Full wwPDB EM Validation Report ⓘ

Jul 3, 2024 – 02:21 am BST

PDB ID	:	7OE0
EMDB ID	:	EMD-12856
Title	:	E. coli pre-30S delta rbfA ribosomal subunit class F
Authors	:	Maksimova, E.; Korepanov, A.; Baymukhametov, T.; Kravchenko, O.; Stolboushkina, E.
Deposited on	:	2021-04-30
Resolution	:	2.69 Å(reported)
Based on initial model	:	4V4Q

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:

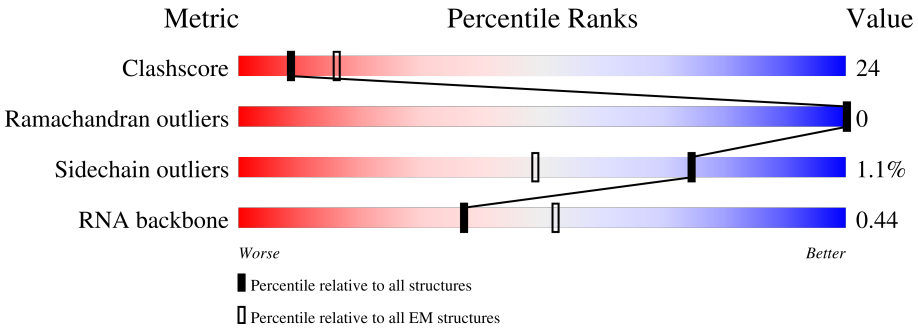
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.69 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.



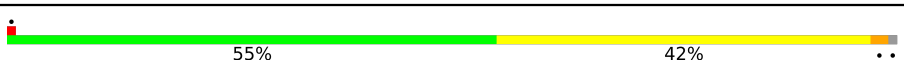
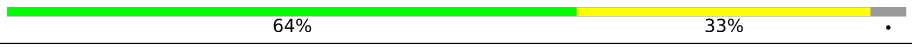
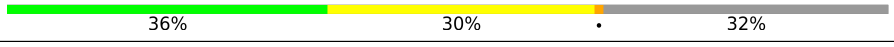
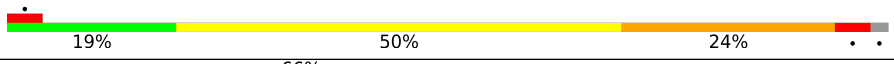
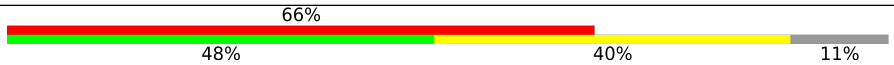
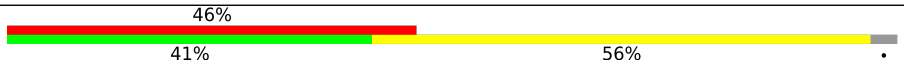
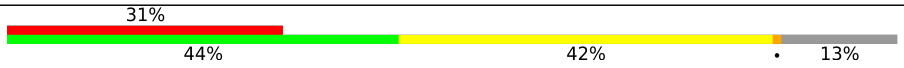
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	B	240	27%, 44%, 45%, ·, 9%
2	D	205	60%, 40%, ·
3	E	166	57%, 33%, 10%
4	F	135	5%, 33%, 41%, ·, 26%
5	H	129	59%, 40%, ·
6	K	128	41%, 31%, 41%, ·, 26%
7	L	123	·, 57%, 43%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	O	89	
9	P	82	
10	Q	83	
11	R	74	
12	T	86	
13	A	1542	
14	C	232	
15	G	178	
16	I	129	
17	J	103	
18	M	117	
19	N	100	
20	S	91	

2 Entry composition (i)

There are 21 unique types of molecules in this entry. The entry contains 50296 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 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	218	1704	1081	305	311	7	0	0

- Molecule 2 is a protein called 30S ribosomal protein S4.

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

- Molecule 3 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	150	1105	687	211	201	6	0	0

- Molecule 4 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	F	100	817	515	148	148	6	0	0

- Molecule 5 is a protein called 30S ribosomal protein S8.

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

- Molecule 6 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	K	95	702	433	137	130	2	0	0

- Molecule 7 is a protein called 30S ribosomal protein S12.

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

- Molecule 8 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 9 is a protein called 30S ribosomal protein S16.

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

- Molecule 10 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 11 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	50	Total	C	N	O	0	0
			407	259	76	72		

- Molecule 12 is a protein called 30S ribosomal protein S20.

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

- Molecule 13 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A	1510	Total	C	N	O	P	0	0
			32408	14454	5952	10493	1509		

- Molecule 14 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 15 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	83	Total	C	N	O	S	0	0
			642	406	119	114	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 18 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 19 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 20 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 21 is water.

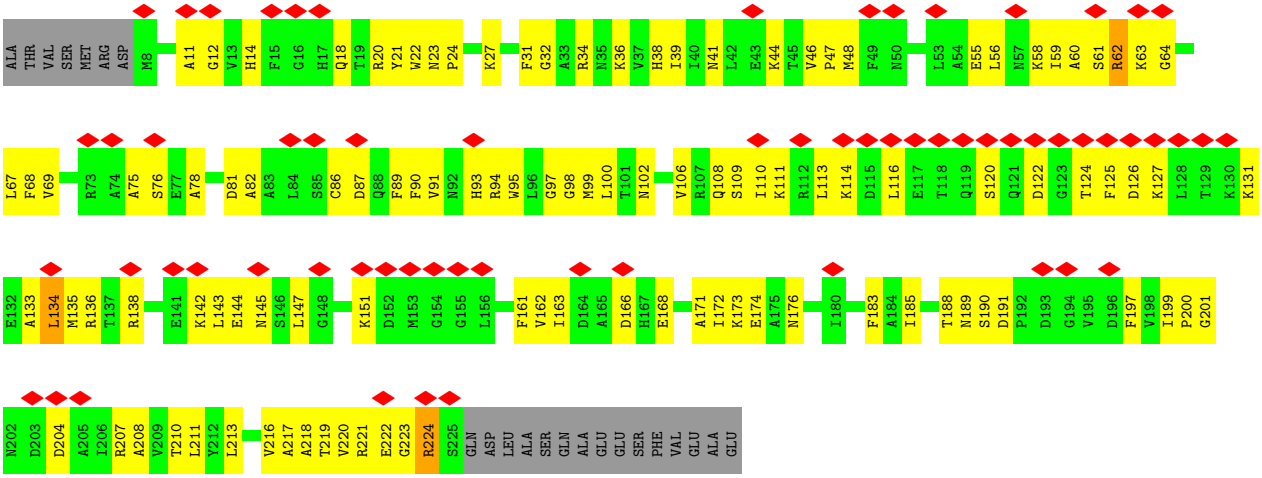
Mol	Chain	Residues	Atoms	AltConf
21	D	7	Total O 7 7	0
21	H	9	Total O 9 9	0
21	L	6	Total O 6 6	0
21	O	1	Total O 1 1	0
21	P	9	Total O 9 9	0
21	Q	3	Total O 3 3	0
21	R	1	Total O 1 1	0
21	T	10	Total O 10 10	0
21	A	484	Total O 484 484	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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: 30S ribosomal protein S2

Chain B:

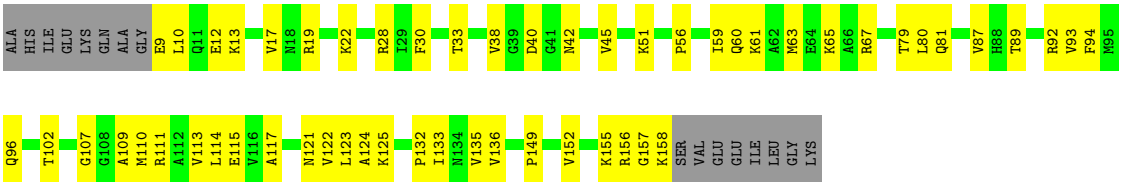


• Molecule 2: 30S ribosomal protein S4

Chain D:

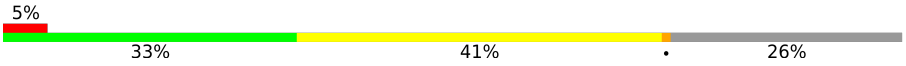
• Molecule 3: 30S ribosomal protein S5

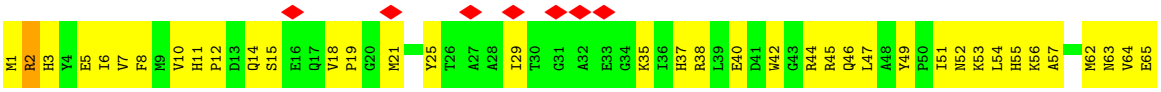
Chain E:



• Molecule 4: 30S ribosomal protein S6, fully modified isoform

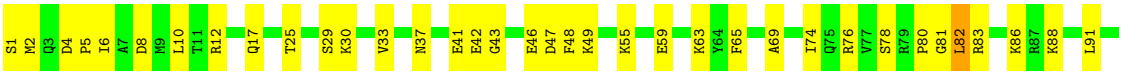
Chain F:





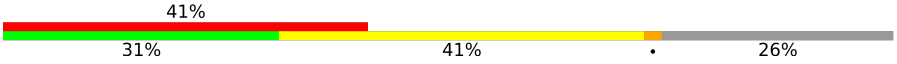
• Molecule 5: 30S ribosomal protein S8

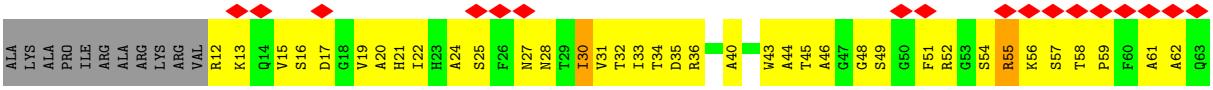
Chain H:

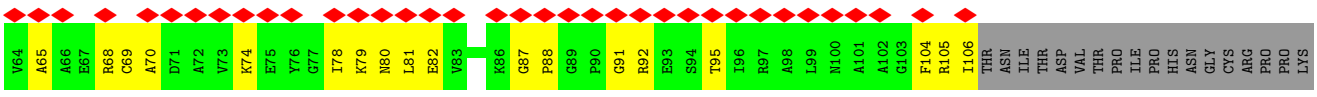


• Molecule 6: 30S ribosomal protein S11

Chain K:

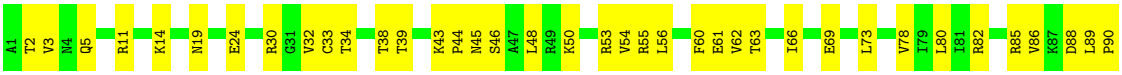






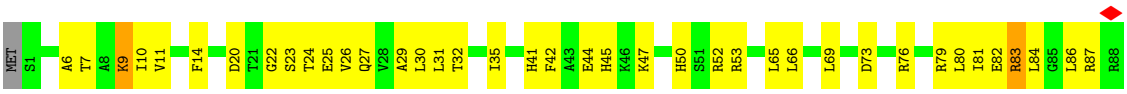
• Molecule 7: 30S ribosomal protein S12

Chain L:



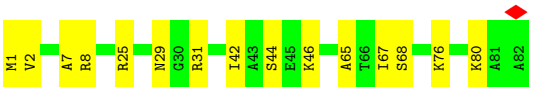
• Molecule 8: 30S ribosomal protein S15

Chain O:



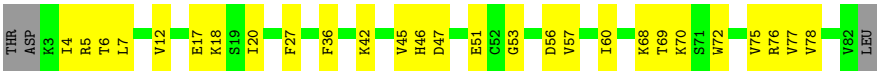
• Molecule 9: 30S ribosomal protein S16

Chain P:



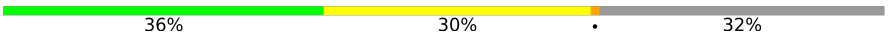
• Molecule 10: 30S ribosomal protein S17

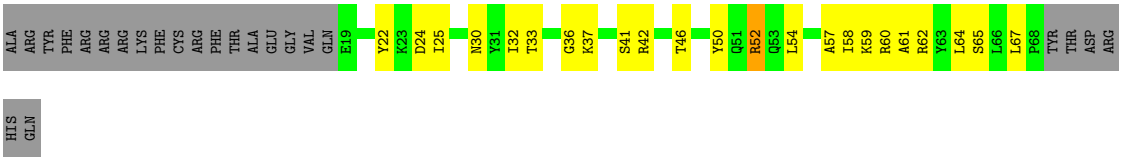
Chain Q:



• Molecule 11: 30S ribosomal protein S18

Chain R:



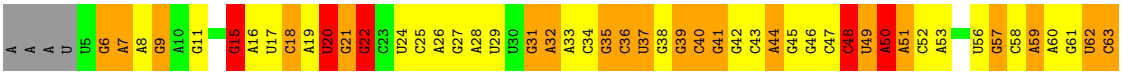


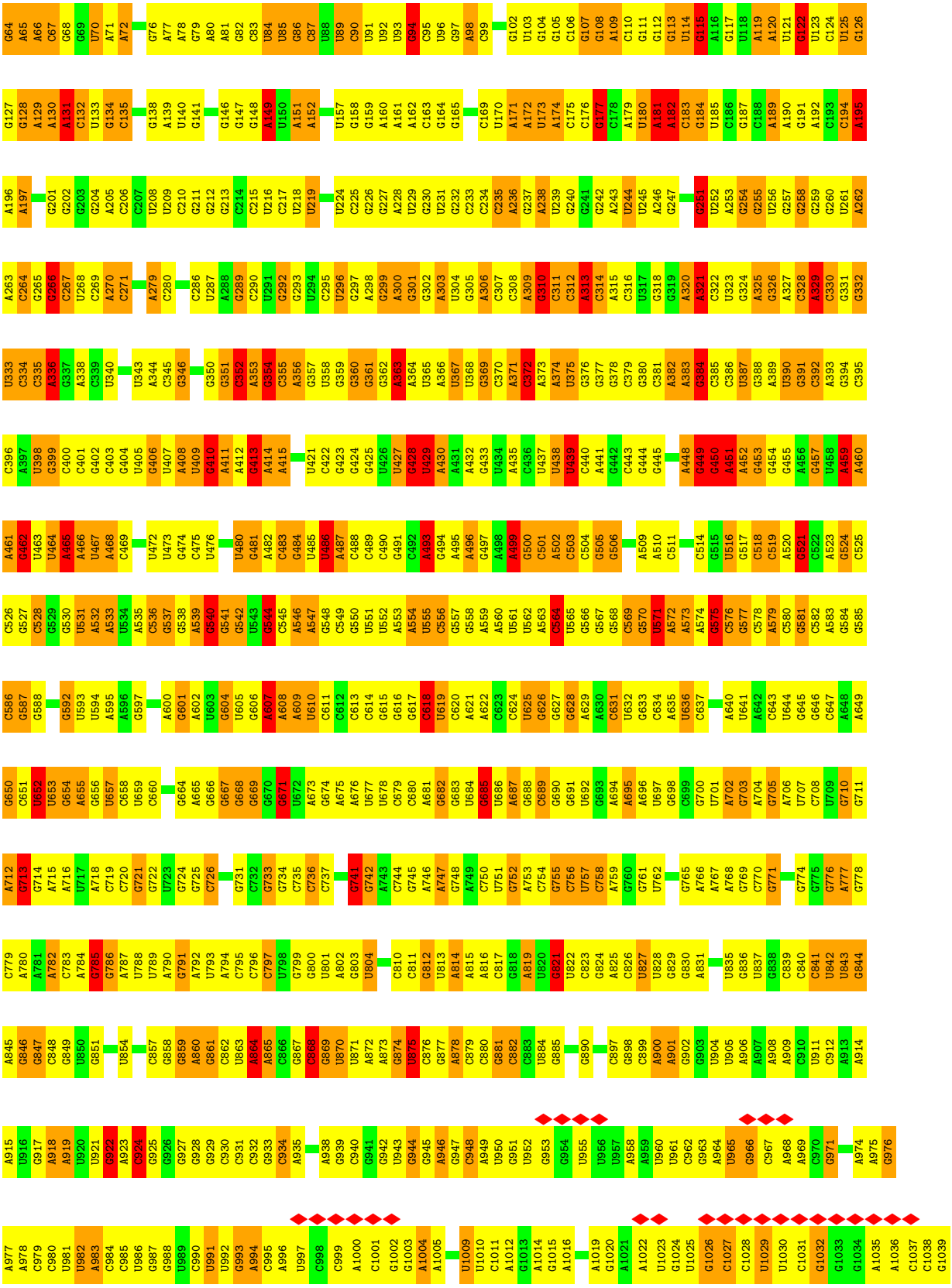
• Molecule 12: 30S ribosomal protein S20

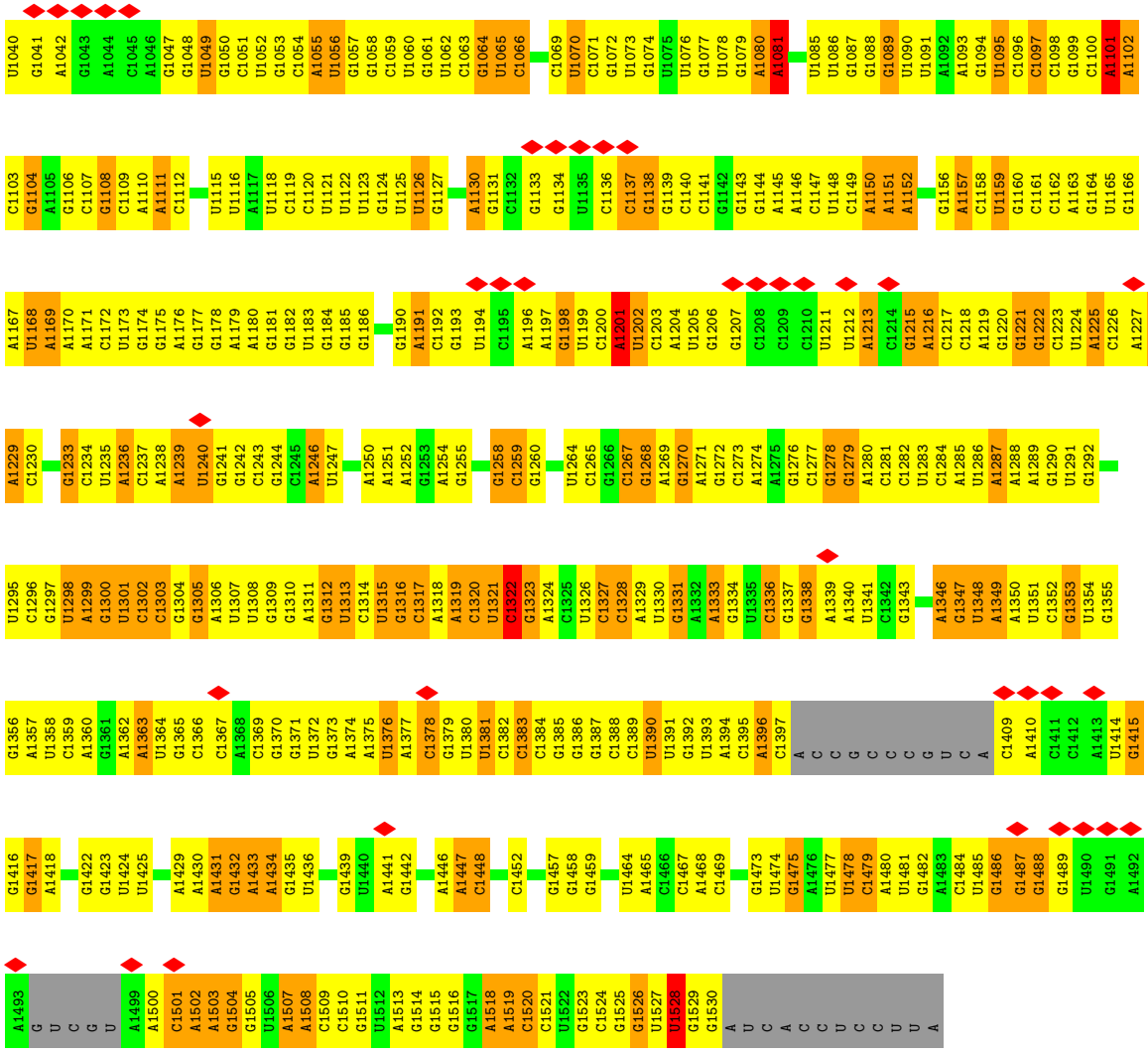
Chain T:

• Molecule 13: 16S rRNA

Chain A:

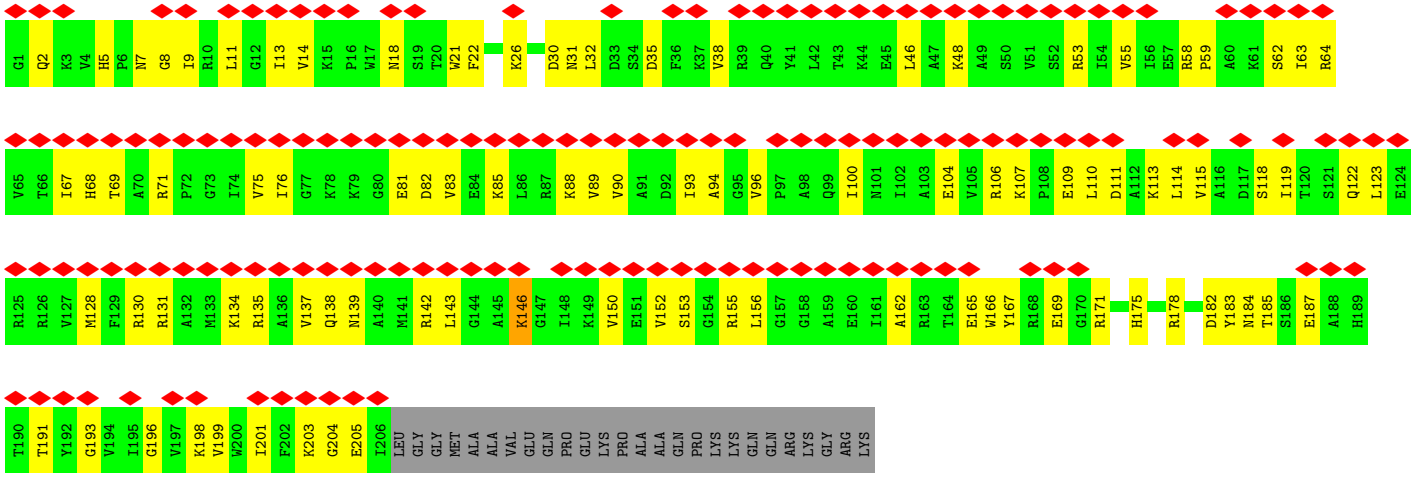






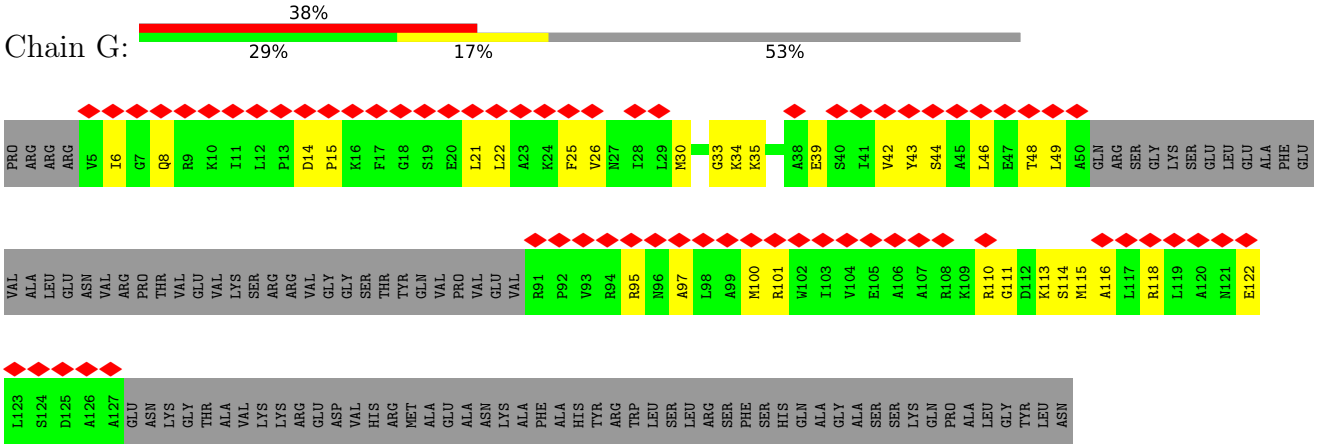
• Molecule 14: 30S ribosomal protein S3

Chain C:



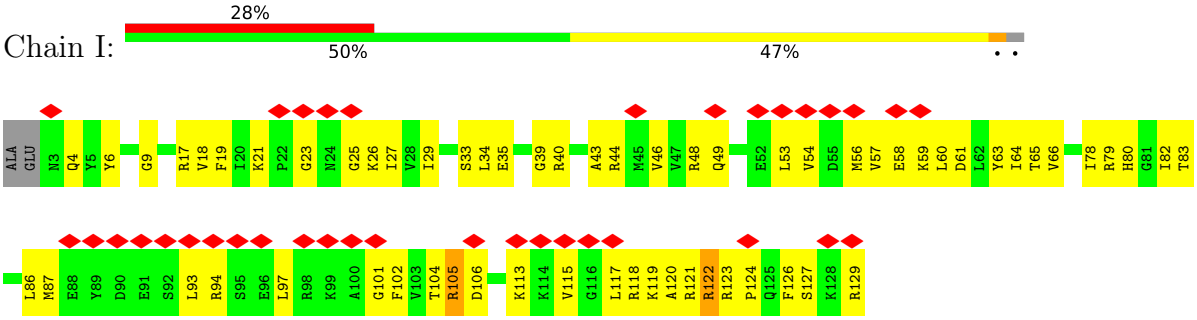
• Molecule 15: 30S ribosomal protein S7

Chain G:



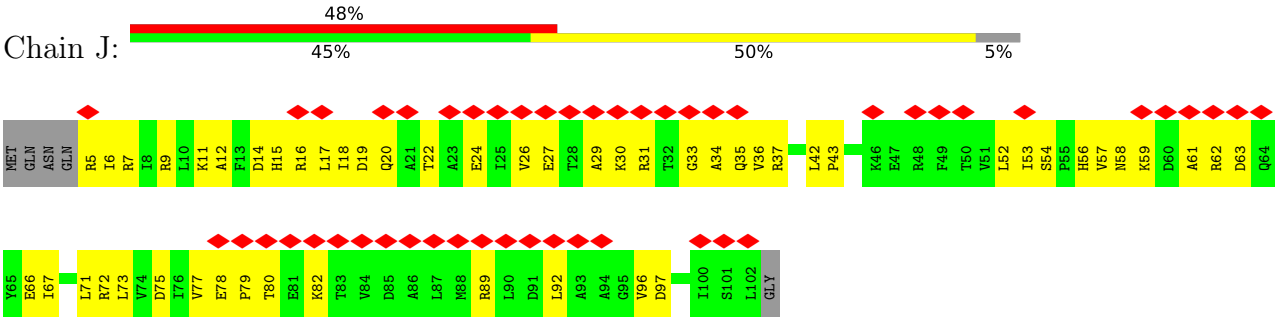
• Molecule 16: 30S ribosomal protein S9

Chain I:



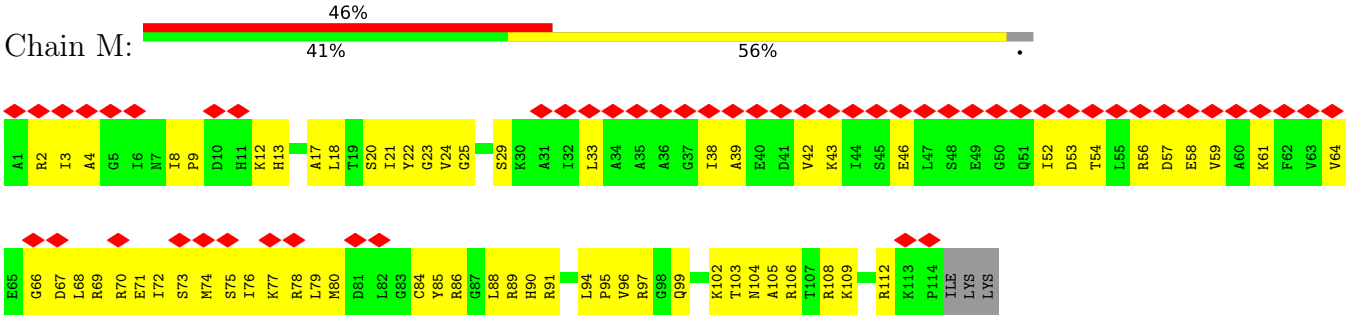
• Molecule 17: 30S ribosomal protein S10

Chain J:



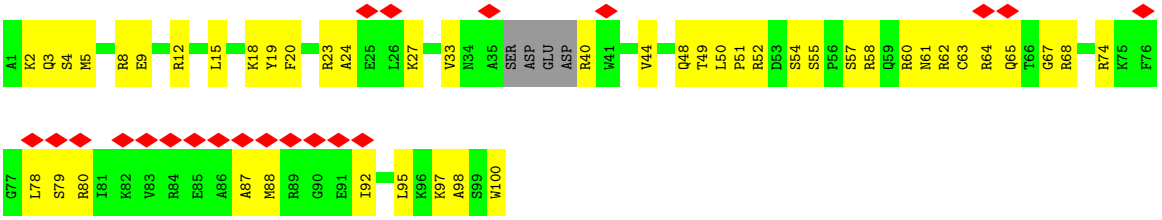
• Molecule 18: 30S ribosomal protein S13

Chain M:

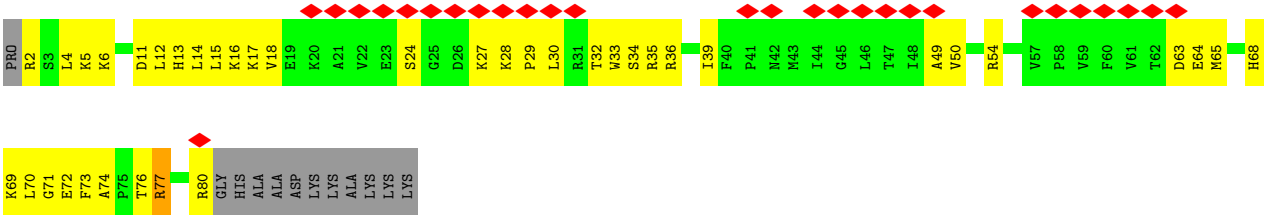


• Molecule 19: 30S ribosomal protein S14

Chain N:



• Molecule 20: 30S ribosomal protein S19



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	138247	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	6.844	Depositor
Minimum map value	-2.889	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.29	Depositor
Map size (Å)	378.4, 378.4, 378.4	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality

5.1 Standard geometry

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	B	0.32	0/1735	0.55	1/2338 (0.0%)
2	D	0.72	0/1665	0.73	0/2227
3	E	0.69	0/1118	0.71	0/1504
4	F	0.30	0/835	0.50	0/1128
5	H	0.82	1/989 (0.1%)	0.75	2/1326 (0.2%)
6	K	0.31	0/713	0.52	1/960 (0.1%)
7	L	0.80	0/969	0.81	0/1300
8	O	0.54	0/724	0.71	0/966
9	P	0.98	0/659	0.76	0/884
10	Q	0.83	0/657	0.73	0/881
11	R	0.37	0/412	0.59	0/553
12	T	0.75	0/671	0.75	0/888
13	A	1.73	833/36289 (2.3%)	1.22	230/56610 (0.4%)
14	C	0.25	0/1651	0.48	0/2225
15	G	0.23	0/648	0.51	0/868
16	I	0.29	0/1034	0.54	0/1375
17	J	0.26	0/796	0.54	0/1077
18	M	0.24	0/892	0.50	0/1193
19	N	0.24	0/785	0.46	0/1043
20	S	0.28	0/652	0.57	0/877
All	All	1.45	834/53894 (1.5%)	1.08	234/80223 (0.3%)

All (834) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	452	A	N9-C4	-13.21	1.29	1.37
13	A	354	G	C6-N1	-9.41	1.32	1.39
13	A	390	U	C2-N3	-9.24	1.31	1.37
13	A	113	G	C6-N1	-9.09	1.33	1.39
13	A	618	C	N3-C4	-8.53	1.27	1.33
13	A	387	U	C2-N3	-8.43	1.31	1.37
13	A	392	C	C2-N3	-8.28	1.29	1.35
13	A	482	A	N7-C5	-8.23	1.34	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	383	A	N7-C5	-8.21	1.34	1.39
13	A	570	G	C8-N7	-8.20	1.26	1.30
13	A	107	G	N9-C8	-8.14	1.32	1.37
13	A	61	G	C8-N7	-8.12	1.26	1.30
13	A	195	A	N9-C4	-8.05	1.33	1.37
13	A	39	G	C6-N1	-7.93	1.33	1.39
13	A	568	G	C6-N1	-7.93	1.34	1.39
13	A	107	G	C8-N7	-7.90	1.26	1.30
13	A	610	U	C2-N3	-7.88	1.32	1.37
13	A	105	G	C5-C4	-7.85	1.32	1.38
13	A	329	A	N7-C5	-7.83	1.34	1.39
13	A	377	G	C2-N3	-7.82	1.26	1.32
13	A	405	U	C2-N3	-7.72	1.32	1.37
13	A	353	A	N9-C4	-7.66	1.33	1.37
13	A	557	G	C5-C4	-7.64	1.32	1.38
13	A	388	G	C8-N7	-7.63	1.26	1.30
13	A	548	G	C6-N1	-7.62	1.34	1.39
13	A	323	U	C2-N3	-7.57	1.32	1.37
13	A	391	G	C6-N1	-7.56	1.34	1.39
13	A	310	G	C5-C4	-7.50	1.33	1.38
13	A	354	G	C5-C6	-7.50	1.34	1.42
13	A	396	C	N3-C4	-7.47	1.28	1.33
13	A	376	G	C8-N7	-7.46	1.26	1.30
13	A	289	G	C8-N7	-7.46	1.26	1.30
13	A	109	A	N7-C5	-7.45	1.34	1.39
13	A	387	U	N3-C4	-7.42	1.31	1.38
13	A	384	G	C6-N1	-7.40	1.34	1.39
13	A	42	G	C6-N1	-7.36	1.34	1.39
13	A	353	A	N3-C4	-7.34	1.30	1.34
13	A	61	G	N7-C5	-7.33	1.34	1.39
13	A	401	C	N3-C4	-7.33	1.28	1.33
13	A	120	A	N9-C4	-7.32	1.33	1.37
13	A	376	G	N7-C5	-7.30	1.34	1.39
13	A	449	G	C6-N1	-7.27	1.34	1.39
13	A	35	G	C6-N1	-7.25	1.34	1.39
13	A	35	G	N7-C5	-7.25	1.34	1.39
13	A	292	G	N1-C2	-7.24	1.31	1.37
13	A	581	G	C5-C4	-7.23	1.33	1.38
13	A	41	G	C8-N7	-7.21	1.26	1.30
13	A	516	U	C2-N3	-7.19	1.32	1.37
13	A	880	C	N3-C4	-7.18	1.28	1.33
13	A	482	A	C8-N7	-7.17	1.26	1.31

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	757	U	C2-N3	-7.16	1.32	1.37
13	A	21	G	C5-C4	-7.15	1.33	1.38
13	A	327	A	N7-C5	-7.14	1.34	1.39
13	A	304	U	C2-N3	-7.13	1.32	1.37
13	A	131	A	N3-C4	-7.13	1.30	1.34
13	A	388	G	C5-C4	-7.12	1.33	1.38
13	A	622	A	C5-C4	-7.10	1.33	1.38
13	A	308	C	N3-C4	-7.08	1.28	1.33
13	A	875	U	C2-N3	-7.06	1.32	1.37
13	A	127	G	C6-N1	-7.05	1.34	1.39
13	A	865	A	C5-C4	-7.03	1.33	1.38
13	A	482	A	N9-C4	-7.03	1.33	1.37
13	A	546	A	N9-C4	-7.01	1.33	1.37
13	A	584	G	C6-N1	-7.01	1.34	1.39
13	A	355	C	N3-C4	-7.00	1.29	1.33
13	A	332	G	C2-N3	-7.00	1.27	1.32
13	A	876	C	N3-C4	-6.99	1.29	1.33
13	A	62	U	C2-N3	-6.98	1.32	1.37
13	A	41	G	C5-C4	-6.98	1.33	1.38
13	A	111	G	C5-C4	-6.98	1.33	1.38
13	A	540	G	C6-N1	-6.98	1.34	1.39
13	A	326	G	C5-C4	-6.98	1.33	1.38
13	A	753	A	N9-C4	-6.98	1.33	1.37
13	A	313	A	C2-N3	-6.97	1.27	1.33
13	A	63	C	N3-C4	-6.96	1.29	1.33
13	A	57	G	C8-N7	-6.96	1.26	1.30
13	A	402	G	C2-N3	-6.93	1.27	1.32
13	A	41	G	C6-N1	-6.93	1.34	1.39
13	A	313	A	C5-C4	-6.93	1.33	1.38
13	A	484	G	C6-N1	-6.93	1.34	1.39
13	A	484	G	C8-N7	-6.93	1.26	1.30
13	A	601	G	C5-C4	-6.93	1.33	1.38
13	A	917	G	C8-N7	-6.92	1.26	1.30
13	A	107	G	C5-C4	-6.90	1.33	1.38
13	A	366	A	N3-C4	-6.90	1.30	1.34
13	A	336	A	N9-C4	-6.87	1.33	1.37
13	A	113	G	N1-C2	-6.87	1.32	1.37
13	A	321	A	C5-C4	-6.86	1.33	1.38
13	A	391	G	N7-C5	-6.86	1.35	1.39
13	A	117	G	C8-N7	-6.84	1.26	1.30
13	A	859	G	C5-C4	-6.84	1.33	1.38
13	A	361	G	C5-C4	-6.84	1.33	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	287	U	C2-N3	-6.83	1.32	1.37
13	A	378	G	C6-N1	-6.82	1.34	1.39
13	A	112	G	C8-N7	-6.81	1.26	1.30
13	A	109	A	C8-N7	-6.80	1.26	1.31
13	A	873	A	N7-C5	-6.79	1.35	1.39
13	A	134	G	C8-N7	-6.79	1.26	1.30
13	A	404	G	C5-C4	-6.78	1.33	1.38
13	A	606	G	C5-C4	-6.77	1.33	1.38
13	A	450	G	C6-N1	-6.77	1.34	1.39
13	A	544	G	C5-C4	-6.77	1.33	1.38
13	A	309	A	C6-N1	-6.76	1.30	1.35
13	A	42	G	C5-C4	-6.76	1.33	1.38
13	A	386	C	N3-C4	-6.76	1.29	1.33
13	A	489	C	N3-C4	-6.76	1.29	1.33
13	A	19	A	C5-C4	-6.74	1.34	1.38
13	A	174	A	C6-N1	-6.73	1.30	1.35
13	A	357	G	C2-N3	-6.73	1.27	1.32
13	A	551	U	C2-N3	-6.73	1.33	1.37
13	A	329	A	N9-C8	-6.72	1.32	1.37
13	A	324	G	C5-C4	-6.72	1.33	1.38
13	A	552	U	C2-N3	-6.72	1.33	1.37
13	A	27	G	C2-N3	-6.72	1.27	1.32
13	A	394	G	C5-C4	-6.71	1.33	1.38
13	A	191	G	C6-N1	-6.69	1.34	1.39
13	A	881	G	C5-C4	-6.69	1.33	1.38
13	A	481	G	C6-N1	-6.69	1.34	1.39
13	A	112	G	C6-N1	-6.69	1.34	1.39
13	A	452	A	C6-N6	-6.68	1.28	1.33
13	A	133	U	C2-N3	-6.68	1.33	1.37
13	A	292	G	C6-N1	-6.68	1.34	1.39
13	A	597	G	C5-C4	-6.68	1.33	1.38
13	A	378	G	C8-N7	-6.67	1.26	1.30
13	A	255	G	C5-C4	-6.67	1.33	1.38
13	A	354	G	C8-N7	-6.65	1.26	1.30
13	A	117	G	C6-N1	-6.65	1.34	1.39
13	A	449	G	C8-N7	-6.65	1.26	1.30
13	A	126	G	C6-N1	-6.64	1.34	1.39
13	A	375	U	C4-C5	-6.64	1.37	1.43
13	A	880	C	C2-N3	-6.63	1.30	1.35
13	A	326	G	C8-N7	-6.63	1.26	1.30
13	A	541	G	C6-N1	-6.63	1.34	1.39
13	A	761	G	C6-N1	-6.62	1.34	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	18	C	N3-C4	-6.62	1.29	1.33
13	A	545	C	N1-C6	-6.61	1.33	1.37
13	A	450	G	C5-C4	-6.61	1.33	1.38
13	A	45	G	C5-C4	-6.59	1.33	1.38
13	A	373	A	C6-N1	-6.59	1.30	1.35
13	A	403	C	C2-N3	-6.58	1.30	1.35
13	A	389	A	C5-C4	-6.58	1.34	1.38
13	A	607	A	N3-C4	-6.58	1.30	1.34
13	A	324	G	N9-C8	-6.57	1.33	1.37
13	A	131	A	C6-N1	-6.56	1.30	1.35
13	A	270	A	C5-C6	-6.56	1.35	1.41
13	A	332	G	N9-C4	-6.56	1.32	1.38
13	A	395	C	C2-N3	-6.56	1.30	1.35
13	A	609	A	N9-C4	-6.56	1.33	1.37
13	A	378	G	C5-C4	-6.55	1.33	1.38
13	A	393	A	N9-C4	-6.55	1.33	1.37
13	A	22	G	C8-N7	-6.54	1.27	1.30
13	A	616	G	C6-N1	-6.53	1.34	1.39
13	A	292	G	C8-N7	-6.52	1.27	1.30
13	A	369	G	C6-N1	-6.51	1.34	1.39
13	A	394	G	C8-N7	-6.51	1.27	1.30
13	A	452	A	C6-N1	-6.51	1.30	1.35
13	A	753	A	N7-C5	-6.50	1.35	1.39
13	A	22	G	C5-C4	-6.50	1.33	1.38
13	A	308	C	C2-N3	-6.50	1.30	1.35
13	A	486	U	C2-N3	-6.50	1.33	1.37
13	A	44	A	C6-N1	-6.50	1.31	1.35
13	A	542	G	C5-C4	-6.49	1.33	1.38
13	A	631	C	N3-C4	-6.49	1.29	1.33
13	A	652	U	C2-N3	-6.49	1.33	1.37
13	A	135	C	N3-C4	-6.48	1.29	1.33
13	A	313	A	N3-C4	-6.48	1.30	1.34
13	A	105	G	C8-N7	-6.48	1.27	1.30
13	A	103	U	C2-N3	-6.48	1.33	1.37
13	A	327	A	C6-N6	-6.47	1.28	1.33
13	A	58	C	N3-C4	-6.47	1.29	1.33
13	A	44	A	C5-C4	-6.46	1.34	1.38
13	A	821	G	C8-N7	-6.46	1.27	1.30
13	A	332	G	C8-N7	-6.44	1.27	1.30
13	A	881	G	C6-N1	-6.44	1.35	1.39
13	A	823	C	N3-C4	-6.44	1.29	1.33
13	A	57	G	C6-N1	-6.44	1.35	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	567	G	C6-N1	-6.42	1.35	1.39
13	A	320	A	C5-C4	-6.41	1.34	1.38
13	A	332	G	C5-C4	-6.41	1.33	1.38
13	A	261	U	C2-N3	-6.40	1.33	1.37
13	A	401	C	C2-N3	-6.39	1.30	1.35
13	A	104	G	C6-N1	-6.39	1.35	1.39
13	A	824	G	C5-C4	-6.38	1.33	1.38
13	A	313	A	C8-N7	-6.38	1.27	1.31
13	A	823	C	C2-N3	-6.38	1.30	1.35
13	A	873	A	C8-N7	-6.38	1.27	1.31
13	A	877	G	C5-C4	-6.38	1.33	1.38
13	A	881	G	C8-N7	-6.38	1.27	1.30
13	A	374	A	C5-C4	-6.38	1.34	1.38
13	A	877	G	N1-C2	-6.36	1.32	1.37
13	A	451	A	N9-C4	-6.36	1.34	1.37
13	A	610	U	N3-C4	-6.36	1.32	1.38
13	A	378	G	N1-C2	-6.36	1.32	1.37
13	A	108	G	C5-C6	-6.36	1.35	1.42
13	A	111	G	N9-C8	-6.35	1.33	1.37
13	A	313	A	N9-C4	-6.35	1.34	1.37
13	A	363	A	C5-C4	-6.34	1.34	1.38
13	A	821	G	C6-N1	-6.33	1.35	1.39
13	A	128	G	C6-N1	-6.33	1.35	1.39
13	A	621	A	C5-C4	-6.33	1.34	1.38
13	A	569	C	N3-C4	-6.32	1.29	1.33
13	A	302	G	C6-N1	-6.32	1.35	1.39
13	A	377	G	C5-C4	-6.31	1.33	1.38
13	A	372	C	C2-O2	-6.31	1.18	1.24
13	A	384	G	C5-C4	-6.30	1.33	1.38
13	A	299	G	C8-N7	-6.29	1.27	1.30
13	A	110	C	C2-O2	-6.29	1.18	1.24
13	A	105	G	C6-N1	-6.28	1.35	1.39
13	A	402	G	C5-C4	-6.28	1.33	1.38
13	A	366	A	N9-C4	-6.28	1.34	1.37
13	A	370	C	N3-C4	-6.28	1.29	1.33
13	A	626	G	C8-N7	-6.27	1.27	1.30
13	A	873	A	C6-N1	-6.26	1.31	1.35
13	A	865	A	C8-N7	-6.26	1.27	1.31
13	A	327	A	C6-N1	-6.24	1.31	1.35
13	A	636	U	C2-N3	-6.24	1.33	1.37
13	A	369	G	N1-C2	-6.24	1.32	1.37
13	A	402	G	N1-C2	-6.23	1.32	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	391	G	C8-N7	-6.23	1.27	1.30
13	A	357	G	N9-C8	-6.23	1.33	1.37
13	A	231	U	C2-N3	-6.23	1.33	1.37
13	A	481	G	C8-N7	-6.23	1.27	1.30
13	A	374	A	N7-C5	-6.23	1.35	1.39
13	A	61	G	C6-N1	-6.22	1.35	1.39
13	A	174	A	N3-C4	-6.22	1.31	1.34
13	A	230	G	C5-C4	-6.21	1.34	1.38
13	A	321	A	N3-C4	-6.21	1.31	1.34
13	A	609	A	C5-C4	-6.21	1.34	1.38
13	A	113	G	C2-N3	-6.21	1.27	1.32
13	A	387	U	C4-O4	-6.20	1.18	1.23
13	A	572	A	N7-C5	-6.20	1.35	1.39
13	A	354	G	C5-C4	-6.20	1.34	1.38
13	A	59	A	C8-N7	-6.19	1.27	1.31
13	A	42	G	N3-C4	-6.19	1.31	1.35
13	A	502	A	C5-C4	-6.19	1.34	1.38
13	A	372	C	N3-C4	-6.18	1.29	1.33
13	A	452	A	N3-C4	-6.18	1.31	1.34
13	A	28	A	C5-C4	-6.18	1.34	1.38
13	A	41	G	N1-C2	-6.18	1.32	1.37
13	A	33	A	C5-C6	-6.17	1.35	1.41
13	A	363	A	N3-C4	-6.17	1.31	1.34
13	A	393	A	C5-C4	-6.17	1.34	1.38
13	A	182	A	N9-C4	-6.16	1.34	1.37
13	A	361	G	C8-N7	-6.16	1.27	1.30
13	A	19	A	C8-N7	-6.16	1.27	1.31
13	A	311	C	N3-C4	-6.15	1.29	1.33
13	A	43	C	N1-C6	-6.15	1.33	1.37
13	A	378	G	C2-N3	-6.15	1.27	1.32
13	A	480	U	N1-C2	-6.15	1.33	1.38
13	A	286	C	N3-C4	-6.14	1.29	1.33
13	A	755	G	C6-N1	-6.14	1.35	1.39
13	A	326	G	N7-C5	-6.13	1.35	1.39
13	A	617	G	C8-N7	-6.13	1.27	1.30
13	A	859	G	C2-N3	-6.13	1.27	1.32
13	A	51	A	N7-C5	-6.13	1.35	1.39
13	A	499	A	N7-C5	-6.13	1.35	1.39
13	A	46	G	C6-N1	-6.12	1.35	1.39
13	A	452	A	N7-C5	-6.12	1.35	1.39
13	A	568	G	C5-C4	-6.12	1.34	1.38
13	A	119	A	C5-C4	-6.12	1.34	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	377	G	C6-N1	-6.11	1.35	1.39
13	A	233	C	C2-N3	-6.10	1.30	1.35
13	A	1080	A	C5-C4	-6.09	1.34	1.38
13	A	392	C	N3-C4	-6.09	1.29	1.33
13	A	399	G	C6-N1	-6.09	1.35	1.39
13	A	647	C	N3-C4	-6.09	1.29	1.33
13	A	548	G	C2-N3	-6.09	1.27	1.32
13	A	327	A	C5-C4	-6.08	1.34	1.38
13	A	604	G	C2-N3	-6.08	1.27	1.32
13	A	366	A	N7-C5	-6.08	1.35	1.39
13	A	232	G	C5-C4	-6.07	1.34	1.38
13	A	622	A	C6-N1	-6.06	1.31	1.35
13	A	482	A	C5-C4	-6.06	1.34	1.38
13	A	502	A	C8-N7	-6.06	1.27	1.31
13	A	391	G	C5-C4	-6.06	1.34	1.38
13	A	113	G	C8-N7	-6.05	1.27	1.30
13	A	301	G	C6-N1	-6.05	1.35	1.39
13	A	240	G	N9-C4	-6.05	1.33	1.38
13	A	329	A	C8-N7	-6.04	1.27	1.31
13	A	391	G	N9-C8	-6.04	1.33	1.37
13	A	104	G	C5-C4	-6.04	1.34	1.38
13	A	874	G	C2-N3	-6.04	1.27	1.32
13	A	356	A	N3-C4	-6.03	1.31	1.34
13	A	550	G	C6-N1	-6.03	1.35	1.39
13	A	106	C	C2-N3	-6.03	1.30	1.35
13	A	255	G	C6-N1	-6.03	1.35	1.39
13	A	322	C	N1-C6	-6.03	1.33	1.37
13	A	112	G	C5-C4	-6.02	1.34	1.38
13	A	127	G	C5-C4	-6.02	1.34	1.38
13	A	316	C	N3-C4	-6.01	1.29	1.33
13	A	151	A	N9-C4	-6.00	1.34	1.37
13	A	500	G	C6-N1	-6.00	1.35	1.39
13	A	46	G	C8-N7	-5.99	1.27	1.30
13	A	126	G	C5-C4	-5.99	1.34	1.38
13	A	394	G	C6-N1	-5.99	1.35	1.39
13	A	573	A	N9-C4	-5.99	1.34	1.37
13	A	600	A	C5-C4	-5.99	1.34	1.38
13	A	377	G	C8-N7	-5.99	1.27	1.30
13	A	865	A	N7-C5	-5.98	1.35	1.39
13	A	109	A	N9-C8	-5.98	1.32	1.37
13	A	290	C	N3-C4	-5.98	1.29	1.33
13	A	429	U	N1-C2	-5.98	1.33	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	289	G	C5-C4	-5.97	1.34	1.38
13	A	384	G	C8-N7	-5.97	1.27	1.30
13	A	399	G	C8-N7	-5.96	1.27	1.30
13	A	379	C	C2-N3	-5.95	1.30	1.35
13	A	567	G	C8-N7	-5.95	1.27	1.30
13	A	379	C	N3-C4	-5.95	1.29	1.33
13	A	542	G	C8-N7	-5.95	1.27	1.30
13	A	395	C	N3-C4	-5.95	1.29	1.33
13	A	579	A	C6-N1	-5.95	1.31	1.35
13	A	500	G	C2-N3	-5.95	1.27	1.32
13	A	115	G	C6-N1	-5.94	1.35	1.39
13	A	878	A	C5-C4	-5.94	1.34	1.38
13	A	540	G	C5-C4	-5.94	1.34	1.38
13	A	501	C	N3-C4	-5.93	1.29	1.33
13	A	394	G	N1-C2	-5.93	1.33	1.37
13	A	647	C	C2-N3	-5.92	1.31	1.35
13	A	57	G	C5-C4	-5.92	1.34	1.38
13	A	109	A	C5-C4	-5.92	1.34	1.38
13	A	616	G	C2-N3	-5.92	1.28	1.32
13	A	251	G	C5-C4	5.91	1.42	1.38
13	A	388	G	C6-N1	-5.91	1.35	1.39
13	A	388	G	N9-C4	-5.91	1.33	1.38
13	A	360	G	C5-C4	-5.91	1.34	1.38
13	A	553	A	C5-C4	-5.91	1.34	1.38
13	A	310	G	C6-N1	-5.90	1.35	1.39
13	A	755	G	C8-N7	-5.90	1.27	1.30
13	A	862	C	C2-N3	-5.90	1.31	1.35
13	A	483	C	N1-C2	-5.89	1.34	1.40
13	A	240	G	C6-N1	-5.89	1.35	1.39
13	A	404	G	C8-N7	-5.89	1.27	1.30
13	A	42	G	C2-N3	-5.88	1.28	1.32
13	A	127	G	N1-C2	-5.88	1.33	1.37
13	A	359	G	N9-C4	-5.88	1.33	1.38
13	A	296	U	C2-N3	-5.88	1.33	1.37
13	A	918	A	C6-N1	-5.87	1.31	1.35
13	A	548	G	N3-C4	-5.86	1.31	1.35
13	A	32	A	C8-N7	-5.86	1.27	1.31
13	A	867	G	C6-N1	-5.86	1.35	1.39
13	A	1080	A	N7-C5	-5.86	1.35	1.39
13	A	113	G	C5-C4	-5.85	1.34	1.38
13	A	482	A	C5-C6	-5.85	1.35	1.41
13	A	122	G	C6-N1	-5.85	1.35	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	548	G	C5-C4	-5.85	1.34	1.38
13	A	32	A	C6-N1	-5.84	1.31	1.35
13	A	545	C	N3-C4	-5.83	1.29	1.33
13	A	885	G	C5-C4	-5.83	1.34	1.38
13	A	115	G	C8-N7	-5.83	1.27	1.30
13	A	600	A	N9-C4	-5.83	1.34	1.37
13	A	240	G	N3-C4	-5.83	1.31	1.35
13	A	607	A	C6-N1	-5.83	1.31	1.35
13	A	645	G	C5-C4	-5.83	1.34	1.38
13	A	255	G	C2-N3	-5.82	1.28	1.32
13	A	20	U	C2-N3	-5.81	1.33	1.37
13	A	570	G	N7-C5	-5.81	1.35	1.39
13	A	115	G	C5-C4	-5.81	1.34	1.38
13	A	545	C	C4-C5	-5.81	1.38	1.43
13	A	28	A	C6-N1	-5.80	1.31	1.35
13	A	351	G	C5-C4	-5.80	1.34	1.38
13	A	279	A	N9-C4	-5.80	1.34	1.37
13	A	541	G	C8-N7	-5.80	1.27	1.30
13	A	171	A	N7-C5	-5.79	1.35	1.39
13	A	570	G	N9-C8	-5.79	1.33	1.37
13	A	655	A	C6-N1	-5.79	1.31	1.35
13	A	541	G	C5-C4	-5.79	1.34	1.38
13	A	117	G	C2-N3	-5.78	1.28	1.32
13	A	22	G	C6-N1	-5.78	1.35	1.39
13	A	608	A	N7-C5	-5.78	1.35	1.39
13	A	404	G	N3-C4	-5.78	1.31	1.35
13	A	40	C	N3-C4	-5.78	1.29	1.33
13	A	46	G	C5-C4	-5.78	1.34	1.38
13	A	481	G	N1-C2	-5.78	1.33	1.37
13	A	483	C	N1-C6	-5.78	1.33	1.37
13	A	762	U	C2-N3	-5.78	1.33	1.37
13	A	761	G	C8-N7	-5.78	1.27	1.30
13	A	325	A	C6-N1	-5.77	1.31	1.35
13	A	61	G	N9-C8	-5.76	1.33	1.37
13	A	141	G	C2-N3	-5.75	1.28	1.32
13	A	266	G	C5-C4	5.75	1.42	1.38
13	A	585	G	C8-N7	-5.75	1.27	1.30
13	A	102	G	C6-N1	-5.75	1.35	1.39
13	A	394	G	C2-N3	-5.75	1.28	1.32
13	A	548	G	C8-N7	-5.74	1.27	1.30
13	A	550	G	C8-N7	-5.74	1.27	1.30
13	A	45	G	N1-C2	-5.74	1.33	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	567	G	C5-C4	-5.74	1.34	1.38
13	A	402	G	C6-N1	-5.72	1.35	1.39
13	A	741	G	C5-C4	-5.72	1.34	1.38
13	A	865	A	N9-C8	-5.72	1.33	1.37
13	A	184	G	N7-C5	-5.71	1.35	1.39
13	A	359	G	N7-C5	-5.71	1.35	1.39
13	A	445	G	C2-N3	-5.71	1.28	1.32
13	A	404	G	C6-N1	-5.71	1.35	1.39
13	A	597	G	N7-C5	-5.71	1.35	1.39
13	A	566	G	C5-C4	-5.70	1.34	1.38
13	A	227	G	C2-N3	-5.70	1.28	1.32
13	A	826	C	N1-C6	-5.70	1.33	1.37
13	A	238	A	C2-N3	-5.70	1.28	1.33
13	A	130	A	C5-C4	-5.70	1.34	1.38
13	A	427	U	C2-N3	-5.69	1.33	1.37
13	A	510	A	N9-C4	-5.69	1.34	1.37
13	A	195	A	C5-C4	-5.69	1.34	1.38
13	A	34	C	N1-C6	-5.68	1.33	1.37
13	A	389	A	C8-N7	-5.67	1.27	1.31
13	A	322	C	N3-C4	-5.67	1.29	1.33
13	A	825	A	C5-C4	-5.67	1.34	1.38
13	A	1079	G	N9-C4	-5.67	1.33	1.38
13	A	234	C	N3-C4	-5.67	1.29	1.33
13	A	585	G	C6-N1	-5.67	1.35	1.39
13	A	357	G	C5-C4	-5.67	1.34	1.38
13	A	352	C	N1-C2	-5.66	1.34	1.40
13	A	11	G	C5-C4	-5.66	1.34	1.38
13	A	192	A	C5-C4	-5.66	1.34	1.38
13	A	377	G	N1-C2	-5.66	1.33	1.37
13	A	504	C	N3-C4	-5.66	1.29	1.33
13	A	592	G	C6-N1	-5.66	1.35	1.39
13	A	354	G	C6-O6	-5.65	1.19	1.24
13	A	372	C	C2-N3	-5.65	1.31	1.35
13	A	864	A	N7-C5	-5.64	1.35	1.39
13	A	544	G	C6-N1	-5.64	1.35	1.39
13	A	326	G	C6-O6	-5.64	1.19	1.24
13	A	874	G	C8-N7	-5.64	1.27	1.30
13	A	403	C	C5-C6	-5.64	1.29	1.34
13	A	568	G	C8-N7	-5.63	1.27	1.30
13	A	385	C	N3-C4	-5.62	1.30	1.33
13	A	376	G	N1-C2	-5.62	1.33	1.37
13	A	27	G	C6-N1	-5.62	1.35	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	502	A	C5-C6	-5.62	1.35	1.41
13	A	393	A	C8-N7	-5.62	1.27	1.31
13	A	182	A	C5-C6	-5.61	1.36	1.41
13	A	635	A	C5-C4	-5.61	1.34	1.38
13	A	103	U	N3-C4	-5.61	1.33	1.38
13	A	44	A	C2-N3	-5.60	1.28	1.33
13	A	326	G	N9-C8	-5.60	1.33	1.37
13	A	394	G	N3-C4	-5.60	1.31	1.35
13	A	58	C	N1-C6	-5.59	1.33	1.37
13	A	41	G	C2-N3	-5.59	1.28	1.32
13	A	863	U	C2-N3	-5.59	1.33	1.37
13	A	578	C	N3-C4	-5.59	1.30	1.33
13	A	224	U	C2-N3	-5.59	1.33	1.37
13	A	389	A	N7-C5	-5.58	1.35	1.39
13	A	117	G	N1-C2	-5.58	1.33	1.37
13	A	361	G	C6-N1	-5.58	1.35	1.39
13	A	1526	G	C5-C4	-5.58	1.34	1.38
13	A	624	C	C2-N3	-5.58	1.31	1.35
13	A	374	A	N9-C4	-5.57	1.34	1.37
13	A	872	A	N3-C4	-5.57	1.31	1.34
13	A	821	G	C5-C4	-5.57	1.34	1.38
13	A	194	C	N3-C4	-5.57	1.30	1.33
13	A	312	C	C4-C5	-5.56	1.38	1.43
13	A	563	A	C8-N7	-5.56	1.27	1.31
13	A	611	C	N3-C4	-5.56	1.30	1.33
13	A	53	A	C5-C6	-5.56	1.36	1.41
13	A	575	G	N7-C5	-5.56	1.35	1.39
13	A	393	A	C2-N3	-5.56	1.28	1.33
13	A	230	G	C6-N1	-5.55	1.35	1.39
13	A	428	G	N9-C4	-5.55	1.33	1.38
13	A	620	C	N3-C4	-5.55	1.30	1.33
13	A	45	G	C8-N7	-5.55	1.27	1.30
13	A	554	A	N3-C4	-5.55	1.31	1.34
13	A	575	G	C8-N7	-5.54	1.27	1.30
13	A	585	G	C5-C4	-5.54	1.34	1.38
13	A	621	A	C8-N7	-5.54	1.27	1.31
13	A	297	G	C8-N7	-5.54	1.27	1.30
13	A	65	A	N9-C4	-5.54	1.34	1.37
13	A	254	G	N3-C4	-5.53	1.31	1.35
13	A	572	A	C5-C4	-5.53	1.34	1.38
13	A	646	G	C8-N7	-5.53	1.27	1.30
13	A	107	G	C2-N3	-5.53	1.28	1.32

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	554	A	C5-C4	-5.53	1.34	1.38
13	A	66	A	N7-C5	-5.53	1.35	1.39
13	A	327	A	N9-C4	-5.53	1.34	1.37
13	A	391	G	C5-C6	-5.53	1.36	1.42
13	A	881	G	N9-C8	-5.52	1.33	1.37
13	A	354	G	N3-C4	-5.52	1.31	1.35
13	A	21	G	C8-N7	-5.52	1.27	1.30
13	A	229	U	N3-C4	-5.52	1.33	1.38
13	A	640	A	N3-C4	-5.51	1.31	1.34
13	A	293	G	C8-N7	-5.51	1.27	1.30
13	A	558	G	C5-C4	-5.51	1.34	1.38
13	A	141	G	C5-C4	-5.51	1.34	1.38
13	A	378	G	N3-C4	-5.51	1.31	1.35
13	A	392	C	C4-C5	-5.51	1.38	1.43
13	A	487	A	C8-N7	-5.51	1.27	1.31
13	A	297	G	C5-C4	-5.50	1.34	1.38
13	A	356	A	C5-C4	-5.50	1.34	1.38
13	A	376	G	N9-C8	-5.50	1.34	1.37
13	A	37	U	C2-N3	-5.50	1.33	1.37
13	A	259	G	C6-N1	-5.50	1.35	1.39
13	A	389	A	C6-N6	-5.50	1.29	1.33
13	A	24	U	C2-N3	-5.49	1.33	1.37
13	A	391	G	C6-O6	-5.49	1.19	1.24
13	A	585	G	N3-C4	-5.49	1.31	1.35
13	A	628	G	C2-N3	-5.49	1.28	1.32
13	A	822	U	C2-N3	-5.48	1.33	1.37
13	A	48	C	N1-C2	-5.48	1.34	1.40
13	A	128	G	C5-C4	-5.48	1.34	1.38
13	A	149	A	N9-C4	-5.48	1.34	1.37
13	A	312	C	C5-C6	-5.48	1.29	1.34
13	A	322	C	C5-C6	-5.48	1.29	1.34
13	A	106	C	N1-C6	-5.48	1.33	1.37
13	A	114	U	C2-N3	-5.47	1.33	1.37
13	A	300	A	N7-C5	-5.47	1.35	1.39
13	A	604	G	C5-C4	-5.47	1.34	1.38
13	A	38	G	C5-C4	-5.47	1.34	1.38
13	A	122	G	C5-C4	-5.47	1.34	1.38
13	A	321	A	C8-N7	-5.46	1.27	1.31
13	A	858	G	C5-C4	-5.46	1.34	1.38
13	A	627	G	C6-N1	-5.46	1.35	1.39
13	A	358	U	C2-N3	-5.46	1.33	1.37
13	A	40	C	C2-N3	-5.46	1.31	1.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	575	G	C6-N1	-5.46	1.35	1.39
13	A	149	A	C6-N1	-5.46	1.31	1.35
13	A	326	G	N1-C2	-5.46	1.33	1.37
13	A	107	G	N7-C5	-5.45	1.35	1.39
13	A	112	G	N9-C8	-5.45	1.34	1.37
13	A	625	U	C2-N3	-5.45	1.33	1.37
13	A	364	A	N9-C4	-5.44	1.34	1.37
13	A	353	A	N7-C5	-5.44	1.35	1.39
13	A	819	A	C8-N7	-5.44	1.27	1.31
13	A	865	A	C6-N1	-5.44	1.31	1.35
13	A	33	A	C6-N1	-5.44	1.31	1.35
13	A	451	A	N3-C4	-5.43	1.31	1.34
13	A	309	A	C8-N7	-5.43	1.27	1.31
13	A	135	C	C2-N3	-5.42	1.31	1.35
13	A	402	G	C8-N7	-5.42	1.27	1.30
13	A	128	G	C2-N3	-5.42	1.28	1.32
13	A	111	G	C8-N7	-5.41	1.27	1.30
13	A	481	G	C5-C4	-5.41	1.34	1.38
13	A	584	G	N1-C2	-5.41	1.33	1.37
13	A	556	C	N3-C4	-5.41	1.30	1.33
13	A	752	G	C5-C4	-5.41	1.34	1.38
13	A	382	A	C5-C4	-5.40	1.34	1.38
13	A	617	G	C5-C4	-5.40	1.34	1.38
13	A	376	G	C5-C4	-5.40	1.34	1.38
13	A	481	G	N9-C8	-5.40	1.34	1.37
13	A	549	C	N3-C4	-5.40	1.30	1.33
13	A	861	G	C8-N7	-5.40	1.27	1.30
13	A	42	G	C8-N7	-5.39	1.27	1.30
13	A	44	A	C5-C6	-5.39	1.36	1.41
13	A	360	G	N1-C2	-5.39	1.33	1.37
13	A	365	U	C2-N3	-5.39	1.33	1.37
13	A	333	U	C2-N3	-5.39	1.33	1.37
13	A	310	G	N9-C8	-5.39	1.34	1.37
13	A	600	A	C5-C6	-5.39	1.36	1.41
13	A	67	C	C2-N3	-5.38	1.31	1.35
13	A	33	A	C8-N7	-5.38	1.27	1.31
13	A	824	G	C6-N1	-5.38	1.35	1.39
13	A	50	A	N3-C4	-5.38	1.31	1.34
13	A	108	G	N3-C4	-5.37	1.31	1.35
13	A	45	G	C5-C6	-5.37	1.36	1.42
13	A	266	G	C6-O6	-5.37	1.19	1.24
13	A	606	G	N9-C8	-5.37	1.34	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	263	A	C8-N7	-5.37	1.27	1.31
13	A	404	G	C2-N3	-5.37	1.28	1.32
13	A	528	C	N3-C4	-5.37	1.30	1.33
13	A	172	A	C6-N6	-5.37	1.29	1.33
13	A	581	G	C8-N7	-5.37	1.27	1.30
13	A	634	C	N3-C4	-5.36	1.30	1.33
13	A	483	C	C4-C5	-5.36	1.38	1.43
13	A	640	A	N9-C4	-5.36	1.34	1.37
13	A	66	A	N3-C4	-5.35	1.31	1.34
13	A	182	A	N3-C4	-5.35	1.31	1.34
13	A	401	C	N1-C6	-5.35	1.33	1.37
13	A	558	G	N9-C4	-5.34	1.33	1.38
13	A	356	A	N7-C5	-5.34	1.36	1.39
13	A	358	U	N3-C4	-5.34	1.33	1.38
13	A	621	A	N7-C5	-5.34	1.36	1.39
13	A	524	G	C6-N1	-5.34	1.35	1.39
13	A	112	G	C6-O6	-5.33	1.19	1.24
13	A	650	G	C8-N7	-5.33	1.27	1.30
13	A	652	U	N3-C4	-5.33	1.33	1.38
13	A	33	A	C6-N6	-5.33	1.29	1.33
13	A	326	G	C2-N3	-5.33	1.28	1.32
13	A	765	G	N7-C5	-5.33	1.36	1.39
13	A	108	G	N7-C5	-5.33	1.36	1.39
13	A	502	A	N9-C4	-5.33	1.34	1.37
13	A	33	A	C5-C4	-5.32	1.35	1.38
13	A	41	G	N9-C8	-5.32	1.34	1.37
13	A	61	G	C2-N2	-5.32	1.29	1.34
13	A	488	C	N3-C4	-5.32	1.30	1.33
13	A	107	G	N9-C4	-5.32	1.33	1.38
13	A	568	G	C2-N3	-5.32	1.28	1.32
13	A	262	A	N9-C4	-5.32	1.34	1.37
13	A	375	U	N1-C6	-5.32	1.33	1.38
13	A	377	G	N9-C4	-5.32	1.33	1.38
13	A	539	A	C5-C4	-5.32	1.35	1.38
13	A	35	G	C8-N7	-5.31	1.27	1.30
13	A	374	A	N3-C4	-5.31	1.31	1.34
13	A	617	G	C6-N1	-5.31	1.35	1.39
13	A	540	G	N7-C5	-5.31	1.36	1.39
13	A	879	C	N3-C4	-5.31	1.30	1.33
13	A	617	G	N1-C2	-5.31	1.33	1.37
13	A	919	A	N9-C4	-5.31	1.34	1.37
13	A	376	G	C6-N1	-5.31	1.35	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	882	C	C2-N3	-5.30	1.31	1.35
13	A	27	G	N1-C2	-5.30	1.33	1.37
13	A	755	G	N1-C2	-5.30	1.33	1.37
13	A	558	G	C8-N7	-5.30	1.27	1.30
13	A	1079	G	C5-C4	-5.30	1.34	1.38
13	A	355	C	C4-C5	-5.29	1.38	1.43
13	A	383	A	C8-N7	-5.29	1.27	1.31
13	A	104	G	C8-N7	-5.29	1.27	1.30
13	A	238	A	C6-N1	-5.29	1.31	1.35
13	A	506	G	C2-N3	-5.29	1.28	1.32
13	A	59	A	C5-C4	-5.29	1.35	1.38
13	A	112	G	N1-C2	-5.29	1.33	1.37
13	A	237	G	C2-N3	-5.29	1.28	1.32
13	A	536	C	N3-C4	-5.29	1.30	1.33
13	A	918	A	N3-C4	-5.29	1.31	1.34
13	A	567	G	N1-C2	-5.28	1.33	1.37
13	A	59	A	N7-C5	-5.28	1.36	1.39
13	A	486	U	N3-C4	-5.28	1.33	1.38
13	A	487	A	N7-C5	-5.28	1.36	1.39
13	A	821	G	N1-C2	-5.28	1.33	1.37
13	A	391	G	C2-N3	-5.28	1.28	1.32
13	A	655	A	N3-C4	-5.28	1.31	1.34
13	A	356	A	N9-C4	-5.27	1.34	1.37
13	A	402	G	N9-C4	-5.27	1.33	1.38
13	A	408	A	N9-C4	-5.27	1.34	1.37
13	A	34	C	C5-C6	-5.27	1.30	1.34
13	A	197	A	C5-C4	-5.27	1.35	1.38
13	A	553	A	C6-N1	-5.27	1.31	1.35
13	A	233	C	N3-C4	-5.26	1.30	1.33
13	A	312	C	N3-C4	-5.26	1.30	1.33
13	A	654	G	C5-C4	-5.26	1.34	1.38
13	A	327	A	C8-N7	-5.26	1.27	1.31
13	A	39	G	C5-C4	-5.26	1.34	1.38
13	A	184	G	C8-N7	-5.26	1.27	1.30
13	A	574	A	C5-C4	-5.25	1.35	1.38
13	A	332	G	N3-C4	-5.25	1.31	1.35
13	A	255	G	N3-C4	-5.25	1.31	1.35
13	A	449	G	N9-C8	-5.25	1.34	1.37
13	A	117	G	C5-C4	-5.25	1.34	1.38
13	A	858	G	C8-N7	-5.25	1.27	1.30
13	A	331	G	C5-C4	-5.25	1.34	1.38
13	A	45	G	C6-N1	-5.24	1.35	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	371	A	C2-N3	-5.24	1.28	1.33
13	A	635	A	C6-N1	-5.24	1.31	1.35
5	H	102	VAL	CB-CG1	-5.23	1.41	1.52
13	A	232	G	C2-N3	-5.23	1.28	1.32
13	A	379	C	C4-C5	-5.23	1.38	1.43
13	A	60	A	C8-N7	-5.23	1.27	1.31
13	A	484	G	N1-C2	-5.23	1.33	1.37
13	A	539	A	C8-N7	-5.23	1.27	1.31
13	A	263	A	C5-C4	-5.23	1.35	1.38
13	A	66	A	C5-C6	-5.23	1.36	1.41
13	A	877	G	C6-N1	-5.23	1.35	1.39
13	A	505	G	C6-N1	-5.23	1.35	1.39
13	A	177	G	C2-N3	-5.22	1.28	1.32
13	A	555	U	N3-C4	-5.22	1.33	1.38
13	A	410	G	C8-N7	-5.22	1.27	1.30
13	A	528	C	C2-N3	-5.22	1.31	1.35
13	A	251	G	N9-C8	5.22	1.41	1.37
13	A	500	G	C5-C4	-5.22	1.34	1.38
13	A	538	G	N1-C2	-5.21	1.33	1.37
13	A	313	A	C5-C6	-5.20	1.36	1.41
13	A	542	G	C6-N1	-5.20	1.35	1.39
13	A	138	G	N9-C4	-5.20	1.33	1.38
13	A	46	G	C2-N3	-5.20	1.28	1.32
13	A	219	U	C2-N3	-5.20	1.34	1.37
13	A	246	A	N9-C4	-5.20	1.34	1.37
13	A	504	C	N1-C6	-5.20	1.34	1.37
13	A	601	G	C6-N1	-5.20	1.35	1.39
13	A	236	A	C6-N1	-5.20	1.31	1.35
13	A	310	G	C8-N7	-5.20	1.27	1.30
13	A	601	G	C5-C6	-5.20	1.37	1.42
13	A	645	G	C8-N7	-5.19	1.27	1.30
13	A	318	G	C5-C4	-5.19	1.34	1.38
13	A	650	G	C5-C4	-5.19	1.34	1.38
13	A	753	A	C5-C4	-5.19	1.35	1.38
13	A	377	G	N3-C4	-5.19	1.31	1.35
13	A	240	G	C5-C4	-5.19	1.34	1.38
13	A	41	G	N7-C5	-5.18	1.36	1.39
13	A	43	C	C2-N3	-5.18	1.31	1.35
13	A	502	A	N9-C8	-5.18	1.33	1.37
13	A	369	G	C2-N3	-5.18	1.28	1.32
13	A	537	G	C6-N1	-5.18	1.35	1.39
13	A	66	A	C8-N7	-5.18	1.27	1.31

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	361	G	N1-C2	-5.18	1.33	1.37
13	A	292	G	C5-C4	-5.18	1.34	1.38
13	A	878	A	C8-N7	-5.18	1.27	1.31
13	A	336	A	C8-N7	-5.17	1.27	1.31
13	A	657	U	C2-N3	-5.17	1.34	1.37
13	A	395	C	C5-C6	-5.17	1.30	1.34
13	A	400	C	C2-N3	-5.17	1.31	1.35
13	A	448	A	N9-C4	-5.17	1.34	1.37
13	A	229	U	C2-N3	-5.17	1.34	1.37
13	A	824	G	C8-N7	-5.17	1.27	1.30
13	A	117	G	N7-C5	-5.17	1.36	1.39
13	A	194	C	C2-N3	-5.17	1.31	1.35
13	A	105	G	C2-N3	-5.17	1.28	1.32
13	A	34	C	C2-N3	-5.16	1.31	1.35
13	A	353	A	C5-C6	-5.16	1.36	1.41
13	A	354	G	N1-C2	-5.16	1.33	1.37
13	A	363	A	N9-C4	-5.16	1.34	1.37
13	A	609	A	C8-N7	-5.16	1.27	1.31
13	A	918	A	C5-C4	-5.16	1.35	1.38
13	A	300	A	C8-N7	-5.16	1.27	1.31
13	A	369	G	C5-C4	-5.16	1.34	1.38
13	A	753	A	C8-N7	-5.16	1.27	1.31
13	A	487	A	C6-N1	-5.15	1.31	1.35
13	A	21	G	N3-C4	-5.15	1.31	1.35
13	A	125	U	N3-C4	-5.15	1.33	1.38
13	A	452	A	C5-C6	-5.15	1.36	1.41
13	A	566	G	N9-C4	-5.15	1.33	1.38
13	A	575	G	N9-C8	-5.15	1.34	1.37
13	A	588	G	N7-C5	-5.15	1.36	1.39
13	A	462	G	C8-N7	-5.15	1.27	1.30
13	A	624	C	C4-C5	-5.14	1.38	1.43
13	A	59	A	C6-N6	-5.14	1.29	1.33
13	A	548	G	N1-C2	-5.14	1.33	1.37
13	A	587	G	N1-C2	-5.14	1.33	1.37
13	A	263	A	N9-C4	-5.14	1.34	1.37
13	A	503	C	C4-C5	-5.14	1.38	1.43
13	A	575	G	C2-N3	-5.14	1.28	1.32
13	A	260	G	C5-C4	-5.13	1.34	1.38
13	A	814	A	N9-C4	-5.13	1.34	1.37
13	A	28	A	N3-C4	-5.13	1.31	1.34
13	A	336	A	C5-C6	-5.13	1.36	1.41
13	A	228	A	N9-C4	-5.13	1.34	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	327	A	N3-C4	-5.13	1.31	1.34
13	A	587	G	C5-C4	-5.13	1.34	1.38
13	A	336	A	C5-C4	-5.13	1.35	1.38
13	A	406	G	C6-N1	-5.13	1.35	1.39
13	A	122	G	N1-C2	-5.12	1.33	1.37
13	A	393	A	N7-C5	-5.12	1.36	1.39
13	A	42	G	N9-C4	-5.12	1.33	1.38
13	A	389	A	N9-C8	-5.11	1.33	1.37
13	A	521	G	C6-N1	-5.11	1.35	1.39
13	A	812	G	N3-C4	-5.11	1.31	1.35
13	A	1081	A	C6-N1	-5.11	1.31	1.35
13	A	861	G	C6-N1	-5.11	1.35	1.39
13	A	766	A	C6-N1	-5.11	1.31	1.35
13	A	15	G	C6-N1	-5.11	1.35	1.39
13	A	152	A	N9-C4	-5.11	1.34	1.37
13	A	185	U	C4-C5	-5.11	1.39	1.43
13	A	756	C	N3-C4	-5.10	1.30	1.33
13	A	510	A	C5-C4	-5.10	1.35	1.38
13	A	227	G	N3-C4	-5.10	1.31	1.35
13	A	394	G	N9-C4	-5.10	1.33	1.38
13	A	49	U	C2-N3	-5.09	1.34	1.37
13	A	184	G	C6-N1	-5.09	1.35	1.39
13	A	191	G	C5-C4	-5.09	1.34	1.38
13	A	575	G	C5-C4	-5.09	1.34	1.38
13	A	21	G	N9-C4	-5.09	1.33	1.38
13	A	885	G	C2-N3	-5.09	1.28	1.32
13	A	29	U	C2-N3	-5.08	1.34	1.37
13	A	380	G	C6-O6	-5.08	1.19	1.24
13	A	402	G	C2-N2	-5.08	1.29	1.34
13	A	622	A	N9-C4	-5.08	1.34	1.37
13	A	812	G	N9-C4	-5.08	1.33	1.38
13	A	219	U	N3-C4	-5.08	1.33	1.38
13	A	354	G	N7-C5	-5.08	1.36	1.39
13	A	428	G	N3-C4	-5.08	1.31	1.35
13	A	449	G	N7-C5	-5.08	1.36	1.39
13	A	915	A	N9-C4	-5.08	1.34	1.37
13	A	119	A	N9-C4	-5.08	1.34	1.37
13	A	501	C	N1-C6	-5.08	1.34	1.37
13	A	761	G	N1-C2	-5.08	1.33	1.37
13	A	859	G	N3-C4	-5.07	1.31	1.35
13	A	374	A	C8-N7	-5.07	1.28	1.31
13	A	879	C	C2-N3	-5.07	1.31	1.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	259	G	N1-C2	-5.07	1.33	1.37
13	A	134	G	C6-N1	-5.07	1.36	1.39
13	A	315	A	C8-N7	-5.07	1.28	1.31
13	A	500	G	N1-C2	-5.07	1.33	1.37
13	A	654	G	C5-C6	-5.07	1.37	1.42
13	A	303	A	C5-C4	-5.06	1.35	1.38
13	A	604	G	N3-C4	-5.06	1.31	1.35
13	A	455	G	C5-C4	-5.06	1.34	1.38
13	A	610	U	C2-O2	-5.06	1.17	1.22
13	A	535	A	N9-C4	-5.06	1.34	1.37
13	A	52	C	N3-C4	-5.06	1.30	1.33
13	A	351	G	C2-N3	-5.06	1.28	1.32
13	A	367	U	C2-N3	-5.06	1.34	1.37
13	A	765	G	C5-C6	-5.06	1.37	1.42
13	A	860	A	N3-C4	-5.06	1.31	1.34
13	A	66	A	C6-N1	-5.05	1.32	1.35
13	A	826	C	C2-N3	-5.05	1.31	1.35
13	A	401	C	C5-C6	-5.05	1.30	1.34
13	A	329	A	N9-C4	-5.05	1.34	1.37
13	A	393	A	N3-C4	-5.05	1.31	1.34
13	A	546	A	C5-C4	-5.05	1.35	1.38
13	A	503	C	N1-C6	-5.05	1.34	1.37
13	A	574	A	C8-N7	-5.05	1.28	1.31
13	A	132	C	C2-N3	-5.04	1.31	1.35
13	A	392	C	N1-C2	-5.04	1.35	1.40
13	A	509	A	C8-N7	-5.04	1.28	1.31
13	A	626	G	C6-N1	-5.04	1.36	1.39
13	A	582	C	N3-C4	-5.04	1.30	1.33
13	A	373	A	C8-N7	-5.04	1.28	1.31
13	A	36	C	N3-C4	-5.04	1.30	1.33
13	A	16	A	N7-C5	-5.04	1.36	1.39
13	A	510	A	N7-C5	-5.04	1.36	1.39
13	A	181	A	N9-C4	-5.03	1.34	1.37
13	A	104	G	N1-C2	-5.03	1.33	1.37
13	A	321	A	C6-N1	-5.03	1.32	1.35
13	A	152	A	C5-C4	-5.03	1.35	1.38
13	A	392	C	N1-C6	-5.03	1.34	1.37
13	A	752	G	N1-C2	-5.03	1.33	1.37
13	A	270	A	C5-C4	-5.03	1.35	1.38
13	A	292	G	C2-N3	-5.03	1.28	1.32
13	A	396	C	C4-N4	-5.03	1.29	1.33
13	A	22	G	N9-C4	-5.03	1.33	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	105	G	N1-C2	-5.03	1.33	1.37
13	A	299	G	C6-N1	-5.03	1.36	1.39
13	A	327	A	N9-C8	-5.03	1.33	1.37
13	A	106	C	C2-O2	-5.02	1.20	1.24
13	A	374	A	C6-N1	-5.02	1.32	1.35
13	A	547	A	N9-C8	-5.02	1.33	1.37
13	A	359	G	C6-N1	-5.02	1.36	1.39
13	A	131	A	C5-C4	-5.02	1.35	1.38
13	A	230	G	C2-N3	-5.02	1.28	1.32
13	A	550	G	C5-C4	-5.02	1.34	1.38
13	A	608	A	N9-C4	-5.02	1.34	1.37
13	A	34	C	C4-N4	-5.02	1.29	1.33
13	A	357	G	C2-N2	-5.01	1.29	1.34
13	A	583	A	N7-C5	-5.01	1.36	1.39
13	A	26	A	C8-N7	-5.01	1.28	1.31
13	A	51	A	C8-N7	-5.01	1.28	1.31
13	A	128	G	N1-C2	-5.01	1.33	1.37
13	A	567	G	C2-N3	-5.01	1.28	1.32
13	A	604	G	N1-C2	-5.01	1.33	1.37
13	A	654	G	C2-N3	-5.01	1.28	1.32
13	A	654	G	C8-N7	-5.00	1.27	1.30
13	A	122	G	C2-N3	-5.00	1.28	1.32
13	A	242	G	C5-C4	-5.00	1.34	1.38
13	A	864	A	C8-N7	-5.00	1.28	1.31
13	A	33	A	N1-C2	-5.00	1.29	1.34
13	A	453	G	C5-C4	-5.00	1.34	1.38
13	A	579	A	N7-C5	-5.00	1.36	1.39
13	A	597	G	C6-N1	-5.00	1.36	1.39

All (234) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	A	108	G	C4-C5-N7	16.49	117.40	110.80
13	A	452	A	C2-N3-C4	-14.94	103.13	110.60
13	A	108	G	C5-N7-C8	-14.52	97.04	104.30
13	A	108	G	C6-C5-N7	-14.29	121.83	130.40
13	A	108	G	C5-C6-O6	-11.68	121.59	128.60
13	A	108	G	N7-C8-N9	10.97	118.59	113.10
13	A	108	G	N1-C6-O6	10.51	126.20	119.90
13	A	372	C	C6-N1-C2	-10.47	116.11	120.30
13	A	452	A	N3-C4-C5	10.39	134.07	126.80
13	A	108	G	C4-N9-C1'	10.12	139.66	126.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	A	452	A	N3-C4-N9	-9.86	119.51	127.40
13	A	462	G	C6-C5-N7	-9.43	124.74	130.40
13	A	108	G	C8-N9-C1'	-9.27	114.95	127.00
13	A	610	U	N3-C2-O2	-8.94	115.95	122.20
13	A	571	U	O5'-P-OP1	-8.70	97.87	105.70
13	A	573	A	O5'-P-OP1	-8.52	98.04	105.70
13	A	462	G	C4-N9-C1'	8.51	137.56	126.50
13	A	752	G	O4'-C1'-N9	8.47	114.98	108.20
13	A	353	A	C5-N7-C8	-8.42	99.69	103.90
13	A	462	G	C8-N9-C1'	-8.09	116.49	127.00
13	A	266	G	C8-N9-C4	8.02	109.61	106.40
13	A	872	A	O4'-C1'-N9	7.99	114.59	108.20
13	A	438	U	O4'-C1'-N1	7.85	114.48	108.20
13	A	108	G	N9-C4-C5	-7.82	102.27	105.40
13	A	25	C	N3-C4-C5	7.55	124.92	121.90
13	A	314	C	N3-C4-C5	7.44	124.88	121.90
13	A	384	G	N3-C4-N9	7.43	130.46	126.00
13	A	21	G	C5-C6-O6	-7.39	124.17	128.60
13	A	353	A	N7-C8-N9	7.38	117.49	113.80
13	A	401	C	C5-C6-N1	-7.36	117.32	121.00
13	A	254	G	O5'-P-OP1	-7.22	99.20	105.70
13	A	175	C	N3-C4-C5	7.21	124.78	121.90
13	A	182	A	C2-N3-C4	-7.19	107.01	110.60
13	A	106	C	O5'-P-OP1	-7.17	99.25	105.70
13	A	103	U	N3-C2-O2	-7.14	117.20	122.20
13	A	395	C	N3-C4-C5	7.12	124.75	121.90
13	A	618	C	N3-C4-N4	-7.09	113.04	118.00
13	A	371	A	N1-C2-N3	-7.01	125.80	129.30
13	A	462	G	C4-C5-N7	6.94	113.58	110.80
13	A	671	G	N3-C4-N9	-6.89	121.86	126.00
13	A	271	C	N3-C4-C5	6.86	124.64	121.90
13	A	708	C	N3-C2-O2	-6.80	117.14	121.90
13	A	618	C	C5-C4-N4	6.79	124.95	120.20
13	A	439	U	N3-C2-O2	-6.78	117.45	122.20
13	A	353	A	O4'-C1'-N9	6.76	113.61	108.20
13	A	266	G	N9-C4-C5	-6.75	102.70	105.40
13	A	483	C	O5'-P-OP1	-6.75	99.63	105.70
13	A	667	G	C4-C5-N7	6.73	113.49	110.80
13	A	516	U	N3-C4-O4	-6.72	114.69	119.40
13	A	383	A	N7-C8-N9	6.72	117.16	113.80
13	A	823	C	N3-C4-C5	6.71	124.58	121.90
13	A	138	G	N3-C4-C5	6.70	131.95	128.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	A	21	G	N1-C6-O6	6.69	123.92	119.90
13	A	328	C	P-O3'-C3'	6.69	127.72	119.70
13	A	235	C	N3-C4-C5	6.67	124.57	121.90
13	A	462	G	N9-C4-C5	-6.67	102.73	105.40
13	A	922	G	O4'-C1'-N9	6.63	113.51	108.20
13	A	67	C	N1-C2-O2	-6.59	114.95	118.90
13	A	733	G	O4'-C1'-N9	6.58	113.47	108.20
13	A	34	C	N3-C4-C5	6.58	124.53	121.90
13	A	823	C	C5-C6-N1	-6.55	117.72	121.00
13	A	462	G	N7-C8-N9	6.55	116.37	113.10
13	A	29	U	N3-C2-O2	-6.54	117.62	122.20
13	A	396	C	N3-C4-C5	6.53	124.51	121.90
13	A	387	U	N3-C4-O4	-6.52	114.84	119.40
13	A	754	C	C6-N1-C2	-6.47	117.71	120.30
13	A	425	G	N3-C2-N2	-6.46	115.38	119.90
13	A	668	G	N1-C6-O6	6.45	123.77	119.90
5	H	82	LEU	CB-CG-CD1	-6.43	100.07	111.00
13	A	383	A	C6-C5-N7	-6.41	127.82	132.30
13	A	392	C	N3-C4-C5	6.40	124.46	121.90
13	A	40	C	N3-C4-C5	6.38	124.45	121.90
13	A	830	G	C8-N9-C4	6.36	108.94	106.40
13	A	454	G	C4-C5-N7	6.35	113.34	110.80
13	A	415	A	C8-N9-C4	-6.22	103.31	105.80
13	A	235	C	C2-N3-C4	-6.21	116.79	119.90
13	A	130	A	C8-N9-C4	6.21	108.28	105.80
13	A	371	A	C6-N1-C2	6.21	122.33	118.60
13	A	330	C	N1-C2-O2	6.20	122.62	118.90
13	A	413	G	O4'-C1'-N9	6.15	113.12	108.20
13	A	48	C	C2-N1-C1'	-6.15	112.04	118.80
13	A	383	A	C8-N9-C4	-6.15	103.34	105.80
13	A	459	A	N9-C4-C5	-6.14	103.34	105.80
13	A	586	C	O5'-P-OP1	-6.12	100.19	105.70
13	A	618	C	N3-C2-O2	-6.12	117.62	121.90
13	A	403	C	N3-C4-C5	6.11	124.34	121.90
13	A	762	U	N3-C2-O2	-6.02	117.99	122.20
13	A	251	G	C4-C5-N7	5.99	113.20	110.80
13	A	429	U	C2-N1-C1'	-5.98	110.52	117.70
13	A	353	A	C4-C5-N7	5.97	113.68	110.70
13	A	387	U	C5-C4-O4	5.97	129.48	125.90
13	A	610	U	N3-C4-O4	-5.96	115.23	119.40
13	A	786	G	C2-N3-C4	-5.92	108.94	111.90
13	A	295	C	N3-C4-C5	5.91	124.26	121.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	A	654	G	C4-C5-N7	5.90	113.16	110.80
13	A	195	A	C6-C5-N7	5.86	136.40	132.30
13	A	351	G	O5'-P-OP1	-5.85	100.43	105.70
13	A	270	A	C8-N9-C4	5.85	108.14	105.80
13	A	462	G	C5-N7-C8	-5.82	101.39	104.30
13	A	384	G	C5-C6-O6	-5.81	125.11	128.60
13	A	462	G	N3-C4-N9	5.80	129.48	126.00
13	A	610	U	C5-C6-N1	-5.80	119.80	122.70
13	A	465	A	N9-C1'-C2'	-5.79	105.63	112.00
13	A	109	A	O4'-C1'-N9	-5.79	103.57	108.20
13	A	48	C	N1-C2-O2	-5.79	115.43	118.90
13	A	542	G	N3-C2-N2	-5.78	115.85	119.90
13	A	387	U	C5-C6-N1	-5.78	119.81	122.70
13	A	880	C	C5-C6-N1	-5.78	118.11	121.00
13	A	754	C	C2-N1-C1'	5.77	125.15	118.80
13	A	880	C	N3-C4-C5	5.76	124.20	121.90
13	A	195	A	C4-C5-C6	-5.76	114.12	117.00
13	A	331	G	C8-N9-C4	5.75	108.70	106.40
13	A	396	C	OP2-P-O3'	5.75	117.85	105.20
13	A	353	A	C8-N9-C4	-5.74	103.50	105.80
13	A	516	U	C5-C6-N1	-5.73	119.83	122.70
13	A	736	C	N3-C2-O2	-5.72	117.90	121.90
13	A	45	G	C4-C5-N7	5.71	113.08	110.80
13	A	1141	C	N3-C2-O2	-5.71	117.91	121.90
13	A	430	A	O5'-P-OP2	-5.70	100.57	105.70
13	A	108	G	N3-C4-N9	5.69	129.42	126.00
13	A	827	U	C2-N3-C4	-5.69	123.59	127.00
13	A	234	C	N3-C4-C5	5.69	124.17	121.90
13	A	1396	A	C8-N9-C4	-5.67	103.53	105.80
13	A	785	G	C8-N9-C4	-5.67	104.13	106.40
13	A	713	G	N3-C4-N9	-5.67	122.60	126.00
13	A	868	C	N3-C4-C5	5.66	124.17	121.90
13	A	354	G	C5-C6-O6	-5.66	125.20	128.60
13	A	427	U	C5-C6-N1	-5.66	119.87	122.70
13	A	1078	U	N3-C4-O4	-5.65	115.44	119.40
13	A	459	A	C4-C5-N7	5.65	113.53	110.70
13	A	372	C	N1-C2-N3	5.64	123.15	119.20
13	A	1322	C	C2-N1-C1'	5.64	125.00	118.80
13	A	604	G	N3-C4-N9	-5.63	122.62	126.00
13	A	480	U	C2-N1-C1'	-5.62	110.95	117.70
13	A	94	G	N3-C2-N2	-5.62	115.96	119.90
13	A	1322	C	N1-C2-O2	5.61	122.26	118.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	A	264	C	C6-N1-C2	-5.60	118.06	120.30
13	A	255	G	N3-C4-N9	-5.59	122.65	126.00
13	A	279	A	C2-N3-C4	-5.58	107.81	110.60
13	A	797	C	N3-C2-O2	-5.58	118.00	121.90
13	A	132	C	N3-C4-C5	5.57	124.13	121.90
13	A	384	G	N9-C4-C5	-5.54	103.18	105.40
13	A	353	A	C2-N3-C4	-5.54	107.83	110.60
13	A	924	C	N1-C2-O2	5.53	122.22	118.90
13	A	379	C	N3-C4-C5	5.53	124.11	121.90
13	A	685	G	N3-C4-N9	-5.52	122.69	126.00
13	A	21	G	C4-C5-N7	5.52	113.01	110.80
13	A	671	G	N3-C4-C5	5.52	131.36	128.60
13	A	823	C	C2-N3-C4	-5.52	117.14	119.90
13	A	402	G	C4-C5-C6	-5.52	115.49	118.80
13	A	667	G	N9-C4-C5	-5.51	103.19	105.40
13	A	182	A	N1-C6-N6	5.51	121.91	118.60
13	A	332	G	N3-C4-C5	5.50	131.35	128.60
13	A	251	G	C2-N3-C4	-5.50	109.15	111.90
13	A	175	C	O5'-P-OP1	-5.50	100.75	105.70
13	A	189	A	C8-N9-C4	5.50	108.00	105.80
13	A	496	A	O4'-C1'-N9	5.49	112.59	108.20
13	A	108	G	N9-C1'-C2'	-5.48	105.97	112.00
13	A	67	C	C2-N3-C4	-5.47	117.17	119.90
13	A	610	U	N1-C2-N3	5.47	118.18	114.90
13	A	182	A	C4-C5-N7	5.45	113.43	110.70
13	A	462	G	N1-C6-O6	5.44	123.17	119.90
13	A	812	G	N3-C4-N9	-5.43	122.74	126.00
13	A	545	C	N3-C4-C5	5.42	124.07	121.90
13	A	439	U	N1-C2-O2	5.42	126.59	122.80
13	A	309	A	N1-C6-N6	-5.41	115.35	118.60
13	A	564	C	C6-N1-C2	-5.41	118.14	120.30
13	A	415	A	N7-C8-N9	5.41	116.50	113.80
13	A	428	G	N3-C2-N2	-5.40	116.12	119.90
13	A	754	C	N3-C4-C5	-5.37	119.75	121.90
13	A	233	C	N3-C4-C5	5.37	124.05	121.90
13	A	380	G	N9-C1'-C2'	-5.37	106.09	112.00
13	A	868	C	C2-N3-C4	-5.36	117.22	119.90
13	A	372	C	N3-C2-O2	-5.35	118.16	121.90
13	A	151	A	N1-C2-N3	-5.32	126.64	129.30
13	A	103	U	N1-C2-O2	5.31	126.52	122.80
13	A	194	C	C4-C5-C6	-5.31	114.75	117.40
13	A	812	G	OP1-P-O3'	5.29	116.85	105.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	A	452	A	N1-C2-N3	5.29	131.95	129.30
13	A	862	C	N3-C4-C5	5.29	124.02	121.90
13	A	320	A	N1-C2-N3	-5.28	126.66	129.30
13	A	785	G	N7-C8-N9	5.28	115.74	113.10
13	A	1528	U	P-O3'-C3'	5.28	126.03	119.70
13	A	465	A	C3'-C2'-C1'	-5.27	97.28	101.50
13	A	824	G	C5-C6-N1	5.26	114.13	111.50
13	A	361	G	C8-N9-C4	5.25	108.50	106.40
13	A	227	G	N3-C2-N2	-5.23	116.24	119.90
13	A	59	A	O5'-P-OP2	-5.22	101.00	105.70
13	A	480	U	C6-N1-C1'	5.22	128.51	121.20
13	A	254	G	OP1-P-OP2	5.21	127.42	119.60
13	A	184	G	C6-C5-N7	-5.21	127.28	130.40
13	A	383	A	N1-C6-N6	5.21	121.72	118.60
13	A	182	A	N3-C4-C5	5.20	130.44	126.80
13	A	383	A	C4-C5-C6	5.20	119.60	117.00
13	A	390	U	N3-C4-C5	5.20	117.72	114.60
13	A	328	C	OP2-P-O3'	5.18	116.59	105.20
13	A	1101	A	P-O3'-C3'	5.18	125.91	119.70
1	B	134	LEU	CA-CB-CG	5.17	127.19	115.30
13	A	624	C	N3-C4-C5	5.17	123.97	121.90
13	A	332	G	N3-C2-N2	-5.14	116.30	119.90
13	A	58	C	N3-C4-C5	5.13	123.95	121.90
13	A	326	G	O5'-P-OP2	5.13	116.86	110.70
13	A	644	U	C2-N3-C4	-5.12	123.93	127.00
13	A	705	G	N1-C2-N2	5.12	120.80	116.20
13	A	668	G	C6-C5-N7	-5.11	127.33	130.40
13	A	726	C	C5-C6-N1	5.11	123.56	121.00
13	A	873	A	N1-C6-N6	-5.11	115.53	118.60
13	A	266	G	OP2-P-O3'	5.10	116.42	105.20
13	A	539	A	N9-C4-C5	-5.09	103.76	105.80
13	A	354	G	C2-N3-C4	-5.09	109.36	111.90
13	A	135	C	N3-C4-N4	-5.09	114.44	118.00
13	A	61	G	C2-N3-C4	-5.09	109.36	111.90
13	A	176	C	N3-C4-C5	5.09	123.93	121.90
13	A	586	C	C2-N3-C4	-5.08	117.36	119.90
13	A	113	G	O5'-P-OP1	-5.07	101.13	105.70
13	A	869	G	C4-C5-N7	5.06	112.83	110.80
13	A	321	A	N9-C4-C5	-5.06	103.78	105.80
6	K	30	ILE	CG1-CB-CG2	-5.05	100.30	111.40
13	A	372	C	C5-C4-N4	5.04	123.73	120.20
13	A	182	A	O4'-C1'-N9	5.04	112.23	108.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	A	606	G	C8-N9-C4	5.04	108.42	106.40
13	A	647	C	C5-C6-N1	-5.03	118.48	121.00
13	A	493	A	C6-C5-N7	-5.03	128.78	132.30
13	A	1078	U	C5-C4-O4	5.03	128.92	125.90
13	A	195	A	N1-C6-N6	-5.02	115.59	118.60
13	A	1201	A	P-O3'-C3'	5.02	125.73	119.70
5	H	82	LEU	CA-CB-CG	5.02	126.85	115.30
13	A	650	G	C6-C5-N7	-5.02	127.39	130.40
13	A	671	G	C5-C6-O6	5.02	131.61	128.60
13	A	106	C	C2-N3-C4	-5.01	117.39	119.90
13	A	331	G	N9-C4-C5	-5.01	103.40	105.40
13	A	225	C	N1-C2-O2	-5.01	115.90	118.90
13	A	897	C	N1-C2-O2	-5.00	115.90	118.90
13	A	362	G	C8-N9-C1'	5.00	133.50	127.00

There are no chirality outliers.

There are no planarity outliers.

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	B	1704	0	1732	96	0
2	D	1643	0	1710	87	0
3	E	1105	0	1148	51	0
4	F	817	0	808	64	0
5	H	979	0	1034	54	0
6	K	702	0	702	52	0
7	L	955	0	1019	68	0
8	O	716	0	742	57	0
9	P	649	0	666	15	0
10	Q	648	0	691	22	0
11	R	407	0	438	28	0
12	T	665	0	714	18	0
13	A	32408	0	16290	1119	0
14	C	1624	0	1699	79	0
15	G	642	0	685	30	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	I	1022	0	1070	70	0
17	J	786	0	828	40	0
18	M	883	0	944	76	0
19	N	774	0	827	53	0
20	S	637	0	665	48	0
21	A	484	0	0	24	0
21	D	7	0	0	0	0
21	H	9	0	0	0	0
21	L	6	0	0	2	0
21	O	1	0	0	0	0
21	P	9	0	0	1	0
21	Q	3	0	0	0	0
21	R	1	0	0	0	0
21	T	10	0	0	1	0
All	All	50296	0	34412	1900	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 24.

All (1900) 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)
4:F:51:ILE:CD1	4:F:86:ARG:HH22	1.24	1.46
9:P:8:ARG:NH1	13:A:391:G:H4'	1.59	1.18
13:A:771:G:H4'	21:A:1894:HOH:O	1.44	1.18
4:F:51:ILE:CD1	4:F:86:ARG:NH2	2.05	1.16
4:F:51:ILE:HD13	4:F:86:ARG:HH22	1.15	1.09
13:A:687:A:H62	13:A:703:G:N2	1.48	1.09
13:A:195:A:H8	21:A:1604:HOH:O	1.39	1.05
2:D:151:GLN:NE2	13:A:437:U:H4'	1.71	1.05
7:L:38:THR:HG22	7:L:48:LEU:HB3	1.36	1.04
4:F:21:MET:SD	4:F:25:TYR:CE2	2.51	1.03
13:A:978:A:C2	13:A:1316:G:N2	2.25	1.03
7:L:113:ARG:HG2	7:L:118:VAL:O	1.59	1.03
4:F:51:ILE:HD11	4:F:86:ARG:HH12	1.17	1.03
13:A:687:A:N6	13:A:703:G:H21	1.58	1.01
7:L:38:THR:CG2	7:L:48:LEU:HB3	1.89	1.01
4:F:51:ILE:HD11	4:F:86:ARG:NH1	1.76	1.01
8:O:6:ALA:O	8:O:9:LYS:HG3	1.61	0.99
13:A:1026:G:N1	13:A:1035:A:H2	1.59	0.99
13:A:1392:G:H21	13:A:1502:A:H3'	1.26	0.99

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:P:8:ARG:HD2	21:P:105:HOH:O	1.63	0.98
4:F:90:MET:SD	11:R:60:ARG:NH1	2.37	0.98
9:P:8:ARG:HH12	13:A:391:G:H4'	1.24	0.97
13:A:978:A:H2	13:A:1316:G:N2	1.61	0.97
7:L:14:LYS:HE3	21:L:201:HOH:O	1.65	0.97
13:A:94:G:N2	13:A:97:G:N7	2.13	0.97
13:A:1115:U:H3	13:A:1185:G:H1	1.00	0.96
13:A:1026:G:N1	13:A:1035:A:C2	2.31	0.96
13:A:444:G:N2	13:A:490:C:O2	1.98	0.96
3:E:87:VAL:HG12	3:E:92:ARG:HG3	1.44	0.96
7:L:113:ARG:CG	7:L:118:VAL:O	2.14	0.95
13:A:202:G:HO2'	13:A:468:A:H8	1.08	0.95
13:A:658:C:O2	13:A:748:G:N2	1.98	0.95
2:D:151:GLN:HE22	13:A:437:U:H4'	1.22	0.95
13:A:517:G:N2	13:A:533:A:OP1	2.01	0.94
4:F:51:ILE:HD12	4:F:86:ARG:HH22	1.32	0.94
4:F:45:ARG:HG2	4:F:46:GLN:H	1.30	0.93
13:A:658:C:N3	13:A:748:G:N1	2.16	0.93
13:A:978:A:H2	13:A:1316:G:H21	0.95	0.93
1:B:135:MET:HG2	1:B:138:ARG:HH21	1.29	0.92
7:L:105:GLY:HA2	7:L:116:TYR:O	1.68	0.92
13:A:448:A:N6	13:A:486:U:O2	2.02	0.92
13:A:1088:G:H21	13:A:1167:A:H61	1.18	0.92
7:L:80:LEU:HB2	7:L:101:LEU:HD13	1.52	0.92
13:A:1357:A:H61	13:A:1365:G:H1	1.19	0.90
11:R:42:ARG:HH12	13:A:721:G:H5"	1.36	0.90
13:A:1159:U:O2	13:A:1161:C:N4	2.05	0.89
13:A:182:A:H2	13:A:194:C:H42	1.17	0.88
5:H:1:SER:N	5:H:5:PRO:HA	1.86	0.88
13:A:1304:G:N2	13:A:1333:A:H62	1.71	0.88
13:A:457:G:N1	13:A:475:C:N3	2.22	0.87
7:L:98:ARG:HA	7:L:103:CYS:SG	2.13	0.87
13:A:1304:G:H21	13:A:1333:A:H62	1.22	0.86
13:A:898:G:O2'	13:A:901:A:N6	2.08	0.86
5:H:47:ASP:OD1	5:H:48:PHE:N	2.09	0.86
13:A:1312:G:H5'	20:S:5:LYS:HE3	1.56	0.86
8:O:9:LYS:CE	8:O:10:ILE:HG13	2.06	0.86
13:A:187:G:N2	13:A:190:A:OP2	2.09	0.86
13:A:1026:G:H1	13:A:1035:A:H2	0.90	0.86
13:A:414:A:OP2	13:A:428:G:N2	2.08	0.85
13:A:687:A:H62	13:A:703:G:H21	0.88	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:79:G:N1	13:A:90:C:N3	2.24	0.85
13:A:770:C:H4'	13:A:900:A:H61	1.39	0.85
13:A:674:G:H2'	13:A:675:A:H8	1.42	0.84
7:L:78:VAL:N	7:L:102:ASP:OD2	2.10	0.84
13:A:152:A:N6	13:A:169:C:O2	2.11	0.84
13:A:443:C:N3	13:A:491:G:N1	2.25	0.84
13:A:839:C:N3	13:A:847:G:N1	2.26	0.84
13:A:79:G:N2	13:A:90:C:O2	2.10	0.83
2:D:151:GLN:HE21	13:A:437:U:C5'	1.91	0.83
4:F:51:ILE:HD11	4:F:86:ARG:NH2	1.93	0.83
13:A:473:U:N3	13:A:474:G:N7	2.27	0.83
13:A:1329:A:H5"	18:M:24:VAL:HA	1.61	0.83
2:D:151:GLN:NE2	13:A:437:U:C5'	2.42	0.83
13:A:1115:U:O2	13:A:1185:G:N2	2.12	0.82
13:A:839:C:O2	13:A:847:G:N2	2.12	0.82
13:A:1150:A:H4'	17:J:43:PRO:HG3	1.61	0.82
5:H:2:MET:HE1	13:A:756:C:H4'	1.61	0.82
7:L:90:PRO:HG3	13:A:912:C:OP1	1.80	0.82
13:A:360:G:C8	21:A:1677:HOH:O	2.33	0.82
14:C:59:PRO:HG3	14:C:64:ARG:HE	1.45	0.81
4:F:51:ILE:HD11	4:F:86:ARG:CZ	2.10	0.81
13:A:785:G:H2'	13:A:786:G:C8	2.15	0.81
6:K:46:ALA:HB2	6:K:65:ALA:HB2	1.60	0.81
13:A:1393:U:H3	13:A:1501:C:HO2'	1.29	0.81
13:A:1162:C:H2'	13:A:1163:A:H8	1.44	0.81
13:A:682:G:H2'	13:A:683:G:C8	2.16	0.81
13:A:444:G:N1	13:A:490:C:N3	2.26	0.81
13:A:157:U:O2	13:A:164:G:O6	1.99	0.80
13:A:664:G:H22	13:A:741:G:H1	1.27	0.80
2:D:58:GLN:O	2:D:62:ARG:HG2	1.81	0.80
13:A:1069:C:N3	13:A:1106:G:N1	2.28	0.80
14:C:13:ILE:HG22	14:C:14:VAL:H	1.47	0.80
11:R:37:LYS:NZ	13:A:718:A:N7	2.30	0.80
2:D:151:GLN:NE2	13:A:437:U:C4'	2.45	0.80
3:E:19:ARG:HD2	3:E:19:ARG:O	1.82	0.80
13:A:674:G:O6	13:A:716:A:N1	2.14	0.80
13:A:837:U:O2	13:A:849:G:O6	2.00	0.80
13:A:202:G:N2	13:A:465:A:N1	2.29	0.79
13:A:1396:A:H2'	13:A:1397:C:C2	2.17	0.79
13:A:94:G:N1	13:A:97:G:O6	2.16	0.79
13:A:925:G:H2'	13:A:1391:U:H3	1.44	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:114:LEU:HD13	3:E:122:VAL:HG11	1.64	0.79
19:N:65:GLN:HG2	19:N:78:LEU:HD22	1.64	0.79
13:A:1373:G:H4'	15:G:30:MET:HE1	1.65	0.79
13:A:465:A:N6	13:A:468:A:N7	2.30	0.78
13:A:1237:C:HO2'	13:A:1300:G:H1	1.31	0.78
4:F:21:MET:SD	4:F:25:TYR:CZ	2.76	0.78
13:A:1309:G:H2'	13:A:1310:G:H8	1.46	0.78
13:A:86:G:H1'	13:A:87:C:H5	1.49	0.78
13:A:673:A:H2'	13:A:674:G:C8	2.19	0.78
13:A:1425:U:O2	13:A:1475:G:N1	2.14	0.78
18:M:21:ILE:HG22	18:M:23:GLY:H	1.47	0.78
2:D:115:GLN:HG2	2:D:153:ARG:HH12	1.48	0.78
8:O:24:THR:HG23	8:O:65:LEU:HD12	1.64	0.78
13:A:76:G:H1	13:A:93:U:H3	0.81	0.77
13:A:1026:G:O6	13:A:1035:A:N1	2.17	0.77
7:L:14:LYS:CE	21:L:201:HOH:O	2.28	0.77
13:A:695:A:H61	13:A:786:G:H21	1.31	0.77
11:R:50:TYR:HE1	11:R:54:LEU:HD22	1.49	0.76
2:D:56:GLU:OE2	2:D:198:LEU:HB2	1.85	0.76
13:A:1053:G:H5"	13:A:1200:C:H41	1.50	0.76
13:A:1305:G:N2	13:A:1331:G:O2'	2.15	0.76
4:F:51:ILE:HD13	4:F:86:ARG:NH2	1.81	0.76
13:A:76:G:O6	13:A:93:U:O4	2.04	0.76
13:A:452:A:N6	13:A:480:U:O2	2.19	0.76
3:E:96:GLN:HE21	3:E:123:LEU:HD23	1.50	0.76
6:K:16:SER:HA	6:K:78:ILE:HA	1.65	0.76
13:A:1268:G:HO2'	13:A:1326:U:HO2'	1.30	0.76
14:C:182:ASP:HB3	14:C:201:ILE:HB	1.68	0.76
13:A:1086:U:N3	13:A:1100:C:O2	2.18	0.75
6:K:45:THR:HG23	6:K:49:SER:HB3	1.69	0.75
13:A:1200:C:H5"	13:A:1201:A:H3'	1.68	0.75
1:B:144:GLU:HA	1:B:147:LEU:HB3	1.69	0.75
3:E:123:LEU:HD21	13:A:6:G:H2'	1.69	0.74
11:R:50:TYR:CE1	11:R:54:LEU:HD22	2.21	0.74
13:A:801:U:H2'	13:A:802:A:H8	1.52	0.74
13:A:770:C:O2'	13:A:900:A:N6	2.21	0.74
13:A:981:U:H5'	19:N:60:ARG:HH11	1.51	0.74
13:A:1052:U:H3	13:A:1206:G:H1	1.34	0.74
13:A:1162:C:H2'	13:A:1163:A:C8	2.22	0.74
13:A:924:C:H3'	13:A:925:G:H8	1.53	0.74
5:H:112:ASP:OD2	5:H:116:ARG:NH2	2.21	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:678:U:H3	13:A:713:G:H22	1.35	0.74
13:A:1160:G:O6	13:A:1182:G:O6	2.05	0.74
7:L:39:THR:OG1	7:L:89:LEU:CD2	2.35	0.74
13:A:1218:C:H2'	13:A:1219:A:C8	2.23	0.74
17:J:52:LEU:HB3	19:N:80:ARG:HD2	1.70	0.74
13:A:1348:U:H2'	13:A:1349:A:H8	1.52	0.73
4:F:2:ARG:HH12	4:F:68:GLN:HG3	1.52	0.73
13:A:70:U:O2'	13:A:94:G:N7	2.19	0.73
13:A:1149:C:H2'	13:A:1150:A:H8	1.52	0.73
2:D:8:LEU:HD13	13:A:429:U:H3'	1.69	0.73
13:A:674:G:H1	13:A:716:A:H2	1.35	0.73
13:A:204:G:C8	13:A:465:A:H1'	2.23	0.73
2:D:195:ASN:OD1	2:D:197:HIS:ND1	2.21	0.73
7:L:82:ARG:NH2	7:L:95:HIS:CE1	2.57	0.73
13:A:1304:G:H21	13:A:1333:A:N6	1.85	0.73
13:A:1357:A:N6	13:A:1365:G:H1	1.86	0.73
13:A:427:U:OP2	13:A:428:G:O2'	2.07	0.72
17:J:30:LYS:HA	17:J:34:ALA:HB3	1.71	0.72
2:D:115:GLN:CG	2:D:153:ARG:HH12	2.02	0.72
7:L:106:VAL:O	7:L:118:VAL:CG2	2.37	0.72
13:A:993:G:O2'	13:A:994:A:N7	2.20	0.72
13:A:1178:G:N2	13:A:1181:G:OP2	2.19	0.72
13:A:1315:U:O2'	13:A:1360:A:N3	2.22	0.72
13:A:658:C:N4	13:A:748:G:O6	2.19	0.72
13:A:722:G:N1	13:A:733:G:O6	2.17	0.72
13:A:1269:A:H1'	13:A:1312:G:H21	1.54	0.72
11:R:46:THR:HG23	11:R:50:TYR:HD1	1.55	0.72
13:A:932:C:H2'	13:A:933:G:C8	2.25	0.72
13:A:1320:C:H42	20:S:36:ARG:HA	1.55	0.71
4:F:45:ARG:HG2	4:F:46:GLN:N	2.04	0.71
13:A:181:A:O2'	13:A:194:C:N4	2.24	0.71
16:I:39:GLY:HA2	16:I:44:ARG:HB2	1.71	0.71
7:L:33:CYS:H	7:L:54:VAL:HG23	1.55	0.71
13:A:1423:G:N2	13:A:1477:U:O2	2.24	0.71
17:J:53:ILE:HD12	17:J:61:ALA:HB1	1.73	0.71
9:P:8:ARG:NH1	13:A:391:G:C4'	2.48	0.71
13:A:1321:U:O2	20:S:35:ARG:NH2	2.24	0.71
8:O:9:LYS:HE3	8:O:10:ILE:CD1	2.21	0.71
13:A:1393:U:H3'	13:A:1394:A:H8	1.56	0.71
13:A:1516:G:N2	13:A:1518:A:H2'	2.06	0.71
13:A:697:U:O2'	13:A:785:G:N3	2.22	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C:7:ASN:ND2	14:C:183:TYR:O	2.21	0.70
2:D:151:GLN:NE2	13:A:437:U:H5"	2.05	0.70
13:A:514:C:H5"	13:A:532:A:H61	1.55	0.70
13:A:1307:U:OP1	18:M:99:GLN:NE2	2.24	0.70
12:T:78:LEU:O	12:T:82:ILE:HG12	1.90	0.70
13:A:982:U:N3	13:A:1223:C:O2	2.24	0.70
13:A:159:G:N2	13:A:162:A:OP2	2.25	0.70
16:I:21:LYS:HB2	16:I:61:ASP:HB3	1.73	0.70
18:M:74:MET:HA	18:M:77:LYS:HB2	1.72	0.70
20:S:13:HIS:HB2	20:S:34:SER:HB3	1.73	0.70
20:S:32:THR:HG22	20:S:34:SER:H	1.55	0.70
11:R:41:SER:OG	11:R:42:ARG:NH2	2.25	0.70
13:A:1227:A:N7	20:S:80:ARG:NH2	2.39	0.70
4:F:5:GLU:HB2	4:F:90:MET:HB3	1.73	0.70
2:D:98:ASP:OD1	2:D:114:ARG:HB2	1.92	0.69
12:T:27:MET:HE1	12:T:66:ILE:HD13	1.73	0.69
12:T:84:LYS:NZ	13:A:258:G:OP1	2.24	0.69
13:A:1351:U:O4	13:A:1371:G:O6	2.11	0.69
8:O:47:LYS:NZ	13:A:669:G:H5'	2.06	0.69
13:A:356:A:N3	13:A:368:U:O2'	2.24	0.69
14:C:63:ILE:HG23	14:C:96:VAL:HG21	1.73	0.69
14:C:138:GLN:HB3	14:C:142:ARG:HH12	1.58	0.69
16:I:18:VAL:HG22	16:I:64:ILE:HG12	1.73	0.69
19:N:87:ALA:HB2	19:N:92:ILE:HD12	1.74	0.69
17:J:52:LEU:HD11	17:J:59:LYS:HA	1.74	0.69
10:Q:7:LEU:HD13	10:Q:72:TRP:CZ3	2.28	0.69
13:A:1058:G:H1	13:A:1199:U:H3	1.40	0.69
13:A:1147:C:O2	16:I:17:ARG:NH1	2.24	0.69
1:B:86:CYS:O	1:B:221:ARG:NH2	2.25	0.69
13:A:1009:U:H3	13:A:1020:G:H1	0.75	0.69
2:D:31:CYS:SG	13:A:429:U:H5"	2.32	0.69
13:A:382:A:H2'	13:A:383:A:C8	2.27	0.69
18:M:8:ILE:HD12	18:M:9:PRO:HD2	1.75	0.69
1:B:97:GLY:O	13:A:1102:A:O2'	2.10	0.69
2:D:86:GLY:HA3	2:D:196:GLU:HG3	1.75	0.69
4:F:38:ARG:NH1	4:F:98:GLU:O	2.25	0.69
13:A:981:U:OP1	19:N:8:ARG:NH2	2.25	0.69
20:S:11:ASP:HB2	20:S:34:SER:HB2	1.75	0.69
13:A:202:G:O2'	13:A:468:A:H8	1.76	0.69
13:A:251:G:C6	13:A:266:G:C2	2.81	0.68
13:A:216:U:H2'	13:A:217:C:C6	2.28	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:1502:A:C5	13:A:1530:G:H4'	2.28	0.68
20:S:35:ARG:HA	20:S:70:LEU:HD22	1.76	0.68
20:S:65:MET:HG3	20:S:68:HIS:HB2	1.74	0.68
3:E:9:GLU:O	3:E:10:LEU:HD12	1.92	0.68
6:K:52:ARG:NE	13:A:691:G:O6	2.26	0.68
7:L:89:LEU:HD12	7:L:89:LEU:O	1.93	0.68
8:O:9:LYS:HD2	8:O:10:ILE:HG13	1.76	0.68
13:A:829:G:N1	13:A:857:C:N3	2.37	0.68
1:B:113:LEU:HD12	1:B:116:LEU:HD21	1.76	0.68
18:M:12:LYS:HB3	18:M:17:ALA:HB2	1.76	0.68
2:D:169:TRP:CD2	2:D:185:PRO:HB3	2.29	0.68
13:A:1111:A:H61	14:C:175:HIS:HB3	1.59	0.68
19:N:87:ALA:HB1	19:N:95:LEU:HD22	1.74	0.68
13:A:457:G:N2	13:A:475:C:O2	2.19	0.67
13:A:703:G:H4'	13:A:704:A:H8	1.59	0.67
13:A:861:G:HO2'	13:A:874:G:HO2'	1.41	0.67
16:I:86:LEU:HD13	16:I:93:LEU:HD11	1.76	0.67
13:A:360:G:H8	21:A:1677:HOH:O	1.74	0.67
13:A:976:G:O5'	13:A:1358:U:O2'	2.12	0.67
13:A:1391:U:O2	13:A:1503:A:N6	2.27	0.67
13:A:149:A:O5'	13:A:1446:A:O2'	2.11	0.67
13:A:1152:A:OP1	17:J:72:ARG:NH2	2.27	0.67
16:I:105:ARG:NH1	16:I:106:ASP:O	2.27	0.67
3:E:33:THR:HG22	3:E:51:LYS:HG2	1.77	0.67
16:I:113:LYS:HA	16:I:120:ALA:HB2	1.76	0.67
13:A:122:G:H1'	21:A:1647:HOH:O	1.93	0.67
13:A:1025:U:H4'	13:A:1026:G:H8	1.60	0.67
13:A:770:C:O2'	13:A:899:C:N3	2.26	0.67
13:A:1175:G:H2'	13:A:1176:A:H8	1.59	0.67
13:A:692:U:N3	13:A:695:A:OP2	2.25	0.67
4:F:6:ILE:HB	4:F:62:MET:HG3	1.76	0.67
13:A:67:C:H2'	13:A:68:G:C8	2.30	0.67
16:I:27:ILE:HB	16:I:34:LEU:HD22	1.76	0.67
6:K:12:ARG:NH1	13:A:684:U:O3'	2.28	0.66
13:A:1269:A:N6	13:A:1313:U:OP1	2.28	0.66
13:A:1060:U:H2'	13:A:1061:G:H8	1.60	0.66
13:A:1218:C:H2'	13:A:1219:A:H8	1.60	0.66
1:B:210:THR:HA	1:B:213:LEU:HD12	1.77	0.66
13:A:1096:C:H2'	13:A:1097:C:C6	2.30	0.66
7:L:38:THR:HG21	7:L:48:LEU:HB3	1.75	0.66
1:B:172:ILE:O	1:B:176:ASN:ND2	2.28	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:3:HIS:HB2	4:F:92:THR:HB	1.77	0.66
5:H:1:SER:H1	5:H:5:PRO:HA	1.61	0.66
13:A:459:A:O5'	13:A:474:G:N2	2.27	0.66
13:A:801:U:H2'	13:A:802:A:C8	2.30	0.66
1:B:56:LEU:HD13	1:B:216:VAL:HG23	1.78	0.66
3:E:102:THR:O	3:E:121:ASN:ND2	2.29	0.66
6:K:30:ILE:HG22	6:K:43:TRP:HE1	1.60	0.66
10:Q:7:LEU:HD13	10:Q:72:TRP:CH2	2.31	0.66
13:A:654:G:O6	13:A:752:G:N2	2.20	0.66
13:A:1194:U:O4	14:C:2:GLN:NE2	2.29	0.66
13:A:1220:G:OP1	19:N:52:ARG:NH2	2.26	0.66
5:H:1:SER:N	5:H:5:PRO:CA	2.59	0.66
7:L:62:VAL:HG21	7:L:94:TYR:CE2	2.31	0.66
13:A:457:G:O6	13:A:475:C:N4	2.22	0.66
1:B:94:ARG:NH1	13:A:1099:G:OP2	2.29	0.66
13:A:1301:U:OP2	13:A:1303:C:N4	2.29	0.66
13:A:1351:U:H3	13:A:1371:G:H1	0.75	0.66
8:O:9:LYS:CD	8:O:10:ILE:HG13	2.26	0.66
13:A:1106:G:H5"	14:C:171:ARG:HB3	1.78	0.66
3:E:19:ARG:HD3	3:E:30:PHE:CD2	2.31	0.65
5:H:82:LEU:HD21	7:L:3:VAL:HG21	1.78	0.65
7:L:30:ARG:NH1	13:A:363:A:OP2	2.29	0.65
13:A:946:A:H2'	13:A:947:G:C8	2.31	0.65
13:A:1516:G:N2	13:A:1519:A:C5	2.64	0.65
1:B:59:ILE:HA	1:B:62:ARG:NH1	2.12	0.65
11:R:42:ARG:NH2	13:A:721:G:OP1	2.29	0.65
13:A:148:G:H21	13:A:1447:A:H2	1.43	0.65
13:A:677:U:H2'	13:A:678:U:C6	2.31	0.65
13:A:1313:U:H2'	13:A:1314:C:C6	2.31	0.65
4:F:8:PHE:HB2	4:F:84:VAL:HG11	1.79	0.65
13:A:443:C:O2	13:A:491:G:N2	2.17	0.65
13:A:1047:G:OP1	19:N:3:GLN:NE2	2.25	0.65
7:L:106:VAL:O	7:L:118:VAL:HG21	1.95	0.65
13:A:195:A:C8	21:A:1604:HOH:O	2.26	0.65
18:M:85:TYR:N	20:S:72:GLU:O	2.29	0.65
13:A:82:G:N2	13:A:84:U:O4	2.29	0.65
13:A:147:G:H2'	13:A:148:G:C8	2.32	0.65
13:A:521:G:H5"	21:A:1697:HOH:O	1.96	0.65
16:I:127:SER:O	16:I:129:ARG:NH1	2.29	0.65
8:O:81:ILE:O	8:O:86:LEU:N	2.29	0.65
13:A:829:G:N2	13:A:857:C:O2	2.16	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:1137:C:O2'	13:A:1138:G:N3	2.30	0.65
13:A:1321:U:H3	20:S:35:ARG:HH12	1.43	0.65
13:A:1360:A:OP2	19:N:74:ARG:NH2	2.30	0.65
13:A:1516:G:H22	13:A:1518:A:H2'	1.61	0.65
2:D:12:ARG:HG2	2:D:33:ILE:HD12	1.79	0.65
9:P:44:SER:H	9:P:46:LYS:HE2	1.61	0.65
13:A:1501:C:OP2	13:A:1504:G:O2'	2.13	0.65
19:N:8:ARG:HB2	19:N:60:ARG:HH22	1.62	0.65
6:K:58:THR:HG23	6:K:61:ALA:H	1.62	0.64
13:A:1224:U:O2'	13:A:1322:C:OP1	2.15	0.64
13:A:1323:G:H2'	13:A:1324:A:C8	2.31	0.64
13:A:696:A:O2'	13:A:786:G:O2'	2.15	0.64
13:A:746:A:H2'	13:A:747:A:C8	2.33	0.64
13:A:1309:G:H2'	13:A:1310:G:C8	2.29	0.64
14:C:69:THR:HG21	14:C:75:VAL:HG21	1.79	0.64
13:A:409:U:O2'	13:A:410:G:O5'	2.14	0.64
6:K:19:VAL:HG12	6:K:82:GLU:HB3	1.80	0.64
6:K:62:ALA:HB1	6:K:95:THR:HB	1.78	0.64
13:A:677:U:O2'	13:A:777:A:O2'	2.15	0.64
13:A:899:C:H2'	13:A:900:A:C8	2.32	0.64
14:C:53:ARG:H	14:C:68:HIS:HB2	1.63	0.64
15:G:15:PRO:HB3	16:I:49:GLN:NE2	2.11	0.64
6:K:32:THR:HB	13:A:705:G:H22	1.63	0.64
13:A:1060:U:H2'	13:A:1061:G:C8	2.33	0.64
1:B:185:ILE:HG13	1:B:199:ILE:HB	1.79	0.64
4:F:6:ILE:HB	4:F:62:MET:SD	2.37	0.64
13:A:744:C:H2'	13:A:745:G:C8	2.33	0.64
13:A:1356:G:H2'	13:A:1357:A:H8	1.63	0.64
7:L:98:ARG:NE	7:L:103:CYS:SG	2.70	0.64
8:O:44:GLU:CD	8:O:45:HIS:HD1	2.02	0.64
13:A:1316:G:N1	13:A:1319:A:OP2	2.30	0.64
16:I:27:ILE:HD12	16:I:48:ARG:HE	1.63	0.64
18:M:94:LEU:HD12	18:M:95:PRO:HD2	1.80	0.64
13:A:518:C:H2'	13:A:530:G:C8	2.32	0.64
13:A:1251:A:H2'	13:A:1252:A:C8	2.33	0.64
13:A:1384:C:H2'	13:A:1385:G:C8	2.33	0.64
18:M:88:LEU:HA	18:M:91:ARG:HD2	1.80	0.64
13:A:713:G:O2'	13:A:714:G:O4'	2.07	0.63
13:A:945:G:H1	13:A:1236:A:H61	1.46	0.63
14:C:48:LYS:O	14:C:71:ARG:NH2	2.31	0.63
2:D:94:GLU:OE2	2:D:103:ARG:NH1	2.31	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:O:9:LYS:NZ	8:O:10:ILE:HG13	2.13	0.63
16:I:117:LEU:HD22	16:I:123:ARG:HG2	1.80	0.63
13:A:292:G:H1'	21:A:1742:HOH:O	1.97	0.63
13:A:842:U:O2'	13:A:843:U:OP1	2.16	0.63
13:A:1388:C:H2'	13:A:1389:C:C6	2.33	0.63
19:N:20:PHE:HA	19:N:24:ALA:HB3	1.80	0.63
18:M:4:ALA:HB1	18:M:64:VAL:HG22	1.79	0.63
8:O:53:ARG:HH12	13:A:579:A:HO2'	1.47	0.63
13:A:1291:U:O2'	16:I:40:ARG:NH2	2.21	0.63
13:A:1147:C:HO2'	16:I:6:TYR:HH	1.46	0.63
13:A:687:A:N6	13:A:701:U:O4'	2.32	0.63
13:A:1311:A:OP2	20:S:2:ARG:NH1	2.31	0.63
19:N:33:VAL:HA	19:N:40:ARG:HH21	1.64	0.63
8:O:47:LYS:NZ	13:A:669:G:OP1	2.32	0.62
5:H:2:MET:HE1	13:A:756:C:C4'	2.28	0.62
13:A:569:C:H3'	21:A:1787:HOH:O	1.98	0.62
13:A:695:A:H61	13:A:786:G:N2	1.97	0.62
13:A:1069:C:N4	13:A:1106:G:O6	2.25	0.62
6:K:51:PHE:HB2	6:K:55:ARG:HH22	1.65	0.62
13:A:674:G:H2'	13:A:675:A:C8	2.30	0.62
13:A:685:G:O2'	13:A:686:U:O4'	2.17	0.62
13:A:980:C:O2'	19:N:12:ARG:NH1	2.32	0.62
13:A:1009:U:O4	13:A:1020:G:O6	2.17	0.62
18:M:64:VAL:O	18:M:68:LEU:N	2.27	0.62
2:D:14:GLU:OE1	2:D:55:ARG:NH1	2.32	0.62
13:A:86:G:H1'	13:A:87:C:C5	2.32	0.62
13:A:1055:A:H2	14:C:193:GLY:HA2	1.63	0.62
2:D:195:ASN:HD21	2:D:197:HIS:HE1	1.46	0.62
8:O:24:THR:HG21	8:O:69:LEU:HG	1.82	0.62
13:A:1055:A:N3	14:C:155:ARG:NH1	2.47	0.62
7:L:39:THR:OG1	7:L:89:LEU:HD23	1.99	0.62
10:Q:70:LYS:NZ	13:A:255:G:OP1	2.30	0.62
13:A:575:G:O2'	13:A:821:G:H5'	1.99	0.62
13:A:1143:G:H2'	13:A:1144:G:H8	1.64	0.62
14:C:58:ARG:HG2	14:C:63:ILE:HG22	1.81	0.62
5:H:43:GLY:O	5:H:63:LYS:NZ	2.33	0.62
13:A:1431:A:H1'	13:A:1432:G:H5'	1.82	0.62
4:F:7:VAL:HG11	11:R:64:LEU:HD11	1.82	0.62
13:A:299:G:H2'	13:A:300:A:C8	2.35	0.62
13:A:695:A:H2'	13:A:696:A:O4'	2.00	0.62
4:F:6:ILE:HG13	4:F:62:MET:SD	2.40	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:212:G:H2'	13:A:213:G:H8	1.65	0.62
13:A:571:U:H5"	13:A:819:A:C5	2.35	0.61
13:A:1071:C:H2'	13:A:1072:G:H8	1.65	0.61
16:I:21:LYS:O	16:I:61:ASP:N	2.27	0.61
17:J:27:GLU:O	17:J:31:ARG:NH1	2.33	0.61
19:N:88:MET:HE1	19:N:95:LEU:HD23	1.82	0.61
3:E:22:LYS:HD3	13:A:1081:A:H5"	1.82	0.61
3:E:107:GLY:HA3	13:A:9:G:H5'	1.82	0.61
13:A:796:C:H2'	13:A:797:C:C6	2.35	0.61
17:J:6:ILE:HD11	17:J:79:PRO:HB3	1.83	0.61
11:R:46:THR:HG23	11:R:50:TYR:CD1	2.35	0.61
11:R:59:LYS:HE2	13:A:735:C:H5'	1.82	0.61
13:A:837:U:C2	13:A:849:G:O6	2.53	0.61
13:A:1291:U:O3'	16:I:40:ARG:NH1	2.32	0.61
18:M:80:MET:SD	18:M:84:CYS:SG	2.93	0.61
18:M:86:ARG:O	18:M:90:HIS:ND1	2.28	0.61
13:A:788:U:O2	13:A:795:C:N4	2.33	0.61
13:A:1095:U:OP1	13:A:1108:G:N2	2.27	0.61
5:H:95:MET:HG2	5:H:98:LEU:HB2	1.82	0.61
13:A:697:U:H1'	13:A:785:G:H21	1.65	0.61
13:A:1147:C:H2'	13:A:1148:U:C6	2.35	0.61
3:E:132:PRO:HA	3:E:135:VAL:HG22	1.83	0.61
3:E:59:ILE:O	3:E:63:MET:HG2	2.00	0.61
13:A:1090:U:O2	13:A:1095:U:N3	2.20	0.61
9:P:2:VAL:O	9:P:65:ALA:HA	2.01	0.61
7:L:86:VAL:HG13	13:A:523:A:N6	2.16	0.61
13:A:1095:U:P	13:A:1108:G:H1	2.23	0.61
17:J:53:ILE:HD11	17:J:63:ASP:HB2	1.81	0.61
1:B:99:MET:HG3	1:B:100:LEU:HD22	1.83	0.60
13:A:464:U:H2'	13:A:466:A:OP1	2.01	0.60
13:A:1239:A:H62	13:A:1299:A:H62	1.48	0.60
13:A:1356:G:H2'	13:A:1357:A:C8	2.36	0.60
16:I:25:GLY:HA3	16:I:58:GLU:HA	1.83	0.60
16:I:43:ALA:HA	16:I:46:VAL:HG12	1.83	0.60
2:D:55:ARG:NH2	13:A:544:G:OP1	2.30	0.60
13:A:779:C:O2'	13:A:780:A:O4'	2.18	0.60
13:A:1287:A:H2'	13:A:1288:A:C8	2.35	0.60
13:A:1348:U:H2'	13:A:1349:A:C8	2.34	0.60
17:J:24:GLU:HG3	17:J:92:LEU:HD21	1.82	0.60
13:A:204:G:N9	13:A:465:A:H1'	2.16	0.60
13:A:1086:U:O4	13:A:1100:C:N3	2.33	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:1191:A:H2'	13:A:1192:C:C6	2.37	0.60
10:Q:68:LYS:O	10:Q:69:THR:OG1	2.14	0.60
13:A:171:A:H2'	13:A:172:A:C8	2.36	0.60
13:A:949:A:H2'	13:A:950:U:C6	2.36	0.60
14:C:82:ASP:OD1	14:C:85:LYS:NZ	2.34	0.60
13:A:1181:G:H4'	13:A:1182:G:H5'	1.81	0.60
7:L:90:PRO:HB3	13:A:911:U:H5"	1.84	0.60
13:A:1271:A:H2'	13:A:1272:G:H8	1.67	0.60
2:D:195:ASN:HD21	2:D:197:HIS:CE1	2.19	0.60
13:A:269:C:H2'	13:A:270:A:C8	2.36	0.60
13:A:335:C:O2'	13:A:336:A:H8	1.85	0.60
13:A:79:G:O6	13:A:90:C:N4	2.26	0.60
20:S:29:PRO:HB2	20:S:49:ALA:HB2	1.83	0.60
10:Q:76:ARG:HH12	10:Q:78:VAL:HG12	1.67	0.60
12:T:24:ARG:O	12:T:28:ARG:HG3	2.02	0.60
13:A:715:A:H8	13:A:716:A:C8	2.20	0.60
12:T:35:TYR:O	12:T:38:ILE:N	2.35	0.59
13:A:681:A:N6	13:A:682:G:O6	2.35	0.59
13:A:751:U:H2'	13:A:752:G:O4'	2.02	0.59
18:M:74:MET:O	18:M:78:ARG:N	2.30	0.59
3:E:63:MET:O	3:E:67:ARG:HG3	2.02	0.59
5:H:81:GLY:O	5:H:82:LEU:HD22	2.02	0.59
13:A:499:A:N1	13:A:546:A:O2'	2.32	0.59
13:A:90:C:H2'	13:A:91:U:C6	2.38	0.59
13:A:1311:A:H2'	13:A:1312:G:O4'	2.02	0.59
17:J:56:HIS:ND1	17:J:57:VAL:HG23	2.17	0.59
6:K:30:ILE:HG22	6:K:43:TRP:NE1	2.17	0.59
8:O:44:GLU:OE1	8:O:45:HIS:ND1	2.36	0.59
13:A:1096:C:H2'	13:A:1097:C:C5	2.38	0.59
13:A:1230:C:OP2	18:M:112:ARG:NH2	2.36	0.59
1:B:11:ALA:HB2	1:B:211:LEU:HD13	1.84	0.59
1:B:41:ASN:HB3	1:B:44:LYS:HB2	1.85	0.59
9:P:25:ARG:NH1	13:A:134:G:O6	2.36	0.59
10:Q:76:ARG:NH1	10:Q:78:VAL:HG12	2.16	0.59
13:A:180:U:C2'	13:A:181:A:H5'	2.32	0.59
13:A:802:A:H3'	13:A:803:G:H8	1.68	0.59
13:A:1222:G:OP2	13:A:1322:C:N4	2.35	0.59
7:L:39:THR:OG1	7:L:89:LEU:HD21	2.02	0.59
13:A:407:U:H2'	13:A:408:A:H8	1.67	0.59
13:A:1064:G:O6	13:A:1192:C:N4	2.35	0.59
15:G:44:SER:O	15:G:48:THR:OG1	2.20	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:1095:U:H2'	13:A:1096:C:C6	2.38	0.59
13:A:1481:U:H2'	13:A:1482:G:C8	2.36	0.59
16:I:18:VAL:HG11	16:I:82:ILE:HA	1.84	0.59
16:I:97:LEU:HG	16:I:102:PHE:HD2	1.68	0.59
1:B:220:VAL:O	1:B:224:ARG:NH1	2.35	0.59
4:F:3:HIS:CE1	4:F:95:ALA:HA	2.37	0.59
7:L:113:ARG:CD	7:L:118:VAL:O	2.51	0.59
13:A:678:U:H3	13:A:713:G:N2	2.00	0.59
13:A:1240:U:OP2	15:G:116:ALA:N	2.34	0.59
13:A:1327:C:H2'	13:A:1328:C:O4'	2.03	0.59
11:R:54:LEU:O	11:R:58:ILE:HD12	2.03	0.59
13:A:789:U:N3	13:A:792:A:OP2	2.28	0.59
13:A:985:C:H2'	13:A:986:U:C6	2.38	0.59
13:A:1372:U:H2'	13:A:1373:G:O4'	2.03	0.59
6:K:48:GLY:H	6:K:52:ARG:HG2	1.68	0.58
9:P:1:MET:HB2	13:A:135:C:O2	2.03	0.58
13:A:839:C:N4	13:A:847:G:O6	2.27	0.58
13:A:1175:G:H2'	13:A:1176:A:C8	2.38	0.58
2:D:120:LYS:HG3	13:A:439:U:H5'	1.85	0.58
4:F:11:HIS:O	4:F:15:SER:N	2.36	0.58
6:K:43:TRP:HZ3	13:A:704:A:N1	2.01	0.58
13:A:932:C:H2'	13:A:933:G:H8	1.66	0.58
13:A:1143:G:H2'	13:A:1144:G:C8	2.38	0.58
2:D:151:GLN:HE21	13:A:437:U:H5'	1.69	0.58
13:A:1363:A:O2'	13:A:1365:G:N7	2.33	0.58
16:I:118:ARG:HH21	16:I:124:PRO:HB3	1.67	0.58
13:A:1520:C:H2'	13:A:1521:C:C6	2.39	0.58
13:A:777:A:H2'	13:A:778:G:H8	1.67	0.58
13:A:844:G:H2'	13:A:845:A:O4'	2.04	0.58
13:A:1144:G:O6	13:A:1145:A:N6	2.35	0.58
18:M:68:LEU:HA	18:M:71:GLU:HG2	1.86	0.58
1:B:110:ILE:HG22	1:B:147:LEU:HG	1.84	0.58
13:A:1070:U:H2'	13:A:1071:C:H6	1.69	0.58
16:I:82:ILE:HG22	16:I:86:LEU:HD23	1.85	0.58
19:N:88:MET:CE	19:N:95:LEU:HD23	2.33	0.58
13:A:350:G:H2'	13:A:351:G:C8	2.38	0.58
13:A:987:G:H2'	13:A:988:G:H8	1.69	0.58
15:G:113:LYS:HB3	15:G:118:ARG:HH12	1.69	0.58
17:J:11:LYS:HB2	17:J:97:ASP:HB3	1.85	0.58
19:N:88:MET:CE	19:N:95:LEU:CD2	2.81	0.58
5:H:17:GLN:OE1	5:H:69:ALA:HB1	2.04	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:371:A:H2'	13:A:372:C:O4'	2.04	0.58
13:A:407:U:H2'	13:A:408:A:C8	2.39	0.58
13:A:679:C:H2'	13:A:680:C:C6	2.38	0.58
13:A:1026:G:C6	13:A:1035:A:N1	2.71	0.58
13:A:1229:A:OP1	18:M:112:ARG:NH2	2.37	0.58
16:I:34:LEU:HD21	16:I:48:ARG:NH2	2.18	0.58
13:A:159:G:O2'	13:A:161:A:N7	2.28	0.58
13:A:776:G:N2	13:A:802:A:OP2	2.29	0.58
16:I:97:LEU:O	16:I:101:GLY:N	2.36	0.58
1:B:110:ILE:HA	1:B:147:LEU:HD11	1.86	0.58
13:A:1396:A:H3'	13:A:1397:C:C6	2.38	0.58
15:G:115:MET:HA	15:G:118:ARG:HB2	1.85	0.58
4:F:2:ARG:HE	4:F:91:ARG:CZ	2.17	0.57
8:O:9:LYS:NZ	8:O:10:ILE:CG1	2.67	0.57
8:O:47:LYS:HZ1	13:A:669:G:H5'	1.68	0.57
13:A:1255:G:O2'	13:A:1258:G:N3	2.29	0.57
13:A:1271:A:H2'	13:A:1272:G:C8	2.38	0.57
13:A:1343:G:H4'	16:I:123:ARG:HB2	1.85	0.57
13:A:1377:A:H4'	13:A:1378:C:H5	1.68	0.57
13:A:157:U:O2	13:A:164:G:C6	2.56	0.57
13:A:777:A:H2'	13:A:778:G:C8	2.39	0.57
13:A:1221:G:OP2	20:S:36:ARG:NH2	2.38	0.57
13:A:1301:U:H2'	13:A:1303:C:H5	1.69	0.57
20:S:4:LEU:HD12	20:S:6:LYS:H	1.68	0.57
13:A:925:G:O2'	13:A:1503:A:N6	2.37	0.57
13:A:1032:G:OP2	13:A:1032:G:N2	2.36	0.57
13:A:1330:U:H3'	13:A:1331:G:C8	2.40	0.57
7:L:46:SER:OG	13:A:518:C:O3'	2.22	0.57
13:A:1070:U:H2'	13:A:1071:C:C6	2.39	0.57
16:I:58:GLU:HG2	16:I:59:LYS:HD3	1.85	0.57
5:H:74:ILE:HG13	5:H:128:VAL:HG22	1.86	0.57
13:A:131:A:H2'	13:A:132:C:C6	2.40	0.57
13:A:532:A:H1'	13:A:533:A:H2'	1.86	0.57
13:A:982:U:O2	13:A:1222:G:O6	2.20	0.57
2:D:12:ARG:NH1	2:D:35:GLN:O	2.38	0.57
8:O:31:LEU:O	8:O:35:ILE:HG12	2.05	0.57
13:A:450:G:H5"	13:A:451:A:C5'	2.35	0.57
13:A:676:A:N1	13:A:715:A:N6	2.52	0.57
13:A:1304:G:N2	13:A:1333:A:N6	2.47	0.57
13:A:1320:C:C5	20:S:69:LYS:HG2	2.40	0.57
20:S:17:LYS:HB3	20:S:30:LEU:HD13	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:18:VAL:HB	4:F:19:PRO:HD3	1.87	0.57
7:L:113:ARG:NH2	13:A:501:C:OP1	2.38	0.57
13:A:686:U:O2'	13:A:703:G:N2	2.38	0.57
13:A:334:C:O2'	13:A:335:C:O5'	2.23	0.57
13:A:1025:U:H4'	13:A:1026:G:C8	2.40	0.57
13:A:1124:G:N2	13:A:1125:U:O4	2.31	0.57
13:A:1269:A:H1'	13:A:1312:G:N2	2.20	0.57
13:A:1358:U:OP2	13:A:1359:C:N4	2.38	0.57
13:A:1384:C:H2'	13:A:1385:G:H8	1.70	0.57
19:N:23:ARG:HH21	19:N:51:PRO:HG2	1.69	0.57
5:H:4:ASP:OD1	5:H:76:ARG:NH1	2.38	0.57
7:L:113:ARG:HG3	7:L:118:VAL:HB	1.86	0.57
13:A:925:G:N2	13:A:1392:G:OP2	2.35	0.57
18:M:24:VAL:HG23	18:M:29:SER:HB2	1.87	0.57
2:D:33:ILE:O	2:D:34:GLU:HG3	2.05	0.56
13:A:443:C:N4	13:A:491:G:O6	2.28	0.56
13:A:1090:U:H2'	13:A:1091:U:C6	2.40	0.56
13:A:1306:A:N6	13:A:1331:G:H1'	2.19	0.56
17:J:5:ARG:N	17:J:77:VAL:O	2.38	0.56
2:D:108:ALA:N	2:D:112:GLU:OE1	2.31	0.56
8:O:9:LYS:HE3	8:O:10:ILE:HG13	1.87	0.56
13:A:177:G:O2'	13:A:1448:C:H4'	2.04	0.56
16:I:34:LEU:O	16:I:39:GLY:N	2.36	0.56
20:S:13:HIS:HB3	20:S:33:TRP:H	1.70	0.56
2:D:56:GLU:CD	2:D:198:LEU:HB2	2.25	0.56
2:D:94:GLU:HA	2:D:99:ASN:HD22	1.70	0.56
2:D:109:THR:OG1	13:A:408:A:OP1	2.21	0.56
5:H:55:LYS:NZ	13:A:653:U:O4'	2.38	0.56
6:K:32:THR:HB	13:A:705:G:N2	2.20	0.56
13:A:6:G:HO2'	13:A:7:A:H8	1.50	0.56
13:A:802:A:H3'	13:A:803:G:C8	2.40	0.56
13:A:1086:U:H2'	13:A:1087:G:C8	2.40	0.56
13:A:1148:U:H2'	13:A:1149:C:O4'	2.05	0.56
13:A:1147:C:H2'	13:A:1148:U:H6	1.70	0.56
13:A:1417:G:N1	13:A:1482:G:N7	2.53	0.56
18:M:103:THR:HG22	18:M:104:ASN:H	1.69	0.56
13:A:17:U:H2'	13:A:18:C:C6	2.40	0.56
13:A:97:G:H2'	13:A:98:A:O4'	2.06	0.56
13:A:695:A:N6	13:A:786:G:H21	2.03	0.56
14:C:165:GLU:HB2	14:C:167:TYR:HE1	1.71	0.56
18:M:12:LYS:HG2	18:M:13:HIS:H	1.70	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:37:HIS:ND1	4:F:65:GLU:HG3	2.20	0.56
8:O:9:LYS:CE	8:O:10:ILE:CG1	2.82	0.56
11:R:52:ARG:NH2	13:A:835:U:OP1	2.39	0.56
13:A:309:A:O2'	13:A:607:A:N1	2.30	0.56
13:A:1330:U:H5'	18:M:22:TYR:HB3	1.88	0.56
13:A:1392:G:N2	13:A:1502:A:O5'	2.39	0.56
13:A:1355:G:H2'	13:A:1356:G:H8	1.70	0.56
16:I:40:ARG:H	16:I:44:ARG:HB2	1.71	0.56
1:B:161:PHE:HA	1:B:183:PHE:HB2	1.88	0.56
3:E:125:LYS:NZ	13:A:9:G:OP2	2.33	0.56
4:F:40:GLU:OE2	4:F:42:TRP:NE1	2.39	0.56
13:A:374:A:H5"	13:A:452:A:C2	2.40	0.56
13:A:1097:C:H2'	13:A:1098:C:C6	2.40	0.56
13:A:1237:C:O2'	13:A:1300:G:N1	2.25	0.56
13:A:1392:G:H2'	13:A:1393:U:H6	1.70	0.56
2:D:151:GLN:HG2	2:D:153:ARG:HG2	1.88	0.56
6:K:80:ASN:HA	6:K:105:ARG:H	1.71	0.55
13:A:21:G:H2'	13:A:22:G:C8	2.41	0.55
13:A:687:A:N6	13:A:703:G:N2	2.29	0.55
13:A:908:A:H2'	13:A:909:A:C8	2.41	0.55
13:A:1287:A:H2'	13:A:1288:A:H8	1.71	0.55
13:A:1393:U:N3	13:A:1501:C:O2'	2.34	0.55
7:L:38:THR:HG22	7:L:48:LEU:CB	2.24	0.55
13:A:1347:G:H22	13:A:1374:A:P	2.29	0.55
13:A:1479:C:H2'	13:A:1480:A:C8	2.40	0.55
8:O:66:LEU:HD11	8:O:86:LEU:HD13	1.88	0.55
13:A:148:G:H1	13:A:174:A:H61	1.54	0.55
13:A:1087:G:H2'	13:A:1088:G:H8	1.71	0.55
18:M:64:VAL:HG12	18:M:66:GLY:H	1.70	0.55
13:A:984:C:H2'	13:A:985:C:C6	2.41	0.55
6:K:43:TRP:CZ3	13:A:704:A:N1	2.75	0.55
7:L:33:CYS:N	7:L:54:VAL:HG23	2.20	0.55
13:A:1014:A:H2'	13:A:1015:G:C8	2.42	0.55
13:A:1307:U:O2'	18:M:108:ARG:HD3	2.07	0.55
18:M:97:ARG:HH21	18:M:99:GLN:HB3	1.71	0.55
1:B:218:ALA:O	1:B:221:ARG:N	2.37	0.55
13:A:270:A:H2'	13:A:271:C:C6	2.41	0.55
13:A:1009:U:O2	13:A:1020:G:N2	2.26	0.55
13:A:1270:G:H2'	13:A:1271:A:H8	1.71	0.55
14:C:178:ARG:NH1	14:C:205:GLU:OE1	2.39	0.55
1:B:60:ALA:HB3	1:B:223:GLY:HA3	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:6:ILE:HB	4:F:62:MET:CG	2.37	0.55
6:K:105:ARG:NH1	6:K:106:ILE:O	2.40	0.55
7:L:106:VAL:O	7:L:118:VAL:HG22	2.06	0.55
13:A:594:U:H2'	13:A:595:A:O4'	2.07	0.55
13:A:1191:A:OP1	14:C:2:GLN:HB3	2.07	0.55
13:A:950:U:H2'	13:A:951:G:H8	1.71	0.55
13:A:1048:G:H5"	19:N:2:LYS:HG2	1.88	0.55
14:C:76:ILE:HA	14:C:83:VAL:HG23	1.89	0.55
18:M:56:ARG:HH21	18:M:59:VAL:HG11	1.72	0.55
2:D:7:LYS:HB3	2:D:20:LEU:CD1	2.37	0.55
13:A:1072:G:H2'	13:A:1073:U:C6	2.42	0.55
13:A:208:U:N3	13:A:210:C:O2	2.40	0.55
13:A:987:G:H2'	13:A:988:G:C8	2.42	0.55
13:A:1038:C:H2'	13:A:1039:G:C8	2.42	0.55
13:A:1163:A:H2'	13:A:1164:G:C8	2.42	0.55
13:A:1298:U:H4'	13:A:1299:A:H5'	1.89	0.55
13:A:1355:G:H2'	13:A:1356:G:C8	2.42	0.55
19:N:27:LYS:HE2	19:N:48:GLN:H	1.72	0.55
1:B:102:ASN:ND2	13:A:1073:U:O2	2.40	0.54
10:Q:6:THR:HA	10:Q:60:ILE:O	2.07	0.54
13:A:922:G:O2'	13:A:923:A:H8	1.89	0.54
13:A:1125:U:H2'	13:A:1126:U:H2'	1.89	0.54
1:B:58:LYS:O	1:B:62:ARG:NH1	2.40	0.54
2:D:104:MET:SD	2:D:179:GLY:HA3	2.47	0.54
6:K:54:SER:OG	13:A:694:A:OP1	2.20	0.54
13:A:64:G:H4'	13:A:65:A:H3'	1.89	0.54
13:A:180:U:H2'	13:A:181:A:H5'	1.89	0.54
13:A:516:U:O4	13:A:532:A:C8	2.61	0.54
13:A:1288:A:N3	13:A:1352:C:O2'	2.32	0.54
14:C:46:LEU:HD22	14:C:75:VAL:HG22	1.89	0.54
2:D:195:ASN:OD1	2:D:195:ASN:O	2.25	0.54
2:D:205:LYS:HA	13:A:8:A:N7	2.22	0.54
12:T:27:MET:HE2	12:T:57:VAL:HG22	1.88	0.54
13:A:1415:G:N2	13:A:1486:G:OP1	2.39	0.54
2:D:169:TRP:CE3	2:D:185:PRO:HB3	2.43	0.54
7:L:106:VAL:HG23	7:L:109:ARG:HB2	1.89	0.54
8:O:53:ARG:NH1	13:A:579:A:O2'	2.23	0.54
13:A:1005:A:OP2	13:A:1024:G:N2	2.37	0.54
4:F:45:ARG:CG	4:F:46:GLN:H	2.11	0.54
13:A:1347:G:N2	13:A:1374:A:O5'	2.41	0.54
19:N:60:ARG:HD2	19:N:62:ARG:HE	1.71	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:166:ASP:OD2	1:B:189:ASN:ND2	2.41	0.54
3:E:28:ARG:HH12	3:E:30:PHE:HZ	1.54	0.54
13:A:673:A:H2'	13:A:674:G:H8	1.70	0.54
13:A:700:G:H4'	13:A:704:A:H1'	1.88	0.54
13:A:785:G:N1	13:A:786:G:C6	2.76	0.54
1:B:99:MET:CE	1:B:106:VAL:HG21	2.38	0.54
13:A:71:A:N1	13:A:99:C:O2'	2.40	0.54
13:A:788:U:H3'	13:A:789:U:C6	2.43	0.54
13:A:1120:C:H2'	13:A:1121:U:H6	1.72	0.54
14:C:137:VAL:HG13	14:C:169:GLU:OE2	2.08	0.54
6:K:27:ASN:HA	6:K:57:SER:OG	2.08	0.54
13:A:776:G:N1	13:A:802:A:OP1	2.25	0.54
13:A:840:C:H2'	13:A:841:C:H5"	1.89	0.54
13:A:996:A:H2'	13:A:997:U:C6	2.42	0.54
13:A:1270:G:H2'	13:A:1271:A:C8	2.43	0.54
13:A:1392:G:H2'	13:A:1393:U:C6	2.42	0.54
3:E:109:ALA:HB3	3:E:135:VAL:HG23	1.88	0.54
13:A:1151:A:O2'	13:A:1152:A:H8	1.90	0.54
13:A:1161:C:H2'	13:A:1162:C:C6	2.42	0.54
13:A:1251:A:H2'	13:A:1252:A:H8	1.72	0.54
15:G:46:LEU:HA	15:G:49:LEU:HD23	1.89	0.54
1:B:143:LEU:HD23	1:B:147:LEU:HB2	1.90	0.54
10:Q:17:GLU:OE2	13:A:254:G:N2	2.40	0.54
13:A:440:C:H2'	13:A:441:A:H8	1.72	0.54
13:A:450:G:H5"	13:A:451:A:H5'	1.90	0.54
13:A:890:G:O2'	13:A:906:A:N6	2.41	0.54
13:A:939:G:H2'	13:A:940:C:C6	2.43	0.54
16:I:17:ARG:HE	16:I:65:THR:HB	1.73	0.54
4:F:71:ILE:HD12	4:F:74:LEU:HD12	1.90	0.53
6:K:20:ALA:N	6:K:82:GLU:O	2.39	0.53
6:K:28:ASN:ND2	13:A:689:C:OP1	2.41	0.53
13:A:413:G:H4'	13:A:414:A:O5'	2.07	0.53
13:A:1120:C:H2'	13:A:1121:U:C6	2.43	0.53
13:A:1510:C:H4'	21:A:2074:HOH:O	2.07	0.53
19:N:52:ARG:HE	19:N:58:ARG:HH12	1.56	0.53
8:O:44:GLU:CD	8:O:45:HIS:ND1	2.61	0.53
13:A:785:G:C6	13:A:786:G:C6	2.96	0.53
13:A:1221:G:O2'	20:S:76:THR:HG21	2.08	0.53
13:A:1418:A:H61	13:A:1482:G:H2'	1.73	0.53
17:J:16:ARG:NH2	17:J:19:ASP:OD2	2.41	0.53
13:A:674:G:C6	13:A:716:A:N1	2.77	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:789:U:C2	13:A:791:G:H5”	2.43	0.53
13:A:1288:A:N6	13:A:1371:G:O2’	2.36	0.53
13:A:1326:U:H2’	13:A:1327:C:C6	2.43	0.53
14:C:9:ILE:HG13	19:N:97:LYS:HD3	1.89	0.53
16:I:66:VAL:HG11	16:I:78:ILE:HD11	1.89	0.53
3:E:19:ARG:HD3	3:E:30:PHE:CE2	2.44	0.53
9:P:31:ARG:NH1	13:A:311:C:OP1	2.39	0.53
13:A:783:C:H2’	13:A:784:A:C8	2.43	0.53
13:A:1393:U:H3’	13:A:1394:A:C8	2.41	0.53
14:C:38:VAL:HG12	14:C:93:ILE:HG23	1.90	0.53
6:K:43:TRP:CD1	6:K:44:ALA:N	2.77	0.53
8:O:9:LYS:HD2	8:O:10:ILE:N	2.24	0.53
13:A:179:A:N6	21:A:1604:HOH:O	2.41	0.53
13:A:952:U:H2’	13:A:953:G:C8	2.44	0.53
13:A:1349:A:H1’	13:A:1374:A:N6	2.23	0.53
13:A:785:G:C6	13:A:786:G:O6	2.61	0.53
13:A:846:G:H3’	13:A:847:G:H8	1.73	0.53
13:A:1056:U:H2’	13:A:1057:G:H8	1.73	0.53
17:J:66:GLU:HB2	19:N:98:ALA:HB2	1.89	0.53
18:M:57:ASP:OD1	18:M:58:GLU:N	2.42	0.53
1:B:20:ARG:HD2	13:A:831:A:OP1	2.09	0.53
3:E:19:ARG:O	3:E:19:ARG:CD	2.56	0.53
7:L:63:THR:CG2	7:L:92:VAL:HG22	2.38	0.53
8:O:44:GLU:OE2	8:O:45:HIS:ND1	2.29	0.53
12:T:77:ASN:O	12:T:81:GLN:HG2	2.08	0.53
13:A:1111:A:N6	14:C:175:HIS:HB3	2.22	0.53
13:A:1366:C:H2’	13:A:1367:C:C6	2.43	0.53
13:A:151:A:H2’	13:A:152:A:O4’	2.08	0.53
13:A:946:A:H2’	13:A:947:G:H8	1.73	0.53
13:A:1250:A:H2’	13:A:1251:A:C8	2.44	0.53
14:C:62:SER:HA	14:C:96:VAL:HB	1.90	0.53
16:I:83:THR:C	16:I:87:MET:HE1	2.29	0.53
20:S:4:LEU:O	20:S:5:LYS:HG2	2.08	0.53
7:L:78:VAL:HG12	7:L:101:LEU:HD23	1.90	0.53
13:A:411:A:H4’	13:A:412:A:H5’	1.91	0.53
13:A:1246:A:N6	13:A:1292:G:O6	2.42	0.53
20:S:39:ILE:HD11	20:S:70:LEU:HD12	1.91	0.53
13:A:816:A:OP1	13:A:1526:G:O2’	2.26	0.53
13:A:1087:G:H2’	13:A:1088:G:C8	2.44	0.53
13:A:1205:U:H2’	13:A:1206:G:C8	2.44	0.53
13:A:1377:A:OP2	15:G:8:GLN:NE2	2.41	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:152:VAL:HA	3:E:155:LYS:HE2	1.91	0.52
12:T:27:MET:CE	12:T:66:ILE:HD13	2.39	0.52
13:A:152:A:N6	13:A:169:C:C2	2.77	0.52
13:A:950:U:H2'	13:A:951:G:C8	2.44	0.52
13:A:1383:C:H2'	13:A:1384:C:C6	2.44	0.52
13:A:1507:A:O2'	13:A:1508:A:OP1	2.21	0.52
5:H:102:VAL:HG13	5:H:125:ILE:HB	1.90	0.52
6:K:44:ALA:HB1	6:K:68:ARG:HB3	1.91	0.52
13:A:680:C:H2'	13:A:681:A:C8	2.45	0.52
1:B:69:VAL:HA	1:B:91:VAL:HG22	1.90	0.52
2:D:169:TRP:NE1	2:D:170:LEU:HD23	2.24	0.52
3:E:13:LYS:NZ	3:E:115:GLU:OE1	2.40	0.52
13:A:251:G:C5	13:A:266:G:C2	2.98	0.52
13:A:687:A:N3	13:A:688:G:H1'	2.24	0.52
13:A:1305:G:H22	13:A:1331:G:HO2'	1.54	0.52
14:C:150:VAL:HG13	14:C:199:VAL:HG12	1.91	0.52
17:J:67:ILE:HD11	19:N:95:LEU:HD12	1.91	0.52
19:N:23:ARG:NH1	19:N:48:GLN:HG3	2.25	0.52
2:D:60:VAL:HG22	2:D:194:ILE:HD12	1.91	0.52
13:A:677:U:H2'	13:A:678:U:C5	2.44	0.52
13:A:1321:U:H3'	13:A:1322:C:H2'	1.90	0.52
19:N:63:CYS:HB2	19:N:79:SER:HB3	1.90	0.52
8:O:25:GLU:HG3	8:O:80:LEU:HD22	1.90	0.52
13:A:1309:G:OP1	18:M:90:HIS:NE2	2.42	0.52
5:H:17:GLN:CD	5:H:69:ALA:HB1	2.30	0.52
11:R:46:THR:CG2	11:R:50:TYR:HD1	2.21	0.52
13:A:182:A:H1'	13:A:183:C:C5	2.44	0.52
13:A:967:C:OP2	13:A:968:A:O2'	2.22	0.52
13:A:1225:A:H1'	20:S:77:ARG:HG2	1.92	0.52
13:A:1277:C:O2'	13:A:1279:G:N3	2.34	0.52
13:A:1359:C:OP2	19:N:74:ARG:NE	2.42	0.52
13:A:1468:A:H2'	13:A:1469:C:O4'	2.09	0.52
16:I:46:VAL:HA	16:I:49:GLN:HG3	1.90	0.52
1:B:221:ARG:HD3	1:B:224:ARG:HH12	1.74	0.52
3:E:113:VAL:HG21	3:E:136:VAL:HG23	1.91	0.52
5:H:80:PRO:O	13:A:878:A:H5"	2.10	0.52
8:O:45:HIS:CD2	13:A:668:G:O2'	2.62	0.52
13:A:298:A:H2'	13:A:299:G:O4'	2.09	0.52
16:I:49:GLN:O	16:I:53:LEU:HG	2.10	0.52
6:K:70:ALA:O	6:K:74:LYS:HG2	2.10	0.52
7:L:69:GLU:OE2	13:A:520:A:O2'	2.27	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:O:66:LEU:HD12	8:O:87:ARG:NH1	2.24	0.52
8:O:81:ILE:HG13	8:O:82:GLU:OE1	2.09	0.52
13:A:343:U:O2'	13:A:346:G:O6	2.20	0.52
13:A:696:A:HO2'	13:A:786:G:HO2'	1.50	0.52
13:A:1052:U:O4	13:A:1206:G:O6	2.28	0.52
14:C:21:TRP:HB3	14:C:58:ARG:H	1.75	0.52
17:J:15:HIS:HA	17:J:18:ILE:HG22	1.92	0.52
17:J:52:LEU:HD13	17:J:62:ARG:HE	1.74	0.52
6:K:52:ARG:NH2	13:A:691:G:N7	2.54	0.52
13:A:122:G:C1'	21:A:1647:HOH:O	2.55	0.52
13:A:493:A:H5'	13:A:494:G:OP2	2.09	0.52
13:A:576:C:H3'	13:A:577:G:H5"	1.91	0.52
12:T:32:LYS:NZ	13:A:1439:G:OP2	2.43	0.52
13:A:462:G:P	13:A:462:G:H8	2.33	0.52
13:A:678:U:H2'	13:A:679:C:C6	2.45	0.52
13:A:711:G:H2'	13:A:712:A:C8	2.44	0.52
13:A:1225:A:H2'	13:A:1225:A:N3	2.24	0.52
16:I:40:ARG:H	16:I:44:ARG:HD3	1.74	0.52
4:F:5:GLU:HA	4:F:63:ASN:CB	2.40	0.51
7:L:11:ARG:HE	13:A:564:C:P	2.33	0.51
7:L:50:LYS:CD	7:L:50:LYS:N	2.73	0.51
13:A:306:A:H5"	21:A:1660:HOH:O	2.09	0.51
13:A:335:C:O3'	13:A:1433:A:O2'	2.28	0.51
13:A:409:U:O2'	13:A:410:G:P	2.68	0.51
13:A:710:G:H2'	13:A:711:G:C8	2.45	0.51
13:A:785:G:P	13:A:785:G:H8	2.33	0.51
13:A:1011:C:H2'	13:A:1012:A:C8	2.45	0.51
13:A:1055:A:C2	14:C:193:GLY:HA2	2.44	0.51
13:A:1065:U:H4'	13:A:1066:C:O5'	2.10	0.51
13:A:1221:G:OP1	20:S:35:ARG:NE	2.43	0.51
13:A:1251:A:H1'	13:A:1370:G:H4'	1.92	0.51
18:M:78:ARG:NH2	20:S:63:ASP:O	2.42	0.51
19:N:23:ARG:HH12	19:N:48:GLN:HG3	1.73	0.51
13:A:76:G:N2	13:A:93:U:O2	2.33	0.51
13:A:374:A:H5"	13:A:452:A:H2	1.74	0.51
13:A:461:A:O2'	13:A:467:U:OP1	2.16	0.51
13:A:496:A:H5'	13:A:497:G:OP2	2.10	0.51
13:A:554:A:H2'	13:A:555:U:C6	2.45	0.51
13:A:704:A:H2'	13:A:704:A:N3	2.25	0.51
13:A:1059:C:OP2	14:C:198:LYS:NZ	2.28	0.51
13:A:1166:G:N2	13:A:1169:A:OP2	2.44	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:1216:A:H2'	13:A:1217:C:C6	2.44	0.51
13:A:1313:U:H2'	13:A:1314:C:H6	1.75	0.51
13:A:1348:U:H4'	16:I:121:ARG:HD2	1.92	0.51
1:B:75:ALA:HA	1:B:78:ALA:HB3	1.92	0.51
1:B:135:MET:CG	1:B:138:ARG:HH21	2.14	0.51
13:A:123:U:H2'	13:A:124:C:C6	2.45	0.51
13:A:714:G:H1'	13:A:777:A:C8	2.45	0.51
13:A:783:C:H2'	13:A:784:A:H8	1.75	0.51
13:A:800:G:H2'	13:A:801:U:C5	2.45	0.51
14:C:107:LYS:HG2	14:C:110:LEU:HB2	1.92	0.51
2:D:123:MET:HG3	2:D:145:ARG:HG2	1.93	0.51
8:O:20:ASP:O	8:O:26:VAL:HG21	2.10	0.51
8:O:47:LYS:HZ3	13:A:669:G:H5'	1.75	0.51
13:A:381:C:H2'	13:A:382:A:O4'	2.11	0.51
13:A:1163:A:H2'	13:A:1164:G:H8	1.75	0.51
14:C:107:LYS:HG3	14:C:143:LEU:HD23	1.93	0.51
13:A:1250:A:H2	13:A:1370:G:H1'	1.74	0.51
13:A:1011:C:H2'	13:A:1012:A:H8	1.75	0.51
13:A:1048:G:H2'	13:A:1050:G:H8	1.76	0.51
13:A:1320:C:H4'	18:M:86:ARG:HH21	1.76	0.51
13:A:1467:C:H2'	13:A:1468:A:H8	1.76	0.51
13:A:1057:G:H5"	14:C:153:SER:HB3	1.92	0.51
13:A:1077:G:N2	13:A:1080:A:OP2	2.37	0.51
13:A:1250:A:N3	13:A:1370:G:O2'	2.31	0.51
14:C:146:LYS:O	14:C:146:LYS:HD2	2.11	0.51
2:D:74:TYR:OH	2:D:96:ARG:NH1	2.44	0.51
3:E:12:GLU:OE1	3:E:38:VAL:HG22	2.10	0.51
3:E:80:LEU:HD11	3:E:122:VAL:HG23	1.93	0.51
4:F:29:ILE:HG21	4:F:64:VAL:HG21	1.92	0.51
13:A:452:A:N6	13:A:480:U:C2	2.79	0.51
13:A:770:C:C4'	13:A:900:A:H61	2.17	0.51
13:A:982:U:O2	13:A:1222:G:C6	2.64	0.51
13:A:1373:G:H4'	15:G:30:MET:CE	2.40	0.51
13:A:1386:G:H2'	13:A:1387:G:C8	2.46	0.51
1:B:131:LYS:O	1:B:134:LEU:HG	2.10	0.51
1:B:216:VAL:HA	1:B:219:THR:HG22	1.93	0.51
2:D:123:MET:SD	2:D:145:ARG:HG2	2.51	0.51
4:F:1:MET:N	4:F:67:PRO:HA	2.26	0.51
5:H:107:LYS:HG2	5:H:120:LEU:HD11	1.93	0.51
13:A:771:G:C4'	21:A:1894:HOH:O	2.25	0.51
17:J:29:ALA:O	17:J:82:LYS:NZ	2.43	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:M:3:ILE:HD12	18:M:21:ILE:HD11	1.92	0.51
1:B:23:ASN:N	1:B:188:THR:O	2.31	0.51
2:D:84:ASN:OD1	2:D:87:GLU:HB3	2.11	0.51
3:E:157:GLY:C	3:E:158:LYS:HD3	2.31	0.51
4:F:2:ARG:NH1	4:F:68:GLN:OE1	2.44	0.51
13:A:613:C:H2'	13:A:614:C:C6	2.45	0.51
13:A:736:C:H2'	13:A:737:C:H6	1.76	0.51
13:A:952:U:H2'	13:A:953:G:H8	1.75	0.51
13:A:1278:G:H21	14:C:26:LYS:HE2	1.76	0.51
13:A:1409:C:H2'	13:A:1410:A:H8	1.76	0.51
6:K:25:SER:OG	6:K:28:ASN:O	2.23	0.50
13:A:999:C:N3	13:A:1042:A:N6	2.58	0.50
13:A:1071:C:H2'	13:A:1072:G:C8	2.44	0.50
1:B:126:ASP:OD1	1:B:127:LYS:N	2.44	0.50
3:E:28:ARG:NH1	3:E:30:PHE:CE1	2.79	0.50
11:R:22:TYR:HA	11:R:57:ALA:HB1	1.93	0.50
13:A:79:G:H2'	13:A:80:A:C8	2.47	0.50
13:A:868:C:H2'	13:A:869:G:O4'	2.11	0.50
13:A:1298:U:H5	15:G:111:GLY:HA2	1.74	0.50
13:A:1423:G:H1	13:A:1477:U:H3	1.58	0.50
13:A:1518:A:O2'	13:A:1519:A:O4'	2.30	0.50
3:E:61:LYS:O	3:E:65:LYS:HG2	2.10	0.50
6:K:36:ARG:HH22	6:K:82:GLU:HB2	1.77	0.50
8:O:41:HIS:O	8:O:44:GLU:HG3	2.11	0.50
13:A:502:A:H2'	13:A:503:C:O4'	2.11	0.50
13:A:1137:C:O2'	13:A:1138:G:H5"	2.12	0.50
18:M:79:LEU:HA	20:S:64:GLU:HB2	1.94	0.50
13:A:89:U:C2	13:A:90:C:C5	3.00	0.50
13:A:931:C:H2'	13:A:932:C:C6	2.46	0.50
13:A:978:A:N1	13:A:1316:G:N3	2.59	0.50
13:A:1181:G:H1'	13:A:1182:G:C8	2.47	0.50
13:A:1393:U:C2	13:A:1502:A:H5'	2.46	0.50
13:A:1467:C:H2'	13:A:1468:A:C8	2.46	0.50
3:E:56:PRO:O	3:E:60:GLN:HG2	2.12	0.50
4:F:37:HIS:HB2	4:F:97:THR:HG23	1.94	0.50
10:Q:47:ASP:N	10:Q:47:ASP:OD1	2.44	0.50
13:A:89:U:H2'	13:A:90:C:C6	2.47	0.50
13:A:1185:G:H2'	13:A:1186:G:H8	1.77	0.50
13:A:1359:C:H4'	13:A:1362:A:H62	1.76	0.50
19:N:49:THR:HG21	20:S:15:LEU:HD21	1.93	0.50
1:B:204:ASP:OD1	1:B:204:ASP:N	2.44	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:89:THR:HG23	13:A:864:A:H4'	1.93	0.50
6:K:21:HIS:CE1	13:A:706:A:H4'	2.47	0.50
13:A:945:G:H1	13:A:1236:A:N6	2.10	0.50
13:A:978:A:C8	13:A:979:C:H5	2.30	0.50
13:A:1149:C:H2'	13:A:1150:A:C8	2.41	0.50
18:M:56:ARG:HA	18:M:59:VAL:HG12	1.91	0.50
5:H:17:GLN:OE1	5:H:69:ALA:CB	2.59	0.50
6:K:13:LYS:NZ	6:K:35:ASP:OD2	2.45	0.50
14:C:134:LYS:HA	14:C:137:VAL:HB	1.93	0.50
3:E:28:ARG:HD2	13:A:1397:C:O2'	2.12	0.50
3:E:155:LYS:HA	5:H:65:PHE:CD1	2.47	0.50
13:A:1125:U:OP1	17:J:37:ARG:HD3	2.12	0.50
13:A:1144:G:N2	13:A:1146:A:H62	2.10	0.50
13:A:1267:C:O2'	13:A:1327:C:H4'	2.12	0.50
13:A:1508:A:H2'	13:A:1509:C:O4'	2.12	0.50
16:I:87:MET:HG2	16:I:94:ARG:CZ	2.41	0.50
5:H:47:ASP:OD1	5:H:48:PHE:O	2.29	0.50
11:R:61:ALA:O	11:R:65:SER:N	2.45	0.50
13:A:473:U:N3	13:A:474:G:C8	2.79	0.50
13:A:799:G:H2'	13:A:800:G:O4'	2.12	0.50
13:A:1119:C:H2'	13:A:1120:C:C6	2.47	0.50
7:L:100:ALA:C	7:L:101:LEU:HD12	2.32	0.49
11:R:36:GLY:O	11:R:62:ARG:NH1	2.44	0.49
13:A:782:A:H3'	13:A:783:C:H6	1.77	0.49
13:A:974:A:OP2	19:N:80:ARG:NE	2.45	0.49
13:A:1147:C:H4'	16:I:6:TYR:CE2	2.47	0.49
13:A:1279:G:OP1	17:J:9:ARG:NH2	2.44	0.49
13:A:1396:A:H3'	13:A:1397:C:C5	2.47	0.49
1:B:142:LYS:O	1:B:145:ASN:ND2	2.45	0.49
13:A:1119:C:H2'	13:A:1120:C:H6	1.77	0.49
13:A:1151:A:O2'	13:A:1152:A:O5'	2.27	0.49
13:A:1295:U:H2'	13:A:1296:C:C6	2.47	0.49
13:A:1375:A:H2'	13:A:1376:U:C6	2.47	0.49
18:M:25:GLY:O	18:M:29:SER:HB3	2.12	0.49
1:B:12:GLY:HA2	1:B:14:HIS:CE1	2.46	0.49
7:L:62:VAL:HG22	7:L:63:THR:H	1.76	0.49
8:O:9:LYS:HE3	8:O:10:ILE:CG1	2.42	0.49
9:P:8:ARG:NH1	13:A:391:G:C5'	2.75	0.49
13:A:769:G:H4'	13:A:1513:A:H4'	1.94	0.49
13:A:846:G:H3'	13:A:847:G:C8	2.47	0.49
13:A:965:U:H5"	13:A:966:G:OP1	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:1348:U:N3	13:A:1374:A:C8	2.76	0.49
14:C:67:ILE:HG22	14:C:69:THR:HG23	1.94	0.49
6:K:43:TRP:HD1	6:K:44:ALA:H	1.58	0.49
7:L:113:ARG:HD2	7:L:118:VAL:O	2.12	0.49
13:A:680:C:H2'	13:A:681:A:H8	1.77	0.49
13:A:1176:A:H2'	13:A:1177:G:C8	2.47	0.49
13:A:1250:A:C2	13:A:1370:G:H1'	2.48	0.49
13:A:1268:G:O2'	13:A:1326:U:O2'	2.03	0.49
14:C:35:ASP:OD1	14:C:58:ARG:NH2	2.45	0.49
1:B:59:ILE:HA	1:B:62:ARG:CZ	2.42	0.49
4:F:21:MET:SD	4:F:25:TYR:HE2	2.27	0.49
5:H:1:SER:HB3	5:H:8:ASP:OD2	2.13	0.49
13:A:96:U:H2'	13:A:97:G:C8	2.46	0.49
13:A:736:C:H2'	13:A:737:C:C6	2.48	0.49
13:A:829:G:O6	13:A:857:C:N4	2.35	0.49
13:A:837:U:O2	13:A:849:G:C6	2.65	0.49
13:A:982:U:C2	13:A:1222:G:O6	2.65	0.49
16:I:126:PHE:CZ	16:I:129:ARG:HG3	2.47	0.49
18:M:103:THR:HG22	18:M:104:ASN:N	2.26	0.49
2:D:172:VAL:HA	2:D:179:GLY:HA2	1.93	0.49
13:A:71:A:O2'	13:A:72:A:O5'	2.31	0.49
13:A:355:C:H2'	13:A:356:A:O4'	2.12	0.49
13:A:847:G:H2'	13:A:848:C:C6	2.47	0.49
13:A:942:G:H2'	13:A:943:U:C6	2.47	0.49
13:A:1435:G:H2'	13:A:1436:U:C6	2.48	0.49
13:A:1502:A:N7	13:A:1530:G:H4'	2.28	0.49
16:I:33:SER:OG	16:I:35:GLU:OE1	2.31	0.49
8:O:65:LEU:HD22	21:A:1938:HOH:O	2.11	0.49
13:A:77:A:H2'	13:A:78:A:O4'	2.13	0.49
13:A:943:U:H2'	13:A:944:G:C8	2.47	0.49
13:A:1000:A:H2'	13:A:1001:C:H6	1.77	0.49
13:A:1169:A:H2'	13:A:1170:A:C8	2.48	0.49
13:A:1198:G:H2'	13:A:1199:U:C6	2.48	0.49
13:A:1216:A:H5"	19:N:4:SER:OG	2.13	0.49
13:A:1375:A:HO2'	15:G:101:ARG:HH21	1.57	0.49
13:A:1392:G:H8	13:A:1392:G:O5'	1.95	0.49
7:L:66:ILE:CD1	7:L:73:LEU:HD22	2.43	0.49
13:A:519:C:H2'	13:A:520:A:O4'	2.12	0.49
13:A:1161:C:H2'	13:A:1162:C:H6	1.78	0.49
18:M:76:ILE:O	18:M:80:MET:HB3	2.13	0.49
7:L:50:LYS:N	7:L:50:LYS:HD2	2.28	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:56:U:H2'	13:A:57:G:C8	2.47	0.49
13:A:76:G:N1	13:A:93:U:N3	2.27	0.49
13:A:91:U:H2'	13:A:92:U:C6	2.48	0.49
13:A:517:G:O6	13:A:532:A:H8	1.96	0.49
13:A:655:A:H2'	13:A:656:G:O4'	2.12	0.49
13:A:1064:G:H1'	13:A:1190:G:H21	1.76	0.49
13:A:1133:G:H2'	13:A:1134:G:C8	2.47	0.49
13:A:1201:A:H1'	13:A:1202:U:OP2	2.13	0.49
13:A:1301:U:H2'	13:A:1303:C:C5	2.48	0.49
14:C:182:ASP:O	14:C:201:ILE:N	2.41	0.49
7:L:86:VAL:CG1	13:A:523:A:N6	2.76	0.49
13:A:1185:G:H2'	13:A:1186:G:C8	2.47	0.49
13:A:1317:C:O3'	19:N:48:GLN:NE2	2.45	0.49
16:I:6:TYR:HE1	16:I:17:ARG:HB3	1.77	0.49
2:D:8:LEU:HD11	2:D:21:LYS:HG2	1.94	0.48
2:D:150:LYS:HD2	2:D:150:LYS:C	2.32	0.48
14:C:128:MET:HG2	14:C:130:ARG:NH1	2.28	0.48
2:D:137:SER:N	2:D:140:ASP:OD1	2.45	0.48
3:E:28:ARG:NH2	13:A:15:G:O2'	2.42	0.48
3:E:79:THR:HB	3:E:121:ASN:HB2	1.94	0.48
13:A:204:G:H2'	13:A:205:A:O4'	2.13	0.48
13:A:398:U:H2'	13:A:399:G:C8	2.48	0.48
13:A:1137:C:H1'	13:A:1138:G:C2	2.47	0.48
13:A:1229:A:P	18:M:112:ARG:HH21	2.36	0.48
14:C:76:ILE:HD13	14:C:83:VAL:HG21	1.94	0.48
14:C:119:ILE:O	14:C:123:LEU:HB2	2.13	0.48
13:A:555:U:H2'	13:A:556:C:C6	2.48	0.48
13:A:636:U:H2'	13:A:637:C:C6	2.48	0.48
13:A:1423:G:H2'	13:A:1424:U:C6	2.47	0.48
13:A:1434:A:H3'	13:A:1435:G:H8	1.79	0.48
14:C:109:GLU:HG3	14:C:139:ASN:HB3	1.94	0.48
18:M:86:ARG:HG2	18:M:90:HIS:CE1	2.49	0.48
1:B:133:ALA:HA	1:B:136:ARG:HE	1.78	0.48
2:D:94:GLU:HA	2:D:99:ASN:ND2	2.28	0.48
2:D:96:ARG:HG3	2:D:133:SER:HA	1.95	0.48
13:A:20:U:H2'	13:A:21:G:O4'	2.13	0.48
13:A:189:A:H2'	13:A:190:A:C8	2.49	0.48
13:A:204:G:C4	13:A:205:A:C8	3.01	0.48
13:A:712:A:C2	13:A:713:G:N2	2.82	0.48
13:A:925:G:H1'	13:A:1392:G:O6	2.13	0.48
13:A:1297:G:N2	15:G:113:LYS:HG3	2.28	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C:185:THR:HG22	14:C:198:LYS:HG2	1.95	0.48
16:I:23:GLY:O	16:I:61:ASP:HB2	2.14	0.48
17:J:77:VAL:HG13	17:J:78:GLU:OE1	2.13	0.48
1:B:114:LYS:HD2	1:B:151:LYS:HD2	1.96	0.48
13:A:714:G:C5	13:A:715:A:C6	3.01	0.48
13:A:786:G:C5	13:A:787:A:N6	2.81	0.48
13:A:996:A:H2'	13:A:997:U:H6	1.78	0.48
13:A:1485:U:H2'	13:A:1486:G:C8	2.48	0.48
14:C:131:ARG:O	14:C:135:ARG:HG2	2.13	0.48
7:L:89:LEU:HD12	7:L:89:LEU:C	2.32	0.48
13:A:679:C:H2'	13:A:680:C:H6	1.76	0.48
13:A:946:A:H1'	13:A:1334:G:H4'	1.96	0.48
13:A:948:C:OP1	18:M:106:ARG:N	2.45	0.48
13:A:1091:U:C2	13:A:1095:U:C4	3.02	0.48
13:A:1238:A:N7	13:A:1303:C:H1'	2.28	0.48
13:A:1464:U:O4	13:A:1465:A:N6	2.46	0.48
13:A:1527:U:O2'	13:A:1528:U:H5'	2.13	0.48
18:M:18:LEU:HG	18:M:33:LEU:HD21	1.96	0.48
1:B:221:ARG:HH11	1:B:224:ARG:HH12	1.61	0.48
4:F:72:ASP:O	4:F:75:GLU:HG3	2.14	0.48
13:A:37:U:O2'	13:A:500:G:H4'	2.14	0.48
13:A:161:A:H2'	13:A:162:A:C8	2.49	0.48
13:A:409:U:O2'	13:A:410:G:C8	2.67	0.48
13:A:459:A:P	13:A:474:G:H22	2.37	0.48
13:A:757:U:H2'	13:A:758:C:O4'	2.13	0.48
13:A:827:U:H2'	13:A:870:U:O4	2.14	0.48
13:A:1228:C:H41	18:M:102:LYS:HG2	1.78	0.48
13:A:1360:A:C8	19:N:57:SER:HA	2.48	0.48
13:A:1380:U:O2	13:A:1382:C:N4	2.45	0.48
18:M:66:GLY:HA2	18:M:70:ARG:NH2	2.29	0.48
13:A:741:G:H2'	13:A:742:G:O4'	2.13	0.48
13:A:1124:G:H1'	13:A:1125:U:H5	1.79	0.48
13:A:1258:G:H2'	13:A:1259:C:C6	2.48	0.48
1:B:32:GLY:HA3	1:B:34:ARG:HH22	1.79	0.48
1:B:81:ASP:N	1:B:81:ASP:OD1	2.45	0.48
1:B:163:ILE:HA	1:B:185:ILE:HD13	1.96	0.48
7:L:86:VAL:C	7:L:88:ASP:H	2.16	0.48
8:O:73:ASP:OD2	8:O:76:ARG:NH1	2.47	0.48
13:A:62:U:H2'	13:A:63:C:C6	2.48	0.48
13:A:146:G:H8	21:A:2069:HOH:O	1.97	0.48
13:A:202:G:H21	13:A:465:A:N6	2.12	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:524:G:H2'	13:A:525:C:C6	2.48	0.48
13:A:1375:A:O2'	15:G:101:ARG:NH2	2.26	0.48
13:A:1524:C:H2'	13:A:1525:G:C8	2.49	0.48
17:J:7:ARG:HD3	17:J:73:LEU:HD11	1.95	0.48
19:N:68:ARG:HH22	19:N:80:ARG:HH21	1.61	0.48
1:B:86:CYS:HB3	1:B:217:ALA:HB1	1.95	0.48
2:D:195:ASN:OD1	2:D:195:ASN:C	2.51	0.48
6:K:28:ASN:OD1	6:K:46:ALA:HB3	2.14	0.48
13:A:119:A:C2	21:A:1608:HOH:O	2.67	0.48
13:A:212:G:N3	13:A:213:G:C8	2.82	0.48
13:A:452:A:N6	13:A:480:U:H3	2.11	0.48
13:A:481:G:O2'	13:A:483:C:N4	2.47	0.48
13:A:608:A:H2'	13:A:609:A:O4'	2.14	0.48
13:A:1122:U:H2'	13:A:1123:U:C6	2.49	0.48
4:F:1:MET:H1	4:F:67:PRO:HA	1.78	0.47
5:H:111:THR:HG23	5:H:114:ALA:H	1.78	0.47
13:A:1520:C:H2'	13:A:1521:C:H6	1.79	0.47
14:C:146:LYS:HE3	14:C:204:GLY:HA2	1.96	0.47
2:D:137:SER:O	2:D:140:ASP:OD1	2.31	0.47
3:E:111:ARG:NH2	13:A:8:A:C6	2.82	0.47
4:F:1:MET:SD	4:F:67:PRO:HG3	2.54	0.47
9:P:31:ARG:HB2	13:A:310:G:H5"	1.95	0.47
13:A:160:A:H2'	13:A:161:A:O4'	2.13	0.47
13:A:631:C:H3'	13:A:632:U:H5'	1.96	0.47
13:A:1160:G:C6	13:A:1161:C:C4	3.01	0.47
13:A:1191:A:H2'	13:A:1192:C:H6	1.78	0.47
19:N:15:LEU:HG	19:N:18:LYS:HE3	1.96	0.47
2:D:33:ILE:HG13	2:D:34:GLU:N	2.29	0.47
4:F:6:ILE:CG1	4:F:62:MET:SD	3.02	0.47
8:O:47:LYS:NZ	13:A:669:G:P	2.87	0.47
13:A:441:A:H61	13:A:493:A:N6	2.12	0.47
13:A:962:C:H2'	13:A:963:G:C8	2.49	0.47
13:A:1380:U:H4'	13:A:1381:U:H5'	1.96	0.47
1:B:108:GLN:HA	1:B:111:LYS:NZ	2.29	0.47
5:H:55:LYS:NZ	13:A:653:U:O5'	2.36	0.47
13:A:334:C:HO2'	13:A:335:C:H6	1.61	0.47
13:A:685:G:H2'	13:A:686:U:C6	2.49	0.47
13:A:1314:C:H2'	13:A:1315:U:C6	2.49	0.47
1:B:18:GLN:NE2	1:B:21:TYR:HB2	2.29	0.47
1:B:58:LYS:O	1:B:61:SER:OG	2.27	0.47
2:D:165:GLU:OE2	2:D:166:LYS:N	2.47	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:T:80:ALA:O	12:T:84:LYS:HG2	2.13	0.47
13:A:172:A:O2'	13:A:173:U:H5'	2.15	0.47
13:A:334:C:O2'	13:A:335:C:P	2.73	0.47
13:A:1019:A:H2'	13:A:1020:G:O4'	2.14	0.47
13:A:1156:G:O2'	13:A:1180:A:N6	2.47	0.47
13:A:1278:G:H5"	13:A:1279:G:O4'	2.14	0.47
13:A:1484:C:H2'	13:A:1485:U:O4'	2.15	0.47
1:B:110:ILE:HG13	1:B:111:LYS:N	2.30	0.47
7:L:66:ILE:HD11	7:L:73:LEU:HD22	1.97	0.47
8:O:42:PHE:HB3	8:O:52:ARG:NH2	2.30	0.47
11:R:32:ILE:HG22	11:R:33:THR:N	2.29	0.47
13:A:703:G:C4'	13:A:704:A:H8	2.26	0.47
13:A:778:G:C5	13:A:779:C:C4	3.03	0.47
13:A:898:G:H2'	13:A:900:A:OP2	2.15	0.47
13:A:921:U:C2'	13:A:922:G:H5'	2.44	0.47
13:A:947:G:H2'	13:A:948:C:C6	2.48	0.47
13:A:1287:A:H1'	13:A:1353:G:O2'	2.15	0.47
14:C:115:VAL:HG12	14:C:199:VAL:HG11	1.95	0.47
1:B:20:ARG:HA	1:B:38:HIS:NE2	2.29	0.47
1:B:76:SER:HB3	1:B:93:HIS:CE1	2.49	0.47
4:F:90:MET:HG3	4:F:91:ARG:N	2.30	0.47
7:L:63:THR:HG22	7:L:92:VAL:HG22	1.96	0.47
8:O:9:LYS:HZ1	8:O:10:ILE:HD11	1.80	0.47
8:O:27:GLN:O	8:O:31:LEU:HD23	2.14	0.47
11:R:33:THR:HG22	11:R:37:LYS:H	1.79	0.47
13:A:49:U:C2	13:A:361:G:N2	2.82	0.47
13:A:113:G:H21	13:A:353:A:H8	1.62	0.47
13:A:208:U:O2'	13:A:211:G:O6	2.21	0.47
13:A:251:G:C8	13:A:266:G:C4	3.03	0.47
13:A:703:G:H4'	13:A:704:A:C8	2.45	0.47
13:A:1271:A:C2	13:A:1272:G:C5	3.03	0.47
13:A:1321:U:H2'	13:A:1322:C:C2	2.50	0.47
13:A:1385:G:H2'	13:A:1386:G:C8	2.50	0.47
20:S:50:VAL:HG21	20:S:70:LEU:HD21	1.97	0.47
2:D:56:GLU:OE2	2:D:199:ILE:N	2.48	0.47
2:D:106:PHE:CG	2:D:144:ILE:HD11	2.50	0.47
7:L:43:LYS:N	7:L:44:PRO:HD2	2.30	0.47
13:A:649:A:H2'	13:A:650:G:O4'	2.15	0.47
13:A:964:A:H1'	17:J:57:VAL:HG21	1.95	0.47
13:A:1048:G:H2'	13:A:1050:G:C8	2.50	0.47
13:A:1131:G:P	16:I:4:GLN:HE22	2.38	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:1164:G:H2'	13:A:1165:U:H6	1.79	0.47
17:J:26:VAL:HG13	17:J:36:VAL:HG11	1.97	0.47
19:N:88:MET:HE1	19:N:95:LEU:CD2	2.43	0.47
1:B:98:GLY:N	1:B:174:GLU:OE2	2.40	0.47
10:Q:18:LYS:HE2	13:A:255:G:H4'	1.97	0.47
13:A:123:U:H2'	13:A:124:C:H6	1.80	0.47
13:A:383:A:C5	13:A:384:G:H1'	2.50	0.47
13:A:398:U:H2'	13:A:399:G:H8	1.80	0.47
13:A:1023:U:H2'	13:A:1024:G:C8	2.50	0.47
13:A:1090:U:H2'	13:A:1091:U:H6	1.79	0.47
13:A:1288:A:H2'	13:A:1289:A:O4'	2.15	0.47
13:A:1326:U:C2	13:A:1327:C:C5	3.03	0.47
13:A:1385:G:H2'	13:A:1386:G:H8	1.80	0.47
1:B:207:ARG:HD2	1:B:208:ALA:N	2.30	0.47
13:A:76:G:O6	13:A:93:U:C4	2.68	0.47
13:A:948:C:H3'	18:M:104:ASN:HB3	1.96	0.47
13:A:1091:U:O2'	13:A:1093:A:N7	2.40	0.47
13:A:1127:G:H22	13:A:1145:A:H2	1.61	0.47
6:K:79:LYS:O	6:K:104:PHE:HA	2.15	0.46
7:L:24:GLU:OE2	7:L:60:PHE:HE2	1.98	0.46
13:A:1341:U:H5"	16:I:129:ARG:HH22	1.80	0.46
13:A:1485:U:H3'	13:A:1486:G:H2'	1.98	0.46
14:C:155:ARG:H	14:C:162:ALA:HA	1.80	0.46
16:I:56:MET:HG3	16:I:57:VAL:H	1.79	0.46
17:J:33:GLY:O	17:J:80:THR:OG1	2.23	0.46
18:M:3:ILE:HA	18:M:56:ARG:CZ	2.45	0.46
2:D:50:TYR:CZ	2:D:54:LEU:HD12	2.50	0.46
6:K:51:PHE:HE2	6:K:56:LYS:HG3	1.80	0.46
11:R:25:ILE:HD11	11:R:67:LEU:HD21	1.97	0.46
12:T:75:LYS:O	12:T:79:THR:HG23	2.15	0.46
13:A:464:U:C2	13:A:466:A:OP1	2.68	0.46
13:A:691:G:H1'	13:A:696:A:N6	2.30	0.46
13:A:958:A:N3	13:A:985:C:O2'	2.38	0.46
13:A:958:A:H1'	13:A:985:C:O2'	2.15	0.46
13:A:1357:A:N1	13:A:1365:G:N2	2.55	0.46
2:D:60:VAL:HG21	2:D:199:ILE:HD11	1.96	0.46
3:E:28:ARG:NH1	3:E:30:PHE:CZ	2.84	0.46
13:A:715:A:C8	13:A:716:A:C8	3.03	0.46
13:A:745:G:H5'	13:A:851:G:H21	1.79	0.46
13:A:1237:C:H3'	13:A:1336:C:H41	1.81	0.46
14:C:138:GLN:O	14:C:142:ARG:NH1	2.48	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:I:39:GLY:HA2	16:I:44:ARG:CB	2.43	0.46
16:I:115:VAL:HG11	17:J:62:ARG:HB2	1.97	0.46
1:B:48:MET:HG3	1:B:199:ILE:HG23	1.96	0.46
1:B:144:GLU:HA	1:B:147:LEU:CB	2.42	0.46
5:H:91:LEU:HB3	5:H:112:ASP:OD1	2.15	0.46
11:R:59:LYS:NZ	13:A:734:G:O3'	2.34	0.46
12:T:83:ASN:HD22	12:T:83:ASN:N	2.13	0.46
13:A:462:G:P	13:A:462:G:C8	3.09	0.46
13:A:674:G:N3	13:A:675:A:C8	2.83	0.46
13:A:864:A:H2'	13:A:865:A:C8	2.50	0.46
14:C:182:ASP:OD2	14:C:203:LYS:NZ	2.47	0.46
16:I:93:LEU:HD23	16:I:93:LEU:H	1.80	0.46
18:M:53:ASP:OD1	18:M:54:THR:N	2.49	0.46
1:B:87:ASP:OD1	1:B:221:ARG:NH2	2.45	0.46
5:H:78:SER:OG	5:H:83:ARG:HA	2.16	0.46
7:L:54:VAL:O	7:L:61:GLU:OE1	2.34	0.46
7:L:85:ARG:HA	7:L:93:ARG:HA	1.96	0.46
9:P:76:LYS:O	9:P:80:LYS:HG2	2.15	0.46
13:A:91:U:H2'	13:A:92:U:H6	1.80	0.46
13:A:346:G:N3	13:A:346:G:H5"	2.31	0.46
13:A:475:C:H2'	13:A:476:U:C6	2.51	0.46
13:A:938:A:N3	13:A:1376:U:O2'	2.37	0.46
13:A:1003:G:N2	13:A:1005:A:O5'	2.48	0.46
13:A:1321:U:O2'	20:S:77:ARG:NH2	2.49	0.46
15:G:39:GLU:O	15:G:43:TYR:HB2	2.15	0.46
1:B:63:LYS:HG2	1:B:224:ARG:HD2	1.98	0.46
1:B:98:GLY:O	1:B:102:ASN:HB3	2.15	0.46
2:D:39:GLN:OE1	2:D:40:HIS:NE2	2.48	0.46
7:L:34:THR:OG1	7:L:53:ARG:O	2.24	0.46
10:Q:45:VAL:HG21	10:Q:60:ILE:HG21	1.97	0.46
11:R:32:ILE:HG22	11:R:33:THR:O	2.16	0.46
13:A:84:U:H3'	13:A:85:U:O2	2.16	0.46
13:A:266:G:O2'	13:A:267:C:O5'	2.34	0.46
13:A:1107:C:C4	13:A:1108:G:C8	3.03	0.46
17:J:53:ILE:HG13	17:J:63:ASP:H	1.81	0.46
1:B:48:MET:N	1:B:48:MET:SD	2.88	0.46
5:H:86:LYS:HB2	5:H:91:LEU:HD23	1.98	0.46
6:K:22:ILE:HA	6:K:31:VAL:HG22	1.98	0.46
13:A:1272:G:H2'	13:A:1273:C:C6	2.50	0.46
13:A:1370:G:H2'	13:A:1371:G:H8	1.81	0.46
16:I:79:ARG:O	16:I:83:THR:HG23	2.14	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:M:86:ARG:HG2	18:M:90:HIS:HE1	1.81	0.46
4:F:10:VAL:HG11	4:F:18:VAL:HG22	1.98	0.46
4:F:85:ILE:HG22	4:F:86:ARG:HG3	1.97	0.46
5:H:25:THR:HG22	5:H:59:GLU:OE1	2.16	0.46
6:K:56:LYS:HG2	6:K:57:SER:H	1.81	0.46
13:A:978:A:N1	13:A:1316:G:C2	2.84	0.46
13:A:1074:G:O2'	13:A:1101:A:N1	2.37	0.46
13:A:1130:A:H61	13:A:1144:G:H1'	1.80	0.46
13:A:1340:A:H2'	13:A:1341:U:O4'	2.15	0.46
13:A:1369:C:H2'	13:A:1370:G:C8	2.50	0.46
1:B:94:ARG:HD3	13:A:1099:G:O5'	2.16	0.46
2:D:9:LYS:NZ	13:A:428:G:OP2	2.45	0.46
2:D:151:GLN:HB3	2:D:154:VAL:HG22	1.96	0.46
5:H:82:LEU:CD2	7:L:3:VAL:HG21	2.43	0.46
13:A:767:A:H2'	13:A:768:A:O4'	2.15	0.46
13:A:1026:G:C2	13:A:1027:C:C5	3.04	0.46
13:A:1396:A:H5"	13:A:1397:C:OP2	2.16	0.46
1:B:173:LYS:NZ	13:A:1076:U:OP1	2.38	0.46
2:D:8:LEU:O	2:D:11:SER:OG	2.30	0.46
7:L:98:ARG:NH1	7:L:106:VAL:HG12	2.31	0.46
13:A:182:A:H1'	13:A:183:C:C6	2.51	0.46
13:A:689:C:H2'	13:A:690:G:O4'	2.16	0.46
13:A:712:A:C5	13:A:713:G:N1	2.84	0.46
13:A:1236:A:H2'	13:A:1237:C:C6	2.51	0.46
13:A:1321:U:H5"	13:A:1322:C:OP2	2.16	0.46
13:A:1507:A:HO2'	13:A:1508:A:P	2.38	0.46
17:J:7:ARG:NE	17:J:75:ASP:OD2	2.35	0.46
18:M:52:ILE:O	18:M:56:ARG:HG2	2.16	0.46
19:N:62:ARG:NH1	19:N:67:GLY:O	2.49	0.46
20:S:28:LYS:HG2	20:S:29:PRO:HD2	1.97	0.46
1:B:82:ALA:HB2	1:B:213:LEU:HB3	1.97	0.45
2:D:75:TYR:HE1	2:D:200:VAL:HG23	1.80	0.45
4:F:3:HIS:HB2	4:F:92:THR:CB	2.44	0.45
13:A:1213:A:H2'	13:A:1215:G:C8	2.52	0.45
13:A:1329:A:P	18:M:25:GLY:H	2.35	0.45
1:B:131:LYS:NZ	13:A:1157:A:OP2	2.44	0.45
3:E:40:ASP:C	3:E:42:ASN:H	2.19	0.45
13:A:1390:U:H2'	13:A:1391:U:C6	2.51	0.45
15:G:26:VAL:HG12	15:G:42:VAL:HG11	1.98	0.45
17:J:12:ALA:HB2	17:J:96:VAL:HG22	1.99	0.45
5:H:49:LYS:HG2	5:H:59:GLU:HB3	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:P:42:ILE:O	9:P:42:ILE:HG13	2.16	0.45
13:A:934:C:O2	13:A:938:A:N6	2.49	0.45
13:A:978:A:H61	13:A:1316:G:H1'	1.81	0.45
13:A:1387:G:H2'	13:A:1388:C:C6	2.52	0.45
13:A:1431:A:HO2'	13:A:1432:G:C5'	2.28	0.45
1:B:122:ASP:HA	1:B:125:PHE:CD2	2.52	0.45
4:F:2:ARG:HE	4:F:91:ARG:NH2	2.15	0.45
13:A:15:G:OP1	13:A:1397:C:N4	2.49	0.45
13:A:264:C:N4	21:A:1609:HOH:O	2.42	0.45
13:A:666:G:H5'	13:A:726:C:H1'	1.99	0.45
13:A:675:A:C4	13:A:676:A:C8	3.04	0.45
13:A:785:G:H8	13:A:785:G:OP1	1.99	0.45
13:A:791:G:H2'	13:A:792:A:H5'	1.98	0.45
13:A:846:G:H2'	13:A:846:G:N3	2.32	0.45
13:A:1304:G:C2	13:A:1333:A:N6	2.84	0.45
13:A:1341:U:H4'	16:I:129:ARG:HH12	1.81	0.45
13:A:1434:A:H3'	13:A:1435:G:C8	2.52	0.45
3:E:40:ASP:O	3:E:42:ASN:N	2.48	0.45
7:L:2:THR:HB	7:L:5:GLN:HG3	1.98	0.45
13:A:159:G:H1'	13:A:162:A:N6	2.31	0.45
13:A:201:G:H1	13:A:216:U:H3	1.64	0.45
13:A:676:A:C6	13:A:677:U:C4	3.04	0.45
13:A:927:G:N2	13:A:1390:U:H3	2.14	0.45
13:A:1130:A:O3'	16:I:4:GLN:NE2	2.44	0.45
13:A:1395:C:H2'	13:A:1396:A:C8	2.51	0.45
14:C:111:ASP:HB3	14:C:114:LEU:HB2	1.98	0.45
20:S:12:LEU:HD21	20:S:16:LYS:HD2	1.97	0.45
1:B:82:ALA:CB	1:B:213:LEU:HB3	2.47	0.45
3:E:93:VAL:HB	3:E:110:MET:CE	2.46	0.45
13:A:438:U:O2'	13:A:494:G:O6	2.15	0.45
13:A:520:A:H2'	13:A:521:G:O4'	2.17	0.45
13:A:1014:A:C2	13:A:1219:A:H1'	2.52	0.45
13:A:1168:U:O2'	13:A:1169:A:H5'	2.17	0.45
13:A:1478:U:O2'	13:A:1479:C:OP1	2.33	0.45
14:C:18:ASN:O	14:C:55:VAL:HA	2.17	0.45
2:D:116:LEU:HD11	2:D:154:VAL:HG12	1.97	0.45
3:E:113:VAL:CG2	3:E:136:VAL:HG23	2.47	0.45
13:A:984:C:H2'	13:A:985:C:H6	1.81	0.45
13:A:993:G:H2'	13:A:995:C:H41	1.81	0.45
13:A:1203:C:H2'	13:A:1204:A:H8	1.82	0.45
13:A:1299:A:H62	13:A:1302:C:H41	1.64	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:J:20:GLN:OE1	17:J:20:GLN:N	2.49	0.45
2:D:38:GLY:HA3	13:A:542:G:H5'	1.97	0.45
5:H:37:ASN:ND2	5:H:48:PHE:HZ	2.14	0.45
13:A:40:C:H2'	13:A:41:G:O4'	2.15	0.45
13:A:1234:C:H2'	13:A:1235:U:C6	2.52	0.45
13:A:1422:G:H2'	13:A:1423:G:C8	2.52	0.45
2:D:39:GLN:OE1	2:D:40:HIS:CE1	2.70	0.45
8:O:26:VAL:O	8:O:30:LEU:HD13	2.16	0.45
13:A:450:G:H5"	13:A:451:A:H5"	1.97	0.45
13:A:859:G:H2'	13:A:860:A:C8	2.51	0.45
13:A:983:A:O2'	13:A:1049:U:O3'	2.35	0.45
13:A:1088:G:N2	13:A:1167:A:H61	2.00	0.45
1:B:56:LEU:HA	1:B:59:ILE:HG12	1.98	0.45
4:F:53:LYS:HD3	4:F:53:LYS:HA	1.87	0.45
10:Q:4:ILE:HG23	10:Q:5:ARG:H	1.82	0.45
13:A:212:G:C4	13:A:213:G:C8	3.05	0.45
13:A:343:U:O3'	13:A:344:A:H8	1.99	0.45
13:A:846:G:C2	13:A:847:G:C5	3.05	0.45
13:A:924:C:H3'	13:A:925:G:C8	2.43	0.45
13:A:928:G:C6	13:A:1390:U:C5	3.05	0.45
13:A:1038:C:H2'	13:A:1039:G:H8	1.81	0.45
13:A:1125:U:OP2	13:A:1145:A:N6	2.50	0.45
14:C:85:LYS:O	14:C:89:VAL:HG23	2.16	0.45
18:M:68:LEU:O	18:M:72:ILE:HG12	2.17	0.45
18:M:89:ARG:HD2	18:M:95:PRO:O	2.17	0.45
19:N:50:LEU:HA	20:S:12:LEU:HD12	1.99	0.45
1:B:22:TRP:CZ3	1:B:24:PRO:HA	2.52	0.44
2:D:176:LYS:O	2:D:176:LYS:HG3	2.17	0.44
13:A:244:U:O4	13:A:906:A:H1'	2.17	0.44
13:A:321:A:N6	13:A:329:A:OP2	2.50	0.44
13:A:1305:G:HO2'	13:A:1306:A:H8	1.64	0.44
13:A:1386:G:H2'	13:A:1387:G:H8	1.82	0.44
14:C:165:GLU:HB2	14:C:167:TYR:CE1	2.52	0.44
14:C:187:GLU:HA	14:C:196:GLY:HA2	1.98	0.44
16:I:122:ARG:NH1	16:I:123:ARG:O	2.50	0.44
17:J:19:ASP:HA	17:J:22:THR:HG22	1.98	0.44
18:M:43:LYS:HD3	18:M:43:LYS:HA	1.73	0.44
4:F:79:ARG:NH2	13:A:671:G:H4'	2.32	0.44
5:H:29:SER:HB2	21:A:1819:HOH:O	2.18	0.44
13:A:771:G:C5'	21:A:1894:HOH:O	2.61	0.44
13:A:860:A:H2'	13:A:861:G:O4'	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:1329:A:H4'	18:M:23:GLY:O	2.17	0.44
13:A:1338:G:H2'	13:A:1339:A:C4	2.52	0.44
16:I:43:ALA:HA	16:I:46:VAL:CG1	2.46	0.44
3:E:152:VAL:HA	3:E:155:LYS:HG2	1.99	0.44
5:H:37:ASN:O	5:H:41:GLU:HG2	2.17	0.44
8:O:22:GLY:HA2	13:A:657:U:H1'	1.99	0.44
12:T:68:LYS:HG3	21:T:108:HOH:O	2.17	0.44
13:A:325:A:H2'	13:A:326:G:O4'	2.17	0.44
13:A:501:C:H2'	13:A:502:A:C8	2.52	0.44
13:A:783:C:C2	13:A:784:A:C8	3.05	0.44
13:A:789:U:N3	13:A:791:G:H5"	2.33	0.44
13:A:1106:G:H2'	13:A:1107:C:C6	2.52	0.44
13:A:1216:A:H2'	13:A:1217:C:H6	1.81	0.44
13:A:1326:U:H2'	13:A:1327:C:C5	2.53	0.44
13:A:1329:A:OP1	18:M:25:GLY:N	2.34	0.44
13:A:1396:A:H2'	13:A:1397:C:O2	2.18	0.44
15:G:110:ARG:HH12	15:G:122:GLU:HG3	1.81	0.44
1:B:48:MET:HE2	1:B:200:PRO:HD2	1.99	0.44
13:A:251:G:C6	13:A:266:G:N2	2.85	0.44
13:A:1251:A:H61	13:A:1354:U:HO2'	1.64	0.44
13:A:1356:G:C2	13:A:1357:A:C5	3.05	0.44
19:N:2:LYS:HB2	19:N:5:MET:HG2	1.99	0.44
20:S:39:ILE:HD11	20:S:70:LEU:HB2	1.99	0.44
1:B:69:VAL:CG2	1:B:162:VAL:HG23	2.47	0.44
2:D:197:HIS:HA	2:D:200:VAL:HG12	1.99	0.44
3:E:45:VAL:HB	3:E:117:ALA:HB2	1.99	0.44
10:Q:46:HIS:HB2	10:Q:70:LYS:HE2	2.00	0.44
13:A:83:C:H4'	13:A:84:U:C5	2.51	0.44
13:A:89:U:H2'	13:A:90:C:H6	1.82	0.44
13:A:182:A:N1	13:A:194:C:N3	2.64	0.44
13:A:700:G:H4'	13:A:704:A:C1'	2.47	0.44
13:A:705:G:H2'	13:A:706:A:C8	2.52	0.44
13:A:1206:G:H2'	13:A:1207:G:C8	2.53	0.44
13:A:1377:A:N1	15:G:6:ILE:HD11	2.31	0.44
13:A:1434:A:H5'	13:A:1435:G:OP2	2.17	0.44
18:M:70:ARG:HA	18:M:73:SER:HB3	2.00	0.44
1:B:67:LEU:HD13	1:B:89:PHE:HB3	1.98	0.44
2:D:189:ASP:OD1	2:D:189:ASP:N	2.41	0.44
5:H:6:ILE:O	5:H:10:LEU:HG	2.18	0.44
8:O:47:LYS:NZ	13:A:668:G:O3'	2.51	0.44
10:Q:75:VAL:HG12	10:Q:76:ARG:HG3	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:500:G:H2'	13:A:501:C:C6	2.52	0.44
13:A:786:G:C5	13:A:787:A:C6	3.06	0.44
17:J:54:SER:HB3	17:J:58:ASN:O	2.18	0.44
18:M:76:ILE:HA	18:M:80:MET:HB3	2.00	0.44
20:S:32:THR:HB	20:S:50:VAL:HG22	1.99	0.44
1:B:218:ALA:O	1:B:222:GLU:OE1	2.36	0.44
10:Q:51:GLU:OE1	10:Q:77:VAL:CG2	2.66	0.44
13:A:50:A:O2'	13:A:360:G:N2	2.50	0.44
13:A:472:U:H2'	13:A:473:U:O4'	2.17	0.44
13:A:687:A:N6	13:A:703:G:C2	2.82	0.44
13:A:1330:U:H5"	13:A:1331:G:C8	2.53	0.44
13:A:1349:A:OP2	16:I:119:LYS:NZ	2.47	0.44
15:G:15:PRO:HB3	16:I:49:GLN:HE22	1.81	0.44
17:J:42:LEU:HB2	17:J:71:LEU:HG	1.98	0.44
17:J:56:HIS:CE1	17:J:57:VAL:HG23	2.53	0.44
18:M:105:ALA:O	18:M:109:LYS:HB3	2.18	0.44
19:N:15:LEU:HD23	19:N:54:SER:HB2	1.99	0.44
20:S:4:LEU:HD12	20:S:6:LYS:N	2.32	0.44
4:F:29:ILE:HD13	4:F:64:VAL:HG11	1.99	0.44
13:A:441:A:H61	13:A:493:A:H61	1.65	0.44
13:A:466:A:H3'	13:A:467:U:H6	1.83	0.44
13:A:958:A:N6	20:S:54:ARG:HG3	2.33	0.44
17:J:22:THR:O	17:J:26:VAL:HG23	2.17	0.44
18:M:33:LEU:HB3	18:M:38:ILE:HG21	2.00	0.44
18:M:72:ILE:O	18:M:75:SER:OG	2.28	0.44
2:D:158:LEU:O	2:D:161:ALA:HB3	2.18	0.44
3:E:156:ARG:HA	5:H:63:LYS:HZ1	1.82	0.44
8:O:44:GLU:OE1	8:O:45:HIS:CE1	2.70	0.44
10:Q:51:GLU:O	10:Q:51:GLU:CD	2.57	0.44
12:T:3:ILE:O	12:T:7:LYS:HG3	2.17	0.44
13:A:139:A:H2'	13:A:140:U:C6	2.53	0.44
13:A:713:G:C4	13:A:714:G:N1	2.85	0.44
13:A:1004:A:C5	13:A:1026:G:C8	3.06	0.44
13:A:1077:G:N1	13:A:1080:A:OP2	2.47	0.44
13:A:1487:G:H1'	13:A:1488:G:N7	2.33	0.44
14:C:31:ASN:O	14:C:58:ARG:NH2	2.51	0.44
15:G:30:MET:HE2	15:G:33:GLY:HA2	2.00	0.44
2:D:115:GLN:HG3	2:D:153:ARG:HH22	1.83	0.43
13:A:212:G:C2	13:A:213:G:C8	3.06	0.43
13:A:462:G:C8	13:A:462:G:OP1	2.71	0.43
13:A:473:U:C2	13:A:474:G:C8	3.06	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:592:G:H2'	13:A:593:U:O4'	2.18	0.43
13:A:696:A:H2'	13:A:697:U:O4'	2.18	0.43
13:A:939:G:H2'	13:A:940:C:H6	1.82	0.43
1:B:32:GLY:O	1:B:34:ARG:NH1	2.52	0.43
2:D:56:GLU:O	2:D:60:VAL:HG23	2.18	0.43
6:K:31:VAL:HB	6:K:69:CYS:SG	2.58	0.43
6:K:59:PRO:HA	6:K:91:GLY:HA3	1.99	0.43
13:A:71:A:O2'	13:A:72:A:O4'	2.26	0.43
13:A:205:A:H2'	13:A:206:C:H6	1.83	0.43
13:A:530:G:H5"	13:A:531:U:H5"	2.00	0.43
13:A:702:A:H8	13:A:702:A:OP1	2.01	0.43
13:A:706:A:H2'	13:A:707:U:C6	2.54	0.43
13:A:1296:C:H4'	18:M:12:LYS:HE2	1.99	0.43
13:A:1320:C:C6	20:S:69:LYS:HE3	2.52	0.43
13:A:1393:U:H2'	13:A:1394:A:O4'	2.18	0.43
13:A:1518:A:O2'	13:A:1519:A:O5'	2.35	0.43
2:D:10:LEU:HD11	2:D:62:ARG:HD2	2.00	0.43
3:E:156:ARG:NH1	5:H:42:GLU:O	2.50	0.43
13:A:235:C:H2'	13:A:236:A:C8	2.53	0.43
13:A:390:U:H2'	13:A:391:G:C8	2.54	0.43
13:A:710:G:H2'	13:A:711:G:H8	1.82	0.43
13:A:714:G:H1'	13:A:777:A:N7	2.33	0.43
13:A:908:A:H2'	13:A:909:A:H8	1.83	0.43
13:A:1069:C:O2	13:A:1106:G:N2	2.19	0.43
13:A:1346:A:N1	13:A:1374:A:H5"	2.33	0.43
13:A:1366:C:H2'	13:A:1367:C:H6	1.82	0.43
13:A:1431:A:O2'	13:A:1432:G:O5'	2.36	0.43
14:C:104:GLU:O	14:C:106:ARG:NH1	2.51	0.43
16:I:19:PHE:HB2	16:I:63:TYR:HB3	2.00	0.43
19:N:55:SER:HB2	19:N:58:ARG:HG2	2.00	0.43
1:B:68:PHE:H	1:B:90:PHE:HA	1.82	0.43
1:B:126:ASP:OD1	1:B:127:LYS:HG2	2.19	0.43
1:B:166:ASP:HB3	1:B:190:SER:HB3	1.99	0.43
7:L:63:THR:HG21	7:L:92:VAL:HG22	2.01	0.43
8:O:6:ALA:HA	8:O:9:LYS:HG2	2.00	0.43
8:O:23:SER:OG	8:O:26:VAL:HG23	2.19	0.43
10:Q:53:GLY:N	10:Q:56:ASP:OD2	2.31	0.43
13:A:6:G:O2'	13:A:7:A:H8	2.01	0.43
13:A:157:U:H1'	13:A:165:G:C2	2.52	0.43
13:A:675:A:C6	13:A:676:A:C5	3.07	0.43
13:A:1049:U:H2'	19:N:2:LYS:HD2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:1162:C:C2	13:A:1163:A:N7	2.86	0.43
13:A:1430:A:N6	13:A:1431:A:N1	2.66	0.43
13:A:1519:A:O2'	13:A:1520:C:OP2	2.30	0.43
15:G:21:LEU:HD23	15:G:21:LEU:H	1.83	0.43
1:B:55:GLU:HA	1:B:58:LYS:HE2	2.00	0.43
4:F:37:HIS:ND1	4:F:65:GLU:CG	2.81	0.43
5:H:37:ASN:HD21	5:H:48:PHE:HZ	1.65	0.43
6:K:16:SER:H	6:K:78:ILE:HD13	1.83	0.43
6:K:52:ARG:HA	6:K:52:ARG:HD2	1.78	0.43
13:A:1072:G:H2'	13:A:1073:U:H6	1.82	0.43
13:A:1087:G:C6	13:A:1099:G:N1	2.86	0.43
13:A:1111:A:H2'	13:A:1112:C:C6	2.53	0.43
13:A:1203:C:H2'	13:A:1204:A:C8	2.54	0.43
13:A:1458:G:H2'	13:A:1459:G:C8	2.53	0.43
1:B:183:PHE:HE1	1:B:197:PHE:CD2	2.36	0.43
3:E:133:ILE:O	3:E:136:VAL:HG12	2.18	0.43
7:L:105:GLY:CA	7:L:116:TYR:O	2.53	0.43
8:O:14:PHE:CZ	8:O:84:LEU:HD13	2.53	0.43
13:A:96:U:H2'	13:A:97:G:H8	1.84	0.43
13:A:264:C:H2'	13:A:265:G:O4'	2.19	0.43
13:A:715:A:H8	13:A:716:A:N7	2.15	0.43
13:A:1091:U:N3	13:A:1095:U:C4	2.87	0.43
13:A:1239:A:O2'	15:G:114:SER:HA	2.18	0.43
13:A:1381:U:H2'	13:A:1382:C:O4'	2.18	0.43
13:A:1516:G:N2	13:A:1519:A:C6	2.86	0.43
14:C:13:ILE:HG22	14:C:14:VAL:N	2.24	0.43
1:B:59:ILE:O	1:B:64:GLY:N	2.44	0.43
1:B:95:TRP:CZ3	1:B:171:ALA:HB2	2.54	0.43
1:B:120:SER:O	1:B:124:THR:HG23	2.18	0.43
3:E:51:LYS:HD2	13:A:1080:A:OP1	2.19	0.43
6:K:34:THR:HA	6:K:40:ALA:HA	2.00	0.43
6:K:49:SER:HB2	6:K:68:ARG:NH2	2.33	0.43
13:A:128:G:H2'	13:A:129:A:C8	2.54	0.43
13:A:1124:G:O6	13:A:1150:A:N6	2.52	0.43
13:A:1179:A:H4'	16:I:104:THR:HA	1.99	0.43
13:A:1273:C:H2'	13:A:1274:A:O4'	2.19	0.43
19:N:5:MET:SD	19:N:8:ARG:NH2	2.92	0.43
4:F:52:ASN:HD22	4:F:85:ILE:HG13	1.84	0.43
4:F:55:HIS:C	4:F:56:LYS:HD3	2.39	0.43
5:H:101:ALA:HB3	5:H:112:ASP:HB2	2.00	0.43
8:O:50:HIS:ND1	13:A:667:G:H4'	2.34	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:486:U:H2'	13:A:487:A:C8	2.53	0.43
13:A:875:U:H5"	21:A:1998:HOH:O	2.17	0.43
16:I:54:VAL:HG11	16:I:93:LEU:HD13	2.00	0.43
18:M:29:SER:O	18:M:29:SER:OG	2.36	0.43
1:B:113:LEU:HD12	1:B:113:LEU:HA	1.91	0.43
4:F:44:ARG:HG3	4:F:57:ALA:C	2.39	0.43
5:H:103:VAL:HG23	5:H:105:THR:HG23	2.01	0.43
13:A:843:U:H2'	13:A:844:G:C5	2.54	0.43
13:A:928:G:H2'	13:A:929:G:O4'	2.19	0.43
13:A:947:G:H2'	13:A:948:C:H6	1.84	0.43
13:A:981:U:H2'	13:A:982:U:H5	1.83	0.43
13:A:1087:G:O5'	13:A:1087:G:H8	2.02	0.43
13:A:1164:G:H2'	13:A:1165:U:C6	2.53	0.43
13:A:1193:G:OP1	14:C:166:TRP:NE1	2.49	0.43
13:A:1283:U:H2'	13:A:1284:C:O4'	2.19	0.43
13:A:1326:U:H2'	13:A:1327:C:H6	1.83	0.43
14:C:152:VAL:HG23	14:C:156:LEU:HD11	2.01	0.43
19:N:19:TYR:HB2	19:N:54:SER:OG	2.18	0.43
20:S:11:ASP:HB2	20:S:34:SER:CB	2.47	0.43
2:D:18:LEU:HD13	2:D:62:ARG:HB2	2.01	0.43
2:D:44:LYS:HZ3	2:D:46:ARG:HE	1.65	0.43
2:D:115:GLN:HG3	2:D:153:ARG:HH12	1.81	0.43
8:O:79:ARG:O	8:O:83:ARG:CB	2.67	0.43
11:R:64:LEU:HD23	11:R:64:LEU:O	2.18	0.43
13:A:320:A:H2'	13:A:321:A:O4'	2.19	0.43
13:A:984:C:C2	13:A:1222:G:C2	3.07	0.43
13:A:990:C:H2'	13:A:991:U:O4'	2.19	0.43
13:A:1015:G:H2'	13:A:1016:A:C8	2.54	0.43
13:A:1242:G:H2'	13:A:1243:C:C6	2.54	0.43
13:A:1243:C:H2'	13:A:1244:G:H8	1.84	0.43
13:A:1446:A:H8	13:A:1446:A:OP1	2.02	0.43
14:C:83:VAL:HG13	14:C:100:ILE:HB	2.01	0.43
1:B:131:LYS:HB3	13:A:1158:C:H1'	2.01	0.42
2:D:31:CYS:HB3	13:A:413:G:H1	1.84	0.42
2:D:169:TRP:HE1	2:D:170:LEU:HD23	1.83	0.42
4:F:92:THR:HG23	4:F:93:LYS:N	2.34	0.42
5:H:2:MET:CE	13:A:756:C:C4'	2.97	0.42
6:K:24:ALA:HB3	6:K:87:GLY:O	2.19	0.42
6:K:43:TRP:CH2	13:A:705:G:N3	2.87	0.42
7:L:78:VAL:O	7:L:102:ASP:HB2	2.18	0.42
10:Q:27:PHE:CE2	10:Q:36:PHE:HB3	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:90:C:C2	13:A:91:U:C5	3.07	0.42
13:A:352:C:O2'	13:A:354:G:OP1	2.31	0.42
13:A:628:G:H2'	13:A:629:A:C8	2.54	0.42
13:A:689:C:C4	13:A:690:G:C5	3.07	0.42
13:A:1056:U:H2'	13:A:1057:G:C8	2.54	0.42
14:C:118:SER:O	14:C:122:GLN:HG3	2.18	0.42
1:B:31:PHE:HB2	1:B:41:ASN:HA	2.01	0.42
2:D:33:ILE:HG13	2:D:34:GLU:H	1.84	0.42
5:H:8:ASP:O	5:H:12:ARG:HG3	2.19	0.42
10:Q:20:ILE:HG23	10:Q:47:ASP:OD1	2.19	0.42
11:R:60:ARG:NE	13:A:736:C:OP1	2.51	0.42
12:T:42:ASP:OD1	12:T:43:LYS:N	2.52	0.42
13:A:114:U:O2'	13:A:115:G:H5'	2.19	0.42
13:A:745:G:H2'	13:A:746:A:C8	2.54	0.42
13:A:965:U:H4'	13:A:966:G:O5'	2.18	0.42
13:A:1025:U:H5"	13:A:1026:G:C5'	2.49	0.42
13:A:1026:G:H2'	13:A:1026:G:N3	2.33	0.42
13:A:1300:G:H4'	13:A:1301:U:O5'	2.19	0.42
13:A:1348:U:C2	13:A:1374:A:N7	2.87	0.42
14:C:22:PHE:CZ	17:J:11:LYS:HB3	2.53	0.42
16:I:9:GLY:HA2	16:I:80:HIS:ND1	2.33	0.42
18:M:3:ILE:HG12	18:M:8:ILE:HD13	2.01	0.42
8:O:9:LYS:CE	8:O:10:ILE:CD1	2.95	0.42
13:A:769:G:H21	13:A:901:A:H2	1.66	0.42
13:A:974:A:H4'	13:A:975:A:H3'	2.02	0.42
13:A:1055:A:C6	13:A:1206:G:C5	3.08	0.42
13:A:1172:C:H2'	13:A:1173:U:C6	2.54	0.42
13:A:1174:G:H2'	13:A:1175:G:C8	2.55	0.42
13:A:1240:U:OP2	15:G:115:MET:N	2.52	0.42
20:S:14:LEU:HB2	20:S:18:VAL:HG23	2.01	0.42
5:H:95:MET:O	5:H:95:MET:CG	2.68	0.42
8:O:23:SER:O	8:O:27:GLN:HG3	2.18	0.42
13:A:131:A:O2'	13:A:262:A:N3	2.43	0.42
13:A:1166:G:C2	13:A:1171:A:C6	3.08	0.42
13:A:1255:G:H2'	13:A:1258:G:H21	1.85	0.42
14:C:32:LEU:HD11	19:N:92:ILE:HG12	2.02	0.42
18:M:9:PRO:HD3	18:M:20:SER:HB3	2.00	0.42
19:N:27:LYS:NZ	19:N:44:VAL:O	2.32	0.42
1:B:109:SER:O	1:B:113:LEU:HB2	2.19	0.42
2:D:173:ASP:O	2:D:177:MET:HA	2.20	0.42
9:P:7:ALA:HB1	9:P:29:ASN:HB3	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:413:G:OP1	13:A:413:G:H3'	2.19	0.42
13:A:618:C:H3'	13:A:619:U:H5"	2.01	0.42
13:A:981:U:C4	13:A:982:U:C4	3.07	0.42
13:A:1147:C:O2'	16:I:6:TYR:OH	2.21	0.42
13:A:1423:G:H2'	13:A:1424:U:H6	1.84	0.42
14:C:8:GLY:HA2	14:C:11:LEU:HG	2.02	0.42
14:C:81:GLU:HG2	14:C:85:LYS:NZ	2.35	0.42
18:M:67:ASP:O	18:M:71:GLU:N	2.48	0.42
20:S:14:LEU:HB3	20:S:32:THR:HG23	2.00	0.42
1:B:34:ARG:HH11	1:B:39:ILE:HG13	1.85	0.42
1:B:124:THR:HG22	1:B:133:ALA:CB	2.50	0.42
10:Q:12:VAL:HG21	10:Q:42:LYS:HE3	2.02	0.42
13:A:120:A:H1'	13:A:122:G:N7	2.35	0.42
13:A:922:G:O2'	13:A:923:A:OP2	2.30	0.42
13:A:928:G:C6	13:A:1390:U:H5	2.38	0.42
13:A:1287:A:N3	13:A:1353:G:O2'	2.36	0.42
13:A:1349:A:H5'	16:I:122:ARG:HB2	2.01	0.42
16:I:54:VAL:HG21	16:I:93:LEU:HD12	2.01	0.42
17:J:14:ASP:OD1	17:J:17:LEU:HB2	2.19	0.42
18:M:88:LEU:HD23	18:M:91:ARG:HD2	2.01	0.42
2:D:10:LEU:HD21	2:D:62:ARG:HD2	2.02	0.42
4:F:37:HIS:CD2	4:F:38:ARG:HE	2.38	0.42
5:H:95:MET:CE	5:H:129:ALA:HB1	2.50	0.42
11:R:24:ASP:OD1	11:R:24:ASP:N	2.45	0.42
13:A:725:G:H2'	13:A:726:C:C6	2.55	0.42
13:A:803:G:H2'	13:A:804:U:O4'	2.19	0.42
13:A:942:G:H1	13:A:1341:U:H3	1.68	0.42
13:A:1037:C:H2'	13:A:1038:C:C6	2.55	0.42
13:A:1101:A:N3	13:A:1102:A:H1'	2.35	0.42
13:A:1115:U:H2'	13:A:1116:U:C6	2.55	0.42
13:A:1326:U:O2'	13:A:1327:C:H5'	2.19	0.42
13:A:1510:C:H2'	13:A:1511:G:C8	2.55	0.42
4:F:12:PRO:HD2	4:F:54:LEU:HD21	2.02	0.42
7:L:32:VAL:HG23	7:L:55:ARG:O	2.20	0.42
8:O:6:ALA:C	8:O:9:LYS:HG3	2.35	0.42
13:A:31:G:O2'	13:A:48:C:N4	2.52	0.42
13:A:335:C:O2'	13:A:336:A:P	2.77	0.42
13:A:494:G:O2'	13:A:496:A:H1'	2.20	0.42
13:A:539:A:H2'	13:A:540:G:C8	2.54	0.42
13:A:580:C:H2'	13:A:581:G:O4'	2.20	0.42
13:A:744:C:H2'	13:A:745:G:H8	1.80	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:841:C:C4	13:A:846:G:C4	3.08	0.42
13:A:900:A:C8	13:A:901:A:C8	3.07	0.42
13:A:947:G:OP2	18:M:106:ARG:NE	2.53	0.42
13:A:1014:A:H5'	20:S:13:HIS:HA	2.02	0.42
13:A:1014:A:P	20:S:17:LYS:HE2	2.60	0.42
13:A:1054:C:H4'	13:A:1056:U:OP2	2.20	0.42
13:A:1072:G:C6	13:A:1104:G:C2	3.07	0.42
13:A:1308:U:P	18:M:96:VAL:HG22	2.60	0.42
13:A:1322:C:OP2	18:M:89:ARG:NH2	2.53	0.42
14:C:90:VAL:HA	14:C:93:ILE:HG22	2.02	0.42
14:C:134:LYS:HZ1	14:C:167:TYR:HD2	1.62	0.42
18:M:2:ARG:HD3	18:M:2:ARG:HA	1.88	0.42
18:M:69:ARG:HD3	18:M:69:ARG:HA	1.83	0.42
19:N:27:LYS:HE2	19:N:48:GLN:N	2.33	0.42
3:E:109:ALA:HB3	3:E:135:VAL:CG2	2.50	0.42
4:F:38:ARG:NH2	4:F:96:VAL:O	2.53	0.42
11:R:30:ASN:N	11:R:30:ASN:OD1	2.50	0.42
13:A:148:G:H1	13:A:174:A:N6	2.16	0.42
13:A:162:A:O5'	13:A:162:A:H8	2.02	0.42
13:A:652:U:H5	21:A:2015:HOH:O	2.03	0.42
13:A:782:A:H3'	13:A:783:C:C6	2.54	0.42
13:A:1000:A:H2'	13:A:1001:C:C6	2.53	0.42
13:A:1118:U:H1'	13:A:1179:A:C4	2.55	0.42
13:A:1118:U:H2'	13:A:1119:C:C6	2.54	0.42
13:A:1186:G:H21	19:N:100:TRP:C	2.22	0.42
13:A:1351:U:O2	13:A:1371:G:N2	2.30	0.42
16:I:119:LYS:O	16:I:119:LYS:HG2	2.19	0.42
20:S:71:GLY:HA2	20:S:74:ALA:HB3	2.02	0.42
1:B:56:LEU:HD23	1:B:59:ILE:HD11	2.01	0.42
4:F:11:HIS:HB2	4:F:14:GLN:OE1	2.19	0.42
7:L:45:ASN:OD1	13:A:528:C:N4	2.32	0.42
8:O:66:LEU:HA	8:O:66:LEU:HD23	1.83	0.42
13:A:134:G:H1'	13:A:325:A:C5	2.54	0.42
13:A:160:A:H8	13:A:160:A:OP1	2.03	0.42
13:A:312:C:H2'	13:A:313:A:C8	2.55	0.42
13:A:448:A:C2'	13:A:449:G:H5'	2.50	0.42
13:A:845:A:C8	13:A:846:G:C8	3.08	0.42
13:A:1022:A:C6	13:A:1023:U:C4	3.07	0.42
13:A:1359:C:H4'	13:A:1362:A:N6	2.35	0.42
19:N:97:LYS:HE3	19:N:97:LYS:HB3	1.84	0.42
20:S:14:LEU:HB3	20:S:32:THR:CG2	2.49	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:94:PHE:O	3:E:124:ALA:HA	2.20	0.41
4:F:6:ILE:CB	4:F:62:MET:SD	3.06	0.41
4:F:47:LEU:HD21	4:F:57:ALA:HB3	2.02	0.41
6:K:49:SER:HB2	6:K:68:ARG:CZ	2.50	0.41
11:R:37:LYS:HD3	13:A:719:C:H1'	2.01	0.41
13:A:432:A:H2'	13:A:433:G:O4'	2.20	0.41
13:A:505:G:H2'	13:A:506:G:C8	2.55	0.41
13:A:924:C:H1'	13:A:1501:C:N4	2.35	0.41
13:A:1040:U:H2'	13:A:1041:G:C8	2.55	0.41
13:A:1289:A:H2	13:A:1372:U:O4'	2.02	0.41
13:A:1514:G:H2'	13:A:1515:G:C8	2.55	0.41
2:D:180:THR:HG22	2:D:182:LYS:HD2	2.03	0.41
5:H:103:VAL:HG12	5:H:124:ILE:HD13	2.02	0.41
6:K:21:HIS:HB3	6:K:32:THR:HG22	2.02	0.41
7:L:19:ASN:O	7:L:93:ARG:HD2	2.20	0.41
7:L:30:ARG:NH1	21:A:1617:HOH:O	2.53	0.41
7:L:62:VAL:HG22	7:L:63:THR:N	2.35	0.41
8:O:22:GLY:HA3	13:A:750:C:O2	2.19	0.41
13:A:15:G:C4'	13:A:1397:C:H2'	2.50	0.41
13:A:945:G:C2	13:A:1337:G:C2	3.08	0.41
13:A:1217:C:H2'	13:A:1218:C:C6	2.54	0.41
13:A:1390:U:H2'	13:A:1391:U:H6	1.85	0.41
16:I:46:VAL:HA	16:I:49:GLN:NE2	2.35	0.41
20:S:24:SER:HB2	20:S:27:LYS:NZ	2.34	0.41
1:B:62:ARG:H	1:B:62:ARG:HD3	1.83	0.41
2:D:33:ILE:C	2:D:34:GLU:HG3	2.41	0.41
2:D:56:GLU:HG3	2:D:57:LYS:N	2.36	0.41
6:K:15:VAL:HG13	6:K:17:ASP:H	1.85	0.41
13:A:211:G:C5	13:A:212:G:H1'	2.55	0.41
13:A:251:G:O6	13:A:266:G:N2	2.53	0.41
13:A:468:A:H3'	13:A:469:C:H6	1.84	0.41
13:A:1053:G:N2	13:A:1058:G:O6	2.53	0.41
13:A:1206:G:H4'	14:C:191:THR:O	2.21	0.41
13:A:1309:G:C6	13:A:1329:A:C6	3.09	0.41
15:G:114:SER:O	15:G:118:ARG:HG2	2.20	0.41
20:S:35:ARG:C	20:S:35:ARG:HD2	2.40	0.41
6:K:32:THR:O	6:K:33:ILE:HD13	2.19	0.41
11:R:41:SER:HG	11:R:42:ARG:HH21	1.66	0.41
13:A:525:C:H2'	13:A:526:C:O4'	2.20	0.41
13:A:951:G:H2'	13:A:952:U:H6	1.85	0.41
16:I:25:GLY:HA2	16:I:60:LEU:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:81:GLN:OE1	3:E:149:PRO:HD3	2.21	0.41
8:O:66:LEU:CD1	8:O:87:ARG:NH1	2.84	0.41
13:A:673:A:C4	13:A:734:G:N2	2.88	0.41
13:A:839:C:H2'	13:A:840:C:C6	2.55	0.41
13:A:968:A:C4	13:A:1062:U:H4'	2.56	0.41
13:A:1254:A:H2'	13:A:1255:G:C8	2.55	0.41
13:A:1312:G:H3'	20:S:5:LYS:CE	2.51	0.41
14:C:13:ILE:CG2	14:C:14:VAL:H	2.26	0.41
15:G:30:MET:SD	15:G:35:LYS:HE3	2.61	0.41
18:M:78:ARG:HD3	18:M:79:LEU:HD12	2.02	0.41
20:S:4:LEU:HD12	20:S:5:LYS:N	2.35	0.41
1:B:191:ASP:N	1:B:191:ASP:OD1	2.52	0.41
5:H:30:LYS:HE3	13:A:643:C:OP1	2.21	0.41
6:K:45:THR:HG21	13:A:688:G:H4'	2.01	0.41
6:K:51:PHE:HB2	6:K:55:ARG:NH2	2.32	0.41
7:L:56:LEU:HD23	7:L:56:LEU:HA	1.82	0.41
8:O:7:THR:O	8:O:11:VAL:HG23	2.21	0.41
10:Q:4:ILE:HG23	10:Q:5:ARG:N	2.36	0.41
12:T:56:ILE:O	12:T:60:GLN:HG2	2.21	0.41
13:A:409:U:O2'	13:A:410:G:O4'	2.38	0.41
13:A:459:A:O4'	13:A:474:G:N2	2.54	0.41
13:A:1205:U:H2'	13:A:1206:G:H8	1.83	0.41
14:C:113:LYS:HB2	14:C:184:ASN:ND2	2.34	0.41
14:C:128:MET:HB3	14:C:131:ARG:NH1	2.36	0.41
19:N:9:GLU:HG2	19:N:60:ARG:HH21	1.85	0.41
1:B:36:LYS:NZ	13:A:848:C:OP1	2.38	0.41
5:H:46:GLU:OE2	5:H:63:LYS:HG3	2.21	0.41
6:K:88:PRO:HA	6:K:92:ARG:HH11	1.86	0.41
8:O:29:ALA:HA	8:O:84:LEU:HD21	2.02	0.41
13:A:460:A:C8	13:A:462:G:OP2	2.73	0.41
13:A:486:U:H2'	13:A:487:A:H8	1.85	0.41
13:A:586:C:O2'	13:A:587:G:H5'	2.21	0.41
13:A:1053:G:O2'	13:A:1199:U:OP2	2.30	0.41
13:A:1376:U:H3'	15:G:8:GLN:HE22	1.85	0.41
1:B:114:LYS:HD2	1:B:151:LYS:CD	2.50	0.41
5:H:95:MET:HE2	5:H:129:ALA:HB1	2.02	0.41
12:T:34:VAL:HG11	12:T:78:LEU:HD13	2.03	0.41
13:A:187:G:O2'	13:A:189:A:N7	2.47	0.41
13:A:268:U:H2'	13:A:269:C:C6	2.55	0.41
13:A:464:U:O2	13:A:466:A:H5'	2.21	0.41
13:A:466:A:O5'	13:A:467:U:H5	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:625:U:H2'	13:A:626:G:C8	2.55	0.41
13:A:685:G:N2	13:A:706:A:N6	2.68	0.41
13:A:899:C:H2'	13:A:900:A:H8	1.81	0.41
14:C:104:GLU:HG3	14:C:106:ARG:HD3	2.01	0.41
1:B:24:PRO:O	1:B:27:LYS:HG3	2.20	0.41
2:D:6:PRO:HB2	2:D:9:LYS:HD2	2.03	0.41
2:D:106:PHE:CD1	2:D:144:ILE:HD11	2.55	0.41
2:D:173:ASP:OD2	2:D:176:LYS:HG2	2.21	0.41
4:F:49:TYR:O	4:F:51:ILE:N	2.53	0.41
6:K:33:ILE:HD12	6:K:81:LEU:HD13	2.02	0.41
8:O:6:ALA:HA	8:O:9:LYS:CG	2.51	0.41
8:O:29:ALA:HA	8:O:32:THR:HG22	2.02	0.41
12:T:27:MET:CE	12:T:57:VAL:HG22	2.51	0.41
13:A:107:G:C2	13:A:108:G:H1'	2.56	0.41
13:A:163:C:H2'	13:A:164:G:O4'	2.21	0.41
13:A:215:C:H2'	13:A:216:U:C6	2.56	0.41
13:A:218:U:H2'	13:A:219:U:O4'	2.21	0.41
13:A:313:A:H2'	13:A:314:C:C6	2.55	0.41
13:A:475:C:H2'	13:A:476:U:H6	1.86	0.41
13:A:610:U:O2	13:A:610:U:O4'	2.38	0.41
13:A:688:G:C2	13:A:700:G:H1'	2.56	0.41
13:A:813:U:H4'	21:A:1630:HOH:O	2.21	0.41
13:A:845:A:H8	13:A:846:G:H8	1.68	0.41
13:A:904:U:H2'	13:A:905:U:C6	2.55	0.41
13:A:981:U:H4'	19:N:60:ARG:HG2	2.02	0.41
13:A:981:U:H3'	13:A:982:U:H6	1.84	0.41
13:A:1065:U:H5"	13:A:1190:G:N2	2.36	0.41
13:A:1350:A:P	16:I:122:ARG:HG3	2.60	0.41
13:A:1429:A:H2'	13:A:1430:A:C8	2.56	0.41
13:A:1510:C:H2'	13:A:1511:G:H8	1.86	0.41
13:A:1516:G:P	13:A:1516:G:H8	2.44	0.41
14:C:30:ASP:HA	19:N:64:ARG:HH22	1.86	0.41
14:C:38:VAL:HG11	14:C:94:ALA:HB2	2.02	0.41
15:G:14:ASP:OD2	15:G:22:LEU:HD22	2.21	0.41
16:I:17:ARG:O	16:I:64:ILE:HA	2.21	0.41
16:I:40:ARG:N	16:I:44:ARG:HB2	2.35	0.41
18:M:39:ALA:HB3	18:M:42:VAL:HG13	2.02	0.41
18:M:84:CYS:HB3	20:S:73:PHE:CZ	2.55	0.41
5:H:2:MET:HE2	13:A:756:C:H1'	2.02	0.41
13:A:560:A:H4'	13:A:561:U:H5"	2.03	0.41
13:A:719:C:OP2	13:A:720:C:N4	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:962:C:H2'	13:A:963:G:H8	1.86	0.41
13:A:985:C:H2'	13:A:986:U:C5	2.56	0.41
13:A:1093:A:O2'	13:A:1095:U:OP1	2.26	0.41
13:A:1124:G:H5"	17:J:37:ARG:HG3	2.03	0.41
13:A:1278:G:N2	14:C:26:LYS:HE2	2.34	0.41
13:A:1285:A:H62	13:A:1355:G:H5'	1.85	0.41
13:A:1341:U:O3'	16:I:129:ARG:NH1	2.54	0.41
14:C:5:HIS:CE1	14:C:183:TYR:HE2	2.39	0.41
16:I:35:GLU:OE1	16:I:35:GLU:N	2.52	0.41
18:M:43:LYS:HB2	18:M:46:GLU:HB2	2.03	0.41
18:M:97:ARG:O	18:M:97:ARG:HD2	2.21	0.41
1:B:63:LYS:HE2	1:B:63:LYS:HB2	1.88	0.40
2:D:171:GLU:CD	2:D:182:LYS:HZ2	2.24	0.40
4:F:38:ARG:HH22	4:F:96:VAL:HG12	1.86	0.40
5:H:105:THR:HG22	5:H:121:GLY:O	2.21	0.40
7:L:82:ARG:CZ	7:L:95:HIS:ND1	2.84	0.40
13:A:459:A:C8	13:A:474:G:N1	2.89	0.40
13:A:601:G:H2'	13:A:602:A:O4'	2.21	0.40
13:A:918:A:H2'	13:A:919:A:C8	2.56	0.40
13:A:938:A:H2'	13:A:939:G:C8	2.56	0.40
13:A:979:C:O2	19:N:58:ARG:NH1	2.54	0.40
13:A:1024:G:H2'	13:A:1025:U:O4'	2.21	0.40
13:A:1089:G:C5	13:A:1090:U:C5	3.08	0.40
13:A:1160:G:N1	13:A:1176:A:C2	2.79	0.40
17:J:35:GLN:N	17:J:78:GLU:OE2	2.54	0.40
18:M:102:LYS:HE3	18:M:102:LYS:HB3	1.86	0.40
1:B:199:ILE:O	1:B:201:GLY:N	2.54	0.40
7:L:80:LEU:HB2	7:L:101:LEU:CD1	2.37	0.40
13:A:125:U:H2'	13:A:126:G:O4'	2.22	0.40
13:A:151:A:N7	13:A:170:U:O2	2.54	0.40
13:A:205:A:H2'	13:A:206:C:C6	2.57	0.40
13:A:604:G:H2'	13:A:605:U:O4'	2.21	0.40
13:A:827:U:C2	13:A:874:G:N2	2.89	0.40
13:A:923:A:N1	13:A:924:C:N4	2.70	0.40
13:A:939:G:N3	13:A:1375:A:H2	2.19	0.40
13:A:1295:U:HO2'	18:M:13:HIS:CD2	2.32	0.40
15:G:33:GLY:O	15:G:34:LYS:HE2	2.22	0.40
1:B:46:VAL:HG23	1:B:47:PRO:HD3	2.04	0.40
1:B:168:GLU:O	1:B:168:GLU:HG3	2.21	0.40
2:D:139:ASN:N	2:D:181:PHE:O	2.30	0.40
3:E:17:VAL:HA	3:E:33:THR:O	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:96:GLN:NE2	3:E:123:LEU:HD23	2.27	0.40
5:H:37:ASN:ND2	5:H:48:PHE:CZ	2.89	0.40
9:P:67:ILE:HG22	9:P:68:SER:O	2.21	0.40
13:A:15:G:H4'	13:A:1397:C:H2'	2.02	0.40
13:A:59:A:H5"	13:A:387:U:H5"	2.03	0.40
13:A:81:A:H2'	13:A:82:G:C8	2.56	0.40
13:A:776:G:H1	13:A:802:A:P	2.38	0.40
13:A:925:G:H2'	13:A:1391:U:N3	2.24	0.40
13:A:948:C:P	18:M:106:ARG:H	2.44	0.40
13:A:952:U:H5"	13:A:964:A:H61	1.85	0.40
13:A:1027:C:H2'	13:A:1028:C:H6	1.85	0.40
13:A:1041:G:H2'	13:A:1042:A:C8	2.57	0.40
13:A:1264:U:H2'	13:A:1265:C:C6	2.56	0.40
13:A:1276:G:H2'	13:A:1277:C:C6	2.57	0.40
14:C:85:LYS:HA	14:C:88:LYS:NZ	2.36	0.40
4:F:52:ASN:ND2	4:F:85:ILE:HG13	2.37	0.40
10:Q:57:VAL:O	10:Q:78:VAL:HG22	2.21	0.40
13:A:333:U:C2'	13:A:334:C:H5'	2.52	0.40
13:A:680:C:C2	13:A:681:A:C8	3.09	0.40
13:A:881:G:H2'	13:A:882:C:O4'	2.22	0.40
13:A:994:A:C6	13:A:1216:A:H4'	2.56	0.40
13:A:1028:C:H2'	13:A:1029:U:H5'	2.04	0.40
13:A:1109:C:OP1	14:C:175:HIS:NE2	2.54	0.40
13:A:1233:G:H2'	13:A:1234:C:C6	2.56	0.40
15:G:25:PHE:CE2	15:G:100:MET:HG3	2.57	0.40
15:G:97:ALA:O	15:G:101:ARG:HG3	2.22	0.40
3:E:152:VAL:HG11	5:H:98:LEU:HG	2.02	0.40
5:H:10:LEU:HD22	5:H:74:ILE:HD11	2.03	0.40
5:H:33:VAL:O	5:H:37:ASN:OD1	2.39	0.40
13:A:35:G:H2'	13:A:36:C:C6	2.57	0.40
13:A:810:C:H2'	13:A:811:C:O4'	2.22	0.40
13:A:949:A:H1'	13:A:971:G:O6	2.21	0.40
13:A:1144:G:C6	13:A:1145:A:C6	3.10	0.40
13:A:1236:A:H2	13:A:1334:G:O2'	2.05	0.40
13:A:1376:U:H3'	15:G:8:GLN:NE2	2.37	0.40
16:I:29:ILE:HG12	16:I:64:ILE:HD12	2.04	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	B	216/240 (90%)	188 (87%)	28 (13%)	0	100	100
2	D	203/205 (99%)	181 (89%)	22 (11%)	0	100	100
3	E	148/166 (89%)	131 (88%)	17 (12%)	0	100	100
4	F	98/135 (73%)	89 (91%)	9 (9%)	0	100	100
5	H	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
6	K	93/128 (73%)	87 (94%)	6 (6%)	0	100	100
7	L	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
8	O	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
9	P	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
10	Q	78/83 (94%)	68 (87%)	10 (13%)	0	100	100
11	R	48/74 (65%)	41 (85%)	7 (15%)	0	100	100
12	T	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
14	C	204/232 (88%)	185 (91%)	19 (9%)	0	100	100
15	G	79/178 (44%)	72 (91%)	7 (9%)	0	100	100
16	I	125/129 (97%)	111 (89%)	14 (11%)	0	100	100
17	J	96/103 (93%)	77 (80%)	19 (20%)	0	100	100
18	M	112/117 (96%)	100 (89%)	12 (11%)	0	100	100
19	N	92/100 (92%)	87 (95%)	5 (5%)	0	100	100
20	S	77/91 (85%)	66 (86%)	11 (14%)	0	100	100
All	All	2166/2490 (87%)	1947 (90%)	219 (10%)	0	100	100

There are no Ramachandran outliers to report.

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	B	180/198 (91%)	178 (99%)	2 (1%)	73 90
2	D	172/172 (100%)	170 (99%)	2 (1%)	71 88
3	E	113/125 (90%)	113 (100%)	0	100 100
4	F	87/116 (75%)	85 (98%)	2 (2%)	50 78
5	H	104/104 (100%)	103 (99%)	1 (1%)	76 91
6	K	69/98 (70%)	68 (99%)	1 (1%)	67 86
7	L	103/103 (100%)	103 (100%)	0	100 100
8	O	76/77 (99%)	74 (97%)	2 (3%)	46 75
9	P	65/65 (100%)	65 (100%)	0	100 100
10	Q	74/77 (96%)	74 (100%)	0	100 100
11	R	43/64 (67%)	42 (98%)	1 (2%)	50 78
12	T	65/65 (100%)	65 (100%)	0	100 100
14	C	170/189 (90%)	169 (99%)	1 (1%)	86 95
15	G	67/146 (46%)	66 (98%)	1 (2%)	65 86
16	I	105/106 (99%)	102 (97%)	3 (3%)	42 71
17	J	86/90 (96%)	85 (99%)	1 (1%)	71 88
18	M	92/95 (97%)	91 (99%)	1 (1%)	73 90
19	N	79/83 (95%)	78 (99%)	1 (1%)	69 87
20	S	70/78 (90%)	69 (99%)	1 (1%)	67 86
All	All	1820/2051 (89%)	1800 (99%)	20 (1%)	74 90

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	62	ARG
1	B	224	ARG
2	D	44	LYS
2	D	150	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	F	2	ARG
4	F	35	LYS
5	H	88	LYS
6	K	55	ARG
8	O	9	LYS
8	O	83	ARG
11	R	52	ARG
14	C	146	LYS
15	G	95	ARG
16	I	26	LYS
16	I	105	ARG
16	I	122	ARG
17	J	89	ARG
18	M	61	LYS
19	N	61	ASN
20	S	77	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	176	ASN
2	D	99	ASN
2	D	151	GLN
3	E	96	GLN
4	F	3	HIS
10	Q	8	GLN
16	I	49	GLN
16	I	125	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	A	1507/1542 (97%)	403 (26%)	21 (1%)

All (403) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
13	A	6	G
13	A	7	A
13	A	9	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	15	G
13	A	20	U
13	A	22	G
13	A	31	G
13	A	32	A
13	A	39	G
13	A	44	A
13	A	47	C
13	A	48	C
13	A	50	A
13	A	51	A
13	A	64	G
13	A	66	A
13	A	70	U
13	A	72	A
13	A	84	U
13	A	85	U
13	A	86	G
13	A	87	C
13	A	89	U
13	A	90	C
13	A	94	G
13	A	95	C
13	A	98	A
13	A	109	A
13	A	115	G
13	A	121	U
13	A	122	G
13	A	129	A
13	A	130	A
13	A	131	A
13	A	149	A
13	A	158	G
13	A	173	U
13	A	177	G
13	A	180	U
13	A	181	A
13	A	182	A
13	A	183	C
13	A	184	G
13	A	195	A
13	A	196	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	197	A
13	A	209	U
13	A	226	G
13	A	239	U
13	A	243	A
13	A	244	U
13	A	245	U
13	A	247	G
13	A	251	G
13	A	252	U
13	A	253	A
13	A	256	U
13	A	257	G
13	A	258	G
13	A	266	G
13	A	267	C
13	A	279	A
13	A	280	C
13	A	289	G
13	A	296	U
13	A	301	G
13	A	303	A
13	A	305	G
13	A	306	A
13	A	307	C
13	A	310	G
13	A	313	A
13	A	321	A
13	A	328	C
13	A	329	A
13	A	330	C
13	A	332	G
13	A	334	C
13	A	335	C
13	A	336	A
13	A	338	A
13	A	340	U
13	A	345	C
13	A	346	G
13	A	352	C
13	A	354	G
13	A	363	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	367	U
13	A	369	G
13	A	372	C
13	A	375	U
13	A	384	G
13	A	392	C
13	A	398	U
13	A	406	G
13	A	409	U
13	A	410	G
13	A	411	A
13	A	413	G
13	A	414	A
13	A	415	A
13	A	421	U
13	A	422	C
13	A	423	G
13	A	424	G
13	A	429	U
13	A	430	A
13	A	435	A
13	A	439	U
13	A	449	G
13	A	450	G
13	A	451	A
13	A	453	G
13	A	457	G
13	A	459	A
13	A	460	A
13	A	461	A
13	A	462	G
13	A	463	U
13	A	464	U
13	A	465	A
13	A	466	A
13	A	467	U
13	A	468	A
13	A	484	G
13	A	485	U
13	A	486	U
13	A	493	A
13	A	495	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	499	A
13	A	511	C
13	A	518	C
13	A	519	C
13	A	521	G
13	A	527	G
13	A	531	U
13	A	532	A
13	A	533	A
13	A	536	C
13	A	537	G
13	A	540	G
13	A	541	G
13	A	544	G
13	A	547	A
13	A	559	A
13	A	562	U
13	A	564	C
13	A	565	U
13	A	570	G
13	A	571	U
13	A	572	A
13	A	573	A
13	A	575	G
13	A	576	C
13	A	577	G
13	A	607	A
13	A	615	G
13	A	618	C
13	A	619	U
13	A	633	G
13	A	641	U
13	A	651	C
13	A	652	U
13	A	653	U
13	A	659	U
13	A	660	C
13	A	665	A
13	A	669	G
13	A	671	G
13	A	682	G
13	A	685	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	687	A
13	A	689	C
13	A	695	A
13	A	698	G
13	A	702	A
13	A	703	G
13	A	710	G
13	A	712	A
13	A	713	G
13	A	721	G
13	A	724	G
13	A	731	G
13	A	741	G
13	A	742	G
13	A	747	A
13	A	755	G
13	A	758	C
13	A	759	A
13	A	771	G
13	A	774	G
13	A	776	G
13	A	777	A
13	A	782	A
13	A	785	G
13	A	790	A
13	A	791	G
13	A	793	U
13	A	794	A
13	A	804	U
13	A	812	G
13	A	814	A
13	A	815	A
13	A	817	C
13	A	821	G
13	A	828	U
13	A	836	G
13	A	841	C
13	A	842	U
13	A	843	U
13	A	844	G
13	A	846	G
13	A	847	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	854	U
13	A	864	A
13	A	868	C
13	A	870	U
13	A	871	U
13	A	875	U
13	A	884	U
13	A	900	A
13	A	901	A
13	A	902	G
13	A	914	A
13	A	922	G
13	A	924	C
13	A	930	C
13	A	934	C
13	A	935	A
13	A	944	G
13	A	946	A
13	A	948	C
13	A	955	U
13	A	960	U
13	A	961	U
13	A	966	G
13	A	969	A
13	A	971	G
13	A	976	G
13	A	977	A
13	A	982	U
13	A	983	A
13	A	991	U
13	A	992	U
13	A	993	G
13	A	994	A
13	A	1002	G
13	A	1004	A
13	A	1009	U
13	A	1010	U
13	A	1026	G
13	A	1027	C
13	A	1029	U
13	A	1030	U
13	A	1031	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	1032	G
13	A	1036	A
13	A	1049	U
13	A	1051	C
13	A	1055	A
13	A	1056	U
13	A	1063	C
13	A	1064	G
13	A	1065	U
13	A	1066	C
13	A	1070	U
13	A	1081	A
13	A	1085	U
13	A	1089	G
13	A	1094	G
13	A	1095	U
13	A	1097	C
13	A	1101	A
13	A	1102	A
13	A	1103	C
13	A	1104	G
13	A	1108	G
13	A	1110	A
13	A	1111	A
13	A	1126	U
13	A	1130	A
13	A	1136	C
13	A	1137	C
13	A	1138	G
13	A	1139	G
13	A	1140	C
13	A	1150	A
13	A	1151	A
13	A	1152	A
13	A	1157	A
13	A	1159	U
13	A	1168	U
13	A	1169	A
13	A	1183	U
13	A	1184	G
13	A	1191	A
13	A	1196	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	1197	A
13	A	1198	G
13	A	1202	U
13	A	1211	U
13	A	1212	U
13	A	1213	A
13	A	1215	G
13	A	1216	A
13	A	1221	G
13	A	1222	G
13	A	1225	A
13	A	1226	C
13	A	1228	C
13	A	1229	A
13	A	1233	G
13	A	1236	A
13	A	1239	A
13	A	1240	U
13	A	1241	G
13	A	1247	U
13	A	1258	G
13	A	1259	C
13	A	1260	G
13	A	1267	C
13	A	1268	G
13	A	1270	G
13	A	1279	G
13	A	1280	A
13	A	1281	C
13	A	1282	C
13	A	1286	U
13	A	1287	A
13	A	1290	G
13	A	1298	U
13	A	1299	A
13	A	1300	G
13	A	1301	U
13	A	1302	C
13	A	1303	C
13	A	1305	G
13	A	1312	G
13	A	1313	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	1315	U
13	A	1316	G
13	A	1317	C
13	A	1318	A
13	A	1319	A
13	A	1320	C
13	A	1321	U
13	A	1322	C
13	A	1323	G
13	A	1327	C
13	A	1328	C
13	A	1331	G
13	A	1333	A
13	A	1336	C
13	A	1338	G
13	A	1346	A
13	A	1347	G
13	A	1348	U
13	A	1349	A
13	A	1353	G
13	A	1363	A
13	A	1364	U
13	A	1376	U
13	A	1378	C
13	A	1379	G
13	A	1381	U
13	A	1383	C
13	A	1390	U
13	A	1414	U
13	A	1415	G
13	A	1416	G
13	A	1417	G
13	A	1431	A
13	A	1432	G
13	A	1433	A
13	A	1434	A
13	A	1441	A
13	A	1442	G
13	A	1447	A
13	A	1448	C
13	A	1452	C
13	A	1457	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	1473	G
13	A	1474	U
13	A	1475	G
13	A	1478	U
13	A	1479	C
13	A	1486	G
13	A	1487	G
13	A	1488	G
13	A	1489	G
13	A	1500	A
13	A	1501	C
13	A	1502	A
13	A	1503	A
13	A	1504	G
13	A	1505	G
13	A	1507	A
13	A	1508	A
13	A	1518	A
13	A	1519	A
13	A	1520	C
13	A	1523	G
13	A	1529	G

All (21) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
13	A	238	A
13	A	266	G
13	A	328	C
13	A	413	G
13	A	428	G
13	A	429	U
13	A	532	A
13	A	842	U
13	A	843	U
13	A	900	A
13	A	960	U
13	A	965	U
13	A	1065	U
13	A	1101	A
13	A	1201	A
13	A	1246	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	A	1278	G
13	A	1300	G
13	A	1507	A
13	A	1518	A
13	A	1528	U

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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.

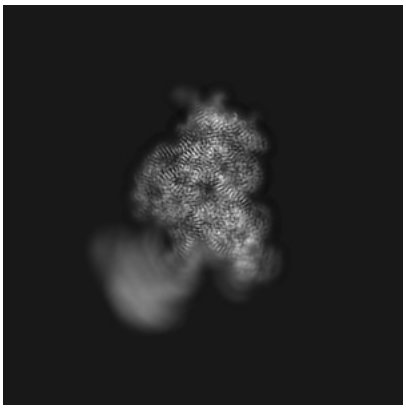
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-12856. These allow visual inspection of the internal detail of the map and identification of artifacts.

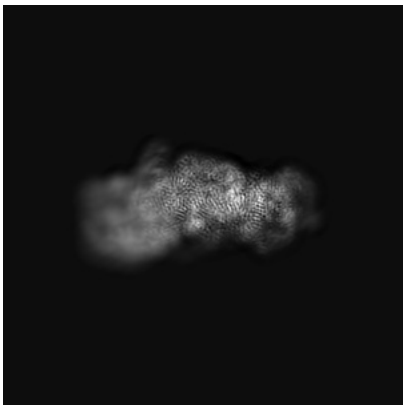
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

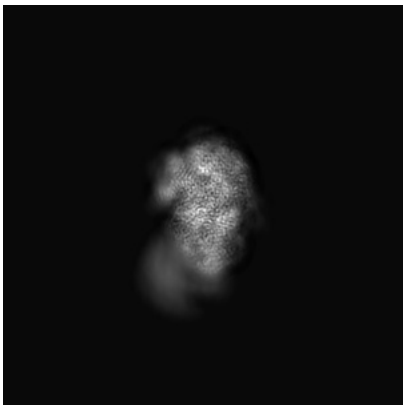
6.1.1 Primary map



X

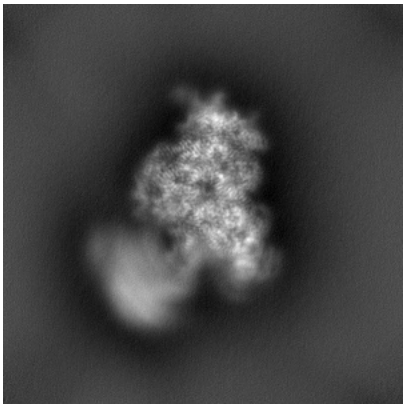


Y

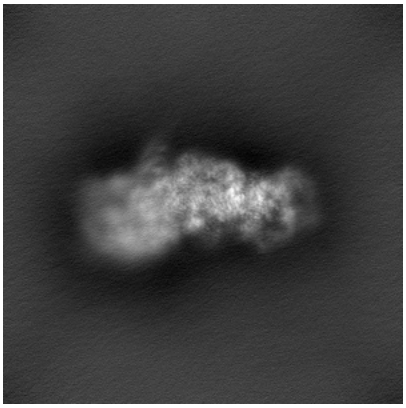


Z

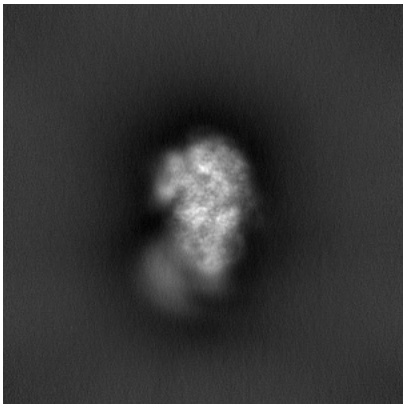
6.1.2 Raw map



X



Y

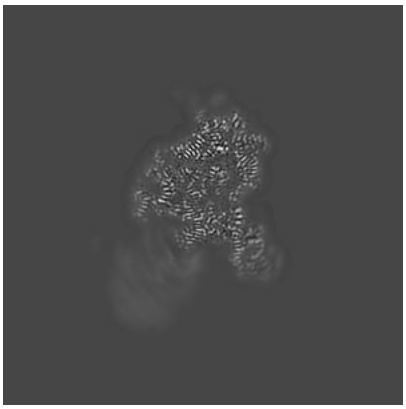


Z

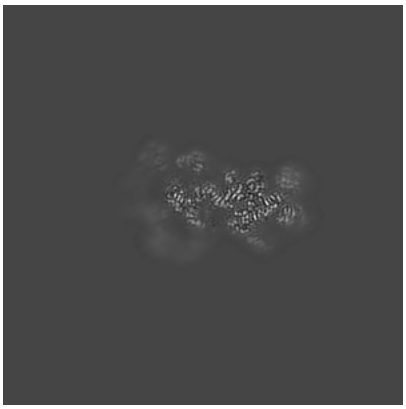
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

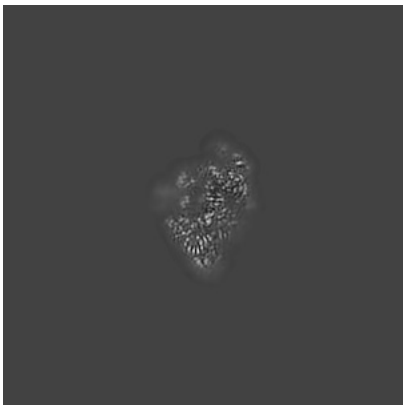
6.2.1 Primary map



X Index: 220

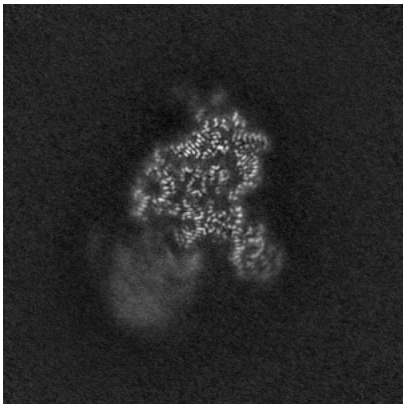


Y Index: 220

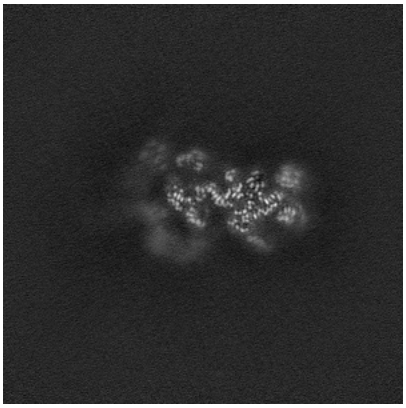


Z Index: 220

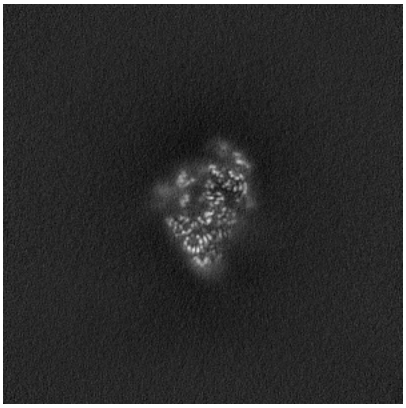
6.2.2 Raw map



X Index: 220



Y Index: 220

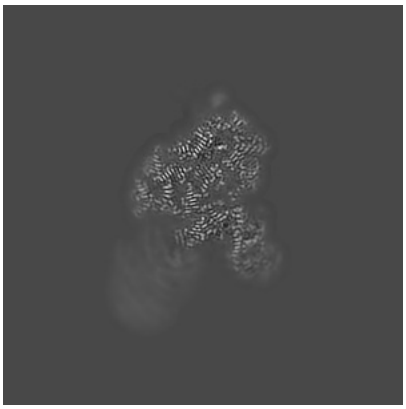


Z Index: 220

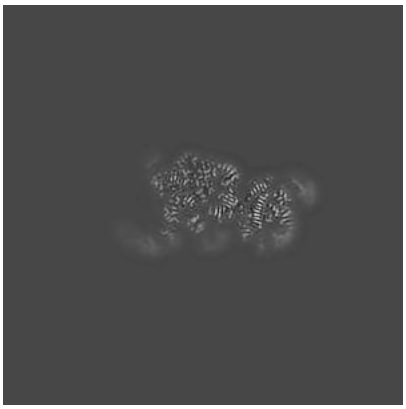
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

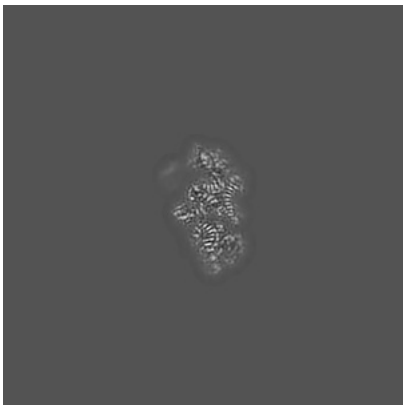
6.3.1 Primary map



X Index: 224

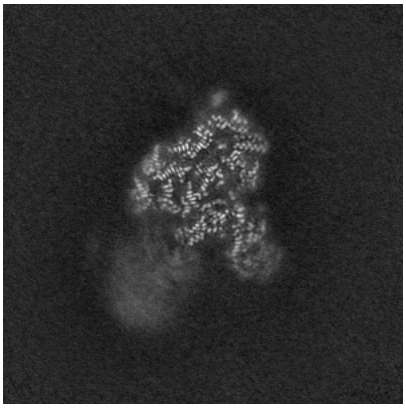


Y Index: 239

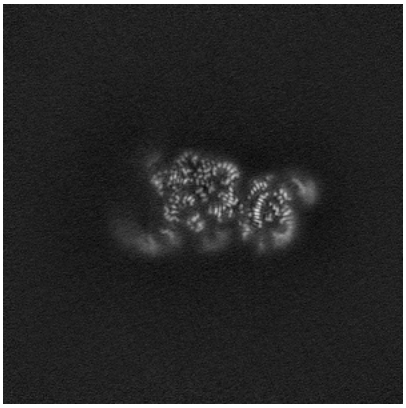


Z Index: 251

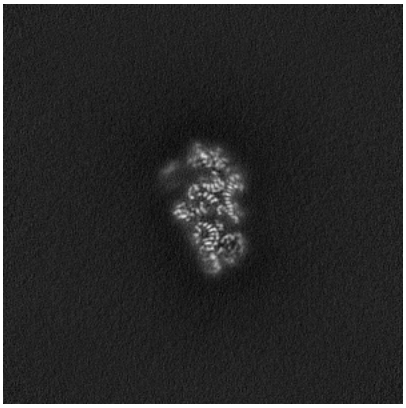
6.3.2 Raw map



X Index: 225



Y Index: 239

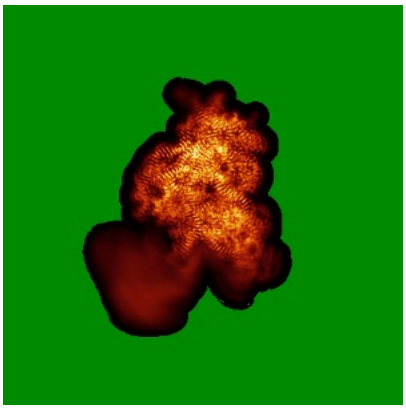


Z Index: 251

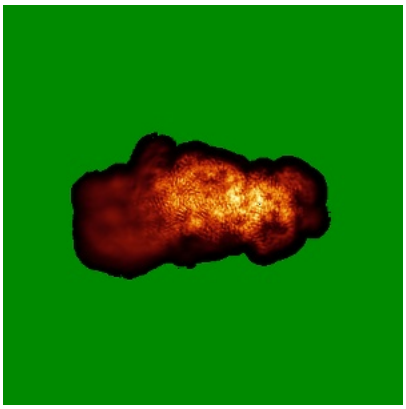
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

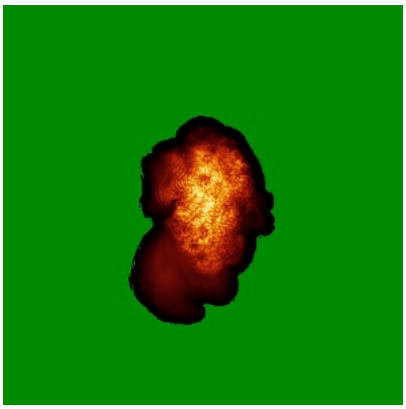
6.4.1 Primary map



X

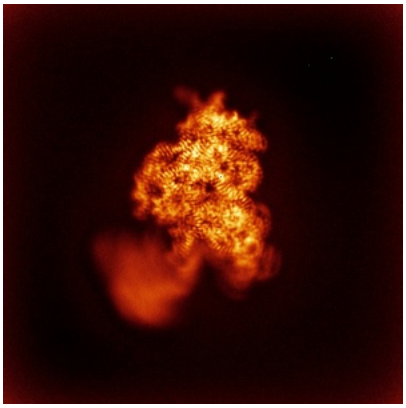


Y



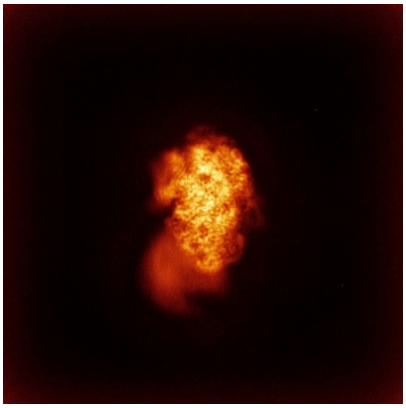
Z

6.4.2 Raw map



X

Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.29. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

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

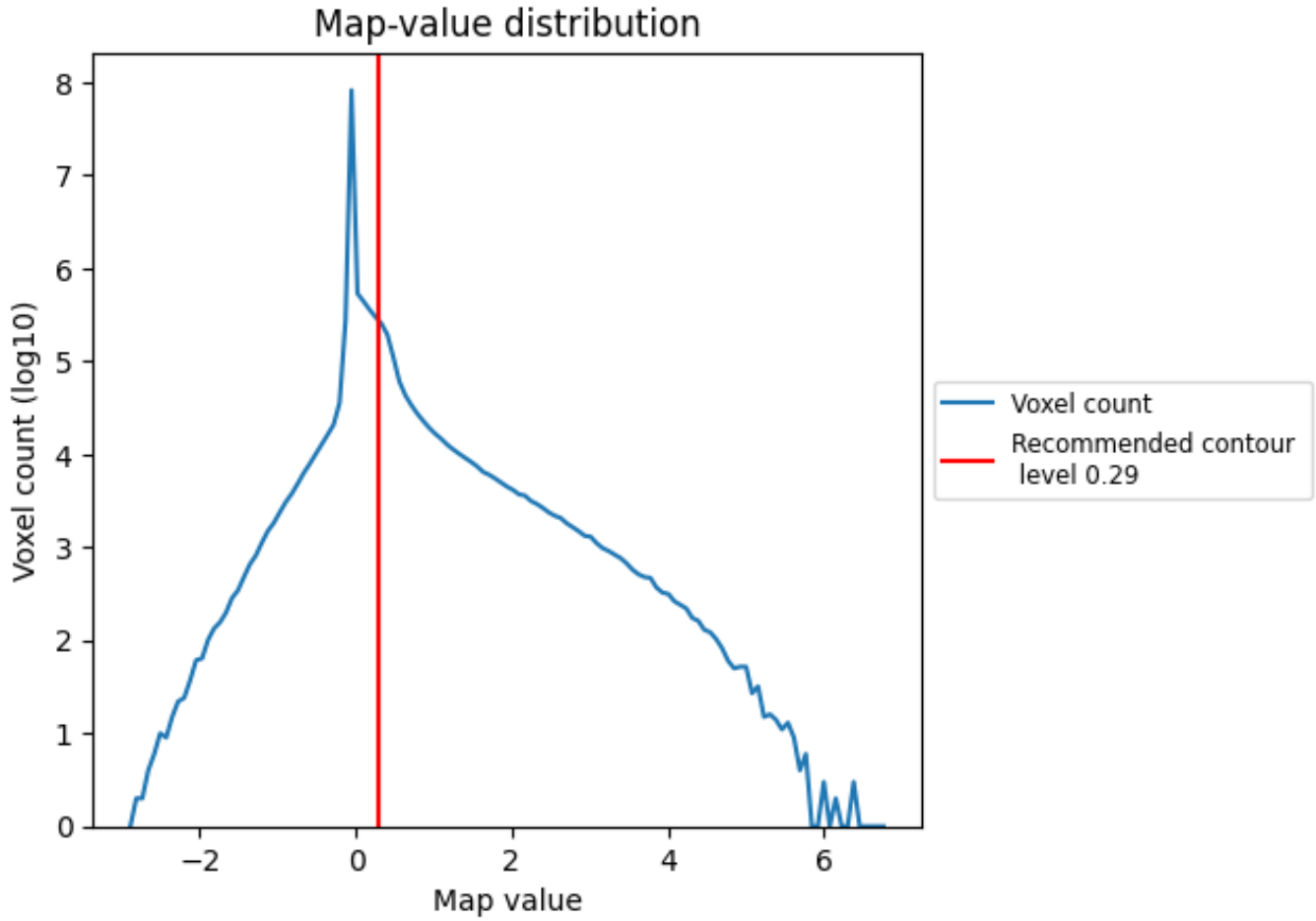
6.6 Mask visualisation (i)

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

7 Map analysis

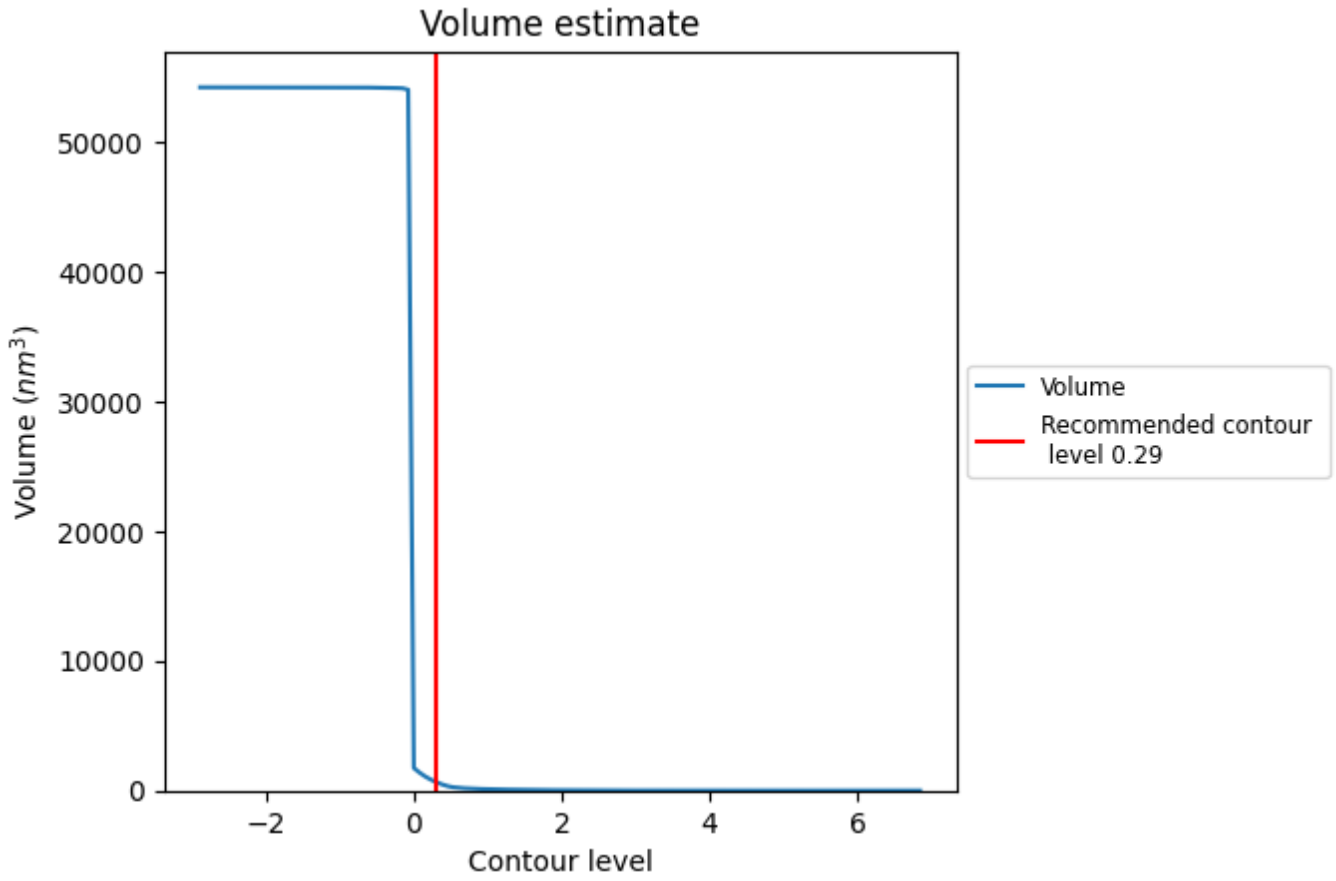
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

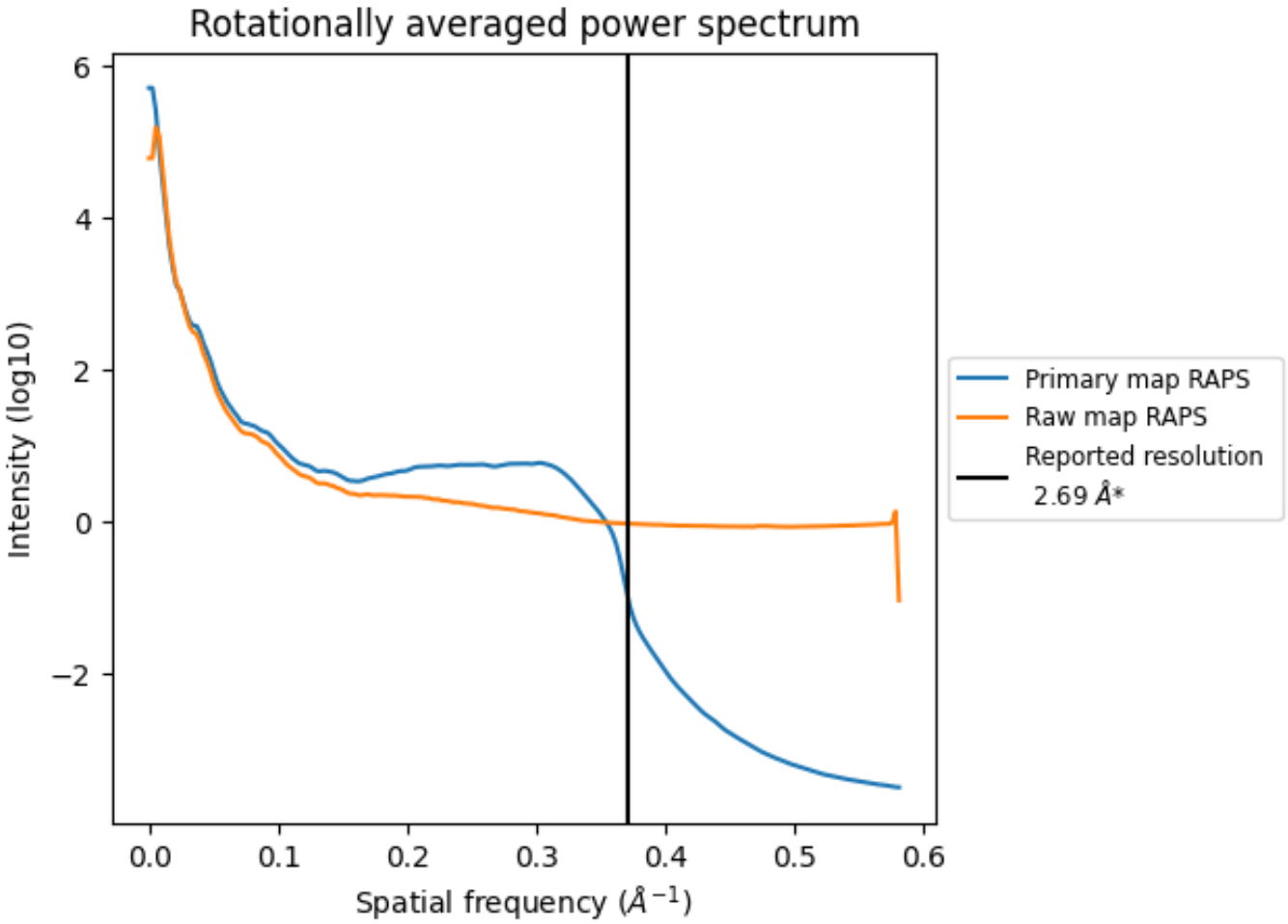
7.2 Volume estimate



The volume at the recommended contour level is 688 nm^3; this corresponds to an approximate mass of 622 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 (i)

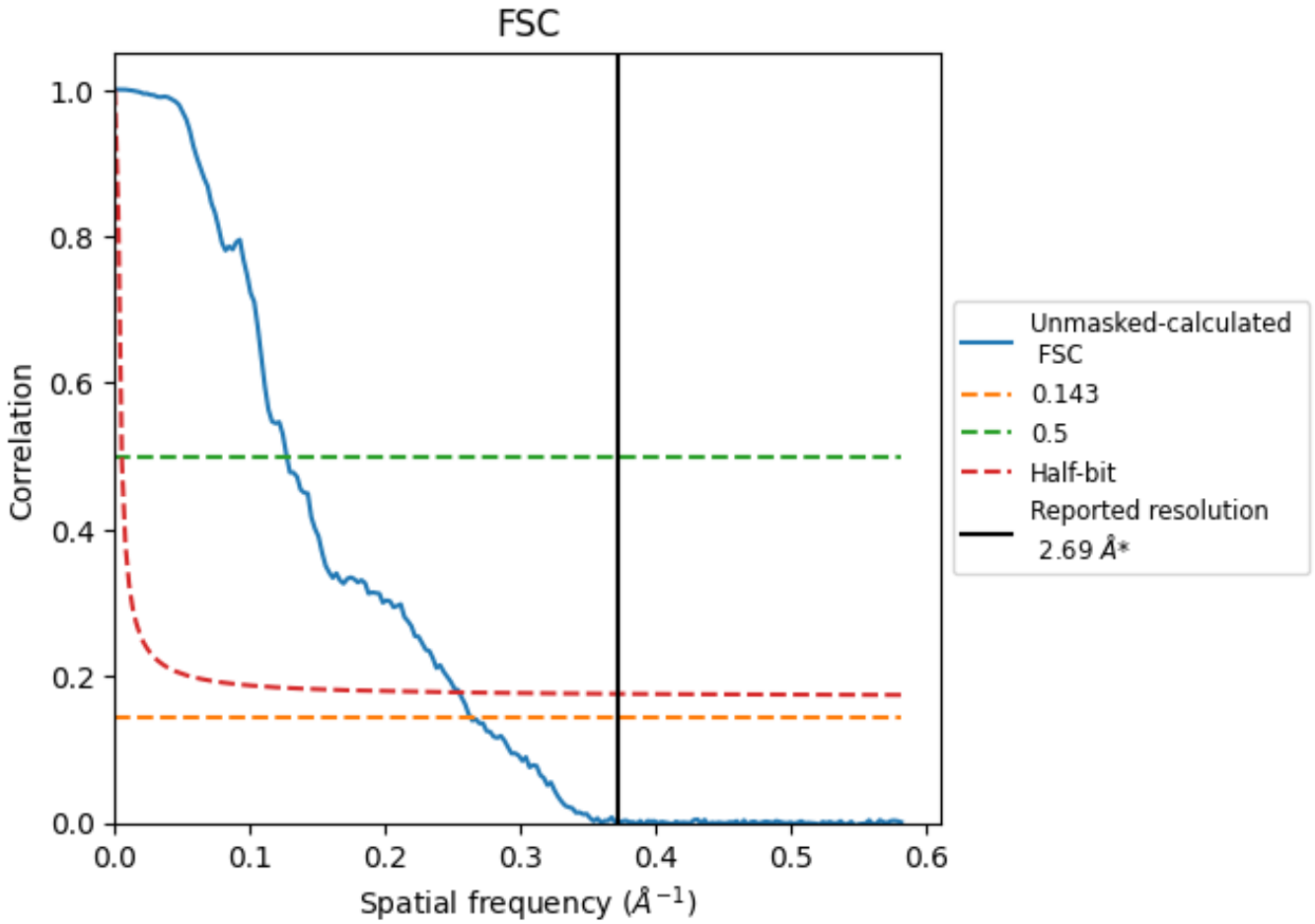


*Reported resolution corresponds to spatial frequency of 0.372 $Å^{-1}$

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.372 Å^{-1}

8.2 Resolution estimates (i)

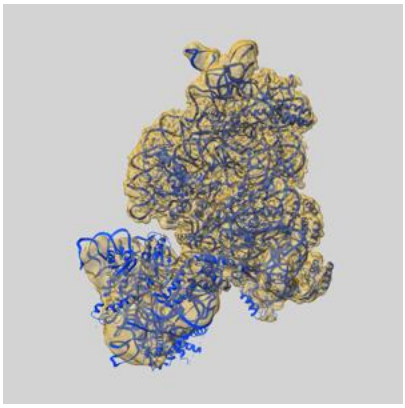
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.69	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.80	7.87	3.93

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.80 differs from the reported value 2.69 by more than 10 %

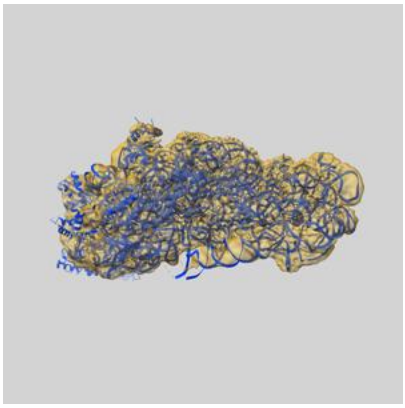
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-12856 and PDB model 7OE0. Per-residue inclusion information can be found in section 3 on page 8.

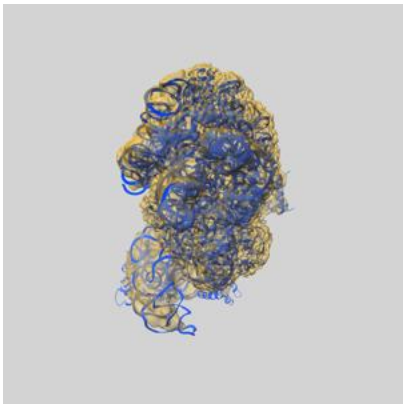
9.1 Map-model overlay



X



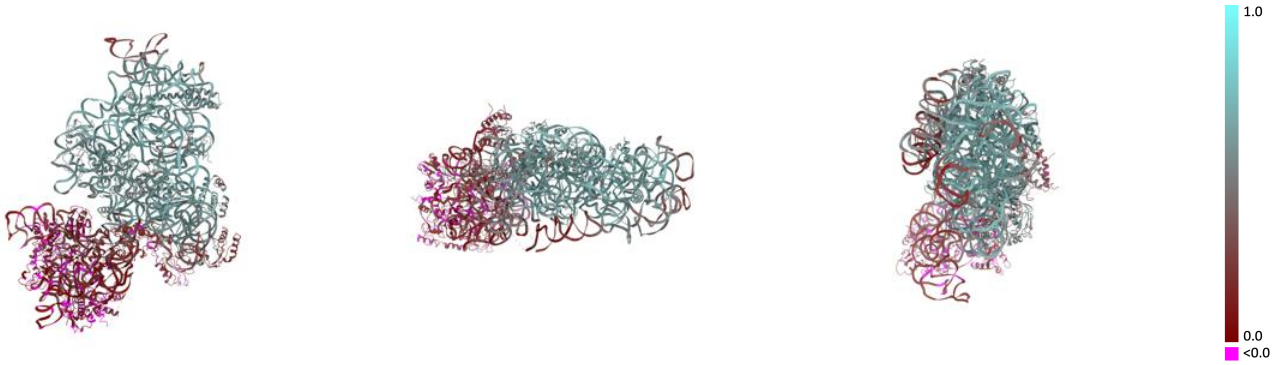
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.29 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.

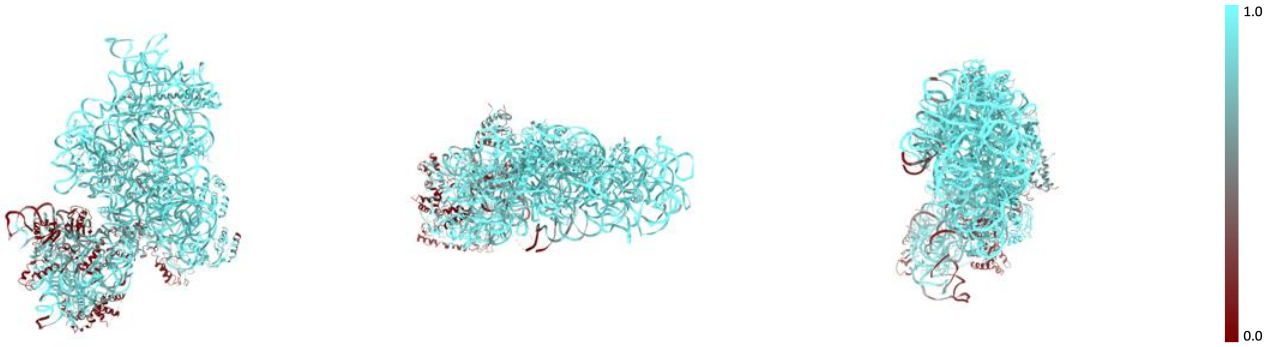
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

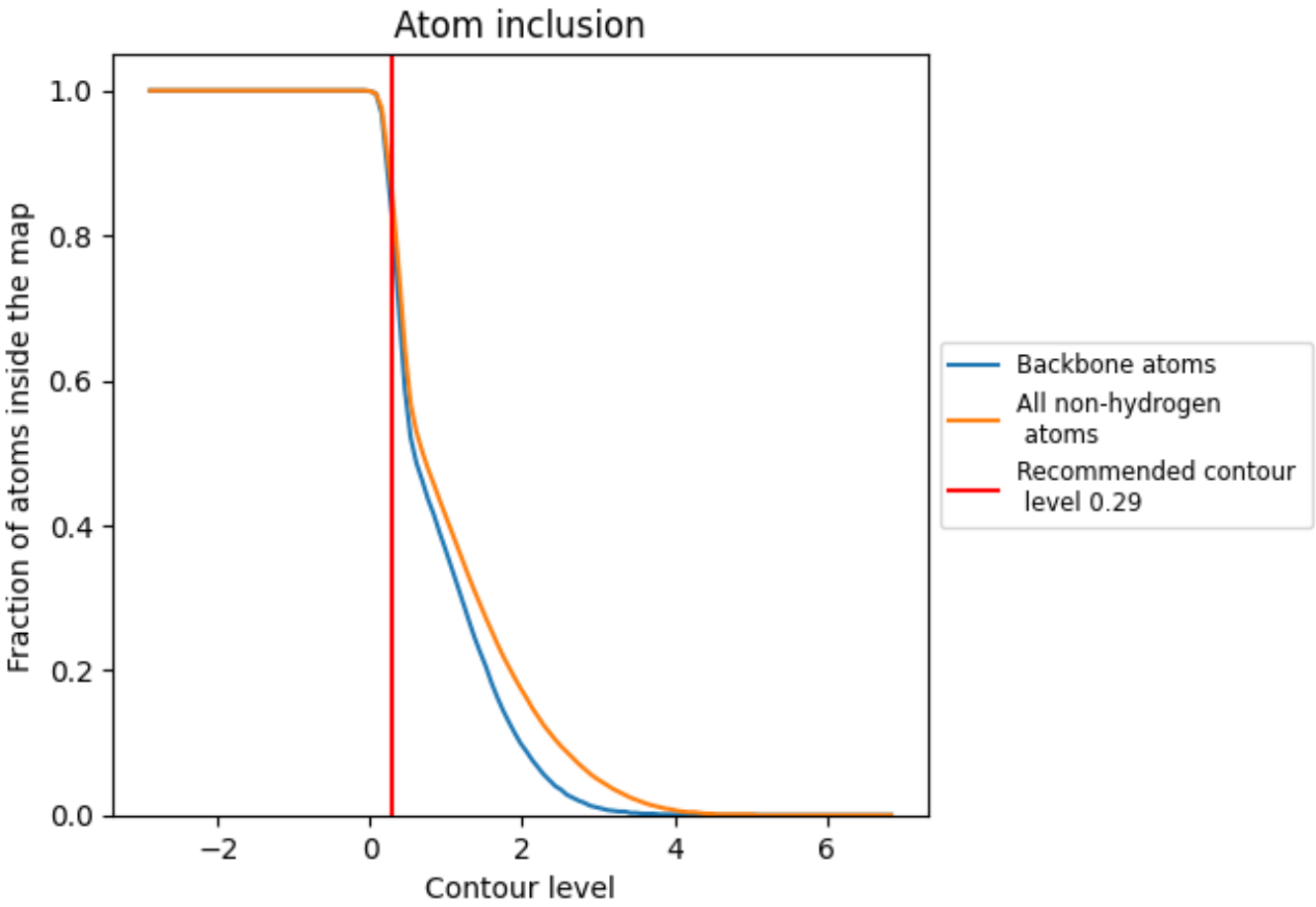
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.29).

9.4 Atom inclusion (i)



At the recommended contour level, 82% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.29) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8590	0.3890
A	0.9340	0.4270
B	0.5730	0.2560
C	0.2430	0.0910
D	0.9670	0.5470
E	0.9760	0.5780
F	0.8220	0.2890
G	0.1910	0.0230
H	0.9720	0.5960
I	0.6570	0.0520
J	0.4870	0.0560
K	0.3900	0.1240
L	0.9650	0.5870
M	0.5050	0.0370
N	0.7480	0.0230
O	0.9520	0.5060
P	0.9650	0.6260
Q	0.9860	0.5940
R	0.9260	0.4250
S	0.6230	0.0670
T	0.9940	0.5990