



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2017 – 08:10 PM EDT

PDB ID : 3CCR  
Title : Structure of Anisomycin resistant 50S Ribosomal Subunit: 23S rRNA mutation A2488C. Density for anisomycin is visible but not included in the model.  
Authors : Blaha, G.; Gurel, G.  
Deposited on : unknown  
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

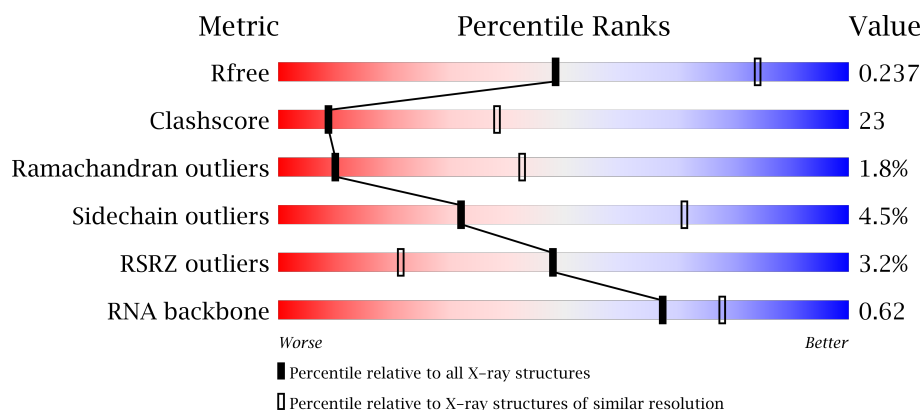
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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.









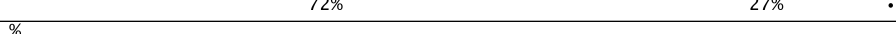
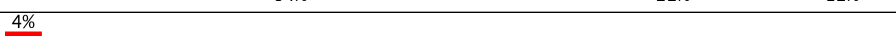
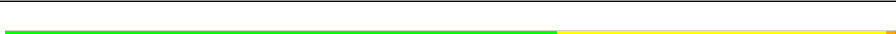









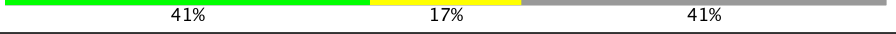

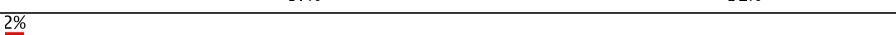




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)
RNA backbone	2435	1007 (3.34-2.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	240	<div> <div>62%</div> <div>33%</div> <div>..</div> </div>
2	B	338	<div> <div>58%</div> <div>37%</div> <div>.</div> </div>
3	C	246	<div> <div>68%</div> <div>27%</div> <div>5%</div> </div>
4	D	177	<div> <div>8%</div> <div>42%</div> <div>35%</div> <div>..</div> <div>21%</div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	E	178	
6	F	120	
7	G	348	
8	H	177	
9	I	162	
10	J	145	
11	K	132	
12	L	165	
13	M	196	
14	N	187	
15	O	116	
16	P	149	
17	Q	96	
18	R	155	
19	S	85	
20	T	120	
21	U	67	
22	V	71	
23	W	154	
24	X	92	
25	Y	241	
26	Z	116	
27	1	57	
28	2	50	
29	3	92	

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
30	0	2923	
31	9	122	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
32	MG	0	8009	-	-	-	X
32	MG	0	8011	-	-	-	X
32	MG	0	8014	-	-	-	X
32	MG	0	8016	-	-	-	X
32	MG	0	8044	-	-	-	X
32	MG	A	8051	-	-	-	X
33	CL	0	8805	-	-	-	X
33	CL	0	8811	-	-	-	X
33	CL	0	8816	-	-	-	X
33	CL	3	8804	-	-	X	-
33	CL	B	8819	-	-	X	-
33	CL	M	8818	-	-	X	-
34	SR	0	8904	-	-	-	X
34	SR	0	8947	-	-	-	X
34	SR	0	8957	-	-	-	X
34	SR	0	8969	-	-	-	X
34	SR	B	8987	-	-	-	X
35	NA	0	8513	-	-	-	X
35	NA	0	8519	-	-	-	X
35	NA	0	8521	-	-	-	X
35	NA	0	8522	-	-	-	X
35	NA	0	8528	-	-	-	X
35	NA	0	8530	-	-	-	X
35	NA	0	8535	-	-	-	X
35	NA	0	8545	-	-	-	X
35	NA	0	8546	-	-	-	X
35	NA	0	8550	-	-	-	X
35	NA	0	8552	-	-	-	X
35	NA	0	8553	-	-	-	X
35	NA	0	8555	-	-	-	X
35	NA	0	8556	-	-	-	X
35	NA	0	8558	-	-	-	X
35	NA	0	8559	-	-	-	X

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	NA	0	8560	-	-	-	X
35	NA	0	8562	-	-	-	X
35	NA	0	8564	-	-	-	X
35	NA	0	8567	-	-	-	X
35	NA	0	8569	-	-	-	X
35	NA	0	8571	-	-	-	X
35	NA	R	8575	-	-	-	X
37	CD	3	8704	-	-	-	X

## 2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 99120 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 L2P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	0	0	0
			1753	1072	352	324	5			

- Molecule 2 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	337	Total	C	N	O	S	0	0	0
			2625	1616	493	511	5			

- Molecule 3 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	246	Total	C	N	O	S	0	0	0
			1860	1130	345	384	1			

- Molecule 4 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	140	Total	C	N	O	S	0	0	0
			1094	685	195	210	4			

- Molecule 5 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	172	Total	C	N	O	S	0	0	0
			1357	840	224	289	4			

- Molecule 6 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	119	Total	C	N	O	S	0	0	0
			890	551	141	197	1			

- Molecule 7 is a protein called 50S ribosomal protein L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	29	Total	C	N	O	S	0	0	0
			240	149	39	51	1			

- Molecule 8 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	160	Total	C	N	O	S	0	0	0
			1282	798	240	238	6			

- Molecule 9 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	70	Total	C	N	O	S	0	0	0
			519	323	81	114	1			

- Molecule 10 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	142	Total	C	N	O	S	0	0	0
			1120	696	199	222	3			

- Molecule 11 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	132	Total	C	N	O	S	0	0	0
			994	609	189	192	4			

- Molecule 12 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	L	145	Total	C	N	O	0	0	0
			1118	670	222	226			

- Molecule 13 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	194	Total	C	N	O	S	0	0	0
			1558	943	333	281	1			

- Molecule 14 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	186	Total	C	N	O	S	0	0	0
			1445	895	262	286	2			

- Molecule 15 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	115	Total	C	N	O		0	0	0
			865	529	161	175				

- Molecule 16 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	143	Total	C	N	O		0	0	0
			1136	683	229	224				

- Molecule 17 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	95	Total	C	N	O		0	0	0
			735	450	141	144				

- Molecule 18 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	R	150	Total	C	N	O	S	0	0	0
			1149	713	209	223	4			

- Molecule 19 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	0
			641	389	111	138	3			

- Molecule 20 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	119	Total	C	N	O		0	0	0
			950	568	180	202				

- Molecule 21 is a protein called 50S ribosomal protein L24e.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	53	Total	C	N	O	S	0	0	0
			410	244	75	86	5			

- Molecule 22 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	65	Total	C	N	O	S	0	0	0
			499	304	94	100	1			

- Molecule 23 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	W	154	Total	C	N	O	S	0	0	0
			1196	737	209	244	6			

- Molecule 24 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	X	82	Total	C	N	O	S	0	0	0
			654	402	129	122	1			

- Molecule 25 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	Y	142	Total	C	N	O		0	0	0
			1130	686	228	216				

- Molecule 26 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Z	73	Total	C	N	O	S	0	0	0
			573	343	113	112	5			

- Molecule 27 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 28 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

- Molecule 29 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 30 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	0	2754	Total	C	N	O	P	0	0	0
			59018	26348	10871	19054	2745			

- Molecule 31 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	9	122	Total	C	N	O	P	0	0	0
			2599	1160	471	847	121			

- Molecule 32 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	0	84	Total	Mg	0	0
			84	84		
32	9	1	Total	Mg	0	0
			1	1		
32	K	1	Total	Mg	0	0
			1	1		
32	B	2	Total	Mg	0	0
			2	2		
32	A	1	Total	Mg	0	0
			1	1		
32	T	1	Total	Mg	0	0
			1	1		
32	2	1	Total	Mg	0	0
			1	1		
32	Y	1	Total	Mg	0	0
			1	1		
32	3	1	Total	Mg	0	0
			1	1		

- Molecule 33 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	9	Total 9	Cl 9	0	0
33	J	3	Total 3	Cl 3	0	0
33	K	1	Total 1	Cl 1	0	0
33	B	1	Total 1	Cl 1	0	0
33	A	1	Total 1	Cl 1	0	0
33	N	1	Total 1	Cl 1	0	0
33	O	1	Total 1	Cl 1	0	0
33	R	1	Total 1	Cl 1	0	0
33	Y	1	Total 1	Cl 1	0	0
33	L	1	Total 1	Cl 1	0	0
33	3	1	Total 1	Cl 1	0	0
33	M	1	Total 1	Cl 1	0	0

- Molecule 34 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	93	Total 93	Sr 93	0	0
34	1	2	Total 2	Sr 2	0	0
34	B	2	Total 2	Sr 2	0	0
34	3	2	Total 2	Sr 2	0	0
34	A	3	Total 3	Sr 3	0	0
34	R	1	Total 1	Sr 1	0	0
34	9	3	Total 3	Sr 3	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	S	1	Total 1	Sr 1	0	0
34	F	1	Total 1	Sr 1	0	0

- Molecule 35 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	66	Total 66	Na 66	0	0
35	J	1	Total 1	Na 1	0	0
35	Q	1	Total 1	Na 1	0	0
35	C	1	Total 1	Na 1	0	0
35	R	2	Total 2	Na 2	0	0
35	9	2	Total 2	Na 2	0	0
35	S	1	Total 1	Na 1	0	0
35	M	1	Total 1	Na 1	0	0

- Molecule 36 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	0	1	Total 1	K 1	0	0
36	M	1	Total 1	K 1	0	0

- Molecule 37 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	O	1	Total 1	Cd 1	0	0
37	Z	1	Total 1	Cd 1	0	0
37	1	1	Total 1	Cd 1	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	3	1	Total	Cd	0	0
			1	1		
37	U	1	Total	Cd	0	0
			1	1		

- Molecule 38 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	A	121	Total	O	0	0
			121	121		
38	B	145	Total	O	0	0
			145	145		
38	C	166	Total	O	0	0
			166	166		
38	D	46	Total	O	0	0
			46	46		
38	E	43	Total	O	0	0
			43	43		
38	F	31	Total	O	0	0
			31	31		
38	G	17	Total	O	0	0
			17	17		
38	H	72	Total	O	0	0
			72	72		
38	I	5	Total	O	0	0
			5	5		
38	J	52	Total	O	0	0
			52	52		
38	K	52	Total	O	0	0
			52	52		
38	L	81	Total	O	0	0
			81	81		
38	M	133	Total	O	0	0
			133	133		
38	N	56	Total	O	0	0
			56	56		
38	O	41	Total	O	0	0
			41	41		
38	P	63	Total	O	0	0
			63	63		
38	Q	52	Total	O	0	0
			52	52		

*Continued on next page...*

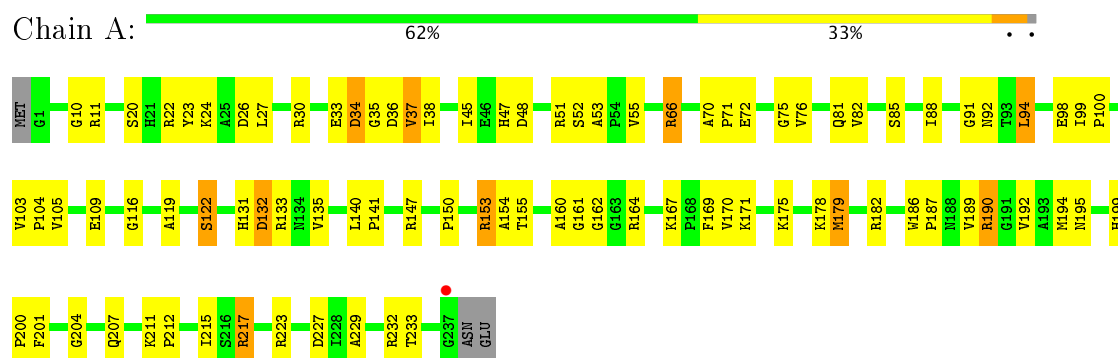
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	R	75	Total 75	O 75	0	0
38	S	37	Total 37	O 37	0	0
38	T	40	Total 40	O 40	0	0
38	U	28	Total 28	O 28	0	0
38	V	15	Total 15	O 15	0	0
38	W	69	Total 69	O 69	0	0
38	X	22	Total 22	O 22	0	0
38	Y	100	Total 100	O 100	0	0
38	Z	28	Total 28	O 28	0	0
38	1	61	Total 61	O 61	0	0
38	2	45	Total 45	O 45	0	0
38	3	76	Total 76	O 76	0	0
38	0	5897	Total 5897	O 5897	0	0
38	9	154	Total 154	O 154	0	0

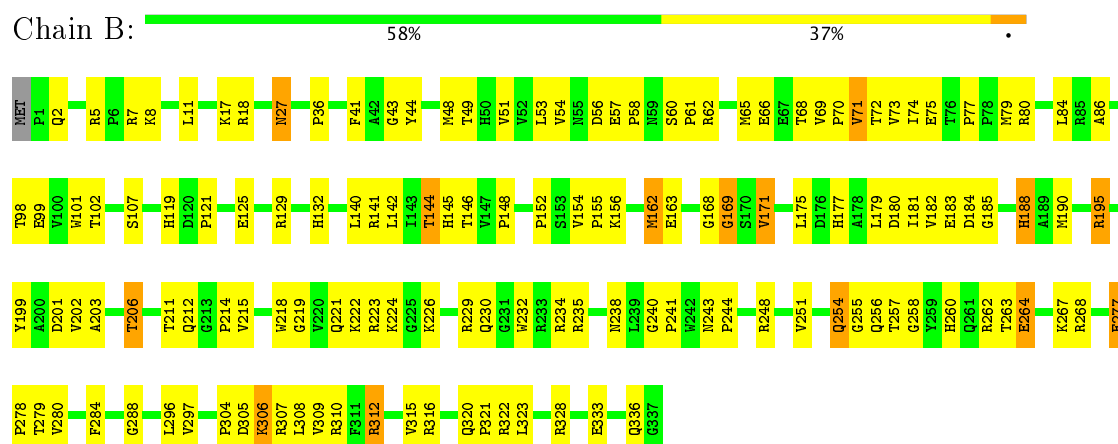
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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 electron 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

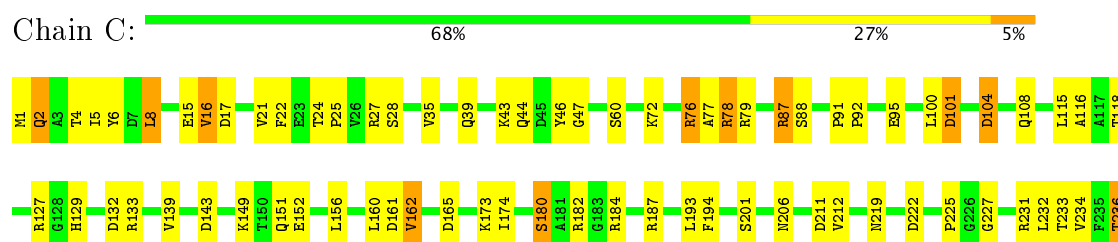
#### • Molecule 1: 50S ribosomal protein L2P



#### • Molecule 2: 50S ribosomal protein L3P

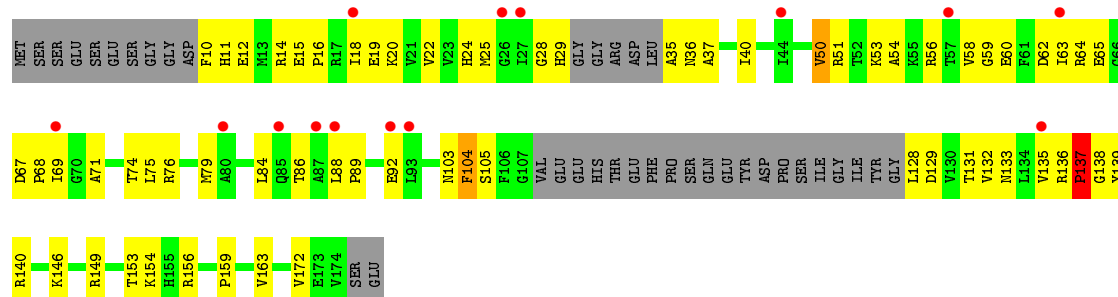
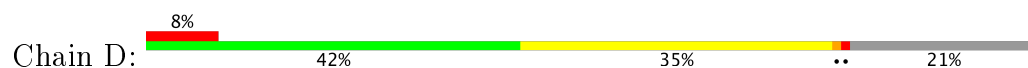


#### • Molecule 3: 50S ribosomal protein L4P

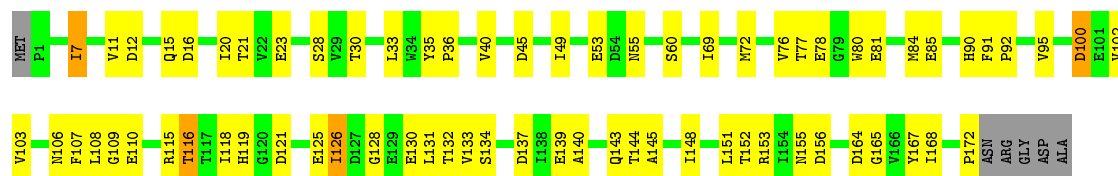




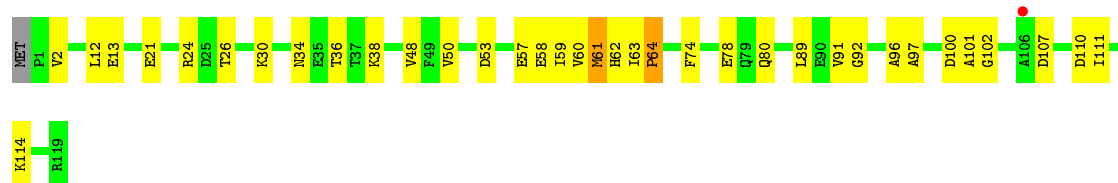
- Molecule 4: 50S ribosomal protein L5P



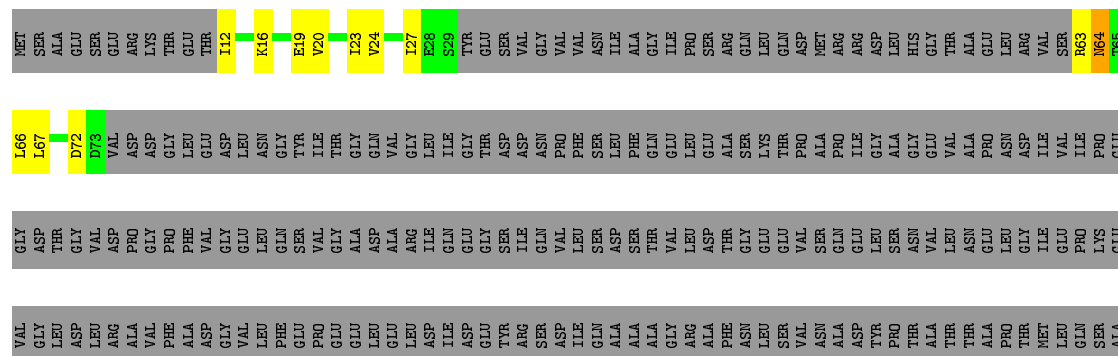
- Molecule 5: 50S ribosomal protein L6P



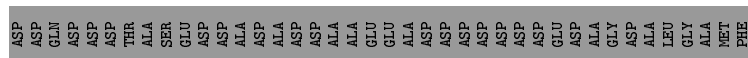
- Molecule 6: 50S ribosomal protein L7Ae



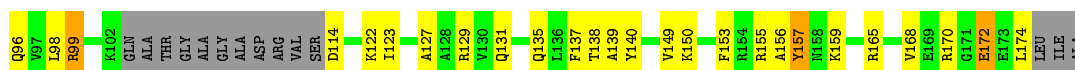
- Molecule 7: 50S ribosomal protein L10E



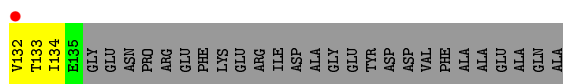




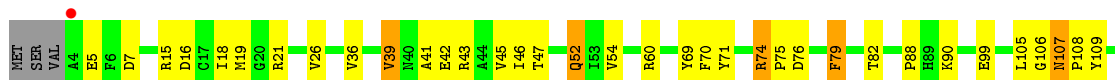
- Chain H:  57% 28% 5% 10%



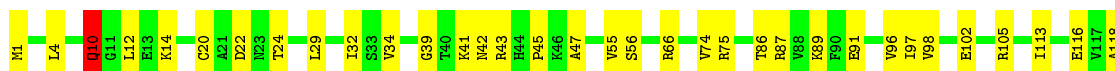
- Chain I: 



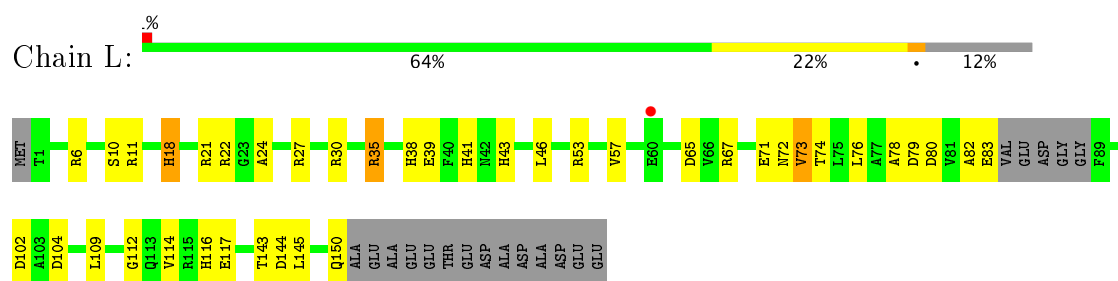
- Chain J:  67% 27% . .



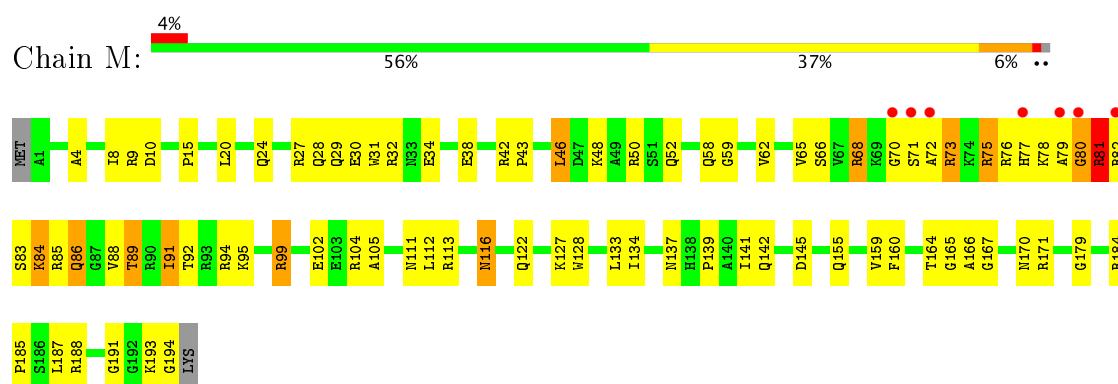
- Chain K:  72% 27%



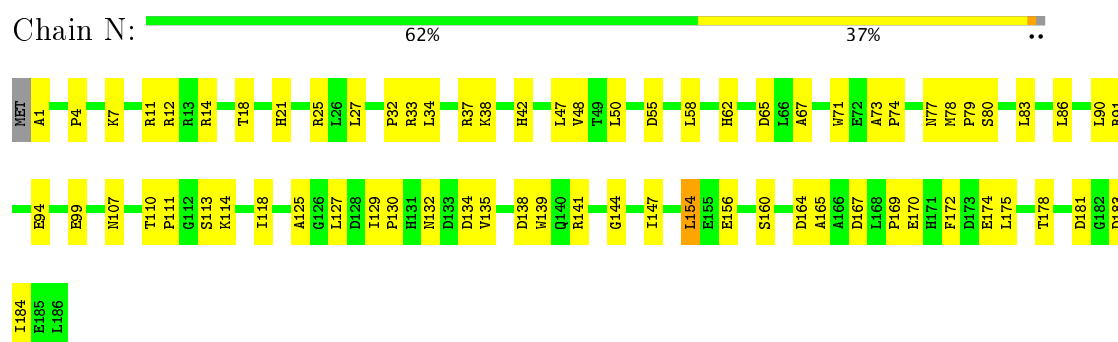
- WORLDWIDE  
 PDB  
PROTEIN DATA BANK



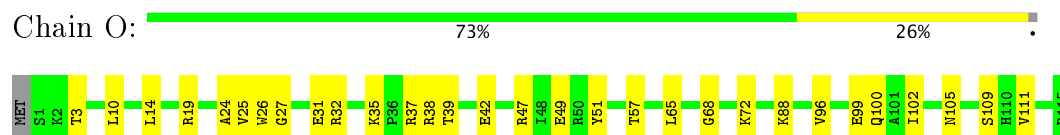
- Molecule 13: 50S ribosomal protein L15e



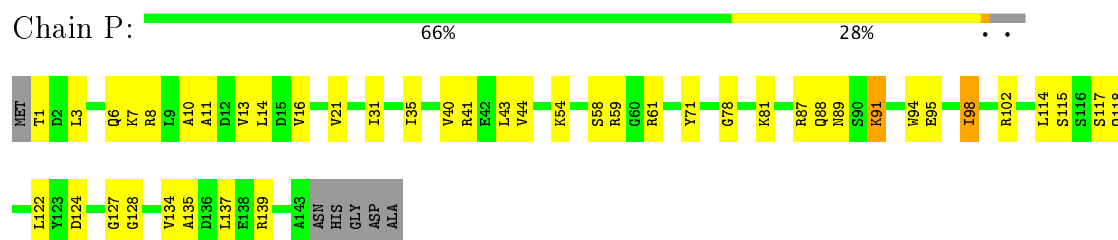
- Molecule 14: 50S ribosomal protein L18P



- Molecule 15: 50S ribosomal protein L18e



- Molecule 16: 50S ribosomal protein L19e



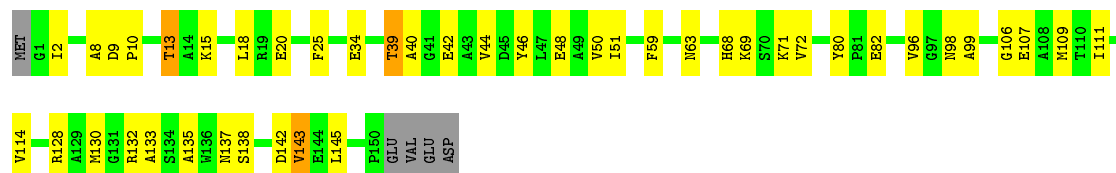
- Molecule 17: 50S ribosomal protein L21e

Chain Q:  69% 27% ..



- Molecule 18: 50S ribosomal protein L22P

Chain R:  68% 26% . .



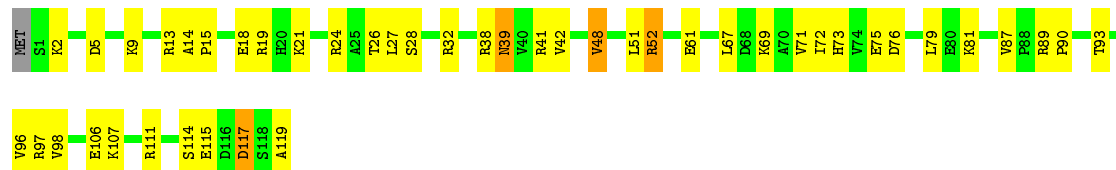
- Molecule 19: 50S ribosomal protein L23P

Chain S:  67% 28% 5% .%



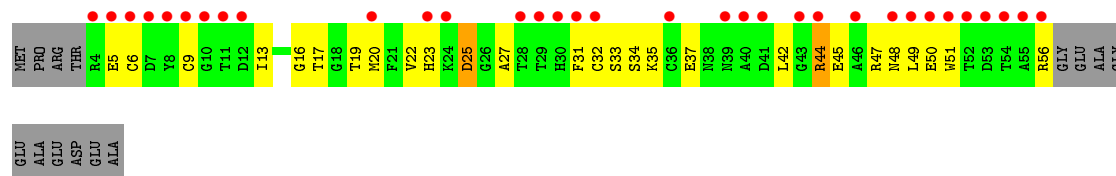
- Molecule 20: 50S ribosomal protein L24P

Chain T:  62% 34% ..



- Molecule 21: 50S ribosomal protein L24e

Chain U:  49% 39% 37% 21%

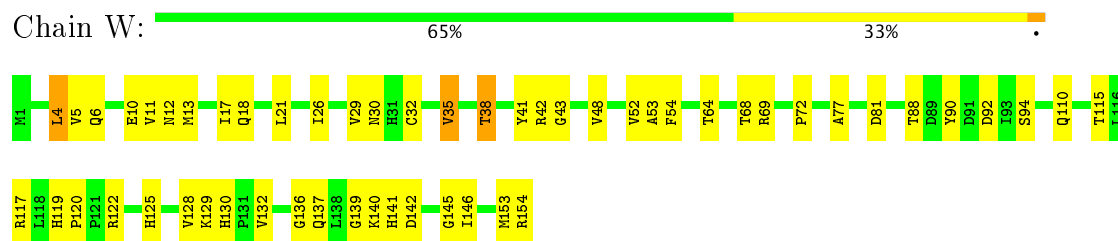


- Molecule 22: 50S ribosomal protein L29P

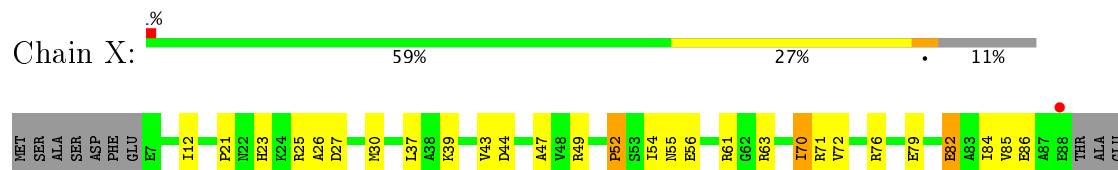
Chain V:  6% 62% 28% 8%



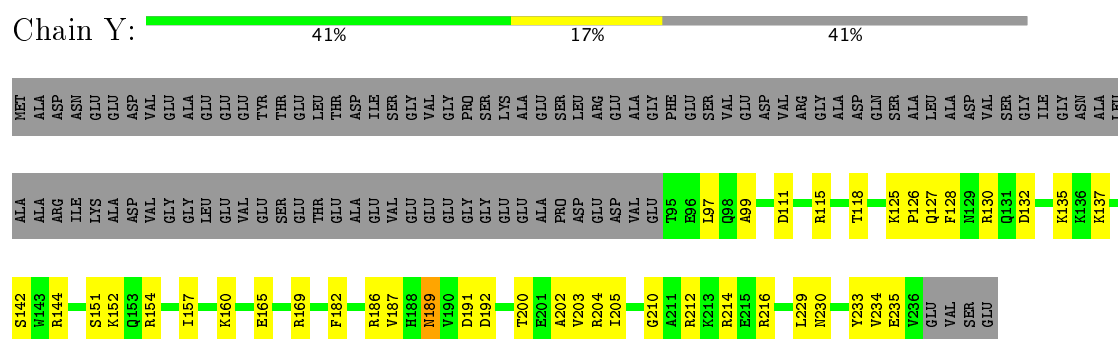
- Molecule 23: 50S ribosomal protein L30P



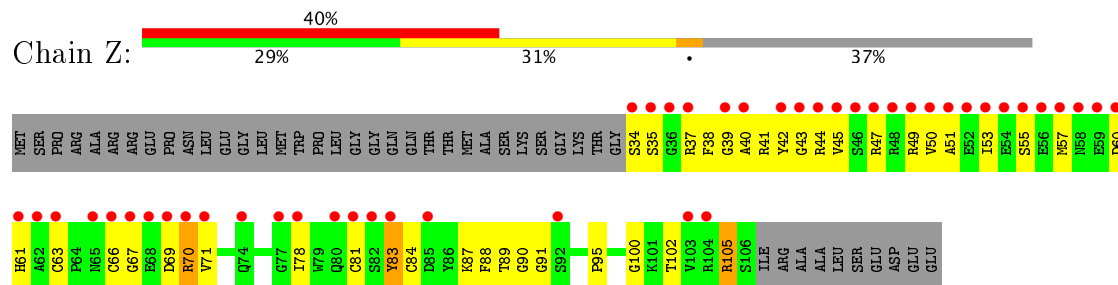
- Molecule 24: 50S ribosomal protein L31e



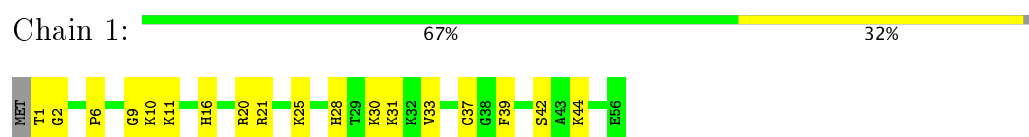
- Molecule 25: 50S ribosomal protein L32e



- Molecule 26: 50S ribosomal protein L37Ae

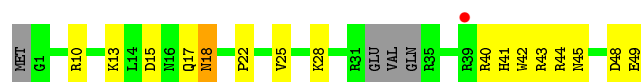


- Molecule 27: 50S ribosomal protein L37e

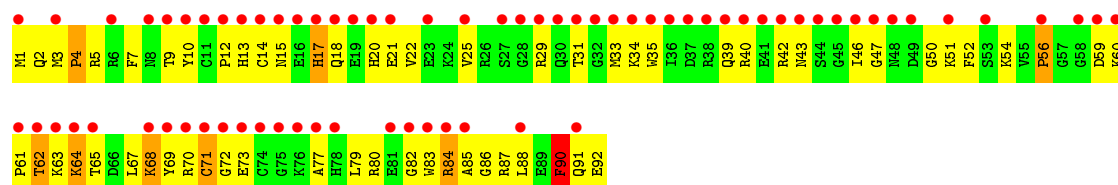
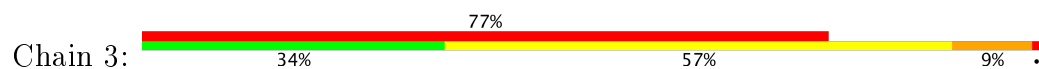


- Molecule 28: 50S ribosomal protein L39e

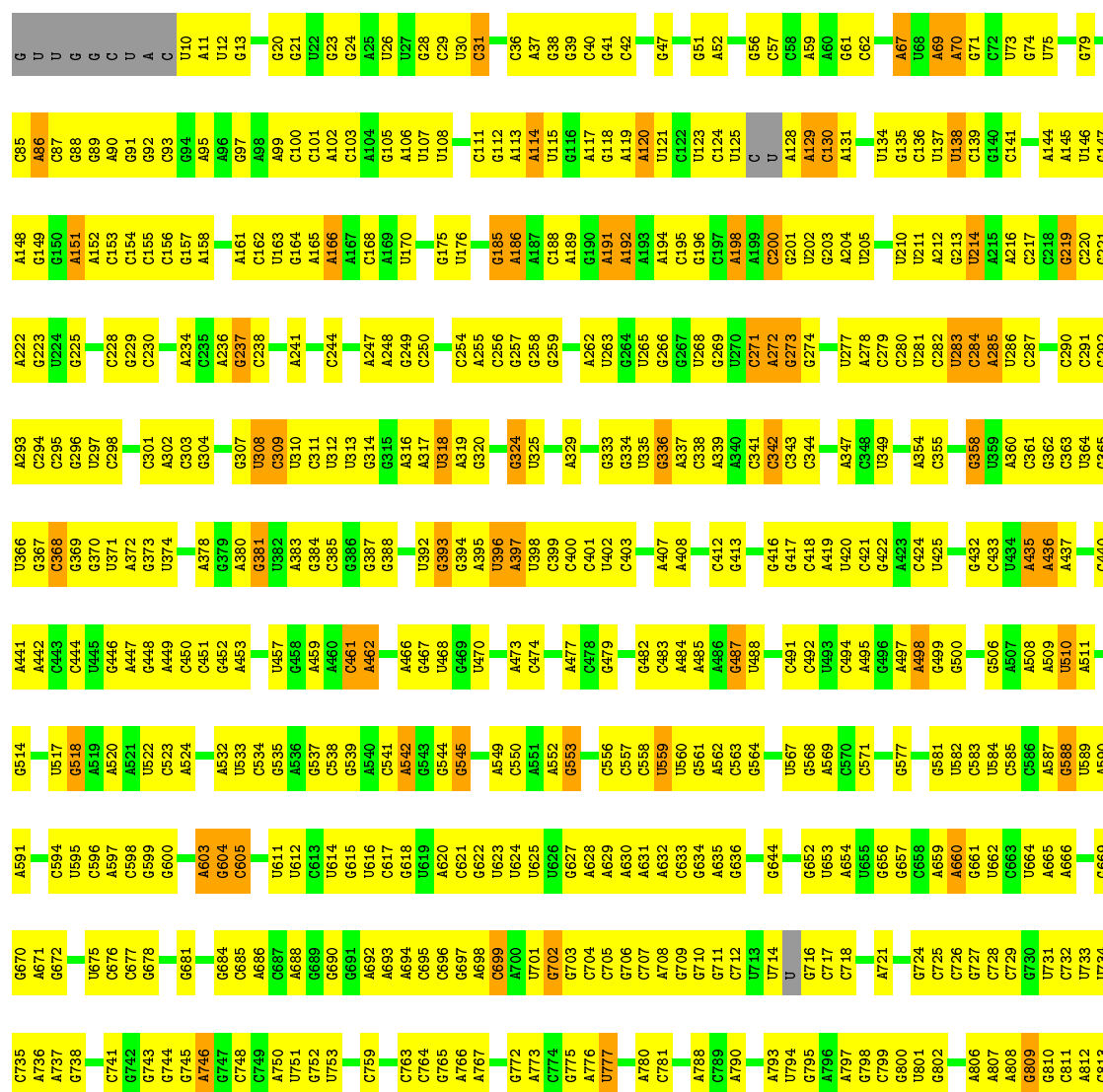




- Molecule 29: 50S ribosomal protein L44E



- Molecule 30: 23S RIBOSOMAL RNA



A1924	C1856	A1778	C1705	G1823	G1555	G1475	U1405	U1251	C1243	C1256	C1255	U1187	G1112	G1025	G964	G887	G814
G1925	A1857	A1778	G1706	A1624	G1556	A1476	A1406	C1255	U1333	C1256	U1255	A1188	U1115	U1026	A965	U888	U815
G1926	A1858	C1787	G1707	U1625	G1557	A1477	A1407	C1256	C1334	C1256	U1255	A1189	U1116	U1027	U966	U889	G816
A1927	A1859	C1787	G1708	A1626	C1558	U1478	U1408	C1256	C1334	C1256	U1255	A1189	U1116	U1028	U967	C890	G817
G1928	U1860	C1787	G1709	G1627	U1559	U1478	G1410	C1256	C1334	C1256	U1255	A1189	U1116	U1029	G968	A818	A819
G1929	C1861	C1787	A1710	U1630	U1561	G1484	G1410	C1256	C1334	C1256	U1255	A1189	U1116	U1030	G969	A819	A819
A1930	C1862	C1787	A1711	A1631	U1562	A1485	G1410	C1256	C1334	C1256	U1255	A1189	U1116	U1031	U970	A820	G820
A1931	C1863	C1787	A1712	A1632	C1563	A1485	A1413	C1256	C1334	C1256	U1255	A1189	U1116	U1032	U	A821	U821
G1932	C1864	C1787	A1713	A1633	C1564	G1490	A1414	C1256	C1334	C1256	U1255	A1189	U1116	U1041	G	C822	C822
G1933	A1865	C1787	A1716	C1634	C1566	C1495	G1415	C1256	C1334	C1256	U1255	A1189	U1116	U1042	G	G823	U823
A1934	A1866	C1787	A1717	U1635	G1567	A1496	G1416	C1256	C1334	C1256	U1255	A1189	U1116	U1043	U	U825	G824
G1935	G1867	C1787	A1718	U1635	G1568	G1497	G1417	C1256	C1334	C1256	U1255	A1189	U1116	U1044	C	U826	U826
G1936	G1868	C1787	A1719	U1636	U1569	G1497	G1418	C1256	C1334	C1256	U1255	A1189	U1116	U1045	G	U827	A827
U1937	A1869	C1787	G1719	A1641	U1569	U1500	U1419	C1256	C1334	C1256	U1255	A1189	U1116	U1046	C	U828	G828
G1938	C1871	C1787	U1722	A1642	A1572	U1500	C1420	C1256	C1334	C1256	U1255	A1189	U1116	U1047	C	U829	A829
U1939	C1872	C1787	U1722	A1643	A1573	U1503	C1421	C1256	C1334	C1256	U1255	A1189	U1116	U1048	C	C905	G830
G1940	C1873	C1787	G1723	U1644	C1574	A1504	C1422	C1256	C1334	C1256	U1255	A1189	U1116	U1049	U	U831	U831
A1941	U1874	C1787	U1724	C1645	C1575	U1505	C1423	C1256	C1334	C1256	U1255	A1189	U1116	U1052	C	C910	G911
A1942	A1875	C1787	C1725	C1646	G1576	U1506	C1424	C1256	C1334	C1256	U1255	A1189	U1116	U1053	C	A912	A912
C1943	C1876	C1787	C1725	C1647	G1577	C1507	C1425	C1256	C1334	C1256	U1255	A1189	U1116	U1054	G	A913	A913
G1947	C1877	C1787	G1730	A1653	U1577	C1507	C1426	C1256	C1334	C1256	U1255	A1189	U1116	U1055	A	U835	U835
G1948	U1878	C1787	C1731	A1654	C1578	C1507	C1427	C1256	C1334	C1256	U1255	A1189	U1116	U1056	G	A916	C838
G1949	C1880	C1787	A1733	G1655	U1583	G1512	U1429	C1256	C1334	C1256	U1255	A1189	U1116	U1057	A	U917	C839
G1950	A1881	C1787	C1734	A1656	C1584	G1513	G1430	C1256	C1334	C1256	U1255	A1189	U1116	U1058	G	U840	U840
G1951	C1882	C1787	C1735	A1657	C1585	G1514	G1431	C1256	C1334	C1256	U1255	A1189	U1116	U1059	G	A841	A841
U	U1883	C1787	A1736	C1662	C1586	G1515	A1434	C1256	C1334	C1256	U1255	A1189	U1116	U1060	A	C920	C842
A	C1884	C1787	C1736	C1663	C1587	G1516	A1435	C1256	C1334	C1256	U1255	A1189	U1116	U1061	G	G921	G843
A	A1885	C1787	U1741	C1664	C1588	U1517	C1436	C1256	C1334	C1256	U1255	A1189	U1116	U1062	U	A923	A844
C	A1886	C1787	A1742	C1665	G1589	A1518	C1437	C1256	C1334	C1256	U1255	A1189	U1116	U1063	C	G924	A844
C	A1887	C1787	G1743	C1666	G1590	A1519	C1438	C1256	C1334	C1256	U1255	A1189	U1116	U1064	G	C925	C848
U	A1888	C1787	G1744	C1667	A1591	G1520	C1439	C1256	C1334	C1256	U1255	A1189	U1116	U1065	C	A926	C848
U	U1889	C1787	C1745	C1668	A1592	G1521	C1440	C1256	C1334	C1256	U1255	A1189	U1116	U1066	C	U927	C853
U	U1890	C1787	G1745	C1669	C1593	G1522	C1441	C1256	C1334	C1256	U1255	A1189	U1116	U1067	A	G928	C854
G	C1891	C1787	U1748	C1670	C1594	G1523	A1442	C1256	C1334	C1256	U1255	A1189	U1116	U1068	C	A929	U855
A	C1892	C1787	U1749	U1671	G1595	U1524	C1443	C1256	C1334	C1256	U1255	A1189	U1116	U1069	A	U856	U856
C	C1893	C1787	U1749	U1672	G1596	U1525	G1444	C1256	C1334	C1256	U1255	A1189	U1116	U1070	C999	G857	A857
C	G1898	C1787	C1752	C1675	U1597	G1526	G1445	C1256	C1334	C1256	U1255	A1189	U1116	U1071	C1000	G858	A857
U1964	C1899	C1787	C1753	G1676	A1598	A1527	G1446	C1256	C1334	C1256	U1255	A1189	U1116	U1072	U	U859	U859
C1965	G1902	C1787	A1754	U1677	U1599	A1528	U1447	C1256	C1334	C1256	U1255	A1189	U1116	U1073	U1003	G860	U860
U1966	U1903	C1787	A1755	C1678	U1600	G1529	A1448	C1256	C1334	C1256	U1255	A1189	U1116	U1074	C1004	G861	U861
U1967	U1904	C1787	C1756	C1679	G1601	G1530	G1449	C1256	C1334	C1256	U1255	A1189	U1116	U1075	C1005	U862	U862
A1968	U1905	C1787	U1757	C1680	G1602	A1533	G1450	C1256	C1334	C1256	U1255	A1189	U1116	U1076	C1006	U863	U863
U1969	C1906	C1787	U1758	C1681	G1603	A1534	C1451	C1256	C1334	C1256	U1255	A1189	U1116	U1077	C1007	U864	U864
G1970	U1907	C1787	A1759	A1682	G1604	C1537	G1452	C1256	C1334	C1256	U1255	A1189	U1116	U1078	U1008	U865	U865
U1971	G1908	C1787	C1760	C1683	G1605	C1538	U1453	C1256	C1334	C1256	U1255	A1189	U1116	U1079	U1009	U866	U866
G1972	A1909	C1787	U1761	A1684	G1606	U1539	U1454	C1256	C1334	C1256	U1255	A1189	U1116	U1080	C1010	U867	U867
A1973	C1910	C1787	C1762	A1685	A1607	G1540	U1461	C1256	C1334	C1256	U1255	A1189	U1116	U1081	C1011	U868	U868
G1974	C1911	C1787	C1763	A1686	G1608	G1541	U1462	C1256	C1334	C1256	U1255	A1189	U1116	U1082	C1012	U869	U869
U1975	C1912	C1787	G1764	C1687	G1609	G1542	U1463	C1256	C1334	C1256	U1255	A1189	U1116	U1083	C1013	U870	U870
U1976	C1913	C1787	C1765	C1688	C1613	G1543	U1464	C1256	C1334	C1256	U1255	A1189	U1116	U1084	C1014	U871	U871
U1977	C1914	C1787	U1766	A1691	G1614	G1544	U1465	C1256	C1334	C1256	U1255	A1189	U1116	U1085	C1015	U872	U872
U1978	C1915	C1787	U1767	C1692	A1615	U1545	U1466	C1256	C1334	C1256	U1255	A1189	U1116	U1086	C1016	U873	U873
G1979	C1916	C1787	C1769	C1693	A1616	G1546	U1467	C1256	C1334	C1256	U1255	A1189	U1116	U1087	C1017	U874	U874
U1980	C1917	C1787	U1770	G1697	C1617	U1547	C1469	C1256	C1334	C1256	U1255	A1189	U1116	U1088	C1018	U875	U875
A1981	U1918	C1787	U1771	G1698	C1618	U1548	C1470	C1256	C1334	C1256	U1255	A1189	U1116	U1089	C1019	U876	U876
U1982	C1919	C1787	U1772	A1701	G1619	U1549	A1471	C1256	C1334	C1256	U1255	A1189	U1116	U1090	C1020	U877	U877
U1983	C1920	C1787	C1772	C1620	G1620	G1552	U1472	C1256	C1334	C1256	U1255	A1189	U1116	U1091	C1021	U878	U878
G1984	C1921	C1787	G1773	C1621	C1621	G1553	U1473	C1256	C1334	C1256	U1255	A1189	U1116	U1092	C1022	U879	U879
U1985	C1922	C1787	A1774	C1622	C1622	G1554	C1474	C1256	C1334	C1256	U1255	A1189	U1116	U1093	C1023	U880	U880
G1986	C1923	C1787	A1775	C1623	C1623	G1555	C1475	C1256	C1334	C1256	U1255	A1189	U1116	U1094	C1024	U881	U881



A62	C63	C64	A65	G66	C67	G68	U69		C72	A73	G74	G75	G76	A77		C81	U82	G83		U87	G88	C89	G90	C91	G92	A93		A105	U106	C107	C108	G109	G110	U111	U112	C113	G114	C115	C116		C122
-----	-----	-----	-----	-----	-----	-----	-----	--	-----	-----	-----	-----	-----	-----	--	-----	-----	-----	--	-----	-----	-----	-----	-----	-----	-----	--	------	------	------	------	------	------	------	------	------	------	------	------	--	------



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	212.41Å 299.52Å 574.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.81 – 3.00 85.66 – 2.40	Depositor EDS
% Data completeness (in resolution range)	77.8 (49.81-3.00) 77.4 (85.66-2.40)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.00 (at 2.40Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.180 , 0.247 0.178 , 0.237	Depositor DCC
$R_{free}$ test set	2780 reflections (1.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	52.9	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 82.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	99120	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.09% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, OMG, CL, SR, NA, K, CD, OMU, UR3, 1MA, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.34	0/1786	0.65	0/2408
2	B	0.34	0/2690	0.64	0/3652
3	C	0.38	0/1885	0.65	0/2552
4	D	0.32	0/1111	0.56	0/1498
5	E	0.34	0/1382	0.59	0/1880
6	F	0.34	0/901	0.58	0/1224
7	G	0.33	0/241	0.48	0/324
8	H	0.34	0/1302	0.65	0/1743
9	I	0.31	0/526	0.51	0/716
10	J	0.38	0/1136	0.62	0/1530
11	K	0.36	0/1004	0.67	0/1351
12	L	0.33	0/1130	0.62	0/1509
13	M	0.38	0/1582	0.63	0/2116
14	N	0.32	0/1474	0.63	0/1999
15	O	0.37	0/874	0.60	0/1181
16	P	0.34	0/1147	0.53	0/1528
17	Q	0.33	0/749	0.69	0/1005
18	R	0.37	0/1172	0.63	0/1578
19	S	0.38	0/648	0.60	0/875
20	T	0.34	0/958	0.66	1/1289 (0.1%)
21	U	0.45	0/417	0.67	0/562
22	V	0.32	0/502	0.55	0/675
23	W	0.36	0/1219	0.64	0/1655
24	X	0.35	0/664	0.61	0/895
25	Y	0.36	0/1146	0.62	0/1536
26	Z	0.45	0/584	0.63	0/781
27	1	0.43	0/438	0.57	0/578
28	2	0.35	0/401	0.60	0/529
29	3	0.48	0/771	0.66	0/1024
30	0	0.41	0/65954	0.68	4/102862 (0.0%)
31	9	0.35	0/2904	0.68	0/4526
All	All	0.39	0/98698	0.67	5/147581 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
23	W	0	1
30	0	0	18
31	9	0	1
All	All	0	20

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	1819	G	C5'-C4'-C3'	5.99	125.59	116.00
30	0	871	G	C5'-C4'-O4'	-5.85	102.08	109.10
30	0	1504	A	C1'-O4'-C4'	-5.36	105.62	109.90
20	T	52	ARG	N-CA-C	5.08	124.73	111.00
30	0	2726	U	N1-C1'-C2'	5.01	120.52	114.00

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	0	1266	U	Sidechain
30	0	1430	G	Sidechain
30	0	2076	U	Sidechain
30	0	2078	U	Sidechain
30	0	214	U	Sidechain
30	0	2412	G	Sidechain
30	0	2465	A	Sidechain
30	0	2552	C	Sidechain
30	0	2607	U	Sidechain
30	0	2726	U	Sidechain
30	0	324	G	Sidechain
30	0	393	G	Sidechain
30	0	435	A	Sidechain
30	0	436	A	Sidechain
30	0	462	A	Sidechain
30	0	518	G	Sidechain
30	0	664	U	Sidechain
30	0	868	G	Sidechain

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Group
31	9	76	G	Sidechain
23	W	90	TYR	Sidechain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1753	0	1766	97	0
2	B	2625	0	2532	127	0
3	C	1860	0	1813	70	0
4	D	1094	0	1085	50	0
5	E	1357	0	1266	55	0
6	F	890	0	843	27	0
7	G	240	0	231	11	0
8	H	1282	0	1292	55	0
9	I	519	0	500	26	0
10	J	1120	0	1098	44	0
11	K	994	0	1027	39	0
12	L	1118	0	1076	29	0
13	M	1558	0	1573	98	0
14	N	1445	0	1401	59	0
15	O	865	0	873	32	0
16	P	1136	0	1123	44	0
17	Q	735	0	729	21	0
18	R	1149	0	1122	37	0
19	S	641	0	605	16	0
20	T	950	0	924	33	0
21	U	410	0	368	38	0
22	V	499	0	511	19	0
23	W	1196	0	1137	52	0
24	X	654	0	653	24	0
25	Y	1130	0	1133	44	0
26	Z	573	0	535	64	0
27	1	431	0	426	20	0
28	2	396	0	413	21	0
29	3	755	0	732	90	0
30	0	59018	0	29810	2239	0
31	9	2599	0	1325	161	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	0	84	0	0	0	0
32	2	1	0	0	0	0
32	3	1	0	0	0	0
32	9	1	0	0	0	0
32	A	1	0	0	0	0
32	B	2	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0
32	Y	1	0	0	0	0
33	0	9	0	0	2	0
33	3	1	0	0	3	0
33	A	1	0	0	1	0
33	B	1	0	0	2	0
33	J	3	0	0	2	0
33	K	1	0	0	0	0
33	L	1	0	0	1	0
33	M	1	0	0	2	0
33	N	1	0	0	0	0
33	O	1	0	0	0	0
33	R	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	93	0	0	0	0
34	1	2	0	0	0	0
34	3	2	0	0	0	0
34	9	3	0	0	0	0
34	A	3	0	0	0	0
34	B	2	0	0	0	0
34	F	1	0	0	0	0
34	R	1	0	0	0	0
34	S	1	0	0	0	0
35	0	66	0	0	0	0
35	9	2	0	0	0	0
35	C	1	0	0	0	0
35	J	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	2	0	0	0	0
35	S	1	0	0	0	0
36	0	1	0	0	0	0
36	M	1	0	0	0	0
37	1	1	0	0	0	0
37	3	1	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	O	1	0	0	0	0
37	U	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5897	0	0	323	0
38	1	61	0	0	3	0
38	2	45	0	0	1	0
38	3	76	0	0	7	0
38	9	154	0	0	11	0
38	A	121	0	0	3	0
38	B	145	0	0	20	0
38	C	166	0	0	13	0
38	D	46	0	0	7	0
38	E	43	0	0	4	0
38	F	31	0	0	1	0
38	G	17	0	0	0	0
38	H	72	0	0	10	0
38	I	5	0	0	2	0
38	J	52	0	0	4	0
38	K	52	0	0	3	0
38	L	81	0	0	4	0
38	M	133	0	0	12	0
38	N	56	0	0	6	0
38	O	41	0	0	2	0
38	P	63	0	0	5	0
38	Q	52	0	0	1	0
38	R	75	0	0	2	0
38	S	37	0	0	0	0
38	T	40	0	0	3	0
38	U	28	0	0	5	0
38	V	15	0	0	1	0
38	W	69	0	0	7	0
38	X	22	0	0	4	0
38	Y	100	0	0	5	0
38	Z	28	0	0	5	0
All	All	99120	0	59922	3377	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 23.

All (3377) 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)
30:0:871:G:C8	30:0:871:G:H5'	1.74	1.22
30:0:1160:G:H5'	30:0:1161:A:C5'	1.70	1.20
30:0:1160:G:C5'	30:0:1161:A:H5'	1.73	1.18
30:0:1278:A:H4'	30:0:1279:U:C4	1.81	1.16
13:M:171:ARG:HD3	30:0:156:C:H5''	1.15	1.13
14:N:37:ARG:NH1	31:9:6:C:H5''	1.65	1.12
30:0:1559:A:H1'	38:0:5836:HOH:O	1.48	1.11
10:J:82:THR:HG23	30:0:1242:A:H5'	1.30	1.10
30:0:236:A:H4'	30:0:237:G:H5'	1.26	1.09
14:N:37:ARG:HH12	31:9:6:C:H5''	1.04	1.08
30:0:1205:U:H2'	30:0:1206:U:C5'	1.83	1.07
30:0:1205:U:H2'	30:0:1206:U:H5'	1.32	1.06
2:B:264:GLU:HG2	2:B:267:LYS:HE2	1.35	1.06
30:0:545:G:H8	30:0:545:G:H5'	1.18	1.05
29:3:88:LEU:HD22	33:3:8804:CL:CL	1.95	1.03
30:0:871:G:H5'	30:0:871:G:H8	0.89	1.02
31:9:54:A:O2'	31:9:55:U:H5'	1.58	1.02
30:0:2506:A:HO2'	30:0:2507:G:H8	1.04	1.01
30:0:1118:A:H3'	30:0:1118:A:H8	1.24	1.01
31:9:14:G:H5'	31:9:14:G:H8	1.25	1.01
22:V:50:ARG:HH12	30:0:56:G:H5''	1.25	1.01
30:0:960:G:H4'	38:0:7414:HOH:O	1.61	0.99
30:0:558:C:C2'	30:0:559:U:H5''	1.92	0.99
30:0:2372:A:H2'	30:0:2373:U:H6	1.28	0.99
29:3:68:LYS:HD3	29:3:70:ARG:HH21	1.28	0.99
30:0:1603:A:H5'	30:0:1605:G:O4'	1.61	0.98
30:0:1834:C:H2'	30:0:1840:A:N6	1.78	0.98
31:9:76:G:H3'	31:9:77:A:H5''	1.44	0.98
29:3:47:GLY:HA2	30:0:2121:G:H4'	1.43	0.98
30:0:1666:C:O2'	30:0:1667:A:H5''	1.62	0.98
18:R:8:ALA:HB1	18:R:13:THR:HG21	1.46	0.97
30:0:694:A:H2'	30:0:695:C:H5'	1.44	0.97
30:0:877:G:H5'	30:0:878:G:OP1	1.65	0.97
2:B:238:ASN:HD22	2:B:240:GLY:H	1.09	0.97
30:0:2717:C:C2'	30:0:2718:C:H5''	1.95	0.96
21:U:51:TRP:HD1	30:0:2865:G:HO2'	1.07	0.96
30:0:1118:A:H3'	30:0:1118:A:C8	1.99	0.96
30:0:1305:C:H5'	38:0:9833:HOH:O	1.66	0.96
30:0:1209:C:H2'	30:0:1210:G:H8	1.31	0.95
31:9:29:C:H2'	31:9:30:C:H5'	1.49	0.95
30:0:2717:C:O2'	30:0:2718:C:H5''	1.65	0.95
30:0:363:C:H1'	38:0:5247:HOH:O	1.67	0.95

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:545:G:C8	30:0:545:G:H5'	2.01	0.95
15:O:3:THR:HG22	30:0:656:G:H5'	1.46	0.95
38:M:8869:HOH:O	30:0:381:G:H5''	1.67	0.95
26:Z:44:ARG:HH21	30:0:1771:U:H5'	1.31	0.95
30:0:2420:G:O2'	30:0:2421:G:H5'	1.64	0.94
31:9:59:C:H2'	31:9:60:C:H6	1.33	0.94
30:0:1118:A:H62	30:0:1244:U:H3	1.14	0.93
30:0:2321:A:H2	30:0:2378:U:H3	1.12	0.93
30:0:871:G:C5'	30:0:871:G:H8	1.81	0.93
3:C:127:ARG:NH2	3:C:225:PRO:HG2	1.82	0.93
30:0:2748:G:H2'	38:0:7523:HOH:O	1.68	0.93
30:0:559:U:H6	30:0:559:U:H5'	1.34	0.92
31:9:54:A:C2'	31:9:55:U:H5'	1.99	0.92
30:0:1116:U:H3	30:0:1246:A:H62	1.17	0.92
30:0:2586:U:H3	30:0:2592:G:H22	1.18	0.91
30:0:2710:U:H1'	38:0:7601:HOH:O	1.69	0.91
30:0:2649:A:H3'	38:0:9829:HOH:O	1.70	0.91
30:0:1856:C:H1'	38:0:5846:HOH:O	1.70	0.91
30:0:1170:U:H2'	30:0:1172:G:OP2	1.71	0.91
30:0:1835:U:H5	30:0:1840:A:N7	1.68	0.91
30:0:1595:G:O2'	30:0:1596:U:H5'	1.71	0.91
30:0:2769:C:C2'	30:0:2770:G:H5'	2.01	0.90
8:H:49:GLN:HE21	8:H:140:TYR:HE2	1.18	0.90
30:0:870:G:H2'	30:0:871:G:H5''	1.51	0.90
13:M:58:GLN:HE22	30:0:259:G:H21	1.13	0.90
30:0:963:C:H2'	30:0:964:G:C8	2.05	0.90
10:J:52:GLN:HE22	30:0:1119:G:H2'	1.37	0.90
30:0:615:G:H1'	38:0:5221:HOH:O	1.72	0.90
23:W:4:LEU:HD13	23:W:52:VAL:HG21	1.51	0.90
30:0:1835:U:H2'	38:0:3618:HOH:O	1.72	0.90
30:0:625:U:H5''	30:0:1044:C:N4	1.87	0.89
30:0:969:G:H1	30:0:999:C:N4	1.71	0.89
30:0:1701:A:H4'	30:0:1702:U:H5''	1.55	0.89
16:P:115:SER:H	16:P:118:GLN:HE21	0.89	0.89
10:J:52:GLN:NE2	30:0:1119:G:H2'	1.88	0.88
13:M:73:ARG:NH2	30:0:2263:G:H5''	1.87	0.88
1:A:199:HIS:HD2	1:A:201:PHE:H	1.21	0.88
28:2:43:ARG:HH22	30:0:1684:A:H1'	1.37	0.87
30:0:542:A:H5'	30:0:542:A:H8	1.39	0.87
30:0:2502:C:H2'	30:0:2503:A:H5'	1.57	0.87
30:0:814:G:H4'	38:0:3128:HOH:O	1.73	0.87

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1666:C:H2'	30:0:1667:A:H5'	1.55	0.87
30:0:2005:G:OP2	30:0:2005:G:H3'	1.75	0.87
25:Y:187:VAL:HG23	25:Y:192:ASP:HB2	1.57	0.87
30:0:506:G:H22	30:0:509:A:C5'	1.87	0.86
31:9:56:A:H2'	31:9:57:A:H5''	1.57	0.86
30:0:2637:A:H4'	38:0:6039:HOH:O	1.75	0.86
30:0:2908:A:H2'	30:0:2909:G:O4'	1.75	0.86
30:0:506:G:H22	30:0:509:A:H5''	1.40	0.86
30:0:2248:C:H3'	38:0:5403:HOH:O	1.76	0.86
30:0:2372:A:H2'	30:0:2373:U:C6	2.09	0.86
13:M:71:SER:HB2	13:M:92:THR:HG22	1.56	0.86
11:K:10:GLN:HE21	11:K:10:GLN:H	1.18	0.86
30:0:553:G:H3'	38:0:4066:HOH:O	1.76	0.86
30:0:969:G:H1	30:0:999:C:H42	1.24	0.86
16:P:115:SER:H	16:P:118:GLN:NE2	1.73	0.86
6:F:63:ILE:HB	6:F:64:PRO:HD3	1.57	0.86
30:0:1183:C:H2'	38:0:6223:HOH:O	1.75	0.85
30:0:558:C:H2'	30:0:559:U:H5''	1.57	0.85
13:M:99:ARG:HE	13:M:170:ASN:HD22	1.19	0.85
30:0:2419:U:H5''	30:0:2420:G:H5'	1.57	0.85
29:3:20:HIS:CD2	29:3:69:TYR:HB3	2.12	0.85
30:0:2421:G:H1'	38:0:7004:HOH:O	1.75	0.85
30:0:2505:G:O2'	30:0:2506:A:H5'	1.76	0.85
30:0:308:U:H5'	30:0:309:C:OP1	1.75	0.85
30:0:1474:C:H6	30:0:1474:C:H5'	1.40	0.85
30:0:200:C:H2'	38:0:3433:HOH:O	1.75	0.84
30:0:2345:A:H3'	30:0:2346:C:H6	1.43	0.84
30:0:1474:C:C6	30:0:1474:C:H5'	2.13	0.84
30:0:870:G:C2'	30:0:871:G:H5''	2.07	0.84
31:9:13:A:O2'	31:9:14:G:H5''	1.77	0.84
30:0:1080:C:H4'	30:0:1081:A:OP1	1.76	0.84
11:K:39:GLY:HA2	38:0:5187:HOH:O	1.75	0.84
23:W:137:GLN:HE21	23:W:141:HIS:HE1	1.23	0.83
31:9:73:A:H2'	31:9:74:G:H8	1.43	0.83
16:P:115:SER:N	16:P:118:GLN:HE21	1.74	0.83
30:0:12:U:H2'	30:0:13:G:H5'	1.57	0.83
30:0:2717:C:H2'	30:0:2718:C:H5''	1.59	0.83
30:0:558:C:H2'	30:0:559:U:C5'	2.08	0.83
31:9:92:G:H2'	31:9:93:A:C8	2.14	0.83
30:0:2570:G:H5''	38:0:4880:HOH:O	1.78	0.83
13:M:68:ARG:NH2	13:M:73:ARG:HD3	1.94	0.83

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2896:A:H5''	38:0:6075:HOH:O	1.77	0.83
31:9:14:G:C8	31:9:14:G:H5'	2.14	0.83
30:0:271:C:H41	30:0:378:A:H2	1.22	0.82
30:0:1644:C:H2'	30:0:1645:U:H6	1.44	0.82
30:0:810:G:H2'	30:0:811:C:C6	2.13	0.82
30:0:2437:A:H2'	30:0:2438:G:C8	2.14	0.82
22:V:12:THR:HG22	22:V:15:GLU:HG3	1.60	0.82
30:0:1205:U:C2'	30:0:1206:U:C5'	2.57	0.82
30:0:1206:U:H5'	30:0:1206:U:H6	1.43	0.82
30:0:236:A:C4'	30:0:237:G:H5'	2.09	0.82
4:D:25:MET:SD	4:D:40:ILE:HD11	2.19	0.82
15:O:3:THR:CG2	30:0:656:G:H5'	2.09	0.82
3:C:236:THR:HG22	3:C:239:ALA:H	1.44	0.82
30:0:2345:A:H3'	30:0:2346:C:C6	2.15	0.82
30:0:2426:G:H1'	38:0:6068:HOH:O	1.79	0.82
30:0:2502:C:C2'	30:0:2503:A:H5'	2.10	0.82
13:M:134:ILE:HG23	13:M:141:ILE:HD13	1.62	0.81
30:0:1116:U:O2'	30:0:1118:A:H2	1.62	0.81
30:0:1191:A:H2'	30:0:1193:A:H5'	1.62	0.81
30:0:1278:A:H4'	30:0:1279:U:C5	2.15	0.81
30:0:614:U:O2'	30:0:615:G:H5'	1.80	0.81
30:0:2604:A:H5'	38:0:5760:HOH:O	1.79	0.81
30:0:185:G:H4'	30:0:186:A:OP1	1.78	0.81
26:Z:42:TYR:HA	30:0:1829:A:H61	1.45	0.81
30:0:282:C:O2'	30:0:283:U:H5'	1.79	0.81
14:N:67:ALA:HA	14:N:71:TRP:HB3	1.62	0.81
18:R:39:THR:HG22	18:R:42:GLU:H	1.44	0.80
13:M:171:ARG:CD	30:0:156:C:H5''	2.06	0.80
31:9:56:A:C2'	31:9:57:A:H5''	2.11	0.80
30:0:1632:A:H2'	30:0:1633:C:H5'	1.61	0.80
29:3:2:GLN:O	30:0:2320:U:H2'	1.80	0.80
6:F:91:VAL:HG12	6:F:92:GLY:H	1.47	0.80
30:0:1119:G:N2	30:0:1246:A:C2	2.48	0.80
30:0:2467:A:H3'	38:0:5416:HOH:O	1.82	0.80
31:9:59:C:H2'	31:9:60:C:C6	2.16	0.80
30:0:558:C:O2'	30:0:559:U:H5''	1.81	0.80
30:0:1185:U:H2'	30:0:1186:C:H6	1.46	0.80
22:V:50:ARG:NH1	30:0:56:G:H5''	1.95	0.80
11:K:14:LYS:HB2	11:K:45:PRO:HG2	1.63	0.80
31:9:29:C:C2'	31:9:30:C:H5'	2.12	0.79
19:S:55:GLN:NE2	30:0:1446:U:H2'	1.97	0.79

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:LYS:HE2	26:Z:50:VAL:HG13	1.63	0.79
30:0:1116:U:HO2'	30:0:1118:A:H2	0.80	0.79
30:0:1603:A:H5''	30:0:1605:G:H5'	1.65	0.79
28:2:41:HIS:H	28:2:45:ASN:HD22	1.31	0.79
21:U:56:ARG:HD2	30:0:2890:A:N9	1.97	0.79
13:M:58:GLN:NE2	30:0:259:G:H21	1.81	0.79
30:0:2506:A:O2'	30:0:2507:G:H8	1.66	0.79
1:A:199:HIS:CD2	1:A:201:PHE:H	2.00	0.79
13:M:159:VAL:HG12	33:M:8818:CL:CL	2.20	0.79
30:0:2717:C:H2'	30:0:2718:C:C5'	2.13	0.79
31:9:73:A:H2'	31:9:74:G:C8	2.17	0.79
30:0:2604:A:H4'	38:0:7586:HOH:O	1.83	0.79
30:0:282:C:H1'	30:0:368:C:H41	1.46	0.79
30:0:282:C:H1'	30:0:368:C:N4	1.98	0.79
30:0:2783:A:H3'	38:0:5197:HOH:O	1.82	0.78
30:0:2769:C:O2'	30:0:2770:G:H5'	1.84	0.78
30:0:1829:A:H2'	30:0:1830:C:H5'	1.65	0.78
30:0:2533:C:H5'	30:0:2533:C:H6	1.47	0.78
30:0:2906:A:H5'	30:0:2907:C:O4'	1.83	0.78
31:9:55:U:H5''	38:9:9146:HOH:O	1.82	0.78
30:0:541:C:C2'	30:0:542:A:H5''	2.13	0.78
30:0:853:C:H3'	38:0:4528:HOH:O	1.83	0.78
30:0:2416:G:H2'	30:0:2417:C:H6	1.49	0.78
2:B:221:GLN:HE22	11:K:42:ASN:HD22	1.32	0.78
10:J:74:ARG:HB3	10:J:74:ARG:HH11	1.48	0.78
13:M:70:GLY:HA3	13:M:73:ARG:NH2	1.99	0.78
30:0:2237:G:H1'	38:0:4824:HOH:O	1.83	0.78
30:0:297:U:H2'	30:0:298:C:H6	1.49	0.78
31:9:56:A:C3'	31:9:57:A:H5''	2.12	0.78
30:0:1189:A:H1'	30:0:1209:C:O4'	1.84	0.77
30:0:1426:C:H2'	38:0:9600:HOH:O	1.83	0.77
30:0:1617:C:C4	30:0:1643:C:H4'	2.19	0.77
30:0:1741:U:H5'	30:0:1742:A:OP1	1.83	0.77
13:M:171:ARG:HD3	30:0:156:C:C5'	2.07	0.77
30:0:1942:A:H5'	38:0:7329:HOH:O	1.84	0.77
30:0:2440:C:H5''	38:0:3808:HOH:O	1.83	0.77
30:0:603:A:H1'	30:0:605:C:C2	2.19	0.77
30:0:1118:A:C3'	30:0:1118:A:C8	2.66	0.77
30:0:2769:C:H2'	30:0:2770:G:O4'	1.82	0.77
4:D:105:SER:OG	30:0:2338:G:H1'	1.83	0.77
10:J:70:PHE:CE1	30:0:2676:C:H4'	2.19	0.77

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2578:G:H5'	30:0:2578:G:H8	1.49	0.77
8:H:91:ARG:O	30:0:1003:U:H4'	1.84	0.77
30:0:2335:C:H2'	30:0:2336:G:C8	2.20	0.76
30:0:2469:A:H1'	38:0:3231:HOH:O	1.85	0.76
30:0:247:A:H2'	38:0:3913:HOH:O	1.85	0.76
29:3:64:LYS:HA	29:3:84:ARG:HA	1.67	0.76
11:K:10:GLN:NE2	11:K:10:GLN:H	1.83	0.76
30:0:1205:U:H2'	30:0:1206:U:H5''	1.66	0.76
30:0:1834:C:H2'	30:0:1840:A:H62	1.48	0.76
20:T:71:VAL:HG11	20:T:90:PRO:HB3	1.65	0.76
30:0:1249:U:H2'	30:0:1250:C:H6	1.51	0.76
30:0:1170:U:H1'	30:0:1172:G:N7	2.00	0.76
30:0:136:C:H2'	30:0:137:U:O4'	1.86	0.76
30:0:960:G:N3	30:0:960:G:H3'	2.00	0.76
31:9:36:C:H4'	38:9:9029:HOH:O	1.85	0.76
30:0:1634:G:H3'	38:0:3885:HOH:O	1.85	0.76
30:0:146:U:O2'	30:0:147:G:H5'	1.86	0.76
30:0:541:C:H2'	30:0:542:A:C5'	2.15	0.75
31:9:75:G:H1	31:9:106:U:H3	1.33	0.75
30:0:2083:A:H3'	38:0:7559:HOH:O	1.86	0.75
30:0:564:G:H1'	38:0:6290:HOH:O	1.85	0.75
2:B:18:ARG:HE	2:B:256:GLN:HE21	1.31	0.75
13:M:88:VAL:HG21	30:0:2122:C:O2'	1.86	0.75
26:Z:63:CYS:SG	26:Z:81:CYS:HB2	2.26	0.75
30:0:1434:A:HO2'	30:0:1435:U:H6	1.32	0.75
30:0:1189:A:H3'	38:0:7661:HOH:O	1.86	0.75
30:0:297:U:H2'	30:0:298:C:C6	2.21	0.75
30:0:1524:U:H4'	30:0:1524:U:OP1	1.87	0.75
30:0:281:U:O2'	30:0:282:C:H5'	1.85	0.75
30:0:1184:C:H1'	38:0:7447:HOH:O	1.86	0.75
30:0:40:C:H4'	38:0:6986:HOH:O	1.86	0.75
30:0:1377:C:H6	30:0:1377:C:H5'	1.52	0.74
30:0:69:A:H5'	30:0:69:A:C8	2.22	0.74
30:0:718:C:H2'	30:0:718:C:O2	1.87	0.74
8:H:44:ASP:HA	8:H:170:ARG:HH12	1.50	0.74
30:0:1279:U:O2	30:0:1279:U:H2'	1.85	0.74
30:0:1787:C:O2'	30:0:1788:U:H5'	1.87	0.74
30:0:279:C:O2'	30:0:280:C:H5'	1.87	0.74
30:0:635:A:H2'	30:0:636:G:H5''	1.68	0.74
30:0:1972:U:H2'	30:0:1973:A:C5'	2.18	0.74
1:A:223:ARG:NH2	30:0:2271:G:H5'	2.02	0.74

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:848:C:H5'	38:0:7257:HOH:O	1.87	0.74
10:J:26:VAL:HG13	10:J:36:VAL:HG11	1.69	0.74
30:0:1589:G:N2	30:0:1605:G:H1'	2.02	0.74
30:0:1165:G:O3'	30:0:1174:A:H4'	1.88	0.74
1:A:47:HIS:CD2	30:0:1654:U:H2'	2.22	0.74
30:0:2831:C:C2'	30:0:2832:C:H5'	2.18	0.74
30:0:629:A:H4'	38:0:4498:HOH:O	1.88	0.74
30:0:694:A:C2'	30:0:695:C:H5'	2.18	0.74
30:0:1185:U:H5'	38:0:7447:HOH:O	1.88	0.73
30:0:2100:A:H5'	38:0:7373:HOH:O	1.88	0.73
30:0:2703:A:H2'	30:0:2704:C:H6	1.52	0.73
21:U:44:ARG:HD3	21:U:49:LEU:HD11	1.70	0.73
30:0:2011:A:H5''	38:0:4388:HOH:O	1.87	0.73
29:3:68:LYS:CD	29:3:70:ARG:HH21	2.01	0.73
30:0:1603:A:C5'	30:0:1605:G:H5'	2.19	0.73
30:0:254:C:H2'	30:0:254:C:O2	1.88	0.73
30:0:1855:G:H4'	30:0:1856:C:O5'	1.88	0.73
30:0:2769:C:H2'	30:0:2770:G:H5'	1.69	0.73
31:9:1:U:H4'	31:9:3:A:OP1	1.88	0.73
2:B:18:ARG:HE	2:B:256:GLN:NE2	1.86	0.73
30:0:137:U:H2'	30:0:139:C:C5	2.23	0.73
2:B:201:ASP:HB2	2:B:312:ARG:HD2	1.70	0.73
30:0:1589:G:H22	30:0:1605:G:H1'	1.53	0.73
30:0:1835:U:C5	30:0:1840:A:N7	2.53	0.73
30:0:2505:G:C2'	30:0:2506:A:H5'	2.19	0.73
30:0:69:A:H5'	30:0:69:A:H8	1.54	0.73
31:9:3:A:N6	31:9:22:G:H1'	2.03	0.73
30:0:2064:U:H5'	30:0:2652:U:O3'	1.89	0.73
30:0:2472:C:O2'	30:0:2634:G:H4'	1.89	0.73
30:0:871:G:C8	30:0:871:G:C5'	2.63	0.73
10:J:47:THR:HG21	30:0:1244:U:H2'	1.69	0.73
30:0:2635:A:O2'	30:0:2636:C:H5'	1.88	0.72
38:B:9106:HOH:O	30:0:2672:C:H1'	1.87	0.72
30:0:1625:U:H6	30:0:1625:U:H3'	1.54	0.72
30:0:1666:C:H2'	30:0:1667:A:C5'	2.19	0.72
30:0:283:U:H5	30:0:284:C:N3	1.87	0.72
1:A:109:GLU:HG2	1:A:116:GLY:H	1.53	0.72
30:0:1733:A:C6	30:0:1734:C:C2	2.77	0.72
13:M:99:ARG:HD2	13:M:167:GLY:HA2	1.71	0.72
1:A:48:ASP:HB3	38:A:9085:HOH:O	1.90	0.72
13:M:79:ALA:HB1	38:0:4442:HOH:O	1.89	0.72

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:58:VAL:HB	4:D:62:ASP:HB3	1.72	0.72
13:M:76:ARG:HB2	13:M:88:VAL:HG13	1.72	0.72
30:0:1372:A:H3'	38:0:7172:HOH:O	1.88	0.72
18:R:132:ARG:NH2	30:0:2055:A:H4'	2.05	0.72
30:0:2467:A:H1'	38:0:9049:HOH:O	1.89	0.72
30:0:2898:G:O2'	30:0:2899:A:H5'	1.89	0.72
30:0:1316:G:H5''	38:0:5285:HOH:O	1.88	0.72
30:0:2831:C:O2'	30:0:2832:C:H5'	1.88	0.72
30:0:1178:G:H2'	30:0:1179:C:C6	2.25	0.72
30:0:1713:G:H1'	38:0:5039:HOH:O	1.89	0.72
30:0:2297:U:H1'	38:0:5144:HOH:O	1.88	0.72
30:0:272:A:H5'	30:0:273:G:OP2	1.90	0.72
30:0:2253:G:H2'	30:0:2254:G:H8	1.55	0.72
30:0:595:U:O2'	30:0:596:C:H5'	1.90	0.71
30:0:603:A:H5''	30:0:604:G:OP1	1.89	0.71
31:9:26:C:O2'	31:9:27:C:H5'	1.91	0.71
30:0:1979:G:H3'	38:0:3283:HOH:O	1.88	0.71
30:0:958:G:H2'	30:0:959:C:C6	2.24	0.71
30:0:1477:C:H5'	30:0:1868:G:H5'	1.72	0.71
18:R:2:ILE:HG22	30:0:21:G:H4'	1.71	0.71
30:0:1801:A:H3'	38:0:7596:HOH:O	1.90	0.71
30:0:2321:A:H2	30:0:2378:U:N3	1.88	0.71
27:1:25:LYS:HD2	28:2:49:GLU:H	1.55	0.71
23:W:125:HIS:CE1	30:0:1097:A:H5''	2.25	0.71
25:Y:187:VAL:HG23	25:Y:192:ASP:CB	2.21	0.71
30:0:1197:G:H1'	30:0:1203:G:N2	2.06	0.71
30:0:1398:G:H2'	30:0:1399:A:C8	2.25	0.71
30:0:2769:C:H2'	30:0:2770:G:C5'	2.20	0.71
26:Z:84:CYS:HB3	30:0:1604:G:H22	1.56	0.71
5:E:143:GLN:NE2	30:0:2779:G:H21	1.89	0.71
30:0:2780:C:H2'	30:0:2781:U:C6	2.26	0.71
30:0:920:C:H4'	30:0:921:G:C2	2.26	0.71
14:N:33:ARG:HH21	14:N:48:VAL:HG11	1.55	0.71
31:9:55:U:H4'	31:9:56:A:C8	2.25	0.71
21:U:56:ARG:HG3	21:U:56:ARG:HH11	1.56	0.71
30:0:1666:C:C2'	30:0:1667:A:C5'	2.69	0.71
3:C:139:VAL:HG13	38:C:8645:HOH:O	1.91	0.70
30:0:1185:U:H2'	30:0:1186:C:C6	2.25	0.70
30:0:2321:A:C2	30:0:2378:U:N3	2.55	0.70
30:0:2524:G:H21	30:0:2526:C:N4	1.88	0.70
30:0:1118:A:N6	30:0:1244:U:H3	1.89	0.70

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2416:G:H2'	30:0:2417:C:C6	2.26	0.70
3:C:78:ARG:HH11	3:C:78:ARG:HG3	1.56	0.70
30:0:1972:U:H2'	30:0:1973:A:H5'	1.73	0.70
30:0:2312:G:H2'	30:0:2313:C:H5'	1.72	0.70
30:0:2717:C:C2'	30:0:2718:C:C5'	2.68	0.70
22:V:57:LYS:HA	22:V:60:GLN:HE21	1.57	0.70
30:0:1596:U:H2'	30:0:1598:A:OP2	1.90	0.70
30:0:2565:C:H4'	38:0:4806:HOH:O	1.91	0.70
14:N:4:PRO:HB2	30:0:1010:C:H4'	1.73	0.70
26:Z:43:GLY:O	26:Z:47:ARG:HG2	1.91	0.70
30:0:1829:A:C2'	30:0:1830:C:H5'	2.21	0.70
30:0:2539:U:H1'	38:0:7770:HOH:O	1.90	0.70
13:M:164:THR:HG22	13:M:166:ALA:H	1.57	0.70
1:A:223:ARG:HH12	30:0:2270:G:H4'	1.55	0.70
14:N:11:ARG:HD3	31:9:114:G:O6	1.90	0.70
38:C:8565:HOH:O	20:T:2:LYS:HE3	1.92	0.70
29:3:40:ARG:HA	29:3:52:PHE:CE1	2.26	0.70
30:0:1226:G:H2'	30:0:1227:C:H6	1.57	0.70
31:9:59:C:O5'	31:9:59:C:H6	1.74	0.69
30:0:1589:G:H5'	38:0:6843:HOH:O	1.91	0.69
30:0:2415:A:H2'	30:0:2416:G:H5'	1.74	0.69
30:0:522:U:O2'	30:0:1366:C:H5'	1.92	0.69
30:0:1181:A:C2'	30:0:1182:C:H5'	2.22	0.69
30:0:2404:G:H5''	38:0:5177:HOH:O	1.91	0.69
30:0:714:U:H4'	38:0:5705:HOH:O	1.93	0.69
1:A:135:VAL:HG11	1:A:147:ARG:NH2	2.07	0.69
7:G:64:ASN:N	7:G:64:ASN:HD22	1.90	0.69
10:J:70:PHE:CD1	30:0:2676:C:H4'	2.27	0.69
30:0:2667:G:H1'	30:0:2914:A:N3	2.08	0.69
8:H:168:VAL:HG13	38:H:218:HOH:O	1.91	0.69
29:3:20:HIS:HD2	29:3:69:TYR:HB3	1.56	0.69
26:Z:37:ARG:HB3	38:0:4665:HOH:O	1.91	0.69
30:0:1205:U:C2'	30:0:1206:U:H5''	2.23	0.69
30:0:545:G:C5'	30:0:545:G:H8	1.99	0.69
14:N:37:ARG:NH1	31:9:6:C:C5'	2.50	0.69
30:0:735:C:H2'	30:0:736:A:O4'	1.93	0.69
2:B:258:GLY:H	2:B:260:HIS:CE1	2.10	0.69
3:C:76:ARG:HH11	3:C:76:ARG:HB3	1.57	0.69
30:0:1741:U:O2'	30:0:2723:G:H4'	1.91	0.69
15:O:32:ARG:HE	15:O:35:LYS:HD2	1.58	0.69
30:0:2705:U:H2'	30:0:2706:A:C8	2.28	0.69

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:128:ARG:NH2	30:0:2054:A:N3	2.41	0.69
30:0:2827:A:H2'	30:0:2828:G:O4'	1.92	0.69
13:M:81:ARG:HD2	13:M:85:ARG:HG3	1.74	0.69
30:0:596:C:H2'	30:0:597:A:H8	1.58	0.69
30:0:1632:A:C2'	30:0:1633:C:H5'	2.22	0.68
30:0:2795:C:O2'	30:0:2796:U:H5'	1.93	0.68
21:U:56:ARG:HB2	30:0:2890:A:C8	2.27	0.68
11:K:74:VAL:HG21	11:K:96:VAL:HG23	1.75	0.68
18:R:138:SER:HB3	30:0:2053:G:OP1	1.94	0.68
16:P:117:SER:HB3	30:0:1593:C:OP1	1.92	0.68
30:0:1702:U:H5'	38:0:3414:HOH:O	1.92	0.68
26:Z:47:ARG:NH2	30:0:1771:U:H1'	2.08	0.68
30:0:2111:G:H1'	38:0:9052:HOH:O	1.94	0.68
30:0:2635:A:C2'	30:0:2636:C:H5'	2.23	0.68
23:W:137:GLN:HE21	23:W:141:HIS:CE1	2.10	0.68
30:0:2637:A:H5'	38:0:4897:HOH:O	1.94	0.68
30:0:333:G:O2'	30:0:334:G:H5'	1.94	0.68
2:B:264:GLU:HG2	2:B:267:LYS:CE	2.19	0.68
23:W:125:HIS:NE2	30:0:1097:A:H5''	2.09	0.68
30:0:1197:G:H1'	30:0:1203:G:C2	2.28	0.68
29:3:50:GLY:HA3	30:0:170:U:H1'	1.75	0.68
30:0:585:C:H5''	38:0:4840:HOH:O	1.94	0.68
30:0:1209:C:H2'	30:0:1210:G:C8	2.23	0.68
26:Z:42:TYR:CA	30:0:1829:A:H61	2.07	0.68
30:0:685:C:O2	30:0:748:C:H4'	1.94	0.68
2:B:267:LYS:HD3	38:B:8996:HOH:O	1.93	0.68
30:0:1151:G:H2'	38:0:5713:HOH:O	1.92	0.68
2:B:206:THR:HG21	30:0:2716:G:H5''	1.76	0.68
30:0:2840:A:H3'	38:0:7629:HOH:O	1.94	0.68
10:J:18:ILE:HD13	30:0:1244:U:OP1	1.94	0.68
10:J:74:ARG:CB	10:J:74:ARG:HH11	2.07	0.68
13:M:95:LYS:HE2	30:0:157:G:H4'	1.76	0.67
30:0:1625:U:C6	30:0:1625:U:H3'	2.29	0.67
29:3:90:PHE:HD1	29:3:90:PHE:H	1.42	0.67
3:C:76:ARG:NH1	3:C:76:ARG:HB3	2.09	0.67
10:J:39:VAL:HG22	10:J:106:GLY:O	1.94	0.67
18:R:98:ASN:HD21	30:0:500:G:H21	1.40	0.67
30:0:1118:A:C8	30:0:1119:G:H5''	2.29	0.67
21:U:42:LEU:HD22	30:0:1810:C:H1'	1.76	0.67
30:0:1813:U:H2'	38:0:6701:HOH:O	1.94	0.67
13:M:70:GLY:HA2	30:0:2263:G:H4'	1.76	0.67

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1528:A:H2'	30:0:1529:G:O4'	1.95	0.67
30:0:541:C:H2'	30:0:542:A:H5''	1.74	0.67
8:H:57:THR:HG23	8:H:131:GLN:HA	1.76	0.67
30:0:2524:G:H5''	38:0:4698:HOH:O	1.94	0.67
30:0:1787:C:H4'	30:0:2883:A:O4'	1.94	0.67
13:M:91:ILE:HG23	38:0:7530:HOH:O	1.94	0.67
30:0:2894:C:O2'	30:0:2895:C:H5'	1.95	0.67
28:2:28:LYS:HE2	30:0:86:A:H1'	1.77	0.67
13:M:73:ARG:HH22	30:0:2263:G:H5''	1.58	0.67
21:U:19:THR:HG22	21:U:20:MET:H	1.59	0.67
30:0:119:A:H2'	30:0:120:A:H5''	1.77	0.67
30:0:370:G:O2'	30:0:371:U:H5'	1.93	0.67
31:9:76:G:C3'	31:9:77:A:H5''	2.23	0.67
30:0:2780:C:H2'	30:0:2781:U:H6	1.59	0.67
30:0:2829:G:N2	30:0:2912:C:C2	2.63	0.67
12:L:46:LEU:O	30:0:2430:A:H4'	1.95	0.67
30:0:1641:A:H2'	30:0:1642:A:H5'	1.77	0.67
30:0:256:C:H2'	30:0:257:G:O4'	1.95	0.67
5:E:91:PHE:HE1	30:0:2694:A:H4'	1.58	0.67
30:0:810:G:H2'	30:0:811:C:H6	1.56	0.67
29:3:60:LYS:HG3	29:3:61:PRO:HD2	1.77	0.67
4:D:154:LYS:HD2	4:D:154:LYS:H	1.60	0.67
10:J:75:PRO:HG2	10:J:105:LEU:HD21	1.77	0.67
11:K:20:CYS:HB2	11:K:29:LEU:HG	1.77	0.67
16:P:59:ARG:HD3	38:0:6249:HOH:O	1.95	0.66
1:A:135:VAL:HG21	1:A:147:ARG:HB3	1.77	0.66
30:0:2785:C:H5'	38:0:7694:HOH:O	1.95	0.66
30:0:596:C:H2'	30:0:597:A:C8	2.29	0.66
14:N:33:ARG:NH2	14:N:48:VAL:HG11	2.10	0.66
30:0:468:U:H3'	38:0:7549:HOH:O	1.93	0.66
29:3:68:LYS:HD3	29:3:70:ARG:NH2	2.07	0.66
15:O:14:LEU:HD23	15:O:102:ILE:HD11	1.77	0.66
30:0:1041:U:H2'	30:0:1042:U:H5'	1.78	0.66
30:0:869:G:H1'	38:0:3302:HOH:O	1.95	0.66
13:M:48:LYS:HE3	13:M:52:GLN:HE21	1.60	0.66
30:0:1120:U:H5'	30:0:1121:G:OP2	1.95	0.66
11:K:12:LEU:HB2	11:K:47:ALA:HB3	1.77	0.66
30:0:1205:U:C2'	30:0:1206:U:H5'	2.18	0.66
30:0:123:U:H5'	38:0:6635:HOH:O	1.96	0.66
30:0:1942:A:H3'	38:0:7329:HOH:O	1.95	0.66
30:0:2329:C:O2'	30:0:2330:U:H5'	1.95	0.66

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:113:SER:HB2	38:N:8852:HOH:O	1.94	0.66
30:0:1063:G:H5''	38:0:9856:HOH:O	1.94	0.66
30:0:1167:G:H2'	30:0:1168:C:C6	2.31	0.66
28:2:43:ARG:NH2	30:0:1684:A:H1'	2.10	0.66
30:0:2032:U:H2'	30:0:2033:G:C5'	2.26	0.66
30:0:2760:C:H5''	38:0:5294:HOH:O	1.95	0.66
30:0:318:U:H5'	30:0:339:A:C2	2.31	0.66
30:0:704:C:H2'	30:0:705:C:H6	1.60	0.66
31:9:7:G:H5'	38:9:9102:HOH:O	1.95	0.66
2:B:27:ASN:H	2:B:27:ASN:HD22	1.44	0.66
30:0:2533:C:C6	30:0:2533:C:H5'	2.31	0.66
3:C:184:ARG:NH2	30:0:450:C:OP1	2.29	0.66
30:0:559:U:C6	30:0:559:U:H5'	2.23	0.66
30:0:921:G:H4'	30:0:924:G:N1	2.11	0.66
30:0:1249:U:H2'	30:0:1250:C:C6	2.30	0.65
30:0:1603:A:H5'	30:0:1605:G:C4'	2.26	0.65
30:0:449:A:H3'	38:0:6214:HOH:O	1.95	0.65
26:Z:44:ARG:NH2	30:0:1771:U:H5'	2.09	0.65
30:0:2851:G:H2'	30:0:2902:A:H61	1.60	0.65
30:0:559:U:H6	30:0:559:U:C5'	2.09	0.65
2:B:179:LEU:O	2:B:183:GLU:HG2	1.96	0.65
12:L:143:THR:HG22	12:L:144:ASP:H	1.61	0.65
14:N:80:SER:HB2	38:N:8833:HOH:O	1.95	0.65
20:T:9:LYS:HE3	20:T:13:ARG:NH1	2.12	0.65
30:0:368:C:H2'	30:0:369:G:H5'	1.77	0.65
31:9:29:C:C5	31:9:30:C:C6	2.84	0.65
26:Z:78:ILE:HG21	26:Z:87:LYS:HE2	1.78	0.65
30:0:2707:C:H2'	30:0:2707:C:O2	1.96	0.65
38:D:7597:HOH:O	31:9:56:A:H2	1.79	0.65
1:A:122:SER:HB2	1:A:164:ARG:NH1	2.11	0.65
16:P:88:GLN:NE2	30:0:1800:G:H1'	2.10	0.65
21:U:56:ARG:HD2	30:0:2890:A:C1'	2.25	0.65
30:0:1061:C:H3'	38:0:5051:HOH:O	1.97	0.65
30:0:1132:A:N6	30:0:1229:C:H2'	2.12	0.65
9:I:110:ASP:O	30:0:1163:G:H5'	1.95	0.65
30:0:1666:C:C2'	30:0:1667:A:H5''	2.27	0.65
30:0:213:G:N2	30:0:225:G:H2'	2.11	0.65
30:0:2597:U:H2'	30:0:2598:U:H5'	1.77	0.65
5:E:91:PHE:CE1	30:0:2694:A:H4'	2.32	0.65
30:0:416:G:H5''	38:0:7402:HOH:O	1.96	0.65
30:0:696:C:H4'	38:0:7263:HOH:O	1.96	0.65

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:115:ARG:HH21	30:0:1266:U:H4'	1.60	0.65
30:0:1385:G:H1'	38:0:4024:HOH:O	1.97	0.65
30:0:290:C:O2'	30:0:291:C:H5'	1.96	0.65
30:0:42:C:H1'	38:0:4645:HOH:O	1.97	0.65
38:O:1484:HOH:O	30:0:710:G:H1'	1.97	0.65
30:0:812:A:H2'	30:0:813:C:C6	2.31	0.65
2:B:238:ASN:HD22	2:B:240:GLY:N	1.90	0.65
16:P:81:LYS:O	30:0:1761:U:H5'	1.97	0.65
30:0:2119:C:O2'	30:0:2120:U:H5'	1.97	0.65
30:0:1586:G:O2'	30:0:1587:U:H5'	1.97	0.64
30:0:2892:G:C6	30:0:2893:C:C4	2.85	0.64
30:0:696:C:O2'	30:0:697:G:H5'	1.97	0.64
31:9:61:C:H2'	31:9:62:A:H8	1.62	0.64
30:0:1377:C:H5'	30:0:1377:C:C6	2.33	0.64
30:0:1422:U:H2'	30:0:1423:C:C6	2.32	0.64
30:0:1735:C:O2'	30:0:1736:A:H5'	1.97	0.64
30:0:1862:C:H1'	38:0:7203:HOH:O	1.96	0.64
38:B:8996:HOH:O	30:0:2766:A:H5'	1.97	0.64
30:0:441:A:H1'	30:0:442:A:N7	2.13	0.64
1:A:47:HIS:HD2	30:0:1654:U:H2'	1.61	0.64
30:0:1819:G:H5'	38:0:4680:HOH:O	1.96	0.64
30:0:1972:U:C2'	30:0:1973:A:H5''	2.27	0.64
30:0:671:A:O2'	30:0:672:G:H2'	1.97	0.64
2:B:36:PRO:HA	2:B:168:GLY:HA3	1.78	0.64
21:U:56:ARG:HD2	30:0:2890:A:C8	2.33	0.64
27:1:9:GLY:HA2	30:0:1687:C:O2	1.98	0.64
30:0:281:U:H2'	30:0:282:C:O4'	1.98	0.64
30:0:693:A:H2'	30:0:694:A:C8	2.33	0.64
2:B:312:ARG:HD3	2:B:315:VAL:HG13	1.80	0.64
30:0:1706:G:H1'	30:0:1712:A:H61	1.61	0.64
30:0:2768:A:O2'	30:0:2769:C:H5'	1.97	0.64
5:E:143:GLN:HE22	30:0:2779:G:H21	1.44	0.64
27:1:21:ARG:HD2	27:1:37:CYS:SG	2.38	0.64
5:E:20:ILE:HD11	5:E:40:VAL:HG11	1.79	0.64
23:W:6:GLN:HB2	23:W:26:ILE:HD11	1.79	0.64
26:Z:70:ARG:HH11	26:Z:83:TYR:HD1	1.46	0.64
3:C:78:ARG:HG3	3:C:78:ARG:NH1	2.13	0.64
30:0:1181:A:H2'	30:0:1182:C:H5'	1.80	0.64
30:0:1973:A:H2'	30:0:1974:G:O4'	1.96	0.64
30:0:2088:C:H2'	30:0:2089:A:H8	1.62	0.64
25:Y:154:ARG:HH22	30:0:1071:G:H4'	1.63	0.64

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:169:ARG:HD2	30:0:1328:A:OP1	1.98	0.64
30:0:459:A:H5''	38:0:9055:HOH:O	1.96	0.64
3:C:16:VAL:HG12	3:C:17:ASP:H	1.62	0.64
14:N:86:LEU:HD12	14:N:125:ALA:HB2	1.78	0.64
30:0:1748:U:C5	30:0:1749:U:C5	2.85	0.63
8:H:27:PRO:HD3	8:H:123:ILE:HG22	1.79	0.63
11:K:66:ARG:HH22	30:0:1994:A:P	2.21	0.63
21:U:23:HIS:HD2	21:U:27:ALA:HB3	1.63	0.63
30:0:2867:G:H2'	30:0:2868:C:C6	2.33	0.63
30:0:541:C:H2'	30:0:542:A:H5'	1.77	0.63
3:C:132:ASP:O	3:C:133:ARG:HG3	1.98	0.63
3:C:236:THR:HG21	38:C:8571:HOH:O	1.97	0.63
11:K:98:VAL:CG1	11:K:102:GLU:HA	2.28	0.63
18:R:40:ALA:O	18:R:44:VAL:HG23	1.99	0.63
8:H:19:ARG:HH12	30:0:1008:C:H5''	1.63	0.63
30:0:1116:U:O2'	30:0:1118:A:C2	2.40	0.63
30:0:2727:A:H2'	30:0:2728:C:H5'	1.80	0.63
30:0:541:C:O2'	30:0:542:A:H5''	1.97	0.63
31:9:17:G:O2'	31:9:18:U:H5'	1.97	0.63
17:Q:26:PRO:O	17:Q:30:VAL:HG23	1.97	0.63
30:0:1835:U:H3'	38:0:5539:HOH:O	1.97	0.63
30:0:2032:U:O2'	30:0:2033:G:H5''	1.98	0.63
13:M:66:SER:HB3	13:M:128:TRP:CD1	2.33	0.63
13:M:164:THR:HG22	13:M:166:ALA:N	2.13	0.63
30:0:2659:U:H5''	38:0:4112:HOH:O	1.98	0.63
30:0:506:G:H22	30:0:509:A:H5'	1.63	0.63
23:W:88:THR:HG22	23:W:110:GLN:HB3	1.81	0.63
30:0:1985:U:H1'	38:0:4497:HOH:O	1.98	0.63
30:0:90:A:H2'	30:0:91:G:O4'	1.98	0.63
29:3:65:THR:O	29:3:82:GLY:HA3	1.99	0.63
31:9:91:C:H2'	31:9:92:G:O4'	1.99	0.63
1:A:211:LYS:HB3	1:A:212:PRO:HD2	1.79	0.63
26:Z:38:PHE:HB3	26:Z:42:TYR:CD1	2.33	0.63
30:0:1149:U:H5''	30:0:1151:G:O4'	1.98	0.63
30:0:1644:C:H2'	30:0:1645:U:C6	2.31	0.63
30:0:2291:A:H8	38:0:6453:HOH:O	1.81	0.63
30:0:2675:A:H1'	30:0:2813:A:C2	2.34	0.63
30:0:2824:C:H5''	30:0:2825:C:H5'	1.80	0.63
14:N:164:ASP:OD1	14:N:167:ASP:HA	1.98	0.63
14:N:37:ARG:HH12	31:9:6:C:C5'	1.95	0.63
30:0:2250:G:H2'	30:0:2251:G:O4'	1.99	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:131:THR:HG21	30:0:2348:C:H1'	1.79	0.63
30:0:2766:A:O2'	30:0:2767:C:H5'	1.99	0.63
29:3:59:ASP:HB3	29:3:63:LYS:NZ	2.13	0.63
29:3:2:GLN:HB3	29:3:91:GLN:CD	2.19	0.63
2:B:280:VAL:HG13	2:B:333:GLU:O	1.99	0.63
22:V:42:ASN:HB3	38:V:7247:HOH:O	1.98	0.63
30:0:2782:G:H3'	38:0:5004:HOH:O	1.98	0.63
30:0:279:C:C2'	30:0:280:C:H5'	2.29	0.63
30:0:630:A:H5''	38:0:4722:HOH:O	1.99	0.63
30:0:956:G:C8	38:0:9387:HOH:O	2.50	0.63
28:2:41:HIS:HB3	28:2:44:ARG:HB2	1.80	0.63
5:E:60:SER:OG	30:0:2784:A:H1'	1.98	0.63
11:K:74:VAL:CG1	11:K:113:ILE:HG12	2.29	0.63
30:0:1165:G:H21	30:0:1173:A:C5'	2.12	0.62
26:Z:41:ARG:HD2	30:0:1830:C:O2	1.98	0.62
30:0:2349:G:H2'	30:0:2350:G:H8	1.62	0.62
27:1:2:GLY:O	27:1:6:PRO:HG2	1.99	0.62
12:L:57:VAL:HG21	30:0:2443:C:H5'	1.80	0.62
20:T:72:ILE:HD13	20:T:93:THR:HG22	1.81	0.62
26:Z:34:SER:HB2	38:0:7481:HOH:O	1.99	0.62
30:0:1921:A:O2'	30:0:1922:A:H5'	1.98	0.62
29:3:54:LYS:HE2	30:0:2468:A:N7	2.14	0.62
30:0:1527:A:H1'	30:0:1528:A:C8	2.34	0.62
30:0:1351:G:H5'	38:0:3619:HOH:O	1.99	0.62
30:0:1878:G:H1'	38:0:6097:HOH:O	2.00	0.62
30:0:1889:C:H2'	30:0:1890:U:O4'	2.00	0.62
4:D:54:ALA:HB2	4:D:69:ILE:HD12	1.80	0.62
14:N:160:SER:HB3	31:9:51:A:H5'	1.82	0.62
21:U:49:LEU:HD12	38:U:3805:HOH:O	1.99	0.62
30:0:1477:C:H5'	30:0:1868:G:C5'	2.29	0.62
30:0:229:G:O2'	30:0:230:C:H5'	2.00	0.62
5:E:153:ARG:HH12	30:0:2778:A:H1'	1.65	0.62
30:0:790:A:H1'	30:0:1710:A:O2'	1.99	0.62
8:H:15:PRO:HG3	30:0:1053:G:OP1	2.00	0.62
20:T:61:GLU:HG2	38:T:3851:HOH:O	1.99	0.62
30:0:1226:G:H5'	38:0:4509:HOH:O	1.98	0.62
29:3:68:LYS:NZ	30:0:2436:U:H5'	2.14	0.62
3:C:246:ARG:NH2	30:0:677:C:H4'	2.14	0.62
30:0:2510:C:H5'	30:0:2511:A:OP2	1.99	0.62
30:0:920:C:H4'	30:0:921:G:N2	2.14	0.62
28:2:22:PRO:HG2	28:2:25:VAL:HG23	1.82	0.62

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:51:TYR:CE2	30:0:721:A:H5''	2.35	0.62
22:V:39:ALA:H	22:V:40:PRO:HD2	1.65	0.62
26:Z:53:ILE:O	26:Z:57:MET:HB2	2.00	0.62
30:0:1752:G:H2'	38:0:7531:HOH:O	2.00	0.62
30:0:303:C:O2'	30:0:304:G:H5'	2.00	0.62
30:0:630:A:H5'	38:0:9372:HOH:O	1.98	0.62
17:Q:14:LEU:HD21	17:Q:43:ILE:HD12	1.82	0.62
30:0:1131:G:H1'	38:0:3907:HOH:O	1.99	0.61
30:0:1279:U:C2'	30:0:1279:U:O2	2.48	0.61
30:0:2251:G:H2'	30:0:2252:A:C8	2.35	0.61
30:0:2300:A:H4'	30:0:2301:A:O5'	2.00	0.61
30:0:236:A:H4'	30:0:237:G:C5'	2.17	0.61
30:0:2439:C:H5'	38:0:5449:HOH:O	1.99	0.61
30:0:2775:A:C6	30:0:2799:A:C8	2.88	0.61
31:9:91:C:H1'	38:9:9149:HOH:O	1.98	0.61
3:C:129:HIS:CE1	3:C:231:ARG:HA	2.35	0.61
23:W:64:THR:O	23:W:68:THR:HG22	2.00	0.61
30:0:1477:C:O2'	30:0:1478:U:H5'	1.99	0.61
30:0:2576:A:H2'	38:0:7732:HOH:O	2.00	0.61
30:0:825:U:H5''	30:0:826:U:OP1	2.00	0.61
9:I:130:LEU:CD2	30:0:1167:G:H4'	2.29	0.61
22:V:55:ARG:O	22:V:59:ILE:HG12	2.01	0.61
30:0:2314:G:C2'	30:0:2315:C:H5'	2.30	0.61
25:Y:186:ARG:HG2	25:Y:186:ARG:HH11	1.65	0.61
30:0:1711:A:O2'	30:0:1712:A:H5'	2.00	0.61
2:B:262:ARG:HG3	30:0:2716:G:H5'	1.83	0.61
30:0:2912:C:O5'	30:0:2912:C:H6	1.83	0.61
30:0:301:C:O2'	30:0:302:A:H5'	2.00	0.61
7:G:12:ILE:HG23	38:0:5418:HOH:O	1.98	0.61
13:M:75:ARG:NH2	13:M:78:LYS:HE2	2.16	0.61
23:W:52:VAL:HG22	23:W:53:ALA:H	1.63	0.61
24:X:71:ARG:HD2	38:X:7542:HOH:O	1.99	0.61
30:0:1118:A:H8	30:0:1119:G:H5''	1.64	0.61
1:A:20:SER:HB3	30:0:1872:C:H5	1.65	0.61
30:0:39:G:N2	30:0:444:C:C2	2.68	0.61
2:B:320:GLN:HE21	2:B:321:PRO:HD2	1.65	0.61
2:B:336:GLN:O	30:0:2862:G:H4'	2.00	0.61
9:I:91:PHE:HD2	9:I:131:GLY:HA2	1.66	0.61
12:L:67:ARG:HB2	12:L:112:GLY:HA3	1.83	0.61
30:0:2526:C:H3'	30:0:2526:C:H6	1.65	0.61
30:0:705:C:H2'	30:0:705:C:O2	1.99	0.61

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:130:LEU:HD21	30:0:1167:G:H4'	1.81	0.61
23:W:13:MET:HE1	23:W:18:GLN:HA	1.81	0.61
30:0:1774:G:O2'	30:0:1775:A:H5'	2.01	0.61
30:0:228:C:H2'	30:0:229:G:H5'	1.80	0.61
30:0:877:G:C5'	30:0:878:G:OP1	2.46	0.61
31:9:20:G:H3'	38:9:9057:HOH:O	2.00	0.61
22:V:12:THR:HG22	22:V:15:GLU:CG	2.31	0.61
30:0:1676:G:O2'	30:0:1677:U:H5'	2.01	0.61
30:0:1856:C:H5'	30:0:1858:A:O4'	2.01	0.61
30:0:282:C:O2	30:0:282:C:H2'	2.00	0.61
30:0:2834:G:C2	30:0:2835:C:H1'	2.35	0.61
23:W:145:GLY:HA3	38:W:6373:HOH:O	2.00	0.61
30:0:1398:G:H2'	30:0:1399:A:H8	1.64	0.61
30:0:283:U:C5	30:0:284:C:C4	2.88	0.61
30:0:807:A:H2'	30:0:808:A:C8	2.36	0.61
31:9:39:U:HO2'	31:9:42:C:H5	1.48	0.61
8:H:174:LEU:HD21	30:0:1220:U:H4'	1.82	0.61
30:0:1701:A:H4'	30:0:1702:U:C5'	2.30	0.61
30:0:558:C:H2'	30:0:559:U:H5'	1.81	0.61
11:K:10:GLN:N	11:K:10:GLN:HE21	1.96	0.61
30:0:1878:G:HO2'	30:0:1879:U:H6	1.42	0.60
38:3:9025:HOH:O	30:0:2468:A:H5'	2.00	0.60
30:0:31:C:H4'	38:0:7408:HOH:O	2.00	0.60
1:A:140:LEU:HB3	1:A:141:PRO:HD2	1.83	0.60
10:J:47:THR:HB	38:0:4807:HOH:O	2.01	0.60
30:0:1175:G:H1'	30:0:1193:A:C2'	2.31	0.60
30:0:1697:G:H4'	38:0:9347:HOH:O	2.02	0.60
30:0:2281:C:H2'	30:0:2282:U:H5'	1.82	0.60
29:3:9:THR:HG23	29:3:20:HIS:ND1	2.15	0.60
2:B:102:THR:HG23	2:B:182:VAL:HG12	1.81	0.60
2:B:320:GLN:HE21	2:B:321:PRO:CD	2.14	0.60
3:C:27:ARG:NH2	30:0:657:G:OP1	2.34	0.60
30:0:2071:C:H5'	38:0:9540:HOH:O	2.00	0.60
30:0:2312:G:C2'	30:0:2313:C:H5'	2.30	0.60
30:0:282:C:O2'	30:0:283:U:C5'	2.49	0.60
30:0:2872:U:H2'	30:0:2873:C:O4'	2.02	0.60
11:K:74:VAL:HG12	11:K:75:ARG:HG3	1.83	0.60
30:0:1201:C:H5''	38:0:6211:HOH:O	2.00	0.60
30:0:1495:C:H1'	30:0:1573:A:H1'	1.83	0.60
26:Z:84:CYS:HB3	30:0:1604:G:N2	2.15	0.60
30:0:38:G:O2'	30:0:39:G:H5'	2.02	0.60

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:407:A:H3'	38:0:4438:HOH:O	2.01	0.60
25:Y:126:PRO:HG2	25:Y:128:PHE:CE1	2.36	0.60
30:0:1205:U:O2'	30:0:1206:U:H5''	2.01	0.60
30:0:1398:G:O2'	30:0:1399:A:H5'	2.02	0.60
30:0:1407:A:O2'	30:0:1408:U:H3'	2.01	0.60
30:0:1972:U:C2'	30:0:1973:A:C5'	2.80	0.60
30:0:2420:G:C2'	30:0:2421:G:H5'	2.30	0.60
30:0:51:G:H1'	38:0:9033:HOH:O	2.01	0.60
30:0:947:U:H2'	30:0:948:G:C8	2.36	0.60
2:B:72:THR:HB	38:B:9076:HOH:O	2.02	0.60
11:K:74:VAL:HG13	11:K:113:ILE:HG12	1.82	0.60
20:T:48:VAL:HG22	20:T:97:ARG:O	2.01	0.60
30:0:146:U:C2'	30:0:147:G:H5'	2.31	0.60
30:0:2893:C:O2'	30:0:2894:C:H5'	2.01	0.60
31:9:18:U:H2'	31:9:19:G:C8	2.37	0.60
31:9:23:U:O2'	31:9:24:U:H4'	2.01	0.60
7:G:16:LYS:HE2	7:G:63:ARG:HH12	1.67	0.60
13:M:102:GLU:OE1	13:M:164:THR:HG21	2.01	0.60
16:P:41:ARG:HH22	30:0:1500:U:P	2.24	0.60
30:0:2353:A:H4'	30:0:2354:A:O5'	2.01	0.60
29:3:31:THR:OG1	29:3:34:LYS:HD3	2.01	0.60
8:H:72:ALA:HB2	8:H:156:ALA:HB2	1.81	0.60
15:O:14:LEU:CD2	15:O:102:ILE:HD11	2.32	0.60
18:R:135:ALA:HB1	18:R:137:ASN:HD21	1.67	0.60
30:0:1844:C:H6	30:0:1844:C:O5'	1.84	0.60
30:0:2608:C:H3'	38:0:7790:HOH:O	2.02	0.60
31:9:3:A:C6	31:9:22:G:H1'	2.36	0.60
31:9:26:C:H2'	31:9:27:C:C6	2.36	0.60
31:9:29:C:H2'	31:9:30:C:C5'	2.28	0.60
33:B:8819:CL:CL	38:B:8997:HOH:O	2.54	0.60
13:M:188:ARG:HD3	30:0:155:C:OP2	2.02	0.60
10:J:82:THR:CG2	30:0:1242:A:H5'	2.20	0.60
30:0:307:G:H3'	38:0:6667:HOH:O	2.01	0.60
30:0:567:U:H5''	38:0:5254:HOH:O	2.02	0.60
2:B:79:MET:HB2	2:B:188:HIS:CE1	2.36	0.60
18:R:46:TYR:O	18:R:50:VAL:HG23	2.00	0.60
30:0:74:G:H2'	30:0:75:U:C6	2.37	0.60
30:0:947:U:H2'	30:0:948:G:H8	1.65	0.60
29:3:43:ASN:HB2	29:3:52:PHE:CE1	2.36	0.60
6:F:58:GLU:CD	13:M:27:ARG:HH22	2.05	0.60
30:0:1878:G:O2'	30:0:1879:U:C6	2.50	0.59

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:324:G:O2'	30:0:325:U:H5'	2.02	0.59
30:0:319:A:H4'	30:0:338:C:C4	2.37	0.59
31:9:63:C:O2'	31:9:64:C:H5'	2.01	0.59
2:B:235:ARG:HD3	30:0:2091:G:H5''	1.83	0.59
16:P:91:LYS:O	16:P:95:GLU:HG3	2.02	0.59
30:0:1590:A:H1'	30:0:1606:A:C2	2.36	0.59
30:0:2686:C:C2	30:0:2709:G:N2	2.70	0.59
27:1:20:ARG:HG2	30:0:111:C:O2'	2.01	0.59
31:9:65:A:N6	31:9:112:U:C6	2.71	0.59
11:K:130:MET:SD	21:U:25:ASP:O	2.60	0.59
13:M:82:ARG:HH22	13:M:85:ARG:HH21	1.49	0.59
30:0:2403:C:H5'	38:0:6001:HOH:O	2.01	0.59
30:0:2718:C:H6	30:0:2718:C:H5'	1.67	0.59
30:0:2820:A:H2'	30:0:2821:C:C6	2.36	0.59
1:A:94:LEU:HG	1:A:99:ILE:HD11	1.84	0.59
3:C:236:THR:HA	38:C:8648:HOH:O	2.01	0.59
5:E:145:ALA:HB1	5:E:168:ILE:HD11	1.85	0.59
2:B:156:LYS:HB3	30:0:2846:C:H4'	1.84	0.59
30:0:2867:G:H2'	30:0:2868:C:H6	1.67	0.59
30:0:653:U:H2'	30:0:654:A:C8	2.37	0.59
30:0:834:G:H4'	30:0:835:U:OP2	2.02	0.59
2:B:101:TRP:HB2	2:B:119:HIS:CD2	2.38	0.59
12:L:79:ASP:HB3	38:L:8859:HOH:O	2.03	0.59
14:N:86:LEU:O	14:N:90:LEU:HG	2.02	0.59
30:0:1585:C:H2'	30:0:1586:G:C8	2.37	0.59
30:0:2809:G:H2'	30:0:2810:G:C8	2.37	0.59
30:0:2831:C:H2'	30:0:2832:C:H5'	1.82	0.59
30:0:2874:G:H3'	38:0:9586:HOH:O	2.02	0.59
30:0:652:G:C2	30:0:653:U:H1'	2.37	0.59
1:A:179:MET:HG2	1:A:186:TRP:CB	2.32	0.59
1:A:33:GLU:H	1:A:33:GLU:CD	2.06	0.59
2:B:62:ARG:HG2	2:B:65:MET:HE3	1.85	0.59
6:F:13:GLU:OE2	6:F:78:GLU:HG2	2.01	0.59
38:B:8993:HOH:O	30:0:2549:C:H1'	2.03	0.59
4:D:58:VAL:HG12	4:D:60:GLU:HG2	1.83	0.59
30:0:1702:U:H5''	38:0:7201:HOH:O	2.01	0.59
30:0:2846:C:H4'	38:0:5047:HOH:O	2.03	0.59
30:0:812:A:H2'	30:0:813:C:H6	1.68	0.59
8:H:37:GLY:HA3	8:H:87:LYS:HA	1.85	0.59
30:0:1380:U:C4	30:0:2748:G:C4	2.91	0.59
30:0:2065:C:O2'	30:0:2066:C:H5'	2.02	0.59

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:155:ARG:NH1	30:0:2503:A:H5''	2.18	0.59
30:0:542:A:H5'	30:0:542:A:C8	2.29	0.59
30:0:590:A:H2'	30:0:591:A:H5'	1.83	0.59
2:B:215:VAL:HB	38:B:9089:HOH:O	2.02	0.59
30:0:1563:G:H4'	38:0:4215:HOH:O	2.01	0.59
30:0:1566:C:O2'	30:0:1567:G:H5'	2.03	0.59
30:0:1972:U:H2'	30:0:1973:A:H5''	1.83	0.59
11:K:41:LYS:HA	30:0:2582:G:O3'	2.03	0.59
30:0:499:G:O2'	30:0:500:G:H5'	2.02	0.59
30:0:702:G:O2'	30:0:703:G:H5'	2.02	0.59
30:0:921:G:H4'	30:0:924:G:C6	2.37	0.59
31:9:54:A:C2	31:9:55:U:C2	2.91	0.59
2:B:145:HIS:HD2	2:B:146:THR:O	1.85	0.59
4:D:159:PRO:O	4:D:163:VAL:HG23	2.02	0.59
16:P:7:LYS:HD3	16:P:21:VAL:HG22	1.85	0.59
18:R:39:THR:HG23	18:R:107:GLU:O	2.03	0.59
24:X:37:LEU:HD13	24:X:85:VAL:HG21	1.84	0.59
13:M:137:ASN:ND2	30:0:145:A:H4'	2.18	0.59
30:0:255:A:H2'	30:0:256:C:H6	1.67	0.59
30:0:281:U:C2'	30:0:282:C:H5'	2.33	0.59
6:F:30:LYS:HB2	6:F:97:ALA:HB3	1.84	0.59
10:J:69:TYR:CE1	30:0:2081:A:H4'	2.38	0.59
10:J:88:PRO:HD3	30:0:1104:C:H4'	1.85	0.59
30:0:1568:G:O2'	30:0:1569:U:H5'	2.03	0.58
26:Z:40:ALA:HA	30:0:1773:G:C8	2.38	0.58
30:0:2563:U:H2'	30:0:2565:C:O5'	2.02	0.58
30:0:2724:U:H2'	30:0:2725:G:O4'	2.03	0.58
30:0:2826:G:C6	30:0:2913:A:C6	2.90	0.58
30:0:925:C:H3'	38:0:3826:HOH:O	2.02	0.58
30:0:1245:C:O5'	30:0:1245:C:H6	1.85	0.58
30:0:2825:C:H4'	30:0:2826:G:O5'	2.03	0.58
30:0:28:G:H1'	38:0:4650:HOH:O	2.03	0.58
29:3:47:GLY:HA2	30:0:2121:G:C4'	2.25	0.58
2:B:243:ASN:HB3	38:0:6624:HOH:O	2.02	0.58
2:B:297:VAL:HB	38:B:9076:HOH:O	2.03	0.58
8:H:98:LEU:HD11	8:H:127:ALA:HB2	1.85	0.58
25:Y:169:ARG:HD3	30:0:1328:A:C8	2.38	0.58
30:0:1158:G:O2'	30:0:1159:G:H5'	2.03	0.58
9:I:83:GLY:H	30:0:1168:C:H5''	1.68	0.58
30:0:1187:U:H2'	38:0:6880:HOH:O	2.01	0.58
30:0:1290:G:H4'	38:0:7465:HOH:O	2.02	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2467:A:H5''	38:0:4285:HOH:O	2.03	0.58
30:0:951:A:C2'	30:0:952:G:H5'	2.33	0.58
3:C:79:ARG:O	3:C:87:ARG:HG2	2.04	0.58
4:D:28:GLY:HA2	4:D:69:ILE:HG23	1.85	0.58
12:L:145:LEU:HB2	38:L:8836:HOH:O	2.03	0.58
13:M:28:GLN:HA	13:M:31:TRP:HB2	1.85	0.58
26:Z:34:SER:HA	30:0:797:A:H4'	1.83	0.58
30:0:1186:C:H42	30:0:1190:G:H22	1.48	0.58
30:0:2590:U:H2'	30:0:2591:C:H5'	1.85	0.58
30:0:293:A:C4	30:0:360:A:C2	2.91	0.58
20:T:52:ARG:HD2	30:0:317:A:H5''	1.85	0.58
30:0:1711:A:C2'	30:0:1712:A:H5'	2.33	0.58
30:0:204:A:H2'	30:0:205:U:H5'	1.85	0.58
30:0:2784:A:H8	30:0:2784:A:O5'	1.87	0.58
3:C:182:ARG:HH12	30:0:450:C:H3'	1.67	0.58
12:L:18:HIS:HD2	30:0:902:G:N7	2.01	0.58
25:Y:234:VAL:HG12	25:Y:235:GLU:H	1.66	0.58
30:0:1520:G:C6	30:0:1521:C:C4	2.92	0.58
10:J:127:ILE:HG22	33:J:8801:CL:CL	2.40	0.58
26:Z:70:ARG:HB2	26:Z:81:CYS:SG	2.44	0.58
30:0:1503:U:C2'	30:0:1504:A:H5'	2.34	0.58
30:0:164:G:H3'	38:0:3636:HOH:O	2.03	0.58
30:0:368:C:C2'	30:0:369:G:H5'	2.34	0.58
30:0:271:C:N4	30:0:378:A:C2	2.66	0.58
31:9:39:U:H1'	31:9:44:A:N6	2.19	0.58
2:B:162:MET:HG3	2:B:310:ARG:HD3	1.84	0.58
5:E:100:ASP:HB3	38:E:2789:HOH:O	2.02	0.58
30:0:1662:C:H2'	30:0:1663:G:O4'	2.03	0.58
30:0:2073:G:OP2	30:0:2490:A:H5'	2.03	0.58
30:0:2493:C:O2	30:0:2493:C:H2'	2.02	0.58
30:0:2505:G:H2'	30:0:2506:A:H5'	1.86	0.58
30:0:2624:A:H1'	38:0:9769:HOH:O	2.04	0.58
30:0:482:G:H4'	30:0:508:A:N1	2.19	0.58
30:0:951:A:O2'	30:0:952:G:H5'	2.03	0.58
31:9:54:A:C2	31:9:55:U:N3	2.72	0.58
2:B:267:LYS:HA	38:B:8996:HOH:O	2.04	0.58
17:Q:11:ARG:NH2	30:0:2363:G:H5''	2.19	0.58
26:Z:42:TYR:HA	30:0:1829:A:N6	2.16	0.58
30:0:1585:C:H2'	30:0:1586:G:H8	1.68	0.58
30:0:1634:G:H2'	30:0:1635:U:C6	2.38	0.58
30:0:1973:A:H5'	30:0:1973:A:H8	1.69	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2511:A:H2'	30:0:2512:U:O4'	2.03	0.58
30:0:2581:U:H1'	38:0:4452:HOH:O	2.03	0.58
30:0:412:C:O2'	30:0:413:G:H5'	2.02	0.58
30:0:544:G:H2'	30:0:545:G:H5''	1.85	0.58
30:0:625:U:H3'	38:0:3244:HOH:O	2.03	0.58
8:H:172:GLU:HB2	38:H:248:HOH:O	2.04	0.58
22:V:1:THR:HG23	22:V:2:VAL:H	1.69	0.58
30:0:1041:U:C2'	30:0:1042:U:H5'	2.34	0.58
30:0:1160:G:H5'	30:0:1161:A:H5'	0.78	0.58
30:0:1300:G:H1'	38:0:4652:HOH:O	2.03	0.58
30:0:2812:A:N7	38:0:7497:HOH:O	2.32	0.58
30:0:51:G:O2'	30:0:52:A:H5'	2.03	0.58
30:0:12:U:C2'	30:0:13:G:H5'	2.32	0.57
30:0:1057:A:H1'	30:0:2492:U:O2'	2.03	0.57
4:D:76:ARG:CZ	31:9:44:A:H1'	2.34	0.57
2:B:125:GLU:O	2:B:129:ARG:HG3	2.03	0.57
3:C:236:THR:CG2	3:C:239:ALA:H	2.16	0.57
11:K:20:CYS:SG	11:K:22:ASP:OD1	2.62	0.57
15:O:10:LEU:HD13	15:O:99:GLU:HG3	1.84	0.57
1:A:75:GLY:HA2	26:Z:88:PHE:HA	1.86	0.57
30:0:2705:U:H2'	30:0:2706:A:H8	1.68	0.57
30:0:2748:G:H5'	38:0:7523:HOH:O	2.04	0.57
30:0:820:G:H5'	30:0:821:U:H5'	1.86	0.57
10:J:70:PHE:HE1	30:0:2676:C:H4'	1.68	0.57
20:T:111:ARG:HB3	20:T:119:ALA:HB2	1.85	0.57
30:0:1166:A:H61	30:0:1180:U:H3	1.51	0.57
30:0:1216:G:H2'	30:0:1217:G:O4'	2.03	0.57
30:0:1256:C:H6	38:0:7140:HOH:O	1.87	0.57
30:0:1342:C:C2'	30:0:1343:C:H5'	2.34	0.57
30:0:590:A:C2'	30:0:591:A:H5'	2.33	0.57
30:0:821:U:H3'	38:0:3764:HOH:O	2.03	0.57
1:A:53:ALA:HB2	1:A:122:SER:OG	2.05	0.57
14:N:48:VAL:HG13	14:N:55:ASP:HB3	1.86	0.57
26:Z:90:GLY:HA3	26:Z:95:PRO:O	2.04	0.57
30:0:1503:U:O2'	30:0:1504:A:H5'	2.04	0.57
30:0:2712:G:H5'	38:0:5187:HOH:O	2.02	0.57
30:0:283:U:H5	30:0:284:C:C4	2.22	0.57
30:0:916:A:C2	30:0:928:G:C4	2.93	0.57
3:C:236:THR:HG22	3:C:239:ALA:N	2.15	0.57
20:T:18:GLU:O	20:T:21:LYS:HG2	2.03	0.57
30:0:1552:G:H2'	30:0:1553:C:C6	2.40	0.57

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1555:G:H4'	30:0:1630:A:H2	1.69	0.57
30:0:1883:U:C2'	30:0:1884:G:H5'	2.34	0.57
30:0:694:A:H2'	30:0:695:C:C5'	2.27	0.57
30:0:727:G:H3'	30:0:728:C:H6	1.68	0.57
29:3:51:LYS:HG3	29:3:52:PHE:CD2	2.40	0.57
11:K:14:LYS:CB	11:K:45:PRO:HG2	2.35	0.57
30:0:1754:A:H5''	38:0:9757:HOH:O	2.04	0.57
30:0:1819:G:H2'	30:0:1820:G:H4'	1.85	0.57
30:0:2078:U:O2'	30:0:2079:G:H5'	2.05	0.57
30:0:2240:U:O2'	30:0:2241:C:H5'	2.04	0.57
30:0:2335:C:H2'	30:0:2336:G:H8	1.67	0.57
30:0:2828:G:H8	30:0:2828:G:O5'	1.87	0.57
30:0:544:G:C2'	30:0:545:G:H5''	2.35	0.57
3:C:8:LEU:HD11	3:C:143:ASP:O	2.04	0.57
5:E:125:GLU:HB2	5:E:132:THR:HG23	1.86	0.57
30:0:1189:A:H1'	30:0:1209:C:C1'	2.35	0.57
30:0:1577:U:O2'	30:0:1578:C:H5'	2.05	0.57
30:0:2001:G:O2'	30:0:2002:C:H5'	2.04	0.57
3:C:127:ARG:HD3	3:C:129:HIS:HE1	1.70	0.57
21:U:56:ARG:HG3	21:U:56:ARG:NH1	2.19	0.57
24:X:43:VAL:HG22	24:X:76:ARG:NH1	2.20	0.57
30:0:138:U:OP2	30:0:139:C:C5	2.58	0.57
30:0:1718:G:O2'	30:0:1719:G:H5'	2.04	0.57
30:0:2010:A:H2'	38:0:5933:HOH:O	2.03	0.57
5:E:153:ARG:NH1	30:0:2778:A:H1'	2.19	0.57
18:R:68:HIS:O	30:0:2842:G:H5'	2.05	0.57
30:0:371:U:O2'	30:0:372:A:H5'	2.05	0.57
30:0:403:C:H3'	38:0:6286:HOH:O	2.05	0.57
14:N:160:SER:CB	31:9:51:A:H5'	2.34	0.57
1:A:153:ARG:HD3	38:A:9011:HOH:O	2.04	0.57
2:B:214:PRO:HD2	38:B:8989:HOH:O	2.05	0.57
15:O:19:ARG:NH1	30:0:1276:U:H3'	2.19	0.57
21:U:13:ILE:HG12	21:U:32:CYS:HB3	1.86	0.57
21:U:33:SER:O	21:U:37:GLU:HG3	2.04	0.57
25:Y:216:ARG:HD2	38:Y:8871:HOH:O	2.03	0.57
26:Z:45:VAL:HG13	26:Z:49:ARG:HE	1.70	0.57
30:0:1182:C:H1'	30:0:1192:A:H8	1.69	0.57
1:A:190:ARG:HD2	30:0:1884:G:O6	2.03	0.57
30:0:1971:G:H5'	38:0:7053:HOH:O	2.05	0.57
30:0:2407:G:O2'	30:0:2408:A:H5'	2.05	0.57
31:9:23:U:H2'	31:9:24:U:H4'	1.87	0.57

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:64:C:C2'	31:9:65:A:H5'	2.35	0.57
2:B:41:PHE:CZ	2:B:79:MET:HG3	2.40	0.57
13:M:68:ARG:HD3	13:M:68:ARG:O	2.05	0.57
20:T:24:ARG:HH21	20:T:39:ASN:HD22	1.53	0.57
24:X:30:MET:HE1	24:X:55:ASN:HA	1.86	0.57
30:0:1079:A:OP2	30:0:1080:C:N4	2.36	0.56
30:0:10:U:C4	30:0:532:A:C8	2.94	0.56
30:0:2251:G:H2'	30:0:2252:A:H8	1.70	0.56
30:0:2769:C:C2'	30:0:2770:G:C5'	2.78	0.56
30:0:312:U:O2'	30:0:313:U:H5'	2.05	0.56
30:0:407:A:H2'	30:0:408:A:C8	2.40	0.56
10:J:116:LEU:HB2	10:J:119:THR:HG21	1.87	0.56
30:0:1020:A:H2'	30:0:1021:G:C8	2.40	0.56
30:0:1173:A:H4'	30:0:1174:A:C8	2.40	0.56
30:0:2110:G:O2'	30:0:2111:G:H5'	2.05	0.56
30:0:2265:U:H2'	30:0:2266:A:C8	2.40	0.56
30:0:2698:G:H2'	30:0:2699:A:O4'	2.05	0.56
30:0:2700:G:H3'	38:0:3575:HOH:O	2.05	0.56
31:9:54:A:HO2'	31:9:55:U:H5'	1.67	0.56
11:K:32:ILE:HD11	11:K:56:SER:HB2	1.86	0.56
13:M:82:ARG:HD2	30:0:170:U:OP2	2.05	0.56
30:0:1616:A:H5''	30:0:1617:C:OP1	2.05	0.56
30:0:1948:G:O2'	30:0:1949:G:H5'	2.05	0.56
30:0:2011:A:H5'	30:0:2013:G:H1'	1.87	0.56
30:0:695:C:O2'	30:0:696:C:H5'	2.04	0.56
30:0:947:U:O2'	30:0:948:G:H5'	2.05	0.56
14:N:48:VAL:CG1	14:N:55:ASP:HB3	2.35	0.56
23:W:38:THR:O	23:W:42:ARG:HB2	2.04	0.56
30:0:1183:C:N4	30:0:1184:C:H41	2.03	0.56
30:0:1928:C:H2'	30:0:1929:G:O4'	2.05	0.56
30:0:280:C:H2'	30:0:281:U:O4'	2.06	0.56
28:2:40:ARG:HG3	28:2:45:ASN:HB2	1.85	0.56
29:3:34:LYS:HB3	38:3:9001:HOH:O	2.05	0.56
11:K:98:VAL:HG13	11:K:102:GLU:HA	1.85	0.56
14:N:141:ARG:NH2	31:9:48:C:H4'	2.21	0.56
30:0:162:C:H2'	30:0:163:U:H5'	1.87	0.56
30:0:1735:C:H2'	30:0:1736:A:C8	2.40	0.56
17:Q:45:PRO:O	30:0:2365:G:H4'	2.06	0.56
30:0:2659:U:H3'	38:0:4379:HOH:O	2.05	0.56
31:9:33:U:H2'	38:9:9068:HOH:O	2.04	0.56
2:B:17:LYS:O	2:B:260:HIS:HD2	1.88	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:49:GLN:NE2	8:H:140:TYR:HE2	1.95	0.56
13:M:171:ARG:NH2	30:0:189:A:OP1	2.38	0.56
15:O:24:ALA:HB3	30:0:710:G:OP1	2.05	0.56
13:M:68:ARG:HG3	30:0:1469:C:OP1	2.05	0.56
30:0:1904:A:H2'	30:0:1905:U:O4'	2.05	0.56
30:0:2289:G:O2'	30:0:2290:U:H5'	2.06	0.56
30:0:2349:G:H2'	30:0:2350:G:C8	2.38	0.56
30:0:2064:U:H4'	30:0:2653:A:OP1	2.05	0.56
30:0:26:U:H5	38:0:3099:HOH:O	1.89	0.56
30:0:1042:U:O2'	30:0:1043:C:H5'	2.05	0.56
30:0:113:A:OP2	30:0:114:A:H2'	2.06	0.56
30:0:1434:A:O2'	30:0:1435:U:H2'	2.05	0.56
30:0:2502:C:H2'	30:0:2503:A:C5'	2.34	0.56
30:0:473:A:O2'	30:0:474:C:H5'	2.06	0.56
30:0:799:C:O2'	30:0:800:G:H5'	2.05	0.56
29:3:65:THR:HG23	33:3:8804:CL:CL	2.43	0.56
2:B:223:ARG:HD3	33:B:8819:CL:CL	2.43	0.56
30:0:1127:C:C5	30:0:1128:U:C4	2.94	0.56
30:0:138:U:OP2	30:0:139:C:H5	1.88	0.56
30:0:2595:U:O2'	30:0:2596:A:H5'	2.05	0.56
26:Z:34:SER:HA	30:0:797:A:C4'	2.36	0.56
29:3:18:GLN:HB3	38:3:9013:HOH:O	2.06	0.56
31:9:54:A:H2'	31:9:55:U:H5'	1.82	0.56
2:B:199:TYR:HE2	2:B:268:ARG:HB2	1.71	0.56
12:L:27:ARG:NH2	12:L:30:ARG:HD3	2.21	0.56
16:P:127:GLY:HA3	38:P:152:HOH:O	2.05	0.56
25:Y:165:GLU:HB3	38:0:6689:HOH:O	2.05	0.56
30:0:1292:G:HO2'	30:0:1293:U:H6	1.52	0.56
13:M:94:ARG:HD2	30:0:158:A:OP2	2.06	0.56
30:0:2241:C:O2'	30:0:2242:U:H5'	2.05	0.56
30:0:2514:U:OP1	30:0:2572:G:H1'	2.04	0.56
21:U:56:ARG:HD2	30:0:2890:A:H1'	1.87	0.56
30:0:473:A:O2'	30:0:890:C:H5'	2.05	0.56
27:1:28:HIS:HE1	30:0:776:A:OP1	1.88	0.56
1:A:27:LEU:HD21	1:A:55:VAL:HG21	1.88	0.56
3:C:4:THR:HA	3:C:15:GLU:HB3	1.88	0.56
13:M:24:GLN:HE22	13:M:27:ARG:HH11	1.53	0.56
21:U:44:ARG:HD3	21:U:49:LEU:CD1	2.35	0.56
30:0:1679:C:H5'	38:0:9332:HOH:O	2.06	0.56
30:0:1788:U:C2	30:0:1805:G:N2	2.73	0.56
30:0:2673:U:C4	30:0:2674:G:C6	2.94	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:18:U:H2'	31:9:19:G:H8	1.71	0.56
15:O:47:ARG:HG3	15:O:47:ARG:HH11	1.71	0.56
30:0:1020:A:H2'	30:0:1021:G:H8	1.71	0.56
30:0:1181:A:H2'	30:0:1182:C:O4'	2.06	0.56
30:0:2314:G:H2'	30:0:2315:C:H5'	1.87	0.56
30:0:2578:G:C8	30:0:2578:G:H5'	2.36	0.56
30:0:2911:C:H2'	30:0:2912:C:C6	2.42	0.56
30:0:660:A:H4'	30:0:661:G:O5'	2.06	0.56
12:L:41:HIS:HD2	30:0:926:A:O2'	1.89	0.56
31:9:49:G:H2'	31:9:50:G:O4'	2.06	0.56
3:C:174:ILE:HD11	30:0:338:C:H4'	1.89	0.56
2:B:68:THR:HG21	21:U:16:GLY:HA3	1.87	0.56
21:U:23:HIS:CD2	21:U:27:ALA:HB3	2.40	0.56
25:Y:142:SER:HB2	38:Y:8902:HOH:O	2.05	0.56
30:0:1116:U:H3	30:0:1246:A:N6	1.96	0.55
1:A:47:HIS:HD2	30:0:1654:U:C2'	2.18	0.55
30:0:1878:G:C1'	38:0:6097:HOH:O	2.53	0.55
30:0:558:C:C2'	30:0:559:U:C5'	2.68	0.55
30:0:1613:C:H2'	30:0:1614:G:O4'	2.06	0.55
30:0:2271:G:N3	30:0:2271:G:H2'	2.20	0.55
30:0:2325:U:O2'	30:0:2411:C:H1'	2.06	0.55
30:0:2852:A:H5''	38:0:5199:HOH:O	2.05	0.55
30:0:339:A:H2'	38:0:4203:HOH:O	2.06	0.55
30:0:684:G:H5''	38:0:4053:HOH:O	2.06	0.55
30:0:858:U:H2'	30:0:859:C:H6	1.71	0.55
29:3:33:MET:HG2	30:0:1922:A:H2'	1.88	0.55
5:E:49:ILE:HD11	5:E:69:ILE:HD12	1.88	0.55
25:Y:99:ALA:HB2	25:Y:233:TYR:CZ	2.42	0.55
30:0:1172:G:H1'	38:0:4940:HOH:O	2.05	0.55
30:0:1165:G:H21	30:0:1173:A:H5''	1.72	0.55
30:0:1183:C:H41	30:0:1192:A:H5'	1.72	0.55
30:0:1512:G:O2'	30:0:1513:C:H5'	2.05	0.55
30:0:2113:G:C6	30:0:2114:C:C4	2.94	0.55
30:0:735:C:C6	30:0:736:A:C8	2.94	0.55
3:C:115:LEU:HD21	3:C:243:VAL:HG13	1.86	0.55
23:W:52:VAL:HG22	23:W:53:ALA:N	2.20	0.55
30:0:2668:G:H2'	30:0:2669:U:C6	2.42	0.55
30:0:913:A:O5'	30:0:913:A:H8	1.90	0.55
30:0:920:C:H5'	30:0:921:G:C4	2.41	0.55
3:C:1:MET:HG2	3:C:2:GLN:H	1.72	0.55
25:Y:210:GLY:HA2	38:0:5285:HOH:O	2.06	0.55

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:44:ARG:HB2	30:0:1886:A:O2'	2.05	0.55
30:0:1625:U:C6	30:0:1625:U:C3'	2.85	0.55
2:B:229:ARG:NH2	30:0:1753:C:O2	2.39	0.55
30:0:2250:G:N2	30:0:2251:G:H1'	2.21	0.55
30:0:310:U:H2'	30:0:311:C:C6	2.41	0.55
29:3:59:ASP:HB3	29:3:63:LYS:HZ3	1.72	0.55
3:C:21:VAL:HG13	38:C:8594:HOH:O	2.05	0.55
7:G:16:LYS:HE2	7:G:63:ARG:NH1	2.21	0.55
24:X:76:ARG:HH11	24:X:76:ARG:HG3	1.72	0.55
38:Y:8879:HOH:O	30:0:1355:A:H5''	2.06	0.55
30:0:1562:C:N4	38:0:5836:HOH:O	2.38	0.55
30:0:1909:A:H2'	30:0:1910:A:C8	2.42	0.55
29:3:47:GLY:CA	30:0:2121:G:H4'	2.29	0.55
30:0:956:G:H3'	38:0:9387:HOH:O	2.06	0.55
3:C:149:LYS:HB2	3:C:152:GLU:HG3	1.89	0.55
3:C:162:VAL:HG22	3:C:232:LEU:HD21	1.87	0.55
10:J:19:MET:HE1	10:J:132:LEU:HD21	1.87	0.55
26:Z:63:CYS:SG	26:Z:81:CYS:CB	2.94	0.55
30:0:1691:A:H5''	38:0:3140:HOH:O	2.06	0.55
30:0:1736:A:H1'	38:0:7566:HOH:O	2.07	0.55
30:0:212:A:O4'	30:0:214:U:C6	2.59	0.55
30:0:545:G:C5'	30:0:545:G:C8	2.81	0.55
30:0:571:C:O5'	30:0:571:C:H6	1.90	0.55
30:0:822:C:C2	30:0:823:U:C5	2.94	0.55
30:0:835:U:H3'	38:0:9381:HOH:O	2.06	0.55
2:B:36:PRO:HA	2:B:168:GLY:CA	2.36	0.55
23:W:119:HIS:HD2	23:W:120:PRO:O	1.89	0.55
30:0:2274:A:H2'	30:0:2275:G:C8	2.42	0.55
30:0:2868:C:H1'	38:0:7107:HOH:O	2.07	0.55
30:0:401:C:H2'	30:0:402:U:H6	1.72	0.55
30:0:696:C:HO2'	30:0:697:G:H5'	1.71	0.55
29:3:90:PHE:CD1	29:3:90:PHE:N	2.75	0.55
31:9:59:C:C2	31:9:60:C:C5	2.94	0.55
2:B:102:THR:HG21	2:B:182:VAL:O	2.07	0.55
4:D:140:ARG:HG3	4:D:140:ARG:HH11	1.72	0.55
13:M:111:ASN:HB2	38:M:8852:HOH:O	2.07	0.55
30:0:1156:C:O2'	30:0:1157:C:H5'	2.07	0.55
30:0:1175:G:H2'	30:0:1176:C:C6	2.42	0.55
30:0:1166:A:C6	30:0:1181:A:C2	2.95	0.55
30:0:1200:A:N1	30:0:1201:C:C2	2.75	0.55
30:0:130:C:O2'	30:0:131:A:N7	2.39	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:70:GLY:CA	30:0:2263:G:H4'	2.37	0.55
30:0:291:C:H2'	30:0:292:G:O4'	2.07	0.55
28:2:43:ARG:HH22	30:0:1684:A:C1'	2.16	0.55
5:E:132:THR:HB	38:E:2227:HOH:O	2.06	0.55
19:S:37:VAL:O	19:S:41:VAL:HG23	2.05	0.55
30:0:1849:G:H1'	30:0:2011:A:N1	2.22	0.55
30:0:1905:U:H2'	30:0:1906:C:H6	1.72	0.55
30:0:2584:G:H4'	38:0:7102:HOH:O	2.07	0.55
30:0:2689:A:C2'	30:0:2690:U:H5'	2.37	0.55
30:0:2790:C:HO2'	30:0:2791:U:H6	1.55	0.55
30:0:777:U:OP2	30:0:777:U:H4'	2.07	0.55
5:E:118:ILE:HG23	5:E:144:THR:HG21	1.89	0.55
5:E:53:GLU:HB3	5:E:55:ASN:ND2	2.21	0.55
30:0:1377:C:H6	30:0:1377:C:C5'	2.20	0.54
30:0:1903:U:O2'	30:0:1904:A:N7	2.40	0.54
30:0:1909:A:N1	30:0:2128:G:H1'	2.22	0.54
30:0:2782:G:N2	30:0:2783:A:N6	2.55	0.54
30:0:690:G:H4'	30:0:741:C:O2	2.06	0.54
30:0:820:G:H5'	30:0:821:U:C5'	2.37	0.54
30:0:941:G:C5	30:0:942:U:C4	2.95	0.54
3:C:132:ASP:HB2	3:C:161:ASP:HB3	1.89	0.54
3:C:2:GLN:HB3	38:C:8581:HOH:O	2.07	0.54
14:N:110:THR:HB	14:N:113:SER:OG	2.07	0.54
1:A:76:VAL:HG23	26:Z:87:LYS:HB3	1.88	0.54
30:0:1593:C:H1'	38:0:6083:HOH:O	2.06	0.54
30:0:363:C:O2'	30:0:364:U:H5'	2.07	0.54
30:0:814:G:H2'	30:0:815:U:O4'	2.07	0.54
30:0:960:G:H8	38:0:5945:HOH:O	1.89	0.54
29:3:12:PRO:HG2	29:3:13:HIS:HD2	1.71	0.54
31:9:58:G:N7	31:9:59:C:C4	2.75	0.54
2:B:232:TRP:CZ3	30:0:2614:C:H5''	2.41	0.54
4:D:146:LYS:NZ	14:N:107:ASN:HD21	2.05	0.54
5:E:108:LEU:HD11	5:E:164:ASP:HB2	1.88	0.54
30:0:1015:C:H4'	38:0:6566:HOH:O	2.06	0.54
30:0:1175:G:H4'	38:0:6842:HOH:O	2.07	0.54
30:0:2032:U:C2'	30:0:2033:G:C5'	2.86	0.54
30:0:2032:U:C2'	30:0:2033:G:H5''	2.38	0.54
30:0:2524:G:H21	30:0:2526:C:H41	1.55	0.54
30:0:2869:G:H5'	38:0:5457:HOH:O	2.07	0.54
27:1:28:HIS:HD2	27:1:30:LYS:H	1.53	0.54
2:B:140:LEU:HA	38:B:9051:HOH:O	2.05	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:41:PHE:CE1	2:B:79:MET:HG3	2.43	0.54
9:I:78:ALA:HB2	9:I:95:LEU:HD21	1.89	0.54
14:N:114:LYS:O	14:N:118:ILE:HG13	2.07	0.54
14:N:130:PRO:HA	38:N:8837:HOH:O	2.06	0.54
30:0:1447:U:OP1	30:0:1506:U:N3	2.39	0.54
30:0:1876:C:H4'	30:0:1877:G:OP2	2.08	0.54
30:0:2281:C:C2'	30:0:2282:U:H5'	2.38	0.54
31:9:27:C:H2'	31:9:28:U:O4'	2.08	0.54
5:E:85:GLU:HG2	5:E:130:GLU:HG2	1.89	0.54
6:F:2:VAL:HG22	6:F:57:GLU:OE1	2.08	0.54
13:M:59:GLY:HA3	13:M:141:ILE:HD12	1.90	0.54
30:0:1139:U:H2'	30:0:1140:C:H6	1.72	0.54
15:O:19:ARG:HH22	30:0:1278:A:P	2.31	0.54
1:A:223:ARG:NH1	30:0:2270:G:H4'	2.22	0.54
30:0:2477:C:O2'	30:0:2478:U:H5'	2.07	0.54
31:9:36:C:C5	31:9:37:C:C5	2.96	0.54
1:A:192:VAL:CG1	1:A:207:GLN:HB3	2.38	0.54
9:I:91:PHE:CD2	9:I:131:GLY:HA2	2.42	0.54
9:I:87:PRO:HD2	30:0:1180:U:H1'	1.89	0.54
12:L:143:THR:HG22	12:L:144:ASP:N	2.22	0.54
13:M:99:ARG:HE	13:M:170:ASN:ND2	1.96	0.54
30:0:1697:G:H5'	38:0:5475:HOH:O	2.08	0.54
30:0:2081:A:H2'	30:0:2082:G:O4'	2.08	0.54
30:0:2107:U:O2'	30:0:2108:A:H5'	2.07	0.54
30:0:2321:A:C4	30:0:2323:G:C8	2.95	0.54
30:0:236:A:H4'	30:0:237:G:OP1	2.08	0.54
30:0:2831:C:H3'	38:0:7197:HOH:O	2.07	0.54
30:0:312:U:C2	30:0:320:G:N2	2.76	0.54
30:0:710:G:O2'	30:0:711:G:H5'	2.08	0.54
1:A:195:ASN:ND2	30:0:877:G:C8	2.76	0.54
30:0:963:C:O2	30:0:1005:A:N1	2.40	0.54
29:3:60:LYS:HB3	29:3:62:THR:O	2.07	0.54
12:L:67:ARG:O	12:L:71:GLU:HG3	2.08	0.54
30:0:1617:C:C5	30:0:1643:C:H4'	2.42	0.54
30:0:2078:U:H2'	30:0:2079:G:C8	2.42	0.54
30:0:2892:G:C5	30:0:2893:C:C5	2.95	0.54
30:0:461:C:N3	30:0:479:G:H5'	2.22	0.54
30:0:623:U:O2'	30:0:624:U:H5'	2.08	0.54
30:0:661:G:C5	30:0:686:A:C2	2.96	0.54
30:0:706:G:HO2'	30:0:707:C:H6	1.53	0.54
30:0:960:G:N3	30:0:960:G:C3'	2.71	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:35:ILE:HD13	38:P:171:HOH:O	2.08	0.54
17:Q:19:ARG:HH21	31:9:11:A:P	2.30	0.54
30:0:1175:G:H1'	30:0:1193:A:H2'	1.89	0.54
30:0:1676:G:H1'	38:0:9441:HOH:O	2.08	0.54
30:0:1850:U:H2'	30:0:1851:G:H8	1.73	0.54
30:0:2045:G:H5''	38:0:7204:HOH:O	2.06	0.54
30:0:2256:G:O2'	30:0:2257:G:H5'	2.08	0.54
30:0:2670:G:O2'	30:0:2671:U:H5'	2.08	0.54
27:1:16:HIS:HD2	30:0:470:U:O2'	1.91	0.54
31:9:30:C:O2	31:9:30:C:H2'	2.08	0.54
2:B:62:ARG:HA	2:B:65:MET:HE3	1.88	0.54
4:D:135:VAL:HG21	4:D:139:TYR:CD1	2.43	0.54
5:E:116:THR:HG22	5:E:151:LEU:HD22	1.90	0.54
18:R:99:ALA:HB1	18:R:109:MET:CE	2.37	0.54
15:O:19:ARG:HH11	30:0:1276:U:H3'	1.73	0.54
30:0:1625:U:H5''	38:0:5995:HOH:O	2.07	0.54
30:0:2487:C:H5	38:0:4858:HOH:O	1.91	0.54
30:0:2787:C:H5	38:0:4605:HOH:O	1.90	0.54
30:0:2908:A:H8	30:0:2908:A:O5'	1.91	0.54
30:0:334:G:C4	30:0:335:U:C6	2.96	0.54
13:M:164:THR:CG2	13:M:165:GLY:N	2.70	0.54
30:0:2831:C:H2'	30:0:2832:C:C5'	2.38	0.54
30:0:541:C:C2'	30:0:542:A:C5'	2.78	0.54
30:0:853:C:H2'	30:0:854:G:O4'	2.08	0.54
28:2:13:LYS:O	28:2:17:GLN:HG3	2.07	0.54
31:9:23:U:C2'	31:9:24:U:H4'	2.38	0.54
8:H:99:ARG:NH1	30:0:1055:G:OP2	2.41	0.53
30:0:1453:G:H2'	30:0:1454:U:O4'	2.07	0.53
30:0:1525:G:H5'	30:0:1526:A:OP2	2.08	0.53
30:0:2106:C:H2'	30:0:2107:U:C6	2.43	0.53
30:0:2599:A:H5''	38:0:3367:HOH:O	2.08	0.53
30:0:30:U:H5''	38:0:5777:HOH:O	2.08	0.53
30:0:338:C:H5''	38:0:3793:HOH:O	2.07	0.53
30:0:354:A:H2'	30:0:355:C:H6	1.73	0.53
1:A:179:MET:HG2	1:A:186:TRP:HB2	1.91	0.53
2:B:238:ASN:ND2	2:B:240:GLY:H	1.92	0.53
14:N:132:ASN:HD22	30:0:2413:A:H4'	1.72	0.53
25:Y:97:LEU:HA	25:Y:234:VAL:O	2.08	0.53
30:0:1268:C:H2'	30:0:1269:G:H8	1.73	0.53
30:0:2321:A:C5	30:0:2323:G:C8	2.96	0.53
30:0:2379:G:N3	30:0:2418:G:H2'	2.22	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2553:A:N3	30:0:2553:A:H2'	2.23	0.53
30:0:2563:U:O2'	30:0:2564:G:H3'	2.08	0.53
30:0:2769:C:H2'	30:0:2770:G:C4'	2.37	0.53
9:I:111:LEU:HD23	30:0:1163:G:H4'	1.90	0.53
15:O:105:ASN:HD21	15:O:109:SER:H	1.56	0.53
16:P:7:LYS:HD3	16:P:21:VAL:CG2	2.38	0.53
30:0:1226:G:C4	30:0:1227:C:C5	2.96	0.53
30:0:1311:G:C2	30:0:1312:G:C8	2.97	0.53
30:0:2465:A:H5'	38:0:6910:HOH:O	2.07	0.53
30:0:421:C:H2'	30:0:422:G:H8	1.74	0.53
31:9:73:A:H61	31:9:108:C:H42	1.57	0.53
1:A:33:GLU:O	1:A:34:ASP:HB2	2.08	0.53
2:B:212:GLN:HA	30:0:1733:A:H4'	1.89	0.53
18:R:25:PHE:HB3	38:R:8914:HOH:O	2.07	0.53
23:W:35:VAL:HG23	23:W:41:TYR:CD2	2.43	0.53
30:0:1754:A:H2'	30:0:1755:A:O4'	2.09	0.53
1:A:20:SER:HB3	30:0:1872:C:C5	2.44	0.53
30:0:2703:A:H2'	30:0:2704:C:C6	2.40	0.53
30:0:491:C:O2'	30:0:492:C:H5'	2.09	0.53
30:0:869:G:OP2	30:0:869:G:C8	2.62	0.53
31:9:114:G:H2'	31:9:115:C:C6	2.43	0.53
12:L:11:ARG:O	30:0:903:U:C2	2.61	0.53
23:W:5:VAL:HG22	23:W:32:CYS:HB2	1.91	0.53
30:0:1271:A:H2'	30:0:1272:C:C6	2.43	0.53
30:0:1741:U:C4	30:0:2033:G:C8	2.96	0.53
30:0:1762:C:O2'	30:0:1763:C:H5'	2.08	0.53
16:P:71:TYR:CE2	30:0:1790:C:H5	2.26	0.53
30:0:2119:C:C2'	30:0:2120:U:H5'	2.38	0.53
30:0:213:G:H22	30:0:225:G:H2'	1.72	0.53
30:0:2831:C:C2	30:0:2910:A:C2	2.96	0.53
30:0:2895:C:H2'	38:0:9579:HOH:O	2.08	0.53
30:0:549:A:C2	30:0:550:C:C2	2.97	0.53
30:0:597:A:O2'	30:0:598:C:H5'	2.08	0.53
30:0:718:C:C2'	30:0:718:C:O2	2.55	0.53
8:H:49:GLN:HG3	8:H:140:TYR:CE2	2.43	0.53
30:0:1278:A:C4'	30:0:1279:U:C4	2.74	0.53
30:0:535:G:C5	30:0:2063:U:C4	2.96	0.53
30:0:2078:U:H2'	30:0:2079:G:H8	1.74	0.53
30:0:2321:A:H2'	30:0:2321:A:N3	2.24	0.53
29:3:68:LYS:HZ1	30:0:2436:U:H5'	1.73	0.53
30:0:2501:G:H1	30:0:2519:C:H42	1.56	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:466:A:H2'	30:0:467:G:O4'	2.08	0.53
31:9:58:G:C8	31:9:59:C:C5	2.97	0.53
8:H:69:ARG:HD3	38:H:239:HOH:O	2.08	0.53
11:K:89:LYS:HA	38:K:7064:HOH:O	2.08	0.53
21:U:56:ARG:CD	30:0:2890:A:H1'	2.38	0.53
30:0:1706:G:C6	30:0:1707:G:C6	2.97	0.53
30:0:1806:G:C5	30:0:1807:U:C5	2.97	0.53
30:0:1819:G:H5'	38:0:5785:HOH:O	2.07	0.53
30:0:195:C:H2'	30:0:196:G:H5'	1.91	0.53
30:0:1972:U:O2'	30:0:1973:A:H5''	2.09	0.53
30:0:2321:A:H4'	30:0:2322:U:OP1	2.08	0.53
30:0:398:U:H2'	30:0:399:C:C6	2.44	0.53
30:0:561:G:N3	30:0:562:A:C8	2.77	0.53
29:3:31:THR:O	30:0:1923:G:H4'	2.09	0.53
2:B:305:ASP:O	2:B:306:LYS:HB2	2.09	0.53
14:N:11:ARG:HG3	14:N:14:ARG:NH1	2.23	0.53
30:0:1167:G:H2'	30:0:1168:C:H6	1.71	0.53
30:0:1769:C:O2'	30:0:1770:U:H5'	2.09	0.53
30:0:2250:G:C2	30:0:2251:G:H1'	2.44	0.53
30:0:2613:G:O2'	30:0:2614:C:H5'	2.09	0.53
30:0:2864:U:C2'	30:0:2865:G:H5'	2.38	0.53
30:0:424:C:H2'	30:0:425:U:C6	2.44	0.53
30:0:191:A:H61	30:0:435:A:N6	2.06	0.53
30:0:69:A:H2'	30:0:70:A:OP2	2.09	0.53
30:0:735:C:C5	30:0:736:A:C5	2.97	0.53
1:A:164:ARG:HB3	1:A:164:ARG:HH11	1.73	0.53
1:A:199:HIS:HD2	1:A:201:PHE:N	2.00	0.53
2:B:141:ARG:HD2	2:B:163:GLU:OE2	2.08	0.53
10:J:39:VAL:HG22	10:J:107:ASN:HA	1.91	0.53
11:K:41:LYS:O	11:K:42:ASN:HB2	2.09	0.53
13:M:179:GLY:O	30:0:399:C:H5'	2.08	0.53
13:M:187:LEU:CD2	13:M:194:GLY:HA3	2.38	0.53
14:N:154:LEU:C	14:N:156:GLU:H	2.11	0.53
22:V:44:GLY:O	22:V:48:GLU:HG2	2.08	0.53
23:W:154:ARG:NH1	30:0:588:G:O6	2.40	0.53
25:Y:154:ARG:NH2	30:0:1071:G:H4'	2.23	0.53
30:0:1158:G:C2'	30:0:1159:G:H5'	2.39	0.53
30:0:1913:C:H2'	30:0:1914:C:H6	1.73	0.53
30:0:1922:A:N1	30:0:2449:G:O2'	2.38	0.53
30:0:1968:A:H2'	30:0:1969:A:C8	2.44	0.53
30:0:2336:G:H2'	38:0:6275:HOH:O	2.09	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:334:G:H2'	30:0:335:U:O4'	2.08	0.53
2:B:62:ARG:HA	2:B:65:MET:CE	2.38	0.53
8:H:6:ALA:HA	8:H:61:ARG:HH12	1.74	0.53
10:J:41:ALA:HB3	38:J:8863:HOH:O	2.09	0.53
16:P:115:SER:OG	16:P:118:GLN:HG3	2.08	0.53
30:0:74:G:H1	30:0:103:C:H42	1.55	0.53
30:0:1844:C:O2'	30:0:1845:A:H5'	2.08	0.53
30:0:2642:G:H2'	30:0:2643:G:O4'	2.09	0.53
9:I:108:HIS:H	9:I:109:PRO:HD2	1.74	0.53
14:N:38:LYS:HE2	14:N:107:ASN:ND2	2.24	0.53
30:0:1014:A:H2'	30:0:1015:C:H5'	1.90	0.52
30:0:1188:A:C6	30:0:1189:A:C6	2.97	0.52
30:0:1244:U:H4'	30:0:1246:A:O4'	2.09	0.52
30:0:1451:C:H5'	30:0:1505:U:C5	2.44	0.52
30:0:2037:C:H3'	38:0:6684:HOH:O	2.09	0.52
30:0:216:A:O2'	30:0:217:C:H5'	2.09	0.52
8:H:159:LYS:HG2	30:0:2519:C:O2	2.09	0.52
30:0:2719:A:H2'	30:0:2720:C:H5'	1.90	0.52
30:0:488:U:H2'	38:0:3993:HOH:O	2.08	0.52
31:9:20:G:O2'	31:9:21:G:H5'	2.09	0.52
31:9:37:C:O2	31:9:47:A:H1'	2.09	0.52
31:9:58:G:C6	31:9:59:C:C2	2.97	0.52
1:A:105:VAL:HG13	1:A:155:THR:O	2.09	0.52
8:H:26:ILE:HA	8:H:123:ILE:HG21	1.91	0.52
1:A:45:ILE:HG22	26:Z:78:ILE:HG12	1.89	0.52
30:0:1164:U:H5	38:0:6024:HOH:O	1.91	0.52
30:0:675:U:H2'	30:0:676:C:H5'	1.90	0.52
15:O:25:VAL:HG13	30:0:709:G:O3'	2.10	0.52
23:W:4:LEU:HD22	23:W:54:PHE:HB3	1.90	0.52
30:0:125:U:H2'	38:0:3760:HOH:O	2.10	0.52
30:0:1515:A:H2'	30:0:1516:U:C6	2.44	0.52
30:0:1557:G:O2'	30:0:1558:C:H5'	2.09	0.52
30:0:1684:A:O2'	30:0:1685:A:H5''	2.10	0.52
13:M:73:ARG:HH21	30:0:2263:G:H5''	1.70	0.52
30:0:271:C:C2	30:0:273:G:O4'	2.61	0.52
30:0:2901:C:H6	30:0:2901:C:O5'	1.93	0.52
30:0:622:G:O2'	30:0:623:U:H5'	2.10	0.52
31:9:1:U:C4'	31:9:3:A:OP1	2.58	0.52
3:C:43:LYS:HG2	30:0:449:A:N7	2.24	0.52
5:E:126:ILE:HA	5:E:131:LEU:HD23	1.91	0.52
13:M:24:GLN:NE2	13:M:27:ARG:HH11	2.07	0.52

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:33:SER:O	19:S:37:VAL:HG23	2.10	0.52
30:0:1359:U:O5'	30:0:1360:C:H5''	2.10	0.52
30:0:1664:A:OP1	30:0:1664:A:H8	1.92	0.52
30:0:1865:A:H2'	30:0:1866:A:C8	2.44	0.52
11:K:66:ARG:HH12	30:0:1992:U:H3'	1.75	0.52
30:0:2320:U:H4'	30:0:2321:A:O4'	2.09	0.52
30:0:2407:G:H2'	30:0:2408:A:O4'	2.09	0.52
30:0:249:G:N2	30:0:250:C:C2	2.77	0.52
30:0:2783:A:O2'	30:0:2784:A:H5'	2.09	0.52
30:0:40:C:H6	30:0:40:C:O5'	1.93	0.52
30:0:24:G:N2	30:0:518:G:H1'	2.24	0.52
28:2:49:GLU:HB2	38:2:131:HOH:O	2.08	0.52
31:9:38:A:C2	31:9:39:U:C4	2.97	0.52
20:T:26:THR:HG23	20:T:97:ARG:HG3	1.90	0.52
23:W:130:HIS:NE2	31:9:88:G:OP1	2.42	0.52
30:0:1590:A:C2	30:0:1606:A:H1'	2.44	0.52
30:0:204:A:C2'	30:0:205:U:H5'	2.39	0.52
30:0:916:A:C2	30:0:928:G:N3	2.78	0.52
29:3:68:LYS:HG2	29:3:77:ALA:HB3	1.91	0.52
2:B:226:LYS:HG2	2:B:230:GLN:NE2	2.25	0.52
6:F:53:ASP:OD1	6:F:80:GLN:HB2	2.10	0.52
13:M:81:ARG:HB3	13:M:86:GLN:HG2	1.91	0.52
14:N:55:ASP:OD2	31:9:7:G:H4'	2.09	0.52
30:0:1139:U:H2'	30:0:1140:C:C6	2.45	0.52
30:0:1180:U:O2'	30:0:1181:A:H5'	2.10	0.52
30:0:1641:A:C2'	30:0:1642:A:H5'	2.40	0.52
30:0:1649:G:H1'	38:0:5498:HOH:O	2.09	0.52
18:R:132:ARG:HH22	30:0:2055:A:H4'	1.74	0.52
30:0:1087:G:O2'	33:0:8822:CL:CL	2.55	0.52
31:9:49:G:O2'	31:9:50:G:H5'	2.08	0.52
1:A:66:ARG:HH11	1:A:66:ARG:HB2	1.74	0.52
4:D:18:ILE:HD13	4:D:84:LEU:HD12	1.91	0.52
5:E:153:ARG:HH12	30:0:2778:A:C1'	2.22	0.52
18:R:111:ILE:HG23	18:R:145:LEU:HD11	1.90	0.52
20:T:106:GLU:HG3	38:T:4913:HOH:O	2.09	0.52
30:0:1052:G:H2'	30:0:1052:G:N3	2.24	0.52
30:0:1886:A:H4'	38:0:9333:HOH:O	2.09	0.52
30:0:1930:A:H2'	30:0:1931:A:C8	2.44	0.52
30:0:1890:U:H4'	30:0:2010:A:C6	2.44	0.52
30:0:2041:G:O2'	30:0:2042:U:H5'	2.10	0.52
30:0:228:C:C2'	30:0:229:G:H5'	2.40	0.52

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2526:C:C6	30:0:2526:C:C3'	2.93	0.52
28:2:18:ASN:HD21	28:2:40:ARG:HB3	1.74	0.52
31:9:58:G:C5	31:9:59:C:C2	2.98	0.52
2:B:223:ARG:HG3	2:B:232:TRP:O	2.10	0.52
25:Y:132:ASP:OD2	30:0:621:C:H5'	2.10	0.52
38:I:1549:HOH:O	30:0:1180:U:H1'	2.10	0.52
30:0:2637:A:C5'	38:0:4897:HOH:O	2.55	0.52
30:0:2651:C:H2'	30:0:2652:U:O4'	2.10	0.52
30:0:506:G:N2	30:0:509:A:H5''	2.18	0.52
30:0:595:U:H3'	38:0:6474:HOH:O	2.09	0.52
30:0:734:U:O2'	30:0:736:A:N7	2.33	0.52
30:0:800:G:H2'	30:0:801:U:C6	2.45	0.52
27:1:11:LYS:HG2	30:0:777:U:O2'	2.10	0.52
31:9:34:A:H2'	31:9:35:C:O4'	2.10	0.52
18:R:18:LEU:HB2	18:R:143:VAL:HG13	1.91	0.52
30:0:1183:C:C4	30:0:1184:C:N4	2.78	0.52
30:0:1522:A:C2'	30:0:1523:G:H5'	2.40	0.52
2:B:243:ASN:HB2	30:0:2607:U:OP2	2.10	0.52
30:0:2672:C:H2'	30:0:2673:U:H6	1.74	0.52
30:0:599:G:H2'	30:0:600:G:H8	1.74	0.52
30:0:615:G:H2'	30:0:616:U:C6	2.44	0.52
30:0:793:A:C5	30:0:794:U:C5	2.98	0.52
6:F:91:VAL:HG12	6:F:92:GLY:N	2.20	0.52
7:G:63:ARG:O	7:G:67:LEU:HG	2.10	0.52
12:L:73:VAL:HG23	12:L:74:THR:H	1.75	0.52
30:0:1154:A:H2'	30:0:1155:G:C8	2.44	0.52
30:0:1422:U:H2'	30:0:1423:C:H6	1.72	0.52
30:0:1504:A:H5'	38:0:4396:HOH:O	2.10	0.52
30:0:2088:C:H2'	30:0:2089:A:C8	2.44	0.52
30:0:308:U:C4	30:0:342:C:H1'	2.45	0.52
30:0:818:A:C6	30:0:819:A:N1	2.78	0.52
29:3:4:PRO:HA	29:3:91:GLN:O	2.09	0.52
13:M:73:ARG:HD2	13:M:73:ARG:N	2.25	0.52
30:0:1175:G:N7	30:0:1176:C:C4	2.78	0.51
30:0:1191:A:C2'	30:0:1193:A:H5'	2.38	0.51
30:0:1309:U:O2'	30:0:1310:U:H5'	2.10	0.51
30:0:1743:G:H2'	30:0:1744:G:O4'	2.10	0.51
30:0:2872:U:H2'	30:0:2873:C:H6	1.76	0.51
30:0:818:A:C6	30:0:819:A:C2	2.98	0.51
12:L:78:ALA:HB3	38:L:8860:HOH:O	2.11	0.51
13:M:43:PRO:HG3	13:M:62:VAL:HG21	1.91	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:49:ARG:HD3	24:X:84:ILE:HG12	1.92	0.51
30:0:1395:C:H2'	30:0:1396:C:C6	2.46	0.51
30:0:2498:C:O2'	30:0:2499:U:H5'	2.10	0.51
30:0:2900:G:H2'	30:0:2901:C:O4'	2.10	0.51
30:0:395:A:H2'	30:0:397:A:H62	1.74	0.51
2:B:144:THR:HB	38:B:9096:HOH:O	2.10	0.51
14:N:7:LYS:HE3	17:Q:21:ARG:O	2.09	0.51
17:Q:87:THR:HB	38:Q:1295:HOH:O	2.10	0.51
20:T:52:ARG:HH12	30:0:308:U:H2'	1.75	0.51
26:Z:38:PHE:HB3	26:Z:42:TYR:CE1	2.46	0.51
30:0:1667:A:H8	30:0:1667:A:H5'	1.75	0.51
30:0:1992:U:H2'	30:0:1994:A:OP2	2.10	0.51
30:0:20:G:H5''	30:0:510:U:O4	2.09	0.51
30:0:2544:G:H5'	38:0:3418:HOH:O	2.10	0.51
25:Y:205:ILE:HB	25:Y:230:ASN:HD21	1.75	0.51
30:0:1641:A:H2'	30:0:1642:A:C5'	2.40	0.51
30:0:2032:U:H2'	30:0:2033:G:H5''	1.92	0.51
30:0:2614:C:O2'	30:0:2615:U:H5'	2.10	0.51
29:3:54:LYS:HE2	30:0:2468:A:C8	2.45	0.51
9:I:120:ALA:O	9:I:124:VAL:HG23	2.09	0.51
30:0:1160:G:H2'	38:0:5597:HOH:O	2.11	0.51
30:0:1167:G:H2'	30:0:1168:C:O4'	2.11	0.51
30:0:1395:C:H2'	30:0:1396:C:H6	1.76	0.51
31:9:56:A:H3'	31:9:57:A:H5''	1.89	0.51
1:A:175:LYS:HE2	33:A:8809:CL:CL	2.48	0.51
15:O:65:LEU:HD13	30:0:746:A:C6	2.45	0.51
30:0:254:C:C2'	30:0:254:C:O2	2.57	0.51
30:0:2700:G:O2'	30:0:2701:G:H5'	2.09	0.51
30:0:2846:C:H3'	38:0:7070:HOH:O	2.11	0.51
30:0:2851:G:H2'	30:0:2902:A:N6	2.26	0.51
30:0:660:A:N6	30:0:746:A:O4'	2.43	0.51
30:0:702:G:C2	30:0:703:G:C8	2.98	0.51
31:9:58:G:H3'	31:9:59:C:C5	2.45	0.51
3:C:127:ARG:HD3	3:C:129:HIS:CE1	2.45	0.51
10:J:21:ARG:HH21	30:0:1244:U:H5''	1.76	0.51
11:K:91:GLU:HG3	38:U:151:HOH:O	2.11	0.51
17:Q:7:LEU:HD12	30:0:2424:U:H1'	1.93	0.51
30:0:1019:C:O2'	30:0:1020:A:H5'	2.11	0.51
30:0:128:A:O2'	30:0:129:A:H5'	2.10	0.51
30:0:1947:G:N2	30:0:1966:U:C2	2.79	0.51
30:0:2032:U:H2'	30:0:2033:G:H5'	1.93	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:83:TRP:NE1	30:0:2380:A:H2	2.09	0.51
30:0:2719:A:C2'	30:0:2720:C:H5'	2.41	0.51
30:0:37:A:H2'	30:0:38:G:C8	2.46	0.51
30:0:633:C:O2'	30:0:634:G:H5'	2.10	0.51
29:3:40:ARG:HA	29:3:52:PHE:HE1	1.73	0.51
2:B:234:ARG:HG3	30:0:1735:C:OP2	2.11	0.51
5:E:137:ASP:OD1	5:E:139:GLU:HB2	2.11	0.51
8:H:114:ASP:HA	38:H:204:HOH:O	2.11	0.51
17:Q:94:GLN:O	17:Q:95:GLU:HB2	2.11	0.51
24:X:56:GLU:HG2	30:0:1400:C:H4'	1.92	0.51
30:0:1236:A:O2'	30:0:1237:U:H5'	2.11	0.51
30:0:2047:C:H5'	38:0:9814:HOH:O	2.10	0.51
30:0:210:U:O2'	30:0:211:U:H5'	2.11	0.51
30:0:2456:A:O2'	30:0:2457:U:H5'	2.10	0.51
30:0:2689:A:H2'	30:0:2690:U:H5'	1.92	0.51
15:O:37:ARG:HD2	30:0:656:G:OP2	2.11	0.51
30:0:727:G:H3'	30:0:728:C:C6	2.45	0.51
30:0:822:C:N3	30:0:823:U:C5	2.79	0.51
3:C:149:LYS:HE3	38:0:4023:HOH:O	2.10	0.51
3:C:219:ASN:O	3:C:222:ASP:HB2	2.11	0.51
6:F:36:THR:HG23	6:F:97:ALA:HB2	1.93	0.51
6:F:91:VAL:HG11	30:0:262:A:OP2	2.10	0.51
7:G:64:ASN:HD22	7:G:64:ASN:H	1.58	0.51
13:M:28:GLN:O	13:M:32:ARG:HG3	2.10	0.51
20:T:32:ARG:NH1	20:T:38:ARG:NH1	2.58	0.51
26:Z:53:ILE:HG23	38:Z:8719:HOH:O	2.10	0.51
26:Z:78:ILE:HD12	38:Z:8715:HOH:O	2.11	0.51
11:K:66:ARG:NH2	30:0:1994:A:OP1	2.44	0.51
30:0:1890:U:H1'	30:0:2013:G:N2	2.26	0.51
30:0:2589:U:H2'	30:0:2590:U:C6	2.46	0.51
30:0:2712:G:C5'	38:0:5187:HOH:O	2.58	0.51
30:0:523:C:H2'	30:0:524:A:C8	2.46	0.51
16:P:128:GLY:HA3	30:0:801:U:O4'	2.11	0.51
8:H:61:ARG:HH11	8:H:61:ARG:HG3	1.75	0.51
24:X:61:ARG:O	30:0:2744:G:H5''	2.11	0.51
25:Y:127:GLN:HA	38:Y:8909:HOH:O	2.11	0.51
30:0:1186:C:N4	30:0:1187:U:C4	2.79	0.51
30:0:1568:G:H2'	30:0:1569:U:O4'	2.10	0.51
30:0:1819:G:H2'	30:0:1820:G:C5'	2.41	0.51
30:0:2526:C:O2'	30:0:2527:U:H5'	2.10	0.51
30:0:255:A:H2'	30:0:256:C:C6	2.46	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:39:G:C2	30:0:444:C:C2	2.99	0.51
30:0:617:C:H2'	30:0:618:G:O4'	2.11	0.51
29:3:22:VAL:HG12	29:3:90:PHE:CE2	2.46	0.51
2:B:80:ARG:HB2	2:B:145:HIS:CE1	2.45	0.51
8:H:31:ILE:HD11	8:H:65:LEU:HB3	1.93	0.51
16:P:118:GLN:O	16:P:122:LEU:HG	2.11	0.51
9:I:83:GLY:HA3	30:0:1168:C:H5'	1.93	0.50
30:0:1226:G:C5	30:0:1227:C:C5	2.99	0.50
30:0:1441:G:O2'	30:0:1442:A:H5'	2.11	0.50
30:0:1511:U:O2'	30:0:1512:G:H5'	2.11	0.50
30:0:1642:A:C8	30:0:1643:C:C5	2.99	0.50
30:0:1796:A:H8	30:0:1796:A:O5'	1.94	0.50
30:0:1805:G:O2'	30:0:1806:G:H5'	2.11	0.50
30:0:2587:OMU:H2'	30:0:2589:U:H5''	1.93	0.50
30:0:553:G:O4'	30:0:1325:G:H5'	2.10	0.50
30:0:560:U:H2'	30:0:561:G:H8	1.75	0.50
2:B:71:VAL:HG21	2:B:296:LEU:HB3	1.92	0.50
7:G:20:VAL:O	7:G:24:VAL:HG23	2.11	0.50
11:K:97:ILE:HG22	11:K:98:VAL:N	2.25	0.50
22:V:12:THR:HG23	22:V:14:ALA:H	1.76	0.50
26:Z:102:THR:HG23	26:Z:105:ARG:HD2	1.93	0.50
30:0:1167:G:N2	30:0:1180:U:C2	2.79	0.50
25:Y:210:GLY:N	30:0:1313:A:H5''	2.27	0.50
30:0:134:U:O2	30:0:145:A:C2	2.63	0.50
30:0:2087:C:O2'	30:0:2088:C:H5'	2.11	0.50
30:0:2672:C:C2	30:0:2673:U:C6	3.00	0.50
30:0:2847:G:O2'	30:0:2848:G:H5'	2.11	0.50
3:C:127:ARG:HH21	3:C:225:PRO:HG2	1.71	0.50
30:0:1087:G:H4'	30:0:1088:A:OP1	2.12	0.50
30:0:1216:G:N2	30:0:1217:G:H1'	2.26	0.50
30:0:1461:U:H2'	30:0:1462:C:C6	2.46	0.50
30:0:1735:C:H2'	30:0:1736:A:H8	1.75	0.50
21:U:35:LYS:HA	30:0:2755:G:OP1	2.11	0.50
30:0:2899:A:O2'	30:0:2900:G:H5'	2.12	0.50
30:0:523:C:H2'	30:0:524:A:H8	1.76	0.50
30:0:876:A:H2'	30:0:876:A:N3	2.26	0.50
27:1:16:HIS:CD2	30:0:470:U:O2'	2.64	0.50
29:3:29:ARG:HA	38:3:9012:HOH:O	2.11	0.50
2:B:248:ARG:O	2:B:251:VAL:HG22	2.11	0.50
3:C:193:LEU:HA	3:C:211:ASP:O	2.10	0.50
3:C:236:THR:HG22	3:C:239:ALA:CB	2.41	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:7:ILE:HG13	5:E:11:VAL:HB	1.93	0.50
30:0:1181:A:H2'	30:0:1182:C:C5'	2.41	0.50
30:0:1463:U:H2'	30:0:1464:C:C6	2.47	0.50
30:0:1474:C:H6	30:0:1474:C:C5'	2.17	0.50
30:0:1522:A:H2'	30:0:1523:G:H5'	1.92	0.50
30:0:2564:G:OP2	30:0:2565:C:H5''	2.11	0.50
30:0:2635:A:HO2'	30:0:2636:C:H5'	1.76	0.50
30:0:1811:A:C2	30:0:2752:C:H1'	2.46	0.50
30:0:40:C:H2'	30:0:41:G:C8	2.46	0.50
29:3:10:TYR:CE1	30:0:2408:A:H1'	2.46	0.50
29:3:10:TYR:HB2	29:3:17:HIS:HE1	1.76	0.50
10:J:107:ASN:HD22	10:J:107:ASN:C	2.15	0.50
12:L:65:ASP:HA	12:L:109:LEU:O	2.11	0.50
30:0:1015:C:O5'	30:0:1015:C:H6	1.94	0.50
30:0:105:G:O2'	30:0:106:A:H5'	2.11	0.50
30:0:1187:U:O2'	30:0:1189:A:H2	1.94	0.50
30:0:1149:U:C5	30:0:1215:A:C5	3.00	0.50
2:B:235:ARG:HH11	30:0:2092:G:P	2.33	0.50
30:0:73:U:H2'	30:0:74:G:C8	2.46	0.50
17:Q:95:GLU:HA	30:0:949:U:H4'	1.94	0.50
7:G:16:LYS:O	7:G:20:VAL:HG23	2.11	0.50
13:M:71:SER:HB2	13:M:92:THR:CG2	2.35	0.50
30:0:119:A:H2'	30:0:120:A:C5'	2.42	0.50
38:B:8995:HOH:O	30:0:2093:G:H5''	2.11	0.50
30:0:2295:G:N3	30:0:2361:A:C2	2.80	0.50
30:0:2344:G:N3	30:0:2344:G:H2'	2.26	0.50
30:0:2506:A:C1'	38:0:6031:HOH:O	2.58	0.50
30:0:372:A:C2	30:0:373:G:C4	2.99	0.50
30:0:451:C:O2'	30:0:452:G:H5'	2.12	0.50
30:0:556:C:O2'	30:0:557:C:H5'	2.11	0.50
30:0:738:G:O5'	30:0:738:G:H8	1.95	0.50
30:0:819:A:C4	30:0:821:U:C5	3.00	0.50
30:0:929:A:H5''	38:0:7060:HOH:O	2.11	0.50
8:H:59:GLN:NE2	8:H:129:ARG:HE	2.10	0.50
14:N:37:ARG:NH1	31:9:6:C:OP1	2.44	0.50
16:P:114:LEU:HD22	16:P:118:GLN:HB3	1.93	0.50
16:P:135:ALA:O	16:P:139:ARG:HG3	2.11	0.50
30:0:10:U:O4	30:0:532:A:H8	1.95	0.50
1:A:178:LYS:HA	30:0:1653:A:H5'	1.94	0.50
30:0:1666:C:H42	30:0:1667:A:N6	2.10	0.50
30:0:1705:C:O2	30:0:2735:U:H5''	2.11	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2415:A:C2'	30:0:2416:G:H5'	2.40	0.50
30:0:2803:C:H2'	30:0:2804:C:H6	1.77	0.50
30:0:2823:G:O2'	30:0:2824:C:H5'	2.12	0.50
30:0:69:A:C5'	30:0:69:A:H8	2.24	0.50
30:0:716:G:C6	30:0:717:C:N4	2.80	0.50
30:0:79:G:N2	30:0:97:G:H1'	2.26	0.50
29:3:3:MET:O	29:3:90:PHE:HA	2.11	0.50
31:9:75:G:N2	31:9:106:U:O2	2.36	0.50
31:9:92:G:H2'	31:9:93:A:H8	1.73	0.50
1:A:132:ASP:CG	1:A:133:ARG:H	2.15	0.50
26:Z:42:TYR:N	30:0:1829:A:H61	2.10	0.50
30:0:1878:G:C4'	38:0:6097:HOH:O	2.60	0.50
30:0:282:C:O2'	30:0:283:U:C4'	2.60	0.50
30:0:59:A:C5'	38:0:4313:HOH:O	2.60	0.50
30:0:74:G:H1	30:0:103:C:N4	2.10	0.50
30:0:764:C:H2'	30:0:765:G:O4'	2.12	0.50
29:3:10:TYR:HB2	29:3:17:HIS:CE1	2.47	0.50
31:9:23:U:H2'	31:9:23:U:O2	2.12	0.50
1:A:100:PRO:HG2	1:A:103:VAL:HG21	1.94	0.50
3:C:22:PHE:HA	3:C:116:ALA:HA	1.94	0.50
13:M:77:HIS:CE1	13:M:86:GLN:HG2	2.47	0.50
13:M:82:ARG:HH22	13:M:85:ARG:NH2	2.08	0.50
14:N:38:LYS:HE2	14:N:107:ASN:HD21	1.75	0.50
22:V:56:ILE:O	22:V:60:GLN:HG3	2.12	0.50
30:0:2253:G:O2'	30:0:2254:G:H5'	2.11	0.50
30:0:2465:A:H3'	38:0:3637:HOH:O	2.12	0.50
30:0:561:G:C2	30:0:562:A:C8	3.00	0.50
30:0:814:G:H2'	30:0:815:U:H6	1.77	0.50
29:3:3:MET:SD	29:3:88:LEU:HD23	2.52	0.50
31:9:42:C:H5'	31:9:43:G:OP2	2.12	0.50
1:A:141:PRO:HG2	30:0:1855:G:O6	2.12	0.50
2:B:18:ARG:HG3	2:B:256:GLN:HG3	1.93	0.50
3:C:101:ASP:HB2	30:0:750:A:O3'	2.12	0.50
12:L:24:ALA:HB2	12:L:30:ARG:HE	1.76	0.50
13:M:145:ASP:HB2	38:M:8865:HOH:O	2.11	0.50
20:T:71:VAL:HG11	20:T:90:PRO:CB	2.38	0.50
23:W:130:HIS:O	23:W:136:GLY:HA3	2.12	0.50
23:W:6:GLN:CB	23:W:26:ILE:HD11	2.40	0.50
24:X:26:ALA:HB2	24:X:63:ARG:HA	1.93	0.50
30:0:1165:G:H21	30:0:1173:A:H5'	1.74	0.49
30:0:1268:C:H2'	30:0:1269:G:C8	2.46	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1393:A:H2'	30:0:1394:C:C6	2.47	0.49
30:0:1601:G:H1'	38:0:9891:HOH:O	2.11	0.49
30:0:1933:G:O2'	30:0:1934:A:H5'	2.12	0.49
30:0:952:G:N3	30:0:2302:A:H2'	2.26	0.49
30:0:2854:A:C6	30:0:2905:A:C6	3.00	0.49
30:0:47:G:N3	30:0:114:A:C2	2.80	0.49
31:9:28:U:O2	31:9:57:A:N6	2.44	0.49
31:9:39:U:H1'	31:9:44:A:H61	1.77	0.49
2:B:66:GLU:OE1	2:B:328:ARG:HD2	2.12	0.49
4:D:58:VAL:CG1	4:D:60:GLU:HG2	2.41	0.49
13:M:159:VAL:CG1	33:M:8818:CL:CL	2.95	0.49
16:P:87:ARG:HG2	38:0:5919:HOH:O	2.10	0.49
30:0:1226:G:H2'	30:0:1227:C:C6	2.44	0.49
30:0:134:U:C2	30:0:145:A:C2	2.99	0.49
30:0:1662:C:H6	30:0:1662:C:O5'	1.94	0.49
30:0:1902:G:N2	30:0:1936:C:C2	2.80	0.49
30:0:589:U:H2'	30:0:590:A:H8	1.76	0.49
30:0:873:G:N2	38:0:9173:HOH:O	2.43	0.49
29:3:60:LYS:C	29:3:62:THR:H	2.15	0.49
31:9:55:U:H4'	31:9:56:A:H8	1.71	0.49
4:D:35:ALA:HB2	38:D:5576:HOH:O	2.11	0.49
8:H:32:ALA:HB3	8:H:69:ARG:HH12	1.77	0.49
16:P:98:ILE:HD12	16:P:102:ARG:NE	2.27	0.49
18:R:18:LEU:O	18:R:142:ASP:HA	2.12	0.49
30:0:1194:A:C2	30:0:1206:U:H1'	2.47	0.49
30:0:1787:C:C4'	30:0:2883:A:O4'	2.59	0.49
30:0:1800:G:H2'	30:0:1801:A:H8	1.77	0.49
30:0:2291:A:N3	30:0:2291:A:H2'	2.28	0.49
30:0:2617:G:C2	30:0:2618:G:C8	3.00	0.49
30:0:2846:C:H2'	30:0:2847:G:H8	1.77	0.49
30:0:316:A:N3	30:0:336:G:O2'	2.41	0.49
30:0:400:C:H2'	30:0:401:C:C6	2.47	0.49
10:J:131:THR:HG22	10:J:134:GLU:H	1.77	0.49
11:K:34:VAL:HB	38:K:7169:HOH:O	2.12	0.49
25:Y:212:ARG:HB2	30:0:1315:G:C4	2.47	0.49
30:0:1206:U:C5'	30:0:1206:U:H6	2.21	0.49
30:0:1255:A:H1'	38:0:7741:HOH:O	2.11	0.49
25:Y:115:ARG:NH2	30:0:1266:U:H4'	2.27	0.49
30:0:1339:G:C6	30:0:1340:G:N1	2.81	0.49
30:0:1381:A:N3	30:0:1382:G:H1'	2.28	0.49
30:0:1947:G:N2	30:0:1966:U:N3	2.60	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2133:U:H4'	30:0:2134:G:H5'	1.93	0.49
29:3:79:LEU:CD1	30:0:2456:A:H2	2.25	0.49
30:0:2632:G:H2'	30:0:2633:A:C8	2.46	0.49
30:0:2632:G:C6	30:0:2633:A:N6	2.81	0.49
30:0:36:C:C2	30:0:447:A:C2	3.00	0.49
30:0:814:G:H2'	30:0:815:U:C6	2.47	0.49
30:0:816:G:H5'	30:0:1598:A:H4'	1.94	0.49
29:3:79:LEU:HD22	38:0:7515:HOH:O	2.13	0.49
1:A:47:HIS:CD2	30:0:1654:U:C2'	2.92	0.49
2:B:44:TYR:OH	2:B:148:PRO:HG3	2.11	0.49
2:B:215:VAL:O	2:B:219:GLY:HA2	2.13	0.49
6:F:110:ASP:O	6:F:114:LYS:HG3	2.12	0.49
9:I:93:ALA:HB3	9:I:132:VAL:HG22	1.95	0.49
17:Q:66:LYS:HB2	17:Q:70:ALA:O	2.13	0.49
26:Z:60:ASP:HB3	26:Z:69:ASP:HB3	1.92	0.49
30:0:1370:G:H5''	38:0:5497:HOH:O	2.12	0.49
30:0:1555:G:H4'	30:0:1630:A:C2	2.47	0.49
30:0:1559:A:HO2'	30:0:1561:U:H5	1.60	0.49
30:0:1733:A:C5	30:0:1734:C:C2	3.00	0.49
30:0:1878:G:O2'	30:0:1879:U:H6	1.90	0.49
30:0:2118:A:H5'	38:0:3996:HOH:O	2.13	0.49
30:0:2366:C:O5'	30:0:2366:C:H6	1.95	0.49
30:0:1787:C:O4'	30:0:2883:A:H1'	2.11	0.49
30:0:494:C:H1'	30:0:498:A:N6	2.27	0.49
2:B:304:PRO:HD2	2:B:307:ARG:HE	1.78	0.49
14:N:58:LEU:HD12	14:N:58:LEU:N	2.27	0.49
30:0:1174:A:C5	30:0:1201:C:H4'	2.47	0.49
30:0:1189:A:O2'	30:0:1208:C:H2'	2.12	0.49
30:0:1626:A:O2'	30:0:1627:G:H5'	2.13	0.49
30:0:1517:C:O2	30:0:1670:A:C2	2.66	0.49
30:0:1682:A:O2'	30:0:1683:G:H5''	2.12	0.49
30:0:1871:U:O4'	30:0:1873:G:C8	2.66	0.49
30:0:2335:C:C2	30:0:2350:G:C2	3.01	0.49
30:0:29:C:O2'	30:0:30:U:H5'	2.12	0.49
8:H:27:PRO:HD3	8:H:123:ILE:CG2	2.43	0.49
10:J:130:VAL:HG12	10:J:131:THR:H	1.78	0.49
14:N:37:ARG:HG3	14:N:37:ARG:HH11	1.77	0.49
20:T:107:LYS:HD2	30:0:97:G:C2	2.47	0.49
30:0:1226:G:N3	30:0:1227:C:C6	2.81	0.49
29:3:33:MET:HG2	30:0:1922:A:C2'	2.42	0.49
30:0:2478:U:H2'	30:0:2479:A:C8	2.48	0.49

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:285:A:H2'	30:0:286:U:O4'	2.13	0.49
30:0:316:A:H1'	30:0:336:G:N3	2.27	0.49
30:0:549:A:C6	30:0:550:C:C4	3.00	0.49
30:0:862:U:H2'	30:0:863:G:H8	1.77	0.49
30:0:889:C:H4'	38:0:6368:HOH:O	2.13	0.49
29:3:12:PRO:HB3	30:0:2382:A:O2'	2.12	0.49
2:B:307:ARG:HD2	38:B:9123:HOH:O	2.12	0.49
6:F:110:ASP:O	6:F:114:LYS:N	2.44	0.49
18:R:71:LYS:HE2	30:0:2831:C:O3'	2.13	0.49
21:U:9:CYS:HB2	38:U:6796:HOH:O	2.11	0.49
30:0:1183:C:N4	30:0:1184:C:N4	2.60	0.49
30:0:1583:U:O2'	30:0:1584:C:H5'	2.13	0.49
30:0:1706:G:C5	30:0:1707:G:C6	3.00	0.49
30:0:1760:G:H5'	30:0:1818:C:O2'	2.12	0.49
30:0:1921:A:C6	30:0:1922:A:C2	3.00	0.49
30:0:2326:C:H4'	30:0:2412:G:H4'	1.94	0.49
30:0:2826:G:H1'	30:0:2914:A:N6	2.28	0.49
30:0:447:A:O2'	30:0:448:G:H5'	2.13	0.49
31:9:110:G:N2	31:9:111:U:H1'	2.28	0.49
1:A:109:GLU:HG2	1:A:116:GLY:N	2.25	0.49
2:B:162:MET:CE	2:B:308:LEU:HD21	2.42	0.49
2:B:98:THR:HG22	2:B:99:GLU:N	2.28	0.49
3:C:233:THR:HG22	3:C:234:VAL:N	2.26	0.49
8:H:29:SER:HA	8:H:62:HIS:HD2	1.77	0.49
26:Z:47:ARG:HH22	30:0:1771:U:H1'	1.77	0.49
30:0:1116:U:C2	30:0:1246:A:N6	2.81	0.49
30:0:1343:C:H2'	30:0:1344:G:O5'	2.12	0.49
30:0:1453:G:C2	30:0:1675:C:C2	3.00	0.49
30:0:2103:A:N3	30:0:2103:A:H2'	2.28	0.49
30:0:2269:C:H2'	30:0:2270:G:O4'	2.12	0.49
30:0:717:C:H2'	30:0:718:C:H6	1.78	0.49
30:0:731:U:O2'	30:0:732:C:H5'	2.13	0.49
29:3:1:MET:HG2	29:3:87:ARG:O	2.11	0.49
31:9:105:A:H2'	31:9:106:U:O4'	2.12	0.49
1:A:36:ASP:HB2	1:A:85:SER:H	1.77	0.49
14:N:25:ARG:HB3	30:0:2415:A:C2	2.47	0.49
25:Y:235:GLU:CD	25:Y:235:GLU:H	2.16	0.49
30:0:1119:G:H22	30:0:1246:A:H2	1.46	0.49
30:0:1351:G:H1'	38:0:4648:HOH:O	2.13	0.49
30:0:1607:A:C4	30:0:1608:G:C8	3.01	0.49
30:0:1615:A:H5'	38:0:4169:HOH:O	2.12	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2497:A:C2	30:0:2524:G:C2	3.01	0.49
30:0:2536:C:H6	38:0:4998:HOH:O	1.95	0.49
30:0:271:C:N4	30:0:378:A:H2	2.01	0.49
27:1:21:ARG:HD2	27:1:39:PHE:HB2	1.95	0.49
31:9:60:C:O2'	31:9:61:C:H5'	2.13	0.49
31:9:8:G:C6	31:9:9:C:C4	3.00	0.49
14:N:178:THR:O	14:N:181:ASP:HB3	2.13	0.49
20:T:69:LYS:O	20:T:71:VAL:HG23	2.13	0.49
30:0:1063:G:H4'	30:0:2307:A:H1'	1.95	0.48
30:0:1240:G:H1'	38:0:9360:HOH:O	2.12	0.48
3:C:173:LYS:HE3	30:0:1311:G:O6	2.12	0.48
30:0:1586:G:C2'	30:0:1587:U:H5'	2.43	0.48
30:0:1644:C:C2	30:0:1645:U:C5	3.01	0.48
30:0:191:A:H2'	30:0:237:G:O6	2.12	0.48
30:0:2297:U:H2'	30:0:2298:C:H6	1.78	0.48
30:0:2639:G:C5	30:0:2640:U:C5	3.01	0.48
30:0:419:A:H1'	30:0:1921:A:C2	2.48	0.48
30:0:788:A:H4'	38:0:7005:HOH:O	2.12	0.48
29:3:88:LEU:HB3	29:3:90:PHE:CE1	2.48	0.48
4:D:92:GLU:HB2	38:D:3862:HOH:O	2.13	0.48
6:F:63:ILE:HB	6:F:64:PRO:CD	2.37	0.48
13:M:52:GLN:OE1	13:M:116:ASN:HB3	2.13	0.48
25:Y:137:LYS:HD2	38:0:7590:HOH:O	2.11	0.48
30:0:1066:U:H2'	30:0:1067:A:C8	2.48	0.48
30:0:106:A:C6	30:0:107:U:C4	3.00	0.48
30:0:1765:G:O2'	30:0:1766:U:H5'	2.12	0.48
30:0:1916:C:O2'	30:0:1917:G:H5'	2.14	0.48
30:0:2646:G:C4	30:0:2647:C:C5	3.02	0.48
30:0:2713:G:O2'	30:0:2714:U:H5'	2.12	0.48
30:0:2864:U:O2'	30:0:2865:G:H5'	2.14	0.48
31:9:19:G:C2	31:9:20:G:C8	3.00	0.48
31:9:2:U:H4'	38:9:9107:HOH:O	2.13	0.48
4:D:22:VAL:HG22	4:D:74:THR:HG22	1.95	0.48
5:E:11:VAL:HG12	5:E:12:ASP:N	2.28	0.48
11:K:98:VAL:HG11	11:K:102:GLU:HA	1.94	0.48
13:M:134:ILE:CG2	13:M:141:ILE:HD13	2.36	0.48
20:T:28:SER:O	20:T:32:ARG:HG3	2.14	0.48
21:U:19:THR:HG22	21:U:20:MET:N	2.28	0.48
30:0:1832:G:C2	30:0:1833:U:C6	3.00	0.48
30:0:1883:U:H2'	30:0:1884:G:H5'	1.94	0.48
30:0:2480:G:O2'	30:0:2481:G:H5'	2.13	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2526:C:H3'	30:0:2526:C:C6	2.47	0.48
30:0:2827:A:C2	30:0:2914:A:C2	3.01	0.48
30:0:2898:G:H1'	38:0:7555:HOH:O	2.13	0.48
30:0:334:G:C5	30:0:335:U:C5	3.00	0.48
30:0:595:U:O4'	33:0:8817:CL:CL	2.69	0.48
30:0:681:G:N3	30:0:681:G:H5'	2.28	0.48
16:P:124:ASP:O	30:0:801:U:H4'	2.13	0.48
31:9:3:A:H2	31:9:21:G:N3	2.12	0.48
8:H:52:LEU:HD13	8:H:153:PHE:HB3	1.95	0.48
30:0:1015:C:H2'	30:0:1016:U:C6	2.48	0.48
30:0:120:A:H2'	30:0:120:A:N3	2.29	0.48
30:0:1557:G:H2'	30:0:1558:C:H6	1.78	0.48
30:0:1632:A:C3'	30:0:1633:C:H5'	2.43	0.48
30:0:2700:G:H2'	30:0:2701:G:C5'	2.43	0.48
2:B:152:PRO:HD2	38:B:9102:HOH:O	2.12	0.48
8:H:35:LYS:HE3	30:0:968:G:H1'	1.95	0.48
13:M:84:LYS:HA	29:3:46:ILE:O	2.12	0.48
16:P:31:ILE:HG12	16:P:43:LEU:HD13	1.96	0.48
26:Z:42:TYR:H	30:0:1829:A:H61	1.61	0.48
30:0:100:C:C4	30:0:101:C:C5	3.01	0.48
30:0:1434:A:O2'	30:0:1435:U:H6	1.92	0.48
30:0:1496:A:H5'	30:0:1572:A:H1'	1.94	0.48
30:0:1634:G:H2'	30:0:1635:U:H6	1.76	0.48
30:0:222:A:H2'	30:0:223:G:O4'	2.13	0.48
30:0:2255:A:C2	30:0:2256:G:C4	3.02	0.48
30:0:2505:G:C2'	30:0:2506:A:C5'	2.91	0.48
30:0:2672:C:H2'	30:0:2673:U:O4'	2.14	0.48
30:0:2755:G:H1'	38:0:4651:HOH:O	2.13	0.48
30:0:2772:G:O2'	30:0:2773:G:H5'	2.13	0.48
30:0:2854:A:H2'	30:0:2855:G:H8	1.78	0.48
30:0:2860:G:H2'	30:0:2861:G:C8	2.48	0.48
30:0:677:C:H2'	30:0:678:G:H8	1.77	0.48
30:0:707:C:C2	30:0:708:A:C8	3.02	0.48
29:3:64:LYS:HE2	38:0:7638:HOH:O	2.12	0.48
4:D:37:ALA:O	4:D:40:ILE:HG12	2.13	0.48
11:K:43:ARG:NH1	30:0:2712:G:OP1	2.46	0.48
12:L:117:GLU:HG3	12:L:117:GLU:O	2.13	0.48
14:N:78:MET:HB2	14:N:79:PRO:HD3	1.95	0.48
18:R:132:ARG:HG2	18:R:133:ALA:N	2.27	0.48
19:S:6:LYS:HB2	19:S:27:ALA:O	2.13	0.48
20:T:27:LEU:HB2	20:T:32:ARG:HG2	1.95	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1182:C:C1'	30:0:1192:A:H8	2.26	0.48
30:0:1207:A:OP2	30:0:1208:C:H5	1.96	0.48
30:0:1970:G:H1'	38:0:3662:HOH:O	2.13	0.48
30:0:1970:G:H4'	30:0:1971:G:C5'	2.43	0.48
30:0:200:C:H6	38:0:3433:HOH:O	1.96	0.48
30:0:2133:U:H4'	30:0:2134:G:C5'	2.44	0.48
30:0:2598:U:O2	30:0:2600:A:C8	2.66	0.48
30:0:2617:G:H4'	38:0:4487:HOH:O	2.13	0.48
30:0:611:U:H2'	30:0:612:U:C6	2.48	0.48
29:3:43:ASN:HB2	29:3:52:PHE:CD1	2.48	0.48
2:B:36:PRO:HG3	2:B:169:GLY:H	1.77	0.48
4:D:51:ARG:HH11	4:D:68:PRO:HB3	1.78	0.48
5:E:139:GLU:OE2	30:0:2781:U:H1'	2.13	0.48
10:J:60:ARG:HD3	10:J:71:TYR:CE1	2.47	0.48
15:O:88:LYS:HB3	38:O:7061:HOH:O	2.13	0.48
30:0:1224:G:H2'	30:0:1225:C:C6	2.48	0.48
30:0:1520:G:H2'	30:0:1521:C:C6	2.49	0.48
30:0:1878:G:C2	30:0:1879:U:C2	3.02	0.48
30:0:1908:G:N1	30:0:1930:A:OP2	2.46	0.48
30:0:2569:A:O5'	30:0:2569:A:H8	1.96	0.48
30:0:2707:C:C2'	30:0:2707:C:O2	2.59	0.48
30:0:31:C:H2'	38:0:7668:HOH:O	2.13	0.48
30:0:627:G:H2'	30:0:2071:C:C4	2.49	0.48
30:0:705:C:C2'	30:0:705:C:O2	2.62	0.48
27:1:25:LYS:CD	28:2:49:GLU:H	2.25	0.48
5:E:80:TRP:O	5:E:134:SER:HA	2.12	0.48
6:F:107:ASP:O	6:F:111:ILE:HG13	2.13	0.48
13:M:139:PRO:HA	13:M:142:GLN:HB2	1.95	0.48
16:P:94:TRP:CZ2	16:P:98:ILE:HG13	2.49	0.48
17:Q:28:ARG:HG2	38:9:9083:HOH:O	2.12	0.48
18:R:138:SER:HB2	38:0:5570:HOH:O	2.14	0.48
23:W:26:ILE:HB	38:W:5420:HOH:O	2.14	0.48
30:0:99:A:C8	30:0:100:C:C6	3.02	0.48
30:0:1023:C:O2'	30:0:1024:G:H5'	2.14	0.48
30:0:1063:G:H8	38:0:9856:HOH:O	1.96	0.48
28:2:10:ARG:NH2	30:0:121:U:OP2	2.44	0.48
30:0:1029:U:O2'	30:0:1273:C:OP1	2.27	0.48
30:0:2354:A:C2	30:0:2367:A:C8	3.02	0.48
30:0:2717:C:H2'	30:0:2718:C:H5'	1.93	0.48
30:0:808:A:C5	30:0:809:G:H1'	2.48	0.48
30:0:858:U:H2'	30:0:859:C:C6	2.47	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:1:THR:HB	38:1:2852:HOH:O	2.12	0.48
29:3:25:VAL:HA	38:3:9036:HOH:O	2.12	0.48
29:3:40:ARG:C	29:3:42:ARG:H	2.16	0.48
1:A:162:GLY:N	26:Z:91:GLY:HA2	2.29	0.48
9:I:133:THR:HG22	9:I:134:ILE:N	2.28	0.48
16:P:11:ALA:HB1	16:P:16:VAL:O	2.14	0.48
23:W:117:ARG:HH22	30:0:1264:U:P	2.36	0.48
30:0:1177:A:N3	30:0:1177:A:H2'	2.28	0.48
30:0:1204:C:H2'	30:0:1205:U:O4'	2.14	0.48
30:0:2254:G:C2	30:0:2255:A:C8	3.01	0.48
30:0:2281:C:H5	38:0:3756:HOH:O	1.97	0.48
30:0:2505:G:H2'	30:0:2506:A:C5'	2.43	0.48
30:0:2587:OMU:H5	38:0:7464:HOH:O	2.13	0.48
30:0:2777:G:O2'	30:0:2778:A:H5'	2.13	0.48
30:0:432:G:H5''	38:0:6860:HOH:O	2.12	0.48
30:0:69:A:C2'	30:0:70:A:OP2	2.62	0.48
30:0:763:C:O2'	30:0:764:C:H5'	2.14	0.48
30:0:842:C:H4'	38:0:3427:HOH:O	2.13	0.48
30:0:920:C:C4'	30:0:921:G:C2	2.95	0.48
31:9:39:U:C2'	31:9:40:C:OP1	2.62	0.48
1:A:71:PRO:HG2	1:A:91:GLY:HA2	1.95	0.48
4:D:51:ARG:NH1	4:D:68:PRO:HB3	2.28	0.48
8:H:157:TYR:C	8:H:157:TYR:HD1	2.18	0.48
30:0:1186:C:C4	30:0:1187:U:C4	3.02	0.48
30:0:1626:A:H2'	30:0:1627:G:O4'	2.14	0.48
30:0:202:U:C4	30:0:203:G:C6	3.01	0.48
11:K:1:MET:N	30:0:2686:C:O2'	2.38	0.48
29:3:51:LYS:HG3	29:3:52:PHE:HD2	1.76	0.48
29:3:83:TRP:HB2	38:0:5759:HOH:O	2.14	0.48
1:A:161:GLY:HA3	38:Z:8705:HOH:O	2.13	0.48
1:A:217:ARG:HG2	1:A:229:ALA:HB2	1.95	0.48
2:B:226:LYS:HG2	2:B:230:GLN:HE21	1.78	0.48
6:F:58:GLU:HA	6:F:61:MET:SD	2.54	0.48
13:M:9:ARG:HD2	30:0:380:A:OP2	2.14	0.48
14:N:4:PRO:HG3	31:9:69:U:OP1	2.13	0.48
9:I:69:PRO:HA	30:0:1164:U:OP1	2.14	0.47
30:0:1188:A:C5	30:0:1189:A:C2	3.02	0.47
30:0:1337:G:C5	30:0:1338:U:C5	3.02	0.47
30:0:1337:G:C6	30:0:1338:U:C4	3.01	0.47
30:0:1471:A:H2'	30:0:1472:C:C6	2.48	0.47
30:0:151:A:H2'	30:0:152:A:O4'	2.14	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:50:GLY:CA	30:0:170:U:H1'	2.43	0.47
30:0:1745:G:H5'	38:0:4312:HOH:O	2.14	0.47
30:0:2458:U:H3'	38:0:3241:HOH:O	2.13	0.47
30:0:2474:A:N7	30:0:2621:PSU:H4'	2.29	0.47
30:0:2474:A:H5'	30:0:2476:C:O5'	2.14	0.47
30:0:2598:U:O2	30:0:2600:A:H8	1.96	0.47
30:0:2830:U:H2'	30:0:2831:C:H6	1.79	0.47
30:0:2848:G:O4'	30:0:2906:A:C2	2.66	0.47
30:0:625:U:H5''	30:0:1044:C:H42	1.71	0.47
30:0:870:G:H2'	30:0:871:G:C5'	2.34	0.47
3:C:162:VAL:HG13	3:C:162:VAL:O	2.13	0.47
18:R:15:LYS:HE3	38:R:8976:HOH:O	2.14	0.47
30:0:2385:G:H2'	30:0:2386:U:C6	2.49	0.47
30:0:2855:G:C2	30:0:2904:U:N3	2.82	0.47
30:0:373:G:O2'	30:0:374:U:H5'	2.14	0.47
30:0:968:G:O2'	30:0:969:G:H5'	2.14	0.47
1:A:27:LEU:HD21	1:A:55:VAL:CG2	2.44	0.47
2:B:84:LEU:O	2:B:99:GLU:HA	2.14	0.47
21:U:50:GLU:OE1	30:0:2866:U:H2'	2.13	0.47
26:Z:40:ALA:HA	30:0:1773:G:H8	1.79	0.47
30:0:1947:G:OP1	30:0:1971:G:N7	2.47	0.47
30:0:2087:C:H2'	30:0:2088:C:H6	1.80	0.47
30:0:361:C:H2'	30:0:362:G:O4'	2.13	0.47
30:0:834:G:H3'	30:0:835:U:H4'	1.97	0.47
11:K:132:VAL:HG11	21:U:22:VAL:HG22	1.96	0.47
25:Y:234:VAL:HG12	25:Y:235:GLU:N	2.28	0.47
30:0:1275:C:H2'	30:0:1276:U:H5'	1.96	0.47
30:0:1389:G:N2	30:0:1391:G:H3'	2.29	0.47
30:0:1619:G:H2'	30:0:1620:C:C6	2.49	0.47
30:0:2379:G:H4'	30:0:2380:A:O5'	2.13	0.47
30:0:2719:A:H2'	30:0:2720:C:C5'	2.44	0.47
30:0:2724:U:H6	30:0:2724:U:O5'	1.96	0.47
30:0:2857:C:H1'	38:0:5328:HOH:O	2.15	0.47
30:0:407:A:H5'	38:0:6000:HOH:O	2.14	0.47
30:0:681:G:N3	30:0:681:G:H2'	2.30	0.47
30:0:699:C:C2	30:0:744:G:C2	3.03	0.47
30:0:965:A:H5'	30:0:966:U:OP2	2.14	0.47
2:B:162:MET:HE1	2:B:308:LEU:HD21	1.96	0.47
2:B:201:ASP:CB	2:B:312:ARG:HD2	2.42	0.47
2:B:74:ILE:HD13	2:B:309:VAL:HG21	1.95	0.47
8:H:88:MET:HA	8:H:139:ALA:HA	1.96	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:56:ARG:HB2	30:0:2890:A:N7	2.29	0.47
22:V:12:THR:CG2	22:V:15:GLU:HG3	2.40	0.47
24:X:85:VAL:HG12	24:X:86:GLU:N	2.29	0.47
1:A:70:ALA:HB1	26:Z:89:THR:HG21	1.97	0.47
30:0:1210:G:N2	30:0:1211:G:H1'	2.29	0.47
30:0:1226:G:C4	30:0:1227:C:C6	3.02	0.47
30:0:1503:U:H2'	30:0:1504:A:C5'	2.45	0.47
30:0:1733:A:N7	30:0:1734:C:C4	2.82	0.47
30:0:1477:C:H4'	30:0:1868:G:OP1	2.15	0.47
30:0:2265:U:H2'	30:0:2266:A:H8	1.80	0.47
30:0:2781:U:C2'	30:0:2782:G:H5'	2.45	0.47
30:0:287:C:H6	30:0:287:C:O5'	1.97	0.47
30:0:371:U:C4	30:0:372:A:N7	2.83	0.47
30:0:558:C:HO2'	30:0:559:U:H5''	1.78	0.47
30:0:699:C:C6	30:0:744:G:N3	2.82	0.47
30:0:820:G:O2'	30:0:856:G:H4'	2.14	0.47
28:2:15:ASP:O	28:2:18:ASN:HB2	2.15	0.47
29:3:68:LYS:HG2	29:3:77:ALA:CB	2.44	0.47
29:3:88:LEU:CD2	33:3:8804:CL:CL	2.86	0.47
31:9:39:U:H3	31:9:42:C:H5''	1.79	0.47
31:9:73:A:H61	31:9:108:C:N4	2.13	0.47
8:H:59:GLN:HE22	8:H:96:GLN:HG2	1.79	0.47
11:K:118:ALA:HA	11:K:125:ALA:HB2	1.96	0.47
17:Q:11:ARG:HD3	38:0:6238:HOH:O	2.13	0.47
30:0:625:U:C5'	30:0:1044:C:N4	2.71	0.47
30:0:1667:A:H5'	30:0:1667:A:C8	2.50	0.47
30:0:1760:G:C5	30:0:1761:U:C4	3.03	0.47
2:B:234:ARG:NH2	30:0:2039:A:OP2	2.47	0.47
30:0:2375:A:H2'	30:0:2376:C:C6	2.50	0.47
30:0:2597:U:C2'	30:0:2598:U:H5'	2.45	0.47
30:0:724:G:O2'	30:0:725:C:H5'	2.15	0.47
30:0:731:U:H2'	30:0:732:C:C6	2.50	0.47
29:3:9:THR:HG23	29:3:20:HIS:CE1	2.49	0.47
31:9:5:G:C2'	31:9:6:C:H5'	2.45	0.47
1:A:135:VAL:HA	1:A:150:PRO:HD3	1.96	0.47
7:G:64:ASN:ND2	7:G:64:ASN:N	2.62	0.47
11:K:97:ILE:HG22	11:K:98:VAL:H	1.79	0.47
13:M:68:ARG:HD2	30:0:1469:C:OP2	2.15	0.47
20:T:71:VAL:CG1	20:T:90:PRO:HB3	2.40	0.47
26:Z:34:SER:CA	30:0:797:A:H4'	2.44	0.47
30:0:1181:A:N1	30:0:1192:A:O2'	2.45	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1210:G:O2'	30:0:1211:G:H5'	2.14	0.47
30:0:2509:A:H2'	30:0:2510:C:O4'	2.14	0.47
8:H:6:ALA:HB3	30:0:2521:A:OP2	2.14	0.47
30:0:2781:U:H2'	30:0:2782:G:H5'	1.95	0.47
30:0:2860:G:H2'	30:0:2861:G:H8	1.80	0.47
30:0:432:G:H2'	30:0:433:C:H6	1.80	0.47
1:A:94:LEU:HG	1:A:99:ILE:CD1	2.44	0.47
8:H:123:ILE:HD12	8:H:123:ILE:N	2.30	0.47
10:J:39:VAL:CG2	10:J:107:ASN:HA	2.44	0.47
15:O:42:GLU:HB2	38:0:3736:HOH:O	2.15	0.47
20:T:41:ARG:NH1	20:T:42:VAL:O	2.47	0.47
20:T:51:LEU:HD11	20:T:97:ARG:HB2	1.97	0.47
23:W:21:LEU:HD21	23:W:48:VAL:HG11	1.96	0.47
25:Y:151:SER:HB3	25:Y:154:ARG:HB3	1.97	0.47
30:0:1333:U:H2'	30:0:1334:C:H6	1.80	0.47
30:0:790:A:H1'	30:0:1710:A:H2'	1.97	0.47
30:0:1858:A:H2'	30:0:1859:A:C8	2.50	0.47
30:0:1988:C:H2'	30:0:1989:G:O4'	2.15	0.47
30:0:2727:A:C2'	30:0:2728:C:H5'	2.45	0.47
30:0:2837:U:H2'	38:0:6824:HOH:O	2.15	0.47
30:0:2858:U:H2'	30:0:2859:C:C6	2.49	0.47
30:0:711:G:O2'	30:0:712:C:H5'	2.15	0.47
23:W:129:LYS:HE3	31:9:87:U:H2'	1.97	0.47
2:B:171:VAL:O	2:B:175:LEU:HB2	2.15	0.47
3:C:180:SER:HB2	38:C:8643:HOH:O	2.14	0.47
4:D:59:GLY:HA3	38:D:4886:HOH:O	2.14	0.47
13:M:15:PRO:HA	13:M:20:LEU:HD23	1.95	0.47
14:N:71:TRP:HZ2	38:N:8833:HOH:O	1.97	0.47
16:P:13:VAL:HG13	16:P:14:LEU:N	2.29	0.47
23:W:77:ALA:HB3	38:W:5763:HOH:O	2.14	0.47
30:0:1168:C:H2'	30:0:1169:U:H5'	1.96	0.47
30:0:1446:U:H4'	30:0:1447:U:OP2	2.14	0.47
30:0:1857:A:N6	30:0:2247:C:H1'	2.30	0.47
30:0:2059:U:H1'	38:0:4439:HOH:O	2.14	0.47
30:0:2460:A:C2	30:0:2461:U:C2	3.02	0.47
30:0:800:G:H8	30:0:800:G:O5'	1.98	0.47
30:0:835:U:H5''	38:0:9381:HOH:O	2.14	0.47
31:9:22:G:N7	31:9:55:U:C6	2.82	0.47
1:A:105:VAL:CG1	1:A:154:ALA:HB1	2.44	0.47
3:C:28:SER:HB2	38:C:8659:HOH:O	2.14	0.47
14:N:27:LEU:HD22	14:N:50:LEU:HD13	1.97	0.47

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:3:LEU:HA	16:P:6:GLN:OE1	2.14	0.47
22:V:64:GLY:O	22:V:65:ASP:HB2	2.15	0.47
23:W:128:VAL:HG22	30:0:1098:A:OP1	2.15	0.47
16:P:1:THR:O	30:0:1396:C:H1'	2.15	0.47
30:0:1889:C:O2'	30:0:1890:U:H5'	2.15	0.47
30:0:2490:A:H5''	38:0:7023:HOH:O	2.15	0.47
30:0:2858:U:H2'	30:0:2859:C:H6	1.80	0.47
30:0:2878:U:H2'	30:0:2879:A:O4'	2.14	0.47
30:0:292:G:H2'	30:0:358:G:N2	2.30	0.47
30:0:561:G:H2'	30:0:562:A:H8	1.79	0.47
1:A:171:LYS:HB2	30:0:820:G:C5	2.50	0.47
2:B:212:GLN:HB2	2:B:257:THR:OG1	2.15	0.47
6:F:21:GLU:O	6:F:24:ARG:HG2	2.15	0.47
18:R:69:LYS:HB2	18:R:72:VAL:HG23	1.97	0.47
22:V:1:THR:HG23	22:V:2:VAL:N	2.29	0.47
23:W:72:PRO:HG2	38:W:5763:HOH:O	2.15	0.47
30:0:1056:U:H2'	30:0:1057:A:O4'	2.14	0.47
23:W:125:HIS:CE1	30:0:1097:A:C5'	2.95	0.47
16:P:41:ARG:NH2	30:0:1500:U:OP2	2.47	0.47
30:0:1806:G:C4	30:0:1807:U:C6	3.03	0.47
30:0:1928:C:O2'	30:0:1929:G:H5'	2.15	0.47
30:0:2301:A:H5''	30:0:2302:A:H5'	1.96	0.47
30:0:249:G:O2'	30:0:250:C:H5'	2.15	0.47
13:M:193:LYS:HB3	30:0:392:U:C5'	2.45	0.47
14:N:170:GLU:O	14:N:174:GLU:HG3	2.14	0.47
17:Q:34:ASP:O	17:Q:37:GLU:HB2	2.15	0.47
30:0:1159:G:H1	30:0:1208:C:H42	1.63	0.46
30:0:1177:A:N1	30:0:1178:G:C4	2.82	0.46
30:0:137:U:OP1	30:0:259:G:O2'	2.33	0.46
24:X:30:MET:HG2	30:0:1384:C:H5'	1.96	0.46
30:0:1760:G:C6	30:0:1761:U:C4	3.03	0.46
30:0:1854:C:H2'	30:0:1875:A:H61	1.80	0.46
30:0:1942:A:O2'	30:0:1943:C:H5'	2.15	0.46
30:0:2019:A:H2'	30:0:2020:C:C6	2.49	0.46
30:0:2379:G:H4'	30:0:2380:A:C5'	2.45	0.46
30:0:2388:C:O2'	30:0:2389:U:H5'	2.14	0.46
30:0:40:C:H5'	38:0:3836:HOH:O	2.14	0.46
30:0:589:U:H2'	30:0:590:A:C8	2.50	0.46
30:0:737:A:H2'	30:0:738:G:C8	2.49	0.46
30:0:806:A:H2'	30:0:807:A:O4'	2.15	0.46
31:9:54:A:C2'	31:9:55:U:C5'	2.85	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:22:VAL:HG21	30:0:2348:C:C5'	2.45	0.46
13:M:184:ARG:HG3	13:M:185:PRO:HA	1.97	0.46
16:P:13:VAL:HG13	16:P:14:LEU:H	1.80	0.46
19:S:6:LYS:HE3	19:S:29:ASP:HA	1.97	0.46
30:0:11:A:N3	30:0:11:A:H2'	2.30	0.46
30:0:1409:G:C2	30:0:1410:G:C8	3.03	0.46
30:0:154:C:O2'	30:0:155:C:H5'	2.14	0.46
30:0:1925:G:O2'	30:0:1926:G:H5'	2.15	0.46
30:0:2461:U:O2	30:0:2466:G:H1'	2.14	0.46
30:0:61:G:C6	30:0:86:A:N6	2.83	0.46
30:0:703:G:C6	30:0:704:C:N4	2.83	0.46
27:1:10:LYS:HG3	38:1:2979:HOH:O	2.14	0.46
29:3:79:LEU:HD12	30:0:2456:A:C2	2.50	0.46
2:B:162:MET:CE	2:B:310:ARG:HD3	2.45	0.46
10:J:42:GLU:HG2	10:J:43:ARG:N	2.30	0.46
21:U:47:ARG:HG3	38:U:4381:HOH:O	2.15	0.46
26:Z:70:ARG:NH1	26:Z:83:TYR:HD1	2.11	0.46
30:0:1016:U:H1'	38:0:3652:HOH:O	2.15	0.46
38:W:7804:HOH:O	30:0:1286:A:H5''	2.15	0.46
30:0:1398:G:H4'	38:0:6650:HOH:O	2.15	0.46
30:0:1415:G:O2'	30:0:1416:G:H5'	2.15	0.46
30:0:168:C:H6	30:0:168:C:O5'	1.98	0.46
30:0:1790:C:H2'	30:0:1791:U:H6	1.80	0.46
30:0:1825:U:O2'	30:0:1826:C:H5'	2.15	0.46
30:0:214:U:H5'	38:0:6117:HOH:O	2.15	0.46
30:0:2259:C:C2	30:0:2260:A:C8	3.04	0.46
30:0:2658:G:C2	30:0:2659:U:C6	3.03	0.46
30:0:2871:G:C6	30:0:2887:G:N1	2.83	0.46
30:0:400:C:H2'	30:0:401:C:H6	1.80	0.46
13:M:92:THR:HB	30:0:401:C:O2'	2.15	0.46
30:0:432:G:C2	30:0:433:C:C5	3.02	0.46
30:0:604:G:H4'	30:0:605:C:O5'	2.15	0.46
29:3:67:LEU:HD13	29:3:69:TYR:HE1	1.81	0.46
1:A:88:ILE:HD13	1:A:100:PRO:HD3	1.97	0.46
2:B:5:ARG:HD2	2:B:8:LYS:NZ	2.31	0.46
12:L:38:HIS:O	30:0:926:A:H1'	2.15	0.46
30:0:100:C:H2'	30:0:101:C:H6	1.81	0.46
30:0:10:U:C4	30:0:532:A:N7	2.84	0.46
30:0:128:A:O2'	30:0:129:A:C5'	2.64	0.46
27:1:42:SER:HB3	30:0:1473:U:C1'	2.45	0.46
30:0:1484:G:H2'	38:0:9110:HOH:O	2.16	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1603:A:C5'	30:0:1605:G:C5'	2.91	0.46
30:0:1806:G:H2'	30:0:1807:U:H6	1.78	0.46
30:0:2520:G:O2'	30:0:2521:A:H5'	2.16	0.46
30:0:247:A:C2	30:0:265:U:C2	3.03	0.46
30:0:440:C:C4	30:0:441:A:C6	3.04	0.46
30:0:732:C:O2'	30:0:733:U:H5'	2.14	0.46
30:0:959:C:H1'	30:0:961:A:C6	2.50	0.46
29:3:64:LYS:HD3	29:3:82:GLY:O	2.14	0.46
31:9:3:A:H2'	38:9:9044:HOH:O	2.14	0.46
1:A:36:ASP:CB	1:A:85:SER:HB2	2.45	0.46
3:C:72:LYS:HG2	3:C:77:ALA:HA	1.96	0.46
4:D:138:GLY:HA2	31:9:29:C:O3'	2.15	0.46
10:J:90:LYS:HB2	33:J:8802:CL:CL	2.53	0.46
23:W:81:ASP:OD1	23:W:92:ASP:HB2	2.16	0.46
30:0:1590:A:C2	30:0:1606:A:C1'	2.99	0.46
30:0:1626:A:H2'	30:0:1627:G:C5'	2.45	0.46
30:0:1477:C:C5'	30:0:1868:G:C5'	2.94	0.46
30:0:2004:U:H4'	38:0:5274:HOH:O	2.14	0.46
30:0:2355:G:N3	30:0:2355:G:H2'	2.31	0.46
30:0:2356:A:H2'	30:0:2357:G:O4'	2.16	0.46
30:0:2911:C:O2'	30:0:2912:C:H5'	2.15	0.46
30:0:364:U:H2'	30:0:365:G:O4'	2.15	0.46
30:0:780:A:H2'	30:0:781:C:C6	2.50	0.46
30:0:815:U:H5	38:0:7423:HOH:O	1.98	0.46
1:A:212:PRO:HB2	38:0:4344:HOH:O	2.16	0.46
2:B:199:TYR:CE2	2:B:268:ARG:HB2	2.49	0.46
30:0:1215:A:O3'	30:0:1216:G:H4'	2.16	0.46
30:0:1524:U:H5''	30:0:1524:U:H6	1.81	0.46
30:0:2626:C:H2'	30:0:2627:G:C8	2.51	0.46
30:0:307:G:N2	30:0:309:C:C2	2.84	0.46
30:0:396:U:O2'	30:0:397:A:P	2.73	0.46
30:0:39:G:O6	30:0:441:A:C2	2.68	0.46
1:A:94:LEU:HD12	1:A:98:GLU:HB2	1.96	0.46
2:B:304:PRO:HD2	2:B:307:ARG:NE	2.31	0.46
4:D:64:ARG:HB3	4:D:67:ASP:OD2	2.15	0.46
8:H:6:ALA:HA	8:H:61:ARG:NH1	2.30	0.46
9:I:87:PRO:HD3	38:0:7103:HOH:O	2.14	0.46
10:J:130:VAL:HG12	10:J:131:THR:N	2.31	0.46
14:N:147:ILE:HD12	38:9:9091:HOH:O	2.15	0.46
18:R:48:GLU:HA	18:R:51:ILE:HD12	1.98	0.46
23:W:68:THR:HG23	23:W:69:ARG:H	1.81	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:112:LEU:CD1	30:0:1162:G:H1'	2.45	0.46
30:0:1187:U:C2	30:0:1189:A:OP2	2.68	0.46
30:0:1200:A:H3'	38:0:5722:HOH:O	2.15	0.46
30:0:1427:A:O2'	30:0:1428:C:H5'	2.16	0.46
30:0:1773:G:H2'	30:0:1774:G:H5'	1.98	0.46
30:0:1829:A:H2'	30:0:1830:C:C5'	2.41	0.46
30:0:2017:U:O2'	30:0:2018:A:C8	2.53	0.46
30:0:2100:A:C5'	38:0:7373:HOH:O	2.57	0.46
30:0:2314:G:O2'	30:0:2315:C:H5'	2.15	0.46
30:0:2397:G:N2	38:0:6910:HOH:O	2.49	0.46
30:0:2471:G:C5	30:0:2472:C:C5	3.03	0.46
30:0:2828:G:O5'	30:0:2828:G:C8	2.68	0.46
30:0:421:C:H2'	30:0:422:G:C8	2.50	0.46
30:0:497:A:H5''	38:0:3588:HOH:O	2.16	0.46
30:0:662:U:H1'	30:0:748:C:H1'	1.98	0.46
6:F:89:LEU:HD21	30:0:262:A:C6	2.51	0.46
14:N:42:HIS:HB3	14:N:62:HIS:HE1	1.80	0.46
15:O:51:TYR:CD2	30:0:721:A:H5''	2.51	0.46
24:X:43:VAL:HG12	24:X:47:ALA:HB3	1.98	0.46
30:0:1187:U:O2'	30:0:1188:A:C8	2.69	0.46
30:0:1209:C:C2	30:0:1210:G:C8	3.03	0.46
30:0:1497:G:H4'	30:0:1627:G:O2'	2.16	0.46
30:0:2326:C:H4'	30:0:2412:G:C4'	2.46	0.46
30:0:2401:A:H2'	30:0:2402:A:C8	2.51	0.46
30:0:2612:A:H4'	38:0:3676:HOH:O	2.15	0.46
30:0:277:U:O2'	30:0:278:A:H5'	2.16	0.46
30:0:282:C:HO2'	30:0:368:C:N4	2.13	0.46
30:0:2912:C:C6	30:0:2912:C:O5'	2.66	0.46
30:0:334:G:H2'	30:0:335:U:H6	1.81	0.46
30:0:567:U:C5'	38:0:5254:HOH:O	2.62	0.46
30:0:920:C:H5''	30:0:921:G:O5'	2.16	0.46
30:0:969:G:N1	30:0:999:C:N4	2.53	0.46
9:I:124:VAL:C	9:I:126:THR:H	2.18	0.46
18:R:135:ALA:HB1	18:R:137:ASN:ND2	2.29	0.46
30:0:1058:A:H2'	30:0:1060:C:H5''	1.97	0.46
30:0:1157:C:H2'	30:0:1158:G:H8	1.80	0.46
30:0:1790:C:H2'	30:0:1791:U:C6	2.51	0.46
30:0:1812:G:H4'	30:0:1814:G:O4'	2.15	0.46
30:0:2038:A:C2	30:0:2039:A:C5	3.04	0.46
30:0:2241:C:H2'	30:0:2242:U:C6	2.50	0.46
30:0:2456:A:H1'	38:0:6579:HOH:O	2.16	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:488:U:C2'	38:0:3993:HOH:O	2.64	0.46
30:0:562:A:H2'	30:0:563:C:O4'	2.15	0.46
30:0:735:C:C5	30:0:736:A:C4	3.03	0.46
30:0:897:A:H2'	30:0:899:C:C5	2.50	0.46
31:9:15:C:N4	31:9:16:G:C6	2.84	0.46
31:9:47:A:C2	31:9:48:C:C2	3.03	0.46
10:J:131:THR:HG22	10:J:134:GLU:HG3	1.97	0.46
14:N:34:LEU:HD22	14:N:129:ILE:HD13	1.98	0.46
15:O:38:ARG:HD3	30:0:654:A:OP2	2.16	0.46
19:S:12:GLU:OE1	30:0:1444:G:H4'	2.15	0.46
20:T:48:VAL:HG23	20:T:98:VAL:HA	1.97	0.46
23:W:29:VAL:O	23:W:30:ASN:HB2	2.16	0.46
26:Z:34:SER:CB	30:0:797:A:H4'	2.46	0.46
30:0:1119:G:N2	30:0:1246:A:H2	2.04	0.46
30:0:1236:A:C2'	30:0:1237:U:H5'	2.46	0.46
30:0:1504:A:C5'	38:0:4396:HOH:O	2.63	0.46
30:0:1512:G:H4'	38:0:4618:HOH:O	2.15	0.46
30:0:1707:G:H1'	30:0:1711:A:N6	2.31	0.46
30:0:1809:G:H2'	30:0:1811:A:OP2	2.16	0.46
30:0:1902:G:H2'	30:0:1903:U:O4'	2.16	0.46
30:0:2011:A:H5'	30:0:2013:G:C1'	2.46	0.46
30:0:212:A:H5'	30:0:214:U:H1'	1.98	0.46
30:0:2694:A:H3'	30:0:2695:C:H6	1.81	0.46
30:0:2831:C:C2	30:0:2910:A:N1	2.84	0.46
30:0:2860:G:H1'	38:0:6785:HOH:O	2.15	0.46
30:0:938:G:C4	30:0:1031:G:N2	2.84	0.46
29:3:20:HIS:CE1	29:3:71:CYS:SG	3.09	0.46
13:M:164:THR:HG22	13:M:165:GLY:N	2.30	0.46
13:M:94:ARG:NH2	30:0:175:G:O6	2.49	0.46
20:T:79:LEU:HG	20:T:89:ARG:HB2	1.98	0.46
24:X:21:PRO:HD3	38:X:6179:HOH:O	2.16	0.46
25:Y:214:ARG:HH12	25:Y:230:ASN:ND2	2.13	0.46
30:0:1217:G:C2	30:0:1218:U:C2	3.04	0.45
30:0:1490:G:H4'	30:0:1533:A:OP1	2.16	0.45
30:0:1516:U:H2'	30:0:1517:C:O4'	2.17	0.45
30:0:1864:C:H2'	30:0:1865:A:O4'	2.16	0.45
30:0:56:G:H1'	38:0:5300:HOH:O	2.16	0.45
3:C:35:VAL:HG21	3:C:227:GLY:HA2	1.98	0.45
4:D:63:ILE:HG13	4:D:64:ARG:N	2.32	0.45
5:E:103:VAL:HG22	5:E:115:ARG:HB3	1.96	0.45
13:M:133:LEU:O	13:M:134:ILE:HD13	2.16	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:64:GLU:HG3	17:Q:74:ASP:CG	2.36	0.45
30:0:1018:A:H8	30:0:1018:A:O5'	1.99	0.45
30:0:1074:G:H4'	30:0:1260:G:C6	2.52	0.45
30:0:1362:U:O2'	30:0:1363:G:H5'	2.17	0.45
30:0:1400:C:C2'	30:0:1401:G:H5'	2.46	0.45
30:0:1444:G:C6	30:0:1445:G:C5	3.05	0.45
30:0:1503:U:H2'	30:0:1504:A:H5'	1.98	0.45
30:0:1831:U:H2'	30:0:1832:G:H5'	1.98	0.45
30:0:1908:G:H1'	30:0:1931:A:N6	2.31	0.45
30:0:1987:C:O2'	30:0:1988:C:H5'	2.16	0.45
30:0:2134:G:N2	30:0:2242:U:C2	2.85	0.45
30:0:2577:A:H8	38:0:9606:HOH:O	1.99	0.45
30:0:2812:A:C2	30:0:2814:A:N7	2.85	0.45
30:0:369:G:O2'	30:0:370:G:H5'	2.16	0.45
30:0:743:G:O2'	30:0:744:G:H5'	2.16	0.45
30:0:940:G:C5	30:0:1027:G:C2	3.04	0.45
31:9:39:U:N3	31:9:42:C:H5''	2.31	0.45
4:D:76:ARG:HD2	31:9:42:C:O2	2.16	0.45
1:A:186:TRP:CG	1:A:187:PRO:HA	2.50	0.45
1:A:35:GLY:O	1:A:37:VAL:HG22	2.17	0.45
1:A:94:LEU:N	1:A:94:LEU:HD23	2.31	0.45
2:B:320:GLN:HA	2:B:321:PRO:HD3	1.83	0.45
8:H:157:TYR:CD1	8:H:157:TYR:C	2.89	0.45
9:I:83:GLY:H	30:0:1168:C:C5'	2.28	0.45
15:O:32:ARG:HH21	15:O:35:LYS:NZ	2.14	0.45
11:K:132:VAL:HG21	21:U:22:VAL:HG13	1.97	0.45
30:0:1116:U:N3	30:0:1246:A:N6	2.60	0.45
9:I:113:SER:HA	30:0:1186:C:H5'	1.98	0.45
30:0:1213:C:O2'	30:0:1214:G:H5'	2.17	0.45
30:0:154:C:H2'	30:0:155:C:H6	1.82	0.45
30:0:1603:A:H5'	30:0:1605:G:C5'	2.46	0.45
30:0:1670:A:H2'	30:0:1671:U:O4'	2.16	0.45
30:0:1759:A:N3	30:0:1818:C:H2'	2.31	0.45
30:0:191:A:N6	30:0:435:A:H62	2.14	0.45
30:0:1948:G:H2'	30:0:1949:G:O4'	2.16	0.45
30:0:2293:G:C6	30:0:2294:C:C5	3.04	0.45
30:0:2757:A:H2'	30:0:2758:G:O4'	2.16	0.45
30:0:360:A:H2'	30:0:361:C:O4'	2.16	0.45
30:0:400:C:O2'	30:0:401:C:H5'	2.17	0.45
30:0:595:U:H2'	30:0:596:C:C6	2.52	0.45
30:0:793:A:H2'	30:0:794:U:H6	1.81	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:99:A:C8	30:0:100:C:C5	3.05	0.45
29:3:12:PRO:HG2	29:3:13:HIS:CD2	2.49	0.45
31:9:59:C:O5'	31:9:59:C:C6	2.63	0.45
1:A:51:ARG:O	1:A:52:SER:HB2	2.16	0.45
8:H:46:TYR:HA	8:H:47:PRO:HD3	1.81	0.45
20:T:114:SER:OG	20:T:117:ASP:HB2	2.16	0.45
30:0:1178:G:C6	30:0:1179:C:N4	2.84	0.45
30:0:912:A:C4	30:0:1294:A:C2	3.04	0.45
30:0:1819:G:H2'	30:0:1820:G:C4'	2.46	0.45
30:0:1964:U:O2	30:0:1964:U:H2'	2.15	0.45
30:0:1970:G:N3	30:0:1970:G:H2'	2.31	0.45
30:0:2005:G:P	30:0:2005:G:H3'	2.55	0.45
30:0:2092:G:H2'	30:0:2613:G:OP1	2.17	0.45
17:Q:15:LYS:HG3	30:0:2364:A:O3'	2.16	0.45
30:0:2438:G:H2'	30:0:2439:C:C6	2.51	0.45
30:0:304:G:O5'	30:0:304:G:H8	2.00	0.45
30:0:734:U:H2'	30:0:736:A:OP2	2.16	0.45
30:0:790:A:H1'	30:0:1710:A:C2'	2.46	0.45
30:0:876:A:C2'	30:0:876:A:N3	2.79	0.45
31:9:29:C:C5	31:9:30:C:C5	3.04	0.45
2:B:254:GLN:HG2	2:B:255:GLY:N	2.30	0.45
13:M:122:GLN:HB2	13:M:127:LYS:HG2	1.98	0.45
13:M:30:GLU:HG2	38:M:8864:HOH:O	2.17	0.45
14:N:144:GLY:O	14:N:147:ILE:HG23	2.15	0.45
18:R:96:VAL:HG13	18:R:106:GLY:HA3	1.98	0.45
25:Y:144:ARG:CZ	38:Y:8916:HOH:O	2.65	0.45
26:Z:70:ARG:O	26:Z:81:CYS:SG	2.74	0.45
30:0:1524:U:H5''	30:0:1524:U:C6	2.51	0.45
30:0:1547:A:H2'	30:0:1548:U:C6	2.52	0.45
30:0:420:U:O4'	30:0:1920:C:C4	2.70	0.45
30:0:1940:C:H1'	38:0:9382:HOH:O	2.17	0.45
30:0:2697:A:H2'	30:0:2697:A:N3	2.32	0.45
30:0:2718:C:C6	30:0:2718:C:H5'	2.50	0.45
30:0:2728:C:O5'	30:0:2728:C:H6	1.99	0.45
30:0:659:A:H5''	38:0:7082:HOH:O	2.17	0.45
38:C:8558:HOH:O	30:0:751:U:H5'	2.16	0.45
30:0:940:G:N3	30:0:1032:A:C2	2.84	0.45
28:2:40:ARG:HG3	28:2:45:ASN:CB	2.45	0.45
29:3:59:ASP:OD1	30:0:2460:A:H5''	2.16	0.45
2:B:162:MET:HE2	2:B:310:ARG:HD3	1.97	0.45
5:E:152:THR:HG21	5:E:165:GLY:HA2	1.99	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:72:ASN:O	12:L:76:LEU:HG	2.17	0.45
18:R:18:LEU:HB2	18:R:143:VAL:CG1	2.46	0.45
23:W:5:VAL:HG11	23:W:153:MET:HE1	1.99	0.45
30:0:1149:U:C5	30:0:1215:A:N7	2.84	0.45
30:0:1151:G:N2	30:0:1214:G:C4	2.85	0.45
30:0:1406:A:H4'	30:0:1407:A:H5''	1.98	0.45
30:0:1434:A:H4'	30:0:1435:U:H5	1.82	0.45
30:0:1523:G:C6	30:0:1524:U:C4	3.05	0.45
30:0:1883:U:H5''	30:0:2013:G:OP2	2.17	0.45
30:0:2475:C:H5'	38:0:3664:HOH:O	2.16	0.45
30:0:418:C:H2'	30:0:419:A:C8	2.52	0.45
30:0:790:A:H8	38:0:6078:HOH:O	1.98	0.45
30:0:960:G:N3	30:0:960:G:C2'	2.79	0.45
31:9:61:C:H2'	31:9:62:A:C8	2.46	0.45
1:A:11:ARG:HD3	38:0:9222:HOH:O	2.16	0.45
1:A:204:GLY:N	30:0:2634:G:OP2	2.49	0.45
6:F:34:ASN:HA	13:M:4:ALA:HB2	1.98	0.45
9:I:82:THR:HG22	30:0:1168:C:H5''	1.97	0.45
12:L:57:VAL:O	12:L:57:VAL:HG12	2.17	0.45
13:M:34:GLU:HB3	13:M:38:GLU:HG3	1.99	0.45
14:N:33:ARG:HG3	38:N:8841:HOH:O	2.17	0.45
15:O:27:GLY:O	15:O:31:GLU:HG3	2.17	0.45
1:A:189:VAL:HA	30:0:1845:A:OP1	2.16	0.45
30:0:2385:G:H2'	30:0:2386:U:H6	1.81	0.45
29:3:35:TRP:HZ3	30:0:2432:C:OP1	2.00	0.45
30:0:2515:C:H2'	30:0:2516:G:O4'	2.16	0.45
27:1:16:HIS:HE1	30:0:775:G:OP1	1.99	0.45
30:0:92:G:H2'	30:0:93:C:H6	1.82	0.45
2:B:119:HIS:O	2:B:121:PRO:HD3	2.16	0.45
30:0:1405:U:H4'	30:0:1406:A:H5''	1.98	0.45
30:0:1902:G:O2'	30:0:1903:U:H5'	2.16	0.45
30:0:2361:A:H2'	30:0:2362:A:C8	2.51	0.45
30:0:2887:G:H2'	30:0:2888:U:O4'	2.17	0.45
30:0:342:C:N4	30:0:343:C:H41	2.15	0.45
30:0:343:C:O2'	30:0:344:C:H5'	2.17	0.45
30:0:387:G:C2'	30:0:388:G:H5'	2.46	0.45
30:0:916:A:C6	30:0:917:U:C4	3.05	0.45
31:9:30:C:C2'	31:9:30:C:O2	2.65	0.45
31:9:72:C:O2'	31:9:73:A:H5'	2.15	0.45
2:B:43:GLY:O	2:B:308:LEU:HD12	2.16	0.45
4:D:50:VAL:O	4:D:71:ALA:HA	2.17	0.45

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:96:ALA:HA	38:F:3111:HOH:O	2.15	0.45
10:J:43:ARG:HD3	38:J:8858:HOH:O	2.17	0.45
30:0:1576:G:C2	30:0:1577:U:C2	3.05	0.45
30:0:1626:A:C2'	30:0:1627:G:H5'	2.46	0.45
30:0:1850:U:H2'	30:0:1851:G:C8	2.52	0.45
30:0:228:C:H2'	30:0:229:G:C5'	2.46	0.45
30:0:281:U:H5	38:0:7575:HOH:O	1.99	0.45
30:0:2842:G:H2'	30:0:2843:A:H5'	1.98	0.45
30:0:862:U:H2'	30:0:863:G:C8	2.52	0.45
30:0:957:A:H8	30:0:957:A:O5'	2.00	0.45
2:B:307:ARG:HG3	2:B:307:ARG:HH11	1.82	0.45
2:B:86:ALA:HA	38:B:9051:HOH:O	2.16	0.45
3:C:95:GLU:HG3	38:C:8669:HOH:O	2.16	0.45
5:E:121:ASP:HB2	38:E:5899:HOH:O	2.16	0.45
5:E:102:VAL:HG11	5:E:148:ILE:HG12	1.98	0.45
21:U:6:CYS:SG	21:U:31:PHE:HA	2.56	0.45
26:Z:35:SER:HB3	26:Z:47:ARG:HB2	1.98	0.45
30:0:1041:U:H2'	30:0:1042:U:C5'	2.46	0.45
30:0:1477:C:C5'	30:0:1868:G:H5''	2.47	0.45
30:0:1543:G:N1	30:0:1641:A:OP2	2.36	0.45
30:0:1801:A:C2	30:0:1802:G:C4	3.04	0.45
30:0:2311:A:O2'	30:0:2312:G:H5'	2.17	0.45
30:0:2511:A:H2'	30:0:2512:U:H6	1.82	0.45
30:0:958:G:H2'	30:0:959:C:H6	1.75	0.45
30:0:969:G:N2	30:0:1000:C:C2	2.85	0.45
31:9:33:U:C6	31:9:43:G:C8	3.05	0.45
3:C:88:SER:O	3:C:91:PRO:HD3	2.17	0.45
13:M:86:GLN:NE2	38:M:8882:HOH:O	2.50	0.45
30:0:1181:A:O2'	30:0:1182:C:H5'	2.17	0.44
30:0:1392:A:C6	30:0:1395:C:C2	3.05	0.44
30:0:1524:U:C5'	30:0:1524:U:H6	2.29	0.44
30:0:1584:C:O2'	30:0:1585:C:H5'	2.17	0.44
30:0:163:U:O3'	30:0:896:C:H4'	2.16	0.44
30:0:1748:U:C5	30:0:1749:U:C4	3.06	0.44
30:0:2293:G:C6	30:0:2294:C:C4	3.05	0.44
30:0:198:A:C2	30:0:2444:U:H1'	2.53	0.44
30:0:2826:G:O6	30:0:2913:A:N6	2.50	0.44
30:0:283:U:H5''	30:0:284:C:OP2	2.17	0.44
30:0:339:A:C6	30:0:342:C:N3	2.85	0.44
30:0:581:G:H5'	38:0:7663:HOH:O	2.17	0.44
31:9:107:C:O2'	31:9:108:C:H5'	2.17	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:3:A:OP2	31:9:25:G:N2	2.50	0.44
1:A:164:ARG:NH1	1:A:164:ARG:HB3	2.31	0.44
4:D:128:LEU:HD23	4:D:129:ASP:N	2.32	0.44
5:E:153:ARG:NH1	30:0:2778:A:C1'	2.81	0.44
8:H:83:GLU:HA	38:H:243:HOH:O	2.18	0.44
10:J:107:ASN:HD21	10:J:109:TYR:HB2	1.82	0.44
16:P:81:LYS:HE3	30:0:1813:U:O2'	2.18	0.44
18:R:34:GLU:HG2	18:R:46:TYR:OH	2.17	0.44
23:W:48:VAL:HG12	23:W:52:VAL:HB	1.98	0.44
26:Z:47:ARG:O	26:Z:51:ALA:HB2	2.16	0.44
30:0:1246:A:O2'	30:0:1247:A:H3'	2.17	0.44
30:0:1362:U:H2'	30:0:1363:G:C8	2.52	0.44
30:0:1434:A:H2'	30:0:1436:C:C5	2.52	0.44
30:0:440:C:O5'	30:0:440:C:H6	2.00	0.44
18:R:98:ASN:ND2	30:0:500:G:H21	2.12	0.44
30:0:711:G:C2'	30:0:712:C:H5'	2.47	0.44
14:N:1:ALA:HB2	31:9:14:G:O2'	2.18	0.44
2:B:51:VAL:HG13	2:B:53:LEU:HD13	1.98	0.44
3:C:129:HIS:HD2	3:C:165:ASP:OD2	2.01	0.44
3:C:60:SER:HA	38:C:8575:HOH:O	2.17	0.44
10:J:15:ARG:HG2	10:J:16:ASP:OD1	2.17	0.44
12:L:41:HIS:CD2	30:0:926:A:O2'	2.69	0.44
13:M:76:ARG:HG3	38:M:8827:HOH:O	2.17	0.44
20:T:81:LYS:HD2	20:T:87:VAL:HG11	1.98	0.44
23:W:10:GLU:O	23:W:13:MET:HB3	2.18	0.44
30:0:1069:C:H2'	30:0:1070:A:O4'	2.18	0.44
30:0:1132:A:H2'	30:0:1133:A:C8	2.52	0.44
30:0:1202:A:C2'	30:0:1203:G:H5'	2.48	0.44
30:0:1391:G:N2	30:0:1434:A:H5''	2.32	0.44
30:0:1649:G:H1'	38:0:5049:HOH:O	2.17	0.44
30:0:1680:C:H2'	30:0:1681:G:O4'	2.17	0.44
30:0:1701:A:H5''	30:0:1702:U:H3'	1.99	0.44
30:0:2276:U:H2'	30:0:2277:U:C6	2.52	0.44
30:0:372:A:O2'	30:0:373:G:H5'	2.17	0.44
30:0:57:C:H42	30:0:89:G:H1	1.64	0.44
30:0:729:C:C2	30:0:743:G:C2	3.05	0.44
30:0:877:G:N7	30:0:885:G:C5	2.85	0.44
29:3:10:TYR:CD1	30:0:2408:A:H1'	2.52	0.44
9:I:130:LEU:HD21	30:0:1167:G:C4'	2.46	0.44
11:K:86:THR:HG22	11:K:87:ARG:N	2.32	0.44
13:M:71:SER:OG	13:M:72:ALA:N	2.51	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:59:PHE:O	18:R:63:ASN:HB3	2.18	0.44
22:V:12:THR:CG2	22:V:15:GLU:H	2.30	0.44
30:0:1415:G:C2'	30:0:1416:G:H5'	2.47	0.44
30:0:1556:G:O2'	30:0:1557:G:H5'	2.17	0.44
30:0:2507:G:H2'	30:0:2510:C:H42	1.81	0.44
30:0:2509:A:OP2	30:0:2510:C:H5	2.00	0.44
30:0:2775:A:N6	30:0:2799:A:C8	2.86	0.44
30:0:2911:C:H2'	30:0:2912:C:H6	1.82	0.44
30:0:625:U:H5'	38:0:3177:HOH:O	2.16	0.44
29:3:5:ARG:HD2	29:3:21:GLU:HG2	1.98	0.44
2:B:244:PRO:HB3	30:0:1234:U:N3	2.32	0.44
4:D:153:THR:O	4:D:156:ARG:HB2	2.16	0.44
5:E:20:ILE:O	5:E:30:THR:HA	2.17	0.44
8:H:14:LYS:HG3	38:H:183:HOH:O	2.17	0.44
12:L:22:ARG:HG2	38:0:3223:HOH:O	2.15	0.44
19:S:11:THR:H	19:S:14:ALA:HB3	1.81	0.44
25:Y:182:PHE:HD2	25:Y:200:THR:O	2.00	0.44
25:Y:189:ASN:HD22	25:Y:189:ASN:C	2.21	0.44
26:Z:69:ASP:O	26:Z:71:VAL:N	2.45	0.44
30:0:1043:C:H2'	38:0:3185:HOH:O	2.18	0.44
30:0:2345:A:C3'	30:0:2346:C:H6	2.23	0.44
18:R:80:TYR:O	30:0:2050:G:H5''	2.16	0.44
23:W:5:VAL:HG11	23:W:153:MET:CE	2.48	0.44
9:I:87:PRO:HG2	30:0:1181:A:O4'	2.18	0.44
30:0:1112:G:H1	30:0:1251:C:H42	1.65	0.44
30:0:1330:A:H2	38:0:4652:HOH:O	2.00	0.44
30:0:1519:U:O2'	30:0:1520:G:H5'	2.16	0.44
30:0:1706:G:C6	30:0:1707:G:N1	2.86	0.44
30:0:1711:A:H2'	30:0:1712:A:H5'	1.99	0.44
30:0:1762:C:H2'	30:0:1763:C:H6	1.82	0.44
1:A:233:THR:HB	30:0:1942:A:H5''	1.99	0.44
30:0:2005:G:OP2	30:0:2006:C:C5'	2.66	0.44
30:0:1016:U:O2'	30:0:2303:A:N7	2.40	0.44
30:0:2377:U:O2'	30:0:2378:U:H5'	2.17	0.44
30:0:2457:U:H1'	38:0:7515:HOH:O	2.17	0.44
30:0:2552:C:C6	30:0:2577:A:N7	2.85	0.44
30:0:2781:U:H2'	30:0:2782:G:C5'	2.48	0.44
30:0:2834:G:H2'	30:0:2835:C:O5'	2.17	0.44
30:0:2854:A:C6	30:0:2905:A:N1	2.86	0.44
30:0:2872:U:C2	30:0:2873:C:C6	3.05	0.44
30:0:569:A:H5''	30:0:587:A:N1	2.32	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:821:U:H2'	30:0:822:C:H6	1.81	0.44
27:1:20:ARG:HB2	38:1:513:HOH:O	2.18	0.44
23:W:129:LYS:CD	31:9:87:U:H2'	2.47	0.44
3:C:6:TYR:N	3:C:6:TYR:CD1	2.86	0.44
5:E:69:ILE:HA	5:E:72:MET:CE	2.48	0.44
8:H:8:MET:CE	30:0:2494:G:H4'	2.48	0.44
13:M:66:SER:HB3	13:M:128:TRP:NE1	2.32	0.44
17:Q:40:HIS:HE1	30:0:949:U:O2'	2.01	0.44
20:T:97:ARG:NH2	30:0:309:C:OP1	2.51	0.44
25:Y:99:ALA:HB2	25:Y:233:TYR:CE2	2.52	0.44
30:0:1309:U:C2'	30:0:1310:U:H5'	2.48	0.44
30:0:1427:A:C2'	30:0:1428:C:H5'	2.47	0.44
19:S:55:GLN:CD	30:0:1446:U:H2'	2.37	0.44
1:A:192:VAL:HG23	30:0:1882:C:OP1	2.17	0.44
30:0:2250:G:N1	30:0:2251:G:N3	2.66	0.44
2:B:5:ARG:NH1	30:0:2547:C:OP2	2.51	0.44
30:0:2566:A:C2	30:0:2696:G:O4'	2.71	0.44
2:B:241:PRO:HB3	30:0:2609:G:N3	2.33	0.44
30:0:2541:U:H5'	30:0:2611:G:O6	2.18	0.44
38:T:2151:HOH:O	30:0:317:A:H5'	2.17	0.44
30:0:929:A:H8	30:0:929:A:O5'	2.01	0.44
4:D:62:ASP:HA	38:D:4233:HOH:O	2.18	0.44
4:D:86:THR:O	4:D:89:PRO:HD2	2.18	0.44
21:U:45:GLU:HB2	21:U:48:ASN:ND2	2.32	0.44
25:Y:204:ARG:NH2	30:0:1324:G:N2	2.65	0.44
30:0:1202:A:H2'	30:0:1203:G:H5'	2.00	0.44
30:0:157:G:H3'	38:0:3945:HOH:O	2.18	0.44
30:0:1789:G:H2'	30:0:1790:C:O5'	2.17	0.44
30:0:1950:G:H2'	30:0:1951:G:C8	2.53	0.44
30:0:1986:G:C6	30:0:1987:C:N4	2.86	0.44
30:0:2061:C:H2'	30:0:2062:A:H5'	1.99	0.44
30:0:2104:C:O2	30:0:2485:A:N1	2.50	0.44
30:0:304:G:H1'	30:0:347:A:N6	2.32	0.44
30:0:582:U:H2'	30:0:583:C:C6	2.53	0.44
30:0:703:G:C6	30:0:704:C:C4	3.06	0.44
30:0:821:U:O2'	30:0:822:C:H5'	2.18	0.44
1:A:194:MET:SD	30:0:875:A:C2	3.11	0.44
30:0:868:G:C4	30:0:887:G:C8	3.06	0.44
31:9:26:C:H2'	31:9:27:C:H6	1.79	0.44
31:9:31:C:C2	31:9:50:G:C2	3.05	0.44
31:9:81:C:C2'	31:9:82:U:H5'	2.48	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:VAL:HA	1:A:104:PRO:HD3	1.89	0.44
2:B:195:ARG:HE	2:B:323:LEU:HD13	1.83	0.44
8:H:59:GLN:HE21	8:H:129:ARG:HE	1.65	0.44
8:H:87:LYS:HG3	8:H:140:TYR:HD1	1.83	0.44
8:H:66:GLU:HA	38:H:239:HOH:O	2.17	0.44
13:M:80:GLY:O	13:M:81:ARG:HB2	2.18	0.44
14:N:47:LEU:HA	14:N:47:LEU:HD13	1.86	0.44
16:P:13:VAL:HG11	16:P:40:VAL:CG1	2.48	0.44
20:T:19:ARG:HD3	20:T:67:LEU:O	2.18	0.44
30:0:1522:A:H2'	30:0:1523:G:C5'	2.48	0.44
16:P:54:LYS:HB2	30:0:1717:A:H5''	1.98	0.44
30:0:1937:U:O2'	30:0:1938:G:H5'	2.18	0.44
30:0:2250:G:C2	30:0:2251:G:C4	3.06	0.44
29:3:10:TYR:CE2	30:0:2382:A:H1'	2.53	0.44
30:0:2431:C:H2'	30:0:2432:C:C6	2.53	0.44
5:E:90:HIS:CE1	30:0:2694:A:H5''	2.53	0.44
30:0:2729:C:O2'	30:0:2730:G:H5'	2.18	0.44
30:0:483:C:H2'	30:0:484:A:O4'	2.18	0.44
30:0:727:G:C2	30:0:728:C:C2	3.06	0.44
1:A:182:ARG:HB3	38:0:5133:HOH:O	2.18	0.44
2:B:279:THR:HG22	2:B:280:VAL:N	2.33	0.44
2:B:54:VAL:HB	38:B:9083:HOH:O	2.17	0.44
8:H:39:LYS:O	30:0:969:G:H4'	2.18	0.44
10:J:75:PRO:HD3	10:J:136:SER:OG	2.18	0.44
16:P:88:GLN:HB3	38:P:185:HOH:O	2.16	0.44
17:Q:25:PRO:HA	17:Q:26:PRO:HD3	1.78	0.44
30:0:1166:A:C6	30:0:1167:G:C5	3.06	0.43
30:0:1167:G:O2'	30:0:1168:C:H5'	2.18	0.43
30:0:1185:U:C5'	38:0:7447:HOH:O	2.59	0.43
30:0:634:G:O2'	30:0:1358:A:OP1	2.31	0.43
30:0:1421:C:O2'	30:0:1422:U:H5'	2.18	0.43
30:0:1544:U:H2'	30:0:1545:C:H6	1.82	0.43
30:0:1592:G:O2'	30:0:1593:C:O4'	2.36	0.43
30:0:1642:A:N7	30:0:1643:C:C4	2.86	0.43
30:0:175:G:O2'	30:0:176:U:OP2	2.36	0.43
30:0:2090:G:H2'	30:0:2091:G:C8	2.53	0.43
30:0:2435:U:H4'	38:0:9269:HOH:O	2.17	0.43
30:0:2851:G:O2'	30:0:2852:A:H5'	2.17	0.43
30:0:293:A:C5	30:0:360:A:C2	3.06	0.43
30:0:324:G:C6	30:0:325:U:C5	3.06	0.43
30:0:39:G:O2'	30:0:40:C:H5'	2.18	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:533:U:H3'	38:0:3742:HOH:O	2.18	0.43
30:0:838:C:H4'	38:0:9187:HOH:O	2.18	0.43
31:9:74:G:O2'	31:9:75:G:H5'	2.18	0.43
3:C:174:ILE:CD1	30:0:338:C:H4'	2.48	0.43
4:D:103:ASN:ND2	4:D:133:ASN:HA	2.33	0.43
13:M:104:ARG:HG3	38:M:8866:HOH:O	2.18	0.43
14:N:12:ARG:HD3	14:N:18:THR:OG1	2.18	0.43
23:W:119:HIS:HE1	38:0:9568:HOH:O	2.00	0.43
25:Y:182:PHE:CG	25:Y:202:ALA:HB2	2.53	0.43
26:Z:45:VAL:O	26:Z:49:ARG:HG3	2.18	0.43
30:0:1130:U:C2'	30:0:1131:G:H5'	2.48	0.43
30:0:117:A:H2'	30:0:118:G:C8	2.53	0.43
30:0:1706:G:H1'	30:0:1712:A:N6	2.30	0.43
30:0:1916:C:C2	30:0:1924:A:C2	3.06	0.43
30:0:2135:A:O4'	30:0:2243:C:N4	2.51	0.43
30:0:2871:G:C4	30:0:2887:G:N2	2.86	0.43
30:0:692:A:N6	30:0:693:A:C2	2.86	0.43
30:0:827:A:H2'	30:0:828:G:O4'	2.18	0.43
31:9:2:U:OP2	31:9:3:A:H5'	2.18	0.43
1:A:215:ILE:HG22	1:A:227:ASP:O	2.18	0.43
1:A:94:LEU:HD12	1:A:98:GLU:CB	2.48	0.43
2:B:84:LEU:HD23	2:B:142:LEU:HD23	2.00	0.43
2:B:202:VAL:HA	2:B:310:ARG:O	2.18	0.43
3:C:193:LEU:HD12	3:C:211:ASP:O	2.18	0.43
4:D:10:PHE:CG	4:D:11:HIS:N	2.86	0.43
13:M:65:VAL:HG21	13:M:105:ALA:HB2	2.00	0.43
23:W:115:THR:HG23	38:W:5420:HOH:O	2.18	0.43
23:W:142:ASP:HB3	23:W:145:GLY:H	1.83	0.43
23:W:13:MET:HE2	23:W:17:ILE:HG22	2.00	0.43
24:X:39:LYS:HE2	30:0:2834:G:OP1	2.17	0.43
26:Z:61:HIS:O	26:Z:69:ASP:HA	2.17	0.43
30:0:1210:G:C2	30:0:1211:G:C8	3.06	0.43
25:Y:154:ARG:HH21	30:0:1293:U:H5'	1.83	0.43
30:0:1298:U:H2'	30:0:1299:G:C8	2.53	0.43
30:0:1363:G:H2'	30:0:1364:G:C8	2.54	0.43
30:0:1815:A:H4'	30:0:2751:C:O4'	2.19	0.43
30:0:1816:C:H2'	30:0:1817:U:O4'	2.17	0.43
30:0:1949:G:N2	30:0:1964:U:C2	2.87	0.43
30:0:2112:A:H2'	30:0:2113:G:C8	2.53	0.43
30:0:219:G:O5'	30:0:220:C:H5''	2.18	0.43
30:0:2277:U:H1'	30:0:2469:A:N3	2.33	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2429:A:C4'	38:0:7716:HOH:O	2.66	0.43
30:0:2594:C:O2'	30:0:2595:U:H5'	2.19	0.43
30:0:2793:A:N6	38:0:5853:HOH:O	2.50	0.43
30:0:2847:G:C2'	30:0:2848:G:H5'	2.48	0.43
30:0:385:C:O5'	30:0:385:C:H6	2.02	0.43
30:0:665:A:C6	30:0:666:A:C6	3.06	0.43
30:0:820:G:H3'	30:0:820:G:N3	2.33	0.43
1:A:38:ILE:HB	1:A:82:VAL:O	2.18	0.43
3:C:44:GLN:HA	38:C:8605:HOH:O	2.18	0.43
3:C:47:GLY:HA2	3:C:92:PRO:HB2	2.00	0.43
4:D:75:LEU:HD22	4:D:79:MET:HB3	2.00	0.43
20:T:14:ALA:HA	20:T:15:PRO:HD3	1.90	0.43
30:0:1537:C:H2'	30:0:1538:C:H6	1.83	0.43
30:0:152:A:O2'	30:0:153:C:H5'	2.18	0.43
30:0:1878:G:O2'	30:0:1879:U:OP2	2.36	0.43
30:0:1980:U:O2	30:0:2008:U:H4'	2.18	0.43
30:0:234:A:H4'	30:0:437:A:O4'	2.18	0.43
30:0:36:C:H1'	38:0:3051:HOH:O	2.17	0.43
30:0:41:G:H8	30:0:41:G:O5'	2.00	0.43
31:9:115:C:C4	31:9:116:C:C5	3.06	0.43
3:C:6:TYR:HD1	3:C:6:TYR:N	2.17	0.43
5:E:126:ILE:HA	5:E:131:LEU:CD2	2.47	0.43
5:E:84:MET:SD	38:E:3134:HOH:O	2.61	0.43
5:E:91:PHE:HA	5:E:92:PRO:HD3	1.89	0.43
11:K:4:LEU:HD22	11:K:116:GLU:HB3	2.00	0.43
14:N:139:TRP:CE3	14:N:139:TRP:HA	2.53	0.43
30:0:1024:G:C6	30:0:1025:C:C4	3.07	0.43
30:0:148:A:O2'	30:0:149:G:H5'	2.19	0.43
30:0:1503:U:H2'	30:0:1504:A:O4'	2.19	0.43
30:0:1520:G:C2	30:0:1521:C:C2	3.07	0.43
30:0:2070:G:H2'	30:0:2072:G:OP1	2.18	0.43
30:0:2354:A:H5'	30:0:2355:G:N7	2.33	0.43
30:0:2361:A:H5'	38:0:9191:HOH:O	2.19	0.43
30:0:2429:A:H4'	38:0:7716:HOH:O	2.16	0.43
30:0:2445:U:H2'	30:0:2446:G:C8	2.54	0.43
30:0:2451:G:N3	30:0:2451:G:H2'	2.32	0.43
30:0:2531:U:H2'	30:0:2532:A:O4'	2.19	0.43
30:0:2748:G:H1'	38:0:7881:HOH:O	2.18	0.43
30:0:2768:A:H3'	30:0:2768:A:N3	2.33	0.43
30:0:772:G:H2'	30:0:773:A:O4'	2.18	0.43
31:9:39:U:O2'	31:9:42:C:H5	2.01	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:154:VAL:HA	2:B:155:PRO:HD3	1.88	0.43
3:C:39:GLN:O	3:C:43:LYS:HD3	2.18	0.43
9:I:73:LEU:HD12	9:I:107:LYS:NZ	2.33	0.43
16:P:8:ARG:HG3	38:P:188:HOH:O	2.17	0.43
23:W:6:GLN:HB2	23:W:26:ILE:CD1	2.48	0.43
30:0:1167:G:C2	30:0:1168:C:C2	3.06	0.43
30:0:1175:G:N3	30:0:1193:A:C6	2.86	0.43
30:0:1275:C:C2'	30:0:1276:U:H5'	2.49	0.43
30:0:1284:G:O2'	30:0:1285:U:H5'	2.18	0.43
30:0:1421:C:C2	30:0:1444:G:N2	2.87	0.43
30:0:1985:U:C2	30:0:1996:U:O4'	2.72	0.43
30:0:2429:A:N6	38:0:3326:HOH:O	2.51	0.43
30:0:2569:A:H2'	30:0:2570:G:O5'	2.19	0.43
30:0:2668:G:H2'	30:0:2669:U:H6	1.81	0.43
30:0:2692:G:N2	30:0:2701:G:C8	2.87	0.43
30:0:2886:C:O2'	30:0:2887:G:H5'	2.18	0.43
30:0:629:A:C2	30:0:2074:A:C2	3.07	0.43
29:3:59:ASP:HB3	29:3:63:LYS:HZ1	1.83	0.43
29:3:67:LEU:CD1	29:3:69:TYR:HE1	2.31	0.43
31:9:108:C:H2'	31:9:109:G:H8	1.82	0.43
31:9:65:A:C4	31:9:113:C:C4	3.07	0.43
31:9:5:G:O2'	31:9:6:C:H5'	2.18	0.43
1:A:71:PRO:O	1:A:160:ALA:HB2	2.18	0.43
4:D:128:LEU:HB2	38:D:6007:HOH:O	2.18	0.43
4:D:104:PHE:CE2	4:D:132:VAL:HB	2.54	0.43
5:E:107:PHE:CE2	5:E:108:LEU:HD13	2.54	0.43
6:F:60:VAL:O	6:F:62:HIS:N	2.52	0.43
10:J:70:PHE:HE1	30:0:2676:C:C4'	2.32	0.43
13:M:164:THR:HB	38:M:8820:HOH:O	2.17	0.43
14:N:32:PRO:HD2	14:N:99:GLU:O	2.18	0.43
14:N:77:ASN:OD1	14:N:79:PRO:HD2	2.18	0.43
17:Q:11:ARG:NH2	30:0:2363:G:C5'	2.81	0.43
26:Z:55:SER:HA	38:0:7562:HOH:O	2.19	0.43
30:0:102:A:C6	30:0:103:C:C4	3.06	0.43
30:0:1178:G:C5	30:0:1179:C:C4	3.07	0.43
30:0:1333:U:H2'	30:0:1334:C:C6	2.53	0.43
30:0:1519:U:H1'	38:0:3898:HOH:O	2.18	0.43
30:0:1552:G:C6	30:0:1634:G:C6	3.07	0.43
30:0:1602:C:H5'	38:0:6467:HOH:O	2.18	0.43
30:0:1665:G:C2	30:0:1666:C:C6	3.07	0.43
30:0:1705:C:O2	30:0:2735:U:C5'	2.65	0.43

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:29:GLN:OE1	30:0:2244:A:H5''	2.18	0.43
30:0:2473:U:H2'	30:0:2476:C:H5	1.84	0.43
30:0:2507:G:H22	30:0:2512:U:H5''	1.84	0.43
30:0:273:G:H2'	30:0:274:G:O4'	2.18	0.43
30:0:2803:C:H2'	30:0:2804:C:C6	2.54	0.43
2:B:27:ASN:HD21	30:0:2807:U:P	2.41	0.43
30:0:284:C:OP2	30:0:284:C:H6	2.01	0.43
30:0:2855:G:C2	30:0:2904:U:C2	3.06	0.43
30:0:624:U:O4	30:0:628:1MA:H8	2.01	0.43
30:0:85:C:H3'	30:0:86:A:H2'	2.01	0.43
30:0:877:G:H3'	38:0:3106:HOH:O	2.19	0.43
31:9:111:U:O2'	31:9:112:U:H5'	2.19	0.43
13:M:70:GLY:HA3	13:M:73:ARG:HH21	1.77	0.43
14:N:91:ARG:O	14:N:94:GLU:HB2	2.19	0.43
26:Z:41:ARG:HD2	30:0:820:G:H22	1.83	0.43
30:0:1159:G:C6	30:0:1160:G:C4	3.07	0.43
30:0:1202:A:H2'	30:0:1203:G:O4'	2.19	0.43
30:0:1255:A:H2'	30:0:1256:C:O5'	2.18	0.43
30:0:1703:G:C2	30:0:1716:A:C4	3.06	0.43
30:0:1788:U:C2	30:0:1805:G:C2	3.07	0.43
30:0:2510:C:H42	30:0:2564:G:H22	1.66	0.43
30:0:2094:G:C2	30:0:2652:U:O2	2.71	0.43
30:0:2727:A:C6	30:0:2756:U:N3	2.87	0.43
30:0:2780:C:C4	30:0:2781:U:C4	3.06	0.43
30:0:2812:A:H2	30:0:2814:A:H62	1.63	0.43
30:0:432:G:C2	30:0:433:C:C6	3.07	0.43
30:0:816:G:C6	30:0:817:G:N1	2.87	0.43
30:0:79:G:H22	30:0:97:G:H1'	1.82	0.43
29:3:22:VAL:HG12	29:3:90:PHE:HE2	1.83	0.43
14:N:65:ASP:HB3	38:N:8820:HOH:O	2.19	0.43
16:P:58:SER:HB3	38:0:5593:HOH:O	2.18	0.43
21:U:6:CYS:HB2	21:U:13:ILE:CG1	2.49	0.43
25:Y:144:ARG:HB3	38:0:4369:HOH:O	2.18	0.43
1:A:167:LYS:CE	26:Z:50:VAL:HG13	2.42	0.43
30:0:1399:A:H2'	30:0:1400:C:C6	2.54	0.43
30:0:1667:A:H2'	30:0:1668:U:O4'	2.19	0.43
30:0:1697:G:H1'	38:0:7261:HOH:O	2.19	0.43
30:0:1712:A:H2'	30:0:1713:G:O4'	2.19	0.43
30:0:1882:C:H2'	30:0:1883:U:C6	2.53	0.43
30:0:191:A:H61	30:0:435:A:H62	1.67	0.43
30:0:2080:G:H2'	30:0:2081:A:C8	2.54	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2328:U:C4	30:0:2329:C:C5	3.07	0.43
30:0:2332:A:H3'	30:0:2333:G:H8	1.84	0.43
29:3:17:HIS:ND1	30:0:2408:A:O2'	2.48	0.43
29:3:54:LYS:HE3	38:0:3005:HOH:O	2.18	0.43
31:9:39:U:H2'	31:9:40:C:OP1	2.18	0.43
31:9:11:A:H2	31:9:68:G:N3	2.17	0.43
1:A:105:VAL:HG11	1:A:154:ALA:HB1	2.00	0.43
2:B:305:ASP:O	2:B:306:LYS:CB	2.66	0.43
5:E:95:VAL:O	5:E:126:ILE:HD12	2.18	0.43
5:E:7:ILE:HG23	5:E:45:ASP:O	2.19	0.43
10:J:99:GLU:HA	38:J:8871:HOH:O	2.19	0.43
16:P:134:VAL:O	16:P:137:LEU:HB3	2.19	0.43
18:R:18:LEU:HD12	18:R:143:VAL:CG1	2.49	0.43
18:R:39:THR:HB	18:R:42:GLU:CD	2.39	0.43
25:Y:235:GLU:CD	25:Y:235:GLU:N	2.72	0.43
30:0:1192:A:H4'	38:0:4383:HOH:O	2.18	0.43
12:L:6:ARG:HD3	30:0:1299:G:O6	2.18	0.43
30:0:1342:C:H2'	30:0:1343:C:H5'	1.99	0.43
30:0:135:G:C2	30:0:144:A:N3	2.86	0.43
30:0:1383:U:H2'	30:0:1384:C:C6	2.54	0.43
30:0:1504:A:H4'	30:0:1506:U:C5	2.53	0.43
30:0:1600:G:H8	30:0:1600:G:OP2	2.02	0.43
30:0:1933:G:C2'	30:0:1934:A:H5'	2.48	0.43
30:0:2095:A:OP1	30:0:2096:A:H4'	2.19	0.43
30:0:2293:G:C5	30:0:2294:C:C5	3.07	0.43
30:0:2476:C:H2'	30:0:2476:C:O2	2.19	0.43
30:0:2779:G:N7	30:0:2790:C:C2	2.86	0.43
30:0:2896:A:H2'	30:0:2896:A:N3	2.34	0.43
30:0:393:G:C2	30:0:394:G:C4	3.06	0.43
30:0:435:A:O2'	30:0:436:A:H5'	2.19	0.43
30:0:699:C:C2	30:0:744:G:N2	2.87	0.43
30:0:67:A:H5''	30:0:69:A:C8	2.54	0.43
30:0:816:G:H8	30:0:816:G:O5'	2.02	0.43
30:0:793:A:C2	30:0:822:C:C2	3.06	0.43
31:9:11:A:H4'	31:9:13:A:C8	2.54	0.43
1:A:72:GLU:HG2	26:Z:100:GLY:HA3	2.01	0.43
4:D:12:GLU:O	4:D:15:GLU:HG2	2.18	0.43
13:M:48:LYS:HE3	13:M:52:GLN:NE2	2.28	0.43
6:F:58:GLU:HB3	13:M:8:ILE:HG23	2.01	0.43
19:S:57:THR:C	19:S:59:ASP:H	2.21	0.43
20:T:28:SER:HA	20:T:97:ARG:HD3	1.99	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1287:A:H8	38:0:7887:HOH:O	2.02	0.42
30:0:248:A:H5'	30:0:249:G:OP2	2.19	0.42
30:0:349:U:O5'	30:0:349:U:H6	2.02	0.42
30:0:577:G:C2	30:0:581:G:C6	3.07	0.42
30:0:729:C:C2	30:0:743:G:N2	2.87	0.42
30:0:877:G:N7	30:0:885:G:C6	2.87	0.42
30:0:970:U:H2'	38:0:6308:HOH:O	2.18	0.42
31:9:110:G:C6	31:9:111:U:C5	3.07	0.42
31:9:16:G:C2	31:9:66:G:O6	2.72	0.42
1:A:23:TYR:HB2	30:0:1872:C:C5	2.54	0.42
1:A:81:GLN:H	1:A:92:ASN:ND2	2.17	0.42
3:C:156:LEU:O	3:C:160:LEU:HG	2.19	0.42
4:D:67:ASP:HA	4:D:68:PRO:HD3	1.92	0.42
5:E:81:GLU:O	5:E:172:PRO:HD3	2.19	0.42
13:M:42:ARG:HA	13:M:43:PRO:HD3	1.86	0.42
15:O:57:THR:O	15:O:111:VAL:HG23	2.19	0.42
19:S:42:GLU:O	19:S:46:ASP:HA	2.19	0.42
21:U:34:SER:HB3	38:0:3126:HOH:O	2.17	0.42
30:0:1183:C:N3	30:0:1184:C:N4	2.67	0.42
30:0:1184:C:O2'	30:0:1185:U:OP2	2.32	0.42
24:X:49:ARG:NH1	30:0:1385:G:O3'	2.51	0.42
30:0:1568:G:C2'	30:0:1569:U:H5'	2.49	0.42
30:0:188:C:O5'	30:0:188:C:H6	2.02	0.42
30:0:1970:G:H4'	30:0:1971:G:O5'	2.19	0.42
30:0:1981:A:C6	30:0:2005:G:H4'	2.54	0.42
30:0:2005:G:OP2	30:0:2006:C:H5''	2.19	0.42
30:0:2512:U:H4'	30:0:2514:U:O4	2.19	0.42
30:0:2531:U:H4'	38:0:9596:HOH:O	2.17	0.42
30:0:2600:A:H2'	30:0:2601:A:O4'	2.19	0.42
30:0:2853:U:C4	30:0:2906:A:N6	2.87	0.42
30:0:726:C:C2	30:0:727:G:C8	3.07	0.42
30:0:95:A:H5''	30:0:97:G:O4'	2.19	0.42
27:1:44:LYS:HG2	30:0:148:A:H5''	2.01	0.42
4:D:137:PRO:O	31:9:30:C:OP1	2.37	0.42
3:C:24:THR:HG23	3:C:25:PRO:HD2	2.02	0.42
13:M:112:LEU:HB3	13:M:133:LEU:HB3	2.02	0.42
23:W:11:VAL:O	23:W:12:ASN:HB2	2.19	0.42
24:X:43:VAL:HG12	24:X:44:ASP:N	2.34	0.42
30:0:107:U:H2'	30:0:108:U:H5'	2.01	0.42
30:0:111:C:H2'	30:0:112:G:O4'	2.19	0.42
30:0:1115:U:H5''	30:0:1140:C:O2'	2.20	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1474:C:O2'	30:0:1475:G:H5'	2.18	0.42
30:0:2248:C:O2'	30:0:2249:G:H5'	2.19	0.42
30:0:2374:G:H2'	30:0:2375:A:C8	2.53	0.42
30:0:314:G:N2	30:0:317:A:C8	2.87	0.42
30:0:354:A:H2'	30:0:355:C:C6	2.52	0.42
30:0:752:G:H2'	30:0:753:U:O4'	2.19	0.42
30:0:830:G:O2'	30:0:831:U:H5'	2.19	0.42
3:C:151:GLN:HA	3:C:151:GLN:HE21	1.84	0.42
3:C:194:PHE:HB2	3:C:212:VAL:HG12	2.00	0.42
3:C:46:TYR:CE1	30:0:450:C:H4'	2.54	0.42
4:D:76:ARG:NE	31:9:44:A:O4'	2.52	0.42
5:E:21:THR:HG23	5:E:30:THR:OG1	2.19	0.42
8:H:65:LEU:HA	8:H:65:LEU:HD12	1.80	0.42
26:Z:34:SER:HB3	30:0:797:A:H4'	2.00	0.42
30:0:1195:G:N2	30:0:1205:U:C2	2.87	0.42
30:0:1350:U:H5''	38:0:5090:HOH:O	2.20	0.42
30:0:1789:G:C2'	30:0:1790:C:O5'	2.67	0.42
30:0:2362:A:H2'	30:0:2363:G:C8	2.54	0.42
29:3:80:ARG:HH22	30:0:2381:C:H4'	1.84	0.42
30:0:2502:C:O2'	30:0:2503:A:H5'	2.19	0.42
30:0:2655:U:C4	30:0:2656:G:N7	2.87	0.42
30:0:282:C:O2'	30:0:368:C:N4	2.52	0.42
30:0:2893:C:C2'	30:0:2894:C:H5'	2.49	0.42
30:0:652:G:H2'	30:0:653:U:O4'	2.20	0.42
30:0:877:G:C6	30:0:885:G:C4	3.08	0.42
28:2:22:PRO:HG2	28:2:25:VAL:CG2	2.49	0.42
31:9:36:C:C5	31:9:37:C:C4	3.08	0.42
31:9:57:A:N3	31:9:57:A:H5'	2.34	0.42
31:9:65:A:C2'	31:9:66:G:OP2	2.68	0.42
2:B:57:GLU:HA	2:B:58:PRO:HD2	1.85	0.42
2:B:60:SER:HA	2:B:61:PRO:HD3	1.90	0.42
5:E:106:ASN:ND2	5:E:109:GLY:HA2	2.34	0.42
5:E:35:TYR:CD2	5:E:36:PRO:HD2	2.55	0.42
5:E:72:MET:O	5:E:76:VAL:HG22	2.19	0.42
12:L:38:HIS:CD2	12:L:39:GLU:HG3	2.54	0.42
19:S:57:THR:HG22	19:S:58:MET:N	2.34	0.42
20:T:24:ARG:HH21	20:T:39:ASN:ND2	2.17	0.42
26:Z:66:CYS:SG	26:Z:67:GLY:N	2.93	0.42
30:0:1342:C:O2'	30:0:1343:C:H5'	2.18	0.42
30:0:138:U:P	30:0:139:C:H5	2.42	0.42
30:0:161:A:H2'	30:0:162:C:C6	2.53	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:165:A:H2'	30:0:166:A:OP1	2.19	0.42
30:0:1754:A:O5'	30:0:1754:A:H8	2.02	0.42
30:0:1757:U:H5	38:0:3214:HOH:O	2.02	0.42
30:0:1848:G:O2'	30:0:1849:G:H5'	2.19	0.42
30:0:1998:G:O2'	30:0:2026:C:H1'	2.20	0.42
30:0:2346:C:O2	30:0:2346:C:H2'	2.18	0.42
30:0:2470:A:H2'	30:0:2471:G:O5'	2.19	0.42
30:0:265:U:C2	30:0:266:G:C8	3.07	0.42
30:0:690:G:H1'	30:0:731:U:O2'	2.20	0.42
30:0:776:A:C2	30:0:780:A:C6	3.08	0.42
29:3:10:TYR:CD2	30:0:2382:A:H1'	2.55	0.42
31:9:22:G:C6	31:9:55:U:C2	3.07	0.42
1:A:223:ARG:HH12	30:0:2270:G:C4'	2.27	0.42
1:A:81:GLN:HB2	1:A:92:ASN:ND2	2.35	0.42
2:B:162:MET:HG3	2:B:310:ARG:NH1	2.35	0.42
2:B:177:HIS:O	2:B:181:ILE:HG13	2.19	0.42
2:B:307:ARG:HG2	2:B:308:LEU:N	2.34	0.42
3:C:211:ASP:HB2	3:C:231:ARG:HH12	1.85	0.42
4:D:88:LEU:HB2	4:D:89:PRO:HD3	2.00	0.42
8:H:91:ARG:NH2	8:H:135:GLN:NE2	2.68	0.42
12:L:10:SER:O	12:L:11:ARG:HB3	2.19	0.42
15:O:105:ASN:HD21	15:O:109:SER:N	2.18	0.42
16:P:10:ALA:HA	16:P:13:VAL:HG12	2.02	0.42
24:X:12:ILE:HB	24:X:70:ILE:CG2	2.49	0.42
26:Z:38:PHE:HB3	26:Z:42:TYR:HD1	1.82	0.42
30:0:1047:U:O5'	30:0:1047:U:H6	2.03	0.42
30:0:1097:A:H2'	30:0:1098:A:C8	2.54	0.42
30:0:1367:A:H2'	30:0:1368:U:O4'	2.20	0.42
30:0:1391:G:H2'	30:0:1392:A:H5'	2.01	0.42
30:0:1573:A:C8	30:0:1574:C:C6	3.08	0.42
30:0:1603:A:H5'	30:0:1605:G:H5'	1.99	0.42
30:0:1643:C:O2'	30:0:1644:C:H5'	2.19	0.42
30:0:1680:C:H5'	30:0:1685:A:N6	2.34	0.42
30:0:1709:G:C6	30:0:1711:A:C5	3.07	0.42
29:3:33:MET:CG	30:0:1922:A:H2'	2.50	0.42
30:0:221:G:H2'	30:0:222:A:C8	2.55	0.42
30:0:2499:U:H2'	30:0:2500:C:O4'	2.20	0.42
30:0:2805:A:C8	30:0:2806:C:C5	3.07	0.42
30:0:2842:G:C2'	30:0:2843:A:H5'	2.50	0.42
30:0:453:A:C4	30:0:479:G:N7	2.87	0.42
30:0:685:C:O2'	30:0:748:C:H5''	2.19	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:37:CYS:SG	27:1:39:PHE:HB2	2.59	0.42
31:9:108:C:H2'	31:9:109:G:C8	2.55	0.42
1:A:10:GLY:HA2	30:0:1861:C:O2	2.20	0.42
2:B:48:MET:O	30:0:2719:A:H5'	2.20	0.42
8:H:48:VAL:HG13	38:H:218:HOH:O	2.18	0.42
9:I:133:THR:HG22	9:I:134:ILE:H	1.83	0.42
13:M:185:PRO:HD3	38:0:9800:HOH:O	2.19	0.42
13:M:191:GLY:O	30:0:175:G:H3'	2.19	0.42
24:X:71:ARG:HD3	38:X:2171:HOH:O	2.20	0.42
30:0:1060:C:H5'	30:0:1060:C:H6	1.85	0.42
30:0:1255:A:C2'	30:0:1256:C:O5'	2.68	0.42
30:0:1523:G:C6	30:0:1524:U:O4	2.73	0.42
30:0:1965:C:H6	30:0:1965:C:O5'	2.02	0.42
30:0:2492:U:C4	30:0:2493:C:C4	3.07	0.42
30:0:2812:A:H2	30:0:2814:A:N7	2.17	0.42
30:0:2864:U:H2'	30:0:2865:G:H5'	2.02	0.42
30:0:462:A:N6	30:0:477:A:C2	2.88	0.42
30:0:583:C:H2'	30:0:584:U:H6	1.85	0.42
30:0:590:A:H2'	30:0:591:A:C5'	2.48	0.42
30:0:669:G:C4	30:0:670:G:C8	3.07	0.42
30:0:795:G:H2'	38:0:9823:HOH:O	2.20	0.42
1:A:26:ASP:HB2	38:0:7291:HOH:O	2.18	0.42
2:B:223:ARG:HG3	2:B:232:TRP:C	2.40	0.42
8:H:59:GLN:HE21	8:H:129:ARG:HG2	1.85	0.42
10:J:116:LEU:HB2	10:J:119:THR:CG2	2.49	0.42
10:J:131:THR:O	10:J:134:GLU:HB2	2.19	0.42
13:M:159:VAL:HG13	13:M:160:PHE:N	2.35	0.42
13:M:70:GLY:HA3	13:M:73:ARG:CZ	2.50	0.42
14:N:169:PRO:O	14:N:172:PHE:HB3	2.20	0.42
20:T:75:GLU:O	20:T:76:ASP:HB2	2.19	0.42
30:0:1241:G:H2'	30:0:1242:A:O4'	2.19	0.42
30:0:1537:C:O2'	30:0:1538:C:H5'	2.18	0.42
30:0:1541:G:O2'	30:0:1542:G:H5'	2.18	0.42
30:0:2256:G:H2'	30:0:2257:G:C5'	2.50	0.42
38:C:8619:HOH:O	30:0:338:C:H5'	2.19	0.42
30:0:451:C:C2'	30:0:452:G:H5'	2.50	0.42
30:0:711:G:N2	30:0:718:C:N1	2.67	0.42
30:0:802:G:N2	30:0:812:A:C4	2.88	0.42
30:0:877:G:C2	30:0:885:G:O4'	2.73	0.42
4:D:104:PHE:N	4:D:104:PHE:CD2	2.88	0.42
13:M:30:GLU:O	13:M:34:GLU:HG3	2.19	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:92:ASP:OD2	23:W:94:SER:HB2	2.20	0.42
24:X:25:ARG:HD2	38:X:5356:HOH:O	2.19	0.42
26:Z:37:ARG:HG3	26:Z:38:PHE:CD2	2.54	0.42
1:A:160:ALA:CB	26:Z:89:THR:HB	2.49	0.42
30:0:1187:U:O2	30:0:1189:A:H5''	2.20	0.42
30:0:1183:C:H1'	30:0:1192:A:N6	2.35	0.42
30:0:1413:A:H2'	30:0:1414:A:O4'	2.20	0.42
30:0:1819:G:H2'	30:0:1820:G:H5'	2.01	0.42
30:0:1840:A:H4'	30:0:1841:C:O5'	2.20	0.42
30:0:2355:G:N3	30:0:2355:G:C2'	2.83	0.42
30:0:2523:U:O2'	30:0:2524:G:H5'	2.19	0.42
2:B:316:ARG:HB2	30:0:2768:A:C8	2.55	0.42
30:0:325:U:H3'	38:0:5512:HOH:O	2.19	0.42
30:0:387:G:O2'	30:0:388:G:H5'	2.20	0.42
30:0:473:A:C2'	30:0:474:C:H5'	2.49	0.42
30:0:485:A:N3	30:0:487:G:H5''	2.34	0.42
3:C:87:ARG:NH2	30:0:894:A:C2	2.88	0.42
31:9:74:G:C2	31:9:75:G:C8	3.08	0.42
31:9:92:G:C6	31:9:93:A:N6	2.88	0.42
1:A:169:PHE:O	1:A:170:VAL:HB	2.20	0.42
2:B:8:LYS:HB3	2:B:218:TRP:O	2.19	0.42
30:0:1015:C:H2'	30:0:1016:U:H6	1.82	0.42
28:2:41:HIS:CE1	30:0:1439:C:H5''	2.54	0.42
30:0:2700:G:C2'	30:0:2701:G:H5'	2.49	0.42
30:0:2909:G:N2	30:0:2910:A:C5	2.88	0.42
30:0:293:A:C2	30:0:294:C:C6	3.08	0.42
30:0:59:A:H5''	38:0:4313:HOH:O	2.18	0.42
30:0:67:A:H3'	30:0:67:A:OP2	2.20	0.42
30:0:868:G:H2'	38:0:3039:HOH:O	2.18	0.42
29:3:14:CYS:SG	38:3:9063:HOH:O	2.62	0.42
29:3:83:TRP:O	29:3:85:ALA:N	2.53	0.42
31:9:114:G:C6	31:9:115:C:N4	2.88	0.42
5:E:77:THR:OG1	5:E:78:GLU:N	2.50	0.42
8:H:149:VAL:HG13	8:H:150:LYS:N	2.35	0.42
11:K:105:ARG:HD2	38:K:3385:HOH:O	2.19	0.42
16:P:40:VAL:O	16:P:44:VAL:HG23	2.20	0.42
17:Q:27:GLN:HB3	38:9:9083:HOH:O	2.20	0.42
23:W:10:GLU:HB3	38:W:1223:HOH:O	2.20	0.42
24:X:70:ILE:O	24:X:70:ILE:HG23	2.18	0.42
26:Z:61:HIS:CG	26:Z:95:PRO:HG3	2.55	0.42
30:0:1006:A:N3	30:0:2298:C:O2'	2.45	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:I:3512:HOH:O	30:0:1163:G:N2	2.53	0.41
30:0:1182:C:H4'	30:0:1192:A:N7	2.35	0.41
30:0:1210:G:C2	30:0:1211:G:N9	2.88	0.41
30:0:1588:G:C6	30:0:1589:G:C6	3.08	0.41
30:0:1624:A:O4'	30:0:1626:A:C8	2.73	0.41
30:0:1789:G:N2	30:0:1790:C:H1'	2.35	0.41
30:0:1919:A:H4'	38:0:4820:HOH:O	2.19	0.41
30:0:2433:A:H2'	30:0:2434:A:C8	2.54	0.41
30:0:2478:U:H2'	30:0:2479:A:H8	1.85	0.41
30:0:2799:A:H5'	30:0:2800:A:P	2.59	0.41
21:U:56:ARG:NH1	30:0:2890:A:C2	2.88	0.41
30:0:314:G:C2	30:0:317:A:C8	3.08	0.41
30:0:335:U:C2'	30:0:336:G:OP1	2.68	0.41
30:0:371:U:H2'	30:0:372:A:H8	1.85	0.41
30:0:628:1MA:H4'	38:0:3136:HOH:O	2.19	0.41
30:0:887:G:H2'	30:0:888:U:C6	2.54	0.41
28:2:48:ASP:O	28:2:49:GLU:HB2	2.20	0.41
29:3:62:THR:CG2	29:3:63:LYS:N	2.83	0.41
2:B:203:ALA:HA	2:B:263:THR:HA	2.02	0.41
2:B:224:LYS:HA	2:B:224:LYS:HD3	1.83	0.41
12:L:73:VAL:HG21	12:L:116:HIS:CE1	2.54	0.41
12:L:35:ARG:HB2	12:L:43:HIS:CD2	2.55	0.41
12:L:53:ARG:N	33:L:8810:CL:CL	2.66	0.41
13:M:89:THR:HA	38:M:8950:HOH:O	2.19	0.41
15:O:39:THR:HB	38:0:4589:HOH:O	2.19	0.41
15:O:68:GLY:HA3	30:0:745:G:O6	2.20	0.41
22:V:39:ALA:C	22:V:41:GLU:H	2.23	0.41
30:0:102:A:C6	30:0:103:C:N4	2.88	0.41
30:0:1163:G:C2	30:0:1184:C:N3	2.87	0.41
30:0:1178:G:H2'	30:0:1179:C:H6	1.79	0.41
30:0:1449:G:H4'	38:0:9213:HOH:O	2.20	0.41
30:0:1507:C:H4'	38:0:3595:HOH:O	2.20	0.41
30:0:1519:U:H6	30:0:1519:U:O5'	2.04	0.41
30:0:1915:U:O2	30:0:1925:G:C2	2.73	0.41
30:0:2004:U:H2'	30:0:2004:U:O2	2.20	0.41
30:0:201:G:H1'	38:0:4539:HOH:O	2.19	0.41
30:0:2020:C:O2'	30:0:2021:C:H5'	2.20	0.41
30:0:2061:C:C2'	30:0:2062:A:H5'	2.51	0.41
30:0:2912:C:C2'	30:0:2913:A:H5'	2.50	0.41
30:0:272:A:N1	30:0:369:G:H5''	2.34	0.41
30:0:412:C:C2'	30:0:413:G:H5'	2.50	0.41

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:446:G:H3'	38:0:9539:HOH:O	2.20	0.41
30:0:495:A:O4'	30:0:1390:A:H1'	2.20	0.41
27:1:31:LYS:O	27:1:33:VAL:HG23	2.20	0.41
29:3:5:ARG:HA	29:3:22:VAL:HG23	2.02	0.41
31:9:50:G:C6	31:9:51:A:C6	3.08	0.41
31:9:56:A:C3'	31:9:57:A:C5'	2.93	0.41
1:A:199:HIS:CD2	1:A:200:PRO:HD2	2.55	0.41
1:A:51:ARG:NH2	1:A:53:ALA:HB3	2.35	0.41
4:D:76:ARG:CZ	31:9:44:A:C1'	2.98	0.41
9:I:96:SER:H	9:I:99:GLN:CD	2.22	0.41
10:J:19:MET:HE2	10:J:79:PHE:HA	2.02	0.41
11:K:4:LEU:HD23	11:K:4:LEU:HA	1.84	0.41
16:P:94:TRP:CH2	16:P:98:ILE:HG13	2.55	0.41
18:R:99:ALA:HB1	18:R:109:MET:HE2	2.01	0.41
22:V:23:LEU:HD22	22:V:49:LEU:HD23	2.01	0.41
23:W:13:MET:CE	23:W:17:ILE:HG22	2.50	0.41
26:Z:78:ILE:HB	38:Z:8715:HOH:O	2.19	0.41
30:0:1079:A:N1	30:0:2068:G:O2'	2.43	0.41
30:0:1212:C:C5	30:0:1213:C:C5	3.09	0.41
30:0:1303:C:O2	30:0:1353:C:H1'	2.20	0.41
30:0:1419:U:H5'	30:0:1420:C:OP2	2.21	0.41
30:0:1554:C:O2'	30:0:1631:A:H1'	2.19	0.41
30:0:1804:A:H2'	30:0:1805:G:C8	2.55	0.41
30:0:1826:C:O2'	30:0:1827:G:H5'	2.21	0.41
30:0:1878:G:O2'	30:0:1879:U:P	2.78	0.41
30:0:2256:G:C2'	30:0:2257:G:H5'	2.51	0.41
30:0:236:A:H8	30:0:236:A:OP1	2.03	0.41
30:0:2474:A:C8	30:0:2621:PSU:H4'	2.55	0.41
38:H:216:HOH:O	30:0:2517:A:H2	1.99	0.41
30:0:2782:G:O6	30:0:2790:C:H5''	2.19	0.41
30:0:2795:C:O2'	30:0:2796:U:C5'	2.65	0.41
30:0:2799:A:N6	30:0:2801:A:C2	2.89	0.41
30:0:38:G:C2'	30:0:39:G:H5'	2.50	0.41
26:Z:34:SER:HA	30:0:797:A:C5'	2.50	0.41
2:B:211:THR:HG21	38:0:7438:HOH:O	2.20	0.41
2:B:75:GLU:C	2:B:77:PRO:HD3	2.40	0.41
4:D:84:LEU:HD23	4:D:84:LEU:HA	1.92	0.41
5:E:69:ILE:HA	5:E:72:MET:HE3	2.02	0.41
8:H:59:GLN:NE2	8:H:96:GLN:HG2	2.35	0.41
12:L:150:GLN:HB3	38:L:8869:HOH:O	2.19	0.41
21:U:31:PHE:CG	21:U:37:GLU:HG2	2.55	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:54:ILE:HD11	24:X:85:VAL:HG12	2.03	0.41
25:Y:157:ILE:HD13	38:0:4836:HOH:O	2.20	0.41
30:0:107:U:C2'	30:0:108:U:H5'	2.50	0.41
30:0:1607:A:C5	30:0:1608:G:C8	3.09	0.41
30:0:1757:U:H6	30:0:1757:U:O5'	2.04	0.41
30:0:1769:C:C2'	30:0:1770:U:H5'	2.51	0.41
30:0:1819:G:C2'	30:0:1820:G:H5'	2.50	0.41
30:0:1928:C:C2'	30:0:1929:G:H5'	2.50	0.41
30:0:1894:C:N4	30:0:1939:U:H2'	2.34	0.41
30:0:1942:A:C1'	38:0:9045:HOH:O	2.69	0.41
30:0:1997:A:H2	30:0:2026:C:O2'	2.04	0.41
30:0:2710:U:H2'	30:0:2711:U:C6	2.55	0.41
30:0:2723:G:H1'	38:0:4812:HOH:O	2.19	0.41
30:0:2815:G:H4'	30:0:2816:A:OP2	2.20	0.41
30:0:281:U:C2'	30:0:282:C:C5'	2.98	0.41
30:0:517:U:H2'	30:0:518:G:H5'	2.02	0.41
30:0:552:A:H5'	38:0:5878:HOH:O	2.19	0.41
26:Z:34:SER:HA	30:0:797:A:H5'	2.02	0.41
31:9:110:G:C6	31:9:111:U:C4	3.08	0.41
31:9:58:G:C8	31:9:59:C:C4	3.08	0.41
2:B:69:VAL:HA	2:B:70:PRO:HD3	1.77	0.41
5:E:107:PHE:O	5:E:110:GLU:HG3	2.20	0.41
15:O:26:TRP:CE3	15:O:26:TRP:HA	2.55	0.41
19:S:17:ASP:HB3	19:S:23:LYS:HB2	2.01	0.41
24:X:23:HIS:HE1	30:0:2044:G:OP1	2.03	0.41
30:0:1063:G:O5'	30:0:2307:A:H1'	2.21	0.41
30:0:10:U:O4	30:0:532:A:OP2	2.38	0.41
30:0:1271:A:H2'	30:0:1272:C:H6	1.84	0.41
30:0:1423:C:O2'	30:0:1424:A:H5'	2.20	0.41
30:0:1882:C:H2'	30:0:1883:U:H6	1.86	0.41
30:0:1898:G:H2'	30:0:1899:C:C6	2.55	0.41
11:K:66:ARG:NH1	30:0:1992:U:H3'	2.35	0.41
2:B:222:LYS:HG3	30:0:2038:A:H5''	2.01	0.41
30:0:2470:A:C2'	30:0:2471:G:O5'	2.68	0.41
30:0:2511:A:H2'	30:0:2512:U:C6	2.56	0.41
30:0:2854:A:N6	30:0:2905:A:N6	2.69	0.41
30:0:343:C:H1'	38:0:5552:HOH:O	2.19	0.41
30:0:594:C:C4	30:0:595:U:C4	3.08	0.41
30:0:910:C:H2'	30:0:911:G:O4'	2.21	0.41
1:A:212:PRO:HA	30:0:1943:C:O4'	2.20	0.41
2:B:320:GLN:HE21	2:B:321:PRO:HD3	1.84	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:5:ILE:HG12	3:C:139:VAL:CG1	2.50	0.41
6:F:26:THR:HB	6:F:102:GLY:HA3	2.02	0.41
7:G:23:ILE:O	7:G:27:ILE:HG13	2.20	0.41
8:H:165:ARG:HD2	38:H:241:HOH:O	2.21	0.41
10:J:54:VAL:HG11	10:J:138:THR:HG21	2.02	0.41
10:J:76:ASP:HA	38:J:8863:HOH:O	2.20	0.41
14:N:132:ASN:O	14:N:135:VAL:HG12	2.21	0.41
19:S:51:GLN:HE21	19:S:53:ASN:HD21	1.67	0.41
21:U:5:GLU:HG2	21:U:6:CYS:N	2.36	0.41
25:Y:130:ARG:HB2	25:Y:142:SER:O	2.20	0.41
25:Y:152:LYS:CB	25:Y:160:LYS:HG3	2.51	0.41
25:Y:189:ASN:HD22	25:Y:191:ASP:N	2.19	0.41
30:0:1278:A:O2'	30:0:1279:U:C2	2.65	0.41
30:0:1540:G:C4	30:0:1541:G:C8	3.09	0.41
30:0:165:A:C2'	30:0:166:A:OP1	2.67	0.41
30:0:1666:C:C2'	30:0:1667:A:H5'	2.32	0.41
30:0:1679:C:O2	30:0:1685:A:C2	2.73	0.41
30:0:2057:U:O5'	30:0:2057:U:H6	2.03	0.41
30:0:2255:A:H2'	30:0:2256:G:O4'	2.20	0.41
30:0:2692:G:N2	30:0:2701:G:C5	2.88	0.41
30:0:307:G:C2	30:0:309:C:C4	3.08	0.41
31:9:60:C:O2	31:9:60:C:H2'	2.19	0.41
1:A:70:ALA:HA	1:A:71:PRO:HD3	1.82	0.41
2:B:241:PRO:HD2	38:B:9125:HOH:O	2.20	0.41
18:R:9:ASP:HA	18:R:10:PRO:HD2	1.90	0.41
19:S:52:VAL:HG22	19:S:66:VAL:HG13	2.03	0.41
23:W:122:ARG:NH2	38:0:5254:HOH:O	2.52	0.41
30:0:1012:A:H8	30:0:1012:A:O5'	2.04	0.41
30:0:1191:A:O5'	30:0:1191:A:C8	2.74	0.41
30:0:1196:C:H2'	30:0:1197:G:H5'	2.02	0.41
30:0:1438:G:N3	30:0:1438:G:H2'	2.35	0.41
30:0:1544:U:O2'	30:0:1545:C:H5'	2.20	0.41
30:0:1798:C:OP2	30:0:1799:G:H5''	2.20	0.41
30:0:213:G:O2'	30:0:214:U:OP2	2.39	0.41
30:0:2325:U:C2	30:0:2326:C:C6	3.09	0.41
30:0:2383:G:C6	30:0:2384:U:C4	3.08	0.41
30:0:2668:G:N2	30:0:2669:U:C2	2.88	0.41
30:0:2668:G:O4'	30:0:2827:A:C2	2.73	0.41
30:0:268:U:O4	30:0:269:G:N1	2.54	0.41
30:0:393:G:C6	30:0:394:G:C6	3.09	0.41
30:0:631:A:C6	30:0:2074:A:H5'	2.56	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:677:C:H6	30:0:677:C:O5'	2.03	0.41
30:0:69:A:C3'	30:0:69:A:C8	3.04	0.41
30:0:812:A:H1'	38:0:3946:HOH:O	2.20	0.41
30:0:862:U:O2'	30:0:863:G:H5'	2.20	0.41
30:0:870:G:C3'	30:0:871:G:H5''	2.51	0.41
29:3:91:GLN:O	29:3:92:GLU:HB2	2.21	0.41
8:H:89:THR:O	8:H:137:PHE:HD2	2.04	0.41
21:U:17:THR:HG21	38:U:2221:HOH:O	2.21	0.41
21:U:42:LEU:HB3	30:0:1810:C:O4'	2.21	0.41
26:Z:70:ARG:HB2	26:Z:81:CYS:HG	1.86	0.41
30:0:1173:A:H2'	30:0:1177:A:H62	1.85	0.41
30:0:1209:C:O2'	30:0:1210:G:H5'	2.20	0.41
30:0:1621:G:H2'	30:0:1622:G:H8	1.86	0.41
30:0:1774:G:C2'	30:0:1775:A:H5'	2.51	0.41
30:0:1803:C:H2'	30:0:1804:A:C8	2.56	0.41
30:0:1913:C:H2'	30:0:1914:C:C6	2.54	0.41
30:0:1977:U:OP1	30:0:1977:U:H3'	2.20	0.41
30:0:2039:A:H2'	30:0:2040:C:C6	2.56	0.41
30:0:189:A:H2	30:0:205:U:O2	2.04	0.41
30:0:2324:G:H2'	30:0:2325:U:C6	2.56	0.41
30:0:241:A:C2	30:0:378:A:H4'	2.55	0.41
30:0:2700:G:H2'	30:0:2701:G:O5'	2.21	0.41
30:0:383:A:H2'	30:0:384:G:O4'	2.21	0.41
23:W:43:GLY:HA3	30:0:945:U:O2'	2.20	0.41
31:9:82:U:H2'	31:9:83:G:C8	2.56	0.41
1:A:199:HIS:HE1	30:0:1881:A:OP1	2.04	0.41
1:A:232:ARG:CZ	30:0:1939:U:H4'	2.50	0.41
1:A:47:HIS:HD2	30:0:1654:U:O2'	2.03	0.41
2:B:195:ARG:HG2	2:B:323:LEU:HD22	2.03	0.41
4:D:20:LYS:HG2	4:D:133:ASN:HB3	2.02	0.41
8:H:91:ARG:NH1	8:H:138:THR:OG1	2.53	0.41
10:J:107:ASN:HA	10:J:108:PRO:HD2	1.98	0.41
14:N:83:LEU:HD13	14:N:175:LEU:HD23	2.03	0.41
16:P:89:ASN:HA	38:P:165:HOH:O	2.20	0.41
18:R:114:VAL:HG13	18:R:114:VAL:O	2.20	0.41
30:0:1193:A:C2	30:0:1194:A:N6	2.89	0.41
30:0:1089:G:H1'	30:0:1290:G:N2	2.36	0.41
30:0:1596:U:O2'	30:0:1598:A:N7	2.46	0.41
30:0:1476:A:H1'	30:0:1867:G:O2'	2.21	0.41
30:0:1973:A:C8	30:0:1973:A:H5'	2.53	0.41
30:0:20:G:H2'	30:0:21:G:O5'	2.21	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2453:G:H2'	30:0:2454:C:C6	2.55	0.41
30:0:2599:A:C6	30:0:2600:A:N1	2.89	0.41
30:0:2695:C:N4	30:0:2701:G:N2	2.69	0.41
30:0:2801:A:C4	30:0:2802:C:C5	3.08	0.41
30:0:51:G:C2	30:0:111:C:C2	3.08	0.41
30:0:844:A:C6	30:0:882:A:C6	3.09	0.41
31:9:29:C:C6	31:9:30:C:C6	3.08	0.41
1:A:171:LYS:HB2	30:0:820:G:C6	2.55	0.41
5:E:119:HIS:O	5:E:140:ALA:HB1	2.21	0.41
5:E:145:ALA:HB1	5:E:168:ILE:CD1	2.49	0.41
5:E:20:ILE:HD12	5:E:33:LEU:HD12	2.03	0.41
6:F:61:MET:O	6:F:64:PRO:HD2	2.21	0.41
19:S:73:ASP:OD1	19:S:76:GLU:HG3	2.21	0.41
21:U:56:ARG:NH1	30:0:2890:A:C4	2.89	0.41
26:Z:47:ARG:HD2	38:Z:8718:HOH:O	2.20	0.41
30:0:1024:G:C5	30:0:1025:C:C4	3.09	0.41
30:0:1168:C:C2'	30:0:1169:U:H5'	2.51	0.41
30:0:1207:A:H5'	30:0:1208:C:OP2	2.21	0.41
30:0:1226:G:C2	30:0:1227:C:C6	3.08	0.41
30:0:1339:G:C5	30:0:1340:G:C6	3.09	0.41
30:0:1362:U:H2'	30:0:1363:G:H8	1.86	0.41
30:0:1416:G:C2'	30:0:1417:G:H5'	2.51	0.41
30:0:1543:G:H2'	30:0:1544:U:C5	2.56	0.41
30:0:1553:C:H6	30:0:1553:C:O5'	2.04	0.41
30:0:1619:G:H2'	30:0:1620:C:O4'	2.21	0.41
30:0:1748:U:C6	30:0:1749:U:C5	3.09	0.41
30:0:2366:C:P	38:0:6939:HOH:O	2.79	0.41
30:0:265:U:C4	30:0:266:G:N7	2.89	0.41
16:P:61:ARG:NH2	30:0:2737:C:OP2	2.40	0.41
30:0:279:C:H2'	30:0:280:C:H5'	2.01	0.41
30:0:61:G:C2	30:0:62:C:C2	3.09	0.41
2:B:74:ILE:HG13	38:B:9076:HOH:O	2.20	0.41
4:D:36:ASN:HA	38:D:7500:HOH:O	2.20	0.41
5:E:15:GLN:HG2	5:E:16:ASP:N	2.36	0.41
14:N:73:ALA:HB1	14:N:74:PRO:CD	2.51	0.41
17:Q:41:LEU:HB3	17:Q:52:PHE:CZ	2.56	0.41
23:W:120:PRO:HG2	30:0:1095:U:O2	2.20	0.41
25:Y:152:LYS:HB3	25:Y:160:LYS:HG3	2.02	0.41
30:0:1103:C:C2	30:0:1241:G:N2	2.89	0.41
30:0:1195:G:N1	30:0:1205:U:N3	2.69	0.41
30:0:1208:C:H2'	30:0:1208:C:O2	2.19	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:123:U:O2'	30:0:124:C:H5'	2.21	0.41
30:0:1591:A:H5'	30:0:1603:A:H61	1.86	0.41
30:0:1634:G:C4	30:0:1635:U:C5	3.08	0.41
30:0:2016:U:H2'	30:0:2017:U:O4'	2.21	0.41
30:0:2098:C:O5'	30:0:2098:C:H6	2.04	0.41
30:0:2269:C:C4	30:0:2270:G:C5	3.08	0.41
30:0:23:G:H1'	30:0:520:A:N6	2.35	0.41
30:0:2526:C:H5'	30:0:2526:C:C6	2.56	0.41
30:0:2617:G:H5''	38:0:3896:HOH:O	2.20	0.41
38:B:9106:HOH:O	30:0:2818:A:H2	2.04	0.41
30:0:282:C:O2	30:0:282:C:C2'	2.62	0.41
2:B:288:GLY:HA2	30:0:2898:G:H4'	2.02	0.41
30:0:714:U:O4'	30:0:716:G:C2	2.74	0.41
30:0:736:A:H5''	38:0:4253:HOH:O	2.21	0.41
30:0:965:A:H2'	30:0:965:A:N3	2.36	0.41
31:9:110:G:H2'	31:9:110:G:N3	2.35	0.41
31:9:14:G:C5'	31:9:14:G:H8	2.13	0.41
1:A:37:VAL:HG13	38:A:9088:HOH:O	2.21	0.41
5:E:81:GLU:HA	5:E:133:VAL:O	2.21	0.41
5:E:23:GLU:HG2	5:E:28:SER:CB	2.51	0.41
13:M:68:ARG:HB2	38:M:8932:HOH:O	2.19	0.41
18:R:130:MET:HG3	38:0:7551:HOH:O	2.21	0.41
23:W:132:VAL:HG21	23:W:140:LYS:O	2.21	0.41
30:0:1170:U:O2	30:0:1172:G:H8	2.04	0.40
30:0:1175:G:C5	30:0:1193:A:C2	3.10	0.40
30:0:1177:A:C6	30:0:1178:G:C5	3.09	0.40
28:2:42:TRP:HZ2	30:0:1438:G:H1'	1.87	0.40
19:S:11:THR:CG2	30:0:1444:G:H5''	2.50	0.40
30:0:1832:G:N3	30:0:1833:U:C6	2.89	0.40
30:0:2330:U:H4'	30:0:2331:C:OP1	2.20	0.40
30:0:2414:A:N1	30:0:2415:A:C6	2.90	0.40
6:F:38:LYS:HE3	30:0:244:C:OP2	2.21	0.40
30:0:257:G:N2	30:0:258:G:C4	2.89	0.40
30:0:2635:A:H2'	30:0:2636:C:H5'	1.98	0.40
30:0:2692:G:N2	30:0:2701:G:C4	2.88	0.40
30:0:797:A:H2'	30:0:798:G:O4'	2.21	0.40
29:3:86:GLY:HA2	38:3:9032:HOH:O	2.21	0.40
3:C:118:THR:HG21	3:C:233:THR:HB	2.03	0.40
4:D:28:GLY:CA	4:D:69:ILE:HG23	2.51	0.40
13:M:72:ALA:HB3	38:M:8950:HOH:O	2.21	0.40
13:M:75:ARG:HG3	38:M:8868:HOH:O	2.20	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:110:THR:HA	14:N:111:PRO:HD3	1.98	0.40
23:W:48:VAL:HG12	23:W:48:VAL:O	2.21	0.40
23:W:4:LEU:CD2	23:W:54:PHE:HB3	2.51	0.40
25:Y:125:LYS:HB2	25:Y:126:PRO:HD2	2.03	0.40
30:0:1634:G:C6	30:0:1635:U:C4	3.10	0.40
30:0:1681:G:H5''	30:0:1682:A:H5'	2.03	0.40
30:0:1774:G:H2'	30:0:1775:A:C5'	2.51	0.40
30:0:2121:G:C2'	30:0:2122:C:H5'	2.51	0.40
30:0:2245:C:O5'	30:0:2245:C:H6	2.04	0.40
30:0:2300:A:H4'	30:0:2301:A:N3	2.37	0.40
30:0:2335:C:N3	30:0:2350:G:C2	2.89	0.40
30:0:2501:G:H1	30:0:2519:C:N4	2.18	0.40
30:0:2831:C:C2'	30:0:2832:C:C5'	2.93	0.40
30:0:2834:G:C2'	30:0:2835:C:O5'	2.69	0.40
30:0:312:U:O2	30:0:320:G:C2	2.75	0.40
30:0:366:U:H2'	30:0:367:G:O4'	2.20	0.40
30:0:534:C:H2'	30:0:2083:A:C2	2.57	0.40
30:0:594:C:H2'	30:0:595:U:C6	2.56	0.40
30:0:596:C:H6	30:0:596:C:O5'	2.03	0.40
30:0:69:A:C5'	30:0:69:A:C8	2.98	0.40
30:0:962:C:H2'	30:0:963:C:H5'	2.03	0.40
3:C:206:ASN:HB2	30:0:329:A:OP2	2.20	0.40
6:F:48:VAL:CG2	6:F:74:PHE:HB3	2.51	0.40
13:M:113:ARG:NH1	13:M:155:GLN:HB2	2.36	0.40
15:O:32:ARG:HD3	15:O:32:ARG:O	2.22	0.40
24:X:26:ALA:HB3	24:X:63:ARG:HG3	2.03	0.40
30:0:1133:A:H2'	30:0:1134:G:H5'	2.03	0.40
30:0:1325:G:O2'	30:0:1326:C:H5'	2.21	0.40
30:0:1474:C:C6	30:0:1474:C:C5'	2.94	0.40
30:0:1521:C:O2'	30:0:1522:A:H5'	2.22	0.40
30:0:1613:C:C6	30:0:1613:C:H3'	2.57	0.40
30:0:2311:A:H3'	38:0:7660:HOH:O	2.20	0.40
30:0:2325:U:H5''	30:0:2417:C:O2'	2.22	0.40
30:0:2493:C:C2'	30:0:2493:C:O2	2.67	0.40
30:0:249:G:O2'	30:0:266:G:H5'	2.21	0.40
30:0:2510:C:H42	30:0:2564:G:N2	2.19	0.40
2:B:5:ARG:NH2	30:0:2548:C:OP2	2.55	0.40
30:0:238:C:H4'	30:0:287:C:OP1	2.22	0.40
30:0:462:A:H2'	38:0:4853:HOH:O	2.21	0.40
30:0:568:G:H21	30:0:590:A:H62	1.69	0.40
30:0:603:A:H4'	30:0:604:G:O5'	2.22	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:822:C:H2'	30:0:823:U:H6	1.86	0.40
29:3:39:GLN:O	29:3:52:PHE:HE1	2.04	0.40
2:B:188:HIS:ND1	2:B:188:HIS:N	2.69	0.40
2:B:277:GLU:N	2:B:278:PRO:CD	2.84	0.40
6:F:50:VAL:HG11	6:F:60:VAL:HG11	2.03	0.40
13:M:46:LEU:O	13:M:50:ARG:HG3	2.21	0.40
22:V:12:THR:HG23	22:V:15:GLU:H	1.86	0.40
24:X:43:VAL:HG11	24:X:82:GLU:HA	2.04	0.40
30:0:1102:C:H5	38:0:3479:HOH:O	2.04	0.40
30:0:1159:G:C2	30:0:1209:C:N3	2.89	0.40
30:0:1520:G:C6	30:0:1521:C:N4	2.89	0.40
30:0:192:A:N6	30:0:194:A:C2	2.89	0.40
30:0:1979:G:H1'	38:0:3061:HOH:O	2.21	0.40
30:0:2102:G:N2	30:0:2103:A:N1	2.69	0.40
30:0:2532:A:OP2	30:0:2532:A:H8	2.05	0.40
30:0:2672:C:H2'	30:0:2673:U:C6	2.53	0.40
31:9:81:C:O2'	31:9:82:U:H5'	2.21	0.40
31:9:89:C:O2'	31:9:90:G:H5'	2.22	0.40
1:A:33:GLU:CD	1:A:33:GLU:N	2.75	0.40
2:B:73:VAL:HG21	2:B:284:PHE:HZ	1.86	0.40
3:C:100:LEU:HD22	30:0:751:U:H5''	2.03	0.40
4:D:14:ARG:HD3	31:9:56:A:O2'	2.22	0.40
5:E:23:GLU:HG2	5:E:28:SER:HB3	2.03	0.40
7:G:19:GLU:HG2	7:G:66:LEU:HD13	2.03	0.40
8:H:91:ARG:H	8:H:91:ARG:HG2	1.43	0.40
15:O:96:VAL:HG13	15:O:100:GLN:OE1	2.21	0.40
15:O:47:ARG:NH1	15:O:47:ARG:HG3	2.36	0.40
15:O:49:GLU:OE1	15:O:72:LYS:HG3	2.22	0.40
25:Y:132:ASP:OD1	25:Y:135:LYS:HD2	2.20	0.40
30:0:1016:U:H2'	30:0:1017:U:O4'	2.21	0.40
28:2:41:HIS:HE1	30:0:1439:C:OP1	2.05	0.40
30:0:146:U:C4	30:0:147:G:C6	3.09	0.40
30:0:1525:G:OP1	30:0:1525:G:H4'	2.21	0.40
30:0:1557:G:H2'	30:0:1558:C:C6	2.57	0.40
30:0:2004:U:H5''	30:0:2005:G:C8	2.57	0.40
30:0:2273:C:O2'	30:0:2274:A:H5'	2.22	0.40
30:0:295:C:H2'	30:0:296:G:O4'	2.22	0.40
30:0:37:A:H2'	30:0:38:G:H8	1.84	0.40
25:Y:229:LEU:O	30:0:552:A:H5''	2.22	0.40
30:0:766:A:HO2'	30:0:767:A:H8	1.68	0.40
30:0:920:C:H5'	30:0:921:G:N3	2.37	0.40

*Continued on next page...*



Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:17:HIS:CG	30:0:2409:C:H4'	2.57	0.40
31:9:2:U:OP2	31:9:2:U:H4'	2.22	0.40
1:A:20:SER:C	1:A:22:ARG:H	2.25	0.40
2:B:201:ASP:N	2:B:312:ARG:O	2.53	0.40
3:C:104:ASP:O	3:C:108:GLN:HG3	2.22	0.40
3:C:1:MET:HG2	3:C:2:GLN:N	2.34	0.40
4:D:135:VAL:HG22	4:D:136:ARG:N	2.36	0.40
5:E:84:MET:HA	5:E:167:TYR:O	2.22	0.40
6:F:59:ILE:CD1	30:0:263:U:C2	3.04	0.40
14:N:127:LEU:HD12	14:N:127:LEU:HA	1.93	0.40
15:O:32:ARG:NE	15:O:32:ARG:HA	2.35	0.40
16:P:13:VAL:HG21	16:P:41:ARG:HG2	2.03	0.40
16:P:78:GLY:O	30:0:1813:U:H4'	2.22	0.40
20:T:26:THR:HA	20:T:39:ASN:HB3	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	235/240 (98%)	200 (85%)	30 (13%)	5 (2%)	8	38
2	B	335/338 (99%)	305 (91%)	23 (7%)	7 (2%)	8	38
3	C	244/246 (99%)	216 (88%)	26 (11%)	2 (1%)	22	64
4	D	134/177 (76%)	105 (78%)	23 (17%)	6 (4%)	3	17
5	E	170/178 (96%)	158 (93%)	11 (6%)	1 (1%)	28	70
6	F	117/120 (98%)	97 (83%)	16 (14%)	4 (3%)	4	24
7	G	25/348 (7%)	22 (88%)	3 (12%)	0	100	100
8	H	156/177 (88%)	139 (89%)	16 (10%)	1 (1%)	28	70
9	I	68/162 (42%)	49 (72%)	16 (24%)	3 (4%)	3	17

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	140/145 (97%)	128 (91%)	10 (7%)	2 (1%)	13	49
11	K	130/132 (98%)	120 (92%)	9 (7%)	1 (1%)	22	64
12	L	141/165 (86%)	116 (82%)	22 (16%)	3 (2%)	8	38
13	M	192/196 (98%)	171 (89%)	17 (9%)	4 (2%)	8	38
14	N	184/187 (98%)	163 (89%)	17 (9%)	4 (2%)	8	36
15	O	113/116 (97%)	106 (94%)	7 (6%)	0	100	100
16	P	141/149 (95%)	133 (94%)	8 (6%)	0	100	100
17	Q	93/96 (97%)	86 (92%)	5 (5%)	2 (2%)	8	36
18	R	148/155 (96%)	138 (93%)	9 (6%)	1 (1%)	25	67
19	S	79/85 (93%)	75 (95%)	4 (5%)	0	100	100
20	T	117/120 (98%)	108 (92%)	9 (8%)	0	100	100
21	U	51/67 (76%)	44 (86%)	6 (12%)	1 (2%)	9	39
22	V	63/71 (89%)	58 (92%)	4 (6%)	1 (2%)	11	46
23	W	152/154 (99%)	142 (93%)	9 (6%)	1 (1%)	25	67
24	X	80/92 (87%)	72 (90%)	6 (8%)	2 (2%)	6	32
25	Y	140/241 (58%)	132 (94%)	7 (5%)	1 (1%)	25	67
26	Z	71/116 (61%)	55 (78%)	12 (17%)	4 (6%)	2	12
27	1	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
28	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
29	3	90/92 (98%)	64 (71%)	17 (19%)	9 (10%)	1	3
All	All	3705/4472 (83%)	3292 (89%)	348 (9%)	65 (2%)	10	43

All (65) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	206	THR
2	B	306	LYS
4	D	137	PRO
6	F	61	MET
6	F	101	ALA
10	J	5	GLU
12	L	80	ASP
13	M	75	ARG
14	N	154	LEU
14	N	183	ASP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
14	N	184	ILE
21	U	44	ARG
26	Z	70	ARG
29	3	56	PRO
29	3	64	LYS
29	3	84	ARG
1	A	34	ASP
3	C	8	LEU
3	C	201	SER
5	E	128	GLY
12	L	21	ARG
12	L	82	ALA
13	M	81	ARG
17	Q	21	ARG
23	W	139	GLY
24	X	70	ILE
26	Z	39	GLY
29	3	4	PRO
29	3	68	LYS
29	3	72	GLY
29	3	73	GLU
2	B	169	GLY
4	D	56	ARG
9	I	83	GLY
9	I	107	LYS
11	K	10	GLN
14	N	165	ALA
26	Z	83	TYR
29	3	90	PHE
1	A	119	ALA
2	B	107	SER
2	B	184	ASP
4	D	65	GLU
10	J	7	ASP
13	M	86	GLN
17	Q	18	PRO
18	R	20	GLU
1	A	24	LYS
1	A	122	SER
1	A	132	ASP
2	B	2	GLN
2	B	185	GLY

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
4	D	172	VAL
6	F	100	ASP
9	I	76	ASP
13	M	80	GLY
24	X	52	PRO
26	Z	105	ARG
29	3	62	THR
4	D	16	PRO
4	D	53	LYS
6	F	64	PRO
8	H	19	ARG
22	V	39	ALA
25	Y	111	ASP

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	179/182 (98%)	170 (95%)	9 (5%)	28	67
2	B	282/283 (100%)	263 (93%)	19 (7%)	19	54
3	C	193/193 (100%)	180 (93%)	13 (7%)	19	54
4	D	117/148 (79%)	110 (94%)	7 (6%)	22	60
5	E	152/156 (97%)	146 (96%)	6 (4%)	37	75
6	F	93/94 (99%)	92 (99%)	1 (1%)	78	93
7	G	27/282 (10%)	25 (93%)	2 (7%)	16	49
8	H	134/145 (92%)	124 (92%)	10 (8%)	16	49
9	I	58/130 (45%)	57 (98%)	1 (2%)	66	89
10	J	118/121 (98%)	109 (92%)	9 (8%)	15	48
11	K	106/106 (100%)	103 (97%)	3 (3%)	49	82
12	L	113/127 (89%)	106 (94%)	7 (6%)	21	58
13	M	158/160 (99%)	147 (93%)	11 (7%)	18	53
14	N	149/150 (99%)	146 (98%)	3 (2%)	60	87

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	O	93/94 (99%)	93 (100%)	0	100	100
16	P	113/117 (97%)	111 (98%)	2 (2%)	64	89
17	Q	79/80 (99%)	74 (94%)	5 (6%)	21	57
18	R	117/122 (96%)	113 (97%)	4 (3%)	42	78
19	S	71/74 (96%)	70 (99%)	1 (1%)	71	91
20	T	105/106 (99%)	98 (93%)	7 (7%)	19	54
21	U	44/53 (83%)	43 (98%)	1 (2%)	56	85
22	V	51/57 (90%)	51 (100%)	0	100	100
23	W	130/130 (100%)	126 (97%)	4 (3%)	45	80
24	X	66/74 (89%)	61 (92%)	5 (8%)	15	48
25	Y	120/196 (61%)	117 (98%)	3 (2%)	53	84
26	Z	60/94 (64%)	60 (100%)	0	100	100
27	1	46/47 (98%)	46 (100%)	0	100	100
28	2	42/46 (91%)	41 (98%)	1 (2%)	54	85
29	3	79/79 (100%)	73 (92%)	6 (8%)	15	48
All	All	3095/3646 (85%)	2955 (96%)	140 (4%)	32	71

All (140) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ARG
1	A	37	VAL
1	A	66	ARG
1	A	94	LEU
1	A	131	HIS
1	A	153	ARG
1	A	179	MET
1	A	190	ARG
1	A	217	ARG
2	B	7	ARG
2	B	11	LEU
2	B	27	ASN
2	B	49	THR
2	B	56	ASP
2	B	71	VAL
2	B	132	HIS
2	B	144	THR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
2	B	162	MET
2	B	171	VAL
2	B	180	ASP
2	B	188	HIS
2	B	190	MET
2	B	195	ARG
2	B	254	GLN
2	B	264	GLU
2	B	277	GLU
2	B	312	ARG
2	B	322	ARG
3	C	2	GLN
3	C	16	VAL
3	C	76	ARG
3	C	78	ARG
3	C	87	ARG
3	C	101	ASP
3	C	104	ASP
3	C	162	VAL
3	C	180	SER
3	C	187	ARG
3	C	236	THR
3	C	240	LEU
3	C	243	VAL
4	D	19	GLU
4	D	24	HIS
4	D	29	HIS
4	D	50	VAL
4	D	104	PHE
4	D	137	PRO
4	D	149	ARG
5	E	7	ILE
5	E	100	ASP
5	E	116	THR
5	E	126	ILE
5	E	155	ASN
5	E	156	ASP
6	F	12	LEU
7	G	64	ASN
7	G	72	ASP
8	H	33	GLN
8	H	62	HIS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
8	H	65	LEU
8	H	87	LYS
8	H	89	THR
8	H	91	ARG
8	H	99	ARG
8	H	122	LYS
8	H	157	TYR
8	H	172	GLU
9	I	110	ASP
10	J	39	VAL
10	J	45	VAL
10	J	46	ILE
10	J	52	GLN
10	J	74	ARG
10	J	79	PHE
10	J	107	ASN
10	J	120	SER
10	J	131	THR
11	K	10	GLN
11	K	24	THR
11	K	55	VAL
12	L	18	HIS
12	L	35	ARG
12	L	73	VAL
12	L	83	GLU
12	L	102	ASP
12	L	104	ASP
12	L	114	VAL
13	M	10	ASP
13	M	46	LEU
13	M	68	ARG
13	M	73	ARG
13	M	81	ARG
13	M	83	SER
13	M	84	LYS
13	M	89	THR
13	M	91	ILE
13	M	99	ARG
13	M	116	ASN
14	N	21	HIS
14	N	134	ASP
14	N	138	ASP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
16	P	91	LYS
16	P	98	ILE
17	Q	16	ASN
17	Q	18	PRO
17	Q	54	PRO
17	Q	75	ILE
17	Q	95	GLU
18	R	13	THR
18	R	39	THR
18	R	82	GLU
18	R	143	VAL
19	S	30	ASP
20	T	5	ASP
20	T	39	ASN
20	T	48	VAL
20	T	73	HIS
20	T	96	VAL
20	T	115	GLU
20	T	117	ASP
21	U	25	ASP
23	W	4	LEU
23	W	35	VAL
23	W	38	THR
23	W	146	ILE
24	X	27	ASP
24	X	52	PRO
24	X	72	VAL
24	X	79	GLU
24	X	82	GLU
25	Y	118	THR
25	Y	189	ASN
25	Y	203	VAL
28	2	18	ASN
29	3	7	PHE
29	3	15	ASN
29	3	17	HIS
29	3	56	PRO
29	3	71	CYS
29	3	90	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (88) such sidechains are listed below:



Mol	Chain	Res	Type
1	A	47	HIS
1	A	92	ASN
1	A	176	HIS
1	A	177	HIS
1	A	199	HIS
2	B	27	ASN
2	B	106	HIS
2	B	145	HIS
2	B	238	ASN
2	B	256	GLN
2	B	260	HIS
2	B	320	GLN
2	B	332	ASN
3	C	73	GLN
3	C	129	HIS
4	D	103	ASN
4	D	133	ASN
5	E	55	ASN
5	E	68	HIS
5	E	74	HIS
5	E	90	HIS
5	E	106	ASN
5	E	143	GLN
7	G	64	ASN
8	H	59	GLN
8	H	135	GLN
9	I	106	GLN
10	J	25	GLN
10	J	52	GLN
10	J	107	ASN
10	J	126	ASN
11	K	10	GLN
11	K	42	ASN
11	K	44	HIS
11	K	119	GLN
12	L	18	HIS
12	L	38	HIS
12	L	41	HIS
12	L	43	HIS
12	L	116	HIS
13	M	24	GLN
13	M	58	GLN
13	M	77	HIS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
13	M	86	GLN
13	M	137	ASN
13	M	142	GLN
13	M	170	ASN
14	N	107	ASN
14	N	132	ASN
16	P	50	GLN
16	P	66	GLN
16	P	88	GLN
16	P	118	GLN
17	Q	27	GLN
17	Q	40	HIS
18	R	61	GLN
18	R	94	ASN
18	R	98	ASN
18	R	117	HIS
19	S	9	HIS
19	S	44	GLN
19	S	53	ASN
20	T	39	ASN
20	T	43	ASN
21	U	39	ASN
22	V	34	GLN
22	V	60	GLN
23	W	12	ASN
23	W	110	GLN
23	W	119	HIS
23	W	141	HIS
24	X	23	HIS
25	Y	129	ASN
25	Y	134	HIS
25	Y	149	GLN
25	Y	189	ASN
27	1	16	HIS
27	1	28	HIS
28	2	16	ASN
28	2	18	ASN
28	2	41	HIS
28	2	45	ASN
29	3	2	GLN
29	3	13	HIS
29	3	18	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
29	3	20	HIS
29	3	30	GLN
29	3	78	HIS

### 5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	0	2745/2923 (93%)	243 (8%)	22 (0%)
31	9	121/122 (99%)	19 (15%)	2 (1%)
All	All	2866/3045 (94%)	262 (9%)	24 (0%)

All (262) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	0	31	C
30	0	67	A
30	0	69	A
30	0	70	A
30	0	71	G
30	0	86	A
30	0	87	C
30	0	88	G
30	0	114	A
30	0	115	U
30	0	120	A
30	0	130	C
30	0	138	U
30	0	141	C
30	0	151	A
30	0	166	A
30	0	185	G
30	0	186	A
30	0	191	A
30	0	192	A
30	0	198	A
30	0	200	C
30	0	219	G
30	0	237	G
30	0	271	C
30	0	272	A
30	0	273	G

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
30	0	283	U
30	0	284	C
30	0	285	A
30	0	308	U
30	0	309	C
30	0	318	U
30	0	336	G
30	0	337	A
30	0	342	C
30	0	358	G
30	0	368	C
30	0	381	G
30	0	397	A
30	0	417	G
30	0	457	U
30	0	461	C
30	0	487	G
30	0	498	A
30	0	510	U
30	0	511	A
30	0	514	G
30	0	537	G
30	0	538	C
30	0	539	G
30	0	542	A
30	0	545	G
30	0	553	G
30	0	559	U
30	0	588	G
30	0	604	G
30	0	605	C
30	0	620	A
30	0	632	A
30	0	644	G
30	0	660	A
30	0	688	A
30	0	698	A
30	0	701	U
30	0	702	G
30	0	746	A
30	0	759	C
30	0	777	U

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
30	0	809	G
30	0	821	U
30	0	835	U
30	0	840	U
30	0	857	A
30	0	858	U
30	0	868	G
30	0	869	G
30	0	871	G
30	0	872	U
30	0	875	A
30	0	877	G
30	0	878	G
30	0	884	C
30	0	885	G
30	0	898	G
30	0	905	C
30	0	920	C
30	0	921	G
30	0	923	A
30	0	953	G
30	0	960	G
30	0	961	A
30	0	1006	A
30	0	1008	C
30	0	1011	C
30	0	1029	U
30	0	1045	G
30	0	1059	G
30	0	1060	C
30	0	1072	G
30	0	1080	C
30	0	1081	A
30	0	1088	A
30	0	1109	U
30	0	1110	G
30	0	1119	G
30	0	1130	U
30	0	1137	G
30	0	1151	G
30	0	1161	A
30	0	1166	A

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
30	0	1174	A
30	0	1175	G
30	0	1185	U
30	0	1192	A
30	0	1193	A
30	0	1205	U
30	0	1206	U
30	0	1208	C
30	0	1216	G
30	0	1238	C
30	0	1239	G
30	0	1279	U
30	0	1289	C
30	0	1342	C
30	0	1353	C
30	0	1354	G
30	0	1360	C
30	0	1377	C
30	0	1378	G
30	0	1407	A
30	0	1460	G
30	0	1474	C
30	0	1485	A
30	0	1505	U
30	0	1506	U
30	0	1524	U
30	0	1525	G
30	0	1526	A
30	0	1528	A
30	0	1562	C
30	0	1592	G
30	0	1605	G
30	0	1617	C
30	0	1625	U
30	0	1626	A
30	0	1634	G
30	0	1656	A
30	0	1667	A
30	0	1682	A
30	0	1684	A
30	0	1685	A
30	0	1692	C

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
30	0	1701	A
30	0	1710	A
30	0	1722	U
30	0	1723	G
30	0	1725	C
30	0	1730	G
30	0	1731	C
30	0	1752	G
30	0	1778	A
30	0	1798	C
30	0	1820	G
30	0	1829	A
30	0	1856	C
30	0	1879	U
30	0	1919	A
30	0	1942	A
30	0	1967	U
30	0	1968	A
30	0	1971	G
30	0	1973	A
30	0	1978	A
30	0	1979	G
30	0	1996	U
30	0	2006	C
30	0	2008	U
30	0	2011	A
30	0	2012	U
30	0	2013	G
30	0	2033	G
30	0	2034	U
30	0	2064	U
30	0	2072	G
30	0	2073	G
30	0	2074	A
30	0	2096	A
30	0	2101	A
30	0	2102	G
30	0	2110	G
30	0	2238	A
30	0	2243	C
30	0	2258	A
30	0	2271	G

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
30	0	2272	G
30	0	2317	C
30	0	2321	A
30	0	2354	A
30	0	2361	A
30	0	2369	A
30	0	2422	U
30	0	2462	G
30	0	2465	A
30	0	2469	A
30	0	2476	C
30	0	2480	G
30	0	2483	A
30	0	2507	G
30	0	2509	A
30	0	2511	A
30	0	2533	C
30	0	2537	G
30	0	2541	U
30	0	2553	A
30	0	2564	G
30	0	2589	U
30	0	2601	A
30	0	2602	G
30	0	2608	C
30	0	2613	G
30	0	2638	G
30	0	2664	A
30	0	2681	A
30	0	2682	C
30	0	2718	C
30	0	2726	U
30	0	2747	C
30	0	2748	G
30	0	2749	U
30	0	2750	G
30	0	2762	C
30	0	2768	A
30	0	2792	A
30	0	2800	A
30	0	2811	A
30	0	2812	A

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
30	0	2825	C
30	0	2876	G
30	0	2890	A
30	0	2896	A
30	0	2903	C
30	0	2914	A
31	9	2	U
31	9	7	G
31	9	14	G
31	9	22	G
31	9	23	U
31	9	24	U
31	9	25	G
31	9	39	U
31	9	40	C
31	9	41	C
31	9	43	G
31	9	44	A
31	9	52	A
31	9	57	A
31	9	65	A
31	9	66	G
31	9	77	A
31	9	114	G
31	9	122	C

All (24) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	0	129	A
30	0	341	C
30	0	396	U
30	0	545	G
30	0	603	A
30	0	604	G
30	0	644	G
30	0	699	C
30	0	834	G
30	0	857	A
30	0	871	G
30	0	877	G
30	0	1080	C

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
30	0	1237	U
30	0	1352	A
30	0	1685	A
30	0	1970	G
30	0	2011	A
30	0	2536	C
30	0	2718	C
30	0	2761	A
30	0	2791	U
31	9	43	G
31	9	65	A

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

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
30	OMU	0	2587	30,35	14,22,23	0.97	1 (7%)	18,31,34	3.68	2 (11%)
30	OMG	0	2588	30	18,26,27	1.10	2 (11%)	22,38,41	2.45	4 (18%)
30	UR3	0	2619	30	14,22,23	0.71	0	16,32,35	0.66	0
30	PSU	0	2621	30	16,21,22	1.65	3 (18%)	20,30,33	6.06	4 (20%)
30	1MA	0	628	30,35	16,25,26	1.09	1 (6%)	13,37,40	1.19	1 (7%)

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
30	OMU	0	2587	30,35	-	0/5/27/28	0/2/2/2
30	OMG	0	2588	30	-	0/5/27/28	0/3/3/3
30	UR3	0	2619	30	-	0/3/25/26	0/2/2/2
30	PSU	0	2621	30	-	0/7/25/26	0/2/2/2

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	1MA	0	628	30,35	-	0/3/25/26	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	0	2621	PSU	C5-C1'	-5.10	1.47	1.52
30	0	2588	OMG	C8-N7	-2.05	1.30	1.34
30	0	2621	PSU	C4-N3	2.56	1.37	1.33
30	0	2621	PSU	C2-N1	2.59	1.43	1.38
30	0	2587	OMU	C4-N3	2.61	1.37	1.33
30	0	628	1MA	C6-N6	2.87	1.34	1.27
30	0	2588	OMG	C6-N1	3.57	1.39	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	2621	PSU	N1-C2-N3	-19.01	114.73	128.40
30	0	2621	PSU	C5-C4-N3	-12.79	114.94	125.43
30	0	2588	OMG	C5-C6-N1	-8.28	111.69	123.48
30	0	628	1MA	C2-N3-C4	-3.72	110.71	116.41
30	0	2587	OMU	C5-C4-N3	-3.59	114.53	123.12
30	0	2588	OMG	C2-N3-C4	-2.91	111.76	115.16
30	0	2588	OMG	N3-C2-N1	-2.44	123.89	127.46
30	0	2621	PSU	C6-N1-C2	2.77	119.80	115.36
30	0	2588	OMG	C6-N1-C2	6.27	125.08	116.06
30	0	2621	PSU	C4-N3-C2	13.72	127.16	115.16
30	0	2587	OMU	C4-N3-C2	15.04	127.05	114.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	0	2587	OMU	2	0
30	0	2621	PSU	2	0
30	0	628	1MA	2	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 305 ligands modelled in this entry, 305 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	237/240 (98%)	-0.60	1 (0%) 92 77	29, 65, 98, 115	0
2	B	337/338 (99%)	-0.73	0 100 100	31, 59, 87, 97	0
3	C	246/246 (100%)	-0.82	0 100 100	23, 47, 69, 80	0
4	D	140/177 (79%)	0.45	14 (10%) 8 3	74, 109, 132, 140	0
5	E	172/178 (96%)	-0.64	0 100 100	50, 74, 97, 103	0
6	F	119/120 (99%)	-0.31	1 (0%) 86 64	50, 73, 106, 113	0
7	G	29/348 (8%)	0.05	0 100 100	75, 96, 105, 109	0
8	H	160/177 (90%)	-0.50	0 100 100	48, 67, 99, 109	0
9	I	70/162 (43%)	1.80	30 (42%) 0 0	134, 152, 167, 169	0
10	J	142/145 (97%)	-0.80	1 (0%) 87 67	40, 58, 75, 97	0
11	K	132/132 (100%)	-0.87	0 100 100	39, 55, 81, 86	0
12	L	145/165 (87%)	-0.25	1 (0%) 87 67	35, 72, 113, 129	0
13	M	194/196 (98%)	-0.52	7 (3%) 43 18	31, 46, 99, 106	0
14	N	186/187 (99%)	-0.33	0 100 100	60, 80, 126, 132	0
15	O	115/116 (99%)	-0.87	0 100 100	43, 56, 74, 80	0
16	P	143/149 (95%)	-0.75	0 100 100	40, 59, 79, 85	0
17	Q	95/96 (98%)	-0.71	0 100 100	44, 56, 72, 88	0
18	R	150/155 (96%)	-0.83	0 100 100	33, 49, 70, 83	0
19	S	81/85 (95%)	-0.68	1 (1%) 79 53	40, 62, 82, 92	0
20	T	119/120 (99%)	-0.55	0 100 100	40, 59, 87, 116	0
21	U	53/67 (79%)	2.67	33 (62%) 0 0	107, 117, 125, 126	0
22	V	65/71 (91%)	-0.03	4 (6%) 21 8	47, 74, 118, 123	0
23	W	154/154 (100%)	-0.68	0 100 100	39, 54, 73, 87	0
24	X	82/92 (89%)	-0.46	1 (1%) 79 53	46, 65, 94, 108	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	Y	142/241 (58%)	-0.88	0 100 100	30, 49, 71, 92	0
26	Z	73/116 (62%)	3.60	46 (63%) 0 0	98, 116, 126, 130	0
27	1	56/57 (98%)	-0.77	0 100 100	28, 36, 43, 48	0
28	2	46/50 (92%)	-0.58	1 (2%) 62 33	31, 66, 97, 104	0
29	3	92/92 (100%)	4.22	71 (77%) 0 0	104, 119, 130, 134	0
30	0	2749/2923 (94%)	-0.82	2 (0%) 95 88	23, 51, 96, 175	0
31	9	122/122 (100%)	-0.96	1 (0%) 86 64	45, 75, 103, 154	0
All	All	6646/7517 (88%)	-0.53	215 (3%) 48 21	23, 57, 116, 175	0

All (215) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
26	Z	46	SER	17.2
26	Z	58	ASN	12.8
29	3	39	GLN	12.2
26	Z	36	GLY	11.4
29	3	34	LYS	11.4
29	3	38	ARG	10.8
29	3	35	TRP	10.7
26	Z	55	SER	10.6
29	3	41	GLU	10.4
29	3	37	ASP	9.9
26	Z	35	SER	9.9
26	Z	50	VAL	9.7
29	3	42	ARG	9.1
29	3	20	HIS	9.1
29	3	33	MET	9.0
26	Z	43	GLY	8.8
29	3	36	ILE	8.4
29	3	82	GLY	8.1
26	Z	59	GLU	7.9
26	Z	69	ASP	7.8
29	3	19	GLU	7.6
29	3	31	THR	7.5
21	U	54	THR	7.3
13	M	71	SER	7.3
29	3	14	CYS	7.2
26	Z	49	ARG	7.1
29	3	11	CYS	7.1
29	3	15	ASN	7.0

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
13	M	70	GLY	7.0
29	3	32	GLY	6.7
29	3	40	ARG	6.6
26	Z	44	ARG	6.2
26	Z	53	ILE	6.2
26	Z	54	GLU	6.1
29	3	43	ASN	6.1
26	Z	34	SER	6.1
21	U	46	ALA	6.1
29	3	71	CYS	6.0
29	3	62	THR	5.9
26	Z	42	TYR	5.7
29	3	56	PRO	5.6
26	Z	48	ARG	5.5
21	U	9	CYS	5.5
21	U	11	THR	5.4
29	3	78	HIS	5.4
29	3	16	GLU	5.4
26	Z	57	MET	5.4
13	M	80	GLY	5.3
26	Z	47	ARG	5.3
29	3	48	ASN	5.3
21	U	39	ASN	5.2
29	3	51	LYS	5.1
26	Z	77	GLY	5.0
9	I	74	ILE	5.0
26	Z	82	SER	5.0
29	3	47	GLY	4.9
26	Z	60	ASP	4.9
26	Z	45	VAL	4.9
29	3	44	SER	4.9
26	Z	81	CYS	4.9
26	Z	67	GLY	4.8
29	3	18	GLN	4.7
29	3	12	PRO	4.7
29	3	81	GLU	4.7
21	U	55	ALA	4.6
26	Z	51	ALA	4.6
26	Z	56	GLU	4.5
29	3	21	GLU	4.5
9	I	93	ALA	4.5
29	3	85	ALA	4.4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
9	I	71	ALA	4.4
29	3	28	GLY	4.4
21	U	40	ALA	4.3
21	U	32	CYS	4.3
29	3	27	SER	4.3
29	3	30	GLN	4.2
29	3	59	ASP	4.2
9	I	92	VAL	4.2
29	3	53	SER	4.2
29	3	13	HIS	4.1
9	I	106	GLN	4.1
29	3	74	CYS	4.1
1	A	237	GLY	4.1
21	U	53	ASP	4.1
4	D	57	THR	4.1
9	I	66	GLY	4.1
21	U	5	GLU	4.0
29	3	23	GLU	4.0
21	U	12	ASP	4.0
9	I	100	VAL	4.0
21	U	6	CYS	4.0
21	U	48	ASN	3.9
29	3	76	LYS	3.9
29	3	10	TYR	3.8
9	I	102	GLN	3.8
26	Z	63	CYS	3.8
29	3	75	GLY	3.7
29	3	29	ARG	3.7
9	I	70	THR	3.7
29	3	84	ARG	3.6
22	V	1	THR	3.6
31	9	1	U	3.6
21	U	52	THR	3.6
26	Z	71	VAL	3.6
29	3	45	GLY	3.5
29	3	60	LYS	3.5
29	3	77	ALA	3.5
9	I	67	VAL	3.5
21	U	10	GLY	3.5
9	I	112	LEU	3.5
29	3	9	THR	3.3
29	3	91	GLN	3.3

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
21	U	36	CYS	3.3
29	3	61	PRO	3.3
26	Z	61	HIS	3.3
9	I	78	ALA	3.3
9	I	104	ALA	3.2
4	D	18	ILE	3.2
29	3	25	VAL	3.2
9	I	99	GLN	3.2
9	I	72	GLU	3.2
21	U	29	THR	3.2
4	D	88	LEU	3.2
21	U	31	PHE	3.2
29	3	17	HIS	3.2
4	D	69	ILE	3.2
21	U	56	ARG	3.2
29	3	83	TRP	3.2
29	3	58	GLY	3.2
22	V	38	GLY	3.1
29	3	63	LYS	3.1
26	Z	80	GLN	3.1
26	Z	52	GLU	3.1
29	3	72	GLY	3.1
29	3	69	TYR	3.1
9	I	132	VAL	3.1
9	I	76	ASP	3.0
26	Z	65	ASN	3.0
26	Z	68	GLU	3.0
21	U	28	THR	3.0
9	I	73	LEU	2.9
29	3	64	LYS	2.9
24	X	88	GLU	2.9
9	I	110	ASP	2.9
26	Z	40	ALA	2.9
26	Z	39	GLY	2.8
26	Z	104	ARG	2.8
4	D	92	GLU	2.8
22	V	39	ALA	2.8
21	U	30	HIS	2.8
22	V	40	PRO	2.8
29	3	73	GLU	2.8
26	Z	70	ARG	2.8
4	D	63	ILE	2.8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
9	I	128	THR	2.7
21	U	24	LYS	2.7
21	U	51	TRP	2.7
13	M	79	ALA	2.7
29	3	70	ARG	2.7
13	M	82	ARG	2.7
21	U	8	TYR	2.7
29	3	8	ASN	2.7
29	3	49	ASP	2.6
30	0	1198	U	2.6
29	3	6	ARG	2.6
26	Z	37	ARG	2.6
29	3	1	MET	2.6
10	J	4	ALA	2.6
21	U	43	GLY	2.6
21	U	4	ARG	2.5
4	D	44	ILE	2.5
4	D	26	GLY	2.5
9	I	68	PRO	2.5
29	3	65	THR	2.5
26	Z	83	TYR	2.5
29	3	68	LYS	2.5
9	I	105	GLU	2.5
26	Z	92	SER	2.4
26	Z	62	ALA	2.4
4	D	93	LEU	2.4
13	M	72	ALA	2.4
29	3	3	MET	2.4
21	U	7	ASP	2.4
26	Z	78	ILE	2.4
9	I	108	HIS	2.3
21	U	23	HIS	2.3
4	D	87	ALA	2.3
21	U	49	LEU	2.3
9	I	75	LYS	2.3
30	0	1172	G	2.3
9	I	79	GLY	2.3
29	3	46	ILE	2.3
19	S	81	ILE	2.3
9	I	113	SER	2.3
21	U	41	ASP	2.2
12	L	60	GLU	2.2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
9	I	81	GLU	2.2
9	I	94	ASP	2.2
29	3	88	LEU	2.2
4	D	135	VAL	2.2
9	I	80	PHE	2.2
26	Z	85	ASP	2.2
4	D	80	ALA	2.1
26	Z	74	GLN	2.1
4	D	85	GLN	2.1
26	Z	103	VAL	2.1
4	D	27	ILE	2.1
13	M	77	HIS	2.0
21	U	50	GLU	2.0
26	Z	66	CYS	2.0
6	F	106	ALA	2.0
28	2	39	ARG	2.0
21	U	44	ARG	2.0
9	I	69	PRO	2.0
21	U	20	MET	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
30	OMG	0	2588	24/25	0.98	0.13	-	39,41,42,45	0
30	UR3	0	2619	21/22	0.98	0.14	-	39,43,45,48	0
30	1MA	0	628	23/24	0.98	0.15	-	31,36,38,38	0
30	PSU	0	2621	20/21	0.98	0.18	-	40,43,44,44	0
30	OMU	0	2587	21/22	0.98	0.12	-	41,44,50,50	0

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
35	NA	0	8559	1/1	0.79	0.45	33.62	122,122,122,122	0
35	NA	0	8528	1/1	0.64	0.91	31.75	83,83,83,83	0
35	NA	0	8562	1/1	0.88	0.53	29.60	89,89,89,89	0
34	SR	0	8957	1/1	0.56	0.75	22.57	200,200,200,200	0
35	NA	0	8545	1/1	0.88	0.24	19.26	33,33,33,33	0
35	NA	0	8564	1/1	0.86	0.35	13.61	57,57,57,57	0
33	CL	0	8816	1/1	0.96	0.39	12.34	94,94,94,94	0
34	SR	0	8947	1/1	0.83	0.30	10.53	194,194,194,194	0
35	NA	R	8575	1/1	0.98	0.34	10.32	89,89,89,89	0
35	NA	0	8530	1/1	0.88	0.36	8.58	49,49,49,49	0
35	NA	0	8546	1/1	0.86	0.48	8.53	80,80,80,80	0
34	SR	0	8969	1/1	0.78	0.30	8.16	192,192,192,192	0
35	NA	0	8553	1/1	0.63	0.32	8.15	70,70,70,70	0
35	NA	0	8535	1/1	0.83	0.20	7.84	64,64,64,64	0
34	SR	B	8987	1/1	0.87	0.39	7.69	200,200,200,200	0
35	NA	0	8513	1/1	0.96	0.34	7.62	66,66,66,66	0
35	NA	0	8567	1/1	0.51	0.30	7.25	68,68,68,68	0
32	MG	0	8016	1/1	0.93	0.21	6.97	48,48,48,48	0
35	NA	0	8519	1/1	0.92	0.26	6.82	51,51,51,51	0
35	NA	0	8550	1/1	0.96	0.28	6.15	47,47,47,47	0
35	NA	0	8556	1/1	0.81	0.45	5.38	63,63,63,63	0
35	NA	0	8555	1/1	0.98	0.34	5.04	50,50,50,50	0
32	MG	0	8014	1/1	0.98	0.19	4.75	21,21,21,21	0
35	NA	0	8552	1/1	0.90	0.26	4.61	58,58,58,58	0
35	NA	0	8521	1/1	0.93	0.21	4.17	53,53,53,53	0
35	NA	0	8558	1/1	0.98	0.21	3.42	44,44,44,44	0
35	NA	0	8571	1/1	0.82	0.17	3.27	46,46,46,46	0
32	MG	0	8011	1/1	1.00	0.21	3.02	24,24,24,24	0
35	NA	0	8522	1/1	0.90	0.21	2.97	45,45,45,45	0
33	CL	0	8811	1/1	0.99	0.37	2.88	79,79,79,79	0
32	MG	0	8009	1/1	0.98	0.21	2.69	24,24,24,24	0
34	SR	0	8904	1/1	1.00	0.17	2.50	58,58,58,58	0
33	CL	0	8805	1/1	0.99	0.14	2.38	70,70,70,70	0
32	MG	0	8044	1/1	0.99	0.14	2.28	52,52,52,52	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
32	MG	A	8051	1/1	0.84	0.22	2.09	101,101,101,101	0
35	NA	0	8569	1/1	0.99	0.21	2.06	67,67,67,67	0
32	MG	0	8004	1/1	0.96	0.18	1.74	21,21,21,21	0
32	MG	0	8008	1/1	0.99	0.14	1.74	26,26,26,26	0
32	MG	0	8003	1/1	0.99	0.17	1.61	22,22,22,22	0
35	NA	0	8517	1/1	0.99	0.15	1.54	21,21,21,21	0
32	MG	0	8015	1/1	0.99	0.13	1.28	25,25,25,25	0
32	MG	0	8088	1/1	0.94	0.16	1.25	35,35,35,35	0
34	SR	0	8903	1/1	1.00	0.13	1.24	46,46,46,46	0
35	NA	0	8507	1/1	0.86	0.16	1.23	32,32,32,32	0
32	MG	0	8062	1/1	0.95	0.20	1.23	57,57,57,57	0
32	MG	0	8085	1/1	0.99	0.12	1.22	67,67,67,67	0
34	SR	0	8902	1/1	0.99	0.16	1.03	67,67,67,67	0
35	NA	0	8534	1/1	0.97	0.18	0.99	37,37,37,37	0
32	MG	0	8010	1/1	0.93	0.17	0.91	24,24,24,24	0
35	NA	0	8537	1/1	1.00	0.17	0.91	29,29,29,29	0
35	NA	0	8560	1/1	0.94	0.79	0.89	74,74,74,74	0
32	MG	0	8084	1/1	0.99	0.14	0.72	24,24,24,24	0
32	MG	0	8065	1/1	0.95	0.12	0.57	50,50,50,50	0
34	SR	0	8975	1/1	0.64	0.11	0.52	171,171,171,171	0
34	SR	0	8985	1/1	0.44	0.12	0.50	182,182,182,182	0
35	NA	0	8515	1/1	0.87	0.15	0.06	44,44,44,44	0
37	CD	3	8704	1/1	0.90	0.71	-0.04	200,200,200,200	0
32	MG	0	8080	1/1	0.95	0.30	-0.13	68,68,68,68	0
33	CL	B	8819	1/1	0.99	0.15	-0.15	59,59,59,59	0
34	SR	0	8923	1/1	0.98	0.12	-0.25	85,85,85,85	0
32	MG	0	8006	1/1	0.98	0.13	-0.34	20,20,20,20	0
37	CD	1	8702	1/1	1.00	0.13	-0.35	61,61,61,61	0
32	MG	0	8021	1/1	0.98	0.11	-0.43	25,25,25,25	0
32	MG	0	8028	1/1	1.00	0.13	-0.47	19,19,19,19	0
35	NA	0	8557	1/1	0.40	0.08	-0.52	59,59,59,59	0
32	MG	0	8047	1/1	0.90	0.15	-0.57	67,67,67,67	0
32	MG	0	8045	1/1	0.99	0.10	-0.63	24,24,24,24	0
35	NA	0	8523	1/1	0.99	0.11	-0.66	51,51,51,51	0
35	NA	Q	8540	1/1	0.96	0.11	-0.70	67,67,67,67	0
35	NA	0	8542	1/1	0.98	0.17	-0.70	51,51,51,51	0
33	CL	J	8821	1/1	0.94	0.12	-0.72	66,66,66,66	0
36	K	M	8402	1/1	0.98	0.11	-0.79	60,60,60,60	0
32	MG	0	8034	1/1	0.98	0.13	-0.90	53,53,53,53	0
34	SR	0	8943	1/1	0.96	0.09	-0.94	72,72,72,72	0
34	SR	0	8972	1/1	0.96	0.10	-1.00	150,150,150,150	0
32	MG	B	8043	1/1	0.96	0.11	-1.21	53,53,53,53	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
32	MG	0	8001	1/1	0.99	0.13	-1.26	26,26,26,26	0
34	SR	0	8964	1/1	0.88	0.08	-1.32	129,129,129,129	0
34	SR	0	8944	1/1	0.80	0.08	-1.42	165,165,165,165	0
35	NA	J	8538	1/1	0.94	0.08	-1.42	49,49,49,49	0
32	MG	0	8012	1/1	0.99	0.15	-1.50	15,15,15,15	0
34	SR	3	8932	1/1	0.82	0.08	-1.51	158,158,158,158	0
33	CL	O	8808	1/1	0.99	0.10	-1.53	87,87,87,87	0
37	CD	U	8701	1/1	0.74	0.35	-1.61	200,200,200,200	0
32	MG	0	8058	1/1	0.99	0.06	-1.74	22,22,22,22	0
35	NA	M	8539	1/1	0.96	0.09	-1.85	32,32,32,32	0
34	SR	A	8930	1/1	0.99	0.07	-2.06	125,125,125,125	0
37	CD	Z	8703	1/1	0.86	0.28	-2.09	200,200,200,200	0
34	SR	0	8936	1/1	0.98	0.08	-2.17	87,87,87,87	0
35	NA	0	8533	1/1	0.96	0.08	-2.19	53,53,53,53	0
35	NA	0	8504	1/1	0.95	0.10	-2.27	27,27,27,27	0
34	SR	0	8984	1/1	0.91	0.07	-2.34	105,105,105,105	0
34	SR	A	8929	1/1	0.96	0.04	-2.47	117,117,117,117	0
34	SR	0	9001	1/1	0.55	0.08	-2.53	166,166,166,166	0
32	MG	T	8057	1/1	0.97	0.04	-2.71	63,63,63,63	0
35	NA	0	8568	1/1	0.99	0.10	-2.75	38,38,38,38	0
33	CL	K	8812	1/1	0.95	0.07	-2.82	48,48,48,48	0
33	CL	3	8804	1/1	0.90	0.19	-2.98	120,120,120,120	0
32	MG	0	8025	1/1	0.97	0.10	-3.14	30,30,30,30	0
34	SR	0	8910	1/1	0.94	0.08	-3.23	99,99,99,99	0
34	SR	0	8992	1/1	0.98	0.08	-3.40	130,130,130,130	0
32	MG	0	8052	1/1	0.91	0.04	-3.67	51,51,51,51	0
34	SR	0	8948	1/1	0.97	0.08	-3.90	103,103,103,103	0
32	MG	Y	8086	1/1	0.97	0.06	-4.07	37,37,37,37	0
33	CL	M	8818	1/1	0.99	0.05	-4.17	39,39,39,39	0
32	MG	0	8087	1/1	0.98	0.09	-4.79	26,26,26,26	0
32	MG	0	8050	1/1	0.91	0.08	-4.90	52,52,52,52	0
32	MG	0	8072	1/1	0.99	0.08	-5.76	47,47,47,47	0
32	MG	0	8002	1/1	0.98	0.08	-6.07	29,29,29,29	0
32	MG	0	8013	1/1	0.99	0.04	-7.18	24,24,24,24	0
34	SR	0	8945	1/1	0.95	0.06	-8.05	107,107,107,107	0
34	SR	0	8949	1/1	0.99	0.05	-11.90	102,102,102,102	0
33	CL	0	8803	1/1	0.95	0.14	-	69,69,69,69	0
32	MG	0	8040	1/1	0.96	0.21	-	54,54,54,54	0
32	MG	0	8007	1/1	1.00	0.19	-	18,18,18,18	0
35	NA	0	8501	1/1	0.96	0.14	-	43,43,43,43	0
34	SR	1	8913	1/1	0.99	0.11	-	100,100,100,100	0
34	SR	0	8982	1/1	0.78	1.84	-	200,200,200,200	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
35	NA	0	8563	1/1	0.52	0.67	-	65,65,65,65	0
34	SR	0	8995	1/1	0.97	0.14	-	140,140,140,140	0
34	SR	0	8914	1/1	0.95	0.20	-	105,105,105,105	0
32	MG	0	8026	1/1	1.00	0.04	-	27,27,27,27	0
34	SR	0	8908	1/1	0.98	0.13	-	77,77,77,77	0
35	NA	S	8510	1/1	0.96	0.04	-	26,26,26,26	0
34	SR	0	8990	1/1	0.96	0.15	-	125,125,125,125	0
34	SR	0	8968	1/1	0.82	0.15	-	177,177,177,177	0
34	SR	0	8973	1/1	0.80	0.14	-	112,112,112,112	0
35	NA	0	8544	1/1	0.94	0.11	-	41,41,41,41	0
32	MG	0	8033	1/1	0.94	0.13	-	40,40,40,40	0
34	SR	0	8931	1/1	0.83	0.07	-	110,110,110,110	0
34	SR	1	8952	1/1	1.00	0.12	-	72,72,72,72	0
34	SR	F	9005	1/1	0.92	0.09	-	131,131,131,131	0
34	SR	0	8965	1/1	0.91	0.07	-	127,127,127,127	0
32	MG	0	8019	1/1	0.99	0.15	-	23,23,23,23	0
35	NA	0	8514	1/1	0.99	0.19	-	17,17,17,17	0
35	NA	0	8509	1/1	0.92	0.14	-	54,54,54,54	0
34	SR	0	8924	1/1	0.97	0.17	-	133,133,133,133	0
32	MG	0	8056	1/1	0.99	0.09	-	75,75,75,75	0
34	SR	0	8905	1/1	0.99	0.23	-	62,62,62,62	0
34	SR	0	9008	1/1	0.99	0.17	-	97,97,97,97	0
34	SR	0	8988	1/1	0.81	0.14	-	170,170,170,170	0
34	SR	0	8907	1/1	1.00	0.12	-	40,40,40,40	0
35	NA	0	8520	1/1	0.98	0.10	-	39,39,39,39	0
32	MG	0	8023	1/1	0.98	0.18	-	24,24,24,24	0
35	NA	0	8548	1/1	0.85	0.13	-	68,68,68,68	0
33	CL	0	8817	1/1	0.96	0.19	-	69,69,69,69	0
32	MG	0	8066	1/1	0.98	0.31	-	75,75,75,75	0
32	MG	0	8031	1/1	0.99	0.23	-	52,52,52,52	0
34	SR	0	8909	1/1	0.98	0.13	-	89,89,89,89	0
32	MG	0	8079	1/1	1.00	0.11	-	36,36,36,36	0
35	NA	0	8518	1/1	0.79	0.26	-	75,75,75,75	0
34	SR	0	8953	1/1	0.89	0.07	-	200,200,200,200	0
34	SR	0	8911	1/1	0.98	0.06	-	79,79,79,79	0
34	SR	0	9000	1/1	0.93	0.32	-	200,200,200,200	0
34	SR	0	8974	1/1	0.57	0.14	-	164,164,164,164	0
35	NA	0	8551	1/1	0.98	0.15	-	55,55,55,55	0
34	SR	0	8938	1/1	0.98	0.07	-	164,164,164,164	0
33	CL	0	8814	1/1	0.78	0.18	-	72,72,72,72	0
35	NA	0	8554	1/1	0.96	0.55	-	65,65,65,65	0
34	SR	0	8921	1/1	0.98	0.09	-	75,75,75,75	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
35	NA	0	8516	1/1	0.96	0.08	-	20,20,20,20	0
35	NA	0	8566	1/1	0.81	0.33	-	62,62,62,62	0
34	SR	0	8956	1/1	0.91	0.05	-	151,151,151,151	0
34	SR	9	9003	1/1	0.90	0.09	-	177,177,177,177	0
32	MG	0	8036	1/1	0.90	0.05	-	37,37,37,37	0
35	NA	0	8549	1/1	0.90	0.17	-	77,77,77,77	0
32	MG	0	8038	1/1	0.99	0.05	-	61,61,61,61	0
34	SR	0	8954	1/1	1.00	0.12	-	103,103,103,103	0
34	SR	0	8983	1/1	0.95	0.28	-	191,191,191,191	0
32	MG	0	8070	1/1	0.99	0.10	-	40,40,40,40	0
35	NA	0	8526	1/1	0.95	0.13	-	33,33,33,33	0
34	SR	0	8920	1/1	0.97	0.05	-	106,106,106,106	0
35	NA	0	8541	1/1	0.83	0.24	-	54,54,54,54	0
33	CL	0	8813	1/1	0.99	0.03	-	46,46,46,46	0
34	SR	0	8997	1/1	0.54	0.85	-	194,194,194,194	0
33	CL	Y	8820	1/1	0.94	0.11	-	47,47,47,47	0
34	SR	0	8979	1/1	0.61	0.18	-	198,198,198,198	0
37	CD	O	8705	1/1	0.98	0.08	-	93,93,93,93	0
32	MG	0	8082	1/1	0.95	0.12	-	66,66,66,66	0
32	MG	2	8060	1/1	0.86	0.10	-	35,35,35,35	0
34	SR	0	8998	1/1	0.76	0.31	-	184,184,184,184	0
32	MG	0	8089	1/1	0.97	0.17	-	59,59,59,59	0
34	SR	9	8978	1/1	1.00	0.07	-	125,125,125,125	0
32	MG	0	8024	1/1	0.98	0.12	-	96,96,96,96	0
34	SR	0	8939	1/1	0.88	0.08	-	152,152,152,152	0
35	NA	0	8505	1/1	0.90	1.17	-	53,53,53,53	0
34	SR	0	8916	1/1	0.94	0.10	-	114,114,114,114	0
35	NA	0	8502	1/1	0.99	0.05	-	56,56,56,56	0
34	SR	0	8934	1/1	0.99	0.09	-	99,99,99,99	0
34	SR	0	8922	1/1	0.75	0.29	-	169,169,169,169	0
35	NA	9	8572	1/1	0.82	0.17	-	71,71,71,71	0
34	SR	0	8901	1/1	0.98	0.14	-	63,63,63,63	0
34	SR	0	8958	1/1	0.98	0.07	-	114,114,114,114	0
34	SR	0	8933	1/1	0.99	0.07	-	126,126,126,126	0
34	SR	0	8989	1/1	0.86	0.19	-	200,200,200,200	0
32	MG	0	8017	1/1	0.98	0.11	-	20,20,20,20	0
32	MG	0	8068	1/1	0.92	0.11	-	49,49,49,49	0
32	MG	9	8074	1/1	0.99	0.05	-	63,63,63,63	0
32	MG	0	8037	1/1	0.94	0.16	-	76,76,76,76	0
32	MG	0	8029	1/1	0.97	0.07	-	68,68,68,68	0
33	CL	A	8809	1/1	0.97	0.34	-	100,100,100,100	0
34	SR	0	8942	1/1	0.88	0.07	-	130,130,130,130	0

*Continued on next page...*



*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
32	MG	0	8075	1/1	0.91	0.09	-	83,83,83,83	0
32	MG	0	8078	1/1	0.98	0.23	-	51,51,51,51	0
36	K	0	8401	1/1	0.75	0.14	-	156,156,156,156	0
32	MG	0	8020	1/1	0.97	0.14	-	29,29,29,29	0
32	MG	0	8063	1/1	0.79	0.23	-	86,86,86,86	0
32	MG	0	8067	1/1	0.98	0.14	-	32,32,32,32	0
32	MG	0	8076	1/1	0.99	0.10	-	27,27,27,27	0
32	MG	0	8059	1/1	0.99	0.12	-	53,53,53,53	0
32	MG	0	8030	1/1	0.99	0.34	-	86,86,86,86	0
34	SR	0	8940	1/1	0.98	0.11	-	77,77,77,77	0
32	MG	0	8077	1/1	0.99	0.10	-	43,43,43,43	0
34	SR	0	8963	1/1	0.98	0.06	-	123,123,123,123	0
35	NA	0	8547	1/1	0.94	0.68	-	47,47,47,47	0
35	NA	0	8531	1/1	0.99	0.10	-	15,15,15,15	0
34	SR	0	8960	1/1	0.76	0.05	-	152,152,152,152	0
34	SR	0	8962	1/1	0.67	0.08	-	179,179,179,179	0
32	MG	0	8005	1/1	0.98	0.22	-	34,34,34,34	0
34	SR	R	8912	1/1	1.00	0.12	-	86,86,86,86	0
35	NA	0	8511	1/1	0.93	0.10	-	48,48,48,48	0
35	NA	0	8524	1/1	0.99	0.39	-	54,54,54,54	0
32	MG	0	8048	1/1	0.99	0.21	-	20,20,20,20	0
33	CL	0	8815	1/1	0.84	0.09	-	87,87,87,87	0
32	MG	3	8090	1/1	0.96	0.12	-	80,80,80,80	0
34	SR	3	8999	1/1	0.91	0.28	-	172,172,172,172	0
32	MG	0	8053	1/1	0.98	0.05	-	45,45,45,45	0
34	SR	0	8971	1/1	0.55	0.10	-	170,170,170,170	0
32	MG	0	8081	1/1	0.86	0.32	-	80,80,80,80	0
35	NA	0	8561	1/1	0.96	0.36	-	57,57,57,57	0
34	SR	0	8986	1/1	0.62	0.47	-	200,200,200,200	0
34	SR	0	9006	1/1	0.31	0.83	-	180,180,180,180	0
34	SR	0	8928	1/1	0.89	0.09	-	146,146,146,146	0
34	SR	B	8950	1/1	0.98	0.15	-	113,113,113,113	0
34	SR	0	8976	1/1	0.91	0.24	-	197,197,197,197	0
32	MG	0	8055	1/1	0.97	0.10	-	45,45,45,45	0
34	SR	0	8955	1/1	0.85	0.18	-	200,200,200,200	0
32	MG	0	8039	1/1	0.94	0.18	-	71,71,71,71	0
34	SR	0	8996	1/1	0.96	0.21	-	199,199,199,199	0
34	SR	0	8951	1/1	0.98	0.08	-	139,139,139,139	0
32	MG	K	8054	1/1	0.92	0.15	-	40,40,40,40	0
34	SR	0	8981	1/1	0.91	0.14	-	157,157,157,157	0
32	MG	0	8092	1/1	0.98	0.02	-	44,44,44,44	0
35	NA	0	8570	1/1	0.88	0.07	-	25,25,25,25	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
34	SR	0	9004	1/1	0.45	1.04	-	200,200,200,200	0
35	NA	C	8503	1/1	0.98	0.17	-	45,45,45,45	0
33	CL	R	8806	1/1	0.95	0.11	-	47,47,47,47	0
35	NA	0	8527	1/1	0.96	0.15	-	54,54,54,54	0
34	SR	0	8937	1/1	0.93	0.17	-	100,100,100,100	0
34	SR	0	8970	1/1	0.94	0.04	-	131,131,131,131	0
32	MG	B	8042	1/1	0.90	0.08	-	56,56,56,56	0
32	MG	0	8022	1/1	0.99	0.12	-	17,17,17,17	0
32	MG	0	8027	1/1	0.97	0.12	-	26,26,26,26	0
34	SR	0	8994	1/1	0.93	0.24	-	200,200,200,200	0
32	MG	0	8041	1/1	0.96	0.31	-	36,36,36,36	0
33	CL	J	8801	1/1	0.96	0.13	-	71,71,71,71	0
33	CL	0	8822	1/1	0.95	0.60	-	97,97,97,97	0
35	NA	0	8506	1/1	0.95	0.53	-	58,58,58,58	0
34	SR	0	8926	1/1	0.98	0.09	-	109,109,109,109	0
35	NA	0	8525	1/1	0.86	0.26	-	85,85,85,85	0
32	MG	0	8073	1/1	0.98	0.06	-	51,51,51,51	0
34	SR	S	8961	1/1	0.98	0.05	-	126,126,126,126	0
35	NA	0	8512	1/1	0.99	0.08	-	36,36,36,36	0
34	SR	0	8959	1/1	0.56	0.29	-	200,200,200,200	0
32	MG	0	8018	1/1	0.98	0.14	-	34,34,34,34	0
35	NA	0	8573	1/1	0.82	0.27	-	55,55,55,55	0
34	SR	0	8967	1/1	0.81	0.05	-	133,133,133,133	0
34	SR	0	9007	1/1	0.82	0.23	-	179,179,179,179	0
33	CL	N	8807	1/1	0.94	0.35	-	99,99,99,99	0
34	SR	0	8966	1/1	0.99	0.07	-	97,97,97,97	0
32	MG	0	8061	1/1	0.99	0.18	-	19,19,19,19	0
34	SR	0	8977	1/1	0.72	0.12	-	181,181,181,181	0
34	SR	0	8919	1/1	0.75	0.32	-	200,200,200,200	0
33	CL	J	8802	1/1	0.54	0.08	-	76,76,76,76	0
32	MG	0	8046	1/1	0.92	0.13	-	26,26,26,26	0
34	SR	A	8993	1/1	0.86	0.08	-	159,159,159,159	0
32	MG	0	8083	1/1	0.97	0.12	-	71,71,71,71	0
34	SR	0	8917	1/1	0.96	0.10	-	109,109,109,109	0
32	MG	0	8093	1/1	0.87	0.06	-	28,28,28,28	0
34	SR	0	8918	1/1	0.98	0.10	-	71,71,71,71	0
32	MG	0	8064	1/1	0.97	0.06	-	33,33,33,33	0
34	SR	9	8980	1/1	0.75	0.14	-	182,182,182,182	0
32	MG	0	8049	1/1	0.92	0.38	-	74,74,74,74	0
33	CL	L	8810	1/1	0.93	0.09	-	64,64,64,64	0
35	NA	0	8565	1/1	0.92	0.95	-	70,70,70,70	0
34	SR	0	8915	1/1	0.87	0.07	-	118,118,118,118	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
34	SR	0	8946	1/1	0.85	0.12	-	123,123,123,123	0
34	SR	0	8906	1/1	1.00	0.20	-	64,64,64,64	0
35	NA	0	8508	1/1	0.95	0.56	-	61,61,61,61	0
32	MG	0	8032	1/1	0.91	0.05	-	27,27,27,27	0
32	MG	0	8071	1/1	0.89	0.13	-	31,31,31,31	0
32	MG	0	8091	1/1	0.73	0.07	-	58,58,58,58	0
34	SR	0	8941	1/1	0.98	0.18	-	122,122,122,122	0
34	SR	0	9002	1/1	0.84	0.06	-	157,157,157,157	0
32	MG	0	8069	1/1	0.90	0.19	-	55,55,55,55	0
35	NA	9	8543	1/1	0.99	0.12	-	38,38,38,38	0
34	SR	0	8935	1/1	0.98	0.09	-	87,87,87,87	0
35	NA	0	8536	1/1	0.97	0.07	-	40,40,40,40	0
35	NA	0	8574	1/1	0.96	0.35	-	54,54,54,54	0
35	NA	R	8532	1/1	0.94	0.13	-	37,37,37,37	0
35	NA	0	8529	1/1	0.98	0.18	-	41,41,41,41	0
32	MG	0	8035	1/1	0.96	0.10	-	61,61,61,61	0
34	SR	0	8991	1/1	0.88	0.34	-	193,193,193,193	0
34	SR	0	8927	1/1	0.94	0.20	-	196,196,196,196	0
34	SR	0	8925	1/1	0.99	0.15	-	94,94,94,94	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.