



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 06:40 AM UTC

PDB ID : 3J16 / pdb_00003j16
EMDB ID : EMD-2010
Title : Models of ribosome-bound Dom34p and Rli1p and their ribosomal binding partners
Authors : Becker, T.; Franckenberg, S.; Wickles, S.; Shoemaker, C.J.; Anger, A.M.; Armache, J.-P.; Sieber, H.; Ungewickell, C.; Berninghausen, O.; Daberkow, I.; Karcher, A.; Thomm, M.; Hopfner, K.-P.; Green, R.; Beckmann, R.
Deposited on : 2011-12-12
Resolution : 7.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

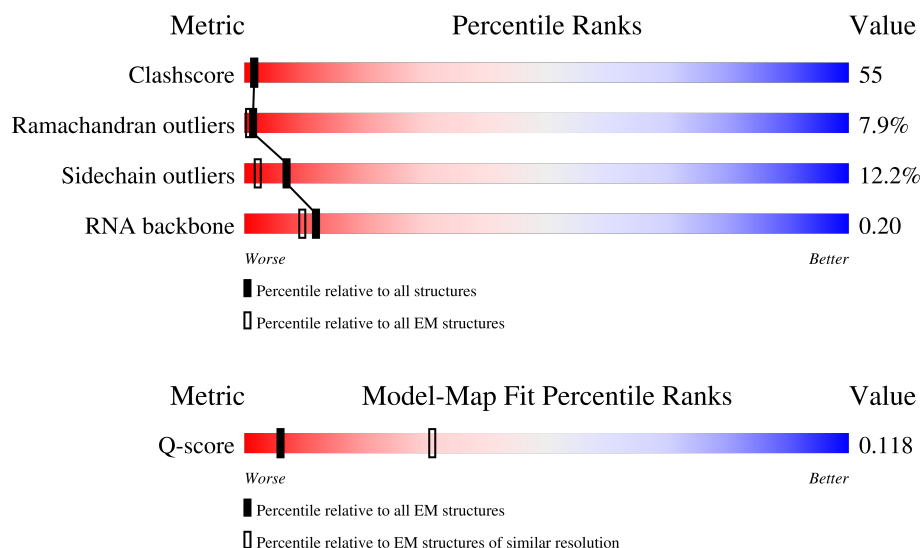
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 7.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	444 (6.70 - 7.70)

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

Mol	Chain	Length	Quality of chain
1	A	386	
2	B	608	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	J	233	
4	K	155	
5	L	75	
6	F	191	
7	E	63	
8	G	312	
9	C	236	
10	H	165	
11	I	137	
12	D	135	

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
13	MG	B	701	-	-	X	-
14	ATP	B	702	-	-	X	-
15	SF4	B	703	-	-	X	-
15	SF4	B	704	-	-	X	-

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 26208 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Dom34p.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	386	Total	C	N	O	S	0	0
			3097	1996	483	603	15		

- Molecule 2 is a protein called Rli1p.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	608	Total	C	N	O	S	0	0
			4804	3065	831	884	24		

- Molecule 3 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	233	Total	C	N	O	P	0	0
			4942	2222	899	1598	223		

- Molecule 4 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	155	Total	C	N	O	P	0	0
			3286	1476	591	1069	150		

- Molecule 5 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	75	Total	C	N	O	P	0	0
			1595	712	280	529	74		

- Molecule 6 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	191	Total	C	N	O	S	0	0
			1519	963	274	278	4		

- Molecule 7 is a protein called 40S ribosomal protein S30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	55	Total	C	N	O	S	0	0
			440	277	90	72	1		

- Molecule 8 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	199	Total	C	N	O	S	0	0
			1541	986	268	282	5		

- Molecule 9 is a protein called 40S ribosomal protein S6E.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 10 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	138	Total	C	N	O	S	0	0
			1037	651	190	194	2		

- Molecule 11 is a protein called 40S ribosomal protein S24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	136	Total	C	N	O	S	0	0
			1004	628	189	180	7		

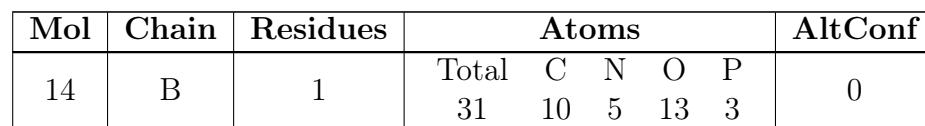
- Molecule 12 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	D	134	Total	C	N	O	0	0
			1074	676	208	190		

- Molecule 13 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
13	B	1	Total	Mg	0
			1	1	

- Molecule 14 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



-
- A chemical structure diagram of a cubane-like cluster, [Fe₄S₄]²⁺. The cluster consists of four iron (Fe) atoms at the corners of a cube and four sulfur (S) atoms at the centers of the edges. The atoms are color-coded: Fe atoms are purple and S atoms are yellow. The cluster is labeled with SF₄ at the top, S₃, FE₁, FE₄, FE₂, S₂, S₄, S₁, and FE₃ at the bottom.

Mol	Chain	Residues	Atoms			AltConf
15	B	1	Total 8	Fe 4	S 4	0
15	B	1	Total 8	Fe 4	S 4	0

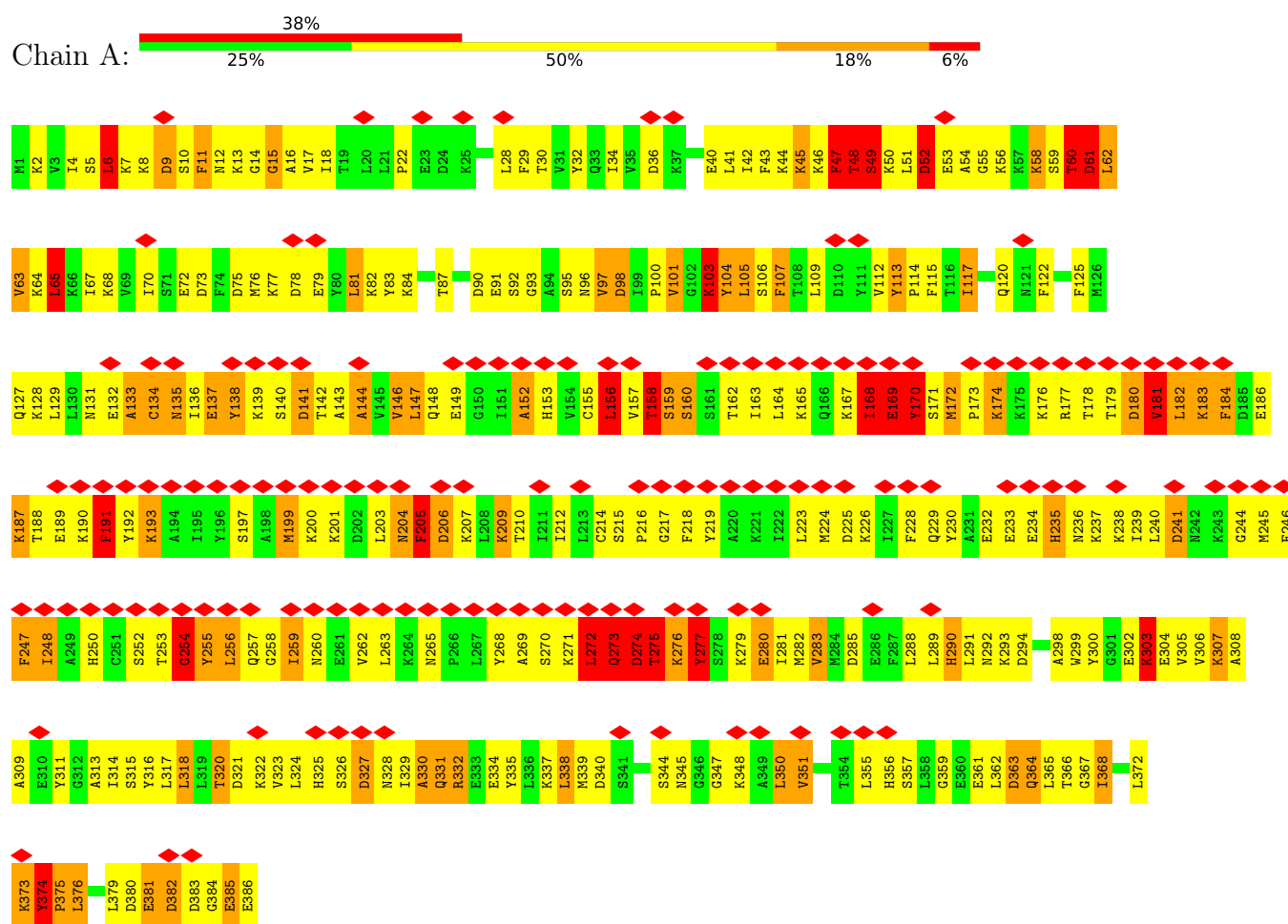
- 

Mol	Chain	Residues	Atoms		AltConf
16	B	1	Total	O	0
			1	1	

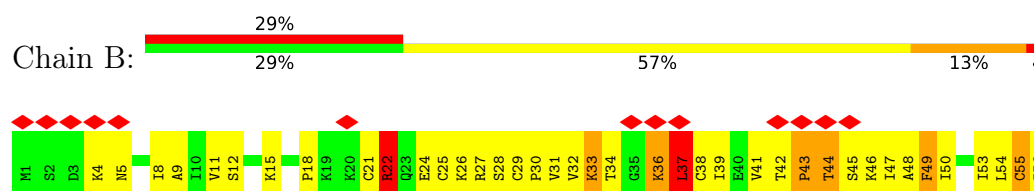
3 Residue-property plots

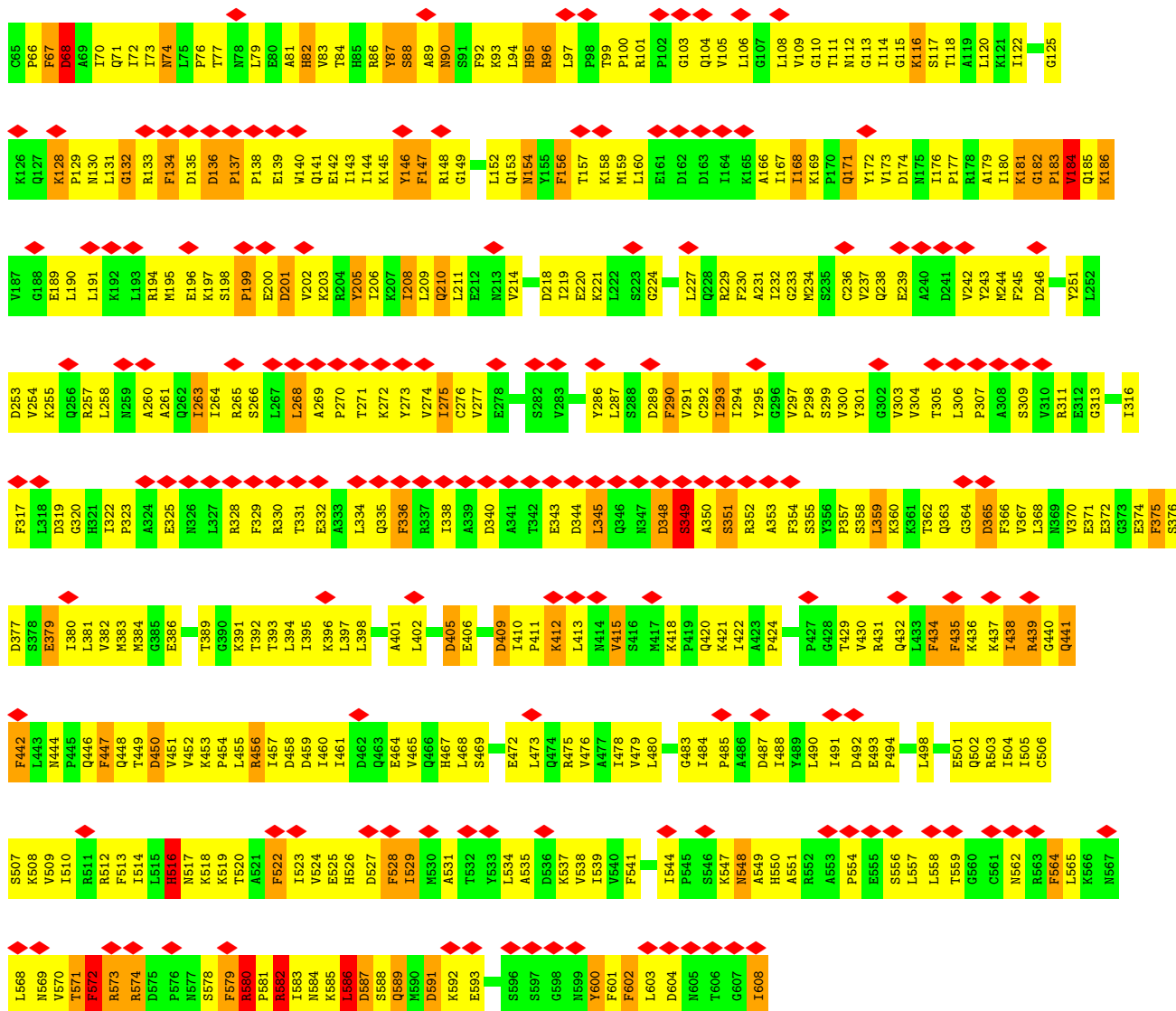
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Dom34p



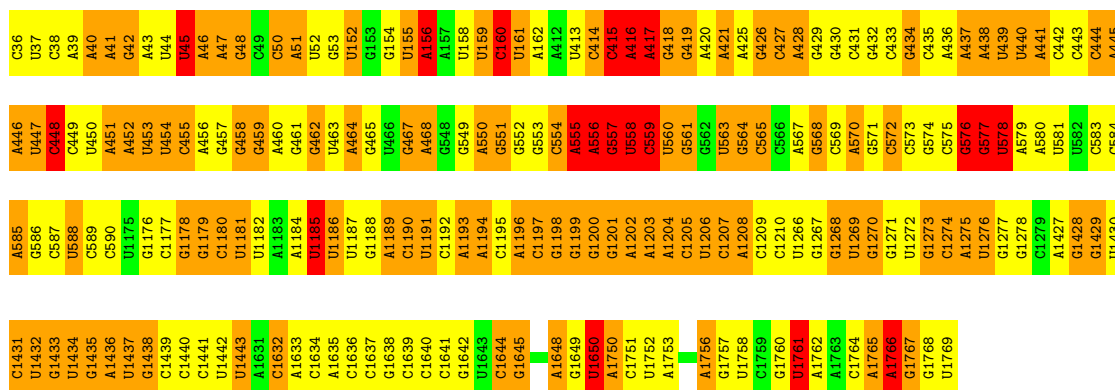
• Molecule 2: Rli1p





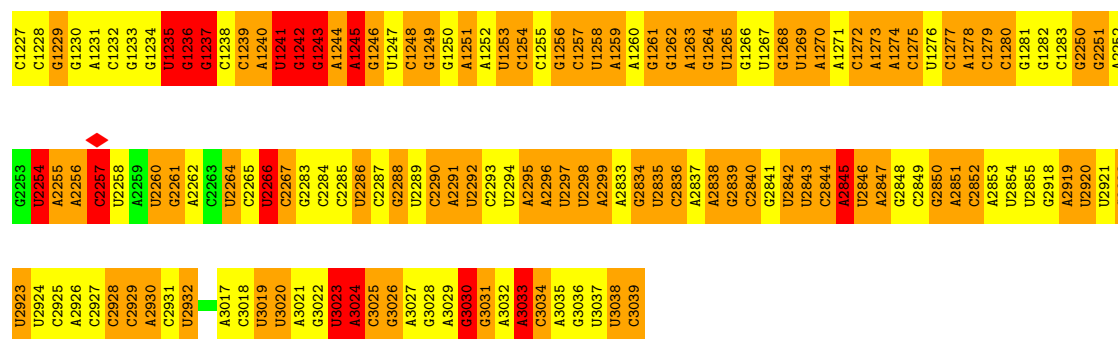
• Molecule 3: 28S ribosomal RNA

Chain J: 9% 39% 44% 8%



• Molecule 4: 18S ribosomal RNA

Chain K: 



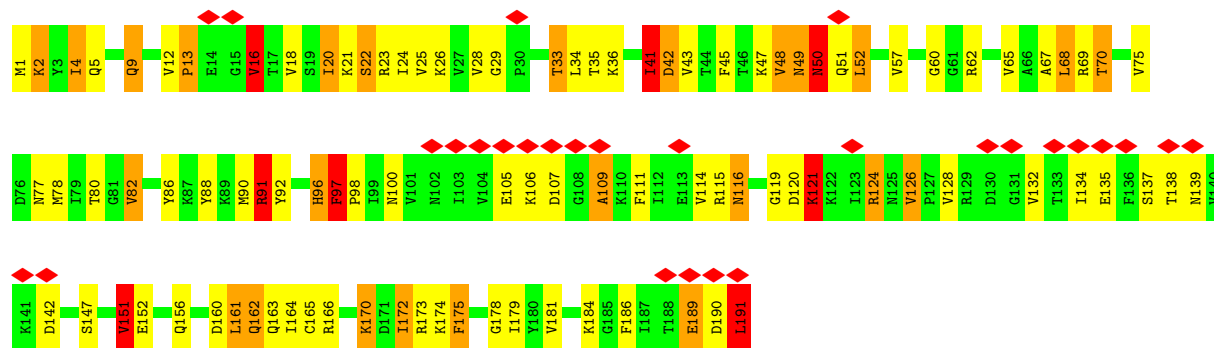
• Molecule 5: P-site tRNA

Chain L: 



• Molecule 6: 60S ribosomal protein L6

Chain F: 



• Molecule 7: 40S ribosomal protein S30E

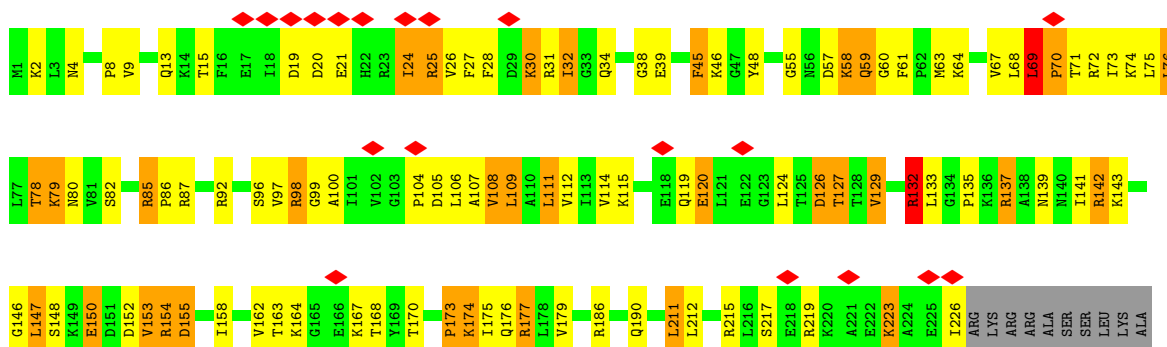
Chain E: 



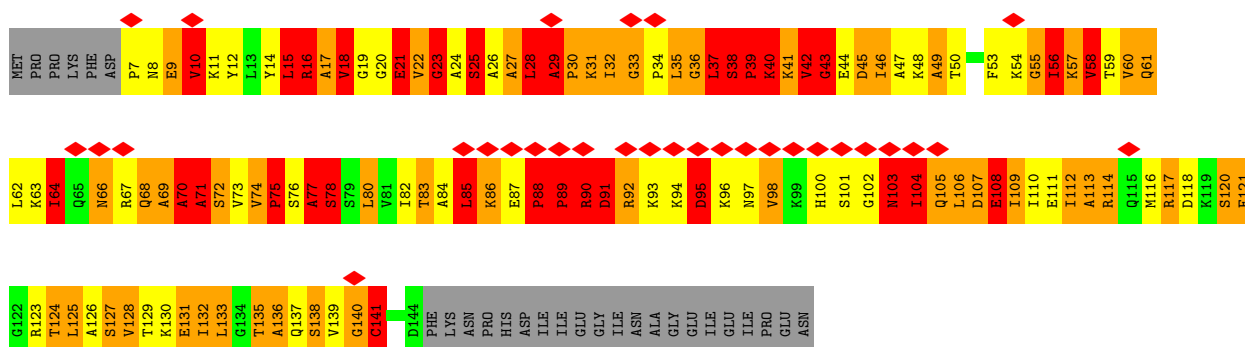
• Molecule 8: 60S ribosomal protein L10

Chain G: 

- Molecule 9: 40S ribosomal protein S6E

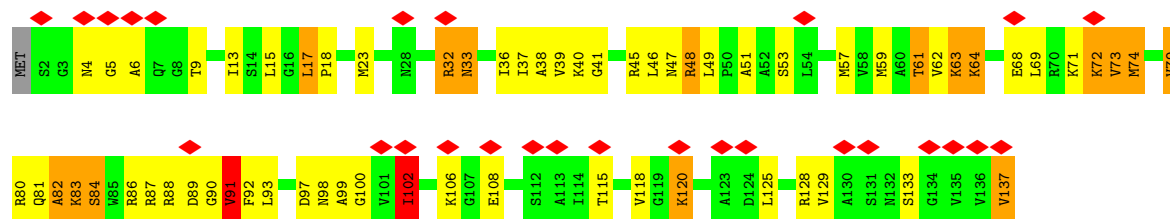


- Molecule 10: 60S ribosomal protein L11

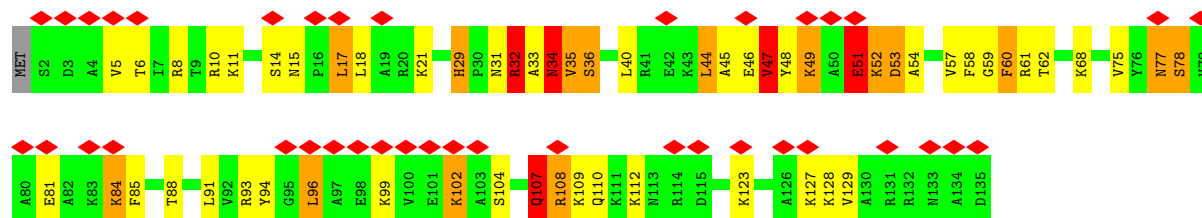


- Molecule 11: 40S ribosomal protein S24E





• Molecule 12: 40S ribosomal protein S24-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	45700	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	75000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	1.731	Depositor
Minimum map value	-0.781	Depositor
Average map value	0.022	Depositor
Map value standard deviation	0.147	Depositor
Recommended contour level	0.32	Depositor
Map size ($\text{\AA}$)	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.2375, 1.2375, 1.2375	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SF4, ATP

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	2.26	116/3149 (3.7%)	2.72	292/4230 (6.9%)
2	B	1.39	13/4893 (0.3%)	1.72	93/6603 (1.4%)
3	J	1.09	26/5523 (0.5%)	1.18	80/8591 (0.9%)
4	K	1.03	13/3671 (0.4%)	1.10	42/5709 (0.7%)
5	L	1.87	53/1781 (3.0%)	2.02	99/2775 (3.6%)
6	F	1.24	13/1540 (0.8%)	1.44	20/2073 (1.0%)
7	E	1.16	2/447 (0.4%)	1.76	16/595 (2.7%)
8	G	2.54	54/1568 (3.4%)	3.19	122/2119 (5.8%)
9	C	0.85	2/1844 (0.1%)	1.20	10/2464 (0.4%)
10	H	2.49	35/1048 (3.3%)	3.16	137/1408 (9.7%)
11	I	1.20	3/1019 (0.3%)	1.37	11/1369 (0.8%)
12	D	0.86	2/1088 (0.2%)	1.21	7/1449 (0.5%)
All	All	1.54	332/27571 (1.2%)	1.82	929/39385 (2.4%)

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	0	18
2	B	0	4
3	J	0	25
4	K	0	20
5	L	0	5
6	F	0	2
7	E	0	2
8	G	0	13
10	H	0	13
12	D	0	1
All	All	0	103

All (332) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	H	88	PRO	CG-CD	49.45	3.18	1.50
8	G	72	ASP	C-O	-41.90	0.93	1.24
8	G	5	ARG	C-O	-32.83	0.84	1.23
5	L	41	G	C2'-C1'	-15.96	1.29	1.53
10	H	46	ILE	CA-CB	-15.26	1.36	1.54
5	L	36	C	O4'-C1'	12.47	1.60	1.41
3	J	578	U	C1'-N1	12.12	1.65	1.47
10	H	89	PRO	CG-CD	12.02	1.91	1.50
5	L	22	G	C2'-C1'	-11.62	1.35	1.53
8	G	199	SER	C-O	-11.57	1.00	1.23
9	C	226	ILE	C-O	-11.56	1.00	1.23
6	F	191	LEU	C-OXT	-11.56	1.00	1.23
11	I	137	VAL	C-O	-11.55	1.00	1.23
2	B	608	ILE	C-OXT	-11.55	1.00	1.23
2	B	608	ILE	C-O	-11.54	1.00	1.23
6	F	191	LEU	C-O	-11.53	1.00	1.23
11	I	137	VAL	C-OXT	-11.53	1.00	1.23
5	L	25	U	C2'-C1'	-11.21	1.36	1.53
10	H	7	PRO	N-CD	11.16	1.63	1.47
5	L	61	C	O4'-C1'	10.94	1.58	1.41
5	L	41	G	O4'-C1'	10.93	1.58	1.41
5	L	43	C	O4'-C1'	10.90	1.58	1.41
3	J	578	U	C4'-O4'	-10.75	1.29	1.45
5	L	2	C	O4'-C1'	10.30	1.57	1.41
8	G	72	ASP	N-CA	10.31	1.62	1.46
5	L	28	G	C2'-C1'	-10.24	1.38	1.53
5	L	48	C	O4'-C1'	10.23	1.57	1.41
5	L	36	C	C2'-C1'	-10.02	1.38	1.53
5	L	45	G	C2'-C1'	-10.00	1.38	1.53
1	A	348	LYS	C-N	9.92	1.45	1.33
8	G	5	ARG	C-N	9.81	1.47	1.33
5	L	64	G	C2'-C1'	-9.71	1.38	1.53
5	L	43	C	C2'-C1'	-9.61	1.39	1.53
5	L	75	A	C2'-C1'	9.54	1.67	1.53
5	L	23	A	C2'-C1'	-9.38	1.39	1.53
5	L	66	C	O4'-C1'	9.32	1.55	1.41
8	G	5	ARG	CA-CB	-9.13	1.38	1.53
8	G	55	LYS	CA-CB	9.10	1.68	1.53
2	B	572	PHE	C-N	9.09	1.46	1.33
2	B	572	PHE	CA-C	-9.04	1.40	1.53
10	H	58	VAL	N-CA	-9.01	1.35	1.46
1	A	180	ASP	CA-C	-8.94	1.40	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	45	G	O4'-C1'	8.87	1.55	1.42
2	B	311	ARG	CD-NE	8.80	1.58	1.46
5	L	29	C	O4'-C1'	8.79	1.54	1.41
8	G	5	ARG	N-CA	8.74	1.56	1.46
5	L	62	C	O4'-C1'	8.64	1.54	1.41
1	A	381	GLU	CA-C	-8.60	1.41	1.52
5	L	26	G	C2'-C1'	-8.52	1.40	1.53
5	L	73	C	O4'-C1'	8.52	1.54	1.41
5	L	2	C	C2'-C1'	-8.49	1.40	1.53
1	A	233	GLU	N-CA	-8.49	1.36	1.46
2	B	583	ILE	CA-CB	-8.46	1.45	1.54
5	L	65	U	C2'-C1'	-8.41	1.40	1.53
5	L	63	C	O4'-C1'	8.32	1.54	1.41
8	G	73	PHE	N-CA	8.29	1.56	1.46
2	B	572	PHE	N-CA	-8.25	1.34	1.46
1	A	384	GLY	C-N	8.21	1.42	1.33
5	L	38	C	O4'-C1'	8.10	1.53	1.41
1	A	288	LEU	C-N	8.09	1.44	1.33
8	G	72	ASP	C-N	8.07	1.45	1.33
8	G	46	ARG	CA-C	-8.05	1.42	1.52
1	A	34	ILE	CA-CB	-8.05	1.47	1.55
1	A	280	GLU	N-CA	-8.02	1.36	1.46
5	L	37	G	C2'-C1'	-8.02	1.41	1.53
8	G	81	LYS	CA-C	-7.95	1.42	1.52
5	L	68	C	O4'-C1'	7.89	1.53	1.41
1	A	171	SER	CA-CB	7.84	1.62	1.52
5	L	74	C	O4'-C1'	7.78	1.53	1.41
10	H	41	LYS	CA-C	-7.67	1.42	1.52
1	A	5	SER	CA-C	-7.61	1.42	1.52
10	H	58	VAL	CA-CB	-7.60	1.44	1.54
1	A	63	VAL	N-CA	-7.58	1.37	1.46
1	A	367	GLY	C-N	7.58	1.42	1.33
8	G	102	SER	CA-C	-7.57	1.43	1.52
1	A	206	ASP	N-CA	-7.57	1.38	1.46
5	L	18	G	C2'-C1'	-7.57	1.41	1.53
1	A	115	PHE	CA-C	-7.56	1.43	1.52
1	A	51	LEU	N-CA	-7.53	1.35	1.45
5	L	65	U	O4'-C1'	7.49	1.52	1.41
2	B	516	HIS	CB-CG	-7.49	1.39	1.50
1	A	351	VAL	CA-CB	7.45	1.62	1.54
8	G	192	ASP	N-CA	-7.45	1.37	1.46
8	G	33	VAL	CA-C	-7.45	1.43	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	60	THR	CA-C	7.44	1.62	1.52
10	H	96	LYS	C-N	7.34	1.44	1.33
10	H	138	SER	C-O	-7.33	1.13	1.23
8	G	72	ASP	CA-CB	7.30	1.63	1.54
5	L	69	G	C2'-C1'	-7.25	1.42	1.53
8	G	42	ARG	C-N	7.24	1.43	1.33
1	A	95	SER	CA-C	-7.23	1.43	1.53
12	D	33	ALA	CA-CB	-7.16	1.43	1.53
1	A	200	LYS	CA-CB	7.14	1.64	1.53
1	A	7	LYS	C-N	7.11	1.42	1.33
3	J	555	A	O3'-P	-7.08	1.50	1.61
1	A	214	CYS	C-N	7.08	1.42	1.33
1	A	2	LYS	N-CA	-7.07	1.37	1.46
3	J	1644	C	C5'-C4'	7.06	1.61	1.51
5	L	75	A	O4'-C1'	-7.01	1.31	1.42
10	H	44	GLU	C-N	6.99	1.43	1.33
1	A	6	LEU	N-CA	-6.92	1.37	1.46
1	A	184	PHE	CA-C	-6.89	1.44	1.52
1	A	90	ASP	CA-C	-6.87	1.44	1.53
8	G	156	VAL	CA-CB	6.86	1.62	1.55
3	J	160	C	C4'-C3'	6.86	1.62	1.52
1	A	117	ILE	CA-CB	6.84	1.62	1.53
8	G	177	ASN	CA-C	-6.84	1.43	1.52
10	H	32	ILE	CA-CB	6.83	1.63	1.54
1	A	305	VAL	CA-CB	-6.79	1.45	1.54
1	A	127	GLN	C-N	6.79	1.42	1.33
1	A	263	LEU	CA-C	-6.78	1.43	1.52
3	J	578	U	O3'-P	-6.74	1.51	1.61
8	G	62	ALA	C-N	6.73	1.42	1.33
1	A	209	LYS	N-CA	-6.72	1.36	1.46
8	G	104	ARG	NE-CZ	6.68	1.40	1.33
10	H	75	PRO	CA-C	6.67	1.61	1.52
3	J	1641	C	C1'-N1	6.67	1.58	1.48
7	E	9	ALA	CA-C	-6.64	1.43	1.52
8	G	33	VAL	C-N	6.64	1.42	1.33
5	L	21	A	O4'-C1'	6.64	1.51	1.41
1	A	255	TYR	CA-CB	6.63	1.64	1.53
8	G	48	ARG	CA-C	6.63	1.61	1.52
8	G	93	LEU	CA-C	-6.61	1.44	1.52
8	G	148	GLY	C-N	6.61	1.42	1.33
3	J	1185	U	O3'-P	-6.59	1.51	1.61
8	G	83	ASN	N-CA	-6.59	1.37	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	41	LEU	C-N	6.59	1.41	1.33
1	A	28	LEU	CA-CB	6.54	1.63	1.53
1	A	204	ASN	N-CA	-6.53	1.38	1.46
1	A	235	HIS	CE1-NE2	-6.50	1.26	1.32
10	H	58	VAL	CA-C	6.49	1.60	1.52
5	L	42	C	O4'-C1'	6.48	1.51	1.41
1	A	129	LEU	CA-C	-6.46	1.43	1.52
1	A	236	ASN	CA-C	-6.45	1.45	1.53
10	H	57	LYS	CA-CB	6.44	1.64	1.53
8	G	132	LYS	C-N	6.42	1.42	1.34
1	A	332	ARG	CA-C	-6.38	1.44	1.52
1	A	347	GLY	C-N	6.37	1.42	1.33
5	L	17	G	O4'-C1'	6.37	1.51	1.42
10	H	61	GLN	CA-C	-6.36	1.44	1.53
9	C	87	ARG	NE-CZ	6.36	1.40	1.33
1	A	306	VAL	C-N	6.34	1.42	1.33
1	A	289	LEU	C-N	6.33	1.42	1.33
5	L	16	U	O4'-C1'	6.32	1.51	1.41
5	L	27	G	C2'-C1'	-6.30	1.44	1.53
1	A	223	LEU	CA-C	-6.27	1.44	1.52
1	A	113	TYR	CA-C	-6.26	1.45	1.52
6	F	96	HIS	CA-C	-6.25	1.44	1.52
1	A	109	LEU	CA-C	-6.25	1.44	1.52
10	H	107	ASP	N-CA	-6.23	1.38	1.46
1	A	184	PHE	CA-CB	6.22	1.63	1.53
8	G	132	LYS	N-CA	-6.21	1.38	1.46
8	G	198	PRO	CA-C	-6.21	1.47	1.53
5	L	72	G	C5'-C4'	6.16	1.60	1.51
10	H	90	ARG	NE-CZ	6.16	1.39	1.33
11	I	102	ILE	CA-CB	6.14	1.61	1.54
10	H	16	ARG	CD-NE	6.12	1.54	1.46
10	H	76	SER	CA-C	-6.12	1.45	1.53
1	A	277	TYR	CA-CB	6.12	1.63	1.53
8	G	104	ARG	CD-NE	6.12	1.54	1.46
1	A	368	ILE	CA-C	-6.10	1.44	1.52
1	A	98	ASP	C-N	6.08	1.40	1.33
10	H	106	LEU	CA-C	-6.07	1.44	1.52
6	F	173	ARG	CZ-NH2	6.07	1.41	1.33
6	F	174	LYS	N-CA	-6.07	1.38	1.46
1	A	317	LEU	C-N	6.06	1.41	1.33
1	A	9	ASP	CA-C	-6.06	1.44	1.52
1	A	339	MET	N-CA	-6.04	1.39	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	116	ASN	N-CA	-6.04	1.38	1.46
7	E	55	ARG	CZ-NH1	6.03	1.41	1.32
1	A	45	LYS	C-N	6.02	1.42	1.33
1	A	60	THR	N-CA	-5.96	1.38	1.46
8	G	42	ARG	N-CA	-5.95	1.39	1.46
12	D	108	ARG	NE-CZ	5.95	1.39	1.33
1	A	15	GLY	C-N	5.94	1.40	1.33
1	A	357	SER	CA-CB	5.93	1.62	1.53
5	L	67	G	C2'-C1'	-5.93	1.44	1.53
8	G	56	ASN	N-CA	-5.93	1.38	1.46
1	A	177	ARG	NE-CZ	5.93	1.39	1.33
10	H	137	GLN	N-CA	-5.93	1.37	1.45
1	A	153	HIS	ND1-CE1	5.92	1.38	1.32
4	K	1236	G	C5'-C4'	5.90	1.60	1.51
4	K	3023	U	O3'-P	-5.90	1.52	1.61
1	A	58	LYS	N-CA	-5.88	1.40	1.46
3	J	1649	G	P-O5'	-5.88	1.50	1.59
8	G	123	ALA	C-N	5.88	1.41	1.33
5	L	72	G	C2'-C1'	-5.88	1.44	1.53
1	A	100	PRO	C-N	5.87	1.40	1.33
8	G	5	ARG	CA-C	5.87	1.60	1.52
8	G	48	ARG	CD-NE	5.85	1.54	1.46
10	H	15	LEU	CA-C	-5.85	1.45	1.52
6	F	124	ARG	NE-CZ	5.83	1.39	1.33
10	H	23	GLY	CA-C	-5.82	1.43	1.51
1	A	128	LYS	CA-C	-5.81	1.45	1.52
1	A	193	LYS	N-CA	-5.80	1.39	1.46
1	A	82	LYS	C-N	5.80	1.41	1.33
5	L	72	G	O3'-P	-5.77	1.52	1.61
5	L	64	G	O4'-C1'	5.76	1.50	1.41
5	L	68	C	C2'-C1'	-5.76	1.44	1.53
1	A	148	GLN	N-CA	-5.76	1.38	1.46
8	G	175	LEU	CB-CG	5.75	1.65	1.53
3	J	457	G	C2'-C1'	-5.74	1.44	1.53
1	A	79	GLU	CA-CB	5.72	1.62	1.53
1	A	187	LYS	N-CA	-5.71	1.39	1.46
1	A	101	VAL	CA-C	-5.71	1.44	1.52
8	G	122	ARG	CA-C	-5.71	1.45	1.53
6	F	96	HIS	N-CA	-5.70	1.38	1.46
10	H	16	ARG	NE-CZ	5.69	1.39	1.33
8	G	64	ARG	NE-CZ	5.67	1.39	1.33
10	H	56	ILE	N-CA	-5.67	1.39	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	29	C	C2'-C1'	-5.66	1.44	1.53
1	A	240	LEU	C-N	5.65	1.41	1.33
4	K	3025	C	C2'-C1'	-5.64	1.44	1.53
10	H	21	GLU	CA-CB	5.64	1.63	1.53
6	F	172	ILE	CA-CB	5.63	1.61	1.54
10	H	27	ALA	CA-C	-5.63	1.45	1.52
8	G	13	ALA	CA-C	-5.62	1.45	1.52
4	K	3026	G	P-O5'	-5.61	1.51	1.59
1	A	142	THR	C-O	-5.60	1.16	1.23
3	J	576	G	O3'-P	-5.60	1.52	1.61
1	A	294	ASP	CA-CB	-5.59	1.43	1.53
3	J	1644	C	O3'-P	-5.58	1.52	1.61
1	A	368	ILE	C-O	-5.58	1.18	1.23
3	J	1638	G	P-O5'	-5.58	1.51	1.59
3	J	1181	U	C4'-O4'	-5.57	1.37	1.45
8	G	122	ARG	NE-CZ	5.57	1.39	1.33
6	F	97	PHE	N-CA	-5.56	1.39	1.46
6	F	96	HIS	ND1-CE1	5.55	1.38	1.32
1	A	302	GLU	CA-CB	5.54	1.62	1.53
8	G	68	SER	CA-C	-5.53	1.46	1.53
10	H	44	GLU	CA-C	-5.53	1.45	1.52
3	J	1634	C	C4'-C3'	5.52	1.60	1.52
1	A	337	LYS	C-O	-5.51	1.17	1.24
2	B	571	THR	C-N	-5.50	1.26	1.33
1	A	252	SER	CA-C	5.50	1.59	1.52
3	J	1761	U	C5'-C4'	5.50	1.59	1.51
6	F	120	ASP	CA-C	-5.49	1.45	1.52
8	G	102	SER	CA-CB	5.49	1.62	1.53
5	L	63	C	C2'-C1'	-5.48	1.45	1.53
3	J	159	U	O3'-P	-5.47	1.52	1.61
3	J	556	A	P-O5'	5.47	1.68	1.59
1	A	18	ILE	CA-CB	-5.46	1.47	1.54
4	K	2250	G	C1'-N9	-5.45	1.39	1.48
1	A	114	PRO	C-N	5.45	1.40	1.33
3	J	1180	C	O3'-P	-5.43	1.53	1.61
1	A	103	LYS	CA-CB	5.43	1.62	1.53
8	G	122	ARG	CD-NE	5.42	1.53	1.46
1	A	282	MET	CA-CB	5.42	1.61	1.53
4	K	1241	U	O3'-P	-5.42	1.53	1.61
2	B	583	ILE	CA-C	-5.41	1.46	1.52
4	K	2255	A	O3'-P	-5.40	1.53	1.61
10	H	31	LYS	CA-CB	5.39	1.63	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	G	42	ARG	CD-NE	5.39	1.53	1.46
8	G	67	LEU	N-CA	-5.38	1.39	1.46
1	A	322	LYS	CA-C	-5.37	1.45	1.52
1	A	73	ASP	N-CA	-5.36	1.40	1.46
10	H	25	SER	C-O	-5.36	1.17	1.24
1	A	250	HIS	CB-CG	5.36	1.57	1.50
5	L	40	U	C2'-C1'	5.36	1.61	1.53
10	H	58	VAL	C-N	5.36	1.41	1.33
1	A	203	LEU	N-CA	-5.35	1.39	1.45
4	K	1238	C	C2'-C1'	-5.34	1.45	1.53
1	A	327	ASP	C-N	5.34	1.41	1.33
10	H	95	ASP	CA-C	-5.33	1.45	1.52
3	J	1638	G	O4'-C1'	5.31	1.49	1.41
8	G	174	ASN	C-N	5.31	1.40	1.33
3	J	1650	U	C4'-C3'	5.31	1.60	1.52
8	G	52	LEU	C-N	5.31	1.41	1.33
1	A	186	GLU	N-CA	5.30	1.52	1.46
1	A	332	ARG	NE-CZ	5.30	1.38	1.33
4	K	3030	G	C2'-C1'	-5.29	1.45	1.53
1	A	241	ASP	CA-C	-5.28	1.45	1.52
1	A	234	GLU	C-N	5.28	1.41	1.33
5	L	61	C	C2'-C1'	-5.27	1.45	1.53
8	G	56	ASN	C-N	5.27	1.41	1.34
1	A	262	VAL	N-CA	-5.27	1.40	1.46
4	K	2254	U	O5'-C5'	5.25	1.50	1.42
1	A	326	SER	CA-CB	5.25	1.62	1.53
1	A	13	LYS	C-N	5.24	1.40	1.33
3	J	1636	C	C2'-C1'	-5.23	1.45	1.53
1	A	32	TYR	N-CA	-5.23	1.39	1.46
1	A	163	ILE	N-CA	5.22	1.53	1.46
1	A	172	MET	CG-SD	5.22	1.93	1.80
4	K	1236	G	O3'-P	-5.21	1.53	1.61
1	A	356	HIS	ND1-CE1	5.21	1.37	1.32
3	J	155	U	C4'-C3'	-5.21	1.44	1.52
1	A	58	LYS	CA-C	-5.21	1.48	1.53
8	G	189	GLN	C-N	5.21	1.41	1.33
2	B	580	ARG	NE-CZ	5.20	1.38	1.33
1	A	340	ASP	C-N	5.20	1.41	1.33
3	J	155	U	C3'-O3'	5.19	1.50	1.42
3	J	1650	U	C5'-C4'	5.19	1.59	1.51
5	L	14	A	O4'-C1'	5.18	1.49	1.41
1	A	239	ILE	C-N	5.17	1.41	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	3030	G	C2'-O2'	-5.17	1.34	1.42
8	G	125	ASN	CA-CB	5.15	1.60	1.53
1	A	191	PHE	C-O	-5.15	1.18	1.24
1	A	72	GLU	CA-C	-5.15	1.46	1.52
1	A	191	PHE	CA-C	-5.14	1.46	1.52
10	H	43	GLY	C-N	5.13	1.41	1.33
1	A	152	ALA	CA-C	-5.13	1.46	1.52
10	H	40	LYS	CA-CB	5.13	1.61	1.53
1	A	182	LEU	C-N	5.12	1.40	1.33
1	A	160	SER	C-O	-5.12	1.16	1.23
1	A	42	ILE	CA-C	-5.12	1.46	1.52
1	A	279	LYS	CA-CB	5.12	1.62	1.53
1	A	320	THR	C-N	5.12	1.40	1.33
6	F	174	LYS	CA-C	-5.12	1.45	1.52
1	A	29	PHE	N-CA	-5.11	1.40	1.46
8	G	50	VAL	C-N	5.11	1.40	1.33
1	A	129	LEU	CB-CG	5.11	1.63	1.53
4	K	3024	A	O3'-P	-5.10	1.53	1.61
5	L	31	C	C2'-C1'	-5.10	1.45	1.53
1	A	41	LEU	CA-C	-5.10	1.46	1.52
1	A	293	LYS	CA-CB	5.09	1.61	1.53
1	A	263	LEU	CA-CB	5.09	1.61	1.53
5	L	54	U	C5'-C4'	5.08	1.58	1.51
2	B	517	ASN	CA-C	-5.08	1.45	1.52
8	G	36	GLN	CA-CB	5.07	1.61	1.53
1	A	156	LEU	C-N	-5.07	1.27	1.33
8	G	48	ARG	CZ-NH2	5.07	1.40	1.33
1	A	197	SER	CA-CB	5.06	1.61	1.53
1	A	164	LEU	CA-C	5.05	1.59	1.52
5	L	49	G	C2'-C1'	-5.03	1.45	1.53
1	A	52	ASP	CA-CB	5.03	1.61	1.53
10	H	45	ASP	CA-CB	5.03	1.62	1.53
5	L	23	A	O4'-C1'	5.03	1.49	1.41
2	B	33	LYS	CA-C	-5.02	1.46	1.52
3	J	1649	G	C5'-C4'	5.02	1.58	1.51
1	A	64	LYS	CA-CB	5.02	1.60	1.53
1	A	309	ALA	C-N	5.01	1.40	1.34
8	G	35	SER	CA-C	-5.01	1.45	1.52

All (929) bond angle outliers are listed below:

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
-----	-------	-----	------	-------	---	-------------	----------

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	G	72	ASP	CA-C-O	-51.28	70.82	120.56
8	G	5	ARG	O-C-N	-44.24	66.20	122.82
8	G	5	ARG	CA-C-O	-43.66	74.28	121.44
8	G	72	ASP	O-C-N	-42.55	73.94	122.88
10	H	88	PRO	N-CD-CG	-34.39	51.62	103.20
1	A	272	LEU	O-C-N	-22.81	96.81	123.27
5	L	73	C	P-O3'-C3'	17.88	147.02	120.20
5	L	12	U	P-O3'-C3'	17.20	146.00	120.20
10	H	40	LYS	N-CA-C	16.72	136.44	113.37
10	H	40	LYS	CA-C-N	16.30	152.67	121.54
10	H	40	LYS	C-N-CA	16.30	152.67	121.54
2	B	572	PHE	CA-C-O	-15.56	95.79	121.94
7	E	9	ALA	N-CA-C	15.47	130.04	111.33
2	B	434	PHE	CA-CB-CG	-15.31	98.48	113.80
10	H	29	ALA	O-C-N	-15.08	103.97	121.32
10	H	41	LYS	N-CA-CB	-14.55	85.89	110.49
5	L	67	G	P-O3'-C3'	14.41	141.82	120.20
1	A	47	PHE	CA-CB-CG	14.40	128.20	113.80
5	L	72	G	P-O3'-C3'	14.37	141.75	120.20
5	L	27	G	P-O3'-C3'	14.26	141.59	120.20
8	G	180	PRO	CB-CA-C	-14.20	88.13	111.56
10	H	38	SER	CA-C-O	-13.94	101.06	120.16
1	A	276	LYS	CA-C-N	13.90	148.10	121.54
1	A	276	LYS	C-N-CA	13.90	148.10	121.54
4	K	1235	U	P-O3'-C3'	13.70	140.76	120.20
10	H	29	ALA	N-CA-C	13.45	139.54	109.81
10	H	43	GLY	N-CA-C	13.45	145.06	113.18
1	A	204	ASN	N-CA-C	-13.34	84.68	108.02
10	H	42	VAL	CA-C-N	13.09	147.06	121.41
10	H	42	VAL	C-N-CA	13.09	147.06	121.41
4	K	2254	U	P-O3'-C3'	12.92	139.58	120.20
10	H	47	ALA	N-CA-C	-12.88	97.82	113.15
8	G	72	ASP	N-CA-C	-12.80	90.57	108.23
1	A	184	PHE	CA-CB-CG	12.67	126.47	113.80
2	B	572	PHE	N-CA-C	-12.49	92.43	109.54
10	H	33	GLY	CA-C-O	-12.43	103.75	121.52
10	H	44	GLU	N-CA-C	12.32	128.54	113.38
5	L	64	G	P-O3'-C3'	12.26	138.58	120.20
3	J	578	U	P-O3'-C3'	12.21	138.51	120.20
10	H	33	GLY	O-C-N	-12.13	109.64	121.77
1	A	132	GLU	N-CA-C	-12.03	100.91	114.62

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	H	18	VAL	CB-CA-C	11.92	130.84	111.29
5	L	40	U	P-O3'-C3'	11.89	138.04	120.20
2	B	375	PHE	CA-CB-CG	-11.85	101.95	113.80
8	G	55	LYS	CA-CB-CG	11.65	137.41	114.10
1	A	276	LYS	N-CA-C	11.62	127.27	113.20
3	J	559	C	C5'-C4'-C3'	-11.60	98.60	116.00
7	E	10	ARG	N-CA-C	-11.52	98.87	113.16
5	L	41	G	N9-C1'-C2'	11.18	128.77	112.00
1	A	49	SER	CB-CA-C	11.10	137.70	111.83
5	L	75	A	O4'-C1'-N9	10.95	124.63	108.20
5	L	29	C	O3'-P-O5'	-10.94	87.59	104.00
10	H	41	LYS	N-CA-C	10.88	133.97	110.80
2	B	447	PHE	CA-CB-CG	-10.87	102.93	113.80
5	L	36	C	N1-C1'-C2'	10.82	128.23	112.00
1	A	49	SER	CA-C-N	10.80	142.17	121.54
1	A	49	SER	C-N-CA	10.80	142.17	121.54
8	G	84	VAL	CA-C-N	10.64	131.94	122.47
8	G	84	VAL	C-N-CA	10.64	131.94	122.47
10	H	28	LEU	CA-C-N	10.60	147.65	121.80
10	H	28	LEU	C-N-CA	10.60	147.65	121.80
1	A	373	LYS	N-CA-CB	10.55	126.16	110.33
8	G	42	ARG	CB-CA-C	10.55	128.79	110.85
10	H	57	LYS	CB-CG-CD	10.52	135.49	111.30
1	A	112	VAL	N-CA-C	-10.50	102.53	111.56
10	H	74	VAL	N-CA-CB	-10.36	96.71	111.21
3	J	155	U	C4'-C3'-C2'	10.32	112.92	102.60
10	H	28	LEU	CB-CA-C	-10.30	92.34	109.03
1	A	374	TYR	CA-CB-CG	10.29	132.43	113.90
4	K	2266	U	P-O3'-C3'	10.28	135.61	120.20
10	H	34	PRO	N-CA-C	10.28	128.14	114.27
3	J	416	A	P-O3'-C3'	10.26	135.60	120.20
1	A	156	LEU	CA-C-N	10.24	134.05	122.48
1	A	156	LEU	C-N-CA	10.24	134.05	122.48
3	J	1761	U	P-O3'-C3'	10.10	135.34	120.20
8	G	39	HIS	CB-CA-C	10.06	127.50	110.79
5	L	43	C	N1-C1'-C2'	10.03	127.04	112.00
5	L	30	G	P-O3'-C3'	9.92	135.08	120.20
3	J	557	G	P-O3'-C3'	9.92	135.07	120.20
8	G	34	SER	N-CA-CB	9.67	123.72	110.38
8	G	5	ARG	N-CA-C	-9.67	97.67	110.24
5	L	2	C	N1-C1'-C2'	9.63	126.44	112.00
2	B	147	PHE	CA-CB-CG	-9.58	104.22	113.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	577	G	P-O3'-C3'	9.52	134.47	120.20
1	A	180	ASP	CA-CB-CG	-9.48	103.12	112.60
10	H	58	VAL	CB-CA-C	9.46	126.81	111.29
4	K	3023	U	P-O3'-C3'	9.43	134.34	120.20
5	L	11	U	P-O3'-C3'	9.40	134.30	120.20
2	B	183	PRO	CA-C-N	9.37	138.83	121.97
2	B	183	PRO	C-N-CA	9.37	138.83	121.97
10	H	30	PRO	CA-C-N	-9.37	105.43	122.38
10	H	30	PRO	C-N-CA	-9.37	105.43	122.38
5	L	25	U	P-O3'-C3'	9.36	134.24	120.20
1	A	34	ILE	N-CA-C	-9.35	102.69	111.48
3	J	448	C	O4'-C4'-C3'	-9.34	94.66	104.00
2	B	137	PRO	N-CA-C	-9.32	99.33	110.70
2	B	442	PHE	CA-CB-CG	-9.26	104.54	113.80
10	H	138	SER	CA-C-N	9.26	138.63	121.97
10	H	138	SER	C-N-CA	9.26	138.63	121.97
5	L	37	G	P-O3'-C3'	9.23	134.04	120.20
10	H	40	LYS	CB-CA-C	-9.22	92.77	110.57
5	L	22	G	N9-C1'-C2'	9.21	125.82	112.00
2	B	183	PRO	N-CA-C	-9.21	93.49	112.47
3	J	417	A	P-O3'-C3'	9.20	134.00	120.20
1	A	304	GLU	CB-CA-C	9.17	126.44	110.85
10	H	41	LYS	CA-CB-CG	9.17	132.43	114.10
1	A	327	ASP	N-CA-CB	9.14	125.94	110.49
1	A	218	PHE	CA-C-N	9.13	132.51	120.28
1	A	218	PHE	C-N-CA	9.13	132.51	120.28
8	G	50	VAL	N-CA-CB	-9.12	100.84	112.60
8	G	5	ARG	CB-CA-C	9.10	125.75	109.64
2	B	156	PHE	CA-CB-CG	-9.06	104.74	113.80
10	H	43	GLY	CA-C-N	-9.02	106.65	122.26
10	H	43	GLY	C-N-CA	-9.02	106.65	122.26
5	L	61	C	N1-C1'-C2'	9.02	125.53	112.00
7	E	9	ALA	CB-CA-C	-9.01	95.37	110.68
8	G	45	LEU	CA-C-N	8.97	132.29	120.28
8	G	45	LEU	C-N-CA	8.97	132.29	120.28
7	E	57	ASN	O-C-N	-8.95	111.03	121.32
2	B	528	PHE	CB-CA-C	-8.93	96.86	110.88
1	A	226	LYS	N-CA-CB	8.92	123.44	110.06
10	H	16	ARG	N-CA-C	-8.86	91.92	110.80
5	L	74	C	O4'-C1'-C2'	-8.86	98.74	107.60
1	A	273	GLN	N-CA-C	8.79	129.51	110.80
1	A	290	HIS	CE1-NE2-CD2	-8.76	100.25	109.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	373	LYS	N-CA-C	-8.75	101.44	112.90
1	A	141	ASP	CA-CB-CG	8.73	121.33	112.60
5	L	13	U	P-O3'-C3'	8.69	133.24	120.20
1	A	274	ASP	CA-CB-CG	-8.68	103.92	112.60
10	H	33	GLY	N-CA-C	8.63	129.94	112.34
5	L	13	U	O4'-C1'-N1	8.56	121.34	108.50
10	H	42	VAL	O-C-N	-8.53	111.90	122.57
10	H	42	VAL	CA-C-O	-8.53	110.11	120.78
8	G	180	PRO	N-CA-C	8.53	130.04	112.47
10	H	45	ASP	CA-C-N	8.49	131.96	121.85
10	H	45	ASP	C-N-CA	8.49	131.96	121.85
8	G	33	VAL	CA-C-O	-8.46	110.27	121.02
1	A	157	VAL	CB-CA-C	8.45	123.19	111.70
1	A	180	ASP	N-CA-CB	8.44	124.76	110.49
3	J	1181	U	C4'-C3'-C2'	-8.44	94.16	102.60
10	H	44	GLU	N-CA-CB	-8.42	97.99	110.53
8	G	72	ASP	N-CA-CB	-8.41	98.57	110.51
1	A	246	PHE	N-CA-CB	8.34	123.75	110.23
5	L	42	C	P-O3'-C3'	8.32	132.68	120.20
10	H	41	LYS	CB-CA-C	-8.28	93.95	110.42
1	A	338	LEU	O-C-N	-8.26	112.78	122.20
2	B	350	ALA	N-CA-C	-8.23	98.29	110.23
1	A	17	VAL	CB-CA-C	-8.23	101.95	111.09
3	J	160	C	P-O3'-C3'	8.21	132.52	120.20
1	A	303	LYS	CA-C-N	8.20	131.94	120.29
1	A	303	LYS	C-N-CA	8.20	131.94	120.29
8	G	36	GLN	CA-CB-CG	8.19	130.48	114.10
9	C	85	ARG	CA-C-N	8.18	128.18	119.76
9	C	85	ARG	C-N-CA	8.18	128.18	119.76
10	H	88	PRO	N-CA-CB	8.15	110.99	103.08
4	K	2845	A	N1-C6-N6	8.14	143.02	118.60
5	L	74	C	P-O3'-C3'	8.13	132.40	120.20
1	A	325	HIS	ND1-CE1-NE2	8.10	116.50	108.40
8	G	72	ASP	CA-CB-CG	-8.10	104.50	112.60
4	K	1236	G	P-O3'-C3'	8.09	132.33	120.20
1	A	290	HIS	CG-CD2-NE2	8.08	115.28	107.20
1	A	158	THR	N-CA-CB	8.08	123.69	110.69
8	G	35	SER	N-CA-CB	8.08	123.14	110.46
1	A	320	THR	CA-C-N	8.07	131.75	120.29
1	A	320	THR	C-N-CA	8.07	131.75	120.29
3	J	448	C	C5'-C4'-C3'	8.07	128.10	116.00
1	A	90	ASP	CA-C-N	8.06	133.50	120.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	90	ASP	C-N-CA	8.06	133.50	120.60
1	A	230	TYR	CA-C-N	8.05	130.91	120.44
1	A	230	TYR	C-N-CA	8.05	130.91	120.44
8	G	18	TYR	N-CA-C	8.04	120.04	111.28
10	H	33	GLY	CA-C-N	8.02	128.71	120.04
10	H	33	GLY	C-N-CA	8.02	128.71	120.04
2	B	336	PHE	CA-CB-CG	-7.99	105.81	113.80
1	A	16	ALA	O-C-N	-7.99	115.31	123.29
2	B	564	PHE	CA-CB-CG	-7.96	105.84	113.80
2	B	289	ASP	CA-CB-CG	-7.94	104.66	112.60
3	J	1765	A	P-O5'-C5'	-7.94	108.99	120.90
4	K	2845	A	C6-N1-C2	7.94	142.41	118.60
8	G	179	SER	C-N-CD	-7.94	92.46	125.00
1	A	374	TYR	N-CA-CB	-7.93	97.69	111.17
1	A	279	LYS	N-CA-C	-7.88	103.65	113.18
6	F	97	PHE	N-CA-CB	-7.88	100.17	110.17
3	J	1764	C	P-O3'-C3'	7.88	132.01	120.20
5	L	41	G	C1'-O4'-C4'	-7.85	102.05	109.90
10	H	95	ASP	N-CA-CB	7.81	123.69	110.49
1	A	160	SER	CB-CA-C	-7.80	97.83	110.08
1	A	350	LEU	CB-CA-C	-7.79	99.96	110.79
1	A	241	ASP	CA-CB-CG	7.78	120.38	112.60
5	L	68	C	N1-C1'-C2'	7.78	123.66	112.00
5	L	12	U	C4'-C3'-C2'	-7.77	94.83	102.60
3	J	578	U	C5'-C4'-C3'	7.76	126.84	115.20
3	J	1767	G	C2'-C3'-O3'	7.74	121.10	109.50
1	A	323	VAL	CA-C-N	7.73	131.14	120.63
1	A	323	VAL	C-N-CA	7.73	131.14	120.63
1	A	141	ASP	N-CA-CB	7.68	123.47	110.49
2	B	67	PHE	CA-CB-CG	-7.67	106.14	113.80
3	J	578	U	C4'-C3'-O3'	-7.66	97.91	109.40
8	G	33	VAL	CB-CA-C	-7.64	100.75	111.21
3	J	152	U	O3'-P-O5'	-7.63	92.55	104.00
1	A	70	ILE	N-CA-C	-7.60	105.61	111.62
1	A	318	LEU	CB-CA-C	-7.60	97.55	110.16
1	A	285	ASP	CA-C-N	7.59	130.44	120.28
1	A	285	ASP	C-N-CA	7.59	130.44	120.28
4	K	3024	A	P-O3'-C3'	7.56	131.54	120.20
3	J	577	G	N9-C1'-C2'	7.54	123.32	112.00
3	J	155	U	P-O3'-C3'	-7.54	108.90	120.20
3	J	1185	U	P-O5'-C5'	7.51	132.16	120.90
1	A	332	ARG	CA-C-N	7.50	130.64	120.44

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	332	ARG	C-N-CA	7.50	130.64	120.44
7	E	57	ASN	N-CA-CB	7.50	123.71	110.37
1	A	165	LYS	N-CA-C	-7.49	104.65	114.31
10	H	22	VAL	CB-CA-C	7.49	123.57	111.29
1	A	173	PRO	N-CA-C	7.49	122.11	110.80
1	A	255	TYR	O-C-N	-7.48	112.64	122.59
10	H	46	ILE	O-C-N	7.47	130.39	122.17
10	H	108	GLU	CA-C-N	-7.47	108.53	121.97
10	H	108	GLU	C-N-CA	-7.47	108.53	121.97
2	B	201	ASP	CA-CB-CG	-7.45	105.15	112.60
1	A	322	LYS	N-CA-CB	7.45	121.29	110.20
8	G	88	PHE	CA-CB-CG	-7.44	106.36	113.80
11	I	9	THR	N-CA-C	-7.42	99.23	110.14
1	A	191	PHE	CA-CB-CG	7.42	121.22	113.80
8	G	46	ARG	N-CA-C	7.41	119.36	111.28
1	A	6	LEU	N-CA-C	-7.41	95.01	110.80
1	A	60	THR	CA-C-N	7.40	135.68	121.54
1	A	60	THR	C-N-CA	7.40	135.68	121.54
2	B	199	PRO	N-CA-C	-7.39	104.62	113.86
5	L	7	A	P-O3'-C3'	7.39	131.28	120.20
1	A	75	ASP	CA-C-N	7.39	130.04	120.44
1	A	75	ASP	C-N-CA	7.39	130.04	120.44
1	A	131	ASN	CA-CB-CG	-7.38	105.22	112.60
1	A	274	ASP	N-CA-CB	7.38	122.95	110.49
8	G	179	SER	O-C-N	7.37	129.80	121.32
8	G	180	PRO	CA-N-CD	-7.37	101.68	112.00
1	A	87	THR	O-C-N	-7.36	113.82	122.95
4	K	1241	U	P-O5'-C5'	7.35	131.93	120.90
1	A	181	VAL	CA-C-N	7.34	135.56	121.54
1	A	181	VAL	C-N-CA	7.34	135.56	121.54
2	B	182	GLY	N-CA-C	-7.34	97.37	112.34
10	H	106	LEU	CA-C-N	7.33	135.53	121.54
10	H	106	LEU	C-N-CA	7.33	135.53	121.54
8	G	4	ILE	CA-C-N	7.31	131.57	120.82
8	G	4	ILE	C-N-CA	7.31	131.57	120.82
10	H	39	PRO	O-C-N	-7.26	112.84	122.64
1	A	90	ASP	CA-CB-CG	-7.25	105.35	112.60
9	C	86	PRO	N-CA-CB	7.22	109.73	103.31
1	A	12	ASN	CA-C-N	7.22	130.28	120.54
1	A	12	ASN	C-N-CA	7.22	130.28	120.54
7	E	9	ALA	O-C-N	7.21	129.76	122.12
1	A	334	GLU	CB-CA-C	-7.20	99.57	110.88

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	66	C	O4'-C1'-C2'	-7.20	100.40	107.60
11	I	91	VAL	N-CA-C	7.20	119.44	108.71
4	K	2267	C	P-O5'-C5'	-7.20	110.10	120.90
5	L	12	U	P-O5'-C5'	-7.20	110.10	120.90
4	K	1241	U	C5'-C4'-C3'	-7.19	105.21	116.00
2	B	572	PHE	CA-C-N	7.19	135.27	121.54
2	B	572	PHE	C-N-CA	7.19	135.27	121.54
10	H	21	GLU	CA-CB-CG	7.18	128.46	114.10
2	B	572	PHE	CA-CB-CG	-7.17	106.63	113.80
1	A	184	PHE	CA-C-N	7.16	130.45	120.29
1	A	184	PHE	C-N-CA	7.16	130.45	120.29
3	J	557	G	O3'-P-O5'	7.15	114.73	104.00
2	B	439	ARG	CA-C-N	-7.15	114.93	123.44
2	B	439	ARG	C-N-CA	-7.15	114.93	123.44
3	J	1181	U	O4'-C1'-C2'	-7.15	100.45	107.60
1	A	206	ASP	CA-CB-CG	7.14	119.74	112.60
5	L	11	U	N1-C1'-C2'	-7.14	101.29	112.00
2	B	43	PRO	N-CA-CB	7.13	106.91	102.92
1	A	47	PHE	CB-CG-CD1	7.12	132.81	120.70
11	I	49	LEU	CA-C-N	-7.11	112.67	119.85
11	I	49	LEU	C-N-CA	-7.11	112.67	119.85
1	A	61	ASP	CA-CB-CG	7.10	119.70	112.60
1	A	254	GLY	O-C-N	-7.10	113.47	122.70
10	H	70	ALA	O-C-N	-7.09	113.16	122.59
1	A	93	GLY	CA-C-N	7.09	129.78	120.28
1	A	93	GLY	C-N-CA	7.09	129.78	120.28
8	G	65	GLY	O-C-N	7.09	128.99	122.19
10	H	136	ALA	CA-C-N	7.08	133.52	122.26
10	H	136	ALA	C-N-CA	7.08	133.52	122.26
1	A	132	GLU	CB-CA-C	7.07	118.68	109.28
1	A	277	TYR	N-CA-C	7.06	125.84	110.80
1	A	276	LYS	N-CA-CB	-7.05	98.99	110.42
10	H	74	VAL	CA-CB-CG1	7.04	122.37	110.40
10	H	15	LEU	CA-C-N	7.04	134.98	121.54
10	H	15	LEU	C-N-CA	7.04	134.98	121.54
1	A	279	LYS	CA-C-N	7.01	130.25	120.29
1	A	279	LYS	C-N-CA	7.01	130.25	120.29
1	A	273	GLN	CA-C-N	7.01	134.92	121.54
1	A	273	GLN	C-N-CA	7.01	134.92	121.54
5	L	8	U	O4'-C1'-C2'	-6.99	100.61	107.60
8	G	90	ASN	CA-C-N	6.99	130.16	120.65
8	G	90	ASN	C-N-CA	6.99	130.16	120.65

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	274	ASP	O-C-N	-6.97	113.33	122.59
5	L	13	U	P-O5'-C5'	-6.94	110.49	120.90
8	G	199	SER	CA-C-O	-6.94	109.00	120.80
1	A	209	LYS	CB-CA-C	6.94	121.50	109.15
9	C	226	ILE	CA-C-O	-6.94	109.01	120.80
5	L	26	G	O4'-C1'-C2'	6.92	114.52	107.60
3	J	1765	A	C1'-O4'-C4'	-6.92	102.78	109.70
1	A	158	THR	CA-C-O	6.92	128.04	120.71
5	L	75	A	N9-C1'-C2'	-6.91	103.64	114.00
1	A	275	THR	CA-CB-CG2	6.90	122.23	110.50
12	D	109	LYS	CA-C-N	6.90	129.85	120.54
12	D	109	LYS	C-N-CA	6.90	129.85	120.54
5	L	44	A	P-O3'-C3'	6.90	130.55	120.20
10	H	9	GLU	N-CA-CB	-6.90	99.79	111.31
2	B	205	TYR	CA-CB-CG	-6.89	101.49	113.90
1	A	190	LYS	N-CA-CB	6.89	120.25	110.12
10	H	18	VAL	CA-C-N	6.89	134.92	121.41
10	H	18	VAL	C-N-CA	6.89	134.92	121.41
1	A	362	LEU	CA-C-N	6.88	130.06	120.29
1	A	362	LEU	C-N-CA	6.88	130.06	120.29
3	J	1632	C	O4'-C1'-N1	6.88	118.82	108.50
1	A	29	PHE	CA-CB-CG	6.88	120.67	113.80
4	K	1243	G	C3'-C2'-C1'	-6.87	94.44	101.30
8	G	189	GLN	N-CA-C	6.87	118.99	108.07
8	G	19	LEU	N-CA-CB	6.86	120.21	110.12
1	A	362	LEU	O-C-N	-6.86	114.20	122.22
5	L	71	A	P-O3'-C3'	6.84	130.47	120.20
4	K	1238	C	C4'-C3'-C2'	-6.84	95.76	102.60
1	A	337	LYS	CB-CA-C	-6.83	100.06	110.92
2	B	36	LYS	CA-C-N	6.83	134.90	121.58
2	B	36	LYS	C-N-CA	6.83	134.90	121.58
10	H	34	PRO	N-CA-CB	-6.83	96.72	103.20
8	G	53	MET	N-CA-CB	-6.82	99.26	110.52
1	A	235	HIS	ND1-CE1-NE2	6.82	115.22	108.40
10	H	89	PRO	N-CA-CB	6.80	110.39	103.25
10	H	105	GLN	CA-C-N	6.79	134.52	121.54
10	H	105	GLN	C-N-CA	6.79	134.52	121.54
1	A	339	MET	CB-CA-C	-6.79	100.18	110.90
8	G	60	ARG	CA-C-N	6.79	131.46	120.60
8	G	60	ARG	C-N-CA	6.79	131.46	120.60
2	B	245	PHE	CA-CB-CG	-6.78	107.02	113.80
5	L	28	G	O3'-P-O5'	6.78	114.17	104.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	H	7	PRO	N-CA-CB	6.78	110.45	103.00
8	G	55	LYS	CB-CA-C	-6.77	96.94	110.42
7	E	57	ASN	CA-C-O	-6.77	110.88	120.16
8	G	83	ASN	CB-CA-C	6.77	123.88	110.42
8	G	114	VAL	N-CA-C	-6.76	99.97	108.89
2	B	311	ARG	NE-CZ-NH1	-6.75	114.75	121.50
1	A	172	MET	CG-SD-CE	6.75	115.75	100.90
1	A	22	PRO	N-CA-CB	6.74	109.61	103.34
5	L	62	C	O4'-C1'-C2'	-6.73	100.87	107.60
10	H	78	SER	CA-C-N	6.73	134.39	121.54
10	H	78	SER	C-N-CA	6.73	134.39	121.54
1	A	157	VAL	O-C-N	6.72	128.94	122.69
3	J	1761	U	C2'-C3'-O3'	6.72	119.58	109.50
8	G	39	HIS	ND1-CE1-NE2	6.72	115.12	108.40
2	B	134	PHE	CA-CB-CG	-6.72	107.08	113.80
1	A	153	HIS	N-CA-CB	6.71	121.31	110.77
8	G	115	ALA	CA-C-N	6.71	126.33	119.56
8	G	115	ALA	C-N-CA	6.71	126.33	119.56
1	A	186	GLU	CB-CA-C	-6.70	99.45	110.85
3	J	1767	G	C4'-C3'-O3'	6.68	119.43	109.40
1	A	375	PRO	CA-C-O	-6.64	114.29	121.27
8	G	39	HIS	CE1-NE2-CD2	-6.64	102.36	109.00
1	A	259	ILE	N-CA-C	6.64	118.19	110.62
8	G	145	ILE	N-CA-CB	6.62	118.55	111.00
5	L	28	G	C4'-C3'-C2'	-6.61	95.99	102.60
10	H	138	SER	N-CA-C	-6.61	105.75	113.88
5	L	64	G	N9-C1'-C2'	6.61	121.91	112.00
6	F	174	LYS	CA-C-O	-6.60	111.94	120.00
6	F	91	ARG	NE-CZ-NH2	6.60	125.14	119.20
1	A	225	ASP	CA-C-N	6.60	129.42	120.38
1	A	225	ASP	C-N-CA	6.60	129.42	120.38
8	G	98	ASN	CA-CB-CG	-6.59	106.01	112.60
7	E	10	ARG	N-CA-CB	-6.59	100.36	110.44
4	K	3025	C	P-O5'-C5'	-6.57	111.05	120.90
8	G	42	ARG	CD-NE-CZ	-6.56	115.22	124.40
1	A	135	ASN	CA-CB-CG	6.56	119.16	112.60
1	A	383	ASP	CA-CB-CG	6.54	119.14	112.60
10	H	58	VAL	CA-CB-CG2	6.54	121.51	110.40
1	A	334	GLU	N-CA-CB	6.53	119.48	110.01
3	J	559	C	C4'-C3'-C2'	-6.53	96.07	102.60
4	K	3033	A	O3'-P-O5'	-6.53	94.20	104.00
10	H	37	LEU	CA-C-O	-6.52	113.62	121.32

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	47	U	N1-C1'-C2'	-6.51	104.24	114.00
1	A	163	ILE	N-CA-CB	6.50	120.09	111.64
10	H	141	CYS	N-CA-CB	6.49	121.45	110.49
10	H	63	LYS	N-CA-CB	6.48	120.24	110.19
1	A	356	HIS	CA-C-N	6.47	129.28	120.54
1	A	356	HIS	C-N-CA	6.47	129.28	120.54
10	H	28	LEU	O-C-N	-6.47	113.68	122.36
10	H	28	LEU	CD1-CG-CD2	-6.47	96.56	110.80
12	D	45	ALA	N-CA-C	-6.46	104.23	111.28
2	B	456	ARG	CA-C-N	6.46	131.36	120.64
2	B	456	ARG	C-N-CA	6.46	131.36	120.64
2	B	600	TYR	CA-CB-CG	-6.46	102.27	113.90
1	A	325	HIS	CA-CB-CG	6.45	120.25	113.80
10	H	24	ALA	CA-C-N	6.43	133.83	121.54
10	H	24	ALA	C-N-CA	6.43	133.83	121.54
1	A	192	TYR	CA-C-N	6.43	128.90	120.28
1	A	192	TYR	C-N-CA	6.43	128.90	120.28
8	G	28	VAL	CA-C-N	6.43	134.01	121.41
8	G	28	VAL	C-N-CA	6.43	134.01	121.41
5	L	6	G	N9-C1'-C2'	6.43	121.64	112.00
8	G	133	THR	CA-C-N	6.43	129.53	120.28
8	G	133	THR	C-N-CA	6.43	129.53	120.28
3	J	1185	U	P-O3'-C3'	6.42	129.84	120.20
1	A	307	LYS	CA-C-O	-6.41	113.63	120.42
1	A	176	LYS	N-CA-CB	6.41	120.16	110.42
10	H	72	SER	N-CA-CB	6.40	121.30	110.49
1	A	188	THR	CA-C-N	6.39	128.84	120.28
1	A	188	THR	C-N-CA	6.39	128.84	120.28
10	H	46	ILE	CA-CB-CG1	6.38	121.24	110.40
9	C	147	LEU	N-CA-C	6.37	121.88	114.62
10	H	89	PRO	CA-C-N	6.37	133.70	121.54
10	H	89	PRO	C-N-CA	6.37	133.70	121.54
1	A	224	MET	N-CA-C	-6.36	104.43	111.36
5	L	13	U	C5'-C4'-C3'	-6.36	106.46	116.00
5	L	38	C	O4'-C1'-C2'	-6.36	101.24	107.60
10	H	138	SER	CA-C-O	-6.35	112.06	119.24
10	H	76	SER	CA-C-N	6.35	133.66	121.54
10	H	76	SER	C-N-CA	6.35	133.66	121.54
1	A	76	MET	N-CA-CB	-6.33	100.82	110.01
1	A	235	HIS	CA-C-N	6.33	132.38	122.26
1	A	235	HIS	C-N-CA	6.33	132.38	122.26
10	H	43	GLY	CA-C-O	-6.32	109.58	120.57

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	382	ASP	N-CA-CB	6.32	121.16	110.49
3	J	577	G	C4'-C3'-O3'	-6.29	103.57	113.00
10	H	77	ALA	O-C-N	-6.29	114.23	122.59
5	L	10	G	C5'-C4'-C3'	-6.27	106.59	116.00
8	G	179	SER	CA-C-N	6.27	127.68	119.84
8	G	179	SER	C-N-CA	6.27	127.68	119.84
2	B	459	ASP	CA-CB-CG	-6.27	106.33	112.60
3	J	578	U	C1'-O4'-C4'	6.25	115.95	109.70
10	H	34	PRO	CB-CA-C	-6.25	101.60	111.04
6	F	120	ASP	N-CA-CB	6.24	119.52	109.28
7	E	59	GLY	CA-C-O	-6.24	112.59	121.52
1	A	17	VAL	N-CA-CB	6.24	119.78	112.35
5	L	13	U	C2'-C3'-O3'	6.24	123.06	113.70
6	F	4	ILE	N-CA-C	6.24	116.41	110.42
1	A	122	PHE	CA-CB-CG	6.22	120.03	113.80
1	A	169	GLU	N-CA-CB	6.22	121.01	110.49
1	A	233	GLU	N-CA-CB	6.22	119.09	110.07
3	J	1644	C	P-O5'-C5'	6.22	130.23	120.90
10	H	7	PRO	CA-N-CD	-6.22	103.29	112.00
3	J	1636	C	O4'-C4'-C3'	-6.22	99.88	106.10
8	G	177	ASN	CA-C-N	6.22	130.50	121.80
8	G	177	ASN	C-N-CA	6.22	130.50	121.80
5	L	40	U	O4'-C1'-N1	6.21	117.82	108.50
1	A	59	SER	CA-C-N	6.21	133.39	121.54
1	A	59	SER	C-N-CA	6.21	133.39	121.54
4	K	1236	G	C3'-C2'-C1'	-6.21	95.30	101.50
8	G	88	PHE	N-CA-C	-6.20	99.61	109.59
8	G	144	LYS	N-CA-C	-6.18	99.58	108.60
1	A	329	ILE	CA-C-N	6.18	133.34	121.54
1	A	329	ILE	C-N-CA	6.18	133.34	121.54
5	L	19	U	P-O5'-C5'	6.17	130.16	120.90
3	J	1648	A	C5'-C4'-C3'	-6.17	106.75	116.00
9	C	129	VAL	CA-C-N	6.16	126.48	119.83
9	C	129	VAL	C-N-CA	6.16	126.48	119.83
2	B	435	PHE	CA-CB-CG	-6.16	107.64	113.80
4	K	3030	G	O4'-C1'-N9	6.15	117.73	108.50
3	J	154	G	P-O3'-C3'	6.15	129.42	120.20
3	J	448	C	N1-C1'-C2'	6.15	121.22	112.00
2	B	440	GLY	N-CA-C	-6.15	106.60	113.79
2	B	569	ASN	CA-CB-CG	-6.14	106.46	112.60
8	G	55	LYS	CA-C-N	6.14	129.65	120.31
8	G	55	LYS	C-N-CA	6.14	129.65	120.31

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	H	10	VAL	O-C-N	-6.14	114.89	122.57
12	D	107	GLN	CA-C-N	6.12	128.49	120.28
12	D	107	GLN	C-N-CA	6.12	128.49	120.28
1	A	363	ASP	CA-CB-CG	6.12	118.72	112.60
5	L	16	U	P-O3'-C3'	6.12	129.38	120.20
3	J	1648	A	O5'-C5'-C4'	-6.12	102.32	111.50
7	E	8	LEU	N-CA-C	-6.12	105.77	113.72
5	L	67	G	O3'-P-O5'	6.11	113.16	104.00
9	C	38	GLY	N-CA-C	6.10	119.87	112.49
2	B	311	ARG	NE-CZ-NH2	6.10	124.69	119.20
10	H	74	VAL	CA-C-O	-6.10	111.78	119.95
10	H	74	VAL	O-C-N	6.08	128.04	121.10
3	J	45	U	C2-N1-C1'	6.08	135.95	117.70
5	L	47	U	O4'-C1'-C2'	-6.08	99.72	105.80
8	G	132	LYS	CA-C-N	6.08	129.55	120.31
8	G	132	LYS	C-N-CA	6.08	129.55	120.31
10	H	55	GLY	N-CA-C	6.08	127.58	113.18
5	L	12	U	C5'-C4'-C3'	-6.08	106.89	116.00
1	A	159	SER	CA-C-O	-6.06	111.84	120.51
10	H	74	VAL	C-N-CD	-6.06	100.16	125.00
5	L	20	C	O4'-C1'-C2'	-6.06	101.54	107.60
10	H	114	ARG	N-CA-C	-6.06	105.85	113.18
1	A	30	THR	N-CA-C	6.05	117.55	111.07
1	A	331	GLN	O-C-N	-6.05	114.54	122.59
3	J	1751	C	O4'-C1'-N1	6.05	117.57	108.50
8	G	52	LEU	CA-C-N	6.05	131.66	122.65
8	G	52	LEU	C-N-CA	6.05	131.66	122.65
1	A	345	ASN	N-CA-C	-6.04	106.89	114.56
10	H	88	PRO	CB-CG-CD	-6.04	86.77	106.10
1	A	340	ASP	CA-C-O	6.04	127.16	120.82
5	L	17	G	C3'-C2'-C1'	6.04	107.54	101.50
1	A	95	SER	N-CA-C	-6.03	101.00	109.69
10	H	29	ALA	CA-C-O	-6.03	111.90	120.16
4	K	3025	C	O5'-C5'-C4'	-6.02	102.47	111.50
1	A	276	LYS	O-C-N	-6.02	113.48	122.39
4	K	1241	U	C4'-C3'-O3'	-6.01	103.98	113.00
8	G	124	VAL	CB-CA-C	6.01	121.15	111.29
1	A	180	ASP	CA-C-N	6.00	132.78	121.97
1	A	180	ASP	C-N-CA	6.00	132.78	121.97
5	L	40	U	O3'-P-O5'	6.00	113.00	104.00
1	A	129	LEU	N-CA-C	-6.00	105.94	113.20
7	E	10	ARG	CA-C-N	-6.00	112.14	121.02

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	E	10	ARG	C-N-CA	-6.00	112.14	121.02
3	J	559	C	O4'-C1'-N1	6.00	117.50	108.50
1	A	133	ALA	N-CA-CB	6.00	120.62	110.49
2	B	22	ARG	N-CA-C	-5.99	98.04	110.80
10	H	104	ILE	N-CA-CB	5.99	121.11	111.23
8	G	55	LYS	CB-CG-CD	5.99	125.07	111.30
5	L	73	C	O4'-C1'-C2'	-5.98	101.62	107.60
4	K	2845	A	C5-C6-N1	-5.97	99.78	117.70
10	H	21	GLU	N-CA-CB	-5.97	100.40	110.49
10	H	46	ILE	N-CA-C	5.97	120.40	113.42
10	H	135	THR	O-C-N	-5.96	114.64	122.39
7	E	9	ALA	CA-C-O	5.96	127.06	120.63
1	A	246	PHE	CA-CB-CG	-5.95	107.85	113.80
8	G	77	LEU	N-CA-C	-5.95	96.65	109.81
4	K	3030	G	O4'-C4'-C3'	5.95	109.95	104.00
4	K	2256	A	O3'-P-O5'	-5.94	95.09	104.00
4	K	3026	G	O4'-C4'-C3'	-5.93	98.07	104.00
1	A	92	SER	O-C-N	-5.93	114.28	122.46
2	B	441	GLN	N-CA-C	-5.93	104.76	112.23
5	L	50	G	O4'-C1'-C2'	5.92	113.52	107.60
11	I	90	GLY	CA-C-N	-5.92	114.44	122.91
11	I	90	GLY	C-N-CA	-5.92	114.44	122.91
1	A	62	LEU	N-CA-C	-5.92	98.19	110.80
1	A	97	VAL	CA-C-N	5.92	132.84	121.54
1	A	97	VAL	C-N-CA	5.92	132.84	121.54
4	K	2251	G	P-O5'-C5'	5.92	129.78	120.90
10	H	90	ARG	NE-CZ-NH2	5.92	124.52	119.20
1	A	137	GLU	N-CA-C	-5.92	105.31	113.18
6	F	119	GLY	CA-C-N	5.92	130.66	121.26
6	F	119	GLY	C-N-CA	5.92	130.66	121.26
2	B	33	LYS	N-CA-CB	5.91	118.80	110.12
5	L	22	G	O4'-C1'-C2'	5.91	113.51	107.60
1	A	177	ARG	CA-C-N	5.90	132.81	121.54
1	A	177	ARG	C-N-CA	5.90	132.81	121.54
1	A	238	LYS	CA-C-N	5.90	129.31	122.35
1	A	238	LYS	C-N-CA	5.90	129.31	122.35
5	L	28	G	O4'-C1'-N9	5.89	117.33	108.50
1	A	81	LEU	CA-C-O	5.88	126.71	120.36
1	A	47	PHE	CB-CG-CD2	-5.88	110.70	120.70
8	G	12	PHE	CB-CA-C	-5.88	101.03	110.79
2	B	365	ASP	N-CA-C	-5.88	107.10	114.56
11	I	61	THR	N-CA-C	-5.88	100.41	109.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	27	G	O3'-P-O5'	5.87	112.81	104.00
1	A	173	PRO	CA-C-O	-5.87	114.34	121.03
1	A	228	PHE	CA-CB-CG	-5.86	107.94	113.80
8	G	58	MET	CB-CA-C	-5.85	101.69	110.88
1	A	36	ASP	N-CA-C	-5.84	101.08	110.14
1	A	263	LEU	N-CA-C	5.84	121.01	111.37
8	G	55	LYS	N-CA-CB	5.84	120.36	110.49
2	B	409	ASP	CA-CB-CG	-5.84	106.76	112.60
10	H	27	ALA	CA-C-N	5.83	132.39	122.36
10	H	27	ALA	C-N-CA	5.83	132.39	122.36
8	G	26	PHE	N-CA-CB	5.83	121.05	111.08
3	J	1767	G	P-O3'-C3'	5.83	128.94	120.20
3	J	558	U	O5'-C5'-C4'	5.81	120.21	111.50
1	A	228	PHE	CA-C-N	5.80	128.52	120.63
1	A	228	PHE	C-N-CA	5.80	128.52	120.63
1	A	262	VAL	CA-C-N	5.80	129.52	120.82
1	A	262	VAL	C-N-CA	5.80	129.52	120.82
3	J	1766	A	O4'-C4'-C3'	-5.79	100.31	106.10
6	F	173	ARG	NE-CZ-NH1	-5.79	115.71	121.50
10	H	83	THR	N-CA-C	-5.79	105.92	112.87
1	A	8	LYS	CB-CA-C	-5.78	101.91	111.51
1	A	339	MET	N-CA-CB	5.78	118.46	110.07
8	G	177	ASN	N-CA-CB	5.78	120.25	110.49
1	A	250	HIS	CA-CB-CG	5.77	119.57	113.80
1	A	290	HIS	ND1-CE1-NE2	5.77	114.17	108.40
1	A	207	LYS	N-CA-C	-5.77	105.51	113.18
8	G	36	GLN	N-CA-C	-5.77	105.08	111.36
1	A	385	GLU	N-CA-CB	5.76	116.05	108.96
1	A	81	LEU	O-C-N	-5.76	116.45	123.30
2	B	146	TYR	CA-CB-CG	-5.75	103.54	113.90
8	G	46	ARG	CA-C-N	5.75	126.32	119.94
8	G	46	ARG	C-N-CA	5.75	126.32	119.94
4	K	1238	C	O3'-P-O5'	-5.75	95.38	104.00
1	A	112	VAL	O-C-N	5.75	127.09	121.98
1	A	155	CYS	N-CA-C	-5.74	98.57	110.80
6	F	16	VAL	N-CA-C	5.74	118.21	108.86
8	G	81	LYS	CA-C-O	-5.73	114.93	121.58
1	A	205	PHE	CA-C-N	5.73	131.75	121.15
1	A	205	PHE	C-N-CA	5.73	131.75	121.15
8	G	180	PRO	N-CA-CB	-5.72	97.24	103.25
1	A	40	GLU	N-CA-CB	5.72	120.86	111.08
1	A	357	SER	CB-CA-C	-5.72	101.66	110.81

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	12	U	O4'-C1'-C2'	-5.72	101.88	107.60
1	A	339	MET	CA-C-O	-5.71	114.82	120.70
8	G	23	LYS	CA-C-N	-5.71	114.94	122.99
8	G	23	LYS	C-N-CA	-5.71	114.94	122.99
10	H	75	PRO	CA-N-CD	-5.71	104.00	112.00
8	G	46	ARG	N-CA-CB	-5.71	101.73	110.12
1	A	321	ASP	CA-CB-CG	5.71	118.31	112.60
10	H	29	ALA	N-CA-CB	-5.71	100.22	110.37
6	F	126	VAL	CA-C-N	-5.70	114.06	119.76
6	F	126	VAL	C-N-CA	-5.70	114.06	119.76
3	J	1640	C	O4'-C1'-N1	5.70	117.05	108.50
8	G	86	PHE	CA-CB-CG	5.70	119.50	113.80
10	H	93	LYS	N-CA-CB	-5.70	100.91	110.99
1	A	290	HIS	CA-CB-CG	-5.69	108.11	113.80
3	J	414	C	P-O3'-C3'	-5.69	111.66	120.20
5	L	50	G	O4'-C1'-N9	5.69	117.04	108.50
5	L	37	G	N9-C1'-C2'	5.69	120.53	112.00
1	A	48	THR	CA-C-N	-5.69	114.68	122.87
1	A	48	THR	C-N-CA	-5.69	114.68	122.87
8	G	30	VAL	CA-CB-CG1	5.69	120.07	110.40
7	E	57	ASN	CA-CB-CG	5.68	118.28	112.60
8	G	115	ALA	CA-C-O	-5.68	114.12	119.80
1	A	275	THR	O-C-N	-5.68	115.04	122.59
11	I	36	ILE	N-CA-C	5.67	116.33	108.84
1	A	363	ASP	N-CA-CB	5.67	118.55	110.16
3	J	578	U	P-O5'-C5'	-5.67	112.39	120.90
1	A	245	MET	CB-CA-C	5.66	116.47	109.16
1	A	265	ASN	O-C-N	-5.66	115.62	121.28
3	J	1766	A	P-O3'-C3'	5.66	128.69	120.20
3	J	45	U	C6-N1-C1'	-5.66	104.22	121.20
1	A	376	LEU	CA-C-N	5.66	126.91	119.84
1	A	376	LEU	C-N-CA	5.66	126.91	119.84
6	F	41	ILE	N-CA-C	5.66	121.11	109.34
1	A	293	LYS	N-CA-CB	5.66	118.36	110.56
5	L	75	A	C1'-O4'-C4'	5.65	115.35	109.70
3	J	158	U	P-O5'-C5'	5.65	129.38	120.90
1	A	98	ASP	CA-CB-CG	-5.65	106.95	112.60
1	A	274	ASP	CA-C-N	5.65	132.33	121.54
1	A	274	ASP	C-N-CA	5.65	132.33	121.54
2	B	82	HIS	N-CA-C	5.65	120.04	113.20
2	B	340	ASP	CA-C-N	5.64	128.88	120.31
2	B	340	ASP	C-N-CA	5.64	128.88	120.31

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	LYS	CA-C-O	-5.64	112.83	119.48
5	L	21	A	P-O5'-C5'	5.64	129.36	120.90
3	J	1765	A	C2'-C3'-O3'	5.64	117.96	109.50
1	A	325	HIS	CE1-NE2-CD2	-5.63	103.36	109.00
2	B	68	ASP	CA-C-N	5.63	128.88	120.31
2	B	68	ASP	C-N-CA	5.63	128.88	120.31
4	K	2257	C	O4'-C4'-C3'	-5.63	98.37	104.00
5	L	19	U	C1'-C2'-O2'	5.63	120.24	111.80
10	H	105	GLN	N-CA-C	-5.63	102.43	110.59
8	G	34	SER	N-CA-C	-5.62	102.59	110.35
1	A	167	LYS	CA-C-O	-5.62	114.01	122.38
5	L	24	A	O4'-C1'-C2'	-5.62	101.98	107.60
10	H	57	LYS	CA-C-N	5.62	132.08	121.97
10	H	57	LYS	C-N-CA	5.62	132.08	121.97
10	H	137	GLN	N-CA-C	-5.62	106.42	113.72
1	A	117	ILE	N-CA-CB	5.61	118.74	111.67
2	B	81	ALA	CA-C-N	5.61	133.16	121.94
2	B	81	ALA	C-N-CA	5.61	133.16	121.94
6	F	98	PRO	N-CA-CB	5.61	107.79	103.30
1	A	359	GLY	N-CA-C	-5.60	105.87	113.37
3	J	1765	A	O4'-C1'-N9	5.59	116.58	108.20
5	L	32	U	N1-C1'-C2'	5.59	120.38	112.00
1	A	189	GLU	N-CA-C	-5.59	105.19	111.28
1	A	47	PHE	O-C-N	5.58	130.30	123.21
10	H	25	SER	CA-C-N	5.58	132.16	122.56
10	H	25	SER	C-N-CA	5.58	132.16	122.56
1	A	199	MET	N-CA-CB	-5.58	101.91	110.16
8	G	101	VAL	N-CA-CB	5.58	118.94	110.58
1	A	164	LEU	CB-CA-C	5.57	119.72	109.46
10	H	104	ILE	CA-CB-CG1	5.57	119.88	110.40
9	C	108	VAL	N-CA-CB	5.57	120.42	111.23
1	A	217	GLY	CA-C-O	-5.56	116.61	122.01
7	E	10	ARG	CA-C-O	-5.56	112.55	119.28
1	A	236	ASN	N-CA-CB	-5.56	102.57	110.58
9	C	19	ASP	N-CA-C	-5.56	101.11	109.95
10	H	18	VAL	CA-CB-CG1	5.56	119.85	110.40
3	J	417	A	C2'-C3'-O3'	5.56	117.83	109.50
3	J	578	U	O5'-C5'-C4'	5.56	120.03	111.70
1	A	34	ILE	CB-CA-C	5.55	116.43	111.71
1	A	293	LYS	CA-C-N	5.55	130.29	122.46
1	A	293	LYS	C-N-CA	5.55	130.29	122.46
3	J	1639	C	P-O5'-C5'	-5.55	112.57	120.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	140	SER	CA-C-N	5.54	132.12	121.54
1	A	140	SER	C-N-CA	5.54	132.12	121.54
1	A	361	GLU	CA-C-N	5.54	128.26	120.28
1	A	361	GLU	C-N-CA	5.54	128.26	120.28
5	L	26	G	C1'-O4'-C4'	-5.54	104.36	109.90
5	L	68	C	P-O5'-C5'	5.54	129.21	120.90
5	L	27	G	C4'-C3'-C2'	-5.54	97.06	102.60
1	A	144	ALA	CA-C-O	5.54	128.00	121.58
5	L	58	U	O4'-C1'-N1	5.53	116.80	108.50
2	B	149	GLY	N-CA-C	-5.53	107.69	115.32
2	B	37	LEU	N-CA-C	5.53	119.87	113.18
10	H	39	PRO	CA-N-CD	-5.52	104.27	112.00
4	K	2252	A	P-O5'-C5'	5.52	129.18	120.90
1	A	200	LYS	N-CA-CB	5.52	118.01	110.01
1	A	271	LYS	N-CA-C	-5.52	104.98	112.26
8	G	123	ALA	CA-C-N	5.52	131.90	121.97
8	G	123	ALA	C-N-CA	5.52	131.90	121.97
10	H	61	GLN	N-CA-CB	-5.52	102.64	111.58
8	G	197	PHE	CA-CB-CG	-5.52	108.28	113.80
5	L	25	U	C4'-C3'-C2'	-5.51	97.09	102.60
3	J	578	U	C5'-C4'-O4'	-5.51	100.83	109.10
3	J	160	C	C2'-C3'-O3'	5.51	121.97	113.70
1	A	188	THR	CB-CA-C	5.50	120.21	110.85
1	A	247	PHE	CA-C-N	5.50	129.94	122.90
1	A	247	PHE	C-N-CA	5.50	129.94	122.90
1	A	201	LYS	CA-C-N	5.50	127.59	120.44
1	A	201	LYS	C-N-CA	5.50	127.59	120.44
10	H	95	ASP	CA-CB-CG	5.50	118.10	112.60
8	G	189	GLN	CB-CG-CD	-5.49	103.26	112.60
8	G	101	VAL	CG1-CB-CG2	5.49	122.88	110.80
5	L	47	U	O4'-C1'-N1	5.49	116.43	108.20
2	B	364	GLY	N-CA-C	-5.48	106.96	114.64
3	J	577	G	C2'-C3'-O3'	5.48	121.91	113.70
5	L	22	G	C1'-O4'-C4'	-5.47	104.43	109.90
8	G	58	MET	CG-SD-CE	-5.47	88.85	100.90
1	A	51	LEU	O-C-N	5.47	129.15	122.14
3	J	1764	C	C3'-C2'-C1'	5.47	106.77	101.30
1	A	368	ILE	O-C-N	-5.47	116.74	123.03
10	H	74	VAL	CB-CA-C	5.47	121.31	111.36
4	K	1245	A	O4'-C1'-C2'	5.46	111.26	105.80
1	A	170	TYR	CA-C-O	-5.46	112.70	120.51
1	A	364	GLN	CA-C-N	5.46	131.05	122.49

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	364	GLN	C-N-CA	5.46	131.05	122.49
5	L	5	U	O3'-P-O5'	-5.45	95.82	104.00
3	J	577	G	C5'-C4'-O4'	5.45	117.97	109.80
7	E	59	GLY	N-CA-C	-5.45	101.22	112.34
1	A	64	LYS	CA-C-N	5.45	130.01	122.77
1	A	64	LYS	C-N-CA	5.45	130.01	122.77
5	L	66	C	C3'-C2'-C1'	5.45	106.75	101.30
1	A	183	LYS	CG-CD-CE	5.44	123.81	111.30
1	A	120	GLN	N-CA-CB	5.44	118.74	110.42
10	H	76	SER	CA-C-O	-5.44	115.09	120.80
1	A	188	THR	N-CA-CB	5.43	118.20	110.16
5	L	66	C	P-O3'-C3'	5.43	128.34	120.20
1	A	157	VAL	CA-CB-CG1	5.42	119.62	110.40
4	K	1251	A	O4'-C4'-C3'	5.42	109.42	104.00
1	A	335	TYR	N-CA-C	5.42	117.94	111.71
4	K	3025	C	O4'-C1'-N1	5.42	116.63	108.50
8	G	86	PHE	CA-C-O	-5.42	114.51	120.36
1	A	330	ALA	CA-C-O	-5.42	112.76	120.51
1	A	11	PHE	CB-CA-C	-5.41	99.33	109.72
5	L	40	U	O4'-C1'-C2'	-5.40	102.20	107.60
6	F	178	GLY	N-CA-C	5.40	118.87	110.88
2	B	522	PHE	CA-CB-CG	-5.40	108.40	113.80
2	B	571	THR	CA-C-N	-5.40	115.10	122.87
2	B	571	THR	C-N-CA	-5.40	115.10	122.87
5	L	69	G	N9-C1'-C2'	5.40	120.09	112.00
6	F	121	LYS	N-CA-CB	5.40	118.65	110.28
6	F	175	PHE	CA-CB-CG	-5.40	108.40	113.80
4	K	3025	C	C5'-C4'-C3'	-5.39	107.91	116.00
1	A	270	SER	N-CA-CB	5.39	119.60	110.49
10	H	64	ILE	N-CA-CB	5.38	120.11	111.23
6	F	50	ASN	N-CA-C	5.38	122.26	110.80
8	G	150	ILE	N-CA-C	-5.38	101.79	108.89
2	B	579	PHE	CA-CB-CG	-5.38	108.42	113.80
4	K	2265	C	O4'-C1'-N1	5.37	116.56	108.50
4	K	3026	G	O3'-P-O5'	-5.37	95.94	104.00
1	A	307	LYS	N-CA-CB	5.37	118.11	110.16
8	G	163	ASN	CA-CB-CG	-5.37	107.23	112.60
10	H	90	ARG	NE-CZ-NH1	-5.37	116.14	121.50
1	A	289	LEU	CA-C-N	5.36	127.73	120.44
1	A	289	LEU	C-N-CA	5.36	127.73	120.44
3	J	1437	U	C2-N1-C1'	-5.36	101.61	117.70
3	J	152	U	P-O3'-C3'	-5.36	112.17	120.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	578	U	C3'-C2'-O2'	-5.35	106.57	114.60
1	A	361	GLU	N-CA-CB	5.35	117.82	110.07
5	L	61	C	O4'-C1'-C2'	-5.35	102.25	107.60
1	A	47	PHE	CA-C-O	-5.34	115.05	120.71
1	A	206	ASP	N-CA-C	-5.34	104.48	112.54
8	G	26	PHE	CA-CB-CG	-5.34	108.46	113.80
5	L	26	G	C3'-C2'-C1'	-5.34	95.96	101.30
1	A	52	ASP	CA-CB-CG	5.34	117.94	112.60
2	B	405	ASP	N-CA-C	-5.33	105.38	111.14
5	L	11	U	O4'-C1'-C2'	-5.33	102.27	107.60
10	H	96	LYS	N-CA-C	5.33	118.78	111.54
1	A	174	LYS	O-C-N	5.32	128.63	122.19
3	J	559	C	O4'-C1'-C2'	-5.32	102.28	107.60
1	A	229	GLN	OE1-CD-NE2	5.32	127.92	122.60
1	A	224	MET	CG-SD-CE	-5.31	89.21	100.90
12	D	35	VAL	N-CA-C	5.31	116.13	111.56
2	B	184	VAL	N-CA-C	-5.31	98.29	109.34
2	B	210	GLN	CA-C-N	5.30	132.55	121.94
2	B	210	GLN	C-N-CA	5.30	132.55	121.94
1	A	44	LYS	CB-CA-C	-5.30	100.18	109.71
2	B	125	GLY	N-CA-C	-5.29	108.02	115.32
3	J	1644	C	C4'-C3'-O3'	-5.29	105.06	113.00
3	J	1645	G	C4'-C3'-C2'	-5.29	97.31	102.60
12	D	110	GLN	CG-CD-NE2	-5.29	108.46	116.40
10	H	92	ARG	CD-NE-CZ	-5.29	116.99	124.40
1	A	375	PRO	N-CD-CG	5.28	111.12	103.20
2	B	574	ARG	CD-NE-CZ	-5.28	117.02	124.40
4	K	2254	U	C4'-C3'-C2'	-5.28	97.32	102.60
3	J	1756	A	O4'-C4'-C3'	-5.27	98.73	104.00
5	L	63	C	N1-C1'-C2'	5.27	119.91	112.00
2	B	57	GLY	N-CA-C	-5.27	108.00	115.43
3	J	1751	C	C4'-C3'-O3'	-5.27	105.10	113.00
2	B	200	GLU	N-CA-C	-5.27	105.71	111.82
4	K	1245	A	O3'-P-O5'	-5.27	96.10	104.00
1	A	133	ALA	N-CA-C	5.26	122.01	110.80
3	J	578	U	C2'-C3'-O3'	5.26	117.40	109.50
5	L	25	U	O4'-C1'-N1	5.26	116.39	108.50
8	G	126	THR	N-CA-C	-5.26	105.72	111.82
11	I	17	LEU	CA-C-N	-5.26	115.31	120.52
11	I	17	LEU	C-N-CA	-5.26	115.31	120.52
2	B	580	ARG	N-CA-CB	5.25	115.83	109.74
2	B	74	ASN	CA-CB-CG	-5.25	107.35	112.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	562	ASN	CA-CB-CG	-5.25	107.35	112.60
6	F	151	VAL	CB-CA-C	-5.24	102.70	111.29
1	A	14	GLY	CA-C-N	5.24	131.67	121.41
1	A	14	GLY	C-N-CA	5.24	131.67	121.41
5	L	74	C	C3'-C2'-C1'	5.24	106.53	101.30
2	B	87	TYR	CA-CB-CG	-5.23	104.48	113.90
8	G	52	LEU	N-CA-CB	5.23	120.05	111.31
3	J	155	U	O3'-P-O5'	5.23	111.84	104.00
1	A	139	LYS	N-CA-C	-5.22	107.28	113.97
10	H	40	LYS	N-CA-CB	-5.22	99.81	110.67
1	A	327	ASP	CA-C-N	5.22	131.51	121.54
1	A	327	ASP	C-N-CA	5.22	131.51	121.54
5	L	42	C	N1-C1'-C2'	5.22	119.83	112.00
5	L	23	A	N9-C1'-C2'	5.22	119.83	112.00
8	G	86	PHE	O-C-N	5.22	129.51	123.30
8	G	189	GLN	O-C-N	5.22	128.11	123.41
1	A	60	THR	N-CA-CB	5.22	119.31	110.49
5	L	5	U	O4'-C1'-N1	5.22	116.32	108.50
1	A	351	VAL	N-CA-C	5.21	115.60	107.99
10	H	28	LEU	CA-C-O	5.21	125.13	119.24
5	L	11	U	O4'-C1'-N1	5.21	116.31	108.50
1	A	183	LYS	CB-CA-C	-5.21	100.05	110.42
3	J	555	A	P-O3'-C3'	5.21	128.01	120.20
3	J	1767	G	C4'-C3'-C2'	-5.20	97.40	102.60
5	L	28	G	C1'-O4'-C4'	-5.20	104.70	109.90
5	L	19	U	O4'-C1'-N1	5.20	116.00	108.20
10	H	103	ASN	CA-CB-CG	5.20	117.80	112.60
1	A	103	LYS	N-CA-C	-5.20	99.73	110.80
8	G	43	LYS	N-CA-CB	5.20	117.86	110.06
3	J	459	G	O3'-P-O5'	-5.20	96.20	104.00
10	H	21	GLU	CB-CA-C	-5.19	100.09	110.42
10	H	58	VAL	CA-C-O	-5.19	114.30	120.78
3	J	1637	C	O4'-C1'-N1	5.18	115.98	108.20
3	J	1758	U	C4'-C3'-O3'	-5.18	105.22	113.00
1	A	366	THR	CB-CA-C	5.18	122.06	110.76
5	L	40	U	P-O5'-C5'	5.18	128.67	120.90
5	L	12	U	C4'-C3'-O3'	-5.18	105.23	113.00
2	B	90	ASN	CA-CB-CG	-5.17	107.43	112.60
2	B	459	ASP	CA-C-N	5.17	129.22	120.64
2	B	459	ASP	C-N-CA	5.17	129.22	120.64
1	A	257	GLN	O-C-N	5.17	127.61	122.08
1	A	260	ASN	N-CA-C	-5.17	106.82	113.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	THR	CA-C-N	5.16	129.97	123.10
1	A	162	THR	C-N-CA	5.16	129.97	123.10
8	G	2	GLY	CA-C-N	5.16	126.59	120.14
8	G	2	GLY	C-N-CA	5.16	126.59	120.14
11	I	72	LYS	N-CA-C	5.16	116.91	109.07
5	L	72	G	P-O5'-C5'	5.16	128.63	120.90
2	B	55	CYS	CA-C-N	5.15	129.15	120.29
2	B	55	CYS	C-N-CA	5.15	129.15	120.29
2	B	154	ASN	CA-CB-CG	-5.15	107.45	112.60
6	F	128	VAL	CB-CA-C	-5.15	103.66	111.33
2	B	349	SER	CA-C-N	-5.14	113.41	120.71
2	B	349	SER	C-N-CA	-5.14	113.41	120.71
8	G	121	VAL	N-CA-C	-5.14	101.08	108.48
3	J	458	G	P-O5'-C5'	5.14	128.61	120.90
1	A	209	LYS	N-CA-C	-5.14	107.67	114.04
1	A	355	LEU	N-CA-C	-5.14	106.98	113.20
8	G	91	GLU	CA-C-N	5.14	125.12	120.03
8	G	91	GLU	C-N-CA	5.14	125.12	120.03
1	A	73	ASP	N-CA-CB	5.13	118.76	110.65
10	H	42	VAL	N-CA-C	5.13	120.02	109.34
3	J	160	C	C4'-C3'-C2'	-5.13	97.47	102.60
1	A	277	TYR	O-C-N	-5.13	115.77	122.59
10	H	91	ASP	CB-CA-C	-5.13	100.22	110.42
4	K	3034	C	C2'-C3'-O3'	5.13	121.39	113.70
10	H	42	VAL	CA-CB-CG1	5.13	119.12	110.40
8	G	70	LEU	O-C-N	-5.12	115.43	121.32
6	F	173	ARG	N-CA-CB	5.12	118.43	110.44
1	A	385	GLU	O-C-N	5.12	128.61	123.13
2	B	319	ASP	CA-CB-CG	-5.11	107.49	112.60
4	K	2264	U	C3'-C2'-C1'	-5.11	96.19	101.30
5	L	24	A	P-O3'-C3'	5.11	127.87	120.20
8	G	7	LYS	N-CA-CB	5.11	117.53	110.17
3	J	160	C	C3'-C2'-O2'	5.11	118.37	110.70
2	B	174	ASP	CA-CB-CG	-5.11	107.49	112.60
2	B	450	ASP	N-CA-C	5.11	117.63	111.40
2	B	340	ASP	CA-CB-CG	-5.10	107.50	112.60
8	G	42	ARG	N-CA-C	-5.10	105.80	111.36
4	K	1243	G	P-O3'-C3'	-5.10	112.55	120.20
5	L	32	U	O4'-C1'-N1	5.10	116.15	108.50
8	G	14	LYS	CA-C-N	5.10	127.62	120.28
8	G	14	LYS	C-N-CA	5.10	127.62	120.28
1	A	302	GLU	CB-CA-C	-5.09	102.02	110.68

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	G	88	PHE	N-CA-CB	5.09	118.89	110.69
1	A	58	LYS	N-CA-C	-5.09	102.64	108.49
1	A	216	PRO	CA-C-O	-5.09	115.61	121.11
8	G	38	MET	CA-C-N	5.09	127.10	120.28
8	G	38	MET	C-N-CA	5.09	127.10	120.28
10	H	45	ASP	CA-CB-CG	5.09	117.69	112.60
2	B	379	GLU	CB-CA-C	-5.08	101.65	110.45
1	A	107	PHE	CB-CA-C	-5.08	102.94	110.62
8	G	14	LYS	CB-CA-C	-5.08	102.90	110.88
2	B	548	ASN	CA-CB-CG	-5.08	107.52	112.60
3	J	578	U	O4'-C1'-N1	5.08	115.82	108.20
2	B	49	PHE	CA-C-N	-5.07	116.50	123.14
2	B	49	PHE	C-N-CA	-5.07	116.50	123.14
4	K	1238	C	C1'-O4'-C4'	-5.07	104.83	109.90
4	K	2254	U	C3'-C2'-O2'	5.07	118.31	110.70
3	J	558	U	P-O5'-C5'	5.07	128.50	120.90
1	A	70	ILE	CA-C-O	-5.07	116.29	120.80
1	A	11	PHE	CB-CG-CD2	-5.07	112.09	120.70
1	A	67	ILE	N-CA-CB	-5.07	102.75	110.86
1	A	235	HIS	CE1-NE2-CD2	-5.07	103.93	109.00
10	H	32	ILE	CA-CB-CG1	5.07	119.01	110.40
1	A	83	TYR	CA-CB-CG	-5.06	104.78	113.90
1	A	64	LYS	CG-CD-CE	5.05	122.93	111.30
5	L	9	A	O4'-C1'-C2'	-5.05	100.75	105.80
1	A	156	LEU	CB-CA-C	-5.05	100.37	110.42
2	B	602	PHE	CA-CB-CG	-5.05	108.75	113.80
4	K	1236	G	C2'-C3'-O3'	5.05	117.07	109.50
2	B	95	HIS	CA-CB-CG	-5.04	108.75	113.80
8	G	66	PHE	CA-C-N	5.04	127.04	120.28
8	G	66	PHE	C-N-CA	5.04	127.04	120.28
10	H	75	PRO	CB-CA-C	-5.04	103.25	111.56
1	A	137	GLU	CA-C-N	5.03	131.14	121.54
1	A	137	GLU	C-N-CA	5.03	131.14	121.54
3	J	558	U	N1-C1'-C2'	5.02	119.53	112.00
8	G	99	VAL	N-CA-CB	-5.02	104.67	110.55
1	A	304	GLU	N-CA-C	5.02	116.83	111.36
2	B	582	ARG	O-C-N	-5.02	117.35	123.27
2	B	132	GLY	N-CA-C	-5.01	106.16	114.48
1	A	65	LEU	O-C-N	-5.01	117.51	123.22
1	A	289	LEU	CA-C-O	-5.01	115.54	120.90
8	G	42	ARG	NE-CZ-NH1	5.01	126.51	121.50
1	A	11	PHE	N-CA-C	-5.01	107.17	113.28

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	G	131	GLY	N-CA-C	-5.01	101.31	113.18
1	A	125	PHE	O-C-N	5.01	127.50	122.09
10	H	45	ASP	CB-CA-C	5.01	118.45	110.09
1	A	292	ASN	N-CA-CB	-5.00	102.63	110.44
10	H	78	SER	CB-CA-C	5.00	120.38	110.42
4	K	2260	U	O4'-C1'-N1	5.00	116.00	108.50

There are no chirality outliers.

All (103) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	104	TYR	Sidechain
1	A	113	TYR	Sidechain
1	A	158	THR	Peptide
1	A	170	TYR	Sidechain
1	A	191	PHE	Sidechain
1	A	215	SER	Peptide
1	A	241	ASP	Peptide
1	A	244	GLY	Peptide
1	A	253	THR	Peptide
1	A	254	GLY	Peptide
1	A	268	TYR	Sidechain
1	A	272	LEU	Mainchain
1	A	274	ASP	Peptide
1	A	276	LYS	Peptide
1	A	277	TYR	Mainchain
1	A	311	TYR	Sidechain
1	A	374	TYR	Sidechain
1	A	48	THR	Peptide
2	B	516	HIS	Sidechain
2	B	572	PHE	Mainchain
2	B	580	ARG	Sidechain
2	B	582	ARG	Sidechain
12	D	108	ARG	Sidechain
7	E	10	ARG	Mainchain
7	E	8	LEU	Peptide
6	F	21	LYS	Peptide
6	F	97	PHE	Sidechain
8	G	26	PHE	Sidechain
8	G	30	VAL	Peptide
8	G	42	ARG	Sidechain
8	G	46	ARG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
8	G	49	ALA	Peptide
8	G	5	ARG	Peptide,Mainchain
8	G	52	LEU	Peptide
8	G	55	LYS	Peptide
8	G	60	ARG	Sidechain
8	G	64	ARG	Sidechain
8	G	72	ASP	Peptide,Mainchain
10	H	12	TYR	Sidechain
10	H	16	ARG	Sidechain,Peptide
10	H	28	LEU	Peptide
10	H	29	ALA	Peptide
10	H	30	PRO	Peptide
10	H	33	GLY	Peptide
10	H	39	PRO	Mainchain
10	H	40	LYS	Peptide
10	H	42	VAL	Peptide
10	H	43	GLY	Peptide
10	H	71	ALA	Peptide
10	H	77	ALA	Peptide
3	J	1181	U	Sidechain
3	J	1182	U	Sidechain
3	J	1184	A	Sidechain
3	J	1185	U	Sidechain
3	J	156	A	Sidechain
3	J	1632	C	Sidechain
3	J	1633	A	Sidechain
3	J	1635	A	Sidechain
3	J	1642	G	Sidechain
3	J	1644	C	Sidechain
3	J	1650	U	Sidechain
3	J	1750	A	Sidechain
3	J	1752	U	Sidechain
3	J	1760	G	Sidechain
3	J	1761	U	Sidechain
3	J	1766	A	Sidechain
3	J	415	C	Sidechain
3	J	416	A	Sidechain
3	J	417	A	Sidechain
3	J	556	A	Sidechain
3	J	559	C	Sidechain
3	J	576	G	Sidechain
3	J	577	G	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
3	J	578	U	Sidechain
3	J	588	U	Sidechain
4	K	1236	G	Sidechain
4	K	1237	G	Sidechain
4	K	1242	G	Sidechain
4	K	1243	G	Sidechain
4	K	1245	A	Sidechain
4	K	2250	G	Sidechain
4	K	2251	G	Sidechain
4	K	2254	U	Sidechain
4	K	2257	C	Sidechain
4	K	2258	U	Sidechain
4	K	2260	U	Sidechain
4	K	2261	G	Sidechain
4	K	2262	A	Sidechain
4	K	2264	U	Sidechain
4	K	2266	U	Sidechain
4	K	3024	A	Sidechain
4	K	3026	G	Sidechain
4	K	3030	G	Sidechain
4	K	3033	A	Sidechain
4	K	3034	C	Sidechain
5	L	1	U	Sidechain
5	L	55	C	Sidechain
5	L	56	A	Sidechain
5	L	57	A	Sidechain
5	L	72	G	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3097	0	3157	160	0
2	B	4804	0	4938	1008	0
3	J	4942	0	2531	523	0
4	K	3286	0	1680	562	0
5	L	1595	0	808	25	0
6	F	1519	0	1587	78	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	E	440	0	488	20	0
8	G	1541	0	1584	82	0
9	C	1820	0	1916	120	0
10	H	1037	0	1108	289	0
11	I	1004	0	1048	96	0
12	D	1074	0	1132	24	0
13	B	1	0	0	2	0
14	B	31	0	12	42	0
15	B	16	0	0	24	0
16	B	1	0	0	0	0
All	All	26208	0	21989	2655	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 55.

All (2655) 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)
10:H:85:LEU:CD2	10:H:87:GLU:H	1.02	1.62
2:B:56:ILE:HG12	15:B:703:SF4:S3	1.41	1.60
8:G:43:LYS:HG2	10:H:121:PHE:CD1	1.31	1.58
8:G:107:ALA:HB3	8:G:183:PHE:CE2	1.36	1.57
10:H:85:LEU:CD2	10:H:86:LYS:H	1.10	1.56
2:B:518:LYS:NZ	6:F:115:ARG:CD	1.69	1.52
1:A:386:GLU:HG2	2:B:27:ARG:CD	1.32	1.51
4:K:2932:U:H5''	11:I:41:GLY:CA	1.42	1.50
4:K:3032:A:C4	6:F:170:LYS:HE2	1.47	1.50
1:A:386:GLU:CD	2:B:27:ARG:HG3	1.32	1.49
1:A:187:LYS:CE	5:L:66:C:OP1	1.63	1.45
10:H:109:ILE:CD1	10:H:129:THR:OG1	1.66	1.43
10:H:125:LEU:CG	10:H:129:THR:HG21	1.48	1.43
8:G:46:ARG:HD3	10:H:121:PHE:CZ	1.50	1.42
10:H:89:PRO:CG	10:H:89:PRO:CD	1.91	1.42
10:H:101:SER:OG	10:H:140:GLY:CA	1.64	1.42
10:H:125:LEU:CA	10:H:129:THR:HG22	1.46	1.42
10:H:125:LEU:C	10:H:129:THR:HG22	1.45	1.41
4:K:2932:U:C5'	11:I:41:GLY:HA2	1.50	1.40
10:H:85:LEU:CD2	10:H:87:GLU:N	1.80	1.39
2:B:116:LYS:CE	14:B:702:ATP:PG	2.12	1.37
10:H:85:LEU:HD21	10:H:87:GLU:N	1.35	1.37
2:B:116:LYS:CE	14:B:702:ATP:O3G	1.71	1.37

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:518:LYS:NZ	6:F:115:ARG:HD3	1.04	1.36
4:K:2295:A:N3	11:I:37:ILE:HD12	1.42	1.34
10:H:85:LEU:HD23	10:H:86:LYS:N	1.03	1.34
10:H:125:LEU:CA	10:H:129:THR:CG2	2.06	1.33
2:B:589:GLN:NE2	9:C:58:LYS:CB	1.82	1.32
4:K:3032:A:N3	6:F:170:LYS:HE2	1.41	1.32
3:J:418:G:O2'	9:C:72:ARG:NH2	1.60	1.31
1:A:386:GLU:CG	2:B:27:ARG:CD	2.09	1.30
1:A:386:GLU:CD	2:B:27:ARG:CG	2.03	1.30
1:A:187:LYS:HE2	5:L:66:C:P	1.72	1.29
4:K:1279:C:O5'	8:G:1:MET:HE1	1.17	1.29
4:K:1239:C:H1'	10:H:97:ASN:ND2	1.47	1.29
10:H:125:LEU:HA	10:H:129:THR:CG2	1.61	1.27
4:K:1234:G:H1'	10:H:131:GLU:OE1	1.27	1.26
2:B:116:LYS:HE2	14:B:702:ATP:PG	1.62	1.26
8:G:107:ALA:HB3	8:G:183:PHE:CD2	1.71	1.25
2:B:116:LYS:NZ	14:B:702:ATP:O3G	1.68	1.24
1:A:237:LYS:HE3	4:K:2839:G:O2'	1.10	1.24
10:H:80:LEU:O	10:H:80:LEU:HD23	1.32	1.24
4:K:3032:A:C4	6:F:170:LYS:CE	2.21	1.24
4:K:1279:C:H5''	8:G:1:MET:SD	1.78	1.23
1:A:386:GLU:OE1	2:B:28:SER:OG	1.56	1.22
3:J:420:A:OP2	9:C:74:LYS:HE2	1.14	1.22
8:G:46:ARG:CD	10:H:121:PHE:CZ	2.23	1.22
8:G:46:ARG:CD	10:H:121:PHE:HZ	1.50	1.22
3:J:420:A:P	9:C:96:SER:OG	1.99	1.21
10:H:120:SER:OG	10:H:128:VAL:CG2	1.88	1.21
3:J:1201:G:H3'	3:J:1201:G:N3	1.55	1.20
10:H:109:ILE:HD12	10:H:129:THR:OG1	1.07	1.20
3:J:152:U:O4'	9:C:13:GLN:HG3	1.42	1.20
10:H:109:ILE:CD1	10:H:129:THR:CB	2.19	1.20
2:B:115:GLY:HA2	14:B:702:ATP:O2A	1.39	1.19
10:H:125:LEU:C	10:H:129:THR:CG2	2.15	1.19
4:K:2295:A:C8	11:I:37:ILE:HG21	1.77	1.19
2:B:67:PHE:HE1	15:B:704:SF4:S1	1.64	1.19
10:H:101:SER:OG	10:H:140:GLY:HA3	1.09	1.19
4:K:1279:C:C5'	8:G:1:MET:HE1	1.70	1.18
2:B:571:THR:HG23	2:B:584:ASN:OD1	1.44	1.17
10:H:132:ILE:O	10:H:135:THR:HG22	1.40	1.17
10:H:125:LEU:O	10:H:129:THR:HG22	1.41	1.17
2:B:37:LEU:HB2	2:B:54:LEU:HD12	1.17	1.17

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:574:ARG:HD3	2:B:602:PHE:CB	1.75	1.17
2:B:574:ARG:NH2	2:B:601:PHE:CE2	2.12	1.16
3:J:584:C:O2'	7:E:18:THR:HG21	1.41	1.16
4:K:1279:C:O5'	8:G:1:MET:CE	1.93	1.16
8:G:37:GLN:HG2	8:G:105:VAL:HG11	1.27	1.16
10:H:109:ILE:CG1	10:H:129:THR:OG1	1.93	1.16
10:H:120:SER:OG	10:H:128:VAL:HG22	1.03	1.16
2:B:67:PHE:CE1	15:B:704:SF4:S1	2.39	1.15
8:G:43:LYS:HA	10:H:121:PHE:HE1	1.02	1.15
2:B:396:LYS:HB3	2:B:402:LEU:HD13	1.18	1.15
8:G:43:LYS:CG	10:H:121:PHE:CD1	2.28	1.15
3:J:1273:G:C4'	3:J:1274:C:H5'	1.77	1.14
4:K:1234:G:C1'	10:H:131:GLU:OE1	1.95	1.14
8:G:107:ALA:CB	8:G:183:PHE:CE2	2.28	1.14
2:B:589:GLN:NE2	9:C:58:LYS:HB3	0.88	1.14
3:J:1201:G:H2'	3:J:1202:A:H4'	1.18	1.14
4:K:1239:C:O2'	10:H:97:ASN:HA	1.43	1.14
2:B:571:THR:CG2	2:B:584:ASN:HB2	1.77	1.14
3:J:418:G:C8	9:C:59:GLN:HG2	1.82	1.14
4:K:3027:A:H2'	4:K:3028:G:C8	1.83	1.13
2:B:56:ILE:CG1	15:B:703:SF4:S3	2.36	1.12
3:J:152:U:O4'	9:C:13:GLN:CG	1.96	1.12
8:G:43:LYS:CG	10:H:121:PHE:HD1	1.63	1.11
4:K:2930:A:O2'	11:I:38:ALA:CB	1.99	1.11
2:B:574:ARG:HD3	2:B:602:PHE:HB2	1.16	1.10
2:B:574:ARG:CD	2:B:602:PHE:HB2	1.80	1.10
3:J:1204:A:H3'	3:J:1205:C:H5''	1.20	1.10
4:K:1239:C:C1'	10:H:97:ASN:ND2	2.14	1.10
2:B:227:LEU:HD12	2:B:230:PHE:HE2	1.13	1.09
1:A:84:LYS:NZ	3:J:564:G:OP2	1.82	1.09
10:H:125:LEU:O	10:H:129:THR:CG2	1.99	1.09
2:B:92:PHE:HB3	14:B:702:ATP:H1'	1.26	1.09
4:K:1239:C:HO2'	10:H:97:ASN:HA	1.05	1.09
1:A:237:LYS:CE	4:K:2839:G:O2'	2.00	1.09
4:K:2295:A:C4	11:I:37:ILE:CD1	2.36	1.09
10:H:110:ILE:HG13	10:H:114:ARG:HD2	1.30	1.09
2:B:451:VAL:HG11	2:B:479:VAL:HG21	1.32	1.08
2:B:31:VAL:HG21	2:B:38:CYS:HB3	1.35	1.08
3:J:419:G:O2'	9:C:61:PHE:HZ	1.32	1.08
4:K:3032:A:N3	6:F:170:LYS:CE	2.14	1.08
10:H:109:ILE:HG13	10:H:129:THR:CB	1.83	1.08

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:460:ILE:HD11	2:B:468:LEU:HD11	1.34	1.08
3:J:1273:G:H4'	3:J:1274:C:C5'	1.83	1.08
1:A:385:GLU:CD	2:B:27:ARG:HH12	1.61	1.07
10:H:117:ARG:HG2	10:H:118:ASP:H	1.11	1.07
10:H:125:LEU:CB	10:H:129:THR:HG21	1.83	1.07
2:B:66:PRO:HD2	15:B:704:SF4:S4	1.93	1.07
4:K:2295:A:C2	11:I:37:ILE:HD12	1.91	1.06
1:A:386:GLU:OE1	2:B:27:ARG:HG3	1.54	1.06
4:K:2932:U:C5'	11:I:41:GLY:CA	2.21	1.06
2:B:453:LYS:HG3	2:B:454:PRO:HD3	1.31	1.05
4:K:1239:C:O2'	10:H:97:ASN:CA	2.03	1.05
4:K:2295:A:C4	11:I:37:ILE:HD12	1.91	1.05
1:A:386:GLU:CG	2:B:27:ARG:HD3	1.78	1.05
2:B:574:ARG:CZ	2:B:602:PHE:O	2.04	1.05
2:B:431:ARG:HB2	2:B:461:ILE:HG23	1.34	1.05
2:B:382:VAL:HG23	2:B:535:ALA:HB2	1.33	1.05
2:B:392:THR:HG22	2:B:396:LYS:HE2	1.37	1.05
2:B:544:ILE:HG13	2:B:547:LYS:HB2	1.35	1.05
10:H:85:LEU:CD2	10:H:86:LYS:N	1.84	1.04
2:B:449:THR:HA	2:B:453:LYS:HE2	1.38	1.03
3:J:420:A:OP2	9:C:74:LYS:CE	2.05	1.03
2:B:116:LYS:HE3	14:B:702:ATP:PG	1.92	1.03
2:B:437:LYS:HE2	2:B:480:LEU:HD21	1.40	1.03
8:G:43:LYS:HA	10:H:121:PHE:CE1	1.93	1.03
2:B:435:PHE:CE2	8:G:145:ILE:CD1	2.42	1.02
2:B:115:GLY:N	14:B:702:ATP:O2B	1.91	1.02
3:J:1197:C:H4'	3:J:1197:C:OP1	1.59	1.02
6:F:91:ARG:HH21	6:F:91:ARG:HG3	1.22	1.02
2:B:50:ILE:HD11	15:B:703:SF4:S4	1.99	1.02
2:B:571:THR:HG22	2:B:584:ASN:HB2	1.40	1.02
3:J:1273:G:H4'	3:J:1274:C:H5'	1.02	1.02
4:K:2295:A:O5'	11:I:61:THR:HG21	1.60	1.02
2:B:58:CYS:SG	15:B:703:SF4:FE4	1.52	1.01
10:H:125:LEU:HG	10:H:129:THR:HG21	1.08	1.01
2:B:29:CYS:SG	15:B:703:SF4:FE1	1.52	1.01
2:B:360:LYS:HB3	2:B:406:GLU:HG2	1.43	1.01
2:B:430:VAL:HG11	2:B:460:ILE:HG23	1.38	1.01
2:B:299:SER:HA	14:B:702:ATP:O3'	1.59	1.01
3:J:1204:A:H3'	3:J:1205:C:C5'	1.89	1.01
4:K:1279:C:C5'	8:G:1:MET:CE	2.37	1.01
10:H:109:ILE:CG1	10:H:129:THR:CB	2.38	1.01

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:420:A:OP1	9:C:96:SER:N	1.92	1.01
3:J:418:G:H8	9:C:59:GLN:HG2	1.20	1.01
2:B:518:LYS:NZ	6:F:115:ARG:HD2	1.70	1.00
4:K:2295:A:N3	11:I:37:ILE:CD1	2.22	1.00
4:K:3032:A:C2	6:F:170:LYS:HD2	1.96	1.00
2:B:435:PHE:CD2	8:G:145:ILE:HD12	1.95	1.00
4:K:2295:A:C6	11:I:37:ILE:HB	1.96	1.00
4:K:3022:G:O2'	4:K:3023:U:OP2	1.78	1.00
4:K:2295:A:C5	11:I:37:ILE:HB	1.96	1.00
10:H:125:LEU:HA	10:H:129:THR:HG22	1.12	1.00
2:B:448:GLN:HA	2:B:452:VAL:HG12	1.44	0.99
1:A:232:GLU:HB3	4:K:2851:A:O3'	1.62	0.99
10:H:125:LEU:CG	10:H:129:THR:CG2	2.39	0.99
3:J:420:A:OP1	9:C:96:SER:CB	2.11	0.99
2:B:434:PHE:HE2	2:B:480:LEU:HB2	1.26	0.99
2:B:589:GLN:O	2:B:593:GLU:HG3	1.63	0.98
3:J:1200:G:H4'	3:J:1201:G:OP2	1.61	0.98
1:A:385:GLU:OE1	2:B:27:ARG:NH1	1.96	0.98
2:B:92:PHE:CB	14:B:702:ATP:H1'	1.93	0.98
10:H:85:LEU:HD23	10:H:86:LYS:CA	1.93	0.98
2:B:435:PHE:CE2	8:G:145:ILE:HD11	1.99	0.98
2:B:435:PHE:HE1	2:B:439:ARG:HD3	1.29	0.97
3:J:40:A:H2'	3:J:41:A:H8	1.29	0.97
10:H:132:ILE:O	10:H:135:THR:CG2	2.12	0.97
4:K:1279:C:C5'	8:G:1:MET:SD	2.52	0.97
4:K:3037:U:O2'	4:K:3038:U:H5'	1.63	0.97
2:B:334:LEU:HG	2:B:504:ILE:HD12	1.46	0.97
2:B:106:LEU:HD22	2:B:290:PHE:HD2	1.27	0.96
10:H:125:LEU:HG	10:H:129:THR:CG2	1.95	0.96
2:B:49:PHE:HE1	2:B:89:ALA:HB1	1.31	0.96
3:J:452:A:H2'	3:J:453:U:H5''	1.44	0.96
3:J:44:U:H5'	3:J:45:U:C5	2.01	0.96
2:B:518:LYS:HG3	6:F:100:ASN:HD22	1.30	0.96
4:K:1279:C:P	8:G:1:MET:HE1	2.06	0.96
1:A:187:LYS:HE2	5:L:66:C:OP1	0.78	0.95
4:K:1274:A:H2'	4:K:1275:C:H5''	1.47	0.95
4:K:2847:A:H5'	4:K:2848:G:OP2	1.65	0.95
2:B:144:ILE:HG23	2:B:153:GLN:HG3	1.46	0.95
2:B:529:ILE:HD13	2:B:529:ILE:H	1.27	0.95
1:A:386:GLU:CG	2:B:27:ARG:HG3	1.96	0.95
2:B:191:LEU:HD13	2:B:206:ILE:HD11	1.45	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:1264:G:H2'	4:K:1264:G:OP2	1.67	0.95
1:A:101:VAL:HG21	3:J:1272:U:O3'	1.67	0.95
2:B:31:VAL:HG21	2:B:38:CYS:CB	1.97	0.94
10:H:109:ILE:HG13	10:H:129:THR:HB	1.49	0.94
2:B:434:PHE:HB3	2:B:442:PHE:HZ	1.31	0.94
2:B:261:ALA:HA	2:B:287:LEU:HD21	1.46	0.94
4:K:2285:C:H5	4:K:2286:U:C2	1.85	0.94
4:K:3032:A:C2	6:F:170:LYS:CD	2.51	0.94
4:K:1239:C:O2'	10:H:97:ASN:O	1.84	0.93
4:K:1279:C:H5''	8:G:1:MET:CE	1.98	0.93
2:B:434:PHE:HB3	2:B:442:PHE:CZ	2.01	0.93
4:K:2287:C:O2	4:K:2298:U:O4'	1.85	0.93
2:B:574:ARG:CZ	2:B:601:PHE:CE2	2.52	0.93
2:B:106:LEU:HB3	2:B:290:PHE:CE2	2.03	0.93
4:K:2293:C:H5	4:K:2294:U:H5	1.14	0.93
4:K:1239:C:H1'	10:H:97:ASN:HD21	1.27	0.93
10:H:101:SER:OG	10:H:140:GLY:N	2.01	0.93
2:B:396:LYS:CB	2:B:402:LEU:HD13	1.99	0.92
2:B:447:PHE:CE1	2:B:479:VAL:HG13	2.03	0.92
2:B:227:LEU:HD12	2:B:230:PHE:CE2	2.03	0.92
3:J:1435:G:H4'	3:J:1436:A:OP2	1.70	0.92
4:K:3027:A:H2'	4:K:3028:G:H8	1.24	0.92
4:K:3032:A:N9	6:F:170:LYS:HE2	1.84	0.92
1:A:187:LYS:CE	5:L:66:C:H5''	1.99	0.92
3:J:418:G:C2'	9:C:72:ARG:NH2	2.31	0.92
3:J:40:A:H2'	3:J:41:A:C8	2.04	0.92
4:K:2850:G:H4'	4:K:2850:G:OP1	1.66	0.92
8:G:43:LYS:HG2	10:H:121:PHE:CE1	2.04	0.92
2:B:148:ARG:HH22	3:J:439:U:C3'	1.84	0.91
2:B:334:LEU:HG	2:B:504:ILE:CD1	2.00	0.91
2:B:574:ARG:NE	2:B:602:PHE:O	2.01	0.91
4:K:1239:C:O2'	10:H:97:ASN:C	2.12	0.91
4:K:1278:A:O2'	4:K:1279:C:H6	1.51	0.91
4:K:2833:A:H2'	4:K:2834:G:H5'	1.52	0.91
1:A:152:ALA:H	1:A:172:MET:HE2	1.35	0.91
10:H:120:SER:CB	10:H:128:VAL:HG22	1.99	0.91
2:B:112:ASN:HB3	14:B:702:ATP:O1G	1.71	0.91
1:A:375:PRO:HD2	4:K:1270:A:O4'	1.71	0.91
2:B:468:LEU:HG	2:B:469:SER:H	1.35	0.91
3:J:1196:A:H4'	3:J:1197:C:H5''	1.49	0.91
4:K:1272:C:H2'	4:K:1273:A:O4'	1.71	0.91

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:124:THR:HG23	10:H:125:LEU:H	1.36	0.91
1:A:385:GLU:HA	2:B:27:ARG:NH1	1.86	0.91
2:B:18:PRO:HA	15:B:704:SF4:S3	2.10	0.91
1:A:52:ASP:OD2	3:J:575:C:OP1	1.89	0.90
4:K:2295:A:C4	11:I:37:ILE:HD13	2.05	0.90
2:B:117:SER:OG	13:B:701:MG:MG	1.12	0.90
2:B:381:LEU:HD21	2:B:539:ILE:HG13	1.53	0.90
3:J:1198:G:H3'	3:J:1199:G:C5'	2.00	0.90
1:A:386:GLU:CG	2:B:27:ARG:CG	2.42	0.90
3:J:427:C:H6	3:J:427:C:C5'	1.83	0.90
10:H:120:SER:CB	10:H:128:VAL:CG2	2.49	0.90
1:A:187:LYS:HE3	5:L:66:C:H5''	1.53	0.90
1:A:386:GLU:CG	2:B:27:ARG:HD2	1.99	0.90
4:K:1239:C:O2'	10:H:97:ASN:ND2	2.04	0.90
4:K:2918:G:C2	4:K:2919:A:N7	2.40	0.90
3:J:1190:C:H4'	3:J:1191:U:OP1	1.71	0.90
2:B:242:VAL:HG23	2:B:273:TYR:CD2	2.07	0.90
2:B:435:PHE:CE2	8:G:145:ILE:HD12	2.06	0.90
3:J:152:U:C4'	9:C:13:GLN:HG3	2.02	0.90
6:F:49:ASN:O	6:F:51:GLN:N	2.03	0.90
1:A:364:GLN:OE1	2:B:58:CYS:HA	1.70	0.90
4:K:1273:A:C8	4:K:1274:A:C8	2.60	0.90
4:K:2851:A:H2'	4:K:2852:C:O4'	1.71	0.90
2:B:258:LEU:HD11	2:B:568:LEU:HD11	1.52	0.89
2:B:603:LEU:HG	2:B:604:ASP:H	1.35	0.89
4:K:2295:A:N7	11:I:37:ILE:CG2	2.35	0.89
3:J:1197:C:H5'	3:J:1198:G:OP2	1.71	0.89
4:K:3032:A:N3	6:F:170:LYS:CD	2.35	0.89
2:B:58:CYS:HG	15:B:703:SF4:FE4	0.87	0.89
3:J:1274:C:H6	3:J:1427:A:H62	1.19	0.89
2:B:37:LEU:CB	2:B:54:LEU:HD12	2.00	0.89
3:J:419:G:O2'	9:C:61:PHE:CZ	2.12	0.89
3:J:450:U:H2'	3:J:451:A:C8	2.08	0.89
2:B:451:VAL:CG1	2:B:479:VAL:HG21	2.02	0.89
3:J:1271:G:H2'	3:J:1272:U:C6	2.08	0.89
1:A:386:GLU:HG2	2:B:27:ARG:CG	2.01	0.89
3:J:418:G:H1'	9:C:59:GLN:HE21	1.35	0.89
3:J:419:G:O3'	9:C:96:SER:OG	1.89	0.89
1:A:386:GLU:CD	2:B:27:ARG:CD	2.42	0.89
2:B:434:PHE:CE2	2:B:480:LEU:HB2	2.08	0.89
2:B:431:ARG:CB	2:B:461:ILE:HG23	2.03	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:2834:G:HO2'	4:K:2835:U:H6	0.93	0.88
8:G:46:ARG:HD3	10:H:121:PHE:HZ	0.72	0.88
3:J:43:A:C2'	3:J:44:U:H5''	2.02	0.88
4:K:1257:C:O2	4:K:1257:C:H2'	1.73	0.88
4:K:2293:C:C5	4:K:2294:U:H5	1.91	0.88
4:K:3028:G:N2	4:K:3029:A:N3	2.22	0.88
10:H:80:LEU:HD23	10:H:83:THR:CG2	2.03	0.87
3:J:452:A:H2'	3:J:453:U:C5'	2.04	0.87
4:K:2931:C:OP1	11:I:40:LYS:NZ	2.06	0.87
2:B:92:PHE:HB2	14:B:702:ATP:O2'	1.75	0.87
2:B:173:VAL:HB	2:B:251:TYR:HE2	1.39	0.87
2:B:571:THR:HG23	2:B:584:ASN:CG	1.98	0.87
2:B:571:THR:CG2	2:B:584:ASN:OD1	2.22	0.87
2:B:28:SER:HB3	2:B:64:LYS:HZ2	1.38	0.87
3:J:1434:U:O3'	3:J:1435:G:H3'	1.72	0.86
2:B:413:LEU:HD12	2:B:487:ASP:CB	2.05	0.86
3:J:419:G:HO2'	9:C:61:PHE:HZ	0.98	0.86
10:H:110:ILE:CG1	10:H:114:ARG:HD2	2.04	0.86
2:B:182:GLY:HA2	2:B:186:LYS:H	1.40	0.86
2:B:86:ARG:HB3	2:B:93:LYS:HG2	1.58	0.86
3:J:152:U:H1'	9:C:13:GLN:OE1	1.74	0.86
2:B:86:ARG:CB	2:B:93:LYS:HG2	2.06	0.86
2:B:95:HIS:HB2	2:B:303:VAL:HG22	1.57	0.86
10:H:109:ILE:HD12	10:H:129:THR:CB	1.96	0.86
2:B:142:GLU:HA	2:B:145:LYS:HE3	1.57	0.86
10:H:109:ILE:CG1	10:H:129:THR:HB	2.05	0.86
2:B:29:CYS:SG	2:B:31:VAL:HG22	2.16	0.86
2:B:571:THR:CG2	2:B:584:ASN:CB	2.53	0.86
1:A:91:GLU:HB3	3:J:1272:U:OP1	1.76	0.86
2:B:574:ARG:NH2	2:B:601:PHE:HE2	1.69	0.86
4:K:2834:G:C4	4:K:2835:U:C5	2.63	0.86
1:A:375:PRO:HD2	4:K:1270:A:C1'	2.06	0.85
2:B:49:PHE:CE1	2:B:89:ALA:HB1	2.11	0.85
2:B:415:VAL:HG23	2:B:488:ILE:HG23	1.56	0.85
3:J:1204:A:OP1	3:J:1204:A:H4'	1.74	0.85
10:H:80:LEU:O	10:H:80:LEU:CD2	2.23	0.85
2:B:133:ARG:HG2	2:B:134:PHE:H	1.41	0.85
2:B:114:ILE:HB	2:B:294:ILE:HG21	1.57	0.85
2:B:488:ILE:HD11	2:B:522:PHE:CE1	2.12	0.85
3:J:1274:C:OP2	3:J:1428:G:P	2.34	0.85
2:B:166:ALA:HA	2:B:242:VAL:HG13	1.59	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:568:LEU:HD22	2:B:570:VAL:HG22	1.58	0.85
3:J:418:G:H1'	9:C:59:GLN:NE2	1.92	0.85
4:K:2295:A:C8	11:I:37:ILE:CG2	2.58	0.85
2:B:92:PHE:CD2	14:B:702:ATP:O4'	2.30	0.85
2:B:268:LEU:HD13	2:B:269:ALA:N	1.92	0.85
1:A:374:TYR:HB2	4:K:1270:A:H1'	1.57	0.84
2:B:205:TYR:CE2	2:B:233:GLY:HA2	2.11	0.84
2:B:394:LEU:HD13	2:B:398:LEU:HD23	1.59	0.84
4:K:2930:A:O2'	11:I:38:ALA:HB1	1.77	0.84
2:B:242:VAL:HG23	2:B:273:TYR:CE2	2.12	0.84
9:C:57:ASP:HA	9:C:106:LEU:HA	1.58	0.84
10:H:85:LEU:HD11	10:H:87:GLU:O	1.78	0.84
2:B:86:ARG:CZ	2:B:93:LYS:HD2	2.08	0.84
2:B:434:PHE:CE2	2:B:480:LEU:HD12	2.11	0.84
3:J:555:A:H3'	3:J:555:A:OP2	1.77	0.84
4:K:2930:A:O2'	11:I:38:ALA:HB2	1.78	0.84
2:B:26:LYS:O	2:B:32:VAL:HG11	1.78	0.83
2:B:574:ARG:NH1	2:B:601:PHE:CE2	2.46	0.83
3:J:444:C:H42	3:J:460:A:H62	1.22	0.83
3:J:1195:C:OP1	3:J:1197:C:H1'	1.78	0.83
2:B:412:LYS:HA	2:B:412:LYS:HE2	1.58	0.83
10:H:117:ARG:HG2	10:H:118:ASP:N	1.93	0.83
2:B:380:ILE:CG2	2:B:535:ALA:HA	2.08	0.83
2:B:457:ILE:O	2:B:460:ILE:HG22	1.77	0.83
3:J:44:U:C5'	3:J:45:U:H5	1.91	0.83
2:B:168:ILE:H	2:B:168:ILE:HD13	1.43	0.83
10:H:109:ILE:HG23	10:H:110:ILE:H	1.43	0.83
1:A:65:LEU:HD23	1:A:65:LEU:H	1.44	0.83
1:A:386:GLU:OE1	2:B:28:SER:N	2.12	0.83
2:B:608:ILE:HG22	2:B:608:ILE:OXT	1.78	0.83
2:B:114:ILE:HB	2:B:294:ILE:CG2	2.09	0.83
2:B:380:ILE:HG21	2:B:534:LEU:O	1.79	0.83
10:H:125:LEU:HD23	10:H:129:THR:CG2	2.08	0.83
4:K:2295:A:N6	4:K:2296:A:N6	2.27	0.83
2:B:389:THR:CG2	2:B:391:LYS:HG3	2.08	0.83
1:A:375:PRO:HG2	4:K:1270:A:C8	2.14	0.83
2:B:128:LYS:H	2:B:128:LYS:HD2	1.44	0.83
2:B:176:ILE:HG13	2:B:227:LEU:HD21	1.61	0.82
2:B:502:GLN:O	2:B:505:ILE:HG22	1.77	0.82
4:K:1278:A:HO2'	4:K:1279:C:H6	0.85	0.82
4:K:2847:A:H3'	4:K:2848:G:H8	1.42	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:29:CYS:HG	15:B:703:SF4:FE1	0.83	0.82
2:B:448:GLN:O	2:B:453:LYS:HG2	1.79	0.82
2:B:59:GLY:O	2:B:62:VAL:HG12	1.77	0.82
2:B:182:GLY:HA3	2:B:184:VAL:C	2.03	0.82
2:B:194:ARG:HD2	2:B:234:MET:CE	2.09	0.82
2:B:505:ILE:O	2:B:509:VAL:HG23	1.79	0.82
10:H:108:GLU:C	10:H:112:ILE:HG23	2.04	0.82
1:A:237:LYS:HE3	4:K:2839:G:HO2'	1.01	0.82
2:B:397:LEU:HD23	2:B:402:LEU:HB2	1.61	0.82
3:J:1274:C:OP2	3:J:1428:G:OP1	1.96	0.82
4:K:2918:G:N2	4:K:2919:A:N7	2.27	0.82
2:B:449:THR:HA	2:B:453:LYS:CE	2.08	0.82
4:K:2293:C:C5	4:K:2294:U:C5	2.66	0.82
4:K:2932:U:H5''	11:I:41:GLY:C	2.03	0.82
10:H:53:PHE:O	10:H:53:PHE:CD2	2.33	0.82
10:H:85:LEU:HD21	10:H:87:GLU:CA	2.09	0.82
2:B:148:ARG:NH2	3:J:429:G:H5''	1.94	0.82
2:B:334:LEU:HD23	2:B:335:GLN:N	1.95	0.82
3:J:1429:G:H2'	3:J:1430:U:H6	1.45	0.82
2:B:38:CYS:SG	15:B:703:SF4:S4	2.78	0.82
3:J:1275:A:OP1	3:J:1275:A:C8	2.33	0.82
10:H:97:ASN:ND2	10:H:97:ASN:O	2.13	0.82
1:A:104:TYR:CD2	3:J:578:U:C6	2.68	0.82
2:B:275:ILE:HD13	2:B:276:CYS:N	1.95	0.82
1:A:386:GLU:HG2	2:B:27:ARG:HD3	0.82	0.81
2:B:457:ILE:O	2:B:461:ILE:HG13	1.79	0.81
3:J:43:A:H2'	3:J:44:U:H5''	1.60	0.81
2:B:50:ILE:CD1	15:B:703:SF4:S4	2.67	0.81
2:B:94:LEU:HD13	2:B:95:HIS:N	1.95	0.81
2:B:106:LEU:HD22	2:B:290:PHE:CD2	2.14	0.81
2:B:290:PHE:HE1	2:B:307:PRO:HA	1.45	0.81
2:B:293:ILE:HD13	2:B:293:ILE:H	1.46	0.81
2:B:381:LEU:HD21	2:B:539:ILE:CD1	2.11	0.81
3:J:44:U:C5'	3:J:45:U:C5	2.63	0.81
10:H:109:ILE:HD11	10:H:129:THR:CB	2.10	0.81
10:H:125:LEU:HD23	10:H:129:THR:HG23	1.63	0.81
1:A:364:GLN:OE1	2:B:58:CYS:CB	2.29	0.81
3:J:1198:G:H3'	3:J:1199:G:H5'	1.60	0.81
3:J:1204:A:C3'	3:J:1205:C:H5''	2.06	0.81
4:K:2932:U:P	11:I:41:GLY:H	2.03	0.81
1:A:187:LYS:CD	5:L:66:C:OP1	2.27	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:344:ASP:C	2:B:345:LEU:HD22	2.06	0.81
4:K:3037:U:H2'	4:K:3038:U:H6	1.45	0.81
2:B:244:MET:HA	2:B:275:ILE:HG22	1.63	0.81
2:B:154:ASN:O	2:B:157:THR:HG22	1.80	0.81
2:B:518:LYS:HG3	6:F:100:ASN:ND2	1.95	0.81
3:J:420:A:OP1	9:C:96:SER:OG	1.99	0.81
2:B:363:GLN:HG3	2:B:365:ASP:H	1.44	0.80
11:I:137:VAL:OXT	11:I:137:VAL:CG1	2.28	0.80
1:A:78:ASP:HB3	7:E:9:ALA:HB2	1.63	0.80
2:B:448:GLN:HA	2:B:452:VAL:CG1	2.10	0.80
4:K:2285:C:C5	4:K:2286:U:C2	2.69	0.80
4:K:2294:U:O2	4:K:2296:A:H2'	1.80	0.80
2:B:105:VAL:C	2:B:106:LEU:HD23	2.07	0.80
10:H:18:VAL:HG12	10:H:20:GLY:H	1.45	0.80
2:B:343:GLU:HG2	2:B:345:LEU:HD21	1.64	0.80
4:K:3029:A:H3'	4:K:3030:G:H5''	1.64	0.80
2:B:589:GLN:HE22	9:C:58:LYS:HB3	1.00	0.80
3:J:1201:G:N3	3:J:1201:G:C3'	2.42	0.80
2:B:453:LYS:CG	2:B:454:PRO:HD3	2.11	0.80
2:B:382:VAL:HG23	2:B:535:ALA:CB	2.09	0.80
2:B:380:ILE:HG23	2:B:535:ALA:HA	1.62	0.80
4:K:2295:A:C6	4:K:2296:A:N6	2.49	0.80
11:I:137:VAL:OXT	11:I:137:VAL:HG12	1.81	0.80
2:B:116:LYS:HE2	14:B:702:ATP:O3G	1.52	0.79
2:B:176:ILE:HG13	2:B:177:PRO:HD3	1.62	0.79
2:B:9:ALA:HB3	2:B:50:ILE:HG21	1.64	0.79
4:K:1229:G:H2'	4:K:1230:G:C8	2.17	0.79
4:K:2287:C:C2	4:K:2298:U:O2	2.36	0.79
4:K:2928:C:H2'	4:K:2929:C:H5'	1.63	0.79
2:B:108:LEU:HD23	2:B:109:VAL:N	1.96	0.79
2:B:380:ILE:HD13	2:B:534:LEU:O	1.82	0.79
3:J:1201:G:H2'	3:J:1202:A:C4'	2.06	0.79
10:H:123:ARG:HD3	10:H:126:ALA:CB	2.13	0.79
2:B:460:ILE:HD11	2:B:468:LEU:CD1	2.10	0.79
2:B:491:ILE:CG2	2:B:523:ILE:HG13	2.11	0.79
4:K:2295:A:N7	11:I:37:ILE:HG21	1.95	0.79
2:B:306:LEU:HB3	2:B:307:PRO:HD2	1.63	0.79
4:K:2294:U:H5'	4:K:2295:A:OP2	1.81	0.79
2:B:380:ILE:CD1	2:B:534:LEU:HB3	2.11	0.79
10:H:109:ILE:CD1	10:H:125:LEU:HG	2.13	0.79
4:K:1239:C:HO2'	10:H:97:ASN:CA	1.88	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:125:LEU:CA	10:H:129:THR:HG21	1.94	0.79
2:B:95:HIS:CE1	2:B:301:TYR:HB2	2.17	0.79
4:K:2284:C:H2'	4:K:2285:C:O2	1.82	0.79
4:K:2295:A:C5	11:I:37:ILE:CB	2.65	0.79
2:B:255:LYS:HB3	2:B:386:GLU:HG3	1.63	0.79
3:J:1274:C:C6	3:J:1427:A:N7	2.50	0.79
4:K:1230:G:C6	4:K:1231:A:N7	2.51	0.79
4:K:2837:A:H2'	4:K:2845:A:N1	1.97	0.79
2:B:29:CYS:SG	15:B:703:SF4:S2	2.81	0.78
2:B:108:LEU:CD2	2:B:294:ILE:HD13	2.13	0.78
3:J:1274:C:O2	3:J:1274:C:H2'	1.83	0.78
4:K:2853:A:C6	4:K:2854:U:N3	2.51	0.78
2:B:381:LEU:HD21	2:B:539:ILE:CG1	2.13	0.78
8:G:46:ARG:HD2	10:H:121:PHE:CZ	2.19	0.78
2:B:574:ARG:HD3	2:B:602:PHE:C	2.09	0.78
4:K:2286:U:C4	4:K:2288:G:H1'	2.17	0.78
10:H:110:ILE:HA	10:H:114:ARG:HB2	1.64	0.78
4:K:1263:A:H61	10:H:135:THR:HA	1.48	0.78
2:B:60:ILE:HD12	2:B:61:CYS:N	1.99	0.78
3:J:152:U:O2'	9:C:4:ASN:OD1	2.00	0.78
4:K:1278:A:O2'	4:K:1279:C:C6	2.29	0.78
8:G:107:ALA:HB3	8:G:183:PHE:CZ	2.15	0.78
9:C:153:VAL:O	9:C:155:ASP:N	2.16	0.78
1:A:386:GLU:OE1	2:B:28:SER:CB	2.32	0.78
4:K:1271:A:N3	4:K:1271:A:H2'	1.98	0.78
3:J:152:U:O4'	9:C:13:GLN:CD	2.25	0.78
10:H:125:LEU:CD2	10:H:129:THR:CG2	2.62	0.78
1:A:187:LYS:CE	5:L:66:C:C5'	2.61	0.78
2:B:42:THR:HG22	2:B:47:ILE:O	1.82	0.78
2:B:116:LYS:N	14:B:702:ATP:O2B	2.15	0.78
2:B:140:TRP:CG	2:B:160:LEU:HD22	2.19	0.78
2:B:457:ILE:HG23	2:B:460:ILE:CG2	2.14	0.78
8:G:38:MET:HE1	8:G:185:LEU:HG	1.66	0.78
2:B:95:HIS:HE1	2:B:301:TYR:HB2	1.48	0.78
4:K:1278:A:O2'	4:K:1279:C:H5'	1.83	0.78
4:K:2932:U:O2	4:K:2932:U:H2'	1.83	0.78
6:F:22:SER:OG	6:F:23:ARG:N	2.16	0.78
3:J:44:U:H5'	3:J:45:U:C4	2.19	0.78
4:K:2295:A:C5	11:I:37:ILE:CG2	2.67	0.78
2:B:480:LEU:HD23	2:B:480:LEU:O	1.85	0.77
2:B:514:ILE:HG23	2:B:519:LYS:O	1.84	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:569:C:H1'	3:J:583:C:H5'	1.65	0.77
8:G:107:ALA:CB	8:G:183:PHE:CD2	2.61	0.77
2:B:29:CYS:O	2:B:32:VAL:HG12	1.83	0.77
2:B:299:SER:HA	14:B:702:ATP:HO3'	1.47	0.77
3:J:44:U:H3'	3:J:45:U:H5'	1.65	0.77
4:K:1277:C:H2'	4:K:1277:C:OP2	1.84	0.77
10:H:57:LYS:HG3	10:H:58:VAL:N	1.98	0.77
2:B:197:LYS:HB3	2:B:201:ASP:OD2	1.83	0.77
2:B:258:LEU:CD1	2:B:568:LEU:HD11	2.13	0.77
3:J:1269:U:H4'	3:J:1270:G:O5'	1.84	0.77
2:B:199:PRO:O	2:B:202:VAL:HG22	1.85	0.77
2:B:435:PHE:CD2	8:G:145:ILE:CD1	2.67	0.77
4:K:1239:C:C1'	10:H:97:ASN:HD21	1.87	0.77
4:K:1269:U:H3	4:K:1271:A:N6	1.81	0.77
2:B:173:VAL:HB	2:B:251:TYR:CE2	2.20	0.77
4:K:2838:A:C2	4:K:2851:A:C4	2.72	0.77
6:F:48:VAL:HG13	6:F:52:LEU:HB3	1.67	0.77
2:B:176:ILE:CG1	2:B:177:PRO:HD3	2.15	0.77
2:B:194:ARG:HD2	2:B:234:MET:HE3	1.67	0.77
8:G:37:GLN:CG	8:G:105:VAL:HG11	2.10	0.77
2:B:114:ILE:HD12	2:B:294:ILE:CB	2.14	0.76
3:J:440:U:H3'	3:J:441:A:H5'	1.67	0.76
3:J:445:A:H2'	3:J:446:A:H8	1.50	0.76
3:J:1193:A:H4'	3:J:1194:A:OP2	1.83	0.76
1:A:364:GLN:OE1	2:B:58:CYS:CA	2.32	0.76
2:B:9:ALA:CB	2:B:50:ILE:HG21	2.15	0.76
2:B:322:ILE:HG13	2:B:325:GLU:HB2	1.67	0.76
3:J:44:U:O5'	3:J:45:U:H5	1.67	0.76
2:B:37:LEU:HB2	2:B:54:LEU:CD1	2.09	0.76
10:H:85:LEU:CD2	10:H:86:LYS:C	2.58	0.76
4:K:2289:U:C2	4:K:2290:C:C5	2.74	0.76
2:B:434:PHE:CZ	2:B:476:VAL:HG12	2.20	0.76
2:B:435:PHE:CE1	2:B:439:ARG:HB2	2.20	0.76
4:K:2923:U:C2	4:K:2924:U:H5	2.04	0.76
10:H:109:ILE:CD1	10:H:129:THR:HB	2.10	0.76
2:B:383:MET:HE3	2:B:524:VAL:HG22	1.67	0.76
10:H:85:LEU:HD21	10:H:87:GLU:H	0.59	0.76
3:J:420:A:P	9:C:74:LYS:HE2	2.24	0.76
2:B:202:VAL:O	2:B:206:ILE:HD13	1.86	0.76
4:K:1229:G:H2'	4:K:1230:G:H8	1.51	0.76
10:H:125:LEU:O	10:H:129:THR:HG23	1.85	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:79:LEU:O	2:B:79:LEU:HD23	1.84	0.75
2:B:261:ALA:CA	2:B:287:LEU:HD21	2.15	0.75
2:B:383:MET:HE3	2:B:524:VAL:CG2	2.16	0.75
3:J:1196:A:H4'	3:J:1197:C:C5'	2.16	0.75
1:A:48:THR:HG21	1:A:60:THR:CA	2.17	0.75
2:B:571:THR:HG23	2:B:584:ASN:HB2	1.66	0.75
3:J:439:U:H1'	3:J:440:U:OP1	1.85	0.75
4:K:1239:C:C2'	10:H:97:ASN:HD22	1.99	0.75
8:G:46:ARG:HD2	10:H:121:PHE:CE1	2.21	0.75
2:B:176:ILE:CG1	2:B:227:LEU:HD21	2.17	0.75
10:H:132:ILE:C	10:H:135:THR:HG22	2.11	0.75
2:B:244:MET:HG2	2:B:275:ILE:HG21	1.69	0.75
4:K:2834:G:N3	4:K:2835:U:C6	2.54	0.75
10:H:23:GLY:CA	10:H:46:ILE:HD11	2.17	0.75
2:B:39:ILE:HD13	2:B:50:ILE:HG13	1.69	0.75
2:B:114:ILE:HD12	2:B:294:ILE:HB	1.67	0.75
2:B:195:MET:HE3	2:B:202:VAL:CA	2.17	0.75
2:B:208:ILE:O	2:B:208:ILE:HD13	1.85	0.75
2:B:273:TYR:OH	2:B:275:ILE:HB	1.86	0.75
2:B:544:ILE:CG1	2:B:547:LYS:HB2	2.15	0.75
3:J:1200:G:H5'	3:J:1201:G:C8	2.22	0.74
4:K:1246:G:C6	4:K:1264:G:N2	2.55	0.74
10:H:125:LEU:CD2	10:H:129:THR:HG21	2.15	0.74
3:J:1197:C:O2	3:J:1197:C:H2'	1.87	0.74
2:B:140:TRP:HB3	2:B:160:LEU:CD2	2.16	0.74
2:B:166:ALA:HA	2:B:242:VAL:CG1	2.17	0.74
2:B:437:LYS:CE	2:B:480:LEU:HD21	2.17	0.74
4:K:2295:A:C5	4:K:2296:A:N6	2.55	0.74
1:A:52:ASP:CG	3:J:575:C:OP1	2.29	0.74
2:B:9:ALA:HB3	2:B:50:ILE:CG2	2.17	0.74
2:B:571:THR:HG23	2:B:584:ASN:CB	2.16	0.74
4:K:1268:G:H5'	4:K:1269:U:OP2	1.87	0.74
4:K:2834:G:O2'	4:K:2835:U:O5'	2.05	0.74
4:K:2842:U:O2	4:K:2842:U:H2'	1.84	0.74
3:J:1274:C:OP2	3:J:1428:G:O5'	2.05	0.74
4:K:2839:G:C5	4:K:2850:G:N2	2.56	0.74
2:B:263:ILE:O	2:B:263:ILE:HD13	1.86	0.74
4:K:2295:A:O4'	11:I:61:THR:HG21	1.88	0.74
4:K:3027:A:C2'	4:K:3028:G:C8	2.69	0.74
4:K:3028:G:C2	4:K:3029:A:N3	2.56	0.74
2:B:358:SER:N	2:B:372:GLU:HG3	2.01	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:427:C:H6	3:J:427:C:H5'	1.52	0.73
4:K:1258:U:H2'	4:K:1259:A:O5'	1.88	0.73
1:A:385:GLU:HB3	2:B:27:ARG:HH11	1.51	0.73
2:B:363:GLN:HG2	2:B:366:PHE:H	1.52	0.73
3:J:418:G:C1'	9:C:59:GLN:HE21	2.00	0.73
10:H:120:SER:HG	10:H:128:VAL:CG2	1.80	0.73
1:A:48:THR:HG21	1:A:60:THR:HA	1.71	0.73
2:B:140:TRP:O	2:B:143:ILE:HG12	1.87	0.73
2:B:380:ILE:HD13	2:B:534:LEU:C	2.13	0.73
3:J:1199:G:C5	3:J:1200:G:H1'	2.23	0.73
4:K:2293:C:H5	4:K:2294:U:C5	2.00	0.73
4:K:2834:G:O2'	4:K:2835:U:H6	1.70	0.73
2:B:136:ASP:H	2:B:137:PRO:HD2	1.54	0.73
2:B:491:ILE:CD1	2:B:494:PRO:HG3	2.18	0.73
4:K:1232:C:C2	4:K:1261:G:C6	2.77	0.73
2:B:195:MET:HE3	2:B:202:VAL:HA	1.69	0.73
10:H:80:LEU:HD23	10:H:83:THR:HG21	1.69	0.73
10:H:85:LEU:HD21	10:H:87:GLU:O	1.88	0.73
2:B:34:THR:OG1	2:B:36:LYS:HD3	1.88	0.73
2:B:76:PRO:O	2:B:77:THR:HG22	1.89	0.73
10:H:85:LEU:CG	10:H:86:LYS:H	2.01	0.73
1:A:78:ASP:CB	7:E:9:ALA:HB2	2.18	0.73
2:B:114:ILE:CG1	2:B:116:LYS:HD2	2.18	0.73
3:J:569:C:O4'	3:J:583:C:H4'	1.88	0.73
2:B:343:GLU:CG	2:B:345:LEU:HD21	2.19	0.73
3:J:1201:G:C4	3:J:1202:A:O4'	2.42	0.73
4:K:2285:C:H5	4:K:2286:U:N3	1.86	0.73
4:K:2930:A:HO2'	11:I:38:ALA:CB	2.02	0.73
8:G:104:ARG:CB	8:G:182:THR:HB	2.19	0.73
8:G:104:ARG:HB2	8:G:182:THR:HB	1.69	0.73
10:H:117:ARG:CG	10:H:118:ASP:H	1.92	0.73
2:B:67:PHE:CD1	15:B:704:SF4:S1	2.81	0.73
2:B:114:ILE:HD12	2:B:294:ILE:CG2	2.19	0.73
2:B:588:SER:HB3	2:B:591:ASP:HB3	1.70	0.73
4:K:1259:A:H5''	4:K:1260:A:OP2	1.88	0.72
10:H:125:LEU:C	10:H:125:LEU:HD23	2.13	0.72
2:B:195:MET:HE3	2:B:202:VAL:CG1	2.18	0.72
3:J:553:G:H3'	3:J:554:C:H5''	1.71	0.72
3:J:1186:U:H2'	3:J:1187:U:O4'	1.88	0.72
2:B:60:ILE:HG13	15:B:703:SF4:S2	2.30	0.72
2:B:176:ILE:HD11	2:B:227:LEU:HG	1.71	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:108:LEU:HG	2:B:294:ILE:HD11	1.72	0.72
3:J:560:U:H2'	3:J:561:G:H8	1.55	0.72
4:K:2290:C:O2'	4:K:2291:A:O4'	2.06	0.72
4:K:2854:U:O2'	4:K:2855:U:H5'	1.89	0.72
2:B:182:GLY:HA3	2:B:185:GLN:CA	2.20	0.72
3:J:551:G:C2	3:J:552:G:C5	2.77	0.72
4:K:1234:G:H3'	4:K:1235:U:H2'	1.72	0.72
4:K:2928:C:C2'	4:K:2929:C:H5'	2.18	0.72
2:B:53:ILE:HG13	2:B:54:LEU:N	2.05	0.72
2:B:60:ILE:HD11	15:B:703:SF4:S2	2.30	0.72
2:B:180:ILE:HG21	2:B:183:PRO:HA	1.72	0.72
2:B:173:VAL:CB	2:B:251:TYR:HE2	2.03	0.72
2:B:568:LEU:HD22	2:B:570:VAL:HG13	1.71	0.72
4:K:1263:A:N6	10:H:135:THR:HA	2.04	0.72
4:K:1264:G:H4'	4:K:1265:U:OP1	1.89	0.72
4:K:3032:A:C4	6:F:170:LYS:NZ	2.58	0.72
2:B:464:GLU:HB2	2:B:467:HIS:ND1	2.04	0.72
4:K:2287:C:N3	4:K:2298:U:O2	2.23	0.72
9:C:24:ILE:O	9:C:26:VAL:N	2.23	0.72
2:B:376:SER:HB2	2:B:379:GLU:OE2	1.90	0.71
3:J:1269:U:O2	3:J:1269:U:O4'	2.07	0.71
3:J:1274:C:H6	3:J:1427:A:N6	1.87	0.71
10:H:85:LEU:HD22	10:H:87:GLU:N	1.98	0.71
3:J:36:C:H2'	3:J:37:U:C6	2.25	0.71
2:B:424:PRO:CG	2:B:465:VAL:HG12	2.20	0.71
2:B:392:THR:O	2:B:395:ILE:HG22	1.89	0.71
3:J:1188:G:H2'	3:J:1189:A:H8	1.55	0.71
2:B:56:ILE:CD1	2:B:58:CYS:HB3	2.20	0.71
3:J:467:G:H5''	3:J:468:A:OP2	1.91	0.71
2:B:537:LYS:HD3	2:B:554:PRO:HB2	1.72	0.71
2:B:72:ILE:C	2:B:73:ILE:HD12	2.15	0.71
2:B:56:ILE:HD11	2:B:58:CYS:SG	2.30	0.71
2:B:266:SER:O	2:B:270:PRO:HD2	1.90	0.71
2:B:455:LEU:HD11	2:B:475:ARG:NH1	2.06	0.71
4:K:2846:U:O2	4:K:2850:G:O6	2.09	0.71
10:H:104:ILE:HG12	10:H:105:GLN:H	1.54	0.71
1:A:65:LEU:H	1:A:65:LEU:CD2	2.04	0.71
2:B:343:GLU:HG2	2:B:345:LEU:CD2	2.21	0.71
4:K:3028:G:O2'	4:K:3029:A:O4'	2.08	0.71
11:I:33:ASN:HD22	11:I:33:ASN:C	1.98	0.71
1:A:106:SER:HB2	3:J:565:C:OP1	1.91	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:544:ILE:CD1	2:B:547:LYS:HG3	2.20	0.70
3:J:1272:U:H5''	3:J:1273:G:OP2	1.91	0.70
2:B:106:LEU:CD2	2:B:290:PHE:HD2	2.02	0.70
2:B:182:GLY:HA2	2:B:186:LYS:N	2.06	0.70
2:B:234:MET:HA	2:B:237:VAL:CG2	2.20	0.70
2:B:255:LYS:HB3	2:B:386:GLU:CG	2.20	0.70
3:J:551:G:H5''	3:J:552:G:OP2	1.90	0.70
1:A:385:GLU:CB	2:B:27:ARG:NH1	2.54	0.70
2:B:148:ARG:NH2	3:J:439:U:H3'	2.06	0.70
2:B:182:GLY:HA3	2:B:185:GLN:HA	1.72	0.70
6:F:49:ASN:O	6:F:49:ASN:ND2	2.23	0.70
10:H:85:LEU:HD21	10:H:87:GLU:C	2.16	0.70
11:I:32:ARG:HB3	11:I:64:LYS:HB3	1.73	0.70
2:B:58:CYS:SG	15:B:703:SF4:S2	2.90	0.70
2:B:156:PHE:O	2:B:160:LEU:HG	1.91	0.70
4:K:2294:U:C5'	4:K:2295:A:OP2	2.40	0.70
2:B:117:SER:HG	13:B:701:MG:MG	0.97	0.70
2:B:322:ILE:HD12	2:B:325:GLU:OE1	1.92	0.70
3:J:553:G:H3'	3:J:554:C:C5'	2.20	0.70
4:K:2932:U:OP1	11:I:40:LYS:HB3	1.92	0.70
1:A:232:GLU:OE1	4:K:2851:A:O4'	2.10	0.70
2:B:205:TYR:HE1	2:B:263:ILE:CD1	2.03	0.70
4:K:2295:A:N7	11:I:37:ILE:HG22	2.05	0.70
3:J:438:A:O2'	3:J:439:U:H5''	1.91	0.70
1:A:318:LEU:HD13	1:A:350:LEU:HD22	1.72	0.70
2:B:290:PHE:CE1	2:B:307:PRO:HA	2.27	0.70
3:J:450:U:H5''	3:J:451:A:OP2	1.92	0.70
3:J:560:U:H2'	3:J:561:G:C8	2.26	0.70
3:J:1429:G:C4	3:J:1430:U:C5	2.79	0.70
1:A:386:GLU:CD	2:B:27:ARG:HD2	2.15	0.69
4:K:1239:C:H2'	4:K:1240:A:C8	2.26	0.69
8:G:104:ARG:HD3	8:G:182:THR:O	1.92	0.69
10:H:38:SER:H	10:H:68:GLN:HA	1.57	0.69
11:I:79:VAL:HG13	11:I:100:GLY:HA2	1.74	0.69
2:B:133:ARG:HG2	2:B:134:PHE:CD2	2.27	0.69
4:K:3019:U:C5	4:K:3020:U:C5	2.80	0.69
10:H:88:PRO:HD2	10:H:89:PRO:N	2.08	0.69
2:B:87:TYR:CB	14:B:702:ATP:C2	2.75	0.69
3:J:437:A:H5''	3:J:438:A:OP1	1.92	0.69
4:K:1239:C:C2'	10:H:97:ASN:ND2	2.55	0.69
4:K:2299:A:H8	4:K:2299:A:H5'	1.56	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:79:LEU:HD21	2:B:95:HIS:NE2	2.06	0.69
2:B:148:ARG:HH21	3:J:429:G:H5''	1.56	0.69
2:B:269:ALA:HB3	2:B:270:PRO:HD3	1.75	0.69
2:B:380:ILE:HD11	2:B:534:LEU:HB3	1.74	0.69
4:K:2289:U:C2'	4:K:2290:C:H5'	2.22	0.69
4:K:2296:A:O2'	4:K:2297:U:H5'	1.92	0.69
10:H:108:GLU:C	10:H:112:ILE:CG2	2.65	0.69
2:B:114:ILE:HD12	2:B:294:ILE:HG21	1.73	0.69
3:J:1199:G:C6	3:J:1200:G:H1'	2.28	0.69
4:K:3032:A:C1'	6:F:170:LYS:HE2	2.22	0.69
2:B:389:THR:HG21	2:B:391:LYS:HG3	1.75	0.69
10:H:133:LEU:C	10:H:133:LEU:HD23	2.18	0.69
2:B:39:ILE:HD11	2:B:50:ILE:HD12	1.74	0.69
2:B:106:LEU:HB3	2:B:290:PHE:CD2	2.28	0.69
4:K:2287:C:O2	4:K:2298:U:O2	2.11	0.69
4:K:2932:U:H5''	11:I:41:GLY:HA2	0.70	0.69
1:A:237:LYS:NZ	4:K:2839:G:H4'	2.07	0.69
2:B:120:LEU:CD2	2:B:246:ASP:HB2	2.23	0.69
2:B:180:ILE:HG23	2:B:183:PRO:O	1.92	0.69
3:J:446:A:C5	3:J:447:U:C5	2.81	0.69
4:K:1256:G:C4	4:K:1257:C:C6	2.81	0.69
4:K:2295:A:O4'	11:I:61:THR:CG2	2.40	0.69
9:C:164:LYS:HB3	9:C:167:LYS:HB3	1.75	0.69
2:B:24:GLU:HA	2:B:27:ARG:HG2	1.75	0.69
2:B:179:ALA:CB	2:B:180:ILE:HD12	2.22	0.69
6:F:57:VAL:HG23	6:F:68:LEU:HG	1.75	0.69
10:H:46:ILE:HD12	10:H:71:ALA:CB	2.22	0.69
2:B:458:ASP:HA	2:B:461:ILE:CD1	2.23	0.69
4:K:1256:G:C4	4:K:1257:C:H6	2.11	0.69
4:K:2295:A:N9	11:I:37:ILE:HD13	2.08	0.69
2:B:56:ILE:HG13	2:B:58:CYS:H	1.58	0.68
3:J:1203:A:H4'	3:J:1204:A:OP2	1.92	0.68
4:K:2289:U:H2'	4:K:2290:C:H5'	1.75	0.68
1:A:283:VAL:HB	1:A:350:LEU:HD21	1.74	0.68
2:B:42:THR:HG21	2:B:47:ILE:HG22	1.73	0.68
2:B:183:PRO:HD2	2:B:185:GLN:C	2.17	0.68
2:B:205:TYR:CE1	2:B:263:ILE:HG13	2.28	0.68
2:B:544:ILE:HD12	2:B:547:LYS:HG3	1.74	0.68
3:J:420:A:P	9:C:96:SER:CB	2.80	0.68
10:H:87:GLU:HG2	10:H:89:PRO:HD3	1.75	0.68
10:H:120:SER:HG	10:H:128:VAL:HG22	0.85	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:GLU:OE1	3:J:1272:U:OP1	2.10	0.68
2:B:255:LYS:HD3	2:B:386:GLU:HG2	1.75	0.68
2:B:574:ARG:HD3	2:B:602:PHE:CA	2.22	0.68
3:J:152:U:C1'	9:C:13:GLN:OE1	2.42	0.68
4:K:2833:A:C6	4:K:2834:G:C8	2.82	0.68
4:K:2847:A:H2'	4:K:2847:A:N3	2.08	0.68
3:J:1274:C:O2'	3:J:1275:A:OP2	2.11	0.68
4:K:2931:C:C4	4:K:2932:U:C5	2.81	0.68
6:F:13:PRO:HD2	6:F:16:VAL:HG22	1.74	0.68
2:B:106:LEU:HB3	2:B:290:PHE:HE2	1.56	0.68
2:B:574:ARG:NH2	2:B:601:PHE:CZ	2.48	0.68
3:J:420:A:OP1	9:C:96:SER:CA	2.42	0.68
9:C:67:VAL:HG21	9:C:99:GLY:HA2	1.76	0.68
10:H:109:ILE:HG13	10:H:129:THR:OG1	1.85	0.68
3:J:44:U:H3'	3:J:45:U:C5'	2.24	0.68
3:J:1431:C:C4'	3:J:1432:U:H5'	2.24	0.68
1:A:386:GLU:OE2	2:B:27:ARG:CG	2.41	0.68
3:J:461:G:H2'	3:J:462:G:H8	1.59	0.68
4:K:1248:C:H2'	4:K:1249:G:H5'	1.76	0.68
4:K:1252:A:H2'	4:K:1253:U:H5'	1.74	0.68
4:K:2918:G:C2	4:K:2919:A:C8	2.81	0.68
11:I:108:GLU:HG2	11:I:128:ARG:HH11	1.58	0.68
2:B:87:TYR:HB3	14:B:702:ATP:C2	2.28	0.68
3:J:587:C:O5'	3:J:587:C:H6	1.77	0.68
2:B:114:ILE:HG12	2:B:116:LYS:HD2	1.76	0.67
2:B:148:ARG:HH22	3:J:439:U:H3'	1.57	0.67
4:K:2288:G:C4	4:K:2289:U:C5	2.82	0.67
11:I:40:LYS:HD3	11:I:59:MET:HE2	1.76	0.67
2:B:31:VAL:CG2	2:B:38:CYS:HB3	2.21	0.67
2:B:115:GLY:CA	14:B:702:ATP:O2A	2.31	0.67
3:J:427:C:C5'	3:J:427:C:C6	2.72	0.67
4:K:2919:A:H3'	4:K:2920:U:H5'	1.76	0.67
2:B:9:ALA:HB2	2:B:72:ILE:CD1	2.25	0.67
2:B:92:PHE:CB	14:B:702:ATP:C1'	2.72	0.67
2:B:305:THR:HG22	2:B:306:LEU:H	1.58	0.67
2:B:382:VAL:CG2	2:B:535:ALA:HB2	2.18	0.67
2:B:441:GLN:HE21	2:B:447:PHE:HE2	1.41	0.67
2:B:589:GLN:CG	9:C:107:ALA:HB2	2.24	0.67
3:J:436:A:H5''	3:J:437:A:OP2	1.95	0.67
4:K:2836:C:O2	4:K:2836:C:C2'	2.42	0.67
4:K:2932:U:C5'	11:I:41:GLY:N	2.57	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1209:C:H2'	3:J:1210:C:H6	1.59	0.67
1:A:84:LYS:HZ1	3:J:564:G:P	2.13	0.67
2:B:475:ARG:O	2:B:479:VAL:HG23	1.95	0.67
2:B:608:ILE:OXT	2:B:608:ILE:CG2	2.38	0.67
3:J:426:G:H2'	3:J:427:C:H5''	1.75	0.67
3:J:564:G:O2'	3:J:577:G:H4'	1.94	0.67
4:K:1257:C:H3'	4:K:1258:U:H6	1.59	0.67
11:I:81:GLN:O	11:I:98:ASN:ND2	2.28	0.67
3:J:44:U:H5'	3:J:45:U:O4	1.93	0.67
3:J:445:A:H2'	3:J:446:A:C8	2.29	0.67
2:B:95:HIS:CB	2:B:303:VAL:HG22	2.24	0.67
2:B:148:ARG:NH2	3:J:439:U:C3'	2.57	0.67
2:B:415:VAL:HG23	2:B:488:ILE:CG2	2.25	0.67
4:K:3022:G:HO2'	4:K:3023:U:P	2.11	0.67
4:K:3037:U:H2'	4:K:3038:U:C6	2.27	0.67
2:B:450:ASP:OD2	2:B:509:VAL:HG22	1.95	0.67
3:J:1431:C:C3'	3:J:1432:U:H5'	2.25	0.67
2:B:574:ARG:NH1	2:B:601:PHE:CD2	2.63	0.67
3:J:429:G:H5''	3:J:439:U:H3'	1.75	0.67
4:K:1256:G:C2	4:K:1257:C:H1'	2.30	0.67
4:K:1260:A:H1'	4:K:1280:C:H1'	1.77	0.67
4:K:3021:A:C4	4:K:3023:U:O4	2.48	0.67
2:B:103:GLY:O	2:B:268:LEU:HD23	1.96	0.66
2:B:395:ILE:HD11	2:B:490:LEU:HB3	1.77	0.66
4:K:1248:C:C5	4:K:1249:G:C8	2.82	0.66
6:F:75:VAL:HA	6:F:78:MET:HE2	1.77	0.66
6:F:90:MET:HE3	6:F:181:VAL:HG23	1.76	0.66
10:H:120:SER:HB3	10:H:128:VAL:HG21	1.77	0.66
2:B:265:ARG:O	2:B:268:LEU:HD12	1.94	0.66
2:B:568:LEU:HD22	2:B:570:VAL:CG2	2.26	0.66
2:B:568:LEU:O	2:B:568:LEU:HD23	1.96	0.66
3:J:1429:G:H2'	3:J:1430:U:C6	2.29	0.66
10:H:112:ILE:HG12	10:H:112:ILE:O	1.95	0.66
10:H:125:LEU:HA	10:H:129:THR:CB	2.25	0.66
11:I:68:GLU:OE1	11:I:68:GLU:N	2.23	0.66
2:B:179:ALA:HB3	2:B:180:ILE:HD12	1.78	0.66
2:B:320:GLY:HA2	2:B:329:PHE:CZ	2.30	0.66
2:B:568:LEU:CD2	2:B:570:VAL:HG13	2.26	0.66
3:J:427:C:H6	3:J:427:C:H5''	1.58	0.66
3:J:564:G:N7	3:J:578:U:C6	2.63	0.66
2:B:501:GLU:O	2:B:504:ILE:HG22	1.96	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:446:A:C4	3:J:447:U:C5	2.84	0.66
4:K:1269:U:H3	4:K:1272:C:N4	1.92	0.66
10:H:101:SER:OG	10:H:140:GLY:C	2.37	0.66
2:B:148:ARG:NH2	3:J:439:U:O3'	2.20	0.66
6:F:25:VAL:HG11	6:F:78:MET:HE1	1.76	0.66
2:B:588:SER:O	2:B:592:LYS:HB3	1.96	0.66
3:J:1269:U:N3	3:J:1432:U:O4'	2.29	0.66
4:K:2837:A:C8	4:K:2845:A:C2	2.83	0.66
4:K:2841:G:C6	4:K:2844:C:C4	2.84	0.66
2:B:332:GLU:OE2	4:K:3022:G:H5'	1.95	0.66
3:J:553:G:C6	3:J:554:C:N3	2.63	0.66
4:K:2923:U:C2	4:K:2924:U:C5	2.84	0.66
10:H:16:ARG:HD2	10:H:60:VAL:HG23	1.78	0.66
10:H:80:LEU:HD23	10:H:80:LEU:C	2.16	0.66
2:B:112:ASN:CB	14:B:702:ATP:O1G	2.42	0.65
2:B:568:LEU:HD13	2:B:570:VAL:CG2	2.26	0.65
1:A:49:SER:HB3	3:J:565:C:N4	2.10	0.65
2:B:437:LYS:HG3	2:B:480:LEU:HD21	1.78	0.65
4:K:1240:A:H3'	4:K:1241:U:H5''	1.78	0.65
4:K:1262:G:OP2	4:K:1262:G:C8	2.49	0.65
4:K:2853:A:N6	4:K:2854:U:H3	1.92	0.65
1:A:104:TYR:CD2	3:J:578:U:H6	2.15	0.65
2:B:313:GLY:O	2:B:316:ILE:HG22	1.96	0.65
2:B:475:ARG:CZ	2:B:502:GLN:HG2	2.26	0.65
4:K:1254:C:H5	4:K:1263:A:OP1	1.79	0.65
2:B:357:PRO:C	2:B:372:GLU:HG3	2.22	0.65
2:B:591:ASP:C	2:B:591:ASP:OD1	2.40	0.65
3:J:1196:A:H5''	3:J:1196:A:N3	2.12	0.65
4:K:2285:C:C5	4:K:2286:U:N3	2.65	0.65
4:K:2932:U:OP1	11:I:40:LYS:HE3	1.96	0.65
1:A:385:GLU:CD	2:B:27:ARG:NH1	2.44	0.65
2:B:86:ARG:HB2	2:B:93:LYS:HG2	1.77	0.65
3:J:152:U:H4'	9:C:13:GLN:C	2.21	0.65
4:K:1257:C:H3'	4:K:1258:U:C6	2.32	0.65
4:K:1277:C:OP2	4:K:1277:C:H6	1.80	0.65
4:K:3032:A:N9	6:F:170:LYS:CE	2.51	0.65
1:A:300:TYR:OH	2:B:64:LYS:HE2	1.96	0.65
2:B:176:ILE:CD1	2:B:227:LEU:HG	2.27	0.65
2:B:305:THR:HG22	2:B:306:LEU:N	2.11	0.65
2:B:447:PHE:O	2:B:451:VAL:HG22	1.97	0.65
8:G:12:PHE:CZ	8:G:57:THR:HG22	2.32	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:108:LEU:HG	2:B:294:ILE:CD1	2.26	0.65
2:B:437:LYS:HG3	2:B:480:LEU:CD2	2.26	0.65
4:K:2836:C:O2	4:K:2836:C:H3'	1.97	0.65
4:K:2288:G:H2'	4:K:2289:U:C6	2.32	0.65
2:B:343:GLU:OE2	6:F:121:LYS:HA	1.97	0.65
3:J:46:A:N6	3:J:433:C:H4'	2.12	0.65
4:K:1236:G:C5	10:H:57:LYS:HE2	2.32	0.65
1:A:313:ALA:O	1:A:372:LEU:HD22	1.97	0.64
2:B:244:MET:HA	2:B:275:ILE:CG2	2.27	0.64
2:B:260:ALA:O	2:B:263:ILE:HG22	1.97	0.64
1:A:385:GLU:CA	2:B:27:ARG:NH1	2.58	0.64
2:B:460:ILE:CD1	2:B:468:LEU:HD11	2.19	0.64
6:F:28:VAL:HG22	6:F:33:THR:HB	1.78	0.64
1:A:386:GLU:CD	2:B:28:SER:OG	2.39	0.64
2:B:413:LEU:HD12	2:B:487:ASP:HB2	1.79	0.64
2:B:444:ASN:OD1	2:B:447:PHE:HB2	1.97	0.64
3:J:48:G:C6	3:J:432:G:N2	2.64	0.64
10:H:120:SER:CB	10:H:128:VAL:HG21	2.27	0.64
1:A:385:GLU:HB3	2:B:27:ARG:NH1	2.13	0.64
3:J:450:U:C2	3:J:451:A:N7	2.65	0.64
4:K:2932:U:O2	4:K:2932:U:C2'	2.45	0.64
10:H:110:ILE:HG13	10:H:114:ARG:CD	2.20	0.64
2:B:516:HIS:CE1	6:F:116:ASN:HB3	2.33	0.64
3:J:420:A:OP1	9:C:96:SER:HB2	1.95	0.64
4:K:1232:C:N3	4:K:1261:G:C2	2.66	0.64
1:A:386:GLU:OE1	2:B:28:SER:CA	2.44	0.64
2:B:86:ARG:NH1	2:B:93:LYS:HD2	2.12	0.64
2:B:176:ILE:HD11	2:B:227:LEU:CD2	2.27	0.64
2:B:380:ILE:HD13	2:B:534:LEU:HB3	1.80	0.64
4:K:1232:C:C4	4:K:1261:G:C2	2.85	0.64
4:K:2289:U:O2'	4:K:2290:C:H5'	1.98	0.64
2:B:28:SER:HB3	2:B:64:LYS:NZ	2.12	0.64
2:B:557:LEU:O	2:B:557:LEU:HD23	1.98	0.64
2:B:603:LEU:HG	2:B:604:ASP:N	2.09	0.64
3:J:572:C:H5''	3:J:573:C:OP2	1.98	0.64
4:K:1279:C:O2'	4:K:1280:C:O5'	2.16	0.64
10:H:136:ALA:HB1	10:H:139:VAL:HB	1.79	0.64
3:J:442:C:O2'	3:J:443:C:H5'	1.98	0.64
6:F:9:GLN:HG2	6:F:52:LEU:HD21	1.78	0.64
12:D:91:LEU:HA	12:D:96:LEU:HD12	1.80	0.64
1:A:187:LYS:NZ	5:L:66:C:H5'	2.12	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:435:PHE:CE1	2:B:439:ARG:HD3	2.22	0.64
2:B:468:LEU:HG	2:B:469:SER:N	2.12	0.64
3:J:152:U:C1'	9:C:13:GLN:CD	2.71	0.64
4:K:2847:A:C4	4:K:2848:G:C8	2.86	0.64
2:B:182:GLY:HA3	2:B:185:GLN:N	2.12	0.64
2:B:368:LEU:HD22	2:B:393:THR:OG1	1.98	0.64
2:B:386:GLU:O	2:B:391:LYS:HE2	1.98	0.64
10:H:120:SER:HB3	10:H:128:VAL:CG2	2.27	0.64
2:B:104:GLN:OE1	2:B:106:LEU:HD21	1.97	0.63
7:E:14:VAL:O	7:E:18:THR:HG23	1.97	0.63
2:B:140:TRP:HE3	2:B:143:ILE:CD1	2.11	0.63
4:K:2294:U:O2	4:K:2294:U:H2'	1.98	0.63
4:K:2931:C:C4	4:K:2932:U:H5	2.15	0.63
8:G:106:ALA:O	8:G:107:ALA:HB2	1.99	0.63
2:B:392:THR:CG2	2:B:396:LYS:HE2	2.22	0.63
2:B:430:VAL:O	2:B:434:PHE:HD1	1.82	0.63
2:B:571:THR:CG2	2:B:584:ASN:CG	2.69	0.63
3:J:1179:G:C6	3:J:1180:C:C2	2.86	0.63
2:B:42:THR:CG2	2:B:47:ILE:HG22	2.28	0.63
2:B:101:ARG:O	2:B:273:TYR:HD1	1.81	0.63
2:B:135:ASP:CG	2:B:139:GLU:HB2	2.22	0.63
2:B:142:GLU:HA	2:B:145:LYS:CE	2.27	0.63
3:J:418:G:H8	9:C:59:GLN:CG	2.05	0.63
4:K:3028:G:C2	4:K:3029:A:C2	2.86	0.63
10:H:109:ILE:HD12	10:H:125:LEU:HG	1.81	0.63
2:B:60:ILE:CD1	15:B:703:SF4:S2	2.87	0.63
2:B:338:ILE:HA	2:B:603:LEU:HD21	1.81	0.63
3:J:1273:G:H4'	3:J:1274:C:C4'	2.28	0.63
4:K:2295:A:OP1	11:I:63:LYS:NZ	2.20	0.63
2:B:58:CYS:SG	2:B:60:ILE:HG13	2.39	0.63
3:J:161:U:OP2	9:C:85:ARG:N	2.31	0.63
11:I:17:LEU:HD21	11:I:98:ASN:ND2	2.13	0.63
2:B:8:ILE:HD13	2:B:79:LEU:HD13	1.80	0.62
2:B:144:ILE:HG23	2:B:153:GLN:CG	2.27	0.62
2:B:448:GLN:CA	2:B:452:VAL:HG12	2.26	0.62
4:K:2834:G:N3	4:K:2835:U:C5	2.66	0.62
10:H:18:VAL:HG12	10:H:20:GLY:N	2.14	0.62
10:H:80:LEU:CD2	10:H:83:THR:HG21	2.29	0.62
2:B:360:LYS:HE3	2:B:367:VAL:HG11	1.80	0.62
3:J:1435:G:C4'	3:J:1436:A:OP2	2.46	0.62
4:K:2921:U:H3'	4:K:2923:U:OP2	1.99	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:59:THR:HG22	10:H:74:VAL:O	1.97	0.62
2:B:194:ARG:HD2	2:B:234:MET:HE2	1.79	0.62
2:B:357:PRO:O	2:B:359:LEU:HD22	1.98	0.62
2:B:451:VAL:HG23	2:B:452:VAL:N	2.15	0.62
4:K:2295:A:C5	11:I:37:ILE:HG21	2.33	0.62
4:K:2852:C:C5	4:K:2853:A:C4	2.86	0.62
1:A:386:GLU:OE2	2:B:27:ARG:HD2	1.99	0.62
2:B:143:ILE:O	2:B:147:PHE:HD2	1.82	0.62
2:B:457:ILE:HG23	2:B:460:ILE:HG21	1.81	0.62
2:B:491:ILE:HG23	2:B:523:ILE:HG13	1.79	0.62
4:K:2294:U:C6	4:K:2297:U:H5	2.17	0.62
4:K:2836:C:H5	4:K:2853:A:N1	1.98	0.62
8:G:37:GLN:HG2	8:G:105:VAL:CG1	2.18	0.62
1:A:84:LYS:NZ	3:J:564:G:P	2.70	0.62
2:B:140:TRP:HB3	2:B:160:LEU:HD22	1.81	0.62
2:B:244:MET:HG2	2:B:275:ILE:CG2	2.30	0.62
2:B:450:ASP:OD1	2:B:505:ILE:HD11	2.00	0.62
3:J:1273:G:C5'	3:J:1274:C:H5'	2.30	0.62
10:H:109:ILE:CD1	10:H:129:THR:CG2	2.77	0.62
2:B:120:LEU:HD22	2:B:246:ASP:HB2	1.80	0.62
2:B:194:ARG:HG2	2:B:234:MET:HG3	1.81	0.62
2:B:236:CYS:SG	2:B:263:ILE:HD12	2.40	0.62
2:B:322:ILE:CD1	2:B:325:GLU:HB2	2.29	0.62
3:J:39:A:C5	3:J:467:G:N2	2.67	0.62
3:J:1196:A:O2'	3:J:1197:C:OP2	2.14	0.62
4:K:1273:A:C8	4:K:1274:A:N7	2.68	0.62
4:K:1279:C:C2	4:K:1280:C:C5	2.88	0.62
10:H:123:ARG:HD3	10:H:126:ALA:HB3	1.80	0.62
3:J:584:C:O2'	7:E:18:THR:CG2	2.33	0.62
4:K:1240:A:H3'	4:K:1241:U:C5'	2.27	0.62
4:K:2833:A:N1	4:K:2834:G:C8	2.68	0.62
1:A:52:ASP:OD1	3:J:575:C:OP1	2.17	0.62
2:B:242:VAL:HG23	2:B:273:TYR:HD2	1.62	0.62
3:J:1200:G:H8	3:J:1200:G:H5''	1.65	0.62
2:B:104:GLN:HG3	2:B:106:LEU:HD21	1.82	0.62
2:B:268:LEU:O	2:B:268:LEU:HD22	2.00	0.62
2:B:452:VAL:HG13	2:B:453:LYS:N	2.15	0.62
3:J:445:A:N3	3:J:446:A:C8	2.68	0.62
2:B:173:VAL:CG2	2:B:251:TYR:HE2	2.13	0.61
4:K:2919:A:C3'	4:K:2920:U:H5'	2.30	0.61
9:C:114:VAL:HG12	9:C:115:LYS:HD3	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:1234:G:O4'	10:H:131:GLU:OE1	2.18	0.61
4:K:1282:G:H2'	4:K:1283:C:O4'	1.99	0.61
4:K:2290:C:H2'	4:K:2291:A:H8	1.64	0.61
4:K:2297:U:O2	4:K:2299:A:C5	2.53	0.61
4:K:2849:C:O2	4:K:2849:C:H2'	2.00	0.61
2:B:37:LEU:HD22	2:B:37:LEU:N	2.15	0.61
2:B:293:ILE:HD13	2:B:293:ILE:N	2.14	0.61
2:B:568:LEU:HD13	2:B:570:VAL:HG22	1.80	0.61
4:K:1272:C:H2'	4:K:1273:A:C4'	2.31	0.61
4:K:2847:A:C2	4:K:2848:G:H1'	2.35	0.61
2:B:135:ASP:OD1	2:B:139:GLU:HB2	2.00	0.61
3:J:448:C:H2'	3:J:449:C:C6	2.35	0.61
4:K:1255:C:O2'	10:H:131:GLU:HA	2.01	0.61
4:K:1256:G:N2	4:K:1257:C:H1'	2.14	0.61
4:K:3019:U:C4	4:K:3020:U:C5	2.88	0.61
11:I:129:VAL:O	11:I:133:SER:OG	2.17	0.61
2:B:568:LEU:CD2	2:B:570:VAL:HG22	2.28	0.61
2:B:116:LYS:H	2:B:116:LYS:HD3	1.64	0.61
3:J:461:G:H2'	3:J:462:G:C8	2.34	0.61
4:K:2931:C:H2'	4:K:2932:U:H6	1.66	0.61
2:B:363:GLN:CG	2:B:366:PHE:H	2.14	0.61
3:J:452:A:C2	3:J:454:U:O5'	2.54	0.61
3:J:1204:A:H2'	3:J:1204:A:N3	2.15	0.61
4:K:2295:A:N9	11:I:37:ILE:HG21	2.16	0.61
10:H:10:VAL:HG12	10:H:11:LYS:N	2.15	0.61
4:K:2851:A:H3'	4:K:2852:C:H5''	1.82	0.61
1:A:237:LYS:HZ2	4:K:2839:G:H4'	1.64	0.61
2:B:73:ILE:HD12	2:B:73:ILE:N	2.15	0.61
2:B:131:LEU:CD1	2:B:142:GLU:HG2	2.31	0.61
2:B:360:LYS:CB	2:B:406:GLU:HG2	2.26	0.61
2:B:529:ILE:H	2:B:529:ILE:CD1	2.08	0.61
3:J:554:C:O3'	3:J:555:A:H2'	2.01	0.61
3:J:586:G:H2'	3:J:587:C:C6	2.35	0.61
3:J:553:G:N2	3:J:572:C:N3	2.49	0.61
3:J:568:G:C2'	3:J:569:C:H5'	2.30	0.61
1:A:78:ASP:CG	7:E:9:ALA:HA	2.26	0.60
4:K:2931:C:C5	4:K:2932:U:H5	2.19	0.60
1:A:187:LYS:CE	5:L:66:C:P	2.66	0.60
2:B:110:GLY:HA3	2:B:114:ILE:HD13	1.82	0.60
2:B:322:ILE:CG1	2:B:325:GLU:HB2	2.30	0.60
4:K:2850:G:H5''	4:K:2850:G:C8	2.35	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:2925:C:H2'	4:K:2926:A:O4'	2.00	0.60
8:G:180:PRO:HD2	8:G:181:PHE:H	1.66	0.60
2:B:116:LYS:HE3	14:B:702:ATP:O2G	2.00	0.60
2:B:458:ASP:HA	2:B:461:ILE:HD11	1.81	0.60
3:J:1433:G:N2	3:J:1434:U:C4	2.68	0.60
4:K:3032:A:H2'	6:F:170:LYS:NZ	2.16	0.60
10:H:40:LYS:N	10:H:68:GLN:HG2	2.16	0.60
1:A:187:LYS:NZ	5:L:66:C:C5'	2.65	0.60
2:B:328:ARG:O	2:B:328:ARG:HG3	2.00	0.60
4:K:2931:C:O2'	4:K:2932:U:H5'	2.00	0.60
2:B:194:ARG:HA	2:B:194:ARG:HE	1.66	0.60
2:B:202:VAL:HG23	2:B:203:LYS:N	2.17	0.60
2:B:491:ILE:HG12	2:B:494:PRO:HG3	1.82	0.60
10:H:46:ILE:HD12	10:H:71:ALA:HB3	1.82	0.60
2:B:28:SER:HB3	2:B:64:LYS:CD	2.31	0.60
2:B:111:THR:O	2:B:114:ILE:HG23	2.01	0.60
2:B:195:MET:CE	2:B:202:VAL:HA	2.32	0.60
2:B:558:LEU:H	2:B:558:LEU:HD12	1.66	0.60
3:J:418:G:H2'	9:C:72:ARG:NH2	2.16	0.60
3:J:463:U:H2'	3:J:464:A:O4'	2.01	0.60
3:J:1189:A:H2'	3:J:1189:A:N3	2.15	0.60
4:K:1277:C:OP2	4:K:1277:C:C6	2.54	0.60
2:B:300:VAL:HG12	2:B:301:TYR:HD1	1.64	0.60
2:B:435:PHE:CD1	2:B:439:ARG:HB2	2.37	0.60
3:J:38:C:C3'	3:J:39:A:H5''	2.32	0.60
4:K:2833:A:C2'	4:K:2834:G:H5'	2.31	0.60
1:A:158:THR:HB	1:A:160:SER:H	1.67	0.60
1:A:315:SER:HB3	1:A:373:LYS:HG2	1.82	0.60
2:B:30:PRO:HG2	2:B:56:ILE:CD1	2.32	0.60
2:B:234:MET:HA	2:B:237:VAL:HG22	1.82	0.60
3:J:426:G:N1	3:J:427:C:C4	2.70	0.60
1:A:237:LYS:HZ1	4:K:2839:G:C3'	2.14	0.60
2:B:179:ALA:C	2:B:180:ILE:HD12	2.26	0.60
4:K:1256:G:C5	4:K:1257:C:C6	2.90	0.60
2:B:130:ASN:HA	2:B:135:ASP:HB3	1.84	0.60
2:B:424:PRO:HB3	2:B:465:VAL:CG1	2.32	0.60
3:J:550:A:H5''	3:J:551:G:OP1	2.01	0.60
3:J:1428:G:H2'	3:J:1428:G:N3	2.16	0.60
4:K:3032:A:C1'	6:F:170:LYS:CE	2.80	0.60
9:C:219:ARG:O	9:C:223:LYS:HB2	2.01	0.60
2:B:31:VAL:HG23	2:B:32:VAL:N	2.16	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:167:ILE:HD12	2:B:238:GLN:CB	2.32	0.59
2:B:338:ILE:HD12	2:B:338:ILE:N	2.17	0.59
3:J:1196:A:C4'	3:J:1197:C:H5''	2.29	0.59
4:K:1232:C:H41	4:K:1261:G:H3'	1.67	0.59
4:K:2918:G:N2	4:K:2919:A:C8	2.70	0.59
4:K:3019:U:C4	4:K:3020:U:C4	2.90	0.59
4:K:2290:C:O2'	4:K:2291:A:O5'	2.20	0.59
2:B:87:TYR:CD2	14:B:702:ATP:C6	2.90	0.59
2:B:94:LEU:HD13	2:B:95:HIS:H	1.66	0.59
2:B:234:MET:C	2:B:237:VAL:HG22	2.27	0.59
2:B:558:LEU:HD12	2:B:558:LEU:N	2.17	0.59
3:J:425:A:H8	3:J:425:A:H5'	1.68	0.59
4:K:1249:G:H2'	4:K:1250:G:C8	2.37	0.59
4:K:1274:A:C6	4:K:1275:C:C5	2.91	0.59
4:K:3018:C:C4	4:K:3019:U:C5	2.90	0.59
9:C:8:PRO:HG3	9:C:112:VAL:HG13	1.84	0.59
9:C:135:PRO:HB2	9:C:141:ILE:HG12	1.84	0.59
10:H:101:SER:HA	10:H:138:SER:O	2.02	0.59
2:B:25:CYS:SG	2:B:70:ILE:HD11	2.42	0.59
2:B:60:ILE:CG1	15:B:703:SF4:S2	2.89	0.59
2:B:116:LYS:O	2:B:120:LEU:HD13	2.02	0.59
2:B:196:GLU:HG3	2:B:239:GLU:HG2	1.83	0.59
6:F:86:TYR:CD1	6:F:151:VAL:HG13	2.37	0.59
10:H:109:ILE:CB	10:H:129:THR:OG1	2.50	0.59
1:A:187:LYS:CG	5:L:66:C:OP1	2.51	0.59
2:B:140:TRP:CB	2:B:160:LEU:HD22	2.32	0.59
2:B:186:LYS:HG3	2:B:218:ASP:OD1	2.02	0.59
3:J:426:G:C6	3:J:427:C:N4	2.71	0.59
4:K:3032:A:N9	6:F:170:LYS:NZ	2.49	0.59
2:B:140:TRP:HB3	2:B:160:LEU:CD1	2.32	0.59
2:B:588:SER:O	2:B:592:LYS:CB	2.50	0.59
3:J:567:A:H1'	7:E:14:VAL:HG23	1.85	0.59
3:J:1275:A:N6	3:J:1431:C:N3	2.51	0.59
1:A:364:GLN:OE1	2:B:58:CYS:HB3	2.03	0.59
4:K:1270:A:C8	4:K:1271:A:C8	2.90	0.59
2:B:510:ILE:HG22	2:B:514:ILE:HD12	1.83	0.59
3:J:44:U:O5'	3:J:45:U:C5	2.54	0.59
3:J:450:U:H2'	3:J:451:A:H8	1.64	0.59
4:K:2289:U:N3	4:K:2290:C:C5	2.71	0.59
2:B:140:TRP:CB	2:B:160:LEU:HD13	2.33	0.59
2:B:420:GLN:HG3	2:B:421:LYS:N	2.18	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:1277:C:O2'	4:K:1278:A:P	2.61	0.59
8:G:43:LYS:CA	10:H:121:PHE:HE1	1.95	0.59
10:H:67:ARG:HG2	10:H:67:ARG:O	2.02	0.59
2:B:62:VAL:HG23	2:B:70:ILE:O	2.03	0.59
2:B:180:ILE:HD12	2:B:180:ILE:N	2.17	0.59
3:J:1199:G:N2	3:J:1201:G:OP2	2.36	0.59
4:K:2833:A:C6	4:K:2834:G:N7	2.71	0.59
4:K:3021:A:C4	4:K:3023:U:C4	2.91	0.59
10:H:109:ILE:HD11	10:H:129:THR:HB	1.78	0.59
2:B:195:MET:HE3	2:B:202:VAL:HG12	1.84	0.58
2:B:268:LEU:HD22	2:B:268:LEU:C	2.27	0.58
2:B:360:LYS:HE3	2:B:367:VAL:CG1	2.33	0.58
4:K:1229:G:H2'	4:K:1230:G:O4'	2.03	0.58
4:K:1258:U:H2'	4:K:1258:U:O2	2.02	0.58
4:K:1270:A:H5'	4:K:1271:A:OP2	2.03	0.58
10:H:23:GLY:HA2	10:H:46:ILE:HD11	1.85	0.58
1:A:47:PHE:HA	3:J:577:G:C6	2.37	0.58
2:B:397:LEU:HD23	2:B:402:LEU:CB	2.31	0.58
4:K:2295:A:H1'	11:I:37:ILE:HD13	1.84	0.58
12:D:104:SER:HB3	12:D:107:GLN:HB2	1.85	0.58
2:B:143:ILE:HD12	2:B:156:PHE:CD1	2.37	0.58
2:B:509:VAL:O	2:B:513:PHE:HD2	1.86	0.58
3:J:426:G:C2	3:J:427:C:C5	2.92	0.58
4:K:1252:A:H2'	4:K:1253:U:C5'	2.33	0.58
4:K:2931:C:H4'	11:I:39:VAL:O	2.03	0.58
1:A:143:ALA:HA	1:A:156:LEU:HA	1.86	0.58
2:B:140:TRP:HB2	2:B:160:LEU:HD13	1.83	0.58
2:B:424:PRO:CB	2:B:465:VAL:HG12	2.33	0.58
3:J:1433:G:N2	3:J:1434:U:C5	2.67	0.58
4:K:1271:A:N6	4:K:1272:C:N4	2.52	0.58
4:K:2919:A:C3'	4:K:2920:U:C5'	2.81	0.58
2:B:8:ILE:CD1	2:B:79:LEU:HD13	2.33	0.58
2:B:100:PRO:HB3	2:B:273:TYR:CZ	2.37	0.58
2:B:133:ARG:HG2	2:B:134:PHE:HD2	1.67	0.58
2:B:136:ASP:HB3	2:B:137:PRO:HD3	1.85	0.58
2:B:195:MET:HE3	2:B:202:VAL:N	2.19	0.58
2:B:589:GLN:NE2	2:B:589:GLN:H	2.01	0.58
3:J:45:U:H5'	3:J:45:U:C6	2.39	0.58
3:J:1431:C:H3'	3:J:1432:U:C5'	2.34	0.58
8:G:15:LEU:HD21	8:G:53:MET:H	1.68	0.58
2:B:195:MET:CE	2:B:237:VAL:HG12	2.34	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:275:ILE:HD13	2:B:276:CYS:H	1.67	0.58
2:B:394:LEU:HD13	2:B:394:LEU:C	2.28	0.58
2:B:424:PRO:HB3	2:B:465:VAL:HG12	1.85	0.58
2:B:491:ILE:HG21	2:B:523:ILE:HG13	1.86	0.58
4:K:2839:G:C6	4:K:2850:G:C2	2.91	0.58
2:B:180:ILE:HG21	2:B:219:ILE:HD12	1.84	0.58
2:B:295:TYR:HE1	2:B:305:THR:HG1	1.48	0.58
3:J:1199:G:C5	3:J:1200:G:C1'	2.86	0.58
3:J:1199:G:N1	3:J:1201:G:OP1	2.37	0.58
6:F:91:ARG:HG3	6:F:91:ARG:NH2	1.99	0.58
9:C:186:ARG:O	9:C:190:GLN:HG2	2.04	0.58
10:H:85:LEU:CD2	10:H:86:LYS:CA	2.66	0.58
10:H:85:LEU:HD23	10:H:86:LYS:C	2.24	0.58
2:B:176:ILE:HD11	2:B:227:LEU:CG	2.34	0.58
2:B:294:ILE:N	2:B:294:ILE:HD12	2.19	0.58
4:K:2833:A:H2'	4:K:2833:A:N3	2.18	0.58
9:C:142:ARG:HA	9:C:147:LEU:HD12	1.85	0.58
2:B:491:ILE:HD13	2:B:494:PRO:HG3	1.85	0.57
4:K:2853:A:N6	4:K:2854:U:N3	2.51	0.57
2:B:92:PHE:HB2	14:B:702:ATP:HO2'	1.69	0.57
2:B:488:ILE:HG13	2:B:520:THR:HG23	1.85	0.57
3:J:1200:G:H5''	3:J:1200:G:C8	2.39	0.57
4:K:1246:G:C2	4:K:1247:U:O2	2.56	0.57
2:B:117:SER:HB2	14:B:702:ATP:O1A	2.04	0.57
2:B:271:THR:O	2:B:271:THR:HG22	2.03	0.57
2:B:444:ASN:HD21	2:B:447:PHE:HD2	1.53	0.57
1:A:299:TRP:CD1	1:A:379:LEU:HD12	2.39	0.57
4:K:2295:A:O2'	11:I:73:VAL:HG11	2.04	0.57
4:K:2836:C:O2	4:K:2836:C:H2'	2.04	0.57
10:H:46:ILE:C	10:H:48:LYS:H	2.12	0.57
3:J:1177:C:H2'	3:J:1178:G:O4'	2.04	0.57
4:K:1269:U:C4	4:K:1271:A:C5	2.92	0.57
4:K:2850:G:H5''	4:K:2850:G:H8	1.70	0.57
10:H:40:LYS:HB2	10:H:68:GLN:HB3	1.85	0.57
2:B:160:LEU:HD23	2:B:160:LEU:N	2.19	0.57
2:B:234:MET:CA	2:B:237:VAL:HG22	2.35	0.57
3:J:463:U:H2'	3:J:464:A:C8	2.39	0.57
3:J:1437:U:O2	3:J:1437:U:C2'	2.40	0.57
4:K:3027:A:C5	4:K:3028:G:C5	2.92	0.57
2:B:31:VAL:CG1	2:B:56:ILE:HG23	2.35	0.57
2:B:194:ARG:CG	2:B:237:VAL:HG23	2.35	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:491:ILE:CG1	2:B:494:PRO:HG3	2.34	0.57
4:K:1248:C:C5	4:K:1249:G:H8	2.22	0.57
4:K:1274:A:C2'	4:K:1275:C:H5''	2.30	0.57
4:K:2295:A:C6	4:K:2296:A:C6	2.92	0.57
10:H:80:LEU:CG	10:H:83:THR:HG21	2.34	0.57
10:H:82:ILE:C	10:H:84:ALA:N	2.62	0.57
2:B:29:CYS:HA	2:B:60:ILE:HD11	1.85	0.57
2:B:114:ILE:CD1	2:B:294:ILE:HB	2.34	0.57
2:B:574:ARG:CD	2:B:602:PHE:O	2.53	0.57
3:J:1438:G:H2'	3:J:1439:C:O4'	2.05	0.57
4:K:2285:C:C5	4:K:2286:U:C4	2.93	0.57
1:A:374:TYR:CE2	4:K:1242:G:C2	2.93	0.57
2:B:410:ILE:HG23	2:B:410:ILE:O	2.05	0.57
2:B:488:ILE:HD11	2:B:522:PHE:HE1	1.65	0.57
3:J:440:U:O2'	3:J:441:A:OP1	2.22	0.57
4:K:1269:U:H2'	4:K:1270:A:H5''	1.85	0.57
4:K:2297:U:C2	4:K:2299:A:C6	2.93	0.57
10:H:109:ILE:HD11	10:H:125:LEU:HG	1.87	0.57
12:D:51:GLU:OE2	12:D:53:ASP:N	2.33	0.57
1:A:237:LYS:NZ	4:K:2839:G:O3'	2.25	0.57
2:B:79:LEU:HG	2:B:95:HIS:CE1	2.40	0.57
2:B:97:LEU:HB2	2:B:152:LEU:CD1	2.34	0.57
2:B:527:ASP:OD2	2:B:529:ILE:HG12	2.05	0.57
3:J:48:G:C5	3:J:432:G:N2	2.72	0.57
4:K:2288:G:N3	4:K:2289:U:C5	2.73	0.57
10:H:109:ILE:HD11	10:H:129:THR:CG2	2.34	0.57
2:B:31:VAL:HG21	2:B:38:CYS:HB2	1.86	0.56
2:B:77:THR:HG23	2:B:77:THR:O	2.05	0.56
2:B:363:GLN:HG3	2:B:365:ASP:N	2.19	0.56
2:B:568:LEU:HD22	2:B:570:VAL:CG1	2.35	0.56
4:K:1269:U:H3	4:K:1271:A:H62	1.53	0.56
4:K:2931:C:O3'	11:I:41:GLY:N	2.31	0.56
8:G:107:ALA:CB	8:G:183:PHE:CZ	2.80	0.56
12:D:77:ASN:O	12:D:78:SER:HB3	2.05	0.56
1:A:308:ALA:HA	1:A:379:LEU:HD13	1.87	0.56
2:B:105:VAL:O	2:B:106:LEU:HD23	2.05	0.56
2:B:168:ILE:HD13	2:B:168:ILE:N	2.19	0.56
2:B:345:LEU:HD22	2:B:345:LEU:N	2.18	0.56
3:J:155:U:H1'	9:C:60:GLY:HA3	1.87	0.56
3:J:553:G:C5	3:J:554:C:C4	2.93	0.56
2:B:12:SER:OG	2:B:15:LYS:HD2	2.05	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:205:TYR:OH	2:B:232:ILE:HG22	2.05	0.56
2:B:338:ILE:HD12	2:B:338:ILE:H	1.69	0.56
2:B:424:PRO:HG3	2:B:465:VAL:HG12	1.87	0.56
2:B:444:ASN:ND2	2:B:447:PHE:HD2	2.02	0.56
2:B:508:LYS:CE	2:B:512:ARG:HD2	2.34	0.56
2:B:572:PHE:O	2:B:573:ARG:O	2.23	0.56
3:J:427:C:H5'	3:J:427:C:C6	2.37	0.56
3:J:438:A:H8	3:J:438:A:O5'	1.88	0.56
3:J:445:A:N6	3:J:461:G:N2	2.52	0.56
3:J:450:U:H2'	3:J:450:U:O2	2.05	0.56
4:K:1265:U:O4	4:K:1277:C:C4	2.58	0.56
4:K:2931:C:H2'	4:K:2932:U:O4'	2.05	0.56
4:K:3020:U:H2'	4:K:3021:A:H8	1.70	0.56
4:K:3038:U:C2'	4:K:3039:C:O5'	2.52	0.56
10:H:23:GLY:O	10:H:27:ALA:HB3	2.05	0.56
2:B:133:ARG:HG2	2:B:134:PHE:N	2.18	0.56
2:B:234:MET:HA	2:B:237:VAL:HG21	1.88	0.56
4:K:1239:C:H2'	4:K:1240:A:O4'	2.04	0.56
4:K:1258:U:C2'	4:K:1259:A:O5'	2.50	0.56
4:K:2836:C:O2	4:K:2837:A:C8	2.59	0.56
4:K:3020:U:H2'	4:K:3021:A:C8	2.40	0.56
8:G:37:GLN:O	8:G:41:VAL:HG23	2.05	0.56
10:H:125:LEU:CB	10:H:129:THR:CG2	2.56	0.56
2:B:73:ILE:HG22	2:B:74:ASN:N	2.20	0.56
2:B:293:ILE:HD11	2:B:305:THR:CB	2.36	0.56
3:J:432:G:O2'	3:J:433:C:H5'	2.06	0.56
3:J:575:C:N4	3:J:576:G:C6	2.74	0.56
4:K:3030:G:H2'	4:K:3031:G:O4'	2.05	0.56
2:B:28:SER:OG	2:B:64:LYS:HD3	2.06	0.56
2:B:112:ASN:HA	14:B:702:ATP:O3G	2.05	0.56
2:B:573:ARG:HG2	2:B:574:ARG:H	1.69	0.56
3:J:571:G:H2'	3:J:571:G:N3	2.21	0.56
3:J:1205:C:C6	3:J:1206:U:O2	2.59	0.56
4:K:2834:G:C4	4:K:2835:U:H5	2.19	0.56
9:C:78:THR:HG23	9:C:92:ARG:HG2	1.86	0.56
1:A:313:ALA:HB1	1:A:372:LEU:HD13	1.87	0.56
2:B:38:CYS:SG	2:B:55:CYS:HA	2.45	0.56
2:B:243:TYR:CE2	2:B:272:LYS:HD3	2.41	0.56
2:B:375:PHE:CZ	2:B:381:LEU:HB2	2.41	0.56
3:J:152:U:O4'	9:C:13:GLN:CB	2.54	0.56
3:J:418:G:C2'	9:C:72:ARG:HH21	2.12	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1198:G:C3'	3:J:1199:G:H5'	2.31	0.56
11:I:33:ASN:HD21	11:I:63:LYS:H	1.54	0.56
2:B:224:GLY:HA3	2:B:251:TYR:CD1	2.41	0.56
3:J:428:A:H2	3:J:440:U:O2	1.88	0.56
3:J:586:G:C4'	7:E:21:VAL:HG22	2.35	0.56
4:K:2296:A:C2	4:K:2919:A:H1'	2.41	0.56
2:B:180:ILE:CG2	2:B:219:ILE:HD12	2.36	0.56
2:B:349:SER:OG	2:B:377:ASP:HB3	2.05	0.56
2:B:589:GLN:HG3	9:C:107:ALA:HB2	1.87	0.56
4:K:1235:U:O4	10:H:135:THR:OG1	2.16	0.56
10:H:43:GLY:HA2	10:H:46:ILE:CG2	2.36	0.56
10:H:125:LEU:C	10:H:125:LEU:CD2	2.78	0.56
1:A:149:GLU:O	1:A:174:LYS:HA	2.06	0.55
3:J:38:C:H3'	3:J:39:A:H5''	1.88	0.55
3:J:40:A:H2'	3:J:41:A:O4'	2.06	0.55
4:K:1257:C:N3	4:K:1258:U:C4	2.74	0.55
4:K:2295:A:H62	4:K:2296:A:N6	2.00	0.55
4:K:2836:C:O2	4:K:2836:C:C3'	2.54	0.55
4:K:2842:U:C6	4:K:2842:U:O5'	2.59	0.55
4:K:2918:G:N3	4:K:2919:A:C8	2.74	0.55
4:K:2932:U:O5'	11:I:41:GLY:HA2	2.04	0.55
8:G:15:LEU:HB3	8:G:64:ARG:HH21	1.71	0.55
10:H:109:ILE:O	10:H:113:ALA:N	2.39	0.55
2:B:195:MET:CE	2:B:202:VAL:HG12	2.37	0.55
2:B:375:PHE:CE1	2:B:522:PHE:CE2	2.95	0.55
2:B:518:LYS:HE3	6:F:116:ASN:HD22	1.72	0.55
2:B:556:SER:OG	2:B:559:THR:HG23	2.06	0.55
3:J:452:A:N1	3:J:454:U:C6	2.74	0.55
3:J:581:U:O2	3:J:581:U:H2'	2.05	0.55
3:J:1272:U:O4	3:J:1431:C:O2	2.23	0.55
5:L:67:G:H2'	5:L:68:C:H5''	1.88	0.55
10:H:85:LEU:HD22	10:H:86:LYS:N	2.08	0.55
10:H:109:ILE:HD11	10:H:129:THR:HG21	1.88	0.55
2:B:574:ARG:CD	2:B:602:PHE:C	2.78	0.55
4:K:2931:C:C2	4:K:2932:U:C6	2.94	0.55
2:B:42:THR:HG23	2:B:42:THR:O	2.05	0.55
2:B:99:THR:O	2:B:106:LEU:HD12	2.06	0.55
2:B:108:LEU:HD23	2:B:294:ILE:HD13	1.85	0.55
3:J:551:G:N1	3:J:552:G:C5	2.75	0.55
3:J:587:C:H2'	3:J:588:U:O4'	2.07	0.55
4:K:3035:A:H1'	6:F:121:LYS:HB2	1.87	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:13:PRO:HD2	6:F:16:VAL:CG2	2.37	0.55
6:F:86:TYR:CE2	6:F:151:VAL:HG22	2.41	0.55
10:H:108:GLU:HA	10:H:112:ILE:CG2	2.36	0.55
11:I:86:ARG:HG3	11:I:92:PHE:CE2	2.42	0.55
2:B:205:TYR:CE2	2:B:209:LEU:HD12	2.42	0.55
3:J:454:U:O2'	3:J:455:C:O4'	2.20	0.55
3:J:568:G:O2'	3:J:569:C:H5'	2.06	0.55
3:J:1275:A:OP1	3:J:1275:A:H8	1.85	0.55
4:K:3021:A:C5	4:K:3023:U:O4	2.59	0.55
1:A:101:VAL:HG21	3:J:1272:U:C3'	2.36	0.55
2:B:49:PHE:HE1	2:B:89:ALA:CB	2.13	0.55
2:B:108:LEU:HD13	2:B:277:VAL:HG22	1.89	0.55
2:B:413:LEU:HD22	2:B:413:LEU:N	2.20	0.55
3:J:434:G:N2	3:J:437:A:H2	2.05	0.55
4:K:2295:A:C1'	11:I:37:ILE:HD13	2.37	0.55
10:H:57:LYS:C	10:H:58:VAL:HG22	2.31	0.55
10:H:123:ARG:CD	10:H:126:ALA:CB	2.84	0.55
2:B:195:MET:HG2	2:B:202:VAL:HG13	1.88	0.55
2:B:331:THR:HG23	2:B:332:GLU:N	2.22	0.55
2:B:480:LEU:HD23	2:B:480:LEU:C	2.32	0.55
3:J:557:G:H3'	3:J:558:U:H4'	1.87	0.55
3:J:1277:G:O6	3:J:1278:G:C2	2.59	0.55
4:K:1232:C:C4	4:K:1261:G:N3	2.75	0.55
4:K:3037:U:HO2'	4:K:3038:U:H5'	1.70	0.55
4:K:2286:U:C4	4:K:2288:G:C1'	2.89	0.55
6:F:77:ASN:HB3	6:F:151:VAL:HG21	1.89	0.55
9:C:109:LEU:HD13	9:C:111:LEU:HD21	1.87	0.55
2:B:380:ILE:HG21	2:B:535:ALA:HA	1.87	0.55
2:B:430:VAL:HG12	2:B:461:ILE:HA	1.89	0.55
3:J:47:A:O5'	3:J:48:G:H5''	2.07	0.55
4:K:2841:G:H3'	4:K:2842:U:H5'	1.88	0.55
4:K:2847:A:N3	4:K:2848:G:C8	2.75	0.55
2:B:39:ILE:HD13	2:B:50:ILE:CG1	2.35	0.55
2:B:92:PHE:CD2	14:B:702:ATP:C4'	2.90	0.55
2:B:380:ILE:HG23	2:B:380:ILE:O	2.06	0.55
3:J:52:U:H6	3:J:52:U:O5'	1.89	0.55
1:A:290:HIS:HB2	1:A:298:ALA:HB2	1.89	0.54
2:B:136:ASP:N	2:B:137:PRO:HD2	2.20	0.54
2:B:435:PHE:CZ	8:G:145:ILE:HD11	2.40	0.54
3:J:551:G:C2	3:J:552:G:N7	2.75	0.54
3:J:1206:U:H5'	3:J:1207:C:OP2	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:21:GLU:CA	10:H:50:THR:HG22	2.37	0.54
2:B:79:LEU:HD23	2:B:79:LEU:C	2.32	0.54
3:J:1431:C:H5'	3:J:1432:U:H5'	1.90	0.54
4:K:1269:U:C4	4:K:1271:A:N7	2.75	0.54
6:F:29:GLY:HA3	6:F:82:VAL:HG13	1.89	0.54
9:C:58:LYS:C	9:C:60:GLY:H	2.15	0.54
9:C:70:PRO:C	9:C:98:ARG:HH11	2.14	0.54
10:H:16:ARG:HB2	10:H:60:VAL:HB	1.89	0.54
10:H:66:ASN:C	10:H:66:ASN:HD22	2.15	0.54
2:B:140:TRP:HE3	2:B:143:ILE:HD13	1.72	0.54
2:B:362:THR:OG1	2:B:367:VAL:HG22	2.08	0.54
3:J:39:A:C4	3:J:467:G:N2	2.75	0.54
3:J:47:A:H4'	3:J:48:G:H5'	1.89	0.54
3:J:448:C:H2'	3:J:449:C:H6	1.70	0.54
3:J:451:A:C2	3:J:454:U:O4	2.61	0.54
4:K:1276:U:N3	4:K:1277:C:C5	2.75	0.54
4:K:2295:A:N6	4:K:2296:A:H61	2.03	0.54
12:D:94:TYR:HD2	12:D:96:LEU:HD11	1.72	0.54
3:J:446:A:C2'	3:J:447:U:H5'	2.37	0.54
3:J:551:G:N3	3:J:552:G:C8	2.75	0.54
2:B:457:ILE:HG23	2:B:460:ILE:HG22	1.87	0.54
2:B:468:LEU:CG	2:B:469:SER:H	2.16	0.54
3:J:432:G:H2'	3:J:433:C:O4'	2.07	0.54
3:J:567:A:N6	3:J:568:G:C4	2.75	0.54
3:J:1209:C:H2'	3:J:1210:C:C6	2.42	0.54
4:K:2290:C:C2	4:K:2291:A:C8	2.95	0.54
2:B:413:LEU:HD12	2:B:487:ASP:HB3	1.89	0.54
3:J:45:U:C3'	3:J:45:U:H6	2.20	0.54
3:J:1194:A:H2'	3:J:1195:C:H5'	1.89	0.54
4:K:1244:A:OP1	10:H:18:VAL:HA	2.08	0.54
4:K:2847:A:C2	4:K:2848:G:C1'	2.90	0.54
2:B:136:ASP:HB3	2:B:137:PRO:CD	2.36	0.54
3:J:44:U:OP2	3:J:45:U:O4	2.25	0.54
3:J:419:G:O3'	9:C:96:SER:CB	2.56	0.54
3:J:1429:G:C5	3:J:1430:U:C5	2.95	0.54
4:K:3027:A:C2'	4:K:3028:G:H8	2.07	0.54
4:K:3032:A:C2	6:F:170:LYS:HD3	2.41	0.54
10:H:108:GLU:HA	10:H:112:ILE:HG21	1.88	0.54
1:A:101:VAL:HG23	3:J:1272:U:O2'	2.08	0.54
2:B:362:THR:HG22	2:B:405:ASP:OD2	2.08	0.54
3:J:47:A:C8	3:J:425:A:C5	2.96	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:449:C:O2	3:J:449:C:H2'	2.08	0.54
3:J:1431:C:H3'	3:J:1432:U:H5'	1.90	0.54
4:K:2848:G:C6	4:K:2849:C:C5	2.96	0.54
10:H:138:SER:C	10:H:140:GLY:H	2.14	0.54
1:A:170:TYR:CG	1:A:191:PHE:HB2	2.42	0.54
2:B:468:LEU:HD23	2:B:473:LEU:HB2	1.88	0.54
3:J:569:C:H1'	3:J:583:C:C5'	2.37	0.54
2:B:140:TRP:CZ3	2:B:159:MET:HE3	2.43	0.54
4:K:2298:U:O4'	4:K:2298:U:O2	2.23	0.54
6:F:156:GLN:NE2	6:F:160:ASP:OD1	2.38	0.54
2:B:182:GLY:HA3	2:B:184:VAL:O	2.07	0.53
3:J:42:G:O4'	3:J:437:A:C8	2.61	0.53
4:K:1234:G:O3'	10:H:116:MET:HE1	2.08	0.53
2:B:183:PRO:CD	2:B:184:VAL:H	2.13	0.53
2:B:293:ILE:CD1	2:B:305:THR:HB	2.38	0.53
3:J:1277:G:O2'	3:J:1278:G:H5'	2.08	0.53
12:D:36:SER:O	12:D:40:LEU:HG	2.08	0.53
1:A:49:SER:HB3	3:J:565:C:C4	2.44	0.53
2:B:11:VAL:HG22	2:B:90:ASN:HB3	1.89	0.53
3:J:52:U:O2'	3:J:53:G:H5'	2.09	0.53
10:H:123:ARG:O	10:H:124:THR:O	2.26	0.53
1:A:104:TYR:CE2	3:J:578:U:C6	2.96	0.53
2:B:183:PRO:HD3	2:B:186:LYS:O	2.08	0.53
2:B:334:LEU:CG	2:B:504:ILE:HD12	2.31	0.53
2:B:429:THR:HG22	2:B:432:GLN:HG3	1.91	0.53
3:J:445:A:C2	3:J:446:A:C5	2.97	0.53
3:J:1196:A:C4'	3:J:1197:C:C5'	2.86	0.53
3:J:1209:C:C2	3:J:1210:C:C5	2.96	0.53
4:K:1278:A:H1'	4:K:1279:C:H5'	1.90	0.53
6:F:96:HIS:CE1	6:F:97:PHE:CE1	2.96	0.53
10:H:22:VAL:HG13	10:H:28:LEU:HD12	1.90	0.53
2:B:140:TRP:CE3	2:B:143:ILE:HD13	2.42	0.53
2:B:422:ILE:HD13	2:B:473:LEU:HG	1.90	0.53
3:J:454:U:O2'	3:J:455:C:P	2.66	0.53
4:K:1269:U:N3	4:K:1271:A:N6	2.56	0.53
4:K:2836:C:C5	4:K:2853:A:C2	2.97	0.53
8:G:42:ARG:HB2	8:G:46:ARG:CZ	2.39	0.53
12:D:49:LYS:HD3	12:D:49:LYS:N	2.24	0.53
1:A:49:SER:CB	3:J:565:C:N4	2.71	0.53
1:A:374:TYR:CB	4:K:1270:A:H1'	2.32	0.53
2:B:53:ILE:HG13	2:B:54:LEU:H	1.72	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:214:VAL:O	2:B:214:VAL:HG12	2.09	0.53
3:J:1197:C:O2	3:J:1197:C:C2'	2.56	0.53
4:K:1244:A:C6	4:K:1248:C:N3	2.76	0.53
4:K:2285:C:H5	4:K:2286:U:C4	2.25	0.53
2:B:28:SER:CB	2:B:64:LYS:HD3	2.39	0.53
2:B:393:THR:HA	2:B:396:LYS:HD2	1.90	0.53
2:B:430:VAL:HG11	2:B:460:ILE:CG2	2.27	0.53
2:B:437:LYS:HG3	2:B:480:LEU:HG	1.90	0.53
2:B:510:ILE:HG22	2:B:514:ILE:CD1	2.38	0.53
3:J:1192:C:C6	3:J:1193:A:C8	2.97	0.53
3:J:1204:A:H5'	3:J:1205:C:H5''	1.89	0.53
10:H:116:MET:O	10:H:116:MET:HG2	2.07	0.53
2:B:87:TYR:O	2:B:88:SER:HB2	2.09	0.53
4:K:1262:G:N7	4:K:1264:G:C4	2.76	0.53
4:K:2834:G:O2'	4:K:2835:U:C6	2.53	0.53
4:K:2847:A:C5'	4:K:2848:G:OP2	2.47	0.53
4:K:2929:C:H3'	4:K:2929:C:C6	2.44	0.53
11:I:86:ARG:HA	11:I:91:VAL:O	2.08	0.53
2:B:58:CYS:SG	15:B:703:SF4:S1	3.06	0.53
2:B:182:GLY:O	2:B:219:ILE:HD12	2.09	0.53
2:B:492:ASP:OD1	2:B:493:GLU:HG3	2.09	0.53
3:J:430:G:H2'	3:J:431:C:H6	1.74	0.53
3:J:1200:G:H5'	3:J:1201:G:H8	1.73	0.53
4:K:1259:A:H2'	4:K:1280:C:O2'	2.09	0.53
11:I:23:MET:HB2	11:I:99:ALA:HA	1.90	0.53
11:I:108:GLU:HG2	11:I:128:ARG:NH1	2.24	0.53
2:B:394:LEU:O	2:B:398:LEU:HD23	2.09	0.53
2:B:565:LEU:CD1	2:B:600:TYR:HB3	2.39	0.53
3:J:553:G:C6	3:J:554:C:C4	2.96	0.53
4:K:2925:C:C6	4:K:2926:A:C8	2.97	0.53
10:H:131:GLU:O	10:H:132:ILE:C	2.52	0.53
2:B:291:VAL:HG12	2:B:309:SER:O	2.09	0.52
3:J:418:G:N2	3:J:419:G:C4	2.78	0.52
5:L:17:G:H3'	5:L:18:G:H5''	1.91	0.52
10:H:16:ARG:HB3	10:H:57:LYS:HD2	1.91	0.52
2:B:103:GLY:HA2	2:B:271:THR:HA	1.91	0.52
2:B:422:ILE:HG23	2:B:422:ILE:O	2.09	0.52
2:B:508:LYS:HE3	2:B:512:ARG:HD2	1.91	0.52
4:K:1239:C:H2'	4:K:1240:A:H8	1.74	0.52
4:K:2294:U:C6	4:K:2297:U:C5	2.97	0.52
9:C:139:ASN:HA	9:C:142:ARG:HB2	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1198:G:H5''	3:J:1199:G:H8	1.74	0.52
4:K:2299:A:H8	4:K:2299:A:C5'	2.20	0.52
8:G:42:ARG:CB	8:G:46:ARG:CZ	2.88	0.52
10:H:10:VAL:HG12	10:H:11:LYS:H	1.73	0.52
3:J:427:C:C6	3:J:427:C:H5''	2.41	0.52
3:J:1201:G:C5	3:J:1202:A:O4'	2.63	0.52
3:J:1203:A:C4'	3:J:1204:A:OP2	2.58	0.52
9:C:67:VAL:O	9:C:68:LEU:HB2	2.10	0.52
2:B:167:ILE:HG21	2:B:243:TYR:CD1	2.45	0.52
2:B:180:ILE:CG2	2:B:183:PRO:HA	2.37	0.52
2:B:242:VAL:HG13	2:B:242:VAL:O	2.08	0.52
2:B:383:MET:HE3	2:B:524:VAL:HG23	1.91	0.52
2:B:435:PHE:HE1	2:B:439:ARG:CD	2.13	0.52
2:B:493:GLU:N	2:B:494:PRO:HD3	2.24	0.52
3:J:426:G:C6	3:J:427:C:C4	2.98	0.52
3:J:1271:G:H2'	3:J:1272:U:H6	1.66	0.52
3:J:1435:G:H4'	3:J:1436:A:H5'	1.91	0.52
4:K:1265:U:O4	4:K:1277:C:C5	2.62	0.52
4:K:2932:U:C5'	11:I:41:GLY:H	2.22	0.52
10:H:17:ALA:H	10:H:57:LYS:HD3	1.73	0.52
10:H:23:GLY:C	10:H:25:SER:H	2.18	0.52
2:B:143:ILE:HG13	2:B:144:ILE:HD12	1.92	0.52
2:B:195:MET:SD	2:B:237:VAL:HG12	2.50	0.52
2:B:290:PHE:HZ	2:B:292:CYS:HG	1.55	0.52
2:B:352:ARG:HG2	2:B:353:ALA:N	2.24	0.52
2:B:437:LYS:HG3	2:B:480:LEU:CG	2.40	0.52
2:B:446:GLN:CD	6:F:96:HIS:CD2	2.88	0.52
3:J:156:A:H5'	3:J:416:A:C8	2.45	0.52
4:K:2922:G:H2'	4:K:2923:U:O4'	2.09	0.52
10:H:109:ILE:CD1	10:H:129:THR:HG21	2.39	0.52
2:B:67:PHE:O	2:B:68:ASP:HB2	2.10	0.52
2:B:101:ARG:HB2	2:B:104:GLN:CG	2.40	0.52
2:B:148:ARG:HH12	3:J:440:U:P	2.31	0.52
2:B:381:LEU:HD13	2:B:554:PRO:HB3	1.92	0.52
2:B:392:THR:O	2:B:396:LYS:HG3	2.10	0.52
4:K:3038:U:C2	4:K:3039:C:C6	2.97	0.52
10:H:112:ILE:O	10:H:132:ILE:HD12	2.10	0.52
10:H:120:SER:O	10:H:121:PHE:HB3	2.09	0.52
2:B:114:ILE:HB	2:B:294:ILE:HG22	1.90	0.52
2:B:381:LEU:HD11	2:B:538:VAL:C	2.35	0.52
3:J:452:A:N1	3:J:454:U:OP2	2.43	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:47:ILE:HG13	2:B:48:ALA:N	2.25	0.52
2:B:100:PRO:HD2	2:B:152:LEU:HD23	1.92	0.52
3:J:39:A:N7	3:J:467:G:N1	2.57	0.52
3:J:563:U:C5'	3:J:564:G:OP2	2.58	0.52
3:J:1176:G:C6	3:J:1177:C:C4	2.98	0.52
3:J:1268:G:O2'	3:J:1269:U:H3'	2.09	0.52
4:K:1236:G:H1	10:H:17:ALA:HA	1.73	0.52
4:K:2290:C:C2'	4:K:2291:A:O5'	2.58	0.52
4:K:3019:U:C5	4:K:3020:U:C4	2.97	0.52
9:C:57:ASP:OD1	9:C:72:ARG:NH1	2.42	0.52
10:H:111:GLU:O	10:H:111:GLU:HG2	2.09	0.52
2:B:491:ILE:HG22	2:B:523:ILE:HA	1.91	0.52
3:J:1210:C:O2	3:J:1210:C:H2'	2.08	0.52
3:J:1429:G:C6	3:J:1430:U:C4	2.98	0.52
4:K:1229:G:C4	4:K:1230:G:C8	2.98	0.52
2:B:60:ILE:HD12	2:B:60:ILE:C	2.35	0.51
2:B:472:GLU:O	2:B:476:VAL:HG23	2.09	0.51
3:J:452:A:H2	3:J:454:U:O5'	1.94	0.51
4:K:1236:G:C6	10:H:57:LYS:HE2	2.45	0.51
4:K:1273:A:H3'	4:K:1274:A:H8	1.75	0.51
10:H:88:PRO:HD2	10:H:89:PRO:CD	2.40	0.51
10:H:109:ILE:HG23	10:H:110:ILE:N	2.20	0.51
2:B:205:TYR:CE2	2:B:209:LEU:CD1	2.94	0.51
2:B:510:ILE:CG2	2:B:514:ILE:HD11	2.40	0.51
3:J:1204:A:N3	3:J:1204:A:C2'	2.73	0.51
4:K:2841:G:C4	4:K:2844:C:N4	2.79	0.51
10:H:23:GLY:HA3	10:H:46:ILE:HD11	1.93	0.51
10:H:87:GLU:HG2	10:H:89:PRO:CD	2.40	0.51
11:I:33:ASN:HD21	11:I:63:LYS:N	2.08	0.51
11:I:87:ARG:HH22	11:I:137:VAL:HG22	1.74	0.51
2:B:60:ILE:O	2:B:63:LYS:HG2	2.10	0.51
2:B:293:ILE:C	2:B:294:ILE:HD12	2.35	0.51
2:B:570:VAL:HG23	2:B:570:VAL:O	2.09	0.51
2:B:572:PHE:C	2:B:573:ARG:O	2.52	0.51
3:J:555:A:H2'	3:J:555:A:P	2.50	0.51
4:K:1236:G:H22	10:H:18:VAL:H	1.59	0.51
4:K:1260:A:H2'	4:K:1261:G:O4'	2.10	0.51
4:K:2288:G:C6	4:K:2289:U:O4	2.62	0.51
4:K:2925:C:C5	4:K:2926:A:C5	2.98	0.51
10:H:104:ILE:CG1	10:H:105:GLN:H	2.22	0.51
10:H:133:LEU:C	10:H:133:LEU:CD2	2.83	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:41:A:H2'	3:J:438:A:H62	1.75	0.51
3:J:445:A:H61	3:J:461:G:N2	2.09	0.51
3:J:555:A:OP2	3:J:555:A:C3'	2.55	0.51
3:J:1205:C:C5	3:J:1206:U:O2	2.63	0.51
4:K:1230:G:C5	4:K:1231:A:N7	2.78	0.51
4:K:3028:G:N2	4:K:3029:A:C2	2.78	0.51
10:H:124:THR:HG23	10:H:125:LEU:N	2.17	0.51
2:B:106:LEU:HD23	2:B:106:LEU:N	2.24	0.51
2:B:205:TYR:HE2	2:B:209:LEU:HD12	1.73	0.51
2:B:434:PHE:CZ	2:B:476:VAL:CG1	2.94	0.51
3:J:561:G:C6	3:J:585:A:N1	2.78	0.51
10:H:42:VAL:HG21	10:H:69:ALA:HB3	1.92	0.51
10:H:80:LEU:CD2	10:H:80:LEU:C	2.80	0.51
2:B:144:ILE:CD1	2:B:160:LEU:HD11	2.40	0.51
2:B:518:LYS:NZ	6:F:115:ARG:CB	2.74	0.51
2:B:565:LEU:HD13	2:B:600:TYR:HB3	1.93	0.51
3:J:564:G:C6	3:J:578:U:O4'	2.64	0.51
3:J:1179:G:H3'	3:J:1180:C:H6	1.75	0.51
4:K:2834:G:C2	4:K:2835:U:C5	2.99	0.51
5:L:30:G:H1	5:L:40:U:H3	1.58	0.51
10:H:109:ILE:N	10:H:112:ILE:CG2	2.74	0.51
2:B:144:ILE:HD11	2:B:160:LEU:HD11	1.92	0.51
2:B:395:ILE:HG23	2:B:396:LYS:N	2.24	0.51
3:J:446:A:H2'	3:J:447:U:H6	1.76	0.51
4:K:2297:U:N3	4:K:2299:A:C6	2.78	0.51
4:K:2850:G:OP1	4:K:2850:G:C4'	2.49	0.51
4:K:3020:U:C2'	4:K:3021:A:OP1	2.58	0.51
4:K:3032:A:H1'	6:F:170:LYS:HE2	1.93	0.51
5:L:20:C:H3'	5:L:21:A:H5'	1.93	0.51
10:H:88:PRO:CD	10:H:89:PRO:CD	2.89	0.51
10:H:109:ILE:HG13	10:H:129:THR:CA	2.39	0.51
2:B:144:ILE:CG2	2:B:153:GLN:HG3	2.31	0.51
2:B:183:PRO:HB3	2:B:190:LEU:HB2	1.92	0.51
3:J:44:U:OP1	3:J:47:A:OP2	2.29	0.51
3:J:152:U:C4'	9:C:13:GLN:CG	2.79	0.51
3:J:439:U:C5	3:J:465:G:N2	2.79	0.51
3:J:463:U:C2	3:J:464:A:C8	2.99	0.51
3:J:1274:C:OP2	3:J:1427:A:H3'	2.11	0.51
3:J:1431:C:C3'	3:J:1432:U:C5'	2.89	0.51
4:K:2837:A:C8	4:K:2845:A:N1	2.79	0.51
1:A:4:ILE:H	1:A:4:ILE:HD12	1.76	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:100:PRO:HA	2:B:273:TYR:CE1	2.46	0.51
2:B:455:LEU:O	2:B:456:ARG:HB2	2.11	0.51
3:J:418:G:O2'	9:C:59:GLN:NE2	2.43	0.51
4:K:2295:A:C4	11:I:37:ILE:HG21	2.45	0.51
6:F:12:VAL:HB	6:F:51:GLN:HA	1.92	0.51
1:A:65:LEU:HD12	1:A:105:LEU:HB3	1.93	0.51
3:J:40:A:C8	3:J:41:A:N7	2.79	0.51
3:J:41:A:C2	3:J:438:A:C5	2.99	0.51
5:L:27:G:H2'	5:L:28:G:H8	1.76	0.51
8:G:43:LYS:CG	10:H:121:PHE:CE1	2.81	0.51
2:B:66:PRO:CD	15:B:704:SF4:S4	2.84	0.50
2:B:118:THR:O	2:B:122:ILE:HD13	2.11	0.50
3:J:549:G:C2	3:J:550:A:C8	2.99	0.50
3:J:586:G:C5	3:J:587:C:C4	2.99	0.50
4:K:1232:C:C2	4:K:1261:G:N1	2.79	0.50
8:G:70:LEU:CB	8:G:71:PRO:HD3	2.41	0.50
1:A:101:VAL:HG21	3:J:1272:U:H4'	1.93	0.50
1:A:101:VAL:CG2	3:J:1272:U:O3'	2.52	0.50
2:B:95:HIS:HE1	2:B:301:TYR:CB	2.21	0.50
2:B:295:TYR:HE1	2:B:305:THR:OG1	1.95	0.50
2:B:334:LEU:HD21	2:B:336:PHE:CZ	2.46	0.50
2:B:538:VAL:HG12	2:B:539:ILE:N	2.26	0.50
3:J:1192:C:H3'	3:J:1193:A:H2'	1.93	0.50
4:K:1239:C:H4'	10:H:97:ASN:O	2.12	0.50
4:K:1270:A:H3'	4:K:1271:A:H8	1.75	0.50
4:K:2294:U:H3'	4:K:2295:A:H5''	1.93	0.50
4:K:3037:U:C2	4:K:3038:U:C5	2.99	0.50
2:B:50:ILE:HG23	2:B:50:ILE:O	2.11	0.50
2:B:140:TRP:CZ3	2:B:159:MET:CE	2.95	0.50
2:B:359:LEU:HD23	2:B:370:VAL:HG11	1.94	0.50
3:J:449:C:H2'	3:J:450:U:C6	2.46	0.50
3:J:586:G:H4'	7:E:21:VAL:HG22	1.92	0.50
4:K:1269:U:N3	4:K:1272:C:N4	2.58	0.50
4:K:2289:U:C2'	4:K:2290:C:C5'	2.89	0.50
4:K:2834:G:C2	4:K:2835:U:C6	3.00	0.50
10:H:109:ILE:HD12	10:H:129:THR:CG2	2.39	0.50
2:B:183:PRO:HA	2:B:219:ILE:HD12	1.93	0.50
4:K:2837:A:H2'	4:K:2845:A:C2	2.45	0.50
4:K:2931:C:C2'	4:K:2932:U:H5'	2.42	0.50
10:H:23:GLY:H	10:H:46:ILE:HG12	1.77	0.50
10:H:46:ILE:HA	10:H:49:ALA:H	1.77	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:128:VAL:O	10:H:131:GLU:HB3	2.11	0.50
1:A:280:GLU:HA	1:A:350:LEU:HD23	1.94	0.50
2:B:9:ALA:HB2	2:B:72:ILE:HD13	1.94	0.50
2:B:41:VAL:HG13	2:B:43:PRO:HD3	1.92	0.50
2:B:133:ARG:CG	2:B:134:PHE:H	2.09	0.50
3:J:38:C:H2'	3:J:39:A:H5''	1.92	0.50
3:J:152:U:C5'	9:C:13:GLN:HG3	2.40	0.50
3:J:572:C:N4	3:J:573:C:N4	2.58	0.50
3:J:1199:G:C4	3:J:1200:G:O4'	2.65	0.50
4:K:1254:C:C2	4:K:1263:A:N1	2.79	0.50
4:K:1279:C:H4'	8:G:1:MET:SD	2.52	0.50
4:K:2285:C:H5	4:K:2286:U:N1	2.09	0.50
4:K:2932:U:P	11:I:41:GLY:N	2.80	0.50
10:H:8:ASN:HD22	10:H:8:ASN:C	2.20	0.50
11:I:15:LEU:HD23	11:I:53:SER:HB3	1.93	0.50
12:D:31:ASN:O	12:D:32:ARG:HB2	2.11	0.50
2:B:589:GLN:NE2	9:C:58:LYS:CG	2.54	0.50
3:J:428:A:C2	3:J:440:U:O2	2.64	0.50
4:K:1229:G:C2	4:K:1230:G:C4	2.99	0.50
4:K:2841:G:C5	4:K:2844:C:N4	2.80	0.50
2:B:30:PRO:HD2	15:B:703:SF4:S2	2.52	0.50
2:B:457:ILE:CG2	2:B:460:ILE:HG22	2.42	0.50
3:J:439:U:C4	3:J:465:G:C2	3.00	0.50
3:J:1188:G:H2'	3:J:1189:A:C8	2.42	0.50
9:C:28:PHE:CE1	9:C:104:PRO:HG3	2.46	0.50
10:H:37:LEU:HD23	10:H:37:LEU:C	2.36	0.50
11:I:62:VAL:HG23	11:I:74:MET:HE1	1.94	0.50
2:B:348:ASP:O	2:B:349:SER:HB2	2.11	0.50
2:B:418:LYS:HD3	2:B:478:ILE:HA	1.94	0.50
2:B:488:ILE:HG13	2:B:520:THR:CG2	2.41	0.50
3:J:553:G:N2	3:J:571:G:N2	2.60	0.50
4:K:2293:C:OP2	11:I:71:LYS:HE3	2.12	0.50
4:K:2836:C:H5	4:K:2853:A:C2	2.28	0.50
9:C:141:ILE:HG21	9:C:153:VAL:HG13	1.94	0.50
10:H:37:LEU:HB2	10:H:68:GLN:C	2.37	0.50
11:I:120:LYS:HB3	11:I:137:VAL:HG21	1.94	0.50
2:B:30:PRO:HG2	2:B:56:ILE:HD13	1.93	0.50
2:B:87:TYR:CD2	14:B:702:ATP:C5	2.99	0.50
2:B:381:LEU:HD12	2:B:537:LYS:C	2.36	0.50
3:J:439:U:C1'	3:J:440:U:OP1	2.57	0.50
2:B:21:CYS:SG	2:B:66:PRO:HG2	2.52	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:143:ILE:CD1	2:B:156:PHE:CD1	2.94	0.49
2:B:263:ILE:HG23	2:B:264:ILE:N	2.27	0.49
2:B:382:VAL:HG12	2:B:383:MET:N	2.26	0.49
2:B:439:ARG:NH1	2:B:439:ARG:HB3	2.26	0.49
3:J:48:G:C6	3:J:432:G:C2	2.99	0.49
3:J:583:C:C2	3:J:584:C:C6	2.99	0.49
3:J:1267:G:O2'	3:J:1268:G:H5'	2.12	0.49
4:K:1236:G:C2	10:H:57:LYS:CB	2.94	0.49
4:K:2833:A:C2	4:K:2834:G:C8	3.00	0.49
8:G:43:LYS:HG2	10:H:121:PHE:HD1	0.79	0.49
8:G:105:VAL:O	8:G:106:ALA:O	2.30	0.49
2:B:194:ARG:HG3	2:B:237:VAL:HG23	1.92	0.49
3:J:454:U:O2'	3:J:455:C:O5'	2.30	0.49
4:K:1236:G:H3'	4:K:1237:G:C5'	2.42	0.49
4:K:1258:U:O2	4:K:1258:U:C2'	2.58	0.49
8:G:91:GLU:HB2	8:G:96:ILE:HD11	1.93	0.49
1:A:53:GLU:HG3	1:A:54:ALA:H	1.76	0.49
2:B:129:PRO:HG2	2:B:143:ILE:HG21	1.94	0.49
3:J:418:G:C2'	9:C:59:GLN:HE21	2.25	0.49
3:J:568:G:C2	3:J:569:C:C6	3.00	0.49
4:K:1234:G:C5'	4:K:1235:U:OP2	2.60	0.49
4:K:1245:A:C5	4:K:1272:C:OP1	2.65	0.49
1:A:300:TYR:OH	2:B:64:LYS:CE	2.60	0.49
2:B:239:GLU:HG3	2:B:239:GLU:O	2.12	0.49
2:B:438:ILE:HG21	2:B:483:GLY:O	2.12	0.49
2:B:523:ILE:HG23	2:B:523:ILE:O	2.13	0.49
4:K:1257:C:O2	4:K:1257:C:C2'	2.48	0.49
4:K:1257:C:C4	4:K:1258:U:C4	3.01	0.49
10:H:87:GLU:CG	10:H:89:PRO:HD3	2.41	0.49
12:D:15:ASN:OD1	12:D:17:LEU:HD12	2.12	0.49
3:J:160:C:H2'	3:J:161:U:O4'	2.13	0.49
3:J:1202:A:OP1	3:J:1203:A:OP2	2.31	0.49
8:G:70:LEU:HB2	8:G:71:PRO:HD3	1.94	0.49
2:B:30:PRO:HG2	2:B:56:ILE:HD11	1.94	0.49
2:B:568:LEU:CD1	2:B:570:VAL:HG22	2.42	0.49
3:J:1186:U:O2'	3:J:1187:U:H5'	2.12	0.49
3:J:1431:C:C5'	3:J:1432:U:H5'	2.42	0.49
11:I:74:MET:HE3	11:I:102:ILE:HB	1.95	0.49
2:B:106:LEU:CB	2:B:290:PHE:CD2	2.94	0.49
2:B:254:VAL:HG22	2:B:526:HIS:O	2.13	0.49
2:B:303:VAL:HG12	2:B:304:VAL:N	2.25	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1204:A:C5	3:J:1205:C:N3	2.80	0.49
4:K:1237:G:N1	4:K:1252:A:C2	2.80	0.49
4:K:1245:A:C4	4:K:1272:C:OP1	2.66	0.49
4:K:1279:C:HO2'	4:K:1280:C:P	2.33	0.49
9:C:67:VAL:HG23	9:C:68:LEU:O	2.13	0.49
10:H:45:ASP:HA	10:H:48:LYS:HB3	1.95	0.49
10:H:103:ASN:H	10:H:141:CYS:HB3	1.77	0.49
2:B:208:ILE:HG23	2:B:209:LEU:N	2.27	0.49
2:B:263:ILE:HD13	2:B:263:ILE:C	2.38	0.49
2:B:362:THR:HG23	2:B:362:THR:O	2.11	0.49
2:B:363:GLN:CG	2:B:365:ASP:H	2.21	0.49
3:J:1206:U:C6	3:J:1207:C:C6	3.01	0.49
3:J:1428:G:O5'	3:J:1429:G:OP2	2.31	0.49
4:K:1271:A:N3	4:K:1271:A:C2'	2.74	0.49
4:K:1275:C:N4	4:K:1276:U:C4	2.81	0.49
6:F:189:GLU:C	6:F:191:LEU:H	2.21	0.49
2:B:375:PHE:CD1	2:B:522:PHE:CZ	3.01	0.49
2:B:455:LEU:HD12	2:B:472:GLU:HG2	1.94	0.49
2:B:558:LEU:H	2:B:558:LEU:CD1	2.26	0.49
3:J:44:U:C3'	3:J:45:U:H5'	2.38	0.49
4:K:1257:C:C4	4:K:1261:G:N2	2.81	0.49
4:K:2295:A:O5'	11:I:61:THR:CG2	2.47	0.49
6:F:162:GLN:HG3	6:F:163:GLN:N	2.21	0.49
10:H:38:SER:H	10:H:68:GLN:CA	2.25	0.49
11:I:89:ASP:OD1	11:I:91:VAL:HG13	2.12	0.49
2:B:290:PHE:HZ	2:B:292:CYS:SG	2.34	0.49
2:B:418:LYS:HE2	2:B:478:ILE:HG12	1.94	0.49
3:J:1275:A:C8	3:J:1438:G:N2	2.81	0.49
3:J:1437:U:H2'	3:J:1438:G:H5'	1.95	0.49
4:K:1246:G:C5	4:K:1264:G:C2	3.01	0.49
4:K:1274:A:C2	4:K:1275:C:C6	3.01	0.49
4:K:2297:U:OP2	4:K:2297:U:H6	1.96	0.49
10:H:26:ALA:C	10:H:28:LEU:H	2.21	0.49
11:I:46:LEU:HG	11:I:47:ASN:OD1	2.13	0.49
2:B:108:LEU:HD23	2:B:108:LEU:C	2.37	0.48
2:B:137:PRO:O	2:B:139:GLU:HG3	2.13	0.48
2:B:194:ARG:HG2	2:B:234:MET:CG	2.43	0.48
2:B:334:LEU:CD2	2:B:336:PHE:CZ	2.95	0.48
3:J:1199:G:C6	3:J:1200:G:C1'	2.96	0.48
4:K:1236:G:C6	4:K:1245:A:C2	3.01	0.48
9:C:126:ASP:OD2	9:C:127:THR:HG22	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:123:ARG:CD	10:H:126:ALA:HB3	2.42	0.48
2:B:131:LEU:HD12	2:B:142:GLU:OE1	2.13	0.48
2:B:140:TRP:HE3	2:B:143:ILE:HD11	1.78	0.48
2:B:140:TRP:CE3	2:B:143:ILE:CD1	2.95	0.48
2:B:334:LEU:HG	2:B:504:ILE:HD11	1.89	0.48
2:B:503:ARG:O	2:B:506:CYS:HB2	2.13	0.48
3:J:551:G:C2	3:J:552:G:C8	3.01	0.48
3:J:1176:G:C6	3:J:1177:C:N4	2.81	0.48
4:K:1275:C:H2'	4:K:1276:U:O4'	2.13	0.48
4:K:3019:U:O2	4:K:3019:U:H2'	2.11	0.48
7:E:53:LYS:HG3	7:E:54:ARG:H	1.79	0.48
2:B:322:ILE:HD12	2:B:325:GLU:CD	2.38	0.48
3:J:581:U:O2	3:J:581:U:C2'	2.61	0.48
3:J:1432:U:OP2	3:J:1432:U:H4'	2.12	0.48
4:K:2929:C:C6	4:K:2929:C:C3'	2.97	0.48
1:A:43:PHE:CZ	1:A:107:PHE:HB2	2.48	0.48
1:A:47:PHE:CE1	3:J:577:G:C8	3.02	0.48
2:B:484:ILE:HG13	2:B:485:PRO:HD2	1.94	0.48
3:J:454:U:O4	3:J:456:A:C4	2.67	0.48
4:K:2841:G:C5	4:K:2844:C:C4	3.01	0.48
6:F:186:PHE:HD1	6:F:191:LEU:OXT	1.97	0.48
10:H:112:ILE:HG12	10:H:132:ILE:CD1	2.43	0.48
1:A:247:PHE:CE1	1:A:273:GLN:O	2.65	0.48
1:A:248:ILE:N	1:A:248:ILE:HD12	2.28	0.48
1:A:291:LEU:HB2	1:A:298:ALA:HB3	1.96	0.48
2:B:92:PHE:CE2	14:B:702:ATP:H4'	2.49	0.48
2:B:269:ALA:HB3	2:B:270:PRO:CD	2.40	0.48
2:B:475:ARG:NH2	2:B:502:GLN:HG2	2.28	0.48
3:J:549:G:N1	3:J:550:A:C5	2.81	0.48
3:J:1204:A:C3'	3:J:1205:C:C5'	2.77	0.48
4:K:2929:C:H3'	4:K:2929:C:H6	1.79	0.48
9:C:45:PHE:HA	9:C:48:TYR:HD2	1.79	0.48
10:H:43:GLY:HA2	10:H:46:ILE:HG22	1.95	0.48
10:H:123:ARG:O	10:H:124:THR:C	2.55	0.48
2:B:268:LEU:HD13	2:B:269:ALA:H	1.72	0.48
2:B:375:PHE:CE1	2:B:381:LEU:HB2	2.48	0.48
2:B:438:ILE:HG23	2:B:438:ILE:O	2.13	0.48
3:J:1186:U:C2'	3:J:1187:U:H5'	2.44	0.48
3:J:1196:A:C4'	3:J:1197:C:O5'	2.62	0.48
4:K:1232:C:C4	4:K:1261:G:C4	3.02	0.48
4:K:3032:A:H4'	4:K:3032:A:OP1	2.12	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:80:ARG:NE	11:I:97:ASP:OD2	2.39	0.48
2:B:56:ILE:HD12	2:B:58:CYS:HB3	1.95	0.48
2:B:100:PRO:HA	2:B:106:LEU:HD12	1.94	0.48
2:B:269:ALA:CB	2:B:270:PRO:HD3	2.43	0.48
2:B:523:ILE:HD13	2:B:534:LEU:CD1	2.43	0.48
4:K:1234:G:H4'	10:H:116:MET:HE2	1.94	0.48
4:K:2838:A:C2	4:K:2851:A:N9	2.82	0.48
10:H:100:HIS:O	10:H:138:SER:O	2.31	0.48
1:A:4:ILE:HD12	1:A:4:ILE:N	2.28	0.48
2:B:238:GLN:HG3	2:B:239:GLU:N	2.29	0.48
2:B:394:LEU:HD13	2:B:394:LEU:O	2.14	0.48
3:J:1438:G:H5'	3:J:1438:G:H8	1.78	0.48
4:K:2294:U:C2	4:K:2296:A:OP2	2.67	0.48
4:K:2924:U:C4	4:K:2925:C:O2	2.66	0.48
8:G:33:VAL:CG2	8:G:184:GLY:O	2.62	0.48
8:G:43:LYS:CA	10:H:121:PHE:CE1	2.82	0.48
2:B:56:ILE:HD11	2:B:58:CYS:CB	2.44	0.48
2:B:56:ILE:HD11	2:B:58:CYS:HB3	1.93	0.48
2:B:106:LEU:HD22	2:B:290:PHE:HB3	1.96	0.48
2:B:205:TYR:O	2:B:208:ILE:HG22	2.14	0.48
2:B:274:VAL:HG12	2:B:275:ILE:N	2.29	0.48
2:B:444:ASN:OD1	2:B:447:PHE:HD2	1.97	0.48
2:B:574:ARG:NH1	2:B:602:PHE:H	2.11	0.48
3:J:551:G:N1	3:J:552:G:C6	2.82	0.48
4:K:1245:A:C2	4:K:1272:C:O4'	2.67	0.48
8:G:46:ARG:CD	10:H:121:PHE:CE1	2.78	0.48
10:H:21:GLU:N	10:H:50:THR:HG21	2.29	0.48
11:I:79:VAL:HG23	11:I:80:ARG:HG3	1.96	0.48
12:D:59:GLY:O	12:D:60:PHE:HB2	2.14	0.48
1:A:144:ALA:CB	1:A:259:ILE:HD12	2.44	0.48
2:B:156:PHE:HD1	2:B:159:MET:HE2	1.79	0.48
3:J:551:G:O4'	3:J:581:U:O2	2.32	0.48
3:J:1192:C:C4	3:J:1193:A:C5	3.02	0.48
3:J:1439:C:O5'	3:J:1439:C:H6	1.97	0.48
4:K:1246:G:N3	4:K:1264:G:O2'	2.39	0.48
4:K:1254:C:C4	4:K:1255:C:C5	3.01	0.48
4:K:2833:A:C2	4:K:2834:G:O4'	2.67	0.48
8:G:33:VAL:HG21	8:G:184:GLY:O	2.14	0.48
10:H:23:GLY:CA	10:H:46:ILE:CD1	2.89	0.48
10:H:88:PRO:CD	10:H:89:PRO:HD3	2.44	0.48
1:A:385:GLU:HA	2:B:27:ARG:HH12	1.72	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:316:ILE:HG23	2:B:317:PHE:N	2.29	0.47
4:K:3017:A:O2'	4:K:3018:C:H5'	2.14	0.47
8:G:37:GLN:HB3	8:G:105:VAL:HB	1.95	0.47
9:C:215:ARG:HD3	9:C:215:ARG:HA	1.57	0.47
11:I:48:ARG:HG3	11:I:48:ARG:HH11	1.79	0.47
2:B:42:THR:HG21	2:B:47:ILE:CG2	2.42	0.47
2:B:205:TYR:HE1	2:B:263:ILE:CG1	2.26	0.47
2:B:457:ILE:C	2:B:460:ILE:HG22	2.39	0.47
3:J:418:G:N2	3:J:419:G:C5	2.82	0.47
3:J:587:C:H2'	3:J:588:U:C6	2.49	0.47
4:K:1232:C:C5	4:K:1261:G:C4	3.02	0.47
4:K:1266:G:N1	4:K:1276:U:C2	2.81	0.47
10:H:46:ILE:C	10:H:48:LYS:N	2.72	0.47
2:B:92:PHE:CD2	14:B:702:ATP:H4'	2.50	0.47
2:B:167:ILE:HG23	2:B:167:ILE:O	2.13	0.47
2:B:437:LYS:HE2	2:B:480:LEU:CD2	2.29	0.47
2:B:455:LEU:HD11	2:B:475:ARG:HH11	1.78	0.47
3:J:446:A:N6	3:J:461:G:H21	2.12	0.47
4:K:1233:G:C2	4:K:1234:G:C8	3.02	0.47
4:K:1246:G:C6	4:K:1264:G:C2	3.01	0.47
4:K:1260:A:H1'	4:K:1280:C:C1'	2.42	0.47
4:K:1279:C:P	8:G:1:MET:CE	2.90	0.47
4:K:2296:A:N3	4:K:2919:A:H1'	2.30	0.47
9:C:63:MET:HG2	9:C:99:GLY:O	2.14	0.47
10:H:109:ILE:HB	10:H:129:THR:OG1	2.13	0.47
2:B:295:TYR:N	2:B:295:TYR:CD1	2.83	0.47
2:B:524:VAL:O	2:B:525:GLU:HG2	2.14	0.47
3:J:436:A:H5''	3:J:437:A:P	2.55	0.47
3:J:550:A:O4'	3:J:556:A:C2	2.68	0.47
3:J:1196:A:N3	3:J:1196:A:O4'	2.48	0.47
6:F:25:VAL:CG1	6:F:78:MET:HE1	2.43	0.47
6:F:170:LYS:HB3	6:F:175:PHE:CD2	2.50	0.47
9:C:63:MET:HE2	9:C:106:LEU:HD22	1.96	0.47
1:A:235:HIS:CE1	1:A:237:LYS:HD3	2.49	0.47
2:B:108:LEU:HD21	2:B:294:ILE:HD13	1.96	0.47
2:B:116:LYS:H	2:B:116:LYS:CD	2.26	0.47
2:B:194:ARG:CD	2:B:234:MET:HE2	2.44	0.47
2:B:290:PHE:CE1	2:B:307:PRO:CA	2.97	0.47
2:B:334:LEU:HD23	2:B:334:LEU:C	2.39	0.47
3:J:563:U:C4	3:J:564:G:C6	3.02	0.47
4:K:1232:C:N3	4:K:1261:G:N1	2.63	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:2287:C:O2	4:K:2298:U:C4'	2.62	0.47
4:K:2294:U:N1	4:K:2297:U:H5	2.13	0.47
4:K:2296:A:C2	4:K:2919:A:C1'	2.96	0.47
4:K:3037:U:O2'	4:K:3038:U:C5'	2.50	0.47
8:G:72:ASP:O	8:G:74:GLU:N	2.45	0.47
2:B:179:ALA:HB3	2:B:180:ILE:CD1	2.43	0.47
2:B:290:PHE:CD1	2:B:291:VAL:N	2.82	0.47
2:B:444:ASN:CG	2:B:447:PHE:HD2	2.22	0.47
3:J:450:U:O2	3:J:450:U:C2'	2.62	0.47
3:J:450:U:N3	3:J:451:A:N6	2.63	0.47
3:J:551:G:N3	3:J:551:G:H2'	2.30	0.47
4:K:1240:A:O3'	10:H:94:LYS:HA	2.15	0.47
4:K:1265:U:C4	4:K:1277:C:C2	3.02	0.47
4:K:2288:G:C2	4:K:2289:U:C4	3.03	0.47
8:G:124:VAL:CG1	8:G:125:ASN:H	2.28	0.47
10:H:108:GLU:CA	10:H:112:ILE:CG2	2.92	0.47
2:B:39:ILE:CD1	2:B:50:ILE:HG13	2.40	0.47
2:B:171:GLN:HB3	2:B:246:ASP:OD2	2.15	0.47
2:B:206:ILE:HG23	2:B:211:LEU:HB2	1.97	0.47
2:B:334:LEU:HD21	2:B:336:PHE:CE1	2.50	0.47
2:B:412:LYS:HE2	2:B:412:LYS:CA	2.39	0.47
2:B:589:GLN:HG3	9:C:107:ALA:CB	2.44	0.47
3:J:38:C:C2'	3:J:39:A:H5''	2.44	0.47
3:J:415:C:O2	3:J:419:G:C2	2.67	0.47
3:J:451:A:H2'	3:J:451:A:N3	2.29	0.47
3:J:564:G:O6	3:J:578:U:C1'	2.62	0.47
3:J:1198:G:C5'	3:J:1199:G:H8	2.27	0.47
3:J:1269:U:H4'	3:J:1270:G:C5'	2.45	0.47
4:K:1256:G:C6	4:K:1261:G:N2	2.83	0.47
4:K:1264:G:H2'	4:K:1264:G:P	2.55	0.47
4:K:2289:U:H2'	4:K:2289:U:O2	2.14	0.47
6:F:26:LYS:HA	6:F:35:THR:HG22	1.97	0.47
6:F:47:LYS:HE3	6:F:50:ASN:H	1.80	0.47
6:F:88:TYR:CE2	6:F:184:LYS:HG2	2.50	0.47
9:C:148:SER:C	9:C:150:GLU:H	2.22	0.47
10:H:37:LEU:HB3	10:H:64:ILE:HG12	1.95	0.47
10:H:57:LYS:C	10:H:58:VAL:CG2	2.86	0.47
10:H:66:ASN:C	10:H:66:ASN:ND2	2.73	0.47
10:H:80:LEU:HG	10:H:83:THR:HG21	1.96	0.47
2:B:11:VAL:HG22	2:B:90:ASN:CB	2.44	0.47
2:B:437:LYS:CG	2:B:480:LEU:HD21	2.43	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:446:A:O2'	3:J:447:U:H5'	2.15	0.47
4:K:1276:U:C2	4:K:1277:C:C5	3.03	0.47
4:K:2299:A:H5'	4:K:2299:A:C8	2.44	0.47
6:F:41:ILE:O	6:F:42:ASP:HB2	2.15	0.47
6:F:67:ALA:HA	6:F:70:THR:HG23	1.97	0.47
9:C:78:THR:HG22	9:C:79:LYS:H	1.80	0.47
10:H:16:ARG:HB3	10:H:57:LYS:CD	2.44	0.47
1:A:232:GLU:OE1	4:K:2851:A:C1'	2.63	0.47
2:B:435:PHE:CE1	2:B:439:ARG:CB	2.95	0.47
3:J:40:A:C8	3:J:41:A:C8	3.02	0.47
3:J:552:G:N1	3:J:553:G:C2	2.83	0.47
3:J:565:C:C6	3:J:577:G:C6	3.02	0.47
2:B:557:LEU:HD23	2:B:557:LEU:C	2.39	0.47
3:J:1200:G:O3'	3:J:1201:G:O4'	2.33	0.47
4:K:1279:C:C4'	8:G:1:MET:SD	3.02	0.47
12:D:84:LYS:HD2	12:D:85:PHE:CE1	2.50	0.47
1:A:386:GLU:OE2	2:B:27:ARG:CD	2.57	0.46
2:B:352:ARG:HD2	2:B:374:GLU:HB2	1.96	0.46
2:B:363:GLN:HG2	2:B:366:PHE:N	2.24	0.46
2:B:430:VAL:CG1	2:B:461:ILE:HA	2.45	0.46
2:B:432:GLN:O	2:B:436:LYS:HG3	2.16	0.46
4:K:1271:A:N6	4:K:1272:C:H42	2.13	0.46
4:K:3018:C:N4	4:K:3019:U:O4	2.49	0.46
6:F:105:GLU:HA	6:F:109:ALA:HB3	1.96	0.46
12:D:102:LYS:H	12:D:102:LYS:HD2	1.79	0.46
2:B:84:THR:O	2:B:131:LEU:HA	2.15	0.46
2:B:582:ARG:HG3	3:J:416:A:H2	1.80	0.46
3:J:461:G:O2'	3:J:462:G:O5'	2.32	0.46
3:J:1437:U:O2'	3:J:1438:G:H5''	2.15	0.46
2:B:182:GLY:CA	2:B:185:GLN:HA	2.41	0.46
3:J:1274:C:O2'	3:J:1275:A:P	2.74	0.46
4:K:2847:A:H3'	4:K:2848:G:C8	2.33	0.46
4:K:3038:U:O2'	4:K:3039:C:P	2.74	0.46
9:C:137:ARG:HD3	9:C:177:ARG:HE	1.81	0.46
10:H:21:GLU:HA	10:H:50:THR:HG22	1.96	0.46
1:A:363:ASP:C	1:A:365:LEU:H	2.24	0.46
2:B:156:PHE:CD1	2:B:159:MET:HE2	2.50	0.46
2:B:574:ARG:NH1	2:B:601:PHE:CZ	2.75	0.46
2:B:589:GLN:C	9:C:58:LYS:HZ3	2.24	0.46
3:J:44:U:C3'	3:J:45:U:C5'	2.93	0.46
3:J:1270:G:C6	3:J:1271:G:N7	2.84	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:1278:A:O2'	4:K:1279:C:C5'	2.61	0.46
4:K:2283:G:H1'	4:K:2284:C:H5	1.79	0.46
4:K:2285:C:H41	4:K:2286:U:H3	1.61	0.46
4:K:2839:G:O6	4:K:2845:A:O2'	2.29	0.46
10:H:48:LYS:HG2	10:H:48:LYS:O	2.14	0.46
1:A:385:GLU:CB	2:B:27:ARG:HH11	2.17	0.46
2:B:115:GLY:HA2	14:B:702:ATP:PA	2.48	0.46
2:B:167:ILE:HD12	2:B:238:GLN:HG2	1.96	0.46
2:B:194:ARG:CG	2:B:237:VAL:CG2	2.94	0.46
2:B:290:PHE:CZ	2:B:292:CYS:SG	3.06	0.46
2:B:293:ILE:HD13	2:B:305:THR:HB	1.98	0.46
2:B:300:VAL:CG1	2:B:301:TYR:HD1	2.27	0.46
3:J:450:U:H2'	3:J:451:A:N7	2.30	0.46
3:J:1273:G:C3'	3:J:1274:C:H5'	2.42	0.46
4:K:2295:A:H62	4:K:2296:A:H61	1.60	0.46
4:K:2298:U:C3'	4:K:2299:A:H5''	2.46	0.46
8:G:61:ARG:HA	8:G:64:ARG:HH11	1.80	0.46
9:C:70:PRO:O	9:C:98:ARG:NH1	2.42	0.46
1:A:313:ALA:CB	1:A:372:LEU:HD13	2.46	0.46
2:B:100:PRO:HD2	2:B:152:LEU:CD2	2.45	0.46
2:B:332:GLU:OE2	4:K:3022:G:C5'	2.63	0.46
2:B:523:ILE:HD13	2:B:534:LEU:HD12	1.97	0.46
3:J:435:C:H2'	3:J:436:A:O4'	2.15	0.46
3:J:1201:G:OP2	3:J:1201:G:C4	2.68	0.46
3:J:1274:C:P	3:J:1428:G:OP1	2.73	0.46
4:K:3032:A:C8	4:K:3032:A:H3'	2.51	0.46
10:H:28:LEU:HG	10:H:43:GLY:H	1.80	0.46
2:B:141:GLN:OE1	2:B:141:GLN:HA	2.16	0.46
2:B:195:MET:HA	2:B:237:VAL:HB	1.98	0.46
2:B:242:VAL:HG23	2:B:273:TYR:HE2	1.75	0.46
2:B:488:ILE:CD1	2:B:522:PHE:HE1	2.28	0.46
2:B:541:PHE:CE2	2:B:551:ALA:HB2	2.50	0.46
3:J:568:G:H2'	3:J:569:C:H5'	1.98	0.46
3:J:1186:U:H2'	3:J:1187:U:C5'	2.46	0.46
4:K:1255:C:O2	4:K:1255:C:H2'	2.14	0.46
10:H:21:GLU:CA	10:H:50:THR:CG2	2.94	0.46
10:H:131:GLU:O	10:H:133:LEU:N	2.49	0.46
11:I:120:LYS:HB3	11:I:137:VAL:CG2	2.45	0.46
1:A:373:LYS:HG3	4:K:1242:G:H1	1.80	0.46
3:J:42:G:C8	3:J:437:A:H3'	2.50	0.46
4:K:1242:G:C8	4:K:1242:G:OP1	2.68	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:211:LEU:O	9:C:215:ARG:HB2	2.16	0.46
10:H:32:ILE:HA	10:H:37:LEU:CD2	2.46	0.46
1:A:256:LEU:H	1:A:256:LEU:HD22	1.81	0.46
2:B:322:ILE:HD12	2:B:325:GLU:CG	2.45	0.46
2:B:401:ALA:C	2:B:402:LEU:HD12	2.41	0.46
3:J:446:A:C5	3:J:447:U:H5	2.28	0.46
3:J:1274:C:HO2'	3:J:1275:A:P	2.34	0.46
3:J:1276:U:O2'	3:J:1277:G:H5'	2.16	0.46
4:K:1234:G:O2'	10:H:116:MET:HE1	2.16	0.46
4:K:1262:G:O6	4:K:1264:G:C2	2.69	0.46
4:K:3020:U:H2'	4:K:3021:A:OP1	2.16	0.46
6:F:92:TYR:HB2	6:F:142:ASP:HB3	1.98	0.46
9:C:73:ILE:HD12	9:C:75:LEU:HD21	1.98	0.46
10:H:22:VAL:HG13	10:H:28:LEU:CD1	2.46	0.46
10:H:53:PHE:O	10:H:53:PHE:CG	2.69	0.46
1:A:65:LEU:CD2	1:A:65:LEU:N	2.78	0.46
2:B:183:PRO:HD3	2:B:186:LYS:C	2.41	0.46
2:B:230:PHE:CD1	2:B:230:PHE:C	2.94	0.46
2:B:260:ALA:O	2:B:264:ILE:HG13	2.16	0.46
2:B:322:ILE:CD1	2:B:325:GLU:CB	2.94	0.46
2:B:591:ASP:OD1	2:B:592:LYS:N	2.48	0.46
3:J:450:U:C2'	3:J:451:A:C8	2.91	0.46
3:J:1201:G:N7	3:J:1202:A:N3	2.64	0.46
3:J:1207:C:C4	3:J:1208:A:N6	2.84	0.46
3:J:1440:C:O2'	3:J:1441:C:H5'	2.15	0.46
4:K:1277:C:O2'	4:K:1278:A:OP2	2.30	0.46
4:K:2837:A:H2'	4:K:2845:A:C6	2.48	0.46
10:H:123:ARG:O	10:H:127:SER:HB3	2.16	0.46
11:I:33:ASN:ND2	11:I:63:LYS:H	2.14	0.46
2:B:28:SER:CB	2:B:64:LYS:CD	2.94	0.45
2:B:447:PHE:HE1	2:B:479:VAL:HG13	1.73	0.45
3:J:152:U:C4'	9:C:13:GLN:HB2	2.45	0.45
3:J:439:U:O2'	3:J:440:U:H4'	2.17	0.45
3:J:571:G:N3	3:J:571:G:C2'	2.78	0.45
3:J:1272:U:O4	3:J:1431:C:C2	2.69	0.45
3:J:1428:G:C2	3:J:1429:G:N7	2.83	0.45
4:K:1278:A:C2'	4:K:1279:C:H5'	2.45	0.45
4:K:2853:A:C6	4:K:2854:U:C2	3.04	0.45
4:K:3028:G:N1	4:K:3029:A:C2	2.84	0.45
10:H:28:LEU:HA	10:H:42:VAL:HG12	1.98	0.45
10:H:46:ILE:C	10:H:49:ALA:H	2.25	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:PHE:CD1	3:J:577:G:C8	3.04	0.45
1:A:187:LYS:HZ3	5:L:66:C:H5'	1.79	0.45
2:B:194:ARG:HG2	2:B:237:VAL:CG2	2.46	0.45
3:J:152:U:H5'	9:C:13:GLN:HG3	1.98	0.45
3:J:429:G:H5''	3:J:439:U:C3'	2.45	0.45
3:J:1201:G:H3'	3:J:1201:G:C4	2.42	0.45
4:K:2834:G:C5	4:K:2835:U:C5	3.04	0.45
7:E:9:ALA:HB3	7:E:10:ARG:HG3	1.99	0.45
10:H:46:ILE:HD13	10:H:46:ILE:HG21	1.72	0.45
2:B:42:THR:CG2	2:B:47:ILE:CG2	2.95	0.45
2:B:70:ILE:HG22	2:B:71:GLN:N	2.30	0.45
2:B:87:TYR:CE2	14:B:702:ATP:C5	3.04	0.45
2:B:157:THR:HG23	2:B:158:LYS:N	2.29	0.45
2:B:173:VAL:CG2	2:B:251:TYR:CE2	2.97	0.45
2:B:233:GLY:O	2:B:237:VAL:HG13	2.16	0.45
3:J:430:G:C5	3:J:431:C:C5	3.04	0.45
3:J:1198:G:OP2	3:J:1199:G:N7	2.50	0.45
4:K:1259:A:N3	4:K:1280:C:O2'	2.39	0.45
4:K:2839:G:C6	4:K:2850:G:N2	2.84	0.45
4:K:3029:A:H3'	4:K:3030:G:C5'	2.42	0.45
4:K:3032:A:H2'	6:F:170:LYS:HZ3	1.79	0.45
4:K:3036:G:C2'	4:K:3037:U:O5'	2.64	0.45
9:C:4:ASN:HA	9:C:15:THR:HG22	1.98	0.45
9:C:153:VAL:HG12	9:C:154:ARG:N	2.31	0.45
12:D:29:HIS:CE1	12:D:68:LYS:N	2.85	0.45
1:A:47:PHE:HB3	1:A:63:VAL:CG2	2.46	0.45
2:B:24:GLU:HG3	2:B:27:ARG:HD2	1.99	0.45
2:B:94:LEU:CD2	2:B:115:GLY:HA3	2.46	0.45
2:B:291:VAL:HG11	2:B:313:GLY:HA3	1.99	0.45
2:B:380:ILE:HG23	2:B:535:ALA:CA	2.40	0.45
2:B:510:ILE:CG2	2:B:514:ILE:CD1	2.95	0.45
3:J:450:U:C2'	3:J:451:A:H8	2.29	0.45
3:J:567:A:N1	3:J:583:C:H1'	2.31	0.45
3:J:1433:G:O2'	3:J:1434:U:H6	1.98	0.45
3:J:1437:U:O2	3:J:1437:U:H2'	2.16	0.45
4:K:1275:C:C4	4:K:1276:U:C5	3.05	0.45
4:K:2853:A:C5	4:K:2854:U:C4	3.04	0.45
5:L:12:U:H2'	5:L:13:U:C6	2.51	0.45
12:D:35:VAL:O	12:D:36:SER:HB3	2.16	0.45
2:B:92:PHE:CG	14:B:702:ATP:C1'	2.98	0.45
2:B:176:ILE:CD1	2:B:227:LEU:CD2	2.95	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:255:LYS:CB	2:B:386:GLU:CG	2.93	0.45
2:B:394:LEU:HD13	2:B:398:LEU:CD2	2.38	0.45
3:J:551:G:C4	3:J:552:G:N7	2.84	0.45
3:J:569:C:C2'	3:J:570:A:O5'	2.65	0.45
4:K:1243:G:O3'	10:H:18:VAL:HG13	2.16	0.45
4:K:2843:U:H3'	4:K:2843:U:OP2	2.17	0.45
4:K:3021:A:O4'	4:K:3023:U:C2	2.69	0.45
7:E:57:ASN:O	7:E:57:ASN:CG	2.60	0.45
1:A:204:ASN:C	1:A:206:ASP:H	2.25	0.45
2:B:130:ASN:O	2:B:131:LEU:HB2	2.16	0.45
2:B:189:GLU:OE1	2:B:189:GLU:HA	2.17	0.45
2:B:507:SER:HA	2:B:534:LEU:HD21	1.97	0.45
2:B:537:LYS:HD3	2:B:554:PRO:CB	2.43	0.45
3:J:451:A:N6	3:J:456:A:N6	2.65	0.45
3:J:1277:G:C2'	3:J:1278:G:H5'	2.47	0.45
4:K:2931:C:OP1	11:I:59:MET:HE3	2.16	0.45
4:K:3027:A:C8	4:K:3028:G:N7	2.85	0.45
6:F:109:ALA:HB1	6:F:111:PHE:CE2	2.52	0.45
2:B:589:GLN:C	9:C:58:LYS:NZ	2.74	0.45
3:J:571:G:H2'	3:J:572:C:C6	2.51	0.45
4:K:1258:U:N3	4:K:1260:A:OP2	2.50	0.45
10:H:28:LEU:HG	10:H:42:VAL:O	2.17	0.45
10:H:97:ASN:O	10:H:98:VAL:C	2.60	0.45
10:H:101:SER:CA	10:H:138:SER:O	2.65	0.45
2:B:4:LYS:HE3	2:B:5:ASN:O	2.16	0.45
2:B:86:ARG:HG2	2:B:132:GLY:HA2	1.98	0.45
2:B:293:ILE:CD1	2:B:305:THR:CB	2.94	0.45
8:G:38:MET:HE1	8:G:185:LEU:CG	2.41	0.45
9:C:28:PHE:C	9:C:30:LYS:H	2.25	0.45
2:B:39:ILE:CD1	2:B:50:ILE:CG1	2.94	0.45
2:B:578:SER:O	2:B:579:PHE:HB2	2.16	0.45
2:B:585:LYS:C	2:B:586:LEU:O	2.56	0.45
3:J:445:A:C2	3:J:446:A:C8	3.04	0.45
3:J:1270:G:C2	3:J:1271:G:C8	3.05	0.45
3:J:1274:C:C5	3:J:1427:A:N7	2.83	0.45
3:J:1277:G:C6	3:J:1278:G:C2	3.05	0.45
9:C:72:ARG:HG2	9:C:98:ARG:HA	1.99	0.45
1:A:47:PHE:CE2	3:J:577:G:H1'	2.52	0.45
1:A:47:PHE:CG	3:J:577:G:C4	3.05	0.45
2:B:353:ALA:H	2:B:376:SER:HA	1.82	0.45
2:B:434:PHE:CZ	2:B:480:LEU:HD12	2.50	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:2289:U:H2'	4:K:2290:C:C5'	2.44	0.45
4:K:3021:A:C8	4:K:3023:U:N3	2.85	0.45
5:L:27:G:H2'	5:L:28:G:C8	2.51	0.45
9:C:31:ARG:H	9:C:34:GLN:HG3	1.82	0.45
10:H:101:SER:CB	10:H:138:SER:O	2.65	0.45
10:H:109:ILE:N	10:H:112:ILE:HG22	2.31	0.45
11:I:38:ALA:HB3	11:I:59:MET:HB2	1.98	0.45
2:B:24:GLU:CA	2:B:27:ARG:HG2	2.47	0.44
3:J:426:G:C2	3:J:427:C:C6	3.05	0.44
3:J:451:A:H61	3:J:456:A:N6	2.15	0.44
3:J:1201:G:C3'	3:J:1201:G:C4	3.00	0.44
5:L:41:G:C3'	5:L:42:C:H5''	2.47	0.44
1:A:277:TYR:O	1:A:281:ILE:HG13	2.17	0.44
2:B:41:VAL:HG13	2:B:41:VAL:O	2.15	0.44
3:J:1186:U:C1'	3:J:1208:A:C2	2.99	0.44
3:J:1186:U:O4'	3:J:1208:A:C2	2.70	0.44
3:J:1428:G:C2	3:J:1429:G:C5	3.04	0.44
3:J:1431:C:C2	3:J:1437:U:O4	2.70	0.44
8:G:43:LYS:HA	8:G:46:ARG:HD2	1.99	0.44
8:G:104:ARG:HD2	8:G:182:THR:OG1	2.17	0.44
2:B:509:VAL:HG13	2:B:513:PHE:CE2	2.53	0.44
3:J:553:G:C5	3:J:554:C:N3	2.84	0.44
3:J:1441:C:H2'	3:J:1442:U:C6	2.52	0.44
4:K:2843:U:H3'	4:K:2843:U:P	2.57	0.44
8:G:19:LEU:HD22	8:G:25:LEU:HD22	1.99	0.44
8:G:37:GLN:CG	8:G:105:VAL:CG1	2.87	0.44
8:G:38:MET:CE	8:G:185:LEU:HG	2.44	0.44
9:C:173:PRO:HB2	9:C:174:LYS:H	1.55	0.44
1:A:386:GLU:N	2:B:27:ARG:HD3	2.31	0.44
2:B:96:ARG:O	2:B:97:LEU:HD23	2.18	0.44
2:B:166:ALA:HB2	2:B:242:VAL:HG11	1.99	0.44
2:B:565:LEU:HD12	2:B:600:TYR:HB2	1.98	0.44
3:J:413:U:O2'	3:J:414:C:H5'	2.17	0.44
3:J:413:U:C2	3:J:421:A:C2	3.06	0.44
3:J:438:A:O5'	3:J:438:A:C8	2.69	0.44
3:J:555:A:C2	3:J:556:A:C2	3.06	0.44
3:J:589:C:C2	3:J:590:C:C5	3.06	0.44
3:J:1179:G:C2	3:J:1180:C:H1'	2.53	0.44
4:K:1253:U:O4	4:K:1264:G:OP1	2.36	0.44
4:K:1273:A:N7	4:K:1274:A:C8	2.85	0.44
4:K:2288:G:H2'	4:K:2289:U:H6	1.79	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:111:ALA:HB1	8:G:167:GLN:HA	2.00	0.44
10:H:82:ILE:C	10:H:84:ALA:H	2.23	0.44
10:H:132:ILE:O	10:H:135:THR:HG23	2.12	0.44
2:B:39:ILE:HD11	2:B:50:ILE:CD1	2.45	0.44
2:B:195:MET:HE1	2:B:237:VAL:HG12	2.00	0.44
3:J:44:U:C5'	3:J:45:U:O4	2.64	0.44
4:K:2297:U:N3	4:K:2299:A:N6	2.66	0.44
6:F:92:TYR:N	6:F:92:TYR:CD1	2.85	0.44
10:H:88:PRO:O	10:H:90:ARG:N	2.51	0.44
2:B:451:VAL:HG23	2:B:452:VAL:H	1.83	0.44
2:B:544:ILE:HD11	2:B:547:LYS:HG3	1.97	0.44
2:B:574:ARG:HB2	2:B:602:PHE:HB2	1.99	0.44
2:B:586:LEU:O	2:B:587:ASP:C	2.60	0.44
3:J:1431:C:H4'	3:J:1432:U:H5'	2.00	0.44
4:K:1245:A:C8	4:K:1272:C:OP1	2.71	0.44
4:K:1276:U:O2'	4:K:1277:C:H5'	2.17	0.44
9:C:163:THR:HA	9:C:168:THR:HA	1.98	0.44
2:B:113:GLY:H	14:B:702:ATP:PG	2.40	0.44
2:B:171:GLN:HE21	2:B:171:GLN:HB2	1.44	0.44
2:B:194:ARG:CG	2:B:234:MET:HG3	2.46	0.44
2:B:338:ILE:H	2:B:338:ILE:CD1	2.28	0.44
4:K:1236:G:C2	10:H:57:LYS:HB3	2.53	0.44
4:K:2834:G:C4	4:K:2835:U:C6	3.02	0.44
4:K:2923:U:H2'	4:K:2924:U:H6	1.83	0.44
11:I:83:LYS:HE2	11:I:84:SER:H	1.82	0.44
1:A:78:ASP:CB	7:E:9:ALA:CB	2.93	0.44
2:B:437:LYS:CD	2:B:480:LEU:HD21	2.47	0.44
2:B:457:ILE:O	2:B:457:ILE:HG22	2.18	0.44
3:J:464:A:H2'	3:J:464:A:N3	2.33	0.44
3:J:568:G:N1	3:J:569:C:C4	2.86	0.44
3:J:1205:C:H6	3:J:1206:U:O2	2.01	0.44
4:K:1235:U:OP2	4:K:1235:U:H3'	2.18	0.44
4:K:2835:U:O2	4:K:2835:U:H2'	2.16	0.44
5:L:12:U:H2'	5:L:13:U:O4'	2.18	0.44
9:C:211:LEU:HD11	9:C:215:ARG:NH2	2.32	0.44
1:A:168:ILE:HG22	1:A:169:GLU:H	1.83	0.44
1:A:272:LEU:O	1:A:274:ASP:N	2.48	0.44
2:B:44:THR:HB	2:B:45:SER:H	1.51	0.44
2:B:348:ASP:HB3	2:B:351:SER:HA	1.98	0.44
2:B:384:MET:CE	2:B:531:ALA:CB	2.96	0.44
3:J:437:A:C5'	3:J:438:A:OP1	2.65	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1274:C:O2	3:J:1274:C:C2'	2.59	0.44
4:K:1263:A:H4'	4:K:1264:G:O5'	2.18	0.44
10:H:125:LEU:HA	10:H:129:THR:HB	2.00	0.44
10:H:125:LEU:CD2	10:H:129:THR:HG23	2.34	0.44
11:I:40:LYS:HG3	11:I:57:MET:HG2	2.00	0.44
12:D:29:HIS:HE2	12:D:34:ASN:HA	1.83	0.44
1:A:187:LYS:HG2	5:L:66:C:OP1	2.18	0.43
2:B:38:CYS:SG	2:B:55:CYS:HB2	2.58	0.43
2:B:330:ARG:HD2	2:B:501:GLU:OE1	2.18	0.43
2:B:573:ARG:CG	2:B:574:ARG:H	2.28	0.43
3:J:449:C:C2	3:J:450:U:C5	3.06	0.43
3:J:585:A:H2'	3:J:586:G:C8	2.52	0.43
3:J:1266:U:H5''	3:J:1267:G:OP2	2.18	0.43
4:K:1257:C:N3	4:K:1261:G:N2	2.66	0.43
6:F:88:TYR:CZ	6:F:184:LYS:HG2	2.53	0.43
7:E:39:LEU:HD12	7:E:43:ARG:NH2	2.33	0.43
7:E:47:VAL:HG22	7:E:48:THR:H	1.82	0.43
11:I:5:GLY:HA3	11:I:106:LYS:O	2.18	0.43
11:I:45:ARG:O	11:I:46:LEU:C	2.61	0.43
3:J:586:G:H2'	3:J:587:C:O5'	2.17	0.43
4:K:1276:U:C2'	4:K:1277:C:H5'	2.48	0.43
4:K:2286:U:O4	4:K:2288:G:H1'	2.17	0.43
9:C:98:ARG:HD3	9:C:99:GLY:O	2.17	0.43
9:C:132:ARG:HH11	9:C:132:ARG:HG2	1.83	0.43
10:H:40:LYS:O	10:H:40:LYS:CG	2.66	0.43
1:A:48:THR:HG21	1:A:60:THR:N	2.32	0.43
1:A:338:LEU:HD23	1:A:368:ILE:HD11	1.99	0.43
2:B:101:ARG:HB2	2:B:104:GLN:CD	2.43	0.43
2:B:114:ILE:CD1	2:B:294:ILE:HG21	2.45	0.43
2:B:358:SER:HB2	2:B:372:GLU:OE1	2.19	0.43
2:B:391:LYS:HE3	2:B:391:LYS:HB2	1.81	0.43
2:B:396:LYS:HD3	2:B:402:LEU:CD1	2.49	0.43
2:B:568:LEU:CD1	2:B:570:VAL:CG2	2.96	0.43
3:J:452:A:C2'	3:J:453:U:C5'	2.87	0.43
3:J:565:C:H2'	3:J:577:G:C2	2.53	0.43
3:J:1198:G:OP1	3:J:1200:G:N2	2.51	0.43
3:J:1277:G:H2'	3:J:1278:G:O4'	2.18	0.43
4:K:1255:C:O3'	10:H:130:LYS:HE2	2.19	0.43
4:K:1275:C:C5'	4:K:1275:C:H6	2.31	0.43
4:K:1277:C:OP2	4:K:1277:C:C2'	2.61	0.43
4:K:2289:U:C2'	4:K:2289:U:O2	2.66	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:2289:U:O2'	4:K:2290:C:C5'	2.65	0.43
9:C:63:MET:HA	9:C:98:ARG:O	2.18	0.43
9:C:64:LYS:O	9:C:67:VAL:HG22	2.17	0.43
2:B:205:TYR:CE2	2:B:233:GLY:CA	2.94	0.43
2:B:564:PHE:CD2	2:B:564:PHE:C	2.96	0.43
2:B:573:ARG:HA	2:B:602:PHE:CE1	2.53	0.43
3:J:430:G:O2'	3:J:431:C:H5'	2.18	0.43
4:K:1234:G:H4'	10:H:116:MET:CE	2.49	0.43
4:K:2922:G:C2	4:K:2923:U:O2	2.72	0.43
4:K:3023:U:H2'	4:K:3024:A:C8	2.53	0.43
6:F:2:LYS:HA	6:F:60:GLY:O	2.18	0.43
6:F:41:ILE:HG23	6:F:43:VAL:HG13	2.00	0.43
8:G:30:VAL:O	8:G:33:VAL:HG23	2.19	0.43
10:H:124:THR:CG2	10:H:125:LEU:H	2.14	0.43
1:A:303:LYS:HD2	2:B:33:LYS:HE3	2.00	0.43
2:B:4:LYS:HG3	2:B:5:ASN:N	2.34	0.43
2:B:322:ILE:HA	2:B:323:PRO:HD2	1.86	0.43
2:B:413:LEU:HD12	2:B:487:ASP:CG	2.43	0.43
2:B:568:LEU:CD2	2:B:570:VAL:CG1	2.95	0.43
3:J:450:U:C4	3:J:451:A:N6	2.81	0.43
3:J:565:C:C5	3:J:577:G:N7	2.87	0.43
3:J:1205:C:H6	3:J:1206:U:C2	2.36	0.43
4:K:2842:U:O2	4:K:2842:U:C2'	2.53	0.43
4:K:3038:U:O2'	4:K:3039:C:O5'	2.35	0.43
11:I:39:VAL:HG21	11:I:51:ALA:C	2.43	0.43
2:B:194:ARG:HA	2:B:194:ARG:NE	2.33	0.43
3:J:460:A:H2'	3:J:460:A:N3	2.34	0.43
3:J:565:C:C5	3:J:577:G:C5	3.05	0.43
3:J:1429:G:N3	3:J:1430:U:C6	2.87	0.43
4:K:1266:G:C2	4:K:1267:U:C6	3.06	0.43
4:K:2833:A:H2'	4:K:2834:G:C5'	2.37	0.43
4:K:2853:A:C5	4:K:2854:U:N3	2.86	0.43
4:K:2930:A:C6	4:K:2931:C:C4	3.06	0.43
8:G:124:VAL:HG13	8:G:125:ASN:H	1.83	0.43
8:G:183:PHE:CD2	8:G:183:PHE:N	2.87	0.43
9:C:67:VAL:HG23	9:C:100:ALA:H	1.83	0.43
10:H:110:ILE:O	10:H:110:ILE:HG12	2.17	0.43
2:B:92:PHE:CZ	14:B:702:ATP:H4'	2.53	0.43
2:B:100:PRO:CA	2:B:273:TYR:CE1	3.02	0.43
2:B:507:SER:O	2:B:534:LEU:HD21	2.18	0.43
2:B:529:ILE:HD13	2:B:529:ILE:N	2.11	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:43:A:O2'	3:J:44:U:H5''	2.18	0.43
3:J:1442:U:N3	3:J:1443:U:O4	2.52	0.43
3:J:1648:A:C4	3:J:1753:A:C2	3.06	0.43
4:K:2284:C:H2'	4:K:2285:C:C2	2.53	0.43
10:H:8:ASN:C	10:H:8:ASN:ND2	2.77	0.43
10:H:109:ILE:N	10:H:112:ILE:HG23	2.34	0.43
12:D:52:LYS:C	12:D:54:ALA:H	2.26	0.43
1:A:376:LEU:HD21	4:K:1270:A:N1	2.33	0.43
2:B:37:LEU:HD23	2:B:54:LEU:HD11	2.00	0.43
2:B:509:VAL:HG13	2:B:513:PHE:HE2	1.84	0.43
2:B:565:LEU:HD12	2:B:600:TYR:CB	2.48	0.43
3:J:155:U:H4'	9:C:60:GLY:N	2.33	0.43
3:J:1428:G:C2	3:J:1429:G:C8	3.07	0.43
3:J:1442:U:H2'	3:J:1443:U:C5	2.54	0.43
4:K:2295:A:O2'	11:I:73:VAL:CG1	2.66	0.43
1:A:324:LEU:HD22	1:A:332:ARG:HB3	2.00	0.43
2:B:62:VAL:HG13	2:B:63:LYS:N	2.33	0.43
2:B:305:THR:CG2	2:B:306:LEU:H	2.30	0.43
2:B:336:PHE:HE1	2:B:529:ILE:HB	1.83	0.43
2:B:413:LEU:CD2	2:B:413:LEU:H	2.32	0.43
2:B:457:ILE:CA	2:B:460:ILE:HG22	2.49	0.43
3:J:1645:G:C6	3:J:1757:G:C6	3.07	0.43
4:K:1231:A:N6	4:K:1279:C:N4	2.67	0.43
4:K:1265:U:O4	4:K:1276:U:C2	2.72	0.43
4:K:2289:U:O2	4:K:2290:C:C6	2.72	0.43
4:K:2854:U:C2'	4:K:2855:U:H5'	2.48	0.43
10:H:19:GLY:O	10:H:50:THR:HG21	2.18	0.43
10:H:35:LEU:HB3	10:H:36:GLY:H	1.71	0.43
1:A:210:THR:HG23	1:A:275:THR:H	1.83	0.43
3:J:47:A:H4'	3:J:48:G:C5'	2.48	0.43
3:J:161:U:OP2	9:C:85:ARG:HB3	2.18	0.43
3:J:578:U:H4'	3:J:578:U:OP1	2.19	0.43
4:K:1254:C:C2	4:K:1263:A:C2	3.07	0.43
4:K:2287:C:O2	4:K:2298:U:H5''	2.19	0.43
11:I:74:MET:HG3	11:I:102:ILE:HD13	2.01	0.43
2:B:62:VAL:CG1	2:B:63:LYS:N	2.82	0.42
2:B:92:PHE:CG	14:B:702:ATP:C4'	3.02	0.42
2:B:94:LEU:HD23	2:B:115:GLY:HA3	2.01	0.42
2:B:117:SER:HB2	14:B:702:ATP:PA	2.59	0.42
2:B:180:ILE:HG23	2:B:183:PRO:C	2.45	0.42
2:B:195:MET:SD	2:B:201:ASP:HB2	2.59	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:195:MET:SD	2:B:201:ASP:CB	3.07	0.42
2:B:352:ARG:CG	2:B:353:ALA:N	2.82	0.42
3:J:454:U:O2'	3:J:455:C:C6	2.71	0.42
3:J:568:G:C2	3:J:569:C:C5	3.07	0.42
3:J:1201:G:N3	3:J:1201:G:O5'	2.52	0.42
4:K:1271:A:H61	4:K:1272:C:H42	1.66	0.42
4:K:3019:U:O2	4:K:3019:U:C2'	2.67	0.42
11:I:4:ASN:C	11:I:6:ALA:H	2.27	0.42
11:I:40:LYS:HB3	11:I:40:LYS:HE3	1.89	0.42
12:D:14:SER:CB	12:D:21:LYS:HE3	2.49	0.42
1:A:78:ASP:CG	7:E:9:ALA:CA	2.92	0.42
2:B:37:LEU:HD23	2:B:54:LEU:CD1	2.49	0.42
2:B:291:VAL:CG1	2:B:313:GLY:HA3	2.50	0.42
3:J:43:A:C3'	3:J:44:U:H5''	2.50	0.42
3:J:433:C:N4	3:J:434:G:C6	2.88	0.42
3:J:1433:G:HO2'	3:J:1434:U:H6	1.67	0.42
4:K:1256:G:C5	4:K:1257:C:C5	3.07	0.42
4:K:2836:C:H2'	4:K:2837:A:O4'	2.19	0.42
4:K:3032:A:H3'	4:K:3032:A:H8	1.83	0.42
8:G:188:VAL:O	8:G:188:VAL:HG12	2.20	0.42
1:A:47:PHE:HB3	1:A:63:VAL:HG21	2.01	0.42
2:B:31:VAL:CG2	2:B:32:VAL:N	2.82	0.42
2:B:73:ILE:CG2	2:B:74:ASN:N	2.82	0.42
2:B:140:TRP:CD2	2:B:160:LEU:HD22	2.54	0.42
2:B:263:ILE:CG2	2:B:264:ILE:N	2.82	0.42
2:B:338:ILE:O	2:B:603:LEU:HD23	2.18	0.42
2:B:505:ILE:CG2	2:B:506:CYS:N	2.82	0.42
3:J:152:U:C4'	9:C:13:GLN:CB	2.97	0.42
3:J:551:G:C4'	3:J:581:U:O2	2.67	0.42
3:J:576:G:H5''	3:J:577:G:OP2	2.19	0.42
4:K:2291:A:C2	4:K:2292:U:C2	3.07	0.42
4:K:2919:A:H3'	4:K:2920:U:C5'	2.45	0.42
4:K:3024:A:H2'	6:F:175:PHE:CE1	2.53	0.42
6:F:20:ILE:HD12	6:F:45:PHE:CD1	2.54	0.42
8:G:5:ARG:HB3	8:G:7:LYS:HA	2.00	0.42
8:G:93:LEU:HD13	8:G:190:VAL:HG11	2.00	0.42
9:C:55:GLY:C	9:C:63:MET:HE3	2.44	0.42
10:H:18:VAL:CG1	10:H:19:GLY:H	2.32	0.42
2:B:99:THR:HG22	2:B:290:PHE:CZ	2.54	0.42
2:B:176:ILE:HG12	2:B:177:PRO:HD3	1.97	0.42
2:B:181:LYS:HB2	2:B:181:LYS:NZ	2.34	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:243:TYR:HE2	2:B:272:LYS:HD3	1.81	0.42
2:B:413:LEU:N	2:B:413:LEU:CD2	2.82	0.42
2:B:451:VAL:CG2	2:B:452:VAL:N	2.82	0.42
2:B:491:ILE:CG2	2:B:523:ILE:HA	2.49	0.42
2:B:538:VAL:CG1	2:B:539:ILE:N	2.82	0.42
3:J:446:A:C6	3:J:447:U:C4	3.07	0.42
3:J:1196:A:O4'	3:J:1197:C:O5'	2.36	0.42
4:K:2288:G:C2	4:K:2289:U:C5	3.07	0.42
4:K:2849:C:O2	4:K:2849:C:C2'	2.66	0.42
10:H:60:VAL:HG22	10:H:73:VAL:HG22	2.01	0.42
10:H:139:VAL:O	10:H:139:VAL:HG12	2.19	0.42
11:I:33:ASN:HD21	11:I:64:LYS:H	1.66	0.42
2:B:38:CYS:SG	2:B:55:CYS:CA	3.07	0.42
2:B:82:HIS:CD2	2:B:96:ARG:HG3	2.54	0.42
2:B:99:THR:HG23	2:B:106:LEU:HD13	2.00	0.42
2:B:166:ALA:CA	2:B:242:VAL:HG13	2.39	0.42
2:B:202:VAL:CG2	2:B:203:LYS:N	2.82	0.42
2:B:253:ASP:CB	2:B:526:HIS:CE1	3.02	0.42
2:B:430:VAL:HG13	2:B:431:ARG:N	2.35	0.42
2:B:434:PHE:CE2	2:B:476:VAL:HG12	2.54	0.42
3:J:448:C:C2	3:J:449:C:C5	3.08	0.42
4:K:1248:C:C3'	4:K:1248:C:C6	3.03	0.42
11:I:79:VAL:HG22	11:I:99:ALA:O	2.20	0.42
2:B:92:PHE:CD2	14:B:702:ATP:C1'	3.02	0.42
2:B:100:PRO:CB	2:B:273:TYR:CZ	3.02	0.42
2:B:104:GLN:CG	2:B:106:LEU:HD21	2.49	0.42
2:B:167:ILE:HD12	2:B:238:GLN:CG	2.49	0.42
2:B:198:SER:O	2:B:201:ASP:HB2	2.19	0.42
2:B:286:TYR:CD1	2:B:286:TYR:C	2.97	0.42
2:B:371:GLU:HG2	2:B:550:HIS:NE2	2.35	0.42
3:J:152:U:O4'	9:C:13:GLN:HB2	2.19	0.42
3:J:565:C:HO2'	3:J:577:G:H1	1.66	0.42
3:J:571:G:H3'	3:J:572:C:H6	1.85	0.42
3:J:586:G:H5'	7:E:21:VAL:O	2.20	0.42
4:K:2295:A:C5	4:K:2296:A:C6	3.07	0.42
9:C:147:LEU:O	9:C:148:SER:OG	2.34	0.42
10:H:132:ILE:O	10:H:133:LEU:C	2.63	0.42
1:A:60:THR:HG23	1:A:61:ASP:H	1.83	0.42
1:A:283:VAL:CB	1:A:350:LEU:HD21	2.47	0.42
2:B:381:LEU:HD21	2:B:539:ILE:HD12	1.98	0.42
2:B:402:LEU:HD12	2:B:402:LEU:N	2.34	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:498:LEU:HB3	2:B:502:GLN:HB2	2.00	0.42
2:B:510:ILE:HG23	2:B:514:ILE:HD11	2.01	0.42
2:B:570:VAL:HG23	2:B:572:PHE:CE1	2.54	0.42
3:J:434:G:N2	3:J:437:A:C2	2.87	0.42
4:K:1239:C:OP2	4:K:1239:C:H6	2.02	0.42
4:K:1246:G:O2'	4:K:1247:U:H5'	2.19	0.42
4:K:1269:U:O4	4:K:1272:C:C5	2.72	0.42
4:K:1277:C:O2'	4:K:1278:A:H8	2.03	0.42
4:K:2838:A:N1	4:K:2851:A:C8	2.87	0.42
8:G:33:VAL:HG12	8:G:37:GLN:HB2	2.02	0.42
8:G:72:ASP:HB3	8:G:73:PHE:HB2	2.01	0.42
8:G:124:VAL:CG1	8:G:125:ASN:N	2.83	0.42
10:H:88:PRO:HD2	10:H:89:PRO:HD3	2.02	0.42
12:D:35:VAL:HG11	12:D:40:LEU:HD11	2.00	0.42
2:B:106:LEU:HD13	2:B:290:PHE:CE2	2.54	0.42
2:B:166:ALA:CA	2:B:242:VAL:CG1	2.95	0.42
2:B:305:THR:CG2	2:B:306:LEU:N	2.80	0.42
2:B:331:THR:CG2	2:B:332:GLU:N	2.83	0.42
2:B:343:GLU:CD	2:B:345:LEU:HD21	2.44	0.42
2:B:544:ILE:HG12	2:B:548:ASN:OD1	2.20	0.42
2:B:589:GLN:HE22	9:C:58:LYS:CB	1.89	0.42
3:J:1275:A:C6	3:J:1438:G:C6	3.08	0.42
4:K:3024:A:C8	4:K:3032:A:C6	3.08	0.42
9:C:76:LEU:HD22	9:C:92:ARG:HB3	2.01	0.42
9:C:79:LYS:O	9:C:80:ASN:HB2	2.19	0.42
10:H:62:LEU:HG	10:H:69:ALA:HB1	2.01	0.42
1:A:137:GLU:HB3	1:A:324:LEU:HD13	2.01	0.42
2:B:167:ILE:HD12	2:B:238:GLN:HB2	2.01	0.42
2:B:194:ARG:HG2	2:B:237:VAL:HG23	2.01	0.42
2:B:205:TYR:CE1	2:B:236:CYS:SG	3.09	0.42
2:B:338:ILE:N	2:B:338:ILE:CD1	2.83	0.42
2:B:375:PHE:HE2	2:B:520:THR:OG1	2.02	0.42
2:B:382:VAL:CG1	2:B:383:MET:N	2.82	0.42
2:B:389:THR:O	2:B:549:ALA:CB	2.68	0.42
2:B:452:VAL:CG1	2:B:453:LYS:N	2.82	0.42
3:J:1195:C:H5''	3:J:1197:C:C6	2.55	0.42
3:J:1201:G:OP2	3:J:1201:G:C5	2.72	0.42
4:K:1262:G:O6	4:K:1264:G:N2	2.52	0.42
4:K:2291:A:N1	4:K:2292:U:C2	2.88	0.42
4:K:2846:U:H2'	4:K:2847:A:OP2	2.20	0.42
8:G:30:VAL:HG13	8:G:38:MET:HG3	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:2:LYS:HB3	9:C:108:VAL:HG22	2.02	0.42
2:B:108:LEU:CD2	2:B:108:LEU:C	2.93	0.42
2:B:395:ILE:CG2	2:B:396:LYS:N	2.83	0.42
2:B:434:PHE:CD1	2:B:434:PHE:N	2.88	0.42
3:J:446:A:C6	3:J:447:U:C5	3.08	0.42
3:J:1267:G:C2'	3:J:1268:G:H5'	2.50	0.42
3:J:1275:A:C8	3:J:1438:G:C2	3.08	0.42
4:K:1259:A:N6	4:K:1260:A:N1	2.68	0.42
4:K:2919:A:H2'	4:K:2920:U:H5'	2.02	0.42
1:A:77:LYS:HG3	1:A:78:ASP:N	2.35	0.41
2:B:210:GLN:HE22	2:B:255:LYS:HE2	1.84	0.41
2:B:220:GLU:HG3	2:B:221:LYS:N	2.34	0.41
2:B:294:ILE:CD1	2:B:294:ILE:N	2.83	0.41
2:B:574:ARG:HD2	2:B:602:PHE:HB2	1.90	0.41
3:J:549:G:N3	3:J:550:A:C8	2.88	0.41
3:J:1209:C:N3	3:J:1210:C:C5	2.88	0.41
3:J:1277:G:C6	3:J:1278:G:N3	2.88	0.41
4:K:1248:C:OP2	4:K:1268:G:O6	2.37	0.41
4:K:2925:C:C5	4:K:2926:A:N7	2.88	0.41
9:C:70:PRO:C	9:C:98:ARG:NH1	2.78	0.41
10:H:132:ILE:CA	10:H:135:THR:HG22	2.50	0.41
12:D:14:SER:HB3	12:D:21:LYS:HE3	2.02	0.41
12:D:47:VAL:HG23	12:D:48:TYR:HD2	1.84	0.41
1:A:134:CYS:SG	1:A:134:CYS:O	2.78	0.41
2:B:58:CYS:SG	15:B:703:SF4:S3	3.17	0.41
2:B:100:PRO:CB	2:B:273:TYR:CE1	3.02	0.41
2:B:117:SER:N	14:B:702:ATP:O1B	2.46	0.41
2:B:157:THR:CG2	2:B:158:LYS:N	2.82	0.41
2:B:182:GLY:CA	2:B:185:GLN:CA	2.94	0.41
2:B:382:VAL:HB	2:B:538:VAL:HG22	2.03	0.41
4:K:2840:C:N4	4:K:2841:G:C5	2.88	0.41
4:K:2851:A:C8	4:K:2851:A:H5''	2.55	0.41
4:K:2927:C:H2'	4:K:2928:C:O4'	2.21	0.41
7:E:34:ALA:O	7:E:37:ARG:HB3	2.20	0.41
10:H:21:GLU:CB	10:H:50:THR:CG2	2.98	0.41
1:A:283:VAL:HG11	1:A:316:TYR:HB3	2.02	0.41
2:B:73:ILE:N	2:B:73:ILE:CD1	2.82	0.41
2:B:168:ILE:N	2:B:168:ILE:CD1	2.82	0.41
2:B:183:PRO:HD2	2:B:185:GLN:N	2.35	0.41
2:B:227:LEU:O	2:B:230:PHE:CE2	2.73	0.41
2:B:334:LEU:CD2	2:B:334:LEU:C	2.93	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:544:ILE:CD1	2:B:547:LYS:CG	2.95	0.41
2:B:557:LEU:C	2:B:557:LEU:CD2	2.93	0.41
4:K:1227:C:O2	4:K:1227:C:H2'	2.20	0.41
4:K:3035:A:H1'	6:F:121:LYS:CB	2.50	0.41
9:C:27:PHE:C	9:C:30:LYS:HG2	2.45	0.41
9:C:58:LYS:C	9:C:60:GLY:N	2.78	0.41
9:C:119:GLN:HG3	9:C:120:GLU:N	2.35	0.41
10:H:21:GLU:HG2	10:H:22:VAL:H	1.86	0.41
1:A:147:LEU:HD21	1:A:219:TYR:HB3	2.02	0.41
1:A:300:TYR:OH	2:B:64:LYS:NZ	2.52	0.41
2:B:106:LEU:CG	2:B:290:PHE:HD2	2.32	0.41
2:B:114:ILE:HG13	14:B:702:ATP:O2B	2.21	0.41
2:B:176:ILE:CD1	2:B:227:LEU:CG	2.95	0.41
2:B:176:ILE:CD1	2:B:227:LEU:HD21	2.50	0.41
3:J:413:U:N3	3:J:421:A:C2	2.88	0.41
3:J:586:G:C2'	3:J:587:C:O5'	2.68	0.41
3:J:1179:G:C6	3:J:1180:C:N3	2.88	0.41
4:K:1266:G:C6	4:K:1267:U:C5	3.08	0.41
4:K:1281:G:C2	4:K:1282:G:N7	2.89	0.41
11:I:18:PRO:HA	11:I:51:ALA:HA	2.02	0.41
1:A:170:TYR:CE1	1:A:172:MET:HA	2.55	0.41
1:A:307:LYS:HD2	1:A:307:LYS:HA	1.96	0.41
2:B:83:VAL:O	2:B:146:TYR:CZ	2.74	0.41
2:B:171:GLN:OE1	2:B:172:TYR:CZ	2.74	0.41
2:B:229:ARG:HA	2:B:232:ILE:HD12	2.03	0.41
2:B:303:VAL:CG1	2:B:304:VAL:N	2.83	0.41
3:J:572:C:C5'	3:J:573:C:OP2	2.66	0.41
3:J:1267:G:C2	3:J:1268:G:C4	3.08	0.41
10:H:28:LEU:HA	10:H:42:VAL:O	2.20	0.41
10:H:123:ARG:CD	10:H:126:ALA:HB2	2.48	0.41
1:A:146:VAL:HG11	1:A:258:GLY:HA3	2.02	0.41
1:A:381:GLU:OE1	2:B:22:ARG:NH1	2.53	0.41
2:B:295:TYR:CZ	2:B:325:GLU:HG2	2.55	0.41
2:B:389:THR:HG23	2:B:391:LYS:HG3	1.97	0.41
3:J:428:A:O3'	3:J:439:U:H2'	2.20	0.41
4:K:1257:C:C2	4:K:1258:U:C6	3.08	0.41
10:H:57:LYS:O	10:H:58:VAL:HG22	2.20	0.41
11:I:93:LEU:N	11:I:93:LEU:HD23	2.35	0.41
11:I:93:LEU:HD23	11:I:93:LEU:H	1.86	0.41
12:D:18:LEU:HD23	12:D:18:LEU:HA	1.89	0.41
12:D:44:LEU:HA	12:D:47:VAL:CG2	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:116:LYS:N	2:B:116:LYS:HD3	2.35	0.41
2:B:208:ILE:CG2	2:B:209:LEU:N	2.84	0.41
2:B:254:VAL:HA	2:B:257:ARG:CD	2.51	0.41
2:B:320:GLY:HA2	2:B:329:PHE:CE2	2.55	0.41
2:B:349:SER:CB	2:B:377:ASP:HB3	2.51	0.41
2:B:394:LEU:C	2:B:394:LEU:CD1	2.94	0.41
2:B:572:PHE:HB3	2:B:581:PRO:CB	2.51	0.41
3:J:445:A:C2	3:J:446:A:N7	2.88	0.41
3:J:1187:U:O5'	3:J:1187:U:H6	2.04	0.41
4:K:1269:U:O4	4:K:1271:A:C5	2.74	0.41
5:L:66:C:H2'	5:L:67:G:C8	2.55	0.41
6:F:96:HIS:CD2	6:F:96:HIS:C	2.98	0.41
6:F:165:CYS:SG	6:F:179:ILE:HD12	2.61	0.41
9:C:55:GLY:CA	9:C:63:MET:HE3	2.51	0.41
2:B:79:LEU:C	2:B:79:LEU:CD2	2.94	0.41
2:B:205:TYR:CD2	2:B:233:GLY:HA2	2.55	0.41
2:B:218:ASP:H	2:B:221:LYS:HD2	1.84	0.41
2:B:510:ILE:HB	2:B:534:LEU:HD22	2.02	0.41
3:J:50:C:O2	3:J:50:C:H2'	2.21	0.41
3:J:552:G:C6	3:J:553:G:N1	2.89	0.41
3:J:1190:C:N3	3:J:1194:A:C2	2.89	0.41
4:K:2295:A:OP1	11:I:61:THR:OG1	2.31	0.41
4:K:3032:A:C8	4:K:3032:A:C3'	3.04	0.41
9:C:32:ILE:HD12	9:C:100:ALA:HB1	2.02	0.41
9:C:39:GLU:HB2	9:C:46:LYS:HG3	2.03	0.41
1:A:135:ASN:HB3	1:A:138:TYR:H	1.85	0.41
1:A:144:ALA:HB3	1:A:259:ILE:HD12	2.02	0.41
1:A:232:GLU:O	4:K:2851:A:O2'	2.39	0.41
2:B:112:ASN:HA	14:B:702:ATP:PG	2.60	0.41
2:B:265:ARG:HD2	2:B:286:TYR:O	2.21	0.41
2:B:345:LEU:CD2	2:B:345:LEU:N	2.84	0.41
2:B:409:ASP:C	2:B:411:PRO:HD3	2.46	0.41
2:B:420:GLN:CG	2:B:421:LYS:N	2.84	0.41
2:B:430:VAL:CG1	2:B:431:ARG:N	2.83	0.41
2:B:431:ARG:HB3	2:B:461:ILE:HG23	1.98	0.41
2:B:580:ARG:HH12	2:B:582:ARG:HH11	1.69	0.41
3:J:51:A:C6	3:J:52:U:C2	3.09	0.41
3:J:425:A:C2'	3:J:426:G:OP2	2.68	0.41
3:J:461:G:C2	3:J:462:G:C5	3.09	0.41
3:J:1429:G:C4	3:J:1430:U:C6	3.09	0.41
4:K:2834:G:O2'	4:K:2835:U:P	2.78	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:2852:C:H5	4:K:2853:A:C4	2.36	0.41
4:K:3036:G:H2'	4:K:3037:U:O5'	2.21	0.41
5:L:67:G:C2'	5:L:68:C:H5''	2.51	0.41
9:C:28:PHE:CZ	9:C:104:PRO:HG3	2.56	0.41
9:C:109:LEU:HD23	9:C:109:LEU:HA	1.85	0.41
10:H:23:GLY:N	10:H:46:ILE:CD1	2.83	0.41
10:H:70:ALA:O	10:H:72:SER:N	2.54	0.41
11:I:33:ASN:ND2	11:I:64:LYS:H	2.19	0.41
12:D:94:TYR:CD2	12:D:96:LEU:HD11	2.55	0.41
1:A:199:MET:HE3	1:A:205:PHE:CZ	2.56	0.41
2:B:46:LYS:HG3	2:B:46:LYS:O	2.21	0.41
2:B:112:ASN:OD1	14:B:702:ATP:O3G	2.39	0.41
2:B:168:ILE:O	2:B:168:ILE:HG12	2.19	0.41
2:B:354:PHE:CE2	2:B:355:SER:O	2.74	0.41
2:B:441:GLN:NE2	2:B:447:PHE:HE2	2.14	0.41
2:B:528:PHE:HE2	2:B:572:PHE:CE1	2.39	0.41
2:B:544:ILE:CD1	2:B:547:LYS:CB	2.99	0.41
2:B:568:LEU:HD23	2:B:568:LEU:C	2.45	0.41
3:J:461:G:C2	3:J:462:G:C4	3.09	0.41
4:K:1254:C:N3	4:K:1255:C:C5	2.89	0.41
4:K:1262:G:H5''	4:K:1263:A:OP2	2.21	0.41
4:K:2852:C:H5	4:K:2853:A:C5	2.39	0.41
6:F:106:LYS:H	6:F:109:ALA:CB	2.33	0.41
9:C:58:LYS:HB2	9:C:59:GLN:OE1	2.21	0.41
9:C:63:MET:HE2	9:C:106:LEU:CD2	2.51	0.41
9:C:69:LEU:HD12	9:C:69:LEU:HA	1.82	0.41
2:B:169:LYS:HG2	2:B:231:ALA:HB1	2.03	0.40
2:B:211:LEU:HD21	2:B:229:ARG:HB3	2.03	0.40
2:B:293:ILE:N	2:B:293:ILE:CD1	2.83	0.40
2:B:366:PHE:CD1	2:B:547:LYS:O	2.75	0.40
2:B:518:LYS:NZ	6:F:115:ARG:HB3	2.37	0.40
3:J:567:A:C6	3:J:568:G:C4	3.09	0.40
3:J:586:G:H4'	7:E:21:VAL:CG2	2.51	0.40
5:L:1:U:H2'	5:L:2:C:C6	2.56	0.40
6:F:34:LEU:HA	6:F:34:LEU:HD23	1.91	0.40
6:F:90:MET:HG2	6:F:181:VAL:HG22	2.03	0.40
7:E:38:LEU:O	7:E:42:ARG:HB2	2.21	0.40
1:A:237:LYS:HZ1	4:K:2839:G:H4'	1.85	0.40
2:B:29:CYS:HA	2:B:30:PRO:HD2	1.88	0.40
2:B:108:LEU:CD2	2:B:294:ILE:CD1	2.95	0.40
2:B:140:TRP:CB	2:B:160:LEU:CD1	2.94	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:253:ASP:HA	2:B:526:HIS:CE1	2.57	0.40
2:B:297:VAL:HG12	2:B:298:PRO:N	2.36	0.40
2:B:498:LEU:HD22	2:B:502:GLN:OE1	2.21	0.40
3:J:155:U:C1'	9:C:60:GLY:HA3	2.50	0.40
4:K:1229:G:C6	4:K:1230:G:C5	3.10	0.40
10:H:91:ASP:OD2	10:H:95:ASP:HB3	2.21	0.40
11:I:81:GLN:O	11:I:82:ALA:HB3	2.22	0.40
2:B:37:LEU:N	2:B:37:LEU:CD2	2.83	0.40
2:B:171:GLN:HB3	2:B:246:ASP:CG	2.46	0.40
2:B:180:ILE:HG22	2:B:181:LYS:N	2.37	0.40
2:B:197:LYS:HB3	2:B:198:SER:H	1.54	0.40
2:B:208:ILE:HD13	2:B:208:ILE:C	2.47	0.40
2:B:209:LEU:HD23	2:B:209:LEU:HA	1.79	0.40
2:B:236:CYS:SG	2:B:263:ILE:CD1	3.07	0.40
2:B:304:VAL:HG12	2:B:305:THR:O	2.21	0.40
2:B:368:LEU:HD22	2:B:393:THR:HG1	1.86	0.40
2:B:573:ARG:HG2	2:B:574:ARG:N	2.36	0.40
3:J:1269:U:C2	3:J:1432:U:O4'	2.74	0.40
4:K:1246:G:N2	4:K:1247:U:O2	2.55	0.40
4:K:1248:C:C6	4:K:1248:C:H3'	2.57	0.40
4:K:2919:A:C2'	4:K:2920:U:C5'	2.99	0.40
6:F:189:GLU:C	6:F:191:LEU:N	2.79	0.40
10:H:61:GLN:HB3	10:H:72:SER:HB3	2.04	0.40
1:A:101:VAL:HG21	3:J:1272:U:C4'	2.52	0.40
2:B:21:CYS:O	2:B:22:ARG:HG3	2.22	0.40
2:B:173:VAL:HG21	2:B:251:TYR:CE2	2.57	0.40
2:B:180:ILE:N	2:B:180:ILE:CD1	2.83	0.40
2:B:382:VAL:HG11	2:B:384:MET:HE3	2.03	0.40
2:B:452:VAL:HG13	2:B:453:LYS:H	1.86	0.40
2:B:457:ILE:HA	2:B:460:ILE:CG2	2.51	0.40
2:B:501:GLU:OE1	2:B:501:GLU:HA	2.21	0.40
3:J:561:G:C2	3:J:585:A:C2	3.09	0.40
4:K:2931:C:N3	4:K:2932:U:C5	2.89	0.40
6:F:126:VAL:HG21	6:F:161:LEU:HA	2.03	0.40
10:H:42:VAL:HG12	10:H:42:VAL:O	2.22	0.40
10:H:46:ILE:HA	10:H:49:ALA:N	2.36	0.40
10:H:101:SER:HB2	10:H:138:SER:O	2.21	0.40
10:H:130:LYS:O	10:H:131:GLU:C	2.64	0.40
12:D:47:VAL:O	12:D:49:LYS:NZ	2.49	0.40
2:B:146:TYR:O	2:B:146:TYR:CD2	2.75	0.40
2:B:371:GLU:HA	2:B:371:GLU:OE1	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:505:ILE:HG23	2:B:506:CYS:N	2.37	0.40
3:J:438:A:C1'	3:J:439:U:OP1	2.69	0.40
4:K:1234:G:O5'	4:K:1235:U:OP2	2.39	0.40
4:K:1257:C:C2	4:K:1261:G:N2	2.89	0.40
4:K:2932:U:C5'	11:I:41:GLY:C	2.83	0.40
6:F:114:VAL:HB	6:F:124:ARG:HB2	2.04	0.40
10:H:9:GLU:C	10:H:10:VAL:HG23	2.47	0.40
10:H:87:GLU:HA	10:H:88:PRO:HD3	1.91	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	384/386 (100%)	289 (75%)	50 (13%)	45 (12%)	0	4
2	B	606/608 (100%)	561 (93%)	29 (5%)	16 (3%)	4	25
6	F	189/191 (99%)	167 (88%)	16 (8%)	6 (3%)	3	21
7	E	53/63 (84%)	42 (79%)	7 (13%)	4 (8%)	1	10
8	G	197/312 (63%)	170 (86%)	15 (8%)	12 (6%)	1	13
9	C	224/236 (95%)	190 (85%)	22 (10%)	12 (5%)	1	15
10	H	136/165 (82%)	47 (35%)	35 (26%)	54 (40%)	0	0
11	I	134/137 (98%)	124 (92%)	9 (7%)	1 (1%)	18	56
12	D	132/135 (98%)	106 (80%)	13 (10%)	13 (10%)	0	7
All	All	2055/2233 (92%)	1696 (82%)	196 (10%)	163 (8%)	1	9

All (163) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	ASP
1	A	15	GLY
1	A	46	LYS
1	A	48	THR
1	A	56	LYS
1	A	60	THR
1	A	61	ASP
1	A	62	LEU
1	A	103	LYS
1	A	133	ALA
1	A	141	ASP
1	A	156	LEU
1	A	159	SER
1	A	180	ASP
1	A	181	VAL
1	A	255	TYR
1	A	273	GLN
1	A	274	ASP
1	A	275	THR
1	A	327	ASP
1	A	328	ASN
1	A	330	ALA
1	A	331	GLN
1	A	382	ASP
2	B	44	THR
2	B	68	ASP
2	B	186	LYS
2	B	573	ARG
6	F	50	ASN
6	F	109	ALA
7	E	47	VAL
7	E	57	ASN
8	G	60	ARG
8	G	70	LEU
8	G	71	PRO
8	G	73	PHE
8	G	83	ASN
8	G	106	ALA
8	G	124	VAL
8	G	179	SER
8	G	180	PRO
9	C	20	ASP
9	C	25	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	C	154	ARG
9	C	173	PRO
9	C	174	LYS
10	H	10	VAL
10	H	17	ALA
10	H	18	VAL
10	H	25	SER
10	H	38	SER
10	H	39	PRO
10	H	49	ALA
10	H	56	ILE
10	H	58	VAL
10	H	75	PRO
10	H	77	ALA
10	H	78	SER
10	H	88	PRO
10	H	90	ARG
10	H	104	ILE
10	H	106	LEU
10	H	109	ILE
10	H	112	ILE
10	H	113	ALA
10	H	124	THR
10	H	141	CYS
12	D	32	ARG
12	D	36	SER
12	D	78	SER
1	A	55	GLY
1	A	168	ILE
1	A	169	GLU
1	A	178	THR
1	A	179	THR
1	A	205	PHE
1	A	269	ALA
2	B	22	ARG
2	B	349	SER
2	B	586	LEU
2	B	587	ASP
8	G	49	ALA
9	C	24	ILE
9	C	146	GLY
9	C	152	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	C	153	VAL
10	H	14	TYR
10	H	21	GLU
10	H	55	GLY
10	H	60	VAL
10	H	66	ASN
10	H	70	ALA
10	H	91	ASP
10	H	107	ASP
10	H	117	ARG
10	H	127	SER
10	H	140	GLY
11	I	82	ALA
12	D	5	VAL
12	D	11	LYS
1	A	52	ASP
1	A	98	ASP
1	A	136	ILE
1	A	182	LEU
1	A	183	LYS
1	A	344	SER
2	B	96	ARG
2	B	136	ASP
2	B	138	PRO
2	B	348	ASP
2	B	351	SER
6	F	42	ASP
8	G	6	GLU
10	H	15	LEU
10	H	69	ALA
10	H	71	ALA
10	H	86	LYS
10	H	131	GLU
12	D	34	ASN
12	D	51	GLU
12	D	53	ASP
1	A	6	LEU
1	A	50	LYS
1	A	96	ASN
6	F	13	PRO
7	E	50	VAL
7	E	58	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	C	69	LEU
10	H	54	LYS
10	H	89	PRO
10	H	92	ARG
10	H	95	ASP
10	H	120	SER
10	H	128	VAL
12	D	60	PHE
1	A	134	CYS
1	A	138	TYR
1	A	314	ILE
2	B	88	SER
6	F	2	LYS
6	F	107	ASP
10	H	29	ALA
10	H	41	LYS
10	H	103	ASN
10	H	108	GLU
10	H	121	PHE
12	D	6	THR
12	D	47	VAL
1	A	254	GLY
8	G	107	ALA
9	C	132	ARG
10	H	85	LEU
10	H	98	VAL
12	D	58	PHE
12	D	77	ASN
2	B	438	ILE
10	H	132	ILE
1	A	97	VAL
10	H	102	GLY
9	C	70	PRO
10	H	23	GLY
10	H	36	GLY
2	B	184	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	348/348 (100%)	316 (91%)	32 (9%)	8	26
2	B	537/537 (100%)	516 (96%)	21 (4%)	28	49
6	F	171/171 (100%)	129 (75%)	42 (25%)	1	4
7	E	48/54 (89%)	39 (81%)	9 (19%)	1	8
8	G	167/254 (66%)	162 (97%)	5 (3%)	36	57
9	C	193/201 (96%)	151 (78%)	42 (22%)	1	6
10	H	112/136 (82%)	94 (84%)	18 (16%)	2	11
11	I	104/105 (99%)	84 (81%)	20 (19%)	1	8
12	D	112/113 (99%)	83 (74%)	29 (26%)	0	3
All	All	1792/1919 (93%)	1574 (88%)	218 (12%)	7	17

All (218) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	10	SER
1	A	11	PHE
1	A	45	LYS
1	A	47	PHE
1	A	49	SER
1	A	52	ASP
1	A	58	LYS
1	A	65	LEU
1	A	68	LYS
1	A	81	LEU
1	A	103	LYS
1	A	105	LEU
1	A	117	ILE
1	A	146	VAL
1	A	147	LEU
1	A	156	LEU
1	A	158	THR
1	A	168	ILE
1	A	181	VAL
1	A	184	PHE
1	A	193	LYS
1	A	209	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	212	ILE
1	A	248	ILE
1	A	256	LEU
1	A	275	THR
1	A	283	VAL
1	A	303	LYS
1	A	320	THR
1	A	351	VAL
1	A	380	ASP
2	B	37	LEU
2	B	63	LYS
2	B	116	LYS
2	B	128	LYS
2	B	168	ILE
2	B	171	GLN
2	B	181	LYS
2	B	208	ILE
2	B	263	ILE
2	B	268	LEU
2	B	275	ILE
2	B	290	PHE
2	B	293	ILE
2	B	345	LEU
2	B	359	LEU
2	B	412	LYS
2	B	415	VAL
2	B	529	ILE
2	B	586	LEU
2	B	589	GLN
2	B	591	ASP
6	F	1	MET
6	F	4	ILE
6	F	5	GLN
6	F	9	GLN
6	F	16	VAL
6	F	18	VAL
6	F	20	ILE
6	F	22	SER
6	F	24	ILE
6	F	33	THR
6	F	36	LYS
6	F	41	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	F	48	VAL
6	F	49	ASN
6	F	52	LEU
6	F	62	ARG
6	F	65	VAL
6	F	68	LEU
6	F	69	ARG
6	F	70	THR
6	F	80	THR
6	F	82	VAL
6	F	91	ARG
6	F	121	LYS
6	F	132	VAL
6	F	134	ILE
6	F	135	GLU
6	F	137	SER
6	F	138	THR
6	F	139	ASN
6	F	147	SER
6	F	151	VAL
6	F	152	GLU
6	F	161	LEU
6	F	162	GLN
6	F	164	ILE
6	F	166	ARG
6	F	170	LYS
6	F	172	ILE
6	F	189	GLU
6	F	190	ASP
6	F	191	LEU
7	E	20	LYS
7	E	21	VAL
7	E	25	GLU
7	E	28	LYS
7	E	29	LYS
7	E	42	ARG
7	E	48	THR
7	E	49	LEU
7	E	50	VAL
8	G	36	GLN
8	G	50	VAL
8	G	73	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	G	84	VAL
8	G	89	THR
9	C	9	VAL
9	C	21	GLU
9	C	25	ARG
9	C	30	LYS
9	C	32	ILE
9	C	45	PHE
9	C	58	LYS
9	C	59	GLN
9	C	69	LEU
9	C	71	THR
9	C	76	LEU
9	C	78	THR
9	C	79	LYS
9	C	82	SER
9	C	97	VAL
9	C	98	ARG
9	C	105	ASP
9	C	109	LEU
9	C	111	LEU
9	C	120	GLU
9	C	124	LEU
9	C	126	ASP
9	C	127	THR
9	C	129	VAL
9	C	132	ARG
9	C	133	LEU
9	C	137	ARG
9	C	142	ARG
9	C	143	LYS
9	C	150	GLU
9	C	155	ASP
9	C	158	ILE
9	C	162	VAL
9	C	170	THR
9	C	175	ILE
9	C	176	GLN
9	C	177	ARG
9	C	179	VAL
9	C	211	LEU
9	C	212	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	C	217	SER
9	C	223	LYS
10	H	15	LEU
10	H	31	LYS
10	H	35	LEU
10	H	37	LEU
10	H	42	VAL
10	H	56	ILE
10	H	58	VAL
10	H	64	ILE
10	H	68	GLN
10	H	75	PRO
10	H	78	SER
10	H	80	LEU
10	H	85	LEU
10	H	103	ASN
10	H	104	ILE
10	H	108	GLU
10	H	125	LEU
10	H	133	LEU
11	I	13	ILE
11	I	32	ARG
11	I	33	ASN
11	I	48	ARG
11	I	63	LYS
11	I	64	LYS
11	I	69	LEU
11	I	72	LYS
11	I	73	VAL
11	I	74	MET
11	I	79	VAL
11	I	83	LYS
11	I	84	SER
11	I	88	ARG
11	I	91	VAL
11	I	102	ILE
11	I	115	THR
11	I	118	VAL
11	I	120	LYS
11	I	125	LEU
12	D	8	ARG
12	D	10	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	D	17	LEU
12	D	29	HIS
12	D	32	ARG
12	D	34	ASN
12	D	44	LEU
12	D	46	GLU
12	D	47	VAL
12	D	49	LYS
12	D	51	GLU
12	D	52	LYS
12	D	57	VAL
12	D	61	ARG
12	D	62	THR
12	D	75	VAL
12	D	81	GLU
12	D	84	LYS
12	D	88	THR
12	D	93	ARG
12	D	96	LEU
12	D	99	LYS
12	D	102	LYS
12	D	107	GLN
12	D	112	LYS
12	D	123	LYS
12	D	127	LYS
12	D	128	LYS
12	D	129	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	ASN
1	A	131	ASN
1	A	148	GLN
1	A	235	HIS
1	A	250	HIS
1	A	257	GLN
1	A	260	ASN
1	A	265	ASN
1	A	273	GLN
1	A	325	HIS
2	B	74	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	78	ASN
2	B	82	HIS
2	B	95	HIS
2	B	171	GLN
2	B	210	GLN
2	B	256	GLN
2	B	259	ASN
2	B	262	GLN
2	B	279	HIS
2	B	321	HIS
2	B	326	ASN
2	B	347	ASN
2	B	387	ASN
2	B	448	GLN
2	B	463	GLN
2	B	474	GLN
2	B	589	GLN
6	F	5	GLN
6	F	50	ASN
6	F	96	HIS
6	F	100	ASN
6	F	116	ASN
7	E	46	ASN
8	G	189	GLN
8	G	195	GLN
9	C	22	HIS
9	C	59	GLN
10	H	8	ASN
10	H	65	GLN
10	H	66	ASN
10	H	68	GLN
10	H	97	ASN
10	H	100	HIS
10	H	115	GLN
11	I	33	ASN
11	I	98	ASN
12	D	133	ASN

5.3.3 RNA ⓘ

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	J	224/233 (96%)	113 (50%)	26 (11%)
4	K	149/155 (96%)	86 (57%)	13 (8%)
5	L	74/75 (98%)	26 (35%)	10 (13%)
All	All	447/463 (96%)	225 (50%)	49 (10%)

All (225) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	J	40	A
3	J	41	A
3	J	42	G
3	J	45	U
3	J	46	A
3	J	47	A
3	J	48	G
3	J	50	C
3	J	51	A
3	J	156	A
3	J	159	U
3	J	160	C
3	J	161	U
3	J	162	A
3	J	415	C
3	J	416	A
3	J	417	A
3	J	418	G
3	J	419	G
3	J	421	A
3	J	426	G
3	J	427	C
3	J	428	A
3	J	434	G
3	J	437	A
3	J	438	A
3	J	439	U
3	J	440	U
3	J	441	A
3	J	444	C
3	J	445	A
3	J	446	A
3	J	447	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	J	448	C
3	J	451	A
3	J	452	A
3	J	453	U
3	J	454	U
3	J	455	C
3	J	458	G
3	J	459	G
3	J	462	G
3	J	464	A
3	J	467	G
3	J	468	A
3	J	550	A
3	J	551	G
3	J	554	C
3	J	555	A
3	J	556	A
3	J	557	G
3	J	558	U
3	J	559	C
3	J	560	U
3	J	561	G
3	J	563	U
3	J	564	G
3	J	565	C
3	J	568	G
3	J	570	A
3	J	572	C
3	J	574	G
3	J	577	G
3	J	578	U
3	J	579	A
3	J	580	A
3	J	585	A
3	J	1178	G
3	J	1179	G
3	J	1185	U
3	J	1186	U
3	J	1189	A
3	J	1190	C
3	J	1191	U
3	J	1193	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	J	1194	A
3	J	1196	A
3	J	1197	C
3	J	1198	G
3	J	1199	G
3	J	1200	G
3	J	1201	G
3	J	1202	A
3	J	1203	A
3	J	1204	A
3	J	1205	C
3	J	1206	U
3	J	1207	C
3	J	1208	A
3	J	1268	G
3	J	1270	G
3	J	1273	G
3	J	1274	C
3	J	1275	A
3	J	1276	U
3	J	1428	G
3	J	1429	G
3	J	1431	C
3	J	1432	U
3	J	1433	G
3	J	1434	U
3	J	1435	G
3	J	1436	A
3	J	1438	G
3	J	1443	U
3	J	1650	U
3	J	1761	U
3	J	1762	A
3	J	1765	A
3	J	1766	A
3	J	1767	G
3	J	1768	G
3	J	1769	U
4	K	1228	C
4	K	1229	G
4	K	1235	U
4	K	1236	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	K	1237	G
4	K	1239	C
4	K	1240	A
4	K	1241	U
4	K	1242	G
4	K	1244	A
4	K	1245	A
4	K	1246	G
4	K	1248	C
4	K	1249	G
4	K	1251	A
4	K	1253	U
4	K	1254	C
4	K	1256	G
4	K	1257	C
4	K	1258	U
4	K	1259	A
4	K	1261	G
4	K	1262	G
4	K	1263	A
4	K	1264	G
4	K	1265	U
4	K	1268	G
4	K	1269	U
4	K	1270	A
4	K	1272	C
4	K	1273	A
4	K	1274	A
4	K	1275	C
4	K	1277	C
4	K	1278	A
4	K	1279	C
4	K	1280	C
4	K	2255	A
4	K	2256	A
4	K	2257	C
4	K	2261	G
4	K	2266	U
4	K	2267	C
4	K	2286	U
4	K	2288	G
4	K	2290	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	K	2291	A
4	K	2292	U
4	K	2295	A
4	K	2296	A
4	K	2297	U
4	K	2298	U
4	K	2299	A
4	K	2834	G
4	K	2835	U
4	K	2836	C
4	K	2838	A
4	K	2839	G
4	K	2840	C
4	K	2842	U
4	K	2843	U
4	K	2844	C
4	K	2845	A
4	K	2846	U
4	K	2847	A
4	K	2850	G
4	K	2851	A
4	K	2852	C
4	K	2919	A
4	K	2920	U
4	K	2922	G
4	K	2923	U
4	K	2928	C
4	K	2929	C
4	K	2930	A
4	K	2932	U
4	K	3019	U
4	K	3020	U
4	K	3023	U
4	K	3024	A
4	K	3025	C
4	K	3030	G
4	K	3031	G
4	K	3033	A
4	K	3038	U
4	K	3039	C
5	L	8	U
5	L	12	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	L	13	U
5	L	14	A
5	L	17	G
5	L	18	G
5	L	19	U
5	L	20	C
5	L	21	A
5	L	22	G
5	L	26	G
5	L	28	G
5	L	32	U
5	L	33	U
5	L	37	G
5	L	38	C
5	L	42	C
5	L	45	G
5	L	47	U
5	L	51	G
5	L	60	C
5	L	65	U
5	L	68	C
5	L	73	C
5	L	74	C
5	L	75	A

All (49) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	J	40	A
3	J	45	U
3	J	160	C
3	J	416	A
3	J	417	A
3	J	427	C
3	J	438	A
3	J	439	U
3	J	447	U
3	J	557	G
3	J	1185	U
3	J	1190	C
3	J	1196	A
3	J	1200	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	J	1202	A
3	J	1203	A
3	J	1204	A
3	J	1207	C
3	J	1269	U
3	J	1274	C
3	J	1435	G
3	J	1750	A
3	J	1756	A
3	J	1761	U
3	J	1765	A
3	J	1767	G
4	K	1235	U
4	K	1264	G
4	K	1272	C
4	K	2254	U
4	K	2266	U
4	K	2290	C
4	K	2297	U
4	K	2834	G
4	K	2850	G
4	K	2851	A
4	K	3023	U
4	K	3030	G
4	K	3038	U
5	L	11	U
5	L	12	U
5	L	13	U
5	L	25	U
5	L	32	U
5	L	37	G
5	L	44	A
5	L	64	G
5	L	72	G
5	L	73	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	$\# Z > 2$
15	SF4	B	703	2	0,12,12	-	-	-		
15	SF4	B	704	2	0,12,12	-	-	-		
14	ATP	B	702	13	32,33,33	2.38	6 (18%)	48,52,52	3.07	15 (31%)

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
15	SF4	B	703	2	-	-	0/6/5/5
15	SF4	B	704	2	-	-	0/6/5/5
14	ATP	B	702	13	-	2/22/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	B	702	ATP	PB-O3A	8.96	1.69	1.59
14	B	702	ATP	C4-N3	5.11	1.44	1.34
14	B	702	ATP	O5'-C5'	-4.58	1.27	1.44
14	B	702	ATP	PA-O5'	-3.09	1.47	1.59
14	B	702	ATP	PB-O2B	-2.58	1.43	1.55
14	B	702	ATP	C3'-C4'	-2.21	1.47	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	B	702	ATP	O5'-C5'-C4'	12.43	151.30	108.99
14	B	702	ATP	O2B-PB-O3A	-7.67	86.54	107.27
14	B	702	ATP	O5'-PA-O1A	-6.37	83.69	108.94
14	B	702	ATP	PA-O5'-C5'	5.84	154.82	121.35
14	B	702	ATP	C5'-C4'-C3'	-5.45	95.59	115.21
14	B	702	ATP	O2A-PA-O3A	4.78	120.18	107.27
14	B	702	ATP	O4'-C4'-C3'	4.67	114.42	105.15
14	B	702	ATP	O2B-PB-O3B	3.55	116.86	107.27
14	B	702	ATP	O3B-PB-O1B	2.81	119.17	110.70
14	B	702	ATP	O3A-PB-O1B	-2.68	102.63	110.70
14	B	702	ATP	C3'-C2'-C1'	2.59	106.36	101.46
14	B	702	ATP	O2G-PG-O3B	2.44	112.83	104.64
14	B	702	ATP	O2A-PA-O1A	2.29	123.08	112.44
14	B	702	ATP	O2A-PA-O5'	-2.16	97.77	107.57
14	B	702	ATP	O2B-PB-O1B	2.10	122.21	112.44

There are no chirality outliers.

All (2) torsion outliers are listed below:

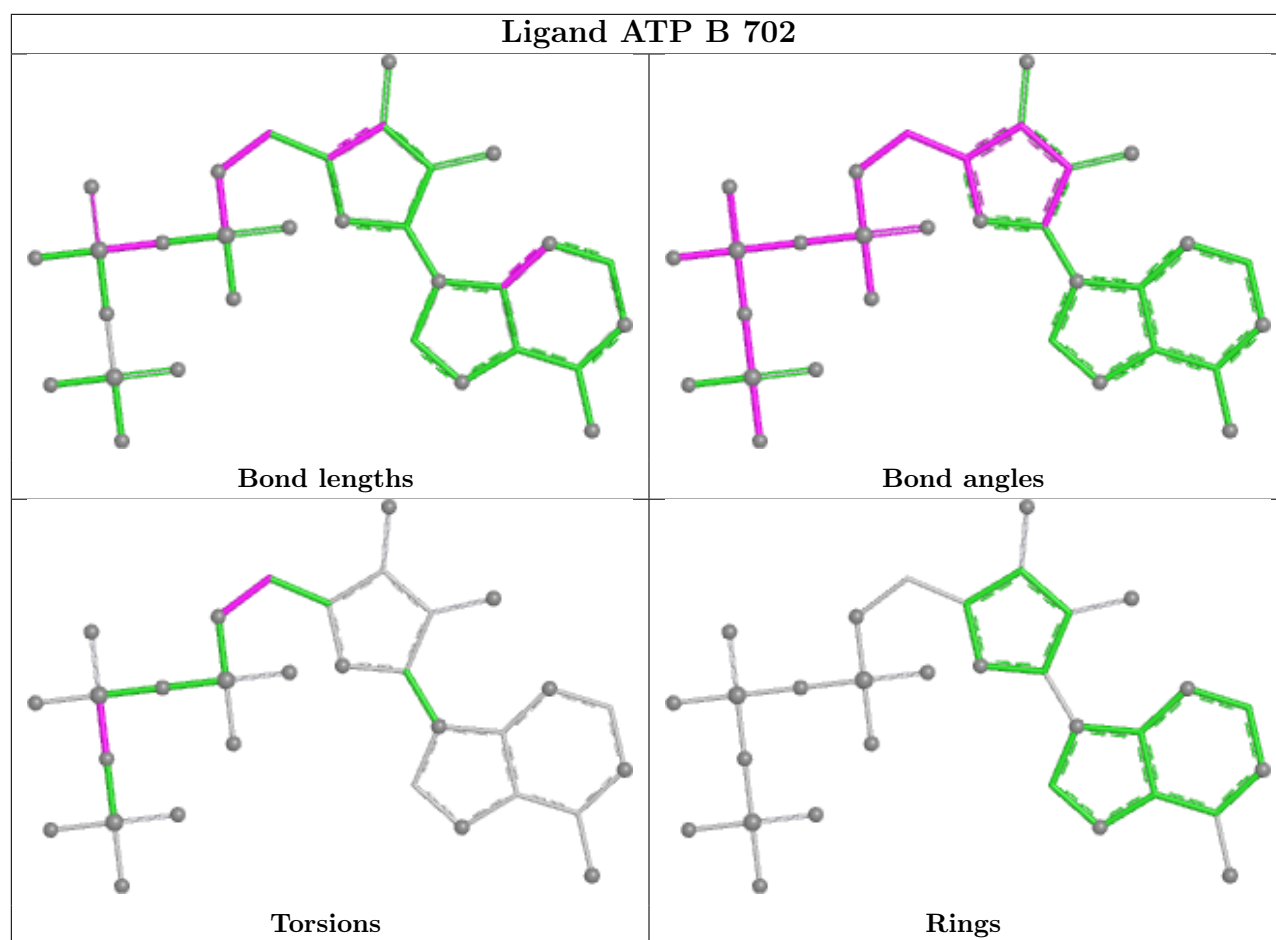
Mol	Chain	Res	Type	Atoms
14	B	702	ATP	C4'-C5'-O5'-PA
14	B	702	ATP	PG-O3B-PB-O1B

There are no ring outliers.

3 monomers are involved in 66 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	B	703	SF4	18	0
15	B	704	SF4	6	0
14	B	702	ATP	42	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

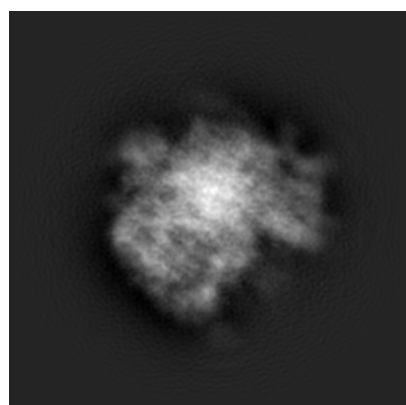
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2010. These allow visual inspection of the internal detail of the map and identification of artifacts.

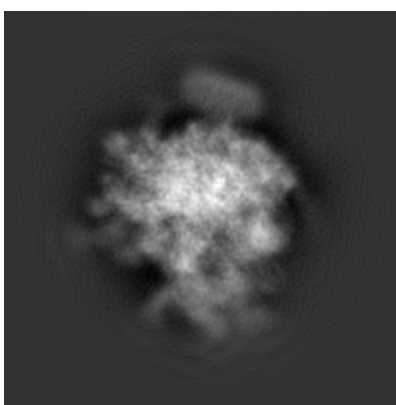
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

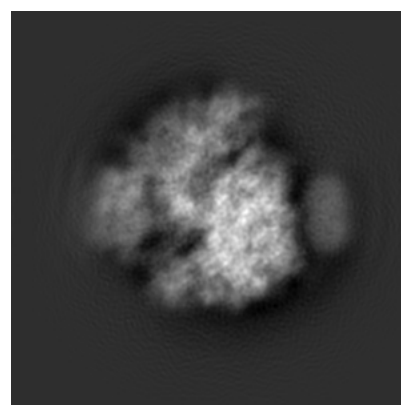
6.1.1 Primary map



X



Y

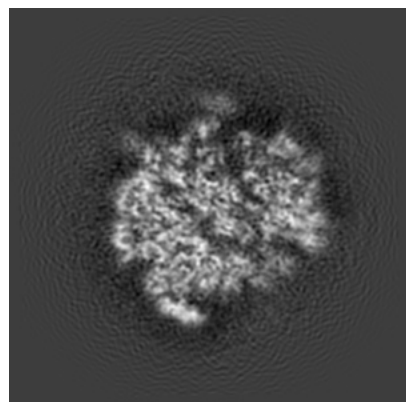


Z

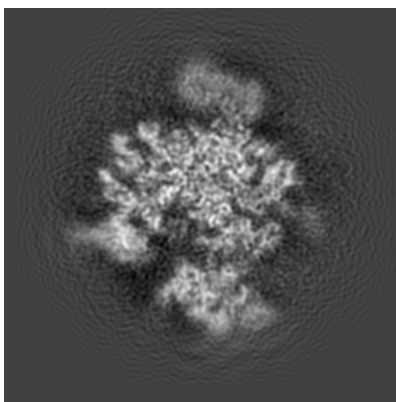
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

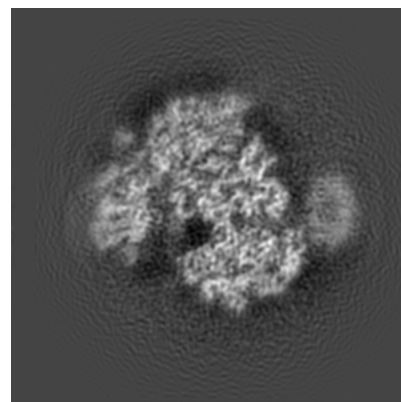
6.2.1 Primary map



X Index: 184



Y Index: 184

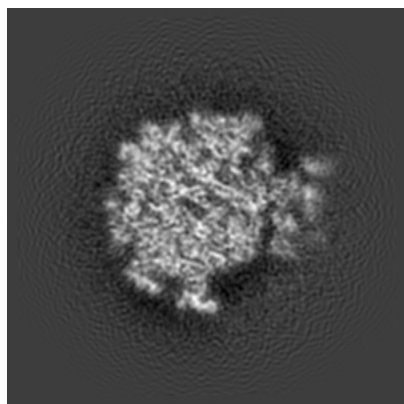


Z Index: 184

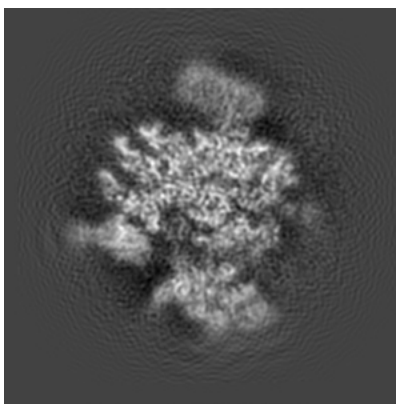
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

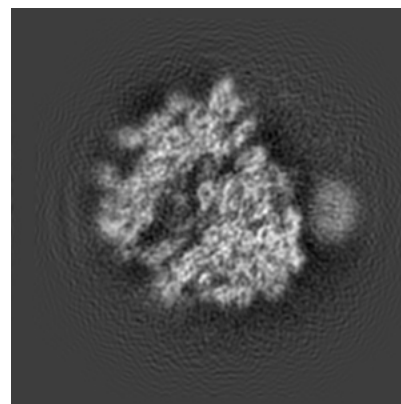
6.3.1 Primary map



X Index: 213



Y Index: 187

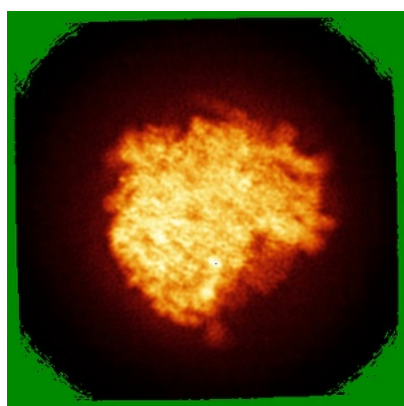


Z Index: 173

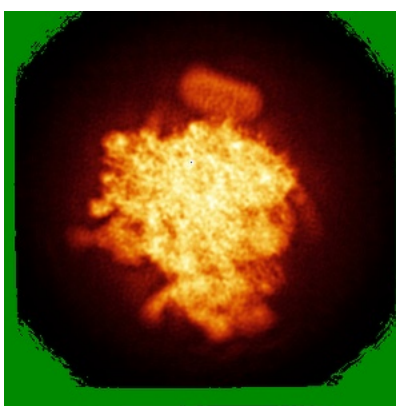
The images above show the largest variance slices of the map in three orthogonal directions.

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

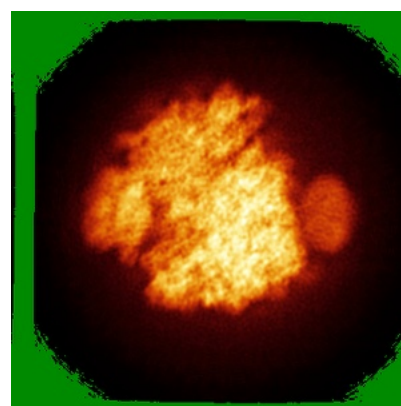
6.4.1 Primary map



X



Y

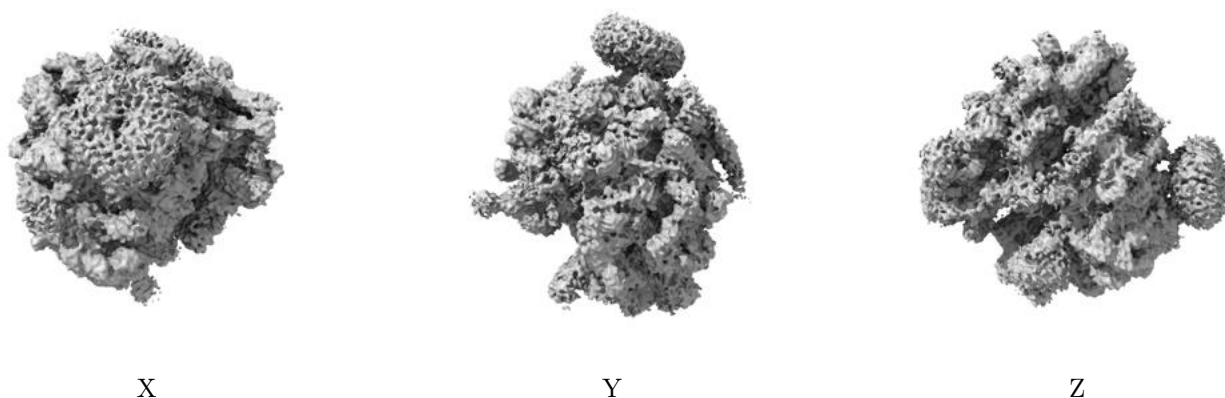


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.32. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

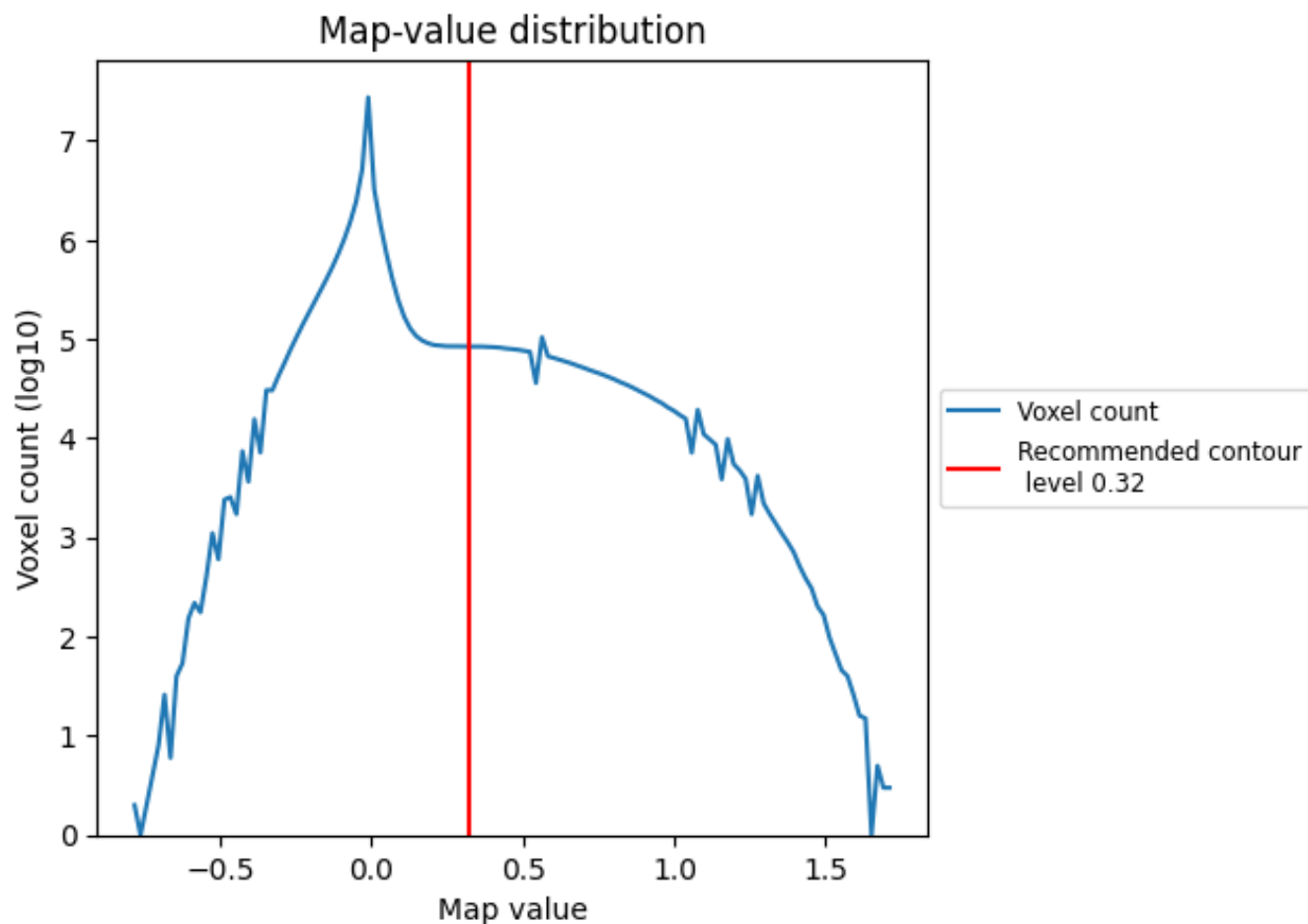
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

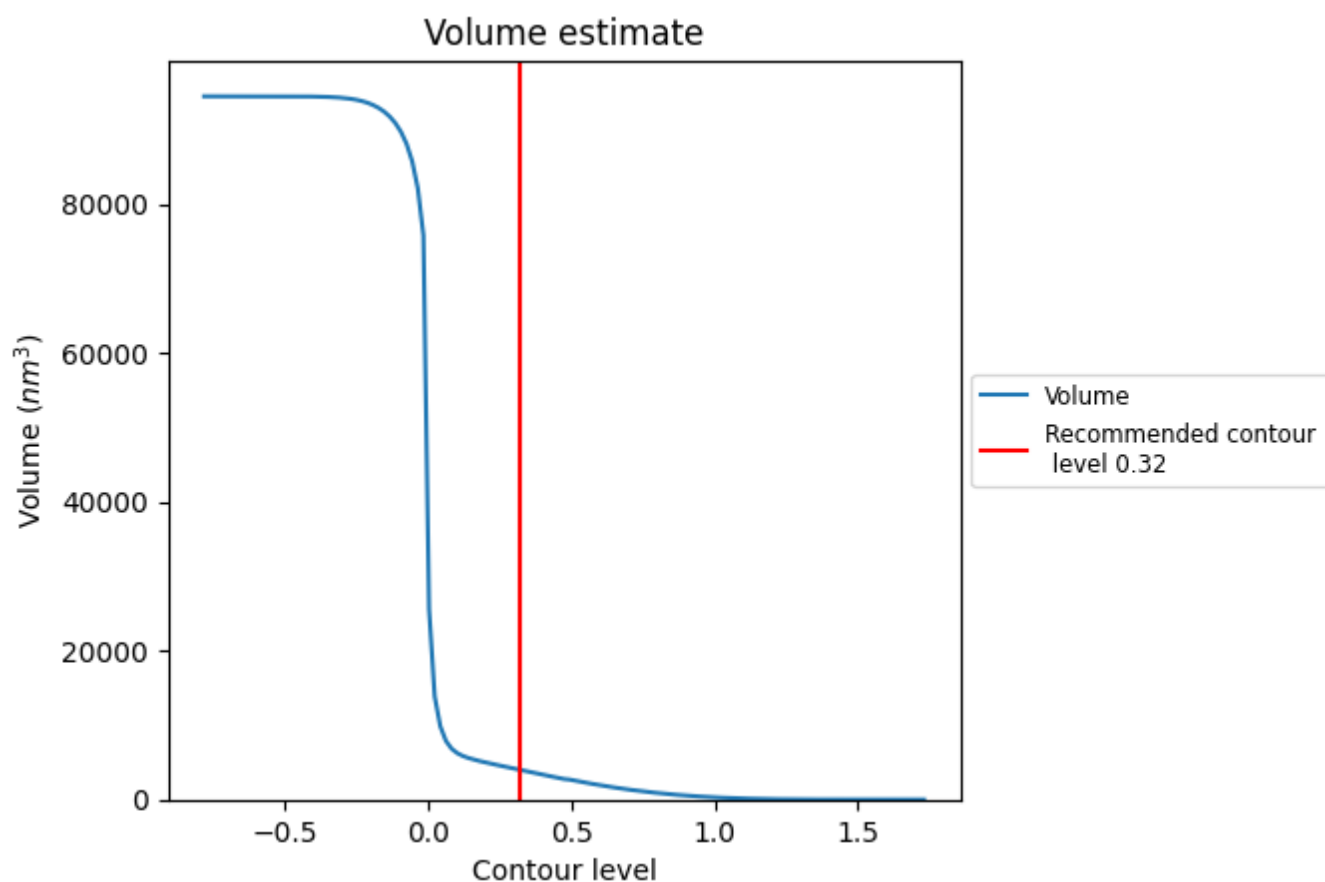
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

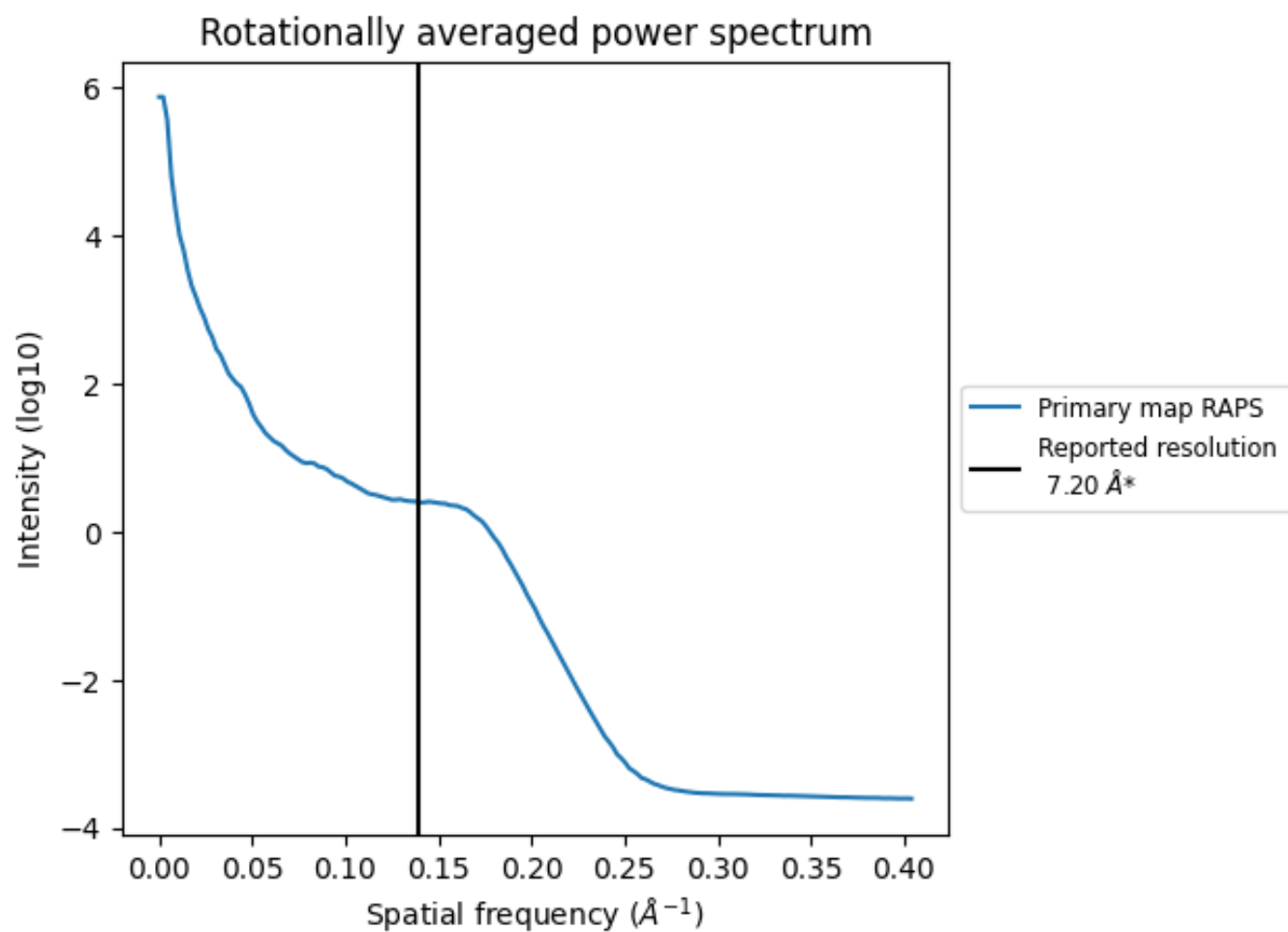
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3997 nm³; this corresponds to an approximate mass of 3610 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.139 Å⁻¹

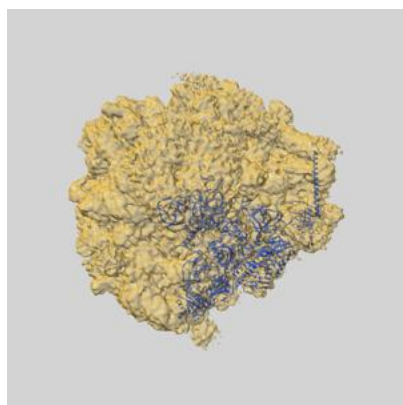
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

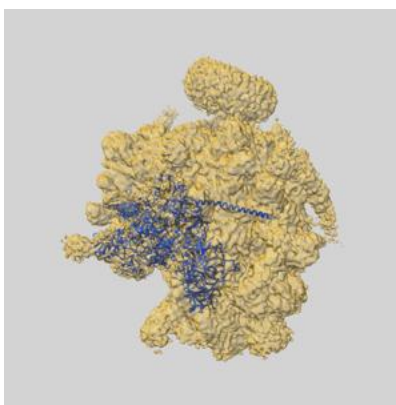
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2010 and PDB model 3J16. Per-residue inclusion information can be found in section [3](#) on page [8](#).

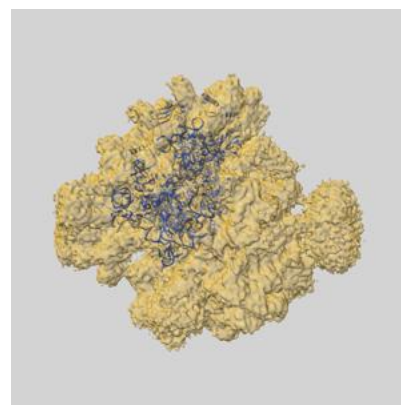
9.1 Map-model overlay [i](#)



X



Y



Z

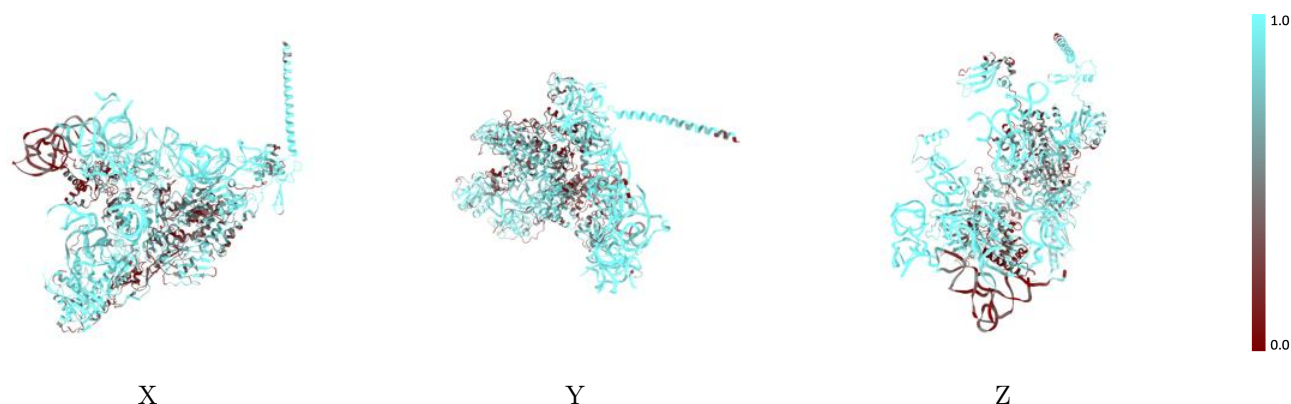
The images above show the 3D surface view of the map at the recommended contour level 0.32 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



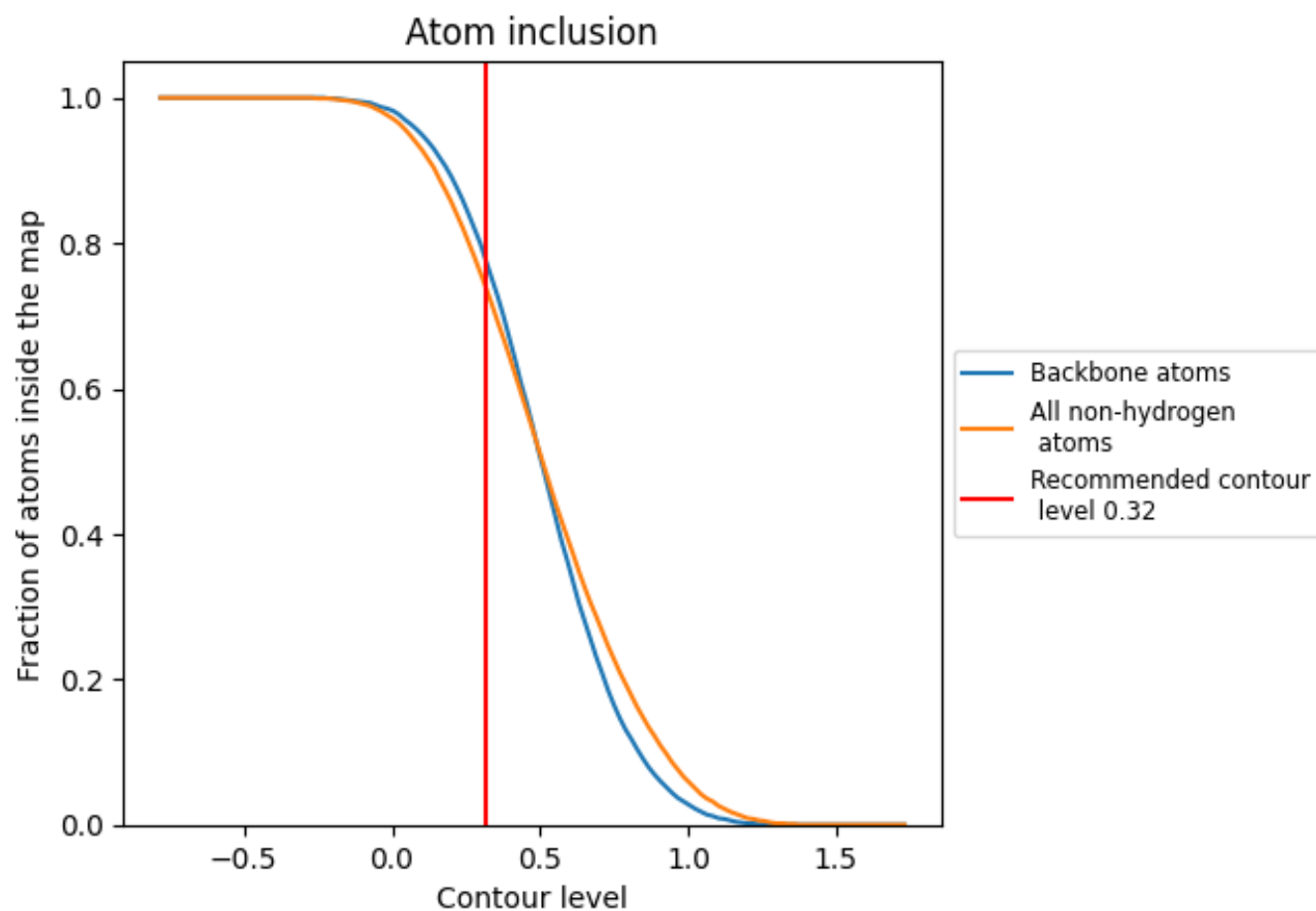
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.32).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.32) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7360	0.1180
A	0.5330	0.0930
B	0.5870	0.0900
C	0.8300	0.1020
D	0.7000	0.0830
E	0.8660	0.1320
F	0.7730	0.1020
G	0.6770	0.0570
H	0.7150	0.1050
I	0.7300	0.1050
J	0.9860	0.1790
K	0.9490	0.1680
L	0.3030	0.0930

1.0

0.0

<0.0