:114:ILE:HG13	1.68	0.76
55:x:58:ARG:HE	55:x:59:ALA:H	1.34	0.76
26:R:9:ALA:HB1	26:R:39:THR:HG21	1.68	0.76
4:3:2312:G:H22	4:3:2320:U:H3	1.32	0.75
32:a:218:ARG:O	32:a:222:ARG:NH1	2.18	0.75
18:J:102:GLU:OE2	28:T:3:LYS:NZ	2.20	0.75
4:3:354:C:O2	34:c:174:ASN:ND2	2.20	0.75
14:F:25:ILE:HB	14:F:100:LEU:HD22	1.68	0.75
35:d:146:ILE:HG22	35:d:148:ARG:H	1.51	0.75
56:y:52:ARG:NH1	56:y:54:LYS:O	2.19	0.75
11:C:151:ILE:HG13	11:C:152:PRO:HD2	1.69	0.75
4:3:395:U:O2'	11:U:41:ARG:NH2	2.20	0.75
48:q:31:LYS:NZ	48:q:33:ILE:HD13	2.01	0.75
4:3:1798:A:OP1	32:a:219:ASN:ND2	2.18	0.74
37:f:5:LEU:HA	37:f:36:ALA:HA	1.68	0.74
4:3:2502:G:H4'	43:l:80:GLU:HG2	1.70	0.74
40:i:3:LYS:HG3	40:i:4:THR:H	1.51	0.74
4:3:2131:G:H1	4:3:2182:C:H42	1.34	0.74
19:K:28:LEU:HD22	19:K:72:ASN:HA	1.69	0.74
11:U:103:ARG:NH1	11:U:103:ARG:O	2.20	0.74
40:i:61:ASN:HB3	40:i:64:GLN:OE1	1.88	0.74
4:3:1173:G:H21	40:i:111:MET:HE2	1.52	0.74
43:l:35:VAL:HG12	43:l:102:VAL:HG22	1.70	0.74
17:I:71:PHE:CE1	21:M:56:VAL:HG13	2.22	0.74
55:x:94:LEU:HD22	55:x:100:LEU:HA	1.70	0.74
4:3:2171:A:H5'	4:3:2181:A:H5'	1.69	0.74
39:h:95:LYS:HD2	39:h:136:ILE:HD12	1.70	0.74
9:A:28:THR:O	9:A:61:GLN:NE2	2.21	0.74
23:O:7:MET:HE1	23:O:20:VAL:HB	1.70	0.74
34:c:134:ASN:OD1	34:c:167:ASN:ND2	2.21	0.74
4:3:935:U:H2'	4:3:936:G:C8	2.23	0.73
38:g:43:LYS:HZ3	38:g:95:ALA:HB1	1.52	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:d:24:SER:HB3	35:d:27:GLN:HG2	1.69	0.73
46:o:21:TYR:CD2	46:o:23:PRO:HD3	2.22	0.73
9:A:203:ASN:HB2	9:A:219:ASN:ND2	2.03	0.73
13:E:114:LYS:O	13:E:117:GLU:HG3	1.88	0.73
47:p:101:GLU:HB3	47:p:104:LYS:HE2	1.70	0.73
4:3:1281:A:H5'	47:p:12:ARG:NH2	2.03	0.73
11:C:81:GLN:HB2	11:C:85:LEU:HD11	1.69	0.73
33:b:17:PHE:HB2	46:o:17:GLN:HE22	1.51	0.73
35:d:171:ARG:HD3	35:d:180:GLY:HA2	1.69	0.73
6:5:1241:G:N2	6:5:1244:A:OP2	2.19	0.73
54:w:98:LEU:HD21	54:w:102:ARG:HH22	1.53	0.73
14:F:135:LYS:NZ	14:F:139:ASP:OD1	2.22	0.73
4:3:1600:A:N3	32:a:62:ASN:ND2	2.35	0.73
4:3:1032:A:H5''	47:p:57:ARG:HH21	1.54	0.73
4:3:2166:U:H2'	4:3:2167:G:H4'	1.69	0.73
17:I:59:ARG:HA	21:M:45:ARG:HE	1.53	0.73
11:U:163:VAL:HG22	11:U:164:SER:H	1.54	0.73
4:3:2475:C:O2	43:l:124:LYS:NZ	2.22	0.72
40:i:80:HIS:HD2	40:i:87:ILE:HB	1.52	0.72
6:5:1196:G:H5'	26:R:36:ARG:CZ	2.19	0.72
11:C:99:ASN:OD1	11:C:110:ARG:NH1	2.22	0.72
13:E:90:LEU:HA	13:E:93:GLU:HG2	1.71	0.72
4:3:2504:C:H5'	43:l:83:MET:HE1	1.69	0.72
10:B:61:THR:HG22	10:B:62:GLN:H	1.54	0.72
12:D:212:ARG:NH1	15:G:53:TYR:CZ	2.57	0.72
6:5:206:G:N2	6:5:209:A:OP2	2.22	0.72
6:5:542:G:OP1	11:C:58:GLN:NE2	2.19	0.72
41:j:90:ASP:O	41:j:91:LYS:HG3	1.89	0.72
55:x:86:GLU:O	55:x:87:GLU:HG3	1.90	0.72
24:P:22:ALA:HB2	24:P:49:ASN:HD21	1.54	0.72
6:5:1048:G:N3	10:B:191:LYS:NZ	2.37	0.72
11:U:13:ARG:HA	53:v:40:THR:HG21	1.70	0.72
34:c:120:LEU:HA	34:c:125:THR:HG21	1.71	0.72
4:3:656:G:H4'	4:3:657:A:H5'	1.71	0.71
4:3:1446:G:O2'	4:3:1613:A:N6	2.23	0.71
6:5:1343:G:H5''	16:H:116:LYS:HB3	1.72	0.71
40:i:39:ILE:HD11	40:i:124:LYS:HB2	1.71	0.71
6:5:813:A:OP1	6:5:1501:G:O2'	2.06	0.71
11:C:25:PHE:HA	11:C:30:LYS:HA	1.70	0.71
4:3:2726:G:O2'	46:o:98:ARG:NH2	2.23	0.71
9:A:201:LEU:O	9:A:219:ASN:ND2	2.17	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:J:90:ILE:HG21	28:T:15:LEU:HD11	1.72	0.71
30:Y:29:A:H2'	30:Y:30:G:O4'	1.90	0.71
23:O:43:LEU:H	23:O:47:LYS:HE3	1.53	0.71
4:3:169:U:O2'	53:v:44:LYS:NZ	2.17	0.71
49:r:24:ILE:HA	49:r:27:LYS:HE2	1.72	0.71
4:3:267:A:OP2	11:U:69:LYS:NZ	2.23	0.71
10:B:156:VAL:HG12	10:B:201:VAL:HG12	1.72	0.71
12:D:55:ARG:HG3	12:D:56:ARG:HG2	1.72	0.71
38:g:41:ARG:NH2	39:h:113:ASN:O	2.21	0.71
4:3:166:A:H1'	37:f:105:GLY:HA3	1.72	0.71
4:3:2852:G:OP2	46:o:98:ARG:NH1	2.23	0.71
6:5:1320:A:H62	6:5:1349:A:H5''	1.55	0.71
11:U:43:ARG:NH1	11:U:44:SER:O	2.24	0.71
11:U:161:GLY:O	11:U:163:VAL:HG12	1.90	0.71
4:3:2465:U:H3	4:3:2502:G:H1	1.37	0.71
16:H:100:LEU:HD23	16:H:103:LYS:HE2	1.72	0.71
49:r:27:LYS:HE3	49:r:32:ALA:HA	1.72	0.71
4:3:2169:G:H4'	4:3:2170:A:H5''	1.73	0.71
36:e:44:LEU:HD12	36:e:55:ILE:HG21	1.73	0.71
41:j:63:VAL:HG12	41:j:106:LEU:HD11	1.72	0.71
4:3:1518:C:N4	4:3:2220:A:OP1	2.24	0.70
26:R:36:ARG:HB3	26:R:72:GLY:HA3	1.73	0.70
4:3:1099:C:O2'	39:h:87:LYS:NZ	2.23	0.70
6:5:169:G:N2	6:5:219:A:O2'	2.25	0.70
30:Y:30:G:H3'	30:Y:31:A:C5'	2.21	0.70
33:b:51:LEU:HD21	33:b:81:LEU:HD11	1.71	0.70
45:n:48:GLN:HG3	45:n:50:ILE:HG12	1.73	0.70
4:3:993:A:H5'	43:l:76:LYS:HD2	1.73	0.70
4:3:2481:U:OP1	4:3:2483:C:N4	2.24	0.70
5:4:40:U:H1'	35:d:63:GLN:HE21	1.55	0.70
8:7:48:G:H1	8:7:64:U:H3	1.37	0.70
46:o:62:GLU:HB3	46:o:81:ILE:HD12	1.72	0.70
4:3:925:C:H1'	4:3:926:U:C2	2.26	0.70
4:3:2580:A:H2'	33:b:151:ARG:NH1	2.04	0.70
6:5:1177:U:P	17:I:62:HIS:HE2	2.15	0.70
4:3:342:G:O2'	51:t:16:LYS:NZ	2.20	0.70
6:5:196:G:O2'	6:5:197:A:OP1	2.08	0.70
16:H:12:ARG:HD2	16:H:79:GLY:HA3	1.73	0.70
48:q:34:GLN:HG3	48:q:56:VAL:HG22	1.73	0.70
4:3:519:A:OP1	51:t:47:LYS:NZ	2.25	0.70
34:c:159:PHE:HB2	34:c:180:VAL:HG12	1.74	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:k:131:VAL:HG12	42:k:148:LEU:HD21	1.74	0.70
6:5:469:C:H5''	23:O:79:TRP:HE1	1.55	0.70
6:5:293:G:N2	6:5:296:A:OP2	2.25	0.70
4:3:2688:C:OP2	33:b:117:ARG:NH2	2.24	0.69
19:K:67:LYS:HD3	19:K:77:LEU:HD23	1.74	0.69
20:L:32:ALA:O	20:L:36:GLN:NE2	2.25	0.69
11:U:144:LEU:HB3	11:U:174:PHE:HB2	1.74	0.69
38:g:57:ASN:OD1	38:g:61:ARG:NH2	2.24	0.69
4:3:195:A:H3'	4:3:196:G:H21	1.56	0.69
4:3:271:G:H5'	11:U:37:GLN:NE2	2.05	0.69
4:3:518:A:O2'	4:3:532:A:N1	2.25	0.69
4:3:2667:G:N2	4:3:2670:A:OP2	2.21	0.69
34:c:9:ILE:HG12	34:c:135:LYS:HD2	1.73	0.69
35:d:54:LEU:HG	35:d:65:PRO:HG2	1.74	0.69
43:l:10:ARG:NH2	43:l:89:ASN:OD1	2.25	0.69
51:t:46:LYS:HE3	51:t:63:VAL:HB	1.74	0.69
4:3:2032:G:OP1	33:b:158:ARG:NH1	2.25	0.69
6:5:1088:C:H5''	9:A:154:ARG:HH21	1.56	0.69
35:d:104:ILE:HA	35:d:108:LEU:HD12	1.73	0.69
16:H:61:LYS:HD2	16:H:63:PHE:CZ	2.28	0.69
23:O:6:LEU:HD13	23:O:17:TYR:CD2	2.28	0.69
51:t:57:LYS:HE3	51:t:59:SER:HB3	1.73	0.69
4:3:1831:G:H21	32:a:263:MET:HE1	1.58	0.69
4:3:2027:G:H5'	56:y:9:SER:HB3	1.74	0.69
4:3:2057:C:O2'	33:b:144:GLN:NE2	2.25	0.69
9:A:20:LEU:HD12	9:A:62:ARG:HH21	1.57	0.69
9:A:182:VAL:HG23	9:A:206:THR:HG22	1.73	0.69
18:J:61:ASP:OD1	18:J:92:SER:OG	2.11	0.69
55:x:94:LEU:HD13	55:x:100:LEU:HD12	1.75	0.69
13:E:25:GLN:HG3	13:E:35:LEU:HD22	1.75	0.69
35:d:117:LEU:H	35:d:177:LEU:HD12	1.55	0.69
56:y:37:LYS:HD3	56:y:43:CYS:HB3	1.73	0.69
4:3:1096:U:H1'	4:3:1105:A:H1'	1.74	0.69
14:F:74:LEU:HD22	14:F:85:GLN:HB3	1.75	0.69
4:3:487:C:N4	4:3:490:A:OP2	2.24	0.68
15:G:90:ILE:HG22	15:G:97:ILE:HG13	1.75	0.68
46:o:33:VAL:HG13	46:o:48:PHE:HB3	1.75	0.68
37:f:96:GLN:NE2	37:f:115:ASP:OD2	2.26	0.68
43:l:78:PRO:HG2	43:l:81:VAL:HG21	1.75	0.68
6:5:954:A:N7	26:R:78:ARG:NH1	2.41	0.68
10:B:46:VAL:HG23	10:B:47:ASN:H	1.58	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:h:72:VAL:HG12	39:h:108:LYS:HD3	1.76	0.68
6:5:93:A:H5'	6:5:94:A:H5''	1.76	0.68
25:Q:103:LYS:HD2	28:T:2:PRO:HA	1.75	0.68
37:f:97:ILE:HA	37:f:100:GLN:HE21	1.59	0.68
4:3:914:G:H2'	4:3:936:G:H22	1.58	0.68
9:A:201:LEU:HG	9:A:228:LEU:HD13	1.73	0.68
25:Q:81:MET:C	25:Q:85:HIS:HD1	2.00	0.68
4:3:477:U:O2	34:c:47:GLN:NE2	2.27	0.68
4:3:2589:G:N2	4:3:2589:G:OP2	2.25	0.68
18:J:87:ASP:OD1	18:J:91:ARG:NH1	2.26	0.68
57:z:27:LYS:O	57:z:29:PRO:HD3	1.93	0.68
9:A:154:ARG:O	9:A:157:GLU:HG3	1.94	0.68
26:R:50:ALA:HB1	26:R:57:PHE:HB3	1.76	0.68
4:3:530:G:N3	49:r:61:ASN:ND2	2.41	0.68
5:4:83:U:H5'	5:4:84:C:H5'	1.75	0.68
25:Q:36:ARG:HH21	25:Q:37:SER:HB3	1.58	0.68
11:U:61:GLN:NE2	11:U:66:ILE:O	2.26	0.68
6:5:1009:G:H21	6:5:1012:A:H2	1.42	0.68
17:I:56:THR:HG23	17:I:70:GLN:HG3	1.76	0.68
56:y:52:ARG:HH22	56:y:55:LYS:HA	1.57	0.68
11:C:41:ARG:O	12:D:59:LYS:NZ	2.26	0.67
11:C:123:LEU:HG	11:C:145:LYS:HG2	1.76	0.67
43:l:43:ASP:HA	43:l:94:VAL:HA	1.74	0.67
46:o:27:ALA:HB3	46:o:96:VAL:HG21	1.76	0.67
51:t:1:MET:HE1	51:t:5:LYS:HD2	1.75	0.67
4:3:2696:G:N1	4:3:2728:U:OP2	2.24	0.67
33:b:180:ARG:HH21	33:b:220:ILE:HG21	1.57	0.67
39:h:76:LEU:HD11	39:h:127:THR:HG23	1.76	0.67
56:y:52:ARG:NH2	56:y:55:LYS:HA	2.09	0.67
4:3:2538:A:N7	36:e:175:LYS:NZ	2.42	0.67
7:6:73:A:H5''	7:6:74:C:H5	1.60	0.67
26:R:68:GLY:HA2	55:x:66:PHE:HZ	1.59	0.67
4:3:2308:U:H2'	4:3:2309:A:H8	1.60	0.67
42:k:76:GLU:O	42:k:110:LEU:HD11	1.94	0.67
56:y:39:PHE:O	56:y:41:ARG:NH1	2.28	0.67
6:5:954:A:HO2'	6:5:979:C:HO2'	1.37	0.67
6:5:983:G:H21	6:5:1012:A:H8	1.43	0.67
18:J:43:MET:HE3	18:J:58:ILE:HG13	1.76	0.67
33:b:36:VAL:HA	33:b:52:LEU:HG	1.77	0.67
53:v:5:ASP:OD1	53:v:6:GLN:N	2.28	0.67
10:B:139:GLN:HG3	10:B:143:LYS:NZ	2.09	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:e:89:LYS:HB3	36:e:168:PHE:CD2	2.30	0.67
44:m:90:TYR:HB3	44:m:97:TYR:CE1	2.30	0.67
4:3:433:A:H3'	53:v:53:ARG:HH12	1.60	0.67
4:3:1343:C:O2'	4:3:1420:A:N3	2.23	0.67
6:5:1269:U:O2'	20:L:14:ARG:NH1	2.28	0.67
4:3:80:U:H5'	54:w:8:ARG:HH22	1.60	0.66
4:3:2106:G:H1	4:3:2198:G:H1	1.42	0.66
4:3:2120:G:H1	4:3:2176:G:H4'	1.61	0.66
16:H:55:ASP:OD1	16:H:56:LEU:N	2.28	0.66
6:5:1197:G:OP2	6:5:1296:C:N4	2.27	0.66
42:k:126:PHE:HB2	42:k:146:VAL:HG22	1.77	0.66
4:3:720:A:OP1	4:3:721:G:N2	2.28	0.66
6:5:1068:G:N2	6:5:1071:A:OP2	2.17	0.66
12:D:212:ARG:NH1	15:G:53:TYR:CG	2.60	0.66
41:j:14:THR:HA	41:j:51:MET:HE1	1.78	0.66
6:5:55:C:H2'	6:5:348:C:H41	1.60	0.66
9:A:32:MET:CE	9:A:281:ARG:HB2	2.26	0.66
13:E:84:ARG:NH1	25:Q:95:TYR:O	2.28	0.66
36:e:38:LEU:HD12	36:e:42:LEU:HD21	1.78	0.66
9:A:286:ARG:O	9:A:287:ASN:ND2	2.29	0.66
12:D:54:ASN:OD1	12:D:58:GLN:NE2	2.29	0.66
20:L:118:ASN:O	26:R:87:ARG:NH2	2.28	0.66
32:a:131:LYS:HG2	32:a:132:PRO:HD2	1.75	0.66
4:3:192:U:H5''	53:v:14:TYR:CD2	2.30	0.66
6:5:416:U:O2'	6:5:421:G:N2	2.28	0.66
34:c:133:PHE:HB3	34:c:165:ASN:HD22	1.60	0.66
36:e:112:TYR:HB2	36:e:116:ILE:HD11	1.78	0.66
37:f:12:LEU:HD12	37:f:19:VAL:HB	1.78	0.66
4:3:1701:G:OP1	41:j:7:ARG:HD3	1.96	0.66
13:E:48:PRO:HB3	13:E:53:LEU:HD22	1.77	0.66
11:U:105:GLY:HA3	11:U:160:SER:HA	1.77	0.66
37:f:83:GLU:O	37:f:84:HIS:ND1	2.29	0.66
48:q:27:ALA:HB1	48:q:31:LYS:HE3	1.78	0.66
4:3:2823:A:O2'	4:3:2825:A:N7	2.27	0.66
12:D:137:TYR:O	15:G:109:ASN:ND2	2.29	0.66
11:U:104:MET:SD	11:U:106:PHE:HD2	2.19	0.66
6:5:386:U:H4'	23:O:28:ARG:HH21	1.59	0.65
18:J:14:ILE:HB	18:J:77:LEU:HD13	1.77	0.65
32:a:136:MET:HG3	32:a:137:PRO:HD2	1.78	0.65
34:c:52:ILE:HG21	34:c:92:GLY:HA3	1.79	0.65
44:m:19:ARG:NH2	44:m:67:LEU:O	2.28	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:201:A:N6	4:3:2438:A:O2'	2.30	0.65
4:3:2383:G:N2	4:3:2386:A:OP2	2.28	0.65
4:3:2653:G:OP2	4:3:2653:G:N2	2.21	0.65
16:H:89:LEU:HA	16:H:92:PHE:CE1	2.31	0.65
23:O:18:ARG:HA	23:O:38:HIS:HA	1.77	0.65
6:5:1425:A:H2'	6:5:1427:U:H3	1.62	0.65
10:B:139:GLN:HG3	10:B:143:LYS:HZ2	1.61	0.65
12:D:143:ARG:NH2	12:D:145:GLY:O	2.29	0.65
22:N:26:VAL:HG11	22:N:78:LEU:HD21	1.78	0.65
23:O:6:LEU:HD22	23:O:17:TYR:HB3	1.78	0.65
11:U:128:THR:HG22	11:U:129:VAL:H	1.61	0.65
12:D:154:ALA:HB1	12:D:158:THR:HG21	1.79	0.65
27:S:11:LEU:HD13	27:S:14:ASN:HD21	1.62	0.65
48:q:36:ASP:OD1	48:q:54:ARG:NH1	2.29	0.65
16:H:12:ARG:NH2	16:H:109:ASP:OD2	2.29	0.65
43:l:89:ASN:OD1	43:l:90:PRO:HD2	1.96	0.65
4:3:519:A:H5'	51:t:47:LYS:HZ1	1.61	0.65
6:5:499:U:OP1	19:K:127:ARG:NH2	2.30	0.65
50:s:25:LYS:HE3	50:s:90:ALA:HB2	1.79	0.65
53:v:39:LYS:HB3	53:v:43:GLY:HA2	1.78	0.65
9:A:46:GLU:HB3	9:A:57:VAL:HG22	1.78	0.65
12:D:127:HIS:HB2	12:D:196:MET:HE2	1.77	0.65
37:f:68:LEU:HD22	37:f:108:LEU:HD11	1.77	0.65
4:3:1806:G:OP1	32:a:268:ARG:NH1	2.29	0.65
6:5:1438:U:H2'	6:5:1439:G:H8	1.62	0.65
11:U:81:GLN:HB2	11:U:85:LEU:HD11	1.79	0.65
38:g:27:PHE:HD1	38:g:106:MET:HE3	1.62	0.65
4:3:1032:A:H5''	47:p:57:ARG:NH2	2.10	0.65
36:e:47:GLU:OE1	36:e:49:LYS:HG3	1.97	0.65
4:3:499:G:N2	4:3:502:A:OP2	2.24	0.64
4:3:1029:A:OP2	47:p:50:ARG:NH2	2.29	0.64
33:b:175:THR:HG21	33:b:208:ARG:HH22	1.61	0.64
48:q:6:VAL:HG22	48:q:11:GLN:HG2	1.77	0.64
53:v:8:THR:HG22	53:v:9:LEU:H	1.63	0.64
11:U:16:PHE:CE2	53:v:61:HIS:HD2	2.14	0.64
4:3:881:A:H1'	4:3:882:C:H5''	1.78	0.64
4:3:2110:U:H4'	4:3:2111:U:OP1	1.96	0.64
4:3:2151:G:H1'	4:3:2154:A:C6	2.32	0.64
6:5:1195:G:O2'	26:R:36:ARG:NH2	2.30	0.64
25:Q:67:TYR:CG	25:Q:103:LYS:HD3	2.32	0.64
42:k:110:LEU:HD12	42:k:111:PRO:HD2	1.78	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:2805:A:H4'	4:3:2807:G:H5''	1.78	0.64
6:5:145:G:N2	6:5:148:A:OP2	2.28	0.64
6:5:1502:G:OP2	28:T:37:ARG:NH2	2.31	0.64
15:G:39:LYS:HG3	15:G:68:ARG:HH22	1.62	0.64
6:5:835:G:OP1	13:E:103:LYS:NZ	2.30	0.64
6:5:1009:G:N2	6:5:1012:A:OP2	2.22	0.64
15:G:31:MET:SD	15:G:73:ASN:HB3	2.37	0.64
11:U:50:TYR:HB3	11:U:53:GLN:HE21	1.61	0.64
36:e:168:PHE:HD1	36:e:169:ASP:OD1	1.81	0.64
41:j:88:LYS:HG2	41:j:94:ARG:HH12	1.63	0.64
43:l:43:ASP:OD2	43:l:45:ARG:NH1	2.31	0.64
43:l:52:ILE:HG22	43:l:56:LYS:HE2	1.79	0.64
4:3:2149:U:H3	4:3:2155:G:H1	1.45	0.64
6:5:838:A:N6	13:E:134:SER:O	2.27	0.64
43:l:36:ALA:HB1	43:l:127:VAL:HG21	1.80	0.64
6:5:1332:U:H3	6:5:1338:A:N6	1.95	0.64
11:U:103:ARG:HH12	11:U:163:VAL:HG23	1.63	0.64
11:U:137:ASN:OD1	11:U:138:PRO:HD2	1.98	0.64
11:U:166:PHE:HD1	11:U:186:GLU:HG2	1.62	0.64
42:k:56:THR:HG23	42:k:60:ARG:HD2	1.79	0.64
4:3:196:G:N2	4:3:196:G:OP2	2.30	0.64
4:3:910:G:H4'	43:l:65:TRP:HD1	1.63	0.64
4:3:2098:U:H3'	4:3:2099:U:H5''	1.80	0.64
6:5:874:C:OP1	19:K:9:ARG:NH2	2.31	0.64
36:e:89:LYS:HB3	36:e:168:PHE:HD2	1.63	0.64
1:0:24:THR:HG23	1:0:27:GLY:H	1.63	0.64
9:A:225:THR:HG22	9:A:229:MET:HE2	1.79	0.64
11:U:157:ALA:O	11:U:171:ASN:ND2	2.30	0.64
45:n:62:LEU:HD13	45:n:69:ASN:HD22	1.63	0.64
4:3:909:U:O2'	43:l:66:ILE:O	2.14	0.63
12:D:93:VAL:HG12	12:D:172:LEU:HG	1.79	0.63
4:3:1830:G:OP1	32:a:58:GLN:NE2	2.31	0.63
4:3:2122:G:H2'	4:3:2124:A:N7	2.13	0.63
4:3:2820:G:N3	4:3:2887:A:O2'	2.31	0.63
37:f:130:ILE:HB	37:f:142:VAL:HB	1.80	0.63
42:k:88:LEU:HD21	42:k:90:LEU:HD12	1.79	0.63
6:5:1177:U:OP2	17:I:62:HIS:NE2	2.32	0.63
32:a:27:THR:HG23	32:a:86:ILE:HG22	1.80	0.63
32:a:72:LYS:HB3	32:a:74:THR:HG22	1.79	0.63
6:5:662:G:H1'	6:5:730:G:H5'	1.80	0.63
14:F:19:ASN:HD22	14:F:58:LEU:HD11	1.64	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:g:24:PHE:N	38:g:112:TYR:O	2.30	0.63
4:3:2103:C:H2'	4:3:2104:A:C8	2.34	0.63
6:5:195:U:H2'	6:5:196:G:H8	1.63	0.63
6:5:1138:U:H3	6:5:1149:G:H1	1.45	0.63
15:G:13:ASP:OD2	15:G:16:ALA:HB3	1.98	0.63
26:R:11:VAL:HG12	26:R:38:SER:HB3	1.81	0.63
11:U:177:THR:HG22	11:U:178:TYR:H	1.63	0.63
32:a:128:ILE:HG22	32:a:129:ASP:H	1.64	0.63
46:o:93:ARG:HE	46:o:118:LYS:HE2	1.61	0.63
46:o:98:ARG:HH11	46:o:99:ALA:H	1.45	0.63
4:3:703:A:H2'	4:3:705:A:H62	1.61	0.63
6:5:499:U:H3	6:5:542:G:H1	1.46	0.63
13:E:94:TYR:HB3	25:Q:85:HIS:HD2	1.62	0.63
17:I:46:LEU:HD21	17:I:79:LEU:HD22	1.80	0.63
34:c:30:LYS:H	34:c:114:THR:HG21	1.62	0.63
12:D:212:ARG:NH2	15:G:51:GLU:O	2.31	0.63
13:E:47:TYR:OH	13:E:84:ARG:NH1	2.32	0.63
43:l:2:LEU:HD12	43:l:47:ILE:HG21	1.79	0.63
45:n:109:ALA:HB1	45:n:114:LEU:HD12	1.81	0.63
49:r:14:PRO:HD2	49:r:99:ARG:HD3	1.80	0.63
4:3:341:G:N1	4:3:344:A:OP2	2.28	0.63
4:3:512:G:N1	4:3:515:A:OP2	2.28	0.63
4:3:1137:C:H2'	4:3:1138:A:H8	1.63	0.63
4:3:1220:A:OP1	48:q:78:HIS:ND1	2.32	0.63
11:C:8:PHE:HE2	11:C:26:SER:HA	1.62	0.63
19:K:4:ILE:HD11	24:P:35:TYR:HB3	1.79	0.63
24:P:70:SER:O	24:P:74:ARG:NH1	2.32	0.63
4:3:333:A:N3	4:3:353:G:O2'	2.28	0.63
4:3:1029:A:OP1	47:p:49:ARG:NH1	2.31	0.63
5:4:40:U:H4'	35:d:64:LYS:HG3	1.80	0.63
6:5:164:C:H2'	6:5:165:A:H8	1.63	0.63
6:5:733:A:OP1	25:Q:92:ARG:NH1	2.32	0.63
6:5:928:G:N7	14:F:1:MET:HE1	2.13	0.63
21:M:21:TYR:HE2	21:M:23:ARG:HE	1.47	0.63
24:P:61:VAL:HG12	24:P:80:ILE:HG12	1.80	0.63
7:6:9:A:O2'	7:6:10:G:N7	2.32	0.62
12:D:67:GLU:OE1	12:D:172:LEU:HD13	1.99	0.62
16:H:12:ARG:HH22	16:H:111:ARG:HH21	1.46	0.62
25:Q:72:PRO:HD2	25:Q:75:ILE:HD12	1.80	0.62
27:S:60:ILE:HD11	27:S:64:ARG:HD3	1.80	0.62
4:3:1619:A:H2'	4:3:1620:A:C8	2.34	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:113:MET:SD	10:B:144:VAL:HG13	2.39	0.62
23:O:11:ARG:HD3	23:O:12:VAL:N	2.14	0.62
25:Q:67:TYR:HB3	25:Q:103:LYS:HD3	1.81	0.62
26:R:22:MET:HE3	26:R:28:LYS:HB2	1.81	0.62
11:U:97:LEU:HD21	11:U:122:VAL:HG11	1.82	0.62
33:b:11:VAL:HG21	46:o:9:LEU:HD12	1.80	0.62
37:f:7:GLN:HB2	37:f:35:LEU:HD13	1.81	0.62
37:f:82:LYS:HD3	37:f:84:HIS:CD2	2.34	0.62
4:3:436:G:O6	53:v:56:ARG:NH2	2.32	0.62
9:A:41:MET:HE2	9:A:204:THR:O	1.99	0.62
9:A:179:ASP:OD1	9:A:180:ASP:N	2.31	0.62
10:B:172:ILE:HG13	10:B:176:MET:CE	2.28	0.62
4:3:2136:A:H3'	4:3:2137:A:H8	1.63	0.62
6:5:257:U:OP1	27:S:64:ARG:NH1	2.33	0.62
6:5:535:A:OP1	19:K:123:ARG:NH2	2.33	0.62
30:Y:32:A:H2'	30:Y:33:A:C8	2.34	0.62
42:k:52:GLU:HB3	42:k:55:GLN:HE21	1.64	0.62
49:r:71:VAL:HA	49:r:107:LEU:HG	1.79	0.62
4:3:1117:U:O2'	38:g:41:ARG:NE	2.32	0.62
13:E:45:LEU:HD11	13:E:49:ILE:HG22	1.82	0.62
48:q:31:LYS:HZ3	48:q:33:ILE:HD13	1.64	0.62
4:3:2854:A:N7	4:3:2872:A:O2'	2.31	0.62
4:3:15:A:O2'	4:3:17:G:N7	2.33	0.62
4:3:940:A:H2'	4:3:941:C:C6	2.35	0.62
4:3:2149:U:H2'	4:3:2150:C:O4'	2.00	0.62
9:A:103:VAL:HG22	9:A:242:MET:HE1	1.80	0.62
10:B:113:MET:HE2	10:B:147:ALA:HB3	1.81	0.62
11:C:68:ASP:OD1	11:C:69:LYS:N	2.33	0.62
29:X:36:LYS:HA	29:X:45:LYS:HE2	1.82	0.62
4:3:2266:C:O2'	4:3:2435:C:OP2	2.18	0.62
11:C:19:LEU:HG	11:C:63:MET:HE2	1.81	0.62
12:D:96:ASN:ND2	12:D:98:LYS:HG2	2.15	0.62
18:J:17:SER:HA	18:J:80:LYS:HB3	1.81	0.62
25:Q:53:LEU:HD22	25:Q:93:ALA:HB2	1.82	0.62
27:S:68:LEU:O	27:S:72:ASN:ND2	2.30	0.62
11:U:161:GLY:N	11:U:171:ASN:HD21	1.97	0.62
46:o:115:LYS:HD2	46:o:116:GLU:O	2.00	0.62
4:3:354:C:H5	34:c:141:LYS:HE3	1.65	0.62
4:3:917:G:H22	4:3:935:U:H1'	1.64	0.62
12:D:69:ARG:HG2	12:D:172:LEU:HD21	1.82	0.62
42:k:39:GLN:OE1	42:k:39:GLN:N	2.31	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:910:G:H1	4:3:941:C:H42	1.48	0.62
6:5:576:A:O2'	6:5:725:A:N3	2.31	0.62
7:6:3:G:H1	7:6:70:U:H3	1.48	0.62
24:P:8:VAL:HG12	24:P:64:VAL:HG12	1.81	0.62
29:X:38:MET:HE2	29:X:57:LEU:HD12	1.82	0.62
49:r:9:ARG:HH21	49:r:82:MET:HE2	1.65	0.62
6:5:136:U:H3	6:5:157:A:H62	1.47	0.61
18:J:66:THR:O	18:J:69:GLU:HG2	2.00	0.61
52:u:60:TYR:CD1	52:u:61:PRO:HD2	2.35	0.61
6:5:542:G:P	11:C:58:GLN:HE22	2.22	0.61
11:C:103:ARG:HH12	11:C:110:ARG:HH22	1.47	0.61
4:3:1386:G:O2'	4:3:1401:A:N6	2.33	0.61
6:5:928:G:C8	14:F:1:MET:HE1	2.35	0.61
6:5:1508:C:H42	9:A:294:GLU:HA	1.65	0.61
11:U:16:PHE:HA	11:U:20:GLU:OE2	2.00	0.61
4:3:2644:U:H4'	33:b:83:GLU:OE2	2.00	0.61
6:5:823:C:O2	15:G:24:ASN:ND2	2.33	0.61
13:E:1:MET:N	13:E:64:GLY:O	2.28	0.61
25:Q:81:MET:HA	25:Q:84:ARG:HG2	1.82	0.61
35:d:17:GLN:HA	35:d:22:PHE:HB2	1.83	0.61
49:r:134:LYS:HA	49:r:137:MET:SD	2.39	0.61
4:3:1798:A:O2'	32:a:213:ILE:O	2.16	0.61
6:5:21:U:OP2	12:D:185:ARG:NH2	2.34	0.61
39:h:41:GLU:HG3	39:h:42:LYS:HG3	1.81	0.61
51:t:71:LEU:HD23	51:t:74:LEU:HD12	1.82	0.61
4:3:2565:G:H4'	52:u:6:PHE:CE1	2.36	0.61
6:5:435:U:O2'	6:5:437:U:O4	2.19	0.61
6:5:945:U:OP2	20:L:101:ARG:HD2	2.01	0.61
16:H:11:ARG:H	16:H:83:LEU:HD23	1.64	0.61
18:J:43:MET:HE1	18:J:59:ALA:HB2	1.83	0.61
35:d:40:VAL:HG22	35:d:42:ASP:H	1.65	0.61
41:j:1:MET:HB2	41:j:32:TYR:HB3	1.82	0.61
44:m:80:ASP:O	44:m:84:SER:OG	2.11	0.61
4:3:1095:U:H1'	4:3:1096:U:H3'	1.83	0.61
4:3:2058:G:N2	4:3:2059:G:O6	2.34	0.61
10:B:5:VAL:HG11	10:B:10:LEU:HD13	1.83	0.61
41:j:53:LYS:N	41:j:56:GLN:OE1	2.30	0.61
4:3:1260:U:O2'	49:r:132:GLN:OE1	2.18	0.61
6:5:394:U:H2'	6:5:395:G:H8	1.66	0.61
14:F:76:VAL:HA	14:F:83:ASN:HD22	1.66	0.61
35:d:29:PRO:HG2	35:d:169:LEU:HD12	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:2123:A:N7	4:3:2169:G:O2'	2.31	0.61
6:5:515:G:N2	6:5:528:G:OP1	2.30	0.61
6:5:1127:A:H5''	17:I:50:THR:HG23	1.81	0.61
23:O:19:ILE:HD11	23:O:72:LEU:HD21	1.82	0.61
43:l:110:PRO:N	43:l:113:GLN:HE22	1.98	0.61
4:3:816:A:OP2	32:a:225:ARG:NH2	2.34	0.61
4:3:2122:G:N1	4:3:2126:A:OP2	2.24	0.61
5:4:2:U:O2	5:4:107:G:N2	2.34	0.61
6:5:44:C:OP1	23:O:11:ARG:NH1	2.33	0.61
6:5:145:G:O2'	6:5:147:A:N6	2.33	0.61
14:F:101:ARG:HG2	14:F:105:MET:HE1	1.83	0.61
27:S:33:LYS:O	27:S:37:LYS:HG3	2.00	0.61
38:g:43:LYS:NZ	38:g:95:ALA:HB1	2.16	0.61
4:3:393:C:O2	11:U:32:LYS:HD2	2.00	0.60
4:3:910:G:H4'	43:l:65:TRP:CD1	2.36	0.60
14:F:117:GLU:OE1	14:F:117:GLU:N	2.30	0.60
35:d:147:LYS:HA	35:d:147:LYS:HE3	1.83	0.60
40:i:139:LYS:O	40:i:139:LYS:HD2	2.00	0.60
4:3:13:C:H3'	4:3:14:U:H5'	1.83	0.60
6:5:305:A:O2'	6:5:605:A:N1	2.33	0.60
6:5:426:U:H3'	11:C:8:PHE:CD1	2.34	0.60
6:5:1448:A:H2'	6:5:1449:G:C8	2.36	0.60
11:C:49:GLY:O	11:C:53:GLN:HG3	2.01	0.60
16:H:54:LEU:HD23	16:H:59:LEU:HD13	1.82	0.60
17:I:24:LEU:HD21	17:I:78:ARG:HG2	1.82	0.60
34:c:115:VAL:HG21	34:c:188:VAL:HG13	1.82	0.60
4:3:410:G:H4'	4:3:411:U:O5'	2.02	0.60
6:5:1281:U:OP1	20:L:100:GLN:NE2	2.33	0.60
6:5:1342:C:H4'	17:I:56:THR:HG21	1.83	0.60
13:E:99:SER:O	13:E:105:GLN:NE2	2.26	0.60
19:K:76:VAL:HG21	19:K:108:TYR:HE1	1.66	0.60
19:K:133:LYS:HG3	19:K:134:LYS:H	1.66	0.60
4:3:1786:U:OP2	4:3:1791:A:N6	2.23	0.60
6:5:923:G:O2'	6:5:1508:C:OP1	2.19	0.60
13:E:162:LYS:HE3	15:G:58:GLN:OE1	2.01	0.60
52:u:82:LYS:HG2	52:u:84:GLN:NE2	2.17	0.60
4:3:1296:G:O2'	4:3:2019:G:O6	2.18	0.60
9:A:84:PHE:CE2	9:A:96:VAL:HG22	2.37	0.60
13:E:17:GLN:HG3	13:E:56:HIS:CD2	2.36	0.60
35:d:178:VAL:HG22	35:d:179:LYS:HG2	1.83	0.60
41:j:8:LEU:H	41:j:18:GLN:HE22	1.50	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:619:A:H62	4:3:1281:A:H2	1.49	0.60
4:3:915:A:C2	4:3:916:U:H1'	2.37	0.60
4:3:1282:G:C2	47:p:32:LYS:HD2	2.36	0.60
4:3:2288:G:O6	52:u:28:ARG:NH2	2.34	0.60
4:3:2698:U:C5'	44:m:14:ARG:HH22	2.09	0.60
6:5:1264:G:OP1	14:F:34:LYS:NZ	2.34	0.60
6:5:1350:A:N7	14:F:9:ARG:NH2	2.45	0.60
33:b:17:PHE:HB2	46:o:17:GLN:NE2	2.17	0.60
34:c:143:MET:HE3	34:c:172:THR:HG22	1.83	0.60
42:k:85:ILE:HD11	42:k:93:ILE:HD13	1.84	0.60
4:3:1092:A:N6	4:3:1122:G:OP1	2.33	0.60
6:5:398:G:OP1	11:C:73:ARG:NH1	2.34	0.60
13:E:83:LEU:H	13:E:83:LEU:HD12	1.66	0.60
48:q:4:ILE:HG13	48:q:40:MET:HB2	1.84	0.60
4:3:944:U:P	43:l:24:ASN:H	2.24	0.60
4:3:2853:U:O2'	4:3:2870:U:O2	2.16	0.60
6:5:373:A:H2'	6:5:374:G:H8	1.65	0.60
6:5:892:G:N2	6:5:895:A:OP2	2.34	0.60
9:A:240:LYS:HD3	9:A:242:MET:HE2	1.82	0.60
16:H:61:LYS:HD2	16:H:63:PHE:CE1	2.37	0.60
11:U:50:TYR:O	11:U:53:GLN:HG2	2.02	0.60
11:U:52:GLN:O	11:U:55:GLN:HG2	2.02	0.60
11:U:53:GLN:OE1	11:U:199:TRP:HB2	2.01	0.60
39:h:120:ALA:HA	39:h:123:MET:HG2	1.83	0.60
43:l:58:LEU:HD11	43:l:62:GLY:HA3	1.83	0.60
54:w:71:LYS:HE2	54:w:72:TYR:HD1	1.66	0.60
2:1:15:LYS:HD3	4:3:664:G:H5''	1.84	0.60
4:3:140:G:N2	4:3:143:A:OP2	2.27	0.60
4:3:1081:A:O4'	38:g:61:ARG:NH2	2.34	0.60
4:3:1353:G:OP1	4:3:1681:G:O2'	2.17	0.60
4:3:1921:C:N4	6:5:1385:A:H5'	2.16	0.60
6:5:408:U:H1'	11:C:29:LYS:H	1.67	0.60
6:5:577:G:H5'	6:5:725:A:H1'	1.84	0.60
7:6:25:C:H42	7:6:45:G:H22	1.50	0.60
9:A:90:ASP:OD1	9:A:91:TYR:N	2.35	0.60
12:D:209:ALA:HA	12:D:212:ARG:HB3	1.83	0.60
43:l:108:ASN:O	43:l:109:ILE:HG23	2.01	0.60
49:r:124:LEU:O	49:r:127:LYS:HG2	2.00	0.60
4:3:2797:C:O2	4:3:2895:A:O2'	2.18	0.60
15:G:26:ARG:HG3	15:G:82:PRO:HG3	1.82	0.60
25:Q:60:LEU:HB3	25:Q:90:LEU:HD21	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Q:93:ALA:HB1	25:Q:98:LEU:HD11	1.84	0.60
4:3:2144:C:H2'	4:3:2145:A:C8	2.30	0.59
4:3:2645:U:O2'	33:b:46:LYS:NZ	2.29	0.59
6:5:258:A:O3'	27:S:63:ASN:ND2	2.34	0.59
6:5:1497:U:H2'	6:5:1498:G:H8	1.67	0.59
14:F:12:LEU:H	14:F:13:PRO:HD2	1.66	0.59
30:Y:49:U:H4'	30:Y:50:U:O5'	2.01	0.59
43:l:54:ILE:HG21	43:l:64:MET:HG3	1.83	0.59
4:3:1833:G:O2'	4:3:1978:U:OP2	2.20	0.59
6:5:550:U:H2'	6:5:551:A:H8	1.67	0.59
6:5:1332:U:OP1	21:M:35:SER:OG	2.20	0.59
12:D:54:ASN:OD1	12:D:55:ARG:N	2.34	0.59
13:E:112:ARG:NH2	13:E:116:ASP:OD1	2.35	0.59
22:N:10:LYS:O	22:N:10:LYS:NZ	2.35	0.59
35:d:148:ARG:HE	35:d:149:ILE:N	1.99	0.59
4:3:1239:G:O2'	4:3:1267:A:N1	2.31	0.59
4:3:2100:G:H4'	37:f:24:GLY:HA3	1.84	0.59
4:3:2427:U:H5''	57:z:20:LEU:HD22	1.84	0.59
6:5:1214:A:H2'	6:5:1272:C:H41	1.66	0.59
7:6:17:U:H5'	7:6:18:G:C5'	2.32	0.59
22:N:41:LEU:O	22:N:44:LYS:NZ	2.34	0.59
11:U:104:MET:HE1	11:U:106:PHE:HB2	1.83	0.59
32:a:233:MET:HE2	32:a:237:ASP:HB2	1.83	0.59
33:b:34:ASN:HB3	33:b:52:LEU:HD23	1.84	0.59
34:c:162:ASN:HB3	34:c:203:VAL:HG22	1.84	0.59
36:e:167:TYR:HB2	36:e:170:GLU:OE1	2.02	0.59
38:g:27:PHE:O	38:g:81:ALA:N	2.35	0.59
42:k:95:ARG:NH2	42:k:110:LEU:O	2.35	0.59
43:l:34:LEU:HD13	43:l:118:LEU:HB3	1.84	0.59
4:3:2107:A:N3	4:3:2198:G:N2	2.50	0.59
4:3:2269:C:N4	52:u:28:ARG:HH21	2.01	0.59
6:5:710:G:H2'	6:5:711:G:C8	2.38	0.59
9:A:26:MET:HG3	9:A:227:LEU:HD22	1.83	0.59
3:2:1:MET:HE1	3:2:33:LYS:HE2	1.84	0.59
4:3:1123:A:N7	39:h:130:GLN:NE2	2.49	0.59
6:5:1022:G:H21	6:5:1026:A:H62	1.48	0.59
6:5:1279:G:H21	6:5:1306:A:H2	1.50	0.59
9:A:140:ASN:OD1	9:A:141:ALA:N	2.35	0.59
10:B:13:GLY:HA3	21:M:57:LYS:HE3	1.84	0.59
4:3:1055:A:N1	4:3:1176:U:O2'	2.32	0.59
6:5:364:U:O2'	6:5:365:U:OP1	2.17	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:J:115:LYS:HE3	28:T:35:HIS:ND1	2.18	0.59
11:U:11:SER:OG	11:U:23:LYS:NZ	2.36	0.59
32:a:147:VAL:HG12	32:a:200:VAL:HG12	1.85	0.59
37:f:5:LEU:HD23	37:f:5:LEU:H	1.68	0.59
40:i:63:ASP:OD1	40:i:64:GLN:NE2	2.35	0.59
4:3:1186:A:O3'	47:p:80:ASN:ND2	2.36	0.59
4:3:2121:A:H3'	4:3:2122:G:H8	1.66	0.59
33:b:34:ASN:ND2	33:b:54:PHE:HB3	2.18	0.59
40:i:101:ASP:HB2	40:i:127:VAL:HG13	1.83	0.59
48:q:67:LYS:HD2	48:q:86:ARG:HD2	1.84	0.59
11:C:154:VAL:HA	11:C:157:ALA:HB3	1.84	0.59
26:R:14:HIS:HA	26:R:17:LYS:NZ	2.18	0.59
35:d:170:LEU:HG	35:d:175:LEU:HB2	1.84	0.59
54:w:23:LYS:HD2	54:w:51:LEU:HD21	1.85	0.59
4:3:271:G:O2'	11:U:34:ILE:HA	2.03	0.59
4:3:2190:G:H5'	4:3:2190:G:H8	1.68	0.59
6:5:352:A:O2'	6:5:364:U:H4'	2.03	0.59
6:5:1062:C:H2'	6:5:1063:G:H8	1.68	0.59
11:C:56:GLU:HB3	11:C:191:ILE:HD13	1.84	0.59
13:E:12:SER:HB3	13:E:16:GLU:OE2	2.03	0.59
41:j:8:LEU:N	41:j:18:GLN:HE22	2.01	0.59
4:3:313:G:H5''	11:U:62:TYR:CE2	2.37	0.59
4:3:799:A:H5''	32:a:217:GLY:HA3	1.85	0.59
4:3:2146:A:H61	4:3:2158:C:H42	1.50	0.59
4:3:2627:U:H5''	33:b:161:LYS:HB3	1.84	0.59
13:E:12:SER:O	13:E:13:LEU:HD22	2.03	0.59
4:3:638:A:H62	4:3:660:U:H3	1.50	0.58
4:3:728:A:O2'	4:3:1381:A:N3	2.36	0.58
9:A:201:LEU:HD12	9:A:217:ALA:HB3	1.85	0.58
12:D:203:LEU:HD21	15:G:85:ASN:ND2	2.18	0.58
12:D:206:ARG:HG2	12:D:210:ILE:HD11	1.85	0.58
28:T:6:VAL:O	28:T:7:LYS:HG2	2.03	0.58
11:U:60:MET:HE3	11:U:64:TYR:HE2	1.68	0.58
38:g:37:ALA:O	38:g:40:ILE:HG22	2.02	0.58
40:i:18:TRP:HB3	40:i:140:PRO:HB3	1.85	0.58
4:3:866:G:H4'	42:k:39:GLN:HE22	1.68	0.58
4:3:947:A:H62	43:l:12:PRO:HA	1.68	0.58
6:5:196:G:HO2'	6:5:197:A:P	2.26	0.58
6:5:386:U:H2'	6:5:387:G:C8	2.38	0.58
12:D:102:GLY:N	12:D:126:LEU:HD23	2.18	0.58
34:c:7:ILE:HD12	34:c:146:PHE:HZ	1.67	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:i:46:ASP:HB3	47:p:99:ILE:HD12	1.85	0.58
45:n:68:ASP:OD1	45:n:69:ASN:N	2.36	0.58
4:3:1129:U:N3	4:3:1132:C:OP2	2.24	0.58
4:3:1553:G:N1	4:3:1577:A:OP2	2.26	0.58
4:3:1699:A:H1'	41:j:1:MET:SD	2.42	0.58
6:5:1136:G:H5''	9:A:146:LYS:HZ1	1.69	0.58
11:C:93:LEU:HA	11:C:96:ARG:HH12	1.68	0.58
33:b:148:GLN:HE22	33:b:151:ARG:HB3	1.68	0.58
4:3:788:G:H2'	4:3:789:A:H8	1.68	0.58
4:3:2794:U:H5''	33:b:72:LYS:HD2	1.84	0.58
6:5:527:G:H22	19:K:61:ALA:HB2	1.68	0.58
9:A:192:ASN:O	9:A:195:ARG:HD2	2.03	0.58
14:F:112:GLU:HG3	14:F:113:LYS:H	1.67	0.58
20:L:2:ALA:N	20:L:8:ASP:OD1	2.37	0.58
4:3:394:C:O4'	11:U:32:LYS:HD3	2.04	0.58
4:3:524:G:N2	4:3:527:A:OP2	2.26	0.58
4:3:695:G:H5''	34:c:101:LEU:HD22	1.85	0.58
4:3:2106:G:N2	4:3:2199:C:O2	2.36	0.58
4:3:2268:C:H42	52:u:28:ARG:NH2	2.01	0.58
6:5:1350:A:OP1	14:F:27:ASN:ND2	2.29	0.58
14:F:67:ASN:O	14:F:137:LYS:NZ	2.31	0.58
37:f:88:PRO:HG2	37:f:89:TYR:HD1	1.68	0.58
48:q:27:ALA:HB1	48:q:31:LYS:CE	2.33	0.58
2:1:9:LYS:O	42:k:65:PHE:N	2.31	0.58
4:3:23:A:H4'	49:r:121:GLN:NE2	2.19	0.58
4:3:343:A:H5'	51:t:16:LYS:HE3	1.86	0.58
4:3:615:G:H2'	4:3:616:G:H8	1.69	0.58
4:3:915:A:OP2	4:3:936:G:N2	2.37	0.58
4:3:1447:A:O2'	4:3:1449:G:N7	2.35	0.58
4:3:2060:G:H5''	33:b:151:ARG:HB2	1.85	0.58
4:3:2386:A:H4'	45:n:27:ARG:NH1	2.18	0.58
6:5:1153:G:N2	6:5:1156:G:OP2	2.37	0.58
17:I:70:GLN:HB3	21:M:61:TRP:CH2	2.38	0.58
11:U:97:LEU:HD13	11:U:129:VAL:HG11	1.84	0.58
33:b:110:VAL:HG11	33:b:197:ILE:HD12	1.83	0.58
4:3:2098:U:O2	53:v:34:GLN:NE2	2.37	0.58
6:5:989:A:O2'	21:M:12:ARG:NH1	2.37	0.58
12:D:132:HIS:O	12:D:133:LYS:HG3	2.03	0.58
15:G:104:LEU:O	15:G:129:ARG:NH2	2.37	0.58
33:b:4:ARG:NH1	33:b:101:LEU:O	2.36	0.58
4:3:1919:A:N1	6:5:1382:C:O2'	2.33	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:22:G:H2'	6:5:23:G:C8	2.39	0.58
13:E:4:ASN:HB3	13:E:88:ILE:HG13	1.86	0.58
23:O:6:LEU:HD13	23:O:17:TYR:HD2	1.67	0.58
36:e:100:ASN:OD1	36:e:107:ASN:ND2	2.36	0.58
40:i:119:ARG:HB3	40:i:120:ARG:NH2	2.19	0.58
43:l:116:LYS:O	43:l:120:ARG:HG2	2.04	0.58
45:n:64:ASN:CG	45:n:65:GLY:H	2.12	0.58
53:v:5:ASP:OD1	53:v:7:LEU:N	2.34	0.58
6:5:373:A:H2'	6:5:374:G:C8	2.39	0.58
6:5:1123:G:O2'	6:5:1124:U:O5'	2.22	0.58
9:A:32:MET:HG3	9:A:33:VAL:H	1.68	0.58
15:G:18:LEU:HD13	15:G:41:LYS:HE2	1.85	0.58
4:3:393:C:C2	11:U:32:LYS:HD2	2.39	0.58
4:3:783:1MG:CM1	49:r:90:LYS:HE2	2.34	0.58
4:3:2107:A:OP2	4:3:2109:A:N6	2.37	0.58
4:3:2504:C:C5'	43:l:83:MET:HE1	2.34	0.58
4:3:2565:G:H4'	52:u:6:PHE:HE1	1.69	0.58
11:C:81:GLN:OE1	11:C:88:ASN:ND2	2.37	0.58
35:d:170:LEU:HG	35:d:175:LEU:HD12	1.85	0.58
39:h:9:ILE:N	39:h:57:ALA:HB3	2.19	0.58
44:m:50:THR:HA	44:m:53:LYS:HE3	1.86	0.58
48:q:54:ARG:HB2	48:q:98:VAL:HB	1.86	0.58
4:3:2195:U:O2'	4:3:2196:G:N7	2.33	0.57
36:e:100:ASN:HA	36:e:128:VAL:HG11	1.86	0.57
41:j:27:SER:OG	41:j:28:THR:N	2.36	0.57
50:s:53:LEU:HD11	50:s:86:PRO:HA	1.86	0.57
4:3:2342:U:N3	45:n:10:LEU:HD21	2.19	0.57
13:E:131:PRO:HB2	13:E:133:THR:HG22	1.84	0.57
34:c:192:MET:HE2	42:k:1:MET:O	2.04	0.57
36:e:110:LEU:HG	36:e:155:ARG:HG3	1.86	0.57
56:y:32:LYS:NZ	56:y:49:GLY:O	2.37	0.57
4:3:314:G:H1'	11:U:36:GLY:HA2	1.85	0.57
4:3:343:A:N3	4:3:363:G:O2'	2.37	0.57
6:5:1052:G:H5'	17:I:59:ARG:NH2	2.18	0.57
6:5:1142:G:O2'	6:5:1144:A:N6	2.34	0.57
9:A:18:VAL:HG13	9:A:22:LYS:HB3	1.87	0.57
11:C:102:TYR:HE2	11:C:103:ARG:HH21	1.52	0.57
12:D:137:TYR:CZ	12:D:205:PRO:HB3	2.39	0.57
15:G:131:LYS:O	15:G:132:LYS:HG3	2.04	0.57
4:3:517:G:OP2	51:t:45:HIS:N	2.30	0.57
4:3:1045:A:N3	4:3:1188:C:O2'	2.34	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:1921:C:H42	6:5:1385:A:H5'	1.66	0.57
4:3:2697:C:OP2	4:3:2727:G:N2	2.27	0.57
4:3:2799:U:OP1	4:3:2896:G:N1	2.22	0.57
10:B:11:ARG:HH22	10:B:185:ILE:HD12	1.69	0.57
17:I:56:THR:HG22	17:I:68:ARG:HG2	1.86	0.57
17:I:61:PRO:HG2	17:I:62:HIS:ND1	2.19	0.57
11:U:166:PHE:CE2	11:U:182:PRO:HG3	2.40	0.57
40:i:19:TYR:HD2	40:i:143:LEU:HD22	1.70	0.57
43:l:43:ASP:HB3	43:l:94:VAL:HG12	1.86	0.57
49:r:23:LEU:O	49:r:27:LYS:NZ	2.36	0.57
4:3:1292:A:H2	56:y:7:ARG:HD3	1.70	0.57
6:5:1110:C:H2'	6:5:1111:G:H8	1.69	0.57
7:6:46:G:H4'	7:6:47:U:OP1	2.04	0.57
10:B:167:ARG:NH2	30:Y:48:C:O2	2.32	0.57
13:E:10:ASP:H	13:E:81:GLN:HB3	1.68	0.57
15:G:59:VAL:HA	15:G:70:VAL:HA	1.86	0.57
21:M:4:LYS:HG3	21:M:5:SER:N	2.19	0.57
32:a:39:VAL:O	32:a:66:TYR:N	2.36	0.57
50:s:12:LEU:HD22	50:s:17:TYR:HE1	1.69	0.57
56:y:46:GLY:O	56:y:47:MET:HE2	2.04	0.57
4:3:2121:A:H3'	4:3:2122:G:C8	2.40	0.57
17:I:59:ARG:HH11	17:I:60:SER:H	1.51	0.57
17:I:70:GLN:HB3	21:M:61:TRP:HH2	1.69	0.57
28:T:19:LYS:HE2	30:Y:31:A:OP2	2.05	0.57
32:a:41:LEU:HG	32:a:66:TYR:HB2	1.85	0.57
37:f:27:ILE:HG12	53:v:64:LEU:HG	1.86	0.57
19:K:121:GLU:HG3	19:K:122:LYS:H	1.69	0.57
11:U:124:LEU:HG	11:U:125:ASN:H	1.70	0.57
11:U:163:VAL:HG22	11:U:164:SER:N	2.20	0.57
50:s:58:LEU:HB2	50:s:80:LEU:HB2	1.84	0.57
4:3:1807:C:OP2	32:a:190:ARG:NH2	2.38	0.57
6:5:1290:G:N1	6:5:1293:A:OP2	2.38	0.57
9:A:228:LEU:HD12	9:A:229:MET:N	2.19	0.57
10:B:87:LYS:NZ	10:B:91:GLN:HE22	2.03	0.57
12:D:63:LYS:NZ	30:Y:55:A:O5'	2.36	0.57
23:O:19:ILE:N	23:O:37:GLY:O	2.38	0.57
11:U:161:GLY:H	11:U:171:ASN:HD21	1.51	0.57
37:f:39:LEU:HD13	37:f:47:ARG:NH2	2.19	0.57
41:j:24:VAL:HG13	41:j:33:ALA:HB2	1.87	0.57
41:j:69:GLN:NE2	41:j:105:GLU:OE2	2.38	0.57
56:y:47:MET:HE1	56:y:52:ARG:CD	2.33	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:11:CYS:HB2	3:2:13:ASP:OD1	2.04	0.57
4:3:2176:G:H22	4:3:2179:A:H2'	1.68	0.57
10:B:160:LEU:HD12	10:B:167:ARG:HB2	1.85	0.57
12:D:215:ASN:HB2	12:D:218:GLU:HB2	1.87	0.57
13:E:3:TYR:HB2	13:E:62:PHE:CE1	2.40	0.57
11:U:81:GLN:OE1	11:U:88:ASN:ND2	2.37	0.57
4:3:620:G:H1	42:k:34:ARG:HH11	1.52	0.57
4:3:1103:G:N2	4:3:1130:A:O2'	2.38	0.57
10:B:192:ALA:HB3	10:B:199:ILE:HB	1.87	0.57
17:I:94:LYS:HA	55:x:94:LEU:HD21	1.87	0.57
11:U:126:ASP:O	11:U:127:ARG:HD2	2.05	0.57
35:d:120:LYS:HD2	35:d:120:LYS:O	2.05	0.57
37:f:39:LEU:HA	37:f:47:ARG:HH21	1.70	0.57
4:3:814:U:OP1	32:a:53:ILE:HD12	2.03	0.56
4:3:1919:A:OP2	4:3:1925:A:N6	2.34	0.56
4:3:2023:U:H3	56:y:7:ARG:HH12	1.52	0.56
6:5:1232:C:H42	55:x:82:LYS:HG2	1.70	0.56
6:5:1289:U:O2'	6:5:1334:A:N3	2.35	0.56
10:B:13:GLY:HA2	10:B:215:LEU:HD21	1.86	0.56
35:d:65:PRO:HB2	35:d:87:CYS:HB2	1.87	0.56
7:6:73:A:H5''	7:6:74:C:C5	2.40	0.56
16:H:86:VAL:HG23	16:H:100:LEU:HD13	1.87	0.56
22:N:18:ASP:OD1	22:N:21:SER:HB2	2.04	0.56
34:c:197:LEU:HD13	34:c:199:VAL:HG23	1.86	0.56
43:l:3:GLN:HE22	43:l:93:TRP:NE1	2.02	0.56
49:r:1:MET:N	49:r:113:GLU:OE2	2.30	0.56
49:r:51:LEU:O	49:r:55:ILE:HG13	2.05	0.56
4:3:1863:G:N2	4:3:2109:A:OP1	2.38	0.56
4:3:2412:A:H4'	42:k:69:ARG:HD3	1.87	0.56
6:5:242:A:N1	6:5:274:A:O2'	2.38	0.56
6:5:1096:A:H2'	6:5:1097:G:H8	1.70	0.56
6:5:1351:U:H2'	6:5:1352:A:C8	2.41	0.56
14:F:142:LYS:O	14:F:145:GLU:HG3	2.05	0.56
23:O:69:VAL:O	23:O:72:LEU:HG	2.06	0.56
24:P:1:MET:HE1	24:P:3:ARG:HB2	1.86	0.56
37:f:54:GLN:O	37:f:58:TYR:HD1	1.88	0.56
45:n:57:SER:OG	45:n:64:ASN:OD1	2.23	0.56
55:x:58:ARG:HG2	55:x:62:LEU:HD13	1.87	0.56
4:3:9:G:H2'	4:3:10:U:C6	2.41	0.56
4:3:2104:A:H2'	4:3:2105:G:C8	2.40	0.56
6:5:1051:U:H3'	10:B:3:GLN:HG2	1.86	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:37:TRP:HZ3	9:A:39:PRO:HA	1.70	0.56
9:A:126:SER:HG	9:A:163:PHE:HE2	1.53	0.56
11:C:56:GLU:HB3	11:C:191:ILE:CD1	2.35	0.56
17:I:9:TYR:CB	17:I:12:LEU:HD21	2.34	0.56
18:J:55:SER:O	18:J:58:ILE:HG12	2.05	0.56
19:K:22:PRO:HD2	19:K:107:ARG:HH21	1.69	0.56
19:K:34:LYS:HD3	19:K:35:VAL:N	2.20	0.56
19:K:68:VAL:HG12	19:K:76:VAL:O	2.06	0.56
37:f:67:LYS:O	37:f:70:GLU:HG2	2.04	0.56
4:3:1926:A:N1	6:5:1470:U:O2'	2.31	0.56
10:B:37:ASP:OD1	10:B:38:GLU:N	2.38	0.56
11:C:73:ARG:O	11:C:76:ARG:HD3	2.05	0.56
17:I:46:LEU:H	17:I:46:LEU:HD23	1.70	0.56
11:U:38:HIS:O	11:U:40:ASN:N	2.38	0.56
37:f:97:ILE:HA	37:f:100:GLN:NE2	2.19	0.56
47:p:53:LYS:O	47:p:57:ARG:HD3	2.06	0.56
48:q:27:ALA:O	48:q:62:HIS:NE2	2.39	0.56
4:3:893:A:H61	4:3:957:G:H1	1.54	0.56
6:5:998:G:H5'	6:5:999:C:C4	2.41	0.56
11:U:64:TYR:HD1	11:U:110:ARG:HH12	1.54	0.56
32:a:128:ILE:HG22	32:a:129:ASP:N	2.20	0.56
4:3:2189:U:H2'	4:3:2190:G:C8	2.40	0.56
4:3:2193:U:H2'	4:3:2194:G:H5''	1.87	0.56
6:5:76:G:N2	6:5:79:A:OP2	2.39	0.56
10:B:57:GLU:HG2	10:B:68:PHE:HB2	1.88	0.56
12:D:177:ASP:N	12:D:177:ASP:OD1	2.39	0.56
14:F:76:VAL:HG22	14:F:83:ASN:ND2	2.20	0.56
17:I:42:ILE:HG23	17:I:80:MET:HE1	1.87	0.56
11:U:24:GLU:O	11:U:24:GLU:HG2	2.05	0.56
41:j:75:THR:HG21	46:o:77:LYS:NZ	2.20	0.56
50:s:53:LEU:HB2	50:s:84:THR:HG23	1.86	0.56
4:3:906:G:O2'	43:l:6:ARG:NH1	2.39	0.56
4:3:2175:U:H2'	4:3:2176:G:O4'	2.05	0.56
4:3:2847:C:H2'	4:3:2848:A:H8	1.70	0.56
6:5:354:U:H2'	6:5:355:A:H8	1.71	0.56
6:5:927:C:C6	14:F:1:MET:HE3	2.41	0.56
6:5:1302:C:O2'	20:L:29:ARG:NH2	2.39	0.56
6:5:1351:U:O3'	14:F:94:ARG:NH2	2.39	0.56
11:C:53:GLN:HG2	11:C:195:TYR:CE2	2.41	0.56
41:j:112:ASN:OD1	41:j:113:LYS:HD3	2.05	0.56
44:m:93:THR:HB	44:m:97:TYR:CE1	2.41	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:v:41:ALA:O	53:v:44:LYS:HG3	2.06	0.56
4:3:86:A:N6	4:3:101:C:O4'	2.38	0.56
4:3:394:C:C1'	11:U:32:LYS:HD3	2.36	0.56
4:3:585:U:H2'	4:3:586:G:H8	1.71	0.56
4:3:1081:A:N7	38:g:4:LYS:NZ	2.54	0.56
4:3:2194:G:H2'	4:3:2195:U:H4'	1.88	0.56
6:5:133:G:H2'	6:5:134:G:C8	2.41	0.56
9:A:159:LEU:O	9:A:163:PHE:HB2	2.05	0.56
10:B:121:ARG:NH1	10:B:190:GLU:OE1	2.39	0.56
12:D:87:ARG:HG2	12:D:109:LEU:HD22	1.88	0.56
19:K:67:LYS:HE2	19:K:75:GLU:HB3	1.88	0.56
43:l:12:PRO:HG2	43:l:72:MET:SD	2.46	0.56
51:t:52:THR:H	51:t:55:ALA:HB3	1.70	0.56
6:5:871:U:H1'	15:G:11:HIS:HE1	1.69	0.56
6:5:1019:G:O2'	6:5:1020:G:OP2	2.21	0.56
17:I:65:LYS:HZ2	17:I:68:ARG:HH21	1.53	0.56
11:U:121:HIS:HD2	11:U:148:THR:HG22	1.69	0.56
11:U:129:VAL:HG13	11:U:134:ILE:HD12	1.87	0.56
37:f:87:ARG:HB2	37:f:88:PRO:HD3	1.88	0.56
41:j:40:VAL:HG22	41:j:59:ARG:HG2	1.88	0.56
4:3:2136:A:H3'	4:3:2137:A:C8	2.42	0.55
6:5:688:G:N7	18:J:21:ASN:ND2	2.55	0.55
6:5:836:C:H1'	13:E:145:ARG:HG2	1.88	0.55
6:5:949:G:H4'	20:L:119:LYS:HD3	1.87	0.55
8:7:27:U:H3	8:7:43:G:H1	1.54	0.55
16:H:50:MET:SD	16:H:81:ILE:HD11	2.46	0.55
17:I:90:ILE:O	17:I:94:LYS:HG2	2.06	0.55
39:h:122:LYS:HA	39:h:125:LEU:HD13	1.87	0.55
8:7:36:C:H2'	8:7:37:A:H8	1.71	0.55
11:C:18:LEU:HA	11:C:63:MET:HE1	1.87	0.55
15:G:23:ASN:HD21	15:G:87:VAL:HG22	1.72	0.55
11:U:14:LEU:HA	53:v:63:ARG:HH12	1.70	0.55
32:a:84:LYS:HE2	32:a:98:LEU:HD23	1.87	0.55
50:s:9:LYS:O	50:s:30:VAL:HG22	2.06	0.55
4:3:388:U:H5''	11:U:109:THR:HG21	1.87	0.55
4:3:1557:G:O6	4:3:1571:G:O2'	2.24	0.55
4:3:2540:G:O2'	4:3:2665:A:N1	2.36	0.55
6:5:832:G:H2'	6:5:833:G:H8	1.70	0.55
8:7:28:C:H5''	26:R:87:ARG:HH11	1.71	0.55
8:7:36:C:H2'	8:7:37:A:C8	2.41	0.55
34:c:64:LYS:NZ	34:c:68:GLN:OE1	2.38	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:l:109:ILE:HD12	43:l:113:GLN:HE21	1.70	0.55
4:3:733:C:O2'	4:3:769:A:N6	2.39	0.55
4:3:2023:U:H1'	56:y:3:VAL:HG22	1.89	0.55
6:5:1105:C:H1'	21:M:60:SER:HB2	1.88	0.55
6:5:1144:A:H2'	6:5:1145:A:C8	2.41	0.55
10:B:20:SER:HB2	21:M:52:ALA:O	2.06	0.55
11:C:100:ILE:CG2	11:C:104:MET:HE3	2.37	0.55
11:C:142:VAL:N	11:C:176:GLY:O	2.38	0.55
14:F:110:ARG:HG2	14:F:112:GLU:HB2	1.87	0.55
16:H:32:VAL:HA	16:H:67:VAL:HB	1.88	0.55
19:K:78:THR:HG21	19:K:95:LEU:HD22	1.89	0.55
32:a:65:LYS:O	32:a:67:ARG:NH1	2.39	0.55
39:h:106:GLN:HA	39:h:109:LEU:HD23	1.87	0.55
53:v:6:GLN:HB2	53:v:48:ILE:HD11	1.88	0.55
4:3:937:A:H2'	4:3:938:A:C8	2.42	0.55
4:3:1245:G:H1	4:3:1264:U:H3	1.55	0.55
4:3:1391:U:O2'	4:3:1816:A:N3	2.34	0.55
4:3:2154:A:H2'	4:3:2155:G:O4'	2.06	0.55
4:3:2688:C:H5'	33:b:198:ALA:HA	1.88	0.55
9:A:134:VAL:O	9:A:137:GLN:HG2	2.07	0.55
10:B:89:THR:HG23	10:B:102:LEU:HD23	1.87	0.55
11:C:19:LEU:HG	11:C:63:MET:CE	2.36	0.55
11:C:100:ILE:HG22	11:C:104:MET:HE3	1.87	0.55
15:G:118:THR:OG1	15:G:123:MET:HE1	2.06	0.55
20:L:118:ASN:HA	26:R:86:ASN:HD21	1.72	0.55
4:3:324:C:OP1	11:U:147:LYS:NZ	2.30	0.55
4:3:1115:G:N3	39:h:123:MET:HE1	2.22	0.55
4:3:2151:G:H2'	4:3:2153:U:C6	2.41	0.55
4:3:2323:U:O2	35:d:125:ARG:NH1	2.38	0.55
6:5:590:G:H1	6:5:644:U:H3	1.55	0.55
6:5:671:G:H2'	6:5:672:A:H8	1.72	0.55
6:5:1361:G:H2'	6:5:1362:G:H8	1.72	0.55
10:B:11:ARG:O	10:B:16:LYS:HG2	2.07	0.55
12:D:95:GLY:N	12:D:172:LEU:HD12	2.22	0.55
33:b:148:GLN:NE2	33:b:151:ARG:HB3	2.22	0.55
3:2:30:GLN:OE1	4:3:2535:C:H5''	2.06	0.55
4:3:354:C:HO2'	4:3:356:A:H8	1.54	0.55
4:3:622:U:H2'	4:3:623:A:C8	2.42	0.55
4:3:1111:C:H2'	4:3:1112:A:O4'	2.06	0.55
4:3:1132:C:H3'	4:3:1133:A:H8	1.72	0.55
6:5:212:G:O2'	6:5:464:A:N6	2.29	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:E:28:THR:HG21	13:E:72:PHE:HA	1.87	0.55
26:R:67:VAL:O	55:x:58:ARG:NH1	2.40	0.55
11:U:109:THR:HG23	11:U:112:SER:H	1.70	0.55
55:x:37:ASP:OD1	55:x:38:ILE:N	2.40	0.55
1:0:2:LYS:HE3	4:3:1654:G:O2'	2.07	0.55
4:3:342:G:H21	4:3:363:G:H21	1.53	0.55
4:3:1909:C:O2'	32:a:251:ARG:O	2.18	0.55
10:B:59:GLU:OE1	17:I:100:VAL:HG21	2.07	0.55
12:D:133:LYS:O	12:D:156:GLN:NE2	2.31	0.55
12:D:152:LYS:HB2	12:D:179:TYR:HB2	1.89	0.55
17:I:15:LYS:HB3	17:I:105:ARG:HB3	1.89	0.55
18:J:76:LYS:HD3	18:J:101:THR:HB	1.89	0.55
4:3:259:A:O2'	4:3:422:A:OP1	2.25	0.55
4:3:2492:G:O2'	43:l:124:LYS:O	2.21	0.55
4:3:2813:A:H2'	4:3:2814:A:C8	2.42	0.55
6:5:96:G:H1	6:5:326:C:H41	1.55	0.55
6:5:190:A:H2'	6:5:191:A:H8	1.72	0.55
14:F:5:ARG:NH2	14:F:8:LYS:HD2	2.21	0.55
19:K:84:GLY:O	19:K:112:ARG:NH2	2.39	0.55
4:3:901:C:H4'	4:3:902:U:C5'	2.37	0.55
4:3:1091:G:H4'	4:3:1121:A:H8	1.72	0.55
6:5:250:G:H2'	6:5:251:G:H8	1.71	0.55
12:D:212:ARG:CZ	15:G:51:GLU:O	2.54	0.55
11:U:14:LEU:HD13	53:v:63:ARG:HH11	1.71	0.55
11:U:56:GLU:HB3	11:U:191:ILE:HD11	1.89	0.55
32:a:34:GLU:O	32:a:38:LEU:HG	2.06	0.55
37:f:130:ILE:HD11	37:f:144:PRO:HG3	1.89	0.55
4:3:930:C:H2'	4:3:931:G:C8	2.42	0.54
7:6:25:C:H42	7:6:45:G:N2	2.05	0.54
12:D:164:GLY:O	12:D:167:ARG:HG2	2.06	0.54
19:K:42:LEU:HD13	19:K:94:LEU:HD21	1.88	0.54
41:j:94:ARG:NE	41:j:94:ARG:HA	2.22	0.54
4:3:227:A:O2'	4:3:456:G:N3	2.34	0.54
4:3:363:G:H1	51:t:16:LYS:HZ3	1.54	0.54
4:3:411:U:H2'	4:3:412:A:H8	1.72	0.54
4:3:716:G:H1	4:3:831:U:H3	1.55	0.54
4:3:897:A:N3	5:4:77:G:O2'	2.40	0.54
4:3:963:U:H2'	4:3:964:A:H8	1.73	0.54
4:3:2493:G:O3'	43:l:126:PRO:HB3	2.07	0.54
7:6:33:U:H6	7:6:33:U:H5''	1.72	0.54
9:A:247:ALA:O	9:A:249:LYS:HG2	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:E:114:LYS:O	13:E:118:ILE:HD12	2.08	0.54
16:H:44:LYS:HG3	16:H:46:VAL:H	1.72	0.54
38:g:55:LYS:HB2	38:g:58:ILE:HG22	1.89	0.54
39:h:125:LEU:HG	39:h:135:VAL:HG21	1.88	0.54
4:3:892:G:H2'	4:3:893:A:C8	2.42	0.54
4:3:1166:G:N2	4:3:1167:U:O4	2.35	0.54
4:3:2119:A:H2'	4:3:2120:G:C8	2.42	0.54
6:5:683:G:H1	6:5:700:G:HO2'	1.55	0.54
13:E:124:ASN:ND2	13:E:129:ASP:HB2	2.23	0.54
22:N:77:ASN:O	22:N:81:THR:HG23	2.08	0.54
11:U:16:PHE:O	11:U:20:GLU:HG3	2.08	0.54
41:j:88:LYS:HE2	41:j:90:ASP:OD2	2.06	0.54
4:3:2173:G:H3'	4:3:2174:G:C8	2.43	0.54
4:3:2698:U:H5'	44:m:14:ARG:NH2	2.11	0.54
6:5:195:U:H2'	6:5:196:G:C8	2.43	0.54
6:5:394:U:H2'	6:5:395:G:C8	2.43	0.54
6:5:452:A:H5''	23:O:70:ARG:HH22	1.71	0.54
6:5:670:G:H2'	6:5:671:G:C8	2.42	0.54
6:5:735:C:OP2	13:E:92:ARG:NH2	2.40	0.54
15:G:101:PHE:HE1	15:G:129:ARG:HA	1.72	0.54
16:H:70:LYS:HD2	16:H:70:LYS:O	2.08	0.54
11:U:44:SER:OG	11:U:52:GLN:HG3	2.07	0.54
36:e:23:ASP:HA	36:e:38:LEU:HB2	1.89	0.54
36:e:118:GLU:OE2	36:e:150:GLU:HG3	2.07	0.54
43:l:64:MET:HE1	43:l:66:ILE:HG13	1.90	0.54
4:3:354:C:C5	34:c:141:LYS:HE3	2.41	0.54
4:3:554:U:H4'	49:r:73:GLU:OE2	2.08	0.54
4:3:2114:C:H2'	4:3:2115:A:C8	2.42	0.54
4:3:2141:A:H2	4:3:2166:U:H1'	1.72	0.54
4:3:2606:A:H5''	32:a:242:GLY:HA3	1.88	0.54
6:5:452:A:N6	6:5:476:U:O2	2.40	0.54
17:I:71:PHE:CZ	17:I:73:LYS:HB2	2.42	0.54
2:1:28:HIS:ND1	2:1:29:LEU:HG	2.22	0.54
4:3:619:A:N1	4:3:844:G:O2'	2.34	0.54
5:4:40:U:O2	35:d:63:GLN:NE2	2.40	0.54
6:5:1197:G:H4'	26:R:78:ARG:NH2	2.17	0.54
13:E:9:VAL:HG23	13:E:56:HIS:HB2	1.90	0.54
14:F:25:ILE:O	14:F:29:ILE:HG12	2.07	0.54
19:K:53:MET:SD	19:K:103:LEU:HD22	2.47	0.54
37:f:27:ILE:CG1	53:v:64:LEU:HG	2.37	0.54
6:5:197:A:H2'	6:5:198:A:C8	2.43	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:941:A:H2'	6:5:942:G:C8	2.43	0.54
6:5:1078:G:H5'	6:5:1078:G:H8	1.72	0.54
10:B:109:ILE:HD11	10:B:222:ILE:HA	1.89	0.54
11:C:60:MET:HB3	11:C:191:ILE:HG12	1.90	0.54
13:E:24:LYS:HE2	13:E:75:THR:HG22	1.88	0.54
17:I:18:SER:HB3	17:I:102:VAL:HA	1.89	0.54
11:U:66:ILE:HD11	11:U:96:ARG:HH12	1.73	0.54
36:e:89:LYS:NZ	36:e:133:GLU:HG3	2.23	0.54
40:i:45:VAL:HG12	47:p:99:ILE:HD13	1.87	0.54
44:m:92:LYS:O	44:m:92:LYS:HD3	2.07	0.54
50:s:43:ALA:O	50:s:47:VAL:HG22	2.07	0.54
4:3:340:U:H1'	4:3:1241:U:H5	1.73	0.54
4:3:622:U:H4'	34:c:97:ARG:HD3	1.88	0.54
4:3:1106:G:N2	4:3:1124:G:O2'	2.40	0.54
4:3:1635:G:OP2	50:s:59:ILE:HD12	2.08	0.54
6:5:789:A:O2'	6:5:791:A:N7	2.41	0.54
9:A:37:TRP:CZ3	9:A:39:PRO:HA	2.42	0.54
9:A:228:LEU:HA	9:A:231:LEU:HD12	1.89	0.54
12:D:219:LEU:H	12:D:219:LEU:HD12	1.73	0.54
13:E:6:ILE:HD11	13:E:59:ARG:HH11	1.72	0.54
14:F:15:PRO:HG3	16:H:45:LEU:HD13	1.89	0.54
17:I:57:ILE:CG2	21:M:41:ARG:HB2	2.38	0.54
21:M:13:ILE:HD12	21:M:14:PRO:HD2	1.89	0.54
24:P:31:LYS:HE3	24:P:36:HIS:HB3	1.89	0.54
11:U:9:LYS:O	11:U:13:ARG:HB2	2.08	0.54
46:o:36:LYS:NZ	46:o:87:SER:OG	2.41	0.54
52:u:10:ILE:HD12	52:u:14:PHE:HZ	1.71	0.54
53:v:63:ARG:C	53:v:65:SER:H	2.14	0.54
4:3:2133:A:N3	4:3:2134:G:O2'	2.39	0.54
4:3:2146:A:H61	4:3:2158:C:N4	2.06	0.54
4:3:2164:G:H4'	4:3:2165:A:H5'	1.90	0.54
4:3:2530:U:O2'	4:3:2655:U:OP1	2.20	0.54
6:5:304:U:H2'	6:5:305:A:H8	1.73	0.54
6:5:1330:A:H2'	6:5:1331:A:C8	2.43	0.54
12:D:67:GLU:CD	12:D:97:ARG:HH21	2.15	0.54
11:U:13:ARG:O	53:v:63:ARG:NH1	2.36	0.54
33:b:97:THR:OG1	33:b:189:MET:HE1	2.08	0.54
4:3:180:A:H5'	4:3:181:G:C8	2.43	0.54
4:3:917:G:N2	4:3:935:U:O2'	2.41	0.54
4:3:2308:U:H2'	4:3:2309:A:C8	2.43	0.54
6:5:1270:C:H5'	20:L:14:ARG:NH1	2.23	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:h:20:LYS:O	39:h:32:MET:HE3	2.08	0.54
54:w:45:ASN:O	54:w:49:ARG:HG3	2.07	0.54
4:3:1076:U:H3	4:3:1149:G:H1	1.55	0.53
4:3:1583:G:O2'	4:3:1584:U:OP1	2.26	0.53
6:5:386:U:H2'	6:5:387:G:H8	1.74	0.53
6:5:1022:G:O2'	6:5:1023:G:O4'	2.25	0.53
11:C:103:ARG:HB3	11:C:167:VAL:HG21	1.91	0.53
23:O:19:ILE:HG22	23:O:36:ILE:HB	1.89	0.53
40:i:20:ILE:HG12	40:i:140:PRO:HB2	1.89	0.53
10:B:134:ARG:HE	10:B:138:ARG:HG3	1.71	0.53
11:C:9:LYS:HG2	11:C:35:PRO:HG3	1.89	0.53
26:R:63:THR:HG23	26:R:66:MET:HE1	1.90	0.53
29:X:29:LYS:HG3	29:X:30:GLN:N	2.20	0.53
51:t:9:LYS:NZ	51:t:21:SER:OG	2.31	0.53
4:3:394:C:O2'	11:U:33:THR:HA	2.09	0.53
4:3:2128:G:H2'	4:3:2129:U:C6	2.43	0.53
4:3:2285:G:H3'	52:u:26:ASN:ND2	2.23	0.53
4:3:2312:G:O2'	35:d:153:ASP:OD1	2.24	0.53
4:3:2798:A:O3'	4:3:2896:G:N2	2.42	0.53
6:5:196:G:H5'	27:S:49:SER:HA	1.90	0.53
8:7:34:G:H1	30:Y:42:U:H3	1.55	0.53
9:A:18:VAL:HG21	9:A:227:LEU:HD11	1.91	0.53
14:F:128:ASN:O	14:F:130:THR:HG23	2.08	0.53
38:g:74:THR:HG22	38:g:110:CYS:HB2	1.89	0.53
47:p:97:LEU:HD11	48:q:4:ILE:HD11	1.90	0.53
49:r:94:ASN:C	49:r:95:MET:HE2	2.34	0.53
4:3:340:U:H2'	4:3:341:G:O4'	2.08	0.53
4:3:940:A:H2'	4:3:941:C:H6	1.72	0.53
4:3:1270:C:H2'	4:3:1271:A:H8	1.72	0.53
12:D:211:LEU:C	12:D:213:ASN:H	2.16	0.53
20:L:73:ILE:O	20:L:77:ILE:HG12	2.09	0.53
23:O:17:TYR:HB2	23:O:39:LEU:HD23	1.90	0.53
26:R:48:THR:OG1	26:R:59:ASN:OD1	2.27	0.53
6:5:585:G:H4'	15:G:12:PHE:CD1	2.43	0.53
6:5:1126:U:O4	6:5:1127:A:N6	2.41	0.53
6:5:1352:A:O2'	14:F:2:ARG:NH2	2.41	0.53
10:B:113:MET:HE1	10:B:149:ALA:HB2	1.90	0.53
14:F:149:ALA:HA	18:J:54:TYR:HD2	1.72	0.53
17:I:83:VAL:HG23	17:I:84:ASP:H	1.74	0.53
26:R:36:ARG:HH12	26:R:77:THR:HG22	1.74	0.53
4:3:50:G:H22	4:3:180:A:H5''	1.73	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:450:C:H1'	4:3:1871:U:H1'	1.91	0.53
4:3:816:A:H5''	4:3:817:A:N7	2.24	0.53
4:3:1529:U:H2'	4:3:1530:G:H8	1.73	0.53
4:3:1569:A:H2'	4:3:1570:A:C2	2.43	0.53
4:3:1812:C:O2	4:3:1819:G:N2	2.34	0.53
4:3:1871:U:OP1	4:3:2418:G:O2'	2.27	0.53
6:5:9:A:N7	11:C:202:ARG:HD2	2.24	0.53
6:5:916:U:O2	12:D:79:THR:OG1	2.23	0.53
19:K:42:LEU:HD13	19:K:94:LEU:HD11	1.89	0.53
22:N:33:ILE:O	22:N:37:THR:HG23	2.09	0.53
23:O:66:THR:HG22	23:O:67:ASP:H	1.73	0.53
32:a:179:TYR:HB3	32:a:191:LYS:HB3	1.89	0.53
34:c:152:LEU:HB3	34:c:157:VAL:HG11	1.91	0.53
35:d:78:LYS:O	35:d:78:LYS:HD3	2.09	0.53
35:d:117:LEU:N	35:d:177:LEU:HD12	2.23	0.53
36:e:142:GLU:OE1	36:e:142:GLU:N	2.39	0.53
37:f:56:GLU:OE1	37:f:56:GLU:N	2.38	0.53
40:i:7:LEU:HD23	40:i:7:LEU:H	1.74	0.53
4:3:314:G:N2	4:3:316:C:H1'	2.24	0.53
4:3:583:U:O4	40:i:3:LYS:HD3	2.08	0.53
4:3:907:A:H2'	4:3:908:A:O4'	2.09	0.53
4:3:944:U:OP1	43:l:24:ASN:N	2.40	0.53
4:3:1280:G:OP2	42:k:22:ARG:NE	2.37	0.53
4:3:2580:A:H2'	33:b:151:ARG:HH22	1.74	0.53
4:3:2630:U:O2'	4:3:2829:G:N7	2.42	0.53
6:5:80:U:H2'	6:5:81:A:H8	1.73	0.53
6:5:353:G:H1'	6:5:364:U:O2	2.09	0.53
6:5:1320:A:H2	6:5:1350:A:H62	1.55	0.53
6:5:1342:C:HO2'	17:I:56:THR:HG1	1.57	0.53
6:5:1387:U:H2'	6:5:1388:A:C8	2.43	0.53
6:5:1388:A:H2	6:5:1462:G:H22	1.57	0.53
16:H:30:ILE:HG23	16:H:37:PRO:HG3	1.89	0.53
16:H:86:VAL:O	16:H:90:LEU:HD23	2.08	0.53
16:H:131:LYS:HE3	16:H:132:ARG:NH1	2.24	0.53
17:I:23:LEU:HD21	17:I:99:PRO:HB2	1.91	0.53
11:U:166:PHE:CD2	11:U:182:PRO:HG3	2.42	0.53
35:d:31:LEU:HD11	35:d:156:LEU:HD12	1.91	0.53
4:3:922:C:H3'	4:3:923:A:H8	1.74	0.53
4:3:1588:A:H2'	4:3:1589:A:C8	2.43	0.53
4:3:2516:G:HO2'	4:3:2562:U:HO2'	1.55	0.53
4:3:2540:G:N2	4:3:2671:G:O2'	2.42	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:2580:A:C2'	33:b:151:ARG:HH22	2.22	0.53
6:5:378:A:H2'	6:5:379:A:C8	2.44	0.53
17:I:13:LYS:HG3	17:I:81:ILE:HB	1.91	0.53
42:k:82:LEU:HA	42:k:85:ILE:HG22	1.90	0.53
45:n:64:ASN:ND2	45:n:65:GLY:H	2.06	0.53
4:3:1414:C:H2'	4:3:1415:A:H8	1.74	0.53
6:5:1115:G:H1'	6:5:1116:U:H5	1.74	0.53
10:B:42:ASN:O	10:B:46:VAL:HG22	2.08	0.53
12:D:169:ILE:HD11	12:D:192:ILE:HG12	1.91	0.53
25:Q:90:LEU:O	25:Q:94:ARG:HG3	2.08	0.53
11:U:19:LEU:HD11	53:v:8:THR:HG23	1.89	0.53
32:a:119:ASP:HB3	32:a:131:LYS:NZ	2.24	0.53
33:b:47:TYR:HB2	33:b:85:ARG:HH21	1.74	0.53
33:b:53:SER:HB2	33:b:78:THR:OG1	2.09	0.53
35:d:60:ILE:HD13	35:d:140:GLU:HG3	1.90	0.53
40:i:20:ILE:HD13	40:i:58:ILE:HB	1.91	0.53
43:l:85:SER:HB3	52:u:22:GLY:HA2	1.89	0.53
4:3:1906:G:H21	4:3:1909:C:H41	1.56	0.53
4:3:1961:A:O2'	4:3:1963:U:O4	2.20	0.53
4:3:2477:A:H2'	4:3:2478:G:O4'	2.09	0.53
6:5:1205:C:N4	20:L:104:THR:OG1	2.42	0.53
9:A:181:PRO:HD3	9:A:200:ALA:HB1	1.90	0.53
20:L:71:ARG:NH1	35:d:113:ASP:OD2	2.41	0.53
55:x:21:ASN:ND2	55:x:39:CYS:SG	2.81	0.53
4:3:615:G:H2'	4:3:616:G:C8	2.44	0.52
4:3:1091:G:H4'	4:3:1121:A:C8	2.44	0.52
6:5:447:G:H5''	6:5:448:A:H3'	1.91	0.52
6:5:855:G:O2'	6:5:868:G:O2'	2.26	0.52
10:B:17:ASN:H	10:B:216:ASN:CG	2.17	0.52
10:B:156:VAL:HG22	10:B:169:LYS:HG2	1.91	0.52
17:I:57:ILE:HG23	21:M:41:ARG:HB2	1.91	0.52
11:U:125:ASN:C	11:U:127:ARG:H	2.16	0.52
42:k:136:LEU:HA	42:k:139:VAL:HG22	1.91	0.52
49:r:28:LYS:HD2	49:r:29:THR:H	1.74	0.52
52:u:8:THR:O	52:u:9:LYS:HB2	2.07	0.52
4:3:2109:A:H2	4:3:2194:G:H1	1.57	0.52
4:3:2566:C:H1'	52:u:5:TYR:HE1	1.74	0.52
6:5:1261:A:H2'	6:5:1262:A:C8	2.44	0.52
9:A:57:VAL:HB	9:A:60:LEU:HB2	1.91	0.52
11:C:117:VAL:HG22	11:C:122:VAL:HG11	1.92	0.52
12:D:65:GLU:O	12:D:67:GLU:N	2.41	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:113:ASN:O	12:D:117:LYS:HG3	2.10	0.52
15:G:16:ALA:HB2	15:G:89:GLN:OE1	2.09	0.52
17:I:59:ARG:NH1	17:I:60:SER:CB	2.72	0.52
24:P:18:ASN:HB2	24:P:21:THR:OG1	2.09	0.52
36:e:18:LEU:HD12	36:e:20:PHE:CZ	2.44	0.52
36:e:38:LEU:HD12	36:e:42:LEU:CD2	2.37	0.52
53:v:38:VAL:O	53:v:45:THR:HA	2.10	0.52
4:3:141:A:H2	4:3:1437:A:H1'	1.74	0.52
4:3:1125:U:H2'	4:3:1126:G:C8	2.44	0.52
4:3:2403:C:H1'	7:6:76:A:H4'	1.91	0.52
4:3:2683:G:OP1	41:j:31:ARG:HG2	2.10	0.52
6:5:1001:A:N7	6:5:1020:G:N2	2.57	0.52
10:B:9:GLY:HA2	10:B:12:PHE:HD2	1.74	0.52
10:B:61:THR:HB	10:B:64:THR:HG22	1.91	0.52
14:F:83:ASN:HD21	14:F:85:GLN:NE2	2.07	0.52
19:K:46:VAL:O	19:K:68:VAL:HG23	2.09	0.52
32:a:83:VAL:HG22	32:a:99:ILE:HG22	1.91	0.52
49:r:127:LYS:O	49:r:130:GLU:HG3	2.08	0.52
51:t:1:MET:HE3	51:t:2:GLN:H	1.74	0.52
4:3:1414:C:H2'	4:3:1415:A:C8	2.44	0.52
4:3:2598:C:H5''	32:a:246:ARG:HG3	1.92	0.52
6:5:134:G:O2'	6:5:1421:A:N3	2.32	0.52
6:5:537:A:OP2	19:K:124:ARG:HD2	2.09	0.52
27:S:40:ASN:ND2	27:S:42:ASP:OD2	2.38	0.52
35:d:135:GLN:HG2	35:d:149:ILE:HG23	1.91	0.52
37:f:127:THR:HG22	37:f:145:ASP:OD1	2.10	0.52
38:g:46:LYS:HG2	38:g:48:GLY:H	1.74	0.52
38:g:72:ASP:O	38:g:76:ILE:HG12	2.10	0.52
39:h:32:MET:O	39:h:36:THR:HG23	2.09	0.52
50:s:12:LEU:HD22	50:s:17:TYR:CE1	2.44	0.52
2:1:10:ARG:HG2	42:k:64:LYS:HA	1.90	0.52
6:5:1332:U:H3	6:5:1338:A:H61	1.58	0.52
9:A:260:GLN:OE1	9:A:261:LYS:HG2	2.08	0.52
10:B:115:SER:HB2	10:B:221:HIS:CD2	2.45	0.52
11:C:122:VAL:HG13	11:C:129:VAL:HG13	1.91	0.52
18:J:103:ILE:HD12	28:T:18:PHE:HB2	1.90	0.52
19:K:76:VAL:HG21	19:K:108:TYR:CE1	2.44	0.52
11:U:96:ARG:HH21	11:U:133:SER:HA	1.74	0.52
38:g:46:LYS:NZ	38:g:86:VAL:O	2.43	0.52
44:m:14:ARG:HD2	44:m:15:VAL:HG23	1.91	0.52
6:5:1087:C:HO2'	6:5:1145:A:HO2'	1.58	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:214:LYS:HZ3	15:G:51:GLU:C	2.12	0.52
15:G:42:ILE:O	15:G:46:GLU:HG2	2.10	0.52
26:R:22:MET:CE	26:R:28:LYS:HB2	2.39	0.52
26:R:68:GLY:HA2	55:x:66:PHE:CZ	2.41	0.52
37:f:41:LYS:O	37:f:42:LYS:HG2	2.10	0.52
38:g:27:PHE:CD1	38:g:106:MET:HE3	2.45	0.52
4:3:632:A:H2'	4:3:633:G:H8	1.75	0.52
4:3:2125:U:P	4:3:2155:G:H4'	2.50	0.52
6:5:92:G:N7	27:S:10:ARG:NH2	2.58	0.52
9:A:32:MET:HG3	9:A:33:VAL:N	2.25	0.52
10:B:8:ASN:OD1	10:B:9:GLY:N	2.42	0.52
10:B:134:ARG:NH1	12:D:110:GLU:OE1	2.43	0.52
16:H:125:ARG:HG2	16:H:126:ALA:H	1.75	0.52
36:e:18:LEU:HD11	36:e:53:LEU:HD13	1.92	0.52
43:l:73:SER:HB2	43:l:93:TRP:CZ3	2.45	0.52
4:3:913:U:H2'	4:3:914:G:O4'	2.09	0.52
6:5:689:U:O2'	6:5:691:A:N7	2.32	0.52
6:5:999:C:OP1	6:5:1023:G:N2	2.42	0.52
6:5:1468:A:H5'	30:Y:44:A:H5'	1.90	0.52
9:A:95:LEU:HD11	9:A:226:CYS:HA	1.92	0.52
17:I:90:ILE:HA	17:I:93:LEU:HD12	1.90	0.52
18:J:12:GLY:HA2	18:J:30:PRO:HD3	1.91	0.52
25:Q:39:LYS:HD3	25:Q:42:ARG:HH12	1.75	0.52
28:T:2:PRO:HB3	28:T:21:VAL:HG11	1.92	0.52
37:f:55:GLN:O	37:f:59:GLU:HG3	2.10	0.52
46:o:31:VAL:HG12	46:o:90:LEU:HA	1.92	0.52
50:s:4:THR:O	50:s:4:THR:HG22	2.09	0.52
56:y:54:LYS:HD2	56:y:55:LYS:O	2.09	0.52
4:3:591:G:H5''	40:i:115:ASN:HD21	1.75	0.52
4:3:2236:G:H22	53:v:34:GLN:HE22	1.58	0.52
4:3:2814:A:H4'	33:b:64:LYS:HD2	1.92	0.52
6:5:275:A:H5''	6:5:276:U:H3'	1.92	0.52
6:5:1510:C:O2'	28:T:55:LYS:HA	2.10	0.52
10:B:158:GLY:HA3	10:B:199:ILE:HD13	1.92	0.52
10:B:159:ARG:HH21	10:B:196:TYR:HB3	1.75	0.52
36:e:42:LEU:HG	36:e:44:LEU:CD2	2.39	0.52
42:k:90:LEU:HD11	42:k:101:LYS:HG3	1.92	0.52
42:k:113:LYS:HE3	42:k:115:ILE:HD11	1.92	0.52
44:m:73:PHE:HB2	44:m:78:LEU:HG	1.91	0.52
54:w:77:LYS:HG2	54:w:78:LYS:H	1.74	0.52
6:5:68:C:H2'	6:5:69:G:C8	2.44	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:972:A:N6	6:5:1199:U:O5'	2.43	0.52
6:5:1406:U:O4	6:5:1407:A:N6	2.43	0.52
9:A:260:GLN:CD	9:A:261:LYS:HG2	2.35	0.52
13:E:142:ARG:O	13:E:145:ARG:N	2.36	0.52
15:G:41:LYS:HA	15:G:44:ILE:HG12	1.92	0.52
19:K:127:ARG:HB2	19:K:132:ALA:HB3	1.92	0.52
35:d:118:SER:C	35:d:120:LYS:H	2.18	0.52
48:q:60:GLU:N	48:q:60:GLU:OE1	2.42	0.52
4:3:339:U:H2'	4:3:340:U:C6	2.45	0.51
4:3:666:G:N2	4:3:669:A:OP2	2.30	0.51
4:3:892:G:H2'	4:3:893:A:H8	1.74	0.51
4:3:1493:A:N7	4:3:1579:G:H2'	2.26	0.51
6:5:18:U:OP1	12:D:74:LYS:HE2	2.10	0.51
6:5:1000:A:O2'	6:5:1029:C:O2'	2.18	0.51
6:5:1174:U:O2'	17:I:62:HIS:CE1	2.63	0.51
7:6:46:G:HO2'	7:6:47:U:H5'	1.75	0.51
11:C:181:PHE:O	11:C:182:PRO:C	2.53	0.51
16:H:33:ASN:O	16:H:35:ARG:HG2	2.10	0.51
16:H:34:ARG:HG2	16:H:34:ARG:HH11	1.74	0.51
17:I:17:GLU:HB2	17:I:77:LYS:HG2	1.91	0.51
18:J:40:SER:HA	18:J:43:MET:CE	2.40	0.51
48:q:1:MET:HE3	48:q:2:HIS:HD2	1.75	0.51
2:1:31:PRO:HD3	57:z:20:LEU:HD21	1.92	0.51
4:3:827:G:N3	4:3:2079:G:O2'	2.40	0.51
4:3:1306:G:H2'	4:3:1307:G:H8	1.74	0.51
4:3:1683:G:O2'	44:m:109:ASP:OD2	2.28	0.51
4:3:2038:A:N3	4:3:2463:G:O2'	2.30	0.51
5:4:2:U:H2'	5:4:3:U:C6	2.46	0.51
6:5:1490:G:H2'	6:5:1491:A:C8	2.45	0.51
9:A:73:LYS:HB3	9:A:235:ALA:HB1	1.93	0.51
11:C:123:LEU:HD21	11:C:145:LYS:HE2	1.91	0.51
11:C:138:PRO:HG3	11:C:181:PHE:HA	1.92	0.51
12:D:207:ARG:HA	12:D:210:ILE:HD12	1.91	0.51
34:c:194:ALA:C	34:c:196:ALA:H	2.17	0.51
39:h:14:LEU:HD13	39:h:19:ALA:HB1	1.90	0.51
57:z:10:GLY:HA2	57:z:17:ILE:HA	1.93	0.51
4:3:881:A:H2	4:3:968:U:H3	1.58	0.51
4:3:1529:U:H2'	4:3:1530:G:C8	2.46	0.51
6:5:460:A:H2'	6:5:461:G:C8	2.45	0.51
14:F:87:PRO:HD2	14:F:151:ALA:HA	1.92	0.51
41:j:22:ILE:HD11	41:j:42:SER:HB3	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:299:A:H2'	4:3:300:G:C8	2.45	0.51
4:3:558:C:H1'	4:3:587:U:H1'	1.93	0.51
4:3:600:U:H5''	42:k:37:LYS:HE3	1.91	0.51
4:3:622:U:H2'	4:3:623:A:H8	1.74	0.51
4:3:749:U:H1'	4:3:752:C:H5	1.76	0.51
4:3:783:1MG:C8	49:r:89:ALA:HB1	2.46	0.51
4:3:1798:A:C2	4:3:1836:A:H4'	2.46	0.51
6:5:369:A:H61	6:5:387:G:H1'	1.74	0.51
6:5:1400:A:H2'	6:5:1401:A:C8	2.46	0.51
6:5:1468:A:H4'	30:Y:43:A:O2'	2.10	0.51
10:B:9:GLY:HA3	21:M:49:TYR:CD1	2.44	0.51
15:G:121:GLY:O	15:G:123:MET:HE2	2.10	0.51
18:J:103:ILE:HD11	28:T:4:ILE:HB	1.92	0.51
11:U:20:GLU:O	11:U:24:GLU:N	2.38	0.51
11:U:198:GLU:HA	11:U:201:LYS:HD3	1.93	0.51
37:f:88:PRO:HG2	37:f:89:TYR:CD1	2.46	0.51
43:l:76:LYS:HB3	43:l:91:GLU:HG3	1.92	0.51
4:3:141:A:C2	4:3:1437:A:H1'	2.46	0.51
4:3:1229:U:H4'	47:p:8:GLN:NE2	2.25	0.51
4:3:2631:G:OP1	4:3:2830:A:O2'	2.21	0.51
4:3:2698:U:O4'	44:m:14:ARG:NH1	2.34	0.51
6:5:808:C:O2'	6:5:895:A:N1	2.43	0.51
6:5:1330:A:H2'	6:5:1331:A:H8	1.74	0.51
9:A:201:LEU:HD13	9:A:215:ILE:HB	1.92	0.51
10:B:34:LEU:HD11	21:M:47:LEU:HD13	1.93	0.51
16:H:35:ARG:HE	16:H:40:TYR:HD2	1.59	0.51
16:H:61:LYS:O	16:H:61:LYS:HD3	2.11	0.51
23:O:23:ASP:HB3	23:O:26:VAL:HG23	1.91	0.51
29:X:44:ARG:HH21	29:X:47:LYS:HE2	1.75	0.51
37:f:41:LYS:HB3	37:f:46:ASP:HB3	1.91	0.51
38:g:25:VAL:HA	38:g:111:GLY:HA3	1.91	0.51
43:l:64:MET:HG2	43:l:106:VAL:HG12	1.93	0.51
46:o:56:ARG:HG2	46:o:57:GLY:N	2.25	0.51
48:q:19:THR:HB	48:q:91:LYS:HE3	1.93	0.51
4:3:299:A:H2'	4:3:300:G:H8	1.75	0.51
4:3:919:C:N4	4:3:930:C:H42	2.08	0.51
4:3:2185:C:O2'	4:3:2186:C:H5'	2.10	0.51
4:3:2238:G:H4'	53:v:30:ASN:HB2	1.91	0.51
4:3:2394:A:O2'	52:u:70:ASP:OD1	2.28	0.51
6:5:387:G:H2'	6:5:388:G:O4'	2.11	0.51
6:5:690:G:H5'	30:Y:36:U:H6	1.76	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:145:THR:O	9:A:149:ASN:ND2	2.36	0.51
10:B:88:ILE:HA	10:B:91:GLN:OE1	2.10	0.51
10:B:114:LEU:HD23	10:B:114:LEU:H	1.76	0.51
13:E:5:ILE:HG21	13:E:72:PHE:CZ	2.45	0.51
18:J:40:SER:HA	18:J:43:MET:HE2	1.91	0.51
11:U:68:ASP:OD1	11:U:69:LYS:N	2.44	0.51
34:c:127:LEU:HD11	34:c:201:LYS:HA	1.92	0.51
37:f:23:ASP:O	37:f:27:ILE:HG22	2.11	0.51
43:l:109:ILE:HD12	43:l:113:GLN:HG2	1.92	0.51
45:n:62:LEU:HD11	45:n:72:LEU:HD23	1.93	0.51
52:u:16:ALA:O	52:u:18:LYS:N	2.43	0.51
4:3:558:C:H5'	4:3:575:C:O2'	2.10	0.51
4:3:816:A:OP1	32:a:225:ARG:NH1	2.38	0.51
4:3:1485:A:H4'	4:3:1486:U:C4	2.46	0.51
4:3:2641:A:O2'	33:b:66:GLN:NE2	2.29	0.51
6:5:311:A:O2'	6:5:326:C:O2'	2.28	0.51
12:D:182:ASN:ND2	12:D:191:MET:SD	2.83	0.51
15:G:125:ASP:OD1	15:G:126:LYS:N	2.44	0.51
28:T:59:MET:SD	28:T:60:VAL:N	2.84	0.51
30:Y:53:A:H2'	30:Y:54:A:C8	2.45	0.51
32:a:150:ILE:HB	32:a:160:ILE:HB	1.93	0.51
36:e:12:ASP:OD1	36:e:12:ASP:N	2.43	0.51
37:f:64:LEU:O	37:f:68:LEU:HG	2.11	0.51
42:k:20:LEU:HB3	42:k:32:SER:HB3	1.91	0.51
43:l:103:MET:HG3	43:l:104:PHE:H	1.75	0.51
49:r:4:PHE:HE2	49:r:6:LYS:HE2	1.75	0.51
4:3:223:A:N3	4:3:238:U:O2'	2.35	0.51
4:3:549:A:N3	4:3:614:C:O2'	2.39	0.51
4:3:993:A:O4'	43:l:76:LYS:NZ	2.40	0.51
4:3:1178:A:N7	40:i:30:LYS:NZ	2.53	0.51
4:3:1296:G:N2	4:3:2020:A:OP2	2.34	0.51
4:3:1544:G:H2'	4:3:1545:A:H8	1.76	0.51
4:3:2024:C:O2	56:y:7:ARG:HD2	2.10	0.51
4:3:2585:A:H2'	4:3:2622:A:H62	1.76	0.51
6:5:1000:A:HO2'	6:5:1029:C:HO2'	1.47	0.51
10:B:64:THR:HA	10:B:101:ASN:OD1	2.11	0.51
15:G:41:LYS:NZ	15:G:45:LEU:HD11	2.25	0.51
11:U:163:VAL:CG2	11:U:164:SER:H	2.23	0.51
35:d:92:ARG:O	35:d:95:ARG:HG2	2.10	0.51
47:p:39:ILE:HG22	47:p:43:LYS:HE3	1.93	0.51
52:u:39:LYS:HG3	52:u:45:ILE:HD12	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:184:A:O2'	4:3:186:A:N7	2.38	0.51
4:3:853:G:N1	4:3:1219:U:OP2	2.34	0.51
4:3:1118:U:O2'	4:3:1120:A:N7	2.38	0.51
4:3:1137:C:H2'	4:3:1138:A:C8	2.44	0.51
4:3:2170:A:H5'	4:3:2174:G:N2	2.26	0.51
4:3:2254:G:H2'	4:3:2255:A:H8	1.76	0.51
6:5:530:A:N6	6:5:1181:G:O2'	2.44	0.51
10:B:46:VAL:HG23	10:B:47:ASN:N	2.24	0.51
13:E:89:ASN:OD1	13:E:91:GLU:HG3	2.10	0.51
15:G:120:ASP:N	15:G:120:ASP:OD1	2.44	0.51
17:I:58:ILE:HD11	17:I:65:LYS:HG3	1.92	0.51
32:a:119:ASP:HB3	32:a:131:LYS:HZ3	1.76	0.51
46:o:54:ARG:HB2	46:o:100:TYR:HD1	1.76	0.51
46:o:98:ARG:HH12	46:o:99:ALA:HB3	1.76	0.51
48:q:85:HIS:NE2	48:q:87:GLN:OE1	2.38	0.51
51:t:24:VAL:HG11	51:t:27:ILE:HD11	1.93	0.51
4:3:930:C:H2'	4:3:931:G:N7	2.26	0.51
4:3:1117:U:H2'	4:3:1118:U:O4'	2.11	0.51
4:3:2863:G:H2'	4:3:2864:A:C8	2.46	0.51
6:5:265:U:H2'	6:5:266:A:C8	2.45	0.51
6:5:1351:U:O4	14:F:9:ARG:NH2	2.44	0.51
15:G:129:ARG:HG2	15:G:129:ARG:HH11	1.75	0.51
16:H:6:TYR:HB2	16:H:21:LEU:HB2	1.92	0.51
19:K:66:ALA:N	19:K:78:THR:O	2.43	0.51
50:s:52:PRO:HB3	50:s:83:ILE:HG23	1.92	0.51
4:3:574:G:H1	4:3:587:U:H3	1.59	0.50
4:3:910:G:H2'	4:3:911:U:O4'	2.11	0.50
4:3:2109:A:H2	4:3:2194:G:H22	1.57	0.50
4:3:2197:U:H3'	4:3:2198:G:C8	2.46	0.50
6:5:18:U:H2'	6:5:19:C:C6	2.46	0.50
6:5:192:A:H2'	6:5:193:G:H8	1.76	0.50
6:5:483:U:H2'	6:5:484:A:H8	1.76	0.50
9:A:31:GLY:N	9:A:54:ASP:O	2.44	0.50
10:B:52:GLN:HB2	10:B:72:ALA:HB3	1.93	0.50
10:B:77:LEU:HD22	10:B:106:ILE:HD13	1.93	0.50
28:T:20:ARG:NH2	30:Y:30:G:O5'	2.44	0.50
53:v:15:GLY:HA3	53:v:29:TRP:HZ3	1.75	0.50
57:z:19:TYR:CD2	57:z:36:LYS:HD2	2.47	0.50
5:4:11:A:H2'	5:4:12:U:H5''	1.93	0.50
9:A:34:LYS:O	9:A:35:ARG:C	2.53	0.50
10:B:113:MET:HG2	10:B:144:VAL:HG22	1.92	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Q:103:LYS:HD2	28:T:2:PRO:CA	2.41	0.50
11:U:66:ILE:CD1	11:U:96:ARG:HH12	2.24	0.50
11:U:166:PHE:CD1	11:U:186:GLU:HG2	2.45	0.50
45:n:65:GLY:HA2	45:n:101:ARG:HH11	1.75	0.50
1:0:32:LYS:O	1:0:36:LYS:HG2	2.12	0.50
4:3:580:U:OP1	4:3:1249:A:O2'	2.25	0.50
4:3:909:U:H2'	4:3:910:G:O4'	2.11	0.50
4:3:2299:U:OP1	4:3:2388:C:O2'	2.29	0.50
6:5:250:G:H2'	6:5:251:G:C8	2.45	0.50
6:5:1212:C:H3'	6:5:1213:A:H5'	1.94	0.50
9:A:38:ASN:HB3	9:A:41:MET:HB2	1.92	0.50
10:B:7:SER:O	10:B:11:ARG:HD3	2.11	0.50
10:B:167:ARG:NH1	30:Y:49:U:O4	2.44	0.50
23:O:1:MET:HE3	23:O:3:LYS:HD2	1.93	0.50
23:O:66:THR:H	23:O:69:VAL:HB	1.75	0.50
34:c:46:ARG:HD2	34:c:99:TYR:CD2	2.47	0.50
40:i:3:LYS:HG3	40:i:4:THR:N	2.23	0.50
47:p:64:LEU:O	47:p:68:LEU:HD23	2.11	0.50
4:3:26:G:H1'	49:r:77:ASN:HB3	1.93	0.50
6:5:941:A:H2'	6:5:942:G:H8	1.76	0.50
6:5:1385:A:H2'	6:5:1386:C:C6	2.46	0.50
6:5:1463:A:H2'	6:5:1464:G:C8	2.46	0.50
9:A:181:PRO:HG2	9:A:206:THR:HG21	1.92	0.50
14:F:67:ASN:ND2	14:F:129:ASN:HB2	2.22	0.50
17:I:7:VAL:HG23	17:I:8:LYS:H	1.77	0.50
17:I:56:THR:HG22	17:I:68:ARG:HD3	1.94	0.50
20:L:69:LEU:O	20:L:73:ILE:HG13	2.11	0.50
28:T:13:LEU:HD11	28:T:17:LYS:HE2	1.93	0.50
37:f:9:VAL:HG13	37:f:11:ASN:O	2.11	0.50
40:i:95:MET:HE3	40:i:99:GLN:O	2.11	0.50
46:o:33:VAL:CG1	46:o:48:PHE:HB3	2.42	0.50
4:3:2145:A:H3'	4:3:2146:A:H8	1.77	0.50
4:3:2403:C:H2'	4:3:2404:G:C8	2.46	0.50
6:5:1384:A:H2'	6:5:1385:A:C8	2.46	0.50
10:B:35:ILE:HG13	21:M:25:GLN:HB3	1.93	0.50
11:C:42:PHE:HA	12:D:59:LYS:HZ1	1.76	0.50
21:M:24:CYS:HB2	21:M:40:CYS:HB3	1.94	0.50
23:O:5:ARG:HA	23:O:69:VAL:HG21	1.93	0.50
32:a:190:ARG:HG3	32:a:278:ILE:HD13	1.93	0.50
35:d:24:SER:HB3	35:d:27:GLN:HE21	1.76	0.50
35:d:100:LEU:O	35:d:104:ILE:HG22	2.11	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:e:35:GLU:N	36:e:35:GLU:OE2	2.45	0.50
37:f:27:ILE:HD11	53:v:64:LEU:O	2.12	0.50
44:m:36:LYS:O	44:m:36:LYS:HD3	2.12	0.50
55:x:19:CYS:SG	55:x:41:LYS:HB2	2.52	0.50
4:3:1446:G:N2	4:3:1613:A:OP2	2.37	0.50
4:3:2153:U:H4'	4:3:2154:A:C8	2.47	0.50
4:3:2299:U:H2'	4:3:2300:A:H8	1.77	0.50
6:5:231:U:H2'	6:5:232:G:H8	1.76	0.50
6:5:1022:G:O2'	6:5:1023:G:O5'	2.29	0.50
12:D:73:LEU:HG	12:D:90:VAL:HG12	1.93	0.50
13:E:142:ARG:O	13:E:144:SER:N	2.45	0.50
32:a:57:HIS:CG	32:a:227:THR:HG22	2.47	0.50
39:h:100:LYS:O	39:h:103:GLU:HG2	2.10	0.50
55:x:94:LEU:O	55:x:94:LEU:HD23	2.12	0.50
4:3:519:A:H5'	51:t:47:LYS:NZ	2.27	0.50
4:3:601:U:OP1	42:k:36:GLN:NE2	2.45	0.50
4:3:922:C:H3'	4:3:923:A:C8	2.47	0.50
4:3:2299:U:H2'	4:3:2300:A:C8	2.46	0.50
4:3:2736:U:O2'	4:3:2737:G:H8	1.94	0.50
6:5:35:C:H2'	6:5:36:G:H8	1.76	0.50
6:5:452:A:OP1	23:O:70:ARG:NH1	2.44	0.50
6:5:487:A:O2'	6:5:488:U:O3'	2.29	0.50
6:5:1158:A:O2'	6:5:1159:A:OP1	2.27	0.50
9:A:17:LEU:HB3	9:A:248:TYR:H	1.77	0.50
11:C:151:ILE:CG1	11:C:152:PRO:HD2	2.40	0.50
13:E:156:LEU:HD22	15:G:63:LYS:NZ	2.27	0.50
15:G:89:GLN:O	15:G:92:LYS:HE2	2.11	0.50
18:J:22:ASN:OD1	18:J:23:THR:N	2.37	0.50
21:M:7:LYS:HE2	21:M:28:GLY:HA3	1.93	0.50
22:N:73:GLU:HG3	22:N:76:ARG:HH21	1.76	0.50
25:Q:67:TYR:CB	25:Q:103:LYS:HD3	2.41	0.50
47:p:65:ASN:O	47:p:69:ARG:HG2	2.11	0.50
48:q:65:GLN:O	48:q:86:ARG:NH2	2.45	0.50
4:3:755:C:H2'	4:3:756:A:H8	1.76	0.50
4:3:1093:U:H3	4:3:1115:G:H1	1.59	0.50
4:3:1460:G:H2'	4:3:1461:A:C8	2.47	0.50
4:3:2334:U:H3	4:3:2397:G:H1	1.60	0.50
6:5:369:A:H4'	6:5:448:A:H62	1.76	0.50
6:5:426:U:P	11:C:12:ARG:HH12	2.35	0.50
6:5:516:C:H4'	6:5:517:C:H5''	1.93	0.50
14:F:107:ALA:HB1	14:F:119:ILE:HG22	1.92	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:62:ASN:CG	15:G:67:LYS:HE3	2.36	0.50
33:b:150:GLY:HA3	33:b:155:SER:HB3	1.94	0.50
41:j:56:GLN:NE2	41:j:58:LEU:HD11	2.27	0.50
42:k:134:GLN:HG3	42:k:137:LYS:HE3	1.92	0.50
45:n:28:VAL:HG13	45:n:89:VAL:HG23	1.94	0.50
47:p:45:ALA:O	47:p:49:ARG:HG3	2.12	0.50
4:3:174:A:H2'	4:3:175:A:H8	1.77	0.50
4:3:1602:G:OP2	32:a:67:ARG:NH2	2.39	0.50
4:3:2115:A:H3'	4:3:2116:U:C6	2.46	0.50
4:3:2534:G:H1	4:3:2545:U:H3	1.59	0.50
6:5:36:G:O2'	19:K:128:SER:O	2.30	0.50
11:C:97:LEU:HD12	11:C:136:LEU:HD21	1.94	0.50
14:F:70:PRO:C	14:F:71:ARG:HD2	2.37	0.50
19:K:86:ASN:HD21	19:K:118:VAL:H	1.60	0.50
20:L:43:LYS:HZ2	20:L:48:LEU:HD13	1.76	0.50
20:L:72:GLU:HA	20:L:75:LEU:HG	1.94	0.50
11:U:60:MET:HB2	11:U:191:ILE:HG12	1.94	0.50
30:Y:35:C:H1'	30:Y:36:U:C2	2.46	0.50
36:e:23:ASP:OD1	36:e:23:ASP:N	2.44	0.50
44:m:60:ARG:O	44:m:64:LYS:HG2	2.12	0.50
53:v:58:LEU:HG	53:v:64:LEU:HD22	1.94	0.50
4:3:1445:U:H2'	4:3:1446:G:O4'	2.12	0.49
5:4:55:A:O4'	35:d:27:GLN:NE2	2.44	0.49
6:5:561:A:H2	19:K:12:ARG:NH1	2.10	0.49
6:5:1215:U:C6	14:F:115:MET:HE3	2.47	0.49
8:7:50:G:H1	8:7:62:C:H42	1.58	0.49
11:C:137:ASN:OD1	11:C:138:PRO:HD2	2.12	0.49
12:D:66:PHE:CZ	12:D:96:ASN:HB3	2.46	0.49
13:E:132:VAL:HG12	13:E:132:VAL:O	2.11	0.49
20:L:29:ARG:O	20:L:33:ILE:HG13	2.11	0.49
24:P:53:VAL:O	24:P:55:ALA:N	2.45	0.49
4:3:928:G:H2'	4:3:929:G:C8	2.47	0.49
4:3:1814:G:N2	4:3:1817:A:OP2	2.42	0.49
6:5:409:G:H22	6:5:425:G:H1'	1.76	0.49
12:D:110:GLU:HG2	12:D:112:PRO:HD2	1.95	0.49
22:N:10:LYS:NZ	22:N:13:GLN:HE21	2.11	0.49
27:S:19:LEU:O	27:S:22:LYS:HG2	2.12	0.49
28:T:56:PHE:HA	28:T:59:MET:HG3	1.94	0.49
44:m:64:LYS:HE3	44:m:75:VAL:HG12	1.94	0.49
46:o:98:ARG:NH1	46:o:99:ALA:HB3	2.26	0.49
57:z:17:ILE:HD11	57:z:50:VAL:HG11	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:5:SER:HA	2:1:8:LYS:HE2	1.94	0.49
4:3:12:A:H2'	4:3:13:C:O4'	2.13	0.49
4:3:1807:C:H2'	32:a:159:GLN:NE2	2.27	0.49
4:3:2189:U:H2'	4:3:2190:G:N7	2.27	0.49
6:5:424:U:OP2	11:C:31:ARG:NH1	2.43	0.49
6:5:473:A:H2'	6:5:474:G:C8	2.47	0.49
6:5:821:U:H2'	6:5:822:A:H8	1.76	0.49
6:5:1113:U:O4	6:5:1114:A:N6	2.45	0.49
6:5:1212:C:H4'	6:5:1274:G:H22	1.77	0.49
9:A:84:PHE:HZ	9:A:229:MET:SD	2.35	0.49
10:B:153:LYS:HB2	10:B:176:MET:CE	2.36	0.49
13:E:124:ASN:HB3	13:E:127:ASN:OD1	2.13	0.49
4:3:357:A:O2'	34:c:174:ASN:O	2.15	0.49
4:3:917:G:H5''	4:3:928:G:OP1	2.13	0.49
4:3:1648:A:N1	49:r:93:SER:OG	2.46	0.49
6:5:335:C:H2'	6:5:336:U:C6	2.48	0.49
11:C:14:LEU:O	11:C:59:ARG:NH2	2.44	0.49
15:G:1:MET:SD	15:G:2:ILE:N	2.86	0.49
19:K:121:GLU:HG3	19:K:122:LYS:N	2.26	0.49
23:O:66:THR:HG22	23:O:67:ASP:OD1	2.12	0.49
24:P:22:ALA:HB2	24:P:49:ASN:ND2	2.25	0.49
29:X:40:ILE:CG1	29:X:43:PHE:HB2	2.42	0.49
35:d:67:ALA:HB3	35:d:84:LEU:HD22	1.92	0.49
41:j:14:THR:HG23	41:j:51:MET:SD	2.52	0.49
46:o:72:GLY:O	46:o:74:PRO:HD3	2.13	0.49
4:3:813:G:H5''	32:a:52:LYS:HE3	1.95	0.49
4:3:1031:U:H5	47:p:52:LYS:HD2	1.77	0.49
4:3:1350:A:O2'	49:r:84:ARG:NH2	2.46	0.49
4:3:1465:U:HO2'	4:3:1542:G:HO2'	1.59	0.49
4:3:1568:C:H3'	4:3:1569:A:C8	2.47	0.49
4:3:2268:C:H42	52:u:28:ARG:CZ	2.25	0.49
6:5:1052:G:H5'	17:I:59:ARG:HH21	1.77	0.49
12:D:176:SER:OG	12:D:177:ASP:N	2.37	0.49
20:L:39:ILE:HG23	20:L:43:LYS:CE	2.42	0.49
23:O:12:VAL:HG22	23:O:13:HIS:CD2	2.47	0.49
54:w:107:ASP:OD1	54:w:108:ALA:N	2.45	0.49
4:3:764:G:OP1	32:a:10:SER:OG	2.31	0.49
4:3:818:A:H2'	4:3:819:U:H4'	1.93	0.49
4:3:2148:U:H2'	4:3:2149:U:C6	2.48	0.49
6:5:388:G:OP1	23:O:12:VAL:HA	2.11	0.49
6:5:510:U:H2'	6:5:511:A:H8	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:34:LYS:O	9:A:37:TRP:CD1	2.56	0.49
13:E:129:ASP:O	13:E:132:VAL:HG23	2.12	0.49
14:F:49:ILE:HG21	14:F:60:VAL:HG11	1.94	0.49
35:d:46:ASP:O	35:d:49:PHE:HB2	2.12	0.49
43:l:103:MET:HG3	43:l:104:PHE:N	2.27	0.49
54:w:51:LEU:O	54:w:55:LEU:HD23	2.13	0.49
55:x:73:LEU:HA	55:x:76:LYS:NZ	2.28	0.49
4:3:914:G:C2	4:3:936:G:N1	2.81	0.49
4:3:935:U:C4	4:3:936:G:C6	3.00	0.49
6:5:388:G:H3'	6:5:389:A:H8	1.78	0.49
6:5:398:G:OP1	11:C:70:GLN:HG3	2.12	0.49
6:5:821:U:H2'	6:5:822:A:C8	2.48	0.49
11:C:59:ARG:HH11	11:C:190:GLY:HA2	1.78	0.49
12:D:68:GLU:HG2	12:D:94:VAL:HG22	1.95	0.49
12:D:68:GLU:HA	12:D:172:LEU:HD11	1.95	0.49
14:F:149:ALA:HA	18:J:54:TYR:CD2	2.47	0.49
32:a:189:THR:HB	32:a:279:ILE:HB	1.94	0.49
41:j:7:ARG:HB2	41:j:18:GLN:NE2	2.28	0.49
4:3:19:G:OP1	56:y:11:HIS:ND1	2.40	0.49
4:3:625:G:H1	4:3:700:U:H3	1.60	0.49
6:5:711:G:H2'	6:5:712:A:C8	2.48	0.49
11:C:100:ILE:O	11:C:104:MET:HG2	2.13	0.49
13:E:107:LEU:HD12	13:E:110:GLN:NE2	2.28	0.49
13:E:156:LEU:HD22	15:G:63:LYS:CE	2.43	0.49
11:U:48:SER:O	11:U:50:TYR:N	2.42	0.49
32:a:126:HIS:HB3	32:a:127:PRO:CD	2.39	0.49
41:j:21:ILE:HA	41:j:41:VAL:HG12	1.94	0.49
43:l:110:PRO:C	43:l:113:GLN:HE22	2.20	0.49
46:o:95:LYS:HD3	46:o:118:LYS:HA	1.95	0.49
47:p:44:TYR:HD1	47:p:47:ARG:HE	1.61	0.49
4:3:1031:U:H4'	47:p:57:ARG:NH1	2.27	0.49
4:3:1618:U:H4'	4:3:1619:A:OP2	2.12	0.49
4:3:1688:A:O2'	33:b:119:PHE:O	2.23	0.49
4:3:2028:G:OP1	56:y:9:SER:OG	2.22	0.49
4:3:2841:A:H2'	4:3:2842:G:H8	1.77	0.49
6:5:38:U:H5''	19:K:134:LYS:HE3	1.95	0.49
6:5:350:G:O2'	6:5:385:A:OP1	2.20	0.49
6:5:677:C:H2'	6:5:678:A:H8	1.77	0.49
6:5:853:A:H2'	6:5:854:A:C8	2.48	0.49
7:6:17:U:H5'	7:6:18:G:H5''	1.95	0.49
10:B:6:ASN:HD22	21:M:49:TYR:HB3	1.78	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:68:GLU:O	12:D:69:ARG:HB3	2.13	0.49
16:H:90:LEU:HD11	16:H:97:LYS:HD3	1.93	0.49
16:H:131:LYS:HE3	16:H:132:ARG:HH12	1.78	0.49
17:I:42:ILE:HG23	17:I:80:MET:CE	2.43	0.49
26:R:67:VAL:HB	55:x:58:ARG:NH2	2.27	0.49
32:a:233:MET:HG3	32:a:234:ASN:N	2.27	0.49
41:j:11:ALA:HB1	41:j:99:PHE:O	2.12	0.49
43:l:29:PHE:HB2	43:l:105:GLU:OE2	2.13	0.49
4:3:652:U:H2'	4:3:653:G:C8	2.48	0.49
4:3:1104:A:H5''	4:3:1105:A:C5	2.48	0.49
4:3:1437:A:H2'	4:3:1438:G:C8	2.47	0.49
4:3:2531:C:O2'	4:3:2772:A:O2'	2.24	0.49
6:5:561:A:O2'	6:5:564:G:O3'	2.30	0.49
6:5:1292:A:H4'	26:R:10:PHE:CD2	2.48	0.49
19:K:79:TYR:O	19:K:81:PRO:HD3	2.13	0.49
20:L:66:GLU:O	20:L:70:ARG:NH1	2.46	0.49
27:S:5:LYS:O	27:S:8:GLU:HG3	2.12	0.49
33:b:188:ASN:ND2	46:o:12:LEU:HD13	2.19	0.49
35:d:70:ALA:HB2	35:d:85:ILE:HD11	1.93	0.49
39:h:55:ILE:HD13	39:h:65:PHE:HE1	1.77	0.49
40:i:33:VAL:HA	40:i:111:MET:SD	2.53	0.49
4:3:984:C:H2'	4:3:985:A:H8	1.78	0.48
4:3:1509:U:H3	4:3:1530:G:H1	1.61	0.48
4:3:2171:A:C2'	4:3:2172:A:H5'	2.44	0.48
6:5:388:G:O5'	23:O:12:VAL:HG23	2.13	0.48
6:5:478:G:H4'	6:5:479:A:OP1	2.12	0.48
6:5:1320:A:N6	6:5:1349:A:H5''	2.26	0.48
6:5:1472:G:H1'	6:5:1493:MA6:H2	1.94	0.48
15:G:65:LYS:HD2	15:G:65:LYS:N	2.28	0.48
21:M:26:ARG:HD2	21:M:27:CYS:N	2.28	0.48
27:S:33:LYS:HA	27:S:36:HIS:NE2	2.28	0.48
11:U:38:HIS:O	11:U:39:GLY:C	2.55	0.48
30:Y:47:U:H3'	30:Y:48:C:H6	1.77	0.48
51:t:8:ASP:OD1	51:t:8:ASP:N	2.46	0.48
55:x:15:LYS:HE2	55:x:33:GLU:CG	2.43	0.48
55:x:16:CYS:SG	55:x:17:ALA:N	2.86	0.48
56:y:16:ARG:HG2	56:y:17:ARG:HH21	1.76	0.48
56:y:32:LYS:HE2	56:y:47:MET:HB3	1.94	0.48
1:0:6:GLN:O	4:3:721:G:H8	1.96	0.48
4:3:87:G:O2'	4:3:104:A:N1	2.37	0.48
4:3:1437:A:H2'	4:3:1438:G:H8	1.78	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:2158:C:H2'	4:3:2159:U:C6	2.47	0.48
4:3:2603:G:N2	4:3:2606:A:OP2	2.36	0.48
4:3:2644:U:HO2'	33:b:47:TYR:HH	1.61	0.48
6:5:374:G:H2'	6:5:375:C:C6	2.49	0.48
6:5:1038:G:H4'	21:M:4:LYS:CE	2.35	0.48
10:B:172:ILE:HG13	10:B:176:MET:HE2	1.94	0.48
19:K:24:LEU:HD21	19:K:41:PRO:O	2.12	0.48
41:j:66:LYS:O	41:j:78:LYS:NZ	2.36	0.48
46:o:48:PHE:CE2	46:o:77:LYS:HG2	2.48	0.48
49:r:1:MET:O	49:r:1:MET:SD	2.71	0.48
49:r:14:PRO:HG3	49:r:101:SER:HB3	1.93	0.48
50:s:86:PRO:HB2	54:w:86:ALA:HB1	1.93	0.48
51:t:3:ARG:NH2	51:t:74:LEU:HB2	2.22	0.48
53:v:8:THR:HG22	53:v:9:LEU:N	2.26	0.48
4:3:920:G:C2	4:3:931:G:C6	3.01	0.48
4:3:1000:U:O2'	4:3:2281:A:N3	2.37	0.48
4:3:2797:C:H5'	4:3:2798:A:O5'	2.14	0.48
6:5:87:G:H2'	6:5:88:A:H8	1.77	0.48
6:5:352:A:H4'	6:5:363:U:O2'	2.14	0.48
6:5:978:A:N1	6:5:1197:G:N2	2.60	0.48
7:6:1:G:O2'	7:6:2:G:OP1	2.29	0.48
9:A:33:VAL:HG21	9:A:281:ARG:H	1.78	0.48
11:C:46:THR:O	11:C:46:THR:HG22	2.14	0.48
11:C:93:LEU:HA	11:C:96:ARG:NH1	2.29	0.48
17:I:85:VAL:HG23	17:I:86:ASN:H	1.78	0.48
23:O:69:VAL:HG12	23:O:73:PHE:CE2	2.49	0.48
34:c:60:GLY:HA3	34:c:80:ARG:HG3	1.96	0.48
35:d:110:ARG:HD3	35:d:137:ILE:O	2.13	0.48
50:s:59:ILE:O	50:s:61:LYS:NZ	2.39	0.48
4:3:606:G:N2	4:3:2038:A:OP1	2.45	0.48
4:3:668:A:H2'	4:3:669:A:C8	2.49	0.48
4:3:1093:U:H3	4:3:1115:G:H22	1.61	0.48
4:3:2107:A:N6	4:3:2195:U:C2	2.82	0.48
4:3:2376:C:H2'	4:3:2377:A:H8	1.77	0.48
12:D:214:LYS:NZ	15:G:51:GLU:C	2.70	0.48
25:Q:103:LYS:O	25:Q:104:ASP:HB2	2.14	0.48
32:a:147:VAL:HA	32:a:200:VAL:HA	1.96	0.48
34:c:127:LEU:HD12	34:c:199:VAL:O	2.13	0.48
35:d:132:ILE:O	35:d:151:GLY:HA3	2.13	0.48
42:k:48:ARG:HG2	42:k:49:PRO:HD2	1.95	0.48
45:n:38:HIS:HB3	45:n:57:SER:HB2	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:517:G:O5'	51:t:44:ARG:NH1	2.46	0.48
4:3:918:G:C2	4:3:932:U:C2	3.02	0.48
4:3:927:A:H2'	4:3:928:G:O4'	2.13	0.48
4:3:1002:A:H4'	4:3:2279:G:H22	1.78	0.48
6:5:20:C:OP2	12:D:185:ARG:NH1	2.47	0.48
9:A:152:LEU:HA	9:A:155:GLU:HG3	1.96	0.48
10:B:215:LEU:O	10:B:217:ARG:HG2	2.14	0.48
11:C:3:TYR:CE1	11:C:65:GLY:HA2	2.49	0.48
17:I:7:VAL:HG23	17:I:8:LYS:N	2.28	0.48
11:U:59:ARG:O	11:U:63:MET:HG2	2.13	0.48
43:l:68:ILE:HG22	43:l:95:ALA:HB1	1.95	0.48
57:z:11:CYS:SG	57:z:12:ASN:N	2.86	0.48
4:3:60:G:OP2	50:s:76:LYS:NZ	2.37	0.48
4:3:125:G:OP1	4:3:1404:C:O2'	2.30	0.48
4:3:388:U:H2'	4:3:389:C:C6	2.49	0.48
4:3:394:C:H2'	4:3:395:U:O4'	2.14	0.48
4:3:652:U:H2'	4:3:653:G:H8	1.78	0.48
4:3:1554:A:OP2	4:3:1576:G:N2	2.47	0.48
4:3:2078:A:H2'	4:3:2079:G:H8	1.78	0.48
4:3:2106:G:H22	4:3:2198:G:H1	1.62	0.48
4:3:2197:U:H3'	4:3:2198:G:H8	1.78	0.48
5:4:76:A:H62	5:4:88:G:H21	1.61	0.48
6:5:47:G:H2'	6:5:362:U:C5	2.49	0.48
6:5:57:U:H2'	6:5:58:G:H8	1.77	0.48
6:5:492:G:O2'	6:5:494:A:H1'	2.14	0.48
10:B:17:ASN:HB2	10:B:216:ASN:HB2	1.95	0.48
10:B:92:ILE:O	10:B:95:ILE:HG22	2.13	0.48
11:U:128:THR:HG22	11:U:129:VAL:N	2.27	0.48
33:b:230:PRO:HD3	46:o:21:TYR:CB	2.42	0.48
35:d:122:PHE:HE2	35:d:167:LEU:HB2	1.78	0.48
37:f:2:LYS:HD3	37:f:18:VAL:HG11	1.95	0.48
37:f:94:THR:O	37:f:98:ILE:HB	2.13	0.48
51:t:97:THR:O	51:t:98:ASN:OD1	2.32	0.48
56:y:55:LYS:HD2	56:y:56:ALA:O	2.13	0.48
4:3:118:G:OP2	4:3:120:A:O2'	2.26	0.48
4:3:474:U:H2'	4:3:475:A:C8	2.48	0.48
4:3:700:U:H2'	4:3:701:A:H8	1.78	0.48
4:3:2026:A:N7	56:y:6:ARG:NH2	2.62	0.48
6:5:35:C:H2'	6:5:36:G:C8	2.49	0.48
6:5:192:A:H2'	6:5:193:G:C8	2.49	0.48
6:5:259:A:H2'	6:5:260:C:C6	2.49	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:60:ARG:HG2	10:B:65:VAL:HG22	1.94	0.48
10:B:133:LEU:HG	10:B:169:LYS:NZ	2.28	0.48
11:C:18:LEU:CA	11:C:63:MET:HE1	2.43	0.48
12:D:132:HIS:CE1	12:D:137:TYR:HB2	2.48	0.48
13:E:21:VAL:HG13	13:E:60:TRP:HZ2	1.79	0.48
17:I:15:LYS:HZ1	17:I:77:LYS:HD2	1.78	0.48
20:L:68:ASP:OD1	20:L:69:LEU:HD22	2.13	0.48
23:O:23:ASP:OD1	23:O:24:SER:N	2.46	0.48
42:k:52:GLU:HB3	42:k:55:GLN:HG2	1.95	0.48
4:3:158:U:H2'	4:3:159:G:C8	2.49	0.48
4:3:159:G:H2'	4:3:160:A:H8	1.79	0.48
4:3:679:A:N1	4:3:2377:A:O2'	2.45	0.48
4:3:912:A:H61	4:3:939:U:H3	1.60	0.48
4:3:2107:A:N3	4:3:2107:A:H2'	2.29	0.48
6:5:1074:U:O2'	6:5:1093:A:OP2	2.29	0.48
6:5:1216:G:H2'	6:5:1217:G:H8	1.79	0.48
6:5:1316:C:H2'	6:5:1317:A:C8	2.48	0.48
9:A:137:GLN:OE1	9:A:156:ILE:HG13	2.13	0.48
11:C:123:LEU:HB3	11:C:143:ARG:NH1	2.29	0.48
11:C:188:PRO:O	11:C:192:ASN:ND2	2.46	0.48
14:F:145:GLU:O	14:F:148:LYS:HG2	2.14	0.48
26:R:11:VAL:HG21	26:R:16:LEU:HD21	1.96	0.48
32:a:138:LEU:HB3	32:a:180:VAL:HG11	1.96	0.48
37:f:56:GLU:O	37:f:60:ILE:HG12	2.13	0.48
39:h:73:SER:HB2	39:h:131:MET:HE3	1.96	0.48
39:h:118:GLU:O	39:h:122:LYS:HG2	2.14	0.48
43:l:74:LYS:HD3	43:l:94:VAL:HG22	1.94	0.48
4:3:1114:C:H3'	4:3:1115:G:H8	1.79	0.48
4:3:1121:A:H5''	4:3:1122:G:H5'	1.94	0.48
4:3:2336:A:H2'	4:3:2337:U:C6	2.49	0.48
6:5:424:U:P	11:C:31:ARG:HH22	2.36	0.48
11:C:113:ALA:O	11:C:116:LEU:HG	2.14	0.48
40:i:40:ARG:HG2	40:i:40:ARG:HH11	1.79	0.48
4:3:629:G:H1	4:3:696:U:H3	1.61	0.48
4:3:934:C:H2'	4:3:935:U:O4'	2.14	0.48
4:3:1098:G:O2'	39:h:84:LYS:NZ	2.46	0.48
6:5:181:G:O2'	24:P:3:ARG:NH1	2.46	0.48
6:5:787:A:OP1	8:7:38:C:O2'	2.32	0.48
9:A:30:VAL:HG13	9:A:53:ASN:HB3	1.96	0.48
12:D:135:SER:HB3	12:D:177:ASP:OD1	2.14	0.48
32:a:268:ARG:O	32:a:270:MET:HE2	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:9:VAL:HG13	33:b:30:TYR:HB3	1.96	0.48
37:f:6:LYS:HA	37:f:58:TYR:HE2	1.78	0.48
46:o:67:ARG:NH2	46:o:105:ARG:HA	2.28	0.48
47:p:80:ASN:O	47:p:84:LYS:HG3	2.14	0.48
1:0:29:LYS:O	1:0:32:LYS:HG2	2.14	0.47
4:3:159:G:H2'	4:3:160:A:C8	2.49	0.47
4:3:516:A:OP2	51:t:44:ARG:HD2	2.14	0.47
4:3:1566:A:H2'	4:3:1567:U:O4'	2.14	0.47
4:3:1583:G:H2'	4:3:1584:U:C6	2.49	0.47
4:3:2171:A:H3'	4:3:2172:A:H8	1.79	0.47
4:3:2200:U:N3	4:3:2201:G:N7	2.61	0.47
4:3:2695:U:H2'	4:3:2696:G:O4'	2.14	0.47
4:3:2813:A:H2'	4:3:2814:A:H8	1.79	0.47
6:5:594:A:C2'	24:P:29:ARG:HH21	2.26	0.47
6:5:1138:U:H2'	6:5:1139:A:H8	1.79	0.47
9:A:70:ASN:O	9:A:73:LYS:HG2	2.14	0.47
10:B:11:ARG:NH2	10:B:178:LEU:O	2.47	0.47
10:B:21:ARG:HA	21:M:54:PRO:HB3	1.95	0.47
10:B:56:VAL:HG23	10:B:69:VAL:HG22	1.96	0.47
11:C:30:LYS:O	11:C:30:LYS:HG3	2.14	0.47
11:C:166:PHE:CE2	11:C:183:GLU:HB2	2.49	0.47
12:D:211:LEU:O	12:D:213:ASN:N	2.46	0.47
13:E:165:ASN:HA	15:G:56:ASN:HB3	1.96	0.47
26:R:67:VAL:HB	55:x:58:ARG:HH22	1.79	0.47
4:3:155:A:H2'	4:3:156:A:H8	1.79	0.47
4:3:631:A:H2'	4:3:632:A:C8	2.49	0.47
4:3:680:A:H2'	4:3:682:A:N7	2.28	0.47
4:3:2070:C:H1'	31:Z:36:ASP:HA	1.97	0.47
4:3:2163:U:H2'	4:3:2164:G:C4	2.49	0.47
6:5:18:U:H2'	6:5:19:C:H6	1.79	0.47
6:5:147:A:H2'	6:5:148:A:C8	2.49	0.47
6:5:483:U:H2'	6:5:484:A:C8	2.49	0.47
6:5:1022:G:H2'	6:5:1023:G:C8	2.50	0.47
13:E:163:MET:HE3	15:G:49:VAL:CG1	2.43	0.47
17:I:59:ARG:H	17:I:59:ARG:HD3	1.79	0.47
25:Q:36:ARG:C	25:Q:38:LYS:H	2.23	0.47
28:T:36:LEU:HD12	28:T:41:ARG:HE	1.78	0.47
30:Y:30:G:C2	30:Y:31:A:H1'	2.49	0.47
32:a:256:THR:HG23	32:a:262:HIS:ND1	2.28	0.47
41:j:88:LYS:NZ	41:j:94:ARG:HH22	2.13	0.47
43:l:20:LYS:CD	43:l:21:ALA:H	2.17	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:383:U:H2'	4:3:384:G:H8	1.79	0.47
4:3:427:A:H1'	4:3:447:G:O4'	2.14	0.47
4:3:916:U:H2'	4:3:917:G:C8	2.49	0.47
4:3:917:G:C6	4:3:918:G:C4	3.03	0.47
4:3:937:A:H2'	4:3:938:A:H8	1.78	0.47
4:3:2119:A:H2'	4:3:2120:G:H8	1.79	0.47
8:7:19:A:H61	8:7:55:C:H42	1.60	0.47
9:A:292:THR:O	9:A:293:ARG:HB3	2.15	0.47
10:B:127:ILE:HD11	10:B:133:LEU:HD13	1.96	0.47
12:D:208:VAL:HG23	12:D:209:ALA:H	1.79	0.47
13:E:71:ASP:N	13:E:71:ASP:OD1	2.47	0.47
17:I:8:LYS:O	17:I:9:TYR:HD1	1.97	0.47
19:K:78:THR:HG23	19:K:108:TYR:O	2.14	0.47
20:L:66:GLU:OE1	20:L:70:ARG:NH1	2.38	0.47
23:O:7:MET:HG3	23:O:29:ASP:H	1.80	0.47
11:U:103:ARG:CZ	11:U:164:SER:HB3	2.44	0.47
33:b:91:GLU:OE2	33:b:94:GLN:HB2	2.14	0.47
4:3:593:C:O2'	47:p:47:ARG:NH1	2.47	0.47
4:3:740:A:H4'	32:a:9:ARG:CZ	2.45	0.47
4:3:2115:A:C2	4:3:2190:G:C6	3.02	0.47
4:3:2134:G:H21	4:3:2181:A:H1'	1.80	0.47
4:3:2838:G:H2'	4:3:2883:A:H61	1.78	0.47
5:4:49:G:OP2	45:n:66:ASN:ND2	2.48	0.47
6:5:295:G:H2'	6:5:296:A:C8	2.49	0.47
8:7:73:C:H5	52:u:17:SER:HB3	1.78	0.47
9:A:46:GLU:OE2	9:A:55:HIS:HB2	2.14	0.47
9:A:223:GLN:HG2	9:A:224:SER:H	1.78	0.47
11:C:70:GLN:O	11:C:74:LEU:HG	2.14	0.47
12:D:115:ILE:O	12:D:119:ILE:HG13	2.15	0.47
13:E:42:LEU:HD21	13:E:56:HIS:CE1	2.50	0.47
13:E:77:ASN:OD1	13:E:78:ILE:HG13	2.15	0.47
13:E:140:GLN:HB2	13:E:141:PRO:HD2	1.96	0.47
22:N:67:LEU:HD23	22:N:67:LEU:O	2.15	0.47
23:O:54:VAL:HB	23:O:58:TRP:CZ3	2.49	0.47
4:3:354:C:O2'	4:3:356:A:H8	1.97	0.47
4:3:783:1MG:HM13	49:r:90:LYS:HE2	1.96	0.47
4:3:2121:A:H2'	4:3:2122:G:O4'	2.14	0.47
4:3:2585:A:H2'	4:3:2622:A:N6	2.29	0.47
6:5:778:A:OP2	6:5:797:G:N1	2.38	0.47
6:5:1049:G:H5''	10:B:202:LYS:HE3	1.95	0.47
6:5:1281:U:H5''	20:L:100:GLN:HE22	1.80	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:M:43:CYS:O	21:M:46:GLU:HG3	2.14	0.47
25:Q:35:LYS:HB3	25:Q:36:ARG:H	1.48	0.47
35:d:85:ILE:HG13	35:d:85:ILE:O	2.14	0.47
35:d:177:LEU:HB2	35:d:180:GLY:C	2.39	0.47
41:j:65:THR:HA	41:j:82:ASN:OD1	2.15	0.47
49:r:29:THR:OG1	49:r:69:LEU:HB2	2.15	0.47
53:v:38:VAL:HG12	53:v:58:LEU:HD11	1.96	0.47
54:w:39:ASP:OD1	54:w:40:LYS:N	2.47	0.47
4:3:145:A:O2'	50:s:42:LEU:HD11	2.15	0.47
4:3:569:U:H2'	4:3:570:C:C6	2.50	0.47
4:3:911:U:H2'	4:3:912:A:H5'	1.96	0.47
4:3:2131:G:H3'	4:3:2132:G:H8	1.79	0.47
6:5:115:A:O2'	6:5:184:U:O4	2.33	0.47
6:5:596:U:H4'	15:G:98:TYR:CG	2.50	0.47
6:5:1019:G:OP2	6:5:1019:G:H8	1.98	0.47
6:5:1180:U:H4'	10:B:193:GLN:HE22	1.80	0.47
6:5:1368:U:O2'	6:5:1476:C:O2'	2.31	0.47
10:B:134:ARG:HH11	12:D:110:GLU:CD	2.22	0.47
11:C:52:GLN:O	11:C:56:GLU:HG2	2.14	0.47
12:D:154:ALA:HB3	12:D:177:ASP:HB2	1.97	0.47
14:F:47:ASP:HA	14:F:50:GLU:OE1	2.14	0.47
16:H:56:LEU:HD21	16:H:103:LYS:HE3	1.96	0.47
18:J:9:VAL:O	18:J:72:MET:HB3	2.15	0.47
24:P:43:LYS:HG2	24:P:45:TYR:CE1	2.49	0.47
32:a:73:ARG:HD3	32:a:109:ILE:HG21	1.96	0.47
35:d:58:HIS:HE2	55:x:7:PHE:HB2	1.79	0.47
39:h:112:LEU:HG	39:h:114:ALA:H	1.79	0.47
41:j:1:MET:HE1	41:j:67:LYS:HG2	1.97	0.47
46:o:49:THR:O	46:o:68:LYS:HE3	2.15	0.47
4:3:332:G:O2'	4:3:356:A:N1	2.40	0.47
4:3:742:G:H1	4:3:759:U:H3	1.62	0.47
4:3:799:A:H5''	32:a:217:GLY:CA	2.45	0.47
4:3:1023:C:O2'	4:3:1036:A:N3	2.41	0.47
4:3:1103:G:O2'	4:3:1104:A:H5'	2.15	0.47
4:3:1229:U:H2'	4:3:1230:U:C6	2.49	0.47
4:3:1306:G:H4'	44:m:31:ILE:HD12	1.96	0.47
4:3:1703:A:H8	41:j:5:MET:SD	2.38	0.47
4:3:1722:U:O2'	4:3:1734:A:N7	2.31	0.47
4:3:1954:C:H2'	4:3:1955:G:H8	1.79	0.47
4:3:2164:G:H4'	4:3:2165:A:C5'	2.43	0.47
6:5:68:C:O2'	6:5:157:A:H1'	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:427:A:OP1	11:C:8:PHE:HB2	2.15	0.47
6:5:470:U:O4	6:5:471:A:N6	2.48	0.47
6:5:737:U:OP1	22:N:35:GLN:NE2	2.48	0.47
6:5:777:A:N6	6:5:798:U:OP2	2.45	0.47
6:5:988:G:O2'	6:5:989:A:N7	2.47	0.47
6:5:1434:C:H2'	6:5:1435:G:C8	2.49	0.47
8:7:10:G:O2'	8:7:11:U:OP1	2.26	0.47
11:C:141:LYS:HA	11:C:177:THR:HB	1.96	0.47
17:I:94:LYS:HA	55:x:94:LEU:CD2	2.44	0.47
19:K:73:GLY:O	19:K:74:PHE:CD1	2.68	0.47
20:L:75:LEU:HD13	20:L:79:HIS:CE1	2.49	0.47
21:M:39:VAL:HG13	21:M:43:CYS:HB2	1.96	0.47
22:N:84:LEU:HD12	22:N:85:ARG:HG2	1.97	0.47
27:S:20:ASN:O	27:S:24:GLN:NE2	2.48	0.47
28:T:36:LEU:H	28:T:41:ARG:HH21	1.61	0.47
11:U:16:PHE:HE2	53:v:61:HIS:HD2	1.61	0.47
32:a:143:GLU:HG2	32:a:170:ILE:O	2.15	0.47
32:a:225:ARG:HG3	32:a:226:PRO:HD2	1.96	0.47
35:d:25:ILE:O	35:d:28:VAL:HG22	2.15	0.47
37:f:45:GLN:O	37:f:49:LEU:HD23	2.15	0.47
40:i:80:HIS:ND1	40:i:81:SER:O	2.48	0.47
2:1:4:LYS:HE2	2:1:58:LEU:HD11	1.97	0.47
4:3:279:U:H2'	4:3:280:A:C8	2.50	0.47
7:6:15:A:H4'	7:6:16:C:OP2	2.15	0.47
11:C:96:ARG:O	11:C:100:ILE:HG12	2.15	0.47
18:J:119:ARG:HB2	28:T:34:TYR:CD2	2.48	0.47
19:K:55:PRO:HG2	19:K:60:SER:HA	1.97	0.47
23:O:17:TYR:O	23:O:39:LEU:N	2.47	0.47
46:o:24:GLU:HA	46:o:55:ARG:HH12	1.79	0.47
49:r:35:ILE:O	49:r:39:THR:HG23	2.14	0.47
4:3:831:U:H2'	4:3:832:C:C6	2.49	0.47
4:3:2311:G:H21	35:d:129:THR:HG21	1.80	0.47
6:5:469:C:C5'	23:O:79:TRP:HE1	2.26	0.47
6:5:515:G:H1	6:5:531:A:P	2.37	0.47
7:6:56:U:H2'	7:6:57:G:C8	2.50	0.47
13:E:49:ILE:HG13	13:E:50:LYS:HG2	1.96	0.47
13:E:86:LEU:HD12	13:E:86:LEU:HA	1.68	0.47
33:b:63:ASN:OD1	33:b:64:LYS:N	2.44	0.47
33:b:107:TYR:OH	33:b:218:LYS:HE2	2.15	0.47
34:c:200:GLU:HB3	34:c:203:VAL:HG23	1.97	0.47
41:j:88:LYS:HG3	41:j:90:ASP:OD1	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:r:64:MET:SD	49:r:66:GLY:N	2.88	0.47
3:2:9:PRO:HD3	3:2:16:ILE:HD11	1.97	0.47
4:3:20:C:OP1	47:p:28:HIS:HE1	1.98	0.47
4:3:823:A:OP1	4:3:826:C:N4	2.40	0.47
4:3:1715:A:O2'	4:3:1769:A:H2'	2.14	0.47
4:3:2137:A:H4'	4:3:2140:G:O2'	2.15	0.47
6:5:354:U:H2'	6:5:355:A:C8	2.50	0.47
6:5:704:U:H2'	6:5:705:A:H8	1.79	0.47
6:5:1354:G:N7	14:F:2:ARG:NH2	2.52	0.47
8:7:10:G:H2'	8:7:11:U:C6	2.50	0.47
9:A:40:LYS:O	9:A:43:PHE:CD2	2.68	0.47
10:B:87:LYS:HZ2	10:B:91:GLN:HE22	1.62	0.47
10:B:111:SER:HB2	10:B:114:LEU:HD21	1.96	0.47
11:C:123:LEU:HD13	11:C:143:ARG:HH12	1.79	0.47
11:C:144:LEU:HD23	11:C:144:LEU:H	1.80	0.47
13:E:80:LYS:O	13:E:81:GLN:C	2.58	0.47
14:F:85:GLN:HB2	14:F:147:ASN:ND2	2.28	0.47
20:L:120:LYS:HG2	26:R:87:ARG:NE	2.30	0.47
23:O:40:ASN:HB3	23:O:43:LEU:HB2	1.97	0.47
11:U:21:ASN:O	11:U:24:GLU:OE1	2.33	0.47
32:a:261:ARG:O	32:a:262:HIS:CG	2.68	0.47
40:i:20:ILE:N	40:i:141:THR:O	2.48	0.47
41:j:88:LYS:HZ3	41:j:94:ARG:HH22	1.63	0.47
46:o:54:ARG:HB2	46:o:100:TYR:CD1	2.50	0.47
54:w:89:GLN:O	54:w:92:GLU:HG3	2.15	0.47
56:y:33:CYS:SG	56:y:35:LYS:HG2	2.56	0.47
4:3:2068:G:N3	4:3:2069:A:N6	2.63	0.46
4:3:2699:C:H4'	4:3:2875:U:O2'	2.15	0.46
6:5:369:A:H2'	6:5:370:A:H8	1.80	0.46
6:5:1071:A:H5''	12:D:76:ILE:HD12	1.97	0.46
7:6:33:U:N3	7:6:36:C:OP2	2.34	0.46
9:A:36:TYR:CE2	9:A:281:ARG:HD3	2.50	0.46
9:A:285:THR:HA	28:T:57:ARG:HH22	1.81	0.46
13:E:40:LEU:HB2	13:E:57:TYR:HB2	1.96	0.46
22:N:15:HIS:O	22:N:18:ASP:HB3	2.15	0.46
23:O:11:ARG:HD3	23:O:12:VAL:H	1.80	0.46
23:O:50:ILE:HG13	23:O:51:ASP:N	2.29	0.46
11:U:17:SER:C	11:U:18:LEU:HD22	2.40	0.46
33:b:230:PRO:HD3	46:o:21:TYR:HB3	1.96	0.46
39:h:72:VAL:O	39:h:73:SER:OG	2.28	0.46
41:j:112:ASN:HA	41:j:115:LEU:HD12	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:r:41:LYS:HE3	56:y:22:LEU:HD11	1.97	0.46
51:t:33:GLN:HB3	51:t:68:PRO:HB2	1.97	0.46
4:3:901:C:H4'	4:3:902:U:O5'	2.15	0.46
4:3:954:A:H5''	4:3:2276:A:H61	1.79	0.46
4:3:2114:C:N4	4:3:2189:U:O4	2.49	0.46
4:3:2254:G:H2'	4:3:2255:A:C8	2.50	0.46
4:3:2324:A:H2'	4:3:2325:U:C6	2.50	0.46
6:5:108:C:OP1	6:5:307:C:O2'	2.32	0.46
6:5:537:A:H2'	6:5:538:G:C8	2.50	0.46
12:D:116:LYS:HA	12:D:119:ILE:HD12	1.97	0.46
16:H:125:ARG:HG2	16:H:126:ALA:N	2.29	0.46
17:I:70:GLN:CB	21:M:61:TRP:HH2	2.28	0.46
26:R:14:HIS:HA	26:R:17:LYS:HZ3	1.79	0.46
11:U:102:TYR:HB3	11:U:110:ARG:HE	1.80	0.46
32:a:252:ASP:N	32:a:252:ASP:OD1	2.47	0.46
36:e:33:GLN:NE2	36:e:34:ILE:O	2.48	0.46
36:e:92:LEU:HA	36:e:165:VAL:HA	1.96	0.46
38:g:123:LEU:O	38:g:126:ILE:HG22	2.16	0.46
4:3:999:U:H1'	4:3:2258:G:O6	2.15	0.46
4:3:1575:C:H2'	4:3:1576:G:O4'	2.15	0.46
4:3:2032:G:H2'	4:3:2033:G:C8	2.49	0.46
4:3:2122:G:H21	4:3:2179:A:H61	1.64	0.46
4:3:2131:G:H1	4:3:2182:C:N4	2.06	0.46
6:5:616:C:H5'	11:C:127:ARG:HH22	1.80	0.46
6:5:1213:A:H5'	6:5:1310:C:H41	1.79	0.46
6:5:1509:A:C2	9:A:293:ARG:HB3	2.50	0.46
17:I:71:PHE:CE1	17:I:72:GLU:O	2.68	0.46
33:b:56:THR:HG22	33:b:78:THR:HG22	1.96	0.46
35:d:38:MET:HB2	35:d:152:PHE:CD1	2.51	0.46
53:v:36:CYS:SG	53:v:48:ILE:HG23	2.55	0.46
4:3:612:G:O2'	4:3:2026:A:OP1	2.32	0.46
4:3:1282:G:C4	47:p:32:LYS:HD2	2.51	0.46
4:3:2005:G:OP2	33:b:142:ARG:NH2	2.49	0.46
4:3:2131:G:N2	4:3:2182:C:N3	2.58	0.46
6:5:707:G:H2'	6:5:708:A:H8	1.81	0.46
9:A:126:SER:O	9:A:129:LYS:HG2	2.15	0.46
11:C:106:PHE:HA	11:C:157:ALA:O	2.14	0.46
12:D:133:LYS:NZ	12:D:154:ALA:O	2.47	0.46
16:H:6:TYR:CE1	16:H:92:PHE:HB3	2.49	0.46
11:U:183:GLU:CD	11:U:185:SER:H	2.23	0.46
32:a:124:SER:OG	32:a:128:ILE:HD11	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:g:11:VAL:HG11	38:g:61:ARG:HD2	1.97	0.46
39:h:14:LEU:HD22	39:h:19:ALA:HA	1.98	0.46
50:s:4:THR:HG21	50:s:47:VAL:HG11	1.97	0.46
51:t:62:LYS:HA	51:t:62:LYS:HD3	1.82	0.46
51:t:81:ALA:HB2	51:t:109:ASN:HD21	1.80	0.46
4:3:51:A:H5''	4:3:53:G:O4'	2.15	0.46
4:3:154:U:H2'	4:3:155:A:H8	1.81	0.46
4:3:912:A:H2'	4:3:913:U:C6	2.51	0.46
4:3:1031:U:O2'	40:i:4:THR:HG21	2.15	0.46
4:3:1436:C:H2'	4:3:1437:A:C8	2.51	0.46
4:3:1672:C:O2	4:3:2706:U:O2'	2.32	0.46
4:3:2794:U:O2'	33:b:65:PRO:O	2.34	0.46
5:4:28:C:OP2	45:n:36:LEU:HD11	2.16	0.46
6:5:894:A:H2'	6:5:895:A:C8	2.50	0.46
13:E:154:GLU:HG3	15:G:3:THR:CG2	2.46	0.46
15:G:48:LEU:HA	15:G:51:GLU:HG3	1.97	0.46
32:a:65:LYS:HB2	32:a:67:ARG:HH12	1.80	0.46
34:c:46:ARG:HD2	34:c:99:TYR:CG	2.51	0.46
4:3:24:U:H2'	4:3:25:G:H8	1.80	0.46
4:3:1124:G:N2	4:3:1125:U:O4	2.47	0.46
4:3:1385:U:H2'	4:3:1386:G:O4'	2.15	0.46
4:3:1536:C:H2'	4:3:1537:A:C8	2.50	0.46
4:3:1691:U:H2'	4:3:1692:A:C8	2.50	0.46
4:3:2011:G:H3'	4:3:2012:A:H8	1.81	0.46
5:4:82:U:H2'	5:4:83:U:H4'	1.96	0.46
6:5:8:G:N7	12:D:152:LYS:HE3	2.30	0.46
9:A:220:HIS:CE1	9:A:279:SER:HA	2.50	0.46
11:C:179:VAL:HG12	11:C:180:ARG:N	2.18	0.46
17:I:40:VAL:HG11	17:I:82:LEU:HD12	1.96	0.46
19:K:78:THR:HA	19:K:106:VAL:HG13	1.97	0.46
21:M:19:ARG:HH11	21:M:19:ARG:HG3	1.80	0.46
23:O:66:THR:HG22	23:O:67:ASP:N	2.31	0.46
11:U:20:GLU:OE2	11:U:21:ASN:ND2	2.49	0.46
11:U:57:LYS:HD2	11:U:199:TRP:HZ3	1.80	0.46
38:g:29:TYR:HB2	38:g:79:LYS:HD3	1.97	0.46
4:3:196:G:O2'	4:3:712:A:N1	2.48	0.46
4:3:1306:G:H2'	4:3:1307:G:C8	2.50	0.46
4:3:2863:G:H8	4:3:2863:G:OP2	1.99	0.46
6:5:510:U:H2'	6:5:511:A:C8	2.51	0.46
6:5:733:A:H2'	6:5:734:A:H8	1.81	0.46
6:5:768:G:H2'	6:5:769:U:C6	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:943:C:H2'	6:5:944:A:H8	1.81	0.46
6:5:998:G:O2'	6:5:1000:A:OP1	2.33	0.46
10:B:156:VAL:HG23	10:B:156:VAL:O	2.16	0.46
11:C:148:THR:O	11:C:151:ILE:HG22	2.15	0.46
12:D:66:PHE:CE1	12:D:96:ASN:HB3	2.51	0.46
20:L:83:ILE:HG23	26:R:66:MET:SD	2.55	0.46
21:M:4:LYS:HG3	21:M:5:SER:H	1.80	0.46
23:O:39:LEU:HD12	23:O:40:ASN:H	1.81	0.46
11:U:16:PHE:CE2	53:v:61:HIS:CD2	3.00	0.46
35:d:25:ILE:H	35:d:25:ILE:HD12	1.80	0.46
39:h:61:LYS:HA	39:h:63:PHE:CE1	2.50	0.46
44:m:13:TRP:O	44:m:16:MET:HG3	2.16	0.46
45:n:29:VAL:HG21	45:n:46:PHE:CE2	2.51	0.46
47:p:92:LYS:HG3	47:p:93:VAL:N	2.31	0.46
4:3:919:C:H2'	4:3:920:G:C8	2.51	0.46
4:3:1464:G:H1	4:3:1590:U:H3	1.63	0.46
4:3:2400:A:OP2	4:3:2430:C:N4	2.42	0.46
4:3:2704:U:H2'	4:3:2705:G:C8	2.51	0.46
4:3:2845:U:H2'	4:3:2846:A:C8	2.51	0.46
8:7:23:C:H2'	8:7:24:A:C8	2.50	0.46
8:7:26:A:H61	8:7:44:G:H1	1.62	0.46
9:A:56:PHE:CD2	9:A:216:PRO:HB3	2.50	0.46
12:D:108:ALA:HB3	12:D:114:ALA:HB2	1.98	0.46
12:D:122:ALA:O	12:D:126:LEU:HG	2.15	0.46
14:F:115:MET:HE2	14:F:115:MET:HB2	1.78	0.46
16:H:6:TYR:CZ	16:H:92:PHE:HB3	2.51	0.46
17:I:59:ARG:NE	17:I:67:SER:OG	2.49	0.46
26:R:36:ARG:NH2	26:R:52:HIS:O	2.48	0.46
27:S:56:ARG:HH12	27:S:57:LYS:NZ	2.13	0.46
33:b:182:VAL:HB	33:b:192:LEU:HB3	1.97	0.46
36:e:124:LEU:HD21	36:e:144:VAL:HA	1.96	0.46
37:f:103:THR:OG1	37:f:108:LEU:O	2.34	0.46
43:l:73:SER:C	43:l:74:LYS:HD2	2.40	0.46
47:p:46:TYR:HA	47:p:49:ARG:NH1	2.31	0.46
49:r:7:GLN:HG3	49:r:10:VAL:HG22	1.97	0.46
55:x:15:LYS:HE2	55:x:33:GLU:HG2	1.97	0.46
4:3:432:G:H1'	53:v:29:TRP:CD1	2.51	0.46
4:3:843:G:O2'	4:3:1284:A:H4'	2.15	0.46
4:3:1809:A:H2'	4:3:1810:A:C8	2.51	0.46
4:3:2120:G:N1	4:3:2176:G:H4'	2.28	0.46
4:3:2713:A:O2'	4:3:2856:G:OP1	2.32	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:87:G:O2'	6:5:137:A:N3	2.45	0.46
6:5:654:U:H4'	22:N:25:GLN:HG3	1.97	0.46
6:5:733:A:H2'	6:5:734:A:C8	2.51	0.46
6:5:991:A:H2'	6:5:992:U:C6	2.51	0.46
6:5:1102:A:N1	10:B:180:THR:HG22	2.31	0.46
24:P:81:ILE:HG22	24:P:82:GLU:HG2	1.98	0.46
25:Q:60:LEU:HD22	25:Q:86:VAL:HG23	1.98	0.46
33:b:10:LYS:HD2	33:b:197:ILE:HB	1.98	0.46
33:b:47:TYR:HD2	33:b:85:ARG:NE	2.14	0.46
34:c:19:LYS:HD3	34:c:20:LEU:N	2.30	0.46
34:c:162:ASN:ND2	34:c:202:GLU:HG3	2.31	0.46
35:d:29:PRO:HB3	35:d:165:GLU:OE1	2.16	0.46
42:k:34:ARG:HB3	42:k:41:ALA:HA	1.97	0.46
47:p:9:THR:HA	47:p:12:ARG:NE	2.30	0.46
49:r:2:ILE:HG21	49:r:106:LYS:HD2	1.97	0.46
2:1:10:ARG:NH1	4:3:254:G:OP2	2.37	0.46
4:3:2124:A:H2	4:3:2170:A:C4	2.34	0.46
4:3:2372:C:H2'	4:3:2373:G:O4'	2.16	0.46
5:4:11:A:N6	5:4:67:G:O2'	2.48	0.46
6:5:714:C:O2'	6:5:731:A:O4'	2.27	0.46
10:B:70:TYR:CD1	10:B:107:ASN:HB3	2.51	0.46
13:E:4:ASN:ND2	13:E:60:TRP:O	2.41	0.46
13:E:153:LYS:HG3	13:E:153:LYS:O	2.16	0.46
14:F:71:ARG:HB2	14:F:141:HIS:CE1	2.51	0.46
21:M:29:ARG:HE	21:M:42:LEU:HD21	1.81	0.46
11:U:100:ILE:O	11:U:104:MET:N	2.48	0.46
34:c:140:THR:HA	34:c:143:MET:HG3	1.96	0.46
34:c:193:LEU:HD23	34:c:193:LEU:O	2.16	0.46
40:i:36:ALA:HA	40:i:39:ILE:HG22	1.97	0.46
56:y:46:GLY:HA3	56:y:54:LYS:HG3	1.98	0.46
1:0:11:LYS:NZ	4:3:721:G:O5'	2.48	0.45
4:3:1691:U:H2'	4:3:1692:A:H8	1.81	0.45
4:3:2078:A:H2'	4:3:2079:G:C8	2.51	0.45
6:5:499:U:H2'	6:5:500:G:H8	1.81	0.45
6:5:719:G:H21	28:T:46:ARG:NH2	2.14	0.45
6:5:1269:U:H2'	6:5:1270:C:C6	2.52	0.45
9:A:29:HIS:HA	9:A:61:GLN:HE22	1.81	0.45
11:C:18:LEU:C	11:C:63:MET:HE1	2.40	0.45
13:E:9:VAL:CG2	13:E:56:HIS:HB2	2.46	0.45
26:R:21:ASP:O	26:R:24:LYS:HG2	2.16	0.45
11:U:17:SER:OG	11:U:18:LEU:N	2.49	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:c:154:ASP:OD1	34:c:154:ASP:N	2.38	0.45
41:j:8:LEU:HB2	41:j:82:ASN:O	2.16	0.45
46:o:102:SER:O	46:o:105:ARG:HG2	2.16	0.45
47:p:10:ARG:HA	47:p:10:ARG:HD2	1.81	0.45
49:r:9:ARG:HH21	49:r:82:MET:CE	2.27	0.45
52:u:99:LYS:HE3	52:u:101:LYS:HE2	1.98	0.45
4:3:274:A:OP2	4:3:294:G:N1	2.49	0.45
4:3:614:C:H2'	4:3:615:G:H8	1.80	0.45
4:3:849:C:H2'	4:3:850:G:H8	1.81	0.45
4:3:910:G:HO2'	43:l:65:TRP:CD1	2.33	0.45
4:3:1440:U:H2'	4:3:1441:A:C8	2.51	0.45
4:3:1703:A:C8	41:j:5:MET:SD	3.08	0.45
4:3:2299:U:O2'	4:3:2382:A:N3	2.49	0.45
6:5:214:U:H2'	6:5:215:C:H6	1.81	0.45
6:5:352:A:C2	6:5:364:U:O2	2.69	0.45
9:A:25:GLU:OE1	9:A:26:MET:HE2	2.16	0.45
10:B:113:MET:HE1	10:B:149:ALA:CB	2.46	0.45
13:E:32:VAL:HG23	13:E:62:PHE:HD2	1.82	0.45
13:E:130:VAL:N	13:E:131:PRO:HD2	2.31	0.45
16:H:129:PHE:CE1	16:H:131:LYS:HB2	2.51	0.45
18:J:16:VAL:HG22	18:J:25:VAL:HG13	1.98	0.45
19:K:29:ASN:HD22	19:K:32:ASN:CG	2.24	0.45
33:b:47:TYR:HD2	33:b:85:ARG:HE	1.63	0.45
34:c:165:ASN:HD21	34:c:168:LEU:HD22	1.81	0.45
41:j:14:THR:HG21	41:j:86:LEU:HD22	1.98	0.45
46:o:93:ARG:HH21	46:o:118:LYS:HE2	1.81	0.45
4:3:756:A:H2'	4:3:757:A:H8	1.82	0.45
4:3:1563:G:N2	4:3:1566:A:OP2	2.33	0.45
4:3:2452:G:OP2	34:c:69:LYS:HD2	2.17	0.45
4:3:2706:U:H2'	4:3:2707:A:C8	2.51	0.45
6:5:403:A:H2'	6:5:404:A:C8	2.51	0.45
6:5:655:G:H2'	6:5:656:U:C6	2.52	0.45
6:5:885:U:H2'	6:5:886:A:H8	1.81	0.45
6:5:1193:U:H2'	6:5:1194:A:C8	2.51	0.45
9:A:197:PRO:HB2	9:A:213:PHE:HE2	1.80	0.45
11:C:25:PHE:HA	11:C:30:LYS:HD2	1.97	0.45
16:H:26:ASP:O	16:H:27:LYS:HB2	2.17	0.45
17:I:13:LYS:HA	17:I:81:ILE:HA	1.99	0.45
19:K:134:LYS:HD3	19:K:136:LYS:HD3	1.97	0.45
35:d:34:ILE:HG12	35:d:100:LEU:HD21	1.97	0.45
39:h:50:MET:O	39:h:70:THR:HG22	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:i:4:THR:HA	48:q:12:TYR:HE2	1.81	0.45
46:o:53:LEU:HD11	46:o:67:ARG:HD2	1.97	0.45
4:3:573:A:H2'	4:3:574:G:O4'	2.17	0.45
4:3:843:G:OP2	42:k:37:LYS:HE2	2.16	0.45
4:3:867:G:H2'	4:3:868:C:C6	2.51	0.45
4:3:869:U:H2'	4:3:870:A:H8	1.81	0.45
4:3:1099:C:H3'	4:3:1100:U:H6	1.82	0.45
4:3:2105:G:C6	4:3:2106:G:C6	3.04	0.45
4:3:2825:A:OP1	33:b:116:GLY:N	2.49	0.45
6:5:1402:U:H2'	6:5:1403:A:H8	1.80	0.45
9:A:116:THR:HA	9:A:123:LEU:HD22	1.98	0.45
14:F:78:ARG:O	14:F:79:ILE:HG23	2.16	0.45
20:L:26:GLY:O	20:L:30:SER:HB3	2.17	0.45
30:Y:47:U:H3'	30:Y:48:C:C6	2.50	0.45
36:e:44:LEU:HD12	36:e:55:ILE:CG2	2.45	0.45
39:h:30:ILE:HG12	39:h:63:PHE:CZ	2.51	0.45
41:j:91:LYS:NZ	41:j:112:ASN:OD1	2.50	0.45
44:m:33:THR:OG1	44:m:34:THR:N	2.49	0.45
4:3:410:G:OP1	11:U:18:LEU:HD21	2.16	0.45
4:3:610:G:H2'	4:3:611:A:C8	2.51	0.45
4:3:916:U:H2'	4:3:917:G:H8	1.82	0.45
4:3:1369:U:OP2	4:3:1422:U:O2'	2.30	0.45
4:3:1696:C:O2'	4:3:2695:U:OP1	2.34	0.45
4:3:2113:U:C2	4:3:2192:U:C2	3.05	0.45
5:4:93:U:H2'	5:4:94:A:C8	2.51	0.45
6:5:426:U:H5'	11:C:8:PHE:CG	2.51	0.45
6:5:503:G:H2'	6:5:504:A:C8	2.52	0.45
6:5:518:A:OP1	19:K:62:LEU:HB3	2.17	0.45
6:5:1142:G:N2	6:5:1145:A:OP2	2.40	0.45
11:C:122:VAL:O	11:C:123:LEU:HD23	2.16	0.45
12:D:166:ILE:H	12:D:166:ILE:HD12	1.81	0.45
19:K:7:LEU:HG	24:P:35:TYR:CE2	2.52	0.45
11:U:123:LEU:HD23	11:U:143:ARG:HD2	1.99	0.45
11:U:153:ILE:O	11:U:155:LYS:N	2.49	0.45
35:d:43:ALA:HB2	35:d:50:LEU:HB2	1.98	0.45
37:f:33:LYS:HB3	37:f:35:LEU:HD23	1.99	0.45
38:g:43:LYS:HE3	38:g:43:LYS:HB3	1.77	0.45
48:q:14:VAL:HB	48:q:94:VAL:HG21	1.99	0.45
4:3:963:U:H2'	4:3:964:A:C8	2.51	0.45
4:3:1095:U:H5''	39:h:68:LYS:HE2	1.98	0.45
4:3:2025:C:H2'	4:3:2026:A:H8	1.81	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:2117:G:C5	4:3:2127:G:C8	3.05	0.45
4:3:2224:A:H2'	4:3:2225:G:H8	1.81	0.45
4:3:2794:U:O3'	33:b:72:LYS:NZ	2.35	0.45
6:5:508:A:N3	6:5:541:C:H1'	2.32	0.45
6:5:918:A:O2'	6:5:1374:C:OP2	2.28	0.45
14:F:42:LEU:HD12	14:F:42:LEU:HA	1.73	0.45
18:J:105:GLU:O	28:T:2:PRO:HD2	2.17	0.45
25:Q:81:MET:O	25:Q:84:ARG:HG2	2.17	0.45
32:a:135:SER:HA	32:a:199:THR:HA	1.98	0.45
35:d:74:ILE:O	35:d:79:LEU:N	2.49	0.45
35:d:100:LEU:HD21	35:d:156:LEU:HD11	1.99	0.45
38:g:18:LEU:HD21	38:g:62:ALA:HB1	1.99	0.45
47:p:32:LYS:HA	47:p:32:LYS:HD3	1.75	0.45
48:q:44:LYS:O	48:q:50:LEU:HD11	2.16	0.45
4:3:915:A:H3'	4:3:916:U:H6	1.81	0.45
4:3:1128:G:H2'	4:3:1129:U:C6	2.52	0.45
4:3:1294:G:OP1	56:y:16:ARG:NH2	2.42	0.45
4:3:1617:U:H5''	4:3:1619:A:C4	2.51	0.45
4:3:2638:G:H2'	4:3:2639:G:H8	1.81	0.45
6:5:20:C:H3'	12:D:185:ARG:NH2	2.32	0.45
6:5:214:U:H2'	6:5:215:C:C6	2.51	0.45
9:A:162:PHE:O	9:A:163:PHE:HD1	1.99	0.45
12:D:101:ILE:C	12:D:126:LEU:HD23	2.42	0.45
15:G:44:ILE:HA	15:G:122:VAL:HG21	1.98	0.45
16:H:121:TYR:HB2	16:H:125:ARG:HD3	1.97	0.45
23:O:73:PHE:O	23:O:78:LEU:N	2.42	0.45
24:P:52:GLU:O	24:P:52:GLU:HG2	2.17	0.45
25:Q:94:ARG:HB3	25:Q:101:PHE:CZ	2.51	0.45
28:T:47:LYS:O	28:T:50:GLN:HG3	2.17	0.45
36:e:121:PRO:HD2	36:e:147:PHE:CE2	2.51	0.45
38:g:42:LYS:HZ1	39:h:113:ASN:C	2.24	0.45
41:j:71:ARG:NH2	41:j:104:ARG:HB3	2.32	0.45
51:t:32:GLN:HG3	51:t:71:LEU:HB2	1.98	0.45
51:t:76:LEU:HD22	51:t:89:ILE:HG21	1.97	0.45
53:v:15:GLY:O	53:v:26:ARG:HD3	2.17	0.45
55:x:14:PHE:O	55:x:22:SER:HA	2.17	0.45
56:y:7:ARG:HA	56:y:7:ARG:HE	1.82	0.45
4:3:2102:U:O2'	4:3:2103:C:H5'	2.16	0.45
6:5:93:A:H62	27:S:10:ARG:HG2	1.82	0.45
6:5:828:U:H5''	9:A:35:ARG:HE	1.81	0.45
6:5:1401:A:H2'	6:5:1402:U:H6	1.82	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:212:ARG:HH12	15:G:53:TYR:CD1	1.75	0.45
15:G:101:PHE:HA	15:G:104:LEU:HG	1.99	0.45
17:I:86:ASN:O	17:I:90:ILE:HG13	2.17	0.45
18:J:119:ARG:HB2	28:T:34:TYR:CG	2.52	0.45
22:N:15:HIS:CE1	22:N:18:ASP:HB2	2.52	0.45
41:j:17:LYS:N	41:j:45:ASP:O	2.48	0.45
46:o:54:ARG:HD3	46:o:56:ARG:HB2	1.99	0.45
50:s:19:ASN:HB3	50:s:26:LYS:HB2	1.99	0.45
55:x:90:LYS:HE3	55:x:92:ARG:NH1	2.32	0.45
4:3:848:U:H2'	4:3:849:C:C6	2.52	0.45
4:3:1036:A:OP2	4:3:1189:G:N1	2.33	0.45
4:3:1444:C:N4	4:3:1616:G:O6	2.49	0.45
4:3:1585:A:N3	4:3:1585:A:H2'	2.32	0.45
4:3:2176:G:N2	4:3:2178:A:H3'	2.32	0.45
6:5:476:U:H5'	6:5:477:U:OP1	2.17	0.45
6:5:825:A:H2'	6:5:826:G:O4'	2.17	0.45
6:5:828:U:H4'	9:A:35:ARG:HH21	1.81	0.45
8:7:35:U:H2'	8:7:36:C:C6	2.51	0.45
9:A:41:MET:SD	9:A:41:MET:C	2.99	0.45
12:D:168:ALA:O	12:D:172:LEU:HD23	2.17	0.45
18:J:106:LYS:HE3	18:J:106:LYS:HB3	1.64	0.45
19:K:86:ASN:OD1	19:K:86:ASN:N	2.47	0.45
19:K:99:ARG:HD2	19:K:99:ARG:HA	1.84	0.45
27:S:19:LEU:HA	27:S:22:LYS:HZ2	1.82	0.45
11:U:140:ASP:O	11:U:177:THR:HG23	2.16	0.45
34:c:7:ILE:HG22	34:c:13:PHE:CE1	2.52	0.45
41:j:1:MET:HE1	41:j:67:LYS:NZ	2.31	0.45
41:j:18:GLN:HB3	41:j:45:ASP:HB2	1.98	0.45
42:k:120:LEU:HD23	42:k:120:LEU:H	1.82	0.45
43:l:73:SER:HB2	43:l:93:TRP:CE3	2.52	0.45
46:o:36:LYS:HE2	46:o:85:ASN:HA	1.99	0.45
51:t:36:VAL:HG12	51:t:69:ILE:HD12	1.99	0.45
4:3:631:A:H2'	4:3:632:A:H8	1.81	0.45
4:3:1273:U:H1'	42:k:4:ASN:O	2.16	0.45
4:3:1777:G:H1	4:3:1989:U:H3	1.64	0.45
4:3:2068:G:O6	59:3:3001:CLM:O4	2.24	0.45
4:3:2361:G:N2	52:u:48:GLY:O	2.33	0.45
6:5:56:A:OP2	6:5:348:C:N4	2.50	0.45
6:5:369:A:N1	6:5:387:G:O2'	2.47	0.45
6:5:631:C:H2'	6:5:632:A:C8	2.52	0.45
6:5:1389:U:H2'	6:5:1390:G:H8	1.81	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:167:ARG:NH2	30:Y:48:C:H1'	2.32	0.45
19:K:73:GLY:O	19:K:74:PHE:HD1	2.00	0.45
23:O:20:VAL:HG13	23:O:34:ALA:O	2.16	0.45
25:Q:51:ILE:HD13	25:Q:85:HIS:HB3	1.98	0.45
11:U:97:LEU:O	11:U:101:VAL:HG23	2.17	0.45
11:U:169:THR:HG23	11:U:175:GLU:O	2.16	0.45
31:Z:2:UNK:HA	51:t:50:GLN:HB2	1.99	0.45
43:l:13:HIS:O	43:l:72:MET:HE3	2.17	0.45
46:o:42:LYS:HG2	46:o:43:VAL:H	1.82	0.45
48:q:56:VAL:HG11	48:q:96:ARG:NH2	2.31	0.45
55:x:94:LEU:HD13	55:x:100:LEU:CD1	2.46	0.45
1:0:1:MET:SD	1:0:3:ARG:HD3	2.58	0.44
4:3:155:A:H2'	4:3:156:A:C8	2.52	0.44
4:3:356:A:H5'	4:3:374:A:H1'	1.99	0.44
4:3:567:U:H4'	4:3:568:G:C8	2.52	0.44
4:3:1521:A:N3	4:3:1611:C:O2'	2.46	0.44
4:3:1665:G:N1	4:3:1668:G:OP2	2.41	0.44
4:3:1698:A:H61	4:3:2003:C:H42	1.65	0.44
4:3:2039:G:H21	33:b:154:ALA:HB3	1.82	0.44
4:3:2112:A:C6	4:3:2192:U:C4	3.05	0.44
4:3:2163:U:H2'	4:3:2164:G:C5	2.52	0.44
4:3:2238:G:H1'	53:v:32:ASN:OD1	2.17	0.44
6:5:212:G:H2'	6:5:213:U:C6	2.51	0.44
10:B:182:ARG:NH1	10:B:209:MET:SD	2.90	0.44
15:G:2:ILE:HB	15:G:60:LEU:HD21	1.99	0.44
38:g:112:TYR:OH	38:g:115:ASN:HA	2.17	0.44
4:3:393:C:H2'	11:U:32:LYS:HD2	1.98	0.44
4:3:1279:U:H5'	47:p:3:ILE:HB	1.99	0.44
4:3:1619:A:H2'	4:3:1620:A:H8	1.82	0.44
4:3:2133:A:O3'	4:3:2134:G:H4'	2.17	0.44
6:5:573:G:O2'	6:5:818:A:H5'	2.17	0.44
6:5:1215:U:O4	14:F:108:ARG:NH2	2.50	0.44
8:7:35:U:P	16:H:132:ARG:HH21	2.41	0.44
8:7:46:U:O2'	8:7:47:U:OP1	2.24	0.44
9:A:201:LEU:HG	9:A:228:LEU:CD1	2.43	0.44
9:A:223:GLN:HG2	9:A:224:SER:N	2.33	0.44
11:C:103:ARG:HD3	11:C:164:SER:OG	2.18	0.44
11:C:121:HIS:HB3	11:C:148:THR:HG21	1.99	0.44
15:G:89:GLN:CD	15:G:92:LYS:HD3	2.42	0.44
18:J:77:LEU:HD23	18:J:100:ILE:HG23	1.99	0.44
38:g:106:MET:HG3	38:g:107:ASN:O	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:i:7:LEU:HD13	47:p:60:TRP:HE1	1.82	0.44
46:o:38:LYS:HG2	46:o:43:VAL:HG12	2.00	0.44
47:p:89:ILE:HG12	48:q:39:LEU:HD13	1.99	0.44
55:x:14:PHE:N	55:x:23:PHE:O	2.47	0.44
4:3:258:G:H4'	4:3:422:A:H4'	1.99	0.44
4:3:860:C:H4'	4:3:2436:G:C5	2.52	0.44
4:3:1102:A:H2'	4:3:1102:A:N3	2.32	0.44
4:3:2108:C:O2	4:3:2196:G:N1	2.33	0.44
6:5:111:A:H2'	6:5:112:U:O4'	2.18	0.44
6:5:625:U:H2'	6:5:626:G:H8	1.83	0.44
10:B:59:GLU:HB3	10:B:66:ASP:HB3	1.99	0.44
11:C:7:ILE:H	11:C:7:ILE:HD12	1.82	0.44
11:C:26:SER:OG	11:C:27:LYS:N	2.50	0.44
11:C:68:ASP:O	11:C:72:ARG:HG3	2.17	0.44
13:E:82:VAL:HG12	13:E:82:VAL:O	2.17	0.44
14:F:26:ILE:HD13	14:F:39:GLN:OE1	2.17	0.44
17:I:71:PHE:CZ	21:M:56:VAL:HG13	2.52	0.44
18:J:43:MET:CE	18:J:59:ALA:HB2	2.45	0.44
28:T:6:VAL:C	28:T:8:ASN:H	2.25	0.44
28:T:56:PHE:O	28:T:59:MET:HG3	2.17	0.44
11:U:44:SER:HA	11:U:51:ALA:CB	2.47	0.44
33:b:22:GLU:HG2	41:j:72:LYS:HE2	1.98	0.44
33:b:98:PRO:HD2	33:b:189:MET:HE1	1.99	0.44
33:b:165:MET:SD	33:b:165:MET:N	2.90	0.44
37:f:33:LYS:HD3	37:f:113:PHE:HB2	1.98	0.44
37:f:58:TYR:HA	37:f:61:ASN:HD21	1.81	0.44
38:g:9:GLN:NE2	38:g:13:ASP:OD2	2.49	0.44
49:r:65:ASN:OD1	49:r:66:GLY:N	2.50	0.44
52:u:6:PHE:HD2	52:u:7:LEU:H	1.65	0.44
54:w:53:THR:O	54:w:57:ILE:HD12	2.17	0.44
3:2:19:ARG:O	3:2:22:ILE:HG22	2.17	0.44
4:3:913:U:H3	4:3:938:A:H61	1.66	0.44
4:3:1120:A:H2'	4:3:1121:A:N9	2.32	0.44
4:3:1436:C:H2'	4:3:1437:A:H8	1.82	0.44
4:3:1697:C:HO2'	4:3:1698:A:H8	1.66	0.44
4:3:1854:A:H3'	4:3:1855:A:H8	1.82	0.44
4:3:2141:A:C2	4:3:2166:U:H1'	2.52	0.44
5:4:3:U:O2'	5:4:24:A:N1	2.50	0.44
6:5:682:G:N2	6:5:701:A:OP2	2.47	0.44
6:5:690:G:H4'	30:Y:36:U:OP2	2.18	0.44
6:5:1076:U:H3'	6:5:1077:U:C5	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:1482:A:H2'	6:5:1483:C:C6	2.53	0.44
9:A:68:ALA:O	9:A:72:VAL:HG12	2.17	0.44
11:C:74:LEU:O	11:C:78:VAL:HG12	2.18	0.44
12:D:178:ILE:HG22	12:D:180:THR:HG23	1.99	0.44
13:E:24:LYS:HE3	13:E:79:ASN:HD22	1.81	0.44
16:H:65:ILE:HG22	16:H:67:VAL:HG23	2.00	0.44
11:U:16:PHE:O	11:U:17:SER:C	2.60	0.44
11:U:129:VAL:HG13	11:U:134:ILE:CD1	2.47	0.44
32:a:190:ARG:NH2	32:a:274:SER:HB2	2.32	0.44
35:d:132:ILE:HB	35:d:152:PHE:HB2	1.99	0.44
48:q:60:GLU:OE2	48:q:91:LYS:HG2	2.18	0.44
48:q:77:LYS:HD3	48:q:77:LYS:HA	1.81	0.44
54:w:16:VAL:O	54:w:19:VAL:HG12	2.17	0.44
4:3:1032:A:O5'	47:p:92:LYS:HD3	2.17	0.44
4:3:1623:U:H2'	4:3:1624:A:C8	2.53	0.44
4:3:1906:G:H21	4:3:1909:C:N4	2.14	0.44
6:5:1002:A:H2'	6:5:1003:A:O4'	2.18	0.44
6:5:1199:U:O2'	6:5:1296:C:OP1	2.35	0.44
9:A:160:GLU:O	9:A:164:GLY:N	2.50	0.44
10:B:201:VAL:O	10:B:202:LYS:HD3	2.17	0.44
13:E:21:VAL:HG13	13:E:60:TRP:CZ2	2.52	0.44
17:I:47:PRO:HA	17:I:78:ARG:HD2	1.99	0.44
18:J:105:GLU:HB3	28:T:2:PRO:HG2	2.00	0.44
20:L:2:ALA:N	20:L:8:ASP:HA	2.33	0.44
23:O:5:ARG:NH2	23:O:26:VAL:O	2.45	0.44
32:a:218:ARG:O	32:a:222:ARG:HG2	2.18	0.44
35:d:104:ILE:HG23	35:d:105:TYR:CD1	2.52	0.44
38:g:69:GLU:N	38:g:69:GLU:OE2	2.51	0.44
52:u:57:THR:HG23	52:u:57:THR:O	2.18	0.44
55:x:87:GLU:OE1	55:x:88:TYR:N	2.50	0.44
4:3:756:A:H2'	4:3:757:A:C8	2.52	0.44
4:3:776:U:H2'	4:3:777:C:H6	1.82	0.44
4:3:863:U:O2'	4:3:866:G:O6	2.36	0.44
4:3:1598:U:H2'	4:3:1599:C:C6	2.53	0.44
4:3:2726:G:H4'	46:o:98:ARG:HH21	1.82	0.44
6:5:190:A:H2'	6:5:191:A:C8	2.49	0.44
6:5:204:C:O2'	6:5:465:A:O2'	2.33	0.44
9:A:147:LYS:O	9:A:150:LEU:HG	2.17	0.44
16:H:41:PHE:CE2	16:H:50:MET:HE1	2.52	0.44
11:U:119:HIS:HB2	11:U:121:HIS:CE1	2.53	0.44
11:U:160:SER:HB3	11:U:171:ASN:ND2	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:31:CYS:O	33:b:189:MET:HG3	2.17	0.44
34:c:162:ASN:HD21	34:c:202:GLU:HG3	1.83	0.44
39:h:11:LYS:HZ1	39:h:68:LYS:NZ	2.15	0.44
40:i:4:THR:HA	48:q:12:TYR:CE2	2.52	0.44
45:n:5:THR:O	45:n:9:ARG:HG3	2.17	0.44
50:s:41:LYS:O	50:s:45:GLU:HG2	2.18	0.44
54:w:10:LYS:CE	54:w:14:GLU:HG2	2.47	0.44
57:z:48:LYS:HG2	57:z:49:GLU:N	2.32	0.44
1:0:26:SER:HB2	4:3:717:U:H5'	1.99	0.44
2:1:12:LYS:HE3	4:3:667:A:H5''	1.98	0.44
4:3:196:G:O2'	4:3:837:A:N3	2.46	0.44
4:3:314:G:H22	11:U:32:LYS:HG3	1.82	0.44
4:3:708:C:OP1	34:c:55:LYS:NZ	2.35	0.44
4:3:912:A:C5	4:3:913:U:C4	3.06	0.44
4:3:1837:C:H2'	4:3:1838:A:H8	1.83	0.44
4:3:2124:A:C6	4:3:2179:A:C6	3.06	0.44
4:3:2311:G:O2'	35:d:121:SER:O	2.21	0.44
4:3:2561:G:C2	4:3:2591:G:H1'	2.53	0.44
4:3:2655:U:H2'	4:3:2656:G:H8	1.82	0.44
6:5:933:A:O2'	14:F:94:ARG:NH2	2.42	0.44
6:5:1024:U:O2'	6:5:1025:U:OP1	2.34	0.44
9:A:280:GLN:HG2	9:A:282:LEU:HG	1.99	0.44
12:D:131:ILE:HD12	12:D:134:GLY:HA2	2.00	0.44
13:E:45:LEU:HD21	13:E:52:GLN:O	2.18	0.44
26:R:32:LYS:HA	26:R:50:ALA:HB3	2.00	0.44
11:U:9:LYS:HD2	11:U:12:ARG:HH21	1.81	0.44
11:U:37:GLN:HG3	11:U:41:ARG:NH2	2.33	0.44
35:d:93:GLY:O	35:d:96:MET:HG2	2.18	0.44
37:f:68:LEU:HB3	37:f:108:LEU:HD21	1.99	0.44
38:g:98:GLY:HA2	38:g:101:LYS:HE2	1.99	0.44
41:j:18:GLN:NE2	41:j:19:VAL:H	2.16	0.44
41:j:51:MET:SD	41:j:51:MET:N	2.91	0.44
41:j:91:LYS:NZ	41:j:112:ASN:H	2.15	0.44
47:p:9:THR:HB	47:p:12:ARG:HH21	1.83	0.44
47:p:86:ASN:HB3	48:q:47:ALA:HB1	2.00	0.44
4:3:768:G:N2	4:3:769:A:N7	2.66	0.44
4:3:1005:G:H2'	4:3:1006:U:C6	2.53	0.44
6:5:259:A:OP1	27:S:67:ARG:NH1	2.51	0.44
6:5:473:A:H2'	6:5:474:G:H8	1.83	0.44
9:A:41:MET:SD	9:A:45:ILE:HD12	2.57	0.44
9:A:225:THR:CG2	9:A:229:MET:HE2	2.47	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:C:97:LEU:O	11:C:101:VAL:HG23	2.18	0.44
13:E:5:ILE:HG22	13:E:7:LEU:HD12	2.00	0.44
13:E:81:GLN:O	13:E:83:LEU:N	2.50	0.44
17:I:59:ARG:HD3	17:I:59:ARG:N	2.33	0.44
32:a:128:ILE:HB	32:a:136:MET:SD	2.58	0.44
36:e:20:PHE:CD1	36:e:25:ILE:HG12	2.52	0.44
37:f:75:THR:HG22	37:f:77:LEU:H	1.81	0.44
42:k:131:VAL:HG11	42:k:136:LEU:HD21	2.00	0.44
4:3:411:U:H2'	4:3:412:A:C8	2.52	0.44
4:3:603:G:H2'	4:3:2037:A:N7	2.33	0.44
4:3:1119:A:C4	38:g:53:VAL:HG21	2.53	0.44
4:3:2160:U:H2'	4:3:2161:G:C8	2.52	0.44
4:3:2198:G:C2	4:3:2199:C:H1'	2.52	0.44
4:3:2764:U:H1'	4:3:2765:A:H5''	2.00	0.44
6:5:37:C:O2'	6:5:499:U:OP1	2.36	0.44
6:5:80:U:H2'	6:5:81:A:C8	2.53	0.44
6:5:1248:U:H2'	6:5:1249:G:O4'	2.18	0.44
10:B:70:TYR:HA	10:B:107:ASN:O	2.18	0.44
11:C:91:ARG:NH2	11:C:181:PHE:HB3	2.33	0.44
15:G:118:THR:OG1	15:G:119:SER:N	2.51	0.44
15:G:118:THR:H	15:G:123:MET:CE	2.31	0.44
19:K:96:ARG:HG2	19:K:111:VAL:HG23	2.00	0.44
20:L:55:ALA:O	20:L:59:VAL:HG23	2.18	0.44
11:U:16:PHE:HE2	53:v:61:HIS:CD2	2.36	0.44
11:U:163:VAL:HG22	11:U:164:SER:O	2.18	0.44
11:U:172:LYS:HE2	11:U:172:LYS:HA	2.00	0.44
33:b:225:GLN:HE22	46:o:84:PRO:HA	1.83	0.44
34:c:43:ALA:C	34:c:45:TRP:H	2.26	0.44
37:f:131:PHE:HA	37:f:140:VAL:O	2.18	0.44
38:g:24:PHE:HB2	38:g:112:TYR:HB3	1.99	0.44
42:k:34:ARG:NE	42:k:40:LYS:O	2.50	0.44
43:l:24:ASN:O	43:l:102:VAL:N	2.39	0.44
49:r:21:CYS:O	49:r:25:VAL:HG23	2.18	0.44
55:x:19:CYS:SG	55:x:21:ASN:ND2	2.91	0.44
4:3:38:G:N3	4:3:486:G:O2'	2.50	0.43
4:3:1104:A:H4'	4:3:1105:A:H2'	2.00	0.43
4:3:1135:C:H2'	4:3:1136:U:O4'	2.18	0.43
4:3:1670:U:H2'	4:3:1671:C:C6	2.53	0.43
4:3:1836:A:H3'	4:3:1837:C:H6	1.83	0.43
4:3:2140:G:H2'	4:3:2164:G:N2	2.33	0.43
4:3:2335:A:H2'	4:3:2336:A:C8	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:65:LEU:HD21	9:A:231:LEU:HD13	2.00	0.43
11:C:106:PHE:CE1	11:C:158:SER:HA	2.53	0.43
17:I:8:LYS:O	17:I:9:TYR:CD1	2.71	0.43
20:L:18:ALA:HA	20:L:21:TYR:HD2	1.83	0.43
38:g:121:ALA:HA	38:g:124:GLU:OE1	2.18	0.43
43:l:3:GLN:NE2	43:l:4:PRO:HD2	2.33	0.43
45:n:28:VAL:HG21	45:n:52:LEU:HD21	2.00	0.43
46:o:67:ARG:CZ	46:o:105:ARG:HA	2.49	0.43
2:1:4:LYS:HG2	2:1:6:ALA:H	1.82	0.43
4:3:1386:G:N1	4:3:1400:U:OP2	2.29	0.43
4:3:1522:U:H5''	4:3:1523:C:H5	1.82	0.43
4:3:1959:A:N3	4:3:2568:G:O2'	2.40	0.43
6:5:836:C:H3'	6:5:837:G:C8	2.53	0.43
6:5:1146:A:H2'	6:5:1147:U:C6	2.53	0.43
6:5:1329:G:H2'	6:5:1330:A:C8	2.53	0.43
9:A:254:ILE:O	9:A:256:ILE:HG23	2.18	0.43
19:K:96:ARG:HG2	19:K:111:VAL:CG2	2.48	0.43
23:O:12:VAL:O	23:O:13:HIS:HB2	2.18	0.43
11:U:150:LYS:O	11:U:152:PRO:HD3	2.18	0.43
33:b:40:LYS:HD2	33:b:45:ASP:OD2	2.17	0.43
35:d:91:LEU:HB3	35:d:95:ARG:HG3	1.99	0.43
39:h:92:ILE:HD13	39:h:134:GLU:HG3	2.00	0.43
57:z:14:CYS:O	57:z:15:ARG:HG3	2.18	0.43
4:3:65:A:H2	50:s:66:ARG:HH22	1.65	0.43
4:3:226:A:H61	4:3:236:G:H1'	1.83	0.43
4:3:315:A:H2'	11:U:35:PRO:HB3	1.99	0.43
4:3:840:G:C1'	42:k:39:GLN:HE21	2.31	0.43
4:3:915:A:H3'	4:3:916:U:C6	2.54	0.43
4:3:1296:G:N7	49:r:16:LYS:HE2	2.33	0.43
4:3:1605:A:H2'	4:3:1606:A:H8	1.83	0.43
4:3:1797:C:O2'	32:a:216:ALA:HB2	2.18	0.43
4:3:2223:C:H2'	4:3:2224:A:H8	1.83	0.43
4:3:2438:A:H2'	4:3:2438:A:N3	2.33	0.43
6:5:366:C:H42	6:5:387:G:H1	1.67	0.43
6:5:1505:G:H2'	6:5:1506:A:C8	2.53	0.43
9:A:58:LEU:HD13	9:A:61:GLN:OE1	2.17	0.43
10:B:124:ALA:O	10:B:128:GLU:OE1	2.37	0.43
11:C:123:LEU:HD22	11:C:128:THR:HG22	2.00	0.43
20:L:19:LEU:HB3	20:L:30:SER:HB2	1.99	0.43
20:L:64:LYS:NZ	20:L:72:GLU:OE1	2.48	0.43
32:a:98:LEU:HB2	32:a:108:TYR:CE1	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:c:34:VAL:O	34:c:38:VAL:HG23	2.18	0.43
38:g:26:ILE:HG21	38:g:80:LEU:HD22	2.00	0.43
47:p:82:LEU:HD23	47:p:87:ILE:HB	2.00	0.43
49:r:33:GLN:OE1	49:r:51:LEU:HD23	2.17	0.43
4:3:841:C:O2	4:3:2452:G:O2'	2.37	0.43
6:5:182:C:H41	24:P:3:ARG:HG2	1.82	0.43
6:5:381:C:H2'	6:5:382:U:C6	2.53	0.43
6:5:458:G:H2'	6:5:459:C:C6	2.53	0.43
6:5:506:U:H5''	11:C:50:TYR:CE1	2.53	0.43
6:5:579:G:OP1	22:N:62:ARG:NH1	2.51	0.43
6:5:659:U:H4'	6:5:833:G:H5''	2.00	0.43
6:5:1108:A:O3'	16:H:108:ARG:HG2	2.18	0.43
9:A:70:ASN:O	9:A:74:GLU:HG2	2.18	0.43
9:A:156:ILE:O	9:A:160:GLU:OE1	2.36	0.43
10:B:133:LEU:HG	10:B:169:LYS:HZ2	1.84	0.43
10:B:137:MET:O	10:B:141:LEU:HD13	2.19	0.43
11:C:123:LEU:HB3	11:C:143:ARG:HH12	1.83	0.43
17:I:94:LYS:HE3	55:x:98:ASN:OD1	2.19	0.43
28:T:45:LYS:O	28:T:48:ILE:HG22	2.19	0.43
34:c:43:ALA:O	34:c:44:SER:OG	2.30	0.43
37:f:41:LYS:O	37:f:41:LYS:HG3	2.18	0.43
41:j:14:THR:HA	41:j:51:MET:CE	2.47	0.43
43:l:24:ASN:HD22	43:l:68:ILE:HD13	1.83	0.43
43:l:77:LYS:HE2	43:l:77:LYS:HB3	1.72	0.43
46:o:51:THR:HG22	46:o:67:ARG:O	2.18	0.43
49:r:125:VAL:O	49:r:129:VAL:HG23	2.19	0.43
4:3:355:A:O2'	4:3:374:A:N3	2.52	0.43
4:3:2146:A:N6	4:3:2158:C:H42	2.15	0.43
4:3:2171:A:H3'	4:3:2172:A:C8	2.54	0.43
5:4:12:U:OP2	5:4:68:C:O2'	2.35	0.43
6:5:260:C:H2'	6:5:261:G:O4'	2.19	0.43
6:5:792:C:O2'	18:J:121:ARG:OXT	2.31	0.43
6:5:1273:A:H2'	6:5:1273:A:N3	2.32	0.43
6:5:1384:A:H2'	6:5:1385:A:H8	1.82	0.43
10:B:83:LYS:HD3	10:B:84:ASN:N	2.34	0.43
11:C:124:LEU:HD11	11:C:129:VAL:HB	1.99	0.43
16:H:85:ILE:O	16:H:89:LEU:HD13	2.18	0.43
16:H:118:PHE:HD2	17:I:70:GLN:NE2	2.16	0.43
19:K:67:LYS:HD3	19:K:77:LEU:CD2	2.46	0.43
33:b:6:ILE:HG22	33:b:207:ILE:HB	2.00	0.43
35:d:14:LYS:O	35:d:18:LYS:HE2	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:d:34:ILE:HG13	35:d:156:LEU:HD13	2.00	0.43
36:e:128:VAL:HG13	36:e:128:VAL:O	2.19	0.43
37:f:96:GLN:O	37:f:100:GLN:NE2	2.51	0.43
37:f:96:GLN:CD	37:f:100:GLN:HE22	2.26	0.43
41:j:1:MET:CE	41:j:67:LYS:HG2	2.49	0.43
43:l:44:ALA:O	43:l:48:GLU:OE1	2.35	0.43
46:o:115:LYS:HE3	46:o:115:LYS:HB3	1.79	0.43
50:s:48:TYR:HD2	50:s:91:ILE:HD13	1.84	0.43
52:u:73:LEU:HD13	52:u:95:VAL:HG11	2.01	0.43
4:3:408:G:OP2	4:3:459:A:N6	2.51	0.43
4:3:1009:A:H5'	4:3:1219:U:H1'	2.00	0.43
4:3:1092:A:H2'	4:3:1093:U:C6	2.53	0.43
4:3:1854:A:H1'	6:5:699:A:C4	2.54	0.43
4:3:2068:G:H2'	4:3:2509:C:O2'	2.18	0.43
4:3:2100:G:H21	4:3:2206:A:N6	2.16	0.43
4:3:2116:U:H2'	4:3:2117:G:C8	2.54	0.43
4:3:2321:C:O4'	35:d:37:ASN:ND2	2.51	0.43
4:3:2353:G:N3	4:3:2389:A:H2'	2.34	0.43
4:3:2580:A:H2'	33:b:151:ARG:NH2	2.33	0.43
6:5:50:U:H4'	19:K:27:ASN:ND2	2.33	0.43
6:5:253:G:H1	6:5:265:U:H3	1.67	0.43
6:5:621:C:H2'	6:5:622:A:C8	2.53	0.43
6:5:1397:G:O5'	41:j:48:PRO:HB3	2.19	0.43
12:D:169:ILE:HD11	12:D:192:ILE:HA	2.00	0.43
20:L:13:LYS:HE2	20:L:21:TYR:OH	2.18	0.43
22:N:45:LYS:HB3	22:N:45:LYS:HE2	1.76	0.43
24:P:50:GLU:HG2	24:P:51:GLY:N	2.33	0.43
24:P:77:ILE:H	24:P:77:ILE:HD12	1.82	0.43
26:R:30:PRO:HA	26:R:48:THR:HG23	1.99	0.43
32:a:125:GLU:HG3	32:a:125:GLU:O	2.19	0.43
33:b:123:ILE:HA	33:b:128:PHE:HB2	2.01	0.43
41:j:54:LYS:HE3	41:j:54:LYS:HB3	1.81	0.43
4:3:230:G:O2'	4:3:232:A:N6	2.51	0.43
4:3:600:U:OP2	42:k:30:LYS:NZ	2.52	0.43
4:3:614:C:H2'	4:3:615:G:C8	2.53	0.43
4:3:900:G:H2'	4:3:901:C:C6	2.53	0.43
4:3:917:G:N2	4:3:935:U:H1'	2.31	0.43
4:3:1141:U:H2'	4:3:1142:G:C8	2.54	0.43
4:3:1572:U:H2'	4:3:1573:A:H8	1.84	0.43
4:3:2124:A:C6	4:3:2174:G:N2	2.87	0.43
4:3:2794:U:H5''	33:b:72:LYS:CD	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:2802:C:N4	4:3:2803:G:H21	2.17	0.43
4:3:2841:A:H2'	4:3:2842:G:C8	2.52	0.43
6:5:1226:A:H2'	6:5:1227:A:C8	2.54	0.43
9:A:38:ASN:HB3	9:A:41:MET:CB	2.49	0.43
12:D:96:ASN:CG	12:D:98:LYS:HG2	2.44	0.43
14:F:151:ALA:O	14:F:152:HIS:C	2.62	0.43
19:K:122:LYS:HG2	19:K:122:LYS:O	2.19	0.43
21:M:34:LEU:O	21:M:38:GLY:N	2.51	0.43
23:O:40:ASN:O	23:O:47:LYS:HE2	2.18	0.43
11:U:52:GLN:HA	11:U:55:GLN:OE1	2.18	0.43
11:U:141:LYS:HD3	11:U:175:GLU:OE1	2.19	0.43
34:c:26:ALA:HB2	34:c:113:HIS:NE2	2.33	0.43
46:o:25:PHE:CE2	46:o:55:ARG:HD2	2.54	0.43
52:u:86:PHE:CE1	52:u:92:LYS:HB3	2.54	0.43
1:0:3:ARG:NE	4:3:1647:A:O2'	2.52	0.43
4:3:322:A:H2'	4:3:323:A:C8	2.53	0.43
4:3:479:A:OP1	34:c:47:GLN:N	2.49	0.43
4:3:630:C:O2'	42:k:11:LYS:O	2.36	0.43
4:3:710:A:N3	4:3:2451:C:O2'	2.49	0.43
4:3:2190:G:H2'	4:3:2191:G:C8	2.54	0.43
4:3:2781:C:H2'	4:3:2782:A:C8	2.53	0.43
6:5:172:C:O2'	27:S:48:TYR:OH	2.22	0.43
6:5:406:G:O5'	11:C:27:LYS:NZ	2.38	0.43
9:A:40:LYS:O	9:A:43:PHE:HD2	2.02	0.43
9:A:227:LEU:O	9:A:231:LEU:HG	2.19	0.43
12:D:132:HIS:ND1	12:D:137:TYR:HB2	2.34	0.43
12:D:212:ARG:HA	12:D:212:ARG:HD2	1.89	0.43
13:E:80:LYS:HB2	13:E:81:GLN:OE1	2.19	0.43
23:O:9:MET:HE1	23:O:18:ARG:HG2	2.01	0.43
11:U:68:ASP:O	11:U:72:ARG:HG3	2.19	0.43
11:U:111:ARG:NH1	11:U:114:ARG:HG2	2.33	0.43
32:a:26:LEU:HD11	32:a:88:TYR:HB2	2.01	0.43
34:c:161:VAL:O	34:c:182:HIS:HA	2.18	0.43
35:d:50:LEU:O	35:d:53:ALA:HB3	2.18	0.43
36:e:120:ILE:HA	36:e:147:PHE:HE2	1.84	0.43
43:l:41:TRP:HE1	43:l:96:VAL:HG22	1.84	0.43
53:v:10:ARG:NH2	53:v:51:SER:OG	2.52	0.43
55:x:60:GLU:O	55:x:63:SER:OG	2.27	0.43
4:3:185:U:O4	34:c:59:ARG:NH2	2.51	0.43
4:3:397:G:H2'	4:3:398:C:C6	2.54	0.43
4:3:433:A:H3'	53:v:53:ARG:NH1	2.31	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:1293:U:H1'	56:y:7:ARG:CZ	2.48	0.43
4:3:1699:A:N1	4:3:2003:C:N4	2.67	0.43
4:3:1755:A:H2'	4:3:1756:A:C8	2.54	0.43
4:3:2164:G:O2'	4:3:2165:A:P	2.76	0.43
4:3:2204:C:H2'	4:3:2205:U:C6	2.54	0.43
4:3:2267:G:H2'	4:3:2268:C:C6	2.54	0.43
6:5:380:G:H2'	6:5:381:C:O4'	2.19	0.43
6:5:1279:G:O2'	6:5:1280:A:O4'	2.37	0.43
9:A:228:LEU:HD12	9:A:229:MET:HG3	2.01	0.43
10:B:70:TYR:HB3	10:B:109:ILE:HD13	2.01	0.43
11:C:170:ASN:HB2	11:C:175:GLU:HG2	1.99	0.43
11:C:179:VAL:CG1	11:C:180:ARG:H	2.17	0.43
20:L:20:THR:HG22	20:L:27:LEU:HA	1.99	0.43
20:L:65:ILE:HG22	20:L:67:GLY:H	1.83	0.43
20:L:79:HIS:O	20:L:82:GLU:HG2	2.19	0.43
25:Q:41:CYS:HA	25:Q:78:ASN:HA	2.01	0.43
26:R:14:HIS:HA	26:R:17:LYS:HZ2	1.84	0.43
11:U:124:LEU:HB2	11:U:129:VAL:HG23	2.01	0.43
49:r:64:MET:HE2	49:r:64:MET:HB2	1.93	0.43
51:t:3:ARG:NH1	51:t:74:LEU:O	2.50	0.43
4:3:9:G:H5'	40:i:135:MET:HE1	2.01	0.43
4:3:227:A:H5'	4:3:228:A:H5'	2.01	0.43
4:3:279:U:H2'	4:3:280:A:H8	1.83	0.43
4:3:1619:A:H8	4:3:1619:A:H5''	1.84	0.43
4:3:2105:G:N2	4:3:2200:U:C2	2.87	0.43
4:3:2113:U:C4	4:3:2191:G:C6	3.07	0.43
4:3:2340:U:OP1	52:u:92:LYS:NZ	2.51	0.43
6:5:256:G:OP2	27:S:71:ARG:NH1	2.52	0.43
6:5:499:U:H2'	6:5:500:G:C8	2.53	0.43
6:5:520:C:H41	19:K:63:ARG:NH2	2.17	0.43
6:5:704:U:OP1	18:J:80:LYS:NZ	2.33	0.43
6:5:1076:U:H3'	6:5:1077:U:C6	2.54	0.43
8:7:28:C:H2'	8:7:29:U:C6	2.54	0.43
12:D:211:LEU:C	12:D:213:ASN:N	2.77	0.43
16:H:83:LEU:HA	16:H:86:VAL:HG12	2.01	0.43
19:K:49:ARG:CZ	19:K:67:LYS:HG2	2.49	0.43
19:K:99:ARG:NH1	19:K:100:VAL:O	2.52	0.43
26:R:69:HIS:HB2	26:R:74:PHE:CZ	2.53	0.43
28:T:16:LYS:NZ	30:Y:30:G:OP1	2.45	0.43
37:f:33:LYS:CB	37:f:35:LEU:HD23	2.49	0.43
4:3:54:A:OP2	4:3:118:G:N1	2.45	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:174:A:H2'	4:3:175:A:C8	2.53	0.42
4:3:2376:C:H2'	4:3:2377:A:C8	2.54	0.42
4:3:2565:G:H2'	4:3:2566:C:C6	2.55	0.42
4:3:2657:C:H2'	4:3:2658:U:C6	2.54	0.42
6:5:616:C:H5''	6:5:617:U:H5''	2.00	0.42
6:5:674:U:O2	6:5:774:A:O2'	2.37	0.42
6:5:1048:G:H5'	10:B:158:GLY:HA2	2.01	0.42
7:6:17:U:H5'	7:6:18:G:H5'	2.01	0.42
9:A:16:GLU:HG3	9:A:249:LYS:O	2.19	0.42
9:A:126:SER:HA	9:A:129:LYS:NZ	2.34	0.42
11:C:67:THR:HG22	11:C:69:LYS:H	1.84	0.42
12:D:55:ARG:C	12:D:56:ARG:HH11	2.27	0.42
13:E:16:GLU:OE2	13:E:17:GLN:HG2	2.20	0.42
14:F:26:ILE:HG21	14:F:39:GLN:OE1	2.19	0.42
14:F:84:TYR:O	14:F:85:GLN:C	2.60	0.42
15:G:76:TYR:CE1	15:G:82:PRO:HB3	2.54	0.42
17:I:70:GLN:CB	21:M:61:TRP:CH2	3.01	0.42
11:U:95:SER:OG	11:U:136:LEU:N	2.51	0.42
38:g:55:LYS:HB2	38:g:58:ILE:CG2	2.47	0.42
39:h:94:GLY:O	39:h:133:ILE:HG23	2.19	0.42
4:3:449:C:H2'	4:3:450:C:C6	2.54	0.42
4:3:848:U:OP2	42:k:25:GLY:N	2.41	0.42
4:3:849:C:H1'	4:3:1255:G:H21	1.83	0.42
4:3:868:C:H2'	4:3:869:U:C6	2.54	0.42
4:3:1063:A:N6	4:3:1160:G:H2'	2.34	0.42
4:3:1334:U:H2'	4:3:1335:A:H8	1.83	0.42
4:3:1495:A:H2'	4:3:1496:A:C8	2.54	0.42
4:3:2104:A:H2'	4:3:2105:G:H8	1.82	0.42
6:5:1509:A:H2	9:A:293:ARG:HD2	1.84	0.42
9:A:27:ARG:HE	9:A:221:GLN:NE2	2.17	0.42
10:B:90:LYS:HE3	10:B:93:LYS:NZ	2.33	0.42
10:B:109:ILE:CD1	10:B:222:ILE:HA	2.48	0.42
10:B:116:ALA:HB1	10:B:203:VAL:HG13	2.00	0.42
13:E:116:ASP:O	13:E:119:ILE:HG22	2.19	0.42
15:G:132:LYS:HD2	15:G:132:LYS:O	2.19	0.42
16:H:41:PHE:HB3	16:H:42:PRO:HD2	2.01	0.42
16:H:57:THR:O	16:H:58:ASP:HB3	2.20	0.42
20:L:43:LYS:NZ	20:L:48:LEU:HD13	2.34	0.42
22:N:29:LEU:O	22:N:33:ILE:HG12	2.19	0.42
25:Q:73:ARG:NH1	25:Q:79:CYS:HA	2.35	0.42
26:R:80:PHE:HZ	26:R:83:HIS:CD2	2.38	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:S:9:LYS:HE2	27:S:13:GLN:NE2	2.34	0.42
45:n:66:ASN:HB2	45:n:68:ASP:OD1	2.19	0.42
46:o:24:GLU:HA	46:o:55:ARG:NH1	2.35	0.42
46:o:56:ARG:HG2	46:o:57:GLY:H	1.84	0.42
4:3:153:U:H2'	4:3:154:U:C6	2.55	0.42
4:3:334:A:H2'	4:3:368:C:H1'	2.01	0.42
4:3:477:U:O2'	34:c:47:GLN:OE1	2.35	0.42
4:3:526:G:H2'	4:3:527:A:C8	2.54	0.42
4:3:880:C:H41	4:3:968:U:H2'	1.84	0.42
4:3:912:A:H2'	4:3:913:U:O4'	2.19	0.42
4:3:1261:U:H2'	4:3:1262:G:C8	2.54	0.42
4:3:1826:A:N1	32:a:282:ARG:NH2	2.67	0.42
4:3:1889:U:H2'	4:3:1890:U:C6	2.54	0.42
4:3:2176:G:H2'	4:3:2178:A:OP2	2.20	0.42
4:3:2541:C:H2'	4:3:2542:A:O4'	2.19	0.42
4:3:2586:G:H1'	33:b:143:PHE:CZ	2.55	0.42
6:5:433:C:H1'	11:C:153:ILE:HD11	2.01	0.42
6:5:573:G:H4'	6:5:574:C:O5'	2.19	0.42
6:5:818:A:H2'	6:5:819:G:H8	1.84	0.42
9:A:162:PHE:O	9:A:163:PHE:CD1	2.72	0.42
9:A:238:GLU:HG2	9:A:244:THR:OG1	2.20	0.42
11:C:53:GLN:OE1	11:C:199:TRP:CE3	2.72	0.42
11:C:123:LEU:CD1	11:C:143:ARG:HH12	2.32	0.42
13:E:45:LEU:HD12	25:Q:97:ALA:HB1	1.99	0.42
14:F:121:ASN:HA	14:F:124:ILE:HG22	2.01	0.42
14:F:142:LYS:HA	14:F:142:LYS:HD3	1.78	0.42
27:S:33:LYS:HA	27:S:36:HIS:CD2	2.54	0.42
34:c:116:TRP:CZ2	34:c:207:LEU:HD11	2.55	0.42
39:h:46:LYS:HB2	39:h:51:ILE:HD11	2.00	0.42
44:m:57:PHE:O	44:m:61:ARG:HG3	2.19	0.42
47:p:50:ARG:H	47:p:50:ARG:HG2	1.68	0.42
52:u:6:PHE:CD2	52:u:7:LEU:N	2.86	0.42
3:2:1:MET:SD	3:2:33:LYS:HE2	2.59	0.42
4:3:665:C:O2	4:3:675:U:O2'	2.37	0.42
4:3:2638:G:H2'	4:3:2639:G:C8	2.54	0.42
5:4:65:G:H2'	5:4:66:A:H8	1.83	0.42
6:5:335:C:H2'	6:5:336:U:H6	1.84	0.42
6:5:664:A:H2'	6:5:665:G:C8	2.54	0.42
6:5:690:G:H5'	30:Y:36:U:C6	2.54	0.42
6:5:1070:G:H2'	6:5:1071:A:C8	2.54	0.42
6:5:1485:C:H2'	6:5:1486:C:C6	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:54:U:H2'	7:6:55:U:C6	2.55	0.42
9:A:127:ILE:HD13	9:A:163:PHE:HB3	2.00	0.42
9:A:161:LYS:HG3	9:A:162:PHE:CD2	2.54	0.42
12:D:54:ASN:CG	12:D:55:ARG:H	2.27	0.42
14:F:15:PRO:HB3	16:H:45:LEU:HD13	2.01	0.42
15:G:27:LYS:HD3	15:G:27:LYS:HA	1.92	0.42
15:G:45:LEU:HD13	15:G:57:PHE:HB2	2.02	0.42
15:G:56:ASN:OD1	15:G:73:ASN:HB2	2.20	0.42
15:G:87:VAL:HG12	15:G:141:VAL:HG22	2.00	0.42
19:K:21:SER:HB2	19:K:108:TYR:HE2	1.84	0.42
33:b:56:THR:HA	33:b:78:THR:HG22	2.00	0.42
34:c:182:HIS:O	34:c:186:VAL:HG13	2.20	0.42
36:e:174:ARG:HD3	36:e:174:ARG:H	1.84	0.42
41:j:88:LYS:HG2	41:j:94:ARG:NH1	2.33	0.42
41:j:104:ARG:NH1	41:j:122:VAL:OXT	2.52	0.42
52:u:44:MET:N	52:u:44:MET:SD	2.92	0.42
53:v:63:ARG:C	53:v:65:SER:N	2.78	0.42
55:x:15:LYS:O	55:x:36:ILE:HG22	2.20	0.42
4:3:915:A:C6	4:3:916:U:C2	3.08	0.42
4:3:1090:G:H4'	38:g:32:MET:O	2.19	0.42
4:3:1094:G:H2'	4:3:1095:U:C5	2.55	0.42
4:3:2342:U:C4	45:n:10:LEU:HD21	2.55	0.42
4:3:2343:A:H5''	4:3:2343:A:H8	1.85	0.42
4:3:2453:G:OP1	34:c:75:ARG:NH2	2.46	0.42
4:3:2843:G:N2	44:m:94:PRO:O	2.42	0.42
6:5:681:U:H1'	18:J:33:ASN:HA	2.00	0.42
6:5:951:U:H3	6:5:955:U:H3	1.67	0.42
6:5:1058:A:N1	6:5:1099:G:O2'	2.49	0.42
6:5:1374:C:O2	6:5:1477:A:N6	2.52	0.42
7:6:1:G:HO2'	7:6:2:G:P	2.42	0.42
10:B:189:LEU:HG	10:B:202:LYS:HZ2	1.84	0.42
12:D:199:ILE:HD12	12:D:199:ILE:HA	1.93	0.42
15:G:47:ILE:HD11	15:G:115:ILE:HG23	2.02	0.42
15:G:114:ALA:HB3	15:G:125:ASP:HB3	2.01	0.42
17:I:50:THR:HB	17:I:74:ASN:OD1	2.19	0.42
18:J:10:SER:O	18:J:72:MET:HB2	2.19	0.42
28:T:34:TYR:CE2	28:T:36:LEU:HD23	2.54	0.42
30:Y:44:A:H2'	30:Y:45:G:C8	2.55	0.42
32:a:137:PRO:HA	32:a:197:ARG:HA	2.02	0.42
4:3:1815:U:O2'	4:3:1816:A:O4'	2.37	0.42
4:3:2094:A:H2'	4:3:2095:A:H8	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:2190:G:H5'	4:3:2190:G:C8	2.52	0.42
4:3:2537:G:H5''	4:3:2538:A:H5''	2.01	0.42
6:5:388:G:H3'	6:5:389:A:C8	2.54	0.42
6:5:680:G:H21	18:J:33:ASN:H	1.68	0.42
6:5:818:A:H2'	6:5:819:G:C8	2.55	0.42
6:5:989:A:C5	6:5:1191:U:H4'	2.55	0.42
6:5:1078:G:H5'	6:5:1078:G:C8	2.54	0.42
9:A:253:GLU:OE2	9:A:254:ILE:HG13	2.20	0.42
11:C:125:ASN:HA	11:C:141:LYS:O	2.20	0.42
12:D:61:ALA:O	12:D:62:PHE:C	2.62	0.42
13:E:81:GLN:O	13:E:82:VAL:C	2.62	0.42
13:E:139:THR:OG1	13:E:140:GLN:N	2.51	0.42
15:G:40:LEU:O	15:G:44:ILE:HG23	2.20	0.42
15:G:131:LYS:HB3	15:G:133:ILE:HG12	2.01	0.42
17:I:56:THR:HG23	17:I:70:GLN:CG	2.45	0.42
17:I:100:VAL:HG23	17:I:101:GLY:H	1.84	0.42
11:U:97:LEU:HD12	11:U:136:LEU:HD21	2.01	0.42
32:a:128:ILE:HD12	32:a:136:MET:SD	2.59	0.42
32:a:151:GLU:HG2	32:a:157:GLY:C	2.44	0.42
35:d:7:HIS:CE1	35:d:11:THR:HG21	2.55	0.42
38:g:97:ASP:HA	38:g:100:VAL:HG22	2.00	0.42
4:3:313:G:H5''	11:U:62:TYR:HE2	1.84	0.42
4:3:450:C:H2'	4:3:451:A:C8	2.55	0.42
4:3:852:C:H2'	4:3:853:G:O4'	2.19	0.42
4:3:921:C:C4	4:3:922:C:C4	3.07	0.42
4:3:934:C:C4	4:3:935:U:C4	3.08	0.42
4:3:1372:U:O2	4:3:1413:A:H5'	2.20	0.42
4:3:1564:U:H2'	4:3:1565:G:C8	2.55	0.42
4:3:1780:A:N7	4:3:1836:A:H1'	2.35	0.42
4:3:2691:C:H5'	46:o:61:SER:HB3	2.02	0.42
6:5:38:U:OP1	19:K:133:LYS:NZ	2.49	0.42
6:5:883:A:N1	6:5:901:A:H5''	2.34	0.42
6:5:1215:U:H4'	14:F:37:LEU:HD21	2.02	0.42
10:B:49:ARG:C	10:B:51:ALA:H	2.28	0.42
10:B:113:MET:HE2	10:B:144:VAL:O	2.19	0.42
15:G:57:PHE:HA	15:G:72:PHE:HA	2.02	0.42
23:O:43:LEU:HB3	23:O:47:LYS:HD2	2.00	0.42
25:Q:38:LYS:HE2	25:Q:74:ARG:HA	2.00	0.42
27:S:28:LEU:HD22	27:S:54:LEU:HD12	2.02	0.42
11:U:4:THR:HG23	11:U:4:THR:O	2.20	0.42
11:U:41:ARG:O	11:U:42:PHE:HB3	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:U:82:ARG:O	11:U:82:ARG:NH1	2.49	0.42
32:a:262:HIS:CD2	32:a:263:MET:HE2	2.55	0.42
35:d:92:ARG:HA	35:d:96:MET:SD	2.59	0.42
40:i:135:MET:HA	40:i:135:MET:HE3	2.01	0.42
43:l:37:THR:O	43:l:37:THR:HG22	2.19	0.42
4:3:916:U:C2	4:3:917:G:C8	3.08	0.42
4:3:929:G:H3'	4:3:930:C:C6	2.55	0.42
4:3:1688:A:N7	4:3:2012:A:H2	2.18	0.42
4:3:1915:C:O2'	8:7:12:G:H5''	2.20	0.42
4:3:1956:G:H2'	4:3:1957:G:H8	1.85	0.42
4:3:2081:U:H2'	4:3:2082:U:C6	2.54	0.42
4:3:2568:G:H2'	4:3:2569:A:C8	2.55	0.42
5:4:81:U:H2'	5:4:82:U:O4'	2.20	0.42
6:5:133:G:H2'	6:5:134:G:H8	1.85	0.42
6:5:660:A:H2'	6:5:661:G:O4'	2.20	0.42
6:5:1032:G:H2'	6:5:1033:U:O4'	2.19	0.42
6:5:1098:C:H2'	6:5:1099:G:O4'	2.20	0.42
6:5:1488:A:H2'	6:5:1489:C:C6	2.54	0.42
9:A:148:GLU:HA	9:A:151:MET:HG2	2.02	0.42
11:C:8:PHE:CE1	11:C:23:LYS:HE2	2.55	0.42
24:P:55:ALA:HB2	24:P:80:ILE:HD11	2.02	0.42
25:Q:48:GLN:HG3	25:Q:50:ARG:O	2.20	0.42
26:R:17:LYS:HA	26:R:20:ILE:HG22	2.01	0.42
32:a:27:THR:HG21	32:a:85:SER:HA	2.01	0.42
33:b:14:SER:OG	33:b:15:GLN:N	2.53	0.42
36:e:34:ILE:HD11	36:e:139:ILE:HG13	2.02	0.42
37:f:66:HIS:CE1	37:f:138:LEU:HD11	2.55	0.42
40:i:118:SER:HA	40:i:121:TRP:HB2	2.02	0.42
43:l:65:TRP:HB2	43:l:105:GLU:CG	2.49	0.42
44:m:17:THR:O	44:m:21:GLN:HG3	2.19	0.42
4:3:2128:G:H2'	4:3:2129:U:H6	1.84	0.42
4:3:2167:G:C2'	4:3:2168:C:H5'	2.49	0.42
4:3:2529:C:O2'	4:3:2572:A:N3	2.44	0.42
6:5:20:C:O2'	6:5:570:A:N1	2.51	0.42
6:5:331:C:H2'	6:5:332:A:C8	2.54	0.42
6:5:906:C:H2'	6:5:907:A:C8	2.54	0.42
7:6:18:G:N7	7:6:57:G:N2	2.68	0.42
8:7:50:G:H2'	8:7:51:G:C8	2.55	0.42
9:A:152:LEU:O	9:A:155:GLU:HG3	2.20	0.42
9:A:185:LYS:HA	9:A:188:VAL:HG12	2.01	0.42
10:B:40:ILE:HG12	10:B:95:ILE:HG21	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:67:VAL:HB	10:B:104:LEU:HD23	2.02	0.42
12:D:160:ILE:HG13	12:D:176:SER:O	2.19	0.42
16:H:23:PRO:HB3	16:H:61:LYS:NZ	2.34	0.42
16:H:34:ARG:HG2	16:H:34:ARG:NH1	2.34	0.42
16:H:129:PHE:HE1	16:H:131:LYS:HB2	1.85	0.42
32:a:84:LYS:CE	32:a:98:LEU:HD23	2.49	0.42
37:f:75:THR:HG22	37:f:77:LEU:HB2	2.01	0.42
40:i:48:THR:HG22	40:i:50:ASN:OD1	2.20	0.42
41:j:92:SER:HA	41:j:93:PRO:HD3	1.90	0.42
42:k:20:LEU:O	42:k:32:SER:OG	2.25	0.42
52:u:78:ASP:HB3	52:u:100:HIS:NE2	2.35	0.42
3:2:4:ARG:HB3	4:3:2474:C:OP1	2.19	0.42
4:3:10:U:H2'	4:3:11:U:H4'	2.01	0.42
4:3:618:G:H3'	4:3:1281:A:H61	1.84	0.42
4:3:859:G:H2'	4:3:860:C:C6	2.54	0.42
4:3:914:G:C8	4:3:914:G:H5''	2.54	0.42
4:3:1092:A:N7	4:3:1121:A:H2'	2.35	0.42
4:3:1120:A:H2'	4:3:1121:A:C4	2.54	0.42
4:3:1859:U:H5''	7:6:72:C:OP1	2.20	0.42
4:3:1879:A:H2'	4:3:1880:G:O4'	2.20	0.42
4:3:2054:C:H2'	4:3:2055:A:H8	1.85	0.42
4:3:2624:C:C4	4:3:2625:U:C4	3.08	0.42
4:3:2743:U:H2'	4:3:2744:A:H8	1.84	0.42
6:5:516:C:H2'	6:5:528:G:C4	2.55	0.42
6:5:945:U:H2'	6:5:946:G:H8	1.84	0.42
6:5:1087:C:O2'	6:5:1145:A:O2'	2.32	0.42
6:5:1163:A:O2'	21:M:58:LYS:NZ	2.35	0.42
9:A:144:LEU:HB3	9:A:149:ASN:CG	2.45	0.42
13:E:31:ASN:HB2	13:E:65:ASP:OD1	2.19	0.42
13:E:75:THR:O	13:E:79:ASN:HB2	2.20	0.42
14:F:138:ASP:O	14:F:142:LYS:HG2	2.19	0.42
19:K:50:VAL:HG21	19:K:87:LEU:HB3	2.01	0.42
26:R:86:ASN:OD1	26:R:87:ARG:N	2.53	0.42
27:S:11:LEU:O	27:S:15:ILE:HG13	2.20	0.42
28:T:30:GLN:O	28:T:33:GLU:HG3	2.19	0.42
35:d:104:ILE:HG23	35:d:105:TYR:HD1	1.85	0.42
40:i:93:ARG:HG3	40:i:97:LYS:HE3	2.02	0.42
3:2:25:VAL:O	3:2:33:LYS:HA	2.20	0.41
4:3:190:G:H2'	4:3:191:G:H8	1.85	0.41
4:3:547:G:OP1	4:3:1264:U:O2'	2.33	0.41
4:3:634:C:O2'	4:3:639:G:H5''	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:648:G:O6	34:c:181:LYS:NZ	2.52	0.41
4:3:755:C:H2'	4:3:756:A:C8	2.54	0.41
4:3:784:A:H4'	4:3:1301:G:N3	2.35	0.41
4:3:847:C:H5''	4:3:1280:G:O2'	2.20	0.41
4:3:923:A:H1'	4:3:927:A:H61	1.85	0.41
4:3:1003:U:H2'	4:3:1004:U:C6	2.55	0.41
4:3:1392:G:N2	4:3:1395:A:OP2	2.45	0.41
4:3:1709:C:H2'	4:3:1710:A:O4'	2.20	0.41
4:3:2060:G:C5'	33:b:151:ARG:HB2	2.50	0.41
4:3:2207:A:N1	4:3:2234:C:N4	2.67	0.41
6:5:20:C:H2'	6:5:21:U:C6	2.55	0.41
6:5:725:A:H2'	6:5:726:A:C8	2.55	0.41
6:5:1243:A:H1'	6:5:1300:C:O2'	2.20	0.41
6:5:1378:C:H6	6:5:1378:C:O5'	2.03	0.41
10:B:52:GLN:HE22	10:B:122:ASP:CG	2.28	0.41
11:C:27:LYS:HD3	11:C:27:LYS:HA	1.90	0.41
11:C:84:ASN:HB3	12:D:156:GLN:O	2.20	0.41
12:D:59:LYS:HB3	12:D:59:LYS:HE2	1.82	0.41
13:E:10:ASP:O	13:E:56:HIS:HD2	2.03	0.41
17:I:79:LEU:HD23	17:I:80:MET:N	2.35	0.41
19:K:48:THR:O	19:K:49:ARG:HB3	2.20	0.41
19:K:70:LEU:HD12	19:K:70:LEU:H	1.85	0.41
26:R:36:ARG:CZ	26:R:52:HIS:O	2.68	0.41
28:T:47:LYS:HE2	28:T:51:LYS:HE3	2.02	0.41
32:a:98:LEU:HD12	32:a:107:SER:O	2.20	0.41
33:b:123:ILE:H	33:b:123:ILE:HD12	1.86	0.41
33:b:182:VAL:HA	33:b:220:ILE:HD11	2.01	0.41
39:h:99:ALA:HA	39:h:102:LYS:HG2	2.02	0.41
40:i:99:GLN:O	40:i:99:GLN:HG2	2.19	0.41
44:m:93:THR:HB	44:m:97:TYR:HE1	1.85	0.41
46:o:28:GLY:HA3	46:o:96:VAL:HG11	2.01	0.41
3:2:1:MET:CE	3:2:33:LYS:HE2	2.50	0.41
4:3:410:G:OP1	11:U:18:LEU:HD11	2.20	0.41
4:3:481:C:N4	4:3:482:G:O6	2.53	0.41
4:3:910:G:H1'	43:l:29:PHE:CE2	2.55	0.41
4:3:1456:C:C5	4:3:1603:A:H5''	2.55	0.41
4:3:2811:G:H2'	4:3:2812:U:C6	2.55	0.41
6:5:57:U:H2'	6:5:58:G:C8	2.53	0.41
6:5:111:A:OP1	6:5:603:U:O2'	2.37	0.41
6:5:196:G:H2'	6:5:197:A:H5''	2.02	0.41
6:5:474:G:O2'	6:5:475:U:H5'	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:594:A:H2'	24:P:29:ARG:HH21	1.84	0.41
6:5:909:A:O2'	6:5:911:G:H5''	2.19	0.41
6:5:1023:G:O2'	6:5:1024:U:H5''	2.20	0.41
9:A:22:LYS:O	9:A:26:MET:HG2	2.19	0.41
9:A:286:ARG:NH1	9:A:287:ASN:OD1	2.53	0.41
10:B:78:ILE:HG23	10:B:82:ASN:OD1	2.21	0.41
10:B:223:LEU:O	10:B:225:PRO:HD2	2.20	0.41
11:C:87:VAL:HG23	11:C:184:ARG:HD2	2.02	0.41
13:E:157:TRP:HB3	15:G:60:LEU:HB3	2.01	0.41
13:E:163:MET:HE3	15:G:49:VAL:HG11	2.02	0.41
14:F:12:LEU:H	14:F:13:PRO:CD	2.31	0.41
14:F:59:THR:HA	14:F:62:GLU:HG2	2.02	0.41
16:H:99:ILE:HG13	16:H:103:LYS:NZ	2.35	0.41
18:J:79:VAL:N	18:J:104:ASN:O	2.50	0.41
20:L:64:LYS:HZ1	20:L:72:GLU:CD	2.26	0.41
22:N:3:ILE:HD11	22:N:32:GLN:OE1	2.20	0.41
22:N:41:LEU:HD12	22:N:44:LYS:HZ1	1.85	0.41
23:O:50:ILE:HG13	23:O:51:ASP:H	1.86	0.41
27:S:11:LEU:HA	27:S:14:ASN:ND2	2.35	0.41
32:a:148:HIS:HB2	32:a:161:ALA:O	2.20	0.41
34:c:143:MET:SD	34:c:143:MET:C	3.03	0.41
36:e:16:VAL:HA	36:e:28:LYS:O	2.20	0.41
37:f:103:THR:HG23	37:f:104:LYS:N	2.35	0.41
38:g:58:ILE:HA	38:g:61:ARG:NH1	2.35	0.41
45:n:32:VAL:HG12	45:n:41:VAL:HG23	2.02	0.41
46:o:93:ARG:NH2	46:o:118:LYS:O	2.53	0.41
55:x:61:LYS:HG3	55:x:62:LEU:HD12	2.02	0.41
1:0:29:LYS:HA	1:0:32:LYS:HE3	2.02	0.41
3:2:27:CYS:SG	3:2:28:LYS:N	2.94	0.41
4:3:28:G:H1'	4:3:549:A:H61	1.85	0.41
4:3:180:A:H5'	4:3:181:G:N7	2.35	0.41
4:3:1621:U:H2'	4:3:1622:C:C6	2.55	0.41
4:3:1801:U:H2'	4:3:1802:C:C6	2.55	0.41
4:3:1803:U:H2'	4:3:1804:A:C8	2.55	0.41
4:3:2194:G:H3'	4:3:2195:U:H5''	2.02	0.41
4:3:2294:A:H4'	4:3:2295:A:O4'	2.20	0.41
5:4:37:A:H2'	5:4:38:U:C6	2.56	0.41
6:5:63:U:H1'	6:5:375:C:H1'	2.02	0.41
6:5:459:C:H2'	6:5:460:A:O4'	2.19	0.41
6:5:649:U:H1'	6:5:650:A:C8	2.55	0.41
6:5:672:A:H1'	18:J:111:HIS:CE1	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:1026:A:N3	6:5:1026:A:H2'	2.35	0.41
6:5:1306:A:H2'	6:5:1307:A:O4'	2.19	0.41
6:5:1347:U:H2'	6:5:1348:G:O4'	2.20	0.41
9:A:32:MET:HE3	9:A:33:VAL:HG23	2.03	0.41
11:C:191:ILE:HG23	11:C:191:ILE:O	2.20	0.41
12:D:78:LYS:HG2	12:D:85:ASN:HB2	2.01	0.41
14:F:9:ARG:HG3	14:F:9:ARG:O	2.19	0.41
14:F:83:ASN:HD21	14:F:85:GLN:CD	2.28	0.41
15:G:54:LEU:H	15:G:54:LEU:HD23	1.86	0.41
16:H:36:ASP:OD2	16:H:38:SER:OG	2.36	0.41
17:I:59:ARG:HA	21:M:45:ARG:HH21	1.84	0.41
17:I:85:VAL:HG23	17:I:86:ASN:N	2.34	0.41
17:I:98:ILE:O	17:I:98:ILE:HG13	2.19	0.41
27:S:56:ARG:HH12	27:S:57:LYS:HZ2	1.68	0.41
11:U:99:ASN:HA	11:U:110:ARG:NE	2.35	0.41
32:a:255:ARG:C	32:a:262:HIS:HE1	2.28	0.41
39:h:80:ALA:HA	39:h:96:ILE:HD11	2.02	0.41
41:j:94:ARG:HA	41:j:94:ARG:CZ	2.51	0.41
44:m:89:LYS:HE2	44:m:89:LYS:HB3	1.84	0.41
47:p:6:GLY:O	47:p:7:LYS:HB3	2.18	0.41
47:p:68:LEU:HD11	47:p:78:PHE:CD1	2.56	0.41
49:r:58:ALA:O	49:r:64:MET:HG3	2.20	0.41
50:s:19:ASN:C	50:s:21:MET:H	2.28	0.41
54:w:58:LEU:HD23	54:w:65:TRP:HB3	2.01	0.41
3:2:1:MET:HE3	4:3:2534:G:O2'	2.20	0.41
4:3:2054:C:O2'	4:3:2827:A:N1	2.46	0.41
4:3:2122:G:H1	4:3:2126:A:P	2.39	0.41
4:3:2623:U:H1'	56:y:4:GLN:HG3	2.02	0.41
5:4:31:G:O6	5:4:48:A:N6	2.53	0.41
6:5:954:A:N7	26:R:78:ARG:CZ	2.83	0.41
6:5:1105:C:H1'	21:M:60:SER:CB	2.50	0.41
6:5:1258:U:H2'	6:5:1259:G:C8	2.55	0.41
6:5:1438:U:H2'	6:5:1439:G:C8	2.50	0.41
7:6:74:C:O2'	7:6:75:C:P	2.78	0.41
11:C:49:GLY:HA2	11:C:52:GLN:HE21	1.85	0.41
12:D:166:ILE:HG21	12:D:180:THR:HG21	2.01	0.41
15:G:23:ASN:ND2	15:G:87:VAL:HG22	2.35	0.41
16:H:121:TYR:HE1	16:H:127:PRO:HG3	1.84	0.41
17:I:31:ILE:HG13	17:I:32:VAL:N	2.35	0.41
34:c:79:THR:O	34:c:80:ARG:NH1	2.52	0.41
42:k:47:THR:OG1	42:k:48:ARG:N	2.52	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:l:73:SER:O	43:l:74:LYS:HD2	2.19	0.41
48:q:2:HIS:HB3	48:q:15:HIS:CE1	2.56	0.41
51:t:26:LYS:NZ	51:t:28:MET:SD	2.77	0.41
51:t:34:ALA:HB3	51:t:74:LEU:HD11	2.03	0.41
55:x:94:LEU:O	55:x:98:ASN:OD1	2.39	0.41
4:3:1230:U:H2'	4:3:1231:G:C8	2.56	0.41
4:3:1573:A:H2'	4:3:1574:G:O4'	2.20	0.41
4:3:1778:G:H2'	4:3:1779:G:C8	2.55	0.41
4:3:1825:U:OP2	32:a:162:ARG:NH2	2.53	0.41
4:3:2293:C:OP1	57:z:27:LYS:HG3	2.20	0.41
4:3:2701:A:H2'	4:3:2702:G:H8	1.85	0.41
6:5:421:G:H5''	6:5:422:A:OP2	2.21	0.41
6:5:1351:U:H2'	6:5:1352:A:H8	1.85	0.41
10:B:7:SER:OG	10:B:204:TRP:NE1	2.44	0.41
11:C:17:SER:OG	11:C:21:ASN:N	2.54	0.41
13:E:135:GLY:CA	25:Q:35:LYS:HE2	2.50	0.41
15:G:126:LYS:HA	15:G:126:LYS:HD2	1.80	0.41
16:H:121:TYR:CE1	16:H:127:PRO:HG3	2.55	0.41
17:I:96:ILE:HG22	55:x:94:LEU:HD11	2.02	0.41
24:P:63:ILE:HG23	24:P:75:PHE:HB3	2.02	0.41
28:T:56:PHE:HA	28:T:59:MET:CG	2.50	0.41
29:X:37:ASN:N	29:X:45:LYS:HD3	2.16	0.41
34:c:125:THR:HG22	34:c:125:THR:O	2.20	0.41
35:d:39:GLY:HA2	35:d:86:GLY:HA2	2.02	0.41
35:d:106:VAL:HG12	35:d:139:PRO:HG3	2.03	0.41
43:l:32:TYR:HE2	43:l:111:GLU:OE1	2.04	0.41
47:p:70:GLU:OE1	47:p:70:GLU:N	2.53	0.41
47:p:73:MET:HE2	47:p:81:LEU:HD11	2.02	0.41
47:p:87:ILE:HA	48:q:47:ALA:O	2.20	0.41
52:u:10:ILE:O	52:u:11:ASP:CG	2.63	0.41
4:3:24:U:H2'	4:3:25:G:C8	2.56	0.41
4:3:193:G:O6	4:3:209:G:O2'	2.34	0.41
4:3:764:G:C4	32:a:215:LYS:HD2	2.56	0.41
4:3:767:C:H2'	4:3:768:G:O4'	2.20	0.41
4:3:1275:C:H5''	42:k:13:ARG:NH1	2.35	0.41
4:3:1894:U:H1'	4:3:2109:A:P	2.60	0.41
4:3:1992:C:H2'	4:3:1993:U:C6	2.55	0.41
4:3:2132:G:N2	4:3:2181:A:OP2	2.53	0.41
4:3:2173:G:H3'	4:3:2174:G:H8	1.85	0.41
4:3:2190:G:C2	4:3:2191:G:C4	3.08	0.41
4:3:2321:C:H2'	4:3:2322:G:C8	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:2356:U:H5'	57:z:19:TYR:OH	2.20	0.41
4:3:2820:G:O4'	56:y:40:HIS:ND1	2.54	0.41
5:4:29:C:O2'	5:4:51:A:N1	2.42	0.41
6:5:579:G:N1	6:5:756:A:OP2	2.32	0.41
6:5:648:C:H2'	6:5:649:U:C6	2.55	0.41
9:A:24:GLY:HA2	9:A:29:HIS:ND1	2.36	0.41
9:A:136:LYS:HE3	9:A:136:LYS:HB2	1.84	0.41
10:B:92:ILE:O	10:B:96:ILE:HG12	2.21	0.41
11:C:42:PHE:N	11:C:42:PHE:CD1	2.88	0.41
11:C:76:ARG:O	11:C:80:LYS:NZ	2.41	0.41
15:G:44:ILE:O	15:G:48:LEU:HD13	2.20	0.41
17:I:49:PRO:O	17:I:77:LYS:NZ	2.52	0.41
17:I:93:LEU:O	55:x:94:LEU:HD21	2.21	0.41
11:U:131:THR:HA	11:U:132:PRO:HD3	1.94	0.41
11:U:180:ARG:HD3	11:U:180:ARG:O	2.19	0.41
35:d:171:ARG:NH1	35:d:180:GLY:O	2.54	0.41
39:h:30:ILE:HG12	39:h:63:PHE:CE1	2.56	0.41
44:m:19:ARG:HB3	44:m:68:LEU:CD1	2.51	0.41
46:o:13:VAL:HA	46:o:16:LYS:HD2	2.03	0.41
4:3:474:U:H2'	4:3:475:A:H8	1.86	0.41
4:3:2094:A:H2'	4:3:2095:A:C8	2.55	0.41
4:3:2130:A:H2'	4:3:2131:G:O4'	2.21	0.41
4:3:2143:G:H2'	4:3:2144:C:C2	2.56	0.41
6:5:9:A:N6	11:C:198:GLU:OE1	2.53	0.41
6:5:69:G:H2'	6:5:70:A:O4'	2.21	0.41
6:5:199:A:N1	6:5:216:G:O2'	2.52	0.41
6:5:359:A:H5''	19:K:44:ARG:NH1	2.35	0.41
6:5:515:G:N2	6:5:531:A:OP2	2.35	0.41
6:5:578:C:H2'	6:5:579:G:O4'	2.20	0.41
6:5:661:G:O2'	6:5:722:G:O2'	2.35	0.41
7:6:35:G:H2'	7:6:36:C:C6	2.56	0.41
9:A:22:LYS:HD3	9:A:22:LYS:HA	1.87	0.41
9:A:43:PHE:HD1	9:A:44:PHE:CD1	2.39	0.41
10:B:45:PHE:HE1	10:B:56:VAL:HG12	1.85	0.41
10:B:74:PRO:HD3	10:B:108:GLU:OE1	2.20	0.41
11:C:103:ARG:NH1	11:C:110:ARG:HH22	2.14	0.41
11:C:106:PHE:HA	11:C:157:ALA:HA	2.02	0.41
12:D:70:ILE:HD13	12:D:92:VAL:HG22	2.02	0.41
14:F:21:LEU:HD21	14:F:65:VAL:HG11	2.02	0.41
14:F:62:GLU:HA	14:F:65:VAL:HG12	2.03	0.41
15:G:29:LYS:HG2	15:G:80:ARG:HH21	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:I:40:VAL:CG1	17:I:82:LEU:HD12	2.51	0.41
17:I:100:VAL:HG23	17:I:101:GLY:N	2.35	0.41
19:K:86:ASN:HD21	19:K:117:THR:HA	1.86	0.41
24:P:10:ILE:HG13	24:P:62:GLN:NE2	2.35	0.41
24:P:64:VAL:HG23	24:P:76:ARG:HG2	2.00	0.41
26:R:9:ALA:H	55:x:69:GLY:HA3	1.86	0.41
28:T:19:LYS:C	28:T:19:LYS:HD2	2.45	0.41
11:U:183:GLU:OE1	11:U:185:SER:OG	2.18	0.41
34:c:183:LEU:HD12	34:c:203:VAL:HG13	2.03	0.41
38:g:11:VAL:HG12	38:g:58:ILE:HG13	2.02	0.41
38:g:100:VAL:HG12	38:g:103:LYS:HE3	2.03	0.41
41:j:119:VAL:HG22	41:j:120:GLU:OE1	2.21	0.41
47:p:95:SER:O	47:p:99:ILE:HG12	2.21	0.41
55:x:21:ASN:HB2	55:x:23:PHE:CZ	2.55	0.41
4:3:117:C:H2'	4:3:118:G:O4'	2.19	0.41
4:3:270:G:O2'	11:U:38:HIS:CD2	2.74	0.41
4:3:297:G:N7	4:3:457:U:H2'	2.36	0.41
4:3:488:G:C8	34:c:59:ARG:HD2	2.55	0.41
4:3:1755:A:H2'	4:3:1756:A:H8	1.85	0.41
4:3:1816:A:H2'	4:3:1817:A:C8	2.55	0.41
4:3:1828:A:H2'	4:3:1829:U:C6	2.55	0.41
4:3:2162:U:O5'	4:3:2162:U:H6	2.03	0.41
6:5:271:G:H4'	24:P:18:ASN:OD1	2.21	0.41
6:5:389:A:OP1	23:O:13:HIS:NE2	2.53	0.41
6:5:1127:A:N3	17:I:47:PRO:HG3	2.36	0.41
6:5:1321:G:C8	16:H:111:ARG:HB3	2.56	0.41
9:A:117:LEU:HB3	9:A:194:LEU:HD11	2.02	0.41
12:D:74:LYS:HG3	12:D:75:ARG:H	1.85	0.41
15:G:38:SER:O	15:G:42:ILE:HG12	2.20	0.41
17:I:96:ILE:HD12	17:I:96:ILE:HA	1.88	0.41
25:Q:35:LYS:NZ	25:Q:40:TYR:HB3	2.35	0.41
25:Q:51:ILE:HG13	25:Q:51:ILE:O	2.21	0.41
26:R:67:VAL:HB	55:x:58:ARG:NH1	2.36	0.41
28:T:42:LEU:HD12	28:T:43:ARG:N	2.36	0.41
11:U:96:ARG:HD2	11:U:96:ARG:HA	1.56	0.41
11:U:103:ARG:NH2	11:U:167:VAL:HB	2.35	0.41
33:b:40:LYS:HE2	33:b:40:LYS:HB2	1.89	0.41
34:c:4:LEU:HG	34:c:127:LEU:HB2	2.02	0.41
40:i:78:TYR:HE1	40:i:89:LYS:HB3	1.86	0.41
41:j:88:LYS:NZ	41:j:92:SER:HB2	2.36	0.41
45:n:104:ALA:HA	45:n:107:GLU:HG2	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:t:10:VAL:HG21	51:t:74:LEU:HB3	2.01	0.41
51:t:64:GLN:CD	51:t:64:GLN:H	2.29	0.41
4:3:20:C:O2'	4:3:587:U:H5''	2.21	0.41
4:3:227:A:N1	4:3:443:C:O2'	2.48	0.41
4:3:890:U:H2'	4:3:891:G:C8	2.56	0.41
4:3:936:G:H8	4:3:936:G:H5''	1.85	0.41
4:3:1468:U:H3	4:3:1586:U:H3	1.68	0.41
4:3:1605:A:H2'	4:3:1606:A:C8	2.56	0.41
4:3:1798:A:P	4:3:1798:A:H8	2.43	0.41
4:3:2164:G:H4'	4:3:2165:A:O5'	2.21	0.41
4:3:2170:A:H5'	4:3:2174:G:C2	2.56	0.41
4:3:2176:G:H21	4:3:2178:A:H3'	1.85	0.41
4:3:2181:A:OP2	4:3:2181:A:H8	2.04	0.41
4:3:2269:C:C5	52:u:30:SER:HB3	2.55	0.41
4:3:2406:U:H2'	4:3:2407:G:C8	2.55	0.41
4:3:2698:U:OP2	44:m:14:ARG:NH2	2.54	0.41
4:3:2798:A:OP1	4:3:2798:A:H4'	2.21	0.41
4:3:2813:A:H61	4:3:2894:G:H2'	1.86	0.41
6:5:32:U:O2'	6:5:49:C:N4	2.54	0.41
6:5:348:C:H4'	6:5:350:G:OP1	2.21	0.41
6:5:425:G:H4'	6:5:426:U:O5'	2.19	0.41
6:5:433:C:O2'	6:5:434:U:H5'	2.20	0.41
6:5:735:C:H2'	6:5:736:U:C6	2.56	0.41
6:5:736:U:HO2'	22:N:39:HIS:CE1	2.38	0.41
6:5:853:A:H2'	6:5:854:A:H8	1.85	0.41
6:5:954:A:C5	26:R:78:ARG:NH2	2.88	0.41
6:5:967:C:OP2	17:I:65:LYS:HD3	2.21	0.41
6:5:1096:A:H2'	6:5:1097:G:C8	2.52	0.41
6:5:1135:U:O4'	6:5:1157:G:N2	2.53	0.41
6:5:1244:A:N3	6:5:1300:C:H1'	2.35	0.41
8:7:74:C:H5''	8:7:75:A:OP2	2.20	0.41
9:A:33:VAL:CG2	9:A:281:ARG:H	2.34	0.41
9:A:108:ILE:HD11	9:A:166:VAL:CG1	2.51	0.41
10:B:22:TRP:H	21:M:54:PRO:HG3	1.85	0.41
11:C:47:MET:HG3	11:C:52:GLN:HB3	2.02	0.41
12:D:55:ARG:HD3	12:D:56:ARG:NH1	2.36	0.41
13:E:1:MET:HG3	13:E:2:GLN:H	1.84	0.41
13:E:157:TRP:HB3	15:G:60:LEU:CB	2.51	0.41
15:G:47:ILE:HG13	15:G:48:LEU:HD12	2.03	0.41
15:G:124:THR:OG1	15:G:127:VAL:HG12	2.20	0.41
17:I:24:LEU:O	17:I:28:THR:HG23	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:K:29:ASN:HB3	19:K:32:ASN:OD1	2.19	0.41
19:K:55:PRO:HG3	19:K:63:ARG:HH11	1.85	0.41
19:K:81:PRO:HD3	19:K:110:ILE:HB	2.02	0.41
19:K:133:LYS:CG	19:K:134:LYS:H	2.32	0.41
21:M:7:LYS:O	21:M:11:THR:HG23	2.20	0.41
11:U:42:PHE:HB2	11:U:55:GLN:HB3	2.02	0.41
11:U:112:SER:O	11:U:116:LEU:HG	2.21	0.41
32:a:84:LYS:HE3	32:a:98:LEU:HB3	2.02	0.41
32:a:186:SER:OG	32:a:282:ARG:NE	2.39	0.41
34:c:160:VAL:HG12	34:c:203:VAL:HG11	2.03	0.41
35:d:122:PHE:HB3	35:d:163:ASP:OD2	2.21	0.41
36:e:78:ALA:O	36:e:82:VAL:HG23	2.21	0.41
36:e:108:LEU:HD23	36:e:110:LEU:HD21	2.02	0.41
38:g:60:ARG:HD3	38:g:75:ALA:O	2.21	0.41
39:h:102:LYS:HE2	39:h:102:LYS:HB2	1.88	0.41
41:j:114:ILE:HD12	41:j:114:ILE:H	1.86	0.41
41:j:119:VAL:HG13	41:j:120:GLU:CD	2.46	0.41
44:m:22:VAL:HA	44:m:25:VAL:HG12	2.02	0.41
46:o:98:ARG:NH1	46:o:100:TYR:H	2.19	0.41
47:p:90:ASN:HB3	47:p:92:LYS:HG2	2.03	0.41
48:q:12:TYR:CZ	48:q:22:VAL:HG12	2.56	0.41
49:r:72:PHE:CE1	49:r:113:GLU:HB3	2.56	0.41
50:s:45:GLU:OE2	50:s:51:LYS:HA	2.20	0.41
4:3:154:U:H2'	4:3:155:A:C8	2.56	0.41
4:3:894:G:N3	4:3:2276:A:H2'	2.36	0.41
4:3:1125:U:C2	4:3:1137:C:H1'	2.56	0.41
4:3:1604:A:H2'	4:3:1605:A:C8	2.56	0.41
4:3:2176:G:N2	4:3:2179:A:H2'	2.36	0.41
4:3:2279:G:H5'	52:u:34:ARG:HG3	2.03	0.41
4:3:2845:U:H2'	4:3:2846:A:H8	1.86	0.41
6:5:1266:U:H2'	6:5:1267:G:H8	1.85	0.41
6:5:1307:A:H2'	6:5:1308:G:O4'	2.21	0.41
7:6:58:A:O2'	7:6:60:A:C8	2.72	0.41
12:D:66:PHE:O	12:D:96:ASN:HA	2.21	0.41
12:D:161:ILE:O	12:D:161:ILE:HG22	2.20	0.41
13:E:132:VAL:O	13:E:132:VAL:CG1	2.69	0.41
14:F:112:GLU:HB3	14:F:118:LYS:HG2	2.03	0.41
15:G:54:LEU:HB2	15:G:73:ASN:O	2.21	0.41
18:J:86:LYS:NZ	28:T:26:ARG:HH21	2.19	0.41
19:K:16:LYS:HE3	19:K:16:LYS:HB3	1.91	0.41
23:O:19:ILE:HD13	23:O:19:ILE:HA	1.93	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:U:141:LYS:HD3	11:U:143:ARG:HB2	2.03	0.41
34:c:157:VAL:HA	34:c:196:ALA:O	2.21	0.41
35:d:91:LEU:C	35:d:96:MET:HB3	2.46	0.41
43:l:29:PHE:HB3	43:l:65:TRP:CE2	2.56	0.41
51:t:52:THR:HG22	51:t:53:LYS:N	2.35	0.41
52:u:52:TYR:HB3	52:u:73:LEU:HD12	2.02	0.41
4:3:573:A:O3'	40:i:11:GLN:OE1	2.39	0.40
4:3:1009:A:H5''	48:q:77:LYS:HD2	2.03	0.40
4:3:1096:U:H5	39:h:11:LYS:HG2	1.86	0.40
4:3:2164:G:O2'	4:3:2165:A:OP2	2.33	0.40
4:3:2224:A:H2'	4:3:2225:G:C8	2.55	0.40
4:3:2797:C:H4'	4:3:2895:A:H2	1.87	0.40
4:3:2838:G:H1'	4:3:2887:A:H61	1.86	0.40
6:5:352:A:H1'	6:5:365:U:OP1	2.21	0.40
6:5:747:C:O2	22:N:20:GLY:HA3	2.22	0.40
6:5:832:G:H2'	6:5:833:G:C8	2.53	0.40
11:C:58:GLN:HA	11:C:61:GLN:HG3	2.03	0.40
11:C:117:VAL:HA	11:C:122:VAL:HG12	2.03	0.40
11:C:149:ILE:O	11:C:154:VAL:HG11	2.21	0.40
13:E:47:TYR:CZ	25:Q:97:ALA:HB2	2.55	0.40
14:F:113:LYS:O	14:F:118:LYS:HG3	2.21	0.40
16:H:48:GLN:NE2	16:H:55:ASP:OD2	2.53	0.40
23:O:49:LYS:C	23:O:49:LYS:HD3	2.46	0.40
24:P:83:ARG:NH1	24:P:83:ARG:HB2	2.36	0.40
27:S:38:GLU:OE1	27:S:38:GLU:N	2.38	0.40
11:U:127:ARG:NE	11:U:127:ARG:HA	2.36	0.40
32:a:234:ASN:O	32:a:241:GLY:HA3	2.20	0.40
35:d:2:ASN:HB3	35:d:5:LYS:HB2	2.03	0.40
42:k:69:ARG:HA	42:k:69:ARG:HD2	1.87	0.40
44:m:55:ASP:OD1	44:m:60:ARG:NH1	2.54	0.40
48:q:14:VAL:HG23	48:q:97:PHE:HZ	1.86	0.40
4:3:34:C:H2'	4:3:35:U:C6	2.56	0.40
4:3:322:A:H2'	4:3:323:A:H8	1.86	0.40
4:3:890:U:H2'	4:3:891:G:H8	1.87	0.40
4:3:919:C:N4	4:3:920:G:O6	2.55	0.40
4:3:1166:G:HO2'	4:3:2032:G:HO2'	1.66	0.40
4:3:1275:C:H5''	42:k:13:ARG:HH12	1.85	0.40
4:3:1295:A:H61	4:3:2020:A:H3'	1.85	0.40
4:3:1311:G:N2	4:3:1313:G:H3'	2.36	0.40
4:3:1536:C:H2'	4:3:1537:A:H8	1.85	0.40
4:3:1758:C:H2'	4:3:1759:C:C6	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:2061:A:H2'	56:y:5:GLN:OE1	2.21	0.40
4:3:2101:A:H5'	37:f:25:TYR:HB2	2.03	0.40
6:5:117:U:H2'	6:5:118:C:C6	2.56	0.40
6:5:145:G:N2	6:5:147:A:H3'	2.37	0.40
6:5:449:A:H2'	23:O:47:LYS:NZ	2.36	0.40
6:5:1399:U:H2'	6:5:1400:A:C8	2.56	0.40
8:7:10:G:HO2'	8:7:11:U:P	2.44	0.40
9:A:234:ASP:OD1	9:A:245:MET:HG3	2.21	0.40
12:D:177:ASP:C	12:D:178:ILE:HG12	2.46	0.40
17:I:104:LEU:HD11	55:x:93:SER:O	2.22	0.40
28:T:24:GLU:OE1	28:T:24:GLU:N	2.51	0.40
11:U:99:ASN:OD1	11:U:110:ARG:NH2	2.53	0.40
32:a:193:LEU:HB2	32:a:196:CYS:SG	2.62	0.40
35:d:104:ILE:HD12	35:d:175:LEU:HD23	2.03	0.40
35:d:136:ILE:H	35:d:136:ILE:HD12	1.87	0.40
4:3:193:G:OP1	53:v:26:ARG:HG2	2.21	0.40
4:3:1119:A:C8	38:g:53:VAL:HG21	2.57	0.40
4:3:1830:G:H2'	4:3:1831:G:C8	2.57	0.40
4:3:2099:U:OP2	4:3:2207:A:O2'	2.39	0.40
4:3:2196:G:C8	4:3:2196:G:O5'	2.74	0.40
4:3:2259:OMG:HM23	4:3:2259:OMG:H1'	1.61	0.40
4:3:2691:C:OP1	46:o:56:ARG:NH1	2.51	0.40
4:3:2896:G:H3'	4:3:2897:G:H5'	2.02	0.40
5:4:104:C:H2'	5:4:105:A:C8	2.56	0.40
6:5:262:G:H1'	6:5:264:C:OP2	2.22	0.40
6:5:1051:U:H3	6:5:1172:A:H61	1.69	0.40
10:B:137:MET:HE2	10:B:169:LYS:HE3	2.03	0.40
10:B:153:LYS:NZ	10:B:155:LEU:HB2	2.36	0.40
13:E:59:ARG:CD	25:Q:54:ILE:HD11	2.52	0.40
13:E:135:GLY:O	25:Q:35:LYS:HE2	2.22	0.40
16:H:41:PHE:CD2	16:H:50:MET:HE1	2.56	0.40
17:I:59:ARG:NH2	17:I:67:SER:HB3	2.36	0.40
18:J:98:LEU:H	18:J:98:LEU:HD12	1.86	0.40
18:J:116:PRO:HB2	28:T:33:GLU:O	2.22	0.40
25:Q:51:ILE:HD12	25:Q:89:ALA:HB2	2.03	0.40
11:U:44:SER:HA	11:U:51:ALA:HB1	2.03	0.40
35:d:8:TYR:O	35:d:12:ILE:HG22	2.22	0.40
35:d:34:ILE:HD11	35:d:100:LEU:HD11	2.03	0.40
35:d:122:PHE:HD2	35:d:163:ASP:HB3	1.85	0.40
36:e:18:LEU:HD12	36:e:20:PHE:CE1	2.56	0.40
38:g:50:LYS:HG3	38:g:84:VAL:CG1	2.51	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:h:55:ILE:HG12	39:h:65:PHE:CD1	2.56	0.40
41:j:19:VAL:HG22	41:j:41:VAL:HB	2.04	0.40
46:o:2:LYS:HD3	46:o:2:LYS:HA	1.85	0.40
47:p:9:THR:HB	47:p:12:ARG:NH2	2.36	0.40
55:x:32:LYS:HE3	55:x:34:ILE:HD13	2.03	0.40
4:3:312:U:H2'	4:3:313:G:C8	2.57	0.40
4:3:447:G:OP2	4:3:2414:U:O2'	2.39	0.40
4:3:776:U:H2'	4:3:777:C:C6	2.56	0.40
4:3:2115:A:H3'	4:3:2116:U:H6	1.86	0.40
4:3:2406:U:H2'	4:3:2407:G:H8	1.87	0.40
4:3:2815:G:H5''	33:b:63:ASN:HD21	1.86	0.40
6:5:381:C:H2'	6:5:382:U:H6	1.86	0.40
6:5:452:A:H2'	6:5:453:C:O4'	2.21	0.40
6:5:609:G:O5'	6:5:609:G:H8	2.04	0.40
6:5:688:G:H1'	6:5:693:A:N6	2.37	0.40
6:5:747:C:H2'	6:5:748:U:C6	2.56	0.40
6:5:824:U:H2'	6:5:864:U:O4	2.21	0.40
6:5:961:G:N2	8:7:34:G:H5'	2.35	0.40
6:5:1045:C:H42	30:Y:46:G:N2	2.19	0.40
6:5:1509:A:H2	9:A:293:ARG:HB3	1.85	0.40
9:A:85:VAL:HG21	9:A:112:TRP:HE3	1.86	0.40
10:B:3:GLN:OE1	10:B:3:GLN:N	2.55	0.40
10:B:57:GLU:CG	10:B:68:PHE:HB2	2.52	0.40
10:B:61:THR:HG22	10:B:62:GLN:N	2.29	0.40
12:D:66:PHE:O	12:D:67:GLU:CB	2.69	0.40
12:D:212:ARG:NH1	15:G:53:TYR:CE2	2.84	0.40
13:E:89:ASN:CG	13:E:91:GLU:HG3	2.47	0.40
13:E:159:VAL:HG13	13:E:162:LYS:NZ	2.37	0.40
16:H:97:LYS:HD2	16:H:97:LYS:C	2.46	0.40
17:I:56:THR:HG22	17:I:68:ARG:CG	2.51	0.40
17:I:59:ARG:HA	21:M:45:ARG:NE	2.30	0.40
17:I:69:GLU:OE2	21:M:45:ARG:NH2	2.55	0.40
34:c:67:LYS:HB2	34:c:67:LYS:HE3	1.90	0.40
37:f:58:TYR:HA	37:f:61:ASN:ND2	2.36	0.40
50:s:47:VAL:HG23	50:s:48:TYR:HD1	1.86	0.40
53:v:63:ARG:CZ	53:v:63:ARG:HB3	2.51	0.40
4:3:45:U:H2'	4:3:46:A:O4'	2.21	0.40
4:3:169:U:H4'	53:v:44:LYS:NZ	2.37	0.40
4:3:918:G:N2	4:3:934:C:C4	2.90	0.40
4:3:1031:U:C5	47:p:52:LYS:HD2	2.55	0.40
4:3:1280:G:C8	42:k:22:ARG:HD2	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:1954:C:H2'	4:3:1955:G:C8	2.57	0.40
4:3:2077:A:H2'	4:3:2078:A:C8	2.56	0.40
4:3:2228:U:H5'	37:f:95:LYS:HG2	2.04	0.40
4:3:2299:U:H1'	4:3:2382:A:H1'	2.03	0.40
6:5:826:G:H1	6:5:851:U:H3	1.70	0.40
6:5:972:A:H1'	6:5:977:U:O4	2.22	0.40
6:5:989:A:N1	21:M:4:LYS:NZ	2.63	0.40
6:5:1258:U:H2'	6:5:1259:G:H8	1.86	0.40
9:A:130:LEU:HD13	9:A:159:LEU:HB2	2.03	0.40
9:A:178:VAL:HG13	9:A:184:GLU:HG3	2.03	0.40
10:B:83:LYS:O	10:B:86:GLN:HG3	2.22	0.40
10:B:139:GLN:C	10:B:143:LYS:HZ3	2.27	0.40
15:G:104:LEU:HD23	15:G:104:LEU:HA	1.87	0.40
16:H:45:LEU:HD12	16:H:48:GLN:HB3	2.04	0.40
18:J:51:LYS:HZ3	18:J:84:ARG:H	1.70	0.40
19:K:80:ILE:HG12	19:K:110:ILE:HD12	2.02	0.40
21:M:19:ARG:HG3	21:M:19:ARG:NH1	2.36	0.40
23:O:78:LEU:HD13	23:O:81:LYS:HE2	2.03	0.40
11:U:53:GLN:NE2	11:U:199:TRP:CD1	2.89	0.40
11:U:64:TYR:HD1	11:U:110:ARG:NH1	2.17	0.40
11:U:66:ILE:HG22	11:U:67:THR:O	2.22	0.40
32:a:76:TYR:HB3	32:a:79:ILE:HD12	2.03	0.40
32:a:138:LEU:HD23	32:a:138:LEU:HA	1.94	0.40
33:b:24:LEU:HD21	33:b:194:SER:HB2	2.02	0.40
33:b:121:GLY:HA2	33:b:166:SER:OG	2.21	0.40
39:h:20:LYS:N	39:h:21:PRO:HD2	2.37	0.40
43:l:109:ILE:HB	43:l:113:GLN:HE21	1.87	0.40
44:m:33:THR:O	44:m:114:ALA:N	2.48	0.40
49:r:14:PRO:HG3	49:r:101:SER:CB	2.52	0.40
49:r:28:LYS:HD2	49:r:28:LYS:HA	1.90	0.40
49:r:124:LEU:HD23	49:r:127:LYS:HD3	2.03	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	0	45/48 (94%)	45 (100%)	0	0	100	100
2	1	57/59 (97%)	57 (100%)	0	0	100	100
3	2	35/37 (95%)	35 (100%)	0	0	100	100
9	A	264/294 (90%)	233 (88%)	25 (10%)	6 (2%)	5	28
10	B	223/273 (82%)	197 (88%)	24 (11%)	2 (1%)	14	51
11	C	202/205 (98%)	166 (82%)	33 (16%)	3 (2%)	8	40
11	U	202/205 (98%)	148 (73%)	41 (20%)	13 (6%)	1	12
12	D	171/219 (78%)	141 (82%)	25 (15%)	5 (3%)	3	23
13	E	165/215 (77%)	142 (86%)	18 (11%)	5 (3%)	3	23
14	F	153/155 (99%)	132 (86%)	15 (10%)	6 (4%)	2	19
15	G	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
16	H	127/132 (96%)	115 (91%)	12 (9%)	0	100	100
17	I	102/108 (94%)	88 (86%)	13 (13%)	1 (1%)	12	49
18	J	112/121 (93%)	105 (94%)	7 (6%)	0	100	100
19	K	133/139 (96%)	113 (85%)	15 (11%)	5 (4%)	2	19
20	L	119/124 (96%)	112 (94%)	7 (6%)	0	100	100
21	M	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
22	N	84/86 (98%)	77 (92%)	6 (7%)	1 (1%)	10	44
23	O	85/94 (90%)	78 (92%)	5 (6%)	2 (2%)	4	27
24	P	83/85 (98%)	71 (86%)	11 (13%)	1 (1%)	10	44
25	Q	76/104 (73%)	65 (86%)	9 (12%)	2 (3%)	4	25
26	R	84/87 (97%)	79 (94%)	5 (6%)	0	100	100
27	S	77/87 (88%)	74 (96%)	2 (3%)	1 (1%)	9	42
28	T	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
29	X	28/444 (6%)	24 (86%)	4 (14%)	0	100	100
31	Z	3/36 (8%)	3 (100%)	0	0	100	100
32	a	283/287 (99%)	267 (94%)	15 (5%)	1 (0%)	30	67
33	b	229/287 (80%)	219 (96%)	9 (4%)	1 (0%)	30	67
34	c	209/212 (99%)	198 (95%)	11 (5%)	0	100	100
35	d	177/180 (98%)	169 (96%)	8 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	e	174/184 (95%)	162 (93%)	12 (7%)	0	100	100
37	f	147/149 (99%)	131 (89%)	15 (10%)	1 (1%)	18	56
38	g	123/161 (76%)	117 (95%)	6 (5%)	0	100	100
39	h	126/137 (92%)	121 (96%)	5 (4%)	0	100	100
40	i	142/146 (97%)	133 (94%)	9 (6%)	0	100	100
41	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
42	k	148/151 (98%)	138 (93%)	10 (7%)	0	100	100
43	l	134/139 (96%)	132 (98%)	2 (2%)	0	100	100
44	m	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
45	n	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
46	o	116/119 (98%)	108 (93%)	8 (7%)	0	100	100
47	p	116/127 (91%)	114 (98%)	2 (2%)	0	100	100
48	q	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
49	r	140/159 (88%)	137 (98%)	3 (2%)	0	100	100
50	s	93/237 (39%)	89 (96%)	4 (4%)	0	100	100
51	t	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
52	u	99/104 (95%)	86 (87%)	9 (9%)	4 (4%)	2	18
53	v	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
54	w	108/111 (97%)	102 (94%)	6 (6%)	0	100	100
55	x	85/97 (88%)	64 (75%)	21 (25%)	0	100	100
56	y	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
57	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	6255/7355 (85%)	5717 (91%)	478 (8%)	60 (1%)	15	49

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	D	67	GLU
12	D	69	ARG
12	D	212	ARG
12	D	216	LEU
13	E	81	GLN
13	E	143	LEU
14	F	151	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
24	P	54	LEU
11	U	39	GLY
11	U	126	ASP
11	U	163	VAL
52	u	9	LYS
52	u	11	ASP
52	u	17	SER
52	u	23	SER
11	C	81	GLN
11	C	182	PRO
14	F	9	ARG
14	F	15	PRO
14	F	79	ILE
22	N	4	ASP
27	S	37	LYS
11	U	3	TYR
11	U	24	GLU
11	U	81	GLN
11	U	154	VAL
11	U	155	LYS
9	A	49	ARG
9	A	219	ASN
13	E	163	MET
14	F	12	LEU
19	K	56	LYS
11	U	27	LYS
11	U	30	LYS
37	f	12	LEU
9	A	54	ASP
10	B	216	ASN
13	E	55	ALA
14	F	153	MET
19	K	70	LEU
23	O	47	LYS
23	O	49	LYS
25	Q	37	SER
32	a	128	ILE
9	A	16	GLU
9	A	17	LEU
11	C	188	PRO
12	D	62	PHE
17	I	100	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
19	K	72	ASN
25	Q	35	LYS
11	U	157	ALA
11	U	181	PHE
13	E	82	VAL
11	U	50	TYR
33	b	230	PRO
9	A	198	VAL
10	B	46	VAL
19	K	57	LYS
19	K	55	PRO

5.3.2 Protein sidechains [i](#)

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	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
9	A	239/262 (91%)	239 (100%)	0	100	100
10	B	188/232 (81%)	188 (100%)	0	100	100
11	C	182/183 (100%)	182 (100%)	0	100	100
11	U	182/183 (100%)	182 (100%)	0	100	100
12	D	141/178 (79%)	141 (100%)	0	100	100
13	E	150/196 (76%)	150 (100%)	0	100	100
14	F	132/132 (100%)	132 (100%)	0	100	100
15	G	124/124 (100%)	124 (100%)	0	100	100
16	H	112/115 (97%)	112 (100%)	0	100	100
17	I	97/99 (98%)	97 (100%)	0	100	100
18	J	91/97 (94%)	91 (100%)	0	100	100
19	K	117/120 (98%)	117 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	L	102/105 (97%)	102 (100%)	0	100	100
21	M	47/48 (98%)	47 (100%)	0	100	100
22	N	78/78 (100%)	78 (100%)	0	100	100
23	O	76/82 (93%)	76 (100%)	0	100	100
24	P	75/75 (100%)	75 (100%)	0	100	100
25	Q	69/94 (73%)	69 (100%)	0	100	100
26	R	76/77 (99%)	76 (100%)	0	100	100
27	S	71/77 (92%)	71 (100%)	0	100	100
28	T	55/56 (98%)	55 (100%)	0	100	100
29	X	27/406 (7%)	27 (100%)	0	100	100
31	Z	2/2 (100%)	2 (100%)	0	100	100
32	a	241/243 (99%)	241 (100%)	0	100	100
33	b	188/233 (81%)	188 (100%)	0	100	100
34	c	183/184 (100%)	183 (100%)	0	100	100
35	d	153/154 (99%)	153 (100%)	0	100	100
36	e	153/159 (96%)	153 (100%)	0	100	100
37	f	134/134 (100%)	134 (100%)	0	100	100
38	g	100/129 (78%)	100 (100%)	0	100	100
39	h	102/110 (93%)	102 (100%)	0	100	100
40	i	126/128 (98%)	126 (100%)	0	100	100
41	j	103/103 (100%)	103 (100%)	0	100	100
42	k	125/126 (99%)	125 (100%)	0	100	100
43	l	113/115 (98%)	113 (100%)	0	100	100
44	m	105/109 (96%)	105 (100%)	0	100	100
45	n	99/99 (100%)	99 (100%)	0	100	100
46	o	104/105 (99%)	104 (100%)	0	100	100
47	p	104/108 (96%)	104 (100%)	0	100	100
48	q	90/91 (99%)	90 (100%)	0	100	100
49	r	118/132 (89%)	118 (100%)	0	100	100
50	s	84/208 (40%)	84 (100%)	0	100	100
51	t	96/96 (100%)	96 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	u	82/85 (96%)	82 (100%)	0	100	100
53	v	59/60 (98%)	59 (100%)	0	100	100
54	w	97/98 (99%)	97 (100%)	0	100	100
55	x	79/86 (92%)	79 (100%)	0	100	100
56	y	48/49 (98%)	48 (100%)	0	100	100
57	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5492/6342 (87%)	5492 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (85) such sidechains are listed below:

Mol	Chain	Res	Type
3	2	20	HIS
3	2	21	GLN
3	2	36	GLN
9	A	81	GLN
9	A	221	GLN
10	B	6	ASN
10	B	27	HIS
10	B	91	GLN
10	B	150	ASN
10	B	193	GLN
11	C	58	GLN
11	C	81	GLN
11	C	88	ASN
11	C	115	GLN
13	E	20	GLN
13	E	22	ASN
13	E	79	ASN
13	E	101	ASN
13	E	165	ASN
14	F	19	ASN
14	F	67	ASN
14	F	83	ASN
14	F	85	GLN
15	G	73	ASN
15	G	85	ASN
16	H	48	GLN
19	K	29	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	L	36	GLN
20	L	100	GLN
22	N	13	GLN
22	N	35	GLN
24	P	46	GLN
24	P	49	ASN
24	P	62	GLN
27	S	31	ASN
27	S	63	ASN
11	U	37	GLN
11	U	53	GLN
11	U	88	ASN
11	U	171	ASN
32	a	31	ASN
32	a	240	HIS
33	b	34	ASN
33	b	144	GLN
33	b	171	HIS
33	b	188	ASN
34	c	170	GLN
34	c	179	GLN
35	d	27	GLN
35	d	37	ASN
35	d	63	GLN
36	e	19	ASN
36	e	54	GLN
36	e	63	GLN
37	f	96	GLN
39	h	40	ASN
39	h	47	GLN
40	i	80	HIS
40	i	133	HIS
41	j	18	GLN
42	k	24	HIS
42	k	81	ASN
43	l	3	GLN
43	l	99	GLN
43	l	113	GLN
44	m	81	HIS
45	n	7	GLN
45	n	49	ASN
45	n	66	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
45	n	69	ASN
47	p	40	GLN
47	p	106	ASN
47	p	110	GLN
48	q	2	HIS
48	q	34	GLN
49	r	120	GLN
49	r	121	GLN
49	r	133	GLN
52	u	43	GLN
52	u	100	HIS
53	v	34	GLN
54	w	9	GLN
54	w	42	HIS
55	x	10	GLN
55	x	56	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	Y	28/29 (96%)	16 (57%)	4 (14%)
4	3	2892/2907 (99%)	536 (18%)	18 (0%)
5	4	107/108 (99%)	29 (27%)	0
6	5	1506/1520 (99%)	258 (17%)	10 (0%)
7	6	76/76 (100%)	23 (30%)	5 (6%)
8	7	74/75 (98%)	20 (27%)	2 (2%)
All	All	4683/4715 (99%)	882 (18%)	39 (0%)

All (882) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	3	11	U
4	3	12	A
4	3	13	C
4	3	14	U
4	3	28	G
4	3	37	G
4	3	48	G
4	3	64	U
4	3	65	A
4	3	73	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	76	A
4	3	77	G
4	3	102	A
4	3	103	G
4	3	119	A
4	3	121	U
4	3	126	C
4	3	132	G
4	3	141	A
4	3	142	A
4	3	163	A
4	3	180	A
4	3	184	A
4	3	187	C
4	3	200	A
4	3	203	A
4	3	219	G
4	3	220	A
4	3	225	A
4	3	226	A
4	3	232	A
4	3	234	G
4	3	237	A
4	3	245	U
4	3	246	G
4	3	252	G
4	3	269	A
4	3	276	A
4	3	284	U
4	3	287	G
4	3	295	U
4	3	296	U
4	3	297	G
4	3	298	U
4	3	299	A
4	3	309	A
4	3	310	U
4	3	311	G
4	3	315	A
4	3	316	C
4	3	317	U
4	3	319	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	325	G
4	3	336	C
4	3	345	A
4	3	363	G
4	3	364	A
4	3	365	U
4	3	402	A
4	3	409	A
4	3	410	G
4	3	411	U
4	3	418	G
4	3	419	A
4	3	424	G
4	3	425	U
4	3	426	U
4	3	432	G
4	3	437	A
4	3	440	C
4	3	460	G
4	3	463	U
4	3	483	A
4	3	517	G
4	3	539	U
4	3	540	A
4	3	548	A
4	3	562	C
4	3	565	C
4	3	566	G
4	3	567	U
4	3	573	A
4	3	581	A
4	3	583	U
4	3	596	G
4	3	598	G
4	3	607	U
4	3	608	A
4	3	610	G
4	3	620	G
4	3	636	U
4	3	637	U
4	3	638	A
4	3	648	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	649	A
4	3	650	G
4	3	663	A
4	3	670	G
4	3	673	A
4	3	681	A
4	3	682	A
4	3	689	U
4	3	691	G
4	3	705	A
4	3	712	A
4	3	716	G
4	3	721	G
4	3	722	C
4	3	765	A
4	3	775	C
4	3	782	U
4	3	792	G
4	3	797	U
4	3	800	C
4	3	810	G
4	3	811	G
4	3	817	A
4	3	819	U
4	3	820	U
4	3	824	A
4	3	828	A
4	3	829	A
4	3	840	G
4	3	846	U
4	3	847	C
4	3	854	A
4	3	862	U
4	3	881	A
4	3	882	C
4	3	883	A
4	3	901	C
4	3	902	U
4	3	904	C
4	3	906	G
4	3	911	U
4	3	912	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	914	G
4	3	915	A
4	3	925	C
4	3	929	G
4	3	931	G
4	3	932	U
4	3	933	A
4	3	934	C
4	3	941	C
4	3	942	A
4	3	944	U
4	3	947	A
4	3	949	C
4	3	951	C
4	3	952	U
4	3	953	G
4	3	970	U
4	3	981	A
4	3	982	G
4	3	994	U
4	3	997	G
4	3	998	C
4	3	1008	A
4	3	1010	G
4	3	1016	A
4	3	1019	A
4	3	1026	A
4	3	1032	A
4	3	1039	G
4	3	1045	A
4	3	1049	U
4	3	1058	U
4	3	1060	G
4	3	1061	A
4	3	1068	U
4	3	1074	A
4	3	1080	A
4	3	1082	A
4	3	1084	C
4	3	1096	U
4	3	1097	G
4	3	1098	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	1099	C
4	3	1102	A
4	3	1104	A
4	3	1105	A
4	3	1106	G
4	3	1107	C
4	3	1110	C
4	3	1111	C
4	3	1113	U
4	3	1114	C
4	3	1115	G
4	3	1120	A
4	3	1122	G
4	3	1123	A
4	3	1125	U
4	3	1130	A
4	3	1132	C
4	3	1138	A
4	3	1144	C
4	3	1145	G
4	3	1146	A
4	3	1147	G
4	3	1165	U
4	3	1167	U
4	3	1168	A
4	3	1170	C
4	3	1176	U
4	3	1177	A
4	3	1178	A
4	3	1204	A
4	3	1208	A
4	3	1209	U
4	3	1210	A
4	3	1212	C
4	3	1215	G
4	3	1234	U
4	3	1235	U
4	3	1236	G
4	3	1242	G
4	3	1246	U
4	3	1250	A
4	3	1251	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	1253	G
4	3	1256	A
4	3	1257	G
4	3	1266	G
4	3	1268	U
4	3	1280	G
4	3	1281	A
4	3	1283	A
4	3	1285	U
4	3	1286	G
4	3	1292	A
4	3	1301	G
4	3	1304	U
4	3	1313	G
4	3	1325	C
4	3	1328	A
4	3	1329	U
4	3	1330	U
4	3	1369	U
4	3	1378	C
4	3	1380	U
4	3	1388	G
4	3	1393	A
4	3	1406	A
4	3	1407	U
4	3	1412	A
4	3	1423	A
4	3	1424	U
4	3	1431	A
4	3	1444	C
4	3	1445	U
4	3	1446	G
4	3	1448	U
4	3	1456	C
4	3	1463	G
4	3	1467	U
4	3	1480	A
4	3	1481	U
4	3	1483	G
4	3	1486	U
4	3	1487	U
4	3	1502	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	1504	G
4	3	1508	G
4	3	1510	A
4	3	1513	A
4	3	1514	U
4	3	1515	A
4	3	1519	A
4	3	1522	U
4	3	1534	A
4	3	1535	A
4	3	1541	A
4	3	1546	U
4	3	1550	G
4	3	1569	A
4	3	1570	A
4	3	1571	G
4	3	1580	G
4	3	1582	G
4	3	1584	U
4	3	1585	A
4	3	1588	A
4	3	1589	A
4	3	1603	A
4	3	1612	U
4	3	1617	U
4	3	1618	U
4	3	1619	A
4	3	1641	A
4	3	1642	G
4	3	1643	A
4	3	1644	A
4	3	1645	C
4	3	1650	A
4	3	1651	C
4	3	1661	A
4	3	1668	G
4	3	1680	A
4	3	1681	G
4	3	1682	C
4	3	1688	A
4	3	1694	A
4	3	1708	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	1727	U
4	3	1737	G
4	3	1748	U
4	3	1749	A
4	3	1764	U
4	3	1769	A
4	3	1770	A
4	3	1771	C
4	3	1780	A
4	3	1789	C
4	3	1791	A
4	3	1807	C
4	3	1808	C
4	3	1809	A
4	3	1816	A
4	3	1823	U
4	3	1836	A
4	3	1854	A
4	3	1855	A
4	3	1866	G
4	3	1869	G
4	3	1878	A
4	3	1886	C
4	3	1910	G
4	3	1913	G
4	3	1919	A
4	3	1920	A
4	3	1921	C
4	3	1922	U
4	3	1936	G
4	3	1937	G
4	3	1938	U
4	3	1943	A
4	3	1944	A
4	3	1962	U
4	3	1974	U
4	3	1977	A
4	3	1978	U
4	3	1979	G
4	3	1998	U
4	3	1999	G
4	3	2000	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	2004	G
4	3	2028	G
4	3	2030	A
4	3	2038	A
4	3	2040	A
4	3	2041	C
4	3	2042	A
4	3	2050	G
4	3	2057	C
4	3	2062	C
4	3	2063	G
4	3	2067	A
4	3	2068	G
4	3	2069	A
4	3	2076	G
4	3	2084	A
4	3	2099	U
4	3	2100	G
4	3	2103	C
4	3	2106	G
4	3	2107	A
4	3	2108	C
4	3	2109	A
4	3	2111	U
4	3	2112	A
4	3	2113	U
4	3	2114	C
4	3	2118	U
4	3	2119	A
4	3	2123	A
4	3	2124	A
4	3	2125	U
4	3	2126	A
4	3	2127	G
4	3	2128	G
4	3	2130	A
4	3	2134	G
4	3	2135	C
4	3	2138	U
4	3	2139	C
4	3	2140	G
4	3	2141	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	2145	A
4	3	2146	A
4	3	2152	C
4	3	2153	U
4	3	2157	A
4	3	2158	C
4	3	2163	U
4	3	2164	G
4	3	2165	A
4	3	2166	U
4	3	2167	G
4	3	2168	C
4	3	2169	G
4	3	2170	A
4	3	2171	A
4	3	2172	A
4	3	2173	G
4	3	2175	U
4	3	2179	A
4	3	2180	U
4	3	2181	A
4	3	2186	C
4	3	2190	G
4	3	2193	U
4	3	2194	G
4	3	2195	U
4	3	2196	G
4	3	2197	U
4	3	2198	G
4	3	2199	C
4	3	2200	U
4	3	2202	U
4	3	2207	A
4	3	2211	G
4	3	2212	U
4	3	2219	U
4	3	2220	A
4	3	2221	U
4	3	2227	U
4	3	2228	U
4	3	2233	A
4	3	2246	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	2247	G
4	3	2259	OMG
4	3	2274	A
4	3	2276	A
4	3	2287	G
4	3	2291	U
4	3	2295	A
4	3	2298	G
4	3	2305	C
4	3	2311	G
4	3	2313	U
4	3	2316	G
4	3	2319	A
4	3	2327	U
4	3	2329	G
4	3	2333	G
4	3	2335	A
4	3	2336	A
4	3	2342	U
4	3	2343	A
4	3	2344	A
4	3	2353	G
4	3	2355	C
4	3	2358	U
4	3	2366	A
4	3	2391	G
4	3	2393	C
4	3	2397	G
4	3	2410	C
4	3	2411	C
4	3	2414	U
4	3	2422	G
4	3	2431	U
4	3	2433	A
4	3	2437	G
4	3	2438	A
4	3	2443	A
4	3	2449	U
4	3	2456	A
4	3	2477	A
4	3	2481	U
4	3	2482	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	2483	C
4	3	2484	A
4	3	2486	A
4	3	2488	C
4	3	2499	U
4	3	2510	G
4	3	2513	G
4	3	2521	A
4	3	2526	A
4	3	2537	G
4	3	2543	G
4	3	2574	A
4	3	2575	G
4	3	2580	A
4	3	2585	A
4	3	2593	U
4	3	2594	C
4	3	2605	G
4	3	2610	A
4	3	2617	U
4	3	2618	C
4	3	2621	U
4	3	2623	U
4	3	2637	A
4	3	2638	G
4	3	2654	U
4	3	2668	A
4	3	2669	G
4	3	2697	C
4	3	2698	U
4	3	2722	G
4	3	2734	C
4	3	2737	G
4	3	2741	A
4	3	2752	G
4	3	2756	A
4	3	2760	C
4	3	2764	U
4	3	2765	A
4	3	2773	A
4	3	2786	A
4	3	2798	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	2799	U
4	3	2804	C
4	3	2806	A
4	3	2807	G
4	3	2808	A
4	3	2810	A
4	3	2813	A
4	3	2822	C
4	3	2824	A
4	3	2829	G
4	3	2839	A
4	3	2853	U
4	3	2862	U
4	3	2863	G
4	3	2871	G
4	3	2876	G
4	3	2884	C
4	3	2887	A
4	3	2888	U
4	3	2895	A
4	3	2896	G
4	3	2899	C
5	4	9	C
5	4	10	C
5	4	11	A
5	4	13	G
5	4	14	U
5	4	22	G
5	4	23	A
5	4	28	C
5	4	33	U
5	4	35	C
5	4	39	U
5	4	41	C
5	4	48	A
5	4	49	G
5	4	54	U
5	4	56	A
5	4	60	C
5	4	64	G
5	4	65	G
5	4	80	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	4	82	U
5	4	83	U
5	4	84	C
5	4	85	A
5	4	88	G
5	4	89	A
5	4	99	A
5	4	106	A
5	4	108	C
6	5	6	C
6	5	10	G
6	5	33	A
6	5	40	G
6	5	48	C
6	5	49	C
6	5	52	A
6	5	57	U
6	5	61	A
6	5	106	C
6	5	114	C
6	5	115	A
6	5	117	U
6	5	120	A
6	5	149	G
6	5	154	G
6	5	163	G
6	5	167	A
6	5	171	A
6	5	173	U
6	5	176	G
6	5	180	C
6	5	182	C
6	5	185	G
6	5	186	A
6	5	189	C
6	5	190	A
6	5	197	A
6	5	198	A
6	5	199	A
6	5	220	U
6	5	223	G
6	5	239	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	5	241	C
6	5	243	G
6	5	247	G
6	5	262	G
6	5	263	C
6	5	269	A
6	5	275	A
6	5	285	G
6	5	301	G
6	5	302	A
6	5	324	C
6	5	325	A
6	5	326	C
6	5	328	G
6	5	341	C
6	5	342	G
6	5	344	G
6	5	347	G
6	5	348	C
6	5	350	G
6	5	359	A
6	5	362	U
6	5	363	U
6	5	364	U
6	5	365	U
6	5	368	C
6	5	369	A
6	5	370	A
6	5	374	G
6	5	380	G
6	5	383	U
6	5	388	G
6	5	394	U
6	5	402	G
6	5	408	U
6	5	416	U
6	5	418	U
6	5	419	A
6	5	422	A
6	5	425	G
6	5	426	U
6	5	447	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	5	449	A
6	5	450	U
6	5	452	A
6	5	461	G
6	5	462	G
6	5	464	A
6	5	468	G
6	5	470	U
6	5	475	U
6	5	476	U
6	5	477	U
6	5	480	C
6	5	481	U
6	5	482	G
6	5	488	U
6	5	489	U
6	5	493	A
6	5	494	A
6	5	495	U
6	5	507	A
6	5	509	C
6	5	510	U
6	5	516	C
6	5	517	C
6	5	522	G
6	5	525	7MG
6	5	530	A
6	5	531	A
6	5	545	A
6	5	557	A
6	5	560	U
6	5	562	U
6	5	570	A
6	5	571	A
6	5	574	C
6	5	575	A
6	5	579	G
6	5	586	G
6	5	594	A
6	5	595	G
6	5	628	A
6	5	650	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	5	661	G
6	5	662	G
6	5	683	G
6	5	700	G
6	5	715	A
6	5	719	G
6	5	720	U
6	5	721	G
6	5	728	G
6	5	745	U
6	5	752	G
6	5	768	G
6	5	790	U
6	5	791	A
6	5	811	A
6	5	812	A
6	5	814	C
6	5	818	A
6	5	825	A
6	5	829	G
6	5	836	C
6	5	838	A
6	5	839	U
6	5	867	A
6	5	883	A
6	5	885	U
6	5	908	A
6	5	910	C
6	5	911	G
6	5	921	G
6	5	922	G
6	5	929	C
6	5	930	A
6	5	955	U
6	5	964	A
6	5	970	A
6	5	971	A
6	5	972	A
6	5	982	A
6	5	987	U
6	5	988	G
6	5	989	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	5	994	C
6	5	995	U
6	5	996	U
6	5	997	G
6	5	998	G
6	5	999	C
6	5	1000	A
6	5	1002	A
6	5	1007	U
6	5	1009	G
6	5	1015	U
6	5	1018	U
6	5	1019	G
6	5	1020	G
6	5	1022	G
6	5	1023	G
6	5	1024	U
6	5	1025	U
6	5	1027	A
6	5	1028	C
6	5	1029	C
6	5	1030	G
6	5	1032	G
6	5	1034	G
6	5	1036	C
6	5	1044	G
6	5	1045	C
6	5	1047	U
6	5	1056	U
6	5	1072	G
6	5	1076	U
6	5	1078	G
6	5	1083	A
6	5	1085	G
6	5	1086	U
6	5	1092	A
6	5	1118	A
6	5	1121	U
6	5	1122	U
6	5	1123	G
6	5	1124	U
6	5	1134	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	5	1135	U
6	5	1141	U
6	5	1142	G
6	5	1158	A
6	5	1159	A
6	5	1170	C
6	5	1171	A
6	5	1172	A
6	5	1188	A
6	5	1189	U
6	5	1202	A
6	5	1203	A
6	5	1215	U
6	5	1231	U
6	5	1232	C
6	5	1233	G
6	5	1235	C
6	5	1255	A
6	5	1260	U
6	5	1271	U
6	5	1274	G
6	5	1279	G
6	5	1291	C
6	5	1294	U
6	5	1296	C
6	5	1297	G
6	5	1306	A
6	5	1312	G
6	5	1320	A
6	5	1321	G
6	5	1337	U
6	5	1338	A
6	5	1339	U
6	5	1343	G
6	5	1345	G
6	5	1372	C
6	5	1373	A
6	5	1397	G
6	5	1417	U
6	5	1426	U
6	5	1427	U
6	5	1428	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	5	1429	G
6	5	1462	G
6	5	1467	A
6	5	1468	A
6	5	1472	G
6	5	1478	A
6	5	1480	G
6	5	1481	U
6	5	1482	A
6	5	1492	G
6	5	1494	MA6
6	5	1504	G
6	5	1505	G
6	5	1510	C
6	5	1511	C
7	6	2	G
7	6	3	G
7	6	13	C
7	6	15	A
7	6	16	C
7	6	17	U
7	6	18	G
7	6	19	A
7	6	20	U
7	6	21	A
7	6	33	U
7	6	34	U
7	6	37	A
7	6	46	G
7	6	47	U
7	6	48	U
7	6	59	G
7	6	65	U
7	6	70	U
7	6	71	C
7	6	72	C
7	6	73	A
7	6	75	C
8	7	4	U
8	7	11	U
8	7	13	U
8	7	15	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	7	16	U
8	7	17	G
8	7	19	A
8	7	20	U
8	7	21	A
8	7	22	A
8	7	34	G
8	7	44	G
8	7	46	U
8	7	47	U
8	7	48	G
8	7	51	G
8	7	57	A
8	7	71	C
8	7	73	C
8	7	75	A
30	Y	29	A
30	Y	31	A
30	Y	32	A
30	Y	34	A
30	Y	35	C
30	Y	36	U
30	Y	37	G
30	Y	40	G
30	Y	47	U
30	Y	49	U
30	Y	50	U
30	Y	51	C
30	Y	52	A
30	Y	53	A
30	Y	54	A
30	Y	56	A

All (39) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	3	315	A
4	3	410	G
4	3	881	A
4	3	901	C
4	3	1124	G
4	3	1209	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	3	1583	G
4	3	1618	U
4	3	2107	A
4	3	2110	U
4	3	2124	A
4	3	2152	C
4	3	2164	G
4	3	2169	G
4	3	2180	U
4	3	2199	C
4	3	2410	C
4	3	2764	U
6	5	196	G
6	5	363	U
6	5	364	U
6	5	571	A
6	5	994	C
6	5	995	U
6	5	1024	U
6	5	1123	G
6	5	1158	A
6	5	1338	A
7	6	1	G
7	6	15	A
7	6	33	U
7	6	46	G
7	6	74	C
8	7	10	G
8	7	46	U
30	Y	34	A
30	Y	35	C
30	Y	49	U
30	Y	51	C

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

8 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	$\# Z > 2$
6	B8T	5	1377	6	19,22,23	4.76	13 (68%)	25,31,34	0.98	1 (4%)
6	MA6	5	1494	6	23,26,27	1.40	3 (13%)	33,38,41	3.24	14 (42%)
6	7MG	5	525	6	23,26,27	3.63	11 (47%)	27,39,42	2.17	9 (33%)
4	1MG	3	783	4	23,26,27	0.59	0	33,39,42	0.73	1 (3%)
6	MA6	5	1493	6	23,26,27	1.41	3 (13%)	33,38,41	3.20	14 (42%)
4	2MA	3	2511	4,61	22,25,26	5.06	15 (68%)	32,37,40	3.73	12 (37%)
4	OMG	3	2259	4,8	23,26,27	0.33	0	32,38,41	0.43	0
6	5MC	5	1375	6	19,22,23	0.82	1 (5%)	26,32,35	0.69	1 (3%)

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
6	B8T	5	1377	6	-	0/7/27/28	0/2/2/2
6	MA6	5	1494	6	-	2/11/29/30	0/3/3/3
6	7MG	5	525	6	-	2/7/37/38	0/3/3/3
4	1MG	3	783	4	-	0/7/25/26	0/3/3/3
6	MA6	5	1493	6	-	0/11/29/30	0/3/3/3
4	2MA	3	2511	4,61	-	2/7/25/26	0/3/3/3
4	OMG	3	2259	4,8	-	3/9/27/28	0/3/3/3
6	5MC	5	1375	6	-	0/7/25/26	0/2/2/2

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	3	2511	2MA	C4-N3	12.12	1.50	1.34
6	5	1377	B8T	O4'-C1'	9.11	1.63	1.42
4	3	2511	2MA	O4'-C1'	8.88	1.62	1.42
6	5	525	7MG	C8-N9	8.67	1.51	1.45
4	3	2511	2MA	C2-N3	8.16	1.48	1.34
6	5	1377	B8T	O4'-C4'	-7.67	1.27	1.45
6	5	1377	B8T	C4-N3	7.60	1.45	1.32
6	5	1377	B8T	C2'-C1'	-7.49	1.30	1.53
4	3	2511	2MA	C2'-C1'	-7.39	1.30	1.53
4	3	2511	2MA	C6-N1	7.36	1.44	1.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	5	525	7MG	C5-N7	7.17	1.44	1.35
6	5	1377	B8T	C2-N3	6.59	1.49	1.36
4	3	2511	2MA	C2-N1	6.37	1.45	1.34
4	3	2511	2MA	O4'-C4'	-6.03	1.31	1.45
6	5	525	7MG	C2-N3	5.87	1.47	1.33
6	5	1377	B8T	C6-C5	5.82	1.48	1.35
6	5	525	7MG	C4-N3	5.81	1.47	1.34
6	5	525	7MG	C4-N9	5.38	1.44	1.37
4	3	2511	2MA	C5-C6	5.26	1.55	1.41
6	5	525	7MG	C2-N2	4.86	1.45	1.34
6	5	1377	B8T	C4-N4	4.57	1.45	1.36
6	5	1377	B8T	C2-N1	4.47	1.49	1.40
6	5	1493	MA6	C6-N6	4.19	1.48	1.36
6	5	1494	MA6	C6-N6	4.17	1.48	1.36
6	5	525	7MG	C2-N1	3.92	1.47	1.37
4	3	2511	2MA	C5-N7	-3.80	1.32	1.39
6	5	525	7MG	C5-C6	3.76	1.52	1.43
6	5	1377	B8T	C5-C4	3.57	1.48	1.41
6	5	1377	B8T	O2'-C2'	3.48	1.51	1.43
6	5	525	7MG	C6-N1	3.38	1.45	1.38
6	5	1375	5MC	C5-C4	-3.28	1.41	1.44
4	3	2511	2MA	C8-N7	3.26	1.37	1.31
6	5	1377	B8T	C6-N1	3.04	1.45	1.38
6	5	1377	B8T	O3'-C3'	-2.77	1.36	1.43
6	5	1377	B8T	O2-C2	-2.65	1.18	1.23
4	3	2511	2MA	O3'-C3'	-2.57	1.36	1.43
4	3	2511	2MA	O2'-C2'	2.56	1.49	1.43
6	5	525	7MG	O6-C6	-2.43	1.18	1.23
6	5	1494	MA6	C5-C4	-2.40	1.34	1.39
6	5	1493	MA6	C5-N7	-2.34	1.34	1.39
6	5	1493	MA6	C5-C4	-2.27	1.35	1.39
6	5	1494	MA6	C5-N7	-2.25	1.35	1.39
4	3	2511	2MA	C6-N6	-2.13	1.28	1.34
4	3	2511	2MA	C8-N9	-2.10	1.34	1.37
4	3	2511	2MA	C4-N9	-2.08	1.33	1.37
6	5	525	7MG	C5-C4	2.04	1.44	1.37

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	3	2511	2MA	C1'-N9-C8	-13.21	97.79	127.09
4	3	2511	2MA	C4-N9-C1'	11.51	153.55	126.63

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	5	1494	MA6	N1-C6-N6	-10.41	104.18	116.86
6	5	1493	MA6	N1-C6-N6	-10.08	104.57	116.86
6	5	1494	MA6	C5-C6-N6	6.77	136.05	125.33
6	5	1493	MA6	C5-C6-N6	6.59	135.76	125.33
4	3	2511	2MA	C5-C4-N3	-6.02	120.84	127.18
6	5	1494	MA6	N1-C2-N3	-5.76	119.86	128.58
6	5	1493	MA6	N1-C2-N3	-5.65	120.02	128.58
6	5	1493	MA6	C1'-N9-C8	-5.34	115.25	127.09
6	5	1494	MA6	C1'-N9-C8	-5.17	115.61	127.09
6	5	525	7MG	C5-C6-N1	5.00	119.74	110.94
6	5	1493	MA6	C5-C4-N3	-4.74	120.19	126.72
6	5	1494	MA6	C5-C4-N3	-4.66	120.30	126.72
6	5	525	7MG	C2-N3-C4	4.63	120.28	112.30
6	5	1494	MA6	N9-C8-N7	-4.51	107.54	113.94
4	3	2511	2MA	N9-C8-N7	-4.47	107.59	113.94
6	5	1493	MA6	N9-C8-N7	-4.31	107.82	113.94
6	5	525	7MG	C5-C4-N3	-4.19	120.26	128.13
6	5	1493	MA6	C4-N9-C1'	4.17	136.38	126.63
6	5	1494	MA6	C4-N9-C1'	3.95	135.87	126.63
6	5	1493	MA6	C4-C5-C6	3.92	119.97	115.91
6	5	525	7MG	C4-C5-N7	3.70	109.75	105.38
6	5	1494	MA6	C4-C5-C6	3.68	119.72	115.91
6	5	1494	MA6	C2-N1-C6	3.44	120.24	111.83
4	3	2511	2MA	N3-C4-N9	3.44	131.35	126.99
6	5	1493	MA6	C2-N1-C6	3.42	120.18	111.83
6	5	1494	MA6	C2-N3-C4	3.39	120.11	111.83
6	5	1493	MA6	C2-N3-C4	3.33	119.97	111.83
4	3	2511	2MA	N3-C2-N1	-3.25	120.04	125.77
6	5	525	7MG	C5-C4-N9	3.19	110.42	106.33
6	5	1494	MA6	C5-N7-C8	3.02	108.20	103.45
6	5	1493	MA6	C5-N7-C8	2.91	108.03	103.45
6	5	1493	MA6	N3-C4-N9	2.90	132.10	127.17
6	5	525	7MG	C2-N1-C6	-2.87	119.90	125.11
4	3	2511	2MA	C5-N7-C8	2.81	107.87	103.45
6	5	525	7MG	O6-C6-C5	-2.80	120.75	127.62
4	3	2511	2MA	C4-N9-C8	2.78	108.66	105.74
6	5	1494	MA6	N3-C4-N9	2.77	131.87	127.17
6	5	1494	MA6	C4-N9-C8	2.64	108.51	105.74
6	5	525	7MG	N9-C4-N3	2.64	129.32	125.46
6	5	1493	MA6	C4-N9-C8	2.51	108.38	105.74
4	3	2511	2MA	N6-C6-N1	2.37	120.22	117.03
4	3	2511	2MA	C3'-C2'-C1'	2.34	105.88	101.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	5	1494	MA6	C4-C5-N7	-2.33	107.92	110.58
6	5	525	7MG	N9-C8-N7	2.30	106.62	103.37
6	5	1493	MA6	C4-C5-N7	-2.20	108.06	110.58
4	3	2511	2MA	CM2-C2-N1	2.20	120.42	117.13
4	3	2511	2MA	C4-C5-N7	-2.19	108.07	110.58
6	5	1377	B8T	C6-C5-C4	2.13	119.57	117.00
4	3	783	1MG	N2-C2-N1	-2.07	117.12	118.79
6	5	1375	5MC	O3'-C3'-C2'	-2.02	105.35	111.82

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	3	2259	OMG	C1'-C2'-O2'-CM2
6	5	525	7MG	O4'-C4'-C5'-O5'
6	5	1494	MA6	O4'-C4'-C5'-O5'
6	5	525	7MG	C3'-C4'-C5'-O5'
6	5	1494	MA6	C3'-C4'-C5'-O5'
4	3	2259	OMG	O4'-C4'-C5'-O5'
4	3	2511	2MA	C3'-C4'-C5'-O5'
4	3	2511	2MA	O4'-C4'-C5'-O5'
4	3	2259	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	3	783	1MG	3	0
6	5	1493	MA6	1	0
4	3	2259	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 316 ligands modelled in this entry, 315 are monoatomic - leaving 1 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	$\# Z > 2$
59	CLM	3	3001	-	20,20,20	2.09	2 (10%)	23,27,27	0.85	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
59	CLM	3	3001	-	-	2/20/22/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	3	3001	CLM	C2-N2	7.45	1.50	1.34
59	3	3001	CLM	O9B-N9	-2.61	1.18	1.22

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	3	3001	CLM	C5-C3-C4-O4
59	3	3001	CLM	N2-C3-C4-O4

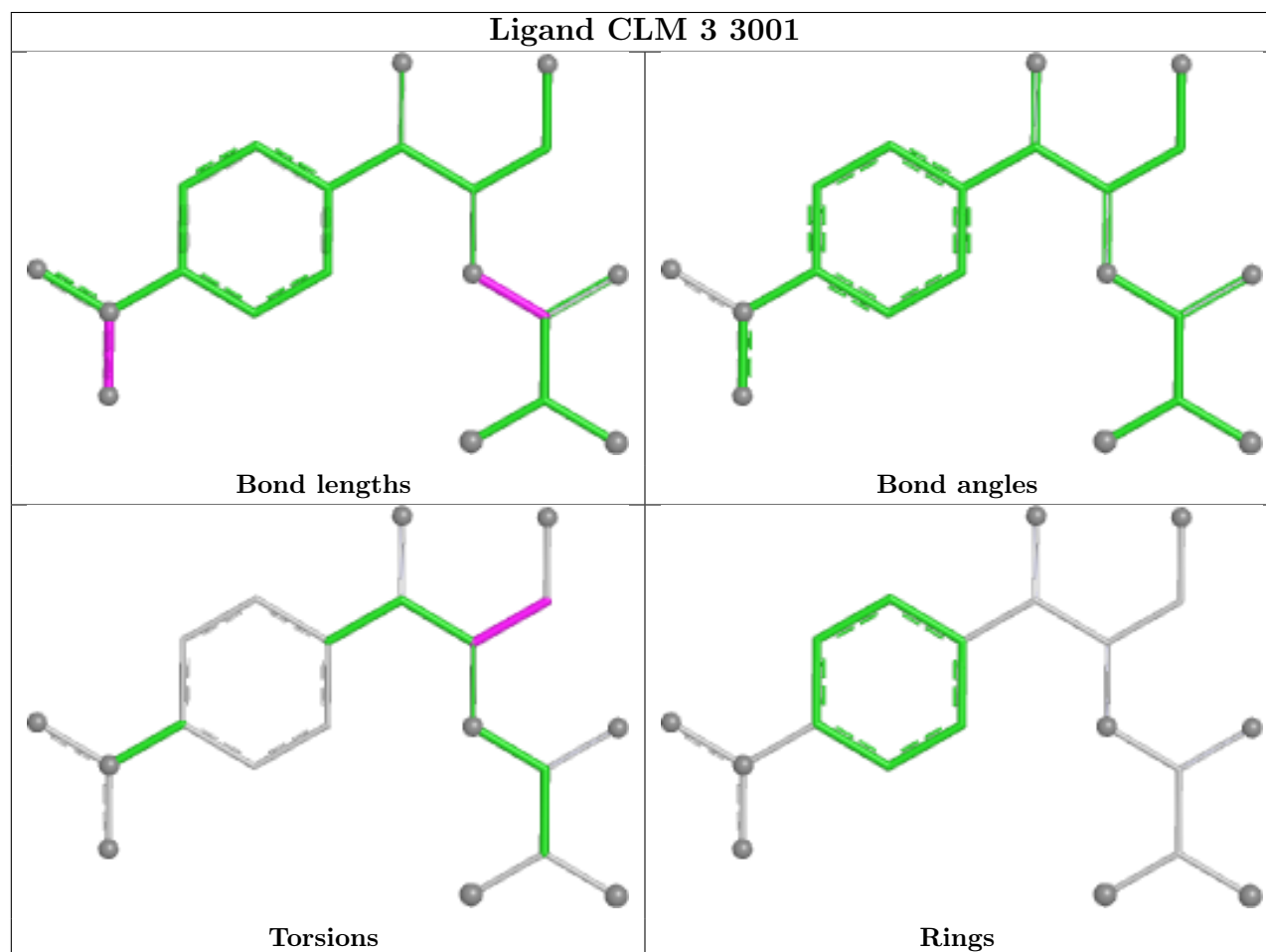
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	3	3001	CLM	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.

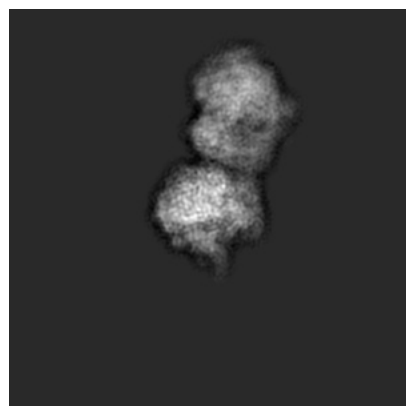
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17145. These allow visual inspection of the internal detail of the map and identification of artifacts.

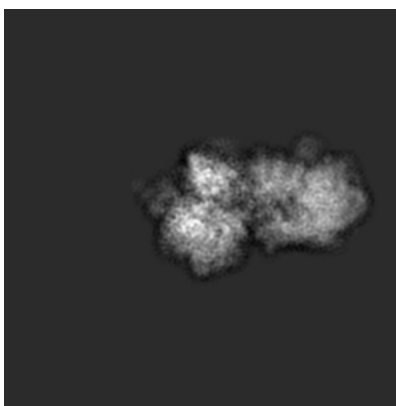
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

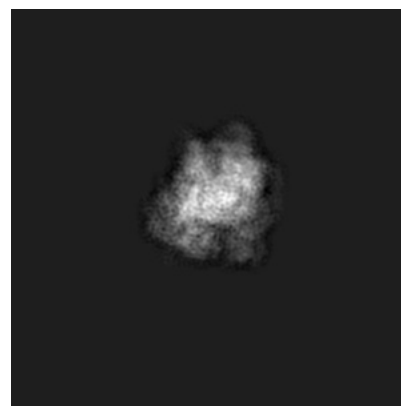
6.1.1 Primary map



X

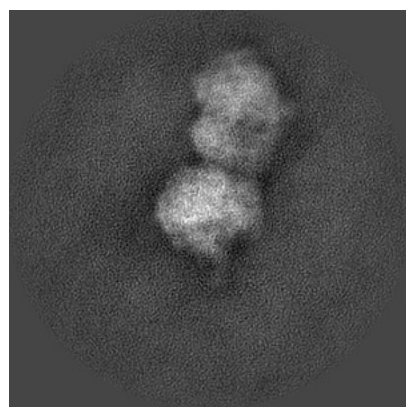


Y

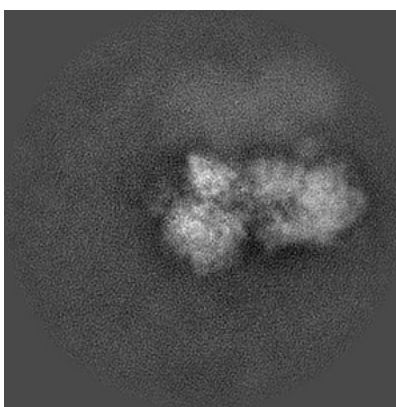


Z

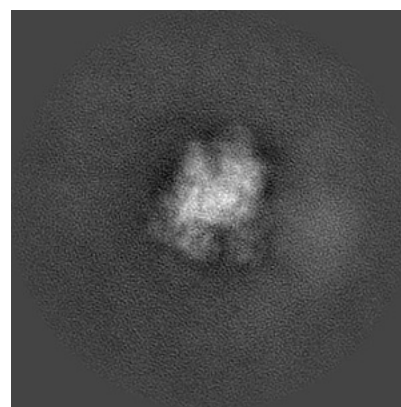
6.1.2 Raw map



X



Y

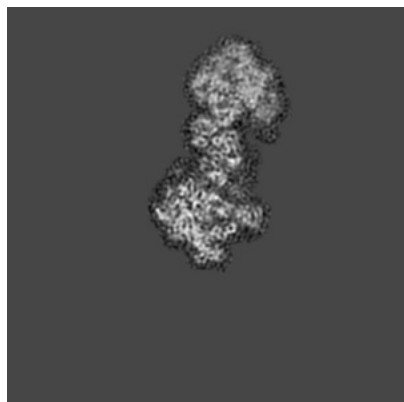


Z

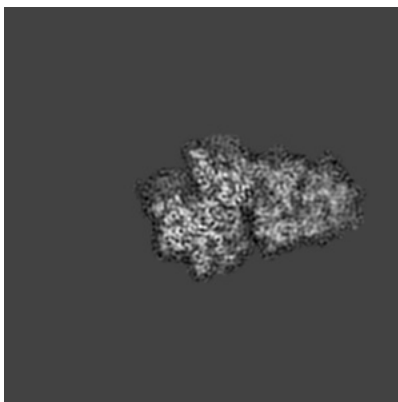
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

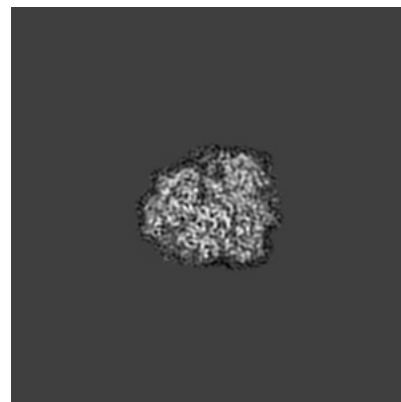
6.2.1 Primary map



X Index: 128

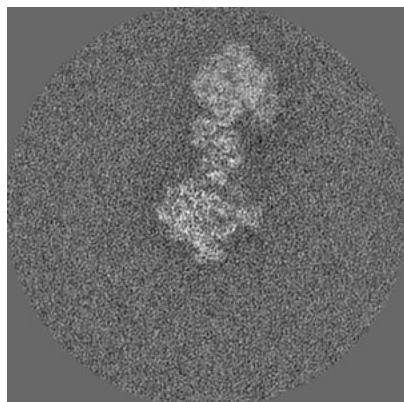


Y Index: 128

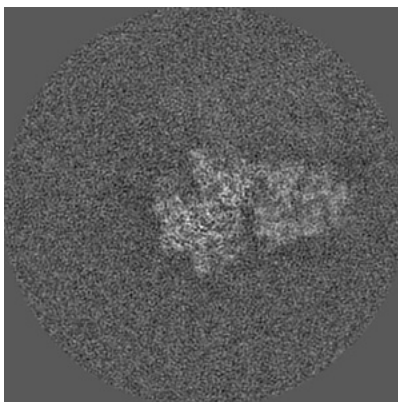


Z Index: 128

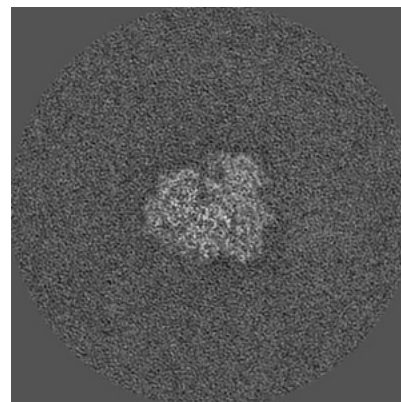
6.2.2 Raw map



X Index: 128



Y Index: 128

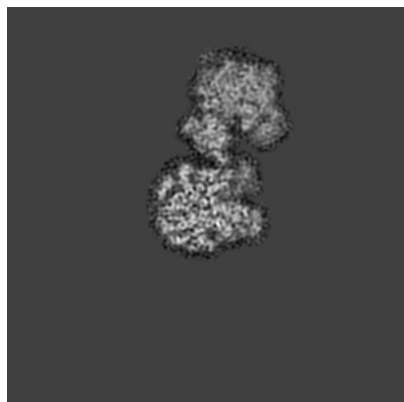


Z Index: 128

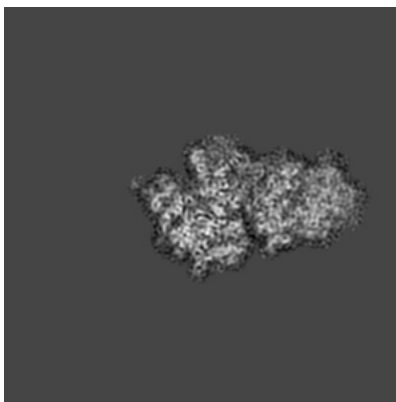
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

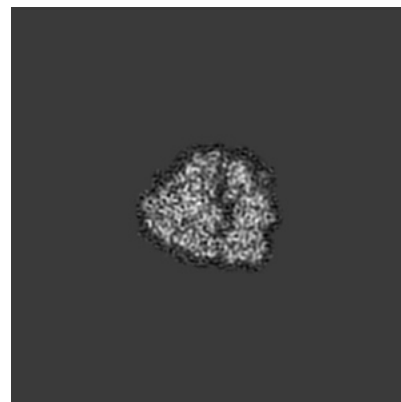
6.3.1 Primary map



X Index: 117

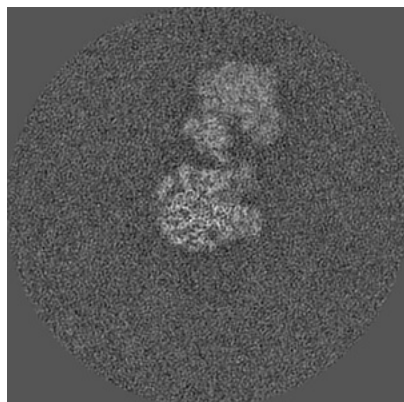


Y Index: 131

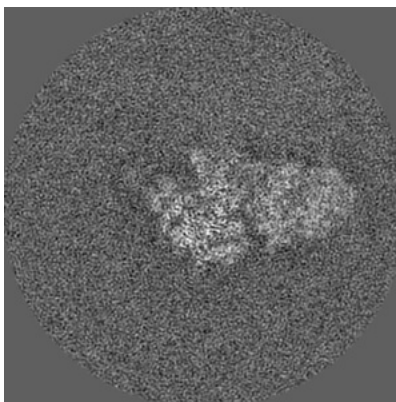


Z Index: 124

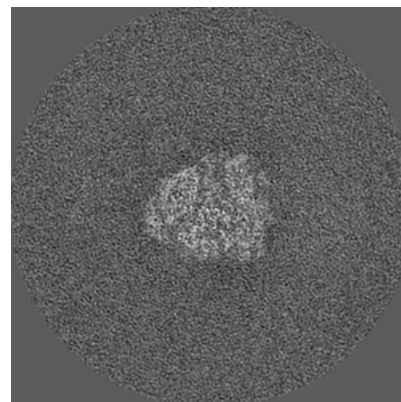
6.3.2 Raw map



X Index: 117



Y Index: 131

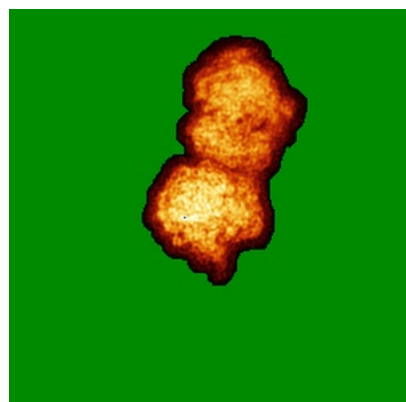


Z Index: 127

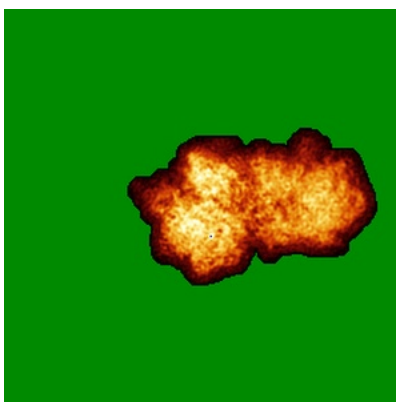
The images above show the largest variance slices of the map in three orthogonal directions.

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

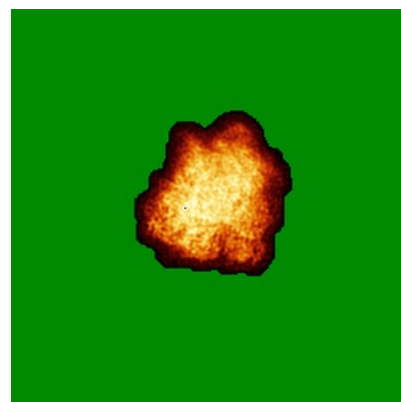
6.4.1 Primary map



X

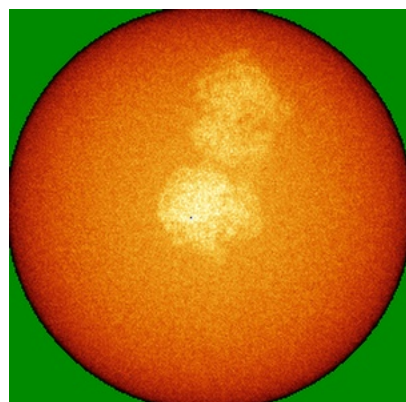


Y

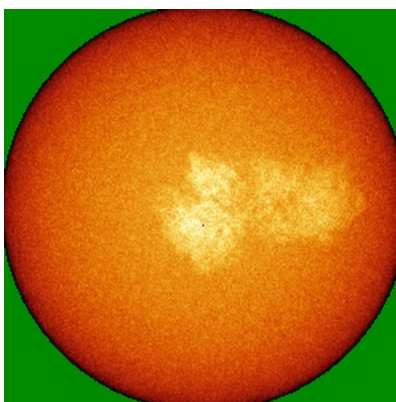


Z

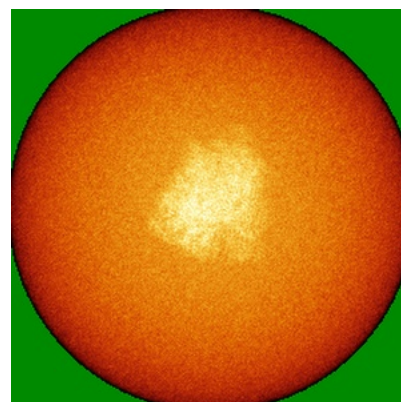
6.4.2 Raw map



X



Y



Z

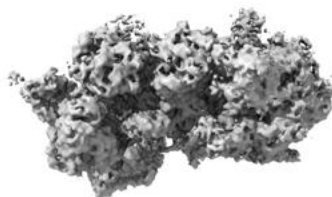
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

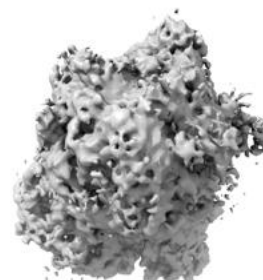
6.5.1 Primary map



X



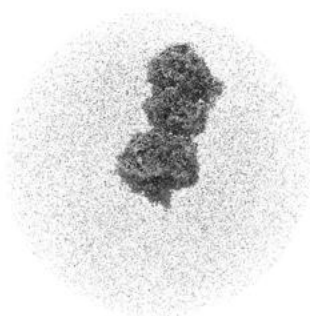
Y



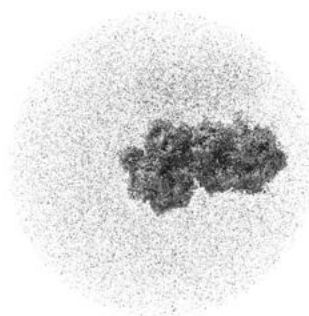
Z

The images above show the 3D surface view of the map at the recommended contour level 1.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

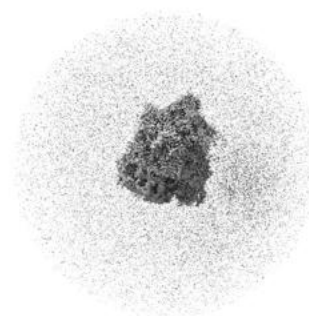
6.5.2 Raw map



X



Y



Z

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

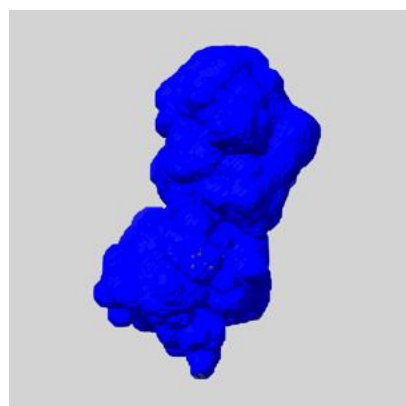
6.6 Mask visualisation [i](#)

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

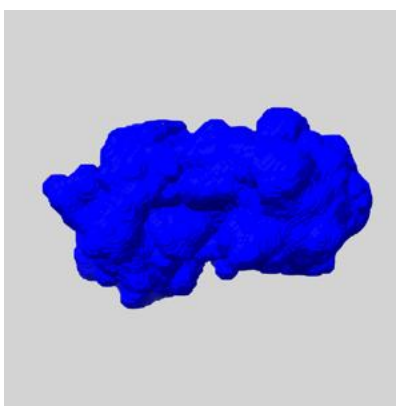
A mask typically either:

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

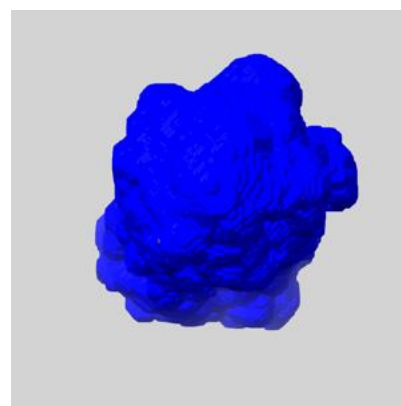
6.6.1 emd_17145_msk_1.map [i](#)



X



Y

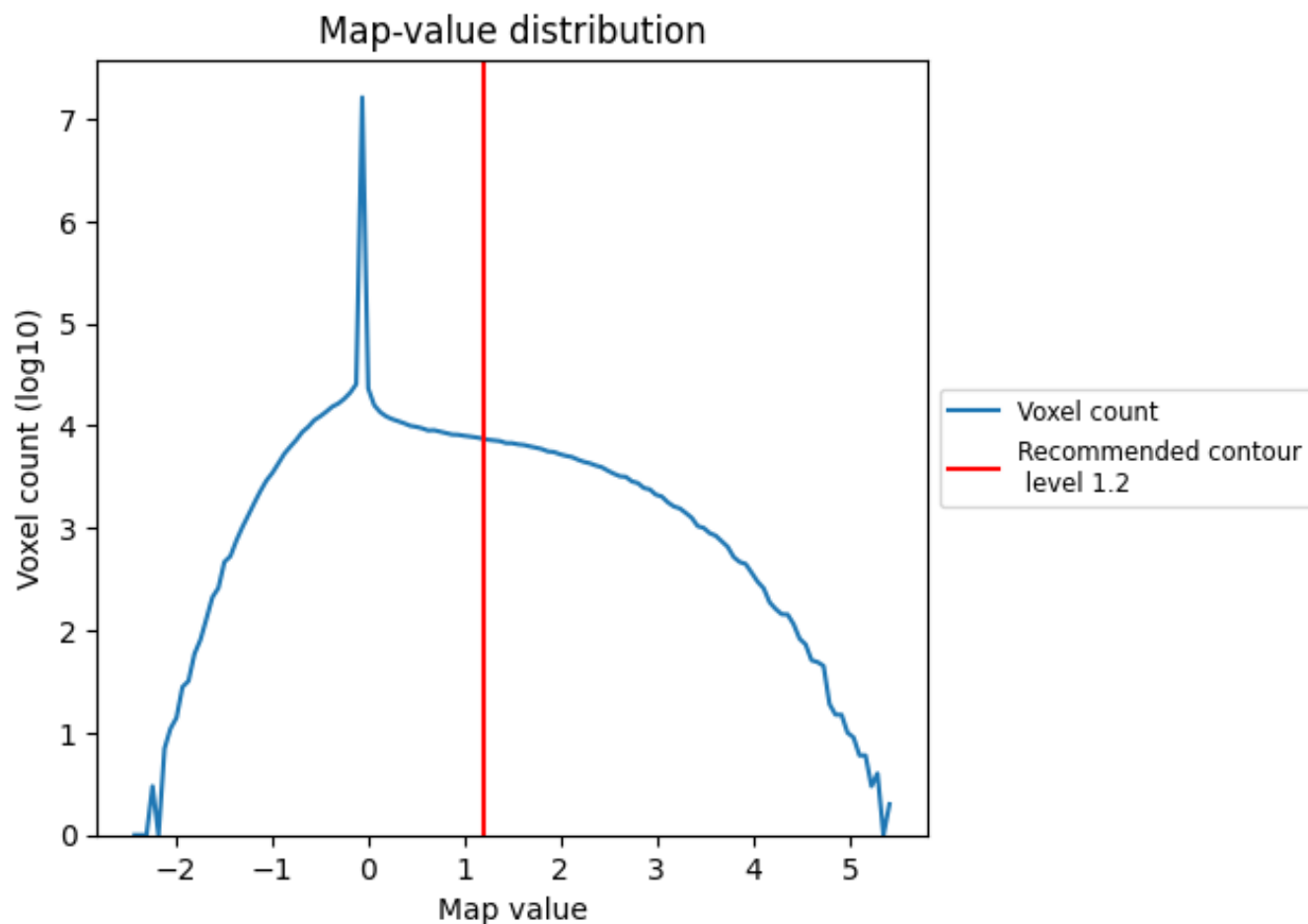


Z

7 Map analysis [i](#)

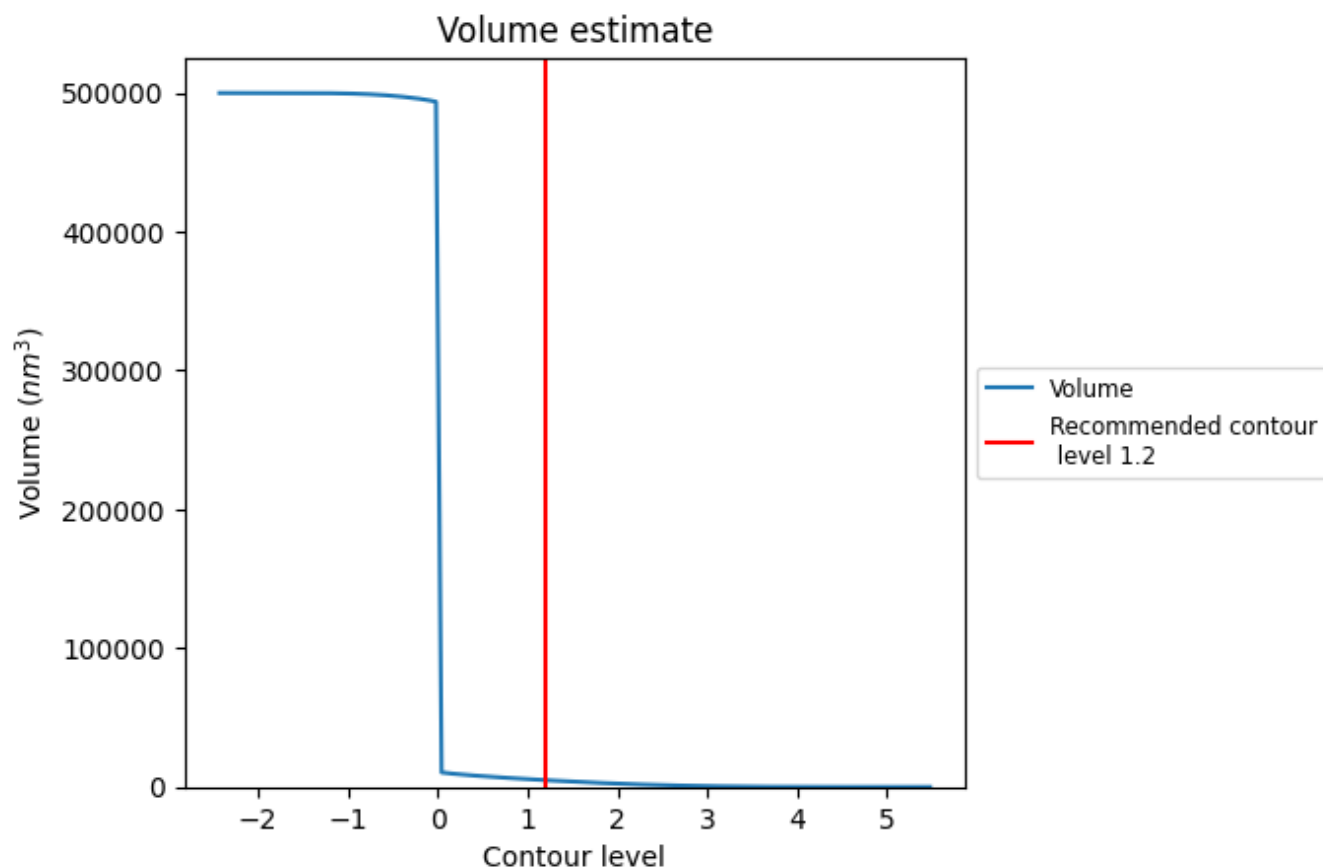
This section contains the results of statistical analysis of the map.

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.

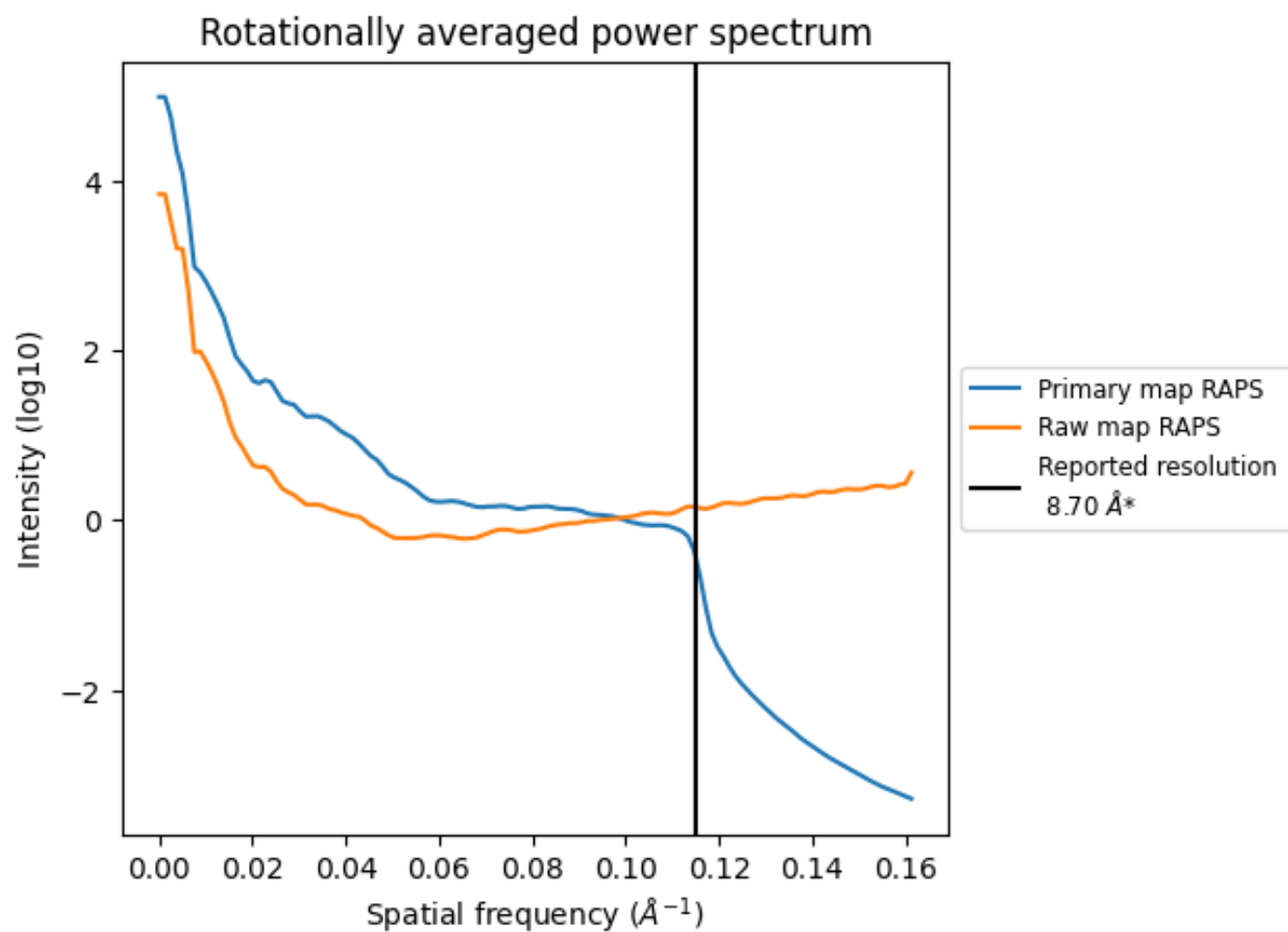
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4893 nm^3 ; this corresponds to an approximate mass of 4420 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 ⓘ

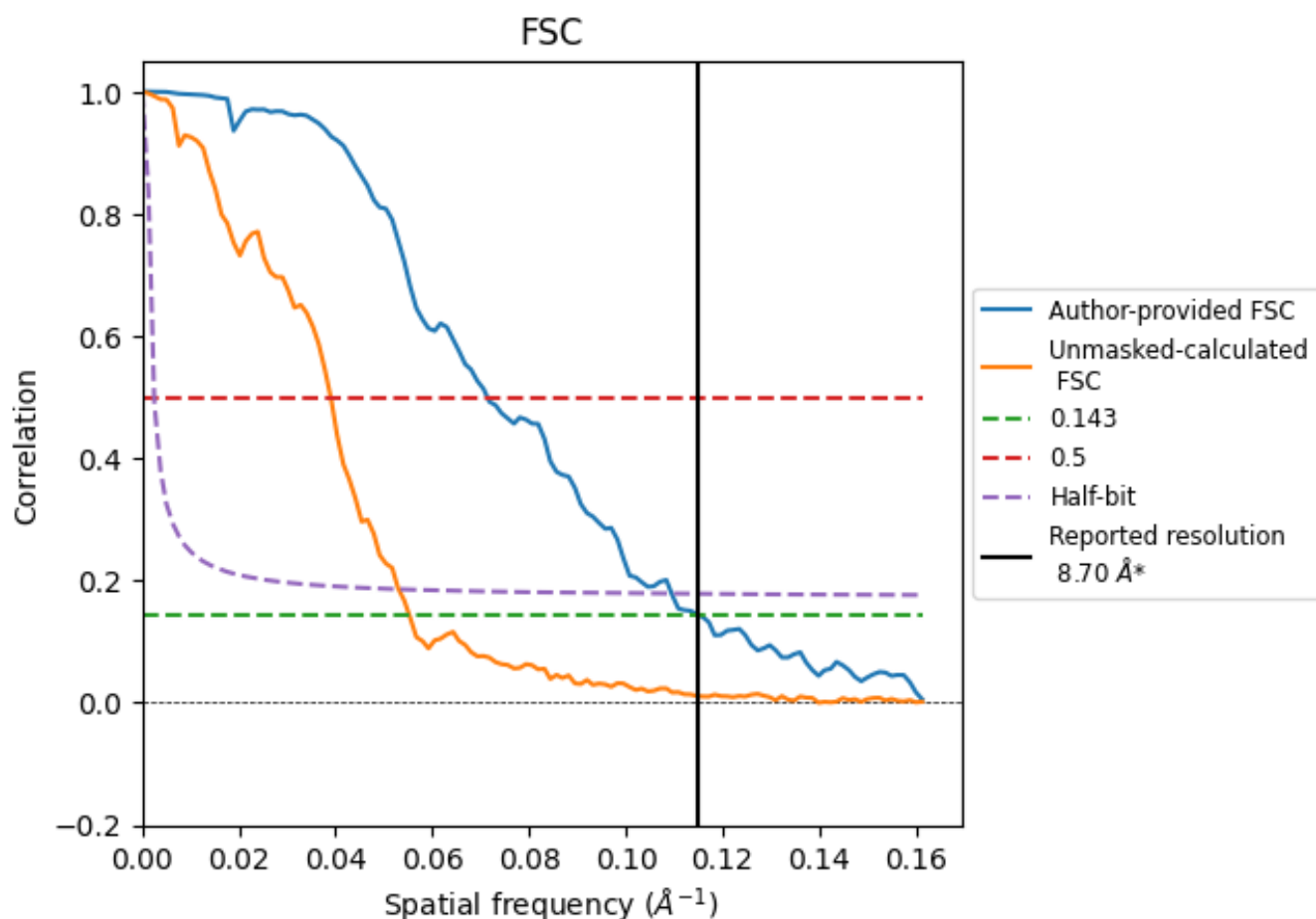


*Reported resolution corresponds to spatial frequency of 0.115 Å⁻¹

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 0.115 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

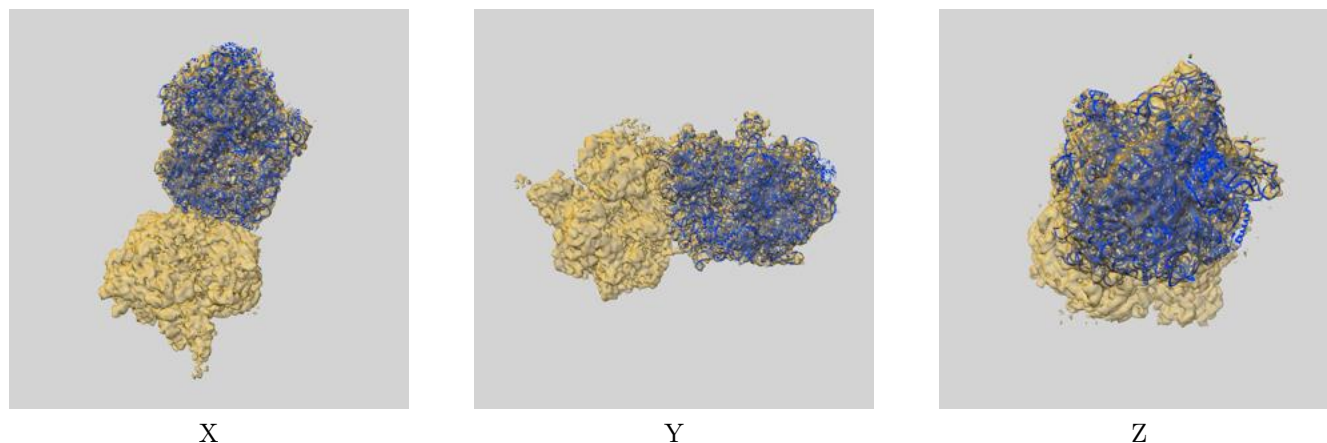
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.70	-	-
Author-provided FSC curve	8.68	14.01	9.13
Unmasked-calculated*	18.08	25.71	18.83

*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 18.08 differs from the reported value 8.7 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17145 and PDB model 8P8W. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



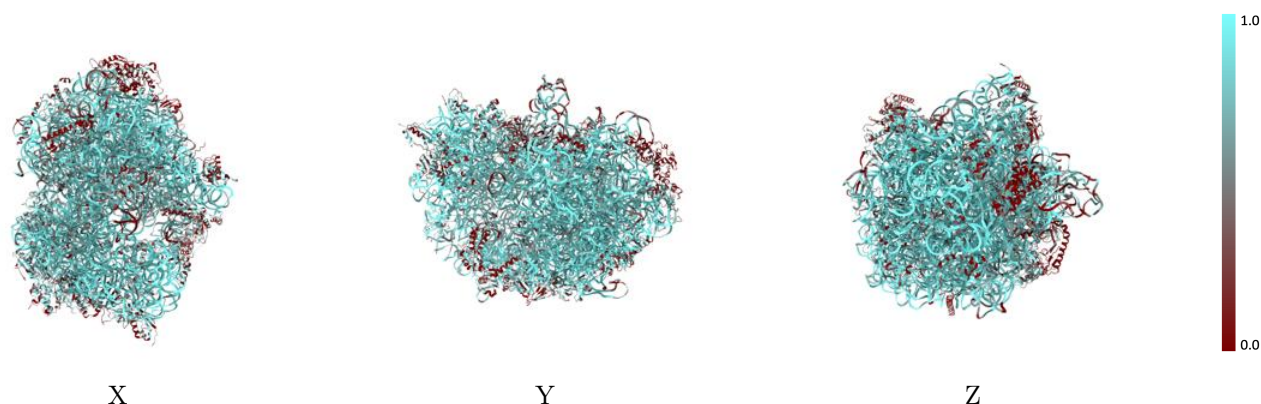
The images above show the 3D surface view of the map at the recommended contour level 1.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



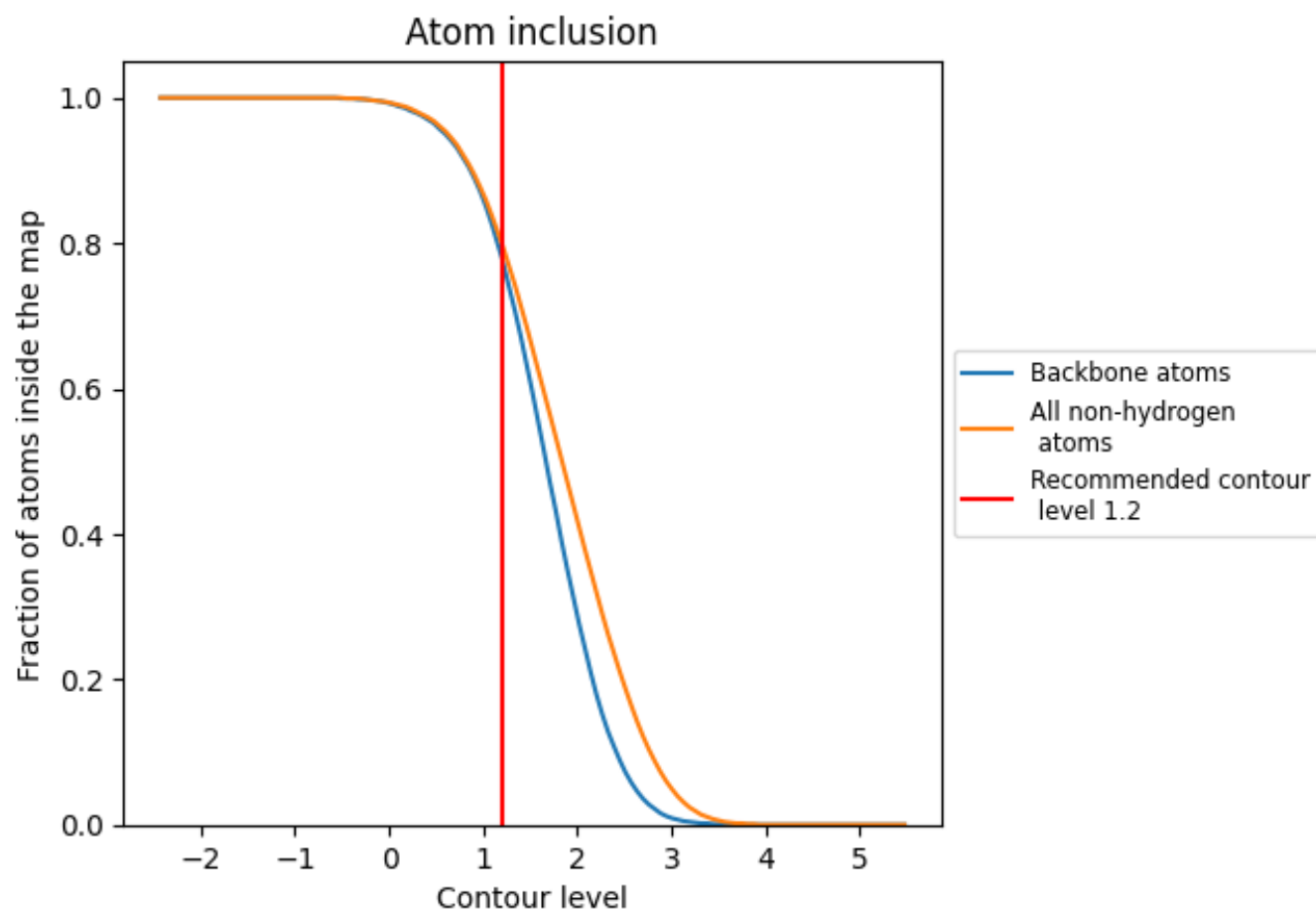
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (1.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8000	 0.1070
0	 0.7730	 0.0600
1	 0.7720	 0.0250
2	 0.8280	 0.0470
3	 0.9090	 0.1110
4	 0.8440	 0.0940
5	 0.9450	 0.1390
6	 0.3120	 0.0370
7	 0.8440	 0.1400
A	 0.5340	 0.1330
B	 0.5980	 0.1260
C	 0.6970	 0.1340
D	 0.5490	 0.1380
E	 0.5910	 0.1420
F	 0.6460	 0.1170
G	 0.6170	 0.1040
H	 0.6700	 0.0840
I	 0.5560	 0.0880
J	 0.7060	 0.1090
K	 0.6840	 0.1020
L	 0.6610	 0.0890
M	 0.7590	 0.0890
N	 0.7240	 0.1390
O	 0.7320	 0.0820
P	 0.6770	 0.1220
Q	 0.6270	 0.1190
R	 0.6910	 0.0810
S	 0.8540	 0.1100
T	 0.6430	 0.1400
U	 0.0650	 0.0250
X	 0.2090	 0.0830
Y	 0.6830	 0.1210
Z	 0.3740	 0.0170
a	 0.6680	 0.0610
b	 0.6670	 0.0530



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	 0.5230	 0.0460
d	 0.4860	 0.0750
e	 0.5300	 0.0720
f	 0.0820	 0.0390
g	 0.3180	 0.0540
h	 0.1740	 0.0270
i	 0.7780	 0.0780
j	 0.5340	 0.0690
k	 0.5770	 0.0380
l	 0.7390	 0.0670
m	 0.8010	 0.0970
n	 0.4970	 0.0520
o	 0.6210	 0.1010
p	 0.7690	 0.0620
q	 0.5270	 0.0470
r	 0.7510	 0.1020
s	 0.7340	 0.0600
t	 0.5020	 0.0800
u	 0.7590	 0.0310
v	 0.6990	 0.0830
w	 0.3980	 0.0770
x	 0.3170	 0.0920
y	 0.8010	 0.0860
z	 0.5130	 0.0190