



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:13 PM UTC

PDB ID : 1XMO / pdb_00001xmo
Title : Crystal Structure of mnm5U34t6A37-tRNA^{Lys}UUU Complexed with AAG-mRNA in the Decoding Center
Authors : Murphy, F.V.; Ramakrishnan, V.; Malkiewicz, A.; Agris, P.F.
Deposited on : 2004-10-04
Resolution : 3.25 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

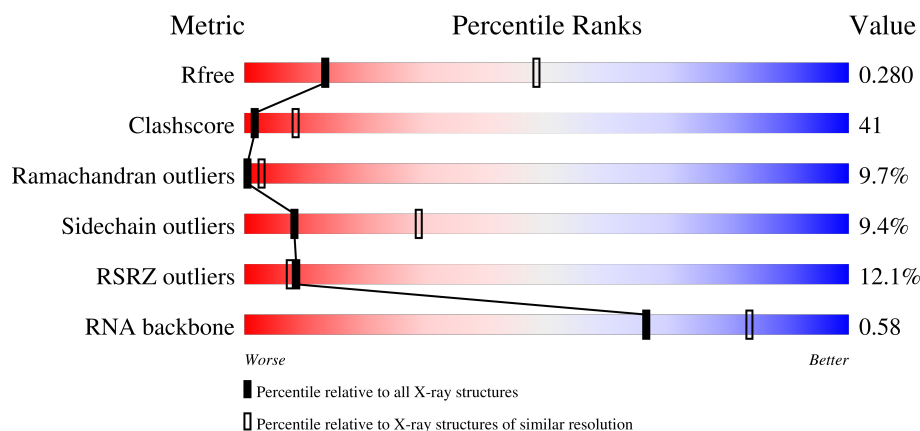
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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.



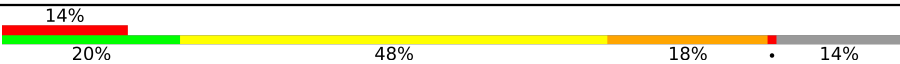
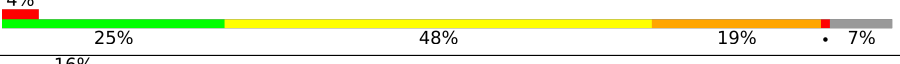
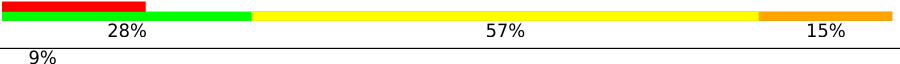
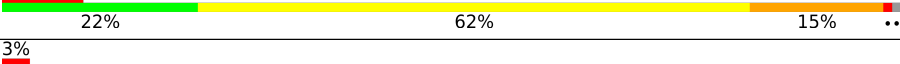
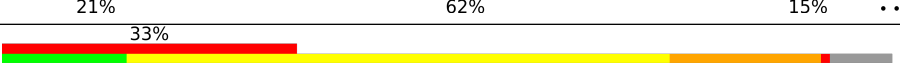
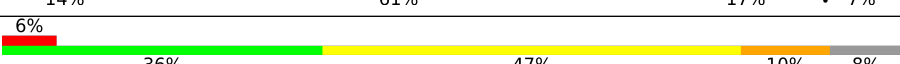
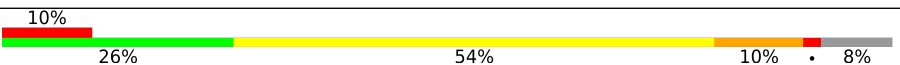
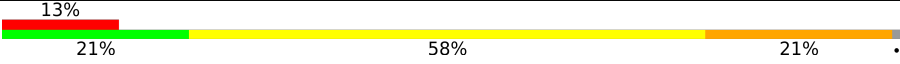
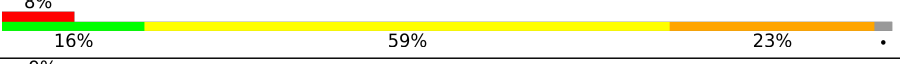
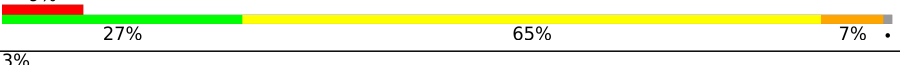
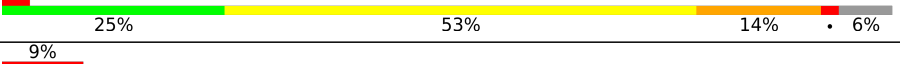
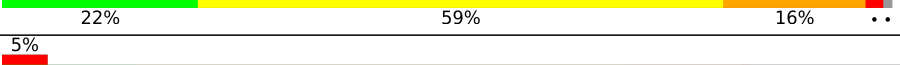
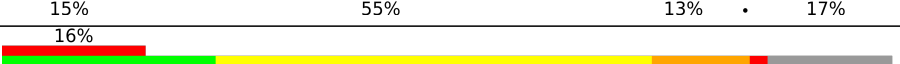
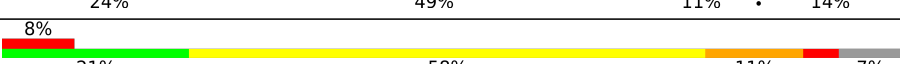
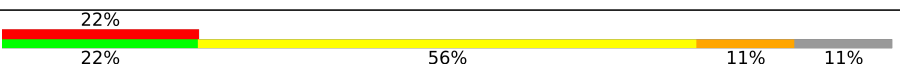
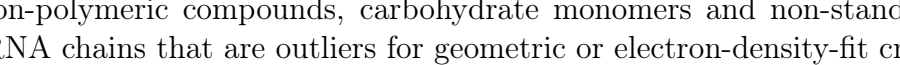
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1605 (3.30-3.22)
Clashscore	190562	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)
RSRZ outliers	180081	1605 (3.30-3.22)
RNA backbone	3983	1006 (3.54-2.98)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1522	12% 27% 55% 13% • •
2	W	3	100%
3	X	11	45% 36% 55% 9%
4	B	256	14% 13% 62% 14% • 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	C	239	
6	D	209	
7	E	162	
8	F	101	
9	G	156	
10	H	138	
11	I	128	
12	J	105	
13	K	129	
14	L	135	
15	M	126	
16	N	61	
17	O	89	
18	P	88	
19	Q	105	
20	R	88	
21	S	93	
22	T	106	
23	V	27	

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
25	MG	A	1562	-	-	-	X
25	MG	A	1615	-	-	-	X
25	MG	A	214	-	-	-	X
3	T6A	X	37	X	-	-	-

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 52063 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 RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1507	Total	C	N	O	P	0	0	0
			32380	14414	5990	10470	1506			

- Molecule 2 is a RNA chain called A-Site Messenger RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	W	3	Total	C	N	O	P	0	0	0
			64	30	15	17	2			

- Molecule 3 is a RNA chain called Anticodon Transfer RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	X	11	Total	C	N	O	P	0	0	0
			239	110	38	81	10			

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	234	Total	C	N	O	S	0	0	0
			1900	1213	341	341	5			

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	206	Total	C	N	O	S	0	0	0
			1612	1016	314	281	1			

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	D	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	150	Total	C	N	O	S	0	0	0
			1146	724	217	201	4			

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	G	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	H	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	I	127	Total	C	N	O		0	0	0
			1011	639	198	174				

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	J	98	Total	C	N	O	S	0	0	0
			792	498	156	137	1			

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	L	124	Total	C	N	O	S	0	0	0
			970	611	195	163	1			

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	M	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			

- Molecule 16 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	N	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	O	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	P	83	Total	C	N	O	S	0	0	0
			700	443	139	117	1			

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	Q	104	Total	C	N	O	S	0	0	0
			857	547	161	147	2			

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
20	R	73	Total	C	N	O	0	0	0
			597	380	118	99			

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	S	80	Total	C	N	O	S	0	0	0
			647	414	119	112	2			

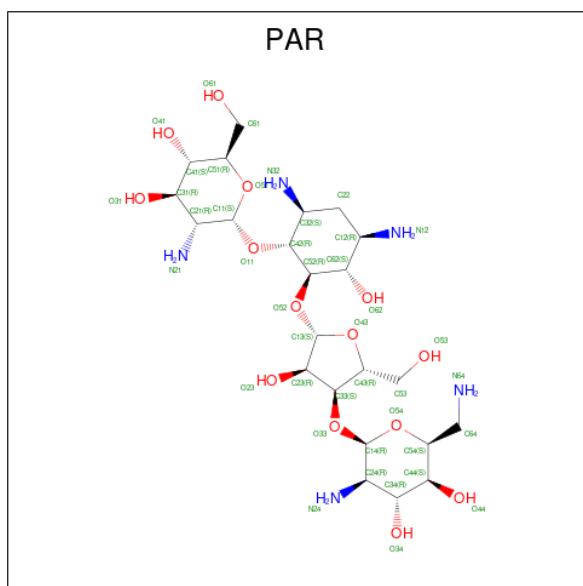
- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	T	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
23	V	24	Total	C	N	O	0	0	0
			208	128	50	30			

- Molecule 24 is PAROMOMYCIN (CCD ID: PAR) (formula: $C_{23}H_{45}N_5O_{14}$).



Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	X	2	Total 2	Mg 2	0	0
25	J	1	Total 1	Mg 1	0	0

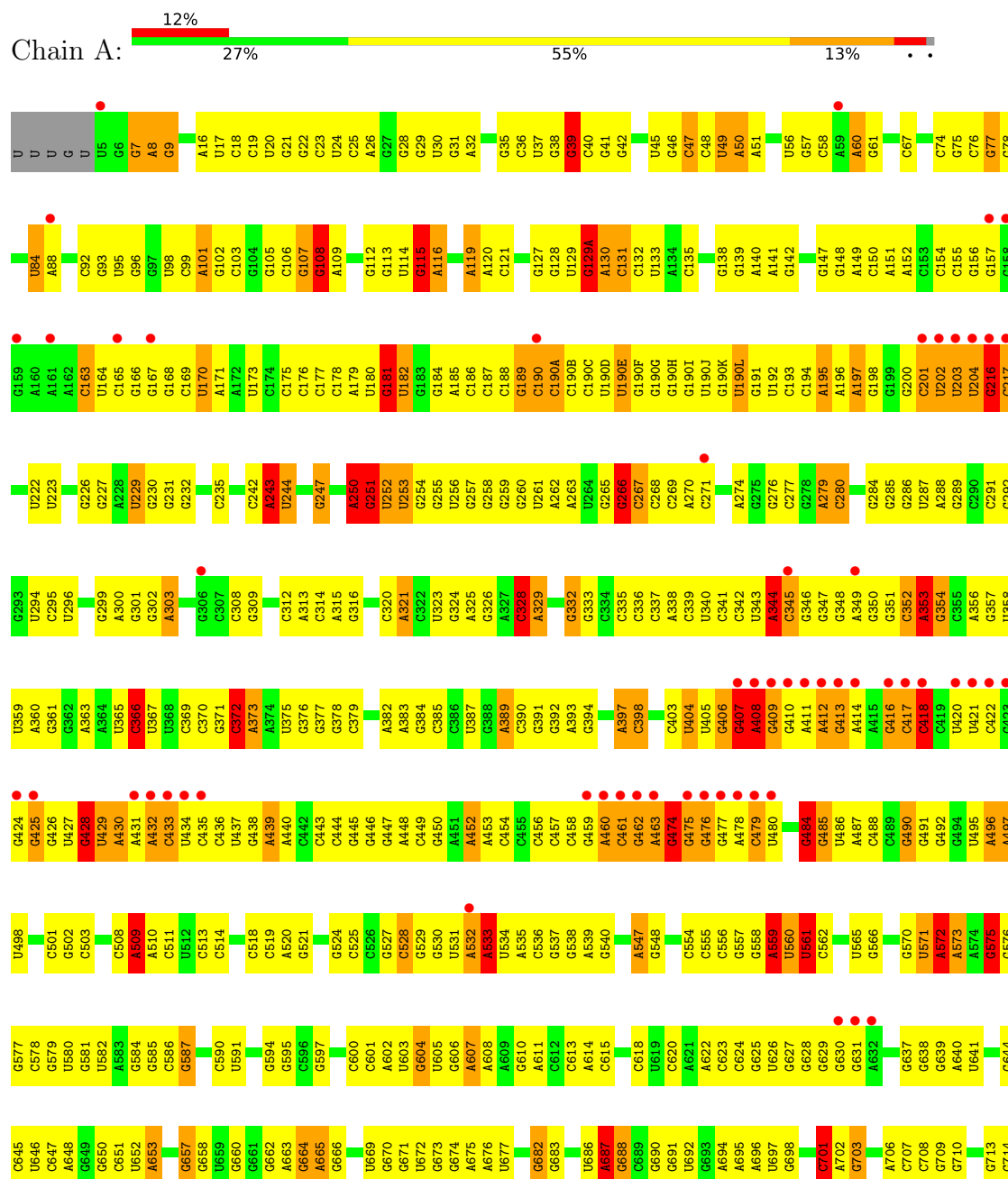
- Molecule 26 is ZINC ION (CCD ID: ZN) (formula: Zn).

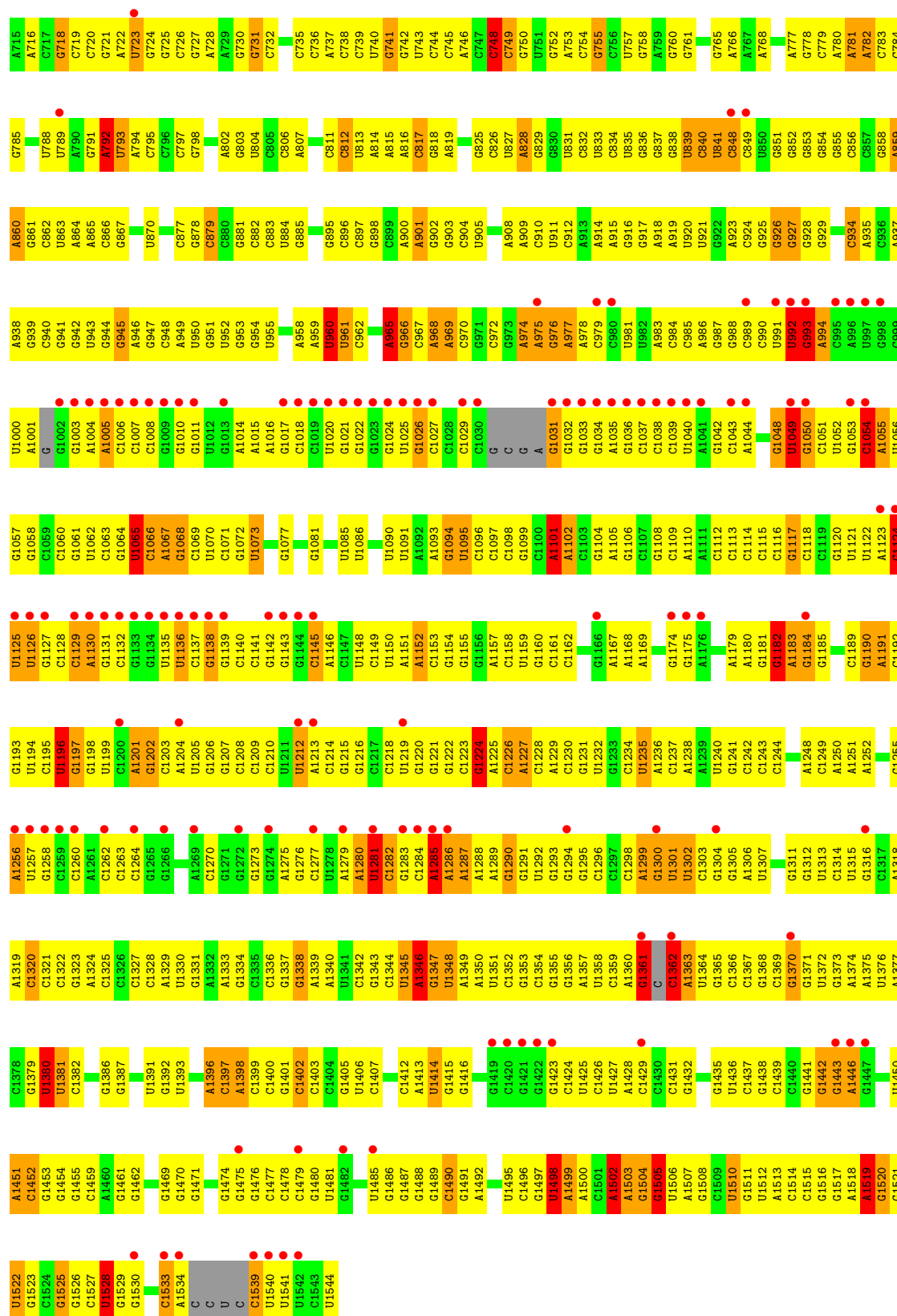
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	D	1	Total 1	Zn 1	0	0
26	N	1	Total 1	Zn 1	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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: 16S ribosomal RNA





Chain W:  100%

A1
A2
G3

• Molecule 3: Anticodon Transfer RNA

Chain X:  45%

G30
A31
C32
U33
U34
U35
U36
A37
A38
U39
C40

• Molecule 4: 30S ribosomal protein S2

Chain B:  14%

MET PRO VAL GLU THR V7 K8 E9 L10 L11 L12 A13 G14 V15 H16 F17 G18 H19 E20 R21 K22 R23 W24 N25 P26 K27 F28 A29 R30 Y31 I32 I33 A34 E35 E36 R37 R38 G39 I39 H40 I41 I42 I43 D44 L45 K46 T47 M48 E49 E50 L51 E52 R53 T54 F55 R56 F57 I58 E59 D60

L61 A62 M63 R64 G65 G66 T67 I68 L69 F70 V71 G72 T73 K74 K75 Q76 A77 Q78 D79 I80 V81 R82 M83 E84 A85 E86 R87 A88 G89 M90 P91 Y92 V93 N94 Q95 E96 R97 L98 G99 G100 H101 M102 L103 T104 N105 F106 K107 T108 S109 Q110 Q111 R112 V113 H114 L115 E116 E117 L118 E119 A120

L121 F122 A123 S124 P125 E126 I127 E128 E129 R130 P131 P132 K133 E134 Q135 V136 R137 L138 R139 H140 E141 L142 E143 E144 L145 Q146 R147 Y148 L149 S150 G151 F152 R153 L154 L155 L156 R157 L158 F159 D160 A161 I162 F163 V164 V165 D166 P167 T168 K169 E170 A171 I172 A173 V174 R175 E176 A177 R178 R179 L180

F181 I182 P183 V184 I185 A186 L187 T190 S192 D193 D194 D195 V196 V197 D198 Y199 I200 T201 T202 G203 N204 E205 D206 A207 I208 R209 S210 T211 Q212 L213 L214 L215 L216 R217 A218 V219 D220 L221 L222 Q223 Q224 A225 R226 V229 V230 E231 P232 S233 P234 A237 L238 V239 Q240 GLU ALA

ALA THR GLU THR PRO GLU GLU SER VAL GLU ALA

• Molecule 5: 30S ribosomal protein S3

Chain C:  14%

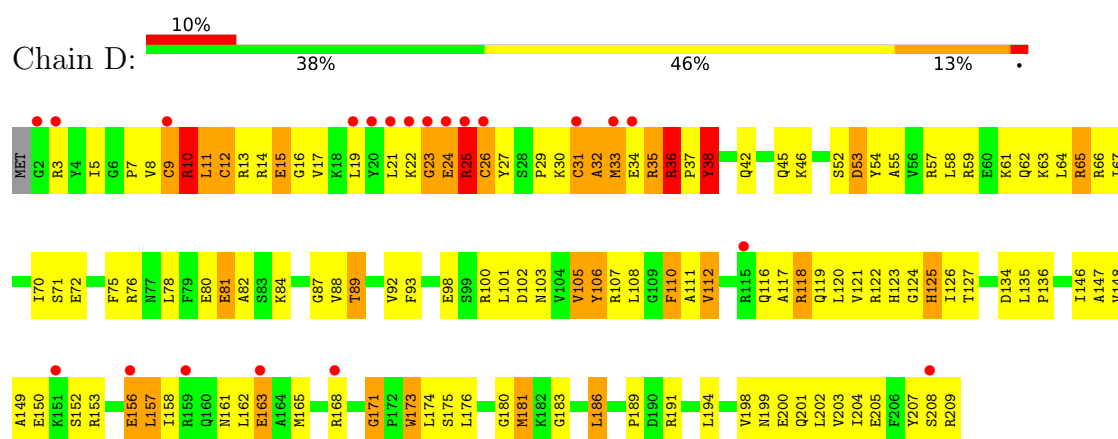
MET G2 K3 K4 I5 H6 P7 I8 G9 R10 R11 R12 G13 G14 I15 I16 D17 V18 R19 S20 R21 R22 R23 R24 R25 R26 R27 R28 R29 R30 R31 R32 R33 R34 R35 R36 R37 R38 R39 R40 L43 L44 E45 E46 E47 Y48 S49 A50 C51 L52 A53 D56 I57 E58 E59 A60 A61 D62

N63 V64 A65 V66 T67 V68 H69 V70 P73 G74 G75 V76 I77 G78 R79 G80 G81 E82 R83 R84 R85 R86 R87 R88 R89 E90 E91 L91 V92 A93 A94 A95 A96 A97 A98 A99 A100 A101 N102 E105 V106 Q107 N108 P109 N110 L111 S112 A113 P114 L115 V116 A117 Q118 R119 V120 A121 E122 I124

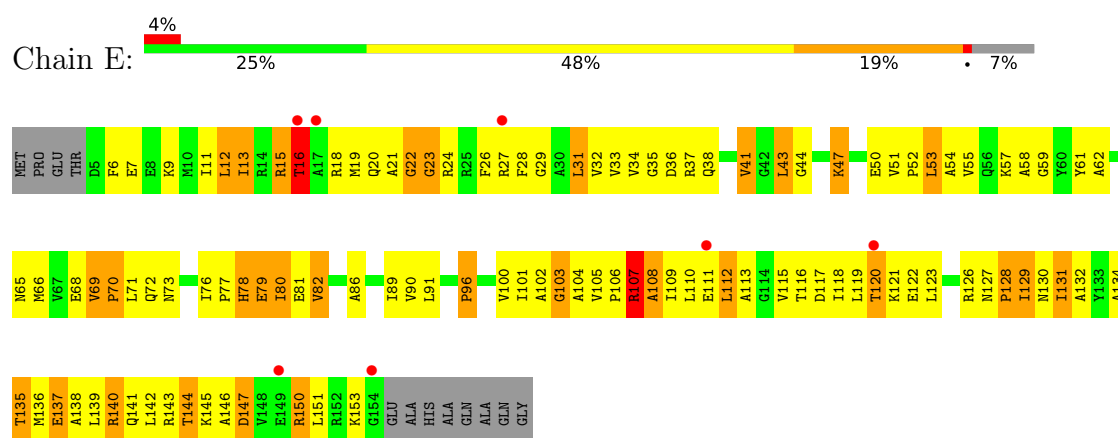
E125 R126 F127 A128 A129 R132 A133 I134 Q136 Q137 A138 V138 Q139 R140 R141 M142 M143 E144 S144 G145 A146 K147 R148 G149 K150 V151 I152 V153 S154 G155 R156 I157 A160 N161 Q162 V163 A164 T165 V166 W167 A168 A169 Q170 G171 R172 T177 L178 R179 A180 N181 F186 A187 L188 A189 R190 T191 T192

Y193 G194 V195 L196 K199 A200 Y201 I202 F203 L204 G205 E206 V207 ILE GLY GLY GLN LYS PRO LYS ALA ARG ARG PRO LEU PRO LYS ALA GLU ARG ARG ARG ARG PRO ALA VAL VAL VAL LYS LYS GLU

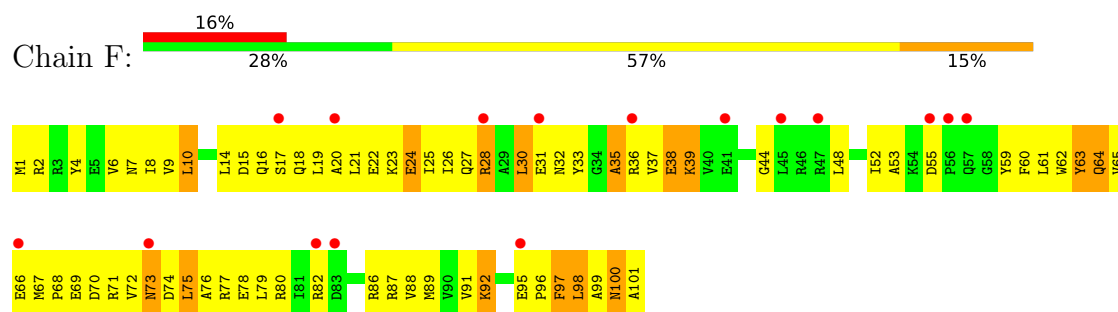
• Molecule 6: 30S ribosomal protein S4



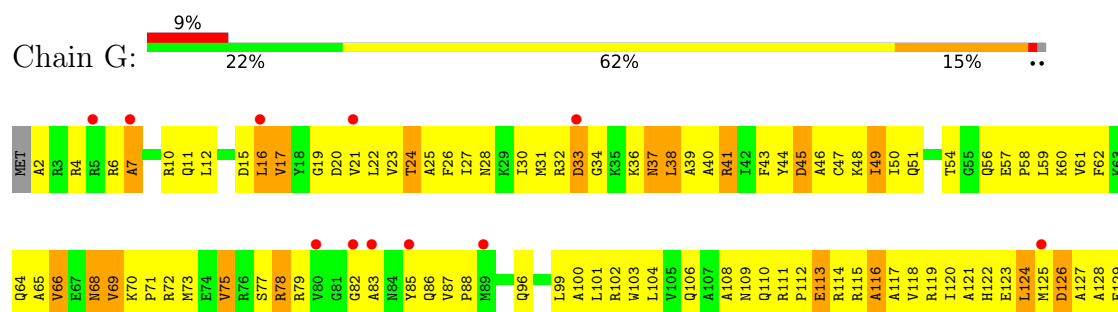
• Molecule 7: 30S ribosomal protein S5



• Molecule 8: 30S ribosomal protein S6

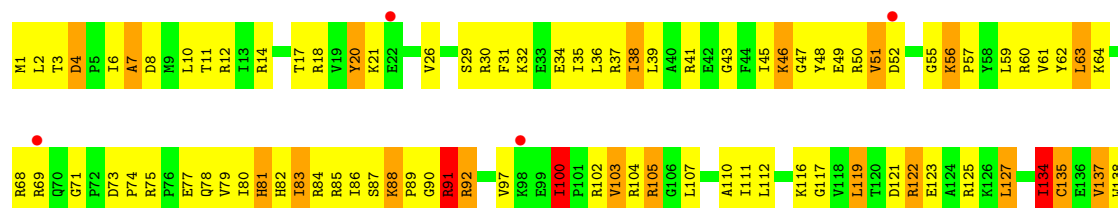


• Molecule 9: 30S ribosomal protein S7

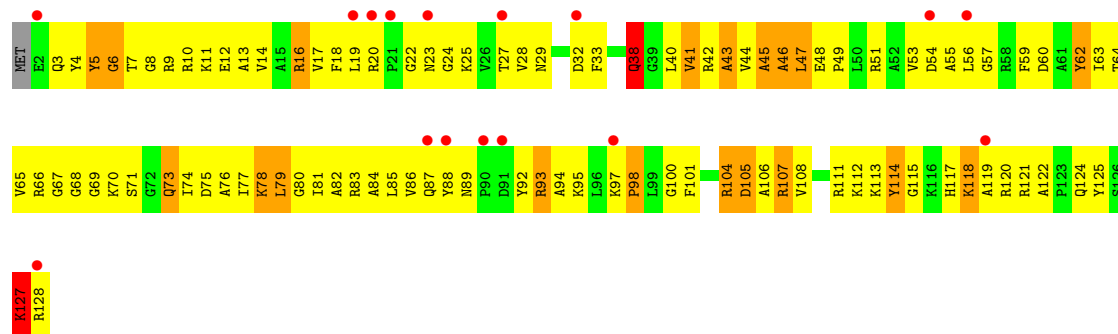




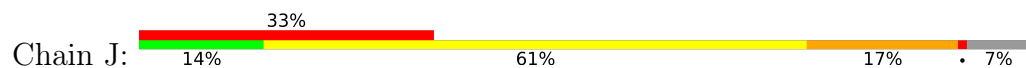
• Molecule 10: 30S ribosomal protein S8



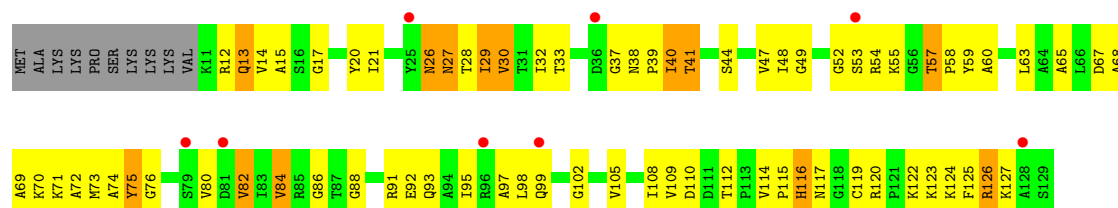
• Molecule 11: 30S ribosomal protein S9



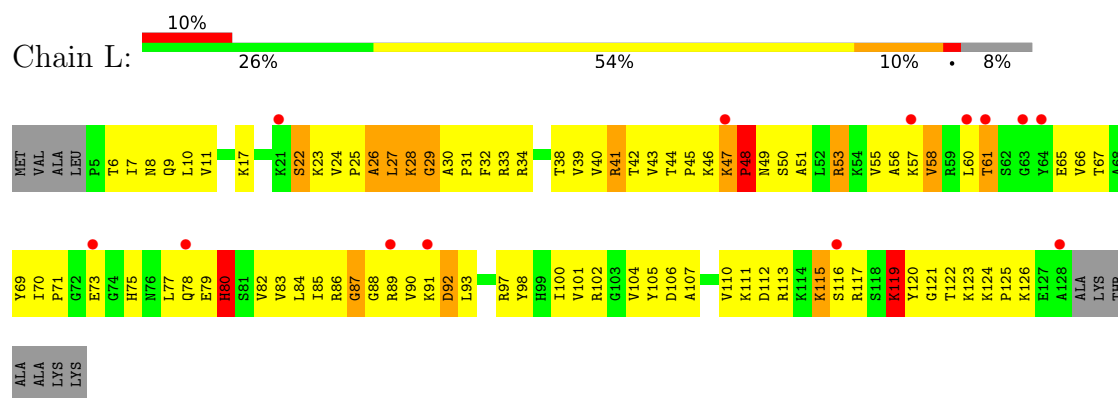
• Molecule 12: 30S ribosomal protein S10



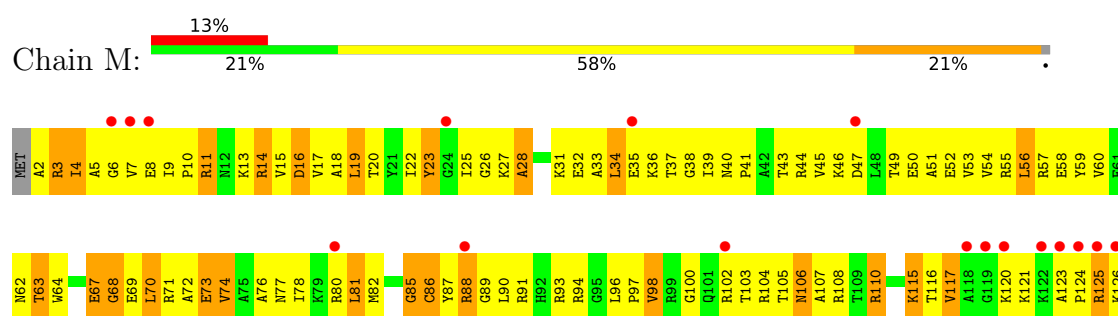
• Molecule 13: 30S ribosomal protein S11



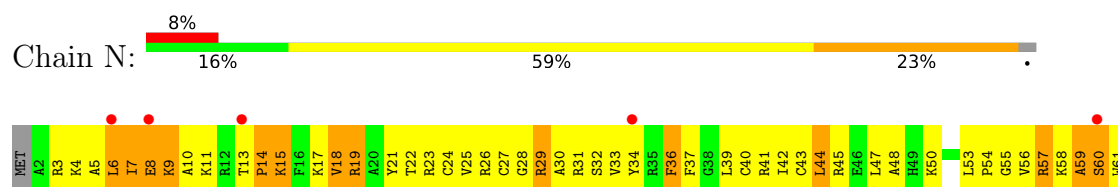
- Molecule 14: 30S ribosomal protein S12



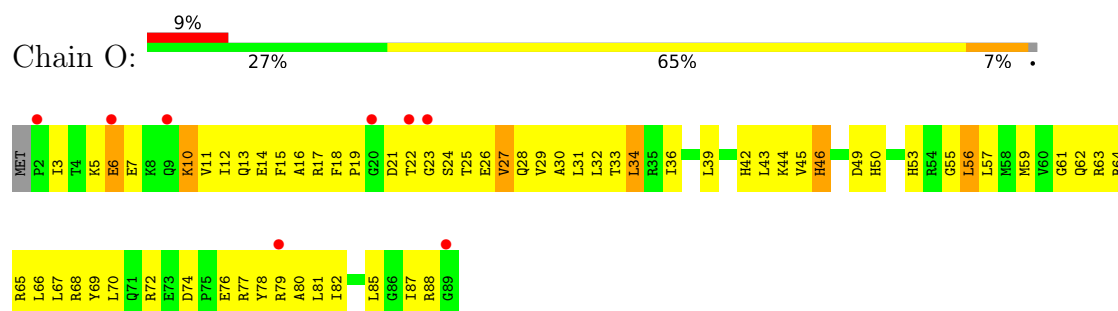
- Molecule 15: 30S ribosomal protein S13



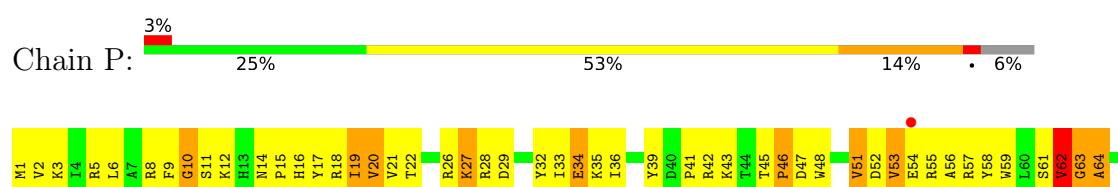
- Molecule 16: 30S ribosomal protein S14

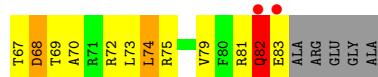


- Molecule 17: 30S ribosomal protein S15

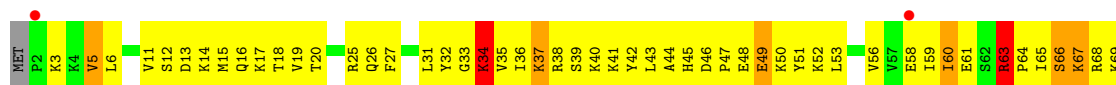


- Molecule 18: 30S ribosomal protein S16

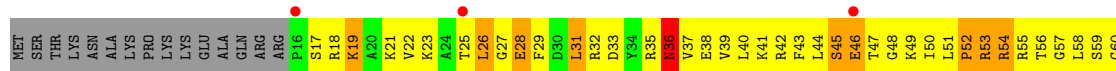
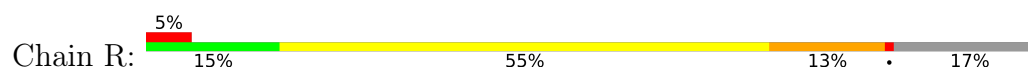




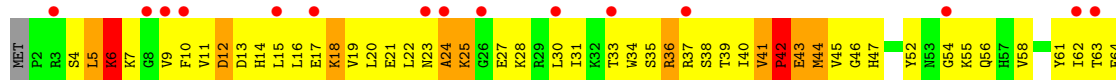
• Molecule 19: 30S ribosomal protein S17



• Molecule 20: 30S ribosomal protein S18



• Molecule 21: 30S ribosomal protein S19



• Molecule 22: 30S ribosomal protein S20



• Molecule 23: 30S ribosomal protein Thx





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	400.81Å 400.81Å 176.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	99.00 – 3.25 99.00 – 3.25	Depositor EDS
% Data completeness (in resolution range)	5.0 (99.00-3.25) 89.2 (99.00-3.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 3.26Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.231 , 0.284 0.228 , 0.280	Depositor DCC
R_{free} test set	10562 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	85.2	Xtriage
Anisotropy	0.267	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 300.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	52063	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: MNU, PAR, ZN, T6A, MG

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	0.47	2/36244 (0.0%)	0.72	65/56567 (0.1%)
2	W	0.53	0/72	1.11	2/111 (1.8%)
3	X	0.52	0/203	0.73	0/311
4	B	0.41	0/1935	1.01	14/2609 (0.5%)
5	C	0.43	0/1636	0.94	3/2205 (0.1%)
6	D	0.51	0/1733	1.02	12/2318 (0.5%)
7	E	0.55	0/1162	1.12	6/1564 (0.4%)
8	F	0.38	0/856	0.86	1/1154 (0.1%)
9	G	0.45	0/1276	0.99	9/1709 (0.5%)
10	H	0.58	0/1136	1.20	14/1527 (0.9%)
11	I	0.41	0/1029	0.97	5/1378 (0.4%)
12	J	0.40	0/805	1.07	4/1082 (0.4%)
13	K	0.57	0/900	1.05	6/1213 (0.5%)
14	L	0.57	0/986	1.20	5/1320 (0.4%)
15	M	0.45	0/1008	1.00	3/1347 (0.2%)
16	N	0.46	0/501	1.09	3/664 (0.5%)
17	O	0.47	0/745	0.88	2/992 (0.2%)
18	P	0.57	0/716	1.13	6/963 (0.6%)
19	Q	0.56	0/870	1.14	6/1159 (0.5%)
20	R	0.42	0/603	1.04	5/799 (0.6%)
21	S	0.38	0/661	1.01	3/890 (0.3%)
22	T	0.56	0/764	1.15	6/1006 (0.6%)
23	V	0.52	0/212	1.06	1/277 (0.4%)
All	All	0.47	2/56053 (0.0%)	0.84	181/83165 (0.2%)

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
1	A	4	60
3	X	1	0
All	All	5	60

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1361	G	O5'-C5'	6.30	1.51	1.42
1	A	1362	C	O5'-C5'	5.90	1.51	1.42

All (181) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	575	G	C2'-C3'-O3'	14.16	130.74	109.50
14	L	26	ALA	N-CA-C	-13.98	98.15	112.97
1	A	115	G	C2'-C3'-O3'	13.96	130.44	109.50
1	A	559	A	C2'-C3'-O3'	13.74	130.12	109.50
1	A	243	A	C2'-C3'-O3'	13.67	130.01	109.50
1	A	1528	U	C2'-C3'-O3'	13.15	129.23	109.50
1	A	181	G	C2'-C3'-O3'	13.04	129.06	109.50
1	A	1498	U	C2'-C3'-O3'	12.27	127.90	109.50
22	T	13	LEU	N-CA-C	-11.75	98.45	113.72
1	A	1503	A	C2'-C3'-O3'	11.32	126.48	109.50
1	A	792	A	C2'-C3'-O3'	10.94	125.91	109.50
1	A	366	C	C2'-C3'-O3'	10.53	125.30	109.50
22	T	75	ASN	N-CA-C	-10.40	100.59	113.28
1	A	965	A	C2'-C3'-O3'	10.13	124.70	109.50
1	A	812	C	C2'-C3'-O3'	9.99	124.48	109.50
1	A	1346	A	C2'-C3'-O3'	9.89	124.34	109.50
1	A	484	G	C2'-C3'-O3'	9.86	124.29	109.50
1	A	372	C	C2'-C3'-O3'	9.62	123.94	109.50
1	A	1528	U	C4'-C3'-O3'	9.50	123.65	109.40
1	A	243	A	C4'-C3'-O3'	9.16	123.13	109.40
1	A	687	A	C2'-C3'-O3'	9.11	123.16	109.50
1	A	60	A	C2'-C3'-O3'	8.98	122.98	109.50
1	A	181	G	C4'-C3'-O3'	8.96	122.83	109.40
1	A	960	U	C2'-C3'-O3'	8.87	122.81	109.50
10	H	56	LYS	CA-C-N	8.69	130.06	119.98
10	H	56	LYS	C-N-CA	8.69	130.06	119.98
16	N	8	GLU	N-CA-C	-8.62	103.28	113.88
1	A	328	C	C2'-C3'-O3'	8.61	122.41	109.50
6	D	110	PHE	N-CA-C	-8.54	100.58	112.45
7	E	69	VAL	N-CA-C	8.46	115.26	107.56

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	559	A	C4'-C3'-O3'	8.45	122.08	109.40
14	L	61	THR	N-CA-C	-8.30	102.41	112.54
19	Q	100	LYS	N-CA-C	-8.02	105.48	114.62
4	B	134	GLU	N-CA-C	-7.84	105.68	114.62
14	L	119	LYS	N-CA-C	-7.79	100.03	110.55
1	A	1067	A	C2'-C3'-O3'	7.74	121.11	109.50
10	H	100	ILE	CA-C-N	7.72	127.77	119.89
10	H	100	ILE	C-N-CA	7.72	127.77	119.89
1	A	509	A	C2'-C3'-O3'	7.65	125.17	113.70
1	A	1505	G	C2'-C3'-O3'	7.63	125.14	113.70
7	E	23	GLY	N-CA-C	7.63	121.67	110.38
4	B	114	ARG	N-CA-C	-7.59	105.97	114.62
20	R	81	PHE	N-CA-C	-7.58	104.55	113.88
1	A	1224	G	C2'-C3'-O3'	7.51	120.76	109.50
1	A	1380	U	C2'-C3'-O3'	7.50	120.75	109.50
6	D	11	LEU	N-CA-C	-7.49	102.61	112.34
10	H	134	ILE	N-CA-C	7.49	118.28	110.72
9	G	33	ASP	N-CA-C	-7.47	104.11	113.23
4	B	220	ASP	N-CA-C	-7.40	103.14	113.20
18	P	19	ILE	N-CA-C	-7.38	99.41	109.37
4	B	152	PHE	N-CA-C	-7.37	104.02	113.16
1	A	533	A	C2'-C3'-O3'	7.37	120.56	109.50
15	M	11	ARG	N-CA-C	7.23	119.38	108.46
21	S	36	ARG	N-CA-C	-7.21	104.36	113.01
19	Q	67	LYS	N-CA-C	-7.14	99.88	110.23
20	R	46	GLU	N-CA-C	-7.12	103.55	113.37
1	A	1101	A	C2'-C3'-O3'	7.03	120.05	109.50
13	K	49	GLY	N-CA-C	7.03	121.10	113.58
20	R	53	ARG	N-CA-C	-7.01	104.36	113.12
1	A	250	A	C2'-C3'-O3'	7.00	120.00	109.50
1	A	1299	A	N9-C1'-C2'	6.92	122.38	112.00
2	W	1	A	O5'-C5'-C4'	6.92	121.88	111.50
10	H	4	ASP	CA-C-N	6.88	128.44	119.84
10	H	4	ASP	C-N-CA	6.88	128.44	119.84
1	A	129(A)	G	C2'-C3'-O3'	6.79	119.68	109.50
1	A	119	A	C2'-C3'-O3'	6.77	119.66	109.50
18	P	63	GLY	N-CA-C	-6.73	105.48	111.67
13	K	26	ASN	N-CA-C	6.71	121.76	113.50
13	K	40	ILE	N-CA-C	-6.70	106.33	111.62
13	K	116	HIS	N-CA-C	-6.68	102.23	110.65
1	A	266	G	C2'-C3'-O3'	6.60	123.60	113.70
1	A	1065	U	C2'-C3'-O3'	6.51	119.27	109.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	I	115	GLY	N-CA-C	-6.50	104.89	114.90
6	D	171	GLY	CA-C-N	6.47	127.93	119.84
6	D	171	GLY	C-N-CA	6.47	127.93	119.84
1	A	7	G	C2'-C3'-O3'	6.45	119.17	109.50
2	W	3	G	C4'-C3'-O3'	6.44	122.66	113.00
15	M	71	ARG	N-CA-C	-6.43	104.32	111.71
1	A	418	C	N1-C1'-C2'	6.42	121.63	112.00
1	A	1346	A	C4'-C3'-O3'	6.41	119.01	109.40
9	G	147	ALA	N-CA-C	-6.40	105.78	113.97
1	A	344	A	C2'-C3'-O3'	6.36	119.04	109.50
14	L	22	SER	N-CA-C	6.35	118.75	110.43
18	P	20	VAL	N-CA-C	6.35	116.74	108.35
9	G	145	ALA	N-CA-C	-6.33	101.61	110.35
12	J	60	ARG	N-CA-C	6.33	124.28	110.80
1	A	428	G	C2'-C3'-O3'	6.32	118.99	109.50
19	Q	39	SER	N-CA-C	6.32	118.79	109.69
1	A	115	G	C4'-C3'-O3'	6.32	118.87	109.40
10	H	103	VAL	N-CA-C	6.26	117.38	108.93
12	J	21	GLN	N-CA-C	-6.21	104.76	112.90
11	I	38	GLN	N-CA-C	6.20	118.28	108.67
1	A	1285	A	C2'-C3'-O3'	6.19	118.79	109.50
11	I	62	TYR	N-CA-C	-6.18	99.16	109.24
4	B	223	ILE	N-CA-C	-6.17	104.62	110.42
7	E	104	ALA	N-CA-C	6.12	117.62	111.07
1	A	992	U	C2'-C3'-O3'	6.12	118.67	109.50
4	B	133	LYS	N-CA-C	-6.05	105.75	113.01
1	A	812	C	C4'-C3'-O3'	6.05	118.47	109.40
16	N	18	VAL	N-CA-C	6.03	116.21	110.42
22	T	89	ARG	N-CA-C	-6.02	104.84	111.82
9	G	4	ARG	N-CA-C	5.98	117.60	111.14
1	A	993	G	C2'-C3'-O3'	5.96	118.45	109.50
10	H	57	PRO	N-CA-C	5.95	120.59	110.95
23	V	24	ARG	N-CA-C	-5.95	104.87	111.71
13	K	102	GLY	N-CA-C	-5.94	106.53	114.25
1	A	1281	U	C2'-C3'-O3'	5.94	118.40	109.50
15	M	23	TYR	N-CA-C	5.83	117.33	110.97
20	R	79	LEU	CA-C-N	5.83	125.80	120.21
20	R	79	LEU	C-N-CA	5.83	125.80	120.21
8	F	73	ASN	N-CA-C	-5.82	105.89	112.87
10	H	137	VAL	CB-CA-C	-5.79	103.75	111.80
9	G	47	CYS	N-CA-C	-5.78	105.94	112.87
6	D	12	CYS	N-CA-C	-5.74	104.66	111.03

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	G	41	ARG	N-CA-C	-5.73	104.24	111.11
4	B	239	VAL	N-CA-C	-5.71	106.73	113.42
1	A	572	A	N9-C1'-C2'	5.70	120.54	112.00
1	A	1361	G	C4'-C3'-O3'	5.70	121.54	113.00
1	A	1182	G	C2'-C3'-O3'	5.69	118.03	109.50
17	O	55	GLY	N-CA-C	-5.68	105.91	112.50
5	C	156	ARG	N-CA-C	-5.68	105.93	112.86
1	A	108	G	O4'-C4'-C3'	-5.66	98.34	104.00
7	E	18	ARG	N-CA-C	-5.65	101.38	110.14
4	B	192	SER	N-CA-C	5.60	117.49	109.14
5	C	99	VAL	N-CA-C	5.59	115.73	108.35
16	N	57	ARG	N-CA-C	5.57	117.00	108.42
9	G	24	THR	N-CA-C	-5.55	104.25	111.02
5	C	68	VAL	N-CA-C	5.53	116.83	109.37
6	D	173	TRP	N-CA-C	-5.51	105.55	114.09
12	J	29	ARG	N-CA-C	-5.51	107.56	114.56
14	L	92	ASP	N-CA-C	5.51	120.00	113.28
4	B	56	ARG	N-CA-C	-5.49	104.52	111.11
17	O	44	LYS	N-CA-C	-5.46	105.43	111.71
4	B	139	LYS	N-CA-C	-5.44	106.69	113.55
1	A	1049	U	C2'-C3'-O3'	5.43	117.65	109.50
1	A	1124	G	N9-C1'-C2'	5.43	120.14	112.00
1	A	353	A	C5'-C4'-O4'	-5.42	101.67	109.80
4	B	219	VAL	N-CA-C	-5.41	107.16	111.81
6	D	186	LEU	N-CA-C	5.41	118.00	111.40
22	T	44	ALA	N-CA-C	-5.38	105.52	111.71
22	T	56	MET	N-CA-C	-5.38	104.66	111.11
21	S	18	LYS	N-CA-C	-5.37	106.86	113.41
1	A	1503	A	C4'-C3'-O3'	5.36	117.44	109.40
6	D	26	CYS	N-CA-C	-5.35	107.06	113.21
18	P	46	PRO	N-CA-C	-5.30	106.16	113.53
19	Q	63	ARG	N-CA-C	-5.29	103.37	109.93
11	I	73	GLN	N-CA-C	-5.29	104.57	111.02
12	J	49	VAL	N-CA-C	5.29	115.89	108.17
1	A	1196	U	C4'-C3'-O3'	5.27	117.30	109.40
4	B	111	ARG	N-CA-C	-5.27	105.62	111.36
18	P	27	LYS	N-CA-C	-5.25	103.68	110.19
19	Q	37	LYS	N-CA-C	-5.25	102.75	110.52
10	H	71	GLY	CA-C-N	5.21	125.46	119.83
10	H	71	GLY	C-N-CA	5.21	125.46	119.83
1	A	618	C	C5'-C4'-C3'	5.21	123.81	116.00
6	D	38	TYR	CA-C-N	5.21	125.74	120.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	38	TYR	C-N-CA	5.21	125.74	120.38
1	A	701	C	C2'-C3'-O3'	5.18	117.28	109.50
4	B	55	PHE	N-CA-C	-5.18	105.63	111.28
1	A	366	C	C4'-C3'-O3'	5.17	117.16	109.40
1	A	1502	A	N9-C1'-C2'	5.17	121.75	114.00
9	G	148	ASN	N-CA-C	-5.16	105.70	112.41
22	T	92	LEU	N-CA-C	-5.16	106.09	112.38
6	D	81	GLU	N-CA-C	-5.15	105.66	111.28
9	G	75	VAL	N-CA-C	5.15	114.16	106.85
1	A	389	A	C5'-C4'-C3'	5.13	123.70	116.00
1	A	1213	A	N9-C1'-C2'	5.13	119.69	112.00
1	A	266	G	N9-C1'-C2'	5.12	119.68	112.00
21	S	78	ARG	N-CA-C	5.11	117.90	109.72
1	A	407	G	C2'-C3'-O3'	5.10	117.14	109.50
11	I	6	GLY	N-CA-C	-5.09	103.11	110.90
13	K	37	GLY	N-CA-C	5.08	120.53	114.48
18	P	11	SER	N-CA-C	-5.06	101.42	108.96
10	H	7	ALA	N-CA-C	-5.06	105.23	111.40
7	E	103	GLY	N-CA-C	-5.05	104.78	112.51
19	Q	35	VAL	CB-CA-C	-5.05	104.56	111.33
4	B	185	ILE	N-CA-C	-5.04	101.08	108.85
7	E	66	MET	N-CA-C	5.04	117.61	109.40
1	A	748	C	N1-C1'-C2'	5.01	119.52	112.00
10	H	20	TYR	N-CA-C	5.01	118.36	111.54
6	D	163	GLU	N-CA-C	-5.00	105.30	111.40

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	181	G	C3'
1	A	243	A	C3'
1	A	559	A	C3'
1	A	1528	U	C3'
3	X	37	T6A	C14

All (60) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1054	C	Sidechain
1	A	107	G	Sidechain
1	A	1073	U	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	A	1077	G	Sidechain
1	A	108	G	Sidechain
1	A	1235	U	Sidechain
1	A	1281	U	Sidechain
1	A	1299	A	Sidechain
1	A	1345	U	Sidechain
1	A	1361	G	Sidechain
1	A	1396	A	Sidechain
1	A	1402	C	Sidechain
1	A	1414	U	Sidechain
1	A	1502	A	Sidechain
1	A	1510	U	Sidechain
1	A	1519	A	Sidechain
1	A	1522	U	Sidechain
1	A	1525	G	Sidechain
1	A	170	U	Sidechain
1	A	197	A	Sidechain
1	A	216	G	Sidechain
1	A	226	G	Sidechain
1	A	229	U	Sidechain
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	253	U	Sidechain
1	A	274	A	Sidechain
1	A	303	A	Sidechain
1	A	387	U	Sidechain
1	A	39	G	Sidechain
1	A	404	U	Sidechain
1	A	408	A	Sidechain
1	A	474	G	Sidechain
1	A	490	G	Sidechain
1	A	528	C	Sidechain
1	A	529	G	Sidechain
1	A	561	U	Sidechain
1	A	571	U	Sidechain
1	A	572	A	Sidechain
1	A	573	A	Sidechain
1	A	575	G	Sidechain
1	A	587	G	Sidechain
1	A	604	G	Sidechain
1	A	657	G	Sidechain
1	A	664	G	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	A	682	G	Sidechain
1	A	727	G	Sidechain
1	A	741	G	Sidechain
1	A	77	G	Sidechain
1	A	785	G	Sidechain
1	A	84	U	Sidechain
1	A	860	A	Sidechain
1	A	870	U	Sidechain
1	A	879	C	Sidechain
1	A	898	G	Sidechain
1	A	901	A	Sidechain
1	A	911	U	Sidechain
1	A	912	C	Sidechain
1	A	960	U	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	32380	0	16346	1334	0
2	W	64	0	35	4	0
3	X	239	0	127	7	0
4	B	1900	0	1951	329	0
5	C	1612	0	1677	257	0
6	D	1703	0	1764	165	0
7	E	1146	0	1207	143	0
8	F	843	0	857	110	0
9	G	1257	0	1296	147	0
10	H	1116	0	1177	120	0
11	I	1011	0	1043	158	0
12	J	792	0	835	129	0
13	K	885	0	904	74	0
14	L	970	0	1057	132	0
15	M	997	0	1072	160	0
16	N	492	0	530	74	0
17	O	734	0	771	85	0
18	P	700	0	720	90	0
19	Q	857	0	930	129	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	R	597	0	668	106	0
21	S	647	0	673	86	0
22	T	762	0	856	98	0
23	V	208	0	221	21	0
24	A	42	0	45	2	0
25	A	104	0	0	0	0
25	J	1	0	0	0	0
25	X	2	0	0	0	0
26	D	1	0	0	0	0
26	N	1	0	0	1	0
All	All	52063	0	36762	3649	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 41.

All (3649) 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)
1:A:1489:G:H2'	1:A:1490:C:H5''	1.26	1.10
6:D:36:ARG:H	6:D:37:PRO:HD3	1.13	1.08
5:C:26:LYS:H	5:C:26:LYS:HD3	1.14	1.06
5:C:179:ARG:HG2	5:C:180:ALA:H	0.98	1.06
4:B:132:LYS:HA	4:B:135:GLN:HB3	1.36	1.05
1:A:1116:C:H2'	1:A:1117:G:H5''	1.36	1.05
1:A:928:G:H4'	1:A:1533:C:H5'	1.39	1.04
1:A:1489:G:C2'	1:A:1490:C:H5''	1.87	1.03
1:A:201:C:C4'	1:A:216:G:H21	1.71	1.03
1:A:929:G:OP1	1:A:1533:C:H2'	1.58	1.03
1:A:243:A:H4'	1:A:244:U:H5'	1.39	1.02
1:A:630:G:H2'	1:A:631:G:H5'	1.37	1.02
5:C:196:LEU:HD23	5:C:196:LEU:H	1.21	1.01
22:T:54:LYS:HG2	22:T:57:ARG:HH22	1.25	1.01
12:J:46:ARG:HD3	12:J:64:GLU:HB3	1.43	1.01
1:A:1057:G:H5''	5:C:154:SER:HB2	1.39	1.00
4:B:80:ILE:HD11	4:B:208:ILE:HG23	1.42	1.00
1:A:839:U:H5'	1:A:840:C:C5	1.97	1.00
1:A:452:A:HO2'	1:A:453:A:H8	1.06	0.98
1:A:190(L):U:H6	1:A:190(L):U:H5'	1.29	0.98
5:C:14:ILE:HG22	5:C:15:THR:H	1.27	0.98
14:L:60:LEU:HD11	14:L:85:ILE:HD12	1.45	0.97
1:A:266:G:H5''	1:A:268:C:H41	1.30	0.96

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:47:LYS:HB3	14:L:48:PRO:HD3	1.47	0.96
6:D:36:ARG:HG3	6:D:38:TYR:HE2	1.30	0.96
14:L:60:LEU:HD21	14:L:66:VAL:HG22	1.48	0.96
11:I:106:ALA:O	11:I:108:VAL:HG23	1.66	0.95
21:S:17:GLU:HA	21:S:20:LEU:HG	1.49	0.95
1:A:972:C:H4'	12:J:57:LYS:HD3	1.47	0.95
7:E:80:ILE:HD11	7:E:91:LEU:HB2	1.47	0.95
21:S:20:LEU:HA	21:S:23:ASN:HD22	1.30	0.94
1:A:838:G:H2'	1:A:839:U:H5''	1.50	0.94
7:E:107:ARG:HH11	7:E:107:ARG:HB2	1.32	0.94
8:F:7:ASN:HB2	8:F:89:MET:HB3	1.48	0.94
5:C:129:ALA:HB3	5:C:132:ARG:HE	1.32	0.94
12:J:90:LEU:H	12:J:91:PRO:HD2	1.32	0.93
1:A:939:G:H5''	9:G:102:ARG:HH22	1.32	0.93
21:S:55:LYS:HG2	21:S:56:GLN:HE21	1.34	0.93
4:B:48:MET:HA	4:B:51:LEU:HD12	1.50	0.92
1:A:582:U:H1'	19:Q:105:ALA:HA	1.50	0.92
16:N:27:CYS:HG	26:N:307:ZN:ZN	0.68	0.92
11:I:114:TYR:H	11:I:114:TYR:HD1	1.12	0.92
5:C:179:ARG:CG	5:C:180:ALA:H	1.81	0.92
5:C:179:ARG:HG2	5:C:180:ALA:N	1.77	0.91
15:M:5:ALA:HB3	15:M:8:GLU:HG3	1.52	0.91
1:A:1095:U:H2'	1:A:1096:C:C6	2.04	0.91
4:B:18:GLY:HA2	4:B:41:ILE:HA	1.52	0.91
12:J:34:VAL:HG22	12:J:74:ILE:HG22	1.54	0.90
12:J:90:LEU:H	12:J:91:PRO:CD	1.84	0.90
14:L:126:LYS:H	14:L:126:LYS:HD2	1.33	0.90
1:A:760:G:H22	19:Q:105:ALA:N	1.68	0.90
17:O:87:ILE:HG22	17:O:88:ARG:HE	1.36	0.90
1:A:1356:G:H2'	1:A:1357:A:C8	2.06	0.90
15:M:81:LEU:HD23	15:M:81:LEU:H	1.37	0.89
1:A:1443:G:H5''	1:A:1446:A:H5'	1.53	0.89
10:H:90:GLY:O	10:H:91:ARG:HB2	1.72	0.89
4:B:92:TYR:CE1	4:B:151:GLY:HA3	2.07	0.89
6:D:36:ARG:HG3	6:D:38:TYR:CE2	2.07	0.89
5:C:179:ARG:HD3	5:C:206:GLU:HB3	1.55	0.89
4:B:178:ARG:HH11	4:B:178:ARG:HG3	1.37	0.89
1:A:1116:C:C2'	1:A:1117:G:H5''	2.03	0.88
17:O:26:GLU:HA	17:O:81:LEU:HD11	1.51	0.88
11:I:9:ARG:HG2	11:I:14:VAL:HG22	1.56	0.88
5:C:108:ASN:ND2	5:C:111:LEU:HG	1.87	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:78:HIS:HD2	10:H:107:LEU:HD12	1.39	0.88
5:C:123:GLN:HE22	5:C:140:ARG:HH22	1.14	0.88
16:N:24:CYS:HB3	16:N:28:GLY:H	1.38	0.88
11:I:43:ALA:HA	11:I:74:ILE:HD13	1.54	0.88
1:A:1034:G:H21	1:A:1035:A:H62	1.22	0.87
14:L:41:ARG:HG2	14:L:42:THR:H	1.40	0.87
1:A:200:G:N2	1:A:216:G:H2'	1.90	0.87
1:A:839:U:H5'	1:A:840:C:H5	1.36	0.87
1:A:953:G:H1'	15:M:125:ARG:HA	1.54	0.87
8:F:101:ALA:HA	20:R:28:GLU:HG3	1.56	0.87
1:A:1016:A:H2'	1:A:1017:G:O4'	1.75	0.87
9:G:22:LEU:O	9:G:25:ALA:HB3	1.74	0.86
1:A:409:G:OP2	1:A:431:A:H5'	1.76	0.86
6:D:36:ARG:N	6:D:37:PRO:HD3	1.89	0.86
7:E:51:VAL:HB	7:E:52:PRO:HD3	1.57	0.86
11:I:10:ARG:HG2	11:I:75:ASP:HB2	1.58	0.86
6:D:81:GLU:HA	6:D:84:LYS:HD2	1.57	0.85
1:A:1124:G:H5'	12:J:35:SER:O	1.76	0.85
1:A:1135:U:H4'	1:A:1136:U:H5	1.40	0.85
1:A:382:A:H2'	1:A:383:A:C8	2.12	0.85
1:A:1316:G:H5''	16:N:17:LYS:HD2	1.58	0.85
14:L:47:LYS:HB3	14:L:48:PRO:CD	2.05	0.85
1:A:459:G:N1	1:A:461:C:H5''	1.90	0.85
23:V:6:ARG:HD3	23:V:15:ARG:NH1	1.91	0.85
1:A:382:A:H2'	1:A:383:A:H8	1.42	0.85
1:A:129(A):G:HO2'	1:A:190(E):U:H2'	1.41	0.85
1:A:371:G:O2'	1:A:372:C:H5'	1.76	0.85
1:A:1435:G:H2'	1:A:1436:U:C6	2.13	0.84
17:O:16:ALA:HB1	17:O:21:ASP:HB3	1.59	0.84
21:S:30:LEU:O	21:S:31:ILE:HD13	1.76	0.84
1:A:406:G:H1	1:A:436:C:H42	1.23	0.84
1:A:630:G:C2'	1:A:631:G:H5'	2.06	0.84
1:A:1201:A:H4'	1:A:1202:G:O5'	1.78	0.84
18:P:21:VAL:HG12	18:P:33:ILE:HD12	1.60	0.84
1:A:328:C:O2	1:A:328:C:H2'	1.75	0.84
5:C:18:TRP:HE3	5:C:18:TRP:H	1.22	0.84
10:H:20:TYR:CE2	10:H:75:ARG:HD2	2.13	0.84
12:J:48:THR:HA	12:J:62:HIS:HD2	1.42	0.83
4:B:200:ILE:HG22	4:B:201:ILE:H	1.41	0.83
8:F:100:ASN:HB2	20:R:23:LYS:HE3	1.60	0.83
1:A:939:G:H5''	9:G:102:ARG:NH2	1.92	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:156:ARG:H	5:C:163:ALA:HA	1.43	0.83
14:L:25:PRO:C	14:L:27:LEU:H	1.87	0.83
10:H:116:LYS:HZ2	10:H:127:LEU:HB3	1.42	0.83
1:A:664:G:H22	1:A:741:G:H1	1.27	0.83
1:A:975:A:O5'	1:A:976:G:H5'	1.78	0.83
1:A:203:U:H4'	1:A:204:U:O3'	1.78	0.82
1:A:235:C:H5'	19:Q:70:ARG:HG2	1.60	0.82
11:I:114:TYR:CD2	12:J:60:ARG:HB2	2.14	0.82
5:C:52:LEU:HD23	5:C:52:LEU:H	1.44	0.82
1:A:476:G:H2'	1:A:479:C:N4	1.94	0.82
14:L:77:LEU:HD21	14:L:107:ALA:HA	1.60	0.82
17:O:36:ILE:HG12	17:O:59:MET:HE3	1.61	0.82
11:I:93:ARG:NH1	11:I:93:ARG:HB3	1.94	0.82
1:A:474:G:H3'	1:A:474:G:N3	1.95	0.82
1:A:1057:G:H5''	5:C:154:SER:CB	2.08	0.82
1:A:476:G:H2'	1:A:479:C:H42	1.45	0.81
9:G:16:LEU:H	9:G:16:LEU:HD22	1.45	0.81
18:P:28:ARG:HG2	18:P:28:ARG:HH11	1.45	0.81
9:G:70:LYS:HB3	9:G:96:GLN:HG2	1.61	0.81
22:T:57:ARG:NH1	22:T:102:GLY:HA3	1.94	0.81
18:P:81:ARG:NE	18:P:81:ARG:HA	1.95	0.81
22:T:67:ALA:HA	22:T:73:HIS:H	1.46	0.81
12:J:38:ILE:HB	12:J:71:LEU:HB2	1.63	0.81
8:F:26:ILE:O	8:F:30:LEU:HB2	1.79	0.81
1:A:579:G:H5'	1:A:728:A:H1'	1.60	0.81
22:T:54:LYS:HG2	22:T:57:ARG:NH2	1.94	0.81
7:E:11:ILE:HG22	7:E:12:LEU:HD12	1.63	0.80
5:C:150:LYS:HE2	5:C:152:ILE:HD11	1.63	0.80
8:F:28:ARG:CZ	8:F:28:ARG:HA	2.11	0.80
12:J:25:GLU:HB3	12:J:29:ARG:HE	1.45	0.80
18:P:81:ARG:HA	18:P:81:ARG:HE	1.46	0.80
4:B:19:HIS:HB2	4:B:204:ASN:ND2	1.97	0.80
5:C:3:ASN:HD22	5:C:3:ASN:N	1.79	0.80
4:B:77:ALA:HB1	4:B:80:ILE:HD12	1.62	0.80
4:B:101:MET:HE2	4:B:108:ILE:HG21	1.62	0.80
9:G:120:ILE:H	9:G:120:ILE:HD12	1.47	0.80
11:I:65:VAL:HG21	11:I:73:GLN:HB3	1.63	0.80
12:J:4:ILE:HD12	12:J:74:ILE:HG13	1.63	0.80
13:K:91:ARG:C	13:K:93:GLN:H	1.87	0.80
1:A:1148:U:H2'	1:A:1149:C:O4'	1.82	0.80
1:A:1349:A:H2'	1:A:1350:A:H8	1.47	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:93:LYS:HE2	5:C:93:LYS:HA	1.63	0.79
9:G:15:ASP:HB3	9:G:19:GLY:N	1.97	0.79
10:H:116:LYS:NZ	10:H:127:LEU:HB3	1.96	0.79
5:C:190:ARG:H	5:C:190:ARG:HD2	1.48	0.79
20:R:47:THR:HA	20:R:83:GLU:HB2	1.64	0.79
4:B:84:GLU:HB3	4:B:219:VAL:HG21	1.64	0.79
4:B:218:ALA:O	4:B:222:ILE:HG13	1.82	0.79
19:Q:98:LEU:HA	19:Q:102:GLY:HA2	1.64	0.79
1:A:1527:C:O2'	1:A:1528:U:H5'	1.81	0.79
4:B:91:PRO:HG3	4:B:154:LEU:HB2	1.64	0.79
19:Q:53:LEU:HD23	19:Q:82:MET:HE1	1.64	0.79
1:A:1137:C:H4'	1:A:1138:G:C2	2.18	0.79
13:K:14:VAL:HG21	13:K:40:ILE:HD11	1.64	0.79
10:H:83:ILE:HG23	10:H:83:ILE:O	1.83	0.78
1:A:406:G:H21	6:D:119:GLN:HE22	1.30	0.78
1:A:1054:C:N4	3:X:34:MNU:H1'	1.98	0.78
4:B:15:VAL:HG11	4:B:209:ARG:HG2	1.63	0.78
5:C:134:ILE:HD11	5:C:153:VAL:HG23	1.65	0.78
19:Q:12:SER:HB3	19:Q:20:THR:HB	1.65	0.78
12:J:84:GLN:O	12:J:88:LEU:HD12	1.83	0.78
6:D:111:ALA:HB2	6:D:120:LEU:HD12	1.65	0.78
9:G:38:LEU:HA	9:G:41:ARG:HG3	1.65	0.78
1:A:1106:G:H5''	5:C:172:ARG:HG2	1.65	0.78
7:E:122:GLU:O	7:E:123:LEU:HD23	1.84	0.78
1:A:376:G:H2'	1:A:377:G:H8	1.48	0.78
1:A:1250:A:H5''	11:I:68:GLY:H	1.48	0.78
4:B:92:TYR:HE1	4:B:151:GLY:HA3	1.47	0.78
6:D:8:VAL:HG11	6:D:21:LEU:HB3	1.66	0.78
1:A:1101:A:H4'	1:A:1102:A:O5'	1.85	0.77
1:A:1250:A:H4'	11:I:68:GLY:H	1.47	0.77
10:H:97:VAL:HA	10:H:100:ILE:HD11	1.65	0.77
18:P:22:THR:HA	18:P:33:ILE:HG13	1.67	0.77
12:J:30:SER:OG	12:J:81:THR:HA	1.83	0.77
15:M:4:ILE:HG22	15:M:5:ALA:N	1.99	0.77
1:A:1229:A:H2'	1:A:1230:C:H6	1.48	0.77
4:B:115:LEU:HD21	4:B:153:ARG:HH22	1.49	0.77
1:A:1490:C:H6	1:A:1490:C:H5'	1.47	0.77
4:B:142:LEU:O	4:B:146:GLN:HG2	1.85	0.77
5:C:86:VAL:O	5:C:89:GLU:HB3	1.85	0.77
1:A:760:G:H22	19:Q:105:ALA:H	1.28	0.77
5:C:56:ASP:O	5:C:57:ILE:HG13	1.84	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:36:LYS:HD2	15:M:59:TYR:CZ	2.19	0.77
1:A:760:G:H1	19:Q:105:ALA:HB2	1.48	0.77
1:A:1154:G:H2'	1:A:1155:G:H8	1.50	0.77
8:F:60:PHE:O	8:F:61:LEU:HD23	1.84	0.77
11:I:8:GLY:HA2	11:I:79:LEU:HD13	1.67	0.77
1:A:1140:C:H2'	1:A:1141:C:H6	1.50	0.77
1:A:1262:C:H42	1:A:1273:G:H1	1.32	0.77
11:I:16:ARG:HD3	11:I:64:THR:HB	1.67	0.77
11:I:114:TYR:CE2	12:J:60:ARG:HB2	2.19	0.77
1:A:190(L):U:H5'	1:A:190(L):U:C6	2.18	0.77
14:L:124:LYS:HD2	14:L:125:PRO:HD2	1.67	0.77
1:A:838:G:C2'	1:A:839:U:H5''	2.13	0.77
16:N:9:LYS:HD3	16:N:10:ALA:N	1.99	0.77
1:A:1140:C:H2'	1:A:1141:C:C6	2.20	0.76
9:G:23:VAL:O	9:G:27:ILE:HG13	1.85	0.76
11:I:11:LYS:O	11:I:12:GLU:HB3	1.83	0.76
13:K:110:ASP:HB2	20:R:88:LYS:HZ2	1.50	0.76
14:L:6:THR:OG1	14:L:9:GLN:HG3	1.84	0.76
14:L:55:VAL:HG12	14:L:56:ALA:N	1.99	0.76
14:L:126:LYS:HD2	14:L:126:LYS:N	1.99	0.76
21:S:17:GLU:HA	21:S:20:LEU:CG	2.13	0.76
1:A:706:A:O2'	13:K:29:ILE:HD11	1.85	0.76
5:C:64:VAL:HG23	5:C:99:VAL:HG11	1.67	0.76
15:M:34:LEU:HD13	15:M:41:PRO:HA	1.66	0.76
15:M:62:ASN:O	15:M:63:THR:HB	1.85	0.76
19:Q:27:PHE:CZ	19:Q:36:ILE:HD11	2.20	0.76
1:A:1391:U:H2'	1:A:1392:G:C8	2.21	0.76
7:E:76:ILE:HG22	7:E:78:HIS:H	1.50	0.76
1:A:1313:U:OP2	21:S:6:LYS:HA	1.85	0.76
4:B:132:LYS:HB3	4:B:136:VAL:HG23	1.67	0.76
5:C:26:LYS:HD3	5:C:26:LYS:N	1.98	0.76
1:A:781:A:H2'	1:A:782:A:H5'	1.68	0.76
1:A:1141:C:O2'	1:A:1142:G:H5'	1.86	0.76
1:A:1502:A:H2	1:A:1505:G:H1	1.32	0.76
1:A:243:A:C4'	1:A:244:U:H5'	2.14	0.76
1:A:954:G:H4'	15:M:120:LYS:HB2	1.67	0.76
1:A:1366:C:H2'	1:A:1367:C:H6	1.50	0.76
14:L:47:LYS:CB	14:L:48:PRO:HD3	2.15	0.76
15:M:78:ILE:HA	15:M:81:LEU:HD21	1.65	0.76
1:A:409:G:OP1	1:A:429:U:H1'	1.86	0.76
5:C:191:THR:HG21	5:C:193:TYR:CZ	2.20	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:38:TYR:CD1	6:D:45:GLN:HG3	2.21	0.75
16:N:14:PRO:O	16:N:15:LYS:HB2	1.84	0.75
1:A:1161:C:H2'	1:A:1162:C:C6	2.20	0.75
4:B:20:GLU:O	4:B:39:ILE:HG23	1.85	0.75
5:C:141:VAL:HG11	5:C:202:ILE:HG12	1.67	0.75
7:E:80:ILE:CD1	7:E:91:LEU:HB2	2.17	0.75
9:G:54:THR:HG22	9:G:56:GLN:H	1.49	0.75
15:M:81:LEU:HD12	15:M:88:ARG:HG2	1.67	0.75
12:J:48:THR:HA	12:J:62:HIS:CD2	2.21	0.75
17:O:65:ARG:NH1	17:O:65:ARG:HB2	2.00	0.75
19:Q:97:SER:HB2	19:Q:102:GLY:O	1.87	0.75
5:C:116:VAL:HG21	5:C:202:ILE:HD11	1.69	0.75
7:E:7:GLU:HB3	7:E:112:LEU:HD11	1.68	0.75
1:A:459:G:H21	1:A:462:G:N2	1.84	0.75
5:C:196:LEU:HD23	5:C:196:LEU:N	2.01	0.75
23:V:6:ARG:HD3	23:V:15:ARG:HH12	1.50	0.75
1:A:201:C:H4'	1:A:216:G:H21	1.48	0.74
14:L:34:ARG:O	14:L:61:THR:HG23	1.87	0.74
17:O:77:ARG:O	17:O:80:ALA:HB3	1.87	0.74
1:A:1360:A:H2'	1:A:1361:G:C8	2.22	0.74
1:A:409:G:H5'	1:A:430:A:C5	2.23	0.74
1:A:1196:U:H5''	1:A:1197:G:H5'	1.69	0.74
7:E:43:LEU:HD11	7:E:132:ALA:HB1	1.68	0.74
1:A:203:U:O3'	1:A:204:U:H4'	1.87	0.74
1:A:406:G:H1	1:A:436:C:N4	1.85	0.74
1:A:877:C:O2	10:H:3:THR:HG21	1.88	0.74
6:D:38:TYR:HE1	6:D:45:GLN:HE21	1.31	0.74
1:A:755:G:OP2	17:O:65:ARG:HD2	1.87	0.74
1:A:1010:G:H2'	1:A:1011:G:H8	1.52	0.74
4:B:178:ARG:HH21	4:B:196:LEU:C	1.95	0.74
6:D:24:GLU:O	6:D:25:ARG:HB2	1.86	0.74
6:D:36:ARG:H	6:D:37:PRO:CD	1.96	0.74
1:A:1250:A:C5'	11:I:68:GLY:H	2.01	0.74
19:Q:45:HIS:NE2	19:Q:47:PRO:HG3	2.02	0.74
1:A:458:C:H42	1:A:463:A:H3'	1.52	0.74
4:B:101:MET:N	4:B:108:ILE:HD12	2.03	0.74
14:L:43:VAL:HG12	14:L:44:THR:N	2.02	0.74
14:L:46:LYS:HE2	14:L:47:LYS:HB2	1.68	0.74
4:B:124:SER:HB2	4:B:125:PRO:HD2	1.67	0.74
11:I:44:VAL:HG12	11:I:51:ARG:HH12	1.52	0.74
14:L:75:HIS:HD2	14:L:77:LEU:H	1.33	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:110:ASN:HD22	5:C:140:ARG:HB3	1.53	0.74
9:G:147:ALA:C	9:G:148:ASN:HD22	1.95	0.74
14:L:53:ARG:HG2	14:L:69:TYR:HE1	1.53	0.74
1:A:1490:C:O2'	1:A:1491:G:H5'	1.88	0.74
4:B:57:PHE:CE2	4:B:61:LEU:HD11	2.22	0.74
8:F:48:LEU:HD13	8:F:52:ILE:HD12	1.69	0.74
14:L:27:LEU:O	14:L:29:GLY:N	2.20	0.74
9:G:75:VAL:HG11	9:G:144:MET:HE3	1.70	0.73
10:H:121:ASP:HB2	10:H:125:ARG:HH21	1.52	0.73
15:M:49:THR:HG22	15:M:51:ALA:H	1.52	0.73
1:A:250:A:H4'	1:A:251:G:O5'	1.88	0.73
4:B:82:ARG:HA	4:B:92:TYR:CE2	2.23	0.73
4:B:219:VAL:C	4:B:221:LEU:H	1.94	0.73
18:P:34:GLU:OE2	18:P:55:ARG:HD3	1.88	0.73
20:R:19:LYS:H	20:R:19:LYS:HD2	1.54	0.73
1:A:1118:C:H1'	1:A:1179:A:C4	2.24	0.73
1:A:1125:U:H3	12:J:5:ARG:HH21	1.34	0.73
6:D:38:TYR:HD1	6:D:45:GLN:HG3	1.53	0.73
1:A:267:C:H2'	1:A:268:C:H6	1.53	0.73
6:D:26:CYS:HA	6:D:31:CYS:HB2	1.71	0.73
1:A:953:G:H1'	15:M:125:ARG:CA	2.19	0.73
5:C:10:PHE:CZ	5:C:178:LEU:HD13	2.23	0.73
1:A:149:A:H2'	1:A:150:C:C6	2.23	0.73
1:A:701:C:H5'	1:A:703:G:O4'	1.88	0.73
1:A:730:G:N2	1:A:765:G:H5''	2.04	0.73
1:A:1443:G:H5''	1:A:1446:A:C5'	2.19	0.73
14:L:110:VAL:O	14:L:122:THR:HG22	1.87	0.73
21:S:15:LEU:HD12	21:S:16:LEU:N	2.03	0.73
1:A:190:C:H4'	1:A:190(A):C:OP1	1.88	0.73
4:B:27:LYS:HE2	4:B:195:ASP:HB2	1.70	0.73
4:B:66:GLY:HA2	4:B:160:ASP:OD2	1.89	0.73
4:B:182:ILE:H	4:B:182:ILE:HD12	1.54	0.72
5:C:134:ILE:HD11	5:C:153:VAL:CG2	2.19	0.72
6:D:118:ARG:HG3	6:D:118:ARG:HH21	1.54	0.72
1:A:954:G:H21	1:A:1227:A:H62	1.35	0.72
1:A:1064:G:H4'	1:A:1065:U:C5'	2.19	0.72
1:A:1135:U:H4'	1:A:1136:U:C5	2.22	0.72
4:B:18:GLY:N	4:B:41:ILE:HG23	2.05	0.72
5:C:150:LYS:HG3	5:C:169:ALA:HB2	1.69	0.72
15:M:3:ARG:HA	15:M:9:ILE:HG13	1.70	0.72
15:M:13:LYS:HG2	15:M:44:ARG:HH21	1.54	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1281:U:H5'	1:A:1282:C:C5	2.25	0.72
11:I:4:TYR:CE2	11:I:88:TYR:HA	2.24	0.72
14:L:86:ARG:HH11	14:L:86:ARG:HG3	1.54	0.72
20:R:53:ARG:NH1	20:R:60:GLY:N	2.37	0.72
1:A:1489:G:H2'	1:A:1490:C:C5'	2.14	0.72
4:B:12:GLU:C	4:B:14:GLY:H	1.97	0.72
1:A:977:A:H2'	1:A:978:A:H5''	1.70	0.72
5:C:47:LEU:HD23	5:C:68:VAL:HG11	1.71	0.72
1:A:1437:C:H2'	1:A:1438:G:H8	1.55	0.72
6:D:3:ARG:HD2	6:D:118:ARG:CZ	2.18	0.72
13:K:110:ASP:HB2	20:R:88:LYS:NZ	2.03	0.72
15:M:23:TYR:HB2	15:M:67:GLU:OE2	1.90	0.72
21:S:14:HIS:O	21:S:18:LYS:HB2	1.89	0.72
12:J:54:PHE:O	12:J:55:LYS:HG2	1.90	0.72
14:L:75:HIS:CD2	14:L:77:LEU:H	2.07	0.72
1:A:335:C:H2'	1:A:336:C:H6	1.55	0.71
4:B:73:THR:HG21	4:B:96:ARG:HH11	1.54	0.71
15:M:69:GLU:O	15:M:72:ALA:HB3	1.90	0.71
20:R:46:GLU:H	20:R:46:GLU:CD	1.97	0.71
9:G:49:ILE:HD12	9:G:49:ILE:N	2.05	0.71
1:A:760:G:N2	19:Q:104:LYS:H	1.87	0.71
5:C:129:ALA:HB3	5:C:132:ARG:NE	2.02	0.71
9:G:145:ALA:C	9:G:147:ALA:H	1.97	0.71
7:E:81:GLU:HG2	7:E:90:VAL:HG22	1.72	0.71
1:A:1142:G:H2'	1:A:1143:G:O4'	1.89	0.71
1:A:1226:C:H4'	1:A:1227:A:OP1	1.89	0.71
1:A:193:C:H2'	1:A:194:C:C6	2.25	0.71
1:A:460:A:H62	1:A:463:A:N6	1.88	0.71
4:B:51:LEU:HD22	4:B:55:PHE:HE1	1.53	0.71
1:A:269:C:H2'	1:A:270:A:C8	2.25	0.71
1:A:408:A:OP1	1:A:408:A:H3'	1.90	0.71
10:H:60:ARG:HH11	10:H:60:ARG:HG3	1.55	0.71
1:A:101:A:O2'	1:A:102:G:H5'	1.90	0.71
5:C:20:SER:HB3	5:C:22:TRP:NE1	2.05	0.71
7:E:105:VAL:HB	7:E:106:PRO:HD3	1.71	0.71
18:P:55:ARG:O	18:P:58:TYR:HB3	1.91	0.71
9:G:113:GLU:HG2	9:G:119:ARG:HG2	1.73	0.71
15:M:81:LEU:H	15:M:81:LEU:CD2	2.04	0.71
1:A:333:G:H4'	22:T:16:HIS:CD2	2.26	0.70
4:B:47:THR:O	4:B:51:LEU:HG	1.90	0.70
10:H:51:VAL:HG12	10:H:52:ASP:H	1.56	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:G:H3'	1:A:424:G:N3	2.06	0.70
1:A:1057:G:O2'	1:A:1058:G:H5'	1.91	0.70
1:A:1106:G:OP1	5:C:172:ARG:HD3	1.91	0.70
1:A:1152:A:H5'	12:J:70:ARG:NH2	2.07	0.70
1:A:1298:C:C4	9:G:114:ARG:HD2	2.26	0.70
1:A:1401:G:N2	1:A:1402:C:H1'	2.05	0.70
5:C:3:ASN:HD22	5:C:3:ASN:H	1.39	0.70
13:K:33:THR:HG22	13:K:39:PRO:HA	1.72	0.70
5:C:15:THR:O	5:C:16:ARG:HB2	1.91	0.70
1:A:1435:G:H2'	1:A:1436:U:H6	1.55	0.70
16:N:59:ALA:O	16:N:60:SER:HB3	1.90	0.70
1:A:1005:A:H1'	1:A:1026:G:N2	2.06	0.70
1:A:1114:C:H2'	1:A:1115:C:H6	1.55	0.70
14:L:27:LEU:C	14:L:29:GLY:H	1.97	0.70
15:M:56:LEU:HD23	15:M:56:LEU:C	2.17	0.70
16:N:9:LYS:HD3	16:N:9:LYS:C	2.17	0.70
1:A:370:C:O2'	1:A:371:G:H5'	1.92	0.70
4:B:71:VAL:O	4:B:165:VAL:HG23	1.92	0.70
1:A:129(A):G:O2'	1:A:190(E):U:H2'	1.90	0.70
6:D:153:ARG:HH22	6:D:180:GLY:HA2	1.56	0.70
6:D:61:LYS:HD2	6:D:207:TYR:OH	1.91	0.70
1:A:163:C:O2'	1:A:164:U:H5'	1.91	0.70
1:A:186:C:H2'	1:A:187:C:H6	1.57	0.70
8:F:31:GLU:HA	8:F:35:ALA:HB2	1.73	0.70
23:V:5:ASP:O	23:V:11:GLY:HA3	1.92	0.70
1:A:186:C:H2'	1:A:187:C:C6	2.27	0.69
1:A:666:G:H5'	1:A:726:C:H1'	1.73	0.69
6:D:191:ARG:O	6:D:191:ARG:HD2	1.92	0.69
21:S:6:LYS:H	21:S:6:LYS:HD3	1.55	0.69
1:A:1352:C:H2'	1:A:1353:G:C8	2.27	0.69
1:A:1397:C:H4'	1:A:1398:A:OP2	1.92	0.69
1:A:1510:U:H2'	1:A:1511:G:C8	2.27	0.69
5:C:190:ARG:HG2	5:C:190:ARG:HH11	1.57	0.69
8:F:100:ASN:HD22	20:R:23:LYS:HG2	1.57	0.69
11:I:44:VAL:HG12	11:I:51:ARG:NH1	2.06	0.69
1:A:190(L):U:H6	1:A:190(L):U:C5'	2.05	0.69
1:A:975:A:H5'	1:A:975:A:H8	1.55	0.69
4:B:101:MET:HE3	4:B:108:ILE:HD13	1.75	0.69
5:C:180:ALA:HB1	5:C:203:PHE:CE1	2.27	0.69
17:O:87:ILE:HG22	17:O:88:ARG:NE	2.08	0.69
22:T:11:SER:HA	22:T:13:LEU:CD1	2.22	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:243:A:H4'	1:A:244:U:C5'	2.18	0.69
1:A:946:A:H2'	1:A:947:G:C8	2.27	0.69
1:A:1368:G:O2'	1:A:1369:C:H5'	1.92	0.69
7:E:78:HIS:CD2	10:H:107:LEU:HD12	2.25	0.69
8:F:44:GLY:HA2	8:F:59:TYR:CZ	2.28	0.69
9:G:22:LEU:HD21	9:G:66:VAL:HG21	1.75	0.69
17:O:39:LEU:HD23	17:O:39:LEU:C	2.16	0.69
1:A:1152:A:H2'	1:A:1153:C:C6	2.27	0.69
20:R:86:VAL:HG12	20:R:87:ARG:H	1.57	0.69
22:T:75:ASN:N	22:T:75:ASN:OD1	2.25	0.69
1:A:269:C:H2'	1:A:270:A:H8	1.56	0.69
4:B:146:GLN:O	4:B:150:SER:HB3	1.93	0.69
8:F:30:LEU:HD22	8:F:35:ALA:CB	2.22	0.69
14:L:55:VAL:HG11	14:L:67:THR:HG23	1.73	0.69
16:N:22:THR:OG1	16:N:33:VAL:HG21	1.92	0.69
19:Q:45:HIS:O	19:Q:47:PRO:HD3	1.92	0.69
1:A:1053:G:C3'	1:A:1054:C:H5'	2.23	0.69
12:J:25:GLU:C	12:J:27:ALA:H	2.00	0.69
1:A:409:G:N2	1:A:433:C:OP1	2.26	0.69
5:C:64:VAL:HG12	5:C:66:VAL:HG23	1.75	0.69
5:C:180:ALA:HB1	5:C:203:PHE:HE1	1.57	0.69
8:F:9:VAL:HB	8:F:87:ARG:HB2	1.74	0.69
9:G:148:ASN:HD22	9:G:148:ASN:N	1.90	0.69
10:H:38:ILE:N	10:H:38:ILE:HD12	2.06	0.69
10:H:38:ILE:HD12	10:H:38:ILE:H	1.58	0.69
11:I:114:TYR:HD1	11:I:114:TYR:N	1.89	0.69
15:M:26:GLY:O	15:M:28:ALA:N	2.26	0.69
1:A:1281:U:H5'	1:A:1282:C:H5	1.58	0.69
15:M:8:GLU:C	15:M:9:ILE:HD12	2.17	0.69
1:A:114:U:O2'	1:A:115:G:H5'	1.93	0.69
1:A:1127:G:H21	1:A:1146:A:H62	1.39	0.69
5:C:26:LYS:H	5:C:26:LYS:CD	1.89	0.69
5:C:52:LEU:HD23	5:C:52:LEU:N	2.07	0.69
17:O:76:GLU:HA	17:O:79:ARG:HH21	1.57	0.69
1:A:338:A:H2'	1:A:339:C:C6	2.28	0.68
18:P:75:ARG:HH11	18:P:75:ARG:HG3	1.57	0.68
1:A:1145:C:HO2'	1:A:1146:A:H8	1.40	0.68
4:B:130:ARG:HD3	4:B:131:PRO:HD2	1.75	0.68
11:I:48:GLU:N	11:I:49:PRO:HD2	2.08	0.68
12:J:6:ILE:HA	12:J:97:GLU:O	1.93	0.68
1:A:975:A:H5'	1:A:975:A:C8	2.28	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:38:ARG:HH11	5:C:38:ARG:HG3	1.58	0.68
14:L:27:LEU:C	14:L:29:GLY:N	2.50	0.68
18:P:20:VAL:HG21	18:P:32:TYR:CG	2.28	0.68
5:C:150:LYS:HB3	5:C:201:TYR:HB2	1.75	0.68
7:E:15:ARG:O	7:E:16:THR:HB	1.93	0.68
8:F:10:LEU:CD1	8:F:59:TYR:HB3	2.23	0.68
15:M:34:LEU:HD22	15:M:39:ILE:HB	1.74	0.68
1:A:1161:C:H2'	1:A:1162:C:H6	1.59	0.68
4:B:87:ARG:HH11	4:B:234:PRO:HD2	1.57	0.68
9:G:15:ASP:HB3	9:G:19:GLY:H	1.59	0.68
11:I:93:ARG:CB	11:I:93:ARG:HH11	2.07	0.68
11:I:104:ARG:O	11:I:104:ARG:HD3	1.93	0.68
12:J:89:ASP:HB2	12:J:91:PRO:HD2	1.74	0.68
17:O:87:ILE:HG22	17:O:88:ARG:H	1.57	0.68
18:P:74:LEU:O	18:P:79:VAL:HG23	1.92	0.68
19:Q:20:THR:HG21	19:Q:41:LYS:HD2	1.75	0.68
4:B:159:PRO:HB2	4:B:161:ALA:O	1.93	0.68
5:C:193:TYR:CD1	5:C:194:GLY:N	2.61	0.68
1:A:1367:C:H4'	12:J:48:THR:HG21	1.76	0.68
4:B:124:SER:O	4:B:127:ILE:HG12	1.94	0.68
6:D:153:ARG:NH1	6:D:181:MET:HB2	2.09	0.68
1:A:1065:U:H4'	1:A:1066:C:O5'	1.93	0.68
4:B:30:ARG:HG3	4:B:31:TYR:CD2	2.29	0.68
5:C:58:GLU:O	5:C:59:ARG:HG3	1.94	0.68
10:H:119:LEU:HD23	10:H:119:LEU:N	2.09	0.68
12:J:35:SER:HB2	12:J:72:VAL:O	1.93	0.68
19:Q:67:LYS:HA	19:Q:70:ARG:HH12	1.59	0.68
1:A:1015:A:H2'	1:A:1016:A:C8	2.29	0.67
1:A:1152:A:H5''	12:J:13:HIS:CD2	2.29	0.67
1:A:1401:G:C2	1:A:1402:C:H1'	2.30	0.67
12:J:71:LEU:O	12:J:72:VAL:HB	1.94	0.67
13:K:67:ASP:OD2	13:K:71:LYS:HE3	1.95	0.67
19:Q:18:THR:HG23	19:Q:69:LYS:HE3	1.75	0.67
1:A:1343:G:H2'	1:A:1344:C:C6	2.29	0.67
11:I:6:GLY:N	11:I:84:ALA:HB2	2.08	0.67
6:D:3:ARG:HA	6:D:3:ARG:NE	2.10	0.67
10:H:46:LYS:HG3	10:H:64:LYS:HG2	1.75	0.67
11:I:11:LYS:O	11:I:11:LYS:HG2	1.93	0.67
21:S:20:LEU:HA	21:S:23:ASN:ND2	2.08	0.67
1:A:919:A:O2'	1:A:920:U:H5'	1.95	0.67
11:I:42:ARG:HG2	11:I:42:ARG:HH11	1.59	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1249:C:H2'	1:A:1250:A:H5'	1.77	0.67
1:A:1347:G:O2'	1:A:1348:U:P	2.52	0.67
7:E:80:ILE:HD12	7:E:80:ILE:H	1.59	0.67
17:O:39:LEU:HD22	17:O:56:LEU:HB2	1.77	0.67
17:O:56:LEU:HA	17:O:59:MET:HE2	1.75	0.67
20:R:52:PRO:HD2	20:R:55:ARG:HG3	1.76	0.67
8:F:10:LEU:HD12	8:F:59:TYR:HB3	1.77	0.67
15:M:8:GLU:OE1	15:M:22:ILE:HA	1.94	0.67
1:A:1229:A:H2'	1:A:1230:C:C6	2.29	0.67
1:A:1250:A:C4'	11:I:68:GLY:H	2.08	0.67
4:B:25:ASN:HD22	4:B:25:ASN:C	2.03	0.67
4:B:71:VAL:HG23	4:B:164:VAL:HA	1.76	0.67
1:A:291:C:O2'	1:A:292:G:H5'	1.95	0.67
1:A:1145:C:O2'	1:A:1146:A:H8	1.78	0.67
4:B:14:GLY:O	4:B:15:VAL:HG13	1.95	0.67
8:F:101:ALA:CA	20:R:28:GLU:HG3	2.24	0.67
11:I:5:TYR:C	11:I:5:TYR:CD1	2.73	0.67
15:M:13:LYS:HA	15:M:44:ARG:HE	1.59	0.67
1:A:969:A:H61	15:M:126:LYS:HE3	1.60	0.66
22:T:11:SER:HA	22:T:13:LEU:HD11	1.76	0.66
5:C:117:ALA:HB2	5:C:200:ALA:HB2	1.77	0.66
6:D:33:MET:O	6:D:37:PRO:HG3	1.95	0.66
11:I:127:LYS:O	11:I:128:ARG:HB2	1.95	0.66
1:A:1329:A:O2'	1:A:1330:U:H5'	1.94	0.66
4:B:19:HIS:ND1	4:B:204:ASN:HB3	2.10	0.66
4:B:63:MET:HG3	4:B:63:MET:O	1.95	0.66
5:C:136:GLN:O	5:C:139:GLN:HB2	1.96	0.66
1:A:736:C:OP1	20:R:68:LYS:HD2	1.95	0.66
1:A:1189:C:OP1	12:J:51:ARG:NH2	2.28	0.66
9:G:26:PHE:CE2	9:G:30:ILE:HD11	2.30	0.66
21:S:42:PRO:O	21:S:45:VAL:HG23	1.95	0.66
1:A:760:G:N2	19:Q:104:LYS:N	2.43	0.66
1:A:860:A:H2'	1:A:861:G:O4'	1.94	0.66
1:A:26:A:N6	1:A:558:G:H1'	2.11	0.66
1:A:190(I):G:O2'	1:A:190(J):U:H5'	1.96	0.66
1:A:328:C:O2	1:A:328:C:C2'	2.44	0.66
1:A:731:G:OP1	1:A:766:A:H1'	1.95	0.66
1:A:1152:A:H5'	12:J:70:ARG:HH22	1.60	0.66
14:L:33:ARG:HD2	14:L:61:THR:OG1	1.96	0.66
15:M:3:ARG:HA	15:M:8:GLU:O	1.96	0.66
1:A:722:A:H4'	1:A:723:U:C4	2.31	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:207:ALA:H	4:B:211:ILE:HD11	1.59	0.66
5:C:10:PHE:O	5:C:178:LEU:HD11	1.95	0.66
15:M:36:LYS:HD2	15:M:59:TYR:OH	1.96	0.66
20:R:55:ARG:NH1	20:R:55:ARG:HB3	2.11	0.66
1:A:1038:C:H2'	1:A:1039:C:C6	2.31	0.66
1:A:1236:A:H2'	1:A:1237:C:C6	2.31	0.66
5:C:14:ILE:HG22	5:C:15:THR:N	2.04	0.66
18:P:54:GLU:OE2	18:P:55:ARG:HG2	1.95	0.66
1:A:1228:C:OP1	15:M:115:LYS:HE3	1.96	0.65
18:P:28:ARG:HG2	18:P:29:ASP:OD2	1.96	0.65
20:R:45:SER:C	20:R:47:THR:H	2.02	0.65
21:S:39:THR:HG22	21:S:40:ILE:N	2.11	0.65
22:T:97:ALA:O	22:T:99:LEU:N	2.29	0.65
1:A:190(H):G:O2'	1:A:190(I):G:H5'	1.97	0.65
1:A:939:G:H2'	1:A:940:C:H6	1.61	0.65
4:B:132:LYS:HA	4:B:135:GLN:CB	2.21	0.65
13:K:91:ARG:C	13:K:93:GLN:N	2.50	0.65
1:A:235:C:H1'	19:Q:61:GLU:OE1	1.96	0.65
1:A:1191:A:OP1	5:C:4:LYS:HE3	1.96	0.65
1:A:1412:C:H2'	1:A:1413:A:C8	2.32	0.65
4:B:17:PHE:HD1	4:B:18:GLY:N	1.95	0.65
6:D:3:ARG:HD2	6:D:118:ARG:NH2	2.12	0.65
1:A:897:C:H5''	19:Q:101:ARG:HH22	1.60	0.65
4:B:115:LEU:HD23	4:B:116:GLU:N	2.10	0.65
7:E:7:GLU:O	7:E:34:VAL:HA	1.97	0.65
9:G:141:VAL:O	9:G:144:MET:HB2	1.96	0.65
20:R:43:PHE:HA	20:R:51:LEU:HD12	1.79	0.65
1:A:130:A:OP2	1:A:190(E):U:H2'	1.97	0.65
1:A:501:C:H2'	1:A:502:G:H8	1.61	0.65
1:A:1000:U:H2'	1:A:1001:A:H8	1.61	0.65
20:R:19:LYS:HD2	20:R:19:LYS:N	2.11	0.65
1:A:1250:A:H4'	11:I:68:GLY:N	2.11	0.65
13:K:33:THR:HG22	13:K:39:PRO:CA	2.27	0.65
23:V:6:ARG:O	23:V:12:LYS:HE3	1.97	0.65
1:A:669:U:H2'	1:A:670:G:H8	1.61	0.65
1:A:1262:C:H2'	1:A:1263:C:H6	1.61	0.65
4:B:143:GLU:O	4:B:147:LYS:HG3	1.97	0.65
8:F:100:ASN:O	20:R:28:GLU:HA	1.97	0.65
9:G:49:ILE:HD12	9:G:49:ILE:H	1.60	0.65
12:J:49:VAL:HG13	16:N:41:ARG:HB2	1.79	0.65
14:L:48:PRO:C	14:L:49:ASN:HD22	2.05	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1032:G:H2'	1:A:1033:G:O4'	1.96	0.65
1:A:1190:G:OP1	5:C:4:LYS:HA	1.97	0.65
6:D:29:PRO:HA	6:D:34:GLU:OE1	1.96	0.65
7:E:12:LEU:HD22	7:E:12:LEU:C	2.21	0.65
7:E:137:GLU:O	7:E:141:GLN:HG3	1.96	0.65
17:O:21:ASP:OD2	17:O:24:SER:HB3	1.96	0.65
1:A:163:C:C2'	1:A:164:U:H5'	2.26	0.65
1:A:404:U:O2'	1:A:405:U:H5'	1.96	0.65
1:A:1226:C:H5''	15:M:103:THR:OG1	1.96	0.65
4:B:212:GLN:NE2	4:B:216:SER:HB3	2.11	0.65
9:G:85:TYR:O	9:G:87:VAL:HG23	1.96	0.65
1:A:761:G:H5'	19:Q:102:GLY:C	2.22	0.65
4:B:101:MET:CE	4:B:108:ILE:HD13	2.26	0.65
4:B:222:ILE:HG22	4:B:226:ARG:NH2	2.11	0.65
5:C:14:ILE:O	5:C:16:ARG:N	2.31	0.65
8:F:19:LEU:HD21	8:F:23:LYS:HD2	1.79	0.65
8:F:69:GLU:O	8:F:72:VAL:HG23	1.97	0.65
1:A:9:G:H5'	7:E:122:GLU:OE2	1.97	0.64
1:A:791:G:H2'	1:A:792:A:H5'	1.78	0.64
1:A:1339:A:H2'	1:A:1340:A:O4'	1.98	0.64
5:C:186:PHE:CG	5:C:187:ALA:N	2.65	0.64
10:H:112:LEU:HD23	10:H:119:LEU:O	1.97	0.64
12:J:34:VAL:HG12	12:J:35:SER:N	2.12	0.64
22:T:53:LEU:HD22	22:T:56:MET:HE3	1.78	0.64
1:A:337:C:H2'	1:A:338:A:H8	1.61	0.64
1:A:1149:C:H2'	1:A:1150:U:H6	1.61	0.64
12:J:90:LEU:N	12:J:91:PRO:HD2	2.10	0.64
17:O:74:ASP:OD1	17:O:76:GLU:HB3	1.97	0.64
21:S:42:PRO:O	21:S:44:MET:N	2.29	0.64
1:A:99:C:H2'	1:A:101:A:C8	2.31	0.64
1:A:1475:G:H2'	1:A:1476:G:H8	1.61	0.64
7:E:33:VAL:HG11	7:E:109:ILE:HA	1.79	0.64
1:A:149:A:H2'	1:A:150:C:H6	1.61	0.64
5:C:64:VAL:CG2	5:C:99:VAL:HG11	2.27	0.64
11:I:9:ARG:HA	11:I:13:ALA:O	1.96	0.64
12:J:76:ASN:HD22	12:J:78:ASN:HD21	1.45	0.64
17:O:65:ARG:HB2	17:O:65:ARG:HH11	1.59	0.64
1:A:76:C:O2'	1:A:77:G:H5'	1.96	0.64
1:A:1056:U:H5'	5:C:163:ALA:HB2	1.78	0.64
1:A:1441:G:H4'	1:A:1442:G:C2	2.33	0.64
5:C:19:GLU:HB3	5:C:40:ARG:HH21	1.63	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:8:VAL:O	6:D:10:ARG:N	2.31	0.64
1:A:1343:G:H2'	1:A:1344:C:H6	1.61	0.64
1:A:1369:C:H2'	1:A:1370:G:C8	2.33	0.64
4:B:116:GLU:HG2	4:B:153:ARG:HH12	1.63	0.64
4:B:132:LYS:HG2	4:B:135:GLN:OE1	1.98	0.64
5:C:20:SER:HB3	5:C:22:TRP:HE1	1.61	0.64
8:F:44:GLY:HA2	8:F:59:TYR:CE1	2.32	0.64
13:K:33:THR:HA	13:K:39:PRO:HA	1.78	0.64
18:P:28:ARG:HG2	18:P:28:ARG:NH1	2.11	0.64
1:A:254:G:OP1	19:Q:67:LYS:O	2.16	0.64
1:A:371:G:C2'	1:A:372:C:H5'	2.28	0.64
5:C:52:LEU:H	5:C:52:LEU:CD2	2.10	0.64
7:E:34:VAL:HG12	7:E:62:ALA:HB1	1.79	0.64
9:G:22:LEU:HD11	9:G:101:LEU:HD21	1.80	0.64
20:R:25:THR:O	20:R:26:LEU:HB2	1.98	0.64
20:R:39:VAL:O	20:R:42:ARG:HB2	1.98	0.64
21:S:16:LEU:O	21:S:19:VAL:HG12	1.97	0.64
7:E:107:ARG:HH11	7:E:107:ARG:CB	2.09	0.64
7:E:150:ARG:HG3	7:E:150:ARG:HH11	1.63	0.64
11:I:93:ARG:C	11:I:95:LYS:H	2.04	0.64
14:L:86:ARG:HG3	14:L:86:ARG:NH1	2.13	0.64
1:A:792:A:H4'	1:A:793:U:H5''	1.78	0.64
1:A:972:C:C4'	12:J:57:LYS:HD3	2.25	0.64
1:A:1330:U:H2'	1:A:1331:G:H5'	1.80	0.64
11:I:81:ILE:O	11:I:85:LEU:HB2	1.98	0.64
12:J:75:ILE:HG22	12:J:76:ASN:H	1.63	0.64
13:K:84:VAL:HG23	13:K:109:VAL:O	1.97	0.64
14:L:110:VAL:HG12	14:L:111:LYS:N	2.12	0.64
1:A:22:G:H2'	1:A:23:C:C6	2.33	0.64
1:A:337:C:H2'	1:A:338:A:C8	2.33	0.64
1:A:463:A:H2	18:P:82:GLN:HG3	1.63	0.64
1:A:794:A:H2'	1:A:795:C:C6	2.32	0.64
4:B:182:ILE:HD12	4:B:182:ILE:N	2.13	0.64
4:B:187:LEU:HD13	4:B:214:ILE:HG21	1.80	0.64
9:G:31:MET:SD	9:G:34:GLY:HA2	2.38	0.64
12:J:6:ILE:HG13	12:J:71:LEU:O	1.97	0.64
15:M:81:LEU:HD23	15:M:81:LEU:N	2.10	0.64
15:M:88:ARG:HG3	15:M:98:VAL:HG11	1.79	0.64
1:A:287:U:O2'	1:A:288:A:H5'	1.97	0.63
1:A:761:G:H5'	19:Q:103:GLY:N	2.13	0.63
1:A:1196:U:H5''	1:A:1197:G:C5'	2.28	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1208:C:H2'	1:A:1209:C:H6	1.61	0.63
11:I:118:LYS:O	11:I:119:ALA:HB3	1.98	0.63
14:L:39:VAL:HA	14:L:79:GLU:CD	2.23	0.63
20:R:36:ASN:O	20:R:39:VAL:HG12	1.97	0.63
22:T:79:ARG:HD2	22:T:83:ARG:HH12	1.62	0.63
4:B:239:VAL:HG12	4:B:240:GLN:NE2	2.12	0.63
5:C:73:PRO:C	5:C:75:VAL:H	2.06	0.63
6:D:25:ARG:HE	6:D:30:LYS:HB2	1.62	0.63
7:E:80:ILE:HD12	7:E:80:ILE:N	2.13	0.63
9:G:41:ARG:O	9:G:45:ASP:HB2	1.97	0.63
11:I:22:GLY:HA3	11:I:60:ASP:HB2	1.79	0.63
14:L:28:LYS:C	14:L:30:ALA:H	2.06	0.63
19:Q:78:GLU:CD	19:Q:81:ARG:HD2	2.23	0.63
19:Q:82:MET:HA	19:Q:85:VAL:HG23	1.77	0.63
21:S:22:LEU:HD22	21:S:28:LYS:HB2	1.79	0.63
1:A:1236:A:H4'	1:A:1304:G:H4'	1.80	0.63
4:B:92:TYR:CD1	4:B:151:GLY:HA3	2.33	0.63
20:R:47:THR:HG22	20:R:48:GLY:H	1.63	0.63
21:S:22:LEU:HD23	21:S:25:LYS:NZ	2.13	0.63
21:S:52:TYR:HA	21:S:56:GLN:O	1.98	0.63
1:A:338:A:H2	1:A:351:G:H22	1.46	0.63
1:A:530:G:O6	2:W:3:G:H1'	1.98	0.63
1:A:959:A:H3'	1:A:960:U:H5''	1.80	0.63
4:B:60:ASP:O	4:B:64:ARG:HB2	1.97	0.63
5:C:64:VAL:HB	5:C:99:VAL:HG21	1.80	0.63
12:J:25:GLU:HA	12:J:28:ARG:HB3	1.81	0.63
19:Q:95:TYR:O	19:Q:97:SER:N	2.31	0.63
21:S:39:THR:HG22	21:S:40:ILE:H	1.64	0.63
1:A:627:G:O2'	1:A:628:G:H5'	1.98	0.63
1:A:1305:G:C5'	23:V:4:GLY:HA3	2.28	0.63
5:C:133:ALA:O	5:C:136:GLN:HB3	1.98	0.63
6:D:76:ARG:HG2	6:D:76:ARG:HH11	1.64	0.63
7:E:129:ILE:H	7:E:129:ILE:HD12	1.64	0.63
14:L:55:VAL:CG1	14:L:67:THR:HG23	2.28	0.63
18:P:17:TYR:HE1	18:P:41:PRO:CG	2.11	0.63
19:Q:97:SER:HB2	19:Q:103:GLY:C	2.23	0.63
1:A:407:G:H3'	1:A:431:A:OP1	1.99	0.63
1:A:524:G:H2'	1:A:525:C:C6	2.34	0.63
1:A:1497:G:O2'	1:A:1498:U:H5'	1.98	0.63
10:H:87:SER:C	10:H:88:LYS:HG2	2.23	0.63
11:I:107:ARG:HB3	11:I:107:ARG:HH11	1.63	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:17:ASP:O	12:J:21:GLN:HB2	1.98	0.63
14:L:110:VAL:CG2	14:L:120:TYR:HB3	2.28	0.63
1:A:353:A:H5'	1:A:353:A:H8	1.64	0.63
1:A:1064:G:H4'	1:A:1065:U:H5'	1.79	0.63
8:F:67:MET:HE2	8:F:72:VAL:HG22	1.79	0.63
21:S:20:LEU:HD12	21:S:21:GLU:N	2.14	0.63
1:A:132:C:O2'	1:A:133:U:H5'	1.98	0.63
1:A:1475:G:H2'	1:A:1476:G:C8	2.33	0.63
7:E:35:GLY:N	7:E:112:LEU:HD12	2.14	0.63
8:F:80:ARG:HG2	8:F:80:ARG:HH11	1.63	0.63
19:Q:60:ILE:HD13	19:Q:61:GLU:H	1.64	0.63
1:A:1319:A:OP1	21:S:5:LEU:HD11	1.99	0.62
4:B:87:ARG:HH21	4:B:219:VAL:HB	1.62	0.62
5:C:6:HIS:NE2	5:C:8:ILE:HB	2.14	0.62
8:F:6:VAL:O	8:F:62:TRP:HA	1.98	0.62
19:Q:69:LYS:O	19:Q:70:ARG:HD2	1.98	0.62
21:S:7:LYS:HG2	21:S:7:LYS:O	1.99	0.62
1:A:333:G:H4'	22:T:16:HIS:NE2	2.13	0.62
1:A:459:G:N2	1:A:462:G:N2	2.46	0.62
1:A:575:G:OP1	1:A:575:G:H4'	1.97	0.62
1:A:1279:A:H5''	1:A:1280:A:OP1	2.00	0.62
5:C:124:ILE:HD11	5:C:153:VAL:HG21	1.81	0.62
6:D:32:ALA:O	6:D:33:MET:C	2.41	0.62
15:M:40:ASN:HD22	15:M:41:PRO:CD	2.13	0.62
15:M:60:VAL:O	15:M:63:THR:HG22	1.98	0.62
15:M:115:LYS:HE3	15:M:115:LYS:H	1.63	0.62
18:P:17:TYR:HE1	18:P:41:PRO:HG2	1.64	0.62
20:R:44:LEU:HD21	20:R:70:ILE:HD13	1.81	0.62
1:A:267:C:H2'	1:A:268:C:C6	2.33	0.62
1:A:376:G:OP2	18:P:67:THR:HG21	2.00	0.62
1:A:445:G:H2'	1:A:446:G:H8	1.63	0.62
1:A:501:C:H2'	1:A:502:G:C8	2.33	0.62
1:A:1086:U:H3	1:A:1099:G:H22	1.46	0.62
4:B:15:VAL:CG1	4:B:209:ARG:HG2	2.29	0.62
14:L:40:VAL:O	14:L:40:VAL:HG12	1.98	0.62
22:T:11:SER:C	22:T:13:LEU:HD12	2.24	0.62
1:A:216:G:H5'	1:A:217:C:O5'	1.99	0.62
1:A:760:G:N1	19:Q:105:ALA:HB2	2.14	0.62
1:A:1525:G:O2'	1:A:1526:G:H5'	1.99	0.62
5:C:14:ILE:CG2	5:C:15:THR:H	2.01	0.62
5:C:59:ARG:HG2	5:C:63:ASN:O	1.99	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:108:ASN:HD22	5:C:111:LEU:HG	1.61	0.62
8:F:95:GLU:CD	8:F:95:GLU:H	2.07	0.62
1:A:190(L):U:O2'	1:A:191:G:H5'	1.98	0.62
7:E:41:VAL:HG13	7:E:113:ALA:HA	1.81	0.62
8:F:67:MET:HE3	8:F:71:ARG:O	1.99	0.62
1:A:791:G:H2'	1:A:792:A:C5'	2.30	0.62
1:A:1125:U:H3	12:J:5:ARG:NH2	1.96	0.62
11:I:97:LYS:HB3	11:I:98:PRO:HD3	1.82	0.62
14:L:43:VAL:HG12	14:L:44:THR:H	1.65	0.62
1:A:737:A:H2'	1:A:738:C:C6	2.35	0.62
1:A:760:G:H1	19:Q:105:ALA:CB	2.12	0.62
1:A:1137:C:H4'	1:A:1138:G:N2	2.14	0.62
1:A:1262:C:H2'	1:A:1263:C:C6	2.34	0.62
7:E:101:ILE:HD12	7:E:119:LEU:HD21	1.82	0.62
8:F:60:PHE:C	8:F:61:LEU:HD23	2.25	0.62
9:G:75:VAL:HG22	9:G:86:GLN:HB3	1.81	0.62
10:H:51:VAL:HG21	10:H:60:ARG:HG2	1.81	0.62
16:N:9:LYS:HG3	16:N:21:TYR:O	2.00	0.62
1:A:1514:C:H2'	1:A:1515:C:H6	1.64	0.62
6:D:146:ILE:N	6:D:146:ILE:HD12	2.13	0.62
8:F:31:GLU:HA	8:F:35:ALA:CB	2.30	0.62
1:A:1205:U:C1'	5:C:195:VAL:HG21	2.30	0.62
1:A:1251:A:H2'	1:A:1252:A:C8	2.34	0.62
13:K:29:ILE:C	13:K:29:ILE:HD12	2.25	0.62
13:K:82:VAL:HG23	13:K:105:VAL:HG13	1.82	0.62
18:P:28:ARG:NH1	18:P:29:ASP:OD2	2.33	0.62
18:P:81:ARG:C	18:P:83:GLU:H	2.08	0.62
4:B:81:VAL:HG12	4:B:92:TYR:HD2	1.65	0.61
5:C:10:PHE:CE2	5:C:178:LEU:HD13	2.35	0.61
9:G:11:GLN:C	9:G:12:LEU:HD12	2.25	0.61
16:N:4:LYS:HA	16:N:7:ILE:CD1	2.30	0.61
19:Q:81:ARG:HE	19:Q:84:LEU:HD11	1.65	0.61
1:A:193:C:H2'	1:A:194:C:H6	1.65	0.61
1:A:475:G:H2'	1:A:476:G:H5''	1.81	0.61
1:A:677:U:H3	1:A:713:G:H22	1.45	0.61
1:A:1355:G:O2'	1:A:1356:G:H5'	2.01	0.61
4:B:35:GLU:HA	4:B:39:ILE:O	1.98	0.61
4:B:178:ARG:HG3	4:B:178:ARG:NH1	2.10	0.61
5:C:64:VAL:HB	5:C:99:VAL:CB	2.30	0.61
6:D:119:GLN:HG2	6:D:123:HIS:CD2	2.35	0.61
1:A:1149:C:H2'	1:A:1150:U:C6	2.35	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1195:C:H3'	1:A:1196:U:H5'	1.82	0.61
5:C:154:SER:O	5:C:165:THR:HA	2.01	0.61
6:D:25:ARG:C	6:D:27:TYR:H	2.07	0.61
6:D:153:ARG:NE	6:D:181:MET:HE3	2.15	0.61
8:F:100:ASN:HD22	20:R:23:LYS:CG	2.12	0.61
10:H:36:LEU:HA	10:H:39:LEU:HD23	1.83	0.61
14:L:55:VAL:CG1	14:L:56:ALA:N	2.63	0.61
1:A:67:C:O2'	1:A:171:A:H1'	1.99	0.61
1:A:620:C:N1	6:D:135:LEU:HD13	2.15	0.61
1:A:1027:C:H1'	1:A:1036:G:H22	1.66	0.61
1:A:1337:G:H5''	1:A:1338:G:OP1	2.01	0.61
9:G:75:VAL:HG13	9:G:75:VAL:O	2.00	0.61
9:G:145:ALA:O	9:G:147:ALA:N	2.34	0.61
14:L:38:THR:HG22	14:L:39:VAL:HG23	1.82	0.61
19:Q:14:LYS:H	19:Q:14:LYS:HD2	1.64	0.61
22:T:54:LYS:HE3	22:T:100:ILE:HD12	1.82	0.61
1:A:299:G:H2'	1:A:300:A:C8	2.36	0.61
1:A:952:U:H1'	15:M:126:LYS:O	2.00	0.61
1:A:1351:U:O2'	1:A:1352:C:H5'	2.01	0.61
7:E:53:LEU:O	7:E:57:LYS:HB2	2.00	0.61
14:L:82:VAL:O	14:L:106:ASP:HB2	2.00	0.61
17:O:53:HIS:HE1	17:O:57:LEU:HD22	1.66	0.61
20:R:37:VAL:HG12	20:R:41:LYS:HE2	1.81	0.61
1:A:653:A:P	10:H:56:LYS:HZ1	2.23	0.61
1:A:760:G:H21	19:Q:104:LYS:H	1.48	0.61
1:A:761:G:H5'	19:Q:102:GLY:HA3	1.81	0.61
1:A:1352:C:H2'	1:A:1353:G:H8	1.63	0.61
4:B:71:VAL:CG2	4:B:164:VAL:HA	2.30	0.61
5:C:155:GLY:HA2	5:C:164:ARG:H	1.65	0.61
13:K:69:ALA:O	13:K:73:MET:HG2	2.00	0.61
1:A:156:G:O2'	1:A:157:G:H5'	2.00	0.61
1:A:761:G:H4'	19:Q:103:GLY:O	2.00	0.61
5:C:196:LEU:H	5:C:196:LEU:CD2	2.01	0.61
11:I:17:VAL:HG21	11:I:80:GLY:HA3	1.82	0.61
11:I:120:ARG:O	11:I:122:ALA:N	2.34	0.61
14:L:89:ARG:HA	14:L:97:ARG:HA	1.83	0.61
17:O:17:ARG:HG3	17:O:17:ARG:HH11	1.65	0.61
22:T:43:LEU:HD13	22:T:51:GLU:HG3	1.83	0.61
1:A:135:C:O2	18:P:1:MET:HB2	2.01	0.61
1:A:975:A:H4'	1:A:976:G:H5'	1.83	0.61
1:A:1034:G:N2	1:A:1035:A:H62	1.96	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:134:GLU:C	4:B:136:VAL:H	2.07	0.61
8:F:82:ARG:HA	8:F:82:ARG:HE	1.65	0.61
19:Q:19:VAL:HG23	19:Q:44:ALA:HB3	1.83	0.61
1:A:393:A:O2'	1:A:394:G:H5'	2.00	0.60
1:A:463:A:C2	18:P:82:GLN:HG3	2.36	0.60
1:A:839:U:O2	1:A:839:U:H2'	2.01	0.60
1:A:921:U:O2	7:E:19:MET:HB2	2.01	0.60
1:A:1386:G:O2'	1:A:1387:G:H5'	2.01	0.60
4:B:18:GLY:H	4:B:41:ILE:HG23	1.63	0.60
6:D:12:CYS:SG	6:D:19:LEU:HB2	2.41	0.60
6:D:25:ARG:HE	6:D:30:LYS:CB	2.14	0.60
10:H:41:ARG:C	10:H:43:GLY:H	2.08	0.60
13:K:14:VAL:HG21	13:K:40:ILE:CD1	2.31	0.60
15:M:54:VAL:O	15:M:58:GLU:HG2	2.01	0.60
19:Q:95:TYR:HA	19:Q:98:LEU:HD11	1.82	0.60
20:R:39:VAL:HG13	20:R:40:LEU:N	2.16	0.60
1:A:1366:C:H2'	1:A:1367:C:C6	2.33	0.60
5:C:149:ALA:O	5:C:150:LYS:HB2	2.01	0.60
6:D:205:GLU:HA	6:D:208:SER:HB2	1.83	0.60
10:H:45:ILE:C	10:H:47:GLY:H	2.09	0.60
16:N:4:LYS:HA	16:N:7:ILE:HD12	1.83	0.60
1:A:1260:C:O5'	1:A:1284:C:H4'	2.01	0.60
4:B:103:THR:HG23	4:B:176:GLU:OE1	2.01	0.60
4:B:178:ARG:NH2	4:B:196:LEU:O	2.34	0.60
7:E:6:PHE:HB3	7:E:34:VAL:HG22	1.82	0.60
16:N:3:ARG:NH1	16:N:6:LEU:HD11	2.15	0.60
1:A:254:G:O2'	1:A:255:G:H5'	2.01	0.60
1:A:452:A:O2'	1:A:453:A:H8	1.79	0.60
1:A:835:U:OP1	20:R:64:ARG:NH2	2.33	0.60
1:A:939:G:H2'	1:A:940:C:C6	2.36	0.60
1:A:1238:A:N7	1:A:1303:C:H1'	2.16	0.60
1:A:1347:G:O2'	1:A:1348:U:OP2	2.18	0.60
4:B:12:GLU:O	4:B:14:GLY:N	2.34	0.60
11:I:43:ALA:CA	11:I:74:ILE:HD13	2.27	0.60
16:N:37:PHE:CE2	16:N:53:LEU:HD13	2.35	0.60
19:Q:27:PHE:C	19:Q:27:PHE:CD1	2.79	0.60
1:A:1182:G:O2'	1:A:1183:A:OP2	2.19	0.60
11:I:10:ARG:O	11:I:11:LYS:C	2.45	0.60
1:A:112:G:N2	1:A:354:G:H5'	2.17	0.60
1:A:538:G:OP2	14:L:115:LYS:HG3	2.01	0.60
1:A:1262:C:N4	1:A:1273:G:H1	1.99	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:107:ARG:O	7:E:108:ALA:C	2.42	0.60
10:H:14:ARG:O	10:H:18:ARG:HD3	2.02	0.60
11:I:12:GLU:HG3	11:I:12:GLU:O	2.00	0.60
18:P:45:THR:HB	18:P:46:PRO:HD2	1.83	0.60
19:Q:59:ILE:CG2	19:Q:71:PHE:HB3	2.32	0.60
21:S:63:THR:HG22	21:S:64:GLU:N	2.15	0.60
22:T:39:LYS:CD	22:T:55:ILE:HD13	2.32	0.60
1:A:865:A:H2'	1:A:866:C:C6	2.37	0.60
4:B:221:LEU:O	4:B:221:LEU:HD13	2.01	0.60
5:C:47:LEU:CD2	5:C:68:VAL:HG11	2.32	0.60
15:M:91:ARG:HB2	15:M:98:VAL:HG13	1.83	0.60
15:M:94:ARG:NH1	21:S:81:ARG:HH11	1.97	0.60
19:Q:78:GLU:HG3	19:Q:78:GLU:O	2.00	0.60
20:R:52:PRO:O	20:R:56:THR:HG23	2.00	0.60
1:A:960:U:O2	1:A:960:U:H2'	2.02	0.60
5:C:156:ARG:O	5:C:157:ILE:C	2.44	0.60
8:F:72:VAL:C	8:F:74:ASP:H	2.08	0.60
10:H:55:GLY:C	10:H:56:LYS:HD2	2.27	0.60
11:I:114:TYR:CE2	12:J:59:SER:O	2.55	0.60
12:J:42:THR:HG23	12:J:67:THR:O	2.02	0.60
18:P:6:LEU:HD11	18:P:73:LEU:HD12	1.82	0.60
1:A:138:G:O2'	1:A:139:G:H5'	2.02	0.60
1:A:344:A:H5''	1:A:345:C:H5	1.67	0.60
1:A:1321:C:H42	21:S:37:ARG:NH1	1.98	0.60
3:X:34:MNU:H2'	3:X:35:U:C6	2.36	0.60
3:X:36:U:H2'	3:X:37:T6A:H8	1.66	0.60
15:M:94:ARG:HH12	21:S:81:ARG:HD3	1.67	0.60
18:P:74:LEU:HB3	18:P:79:VAL:HG21	1.82	0.60
22:T:67:ALA:HA	22:T:73:HIS:N	2.17	0.60
1:A:853:G:O2'	1:A:854:G:H5'	2.02	0.60
1:A:1208:C:H2'	1:A:1209:C:C6	2.36	0.60
1:A:1234:C:O2'	1:A:1235:U:H5'	2.02	0.60
1:A:1342:C:O2'	1:A:1343:G:H5'	2.02	0.60
4:B:60:ASP:OD1	4:B:64:ARG:HD2	2.02	0.60
4:B:84:GLU:OE1	4:B:216:SER:HA	2.01	0.60
5:C:97:LYS:O	5:C:98:ASN:HB3	2.02	0.60
18:P:18:ARG:NH1	18:P:32:TYR:OH	2.35	0.60
22:T:72:LEU:O	22:T:73:HIS:O	2.19	0.60
1:A:129:U:H5'	1:A:129(A):G:OP1	2.02	0.59
1:A:953:G:C1'	15:M:125:ARG:HA	2.28	0.59
4:B:12:GLU:HG2	4:B:44:LEU:HD22	1.82	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:49:ILE:H	9:G:49:ILE:CD1	2.14	0.59
15:M:94:ARG:HH12	21:S:81:ARG:HH11	1.49	0.59
17:O:88:ARG:HE	17:O:88:ARG:N	2.00	0.59
1:A:1072:G:H2'	1:A:1073:U:C6	2.37	0.59
1:A:1250:A:H5''	11:I:68:GLY:N	2.16	0.59
4:B:10:LEU:C	4:B:12:GLU:H	2.11	0.59
4:B:131:PRO:HB2	4:B:133:LYS:HG3	1.84	0.59
5:C:148:GLY:HA3	5:C:172:ARG:O	2.02	0.59
10:H:116:LYS:HD3	10:H:127:LEU:HD12	1.84	0.59
1:A:112:G:H21	1:A:354:G:H5'	1.67	0.59
1:A:556:C:O2'	1:A:557:G:H5'	2.01	0.59
1:A:622:A:C8	1:A:623:C:C6	2.91	0.59
1:A:716:A:N3	13:K:117:ASN:O	2.36	0.59
1:A:750:G:N3	17:O:23:GLY:HA3	2.17	0.59
1:A:1428:A:H2'	1:A:1429:C:C6	2.37	0.59
4:B:27:LYS:CE	4:B:195:ASP:HB2	2.33	0.59
4:B:131:PRO:C	4:B:133:LYS:H	2.10	0.59
5:C:147:LYS:HE2	5:C:205:GLY:HA2	1.84	0.59
14:L:71:PRO:O	14:L:102:ARG:HD2	2.02	0.59
18:P:81:ARG:HE	18:P:81:ARG:CA	2.14	0.59
1:A:418:C:H6	1:A:425:G:H1	1.47	0.59
1:A:974:A:OP1	16:N:31:ARG:HD3	2.01	0.59
1:A:1321:C:O2'	21:S:77:THR:HG21	2.03	0.59
5:C:147:LYS:HE3	5:C:203:PHE:CE2	2.37	0.59
9:G:103:TRP:HD1	9:G:106:GLN:NE2	2.00	0.59
15:M:4:ILE:HG22	15:M:5:ALA:H	1.68	0.59
20:R:33:ASP:OD2	20:R:36:ASN:HB2	2.02	0.59
20:R:53:ARG:NH1	20:R:59:SER:C	2.61	0.59
5:C:58:GLU:HB3	12:J:92:THR:HG21	1.84	0.59
10:H:74:PRO:O	10:H:75:ARG:C	2.46	0.59
14:L:58:VAL:O	14:L:65:GLU:HA	2.02	0.59
15:M:49:THR:C	15:M:51:ALA:H	2.10	0.59
1:A:425:G:H2'	1:A:426:G:O4'	2.03	0.59
1:A:1292:U:H2'	1:A:1293:G:C8	2.38	0.59
1:A:1363:A:H1'	1:A:1365:G:N7	2.17	0.59
1:A:1391:U:H2'	1:A:1392:G:H8	1.65	0.59
4:B:30:ARG:HD2	4:B:31:TYR:CE2	2.37	0.59
4:B:69:LEU:C	4:B:69:LEU:HD23	2.28	0.59
4:B:97:TRP:CE2	4:B:101:MET:HG3	2.37	0.59
4:B:200:ILE:O	4:B:201:ILE:HG13	2.03	0.59
4:B:210:SER:C	4:B:212:GLN:H	2.11	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:76:ARG:HG2	6:D:76:ARG:NH1	2.18	0.59
8:F:10:LEU:HD12	8:F:10:LEU:H	1.66	0.59
8:F:30:LEU:HD22	8:F:35:ALA:HB1	1.85	0.59
19:Q:11:VAL:C	19:Q:53:LEU:HD11	2.28	0.59
21:S:30:LEU:C	21:S:31:ILE:HD13	2.28	0.59
1:A:1490:C:H6	1:A:1490:C:C5'	2.14	0.59
4:B:47:THR:HA	4:B:202:PRO:HG2	1.84	0.59
5:C:23:TYR:CD2	5:C:24:ALA:N	2.71	0.59
5:C:189:ALA:HB3	5:C:196:LEU:O	2.03	0.59
6:D:36:ARG:N	6:D:37:PRO:CD	2.60	0.59
12:J:24:VAL:O	12:J:28:ARG:HD3	2.02	0.59
20:R:43:PHE:C	20:R:51:LEU:HD12	2.28	0.59
1:A:28:G:O2'	1:A:296:U:OP1	2.20	0.59
1:A:1051:C:O2'	1:A:1052:U:H5'	2.02	0.59
1:A:1053:G:C4'	1:A:1054:C:H5'	2.33	0.59
4:B:98:LEU:HB2	4:B:101:MET:HE3	1.83	0.59
7:E:15:ARG:O	7:E:16:THR:CB	2.51	0.59
8:F:98:LEU:HD22	8:F:101:ALA:HB2	1.84	0.59
20:R:53:ARG:C	20:R:55:ARG:N	2.60	0.59
21:S:12:ASP:HB3	21:S:14:HIS:CE1	2.38	0.59
22:T:53:LEU:O	22:T:56:MET:HB3	2.03	0.59
22:T:56:MET:HG2	22:T:84:LEU:CD1	2.32	0.59
1:A:625:G:H4'	18:P:16:HIS:CD2	2.38	0.59
1:A:840:C:H4'	1:A:841:U:OP1	2.02	0.59
1:A:908:A:H2'	1:A:909:A:C8	2.38	0.59
1:A:918:A:H2'	1:A:919:A:C8	2.38	0.59
1:A:1054:C:H42	3:X:34:MNU:H1'	1.66	0.59
1:A:1519:A:H3'	1:A:1520:G:C5'	2.32	0.59
4:B:78:GLN:HG2	4:B:94:ASN:CG	2.28	0.59
4:B:127:ILE:HG13	4:B:128:GLU:OE1	2.03	0.59
6:D:70:ILE:HG22	6:D:71:SER:N	2.17	0.59
8:F:72:VAL:C	8:F:74:ASP:N	2.57	0.59
8:F:97:PHE:HB2	20:R:32:ARG:NH2	2.18	0.59
10:H:127:LEU:N	10:H:127:LEU:HD23	2.18	0.59
13:K:86:GLY:H	13:K:112:THR:HG23	1.66	0.59
15:M:14:ARG:HB3	15:M:14:ARG:NH1	2.18	0.59
1:A:1499:A:O2'	1:A:1500:A:H5'	2.03	0.59
5:C:88:ARG:HE	5:C:101:LEU:HB3	1.67	0.59
6:D:153:ARG:HH12	6:D:180:GLY:C	2.11	0.59
8:F:22:GLU:OE1	8:F:82:ARG:HD3	2.02	0.59
11:I:93:ARG:NH1	11:I:93:ARG:CB	2.63	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:5:ARG:HB2	12:J:99:LYS:O	2.03	0.59
1:A:203:U:H5'	1:A:216:G:OP1	2.03	0.58
1:A:1281:U:H4'	1:A:1282:C:OP2	2.02	0.58
1:A:1289:A:H2'	1:A:1290:G:H5'	1.85	0.58
7:E:126:ARG:CG	7:E:126:ARG:HH11	2.15	0.58
9:G:21:VAL:HG23	9:G:22:LEU:N	2.18	0.58
13:K:84:VAL:HG11	13:K:91:ARG:HD3	1.85	0.58
18:P:42:ARG:O	18:P:43:LYS:C	2.45	0.58
19:Q:31:LEU:HG	19:Q:32:TYR:CE2	2.37	0.58
1:A:151:A:H2'	1:A:152:A:O4'	2.03	0.58
1:A:201:C:H4'	1:A:216:G:N2	2.17	0.58
1:A:738:C:H5''	8:F:69:GLU:HB3	1.85	0.58
1:A:969:A:N6	15:M:126:LYS:HE3	2.17	0.58
4:B:22:LYS:HG3	4:B:35:GLU:OE1	2.02	0.58
9:G:79:ARG:HH11	9:G:83:ALA:N	2.01	0.58
10:H:35:ILE:HG22	10:H:39:LEU:HD21	1.85	0.58
11:I:113:LYS:N	11:I:113:LYS:HD2	2.17	0.58
13:K:54:ARG:O	13:K:57:THR:HG23	2.03	0.58
16:N:9:LYS:C	16:N:11:LYS:H	2.10	0.58
1:A:948:C:O2'	1:A:949:A:H5'	2.03	0.58
5:C:93:LYS:HD3	5:C:94:LEU:HD12	1.85	0.58
13:K:54:ARG:O	13:K:57:THR:CG2	2.51	0.58
14:L:117:ARG:NH2	14:L:124:LYS:HD3	2.19	0.58
1:A:188:C:H5'	1:A:189:G:OP2	2.03	0.58
1:A:669:U:H2'	1:A:670:G:C8	2.38	0.58
4:B:139:LYS:O	4:B:139:LYS:HD3	2.03	0.58
4:B:230:VAL:HG12	4:B:231:GLU:N	2.18	0.58
8:F:36:ARG:HG2	8:F:36:ARG:HH11	1.68	0.58
8:F:89:MET:HA	8:F:89:MET:HE3	1.85	0.58
9:G:44:TYR:C	9:G:46:ALA:N	2.60	0.58
12:J:12:ASP:HB3	12:J:15:THR:CG2	2.33	0.58
17:O:87:ILE:HG22	17:O:88:ARG:N	2.19	0.58
22:T:100:ILE:O	22:T:101:GLY:C	2.46	0.58
1:A:412:A:H2'	1:A:413:G:H5'	1.85	0.58
1:A:1505:G:H2'	1:A:1541:U:OP2	2.04	0.58
5:C:5:ILE:O	5:C:5:ILE:HD12	2.03	0.58
5:C:107:GLN:O	5:C:108:ASN:HB3	2.04	0.58
9:G:145:ALA:C	9:G:147:ALA:N	2.61	0.58
11:I:10:ARG:HG2	11:I:75:ASP:CB	2.31	0.58
19:Q:81:ARG:HE	19:Q:84:LEU:CD1	2.16	0.58
1:A:154:C:H2'	1:A:155:C:H6	1.69	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:G:H5''	1:A:268:C:N4	2.11	0.58
1:A:954:G:H2'	1:A:955:U:H6	1.68	0.58
9:G:44:TYR:C	9:G:46:ALA:H	2.12	0.58
12:J:47:PHE:HB2	12:J:63:PHE:HB2	1.86	0.58
18:P:19:ILE:HG22	18:P:36:ILE:HG13	1.86	0.58
1:A:262:A:C6	1:A:263:A:C6	2.91	0.58
1:A:877:C:H1'	10:H:3:THR:CG2	2.33	0.58
1:A:1184:G:H2'	1:A:1185:G:H8	1.69	0.58
1:A:1218:C:H2'	1:A:1219:U:C6	2.38	0.58
1:A:1513:A:H2'	1:A:1514:C:C6	2.38	0.58
4:B:17:PHE:CD1	4:B:18:GLY:N	2.71	0.58
4:B:88:ALA:CB	4:B:90:MET:HG2	2.33	0.58
4:B:139:LYS:HE3	4:B:143:GLU:OE2	2.03	0.58
5:C:123:GLN:NE2	5:C:140:ARG:HH22	1.94	0.58
10:H:82:HIS:O	10:H:83:ILE:HB	2.01	0.58
12:J:89:ASP:OD2	12:J:91:PRO:HD2	2.04	0.58
14:L:83:VAL:HG22	14:L:100:ILE:HG23	1.86	0.58
16:N:8:GLU:O	16:N:11:LYS:HB2	2.03	0.58
17:O:33:THR:HG23	17:O:63:ARG:NH1	2.19	0.58
18:P:67:THR:HG22	18:P:69:THR:H	1.69	0.58
1:A:357:G:O2'	1:A:358:U:H5'	2.04	0.58
1:A:614:A:H2'	1:A:615:C:C6	2.39	0.58
1:A:1318:A:H4'	21:S:10:PHE:CE2	2.39	0.58
4:B:44:LEU:HA	4:B:47:THR:OG1	2.04	0.58
4:B:82:ARG:HA	4:B:92:TYR:HE2	1.68	0.58
5:C:191:THR:HG21	5:C:193:TYR:CE2	2.39	0.58
1:A:459:G:H1	1:A:461:C:H5''	1.67	0.58
1:A:690:G:H2'	1:A:691:G:O4'	2.04	0.58
1:A:945:G:C2	1:A:946:A:C8	2.91	0.58
1:A:1054:C:O2'	1:A:1055:A:H5''	2.03	0.58
4:B:144:ARG:HG3	4:B:145:LEU:N	2.19	0.58
5:C:40:ARG:HB3	5:C:44:GLU:CD	2.29	0.58
8:F:99:ALA:CB	20:R:31:LEU:HD12	2.34	0.58
10:H:20:TYR:HE2	10:H:75:ARG:HD2	1.65	0.58
10:H:59:LEU:O	10:H:61:VAL:HG23	2.03	0.58
20:R:47:THR:HB	20:R:49:LYS:HG2	1.86	0.58
1:A:21:G:H2'	1:A:22:G:C8	2.38	0.58
1:A:141:A:O2'	1:A:142:G:H5'	2.04	0.58
1:A:335:C:O2'	1:A:336:C:H5'	2.03	0.58
1:A:353:A:H5'	1:A:353:A:C8	2.38	0.58
1:A:547:A:H4'	1:A:548:G:O5'	2.03	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:590:C:O2'	1:A:591:U:H5'	2.04	0.58
1:A:895:G:H2'	1:A:896:C:C6	2.38	0.58
1:A:1095:U:H2'	1:A:1096:C:H6	1.67	0.58
1:A:1127:G:N2	1:A:1146:A:H62	2.01	0.58
5:C:193:TYR:HD1	5:C:194:GLY:N	2.02	0.58
10:H:103:VAL:HG21	10:H:110:ALA:HB2	1.84	0.58
15:M:50:GLU:O	15:M:54:VAL:HG23	2.04	0.58
15:M:56:LEU:HD23	15:M:56:LEU:O	2.03	0.58
17:O:12:ILE:C	17:O:14:GLU:H	2.12	0.58
17:O:26:GLU:O	17:O:27:VAL:C	2.47	0.58
18:P:1:MET:HE3	18:P:3:LYS:HD2	1.85	0.58
1:A:49:U:O2'	1:A:50:A:H2'	2.04	0.57
1:A:420:U:O5'	1:A:424:G:H8	1.86	0.57
1:A:1193:G:O2'	1:A:1194:U:H5'	2.04	0.57
8:F:98:LEU:HD23	8:F:99:ALA:H	1.69	0.57
10:H:6:ILE:HG13	10:H:31:PHE:CE2	2.39	0.57
1:A:184:G:H2'	1:A:185:A:H8	1.67	0.57
1:A:255:G:H1'	19:Q:16:GLN:NE2	2.19	0.57
1:A:314:C:O2'	1:A:315:A:H5'	2.04	0.57
1:A:1153:C:H2'	1:A:1154:G:H8	1.68	0.57
1:A:1437:C:H2'	1:A:1438:G:C8	2.39	0.57
6:D:24:GLU:OE1	6:D:24:GLU:HA	2.03	0.57
7:E:143:ARG:HH12	10:H:77:GLU:CD	2.12	0.57
9:G:149:ARG:HA	9:G:149:ARG:HE	1.69	0.57
11:I:7:THR:HG22	11:I:8:GLY:N	2.19	0.57
19:Q:82:MET:O	19:Q:83:ASP:C	2.47	0.57
1:A:1174:G:O2'	1:A:1175:G:H5'	2.04	0.57
1:A:1349:A:C4	1:A:1350:A:C8	2.92	0.57
1:A:1358:U:H3'	1:A:1359:C:H6	1.69	0.57
4:B:87:ARG:NH1	4:B:233:SER:HA	2.18	0.57
5:C:73:PRO:O	5:C:75:VAL:N	2.30	0.57
11:I:93:ARG:O	11:I:95:LYS:N	2.33	0.57
1:A:195:A:H4'	22:T:68:LYS:HE2	1.86	0.57
1:A:444:C:O2'	1:A:445:G:H5'	2.04	0.57
1:A:983:A:H5'	1:A:984:C:OP2	2.04	0.57
5:C:191:THR:HG22	5:C:192:THR:N	2.18	0.57
14:L:119:LYS:H	14:L:119:LYS:HD2	1.68	0.57
19:Q:76:LEU:C	19:Q:76:LEU:HD23	2.30	0.57
1:A:252:U:H2'	1:A:253:U:C6	2.39	0.57
1:A:308:C:H2'	1:A:309:G:H8	1.70	0.57
1:A:459:G:H3'	1:A:460:A:H5''	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1216:G:H5''	16:N:5:ALA:HB2	1.87	0.57
1:A:1370:G:O2'	1:A:1371:G:H5'	2.04	0.57
1:A:1521:G:H2'	1:A:1522:U:C6	2.40	0.57
7:E:72:GLN:O	7:E:73:ASN:HB3	2.05	0.57
12:J:87:THR:O	12:J:88:LEU:HG	2.04	0.57
13:K:105:VAL:O	13:K:105:VAL:HG12	2.05	0.57
17:O:21:ASP:CG	17:O:24:SER:HB3	2.29	0.57
17:O:26:GLU:OE1	17:O:77:ARG:HD2	2.04	0.57
19:Q:60:ILE:HD13	19:Q:61:GLU:N	2.19	0.57
22:T:43:LEU:HD12	22:T:52:ALA:HA	1.86	0.57
1:A:407:G:O2'	1:A:408:A:OP1	2.21	0.57
1:A:713:G:H2'	1:A:714:G:C8	2.40	0.57
1:A:1342:C:O2'	11:I:124:GLN:HB2	2.05	0.57
1:A:1372:U:OP1	11:I:71:SER:HB3	2.04	0.57
4:B:12:GLU:C	4:B:14:GLY:N	2.60	0.57
4:B:97:TRP:CZ2	4:B:102:LEU:HD13	2.40	0.57
4:B:112:VAL:C	4:B:114:ARG:H	2.13	0.57
4:B:115:LEU:CD2	4:B:153:ARG:HH22	2.17	0.57
4:B:180:LEU:O	4:B:181:PHE:HB2	2.04	0.57
5:C:83:ARG:O	5:C:86:VAL:N	2.37	0.57
5:C:191:THR:HG22	5:C:193:TYR:H	1.69	0.57
7:E:77:PRO:O	7:E:78:HIS:HB3	2.05	0.57
13:K:21:ILE:HG12	13:K:30:VAL:HG13	1.87	0.57
14:L:24:VAL:O	14:L:24:VAL:HG12	2.03	0.57
19:Q:86:GLU:O	19:Q:87:LYS:C	2.47	0.57
20:R:53:ARG:HH12	20:R:60:GLY:N	2.02	0.57
1:A:1243:C:H2'	1:A:1244:C:C6	2.39	0.57
6:D:34:GLU:O	6:D:35:ARG:HB2	2.03	0.57
14:L:92:ASP:C	14:L:93:LEU:HD23	2.30	0.57
1:A:190(A):C:H42	1:A:190(H):G:H1	1.53	0.57
1:A:895:G:H2'	1:A:896:C:H6	1.69	0.57
1:A:1329:A:C2'	1:A:1330:U:H5'	2.35	0.57
5:C:110:ASN:ND2	5:C:140:ARG:HB3	2.20	0.57
6:D:38:TYR:HE1	6:D:45:GLN:NE2	2.03	0.57
7:E:79:GLU:HA	7:E:91:LEU:O	2.05	0.57
13:K:74:ALA:C	13:K:76:GLY:H	2.12	0.57
13:K:95:ILE:HG21	13:K:108:ILE:HD13	1.86	0.57
15:M:74:VAL:O	15:M:77:ASN:HB3	2.04	0.57
19:Q:50:LYS:HG2	19:Q:50:LYS:O	2.04	0.57
19:Q:97:SER:OG	19:Q:103:GLY:HA2	2.05	0.57
4:B:88:ALA:HB3	4:B:90:MET:HG2	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:163:PHE:CD1	4:B:185:ILE:HB	2.40	0.57
4:B:184:VAL:O	4:B:198:ASP:HB2	2.04	0.57
9:G:28:ASN:O	9:G:31:MET:HB3	2.05	0.57
14:L:55:VAL:HG12	14:L:56:ALA:H	1.66	0.57
15:M:14:ARG:CB	15:M:14:ARG:HH11	2.18	0.57
15:M:49:THR:C	15:M:51:ALA:N	2.61	0.57
19:Q:12:SER:HB3	19:Q:20:THR:CB	2.34	0.57
1:A:409:G:H3'	1:A:431:A:N7	2.18	0.57
1:A:1286:A:C2	23:V:18:TYR:OH	2.58	0.57
4:B:101:MET:CA	4:B:108:ILE:HD12	2.34	0.57
9:G:75:VAL:HG23	9:G:87:VAL:C	2.30	0.57
9:G:108:ALA:O	9:G:119:ARG:HD2	2.05	0.57
15:M:15:VAL:HG23	15:M:43:THR:O	2.05	0.57
16:N:27:CYS:SG	16:N:43:CYS:SG	3.02	0.57
19:Q:15:MET:HE1	19:Q:43:LEU:HD13	1.87	0.57
21:S:15:LEU:HD12	21:S:15:LEU:C	2.29	0.57
1:A:1161:C:H2'	1:A:1162:C:C5	2.40	0.56
4:B:97:TRP:HZ2	4:B:102:LEU:HD13	1.70	0.56
9:G:64:GLN:O	9:G:68:ASN:HB2	2.05	0.56
11:I:49:PRO:HG2	11:I:81:ILE:HG22	1.87	0.56
11:I:84:ALA:C	11:I:86:VAL:H	2.13	0.56
1:A:409:G:H2'	1:A:409:G:N3	2.19	0.56
1:A:1375:A:O2'	1:A:1376:U:H5'	2.05	0.56
9:G:138:LYS:HD3	9:G:138:LYS:C	2.30	0.56
10:H:11:THR:HA	10:H:14:ARG:NH1	2.19	0.56
1:A:41:G:H2'	1:A:42:G:H8	1.69	0.56
1:A:231:G:O2'	1:A:232:G:H5'	2.05	0.56
1:A:338:A:H2'	1:A:339:C:H6	1.68	0.56
1:A:409:G:H1	1:A:433:C:C5'	2.19	0.56
1:A:624:C:H2'	1:A:625:G:H8	1.69	0.56
1:A:1038:C:H2'	1:A:1039:C:H6	1.70	0.56
1:A:1064:G:H4'	1:A:1065:U:H5''	1.86	0.56
1:A:1241:G:H2'	1:A:1242:C:C6	2.40	0.56
1:A:1347:G:C2'	1:A:1348:U:OP2	2.54	0.56
1:A:1392:G:O2'	1:A:1393:U:H5'	2.05	0.56
5:C:114:PRO:O	5:C:118:GLN:HB2	2.05	0.56
7:E:76:ILE:HG23	7:E:77:PRO:HD2	1.88	0.56
12:J:9:ARG:HG3	12:J:9:ARG:O	2.05	0.56
13:K:124:LYS:HE2	13:K:125:PHE:CZ	2.40	0.56
14:L:43:VAL:CG1	14:L:44:THR:N	2.68	0.56
18:P:17:TYR:CE1	18:P:41:PRO:HG2	2.40	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:162:LEU:O	6:D:165:MET:HB2	2.05	0.56
10:H:49:GLU:HG2	10:H:62:TYR:HE2	1.71	0.56
11:I:85:LEU:O	11:I:92:TYR:HD1	1.89	0.56
20:R:55:ARG:HB3	20:R:55:ARG:HH11	1.69	0.56
1:A:408:A:H5''	1:A:429:U:O2'	2.05	0.56
5:C:18:TRP:CE3	5:C:18:TRP:N	2.71	0.56
9:G:65:ALA:O	9:G:69:VAL:HG23	2.06	0.56
10:H:38:ILE:H	10:H:38:ILE:CD1	2.18	0.56
15:M:73:GLU:O	15:M:77:ASN:N	2.34	0.56
1:A:16:A:C2'	1:A:17:U:H5'	2.35	0.56
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.21	0.56
1:A:923:A:OP1	7:E:21:ALA:HB2	2.06	0.56
1:A:1329:A:P	15:M:28:ALA:HB3	2.45	0.56
1:A:1402:C:O2	1:A:1500:A:N1	2.39	0.56
4:B:51:LEU:HD22	4:B:55:PHE:CE1	2.38	0.56
4:B:68:ILE:HB	4:B:90:MET:HE3	1.88	0.56
4:B:115:LEU:HD21	4:B:153:ARG:NH2	2.18	0.56
4:B:137:ARG:NH1	4:B:137:ARG:HB3	2.21	0.56
5:C:48:TYR:HA	5:C:52:LEU:HD22	1.87	0.56
6:D:202:LEU:O	6:D:203:VAL:C	2.49	0.56
9:G:115:ARG:O	9:G:116:ALA:C	2.48	0.56
14:L:71:PRO:HG2	14:L:102:ARG:HG3	1.88	0.56
19:Q:59:ILE:HG23	19:Q:71:PHE:HB3	1.87	0.56
1:A:750:G:H21	17:O:23:GLY:HA3	1.71	0.56
1:A:926:G:H5'	1:A:927:G:O5'	2.05	0.56
1:A:1039:C:O2'	1:A:1040:U:H5'	2.05	0.56
4:B:7:VAL:C	4:B:8:LYS:HD2	2.30	0.56
5:C:28:GLN:HA	5:C:31:HIS:HD2	1.71	0.56
7:E:13:ILE:HA	7:E:29:GLY:O	2.06	0.56
11:I:97:LYS:N	11:I:98:PRO:CD	2.68	0.56
12:J:7:LYS:O	12:J:97:GLU:HB2	2.04	0.56
14:L:82:VAL:HG12	14:L:106:ASP:OD1	2.05	0.56
14:L:89:ARG:NE	14:L:97:ARG:HG2	2.21	0.56
1:A:147:G:O2'	1:A:148:G:H5'	2.06	0.56
1:A:200:G:H21	1:A:216:G:H2'	1.68	0.56
1:A:475:G:C2	1:A:476:G:C8	2.94	0.56
1:A:1118:C:O5'	1:A:1118:C:H6	1.89	0.56
10:H:73:ASP:OD2	10:H:75:ARG:HB2	2.06	0.56
11:I:114:TYR:HE2	12:J:59:SER:O	1.89	0.56
1:A:107:G:C2'	1:A:108:G:H5'	2.36	0.56
1:A:190(L):U:C2'	1:A:191:G:H5'	2.36	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:G:H5'	1:A:266:G:C8	2.40	0.56
4:B:10:LEU:HA	4:B:48:MET:SD	2.45	0.56
4:B:100:GLY:C	4:B:108:ILE:HD12	2.31	0.56
7:E:28:PHE:CD2	7:E:51:VAL:HG22	2.41	0.56
7:E:57:LYS:HG2	7:E:61:TYR:CE2	2.41	0.56
12:J:38:ILE:CB	12:J:71:LEU:HB2	2.34	0.56
12:J:39:PRO:O	12:J:69:ASN:O	2.23	0.56
1:A:39:G:O2'	1:A:40:C:H5'	2.06	0.56
4:B:212:GLN:O	4:B:213:LEU:C	2.48	0.56
5:C:30:ARG:HB3	5:C:30:ARG:CZ	2.36	0.56
5:C:138:VAL:HG22	5:C:151:VAL:HG23	1.88	0.56
9:G:38:LEU:C	9:G:38:LEU:HD12	2.31	0.56
11:I:63:ILE:CD1	11:I:81:ILE:HD11	2.36	0.56
22:T:70:SER:HA	22:T:73:HIS:CD2	2.41	0.56
1:A:41:G:H2'	1:A:42:G:C8	2.40	0.55
1:A:900:A:H2'	1:A:901:A:C8	2.40	0.55
1:A:1128:C:H5'	11:I:16:ARG:NH2	2.20	0.55
1:A:1202:G:O2'	1:A:1203:C:H5'	2.06	0.55
7:E:51:VAL:O	7:E:54:ALA:HB3	2.05	0.55
7:E:68:GLU:O	7:E:70:PRO:HD3	2.06	0.55
10:H:84:ARG:O	10:H:135:CYS:HB2	2.06	0.55
11:I:17:VAL:HG11	11:I:81:ILE:HA	1.87	0.55
20:R:73:ALA:CB	20:R:79:LEU:HD12	2.37	0.55
1:A:149:A:O2'	1:A:150:C:H5'	2.06	0.55
1:A:449:C:H2'	1:A:450:G:O4'	2.06	0.55
4:B:15:VAL:HG21	4:B:209:ARG:CG	2.37	0.55
4:B:31:TYR:HE1	4:B:200:ILE:HD13	1.70	0.55
4:B:87:ARG:NH2	4:B:219:VAL:HB	2.22	0.55
4:B:97:TRP:CD2	4:B:101:MET:HG3	2.40	0.55
8:F:14:LEU:HA	8:F:18:GLN:HE21	1.72	0.55
12:J:12:ASP:OD2	12:J:13:HIS:N	2.39	0.55
18:P:51:VAL:HG11	18:P:74:LEU:HD22	1.88	0.55
1:A:333:G:H4'	22:T:16:HIS:HE2	1.71	0.55
1:A:580:U:H2'	1:A:581:G:O4'	2.07	0.55
1:A:1153:C:H2'	1:A:1154:G:C8	2.42	0.55
4:B:239:VAL:HG12	4:B:240:GLN:HE22	1.70	0.55
5:C:3:ASN:N	5:C:3:ASN:ND2	2.50	0.55
5:C:82:GLU:O	5:C:85:ARG:HB3	2.06	0.55
6:D:16:GLY:C	6:D:33:MET:HE1	2.32	0.55
9:G:152:ALA:C	9:G:154:TYR:H	2.14	0.55
1:A:781:A:H2'	1:A:782:A:C5'	2.35	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:865:A:O2'	1:A:866:C:H5'	2.06	0.55
1:A:920:U:H2'	1:A:921:U:C6	2.41	0.55
1:A:974:A:OP2	16:N:41:ARG:NH1	2.37	0.55
1:A:1010:G:H2'	1:A:1011:G:C8	2.38	0.55
1:A:1381:U:O2'	1:A:1382:C:H5'	2.06	0.55
4:B:15:VAL:HG21	4:B:209:ARG:HG3	1.87	0.55
4:B:106:LYS:O	4:B:110:GLN:HG3	2.07	0.55
4:B:178:ARG:HH11	4:B:178:ARG:CG	2.13	0.55
17:O:78:TYR:CZ	17:O:82:ILE:HD11	2.42	0.55
1:A:302:G:H5''	14:L:17:LYS:NZ	2.22	0.55
1:A:437:U:C2'	1:A:438:G:H5'	2.36	0.55
1:A:984:C:H2'	1:A:985:C:C6	2.42	0.55
1:A:1128:C:H6	1:A:1128:C:O5'	1.89	0.55
1:A:1514:C:H2'	1:A:1515:C:C6	2.42	0.55
4:B:23:ARG:NH1	4:B:24:TRP:HA	2.21	0.55
4:B:51:LEU:O	4:B:55:PHE:HD1	1.89	0.55
4:B:219:VAL:C	4:B:221:LEU:N	2.61	0.55
5:C:134:ILE:O	5:C:138:VAL:HG23	2.07	0.55
6:D:62:GLN:NE2	6:D:65:ARG:HH12	2.05	0.55
8:F:98:LEU:HD23	8:F:99:ALA:N	2.21	0.55
11:I:5:TYR:C	11:I:84:ALA:HB2	2.31	0.55
16:N:14:PRO:O	16:N:15:LYS:CB	2.54	0.55
1:A:103:C:P	22:T:17:ARG:HH11	2.29	0.55
1:A:256:U:H2'	1:A:257:G:C8	2.42	0.55
1:A:447:G:H2'	1:A:485:G:N2	2.22	0.55
1:A:463:A:C2	18:P:82:GLN:HB2	2.42	0.55
1:A:475:G:H2'	1:A:476:G:C5'	2.37	0.55
5:C:153:VAL:HG12	5:C:154:SER:N	2.21	0.55
10:H:60:ARG:HH11	10:H:60:ARG:CG	2.20	0.55
12:J:63:PHE:CE1	16:N:45:ARG:HG3	2.42	0.55
17:O:24:SER:OG	17:O:27:VAL:HG23	2.06	0.55
18:P:53:VAL:CG2	18:P:54:GLU:N	2.70	0.55
22:T:13:LEU:HD12	22:T:13:LEU:H	1.71	0.55
22:T:57:ARG:HB2	22:T:57:ARG:HH11	1.72	0.55
22:T:89:ARG:O	22:T:93:GLU:HG2	2.06	0.55
1:A:84:U:H2'	1:A:88:A:C8	2.41	0.55
4:B:16:HIS:HB3	4:B:44:LEU:HD21	1.89	0.55
6:D:70:ILE:HD11	6:D:100:ARG:HD2	1.88	0.55
7:E:135:THR:HG22	7:E:136:MET:N	2.21	0.55
10:H:18:ARG:NH2	10:H:81:HIS:O	2.37	0.55
11:I:45:ALA:O	11:I:48:GLU:N	2.39	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:53:VAL:HG21	11:I:85:LEU:HD21	1.89	0.55
22:T:50:GLU:HG3	22:T:100:ILE:HD12	1.88	0.55
1:A:190(E):U:O2'	19:Q:63:ARG:NH2	2.39	0.55
1:A:404:U:H2'	1:A:405:U:H6	1.71	0.55
1:A:826:C:H2'	1:A:827:U:C6	2.42	0.55
1:A:838:G:C3'	1:A:839:U:H5''	2.37	0.55
1:A:974:A:OP1	1:A:974:A:H8	1.90	0.55
1:A:1249:C:C2'	1:A:1250:A:H5'	2.36	0.55
7:E:126:ARG:HH11	7:E:126:ARG:HG2	1.71	0.55
10:H:39:LEU:HD22	10:H:39:LEU:H	1.72	0.55
12:J:9:ARG:HB3	12:J:9:ARG:NH1	2.22	0.55
20:R:46:GLU:CD	20:R:46:GLU:N	2.64	0.55
1:A:942:G:C2	1:A:943:U:C6	2.95	0.55
1:A:1064:G:C4'	1:A:1065:U:H5'	2.37	0.55
1:A:1330:U:C2'	1:A:1331:G:H5'	2.37	0.55
4:B:88:ALA:HB1	4:B:226:ARG:HH22	1.72	0.55
5:C:64:VAL:HB	5:C:99:VAL:CG2	2.37	0.55
11:I:4:TYR:O	11:I:18:PHE:HA	2.07	0.55
14:L:126:LYS:H	14:L:126:LYS:CD	2.14	0.55
15:M:105:THR:O	15:M:106:ASN:C	2.48	0.55
17:O:10:LYS:HD2	17:O:10:LYS:C	2.32	0.55
19:Q:40:LYS:HD3	19:Q:42:TYR:CZ	2.41	0.55
1:A:554:C:H2'	1:A:555:C:C6	2.42	0.55
1:A:761:G:H5'	19:Q:102:GLY:CA	2.37	0.55
1:A:977:A:C2'	1:A:978:A:H5''	2.36	0.55
1:A:1123:A:H2	12:J:39:PRO:HG3	1.71	0.55
1:A:1318:A:H4'	21:S:10:PHE:CZ	2.42	0.55
1:A:1413:A:O2'	1:A:1414:U:H5'	2.07	0.55
4:B:137:ARG:C	4:B:139:LYS:H	2.14	0.55
4:B:213:LEU:O	4:B:217:ARG:HG2	2.07	0.55
5:C:147:LYS:HE2	5:C:205:GLY:H	1.71	0.55
7:E:59:GLY:O	7:E:62:ALA:HB3	2.07	0.55
9:G:71:PRO:HD3	9:G:103:TRP:CZ3	2.42	0.55
22:T:100:ILE:O	22:T:102:GLY:N	2.39	0.55
1:A:260:G:H2'	1:A:261:U:C6	2.42	0.54
1:A:397:A:H5'	1:A:398:C:OP1	2.07	0.54
1:A:582:U:C1'	19:Q:105:ALA:HA	2.30	0.54
1:A:639:G:O2'	1:A:640:A:H5'	2.06	0.54
1:A:1106:G:H5''	5:C:172:ARG:CG	2.36	0.54
1:A:1205:U:H1'	5:C:195:VAL:HG21	1.90	0.54
1:A:1451:A:H8	1:A:1451:A:O5'	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:48:TYR:CD1	10:H:48:TYR:C	2.82	0.54
21:S:9:VAL:HG12	21:S:10:PHE:N	2.22	0.54
1:A:528:C:H5'	1:A:535:A:C6	2.42	0.54
1:A:744:C:H2'	1:A:745:C:C6	2.42	0.54
1:A:989:C:O2'	1:A:990:C:H5'	2.07	0.54
1:A:1005:A:H1'	1:A:1026:G:C2	2.42	0.54
1:A:1025:U:H5'	1:A:1026:G:OP1	2.07	0.54
4:B:115:LEU:HD23	4:B:115:LEU:C	2.33	0.54
6:D:70:ILE:CG2	6:D:71:SER:N	2.71	0.54
8:F:38:GLU:O	8:F:39:LYS:HB3	2.07	0.54
9:G:125:MET:O	9:G:128:ALA:HB3	2.07	0.54
10:H:41:ARG:C	10:H:43:GLY:N	2.66	0.54
10:H:97:VAL:O	10:H:100:ILE:HG13	2.07	0.54
15:M:5:ALA:O	15:M:6:GLY:C	2.50	0.54
17:O:87:ILE:CG2	17:O:88:ARG:HH21	2.20	0.54
20:R:38:GLU:OE1	20:R:38:GLU:N	2.40	0.54
1:A:445:G:O2'	1:A:446:G:H5'	2.07	0.54
1:A:456:C:H2'	1:A:457:C:C6	2.42	0.54
1:A:478:A:H2'	1:A:479:C:H5''	1.88	0.54
1:A:1305:G:O2'	1:A:1331:G:N2	2.40	0.54
4:B:114:ARG:HD2	4:B:141:GLU:OE2	2.07	0.54
7:E:96:PRO:HA	7:E:117:ASP:OD2	2.07	0.54
10:H:134:ILE:O	10:H:135:CYS:HB3	2.07	0.54
18:P:53:VAL:O	18:P:54:GLU:C	2.51	0.54
1:A:1120:G:H2'	1:A:1121:U:C6	2.42	0.54
1:A:1230:C:O2'	1:A:1231:G:H5'	2.07	0.54
1:A:1300:G:HO2'	1:A:1301:U:H6	1.55	0.54
1:A:1406:U:O2'	1:A:1407:C:H5'	2.07	0.54
4:B:36:ARG:HB2	4:B:41:ILE:HD11	1.89	0.54
4:B:115:LEU:HD12	4:B:145:LEU:HB3	1.88	0.54
5:C:51:GLY:O	5:C:70:VAL:HA	2.08	0.54
6:D:126:ILE:HG22	6:D:127:THR:N	2.23	0.54
9:G:69:VAL:HA	9:G:138:LYS:HG3	1.88	0.54
9:G:152:ALA:O	9:G:154:TYR:N	2.40	0.54
13:K:91:ARG:O	13:K:93:GLN:N	2.40	0.54
19:Q:5:VAL:O	19:Q:6:LEU:HD23	2.08	0.54
22:T:16:HIS:CE1	22:T:20:LEU:HD11	2.42	0.54
1:A:390:C:H2'	1:A:391:G:H8	1.72	0.54
3:X:30:G:H2'	3:X:30:G:N3	2.23	0.54
5:C:93:LYS:HE2	5:C:93:LYS:CA	2.36	0.54
9:G:110:GLN:OE1	9:G:110:GLN:HA	2.06	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:55:VAL:CG1	14:L:56:ALA:H	2.18	0.54
15:M:88:ARG:CB	15:M:88:ARG:HH11	2.19	0.54
18:P:53:VAL:C	18:P:55:ARG:N	2.62	0.54
22:T:100:ILE:O	22:T:100:ILE:HG22	2.06	0.54
1:A:17:U:H2'	1:A:18:C:C6	2.42	0.54
1:A:744:C:H2'	1:A:745:C:H6	1.72	0.54
1:A:811:C:H4'	1:A:900:A:N6	2.22	0.54
1:A:1305:G:N2	1:A:1331:G:H1'	2.22	0.54
1:A:1480:G:H2'	1:A:1481:U:C6	2.42	0.54
4:B:162:ILE:O	4:B:185:ILE:HG13	2.07	0.54
4:B:201:ILE:O	4:B:203:GLY:N	2.41	0.54
5:C:119:ARG:O	5:C:122:GLU:HB2	2.07	0.54
11:I:49:PRO:CG	11:I:81:ILE:HG22	2.38	0.54
15:M:17:VAL:O	15:M:20:THR:HB	2.08	0.54
19:Q:63:ARG:HG2	19:Q:64:PRO:HD2	1.89	0.54
1:A:409:G:N3	1:A:409:G:C2'	2.71	0.54
1:A:673:G:H2'	1:A:674:G:C8	2.43	0.54
1:A:1168:A:H2'	1:A:1169:A:C8	2.43	0.54
1:A:1323:G:H2'	1:A:1324:A:C8	2.42	0.54
5:C:190:ARG:HD2	5:C:190:ARG:N	2.21	0.54
6:D:200:GLU:O	6:D:201:GLN:C	2.51	0.54
1:A:1221:G:O2'	1:A:1222:G:H5'	2.08	0.54
1:A:1256:A:H5'	1:A:1258:G:H1'	1.89	0.54
1:A:1300:G:O2'	1:A:1301:U:H6	1.91	0.54
4:B:14:GLY:C	4:B:15:VAL:HG22	2.32	0.54
7:E:20:GLN:O	7:E:21:ALA:C	2.51	0.54
8:F:2:ARG:CZ	8:F:69:GLU:HG2	2.37	0.54
11:I:25:LYS:HB2	11:I:60:ASP:OD1	2.08	0.54
14:L:45:PRO:HD3	14:L:51:ALA:O	2.08	0.54
15:M:81:LEU:O	15:M:86:CYS:HB3	2.08	0.54
22:T:82:SER:O	22:T:86:ARG:HB2	2.07	0.54
1:A:474:G:N3	1:A:474:G:C3'	2.70	0.54
1:A:594:G:H2'	1:A:595:G:H5'	1.89	0.54
1:A:723:U:O2	1:A:723:U:H2'	2.08	0.54
1:A:1033:G:H2'	1:A:1034:G:H8	1.73	0.54
1:A:1104:G:H2'	1:A:1105:A:H8	1.73	0.54
4:B:101:MET:HA	4:B:108:ILE:HD12	1.90	0.54
6:D:15:GLU:HG2	6:D:63:LYS:HG3	1.90	0.54
15:M:2:ALA:O	15:M:4:ILE:HG13	2.08	0.54
1:A:113:G:H1'	1:A:354:G:H5'	1.89	0.54
1:A:192:U:H4'	22:T:102:GLY:O	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:539:A:H2'	1:A:540:G:C8	2.43	0.54
1:A:975:A:O2'	1:A:976:G:OP2	2.23	0.54
1:A:976:G:C8	1:A:1358:U:O2	2.60	0.54
1:A:1312:G:O2'	1:A:1313:U:H5'	2.08	0.54
6:D:24:GLU:O	6:D:25:ARG:CB	2.55	0.54
6:D:62:GLN:HE22	6:D:65:ARG:HH12	1.56	0.54
7:E:147:ASP:OD1	7:E:147:ASP:N	2.32	0.54
10:H:34:GLU:O	10:H:37:ARG:HB2	2.07	0.54
11:I:63:ILE:HD11	11:I:81:ILE:HD11	1.90	0.54
15:M:121:LYS:N	15:M:121:LYS:HD2	2.23	0.54
19:Q:98:LEU:O	19:Q:99:SER:HB3	2.08	0.54
1:A:390:C:H2'	1:A:391:G:C8	2.43	0.53
1:A:951:G:O2'	1:A:952:U:H5'	2.08	0.53
1:A:1126:U:H2'	1:A:1127:G:O4'	2.08	0.53
4:B:130:ARG:CD	4:B:131:PRO:HD2	2.37	0.53
5:C:20:SER:O	16:N:54:PRO:HB3	2.08	0.53
7:E:91:LEU:HB3	7:E:118:ILE:HD11	1.90	0.53
7:E:128:PRO:HG2	7:E:129:ILE:H	1.74	0.53
8:F:67:MET:CE	8:F:72:VAL:HG22	2.38	0.53
15:M:5:ALA:HB3	15:M:8:GLU:CG	2.32	0.53
20:R:59:SER:OG	20:R:62:GLU:HG3	2.07	0.53
1:A:167:G:O2'	1:A:168:G:H5'	2.07	0.53
1:A:201:C:O4'	1:A:216:G:N2	2.41	0.53
1:A:645:C:O2'	1:A:646:U:H5'	2.07	0.53
1:A:750:G:H1'	17:O:22:THR:OG1	2.08	0.53
4:B:88:ALA:C	4:B:90:MET:H	2.16	0.53
7:E:144:THR:HG22	7:E:147:ASP:OD1	2.08	0.53
8:F:8:ILE:HD11	8:F:79:LEU:HD13	1.89	0.53
8:F:14:LEU:HA	8:F:18:GLN:NE2	2.24	0.53
8:F:28:ARG:HA	8:F:28:ARG:NE	2.24	0.53
12:J:9:ARG:HD2	12:J:95:GLU:OE1	2.08	0.53
22:T:43:LEU:CD1	22:T:52:ALA:HA	2.39	0.53
1:A:403:C:O2'	1:A:404:U:H5'	2.08	0.53
1:A:448:A:C4	1:A:487:A:C2	2.96	0.53
1:A:487:A:H2'	1:A:488:C:O4'	2.08	0.53
4:B:177:ALA:O	4:B:180:LEU:N	2.41	0.53
6:D:108:LEU:HB3	6:D:110:PHE:CE1	2.44	0.53
10:H:4:ASP:OD2	10:H:85:ARG:NH1	2.41	0.53
12:J:28:ARG:HG2	12:J:28:ARG:O	2.08	0.53
16:N:26:ARG:CZ	16:N:47:LEU:HD21	2.38	0.53
19:Q:96:GLN:O	19:Q:97:SER:HB3	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:79:LEU:HD22	20:R:80:PRO:HD2	1.90	0.53
20:R:88:LYS:OXT	20:R:88:LYS:HG2	2.07	0.53
1:A:340:U:H2'	1:A:341:C:C6	2.43	0.53
1:A:929:G:P	1:A:1533:C:H2'	2.49	0.53
1:A:959:A:C2	1:A:1222:G:O4'	2.61	0.53
1:A:1487:G:O2'	1:A:1488:G:H5'	2.07	0.53
4:B:178:ARG:NH1	4:B:178:ARG:CG	2.70	0.53
5:C:30:ARG:CB	5:C:30:ARG:NH1	2.71	0.53
9:G:120:ILE:H	9:G:120:ILE:CD1	2.21	0.53
11:I:17:VAL:CG2	11:I:80:GLY:HA3	2.38	0.53
15:M:3:ARG:CA	15:M:9:ILE:HG13	2.38	0.53
18:P:53:VAL:O	18:P:55:ARG:N	2.42	0.53
21:S:46:GLY:HA2	21:S:61:TYR:HE2	1.73	0.53
4:B:91:PRO:HB3	4:B:151:GLY:O	2.09	0.53
6:D:150:GLU:HA	6:D:153:ARG:HG2	1.90	0.53
15:M:20:THR:HG23	15:M:26:GLY:HA2	1.89	0.53
19:Q:59:ILE:HG22	19:Q:71:PHE:CD1	2.43	0.53
20:R:36:ASN:ND2	20:R:38:GLU:CD	2.67	0.53
1:A:707:C:O2'	1:A:708:C:H5'	2.09	0.53
1:A:975:A:H4'	1:A:976:G:C5'	2.38	0.53
4:B:111:ARG:HB3	4:B:149:LEU:HD11	1.90	0.53
6:D:108:LEU:O	6:D:165:MET:HE2	2.07	0.53
9:G:49:ILE:N	9:G:49:ILE:CD1	2.71	0.53
9:G:151:TYR:HE1	13:K:54:ARG:CZ	2.22	0.53
10:H:83:ILE:O	10:H:83:ILE:CG2	2.55	0.53
12:J:16:LEU:O	12:J:18:ALA:N	2.41	0.53
13:K:41:THR:HG21	13:K:71:LYS:HB3	1.90	0.53
18:P:6:LEU:HD23	18:P:17:TYR:CG	2.44	0.53
18:P:22:THR:HA	18:P:33:ILE:CG1	2.37	0.53
1:A:202:U:H5'	1:A:216:G:O2'	2.08	0.53
1:A:1497:G:C2'	1:A:1498:U:H5'	2.39	0.53
4:B:163:PHE:HD1	4:B:185:ILE:HB	1.73	0.53
5:C:81:GLY:O	5:C:84:ILE:HG22	2.08	0.53
6:D:22:LYS:O	6:D:23:GLY:C	2.51	0.53
8:F:91:VAL:HG11	20:R:72:ARG:NH1	2.24	0.53
9:G:88:PRO:HB2	9:G:149:ARG:HH21	1.73	0.53
13:K:30:VAL:HG21	13:K:65:ALA:HA	1.91	0.53
15:M:33:ALA:C	15:M:35:GLU:H	2.16	0.53
18:P:69:THR:O	18:P:72:ARG:HB3	2.09	0.53
20:R:35:ARG:O	20:R:37:VAL:HG23	2.08	0.53
1:A:92:C:O2'	1:A:93:G:H5'	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:C:O2	1:A:203:U:H1'	2.09	0.53
1:A:254:G:OP1	19:Q:68:ARG:HB3	2.09	0.53
1:A:1054:C:OP1	1:A:1197:G:OP1	2.26	0.53
4:B:45:GLN:O	4:B:49:GLU:HG3	2.09	0.53
4:B:132:LYS:HB3	4:B:136:VAL:CG2	2.39	0.53
4:B:144:ARG:HA	4:B:147:LYS:HD2	1.91	0.53
12:J:31:GLY:CA	12:J:76:ASN:HD21	2.22	0.53
15:M:59:TYR:CG	15:M:59:TYR:O	2.61	0.53
1:A:942:G:H2'	1:A:943:U:H6	1.73	0.53
10:H:103:VAL:CG2	10:H:110:ALA:HB2	2.39	0.53
11:I:117:HIS:C	11:I:118:LYS:HG3	2.33	0.53
18:P:17:TYR:CE1	18:P:41:PRO:CG	2.92	0.53
18:P:75:ARG:HG3	18:P:75:ARG:NH1	2.21	0.53
21:S:71:LEU:C	21:S:73:GLU:H	2.17	0.53
1:A:154:C:H2'	1:A:155:C:C6	2.44	0.53
1:A:941:G:O2'	1:A:942:G:H5'	2.08	0.53
1:A:1195:C:H3'	1:A:1196:U:C5'	2.39	0.53
4:B:23:ARG:HH12	4:B:191:ASP:HA	1.74	0.53
5:C:181:ASN:O	5:C:204:LEU:HD12	2.09	0.53
6:D:199:ASN:ND2	6:D:201:GLN:HB2	2.24	0.53
9:G:120:ILE:HD12	9:G:120:ILE:N	2.18	0.53
11:I:48:GLU:N	11:I:49:PRO:CD	2.71	0.53
12:J:85:LEU:O	12:J:87:THR:N	2.42	0.53
14:L:25:PRO:C	14:L:27:LEU:N	2.59	0.53
14:L:85:ILE:HG23	14:L:98:TYR:HB3	1.91	0.53
15:M:53:VAL:O	15:M:57:ARG:HB2	2.09	0.53
21:S:71:LEU:O	21:S:73:GLU:N	2.42	0.53
1:A:761:G:C5'	19:Q:102:GLY:HA3	2.38	0.52
1:A:1010:G:N2	1:A:1020:U:H1'	2.23	0.52
1:A:1423:G:O2'	1:A:1424:C:H5'	2.10	0.52
4:B:144:ARG:HG3	4:B:145:LEU:H	1.72	0.52
5:C:35:GLU:OE1	5:C:97:LYS:HE3	2.08	0.52
5:C:43:LEU:HD22	5:C:68:VAL:HG21	1.91	0.52
8:F:4:TYR:CE2	8:F:72:VAL:HG21	2.44	0.52
9:G:23:VAL:HG13	9:G:43:PHE:CE2	2.43	0.52
9:G:61:VAL:O	9:G:64:GLN:HB3	2.08	0.52
11:I:49:PRO:HB3	11:I:82:ALA:HB2	1.91	0.52
12:J:63:PHE:HE1	16:N:45:ARG:HG3	1.74	0.52
1:A:650:G:O2'	1:A:651:C:H5'	2.09	0.52
1:A:750:G:N2	17:O:23:GLY:HA3	2.23	0.52
1:A:1035:A:O2'	1:A:1036:G:H5'	2.10	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:69:LEU:HD12	4:B:155:LEU:HD11	1.92	0.52
6:D:11:LEU:HD22	6:D:66:ARG:NE	2.24	0.52
11:I:42:ARG:O	11:I:43:ALA:C	2.52	0.52
11:I:95:LYS:C	11:I:98:PRO:HD2	2.34	0.52
1:A:22:G:H2'	1:A:23:C:H6	1.75	0.52
1:A:1010:G:H22	1:A:1020:U:H1'	1.73	0.52
8:F:99:ALA:HB2	20:R:31:LEU:HD12	1.91	0.52
9:G:111:ARG:HE	9:G:123:GLU:HA	1.75	0.52
11:I:69:GLY:O	11:I:73:GLN:HG3	2.09	0.52
15:M:6:GLY:O	15:M:7:VAL:HG22	2.09	0.52
15:M:56:LEU:C	15:M:56:LEU:CD2	2.82	0.52
16:N:47:LEU:O	16:N:48:ALA:C	2.52	0.52
17:O:82:ILE:HD13	17:O:88:ARG:CG	2.39	0.52
19:Q:66:SER:O	19:Q:70:ARG:NH1	2.43	0.52
1:A:458:C:H2'	1:A:459:G:H8	1.73	0.52
1:A:1060:C:O2'	1:A:1061:G:H5'	2.10	0.52
4:B:222:ILE:HG22	4:B:226:ARG:HH21	1.75	0.52
7:E:129:ILE:HD12	7:E:129:ILE:N	2.24	0.52
12:J:38:ILE:O	12:J:70:ARG:HA	2.09	0.52
14:L:28:LYS:C	14:L:30:ALA:N	2.63	0.52
20:R:53:ARG:HG2	20:R:63:GLN:HG2	1.91	0.52
1:A:16:A:O2'	1:A:17:U:H5'	2.10	0.52
1:A:625:G:H2'	1:A:626:U:C6	2.44	0.52
1:A:975:A:C5'	1:A:976:G:H5'	2.39	0.52
1:A:1513:A:C2	1:A:1523:G:C6	2.97	0.52
4:B:71:VAL:HG21	4:B:164:VAL:HG22	1.91	0.52
6:D:61:LYS:NZ	6:D:72:GLU:OE2	2.43	0.52
6:D:118:ARG:HG3	6:D:118:ARG:NH2	2.23	0.52
12:J:23:ILE:HG22	12:J:72:VAL:HG11	1.90	0.52
15:M:15:VAL:HG12	15:M:19:LEU:HD12	1.90	0.52
15:M:37:THR:CG2	15:M:55:ARG:HD2	2.39	0.52
1:A:74:C:O2'	1:A:75:G:H5'	2.10	0.52
1:A:312:C:H2'	1:A:313:A:C8	2.44	0.52
1:A:407:G:C3'	1:A:431:A:OP1	2.58	0.52
1:A:620:C:C2	6:D:135:LEU:HD13	2.45	0.52
1:A:1068:G:N7	1:A:1094:G:H2'	2.25	0.52
1:A:1427:U:O2'	1:A:1428:A:H5'	2.10	0.52
6:D:10:ARG:C	6:D:12:CYS:N	2.59	0.52
12:J:3:LYS:C	12:J:4:ILE:HG13	2.35	0.52
14:L:9:GLN:O	14:L:10:LEU:C	2.53	0.52
21:S:22:LEU:CD2	21:S:28:LYS:HB2	2.40	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:G:O2'	1:A:408:A:P	2.67	0.52
1:A:509:A:H5'	6:D:54:TYR:HD2	1.75	0.52
4:B:54:THR:O	4:B:58:ILE:HG13	2.10	0.52
5:C:87:LEU:C	5:C:89:GLU:H	2.16	0.52
6:D:45:GLN:O	6:D:46:LYS:C	2.51	0.52
7:E:43:LEU:H	7:E:65:ASN:ND2	2.08	0.52
7:E:103:GLY:O	7:E:106:PRO:HD2	2.09	0.52
9:G:15:ASP:CB	9:G:20:ASP:H	2.23	0.52
10:H:6:ILE:HD12	10:H:35:ILE:HD12	1.91	0.52
12:J:71:LEU:O	12:J:72:VAL:CB	2.58	0.52
14:L:47:LYS:CB	14:L:48:PRO:CD	2.79	0.52
14:L:88:GLY:H	14:L:98:TYR:HA	1.75	0.52
15:M:91:ARG:NH2	15:M:103:THR:HG21	2.25	0.52
18:P:15:PRO:O	18:P:16:HIS:ND1	2.42	0.52
18:P:46:PRO:HG2	18:P:47:ASP:H	1.74	0.52
1:A:460:A:N7	1:A:462:G:N2	2.44	0.52
1:A:738:C:H2'	1:A:739:C:H6	1.75	0.52
1:A:1510:U:H2'	1:A:1511:G:H8	1.71	0.52
6:D:65:ARG:HB2	6:D:75:PHE:CD1	2.45	0.52
10:H:91:ARG:HG3	14:L:7:ILE:HG13	1.91	0.52
11:I:45:ALA:O	11:I:46:ALA:C	2.53	0.52
12:J:4:ILE:CD1	12:J:74:ILE:HG13	2.37	0.52
20:R:48:GLY:H	20:R:82:THR:HA	1.74	0.52
1:A:201:C:C4'	1:A:216:G:N2	2.56	0.52
1:A:222:U:H2'	1:A:223:U:C6	2.45	0.52
1:A:513:C:H2'	1:A:514:C:C6	2.44	0.52
1:A:792:A:H4'	1:A:793:U:C5'	2.40	0.52
1:A:981:U:H5'	16:N:21:TYR:CE1	2.45	0.52
1:A:1193:G:C2'	1:A:1194:U:H5'	2.39	0.52
4:B:144:ARG:HD2	4:B:145:LEU:HD23	1.92	0.52
14:L:33:ARG:O	14:L:84:LEU:HD12	2.09	0.52
16:N:9:LYS:NZ	16:N:22:THR:HA	2.25	0.52
19:Q:104:LYS:O	19:Q:105:ALA:HB3	2.10	0.52
1:A:359:U:O2'	1:A:360:A:H5'	2.10	0.52
1:A:975:A:C4'	1:A:976:G:H5'	2.39	0.52
4:B:187:LEU:HD12	4:B:201:ILE:HG22	1.92	0.52
5:C:39:ILE:HG22	5:C:40:ARG:N	2.25	0.52
7:E:102:ALA:HB2	7:E:120:THR:HB	1.91	0.52
8:F:14:LEU:HD13	8:F:19:LEU:HA	1.91	0.52
10:H:137:VAL:HG12	10:H:138:TRP:N	2.23	0.52
12:J:7:LYS:HB2	12:J:97:GLU:CB	2.39	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:119:LYS:HD2	14:L:119:LYS:N	2.24	0.52
15:M:13:LYS:O	15:M:14:ARG:C	2.52	0.52
15:M:34:LEU:CD2	15:M:39:ILE:HB	2.38	0.52
1:A:586:C:O2'	1:A:587:G:H5'	2.09	0.51
1:A:865:A:H2'	1:A:866:C:H6	1.76	0.51
1:A:943:U:H2'	1:A:944:G:H5'	1.90	0.51
1:A:986:A:H2'	1:A:987:G:C8	2.45	0.51
1:A:1062:U:H2'	1:A:1063:C:C6	2.45	0.51
1:A:1123:A:H4'	12:J:36:GLY:HA3	1.92	0.51
6:D:70:ILE:HD11	6:D:100:ARG:CD	2.40	0.51
7:E:128:PRO:O	7:E:129:ILE:C	2.52	0.51
9:G:73:MET:HE2	9:G:149:ARG:HH22	1.75	0.51
11:I:9:ARG:CG	11:I:14:VAL:HG22	2.34	0.51
15:M:40:ASN:HD22	15:M:41:PRO:HD2	1.74	0.51
20:R:19:LYS:H	20:R:19:LYS:CD	2.22	0.51
20:R:53:ARG:HH11	20:R:59:SER:C	2.19	0.51
22:T:13:LEU:HD12	22:T:13:LEU:N	2.25	0.51
1:A:200:G:H2'	1:A:216:G:N2	2.25	0.51
1:A:984:C:H2'	1:A:985:C:H6	1.74	0.51
1:A:1150:U:O2	12:J:39:PRO:HG3	2.10	0.51
1:A:1372:U:O2'	1:A:1373:G:H5'	2.09	0.51
4:B:92:TYR:HE1	4:B:151:GLY:CA	2.20	0.51
4:B:92:TYR:CD1	4:B:92:TYR:N	2.78	0.51
4:B:200:ILE:HG22	4:B:201:ILE:N	2.18	0.51
5:C:157:ILE:CD1	5:C:166:GLU:HB2	2.40	0.51
5:C:180:ALA:O	5:C:181:ASN:HB3	2.10	0.51
5:C:186:PHE:O	5:C:187:ALA:HB2	2.09	0.51
7:E:11:ILE:HB	7:E:31:LEU:HB3	1.91	0.51
8:F:23:LYS:HA	8:F:26:ILE:HB	1.92	0.51
11:I:111:ARG:HG2	11:I:112:LYS:N	2.23	0.51
12:J:47:PHE:CZ	16:N:37:PHE:HE1	2.28	0.51
17:O:53:HIS:CE1	17:O:57:LEU:HD22	2.44	0.51
20:R:47:THR:HG22	20:R:48:GLY:N	2.25	0.51
1:A:267:C:P	19:Q:67:LYS:HB2	2.51	0.51
1:A:686:U:O4	1:A:703:G:H1'	2.10	0.51
1:A:909:A:H2'	1:A:910:C:O4'	2.10	0.51
1:A:1130:A:OP2	1:A:1131:G:H5''	2.11	0.51
1:A:1288:A:H1'	1:A:1352:C:O2'	2.10	0.51
1:A:1412:C:H2'	1:A:1413:A:H8	1.73	0.51
1:A:1507:A:C2	1:A:1508:G:C4	2.98	0.51
4:B:120:ALA:C	4:B:122:PHE:H	2.18	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:28:GLN:HA	5:C:31:HIS:CD2	2.46	0.51
11:I:4:TYR:HD1	11:I:19:LEU:O	1.93	0.51
11:I:46:ALA:O	11:I:49:PRO:HD2	2.10	0.51
12:J:34:VAL:HG12	12:J:35:SER:H	1.73	0.51
12:J:89:ASP:CB	12:J:91:PRO:HD2	2.41	0.51
13:K:58:PRO:HB2	13:K:93:GLN:HG3	1.93	0.51
17:O:67:LEU:O	17:O:70:LEU:N	2.44	0.51
1:A:45:U:H2'	1:A:46:G:C8	2.46	0.51
1:A:640:A:O2'	1:A:641:U:H5'	2.09	0.51
1:A:818:G:O2'	1:A:819:A:H5'	2.11	0.51
1:A:950:U:OP2	15:M:102:ARG:HD2	2.11	0.51
1:A:1513:A:C2	1:A:1523:G:C5	2.99	0.51
1:A:1515:C:O2'	1:A:1516:G:H5'	2.11	0.51
7:E:11:ILE:CG2	7:E:12:LEU:HD12	2.38	0.51
7:E:129:ILE:H	7:E:129:ILE:CD1	2.23	0.51
8:F:80:ARG:NH1	8:F:88:VAL:HB	2.26	0.51
10:H:86:ILE:HG12	10:H:135:CYS:HA	1.92	0.51
11:I:92:TYR:O	11:I:93:ARG:C	2.53	0.51
14:L:119:LYS:H	14:L:119:LYS:CD	2.23	0.51
15:M:10:PRO:O	15:M:11:ARG:HB2	2.10	0.51
17:O:78:TYR:C	17:O:80:ALA:N	2.66	0.51
18:P:26:ARG:HG3	18:P:27:LYS:N	2.25	0.51
19:Q:56:VAL:CG2	19:Q:81:ARG:HD3	2.41	0.51
21:S:45:VAL:HG12	21:S:46:GLY:N	2.24	0.51
1:A:193:C:O3'	22:T:61:SER:HB2	2.11	0.51
1:A:411:A:C2	1:A:417:C:O2	2.63	0.51
1:A:584:G:H2'	1:A:585:G:C8	2.45	0.51
1:A:1003:G:N1	1:A:1004:A:H1'	2.26	0.51
1:A:1021:G:O2'	1:A:1022:G:H5'	2.10	0.51
1:A:1209:C:O2'	1:A:1210:C:H5'	2.11	0.51
1:A:1392:G:O2'	1:A:1502:A:H5''	2.10	0.51
5:C:6:HIS:CD2	5:C:8:ILE:H	2.29	0.51
9:G:38:LEU:C	9:G:40:ALA:N	2.68	0.51
10:H:104:ARG:CZ	10:H:138:TRP:CZ3	2.93	0.51
11:I:12:GLU:O	11:I:12:GLU:CG	2.58	0.51
11:I:13:ALA:HA	11:I:67:GLY:O	2.10	0.51
12:J:60:ARG:HG2	12:J:60:ARG:HH11	1.76	0.51
21:S:17:GLU:O	21:S:21:GLU:HG3	2.10	0.51
22:T:34:LYS:O	22:T:37:SER:HB2	2.11	0.51
22:T:39:LYS:HD3	22:T:55:ILE:HD13	1.91	0.51
1:A:384:G:H2'	1:A:385:C:C6	2.45	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1064:G:N2	1:A:1190:G:H2'	2.25	0.51
4:B:17:PHE:HD1	4:B:18:GLY:H	1.56	0.51
5:C:38:ARG:HG3	5:C:38:ARG:NH1	2.24	0.51
9:G:15:ASP:HB3	9:G:20:ASP:H	1.76	0.51
9:G:108:ALA:C	9:G:110:GLN:H	2.18	0.51
9:G:135:VAL:O	9:G:139:GLU:HG3	2.11	0.51
19:Q:68:ARG:HG2	19:Q:68:ARG:HH11	1.74	0.51
22:T:72:LEU:O	22:T:73:HIS:C	2.52	0.51
1:A:109:A:H2'	1:A:326:G:N2	2.26	0.51
1:A:376:G:H2'	1:A:377:G:C8	2.36	0.51
1:A:965:A:C6	1:A:969:A:C2	2.99	0.51
5:C:26:LYS:N	5:C:26:LYS:CD	2.67	0.51
7:E:107:ARG:HB2	7:E:107:ARG:NH1	2.14	0.51
8:F:33:TYR:HA	8:F:71:ARG:CZ	2.40	0.51
11:I:112:LYS:HD3	11:I:112:LYS:C	2.35	0.51
1:A:35:G:H2'	1:A:36:C:C6	2.46	0.51
1:A:332:G:O2'	1:A:333:G:H5'	2.11	0.51
1:A:825:G:O2'	1:A:826:C:H5'	2.11	0.51
1:A:1298:C:H2'	9:G:114:ARG:NH1	2.26	0.51
1:A:1425:U:H2'	1:A:1426:C:C6	2.44	0.51
5:C:28:GLN:O	5:C:29:TYR:C	2.53	0.51
11:I:104:ARG:O	11:I:105:ASP:C	2.54	0.51
14:L:83:VAL:HG21	14:L:100:ILE:HD13	1.92	0.51
15:M:91:ARG:HB3	15:M:98:VAL:HG22	1.91	0.51
16:N:25:VAL:HG12	16:N:39:LEU:HD23	1.92	0.51
1:A:538:G:O2'	1:A:539:A:H5'	2.11	0.51
1:A:1006:C:H2'	1:A:1007:C:H6	1.75	0.51
1:A:1358:U:H2'	1:A:1359:C:O4'	2.10	0.51
1:A:1519:A:H3'	1:A:1520:G:H5'	1.91	0.51
4:B:16:HIS:CE1	4:B:214:ILE:HG12	2.46	0.51
4:B:118:LEU:O	4:B:120:ALA:N	2.44	0.51
6:D:207:TYR:C	6:D:209:ARG:H	2.18	0.51
9:G:15:ASP:OD2	9:G:44:TYR:OH	2.28	0.51
9:G:103:TRP:O	9:G:104:LEU:C	2.54	0.51
11:I:53:VAL:CG2	11:I:85:LEU:HD21	2.40	0.51
11:I:107:ARG:HB3	11:I:107:ARG:NH1	2.26	0.51
12:J:7:LYS:HB2	12:J:97:GLU:HB2	1.93	0.51
14:L:26:ALA:O	14:L:27:LEU:O	2.29	0.51
14:L:43:VAL:CG1	14:L:44:THR:H	2.21	0.51
14:L:110:VAL:HG21	14:L:120:TYR:HB3	1.93	0.51
15:M:49:THR:HB	15:M:52:GLU:HG3	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:21:VAL:HG21	18:P:59:TRP:CD1	2.46	0.51
21:S:58:VAL:HG21	21:S:75:ALA:HA	1.91	0.51
1:A:139:G:O2'	1:A:140:A:H5'	2.11	0.51
1:A:427:U:OP1	6:D:13:ARG:NH2	2.43	0.51
1:A:1315:U:H2'	1:A:1316:G:C8	2.46	0.51
1:A:1325:C:H4'	23:V:17:THR:HG21	1.93	0.51
4:B:96:ARG:HH12	4:B:169:LYS:NZ	2.08	0.51
14:L:113:ARG:HB2	14:L:122:THR:HG21	1.93	0.51
20:R:39:VAL:CG1	20:R:40:LEU:N	2.74	0.51
1:A:19:C:O2'	1:A:20:U:H5'	2.11	0.50
1:A:247:G:OP2	19:Q:99:SER:HB2	2.11	0.50
1:A:1003:G:C6	1:A:1004:A:H1'	2.46	0.50
1:A:1367:C:C2	1:A:1368:G:C8	2.99	0.50
4:B:115:LEU:CD2	4:B:116:GLU:N	2.74	0.50
4:B:182:ILE:H	4:B:182:ILE:CD1	2.21	0.50
10:H:36:LEU:CD1	10:H:59:LEU:HD13	2.41	0.50
10:H:97:VAL:HA	10:H:100:ILE:CD1	2.40	0.50
12:J:16:LEU:O	12:J:17:ASP:C	2.52	0.50
12:J:96:ILE:HG22	12:J:97:GLU:N	2.25	0.50
17:O:7:GLU:O	17:O:11:VAL:HG23	2.11	0.50
18:P:8:ARG:C	18:P:9:PHE:HD2	2.19	0.50
19:Q:63:ARG:HG2	19:Q:64:PRO:CD	2.42	0.50
22:T:101:GLY:O	22:T:102:GLY:C	2.53	0.50
1:A:173:U:H6	1:A:198:G:HO2'	1.54	0.50
1:A:959:A:H2'	1:A:960:U:O4'	2.11	0.50
1:A:1182:G:H4'	1:A:1183:A:O5'	2.11	0.50
4:B:15:VAL:HG11	4:B:209:ARG:CG	2.39	0.50
5:C:139:GLN:O	5:C:140:ARG:C	2.54	0.50
1:A:939:G:H5''	9:G:102:ARG:CZ	2.42	0.50
1:A:960:U:H1'	1:A:1223:C:H5'	1.93	0.50
1:A:1226:C:O2'	1:A:1227:A:H5'	2.11	0.50
1:A:1290:G:H2'	1:A:1291:G:H8	1.76	0.50
1:A:1426:C:H2'	1:A:1427:U:H6	1.76	0.50
4:B:80:ILE:CD1	4:B:208:ILE:HG23	2.29	0.50
4:B:105:PHE:O	4:B:106:LYS:C	2.54	0.50
5:C:191:THR:HG21	5:C:193:TYR:CE1	2.47	0.50
12:J:32:ALA:HB2	12:J:76:ASN:OD1	2.11	0.50
14:L:86:ARG:HB3	14:L:101:VAL:HG23	1.94	0.50
14:L:87:GLY:HA2	14:L:98:TYR:HA	1.94	0.50
16:N:36:PHE:O	16:N:36:PHE:CD1	2.65	0.50
17:O:82:ILE:HD13	17:O:88:ARG:HG3	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:A:H61	1:A:558:G:H1'	1.77	0.50
1:A:203:U:H4'	1:A:216:G:P	2.52	0.50
1:A:409:G:N2	1:A:431:A:O2'	2.44	0.50
1:A:456:C:O2'	1:A:457:C:H5'	2.12	0.50
1:A:730:G:H21	1:A:765:G:H5''	1.74	0.50
1:A:836:G:OP1	20:R:61:LYS:NZ	2.44	0.50
1:A:952:U:O2'	1:A:953:G:H5'	2.12	0.50
1:A:1101:A:C8	4:B:172:ILE:HD13	2.46	0.50
1:A:1399:C:C2	1:A:1502:A:N6	2.80	0.50
4:B:77:ALA:HB3	4:B:211:ILE:HD13	1.94	0.50
5:C:20:SER:HB3	5:C:22:TRP:CD1	2.47	0.50
7:E:144:THR:CG2	7:E:146:ALA:H	2.25	0.50
9:G:25:ALA:O	9:G:28:ASN:HB2	2.11	0.50
14:L:53:ARG:CG	14:L:69:TYR:HE1	2.23	0.50
14:L:60:LEU:CD1	14:L:85:ILE:HD12	2.29	0.50
15:M:94:ARG:HH12	21:S:81:ARG:CD	2.25	0.50
1:A:242:C:H2'	1:A:243:A:H5'	1.93	0.50
1:A:646:U:H2'	1:A:647:C:C6	2.46	0.50
1:A:707:C:H2'	1:A:708:C:H6	1.76	0.50
1:A:1056:U:C5'	5:C:163:ALA:HB2	2.42	0.50
1:A:1073:U:OP1	7:E:57:LYS:HE2	2.11	0.50
4:B:28:PHE:CD2	4:B:190:THR:HA	2.47	0.50
4:B:51:LEU:CD2	4:B:55:PHE:HE1	2.22	0.50
4:B:92:TYR:N	4:B:92:TYR:HD1	2.09	0.50
4:B:122:PHE:CZ	4:B:139:LYS:HG2	2.47	0.50
8:F:62:TRP:C	8:F:63:TYR:CD1	2.90	0.50
14:L:55:VAL:HG11	14:L:67:THR:CG2	2.41	0.50
1:A:28:G:O2'	1:A:29:G:H5'	2.12	0.50
1:A:1085:U:H3'	1:A:1086:U:C5	2.46	0.50
1:A:1086:U:H3	1:A:1099:G:N2	2.09	0.50
1:A:1220:G:N3	21:S:54:GLY:HA2	2.27	0.50
4:B:178:ARG:HH21	4:B:196:LEU:HA	1.76	0.50
6:D:121:VAL:O	6:D:134:ASP:HA	2.12	0.50
7:E:16:THR:HG21	7:E:27:ARG:HB2	1.92	0.50
7:E:80:ILE:HD12	7:E:80:ILE:O	2.12	0.50
9:G:75:VAL:CG2	9:G:86:GLN:HB3	2.40	0.50
12:J:25:GLU:C	12:J:27:ALA:N	2.69	0.50
17:O:67:LEU:O	17:O:68:ARG:C	2.54	0.50
19:Q:63:ARG:HG2	19:Q:64:PRO:N	2.27	0.50
19:Q:92:ARG:O	19:Q:95:TYR:HB2	2.12	0.50
1:A:802:A:H2'	1:A:803:G:H5'	1.92	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:938:A:N6	1:A:939:G:C6	2.80	0.50
1:A:1000:U:H2'	1:A:1001:A:C8	2.45	0.50
1:A:1031:G:H2'	1:A:1031:G:N3	2.26	0.50
1:A:1413:A:H2	1:A:1487:G:H22	1.59	0.50
4:B:82:ARG:HG2	4:B:86:GLU:OE1	2.12	0.50
4:B:183:PRO:HA	4:B:198:ASP:OD2	2.10	0.50
5:C:165:THR:O	5:C:165:THR:HG22	2.11	0.50
6:D:163:GLU:C	6:D:165:MET:H	2.20	0.50
8:F:19:LEU:HD23	8:F:20:ALA:N	2.26	0.50
9:G:152:ALA:C	9:G:154:TYR:N	2.67	0.50
10:H:38:ILE:N	10:H:38:ILE:CD1	2.74	0.50
10:H:51:VAL:HG21	10:H:60:ARG:CG	2.40	0.50
12:J:25:GLU:O	12:J:27:ALA:N	2.41	0.50
12:J:80:LYS:HA	12:J:83:GLU:HB2	1.93	0.50
13:K:123:LYS:O	13:K:124:LYS:C	2.55	0.50
14:L:41:ARG:HG2	14:L:42:THR:N	2.20	0.50
15:M:125:ARG:HD2	15:M:125:ARG:C	2.36	0.50
17:O:61:GLY:O	17:O:64:ARG:HG2	2.11	0.50
1:A:168:G:O2'	1:A:169:C:H5'	2.12	0.50
1:A:359:U:H2'	1:A:360:A:H8	1.77	0.50
1:A:408:A:OP1	1:A:431:A:OP2	2.29	0.50
1:A:456:C:H2'	1:A:457:C:H6	1.76	0.50
1:A:1293:G:O2'	1:A:1294:G:H5'	2.12	0.50
4:B:19:HIS:HB2	4:B:204:ASN:HD22	1.74	0.50
4:B:19:HIS:CD2	4:B:204:ASN:HA	2.47	0.50
4:B:178:ARG:HH21	4:B:196:LEU:CA	2.25	0.50
5:C:29:TYR:OH	16:N:54:PRO:HG2	2.12	0.50
5:C:64:VAL:HB	5:C:99:VAL:HB	1.93	0.50
5:C:139:GLN:HA	5:C:139:GLN:NE2	2.27	0.50
7:E:144:THR:O	7:E:145:LYS:C	2.55	0.50
9:G:6:ARG:O	9:G:7:ALA:C	2.55	0.50
9:G:21:VAL:HG23	9:G:22:LEU:H	1.77	0.50
15:M:15:VAL:O	15:M:18:ALA:HB3	2.11	0.50
15:M:34:LEU:HD13	15:M:41:PRO:CA	2.38	0.50
16:N:27:CYS:HB3	16:N:43:CYS:SG	2.52	0.50
17:O:5:LYS:HB2	17:O:6:GLU:OE2	2.11	0.50
19:Q:17:LYS:HA	19:Q:46:ASP:O	2.12	0.50
20:R:45:SER:C	20:R:47:THR:N	2.64	0.50
1:A:102:G:N3	1:A:151:A:H2	2.10	0.50
1:A:594:G:C2'	1:A:595:G:H5'	2.42	0.50
1:A:694:A:H5'	13:K:53:SER:HB3	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:831:U:H2'	1:A:832:C:H6	1.77	0.50
1:A:1428:A:H2'	1:A:1429:C:H6	1.77	0.50
4:B:25:ASN:C	4:B:25:ASN:ND2	2.68	0.50
4:B:210:SER:C	4:B:212:GLN:N	2.68	0.50
6:D:65:ARG:HB2	6:D:75:PHE:CE1	2.47	0.50
6:D:150:GLU:HA	6:D:153:ARG:CG	2.42	0.50
10:H:102:ARG:HG3	10:H:102:ARG:O	2.12	0.50
14:L:89:ARG:HG2	14:L:97:ARG:HG2	1.93	0.50
15:M:85:GLY:O	15:M:86:CYS:O	2.29	0.50
18:P:46:PRO:HG2	18:P:47:ASP:N	2.27	0.50
18:P:67:THR:HG22	18:P:68:ASP:N	2.27	0.50
20:R:43:PHE:CA	20:R:51:LEU:HD12	2.42	0.50
1:A:107:G:H2'	1:A:108:G:H5'	1.94	0.49
1:A:193:C:H4'	22:T:60:GLU:HG2	1.94	0.49
1:A:792:A:C4	1:A:794:A:C6	3.00	0.49
4:B:59:GLU:O	4:B:62:ALA:HB3	2.12	0.49
6:D:35:ARG:O	6:D:36:ARG:CB	2.60	0.49
12:J:34:VAL:HG11	12:J:72:VAL:HG13	1.93	0.49
15:M:20:THR:C	15:M:22:ILE:H	2.19	0.49
15:M:63:THR:HG23	15:M:64:TRP:CG	2.47	0.49
20:R:18:ARG:H	20:R:19:LYS:HD2	1.77	0.49
1:A:190(F):G:H4'	1:A:190(G):G:OP2	2.11	0.49
1:A:192:U:H1'	22:T:103:GLY:HA3	1.94	0.49
1:A:392:G:H2'	1:A:393:A:H8	1.77	0.49
1:A:578:C:O2'	1:A:728:A:N3	2.43	0.49
1:A:1366:C:C2	1:A:1367:C:C5	3.00	0.49
5:C:23:TYR:CG	5:C:24:ALA:N	2.80	0.49
5:C:35:GLU:CD	5:C:59:ARG:HH22	2.20	0.49
5:C:83:ARG:HH11	5:C:83:ARG:HG3	1.77	0.49
5:C:87:LEU:O	5:C:91:LEU:HB2	2.12	0.49
6:D:64:LEU:HD12	6:D:75:PHE:CZ	2.46	0.49
7:E:128:PRO:O	7:E:130:ASN:N	2.45	0.49
9:G:117:ALA:O	9:G:118:VAL:C	2.55	0.49
14:L:124:LYS:O	14:L:125:PRO:C	2.53	0.49
15:M:7:VAL:HG23	15:M:7:VAL:O	2.12	0.49
17:O:3:ILE:HD13	17:O:34:LEU:HD13	1.94	0.49
17:O:78:TYR:C	17:O:80:ALA:H	2.19	0.49
18:P:74:LEU:HD13	18:P:79:VAL:HG21	1.94	0.49
20:R:21:LYS:CG	20:R:57:GLY:HA3	2.42	0.49
20:R:22:VAL:O	20:R:22:VAL:HG12	2.11	0.49
22:T:36:LEU:HD12	22:T:62:LEU:HD12	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:60:GLU:O	22:T:63:ILE:HB	2.12	0.49
1:A:613:C:O2'	1:A:614:A:H5'	2.13	0.49
1:A:780:A:O2'	1:A:781:A:H5''	2.11	0.49
1:A:882:C:O2'	1:A:883:C:H5'	2.12	0.49
1:A:943:U:C2'	1:A:944:G:H5'	2.42	0.49
1:A:1105:A:H2'	1:A:1106:G:H8	1.78	0.49
1:A:1238:A:H5'	1:A:1336:C:H41	1.77	0.49
1:A:1256:A:C5'	1:A:1258:G:H1'	2.43	0.49
4:B:178:ARG:HH22	10:H:68:ARG:HH22	1.60	0.49
7:E:51:VAL:HB	7:E:52:PRO:CD	2.37	0.49
8:F:97:PHE:HB2	20:R:32:ARG:HH21	1.77	0.49
11:I:83:ARG:O	11:I:86:VAL:HB	2.12	0.49
21:S:7:LYS:H	21:S:7:LYS:HD3	1.78	0.49
1:A:131:C:H2'	1:A:132:C:C6	2.48	0.49
1:A:560:U:H5'	1:A:566:G:N2	2.27	0.49
1:A:737:A:H1'	8:F:73:ASN:HD21	1.77	0.49
1:A:1114:C:H2'	1:A:1115:C:C6	2.42	0.49
1:A:1300:G:O2'	1:A:1301:U:P	2.69	0.49
1:A:1415:G:H2'	1:A:1416:G:H8	1.78	0.49
4:B:77:ALA:HB2	4:B:211:ILE:HD12	1.94	0.49
4:B:134:GLU:C	4:B:136:VAL:N	2.71	0.49
4:B:137:ARG:HB3	4:B:137:ARG:HH11	1.78	0.49
7:E:150:ARG:HG3	7:E:150:ARG:NH1	2.26	0.49
8:F:18:GLN:O	8:F:21:LEU:HB3	2.12	0.49
8:F:80:ARG:HG2	8:F:80:ARG:NH1	2.27	0.49
12:J:79:ARG:O	12:J:83:GLU:HB2	2.12	0.49
13:K:27:ASN:HB2	13:K:55:LYS:HB3	1.93	0.49
14:L:24:VAL:HG13	14:L:98:TYR:HE2	1.76	0.49
19:Q:6:LEU:O	19:Q:59:ILE:N	2.45	0.49
19:Q:63:ARG:O	19:Q:64:PRO:C	2.56	0.49
20:R:29:PHE:CE1	20:R:31:LEU:HG	2.47	0.49
20:R:57:GLY:C	20:R:58:LEU:HD23	2.37	0.49
1:A:16:A:H2'	1:A:17:U:H5'	1.94	0.49
1:A:115:G:H1'	1:A:116:A:N7	2.27	0.49
1:A:1112:C:N3	5:C:178:LEU:N	2.61	0.49
1:A:1184:G:H2'	1:A:1185:G:C8	2.48	0.49
1:A:1349:A:P	11:I:118:LYS:NZ	2.85	0.49
6:D:120:LEU:HD23	6:D:125:HIS:HD2	1.77	0.49
9:G:129:GLU:OE1	9:G:131:LYS:HE2	2.12	0.49
10:H:7:ALA:O	10:H:8:ASP:C	2.55	0.49
10:H:35:ILE:HG23	10:H:111:ILE:HG21	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:13:LYS:HA	15:M:44:ARG:NE	2.27	0.49
15:M:37:THR:HG23	15:M:55:ARG:HG2	1.94	0.49
15:M:108:ARG:N	15:M:108:ARG:HD2	2.27	0.49
17:O:6:GLU:O	17:O:7:GLU:C	2.55	0.49
20:R:21:LYS:HG2	20:R:57:GLY:HA3	1.94	0.49
22:T:93:GLU:O	22:T:94:ALA:HB2	2.12	0.49
23:V:9:ARG:NH1	23:V:22:ARG:HG3	2.27	0.49
1:A:127:G:O2'	1:A:128:G:H5'	2.13	0.49
1:A:294:U:H2'	1:A:295:C:C6	2.47	0.49
1:A:409:G:H1	1:A:433:C:H5'	1.77	0.49
1:A:675:A:H1'	13:K:116:HIS:CD2	2.48	0.49
1:A:757:U:O2'	1:A:879:C:H1'	2.13	0.49
1:A:1097:C:H2'	1:A:1098:C:C6	2.47	0.49
1:A:1491:G:C5	24:A:1545:PAR:H21	2.48	0.49
4:B:100:GLY:O	4:B:101:MET:C	2.54	0.49
9:G:37:ASN:O	9:G:40:ALA:HB3	2.13	0.49
9:G:116:ALA:O	9:G:117:ALA:C	2.55	0.49
11:I:4:TYR:CZ	11:I:88:TYR:HD1	2.30	0.49
14:L:50:SER:O	14:L:51:ALA:HB2	2.13	0.49
15:M:91:ARG:CB	15:M:98:VAL:HG22	2.43	0.49
20:R:57:GLY:O	20:R:58:LEU:HD23	2.13	0.49
22:T:72:LEU:C	22:T:73:HIS:O	2.56	0.49
1:A:754:C:O2	1:A:754:C:H3'	2.12	0.49
1:A:1014:A:C2	1:A:1219:U:H1'	2.46	0.49
1:A:1486:G:H2'	1:A:1487:G:O4'	2.13	0.49
5:C:179:ARG:CG	5:C:180:ALA:N	2.52	0.49
6:D:163:GLU:C	6:D:165:MET:N	2.70	0.49
10:H:17:THR:HB	10:H:78:GLN:OE1	2.13	0.49
12:J:12:ASP:HB3	12:J:15:THR:HG22	1.94	0.49
14:L:110:VAL:CG1	14:L:111:LYS:N	2.75	0.49
16:N:37:PHE:CE2	16:N:56:VAL:HG21	2.47	0.49
17:O:39:LEU:CD2	17:O:56:LEU:HB2	2.42	0.49
19:Q:33:GLY:O	19:Q:34:LYS:C	2.53	0.49
22:T:16:HIS:O	22:T:17:ARG:C	2.56	0.49
1:A:349:A:H2'	1:A:350:G:O5'	2.12	0.49
1:A:488:C:O5'	1:A:488:C:H6	1.96	0.49
1:A:750:G:C2	17:O:23:GLY:HA3	2.48	0.49
1:A:840:C:C4'	1:A:841:U:OP1	2.61	0.49
1:A:1101:A:C4'	1:A:1102:A:O5'	2.58	0.49
1:A:1109:C:H2'	1:A:1110:A:O4'	2.12	0.49
1:A:1140:C:C6	1:A:1141:C:H5	2.30	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1285:A:H1'	1:A:1286:A:OP2	2.13	0.49
5:C:30:ARG:HB2	5:C:30:ARG:HH11	1.77	0.49
6:D:30:LYS:O	6:D:32:ALA:N	2.41	0.49
7:E:77:PRO:O	7:E:78:HIS:CB	2.61	0.49
13:K:58:PRO:O	13:K:59:TYR:C	2.55	0.49
14:L:86:ARG:O	14:L:87:GLY:O	2.31	0.49
16:N:21:TYR:HD2	16:N:22:THR:O	1.96	0.49
19:Q:3:LYS:HB3	19:Q:60:ILE:CD1	2.43	0.49
21:S:33:THR:HG22	21:S:35:SER:H	1.78	0.49
22:T:39:LYS:HD3	22:T:55:ILE:HG21	1.94	0.49
1:A:625:G:H2'	1:A:626:U:H6	1.77	0.49
1:A:877:C:O2'	1:A:878:G:H5'	2.12	0.49
1:A:974:A:P	16:N:41:ARG:HH12	2.36	0.49
1:A:1424:C:H2'	1:A:1425:U:C6	2.48	0.49
4:B:77:ALA:CB	4:B:211:ILE:HD13	2.43	0.49
4:B:204:ASN:O	4:B:206:ASP:N	2.45	0.49
5:C:36:ASP:OD2	5:C:36:ASP:N	2.44	0.49
5:C:58:GLU:O	5:C:64:VAL:HA	2.11	0.49
5:C:64:VAL:O	5:C:99:VAL:HB	2.13	0.49
5:C:204:LEU:HD12	5:C:204:LEU:N	2.28	0.49
6:D:105:VAL:HG12	6:D:106:TYR:N	2.28	0.49
7:E:144:THR:HG22	7:E:146:ALA:N	2.28	0.49
12:J:25:GLU:HB3	12:J:29:ARG:NE	2.23	0.49
12:J:39:PRO:O	12:J:40:LEU:HB2	2.12	0.49
14:L:39:VAL:H	14:L:57:LYS:HB2	1.78	0.49
17:O:14:GLU:HG3	17:O:15:PHE:CD1	2.47	0.49
19:Q:45:HIS:CD2	19:Q:47:PRO:HG3	2.48	0.49
20:R:53:ARG:C	20:R:55:ARG:H	2.20	0.49
21:S:71:LEU:C	21:S:73:GLU:N	2.71	0.49
1:A:98:U:O2'	1:A:99:C:H5'	2.12	0.49
1:A:176:C:OP1	22:T:29:LYS:HE2	2.12	0.49
1:A:448:A:O2'	1:A:449:C:H5'	2.12	0.49
1:A:460:A:N6	1:A:463:A:N6	2.61	0.49
1:A:953:G:N7	15:M:104:ARG:NH2	2.58	0.49
1:A:1157:A:H4'	1:A:1158:C:O5'	2.13	0.49
1:A:1250:A:H4'	11:I:68:GLY:CA	2.42	0.49
1:A:1291:G:H4'	11:I:38:GLN:O	2.13	0.49
6:D:64:LEU:O	6:D:64:LEU:HD13	2.13	0.49
6:D:106:TYR:CD2	6:D:106:TYR:C	2.90	0.49
7:E:16:THR:CG2	7:E:27:ARG:HB2	2.42	0.49
7:E:102:ALA:HB1	7:E:120:THR:HG21	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:60:PHE:CE2	20:R:78:LEU:HD21	2.48	0.49
12:J:4:ILE:HB	12:J:74:ILE:HG13	1.95	0.49
15:M:13:LYS:HD3	15:M:14:ARG:N	2.28	0.49
17:O:50:HIS:O	17:O:53:HIS:HB3	2.13	0.49
1:A:363:A:OP1	14:L:33:ARG:HD3	2.12	0.48
1:A:600:C:H2'	1:A:601:C:H6	1.77	0.48
1:A:781:A:OP1	1:A:1523:G:H5'	2.12	0.48
1:A:831:U:O2'	1:A:832:C:H5'	2.13	0.48
1:A:1003:G:H2'	1:A:1003:G:N3	2.28	0.48
1:A:1042:G:O2'	1:A:1043:C:H5'	2.13	0.48
1:A:1054:C:C2'	1:A:1055:A:H5''	2.42	0.48
1:A:1056:U:H5'	5:C:163:ALA:CB	2.42	0.48
1:A:1091:U:O2	1:A:1093:A:C8	2.66	0.48
1:A:1347:G:H2'	1:A:1373:G:H1	1.78	0.48
4:B:10:LEU:C	4:B:12:GLU:N	2.71	0.48
6:D:108:LEU:HD21	6:D:174:LEU:HD22	1.95	0.48
6:D:153:ARG:CD	6:D:181:MET:HE3	2.43	0.48
6:D:165:MET:O	6:D:168:ARG:HB2	2.13	0.48
8:F:19:LEU:C	8:F:21:LEU:N	2.71	0.48
8:F:75:LEU:C	8:F:75:LEU:HD13	2.38	0.48
12:J:25:GLU:O	12:J:29:ARG:HG3	2.13	0.48
12:J:69:ASN:O	12:J:70:ARG:HD3	2.13	0.48
15:M:3:ARG:HH22	15:M:7:VAL:HG12	1.78	0.48
17:O:76:GLU:HA	17:O:79:ARG:HE	1.77	0.48
22:T:75:ASN:O	22:T:78:ALA:HB3	2.13	0.48
1:A:190(K):G:C2'	1:A:190(L):U:H5''	2.44	0.48
1:A:491:G:O2'	1:A:492:G:H5'	2.13	0.48
1:A:718:G:H5'	1:A:719:C:OP2	2.13	0.48
1:A:760:G:H1	19:Q:105:ALA:CA	2.26	0.48
1:A:848:C:H2'	1:A:849:C:H6	1.77	0.48
1:A:934:C:C4	1:A:1345:U:C5	3.02	0.48
1:A:1031:G:H4'	1:A:1032:G:C8	2.48	0.48
1:A:1356:G:H2'	1:A:1357:A:H8	1.73	0.48
1:A:1423:G:H2'	1:A:1424:C:H6	1.78	0.48
1:A:1521:G:H2'	1:A:1522:U:H6	1.78	0.48
5:C:139:GLN:CA	5:C:139:GLN:HE21	2.26	0.48
5:C:157:ILE:HD11	5:C:166:GLU:HB2	1.95	0.48
6:D:38:TYR:CD2	6:D:38:TYR:N	2.80	0.48
9:G:48:LYS:O	9:G:51:GLN:HB2	2.12	0.48
15:M:123:ALA:O	15:M:124:PRO:C	2.56	0.48
16:N:23:ARG:NH1	16:N:30:ALA:HB2	2.28	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:73:HIS:O	22:T:74:LYS:HB2	2.12	0.48
1:A:409:G:H2'	1:A:431:A:C8	2.49	0.48
1:A:519:C:H2'	1:A:520:A:O4'	2.14	0.48
1:A:600:C:H2'	1:A:601:C:C6	2.48	0.48
1:A:954:G:C4	1:A:955:U:C6	3.02	0.48
1:A:1237:C:H4'	1:A:1334:G:N2	2.28	0.48
1:A:1294:G:O2'	1:A:1295:G:H5'	2.13	0.48
4:B:77:ALA:HB2	4:B:211:ILE:CD1	2.43	0.48
7:E:24:ARG:HB3	7:E:24:ARG:NH1	2.28	0.48
7:E:36:ASP:O	7:E:37:ARG:HB2	2.13	0.48
9:G:115:ARG:HB2	9:G:118:VAL:CG2	2.43	0.48
11:I:114:TYR:N	11:I:114:TYR:CD1	2.62	0.48
14:L:65:GLU:CD	14:L:65:GLU:N	2.71	0.48
17:O:66:LEU:O	17:O:69:TYR:HB3	2.12	0.48
18:P:6:LEU:HD23	18:P:17:TYR:CD1	2.48	0.48
1:A:942:G:N3	1:A:943:U:C6	2.81	0.48
1:A:991:U:O2	1:A:993:G:H8	1.97	0.48
1:A:1053:G:C4	1:A:1199:U:C5	3.01	0.48
1:A:1320:C:N4	21:S:37:ARG:HD3	2.29	0.48
1:A:1489:G:C3'	1:A:1490:C:H5''	2.42	0.48
4:B:20:GLU:O	4:B:39:ILE:CG2	2.58	0.48
5:C:60:ALA:O	5:C:61:ALA:HB2	2.12	0.48
5:C:127:ARG:HG2	5:C:127:ARG:O	2.12	0.48
5:C:153:VAL:CG1	5:C:154:SER:N	2.76	0.48
10:H:60:ARG:CG	10:H:60:ARG:NH1	2.75	0.48
10:H:63:LEU:HD22	10:H:63:LEU:N	2.28	0.48
10:H:81:HIS:ND1	10:H:81:HIS:N	2.60	0.48
10:H:112:LEU:HG	10:H:112:LEU:O	2.13	0.48
11:I:3:GLN:HB2	11:I:20:ARG:HG2	1.95	0.48
13:K:52:GLY:H	13:K:55:LYS:HE2	1.77	0.48
14:L:47:LYS:CG	14:L:48:PRO:HD3	2.43	0.48
20:R:74:ARG:O	20:R:75:ILE:C	2.56	0.48
22:T:41:ILE:O	22:T:45:GLN:HB2	2.13	0.48
1:A:445:G:H2'	1:A:446:G:C8	2.47	0.48
1:A:1049:U:H1'	1:A:1201:A:N7	2.28	0.48
1:A:1104:G:P	4:B:111:ARG:HD2	2.54	0.48
1:A:1226:C:H5'	15:M:96:LEU:HD13	1.96	0.48
3:X:31:A:H2'	3:X:32:C:C6	2.48	0.48
4:B:143:GLU:C	4:B:147:LYS:HE3	2.38	0.48
5:C:28:GLN:O	5:C:31:HIS:N	2.46	0.48
5:C:51:GLY:C	5:C:70:VAL:HG12	2.38	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:43:LEU:HB2	7:E:136:MET:HE2	1.94	0.48
8:F:38:GLU:HB2	8:F:64:GLN:HG2	1.96	0.48
8:F:63:TYR:CD1	8:F:63:TYR:N	2.82	0.48
16:N:26:ARG:NH2	16:N:47:LEU:HD21	2.28	0.48
1:A:285:G:O2'	1:A:286:G:H5'	2.14	0.48
1:A:475:G:N2	1:A:476:G:C8	2.82	0.48
1:A:1292:U:H2'	1:A:1293:G:H8	1.79	0.48
4:B:122:PHE:HA	4:B:127:ILE:CG2	2.44	0.48
4:B:184:VAL:N	4:B:198:ASP:OD2	2.34	0.48
5:C:40:ARG:HB3	5:C:44:GLU:HG3	1.96	0.48
20:R:87:ARG:O	20:R:88:LYS:HB3	2.13	0.48
21:S:17:GLU:HA	21:S:20:LEU:CD2	2.43	0.48
1:A:129(A):G:O2'	1:A:190(E):U:H5''	2.14	0.48
1:A:175:C:H2'	1:A:176:C:H6	1.78	0.48
1:A:408:A:H4'	1:A:409:G:OP1	2.14	0.48
1:A:486:U:O2'	1:A:487:A:H5'	2.14	0.48
1:A:604:G:O2'	1:A:605:U:H5'	2.13	0.48
1:A:1029:C:H1'	1:A:1033:G:N2	2.29	0.48
1:A:1064:G:H22	1:A:1190:G:H2'	1.79	0.48
1:A:1207:G:H2'	1:A:1208:C:H6	1.79	0.48
1:A:1221:G:C2'	1:A:1222:G:H5'	2.44	0.48
1:A:1320:C:H41	21:S:37:ARG:HD3	1.78	0.48
7:E:144:THR:HG22	7:E:146:ALA:H	1.78	0.48
11:I:114:TYR:HD2	12:J:60:ARG:HB2	1.72	0.48
15:M:40:ASN:HD22	15:M:41:PRO:N	2.11	0.48
15:M:91:ARG:HH22	15:M:103:THR:HG21	1.79	0.48
22:T:56:MET:HE1	22:T:104:LEU:HG	1.96	0.48
1:A:56:U:H2'	1:A:57:G:C8	2.49	0.48
1:A:797:C:H2'	1:A:798:G:H8	1.79	0.48
1:A:958:A:C8	21:S:55:LYS:HD2	2.48	0.48
1:A:1117:G:O3'	11:I:104:ARG:HD2	2.14	0.48
4:B:9:GLU:OE2	4:B:213:LEU:HD11	2.13	0.48
6:D:153:ARG:HD2	6:D:181:MET:HE3	1.95	0.48
9:G:51:GLN:OE1	9:G:51:GLN:HA	2.14	0.48
10:H:36:LEU:HD12	10:H:59:LEU:HD13	1.94	0.48
11:I:125:TYR:HE1	11:I:128:ARG:HB3	1.79	0.48
12:J:48:THR:HG23	12:J:62:HIS:NE2	2.29	0.48
14:L:56:ALA:HB2	14:L:70:ILE:HD11	1.95	0.48
17:O:28:GLN:O	17:O:29:VAL:C	2.55	0.48
1:A:95:U:O2'	1:A:96:G:H5'	2.14	0.48
1:A:112:G:H4'	1:A:389:A:H5''	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:C:H42	1:A:463:A:C3'	2.23	0.48
1:A:731:G:O2'	1:A:732:C:H5'	2.14	0.48
1:A:861:G:O2'	1:A:862:C:H5'	2.14	0.48
1:A:994:A:H2'	1:A:994:A:N3	2.29	0.48
1:A:1380:U:O2'	1:A:1381:U:OP2	2.28	0.48
4:B:54:THR:O	4:B:57:PHE:HB3	2.14	0.48
5:C:139:GLN:O	5:C:142:MET:N	2.46	0.48
8:F:62:TRP:C	8:F:63:TYR:HD1	2.22	0.48
9:G:38:LEU:C	9:G:40:ALA:H	2.20	0.48
12:J:65:LEU:HD23	12:J:65:LEU:C	2.39	0.48
14:L:32:PHE:HB3	14:L:84:LEU:HD11	1.95	0.48
15:M:4:ILE:CG2	15:M:5:ALA:N	2.70	0.48
15:M:88:ARG:HG3	15:M:98:VAL:CG1	2.42	0.48
19:Q:80:GLY:O	19:Q:81:ARG:HB3	2.14	0.48
21:S:22:LEU:C	21:S:24:ALA:H	2.20	0.48
1:A:176:C:O2'	1:A:177:C:H5'	2.13	0.48
1:A:353:A:H8	1:A:353:A:C5'	2.27	0.48
1:A:408:A:H4'	1:A:429:U:H1'	1.96	0.48
1:A:559:A:H4'	1:A:560:U:O3'	2.13	0.48
1:A:991:U:C4	1:A:1212:U:H1'	2.49	0.48
1:A:1375:A:C2'	1:A:1376:U:H5'	2.44	0.48
1:A:1461:G:O2'	1:A:1462:G:H5'	2.14	0.48
4:B:46:LYS:HA	4:B:49:GLU:HB2	1.96	0.48
4:B:97:TRP:HH2	4:B:176:GLU:CD	2.22	0.48
4:B:107:THR:O	4:B:110:GLN:N	2.41	0.48
6:D:38:TYR:N	6:D:38:TYR:HD2	2.12	0.48
6:D:61:LYS:HD2	6:D:207:TYR:HH	1.77	0.48
11:I:28:VAL:HA	11:I:63:ILE:O	2.14	0.48
12:J:9:ARG:CB	12:J:9:ARG:HH11	2.27	0.48
16:N:41:ARG:HG3	16:N:42:ILE:N	2.28	0.48
17:O:33:THR:HG23	17:O:63:ARG:HH12	1.78	0.48
18:P:19:ILE:HG22	18:P:36:ILE:CG1	2.44	0.48
18:P:56:ALA:O	18:P:57:ARG:C	2.57	0.48
18:P:69:THR:O	18:P:70:ALA:C	2.57	0.48
1:A:163:C:H2'	1:A:164:U:O4'	2.14	0.47
1:A:312:C:H2'	1:A:313:A:H8	1.78	0.47
1:A:760:G:N2	19:Q:105:ALA:N	2.50	0.47
1:A:1248:A:H2'	1:A:1249:C:C6	2.49	0.47
5:C:87:LEU:C	5:C:89:GLU:N	2.70	0.47
14:L:104:VAL:O	14:L:105:TYR:HB2	2.14	0.47
14:L:120:TYR:O	14:L:122:THR:HG23	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:31:LYS:O	15:M:35:GLU:HB2	2.13	0.47
15:M:37:THR:HG22	15:M:55:ARG:HD2	1.96	0.47
16:N:3:ARG:O	16:N:7:ILE:HG13	2.13	0.47
21:S:63:THR:HG22	21:S:65:ASN:H	1.78	0.47
1:A:19:C:H5''	7:E:86:ALA:CB	2.44	0.47
1:A:335:C:H2'	1:A:336:C:C6	2.41	0.47
1:A:459:G:H3'	1:A:460:A:C5'	2.44	0.47
1:A:687:A:H4'	1:A:688:G:O5'	2.14	0.47
1:A:1007:C:H2'	1:A:1008:C:C6	2.49	0.47
1:A:1060:C:C2	1:A:1198:G:C2	3.02	0.47
1:A:1330:U:OP1	15:M:23:TYR:O	2.33	0.47
1:A:1443:G:C5'	1:A:1446:A:H5'	2.36	0.47
5:C:58:GLU:HB3	12:J:92:THR:CG2	2.44	0.47
5:C:178:LEU:O	5:C:179:ARG:HB2	2.14	0.47
8:F:96:PRO:O	8:F:98:LEU:N	2.46	0.47
11:I:55:ALA:O	11:I:57:GLY:N	2.47	0.47
12:J:25:GLU:CB	12:J:29:ARG:HH21	2.26	0.47
13:K:33:THR:HB	13:K:38:ASN:C	2.39	0.47
14:L:7:ILE:O	14:L:11:VAL:HG23	2.14	0.47
19:Q:90:ILE:O	19:Q:93:GLN:HB3	2.14	0.47
22:T:61:SER:O	22:T:62:LEU:C	2.56	0.47
1:A:448:A:H2'	1:A:449:C:C6	2.49	0.47
1:A:474:G:OP1	1:A:475:G:C8	2.67	0.47
1:A:753:A:H2	10:H:1:MET:HE2	1.79	0.47
1:A:828:A:H2'	1:A:829:G:O4'	2.13	0.47
1:A:977:A:O2'	1:A:979:C:OP2	2.32	0.47
1:A:1060:C:C2	1:A:1198:G:N2	2.82	0.47
1:A:1113:C:O2'	1:A:1114:C:H5'	2.15	0.47
1:A:1196:U:H4'	1:A:1197:G:OP2	2.14	0.47
1:A:1227:A:H8	1:A:1227:A:H3'	1.79	0.47
4:B:118:LEU:O	4:B:119:GLU:C	2.56	0.47
4:B:216:SER:O	4:B:219:VAL:HG23	2.14	0.47
7:E:144:THR:CB	7:E:147:ASP:OD1	2.62	0.47
9:G:46:ALA:C	9:G:48:LYS:N	2.72	0.47
9:G:101:LEU:O	9:G:102:ARG:C	2.57	0.47
10:H:104:ARG:NH2	10:H:138:TRP:CZ3	2.82	0.47
11:I:5:TYR:HB2	11:I:18:PHE:CD2	2.48	0.47
13:K:33:THR:HB	13:K:38:ASN:O	2.13	0.47
15:M:20:THR:C	15:M:22:ILE:N	2.72	0.47
17:O:88:ARG:HE	17:O:88:ARG:H	1.63	0.47
20:R:37:VAL:HG12	20:R:41:LYS:CE	2.43	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:4:SER:O	21:S:5:LEU:CB	2.63	0.47
21:S:38:SER:OG	21:S:71:LEU:HD13	2.14	0.47
22:T:10:LEU:O	22:T:12:ALA:N	2.47	0.47
1:A:201:C:O5'	1:A:216:G:N2	2.47	0.47
1:A:321:A:H62	1:A:328:C:H1'	1.79	0.47
1:A:356:A:O2'	1:A:357:G:H5'	2.14	0.47
1:A:408:A:C4'	1:A:429:U:O2'	2.62	0.47
1:A:458:C:N4	1:A:463:A:H3'	2.25	0.47
6:D:3:ARG:HA	6:D:3:ARG:HE	1.79	0.47
8:F:67:MET:CE	8:F:72:VAL:HA	2.45	0.47
9:G:62:PHE:HA	9:G:124:LEU:CD2	2.45	0.47
12:J:10:GLY:H	12:J:16:LEU:HD11	1.79	0.47
14:L:71:PRO:HB2	14:L:120:TYR:HE2	1.78	0.47
16:N:28:GLY:O	16:N:30:ALA:N	2.47	0.47
21:S:40:ILE:HD13	21:S:62:ILE:HG13	1.95	0.47
1:A:279:A:OP2	19:Q:95:TYR:OH	2.26	0.47
1:A:1090:U:H2'	1:A:1091:U:C6	2.49	0.47
1:A:1195:C:H2'	1:A:1197:G:H5'	1.95	0.47
5:C:65:ALA:HB1	5:C:67:THR:OG1	2.13	0.47
8:F:76:ALA:C	8:F:78:GLU:N	2.69	0.47
10:H:6:ILE:HD12	10:H:35:ILE:CD1	2.45	0.47
11:I:106:ALA:O	11:I:107:ARG:C	2.56	0.47
12:J:34:VAL:HG22	12:J:74:ILE:CG2	2.35	0.47
14:L:28:LYS:O	14:L:30:ALA:N	2.47	0.47
23:V:6:ARG:CD	23:V:15:ARG:HH12	2.25	0.47
1:A:408:A:H5''	6:D:22:LYS:NZ	2.30	0.47
1:A:839:U:O2	1:A:839:U:C2'	2.63	0.47
1:A:865:A:C6	1:A:866:C:C4	3.02	0.47
1:A:883:C:O2'	1:A:884:U:H5'	2.15	0.47
1:A:1104:G:OP1	4:B:111:ARG:HD2	2.13	0.47
1:A:1287:A:H2'	1:A:1288:A:C8	2.50	0.47
1:A:1350:A:C2	1:A:1351:U:C2	3.02	0.47
1:A:1474:G:O2'	1:A:1475:G:H5'	2.15	0.47
5:C:5:ILE:HD13	5:C:10:PHE:HB2	1.96	0.47
5:C:66:VAL:O	5:C:66:VAL:HG12	2.14	0.47
6:D:31:CYS:O	6:D:33:MET:N	2.48	0.47
10:H:45:ILE:C	10:H:47:GLY:N	2.73	0.47
11:I:114:TYR:HD2	12:J:60:ARG:HD2	1.80	0.47
12:J:8:LEU:HD12	12:J:20:ALA:HB1	1.96	0.47
13:K:27:ASN:OD1	13:K:28:THR:N	2.48	0.47
16:N:32:SER:HB2	16:N:41:ARG:HB3	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:22:THR:HA	18:P:33:ILE:CD1	2.45	0.47
1:A:370:C:C2'	1:A:371:G:H5'	2.45	0.47
1:A:397:A:H3'	1:A:397:A:N3	2.29	0.47
1:A:409:G:P	1:A:429:U:O2	2.72	0.47
1:A:708:C:O2'	1:A:709:G:H5'	2.15	0.47
1:A:743:U:H2'	1:A:744:C:C6	2.50	0.47
1:A:864:A:H2'	1:A:865:A:C8	2.49	0.47
1:A:865:A:C5	1:A:866:C:C4	3.02	0.47
1:A:897:C:H5''	19:Q:101:ARG:NH2	2.29	0.47
1:A:1197:G:OP1	1:A:1197:G:H3'	2.14	0.47
1:A:1228:C:H4'	15:M:116:THR:HA	1.95	0.47
1:A:1251:A:H1'	1:A:1369:C:O2'	2.13	0.47
1:A:1300:G:C2'	1:A:1301:U:OP2	2.62	0.47
1:A:1358:U:H3'	1:A:1359:C:C6	2.49	0.47
1:A:1405:G:P	24:A:1545:PAR:O34	2.73	0.47
1:A:1441:G:H4'	1:A:1442:G:N1	2.29	0.47
5:C:33:LEU:HD21	16:N:53:LEU:HD21	1.97	0.47
5:C:73:PRO:C	5:C:75:VAL:N	2.68	0.47
5:C:147:LYS:HE2	5:C:205:GLY:CA	2.45	0.47
6:D:15:GLU:CG	6:D:63:LYS:HG3	2.45	0.47
7:E:121:LYS:HE3	7:E:123:LEU:CD2	2.44	0.47
9:G:87:VAL:HG13	9:G:88:PRO:HD2	1.96	0.47
9:G:112:PRO:HD2	9:G:113:GLU:OE2	2.13	0.47
9:G:117:ALA:HA	9:G:120:ILE:HD13	1.97	0.47
10:H:121:ASP:HB2	10:H:125:ARG:NH2	2.25	0.47
11:I:63:ILE:HD13	11:I:77:ILE:HG23	1.97	0.47
11:I:113:LYS:N	11:I:113:LYS:CD	2.78	0.47
11:I:127:LYS:CA	11:I:127:LYS:HE3	2.45	0.47
12:J:44:VAL:HG21	12:J:66:ARG:HH21	1.79	0.47
14:L:40:VAL:HG21	14:L:77:LEU:O	2.13	0.47
15:M:19:LEU:O	15:M:22:ILE:HG13	2.15	0.47
15:M:87:TYR:C	15:M:89:GLY:N	2.71	0.47
17:O:31:LEU:O	17:O:34:LEU:HB3	2.15	0.47
17:O:46:HIS:ND1	17:O:46:HIS:N	2.63	0.47
18:P:53:VAL:HG22	18:P:54:GLU:N	2.29	0.47
22:T:22:ARG:O	22:T:25:ARG:N	2.48	0.47
22:T:53:LEU:O	22:T:56:MET:N	2.48	0.47
22:T:57:ARG:NH1	22:T:57:ARG:HB2	2.29	0.47
1:A:603:U:H2'	1:A:604:G:H8	1.80	0.47
1:A:1296:C:H5''	15:M:14:ARG:HD2	1.97	0.47
1:A:1345:U:C2	1:A:1377:A:C2	3.03	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1495:U:H2'	1:A:1496:C:H6	1.78	0.47
4:B:16:HIS:NE2	4:B:214:ILE:CG1	2.78	0.47
4:B:71:VAL:CG2	4:B:164:VAL:HG22	2.45	0.47
7:E:21:ALA:O	7:E:22:GLY:C	2.56	0.47
7:E:21:ALA:O	7:E:23:GLY:N	2.47	0.47
7:E:57:LYS:HG2	7:E:61:TYR:HE2	1.79	0.47
8:F:76:ALA:O	8:F:80:ARG:HG3	2.15	0.47
10:H:1:MET:HG2	10:H:2:LEU:N	2.30	0.47
11:I:45:ALA:O	11:I:48:GLU:HB2	2.15	0.47
15:M:62:ASN:O	15:M:63:THR:CB	2.61	0.47
20:R:47:THR:HG23	20:R:83:GLU:H	1.79	0.47
21:S:4:SER:O	21:S:5:LEU:HG	2.15	0.47
1:A:325:A:H2'	1:A:326:G:O4'	2.14	0.47
1:A:428:G:OP2	6:D:7:PRO:HG3	2.14	0.47
1:A:848:C:H2'	1:A:849:C:C6	2.50	0.47
1:A:968:A:OP2	11:I:128:ARG:NH2	2.48	0.47
1:A:1018:C:O5'	1:A:1018:C:H6	1.98	0.47
1:A:1154:G:H2'	1:A:1155:G:C8	2.40	0.47
4:B:207:ALA:O	4:B:211:ILE:HG13	2.14	0.47
5:C:92:ALA:HA	5:C:95:THR:OG1	2.15	0.47
5:C:92:ALA:O	5:C:93:LYS:C	2.58	0.47
5:C:172:ARG:NH1	5:C:203:PHE:CE2	2.82	0.47
9:G:57:GLU:O	9:G:60:LYS:HB3	2.15	0.47
10:H:82:HIS:O	10:H:83:ILE:CB	2.63	0.47
11:I:8:GLY:CA	11:I:79:LEU:HB3	2.45	0.47
11:I:40:LEU:O	11:I:41:VAL:C	2.57	0.47
11:I:84:ALA:C	11:I:86:VAL:N	2.73	0.47
12:J:25:GLU:HB2	12:J:29:ARG:HH21	1.79	0.47
15:M:33:ALA:C	15:M:35:GLU:N	2.73	0.47
15:M:80:ARG:C	15:M:82:MET:N	2.71	0.47
18:P:20:VAL:HG23	18:P:35:LYS:HA	1.96	0.47
19:Q:27:PHE:CE1	19:Q:36:ILE:HD11	2.50	0.47
19:Q:76:LEU:C	19:Q:76:LEU:CD2	2.87	0.47
1:A:227:G:O2'	18:P:62:VAL:HG11	2.15	0.47
1:A:459:G:C6	1:A:461:C:H5''	2.49	0.47
1:A:908:A:H2'	1:A:909:A:H8	1.79	0.47
1:A:1126:U:OP2	1:A:1281:U:O2	2.33	0.47
1:A:1190:G:H3'	5:C:3:ASN:OD1	2.14	0.47
1:A:1480:G:H2'	1:A:1481:U:H6	1.79	0.47
5:C:137:ALA:O	5:C:141:VAL:HG23	2.14	0.47
5:C:172:ARG:HB3	5:C:172:ARG:HH11	1.80	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:196:LEU:N	5:C:196:LEU:CD2	2.71	0.47
6:D:98:GLU:HG2	6:D:189:PRO:HG3	1.97	0.47
7:E:57:LYS:HB2	7:E:57:LYS:HE3	1.67	0.47
8:F:19:LEU:HD23	8:F:19:LEU:C	2.39	0.47
8:F:75:LEU:O	8:F:78:GLU:HB3	2.15	0.47
9:G:78:ARG:HB2	9:G:156:TRP:CH2	2.50	0.47
10:H:4:ASP:OD2	10:H:89:PRO:HD3	2.14	0.47
11:I:78:LYS:HE3	11:I:101:PHE:CD2	2.49	0.47
15:M:19:LEU:HD21	15:M:56:LEU:HD21	1.97	0.47
19:Q:52:LYS:N	19:Q:52:LYS:HD2	2.30	0.47
20:R:87:ARG:HG3	20:R:87:ARG:HH11	1.80	0.47
1:A:836:G:C6	1:A:851:G:C6	3.03	0.46
1:A:1290:G:H2'	1:A:1291:G:C8	2.50	0.46
1:A:1329:A:N7	23:V:7:ARG:NH2	2.63	0.46
7:E:24:ARG:CB	7:E:24:ARG:HH11	2.28	0.46
8:F:68:PRO:O	8:F:69:GLU:C	2.58	0.46
13:K:68:ALA:O	13:K:72:ALA:HB2	2.15	0.46
14:L:39:VAL:HA	14:L:79:GLU:OE1	2.15	0.46
15:M:78:ILE:O	15:M:81:LEU:HD23	2.15	0.46
15:M:94:ARG:NH1	21:S:81:ARG:HD3	2.30	0.46
17:O:87:ILE:HG22	17:O:88:ARG:HH21	1.80	0.46
19:Q:69:LYS:C	19:Q:70:ARG:HD2	2.40	0.46
20:R:53:ARG:O	20:R:57:GLY:N	2.42	0.46
21:S:13:ASP:OD2	21:S:14:HIS:N	2.46	0.46
21:S:15:LEU:HD23	21:S:33:THR:HG21	1.97	0.46
21:S:63:THR:CG2	21:S:64:GLU:N	2.78	0.46
22:T:56:MET:HG2	22:T:84:LEU:HD11	1.97	0.46
1:A:448:A:OP2	1:A:485:G:N2	2.37	0.46
1:A:657:G:O2'	1:A:658:G:H5'	2.15	0.46
1:A:697:U:H2'	1:A:698:G:H5'	1.97	0.46
1:A:806:C:O2'	1:A:807:A:H5'	2.16	0.46
1:A:1349:A:H2'	1:A:1350:A:C8	2.37	0.46
5:C:46:GLU:C	5:C:48:TYR:H	2.23	0.46
6:D:98:GLU:OE2	6:D:107:ARG:NE	2.47	0.46
9:G:43:PHE:O	9:G:46:ALA:HB3	2.15	0.46
14:L:28:LYS:O	14:L:28:LYS:HG2	2.15	0.46
14:L:78:GLN:O	14:L:80:HIS:N	2.45	0.46
15:M:31:LYS:C	15:M:33:ALA:N	2.71	0.46
20:R:53:ARG:CG	20:R:63:GLN:HG2	2.44	0.46
1:A:216:G:H5'	1:A:217:C:P	2.55	0.46
1:A:539:A:H2'	1:A:540:G:H8	1.79	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:556:C:C2'	1:A:557:G:H5'	2.46	0.46
1:A:570:G:N2	1:A:571:U:C2	2.83	0.46
1:A:791:G:C2'	1:A:792:A:C5'	2.92	0.46
1:A:858:G:O2'	1:A:859:A:H5'	2.16	0.46
1:A:1055:A:C2	1:A:1056:U:H1'	2.50	0.46
4:B:68:ILE:HG22	4:B:69:LEU:N	2.30	0.46
4:B:144:ARG:HA	4:B:147:LYS:CE	2.45	0.46
6:D:102:ASP:CG	6:D:103:ASN:N	2.74	0.46
9:G:44:TYR:O	9:G:46:ALA:N	2.48	0.46
10:H:104:ARG:CZ	10:H:138:TRP:CH2	2.98	0.46
16:N:3:ARG:O	16:N:4:LYS:C	2.57	0.46
18:P:17:TYR:HE1	18:P:41:PRO:HG3	1.80	0.46
19:Q:81:ARG:HG3	19:Q:81:ARG:O	2.16	0.46
20:R:42:ARG:HG3	20:R:42:ARG:HH11	1.80	0.46
1:A:217:C:P	1:A:461:C:H41	2.38	0.46
1:A:390:C:O3'	18:P:28:ARG:NH2	2.48	0.46
1:A:1097:C:O2'	1:A:1168:A:H1'	2.15	0.46
1:A:1283:G:O2'	1:A:1284:C:H5'	2.15	0.46
8:F:67:MET:HE1	8:F:75:LEU:CB	2.45	0.46
13:K:40:ILE:HG22	13:K:41:THR:OG1	2.15	0.46
15:M:39:ILE:HD12	15:M:56:LEU:HD12	1.98	0.46
15:M:53:VAL:HG12	15:M:57:ARG:HH21	1.80	0.46
15:M:67:GLU:O	15:M:68:GLY:C	2.58	0.46
17:O:32:LEU:O	17:O:33:THR:C	2.59	0.46
18:P:75:ARG:NH1	18:P:82:GLN:HE22	2.13	0.46
21:S:11:VAL:HG22	21:S:39:THR:H	1.81	0.46
1:A:84:U:H2'	1:A:88:A:H8	1.78	0.46
1:A:284:G:H2'	1:A:285:G:H8	1.80	0.46
1:A:333:G:C4'	22:T:16:HIS:CD2	2.98	0.46
1:A:706:A:H1'	13:K:29:ILE:CD1	2.45	0.46
1:A:967:C:O3'	11:I:128:ARG:CZ	2.64	0.46
1:A:1036:G:O2'	1:A:1037:C:H5'	2.16	0.46
1:A:1043:C:O2'	1:A:1044:A:H5'	2.15	0.46
1:A:1057:G:C2'	1:A:1058:G:H5'	2.45	0.46
1:A:1072:G:H2'	1:A:1073:U:H6	1.81	0.46
1:A:1224:G:H1	1:A:1362:C:H42	1.63	0.46
1:A:1438:G:H2'	1:A:1439:C:C6	2.51	0.46
4:B:75:LYS:O	4:B:76:GLN:C	2.59	0.46
7:E:20:GLN:C	7:E:21:ALA:O	2.58	0.46
7:E:43:LEU:HD23	7:E:44:GLY:H	1.81	0.46
9:G:16:LEU:H	9:G:16:LEU:CD2	2.22	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:86:MET:HA	12:J:86:MET:HE3	1.98	0.46
13:K:17:GLY:O	13:K:80:VAL:HA	2.16	0.46
15:M:63:THR:HG23	15:M:64:TRP:CD2	2.50	0.46
17:O:17:ARG:HG3	17:O:17:ARG:NH1	2.29	0.46
19:Q:97:SER:CB	19:Q:103:GLY:C	2.89	0.46
22:T:77:ALA:O	22:T:78:ALA:C	2.58	0.46
22:T:87:LYS:O	22:T:91:LEU:HG	2.16	0.46
1:A:424:G:N3	1:A:424:G:C3'	2.77	0.46
1:A:625:G:O2'	1:A:626:U:H5'	2.15	0.46
1:A:647:C:H2'	1:A:648:A:C8	2.51	0.46
1:A:814:A:N7	1:A:816:A:C4	2.83	0.46
1:A:855:G:H2'	1:A:856:C:C6	2.51	0.46
1:A:1104:G:H2'	1:A:1105:A:C8	2.50	0.46
1:A:1120:G:H2'	1:A:1121:U:H6	1.81	0.46
1:A:1522:U:H2'	1:A:1523:G:H8	1.79	0.46
4:B:78:GLN:HG2	4:B:94:ASN:ND2	2.30	0.46
8:F:21:LEU:O	8:F:24:GLU:HB3	2.15	0.46
9:G:15:ASP:OD2	9:G:16:LEU:N	2.48	0.46
9:G:135:VAL:O	9:G:138:LYS:HB3	2.16	0.46
10:H:35:ILE:HG23	10:H:111:ILE:HD13	1.97	0.46
10:H:64:LYS:O	10:H:79:VAL:HG23	2.16	0.46
19:Q:44:ALA:HB1	19:Q:73:VAL:HG22	1.98	0.46
22:T:45:GLN:HA	22:T:91:LEU:HD13	1.98	0.46
1:A:57:G:H2'	1:A:58:C:C6	2.51	0.46
1:A:302:G:H5''	14:L:17:LYS:HZ1	1.78	0.46
1:A:731:G:H5'	1:A:766:A:H4'	1.97	0.46
1:A:1060:C:H4'	12:J:52:GLY:N	2.31	0.46
1:A:1108:G:H4'	1:A:1191:A:O4'	2.15	0.46
1:A:1190:G:C2'	1:A:1191:A:OP2	2.63	0.46
1:A:1306:A:H2'	1:A:1307:U:O4'	2.16	0.46
1:A:1328:C:O2'	1:A:1329:A:H5'	2.14	0.46
4:B:8:LYS:O	4:B:9:GLU:C	2.58	0.46
4:B:30:ARG:C	4:B:32:ILE:H	2.23	0.46
4:B:33:TYR:HB3	4:B:41:ILE:O	2.15	0.46
4:B:55:PHE:O	4:B:56:ARG:C	2.57	0.46
4:B:143:GLU:O	4:B:147:LYS:HE3	2.16	0.46
6:D:127:THR:CG2	6:D:147:ALA:HB3	2.46	0.46
7:E:43:LEU:HD23	7:E:44:GLY:N	2.31	0.46
10:H:35:ILE:O	10:H:36:LEU:C	2.58	0.46
10:H:46:LYS:HG3	10:H:64:LYS:CG	2.43	0.46
11:I:47:LEU:C	11:I:49:PRO:HD2	2.41	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:28:ARG:HG2	12:J:28:ARG:HH11	1.79	0.46
13:K:97:ALA:O	13:K:98:LEU:C	2.57	0.46
13:K:120:ARG:NH2	13:K:126:ARG:NH1	2.63	0.46
18:P:81:ARG:C	18:P:83:GLU:N	2.74	0.46
20:R:28:GLU:OE1	20:R:28:GLU:N	2.48	0.46
1:A:337:C:N4	1:A:338:A:H62	2.13	0.46
1:A:840:C:O5'	1:A:840:C:H6	1.98	0.46
1:A:1117:G:H21	1:A:1180:A:H1'	1.80	0.46
4:B:26:PRO:C	4:B:28:PHE:H	2.23	0.46
5:C:178:LEU:O	5:C:179:ARG:CB	2.63	0.46
6:D:54:TYR:O	6:D:55:ALA:C	2.58	0.46
6:D:87:GLY:O	6:D:89:THR:N	2.49	0.46
7:E:15:ARG:HG3	7:E:15:ARG:NH1	2.31	0.46
10:H:31:PHE:O	10:H:35:ILE:HG13	2.16	0.46
11:I:117:HIS:O	11:I:118:LYS:HG3	2.16	0.46
13:K:67:ASP:CG	13:K:71:LYS:HE3	2.41	0.46
14:L:7:ILE:HG22	14:L:11:VAL:HG23	1.98	0.46
22:T:100:ILE:O	22:T:100:ILE:CG2	2.63	0.46
23:V:24:ARG:O	23:V:25:LYS:CB	2.64	0.46
1:A:407:G:H2'	1:A:431:A:OP1	2.15	0.46
1:A:501:C:O2'	1:A:502:G:H5'	2.16	0.46
1:A:740:U:H4'	17:O:42:HIS:CD2	2.51	0.46
1:A:954:G:H2'	1:A:955:U:O4'	2.15	0.46
1:A:1357:A:C8	1:A:1358:U:H5	2.34	0.46
4:B:131:PRO:C	4:B:133:LYS:N	2.74	0.46
6:D:162:LEU:HD12	6:D:181:MET:SD	2.56	0.46
7:E:34:VAL:HG13	7:E:34:VAL:O	2.15	0.46
8:F:101:ALA:CB	20:R:28:GLU:HG3	2.45	0.46
9:G:46:ALA:HA	9:G:49:ILE:HD13	1.98	0.46
10:H:31:PHE:O	10:H:34:GLU:HB2	2.16	0.46
11:I:46:ALA:C	11:I:48:GLU:H	2.23	0.46
15:M:73:GLU:O	15:M:74:VAL:C	2.59	0.46
16:N:5:ALA:C	16:N:7:ILE:H	2.23	0.46
17:O:78:TYR:O	17:O:80:ALA:N	2.49	0.46
18:P:43:LYS:HG2	18:P:48:TRP:CE2	2.51	0.46
19:Q:67:LYS:O	19:Q:68:ARG:HB3	2.15	0.46
20:R:79:LEU:CD2	20:R:80:PRO:HD2	2.45	0.46
21:S:14:HIS:O	21:S:18:LYS:HE3	2.16	0.46
22:T:90:GLN:O	22:T:93:GLU:HB2	2.15	0.46
23:V:6:ARG:C	23:V:8:THR:H	2.24	0.46
1:A:346:G:C2'	1:A:347:G:H5'	2.46	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:903:G:H2'	1:A:904:C:C6	2.51	0.46
1:A:1117:G:H4'	11:I:104:ARG:NH1	2.31	0.46
1:A:1439:C:OP1	22:T:38:LYS:NZ	2.45	0.46
4:B:30:ARG:HG3	4:B:31:TYR:N	2.31	0.46
4:B:91:PRO:HG2	4:B:155:LEU:HG	1.97	0.46
5:C:139:GLN:HA	5:C:139:GLN:HE21	1.81	0.46
7:E:50:GLU:O	7:E:51:VAL:C	2.59	0.46
11:I:93:ARG:C	11:I:95:LYS:N	2.71	0.46
11:I:113:LYS:H	11:I:119:ALA:HA	1.80	0.46
1:A:748:C:OP2	1:A:748:C:H6	1.99	0.45
1:A:1401:G:C2	1:A:1402:C:C1'	2.98	0.45
4:B:137:ARG:HA	4:B:140:HIS:HD2	1.80	0.45
6:D:19:LEU:HD22	6:D:67:ILE:HG12	1.97	0.45
6:D:180:GLY:O	6:D:181:MET:C	2.58	0.45
9:G:111:ARG:HE	9:G:123:GLU:CA	2.29	0.45
9:G:148:ASN:N	9:G:148:ASN:ND2	2.62	0.45
11:I:5:TYR:HA	11:I:17:VAL:O	2.16	0.45
11:I:43:ALA:HA	11:I:74:ILE:CD1	2.36	0.45
13:K:74:ALA:C	13:K:76:GLY:N	2.72	0.45
18:P:74:LEU:HB3	18:P:79:VAL:CG2	2.46	0.45
1:A:352:C:N3	1:A:356:A:N6	2.64	0.45
1:A:392:G:H2'	1:A:393:A:C8	2.51	0.45
1:A:730:G:N3	1:A:765:G:H4'	2.32	0.45
1:A:1305:G:OP1	23:V:2:GLY:N	2.50	0.45
1:A:1423:G:H2'	1:A:1424:C:C6	2.51	0.45
1:A:1431:C:C2'	1:A:1432:G:H5'	2.46	0.45
1:A:1504:G:O2'	1:A:1505:G:OP2	2.31	0.45
4:B:102:LEU:N	4:B:102:LEU:HD12	2.32	0.45
4:B:108:ILE:HG22	4:B:152:PHE:CE2	2.52	0.45
4:B:137:ARG:C	4:B:139:LYS:N	2.73	0.45
4:B:221:LEU:HD13	4:B:221:LEU:C	2.42	0.45
6:D:78:LEU:HB3	6:D:93:PHE:HE2	1.81	0.45
7:E:135:THR:O	7:E:138:ALA:HB3	2.17	0.45
13:K:74:ALA:O	13:K:76:GLY:N	2.49	0.45
14:L:39:VAL:HA	14:L:79:GLU:HG2	1.98	0.45
15:M:80:ARG:C	15:M:82:MET:H	2.23	0.45
18:P:10:GLY:HA3	18:P:14:ASN:O	2.15	0.45
18:P:51:VAL:O	18:P:52:ASP:C	2.58	0.45
19:Q:51:TYR:C	19:Q:52:LYS:HD2	2.41	0.45
19:Q:61:GLU:HA	19:Q:71:PHE:CD1	2.50	0.45
20:R:55:ARG:HH11	20:R:55:ARG:CB	2.30	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:U:H2'	1:A:253:U:C5	2.52	0.45
1:A:718:G:O5'	13:K:117:ASN:ND2	2.49	0.45
1:A:720:C:H2'	1:A:721:G:C8	2.51	0.45
1:A:723:U:H5''	1:A:724:G:OP2	2.17	0.45
1:A:934:C:H5	1:A:1344:C:H2'	1.82	0.45
1:A:1249:C:O2'	11:I:73:GLN:NE2	2.50	0.45
1:A:1288:A:C6	1:A:1289:A:C5	3.04	0.45
1:A:1490:C:H5'	1:A:1490:C:C6	2.39	0.45
4:B:27:LYS:HZ3	4:B:195:ASP:HB2	1.80	0.45
4:B:107:THR:O	4:B:108:ILE:C	2.59	0.45
6:D:126:ILE:CG2	6:D:127:THR:N	2.79	0.45
7:E:107:ARG:O	7:E:110:LEU:N	2.49	0.45
10:H:10:LEU:HD23	10:H:83:ILE:HD11	1.99	0.45
12:J:9:ARG:NH1	12:J:9:ARG:CB	2.79	0.45
12:J:32:ALA:H	12:J:76:ASN:HD21	1.65	0.45
15:M:108:ARG:NE	15:M:108:ARG:HA	2.31	0.45
20:R:53:ARG:O	20:R:54:ARG:C	2.58	0.45
1:A:8:A:C6	6:D:209:ARG:HA	2.52	0.45
1:A:163:C:H2'	1:A:164:U:C5'	2.46	0.45
1:A:748:C:O2'	1:A:749:C:C6	2.65	0.45
1:A:939:G:C5'	9:G:102:ARG:HH22	2.18	0.45
4:B:84:GLU:HB3	4:B:219:VAL:CG2	2.40	0.45
4:B:97:TRP:CZ2	4:B:101:MET:HB2	2.51	0.45
7:E:143:ARG:HD3	7:E:143:ARG:HA	1.60	0.45
10:H:105:ARG:HG3	10:H:105:ARG:HH11	1.81	0.45
15:M:14:ARG:HB3	15:M:14:ARG:HH11	1.79	0.45
22:T:80:ARG:O	22:T:81:LYS:C	2.60	0.45
1:A:38:G:N1	1:A:397:A:OP1	2.34	0.45
1:A:277:C:OP1	19:Q:41:LYS:HE3	2.17	0.45
1:A:740:U:O2'	1:A:741:G:H5'	2.17	0.45
1:A:742:G:H2'	1:A:743:U:O4'	2.16	0.45
1:A:938:A:C6	1:A:939:G:C5	3.05	0.45
1:A:1495:U:H2'	1:A:1496:C:C6	2.52	0.45
4:B:16:HIS:O	4:B:17:PHE:C	2.59	0.45
4:B:81:VAL:C	4:B:83:MET:N	2.74	0.45
4:B:139:LYS:HD3	4:B:139:LYS:C	2.41	0.45
6:D:116:GLN:O	6:D:117:ALA:C	2.59	0.45
7:E:35:GLY:H	7:E:112:LEU:HD12	1.81	0.45
7:E:151:LEU:HD11	10:H:77:GLU:OE2	2.16	0.45
9:G:122:HIS:HA	9:G:125:MET:HE3	1.97	0.45
10:H:11:THR:O	10:H:14:ARG:N	2.50	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:35:ILE:O	10:H:39:LEU:HD22	2.17	0.45
10:H:35:ILE:CG2	10:H:111:ILE:HD13	2.47	0.45
11:I:24:GLY:HA3	11:I:57:GLY:HA2	1.98	0.45
13:K:109:VAL:HA	20:R:85:LEU:O	2.16	0.45
14:L:11:VAL:HG21	19:Q:34:LYS:HG2	1.99	0.45
14:L:24:VAL:HG13	14:L:98:TYR:CE2	2.50	0.45
14:L:53:ARG:CD	14:L:93:LEU:HD21	2.47	0.45
15:M:14:ARG:NH1	15:M:14:ARG:CB	2.79	0.45
15:M:31:LYS:O	15:M:32:GLU:C	2.57	0.45
15:M:59:TYR:O	15:M:59:TYR:CD1	2.69	0.45
15:M:116:THR:HG22	15:M:117:VAL:N	2.32	0.45
16:N:8:GLU:O	16:N:9:LYS:C	2.59	0.45
18:P:55:ARG:O	18:P:56:ALA:C	2.58	0.45
19:Q:65:ILE:O	19:Q:66:SER:HB3	2.15	0.45
19:Q:67:LYS:CA	19:Q:70:ARG:HH12	2.29	0.45
21:S:63:THR:HG21	21:S:65:ASN:HD22	1.81	0.45
22:T:22:ARG:C	22:T:24:LEU:N	2.73	0.45
1:A:344:A:H5''	1:A:345:C:C5	2.50	0.45
1:A:432:A:O3'	1:A:433:C:H6	1.99	0.45
1:A:437:U:O2'	1:A:438:G:H5'	2.17	0.45
1:A:502:G:H2'	1:A:503:C:C6	2.52	0.45
1:A:560:U:H4'	1:A:561:U:H5''	1.99	0.45
1:A:660:G:C2	1:A:746:A:C2	3.05	0.45
1:A:662:G:O2'	1:A:663:A:H5'	2.17	0.45
1:A:954:G:C5	1:A:955:U:C5	3.05	0.45
1:A:961:U:H2'	1:A:962:C:O4'	2.16	0.45
1:A:1227:A:OP2	15:M:96:LEU:HD21	2.17	0.45
1:A:1275:A:O2'	1:A:1276:G:H5'	2.16	0.45
1:A:1314:C:OP2	21:S:6:LYS:HD2	2.17	0.45
1:A:1347:G:C2'	1:A:1373:G:H1	2.28	0.45
1:A:1519:A:C3'	1:A:1520:G:H5'	2.47	0.45
5:C:113:ALA:O	5:C:114:PRO:C	2.58	0.45
7:E:15:ARG:O	7:E:27:ARG:O	2.35	0.45
7:E:119:LEU:HA	7:E:119:LEU:HD23	1.59	0.45
9:G:77:SER:O	9:G:156:TRP:HH2	2.00	0.45
10:H:46:LYS:N	10:H:64:LYS:HG3	2.31	0.45
11:I:27:THR:HG22	11:I:28:VAL:N	2.32	0.45
12:J:16:LEU:C	12:J:18:ALA:N	2.74	0.45
12:J:86:MET:N	12:J:86:MET:SD	2.89	0.45
16:N:18:VAL:HG23	16:N:19:ARG:H	1.82	0.45
17:O:11:VAL:O	17:O:14:GLU:HB3	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:45:VAL:HB	17:O:46:HIS:ND1	2.32	0.45
17:O:76:GLU:CA	17:O:79:ARG:HH21	2.25	0.45
19:Q:20:THR:CG2	19:Q:41:LYS:HD2	2.46	0.45
19:Q:25:ARG:O	19:Q:25:ARG:HG2	2.16	0.45
19:Q:58:GLU:HB2	19:Q:74:LEU:HB3	1.98	0.45
1:A:826:C:H2'	1:A:827:U:H6	1.81	0.45
1:A:1347:G:N2	1:A:1373:G:H2'	2.31	0.45
1:A:1402:C:H2'	1:A:1403:C:O4'	2.17	0.45
1:A:1403:C:H1'	1:A:1500:A:N1	2.32	0.45
1:A:1451:A:O2'	1:A:1452:C:OP1	2.31	0.45
4:B:194:PRO:C	4:B:196:LEU:H	2.24	0.45
5:C:34:LEU:HD23	5:C:34:LEU:O	2.15	0.45
5:C:199:LYS:HB3	5:C:201:TYR:HE1	1.82	0.45
7:E:55:VAL:O	7:E:58:ALA:HB3	2.16	0.45
7:E:144:THR:HG23	7:E:145:LYS:N	2.32	0.45
8:F:71:ARG:HA	8:F:74:ASP:OD2	2.17	0.45
10:H:10:LEU:CD2	10:H:83:ILE:HD11	2.47	0.45
12:J:24:VAL:O	12:J:24:VAL:HG12	2.16	0.45
21:S:17:GLU:CA	21:S:20:LEU:HG	2.35	0.45
22:T:39:LYS:CE	22:T:55:ILE:HD13	2.47	0.45
1:A:337:C:N4	1:A:338:A:N6	2.64	0.45
1:A:439:A:C4	1:A:497:A:C2	3.04	0.45
1:A:833:U:H2'	1:A:834:C:H6	1.82	0.45
1:A:969:A:C2'	1:A:970:C:H5'	2.47	0.45
1:A:987:G:O2'	1:A:988:G:H5'	2.17	0.45
1:A:1167:A:C6	1:A:1168:A:C6	3.04	0.45
1:A:1380:U:O2'	1:A:1381:U:P	2.75	0.45
4:B:207:ALA:H	4:B:211:ILE:CD1	2.28	0.45
5:C:155:GLY:C	5:C:157:ILE:N	2.70	0.45
6:D:10:ARG:C	6:D:12:CYS:H	2.24	0.45
6:D:102:ASP:CG	6:D:103:ASN:H	2.25	0.45
9:G:15:ASP:O	9:G:19:GLY:HA2	2.17	0.45
9:G:116:ALA:HA	9:G:119:ARG:CZ	2.46	0.45
12:J:32:ALA:C	12:J:34:VAL:H	2.23	0.45
14:L:41:ARG:CG	14:L:42:THR:H	2.18	0.45
15:M:23:TYR:HB2	15:M:67:GLU:CD	2.41	0.45
16:N:9:LYS:C	16:N:11:LYS:N	2.74	0.45
21:S:15:LEU:HD21	21:S:38:SER:OG	2.16	0.45
1:A:665:A:H2'	1:A:732:C:O2	2.17	0.45
1:A:1069:C:H2'	1:A:1070:U:O5'	2.16	0.45
1:A:1085:U:H3'	1:A:1086:U:H5	1.82	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1137:C:H4'	1:A:1138:G:N1	2.31	0.45
1:A:1280:A:O4'	12:J:41:PRO:HG3	2.17	0.45
1:A:1370:G:C2	1:A:1371:G:C8	3.05	0.45
1:A:1477:C:O2'	1:A:1478:C:H5'	2.17	0.45
4:B:141:GLU:O	4:B:142:LEU:C	2.60	0.45
4:B:144:ARG:HA	4:B:147:LYS:CD	2.46	0.45
5:C:88:ARG:HG2	5:C:101:LEU:HB2	1.99	0.45
6:D:3:ARG:HH12	6:D:70:ILE:HA	1.82	0.45
6:D:64:LEU:HD13	6:D:64:LEU:C	2.42	0.45
6:D:112:VAL:CG2	6:D:161:ASN:HD21	2.29	0.45
7:E:28:PHE:O	7:E:47:LYS:HA	2.17	0.45
8:F:1:MET:HB3	8:F:66:GLU:HG2	1.99	0.45
8:F:30:LEU:HD22	8:F:35:ALA:HB2	1.99	0.45
11:I:98:PRO:C	11:I:100:GLY:H	2.24	0.45
12:J:79:ARG:HG2	12:J:79:ARG:HH11	1.82	0.45
19:Q:97:SER:OG	19:Q:98:LEU:N	2.50	0.45
20:R:72:ARG:O	20:R:73:ALA:C	2.60	0.45
21:S:41:VAL:HB	21:S:42:PRO:HD2	1.99	0.45
1:A:280:C:O2	19:Q:38:ARG:HG3	2.16	0.45
1:A:624:C:H2'	1:A:625:G:C8	2.50	0.45
1:A:690:G:C6	1:A:691:G:C6	3.06	0.45
1:A:781:A:C5	1:A:802:A:C2	3.05	0.45
1:A:1202:G:O4'	16:N:29:ARG:HD3	2.17	0.45
1:A:1321:C:H42	21:S:37:ARG:HH12	1.65	0.45
1:A:1426:C:H2'	1:A:1427:U:C6	2.52	0.45
1:A:1525:G:P	13:K:120:ARG:HH22	2.39	0.45
4:B:11:LEU:C	4:B:13:ALA:N	2.75	0.45
4:B:27:LYS:O	4:B:194:PRO:HG3	2.17	0.45
4:B:69:LEU:C	4:B:69:LEU:CD2	2.90	0.45
4:B:187:LEU:HD12	4:B:201:ILE:CG2	2.47	0.45
5:C:147:LYS:HE2	5:C:205:GLY:N	2.31	0.45
5:C:203:PHE:C	5:C:204:LEU:HG	2.42	0.45
6:D:32:ALA:O	6:D:34:GLU:C	2.60	0.45
6:D:199:ASN:HD21	6:D:201:GLN:HB2	1.81	0.45
7:E:139:LEU:O	7:E:140:ARG:C	2.60	0.45
8:F:36:ARG:HG2	8:F:36:ARG:NH1	2.31	0.45
9:G:115:ARG:HB2	9:G:118:VAL:HG21	1.99	0.45
10:H:38:ILE:O	10:H:39:LEU:C	2.60	0.45
12:J:39:PRO:HA	12:J:70:ARG:HH11	1.82	0.45
14:L:23:LYS:C	14:L:24:VAL:HG23	2.42	0.45
15:M:13:LYS:HG2	15:M:44:ARG:NH2	2.29	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:88:ARG:HH11	15:M:88:ARG:HB2	1.82	0.45
17:O:10:LYS:HD2	17:O:10:LYS:O	2.17	0.45
18:P:1:MET:CE	18:P:3:LYS:HD2	2.47	0.45
1:A:20:U:O2'	1:A:21:G:H5'	2.17	0.44
1:A:37:U:O2'	1:A:38:G:H5'	2.17	0.44
1:A:352:C:H4'	1:A:354:G:OP1	2.17	0.44
1:A:372:C:O2'	1:A:373:A:OP2	2.31	0.44
1:A:532:A:C2'	1:A:533:A:OP1	2.65	0.44
1:A:707:C:H4'	13:K:20:TYR:CG	2.52	0.44
1:A:737:A:H2'	1:A:738:C:H6	1.81	0.44
1:A:778:G:C5	1:A:779:C:C5	3.05	0.44
1:A:1311:G:N2	1:A:1327:C:C2	2.85	0.44
4:B:21:ARG:HB2	4:B:22:LYS:H	1.51	0.44
5:C:6:HIS:CD2	5:C:8:ILE:HB	2.52	0.44
7:E:121:LYS:HE3	7:E:123:LEU:HD23	2.00	0.44
8:F:10:LEU:HD12	8:F:59:TYR:O	2.17	0.44
9:G:58:PRO:O	9:G:59:LEU:C	2.60	0.44
9:G:151:TYR:HE1	13:K:54:ARG:NH2	2.16	0.44
10:H:11:THR:O	10:H:12:ARG:C	2.59	0.44
10:H:119:LEU:N	10:H:119:LEU:CD2	2.80	0.44
10:H:134:ILE:HG22	10:H:135:CYS:N	2.31	0.44
15:M:96:LEU:HB3	15:M:97:PRO:HD2	1.99	0.44
18:P:43:LYS:HG3	18:P:48:TRP:CD2	2.51	0.44
19:Q:58:GLU:OE1	19:Q:74:LEU:HD13	2.17	0.44
1:A:286:G:H2'	1:A:287:U:O4'	2.17	0.44
1:A:407:G:C2'	1:A:408:A:OP1	2.66	0.44
1:A:1227:A:H3'	1:A:1227:A:C8	2.52	0.44
1:A:1237:C:C4'	1:A:1334:G:N2	2.80	0.44
1:A:1344:C:O2'	1:A:1345:U:H5'	2.17	0.44
4:B:63:MET:O	4:B:64:ARG:HB2	2.17	0.44
4:B:200:ILE:CG2	4:B:201:ILE:H	2.20	0.44
5:C:17:ASP:HB2	5:C:21:ARG:HH21	1.82	0.44
7:E:6:PHE:HB3	7:E:34:VAL:CG2	2.47	0.44
7:E:35:GLY:CA	7:E:112:LEU:HD12	2.47	0.44
8:F:25:ILE:HD12	8:F:82:ARG:HD2	1.98	0.44
13:K:69:ALA:O	13:K:72:ALA:HB3	2.17	0.44
14:L:22:SER:OG	14:L:23:LYS:N	2.49	0.44
14:L:23:LYS:O	14:L:24:VAL:HG23	2.17	0.44
19:Q:104:LYS:HD3	19:Q:104:LYS:C	2.42	0.44
20:R:79:LEU:HA	20:R:79:LEU:HD23	1.84	0.44
1:A:201:C:C5'	1:A:216:G:H21	2.28	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:676:A:H1'	13:K:115:PRO:HB3	1.98	0.44
1:A:738:C:H2'	1:A:739:C:C6	2.52	0.44
1:A:969:A:O2'	1:A:970:C:H5'	2.17	0.44
1:A:1070:U:O2'	1:A:1071:C:H5'	2.17	0.44
1:A:1320:C:C2	21:S:72:GLY:HA3	2.53	0.44
4:B:23:ARG:O	4:B:24:TRP:O	2.34	0.44
4:B:107:THR:C	4:B:109:SER:N	2.74	0.44
5:C:178:LEU:HD12	5:C:178:LEU:HA	1.70	0.44
6:D:105:VAL:HG12	6:D:117:ALA:HB1	2.00	0.44
9:G:116:ALA:HA	9:G:119:ARG:NH2	2.32	0.44
9:G:138:LYS:HE2	9:G:142:GLU:OE1	2.17	0.44
11:I:98:PRO:C	11:I:100:GLY:N	2.75	0.44
15:M:53:VAL:O	15:M:53:VAL:HG12	2.16	0.44
20:R:86:VAL:O	20:R:87:ARG:HB2	2.17	0.44
22:T:78:ALA:O	22:T:79:ARG:C	2.58	0.44
1:A:316:G:OP2	1:A:351:G:O2'	2.35	0.44
1:A:324:G:OP1	22:T:22:ARG:NH1	2.51	0.44
1:A:369:C:O2'	1:A:370:C:H5'	2.17	0.44
1:A:622:A:C8	1:A:623:C:C5	3.06	0.44
1:A:644:G:O2'	1:A:645:C:H5'	2.18	0.44
1:A:1060:C:O4'	12:J:52:GLY:HA2	2.17	0.44
1:A:1190:G:O2'	1:A:1191:A:P	2.75	0.44
1:A:1399:C:C2	1:A:1401:G:C5	3.05	0.44
4:B:172:ILE:O	4:B:173:ALA:C	2.59	0.44
5:C:111:LEU:HD21	5:C:144:SER:O	2.17	0.44
8:F:25:ILE:HD12	8:F:82:ARG:HH11	1.82	0.44
12:J:34:VAL:CG1	12:J:35:SER:N	2.79	0.44
17:O:16:ALA:HA	17:O:21:ASP:OD1	2.17	0.44
17:O:76:GLU:OE1	17:O:79:ARG:NH2	2.50	0.44
21:S:45:VAL:C	21:S:47:HIS:H	2.24	0.44
1:A:190(K):G:C3'	1:A:190(L):U:H5''	2.48	0.44
1:A:303:A:P	14:L:17:LYS:HZ1	2.41	0.44
1:A:349:A:C2'	1:A:350:G:O5'	2.66	0.44
1:A:413:G:H1'	1:A:416:G:N2	2.33	0.44
1:A:1060:C:H5''	12:J:51:ARG:HB3	1.99	0.44
1:A:1539:C:C2	1:A:1540:U:H5	2.34	0.44
4:B:48:MET:O	4:B:51:LEU:HB2	2.18	0.44
4:B:80:ILE:HD11	4:B:208:ILE:CG2	2.31	0.44
5:C:91:LEU:O	5:C:95:THR:HG23	2.18	0.44
5:C:134:ILE:CG2	5:C:168:ALA:HB3	2.48	0.44
5:C:151:VAL:C	5:C:152:ILE:HG13	2.42	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:139:LEU:O	7:E:141:GLN:N	2.51	0.44
8:F:67:MET:HB2	8:F:68:PRO:CD	2.47	0.44
9:G:16:LEU:HD22	9:G:16:LEU:N	2.23	0.44
9:G:65:ALA:O	9:G:66:VAL:C	2.60	0.44
9:G:70:LYS:HG2	9:G:100:ALA:HB2	2.00	0.44
9:G:122:HIS:O	9:G:123:GLU:C	2.61	0.44
16:N:11:LYS:C	16:N:13:THR:N	2.74	0.44
16:N:33:VAL:O	16:N:34:TYR:C	2.61	0.44
17:O:70:LEU:HG	17:O:78:TYR:HB2	1.98	0.44
20:R:52:PRO:HB2	20:R:54:ARG:HG3	1.99	0.44
21:S:6:LYS:HB2	21:S:7:LYS:HD3	1.99	0.44
1:A:50:A:N6	1:A:361:G:H4'	2.32	0.44
1:A:142:G:O2'	1:A:196:A:N1	2.46	0.44
1:A:191:G:N2	22:T:85:MET:HE1	2.33	0.44
1:A:409:G:H5'	1:A:430:A:C6	2.52	0.44
1:A:1054:C:O2'	1:A:1055:A:C5'	2.65	0.44
1:A:1121:U:O2'	1:A:1122:U:H5'	2.17	0.44
1:A:1399:C:H4'	1:A:1400:C:O5'	2.17	0.44
1:A:1406:U:C2'	1:A:1407:C:H5'	2.47	0.44
1:A:1431:C:H2'	1:A:1432:G:H5'	1.98	0.44
4:B:27:LYS:NZ	4:B:195:ASP:HB2	2.32	0.44
4:B:104:ASN:OD1	4:B:107:THR:HB	2.17	0.44
5:C:191:THR:CG2	5:C:192:THR:N	2.81	0.44
6:D:25:ARG:C	6:D:27:TYR:N	2.75	0.44
6:D:156:GLU:C	6:D:156:GLU:OE1	2.61	0.44
8:F:25:ILE:HD12	8:F:82:ARG:NH1	2.32	0.44
9:G:111:ARG:NH2	9:G:126:ASP:CG	2.75	0.44
14:L:38:THR:HB	14:L:57:LYS:HB3	1.98	0.44
14:L:46:LYS:O	14:L:47:LYS:C	2.61	0.44
20:R:53:ARG:O	20:R:55:ARG:N	2.50	0.44
21:S:28:LYS:HB3	21:S:31:ILE:HD11	1.99	0.44
1:A:24:U:O2'	1:A:25:C:H5'	2.18	0.44
1:A:707:C:O2	13:K:39:PRO:HD3	2.18	0.44
1:A:1160:G:C6	1:A:1181:G:O6	2.71	0.44
1:A:1197:G:OP1	1:A:1198:G:OP2	2.36	0.44
1:A:1368:G:OP2	11:I:112:LYS:HD3	2.18	0.44
4:B:115:LEU:O	4:B:118:LEU:N	2.49	0.44
5:C:65:ALA:O	5:C:66:VAL:C	2.60	0.44
7:E:15:ARG:HD3	7:E:26:PHE:CD2	2.52	0.44
7:E:71:LEU:O	7:E:72:GLN:HG2	2.17	0.44
7:E:72:GLN:O	7:E:73:ASN:CB	2.65	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:42:ILE:O	16:N:43:CYS:C	2.60	0.44
19:Q:51:TYR:CE1	19:Q:73:VAL:HG11	2.52	0.44
21:S:43:GLU:H	21:S:43:GLU:CD	2.25	0.44
1:A:378:G:O2'	1:A:379:C:H5'	2.18	0.44
1:A:554:C:H2'	1:A:555:C:H6	1.82	0.44
1:A:572:A:H5''	1:A:917:G:H4'	2.00	0.44
1:A:584:G:H2'	1:A:585:G:H8	1.82	0.44
1:A:992:U:O2'	1:A:993:G:P	2.76	0.44
1:A:1053:G:H4'	1:A:1054:C:H5'	1.98	0.44
1:A:1081:G:OP1	7:E:16:THR:HG23	2.18	0.44
1:A:1160:G:C6	1:A:1161:C:C4	3.06	0.44
1:A:1160:G:O2'	1:A:1161:C:H5'	2.18	0.44
1:A:1190:G:C3'	5:C:3:ASN:OD1	2.66	0.44
1:A:1305:G:C8	1:A:1305:G:OP2	2.71	0.44
4:B:9:GLU:O	4:B:12:GLU:N	2.51	0.44
4:B:193:ASP:OD1	4:B:196:LEU:HB2	2.17	0.44
5:C:33:LEU:HD11	16:N:53:LEU:HD23	1.99	0.44
5:C:180:ALA:O	5:C:205:GLY:O	2.36	0.44
5:C:195:VAL:O	5:C:195:VAL:HG12	2.17	0.44
7:E:126:ARG:CG	7:E:126:ARG:NH1	2.75	0.44
9:G:23:VAL:O	9:G:24:THR:C	2.61	0.44
11:I:78:LYS:HE3	11:I:101:PHE:HD2	1.83	0.44
11:I:80:GLY:O	11:I:83:ARG:N	2.51	0.44
16:N:43:CYS:O	16:N:44:LEU:C	2.60	0.44
16:N:59:ALA:O	16:N:60:SER:CB	2.62	0.44
17:O:30:ALA:O	17:O:31:LEU:C	2.61	0.44
19:Q:48:GLU:O	19:Q:49:GLU:C	2.60	0.44
19:Q:85:VAL:O	19:Q:89:LEU:HG	2.18	0.44
20:R:51:LEU:HA	20:R:52:PRO:HD3	1.82	0.44
20:R:62:GLU:O	20:R:63:GLN:C	2.61	0.44
22:T:19:SER:O	22:T:20:LEU:C	2.61	0.44
22:T:63:ILE:HD13	22:T:80:ARG:HB2	1.98	0.44
1:A:391:G:C6	1:A:392:G:C5	3.05	0.44
1:A:407:G:N2	1:A:496:A:O2'	2.50	0.44
1:A:460:A:H62	1:A:463:A:H62	1.64	0.44
1:A:817:C:H4'	1:A:818:G:OP1	2.18	0.44
1:A:1270:C:O5'	1:A:1270:C:H6	2.01	0.44
1:A:1345:U:C4	1:A:1377:A:C2	3.05	0.44
5:C:29:TYR:CZ	16:N:54:PRO:HG2	2.53	0.44
5:C:43:LEU:HD22	5:C:47:LEU:HD22	1.99	0.44
6:D:207:TYR:C	6:D:209:ARG:N	2.73	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:32:VAL:HG12	7:E:33:VAL:N	2.33	0.44
8:F:37:VAL:HA	8:F:65:VAL:HG12	1.98	0.44
14:L:7:ILE:O	14:L:8:ASN:C	2.59	0.44
21:S:16:LEU:C	21:S:18:LYS:H	2.26	0.44
1:A:279:A:H5''	1:A:280:C:H3'	2.00	0.43
1:A:303:A:P	14:L:17:LYS:NZ	2.91	0.43
1:A:1006:C:O2'	1:A:1007:C:H5'	2.18	0.43
1:A:1192:C:C5	1:A:1193:G:C8	3.06	0.43
1:A:1345:U:C2	1:A:1377:A:N1	2.86	0.43
1:A:1370:G:C2	1:A:1371:G:N7	2.85	0.43
4:B:36:ARG:HD2	4:B:41:ILE:CD1	2.48	0.43
5:C:177:THR:O	5:C:179:ARG:N	2.50	0.43
6:D:58:LEU:HD13	6:D:58:LEU:C	2.42	0.43
8:F:67:MET:HE1	8:F:75:LEU:HB3	2.00	0.43
9:G:46:ALA:C	9:G:48:LYS:H	2.25	0.43
9:G:99:LEU:O	9:G:100:ALA:C	2.61	0.43
12:J:23:ILE:CG2	12:J:72:VAL:HG11	2.47	0.43
17:O:6:GLU:CD	17:O:6:GLU:N	2.75	0.43
20:R:27:GLY:O	20:R:29:PHE:HD2	2.01	0.43
20:R:60:GLY:O	20:R:61:LYS:C	2.61	0.43
22:T:74:LYS:HB3	22:T:75:ASN:H	1.53	0.43
1:A:418:C:C5	1:A:426:G:N1	2.86	0.43
1:A:586:C:C2'	1:A:587:G:H5'	2.48	0.43
1:A:975:A:H4'	1:A:976:G:O5'	2.18	0.43
1:A:1060:C:O2	1:A:1198:G:C2	2.72	0.43
1:A:1072:G:H2'	1:A:1073:U:O4'	2.18	0.43
1:A:1168:A:C6	1:A:1169:A:C6	3.06	0.43
1:A:1364:U:O2'	1:A:1365:G:H5'	2.18	0.43
4:B:24:TRP:HB3	4:B:40:HIS:CE1	2.53	0.43
4:B:82:ARG:NH1	4:B:92:TYR:OH	2.51	0.43
5:C:190:ARG:HG2	5:C:190:ARG:NH1	2.28	0.43
5:C:194:GLY:C	5:C:195:VAL:HG23	2.43	0.43
6:D:3:ARG:NE	6:D:3:ARG:CA	2.80	0.43
8:F:30:LEU:HD21	8:F:65:VAL:HG11	1.99	0.43
9:G:139:GLU:O	9:G:143:ARG:HG3	2.17	0.43
10:H:59:LEU:O	10:H:60:ARG:C	2.60	0.43
19:Q:51:TYR:HE2	19:Q:76:LEU:HB2	1.83	0.43
19:Q:82:MET:O	19:Q:85:VAL:N	2.51	0.43
20:R:35:ARG:O	20:R:37:VAL:N	2.47	0.43
1:A:113:G:H1'	1:A:354:G:C5'	2.48	0.43
1:A:328:C:H4'	1:A:329:A:H5'	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:G:H2'	1:A:485:G:H22	1.83	0.43
1:A:597:G:C4	1:A:644:G:C2	3.07	0.43
1:A:783:C:O2'	1:A:784:C:H5'	2.17	0.43
1:A:1354:C:O2'	1:A:1355:G:H5'	2.18	0.43
1:A:1521:G:O2'	1:A:1522:U:H5'	2.17	0.43
6:D:8:VAL:HG11	6:D:21:LEU:CB	2.43	0.43
6:D:61:LYS:O	6:D:62:GLN:C	2.59	0.43
9:G:12:LEU:HD12	9:G:12:LEU:N	2.33	0.43
10:H:29:SER:OG	10:H:32:LYS:HG3	2.17	0.43
10:H:83:ILE:HG13	10:H:137:VAL:HG22	2.00	0.43
10:H:87:SER:OG	10:H:92:ARG:HA	2.18	0.43
17:O:18:PHE:O	17:O:19:PRO:C	2.59	0.43
18:P:67:THR:O	18:P:68:ASP:C	2.61	0.43
1:A:19:C:O2	1:A:572:A:H2	2.00	0.43
1:A:178:C:O2'	1:A:179:A:H5'	2.18	0.43
1:A:252:U:H2'	1:A:253:U:H6	1.81	0.43
1:A:443:C:H2'	1:A:444:C:H6	1.82	0.43
1:A:490:G:H2'	1:A:491:G:H8	1.84	0.43
1:A:602:A:O2'	1:A:603:U:H5'	2.18	0.43
1:A:1112:C:O2	5:C:179:ARG:HB3	2.17	0.43
1:A:1302:U:C5	15:M:17:VAL:HG21	2.52	0.43
5:C:34:LEU:CD1	16:N:25:VAL:HG21	2.48	0.43
5:C:57:ILE:HG23	5:C:64:VAL:HG13	2.01	0.43
6:D:59:ARG:NE	6:D:59:ARG:HA	2.33	0.43
6:D:112:VAL:HG23	6:D:116:GLN:OE1	2.18	0.43
6:D:153:ARG:CZ	6:D:181:MET:HE3	2.49	0.43
7:E:78:HIS:HB2	7:E:79:GLU:OE1	2.19	0.43
8:F:33:TYR:HA	8:F:71:ARG:NH2	2.33	0.43
10:H:48:TYR:HB2	10:H:60:ARG:O	2.18	0.43
11:I:53:VAL:O	11:I:54:ASP:C	2.61	0.43
16:N:57:ARG:CG	16:N:58:LYS:N	2.80	0.43
20:R:74:ARG:HB3	20:R:81:PHE:CE1	2.54	0.43
22:T:14:LYS:O	22:T:18:GLN:HG3	2.19	0.43
1:A:190(K):G:H2'	1:A:190(L):U:H5''	2.00	0.43
1:A:339:C:H2'	1:A:340:U:H6	1.83	0.43
1:A:348:G:H2'	1:A:348:G:N3	2.32	0.43
1:A:607:A:O2'	1:A:608:A:H5'	2.18	0.43
1:A:831:U:H2'	1:A:832:C:C6	2.54	0.43
1:A:1061:G:C6	1:A:1062:U:N3	2.86	0.43
1:A:1108:G:H5'	1:A:1191:A:H4'	2.00	0.43
1:A:1450:U:H2'	1:A:1452:C:C5	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:W:2:A:H8	2:W:2:A:H5'	1.84	0.43
4:B:24:TRP:N	4:B:24:TRP:CD1	2.85	0.43
4:B:57:PHE:CZ	4:B:61:LEU:HD21	2.53	0.43
4:B:130:ARG:HB3	4:B:134:GLU:OE1	2.19	0.43
5:C:50:ALA:CB	5:C:70:VAL:HG11	2.48	0.43
6:D:70:ILE:HG22	6:D:71:SER:O	2.18	0.43
6:D:124:GLY:O	6:D:126:ILE:N	2.52	0.43
7:E:144:THR:HB	7:E:147:ASP:OD1	2.19	0.43
9:G:15:ASP:C	9:G:17:VAL:H	2.25	0.43
10:H:69:ARG:NE	10:H:75:ARG:O	2.48	0.43
11:I:43:ALA:O	11:I:44:VAL:C	2.61	0.43
12:J:14:LYS:C	12:J:16:LEU:H	2.26	0.43
15:M:105:THR:HG22	15:M:106:ASN:H	1.83	0.43
16:N:55:GLY:O	16:N:56:VAL:C	2.62	0.43
17:O:3:ILE:CD1	17:O:34:LEU:HD22	2.48	0.43
18:P:12:LYS:C	18:P:14:ASN:H	2.26	0.43
1:A:131:C:H2'	1:A:132:C:H6	1.83	0.43
1:A:375:U:O2'	18:P:28:ARG:HD2	2.19	0.43
1:A:437:U:H2'	1:A:438:G:H5'	1.99	0.43
1:A:603:U:H2'	1:A:604:G:C8	2.54	0.43
1:A:802:A:C2'	1:A:803:G:H5'	2.48	0.43
1:A:803:G:H2'	1:A:804:U:O4'	2.18	0.43
1:A:958:A:N3	1:A:985:C:O2'	2.45	0.43
1:A:978:A:C5	1:A:1319:A:C2	3.06	0.43
1:A:1157:A:H1'	1:A:1181:G:N2	2.34	0.43
1:A:1179:A:O2'	1:A:1180:A:H5'	2.19	0.43
1:A:1250:A:C5'	11:I:68:GLY:N	2.77	0.43
5:C:5:ILE:O	5:C:5:ILE:CD1	2.66	0.43
5:C:47:LEU:N	5:C:47:LEU:HD12	2.34	0.43
6:D:64:LEU:HD12	6:D:75:PHE:HZ	1.84	0.43
7:E:69:VAL:HG21	7:E:113:ALA:HB1	1.99	0.43
9:G:108:ALA:C	9:G:110:GLN:N	2.76	0.43
14:L:53:ARG:HG2	14:L:69:TYR:CE1	2.43	0.43
14:L:92:ASP:O	14:L:93:LEU:HD23	2.18	0.43
18:P:9:PHE:CE1	18:P:18:ARG:CZ	3.01	0.43
19:Q:19:VAL:CG2	19:Q:44:ALA:HB3	2.49	0.43
21:S:33:THR:HG22	21:S:34:TRP:N	2.32	0.43
1:A:141:A:H1'	1:A:182:U:O2	2.18	0.43
1:A:359:U:H2'	1:A:360:A:C8	2.54	0.43
1:A:416:G:H3'	1:A:416:G:N3	2.33	0.43
1:A:1320:C:O2	21:S:72:GLY:HA3	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1320:C:N3	21:S:36:ARG:HG3	2.34	0.43
1:A:1431:C:H2'	1:A:1432:G:C5'	2.49	0.43
4:B:46:LYS:O	4:B:50:GLU:HB2	2.19	0.43
5:C:89:GLU:O	5:C:93:LYS:HB2	2.19	0.43
5:C:121:ALA:O	5:C:125:GLU:HG3	2.19	0.43
5:C:186:PHE:CE2	5:C:188:LEU:HD22	2.53	0.43
9:G:40:ALA:O	9:G:41:ARG:C	2.62	0.43
9:G:136:LYS:O	9:G:137:LYS:C	2.61	0.43
10:H:137:VAL:CG1	10:H:138:TRP:N	2.79	0.43
11:I:38:GLN:OE1	11:I:38:GLN:HA	2.18	0.43
13:K:69:ALA:O	13:K:70:LYS:C	2.61	0.43
14:L:117:ARG:O	14:L:119:LYS:O	2.37	0.43
15:M:33:ALA:O	15:M:35:GLU:N	2.52	0.43
15:M:94:ARG:HH12	21:S:81:ARG:NH1	2.12	0.43
17:O:53:HIS:O	17:O:56:LEU:N	2.51	0.43
19:Q:74:LEU:O	19:Q:74:LEU:HD23	2.18	0.43
20:R:59:SER:O	20:R:60:GLY:C	2.62	0.43
21:S:45:VAL:HG12	21:S:46:GLY:H	1.84	0.43
22:T:100:ILE:C	22:T:102:GLY:N	2.76	0.43
1:A:77:G:O2'	1:A:78:G:H5'	2.18	0.43
1:A:243:A:C5'	1:A:244:U:H5'	2.48	0.43
1:A:279:A:H4'	1:A:280:C:OP2	2.17	0.43
1:A:294:U:H2'	1:A:295:C:H6	1.83	0.43
1:A:560:U:O2'	1:A:561:U:OP2	2.24	0.43
1:A:601:C:O2'	1:A:602:A:H5'	2.18	0.43
1:A:692:U:OP1	13:K:124:LYS:HE3	2.19	0.43
1:A:718:G:C5'	1:A:719:C:OP2	2.66	0.43
1:A:1346:A:C8	1:A:1348:U:C2	3.07	0.43
1:A:1372:U:H2'	1:A:1373:G:C5'	2.49	0.43
1:A:1520:G:C2	1:A:1521:G:C5	3.07	0.43
4:B:20:GLU:HB2	4:B:190:THR:HB	2.01	0.43
4:B:157:ARG:O	4:B:158:LEU:C	2.61	0.43
4:B:177:ALA:O	4:B:178:ARG:C	2.62	0.43
5:C:151:VAL:O	5:C:152:ILE:HG13	2.19	0.43
6:D:80:GLU:HA	6:D:80:GLU:OE2	2.18	0.43
6:D:116:GLN:O	6:D:119:GLN:N	2.51	0.43
8:F:74:ASP:O	8:F:75:LEU:C	2.61	0.43
9:G:15:ASP:HB3	9:G:19:GLY:CA	2.49	0.43
9:G:26:PHE:HB2	9:G:62:PHE:HZ	1.83	0.43
9:G:32:ARG:O	9:G:33:ASP:HB2	2.18	0.43
11:I:87:GLN:C	11:I:89:ASN:N	2.72	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:96:ILE:CG2	12:J:97:GLU:N	2.82	0.43
14:L:119:LYS:O	14:L:120:TYR:HB2	2.19	0.43
22:T:59:ALA:O	22:T:60:GLU:C	2.60	0.43
1:A:652:U:C5	1:A:752:G:C4	3.07	0.43
1:A:757:U:H2'	1:A:758:G:O4'	2.18	0.43
1:A:791:G:C2'	1:A:792:A:H5'	2.47	0.43
1:A:920:U:H2'	1:A:921:U:H6	1.80	0.43
1:A:1116:C:H2'	1:A:1117:G:C5'	2.27	0.43
1:A:1263:C:O2'	1:A:1264:C:H5'	2.18	0.43
4:B:7:VAL:HG23	4:B:7:VAL:O	2.18	0.43
4:B:9:GLU:HB2	4:B:217:ARG:HH12	1.83	0.43
4:B:58:ILE:O	4:B:61:LEU:HB2	2.19	0.43
5:C:52:LEU:CD2	5:C:118:GLN:HE22	2.32	0.43
5:C:91:LEU:HD21	5:C:99:VAL:HG23	2.00	0.43
6:D:112:VAL:HG22	6:D:161:ASN:ND2	2.34	0.43
8:F:32:ASN:N	8:F:32:ASN:HD22	2.16	0.43
8:F:44:GLY:CA	8:F:59:TYR:CE1	3.01	0.43
10:H:29:SER:O	10:H:30:ARG:C	2.61	0.43
10:H:122:ARG:O	10:H:123:GLU:C	2.61	0.43
17:O:57:LEU:HD12	17:O:57:LEU:HA	1.51	0.43
17:O:76:GLU:O	17:O:77:ARG:C	2.61	0.43
18:P:63:GLY:O	18:P:64:ALA:C	2.61	0.43
20:R:26:LEU:HD11	20:R:39:VAL:HG23	2.01	0.43
22:T:68:LYS:HA	22:T:68:LYS:HD2	1.83	0.43
1:A:41:G:O2'	1:A:42:G:H5'	2.18	0.43
1:A:169:C:O2'	1:A:170:U:H5'	2.19	0.43
1:A:300:A:H2'	1:A:301:G:O4'	2.19	0.43
1:A:647:C:H2'	1:A:648:A:H8	1.83	0.43
1:A:709:G:C6	1:A:710:G:C5	3.06	0.43
1:A:916:G:O2'	1:A:917:G:H5'	2.18	0.43
1:A:1371:G:C2	1:A:1372:U:C6	3.06	0.43
1:A:1424:C:H2'	1:A:1425:U:O4'	2.19	0.43
4:B:36:ARG:C	4:B:38:GLY:N	2.76	0.43
4:B:79:ASP:C	4:B:81:VAL:N	2.74	0.43
4:B:91:PRO:HA	4:B:154:LEU:HD12	2.00	0.43
4:B:124:SER:HB2	4:B:125:PRO:CD	2.44	0.43
4:B:187:LEU:CD1	4:B:214:ILE:HG21	2.45	0.43
5:C:30:ARG:HB3	5:C:30:ARG:NH1	2.33	0.43
5:C:160:ALA:C	5:C:162:GLN:N	2.77	0.43
5:C:179:ARG:O	5:C:180:ALA:HB3	2.19	0.43
7:E:31:LEU:HD22	7:E:43:LEU:HD21	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:48:LEU:HD21	8:F:60:PHE:CE1	2.54	0.43
11:I:93:ARG:HB3	11:I:93:ARG:CZ	2.47	0.43
14:L:69:TYR:HB2	14:L:90:VAL:HG21	2.01	0.43
15:M:40:ASN:HD22	15:M:40:ASN:C	2.26	0.43
16:N:4:LYS:O	16:N:5:ALA:C	2.62	0.43
18:P:14:ASN:O	18:P:14:ASN:CG	2.59	0.43
19:Q:3:LYS:HD3	19:Q:61:GLU:O	2.18	0.43
1:A:342:C:O2'	1:A:343:U:H5'	2.19	0.42
1:A:1203:C:H2'	1:A:1204:A:H8	1.84	0.42
1:A:1478:C:H2'	1:A:1479:C:C6	2.54	0.42
1:A:1516:G:H2'	1:A:1518:A:OP2	2.19	0.42
4:B:23:ARG:C	4:B:23:ARG:HD3	2.44	0.42
4:B:73:THR:HB	4:B:170:GLU:OE2	2.19	0.42
4:B:90:MET:HE2	4:B:222:ILE:HD13	2.01	0.42
4:B:101:MET:HE2	4:B:101:MET:HA	2.01	0.42
5:C:40:ARG:HB3	5:C:44:GLU:OE1	2.18	0.42
5:C:90:GLU:HA	5:C:93:LYS:HB2	2.00	0.42
6:D:162:LEU:HD23	6:D:165:MET:HG3	2.00	0.42
8:F:100:ASN:ND2	20:R:23:LYS:HG2	2.31	0.42
9:G:118:VAL:O	9:G:121:ALA:HB3	2.19	0.42
11:I:65:VAL:O	11:I:66:ARG:HB2	2.19	0.42
11:I:127:LYS:HE3	11:I:127:LYS:HA	2.01	0.42
15:M:23:TYR:CB	15:M:67:GLU:HA	2.49	0.42
18:P:74:LEU:CB	18:P:79:VAL:HG21	2.49	0.42
19:Q:40:LYS:HE2	19:Q:42:TYR:CE2	2.54	0.42
21:S:22:LEU:HA	21:S:25:LYS:NZ	2.33	0.42
22:T:53:LEU:CD1	22:T:101:GLY:HA2	2.49	0.42
1:A:180:U:H2'	1:A:181:G:H5'	2.01	0.42
1:A:190(H):G:C2'	1:A:190(I):G:H5'	2.49	0.42
1:A:344:A:H4'	1:A:345:C:OP2	2.19	0.42
1:A:478:A:H3'	1:A:479:C:C5'	2.49	0.42
1:A:610:G:O2'	1:A:611:A:H5'	2.19	0.42
1:A:929:G:H5''	1:A:1533:C:C5	2.55	0.42
1:A:954:G:H2'	1:A:955:U:C6	2.52	0.42
1:A:1201:A:HO2'	1:A:1202:G:P	2.42	0.42
1:A:1286:A:H2	23:V:18:TYR:HH	1.61	0.42
6:D:110:PHE:CD2	6:D:148:VAL:HG22	2.54	0.42
6:D:156:GLU:O	6:D:157:LEU:C	2.61	0.42
7:E:96:PRO:HA	7:E:117:ASP:CG	2.44	0.42
7:E:115:VAL:HG12	7:E:116:THR:N	2.33	0.42
11:I:93:ARG:HH11	11:I:93:ARG:HB2	1.83	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:59:TYR:O	13:K:60:ALA:C	2.61	0.42
15:M:34:LEU:CD1	15:M:41:PRO:HA	2.43	0.42
17:O:39:LEU:HD23	17:O:39:LEU:O	2.19	0.42
1:A:107:G:N7	22:T:15:ARG:NH2	2.59	0.42
1:A:653:A:P	10:H:56:LYS:NZ	2.91	0.42
1:A:695:A:H2'	1:A:696:A:C8	2.54	0.42
1:A:946:A:C6	1:A:947:G:C6	3.08	0.42
1:A:1123:A:H2'	1:A:1124:G:O4'	2.19	0.42
1:A:1319:A:OP2	21:S:5:LEU:HD21	2.20	0.42
1:A:1357:A:C5	1:A:1358:U:C5	3.07	0.42
4:B:42:ILE:HG21	4:B:202:PRO:O	2.20	0.42
4:B:148:TYR:CD2	4:B:148:TYR:N	2.84	0.42
4:B:224:GLN:C	4:B:226:ARG:H	2.27	0.42
5:C:11:ARG:O	5:C:14:ILE:O	2.38	0.42
5:C:70:VAL:O	5:C:105:GLU:HA	2.18	0.42
6:D:14:ARG:C	6:D:16:GLY:N	2.77	0.42
6:D:33:MET:HA	6:D:37:PRO:HA	2.00	0.42
6:D:149:ALA:HB3	6:D:152:SER:HB2	2.00	0.42
9:G:153:HIS:ND1	9:G:153:HIS:N	2.66	0.42
10:H:91:ARG:NH1	19:Q:33:GLY:HA3	2.35	0.42
11:I:42:ARG:HG2	11:I:42:ARG:NH1	2.30	0.42
12:J:28:ARG:HG2	12:J:28:ARG:NH1	2.33	0.42
13:K:69:ALA:O	13:K:72:ALA:N	2.52	0.42
15:M:2:ALA:HB3	15:M:53:VAL:HG11	2.01	0.42
15:M:90:LEU:HD22	15:M:93:ARG:HD2	2.01	0.42
20:R:86:VAL:HG12	20:R:87:ARG:N	2.30	0.42
21:S:39:THR:CG2	21:S:40:ILE:N	2.80	0.42
1:A:46:G:H2'	1:A:366:C:C5	2.54	0.42
1:A:363:A:C2	14:L:31:PRO:HG2	2.54	0.42
1:A:521:G:OP1	14:L:73:GLU:O	2.36	0.42
1:A:848:C:O2'	1:A:849:C:H5'	2.19	0.42
1:A:866:C:H2'	1:A:867:G:O4'	2.20	0.42
1:A:1206:G:H1'	5:C:193:TYR:O	2.18	0.42
4:B:164:VAL:O	4:B:186:ALA:HA	2.20	0.42
5:C:30:ARG:NH1	5:C:30:ARG:HB2	2.33	0.42
6:D:52:SER:C	6:D:54:TYR:N	2.76	0.42
6:D:150:GLU:C	6:D:152:SER:N	2.74	0.42
7:E:110:LEU:HD13	7:E:118:ILE:HG21	2.01	0.42
8:F:37:VAL:HG22	8:F:65:VAL:CG1	2.50	0.42
8:F:55:ASP:CB	8:F:86:ARG:HH12	2.31	0.42
11:I:10:ARG:O	11:I:13:ALA:N	2.53	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:13:GLN:HA	13:K:75:TYR:O	2.19	0.42
13:K:27:ASN:CG	13:K:28:THR:N	2.77	0.42
13:K:95:ILE:O	13:K:99:GLN:HG3	2.19	0.42
14:L:39:VAL:HA	14:L:79:GLU:CG	2.49	0.42
18:P:33:ILE:O	18:P:34:GLU:HB2	2.19	0.42
19:Q:26:GLN:O	19:Q:27:PHE:HB3	2.19	0.42
19:Q:31:LEU:HG	19:Q:32:TYR:CD2	2.54	0.42
20:R:29:PHE:CZ	20:R:31:LEU:HG	2.55	0.42
1:A:587:G:OP1	10:H:89:PRO:HB3	2.19	0.42
1:A:741:G:O2'	1:A:742:G:H5'	2.19	0.42
1:A:791:G:H2'	1:A:792:A:H5''	2.00	0.42
1:A:966:G:H2'	1:A:967:C:O4'	2.19	0.42
1:A:1453:G:H2'	1:A:1454:G:O4'	2.20	0.42
1:A:1455:G:O2'	1:A:1459:C:H5'	2.19	0.42
4:B:16:HIS:CB	4:B:44:LEU:HD21	2.48	0.42
4:B:24:TRP:CZ3	4:B:26:PRO:HA	2.55	0.42
4:B:174:VAL:O	4:B:175:ARG:C	2.60	0.42
4:B:212:GLN:HE22	4:B:216:SER:HB3	1.81	0.42
4:B:230:VAL:CG1	4:B:231:GLU:N	2.81	0.42
5:C:30:ARG:CZ	5:C:30:ARG:CB	2.98	0.42
5:C:70:VAL:C	5:C:106:VAL:HG23	2.44	0.42
6:D:36:ARG:HA	6:D:38:TYR:CE2	2.55	0.42
9:G:149:ARG:HG2	13:K:59:TYR:CE1	2.55	0.42
11:I:69:GLY:C	11:I:73:GLN:HG3	2.44	0.42
12:J:38:ILE:HD12	12:J:71:LEU:CB	2.50	0.42
14:L:53:ARG:HD2	14:L:93:LEU:HD21	2.00	0.42
14:L:120:TYR:O	14:L:122:THR:N	2.52	0.42
18:P:61:SER:C	18:P:62:VAL:HG22	2.44	0.42
21:S:45:VAL:HA	21:S:62:ILE:HG22	2.02	0.42
1:A:397:A:H5'	1:A:398:C:P	2.60	0.42
1:A:412:A:H2'	1:A:413:G:C5'	2.50	0.42
1:A:420:U:H5'	1:A:424:G:H1'	2.01	0.42
1:A:439:A:H2'	1:A:440:A:O4'	2.20	0.42
1:A:624:C:O2'	1:A:625:G:H5'	2.19	0.42
1:A:990:C:H5''	1:A:1018:C:H5'	2.02	0.42
1:A:1205:U:O2'	5:C:195:VAL:CG2	2.68	0.42
1:A:1237:C:C4'	1:A:1334:G:H21	2.33	0.42
1:A:1305:G:H5'	23:V:4:GLY:HA3	1.99	0.42
1:A:1415:G:C4	1:A:1416:G:C8	3.06	0.42
1:A:1416:G:C2	1:A:1485:U:O2	2.73	0.42
1:A:1470:G:O2'	1:A:1471:G:H5'	2.18	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1511:G:H2'	1:A:1512:U:O4'	2.19	0.42
4:B:16:HIS:NE2	4:B:214:ILE:HG12	2.35	0.42
4:B:170:GLU:O	4:B:173:ALA:HB3	2.19	0.42
5:C:52:LEU:O	5:C:53:ALA:C	2.63	0.42
11:I:23:ASN:O	11:I:23:ASN:ND2	2.52	0.42
13:K:14:VAL:O	13:K:15:ALA:HB3	2.19	0.42
13:K:126:ARG:HB3	13:K:127:LYS:H	1.48	0.42
15:M:2:ALA:O	15:M:3:ARG:C	2.62	0.42
15:M:9:ILE:HD12	15:M:9:ILE:N	2.34	0.42
16:N:47:LEU:O	16:N:50:LYS:N	2.52	0.42
17:O:25:THR:O	17:O:25:THR:HG22	2.19	0.42
18:P:6:LEU:HD21	18:P:73:LEU:HD11	2.02	0.42
20:R:26:LEU:HD21	20:R:39:VAL:CG2	2.50	0.42
22:T:18:GLN:O	22:T:19:SER:C	2.62	0.42
22:T:49:ALA:O	22:T:52:ALA:HB3	2.20	0.42
1:A:105:G:H2'	1:A:106:C:C6	2.54	0.42
1:A:114:U:H2'	1:A:115:G:C8	2.55	0.42
1:A:300:A:H1'	1:A:565:U:O2	2.20	0.42
1:A:320:C:H2'	1:A:321:A:C8	2.54	0.42
1:A:602:A:C2	1:A:637:G:C2	3.07	0.42
1:A:929:G:H5''	1:A:1533:C:C6	2.54	0.42
1:A:1250:A:H2'	1:A:1251:A:C8	2.54	0.42
1:A:1303:C:N4	1:A:1304:G:C6	2.87	0.42
1:A:1305:G:H5''	23:V:4:GLY:HA3	1.99	0.42
1:A:1346:A:C5	9:G:10:ARG:NH2	2.88	0.42
1:A:1505:G:C8	1:A:1505:G:H3'	2.54	0.42
4:B:77:ALA:HB3	4:B:211:ILE:HG21	2.02	0.42
5:C:14:ILE:CG2	5:C:15:THR:N	2.72	0.42
5:C:34:LEU:HD12	16:N:25:VAL:HG21	2.02	0.42
7:E:15:ARG:HG3	7:E:15:ARG:HH11	1.84	0.42
8:F:31:GLU:CA	8:F:35:ALA:HB2	2.47	0.42
9:G:116:ALA:O	9:G:119:ARG:HB2	2.19	0.42
12:J:90:LEU:N	12:J:91:PRO:CD	2.61	0.42
15:M:72:ALA:O	15:M:76:ALA:HB3	2.20	0.42
15:M:110:ARG:HH11	15:M:110:ARG:CG	2.32	0.42
16:N:44:LEU:C	16:N:44:LEU:HD13	2.45	0.42
19:Q:82:MET:C	19:Q:84:LEU:N	2.75	0.42
23:V:6:ARG:O	23:V:8:THR:N	2.45	0.42
1:A:47:C:H5''	1:A:365:U:C6	2.55	0.42
1:A:258:G:O2'	1:A:259:G:H5'	2.19	0.42
1:A:458:C:C2'	1:A:459:G:H8	2.33	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:G:C2'	1:A:476:G:H5''	2.47	0.42
1:A:605:U:O2'	1:A:606:G:H5'	2.19	0.42
1:A:737:A:H1'	8:F:73:ASN:ND2	2.34	0.42
1:A:928:G:H4'	1:A:1533:C:C5'	2.29	0.42
1:A:1053:G:O6	1:A:1199:U:H2'	2.19	0.42
1:A:1333:A:H2'	1:A:1334:G:O4'	2.20	0.42
1:A:1377:A:O2'	9:G:2:ALA:HB3	2.20	0.42
1:A:1396:A:H4'	1:A:1397:C:H5''	2.02	0.42
4:B:36:ARG:C	4:B:38:GLY:H	2.26	0.42
4:B:44:LEU:O	4:B:47:THR:N	2.53	0.42
4:B:87:ARG:O	4:B:88:ALA:HB2	2.20	0.42
5:C:132:ARG:O	5:C:136:GLN:N	2.47	0.42
10:H:117:GLY:O	10:H:119:LEU:CD2	2.68	0.42
11:I:42:ARG:O	11:I:44:VAL:N	2.52	0.42
11:I:44:VAL:O	11:I:51:ARG:NH1	2.52	0.42
12:J:55:LYS:HG3	12:J:56:HIS:N	2.35	0.42
17:O:32:LEU:C	17:O:34:LEU:N	2.73	0.42
17:O:43:LEU:HD11	17:O:53:HIS:HA	2.01	0.42
20:R:17:SER:H	20:R:19:LYS:NZ	2.18	0.42
22:T:54:LYS:CE	22:T:100:ILE:HD12	2.48	0.42
23:V:2:GLY:O	23:V:3:LYS:C	2.63	0.42
1:A:129(A):G:O2'	1:A:130:A:OP2	2.29	0.42
1:A:532:A:H2'	1:A:533:A:OP1	2.20	0.42
1:A:602:A:H2'	1:A:603:U:O4'	2.20	0.42
1:A:904:C:O2'	1:A:905:U:H5'	2.20	0.42
1:A:927:G:H2'	1:A:928:G:H8	1.85	0.42
1:A:1256:A:H2	1:A:1277:C:C4	2.38	0.42
3:X:36:U:H2'	3:X:37:T6A:C8	2.52	0.42
4:B:103:THR:HA	4:B:180:LEU:HD11	2.01	0.42
6:D:61:LYS:NZ	6:D:62:GLN:NE2	2.67	0.42
6:D:101:LEU:HD12	6:D:101:LEU:O	2.19	0.42
7:E:70:PRO:O	7:E:77:PRO:HD3	2.20	0.42
15:M:59:TYR:O	15:M:63:THR:HG21	2.20	0.42
18:P:21:VAL:HG21	18:P:59:TRP:CG	2.55	0.42
19:Q:40:LYS:HD3	19:Q:42:TYR:OH	2.19	0.42
19:Q:81:ARG:CZ	19:Q:81:ARG:HB2	2.50	0.42
22:T:39:LYS:HE3	22:T:55:ILE:HD13	2.02	0.42
22:T:96:GLY:O	22:T:97:ALA:HB3	2.18	0.42
23:V:17:THR:O	23:V:22:ARG:HD3	2.20	0.42
1:A:409:G:OP2	1:A:431:A:C5'	2.57	0.42
1:A:440:A:C6	1:A:495:U:C2	3.08	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:462:G:O2'	18:P:82:GLN:NE2	2.53	0.42
1:A:559:A:P	7:E:126:ARG:NH2	2.93	0.42
1:A:604:G:H2'	1:A:605:U:H6	1.84	0.42
1:A:665:A:H2'	1:A:725:G:N2	2.35	0.42
1:A:735:C:H1'	20:R:75:ILE:HD11	2.02	0.42
1:A:833:U:H2'	1:A:834:C:C6	2.54	0.42
1:A:851:G:O2'	1:A:852:G:H5'	2.19	0.42
1:A:1037:C:H2'	1:A:1038:C:C6	2.55	0.42
1:A:1054:C:H2'	1:A:1055:A:H5''	2.01	0.42
1:A:1520:G:H2'	1:A:1521:G:C8	2.55	0.42
4:B:26:PRO:C	4:B:28:PHE:N	2.78	0.42
4:B:32:ILE:HD13	4:B:40:HIS:CD2	2.55	0.42
4:B:73:THR:O	4:B:74:LYS:C	2.63	0.42
6:D:110:PHE:N	6:D:110:PHE:CD1	2.87	0.42
7:E:50:GLU:OE1	7:E:53:LEU:HD12	2.20	0.42
7:E:76:ILE:HG23	7:E:142:LEU:HD13	2.01	0.42
8:F:19:LEU:C	8:F:21:LEU:H	2.27	0.42
9:G:24:THR:O	9:G:25:ALA:C	2.63	0.42
10:H:82:HIS:CG	10:H:83:ILE:H	2.38	0.42
11:I:78:LYS:HD2	11:I:78:LYS:O	2.20	0.42
15:M:45:VAL:C	15:M:47:ASP:N	2.76	0.42
16:N:29:ARG:HB3	16:N:40:CYS:CB	2.49	0.42
17:O:21:ASP:OD1	17:O:24:SER:HB3	2.20	0.42
19:Q:102:GLY:O	19:Q:103:GLY:O	2.38	0.42
20:R:44:LEU:HD23	20:R:50:ILE:HA	2.01	0.42
20:R:47:THR:CG2	20:R:83:GLU:H	2.33	0.42
1:A:358:U:H2'	1:A:359:U:C6	2.55	0.41
1:A:454:C:H4'	18:P:68:ASP:OD2	2.20	0.41
1:A:625:G:OP1	18:P:9:PHE:O	2.38	0.41
1:A:768:A:H4'	1:A:1523:G:N2	2.35	0.41
1:A:836:G:H2'	1:A:837:G:H8	1.85	0.41
1:A:923:A:O4'	1:A:1398:A:C2	2.72	0.41
1:A:965:A:N1	1:A:969:A:C2	2.88	0.41
1:A:992:U:O2'	1:A:993:G:OP2	2.32	0.41
1:A:1284:C:H3'	1:A:1285:A:C8	2.55	0.41
1:A:1349:A:C6	1:A:1374:A:C8	3.08	0.41
1:A:1539:C:O2	9:G:82:GLY:HA3	2.20	0.41
4:B:120:ALA:C	4:B:122:PHE:N	2.77	0.41
7:E:82:VAL:HG11	7:E:134:ALA:O	2.20	0.41
8:F:15:ASP:O	8:F:16:GLN:C	2.63	0.41
8:F:52:ILE:O	8:F:53:ALA:HB3	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:67:MET:HE2	8:F:72:VAL:HG13	2.01	0.41
8:F:74:ASP:O	8:F:77:ARG:N	2.53	0.41
10:H:11:THR:CB	10:H:14:ARG:HH12	2.32	0.41
10:H:121:ASP:O	10:H:122:ARG:C	2.62	0.41
13:K:48:ILE:CD1	13:K:63:LEU:HB2	2.50	0.41
21:S:35:SER:C	21:S:37:ARG:N	2.78	0.41
22:T:44:ALA:C	22:T:47:GLY:H	2.26	0.41
1:A:484:G:H5'	1:A:486:U:O4'	2.20	0.41
1:A:536:C:H2'	1:A:537:G:C8	2.56	0.41
1:A:575:G:C5	1:A:881:G:C2	3.07	0.41
1:A:673:G:N2	1:A:674:G:C2	2.87	0.41
1:A:754:C:O2	1:A:754:C:C3'	2.67	0.41
1:A:782:A:H2'	1:A:783:C:O4'	2.20	0.41
1:A:915:A:H2'	1:A:916:G:H5'	2.02	0.41
4:B:53:ARG:O	4:B:56:ARG:HB3	2.21	0.41
4:B:83:MET:HE2	4:B:234:PRO:C	2.44	0.41
4:B:169:LYS:HD3	4:B:170:GLU:OE2	2.20	0.41
4:B:201:ILE:HG21	4:B:214:ILE:HG21	2.02	0.41
6:D:52:SER:O	6:D:53:ASP:C	2.63	0.41
6:D:194:LEU:HD22	6:D:194:LEU:N	2.35	0.41
8:F:15:ASP:OD1	8:F:17:SER:HB2	2.20	0.41
11:I:28:VAL:O	11:I:29:ASN:HB2	2.20	0.41
14:L:27:LEU:O	14:L:28:LYS:C	2.61	0.41
14:L:86:ARG:HG3	14:L:86:ARG:O	2.19	0.41
14:L:119:LYS:N	14:L:119:LYS:CD	2.83	0.41
15:M:16:ASP:OD1	15:M:16:ASP:N	2.47	0.41
16:N:17:LYS:HG3	16:N:18:VAL:N	2.34	0.41
16:N:60:SER:O	16:N:61:TRP:HB3	2.20	0.41
1:A:376:G:N3	1:A:389:A:C2	2.88	0.41
1:A:662:G:H2'	1:A:663:A:C8	2.56	0.41
1:A:778:G:O2'	1:A:779:C:H5'	2.20	0.41
1:A:1050:G:O2'	1:A:1051:C:H5'	2.21	0.41
1:A:1255:G:O2'	1:A:1258:G:N3	2.51	0.41
4:B:23:ARG:C	4:B:23:ARG:CD	2.94	0.41
4:B:137:ARG:HA	4:B:140:HIS:CD2	2.55	0.41
4:B:169:LYS:C	4:B:171:ALA:H	2.27	0.41
6:D:10:ARG:O	6:D:13:ARG:N	2.53	0.41
6:D:110:PHE:N	6:D:110:PHE:HD1	2.18	0.41
6:D:146:ILE:N	6:D:146:ILE:CD1	2.82	0.41
7:E:131:ILE:HD13	7:E:131:ILE:HA	1.82	0.41
8:F:63:TYR:N	8:F:63:TYR:HD1	2.18	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:23:VAL:HG12	9:G:27:ILE:HD11	2.02	0.41
11:I:118:LYS:O	11:I:119:ALA:CB	2.64	0.41
15:M:59:TYR:O	15:M:63:THR:CG2	2.69	0.41
1:A:129:U:O2'	1:A:130:A:H2'	2.20	0.41
1:A:276:G:O2'	1:A:277:C:H5'	2.21	0.41
1:A:851:G:H2'	1:A:852:G:H8	1.85	0.41
1:A:924:C:H5'	1:A:1399:C:OP2	2.20	0.41
1:A:974:A:OP1	1:A:974:A:C8	2.73	0.41
1:A:1112:C:O2	5:C:178:LEU:O	2.39	0.41
4:B:194:PRO:C	4:B:196:LEU:N	2.79	0.41
4:B:215:LEU:O	4:B:218:ALA:HB3	2.20	0.41
6:D:176:LEU:HA	6:D:183:GLY:HA2	2.01	0.41
7:E:131:ILE:O	7:E:134:ALA:HB3	2.20	0.41
11:I:42:ARG:O	11:I:45:ALA:N	2.42	0.41
14:L:83:VAL:CG2	14:L:100:ILE:HG23	2.50	0.41
17:O:70:LEU:C	17:O:72:ARG:N	2.78	0.41
1:A:22:G:H4'	1:A:885:G:C8	2.55	0.41
1:A:163:C:H2'	1:A:164:U:H5'	1.98	0.41
1:A:323:U:H2'	1:A:324:G:O4'	2.20	0.41
1:A:346:G:O2'	1:A:347:G:H5'	2.18	0.41
1:A:692:U:H1'	1:A:695:A:N7	2.36	0.41
1:A:1085:U:C2	1:A:1094:G:O6	2.73	0.41
4:B:44:LEU:O	4:B:45:GLN:C	2.61	0.41
4:B:70:PHE:CD1	4:B:70:PHE:N	2.89	0.41
4:B:78:GLN:HG2	4:B:94:ASN:OD1	2.20	0.41
4:B:118:LEU:HD13	4:B:142:LEU:HB2	2.02	0.41
5:C:33:LEU:CD2	16:N:53:LEU:HD21	2.51	0.41
5:C:83:ARG:HG3	5:C:83:ARG:NH1	2.35	0.41
5:C:172:ARG:NH1	5:C:172:ARG:HB3	2.35	0.41
9:G:50:ILE:O	9:G:54:THR:HB	2.21	0.41
10:H:20:TYR:CE1	10:H:78:GLN:NE2	2.88	0.41
10:H:134:ILE:HD12	10:H:134:ILE:HA	1.81	0.41
16:N:53:LEU:HB3	16:N:56:VAL:HB	2.02	0.41
17:O:49:ASP:C	17:O:49:ASP:OD1	2.62	0.41
19:Q:95:TYR:O	19:Q:98:LEU:HD12	2.20	0.41
1:A:103:C:P	22:T:17:ARG:NH1	2.92	0.41
1:A:128:G:C6	1:A:129:U:C4	3.09	0.41
1:A:458:C:H2'	1:A:459:G:O4'	2.20	0.41
1:A:778:G:H1'	13:K:119:CYS:HB3	2.03	0.41
1:A:1151:A:H5''	12:J:42:THR:OG1	2.21	0.41
1:A:1227:A:C8	1:A:1227:A:C3'	3.04	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1234:C:C2'	1:A:1235:U:H5'	2.51	0.41
1:A:1302:U:H5	15:M:17:VAL:HG21	1.85	0.41
1:A:1451:A:O3'	1:A:1452:C:H6	2.04	0.41
5:C:51:GLY:O	5:C:53:ALA:N	2.44	0.41
6:D:105:VAL:HG12	6:D:117:ALA:CB	2.51	0.41
6:D:125:HIS:HA	6:D:149:ALA:HB3	2.03	0.41
10:H:88:LYS:O	10:H:89:PRO:C	2.62	0.41
11:I:48:GLU:OE2	11:I:51:ARG:HD2	2.20	0.41
12:J:78:ASN:O	12:J:82:ILE:HD12	2.20	0.41
15:M:31:LYS:O	15:M:35:GLU:OE1	2.39	0.41
15:M:70:LEU:O	15:M:70:LEU:HD23	2.20	0.41
23:V:13:ILE:O	23:V:16:GLY:N	2.39	0.41
1:A:376:G:H5''	18:P:5:ARG:HD2	2.01	0.41
1:A:533:A:C6	1:A:536:C:N3	2.88	0.41
1:A:664:G:N2	1:A:741:G:H1	2.07	0.41
1:A:748:C:O2'	1:A:749:C:H6	2.03	0.41
4:B:18:GLY:CA	4:B:41:ILE:HG23	2.49	0.41
5:C:6:HIS:HD2	5:C:7:PRO:HD2	1.85	0.41
5:C:15:THR:HB	5:C:181:ASN:HB2	2.02	0.41
6:D:202:LEU:O	6:D:205:GLU:N	2.53	0.41
7:E:24:ARG:NH1	7:E:24:ARG:CB	2.84	0.41
7:E:54:ALA:O	7:E:58:ALA:N	2.44	0.41
7:E:127:ASN:OD1	7:E:127:ASN:C	2.62	0.41
9:G:75:VAL:O	9:G:75:VAL:CG1	2.68	0.41
11:I:17:VAL:HG11	11:I:81:ILE:CA	2.50	0.41
11:I:107:ARG:NH1	11:I:107:ARG:CB	2.84	0.41
19:Q:60:ILE:CD1	19:Q:61:GLU:N	2.84	0.41
1:A:628:G:H2'	1:A:629:G:C8	2.55	0.41
1:A:674:G:H2'	1:A:675:A:H8	1.86	0.41
1:A:760:G:N3	19:Q:103:GLY:HA3	2.36	0.41
1:A:994:A:N7	1:A:1216:G:H4'	2.36	0.41
1:A:1048:G:OP1	16:N:3:ARG:HA	2.21	0.41
1:A:1096:C:H2'	1:A:1097:C:C6	2.55	0.41
1:A:1220:G:O2'	1:A:1221:G:H5'	2.20	0.41
1:A:1431:C:O2'	1:A:1432:G:H5'	2.21	0.41
4:B:102:LEU:N	4:B:102:LEU:CD1	2.84	0.41
4:B:144:ARG:CG	4:B:145:LEU:N	2.83	0.41
5:C:64:VAL:CB	5:C:99:VAL:HG11	2.50	0.41
6:D:173:TRP:O	6:D:186:LEU:HB2	2.20	0.41
7:E:9:LYS:NZ	7:E:111:GLU:OE1	2.53	0.41
7:E:77:PRO:HD2	7:E:142:LEU:HD13	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:38:LEU:O	9:G:40:ALA:N	2.54	0.41
13:K:122:LYS:O	13:K:123:LYS:C	2.63	0.41
18:P:1:MET:HE3	18:P:3:LYS:CG	2.50	0.41
19:Q:13:ASP:O	19:Q:13:ASP:OD2	2.39	0.41
21:S:74:PHE:CD1	21:S:74:PHE:N	2.88	0.41
1:A:165:C:C2	1:A:166:G:C8	3.08	0.41
1:A:253:U:H2'	1:A:254:G:H8	1.86	0.41
1:A:353:A:C8	1:A:353:A:C5'	3.03	0.41
1:A:443:C:H2'	1:A:444:C:C6	2.56	0.41
1:A:792:A:H1'	1:A:794:A:N7	2.36	0.41
1:A:802:A:H2'	1:A:803:G:C5'	2.50	0.41
1:A:1035:A:C2'	1:A:1036:G:H5'	2.51	0.41
1:A:1048:G:H1'	1:A:1215:G:H5'	2.02	0.41
1:A:1207:G:O2'	1:A:1208:C:H5'	2.20	0.41
1:A:1231:G:H2'	1:A:1232:U:C6	2.56	0.41
1:A:1240:U:P	9:G:116:ALA:HB2	2.61	0.41
1:A:1321:C:C5	1:A:1322:C:C2	3.09	0.41
1:A:1424:C:H2'	1:A:1425:U:H6	1.84	0.41
4:B:27:LYS:NZ	4:B:193:ASP:OD2	2.53	0.41
4:B:87:ARG:HH11	4:B:233:SER:HA	1.85	0.41
4:B:101:MET:CE	4:B:108:ILE:HG21	2.41	0.41
4:B:128:GLU:HA	4:B:135:GLN:NE2	2.35	0.41
5:C:8:ILE:HG22	5:C:9:GLY:N	2.36	0.41
5:C:13:GLY:HA2	16:N:57:ARG:CZ	2.51	0.41
5:C:39:ILE:HD12	5:C:57:ILE:CD1	2.51	0.41
5:C:133:ALA:O	5:C:137:ALA:N	2.41	0.41
6:D:11:LEU:HD22	6:D:66:ARG:CZ	2.50	0.41
6:D:61:LYS:HZ1	6:D:62:GLN:NE2	2.19	0.41
6:D:63:LYS:HD2	6:D:198:VAL:HG22	2.02	0.41
7:E:128:PRO:C	7:E:130:ASN:N	2.79	0.41
9:G:31:MET:HA	9:G:39:ALA:HB2	2.03	0.41
9:G:140:ASP:O	9:G:141:VAL:C	2.64	0.41
11:I:8:GLY:HA3	11:I:79:LEU:HB3	2.02	0.41
11:I:44:VAL:O	11:I:51:ARG:NH2	2.54	0.41
12:J:16:LEU:O	12:J:19:SER:N	2.54	0.41
12:J:47:PHE:CD2	16:N:34:TYR:HE2	2.39	0.41
13:K:26:ASN:O	13:K:27:ASN:CB	2.68	0.41
14:L:46:LYS:HG3	14:L:47:LYS:N	2.36	0.41
14:L:111:LYS:O	14:L:112:ASP:HB2	2.21	0.41
15:M:58:GLU:HA	15:M:58:GLU:OE2	2.21	0.41
16:N:29:ARG:HG2	16:N:29:ARG:HH11	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:61:GLY:O	17:O:62:GLN:C	2.64	0.41
18:P:58:TYR:O	18:P:61:SER:N	2.54	0.41
19:Q:84:LEU:O	19:Q:85:VAL:C	2.62	0.41
1:A:791:G:N2	1:A:1497:G:O3'	2.54	0.41
1:A:1096:C:H2'	1:A:1097:C:H6	1.85	0.41
1:A:1223:C:H3'	1:A:1224:G:H5''	2.03	0.41
1:A:1229:A:C2	1:A:1230:C:C4	3.09	0.41
1:A:1320:C:H2'	1:A:1321:C:O4'	2.20	0.41
1:A:1360:A:C2'	1:A:1361:G:C8	3.00	0.41
1:A:1469:G:O2'	1:A:1470:G:H5'	2.21	0.41
1:A:1544:U:O3'	2:W:1:A:C5'	2.68	0.41
2:W:1:A:H2'	2:W:2:A:H5'	2.03	0.41
4:B:134:GLU:HG2	4:B:137:ARG:HH21	1.86	0.41
5:C:48:TYR:HD1	5:C:48:TYR:C	2.29	0.41
6:D:52:SER:O	6:D:54:TYR:N	2.54	0.41
6:D:81:GLU:O	6:D:82:ALA:C	2.64	0.41
6:D:148:VAL:HG11	6:D:158:ILE:HD13	2.03	0.41
7:E:107:ARG:HG2	7:E:111:GLU:OE1	2.20	0.41
9:G:32:ARG:HE	9:G:32:ARG:HB3	1.75	0.41
9:G:66:VAL:HG12	9:G:70:LYS:HE3	2.02	0.41
9:G:124:LEU:O	9:G:127:ALA:HB3	2.20	0.41
11:I:70:LYS:O	11:I:74:ILE:HG13	2.21	0.41
14:L:70:ILE:HG12	14:L:100:ILE:HD12	2.02	0.41
15:M:67:GLU:HB3	15:M:68:GLY:H	1.46	0.41
18:P:20:VAL:HG21	18:P:32:TYR:CD2	2.55	0.41
19:Q:37:LYS:O	19:Q:38:ARG:HB2	2.21	0.41
19:Q:76:LEU:HD23	19:Q:77:VAL:N	2.36	0.41
22:T:15:ARG:O	22:T:16:HIS:C	2.64	0.41
22:T:30:LYS:O	22:T:31:SER:C	2.63	0.41
22:T:61:SER:O	22:T:63:ILE:N	2.54	0.41
1:A:109:A:C6	1:A:326:G:C6	3.09	0.40
1:A:265:G:H2'	1:A:267:C:H5	1.86	0.40
1:A:937:A:C2	1:A:1379:G:C6	3.09	0.40
1:A:961:U:O2'	1:A:962:C:H5'	2.21	0.40
1:A:1017:G:H2'	1:A:1018:C:C6	2.56	0.40
1:A:1129:C:OP1	11:I:62:TYR:OH	2.37	0.40
1:A:1152:A:H5''	12:J:13:HIS:CG	2.55	0.40
1:A:1221:G:OP1	21:S:36:ARG:HD3	2.21	0.40
4:B:97:TRP:CE3	4:B:98:LEU:O	2.74	0.40
4:B:112:VAL:C	4:B:114:ARG:N	2.78	0.40
5:C:96:GLY:C	5:C:97:LYS:HG2	2.46	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:164:ARG:HB3	5:C:164:ARG:HH11	1.86	0.40
7:E:12:LEU:N	7:E:12:LEU:HD13	2.35	0.40
8:F:91:VAL:HG12	8:F:92:LYS:N	2.36	0.40
10:H:80:ILE:O	10:H:80:ILE:HG22	2.20	0.40
10:H:110:ALA:O	10:H:111:ILE:C	2.63	0.40
11:I:46:ALA:O	11:I:78:LYS:HG2	2.21	0.40
11:I:59:PHE:HZ	11:I:88:TYR:CZ	2.39	0.40
15:M:22:ILE:CD1	15:M:25:ILE:HD12	2.51	0.40
18:P:1:MET:HE3	18:P:3:LYS:CD	2.51	0.40
22:T:91:LEU:N	22:T:91:LEU:HD23	2.36	0.40
1:A:559:A:OP2	7:E:126:ARG:NH2	2.54	0.40
1:A:651:C:O2'	1:A:652:U:H5'	2.22	0.40
1:A:741:G:H5'	17:O:39:LEU:HD12	2.03	0.40
1:A:788:U:O2'	1:A:789:U:H5'	2.21	0.40
1:A:1064:G:N2	1:A:1190:G:C2'	2.84	0.40
1:A:1140:C:H2'	1:A:1141:C:C5	2.53	0.40
1:A:1229:A:C4	1:A:1230:C:C5	3.09	0.40
1:A:1240:U:OP2	9:G:116:ALA:HB2	2.21	0.40
1:A:1241:G:H2'	1:A:1242:C:H6	1.86	0.40
4:B:69:LEU:HD22	4:B:71:VAL:HG13	2.02	0.40
4:B:224:GLN:C	4:B:226:ARG:N	2.79	0.40
5:C:40:ARG:HG3	5:C:40:ARG:HH11	1.87	0.40
5:C:167:TRP:HB3	5:C:168:ALA:H	1.44	0.40
5:C:180:ALA:HA	5:C:206:GLU:HA	2.03	0.40
6:D:61:LYS:HD2	6:D:207:TYR:CZ	2.56	0.40
9:G:21:VAL:CG2	9:G:22:LEU:N	2.85	0.40
9:G:36:LYS:HZ2	9:G:36:LYS:HG3	1.70	0.40
12:J:80:LYS:HA	12:J:83:GLU:CB	2.51	0.40
13:K:29:ILE:HD12	13:K:30:VAL:N	2.36	0.40
13:K:54:ARG:O	13:K:57:THR:HG22	2.20	0.40
14:L:69:TYR:CD2	14:L:70:ILE:N	2.89	0.40
15:M:25:ILE:HG22	15:M:26:GLY:N	2.37	0.40
15:M:44:ARG:HB3	15:M:46:LYS:HG2	2.04	0.40
18:P:39:TYR:CE2	18:P:41:PRO:HG3	2.56	0.40
20:R:37:VAL:C	20:R:41:LYS:HE2	2.47	0.40
20:R:40:LEU:C	20:R:42:ARG:N	2.79	0.40
1:A:270:A:H2'	1:A:271:C:C6	2.57	0.40
1:A:339:C:H2'	1:A:340:U:C6	2.57	0.40
1:A:604:G:C5	1:A:605:U:C5	3.09	0.40
1:A:637:G:O2'	1:A:638:G:H5'	2.20	0.40
1:A:671:G:H2'	1:A:672:U:O4'	2.22	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:682:G:O2'	1:A:683:G:H5'	2.21	0.40
1:A:960:U:O2	1:A:960:U:H5'	2.21	0.40
1:A:1014:A:H2	1:A:1219:U:H1'	1.87	0.40
4:B:76:GLN:NE2	4:B:207:ALA:N	2.70	0.40
5:C:58:GLU:HB2	5:C:65:ALA:HB2	2.03	0.40
5:C:79:ARG:HE	5:C:82:GLU:CD	2.30	0.40
5:C:133:ALA:O	5:C:134:ILE:C	2.63	0.40
5:C:200:ALA:C	5:C:201:TYR:CD1	2.99	0.40
6:D:33:MET:O	6:D:35:ARG:N	2.54	0.40
6:D:100:ARG:HB3	6:D:102:ASP:OD1	2.21	0.40
7:E:143:ARG:NH1	10:H:77:GLU:OE2	2.52	0.40
11:I:32:ASP:O	11:I:33:PHE:C	2.64	0.40
12:J:64:GLU:HG2	16:N:59:ALA:HA	2.02	0.40
14:L:71:PRO:HB2	14:L:120:TYR:CE2	2.55	0.40
15:M:19:LEU:O	15:M:22:ILE:CG1	2.69	0.40
20:R:48:GLY:O	20:R:49:LYS:C	2.64	0.40
21:S:4:SER:O	21:S:5:LEU:CG	2.69	0.40
1:A:46:G:O2'	1:A:365:U:H1'	2.21	0.40
1:A:190(L):U:H3	22:T:105:SER:CB	2.33	0.40
1:A:229:U:H2'	1:A:230:G:H8	1.87	0.40
1:A:664:G:OP1	20:R:64:ARG:HD2	2.21	0.40
1:A:925:G:C6	1:A:927:G:N7	2.89	0.40
1:A:953:G:O2'	15:M:125:ARG:HA	2.21	0.40
1:A:1184:G:OP1	1:A:1184:G:H3'	2.22	0.40
1:A:1192:C:H2'	1:A:1193:G:O4'	2.21	0.40
1:A:1345:U:C4	1:A:1377:A:N3	2.90	0.40
1:A:1348:U:H2'	1:A:1349:A:H8	1.86	0.40
1:A:1427:U:H2'	1:A:1428:A:C8	2.57	0.40
4:B:168:THR:O	4:B:171:ALA:HB2	2.22	0.40
4:B:223:ILE:O	4:B:226:ARG:HB2	2.22	0.40
6:D:135:LEU:O	6:D:136:PRO:C	2.64	0.40
6:D:204:ILE:HG22	6:D:208:SER:OG	2.22	0.40
7:E:32:VAL:O	7:E:43:LEU:HD23	2.21	0.40
8:F:37:VAL:O	8:F:39:LYS:N	2.54	0.40
11:I:76:ALA:O	11:I:79:LEU:N	2.54	0.40
13:K:86:GLY:N	13:K:112:THR:HG23	2.34	0.40
15:M:16:ASP:O	15:M:17:VAL:C	2.65	0.40
15:M:69:GLU:O	15:M:69:GLU:HG2	2.21	0.40
16:N:36:PHE:CD1	16:N:36:PHE:C	2.99	0.40
17:O:76:GLU:HA	17:O:79:ARG:NH2	2.31	0.40
20:R:73:ALA:HB3	20:R:79:LEU:HD12	2.04	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:10:LEU:CD1	22:T:12:ALA:H	2.35	0.40
22:T:36:LEU:HD12	22:T:62:LEU:CD1	2.51	0.40
1:A:718:G:C8	13:K:116:HIS:HB3	2.57	0.40
1:A:862:C:H2'	1:A:863:U:C6	2.57	0.40
1:A:1347:G:C6	11:I:107:ARG:NH2	2.75	0.40
4:B:45:GLN:HB3	4:B:49:GLU:OE2	2.21	0.40
4:B:55:PHE:HA	4:B:58:ILE:HG13	2.04	0.40
5:C:40:ARG:HB3	5:C:44:GLU:CG	2.51	0.40
6:D:112:VAL:HG22	6:D:161:ASN:HD21	1.86	0.40
7:E:12:LEU:N	7:E:12:LEU:CD1	2.85	0.40
7:E:90:VAL:O	7:E:91:LEU:HD23	2.22	0.40
7:E:144:THR:HG22	7:E:146:ALA:HB3	2.04	0.40
8:F:25:ILE:C	8:F:27:GLN:N	2.79	0.40
8:F:36:ARG:O	8:F:65:VAL:HA	2.22	0.40
11:I:8:GLY:HA2	11:I:79:LEU:HB3	2.04	0.40
11:I:79:LEU:O	11:I:80:GLY:C	2.65	0.40
22:T:47:GLY:C	22:T:49:ALA:H	2.29	0.40
23:V:5:ASP:OD1	23:V:5:ASP:C	2.64	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	
4	B	232/256 (91%)	129 (56%)	80 (34%)	23 (10%)	0	3
5	C	204/239 (85%)	123 (60%)	48 (24%)	33 (16%)	0	1
6	D	206/209 (99%)	151 (73%)	38 (18%)	17 (8%)	0	4
7	E	148/162 (91%)	120 (81%)	18 (12%)	10 (7%)	1	6
8	F	99/101 (98%)	68 (69%)	24 (24%)	7 (7%)	1	6
9	G	153/156 (98%)	99 (65%)	41 (27%)	13 (8%)	0	4

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	H	136/138 (99%)	106 (78%)	25 (18%)	5 (4%)	2	15
11	I	125/128 (98%)	85 (68%)	27 (22%)	13 (10%)	0	2
12	J	96/105 (91%)	57 (59%)	23 (24%)	16 (17%)	0	1
13	K	117/129 (91%)	85 (73%)	26 (22%)	6 (5%)	1	10
14	L	122/135 (90%)	85 (70%)	24 (20%)	13 (11%)	0	2
15	M	123/126 (98%)	75 (61%)	30 (24%)	18 (15%)	0	1
16	N	58/61 (95%)	34 (59%)	16 (28%)	8 (14%)	0	1
17	O	86/89 (97%)	54 (63%)	28 (33%)	4 (5%)	2	11
18	P	81/88 (92%)	59 (73%)	16 (20%)	6 (7%)	1	5
19	Q	102/105 (97%)	75 (74%)	17 (17%)	10 (10%)	0	3
20	R	71/88 (81%)	50 (70%)	16 (22%)	5 (7%)	1	6
21	S	78/93 (84%)	56 (72%)	14 (18%)	8 (10%)	0	2
22	T	97/106 (92%)	56 (58%)	30 (31%)	11 (11%)	0	2
23	V	22/27 (82%)	18 (82%)	2 (9%)	2 (9%)	0	3
All	All	2356/2541 (93%)	1585 (67%)	543 (23%)	228 (10%)	0	3

All (228) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	13	ALA
4	B	15	VAL
4	B	16	HIS
4	B	21	ARG
4	B	24	TRP
4	B	64	ARG
4	B	205	ASP
5	C	15	THR
5	C	16	ARG
5	C	52	LEU
5	C	53	ALA
5	C	61	ALA
5	C	100	ALA
5	C	179	ARG
5	C	189	ALA
6	D	9	CYS
6	D	32	ALA
6	D	36	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	D	88	VAL
7	E	78	HIS
8	F	35	ALA
8	F	64	GLN
9	G	116	ALA
9	G	155	ARG
10	H	83	ILE
10	H	91	ARG
11	I	41	VAL
11	I	46	ALA
11	I	121	ARG
12	J	34	VAL
12	J	60	ARG
12	J	86	MET
12	J	90	LEU
14	L	27	LEU
14	L	28	LYS
14	L	41	ARG
14	L	47	LYS
14	L	48	PRO
14	L	80	HIS
14	L	87	GLY
14	L	115	LYS
14	L	121	GLY
14	L	123	LYS
15	M	3	ARG
15	M	27	LYS
15	M	67	GLU
15	M	74	VAL
15	M	86	CYS
16	N	29	ARG
16	N	59	ALA
19	Q	81	ARG
19	Q	97	SER
19	Q	103	GLY
20	R	19	LYS
21	S	5	LEU
21	S	6	LYS
21	S	43	GLU
22	T	11	SER
22	T	49	ALA
22	T	73	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
22	T	94	ALA
22	T	98	PRO
22	T	99	LEU
4	B	23	ARG
4	B	62	ALA
4	B	76	GLN
4	B	119	GLU
5	C	18	TRP
5	C	26	LYS
5	C	60	ALA
5	C	91	LEU
5	C	96	GLY
5	C	102	ASN
5	C	150	LYS
5	C	187	ALA
5	C	188	LEU
6	D	10	ARG
6	D	23	GLY
6	D	25	ARG
6	D	89	THR
6	D	125	HIS
6	D	181	MET
7	E	153	LYS
9	G	68	ASN
9	G	153	HIS
11	I	43	ALA
11	I	56	LEU
11	I	94	ALA
12	J	4	ILE
12	J	26	ALA
12	J	27	ALA
12	J	72	VAL
12	J	85	LEU
13	K	75	TYR
13	K	88	GLY
13	K	126	ARG
15	M	63	THR
15	M	68	GLY
15	M	117	VAL
16	N	15	LYS
18	P	62	VAL
19	Q	49	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
19	Q	77	VAL
19	Q	80	GLY
19	Q	96	GLN
19	Q	99	SER
20	R	36	ASN
21	S	25	LYS
21	S	44	MET
22	T	101	GLY
23	V	7	ARG
23	V	9	ARG
4	B	20	GLU
5	C	4	LYS
5	C	81	GLY
5	C	195	VAL
6	D	5	ILE
6	D	175	SER
7	E	16	THR
7	E	22	GLY
7	E	107	ARG
7	E	108	ALA
7	E	140	ARG
8	F	97	PHE
9	G	7	ALA
9	G	66	VAL
9	G	78	ARG
9	G	146	GLU
10	H	122	ARG
11	I	105	ASP
12	J	17	ASP
12	J	57	LYS
12	J	73	ASP
13	K	12	ARG
14	L	91	LYS
15	M	14	ARG
15	M	38	GLY
16	N	36	PHE
16	N	60	SER
17	O	13	GLN
18	P	64	ALA
18	P	82	GLN
19	Q	66	SER
20	R	26	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
21	S	72	GLY
22	T	86	ARG
4	B	74	LYS
4	B	131	PRO
4	B	202	PRO
5	C	47	LEU
5	C	146	ALA
5	C	157	ILE
6	D	31	CYS
6	D	33	MET
8	F	38	GLU
8	F	70	ASP
9	G	37	ASN
9	G	109	ASN
9	G	134	ALA
10	H	46	LYS
11	I	45	ALA
11	I	47	LEU
11	I	107	ARG
11	I	127	LYS
12	J	20	ALA
12	J	40	LEU
15	M	34	LEU
15	M	100	GLY
15	M	125	ARG
16	N	6	LEU
17	O	46	HIS
19	Q	34	LYS
20	R	45	SER
21	S	42	PRO
22	T	9	ASN
4	B	88	ALA
4	B	95	GLN
4	B	113	HIS
4	B	130	ARG
4	B	177	ALA
4	B	229	VAL
5	C	49	SER
5	C	98	ASN
5	C	108	ASN
5	C	168	ALA
6	D	53	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	E	128	PRO
8	F	100	ASN
10	H	135	CYS
14	L	116	SER
15	M	4	ILE
15	M	28	ALA
15	M	73	GLU
15	M	107	ALA
16	N	19	ARG
17	O	85	LEU
18	P	34	GLU
20	R	52	PRO
21	S	24	ALA
22	T	50	GLU
22	T	62	LEU
5	C	82	GLU
5	C	178	LEU
5	C	205	GLY
6	D	35	ARG
6	D	171	GLY
7	E	129	ILE
8	F	39	LYS
9	G	17	VAL
9	G	130	GLY
11	I	93	ARG
13	K	92	GLU
15	M	85	GLY
4	B	165	VAL
4	B	174	VAL
12	J	76	ASN
18	P	10	GLY
12	J	39	PRO
5	C	14	ILE
11	I	98	PRO
13	K	47	VAL
17	O	27	VAL
18	P	51	VAL
5	C	74	GLY
5	C	84	ILE
7	E	70	PRO
14	L	29	GLY
16	N	14	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	
4	B	202/220 (92%)	183 (91%)	19 (9%)	8	29
5	C	160/188 (85%)	145 (91%)	15 (9%)	8	29
6	D	180/181 (99%)	161 (89%)	19 (11%)	6	24
7	E	115/123 (94%)	90 (78%)	25 (22%)	1	4
8	F	90/90 (100%)	82 (91%)	8 (9%)	9	30
9	G	126/127 (99%)	115 (91%)	11 (9%)	9	31
10	H	119/119 (100%)	104 (87%)	15 (13%)	4	19
11	I	98/99 (99%)	89 (91%)	9 (9%)	8	29
12	J	87/92 (95%)	84 (97%)	3 (3%)	32	57
13	K	90/99 (91%)	79 (88%)	11 (12%)	5	20
14	L	104/111 (94%)	99 (95%)	5 (5%)	23	50
15	M	100/101 (99%)	90 (90%)	10 (10%)	7	26
16	N	49/50 (98%)	46 (94%)	3 (6%)	17	44
17	O	79/80 (99%)	75 (95%)	4 (5%)	21	49
18	P	72/74 (97%)	66 (92%)	6 (8%)	10	34
19	Q	96/97 (99%)	88 (92%)	8 (8%)	10	34
20	R	64/77 (83%)	60 (94%)	4 (6%)	16	43
21	S	71/80 (89%)	66 (93%)	5 (7%)	14	40
22	T	75/82 (92%)	68 (91%)	7 (9%)	8	29
23	V	19/22 (86%)	19 (100%)	0	100	100
All	All	1996/2112 (94%)	1809 (91%)	187 (9%)	8	29

All (187) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	9	GLU
4	B	15	VAL
4	B	23	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	B	25	ASN
4	B	64	ARG
4	B	76	GLN
4	B	92	TYR
4	B	102	LEU
4	B	117	GLU
4	B	139	LYS
4	B	144	ARG
4	B	162	ILE
4	B	178	ARG
4	B	185	ILE
4	B	191	ASP
4	B	196	LEU
4	B	215	LEU
4	B	219	VAL
4	B	224	GLN
5	C	3	ASN
5	C	5	ILE
5	C	8	ILE
5	C	18	TRP
5	C	26	LYS
5	C	34	LEU
5	C	36	ASP
5	C	70	VAL
5	C	93	LYS
5	C	101	LEU
5	C	139	GLN
5	C	165	THR
5	C	167	TRP
5	C	196	LEU
5	C	204	LEU
6	D	9	CYS
6	D	10	ARG
6	D	15	GLU
6	D	17	VAL
6	D	24	GLU
6	D	25	ARG
6	D	36	ARG
6	D	38	TYR
6	D	42	GLN
6	D	57	ARG
6	D	65	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	D	92	VAL
6	D	105	VAL
6	D	106	TYR
6	D	112	VAL
6	D	118	ARG
6	D	122	ARG
6	D	156	GLU
6	D	157	LEU
7	E	12	LEU
7	E	13	ILE
7	E	15	ARG
7	E	16	THR
7	E	31	LEU
7	E	38	GLN
7	E	41	VAL
7	E	43	LEU
7	E	47	LYS
7	E	53	LEU
7	E	79	GLU
7	E	80	ILE
7	E	82	VAL
7	E	89	ILE
7	E	96	PRO
7	E	100	VAL
7	E	107	ARG
7	E	112	LEU
7	E	120	THR
7	E	131	ILE
7	E	135	THR
7	E	137	GLU
7	E	144	THR
7	E	147	ASP
7	E	150	ARG
8	F	10	LEU
8	F	24	GLU
8	F	28	ARG
8	F	30	LEU
8	F	63	TYR
8	F	75	LEU
8	F	92	LYS
8	F	98	LEU
9	G	16	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	G	38	LEU
9	G	45	ASP
9	G	49	ILE
9	G	69	VAL
9	G	72	ARG
9	G	113	GLU
9	G	124	LEU
9	G	126	ASP
9	G	148	ASN
9	G	156	TRP
10	H	21	LYS
10	H	26	VAL
10	H	38	ILE
10	H	50	ARG
10	H	51	VAL
10	H	63	LEU
10	H	81	HIS
10	H	88	LYS
10	H	91	ARG
10	H	92	ARG
10	H	100	ILE
10	H	105	ARG
10	H	119	LEU
10	H	127	LEU
10	H	134	ILE
11	I	5	TYR
11	I	16	ARG
11	I	38	GLN
11	I	78	LYS
11	I	79	LEU
11	I	104	ARG
11	I	114	TYR
11	I	118	LYS
11	I	127	LYS
12	J	73	ASP
12	J	75	ILE
12	J	98	ILE
13	K	13	GLN
13	K	27	ASN
13	K	29	ILE
13	K	30	VAL
13	K	32	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	K	41	THR
13	K	44	SER
13	K	57	THR
13	K	82	VAL
13	K	84	VAL
13	K	114	VAL
14	L	48	PRO
14	L	53	ARG
14	L	58	VAL
14	L	80	HIS
14	L	119	LYS
15	M	16	ASP
15	M	19	LEU
15	M	56	LEU
15	M	70	LEU
15	M	81	LEU
15	M	88	ARG
15	M	98	VAL
15	M	106	ASN
15	M	110	ARG
15	M	115	LYS
16	N	7	ILE
16	N	9	LYS
16	N	44	LEU
17	O	6	GLU
17	O	10	LYS
17	O	34	LEU
17	O	56	LEU
18	P	2	VAL
18	P	53	VAL
18	P	62	VAL
18	P	68	ASP
18	P	74	LEU
18	P	82	GLN
19	Q	5	VAL
19	Q	34	LYS
19	Q	60	ILE
19	Q	63	ARG
19	Q	74	LEU
19	Q	78	GLU
19	Q	85	VAL
19	Q	98	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	R	28	GLU
20	R	31	LEU
20	R	36	ASN
20	R	54	ARG
21	S	6	LYS
21	S	12	ASP
21	S	27	GLU
21	S	41	VAL
21	S	42	PRO
22	T	10	LEU
22	T	13	LEU
22	T	42	GLN
22	T	62	LEU
22	T	73	HIS
22	T	74	LYS
22	T	75	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (71) such sidechains are listed below:

Mol	Chain	Res	Type
4	B	19	HIS
4	B	25	ASN
4	B	40	HIS
4	B	110	GLN
4	B	212	GLN
4	B	240	GLN
5	C	6	HIS
5	C	31	HIS
5	C	63	ASN
5	C	69	HIS
5	C	108	ASN
5	C	110	ASN
5	C	118	GLN
5	C	123	GLN
5	C	139	GLN
5	C	181	ASN
6	D	42	GLN
6	D	45	GLN
6	D	62	GLN
6	D	119	GLN
6	D	123	HIS
6	D	161	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	D	199	ASN
6	D	201	GLN
7	E	65	ASN
7	E	73	ASN
7	E	78	HIS
8	F	18	GLN
8	F	27	GLN
8	F	32	ASN
8	F	57	GLN
8	F	64	GLN
8	F	84	ASN
8	F	100	ASN
9	G	37	ASN
9	G	86	GLN
9	G	96	GLN
9	G	97	GLN
9	G	106	GLN
9	G	148	ASN
11	I	23	ASN
11	I	73	GLN
11	I	117	HIS
12	J	56	HIS
12	J	78	ASN
12	J	84	GLN
13	K	22	HIS
13	K	62	GLN
13	K	104	GLN
13	K	116	HIS
13	K	117	ASN
14	L	49	ASN
14	L	75	HIS
15	M	12	ASN
15	M	40	ASN
15	M	62	ASN
15	M	77	ASN
15	M	101	GLN
17	O	13	GLN
17	O	37	ASN
17	O	53	HIS
17	O	71	GLN
18	P	14	ASN
18	P	82	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	R	36	ASN
21	S	23	ASN
21	S	47	HIS
21	S	56	GLN
21	S	65	ASN
21	S	69	HIS
22	T	45	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1522 (98%)	241 (16%)	62 (4%)
2	W	2/3 (66%)	1 (50%)	0
3	X	10/11 (90%)	0	0
All	All	1518/1536 (98%)	242 (15%)	62 (4%)

All (242) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	60	A
1	A	61	G
1	A	101	A
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	163	C
1	A	182	U
1	A	189	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	190	C
1	A	190(A)	C
1	A	190(B)	C
1	A	190(C)	C
1	A	190(D)	U
1	A	190(E)	U
1	A	190(L)	U
1	A	195	A
1	A	197	A
1	A	201	C
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	217	C
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	289	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	345	C
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	397	A
1	A	398	C
1	A	406	G
1	A	407	G
1	A	408	A
1	A	409	G
1	A	410	G
1	A	412	A
1	A	413	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	414	A
1	A	416	G
1	A	417	C
1	A	418	C
1	A	421	U
1	A	422	C
1	A	425	G
1	A	429	U
1	A	430	A
1	A	432	A
1	A	433	C
1	A	434	U
1	A	435	C
1	A	439	A
1	A	452	A
1	A	460	A
1	A	461	C
1	A	462	G
1	A	463	A
1	A	474	G
1	A	475	G
1	A	476	G
1	A	477	G
1	A	479	C
1	A	480	U
1	A	484	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	508	C
1	A	510	A
1	A	511	C
1	A	518	C
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	562	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	607	A
1	A	653	A
1	A	665	A
1	A	687	A
1	A	688	G
1	A	702	A
1	A	703	G
1	A	718	G
1	A	723	U
1	A	731	G
1	A	748	C
1	A	749	C
1	A	755	G
1	A	777	A
1	A	781	A
1	A	782	A
1	A	792	A
1	A	793	U
1	A	812	C
1	A	813	U
1	A	815	A
1	A	817	C
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	859	A
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	961	U
1	A	965	A
1	A	966	G
1	A	968	A
1	A	969	A
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1005	A
1	A	1024	G
1	A	1026	G
1	A	1031	G
1	A	1050	G
1	A	1054	C
1	A	1055	A
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1129	C
1	A	1130	A
1	A	1132	C
1	A	1136	U
1	A	1138	G
1	A	1139	G
1	A	1145	C
1	A	1152	A
1	A	1159	U
1	A	1183	A
1	A	1184	G
1	A	1191	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1196	U
1	A	1197	G
1	A	1201	A
1	A	1202	G
1	A	1212	U
1	A	1214	C
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1256	A
1	A	1257	U
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1286	A
1	A	1287	A
1	A	1290	G
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1320	C
1	A	1338	G
1	A	1346	A
1	A	1347	G
1	A	1348	U
1	A	1361	G
1	A	1362	C
1	A	1363	A
1	A	1370	G
1	A	1381	U
1	A	1398	A
1	A	1442	G
1	A	1443	G
1	A	1446	A
1	A	1452	C
1	A	1490	C
1	A	1492	A
1	A	1498	U
1	A	1499	A
1	A	1502	A
1	A	1504	G
1	A	1505	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1506	U
1	A	1517	G
1	A	1519	A
1	A	1520	G
1	A	1529	G
1	A	1530	G
1	A	1533	C
1	A	1534	A
1	A	1539	C
2	W	2	A

All (62) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	30	U
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	328	C
1	A	344	A
1	A	353	A
1	A	366	C
1	A	372	C
1	A	407	G
1	A	428	G
1	A	429	U
1	A	484	G
1	A	496	A
1	A	509	A
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	701	C
1	A	748	C
1	A	792	A
1	A	812	C
1	A	840	C
1	A	960	U
1	A	965	A
1	A	975	A
1	A	992	U
1	A	993	G
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1101	A
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1196	U
1	A	1201	A
1	A	1224	G
1	A	1226	C
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1346	A
1	A	1347	G
1	A	1380	U
1	A	1397	C
1	A	1451	A
1	A	1498	U
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1528	U

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

2 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	$\# Z > 2$
3	T6A	X	37	3	31,34,35	1.34	6 (19%)	43,49,52	3.15	10 (23%)
3	MNU	X	34	3,2	21,24,25	0.55	0	27,34,37	0.46	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	T6A	X	37	3	1/1/9/11	4/23/41/42	0/3/3/3
3	MNU	X	34	3,2	-	3/10/28/29	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	X	37	T6A	O14-C14	-3.12	1.34	1.43
3	X	37	T6A	ODA-C13	3.07	1.31	1.22
3	X	37	T6A	C15-C14	-2.87	1.43	1.51
3	X	37	T6A	ODB-C13	-2.79	1.21	1.30
3	X	37	T6A	C12-N11	-2.45	1.40	1.45
3	X	37	T6A	C6-N6	-2.24	1.34	1.39

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	X	37	T6A	O14-C14-C15	11.89	145.26	109.68
3	X	37	T6A	ODA-C13-C12	-6.90	98.94	121.86
3	X	37	T6A	O14-C14-C12	-6.88	95.20	109.07
3	X	37	T6A	N6-C10-N11	6.55	122.78	113.77
3	X	37	T6A	C12-N11-C10	6.42	132.66	121.99
3	X	37	T6A	ODB-C13-C12	5.74	134.06	114.15
3	X	37	T6A	C13-C12-N11	5.29	121.79	110.17
3	X	37	T6A	O10-C10-N6	-4.17	116.23	123.64
3	X	37	T6A	C15-C14-C12	3.66	119.52	112.29
3	X	37	T6A	C5-C6-N6	2.03	124.12	118.94

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	X	37	T6A	C14

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	X	34	MNU	C4-C5-C7-N8
3	X	37	T6A	C13-C12-C14-O14
3	X	37	T6A	N11-C12-C14-O14
3	X	37	T6A	C3'-C4'-C5'-O5'
3	X	34	MNU	C6-C5-C7-N8
3	X	37	T6A	O4'-C4'-C5'-O5'
3	X	34	MNU	C2'-C1'-N1-C2

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	X	37	T6A	2	0
3	X	34	MNU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 110 ligands modelled in this entry, 109 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
24	PAR	A	1545	-	44,45,45	1.63	10 (22%)	63,67,67	1.11	4 (6%)

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
24	PAR	A	1545	-	-	4/18/94/94	0/4/4/4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1545	PAR	O54-C14	4.02	1.52	1.41
24	A	1545	PAR	C31-C21	3.66	1.58	1.53
24	A	1545	PAR	O51-C11	2.94	1.49	1.41
24	A	1545	PAR	O33-C14	2.85	1.49	1.41
24	A	1545	PAR	O33-C33	2.82	1.51	1.43
24	A	1545	PAR	C44-C34	2.68	1.59	1.52
24	A	1545	PAR	O51-C51	2.43	1.50	1.44
24	A	1545	PAR	O54-C54	2.31	1.50	1.44
24	A	1545	PAR	C34-C24	2.30	1.56	1.53
24	A	1545	PAR	C11-C21	2.09	1.56	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1545	PAR	O52-C13-O43	-3.40	107.89	111.37
24	A	1545	PAR	O54-C54-C64	3.34	112.49	106.07
24	A	1545	PAR	O33-C14-C24	3.21	113.33	108.08
24	A	1545	PAR	C14-O54-C54	3.13	119.83	113.72

There are no chirality outliers.

All (4) torsion outliers are listed below:

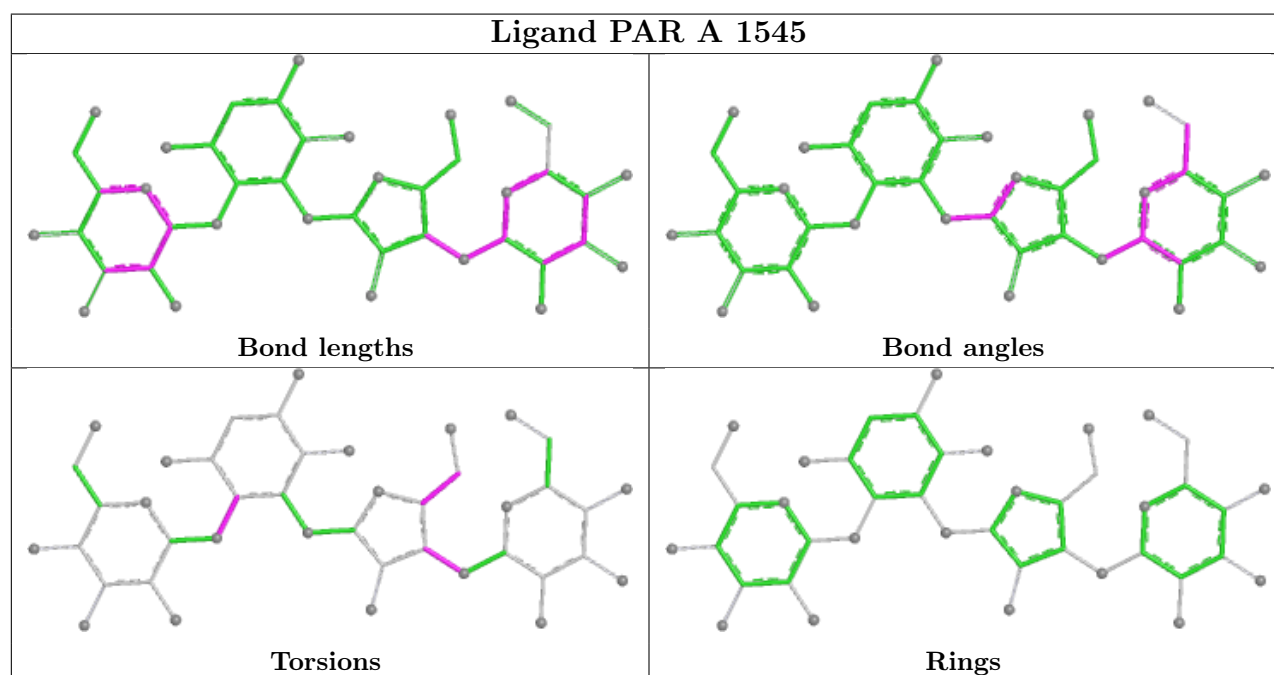
Mol	Chain	Res	Type	Atoms
24	A	1545	PAR	O43-C43-C53-O53
24	A	1545	PAR	C52-C42-O11-C11
24	A	1545	PAR	C23-C33-O33-C14
24	A	1545	PAR	C33-C43-C53-O53

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	1545	PAR	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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, 95th 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 ²)	Q<0.9
1	A	1507/1522 (99%)	0.77	188 (12%) 8 7	30, 65, 160, 200	0
2	W	3/3 (100%)	0.37	0 100 100	56, 56, 63, 72	0
3	X	9/11 (81%)	1.94	5 (55%) 0 0	64, 101, 157, 157	0
4	B	234/256 (91%)	0.90	36 (15%) 5 5	37, 100, 173, 200	0
5	C	206/239 (86%)	0.94	34 (16%) 4 4	44, 93, 169, 200	0
6	D	208/209 (99%)	0.62	21 (10%) 12 10	33, 71, 149, 200	0
7	E	150/162 (92%)	0.36	7 (4%) 36 24	27, 63, 122, 200	0
8	F	101/101 (100%)	0.92	16 (15%) 5 4	48, 103, 154, 174	0
9	G	155/156 (99%)	0.63	14 (9%) 15 12	41, 81, 152, 200	0
10	H	138/138 (100%)	0.28	4 (2%) 53 36	20, 54, 113, 174	0
11	I	127/128 (99%)	0.91	16 (12%) 8 7	35, 90, 149, 178	0
12	J	98/105 (93%)	1.67	35 (35%) 1 1	44, 117, 186, 200	0
13	K	119/129 (92%)	0.36	8 (6%) 24 16	30, 67, 138, 187	0
14	L	124/135 (91%)	0.57	13 (10%) 11 9	31, 64, 139, 175	0
15	M	125/126 (99%)	1.00	17 (13%) 7 6	44, 85, 169, 200	0
16	N	60/61 (98%)	0.88	5 (8%) 17 13	42, 82, 139, 179	0
17	O	88/89 (98%)	0.55	8 (9%) 15 11	23, 76, 142, 192	0
18	P	83/88 (94%)	0.26	3 (3%) 46 31	27, 52, 96, 173	0
19	Q	104/105 (99%)	0.55	9 (8%) 16 12	22, 61, 146, 200	0
20	R	73/88 (82%)	0.49	4 (5%) 30 21	40, 79, 175, 188	0
21	S	80/93 (86%)	1.19	15 (18%) 3 3	62, 111, 162, 193	0
22	T	99/106 (93%)	0.54	9 (9%) 15 11	32, 58, 136, 168	0
23	V	24/27 (88%)	1.23	6 (25%) 2 1	41, 69, 118, 136	0
All	All	3915/4077 (96%)	0.74	473 (12%) 8 7	20, 73, 159, 200	0

All (473) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	217	C	8.6
19	Q	102	GLY	8.3
1	A	409	G	8.3
1	A	216	G	8.1
1	A	202	U	8.0
1	A	407	G	8.0
1	A	1126	U	7.5
1	A	410	G	7.2
15	M	7	VAL	6.9
18	P	83	GLU	6.8
9	G	16	LEU	6.4
6	D	23	GLY	6.4
15	M	120	LYS	6.4
1	A	425	G	6.3
1	A	424	G	6.2
1	A	479	C	6.1
1	A	1034	G	6.0
1	A	1540	U	5.8
1	A	631	G	5.8
8	F	41	GLU	5.8
1	A	463	A	5.8
1	A	201	C	5.7
1	A	1129	C	5.6
9	G	33	ASP	5.5
1	A	1541	U	5.4
1	A	1127	G	5.4
19	Q	103	GLY	5.3
11	I	23	ASN	5.2
6	D	31	CYS	5.2
15	M	122	LYS	5.2
1	A	417	C	5.2
12	J	4	ILE	5.2
1	A	1533	C	5.1
6	D	25	ARG	5.1
1	A	421	U	5.1
12	J	100	THR	5.0
5	C	100	ALA	5.0
1	A	408	A	5.0
1	A	416	G	5.0
1	A	204	U	5.0
1	A	1026	G	4.9
18	P	82	GLN	4.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	190	C	4.8
19	Q	105	ALA	4.8
1	A	1031	G	4.8
6	D	9	CYS	4.7
1	A	1362	C	4.7
1	A	418	C	4.7
1	A	1003	G	4.6
1	A	1361	G	4.6
1	A	1421	G	4.6
1	A	1281	U	4.4
22	T	106	ALA	4.3
1	A	1011	G	4.3
1	A	1035	A	4.3
1	A	432	A	4.3
13	K	36	ASP	4.2
4	B	125	PRO	4.2
15	M	123	ALA	4.2
1	A	996	A	4.2
1	A	462	G	4.2
5	C	110	ASN	4.2
23	V	23	PRO	4.2
12	J	73	ASP	4.1
1	A	1124	G	4.1
12	J	37	PRO	4.1
9	G	82	GLY	4.1
12	J	31	GLY	4.1
1	A	476	G	4.1
3	X	30	G	4.1
1	A	411	A	4.0
1	A	414	A	4.0
1	A	1131	G	4.0
12	J	89	ASP	4.0
6	D	26	CYS	4.0
7	E	154	GLY	4.0
12	J	10	GLY	4.0
1	A	1446	A	4.0
1	A	1258	G	4.0
17	O	22	THR	3.9
1	A	423	G	3.9
1	A	1033	G	3.9
4	B	148	TYR	3.9
6	D	24	GLU	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
6	D	163	GLU	3.9
12	J	88	LEU	3.9
12	J	78	ASN	3.8
6	D	3	ARG	3.8
1	A	1144	G	3.8
1	A	431	A	3.8
1	A	434	U	3.8
17	O	6	GLU	3.8
1	A	1256	A	3.8
15	M	118	ALA	3.7
1	A	1134	G	3.7
15	M	124	PRO	3.7
4	B	15	VAL	3.7
5	C	64	VAL	3.7
1	A	848	C	3.7
21	S	10	PHE	3.7
1	A	1539	C	3.7
1	A	1021	G	3.7
1	A	1138	G	3.7
12	J	90	LEU	3.7
6	D	20	TYR	3.6
21	S	63	THR	3.6
5	C	167	TRP	3.6
5	C	3	ASN	3.6
1	A	1027	C	3.6
4	B	238	LEU	3.6
1	A	1020	U	3.6
21	S	8	GLY	3.6
22	T	101	GLY	3.5
1	A	1004	A	3.5
8	F	95	GLU	3.5
4	B	96	ARG	3.5
1	A	1006	C	3.5
1	A	1054	C	3.5
14	L	91	LYS	3.5
5	C	129	ALA	3.5
20	R	46	GLU	3.5
21	S	30	LEU	3.5
1	A	1174	G	3.5
6	D	159	ARG	3.5
1	A	1542	U	3.5
11	I	2	GLU	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
21	S	24	ALA	3.4
5	C	4	LYS	3.4
15	M	126	LYS	3.4
1	A	203	U	3.4
1	A	413	G	3.4
4	B	237	ALA	3.4
1	A	1005	A	3.4
1	A	1142	G	3.4
1	A	412	A	3.4
1	A	1030	C	3.4
12	J	12	ASP	3.4
1	A	630	G	3.4
1	A	1130	A	3.3
1	A	1024	G	3.3
4	B	12	GLU	3.3
1	A	1257	U	3.3
19	Q	2	PRO	3.3
9	G	7	ALA	3.3
1	A	980	C	3.3
1	A	1029	C	3.3
6	D	156	GLU	3.3
14	L	64	TYR	3.2
12	J	87	THR	3.2
1	A	1010	G	3.2
1	A	1025	U	3.2
14	L	63	GLY	3.2
21	S	54	GLY	3.2
4	B	140	HIS	3.2
1	A	460	A	3.2
1	A	1133	G	3.2
4	B	122	PHE	3.2
1	A	992	U	3.2
12	J	84	GLN	3.2
4	B	220	ASP	3.2
14	L	128	ALA	3.2
1	A	849	C	3.2
1	A	1277	C	3.2
1	A	1316	G	3.1
4	B	113	HIS	3.1
1	A	1019	C	3.1
5	C	58	GLU	3.1
4	B	135	GLN	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	1032	G	3.1
1	A	1050	G	3.1
12	J	5	ARG	3.1
12	J	83	GLU	3.1
12	J	8	LEU	3.0
8	F	47	ARG	3.0
12	J	43	ARG	3.0
1	A	789	U	3.0
5	C	82	GLU	3.0
12	J	95	GLU	3.0
8	F	56	PRO	3.0
15	M	6	GLY	3.0
19	Q	104	LYS	3.0
13	K	79	SER	3.0
11	I	87	GLN	3.0
1	A	532	A	3.0
7	E	120	THR	3.0
9	G	83	ALA	3.0
22	T	95	ALA	3.0
1	A	1125	U	3.0
1	A	1534	A	3.0
21	S	37	ARG	3.0
12	J	79	ARG	2.9
1	A	1259	C	2.9
22	T	100	ILE	2.9
1	A	306	G	2.9
1	A	477	G	2.9
1	A	1266	G	2.9
20	R	83	GLU	2.9
14	L	78	GLN	2.9
21	S	23	ASN	2.9
1	A	433	C	2.9
4	B	133	LYS	2.9
15	M	47	ASP	2.9
12	J	20	ALA	2.9
1	A	632	A	2.9
1	A	1036	G	2.9
6	D	33	MET	2.9
11	I	97	LYS	2.9
12	J	75	ILE	2.9
1	A	1136	U	2.8
1	A	1145	C	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
23	V	5	ASP	2.8
9	G	21	VAL	2.8
5	C	80	GLY	2.8
15	M	119	GLY	2.8
6	D	208	SER	2.8
1	A	167	G	2.8
1	A	475	G	2.8
1	A	1009	G	2.8
15	M	8	GLU	2.8
12	J	77	PRO	2.8
9	G	139	GLU	2.8
5	C	78	GLY	2.8
12	J	7	LYS	2.8
5	C	128	PHE	2.8
23	V	19	GLY	2.8
1	A	1013	G	2.8
1	A	1132	C	2.7
5	C	89	GLU	2.7
21	S	17	GLU	2.7
1	A	1422	G	2.7
11	I	32	ASP	2.7
11	I	20	ARG	2.7
6	D	22	LYS	2.7
13	K	25	TYR	2.7
4	B	141	GLU	2.7
11	I	27	THR	2.7
17	O	20	GLY	2.7
10	H	69	ARG	2.7
19	Q	101	ARG	2.7
6	D	151	LYS	2.7
1	A	1038	C	2.7
19	Q	96	GLN	2.7
20	R	16	PRO	2.7
6	D	168	ARG	2.7
8	F	82	ARG	2.7
1	A	1283	G	2.7
16	N	34	TYR	2.7
13	K	81	ASP	2.7
1	A	478	A	2.6
1	A	271	C	2.6
21	S	15	LEU	2.6
1	A	1370	G	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
4	B	191	ASP	2.6
12	J	86	MET	2.6
1	A	1212	U	2.6
1	A	975	A	2.6
5	C	207	VAL	2.6
3	X	40	C	2.6
14	L	116	SER	2.6
6	D	115	ARG	2.6
15	M	102	ARG	2.6
5	C	51	GLY	2.6
1	A	1135	U	2.6
7	E	149	GLU	2.6
11	I	128	ARG	2.6
14	L	47	LYS	2.6
1	A	422	C	2.6
1	A	1284	C	2.6
7	E	17	ALA	2.6
1	A	1443	G	2.6
11	I	88	TYR	2.6
8	F	17	SER	2.6
1	A	1286	A	2.6
9	G	140	ASP	2.6
1	A	1007	C	2.6
1	A	1420	C	2.6
11	I	119	ALA	2.6
1	A	1040	U	2.5
1	A	1219	U	2.5
10	H	98	LYS	2.5
1	A	1176	A	2.5
4	B	48	MET	2.5
1	A	345	C	2.5
1	A	1008	C	2.5
4	B	232	PRO	2.5
9	G	80	VAL	2.5
5	C	56	ASP	2.5
22	T	12	ALA	2.5
1	A	1044	A	2.5
1	A	1213	A	2.5
1	A	993	G	2.5
1	A	1022	G	2.5
4	B	16	HIS	2.5
1	A	1018	C	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
5	C	13	GLY	2.5
21	S	26	GLY	2.5
5	C	170	GLN	2.5
1	A	1049	U	2.5
3	X	39	U	2.5
11	I	54	ASP	2.5
5	C	67	THR	2.5
12	J	29	ARG	2.5
17	O	9	GLN	2.5
1	A	1166	G	2.5
5	C	143	GLU	2.5
4	B	79	ASP	2.5
19	Q	93	GLN	2.5
13	K	128	ALA	2.4
8	F	31	GLU	2.4
5	C	140	ARG	2.4
1	A	1023	G	2.4
1	A	1137	C	2.4
4	B	131	PRO	2.4
12	J	41	PRO	2.4
1	A	723	U	2.4
17	O	89	GLY	2.4
8	F	57	GLN	2.4
14	L	73	GLU	2.4
9	G	5	ARG	2.4
1	A	1479	C	2.4
5	C	77	ILE	2.4
12	J	58	ASP	2.4
5	C	81	GLY	2.4
9	G	89	MET	2.4
13	K	99	GLN	2.4
1	A	459	G	2.4
12	J	24	VAL	2.4
14	L	89	ARG	2.4
15	M	80	ARG	2.4
17	O	79	ARG	2.4
22	T	105	SER	2.4
7	E	16	THR	2.3
7	E	27	ARG	2.3
1	A	1053	G	2.3
1	A	1300	G	2.3
4	B	126	GLU	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
8	F	66	GLU	2.3
9	G	146	GLU	2.3
11	I	90	PRO	2.3
1	A	88	A	2.3
15	M	125	ARG	2.3
1	A	5	U	2.3
1	A	1260	C	2.3
1	A	1262	C	2.3
1	A	158	G	2.3
1	A	1175	G	2.3
1	A	1274	G	2.3
1	A	1482	G	2.3
6	D	2	GLY	2.3
5	C	32	LEU	2.3
1	A	349	A	2.3
4	B	110	GLN	2.3
5	C	161	GLU	2.3
1	A	435	C	2.3
1	A	1264	C	2.3
17	O	2	PRO	2.3
15	M	24	GLY	2.3
5	C	60	ALA	2.3
8	F	20	ALA	2.3
4	B	19	HIS	2.3
16	N	60	SER	2.3
11	I	56	LEU	2.3
1	A	1143	G	2.3
1	A	1419	G	2.3
1	A	1269	A	2.3
4	B	144	ARG	2.3
1	A	989	C	2.3
5	C	87	LEU	2.3
14	L	61	THR	2.3
5	C	37	GLN	2.3
10	H	52	ASP	2.3
15	M	35	GLU	2.2
22	T	50	GLU	2.2
1	A	1139	G	2.2
1	A	1423	G	2.2
1	A	420	U	2.2
1	A	1485	U	2.2
4	B	206	ASP	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
6	D	34	GLU	2.2
11	I	19	LEU	2.2
17	O	23	GLY	2.2
1	A	1017	G	2.2
1	A	1447	G	2.2
1	A	1475	G	2.2
12	J	99	LYS	2.2
1	A	997	U	2.2
1	A	1204	A	2.2
1	A	1285	A	2.2
13	K	53	SER	2.2
1	A	1043	C	2.2
1	A	1200	C	2.2
4	B	91	PRO	2.2
14	L	60	LEU	2.2
12	J	15	THR	2.2
9	G	85	TYR	2.2
4	B	136	VAL	2.2
4	B	95	GLN	2.2
1	A	157	G	2.2
1	A	998	G	2.2
1	A	1041	A	2.2
7	E	111	GLU	2.2
19	Q	58	GLU	2.2
11	I	91	ASP	2.2
5	C	88	ARG	2.2
1	A	165	C	2.2
1	A	1429	C	2.2
6	D	21	LEU	2.2
4	B	9	GLU	2.2
10	H	22	GLU	2.2
12	J	64	GLU	2.2
18	P	54	GLU	2.2
23	V	25	LYS	2.2
8	F	28	ARG	2.2
4	B	205	ASP	2.2
1	A	59	A	2.2
5	C	48	TYR	2.1
1	A	1039	C	2.1
8	F	73	ASN	2.1
11	I	21	PRO	2.1
15	M	88	ARG	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
4	B	166	ASP	2.1
21	S	33	THR	2.1
1	A	161	A	2.1
1	A	1279	A	2.1
6	D	19	LEU	2.1
1	A	159	G	2.1
1	A	1002	G	2.1
1	A	1184	G	2.1
1	A	1294	G	2.1
8	F	36	ARG	2.1
21	S	3	ARG	2.1
1	A	979	C	2.1
1	A	1037	C	2.1
12	J	68	HIS	2.1
12	J	22	LYS	2.1
16	N	13	THR	2.1
4	B	231	GLU	2.1
12	J	54	PHE	2.1
1	A	1272	G	2.1
1	A	1530	G	2.1
1	A	461	C	2.1
12	J	98	ILE	2.1
20	R	25	THR	2.1
4	B	143	GLU	2.1
4	B	192	SER	2.1
21	S	9	VAL	2.1
1	A	1123	A	2.1
5	C	52	LEU	2.1
13	K	96	ARG	2.1
21	S	62	ILE	2.1
22	T	99	LEU	2.1
8	F	55	ASP	2.1
9	G	125	MET	2.1
1	A	1304	G	2.1
1	A	480	U	2.0
1	A	991	U	2.0
14	L	21	LYS	2.0
4	B	233	SER	2.0
5	C	21	ARG	2.0
8	F	45	LEU	2.0
22	T	86	ARG	2.0
3	X	38	A	2.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
8	F	83	ASP	2.0
5	C	2	GLY	2.0
3	X	32	C	2.0
14	L	57	LYS	2.0
23	V	10	ARG	2.0
4	B	94	ASN	2.0
5	C	28	GLN	2.0
16	N	8	GLU	2.0
23	V	24	ARG	2.0
16	N	6	LEU	2.0
1	A	995	C	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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å ²)	Q<0.9
3	T6A	X	37	32/33	0.88	0.18	76,80,80,80	0
3	MNU	X	34	23/24	0.89	0.18	56,96,115,115	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å ²)	Q<0.9
25	MG	A	1619	1/1	0.45	0.40	23,23,23,23	1
25	MG	A	1631	1/1	0.66	0.21	23,23,23,23	1
25	MG	A	1550	1/1	0.72	0.27	23,23,23,23	1
25	MG	A	1615	1/1	0.74	0.41	23,23,23,23	1
25	MG	A	214	1/1	0.75	0.44	23,23,23,23	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	210	1/1	0.75	0.21	23,23,23,23	1
25	MG	A	1562	1/1	0.79	0.48	23,23,23,23	1
25	MG	A	1621	1/1	0.81	0.20	23,23,23,23	1
25	MG	A	1548	1/1	0.82	0.37	23,23,23,23	1
25	MG	A	1575	1/1	0.82	0.53	23,23,23,23	1
25	MG	A	1628	1/1	0.83	0.25	23,23,23,23	1
25	MG	A	1591	1/1	0.83	0.39	23,23,23,23	1
25	MG	A	1607	1/1	0.84	0.56	23,23,23,23	1
25	MG	A	1582	1/1	0.86	0.19	23,23,23,23	0
25	MG	A	1570	1/1	0.87	0.24	23,23,23,23	0
25	MG	A	1623	1/1	0.87	0.40	23,23,23,23	1
25	MG	A	1588	1/1	0.88	0.35	23,23,23,23	0
25	MG	A	1584	1/1	0.88	0.24	23,23,23,23	0
25	MG	A	1625	1/1	0.88	0.30	23,23,23,23	1
25	MG	A	1616	1/1	0.88	0.15	23,23,23,23	1
25	MG	A	1599	1/1	0.88	0.22	23,23,23,23	1
25	MG	A	1635	1/1	0.88	0.41	23,23,23,23	1
25	MG	A	1614	1/1	0.89	0.26	23,23,23,23	1
25	MG	A	441	1/1	0.89	0.20	23,23,23,23	1
25	MG	A	471	1/1	0.89	0.26	23,23,23,23	1
25	MG	A	1605	1/1	0.89	0.26	23,23,23,23	1
25	MG	A	493	1/1	0.89	0.55	23,23,23,23	1
25	MG	A	86	1/1	0.89	0.14	23,23,23,23	1
25	MG	A	1571	1/1	0.90	0.16	23,23,23,23	0
25	MG	A	1630	1/1	0.90	0.17	23,23,23,23	1
25	MG	A	469	1/1	0.90	0.20	23,23,23,23	1
25	MG	A	1564	1/1	0.90	0.18	23,23,23,23	0
25	MG	A	473	1/1	0.90	0.58	23,23,23,23	1
25	MG	A	1561	1/1	0.90	0.13	23,23,23,23	1
25	MG	A	1551	1/1	0.90	0.30	23,23,23,23	0
25	MG	A	1586	1/1	0.90	0.21	23,23,23,23	1
25	MG	A	1566	1/1	0.91	0.37	23,23,23,23	1
25	MG	A	1622	1/1	0.91	0.56	23,23,23,23	1
24	PAR	A	1545	42/42	0.91	0.12	25,25,25,25	0
25	MG	A	1600	1/1	0.91	0.23	23,23,23,23	1
25	MG	A	1568	1/1	0.91	0.13	23,23,23,23	0
25	MG	A	1565	1/1	0.91	0.13	23,23,23,23	0
25	MG	A	1603	1/1	0.92	0.28	23,23,23,23	1
25	MG	A	1574	1/1	0.92	0.19	23,23,23,23	0
25	MG	A	1595	1/1	0.92	0.39	23,23,23,23	1
25	MG	A	1560	1/1	0.92	0.25	23,23,23,23	0
25	MG	A	1579	1/1	0.92	0.18	23,23,23,23	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	466	1/1	0.93	0.28	23,23,23,23	1
25	MG	A	467	1/1	0.93	0.13	23,23,23,23	1
25	MG	A	1610	1/1	0.93	0.34	23,23,23,23	1
25	MG	A	1576	1/1	0.93	0.18	23,23,23,23	0
25	MG	A	1577	1/1	0.93	0.10	23,23,23,23	0
25	MG	A	1547	1/1	0.93	0.18	23,23,23,23	0
25	MG	A	1632	1/1	0.93	0.15	23,23,23,23	1
25	MG	A	1606	1/1	0.93	0.07	23,23,23,23	1
25	MG	A	1559	1/1	0.93	0.22	23,23,23,23	0
25	MG	A	211	1/1	0.94	0.32	23,23,23,23	0
25	MG	A	1620	1/1	0.94	0.21	23,23,23,23	1
25	MG	A	1546	1/1	0.94	0.21	23,23,23,23	0
25	MG	A	1590	1/1	0.94	0.20	23,23,23,23	0
25	MG	A	1596	1/1	0.94	0.56	23,23,23,23	1
25	MG	A	1569	1/1	0.94	0.24	23,23,23,23	1
25	MG	A	1624	1/1	0.94	0.23	23,23,23,23	1
25	MG	A	1592	1/1	0.94	0.09	23,23,23,23	0
25	MG	A	1626	1/1	0.94	0.17	23,23,23,23	1
25	MG	A	1554	1/1	0.94	0.49	23,23,23,23	1
25	MG	X	502	1/1	0.94	0.46	23,23,23,23	1
25	MG	A	1617	1/1	0.95	0.21	23,23,23,23	1
25	MG	A	1618	1/1	0.95	0.10	23,23,23,23	0
25	MG	A	1558	1/1	0.95	0.07	23,23,23,23	0
25	MG	A	1602	1/1	0.95	0.20	23,23,23,23	0
25	MG	A	1627	1/1	0.95	0.19	23,23,23,23	1
25	MG	A	1587	1/1	0.95	0.19	23,23,23,23	0
25	MG	A	1634	1/1	0.95	0.38	23,23,23,23	1
25	MG	A	1629	1/1	0.95	0.18	23,23,23,23	0
25	MG	A	87	1/1	0.95	0.33	23,23,23,23	1
25	MG	A	1578	1/1	0.95	0.10	23,23,23,23	0
25	MG	J	449	1/1	0.95	0.11	23,23,23,23	1
25	MG	A	1563	1/1	0.96	0.22	23,23,23,23	1
25	MG	A	71	1/1	0.96	0.24	23,23,23,23	1
25	MG	A	1581	1/1	0.96	0.40	23,23,23,23	1
25	MG	A	1608	1/1	0.96	0.29	23,23,23,23	1
25	MG	A	1557	1/1	0.96	0.13	23,23,23,23	0
25	MG	A	1611	1/1	0.96	0.09	23,23,23,23	1
25	MG	A	1552	1/1	0.97	0.16	23,23,23,23	0
25	MG	A	1572	1/1	0.97	0.11	23,23,23,23	0
25	MG	A	1573	1/1	0.97	0.14	23,23,23,23	0
25	MG	A	470	1/1	0.97	0.21	23,23,23,23	1
25	MG	A	1597	1/1	0.97	0.06	23,23,23,23	1

Continued on next page...

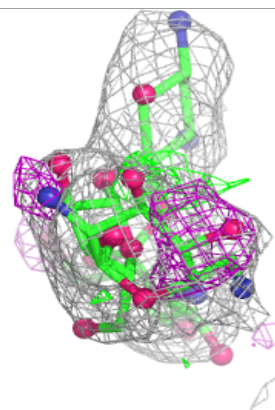
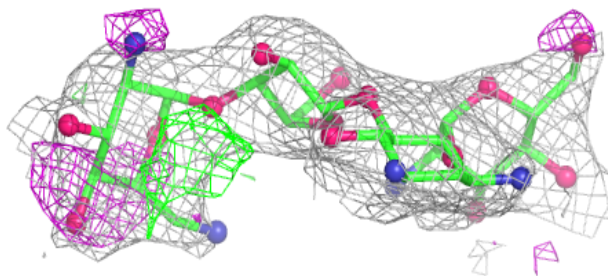
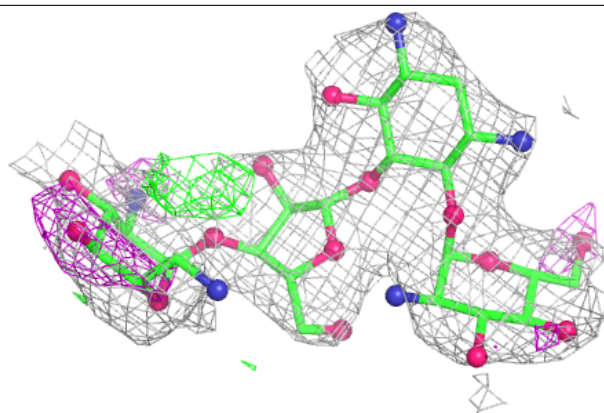
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1598	1/1	0.97	0.06	23,23,23,23	0
25	MG	A	1613	1/1	0.97	0.17	23,23,23,23	1
25	MG	A	1580	1/1	0.97	0.24	23,23,23,23	1
25	MG	A	1549	1/1	0.97	0.25	23,23,23,23	1
25	MG	A	1555	1/1	0.97	0.26	23,23,23,23	0
25	MG	A	1556	1/1	0.97	0.17	23,23,23,23	0
25	MG	X	500	1/1	0.97	0.11	23,23,23,23	1
25	MG	A	1604	1/1	0.97	0.21	23,23,23,23	1
25	MG	A	1585	1/1	0.97	0.32	23,23,23,23	1
25	MG	A	1567	1/1	0.98	0.28	23,23,23,23	0
25	MG	A	1633	1/1	0.98	0.40	23,23,23,23	1
25	MG	A	1612	1/1	0.98	0.14	23,23,23,23	1
25	MG	A	1601	1/1	0.98	0.07	23,23,23,23	1
25	MG	A	1589	1/1	0.98	0.24	23,23,23,23	0
25	MG	A	1593	1/1	0.98	0.30	23,23,23,23	1
25	MG	A	1609	1/1	0.98	0.17	23,23,23,23	0
25	MG	A	1583	1/1	0.98	0.12	23,23,23,23	0
26	ZN	D	306	1/1	0.98	0.12	23,23,23,23	1
25	MG	A	1594	1/1	0.99	0.06	23,23,23,23	1
25	MG	A	1553	1/1	0.99	0.19	23,23,23,23	0
26	ZN	N	307	1/1	1.00	0.04	23,23,23,23	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around PAR A 1545:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.