



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 04:07 PM UTC

PDB ID : 5UYK / pdb_00005uyk
EMDB ID : EMD-8615
Title : 70S ribosome bound with cognate ternary complex not base-paired to A site codon (Structure I)
Authors : Loveland, A.B.; Demo, G.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2017-02-24
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

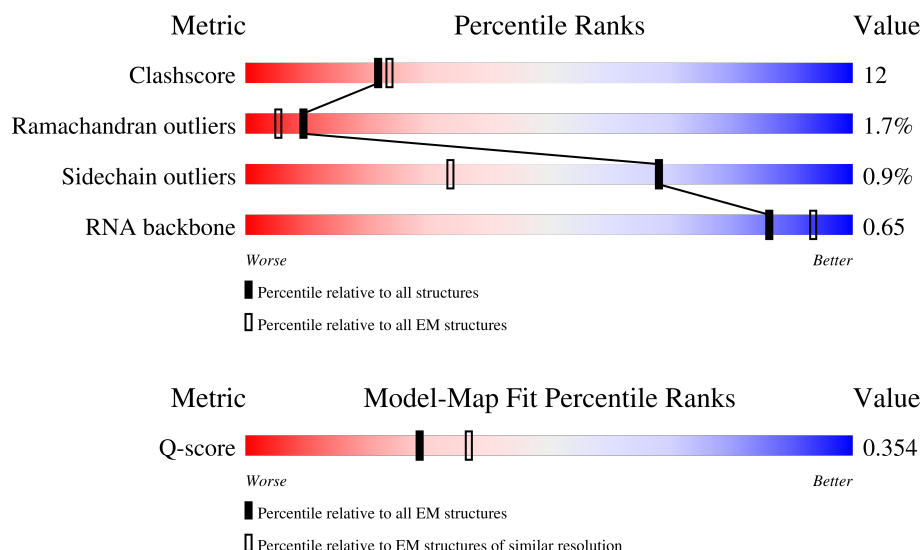
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



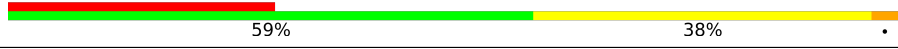
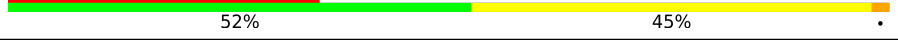
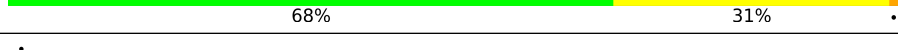
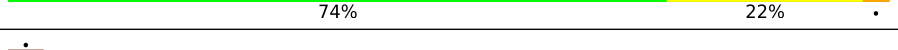
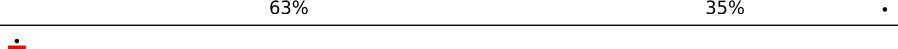
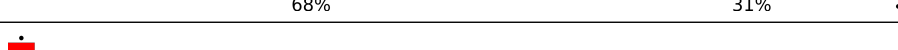
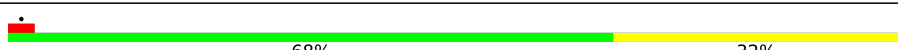
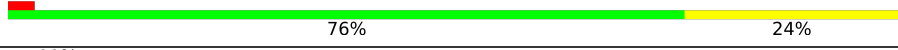
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	04	271	
2	05	209	
3	06	201	

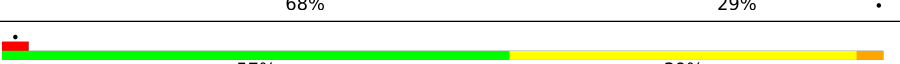
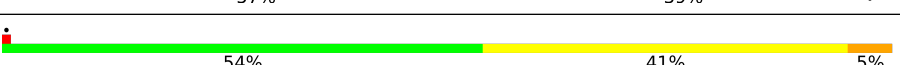
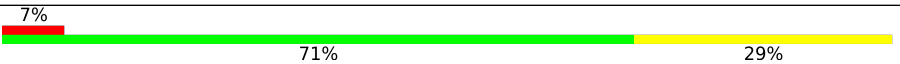
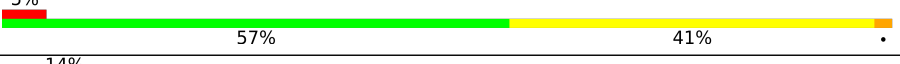
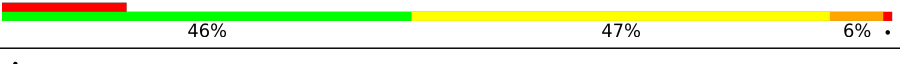
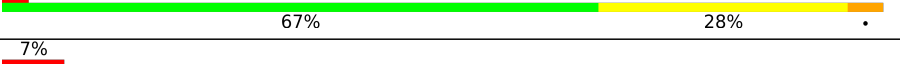
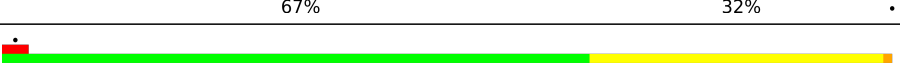
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	07	177	
5	08	176	
6	09	149	
7	10	131	
8	11	141	
9	12	142	
10	13	122	
11	14	143	
12	15	136	
13	16	120	
14	17	116	
15	18	114	
16	19	117	
17	20	103	
18	21	110	
19	22	93	
20	23	102	
21	24	94	
22	25	75	
23	26	77	
24	27	63	
25	28	58	
26	29	66	
27	30	56	
28	31	50	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	32	46	
30	33	64	
31	34	38	
32	B	218	
33	C	206	
34	D	205	
35	E	157	
36	F	100	
37	G	151	
38	H	129	
39	I	127	
40	J	98	
41	K	116	
42	L	123	
43	M	114	
44	N	100	
45	O	88	
46	P	82	
47	Q	80	
48	R	65	
49	S	79	
50	T	85	
51	U	65	
52	03	223	
53	A	1539	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	01	2903	
55	02	120	
56	W	77	
56	X	77	
57	V	20	
58	Y	76	
59	Z	392	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 154412 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	04	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	05	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	06	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	07	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	08	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	10	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	12	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	13	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	14	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	15	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	16	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	17	116	Total	C	N	O	0	0
			892	552	178	162		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
15	18	114	Total	C	N	O	S	0
			917	574	179	163	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
16	19	117	Total	C	N	O		0
			947	604	192	151		0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	20	103	Total	C	N	O	S	0
			816	516	153	145	2	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	21	110	Total	C	N	O	S	0
			857	532	166	156	3	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
19	22	93	Total	C	N	O	S	0
			739	466	139	132	2	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	23	102	Total	C	N	O		0
			780	492	146	142		0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	24	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	25	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	26	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	27	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	28	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	29	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	30	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	31	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	32	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	34	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 33 is a protein called 30S ribosomal protein S3.

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

- Molecule 34 is a protein called 30S ribosomal protein S4.

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

- Molecule 35 is a protein called 30S ribosomal protein S5.

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

- Molecule 36 is a protein called 30S ribosomal protein S6.

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

- Molecule 37 is a protein called 30S ribosomal protein S7.

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

- Molecule 38 is a protein called 30S ribosomal protein S8.

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

- Molecule 39 is a protein called 30S ribosomal protein S9.

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

- Molecule 40 is a protein called 30S ribosomal protein S10.

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

- Molecule 41 is a protein called 30S ribosomal protein S11.

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

- Molecule 42 is a protein called 30S ribosomal protein S12.

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

- Molecule 43 is a protein called 30S ribosomal protein S13.

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

- Molecule 44 is a protein called 30S ribosomal protein S14.

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

- Molecule 45 is a protein called 30S ribosomal protein S15.

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

- Molecule 46 is a protein called 30S ribosomal protein S16.

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

- Molecule 47 is a protein called 30S ribosomal protein S17.

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

- Molecule 48 is a protein called 30S ribosomal protein S18.

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

- Molecule 49 is a protein called 30S ribosomal protein S19.

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

- Molecule 50 is a protein called 30S ribosomal protein S20.

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

- Molecule 51 is a protein called 30S ribosomal protein S21.

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

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	03	223	Total	C	N	O	S	0	0
			1662	1039	302	315	6		

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

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

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	01	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	747	C	U	conflict	GB 802133627

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	02	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

- Molecule 56 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
56	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	V	20	Total	C	N	O	P	0	0
			432	195	86	132	19		

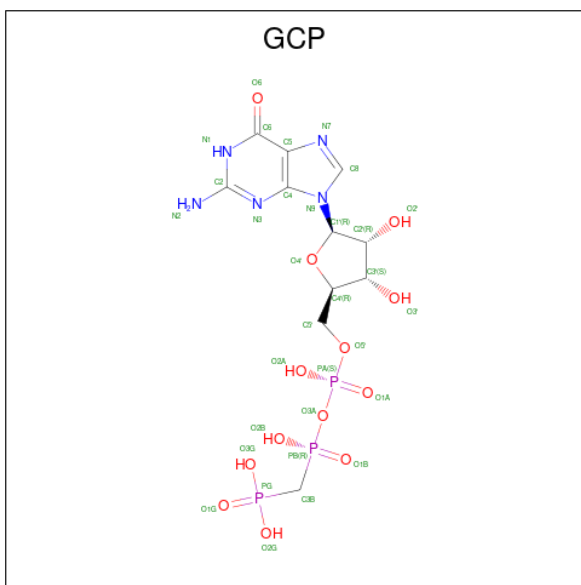
- Molecule 58 is a RNA chain called tRNAPhe.

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

- Molecule 59 is a protein called Elongation factor Tu 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Z	392	Total	C	N	O	S	0	0
			3029	1915	521	580	13		

- Molecule 60 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

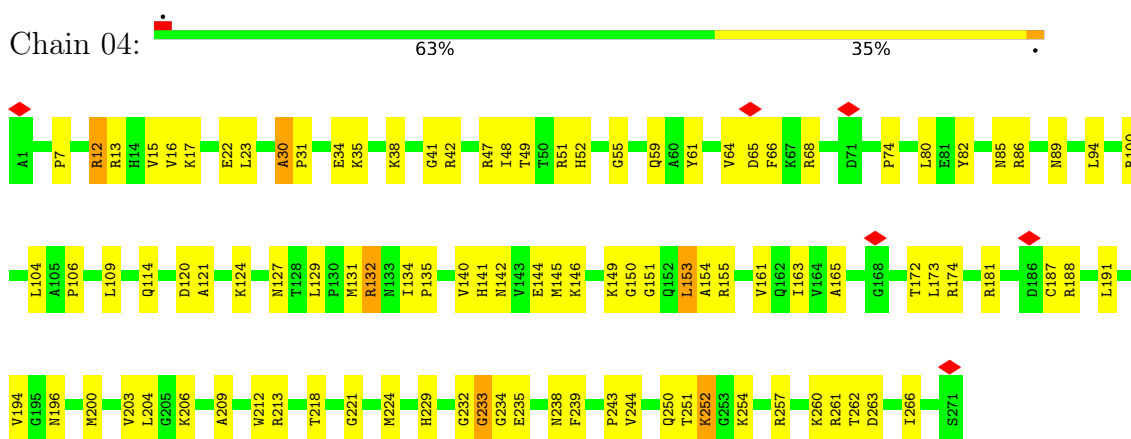


Mol	Chain	Residues	Atoms					AltConf
60	Z	1	Total	C	N	O	P	0
			32	11	5	13	3	

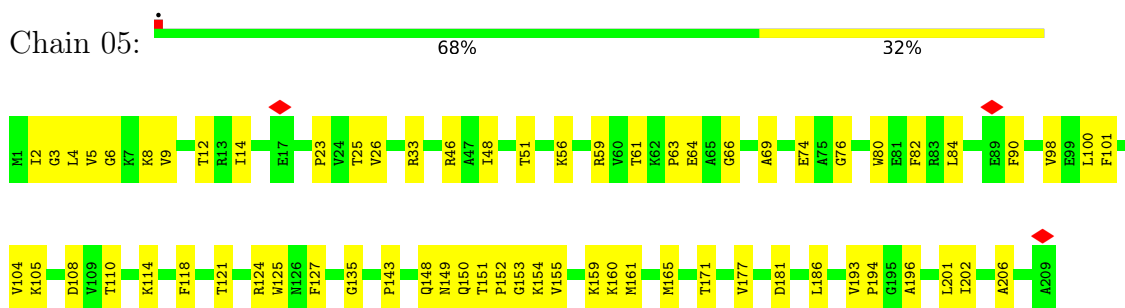
3 Residue-property plots

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

- Molecule 1: 50S ribosomal protein L2



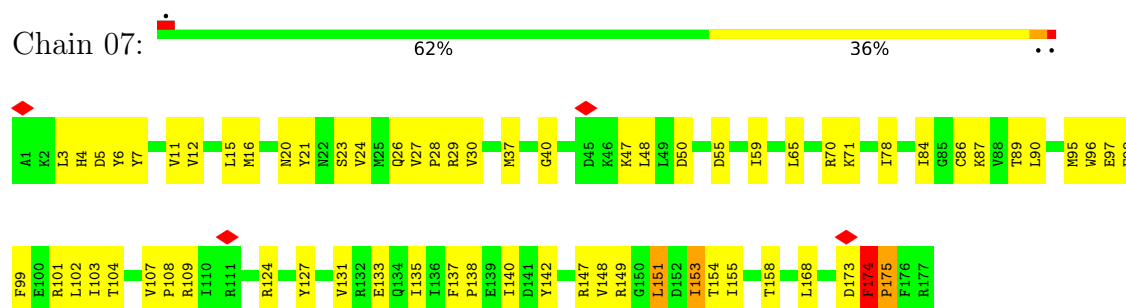
- Molecule 2: 50S ribosomal protein L3



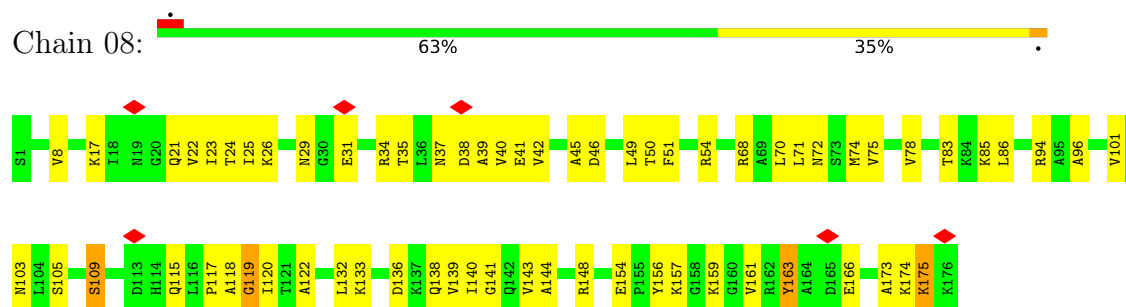
- Molecule 3: 50S ribosomal protein L4



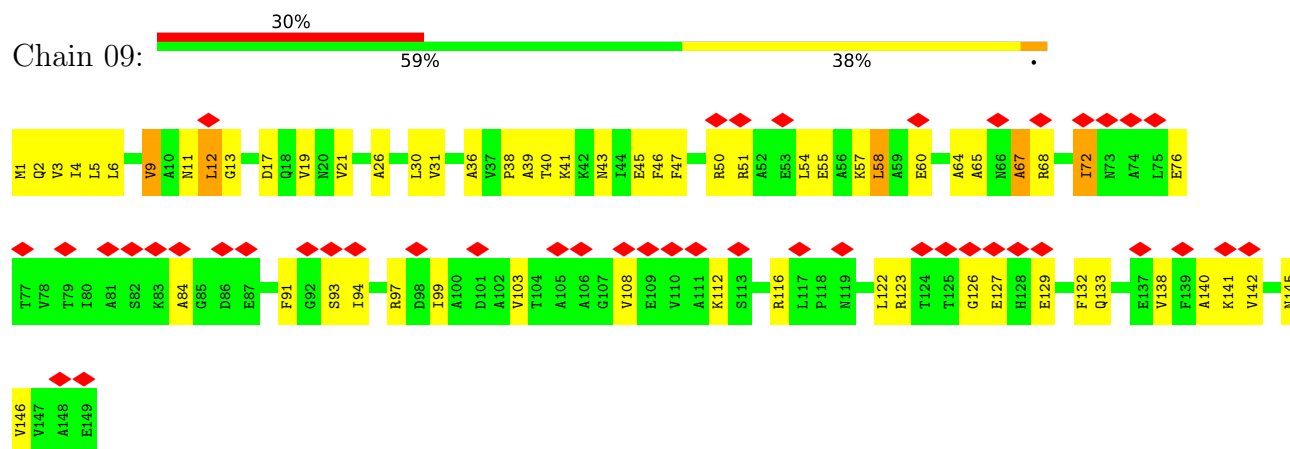
- Molecule 4: 50S ribosomal protein L5



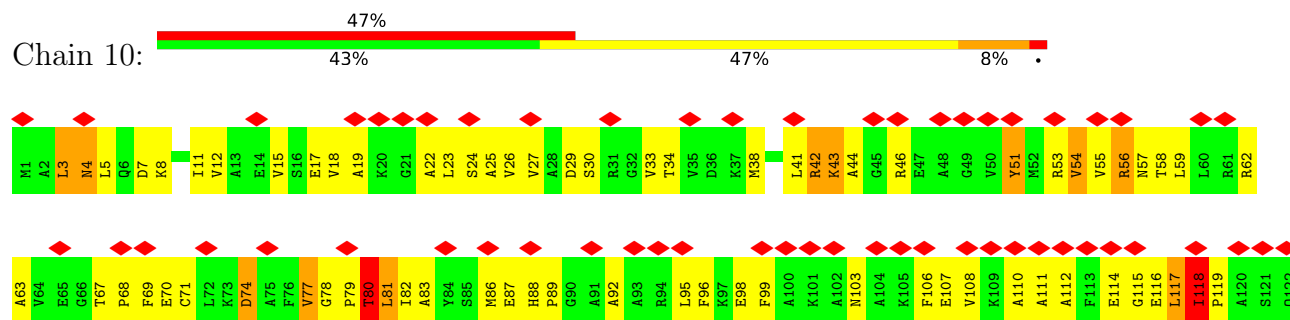
- Molecule 5: 50S ribosomal protein L6

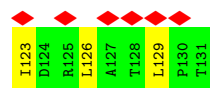


- Molecule 6: 50S ribosomal protein L9

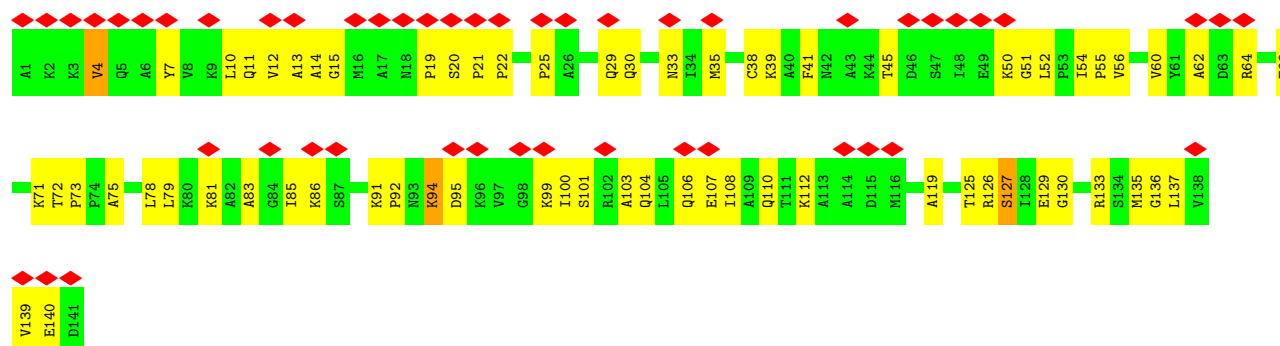


- Molecule 7: 50S ribosomal protein L10

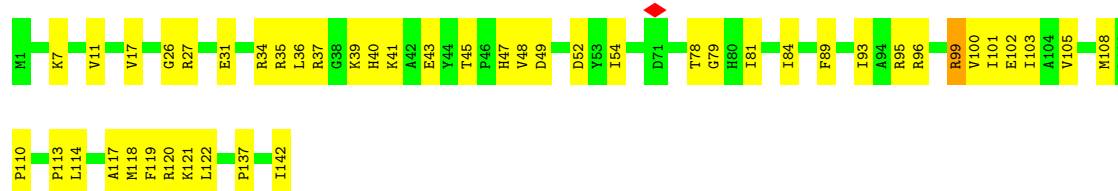




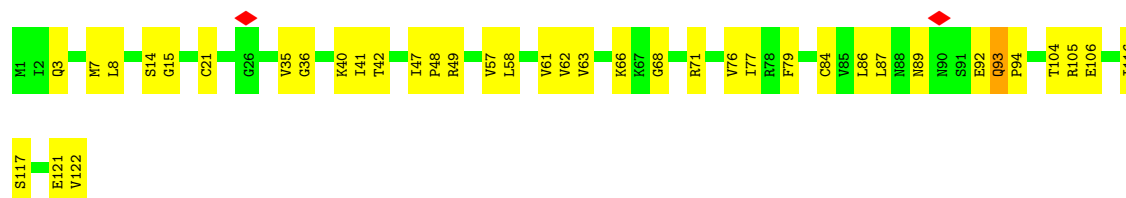
• Molecule 8: 50S ribosomal protein L11



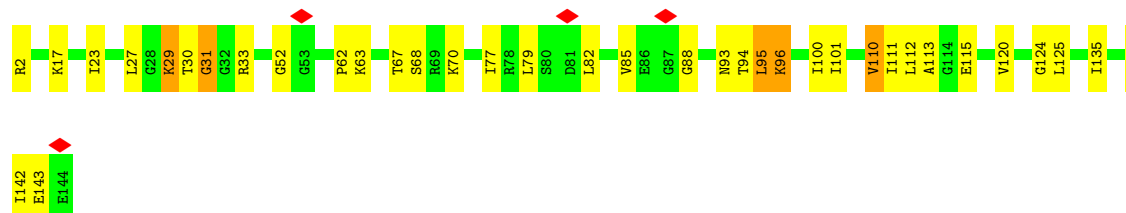
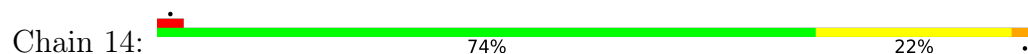
• Molecule 9: 50S ribosomal protein L13



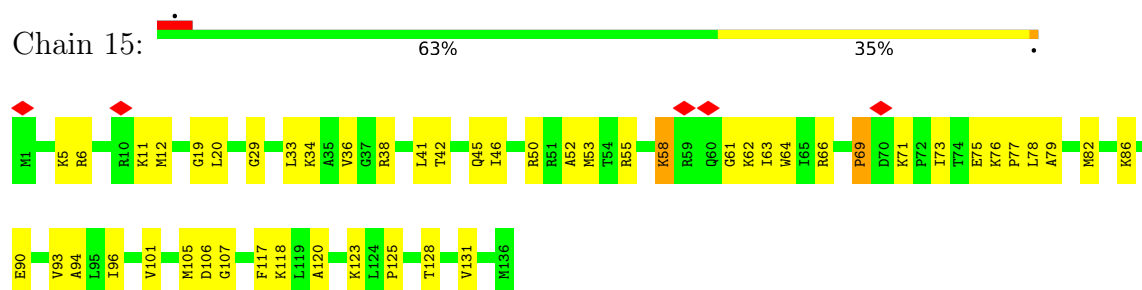
• Molecule 10: 50S ribosomal protein L14



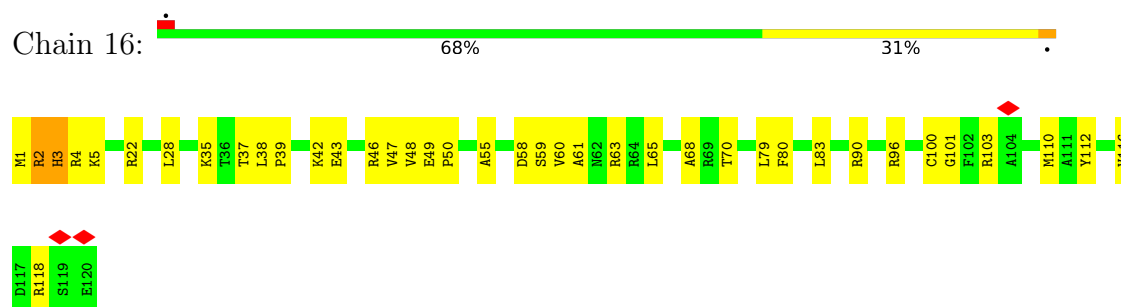
• Molecule 11: 50S ribosomal protein L15



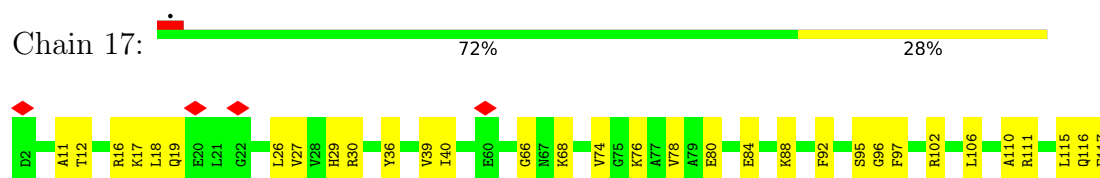
- Molecule 12: 50S ribosomal protein L16



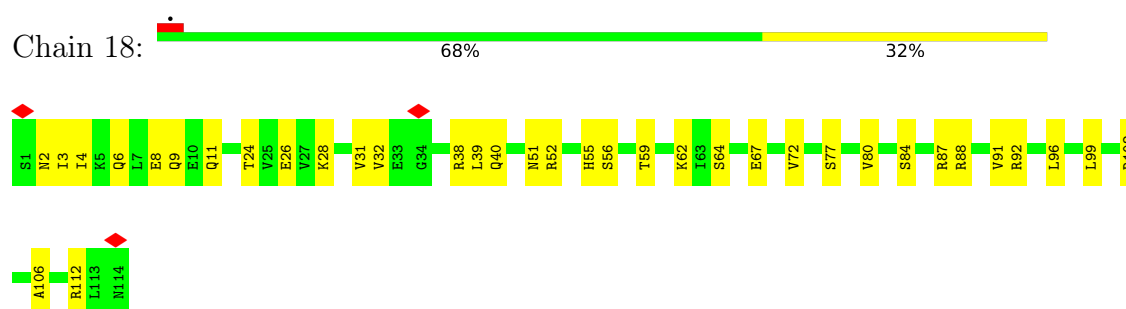
- Molecule 13: 50S ribosomal protein L17



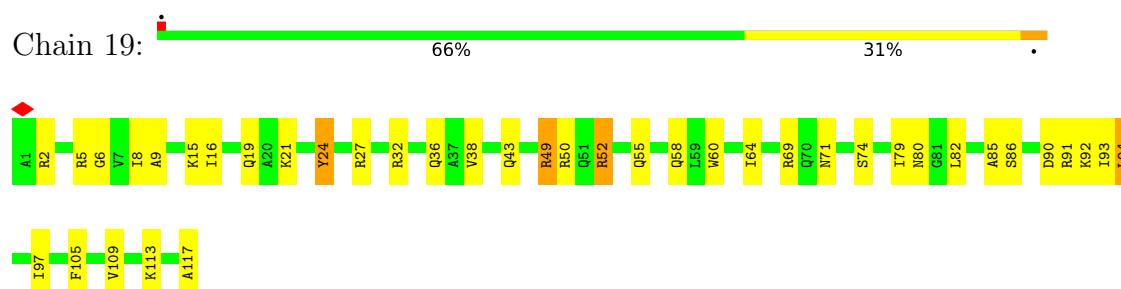
- Molecule 14: 50S ribosomal protein L18



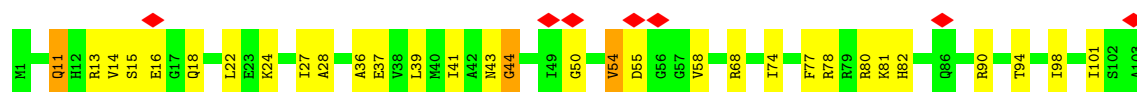
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20



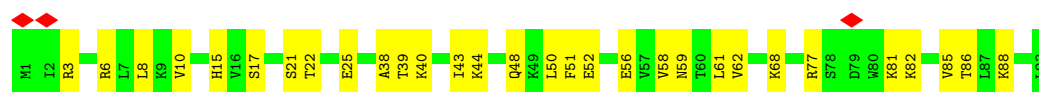
- Molecule 17: 50S ribosomal protein L21



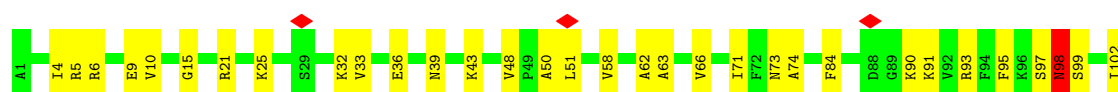
- Molecule 18: 50S ribosomal protein L22



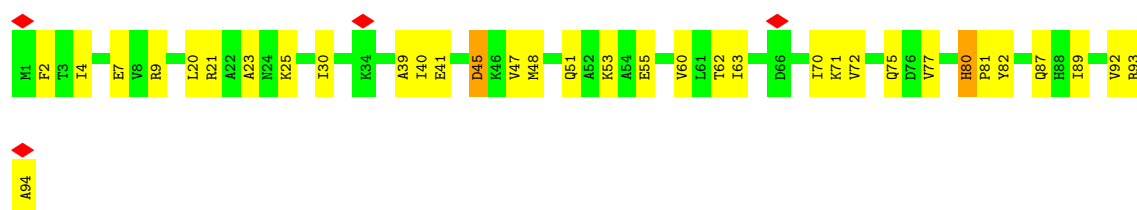
- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25

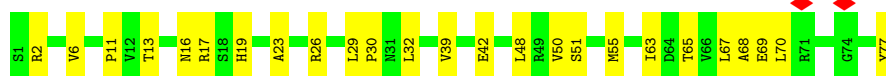


- Molecule 22: 50S ribosomal protein L27

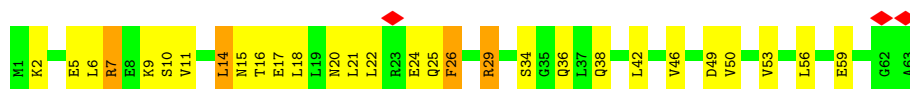




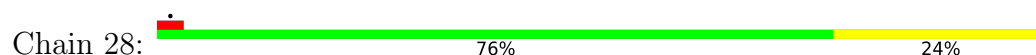
- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30



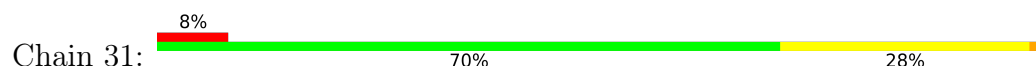
- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32

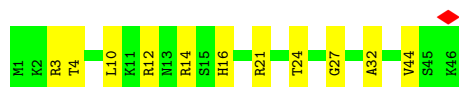


- Molecule 28: 50S ribosomal protein L33



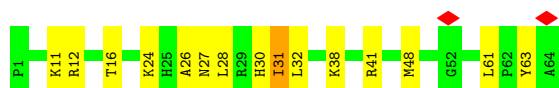
- Molecule 29: 50S ribosomal protein L34

Chain 32:  76% 24%



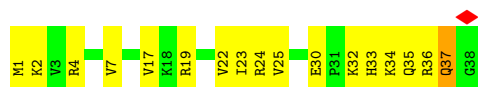
- Molecule 30: 50S ribosomal protein L35

Chain 33:  77% 22%



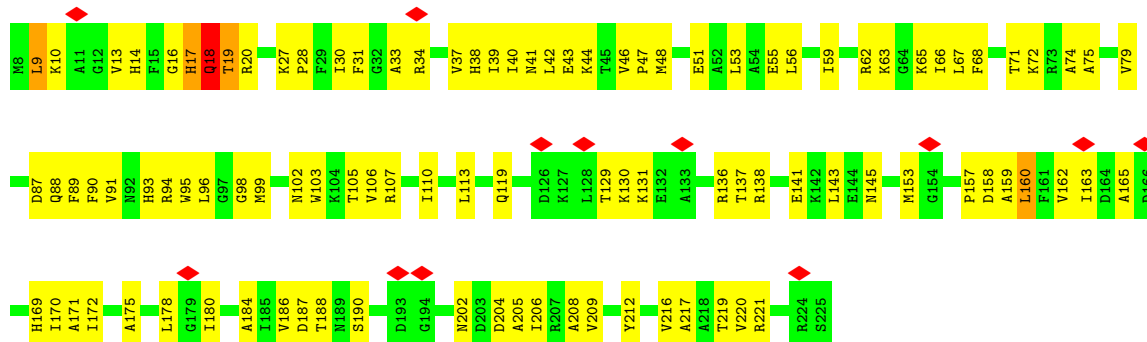
- Molecule 31: 50S ribosomal protein L36

Chain 34:  55% 42%



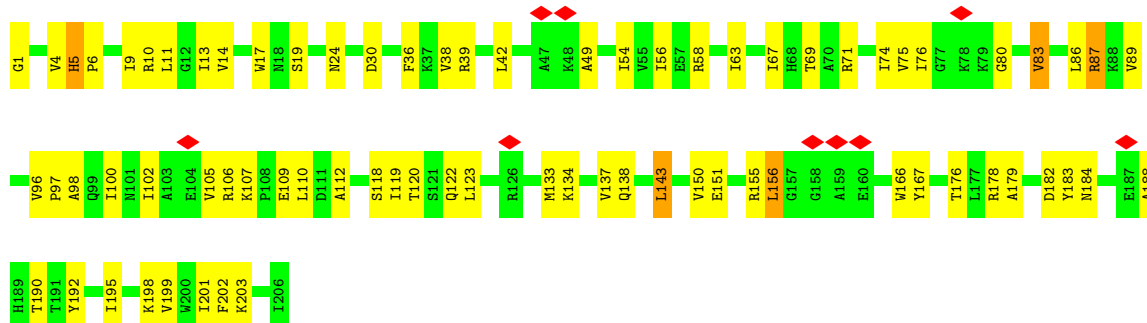
- Molecule 32: 30S ribosomal protein S2

Chain B:  6% 53% 44%

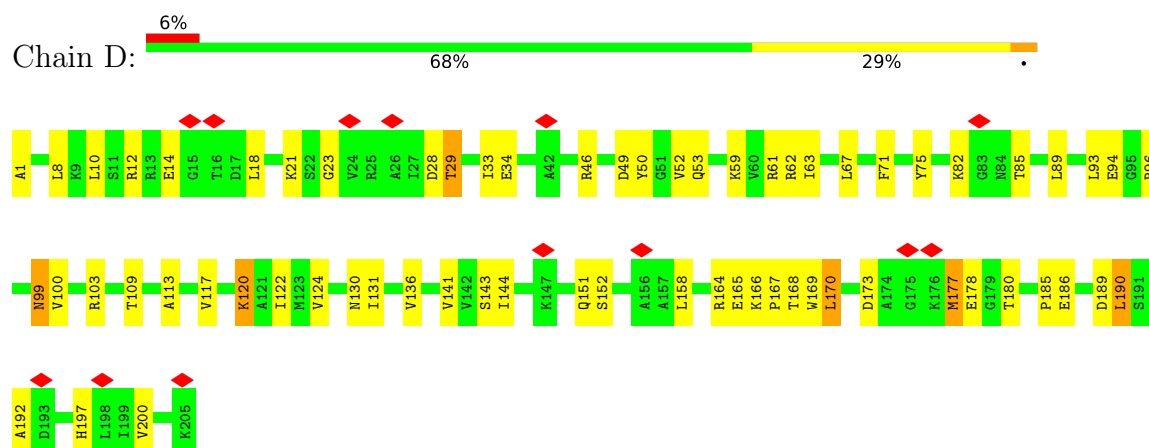


- Molecule 33: 30S ribosomal protein S3

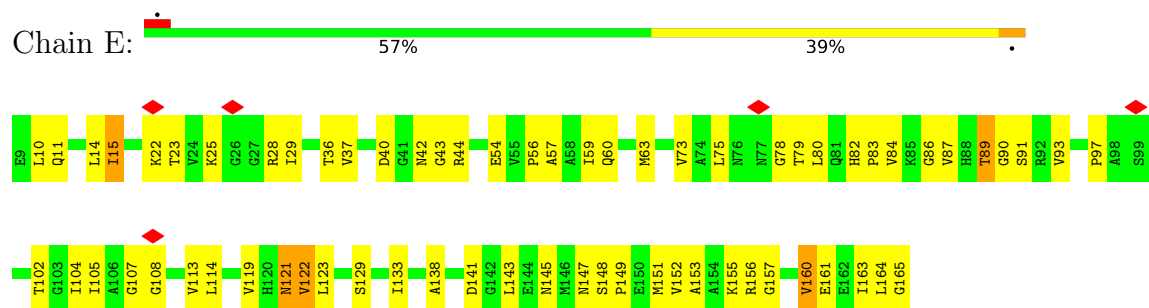
Chain C:  64% 34%



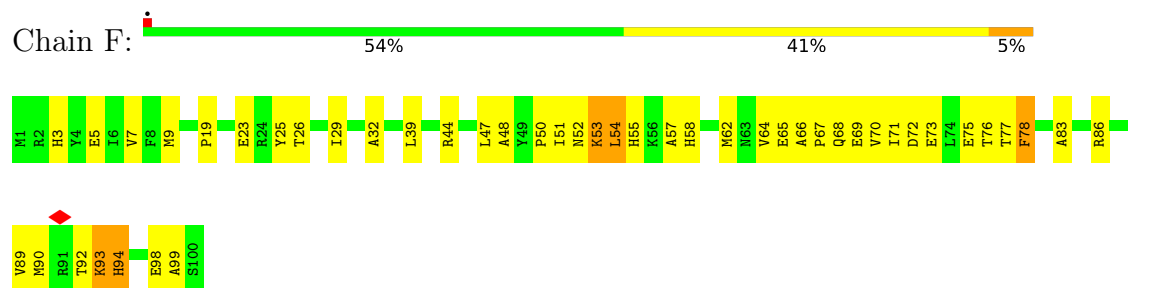
- Molecule 34: 30S ribosomal protein S4



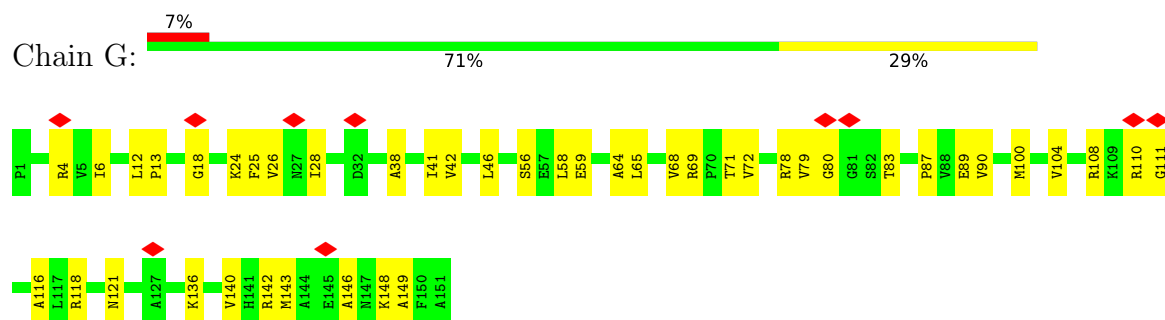
- Molecule 35: 30S ribosomal protein S5



- Molecule 36: 30S ribosomal protein S6

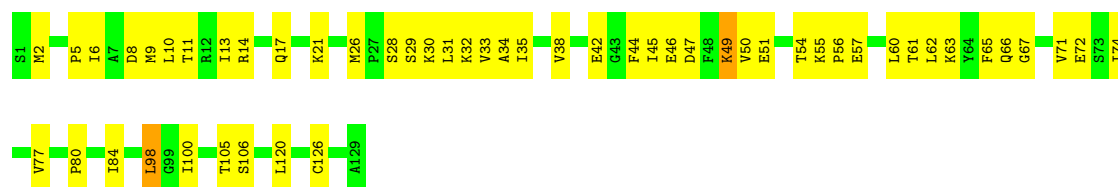


- Molecule 37: 30S ribosomal protein S7



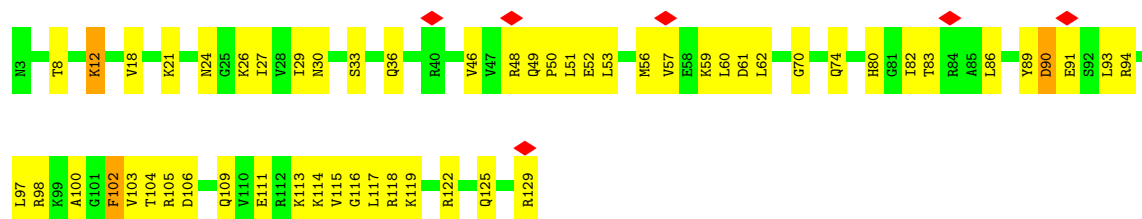
- Molecule 38: 30S ribosomal protein S8

Chain H:  60% 39%



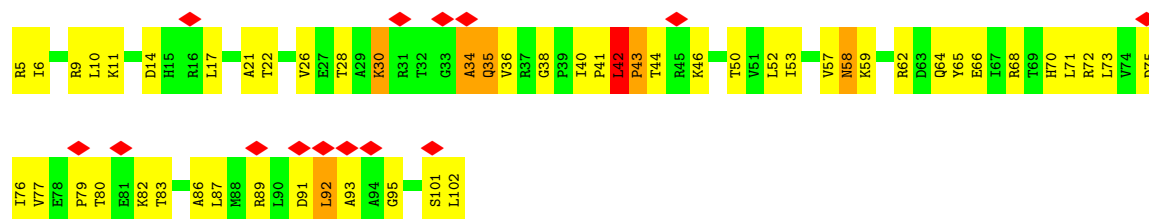
- Molecule 39: 30S ribosomal protein S9

Chain I:  5% 57% 41%



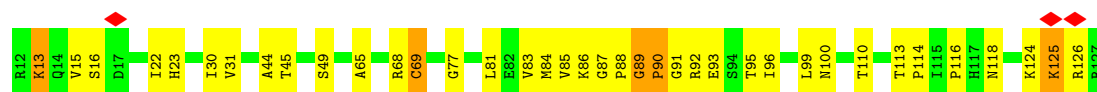
- Molecule 40: 30S ribosomal protein S10

Chain J:  14% 46% 47% 6%



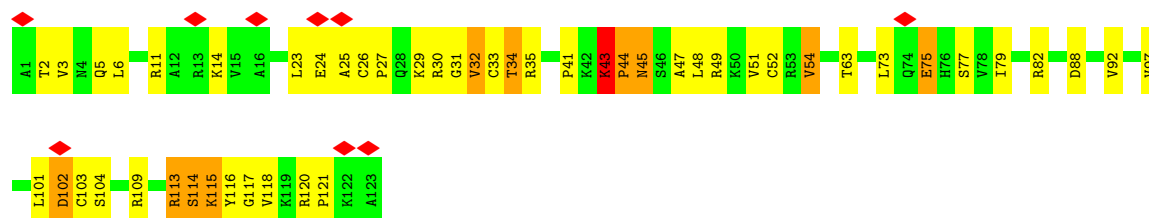
- Molecule 41: 30S ribosomal protein S11

Chain K:  67% 28%



- Molecule 42: 30S ribosomal protein S12

Chain L:  7% 59% 32% 8%



- Molecule 43: 30S ribosomal protein S13

Chain M:  67% 32%



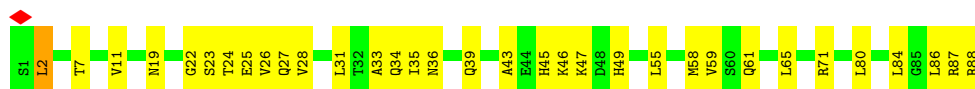
- Molecule 44: 30S ribosomal protein S14

Chain N:  66% 33%



- Molecule 45: 30S ribosomal protein S15

Chain O:  63% 36%



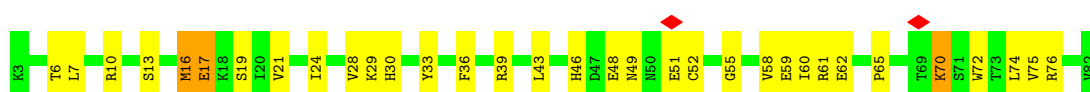
- Molecule 46: 30S ribosomal protein S16

Chain P:  60% 39%



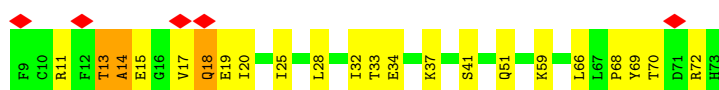
- Molecule 47: 30S ribosomal protein S17

Chain Q:  59% 38%



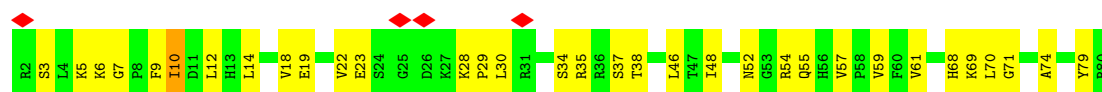
- Molecule 48: 30S ribosomal protein S18

Chain R:  66% 29% 5%



- Molecule 49: 30S ribosomal protein S19

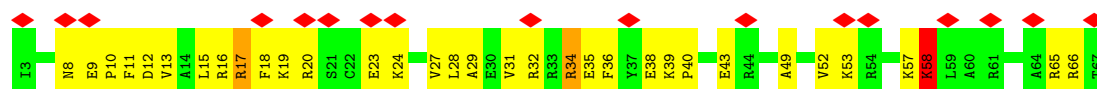
Chain S:  58% 41% 5%



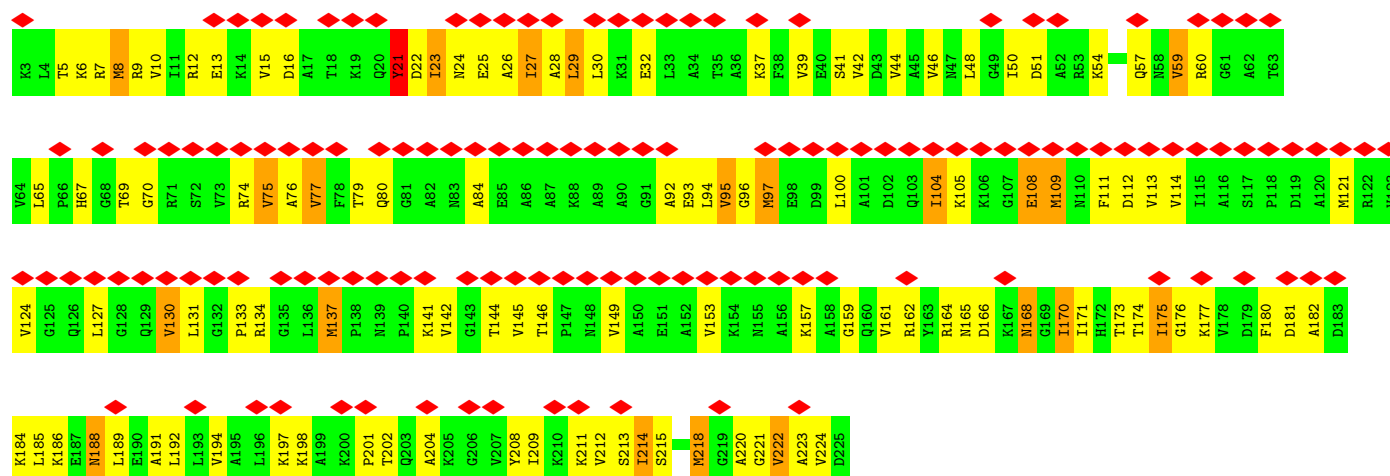
- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21

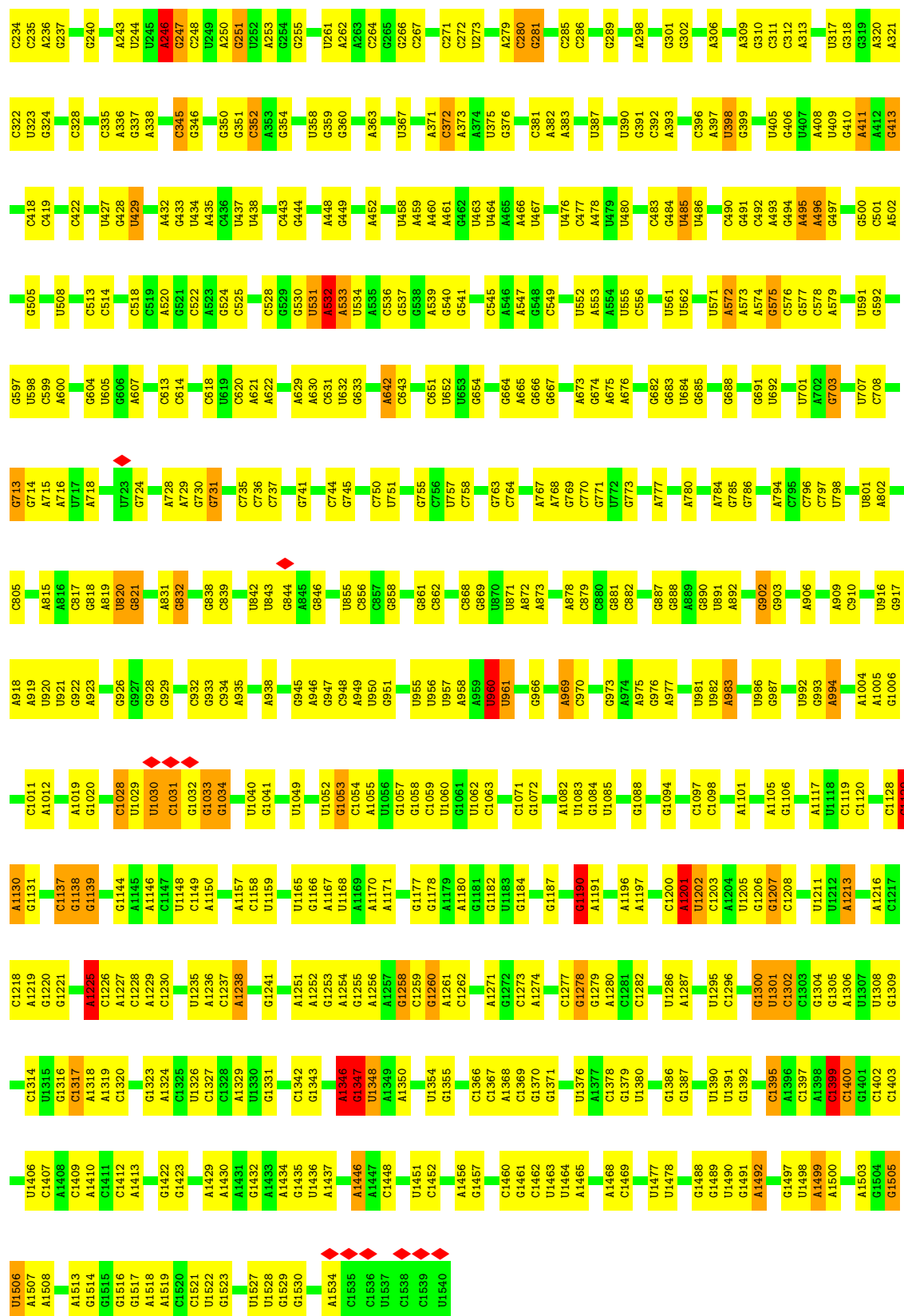


- Molecule 52: 50S ribosomal protein L1



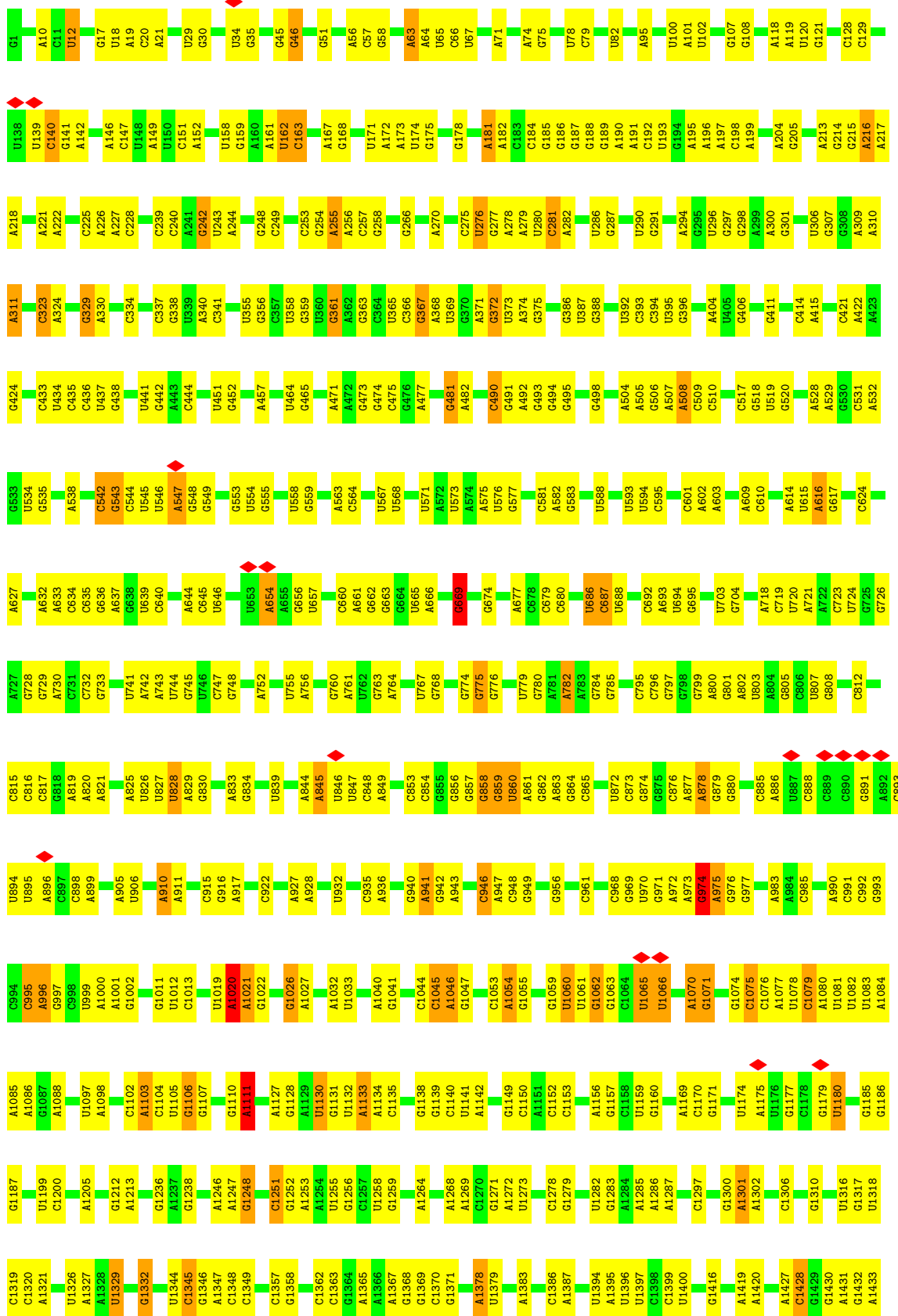
- Molecule 53: 16S ribosomal RNA



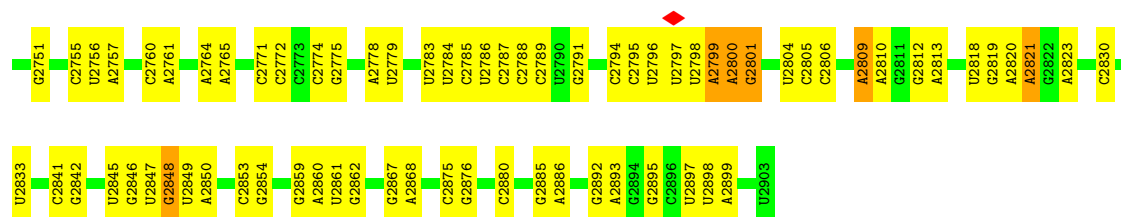


• Molecule 54: 23S ribosomal RNA

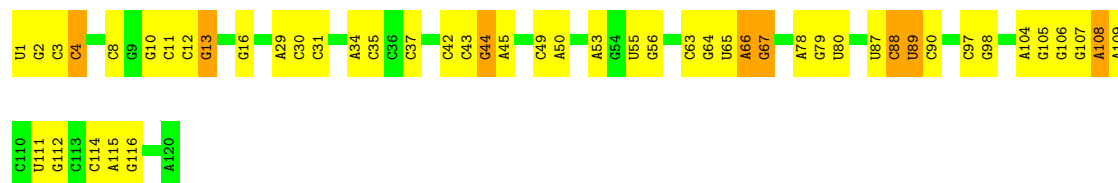
Chain 01:  56% 39%







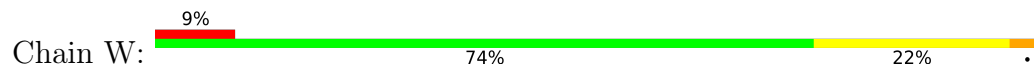
• Molecule 55: 5S ribosomal RNA



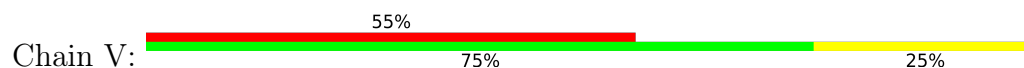
• Molecule 56: tRNAfMet



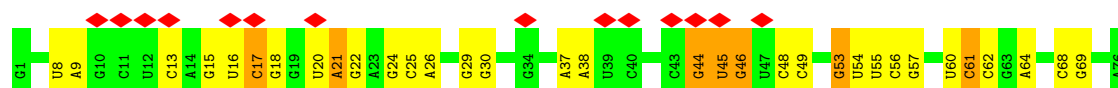
• Molecule 56: tRNAfMet



• Molecule 57: mRNA

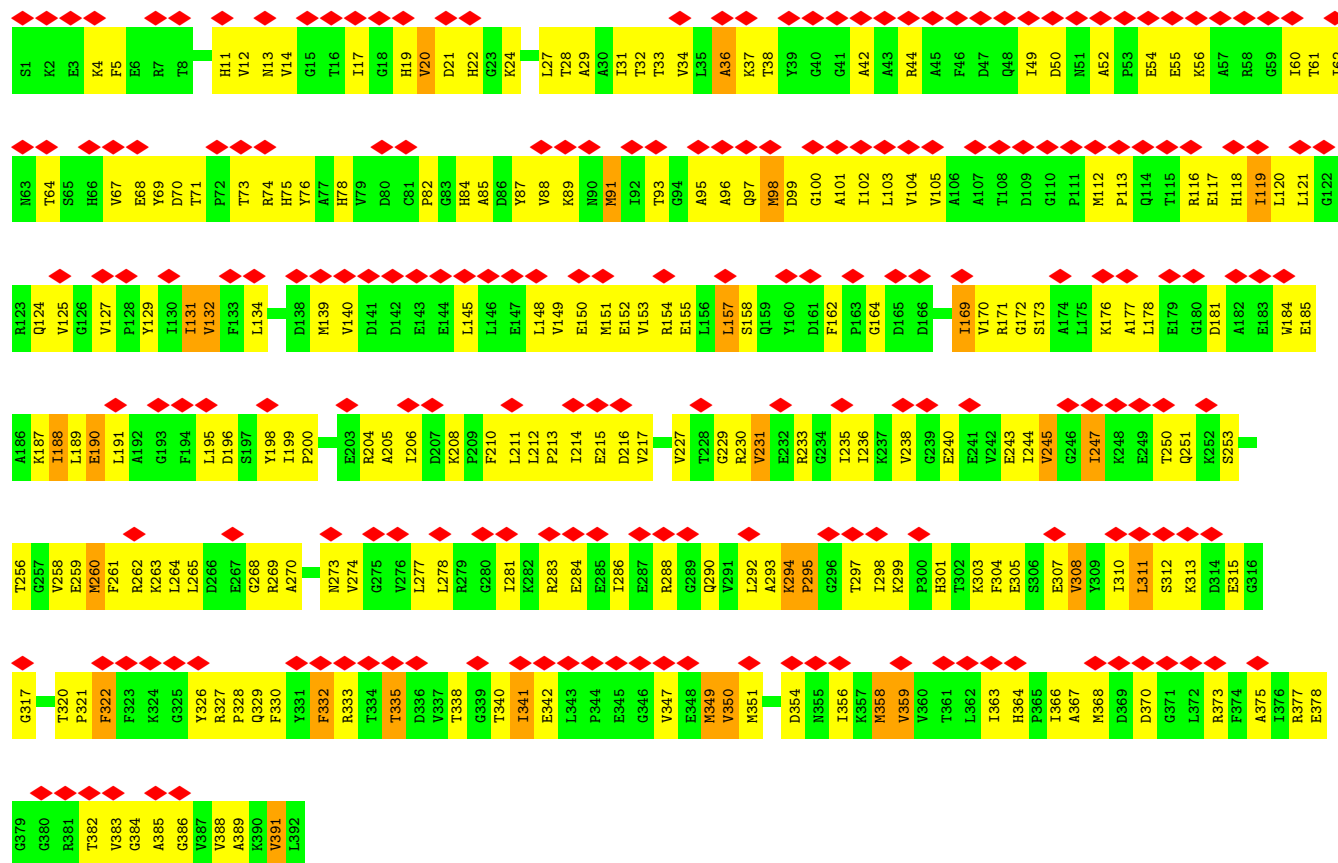


• Molecule 58: tRNAPhe



• Molecule 59: Elongation factor Tu 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6726	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTFFIND3 was used to determine CTF values. FREALIGN applied CTF correction.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	60976	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	17.111	Depositor
Minimum map value	-6.509	Depositor
Average map value	-0.407	Depositor
Map value standard deviation	1.292	Depositor
Recommended contour level	3.47	Depositor
Map size ($\text{\AA}$)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	04	0.37	0/2122	0.89	6/2852 (0.2%)
2	05	0.36	0/1586	0.85	1/2134 (0.0%)
3	06	0.35	0/1571	0.89	5/2113 (0.2%)
4	07	0.35	0/1435	0.93	6/1926 (0.3%)
5	08	0.34	0/1343	0.86	4/1816 (0.2%)
6	09	0.40	0/1122	0.94	3/1515 (0.2%)
7	10	0.45	0/1002	1.13	11/1350 (0.8%)
8	11	0.45	0/1046	0.93	4/1410 (0.3%)
9	12	0.35	0/1152	0.89	4/1551 (0.3%)
10	13	0.34	0/948	0.93	3/1268 (0.2%)
11	14	0.35	0/1054	0.93	3/1403 (0.2%)
12	15	0.37	0/1093	0.86	1/1460 (0.1%)
13	16	0.35	0/974	0.93	3/1301 (0.2%)
14	17	0.33	0/902	0.87	2/1209 (0.2%)
15	18	0.33	0/929	0.83	0/1242
16	19	0.34	0/960	0.95	5/1278 (0.4%)
17	20	0.34	0/829	0.91	2/1107 (0.2%)
18	21	0.33	0/864	0.91	1/1156 (0.1%)
19	22	0.33	0/745	0.82	2/994 (0.2%)
20	23	0.32	0/788	0.94	1/1051 (0.1%)
21	24	0.32	0/766	0.88	3/1025 (0.3%)
22	25	0.32	0/582	0.83	1/769 (0.1%)
23	26	0.35	0/635	0.86	1/848 (0.1%)
24	27	0.31	0/510	1.00	4/677 (0.6%)
25	28	0.35	0/453	0.84	0/605
26	29	0.38	0/532	0.93	0/709
27	30	0.35	0/450	0.92	2/599 (0.3%)
28	31	0.36	0/417	0.89	1/554 (0.2%)
29	32	0.37	0/380	0.88	1/498 (0.2%)
30	33	0.34	0/513	0.90	2/676 (0.3%)
31	34	0.34	0/303	0.80	0/397
32	B	0.36	0/1736	1.07	12/2338 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	C	0.36	0/1652	0.84	5/2225 (0.2%)
34	D	0.34	0/1665	0.96	8/2227 (0.4%)
35	E	0.37	0/1170	1.01	4/1573 (0.3%)
36	F	0.39	0/836	1.04	2/1128 (0.2%)
37	G	0.35	0/1196	1.00	8/1602 (0.5%)
38	H	0.34	0/989	0.95	3/1326 (0.2%)
39	I	0.37	0/1034	0.98	2/1375 (0.1%)
40	J	0.39	0/797	0.99	6/1077 (0.6%)
41	K	0.37	0/886	0.91	3/1195 (0.3%)
42	L	0.36	0/969	1.07	12/1300 (0.9%)
43	M	0.35	0/893	0.95	2/1193 (0.2%)
44	N	0.34	0/817	0.89	2/1088 (0.2%)
45	O	0.34	0/722	0.96	3/964 (0.3%)
46	P	0.37	0/659	0.95	1/884 (0.1%)
47	Q	0.35	0/658	0.92	1/881 (0.1%)
48	R	0.40	0/545	0.97	5/731 (0.7%)
49	S	0.37	0/653	0.84	0/877
50	T	0.35	0/671	0.90	1/888 (0.1%)
51	U	0.39	0/551	1.00	3/728 (0.4%)
52	03	1.62	22/1677 (1.3%)	1.05	7/2259 (0.3%)
53	A	0.45	0/36963	0.54	17/57662 (0.0%)
54	01	0.45	0/69796	0.54	19/108888 (0.0%)
55	02	0.44	0/2872	0.54	1/4479 (0.0%)
56	W	0.48	0/1832	0.51	0/2855
56	X	0.51	0/1832	0.57	0/2855
57	V	0.54	0/486	0.54	0/757
58	Y	0.51	0/1809	0.56	0/2819
59	Z	1.50	26/3085 (0.8%)	1.05	13/4173 (0.3%)
All	All	0.50	48/167457 (0.0%)	0.68	222/249840 (0.1%)

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	03	137	MET	SD-CE	8.81	2.01	1.79
59	Z	368	MET	SD-CE	7.92	1.99	1.79
59	Z	91	MET	SD-CE	7.31	1.97	1.79
52	03	121	MET	SD-CE	7.20	1.97	1.79
52	03	109	MET	SD-CE	7.15	1.97	1.79
59	Z	20	VAL	CA-CB	6.94	1.61	1.54
52	03	218	MET	SD-CE	6.78	1.96	1.79
59	Z	335	THR	CA-CB	6.77	1.61	1.52
52	03	8	MET	SD-CE	6.67	1.96	1.79

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	Z	139	MET	SD-CE	6.53	1.95	1.79
59	Z	350	VAL	CA-CB	6.46	1.60	1.53
59	Z	247	ILE	CA-CB	6.40	1.61	1.54
59	Z	349	MET	SD-CE	6.25	1.95	1.79
52	03	175	ILE	CA-CB	5.99	1.61	1.54
52	03	95	VAL	CA-CB	5.98	1.60	1.53
59	Z	98	MET	SD-CE	5.93	1.94	1.79
52	03	170	ILE	CA-CB	5.86	1.62	1.54
52	03	77	VAL	CA-CB	5.84	1.61	1.53
52	03	222	VAL	CA-CB	5.81	1.60	1.53
52	03	97	MET	SD-CE	5.81	1.94	1.79
59	Z	169	ILE	CA-CB	5.76	1.60	1.53
52	03	59	VAL	CA-CB	5.76	1.59	1.53
52	03	15	VAL	CA-CB	5.68	1.61	1.53
59	Z	112	MET	SD-CE	5.64	1.93	1.79
59	Z	351	MET	SD-CE	5.64	1.93	1.79
59	Z	231	VAL	CA-CB	5.63	1.60	1.53
52	03	75	VAL	CA-CB	5.60	1.60	1.54
59	Z	391	VAL	CA-CB	5.54	1.60	1.54
59	Z	119	ILE	CA-CB	5.46	1.61	1.54
52	03	145	VAL	CA-CB	5.38	1.59	1.53
52	03	146	THR	CA-CB	5.35	1.61	1.54
52	03	113	VAL	CA-CB	5.34	1.61	1.55
52	03	214	ILE	CA-CB	5.30	1.60	1.54
59	Z	105	VAL	CA-CB	5.30	1.60	1.54
59	Z	347	VAL	CA-CB	5.30	1.61	1.53
59	Z	140	VAL	CA-CB	5.27	1.61	1.54
59	Z	132	VAL	CA-CB	5.25	1.60	1.54
59	Z	340	THR	CA-CB	5.24	1.61	1.53
59	Z	341	ILE	CA-CB	5.20	1.59	1.53
59	Z	64	THR	CA-CB	5.19	1.59	1.52
52	03	39	VAL	CA-CB	5.15	1.60	1.53
59	Z	131	ILE	CA-CB	5.15	1.60	1.54
59	Z	260	MET	SD-CE	5.15	1.92	1.79
52	03	104	ILE	CA-CB	5.14	1.60	1.54
52	03	130	VAL	CA-CB	5.11	1.61	1.54
59	Z	71	THR	CA-CB	5.05	1.59	1.53
59	Z	151	MET	SD-CE	5.02	1.92	1.79
52	03	23	ILE	CA-CB	5.01	1.60	1.54

All (222) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	B	17	HIS	N-CA-C	11.51	125.52	109.18
37	G	142	ARG	N-CA-C	-9.43	101.91	113.41
38	H	67	GLY	N-CA-C	-9.34	100.85	113.37
53	A	1201	A	C2'-C3'-O3'	9.04	123.05	109.50
32	B	160	LEU	O-C-N	-8.69	111.65	123.12
32	B	88	GLN	N-CA-C	8.69	121.10	110.41
3	06	178	VAL	N-CA-C	8.64	118.65	110.53
35	E	15	ILE	N-CA-C	-8.46	103.04	110.74
45	O	43	ALA	N-CA-C	-8.39	102.21	111.36
40	J	95	GLY	N-CA-C	-8.23	104.16	113.79
7	10	117	LEU	N-CA-C	8.21	123.09	108.24
9	12	81	ILE	N-CA-C	8.19	118.96	110.36
42	L	114	SER	N-CA-C	-8.20	102.29	111.14
53	A	1190	G	C2'-C3'-O3'	7.87	121.31	109.50
34	D	168	THR	N-CA-C	7.86	120.99	111.40
27	30	53	VAL	N-CA-C	7.77	118.55	110.62
41	K	69	CYS	N-CA-C	-7.73	104.34	114.31
13	16	60	VAL	N-CA-C	-7.72	105.17	111.81
32	B	204	ASP	N-CA-C	7.66	119.71	111.36
41	K	100	ASN	N-CA-C	-7.60	101.09	112.04
48	R	13	THR	N-CA-C	7.60	121.16	112.57
7	10	77	VAL	N-CA-C	-7.48	104.20	112.80
8	11	83	ALA	N-CA-C	-7.36	104.44	113.50
59	Z	44	ARG	N-CA-C	-7.27	101.16	110.53
59	Z	284	GLU	N-CA-C	7.26	118.84	111.07
24	27	26	PHE	N-CA-C	7.26	118.88	110.97
5	08	109	SER	N-CA-C	-7.22	104.09	113.12
42	L	43	LYS	N-CA-C	7.12	125.55	109.81
37	G	146	ALA	N-CA-C	-7.10	104.62	113.28
52	03	188	ASN	N-CA-C	-7.08	102.60	112.45
1	04	30	ALA	N-CA-C	7.04	123.07	113.77
34	D	190	LEU	N-CA-C	7.03	120.38	109.07
51	U	58	LYS	N-CA-C	-6.99	104.56	113.23
42	L	115	LYS	N-CA-C	-6.98	100.15	110.48
53	A	532	A	C2'-C3'-O3'	6.87	119.80	109.50
59	Z	247	ILE	N-CA-C	6.85	117.36	110.23
37	G	143	MET	N-CA-C	-6.82	103.78	111.14
53	A	1300	G	N9-C1'-C2'	6.80	122.21	112.00
37	G	79	VAL	N-CA-C	-6.74	106.08	113.43
27	30	9	ARG	N-CA-C	-6.72	104.03	111.36
54	01	1378	A	C2'-C3'-O3'	6.71	119.57	109.50
32	B	48	MET	N-CA-C	6.70	118.27	110.97
32	B	158	ASP	N-CA-C	-6.69	105.40	113.97

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	B	74	ALA	N-CA-C	-6.62	105.50	113.97
28	31	46	VAL	N-CA-C	6.59	118.09	108.53
21	24	2	PHE	N-CA-C	-6.58	104.82	112.92
18	21	62	ASP	N-CA-C	6.56	116.93	108.34
45	O	39	GLN	N-CA-C	-6.54	104.23	111.82
4	07	4	HIS	N-CA-C	-6.52	104.01	112.23
8	11	62	ALA	N-CA-C	-6.52	105.33	113.28
54	01	1020	A	C2'-C3'-O3'	6.51	119.26	109.50
6	09	67	ALA	N-CA-C	-6.49	104.84	112.89
10	13	89	ASN	N-CA-C	6.49	118.89	111.11
7	10	63	ALA	N-CA-C	-6.47	104.42	112.90
1	04	121	ALA	N-CA-C	6.45	119.38	110.35
52	03	108	GLU	N-CA-C	6.44	118.36	109.54
17	20	36	ALA	N-CA-C	-6.41	105.41	112.72
53	A	438	U	N1-C1'-C2'	6.40	121.59	112.00
51	U	34	ARG	N-CA-C	6.38	118.38	110.91
48	R	15	GLU	N-CA-C	-6.38	105.66	113.50
7	10	42	ARG	N-CA-C	-6.36	104.22	112.23
13	16	68	ALA	N-CA-C	-6.34	104.47	111.82
16	19	6	GLY	N-CA-C	6.31	115.95	110.21
20	23	98	ASN	N-CA-C	-6.30	97.38	110.80
34	D	166	LYS	CA-C-N	6.29	127.70	119.84
34	D	166	LYS	C-N-CA	6.29	127.70	119.84
12	15	118	LYS	N-CA-C	-6.29	103.71	112.45
42	L	45	ASN	N-CA-C	6.28	119.41	111.69
40	J	44	THR	N-CA-C	6.26	119.86	109.46
21	24	45	ASP	N-CA-C	6.26	118.66	111.02
24	27	16	THR	N-CA-C	-6.23	104.56	111.36
59	Z	350	VAL	N-CA-C	6.22	116.21	107.37
44	N	24	ALA	N-CA-C	-6.17	105.51	113.16
39	I	90	ASP	N-CA-C	6.15	123.91	110.80
16	19	52	ARG	N-CA-C	-6.14	104.70	111.82
5	08	72	ASN	N-CA-C	-6.12	104.61	111.28
39	I	18	VAL	N-CA-C	6.12	116.51	107.15
10	13	68	GLY	N-CA-C	6.10	119.86	112.48
54	01	242	G	N9-C1'-C2'	6.10	121.15	112.00
30	33	63	TYR	N-CA-C	6.08	117.99	111.36
52	03	29	LEU	N-CA-C	6.08	117.99	111.36
52	03	168	ASN	N-CA-C	-6.07	105.42	114.64
59	Z	157	LEU	N-CA-C	-6.07	104.75	111.36
1	04	12	ARG	N-CA-C	-6.06	105.64	113.16
7	10	30	SER	N-CA-C	-6.05	105.16	112.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	10	80	THR	N-CA-C	6.02	123.62	110.80
9	12	119	PHE	N-CA-C	-6.02	105.77	113.23
53	A	1301	U	N1-C1'-C2'	6.01	121.02	112.00
16	19	49	ARG	N-CA-C	-6.00	105.53	112.92
35	E	141	ASP	N-CA-C	-6.00	104.67	112.23
48	R	14	ALA	N-CA-C	-5.98	104.88	111.82
23	26	68	ALA	N-CA-C	-5.98	105.07	112.90
4	07	174	PHE	CA-C-N	5.95	127.27	119.84
4	07	174	PHE	C-N-CA	5.95	127.27	119.84
59	Z	36	ALA	N-CA-C	-5.90	104.79	112.23
1	04	35	LYS	N-CA-C	5.89	118.14	110.43
53	A	1346	A	N9-C1'-C2'	5.88	120.83	112.00
22	25	52	ASP	N-CA-C	-5.86	105.71	112.92
4	07	153	ILE	N-CA-C	5.83	116.28	108.11
17	20	44	GLY	N-CA-C	-5.82	105.75	112.73
32	B	62	ARG	N-CA-C	-5.80	106.20	113.28
48	R	69	TYR	N-CA-C	-5.80	105.04	111.36
7	10	115	GLY	N-CA-C	5.78	124.58	112.45
37	G	4	ARG	N-CA-C	5.76	118.71	110.24
36	F	78	PHE	N-CA-C	-5.76	106.80	113.88
32	B	9	LEU	N-CA-C	-5.69	97.65	108.17
51	U	17	ARG	N-CA-C	-5.68	105.85	112.89
42	L	117	GLY	N-CA-C	5.67	126.62	113.18
33	C	143	LEU	N-CA-C	-5.67	105.86	112.89
4	07	5	ASP	N-CA-C	-5.65	105.26	111.82
53	A	246	A	C2'-C3'-O3'	5.63	117.95	109.50
33	C	83	VAL	N-CA-C	5.63	115.76	110.30
6	09	72	ILE	N-CA-C	-5.62	105.25	110.53
21	24	80	HIS	N-CA-C	-5.61	102.04	110.24
54	01	974	G	N9-C1'-C2'	5.61	122.42	114.00
32	B	34	ARG	N-CA-C	5.58	117.44	111.36
43	M	110	GLY	CA-C-N	5.58	126.81	119.84
43	M	110	GLY	C-N-CA	5.58	126.81	119.84
48	R	32	ILE	N-CA-C	-5.57	101.05	108.96
53	A	438	U	C4'-C3'-O3'	-5.56	104.66	113.00
11	14	113	ALA	N-CA-C	-5.55	107.15	114.31
7	10	44	ALA	N-CA-C	-5.54	105.39	111.82
42	L	24	GLU	N-CA-C	5.54	119.03	111.39
10	13	42	THR	N-CA-C	-5.53	101.36	109.81
42	L	54	VAL	N-CA-C	5.50	116.05	108.12
59	Z	190	GLU	N-CA-C	-5.50	104.98	110.97
37	G	28	ILE	N-CA-C	-5.49	107.39	112.83

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	05	69	ALA	N-CA-C	-5.49	106.42	113.23
53	A	1225	A	N9-C1'-C2'	5.48	120.22	112.00
54	01	2296	U	C2'-C3'-O3'	-5.48	105.48	113.70
59	Z	210	PHE	N-CA-C	5.48	117.97	110.24
52	03	27	ILE	N-CA-C	5.45	117.86	111.05
53	A	280	C	C2'-C3'-O3'	5.40	121.79	113.70
53	A	1129	C	N1-C1'-C2'	5.39	120.08	112.00
36	F	83	ALA	N-CA-C	-5.38	106.65	113.43
59	Z	332	PHE	N-CA-C	-5.38	104.18	111.55
52	03	59	VAL	N-CA-C	5.38	115.00	107.37
42	L	75	GLU	N-CA-C	5.37	122.24	110.80
32	B	10	LYS	N-CA-C	5.36	116.81	110.97
59	Z	313	LYS	N-CA-C	-5.35	105.61	111.82
42	L	44	PRO	N-CA-C	5.34	123.84	114.75
47	Q	16	MET	N-CA-C	5.34	116.72	110.41
13	16	3	HIS	N-CA-C	-5.34	101.08	109.25
59	Z	294	LYS	N-CA-C	-5.34	102.72	110.08
54	01	2287	A	N9-C1'-C2'	5.33	120.00	112.00
42	L	102	ASP	N-CA-C	5.32	122.13	110.80
8	11	94	LYS	N-CA-C	-5.31	106.65	113.23
40	J	21	ALA	N-CA-C	-5.31	106.31	112.89
29	32	32	ALA	N-CA-C	-5.31	104.92	111.40
14	17	18	LEU	N-CA-C	5.30	116.87	111.14
54	01	2848	G	N9-C1'-C2'	5.30	119.95	112.00
32	B	130	LYS	N-CA-C	-5.30	105.68	111.82
54	01	669	G	N9-C1'-C2'	5.29	119.94	112.00
9	12	99	ARG	N-CA-C	5.28	117.03	111.28
52	03	191	ALA	N-CA-C	-5.28	105.58	112.23
59	Z	188	ILE	N-CA-C	-5.27	105.25	111.00
42	L	25	ALA	N-CA-C	5.27	118.40	111.28
7	10	54	VAL	N-CA-C	-5.27	107.34	112.29
54	01	490	C	C2'-C3'-O3'	5.27	121.60	113.70
7	10	106	PHE	N-CA-C	5.27	117.07	110.91
24	27	15	ASN	N-CA-C	-5.27	105.59	112.23
53	A	1399	C	C4'-C3'-O3'	5.26	117.30	109.40
3	06	25	GLU	N-CA-C	5.26	117.69	111.33
37	G	108	ARG	N-CA-C	-5.25	105.73	111.82
54	01	481	G	N9-C1'-C2'	5.25	119.88	112.00
1	04	153	LEU	N-CA-C	5.25	117.84	109.81
55	02	66	A	C2'-C3'-O3'	-5.25	105.83	113.70
33	C	87	ARG	N-CA-C	-5.23	105.25	111.69
33	C	5	HIS	CA-C-N	5.23	125.28	119.32

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	C	5	HIS	C-N-CA	5.23	125.28	119.32
5	08	119	GLY	N-CA-C	5.23	125.57	113.18
34	D	21	LYS	N-CA-C	-5.22	104.07	110.65
46	P	54	LEU	N-CA-C	5.22	119.98	111.37
54	01	1669	A	N9-C1'-C2'	5.21	119.82	112.00
41	K	13	LYS	N-CA-C	5.20	121.88	110.80
3	06	81	GLY	N-CA-C	-5.20	100.86	113.18
30	33	26	ALA	N-CA-C	5.20	119.38	107.48
42	L	104	SER	N-CA-C	5.20	117.90	109.79
3	06	46	GLN	N-CA-C	-5.19	102.31	110.36
11	14	115	GLU	N-CA-C	5.19	116.98	110.91
54	01	372	G	N9-C1'-C2'	5.18	119.78	112.00
1	04	213	ARG	N-CA-C	-5.18	105.71	111.36
45	O	49	HIS	N-CA-C	5.18	118.70	112.38
54	01	1320	C	N1-C1'-C2'	5.18	119.76	112.00
6	09	58	LEU	N-CA-C	-5.16	105.10	111.40
4	07	48	LEU	N-CA-C	-5.16	105.73	111.36
38	H	72	GLU	N-CA-C	-5.16	105.30	111.03
5	08	163	TYR	N-CA-C	-5.16	103.23	110.50
34	D	177	MET	N-CA-C	-5.15	104.31	111.52
44	N	21	ALA	N-CA-C	-5.15	105.68	113.51
54	01	2501	C	N1-C1'-C2'	5.15	119.73	112.00
19	22	51	PHE	N-CA-C	-5.15	106.50	112.89
11	14	95	LEU	N-CA-C	-5.14	106.85	113.23
35	E	153	ALA	N-CA-C	-5.14	106.78	113.16
40	J	42	LEU	CA-C-N	5.13	126.25	119.84
40	J	42	LEU	C-N-CA	5.13	126.25	119.84
19	22	3	ARG	N-CA-C	-5.11	105.71	111.28
8	11	127	SER	N-CA-C	-5.11	105.79	111.36
14	17	68	LYS	N-CA-C	5.10	117.57	111.71
40	J	75	ASP	N-CA-C	5.10	117.39	111.02
54	01	858	G	C2'-C3'-O3'	5.10	121.34	113.70
37	G	149	ALA	N-CA-C	-5.09	106.57	112.89
34	D	46	ARG	N-CA-C	-5.09	105.43	111.69
16	19	80	ASN	N-CA-C	-5.08	105.87	111.71
53	A	960	U	C4'-C3'-O3'	5.08	117.02	109.40
50	T	46	ALA	N-CA-C	-5.08	105.83	111.36
53	A	1347	G	N9-C1'-C2'	5.08	119.61	112.00
38	H	98	LEU	N-CA-C	-5.07	107.16	113.55
54	01	1111	A	N9-C1'-C2'	5.07	119.60	112.00
59	Z	308	VAL	N-CA-C	5.07	115.15	107.75
3	06	146	VAL	N-CA-C	5.07	115.00	108.82

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	01	2326	C	C2'-C3'-O3'	5.06	121.29	113.70
54	01	1818	U	N1-C1'-C2'	5.06	119.59	112.00
53	A	983	A	N9-C1'-C2'	5.06	119.58	112.00
7	10	56	ARG	N-CA-C	5.06	117.15	107.75
24	27	14	LEU	N-CA-C	-5.05	106.62	112.89
54	01	1130	U	C2'-C3'-O3'	5.05	121.27	113.70
9	12	79	GLY	N-CA-C	-5.05	107.13	114.90
53	A	1505	G	N9-C1'-C2'	5.04	119.56	112.00
16	19	24	TYR	N-CA-C	5.03	117.81	109.46
34	D	99	ASN	N-CA-C	-5.01	106.34	112.90
35	E	93	VAL	N-CA-C	5.01	119.76	109.34

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	04	2083	0	2157	84	0
2	05	1565	0	1616	54	0
3	06	1552	0	1619	45	0
4	07	1411	0	1447	51	0
5	08	1323	0	1374	47	0
6	09	1111	0	1148	42	0
7	10	989	0	1025	68	0
8	11	1032	0	1088	53	0
9	12	1129	0	1162	43	0
10	13	939	0	1012	27	0
11	14	1045	0	1117	31	0
12	15	1074	0	1157	42	0
13	16	961	0	1000	27	0
14	17	892	0	923	22	0
15	18	917	0	965	32	0
16	19	947	0	1022	35	0
17	20	816	0	839	26	0
18	21	857	0	922	28	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	22	739	0	807	18	0
20	23	780	0	834	23	0
21	24	753	0	780	21	0
22	25	575	0	592	21	0
23	26	625	0	655	16	0
24	27	509	0	543	27	0
25	28	449	0	491	9	0
26	29	523	0	524	17	0
27	30	444	0	461	22	0
28	31	410	0	440	10	0
29	32	377	0	418	9	0
30	33	504	0	574	9	0
31	34	302	0	343	15	0
32	B	1705	0	1732	80	0
33	C	1625	0	1699	64	0
34	D	1643	0	1710	45	0
35	E	1157	0	1199	57	0
36	F	818	0	808	37	0
37	G	1182	0	1240	24	0
38	H	979	0	1034	37	0
39	I	1022	0	1070	41	0
40	J	787	0	828	39	0
41	K	870	0	878	30	0
42	L	955	0	1019	39	0
43	M	884	0	944	32	0
44	N	805	0	847	34	0
45	O	714	0	737	19	0
46	P	649	0	666	27	0
47	Q	649	0	691	32	0
48	R	536	0	552	12	0
49	S	638	0	665	26	0
50	T	665	0	714	20	0
51	U	545	0	579	30	0
52	03	1662	0	1750	104	0
53	A	33012	0	16618	427	0
54	01	62317	0	31346	825	0
55	02	2568	0	1303	43	0
56	W	1640	0	837	10	0
56	X	1640	0	837	23	0
57	V	432	0	218	3	0
58	Y	1619	0	822	23	0
59	Z	3029	0	3043	171	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	Z	32	0	14	4	0
All	All	154412	0	105455	3005	0

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

All (3005) 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)
52:03:137:MET:SD	52:03:137:MET:CE	2.01	1.49
54:01:45:G:H5''	54:01:46:G:H5'	1.31	1.07
52:03:26:ALA:HB2	52:03:224:VAL:HG11	1.41	1.02
36:F:3:HIS:H	36:F:92:THR:HG22	1.30	0.97
37:G:12:LEU:HD11	39:I:49:GLN:HE22	1.30	0.95
33:C:109:GLU:HB2	33:C:143:LEU:HD13	1.49	0.94
54:01:275:C:H2'	54:01:276:U:H4'	1.50	0.93
52:03:21:TYR:HB2	52:03:224:VAL:HG12	1.51	0.92
52:03:27:ILE:HD13	52:03:186:LYS:HD3	1.50	0.91
35:E:80:LEU:HD13	35:E:122:VAL:HG11	1.53	0.91
17:20:15:SER:H	17:20:18:GLN:HE21	1.18	0.91
10:13:121:GLU:HG2	10:13:122:VAL:HG23	1.53	0.91
53:A:1206:G:H2'	53:A:1207:G:H5''	1.52	0.90
33:C:71:ARG:HD3	33:C:74:ILE:HD12	1.53	0.89
56:X:13:C:H2'	56:X:14:A:H5''	1.54	0.89
52:03:133:PRO:HG2	54:01:2169:A:H5'	1.55	0.88
15:18:38:ARG:HH22	15:18:40:GLN:HB3	1.39	0.88
53:A:112:G:H21	53:A:354:G:H5'	1.37	0.88
30:33:16:THR:HG21	30:33:48:MET:HE1	1.55	0.88
32:B:56:LEU:HD23	32:B:59:ILE:HD11	1.57	0.87
35:E:107:GLY:HA3	53:A:9:G:H5'	1.56	0.87
40:J:70:HIS:HB3	40:J:72:ARG:HH12	1.39	0.87
33:C:13:ILE:HG22	33:C:14:VAL:HG23	1.55	0.87
15:18:6:GLN:HA	15:18:9:GLN:HE21	1.38	0.87
3:06:146:VAL:HG12	3:06:185:LYS:HB2	1.56	0.86
52:03:37:LYS:HB2	54:01:2127:G:H5'	1.57	0.86
38:H:46:GLU:HB3	38:H:61:THR:HB	1.56	0.86
54:01:2277:G:H2'	54:01:2278:A:H5''	1.56	0.86
47:Q:46:HIS:HB2	47:Q:70:LYS:HD3	1.56	0.86
52:03:134:ARG:HG3	54:01:2169:A:H5''	1.56	0.85
11:14:67:THR:HG21	54:01:244:A:H5''	1.56	0.85
53:A:531:U:H5'	53:A:532:A:OP1	1.76	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:34:36:ARG:HG2	31:34:37:GLN:H	1.42	0.85
22:25:39:THR:H	54:01:2331:G:H4'	1.43	0.84
34:D:173:ASP:HB3	34:D:178:GLU:HB3	1.59	0.84
54:01:2800:A:H3'	54:01:2801:G:H5'	1.58	0.84
59:Z:134:LEU:HD12	59:Z:171:ARG:HG2	1.60	0.84
12:15:12:MET:HA	54:01:910:A:H62	1.43	0.83
54:01:1645:G:H5''	54:01:1646:C:H5'	1.61	0.83
12:15:45:GLN:HE21	54:01:2485:G:H5''	1.44	0.83
1:04:38:LYS:HB3	54:01:692:C:H5''	1.61	0.82
55:02:13:G:H21	55:02:16:G:H1'	1.43	0.82
32:B:67:LEU:HD21	32:B:91:VAL:HG23	1.60	0.82
48:R:17:VAL:HG22	48:R:18:GLN:H	1.45	0.82
18:21:66:ILE:H	18:21:66:ILE:HD12	1.44	0.82
33:C:30:ASP:HA	44:N:64:ARG:HH12	1.45	0.82
54:01:1394:U:H4'	54:01:1603:A:H4'	1.59	0.82
44:N:84:ARG:HH22	53:A:1059:C:H4'	1.45	0.81
35:E:119:VAL:HG11	35:E:122:VAL:HG22	1.63	0.81
8:11:55:PRO:HG2	8:11:71:LYS:HB2	1.62	0.81
2:05:33:ARG:H	2:05:33:ARG:HD2	1.45	0.81
59:Z:117:GLU:HA	59:Z:120:LEU:HG	1.63	0.81
7:10:24:SER:HB2	7:10:116:GLU:HG3	1.61	0.80
34:D:144:ILE:HD13	34:D:177:MET:HB3	1.62	0.80
8:11:78:LEU:HG	8:11:81:LYS:HE3	1.61	0.80
7:10:43:LYS:HA	7:10:46:ARG:HE	1.44	0.80
33:C:106:ARG:H	33:C:106:ARG:HD2	1.47	0.80
12:15:42:THR:HG22	12:15:93:VAL:HG12	1.64	0.80
43:M:6:ILE:HD11	43:M:21:ILE:HA	1.63	0.80
7:10:71:CYS:HA	7:10:117:LEU:HD12	1.62	0.79
53:A:1137:C:H5'	53:A:1138:G:H5'	1.63	0.79
56:X:25:C:H2'	56:X:26:G:H8	1.46	0.79
55:02:3:C:H2'	55:02:4:C:H5''	1.65	0.79
43:M:6:ILE:HG13	43:M:7:ASN:H	1.46	0.79
54:01:1790:C:H2'	54:01:1791:A:C5	2.18	0.78
59:Z:297:THR:HG23	59:Z:298:ILE:HD12	1.65	0.78
59:Z:206:ILE:HG22	59:Z:270:ALA:H	1.47	0.78
59:Z:332:PHE:HB2	59:Z:335:THR:HB	1.64	0.78
6:09:116:ARG:HG3	6:09:133:GLN:HG3	1.64	0.78
54:01:1053:C:H2'	54:01:1054:A:H5''	1.66	0.78
54:01:2553:G:H3'	54:01:2554:U:H5''	1.65	0.78
53:A:1259:C:H3'	53:A:1260:G:H5''	1.65	0.78
59:Z:238:VAL:HG13	59:Z:256:THR:HA	1.65	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:24:77:VAL:HG23	21:24:89:ILE:HG12	1.67	0.77
49:S:30:LEU:HB2	49:S:48:ILE:HG22	1.67	0.77
5:08:154:GLU:HG2	5:08:156:TYR:H	1.48	0.77
8:11:11:GLN:HB2	8:11:56:VAL:HG12	1.65	0.77
26:29:28:VAL:HG11	26:29:32:LEU:HD13	1.64	0.77
54:01:799:G:H5''	54:01:800:A:H2'	1.66	0.77
8:11:91:LYS:HG3	8:11:94:LYS:HE2	1.67	0.77
53:A:405:U:H3'	53:A:406:G:H5'	1.66	0.77
54:01:1105:U:H2'	54:01:1106:G:H5''	1.65	0.77
7:10:23:LEU:HB2	7:10:118:ILE:HG13	1.67	0.77
9:12:95:ARG:HG2	9:12:96:ARG:HG2	1.67	0.76
32:B:94:ARG:H	32:B:94:ARG:HD2	1.51	0.76
38:H:54:THR:HG23	38:H:55:LYS:HG3	1.66	0.76
8:11:100:ILE:HD11	8:11:137:LEU:HD13	1.68	0.76
53:A:769:G:H4'	53:A:1513:A:H4'	1.66	0.76
59:Z:52:ALA:HB3	59:Z:55:GLU:HG3	1.68	0.76
56:X:35:A:H61	57:V:13:A:H61	1.34	0.75
47:Q:16:MET:HG3	47:Q:19:SER:HB2	1.69	0.75
35:E:160:VAL:HG13	35:E:161:GLU:H	1.51	0.75
59:Z:227:VAL:HG11	59:Z:292:LEU:HD11	1.69	0.75
52:03:67:HIS:HB2	52:03:188:ASN:HD21	1.52	0.74
15:18:59:THR:HG22	15:18:72:VAL:HG12	1.69	0.74
43:M:76:ILE:HG22	43:M:80:MET:HE2	1.69	0.74
32:B:153:MET:HE1	32:B:157:PRO:HG3	1.69	0.74
43:M:15:VAL:HG23	43:M:16:ILE:HD12	1.67	0.74
53:A:1052:U:H2'	53:A:1200:C:H41	1.50	0.74
21:24:20:LEU:HD11	21:24:41:GLU:HG2	1.68	0.74
32:B:165:ALA:HB3	32:B:190:SER:HB3	1.69	0.74
58:Y:8:U:H2'	58:Y:13:C:H41	1.53	0.74
59:Z:305:GLU:HG3	59:Z:359:VAL:HG22	1.69	0.74
1:04:244:VAL:HG12	1:04:250:GLN:HA	1.70	0.73
2:05:151:THR:HB	2:05:152:PRO:HD3	1.70	0.73
6:09:65:ALA:HA	6:09:68:ARG:HD2	1.70	0.73
47:Q:59:GLU:HG3	47:Q:76:ARG:HG2	1.70	0.73
54:01:807:U:H2'	54:01:808:G:H8	1.51	0.73
54:01:1077:A:H2'	54:01:1078:U:H5'	1.70	0.73
10:13:21:CYS:HA	10:13:41:ILE:HG22	1.69	0.73
15:18:92:ARG:HD3	54:01:1753:G:H5''	1.70	0.73
34:D:164:ARG:HG2	34:D:165:GLU:H	1.54	0.73
8:11:12:VAL:HG12	8:11:13:ALA:H	1.53	0.73
52:03:27:ILE:HG21	52:03:186:LYS:HB2	1.71	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:C:39:ARG:HG3	33:C:54:ILE:HD11	1.71	0.72
49:S:5:LYS:HG3	49:S:6:LYS:HG2	1.70	0.72
4:07:133:GLU:HB3	4:07:135:ILE:HG13	1.69	0.72
42:L:3:VAL:HA	42:L:6:LEU:HD12	1.70	0.72
39:I:98:ARG:HG3	39:I:103:VAL:HG21	1.72	0.72
53:A:1033:G:H3'	53:A:1034:G:H5''	1.70	0.72
8:11:11:GLN:HB3	8:11:55:PRO:HA	1.71	0.72
40:J:53:ILE:HG12	53:A:1060:U:H5''	1.71	0.72
16:19:43:GLN:HE21	17:20:77:PHE:HB3	1.55	0.72
7:10:107:GLU:HG2	7:10:110:ALA:HB2	1.71	0.72
1:04:47:ARG:HH21	54:01:774:G:H5''	1.53	0.72
1:04:204:LEU:HD22	1:04:209:ALA:HB1	1.72	0.72
5:08:96:ALA:HB3	5:08:103:ASN:HB3	1.72	0.72
18:21:3:THR:HG21	18:21:58:ALA:HB2	1.72	0.71
42:L:101:LEU:O	42:L:103:CYS:N	2.22	0.71
53:A:85:U:H5''	53:A:86:G:H5'	1.70	0.71
7:10:18:VAL:HA	7:10:86:MET:HE2	1.70	0.71
20:23:33:VAL:HG13	20:23:66:VAL:HG22	1.71	0.71
53:A:1218:C:H2'	53:A:1219:A:C8	2.25	0.71
54:01:1807:G:H2'	54:01:1808:A:H5'	1.72	0.71
9:12:114:LEU:HG	9:12:118:MET:HE3	1.71	0.71
59:Z:258:VAL:HG13	59:Z:274:VAL:HG21	1.72	0.71
2:05:14:ILE:HG23	15:18:11:GLN:HE22	1.54	0.71
3:06:18:THR:HA	3:06:106:LYS:HE3	1.72	0.71
27:30:42:ILE:HG22	27:30:48:TYR:HB2	1.73	0.71
54:01:507:A:H5''	54:01:508:A:H5''	1.73	0.71
54:01:2296:U:H5''	54:01:2297:A:OP1	1.90	0.71
1:04:261:ARG:HD2	1:04:262:THR:HG23	1.72	0.71
1:04:52:HIS:HE2	1:04:218:THR:HG23	1.56	0.70
7:10:87:GLU:HG2	7:10:95:LEU:HD12	1.73	0.70
10:13:76:VAL:H	15:18:72:VAL:HG22	1.56	0.70
32:B:119:GLN:HG2	32:B:136:ARG:HH22	1.56	0.70
10:13:48:PRO:HB3	53:A:1422:G:H5'	1.73	0.70
11:14:95:LEU:HD22	11:14:100:ILE:HD11	1.72	0.70
59:Z:54:GLU:HG2	59:Z:60:ILE:HD11	1.71	0.70
1:04:257:ARG:HE	1:04:266:ILE:HD12	1.57	0.70
17:20:15:SER:H	17:20:18:GLN:NE2	1.87	0.70
42:L:45:ASN:HD22	53:A:528:C:H41	1.37	0.70
40:J:57:VAL:O	40:J:58:ASN:HB2	1.92	0.69
3:06:143:LEU:HD22	3:06:146:VAL:HG11	1.74	0.69
46:P:6:LEU:HD22	46:P:17:TYR:HB3	1.73	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:34:2:LYS:NZ	54:01:2478:A:H5''	2.07	0.69
52:03:30:LEU:HD22	52:03:42:VAL:HG21	1.74	0.69
52:03:97:MET:HB3	52:03:100:LEU:HB2	1.73	0.69
54:01:807:U:H2'	54:01:808:G:C8	2.26	0.69
54:01:2452:C:H42	54:01:2504:U:H3	1.40	0.69
12:15:55:ARG:HD3	54:01:2469:A:H4'	1.73	0.69
59:Z:21:ASP:H	60:Z:401:GCP:H3B1	1.57	0.69
36:F:54:LEU:HD23	36:F:55:HIS:O	1.93	0.69
3:06:175:ILE:HD12	3:06:180:LEU:HD11	1.74	0.69
5:08:17:LYS:HB2	5:08:24:THR:HB	1.74	0.69
11:14:111:ILE:H	11:14:111:ILE:HD12	1.58	0.69
12:15:34:LYS:HE3	12:15:131:VAL:HG11	1.74	0.69
51:U:13:VAL:HG13	51:U:15:LEU:HG	1.75	0.69
58:Y:16:U:H2'	58:Y:17:C:H4'	1.73	0.69
59:Z:17:ILE:HG13	59:Z:103:LEU:HA	1.75	0.69
31:34:25:VAL:HB	31:34:35:GLN:HG3	1.74	0.69
35:E:133:ILE:HD12	35:E:133:ILE:H	1.58	0.69
54:01:1326:U:H2'	54:01:1327:A:H8	1.58	0.69
59:Z:103:LEU:HB3	59:Z:132:VAL:HG22	1.74	0.69
19:22:58:VAL:HG13	19:22:85:VAL:HG22	1.75	0.68
56:W:47:U:H3'	56:W:48:C:H5'	1.75	0.68
34:D:200:VAL:HG11	35:E:102:THR:HG22	1.75	0.68
38:H:5:PRO:HB2	38:H:32:LYS:HE3	1.74	0.68
40:J:9:ARG:HH12	40:J:11:LYS:NZ	1.91	0.68
40:J:10:LEU:HD23	40:J:10:LEU:H	1.58	0.68
54:01:1368:G:H2'	54:01:1369:G:H8	1.59	0.68
2:05:46:ARG:HG2	2:05:84:LEU:HD12	1.76	0.68
32:B:162:VAL:HB	32:B:184:ALA:HB2	1.75	0.68
54:01:546:U:H2'	54:01:547:A:H4'	1.75	0.68
45:O:33:ALA:HA	45:O:36:ASN:HD22	1.59	0.68
59:Z:73:THR:HG22	59:Z:74:ARG:HG3	1.75	0.68
59:Z:321:PRO:HG2	59:Z:349:MET:HE2	1.74	0.68
8:11:20:SER:HB3	8:11:21:PRO:HD3	1.76	0.68
53:A:484:G:H4'	53:A:485:U:H5''	1.74	0.68
1:04:23:LEU:HD13	1:04:82:TYR:HB2	1.76	0.68
33:C:151:GLU:HG3	33:C:166:TRP:HB3	1.76	0.68
53:A:960:U:H4'	53:A:961:U:O5'	1.92	0.68
3:06:5:LEU:HD22	3:06:10:SER:HB3	1.76	0.68
32:B:16:GLY:HA2	32:B:40:ILE:HG13	1.75	0.68
8:11:119:ALA:HB2	54:01:1082:U:H5''	1.76	0.67
54:01:542:C:H2'	54:01:543:G:H5''	1.74	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1026:G:H2'	54:01:1027:A:H8	1.59	0.67
1:04:154:ALA:HB2	1:04:161:VAL:HG23	1.76	0.67
6:09:126:GLY:H	6:09:146:VAL:HB	1.59	0.67
15:18:4:ILE:O	15:18:8:GLU:HG3	1.94	0.67
33:C:76:ILE:HG22	33:C:83:VAL:HG21	1.76	0.67
52:03:166:ASP:OD2	52:03:168:ASN:HB2	1.93	0.67
19:22:61:LEU:HD11	19:22:82:LYS:HD3	1.75	0.67
46:P:5:ARG:HB2	53:A:376:G:H5''	1.76	0.67
34:D:96:ARG:O	34:D:100:VAL:HG23	1.94	0.67
43:M:94:LEU:HB3	43:M:95:PRO:HD2	1.75	0.67
9:12:78:THR:HG22	54:01:2641:G:H5''	1.77	0.67
42:L:113:ARG:HB2	42:L:118:VAL:HB	1.76	0.67
1:04:74:PRO:HB3	1:04:114:GLN:HE21	1.59	0.67
18:21:83:LYS:HG2	18:21:95:ARG:HH12	1.60	0.67
5:08:41:GLU:HG3	5:08:54:ARG:HH21	1.59	0.67
15:18:88:ARG:HH11	15:18:112:ARG:NH2	1.92	0.67
26:29:58:ASP:O	26:29:62:LYS:HG3	1.96	0.66
52:03:197:LYS:HE3	52:03:209:ILE:HD13	1.77	0.66
21:24:72:VAL:HG12	21:24:93:ARG:HA	1.76	0.66
36:F:64:VAL:HG22	36:F:65:GLU:N	2.10	0.66
59:Z:294:LYS:HE2	59:Z:297:THR:HG21	1.77	0.66
7:10:7:ASP:O	7:10:11:ILE:HG12	1.95	0.66
8:11:30:GLN:HB3	8:11:60:VAL:HG11	1.76	0.66
7:10:53:ARG:HB3	7:10:55:VAL:HG22	1.76	0.66
55:02:88:C:H5''	55:02:89:U:OP1	1.96	0.66
16:19:91:ARG:HH11	54:01:997:G:H5''	1.61	0.66
55:02:3:C:C2'	55:02:4:C:H5''	2.26	0.66
1:04:153:LEU:HD11	1:04:181:ARG:NH2	2.10	0.66
41:K:23:HIS:HB3	41:K:30:ILE:HG23	1.76	0.66
40:J:52:LEU:HD12	44:N:80:ARG:NE	2.11	0.66
46:P:67:ILE:H	46:P:67:ILE:HD12	1.61	0.66
59:Z:308:VAL:HG22	59:Z:386:GLY:HA3	1.76	0.66
59:Z:326:TYR:HB3	59:Z:341:ILE:HG13	1.77	0.66
15:18:38:ARG:HH11	53:A:345:C:H5'	1.59	0.66
22:25:12:SER:HB3	54:01:2262:U:H5	1.61	0.66
58:Y:8:U:H2'	58:Y:13:C:N4	2.11	0.66
1:04:235:GLU:H	1:04:238:ASN:ND2	1.94	0.66
52:03:185:LEU:HA	52:03:188:ASN:HB2	1.78	0.66
4:07:140:ILE:HG22	4:07:142:TYR:H	1.60	0.65
32:B:71:THR:HG22	32:B:72:LYS:H	1.61	0.65
39:I:94:ARG:HA	39:I:97:LEU:HB3	1.78	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:K:116:PRO:HB3	53:A:676:A:H1'	1.78	0.65
23:26:2:ARG:HD2	23:26:29:LEU:HD22	1.77	0.65
35:E:23:THR:HA	35:E:28:ARG:HA	1.78	0.65
54:01:121:G:H4'	54:01:149:A:H5'	1.77	0.65
54:01:833:A:H2'	54:01:834:G:H8	1.60	0.65
54:01:833:A:H2'	54:01:834:G:C8	2.31	0.65
45:O:55:LEU:O	45:O:59:VAL:HG23	1.97	0.65
54:01:2277:G:C2'	54:01:2278:A:H5''	2.26	0.65
42:L:45:ASN:ND2	53:A:528:C:H41	1.94	0.65
54:01:1105:U:C2'	54:01:1106:G:H5''	2.26	0.65
54:01:2389:G:H5''	54:01:2390:U:O4'	1.95	0.65
42:L:49:ARG:HH12	53:A:522:C:H41	1.44	0.65
53:A:1205:U:H2'	53:A:1206:G:H8	1.61	0.65
10:13:40:LYS:HE3	10:13:57:VAL:HG12	1.78	0.65
54:01:917:A:H5''	54:01:2268:A:H61	1.61	0.65
58:Y:15:G:H2'	58:Y:16:U:H5'	1.79	0.65
39:I:125:GLN:HE22	53:A:1342:C:H1'	1.61	0.65
53:A:868:C:H2'	53:A:869:G:O4'	1.97	0.65
53:A:1088:G:H21	53:A:1167:A:H61	1.45	0.65
5:08:71:LEU:HA	5:08:74:MET:HB2	1.79	0.65
15:18:28:LYS:HB3	15:18:39:LEU:HD11	1.78	0.65
32:B:16:GLY:HA3	32:B:39:ILE:HA	1.79	0.65
52:03:76:ALA:HB3	52:03:114:VAL:HG22	1.79	0.65
12:15:53:MET:HE3	12:15:63:ILE:HD13	1.79	0.64
20:23:48:VAL:HG22	20:23:50:ALA:H	1.61	0.64
44:N:92:ILE:H	44:N:92:ILE:HD12	1.62	0.64
53:A:212:G:H2'	53:A:213:G:H8	1.62	0.64
15:18:38:ARG:NH2	15:18:40:GLN:HB3	2.10	0.64
38:H:77:VAL:HG12	38:H:84:ILE:HD12	1.79	0.64
41:K:30:ILE:HD13	41:K:45:THR:HG22	1.80	0.64
49:S:18:VAL:O	49:S:22:VAL:HG23	1.97	0.64
2:05:101:PHE:HA	2:05:104:VAL:HG22	1.78	0.64
54:01:729:G:H4'	54:01:763:G:H5'	1.79	0.64
54:01:1509:A:H2'	54:01:1510:G:C8	2.33	0.64
2:05:148:GLN:HB2	2:05:152:PRO:HG2	1.79	0.64
9:12:7:LYS:HG2	54:01:538:A:H4'	1.77	0.64
59:Z:235:ILE:HG22	59:Z:269:ARG:HA	1.80	0.64
15:18:102:ARG:HD3	15:18:106:ALA:HB1	1.78	0.64
54:01:2267:A:H5''	54:01:2268:A:H5'	1.79	0.64
55:02:55:U:H2'	55:02:56:G:C8	2.32	0.64
7:10:57:ASN:HB2	7:10:62:ARG:HG2	1.80	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:14:79:LEU:HD23	11:14:110:VAL:HG12	1.78	0.64
52:03:57:GLN:OE1	52:03:204:ALA:HB2	1.97	0.64
53:A:1052:U:H2'	53:A:1200:C:N4	2.12	0.64
7:10:19:ALA:HA	7:10:70:GLU:HG3	1.79	0.64
32:B:47:PRO:O	32:B:51:GLU:HG3	1.98	0.64
32:B:162:VAL:HG21	32:B:172:ILE:HG12	1.79	0.64
38:H:11:THR:HA	38:H:14:ARG:NH1	2.12	0.64
52:03:65:LEU:HB2	52:03:159:GLY:HA3	1.78	0.64
32:B:31:PHE:HB2	32:B:39:ILE:HB	1.80	0.64
32:B:202:ASN:HD22	32:B:208:ALA:HB2	1.63	0.64
42:L:26:CYS:SG	42:L:29:LYS:HG2	2.38	0.64
52:03:194:VAL:HG12	52:03:198:LYS:NZ	2.12	0.64
2:05:8:LYS:HB2	2:05:201:LEU:HD11	1.80	0.64
19:22:68:LYS:HE3	19:22:77:ARG:NH2	2.13	0.64
32:B:186:VAL:HB	32:B:190:SER:HB2	1.78	0.64
59:Z:307:GLU:HG3	59:Z:389:ALA:HB2	1.79	0.64
1:04:209:ALA:HA	1:04:212:TRP:NE1	2.13	0.63
10:13:104:THR:HG22	10:13:106:GLU:H	1.63	0.63
16:19:8:ILE:HD12	16:19:9:ALA:N	2.11	0.63
12:15:45:GLN:NE2	54:01:2485:G:H5''	2.13	0.63
18:21:1:MET:HG2	18:21:109:ASP:OD2	1.97	0.63
54:01:215:G:H4'	54:01:216:A:H4'	1.78	0.63
1:04:260:LYS:HA	1:04:263:ASP:OD2	1.97	0.63
16:19:24:TYR:HE1	54:01:17:G:H4'	1.64	0.63
25:28:12:ALA:HA	25:28:15:ARG:HD3	1.79	0.63
54:01:528:A:C2	54:01:2042:A:H2'	2.34	0.63
14:17:17:LYS:HZ2	54:01:2380:C:H5'	1.64	0.63
46:P:20:VAL:HG22	46:P:21:VAL:N	2.14	0.63
59:Z:13:ASN:HB3	59:Z:98:MET:HA	1.80	0.63
39:I:60:LEU:HD21	39:I:89:TYR:HE2	1.62	0.63
47:Q:43:LEU:HD21	53:A:236:A:H5''	1.81	0.63
10:13:116:ILE:HD12	10:13:117:SER:N	2.14	0.63
36:F:64:VAL:HG22	36:F:65:GLU:H	1.62	0.63
47:Q:7:LEU:HD22	47:Q:24:ILE:HD13	1.80	0.63
52:03:60:ARG:HB2	52:03:141:LYS:HG3	1.80	0.63
2:05:33:ARG:HD3	2:05:51:THR:HG23	1.81	0.63
24:27:9:LYS:HD3	24:27:11:VAL:H	1.64	0.63
34:D:94:GLU:HA	34:D:99:ASN:ND2	2.14	0.63
37:G:58:LEU:HD12	37:G:59:GLU:N	2.14	0.63
52:03:7:ARG:NH1	52:03:218:MET:HE2	2.13	0.63
54:01:2167:U:H2'	54:01:2169:A:OP2	1.99	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:93:ILE:HD13	9:12:100:VAL:HG21	1.81	0.63
33:C:5:HIS:HB3	44:N:88:MET:HE3	1.81	0.63
50:T:23:ARG:NH2	50:T:60:GLN:HE22	1.96	0.62
53:A:701:U:H4'	53:A:703:G:H1'	1.81	0.62
54:01:2286:G:H5''	54:01:2287:A:OP1	1.98	0.62
52:03:37:LYS:CB	54:01:2127:G:H5'	2.28	0.62
55:02:66:A:H5''	55:02:67:G:OP1	1.99	0.62
7:10:4:ASN:HA	7:10:7:ASP:HB2	1.79	0.62
36:F:47:LEU:HD21	36:F:57:ALA:HB3	1.82	0.62
51:U:16:ARG:HB2	51:U:19:LYS:HD3	1.82	0.62
53:A:1227:A:H2'	53:A:1228:C:H5'	1.80	0.62
59:Z:89:LYS:HG2	59:Z:288:ARG:HH22	1.64	0.62
35:E:105:ILE:HD11	35:E:123:LEU:HD22	1.81	0.62
50:T:59:ARG:NH1	53:A:177:G:H5'	2.15	0.62
52:03:60:ARG:HH11	52:03:164:ARG:HD2	1.64	0.62
6:09:127:GLU:HA	6:09:145:ASN:HA	1.82	0.62
34:D:120:LYS:HG2	34:D:130:ASN:OD1	2.00	0.62
40:J:6:ILE:HB	40:J:76:ILE:HB	1.81	0.62
47:Q:30:HIS:HD2	47:Q:33:TYR:H	1.47	0.62
53:A:1277:C:H2'	53:A:1278:G:H5''	1.81	0.62
54:01:1837:C:H2'	54:01:1899:A:H61	1.62	0.62
59:Z:338:THR:HB	59:Z:363:ILE:HD13	1.82	0.62
14:17:80:GLU:O	14:17:84:GLU:HG3	1.99	0.62
54:01:2249:U:H3'	54:01:2250:G:H5'	1.82	0.62
7:10:22:ALA:HB1	7:10:118:ILE:HD11	1.81	0.62
10:13:63:VAL:HG22	10:13:84:CYS:HA	1.80	0.62
44:N:1:ALA:HB2	53:A:1203:C:H5''	1.82	0.62
1:04:235:GLU:H	1:04:238:ASN:HD22	1.48	0.62
6:09:12:LEU:HD12	6:09:13:GLY:N	2.15	0.62
54:01:2800:A:C2	54:01:2895:G:H1'	2.34	0.62
59:Z:260:MET:HA	59:Z:274:VAL:HG12	1.82	0.62
5:08:26:LYS:HB2	5:08:31:GLU:HG3	1.82	0.62
6:09:17:ASP:HB3	6:09:19:VAL:HG23	1.80	0.62
32:B:66:ILE:HD12	32:B:159:ALA:HB3	1.81	0.62
32:B:75:ALA:O	32:B:79:VAL:HG23	2.00	0.62
39:I:51:LEU:HD13	39:I:56:MET:HG3	1.81	0.62
45:O:34:GLN:HB3	45:O:58:MET:HE1	1.80	0.62
54:01:704:G:H2'	54:01:726:G:N2	2.15	0.62
55:02:3:C:C3'	55:02:4:C:H5''	2.29	0.62
49:S:69:LYS:HE3	53:A:1319:A:H5''	1.82	0.61
55:02:115:A:H2'	55:02:116:G:C8	2.35	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:247:ILE:N	59:Z:290:GLN:HE21	1.98	0.61
6:09:76:GLU:HB3	6:09:142:VAL:HA	1.81	0.61
52:03:44:VAL:HG13	52:03:214:ILE:HG22	1.81	0.61
53:A:532:A:O2'	53:A:533:A:OP1	2.16	0.61
5:08:154:GLU:OE1	5:08:157:LYS:HB2	2.00	0.61
19:22:56:GLU:OE2	19:22:88:LYS:HG2	1.99	0.61
33:C:112:ALA:HB1	33:C:184:ASN:HB2	1.83	0.61
34:D:8:LEU:HD23	53:A:429:U:H5'	1.82	0.61
50:T:82:ILE:HD12	50:T:83:ASN:N	2.14	0.61
7:10:43:LYS:HE3	7:10:98:GLU:HG3	1.82	0.61
11:14:82:LEU:HG	11:14:120:VAL:HG11	1.82	0.61
12:15:11:LYS:HE3	12:15:86:LYS:HB3	1.82	0.61
34:D:61:ARG:HH21	34:D:67:LEU:HA	1.63	0.61
42:L:79:ILE:HG22	42:L:103:CYS:HB2	1.82	0.61
54:01:2636:C:H2'	54:01:2637:U:C6	2.36	0.61
3:06:154:ASP:OD2	3:06:156:ASN:HB3	2.00	0.61
9:12:37:ARG:HD3	9:12:39:LYS:HD2	1.81	0.61
31:34:2:LYS:HZ1	54:01:2478:A:H5''	1.64	0.61
31:34:33:HIS:O	31:34:35:GLN:HG2	1.99	0.61
35:E:82:HIS:HB2	35:E:83:PRO:HD2	1.82	0.61
34:D:33:ILE:HG13	34:D:34:GLU:N	2.14	0.61
53:A:427:U:H4'	53:A:541:G:H5''	1.82	0.61
59:Z:243:GLU:HG3	59:Z:295:PRO:HA	1.81	0.61
16:19:71:ASN:OD1	16:19:109:VAL:HG21	2.00	0.61
26:29:16:CYS:HA	26:29:34:LEU:HB2	1.81	0.61
37:G:111:GLY:HA2	37:G:118:ARG:HD3	1.82	0.61
52:03:51:ASP:HB3	52:03:54:LYS:HG3	1.82	0.61
59:Z:294:LYS:HB3	59:Z:297:THR:HG22	1.81	0.61
7:10:23:LEU:HD21	7:10:96:PHE:HB2	1.81	0.61
56:X:59:A:H2'	56:X:60:U:H5'	1.83	0.61
35:E:59:ILE:O	35:E:63:MET:HG2	2.00	0.61
44:N:100:TRP:HZ2	53:A:1368:A:H5''	1.66	0.61
52:03:75:VAL:HB	52:03:92:ALA:HA	1.83	0.61
59:Z:74:ARG:CZ	59:Z:200:PRO:HA	2.31	0.61
1:04:47:ARG:NH2	54:01:774:G:H5''	2.16	0.60
32:B:41:ASN:ND2	32:B:43:GLU:HB2	2.16	0.60
34:D:100:VAL:HG21	34:D:136:VAL:HG21	1.82	0.60
52:03:7:ARG:HE	54:01:2128:G:H4'	1.65	0.60
14:17:76:LYS:O	14:17:80:GLU:HG3	2.02	0.60
35:E:15:ILE:HD11	35:E:37:VAL:HG23	1.83	0.60
53:A:1296:C:H4'	53:A:1302:C:N4	2.16	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:475:C:H4'	54:01:510:C:H5'	1.81	0.60
59:Z:124:GLN:HA	59:Z:373:ARG:HG2	1.81	0.60
59:Z:312:SER:H	59:Z:315:GLU:HB2	1.66	0.60
13:16:2:ARG:HG2	54:01:1653:G:H3'	1.83	0.60
36:F:26:THR:HA	36:F:29:ILE:HD12	1.83	0.60
44:N:2:LYS:HD3	53:A:1049:U:H2'	1.84	0.60
54:01:2698:U:H2'	54:01:2699:C:C6	2.35	0.60
12:15:5:LYS:HG2	12:15:6:ARG:HG2	1.84	0.60
24:27:42:LEU:O	24:27:46:VAL:HG23	2.01	0.60
53:A:1513:A:H2'	53:A:1514:G:C8	2.37	0.60
54:01:1830:C:H2'	54:01:1831:G:H8	1.65	0.60
54:01:1936:A:H2	54:01:1943:U:H3	1.50	0.60
1:04:165:ALA:HB3	1:04:172:THR:HB	1.83	0.60
14:17:17:LYS:NZ	54:01:2380:C:H5'	2.17	0.60
34:D:12:ARG:HG2	34:D:33:ILE:HD12	1.83	0.60
53:A:1412:C:H2'	53:A:1413:A:C8	2.37	0.60
54:01:1857:G:H2'	54:01:1884:G:H22	1.66	0.60
54:01:2086:U:H2'	54:01:2087:G:C8	2.37	0.60
13:16:47:VAL:C	13:16:50:PRO:HD2	2.26	0.60
46:P:2:VAL:HG23	46:P:65:ALA:HA	1.82	0.60
46:P:43:ALA:HA	46:P:46:LYS:NZ	2.16	0.60
55:02:106:G:H2'	55:02:107:G:O4'	2.02	0.60
56:X:38:A:H3'	56:X:39:C:C6	2.37	0.60
56:W:17:C:H5'	56:W:61:C:OP1	2.02	0.60
59:Z:293:ALA:HB1	59:Z:298:ILE:HD13	1.82	0.60
7:10:8:LYS:O	7:10:12:VAL:HG23	2.02	0.60
9:12:27:ARG:NH2	54:01:1142:A:H4'	2.17	0.60
23:26:65:THR:O	23:26:69:GLU:HG3	2.00	0.60
45:O:86:LEU:HD12	45:O:86:LEU:O	2.02	0.60
52:03:77:VAL:HB	52:03:95:VAL:HG13	1.83	0.60
54:01:1063:G:H1	54:01:1075:C:H42	1.49	0.60
13:16:59:SER:O	13:16:63:ARG:HG2	2.02	0.60
14:17:16:ARG:HD3	14:17:19:GLN:HE21	1.66	0.60
32:B:202:ASN:HD21	32:B:205:ALA:HB3	1.67	0.60
53:A:279:A:H5'	53:A:281:G:H5'	1.82	0.60
15:18:3:ILE:H	15:18:3:ILE:HD12	1.66	0.59
21:24:21:ARG:HE	21:24:87:GLN:HA	1.66	0.59
54:01:704:G:H2'	54:01:726:G:H22	1.66	0.59
7:10:17:GLU:HG2	7:10:88:HIS:NE2	2.17	0.59
7:10:34:THR:HB	7:10:38:MET:HE2	1.84	0.59
8:11:92:PRO:HA	8:11:136:GLY:HA2	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1060:U:H5'	54:01:1062:G:H5'	1.84	0.59
4:07:135:ILE:HG21	4:07:142:TYR:HD1	1.66	0.59
54:01:1186:G:H2'	54:01:1187:G:O4'	2.02	0.59
54:01:2070:A:H2'	54:01:2071:A:C8	2.37	0.59
54:01:2699:C:H2'	54:01:2700:A:H8	1.66	0.59
8:11:14:ALA:HB3	8:11:54:ILE:HD12	1.84	0.59
18:21:82:MET:HB2	18:21:98:LYS:HB2	1.84	0.59
33:C:120:THR:HG23	33:C:188:ALA:HB2	1.83	0.59
53:A:236:A:H2'	53:A:237:G:C8	2.38	0.59
54:01:2215:C:H2'	54:01:2216:G:H8	1.67	0.59
59:Z:67:VAL:CG2	59:Z:78:HIS:HB3	2.32	0.59
2:05:149:ASN:HB3	54:01:2572:A:OP2	2.03	0.59
4:07:16:MET:SD	4:07:21:TYR:HB2	2.42	0.59
6:09:41:LYS:O	6:09:45:GLU:HG3	2.02	0.59
20:23:10:VAL:HG12	20:23:71:ILE:HG22	1.84	0.59
24:27:46:VAL:O	24:27:50:VAL:HG23	2.02	0.59
32:B:41:ASN:HD21	32:B:43:GLU:HB2	1.66	0.59
38:H:77:VAL:HG23	38:H:126:CYS:HA	1.82	0.59
9:12:17:VAL:HG23	9:12:137:PRO:HB2	1.84	0.59
22:25:38:GLY:HA2	54:01:2330:G:H21	1.67	0.59
40:J:46:LYS:HE2	40:J:68:ARG:HG2	1.83	0.59
53:A:571:U:H2'	53:A:572:A:H5''	1.84	0.59
54:01:2800:A:H3'	54:01:2801:G:C5'	2.29	0.59
10:13:79:PHE:HB3	15:18:67:GLU:OE2	2.03	0.59
34:D:10:LEU:HD13	34:D:62:ARG:HD2	1.85	0.59
45:O:23:SER:O	45:O:27:GLN:HG3	2.01	0.59
2:05:59:ARG:HH11	54:01:2830:C:H3'	1.67	0.59
7:10:74:ASP:HA	7:10:77:VAL:HG23	1.84	0.59
8:11:125:THR:O	8:11:129:GLU:HG3	2.03	0.59
33:C:133:MET:HE3	33:C:167:TYR:HB2	1.85	0.59
46:P:20:VAL:HG23	46:P:35:ARG:HA	1.85	0.59
54:01:742:A:H2'	54:01:743:A:C8	2.38	0.59
59:Z:131:ILE:HD12	59:Z:195:LEU:HD12	1.83	0.59
38:H:2:MET:HE1	53:A:654:G:H4'	1.85	0.59
38:H:45:ILE:HD13	38:H:60:LEU:HD13	1.85	0.59
53:A:1391:U:H2'	53:A:1392:G:H8	1.67	0.59
54:01:639:U:H2'	54:01:640:C:C6	2.37	0.59
54:01:968:C:H2'	54:01:969:G:H8	1.67	0.59
54:01:1159:U:H2'	54:01:1160:G:H8	1.68	0.59
11:14:17:LYS:HD3	54:01:663:G:H5''	1.84	0.58
23:26:16:ASN:ND2	54:01:2081:U:H5''	2.18	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:F:92:THR:OG1	36:F:93:LYS:N	2.34	0.58
40:J:80:THR:HG22	40:J:82:LYS:H	1.68	0.58
52:03:104:ILE:O	52:03:109:MET:HG3	2.03	0.58
53:A:70:U:H5''	53:A:71:A:OP1	2.03	0.58
54:01:2190:G:H2'	54:01:2191:A:C8	2.38	0.58
59:Z:54:GLU:OE1	59:Z:62:ILE:HG21	2.03	0.58
22:25:62:LYS:O	22:25:78:ILE:HG23	2.03	0.58
27:30:30:ASP:HB3	27:30:34:GLY:H	1.68	0.58
37:G:136:LYS:O	37:G:140:VAL:HG23	2.03	0.58
47:Q:46:HIS:HB2	47:Q:70:LYS:CD	2.29	0.58
54:01:1794:A:H2'	54:01:1795:C:C6	2.38	0.58
59:Z:27:LEU:O	59:Z:31:ILE:HG13	2.03	0.58
2:05:135:GLY:O	54:01:2580:U:H5''	2.03	0.58
25:28:5:LYS:HG2	25:28:36:GLU:HG3	1.85	0.58
48:R:41:SER:HB3	48:R:51:GLN:HE21	1.68	0.58
54:01:1251:C:O2'	54:01:1252:G:H3'	2.03	0.58
1:04:16:VAL:HB	1:04:203:VAL:HG22	1.85	0.58
1:04:140:VAL:HG12	1:04:191:LEU:HD23	1.84	0.58
3:06:117:ARG:HH12	11:14:2:ARG:HG2	1.69	0.58
8:11:99:LYS:HE3	8:11:140:GLU:HG2	1.85	0.58
51:U:53:LYS:O	51:U:57:LYS:HG2	2.04	0.58
54:01:780:G:H2'	54:01:782:A:N7	2.17	0.58
54:01:2591:C:H2'	54:01:2592:G:C8	2.39	0.58
59:Z:68:GLU:HB2	59:Z:261:PHE:CD2	2.38	0.58
59:Z:155:GLU:HA	59:Z:158:SER:HB2	1.84	0.58
16:19:5:ARG:HB2	16:19:8:ILE:HD11	1.86	0.58
24:27:6:LEU:HD11	24:27:59:GLU:OE2	2.04	0.58
32:B:178:LEU:HG	32:B:180:ILE:HG13	1.85	0.58
33:C:151:GLU:HB3	33:C:198:LYS:HG3	1.85	0.58
35:E:10:LEU:HA	35:E:40:ASP:HA	1.86	0.58
52:03:74:ARG:H	52:03:112:ASP:HB2	1.67	0.58
53:A:902:G:H2'	53:A:903:G:H8	1.68	0.58
54:01:1053:C:C2'	54:01:1054:A:H5''	2.33	0.58
55:02:87:U:H5''	55:02:88:C:OP2	2.04	0.58
8:11:45:THR:HG22	8:11:50:LYS:HG2	1.86	0.58
32:B:67:LEU:HD23	32:B:68:PHE:N	2.19	0.58
52:03:124:VAL:HG13	52:03:127:LEU:HD12	1.86	0.58
54:01:581:C:H2'	54:01:582:A:C8	2.38	0.58
54:01:2646:C:H2'	54:01:2647:U:O4'	2.03	0.58
55:02:3:C:H3'	55:02:4:C:H5''	1.86	0.58
1:04:235:GLU:N	1:04:238:ASN:HD22	2.01	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:09:3:VAL:HG22	6:09:38:PRO:HA	1.86	0.58
40:J:91:ASP:O	40:J:92:LEU:HB2	2.04	0.58
53:A:1206:G:C2'	53:A:1207:G:H5''	2.29	0.58
54:01:2248:C:H2'	54:01:2249:U:H5'	1.85	0.58
5:08:37:ASN:ND2	5:08:39:ALA:HB3	2.19	0.58
8:11:127:SER:HA	54:01:1080:A:H1'	1.85	0.58
9:12:45:THR:HG22	9:12:47:HIS:H	1.69	0.58
9:12:114:LEU:O	9:12:118:MET:HG2	2.04	0.58
12:15:11:LYS:HD2	12:15:86:LYS:HG2	1.86	0.58
46:P:14:ARG:HH12	53:A:618:C:H1'	1.67	0.58
53:A:112:G:N2	53:A:354:G:H5'	2.13	0.58
54:01:1348:C:H2'	54:01:1349:C:H5'	1.86	0.58
59:Z:69:TYR:HE1	59:Z:78:HIS:HB2	1.68	0.58
7:10:41:LEU:HD11	7:10:54:VAL:HG11	1.85	0.58
55:02:66:A:N1	55:02:107:G:H2'	2.19	0.58
51:U:17:ARG:HA	51:U:20:ARG:HH11	1.68	0.58
53:A:770:C:H2'	53:A:771:G:H8	1.68	0.58
56:X:13:C:C2'	56:X:14:A:H5''	2.28	0.58
58:Y:61:C:H6	58:Y:61:C:H5'	1.69	0.58
59:Z:214:ILE:HD12	59:Z:290:GLN:HB2	1.86	0.58
11:14:23:ILE:HD12	11:14:23:ILE:H	1.68	0.57
12:15:52:ALA:HB2	12:15:123:LYS:HE3	1.86	0.57
18:21:55:ILE:O	18:21:59:GLU:HG2	2.04	0.57
26:29:48:GLN:NE2	26:29:52:ALA:HB2	2.19	0.57
39:I:59:LYS:HB3	39:I:60:LEU:HD12	1.86	0.57
53:A:715:A:H2'	53:A:716:A:C8	2.39	0.57
53:A:831:A:H3'	53:A:832:G:H5''	1.86	0.57
53:A:1386:G:H2'	53:A:1387:G:H8	1.69	0.57
54:01:968:C:H2'	54:01:969:G:C8	2.39	0.57
59:Z:187:LYS:HA	59:Z:190:GLU:HG3	1.86	0.57
6:09:3:VAL:HA	6:09:39:ALA:H	1.69	0.57
6:09:132:PHE:HB2	6:09:140:ALA:HB3	1.85	0.57
17:20:68:ARG:HB2	17:20:90:ARG:HH21	1.68	0.57
52:03:46:VAL:HG22	52:03:212:VAL:HG13	1.85	0.57
53:A:950:U:H2'	53:A:951:G:H8	1.69	0.57
54:01:286:U:H2'	54:01:287:G:C8	2.39	0.57
51:U:39:LYS:O	51:U:43:GLU:HG2	2.04	0.57
53:A:1391:U:H2'	53:A:1392:G:C8	2.39	0.57
24:27:49:ASP:O	24:27:53:VAL:HG23	2.04	0.57
32:B:55:GLU:O	32:B:59:ILE:HG12	2.05	0.57
54:01:917:A:H5''	54:01:2268:A:N6	2.19	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1765:U:H2'	54:01:1766:G:C8	2.40	0.57
54:01:2605:U:H2'	54:01:2606:C:C6	2.39	0.57
54:01:2699:C:H2'	54:01:2700:A:C8	2.39	0.57
3:06:40:ARG:HH22	54:01:1246:A:H4'	1.68	0.57
23:26:16:ASN:HD22	54:01:2081:U:H5''	1.70	0.57
44:N:13:VAL:HA	44:N:59:GLN:HE22	1.68	0.57
53:A:501:C:H2'	53:A:502:A:H8	1.68	0.57
53:A:707:U:H2'	53:A:708:C:C6	2.39	0.57
2:05:105:LYS:HA	2:05:177:VAL:HG12	1.87	0.57
18:21:83:LYS:HG2	18:21:95:ARG:NH1	2.19	0.57
52:03:211:LYS:HE2	52:03:213:SER:HB3	1.86	0.57
59:Z:4:LYS:HA	59:Z:264:LEU:HB2	1.85	0.57
2:05:25:THR:HG21	2:05:193:VAL:HG22	1.87	0.57
4:07:90:LEU:HD12	4:07:90:LEU:O	2.05	0.57
5:08:23:ILE:HG22	5:08:25:ILE:HG13	1.86	0.57
5:08:71:LEU:O	5:08:75:VAL:HG23	2.03	0.57
34:D:49:ASP:HA	34:D:52:VAL:HG22	1.85	0.57
39:I:33:SER:H	39:I:36:GLN:HE21	1.52	0.57
44:N:20:PHE:O	44:N:21:ALA:HB3	2.04	0.57
54:01:996:A:H2'	54:01:997:G:H8	1.70	0.57
59:Z:176:LYS:HD2	59:Z:184:TRP:CD1	2.40	0.57
4:07:133:GLU:OE2	4:07:148:VAL:HG13	2.04	0.57
32:B:160:LEU:HD22	32:B:175:ALA:HB2	1.86	0.57
52:03:175:ILE:HB	52:03:188:ASN:HB3	1.86	0.57
53:A:352:C:H4'	53:A:354:G:OP1	2.04	0.57
53:A:1228:C:H2'	53:A:1229:A:H8	1.70	0.57
53:A:1369:C:H2'	53:A:1370:G:C8	2.39	0.57
59:Z:67:VAL:HG23	59:Z:78:HIS:HB3	1.86	0.57
59:Z:214:ILE:HD13	59:Z:286:ILE:HD11	1.85	0.57
6:09:94:ILE:HD11	6:09:122:LEU:HB2	1.85	0.57
33:C:9:ILE:HG23	33:C:10:ARG:HG3	1.85	0.57
53:A:312:C:H2'	53:A:313:A:C8	2.40	0.57
59:Z:328:PRO:HG2	59:Z:330:PHE:CZ	2.40	0.57
7:10:26:VAL:HB	7:10:82:ILE:HD12	1.86	0.57
9:12:45:THR:HB	9:12:48:VAL:HB	1.87	0.57
35:E:148:SER:HB2	35:E:149:PRO:HD2	1.85	0.57
51:U:58:LYS:NZ	51:U:58:LYS:HB2	2.20	0.57
3:06:192:ALA:O	3:06:196:VAL:HG23	2.05	0.56
24:27:7:ARG:HD3	24:27:7:ARG:N	2.20	0.56
35:E:54:GLU:HG2	35:E:56:PRO:HD2	1.87	0.56
39:I:49:GLN:N	39:I:50:PRO:HD2	2.20	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:P:70:ARG:NH1	53:A:452:A:H1'	2.20	0.56
52:03:12:ARG:HG2	52:03:220:ALA:HB2	1.86	0.56
52:03:48:LEU:HD12	52:03:165:ASN:ND2	2.20	0.56
53:A:358:U:H2'	53:A:359:G:H8	1.70	0.56
53:A:398:U:H2'	53:A:399:G:H8	1.69	0.56
53:A:501:C:H2'	53:A:502:A:C8	2.40	0.56
53:A:1129:C:H2'	53:A:1139:G:N7	2.19	0.56
54:01:1268:A:H2'	54:01:1269:A:O4'	2.04	0.56
59:Z:97:GLN:HE21	59:Z:229:GLY:HA2	1.70	0.56
1:04:206:LYS:HD2	54:01:729:G:C8	2.41	0.56
4:07:87:LYS:HD2	54:01:2313:C:H5''	1.87	0.56
13:16:39:PRO:HG2	54:01:1651:G:H4'	1.86	0.56
14:17:29:HIS:HB3	14:17:36:TYR:HB2	1.87	0.56
34:D:117:VAL:HG22	34:D:122:ILE:HG13	1.87	0.56
36:F:52:ASN:O	36:F:53:LYS:HG3	2.04	0.56
53:A:744:C:H2'	53:A:745:G:C8	2.40	0.56
53:A:1429:A:H2'	53:A:1430:A:H8	1.70	0.56
54:01:1717:A:H2'	54:01:1718:G:O4'	2.06	0.56
59:Z:74:ARG:HB2	59:Z:76:TYR:CZ	2.41	0.56
2:05:118:PHE:HB2	54:01:2823:A:OP1	2.04	0.56
3:06:176:ASP:OD1	3:06:179:SER:HB2	2.06	0.56
12:15:82:MET:HE1	54:01:956:G:H4'	1.87	0.56
40:J:28:THR:HG22	40:J:86:ALA:HB1	1.86	0.56
42:L:2:THR:CG2	42:L:5:GLN:HG3	2.35	0.56
52:03:142:VAL:HG11	52:03:162:ARG:HD2	1.87	0.56
53:A:1144:G:H21	53:A:1146:A:H62	1.52	0.56
54:01:473:G:O2'	54:01:474:G:H5'	2.05	0.56
54:01:554:U:H2'	54:01:555:G:O4'	2.04	0.56
54:01:660:C:H2'	54:01:661:A:C8	2.41	0.56
54:01:679:C:H2'	54:01:680:C:C6	2.40	0.56
54:01:1149:G:H2'	54:01:1150:C:C6	2.41	0.56
54:01:2636:C:H2'	54:01:2637:U:H6	1.68	0.56
59:Z:157:LEU:HB3	59:Z:162:PHE:HB2	1.87	0.56
59:Z:366:ILE:HG13	59:Z:367:ALA:N	2.21	0.56
5:08:34:ARG:NE	5:08:70:LEU:HD13	2.19	0.56
20:23:10:VAL:HG12	20:23:71:ILE:HA	1.86	0.56
40:J:5:ARG:HG2	40:J:79:PRO:HB3	1.86	0.56
48:R:70:THR:HG23	48:R:72:ARG:H	1.71	0.56
54:01:2287:A:O2'	54:01:2288:A:H2'	2.06	0.56
54:01:2297:A:N6	54:01:2319:G:H1'	2.19	0.56
1:04:61:TYR:HE1	54:01:1816:C:H3'	1.71	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:18:52:ARG:NH2	54:01:2720:U:H5''	2.21	0.56
31:34:7:VAL:HB	31:34:35:GLN:NE2	2.20	0.56
32:B:160:LEU:HD22	32:B:175:ALA:CB	2.35	0.56
43:M:24:VAL:HA	53:A:1329:A:H5''	1.86	0.56
43:M:47:LEU:HD21	43:M:51:GLN:HB2	1.88	0.56
52:03:46:VAL:O	52:03:171:ILE:HG22	2.05	0.56
52:03:105:LYS:HA	52:03:109:MET:SD	2.46	0.56
15:18:88:ARG:HH11	15:18:112:ARG:HH21	1.52	0.56
22:25:47:VAL:HG13	22:25:56:PHE:O	2.05	0.56
36:F:9:MET:HE3	36:F:86:ARG:HB2	1.87	0.56
54:01:1432:G:H2'	54:01:1433:A:C8	2.40	0.56
59:Z:184:TRP:O	59:Z:188:ILE:HG12	2.05	0.56
1:04:61:TYR:CE1	54:01:1816:C:H3'	2.40	0.56
8:11:78:LEU:HD13	8:11:112:LYS:NZ	2.21	0.56
38:H:6:ILE:HD11	38:H:31:LEU:HD23	1.86	0.56
52:03:27:ILE:HB	52:03:182:ALA:HB1	1.88	0.56
54:01:184:C:H2'	54:01:185:G:H8	1.70	0.56
7:10:78:GLY:N	7:10:79:PRO:HD2	2.21	0.56
33:C:118:SER:O	33:C:122:GLN:HG3	2.06	0.56
52:03:153:VAL:HG12	52:03:157:LYS:HD3	1.87	0.56
53:A:1170:A:H2'	53:A:1171:A:O4'	2.05	0.56
53:A:1399:C:H4'	53:A:1400:C:O5'	2.05	0.56
54:01:100:U:H4'	54:01:101:A:O4'	2.06	0.56
54:01:1071:G:OP1	54:01:1071:G:H3'	2.05	0.56
54:01:1316:U:H2'	54:01:1317:G:C8	2.41	0.56
33:C:69:THR:HG21	33:C:75:VAL:HG21	1.87	0.56
35:E:152:VAL:HG11	38:H:98:LEU:HD13	1.87	0.56
44:N:80:ARG:O	44:N:83:VAL:HG12	2.06	0.56
52:03:22:ASP:H	52:03:25:GLU:HB3	1.70	0.56
53:A:1429:A:H2'	53:A:1430:A:C8	2.41	0.56
59:Z:100:GLY:HA3	59:Z:199:ILE:HD13	1.88	0.56
2:05:124:ARG:HA	2:05:165:MET:SD	2.46	0.56
7:10:59:LEU:HD22	7:10:62:ARG:NH2	2.21	0.56
17:20:78:ARG:HH12	54:01:990:A:H61	1.54	0.56
21:24:62:THR:HG22	21:24:71:LYS:HG2	1.88	0.56
46:P:20:VAL:HG22	46:P:21:VAL:H	1.71	0.56
48:R:17:VAL:HG22	48:R:18:GLN:N	2.19	0.56
53:A:89:U:H2'	53:A:90:C:O4'	2.06	0.56
53:A:797:C:H2'	53:A:798:U:C6	2.41	0.56
14:17:110:ALA:HB1	14:17:115:LEU:HD23	1.88	0.55
20:23:25:LYS:HG2	20:23:36:GLU:OE1	2.05	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:C:76:ILE:HB	33:C:80:GLY:HA2	1.88	0.55
40:J:42:LEU:HD11	40:J:73:LEU:HG	1.88	0.55
44:N:45:LEU:O	49:S:12:LEU:HD11	2.07	0.55
52:O3:48:LEU:HG	52:O3:171:ILE:HB	1.89	0.55
54:O1:2350:C:H2'	54:O1:2351:G:O4'	2.05	0.55
16:19:32:ARG:HB2	54:O1:581:C:OP1	2.05	0.55
18:21:4:ILE:HG22	18:21:106:VAL:HG22	1.88	0.55
32:B:41:ASN:HD22	32:B:44:LYS:HG2	1.71	0.55
43:M:47:LEU:HD23	43:M:48:SER:O	2.06	0.55
54:O1:1138:G:H2'	54:O1:1139:G:O4'	2.06	0.55
54:O1:2537:U:H2'	54:O1:2538:C:C6	2.41	0.55
54:O1:1278:C:H2'	54:O1:1279:G:H8	1.71	0.55
54:O1:1368:G:H2'	54:O1:1369:G:C8	2.41	0.55
54:O1:2329:U:H2'	54:O1:2330:G:H8	1.72	0.55
23:26:70:LEU:HD13	23:26:77:TYR:HB3	1.88	0.55
24:27:21:LEU:HA	24:27:25:GLN:HB3	1.89	0.55
38:H:9:MET:HE1	38:H:35:ILE:HB	1.89	0.55
53:A:744:C:H2'	53:A:745:G:H8	1.72	0.55
54:O1:161:A:H3'	54:O1:162:U:H5''	1.87	0.55
54:O1:703:U:H2'	54:O1:704:G:O4'	2.05	0.55
39:I:104:THR:HG23	53:A:1180:A:H5'	1.89	0.55
54:O1:1283:G:H1'	54:O1:1329:U:O2	2.07	0.55
54:O1:2799:A:H2'	54:O1:2800:A:H5'	1.89	0.55
59:Z:354:ASP:HB3	59:Z:356:ILE:HG23	1.89	0.55
5:O8:8:VAL:HB	5:O8:49:LEU:HB2	1.89	0.55
16:19:21:LYS:HG2	54:O1:19:A:H5''	1.89	0.55
20:23:5:ARG:HG2	20:23:93:ARG:NH2	2.22	0.55
42:L:32:VAL:O	42:L:33:CYS:HB2	2.06	0.55
54:O1:2111:U:H3	54:O1:2147:A:H1'	1.71	0.55
59:Z:212:LEU:HD21	59:Z:229:GLY:HA3	1.89	0.55
8:11:85:ILE:HD11	8:11:137:LEU:HD21	1.88	0.55
11:14:135:ILE:HB	11:14:142:ILE:HD11	1.88	0.55
33:C:106:ARG:HG2	33:C:107:LYS:HD2	1.88	0.55
36:F:51:ILE:C	36:F:53:LYS:H	2.14	0.55
54:O1:1874:C:H2'	54:O1:1875:G:O4'	2.07	0.55
54:O1:2155:U:H2'	54:O1:2156:G:H5'	1.89	0.55
54:O1:2512:C:H2'	54:O1:2513:A:O4'	2.06	0.55
11:14:23:ILE:HD12	11:14:23:ILE:N	2.22	0.55
16:19:49:ARG:HG2	16:19:52:ARG:NH2	2.22	0.55
32:B:9:LEU:HD11	32:B:13:VAL:HG22	1.87	0.55
53:A:1296:C:H4'	53:A:1302:C:H42	1.72	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2182:U:H2'	54:01:2183:A:C8	2.42	0.55
54:01:2423:U:O2'	54:01:2425:A:H2'	2.07	0.55
3:06:71:GLY:N	54:01:674:G:H5''	2.22	0.55
27:30:29:VAL:HB	54:01:2885:G:H1	1.71	0.55
32:B:17:HIS:HB2	32:B:188:THR:HG23	1.88	0.55
32:B:65:LYS:HB3	32:B:89:PHE:HE2	1.72	0.55
44:N:53:ASP:HA	44:N:58:ARG:HD3	1.87	0.55
53:A:220:G:O2'	53:A:221:C:H5'	2.07	0.55
53:A:236:A:H2'	53:A:237:G:H8	1.72	0.55
53:A:398:U:H2'	53:A:399:G:C8	2.42	0.55
53:A:1346:A:O2'	53:A:1347:G:H4'	2.07	0.55
54:01:365:U:H2'	54:01:366:C:C6	2.41	0.55
54:01:593:U:H2'	54:01:594:U:C6	2.42	0.55
59:Z:206:ILE:HG22	59:Z:270:ALA:N	2.19	0.55
5:08:154:GLU:HG2	5:08:157:LYS:H	1.72	0.55
8:11:33:ASN:ND2	8:11:35:MET:HB3	2.21	0.55
33:C:58:ARG:NH1	33:C:58:ARG:HB2	2.22	0.55
37:G:80:GLY:HA3	57:V:11:U:O2'	2.06	0.55
45:O:7:THR:O	45:O:11:VAL:HG23	2.06	0.55
53:A:225:C:H2'	53:A:226:G:H5''	1.89	0.55
54:01:172:A:H2'	54:01:173:A:H8	1.72	0.55
59:Z:317:GLY:HA2	59:Z:383:VAL:HA	1.87	0.55
6:09:51:ARG:HA	6:09:55:GLU:HG3	1.89	0.54
19:22:39:THR:O	19:22:43:ILE:HG13	2.07	0.54
54:01:1906:G:H2'	54:01:1907:G:H5''	1.88	0.54
54:01:2743:U:H3'	54:01:2744:G:H5''	1.88	0.54
59:Z:184:TRP:CE3	59:Z:187:LYS:HG2	2.42	0.54
7:10:51:TYR:HA	7:10:53:ARG:HH12	1.71	0.54
9:12:31:GLU:HG2	9:12:142:ILE:HG12	1.89	0.54
18:21:42:LYS:HB2	54:01:2010:G:H5''	1.88	0.54
31:34:30:GLU:HG3	31:34:32:LYS:H	1.71	0.54
48:R:59:LYS:HD3	53:A:735:C:H5'	1.89	0.54
54:01:741:U:H2'	54:01:742:A:H8	1.72	0.54
54:01:2180:U:H2'	54:01:2181:U:O4'	2.07	0.54
59:Z:13:ASN:HB2	59:Z:99:ASP:H	1.72	0.54
59:Z:21:ASP:N	60:Z:401:GCP:H3B1	2.22	0.54
59:Z:245:VAL:HA	59:Z:250:THR:HG22	1.89	0.54
4:07:55:ASP:O	4:07:59:ILE:HG13	2.07	0.54
17:20:68:ARG:HB2	17:20:90:ARG:NH2	2.22	0.54
30:33:61:LEU:HD12	30:33:61:LEU:O	2.07	0.54
32:B:18:GLN:HG2	32:B:187:ASP:OD2	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:C:133:MET:O	33:C:137:VAL:HG23	2.07	0.54
33:C:134:LYS:O	33:C:138:GLN:HG3	2.06	0.54
49:S:54:ARG:HG3	49:S:55:GLN:HG2	1.90	0.54
54:01:1609:A:H1'	54:01:1616:A:H1'	1.89	0.54
54:01:2185:U:H2'	54:01:2186:G:C8	2.43	0.54
1:04:106:PRO:HG2	1:04:109:LEU:HB2	1.87	0.54
3:06:105:LEU:HD23	3:06:108:ILE:HD11	1.88	0.54
4:07:47:LYS:HA	4:07:50:ASP:OD2	2.05	0.54
5:08:51:PHE:HZ	5:08:71:LEU:HD22	1.72	0.54
19:22:6:ARG:O	19:22:10:VAL:HG23	2.08	0.54
41:K:93:GLU:HG2	41:K:96:ILE:HD11	1.88	0.54
42:L:109:ARG:HB2	42:L:118:VAL:HG21	1.88	0.54
46:P:51:ARG:C	46:P:52:LEU:HD12	2.32	0.54
54:01:2368:C:H2'	54:01:2369:A:C8	2.43	0.54
54:01:2404:U:H2'	54:01:2405:G:O4'	2.07	0.54
54:01:2861:U:H2'	54:01:2862:G:H8	1.73	0.54
6:09:30:LEU:HB3	6:09:36:ALA:HB3	1.89	0.54
16:19:91:ARG:HD2	16:19:91:ARG:N	2.23	0.54
32:B:96:LEU:H	32:B:99:MET:HE3	1.73	0.54
32:B:103:TRP:CH2	32:B:107:ARG:HD3	2.42	0.54
50:T:4:LYS:HG3	50:T:6:ALA:H	1.72	0.54
53:A:434:U:H2'	53:A:435:A:C8	2.42	0.54
53:A:682:G:H2'	53:A:683:G:H8	1.72	0.54
53:A:918:A:H2'	53:A:919:A:C8	2.42	0.54
53:A:1379:G:O2'	53:A:1380:U:H5'	2.07	0.54
54:01:57:C:H2'	54:01:58:G:O4'	2.07	0.54
54:01:969:G:H2'	54:01:970:U:C6	2.43	0.54
54:01:1447:C:H2'	54:01:1448:G:H8	1.71	0.54
54:01:2208:C:H2'	54:01:2209:G:C8	2.42	0.54
54:01:2676:C:H2'	54:01:2677:G:C8	2.43	0.54
58:Y:53:G:H4'	59:Z:320:THR:OG1	2.08	0.54
59:Z:12:VAL:HB	59:Z:76:TYR:CD1	2.43	0.54
33:C:107:LYS:HG2	33:C:110:LEU:HD12	1.90	0.54
40:J:59:LYS:HE2	40:J:62:ARG:HH21	1.73	0.54
49:S:19:GLU:O	49:S:23:GLU:HG2	2.08	0.54
53:A:70:U:H2'	53:A:94:G:N7	2.23	0.54
53:A:235:C:H2'	53:A:236:A:C8	2.43	0.54
53:A:335:C:H2'	53:A:336:A:H8	1.73	0.54
7:10:118:ILE:HB	7:10:119:PRO:HD3	1.89	0.54
10:13:66:LYS:NZ	10:13:66:LYS:HB3	2.22	0.54
24:27:26:PHE:HA	24:27:29:ARG:HE	1.73	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:33:38:LYS:HA	30:33:41:ARG:HH11	1.72	0.54
34:D:49:ASP:O	34:D:53:GLN:HG3	2.07	0.54
54:01:873:C:H2'	54:01:874:G:H8	1.72	0.54
54:01:975:A:H1'	54:01:990:A:C6	2.43	0.54
54:01:1827:U:O2'	54:01:1828:G:H5'	2.07	0.54
59:Z:304:PHE:HD2	59:Z:388:VAL:HG13	1.73	0.54
1:04:12:ARG:HH21	54:01:728:G:C5'	2.21	0.54
2:05:9:VAL:O	2:05:26:VAL:HB	2.07	0.54
4:07:23:SER:HB3	4:07:26:GLN:HG3	1.89	0.54
5:08:118:ALA:O	5:08:120:ILE:N	2.41	0.54
14:17:66:GLY:HA2	14:17:102:ARG:NH2	2.23	0.54
32:B:162:VAL:HB	32:B:184:ALA:CB	2.38	0.54
33:C:67:ILE:HD11	33:C:100:ILE:HD11	1.88	0.54
33:C:86:LEU:HA	33:C:89:VAL:HG22	1.88	0.54
35:E:79:THR:OG1	35:E:80:LEU:N	2.40	0.54
35:E:79:THR:HG23	35:E:80:LEU:O	2.08	0.54
40:J:66:GLU:HG2	44:N:98:ALA:HB2	1.88	0.54
51:U:34:ARG:HB3	51:U:36:PHE:CE2	2.43	0.54
52:03:111:PHE:CE2	52:03:114:VAL:HG23	2.43	0.54
53:A:1201:A:H1'	53:A:1202:U:OP2	2.08	0.54
54:01:290:U:H2'	54:01:291:G:H8	1.71	0.54
54:01:1909:C:H2'	54:01:1910:G:H8	1.72	0.54
54:01:2789:C:H2'	54:01:2893:A:N7	2.23	0.54
55:02:13:G:N2	55:02:16:G:H1'	2.20	0.54
59:Z:70:ASP:HA	59:Z:76:TYR:HD2	1.71	0.54
59:Z:253:SER:HB2	59:Z:281:ILE:HD11	1.87	0.54
40:J:57:VAL:O	40:J:58:ASN:CB	2.55	0.54
47:Q:10:ARG:HH11	47:Q:55:GLY:HA2	1.72	0.54
54:01:1697:G:H4'	54:01:1978:A:H5''	1.89	0.54
59:Z:214:ILE:CD1	59:Z:286:ILE:HD11	2.37	0.54
2:05:125:TRP:CD1	2:05:160:LYS:HB3	2.42	0.54
4:07:40:GLY:HA2	4:07:84:ILE:HG13	1.89	0.54
5:08:8:VAL:HB	5:08:49:LEU:HD12	1.89	0.54
7:10:88:HIS:HB2	7:10:89:PRO:HD3	1.90	0.54
13:16:47:VAL:O	13:16:50:PRO:HD2	2.08	0.54
33:C:110:LEU:HD13	33:C:203:LYS:HE3	1.90	0.54
33:C:182:ASP:HB2	33:C:201:ILE:HB	1.90	0.54
34:D:190:LEU:HD12	34:D:190:LEU:O	2.08	0.54
36:F:50:PRO:HG3	36:F:55:HIS:CE1	2.43	0.54
49:S:54:ARG:HB3	53:A:958:A:C2	2.43	0.54
53:A:1228:C:H2'	53:A:1229:A:C8	2.43	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:741:U:H2'	54:01:742:A:C8	2.43	0.54
54:01:1669:A:H5''	54:01:2550:G:OP1	2.08	0.54
54:01:2144:G:H1'	54:01:2147:A:H61	1.73	0.54
59:Z:124:GLN:NE2	59:Z:385:ALA:HB1	2.22	0.54
59:Z:329:GLN:HE22	59:Z:378:GLU:HA	1.72	0.54
2:05:181:ASP:HB3	2:05:186:LEU:HB2	1.90	0.53
4:07:154:THR:HG21	54:01:2314:A:O4'	2.07	0.53
32:B:27:LYS:HB3	32:B:28:PRO:HD3	1.89	0.53
33:C:87:ARG:HG3	33:C:98:ALA:O	2.07	0.53
42:L:113:ARG:HH12	42:L:121:PRO:HD3	1.72	0.53
52:03:69:THR:HG22	52:03:174:THR:HG23	1.89	0.53
54:01:310:A:C2'	54:01:311:A:H5''	2.38	0.53
54:01:2270:A:H2'	54:01:2271:G:O4'	2.08	0.53
54:01:2398:U:H2'	54:01:2399:G:C8	2.43	0.53
18:21:86:MET:HB2	18:21:96:ILE:HD13	1.89	0.53
53:A:358:U:H2'	53:A:359:G:C8	2.42	0.53
54:01:255:A:H2'	54:01:256:A:O4'	2.08	0.53
54:01:1775:U:H2'	54:01:1776:G:O4'	2.07	0.53
54:01:2162:G:H2'	54:01:2163:A:C8	2.43	0.53
59:Z:68:GLU:HB2	59:Z:261:PHE:HD2	1.72	0.53
1:04:12:ARG:HA	1:04:15:VAL:HG23	1.90	0.53
35:E:59:ILE:HD12	35:E:60:GLN:N	2.23	0.53
41:K:124:LYS:HD3	41:K:124:LYS:H	1.74	0.53
53:A:20:U:H2'	53:A:21:G:O4'	2.08	0.53
53:A:59:A:H5''	53:A:387:U:H5''	1.90	0.53
53:A:1306:A:N6	53:A:1331:G:H1'	2.24	0.53
53:A:1460:C:H2'	53:A:1461:G:H8	1.73	0.53
54:01:1675:C:H2'	54:01:1676:A:O4'	2.07	0.53
54:01:1689:A:H2'	54:01:1690:A:H8	1.74	0.53
59:Z:145:LEU:O	59:Z:149:VAL:HG23	2.09	0.53
1:04:261:ARG:CD	1:04:262:THR:HG23	2.39	0.53
2:05:2:ILE:HG21	2:05:90:PHE:HE2	1.73	0.53
2:05:33:ARG:H	2:05:33:ARG:CD	2.19	0.53
33:C:155:ARG:HG3	33:C:192:TYR:O	2.08	0.53
45:O:45:HIS:O	45:O:47:LYS:N	2.41	0.53
54:01:1316:U:H2'	54:01:1317:G:H8	1.73	0.53
54:01:2329:U:H2'	54:01:2330:G:C8	2.44	0.53
24:27:9:LYS:HE2	24:27:11:VAL:HG23	1.89	0.53
27:30:27:LEU:HD11	27:30:36:LYS:HB3	1.91	0.53
39:I:115:VAL:HG21	40:J:62:ARG:HB2	1.90	0.53
47:Q:48:GLU:HB2	47:Q:51:GLU:OE2	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:859:G:H1'	54:01:860:U:H5	1.73	0.53
54:01:1765:U:H2'	54:01:1766:G:H8	1.74	0.53
54:01:2345:G:N3	54:01:2381:A:H2'	2.24	0.53
56:W:47:U:H3'	56:W:48:C:C5'	2.39	0.53
59:Z:93:THR:HG22	59:Z:215:GLU:HG2	1.91	0.53
32:B:79:VAL:HG12	32:B:90:PHE:HB2	1.89	0.53
34:D:131:ILE:HG12	53:A:620:C:C2	2.43	0.53
38:H:65:PHE:CD2	38:H:66:GLN:HG2	2.43	0.53
53:A:891:U:O2'	53:A:892:A:H5'	2.08	0.53
54:01:435:C:H2'	54:01:436:C:H5'	1.90	0.53
54:01:742:A:H2'	54:01:743:A:H8	1.74	0.53
54:01:1310:G:H1'	54:01:1611:C:H5'	1.88	0.53
16:19:15:LYS:O	16:19:19:GLN:HG3	2.09	0.53
33:C:11:LEU:HD13	33:C:17:TRP:NE1	2.24	0.53
35:E:119:VAL:HG11	35:E:122:VAL:CG2	2.37	0.53
42:L:43:LYS:HB3	42:L:44:PRO:HD3	1.90	0.53
49:S:35:ARG:HH22	49:S:52:ASN:HA	1.74	0.53
54:01:2215:C:H2'	54:01:2216:G:C8	2.44	0.53
59:Z:212:LEU:HG	59:Z:230:ARG:O	2.08	0.53
5:08:94:ARG:HB2	5:08:105:SER:HB2	1.90	0.53
6:09:93:SER:HB3	6:09:123:ARG:HG2	1.90	0.53
8:11:21:PRO:HB2	8:11:22:PRO:HD3	1.90	0.53
12:15:42:THR:O	12:15:46:ILE:HD13	2.09	0.53
16:19:105:PHE:O	16:19:109:VAL:HG23	2.08	0.53
38:H:45:ILE:HG21	38:H:60:LEU:HD22	1.90	0.53
39:I:89:TYR:HB3	39:I:93:LEU:HD12	1.90	0.53
42:L:48:LEU:HB2	53:A:520:A:OP1	2.09	0.53
51:U:11:PHE:O	51:U:13:VAL:HG12	2.09	0.53
53:A:784:A:H2'	53:A:785:G:C8	2.43	0.53
53:A:1402:C:H2'	53:A:1403:C:O4'	2.09	0.53
54:01:575:A:O2'	54:01:576:U:H5'	2.09	0.53
6:09:64:ALA:O	6:09:68:ARG:HG3	2.08	0.53
46:P:70:ARG:HD3	53:A:375:U:OP1	2.09	0.53
52:03:9:ARG:O	52:03:13:GLU:HG3	2.09	0.53
53:A:335:C:H2'	53:A:336:A:C8	2.44	0.53
53:A:411:A:H1'	53:A:413:G:H1'	1.90	0.53
54:01:1141:U:H4'	54:01:1142:A:O4'	2.09	0.53
54:01:1332:G:N7	54:01:1609:A:H2'	2.24	0.53
54:01:2141:G:H2'	54:01:2142:A:C8	2.44	0.53
55:02:114:C:H2'	55:02:115:A:H8	1.72	0.53
2:05:194:PRO:HA	54:01:2680:U:H5'	1.89	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:19:50:ARG:HG2	54:01:1156:A:C8	2.44	0.53
29:32:16:HIS:HA	29:32:21:ARG:HH22	1.72	0.53
33:C:179:ALA:HB1	33:C:202:PHE:HE1	1.73	0.53
40:J:91:ASP:CG	40:J:92:LEU:H	2.17	0.53
50:T:23:ARG:HH21	50:T:60:GLN:HE22	1.57	0.53
53:A:309:A:H2'	53:A:310:G:H8	1.72	0.53
54:01:2317:A:H2'	54:01:2318:G:O4'	2.09	0.53
59:Z:11:HIS:CB	59:Z:269:ARG:HH12	2.22	0.53
4:07:124:ARG:HH21	54:01:2316:G:H4'	1.74	0.52
12:15:29:GLY:HA2	12:15:106:ASP:HB2	1.91	0.52
28:31:47:ILE:HD12	28:31:47:ILE:N	2.23	0.52
33:C:54:ILE:HG22	33:C:67:ILE:HA	1.90	0.52
53:A:483:C:H2'	53:A:484:G:C8	2.43	0.52
54:01:329:G:O4'	54:01:477:A:H1'	2.09	0.52
54:01:1447:C:H2'	54:01:1448:G:C8	2.45	0.52
4:07:107:VAL:HB	4:07:108:PRO:HD3	1.91	0.52
5:08:136:ASP:OD2	5:08:139:VAL:HG23	2.09	0.52
17:20:80:ARG:NH2	54:01:571:U:H3'	2.24	0.52
51:U:17:ARG:HA	51:U:20:ARG:NH1	2.25	0.52
53:A:1409:C:H2'	53:A:1410:A:C8	2.44	0.52
53:A:1498:U:H1'	53:A:1499:A:N7	2.24	0.52
54:01:519:U:H2'	54:01:520:G:C8	2.45	0.52
54:01:1297:C:OP1	54:01:2710:C:H4'	2.08	0.52
54:01:2248:C:C2'	54:01:2249:U:H5'	2.39	0.52
59:Z:230:ARG:HA	59:Z:273:ASN:HA	1.89	0.52
59:Z:370:ASP:OD1	59:Z:391:VAL:HG23	2.09	0.52
6:09:2:GLN:O	6:09:39:ALA:HB3	2.09	0.52
7:10:33:VAL:HG12	7:10:34:THR:N	2.25	0.52
38:H:17:GLN:NE2	38:H:71:VAL:H	2.08	0.52
47:Q:43:LEU:HD13	47:Q:72:TRP:NE1	2.25	0.52
53:A:1527:U:H2'	53:A:1528:U:C6	2.43	0.52
59:Z:310:ILE:HG21	59:Z:350:VAL:HG12	1.92	0.52
12:15:69:PRO:HA	12:15:94:ALA:HB2	1.89	0.52
35:E:163:ILE:HD12	35:E:164:LEU:N	2.24	0.52
38:H:29:SER:HB3	38:H:32:LYS:HD3	1.90	0.52
54:01:546:U:H2'	54:01:547:A:C4'	2.39	0.52
54:01:1047:G:H2'	54:01:1110:G:N2	2.24	0.52
59:Z:172:GLY:HA3	59:Z:187:LYS:HB3	1.91	0.52
53:A:1230:C:H5'	56:W:30:G:H5''	1.92	0.52
54:01:66:C:H2'	54:01:67:U:C6	2.44	0.52
54:01:2861:U:H2'	54:01:2862:G:C8	2.44	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:02:63:C:H2'	55:02:64:G:H8	1.75	0.52
6:09:1:MET:HB3	6:09:3:VAL:HG23	1.91	0.52
11:14:23:ILE:HG13	17:20:82:HIS:NE2	2.25	0.52
28:31:8:ILE:HG21	28:31:24:LYS:HE2	1.90	0.52
32:B:208:ALA:HB1	32:B:212:TYR:HE2	1.73	0.52
38:H:17:GLN:HE21	38:H:71:VAL:HB	1.75	0.52
53:A:418:C:H2'	53:A:419:C:C6	2.45	0.52
54:01:2629:U:O2'	54:01:2630:G:H5''	2.10	0.52
3:06:79:ARG:HH22	54:01:471:A:H5''	1.73	0.52
7:10:23:LEU:HB3	7:10:87:GLU:OE1	2.09	0.52
22:25:45:ALA:O	22:25:47:VAL:HG23	2.10	0.52
33:C:110:LEU:HG	33:C:143:LEU:HD22	1.91	0.52
55:02:37:C:H42	55:02:49:C:H1'	1.74	0.52
35:E:84:VAL:HG23	35:E:145:ASN:HD22	1.75	0.52
52:03:57:GLN:HG2	52:03:201:PRO:HB2	1.92	0.52
53:A:494:G:O2'	53:A:496:A:H1'	2.10	0.52
53:A:1406:U:H2'	53:A:1407:C:O4'	2.10	0.52
2:05:154:LYS:NZ	54:01:2024:G:H4'	2.25	0.52
5:08:23:ILE:HD13	5:08:71:LEU:HD21	1.90	0.52
10:13:15:GLY:O	10:13:47:ILE:HG12	2.10	0.52
12:15:33:LEU:HB2	12:15:117:PHE:CD1	2.45	0.52
12:15:50:ARG:HH21	12:15:50:ARG:HG2	1.74	0.52
16:19:36:GLN:NE2	54:01:564:C:H1'	2.25	0.52
24:27:2:LYS:HD2	54:01:78:U:OP2	2.10	0.52
42:L:26:CYS:SG	42:L:29:LYS:HE2	2.50	0.52
44:N:2:LYS:HB3	44:N:5:MET:HG2	1.92	0.52
47:Q:59:GLU:HB2	47:Q:76:ARG:H	1.74	0.52
51:U:28:LEU:HA	51:U:31:VAL:HG12	1.92	0.52
53:A:235:C:H2'	53:A:236:A:H8	1.75	0.52
53:A:410:G:H2'	53:A:429:U:C4	2.45	0.52
54:01:1437:C:H2'	54:01:1438:U:C6	2.45	0.52
7:10:103:ASN:HA	7:10:107:GLU:HB3	1.92	0.52
21:24:70:ILE:HG22	21:24:72:VAL:HG13	1.91	0.52
29:32:12:ARG:NH1	29:32:44:VAL:HG21	2.25	0.52
32:B:53:LEU:HD23	32:B:56:LEU:HD12	1.91	0.52
34:D:85:THR:HB	35:E:102:THR:HG21	1.91	0.52
34:D:141:VAL:HG12	34:D:180:THR:HG23	1.92	0.52
35:E:147:ASN:HB2	35:E:151:MET:HG3	1.91	0.52
41:K:85:VAL:HG22	41:K:110:THR:O	2.10	0.52
42:L:115:LYS:O	42:L:116:TYR:HB2	2.09	0.52
48:R:11:ARG:CZ	48:R:14:ALA:HB3	2.40	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:129:A:H1'	53:A:130:A:N7	2.25	0.52
54:01:290:U:H2'	54:01:291:G:C8	2.43	0.52
54:01:910:A:H2'	54:01:911:A:C8	2.45	0.52
54:01:927:A:H2'	54:01:928:A:C8	2.45	0.52
54:01:1625:C:H2'	54:01:1626:A:O4'	2.10	0.52
54:01:2082:A:H2'	54:01:2083:G:O4'	2.10	0.52
55:02:114:C:H2'	55:02:115:A:C8	2.44	0.52
59:Z:294:LYS:HB3	59:Z:297:THR:CG2	2.40	0.52
8:11:15:GLY:HA3	8:11:51:GLY:H	1.74	0.51
37:G:111:GLY:HA2	37:G:118:ARG:HH11	1.75	0.51
53:A:948:C:H2'	53:A:949:A:H8	1.74	0.51
54:01:942:G:H2'	54:01:943:A:O4'	2.10	0.51
54:01:2366:A:H2'	54:01:2367:G:O4'	2.10	0.51
59:Z:150:GLU:OE2	59:Z:169:ILE:HB	2.11	0.51
6:09:43:ASN:HA	6:09:46:PHE:HD2	1.75	0.51
32:B:216:VAL:O	32:B:220:VAL:HG23	2.10	0.51
33:C:11:LEU:HD13	33:C:17:TRP:HE1	1.76	0.51
35:E:122:VAL:HG23	35:E:122:VAL:O	2.11	0.51
53:A:106:C:H2'	53:A:107:G:H8	1.75	0.51
53:A:902:G:H2'	53:A:903:G:C8	2.45	0.51
54:01:2538:C:H2'	54:01:2539:C:H6	1.75	0.51
54:01:2898:U:H2'	54:01:2899:A:H8	1.73	0.51
55:02:34:A:N6	55:02:44:G:H2'	2.25	0.51
59:Z:102:ILE:HD11	59:Z:195:LEU:HD11	1.92	0.51
1:04:163:ILE:HA	1:04:173:LEU:HD23	1.92	0.51
2:05:66:GLY:HA3	54:01:2787:C:H5'	1.92	0.51
14:17:26:LEU:HD23	14:17:92:PHE:HD1	1.75	0.51
14:17:74:VAL:O	14:17:78:VAL:HG23	2.11	0.51
19:22:58:VAL:HG22	19:22:85:VAL:HG13	1.92	0.51
22:25:70:PRO:HD3	55:02:12:C:H42	1.74	0.51
33:C:102:ILE:HD12	33:C:102:ILE:O	2.10	0.51
37:G:78:ARG:HB3	37:G:83:THR:HA	1.93	0.51
40:J:41:PRO:HG3	53:A:1150:A:N3	2.25	0.51
42:L:114:SER:HB3	53:A:35:G:H21	1.76	0.51
45:O:23:SER:HB3	45:O:26:VAL:HG23	1.92	0.51
52:03:215:SER:HB3	52:03:221:GLY:HA2	1.92	0.51
54:01:107:G:H2'	54:01:108:G:H8	1.75	0.51
54:01:189:G:H2'	54:01:205:G:H22	1.75	0.51
54:01:1782:U:H2'	54:01:1783:A:H5'	1.91	0.51
54:01:1971:U:H5'	54:01:1972:G:H5''	1.91	0.51
54:01:2849:U:H4'	54:01:2850:A:H5'	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:X:70:G:H2'	56:X:71:C:O4'	2.10	0.51
5:08:148:ARG:HA	5:08:161:VAL:HB	1.93	0.51
15:18:3:ILE:HD12	15:18:3:ILE:N	2.24	0.51
53:A:1062:U:H2'	53:A:1063:C:C6	2.45	0.51
54:01:582:A:H2'	54:01:583:G:C8	2.45	0.51
54:01:940:G:H3'	54:01:941:A:H5''	1.93	0.51
54:01:1761:C:H2'	54:01:1762:A:O4'	2.11	0.51
54:01:2676:C:H2'	54:01:2677:G:H8	1.74	0.51
54:01:2859:G:H2'	54:01:2860:A:C8	2.44	0.51
11:14:124:GLY:C	11:14:125:LEU:HD12	2.35	0.51
19:22:8:LEU:HD11	24:27:22:LEU:HD12	1.91	0.51
20:23:4:ILE:HD12	20:23:4:ILE:N	2.25	0.51
32:B:129:THR:HG22	32:B:131:LYS:H	1.75	0.51
34:D:143:SER:C	34:D:144:ILE:HD12	2.36	0.51
42:L:2:THR:HG21	42:L:5:GLN:HG3	1.92	0.51
47:Q:16:MET:HE2	47:Q:19:SER:HB3	1.92	0.51
51:U:29:ALA:HA	51:U:32:ARG:HD3	1.91	0.51
52:03:149:VAL:O	52:03:153:VAL:HG23	2.10	0.51
53:A:887:G:H2'	53:A:888:G:H5'	1.93	0.51
53:A:1011:C:H2'	53:A:1012:A:C8	2.46	0.51
54:01:56:A:H2'	54:01:57:C:O4'	2.11	0.51
54:01:2185:U:H2'	54:01:2186:G:H8	1.76	0.51
56:X:38:A:H3'	56:X:39:C:H6	1.73	0.51
2:05:2:ILE:HD11	2:05:100:LEU:HD22	1.91	0.51
4:07:90:LEU:HD13	4:07:95:MET:HA	1.93	0.51
5:08:173:ALA:HB1	54:01:2531:A:C8	2.45	0.51
9:12:95:ARG:HH11	9:12:95:ARG:HG3	1.75	0.51
40:J:40:ILE:HD12	40:J:73:LEU:HB2	1.92	0.51
41:K:88:PRO:HG2	41:K:89:GLY:H	1.75	0.51
43:M:24:VAL:HG23	43:M:28:ARG:HB3	1.93	0.51
53:A:382:A:H2'	53:A:383:A:C8	2.44	0.51
53:A:1219:A:H2'	53:A:1220:G:C8	2.46	0.51
54:01:197:A:H4'	54:01:2069:G:OP2	2.10	0.51
54:01:1657:U:H2'	54:01:1658:C:H6	1.76	0.51
54:01:2195:U:H2'	54:01:2196:C:C6	2.46	0.51
55:02:30:C:H2'	55:02:31:C:H5'	1.91	0.51
56:X:32:C:H2'	56:X:33:U:C4	2.45	0.51
1:04:131:MET:HG3	1:04:187:CYS:O	2.11	0.51
11:14:96:LYS:HB2	11:14:96:LYS:NZ	2.26	0.51
28:31:4:ILE:HD13	28:31:27:ARG:NH2	2.26	0.51
32:B:94:ARG:HD2	32:B:94:ARG:N	2.22	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:D:151:GLN:HG3	53:A:437:U:OP1	2.11	0.51
43:M:9:PRO:HG3	43:M:44:ILE:HG13	1.93	0.51
54:01:609:A:H2'	54:01:610:C:O4'	2.11	0.51
54:01:723:C:H2'	54:01:724:U:O4'	2.11	0.51
54:01:2070:A:H2'	54:01:2071:A:H8	1.74	0.51
59:Z:34:VAL:O	59:Z:38:THR:HG23	2.11	0.51
4:07:137:PHE:HB2	4:07:140:ILE:HD13	1.93	0.51
8:11:91:LYS:HA	8:11:94:LYS:HE2	1.93	0.51
12:15:12:MET:CA	54:01:910:A:H62	2.20	0.51
12:15:66:ARG:HG3	12:15:66:ARG:HH11	1.75	0.51
27:30:43:THR:HG23	27:30:47:TYR:O	2.10	0.51
35:E:121:ASN:OD1	35:E:122:VAL:HG13	2.11	0.51
47:Q:13:SER:HB3	47:Q:21:VAL:CG1	2.40	0.51
54:01:2487:G:H2'	54:01:2488:G:C8	2.44	0.51
59:Z:33:THR:O	59:Z:37:LYS:HG3	2.09	0.51
3:06:68:ALA:HA	54:01:1255:U:C6	2.45	0.51
16:19:109:VAL:HG12	16:19:113:LYS:HE2	1.93	0.51
28:31:37:LYS:HB2	28:31:48:TYR:CE2	2.46	0.51
35:E:73:VAL:HG21	35:E:143:LEU:HD13	1.91	0.51
46:P:19:VAL:HG13	46:P:36:VAL:O	2.11	0.51
52:03:41:SER:HB2	52:03:176:GLY:O	2.10	0.51
54:01:2368:C:H2'	54:01:2369:A:H8	1.76	0.51
54:01:2812:G:H2'	54:01:2813:A:C8	2.46	0.51
59:Z:50:ASP:HB3	59:Z:56:LYS:HG3	1.92	0.51
1:04:144:GLU:HG3	1:04:188:ARG:O	2.11	0.51
4:07:102:LEU:O	4:07:107:VAL:HG23	2.11	0.51
13:16:38:LEU:HB3	13:16:39:PRO:HD3	1.91	0.51
13:16:58:ASP:OD1	13:16:63:ARG:HD3	2.11	0.51
18:21:24:ILE:HD13	18:21:36:LEU:HD11	1.93	0.51
39:I:33:SER:HB3	39:I:36:GLN:HG2	1.93	0.51
43:M:56:ARG:HA	43:M:59:VAL:HG22	1.92	0.51
45:O:24:THR:O	45:O:28:VAL:HG23	2.11	0.51
52:03:104:ILE:HG22	52:03:109:MET:HG2	1.92	0.51
52:03:194:VAL:HG12	52:03:198:LYS:HZ2	1.76	0.51
53:A:1144:G:N2	53:A:1146:A:H62	2.09	0.51
54:01:996:A:H2'	54:01:997:G:C8	2.46	0.51
54:01:1063:G:H1	54:01:1075:C:N4	2.08	0.51
54:01:1170:C:H2'	54:01:1171:G:C8	2.46	0.51
54:01:1357:C:H2'	54:01:1358:G:O4'	2.11	0.51
59:Z:120:LEU:HD12	59:Z:121:LEU:HG	1.93	0.51
59:Z:149:VAL:O	59:Z:153:VAL:HG23	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:14:95:LEU:HB3	11:14:100:ILE:HD11	1.92	0.50
14:17:88:LYS:HE2	14:17:116:GLN:HG3	1.92	0.50
33:C:56:ILE:HG22	33:C:63:ILE:HD11	1.92	0.50
33:C:71:ARG:O	33:C:75:VAL:HG23	2.11	0.50
40:J:70:HIS:C	40:J:71:LEU:HD12	2.36	0.50
43:M:104:ASN:O	43:M:105:ALA:HB3	2.11	0.50
45:O:35:ILE:HG13	45:O:58:MET:HE2	1.91	0.50
47:Q:60:ILE:HG23	47:Q:72:TRP:HB3	1.91	0.50
51:U:36:PHE:C	51:U:38:GLU:H	2.19	0.50
53:A:86:G:H4'	53:A:87:C:C5	2.46	0.50
53:A:673:A:H2'	53:A:674:G:C8	2.47	0.50
53:A:1436:U:H2'	53:A:1437:A:C8	2.45	0.50
54:01:296:U:H2'	54:01:297:G:C8	2.47	0.50
54:01:2114:A:N3	54:01:2114:A:H2'	2.26	0.50
59:Z:278:LEU:HD13	59:Z:281:ILE:HG13	1.92	0.50
27:30:8:THR:HG22	54:01:2020:A:H5'	1.93	0.50
27:30:12:ARG:HH11	27:30:16:ARG:CZ	2.24	0.50
32:B:178:LEU:HD23	32:B:178:LEU:H	1.77	0.50
37:G:24:LYS:HD3	37:G:100:MET:HE1	1.92	0.50
45:O:2:LEU:HB2	45:O:34:GLN:HE22	1.76	0.50
49:S:14:LEU:O	49:S:18:VAL:HG23	2.11	0.50
50:T:59:ARG:O	50:T:63:LYS:HG2	2.11	0.50
53:A:29:U:O2'	53:A:30:U:H5'	2.11	0.50
54:01:414:C:H2'	54:01:415:A:C8	2.45	0.50
54:01:576:U:H2'	54:01:577:G:C8	2.46	0.50
54:01:1710:G:H2'	54:01:1711:A:C8	2.46	0.50
8:11:106:GLN:O	8:11:110:GLN:HG2	2.11	0.50
18:21:20:VAL:HG21	18:21:43:ALA:HB3	1.93	0.50
32:B:30:ILE:HB	32:B:38:HIS:HB3	1.94	0.50
32:B:138:ARG:HD2	32:B:141:GLU:OE1	2.10	0.50
37:G:100:MET:O	37:G:104:VAL:HG23	2.10	0.50
38:H:29:SER:O	38:H:33:VAL:HG23	2.11	0.50
38:H:34:ALA:O	38:H:38:VAL:HG23	2.11	0.50
41:K:83:VAL:O	41:K:84:MET:HE2	2.11	0.50
51:U:65:ARG:HA	51:U:65:ARG:HE	1.76	0.50
53:A:77:A:H2'	53:A:78:A:C8	2.46	0.50
53:A:1308:U:H2'	53:A:1309:G:C8	2.46	0.50
53:A:1521:C:H2'	53:A:1522:U:C6	2.47	0.50
54:01:876:C:H2'	54:01:877:A:O4'	2.11	0.50
54:01:2432:A:H1'	56:X:75:C:H5'	1.91	0.50
55:02:66:A:H61	55:02:107:G:H3'	1.76	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:07:127:TYR:HB3	4:07:155:ILE:HB	1.93	0.50
23:26:32:LEU:HA	23:26:51:SER:HA	1.92	0.50
36:F:68:GLN:O	36:F:71:ILE:HG22	2.10	0.50
41:K:49:SER:HB3	41:K:68:ARG:HD3	1.92	0.50
42:L:113:ARG:NH2	42:L:120:ARG:HA	2.27	0.50
53:A:1082:A:H2'	53:A:1083:U:O4'	2.12	0.50
53:A:1252:A:H2'	53:A:1253:G:O4'	2.11	0.50
54:01:732:C:H2'	54:01:733:G:O4'	2.11	0.50
54:01:992:C:H2'	54:01:993:G:C8	2.46	0.50
54:01:1159:U:H2'	54:01:1160:G:C8	2.46	0.50
54:01:2755:C:O5'	54:01:2755:C:H6	1.94	0.50
59:Z:341:ILE:HD12	59:Z:358:MET:HE2	1.92	0.50
1:04:140:VAL:HG12	1:04:191:LEU:HA	1.93	0.50
25:28:23:LEU:HD11	25:28:53:MET:SD	2.51	0.50
29:32:10:LEU:O	29:32:14:ARG:HG2	2.12	0.50
32:B:93:HIS:ND1	32:B:145:ASN:HB2	2.26	0.50
54:01:879:G:H2'	54:01:880:G:H8	1.76	0.50
1:04:224:MET:HG2	54:01:782:A:C2	2.47	0.50
7:10:56:ARG:HD2	54:01:1106:G:O2'	2.12	0.50
8:11:4:VAL:HA	8:11:7:TYR:CE1	2.47	0.50
24:27:18:LEU:HG	24:27:22:LEU:HD13	1.94	0.50
52:03:221:GLY:N	54:01:2176:A:H5''	2.26	0.50
53:A:1128:C:H2'	53:A:1129:C:O4'	2.11	0.50
53:A:1205:U:H2'	53:A:1206:G:C8	2.45	0.50
54:01:355:U:H2'	54:01:356:G:H8	1.76	0.50
54:01:1822:C:H2'	54:01:1823:G:H8	1.77	0.50
54:01:1909:C:H2'	54:01:1910:G:C8	2.47	0.50
54:01:2875:C:H2'	54:01:2876:G:C8	2.47	0.50
1:04:94:LEU:HD13	1:04:100:ARG:HG2	1.92	0.50
3:06:145:ASP:HA	3:06:166:LYS:HB3	1.94	0.50
8:11:130:GLY:HA2	8:11:133:ARG:NH1	2.27	0.50
9:12:31:GLU:OE2	9:12:34:ARG:HD3	2.12	0.50
15:18:24:THR:HB	15:18:87:ARG:H	1.76	0.50
33:C:5:HIS:HB3	44:N:88:MET:CE	2.42	0.50
34:D:1:ALA:HA	34:D:67:LEU:HD11	1.94	0.50
37:G:65:LEU:HA	37:G:68:VAL:HG22	1.93	0.50
49:S:71:GLY:HA3	53:A:1320:C:O2	2.12	0.50
51:U:9:GLU:HB2	51:U:10:PRO:HD3	1.94	0.50
53:A:1207:G:H2'	53:A:1208:C:O4'	2.12	0.50
54:01:594:U:H2'	54:01:595:C:C6	2.47	0.50
54:01:940:G:C3'	54:01:941:A:H5''	2.42	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:971:G:H2'	54:01:972:A:O4'	2.12	0.50
54:01:1872:A:H2'	54:01:1873:G:O4'	2.11	0.50
54:01:2196:C:O2'	54:01:2197:U:H5'	2.11	0.50
54:01:2372:U:H2'	54:01:2373:G:H8	1.76	0.50
59:Z:68:GLU:HG2	59:Z:76:TYR:O	2.12	0.50
3:06:52:VAL:HG13	54:01:452:G:OP1	2.12	0.50
10:13:48:PRO:HG2	10:13:49:ARG:HD2	1.93	0.50
10:13:122:VAL:OXT	10:13:122:VAL:HG12	2.11	0.50
18:21:28:LYS:HB2	18:21:31:GLN:OE1	2.11	0.50
51:U:49:ALA:O	51:U:53:LYS:HG3	2.12	0.50
53:A:48:C:H5'	53:A:49:U:OP2	2.11	0.50
53:A:986:U:H2'	53:A:987:G:C8	2.47	0.50
53:A:1005:A:H2'	53:A:1006:G:O4'	2.12	0.50
53:A:1305:G:H22	53:A:1331:G:H2'	1.76	0.50
54:01:1300:G:H4'	54:01:1301:A:C5'	2.41	0.50
54:01:2623:G:H2'	54:01:2624:G:H8	1.76	0.50
58:Y:56:C:H2'	58:Y:57:G:H8	1.76	0.50
59:Z:5:PHE:CD1	59:Z:263:LYS:HD2	2.46	0.50
59:Z:375:ALA:HA	59:Z:385:ALA:HA	1.93	0.50
11:14:30:THR:O	11:14:33:ARG:HG2	2.11	0.50
12:15:63:ILE:HG12	12:15:105:MET:HE2	1.92	0.50
15:18:26:GLU:HB3	15:18:84:SER:OG	2.12	0.50
20:23:39:ASN:HB3	20:23:62:ALA:HB3	1.94	0.50
21:24:53:LYS:HB3	21:24:55:GLU:OE1	2.11	0.50
27:30:40:HIS:HA	27:30:48:TYR:OH	2.12	0.50
39:I:129:ARG:HG2	39:I:129:ARG:HH11	1.77	0.50
47:Q:6:THR:C	47:Q:7:LEU:HD12	2.36	0.50
53:A:410:G:H2'	53:A:429:U:O4	2.11	0.50
54:01:915:C:H3'	54:01:916:G:C8	2.47	0.50
54:01:1857:G:N2	54:01:1884:G:H2'	2.27	0.50
54:01:2515:C:H2'	54:01:2516:A:C8	2.47	0.50
59:Z:24:LYS:HG2	59:Z:104:VAL:HB	1.93	0.50
1:04:252:LYS:HB2	1:04:252:LYS:NZ	2.27	0.49
2:05:3:GLY:C	2:05:4:LEU:HD12	2.36	0.49
3:06:68:ALA:HA	54:01:1255:U:C5	2.47	0.49
9:12:26:GLY:HA3	54:01:1140:C:H5'	1.93	0.49
16:19:32:ARG:HG2	54:01:1252:G:N2	2.27	0.49
22:25:28:LEU:HA	22:25:60:ASP:OD1	2.12	0.49
22:25:55:LEU:HD12	22:25:76:ILE:HD12	1.93	0.49
32:B:99:MET:HA	32:B:106:VAL:HG21	1.93	0.49
35:E:119:VAL:CG1	35:E:122:VAL:HG22	2.39	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:100:ILE:HD12	38:H:100:ILE:O	2.12	0.49
40:J:65:TYR:OH	44:N:84:ARG:HG3	2.12	0.49
41:K:81:LEU:HD12	41:K:81:LEU:O	2.12	0.49
41:K:86:LYS:NZ	41:K:114:PRO:HD3	2.27	0.49
54:01:257:C:H2'	54:01:258:G:O4'	2.12	0.49
54:01:872:U:H2'	54:01:873:C:C6	2.47	0.49
54:01:1278:C:H2'	54:01:1279:G:C8	2.47	0.49
54:01:1434:A:H2'	54:01:1435:G:C8	2.47	0.49
54:01:1636:U:H2'	54:01:1637:A:H8	1.75	0.49
54:01:1709:U:H2'	54:01:1710:G:H8	1.77	0.49
1:04:66:PHE:HB3	1:04:150:GLY:O	2.12	0.49
3:06:46:GLN:CB	3:06:83:VAL:HG11	2.42	0.49
5:08:29:ASN:HB2	5:08:78:VAL:HA	1.94	0.49
6:09:84:ALA:HA	6:09:91:PHE:H	1.76	0.49
52:03:28:ALA:O	52:03:32:GLU:HG3	2.12	0.49
52:03:41:SER:HA	52:03:177:LYS:HA	1.94	0.49
52:03:50:ILE:HG12	52:03:165:ASN:HD21	1.77	0.49
53:A:212:G:H2'	53:A:213:G:C8	2.46	0.49
53:A:1301:U:O2	53:A:1301:U:H2'	2.11	0.49
53:A:1342:C:H2'	53:A:1343:G:C8	2.46	0.49
54:01:171:U:H2'	54:01:172:A:C8	2.47	0.49
54:01:492:A:H2'	54:01:493:G:O4'	2.12	0.49
54:01:669:G:H2'	54:01:669:G:N3	2.27	0.49
54:01:1527:G:H21	54:01:1545:A:H62	1.60	0.49
54:01:2247:A:H2'	54:01:2248:C:C6	2.47	0.49
54:01:2514:U:H2'	54:01:2515:C:C6	2.47	0.49
54:01:2771:C:H2'	54:01:2772:C:C6	2.47	0.49
54:01:2788:C:H2'	54:01:2789:C:C6	2.47	0.49
4:07:104:THR:HG21	26:29:22:MET:HE1	1.93	0.49
32:B:53:LEU:HA	32:B:56:LEU:HB2	1.94	0.49
42:L:31:GLY:HA3	42:L:54:VAL:CG1	2.43	0.49
42:L:51:VAL:HG22	42:L:52:CYS:N	2.27	0.49
45:O:19:ASN:OD1	53:A:750:C:H5'	2.12	0.49
54:01:553:G:H2'	54:01:554:U:O4'	2.11	0.49
54:01:2804:U:H2'	54:01:2805:C:C6	2.47	0.49
55:02:65:U:H3'	55:02:108:A:N6	2.26	0.49
2:05:61:THR:OG1	2:05:64:GLU:HG3	2.13	0.49
9:12:89:PHE:O	9:12:93:ILE:HG12	2.12	0.49
34:D:75:TYR:HA	34:D:89:LEU:HD13	1.94	0.49
41:K:85:VAL:HG21	51:U:16:ARG:HH22	1.77	0.49
54:01:1370:C:H2'	54:01:1371:G:O4'	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1810:A:H2'	54:01:1811:G:O4'	2.12	0.49
54:01:2186:G:H2'	54:01:2187:U:O4'	2.12	0.49
54:01:2556:C:H2'	54:01:2557:G:O4'	2.11	0.49
54:01:2705:A:H2'	54:01:2706:A:O4'	2.12	0.49
55:02:53:A:H2'	55:02:53:A:N3	2.27	0.49
59:Z:84:HIS:HB3	59:Z:87:TYR:HD2	1.77	0.49
2:05:121:THR:HG21	2:05:143:PRO:HB3	1.93	0.49
13:16:43:GLU:OE2	13:16:46:ARG:HD3	2.13	0.49
17:20:24:LYS:HA	17:20:94:THR:OG1	2.12	0.49
50:T:20:ASN:HD21	50:T:65:LEU:HD11	1.78	0.49
53:A:476:U:H2'	53:A:477:C:C6	2.48	0.49
53:A:1254:A:H2'	53:A:1255:G:C8	2.47	0.49
53:A:1395:C:H6	53:A:1395:C:H5'	1.77	0.49
54:01:1463:C:H2'	54:01:1464:G:C8	2.48	0.49
54:01:2704:C:H2'	54:01:2705:A:O4'	2.13	0.49
59:Z:85:ALA:O	59:Z:88:VAL:HG23	2.12	0.49
3:06:189:THR:O	3:06:193:VAL:HG23	2.12	0.49
9:12:36:LEU:HD11	9:12:122:LEU:HD13	1.95	0.49
12:15:42:THR:OG1	12:15:45:GLN:HG3	2.13	0.49
23:26:19:HIS:HB3	54:01:2080:A:OP1	2.13	0.49
30:33:28:LEU:HD12	30:33:32:LEU:HD22	1.94	0.49
31:34:23:ILE:HD13	54:01:1032:A:H1'	1.93	0.49
32:B:46:VAL:HB	32:B:47:PRO:HD3	1.95	0.49
32:B:96:LEU:H	32:B:99:MET:CE	2.26	0.49
33:C:76:ILE:HA	33:C:83:VAL:HG23	1.94	0.49
41:K:83:VAL:C	41:K:84:MET:HE2	2.38	0.49
42:L:49:ARG:HH22	53:A:522:C:N4	2.11	0.49
49:S:38:THR:HG22	49:S:69:LYS:HG2	1.94	0.49
53:A:181:A:N6	53:A:194:C:H2'	2.27	0.49
54:01:581:C:H2'	54:01:582:A:H8	1.77	0.49
54:01:601:C:H2'	54:01:602:A:O4'	2.13	0.49
54:01:644:A:H2'	54:01:645:C:C4'	2.43	0.49
54:01:660:C:H2'	54:01:661:A:H8	1.77	0.49
54:01:905:A:O2'	54:01:906:U:H5'	2.12	0.49
54:01:915:C:H3'	54:01:916:G:H8	1.76	0.49
54:01:1780:A:O2'	54:01:1781:U:H2'	2.13	0.49
54:01:1857:G:H2'	54:01:1884:G:N2	2.27	0.49
54:01:1932:A:H2'	54:01:1933:G:O4'	2.12	0.49
54:01:2515:C:H2'	54:01:2516:A:H8	1.78	0.49
54:01:2637:U:H2'	54:01:2638:G:O4'	2.12	0.49
54:01:2760:C:O2'	54:01:2761:A:H5'	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:06:63:LYS:HD2	54:01:2444:G:OP2	2.13	0.49
4:07:7:TYR:O	4:07:12:VAL:HG23	2.12	0.49
24:27:9:LYS:HD3	24:27:10:SER:N	2.27	0.49
47:Q:60:ILE:CG2	47:Q:72:TRP:HB3	2.43	0.49
53:A:1202:U:H2'	53:A:1203:C:O4'	2.13	0.49
54:01:18:U:H2'	54:01:19:A:C8	2.48	0.49
54:01:873:C:H2'	54:01:874:G:C8	2.48	0.49
54:01:1474:U:H2'	54:01:1475:G:H5'	1.93	0.49
55:02:29:A:H2'	55:02:30:C:O4'	2.12	0.49
58:Y:64:A:H1'	59:Z:378:GLU:OE2	2.12	0.49
6:09:6:LEU:HD21	6:09:51:ARG:HH11	1.78	0.49
8:11:33:ASN:HB2	8:11:64:ARG:HH22	1.77	0.49
9:12:93:ILE:CD1	9:12:100:VAL:HG21	2.43	0.49
12:15:61:GLY:HA2	12:15:107:GLY:HA3	1.95	0.49
21:24:80:HIS:ND1	21:24:81:PRO:HD2	2.28	0.49
35:E:113:VAL:HG13	35:E:114:LEU:HD12	1.94	0.49
39:I:26:LYS:C	39:I:27:ILE:HD12	2.38	0.49
53:A:1342:C:H2'	53:A:1343:G:H8	1.77	0.49
54:01:687:C:H2'	54:01:688:U:O4'	2.13	0.49
54:01:879:G:H2'	54:01:880:G:C8	2.47	0.49
54:01:1078:U:H4'	54:01:1079:C:H5'	1.95	0.49
54:01:1082:U:H3	54:01:1086:A:H61	1.59	0.49
54:01:1683:U:H2'	54:01:1684:G:C8	2.48	0.49
54:01:2039:U:H2'	54:01:2040:G:C8	2.47	0.49
54:01:2507:C:H2'	54:01:2508:G:H8	1.78	0.49
59:Z:11:HIS:HA	59:Z:75:HIS:HB3	1.95	0.49
5:08:118:ALA:O	5:08:120:ILE:HG12	2.12	0.49
15:18:99:LEU:O	15:18:99:LEU:HD23	2.12	0.49
17:20:37:GLU:O	17:20:39:LEU:HD12	2.13	0.49
23:26:6:VAL:HG23	23:26:50:VAL:HG12	1.95	0.49
44:N:37:ASP:OD1	44:N:39:ASP:HB3	2.13	0.49
53:A:831:A:H2'	53:A:832:G:O4'	2.13	0.49
54:01:1077:A:C2'	54:01:1078:U:H5'	2.40	0.49
54:01:2364:C:H2'	54:01:2365:G:O4'	2.13	0.49
59:Z:366:ILE:HG13	59:Z:367:ALA:H	1.77	0.49
7:10:26:VAL:HB	7:10:82:ILE:HG23	1.94	0.49
14:17:106:LEU:O	14:17:106:LEU:HD23	2.12	0.49
39:I:46:VAL:HA	39:I:49:GLN:HG3	1.95	0.49
39:I:111:GLU:HB3	39:I:114:LYS:NZ	2.27	0.49
40:J:91:ASP:O	40:J:92:LEU:CB	2.60	0.49
41:K:125:LYS:HD2	53:A:797:C:OP1	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:7:ARG:NE	54:01:2128:G:H4'	2.28	0.49
52:03:23:ILE:HG23	52:03:189:LEU:HD23	1.95	0.49
53:A:350:G:H2'	53:A:351:G:C8	2.48	0.49
53:A:1308:U:H2'	53:A:1309:G:H8	1.77	0.49
54:01:1367:A:H2'	54:01:1368:G:H5'	1.94	0.49
54:01:2074:U:H2'	54:01:2075:U:C6	2.48	0.49
54:01:2158:A:H4'	54:01:2159:G:O4'	2.13	0.49
54:01:2898:U:H2'	54:01:2899:A:C8	2.48	0.49
59:Z:97:GLN:NE2	59:Z:229:GLY:HA2	2.27	0.49
59:Z:326:TYR:O	59:Z:341:ILE:HG12	2.13	0.49
2:05:61:THR:HG1	2:05:64:GLU:HG3	1.77	0.48
3:06:88:ARG:HB3	3:06:89:PRO:HD2	1.95	0.48
3:06:149:ILE:CG2	3:06:188:MET:HG2	2.43	0.48
16:19:74:SER:HB2	54:01:1011:G:OP1	2.13	0.48
21:24:30:ILE:HG13	21:24:40:ILE:HG13	1.95	0.48
35:E:119:VAL:HG12	35:E:121:ASN:H	1.78	0.48
42:L:63:THR:HG23	42:L:92:VAL:HA	1.95	0.48
46:P:12:LYS:HD2	53:A:393:A:OP2	2.13	0.48
46:P:70:ARG:HH11	53:A:452:A:H1'	1.77	0.48
52:03:161:VAL:HB	52:03:173:THR:OG1	2.13	0.48
53:A:149:A:H1'	53:A:1446:A:H2	1.78	0.48
53:A:524:G:H2'	53:A:525:C:C6	2.48	0.48
53:A:932:C:H2'	53:A:933:G:C8	2.48	0.48
54:01:1709:U:H2'	54:01:1710:G:C8	2.47	0.48
54:01:1869:G:H3'	54:01:1870:C:C5'	2.43	0.48
1:04:120:ASP:HB2	6:09:91:PHE:HZ	1.78	0.48
16:19:90:ASP:OD2	16:19:92:LYS:HB3	2.13	0.48
18:21:14:ALA:HB2	18:21:78:GLU:HB3	1.96	0.48
24:27:26:PHE:O	24:27:29:ARG:HD3	2.13	0.48
25:28:40:THR:OG1	25:28:41:PRO:HD2	2.13	0.48
31:34:1:MET:HE2	31:34:36:ARG:HD3	1.95	0.48
38:H:106:SER:HA	53:A:642:A:C8	2.48	0.48
40:J:22:THR:O	40:J:26:VAL:HG23	2.13	0.48
47:Q:17:GLU:OE2	53:A:255:G:H1'	2.13	0.48
54:01:296:U:H2'	54:01:297:G:H8	1.78	0.48
54:01:767:U:H2'	54:01:768:G:H8	1.78	0.48
54:01:2141:G:H2'	54:01:2142:A:H8	1.77	0.48
54:01:2195:U:H2'	54:01:2196:C:H6	1.79	0.48
1:04:149:LYS:HD3	54:01:2204:G:H4'	1.95	0.48
4:07:131:VAL:HG22	4:07:151:LEU:O	2.14	0.48
9:12:52:ASP:O	9:12:54:ILE:HG13	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:113:PRO:HD2	54:01:558:U:P	2.53	0.48
16:19:79:ILE:HG21	16:19:91:ARG:NH2	2.28	0.48
49:S:35:ARG:NH2	49:S:52:ASN:HA	2.28	0.48
53:A:757:U:H2'	53:A:758:C:O4'	2.13	0.48
53:A:1432:G:H1'	53:A:1468:A:N6	2.28	0.48
54:01:1947:C:H2'	54:01:1948:G:H8	1.78	0.48
5:08:37:ASN:HB3	5:08:40:VAL:HG23	1.94	0.48
5:08:140:ILE:HD12	5:08:141:GLY:N	2.28	0.48
29:32:24:THR:HG23	29:32:27:GLY:H	1.76	0.48
33:C:1:GLY:HA3	53:A:1060:U:H5	1.78	0.48
39:I:114:LYS:HE3	53:A:1187:G:H5'	1.94	0.48
41:K:87:GLY:H	41:K:113:THR:HG22	1.77	0.48
49:S:38:THR:HA	49:S:69:LYS:HA	1.95	0.48
53:A:195:A:H2'	53:A:196:A:C8	2.48	0.48
53:A:1097:C:H2'	53:A:1098:C:C6	2.48	0.48
8:11:126:ARG:HE	54:01:1081:U:P	2.37	0.48
9:12:41:LYS:HG2	9:12:43:GLU:CD	2.38	0.48
13:16:28:LEU:HD23	13:16:48:VAL:HG11	1.96	0.48
18:21:66:ILE:H	18:21:66:ILE:CD1	2.20	0.48
39:I:119:LYS:HE3	53:A:1350:A:OP2	2.13	0.48
54:01:253:C:H2'	54:01:254:G:O4'	2.14	0.48
54:01:441:U:O2'	54:01:442:G:H5'	2.12	0.48
54:01:2199:A:H2'	54:01:2200:C:O4'	2.12	0.48
2:05:186:LEU:HD21	15:18:3:ILE:HG21	1.96	0.48
4:07:65:LEU:HD22	55:02:42:C:C5	2.48	0.48
4:07:140:ILE:HD12	4:07:140:ILE:N	2.29	0.48
5:08:85:LYS:C	5:08:86:LEU:HD12	2.39	0.48
6:09:50:ARG:O	6:09:55:GLU:HG3	2.13	0.48
6:09:76:GLU:HA	6:09:142:VAL:HG13	1.95	0.48
13:16:90:ARG:HB2	13:16:90:ARG:NH1	2.28	0.48
24:27:9:LYS:HD3	24:27:11:VAL:N	2.27	0.48
29:32:3:ARG:HB3	54:01:1612:C:O2'	2.13	0.48
47:Q:29:LYS:HB2	47:Q:36:PHE:CE1	2.48	0.48
52:03:75:VAL:HG21	52:03:153:VAL:HG13	1.95	0.48
53:A:151:A:H2'	53:A:152:A:O4'	2.14	0.48
53:A:545:C:O2'	53:A:549:C:H5''	2.13	0.48
53:A:909:A:H2'	53:A:910:C:O4'	2.14	0.48
54:01:799:G:H3'	54:01:800:A:C8	2.49	0.48
54:01:1906:G:C3'	54:01:1907:G:H5''	2.44	0.48
54:01:2024:G:H2'	54:01:2025:C:O4'	2.14	0.48
2:05:121:THR:HB	2:05:127:PHE:CD2	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:27:ARG:HH21	54:01:1142:A:H4'	1.79	0.48
40:J:50:THR:HG23	40:J:64:GLN:HG2	1.95	0.48
42:L:30:ARG:HB3	53:A:363:A:OP2	2.14	0.48
45:O:22:GLY:HA3	53:A:750:C:O2	2.13	0.48
52:03:180:PHE:HD2	52:03:185:LEU:HD21	1.76	0.48
53:A:312:C:H2'	53:A:313:A:H8	1.77	0.48
53:A:691:G:H2'	53:A:692:U:C6	2.49	0.48
54:01:225:C:H2'	54:01:226:A:O4'	2.14	0.48
54:01:1825:U:H2'	54:01:1826:G:H8	1.79	0.48
54:01:2710:C:H2'	54:01:2711:A:C8	2.48	0.48
59:Z:181:ASP:O	59:Z:185:GLU:HB3	2.13	0.48
59:Z:243:GLU:CG	59:Z:295:PRO:HA	2.43	0.48
59:Z:327:ARG:NH2	59:Z:363:ILE:HG21	2.29	0.48
1:04:48:ILE:O	1:04:48:ILE:HG23	2.13	0.48
11:14:68:SER:HB2	54:01:632:A:H5''	1.95	0.48
12:15:76:LYS:HD3	12:15:77:PRO:HD2	1.96	0.48
14:17:26:LEU:HD13	14:17:39:VAL:HG22	1.95	0.48
15:18:31:VAL:HG22	15:18:32:VAL:N	2.29	0.48
32:B:96:LEU:N	32:B:99:MET:HE3	2.29	0.48
32:B:98:GLY:O	32:B:102:ASN:HB3	2.12	0.48
40:J:59:LYS:HE2	40:J:62:ARG:NH2	2.29	0.48
42:L:11:ARG:HD2	53:A:562:U:H1'	1.96	0.48
46:P:36:VAL:O	46:P:36:VAL:HG13	2.14	0.48
48:R:33:THR:HG22	48:R:37:LYS:H	1.79	0.48
52:03:105:LYS:O	52:03:109:MET:HE2	2.14	0.48
53:A:359:G:H2'	53:A:360:G:O4'	2.13	0.48
53:A:948:C:H2'	53:A:949:A:C8	2.49	0.48
53:A:1033:G:C3'	53:A:1034:G:H5''	2.40	0.48
54:01:1506:U:H2'	54:01:1507:C:C6	2.49	0.48
54:01:2047:C:H2'	54:01:2048:G:C8	2.48	0.48
54:01:2243:U:H2'	54:01:2244:U:C6	2.49	0.48
54:01:2264:C:H2'	54:01:2265:U:O4'	2.14	0.48
55:02:63:C:H2'	55:02:64:G:C8	2.49	0.48
59:Z:102:ILE:HG23	59:Z:131:ILE:O	2.13	0.48
59:Z:299:LYS:NZ	59:Z:301:HIS:HA	2.28	0.48
59:Z:326:TYR:HB3	59:Z:341:ILE:CG1	2.44	0.48
1:04:144:GLU:HA	1:04:151:GLY:HA2	1.95	0.48
3:06:48:THR:O	3:06:52:VAL:HG23	2.14	0.48
13:16:101:GLY:H	27:30:41:HIS:HD2	1.62	0.48
21:24:75:GLN:HB2	21:24:92:VAL:HG23	1.96	0.48
32:B:102:ASN:O	32:B:105:THR:HG22	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:D:124:VAL:HG23	34:D:141:VAL:O	2.14	0.48
36:F:92:THR:C	36:F:94:HIS:H	2.21	0.48
42:L:113:ARG:HH22	42:L:120:ARG:HA	1.78	0.48
53:A:492:C:H2'	53:A:493:A:C8	2.48	0.48
53:A:1368:A:O2'	53:A:1369:C:H5'	2.13	0.48
54:01:158:U:H2'	54:01:159:G:O4'	2.13	0.48
54:01:181:A:H2'	54:01:182:A:C8	2.49	0.48
54:01:2848:G:O2'	54:01:2849:U:H5'	2.13	0.48
59:Z:19:HIS:HB3	59:Z:22:HIS:CE1	2.49	0.48
59:Z:173:SER:HB3	59:Z:184:TRP:CD2	2.49	0.48
3:06:47:LYS:O	3:06:83:VAL:HB	2.14	0.48
8:11:94:LYS:HZ2	54:01:1076:C:H4'	1.79	0.48
9:12:35:ARG:HA	9:12:40:HIS:HD2	1.78	0.48
13:16:118:ARG:NH1	27:30:55:ALA:HB3	2.28	0.48
15:18:52:ARG:H	15:18:56:SER:HB3	1.79	0.48
22:25:40:LYS:HE3	54:01:2330:G:O2'	2.13	0.48
36:F:71:ILE:HD11	36:F:89:VAL:HG21	1.95	0.48
51:U:11:PHE:C	51:U:13:VAL:H	2.21	0.48
52:03:29:LEU:HD23	52:03:222:VAL:HG13	1.96	0.48
54:01:226:A:H2'	54:01:227:A:O4'	2.13	0.48
54:01:323:C:H2'	54:01:1205:A:N1	2.29	0.48
54:01:1900:A:H1'	54:01:1970:A:H2'	1.94	0.48
54:01:2281:A:O2'	54:01:2282:G:H5'	2.14	0.48
59:Z:55:GLU:HA	59:Z:60:ILE:HG13	1.96	0.48
10:13:7:MET:C	10:13:8:LEU:HD12	2.38	0.47
13:16:96:ARG:NH1	13:16:116:VAL:HG13	2.29	0.47
18:21:24:ILE:HD11	18:21:74:ILE:HD13	1.94	0.47
20:23:32:LYS:HB3	20:23:63:ALA:HB1	1.96	0.47
31:34:25:VAL:HG21	31:34:35:GLN:HE21	1.79	0.47
35:E:54:GLU:HB3	35:E:57:ALA:HB3	1.96	0.47
36:F:93:LYS:O	36:F:94:HIS:HB2	2.14	0.47
41:K:92:ARG:HE	51:U:24:LYS:NZ	2.12	0.47
42:L:114:SER:CB	53:A:35:G:H21	2.27	0.47
52:03:24:ASN:OD1	52:03:27:ILE:HD11	2.14	0.47
53:A:78:A:H2'	53:A:79:G:O4'	2.13	0.47
53:A:202:G:H21	53:A:466:A:H61	1.62	0.47
53:A:494:G:H2'	53:A:496:A:H8	1.79	0.47
53:A:539:A:H2'	53:A:540:G:C8	2.48	0.47
53:A:831:A:C3'	53:A:832:G:H5''	2.43	0.47
54:01:286:U:H2'	54:01:287:G:H8	1.76	0.47
54:01:1020:A:H1'	54:01:1021:A:OP2	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2507:C:H2'	54:01:2508:G:C8	2.49	0.47
59:Z:217:VAL:HB	59:Z:283:ARG:NH1	2.29	0.47
59:Z:297:THR:HG23	59:Z:298:ILE:CD1	2.41	0.47
5:08:41:GLU:HA	5:08:54:ARG:HH21	1.79	0.47
18:21:29:VAL:HG23	18:21:69:LEU:O	2.14	0.47
24:27:7:ARG:HD3	24:27:7:ARG:H	1.79	0.47
32:B:53:LEU:HD22	32:B:219:THR:HG21	1.97	0.47
46:P:46:LYS:HE2	46:P:48:GLU:O	2.14	0.47
51:U:35:GLU:O	51:U:36:PHE:HB2	2.14	0.47
53:A:770:C:H2'	53:A:771:G:C8	2.49	0.47
54:01:1681:G:N3	54:01:1762:A:H2'	2.29	0.47
54:01:1893:C:H2'	54:01:1894:C:H5'	1.96	0.47
56:X:4:G:H2'	56:X:5:G:C8	2.49	0.47
56:X:71:C:H2'	56:X:72:A:C8	2.48	0.47
3:06:77:ILE:HG13	3:06:78:TRP:HD1	1.78	0.47
19:22:40:LYS:HA	19:22:43:ILE:HD12	1.95	0.47
20:23:93:ARG:CB	20:23:102:ILE:HD12	2.45	0.47
34:D:62:ARG:HG3	34:D:62:ARG:HH11	1.79	0.47
34:D:131:ILE:HD12	34:D:131:ILE:N	2.29	0.47
34:D:186:GLU:HB3	34:D:189:ASP:OD2	2.14	0.47
38:H:105:THR:HB	38:H:120:LEU:HD11	1.96	0.47
45:O:71:ARG:HG2	45:O:71:ARG:HH11	1.79	0.47
53:A:81:A:H2	53:A:88:U:H3	1.63	0.47
53:A:271:C:H2'	53:A:272:C:C6	2.49	0.47
53:A:621:A:H2'	53:A:622:A:C8	2.50	0.47
54:01:45:G:H5''	54:01:46:G:C5'	2.23	0.47
54:01:392:U:H2'	54:01:393:C:C6	2.48	0.47
54:01:1053:C:C3'	54:01:1054:A:H5''	2.44	0.47
54:01:2151:U:H2'	54:01:2152:G:C8	2.50	0.47
58:Y:25:C:H2'	58:Y:26:A:O4'	2.14	0.47
59:Z:5:PHE:HD1	59:Z:263:LYS:HD2	1.78	0.47
59:Z:34:VAL:HG21	59:Z:188:ILE:HB	1.96	0.47
2:05:12:THR:HG21	15:18:4:ILE:HG23	1.97	0.47
2:05:159:LYS:HE2	54:01:2512:C:O2'	2.13	0.47
5:08:138:GLN:HE22	54:01:2746:U:H1'	1.80	0.47
7:10:112:ALA:HB1	7:10:123:ILE:HD12	1.95	0.47
12:15:71:LYS:HE3	12:15:73:ILE:HD11	1.96	0.47
37:G:71:THR:O	37:G:90:VAL:HG12	2.15	0.47
38:H:11:THR:HA	38:H:14:ARG:HH12	1.79	0.47
45:O:31:LEU:O	45:O:35:ILE:HG13	2.14	0.47
52:03:218:MET:HG2	54:01:2174:C:O2	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:106:C:H2'	53:A:107:G:C8	2.49	0.47
53:A:838:G:H2'	53:A:839:C:O4'	2.14	0.47
54:01:215:G:C4'	54:01:216:A:H4'	2.43	0.47
54:01:2411:A:H2'	54:01:2412:A:C8	2.49	0.47
54:01:2557:G:H2'	54:01:2558:C:C6	2.49	0.47
3:06:23:PHE:HB2	3:06:114:ARG:HH22	1.80	0.47
3:06:79:ARG:NH2	54:01:471:A:H5''	2.29	0.47
7:10:3:LEU:HB3	54:01:1044:C:OP2	2.14	0.47
8:11:56:VAL:HG21	8:11:68:PHE:HB2	1.96	0.47
33:C:67:ILE:CD1	33:C:100:ILE:HD11	2.45	0.47
36:F:32:ALA:HB1	36:F:70:VAL:HG21	1.95	0.47
36:F:64:VAL:CG2	36:F:65:GLU:N	2.78	0.47
39:I:104:THR:HG22	39:I:106:ASP:H	1.79	0.47
52:03:70:GLY:HA3	52:03:177:LYS:HG2	1.96	0.47
54:01:394:C:H2'	54:01:395:U:O4'	2.14	0.47
54:01:1859:U:H2'	54:01:1860:G:H8	1.79	0.47
54:01:2472:G:H2'	54:01:2475:C:H42	1.80	0.47
54:01:2743:U:C3'	54:01:2744:G:H5''	2.45	0.47
5:08:163:TYR:HB2	5:08:166:GLU:HB2	1.95	0.47
7:10:25:ALA:HB3	7:10:99:PHE:CD2	2.50	0.47
8:11:72:THR:HG23	8:11:73:PRO:HD2	1.96	0.47
9:12:41:LYS:HG2	9:12:43:GLU:OE1	2.14	0.47
39:I:83:THR:HG21	39:I:102:PHE:HB3	1.96	0.47
40:J:36:VAL:HG22	40:J:38:GLY:H	1.78	0.47
40:J:52:LEU:HB2	44:N:80:ARG:HD2	1.96	0.47
42:L:47:ALA:C	42:L:48:LEU:HD12	2.39	0.47
49:S:35:ARG:HD2	53:A:1221:G:OP1	2.15	0.47
53:A:950:U:H2'	53:A:951:G:C8	2.50	0.47
53:A:1500:A:H5''	53:A:1508:A:H5''	1.96	0.47
54:01:2105:U:H2'	54:01:2106:U:O4'	2.14	0.47
54:01:2533:U:H2'	54:01:2534:A:O4'	2.14	0.47
55:02:1:U:H2'	55:02:2:G:C8	2.50	0.47
2:05:33:ARG:HD2	2:05:33:ARG:N	2.23	0.47
2:05:108:ASP:OD2	2:05:206:ALA:HA	2.13	0.47
4:07:29:ARG:CZ	4:07:158:THR:HG21	2.44	0.47
4:07:70:ARG:NH2	4:07:71:LYS:HG2	2.30	0.47
4:07:174:PHE:HA	4:07:175:PRO:HD2	1.70	0.47
5:08:29:ASN:HD22	5:08:78:VAL:C	2.23	0.47
5:08:86:LEU:HG	5:08:163:TYR:HA	1.97	0.47
6:09:47:PHE:HD1	6:09:51:ARG:HD2	1.80	0.47
20:23:95:PHE:O	20:23:99:SER:HA	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:24:21:ARG:HA	21:24:25:LYS:O	2.14	0.47
27:30:3:GLN:HA	54:01:2615:U:C2	2.49	0.47
32:B:91:VAL:HG11	32:B:95:TRP:HD1	1.80	0.47
32:B:137:THR:O	32:B:141:GLU:HG3	2.14	0.47
33:C:13:ILE:N	33:C:13:ILE:HD12	2.30	0.47
34:D:96:ARG:HG2	34:D:96:ARG:HH11	1.78	0.47
36:F:3:HIS:H	36:F:92:THR:CG2	2.14	0.47
39:I:29:ILE:HG12	39:I:30:ASN:OD1	2.15	0.47
42:L:113:ARG:HH22	42:L:120:ARG:HG3	1.79	0.47
43:M:13:HIS:NE2	53:A:1296:C:H5'	2.28	0.47
45:O:87:ARG:HG3	45:O:88:ARG:H	1.80	0.47
50:T:28:ARG:HH12	53:A:1437:A:H5''	1.80	0.47
52:03:131:LEU:HA	52:03:134:ARG:HB2	1.97	0.47
53:A:189:A:H2'	53:A:190:A:O4'	2.14	0.47
53:A:371:A:H2'	53:A:372:C:O4'	2.14	0.47
54:01:20:C:H2'	54:01:21:A:C8	2.50	0.47
54:01:65:U:H2'	54:01:66:C:C6	2.49	0.47
54:01:437:U:H2'	54:01:438:G:C8	2.50	0.47
54:01:729:G:H4'	54:01:763:G:C5'	2.44	0.47
54:01:755:U:H2'	54:01:756:A:C8	2.49	0.47
54:01:1657:U:H2'	54:01:1658:C:C6	2.50	0.47
54:01:1748:C:H2'	54:01:1749:A:C8	2.50	0.47
54:01:2137:U:H2'	54:01:2138:G:H8	1.78	0.47
54:01:2291:U:H2'	54:01:2292:U:C6	2.49	0.47
54:01:2853:C:H2'	54:01:2854:G:C8	2.49	0.47
59:Z:148:LEU:O	59:Z:152:GLU:HG3	2.15	0.47
59:Z:231:VAL:CG1	59:Z:270:ALA:HA	2.45	0.47
59:Z:243:GLU:CD	59:Z:295:PRO:HA	2.39	0.47
59:Z:261:PHE:O	59:Z:262:ARG:HB2	2.15	0.47
1:04:59:GLN:HA	54:01:1568:G:H5'	1.97	0.47
2:05:110:THR:HG23	2:05:171:THR:OG1	2.15	0.47
3:06:44:ARG:HD2	54:01:444:C:OP2	2.15	0.47
8:11:119:ALA:HB2	54:01:1082:U:C5'	2.43	0.47
24:27:2:LYS:HE2	54:01:102:U:H1'	1.96	0.47
30:33:11:LYS:HB2	30:33:11:LYS:NZ	2.30	0.47
34:D:169:TRP:CG	34:D:185:PRO:HG3	2.50	0.47
35:E:14:LEU:HA	35:E:36:THR:HG22	1.96	0.47
35:E:22:LYS:HB3	35:E:29:ILE:CG2	2.44	0.47
35:E:56:PRO:O	35:E:59:ILE:HG13	2.15	0.47
37:G:65:LEU:HD23	37:G:69:ARG:HH21	1.80	0.47
44:N:41:TRP:HA	44:N:44:VAL:HG22	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:93:GLU:C	52:03:94:LEU:HD12	2.39	0.47
54:01:1468:U:H2'	54:01:1522:A:H61	1.78	0.47
54:01:1856:U:H2'	54:01:1857:G:O4'	2.14	0.47
54:01:2065:C:H2'	54:01:2066:C:C6	2.50	0.47
7:10:3:LEU:HD12	7:10:5:LEU:HG	1.96	0.47
9:12:117:ALA:HA	9:12:120:ARG:NH2	2.29	0.47
13:16:103:ARG:NH1	54:01:1287:A:H5'	2.29	0.47
21:24:4:ILE:HB	21:24:63:ILE:HG12	1.97	0.47
22:25:12:SER:HB3	54:01:2262:U:C5	2.45	0.47
36:F:93:LYS:O	36:F:94:HIS:CB	2.63	0.47
49:S:46:LEU:O	49:S:61:VAL:HG23	2.15	0.47
53:A:575:G:O2'	53:A:821:G:H5'	2.14	0.47
53:A:1354:U:H2'	53:A:1355:G:H8	1.80	0.47
54:01:337:C:H2'	54:01:338:G:O4'	2.15	0.47
54:01:1065:U:H5'	54:01:1066:U:OP2	2.14	0.47
54:01:2785:C:H2'	54:01:2786:U:C6	2.49	0.47
55:02:10:G:H2'	55:02:11:C:O4'	2.14	0.47
56:X:31:G:H2'	56:X:32:C:H5'	1.97	0.47
59:Z:11:HIS:HB3	59:Z:204:ARG:HH12	1.78	0.47
59:Z:189:LEU:O	59:Z:189:LEU:HD23	2.15	0.47
2:05:14:ILE:HG23	15:18:11:GLN:NE2	2.28	0.47
7:10:27:VAL:O	7:10:82:ILE:HA	2.15	0.47
8:11:78:LEU:HD21	8:11:108:ILE:HD13	1.97	0.47
8:11:130:GLY:HA2	8:11:133:ARG:HH12	1.80	0.47
10:13:41:ILE:C	10:13:41:ILE:HD12	2.40	0.47
21:24:47:VAL:O	21:24:51:GLN:HG2	2.15	0.47
25:28:14:GLY:C	25:28:15:ARG:HD2	2.39	0.47
26:29:56:ARG:HH12	49:S:68:HIS:CE1	2.33	0.47
32:B:33:ALA:HB3	32:B:37:VAL:HG13	1.97	0.47
44:N:47:LEU:HD21	53:A:1317:C:H4'	1.96	0.47
47:Q:46:HIS:CB	47:Q:70:LYS:HD3	2.36	0.47
54:01:12:U:O2	54:01:2626:C:H4'	2.15	0.47
54:01:760:G:H2'	54:01:761:A:O4'	2.14	0.47
54:01:1040:A:H2'	54:01:1041:G:H8	1.79	0.47
54:01:1139:G:O2'	54:01:1140:C:H5'	2.15	0.47
54:01:1857:G:H1'	54:01:1885:A:N6	2.29	0.47
59:Z:33:THR:HG21	59:Z:178:LEU:HA	1.97	0.47
2:05:56:LYS:HB2	2:05:56:LYS:NZ	2.31	0.46
2:05:149:ASN:CG	2:05:150:GLN:H	2.23	0.46
7:10:54:VAL:HG22	7:10:83:ALA:HB1	1.96	0.46
19:22:21:SER:O	19:22:25:GLU:HG2	2.14	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:26:16:ASN:HB2	23:26:26:ARG:HB3	1.96	0.46
39:I:12:LYS:HG3	39:I:109:GLN:OE1	2.15	0.46
52:03:27:ILE:HG21	52:03:186:LYS:CB	2.43	0.46
53:A:123:U:H5''	53:A:311:C:O2'	2.15	0.46
53:A:477:C:H2'	53:A:478:A:C8	2.49	0.46
53:A:1462:C:H2'	53:A:1463:U:C6	2.50	0.46
53:A:1513:A:H2'	53:A:1514:G:H8	1.80	0.46
54:01:1103:A:H2'	54:01:1103:A:N3	2.30	0.46
54:01:1169:A:H2'	54:01:1170:C:O4'	2.16	0.46
54:01:1752:C:H5''	54:01:2862:G:H5'	1.96	0.46
54:01:2487:G:H2'	54:01:2488:G:H8	1.79	0.46
2:05:125:TRP:CG	2:05:160:LYS:HB3	2.50	0.46
5:08:139:VAL:O	5:08:143:VAL:HG23	2.15	0.46
7:10:92:ALA:HB1	7:10:129:LEU:HB3	1.96	0.46
8:11:101:SER:HB3	8:11:104:GLN:OE1	2.14	0.46
28:31:47:ILE:HD12	28:31:47:ILE:H	1.80	0.46
32:B:208:ALA:HB1	32:B:212:TYR:CE2	2.51	0.46
50:T:23:ARG:HH11	50:T:23:ARG:HG3	1.81	0.46
54:01:306:U:H2'	54:01:307:G:O4'	2.15	0.46
54:01:1468:U:H2'	54:01:1522:A:N6	2.31	0.46
54:01:2006:C:H5'	54:01:2049:G:OP1	2.15	0.46
54:01:2478:A:C2	54:01:2529:G:H2'	2.50	0.46
1:04:17:LYS:HD2	54:01:1565:C:H5''	1.98	0.46
4:07:99:PHE:O	4:07:103:ILE:HG12	2.15	0.46
7:10:33:VAL:HA	54:01:1055:G:H4'	1.97	0.46
26:29:66:ILE:O	26:29:66:ILE:HG12	2.15	0.46
28:31:5:ARG:NH1	28:31:25:ASN:HB2	2.31	0.46
36:F:64:VAL:CG2	36:F:65:GLU:H	2.28	0.46
44:N:15:LEU:CD2	44:N:54:SER:HB3	2.46	0.46
53:A:1273:C:H2'	53:A:1274:A:O4'	2.15	0.46
54:01:542:C:C2'	54:01:543:G:H5''	2.43	0.46
54:01:991:C:H5'	54:01:1185:G:H2'	1.97	0.46
59:Z:173:SER:HB3	59:Z:184:TRP:CG	2.51	0.46
2:05:48:ILE:HG23	2:05:84:LEU:HD21	1.97	0.46
7:10:29:ASP:N	7:10:81:LEU:HD22	2.30	0.46
10:13:105:ARG:HG2	10:13:122:VAL:HG13	1.98	0.46
12:15:75:GLU:HB3	12:15:90:GLU:HG3	1.98	0.46
13:16:79:LEU:HD23	13:16:83:LEU:HD12	1.98	0.46
19:22:50:LEU:HD23	24:27:26:PHE:CE2	2.51	0.46
25:28:40:THR:HG23	25:28:43:ILE:H	1.81	0.46
28:31:12:SER:HA	28:31:48:TYR:CD1	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B:9:LEU:HD11	32:B:13:VAL:HG13	1.98	0.46
33:C:5:HIS:CG	44:N:88:MET:HB3	2.50	0.46
35:E:87:VAL:HA	35:E:91:SER:O	2.15	0.46
39:I:21:LYS:O	39:I:60:LEU:HB3	2.15	0.46
53:A:458:U:H2'	53:A:459:A:C8	2.51	0.46
53:A:490:C:H2'	53:A:491:G:C8	2.51	0.46
53:A:1456:A:H2'	53:A:1457:G:O4'	2.15	0.46
54:01:300:A:H2'	54:01:334:C:H1'	1.97	0.46
54:01:853:C:H2'	54:01:854:C:C6	2.50	0.46
54:01:2841:C:H2'	54:01:2842:G:C8	2.51	0.46
1:04:146:LYS:HB2	1:04:149:LYS:HB2	1.97	0.46
7:10:23:LEU:HD13	7:10:118:ILE:HB	1.98	0.46
8:11:25:PRO:O	8:11:29:GLN:HB2	2.16	0.46
15:18:91:VAL:HG21	15:18:96:LEU:HD21	1.97	0.46
32:B:95:TRP:CZ2	32:B:171:ALA:HA	2.50	0.46
33:C:19:SER:HB2	44:N:91:GLU:O	2.14	0.46
34:D:103:ARG:HB3	34:D:170:LEU:HD21	1.98	0.46
37:G:42:VAL:O	37:G:46:LEU:HD13	2.16	0.46
43:M:3:ILE:H	43:M:7:ASN:HB3	1.80	0.46
54:01:745:G:O2'	54:01:748:G:H1'	2.16	0.46
54:01:1127:A:H2'	54:01:1128:G:H5''	1.97	0.46
54:01:1386:C:H2'	54:01:1387:A:H8	1.80	0.46
54:01:1869:G:H3'	54:01:1870:C:H5''	1.98	0.46
54:01:2102:G:H2'	54:01:2103:C:O4'	2.16	0.46
54:01:2121:G:H2'	54:01:2122:U:O4'	2.16	0.46
54:01:2504:U:C2'	54:01:2505:G:H5'	2.46	0.46
54:01:2508:G:H1	54:01:2580:U:H3	1.64	0.46
56:W:73:A:H5''	56:W:74:C:O4'	2.15	0.46
1:04:131:MET:HA	1:04:134:ILE:HD12	1.98	0.46
8:11:72:THR:HG21	8:11:112:LYS:HG2	1.98	0.46
9:12:99:ARG:O	9:12:103:ILE:HG13	2.15	0.46
13:16:22:ARG:HG3	13:16:70:THR:HA	1.97	0.46
20:23:91:LYS:NZ	54:01:82:U:H5'	2.31	0.46
23:26:55:MET:SD	54:01:2091:C:H4'	2.56	0.46
33:C:143:LEU:HD23	33:C:143:LEU:O	2.15	0.46
44:N:8:ARG:HB3	44:N:12:ARG:HH12	1.81	0.46
48:R:25:ILE:HG21	48:R:66:LEU:HB3	1.98	0.46
51:U:40:PRO:HA	51:U:43:GLU:HG2	1.98	0.46
53:A:1489:G:H2'	53:A:1490:U:C6	2.50	0.46
54:01:162:U:O2'	54:01:163:C:H5'	2.14	0.46
54:01:898:C:H2'	54:01:899:A:O4'	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:11:HIS:HB2	59:Z:269:ARG:HH12	1.81	0.46
1:04:48:ILE:HD11	1:04:51:ARG:HA	1.97	0.46
4:07:30:VAL:HG22	4:07:95:MET:HE1	1.97	0.46
9:12:36:LEU:HG	9:12:54:ILE:HD12	1.97	0.46
12:15:45:GLN:HE21	54:01:2485:G:C5'	2.21	0.46
16:19:27:ARG:HB3	16:19:27:ARG:HH11	1.80	0.46
18:21:9:HIS:HE1	18:21:80:PRO:HG2	1.80	0.46
32:B:113:LEU:HD13	32:B:143:LEU:HG	1.98	0.46
34:D:10:LEU:HD22	34:D:62:ARG:CZ	2.46	0.46
35:E:156:ARG:NE	35:E:163:ILE:HG21	2.30	0.46
37:G:110:ARG:HH12	37:G:121:ASN:CB	2.28	0.46
39:I:61:ASP:C	39:I:62:LEU:HD12	2.41	0.46
52:03:50:ILE:CD1	52:03:165:ASN:HD21	2.29	0.46
53:A:381:C:H2'	53:A:382:A:O4'	2.15	0.46
53:A:513:C:H2'	53:A:514:C:C6	2.50	0.46
53:A:1119:C:H2'	53:A:1120:C:C6	2.50	0.46
54:01:198:C:O2'	54:01:199:A:H5'	2.16	0.46
54:01:576:U:H2'	54:01:577:G:H8	1.79	0.46
54:01:656:G:O2'	54:01:657:U:H5'	2.16	0.46
54:01:1105:U:C3'	54:01:1106:G:H5''	2.45	0.46
54:01:2123:G:H2'	54:01:2124:G:H8	1.81	0.46
3:06:76:PRO:HA	3:06:82:GLY:HA2	1.97	0.46
7:10:42:ARG:O	7:10:46:ARG:HG3	2.16	0.46
16:19:2:ARG:HD2	54:01:1248:G:C2	2.50	0.46
33:C:106:ARG:H	33:C:106:ARG:CD	2.23	0.46
34:D:197:HIS:HE1	35:E:104:ILE:H	1.64	0.46
38:H:9:MET:O	38:H:13:ILE:HG13	2.14	0.46
41:K:124:LYS:NZ	53:A:780:A:H5''	2.31	0.46
42:L:73:LEU:N	42:L:73:LEU:HD12	2.31	0.46
52:03:48:LEU:HD22	52:03:208:TYR:CE1	2.50	0.46
53:A:234:C:H2'	53:A:235:C:C6	2.50	0.46
53:A:434:U:H2'	53:A:435:A:H8	1.80	0.46
53:A:664:G:H22	53:A:741:G:H1	1.64	0.46
54:01:815:C:H2'	54:01:816:C:C6	2.50	0.46
54:01:1133:A:H4'	54:01:1134:A:H5''	1.98	0.46
54:01:1179:G:C5	54:01:1180:U:H1'	2.51	0.46
54:01:1430:G:H2'	54:01:1431:A:O4'	2.16	0.46
54:01:1443:U:H2'	54:01:1444:G:C8	2.50	0.46
54:01:1790:C:H2'	54:01:1791:A:N7	2.30	0.46
56:W:6:G:O2'	56:W:7:G:H5'	2.16	0.46
1:04:221:GLY:H	54:01:1826:G:P	2.39	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:22:44:LYS:O	19:22:48:GLN:HG2	2.15	0.46
20:23:90:LYS:NZ	54:01:100:U:H2'	2.31	0.46
21:24:9:ARG:HD3	21:24:39:ALA:HB1	1.97	0.46
31:34:19:ARG:HD2	31:34:24:ARG:HD2	1.98	0.46
39:I:70:GLY:O	39:I:74:GLN:HG3	2.16	0.46
40:J:34:ALA:O	40:J:35:GLN:HB3	2.16	0.46
50:T:70:LYS:HA	50:T:73:ARG:NH1	2.31	0.46
52:03:133:PRO:O	54:01:2169:A:H4'	2.15	0.46
53:A:56:U:H2'	53:A:57:G:C8	2.50	0.46
53:A:373:A:H61	53:A:391:G:H1'	1.81	0.46
53:A:1499:A:H2'	53:A:1500:A:H8	1.80	0.46
54:01:29:U:H2'	54:01:30:G:C8	2.50	0.46
54:01:2818:U:H2'	54:01:2819:G:H8	1.80	0.46
59:Z:212:LEU:HA	59:Z:213:PRO:HD3	1.74	0.46
59:Z:377:ARG:HD2	59:Z:378:GLU:N	2.31	0.46
3:06:149:ILE:HG21	3:06:188:MET:HG2	1.98	0.46
6:09:116:ARG:CG	6:09:133:GLN:HG3	2.40	0.46
12:15:41:LEU:HA	12:15:45:GLN:OE1	2.16	0.46
33:C:10:ARG:HA	33:C:13:ILE:HD13	1.98	0.46
53:A:861:G:H2'	53:A:862:C:C6	2.51	0.46
53:A:1460:C:H2'	53:A:1461:G:C8	2.50	0.46
54:01:118:A:N3	54:01:178:G:H1'	2.30	0.46
54:01:197:A:H2'	54:01:198:C:O4'	2.16	0.46
54:01:1127:A:C2'	54:01:1128:G:H5''	2.46	0.46
54:01:2066:C:O2'	54:01:2067:G:H5'	2.16	0.46
54:01:2259:U:H2'	54:01:2260:C:C6	2.51	0.46
59:Z:97:GLN:HB3	59:Z:273:ASN:ND2	2.31	0.46
59:Z:303:LYS:HE3	59:Z:342:GLU:OE1	2.16	0.46
3:06:77:ILE:HG13	3:06:78:TRP:CD1	2.52	0.45
5:08:154:GLU:HB3	5:08:159:LYS:H	1.80	0.45
5:08:174:LYS:HG3	54:01:2529:G:H4'	1.98	0.45
9:12:84:ILE:HG23	9:12:84:ILE:O	2.16	0.45
16:19:86:SER:HB3	17:20:50:GLY:O	2.16	0.45
18:21:57:ASN:HD21	54:01:495:G:H1'	1.81	0.45
28:31:36:LYS:HG3	28:31:47:ILE:HG13	1.99	0.45
32:B:42:LEU:O	32:B:46:VAL:HG23	2.17	0.45
34:D:82:LYS:HE2	53:A:2:A:H4'	1.98	0.45
35:E:84:VAL:CG2	35:E:145:ASN:HD22	2.28	0.45
35:E:161:GLU:HA	35:E:164:LEU:HD11	1.98	0.45
44:N:63:CYS:HB3	44:N:67:GLY:H	1.80	0.45
45:O:25:GLU:H	45:O:25:GLU:CD	2.24	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:O:61:GLN:O	45:O:65:LEU:HG	2.16	0.45
53:A:1071:C:H2'	53:A:1072:G:H8	1.81	0.45
53:A:1130:A:H2'	53:A:1131:G:O4'	2.16	0.45
53:A:1219:A:H2'	53:A:1220:G:H8	1.80	0.45
53:A:1271:A:H5'	53:A:1314:C:H5''	1.98	0.45
54:01:693:A:H2'	54:01:694:U:O4'	2.17	0.45
54:01:1386:C:H2'	54:01:1387:A:C8	2.51	0.45
54:01:1434:A:H2'	54:01:1435:G:H8	1.81	0.45
54:01:1482:G:H1'	54:01:1509:A:C2	2.51	0.45
54:01:2853:C:H2'	54:01:2854:G:H8	1.80	0.45
59:Z:304:PHE:CE2	59:Z:388:VAL:HG22	2.51	0.45
2:05:114:LYS:HG2	2:05:196:ALA:HB2	1.98	0.45
18:21:31:GLN:O	18:21:35:ILE:HG13	2.15	0.45
20:23:73:ASN:O	20:23:74:ALA:HB3	2.16	0.45
42:L:47:ALA:HB3	42:L:49:ARG:HE	1.80	0.45
47:Q:58:VAL:HG22	47:Q:59:GLU:N	2.30	0.45
53:A:90:C:H2'	53:A:91:U:C5	2.50	0.45
54:01:20:C:H2'	54:01:21:A:H8	1.81	0.45
54:01:616:A:H2'	54:01:617:G:O4'	2.16	0.45
54:01:861:A:H2'	54:01:862:G:O4'	2.15	0.45
54:01:1111:A:H2'	54:01:1111:A:N3	2.31	0.45
54:01:1773:A:C2'	54:01:1774:C:H5'	2.46	0.45
54:01:2475:C:C2'	54:01:2476:A:H5'	2.46	0.45
54:01:2579:C:O2'	54:01:2580:U:H5'	2.16	0.45
54:01:2584:U:H2'	54:01:2585:U:H2'	1.98	0.45
1:04:51:ARG:HB2	1:04:52:HIS:ND1	2.31	0.45
6:09:67:ALA:HA	6:09:138:VAL:HG11	1.98	0.45
7:10:11:ILE:O	7:10:15:VAL:HG23	2.16	0.45
27:30:39:ARG:HD3	54:01:2886:A:N1	2.31	0.45
33:C:36:PHE:CE2	44:N:65:GLN:HG2	2.51	0.45
35:E:40:ASP:OD1	35:E:44:ARG:HB2	2.16	0.45
38:H:80:PRO:HG2	53:A:878:A:H5''	1.98	0.45
53:A:70:U:H4'	53:A:71:A:H8	1.80	0.45
53:A:552:U:H2'	53:A:553:A:C8	2.50	0.45
53:A:1235:U:O2'	53:A:1305:G:H5'	2.15	0.45
53:A:1434:A:H2'	53:A:1435:G:O4'	2.15	0.45
54:01:718:A:H2'	54:01:719:C:O4'	2.16	0.45
54:01:2193:G:H2'	54:01:2194:U:C6	2.52	0.45
54:01:2469:A:H2'	54:01:2470:G:O4'	2.17	0.45
58:Y:56:C:H2'	58:Y:57:G:C8	2.51	0.45
7:10:67:THR:HG23	7:10:74:ASP:HB2	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:22:62:VAL:HG22	19:22:81:LYS:HE2	1.98	0.45
35:E:156:ARG:HG2	38:H:42:GLU:O	2.17	0.45
37:G:12:LEU:HD12	37:G:13:PRO:HD2	1.98	0.45
38:H:49:LYS:NZ	38:H:49:LYS:HB2	2.31	0.45
38:H:63:LYS:NZ	38:H:63:LYS:HB3	2.32	0.45
42:L:51:VAL:HG22	42:L:52:CYS:H	1.82	0.45
52:03:181:ASP:HB2	52:03:184:LYS:HG2	1.98	0.45
53:A:224:U:H2'	53:A:225:C:C6	2.52	0.45
53:A:250:A:H4'	53:A:251:G:O5'	2.17	0.45
53:A:629:A:H2'	53:A:630:A:O4'	2.17	0.45
53:A:1397:C:H2'	57:V:22:A:N6	2.31	0.45
54:01:189:G:H2'	54:01:205:G:N2	2.31	0.45
54:01:828:U:H2'	54:01:829:A:C8	2.52	0.45
54:01:1326:U:H2'	54:01:1327:A:C8	2.45	0.45
54:01:1937:A:O2'	54:01:1938:A:H3'	2.16	0.45
54:01:2480:C:H2'	54:01:2481:G:O4'	2.16	0.45
54:01:2538:C:H2'	54:01:2539:C:C6	2.51	0.45
59:Z:154:ARG:HG2	59:Z:164:GLY:O	2.17	0.45
1:04:12:ARG:HA	1:04:15:VAL:CG2	2.47	0.45
1:04:42:ARG:HE	1:04:48:ILE:HB	1.82	0.45
4:07:78:ILE:O	4:07:78:ILE:HG13	2.17	0.45
8:11:19:PRO:C	8:11:22:PRO:HD2	2.41	0.45
10:13:14:SER:OG	10:13:86:LEU:HD12	2.17	0.45
11:14:79:LEU:CD1	11:14:112:LEU:HA	2.47	0.45
18:21:6:LYS:HG3	54:01:494:G:H4'	1.99	0.45
19:22:56:GLU:HB2	19:22:86:THR:OG1	2.16	0.45
46:P:33:ILE:N	46:P:33:ILE:HD12	2.32	0.45
53:A:597:G:H2'	53:A:598:U:H5'	1.98	0.45
54:01:893:C:H2'	54:01:894:U:O4'	2.16	0.45
54:01:1246:A:H2'	54:01:1247:A:O4'	2.16	0.45
54:01:2298:A:H2'	54:01:2299:U:O4'	2.17	0.45
59:Z:91:MET:HE3	59:Z:118:HIS:CD2	2.52	0.45
1:04:22:GLU:HB3	1:04:80:LEU:HD12	1.99	0.45
1:04:41:GLY:O	1:04:49:THR:N	2.49	0.45
1:04:174:ARG:HG2	1:04:174:ARG:HH11	1.81	0.45
4:07:3:LEU:HA	4:07:6:TYR:HB3	1.98	0.45
7:10:43:LYS:NZ	7:10:43:LYS:HB3	2.31	0.45
8:11:14:ALA:HB1	8:11:45:THR:OG1	2.16	0.45
12:15:34:LYS:HD3	21:24:82:TYR:HA	1.99	0.45
12:15:62:LYS:HD3	12:15:64:TRP:CZ2	2.52	0.45
18:21:9:HIS:CE1	18:21:80:PRO:HG2	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:27:20:ASN:O	24:27:24:GLU:HB2	2.16	0.45
24:27:26:PHE:HA	24:27:29:ARG:NE	2.32	0.45
27:30:8:THR:CG2	54:01:2020:A:H5'	2.47	0.45
36:F:73:GLU:O	36:F:77:THR:HG23	2.15	0.45
40:J:101:SER:C	40:J:102:LEU:HD12	2.41	0.45
42:L:41:PRO:HD2	42:L:47:ALA:H	1.82	0.45
48:R:25:ILE:HA	48:R:28:LEU:HB3	1.98	0.45
49:S:9:PHE:CD2	53:A:1318:A:H4'	2.52	0.45
50:T:66:ILE:HG21	50:T:71:ALA:HB2	1.99	0.45
53:A:1492:A:H2'	54:01:1913:A:H2	1.82	0.45
54:01:128:C:H2'	54:01:129:C:C6	2.51	0.45
55:02:30:C:C2'	55:02:31:C:H5'	2.46	0.45
56:X:59:A:C2'	56:X:60:U:H5'	2.46	0.45
59:Z:236:ILE:HA	59:Z:240:GLU:OE1	2.16	0.45
1:04:200:MET:HE3	53:A:773:G:H4'	1.98	0.45
2:05:98:VAL:O	2:05:98:VAL:HG22	2.17	0.45
3:06:15:SER:HB2	3:06:18:THR:HB	1.99	0.45
4:07:98:PHE:HD1	4:07:101:ARG:HH11	1.63	0.45
7:10:96:PHE:HE2	7:10:126:LEU:HB2	1.82	0.45
9:12:47:HIS:ND1	9:12:48:VAL:HG23	2.31	0.45
19:22:15:HIS:HE1	19:22:17:SER:HB3	1.82	0.45
26:29:2:LYS:HB2	26:29:5:ILE:HD11	1.98	0.45
26:29:11:GLU:HA	26:29:25:ARG:HA	1.98	0.45
29:32:12:ARG:HH11	29:32:44:VAL:HG21	1.80	0.45
33:C:39:ARG:HH21	33:C:56:ILE:HG12	1.81	0.45
34:D:71:PHE:HE1	34:D:93:LEU:HD11	1.82	0.45
52:03:84:ALA:HA	52:03:95:VAL:HG11	1.97	0.45
53:A:337:G:H2'	53:A:338:A:C8	2.51	0.45
53:A:1251:A:H2'	53:A:1252:A:C8	2.51	0.45
54:01:146:A:H2'	54:01:147:C:C6	2.52	0.45
54:01:582:A:H2'	54:01:583:G:H8	1.80	0.45
54:01:1796:U:H2'	54:01:1797:G:C8	2.51	0.45
54:01:2097:A:H2'	54:01:2098:U:O4'	2.16	0.45
59:Z:95:ALA:HB1	59:Z:125:VAL:HG11	1.99	0.45
5:08:83:THR:HG23	5:08:133:LYS:HG2	1.98	0.45
34:D:29:THR:O	34:D:29:THR:HG22	2.17	0.45
34:D:50:TYR:CD2	53:A:508:U:H4'	2.51	0.45
35:E:43:GLY:O	35:E:73:VAL:N	2.47	0.45
36:F:72:ASP:O	36:F:76:THR:HG23	2.17	0.45
38:H:10:LEU:HD22	38:H:74:ILE:CD1	2.46	0.45
42:L:41:PRO:HG3	42:L:49:ARG:HG2	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Q:59:GLU:HB3	47:Q:75:VAL:HB	1.99	0.45
53:A:460:A:H2'	53:A:461:A:C8	2.52	0.45
53:A:684:U:H2'	53:A:685:G:O4'	2.17	0.45
53:A:871:U:H5''	53:A:872:A:OP2	2.16	0.45
54:01:367:G:H2'	54:01:368:A:O4'	2.16	0.45
54:01:2377:A:H2'	54:01:2378:A:C8	2.52	0.45
59:Z:176:LYS:HB3	59:Z:181:ASP:HB2	1.99	0.45
59:Z:247:ILE:HG12	59:Z:364:HIS:HB3	1.99	0.45
59:Z:310:ILE:HG21	59:Z:350:VAL:CG1	2.47	0.45
7:10:67:THR:CG2	7:10:74:ASP:HB2	2.46	0.45
15:18:52:ARG:HB3	15:18:55:HIS:HB2	1.99	0.45
20:23:93:ARG:HB2	20:23:102:ILE:HD12	1.99	0.45
21:24:60:VAL:HG11	21:24:71:LYS:HE3	1.99	0.45
31:34:22:VAL:O	31:34:24:ARG:HG3	2.16	0.45
34:D:158:LEU:HD23	34:D:158:LEU:O	2.17	0.45
43:M:3:ILE:HG12	43:M:7:ASN:OD1	2.16	0.45
44:N:5:MET:HE3	44:N:62:ARG:HH21	1.82	0.45
46:P:23:ASP:HB3	46:P:26:ASN:OD1	2.17	0.45
51:U:11:PHE:CG	51:U:12:ASP:N	2.85	0.45
51:U:65:ARG:HA	51:U:65:ARG:NE	2.32	0.45
52:03:175:ILE:HD12	52:03:185:LEU:HB3	1.99	0.45
53:A:285:C:H2'	53:A:286:C:C6	2.51	0.45
53:A:881:G:H2'	53:A:882:C:O4'	2.16	0.45
53:A:1148:U:H2'	53:A:1149:C:O4'	2.17	0.45
53:A:1258:G:H2'	53:A:1259:C:C6	2.51	0.45
53:A:1436:U:H2'	53:A:1437:A:H8	1.82	0.45
54:01:63:A:H2'	54:01:64:A:H8	1.81	0.45
54:01:195:A:H2'	54:01:198:C:N4	2.31	0.45
54:01:2806:C:H42	54:01:2892:G:H1	1.64	0.45
2:05:202:ILE:N	2:05:202:ILE:HD12	2.32	0.45
4:07:7:TYR:HA	4:07:11:VAL:CG2	2.46	0.45
4:07:15:LEU:HD11	4:07:168:LEU:HA	1.98	0.45
4:07:24:VAL:O	4:07:27:VAL:HG12	2.17	0.45
4:07:138:PRO:HB3	26:29:32:LEU:HD11	1.99	0.45
9:12:35:ARG:HA	9:12:40:HIS:CD2	2.51	0.45
11:14:70:LYS:HD3	54:01:633:A:H5''	1.99	0.45
12:15:58:LYS:HA	12:15:58:LYS:HD3	1.79	0.45
16:19:82:LEU:HA	16:19:85:ALA:HB3	1.98	0.45
17:20:43:ASN:CG	17:20:44:GLY:H	2.25	0.45
20:23:9:GLU:OE2	20:23:21:ARG:HG2	2.17	0.45
35:E:160:VAL:HG13	35:E:161:GLU:N	2.27	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:G:56:SER:HB3	37:G:59:GLU:HG2	1.99	0.45
39:I:24:ASN:ND2	39:I:26:LYS:HE3	2.32	0.45
40:J:35:GLN:HG2	40:J:77:VAL:HB	1.99	0.45
41:K:118:ASN:OD1	53:A:718:A:H5'	2.16	0.45
44:N:20:PHE:O	44:N:21:ALA:CB	2.65	0.45
51:U:39:LYS:N	51:U:40:PRO:CD	2.80	0.45
53:A:1522:U:H2'	53:A:1523:G:H8	1.81	0.45
54:01:184:C:H2'	54:01:185:G:C8	2.51	0.45
54:01:213:A:H2'	54:01:214:G:C8	2.52	0.45
54:01:1900:A:O4'	54:01:1970:A:H5''	2.17	0.45
54:01:2145:C:H3'	54:01:2146:C:H5'	1.99	0.45
1:04:129:LEU:N	1:04:129:LEU:HD23	2.33	0.44
4:07:147:ARG:HG3	4:07:148:VAL:N	2.32	0.44
34:D:59:LYS:O	34:D:63:ILE:HG13	2.17	0.44
52:03:181:ASP:HB2	52:03:184:LYS:CG	2.47	0.44
54:01:172:A:H2'	54:01:173:A:C8	2.51	0.44
54:01:720:U:H2'	54:01:721:A:C8	2.52	0.44
54:01:1346:G:H2'	54:01:1347:A:H8	1.82	0.44
54:01:2137:U:H2'	54:01:2138:G:C8	2.51	0.44
54:01:2553:G:H1'	54:01:2582:G:H21	1.82	0.44
54:01:2799:A:C2'	54:01:2800:A:H5'	2.47	0.44
54:01:2875:C:H2'	54:01:2876:G:H8	1.82	0.44
59:Z:14:VAL:HG21	59:Z:69:TYR:OH	2.16	0.44
1:04:257:ARG:HE	1:04:266:ILE:CD1	2.28	0.44
9:12:37:ARG:HH22	9:12:110:PRO:HG3	1.83	0.44
10:13:48:PRO:HB3	53:A:1422:G:C5'	2.44	0.44
15:18:62:LYS:HE2	15:18:64:SER:HB3	1.99	0.44
37:G:25:PHE:HD1	37:G:100:MET:HB3	1.82	0.44
41:K:92:ARG:HE	51:U:24:LYS:HZ1	1.64	0.44
52:03:144:THR:HG23	52:03:162:ARG:HD3	2.00	0.44
53:A:1492:A:H2'	54:01:1913:A:C2	2.53	0.44
54:01:281:C:H2'	54:01:282:A:H8	1.82	0.44
54:01:1083:U:H2'	54:01:1085:A:OP2	2.17	0.44
54:01:1440:U:H2'	54:01:1441:G:C8	2.52	0.44
1:04:89:ASN:OD1	1:04:196:ASN:HB2	2.16	0.44
2:05:161:MET:HE1	54:01:2050:C:O2	2.17	0.44
7:10:51:TYR:HA	7:10:53:ARG:NH1	2.32	0.44
8:11:10:LEU:HD21	54:01:1061:U:H5''	1.99	0.44
12:15:19:GLY:C	12:15:20:LEU:HD12	2.43	0.44
12:15:78:LEU:HD23	12:15:79:ALA:N	2.32	0.44
13:16:61:ALA:O	13:16:65:LEU:HD13	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:24:45:ASP:O	21:24:48:MET:HB3	2.16	0.44
38:H:28:SER:HB3	38:H:56:PRO:HB2	1.99	0.44
51:U:34:ARG:HD2	51:U:36:PHE:CZ	2.53	0.44
52:03:96:GLY:HA3	52:03:104:ILE:HD11	1.99	0.44
53:A:128:G:H2'	53:A:129:A:C8	2.53	0.44
54:01:297:G:H2'	54:01:298:G:O4'	2.18	0.44
54:01:974:G:H1'	54:01:975:A:C8	2.53	0.44
54:01:1908:C:O2	56:W:12:G:H4'	2.17	0.44
59:Z:377:ARG:HA	59:Z:382:THR:HA	1.99	0.44
16:19:55:GLN:CD	54:01:559:G:H1'	2.42	0.44
17:20:16:GLU:HB2	17:20:101:ILE:HG12	1.99	0.44
31:34:36:ARG:CG	31:34:37:GLN:H	2.13	0.44
36:F:3:HIS:HB2	36:F:92:THR:HA	1.98	0.44
39:I:82:ILE:O	39:I:86:LEU:HG	2.16	0.44
52:03:5:THR:O	52:03:9:ARG:N	2.48	0.44
53:A:994:A:C8	53:A:1216:A:H4'	2.53	0.44
53:A:1254:A:H2'	53:A:1255:G:H8	1.80	0.44
54:01:279:A:H2'	54:01:280:U:H5'	1.98	0.44
54:01:677:A:O2'	54:01:2071:A:H5'	2.17	0.44
54:01:878:A:H3'	54:01:879:G:H8	1.83	0.44
54:01:2847:U:H2'	54:01:2848:G:O4'	2.17	0.44
55:02:65:U:H3'	55:02:108:A:H61	1.83	0.44
59:Z:117:GLU:HA	59:Z:120:LEU:CG	2.40	0.44
26:29:46:GLY:HA2	26:29:49:ARG:HG2	2.00	0.44
40:J:59:LYS:HD3	53:A:973:G:OP1	2.17	0.44
43:M:6:ILE:O	43:M:8:ILE:HG13	2.16	0.44
50:T:23:ARG:O	50:T:26:MET:HG2	2.17	0.44
53:A:674:G:H2'	53:A:675:A:C8	2.52	0.44
53:A:916:U:H2'	53:A:917:G:H8	1.82	0.44
53:A:946:A:H2'	53:A:947:G:C8	2.52	0.44
53:A:1040:U:H2'	53:A:1041:G:C8	2.52	0.44
53:A:1088:G:N2	53:A:1167:A:H61	2.12	0.44
53:A:1261:A:H3'	53:A:1262:C:H6	1.83	0.44
53:A:1354:U:H2'	53:A:1355:G:C8	2.52	0.44
53:A:1464:U:H2'	53:A:1465:A:C8	2.52	0.44
54:01:1689:A:H2'	54:01:1690:A:C8	2.52	0.44
54:01:1744:A:H3'	54:01:1745:A:H8	1.83	0.44
54:01:1947:C:H2'	54:01:1948:G:C8	2.52	0.44
54:01:2028:U:H2'	54:01:2029:G:C8	2.53	0.44
54:01:2730:C:H2'	54:01:2731:G:H8	1.82	0.44
59:Z:131:ILE:HD11	59:Z:198:TYR:HB3	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:170:VAL:HG13	59:Z:190:GLU:HB2	2.00	0.44
59:Z:211:LEU:HB3	59:Z:233:ARG:HG2	1.99	0.44
7:10:3:LEU:CD1	7:10:5:LEU:HG	2.47	0.44
9:12:108:MET:HE2	54:01:1138:G:H21	1.82	0.44
9:12:113:PRO:O	9:12:117:ALA:N	2.50	0.44
10:13:49:ARG:NH2	53:A:1423:G:H5'	2.33	0.44
13:16:37:THR:HG22	13:16:110:MET:HE1	2.00	0.44
14:17:110:ALA:O	14:17:115:LEU:HB3	2.17	0.44
20:23:84:PHE:HB2	54:01:297:G:H5''	1.99	0.44
29:32:44:VAL:HG13	29:32:44:VAL:O	2.17	0.44
33:C:156:LEU:HD12	33:C:156:LEU:O	2.18	0.44
39:I:116:GLY:C	39:I:117:LEU:HD12	2.43	0.44
41:K:126:ARG:HA	41:K:126:ARG:NE	2.32	0.44
42:L:41:PRO:HB3	42:L:88:ASP:OD1	2.17	0.44
43:M:76:ILE:O	43:M:80:MET:HG3	2.17	0.44
46:P:38:PHE:CE1	46:P:51:ARG:HB2	2.52	0.44
49:S:79:TYR:CZ	53:A:1226:C:H4'	2.52	0.44
53:A:736:C:H2'	53:A:737:C:C6	2.52	0.44
53:A:1236:A:H4'	53:A:1304:G:H4'	2.00	0.44
54:01:186:G:H2'	54:01:187:G:H8	1.83	0.44
54:01:217:A:H2'	54:01:218:A:O4'	2.18	0.44
54:01:1300:G:H4'	54:01:1301:A:H5''	1.99	0.44
54:01:2259:U:H2'	54:01:2260:C:H6	1.83	0.44
56:X:8:U:H5'	56:X:49:G:OP2	2.18	0.44
59:Z:259:GLU:OE1	59:Z:262:ARG:HA	2.17	0.44
4:07:3:LEU:HD12	4:07:96:TRP:HE3	1.83	0.44
8:11:39:LYS:HE2	8:11:39:LYS:HA	1.99	0.44
8:11:79:LEU:HD12	8:11:135:MET:HG3	1.99	0.44
8:11:139:VAL:HG13	8:11:139:VAL:O	2.18	0.44
22:25:17:LEU:HD21	22:25:37:ARG:NH2	2.33	0.44
22:25:22:PHE:HD2	54:01:922:C:H1'	1.82	0.44
34:D:113:ALA:O	34:D:117:VAL:HG23	2.18	0.44
36:F:39:LEU:HD23	36:F:62:MET:HA	1.99	0.44
44:N:5:MET:HE2	53:A:982:U:H5''	2.00	0.44
53:A:32:A:H2'	53:A:33:A:C8	2.53	0.44
53:A:219:U:H2'	53:A:220:G:H8	1.83	0.44
53:A:1057:G:H2'	53:A:1058:G:O4'	2.17	0.44
54:01:66:C:H2'	54:01:67:U:H6	1.81	0.44
54:01:310:A:H2'	54:01:311:A:H5''	1.98	0.44
54:01:310:A:O2'	54:01:311:A:H5''	2.18	0.44
54:01:395:U:H2'	54:01:396:G:C8	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:665:U:H2'	54:01:666:A:C8	2.52	0.44
54:01:665:U:H2'	54:01:666:A:H8	1.83	0.44
54:01:1536:C:H4'	54:01:1537:G:C2	2.52	0.44
54:01:1593:A:H2'	54:01:1594:U:C6	2.53	0.44
54:01:2111:U:N3	54:01:2147:A:H1'	2.32	0.44
54:01:2462:C:H2'	54:01:2463:C:C6	2.52	0.44
54:01:2581:G:H2'	54:01:2581:G:N3	2.33	0.44
55:02:49:C:H2'	55:02:50:A:H8	1.83	0.44
3:06:109:LEU:O	3:06:113:VAL:HG23	2.18	0.44
3:06:188:MET:HE1	3:06:196:VAL:HG21	1.99	0.44
7:10:78:GLY:N	7:10:79:PRO:CD	2.81	0.44
17:20:54:VAL:HG12	17:20:55:ASP:N	2.33	0.44
22:25:16:ARG:HG3	54:01:2270:A:O2'	2.18	0.44
33:C:96:VAL:HB	33:C:97:PRO:HD2	1.99	0.44
35:E:37:VAL:HG11	35:E:113:VAL:HG23	2.00	0.44
39:I:115:VAL:HG23	53:A:1367:C:H5''	1.99	0.44
40:J:9:ARG:HH12	40:J:11:LYS:HZ3	1.65	0.44
43:M:77:LYS:HA	43:M:80:MET:HE3	1.98	0.44
53:A:246:A:O2'	53:A:247:G:O5'	2.31	0.44
53:A:448:A:H3'	53:A:449:G:C8	2.53	0.44
53:A:714:G:H2'	53:A:715:A:C8	2.53	0.44
53:A:820:U:H3'	53:A:821:G:C5'	2.48	0.44
54:01:1019:U:H3	54:01:1142:A:H62	1.65	0.44
54:01:1344:U:H3'	54:01:1345:C:H5'	1.98	0.44
54:01:1664:A:H61	54:01:1996:C:H42	1.66	0.44
54:01:2159:G:H2'	54:01:2160:C:O4'	2.17	0.44
54:01:2756:U:H4'	54:01:2757:A:OP1	2.17	0.44
59:Z:212:LEU:HD12	59:Z:231:VAL:HG22	2.00	0.44
3:06:55:SER:HB2	54:01:797:G:OP1	2.17	0.44
16:19:93:ILE:HG13	17:20:11:GLN:HB3	1.99	0.44
23:26:13:THR:CG2	54:01:188:G:H5'	2.46	0.44
26:29:2:LYS:HB2	26:29:5:ILE:CD1	2.48	0.44
27:30:2:VAL:HG21	54:01:2057:G:H1'	1.99	0.44
32:B:163:ILE:HD11	32:B:209:VAL:HG12	1.99	0.44
33:C:6:PRO:HD2	33:C:183:TYR:CD2	2.53	0.44
35:E:15:ILE:HD12	35:E:15:ILE:N	2.33	0.44
42:L:82:ARG:HD3	42:L:97:VAL:HG22	1.99	0.44
44:N:84:ARG:NH2	53:A:1059:C:H4'	2.23	0.44
49:S:48:ILE:HG13	49:S:59:VAL:HG23	2.00	0.44
51:U:49:ALA:O	51:U:52:VAL:HG12	2.18	0.44
53:A:413:G:H2'	53:A:428:G:N2	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1165:U:H2'	53:A:1166:G:O4'	2.18	0.44
54:01:239:C:H2'	54:01:240:C:O4'	2.17	0.44
54:01:856:G:H2'	54:01:857:G:C8	2.53	0.44
54:01:863:A:H2'	54:01:864:G:C8	2.53	0.44
54:01:2014:A:H2'	54:01:2015:A:C8	2.52	0.44
54:01:2055:C:H2'	54:01:2504:U:H5'	2.00	0.44
54:01:2586:U:H2'	54:01:2587:A:C8	2.52	0.44
54:01:2730:C:H2'	54:01:2731:G:C8	2.52	0.44
59:Z:129:TYR:CE2	59:Z:200:PRO:HD2	2.53	0.44
1:04:233:GLY:HA3	54:01:2598:A:H5''	1.99	0.43
5:08:26:LYS:CB	5:08:31:GLU:HG3	2.46	0.43
5:08:42:VAL:HG23	5:08:50:THR:O	2.17	0.43
6:09:47:PHE:HA	6:09:51:ARG:HB2	2.00	0.43
16:19:93:ILE:O	16:19:97:ILE:HG13	2.18	0.43
17:20:14:VAL:HG21	17:20:98:ILE:HG13	1.99	0.43
17:20:74:ILE:N	17:20:74:ILE:HD12	2.33	0.43
32:B:94:ARG:HH21	51:U:66:ARG:HH11	1.66	0.43
39:I:118:ARG:NH2	39:I:122:ARG:HG2	2.33	0.43
46:P:78:VAL:O	46:P:78:VAL:HG22	2.18	0.43
52:03:21:TYR:CD2	52:03:25:GLU:HG2	2.53	0.43
53:A:147:G:H2'	53:A:148:G:C8	2.53	0.43
53:A:618:C:H3'	53:A:620:C:OP2	2.18	0.43
53:A:1032:G:H21	53:A:1033:G:H4'	1.83	0.43
53:A:1177:G:H2'	53:A:1178:G:O4'	2.18	0.43
53:A:1488:G:O2'	53:A:1489:G:H5'	2.17	0.43
54:01:654:A:H3'	54:01:654:A:N3	2.33	0.43
59:Z:101:ALA:H	59:Z:127:VAL:HG11	1.81	0.43
59:Z:244:ILE:HD13	59:Z:251:GLN:HG3	1.99	0.43
1:04:23:LEU:HD21	1:04:89:ASN:ND2	2.33	0.43
1:04:153:LEU:HD11	1:04:181:ARG:HH22	1.83	0.43
7:10:8:LYS:HD3	54:01:1046:A:N1	2.34	0.43
14:17:92:PHE:HB2	14:17:117:PHE:CD2	2.53	0.43
20:23:90:LYS:HZ1	54:01:100:U:H2'	1.81	0.43
36:F:5:GLU:O	36:F:7:VAL:HG23	2.18	0.43
38:H:50:VAL:HG22	38:H:50:VAL:O	2.17	0.43
46:P:26:ASN:ND2	46:P:31:ARG:HB3	2.33	0.43
47:Q:10:ARG:NH1	47:Q:55:GLY:HA2	2.32	0.43
52:03:57:GLN:HB3	52:03:201:PRO:HG2	1.99	0.43
53:A:1225:A:H2'	53:A:1225:A:N3	2.34	0.43
54:01:848:C:H2'	54:01:849:A:C8	2.53	0.43
54:01:1097:U:H2'	54:01:1098:A:O4'	2.17	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1199:U:H2'	54:01:1200:C:C6	2.52	0.43
54:01:2093:G:H2'	54:01:2094:A:H8	1.83	0.43
54:01:2236:U:H2'	54:01:2237:G:O4'	2.17	0.43
1:04:234:GLY:HA3	1:04:238:ASN:HB2	2.00	0.43
1:04:254:LYS:O	54:01:1797:G:H4'	2.18	0.43
4:07:28:PRO:HB2	4:07:168:LEU:HD22	2.00	0.43
5:08:173:ALA:C	5:08:175:LYS:H	2.25	0.43
10:13:36:GLY:HA2	10:13:62:VAL:O	2.18	0.43
10:13:93:GLN:HA	10:13:94:PRO:HD2	1.83	0.43
19:22:22:THR:HA	19:22:25:GLU:HG2	2.00	0.43
22:25:10:ARG:HH11	22:25:10:ARG:HG3	1.83	0.43
35:E:40:ASP:OD2	35:E:42:ASN:HB3	2.18	0.43
39:I:49:GLN:N	39:I:50:PRO:CD	2.82	0.43
39:I:113:LYS:HE2	39:I:118:ARG:O	2.17	0.43
50:T:34:VAL:HG11	50:T:78:LEU:HD21	1.99	0.43
52:03:180:PHE:HB2	52:03:185:LEU:HD11	2.00	0.43
53:A:452:A:H61	53:A:480:U:H3	1.66	0.43
53:A:631:C:H3'	53:A:632:U:H5'	1.99	0.43
53:A:767:A:H2'	53:A:768:A:O4'	2.19	0.43
53:A:955:U:H3	53:A:1225:A:H61	1.65	0.43
54:01:437:U:H2'	54:01:438:G:H8	1.82	0.43
54:01:635:C:H2'	54:01:636:G:C8	2.52	0.43
54:01:1772:A:H2'	54:01:1773:A:H4'	2.00	0.43
54:01:2207:C:H2'	54:01:2208:C:C6	2.54	0.43
54:01:2277:G:C3'	54:01:2278:A:H5''	2.48	0.43
54:01:2293:G:H2'	54:01:2294:G:C8	2.53	0.43
59:Z:321:PRO:HA	59:Z:350:VAL:O	2.17	0.43
1:04:145:MET:SD	1:04:181:ARG:NH2	2.91	0.43
3:06:123:LYS:HA	3:06:189:THR:HG23	2.00	0.43
4:07:135:ILE:HG21	4:07:142:TYR:CD1	2.49	0.43
6:09:72:ILE:HB	6:09:108:VAL:HG22	2.00	0.43
11:14:93:ASN:O	11:14:94:THR:HB	2.18	0.43
25:28:40:THR:CG2	25:28:43:ILE:HG12	2.48	0.43
25:28:56:VAL:HG22	25:28:57:GLU:N	2.33	0.43
26:29:59:ARG:O	26:29:63:ARG:HG3	2.18	0.43
28:31:14:ALA:HB2	28:31:46:VAL:HG13	2.00	0.43
36:F:66:ALA:HB1	36:F:67:PRO:HD2	2.00	0.43
43:M:7:ASN:ND2	43:M:9:PRO:HD3	2.34	0.43
46:P:13:LYS:HE3	53:A:392:C:H4'	2.00	0.43
46:P:20:VAL:CG2	46:P:21:VAL:N	2.81	0.43
48:R:34:GLU:HB3	51:U:18:PHE:HZ	1.84	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:T:28:ARG:O	50:T:32:LYS:HG2	2.18	0.43
52:03:60:ARG:HB2	52:03:141:LYS:CG	2.47	0.43
53:A:599:C:H2'	53:A:600:A:C8	2.52	0.43
53:A:1316:G:H2'	53:A:1317:C:H5''	1.99	0.43
54:01:1934:C:H2'	54:01:1935:G:O4'	2.18	0.43
54:01:2452:C:N4	54:01:2504:U:H3	2.12	0.43
54:01:2795:C:H2'	54:01:2796:U:O4'	2.18	0.43
59:Z:119:ILE:HG21	59:Z:157:LEU:HD23	2.01	0.43
3:06:149:ILE:HD12	3:06:170:ARG:O	2.18	0.43
4:07:109:ARG:HH11	43:M:2:ARG:NE	2.16	0.43
7:10:118:ILE:HD13	7:10:118:ILE:HA	1.90	0.43
10:13:61:VAL:HB	10:13:87:LEU:HD11	2.00	0.43
11:14:85:VAL:HG11	11:14:95:LEU:HD23	2.00	0.43
32:B:102:ASN:O	32:B:106:VAL:HG23	2.18	0.43
32:B:119:GLN:HG2	32:B:136:ARG:NH2	2.30	0.43
33:C:105:VAL:O	33:C:105:VAL:HG13	2.17	0.43
33:C:190:THR:HG21	33:C:195:ILE:HD12	2.01	0.43
39:I:70:GLY:HA3	53:A:1371:G:O3'	2.18	0.43
53:A:193:C:O2'	53:A:194:C:H5'	2.18	0.43
53:A:1490:U:H2'	53:A:1491:G:O4'	2.18	0.43
53:A:1516:G:H2'	53:A:1518:A:OP2	2.18	0.43
54:01:435:C:C2'	54:01:436:C:H5'	2.48	0.43
54:01:755:U:H2'	54:01:756:A:H8	1.83	0.43
54:01:1499:C:H2'	54:01:1500:G:H8	1.84	0.43
54:01:1654:A:H2'	54:01:1655:A:H8	1.83	0.43
54:01:2327:A:H2'	54:01:2328:A:C8	2.54	0.43
54:01:2417:C:H2'	54:01:2418:A:H8	1.84	0.43
54:01:2743:U:H2'	54:01:2744:G:C4'	2.49	0.43
59:Z:17:ILE:HG13	59:Z:103:LEU:HD12	2.00	0.43
1:04:85:ASN:HD21	54:01:1817:G:H5'	1.84	0.43
1:04:235:GLU:HG2	54:01:2599:G:C8	2.54	0.43
5:08:51:PHE:CE2	5:08:68:ARG:HA	2.54	0.43
12:15:125:PRO:HB3	54:01:2485:G:O3'	2.19	0.43
14:17:40:ILE:HD13	55:02:8:C:O2'	2.19	0.43
32:B:19:THR:OG1	32:B:20:ARG:N	2.51	0.43
33:C:38:VAL:HG23	33:C:39:ARG:N	2.34	0.43
35:E:82:HIS:C	35:E:97:PRO:HD3	2.44	0.43
41:K:22:ILE:HG12	41:K:31:VAL:HG13	2.01	0.43
52:03:65:LEU:H	52:03:159:GLY:C	2.26	0.43
52:03:133:PRO:HG3	54:01:2168:G:O3'	2.18	0.43
52:03:175:ILE:HG23	52:03:192:LEU:HD22	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:86:G:H4'	53:A:87:C:C6	2.53	0.43
53:A:132:C:H5'	53:A:262:A:O2'	2.19	0.43
53:A:243:A:H4'	53:A:244:U:H3'	2.01	0.43
54:01:184:C:H4'	54:01:217:A:H2	1.83	0.43
54:01:825:A:H2'	54:01:826:U:O4'	2.19	0.43
54:01:1783:A:N1	54:01:2587:A:H2'	2.33	0.43
54:01:2139:U:H2'	54:01:2140:G:C8	2.53	0.43
54:01:2190:G:H2'	54:01:2191:A:H8	1.84	0.43
54:01:2660:A:H2'	54:01:2661:G:O4'	2.18	0.43
55:02:79:G:H2'	55:02:80:U:O4'	2.18	0.43
56:X:31:G:C2'	56:X:32:C:H5'	2.48	0.43
56:W:51:C:H2'	56:W:52:G:O4'	2.18	0.43
1:04:132:ARG:HD3	1:04:132:ARG:H	1.84	0.43
5:08:22:VAL:HG22	5:08:35:THR:OG1	2.18	0.43
5:08:144:ALA:HB1	5:08:163:TYR:HE1	1.83	0.43
6:09:5:LEU:HD23	6:09:9:VAL:HG21	2.00	0.43
9:12:99:ARG:HA	9:12:102:GLU:HB3	2.00	0.43
15:18:51:ASN:O	54:01:2845:U:H5''	2.18	0.43
19:22:8:LEU:HD13	24:27:21:LEU:HB3	2.01	0.43
22:25:33:ILE:HD11	22:25:78:ILE:HD11	1.99	0.43
41:K:44:ALA:HB3	41:K:69:CYS:HB2	2.00	0.43
51:U:23:GLU:HB3	51:U:27:VAL:HG22	1.99	0.43
53:A:321:A:O2'	53:A:322:C:H5'	2.18	0.43
53:A:730:G:C5	53:A:731:G:H1'	2.53	0.43
54:01:1906:G:C2'	54:01:1907:G:H5''	2.49	0.43
58:Y:29:G:H2'	58:Y:30:G:C8	2.53	0.43
58:Y:60:U:O2'	58:Y:61:C:H5'	2.18	0.43
59:Z:29:ALA:C	59:Z:178:LEU:HD13	2.44	0.43
7:10:118:ILE:CB	7:10:119:PRO:HD3	2.48	0.43
14:17:111:ARG:HB2	14:17:117:PHE:CE1	2.54	0.43
24:27:38:GLN:O	54:01:95:A:H4'	2.18	0.43
34:D:14:GLU:OE1	34:D:59:LYS:HB2	2.19	0.43
35:E:129:SER:HB2	53:A:20:U:OP2	2.18	0.43
35:E:152:VAL:O	35:E:156:ARG:HB3	2.19	0.43
35:E:156:ARG:HG3	38:H:44:PHE:CZ	2.54	0.43
36:F:19:PRO:O	36:F:23:GLU:HG3	2.19	0.43
37:G:87:PRO:HG3	37:G:148:LYS:HA	1.99	0.43
53:A:728:A:H2'	53:A:729:A:C8	2.53	0.43
53:A:801:U:H2'	53:A:802:A:H8	1.84	0.43
53:A:922:G:H2'	53:A:923:A:C8	2.54	0.43
54:01:796:C:H2'	54:01:797:G:H8	1.84	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1362:C:H2'	54:01:1363:C:O4'	2.19	0.43
54:01:1710:G:H1'	54:01:2859:G:H21	1.83	0.43
54:01:2026:U:H2'	54:01:2027:G:O4'	2.19	0.43
54:01:2725:A:H2'	54:01:2726:A:H2'	2.00	0.43
58:Y:68:C:H2'	58:Y:69:G:C8	2.53	0.43
1:04:64:VAL:HB	1:04:66:PHE:CZ	2.54	0.43
4:07:147:ARG:HG3	4:07:148:VAL:H	1.84	0.43
11:14:141:LYS:HE2	11:14:143:GLU:HB3	2.00	0.43
17:20:27:ILE:HG22	17:20:28:ALA:N	2.34	0.43
17:20:58:VAL:O	17:20:58:VAL:HG13	2.18	0.43
18:21:86:MET:HB2	18:21:96:ILE:CD1	2.48	0.43
24:27:5:GLU:O	24:27:56:LEU:HD13	2.19	0.43
36:F:5:GLU:HB2	36:F:90:MET:HB2	2.00	0.43
36:F:67:PRO:HG2	36:F:70:VAL:HG23	1.99	0.43
38:H:51:GLU:O	38:H:57:GLU:N	2.51	0.43
49:S:10:ILE:HG22	49:S:37:SER:HB2	2.01	0.43
49:S:34:SER:O	49:S:70:LEU:HD12	2.19	0.43
52:03:7:ARG:HH11	54:01:2128:G:H4'	1.84	0.43
52:03:105:LYS:HE3	52:03:130:VAL:HG21	2.01	0.43
53:A:604:G:H2'	53:A:605:U:O4'	2.18	0.43
53:A:763:G:H2'	53:A:764:C:C6	2.54	0.43
53:A:1237:C:OP1	53:A:1238:A:H1'	2.19	0.43
54:01:191:A:H2'	54:01:192:C:C6	2.53	0.43
54:01:374:A:H2'	54:01:375:G:O4'	2.19	0.43
54:01:826:U:H5''	54:01:2429:G:P	2.59	0.43
58:Y:55:U:H2'	58:Y:57:G:OP2	2.18	0.43
59:Z:206:ILE:HB	59:Z:235:ILE:HG23	2.01	0.43
13:16:2:ARG:HA	13:16:5:LYS:HG3	2.00	0.43
20:23:4:ILE:HD12	20:23:4:ILE:H	1.83	0.43
32:B:67:LEU:HD21	32:B:91:VAL:CG2	2.40	0.43
41:K:95:THR:O	41:K:99:LEU:HD13	2.19	0.43
43:M:9:PRO:CG	43:M:44:ILE:HG13	2.49	0.43
53:A:408:A:H2'	53:A:409:U:O4'	2.18	0.43
53:A:591:U:H2'	53:A:592:G:H8	1.84	0.43
53:A:682:G:H2'	53:A:683:G:C8	2.53	0.43
53:A:1157:A:H4'	53:A:1158:C:O5'	2.19	0.43
54:01:193:U:H4'	54:01:803:U:H4'	2.01	0.43
54:01:817:C:O2'	54:01:839:U:H5''	2.18	0.43
54:01:1152:C:H2'	54:01:1153:C:C6	2.54	0.43
54:01:1683:U:H2'	54:01:1684:G:H8	1.84	0.43
54:01:1697:G:C4'	54:01:1978:A:H5''	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:X:68:C:H2'	56:X:69:C:O4'	2.19	0.43
1:04:235:GLU:N	1:04:238:ASN:ND2	2.60	0.42
2:05:154:LYS:HZ2	54:01:2024:G:H4'	1.82	0.42
4:07:97:GLU:CG	26:29:25:ARG:HB2	2.48	0.42
6:09:26:ALA:O	6:09:31:VAL:HG23	2.19	0.42
7:10:58:THR:HG21	7:10:82:ILE:H	1.85	0.42
8:11:12:VAL:HG12	8:11:13:ALA:N	2.28	0.42
36:F:44:ARG:HA	36:F:58:HIS:HA	2.00	0.42
37:G:38:ALA:O	37:G:42:VAL:HG23	2.19	0.42
39:I:62:LEU:HD12	39:I:62:LEU:N	2.34	0.42
51:U:17:ARG:HA	51:U:20:ARG:HG2	2.00	0.42
53:A:227:G:H2'	53:A:228:A:O4'	2.19	0.42
53:A:443:C:H2'	53:A:444:G:H8	1.83	0.42
54:01:1844:C:H2'	54:01:1845:G:H8	1.82	0.42
56:X:21:A:N6	56:X:46:G:H2'	2.34	0.42
1:04:7:PRO:HB3	1:04:13:ARG:HA	2.01	0.42
1:04:257:ARG:HG3	54:01:1799:G:OP1	2.19	0.42
5:08:157:LYS:HD2	54:01:2659:G:OP1	2.19	0.42
20:23:43:LYS:O	20:23:58:VAL:N	2.52	0.42
22:25:22:PHE:CD2	54:01:922:C:H1'	2.54	0.42
22:25:25:GLU:O	22:25:63:VAL:HG23	2.19	0.42
30:33:38:LYS:CA	30:33:41:ARG:HH11	2.32	0.42
47:Q:46:HIS:HB2	47:Q:70:LYS:CG	2.48	0.42
50:T:70:LYS:HA	50:T:73:ARG:HH12	1.83	0.42
53:A:225:C:C3'	53:A:226:G:H5''	2.49	0.42
53:A:666:G:H2'	53:A:667:G:C8	2.54	0.42
53:A:969:A:H2'	53:A:970:C:O4'	2.18	0.42
54:01:548:G:H2'	54:01:549:G:O4'	2.19	0.42
54:01:795:C:H2'	54:01:796:C:C6	2.54	0.42
54:01:992:C:H2'	54:01:993:G:H8	1.84	0.42
54:01:1655:A:H2'	54:01:1656:C:O4'	2.19	0.42
54:01:2123:G:H2'	54:01:2124:G:C8	2.55	0.42
59:Z:29:ALA:HB2	59:Z:49:ILE:HD12	2.00	0.42
59:Z:60:ILE:HA	60:Z:401:GCP:O2G	2.19	0.42
3:06:188:MET:CE	3:06:196:VAL:HG21	2.49	0.42
5:08:132:LEU:HD12	5:08:132:LEU:O	2.19	0.42
15:18:77:SER:O	15:18:80:VAL:HG22	2.19	0.42
17:20:15:SER:N	17:20:18:GLN:HE21	2.01	0.42
25:28:50:VAL:O	25:28:54:VAL:HG22	2.19	0.42
35:E:75:LEU:O	35:E:75:LEU:HD12	2.19	0.42
38:H:30:LYS:HD2	53:A:643:C:OP1	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Q:13:SER:HB3	47:Q:21:VAL:HG11	2.00	0.42
50:T:30:PHE:O	50:T:34:VAL:HG23	2.20	0.42
52:03:5:THR:OG1	52:03:8:MET:HE3	2.19	0.42
53:A:244:U:O4	53:A:906:A:H1'	2.18	0.42
53:A:555:U:H2'	53:A:556:C:C6	2.54	0.42
54:01:190:A:H5''	54:01:204:A:H61	1.84	0.42
54:01:310:A:O2'	54:01:311:A:H2'	2.20	0.42
54:01:433:C:O2'	54:01:434:U:H5'	2.19	0.42
54:01:935:C:H2'	54:01:936:A:C8	2.54	0.42
54:01:1258:U:H2'	54:01:1259:G:C8	2.54	0.42
54:01:1282:U:H2'	54:01:1283:G:O4'	2.20	0.42
54:01:1532:A:H1'	54:01:1540:G:N2	2.34	0.42
54:01:1773:A:H2'	54:01:1774:C:H5'	2.00	0.42
58:Y:15:G:C2'	58:Y:16:U:H5'	2.46	0.42
1:04:48:ILE:HG22	54:01:779:U:OP1	2.20	0.42
5:08:21:GLN:NE2	5:08:38:ASP:HA	2.33	0.42
7:10:43:LYS:CB	7:10:46:ARG:HH21	2.32	0.42
7:10:69:PHE:CD2	7:10:70:GLU:HG2	2.55	0.42
7:10:81:LEU:HA	54:01:1107:G:H4'	2.00	0.42
12:15:53:MET:HB2	12:15:120:ALA:HB2	2.02	0.42
12:15:78:LEU:HD23	12:15:79:ALA:HB2	2.01	0.42
13:16:49:GLU:HB2	13:16:50:PRO:HD3	2.02	0.42
14:17:27:VAL:HG13	14:17:95:SER:OG	2.20	0.42
30:33:30:HIS:ND1	30:33:31:ILE:HG13	2.35	0.42
43:M:16:ILE:HD12	43:M:16:ILE:H	1.84	0.42
44:N:45:LEU:HG	49:S:12:LEU:HD22	2.02	0.42
47:Q:74:LEU:HD12	47:Q:75:VAL:N	2.34	0.42
49:S:28:LYS:HE3	49:S:29:PRO:HD2	2.02	0.42
52:03:6:LYS:O	52:03:10:VAL:HG23	2.19	0.42
52:03:46:VAL:HG13	52:03:212:VAL:HG22	2.02	0.42
53:A:578:C:H2'	53:A:579:A:C8	2.54	0.42
53:A:797:C:H2'	53:A:798:U:H6	1.83	0.42
53:A:945:G:H2'	53:A:945:G:N3	2.34	0.42
53:A:1030:U:H3'	53:A:1031:C:H5'	2.01	0.42
53:A:1030:U:H5	53:A:1033:G:H21	1.67	0.42
54:01:799:G:H3'	54:01:800:A:H8	1.84	0.42
54:01:844:A:H5'	54:01:845:A:OP1	2.20	0.42
54:01:917:A:H2	55:02:79:G:H21	1.68	0.42
54:01:1565:C:O2'	54:01:1566:A:H2'	2.19	0.42
54:01:2149:U:H2'	54:01:2150:C:O4'	2.18	0.42
58:Y:37:A:H2'	58:Y:38:A:O4'	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:06:105:LEU:O	3:06:109:LEU:HD13	2.18	0.42
9:12:113:PRO:HD2	54:01:558:U:OP1	2.20	0.42
11:14:63:LYS:HA	30:33:12:ARG:HG2	2.00	0.42
15:18:2:ASN:ND2	54:01:2876:G:H5''	2.34	0.42
22:25:58:LYS:HE3	54:01:2366:A:H4'	2.02	0.42
27:30:10:SER:O	27:30:14:MET:HG3	2.20	0.42
32:B:102:ASN:ND2	32:B:105:THR:HG21	2.34	0.42
36:F:75:GLU:HA	36:F:78:PHE:HD2	1.83	0.42
50:T:35:TYR:O	50:T:39:GLU:HG2	2.19	0.42
54:01:482:A:H1'	54:01:498:G:N2	2.34	0.42
54:01:1285:A:H2'	54:01:1286:A:H5'	2.01	0.42
54:01:2783:U:H2'	54:01:2784:U:C6	2.54	0.42
54:01:2897:U:H2'	54:01:2898:U:C6	2.54	0.42
59:Z:177:ALA:CB	59:Z:188:ILE:HG13	2.49	0.42
1:04:134:ILE:HA	1:04:135:PRO:HD3	1.94	0.42
1:04:260:LYS:HB3	54:01:2227:A:H5''	2.00	0.42
6:09:1:MET:N	6:09:21:VAL:O	2.43	0.42
6:09:99:ILE:O	6:09:103:VAL:HG23	2.19	0.42
7:10:27:VAL:HG23	7:10:110:ALA:HA	2.02	0.42
7:10:116:GLU:HB3	7:10:117:LEU:H	1.72	0.42
8:11:127:SER:HB2	54:01:1080:A:N3	2.35	0.42
9:12:7:LYS:O	9:12:11:VAL:HG23	2.20	0.42
13:16:55:ALA:HA	13:16:80:PHE:CE1	2.55	0.42
14:17:29:HIS:HA	14:17:97:PHE:CE2	2.55	0.42
20:23:10:VAL:HA	20:23:71:ILE:HA	2.02	0.42
32:B:96:LEU:O	32:B:99:MET:HG2	2.19	0.42
32:B:206:ILE:O	32:B:209:VAL:HG22	2.20	0.42
32:B:217:ALA:O	32:B:221:ARG:HB2	2.19	0.42
35:E:164:LEU:HD12	35:E:165:GLY:N	2.34	0.42
36:F:25:TYR:O	36:F:29:ILE:HG13	2.19	0.42
37:G:72:VAL:HG12	37:G:89:GLU:HA	2.02	0.42
37:G:110:ARG:HH22	37:G:121:ASN:HB3	1.84	0.42
40:J:42:LEU:HA	40:J:43:PRO:HD2	1.73	0.42
43:M:53:ASP:HA	43:M:56:ARG:HH11	1.85	0.42
52:03:57:GLN:HG2	52:03:201:PRO:CB	2.50	0.42
53:A:390:U:H2'	53:A:391:G:C8	2.55	0.42
53:A:878:A:H2'	53:A:879:C:C6	2.55	0.42
53:A:1477:U:H2'	53:A:1478:U:C6	2.54	0.42
54:01:140:C:H3'	54:01:140:C:OP2	2.19	0.42
54:01:1748:C:H2'	54:01:1749:A:H8	1.84	0.42
54:01:2246:G:H2'	54:01:2247:A:C8	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:Y:9:A:C2	58:Y:44:G:H2'	2.54	0.42
8:11:91:LYS:HA	8:11:94:LYS:HZ3	1.85	0.42
10:13:92:GLU:O	10:13:93:GLN:C	2.62	0.42
12:15:38:ARG:CD	55:02:90:C:H4'	2.50	0.42
14:17:12:THR:HB	54:01:2334:U:H4'	2.01	0.42
18:21:25:ARG:NH2	54:01:519:U:H5''	2.34	0.42
24:27:14:LEU:O	24:27:14:LEU:HD23	2.20	0.42
40:J:14:ASP:OD2	40:J:17:LEU:HB2	2.19	0.42
42:L:120:ARG:NH1	53:A:500:G:H5'	2.34	0.42
52:03:104:ILE:HG23	52:03:108:GLU:O	2.20	0.42
52:03:170:ILE:HG21	54:01:2177:C:H1'	2.02	0.42
53:A:17:U:H2'	53:A:18:C:C6	2.54	0.42
53:A:67:C:H2'	53:A:68:G:C8	2.55	0.42
53:A:539:A:H2'	53:A:540:G:H8	1.84	0.42
53:A:651:C:H2'	53:A:652:U:C6	2.55	0.42
53:A:855:U:H2'	53:A:856:C:C6	2.54	0.42
53:A:1053:G:H4'	53:A:1055:A:OP1	2.19	0.42
54:01:151:C:H2'	54:01:152:A:C8	2.54	0.42
54:01:464:U:H1'	54:01:686:U:H5	1.84	0.42
54:01:935:C:H2'	54:01:936:A:H8	1.85	0.42
54:01:995:C:H6	54:01:995:C:H5'	1.85	0.42
54:01:1318:U:H2'	54:01:1319:C:C6	2.54	0.42
54:01:1989:G:H2'	54:01:1990:C:O4'	2.19	0.42
54:01:2415:G:H2'	54:01:2416:C:C6	2.54	0.42
54:01:2818:U:H2'	54:01:2819:G:C8	2.54	0.42
55:02:30:C:H2'	55:02:31:C:C5'	2.49	0.42
56:X:14:A:H2'	56:X:15:G:O4'	2.20	0.42
59:Z:20:VAL:HA	60:Z:401:GCP:O1G	2.19	0.42
59:Z:67:VAL:HG22	59:Z:78:HIS:HB3	1.99	0.42
59:Z:191:LEU:O	59:Z:195:LEU:HB2	2.19	0.42
59:Z:311:LEU:HG	59:Z:384:GLY:HA2	2.01	0.42
59:Z:322:PHE:N	59:Z:322:PHE:CD1	2.87	0.42
3:06:163:ASN:ND2	54:01:323:C:H5''	2.35	0.42
4:07:148:VAL:HG12	4:07:148:VAL:O	2.20	0.42
12:15:36:VAL:HG13	21:24:82:TYR:CD2	2.55	0.42
13:16:103:ARG:HB2	13:16:110:MET:HE3	2.01	0.42
14:17:30:ARG:HG2	14:17:30:ARG:HH11	1.84	0.42
16:19:8:ILE:H	16:19:8:ILE:HG13	1.70	0.42
23:26:17:ARG:HE	23:26:23:ALA:HB2	1.85	0.42
41:K:126:ARG:HH21	53:A:796:C:H4'	1.84	0.42
43:M:97:ARG:HG2	43:M:97:ARG:HH11	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:P:40:ASN:OD1	46:P:42:ILE:HG12	2.20	0.42
53:A:301:G:H2'	53:A:302:G:H8	1.84	0.42
53:A:713:G:H2'	53:A:714:G:C8	2.55	0.42
53:A:1071:C:H2'	53:A:1072:G:C8	2.54	0.42
54:01:355:U:H2'	54:01:356:G:C8	2.54	0.42
54:01:624:C:O2'	54:01:657:U:H5''	2.20	0.42
54:01:633:A:H2'	54:01:634:C:H5'	2.00	0.42
54:01:1474:U:C2'	54:01:1475:G:H5'	2.49	0.42
54:01:2721:A:H2'	54:01:2722:G:O4'	2.20	0.42
55:02:78:A:H2'	55:02:79:G:O4'	2.20	0.42
1:04:30:ALA:HB3	1:04:31:PRO:HD3	2.02	0.42
2:05:135:GLY:HA2	54:01:743:A:OP1	2.20	0.42
4:07:89:THR:O	55:02:43:C:H1'	2.20	0.42
7:10:111:ALA:O	7:10:114:GLU:HG2	2.20	0.42
8:11:99:LYS:O	8:11:100:ILE:HD13	2.20	0.42
11:14:23:ILE:HG13	17:20:82:HIS:CE1	2.55	0.42
11:14:27:LEU:O	11:14:31:GLY:HA2	2.19	0.42
11:14:79:LEU:HD11	11:14:112:LEU:HA	2.02	0.42
20:23:97:SER:O	20:23:98:ASN:CB	2.67	0.42
27:30:33:SER:CB	27:30:35:GLU:HG3	2.50	0.42
33:C:38:VAL:O	33:C:42:LEU:HD13	2.19	0.42
36:F:98:GLU:HB3	36:F:99:ALA:H	1.67	0.42
41:K:44:ALA:HB3	41:K:65:ALA:O	2.20	0.42
53:A:928:G:H2'	53:A:929:G:H8	1.85	0.42
54:01:280:U:H2'	54:01:281:C:C2	2.55	0.42
54:01:767:U:H2'	54:01:768:G:C8	2.55	0.42
54:01:859:G:O2'	54:01:860:U:P	2.77	0.42
54:01:1844:C:H2'	54:01:1845:G:C8	2.55	0.42
54:01:2233:U:H2'	54:01:2234:G:H8	1.84	0.42
54:01:2774:C:H2'	54:01:2775:G:O4'	2.20	0.42
56:X:1:C:H2'	56:X:2:G:C8	2.55	0.42
59:Z:113:PRO:O	59:Z:116:ARG:HB3	2.20	0.42
1:04:65:ASP:OD2	1:04:68:ARG:HD2	2.20	0.42
1:04:104:LEU:HD12	1:04:142:ASN:ND2	2.35	0.42
1:04:243:PRO:O	1:04:251:THR:HG22	2.20	0.42
5:08:34:ARG:HE	5:08:70:LEU:HD13	1.81	0.42
7:10:29:ASP:H	7:10:81:LEU:HD22	1.83	0.42
8:11:75:ALA:O	8:11:79:LEU:N	2.50	0.42
9:12:117:ALA:HA	9:12:120:ARG:HH21	1.83	0.42
11:14:62:PRO:HG2	30:33:24:LYS:HB3	2.02	0.42
13:16:1:MET:O	13:16:2:ARG:HG3	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:20:78:ARG:NH1	54:01:990:A:H61	2.17	0.42
33:C:13:ILE:HD12	33:C:13:ILE:H	1.85	0.42
39:I:80:HIS:CD2	39:I:105:ARG:HA	2.55	0.42
43:M:100:ARG:HH12	43:M:103:THR:CB	2.33	0.42
53:A:1295:U:H2'	53:A:1296:C:C6	2.54	0.42
54:01:358:U:H2'	54:01:359:G:O4'	2.20	0.42
54:01:2292:U:H2'	54:01:2293:G:C8	2.55	0.42
54:01:2520:C:O2'	54:01:2521:C:H5'	2.20	0.42
1:04:55:GLY:H	54:01:692:C:P	2.43	0.41
1:04:86:ARG:HG2	1:04:86:ARG:HH11	1.86	0.41
2:05:6:GLY:O	2:05:201:LEU:N	2.47	0.41
7:10:67:THR:HB	7:10:68:PRO:HD3	2.02	0.41
12:15:33:LEU:HD11	12:15:128:THR:OG1	2.20	0.41
16:19:60:TRP:O	16:19:64:ILE:HG13	2.20	0.41
22:25:61:GLY:HA2	22:25:81:GLU:OXT	2.20	0.41
24:27:9:LYS:HE2	24:27:11:VAL:CG2	2.50	0.41
32:B:63:LYS:HD2	32:B:63:LYS:HA	1.86	0.41
32:B:202:ASN:ND2	32:B:208:ALA:HB2	2.31	0.41
35:E:108:GLY:H	53:A:9:G:H4'	1.85	0.41
47:Q:39:ARG:HG3	47:Q:39:ARG:HH11	1.85	0.41
53:A:6:G:O2'	53:A:298:A:H1'	2.20	0.41
54:01:78:U:H2'	54:01:79:C:C6	2.55	0.41
54:01:195:A:H2'	54:01:198:C:H41	1.84	0.41
54:01:1550:C:H2'	54:01:1551:A:C8	2.55	0.41
54:01:1686:C:H2'	54:01:1687:G:O4'	2.20	0.41
54:01:2114:A:O2'	54:01:2167:U:H5'	2.19	0.41
54:01:2819:G:H2'	54:01:2821:A:N7	2.35	0.41
56:X:1:C:H2'	56:X:2:G:H8	1.84	0.41
2:05:33:ARG:HH22	2:05:74:GLU:HB3	1.85	0.41
2:05:155:VAL:HG21	54:01:2618:G:H21	1.85	0.41
4:07:153:ILE:HD12	4:07:153:ILE:N	2.35	0.41
8:11:30:GLN:CB	8:11:60:VAL:HG21	2.50	0.41
10:13:71:ARG:HH11	10:13:77:ILE:HD11	1.85	0.41
11:14:93:ASN:C	11:14:95:LEU:H	2.29	0.41
27:30:27:LEU:HD12	27:30:37:HIS:O	2.21	0.41
32:B:153:MET:CE	32:B:157:PRO:HG3	2.43	0.41
33:C:112:ALA:HA	33:C:201:ILE:HD12	2.02	0.41
36:F:47:LEU:HD13	36:F:51:ILE:HG13	2.01	0.41
52:03:16:ASP:HB2	52:03:21:TYR:HE1	1.85	0.41
53:A:396:C:H2'	53:A:397:A:H5''	2.01	0.41
53:A:613:C:H2'	53:A:614:C:C6	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:107:G:H2'	54:01:108:G:C8	2.55	0.41
54:01:392:U:H2'	54:01:393:C:H6	1.85	0.41
54:01:946:C:H2'	54:01:947:A:H8	1.85	0.41
54:01:1074:G:H2'	54:01:1075:C:O4'	2.20	0.41
54:01:1548:A:H2'	54:01:1549:A:C8	2.55	0.41
54:01:1595:C:H2'	54:01:1596:A:H8	1.86	0.41
54:01:1720:U:H2'	54:01:1721:G:O4'	2.20	0.41
54:01:1796:U:H2'	54:01:1797:G:H8	1.85	0.41
54:01:2266:A:H4'	54:01:2267:A:N3	2.35	0.41
54:01:2305:U:H2'	54:01:2306:C:C6	2.55	0.41
54:01:2328:A:H2'	54:01:2329:U:C6	2.55	0.41
54:01:2684:U:H2'	54:01:2685:G:O4'	2.20	0.41
55:02:49:C:H2'	55:02:50:A:C8	2.55	0.41
55:02:88:C:C5'	55:02:89:U:OP1	2.67	0.41
3:06:148:ILE:HD13	3:06:187:VAL:HG11	2.02	0.41
4:07:40:GLY:HA2	4:07:84:ILE:CG1	2.50	0.41
4:07:97:GLU:HG2	26:29:25:ARG:HB2	2.02	0.41
9:12:35:ARG:HB2	9:12:54:ILE:HD11	2.02	0.41
10:13:3:GLN:HE21	54:01:1666:G:H1'	1.85	0.41
21:24:7:GLU:HB2	21:24:41:GLU:HB3	2.02	0.41
23:26:63:ILE:O	23:26:67:LEU:HD13	2.20	0.41
32:B:14:HIS:HB2	32:B:202:ASN:HB2	2.01	0.41
32:B:16:GLY:HA2	32:B:40:ILE:H	1.85	0.41
32:B:107:ARG:HA	32:B:110:ILE:HD12	2.02	0.41
33:C:150:VAL:HG12	33:C:199:VAL:HG23	2.01	0.41
33:C:176:THR:HG22	33:C:178:ARG:HG2	2.03	0.41
37:G:41:ILE:HG23	37:G:116:ALA:HA	2.02	0.41
41:K:118:ASN:O	53:A:716:A:H1'	2.20	0.41
49:S:35:ARG:NH1	49:S:74:ALA:HB3	2.35	0.41
53:A:225:C:H2'	53:A:226:G:O4'	2.20	0.41
53:A:459:A:H2'	53:A:460:A:C8	2.55	0.41
54:01:340:A:H2'	54:01:341:C:O4'	2.20	0.41
54:01:2055:C:H5'	54:01:2056:G:O5'	2.19	0.41
54:01:2564:A:OP1	54:01:2648:G:H4'	2.21	0.41
59:Z:32:THR:O	59:Z:36:ALA:N	2.53	0.41
59:Z:205:ALA:HB1	59:Z:208:LYS:HE3	2.02	0.41
59:Z:256:THR:C	59:Z:277:LEU:HD23	2.44	0.41
1:04:124:LYS:HB3	1:04:127:ASN:OD1	2.21	0.41
1:04:154:ALA:CB	1:04:161:VAL:HG23	2.48	0.41
8:11:103:ALA:O	8:11:107:GLU:HG3	2.20	0.41
10:13:76:VAL:H	15:18:72:VAL:CG2	2.28	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:14:29:LYS:HG2	11:14:30:THR:HG23	2.03	0.41
21:24:72:VAL:HA	21:24:94:ALA:H	1.84	0.41
31:34:4:ARG:HB3	54:01:2466:C:OP1	2.20	0.41
32:B:169:HIS:CE1	32:B:170:ILE:HG23	2.55	0.41
33:C:1:GLY:HA3	53:A:1060:U:C5	2.55	0.41
44:N:5:MET:HE3	44:N:62:ARG:NH2	2.35	0.41
44:N:9:GLU:O	44:N:13:VAL:HG23	2.21	0.41
47:Q:59:GLU:O	47:Q:74:LEU:HA	2.20	0.41
47:Q:61:ARG:HD2	47:Q:62:GLU:O	2.20	0.41
52:03:21:TYR:N	52:03:223:ALA:O	2.43	0.41
53:A:323:U:H2'	53:A:324:G:O4'	2.20	0.41
53:A:1084:G:H2'	53:A:1085:U:C5	2.56	0.41
53:A:1323:G:H2'	53:A:1324:A:C8	2.55	0.41
54:01:167:A:H2'	54:01:168:G:O4'	2.20	0.41
54:01:801:G:H3'	54:01:802:A:H5'	2.02	0.41
54:01:2206:C:H2'	54:01:2207:C:C6	2.55	0.41
54:01:2639:A:H2'	54:01:2640:G:O4'	2.20	0.41
54:01:2845:U:H2'	54:01:2846:G:C8	2.55	0.41
55:02:111:U:H2'	55:02:112:G:H8	1.85	0.41
56:X:9:G:H5''	56:X:11:A:N7	2.36	0.41
58:Y:45:U:H3'	58:Y:46:G:H5''	2.03	0.41
59:Z:215:GLU:OE2	59:Z:216:ASP:HB2	2.19	0.41
59:Z:328:PRO:HG2	59:Z:330:PHE:CE1	2.55	0.41
1:04:141:HIS:CD2	1:04:194:VAL:HG22	2.56	0.41
6:09:50:ARG:O	6:09:54:LEU:HB3	2.19	0.41
7:10:80:THR:O	7:10:82:ILE:HG12	2.20	0.41
9:12:118:MET:HA	9:12:121:LYS:HG2	2.01	0.41
11:14:95:LEU:HB3	11:14:100:ILE:CG1	2.50	0.41
13:16:100:CYS:HB3	27:30:42:ILE:HD11	2.02	0.41
17:20:14:VAL:HG23	17:20:18:GLN:NE2	2.36	0.41
23:26:48:LEU:HD21	23:26:77:TYR:HB2	2.03	0.41
27:30:24:VAL:HG22	27:30:26:SER:HB2	2.02	0.41
35:E:84:VAL:HG23	35:E:145:ASN:ND2	2.34	0.41
52:03:7:ARG:HE	54:01:2128:G:C4'	2.29	0.41
52:03:212:VAL:HG12	52:03:214:ILE:HG23	2.02	0.41
53:A:149:A:H1'	53:A:1446:A:C2	2.54	0.41
53:A:219:U:H2'	53:A:220:G:C8	2.56	0.41
53:A:1040:U:H2'	53:A:1041:G:H8	1.85	0.41
53:A:1326:U:O2'	53:A:1327:C:H5'	2.20	0.41
54:01:774:G:O2'	54:01:775:G:H5''	2.21	0.41
54:01:894:U:O2'	54:01:895:U:H5'	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:947:A:H2'	54:01:948:C:C6	2.56	0.41
54:01:1213:A:N6	54:01:1236:G:H1'	2.35	0.41
54:01:1399:C:H2'	54:01:1400:U:C6	2.55	0.41
54:01:1433:A:H2'	54:01:1434:A:O4'	2.21	0.41
55:02:104:A:H2'	55:02:105:G:O4'	2.21	0.41
58:Y:44:G:H1'	58:Y:45:U:C6	2.55	0.41
59:Z:96:ALA:HB2	59:Z:333:ARG:O	2.20	0.41
1:04:224:MET:SD	1:04:229:HIS:HB2	2.60	0.41
2:05:5:VAL:HG11	2:05:80:TRP:CZ3	2.55	0.41
7:10:33:VAL:HG12	7:10:34:THR:H	1.86	0.41
12:15:34:LYS:HA	12:15:101:VAL:HA	2.02	0.41
16:19:55:GLN:HA	16:19:58:GLN:HG2	2.02	0.41
18:21:43:ALA:O	18:21:47:VAL:HG12	2.20	0.41
23:26:11:PRO:HG3	23:26:30:PRO:HD2	2.03	0.41
27:30:9:ARG:O	27:30:13:GLY:N	2.54	0.41
32:B:202:ASN:ND2	32:B:205:ALA:HB3	2.34	0.41
34:D:94:GLU:HA	34:D:99:ASN:HD22	1.83	0.41
35:E:86:GLY:O	35:E:138:ALA:HB1	2.21	0.41
39:I:89:TYR:HB3	39:I:93:LEU:CD1	2.51	0.41
41:K:15:VAL:HG22	41:K:16:SER:N	2.35	0.41
41:K:126:ARG:NH2	53:A:796:C:H4'	2.35	0.41
46:P:59:HIS:O	46:P:63:GLN:HG2	2.19	0.41
47:Q:52:CYS:SG	47:Q:74:LEU:HD22	2.61	0.41
48:R:13:THR:HG21	48:R:20:ILE:HD11	2.02	0.41
52:03:16:ASP:HB2	52:03:21:TYR:CE1	2.55	0.41
53:A:443:C:H2'	53:A:444:G:C8	2.56	0.41
53:A:785:G:H2'	53:A:786:G:H8	1.86	0.41
53:A:785:G:O2'	53:A:786:G:H5'	2.20	0.41
53:A:994:A:C5	53:A:1216:A:H4'	2.56	0.41
53:A:1468:A:O2'	53:A:1469:C:H5'	2.20	0.41
53:A:1497:G:O2'	53:A:1498:U:H5'	2.21	0.41
54:01:999:U:O2'	54:01:1000:A:H5'	2.21	0.41
54:01:1435:G:O2'	54:01:1436:G:H5'	2.20	0.41
54:01:1672:A:C2	54:01:2582:G:H5'	2.55	0.41
54:01:1837:C:H2'	54:01:1899:A:N6	2.34	0.41
54:01:2555:U:H2'	54:01:2556:C:H5'	2.02	0.41
58:Y:24:G:H2'	58:Y:25:C:O4'	2.21	0.41
5:08:101:VAL:HG22	5:08:115:GLN:HG3	2.02	0.41
8:11:10:LEU:HD11	54:01:1070:A:C2	2.56	0.41
9:12:49:ASP:OD1	9:12:118:MET:HE2	2.21	0.41
13:16:38:LEU:HD11	13:16:42:LYS:HE2	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:19:113:LYS:O	16:19:117:ALA:N	2.54	0.41
21:24:23:ALA:O	21:24:25:LYS:HG3	2.20	0.41
36:F:48:ALA:HB1	48:R:68:PRO:HG3	2.02	0.41
36:F:69:GLU:HA	36:F:72:ASP:OD2	2.21	0.41
37:G:6:ILE:HD12	37:G:6:ILE:O	2.20	0.41
39:I:105:ARG:CZ	53:A:1117:A:H5''	2.51	0.41
41:K:90:PRO:HG2	41:K:91:GLY:H	1.84	0.41
42:L:14:LYS:HE3	53:A:562:U:H5	1.85	0.41
53:A:552:U:H2'	53:A:553:A:H8	1.85	0.41
53:A:1028:C:H2'	53:A:1029:U:O4'	2.20	0.41
53:A:1506:U:O2'	53:A:1507:A:H5'	2.20	0.41
54:01:464:U:H2'	54:01:465:G:O4'	2.21	0.41
54:01:948:C:H2'	54:01:949:G:C8	2.56	0.41
54:01:1739:A:H2'	54:01:1740:G:O4'	2.20	0.41
54:01:2093:G:H2'	54:01:2094:A:C8	2.55	0.41
54:01:2623:G:H2'	54:01:2624:G:C8	2.54	0.41
58:Y:61:C:H2'	58:Y:62:C:O4'	2.21	0.41
59:Z:28:THR:HG23	59:Z:78:HIS:CD2	2.56	0.41
3:06:23:PHE:CE1	3:06:28:VAL:HG21	2.56	0.41
8:11:38:CYS:O	8:11:41:PHE:HB3	2.20	0.41
9:12:101:ILE:O	9:12:105:VAL:HG23	2.20	0.41
11:14:77:ILE:N	11:14:77:ILE:HD12	2.35	0.41
13:16:3:HIS:O	13:16:4:ARG:HB2	2.21	0.41
16:19:91:ARG:NH1	54:01:997:G:H5''	2.31	0.41
27:30:39:ARG:HB3	27:30:40:HIS:ND1	2.36	0.41
28:31:7:LYS:HA	28:31:23:THR:HA	2.03	0.41
29:32:21:ARG:HH21	29:32:21:ARG:HG2	1.86	0.41
32:B:106:VAL:O	32:B:110:ILE:HG13	2.21	0.41
33:C:39:ARG:HH21	33:C:56:ILE:CG1	2.33	0.41
34:D:109:THR:HG21	53:A:408:A:OP1	2.21	0.41
43:M:89:ARG:HH21	43:M:95:PRO:HG2	1.85	0.41
45:O:80:LEU:O	45:O:84:LEU:HD13	2.20	0.41
47:Q:65:PRO:O	53:A:264:C:O2'	2.37	0.41
52:03:185:LEU:HD23	52:03:188:ASN:HD22	1.86	0.41
53:A:34:C:H2'	53:A:35:G:C8	2.56	0.41
53:A:536:C:H2'	53:A:537:G:C8	2.56	0.41
53:A:1211:U:H4'	53:A:1213:A:N3	2.36	0.41
53:A:1498:U:H6	53:A:1499:A:H62	1.69	0.41
54:01:193:U:H4'	54:01:803:U:C4'	2.51	0.41
54:01:270:A:N1	54:01:369:U:H4'	2.36	0.41
54:01:615:U:H5''	54:01:616:A:OP2	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:976:G:H2'	54:01:977:G:C8	2.55	0.41
54:01:1794:A:H2'	54:01:1795:C:H6	1.85	0.41
54:01:2417:C:H2'	54:01:2418:A:C8	2.56	0.41
54:01:2809:A:H2'	54:01:2810:A:C8	2.55	0.41
59:Z:305:GLU:HA	59:Z:359:VAL:HA	2.02	0.41
59:Z:312:SER:O	59:Z:317:GLY:N	2.51	0.41
4:07:109:ARG:HE	43:M:2:ARG:NH1	2.19	0.41
6:09:129:GLU:OE2	6:09:141:LYS:HB3	2.20	0.41
9:12:95:ARG:HG3	9:12:95:ARG:NH1	2.34	0.41
12:15:41:LEU:HG	12:15:96:ILE:HG13	2.02	0.41
12:15:66:ARG:HG3	12:15:66:ARG:NH1	2.35	0.41
16:19:93:ILE:HG23	17:20:13:ARG:HB2	2.03	0.41
17:20:81:LYS:HD2	54:01:973:A:H5'	2.03	0.41
18:21:24:ILE:HD11	18:21:74:ILE:CD1	2.51	0.41
22:25:39:THR:HG21	54:01:2336:A:H61	1.86	0.41
23:26:39:VAL:HG12	23:26:42:GLU:H	1.86	0.41
27:30:7:PRO:HG2	54:01:1264:A:H5'	2.02	0.41
29:32:3:ARG:HD3	29:32:4:THR:H	1.86	0.41
32:B:65:LYS:HB3	32:B:89:PHE:CE2	2.53	0.41
34:D:18:LEU:HD22	34:D:63:ILE:HG12	2.03	0.41
34:D:141:VAL:HA	34:D:180:THR:HA	2.03	0.41
35:E:160:VAL:HG22	35:E:161:GLU:N	2.36	0.41
38:H:5:PRO:O	38:H:8:ASP:HB3	2.21	0.41
38:H:9:MET:HG3	38:H:26:MET:SD	2.61	0.41
39:I:48:ARG:O	39:I:52:GLU:HG2	2.21	0.41
43:M:58:GLU:OE2	43:M:61:LYS:HD2	2.20	0.41
52:03:176:GLY:HA3	52:03:180:PHE:CD2	2.56	0.41
53:A:320:A:H2'	53:A:321:A:C8	2.56	0.41
53:A:750:C:H2'	53:A:751:U:C6	2.55	0.41
53:A:981:U:H2'	53:A:982:U:C5	2.56	0.41
53:A:1390:U:H2'	53:A:1391:U:C6	2.55	0.41
54:01:534:U:H2'	54:01:535:G:C8	2.56	0.41
54:01:534:U:H2'	54:01:535:G:H8	1.85	0.41
54:01:662:G:O2'	54:01:663:G:H5'	2.21	0.41
54:01:744:U:H2'	54:01:745:G:O4'	2.21	0.41
54:01:1544:A:H2'	54:01:1545:A:C8	2.56	0.41
54:01:1596:A:H2'	54:01:1597:A:O4'	2.21	0.41
54:01:1605:C:H2'	54:01:1606:C:O4'	2.20	0.41
54:01:1911:U:H2'	54:01:1918:A:N1	2.36	0.41
54:01:2318:G:H2'	54:01:2319:G:O4'	2.20	0.41
54:01:2396:G:H2'	54:01:2397:G:H8	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2687:U:H2'	54:01:2688:G:O4'	2.21	0.41
59:Z:102:ILE:CG2	59:Z:191:LEU:HD11	2.51	0.41
6:09:4:ILE:HB	6:09:39:ALA:HB2	2.03	0.41
6:09:57:LYS:HA	6:09:60:GLU:HB2	2.03	0.41
7:10:96:PHE:CE2	7:10:126:LEU:HB2	2.56	0.41
7:10:118:ILE:H	7:10:119:PRO:HD2	1.86	0.41
13:16:35:LYS:HD2	13:16:112:TYR:CE1	2.56	0.41
19:22:15:HIS:CE1	19:22:17:SER:HB3	2.56	0.41
20:23:15:GLY:C	54:01:309:A:H4'	2.46	0.41
35:E:151:MET:O	35:E:155:LYS:HG3	2.21	0.41
38:H:21:LYS:O	38:H:62:LEU:HD12	2.21	0.41
40:J:26:VAL:O	40:J:30:LYS:N	2.45	0.41
50:T:70:LYS:HE2	53:A:261:U:OP2	2.20	0.41
52:03:59:VAL:O	52:03:164:ARG:HA	2.21	0.41
53:A:463:U:H2'	53:A:464:U:O4'	2.21	0.41
53:A:858:G:O6	53:A:869:G:H3'	2.21	0.41
53:A:956:U:H2'	53:A:957:U:O4'	2.21	0.41
54:01:1001:A:H2'	54:01:1002:G:O4'	2.21	0.41
54:01:1732:C:O2'	54:01:1733:G:H5'	2.21	0.41
54:01:2047:C:H2'	54:01:2048:G:H8	1.85	0.41
59:Z:61:THR:HB	59:Z:82:PRO:HB3	2.02	0.41
1:04:86:ARG:HH12	1:04:155:ARG:HH21	1.69	0.40
3:06:131:THR:HG22	3:06:160:ALA:O	2.21	0.40
4:07:109:ARG:HE	43:M:2:ARG:CZ	2.34	0.40
5:08:122:ALA:HA	5:08:132:LEU:HA	2.03	0.40
6:09:54:LEU:O	6:09:58:LEU:HG	2.21	0.40
6:09:97:ARG:HG2	6:09:112:LYS:HD3	2.03	0.40
18:21:75:PHE:CD1	18:21:75:PHE:N	2.89	0.40
24:27:34:SER:OG	24:27:36:GLN:HG3	2.21	0.40
26:29:9:TYR:CE1	26:29:26:SER:HA	2.55	0.40
26:29:14:ALA:HB2	26:29:24:ILE:HG12	2.03	0.40
33:C:49:ALA:HB1	33:C:75:VAL:HG22	2.03	0.40
35:E:156:ARG:HH12	38:H:100:ILE:HG23	1.87	0.40
40:J:28:THR:CG2	40:J:86:ALA:HB1	2.51	0.40
46:P:67:ILE:HD12	46:P:67:ILE:N	2.33	0.40
53:A:938:A:C2	53:A:1376:U:H1'	2.56	0.40
53:A:982:U:H4'	53:A:983:A:O5'	2.21	0.40
53:A:1347:G:C2'	53:A:1348:U:OP2	2.69	0.40
53:A:1366:C:H2'	53:A:1367:C:C6	2.56	0.40
54:01:1086:A:N3	54:01:1086:A:H3'	2.36	0.40
54:01:1102:C:H2'	54:01:1103:A:O4'	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2144:G:H1'	54:01:2147:A:N6	2.37	0.40
54:01:2238:G:N3	54:01:2238:G:H2'	2.36	0.40
54:01:2640:G:H2'	54:01:2641:G:H8	1.86	0.40
59:Z:212:LEU:HD21	59:Z:229:GLY:CA	2.50	0.40
16:19:64:ILE:HD13	16:19:94:LEU:HD22	2.01	0.40
31:34:17:VAL:HG12	31:34:19:ARG:HG3	2.03	0.40
40:J:83:THR:O	40:J:87:LEU:HG	2.20	0.40
41:K:86:LYS:HZ2	41:K:114:PRO:HD3	1.85	0.40
49:S:57:VAL:O	49:S:57:VAL:HG13	2.21	0.40
53:A:317:U:H2'	53:A:318:G:C8	2.56	0.40
53:A:372:C:N4	53:A:387:U:H2'	2.35	0.40
53:A:495:A:H4'	53:A:496:A:OP1	2.20	0.40
53:A:505:G:H4'	53:A:534:U:C4	2.57	0.40
53:A:620:C:H2'	53:A:621:A:O4'	2.21	0.40
53:A:715:A:H2'	53:A:716:A:H8	1.82	0.40
53:A:920:U:H2'	53:A:921:U:C6	2.56	0.40
54:01:174:U:H2'	54:01:175:G:C8	2.56	0.40
54:01:1318:U:H2'	54:01:1319:C:H6	1.86	0.40
54:01:1636:U:H2'	54:01:1637:A:C8	2.54	0.40
54:01:1637:A:H5'	54:01:1760:C:O2'	2.21	0.40
54:01:2693:G:O2'	54:01:2694:G:H5'	2.21	0.40
55:02:97:C:H2'	55:02:98:G:O4'	2.20	0.40
56:X:28:C:H2'	56:X:29:G:H8	1.86	0.40
56:W:9:G:N3	56:W:45:G:H2'	2.36	0.40
58:Y:21:A:H3'	58:Y:46:G:O6	2.21	0.40
59:Z:265:LEU:HD21	59:Z:268:GLY:HA2	2.03	0.40
1:04:153:LEU:HD11	1:04:181:ARG:HH21	1.83	0.40
2:05:23:PRO:HG2	54:01:2728:U:O2'	2.21	0.40
4:07:173:ASP:O	4:07:174:PHE:C	2.65	0.40
6:09:9:VAL:HG12	6:09:11:ASN:H	1.86	0.40
8:11:86:LYS:HD3	8:11:86:LYS:N	2.37	0.40
10:13:87:LEU:HB3	10:13:92:GLU:O	2.21	0.40
12:15:50:ARG:HG2	12:15:50:ARG:NH2	2.35	0.40
18:21:74:ILE:HG23	18:21:74:ILE:O	2.21	0.40
24:27:17:GLU:HB2	24:27:53:VAL:HG11	2.03	0.40
33:C:4:VAL:HB	53:A:1190:G:OP2	2.21	0.40
37:G:26:VAL:HG13	37:G:42:VAL:HG21	2.03	0.40
43:M:89:ARG:NH2	43:M:94:LEU:HB3	2.37	0.40
47:Q:17:GLU:OE1	53:A:273:U:H1'	2.22	0.40
52:03:48:LEU:HD11	52:03:59:VAL:HG11	2.04	0.40
53:A:202:G:H2'	53:A:203:G:C8	2.57	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:666:G:H2'	53:A:667:G:H8	1.85	0.40
53:A:1019:A:H2'	53:A:1020:G:O4'	2.22	0.40
53:A:1105:A:H2'	53:A:1106:G:H8	1.86	0.40
53:A:1386:G:H2'	53:A:1387:G:C8	2.54	0.40
54:01:493:G:O2'	54:01:494:G:H5'	2.21	0.40
54:01:543:G:H2'	54:01:544:C:O4'	2.21	0.40
54:01:567:U:H2'	54:01:568:U:O4'	2.21	0.40
54:01:820:A:H2'	54:01:821:A:C8	2.56	0.40
54:01:864:G:H2'	54:01:865:C:C6	2.56	0.40
54:01:1443:U:H2'	54:01:1444:G:H8	1.83	0.40
54:01:1563:U:H2'	54:01:1564:C:C6	2.57	0.40
1:04:239:PHE:HE2	54:01:1902:C:H5''	1.87	0.40
6:09:40:THR:HG22	6:09:41:LYS:H	1.86	0.40
7:10:25:ALA:HB3	7:10:99:PHE:CE2	2.57	0.40
9:12:34:ARG:NH2	16:19:69:ARG:HD2	2.37	0.40
11:14:100:ILE:HG13	11:14:101:ILE:HG23	2.02	0.40
16:19:16:ILE:HG23	16:19:38:VAL:HG21	2.03	0.40
17:20:41:ILE:HD12	17:20:54:VAL:HG11	2.04	0.40
36:F:47:LEU:HD21	36:F:57:ALA:CB	2.51	0.40
39:I:53:LEU:HD21	39:I:100:ALA:HB2	2.03	0.40
39:I:105:ARG:HD3	39:I:105:ARG:O	2.21	0.40
40:J:53:ILE:HG12	53:A:1060:U:C5'	2.47	0.40
42:L:113:ARG:NH2	42:L:120:ARG:HG3	2.36	0.40
47:Q:28:VAL:HG22	47:Q:29:LYS:N	2.35	0.40
50:T:42:ASP:CB	50:T:45:ALA:HB3	2.51	0.40
52:03:60:ARG:CB	52:03:141:LYS:HG3	2.48	0.40
54:01:1045:C:H5'	54:01:1046:A:C5'	2.51	0.40
54:01:1396:U:H5''	54:01:1397:U:OP2	2.21	0.40
54:01:1427:A:H4'	54:01:1428:C:O4'	2.21	0.40
54:01:1473:G:H2'	54:01:1474:U:O4'	2.22	0.40
54:01:1635:A:H2'	54:01:1636:U:O4'	2.21	0.40
54:01:2052:A:H2'	54:01:2053:G:H8	1.87	0.40
54:01:2113:U:O5'	54:01:2113:U:H6	2.04	0.40
58:Y:8:U:H5'	58:Y:49:C:OP2	2.21	0.40
59:Z:321:PRO:CG	59:Z:349:MET:HE2	2.49	0.40
2:05:51:THR:OG1	2:05:76:GLY:HA3	2.22	0.40
2:05:61:THR:HB	2:05:63:PRO:HD2	2.03	0.40
2:05:82:PHE:HE1	2:05:202:ILE:HG23	1.86	0.40
3:06:40:ARG:NH2	54:01:1246:A:H4'	2.33	0.40
3:06:46:GLN:HB3	3:06:83:VAL:HG11	2.03	0.40
4:07:37:MET:HB3	4:07:86:CYS:SG	2.61	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:09:40:THR:H	6:09:43:ASN:HB2	1.87	0.40
7:10:118:ILE:H	7:10:119:PRO:CD	2.34	0.40
8:11:52:LEU:O	8:11:54:ILE:HG13	2.22	0.40
14:17:11:ALA:HB2	14:17:96:GLY:N	2.36	0.40
33:C:119:ILE:O	33:C:123:LEU:HG	2.21	0.40
43:M:97:ARG:HG2	43:M:97:ARG:NH1	2.37	0.40
43:M:113:LYS:H	43:M:114:PRO:HD2	1.85	0.40
50:T:20:ASN:HD21	50:T:65:LEU:CD1	2.34	0.40
52:03:79:THR:HB	52:03:80:GLN:H	1.76	0.40
53:A:243:A:H62	53:A:281:G:H1'	1.86	0.40
53:A:247:G:O2'	53:A:248:C:H5'	2.21	0.40
53:A:432:A:H2'	53:A:433:G:O4'	2.21	0.40
53:A:1278:G:OP1	53:A:1279:G:H5'	2.21	0.40
54:01:277:G:H1'	54:01:361:G:O6	2.21	0.40
54:01:517:C:H2'	54:01:518:G:O4'	2.21	0.40
54:01:1766:G:H2'	54:01:1767:G:H8	1.86	0.40
54:01:2086:U:H2'	54:01:2087:G:H8	1.84	0.40
54:01:2112:G:H2'	54:01:2113:U:H5'	2.03	0.40
54:01:2222:C:H2'	54:01:2223:G:O4'	2.22	0.40
54:01:2732:G:O2'	54:01:2733:A:H5'	2.22	0.40
56:W:62:C:H2'	56:W:63:G:C8	2.56	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	04	269/271 (99%)	241 (90%)	26 (10%)	2 (1%)	18	53
2	05	207/209 (99%)	185 (89%)	21 (10%)	1 (0%)	24	59
3	06	199/201 (99%)	174 (87%)	24 (12%)	1 (0%)	24	59
4	07	175/177 (99%)	155 (89%)	16 (9%)	4 (2%)	5	30

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	08	174/176 (99%)	157 (90%)	12 (7%)	5 (3%)	3	26
6	09	147/149 (99%)	124 (84%)	21 (14%)	2 (1%)	9	38
7	10	129/131 (98%)	95 (74%)	27 (21%)	7 (5%)	1	17
8	11	139/141 (99%)	111 (80%)	27 (19%)	1 (1%)	18	53
9	12	140/142 (99%)	130 (93%)	10 (7%)	0	100	100
10	13	120/122 (98%)	100 (83%)	18 (15%)	2 (2%)	7	35
11	14	141/143 (99%)	116 (82%)	21 (15%)	4 (3%)	4	27
12	15	134/136 (98%)	122 (91%)	10 (8%)	2 (2%)	8	37
13	16	118/120 (98%)	103 (87%)	15 (13%)	0	100	100
14	17	114/116 (98%)	105 (92%)	9 (8%)	0	100	100
15	18	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
16	19	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
17	20	101/103 (98%)	82 (81%)	18 (18%)	1 (1%)	12	45
18	21	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
19	22	91/93 (98%)	80 (88%)	10 (11%)	1 (1%)	11	43
20	23	100/102 (98%)	84 (84%)	13 (13%)	3 (3%)	3	26
21	24	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
22	25	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
23	26	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	27	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
25	28	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
26	29	64/66 (97%)	50 (78%)	14 (22%)	0	100	100
27	30	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
28	31	48/50 (96%)	41 (85%)	7 (15%)	0	100	100
29	32	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
30	33	62/64 (97%)	56 (90%)	4 (6%)	2 (3%)	3	25
31	34	36/38 (95%)	28 (78%)	6 (17%)	2 (6%)	1	16
32	B	216/218 (99%)	173 (80%)	40 (18%)	3 (1%)	9	38
33	C	204/206 (99%)	188 (92%)	16 (8%)	0	100	100
34	D	203/205 (99%)	174 (86%)	23 (11%)	6 (3%)	3	26
35	E	155/157 (99%)	119 (77%)	27 (17%)	9 (6%)	1	16

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	F	98/100 (98%)	73 (74%)	21 (21%)	4 (4%)	2	20
37	G	149/151 (99%)	127 (85%)	20 (13%)	2 (1%)	9	40
38	H	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	50
39	I	125/127 (98%)	103 (82%)	16 (13%)	6 (5%)	2	18
40	J	96/98 (98%)	78 (81%)	10 (10%)	8 (8%)	0	10
41	K	114/116 (98%)	95 (83%)	14 (12%)	5 (4%)	2	20
42	L	121/123 (98%)	93 (77%)	19 (16%)	9 (7%)	1	12
43	M	112/114 (98%)	95 (85%)	14 (12%)	3 (3%)	4	28
44	N	98/100 (98%)	83 (85%)	15 (15%)	0	100	100
45	O	86/88 (98%)	80 (93%)	4 (5%)	2 (2%)	5	30
46	P	80/82 (98%)	68 (85%)	11 (14%)	1 (1%)	9	40
47	Q	78/80 (98%)	66 (85%)	9 (12%)	3 (4%)	2	21
48	R	63/65 (97%)	56 (89%)	5 (8%)	2 (3%)	3	25
49	S	77/79 (98%)	65 (84%)	10 (13%)	2 (3%)	4	28
50	T	83/85 (98%)	79 (95%)	3 (4%)	1 (1%)	10	41
51	U	63/65 (97%)	43 (68%)	19 (30%)	1 (2%)	7	36
52	03	221/223 (99%)	193 (87%)	27 (12%)	1 (0%)	24	59
59	Z	390/392 (100%)	349 (90%)	39 (10%)	2 (0%)	24	59
All	All	6457/6563 (98%)	5581 (86%)	765 (12%)	111 (2%)	9	35

All (111) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	04	232	GLY
3	06	83	VAL
4	07	175	PRO
5	08	46	ASP
5	08	119	GLY
6	09	9	VAL
7	10	80	THR
10	13	35	VAL
12	15	58	LYS
17	20	54	VAL
20	23	6	ARG
20	23	98	ASN
31	34	37	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
35	E	25	LYS
35	E	122	VAL
35	E	160	VAL
36	F	53	LYS
36	F	54	LEU
36	F	94	HIS
38	H	47	ASP
39	I	57	VAL
39	I	90	ASP
39	I	91	GLU
40	J	34	ALA
40	J	58	ASN
40	J	89	ARG
40	J	92	LEU
42	L	102	ASP
43	M	65	GLU
45	O	46	LYS
47	Q	49	ASN
48	R	19	GLU
51	U	8	ASN
4	07	149	ARG
5	08	45	ALA
5	08	175	LYS
6	09	12	LEU
7	10	81	LEU
11	14	31	GLY
30	33	27	ASN
32	B	87	ASP
35	E	11	GLN
35	E	89	THR
35	E	157	GLY
39	I	102	PHE
41	K	89	GLY
42	L	23	LEU
42	L	35	ARG
42	L	77	SER
46	P	79	ASN
47	Q	70	LYS
48	R	18	GLN
50	T	68	LYS
52	03	21	TYR
59	Z	295	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	10	4	ASN
10	13	93	GLN
11	14	29	LYS
19	22	38	ALA
34	D	23	GLY
34	D	29	THR
34	D	167	PRO
34	D	192	ALA
37	G	64	ALA
39	I	12	LYS
40	J	35	GLN
40	J	93	ALA
41	K	125	LYS
42	L	32	VAL
42	L	75	GLU
43	M	4	ALA
47	Q	17	GLU
59	Z	42	ALA
1	04	233	GLY
4	07	20	ASN
4	07	174	PHE
30	33	31	ILE
31	34	34	LYS
34	D	152	SER
35	E	78	GLY
35	E	90	GLY
35	E	121	ASN
39	I	8	THR
41	K	13	LYS
42	L	34	THR
45	O	2	LEU
7	10	51	TYR
7	10	108	VAL
7	10	118	ILE
11	14	52	GLY
11	14	88	GLY
20	23	51	LEU
32	B	18	GLN
32	B	19	THR
34	D	120	LYS
36	F	93	LYS
37	G	18	GLY

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
42	L	43	LYS
49	S	3	SER
7	10	74	ASP
40	J	42	LEU
40	J	43	PRO
5	08	117	PRO
8	11	4	VAL
41	K	90	PRO
41	K	77	GLY
42	L	27	PRO
43	M	111	PRO
49	S	7	GLY
2	05	153	GLY
12	15	69	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	04	216/216 (100%)	213 (99%)	3 (1%)	59	71
2	05	164/164 (100%)	164 (100%)	0	100	100
3	06	165/165 (100%)	165 (100%)	0	100	100
4	07	148/148 (100%)	147 (99%)	1 (1%)	76	78
5	08	137/137 (100%)	136 (99%)	1 (1%)	76	78
6	09	114/114 (100%)	114 (100%)	0	100	100
7	10	100/100 (100%)	97 (97%)	3 (3%)	36	57
8	11	109/109 (100%)	108 (99%)	1 (1%)	70	75
9	12	116/116 (100%)	116 (100%)	0	100	100
10	13	103/103 (100%)	102 (99%)	1 (1%)	68	75
11	14	102/102 (100%)	100 (98%)	2 (2%)	48	65
12	15	109/109 (100%)	109 (100%)	0	100	100
13	16	100/100 (100%)	99 (99%)	1 (1%)	68	75

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	17	86/86 (100%)	86 (100%)	0	100	100
15	18	99/99 (100%)	99 (100%)	0	100	100
16	19	89/89 (100%)	88 (99%)	1 (1%)	65	74
17	20	84/84 (100%)	82 (98%)	2 (2%)	43	63
18	21	93/93 (100%)	92 (99%)	1 (1%)	65	74
19	22	80/80 (100%)	78 (98%)	2 (2%)	42	62
20	23	83/83 (100%)	83 (100%)	0	100	100
21	24	78/78 (100%)	78 (100%)	0	100	100
22	25	57/57 (100%)	57 (100%)	0	100	100
23	26	67/67 (100%)	67 (100%)	0	100	100
24	27	55/55 (100%)	53 (96%)	2 (4%)	31	54
25	28	48/48 (100%)	48 (100%)	0	100	100
26	29	59/59 (100%)	59 (100%)	0	100	100
27	30	47/47 (100%)	47 (100%)	0	100	100
28	31	45/45 (100%)	45 (100%)	0	100	100
29	32	38/38 (100%)	38 (100%)	0	100	100
30	33	51/51 (100%)	51 (100%)	0	100	100
31	34	34/34 (100%)	34 (100%)	0	100	100
32	B	180/180 (100%)	179 (99%)	1 (1%)	78	80
33	C	170/170 (100%)	168 (99%)	2 (1%)	63	72
34	D	172/172 (100%)	170 (99%)	2 (1%)	63	72
35	E	119/119 (100%)	118 (99%)	1 (1%)	73	77
36	F	87/87 (100%)	87 (100%)	0	100	100
37	G	124/124 (100%)	124 (100%)	0	100	100
38	H	104/104 (100%)	103 (99%)	1 (1%)	68	75
39	I	105/105 (100%)	105 (100%)	0	100	100
40	J	86/86 (100%)	85 (99%)	1 (1%)	63	72
41	K	89/89 (100%)	89 (100%)	0	100	100
42	L	103/103 (100%)	101 (98%)	2 (2%)	50	66
43	M	92/92 (100%)	90 (98%)	2 (2%)	45	64
44	N	83/83 (100%)	83 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	O	76/76 (100%)	76 (100%)	0	100	100
46	P	65/65 (100%)	63 (97%)	2 (3%)	35	57
47	Q	74/74 (100%)	74 (100%)	0	100	100
48	R	56/56 (100%)	56 (100%)	0	100	100
49	S	70/70 (100%)	69 (99%)	1 (1%)	59	71
50	T	65/65 (100%)	63 (97%)	2 (3%)	35	57
51	U	55/55 (100%)	54 (98%)	1 (2%)	51	67
52	03	174/174 (100%)	172 (99%)	2 (1%)	65	74
59	Z	324/325 (100%)	318 (98%)	6 (2%)	50	66
All	All	5349/5350 (100%)	5302 (99%)	47 (1%)	68	75

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	04	34	GLU
1	04	132	ARG
1	04	252	LYS
4	07	151	LEU
5	08	109	SER
7	10	3	LEU
7	10	43	LYS
7	10	118	ILE
8	11	95	ASP
10	13	58	LEU
11	14	96	LYS
11	14	110	VAL
13	16	2	ARG
16	19	94	LEU
17	20	11	GLN
17	20	22	LEU
18	21	57	ASN
19	22	52	GLU
19	22	59	ASN
24	27	7	ARG
24	27	29	ARG
32	B	18	GLN
33	C	24	ASN
33	C	156	LEU
34	D	28	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	D	170	LEU
35	E	89	THR
38	H	49	LYS
40	J	30	LYS
42	L	34	THR
42	L	113	ARG
43	M	15	VAL
43	M	111	PRO
46	P	19	VAL
46	P	69	ASP
49	S	10	ILE
50	T	29	THR
50	T	53	MET
51	U	58	LYS
52	03	21	TYR
52	03	202	THR
59	Z	196	ASP
59	Z	245	VAL
59	Z	311	LEU
59	Z	322	PHE
59	Z	358	MET
59	Z	359	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (109) such sidechains are listed below:

Mol	Chain	Res	Type
1	04	45	ASN
1	04	59	GLN
1	04	85	ASN
1	04	114	GLN
1	04	142	ASN
1	04	162	GLN
1	04	196	ASN
1	04	238	ASN
2	05	49	GLN
3	06	41	GLN
3	06	92	HIS
3	06	94	GLN
3	06	163	ASN
3	06	165	HIS
3	06	195	GLN
4	07	51	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	07	80	GLN
5	08	21	GLN
5	08	29	ASN
5	08	37	ASN
5	08	138	GLN
6	09	66	ASN
6	09	73	ASN
8	11	18	ASN
8	11	30	GLN
8	11	42	ASN
9	12	40	HIS
9	12	76	HIS
10	13	3	GLN
11	14	38	GLN
12	15	13	HIS
13	16	9	GLN
13	16	23	ASN
13	16	62	ASN
14	17	19	GLN
15	18	9	GLN
16	19	36	GLN
16	19	43	GLN
17	20	18	GLN
18	21	9	HIS
18	21	57	ASN
20	23	39	ASN
20	23	68	ASN
21	24	87	GLN
23	26	16	ASN
23	26	19	HIS
24	27	20	ASN
24	27	41	HIS
25	28	19	HIS
26	29	20	ASN
26	29	33	ASN
26	29	48	GLN
26	29	65	ASN
27	30	4	GLN
27	30	41	HIS
29	32	16	HIS
31	34	35	GLN
32	B	23	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B	38	HIS
32	B	41	ASN
32	B	169	HIS
33	C	24	ASN
33	C	31	ASN
33	C	40	GLN
33	C	139	ASN
33	C	189	HIS
34	D	39	GLN
34	D	88	ASN
34	D	197	HIS
35	E	69	ASN
35	E	145	ASN
36	F	11	HIS
36	F	17	GLN
36	F	37	HIS
36	F	55	HIS
36	F	58	HIS
36	F	68	GLN
37	G	27	ASN
38	H	17	GLN
39	I	36	GLN
39	I	49	GLN
39	I	125	GLN
40	J	20	GLN
40	J	58	ASN
42	L	45	ASN
42	L	95	HIS
44	N	42	ASN
44	N	59	GLN
45	O	36	ASN
46	P	9	HIS
46	P	26	ASN
47	Q	8	GLN
47	Q	30	HIS
48	R	30	ASN
48	R	53	GLN
49	S	55	GLN
49	S	56	HIS
49	S	68	HIS
50	T	20	ASN
50	T	60	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	03	47	ASN
52	03	67	HIS
52	03	148	ASN
52	03	165	ASN
52	03	188	ASN
59	Z	48	GLN
59	Z	97	GLN
59	Z	290	GLN
59	Z	329	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	A	1538/1539 (99%)	161 (10%)	10 (0%)
54	01	2902/2903 (99%)	355 (12%)	12 (0%)
55	02	119/120 (99%)	9 (7%)	1 (0%)
56	W	76/77 (98%)	7 (9%)	0
56	X	76/77 (98%)	11 (14%)	0
57	V	19/20 (95%)	2 (10%)	0
58	Y	75/76 (98%)	12 (16%)	0
All	All	4805/4812 (99%)	557 (11%)	23 (0%)

All (557) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	A	6	G
53	A	7	A
53	A	9	G
53	A	22	G
53	A	31	G
53	A	32	A
53	A	39	G
53	A	51	A
53	A	71	A
53	A	82	G
53	A	86	G
53	A	87	C
53	A	94	G
53	A	95	C
53	A	100	G
53	A	121	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	A	130	A
53	A	183	C
53	A	184	G
53	A	197	A
53	A	209	U
53	A	210	C
53	A	226	G
53	A	240	G
53	A	247	G
53	A	251	G
53	A	253	A
53	A	266	G
53	A	267	C
53	A	281	G
53	A	289	G
53	A	306	A
53	A	328	C
53	A	345	C
53	A	346	G
53	A	352	C
53	A	367	U
53	A	372	C
53	A	398	U
53	A	411	A
53	A	413	G
53	A	422	C
53	A	429	U
53	A	467	U
53	A	485	U
53	A	486	U
53	A	496	A
53	A	497	G
53	A	518	C
53	A	530	G
53	A	531	U
53	A	532	A
53	A	533	A
53	A	547	A
53	A	561	U
53	A	572	A
53	A	573	A
53	A	574	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	A	575	G
53	A	576	C
53	A	577	G
53	A	607	A
53	A	633	G
53	A	642	A
53	A	665	A
53	A	688	G
53	A	703	G
53	A	713	G
53	A	724	G
53	A	731	G
53	A	755	G
53	A	777	A
53	A	794	A
53	A	805	C
53	A	815	A
53	A	817	C
53	A	818	G
53	A	819	A
53	A	820	U
53	A	821	G
53	A	832	G
53	A	842	U
53	A	843	U
53	A	844	G
53	A	846	G
53	A	873	A
53	A	890	G
53	A	902	G
53	A	926	G
53	A	934	C
53	A	935	A
53	A	960	U
53	A	961	U
53	A	966	G
53	A	969	A
53	A	975	A
53	A	976	G
53	A	977	A
53	A	992	U
53	A	993	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	A	994	A
53	A	1004	A
53	A	1028	C
53	A	1030	U
53	A	1031	C
53	A	1033	G
53	A	1034	G
53	A	1053	G
53	A	1054	C
53	A	1094	G
53	A	1101	A
53	A	1129	C
53	A	1130	A
53	A	1137	C
53	A	1138	G
53	A	1139	G
53	A	1159	U
53	A	1168	U
53	A	1182	G
53	A	1184	G
53	A	1191	A
53	A	1196	A
53	A	1197	A
53	A	1201	A
53	A	1202	U
53	A	1207	G
53	A	1213	A
53	A	1225	A
53	A	1238	A
53	A	1241	G
53	A	1256	A
53	A	1258	G
53	A	1260	G
53	A	1278	G
53	A	1280	A
53	A	1282	C
53	A	1286	U
53	A	1287	A
53	A	1300	G
53	A	1302	C
53	A	1317	C
53	A	1346	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	A	1347	G
53	A	1348	U
53	A	1378	C
53	A	1395	C
53	A	1400	C
53	A	1446	A
53	A	1448	C
53	A	1451	U
53	A	1452	C
53	A	1492	A
53	A	1499	A
53	A	1503	A
53	A	1505	G
53	A	1506	U
53	A	1517	G
53	A	1519	A
53	A	1529	G
53	A	1530	G
53	A	1534	A
54	01	10	A
54	01	12	U
54	01	34	U
54	01	35	G
54	01	46	G
54	01	51	G
54	01	63	A
54	01	71	A
54	01	74	A
54	01	75	G
54	01	119	A
54	01	120	U
54	01	139	U
54	01	140	C
54	01	141	G
54	01	142	A
54	01	162	U
54	01	163	C
54	01	181	A
54	01	196	A
54	01	216	A
54	01	221	A
54	01	222	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	228	C
54	01	242	G
54	01	243	U
54	01	248	G
54	01	249	C
54	01	255	A
54	01	266	G
54	01	276	U
54	01	278	A
54	01	281	C
54	01	294	A
54	01	301	G
54	01	311	A
54	01	323	C
54	01	324	A
54	01	329	G
54	01	330	A
54	01	361	G
54	01	363	G
54	01	367	G
54	01	371	A
54	01	372	G
54	01	373	U
54	01	386	G
54	01	387	U
54	01	388	G
54	01	404	A
54	01	406	G
54	01	411	G
54	01	422	A
54	01	424	G
54	01	451	U
54	01	457	A
54	01	481	G
54	01	491	G
54	01	504	A
54	01	505	A
54	01	506	G
54	01	508	A
54	01	509	C
54	01	529	A
54	01	531	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	532	A
54	01	542	C
54	01	543	G
54	01	545	U
54	01	547	A
54	01	563	A
54	01	573	U
54	01	588	U
54	01	603	A
54	01	614	A
54	01	616	A
54	01	627	A
54	01	637	A
54	01	646	U
54	01	654	A
54	01	669	G
54	01	686	U
54	01	687	C
54	01	695	G
54	01	730	A
54	01	747	C
54	01	752	A
54	01	764	A
54	01	775	G
54	01	776	G
54	01	782	A
54	01	784	G
54	01	785	G
54	01	805	G
54	01	812	C
54	01	819	A
54	01	827	U
54	01	828	U
54	01	830	G
54	01	845	A
54	01	846	U
54	01	847	U
54	01	858	G
54	01	859	G
54	01	860	U
54	01	878	A
54	01	885	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	886	A
54	01	888	C
54	01	891	G
54	01	896	A
54	01	910	A
54	01	932	U
54	01	941	A
54	01	946	C
54	01	961	C
54	01	974	G
54	01	975	A
54	01	983	A
54	01	985	C
54	01	995	C
54	01	996	A
54	01	1012	U
54	01	1013	C
54	01	1021	A
54	01	1022	G
54	01	1026	G
54	01	1033	U
54	01	1045	C
54	01	1046	A
54	01	1054	A
54	01	1059	G
54	01	1060	U
54	01	1062	G
54	01	1065	U
54	01	1066	U
54	01	1070	A
54	01	1071	G
54	01	1075	C
54	01	1079	C
54	01	1084	A
54	01	1088	A
54	01	1103	A
54	01	1104	C
54	01	1106	G
54	01	1111	A
54	01	1131	G
54	01	1132	U
54	01	1133	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	1135	C
54	01	1157	G
54	01	1174	U
54	01	1175	A
54	01	1177	G
54	01	1180	U
54	01	1212	G
54	01	1238	G
54	01	1248	G
54	01	1251	C
54	01	1253	A
54	01	1256	G
54	01	1271	G
54	01	1272	A
54	01	1273	U
54	01	1301	A
54	01	1302	A
54	01	1306	C
54	01	1321	A
54	01	1329	U
54	01	1332	G
54	01	1345	C
54	01	1365	A
54	01	1378	A
54	01	1379	U
54	01	1383	A
54	01	1395	A
54	01	1416	G
54	01	1419	A
54	01	1420	A
54	01	1428	C
54	01	1454	C
54	01	1461	C
54	01	1482	G
54	01	1490	A
54	01	1491	G
54	01	1498	C
54	01	1515	A
54	01	1524	G
54	01	1533	C
54	01	1535	A
54	01	1536	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	1555	G
54	01	1559	U
54	01	1560	G
54	01	1569	A
54	01	1581	G
54	01	1584	U
54	01	1585	C
54	01	1608	A
54	01	1611	C
54	01	1616	A
54	01	1634	A
54	01	1647	U
54	01	1648	U
54	01	1651	G
54	01	1674	G
54	01	1694	C
54	01	1715	G
54	01	1729	U
54	01	1730	C
54	01	1732	C
54	01	1738	G
54	01	1758	U
54	01	1764	C
54	01	1773	A
54	01	1780	A
54	01	1787	A
54	01	1800	C
54	01	1801	A
54	01	1808	A
54	01	1816	C
54	01	1821	A
54	01	1829	A
54	01	1833	C
54	01	1871	A
54	01	1901	A
54	01	1906	G
54	01	1907	G
54	01	1913	A
54	01	1914	C
54	01	1929	G
54	01	1930	G
54	01	1931	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	1937	A
54	01	1944	U
54	01	1955	U
54	01	1962	C
54	01	1963	U
54	01	1967	C
54	01	1970	A
54	01	1971	U
54	01	1972	G
54	01	1991	U
54	01	1993	U
54	01	1997	C
54	01	2022	U
54	01	2023	C
54	01	2030	A
54	01	2031	A
54	01	2036	C
54	01	2043	C
54	01	2049	G
54	01	2055	C
54	01	2056	G
54	01	2060	A
54	01	2061	G
54	01	2062	A
54	01	2069	G
54	01	2072	C
54	01	2093	G
54	01	2096	C
54	01	2108	A
54	01	2110	G
54	01	2111	U
54	01	2112	G
54	01	2116	G
54	01	2118	U
54	01	2119	A
54	01	2125	G
54	01	2127	G
54	01	2132	U
54	01	2133	G
54	01	2145	C
54	01	2147	A
54	01	2162	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	2164	C
54	01	2171	A
54	01	2172	U
54	01	2173	A
54	01	2189	U
54	01	2198	A
54	01	2204	G
54	01	2211	A
54	01	2213	U
54	01	2225	A
54	01	2239	G
54	01	2250	G
54	01	2259	U
54	01	2266	A
54	01	2278	A
54	01	2283	C
54	01	2287	A
54	01	2297	A
54	01	2305	U
54	01	2309	A
54	01	2320	U
54	01	2325	G
54	01	2327	A
54	01	2334	U
54	01	2337	G
54	01	2350	C
54	01	2383	G
54	01	2385	C
54	01	2402	U
54	01	2406	A
54	01	2407	A
54	01	2423	U
54	01	2424	C
54	01	2429	G
54	01	2430	A
54	01	2435	A
54	01	2441	U
54	01	2447	G
54	01	2448	A
54	01	2476	A
54	01	2498	C
54	01	2502	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	01	2503	A
54	01	2505	G
54	01	2518	A
54	01	2520	C
54	01	2547	A
54	01	2554	U
54	01	2567	G
54	01	2572	A
54	01	2602	A
54	01	2609	U
54	01	2613	U
54	01	2655	G
54	01	2682	A
54	01	2689	U
54	01	2690	U
54	01	2713	U
54	01	2714	G
54	01	2744	G
54	01	2748	A
54	01	2751	G
54	01	2764	A
54	01	2765	A
54	01	2778	A
54	01	2779	U
54	01	2791	G
54	01	2794	C
54	01	2797	U
54	01	2798	U
54	01	2799	A
54	01	2800	A
54	01	2801	G
54	01	2809	A
54	01	2820	A
54	01	2821	A
54	01	2833	U
54	01	2867	G
54	01	2868	A
54	01	2880	C
55	02	4	C
55	02	13	G
55	02	35	C
55	02	44	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
55	02	45	A
55	02	67	G
55	02	89	U
55	02	108	A
55	02	109	A
56	X	3	C
56	X	8	U
56	X	9	G
56	X	10	G
56	X	14	A
56	X	19	G
56	X	21	A
56	X	22	G
56	X	32	C
56	X	34	C
56	X	38	A
57	V	12	A
57	V	19	U
56	W	9	G
56	W	18	G
56	W	19	G
56	W	20	U
56	W	21	A
56	W	47	U
56	W	48	C
58	Y	17	C
58	Y	18	G
58	Y	20	U
58	Y	21	A
58	Y	22	G
58	Y	44	G
58	Y	45	U
58	Y	46	G
58	Y	48	C
58	Y	53	G
58	Y	54	U
58	Y	61	C

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	A	70	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	A	246	A
53	A	280	C
53	A	495	A
53	A	531	U
53	A	960	U
53	A	1190	G
53	A	1201	A
53	A	1347	G
53	A	1399	C
54	01	242	G
54	01	372	G
54	01	421	C
54	01	490	C
54	01	858	G
54	01	859	G
54	01	1020	A
54	01	1130	U
54	01	1378	A
54	01	1930	G
54	01	2296	U
54	01	2326	C
55	02	88	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
60	GCP	Z	401	-	32,34,34	1.80	7 (21%)	49,54,54	2.56	15 (30%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	GCP	Z	401	-	-	8/19/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	Z	401	GCP	PA-O3A	-5.38	1.53	1.59
60	Z	401	GCP	PB-O3A	-3.97	1.54	1.58
60	Z	401	GCP	C1'-N9	3.34	1.57	1.47
60	Z	401	GCP	O4'-C1'	2.42	1.47	1.42
60	Z	401	GCP	C2'-C3'	2.23	1.59	1.53
60	Z	401	GCP	C5'-C4'	2.05	1.57	1.51
60	Z	401	GCP	PB-O2B	-2.04	1.51	1.56

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	Z	401	GCP	C1'-N9-C4	7.99	150.09	126.49
60	Z	401	GCP	C1'-N9-C8	-7.55	105.27	126.73
60	Z	401	GCP	O1G-PG-C3B	-7.42	95.19	111.37
60	Z	401	GCP	O4'-C1'-C2'	-4.46	97.07	106.62
60	Z	401	GCP	O5'-PA-O1A	-3.94	93.32	108.94
60	Z	401	GCP	O2B-PB-O1B	3.78	122.25	109.95
60	Z	401	GCP	O2A-PA-O3A	-3.51	97.79	107.27
60	Z	401	GCP	O3'-C3'-C4'	-3.31	101.59	111.08
60	Z	401	GCP	PB-O3A-PA	3.22	142.87	132.37
60	Z	401	GCP	C2'-C1'-N9	3.09	121.84	113.25
60	Z	401	GCP	O3G-PG-O1G	3.02	120.21	112.39
60	Z	401	GCP	O2G-PG-C3B	2.95	113.55	106.40
60	Z	401	GCP	O4'-C4'-C5'	2.84	118.43	109.33
60	Z	401	GCP	O2A-PA-O1A	2.23	122.81	112.44
60	Z	401	GCP	C3'-C2'-C1'	-2.03	97.63	101.46

There are no chirality outliers.

All (8) torsion outliers are listed below:

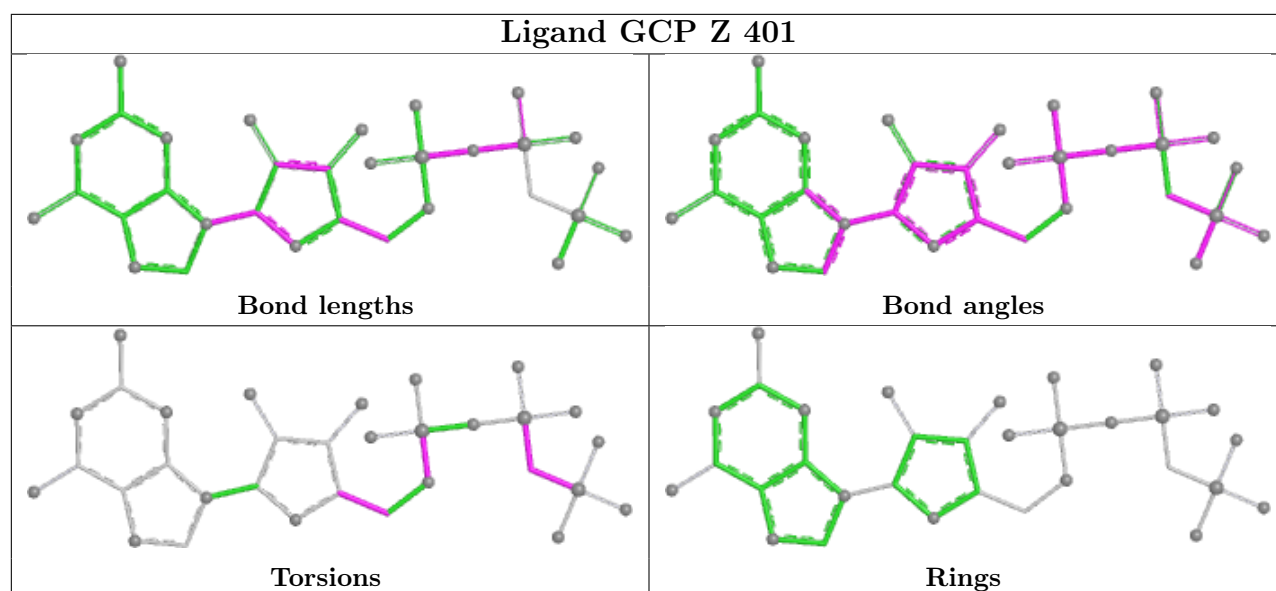
Mol	Chain	Res	Type	Atoms
60	Z	401	GCP	PB-C3B-PG-O1G
60	Z	401	GCP	PB-C3B-PG-O2G
60	Z	401	GCP	PG-C3B-PB-O1B
60	Z	401	GCP	C5'-O5'-PA-O3A
60	Z	401	GCP	O4'-C4'-C5'-O5'
60	Z	401	GCP	C3'-C4'-C5'-O5'
60	Z	401	GCP	PB-C3B-PG-O3G
60	Z	401	GCP	C5'-O5'-PA-O2A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	Z	401	GCP	4	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.

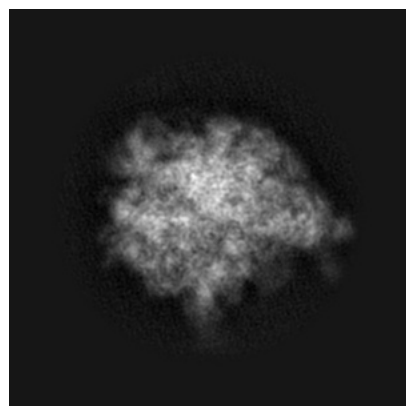
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8615. These allow visual inspection of the internal detail of the map and identification of artifacts.

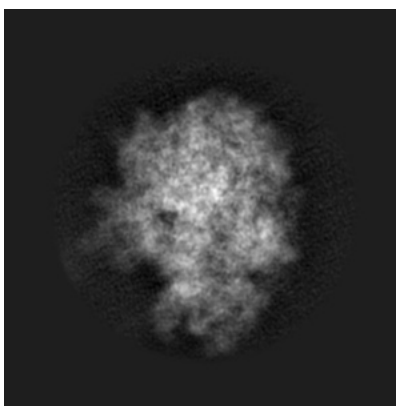
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

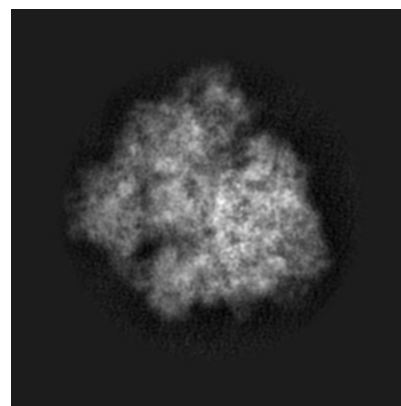
6.1.1 Primary map



X

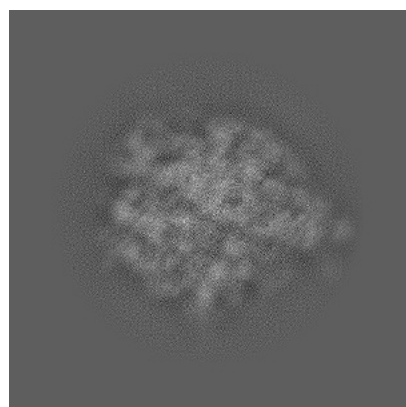


Y

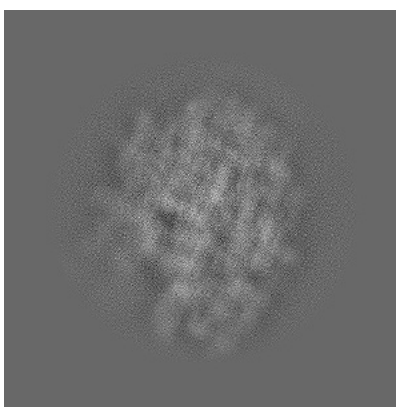


Z

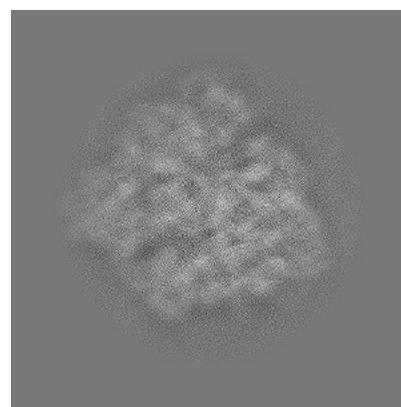
6.1.2 Raw map



X



Y

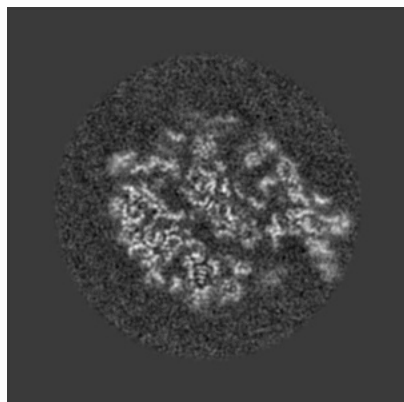


Z

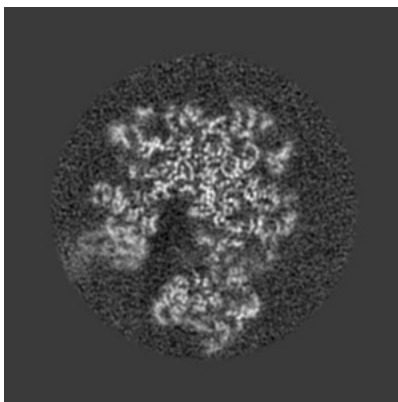
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

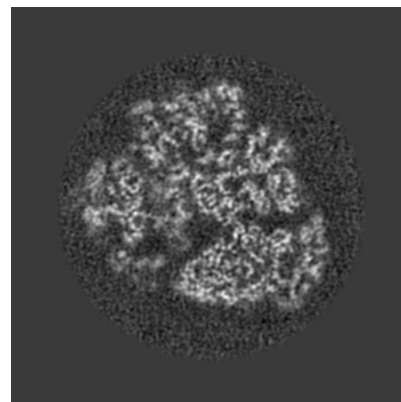
6.2.1 Primary map



X Index: 240

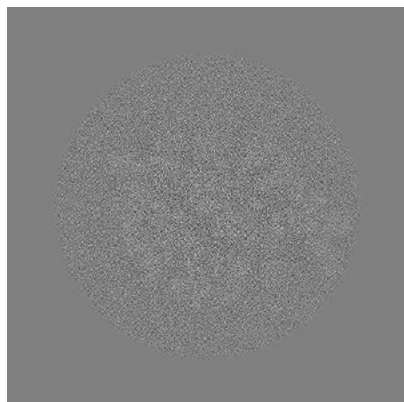


Y Index: 240

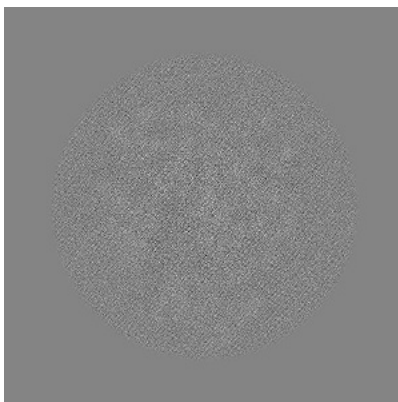


Z Index: 240

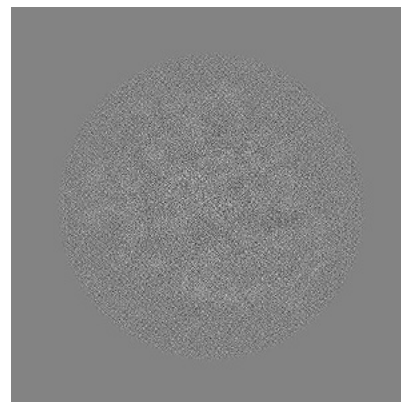
6.2.2 Raw map



X Index: 240



Y Index: 240

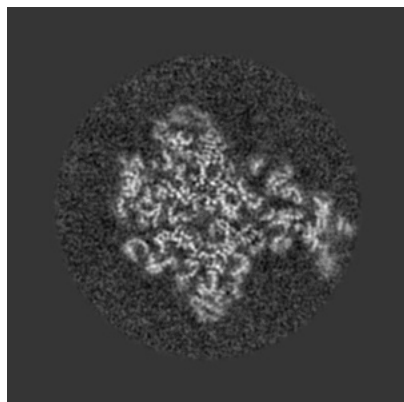


Z Index: 240

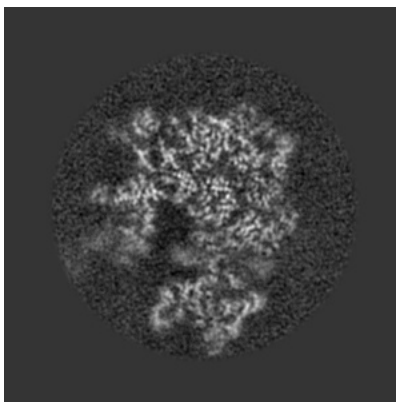
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

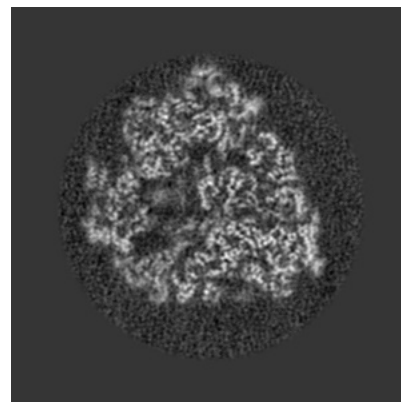
6.3.1 Primary map



X Index: 251

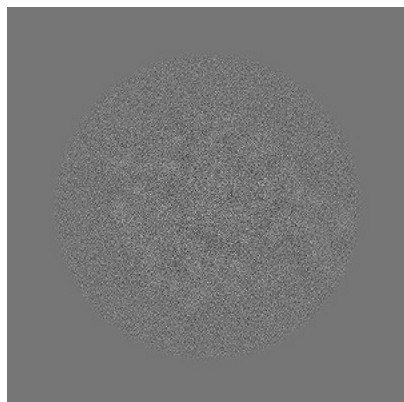


Y Index: 247

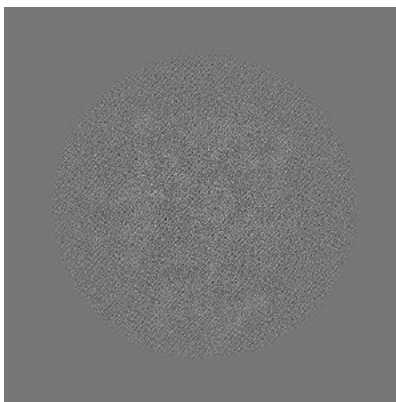


Z Index: 227

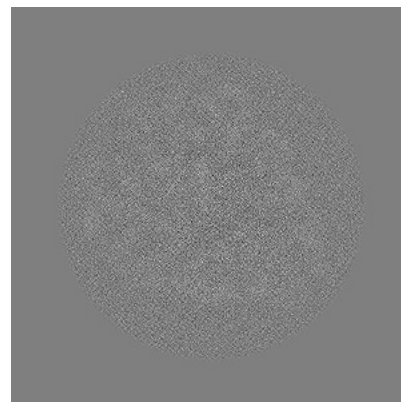
6.3.2 Raw map



X Index: 237



Y Index: 248

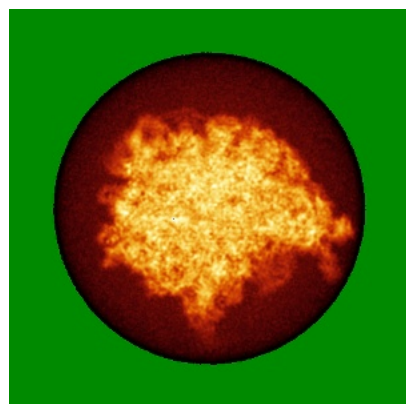


Z Index: 234

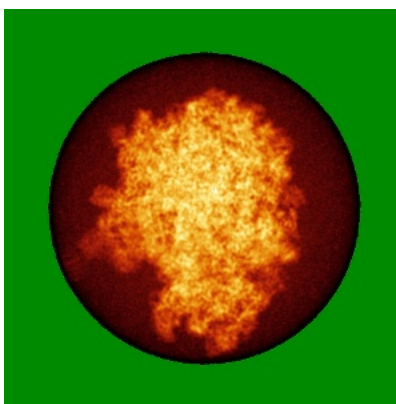
The images above show the largest variance slices of the map in three orthogonal directions.

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

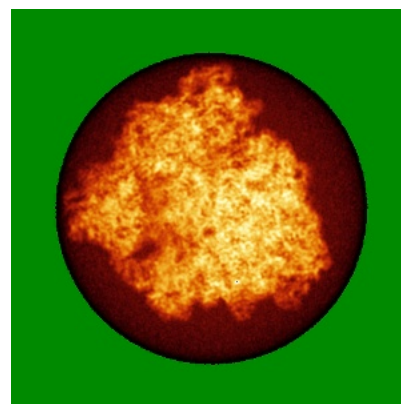
6.4.1 Primary map



X

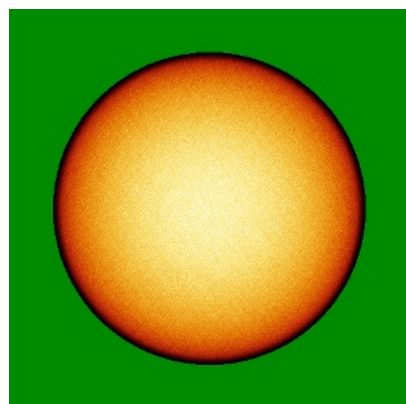


Y

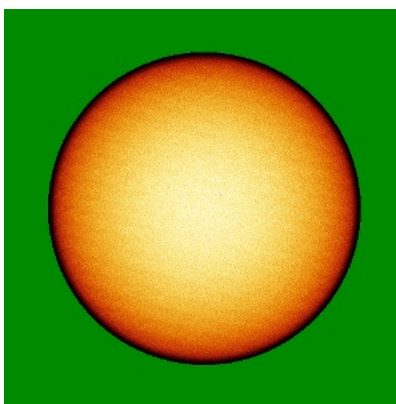


Z

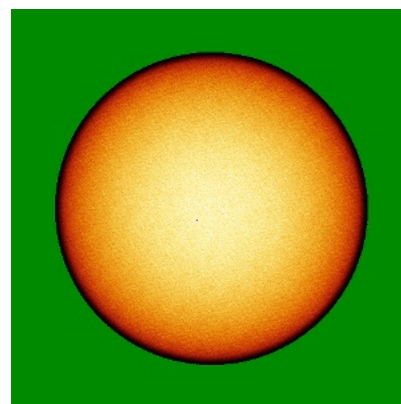
6.4.2 Raw map



X



Y

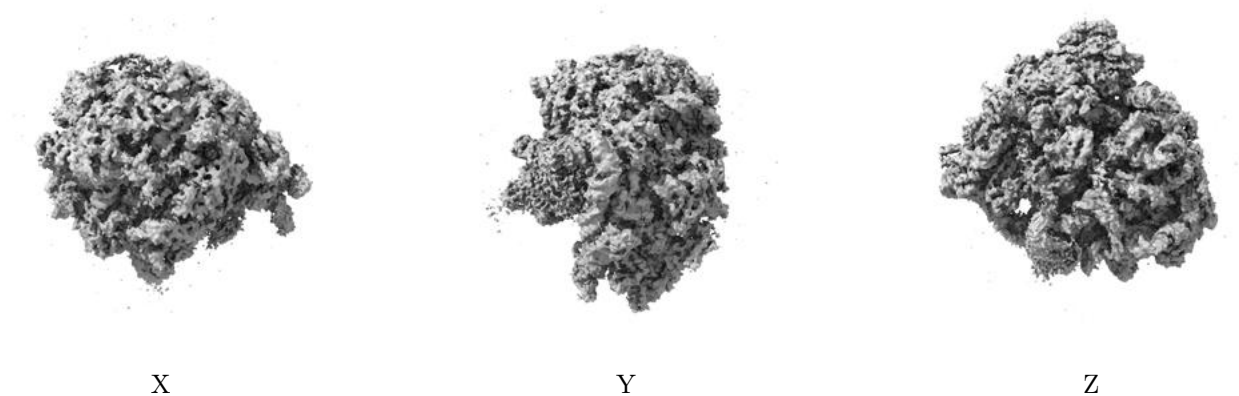


Z

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

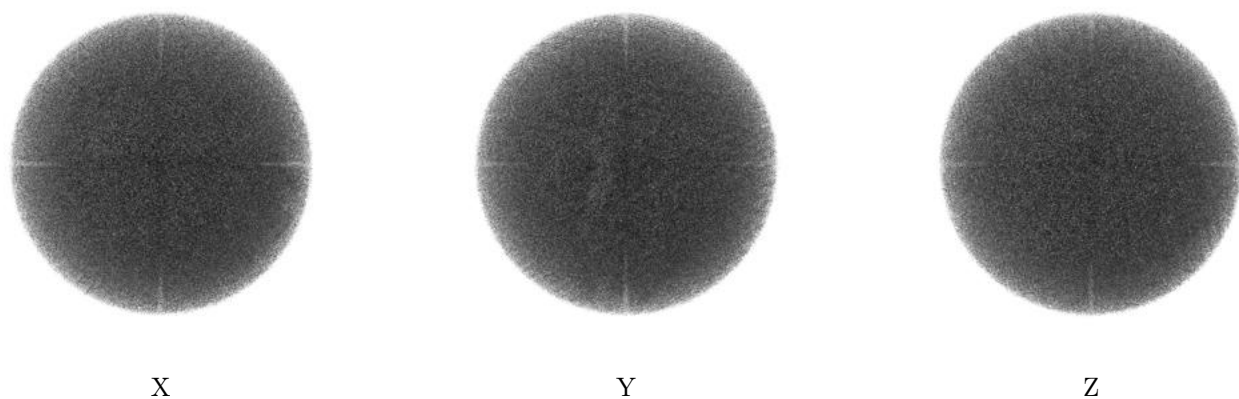
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.47. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

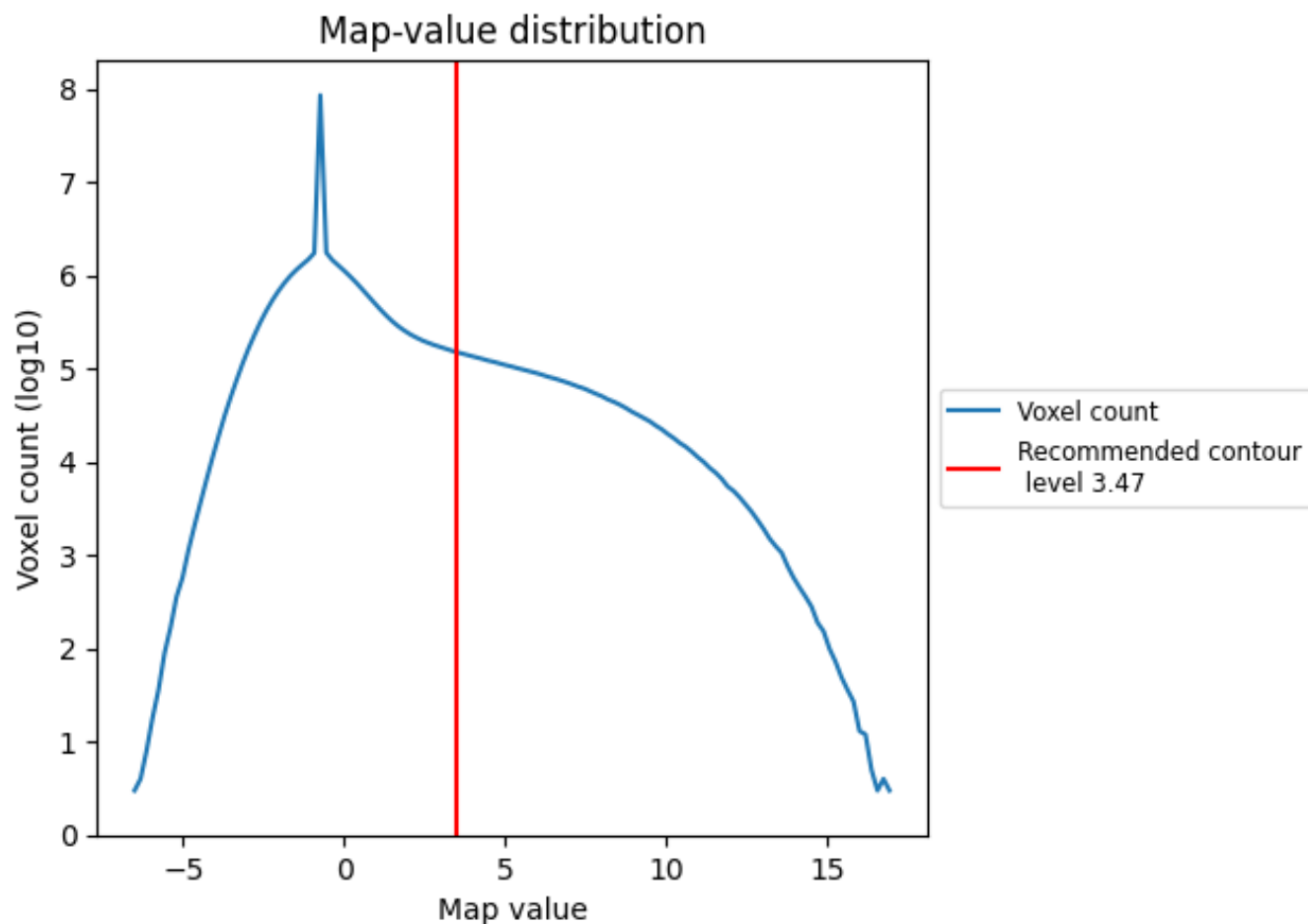
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

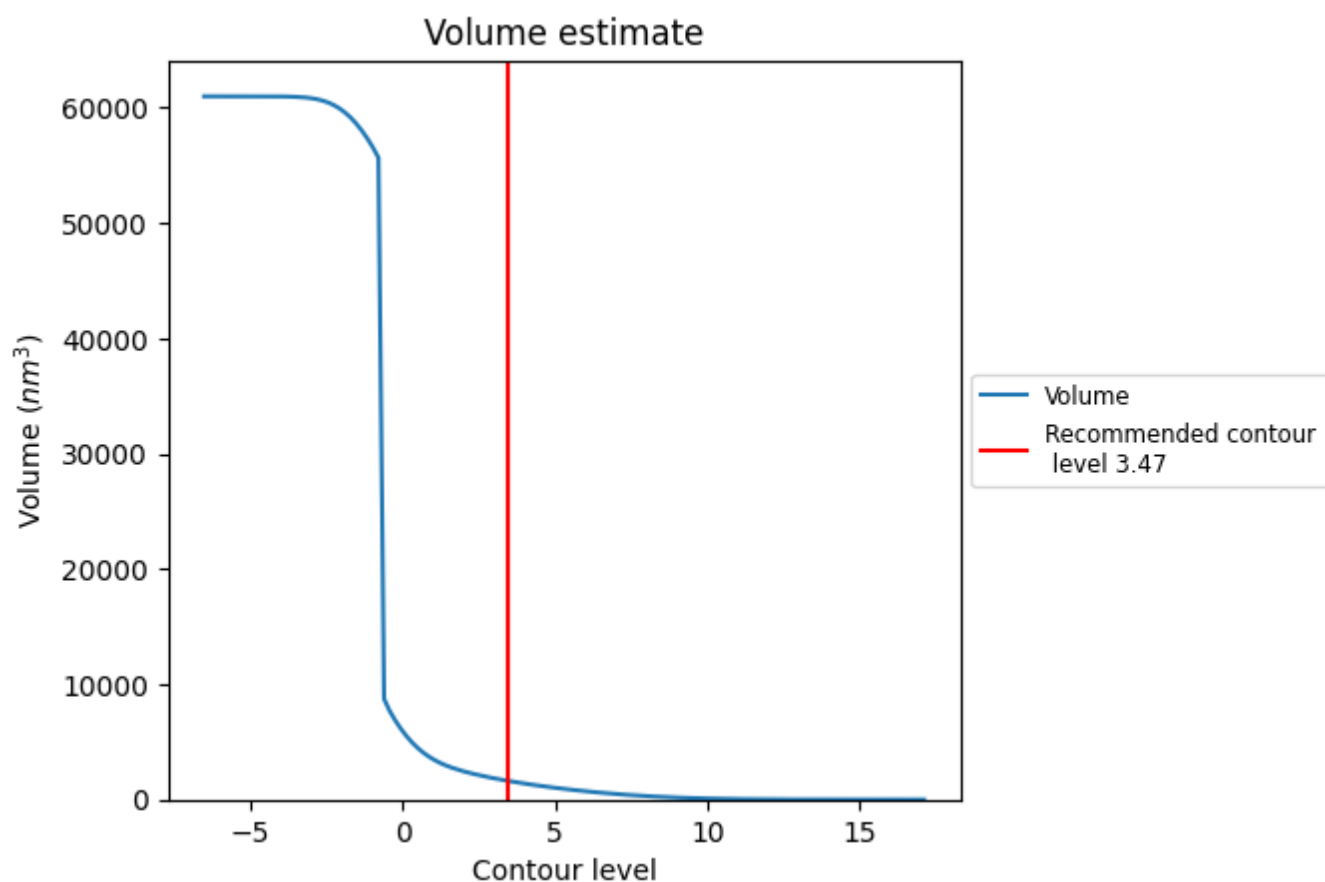
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

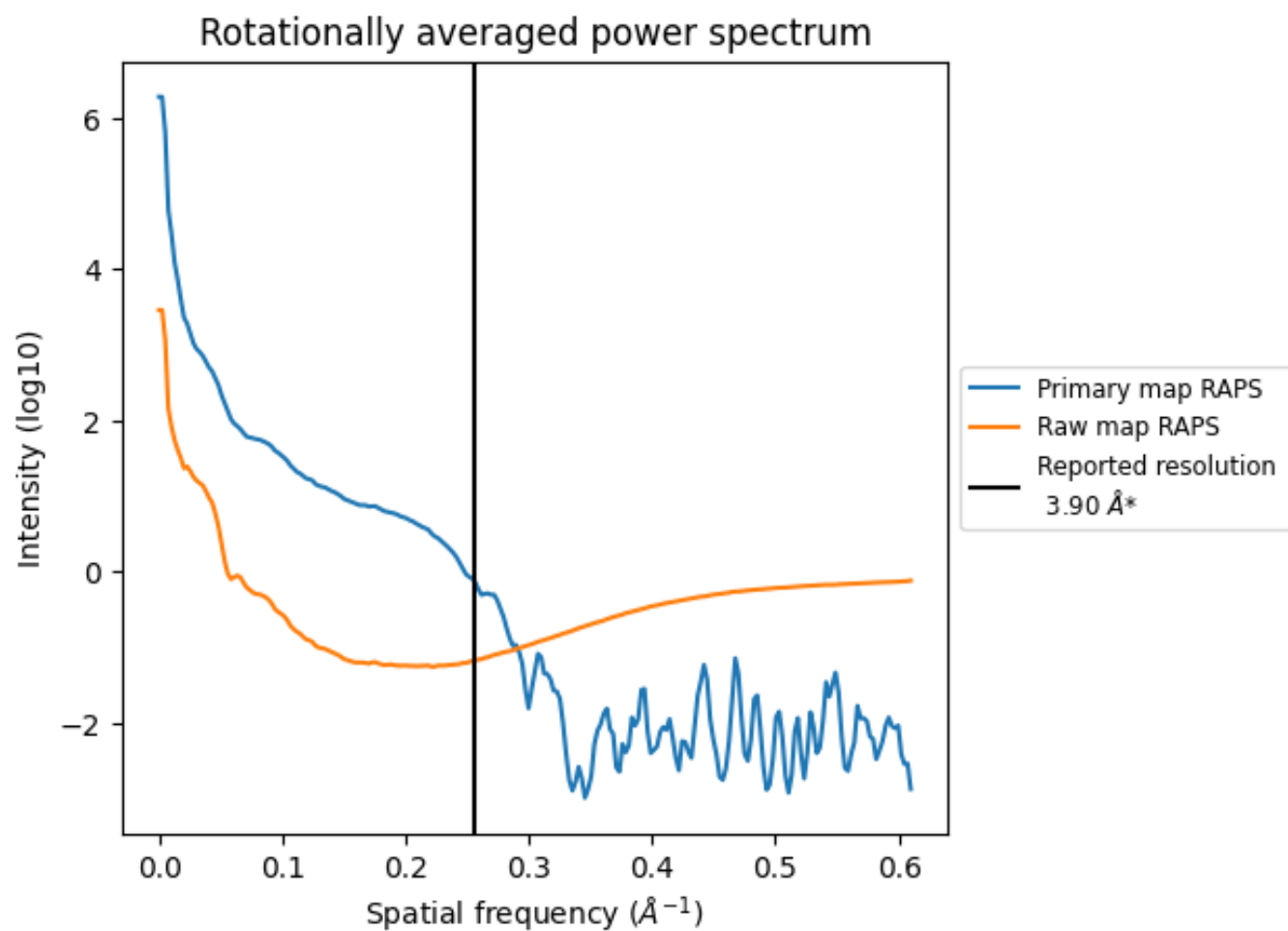
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1616 nm³; this corresponds to an approximate mass of 1460 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

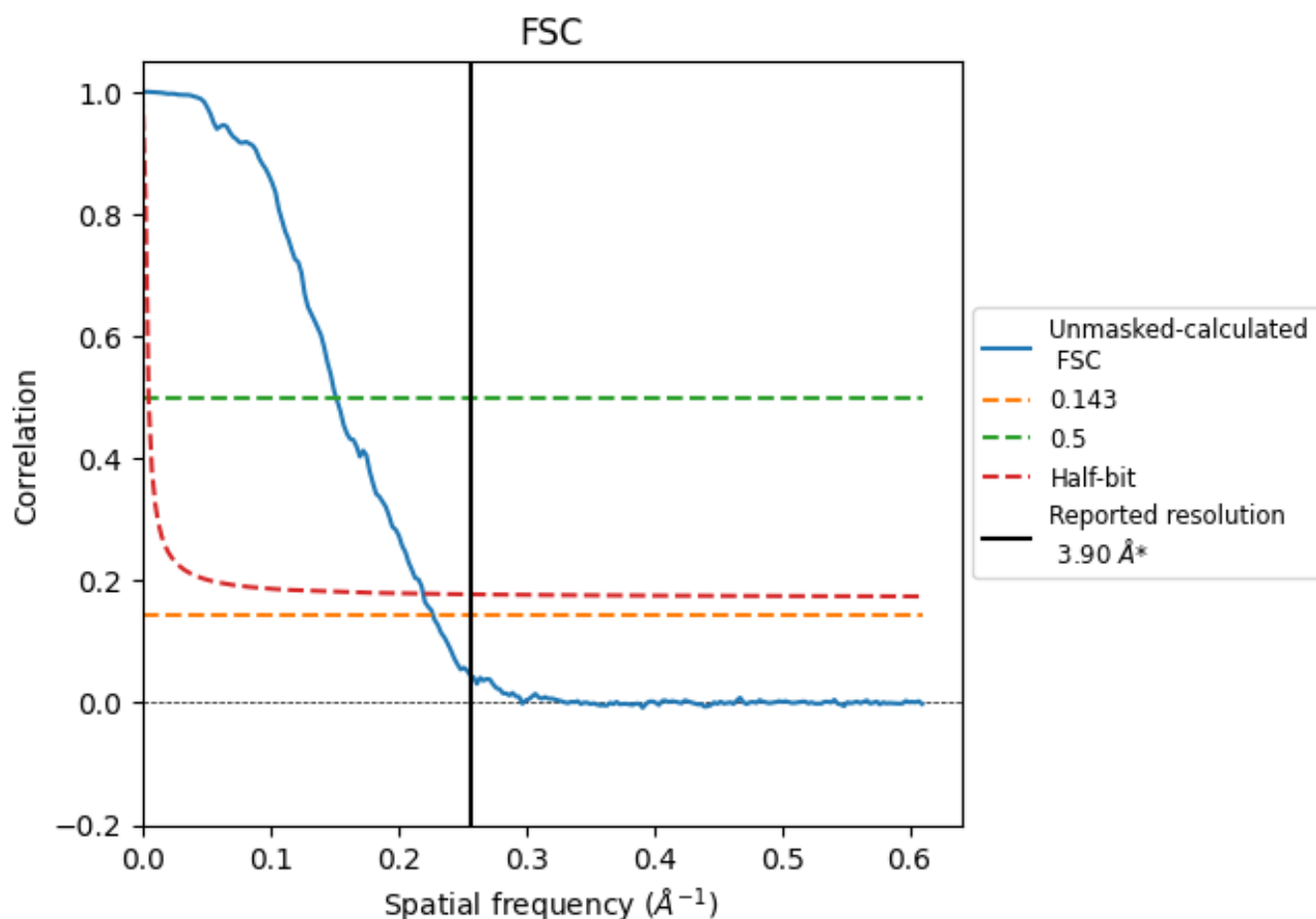


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

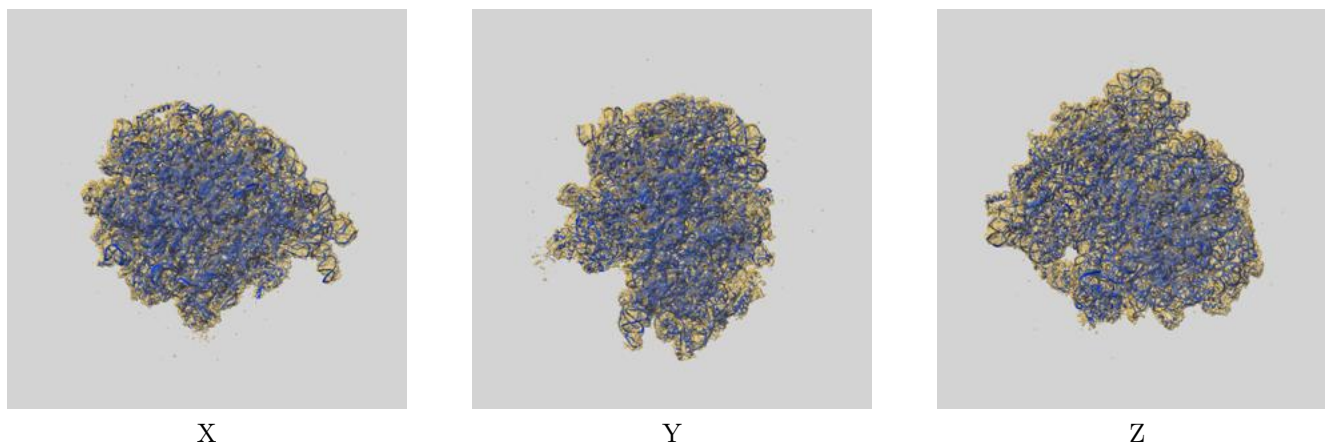
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.40	6.60	4.55

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.40 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

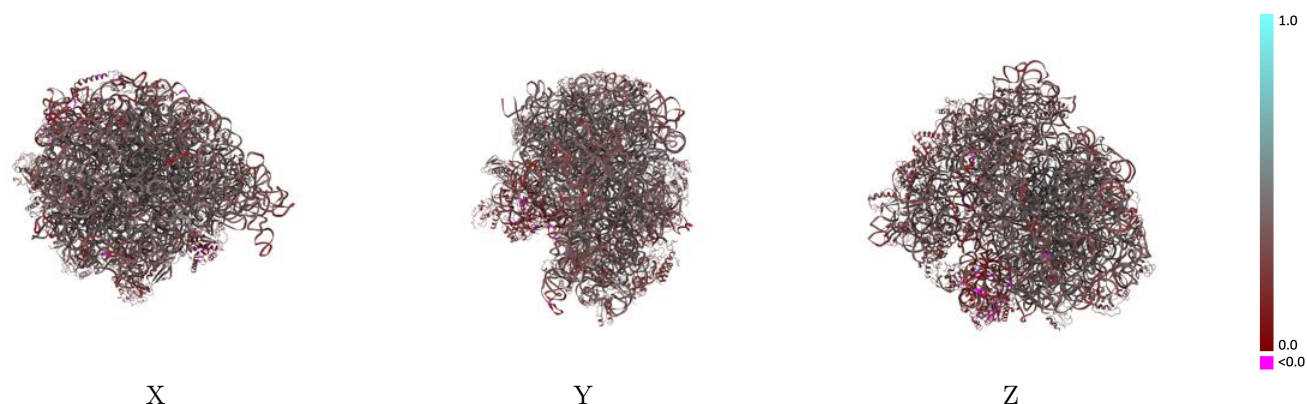
This section contains information regarding the fit between EMDB map EMD-8615 and PDB model 5UYK. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 3.47 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

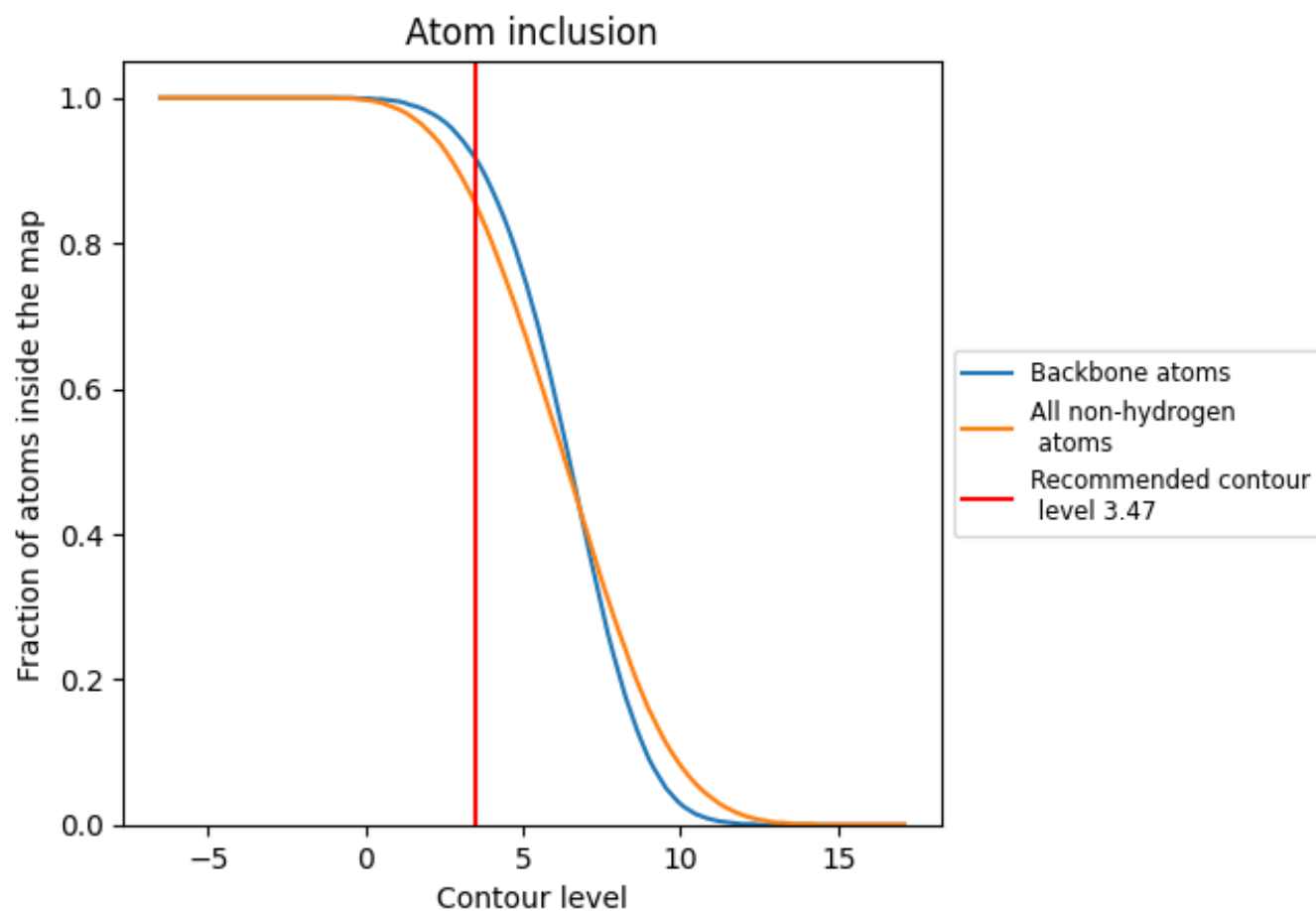


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 86% 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 (3.47) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8560	 0.3540
01	 0.9450	 0.3760
02	 0.9540	 0.3590
03	 0.3760	 0.1730
04	 0.7860	 0.4080
05	 0.7830	 0.3950
06	 0.7510	 0.3530
07	 0.7870	 0.3250
08	 0.7820	 0.3550
09	 0.5250	 0.2890
10	 0.4380	 0.1870
11	 0.5110	 0.1820
12	 0.7790	 0.3820
13	 0.7120	 0.4000
14	 0.7740	 0.3740
15	 0.7090	 0.3840
16	 0.8000	 0.3750
17	 0.7970	 0.3330
18	 0.7250	 0.3680
19	 0.7870	 0.3780
20	 0.7500	 0.3730
21	 0.7440	 0.3770
22	 0.7750	 0.3660
23	 0.7680	 0.3370
24	 0.7790	 0.3520
25	 0.7640	 0.3850
26	 0.7700	 0.3750
27	 0.7520	 0.3000
28	 0.7460	 0.3690
29	 0.7130	 0.2840
30	 0.7640	 0.3680
31	 0.7020	 0.3670
32	 0.8080	 0.3950
33	 0.7700	 0.3980
34	 0.7770	 0.4180



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
A	 0.9410	 0.3650
B	 0.7210	 0.3030
C	 0.7280	 0.3550
D	 0.7330	 0.3220
E	 0.7620	 0.3680
F	 0.8030	 0.3520
G	 0.7290	 0.3230
H	 0.7960	 0.3680
I	 0.7610	 0.3090
J	 0.6680	 0.3140
K	 0.7770	 0.3550
L	 0.7430	 0.3830
M	 0.7610	 0.3260
N	 0.7640	 0.3370
O	 0.7990	 0.3440
P	 0.8040	 0.3630
Q	 0.7520	 0.3550
R	 0.7650	 0.3570
S	 0.7620	 0.3210
T	 0.7570	 0.3270
U	 0.5830	 0.2790
V	 0.3840	 0.2420
W	 0.6670	 0.3220
X	 0.6880	 0.1750
Y	 0.5960	 0.1750
Z	 0.3930	 0.2260