



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 09:22 PM UTC

PDB ID : 8I9W / pdb_00008i9w
EMDB ID : EMD-35286
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- Dbp10-3
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

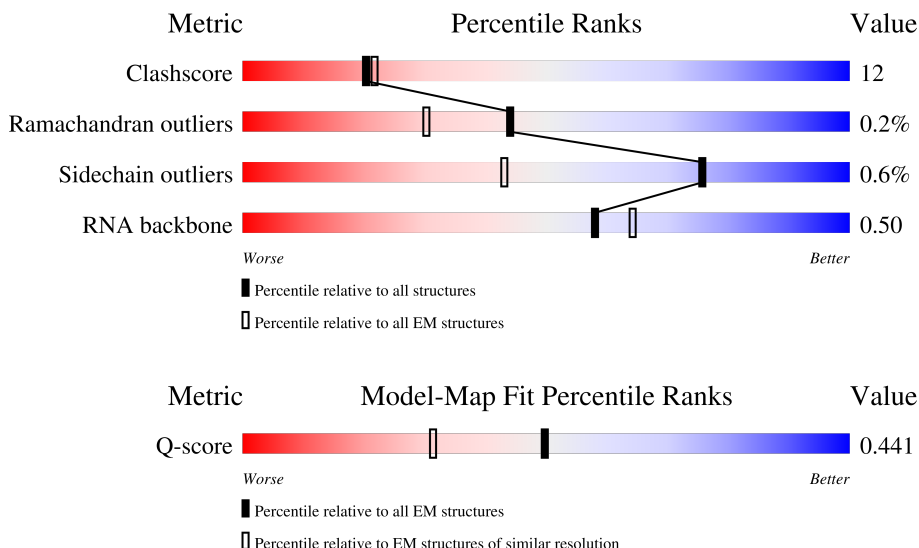
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	C1	3341	
2	C2	319	
3	CA	316	

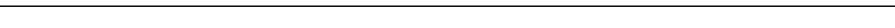
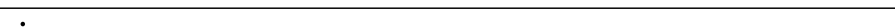
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	CB	391	
5	CC	801	
6	CE	598	
7	CF	270	
8	CG	184	
9	CH	661	
10	CI	414	
11	CJ	679	
12	CK	261	
13	CL	558	
14	CM	249	
14	LF	249	
15	CN	246	
16	CO	120	
17	CP	751	
18	CQ	225	
19	CR	237	
20	CS	834	
21	CT	688	
22	CU	451	
23	CV	147	
24	CX	203	
25	CY	788	
26	Cb	924	
27	Cz	123	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
28	LB	392	
29	LC	365	
30	LE	200	
31	LG	262	
32	LH	192	
33	LK	165	
34	LL	213	
35	LM	142	
36	LN	203	
37	LO	204	
38	LP	187	
39	LQ	213	
40	LS	174	
41	LT	160	
42	LV	139	
43	LX	156	
44	LY	138	
45	Ld	120	
46	Le	131	
47	Lf	109	
48	Lh	935	
49	Li	110	
50	Lj	95	
51	Lq	217	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 136840 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 RNA chain called RNA (3341-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	2163	Total	C	N	O	P	0	0
			46266	20653	8376	15074	2163		

- Molecule 2 is a RNA chain called RNA (319-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	256	Total	C	N	O	P	0	0
			5456	2435	974	1791	256		

- Molecule 3 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CA	251	Total	C	N	O	S	0	0
			2069	1324	381	357	7		

- Molecule 4 is a protein called Ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CB	260	Total	C	N	O	S	0	0
			2063	1322	367	371	3		

- Molecule 5 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	CC	291	Total	C	N	O	P	S	0	0
			2413	1530	403	471	2	7		

- Molecule 6 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CE	463	Total	C	N	O	S	0	0
			3673	2352	643	667	11		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CE	543	LYS	-	insertion	UNP G0RYU9
CE	544	SER	-	insertion	UNP G0RYU9
CE	545	PHE	-	insertion	UNP G0RYU9
CE	546	GLY	-	insertion	UNP G0RYU9
CE	547	PHE	-	insertion	UNP G0RYU9
CE	548	SER	-	insertion	UNP G0RYU9
CE	549	THR	-	insertion	UNP G0RYU9
CE	550	PRO	-	insertion	UNP G0RYU9
CE	551	PRO	-	insertion	UNP G0RYU9
CE	552	ARG	-	insertion	UNP G0RYU9
CE	553	VAL	-	insertion	UNP G0RYU9
CE	554	ASP	-	insertion	UNP G0RYU9
CE	555	ILE	-	insertion	UNP G0RYU9
CE	556	THR	-	insertion	UNP G0RYU9
CE	557	LEU	-	insertion	UNP G0RYU9
CE	558	SER	-	insertion	UNP G0RYU9
CE	559	ALA	-	insertion	UNP G0RYU9
CE	560	SER	-	insertion	UNP G0RYU9
CE	561	LEU	-	insertion	UNP G0RYU9
CE	562	SER	-	insertion	UNP G0RYU9
CE	563	ARG	-	insertion	UNP G0RYU9
CE	564	ASP	-	insertion	UNP G0RYU9
CE	565	LYS	-	insertion	UNP G0RYU9
CE	566	LYS	-	insertion	UNP G0RYU9
CE	567	PRO	-	insertion	UNP G0RYU9
CE	568	GLN	-	insertion	UNP G0RYU9
CE	569	GLY	-	insertion	UNP G0RYU9
CE	570	ARG	-	insertion	UNP G0RYU9
CE	571	ARG	-	insertion	UNP G0RYU9
CE	572	ALA	-	insertion	UNP G0RYU9
CE	573	TYR	-	insertion	UNP G0RYU9
CE	574	GLY	-	insertion	UNP G0RYU9
CE	575	SER	-	insertion	UNP G0RYU9
CE	576	GLN	-	insertion	UNP G0RYU9
CE	577	PRO	-	insertion	UNP G0RYU9
CE	578	ARG	-	insertion	UNP G0RYU9
CE	579	GLN	-	insertion	UNP G0RYU9
CE	580	GLY	-	insertion	UNP G0RYU9
CE	581	GLY	-	insertion	UNP G0RYU9
CE	582	ARG	-	insertion	UNP G0RYU9
CE	583	TYR	-	insertion	UNP G0RYU9
CE	584	LYS	-	insertion	UNP G0RYU9

- Molecule 7 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CF	245	Total	C	N	O	S	0	0
			1945	1222	352	362	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CF	13	ILE	THR	conflict	UNP G0S616
CF	139	THR	PRO	conflict	UNP G0S616
CF	228	ASN	SER	conflict	UNP G0S616
CF	259	ILE	MET	conflict	UNP G0S616

- Molecule 8 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CG	177	Total	C	N	O	S	0	0
			1396	884	247	253	12		

- Molecule 9 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CH	503	Total	C	N	O	S	0	0
			4085	2594	712	763	16		

- Molecule 10 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CI	146	Total	C	N	O	S	0	0
			1196	763	224	204	5		

- Molecule 11 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CJ	379	Total	C	N	O	S	0	0
			3092	1991	543	548	10		

- Molecule 12 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CK	238	Total	C	N	O	S	0	0
			1908	1199	375	330	4		

- Molecule 13 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	CL	397	Total	C	N	O	0	0
			2239	1350	459	430		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CL	69	ARG	ILE	conflict	UNP G0SEW3

- Molecule 14 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CM	223	Total	C	N	O	S	0	0
			1820	1169	340	308	3		
14	LF	247	Total	C	N	O	S	0	0
			2017	1294	376	344	3		

- Molecule 15 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CN	246	Total	C	N	O	S	0	0
			1856	1158	322	369	7		

- Molecule 16 is a protein called DUF2423 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CO	62	Total	C	N	O	S	0	0
			468	290	94	82	2		

- Molecule 17 is a protein called RNA methyltransferase nop2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CP	356	Total	C	N	O	S	0	0
			2798	1777	495	510	16		

- Molecule 18 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CQ	125	Total	C	N	O	S	0	0
			1056	664	219	163	10		

- Molecule 19 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CR	167	Total	C	N	O	S	0	0
			1354	827	278	247	2		

- Molecule 20 is a protein called AdoMet-dependent rRNA methyltransferase SPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CS	235	Total	C	N	O	S	0	0
			1891	1186	359	341	5		

- Molecule 21 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CT	488	Total	C	N	O	S	0	0
			3911	2486	690	719	16		

- Molecule 22 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CU	178	Total	C	N	O	S	0	0
			1415	876	265	271	3		

- Molecule 23 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	CV	139	Total	C	N	O	S	0	0
			1073	672	213	188			

- Molecule 24 is a protein called 60S ribosomal subunit-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	CX	88	Total	C	N	O	S	0	0
			701	435	128	135	3		

- Molecule 25 is a protein called Putative NOC2 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	CY	361	Total	C	N	O	S	0	0
			2919	1874	525	509	11		

- Molecule 26 is a protein called ATP-dependent RNA helicase DBP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Cb	634	Total	C	N	O	S	0	0
			5005	3183	907	902	13		

- Molecule 27 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Cz	70	Total	C	N	O	S	0	0
			592	368	120	101	3		

- Molecule 28 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LB	339	Total	C	N	O	S	0	0
			2696	1713	491	480	12		

- Molecule 29 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LC	362	Total	C	N	O	S	0	0
			2752	1738	526	479	9		

- Molecule 30 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LE	179	Total	C	N	O	S	0	0
			1403	898	255	247	3		

- Molecule 31 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LG	204	Total	C	N	O	S	0	0
			1644	1060	297	282	5		

- Molecule 32 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LH	190	Total	C	N	O	S	0	0
			1496	950	268	272	6		

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	TYR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LEU	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5

- Molecule 33 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LK	146	Total	C	N	O	S	0	0
			1112	701	203	206	2		

- Molecule 34 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LL	117	Total	C	N	O	S	0	0
			964	608	206	148	2		

- Molecule 35 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LM	137	Total	C	N	O	S	0	0
			1101	699	211	190	1		

- Molecule 36 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LN	183	Total	C	N	O	S	0	0
			1563	974	332	253	4		

- Molecule 37 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LO	204	Total	C	N	O	S	0	0
			1618	1039	306	267	6		

- Molecule 38 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LP	153	Total	C	N	O	S	0	0
			1200	747	238	213	2		

- Molecule 39 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LQ	129	Total	C	N	O	S	0	0
			1021	646	200	173	2		

- Molecule 40 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LS	174	Total	C	N	O	S	0	0
			1433	922	267	239	5		

- Molecule 41 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LT	126	Total	C	N	O	S	0	0
			1014	643	196	173	2		

- Molecule 42 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LV	135	Total	C	N	O	S	0	0
			995	633	185	170	7		

- Molecule 43 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	LX	47	Total	C	N	O	0	0
			354	224	72	58		

- Molecule 44 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LY	134	Total	C	N	O	S	0	0
			1065	664	215	184	2		

- Molecule 45 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ld	109	Total	C	N	O	S	0	0
			890	563	171	155	1		

- Molecule 46 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Le	127	Total	C	N	O	S	0	0
			1025	645	209	164	7		

- Molecule 47 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lf	108	Total	C	N	O	S	0	0
			862	546	171	144	1		

- Molecule 48 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	Lh	121	Total	C	N	O	0	0
			995	633	196	166		

- Molecule 49 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	Li	88	Total	C	N	O	S	0
			731	449	162	119	1	0

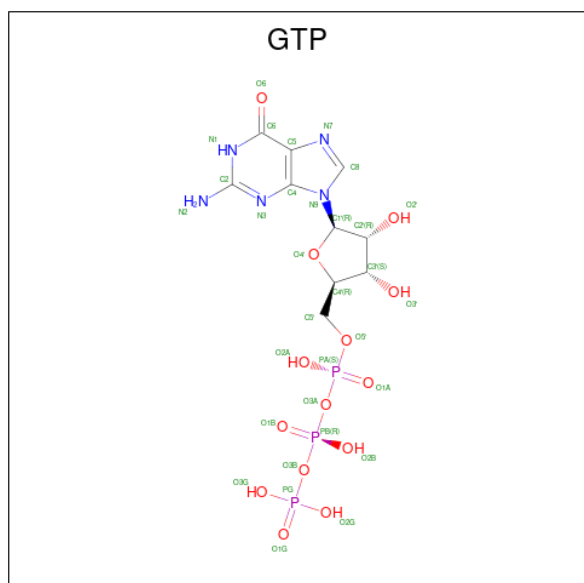
- Molecule 50 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	Lj	74	Total	C	N	O	S	0
			595	365	132	93	5	0

- Molecule 51 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	Lq	207	Total	C	N	O	S	0
			1600	1016	285	291	8	0

- Molecule 52 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms				AltConf
52	CH	1	Total	C	N	O	P
			32	10	5	14	3

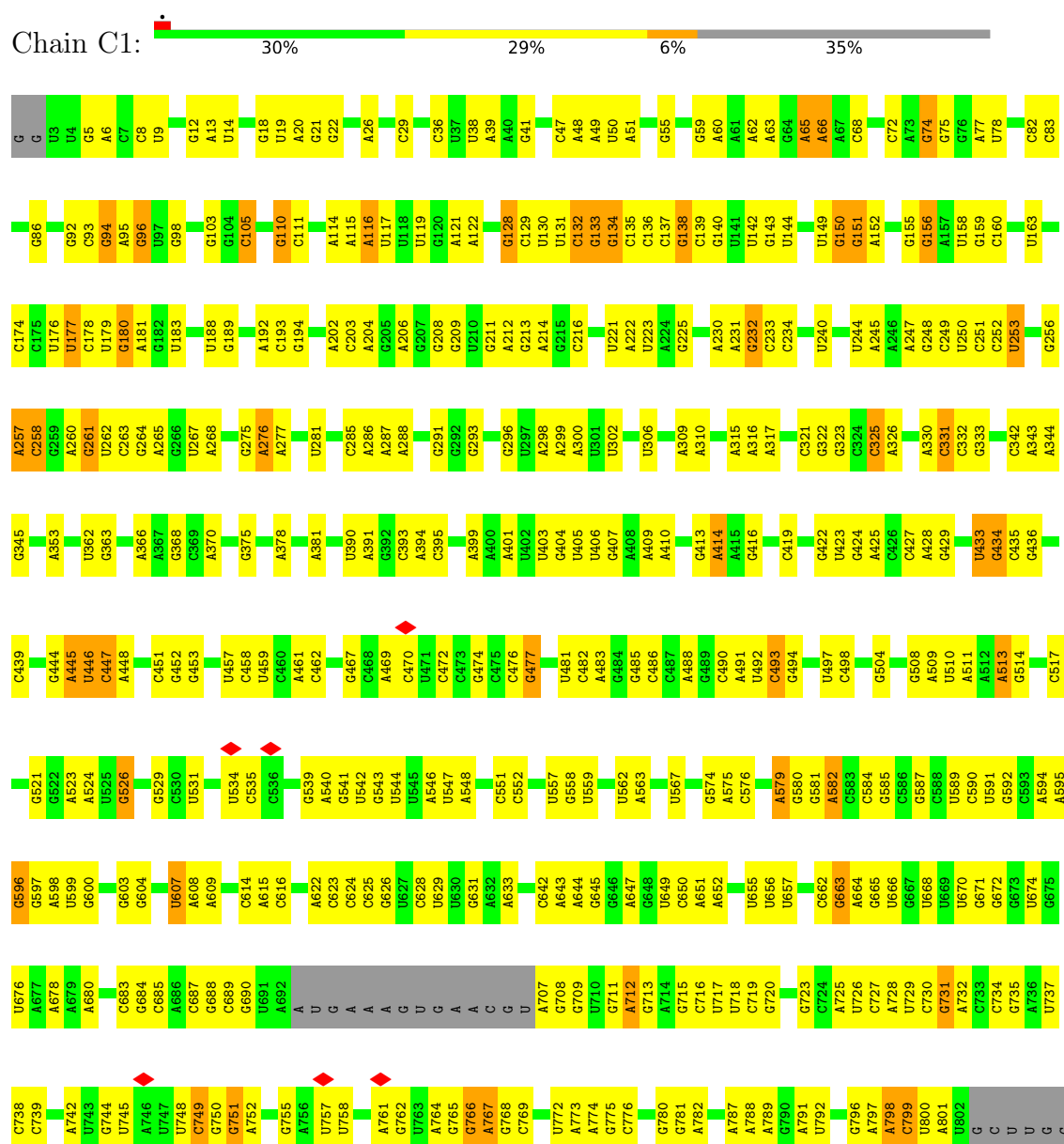
- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
53	CQ	1	Total 1	Zn 1	0
53	Lj	1	Total 1	Zn 1	0

3 Residue-property plots

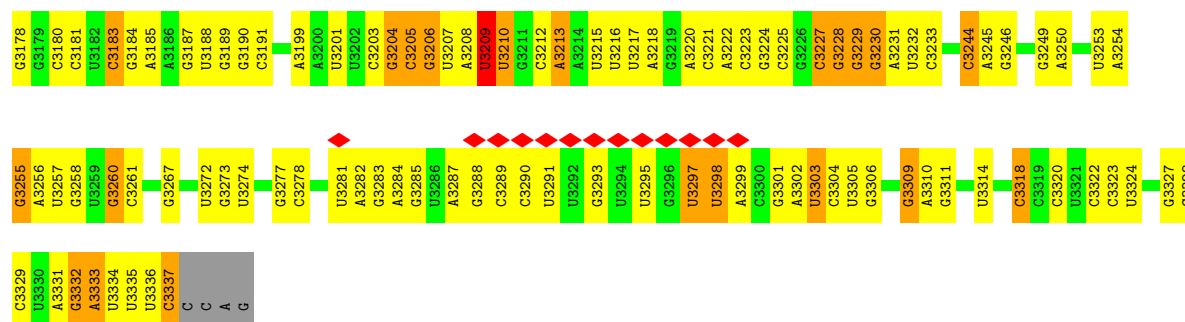
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: RNA (3341-MER)

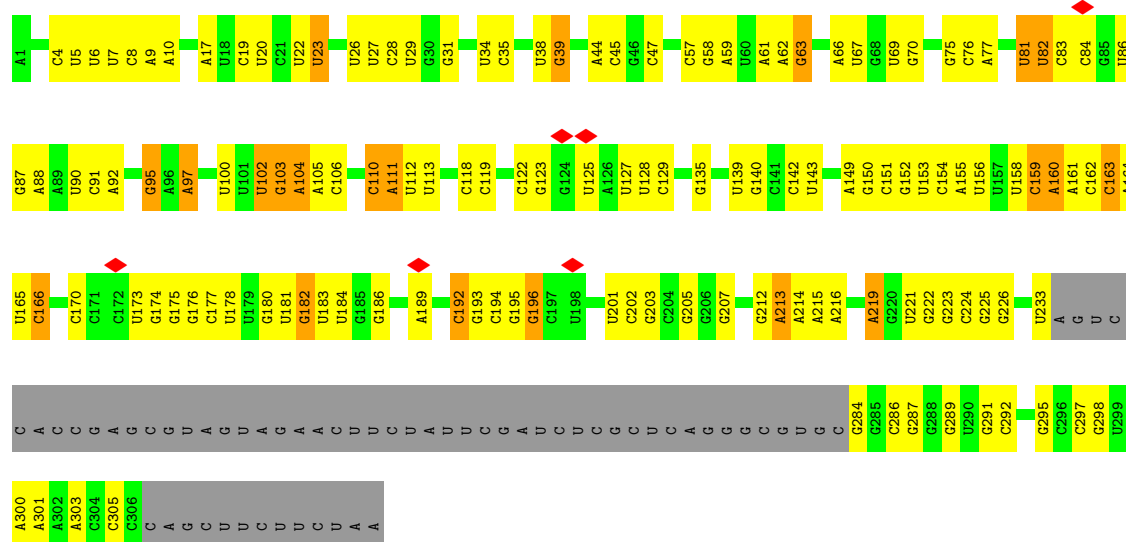




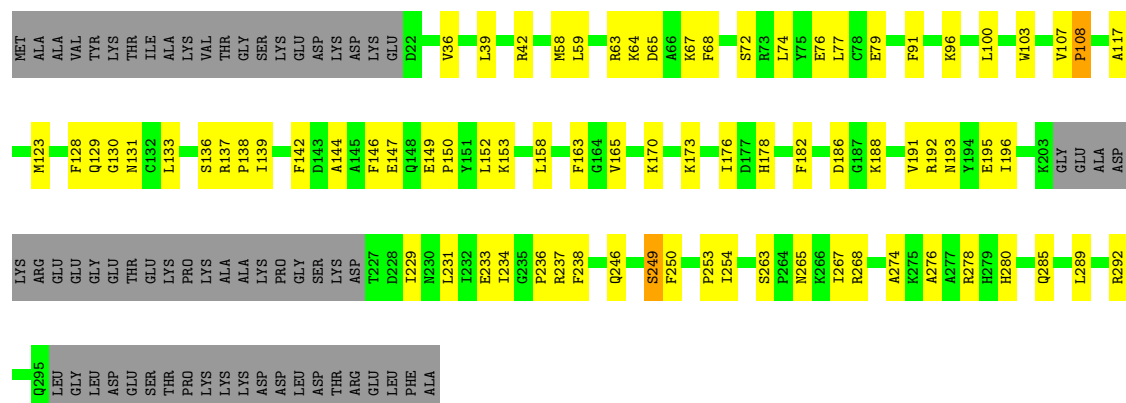




- Molecule 2: RNA (319-MER)

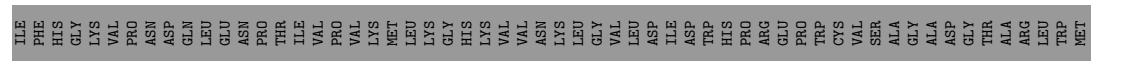


- Molecule 3: Brix domain-containing protein



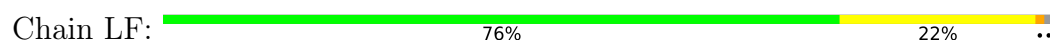
- Molecule 4: Ribosome biogenesis protein C8F11.04

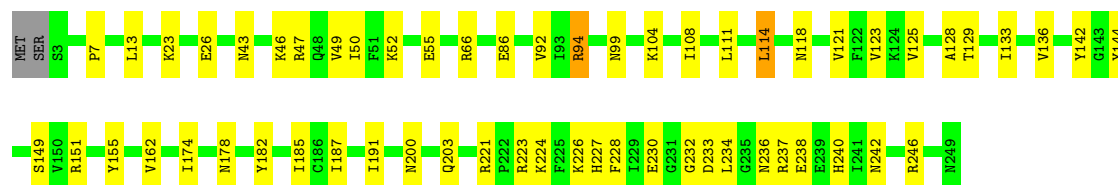




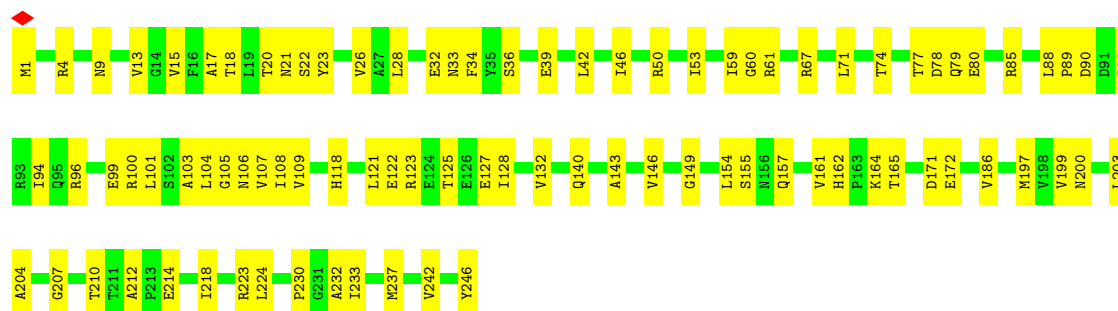




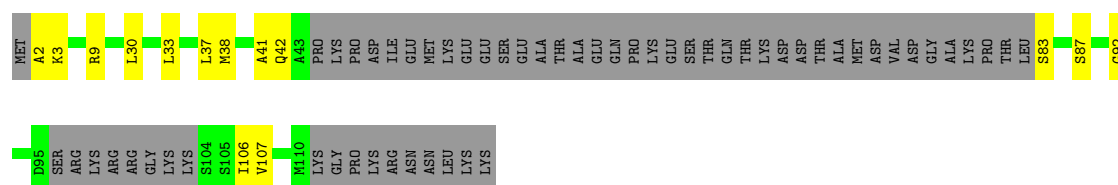




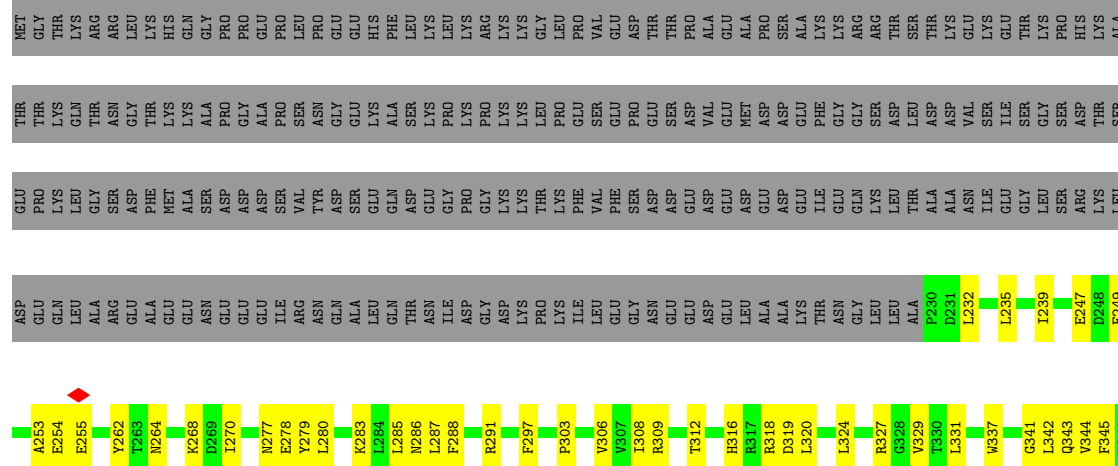
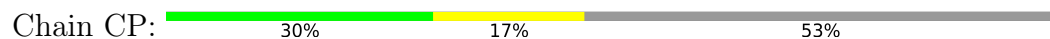
• Molecule 15: Eukaryotic translation initiation factor 6

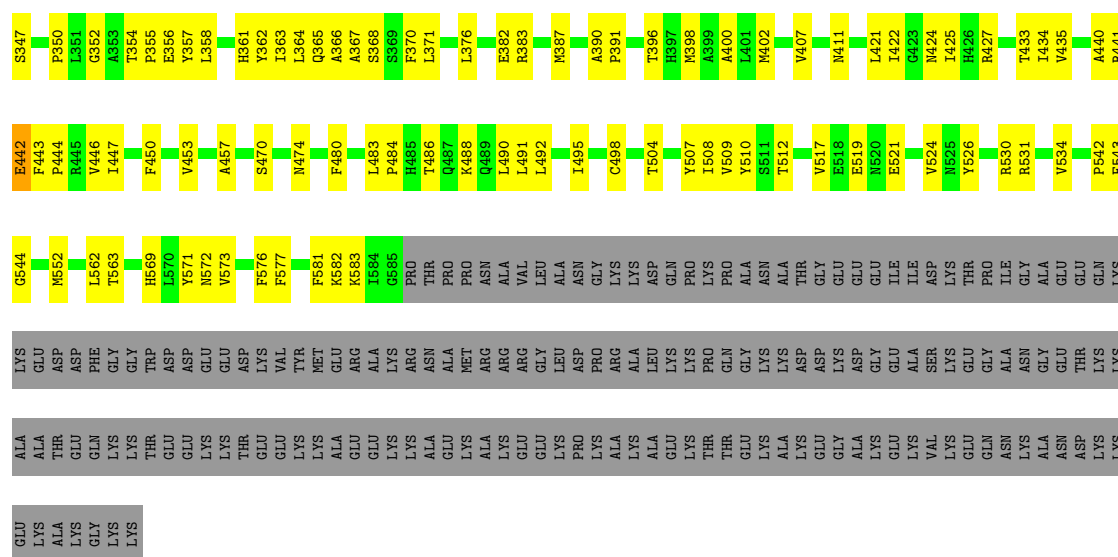


• Molecule 16: DUF2423 domain-containing protein

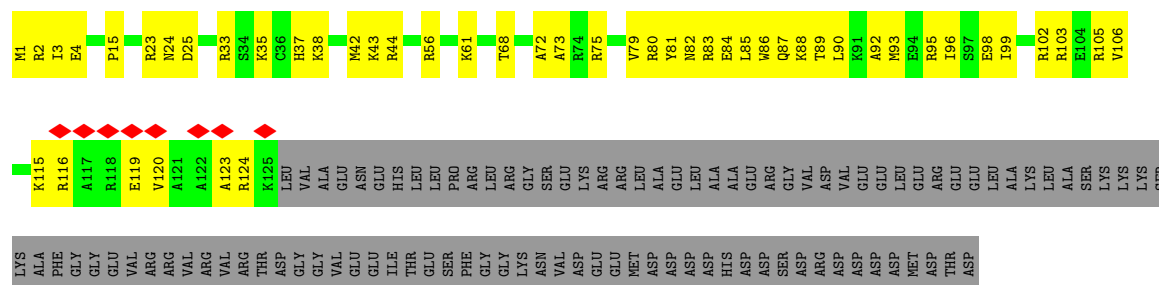
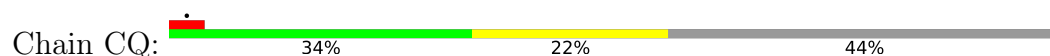


• Molecule 17: RNA methyltransferase nop2-like protein

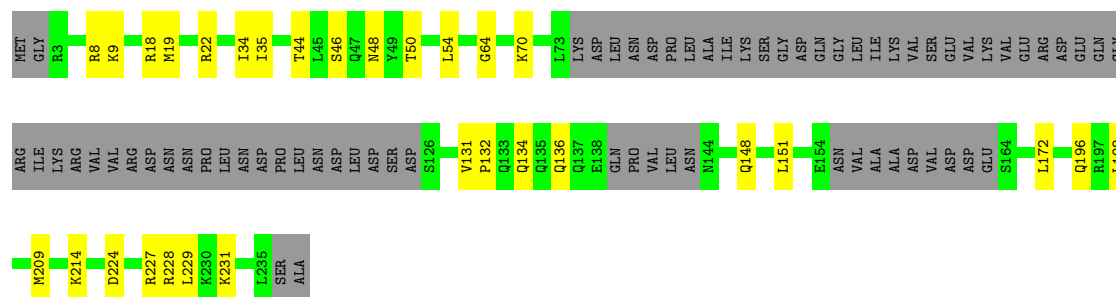




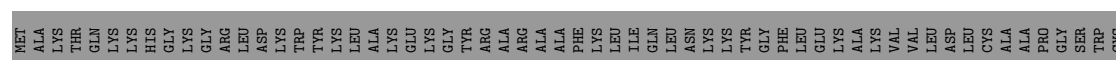
• Molecule 18: Ribosome biogenesis protein RLP24

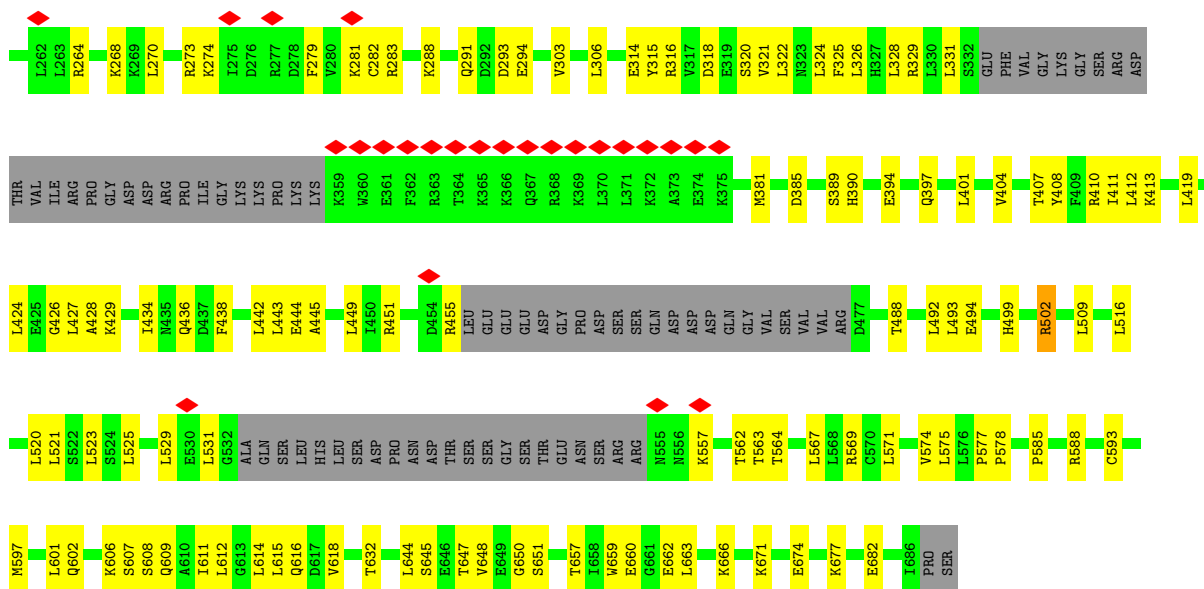


• Molecule 19: Nucleolar protein 16

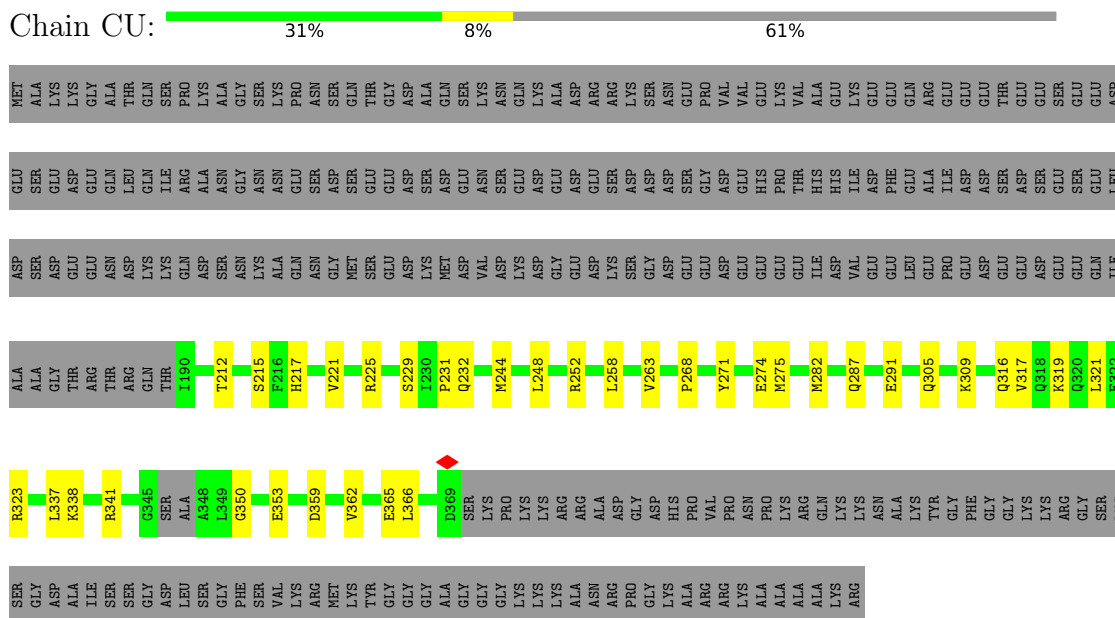


• Molecule 20: AdoMet-dependent rRNA methyltransferase SPB1

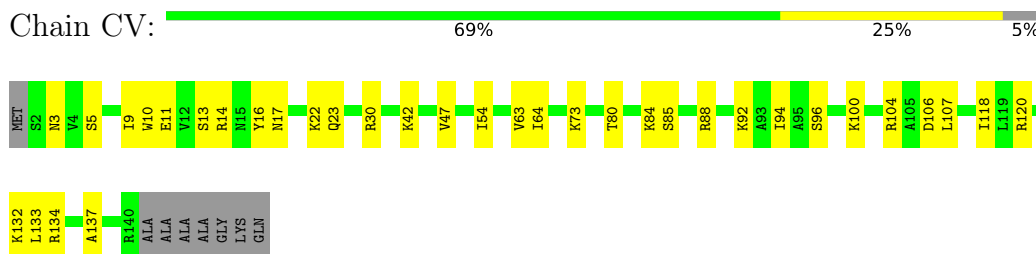




- Molecule 22: rRNA-processing protein EBP2

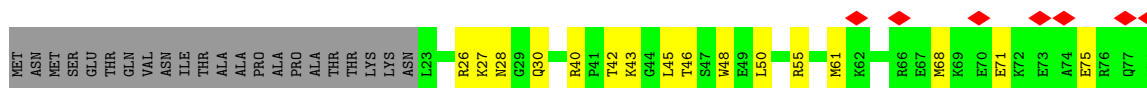
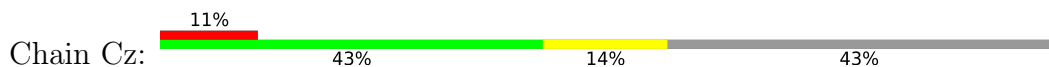


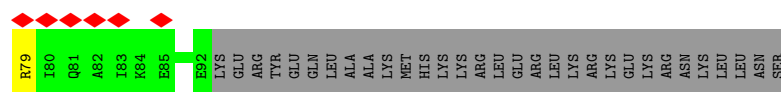
- Molecule 23: Putative 60S ribosomal protein



- Molecule 24: 60S ribosomal subunit-like protein

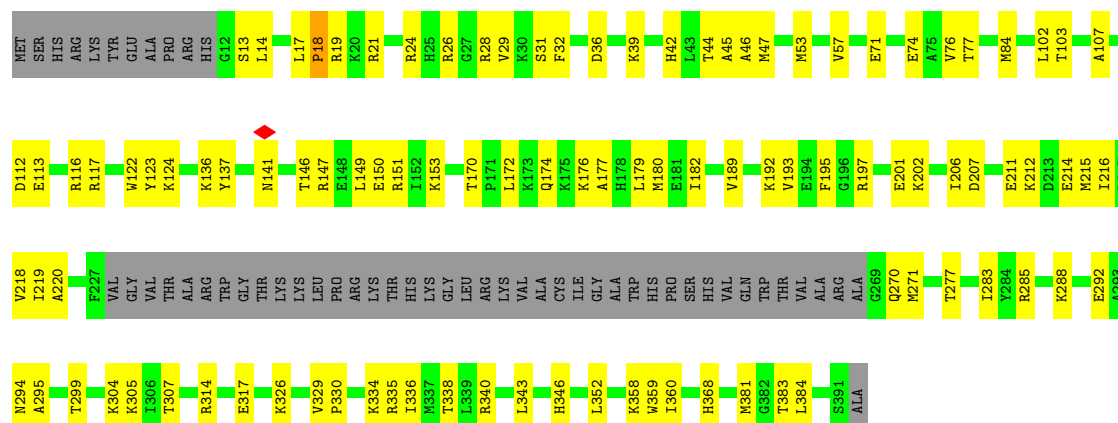
Chain Cb:





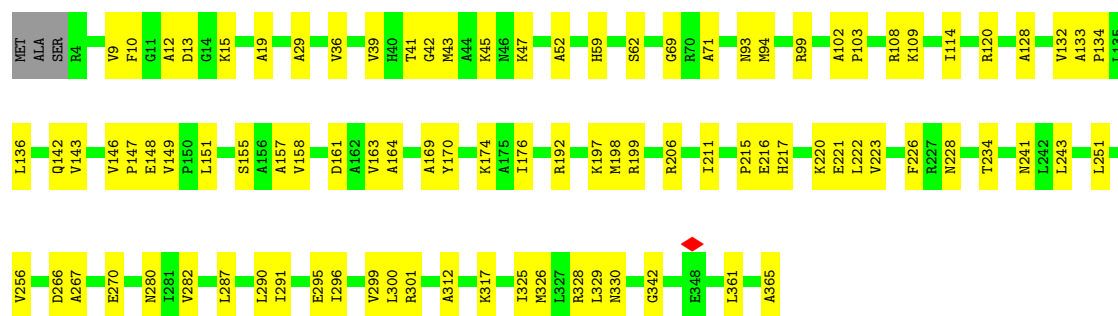
- Molecule 28: 60S ribosomal protein L3-like protein

Chain LB: 60% 26% 14%



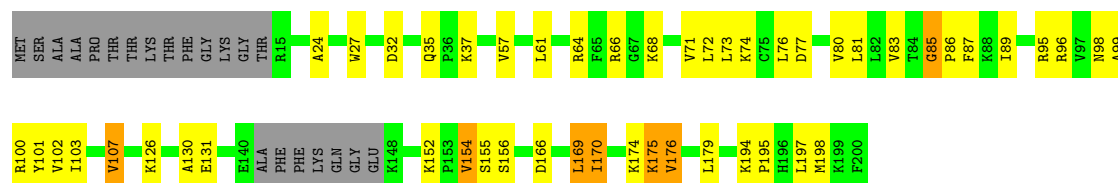
- Molecule 29: 60S ribosomal protein L4-like protein

Chain LC: 74% 25% .



- Molecule 30: 60S ribosomal protein L6

Chain LE: 64% 22% 10%



- Molecule 31: 60S ribosomal protein L8

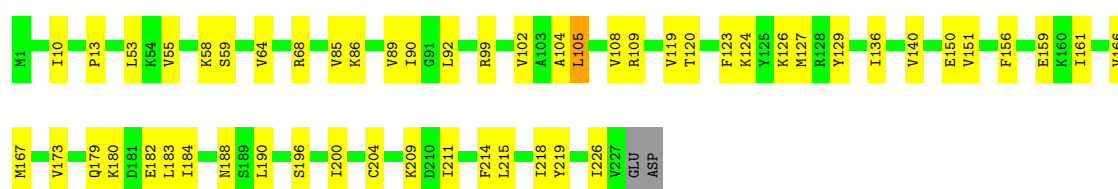
Chain LG: 58% 19% 22%





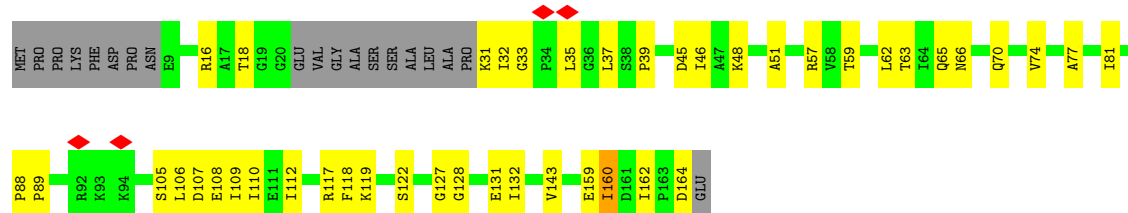
- Molecule 32: 60S ribosomal protein l9-like protein

Chain LH: 71% 27% ..



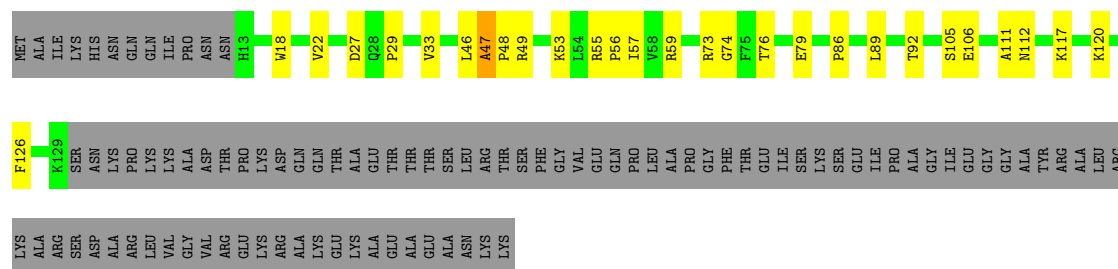
- Molecule 33: 60S ribosomal protein L12-like protein

Chain LK: 62% 26% 12%



- Molecule 34: 60S ribosomal protein L13

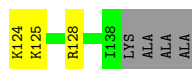
Chain LL: 42% 13% 45%



- Molecule 35: 60S ribosomal protein L14-like protein

Chain LM: 71% 25%





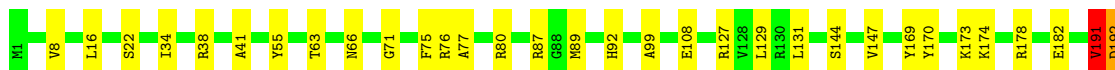
- Molecule 36: Ribosomal protein L15

Chain LN: 67% 21% 10%



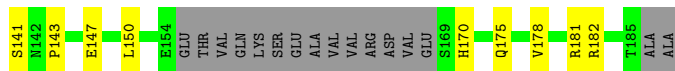
- Molecule 37: 60S ribosomal protein L16-like protein

Chain LO: 83% 16%



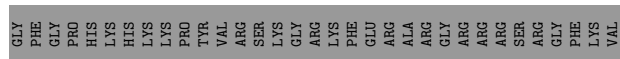
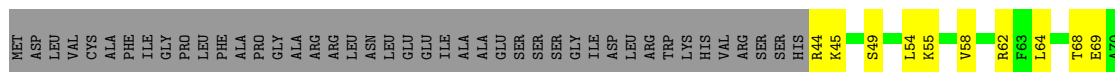
- Molecule 38: 60S ribosomal protein l17-like protein

Chain LP: 65% 17% 18%



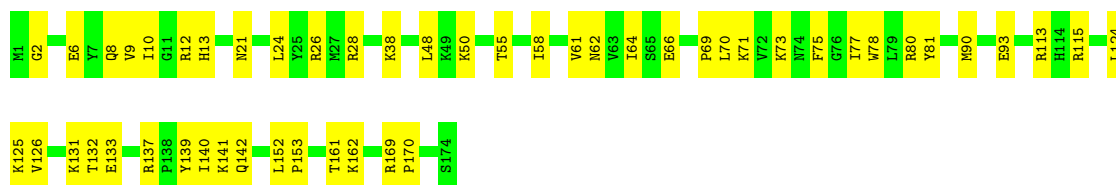
- Molecule 39: Ribosomal protein L18-like protein

Chain LQ: 41% 20% 39%

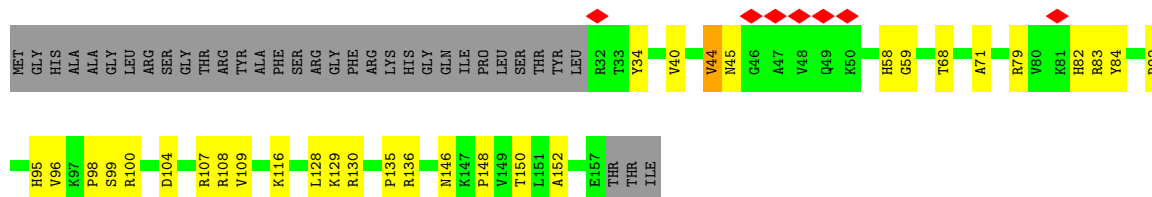


- Molecule 40: 60S ribosomal protein L20

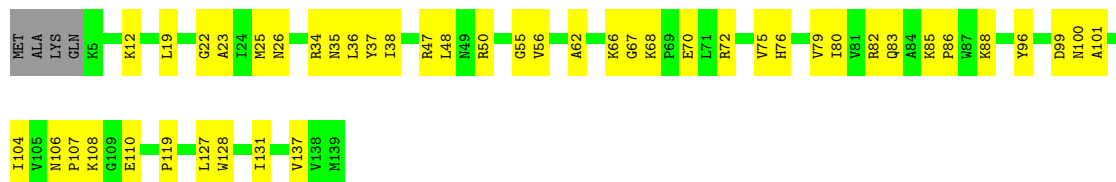
Chain LS: 71% 29%



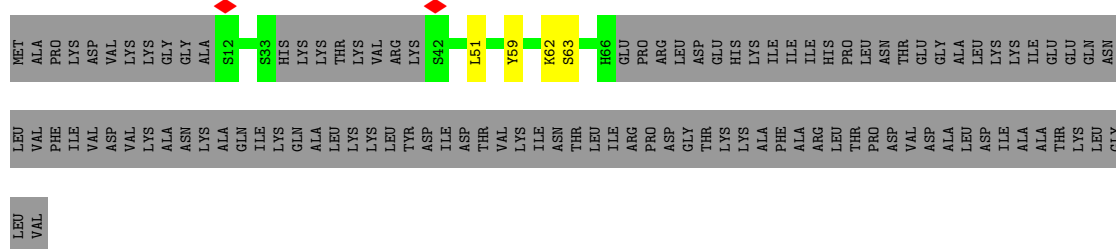
- Molecule 41: 60S ribosomal protein l21-like protein



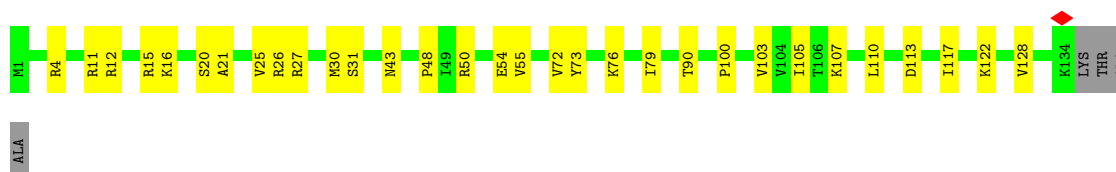
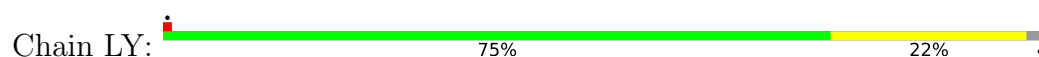
- Molecule 42: 60S ribosomal protein l23-like protein



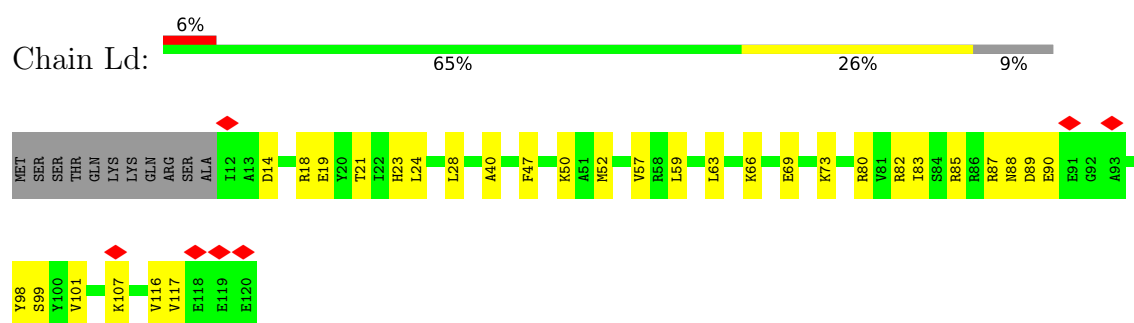
- Molecule 43: 60S ribosomal protein L25-like protein



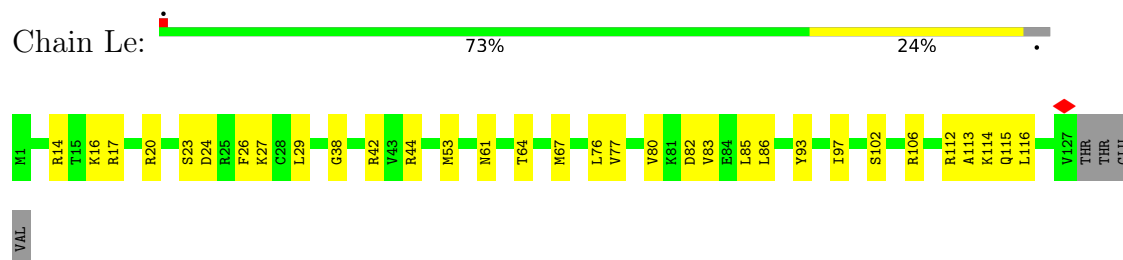
- Molecule 44: 60S ribosomal protein L26-like protein



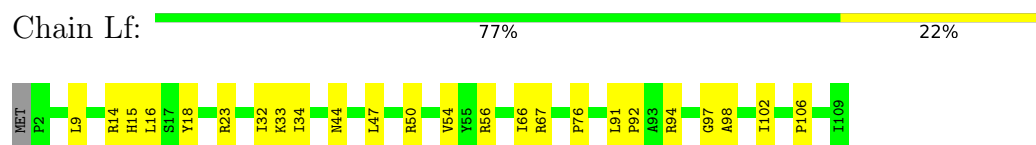
- Molecule 45: Putative 60S ribosomal protein



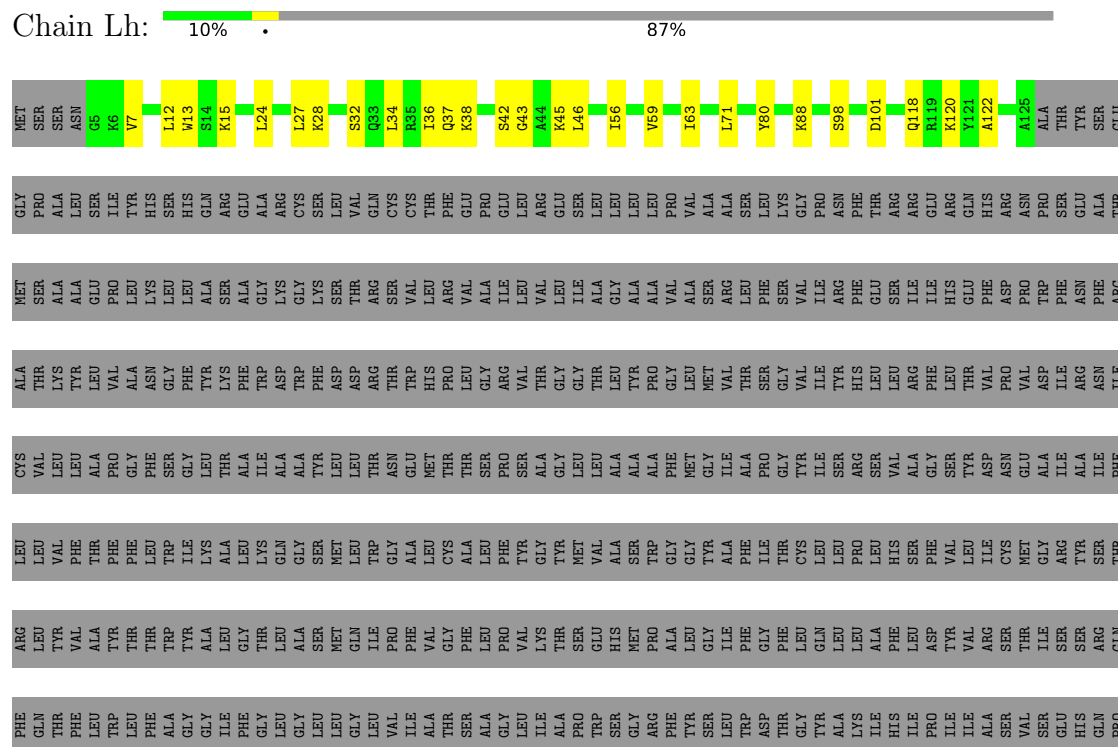
- Molecule 46: 60S ribosomal protein L32-like protein



- Molecule 47: 60S ribosomal protein l33-like protein



- Molecule 48: dolichyl-diphosphooligosaccharide--protein glycotransferase

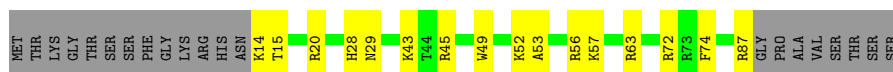


[illegible]

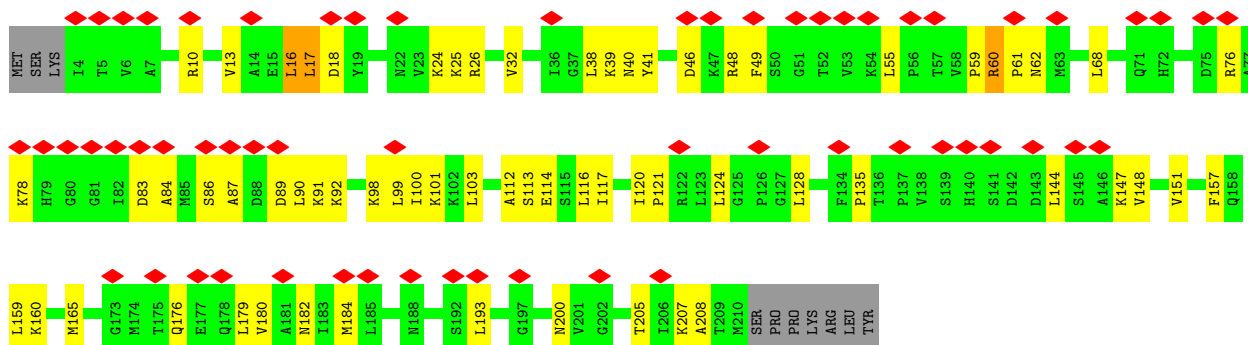
- Molecule 49: 60S ribosomal protein L36



- Molecule 50: Ribosomal protein L37



- Molecule 51: Ribosomal protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	30333	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.497	Depositor
Minimum map value	-0.266	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	438.9, 438.9, 438.9	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, SEP, ZN, GTP

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	C1	0.21	0/51760	0.34	3/80668 (0.0%)
2	C2	0.23	0/6097	0.35	0/9499
3	CA	0.32	0/2115	0.58	1/2840 (0.0%)
4	CB	0.25	0/2109	0.57	1/2866 (0.0%)
5	CC	0.21	0/2461	0.46	0/3348
6	CE	0.18	0/3743	0.47	0/5045
7	CF	0.18	0/1982	0.53	0/2671
8	CG	0.38	0/1422	0.69	1/1920 (0.1%)
9	CH	0.31	0/4162	0.60	0/5618
10	CI	0.25	0/1225	0.71	4/1645 (0.2%)
11	CJ	0.18	0/3171	0.50	1/4286 (0.0%)
12	CK	0.21	0/1940	0.50	0/2601
13	CL	0.16	0/2247	0.43	0/3076
14	CM	0.22	0/1851	0.57	0/2481
14	LF	0.29	0/2055	0.51	0/2758
15	CN	0.17	0/1881	0.47	0/2560
16	CO	0.17	0/470	0.41	0/619
17	CP	0.39	0/2859	0.71	1/3870 (0.0%)
18	CQ	0.28	0/1077	0.60	0/1427
19	CR	0.21	0/1369	0.44	0/1828
20	CS	0.14	0/1912	0.43	0/2534
21	CT	0.19	0/3974	0.49	0/5357
22	CU	0.26	0/1428	0.51	0/1910
23	CV	0.16	0/1091	0.42	0/1468
24	CX	0.18	0/705	0.47	0/938
25	CY	0.21	0/2971	0.59	0/4006
26	Cb	0.28	0/5097	0.57	4/6868 (0.1%)
27	Cz	0.15	0/598	0.42	0/785
28	LB	0.36	0/2748	0.64	1/3684 (0.0%)
29	LC	0.25	0/2809	0.46	1/3787 (0.0%)
30	LE	0.58	0/1428	0.93	1/1921 (0.1%)
31	LG	0.38	0/1667	0.74	5/2230 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LH	0.37	0/1516	0.68	0/2038
33	LK	0.15	0/1124	0.47	0/1507
34	LL	0.33	0/983	0.52	0/1318
35	LM	0.30	0/1120	0.54	0/1507
36	LN	0.40	0/1595	0.68	4/2132 (0.2%)
37	LO	0.30	0/1652	0.54	0/2215
38	LP	0.14	0/1217	0.33	0/1636
39	LQ	0.17	0/1033	0.41	0/1391
40	LS	0.16	0/1468	0.41	0/1975
41	LT	0.11	0/1033	0.29	0/1389
42	LV	0.21	0/1013	0.46	0/1361
43	LX	0.12	0/361	0.30	0/482
44	LY	0.16	0/1079	0.40	0/1443
45	Ld	0.44	0/904	0.58	0/1209
46	Le	0.21	0/1043	0.42	0/1389
47	Lf	0.20	0/883	0.45	0/1187
48	Lh	0.34	0/1006	0.66	2/1338 (0.1%)
49	Li	0.23	0/738	0.46	0/971
50	Lj	0.23	0/606	0.47	0/803
51	Lq	0.26	0/1621	0.57	0/2180
All	All	0.25	0/144419	0.47	30/206585 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
28	LB	0	1
36	LN	0	1
51	Lq	0	1
All	All	0	3

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1134	G	C4'-C3'-O3'	7.57	120.76	109.40
36	LN	39	ALA	CA-C-N	7.51	135.88	121.54
36	LN	39	ALA	C-N-CA	7.51	135.88	121.54
10	CI	313	ARG	CB-CG-CD	7.05	127.52	111.30
36	LN	124	ASP	CA-CB-CG	6.91	119.51	112.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	3267	G	C4'-C3'-C2'	-6.61	96.00	102.60
10	CI	312	ARG	CA-C-N	-6.44	109.88	121.14
10	CI	312	ARG	C-N-CA	-6.44	109.88	121.14
31	LG	192	LEU	N-CA-C	-6.31	104.33	111.14
26	Cb	328	ILE	N-CA-C	-6.10	107.19	113.10
36	LN	98	LEU	N-CA-C	-5.74	105.77	112.89
31	LG	189	LEU	N-CA-C	-5.59	105.18	111.28
11	CJ	119	PRO	CA-N-CD	-5.59	104.17	112.00
1	C1	3209	U	P-O3'-C3'	5.41	128.31	120.20
8	CG	167	GLN	N-CA-C	-5.40	107.70	114.56
10	CI	313	ARG	N-CA-CB	5.32	119.08	110.40
26	Cb	290	PRO	CB-CA-C	-5.29	105.79	111.56
3	CA	108	PRO	CB-CA-C	-5.26	98.84	112.00
4	CB	80	PRO	N-CA-C	5.18	119.61	111.38
29	LC	267	ALA	CA-C-O	-5.14	115.61	121.00
26	Cb	327	ASP	CA-C-N	-5.13	115.59	122.72
26	Cb	327	ASP	C-N-CA	-5.13	115.59	122.72
31	LG	101	ARG	CB-CA-C	5.12	117.50	109.27
30	LE	131	GLU	N-CA-C	-5.10	107.03	113.20
48	Lh	7	VAL	CA-C-N	-5.08	115.72	122.72
48	Lh	7	VAL	C-N-CA	-5.08	115.72	122.72
17	CP	577	PHE	CA-CB-CG	5.01	118.81	113.80
28	LB	14	LEU	N-CA-C	-5.01	107.12	113.18
31	LG	193	VAL	CA-C-N	-5.00	115.71	123.17
31	LG	193	VAL	C-N-CA	-5.00	115.71	123.17

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
28	LB	17	LEU	Peptide
36	LN	39	ALA	Peptide
51	Lq	60	ARG	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C1	46266	0	23326	857	0
2	C2	5456	0	2762	89	0
3	CA	2069	0	2109	59	0
4	CB	2063	0	2131	86	0
5	CC	2413	0	2318	62	0
6	CE	3673	0	3778	97	0
7	CF	1945	0	1965	62	0
8	CG	1396	0	1420	51	0
9	CH	4085	0	4123	133	0
10	CI	1196	0	1202	56	0
11	CJ	3092	0	3102	135	0
12	CK	1908	0	2019	66	0
13	CL	2239	0	1495	19	0
14	CM	1820	0	1938	54	0
14	LF	2017	0	2130	42	0
15	CN	1856	0	1856	66	0
16	CO	468	0	503	11	0
17	CP	2798	0	2812	110	0
18	CQ	1056	0	1110	66	0
19	CR	1354	0	1400	30	0
20	CS	1891	0	1953	38	0
21	CT	3911	0	4023	112	0
22	CU	1415	0	1457	33	0
23	CV	1073	0	1130	36	0
24	CX	701	0	742	23	0
25	CY	2919	0	3020	137	0
26	Cb	5005	0	5159	176	0
27	Cz	592	0	640	16	0
28	LB	2696	0	2797	80	0
29	LC	2752	0	2878	73	0
30	LE	1403	0	1503	37	0
31	LG	1644	0	1793	38	0
32	LH	1496	0	1575	38	0
33	LK	1112	0	1190	30	0
34	LL	964	0	1041	23	0
35	LM	1101	0	1170	28	0
36	LN	1563	0	1618	31	0
37	LO	1618	0	1714	28	0
38	LP	1200	0	1242	28	0
39	LQ	1021	0	1118	34	0
40	LS	1433	0	1496	41	0
41	LT	1014	0	1073	23	0
42	LV	995	0	1055	42	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	LX	354	0	383	5	0
44	LY	1065	0	1156	24	0
45	Ld	890	0	940	20	0
46	Le	1025	0	1104	28	0
47	Lf	862	0	891	18	0
48	Lh	995	0	1110	22	0
49	Li	731	0	797	21	0
50	Lj	595	0	625	20	0
51	Lq	1600	0	1703	48	0
52	CH	32	0	12	0	0
53	CQ	1	0	0	0	0
53	Lj	1	0	0	0	0
All	All	136840	0	113607	3035	0

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

All (3035) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3118:A:H61	1:C1:3225:C:N4	1.34	1.26
1:C1:3118:A:N6	1:C1:3225:C:H42	1.34	1.22
1:C1:2848:A:N6	1:C1:2871:C:H42	1.50	1.10
1:C1:2848:A:H61	1:C1:2871:C:N4	1.52	1.05
1:C1:891:G:H1	1:C1:898:A:N6	1.57	1.02
1:C1:3273:G:H22	1:C1:3309:G:H1'	1.25	1.01
2:C2:196:G:H1	2:C2:201:U:H3	1.01	0.97
1:C1:407:G:H21	1:C1:1381:A:N6	1.63	0.96
21:CT:525:LEU:HG	21:CT:602:GLN:NE2	1.81	0.96
26:Cb:22:PHE:HD2	26:Cb:292:LEU:HB2	1.31	0.95
1:C1:2404:G:H1	1:C1:2467:U:H3	1.05	0.94
1:C1:2091:U:H3	1:C1:2285:G:H1	1.13	0.94
50:Lj:15:THR:O	50:Lj:28:HIS:HA	1.67	0.93
14:CM:148:LYS:HD2	14:CM:246:ARG:HH21	1.34	0.93
1:C1:891:G:H1	1:C1:898:A:H61	0.93	0.92
1:C1:2922:G:O6	1:C1:2926:G:C6	2.23	0.91
23:CV:13:SER:HB2	23:CV:17:ASN:HD21	1.34	0.91
1:C1:1046:A:N6	1:C1:1074:C:C2	2.38	0.90
1:C1:407:G:H21	1:C1:1381:A:H61	0.94	0.88
7:CF:88:GLY:HA3	7:CF:91:ARG:HH11	1.38	0.88
40:LS:6:GLU:HB2	40:LS:64:ILE:O	1.74	0.87

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CP:306:VAL:HG23	17:CP:344:VAL:HB	1.57	0.87
28:LB:207:ASP:OD2	28:LB:288:LYS:NZ	2.09	0.86
7:CF:21:GLU:OE1	7:CF:25:ARG:NH1	2.07	0.86
11:CJ:267:GLU:HB3	11:CJ:381:GLN:HE21	1.39	0.86
1:C1:66:A:N6	1:C1:75:G:N2	2.23	0.85
17:CP:470:SER:OG	17:CP:474:ASN:ND2	2.08	0.85
1:C1:2735:G:H1	1:C1:2741:U:H3	0.87	0.85
1:C1:670:U:O4	1:C1:684:G:O6	1.95	0.85
1:C1:264:G:H1'	49:Li:91:ARG:HH12	1.43	0.84
26:Cb:165:VAL:HG12	26:Cb:239:VAL:HB	1.60	0.83
1:C1:1157:C:N4	37:LO:89:MET:SD	2.51	0.83
15:CN:1:MET:H2	15:CN:224:LEU:HB3	1.43	0.82
29:LC:151:LEU:HD23	29:LC:256:VAL:HG12	1.62	0.82
9:CH:183:VAL:HG21	9:CH:219:ASP:HB2	1.62	0.81
1:C1:2387:G:O6	1:C1:2563:G:C2	2.34	0.81
6:CE:528:ARG:O	6:CE:532:ASP:HB3	1.80	0.81
9:CH:19:ILE:HG23	9:CH:23:ARG:HH21	1.46	0.80
1:C1:1156:G:H21	1:C1:1157:C:H41	1.29	0.80
16:CO:38:MET:O	16:CO:42:GLN:NE2	2.15	0.80
26:Cb:100:ASN:HA	26:Cb:103:ARG:HH11	1.47	0.80
40:LS:8:GLN:HE21	40:LS:62:ASN:HB2	1.44	0.80
21:CT:184:ILE:HD13	21:CT:207:GLU:HB3	1.64	0.79
2:C2:95:G:OP2	50:Lj:72:ARG:NH1	2.15	0.79
1:C1:36:C:H4'	1:C1:789:A:H2	1.46	0.79
8:CG:121:ARG:HH21	8:CG:137:MET:HA	1.48	0.79
26:Cb:322:LEU:HB2	26:Cb:517:ASN:HD21	1.48	0.79
47:Lf:44:ASN:HA	47:Lf:47:LEU:HD13	1.65	0.78
8:CG:161:GLY:HA2	12:CK:141:LYS:HD3	1.63	0.78
9:CH:236:MET:HA	9:CH:239:VAL:HG12	1.65	0.78
1:C1:2433:U:O2	1:C1:2436:G:O6	2.02	0.78
30:LE:89:ILE:HD11	30:LE:170:ILE:HD11	1.66	0.78
9:CH:248:ALA:HB2	9:CH:338:LEU:HD21	1.63	0.77
21:CT:493:LEU:HG	21:CT:509:LEU:HD21	1.65	0.77
25:CY:439:LEU:O	25:CY:443:ASN:ND2	2.17	0.77
39:LQ:138:ARG:HH12	39:LQ:148:THR:HG21	1.49	0.77
1:C1:3118:A:N1	1:C1:3225:C:N3	2.33	0.77
1:C1:529:G:H1	1:C1:542:U:H3	1.29	0.77
1:C1:144:U:OP2	36:LN:49:ARG:NH2	2.17	0.77
21:CT:274:LYS:H	21:CT:279:PHE:HE2	1.30	0.77
1:C1:529:G:O6	1:C1:543:G:C2	2.38	0.77
1:C1:2848:A:N1	1:C1:2871:C:N3	2.32	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2922:G:N2	1:C1:2925:A:C5	2.52	0.77
1:C1:3288:G:H1	1:C1:3297:U:H3	1.33	0.77
21:CT:424:LEU:HB3	21:CT:488:THR:HG21	1.67	0.76
9:CH:309:THR:HG22	9:CH:316:ILE:HD13	1.67	0.76
8:CG:87:LEU:HD21	8:CG:141:PRO:HB2	1.68	0.76
26:Cb:837:VAL:O	26:Cb:841:SER:HB3	1.86	0.76
25:CY:386:PHE:O	25:CY:397:ARG:NH2	2.18	0.76
25:CY:421:LYS:HE3	25:CY:425:GLN:HE22	1.49	0.76
19:CR:209:MET:HE1	19:CR:229:LEU:HD11	1.67	0.76
26:Cb:493:ARG:HH11	26:Cb:581:ALA:HB2	1.51	0.76
1:C1:248:G:O2'	19:CR:148:GLN:NE2	2.19	0.75
1:C1:974:G:O6	1:C1:1038:U:O4	2.04	0.75
10:CI:307:ALA:O	10:CI:310:GLU:HG3	1.85	0.75
9:CH:228:LEU:HB2	26:Cb:593:LYS:HZ3	1.51	0.75
26:Cb:227:GLU:HG3	26:Cb:813:PHE:HB2	1.69	0.75
9:CH:167:ARG:HG3	9:CH:342:ARG:HH11	1.51	0.75
28:LB:45:ALA:H	28:LB:182:ILE:HG23	1.50	0.75
1:C1:66:A:N6	1:C1:75:G:C2	2.55	0.75
19:CR:35:ILE:HG21	34:LL:47:ALA:HB1	1.67	0.75
25:CY:555:ILE:HG23	25:CY:571:LEU:HD13	1.68	0.75
32:LH:68:ARG:NH1	32:LH:188:ASN:OD1	2.20	0.75
10:CI:306:VAL:HA	10:CI:309:GLU:HG3	1.68	0.75
32:LH:140:VAL:HG22	32:LH:151:VAL:HG22	1.69	0.75
44:LY:31:SER:HA	44:LY:48:PRO:HA	1.69	0.75
12:CK:184:VAL:HG21	12:CK:223:VAL:HG21	1.68	0.74
17:CP:425:ILE:HG21	17:CP:433:THR:HG21	1.68	0.74
26:Cb:493:ARG:HH22	26:Cb:577:GLY:H	1.35	0.74
1:C1:1156:G:N2	1:C1:1157:C:H41	1.85	0.74
6:CE:199:ILE:HG22	6:CE:238:ILE:HD13	1.70	0.74
9:CH:202:SER:OG	12:CK:4:ASN:ND2	2.18	0.74
11:CJ:40:LYS:NZ	11:CJ:129:GLU:OE2	2.21	0.74
39:LQ:106:LYS:O	39:LQ:127:GLU:HB3	1.88	0.74
1:C1:2361:A:N6	1:C1:2900:C:C4	2.56	0.74
26:Cb:479:LEU:HD13	26:Cb:559:ARG:HG3	1.70	0.74
25:CY:488:ARG:HH12	25:CY:603:LYS:HD3	1.53	0.73
21:CT:666:LYS:HE3	25:CY:568:TYR:HB2	1.69	0.73
14:LF:94:ARG:HB2	14:LF:114:LEU:HB3	1.71	0.73
39:LQ:82:MET:HE2	39:LQ:86:ASN:HB3	1.71	0.73
21:CT:615:LEU:HA	21:CT:618:VAL:HG22	1.70	0.73
1:C1:1046:A:N1	1:C1:1074:C:C4	2.57	0.73
1:C1:2947:U:H2'	1:C1:2948:G:C8	2.24	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Cb:4:ARG:NH2	26:Cb:537:VAL:O	2.21	0.73
26:Cb:833:LYS:HD2	26:Cb:836:LEU:HD13	1.71	0.73
1:C1:745:U:O2	1:C1:749:C:N3	2.22	0.72
14:LF:86:GLU:OE2	41:LT:136:ARG:NH1	2.22	0.72
2:C2:186:G:OP1	10:CI:228:ARG:NH1	2.23	0.72
4:CB:120:LEU:HA	4:CB:123:LYS:HE2	1.71	0.72
31:LG:66:LYS:HG2	31:LG:70:MET:HE2	1.69	0.72
1:C1:642:C:H2'	1:C1:643:A:H8	1.54	0.72
11:CJ:261:LYS:HG2	11:CJ:266:ALA:HB2	1.70	0.72
15:CN:109:VAL:HG23	15:CN:149:GLY:HA2	1.72	0.72
42:LV:22:GLY:N	42:LV:38:ILE:O	2.22	0.72
27:Cz:50:LEU:HD11	40:LS:133:GLU:HG3	1.71	0.72
2:C2:83:C:N3	44:LY:50:ARG:NH2	2.38	0.72
6:CE:467:LEU:HD13	6:CE:470:LEU:HD13	1.71	0.72
25:CY:723:VAL:HA	25:CY:726:ARG:HE	1.55	0.72
3:CA:100:LEU:HB3	3:CA:117:ALA:HB3	1.72	0.72
10:CI:269:HIS:HD2	10:CI:270:PRO:HD2	1.54	0.72
2:C2:103:G:OP1	50:Lj:20:ARG:NH1	2.23	0.71
26:Cb:224:LEU:HB2	26:Cb:228:MET:HE1	1.72	0.71
28:LB:57:VAL:HG13	28:LB:358:LYS:HB2	1.73	0.71
14:CM:149:SER:HB2	14:CM:245:ILE:HD11	1.73	0.71
26:Cb:479:LEU:HB3	26:Cb:559:ARG:HE	1.56	0.71
1:C1:1868:G:H2'	1:C1:1869:U:C6	2.24	0.71
7:CF:88:GLY:HA3	7:CF:91:ARG:NH1	2.04	0.71
11:CJ:420:ILE:HD11	11:CJ:478:PRO:HG3	1.71	0.71
6:CE:239:ALA:HB1	6:CE:244:LEU:HB2	1.72	0.71
18:CQ:56:ARG:HG2	18:CQ:61:LYS:HB2	1.73	0.71
6:CE:441:TYR:O	6:CE:445:VAL:HG22	1.91	0.71
9:CH:315:GLU:OE1	9:CH:337:ARG:NH2	2.22	0.71
7:CF:187:GLU:CD	7:CF:188:ALA:H	1.99	0.70
9:CH:451:ASP:HB2	18:CQ:75:ARG:HH21	1.56	0.70
23:CV:120:ARG:HG3	23:CV:123:ARG:HE	1.54	0.70
44:LY:72:VAL:HG23	44:LY:79:ILE:HG22	1.72	0.70
44:LY:100:PRO:HA	44:LY:103:VAL:HG22	1.73	0.70
14:LF:233:ASP:OD1	14:LF:237:ARG:NH2	2.25	0.70
17:CP:495:ILE:HD12	17:CP:534:VAL:HG11	1.73	0.70
21:CT:647:THR:HG23	21:CT:650:GLY:H	1.56	0.70
1:C1:2922:G:N2	1:C1:2925:A:C6	2.59	0.70
9:CH:221:PRO:HD2	9:CH:238:SER:HB3	1.71	0.70
32:LH:58:LYS:HG3	32:LH:59:SER:H	1.55	0.70
1:C1:979:A:H5'	40:LS:50:LYS:HE2	1.73	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CX:84:LYS:HD2	24:CX:90:LYS:HB2	1.73	0.70
1:C1:663:G:HO2'	1:C1:665:G:HO2'	1.40	0.70
7:CF:69:LYS:HD2	7:CF:72:LEU:HD23	1.71	0.70
2:C2:219:A:N6	10:CI:218:VAL:O	2.24	0.70
20:CS:740:ARG:O	20:CS:744:GLN:NE2	2.24	0.70
8:CG:29:PRO:HD3	24:CX:98:ARG:HH21	1.57	0.70
12:CK:239:TRP:CD1	17:CP:474:ASN:HD21	2.10	0.70
18:CQ:105:ARG:HE	28:LB:383:THR:HG21	1.55	0.70
26:Cb:367:HIS:HB2	26:Cb:418:ASN:HD21	1.53	0.70
17:CP:387:MET:HE2	17:CP:440:ALA:HB1	1.73	0.70
26:Cb:17:ILE:H	26:Cb:448:LYS:HZ3	1.39	0.70
1:C1:1071:G:H2'	1:C1:1072:G:C8	2.27	0.69
1:C1:1239:C:O2	7:CF:54:LYS:NZ	2.25	0.69
1:C1:3309:G:H4'	1:C1:3310:A:H8	1.57	0.69
25:CY:579:LEU:HD12	25:CY:584:MET:HE1	1.74	0.69
10:CI:218:VAL:HG12	10:CI:231:ALA:HB2	1.73	0.69
46:Le:26:PHE:HB2	46:Le:29:LEU:HD12	1.73	0.69
2:C2:143:U:OP1	36:LN:38:ARG:NH2	2.25	0.69
1:C1:407:G:N2	1:C1:1381:A:H61	1.79	0.69
8:CG:72:GLY:HA2	8:CG:83:HIS:ND1	2.08	0.69
25:CY:420:LEU:HD11	25:CY:463:THR:HG21	1.75	0.69
1:C1:1045:G:H21	1:C1:1048:G:H21	1.40	0.69
1:C1:2922:G:C6	1:C1:2926:G:C6	2.81	0.69
4:CB:71:HIS:ND1	4:CB:237:PRO:O	2.24	0.69
17:CP:453:VAL:HB	17:CP:508:ILE:HG12	1.75	0.69
25:CY:548:PHE:HB3	25:CY:552:PHE:HE2	1.57	0.69
26:Cb:22:PHE:CD2	26:Cb:292:LEU:HB2	2.22	0.69
26:Cb:493:ARG:HE	26:Cb:574:ALA:HA	1.58	0.69
32:LH:173:VAL:HG13	32:LH:183:LEU:HD21	1.74	0.69
4:CB:61:PRO:HD2	4:CB:286:PRO:HG3	1.75	0.69
4:CB:143:GLN:HG3	4:CB:170:THR:HG21	1.74	0.69
25:CY:454:GLY:O	25:CY:457:GLN:NE2	2.25	0.69
26:Cb:396:VAL:HG12	26:Cb:426:ALA:HB1	1.75	0.69
1:C1:1156:G:H21	1:C1:1157:C:N4	1.91	0.69
5:CC:246:LEU:HG	5:CC:247:ILE:HG13	1.75	0.69
16:CO:37:LEU:HG	28:LB:195:PHE:HZ	1.58	0.69
25:CY:485:GLN:HB3	25:CY:488:ARG:HB2	1.75	0.69
8:CG:96:TYR:HB2	8:CG:131:GLY:O	1.92	0.68
9:CH:179:LYS:HA	9:CH:252:PHE:HE1	1.58	0.68
51:Lq:17:LEU:HG	51:Lq:18:ASP:HB2	1.74	0.68
1:C1:2780:U:H4'	9:CH:34:PRO:HB2	1.74	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3143:U:H5''	37:LO:174:LYS:HE2	1.75	0.68
5:CC:403:ARG:CZ	11:CJ:147:MET:HE3	2.24	0.68
1:C1:3309:G:H1	28:LB:381:MET:HE1	1.57	0.68
23:CV:13:SER:HB2	23:CV:17:ASN:ND2	2.09	0.68
25:CY:654:MET:HE3	25:CY:655:LYS:HD2	1.75	0.68
25:CY:696:PHE:HD1	25:CY:704:VAL:HG21	1.58	0.68
1:C1:132:C:O2	1:C1:133:G:N2	2.26	0.68
30:LE:76:LEU:HB2	30:LE:80:VAL:HG23	1.76	0.68
7:CF:158:SER:HB3	7:CF:161:LEU:HD13	1.75	0.68
9:CH:448:ASP:OD2	18:CQ:2:ARG:NH2	2.23	0.68
17:CP:492:LEU:HD11	17:CP:526:TYR:CE1	2.29	0.68
20:CS:485:SER:O	20:CS:491:ARG:NH1	2.27	0.68
21:CT:663:LEU:HD13	21:CT:666:LYS:HE2	1.76	0.68
8:CG:16:LEU:O	8:CG:20:MET:HB2	1.93	0.68
26:Cb:162:ARG:HA	26:Cb:235:ILE:HA	1.75	0.68
1:C1:230:A:H2'	1:C1:231:A:C8	2.29	0.68
1:C1:1189:G:OP1	12:CK:54:ARG:NH2	2.27	0.67
13:CL:62:LYS:HE3	27:Cz:61:MET:HE2	1.76	0.67
1:C1:1045:G:O2'	1:C1:1079:G:N2	2.28	0.67
15:CN:15:VAL:HA	15:CN:61:ARG:HG2	1.77	0.67
1:C1:2294:A:H2'	1:C1:2295:C:C6	2.29	0.67
11:CJ:267:GLU:HB3	11:CJ:381:GLN:NE2	2.10	0.67
25:CY:492:ASN:ND2	25:CY:494:GLN:OE1	2.27	0.67
9:CH:270:PHE:HE1	9:CH:308:LEU:HD11	1.60	0.67
28:LB:57:VAL:CG1	28:LB:358:LYS:HB2	2.25	0.67
7:CF:49:ARG:HE	7:CF:124:PHE:HB2	1.60	0.67
34:LL:47:ALA:HB3	34:LL:48:PRO:HD3	1.77	0.67
1:C1:116:A:OP1	49:Li:45:ARG:NH1	2.26	0.67
2:C2:297:C:H2'	2:C2:298:G:C8	2.30	0.67
15:CN:140:GLN:NE2	15:CN:172:GLU:OE1	2.28	0.67
25:CY:488:ARG:NH1	25:CY:547:TYR:OH	2.28	0.67
11:CJ:372:PHE:HB2	11:CJ:395:ILE:HG12	1.75	0.67
26:Cb:402:GLN:OE1	26:Cb:405:ARG:NH2	2.28	0.67
51:Lq:68:LEU:HB3	51:Lq:116:LEU:HD23	1.77	0.67
9:CH:284:ILE:O	9:CH:316:ILE:HA	1.94	0.66
17:CP:498:CYS:HB2	17:CP:508:ILE:HD11	1.76	0.66
8:CG:20:MET:O	8:CG:95:ARG:NH2	2.28	0.66
11:CJ:131:TYR:OH	11:CJ:140:ASP:OD2	2.14	0.66
17:CP:446:VAL:HG23	17:CP:447:ILE:HD12	1.77	0.66
25:CY:453:TRP:HZ3	25:CY:464:ALA:HB2	1.59	0.66
39:LQ:127:GLU:OE2	39:LQ:147:ARG:NH2	2.28	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CJ:458:PRO:HB2	11:CJ:462:TRP:HZ3	1.60	0.66
14:CM:161:LYS:HE2	14:CM:164:GLY:H	1.61	0.66
49:Li:93:LYS:NZ	49:Li:97:GLU:OE2	2.27	0.66
1:C1:245:A:O3'	5:CC:289:LYS:NZ	2.25	0.66
12:CK:164:ARG:NH1	12:CK:171:PHE:O	2.28	0.66
35:LM:105:GLN:OE1	35:LM:109:ARG:NH1	2.29	0.66
21:CT:322:LEU:HD11	21:CT:419:LEU:HD22	1.77	0.66
35:LM:72:LEU:HD12	35:LM:73:PRO:HD2	1.78	0.66
1:C1:1203:U:H5''	7:CF:71:LYS:HE3	1.78	0.66
1:C1:3332:G:HO2'	1:C1:3333:A:H8	1.44	0.66
11:CJ:224:PHE:HA	11:CJ:227:MET:SD	2.35	0.66
48:Lh:13:TRP:CZ3	50:Lj:87:ARG:CZ	2.79	0.66
1:C1:261:G:OP1	36:LN:47:LYS:NZ	2.29	0.66
6:CE:151:VAL:HG12	6:CE:293:MET:HG2	1.78	0.66
1:C1:1171:C:N3	1:C1:1297:U:O2	2.29	0.66
1:C1:2414:G:H1	1:C1:2456:A:H2	1.42	0.66
1:C1:683:C:H1'	19:CR:64:GLY:H	1.61	0.65
1:C1:1869:U:H2'	1:C1:1870:A:H8	1.61	0.65
1:C1:2813:C:H2'	1:C1:2814:G:H8	1.59	0.65
3:CA:144:ALA:HB3	22:CU:225:ARG:HG3	1.78	0.65
6:CE:329:VAL:HG23	6:CE:331:GLY:H	1.61	0.65
14:CM:172:ASN:HA	14:CM:175:ILE:HD12	1.75	0.65
49:Li:60:ALA:HB3	49:Li:63:GLU:HG3	1.77	0.65
1:C1:891:G:N2	1:C1:898:A:N1	2.36	0.65
1:C1:1332:A:H2	1:C1:1335:C:H41	1.43	0.65
2:C2:159:C:H5''	14:CM:59:LYS:HD3	1.76	0.65
9:CH:97:ILE:HD13	9:CH:142:LEU:HD23	1.77	0.65
7:CF:131:ALA:HB2	7:CF:201:LEU:HD21	1.79	0.65
1:C1:1097:G:H4'	1:C1:1098:G:H5''	1.78	0.65
14:CM:104:LYS:O	14:CM:108:ILE:HG12	1.96	0.65
17:CP:421:LEU:O	17:CP:425:ILE:HG13	1.96	0.65
17:CP:443:PHE:HA	17:CP:446:VAL:HG22	1.77	0.65
25:CY:477:ASN:O	25:CY:481:ASN:ND2	2.29	0.65
26:Cb:140:LYS:HD2	26:Cb:271:PHE:HB3	1.79	0.65
27:Cz:45:LEU:HD23	40:LS:141:LYS:HB2	1.78	0.65
51:Lq:60:ARG:O	51:Lq:62:ASN:N	2.29	0.65
26:Cb:2:PRO:HA	26:Cb:5:ALA:HB2	1.79	0.65
32:LH:86:LYS:HB2	32:LH:89:VAL:HG12	1.79	0.65
32:LH:179:GLN:HB2	32:LH:182:GLU:HG2	1.78	0.65
17:CP:232:LEU:HD23	17:CP:235:LEU:HD12	1.79	0.65
18:CQ:89:THR:O	18:CQ:93:MET:HG2	1.97	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CQ:95:ARG:NH1	18:CQ:98:GLU:OE2	2.29	0.65
36:LN:62:TYR:HD2	36:LN:134:LEU:HD13	1.61	0.65
10:CI:303:GLN:HA	10:CI:306:VAL:HG22	1.77	0.65
1:C1:1157:C:N4	37:LO:22:SER:OG	2.30	0.65
30:LE:166:ASP:O	30:LE:170:ILE:HB	1.97	0.65
33:LK:18:THR:HA	33:LK:57:ARG:HH12	1.62	0.65
10:CI:310:GLU:HB2	10:CI:313:ARG:HH11	1.62	0.64
21:CT:183:ARG:NH2	21:CT:255:HIS:O	2.30	0.64
32:LH:10:ILE:HG12	32:LH:109:ARG:HG3	1.79	0.64
1:C1:725:A:OP1	39:LQ:94:ARG:NH2	2.30	0.64
6:CE:455:LYS:HA	6:CE:455:LYS:HE3	1.78	0.64
51:Lq:99:LEU:HD23	51:Lq:103:LEU:HD23	1.80	0.64
10:CI:200:GLU:OE2	10:CI:218:VAL:HG22	1.98	0.64
35:LM:44:PRO:HG3	35:LM:81:VAL:HG13	1.79	0.64
1:C1:3164:G:C6	1:C1:3206:G:N1	2.65	0.64
40:LS:9:VAL:HG22	40:LS:61:VAL:HG22	1.79	0.64
1:C1:1372:A:N6	1:C1:1400:A:O2'	2.30	0.64
9:CH:426:ILE:O	18:CQ:80:ARG:NH2	2.31	0.64
46:Le:77:VAL:HG21	46:Le:83:VAL:HG13	1.79	0.64
1:C1:3021:U:H2'	1:C1:3022:G:H8	1.62	0.64
10:CI:308:LYS:O	10:CI:311:GLN:HG3	1.97	0.64
1:C1:2317:G:OP1	38:LP:141:SER:OG	2.14	0.64
21:CT:525:LEU:CG	21:CT:602:GLN:NE2	2.60	0.64
26:Cb:329:ILE:HD12	26:Cb:437:ASN:ND2	2.12	0.64
5:CC:270:PRO:HB3	31:LG:148:ASN:HA	1.80	0.64
7:CF:170:MET:HG2	7:CF:192:TYR:CD2	2.32	0.64
30:LE:57:VAL:HB	30:LE:107:VAL:HG13	1.80	0.64
1:C1:381:A:H5''	38:LP:16:ARG:HG3	1.78	0.63
1:C1:975:G:N2	1:C1:976:U:O4	2.30	0.63
1:C1:2725:U:H3	1:C1:2749:G:H1	1.46	0.63
1:C1:3283:G:H21	1:C1:3302:A:H2	1.46	0.63
17:CP:572:ASN:ND2	26:Cb:716:MET:O	2.31	0.63
48:Lh:98:SER:OG	48:Lh:101:ASP:OD2	2.15	0.63
1:C1:407:G:N2	1:C1:1381:A:N6	2.42	0.63
3:CA:123:MET:HE3	3:CA:236:PRO:HD3	1.80	0.63
22:CU:258:LEU:HD22	22:CU:263:VAL:HG11	1.79	0.63
26:Cb:534:LEU:O	26:Cb:538:THR:HG23	1.99	0.63
39:LQ:45:LYS:O	39:LQ:62:ARG:NH2	2.31	0.63
1:C1:68:C:OP2	1:C1:293:G:N2	2.31	0.63
1:C1:3227:C:N4	1:C1:3228:G:O6	2.31	0.63
5:CC:276:GLU:OE1	5:CC:280:ARG:NH1	2.27	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CJ:31:PRO:HD2	11:CJ:32:ASP:H	1.64	0.63
11:CJ:259:GLN:NE2	14:CM:246:ARG:HH12	1.96	0.63
28:LB:74:GLU:OE2	28:LB:326:LYS:NZ	2.31	0.63
34:LL:86:PRO:HG2	34:LL:89:LEU:HB3	1.80	0.63
47:Lf:47:LEU:HD11	47:Lf:76:PRO:HD3	1.79	0.63
5:CC:355:ASN:OD1	5:CC:386:LYS:NZ	2.31	0.63
28:LB:295:ALA:HB3	28:LB:304:LYS:HG3	1.80	0.63
32:LH:64:VAL:HG23	32:LH:119:VAL:HG21	1.81	0.63
33:LK:117:ARG:NH2	33:LK:122:SER:O	2.31	0.63
1:C1:231:A:H2'	1:C1:232:G:C8	2.33	0.63
9:CH:232:ASN:O	9:CH:236:MET:HG3	1.99	0.63
9:CH:253:MET:HB3	9:CH:286:LEU:HD12	1.80	0.63
11:CJ:40:LYS:HZ3	11:CJ:126:ILE:HG22	1.63	0.63
21:CT:557:LYS:O	21:CT:569:ARG:NH1	2.30	0.63
23:CV:23:GLN:HE22	46:Le:76:LEU:HB3	1.63	0.63
42:LV:34:ARG:HB3	42:LV:66:LYS:HG3	1.81	0.63
4:CB:30:LEU:HB2	4:CB:291:LEU:HD11	1.80	0.63
9:CH:484:GLU:OE1	18:CQ:124:ARG:NH2	2.31	0.63
14:CM:114:LEU:HD21	14:CM:121:VAL:HG22	1.81	0.63
21:CT:601:LEU:HD11	21:CT:660:GLU:HB3	1.79	0.63
48:Lh:13:TRP:CZ3	50:Lj:87:ARG:NE	2.66	0.63
51:Lq:48:ARG:NH2	51:Lq:159:LEU:O	2.32	0.63
1:C1:3218:A:N1	38:LP:182:ARG:NH2	2.46	0.63
9:CH:328:GLN:O	9:CH:332:ASN:ND2	2.32	0.63
29:LC:329:LEU:HD22	14:LF:187:ILE:HG13	1.81	0.63
1:C1:676:U:H3	29:LC:234:THR:HG23	1.63	0.63
1:C1:1045:G:N2	1:C1:1048:G:H21	1.96	0.63
1:C1:3314:U:OP1	45:Ld:23:HIS:NE2	2.32	0.63
19:CR:136:GLN:HG3	34:LL:117:LYS:HZ2	1.64	0.63
25:CY:456:ASP:OD2	25:CY:457:GLN:N	2.32	0.63
51:Lq:17:LEU:HD13	51:Lq:176:GLN:HE22	1.63	0.63
1:C1:213:G:C6	1:C1:1371:G:C2	2.87	0.63
1:C1:2788:G:H2'	1:C1:2789:G:C8	2.34	0.63
1:C1:3188:U:H2'	1:C1:3189:G:C8	2.34	0.63
9:CH:282:VAL:HB	9:CH:314:VAL:HG22	1.81	0.63
12:CK:218:GLY:N	12:CK:245:ILE:O	2.30	0.62
19:CR:136:GLN:O	34:LL:117:LYS:NZ	2.32	0.62
1:C1:66:A:H61	1:C1:75:G:N2	1.95	0.62
10:CI:215:ARG:NH2	10:CI:234:GLU:OE2	2.28	0.62
1:C1:65:A:H1'	1:C1:77:A:H1'	1.81	0.62
20:CS:728:ARG:HG2	21:CT:436:GLN:HE22	1.64	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CU:365:GLU:HG3	22:CU:366:LEU:HD12	1.81	0.62
26:Cb:228:MET:HB2	26:Cb:230:LEU:HG	1.81	0.62
1:C1:55:G:OP1	50:Lj:43:LYS:NZ	2.28	0.62
8:CG:71:LEU:HA	8:CG:86:ALA:HB2	1.80	0.62
9:CH:179:LYS:HA	9:CH:252:PHE:CE1	2.34	0.62
21:CT:644:LEU:HD21	25:CY:648:VAL:HG11	1.80	0.62
11:CJ:104:ALA:HB1	11:CJ:108:ARG:HH12	1.63	0.62
21:CT:571:LEU:HA	21:CT:574:VAL:HG12	1.80	0.62
26:Cb:259:LEU:HD11	26:Cb:286:GLY:HA3	1.81	0.62
28:LB:174:GLN:HG2	28:LB:176:LYS:H	1.65	0.62
1:C1:3124:U:O4	47:Lf:56:ARG:NH1	2.32	0.62
1:C1:3110:C:H42	1:C1:3337:C:H2'	1.65	0.62
5:CC:370:TRP:O	5:CC:378:ARG:NH2	2.32	0.62
25:CY:417:GLU:HB3	25:CY:459:LEU:HD12	1.82	0.62
51:Lq:39:LYS:HD2	51:Lq:40:ASN:HB2	1.80	0.62
1:C1:209:G:OP1	44:LY:15:ARG:NH1	2.32	0.62
1:C1:3164:G:C6	1:C1:3206:G:C6	2.87	0.62
1:C1:3213:A:OP2	30:LE:95:ARG:NH2	2.32	0.62
10:CI:217:ARG:NH2	10:CI:272:LEU:O	2.32	0.62
15:CN:230:PRO:HG2	15:CN:232:ALA:HB3	1.82	0.62
32:LH:105:LEU:HA	32:LH:108:VAL:HG22	1.80	0.62
1:C1:642:C:H2'	1:C1:643:A:C8	2.35	0.62
1:C1:663:G:O2'	1:C1:665:G:O2'	2.13	0.62
2:C2:135:G:OP1	43:LX:62:LYS:NZ	2.27	0.62
9:CH:242:LEU:O	9:CH:280:LYS:NZ	2.33	0.62
10:CI:242:ASP:HB3	10:CI:246:ARG:HH12	1.64	0.62
19:CR:50:THR:HG22	19:CR:70:LYS:H	1.65	0.62
26:Cb:132:GLY:HA2	26:Cb:293:VAL:HG12	1.82	0.62
1:C1:526:G:H22	1:C1:543:G:H2'	1.63	0.62
1:C1:933:A:N3	1:C1:1096:U:O2'	2.31	0.62
3:CA:139:ILE:HG13	3:CA:176:ILE:HD11	1.82	0.62
6:CE:222:ASN:O	6:CE:226:GLU:HG3	2.00	0.62
6:CE:539:VAL:HA	6:CE:550:PRO:HG3	1.82	0.62
11:CJ:97:ARG:HH22	31:LG:196:LYS:HA	1.65	0.62
13:CL:223:HIS:O	13:CL:225:VAL:N	2.32	0.62
33:LK:59:THR:OG1	33:LK:74:VAL:O	2.18	0.62
1:C1:2387:G:O6	1:C1:2563:G:N2	2.33	0.61
11:CJ:380:ARG:NH1	11:CJ:401:LEU:O	2.33	0.61
1:C1:476:C:H2'	1:C1:477:G:H8	1.65	0.61
1:C1:1263:U:H2'	1:C1:1264:G:H8	1.65	0.61
6:CE:353:LYS:HD2	6:CE:382:LEU:HD13	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CJ:418:GLN:NE2	11:CJ:419:ILE:O	2.33	0.61
20:CS:728:ARG:O	21:CT:436:GLN:NE2	2.33	0.61
27:Cz:40:ARG:HE	27:Cz:43:LYS:HZ3	1.47	0.61
1:C1:1880:A:OP1	42:LV:37:TYR:OH	2.17	0.61
1:C1:3203:C:H2'	1:C1:3204:G:H8	1.65	0.61
15:CN:79:GLN:OE1	18:CQ:1:MET:N	2.33	0.61
44:LY:54:GLU:HB2	44:LY:107:LYS:HB3	1.82	0.61
7:CF:80:THR:OG1	7:CF:83:GLU:OE1	2.18	0.61
10:CI:310:GLU:HB2	10:CI:313:ARG:NH1	2.15	0.61
18:CQ:81:TYR:HA	18:CQ:86:TRP:CZ3	2.36	0.61
45:Ld:18:ARG:HE	45:Ld:116:VAL:HG22	1.66	0.61
48:Lh:37:GLN:O	48:Lh:45:LYS:NZ	2.31	0.61
26:Cb:875:GLU:O	26:Cb:879:LYS:HG3	2.01	0.61
28:LB:220:ALA:HB3	28:LB:330:PRO:HB2	1.83	0.61
33:LK:162:ILE:HG22	33:LK:164:ASP:H	1.66	0.61
1:C1:298:A:OP2	3:CA:265:ASN:ND2	2.31	0.61
1:C1:887:G:H2'	1:C1:888:G:C8	2.36	0.61
3:CA:231:LEU:HD13	22:CU:248:LEU:HD23	1.82	0.61
20:CS:730:ILE:HG12	21:CT:436:GLN:HG3	1.81	0.61
21:CT:660:GLU:OE1	21:CT:660:GLU:N	2.34	0.61
37:LO:55:TYR:OH	37:LO:75:PHE:O	2.19	0.61
48:Lh:24:LEU:O	48:Lh:28:LYS:HG2	2.00	0.61
1:C1:1171:C:N3	1:C1:1297:U:C2	2.69	0.61
1:C1:2433:U:OP2	51:Lq:26:ARG:NH1	2.34	0.61
9:CH:427:LEU:HD21	18:CQ:81:TYR:HB3	1.82	0.61
9:CH:432:TRP:HB3	18:CQ:81:TYR:CE2	2.35	0.61
11:CJ:267:GLU:CB	11:CJ:381:GLN:HE21	2.11	0.61
15:CN:125:THR:HA	15:CN:128:ILE:HG22	1.83	0.61
26:Cb:796:ILE:HG12	26:Cb:806:ALA:HA	1.81	0.61
29:LC:161:ASP:HA	29:LC:164:ALA:HB3	1.80	0.61
32:LH:13:PRO:HD2	32:LH:53:LEU:HD12	1.81	0.61
1:C1:476:C:H2'	1:C1:477:G:C8	2.35	0.61
1:C1:3309:G:N1	28:LB:381:MET:HE1	2.14	0.61
31:LG:250:GLU:HA	31:LG:253:LYS:HG2	1.81	0.61
1:C1:2456:A:H2'	1:C1:2457:C:C6	2.36	0.61
5:CC:204:LEU:HD11	21:CT:449:LEU:HD21	1.83	0.61
9:CH:232:ASN:N	9:CH:235:GLU:OE2	2.34	0.61
1:C1:115:A:O3'	36:LN:5:LYS:NZ	2.34	0.61
1:C1:2555:U:H2'	1:C1:2556:G:H8	1.66	0.61
8:CG:20:MET:HE1	8:CG:26:LEU:HD11	1.83	0.61
11:CJ:133:THR:HG23	11:CJ:136:ASP:H	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1046:A:N6	1:C1:1074:C:O2	2.34	0.60
7:CF:74:ALA:HB2	7:CF:96:LEU:HD22	1.81	0.60
15:CN:107:VAL:HG23	15:CN:108:ILE:HG13	1.82	0.60
17:CP:354:THR:OG1	17:CP:362:TYR:OH	2.16	0.60
26:Cb:134:ALA:HB3	26:Cb:140:LYS:HD3	1.83	0.60
37:LO:191:VAL:HG13	37:LO:192:ASP:H	1.66	0.60
9:CH:258:GLN:HE22	33:LK:33:GLY:HA3	1.66	0.60
33:LK:63:THR:OG1	33:LK:70:GLN:NE2	2.22	0.60
36:LN:64:VAL:HG11	36:LN:102:ALA:HB1	1.83	0.60
14:CM:91:PHE:HB2	14:CM:145:PRO:HG3	1.83	0.60
29:LC:13:ASP:OD2	29:LC:15:LYS:NZ	2.30	0.60
50:Lj:45:ARG:O	50:Lj:57:LYS:NZ	2.23	0.60
1:C1:1046:A:N1	1:C1:1074:C:N3	2.50	0.60
1:C1:1178:C:H41	1:C1:1302:C:H5''	1.67	0.60
1:C1:2946:C:H5''	37:LO:66:ASN:HB2	1.82	0.60
3:CA:72:SER:OG	3:CA:76:GLU:OE1	2.16	0.60
6:CE:234:VAL:HG11	6:CE:237:LEU:HD13	1.83	0.60
9:CH:270:PHE:CE1	9:CH:308:LEU:HD11	2.37	0.60
9:CH:468:LEU:HB3	9:CH:474:TYR:HE2	1.67	0.60
21:CT:246:ALA:O	21:CT:250:VAL:HG23	2.00	0.60
45:Ld:88:ASN:HB2	45:Ld:98:TYR:HD1	1.64	0.60
1:C1:2432:C:H5''	51:Lq:26:ARG:HD3	1.84	0.60
11:CJ:377:GLU:HG3	11:CJ:421:ASP:HB3	1.84	0.60
19:CR:44:THR:O	19:CR:48:ASN:ND2	2.35	0.60
26:Cb:316:GLU:HG2	26:Cb:518:VAL:HG21	1.84	0.60
11:CJ:388:ARG:NH2	11:CJ:392:CYS:O	2.30	0.60
15:CN:103:ALA:HB1	15:CN:106:ASN:HD22	1.66	0.60
23:CV:88:ARG:NH1	30:LE:24:ALA:O	2.32	0.60
26:Cb:159:PHE:HA	26:Cb:210:ASN:HD21	1.66	0.60
30:LE:176:VAL:HG22	30:LE:179:LEU:HB2	1.83	0.60
1:C1:2445:G:N1	1:C1:2448:A:OP2	2.35	0.60
11:CJ:65:TYR:CE2	11:CJ:67:LYS:HB2	2.37	0.60
17:CP:521:GLU:HA	17:CP:524:VAL:HG12	1.82	0.60
26:Cb:393:VAL:HG22	26:Cb:419:ILE:HB	1.84	0.60
6:CE:351:PHE:HE2	6:CE:430:VAL:HG21	1.67	0.60
7:CF:165:LEU:HD22	7:CF:170:MET:HE2	1.82	0.60
9:CH:13:ALA:HB2	9:CH:143:LYS:HA	1.83	0.60
10:CI:203:LEU:HB3	10:CI:216:LEU:HD11	1.84	0.60
16:CO:41:ALA:O	28:LB:202:LYS:NZ	2.34	0.60
26:Cb:15:VAL:HG12	26:Cb:448:LYS:HZ2	1.67	0.60
29:LC:361:LEU:HD11	41:LT:148:PRO:HG2	1.84	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LF:221:ARG:NH1	14:LF:232:GLY:O	2.34	0.60
1:C1:1877:G:H2'	1:C1:1878:G:H8	1.67	0.60
6:CE:329:VAL:HG22	6:CE:447:ARG:HH22	1.66	0.60
9:CH:177:VAL:HG23	9:CH:254:ASP:HB2	1.83	0.60
9:CH:474:TYR:CD1	18:CQ:106:VAL:HG21	2.37	0.60
20:CS:496:ARG:NH2	21:CT:389:SER:OG	2.34	0.60
21:CT:257:ASN:OD1	21:CT:258:PHE:N	2.35	0.60
1:C1:2972:C:OP2	16:CO:2:ALA:N	2.35	0.59
2:C2:75:G:OP2	44:LY:73:TYR:OH	2.19	0.59
4:CB:251:GLU:HG2	4:CB:252:PRO:HD2	1.84	0.59
14:CM:104:LYS:HG3	14:CM:105:PRO:HD3	1.83	0.59
1:C1:917:A:O2'	1:C1:918:G:H2'	2.02	0.59
1:C1:1046:A:C6	1:C1:1074:C:C2	2.90	0.59
1:C1:2307:A:H2'	1:C1:2308:C:C6	2.37	0.59
11:CJ:149:PHE:HD2	11:CJ:210:VAL:HG22	1.66	0.59
12:CK:17:ARG:NH2	32:LH:219:TYR:OH	2.35	0.59
30:LE:86:PRO:HB3	30:LE:166:ASP:HB2	1.84	0.59
1:C1:155:G:H2'	1:C1:156:G:C8	2.37	0.59
1:C1:562:U:H2'	1:C1:563:A:H8	1.67	0.59
1:C1:643:A:H2'	1:C1:644:A:C8	2.36	0.59
14:CM:104:LYS:CG	14:CM:105:PRO:HD3	2.32	0.59
15:CN:71:LEU:HD21	15:CN:132:VAL:HG11	1.84	0.59
17:CP:367:ALA:HA	17:CP:370:PHE:HD1	1.68	0.59
26:Cb:329:ILE:HD12	26:Cb:437:ASN:HD21	1.66	0.59
34:LL:53:LYS:HB2	34:LL:55:ARG:HH12	1.67	0.59
1:C1:130:U:O2	1:C1:133:G:N2	2.32	0.59
1:C1:894:A:OP1	20:CS:728:ARG:NH1	2.36	0.59
9:CH:212:TYR:HD1	15:CN:212:ALA:HB1	1.67	0.59
17:CP:270:ILE:HD13	17:CP:285:LEU:HD11	1.85	0.59
28:LB:299:THR:HG21	28:LB:358:LYS:HD2	1.84	0.59
39:LQ:108:VAL:HG23	39:LQ:167:LEU:HD13	1.83	0.59
1:C1:110:G:OP2	34:LL:73:ARG:NH2	2.36	0.59
2:C2:203:G:H5'	10:CI:223:LYS:HZ2	1.66	0.59
7:CF:132:PRO:HD2	7:CF:216:LEU:HD23	1.84	0.59
8:CG:21:THR:HA	8:CG:95:ARG:HH21	1.67	0.59
11:CJ:133:THR:OG1	11:CJ:135:GLN:OE1	2.20	0.59
37:LO:127:ARG:HG2	37:LO:131:LEU:HD13	1.84	0.59
50:Lj:14:LYS:O	50:Lj:29:ASN:ND2	2.36	0.59
1:C1:1272:U:H2'	1:C1:1273:A:C8	2.36	0.59
4:CB:70:LYS:HB3	4:CB:277:ASN:HD21	1.67	0.59
1:C1:3015:U:O4	45:Ld:73:LYS:NZ	2.33	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3220:A:H2'	1:C1:3221:C:C6	2.38	0.59
1:C1:1157:C:O2'	1:C1:1158:C:O5'	2.20	0.59
1:C1:2456:A:H2'	1:C1:2457:C:H6	1.68	0.59
1:C1:2480:C:H2'	1:C1:2481:A:H8	1.68	0.59
1:C1:3045:G:H2'	1:C1:3046:C:O4'	2.01	0.59
3:CA:191:VAL:HG21	3:CA:238:PHE:CZ	2.38	0.59
6:CE:334:GLN:O	6:CE:480:VAL:HA	2.03	0.59
8:CG:52:ILE:HG23	17:CP:434:ILE:HD11	1.85	0.59
1:C1:2433:U:O2	1:C1:2436:G:C6	2.56	0.59
20:CS:711:THR:HG23	20:CS:714:ALA:H	1.66	0.59
42:LV:25:MET:HE3	42:LV:38:ILE:HD11	1.85	0.59
1:C1:2376:G:H1	1:C1:2764:U:H3	1.49	0.59
7:CF:241:LYS:HG3	7:CF:242:THR:HG23	1.84	0.59
23:CV:3:ASN:ND2	29:LC:29:ALA:O	2.36	0.59
44:LY:26:ARG:O	44:LY:30:MET:HG3	2.03	0.59
45:Ld:89:ASP:OD1	45:Ld:90:GLU:N	2.32	0.59
1:C1:1336:G:N2	1:C1:1338:U:O2'	2.34	0.58
1:C1:3318:C:H4'	28:LB:314:ARG:HG3	1.85	0.58
15:CN:1:MET:N	15:CN:224:LEU:HB3	2.16	0.58
20:CS:578:ILE:HD12	20:CS:579:PRO:HD2	1.85	0.58
39:LQ:107:THR:HA	39:LQ:127:GLU:O	2.02	0.58
1:C1:603:G:H2'	1:C1:604:G:C8	2.38	0.58
1:C1:2844:U:OP1	13:CL:9:LYS:NZ	2.29	0.58
11:CJ:166:ALA:O	11:CJ:170:ARG:HG2	2.03	0.58
18:CQ:1:MET:SD	28:LB:359:TRP:NE1	2.76	0.58
28:LB:146:THR:O	28:LB:150:GLU:HG2	2.02	0.58
1:C1:1044:A:O2'	41:LT:108:ARG:NH2	2.36	0.58
3:CA:276:ALA:O	3:CA:280:HIS:ND1	2.36	0.58
4:CB:273:GLN:HB2	4:CB:277:ASN:HB2	1.84	0.58
5:CC:389:SER:HB2	5:CC:391:ARG:HG2	1.85	0.58
14:CM:209:TRP:CD1	14:CM:210:PRO:HD2	2.38	0.58
51:Lq:59:PRO:C	51:Lq:61:PRO:HD3	2.29	0.58
1:C1:263:C:O2	49:Li:91:ARG:NH2	2.35	0.58
1:C1:3017:C:O3'	1:C1:3311:G:N2	2.37	0.58
2:C2:29:U:H5''	34:LL:27:ASP:HB3	1.85	0.58
11:CJ:99:ASP:OD2	11:CJ:102:ASN:ND2	2.37	0.58
11:CJ:141:LEU:HD11	11:CJ:238:LEU:HD21	1.85	0.58
26:Cb:163:ALA:HB3	26:Cb:213:ILE:HA	1.86	0.58
2:C2:219:A:H5''	10:CI:222:LYS:HE3	1.85	0.58
7:CF:77:LEU:HD22	7:CF:89:LEU:HD21	1.85	0.58
18:CQ:33:ARG:HH21	18:CQ:35:LYS:HE2	1.68	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CT:328:LEU:HD13	21:CT:331:LEU:HD13	1.86	0.58
1:C1:781:G:H22	29:LC:102:ALA:HA	1.69	0.58
1:C1:2942:C:H2'	1:C1:2943:C:H6	1.68	0.58
5:CC:391:ARG:HD2	5:CC:392:LYS:NZ	2.19	0.58
35:LM:18:ARG:NH1	35:LM:65:THR:O	2.37	0.58
1:C1:773:A:H2'	1:C1:774:A:H8	1.68	0.58
8:CG:122:TRP:CG	8:CG:155:ARG:HH12	2.21	0.58
11:CJ:104:ALA:HB1	11:CJ:108:ARG:NH1	2.19	0.58
14:CM:190:LEU:HD21	14:CM:208:LEU:HD11	1.85	0.58
21:CT:443:LEU:HD21	21:CT:493:LEU:HD21	1.84	0.58
23:CV:10:TRP:HB2	23:CV:47:VAL:HG11	1.86	0.58
1:C1:445:A:H4'	1:C1:446:U:OP1	2.03	0.58
1:C1:2955:U:H2'	1:C1:2956:C:C6	2.39	0.58
9:CH:297:LEU:HB3	9:CH:302:GLN:NE2	2.19	0.58
10:CI:192:ALA:HB3	10:CI:259:THR:HB	1.84	0.58
25:CY:648:VAL:HA	25:CY:651:LYS:HD2	1.86	0.58
1:C1:1869:U:H2'	1:C1:1870:A:C8	2.38	0.58
4:CB:58:ALA:HA	4:CB:249:ASN:HB3	1.86	0.58
9:CH:186:VAL:HG13	9:CH:187:THR:HG23	1.84	0.58
24:CX:126:LEU:O	24:CX:130:ARG:HG3	2.03	0.58
40:LS:12:ARG:HB3	40:LS:24:LEU:HD23	1.85	0.58
42:LV:22:GLY:CA	42:LV:38:ILE:O	2.52	0.58
1:C1:2569:U:H2'	1:C1:2570:U:C6	2.39	0.57
1:C1:2977:U:OP1	9:CH:405:ARG:NH2	2.37	0.57
1:C1:3335:U:H2'	1:C1:3336:U:C6	2.39	0.57
11:CJ:112:LEU:HD12	11:CJ:113:PRO:HD2	1.85	0.57
15:CN:233:ILE:HG23	15:CN:237:MET:HE2	1.86	0.57
26:Cb:817:ARG:HH12	26:Cb:824:ARG:HA	1.69	0.57
44:LY:73:TYR:CD2	44:LY:76:LYS:HG2	2.39	0.57
1:C1:713:G:C5	1:C1:723:G:C2	2.92	0.57
1:C1:2368:C:H1'	22:CU:316:GLN:HG2	1.85	0.57
1:C1:3164:G:O6	1:C1:3206:G:C6	2.57	0.57
21:CT:616:GLN:NE2	21:CT:682:GLU:OE2	2.20	0.57
25:CY:451:GLU:HA	25:CY:509:HIS:HE1	1.69	0.57
14:LF:114:LEU:HD21	14:LF:121:VAL:HG22	1.85	0.57
1:C1:895:A:HO2'	1:C1:896:A:H8	1.53	0.57
2:C2:166:C:OP2	4:CB:158:ARG:NH1	2.36	0.57
4:CB:66:LEU:HB3	4:CB:241:THR:HG22	1.86	0.57
4:CB:78:LEU:HD13	4:CB:178:ARG:NH1	2.19	0.57
5:CC:374:ASP:O	5:CC:378:ARG:NH1	2.38	0.57
8:CG:71:LEU:HD11	8:CG:89:ILE:HD12	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LB:149:LEU:O	28:LB:153:LYS:HG2	2.03	0.57
1:C1:423:U:OP1	47:Lf:67:ARG:NH1	2.37	0.57
1:C1:895:A:O2'	1:C1:896:A:H8	1.87	0.57
1:C1:2461:U:H2'	1:C1:2462:A:C8	2.40	0.57
6:CE:352:LEU:HB3	6:CE:382:LEU:HD21	1.86	0.57
8:CG:29:PRO:HD3	24:CX:98:ARG:HE	1.70	0.57
11:CJ:263:ASP:O	14:CM:146:ASN:ND2	2.36	0.57
24:CX:98:ARG:HH11	24:CX:102:ASN:HD21	1.52	0.57
40:LS:93:GLU:HB3	40:LS:140:ILE:HD12	1.86	0.57
1:C1:663:G:O6	39:LQ:89:PRO:HB3	2.05	0.57
1:C1:1360:U:H2'	1:C1:1361:G:H8	1.69	0.57
2:C2:175:G:H2'	2:C2:176:G:C8	2.39	0.57
4:CB:97:VAL:HG22	4:CB:124:ILE:HA	1.85	0.57
4:CB:215:ARG:HB3	4:CB:219:GLU:OE1	2.05	0.57
10:CI:219:VAL:HG21	10:CI:230:ARG:HE	1.69	0.57
21:CT:521:LEU:HD11	25:CY:645:PRO:HA	1.86	0.57
22:CU:305:GLN:HE22	22:CU:309:LYS:HE2	1.69	0.57
25:CY:572:ALA:O	25:CY:576:LEU:HD23	2.04	0.57
11:CJ:376:ARG:HD2	14:CM:189:ASP:HA	1.86	0.57
18:CQ:82:ASN:H	18:CQ:86:TRP:HZ3	1.50	0.57
26:Cb:435:LEU:O	26:Cb:457:THR:OG1	2.19	0.57
32:LH:129:TYR:HB3	32:LH:218:ILE:HG12	1.86	0.57
34:LL:48:PRO:HG2	48:Lh:120:LYS:HD3	1.86	0.57
36:LN:192:LYS:O	36:LN:196:THR:HG23	2.05	0.57
1:C1:2922:G:O6	1:C1:2926:G:C5	2.58	0.57
10:CI:252:LEU:HD23	31:LG:92:GLN:HG3	1.87	0.57
12:CK:44:GLY:C	12:CK:46:ARG:H	2.13	0.57
25:CY:728:LEU:O	25:CY:731:GLU:HG3	2.04	0.57
1:C1:529:G:O6	1:C1:542:U:O4	2.22	0.57
1:C1:687:C:H2'	1:C1:688:G:H8	1.68	0.57
25:CY:723:VAL:HA	25:CY:726:ARG:NE	2.18	0.57
35:LM:112:LEU:HD11	35:LM:120:VAL:HG21	1.87	0.57
41:LT:68:THR:OG1	41:LT:71:ALA:O	2.18	0.57
47:Lf:18:TYR:OH	47:Lf:91:LEU:O	2.22	0.57
48:Lh:13:TRP:CZ3	50:Lj:87:ARG:NH1	2.73	0.57
1:C1:2091:U:H2'	1:C1:2092:G:C8	2.40	0.57
10:CI:315:ALA:O	10:CI:318:GLU:HG3	2.05	0.57
17:CP:312:THR:HG22	17:CP:400:ALA:HB1	1.87	0.57
21:CT:424:LEU:HD23	21:CT:427:LEU:HD12	1.87	0.57
29:LC:42:GLY:HA3	29:LC:114:ILE:HD11	1.87	0.57
32:LH:167:MET:HE1	32:LH:200:ILE:HD11	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:LN:123:GLN:HG3	36:LN:128:LYS:HG2	1.87	0.57
42:LV:67:GLY:O	42:LV:72:ARG:NH2	2.38	0.57
1:C1:584:C:P	1:C1:596:G:H1	2.28	0.57
1:C1:2973:A:H2'	1:C1:2974:G:H8	1.69	0.57
2:C2:159:C:N4	10:CI:252:LEU:O	2.38	0.57
4:CB:233:VAL:HG23	4:CB:243:ILE:HD11	1.86	0.57
5:CC:391:ARG:HD2	5:CC:392:LYS:HZ3	1.69	0.57
6:CE:399:THR:HA	6:CE:402:GLU:HG2	1.87	0.57
11:CJ:148:LEU:HD12	11:CJ:238:LEU:HD12	1.86	0.57
11:CJ:458:PRO:HB2	11:CJ:462:TRP:CZ3	2.40	0.57
16:CO:106:ILE:HG23	16:CO:107:VAL:HG13	1.87	0.57
17:CP:254:GLU:HG3	17:CP:255:GLU:H	1.70	0.57
21:CT:326:LEU:HG	21:CT:429:LYS:HD3	1.87	0.57
14:LF:227:HIS:HB3	14:LF:230:GLU:OE1	2.05	0.57
1:C1:114:A:H4'	36:LN:49:ARG:HG2	1.86	0.56
15:CN:100:ARG:NH1	18:CQ:25:ASP:OD2	2.38	0.56
34:LL:57:ILE:HD11	34:LL:111:ALA:HB1	1.87	0.56
1:C1:715:G:H5''	39:LQ:71:PRO:HB2	1.87	0.56
1:C1:979:A:H2'	1:C1:980:G:C8	2.40	0.56
1:C1:3189:G:H2'	1:C1:3190:G:H8	1.68	0.56
6:CE:384:VAL:HG23	6:CE:410:THR:HG23	1.88	0.56
8:CG:37:VAL:HG11	8:CG:50:LEU:HD13	1.88	0.56
21:CT:270:LEU:HD21	21:CT:283:ARG:HD2	1.87	0.56
29:LC:158:VAL:HA	29:LC:163:VAL:HG21	1.87	0.56
44:LY:73:TYR:CE2	44:LY:76:LYS:HG2	2.40	0.56
1:C1:115:A:N6	1:C1:149:U:C2	2.73	0.56
1:C1:174:C:N4	1:C1:230:A:H61	2.03	0.56
1:C1:1124:G:H5'	1:C1:1125:A:H2'	1.86	0.56
1:C1:1874:A:N1	26:Cb:815:LYS:HB3	2.20	0.56
1:C1:2926:G:H2'	1:C1:2927:A:C8	2.40	0.56
1:C1:3215:U:C2	47:Lf:66:ILE:HG21	2.41	0.56
2:C2:207:G:OP1	4:CB:175:THR:OG1	2.23	0.56
9:CH:357:ILE:HG23	9:CH:361:LEU:HD23	1.86	0.56
10:CI:219:VAL:HG23	10:CI:228:ARG:HB2	1.88	0.56
11:CJ:141:LEU:HD23	11:CJ:206:ILE:HD13	1.86	0.56
17:CP:443:PHE:N	17:CP:444:PRO:HD2	2.20	0.56
20:CS:661:THR:O	20:CS:665:GLN:HG3	2.05	0.56
21:CT:134:ILE:HG12	21:CT:148:HIS:HD2	1.70	0.56
25:CY:676:LEU:HA	25:CY:679:LYS:HE2	1.86	0.56
25:CY:678:GLN:O	25:CY:682:MET:HG3	2.06	0.56
26:Cb:238:VAL:HG21	26:Cb:262:LEU:HD13	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:LO:77:ALA:HB3	37:LO:80:ARG:HG2	1.87	0.56
40:LS:6:GLU:CB	40:LS:64:ILE:HB	2.36	0.56
40:LS:21:ASN:OD1	41:LT:146:ASN:ND2	2.38	0.56
1:C1:622:A:O3'	46:Le:42:ARG:NH1	2.37	0.56
2:C2:205:G:H4'	4:CB:238:SER:HB2	1.87	0.56
3:CA:131:ASN:HB2	22:CU:282:MET:HE3	1.87	0.56
32:LH:156:PHE:O	32:LH:159:GLU:HG2	2.06	0.56
40:LS:81:TYR:CE1	40:LS:90:MET:HE3	2.41	0.56
6:CE:122:THR:HG21	6:CE:171:GLU:OE2	2.05	0.56
12:CK:154:PRO:HG3	12:CK:249:PRO:HB2	1.88	0.56
18:CQ:1:MET:SD	18:CQ:15:PRO:HG2	2.46	0.56
29:LC:132:VAL:HG12	29:LC:134:PRO:HD2	1.87	0.56
45:Ld:83:ILE:HG12	45:Ld:101:VAL:HG22	1.88	0.56
1:C1:966:U:H2'	1:C1:967:U:H6	1.70	0.56
1:C1:2373:U:H2'	1:C1:2374:G:H8	1.71	0.56
1:C1:2922:G:H21	1:C1:2925:A:N6	2.04	0.56
1:C1:2975:C:OP1	15:CN:9:ASN:ND2	2.27	0.56
1:C1:3334:U:H2'	1:C1:3335:U:C6	2.41	0.56
2:C2:202:C:H2'	2:C2:203:G:H8	1.70	0.56
20:CS:658:GLU:HG3	20:CS:710:ILE:HD11	1.87	0.56
31:LG:229:VAL:O	31:LG:233:ARG:HB3	2.05	0.56
1:C1:137:C:H2'	1:C1:138:G:O4'	2.05	0.56
1:C1:781:G:H1	29:LC:103:PRO:HD2	1.70	0.56
1:C1:2404:G:O6	1:C1:2467:U:O4	2.23	0.56
17:CP:327:ARG:HH12	17:CP:355:PRO:HG2	1.71	0.56
25:CY:439:LEU:HA	25:CY:442:ILE:HG12	1.86	0.56
28:LB:24:ARG:HH22	28:LB:28:ARG:HB3	1.71	0.56
14:LF:23:LYS:HA	14:LF:26:GLU:HG2	1.88	0.56
1:C1:651:A:H2'	1:C1:652:A:C8	2.41	0.56
1:C1:2432:C:OP1	51:Lq:26:ARG:NE	2.38	0.56
3:CA:68:PHE:HA	49:Li:89:PHE:HE2	1.70	0.56
3:CA:130:GLY:HA3	3:CA:234:ILE:HG22	1.88	0.56
6:CE:217:VAL:HG23	6:CE:226:GLU:OE1	2.05	0.56
11:CJ:26:LEU:HD23	11:CJ:73:LEU:HD23	1.87	0.56
11:CJ:149:PHE:CE1	11:CJ:172:CYS:HB2	2.40	0.56
11:CJ:372:PHE:O	11:CJ:395:ILE:HA	2.05	0.56
26:Cb:251:PHE:HA	26:Cb:254:GLN:NE2	2.20	0.56
1:C1:2814:G:H21	12:CK:192:THR:HG21	1.70	0.56
7:CF:227:TRP:HB2	7:CF:234:VAL:HG12	1.86	0.56
25:CY:433:VAL:HG23	25:CY:434:THR:H	1.70	0.56
26:Cb:309:PHE:HB2	26:Cb:506:VAL:HG22	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LG:146:ILE:HG23	31:LG:178:ILE:HD12	1.87	0.56
1:C1:247:A:H2'	1:C1:248:G:H8	1.71	0.56
1:C1:3309:G:H22	18:CQ:56:ARG:NH2	2.04	0.56
11:CJ:47:PRO:HG2	11:CJ:53:VAL:HG21	1.87	0.56
43:LX:63:SER:HB2	48:Lh:71:LEU:HD13	1.88	0.56
1:C1:249:C:O4'	19:CR:148:GLN:NE2	2.39	0.55
1:C1:3244:C:O3'	28:LB:335:ARG:NH2	2.39	0.55
11:CJ:371:THR:HG23	11:CJ:416:THR:H	1.71	0.55
26:Cb:331:MET:HE1	26:Cb:418:ASN:HD22	1.71	0.55
30:LE:126:LYS:O	30:LE:130:ALA:HB2	2.06	0.55
31:LG:222:LYS:O	31:LG:226:LEU:HB2	2.05	0.55
41:LT:45:ASN:H	41:LT:95:HIS:CE1	2.24	0.55
1:C1:189:G:N1	1:C1:192:A:OP2	2.36	0.55
1:C1:3216:U:O2'	1:C1:3218:A:N6	2.37	0.55
1:C1:3332:G:O2'	1:C1:3333:A:H8	1.90	0.55
2:C2:102:U:O2'	2:C2:103:G:OP1	2.22	0.55
19:CR:151:LEU:HD21	34:LL:120:LYS:HD2	1.88	0.55
21:CT:602:GLN:O	21:CT:602:GLN:HG2	2.05	0.55
29:LC:280:ASN:HD22	29:LC:282:VAL:H	1.55	0.55
40:LS:6:GLU:HB2	40:LS:64:ILE:HB	1.86	0.55
1:C1:894:A:C6	20:CS:727:ALA:HB1	2.41	0.55
1:C1:3162:A:O2'	38:LP:182:ARG:NH2	2.38	0.55
2:C2:127:U:O2	11:CJ:15:ASN:ND2	2.30	0.55
20:CS:488:ALA:HA	20:CS:491:ARG:HG3	1.86	0.55
25:CY:467:SER:O	25:CY:470:GLN:HG3	2.06	0.55
25:CY:583:GLU:OE2	25:CY:615:GLN:NE2	2.39	0.55
26:Cb:529:GLU:HG3	42:LV:108:LYS:NZ	2.20	0.55
26:Cb:602:THR:H	26:Cb:625:ARG:HH22	1.54	0.55
26:Cb:868:VAL:O	26:Cb:871:LYS:HG3	2.06	0.55
28:LB:29:VAL:HG12	28:LB:31:SER:H	1.71	0.55
51:Lq:49:PHE:HB2	51:Lq:193:LEU:HG	1.88	0.55
1:C1:897:G:H2'	1:C1:898:A:H8	1.71	0.55
2:C2:44:A:H2'	2:C2:45:C:C6	2.41	0.55
4:CB:87:HIS:CE1	4:CB:254:LYS:HD2	2.42	0.55
7:CF:38:GLN:NE2	7:CF:106:ASN:OD1	2.39	0.55
15:CN:88:LEU:HD12	15:CN:94:ILE:HD11	1.89	0.55
17:CP:264:ASN:CG	17:CP:268:LYS:HZ3	2.14	0.55
21:CT:172:MET:HE2	21:CT:245:CYS:HA	1.88	0.55
24:CX:99:GLU:HA	24:CX:102:ASN:HD22	1.71	0.55
25:CY:556:ARG:NH2	25:CY:624:GLU:OE2	2.33	0.55
26:Cb:322:LEU:HB2	26:Cb:517:ASN:ND2	2.20	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Cb:409:VAL:HG12	26:Cb:413:ARG:HD2	1.89	0.55
35:LM:121:MET:HE3	35:LM:125:LYS:HE3	1.89	0.55
1:C1:1230:C:H2'	26:Cb:622:ARG:HH22	1.71	0.55
1:C1:2387:G:C6	1:C1:2563:G:N2	2.75	0.55
1:C1:3078:U:H1'	1:C1:3079:A:H5''	1.87	0.55
6:CE:182:ASN:O	6:CE:257:ASN:ND2	2.40	0.55
8:CG:128:GLU:O	8:CG:147:THR:OG1	2.16	0.55
9:CH:284:ILE:HB	9:CH:316:ILE:HG13	1.88	0.55
10:CI:191:ILE:HD11	10:CI:258:LEU:HD23	1.87	0.55
15:CN:85:ARG:NH2	15:CN:89:PRO:O	2.40	0.55
23:CV:16:TYR:O	23:CV:17:ASN:ND2	2.40	0.55
33:LK:31:LYS:HG3	33:LK:32:ILE:HG12	1.89	0.55
34:LL:76:THR:HB	34:LL:79:GLU:HG2	1.88	0.55
1:C1:429:G:O6	23:CV:134:ARG:NH1	2.40	0.55
1:C1:1083:G:H1'	14:LF:111:LEU:HD22	1.88	0.55
1:C1:2564:G:C4	8:CG:2:ARG:HD3	2.42	0.55
1:C1:2922:G:N7	1:C1:2926:G:N1	2.55	0.55
4:CB:116:PHE:HZ	4:CB:120:LEU:HD22	1.72	0.55
6:CE:388:HIS:CE1	6:CE:390:LYS:HB2	2.42	0.55
27:Cz:42:THR:HG23	27:Cz:45:LEU:HD22	1.89	0.55
1:C1:713:G:C6	1:C1:723:G:C2	2.95	0.55
1:C1:2414:G:O6	1:C1:2456:A:N1	2.40	0.55
4:CB:48:ASN:OD1	4:CB:49:LEU:N	2.37	0.55
6:CE:571:ARG:HG2	6:CE:572:ALA:N	2.20	0.55
7:CF:64:ARG:NH1	7:CF:65:ILE:O	2.40	0.55
8:CG:28:ALA:HA	24:CX:98:ARG:HH21	1.71	0.55
11:CJ:189:PHE:HB3	11:CJ:196:TYR:HB2	1.89	0.55
17:CP:309:ARG:HG3	17:CP:370:PHE:CE2	2.41	0.55
21:CT:428:ALA:HA	21:CT:492:LEU:HD21	1.87	0.55
30:LE:194:LYS:HD2	30:LE:197:LEU:HD12	1.89	0.55
33:LK:65:GLN:HG2	33:LK:66:ASN:N	2.22	0.55
38:LP:40:LYS:HD2	38:LP:113:ILE:HG22	1.89	0.55
1:C1:38:U:H2'	1:C1:39:A:C8	2.42	0.55
5:CC:367:ARG:HH22	5:CC:385:THR:HA	1.72	0.55
11:CJ:390:PHE:CE2	11:CJ:465:ILE:HG13	2.42	0.55
12:CK:240:GLY:O	12:CK:241:ARG:NH1	2.40	0.55
16:CO:38:MET:HE3	16:CO:42:GLN:NE2	2.22	0.55
18:CQ:1:MET:HE1	28:LB:57:VAL:HG21	1.89	0.55
37:LO:129:LEU:HD11	40:LS:170:PRO:HG2	1.89	0.55
1:C1:649:U:H2'	1:C1:650:C:C6	2.42	0.55
1:C1:3288:G:O6	1:C1:3297:U:O4	2.25	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CH:465:GLU:OE2	18:CQ:103:ARG:NH1	2.40	0.55
26:Cb:546:MET:SD	26:Cb:549:ARG:NH2	2.80	0.55
29:LC:155:SER:HA	29:LC:158:VAL:HG12	1.89	0.55
41:LT:40:VAL:HG21	41:LT:96:VAL:HB	1.89	0.55
1:C1:983:A:N1	1:C1:1032:U:O2'	2.39	0.55
1:C1:2407:A:H2'	1:C1:2408:U:H6	1.71	0.55
1:C1:2926:G:H2'	1:C1:2927:A:H8	1.71	0.55
4:CB:21:ASP:OD1	4:CB:22:GLN:N	2.40	0.55
9:CH:493:GLU:OE1	45:Ld:107:LYS:NZ	2.40	0.55
23:CV:30:ARG:NH2	46:Le:82:ASP:OD1	2.40	0.55
26:Cb:242:GLU:HB3	26:Cb:245:ARG:HG3	1.88	0.55
35:LM:19:VAL:O	35:LM:65:THR:OG1	2.23	0.55
38:LP:23:ARG:O	38:LP:86:LYS:NZ	2.30	0.55
42:LV:83:GLN:HE21	42:LV:85:LYS:HB3	1.71	0.55
51:Lq:205:THR:HG22	51:Lq:207:LYS:H	1.72	0.55
1:C1:2351:C:H2'	1:C1:2352:A:H8	1.72	0.54
1:C1:3205:C:H2'	1:C1:3206:G:H8	1.72	0.54
5:CC:355:ASN:O	11:CJ:485:HIS:N	2.40	0.54
5:CC:403:ARG:NH1	5:CC:406:ARG:HB3	2.21	0.54
6:CE:392:LYS:HE3	6:CE:394:GLN:HB2	1.89	0.54
25:CY:549:PRO:O	25:CY:553:HIS:ND1	2.40	0.54
26:Cb:310:PHE:HB2	26:Cb:469:LEU:HD23	1.88	0.54
35:LM:22:LEU:O	35:LM:25:GLY:N	2.37	0.54
51:Lq:32:VAL:HG23	51:Lq:208:ALA:HA	1.88	0.54
1:C1:399:A:C2	2:C2:17:A:H1'	2.42	0.54
1:C1:2407:A:H2'	1:C1:2408:U:C6	2.42	0.54
1:C1:2907:U:H2'	1:C1:2908:G:C8	2.42	0.54
1:C1:3284:A:H62	1:C1:3301:G:H21	1.55	0.54
9:CH:186:VAL:HG23	9:CH:331:LYS:HD3	1.88	0.54
26:Cb:283:THR:HA	26:Cb:287:LEU:HD13	1.90	0.54
29:LC:151:LEU:HD21	29:LC:176:ILE:HG12	1.88	0.54
1:C1:749:C:H2'	1:C1:750:G:C8	2.41	0.54
1:C1:1202:U:H5'	27:Cz:48:TRP:CZ2	2.42	0.54
1:C1:3297:U:O2'	1:C1:3298:U:OP1	2.24	0.54
2:C2:38:U:O2'	48:Lh:88:LYS:NZ	2.39	0.54
3:CA:108:PRO:HB3	6:CE:573:TYR:CE1	2.42	0.54
9:CH:242:LEU:HB3	9:CH:277:PHE:HE1	1.72	0.54
9:CH:444:LYS:HE2	18:CQ:93:MET:HE3	1.90	0.54
15:CN:61:ARG:NH1	15:CN:105:GLY:O	2.41	0.54
23:CV:123:ARG:HD3	30:LE:27:TRP:CZ2	2.43	0.54
26:Cb:493:ARG:NH2	26:Cb:577:GLY:H	2.03	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:LO:170:TYR:CZ	37:LO:174:LYS:HE3	2.42	0.54
1:C1:643:A:H2'	1:C1:644:A:H8	1.72	0.54
1:C1:1126:U:H6	1:C1:1142:C:H41	1.55	0.54
1:C1:2404:G:H2'	1:C1:2405:A:C8	2.43	0.54
4:CB:33:HIS:CG	10:CI:323:MET:HE1	2.42	0.54
5:CC:142:ASP:HB2	5:CC:146:GLY:H	1.72	0.54
9:CH:315:GLU:CD	9:CH:337:ARG:HH22	2.14	0.54
9:CH:337:ARG:HA	9:CH:340:VAL:HG12	1.89	0.54
9:CH:364:VAL:HG11	15:CN:242:VAL:HG23	1.88	0.54
10:CI:239:GLU:O	10:CI:243:ILE:HD12	2.08	0.54
11:CJ:388:ARG:HG2	11:CJ:388:ARG:HH11	1.71	0.54
21:CT:412:LEU:HD11	21:CT:427:LEU:HD11	1.88	0.54
14:LF:66:ARG:HA	14:LF:66:ARG:HE	1.73	0.54
33:LK:18:THR:O	33:LK:57:ARG:NH2	2.41	0.54
34:LL:29:PRO:O	34:LL:33:VAL:HG23	2.08	0.54
2:C2:156:U:OP1	31:LG:87:LYS:NZ	2.40	0.54
14:CM:92:VAL:O	14:CM:120:GLY:HA2	2.08	0.54
15:CN:20:THR:HG23	15:CN:22:SER:H	1.72	0.54
17:CP:492:LEU:HD11	17:CP:526:TYR:HE1	1.71	0.54
18:CQ:68:THR:HG22	18:CQ:96:ILE:HG23	1.90	0.54
25:CY:631:VAL:HA	25:CY:634:SER:HB3	1.90	0.54
26:Cb:306:GLU:HA	26:Cb:501:ALA:HA	1.90	0.54
26:Cb:375:THR:OG1	26:Cb:378:HIS:ND1	2.41	0.54
14:LF:142:TYR:CZ	14:LF:236:ASN:HB2	2.43	0.54
35:LM:94:TRP:O	35:LM:97:THR:OG1	2.25	0.54
42:LV:23:ALA:HB3	42:LV:38:ILE:HD12	1.90	0.54
1:C1:1171:C:C4	1:C1:1297:U:O2	2.60	0.54
1:C1:3305:U:H2'	1:C1:3306:G:C8	2.42	0.54
4:CB:78:LEU:HD12	4:CB:172:TYR:CD2	2.42	0.54
5:CC:231:LEU:HD11	20:CS:663:ALA:HB1	1.88	0.54
11:CJ:217:ARG:HH11	11:CJ:219:VAL:HB	1.72	0.54
12:CK:112:GLU:OE1	17:CP:232:LEU:HD12	2.08	0.54
12:CK:128:SER:OG	12:CK:130:GLU:OE1	2.26	0.54
18:CQ:23:ARG:HG3	18:CQ:25:ASP:OD1	2.07	0.54
21:CT:381:MET:HE3	21:CT:385:ASP:HB2	1.89	0.54
21:CT:562:THR:HG22	21:CT:564:THR:H	1.72	0.54
26:Cb:308:ALA:HB1	26:Cb:573:HIS:CE1	2.43	0.54
2:C2:69:U:H2'	2:C2:70:G:O4'	2.08	0.54
2:C2:152:G:O3'	31:LG:66:LYS:NZ	2.40	0.54
5:CC:387:TYR:HD1	5:CC:392:LYS:HB3	1.72	0.54
6:CE:438:PRO:HG2	6:CE:527:LEU:HD12	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CF:173:ARG:HH22	32:LH:180:LYS:HG2	1.73	0.54
10:CI:188:VAL:HG22	10:CI:234:GLU:HG3	1.88	0.54
10:CI:225:GLY:HA3	10:CI:282:VAL:HG12	1.88	0.54
31:LG:158:ASN:ND2	31:LG:184:LYS:HG2	2.21	0.54
9:CH:429:ASN:HB3	9:CH:432:TRP:CD2	2.42	0.54
11:CJ:472:PRO:HB2	11:CJ:475:LEU:HB2	1.90	0.54
41:LT:71:ALA:HA	41:LT:92:ARG:HA	1.90	0.54
1:C1:712:A:H3'	1:C1:713:G:H8	1.73	0.54
1:C1:1870:A:H2'	1:C1:1871:G:C8	2.42	0.54
1:C1:2408:U:H2'	1:C1:2409:A:C8	2.42	0.54
1:C1:2777:A:H4'	1:C1:2778:A:OP1	2.07	0.54
1:C1:3075:C:OP2	27:Cz:26:ARG:NH1	2.41	0.54
5:CC:271:LEU:HD21	49:Li:48:PHE:CD2	2.43	0.54
9:CH:208:LEU:HD21	9:CH:331:LYS:HD2	1.89	0.54
9:CH:445:ASN:HD21	18:CQ:3:ILE:HB	1.73	0.54
12:CK:17:ARG:NH1	32:LH:214:PHE:O	2.41	0.54
21:CT:264:ARG:HB3	21:CT:268:LYS:NZ	2.23	0.54
25:CY:631:VAL:HG21	25:CY:722:VAL:HG11	1.89	0.54
29:LC:133:ALA:HB2	29:LC:149:VAL:HG21	1.90	0.54
14:LF:123:VAL:HG11	14:LF:129:THR:HG21	1.90	0.54
33:LK:65:GLN:HG2	33:LK:66:ASN:H	1.72	0.54
33:LK:107:ASP:OD1	33:LK:108:GLU:N	2.41	0.54
1:C1:729:U:H2'	1:C1:730:C:C6	2.43	0.54
1:C1:796:G:H1	1:C1:906:A:N6	2.05	0.54
1:C1:1406:C:OP1	23:CV:22:LYS:NZ	2.39	0.54
1:C1:2857:C:O2'	1:C1:2859:G:OP2	2.26	0.54
1:C1:3159:A:N6	1:C1:3201:U:OP2	2.41	0.54
1:C1:3298:U:H2'	1:C1:3299:A:H8	1.73	0.54
7:CF:91:ARG:HH22	7:CF:233:GLU:HA	1.72	0.54
8:CG:52:ILE:HG12	17:CP:407:VAL:HG22	1.90	0.54
11:CJ:191:SER:O	11:CJ:212:TYR:OH	2.24	0.54
19:CR:132:PRO:HG2	34:LL:106:GLU:HB3	1.89	0.54
31:LG:102:PRO:HG3	31:LG:193:VAL:HA	1.89	0.54
1:C1:745:U:H3	1:C1:749:C:N4	2.05	0.53
1:C1:909:C:H2'	1:C1:910:A:C8	2.44	0.53
1:C1:2361:A:C6	1:C1:2900:C:C4	2.97	0.53
4:CB:67:THR:O	4:CB:279:ARG:HB3	2.07	0.53
4:CB:118:GLU:HA	4:CB:121:ARG:HD2	1.90	0.53
8:CG:84:ILE:HG12	8:CG:170:CYS:HA	1.91	0.53
9:CH:20:VAL:HG11	9:CH:56:CYS:SG	2.48	0.53
35:LM:27:LEU:HD11	35:LM:94:TRP:CG	2.43	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1120:U:H2'	1:C1:1121:G:H8	1.74	0.53
1:C1:2455:U:O2'	1:C1:2456:A:H5'	2.08	0.53
6:CE:332:LEU:HD11	6:CE:446:GLY:HA3	1.90	0.53
7:CF:77:LEU:HB3	7:CF:89:LEU:HG	1.91	0.53
9:CH:149:LEU:HA	9:CH:152:VAL:HG12	1.89	0.53
11:CJ:249:ILE:HG23	11:CJ:251:LEU:H	1.73	0.53
11:CJ:398:ASP:H	11:CJ:401:LEU:HD12	1.73	0.53
17:CP:309:ARG:HB3	17:CP:363:ILE:HG22	1.89	0.53
19:CR:131:VAL:HG13	19:CR:134:GLN:HB2	1.90	0.53
20:CS:466:ASP:CG	20:CS:470:ARG:HE	2.15	0.53
26:Cb:225:LYS:HZ3	26:Cb:232:LEU:HG	1.73	0.53
26:Cb:413:ARG:NH1	26:Cb:431:ASP:O	2.41	0.53
32:LH:126:LYS:HG2	32:LH:184:ILE:HG12	1.90	0.53
32:LH:150:GLU:HG3	32:LH:166:VAL:HG12	1.90	0.53
33:LK:46:ILE:HD11	33:LK:62:LEU:HD21	1.90	0.53
45:Ld:14:ASP:HA	45:Ld:85:ARG:HH21	1.73	0.53
1:C1:890:G:OP1	20:CS:747:LYS:NZ	2.38	0.53
1:C1:3017:C:O2	1:C1:3272:U:O2'	2.24	0.53
1:C1:3254:A:H2'	1:C1:3255:G:H5''	1.91	0.53
6:CE:389:GLY:HA2	6:CE:396:ARG:HH21	1.72	0.53
15:CN:90:ASP:OD1	18:CQ:80:ARG:HD2	2.09	0.53
25:CY:470:GLN:HA	25:CY:473:ILE:HG22	1.90	0.53
31:LG:80:GLN:HE22	31:LG:170:PRO:HG2	1.73	0.53
1:C1:260:A:C5	36:LN:12:LYS:HG2	2.43	0.53
1:C1:1176:G:H2'	1:C1:1177:A:C8	2.44	0.53
1:C1:2078:G:H2'	1:C1:2079:A:C8	2.43	0.53
1:C1:2091:U:H2'	1:C1:2092:G:H8	1.73	0.53
1:C1:2817:U:H4'	1:C1:2818:U:O5'	2.07	0.53
1:C1:2942:C:H2'	1:C1:2943:C:C6	2.42	0.53
6:CE:360:ILE:HD13	6:CE:428:TRP:HB2	1.90	0.53
7:CF:30:ILE:O	7:CF:34:ILE:HG13	2.08	0.53
7:CF:43:PHE:HB3	7:CF:223:LEU:HD13	1.90	0.53
8:CG:116:LYS:HB3	8:CG:159:PRO:HA	1.90	0.53
10:CI:221:ASN:HD22	10:CI:228:ARG:HH12	1.54	0.53
11:CJ:79:GLN:O	11:CJ:83:GLU:HG3	2.08	0.53
17:CP:484:PRO:HG3	17:CP:519:GLU:HG2	1.90	0.53
18:CQ:99:ILE:O	18:CQ:103:ARG:HG2	2.08	0.53
19:CR:8:ARG:HH21	50:Lj:63:ARG:HA	1.72	0.53
37:LO:38:ARG:HB3	37:LO:41:ALA:HB3	1.90	0.53
1:C1:446:U:H4'	1:C1:447:C:OP2	2.07	0.53
1:C1:514:G:H5'	40:LS:70:LEU:HD12	1.89	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:750:G:H2'	1:C1:751:G:C4	2.44	0.53
1:C1:2091:U:O4	1:C1:2285:G:O6	2.26	0.53
3:CA:150:PRO:HA	3:CA:153:LYS:HE3	1.91	0.53
18:CQ:81:TYR:HA	18:CQ:86:TRP:HZ3	1.71	0.53
25:CY:701:ARG:HB2	25:CY:704:VAL:HB	1.90	0.53
28:LB:292:GLU:HA	28:LB:305:LYS:HZ2	1.73	0.53
38:LP:175:GLN:HA	38:LP:178:VAL:HG22	1.90	0.53
1:C1:433:U:H2'	1:C1:434:G:H8	1.73	0.53
1:C1:978:A:H2'	1:C1:979:A:C8	2.43	0.53
1:C1:3203:C:H2'	1:C1:3204:G:C8	2.44	0.53
6:CE:441:TYR:CE1	6:CE:445:VAL:HG21	2.44	0.53
9:CH:448:ASP:CG	18:CQ:2:ARG:HH21	2.15	0.53
15:CN:26:VAL:HG13	15:CN:34:PHE:HD2	1.74	0.53
28:LB:137:TYR:OH	28:LB:197:ARG:NH2	2.41	0.53
39:LQ:92:LEU:HD13	39:LQ:116:ASP:HA	1.91	0.53
1:C1:151:G:OP2	49:Li:35:PRO:HG2	2.09	0.53
1:C1:370:A:H4'	44:LY:90:THR:HG22	1.90	0.53
1:C1:542:U:H2'	1:C1:543:G:O4'	2.08	0.53
1:C1:1870:A:H2'	1:C1:1871:G:H8	1.73	0.53
1:C1:3249:G:OP2	1:C1:3249:G:N2	2.35	0.53
6:CE:351:PHE:CE2	6:CE:430:VAL:HG21	2.44	0.53
9:CH:202:SER:HG	12:CK:4:ASN:HD21	1.54	0.53
25:CY:594:LYS:O	25:CY:608:TYR:OH	2.22	0.53
25:CY:634:SER:HA	25:CY:639:PHE:CE2	2.44	0.53
32:LH:196:SER:O	32:LH:200:ILE:HD12	2.08	0.53
42:LV:35:ASN:CG	42:LV:66:LYS:HG2	2.33	0.53
1:C1:1171:C:H42	1:C1:1297:U:H1'	1.73	0.53
1:C1:1303:G:H2'	1:C1:1304:U:C6	2.44	0.53
1:C1:2342:U:O2'	1:C1:2343:G:H8	1.92	0.53
1:C1:3223:C:H2'	1:C1:3224:G:H8	1.73	0.53
10:CI:221:ASN:HB2	10:CI:228:ARG:NH1	2.24	0.53
11:CJ:388:ARG:HH12	11:CJ:395:ILE:HD12	1.74	0.53
25:CY:451:GLU:HA	25:CY:509:HIS:CE1	2.43	0.53
25:CY:675:VAL:HG22	25:CY:679:LYS:HZ3	1.74	0.53
1:C1:513:A:O2'	40:LS:69:PRO:HD2	2.08	0.53
1:C1:1201:C:H3'	27:Cz:55:ARG:HH12	1.73	0.53
9:CH:20:VAL:HG22	9:CH:55:THR:HG22	1.90	0.53
9:CH:444:LYS:HE2	18:CQ:93:MET:HB3	1.91	0.53
21:CT:606:LYS:O	21:CT:609:GLN:HG3	2.09	0.53
1:C1:433:U:H2'	1:C1:434:G:C8	2.44	0.53
1:C1:1241:A:H2'	1:C1:1242:A:C8	2.44	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1859:U:O4	1:C1:1860:A:N6	2.42	0.53
1:C1:2078:G:H2'	1:C1:2079:A:H8	1.74	0.53
3:CA:137:ARG:HG2	3:CA:165:VAL:HG12	1.89	0.53
4:CB:106:ARG:NH1	4:CB:110:ASN:OD1	2.42	0.53
6:CE:192:THR:HB	6:CE:195:LEU:HD13	1.90	0.53
11:CJ:251:LEU:HD13	11:CJ:273:LEU:HD23	1.90	0.53
14:CM:60:GLU:O	14:CM:64:GLN:HG2	2.09	0.53
26:Cb:2:PRO:HG2	42:LV:75:VAL:HG21	1.91	0.53
26:Cb:331:MET:HE1	26:Cb:418:ASN:ND2	2.24	0.53
1:C1:727:C:H2'	1:C1:728:A:C8	2.45	0.52
2:C2:23:U:H5''	44:LY:12:ARG:HG3	1.90	0.52
9:CH:426:ILE:HG23	18:CQ:80:ARG:HH22	1.74	0.52
9:CH:452:PRO:HD3	18:CQ:79:VAL:HG21	1.91	0.52
14:CM:242:ASN:HA	14:CM:245:ILE:HG12	1.91	0.52
17:CP:382:GLU:HG2	17:CP:504:THR:HG21	1.89	0.52
51:Lq:16:LEU:O	51:Lq:17:LEU:C	2.52	0.52
1:C1:2919:G:H2'	1:C1:2920:U:C6	2.43	0.52
1:C1:3283:G:O2'	1:C1:3302:A:N6	2.40	0.52
15:CN:143:ALA:HB2	15:CN:165:THR:HG22	1.91	0.52
26:Cb:170:ARG:HG3	26:Cb:195:VAL:HG21	1.91	0.52
26:Cb:258:ILE:O	26:Cb:262:LEU:HG	2.09	0.52
42:LV:47:ARG:HG2	42:LV:48:LEU:H	1.75	0.52
46:Le:86:LEU:HD11	46:Le:93:TYR:HB3	1.89	0.52
1:C1:966:U:H2'	1:C1:967:U:C6	2.44	0.52
1:C1:1901:A:H61	1:C1:2073:G:H1	1.57	0.52
1:C1:2361:A:C6	1:C1:2900:C:N3	2.77	0.52
1:C1:3105:C:H2'	1:C1:3106:G:H8	1.75	0.52
9:CH:210:TYR:OH	9:CH:211:LYS:NZ	2.43	0.52
10:CI:290:GLY:O	10:CI:294:GLU:HG2	2.10	0.52
11:CJ:246:TYR:HA	11:CJ:249:ILE:HG22	1.90	0.52
11:CJ:373:PHE:HB3	11:CJ:418:GLN:HG3	1.90	0.52
11:CJ:401:LEU:HD23	14:CM:188:GLU:OE2	2.08	0.52
13:CL:277:PRO:O	13:CL:279:ALA:N	2.42	0.52
21:CT:390:HIS:NE2	21:CT:394:GLU:OE2	2.41	0.52
26:Cb:16:ASP:OD1	26:Cb:19:GLY:N	2.43	0.52
26:Cb:488:ARG:NH2	26:Cb:495:GLU:OE1	2.43	0.52
28:LB:21:ARG:HG2	28:LB:270:GLN:HG2	1.91	0.52
37:LO:199:LEU:HD12	37:LO:204:TYR:HB2	1.91	0.52
1:C1:345:G:O6	50:Lj:52:LYS:NZ	2.32	0.52
1:C1:401:A:OP1	46:Le:27:LYS:NZ	2.31	0.52
1:C1:567:U:OP1	14:LF:246:ARG:NH1	2.43	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2076:C:H2'	1:C1:2077:G:H8	1.74	0.52
11:CJ:169:GLU:HG2	11:CJ:173:HIS:CE1	2.45	0.52
14:CM:119:ASN:HD21	14:CM:212:LYS:HG3	1.74	0.52
48:Lh:59:VAL:O	48:Lh:63:ILE:HG13	2.09	0.52
1:C1:523:A:H2'	1:C1:524:A:C8	2.44	0.52
2:C2:175:G:H2'	2:C2:176:G:H8	1.73	0.52
6:CE:267:ASP:OD2	6:CE:268:ARG:N	2.42	0.52
6:CE:269:ILE:HG21	6:CE:278:MET:HE2	1.90	0.52
6:CE:328:THR:HA	6:CE:447:ARG:HH21	1.73	0.52
8:CG:149:ARG:HB3	8:CG:153:GLU:HB2	1.91	0.52
9:CH:257:GLU:HB2	33:LK:39:PRO:HG2	1.91	0.52
10:CI:249:ASP:HA	10:CI:260:CYS:HB2	1.92	0.52
17:CP:495:ILE:HD11	17:CP:581:PHE:CD2	2.44	0.52
20:CS:497:GLN:NE2	20:CS:498:GLU:O	2.42	0.52
25:CY:558:LEU:HD13	25:CY:571:LEU:HD21	1.90	0.52
1:C1:2329:A:H2'	1:C1:2330:A:H8	1.75	0.52
1:C1:2841:U:H2'	1:C1:2842:C:H6	1.74	0.52
1:C1:2883:C:H2'	1:C1:2884:A:H8	1.74	0.52
4:CB:25:LYS:HA	4:CB:28:LYS:HG2	1.92	0.52
21:CT:143:GLU:HG2	21:CT:202:ARG:HG2	1.91	0.52
25:CY:539:MET:HE1	25:CY:554:LEU:HB2	1.91	0.52
14:LF:144:TYR:CE2	14:LF:238:GLU:HG3	2.45	0.52
42:LV:25:MET:HG2	42:LV:26:ASN:O	2.10	0.52
1:C1:768:G:H2'	1:C1:769:C:C6	2.45	0.52
1:C1:954:G:OP1	39:LQ:44:ARG:NH2	2.39	0.52
1:C1:1398:C:H2'	1:C1:1399:G:C4	2.45	0.52
1:C1:2751:G:H2'	1:C1:2752:G:C8	2.44	0.52
1:C1:3172:U:H2'	1:C1:3173:C:C6	2.45	0.52
17:CP:357:TYR:HE1	17:CP:427:ARG:HH21	1.57	0.52
26:Cb:17:ILE:H	26:Cb:448:LYS:NZ	2.05	0.52
26:Cb:141:THR:HA	26:Cb:144:PHE:CE1	2.45	0.52
36:LN:165:THR:O	36:LN:169:LYS:HG3	2.10	0.52
51:Lq:100:ILE:HD13	51:Lq:124:LEU:HD11	1.90	0.52
1:C1:798:A:O2'	1:C1:799:C:O5'	2.28	0.52
1:C1:1227:A:H2'	1:C1:1254:C:OP1	2.09	0.52
4:CB:30:LEU:O	4:CB:34:ILE:HG12	2.10	0.52
6:CE:359:LYS:HB2	6:CE:427:ASP:H	1.73	0.52
15:CN:78:ASP:OD1	15:CN:96:ARG:NH2	2.41	0.52
46:Le:77:VAL:HG23	46:Le:82:ASP:HB2	1.91	0.52
1:C1:19:U:H2'	1:C1:20:A:C8	2.44	0.52
1:C1:1094:A:H2'	1:C1:1095:G:C8	2.44	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1371:G:H5''	46:Le:102:SER:HB3	1.92	0.52
1:C1:1877:G:H2'	1:C1:1878:G:C8	2.44	0.52
1:C1:3207:U:H2'	30:LE:87:PHE:CZ	2.44	0.52
2:C2:153:U:OP1	31:LG:66:LYS:NZ	2.40	0.52
3:CA:42:ARG:HG2	3:CA:67:LYS:HB3	1.92	0.52
7:CF:31:ARG:NH1	7:CF:76:ALA:O	2.43	0.52
8:CG:112:SER:HB2	12:CK:139:GLY:HA3	1.92	0.52
9:CH:263:LEU:O	9:CH:267:ILE:HG12	2.10	0.52
9:CH:404:ALA:HA	9:CH:407:ILE:HG12	1.92	0.52
11:CJ:419:ILE:HD13	11:CJ:456:VAL:HG23	1.91	0.52
25:CY:411:GLY:O	25:CY:416:ARG:NH1	2.43	0.52
25:CY:656:GLU:HA	25:CY:659:LYS:HE2	1.92	0.52
26:Cb:549:ARG:HD2	26:Cb:550:ASN:O	2.09	0.52
31:LG:85:LEU:HD23	31:LG:181:ALA:HB1	1.92	0.52
1:C1:1188:G:H2'	1:C1:1189:G:H5''	1.91	0.52
1:C1:3272:U:H2'	1:C1:3273:G:O4'	2.10	0.52
3:CA:79:GLU:OE2	6:CE:573:TYR:N	2.43	0.52
5:CC:363:THR:O	5:CC:366:GLU:HG3	2.09	0.52
9:CH:236:MET:HE1	26:Cb:597:TYR:CG	2.45	0.52
18:CQ:95:ARG:NH2	18:CQ:99:ILE:HD11	2.24	0.52
19:CR:46:SER:O	19:CR:50:THR:HG23	2.10	0.52
20:CS:660:MET:HB2	20:CS:718:ILE:HD11	1.92	0.52
21:CT:145:TYR:HB3	21:CT:148:HIS:ND1	2.25	0.52
23:CV:73:LYS:HA	29:LC:148:GLU:H	1.76	0.52
1:C1:155:G:H2'	1:C1:156:G:H8	1.74	0.51
1:C1:773:A:H2'	1:C1:774:A:C8	2.45	0.51
1:C1:895:A:O2'	1:C1:896:A:O5'	2.27	0.51
1:C1:1080:A:OP2	41:LT:130:ARG:NH1	2.43	0.51
1:C1:2737:A:H2'	1:C1:2738:A:O4'	2.10	0.51
2:C2:193:G:H1'	4:CB:240:ASN:ND2	2.25	0.51
4:CB:20:PRO:HA	4:CB:23:THR:HG22	1.93	0.51
7:CF:88:GLY:O	7:CF:91:ARG:HD3	2.10	0.51
12:CK:137:LYS:HE2	12:CK:143:HIS:CG	2.46	0.51
15:CN:28:LEU:HD13	15:CN:50:ARG:HD2	1.93	0.51
17:CP:488:LYS:HZ1	17:CP:526:TYR:HB2	1.75	0.51
33:LK:105:SER:HB3	33:LK:108:GLU:OE1	2.10	0.51
45:Ld:52:MET:HB3	45:Ld:85:ARG:HD3	1.92	0.51
1:C1:717:U:O2'	1:C1:720:G:O6	2.19	0.51
1:C1:889:G:H1	1:C1:900:U:H3	1.57	0.51
4:CB:159:ILE:O	4:CB:163:LEU:HG	2.10	0.51
11:CJ:386:ILE:HD12	11:CJ:465:ILE:HD13	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CM:92:VAL:HG11	14:CM:133:ILE:HD12	1.92	0.51
14:CM:103:PRO:HA	14:CM:106:ARG:NH1	2.25	0.51
1:C1:789:A:H61	1:C1:913:U:H3	1.55	0.51
2:C2:154:C:H2'	2:C2:155:A:C8	2.45	0.51
6:CE:333:GLU:OE2	6:CE:481:VAL:HG13	2.10	0.51
7:CF:91:ARG:HH21	7:CF:234:VAL:HG22	1.75	0.51
9:CH:283:PHE:CE2	9:CH:334:VAL:HG23	2.45	0.51
17:CP:530:ARG:NH1	17:CP:531:ARG:HH12	2.08	0.51
26:Cb:4:ARG:HH21	26:Cb:541:ALA:HB2	1.75	0.51
37:LO:87:ARG:HD3	37:LO:92:HIS:CG	2.45	0.51
42:LV:68:LYS:HZ2	42:LV:70:GLU:HB2	1.75	0.51
1:C1:325:C:OP2	19:CR:9:LYS:NZ	2.29	0.51
1:C1:651:A:H2'	1:C1:652:A:H8	1.73	0.51
1:C1:727:C:H2'	1:C1:728:A:H8	1.75	0.51
1:C1:3204:G:H2'	1:C1:3205:C:C6	2.45	0.51
11:CJ:144:CYS:SG	11:CJ:238:LEU:HG	2.51	0.51
14:CM:94:ARG:O	14:CM:118:ASN:N	2.43	0.51
15:CN:154:LEU:HD12	15:CN:155:SER:H	1.76	0.51
14:LF:104:LYS:O	14:LF:108:ILE:HG12	2.11	0.51
40:LS:38:LYS:HG2	40:LS:58:ILE:HG13	1.92	0.51
25:CY:414:ALA:O	25:CY:417:GLU:HG3	2.10	0.51
26:Cb:833:LYS:NZ	26:Cb:835:ASN:HB2	2.26	0.51
28:LB:29:VAL:HA	28:LB:219:ILE:HD13	1.92	0.51
44:LY:30:MET:HB3	44:LY:100:PRO:HG2	1.93	0.51
51:Lq:86:SER:O	51:Lq:90:LEU:HG	2.11	0.51
1:C1:422:G:H2'	1:C1:423:U:C6	2.46	0.51
1:C1:529:G:C6	1:C1:543:G:N2	2.79	0.51
1:C1:662:C:O2'	1:C1:666:U:OP1	2.22	0.51
1:C1:796:G:H1	1:C1:906:A:H61	1.58	0.51
1:C1:1900:A:H2'	1:C1:1901:A:C8	2.45	0.51
3:CA:292:ARG:NH2	39:LQ:118:ASN:OD1	2.44	0.51
4:CB:117:PRO:O	4:CB:121:ARG:HG3	2.10	0.51
9:CH:210:TYR:HB3	9:CH:215:TYR:HE1	1.75	0.51
14:LF:162:VAL:HG21	14:LF:174:ILE:HD11	1.92	0.51
1:C1:409:A:H2'	1:C1:410:A:H8	1.74	0.51
1:C1:2371:G:H2'	1:C1:2372:U:C6	2.46	0.51
1:C1:2747:U:O4	1:C1:2748:A:N6	2.43	0.51
1:C1:2766:A:N3	22:CU:323:ARG:NH1	2.58	0.51
4:CB:33:HIS:CD2	10:CI:323:MET:HE1	2.46	0.51
7:CF:162:GLU:HB3	7:CF:163:PRO:HD3	1.92	0.51
8:CG:162:ILE:HD11	12:CK:140:LYS:HA	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CM:50:ILE:HG13	14:CM:51:PHE:H	1.75	0.51
25:CY:639:PHE:HB3	25:CY:687:ILE:HG21	1.92	0.51
28:LB:295:ALA:HA	28:LB:360:ILE:HD12	1.93	0.51
45:Ld:47:PHE:HA	45:Ld:50:LYS:HE3	1.93	0.51
1:C1:490:C:H2'	1:C1:491:A:H8	1.76	0.51
1:C1:575:A:H2'	1:C1:576:C:C6	2.45	0.51
1:C1:683:C:OP2	29:LC:120:ARG:NH2	2.40	0.51
1:C1:890:G:H2'	1:C1:891:G:C8	2.46	0.51
1:C1:1242:A:H2'	1:C1:1243:G:C4	2.46	0.51
1:C1:1306:C:H5'	40:LS:2:GLY:HA2	1.92	0.51
5:CC:403:ARG:HH11	5:CC:403:ARG:HA	1.76	0.51
14:CM:171:ASP:N	14:CM:171:ASP:OD1	2.42	0.51
25:CY:548:PHE:HB3	25:CY:552:PHE:CE2	2.42	0.51
46:Le:64:THR:HA	46:Le:67:MET:SD	2.50	0.51
1:C1:745:U:N3	1:C1:749:C:N4	2.59	0.51
1:C1:2290:U:H2'	1:C1:2291:C:H6	1.75	0.51
1:C1:2778:A:H2'	1:C1:2779:C:O4'	2.11	0.51
1:C1:3162:A:HO2'	38:LP:182:ARG:HH22	1.57	0.51
3:CA:263:SER:O	3:CA:267:ILE:HD12	2.11	0.51
17:CP:270:ILE:HD11	17:CP:297:PHE:HD2	1.76	0.51
25:CY:628:GLU:O	25:CY:632:LEU:HB2	2.11	0.51
26:Cb:192:VAL:HG23	26:Cb:206:LEU:HD13	1.91	0.51
1:C1:461:A:OP1	23:CV:92:LYS:NZ	2.38	0.51
1:C1:711:G:H2'	1:C1:712:A:O4'	2.11	0.51
1:C1:1066:A:H2'	1:C1:1067:A:C8	2.45	0.51
2:C2:26:U:H2'	2:C2:27:U:C6	2.46	0.51
3:CA:196:ILE:HG23	3:CA:229:ILE:HG23	1.92	0.51
3:CA:233:GLU:OE1	3:CA:237:ARG:NH2	2.42	0.51
4:CB:259:ILE:HA	4:CB:262:VAL:HG22	1.93	0.51
7:CF:18:LYS:HB3	7:CF:22:ALA:HB2	1.92	0.51
9:CH:305:ILE:O	9:CH:309:THR:HG23	2.10	0.51
14:CM:74:ILE:HD12	14:CM:134:LYS:HZ2	1.74	0.51
17:CP:270:ILE:HD11	17:CP:297:PHE:CD2	2.45	0.51
21:CT:663:LEU:HD23	25:CY:638:ALA:HB3	1.93	0.51
25:CY:379:LEU:O	25:CY:383:VAL:HG23	2.10	0.51
25:CY:722:VAL:HG13	25:CY:726:ARG:HH21	1.76	0.51
26:Cb:11:SER:O	26:Cb:12:GLU:HG3	2.11	0.51
26:Cb:585:GLN:HA	26:Cb:588:ASP:HB2	1.92	0.51
26:Cb:813:PHE:CZ	26:Cb:825:LEU:HD11	2.46	0.51
40:LS:139:TYR:O	40:LS:142:GLN:HG2	2.11	0.51
1:C1:3021:U:H2'	1:C1:3022:G:C8	2.45	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3320:C:H5'	28:LB:317:GLU:OE1	2.10	0.50
2:C2:128:U:H5''	2:C2:129:C:H5	1.76	0.50
2:C2:161:A:H2'	2:C2:162:C:O4'	2.12	0.50
6:CE:331:GLY:O	6:CE:450:ARG:NH2	2.39	0.50
12:CK:260:LEU:HD22	22:CU:338:LYS:HB3	1.93	0.50
25:CY:432:ARG:HG2	25:CY:494:GLN:CG	2.41	0.50
25:CY:617:GLY:O	25:CY:621:GLN:HG2	2.10	0.50
25:CY:640:PRO:O	25:CY:644:LEU:HG	2.10	0.50
26:Cb:591:LEU:O	26:Cb:595:THR:HG23	2.10	0.50
33:LK:16:ARG:HH21	33:LK:57:ARG:HB3	1.76	0.50
33:LK:45:ASP:HA	33:LK:48:LYS:HG3	1.92	0.50
36:LN:64:VAL:CG1	36:LN:102:ALA:HB1	2.40	0.50
40:LS:66:GLU:HB2	40:LS:69:PRO:HG3	1.93	0.50
1:C1:709:G:H1	1:C1:729:U:H3	1.58	0.50
1:C1:2341:U:C2'	1:C1:2342:U:H5'	2.41	0.50
11:CJ:104:ALA:HA	11:CJ:107:GLU:HG2	1.93	0.50
15:CN:22:SER:HB3	15:CN:67:ARG:HG3	1.92	0.50
25:CY:432:ARG:HG2	25:CY:494:GLN:HG2	1.93	0.50
25:CY:457:GLN:O	25:CY:461:TYR:N	2.42	0.50
28:LB:136:LYS:O	28:LB:141:ASN:HB2	2.11	0.50
30:LE:154:VAL:O	30:LE:155:SER:C	2.54	0.50
38:LP:69:ARG:HD3	38:LP:79:SER:HB3	1.93	0.50
1:C1:910:A:O2'	50:Lj:49:TRP:O	2.27	0.50
1:C1:1134:G:C8	13:CL:18:THR:HG21	2.46	0.50
1:C1:2319:A:H2'	1:C1:2320:A:H8	1.76	0.50
1:C1:3190:G:H2'	1:C1:3191:C:C6	2.47	0.50
2:C2:31:G:O2'	19:CR:22:ARG:O	2.30	0.50
2:C2:286:C:H2'	2:C2:287:G:H8	1.76	0.50
5:CC:391:ARG:HG3	5:CC:392:LYS:HD3	1.94	0.50
6:CE:441:TYR:CE2	6:CE:460:LEU:HD12	2.47	0.50
11:CJ:148:LEU:HD11	11:CJ:234:TYR:C	2.36	0.50
29:LC:128:ALA:O	29:LC:132:VAL:HG23	2.11	0.50
30:LE:32:ASP:OD1	30:LE:32:ASP:N	2.44	0.50
46:Le:112:ARG:NH1	46:Le:115:GLN:OE1	2.44	0.50
1:C1:5:G:H2'	1:C1:6:A:H8	1.77	0.50
1:C1:63:A:H5''	36:LN:174:LEU:HD13	1.93	0.50
1:C1:188:U:H2'	1:C1:189:G:O4'	2.10	0.50
1:C1:403:U:H2'	1:C1:404:G:H8	1.75	0.50
1:C1:725:A:H5''	39:LQ:94:ARG:HH22	1.77	0.50
1:C1:2436:G:O2'	1:C1:2437:G:O5'	2.27	0.50
2:C2:128:U:OP1	2:C2:129:C:N4	2.44	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CF:49:ARG:NE	7:CF:124:PHE:HB2	2.26	0.50
8:CG:6:ASP:OD1	8:CG:6:ASP:N	2.43	0.50
18:CQ:83:ARG:O	18:CQ:87:GLN:HG2	2.12	0.50
25:CY:729:ARG:O	25:CY:733:LYS:HG2	2.10	0.50
26:Cb:195:VAL:HG12	26:Cb:217:THR:HG23	1.92	0.50
26:Cb:293:VAL:HG22	26:Cb:294:ARG:H	1.77	0.50
37:LO:8:VAL:HG23	37:LO:34:ILE:HD13	1.92	0.50
42:LV:68:LYS:NZ	42:LV:70:GLU:HB2	2.27	0.50
1:C1:159:G:P	19:CR:227:ARG:HH22	2.34	0.50
1:C1:231:A:H2'	1:C1:232:G:H8	1.75	0.50
1:C1:581:G:H1'	30:LE:37:LYS:HG3	1.92	0.50
1:C1:1072:G:H2'	1:C1:1073:G:C8	2.46	0.50
1:C1:1076:U:O2'	1:C1:1078:C:OP1	2.20	0.50
3:CA:108:PRO:HB3	6:CE:573:TYR:CZ	2.46	0.50
6:CE:146:LEU:HD21	6:CE:171:GLU:HG3	1.94	0.50
17:CP:316:HIS:NE2	17:CP:319:ASP:OD2	2.45	0.50
25:CY:424:TYR:O	25:CY:428:VAL:HG23	2.12	0.50
26:Cb:190:LYS:HB3	26:Cb:211:PRO:HA	1.93	0.50
26:Cb:451:VAL:HG21	26:Cb:484:PHE:HE2	1.76	0.50
26:Cb:495:GLU:HB3	26:Cb:498:PRO:HG3	1.93	0.50
32:LH:129:TYR:HB3	32:LH:218:ILE:CG1	2.42	0.50
38:LP:64:ALA:HB3	38:LP:80:ARG:HH21	1.76	0.50
38:LP:67:THR:HB	38:LP:80:ARG:HD2	1.93	0.50
41:LT:99:SER:OG	41:LT:100:ARG:N	2.44	0.50
1:C1:121:A:O2'	31:LG:108:LYS:NZ	2.41	0.50
1:C1:562:U:H2'	1:C1:563:A:C8	2.45	0.50
1:C1:886:U:HO2'	1:C1:887:G:P	2.32	0.50
1:C1:1429:G:N7	38:LP:25:SER:OG	2.42	0.50
7:CF:145:THR:OG1	7:CF:154:ASP:OD2	2.22	0.50
8:CG:95:ARG:HG2	8:CG:96:TYR:CD2	2.46	0.50
11:CJ:167:ARG:HH12	11:CJ:235:MET:HB3	1.75	0.50
14:CM:102:PRO:HB2	14:CM:105:PRO:HD2	1.93	0.50
26:Cb:97:LEU:HB3	26:Cb:101:LEU:HD23	1.92	0.50
42:LV:36:LEU:HD21	42:LV:104:ILE:HD11	1.94	0.50
1:C1:50:U:H2'	1:C1:51:A:H8	1.77	0.50
1:C1:252:C:OP1	6:CE:229:LYS:HG3	2.12	0.50
1:C1:2431:G:H2'	1:C1:2432:C:H6	1.76	0.50
1:C1:2970:U:H2'	1:C1:2971:U:C6	2.47	0.50
1:C1:3273:G:H1	1:C1:3309:G:H8	1.59	0.50
2:C2:57:C:H4'	2:C2:63:G:N7	2.27	0.50
2:C2:182:G:N1	4:CB:78:LEU:HD23	2.26	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:196:G:O6	2:C2:201:U:O4	2.30	0.50
12:CK:209:TYR:HB3	12:CK:214:VAL:HB	1.94	0.50
14:CM:154:ILE:HG21	14:CM:191:ILE:HG12	1.92	0.50
14:CM:187:ILE:O	14:CM:191:ILE:HG13	2.12	0.50
22:CU:248:LEU:HB3	22:CU:252:ARG:NH1	2.27	0.50
26:Cb:319:GLY:O	26:Cb:517:ASN:ND2	2.44	0.50
14:LF:13:LEU:HD12	14:LF:13:LEU:O	2.12	0.50
32:LH:99:ARG:HA	32:LH:102:VAL:HG22	1.94	0.50
1:C1:416:G:O2'	46:Le:24:ASP:OD2	2.23	0.50
1:C1:582:A:H5'	30:LE:35:GLN:O	2.12	0.50
1:C1:1196:U:H2'	1:C1:1197:A:C8	2.47	0.50
1:C1:2835:G:H1	1:C1:2907:U:H3	1.60	0.50
11:CJ:267:GLU:HG2	11:CJ:381:GLN:NE2	2.27	0.50
15:CN:161:VAL:HG22	15:CN:162:HIS:H	1.75	0.50
16:CO:3:LYS:HG3	16:CO:9:ARG:NH2	2.26	0.50
19:CR:198:LEU:HB3	19:CR:209:MET:HE3	1.92	0.50
24:CX:99:GLU:HG2	24:CX:135:ILE:HG22	1.94	0.50
26:Cb:869:ARG:HA	26:Cb:872:ARG:HG2	1.92	0.50
31:LG:89:LEU:HD21	31:LG:221:VAL:HG23	1.93	0.50
32:LH:127:MET:HE2	32:LH:218:ILE:HG22	1.94	0.50
39:LQ:107:THR:HA	39:LQ:127:GLU:HB3	1.94	0.50
42:LV:79:VAL:HG11	42:LV:131:ILE:HD11	1.93	0.50
1:C1:435:C:H2'	1:C1:436:G:C8	2.47	0.50
1:C1:2371:G:H2'	1:C1:2372:U:H6	1.77	0.50
1:C1:2480:C:H2'	1:C1:2481:A:C8	2.47	0.50
6:CE:126:ILE:HD11	6:CE:167:ILE:HD11	1.93	0.50
21:CT:303:VAL:HG23	21:CT:325:PHE:HE1	1.75	0.50
25:CY:738:GLU:HA	25:CY:741:ARG:HD2	1.93	0.50
26:Cb:493:ARG:NH1	26:Cb:581:ALA:HB2	2.24	0.50
28:LB:219:ILE:HB	28:LB:338:THR:HB	1.94	0.50
29:LC:170:TYR:CE2	29:LC:174:LYS:HD2	2.47	0.50
14:LF:92:VAL:HG13	14:LF:142:TYR:HB3	1.94	0.50
36:LN:9:GLU:HG3	49:Li:49:VAL:HG12	1.94	0.50
38:LP:118:GLN:NE2	38:LP:147:GLU:OE2	2.45	0.50
40:LS:8:GLN:HB3	40:LS:64:ILE:HD11	1.94	0.50
1:C1:86:G:O2'	1:C1:98:G:O6	2.28	0.49
1:C1:2856:G:N7	12:CK:7:ILE:HG12	2.27	0.49
1:C1:3309:G:H4'	1:C1:3310:A:C8	2.44	0.49
7:CF:62:ASP:OD1	7:CF:107:ARG:NH2	2.45	0.49
7:CF:164:GLU:HA	7:CF:167:ARG:HG2	1.94	0.49
8:CG:115:VAL:O	8:CG:119:VAL:HG23	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CK:175:MET:HA	12:CK:178:ARG:HD2	1.94	0.49
12:CK:221:ILE:HD13	12:CK:245:ILE:HD11	1.94	0.49
12:CK:236:LYS:NZ	17:CP:474:ASN:HA	2.27	0.49
13:CL:56:PRO:HD3	40:LS:78:TRP:NE1	2.27	0.49
25:CY:675:VAL:HA	25:CY:678:GLN:OE1	2.12	0.49
27:Cz:68:MET:O	27:Cz:71:GLU:HG3	2.12	0.49
35:LM:124:LYS:HG2	37:LO:199:LEU:HD11	1.93	0.49
1:C1:74:G:O2'	34:LL:59:ARG:O	2.31	0.49
1:C1:119:U:OP1	5:CC:280:ARG:NE	2.37	0.49
1:C1:2548:A:H2'	1:C1:2549:A:C8	2.47	0.49
1:C1:2856:G:C5	9:CH:158:ARG:HD3	2.47	0.49
2:C2:202:C:H2'	2:C2:203:G:C8	2.46	0.49
6:CE:179:LYS:N	6:CE:182:ASN:OD1	2.43	0.49
7:CF:88:GLY:CA	7:CF:91:ARG:HH11	2.18	0.49
13:CL:18:THR:HG22	13:CL:21:ARG:HH12	1.77	0.49
13:CL:262:ARG:HA	13:CL:265:PHE:O	2.11	0.49
15:CN:197:MET:HE1	15:CN:218:ILE:HD13	1.93	0.49
17:CP:277:ASN:OD1	17:CP:278:GLU:N	2.45	0.49
21:CT:225:ALA:HB1	21:CT:243:PHE:HE1	1.75	0.49
21:CT:244:THR:OG1	21:CT:281:LYS:NZ	2.41	0.49
25:CY:379:LEU:O	25:CY:382:THR:OG1	2.27	0.49
25:CY:496:VAL:HG13	25:CY:554:LEU:HD11	1.94	0.49
25:CY:498:SER:HB2	25:CY:502:TRP:HZ3	1.76	0.49
25:CY:733:LYS:HD3	25:CY:736:MET:HE2	1.94	0.49
26:Cb:148:MET:O	26:Cb:152:LEU:HG	2.12	0.49
41:LT:34:TYR:HE1	41:LT:98:PRO:HD3	1.77	0.49
51:Lq:89:ASP:O	51:Lq:92:LYS:HG3	2.12	0.49
1:C1:529:G:C6	1:C1:543:G:C2	2.99	0.49
1:C1:1337:A:OP2	23:CV:14:ARG:NH2	2.45	0.49
4:CB:83:ILE:HD11	4:CB:270:PHE:HE2	1.77	0.49
9:CH:60:PHE:O	9:CH:64:ILE:HG12	2.12	0.49
9:CH:210:TYR:HB3	9:CH:215:TYR:CE1	2.47	0.49
14:CM:108:ILE:HG21	14:CM:132:MET:HB2	1.94	0.49
15:CN:233:ILE:HD12	15:CN:237:MET:HE1	1.94	0.49
17:CP:582:LYS:NZ	17:CP:583:LYS:O	2.41	0.49
26:Cb:833:LYS:HZ3	26:Cb:835:ASN:HB2	1.76	0.49
28:LB:307:THR:HG21	28:LB:317:GLU:HG3	1.94	0.49
30:LE:100:ARG:HH21	47:Lf:106:PRO:HB2	1.76	0.49
32:LH:86:LYS:HB2	32:LH:89:VAL:CG1	2.41	0.49
39:LQ:64:LEU:O	39:LQ:68:THR:OG1	2.20	0.49
42:LV:19:LEU:HD21	42:LV:100:ASN:HB3	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Lq:98:LYS:HA	51:Lq:101:LYS:HE2	1.93	0.49
1:C1:261:G:OP2	36:LN:44:ARG:NH1	2.39	0.49
1:C1:1205:A:N6	1:C1:1267:G:H21	2.10	0.49
1:C1:2360:A:H2'	1:C1:2901:G:H1	1.77	0.49
1:C1:2796:A:H2'	1:C1:2797:G:O4'	2.12	0.49
1:C1:2816:U:OP2	1:C1:2817:U:O2'	2.21	0.49
6:CE:580:GLY:O	6:CE:583:TYR:OH	2.22	0.49
11:CJ:231:VAL:HG12	11:CJ:235:MET:HE2	1.94	0.49
12:CK:128:SER:OG	12:CK:131:GLU:OE2	2.18	0.49
20:CS:494:ARG:NH2	20:CS:497:GLN:OE1	2.45	0.49
26:Cb:322:LEU:CB	26:Cb:517:ASN:HD21	2.21	0.49
30:LE:99:ALA:HA	30:LE:102:VAL:HG22	1.94	0.49
49:Li:35:PRO:HA	49:Li:38:ARG:HB2	1.94	0.49
51:Lq:38:LEU:HD23	51:Lq:39:LYS:N	2.27	0.49
1:C1:95:A:C5	1:C1:96:G:H1'	2.48	0.49
1:C1:909:C:H2'	1:C1:910:A:H8	1.77	0.49
1:C1:2329:A:H2'	1:C1:2330:A:C8	2.48	0.49
1:C1:2815:C:O2'	12:CK:183:ASN:OD1	2.20	0.49
1:C1:2841:U:H2'	1:C1:2842:C:C6	2.48	0.49
2:C2:58:G:N7	50:Lj:63:ARG:NH2	2.60	0.49
2:C2:213:A:C4	4:CB:140:TYR:HE1	2.30	0.49
6:CE:124:LYS:HG2	6:CE:209:TYR:CE2	2.47	0.49
9:CH:55:THR:O	9:CH:59:LYS:HG2	2.11	0.49
12:CK:174:PRO:HG2	12:CK:177:LEU:HD12	1.93	0.49
17:CP:286:ASN:O	17:CP:286:ASN:ND2	2.42	0.49
17:CP:365:GLN:HG2	17:CP:366:ALA:H	1.77	0.49
26:Cb:203:GLN:OE1	26:Cb:220:ARG:NE	2.45	0.49
26:Cb:232:LEU:HB3	26:Cb:235:ILE:HD12	1.93	0.49
46:Le:44:ARG:HA	46:Le:53:MET:HE3	1.93	0.49
1:C1:194:G:OP1	1:C1:213:G:O2'	2.29	0.49
5:CC:292:MET:HA	5:CC:292:MET:HE3	1.94	0.49
9:CH:468:LEU:HB3	9:CH:474:TYR:CE2	2.48	0.49
19:CR:172:LEU:HD22	34:LL:126:PHE:HZ	1.77	0.49
21:CT:516:LEU:O	21:CT:520:LEU:HG	2.11	0.49
21:CT:674:GLU:HA	21:CT:677:LYS:HG2	1.93	0.49
28:LB:285:ARG:NH1	28:LB:294:ASN:O	2.45	0.49
31:LG:75:PRO:HB3	36:LN:17:ASP:OD2	2.13	0.49
41:LT:104:ASP:HA	41:LT:107:ARG:HG2	1.94	0.49
1:C1:114:A:H2'	1:C1:115:A:O4'	2.12	0.49
1:C1:174:C:N3	1:C1:230:A:N1	2.60	0.49
2:C2:154:C:H2'	2:C2:155:A:H8	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CE:377:LEU:HD12	6:CE:382:LEU:HB3	1.94	0.49
17:CP:331:LEU:CD2	17:CP:344:VAL:HG22	2.43	0.49
17:CP:488:LYS:NZ	17:CP:526:TYR:HB2	2.28	0.49
19:CR:54:LEU:HD22	48:Lh:122:ALA:HB1	1.94	0.49
20:CS:650:PRO:HG2	31:LG:261:LYS:HZ2	1.77	0.49
35:LM:94:TRP:CE2	35:LM:100:ALA:HB2	2.48	0.49
36:LN:46:ASP:OD1	36:LN:47:LYS:N	2.46	0.49
1:C1:2361:A:N6	1:C1:2900:C:C5	2.80	0.49
4:CB:65:THR:OG1	4:CB:240:ASN:OD1	2.31	0.49
4:CB:76:HIS:N	4:CB:237:PRO:HG3	2.27	0.49
8:CG:94:ALA:HB3	8:CG:97:LYS:HE3	1.95	0.49
9:CH:486:GLU:OE2	18:CQ:116:ARG:NH2	2.44	0.49
26:Cb:245:ARG:NH1	26:Cb:428:ARG:HE	2.11	0.49
26:Cb:575:ILE:O	26:Cb:576:PHE:C	2.55	0.49
29:LC:169:ALA:HB1	29:LC:226:PHE:CE1	2.48	0.49
51:Lq:144:LEU:HA	51:Lq:147:LYS:HE2	1.95	0.49
1:C1:1134:G:N7	13:CL:18:THR:HG21	2.28	0.49
1:C1:1375:A:N6	1:C1:1399:G:H1'	2.28	0.49
1:C1:2302:U:C2	1:C1:2303:A:C8	3.00	0.49
1:C1:2922:G:C5	1:C1:2926:G:N1	2.81	0.49
5:CC:403:ARG:NH2	11:CJ:147:MET:HE3	2.28	0.49
17:CP:368:SER:OG	17:CP:573:VAL:HG12	2.12	0.49
17:CP:398:MET:O	17:CP:402:MET:HG3	2.12	0.49
23:CV:63:VAL:HG21	23:CV:94:ILE:HG12	1.95	0.49
36:LN:148:ILE:O	36:LN:151:ILE:HG22	2.13	0.49
42:LV:55:GLY:C	42:LV:80:ILE:HD11	2.38	0.49
47:Lf:14:ARG:HA	47:Lf:98:ALA:O	2.13	0.49
1:C1:353:A:O3'	50:Lj:45:ARG:NH2	2.46	0.49
1:C1:628:C:H2'	1:C1:629:U:C6	2.48	0.49
1:C1:947:U:C2	1:C1:948:A:C8	3.01	0.49
1:C1:1394:G:OP1	46:Le:106:ARG:NH2	2.46	0.49
1:C1:2399:G:H1	1:C1:2472:U:H3	1.60	0.49
1:C1:2829:G:H2'	1:C1:2830:A:C8	2.47	0.49
3:CA:253:PRO:HG2	5:CC:142:ASP:HB3	1.94	0.49
16:CO:33:LEU:HD11	28:LB:211:GLU:HB3	1.94	0.49
21:CT:134:ILE:HG23	21:CT:148:HIS:HB3	1.94	0.49
21:CT:632:THR:HG22	21:CT:657:THR:HG21	1.94	0.49
25:CY:374:LYS:HA	25:CY:377:LYS:HG2	1.95	0.49
35:LM:27:LEU:HD12	35:LM:50:LEU:HD23	1.95	0.49
35:LM:120:VAL:O	35:LM:124:LYS:HG3	2.12	0.49
51:Lq:38:LEU:HD11	51:Lq:200:ASN:ND2	2.28	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:296:G:OP1	3:CA:96:LYS:NZ	2.40	0.48
1:C1:1291:U:OP2	13:CL:14:LYS:N	2.43	0.48
1:C1:3042:G:OP2	18:CQ:38:LYS:NZ	2.42	0.48
9:CH:264:LYS:NZ	9:CH:268:ASN:HB2	2.28	0.48
10:CI:203:LEU:HD22	10:CI:233:ILE:HD11	1.95	0.48
11:CJ:25:LYS:HE3	11:CJ:73:LEU:HD11	1.95	0.48
12:CK:125:ARG:HH22	12:CK:180:LYS:HE2	1.77	0.48
16:CO:30:LEU:HD11	28:LB:42:HIS:CG	2.48	0.48
26:Cb:207:MET:HE2	26:Cb:230:LEU:HD22	1.95	0.48
28:LB:76:VAL:HG12	28:LB:326:LYS:HA	1.94	0.48
30:LE:72:LEU:HA	30:LE:83:VAL:HG12	1.94	0.48
38:LP:84:PRO:HB2	38:LP:87:SER:OG	2.12	0.48
48:Lh:43:GLY:O	48:Lh:46:LEU:N	2.47	0.48
1:C1:8:C:H2'	1:C1:9:U:C6	2.49	0.48
1:C1:2980:U:H2'	1:C1:2981:A:H8	1.78	0.48
1:C1:3118:A:H2'	1:C1:3119:C:O4'	2.13	0.48
1:C1:3273:G:N2	1:C1:3309:G:H1'	2.09	0.48
3:CA:146:PHE:HA	3:CA:152:LEU:HB3	1.95	0.48
9:CH:246:ARG:NH2	9:CH:280:LYS:HA	2.28	0.48
12:CK:42:LEU:HD13	12:CK:46:ARG:HG2	1.95	0.48
18:CQ:37:HIS:NE2	42:LV:96:TYR:OH	2.22	0.48
21:CT:315:TYR:OH	21:CT:410:ARG:NE	2.46	0.48
33:LK:106:LEU:O	33:LK:110:ILE:HG12	2.13	0.48
35:LM:20:LEU:HD13	35:LM:62:ALA:HB1	1.93	0.48
39:LQ:95:ILE:HG22	39:LQ:167:LEU:HD22	1.94	0.48
1:C1:551:C:H2'	1:C1:552:C:C6	2.48	0.48
1:C1:780:G:H2'	1:C1:782:A:H62	1.78	0.48
1:C1:2351:C:H2'	1:C1:2352:A:C8	2.48	0.48
2:C2:26:U:O2'	29:LC:52:ALA:O	2.31	0.48
2:C2:76:C:H2'	2:C2:77:A:H8	1.77	0.48
5:CC:306:TYR:HB2	31:LG:113:LEU:HG	1.95	0.48
26:Cb:396:VAL:HB	26:Cb:422:VAL:HG12	1.95	0.48
29:LC:146:VAL:HG21	29:LC:151:LEU:HD22	1.94	0.48
1:C1:174:C:N4	1:C1:230:A:N6	2.61	0.48
1:C1:725:A:H1'	39:LQ:168:ARG:HD2	1.96	0.48
1:C1:1157:C:N3	37:LO:22:SER:HA	2.27	0.48
1:C1:1899:U:H2'	1:C1:1900:A:C8	2.49	0.48
1:C1:2319:A:H2'	1:C1:2320:A:C8	2.48	0.48
1:C1:3131:A:O2'	1:C1:3132:U:OP1	2.29	0.48
4:CB:98:CYS:HB3	4:CB:153:PHE:HD1	1.79	0.48
6:CE:516:ARG:HG2	6:CE:553:VAL:HG12	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CN:186:VAL:HG22	15:CN:218:ILE:HD11	1.94	0.48
15:CN:210:THR:HG23	15:CN:214:GLU:HG3	1.96	0.48
21:CT:607:SER:O	21:CT:611:ILE:HD12	2.13	0.48
25:CY:374:LYS:HB3	25:CY:378:MET:HE1	1.95	0.48
31:LG:204:THR:HG22	31:LG:205:GLU:HG3	1.95	0.48
1:C1:36:C:O2'	1:C1:915:G:N3	2.44	0.48
1:C1:258:C:N4	49:Li:39:LYS:HA	2.28	0.48
1:C1:1046:A:C6	1:C1:1074:C:N3	2.80	0.48
1:C1:1090:C:H2'	1:C1:1091:A:H8	1.78	0.48
1:C1:1218:G:N2	1:C1:1226:A:OP1	2.46	0.48
5:CC:373:MET:HE3	5:CC:378:ARG:NE	2.28	0.48
26:Cb:131:VAL:HG13	26:Cb:270:LEU:HD22	1.95	0.48
46:Le:80:VAL:HA	46:Le:83:VAL:HG22	1.96	0.48
1:C1:36:C:H4'	1:C1:789:A:C2	2.37	0.48
1:C1:117:U:O2'	1:C1:119:U:OP2	2.23	0.48
1:C1:221:U:OP1	44:LY:4:ARG:NH2	2.47	0.48
1:C1:3005:A:H4'	28:LB:53:MET:CE	2.43	0.48
1:C1:3221:C:H2'	1:C1:3222:A:H8	1.79	0.48
3:CA:182:PHE:HD1	3:CA:191:VAL:HG12	1.78	0.48
9:CH:166:THR:O	9:CH:168:THR:HG23	2.14	0.48
17:CP:337:TRP:HB2	17:CP:542:PRO:HG2	1.95	0.48
17:CP:447:ILE:HD13	17:CP:450:PHE:HZ	1.78	0.48
29:LC:290:LEU:HD23	39:LQ:156:LEU:HD21	1.95	0.48
14:LF:46:LYS:HA	14:LF:49:VAL:HG12	1.95	0.48
44:LY:16:LYS:O	44:LY:20:SER:OG	2.19	0.48
51:Lq:24:LYS:HD2	51:Lq:25:LYS:N	2.28	0.48
1:C1:128:G:OP1	48:Lh:80:TYR:OH	2.22	0.48
1:C1:286:A:OP2	36:LN:15:GLN:NE2	2.47	0.48
1:C1:624:C:C2	1:C1:625:C:C5	3.02	0.48
1:C1:1196:U:H2'	1:C1:1197:A:H8	1.78	0.48
1:C1:2867:U:H2'	1:C1:2868:A:O4'	2.14	0.48
1:C1:2963:A:H2'	1:C1:2964:U:O4'	2.14	0.48
3:CA:74:LEU:HB3	3:CA:250:PHE:HB3	1.95	0.48
12:CK:241:ARG:NH2	22:CU:350:GLY:O	2.42	0.48
12:CK:260:LEU:HD13	22:CU:337:LEU:HD22	1.95	0.48
14:CM:203:GLN:CD	14:CM:203:GLN:H	2.22	0.48
17:CP:363:ILE:HG13	17:CP:427:ARG:HH22	1.77	0.48
23:CV:5:SER:O	23:CV:9:ILE:HD12	2.14	0.48
24:CX:97:ASP:O	24:CX:100:SER:OG	2.27	0.48
26:Cb:238:VAL:HG21	26:Cb:266:ARG:HD2	1.95	0.48
30:LE:72:LEU:HD13	30:LE:81:LEU:HB3	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LF:242:ASN:O	14:LF:246:ARG:HG2	2.13	0.48
1:C1:177:U:H2'	1:C1:178:C:C6	2.48	0.48
1:C1:322:G:C2	1:C1:323:G:C8	3.01	0.48
8:CG:2:ARG:HG3	8:CG:2:ARG:HH11	1.78	0.48
8:CG:121:ARG:NH2	8:CG:137:MET:HA	2.25	0.48
17:CP:324:LEU:HD12	17:CP:331:LEU:HD11	1.95	0.48
17:CP:457:ALA:HB3	17:CP:512:THR:HG22	1.96	0.48
26:Cb:101:LEU:HD21	26:Cb:146:ILE:HG23	1.96	0.48
28:LB:26:ARG:NH1	28:LB:179:LEU:O	2.47	0.48
38:LP:122:ALA:HB3	38:LP:143:PRO:HG2	1.96	0.48
47:Lf:15:HIS:O	47:Lf:97:GLY:N	2.47	0.48
49:Li:99:LEU:HD23	49:Li:102:ILE:HD12	1.95	0.48
1:C1:452:G:H2'	1:C1:453:G:H8	1.77	0.48
1:C1:1191:G:OP1	12:CK:36:SER:OG	2.31	0.48
1:C1:1430:U:H5''	38:LP:66:SER:HB2	1.96	0.48
1:C1:2373:U:H2'	1:C1:2374:G:C8	2.49	0.48
1:C1:2374:G:H2'	1:C1:2375:A:H8	1.79	0.48
1:C1:2761:A:H2'	1:C1:2762:A:H8	1.78	0.48
1:C1:3245:A:H2'	1:C1:3246:G:C8	2.49	0.48
4:CB:113:ALA:O	4:CB:121:ARG:NH1	2.44	0.48
4:CB:115:GLU:O	4:CB:115:GLU:HG2	2.12	0.48
5:CC:338:MET:HG3	11:CJ:65:TYR:CZ	2.49	0.48
6:CE:162:THR:HA	6:CE:165:PHE:CE2	2.49	0.48
11:CJ:227:MET:HA	11:CJ:230:PHE:HB2	1.95	0.48
14:CM:153:LEU:HD22	14:CM:249:ASN:HD22	1.78	0.48
20:CS:666:LEU:HD21	20:CS:676:LEU:HD11	1.95	0.48
21:CT:585:PRO:HG2	21:CT:588:ARG:NH2	2.29	0.48
22:CU:212:THR:HG22	22:CU:217:HIS:HD2	1.79	0.48
22:CU:317:VAL:O	22:CU:321:LEU:HD13	2.14	0.48
29:LC:39:VAL:HA	29:LC:114:ILE:HD13	1.94	0.48
1:C1:423:U:H2'	1:C1:424:G:C8	2.48	0.48
4:CB:116:PHE:CZ	4:CB:120:LEU:HD22	2.48	0.48
5:CC:311:GLU:HA	5:CC:314:ARG:HG2	1.96	0.48
7:CF:164:GLU:HG3	7:CF:167:ARG:NH2	2.29	0.48
17:CP:247:GLU:OE1	17:CP:291:ARG:NH1	2.43	0.48
21:CT:288:LYS:HA	21:CT:291:GLN:HG2	1.96	0.48
21:CT:608:SER:O	21:CT:612:LEU:HD23	2.14	0.48
21:CT:645:SER:OG	21:CT:651:SER:HB3	2.14	0.48
29:LC:326:MET:HE3	29:LC:330:ASN:HB3	1.96	0.48
33:LK:77:ALA:O	33:LK:81:ILE:HG12	2.14	0.48
1:C1:788:A:H62	1:C1:915:G:H1	1.60	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:975:G:H4'	1:C1:976:U:H5'	1.95	0.47
1:C1:1259:C:H2'	1:C1:1260:A:H8	1.79	0.47
1:C1:3162:A:H4'	1:C1:3163:G:O5'	2.13	0.47
1:C1:3223:C:H2'	1:C1:3224:G:C8	2.48	0.47
3:CA:58:MET:SD	3:CA:193:ASN:ND2	2.87	0.47
4:CB:22:GLN:OE1	10:CI:325:TYR:OH	2.24	0.47
4:CB:265:GLU:O	4:CB:269:ARG:HG2	2.13	0.47
6:CE:438:PRO:O	6:CE:442:ILE:HD12	2.14	0.47
7:CF:170:MET:HE1	7:CF:212:PHE:HZ	1.78	0.47
11:CJ:75:GLU:HG3	11:CJ:77:LEU:H	1.79	0.47
11:CJ:123:LEU:O	11:CJ:127:ILE:HG12	2.13	0.47
14:CM:126:THR:H	14:CM:129:THR:HB	1.79	0.47
18:CQ:44:ARG:HH11	18:CQ:44:ARG:HG3	1.78	0.47
20:CS:814:MET:HB2	29:LC:69:GLY:HA3	1.95	0.47
21:CT:597:MET:HB3	21:CT:660:GLU:HG2	1.94	0.47
32:LH:204:CYS:SG	32:LH:218:ILE:HD12	2.54	0.47
40:LS:10:ILE:HG13	40:LS:26:ARG:HB2	1.96	0.47
40:LS:71:LYS:NZ	40:LS:73:LYS:HG2	2.28	0.47
45:Ld:59:LEU:HB3	45:Ld:63:LEU:HD23	1.96	0.47
1:C1:451:C:H2'	1:C1:452:G:C8	2.50	0.47
1:C1:481:U:H2'	1:C1:482:C:C6	2.49	0.47
1:C1:1275:U:H2'	1:C1:1276:A:H8	1.78	0.47
1:C1:3026:G:C2	1:C1:3027:A:C8	3.02	0.47
3:CA:170:LYS:HB3	5:CC:167:VAL:HG21	1.95	0.47
4:CB:109:LYS:HA	4:CB:112:VAL:HG12	1.96	0.47
9:CH:69:VAL:HG12	9:CH:71:SER:H	1.79	0.47
9:CH:450:ILE:HD11	18:CQ:85:LEU:CD2	2.44	0.47
12:CK:147:TRP:CD1	12:CK:170:ARG:HH21	2.32	0.47
16:CO:92:GLY:H	28:LB:147:ARG:HD2	1.79	0.47
18:CQ:82:ASN:HB3	18:CQ:85:LEU:CB	2.44	0.47
22:CU:341:ARG:NH2	22:CU:353:GLU:OE1	2.47	0.47
25:CY:675:VAL:HG13	25:CY:679:LYS:NZ	2.29	0.47
26:Cb:480:ASP:OD1	26:Cb:556:SER:OG	2.31	0.47
28:LB:123:TYR:CZ	28:LB:124:LYS:HD2	2.47	0.47
30:LE:73:LEU:HD21	30:LE:169:LEU:HD11	1.96	0.47
40:LS:48:LEU:HD11	41:LT:152:ALA:O	2.14	0.47
41:LT:82:HIS:O	41:LT:83:ARG:NE	2.42	0.47
51:Lq:39:LYS:HD2	51:Lq:40:ASN:N	2.29	0.47
51:Lq:87:ALA:O	51:Lq:91:LYS:HG2	2.14	0.47
1:C1:3305:U:H2'	1:C1:3306:G:H8	1.79	0.47
8:CG:119:VAL:HG11	8:CG:122:TRP:CE2	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CH:330:VAL:O	9:CH:334:VAL:HG12	2.14	0.47
9:CH:360:ARG:HD2	26:Cb:520:TRP:HE1	1.79	0.47
10:CI:242:ASP:HB3	10:CI:246:ARG:NH1	2.29	0.47
15:CN:4:ARG:HG2	15:CN:207:GLY:O	2.13	0.47
16:CO:83:SER:O	16:CO:87:SER:HB3	2.14	0.47
17:CP:341:GLY:O	17:CP:342:LEU:HD23	2.15	0.47
17:CP:488:LYS:HZ1	17:CP:526:TYR:CB	2.27	0.47
17:CP:491:LEU:HD13	17:CP:510:TYR:CD2	2.49	0.47
18:CQ:82:ASN:HB3	18:CQ:85:LEU:HB3	1.95	0.47
18:CQ:86:TRP:HA	18:CQ:89:THR:HB	1.96	0.47
21:CT:294:GLU:HG2	21:CT:329:ARG:NH2	2.30	0.47
22:CU:319:LYS:O	22:CU:323:ARG:HG3	2.13	0.47
25:CY:450:ALA:HA	25:CY:505:VAL:HG22	1.95	0.47
25:CY:658:ARG:NH2	25:CY:667:ALA:HA	2.28	0.47
28:LB:211:GLU:HG3	28:LB:212:LYS:O	2.14	0.47
14:LF:149:SER:OG	14:LF:246:ARG:NH2	2.47	0.47
37:LO:55:TYR:CE1	37:LO:147:VAL:HG21	2.49	0.47
51:Lq:24:LYS:HD2	51:Lq:26:ARG:H	1.80	0.47
1:C1:332:C:H2'	1:C1:333:G:O4'	2.14	0.47
1:C1:734:C:H2'	1:C1:735:G:H8	1.79	0.47
4:CB:156:ASP:O	4:CB:160:ILE:HG12	2.14	0.47
6:CE:172:MET:CE	6:CE:259:LYS:HB2	2.44	0.47
9:CH:365:MET:HA	9:CH:368:ILE:HG22	1.96	0.47
10:CI:302:TRP:O	10:CI:306:VAL:HG13	2.15	0.47
17:CP:309:ARG:HH22	17:CP:396:THR:HB	1.80	0.47
17:CP:544:GLY:HA2	17:CP:571:TYR:CE2	2.48	0.47
21:CT:494:GLU:OE1	21:CT:578:PRO:HD2	2.14	0.47
25:CY:688:GLU:O	25:CY:691:ARG:HG2	2.14	0.47
26:Cb:239:VAL:HG22	26:Cb:269:LEU:HB2	1.95	0.47
28:LB:340:ARG:HH12	28:LB:343:LEU:HG	1.79	0.47
34:LL:92:THR:HG23	48:Lh:118:GLN:HA	1.95	0.47
42:LV:22:GLY:HA2	42:LV:38:ILE:O	2.13	0.47
45:Ld:66:LYS:HA	45:Ld:69:GLU:HG3	1.97	0.47
51:Lq:38:LEU:HD22	51:Lq:41:TYR:HB2	1.97	0.47
1:C1:133:G:O2'	1:C1:134:G:O4'	2.31	0.47
1:C1:409:A:H2'	1:C1:410:A:C8	2.49	0.47
1:C1:542:U:H3'	1:C1:543:G:H8	1.80	0.47
1:C1:926:C:H2'	1:C1:927:C:C6	2.49	0.47
1:C1:3041:C:O2'	1:C1:3272:U:H5''	2.15	0.47
11:CJ:398:ASP:OD1	11:CJ:399:ALA:N	2.48	0.47
14:CM:193:GLU:O	14:CM:197:VAL:HA	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CQ:80:ARG:HG2	18:CQ:80:ARG:HH11	1.78	0.47
20:CS:472:LEU:HD12	31:LG:67:ILE:HG13	1.97	0.47
29:LC:215:PRO:HB3	29:LC:220:LYS:NZ	2.29	0.47
1:C1:74:G:OP1	34:LL:105:SER:HB3	2.14	0.47
1:C1:267:U:H2'	1:C1:268:A:C8	2.49	0.47
1:C1:529:G:O6	1:C1:543:G:N2	2.48	0.47
1:C1:684:G:H2'	1:C1:685:C:C6	2.50	0.47
1:C1:1183:C:H2'	1:C1:1184:A:N7	2.30	0.47
1:C1:2568:G:H2'	1:C1:2569:U:C6	2.50	0.47
1:C1:2772:G:H2'	1:C1:2773:G:H8	1.80	0.47
1:C1:2922:G:O6	1:C1:2926:G:O6	2.31	0.47
6:CE:184:THR:OG1	6:CE:254:VAL:O	2.22	0.47
6:CE:367:CYS:HA	6:CE:370:VAL:HG12	1.96	0.47
8:CG:14:ASP:O	24:CX:112:LYS:NZ	2.45	0.47
9:CH:21:LEU:HA	9:CH:24:THR:HG22	1.96	0.47
9:CH:450:ILE:HD11	18:CQ:85:LEU:HD23	1.95	0.47
10:CI:317:ALA:O	10:CI:321:LYS:HG2	2.15	0.47
11:CJ:35:LYS:HZ3	11:CJ:35:LYS:HB2	1.80	0.47
17:CP:288:PHE:HE1	17:CP:569:HIS:CE1	2.31	0.47
25:CY:706:ALA:HA	25:CY:709:LYS:HD3	1.95	0.47
40:LS:161:THR:HG23	40:LS:162:LYS:HE3	1.96	0.47
48:Lh:12:LEU:HA	48:Lh:15:LYS:HZ3	1.78	0.47
48:Lh:34:LEU:O	48:Lh:38:LYS:HB2	2.15	0.47
51:Lq:76:ARG:HB2	51:Lq:144:LEU:HD21	1.96	0.47
1:C1:179:U:H1'	44:LY:128:VAL:HG21	1.96	0.47
1:C1:208:G:H5''	44:LY:11:ARG:HG3	1.95	0.47
1:C1:422:G:H2'	1:C1:423:U:H6	1.80	0.47
1:C1:707:A:H5''	1:C1:708:G:H5'	1.95	0.47
1:C1:897:G:H2'	1:C1:898:A:C8	2.49	0.47
1:C1:935:U:OP1	1:C1:1098:G:N2	2.46	0.47
1:C1:2073:G:H5'	26:Cb:107:ARG:HD3	1.97	0.47
1:C1:2298:U:H2'	1:C1:2299:C:C6	2.50	0.47
1:C1:2457:C:C2	1:C1:2458:U:C5	3.02	0.47
1:C1:2548:A:H2'	1:C1:2549:A:H8	1.80	0.47
1:C1:3069:G:O6	1:C1:3077:C:H5''	2.15	0.47
1:C1:3250:A:OP1	38:LP:74:LYS:HD2	2.14	0.47
6:CE:428:TRP:CE2	6:CE:457:ARG:HD3	2.50	0.47
9:CH:270:PHE:HA	9:CH:273:ILE:HG22	1.96	0.47
15:CN:36:SER:HA	15:CN:39:GLU:HG2	1.95	0.47
15:CN:101:LEU:HD13	42:LV:137:VAL:HG23	1.95	0.47
15:CN:197:MET:HE1	15:CN:218:ILE:HG21	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CP:357:TYR:HB2	17:CP:362:TYR:CZ	2.50	0.47
21:CT:303:VAL:HG23	21:CT:325:PHE:CE1	2.50	0.47
21:CT:321:VAL:HA	21:CT:324:LEU:HG	1.95	0.47
21:CT:571:LEU:HB3	21:CT:614:LEU:HD21	1.97	0.47
21:CT:588:ARG:HA	21:CT:648:VAL:HG11	1.97	0.47
26:Cb:15:VAL:HG22	26:Cb:274:THR:HB	1.96	0.47
26:Cb:263:PRO:O	26:Cb:266:ARG:NH1	2.41	0.47
26:Cb:444:PRO:HD3	26:Cb:453:ARG:NH2	2.30	0.47
29:LC:280:ASN:ND2	29:LC:282:VAL:H	2.12	0.47
29:LC:328:ARG:O	14:LF:47:ARG:NH1	2.34	0.47
32:LH:55:VAL:HG23	32:LH:64:VAL:HG12	1.97	0.47
34:LL:46:LEU:HD22	34:LL:49:ARG:HD2	1.96	0.47
35:LM:11:TRP:CZ2	40:LS:153:PRO:HB3	2.50	0.47
39:LQ:55:LYS:HA	39:LQ:58:VAL:HG22	1.96	0.47
51:Lq:180:VAL:O	51:Lq:184:MET:HG3	2.15	0.47
1:C1:978:A:H2'	1:C1:979:A:H8	1.79	0.47
1:C1:1883:C:H42	26:Cb:217:THR:HB	1.79	0.47
1:C1:2990:A:H2'	1:C1:2991:C:H6	1.79	0.47
2:C2:203:G:H5'	10:CI:223:LYS:NZ	2.29	0.47
3:CA:147:GLU:HG2	22:CU:221:VAL:HG11	1.96	0.47
5:CC:235:GLU:O	5:CC:239:ILE:HG12	2.14	0.47
11:CJ:166:ALA:HB1	11:CJ:170:ARG:NH2	2.30	0.47
12:CK:236:LYS:CE	17:CP:474:ASN:HA	2.45	0.47
21:CT:279:PHE:HA	21:CT:282:CYS:SG	2.54	0.47
23:CV:54:ILE:HG22	23:CV:118:ILE:HD12	1.97	0.47
32:LH:10:ILE:HB	32:LH:90:ILE:HG12	1.95	0.47
40:LS:77:ILE:HG23	40:LS:126:VAL:HG22	1.97	0.47
46:Le:86:LEU:HD11	46:Le:93:TYR:CB	2.45	0.47
1:C1:174:C:H42	1:C1:230:A:N6	2.13	0.47
1:C1:1430:U:H2'	1:C1:1431:A:H8	1.80	0.47
1:C1:1883:C:H41	26:Cb:251:PHE:HZ	1.63	0.47
1:C1:2776:U:H2'	1:C1:2777:A:C8	2.50	0.47
1:C1:3105:C:H2'	1:C1:3106:G:C8	2.49	0.47
1:C1:3162:A:H5''	1:C1:3163:G:C8	2.50	0.47
2:C2:163:C:H5''	4:CB:162:ARG:NH2	2.30	0.47
4:CB:140:TYR:HA	4:CB:143:GLN:HG2	1.97	0.47
6:CE:435:PRO:O	6:CE:525:HIS:NE2	2.48	0.47
11:CJ:19:ARG:HD2	11:CJ:20:THR:N	2.30	0.47
17:CP:329:VAL:HG22	17:CP:347:SER:HB2	1.96	0.47
23:CV:42:LYS:NZ	23:CV:106:ASP:HB2	2.30	0.47
25:CY:683:ASN:OD1	25:CY:684:ALA:N	2.47	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LB:219:ILE:HG12	28:LB:277:THR:HG23	1.96	0.47
28:LB:288:LYS:HE3	28:LB:288:LYS:HA	1.97	0.47
14:LF:228:PHE:N	14:LF:234:LEU:O	2.46	0.47
33:LK:128:GLY:O	33:LK:132:ILE:HD12	2.15	0.47
45:Ld:57:VAL:HG22	45:Ld:99:SER:OG	2.15	0.47
51:Lq:17:LEU:HD13	51:Lq:176:GLN:NE2	2.29	0.47
1:C1:967:U:O2'	14:LF:128:ALA:O	2.32	0.47
1:C1:2337:G:N2	1:C1:2337:G:OP2	2.48	0.47
1:C1:3017:C:H1'	1:C1:3272:U:H1'	1.97	0.47
5:CC:399:PHE:HE2	11:CJ:150:LEU:HD13	1.79	0.47
9:CH:432:TRP:HB3	18:CQ:81:TYR:HE2	1.76	0.47
15:CN:21:ASN:HB2	15:CN:67:ARG:HB2	1.97	0.47
15:CN:101:LEU:HA	42:LV:137:VAL:HG22	1.97	0.47
15:CN:171:ASP:OD1	15:CN:172:GLU:N	2.48	0.47
21:CT:451:ARG:O	21:CT:455:ARG:HG2	2.15	0.47
27:Cz:46:THR:HG23	27:Cz:50:LEU:HD23	1.97	0.47
28:LB:19:ARG:HH21	28:LB:271:MET:HA	1.80	0.47
29:LC:12:ALA:HB2	29:LC:157:ALA:HB1	1.97	0.47
35:LM:125:LYS:HG2	35:LM:128:ARG:HH21	1.80	0.47
44:LY:21:ALA:HB1	44:LY:25:VAL:HB	1.96	0.47
1:C1:1140:A:H62	14:LF:99:ASN:ND2	2.13	0.46
5:CC:262:PHE:HB3	49:Li:55:GLU:OE1	2.15	0.46
6:CE:336:TYR:CE2	6:CE:482:GLU:HG3	2.49	0.46
9:CH:234:ILE:O	9:CH:237:GLN:HB3	2.15	0.46
9:CH:289:MET:HE3	9:CH:289:MET:HB3	1.71	0.46
17:CP:441:ARG:HG2	17:CP:490:LEU:HD22	1.97	0.46
26:Cb:243:ALA:HA	26:Cb:246:LEU:HD12	1.97	0.46
42:LV:36:LEU:HB3	42:LV:62:ALA:HB1	1.96	0.46
42:LV:85:LYS:HD2	42:LV:86:PRO:HD2	1.97	0.46
51:Lq:148:VAL:HA	51:Lq:151:VAL:HG22	1.96	0.46
1:C1:82:C:H2'	1:C1:83:C:C6	2.50	0.46
1:C1:933:A:H4'	1:C1:949:G:H21	1.79	0.46
1:C1:2959:C:OP1	28:LB:26:ARG:NH1	2.48	0.46
1:C1:3189:G:H2'	1:C1:3190:G:C8	2.49	0.46
6:CE:310:SER:OG	6:CE:311:LEU:HD12	2.16	0.46
9:CH:85:TYR:CD1	9:CH:152:VAL:HG23	2.51	0.46
9:CH:466:GLU:HA	9:CH:469:GLU:OE1	2.15	0.46
11:CJ:373:PHE:HB3	11:CJ:418:GLN:CG	2.45	0.46
11:CJ:397:TRP:HB2	11:CJ:401:LEU:CD1	2.45	0.46
14:CM:101:ILE:O	14:CM:106:ARG:NE	2.46	0.46
20:CS:466:ASP:OD2	20:CS:470:ARG:NE	2.37	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CT:160:ILE:HD12	21:CT:163:ILE:HD12	1.97	0.46
30:LE:71:VAL:HG11	30:LE:169:LEU:HD13	1.95	0.46
14:LF:223:ARG:HB2	14:LF:226:LYS:NZ	2.30	0.46
32:LH:53:LEU:HD11	32:LH:120:THR:OG1	2.15	0.46
1:C1:66:A:N6	1:C1:75:G:H22	2.08	0.46
1:C1:745:U:C2	1:C1:749:C:N3	2.83	0.46
1:C1:1272:U:OP1	7:CF:8:ARG:NH1	2.48	0.46
2:C2:28:C:H2'	2:C2:29:U:C6	2.50	0.46
2:C2:160:A:H2'	2:C2:161:A:C8	2.49	0.46
7:CF:107:ARG:HG2	7:CF:108:ASP:H	1.79	0.46
9:CH:170:LEU:HD11	9:CH:245:LEU:HB2	1.98	0.46
11:CJ:374:LEU:HD13	11:CJ:395:ILE:HG21	1.96	0.46
15:CN:32:GLU:OE1	15:CN:50:ARG:NH1	2.48	0.46
18:CQ:2:ARG:HB3	18:CQ:2:ARG:NH1	2.30	0.46
26:Cb:9:ALA:HB3	26:Cb:10:PRO:HD3	1.96	0.46
49:Li:54:ARG:NH1	49:Li:63:GLU:OE2	2.45	0.46
1:C1:68:C:N4	1:C1:306:U:O2'	2.48	0.46
1:C1:541:G:H2'	1:C1:542:U:C6	2.50	0.46
1:C1:1297:U:H4'	1:C1:1299:A:O4'	2.14	0.46
1:C1:2291:C:C2	1:C1:2292:C:C5	3.03	0.46
1:C1:3260:G:H2'	1:C1:3261:C:O4'	2.15	0.46
4:CB:98:CYS:HB3	4:CB:153:PHE:CD1	2.50	0.46
4:CB:173:LYS:C	4:CB:175:THR:HG23	2.41	0.46
7:CF:59:GLU:HG2	7:CF:115:TYR:CZ	2.50	0.46
8:CG:119:VAL:HG21	8:CG:163:VAL:HG21	1.97	0.46
17:CP:543:PHE:CE2	26:Cb:714:VAL:HG11	2.50	0.46
23:CV:64:ILE:HG22	23:CV:80:THR:HG22	1.98	0.46
25:CY:401:PHE:CD1	25:CY:448:SER:HB2	2.51	0.46
14:LF:52:LYS:O	14:LF:55:GLU:HG2	2.14	0.46
33:LK:159:GLU:OE1	33:LK:159:GLU:N	2.47	0.46
35:LM:44:PRO:HD2	35:LM:85:TRP:CE3	2.51	0.46
36:LN:27:CYS:SG	36:LN:124:ASP:HB3	2.54	0.46
36:LN:28:TRP:O	36:LN:32:GLN:HG2	2.14	0.46
42:LV:106:ASN:ND2	42:LV:110:GLU:HB2	2.30	0.46
1:C1:233:C:H2'	1:C1:234:C:C6	2.51	0.46
1:C1:491:A:H2'	1:C1:492:U:C6	2.49	0.46
1:C1:599:U:H2'	1:C1:600:G:H8	1.79	0.46
1:C1:2320:A:H4'	20:CS:796:GLY:HA2	1.97	0.46
3:CA:149:GLU:HB2	3:CA:152:LEU:HD12	1.98	0.46
3:CA:191:VAL:O	3:CA:192:ARG:HD2	2.15	0.46
6:CE:450:ARG:HB3	6:CE:455:LYS:NZ	2.31	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CJ:384:GLU:O	11:CJ:388:ARG:HG2	2.15	0.46
24:CX:123:ALA:O	24:CX:127:GLU:HG2	2.16	0.46
26:Cb:177:LEU:HD21	26:Cb:193:LEU:HB3	1.98	0.46
28:LB:215:MET:HB2	28:LB:346:HIS:CE1	2.50	0.46
37:LO:178:ARG:NH1	37:LO:178:ARG:HB2	2.30	0.46
1:C1:1334:A:O2'	23:CV:42:LYS:NZ	2.39	0.46
1:C1:3124:U:H5'	1:C1:3125:A:OP1	2.15	0.46
1:C1:3204:G:O2'	1:C1:3205:C:OP1	2.31	0.46
3:CA:136:SER:HB3	3:CA:173:LYS:HB2	1.97	0.46
4:CB:275:TRP:HA	4:CB:278:VAL:HG12	1.97	0.46
5:CC:229:LEU:HD23	20:CS:667:ALA:HB1	1.98	0.46
11:CJ:82:ARG:NH1	43:LX:51:LEU:HD21	2.31	0.46
26:Cb:410:ASP:OD2	26:Cb:414:ARG:NH1	2.42	0.46
29:LC:133:ALA:HB3	29:LC:134:PRO:HD3	1.97	0.46
29:LC:211:ILE:HG23	29:LC:256:VAL:HG23	1.95	0.46
30:LE:61:LEU:HD11	30:LE:103:ILE:HG13	1.97	0.46
37:LO:169:TYR:CE2	37:LO:173:LYS:HD2	2.51	0.46
40:LS:137:ARG:O	40:LS:141:LYS:HG2	2.14	0.46
1:C1:332:C:OP2	29:LC:199:ARG:NH1	2.35	0.46
1:C1:1263:U:H2'	1:C1:1264:G:C8	2.49	0.46
1:C1:1277:G:O2'	40:LS:115:ARG:NH1	2.49	0.46
1:C1:2779:C:H2'	1:C1:2780:U:C6	2.51	0.46
1:C1:2989:A:H2	32:LH:209:LYS:HZ3	1.62	0.46
1:C1:3045:G:OP1	28:LB:314:ARG:NH1	2.48	0.46
1:C1:3231:A:H2'	1:C1:3232:U:C6	2.51	0.46
5:CC:233:ARG:O	5:CC:237:GLU:HG2	2.15	0.46
9:CH:404:ALA:HB3	15:CN:36:SER:OG	2.16	0.46
11:CJ:372:PHE:HA	11:CJ:417:HIS:O	2.15	0.46
12:CK:68:HIS:HA	12:CK:71:ARG:HG2	1.98	0.46
23:CV:54:ILE:HG12	23:CV:63:VAL:HG22	1.98	0.46
23:CV:96:SER:HB2	23:CV:100:LYS:HD2	1.98	0.46
25:CY:529:TYR:HB3	25:CY:530:PRO:HD3	1.97	0.46
28:LB:214:GLU:H	28:LB:283:ILE:HG22	1.80	0.46
29:LC:59:HIS:CE1	29:LC:99:ARG:HD3	2.51	0.46
35:LM:118:PHE:CE2	35:LM:122:ARG:HD2	2.51	0.46
38:LP:178:VAL:O	38:LP:182:ARG:HG2	2.16	0.46
40:LS:13:HIS:CE1	40:LS:55:THR:HB	2.51	0.46
51:Lq:144:LEU:HA	51:Lq:147:LYS:HG2	1.97	0.46
1:C1:656:U:H2'	1:C1:657:U:C6	2.51	0.46
1:C1:1184:A:N7	1:C1:1282:G:H2'	2.30	0.46
1:C1:1303:G:H2'	1:C1:1304:U:H6	1.81	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1323:U:H2'	1:C1:1324:C:C6	2.51	0.46
1:C1:2089:U:P	18:CQ:43:LYS:HZ1	2.36	0.46
1:C1:2387:G:C6	1:C1:2563:G:C2	3.04	0.46
1:C1:2395:U:H2'	1:C1:2396:U:H2'	1.98	0.46
2:C2:184:U:C6	4:CB:169:LYS:HD3	2.51	0.46
2:C2:225:G:H3'	2:C2:226:G:H8	1.80	0.46
7:CF:196:LYS:HE2	7:CF:199:GLU:OE1	2.16	0.46
9:CH:251:TYR:HB3	9:CH:284:ILE:HG12	1.97	0.46
11:CJ:379:PRO:C	11:CJ:382:PRO:HD2	2.41	0.46
12:CK:4:ASN:O	12:CK:6:TYR:N	2.49	0.46
12:CK:9:ARG:CZ	12:CK:13:LEU:HD21	2.45	0.46
12:CK:149:ARG:HH12	12:CK:170:ARG:NH1	2.14	0.46
17:CP:235:LEU:O	17:CP:239:ILE:HG13	2.16	0.46
19:CR:19:MET:HE1	50:Lj:74:PHE:HD2	1.81	0.46
20:CS:694:ASP:O	20:CS:698:GLU:HG3	2.16	0.46
23:CV:11:GLU:HA	23:CV:14:ARG:HD2	1.98	0.46
25:CY:430:GLY:HA3	25:CY:445:MET:HE1	1.96	0.46
25:CY:498:SER:HB2	25:CY:502:TRP:CZ3	2.51	0.46
28:LB:36:ASP:OD1	28:LB:39:LYS:HG3	2.16	0.46
14:LF:237:ARG:HB2	14:LF:240:HIS:HB2	1.98	0.46
1:C1:650:C:H2'	1:C1:651:A:H8	1.80	0.46
1:C1:729:U:H2'	1:C1:730:C:H6	1.81	0.46
1:C1:2304:U:H2'	1:C1:2305:C:C6	2.51	0.46
4:CB:33:HIS:HA	4:CB:36:LYS:HG2	1.96	0.46
5:CC:286:ASN:HA	5:CC:289:LYS:HG3	1.98	0.46
6:CE:388:HIS:HE1	6:CE:390:LYS:HB2	1.80	0.46
11:CJ:144:CYS:SG	11:CJ:237:LEU:HD23	2.56	0.46
11:CJ:252:LYS:NZ	11:CJ:254:PRO:O	2.49	0.46
17:CP:552:MET:HE2	17:CP:552:MET:HB3	1.77	0.46
21:CT:525:LEU:HG	21:CT:602:GLN:HE22	1.73	0.46
25:CY:377:LYS:HA	25:CY:380:ILE:HG22	1.98	0.46
26:Cb:200:LEU:HG	26:Cb:204:PHE:CZ	2.51	0.46
1:C1:580:G:H21	30:LE:37:LYS:HD3	1.81	0.46
1:C1:968:U:H2'	1:C1:969:U:C6	2.51	0.46
1:C1:2374:G:H2'	1:C1:2375:A:C8	2.51	0.46
2:C2:81:U:O2	2:C2:82:U:O2'	2.33	0.46
9:CH:169:LEU:HD12	9:CH:217:VAL:HG22	1.97	0.46
9:CH:488:ILE:HG22	18:CQ:123:ALA:HB1	1.98	0.46
11:CJ:12:ALA:HB1	11:CJ:53:VAL:HG22	1.98	0.46
18:CQ:73:ALA:HB3	18:CQ:75:ARG:HH12	1.80	0.46
24:CX:98:ARG:HH11	24:CX:98:ARG:HG2	1.80	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:433:VAL:HG23	25:CY:434:THR:N	2.30	0.46
26:Cb:273:ALA:HB3	26:Cb:428:ARG:HD3	1.98	0.46
26:Cb:529:GLU:HG3	42:LV:108:LYS:HZ2	1.80	0.46
30:LE:77:ASP:O	30:LE:80:VAL:HG22	2.16	0.46
35:LM:123:LEU:HB3	37:LO:199:LEU:HD21	1.97	0.46
35:LM:125:LYS:HG2	35:LM:128:ARG:NH2	2.31	0.46
46:Le:97:ILE:HG21	46:Le:106:ARG:HG2	1.97	0.46
51:Lq:89:ASP:OD1	51:Lq:92:LYS:HE3	2.15	0.46
1:C1:202:A:H4'	1:C1:204:A:N7	2.31	0.45
1:C1:264:G:H2'	1:C1:265:A:H8	1.81	0.45
1:C1:504:G:N2	29:LC:342:GLY:O	2.48	0.45
1:C1:625:C:C2	1:C1:626:G:C8	3.04	0.45
1:C1:2380:G:H5''	1:C1:2381:A:H5'	1.98	0.45
2:C2:8:C:H2'	2:C2:9:A:H8	1.81	0.45
2:C2:9:A:H2'	2:C2:10:A:C8	2.51	0.45
3:CA:138:PRO:HB3	3:CA:178:HIS:NE2	2.30	0.45
6:CE:130:GLY:HA3	6:CE:394:GLN:OE1	2.16	0.45
7:CF:165:LEU:HD22	7:CF:170:MET:CE	2.45	0.45
19:CR:50:THR:CG2	19:CR:70:LYS:H	2.27	0.45
26:Cb:6:VAL:HG23	26:Cb:7:SER:H	1.81	0.45
36:LN:200:TRP:O	36:LN:203:ARG:NH1	2.47	0.45
51:Lq:176:GLN:OE1	51:Lq:179:LEU:HD21	2.16	0.45
1:C1:288:A:N3	1:C1:291:G:O2'	2.46	0.45
1:C1:316:A:H2'	1:C1:317:A:C8	2.51	0.45
1:C1:452:G:H2'	1:C1:453:G:C8	2.52	0.45
4:CB:118:GLU:O	4:CB:121:ARG:HB2	2.16	0.45
4:CB:215:ARG:NH2	4:CB:219:GLU:OE2	2.50	0.45
11:CJ:6:LYS:HD2	11:CJ:6:LYS:HA	1.79	0.45
11:CJ:178:TYR:HB2	11:CJ:246:TYR:HE1	1.81	0.45
14:CM:113:ARG:NH1	14:CM:210:PRO:HD3	2.31	0.45
20:CS:724:ALA:HB3	20:CS:727:ALA:HB2	1.98	0.45
21:CT:237:PRO:O	21:CT:241:ILE:HG13	2.16	0.45
22:CU:229:SER:O	22:CU:231:PRO:HD3	2.16	0.45
25:CY:723:VAL:O	25:CY:726:ARG:HG2	2.17	0.45
28:LB:112:ASP:O	28:LB:116:ARG:HG3	2.17	0.45
1:C1:285:C:H2'	1:C1:286:A:O4'	2.16	0.45
1:C1:423:U:H2'	1:C1:424:G:H8	1.80	0.45
1:C1:1075:A:H5''	1:C1:1078:C:H5	1.81	0.45
1:C1:1151:A:H4'	14:LF:224:LYS:HD3	1.98	0.45
1:C1:1866:A:O2'	1:C1:1867:U:H5''	2.16	0.45
1:C1:2764:U:O2'	1:C1:2765:U:H5'	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:6:U:H2'	2:C2:7:U:H6	1.81	0.45
3:CA:76:GLU:HA	3:CA:79:GLU:OE1	2.16	0.45
4:CB:220:ILE:O	4:CB:224:ILE:HG12	2.16	0.45
6:CE:362:VAL:HB	6:CE:412:ILE:HG22	1.98	0.45
10:CI:310:GLU:CB	10:CI:313:ARG:HH11	2.29	0.45
21:CT:529:LEU:HA	21:CT:563:THR:OG1	2.17	0.45
25:CY:624:GLU:HG3	25:CY:729:ARG:NH2	2.31	0.45
26:Cb:369:THR:OG1	26:Cb:419:ILE:HG13	2.17	0.45
26:Cb:413:ARG:HH12	26:Cb:431:ASP:HB3	1.81	0.45
39:LQ:158:LYS:HB3	39:LQ:158:LYS:HE2	1.67	0.45
51:Lq:157:PHE:HA	51:Lq:165:MET:HE1	1.99	0.45
1:C1:1238:G:H2'	1:C1:1239:C:C6	2.51	0.45
1:C1:2076:C:H2'	1:C1:2077:G:C8	2.51	0.45
1:C1:2381:A:H2'	1:C1:2382:C:H6	1.82	0.45
1:C1:2427:G:H2'	1:C1:2428:G:C8	2.52	0.45
1:C1:2555:U:H2'	1:C1:2556:G:C8	2.47	0.45
7:CF:238:GLU:HG2	7:CF:238:GLU:O	2.16	0.45
11:CJ:148:LEU:HD23	11:CJ:148:LEU:HA	1.69	0.45
17:CP:495:ILE:HD11	17:CP:581:PHE:HD2	1.81	0.45
25:CY:429:GLN:HA	25:CY:432:ARG:HB2	1.96	0.45
26:Cb:579:GLU:O	26:Cb:582:ASN:HB2	2.17	0.45
29:LC:280:ASN:ND2	29:LC:282:VAL:HG22	2.32	0.45
1:C1:363:G:N1	1:C1:366:A:OP2	2.42	0.45
1:C1:404:G:H2'	1:C1:405:U:C6	2.52	0.45
1:C1:493:C:H2'	1:C1:494:G:H8	1.82	0.45
1:C1:595:A:OP1	29:LC:317:LYS:NZ	2.43	0.45
1:C1:1272:U:H2'	1:C1:1273:A:H8	1.78	0.45
1:C1:2404:G:H2'	1:C1:2405:A:H8	1.79	0.45
1:C1:2821:G:C4	9:CH:94:LEU:HD13	2.52	0.45
4:CB:22:GLN:O	4:CB:25:LYS:HG2	2.17	0.45
9:CH:449:TYR:CZ	18:CQ:72:ALA:HB2	2.51	0.45
17:CP:470:SER:HG	17:CP:474:ASN:HD22	1.55	0.45
22:CU:362:VAL:HA	22:CU:365:GLU:HG2	1.99	0.45
26:Cb:253:ALA:O	26:Cb:256:THR:OG1	2.27	0.45
14:LF:66:ARG:HA	14:LF:66:ARG:NE	2.31	0.45
32:LH:136:ILE:HD11	32:LH:156:PHE:HD1	1.81	0.45
39:LQ:138:ARG:HH11	39:LQ:138:ARG:HG3	1.81	0.45
1:C1:94:G:H2'	1:C1:95:A:C8	2.52	0.45
1:C1:772:U:C2	1:C1:773:A:C8	3.05	0.45
1:C1:1054:G:H2'	1:C1:1055:U:C6	2.51	0.45
1:C1:1201:C:N3	1:C1:1269:A:N1	2.65	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2072:G:H4'	26:Cb:103:ARG:HH21	1.80	0.45
1:C1:2350:U:H4'	38:LP:80:ARG:NH1	2.32	0.45
2:C2:192:C:H2'	2:C2:193:G:H8	1.82	0.45
5:CC:202:ASP:OD2	5:CC:203:ALA:N	2.50	0.45
6:CE:305:ASP:O	6:CE:309:ILE:HG12	2.16	0.45
11:CJ:388:ARG:HG2	11:CJ:388:ARG:NH1	2.31	0.45
15:CN:99:GLU:OE1	15:CN:125:THR:HG21	2.16	0.45
17:CP:345:PHE:CE2	26:Cb:720:PRO:HA	2.51	0.45
26:Cb:239:VAL:HG22	26:Cb:269:LEU:HD12	1.99	0.45
29:LC:287:LEU:O	29:LC:291:ILE:HG12	2.16	0.45
31:LG:243:PHE:O	31:LG:246:GLN:HG2	2.16	0.45
41:LT:44:VAL:HG21	41:LT:58:HIS:HA	1.99	0.45
43:LX:59:TYR:CD1	48:Lh:80:TYR:HB3	2.52	0.45
51:Lq:112:ALA:HB2	51:Lq:135:PRO:HB2	1.99	0.45
1:C1:2077:G:H2'	1:C1:2078:G:C8	2.52	0.45
1:C1:2299:C:H2'	1:C1:2300:C:H6	1.82	0.45
1:C1:2308:C:H2'	1:C1:2309:U:O4'	2.16	0.45
1:C1:3067:C:H2'	1:C1:3068:U:C6	2.51	0.45
5:CC:173:GLY:HA3	22:CU:274:GLU:HB2	1.97	0.45
8:CG:28:ALA:HA	24:CX:98:ARG:NH2	2.31	0.45
8:CG:100:VAL:C	8:CG:137:MET:HE2	2.42	0.45
13:CL:39:ALA:O	13:CL:42:ASN:HB2	2.17	0.45
22:CU:248:LEU:HB3	22:CU:252:ARG:HH12	1.82	0.45
23:CV:22:LYS:HB3	23:CV:22:LYS:HE2	1.71	0.45
33:LK:32:ILE:HG22	33:LK:37:LEU:HB2	1.97	0.45
46:Le:20:ARG:HB3	46:Le:23:SER:OG	2.16	0.45
1:C1:8:C:H2'	1:C1:9:U:H6	1.81	0.45
1:C1:222:A:H2'	1:C1:223:U:C6	2.51	0.45
1:C1:680:A:H4'	29:LC:241:ASN:OD1	2.17	0.45
1:C1:1202:U:H2'	27:Cz:48:TRP:CH2	2.52	0.45
1:C1:2746:C:H2'	1:C1:2747:U:C6	2.52	0.45
1:C1:3229:G:H2'	1:C1:3230:G:H8	1.82	0.45
2:C2:7:U:H2'	2:C2:8:C:H6	1.81	0.45
2:C2:102:U:HO2'	2:C2:103:G:P	2.39	0.45
4:CB:97:VAL:HG12	4:CB:152:VAL:CG1	2.47	0.45
4:CB:103:ASP:HB3	4:CB:104:PRO:HD2	1.98	0.45
5:CC:326:LEU:HB2	11:CJ:240:PHE:CD1	2.51	0.45
5:CC:343:PRO:HD2	14:CM:19:LEU:HD12	1.98	0.45
6:CE:191:PRO:HB3	6:CE:269:ILE:HG12	1.98	0.45
6:CE:450:ARG:HE	6:CE:450:ARG:HB2	1.54	0.45
8:CG:170:CYS:HB3	17:CP:358:LEU:HB3	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CK:133:PHE:CE2	12:CK:148:LYS:HD2	2.52	0.45
15:CN:242:VAL:O	15:CN:246:TYR:HB2	2.17	0.45
20:CS:799:ARG:HG3	29:LC:71:ALA:HB3	1.99	0.45
21:CT:445:ALA:O	21:CT:449:LEU:HG	2.17	0.45
26:Cb:182:GLU:O	26:Cb:185:LYS:NZ	2.42	0.45
26:Cb:474:ASP:HA	26:Cb:477:TYR:HD2	1.82	0.45
26:Cb:487:ARG:NH1	26:Cb:501:ALA:O	2.49	0.45
29:LC:36:VAL:HG11	29:LC:251:LEU:HD21	1.99	0.45
30:LE:175:LYS:HE2	30:LE:175:LYS:HB2	1.74	0.45
31:LG:73:LYS:HE2	31:LG:73:LYS:HB3	1.86	0.45
31:LG:186:LYS:HB2	31:LG:197:THR:HG23	1.99	0.45
50:Lj:53:ALA:O	50:Lj:57:LYS:HG2	2.17	0.45
1:C1:21:G:H3'	1:C1:22:G:H8	1.82	0.45
1:C1:745:U:O2	1:C1:749:C:C4	2.70	0.45
1:C1:1205:A:H62	1:C1:1267:G:H21	1.63	0.45
1:C1:2336:C:H2'	1:C1:2337:G:C2	2.52	0.45
1:C1:2766:A:C6	22:CU:323:ARG:HD2	2.51	0.45
1:C1:2918:C:H2'	1:C1:2919:G:H8	1.82	0.45
1:C1:3066:G:OP1	12:CK:23:ARG:NE	2.50	0.45
1:C1:3302:A:H5''	1:C1:3303:U:C5	2.51	0.45
2:C2:225:G:H1'	2:C2:303:A:H61	1.81	0.45
6:CE:111:GLN:O	6:CE:139:ARG:NH2	2.50	0.45
9:CH:84:LEU:HD22	26:Cb:603:ILE:HG21	1.99	0.45
9:CH:437:ILE:HG21	9:CH:447:TYR:OH	2.17	0.45
12:CK:116:ARG:HG2	12:CK:116:ARG:HH11	1.81	0.45
14:CM:44:LYS:HA	14:CM:44:LYS:HD2	1.67	0.45
38:LP:114:ILE:HA	38:LP:150:LEU:HD23	1.99	0.45
1:C1:180:G:H2'	1:C1:181:A:C8	2.52	0.45
1:C1:490:C:H2'	1:C1:491:A:C8	2.52	0.45
1:C1:1163:U:H5'	40:LS:161:THR:OG1	2.17	0.45
1:C1:1185:A:H61	1:C1:1282:G:H1'	1.81	0.45
1:C1:1880:A:H2'	1:C1:1881:G:H8	1.82	0.45
1:C1:2973:A:H2'	1:C1:2974:G:C8	2.50	0.45
2:C2:6:U:C2	2:C2:7:U:C5	3.05	0.45
6:CE:305:ASP:HA	6:CE:308:ARG:NH1	2.32	0.45
8:CG:110:TYR:CE2	12:CK:127:ILE:HD11	2.51	0.45
12:CK:130:GLU:OE2	12:CK:174:PRO:HA	2.17	0.45
12:CK:196:PRO:HG2	12:CK:224:ASN:HB3	1.98	0.45
20:CS:819:MET:HE2	20:CS:819:MET:HB3	1.93	0.45
23:CV:133:LEU:HD12	23:CV:137:ALA:HB1	1.99	0.45
25:CY:650:LEU:HD11	25:CY:673:LEU:HD12	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:679:LYS:HE3	25:CY:721:TYR:CG	2.52	0.45
26:Cb:323:HIS:HE2	26:Cb:510:LYS:HE3	1.81	0.45
29:LC:220:LYS:O	29:LC:223:VAL:HG22	2.17	0.45
35:LM:15:GLU:OE1	35:LM:15:GLU:N	2.50	0.45
1:C1:1201:C:C2	1:C1:1269:A:C2	3.05	0.44
1:C1:1363:A:H2'	1:C1:1364:G:H8	1.82	0.44
1:C1:1868:G:H2'	1:C1:1869:U:H6	1.78	0.44
1:C1:2451:C:N4	1:C1:2452:C:N4	2.64	0.44
6:CE:433:ASP:HB3	6:CE:434:PRO:HD2	1.99	0.44
9:CH:38:ILE:HA	9:CH:41:ILE:HD12	1.99	0.44
9:CH:299:PRO:HA	9:CH:302:GLN:HG3	1.98	0.44
11:CJ:371:THR:HB	11:CJ:394:ARG:NH1	2.32	0.44
12:CK:239:TRP:NE1	17:CP:474:ASN:HD21	2.15	0.44
18:CQ:84:GLU:O	18:CQ:88:LYS:HG2	2.17	0.44
23:CV:30:ARG:HG2	46:Le:85:LEU:HD11	1.99	0.44
25:CY:415:VAL:O	25:CY:419:VAL:HG23	2.17	0.44
26:Cb:225:LYS:NZ	26:Cb:232:LEU:HG	2.32	0.44
35:LM:59:LEU:HD13	40:LS:152:LEU:HD11	1.98	0.44
39:LQ:83:SER:O	39:LQ:87:ARG:HG3	2.18	0.44
44:LY:55:VAL:HG12	44:LY:105:ILE:HA	1.99	0.44
50:Lj:52:LYS:O	50:Lj:56:ARG:HG3	2.16	0.44
1:C1:607:U:H4'	38:LP:170:HIS:NE2	2.32	0.44
1:C1:1086:U:H2'	1:C1:1087:C:C6	2.52	0.44
1:C1:1139:G:H2'	1:C1:1140:A:O4'	2.17	0.44
1:C1:1322:C:H2'	1:C1:1323:U:C6	2.53	0.44
1:C1:1874:A:N6	26:Cb:819:GLN:HG3	2.32	0.44
1:C1:2774:G:H2'	1:C1:2775:A:C8	2.52	0.44
1:C1:3125:A:O2'	37:LO:99:ALA:HB1	2.17	0.44
1:C1:3137:A:N3	1:C1:3140:G:O2'	2.49	0.44
2:C2:22:U:OP2	29:LC:198:MET:HG2	2.17	0.44
4:CB:49:LEU:HB2	6:CE:483:TYR:HD2	1.82	0.44
4:CB:282:TYR:CD1	4:CB:292:PRO:HA	2.53	0.44
10:CI:221:ASN:OD1	10:CI:223:LYS:N	2.49	0.44
10:CI:303:GLN:O	10:CI:306:VAL:HG22	2.17	0.44
11:CJ:80:LYS:O	11:CJ:84:GLN:HG2	2.18	0.44
11:CJ:259:GLN:HE22	14:CM:246:ARG:HH12	1.65	0.44
11:CJ:263:ASP:C	14:CM:146:ASN:HD21	2.24	0.44
13:CL:59:PHE:CZ	40:LS:125:LYS:HD3	2.52	0.44
19:CR:148:GLN:OE1	34:LL:86:PRO:HB3	2.17	0.44
25:CY:683:ASN:O	25:CY:687:ILE:HG22	2.16	0.44
26:Cb:833:LYS:O	26:Cb:837:VAL:HG23	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LF:46:LYS:NZ	14:LF:185:ILE:HB	2.31	0.44
42:LV:76:HIS:HB2	42:LV:104:ILE:HD12	1.99	0.44
47:Lf:50:ARG:HA	47:Lf:50:ARG:HD2	1.77	0.44
1:C1:579:A:H1'	1:C1:1319:G:H5''	1.98	0.44
1:C1:631:G:H5'	1:C1:1099:G:H1'	1.99	0.44
1:C1:707:A:C6	1:C1:764:A:H4'	2.53	0.44
1:C1:2298:U:H2'	1:C1:2299:C:H6	1.82	0.44
1:C1:2365:G:C2	1:C1:2366:A:H1'	2.53	0.44
1:C1:2775:A:H2'	1:C1:2776:U:O4'	2.18	0.44
1:C1:3304:C:H2'	1:C1:3305:U:H6	1.82	0.44
6:CE:173:LEU:HB3	6:CE:212:GLN:HG2	1.99	0.44
7:CF:74:ALA:HB1	7:CF:93:THR:HG23	2.00	0.44
13:CL:20:LEU:O	13:CL:24:ILE:HG12	2.18	0.44
15:CN:162:HIS:CD2	15:CN:164:LYS:H	2.35	0.44
17:CP:279:TYR:CE2	17:CP:283:LYS:HD2	2.52	0.44
19:CR:34:ILE:HD12	19:CR:172:LEU:HD23	2.00	0.44
20:CS:725:LEU:HD23	21:CT:401:LEU:HB3	1.98	0.44
21:CT:264:ARG:HB3	21:CT:268:LYS:HZ1	1.82	0.44
26:Cb:129:ASP:OD1	26:Cb:268:THR:N	2.26	0.44
1:C1:66:A:C6	1:C1:75:G:N2	2.85	0.44
1:C1:213:G:C6	1:C1:1371:G:N2	2.86	0.44
1:C1:738:C:OP1	22:CU:232:GLN:NE2	2.33	0.44
1:C1:1119:C:H2'	1:C1:1120:U:C6	2.52	0.44
1:C1:1208:G:H2'	1:C1:1209:C:C6	2.53	0.44
1:C1:2859:G:O2'	1:C1:2981:A:N1	2.47	0.44
1:C1:3075:C:H5'	27:Cz:27:LYS:HB3	2.00	0.44
3:CA:138:PRO:HB3	3:CA:178:HIS:CD2	2.52	0.44
3:CA:274:ALA:O	3:CA:278:ARG:NE	2.49	0.44
5:CC:326:LEU:HG	11:CJ:128:ARG:NE	2.32	0.44
6:CE:487:LYS:HA	6:CE:490:ILE:HD12	2.00	0.44
12:CK:236:LYS:HE2	17:CP:474:ASN:HA	2.00	0.44
17:CP:356:GLU:HB2	17:CP:361:HIS:HB2	1.99	0.44
17:CP:443:PHE:N	17:CP:444:PRO:CD	2.80	0.44
18:CQ:120:VAL:O	18:CQ:124:ARG:HG2	2.17	0.44
21:CT:499:HIS:CD2	21:CT:502:ARG:HH21	2.35	0.44
21:CT:523:LEU:HD13	21:CT:567:LEU:HD12	2.00	0.44
23:CV:132:LYS:HE2	23:CV:132:LYS:HB2	1.76	0.44
25:CY:553:HIS:O	25:CY:556:ARG:HB2	2.17	0.44
31:LG:75:PRO:HG2	31:LG:78:ILE:HD12	1.98	0.44
42:LV:12:LYS:HD3	42:LV:127:LEU:HD11	2.00	0.44
1:C1:63:A:N3	1:C1:78:U:O2'	2.41	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1199:A:N6	1:C1:1271:G:O6	2.51	0.44
1:C1:1322:C:H2'	1:C1:1323:U:H6	1.83	0.44
1:C1:1901:A:N6	1:C1:2073:G:H1	2.15	0.44
1:C1:3298:U:H2'	1:C1:3299:A:C8	2.52	0.44
2:C2:47:C:H1'	2:C2:61:A:H2'	1.99	0.44
3:CA:59:LEU:HD11	3:CA:163:PHE:CD1	2.51	0.44
3:CA:186:ASP:C	3:CA:188:LYS:H	2.26	0.44
3:CA:193:ASN:ND2	3:CA:234:ILE:HD11	2.33	0.44
4:CB:260:GLU:HA	4:CB:263:ILE:HG12	1.99	0.44
4:CB:275:TRP:O	4:CB:278:VAL:HG12	2.18	0.44
5:CC:411:TYR:CD2	5:CC:412:LEU:HG	2.53	0.44
6:CE:268:ARG:O	6:CE:272:ILE:HG12	2.18	0.44
12:CK:2:PRO:HB2	12:CK:6:TYR:CD1	2.52	0.44
14:CM:74:ILE:O	14:CM:75:ALA:C	2.60	0.44
15:CN:59:ILE:HG13	15:CN:60:GLY:N	2.33	0.44
25:CY:673:LEU:O	25:CY:677:VAL:HG23	2.17	0.44
26:Cb:105:ILE:HG23	26:Cb:110:PHE:HB2	1.98	0.44
26:Cb:205:GLY:O	26:Cb:209:THR:HG23	2.18	0.44
26:Cb:206:LEU:O	26:Cb:209:THR:OG1	2.20	0.44
31:LG:102:PRO:CG	31:LG:193:VAL:HA	2.48	0.44
36:LN:9:GLU:HB2	49:Li:53:ILE:HG13	1.98	0.44
46:Le:14:ARG:NH2	46:Le:17:ARG:O	2.48	0.44
46:Le:44:ARG:HA	46:Le:53:MET:CE	2.47	0.44
51:Lq:78:LYS:HZ2	51:Lq:84:ALA:H	1.66	0.44
1:C1:3018:G:H4'	1:C1:3273:G:H4'	2.00	0.44
1:C1:3210:U:O4	38:LP:181:ARG:HD3	2.17	0.44
2:C2:149:A:H2'	2:C2:150:G:C8	2.53	0.44
2:C2:194:C:H5'	4:CB:67:THR:HG21	1.98	0.44
3:CA:59:LEU:HD11	3:CA:163:PHE:HD1	1.83	0.44
6:CE:216:VAL:HG22	6:CE:218:ILE:HG23	1.99	0.44
7:CF:41:PHE:CD2	7:CF:226:TYR:HB3	2.53	0.44
8:CG:115:VAL:HG12	8:CG:162:ILE:HA	1.99	0.44
9:CH:179:LYS:HB2	9:CH:179:LYS:HE2	1.72	0.44
11:CJ:397:TRP:HB2	11:CJ:401:LEU:HD12	2.00	0.44
11:CJ:454:ILE:HG22	11:CJ:456:VAL:HG13	2.00	0.44
12:CK:186:HIS:O	12:CK:190:ASN:HA	2.18	0.44
14:CM:65:GLU:O	14:CM:69:ILE:HG12	2.17	0.44
21:CT:314:GLU:HB2	21:CT:316:ARG:HH22	1.83	0.44
25:CY:387:TRP:HE1	25:CY:404:ILE:HG13	1.82	0.44
25:CY:491:TYR:OH	25:CY:538:ALA:O	2.29	0.44
26:Cb:376:LYS:O	26:Cb:380:GLU:HG3	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LB:47:MET:HE2	28:LB:180:MET:HG2	2.00	0.44
28:LB:214:GLU:O	28:LB:283:ILE:HG22	2.18	0.44
37:LO:144:SER:HA	37:LO:147:VAL:HG12	1.98	0.44
39:LQ:49:SER:HB2	39:LQ:54:LEU:HD23	2.00	0.44
39:LQ:96:ALA:O	39:LQ:100:LYS:HG2	2.17	0.44
1:C1:83:C:O2	1:C1:103:G:N2	2.51	0.44
1:C1:105:C:H5'	1:C1:684:G:N2	2.32	0.44
1:C1:276:A:H61	1:C1:296:G:P	2.40	0.44
1:C1:775:G:H2'	1:C1:776:C:H6	1.82	0.44
1:C1:920:U:H2'	1:C1:921:G:C8	2.53	0.44
1:C1:1358:C:O2'	1:C1:1390:G:O2'	2.35	0.44
1:C1:1879:A:H2'	1:C1:1880:A:H8	1.82	0.44
1:C1:2780:U:H2'	1:C1:2781:G:O4'	2.18	0.44
1:C1:3076:U:OP2	27:Cz:28:ASN:ND2	2.46	0.44
1:C1:3335:U:H2'	1:C1:3336:U:H6	1.81	0.44
3:CA:39:LEU:CD1	3:CA:65:ASP:HB3	2.47	0.44
9:CH:170:LEU:HD13	9:CH:242:LEU:HA	2.00	0.44
12:CK:175:MET:SD	12:CK:178:ARG:NH1	2.90	0.44
18:CQ:68:THR:CG2	18:CQ:96:ILE:HG23	2.47	0.44
25:CY:649:ALA:HA	25:CY:652:ARG:HE	1.83	0.44
26:Cb:152:LEU:HD22	26:Cb:162:ARG:HE	1.82	0.44
30:LE:155:SER:O	30:LE:156:SER:C	2.60	0.44
38:LP:64:ALA:HB1	38:LP:80:ARG:HE	1.83	0.44
42:LV:79:VAL:HG21	42:LV:128:TRP:NE1	2.32	0.44
1:C1:250:U:H2'	1:C1:251:C:C6	2.53	0.44
1:C1:540:A:H2'	1:C1:541:G:H8	1.83	0.44
1:C1:1151:A:H2'	1:C1:1152:A:C8	2.53	0.44
1:C1:1171:C:N4	1:C1:1297:U:H1'	2.33	0.44
1:C1:1430:U:H2'	1:C1:1431:A:C8	2.52	0.44
1:C1:2922:G:H2'	1:C1:2922:G:N3	2.33	0.44
1:C1:3001:A:H4'	28:LB:13:SER:HB2	1.99	0.44
1:C1:3115:C:H2'	1:C1:3116:G:C8	2.53	0.44
1:C1:3289:C:C4	1:C1:3290:C:N4	2.85	0.44
3:CA:137:ARG:NH1	22:CU:215:SER:O	2.51	0.44
7:CF:157:VAL:HG22	7:CF:158:SER:H	1.83	0.44
17:CP:411:ASN:HB2	17:CP:443:PHE:CZ	2.53	0.44
17:CP:424:ASN:OD1	17:CP:427:ARG:NH1	2.43	0.44
17:CP:486:THR:O	17:CP:490:LEU:HD23	2.17	0.44
17:CP:507:TYR:HA	17:CP:581:PHE:O	2.17	0.44
21:CT:671:LYS:HA	21:CT:674:GLU:OE1	2.18	0.44
26:Cb:119:LYS:HE3	26:Cb:294:ARG:O	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Cb:218:PRO:HB2	26:Cb:251:PHE:CD1	2.53	0.44
28:LB:172:LEU:HD21	28:LB:334:LYS:HB2	2.00	0.44
14:LF:182:TYR:HB3	14:LF:200:ASN:ND2	2.33	0.44
36:LN:53:TYR:HB2	36:LN:133:ILE:HD13	1.98	0.44
44:LY:27:ARG:HG2	44:LY:48:PRO:HB3	1.99	0.44
51:Lq:55:LEU:HD21	51:Lq:182:ASN:HB3	1.99	0.44
1:C1:140:G:OP2	31:LG:196:LYS:NZ	2.51	0.44
1:C1:247:A:H2'	1:C1:248:G:C8	2.51	0.44
1:C1:580:G:N2	30:LE:37:LYS:HD3	2.33	0.44
1:C1:655:U:H2'	1:C1:656:U:C6	2.53	0.44
1:C1:663:G:H5''	39:LQ:134:THR:HB	1.99	0.44
1:C1:1368:A:H2	29:LC:142:GLN:HE21	1.66	0.44
1:C1:2818:U:N3	9:CH:99:THR:OG1	2.51	0.44
1:C1:3327:G:H2'	1:C1:3328:C:C6	2.52	0.44
2:C2:142:C:H2'	2:C2:143:U:C6	2.53	0.44
3:CA:137:ARG:O	3:CA:176:ILE:HG13	2.18	0.44
9:CH:449:TYR:CG	18:CQ:93:MET:HE1	2.53	0.44
10:CI:207:PHE:C	10:CI:213:ILE:HD11	2.43	0.44
14:CM:128:ALA:O	14:CM:132:MET:HG2	2.17	0.44
23:CV:125:VAL:HG11	46:Le:114:LYS:HG2	2.00	0.44
25:CY:596:LEU:HD21	25:CY:601:ALA:HB2	1.99	0.44
26:Cb:159:PHE:HA	26:Cb:210:ASN:ND2	2.30	0.44
26:Cb:859:ALA:HA	26:Cb:869:ARG:HD3	1.99	0.44
28:LB:103:THR:HG21	28:LB:151:ARG:HD2	2.00	0.44
28:LB:107:ALA:HB1	28:LB:201:GLU:OE2	2.17	0.44
29:LC:301:ARG:HE	39:LQ:69:GLU:HG3	1.83	0.44
49:Li:86:LEU:HD13	49:Li:91:ARG:HB3	2.00	0.44
1:C1:150:G:H1'	49:Li:35:PRO:HB2	2.00	0.43
1:C1:256:G:O6	6:CE:224:ARG:HB3	2.18	0.43
1:C1:1080:A:O5'	41:LT:129:LYS:HG2	2.18	0.43
1:C1:1897:C:H2'	1:C1:1898:G:C8	2.51	0.43
1:C1:2077:G:H2'	1:C1:2078:G:H8	1.83	0.43
3:CA:285:GLN:O	3:CA:289:LEU:HG	2.17	0.43
8:CG:87:LEU:HD23	8:CG:87:LEU:C	2.43	0.43
9:CH:297:LEU:HD23	9:CH:298:ASP:N	2.33	0.43
10:CI:320:LEU:HD12	10:CI:323:MET:HB2	2.00	0.43
11:CJ:127:ILE:HD13	11:CJ:233:PHE:HE1	1.83	0.43
11:CJ:388:ARG:HH21	11:CJ:392:CYS:C	2.22	0.43
12:CK:59:ILE:HG22	12:CK:63:LYS:HE2	1.99	0.43
15:CN:99:GLU:HG3	15:CN:101:LEU:N	2.33	0.43
15:CN:118:HIS:HB3	15:CN:121:LEU:CD1	2.47	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CP:440:ALA:HB3	17:CP:490:LEU:HD11	2.00	0.43
17:CP:507:TYR:CZ	17:CP:582:LYS:HD3	2.53	0.43
21:CT:273:ARG:HD2	21:CT:318:ASP:HB2	2.00	0.43
24:CX:98:ARG:O	24:CX:102:ASN:ND2	2.51	0.43
28:LB:102:LEU:HG	28:LB:103:THR:HG23	2.00	0.43
28:LB:170:THR:HG22	28:LB:172:LEU:HG	2.00	0.43
28:LB:292:GLU:HA	28:LB:305:LYS:NZ	2.32	0.43
33:LK:118:PHE:CE1	33:LK:119:LYS:HG2	2.53	0.43
42:LV:56:VAL:HA	42:LV:80:ILE:HG13	2.00	0.43
1:C1:531:U:O4	1:C1:541:G:O6	2.36	0.43
1:C1:972:G:N2	41:LT:59:GLY:O	2.51	0.43
1:C1:1241:A:H1'	1:C1:1262:C:O2'	2.19	0.43
1:C1:1884:G:H2'	1:C1:1885:G:C8	2.53	0.43
2:C2:223:G:H2'	2:C2:224:C:C6	2.52	0.43
3:CA:246:GLN:HG2	3:CA:254:ILE:HD13	2.00	0.43
4:CB:19:ASP:HB3	4:CB:22:GLN:HG3	2.00	0.43
5:CC:387:TYR:CE1	5:CC:394:PRO:HD3	2.53	0.43
9:CH:141:ARG:HG2	9:CH:141:ARG:NH1	2.33	0.43
17:CP:352:GLY:HA2	17:CP:357:TYR:CE2	2.54	0.43
17:CP:368:SER:HB3	17:CP:576:PHE:CD1	2.53	0.43
21:CT:231:GLU:HG2	21:CT:232:ASP:O	2.19	0.43
26:Cb:489:LEU:HD21	26:Cb:491:LEU:HD21	2.00	0.43
32:LH:211:ILE:H	32:LH:211:ILE:HD12	1.83	0.43
37:LO:63:THR:OG1	37:LO:71:GLY:HA2	2.18	0.43
41:LT:79:ARG:HG3	41:LT:84:TYR:CE2	2.53	0.43
45:Ld:88:ASN:HB2	45:Ld:98:TYR:CD1	2.49	0.43
1:C1:1874:A:C2	26:Cb:815:LYS:HD2	2.54	0.43
1:C1:2735:G:O6	1:C1:2741:U:O4	2.35	0.43
1:C1:3180:C:H2'	1:C1:3181:C:O4'	2.18	0.43
2:C2:7:U:H2'	2:C2:8:C:C6	2.53	0.43
2:C2:111:A:O2'	50:Lj:20:ARG:NE	2.52	0.43
3:CA:147:GLU:CG	22:CU:221:VAL:HG11	2.48	0.43
4:CB:174:THR:O	4:CB:175:THR:OG1	2.31	0.43
15:CN:42:LEU:HD13	15:CN:46:ILE:HD11	2.01	0.43
17:CP:356:GLU:OE2	17:CP:356:GLU:N	2.48	0.43
21:CT:175:TYR:HA	21:CT:178:VAL:HG22	2.01	0.43
21:CT:659:TRP:N	21:CT:660:GLU:OE1	2.51	0.43
25:CY:535:THR:O	25:CY:539:MET:HG2	2.18	0.43
25:CY:616:ASP:O	25:CY:620:GLU:OE1	2.36	0.43
25:CY:644:LEU:N	25:CY:645:PRO:HD2	2.33	0.43
25:CY:688:GLU:HA	25:CY:691:ARG:HD2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LC:136:LEU:HD23	29:LC:143:VAL:HG21	2.00	0.43
29:LC:215:PRO:HB3	29:LC:220:LYS:HZ3	1.81	0.43
30:LE:85:GLY:HA3	30:LE:86:PRO:C	2.43	0.43
14:LF:125:VAL:HG12	41:LT:135:PRO:HG3	1.99	0.43
32:LH:104:ALA:O	32:LH:108:VAL:HG13	2.18	0.43
32:LH:124:LYS:HE3	32:LH:226:ILE:HG12	2.01	0.43
33:LK:35:LEU:HD22	33:LK:37:LEU:HD23	2.00	0.43
44:LY:43:ASN:HB3	44:LY:122:LYS:HG3	2.00	0.43
1:C1:414:A:N1	1:C1:2324:C:O2'	2.49	0.43
1:C1:497:U:H2'	1:C1:498:C:C6	2.54	0.43
1:C1:1881:G:H2'	1:C1:1882:U:C6	2.53	0.43
1:C1:3046:C:H2'	1:C1:3047:U:O4'	2.18	0.43
3:CA:292:ARG:HH21	39:LQ:136:LYS:NZ	2.15	0.43
6:CE:542:ALA:HB1	6:CE:547:PHE:HB2	2.01	0.43
7:CF:185:LYS:HE2	7:CF:185:LYS:HB3	1.84	0.43
8:CG:100:VAL:HG11	8:CG:114:ILE:HG12	1.99	0.43
8:CG:126:CYS:SG	8:CG:130:SER:OG	2.66	0.43
10:CI:228:ARG:HG2	10:CI:230:ARG:NH2	2.34	0.43
11:CJ:167:ARG:NH1	11:CJ:235:MET:HB3	2.32	0.43
11:CJ:266:ALA:HB3	11:CJ:270:ALA:HB2	1.99	0.43
17:CP:320:LEU:HD11	17:CP:362:TYR:HB3	1.99	0.43
17:CP:571:TYR:O	17:CP:573:VAL:N	2.42	0.43
21:CT:169:VAL:O	21:CT:172:MET:HB3	2.18	0.43
21:CT:404:VAL:O	21:CT:407:THR:OG1	2.28	0.43
22:CU:319:LYS:HD3	22:CU:319:LYS:HA	1.76	0.43
25:CY:548:PHE:HB2	25:CY:549:PRO:HD3	2.01	0.43
28:LB:214:GLU:O	28:LB:216:ILE:HG23	2.18	0.43
36:LN:159:ARG:HB3	36:LN:164:LEU:HB2	1.99	0.43
42:LV:25:MET:HE1	42:LV:80:ILE:HG22	2.00	0.43
44:LY:113:ASP:O	44:LY:117:ILE:HG13	2.18	0.43
1:C1:202:A:N3	29:LC:228:ASN:ND2	2.59	0.43
1:C1:405:U:H2'	1:C1:406:U:C6	2.54	0.43
1:C1:539:G:C2	1:C1:540:A:N7	2.86	0.43
1:C1:2768:C:H2'	1:C1:2769:A:C8	2.54	0.43
1:C1:2845:A:H61	9:CH:31:GLN:HG3	1.83	0.43
1:C1:2889:C:H42	1:C1:2893:U:H5''	1.83	0.43
6:CE:347:LEU:HD13	6:CE:485:PHE:CD1	2.54	0.43
8:CG:122:TRP:CD1	8:CG:155:ARG:HH12	2.35	0.43
11:CJ:169:GLU:HA	11:CJ:172:CYS:SG	2.58	0.43
15:CN:122:GLU:HB2	15:CN:125:THR:HG23	2.00	0.43
17:CP:308:ILE:HG22	17:CP:364:LEU:HD23	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CP:309:ARG:HG3	17:CP:370:PHE:HE2	1.82	0.43
17:CP:316:HIS:CE1	17:CP:318:ARG:HG3	2.52	0.43
21:CT:531:LEU:HD11	25:CY:540:ARG:HH21	1.84	0.43
24:CX:125:GLN:O	24:CX:128:GLU:HG2	2.19	0.43
25:CY:730:GLU:O	25:CY:734:ARG:HG2	2.17	0.43
26:Cb:308:ALA:HB1	26:Cb:573:HIS:HE1	1.84	0.43
28:LB:117:ARG:NH2	28:LB:176:LYS:HG2	2.33	0.43
36:LN:154:PRO:O	36:LN:157:LYS:HG3	2.19	0.43
39:LQ:138:ARG:HG3	39:LQ:138:ARG:NH1	2.33	0.43
1:C1:1321:C:H2'	1:C1:1322:C:C6	2.54	0.43
1:C1:2290:U:C2	1:C1:2291:C:C5	3.07	0.43
1:C1:2468:U:H2'	1:C1:2469:U:H6	1.82	0.43
1:C1:3208:A:OP1	30:LE:64:ARG:NH2	2.37	0.43
5:CC:389:SER:O	5:CC:393:VAL:HG23	2.17	0.43
7:CF:21:GLU:O	7:CF:25:ARG:HD3	2.17	0.43
9:CH:93:ALA:O	9:CH:97:ILE:HG12	2.19	0.43
9:CH:236:MET:CA	9:CH:239:VAL:HG12	2.42	0.43
9:CH:255:ILE:HG22	9:CH:292:LYS:HD2	2.00	0.43
10:CI:301:GLN:O	10:CI:304:VAL:HG22	2.18	0.43
11:CJ:45:ARG:NE	11:CJ:65:TYR:HB2	2.34	0.43
12:CK:116:ARG:HG2	12:CK:116:ARG:NH1	2.33	0.43
13:CL:68:GLN:O	13:CL:71:GLU:HG3	2.18	0.43
15:CN:74:THR:HA	15:CN:96:ARG:HD3	2.00	0.43
25:CY:421:LYS:HE3	25:CY:425:GLN:NE2	2.26	0.43
26:Cb:187:THR:HG22	26:Cb:189:LEU:HG	1.99	0.43
28:LB:150:GLU:HA	28:LB:153:LYS:CG	2.48	0.43
29:LC:43:MET:HG2	29:LC:243:LEU:HD11	2.00	0.43
30:LE:73:LEU:HD21	30:LE:169:LEU:CD1	2.49	0.43
40:LS:80:ARG:HB2	40:LS:124:LEU:HD11	2.01	0.43
51:Lq:38:LEU:HD22	51:Lq:41:TYR:CB	2.48	0.43
1:C1:708:G:N2	1:C1:731:G:H1'	2.34	0.43
1:C1:2430:A:O2'	1:C1:2439:G:N2	2.51	0.43
1:C1:3183:C:H5'	1:C1:3184:G:OP2	2.18	0.43
2:C2:44:A:H2'	2:C2:45:C:H6	1.84	0.43
5:CC:171:THR:O	5:CC:171:THR:HG22	2.18	0.43
6:CE:486:PRO:O	6:CE:490:ILE:HG13	2.18	0.43
7:CF:22:ALA:HA	7:CF:25:ARG:CZ	2.48	0.43
7:CF:224:LEU:HD21	7:CF:243:ARG:HD3	2.01	0.43
9:CH:340:VAL:HA	9:CH:343:VAL:HG12	2.01	0.43
11:CJ:32:ASP:HA	11:CJ:35:LYS:HZ3	1.84	0.43
12:CK:126:GLY:HA3	12:CK:161:PHE:HB2	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CN:99:GLU:HG3	15:CN:101:LEU:H	1.83	0.43
17:CP:337:TRP:CD1	17:CP:337:TRP:H	2.37	0.43
17:CP:343:GLN:NE2	26:Cb:716:MET:HB3	2.34	0.43
17:CP:383:ARG:HG2	17:CP:450:PHE:CD2	2.54	0.43
20:CS:655:ILE:HG13	20:CS:722:LEU:HD21	2.00	0.43
22:CU:275:MET:HE3	22:CU:275:MET:HB3	1.94	0.43
25:CY:588:PRO:HB3	25:CY:615:GLN:HG3	2.00	0.43
26:Cb:492:GLY:HA3	26:Cb:571:GLN:CD	2.44	0.43
29:LC:10:PHE:CZ	29:LC:147:PRO:HG2	2.53	0.43
29:LC:295:GLU:O	29:LC:299:VAL:HG23	2.19	0.43
29:LC:326:MET:HE1	14:LF:155:TYR:CZ	2.53	0.43
42:LV:47:ARG:HB3	42:LV:50:ARG:HB3	2.00	0.43
45:Ld:18:ARG:HB3	45:Ld:116:VAL:HA	2.01	0.43
1:C1:281:U:OP2	36:LN:170:LYS:NZ	2.51	0.43
1:C1:424:G:H2'	1:C1:425:A:C8	2.53	0.43
1:C1:596:G:H1'	29:LC:312:ALA:O	2.19	0.43
1:C1:728:A:H2'	1:C1:729:U:C6	2.53	0.43
1:C1:1234:A:H2'	1:C1:1235:U:O4'	2.18	0.43
1:C1:2558:C:H2'	1:C1:2559:A:C8	2.54	0.43
1:C1:3255:G:H5''	1:C1:3255:G:H8	1.84	0.43
2:C2:63:G:H22	2:C2:97:A:H2	1.65	0.43
4:CB:232:LEU:HD13	4:CB:234:HIS:CE1	2.53	0.43
6:CE:189:VAL:HG11	6:CE:278:MET:HE1	2.00	0.43
15:CN:77:THR:OG1	15:CN:80:GLU:HG3	2.18	0.43
21:CT:171:GLN:O	21:CT:175:TYR:HD2	2.01	0.43
21:CT:444:GLU:OE2	24:CX:121:MET:HG2	2.17	0.43
22:CU:244:MET:O	22:CU:248:LEU:HG	2.18	0.43
24:CX:118:SER:HB2	24:CX:121:MET:HG3	2.01	0.43
31:LG:66:LYS:HE2	31:LG:66:LYS:HB2	1.74	0.43
44:LY:79:ILE:HD11	44:LY:103:VAL:HG11	2.00	0.43
1:C1:404:G:OP1	38:LP:62:ARG:NH1	2.44	0.43
1:C1:683:C:H1'	19:CR:64:GLY:N	2.32	0.43
1:C1:2300:C:H2'	1:C1:2301:C:H6	1.84	0.43
1:C1:2313:U:H2'	1:C1:2314:A:H8	1.83	0.43
1:C1:2354:C:H4'	1:C1:2355:G:C2	2.54	0.43
1:C1:2818:U:H3	9:CH:99:THR:HG1	1.65	0.43
1:C1:2933:U:H2'	1:C1:2934:A:H8	1.84	0.43
1:C1:3029:C:H2'	1:C1:3030:G:O4'	2.19	0.43
2:C2:7:U:C2	2:C2:8:C:C5	3.06	0.43
2:C2:39:G:H1'	2:C2:104:A:N6	2.34	0.43
3:CA:182:PHE:CD1	3:CA:191:VAL:HG12	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CA:265:ASN:OD1	3:CA:268:ARG:NH1	2.51	0.43
6:CE:157:THR:HA	6:CE:161:LYS:HE2	2.01	0.43
8:CG:162:ILE:H	12:CK:141:LYS:HZ2	1.66	0.43
9:CH:246:ARG:HH21	9:CH:280:LYS:HA	1.84	0.43
12:CK:165:PRO:O	12:CK:169:GLU:HB3	2.18	0.43
15:CN:18:THR:OG1	15:CN:60:GLY:HA2	2.18	0.43
18:CQ:1:MET:CE	28:LB:57:VAL:HG21	2.48	0.43
21:CT:306:LEU:HD11	21:CT:325:PHE:CE1	2.54	0.43
23:CV:73:LYS:HG3	23:CV:73:LYS:O	2.19	0.43
23:CV:123:ARG:HD3	30:LE:27:TRP:CH2	2.54	0.43
25:CY:627:SER:O	25:CY:631:VAL:HG12	2.19	0.43
14:LF:133:ILE:HA	14:LF:136:VAL:HG22	2.00	0.43
47:Lf:92:PRO:C	47:Lf:94:ARG:H	2.26	0.43
1:C1:1181:C:H2'	1:C1:1182:A:C8	2.54	0.43
1:C1:2292:C:H2'	1:C1:2293:C:C6	2.53	0.43
1:C1:2431:G:H2'	1:C1:2432:C:C6	2.54	0.43
5:CC:261:TRP:HB2	49:Li:105:GLU:HB3	2.00	0.43
9:CH:402:VAL:O	9:CH:406:ASP:HB2	2.18	0.43
11:CJ:178:TYR:HB2	11:CJ:246:TYR:CE1	2.53	0.43
13:CL:187:GLY:HA2	13:CL:188:ALA:HA	1.54	0.43
14:CM:92:VAL:HG12	14:CM:142:TYR:HB3	2.01	0.43
18:CQ:15:PRO:HB2	28:LB:359:TRP:HZ2	1.82	0.43
23:CV:88:ARG:HD3	30:LE:24:ALA:HB3	2.01	0.43
29:LC:192:ARG:O	29:LC:197:LYS:HD3	2.19	0.43
31:LG:52:MET:HB3	31:LG:53:VAL:H	1.66	0.43
47:Lf:9:LEU:HD23	47:Lf:9:LEU:HA	1.82	0.43
47:Lf:23:ARG:HG2	47:Lf:23:ARG:HH11	1.84	0.43
1:C1:264:G:H1'	49:Li:91:ARG:NH1	2.22	0.42
1:C1:362:U:H2'	1:C1:363:G:O4'	2.19	0.42
1:C1:597:G:N1	1:C1:1319:G:OP1	2.41	0.42
1:C1:599:U:H2'	1:C1:600:G:C8	2.54	0.42
1:C1:3086:A:C6	1:C1:3088:U:H1'	2.53	0.42
2:C2:177:C:H2'	2:C2:178:U:C6	2.54	0.42
2:C2:213:A:C4	4:CB:140:TYR:CE1	3.07	0.42
8:CG:162:ILE:H	12:CK:141:LYS:NZ	2.16	0.42
9:CH:338:LEU:O	9:CH:342:ARG:HG3	2.20	0.42
10:CI:219:VAL:CG2	10:CI:228:ARG:HB2	2.48	0.42
10:CI:275:GLY:O	10:CI:278:ARG:HG2	2.18	0.42
12:CK:27:LYS:O	12:CK:31:GLU:HG2	2.19	0.42
12:CK:164:ARG:HD3	12:CK:173:ARG:HH21	1.84	0.42
14:CM:92:VAL:HG12	14:CM:142:TYR:CB	2.48	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CN:199:VAL:HG23	15:CN:204:ALA:HB2	2.00	0.42
25:CY:446:LYS:HG2	25:CY:504:CYS:SG	2.59	0.42
25:CY:637:ILE:O	25:CY:691:ARG:NH2	2.52	0.42
26:Cb:141:THR:O	26:Cb:145:VAL:HG23	2.19	0.42
27:Cz:28:ASN:HB3	27:Cz:30:GLN:HG2	2.00	0.42
28:LB:381:MET:HE2	28:LB:384:LEU:HD21	2.01	0.42
29:LC:266:ASP:O	29:LC:270:GLU:HG3	2.19	0.42
30:LE:195:PRO:HA	30:LE:198:MET:HE2	2.01	0.42
14:LF:162:VAL:HG22	14:LF:178:ASN:ND2	2.34	0.42
51:Lq:46:ASP:OD1	51:Lq:46:ASP:N	2.51	0.42
1:C1:18:G:OP2	43:LX:59:TYR:OH	2.38	0.42
1:C1:159:G:H2'	1:C1:160:C:C6	2.53	0.42
1:C1:404:G:H2'	1:C1:405:U:H6	1.83	0.42
1:C1:889:G:H2'	1:C1:890:G:C8	2.55	0.42
1:C1:1045:G:C6	41:LT:109:VAL:HG22	2.54	0.42
1:C1:1089:A:H2'	1:C1:1090:C:H6	1.84	0.42
1:C1:2289:U:H2'	1:C1:2290:U:H6	1.84	0.42
1:C1:2299:C:H2'	1:C1:2300:C:C6	2.53	0.42
2:C2:119:C:OP1	11:CJ:70:GLN:NE2	2.50	0.42
2:C2:139:U:H2'	2:C2:140:G:H8	1.84	0.42
4:CB:71:HIS:HD1	4:CB:238:SER:HA	1.83	0.42
5:CC:399:PHE:HE1	11:CJ:209:LEU:HD23	1.83	0.42
9:CH:301:MET:O	9:CH:305:ILE:HG12	2.19	0.42
10:CI:243:ILE:O	10:CI:247:THR:HG22	2.18	0.42
11:CJ:265:GLY:HA3	14:CM:147:LEU:HD11	2.00	0.42
18:CQ:115:LYS:O	18:CQ:119:GLU:HG2	2.19	0.42
21:CT:408:TYR:CE2	21:CT:426:GLY:HA3	2.53	0.42
23:CV:84:LYS:HG3	23:CV:84:LYS:O	2.19	0.42
25:CY:373:ARG:C	25:CY:377:LYS:HZ2	2.28	0.42
25:CY:401:PHE:HZ	25:CY:451:GLU:OE2	2.02	0.42
26:Cb:293:VAL:O	26:Cb:294:ARG:HB3	2.19	0.42
26:Cb:559:ARG:O	26:Cb:563:VAL:HG23	2.19	0.42
29:LC:158:VAL:HG22	29:LC:222:LEU:HD22	2.01	0.42
32:LH:167:MET:SD	32:LH:196:SER:HB3	2.60	0.42
33:LK:106:LEU:HD11	33:LK:160:ILE:HG21	2.01	0.42
33:LK:112:ILE:HG22	33:LK:132:ILE:HG12	2.01	0.42
1:C1:72:C:N3	1:C1:74:G:C5	2.87	0.42
1:C1:981:C:H5''	1:C1:982:G:H5'	1.99	0.42
1:C1:1158:C:OP2	1:C1:1159:G:H3'	2.19	0.42
1:C1:1899:U:H2'	1:C1:1900:A:H8	1.83	0.42
5:CC:408:MET:HA	5:CC:411:TYR:CE1	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CF:158:SER:OG	7:CF:160:THR:HG22	2.19	0.42
7:CF:208:LEU:HD23	7:CF:208:LEU:HA	1.92	0.42
10:CI:190:TYR:CZ	10:CI:192:ALA:HB2	2.53	0.42
11:CJ:196:TYR:CZ	11:CJ:209:LEU:HD22	2.54	0.42
15:CN:154:LEU:HD12	15:CN:155:SER:N	2.34	0.42
20:CS:700:GLU:O	20:CS:704:ASP:HB2	2.19	0.42
21:CT:411:ILE:HD13	21:CT:419:LEU:HD13	2.00	0.42
24:CX:95:VAL:HG23	24:CX:100:SER:HB2	2.00	0.42
25:CY:616:ASP:CG	25:CY:666:ASN:HD21	2.25	0.42
29:LC:9:VAL:HB	29:LC:19:ALA:HB3	2.02	0.42
29:LC:41:THR:O	29:LC:45:LYS:HG3	2.19	0.42
29:LC:93:ASN:HA	29:LC:99:ARG:O	2.19	0.42
32:LH:85:VAL:HG23	32:LH:89:VAL:HG13	2.01	0.42
35:LM:16:VAL:HG11	35:LM:74:ARG:HA	2.01	0.42
1:C1:74:G:C2	1:C1:75:G:C8	3.07	0.42
1:C1:133:G:O2'	1:C1:134:G:O5'	2.38	0.42
1:C1:214:A:O2'	1:C1:216:C:OP2	2.31	0.42
1:C1:768:G:H2'	1:C1:769:C:H6	1.84	0.42
1:C1:796:G:H2'	1:C1:797:A:C8	2.55	0.42
1:C1:977:A:C2	1:C1:1036:A:H1'	2.54	0.42
1:C1:1886:C:H41	42:LV:66:LYS:HB2	1.84	0.42
1:C1:2567:A:H2'	1:C1:2568:G:H8	1.84	0.42
1:C1:3162:A:H5''	1:C1:3163:G:C5	2.54	0.42
1:C1:3304:C:H2'	1:C1:3305:U:C6	2.54	0.42
4:CB:49:LEU:HD11	6:CE:459:LEU:HD21	2.00	0.42
6:CE:135:THR:OG1	6:CE:138:GLN:HG3	2.19	0.42
9:CH:117:TYR:HB3	12:CK:177:LEU:HD11	2.02	0.42
9:CH:447:TYR:O	9:CH:450:ILE:HG22	2.18	0.42
11:CJ:386:ILE:HG23	11:CJ:465:ILE:HD12	2.01	0.42
15:CN:162:HIS:HB3	15:CN:165:THR:HG23	2.00	0.42
17:CP:324:LEU:HB2	17:CP:331:LEU:HD11	2.01	0.42
17:CP:367:ALA:O	17:CP:370:PHE:HB2	2.19	0.42
20:CS:573:ASP:O	20:CS:577:LYS:HG2	2.20	0.42
20:CS:820:LYS:HB3	20:CS:820:LYS:HE3	1.86	0.42
25:CY:558:LEU:HD22	25:CY:569:ILE:HG21	2.01	0.42
25:CY:573:SER:O	25:CY:577:GLU:OE1	2.37	0.42
26:Cb:426:ALA:O	26:Cb:430:ILE:HG12	2.20	0.42
14:LF:43:ASN:O	14:LF:47:ARG:HG2	2.19	0.42
1:C1:2087:A:H2'	1:C1:2088:A:O4'	2.19	0.42
1:C1:3277:G:H2'	1:C1:3278:C:C6	2.54	0.42
4:CB:48:ASN:HA	6:CE:484:ASP:OD1	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CI:306:VAL:HA	10:CI:309:GLU:CG	2.45	0.42
11:CJ:266:ALA:HB1	11:CJ:269:ALA:HB3	2.00	0.42
18:CQ:92:ALA:O	18:CQ:93:MET:C	2.63	0.42
25:CY:664:ASN:OD1	25:CY:665:LYS:N	2.52	0.42
26:Cb:158:ARG:HB3	26:Cb:829:GLY:HA2	2.01	0.42
28:LB:24:ARG:HH11	28:LB:26:ARG:HB3	1.84	0.42
40:LS:26:ARG:O	41:LT:150:THR:HA	2.20	0.42
42:LV:25:MET:HE1	42:LV:80:ILE:CG2	2.49	0.42
1:C1:663:G:H2'	1:C1:767:A:H61	1.85	0.42
1:C1:788:A:N6	1:C1:915:G:H22	2.18	0.42
1:C1:1216:G:H2'	1:C1:1217:U:C5	2.54	0.42
1:C1:1323:U:H2'	1:C1:1324:C:H6	1.82	0.42
1:C1:3005:A:H4'	28:LB:53:MET:HE2	2.01	0.42
2:C2:201:U:H2'	2:C2:202:C:C6	2.54	0.42
4:CB:71:HIS:ND1	4:CB:238:SER:HA	2.35	0.42
6:CE:488:ASN:C	6:CE:488:ASN:HD22	2.27	0.42
8:CG:29:PRO:HD3	24:CX:98:ARG:NH2	2.29	0.42
9:CH:468:LEU:HD23	9:CH:468:LEU:HA	1.86	0.42
15:CN:23:TYR:CD2	15:CN:92:ILE:HD13	2.53	0.42
18:CQ:80:ARG:HG2	18:CQ:80:ARG:NH1	2.35	0.42
19:CR:196:GLN:OE1	19:CR:196:GLN:HA	2.20	0.42
19:CR:224:ASP:OD1	19:CR:228:ARG:NH1	2.53	0.42
21:CT:525:LEU:HD11	25:CY:645:PRO:HB2	2.01	0.42
24:CX:98:ARG:HA	24:CX:101:MET:HE3	2.02	0.42
25:CY:380:ILE:CD1	25:CY:419:VAL:HA	2.50	0.42
25:CY:632:LEU:HD22	25:CY:633:TRP:CE2	2.55	0.42
25:CY:738:GLU:O	25:CY:739:ALA:C	2.62	0.42
26:Cb:545:TYR:HA	26:Cb:548:THR:HG22	2.02	0.42
28:LB:189:VAL:O	28:LB:193:VAL:HG23	2.19	0.42
42:LV:88:LYS:HE3	42:LV:88:LYS:HB2	1.78	0.42
47:Lf:34:ILE:HG12	47:Lf:102:ILE:HD13	2.01	0.42
1:C1:461:A:H2'	1:C1:462:C:C6	2.55	0.42
1:C1:764:A:H5''	1:C1:765:G:H5'	2.02	0.42
1:C1:1193:U:O2'	40:LS:113:ARG:NH1	2.53	0.42
1:C1:2295:C:H2'	1:C1:2296:U:C6	2.55	0.42
6:CE:243:ARG:HG3	6:CE:247:HIS:HD2	1.84	0.42
11:CJ:377:GLU:OE2	11:CJ:422:ARG:HG3	2.19	0.42
15:CN:53:ILE:HG12	15:CN:59:ILE:HG22	2.00	0.42
21:CT:410:ARG:O	21:CT:413:LYS:HG3	2.19	0.42
26:Cb:194:LEU:HD13	26:Cb:224:LEU:HD21	2.01	0.42
26:Cb:305:LEU:HD11	26:Cb:466:ALA:HB2	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Cb:602:THR:HG23	26:Cb:625:ARG:HH21	1.84	0.42
33:LK:109:ILE:HD11	33:LK:143:VAL:HG21	2.01	0.42
35:LM:73:PRO:HG2	35:LM:76:ALA:HB2	2.01	0.42
1:C1:435:C:H2'	1:C1:436:G:H8	1.84	0.42
1:C1:557:U:H2'	1:C1:558:G:C8	2.54	0.42
1:C1:731:G:C2	1:C1:732:A:C8	3.07	0.42
1:C1:737:U:H2'	1:C1:738:C:C6	2.55	0.42
1:C1:910:A:OP1	29:LC:62:SER:OG	2.28	0.42
1:C1:2741:U:H2'	1:C1:2742:G:C8	2.54	0.42
1:C1:3152:G:H4'	1:C1:3153:U:H5''	2.00	0.42
5:CC:170:ASN:OD1	5:CC:187:GLY:HA3	2.19	0.42
6:CE:441:TYR:HE2	6:CE:460:LEU:HD12	1.85	0.42
6:CE:460:LEU:HD13	6:CE:469:PHE:CE2	2.54	0.42
7:CF:37:TYR:HA	7:CF:106:ASN:OD1	2.20	0.42
17:CP:508:ILE:HB	17:CP:581:PHE:HB2	2.01	0.42
18:CQ:2:ARG:NH1	18:CQ:4:GLU:OE2	2.52	0.42
21:CT:397:GLN:O	21:CT:401:LEU:HD23	2.20	0.42
25:CY:421:LYS:O	25:CY:424:TYR:HB3	2.20	0.42
25:CY:718:LEU:O	25:CY:722:VAL:HG12	2.20	0.42
26:Cb:137:GLY:HA3	26:Cb:431:ASP:OD2	2.20	0.42
26:Cb:479:LEU:HB3	26:Cb:559:ARG:NE	2.31	0.42
30:LE:98:ASN:HB3	30:LE:101:TYR:HD2	1.83	0.42
31:LG:81:PHE:HA	31:LG:182:ILE:HD13	2.02	0.42
51:Lq:160:LYS:HD3	51:Lq:160:LYS:HA	1.90	0.42
1:C1:174:C:N3	1:C1:230:A:C6	2.88	0.42
1:C1:419:C:OP1	46:Le:16:LYS:HD3	2.20	0.42
1:C1:574:G:H2'	1:C1:575:A:H8	1.84	0.42
1:C1:1162:G:C4	1:C1:1164:G:C8	3.08	0.42
1:C1:2898:A:C5	1:C1:2903:G:C8	3.08	0.42
1:C1:2927:A:O3'	8:CG:149:ARG:NH2	2.53	0.42
1:C1:3023:U:H2'	1:C1:3024:C:C6	2.54	0.42
1:C1:3070:A:H2'	1:C1:3071:A:O4'	2.19	0.42
6:CE:173:LEU:HD23	6:CE:178:PHE:CD2	2.55	0.42
6:CE:512:LYS:HB3	6:CE:512:LYS:HE3	1.88	0.42
9:CH:51:PHE:HA	9:CH:54:GLU:OE1	2.20	0.42
11:CJ:49:ASP:OD2	11:CJ:52:LYS:HG2	2.20	0.42
11:CJ:242:ASN:HB2	11:CJ:253:TYR:HE1	1.84	0.42
15:CN:200:ASN:OD1	15:CN:203:LEU:N	2.53	0.42
17:CP:367:ALA:O	17:CP:371:LEU:HG	2.20	0.42
21:CT:250:VAL:O	21:CT:254:PRO:HG3	2.20	0.42
26:Cb:372:PHE:HB3	26:Cb:453:ARG:NH1	2.35	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Cb:422:VAL:HG21	26:Cb:427:ALA:HB2	2.01	0.42
29:LC:108:ARG:O	29:LC:108:ARG:HG2	2.20	0.42
29:LC:317:LYS:HB2	29:LC:325:ILE:HG13	2.02	0.42
38:LP:67:THR:HB	38:LP:80:ARG:HB3	2.02	0.42
48:Lh:34:LEU:O	48:Lh:38:LYS:CB	2.68	0.42
51:Lq:120:ILE:N	51:Lq:121:PRO:HD3	2.35	0.42
51:Lq:128:LEU:O	51:Lq:128:LEU:HD23	2.19	0.42
1:C1:139:C:H2'	1:C1:140:G:O4'	2.19	0.42
1:C1:917:A:H2'	1:C1:919:C:C5	2.54	0.42
1:C1:975:G:H22	1:C1:1035:A:H2'	1.85	0.42
1:C1:1116:G:H4'	22:CU:317:VAL:HG21	2.02	0.42
1:C1:2323:A:H2'	1:C1:2324:C:C6	2.55	0.42
1:C1:2840:U:H2'	1:C1:2841:U:C6	2.55	0.42
1:C1:2992:C:H5'	32:LH:161:ILE:HD12	2.00	0.42
3:CA:91:PHE:HB3	3:CA:103:TRP:HB2	2.02	0.42
6:CE:361:ILE:HD12	6:CE:426:VAL:HG21	2.02	0.42
9:CH:474:TYR:CE1	18:CQ:102:ARG:NH1	2.88	0.42
10:CI:207:PHE:HB3	10:CI:235:PHE:HZ	1.84	0.42
13:CL:223:HIS:C	13:CL:225:VAL:H	2.28	0.42
15:CN:123:ARG:NH1	15:CN:127:GLU:OE1	2.53	0.42
15:CN:157:GLN:OE1	15:CN:223:ARG:HD2	2.20	0.42
17:CP:280:LEU:HD13	17:CP:480:PHE:CZ	2.55	0.42
17:CP:343:GLN:NE2	17:CP:345:PHE:HE1	2.17	0.42
19:CR:214:LYS:HA	19:CR:214:LYS:HD2	1.83	0.42
21:CT:293:ASP:N	21:CT:329:ARG:HH12	2.18	0.42
25:CY:440:SER:HA	25:CY:443:ASN:HD22	1.83	0.42
26:Cb:210:ASN:HD22	26:Cb:832:GLU:HG3	1.85	0.42
33:LK:128:GLY:HA2	33:LK:131:GLU:OE1	2.20	0.42
35:LM:19:VAL:HG23	35:LM:65:THR:OG1	2.20	0.42
37:LO:178:ARG:O	37:LO:182:GLU:HG3	2.20	0.42
40:LS:71:LYS:HZ2	40:LS:73:LYS:HG2	1.85	0.42
46:Le:61:ASN:HB3	46:Le:64:THR:OG1	2.20	0.42
47:Lf:15:HIS:HA	47:Lf:32:ILE:HD13	2.01	0.42
1:C1:926:C:H2'	1:C1:927:C:H6	1.84	0.41
1:C1:927:C:H2'	1:C1:928:G:H8	1.85	0.41
5:CC:237:GLU:OE1	5:CC:240:ARG:NH2	2.53	0.41
7:CF:45:VAL:HG23	7:CF:45:VAL:O	2.20	0.41
8:CG:152:ALA:O	8:CG:156:ARG:HG3	2.19	0.41
9:CH:90:PHE:HE1	9:CH:152:VAL:HG11	1.85	0.41
10:CI:207:PHE:HB3	10:CI:235:PHE:CZ	2.55	0.41
15:CN:17:ALA:HB2	15:CN:34:PHE:HE2	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CN:104:LEU:HA	15:CN:107:VAL:HG22	2.02	0.41
21:CT:318:ASP:C	21:CT:320:SER:H	2.28	0.41
28:LB:29:VAL:HG13	28:LB:340:ARG:HD3	2.02	0.41
31:LG:175:LYS:HE3	49:Li:48:PHE:HE1	1.85	0.41
37:LO:170:TYR:CE2	37:LO:174:LYS:HE3	2.54	0.41
48:Lh:27:LEU:HG	48:Lh:56:ILE:HG12	2.02	0.41
51:Lq:83:ASP:N	51:Lq:83:ASP:OD1	2.53	0.41
1:C1:920:U:H2'	1:C1:921:G:H8	1.85	0.41
1:C1:1049:C:H5'	1:C1:1050:C:OP2	2.20	0.41
1:C1:1880:A:H2'	1:C1:1881:G:C8	2.55	0.41
1:C1:1903:U:H3	1:C1:2071:U:H3	1.68	0.41
1:C1:2314:A:H5''	38:LP:83:TRP:O	2.20	0.41
1:C1:2409:A:H2'	1:C1:2410:G:O4'	2.21	0.41
2:C2:91:C:H2'	2:C2:92:A:C8	2.55	0.41
2:C2:139:U:H2'	2:C2:140:G:C8	2.55	0.41
5:CC:287:GLU:OE1	31:LG:112:LEU:HD21	2.21	0.41
5:CC:310:GLU:OE2	5:CC:311:GLU:HG3	2.20	0.41
9:CH:331:LYS:HE3	9:CH:331:LYS:HB3	1.90	0.41
11:CJ:178:TYR:CE2	11:CJ:245:LEU:HD13	2.56	0.41
12:CK:17:ARG:NH1	32:LH:215:LEU:HA	2.36	0.41
12:CK:101:ALA:O	12:CK:105:GLN:HG3	2.21	0.41
14:CM:172:ASN:O	14:CM:176:GLU:OE1	2.37	0.41
18:CQ:1:MET:HE3	28:LB:71:GLU:OE1	2.19	0.41
20:CS:494:ARG:CZ	21:CT:185:ARG:HH22	2.33	0.41
21:CT:174:VAL:O	21:CT:178:VAL:HG22	2.20	0.41
28:LB:32:PHE:HD1	28:LB:44:THR:HG21	1.85	0.41
29:LC:164:ALA:HB2	29:LC:221:GLU:HG2	2.02	0.41
31:LG:196:LYS:HB2	31:LG:196:LYS:HE2	1.83	0.41
31:LG:208:SER:HA	31:LG:211:LYS:HG2	2.02	0.41
1:C1:47:C:OP2	1:C1:48:A:O2'	2.38	0.41
1:C1:257:A:H5'	1:C1:258:C:OP2	2.20	0.41
1:C1:403:U:H2'	1:C1:404:G:C8	2.53	0.41
1:C1:485:G:H2'	1:C1:486:C:C6	2.56	0.41
1:C1:523:A:H2'	1:C1:524:A:H8	1.84	0.41
1:C1:615:A:H2'	1:C1:616:C:C6	2.55	0.41
1:C1:626:G:OP1	46:Le:38:GLY:HA3	2.20	0.41
1:C1:1087:C:H2'	1:C1:1088:G:H8	1.84	0.41
4:CB:68:THR:HA	4:CB:279:ARG:HB3	2.03	0.41
5:CC:171:THR:HB	5:CC:188:TYR:O	2.19	0.41
5:CC:326:LEU:HG	11:CJ:128:ARG:CZ	2.50	0.41
5:CC:336:ASN:OD1	5:CC:336:ASN:N	2.52	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CJ:32:ASP:HA	11:CJ:35:LYS:NZ	2.35	0.41
11:CJ:104:ALA:O	11:CJ:107:GLU:HG2	2.20	0.41
11:CJ:387:LEU:HB3	11:CJ:392:CYS:HB3	2.03	0.41
12:CK:148:LYS:NZ	12:CK:172:ILE:HG13	2.35	0.41
14:CM:89:LEU:HD11	14:CM:122:PHE:HB3	2.02	0.41
14:CM:188:GLU:HA	14:CM:191:ILE:HD12	2.02	0.41
17:CP:287:LEU:HG	17:CP:288:PHE:CD2	2.56	0.41
17:CP:303:PRO:O	26:Cb:718:TYR:OH	2.16	0.41
21:CT:154:ARG:HA	21:CT:157:GLU:CD	2.46	0.41
21:CT:525:LEU:CG	21:CT:602:GLN:HE22	2.31	0.41
24:CX:107:MET:HE3	24:CX:133:ARG:NH2	2.36	0.41
25:CY:589:LYS:HA	25:CY:589:LYS:HD2	1.83	0.41
25:CY:675:VAL:C	25:CY:679:LYS:HZ3	2.27	0.41
26:Cb:852:GLN:O	26:Cb:853:MET:HE2	2.20	0.41
45:Ld:19:GLU:HB2	45:Ld:80:ARG:HH21	1.85	0.41
46:Le:113:ALA:HA	46:Le:116:LEU:HB2	2.02	0.41
47:Lf:47:LEU:HD21	47:Lf:76:PRO:HD3	2.02	0.41
1:C1:427:C:H2'	1:C1:428:A:C8	2.55	0.41
1:C1:1156:G:H2'	1:C1:1157:C:C5	2.56	0.41
1:C1:1293:G:H1'	1:C1:2343:G:OP1	2.21	0.41
1:C1:2381:A:H2'	1:C1:2382:C:C6	2.55	0.41
1:C1:3188:U:H2'	1:C1:3189:G:H8	1.83	0.41
1:C1:3333:A:H2'	1:C1:3334:U:C6	2.55	0.41
4:CB:113:ALA:C	4:CB:121:ARG:HH12	2.25	0.41
4:CB:114:ASP:HB2	4:CB:115:GLU:OE1	2.21	0.41
5:CC:348:PRO:HB3	5:CC:352:LEU:HD12	2.02	0.41
5:CC:354:TYR:HD2	5:CC:387:TYR:HB2	1.84	0.41
8:CG:41:GLN:HE22	8:CG:61:ARG:HG3	1.85	0.41
9:CH:242:LEU:HB3	9:CH:277:PHE:CE1	2.52	0.41
11:CJ:367:PHE:HA	11:CJ:370:PHE:HD2	1.86	0.41
21:CT:531:LEU:HD11	25:CY:540:ARG:NH2	2.35	0.41
28:LB:53:MET:HG2	28:LB:77:THR:HA	2.02	0.41
28:LB:189:VAL:HA	28:LB:192:LYS:HG2	2.02	0.41
32:LH:123:PHE:CE2	32:LH:190:LEU:HB2	2.55	0.41
1:C1:29:C:H4'	1:C1:62:A:H4'	2.02	0.41
1:C1:424:G:H2'	1:C1:425:A:H8	1.85	0.41
1:C1:585:G:H1	1:C1:596:G:H5''	1.85	0.41
1:C1:650:C:H2'	1:C1:651:A:C8	2.56	0.41
1:C1:1269:A:H2'	1:C1:1270:U:O4'	2.21	0.41
1:C1:2418:A:H2	1:C1:2445:G:H1'	1.86	0.41
1:C1:2448:A:H1'	1:C1:2449:U:C6	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2774:G:H21	22:CU:316:GLN:CD	2.28	0.41
3:CA:142:PHE:HB2	22:CU:221:VAL:HG22	2.01	0.41
6:CE:276:ASP:O	6:CE:280:GLN:HG3	2.21	0.41
6:CE:427:ASP:O	6:CE:457:ARG:HG2	2.20	0.41
7:CF:160:THR:HG23	7:CF:161:LEU:HD12	2.02	0.41
9:CH:344:SER:O	9:CH:347:LEU:HG	2.21	0.41
11:CJ:66:THR:O	11:CJ:70:GLN:HG2	2.21	0.41
12:CK:38:ASN:O	12:CK:42:LEU:HG	2.20	0.41
13:CL:69:ARG:O	13:CL:73:ARG:HD2	2.20	0.41
21:CT:438:PHE:O	21:CT:442:LEU:HG	2.21	0.41
25:CY:420:LEU:HD22	25:CY:456:ASP:OD1	2.21	0.41
40:LS:131:LYS:HG3	40:LS:132:THR:O	2.19	0.41
45:Ld:24:LEU:O	45:Ld:28:LEU:HB2	2.20	0.41
1:C1:331:C:OP1	1:C1:1362:G:O2'	2.34	0.41
1:C1:542:U:H3'	1:C1:543:G:C8	2.54	0.41
1:C1:907:A:H2'	1:C1:908:C:H6	1.85	0.41
1:C1:1340:C:H2'	1:C1:1341:C:H6	1.86	0.41
2:C2:19:C:C4	2:C2:20:U:C4	3.09	0.41
4:CB:71:HIS:CE1	4:CB:238:SER:HA	2.55	0.41
4:CB:97:VAL:CG2	4:CB:124:ILE:HA	2.48	0.41
8:CG:90:LEU:O	8:CG:94:ALA:HB2	2.21	0.41
9:CH:405:ARG:HH21	15:CN:33:ASN:ND2	2.18	0.41
10:CI:222:LYS:HD2	10:CI:223:LYS:HZ3	1.86	0.41
11:CJ:65:TYR:O	11:CJ:69:ILE:HG12	2.20	0.41
11:CJ:458:PRO:O	11:CJ:462:TRP:HE3	2.03	0.41
11:CJ:483:PRO:HA	11:CJ:484:PRO:HD3	1.96	0.41
12:CK:134:LYS:O	12:CK:138:THR:HG23	2.20	0.41
14:CM:239:GLU:HA	14:CM:242:ASN:HD22	1.85	0.41
18:CQ:24:ASN:O	42:LV:119:PRO:HD3	2.20	0.41
21:CT:238:ILE:HD12	21:CT:238:ILE:HA	1.90	0.41
21:CT:593:CYS:O	21:CT:597:MET:HG2	2.21	0.41
22:CU:268:PRO:HG2	22:CU:271:TYR:HB2	2.02	0.41
25:CY:674:VAL:O	25:CY:677:VAL:HB	2.20	0.41
25:CY:709:LYS:N	25:CY:709:LYS:HD2	2.35	0.41
26:Cb:493:ARG:HH22	26:Cb:576:PHE:HB2	1.86	0.41
26:Cb:603:ILE:HA	26:Cb:606:ILE:HD12	2.02	0.41
28:LB:26:ARG:HA	28:LB:336:ILE:HG21	2.02	0.41
28:LB:206:ILE:HD12	28:LB:206:ILE:HA	1.92	0.41
29:LC:216:GLU:HG3	29:LC:217:HIS:ND1	2.35	0.41
37:LO:16:LEU:HD21	37:LO:131:LEU:HD11	2.02	0.41
37:LO:77:ALA:HB1	37:LO:108:GLU:OE1	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:LP:71:ALA:O	38:LP:74:LYS:HG3	2.20	0.41
46:Le:77:VAL:HG23	46:Le:82:ASP:CB	2.51	0.41
1:C1:1055:U:H2'	1:C1:1056:U:C6	2.55	0.41
1:C1:1090:C:H2'	1:C1:1091:A:C8	2.54	0.41
1:C1:1426:G:H2'	1:C1:1427:U:O4'	2.21	0.41
1:C1:2457:C:H2'	1:C1:2458:U:H6	1.85	0.41
2:C2:110:C:C5	50:Lj:20:ARG:HG3	2.56	0.41
4:CB:57:VAL:O	4:CB:248:ALA:HB3	2.20	0.41
6:CE:172:MET:SD	6:CE:173:LEU:N	2.94	0.41
7:CF:27:PHE:O	7:CF:31:ARG:HG3	2.21	0.41
9:CH:169:LEU:HD23	9:CH:248:ALA:HB3	2.02	0.41
10:CI:310:GLU:O	10:CI:313:ARG:HD3	2.21	0.41
10:CI:320:LEU:HD11	10:CI:325:TYR:HB3	2.02	0.41
11:CJ:78:LEU:O	11:CJ:82:ARG:HG3	2.20	0.41
19:CR:231:LYS:HB3	19:CR:231:LYS:HE2	1.81	0.41
21:CT:662:GLU:OE1	21:CT:662:GLU:N	2.51	0.41
22:CU:287:GLN:O	22:CU:291:GLU:OE1	2.38	0.41
23:CV:30:ARG:HA	46:Le:85:LEU:HD21	2.01	0.41
14:LF:46:LYS:O	14:LF:50:ILE:HG12	2.20	0.41
45:Ld:14:ASP:CB	45:Ld:87:ARG:HH12	2.33	0.41
1:C1:448:A:H62	1:C1:467:G:H1'	1.85	0.41
1:C1:482:C:H2'	1:C1:483:A:C8	2.56	0.41
1:C1:689:C:H2'	1:C1:690:G:C8	2.56	0.41
1:C1:907:A:H2'	1:C1:908:C:C6	2.56	0.41
1:C1:1152:A:H2'	1:C1:1153:G:O4'	2.20	0.41
1:C1:2451:C:H2'	1:C1:2452:C:O4'	2.20	0.41
1:C1:3131:A:HO2'	1:C1:3132:U:P	2.42	0.41
1:C1:3255:G:OP1	28:LB:116:ARG:NH2	2.54	0.41
6:CE:258:LEU:HB3	6:CE:286:PRO:HG2	2.02	0.41
7:CF:21:GLU:CD	7:CF:25:ARG:HH11	2.24	0.41
11:CJ:379:PRO:HB2	11:CJ:382:PRO:HG2	2.03	0.41
15:CN:13:VAL:HG13	15:CN:34:PHE:HZ	1.86	0.41
17:CP:249:PHE:O	17:CP:253:ALA:HB2	2.21	0.41
17:CP:268:LYS:HE2	17:CP:268:LYS:HB2	1.93	0.41
17:CP:376:LEU:HB2	17:CP:509:VAL:CG2	2.50	0.41
18:CQ:42:MET:HB3	18:CQ:44:ARG:NH1	2.36	0.41
23:CV:88:ARG:HB3	14:LF:7:PRO:HD2	2.02	0.41
26:Cb:602:THR:H	26:Cb:625:ARG:NH2	2.17	0.41
27:Cz:40:ARG:HE	27:Cz:43:LYS:NZ	2.15	0.41
27:Cz:75:GLU:OE2	27:Cz:79:ARG:NE	2.54	0.41
28:LB:116:ARG:HG2	28:LB:122:TRP:CD2	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LE:81:LEU:O	30:LE:96:ARG:HA	2.21	0.41
30:LE:170:ILE:HD12	30:LE:174:LYS:HE2	2.03	0.41
51:Lq:10:ARG:HA	51:Lq:13:VAL:HG12	2.03	0.41
1:C1:12:G:H2'	1:C1:13:A:C8	2.56	0.41
1:C1:326:A:H5''	19:CR:18:ARG:NH1	2.36	0.41
1:C1:655:U:H2'	1:C1:656:U:H6	1.85	0.41
1:C1:670:U:H2'	1:C1:671:G:O4'	2.20	0.41
1:C1:731:G:N3	1:C1:731:G:H2'	2.35	0.41
1:C1:1403:G:H2'	1:C1:1404:G:H8	1.86	0.41
1:C1:2882:U:H2'	1:C1:2883:C:C6	2.56	0.41
1:C1:3109:A:H4'	1:C1:3233:C:H1'	2.03	0.41
2:C2:118:C:H2'	2:C2:119:C:C6	2.55	0.41
3:CA:195:GLU:HB2	3:CA:234:ILE:HG21	2.03	0.41
4:CB:60:THR:HA	4:CB:61:PRO:HD3	1.94	0.41
5:CC:149:TYR:HE2	6:CE:571:ARG:HH12	1.62	0.41
5:CC:186:ILE:O	5:CC:186:ILE:HG23	2.21	0.41
6:CE:373:TYR:O	6:CE:377:LEU:HD23	2.21	0.41
9:CH:166:THR:HG22	9:CH:167:ARG:N	2.35	0.41
9:CH:235:GLU:O	9:CH:238:SER:OG	2.33	0.41
9:CH:455:ASP:O	9:CH:459:GLN:HG3	2.20	0.41
11:CJ:84:GLN:HG3	11:CJ:121:TYR:HE1	1.86	0.41
11:CJ:463:ASP:CG	11:CJ:471:LYS:HG3	2.45	0.41
17:CP:254:GLU:HB2	17:CP:262:TYR:OH	2.20	0.41
17:CP:422:ILE:HG12	17:CP:435:VAL:HG21	2.03	0.41
20:CS:730:ILE:H	20:CS:730:ILE:HG13	1.66	0.41
21:CT:279:PHE:O	21:CT:283:ARG:HD3	2.21	0.41
21:CT:444:GLU:OE1	24:CX:120:ILE:HG22	2.21	0.41
21:CT:575:LEU:HD13	21:CT:618:VAL:HG11	2.03	0.41
25:CY:401:PHE:CE1	25:CY:448:SER:HB2	2.56	0.41
25:CY:470:GLN:O	25:CY:473:ILE:HG22	2.21	0.41
25:CY:735:LEU:HD23	25:CY:735:LEU:HA	1.92	0.41
26:Cb:484:PHE:HD2	26:Cb:485:LEU:HD22	1.86	0.41
28:LB:113:GLU:HB2	28:LB:177:ALA:HB2	2.02	0.41
28:LB:218:VAL:HG11	28:LB:329:VAL:HG13	2.03	0.41
29:LC:365:ALA:HB3	40:LS:28:ARG:HD2	2.03	0.41
14:LF:203:GLN:H	14:LF:203:GLN:CD	2.28	0.41
33:LK:127:GLY:O	33:LK:131:GLU:OE1	2.39	0.41
34:LL:79:GLU:OE2	34:LL:112:ASN:HB3	2.21	0.41
35:LM:13:ARG:HG2	35:LM:13:ARG:NH1	2.35	0.41
42:LV:25:MET:CE	42:LV:38:ILE:HD11	2.48	0.41
42:LV:106:ASN:OD1	42:LV:110:GLU:N	2.30	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:LY:110:LEU:HD23	44:LY:110:LEU:HA	1.91	0.41
47:Lf:54:VAL:HG13	47:Lf:66:ILE:HG23	2.02	0.41
51:Lq:113:SER:O	51:Lq:117:ILE:HB	2.21	0.41
51:Lq:205:THR:HG23	51:Lq:207:LYS:HD3	2.02	0.41
1:C1:142:U:C4	31:LG:160:VAL:HG13	2.56	0.41
1:C1:645:G:N2	29:LC:94:MET:HB2	2.36	0.41
1:C1:1864:C:H3'	1:C1:1865:A:H5''	2.02	0.41
1:C1:2738:A:H4'	1:C1:2739:U:OP1	2.21	0.41
2:C2:4:C:C2	2:C2:5:U:C5	3.09	0.41
3:CA:74:LEU:O	3:CA:77:LEU:HB2	2.21	0.41
4:CB:19:ASP:HB3	4:CB:22:GLN:CG	2.51	0.41
4:CB:99:LEU:HB3	4:CB:127:VAL:HG12	2.02	0.41
5:CC:238:LEU:HB3	20:CS:676:LEU:HD13	2.03	0.41
11:CJ:397:TRP:H	11:CJ:405:ALA:HB1	1.86	0.41
21:CT:401:LEU:HD12	21:CT:434:ILE:HD11	2.03	0.41
21:CT:424:LEU:HB3	21:CT:488:THR:CG2	2.42	0.41
25:CY:456:ASP:HB2	25:CY:459:LEU:HD21	2.03	0.41
31:LG:150:LYS:O	31:LG:204:THR:HG23	2.21	0.41
36:LN:142:ILE:HG22	36:LN:152:CYS:SG	2.60	0.41
36:LN:158:HIS:HB3	36:LN:161:CYS:HB2	2.02	0.41
39:LQ:152:ASP:OD1	39:LQ:152:ASP:N	2.54	0.41
42:LV:99:ASP:N	42:LV:99:ASP:OD1	2.54	0.41
45:Ld:28:LEU:HD11	45:Ld:40:ALA:HB2	2.02	0.41
45:Ld:82:ARG:HD2	45:Ld:117:VAL:HG11	2.03	0.41
51:Lq:114:GLU:O	51:Lq:117:ILE:HG22	2.21	0.41
1:C1:253:U:N3	6:CE:368:ASN:ND2	2.65	0.40
1:C1:1201:C:O2'	1:C1:1268:A:N1	2.46	0.40
1:C1:1332:A:O2'	1:C1:1334:A:OP1	2.39	0.40
1:C1:2562:U:H2'	1:C1:2563:G:O4'	2.20	0.40
1:C1:2764:U:H2'	1:C1:2765:U:C6	2.56	0.40
1:C1:2881:U:H2'	1:C1:2882:U:C6	2.55	0.40
1:C1:3209:U:H4'	1:C1:3210:U:O5'	2.20	0.40
3:CA:133:LEU:HB3	3:CA:173:LYS:HG3	2.02	0.40
6:CE:173:LEU:HD22	6:CE:235:ASN:HB3	2.02	0.40
7:CF:170:MET:HE1	7:CF:212:PHE:CZ	2.55	0.40
9:CH:391:LYS:HD3	9:CH:392:LYS:O	2.21	0.40
11:CJ:84:GLN:HG3	11:CJ:121:TYR:CE1	2.56	0.40
12:CK:126:GLY:HA2	17:CP:350:PRO:HG3	2.02	0.40
13:CL:29:ALA:O	13:CL:33:ARG:HG3	2.20	0.40
14:CM:132:MET:O	14:CM:136:VAL:HG22	2.22	0.40
17:CP:571:TYR:HE1	26:Cb:711:ASP:HB2	1.86	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CQ:90:LEU:HA	18:CQ:93:MET:HG2	2.02	0.40
21:CT:283:ARG:HE	21:CT:320:SER:CB	2.33	0.40
23:CV:104:ARG:HB3	23:CV:107:LEU:HB2	2.03	0.40
25:CY:386:PHE:HA	25:CY:389:GLN:HG3	2.03	0.40
25:CY:542:ILE:HG23	25:CY:542:ILE:O	2.21	0.40
29:LC:47:LYS:HA	29:LC:47:LYS:HD2	1.84	0.40
33:LK:88:PRO:HA	33:LK:89:PRO:HD3	1.89	0.40
35:LM:19:VAL:HG12	35:LM:29:ALA:HB2	2.02	0.40
39:LQ:127:GLU:OE2	39:LQ:149:LEU:HD11	2.20	0.40
41:LT:34:TYR:CE1	41:LT:98:PRO:HD3	2.56	0.40
41:LT:116:LYS:HB3	41:LT:128:LEU:HD11	2.03	0.40
42:LV:106:ASN:HB2	42:LV:107:PRO:HD2	2.02	0.40
48:Lh:38:LYS:HG2	48:Lh:42:SER:HA	2.03	0.40
1:C1:671:G:H2'	1:C1:672:G:H8	1.85	0.40
1:C1:1054:G:H2'	1:C1:1055:U:H6	1.86	0.40
1:C1:1172:A:N3	1:C1:1172:A:H2'	2.37	0.40
1:C1:1190:C:H4'	7:CF:4:SER:H	1.87	0.40
1:C1:1210:A:H5''	7:CF:203:SER:HB3	2.03	0.40
1:C1:1332:A:H2'	1:C1:1334:A:C8	2.57	0.40
1:C1:2414:G:C2	1:C1:2424:G:H1'	2.57	0.40
1:C1:2769:A:H2'	1:C1:2770:C:C6	2.56	0.40
1:C1:2772:G:H2'	1:C1:2773:G:C8	2.56	0.40
1:C1:3107:A:H2'	1:C1:3108:U:O4'	2.22	0.40
3:CA:107:VAL:HG12	3:CA:249:SER:OG	2.21	0.40
11:CJ:169:GLU:HG2	11:CJ:173:HIS:HE1	1.87	0.40
12:CK:149:ARG:O	12:CK:149:ARG:HG2	2.22	0.40
17:CP:390:ALA:HB3	17:CP:391:PRO:HD3	2.02	0.40
21:CT:492:LEU:HD23	21:CT:492:LEU:HA	1.87	0.40
24:CX:98:ARG:HH11	24:CX:102:ASN:ND2	2.16	0.40
25:CY:444:LEU:HA	25:CY:447:ASN:OD1	2.21	0.40
26:Cb:22:PHE:HD2	26:Cb:292:LEU:CB	2.17	0.40
26:Cb:144:PHE:HB3	26:Cb:271:PHE:CE1	2.56	0.40
26:Cb:165:VAL:CG2	26:Cb:215:ILE:HG12	2.51	0.40
26:Cb:579:GLU:HG2	26:Cb:580:ALA:N	2.36	0.40
29:LC:223:VAL:O	29:LC:226:PHE:C	2.64	0.40
33:LK:105:SER:O	33:LK:109:ILE:HG13	2.20	0.40
48:Lh:13:TRP:CE3	50:Lj:87:ARG:NH1	2.88	0.40
1:C1:265:A:OP1	3:CA:42:ARG:NH2	2.55	0.40
1:C1:375:G:N2	1:C1:378:A:OP2	2.52	0.40
1:C1:725:A:H2'	1:C1:726:U:O4'	2.21	0.40
1:C1:886:U:O2'	1:C1:887:G:OP1	2.28	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1214:C:O2	7:CF:54:LYS:NZ	2.43	0.40
4:CB:42:ARG:NH2	4:CB:46:LYS:HG3	2.36	0.40
7:CF:143:TYR:HA	7:CF:156:PRO:HA	2.03	0.40
8:CG:20:MET:SD	8:CG:93:ASN:HB2	2.61	0.40
9:CH:172:ALA:HB2	9:CH:242:LEU:HD21	2.03	0.40
9:CH:449:TYR:CE2	18:CQ:72:ALA:HB2	2.56	0.40
11:CJ:78:LEU:O	11:CJ:81:PHE:HB2	2.20	0.40
11:CJ:148:LEU:CD1	11:CJ:238:LEU:HD12	2.50	0.40
11:CJ:160:VAL:HG13	11:CJ:164:MET:SD	2.61	0.40
15:CN:118:HIS:CD2	15:CN:146:VAL:HG22	2.56	0.40
17:CP:447:ILE:HB	17:CP:450:PHE:CE1	2.56	0.40
25:CY:394:ASP:OD1	25:CY:395:SER:N	2.55	0.40
25:CY:635:ARG:CZ	25:CY:713:TRP:HB3	2.52	0.40
26:Cb:135:ARG:O	26:Cb:140:LYS:NZ	2.55	0.40
26:Cb:447:PRO:O	26:Cb:451:VAL:HG23	2.21	0.40
29:LC:296:ILE:HD13	39:LQ:159:PRO:HB3	2.04	0.40
14:LF:151:ARG:HG3	14:LF:191:ILE:HD13	2.02	0.40
34:LL:56:PRO:HG3	34:LL:74:GLY:O	2.21	0.40
37:LO:76:ARG:HD2	37:LO:147:VAL:HG22	2.03	0.40
38:LP:55:LYS:HD2	38:LP:55:LYS:HA	1.92	0.40
40:LS:73:LYS:HE2	40:LS:75:PHE:HZ	1.87	0.40
47:Lf:16:LEU:HD11	47:Lf:33:LYS:HB2	2.02	0.40
48:Lh:32:SER:O	48:Lh:36:ILE:HG12	2.21	0.40
1:C1:791:A:H2'	1:C1:792:U:C6	2.56	0.40
1:C1:1088:G:H2'	1:C1:1089:A:H8	1.86	0.40
1:C1:1366:U:OP2	29:LC:206:ARG:HA	2.21	0.40
1:C1:2874:U:C2	1:C1:2875:G:C8	3.09	0.40
2:C2:66:A:H2'	2:C2:67:U:C6	2.56	0.40
3:CA:128:PHE:O	3:CA:129:GLN:HB2	2.22	0.40
4:CB:156:ASP:OD1	4:CB:156:ASP:N	2.51	0.40
5:CC:403:ARG:NH1	5:CC:406:ARG:HD2	2.36	0.40
11:CJ:123:LEU:HB3	11:CJ:126:ILE:HD11	2.03	0.40
17:CP:442:GLU:C	17:CP:444:PRO:HD2	2.46	0.40
21:CT:577:PRO:HA	21:CT:578:PRO:HD3	1.97	0.40
25:CY:488:ARG:HA	25:CY:488:ARG:NE	2.35	0.40
25:CY:495:TYR:O	25:CY:499:LEU:HD23	2.22	0.40
26:Cb:331:MET:HE3	26:Cb:332:PRO:HD2	2.03	0.40
29:LC:296:ILE:O	29:LC:300:LEU:HG	2.21	0.40
32:LH:123:PHE:CD1	32:LH:190:LEU:HD13	2.56	0.40
34:LL:18:TRP:O	34:LL:22:VAL:HB	2.20	0.40
1:C1:158:U:H2'	1:C1:159:G:C8	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:481:U:H2'	1:C1:482:C:H6	1.86	0.40
1:C1:766:G:H1	39:LQ:117:ASP:HA	1.87	0.40
1:C1:966:U:O2'	14:LF:108:ILE:HD11	2.21	0.40
1:C1:1215:G:C6	1:C1:1238:G:C6	3.09	0.40
1:C1:2782:G:OP2	13:CL:20:LEU:HD21	2.21	0.40
2:C2:122:C:H2'	2:C2:123:G:C8	2.56	0.40
2:C2:233:U:H3	2:C2:284:G:H1	1.69	0.40
3:CA:36:VAL:HG11	3:CA:59:LEU:HD23	2.03	0.40
4:CB:232:LEU:HD13	4:CB:234:HIS:NE2	2.37	0.40
4:CB:282:TYR:HB3	4:CB:290:ALA:HB1	2.03	0.40
14:CM:43:ASN:O	14:CM:47:ARG:HG2	2.21	0.40
14:CM:56:LYS:O	14:CM:57:TYR:C	2.64	0.40
14:CM:93:ILE:HD11	14:CM:245:ILE:HG22	2.04	0.40
25:CY:411:GLY:HA3	25:CY:416:ARG:CZ	2.52	0.40
28:LB:46:ALA:HA	28:LB:84:MET:HE1	2.04	0.40
29:LC:109:LYS:HE3	36:LN:203:ARG:HB2	2.04	0.40
31:LG:246:GLN:O	31:LG:250:GLU:OE1	2.39	0.40
36:LN:2:GLY:HA2	49:Li:45:ARG:HH22	1.85	0.40
39:LQ:101:ASN:C	39:LQ:103:ASN:H	2.30	0.40
40:LS:169:ARG:HA	40:LS:170:PRO:HD3	1.96	0.40
42:LV:82:ARG:HB2	42:LV:101:ALA:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
3	CA	247/316 (78%)	232 (94%)	15 (6%)	0	100	100
4	CB	256/391 (66%)	239 (93%)	17 (7%)	0	100	100
5	CC	283/801 (35%)	268 (95%)	14 (5%)	1 (0%)	30	61
6	CE	459/598 (77%)	444 (97%)	15 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	CF	243/270 (90%)	230 (95%)	11 (4%)	2 (1%)	16	47
8	CG	175/184 (95%)	167 (95%)	8 (5%)	0	100	100
9	CH	499/661 (76%)	470 (94%)	28 (6%)	1 (0%)	43	73
10	CI	144/414 (35%)	134 (93%)	10 (7%)	0	100	100
11	CJ	373/679 (55%)	355 (95%)	18 (5%)	0	100	100
12	CK	234/261 (90%)	221 (94%)	13 (6%)	0	100	100
13	CL	393/558 (70%)	361 (92%)	29 (7%)	3 (1%)	16	47
14	CM	219/249 (88%)	209 (95%)	10 (5%)	0	100	100
14	LF	245/249 (98%)	237 (97%)	7 (3%)	1 (0%)	30	61
15	CN	244/246 (99%)	228 (93%)	16 (7%)	0	100	100
16	CO	56/120 (47%)	55 (98%)	1 (2%)	0	100	100
17	CP	354/751 (47%)	332 (94%)	21 (6%)	1 (0%)	36	67
18	CQ	123/225 (55%)	119 (97%)	4 (3%)	0	100	100
19	CR	159/237 (67%)	156 (98%)	3 (2%)	0	100	100
20	CS	221/834 (26%)	213 (96%)	8 (4%)	0	100	100
21	CT	478/688 (70%)	456 (95%)	21 (4%)	1 (0%)	43	73
22	CU	174/451 (39%)	169 (97%)	4 (2%)	1 (1%)	21	52
23	CV	137/147 (93%)	134 (98%)	2 (2%)	1 (1%)	18	49
24	CX	86/203 (42%)	84 (98%)	2 (2%)	0	100	100
25	CY	351/788 (44%)	323 (92%)	27 (8%)	1 (0%)	36	67
26	Cb	622/924 (67%)	575 (92%)	45 (7%)	2 (0%)	36	67
27	Cz	68/123 (55%)	66 (97%)	2 (3%)	0	100	100
28	LB	335/392 (86%)	315 (94%)	18 (5%)	2 (1%)	21	52
29	LC	360/365 (99%)	344 (96%)	16 (4%)	0	100	100
30	LE	175/200 (88%)	167 (95%)	7 (4%)	1 (1%)	21	52
31	LG	200/262 (76%)	192 (96%)	8 (4%)	0	100	100
32	LH	188/192 (98%)	181 (96%)	7 (4%)	0	100	100
33	LK	142/165 (86%)	134 (94%)	6 (4%)	2 (1%)	9	34
34	LL	115/213 (54%)	106 (92%)	8 (7%)	1 (1%)	14	44
35	LM	135/142 (95%)	128 (95%)	7 (5%)	0	100	100
36	LN	179/203 (88%)	168 (94%)	9 (5%)	2 (1%)	11	39

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	LO	202/204 (99%)	190 (94%)	10 (5%)	2 (1%)	12	41
38	LP	147/187 (79%)	144 (98%)	3 (2%)	0	100	100
39	LQ	127/213 (60%)	122 (96%)	5 (4%)	0	100	100
40	LS	172/174 (99%)	166 (96%)	6 (4%)	0	100	100
41	LT	124/160 (78%)	119 (96%)	4 (3%)	1 (1%)	16	47
42	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
43	LX	43/156 (28%)	43 (100%)	0	0	100	100
44	LY	132/138 (96%)	128 (97%)	4 (3%)	0	100	100
45	Ld	107/120 (89%)	102 (95%)	5 (5%)	0	100	100
46	Le	125/131 (95%)	120 (96%)	5 (4%)	0	100	100
47	Lf	106/109 (97%)	103 (97%)	3 (3%)	0	100	100
48	Lh	119/935 (13%)	111 (93%)	8 (7%)	0	100	100
49	Li	86/110 (78%)	85 (99%)	1 (1%)	0	100	100
50	Lj	72/95 (76%)	69 (96%)	3 (4%)	0	100	100
51	Lq	205/217 (94%)	180 (88%)	25 (12%)	0	100	100
All	All	10572/16590 (64%)	10025 (95%)	521 (5%)	26 (0%)	44	73

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	CF	239	ALA
21	CT	502	ARG
36	LN	40	SER
37	LO	191	VAL
17	CP	442	GLU
22	CU	359	ASP
25	CY	523	PRO
26	Cb	294	ARG
28	LB	18	PRO
33	LK	51	ALA
7	CF	188	ALA
13	CL	224	ASP
13	CL	439	ASP
26	Cb	576	PHE
28	LB	368	HIS
9	CH	197	ALA
23	CV	85	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	LE	85	GLY
14	LF	118	ASN
36	LN	124	ASP
13	CL	446	ASP
33	LK	160	ILE
37	LO	192	ASP
41	LT	44	VAL
34	LL	47	ALA
5	CC	251	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CA	223/276 (81%)	219 (98%)	4 (2%)	51	73
4	CB	222/329 (68%)	222 (100%)	0	100	100
5	CC	266/708 (38%)	263 (99%)	3 (1%)	65	78
6	CE	398/517 (77%)	398 (100%)	0	100	100
7	CF	214/236 (91%)	214 (100%)	0	100	100
8	CG	150/155 (97%)	150 (100%)	0	100	100
9	CH	448/575 (78%)	441 (98%)	7 (2%)	55	75
10	CI	121/336 (36%)	121 (100%)	0	100	100
11	CJ	330/579 (57%)	330 (100%)	0	100	100
12	CK	204/225 (91%)	204 (100%)	0	100	100
13	CL	72/458 (16%)	71 (99%)	1 (1%)	59	76
14	CM	191/215 (89%)	191 (100%)	0	100	100
14	LF	213/215 (99%)	211 (99%)	2 (1%)	70	80
15	CN	206/206 (100%)	206 (100%)	0	100	100
16	CO	48/99 (48%)	48 (100%)	0	100	100
17	CP	302/632 (48%)	298 (99%)	4 (1%)	61	77
18	CQ	107/192 (56%)	107 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	CR	144/206 (70%)	144 (100%)	0	100	100
20	CS	188/716 (26%)	188 (100%)	0	100	100
21	CT	427/600 (71%)	427 (100%)	0	100	100
22	CU	149/376 (40%)	149 (100%)	0	100	100
23	CV	109/112 (97%)	109 (100%)	0	100	100
24	CX	76/172 (44%)	76 (100%)	0	100	100
25	CY	313/686 (46%)	313 (100%)	0	100	100
26	Cb	535/779 (69%)	525 (98%)	10 (2%)	50	73
27	Cz	60/107 (56%)	60 (100%)	0	100	100
28	LB	289/331 (87%)	287 (99%)	2 (1%)	76	82
29	LC	283/285 (99%)	283 (100%)	0	100	100
30	LE	151/166 (91%)	141 (93%)	10 (7%)	15	43
31	LG	175/222 (79%)	173 (99%)	2 (1%)	65	78
32	LH	167/169 (99%)	165 (99%)	2 (1%)	63	78
33	LK	121/136 (89%)	121 (100%)	0	100	100
34	LL	99/176 (56%)	99 (100%)	0	100	100
35	LM	115/117 (98%)	115 (100%)	0	100	100
36	LN	164/180 (91%)	160 (98%)	4 (2%)	43	69
37	LO	163/163 (100%)	162 (99%)	1 (1%)	78	83
38	LP	123/152 (81%)	123 (100%)	0	100	100
39	LQ	110/178 (62%)	110 (100%)	0	100	100
40	LS	154/154 (100%)	154 (100%)	0	100	100
41	LT	109/135 (81%)	109 (100%)	0	100	100
42	LV	99/102 (97%)	99 (100%)	0	100	100
43	LX	36/129 (28%)	36 (100%)	0	100	100
44	LY	117/119 (98%)	117 (100%)	0	100	100
45	Ld	95/105 (90%)	94 (99%)	1 (1%)	65	78
46	Le	110/114 (96%)	110 (100%)	0	100	100
47	Lf	89/90 (99%)	89 (100%)	0	100	100
48	Lh	108/781 (14%)	108 (100%)	0	100	100
49	Li	75/93 (81%)	74 (99%)	1 (1%)	61	77

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	Lj	61/78 (78%)	61 (100%)	0	100	100
51	Lq	179/189 (95%)	177 (99%)	2 (1%)	65	78
All	All	8908/14071 (63%)	8852 (99%)	56 (1%)	76	83

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	CA	63	ARG
3	CA	64	LYS
3	CA	158	LEU
3	CA	249	SER
5	CC	157	VAL
5	CC	161	ASP
5	CC	164	ASP
9	CH	174	PHE
9	CH	179	LYS
9	CH	201	LYS
9	CH	286	LEU
9	CH	289	MET
9	CH	290	ASP
9	CH	291	ILE
13	CL	19	ARG
17	CP	483	LEU
17	CP	517	VAL
17	CP	562	LEU
17	CP	563	THR
26	Cb	291	VAL
26	Cb	301	VAL
26	Cb	509	LEU
26	Cb	512	VAL
26	Cb	572	LEU
26	Cb	583	GLU
26	Cb	584	GLU
26	Cb	586	VAL
26	Cb	587	ARG
26	Cb	589	ASN
28	LB	18	PRO
28	LB	352	LEU
30	LE	66	ARG
30	LE	68	LYS
30	LE	74	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	LE	107	VAL
30	LE	152	LYS
30	LE	154	VAL
30	LE	169	LEU
30	LE	170	ILE
30	LE	175	LYS
30	LE	176	VAL
14	LF	94	ARG
14	LF	114	LEU
31	LG	95	LYS
31	LG	191	THR
32	LH	92	LEU
32	LH	105	LEU
36	LN	27	CYS
36	LN	41	ARG
36	LN	64	VAL
36	LN	66	VAL
37	LO	191	VAL
45	Ld	21	THR
49	Li	74	LYS
51	Lq	16	LEU
51	Lq	17	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (108) such sidechains are listed below:

Mol	Chain	Res	Type
3	CA	118	GLN
3	CA	193	ASN
3	CA	280	HIS
4	CB	33	HIS
4	CB	76	HIS
4	CB	105	GLN
4	CB	234	HIS
6	CE	393	GLN
6	CE	463	GLN
6	CE	494	GLN
7	CF	29	ASN
7	CF	38	GLN
7	CF	47	ASN
8	CG	41	GLN
8	CG	93	ASN
9	CH	14	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	CH	126	GLN
9	CH	258	GLN
10	CI	269	HIS
10	CI	286	ASN
11	CJ	102	ASN
11	CJ	183	HIS
11	CJ	202	GLN
11	CJ	216	GLN
11	CJ	259	GLN
11	CJ	381	GLN
11	CJ	457	GLN
12	CK	4	ASN
12	CK	10	HIS
12	CK	40	GLN
12	CK	248	ASN
14	CM	206	ASN
14	CM	240	HIS
15	CN	191	ASN
16	CO	15	GLN
16	CO	42	GLN
17	CP	265	GLN
17	CP	343	GLN
17	CP	361	HIS
17	CP	437	ASN
17	CP	474	ASN
17	CP	557	HIS
19	CR	148	GLN
19	CR	220	GLN
20	CS	744	GLN
21	CT	251	ASN
21	CT	436	GLN
21	CT	561	GLN
21	CT	595	GLN
21	CT	602	GLN
22	CU	217	HIS
22	CU	245	ASN
22	CU	287	GLN
22	CU	305	GLN
23	CV	17	ASN
23	CV	23	GLN
23	CV	43	HIS
23	CV	48	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
23	CV	101	HIS
24	CX	75	ASN
24	CX	102	ASN
25	CY	425	GLN
25	CY	443	ASN
25	CY	481	ASN
25	CY	485	GLN
25	CY	509	HIS
26	Cb	210	ASN
26	Cb	377	HIS
26	Cb	437	ASN
26	Cb	440	ASN
26	Cb	517	ASN
26	Cb	585	GLN
26	Cb	835	ASN
28	LB	174	GLN
28	LB	183	GLN
28	LB	275	HIS
29	LC	88	GLN
29	LC	205	GLN
29	LC	330	ASN
30	LE	116	GLN
30	LE	124	GLN
14	LF	9	GLN
14	LF	99	ASN
14	LF	116	GLN
14	LF	178	ASN
31	LG	82	GLN
32	LH	72	GLN
32	LH	133	HIS
32	LH	137	ASN
32	LH	195	GLN
32	LH	208	ASN
33	LK	14	HIS
33	LK	70	GLN
35	LM	106	GLN
36	LN	15	GLN
37	LO	66	ASN
38	LP	42	GLN
39	LQ	122	GLN
40	LS	8	GLN
40	LS	122	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
41	LT	95	HIS
41	LT	127	GLN
45	Ld	64	ASN
46	Le	89	HIS
47	Lf	58	GLN
48	Lh	50	HIS
51	Lq	176	GLN
51	Lq	200	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2145/3341 (64%)	456 (21%)	27 (1%)
2	C2	254/319 (79%)	60 (23%)	6 (2%)
All	All	2399/3660 (65%)	516 (21%)	33 (1%)

All (516) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	14	U
1	C1	26	A
1	C1	41	G
1	C1	49	A
1	C1	59	G
1	C1	60	A
1	C1	65	A
1	C1	66	A
1	C1	74	G
1	C1	92	G
1	C1	93	C
1	C1	94	G
1	C1	96	G
1	C1	105	C
1	C1	110	G
1	C1	111	C
1	C1	116	A
1	C1	122	A
1	C1	128	G
1	C1	129	C
1	C1	131	U
1	C1	132	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	133	G
1	C1	134	G
1	C1	135	C
1	C1	136	C
1	C1	138	G
1	C1	143	G
1	C1	150	G
1	C1	151	G
1	C1	152	A
1	C1	156	G
1	C1	163	U
1	C1	176	U
1	C1	177	U
1	C1	180	G
1	C1	183	U
1	C1	193	C
1	C1	203	C
1	C1	206	A
1	C1	211	G
1	C1	212	A
1	C1	225	G
1	C1	232	G
1	C1	240	U
1	C1	244	U
1	C1	253	U
1	C1	257	A
1	C1	258	C
1	C1	261	G
1	C1	262	U
1	C1	275	G
1	C1	276	A
1	C1	277	A
1	C1	287	A
1	C1	299	A
1	C1	300	A
1	C1	302	U
1	C1	309	A
1	C1	310	A
1	C1	315	A
1	C1	321	C
1	C1	325	C
1	C1	330	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	331	C
1	C1	342	C
1	C1	343	A
1	C1	344	A
1	C1	368	G
1	C1	390	U
1	C1	391	A
1	C1	393	C
1	C1	394	A
1	C1	395	C
1	C1	413	G
1	C1	414	A
1	C1	433	U
1	C1	434	G
1	C1	439	C
1	C1	444	G
1	C1	446	U
1	C1	447	C
1	C1	457	U
1	C1	458	C
1	C1	459	U
1	C1	469	A
1	C1	470	C
1	C1	472	C
1	C1	474	G
1	C1	477	G
1	C1	488	A
1	C1	493	C
1	C1	508	G
1	C1	509	A
1	C1	510	U
1	C1	511	A
1	C1	513	A
1	C1	517	C
1	C1	521	G
1	C1	526	G
1	C1	534	U
1	C1	535	C
1	C1	544	U
1	C1	546	A
1	C1	547	U
1	C1	548	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	559	U
1	C1	579	A
1	C1	582	A
1	C1	587	G
1	C1	589	U
1	C1	590	C
1	C1	591	U
1	C1	592	G
1	C1	594	A
1	C1	596	G
1	C1	598	A
1	C1	607	U
1	C1	608	A
1	C1	609	A
1	C1	614	C
1	C1	623	C
1	C1	633	A
1	C1	647	A
1	C1	663	G
1	C1	664	A
1	C1	668	U
1	C1	674	U
1	C1	678	A
1	C1	712	A
1	C1	716	C
1	C1	718	U
1	C1	719	C
1	C1	731	G
1	C1	739	C
1	C1	742	A
1	C1	744	G
1	C1	748	U
1	C1	749	C
1	C1	751	G
1	C1	752	A
1	C1	755	G
1	C1	757	U
1	C1	758	U
1	C1	761	A
1	C1	762	G
1	C1	766	G
1	C1	767	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	787	A
1	C1	798	A
1	C1	799	C
1	C1	800	U
1	C1	801	A
1	C1	887	G
1	C1	889	G
1	C1	896	A
1	C1	898	A
1	C1	925	A
1	C1	932	A
1	C1	933	A
1	C1	934	G
1	C1	941	U
1	C1	942	C
1	C1	943	A
1	C1	944	G
1	C1	959	C
1	C1	960	C
1	C1	965	G
1	C1	974	G
1	C1	975	G
1	C1	976	U
1	C1	982	G
1	C1	983	A
1	C1	1031	C
1	C1	1033	U
1	C1	1039	A
1	C1	1046	A
1	C1	1047	A
1	C1	1048	G
1	C1	1049	C
1	C1	1050	C
1	C1	1054	G
1	C1	1057	A
1	C1	1058	C
1	C1	1063	C
1	C1	1064	U
1	C1	1065	G
1	C1	1073	G
1	C1	1074	C
1	C1	1076	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	1079	G
1	C1	1080	A
1	C1	1085	A
1	C1	1086	U
1	C1	1095	G
1	C1	1097	G
1	C1	1098	G
1	C1	1114	C
1	C1	1122	G
1	C1	1124	G
1	C1	1125	A
1	C1	1126	U
1	C1	1135	A
1	C1	1141	A
1	C1	1157	C
1	C1	1158	C
1	C1	1159	G
1	C1	1163	U
1	C1	1164	G
1	C1	1172	A
1	C1	1174	C
1	C1	1175	A
1	C1	1178	C
1	C1	1179	A
1	C1	1180	C
1	C1	1184	A
1	C1	1189	G
1	C1	1190	C
1	C1	1191	G
1	C1	1204	G
1	C1	1218	G
1	C1	1227	A
1	C1	1228	G
1	C1	1240	U
1	C1	1245	A
1	C1	1247	U
1	C1	1254	C
1	C1	1268	A
1	C1	1269	A
1	C1	1271	G
1	C1	1272	U
1	C1	1286	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	1287	U
1	C1	1288	G
1	C1	1289	G
1	C1	1291	U
1	C1	1294	C
1	C1	1295	G
1	C1	1298	C
1	C1	1312	A
1	C1	1314	A
1	C1	1330	A
1	C1	1331	G
1	C1	1332	A
1	C1	1333	A
1	C1	1334	A
1	C1	1335	C
1	C1	1336	G
1	C1	1337	A
1	C1	1347	G
1	C1	1368	A
1	C1	1374	G
1	C1	1381	A
1	C1	1399	G
1	C1	1401	A
1	C1	1416	G
1	C1	1419	C
1	C1	1434	A
1	C1	1861	G
1	C1	1864	C
1	C1	1865	A
1	C1	1866	A
1	C1	1867	U
1	C1	1874	A
1	C1	1875	A
1	C1	1883	C
1	C1	1886	C
1	C1	1897	C
1	C1	1900	A
1	C1	1901	A
1	C1	2075	A
1	C1	2088	A
1	C1	2287	G
1	C1	2288	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	2294	A
1	C1	2295	C
1	C1	2297	G
1	C1	2298	U
1	C1	2302	U
1	C1	2310	A
1	C1	2325	A
1	C1	2327	C
1	C1	2332	G
1	C1	2335	A
1	C1	2338	G
1	C1	2339	G
1	C1	2342	U
1	C1	2343	G
1	C1	2345	C
1	C1	2347	A
1	C1	2350	U
1	C1	2355	G
1	C1	2356	G
1	C1	2359	A
1	C1	2361	A
1	C1	2362	G
1	C1	2363	A
1	C1	2364	A
1	C1	2396	U
1	C1	2397	G
1	C1	2399	G
1	C1	2407	A
1	C1	2410	G
1	C1	2414	G
1	C1	2415	U
1	C1	2424	G
1	C1	2425	G
1	C1	2428	G
1	C1	2430	A
1	C1	2433	U
1	C1	2434	U
1	C1	2435	C
1	C1	2436	G
1	C1	2437	G
1	C1	2438	C
1	C1	2439	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	2444	U
1	C1	2449	U
1	C1	2453	A
1	C1	2455	U
1	C1	2456	A
1	C1	2464	U
1	C1	2465	G
1	C1	2467	U
1	C1	2484	G
1	C1	2551	A
1	C1	2560	G
1	C1	2564	G
1	C1	2730	C
1	C1	2740	U
1	C1	2749	G
1	C1	2759	A
1	C1	2760	A
1	C1	2761	A
1	C1	2775	A
1	C1	2777	A
1	C1	2778	A
1	C1	2782	G
1	C1	2783	C
1	C1	2784	U
1	C1	2785	U
1	C1	2806	G
1	C1	2818	U
1	C1	2819	U
1	C1	2820	U
1	C1	2845	A
1	C1	2847	C
1	C1	2856	G
1	C1	2857	C
1	C1	2862	U
1	C1	2869	A
1	C1	2889	C
1	C1	2893	U
1	C1	2894	A
1	C1	2899	A
1	C1	2902	U
1	C1	2904	A
1	C1	2917	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	2924	G
1	C1	2925	A
1	C1	2935	G
1	C1	2936	U
1	C1	2942	C
1	C1	2948	G
1	C1	2950	U
1	C1	2951	G
1	C1	2954	C
1	C1	2955	U
1	C1	2956	C
1	C1	2969	A
1	C1	3005	A
1	C1	3006	A
1	C1	3016	G
1	C1	3031	G
1	C1	3035	G
1	C1	3043	A
1	C1	3048	A
1	C1	3049	C
1	C1	3050	C
1	C1	3070	A
1	C1	3074	C
1	C1	3079	A
1	C1	3086	A
1	C1	3087	A
1	C1	3088	U
1	C1	3098	A
1	C1	3099	A
1	C1	3100	C
1	C1	3101	G
1	C1	3112	A
1	C1	3113	C
1	C1	3118	A
1	C1	3121	U
1	C1	3122	U
1	C1	3124	U
1	C1	3125	A
1	C1	3126	G
1	C1	3127	A
1	C1	3130	U
1	C1	3131	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	3132	U
1	C1	3134	A
1	C1	3140	G
1	C1	3145	C
1	C1	3146	G
1	C1	3147	G
1	C1	3153	U
1	C1	3154	A
1	C1	3161	C
1	C1	3162	A
1	C1	3163	G
1	C1	3167	A
1	C1	3170	C
1	C1	3171	C
1	C1	3178	G
1	C1	3183	C
1	C1	3185	A
1	C1	3187	G
1	C1	3199	A
1	C1	3205	C
1	C1	3206	G
1	C1	3210	U
1	C1	3212	C
1	C1	3213	A
1	C1	3217	U
1	C1	3227	C
1	C1	3228	G
1	C1	3229	G
1	C1	3230	G
1	C1	3244	C
1	C1	3253	U
1	C1	3255	G
1	C1	3256	A
1	C1	3257	U
1	C1	3258	G
1	C1	3260	G
1	C1	3274	U
1	C1	3281	U
1	C1	3282	A
1	C1	3285	G
1	C1	3287	A
1	C1	3291	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	3293	G
1	C1	3295	U
1	C1	3298	U
1	C1	3303	U
1	C1	3309	G
1	C1	3318	C
1	C1	3322	C
1	C1	3323	C
1	C1	3324	U
1	C1	3329	C
1	C1	3331	A
1	C1	3332	G
1	C1	3333	A
1	C1	3337	C
2	C2	23	U
2	C2	34	U
2	C2	35	C
2	C2	39	G
2	C2	59	A
2	C2	62	A
2	C2	63	G
2	C2	81	U
2	C2	82	U
2	C2	84	C
2	C2	86	U
2	C2	87	G
2	C2	88	A
2	C2	90	U
2	C2	95	G
2	C2	97	A
2	C2	100	U
2	C2	103	G
2	C2	104	A
2	C2	105	A
2	C2	106	C
2	C2	110	C
2	C2	111	A
2	C2	112	U
2	C2	113	U
2	C2	125	U
2	C2	151	C
2	C2	158	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	C2	159	C
2	C2	160	A
2	C2	163	C
2	C2	164	A
2	C2	165	U
2	C2	166	C
2	C2	170	C
2	C2	173	U
2	C2	174	G
2	C2	180	G
2	C2	181	U
2	C2	182	G
2	C2	183	U
2	C2	189	A
2	C2	192	C
2	C2	195	G
2	C2	196	G
2	C2	212	G
2	C2	213	A
2	C2	214	A
2	C2	215	A
2	C2	216	A
2	C2	219	A
2	C2	221	U
2	C2	222	G
2	C2	289	G
2	C2	291	G
2	C2	292	C
2	C2	295	G
2	C2	300	A
2	C2	301	A
2	C2	305	C

All (33) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	150	G
1	C1	445	A
1	C1	446	U
1	C1	508	G
1	C1	510	U
1	C1	886	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	897	G
1	C1	959	C
1	C1	1063	C
1	C1	1134	G
1	C1	2301	C
1	C1	2360	A
1	C1	2777	A
1	C1	2817	U
1	C1	2898	A
1	C1	3005	A
1	C1	3078	U
1	C1	3112	A
1	C1	3131	A
1	C1	3162	A
1	C1	3204	G
1	C1	3209	U
1	C1	3212	C
1	C1	3229	G
1	C1	3255	G
1	C1	3257	U
1	C1	3297	U
2	C2	87	G
2	C2	102	U
2	C2	163	C
2	C2	164	A
2	C2	180	G
2	C2	181	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	SEP	CC	160	5	8,9,10	0.65	0	7,12,14	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	TPO	CC	163	5	8,10,11	0.68	0	10,14,16	1.03	1 (10%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	SEP	CC	160	5	-	5/6/8/10	-
5	TPO	CC	163	5	-	1/9/11/13	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	CC	163	TPO	O-C-CA	-2.47	118.43	124.77

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	CC	160	SEP	C-CA-CB-OG
5	CC	160	SEP	CB-OG-P-O1P
5	CC	160	SEP	CB-OG-P-O2P
5	CC	160	SEP	CB-OG-P-O3P
5	CC	160	SEP	N-CA-CB-OG
5	CC	163	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
52	GTP	CH	1001	-	33,34,34	0.53	0	50,54,54	0.56	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
52	GTP	CH	1001	-	-	7/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

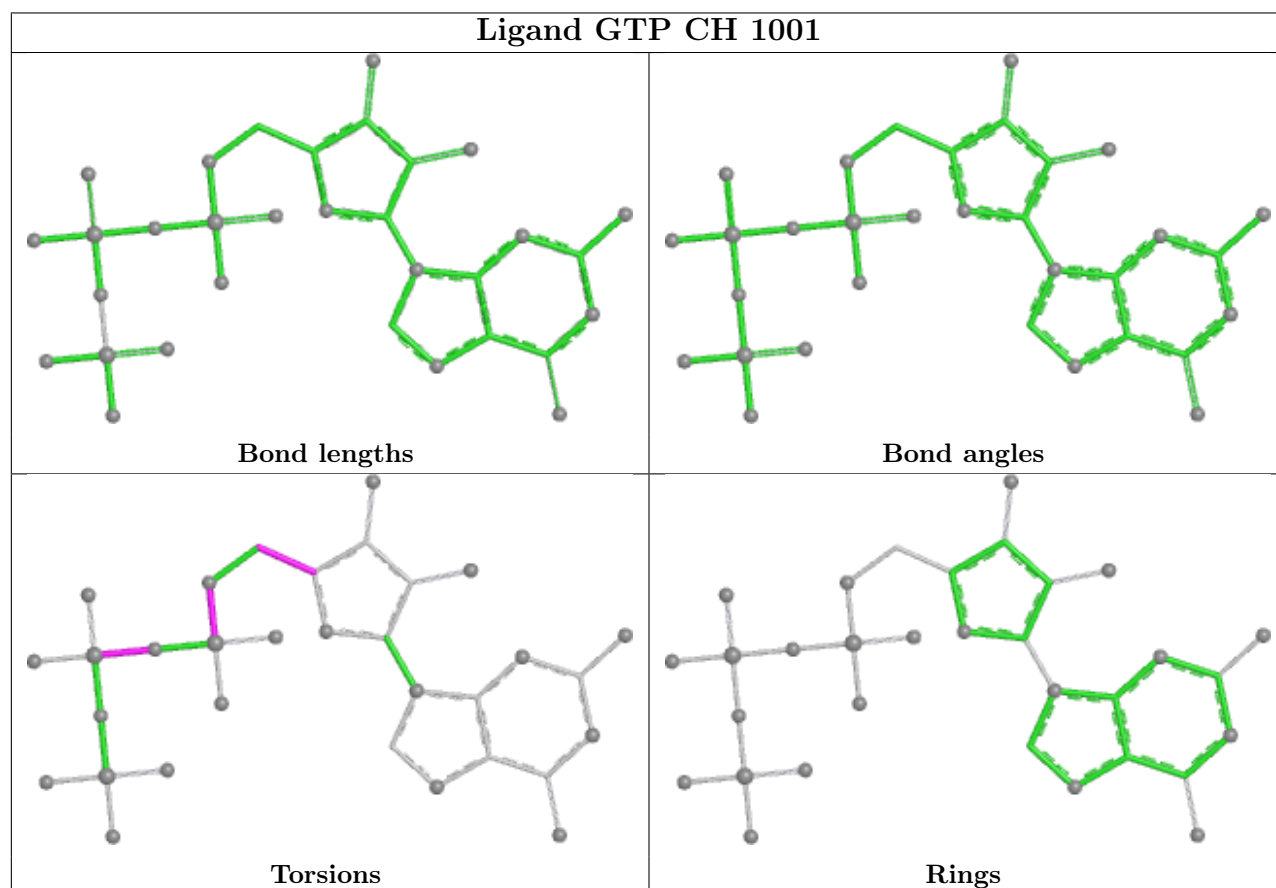
Mol	Chain	Res	Type	Atoms
52	CH	1001	GTP	C5'-O5'-PA-O3A
52	CH	1001	GTP	C5'-O5'-PA-O1A
52	CH	1001	GTP	C5'-O5'-PA-O2A
52	CH	1001	GTP	O4'-C4'-C5'-O5'
52	CH	1001	GTP	C3'-C4'-C5'-O5'
52	CH	1001	GTP	PA-O3A-PB-O2B
52	CH	1001	GTP	PA-O3A-PB-O1B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

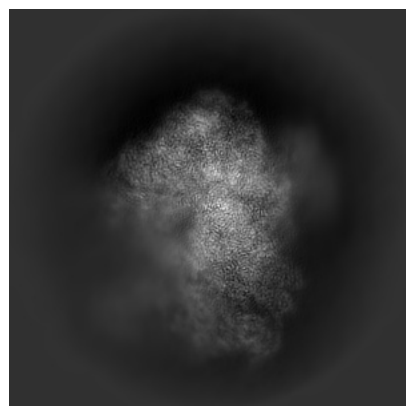
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35286. These allow visual inspection of the internal detail of the map and identification of artifacts.

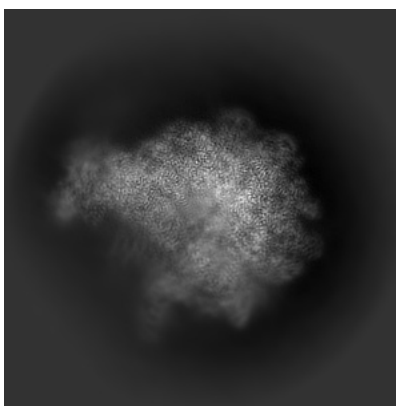
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

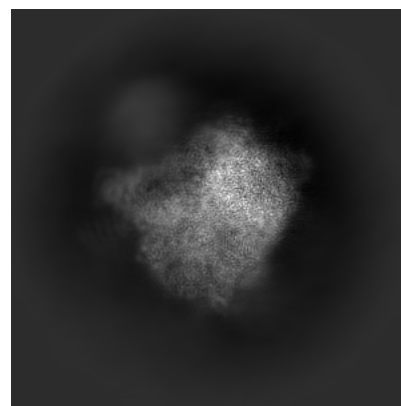
6.1.1 Primary map



X

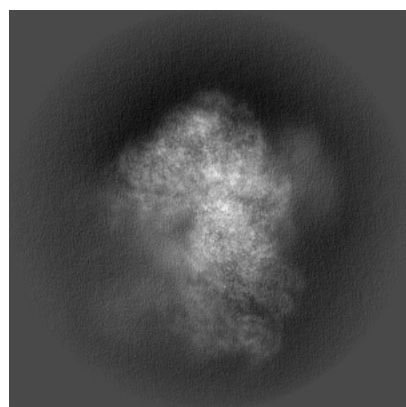


Y

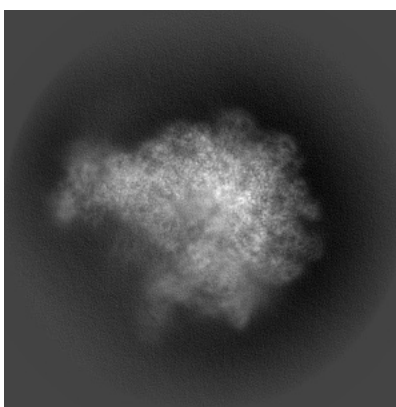


Z

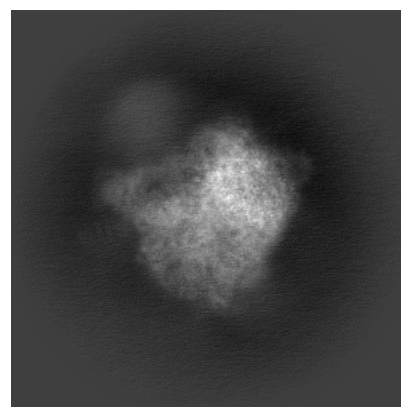
6.1.2 Raw map



X



Y

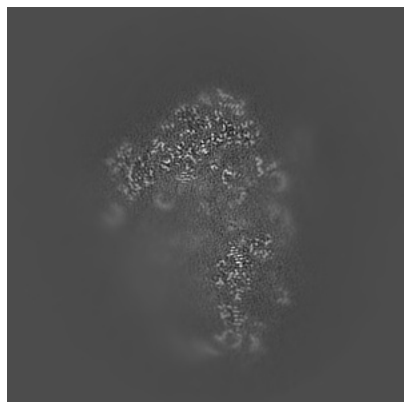


Z

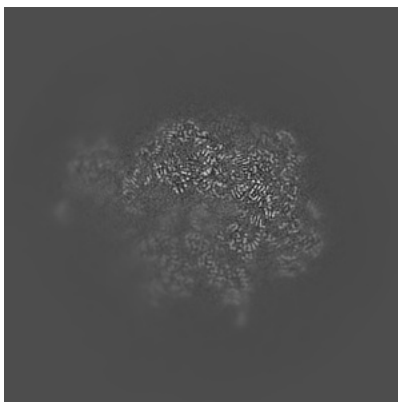
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

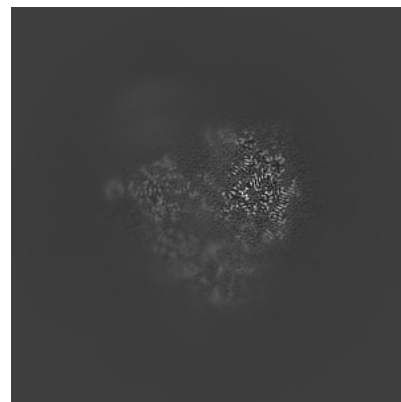
6.2.1 Primary map



X Index: 210

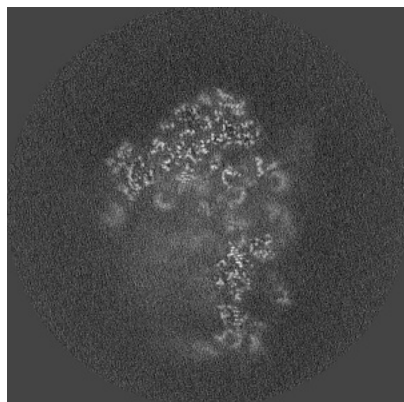


Y Index: 210

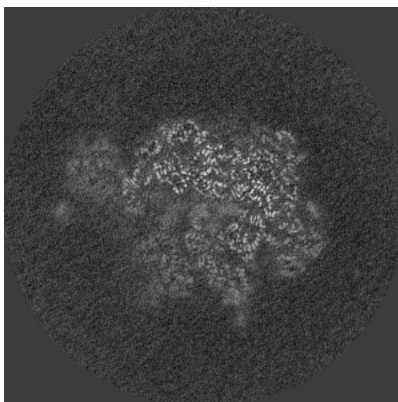


Z Index: 210

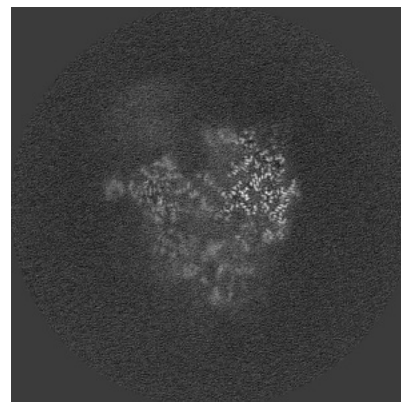
6.2.2 Raw map



X Index: 210



Y Index: 210

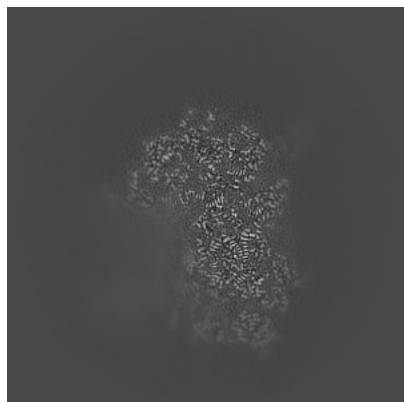


Z Index: 210

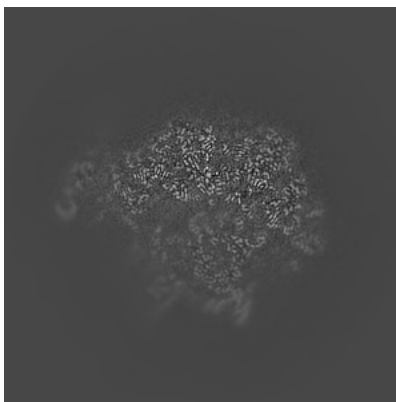
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

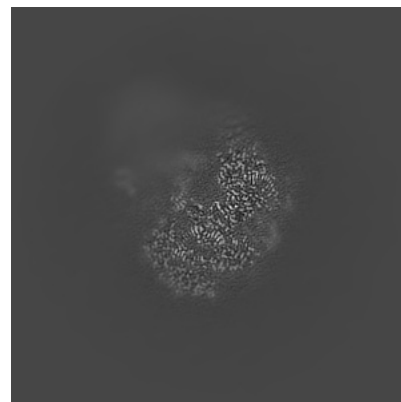
6.3.1 Primary map



X Index: 243

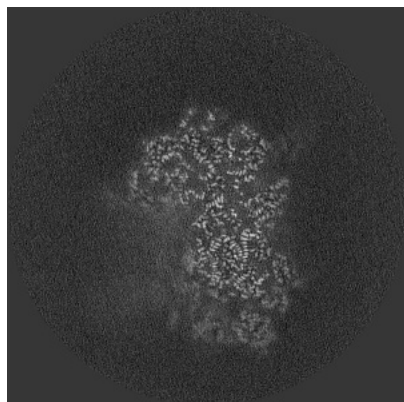


Y Index: 219

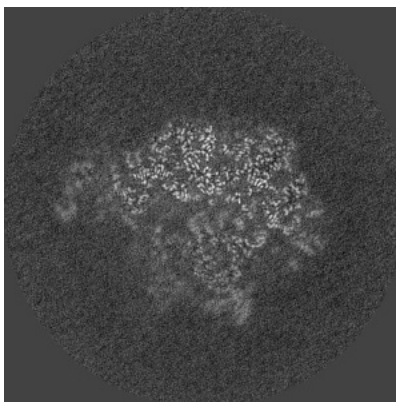


Z Index: 267

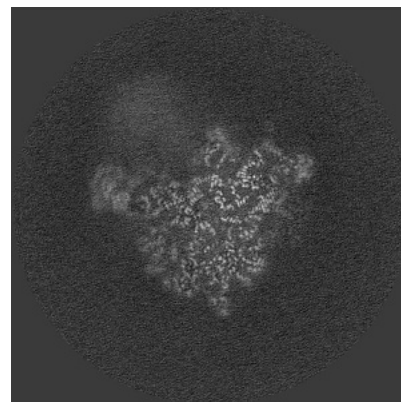
6.3.2 Raw map



X Index: 243



Y Index: 219

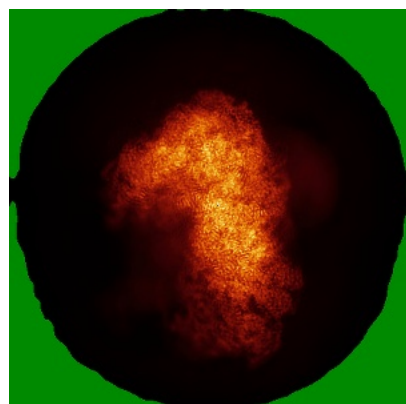


Z Index: 246

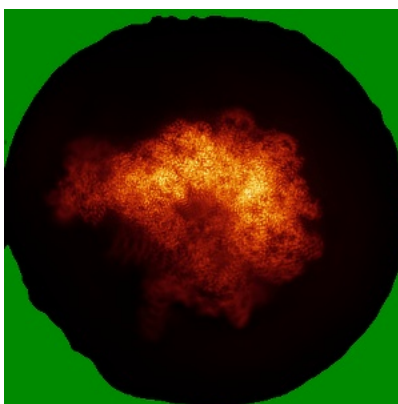
The images above show the largest variance slices of the map in three orthogonal directions.

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

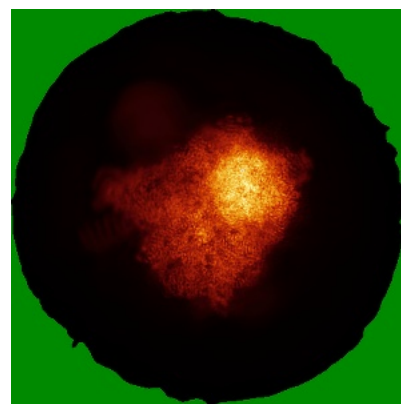
6.4.1 Primary map



X

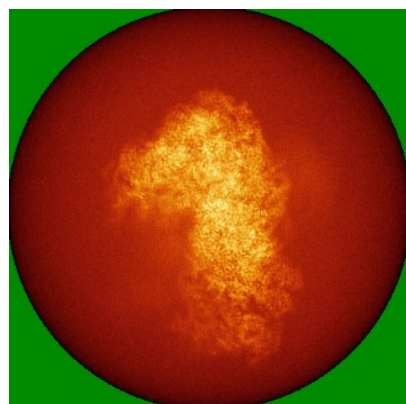


Y

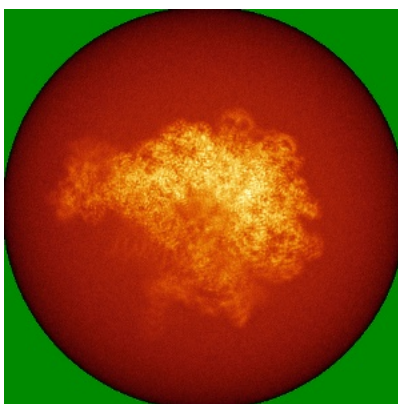


Z

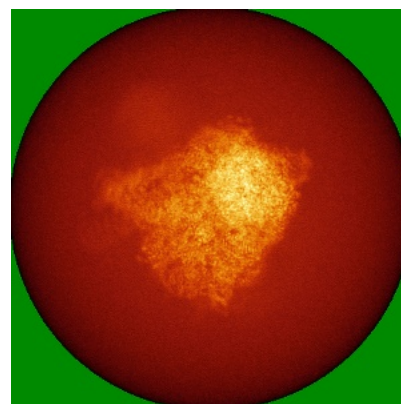
6.4.2 Raw map



X



Y

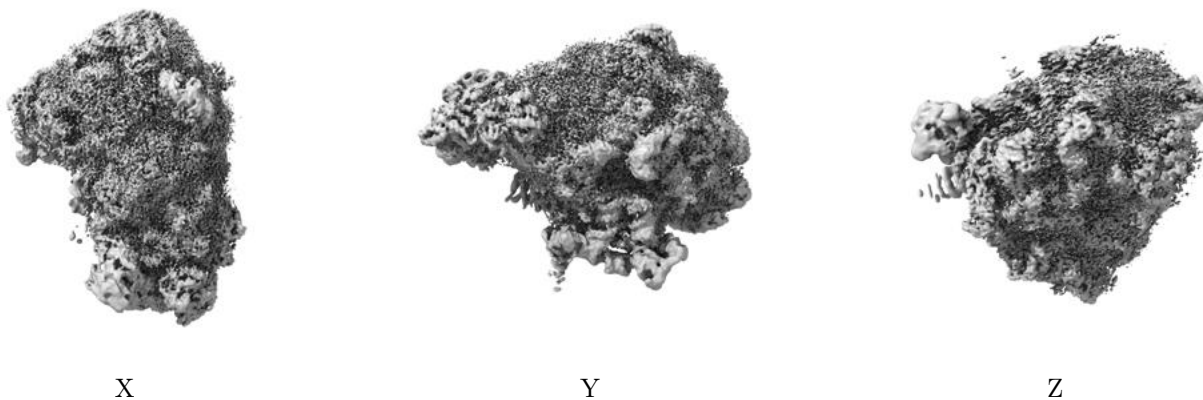


Z

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

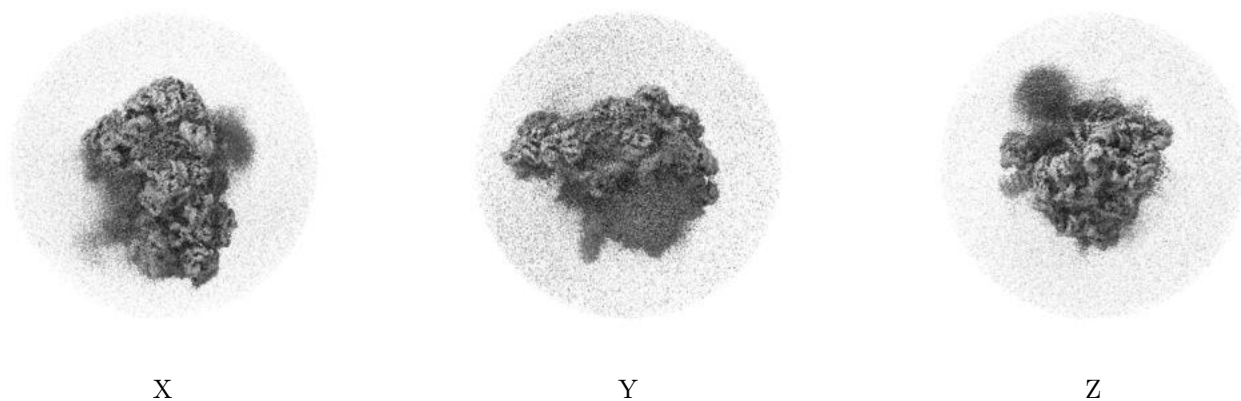
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

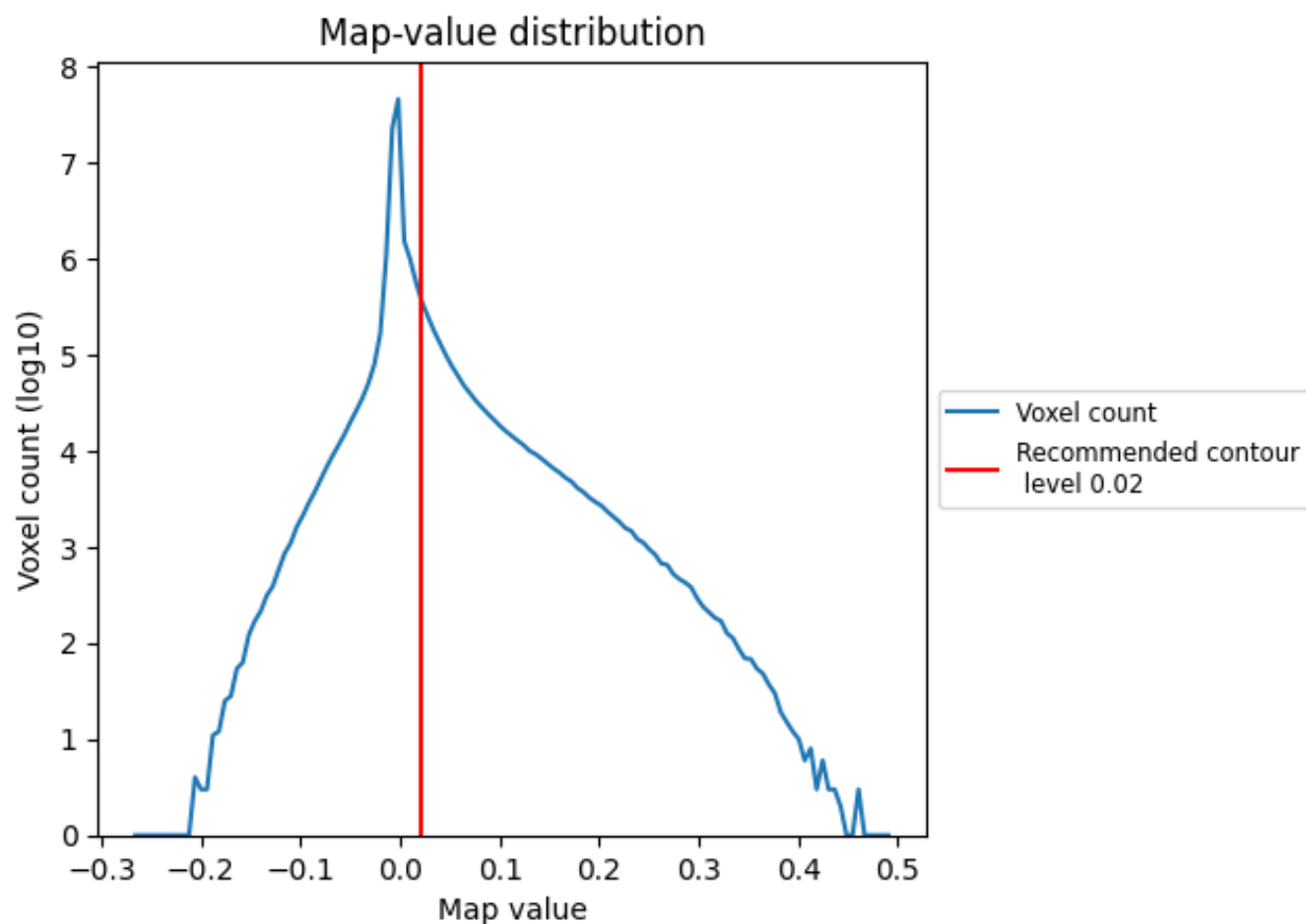
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

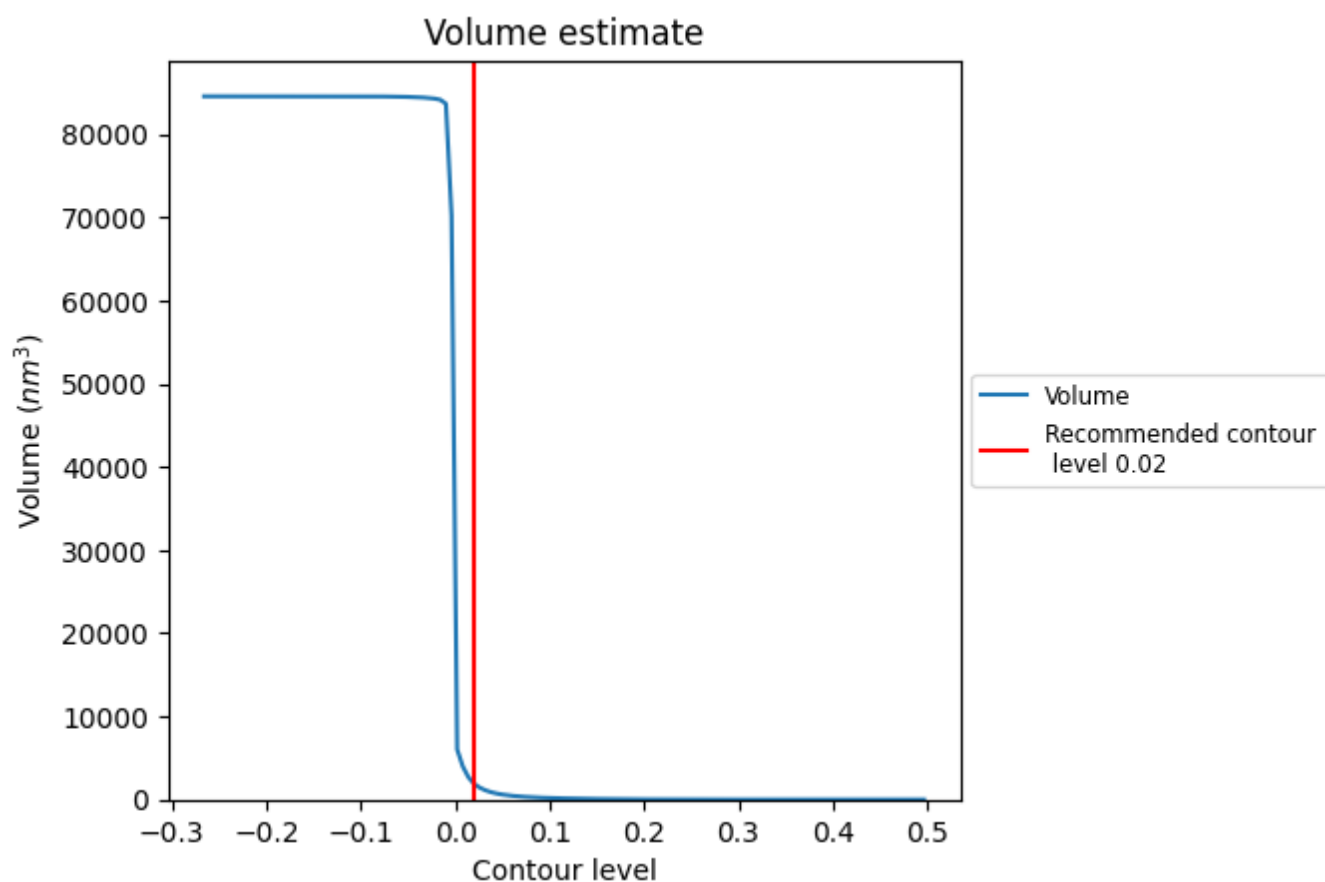
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

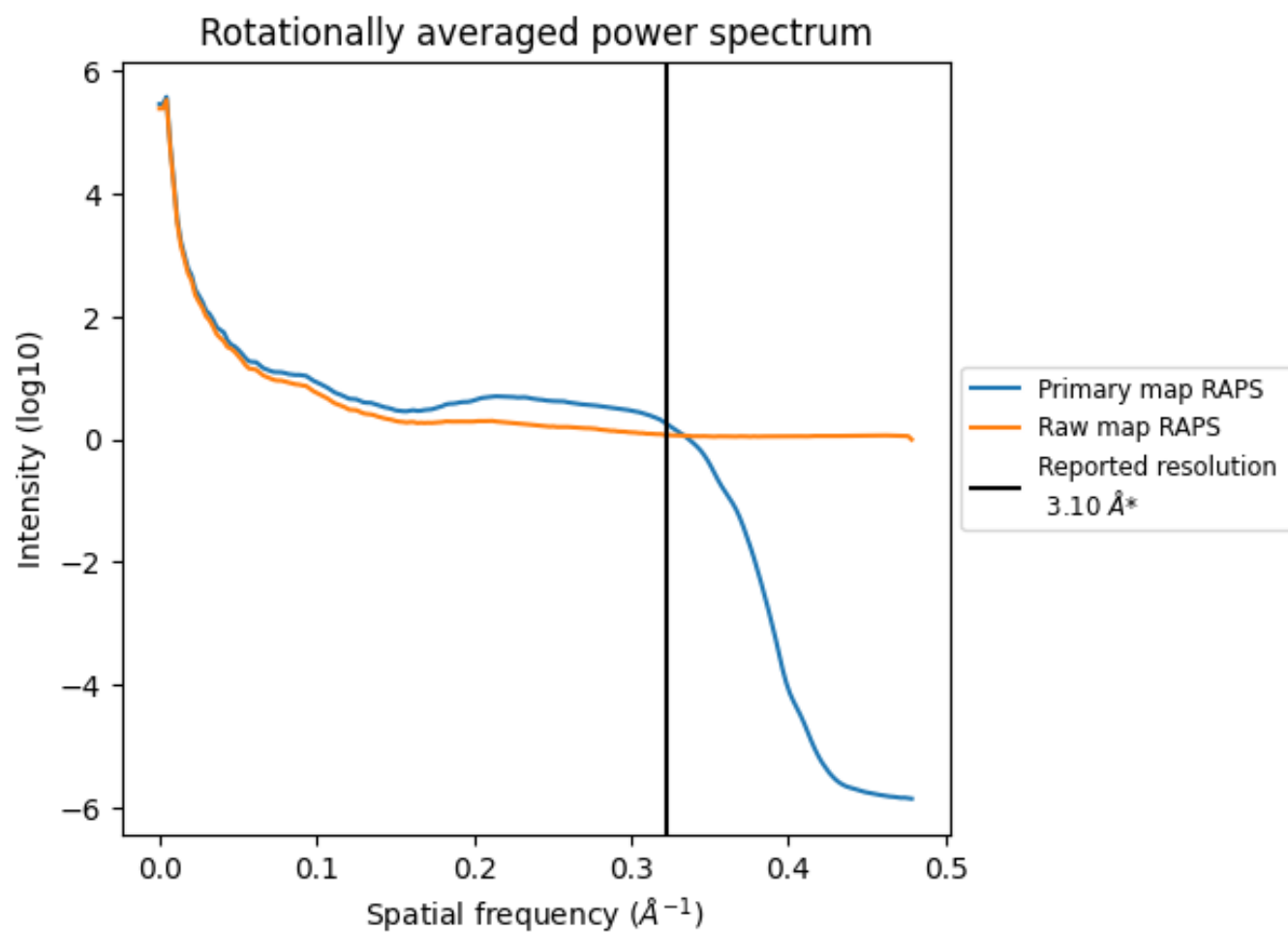
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1891 nm^3 ; this corresponds to an approximate mass of 1708 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

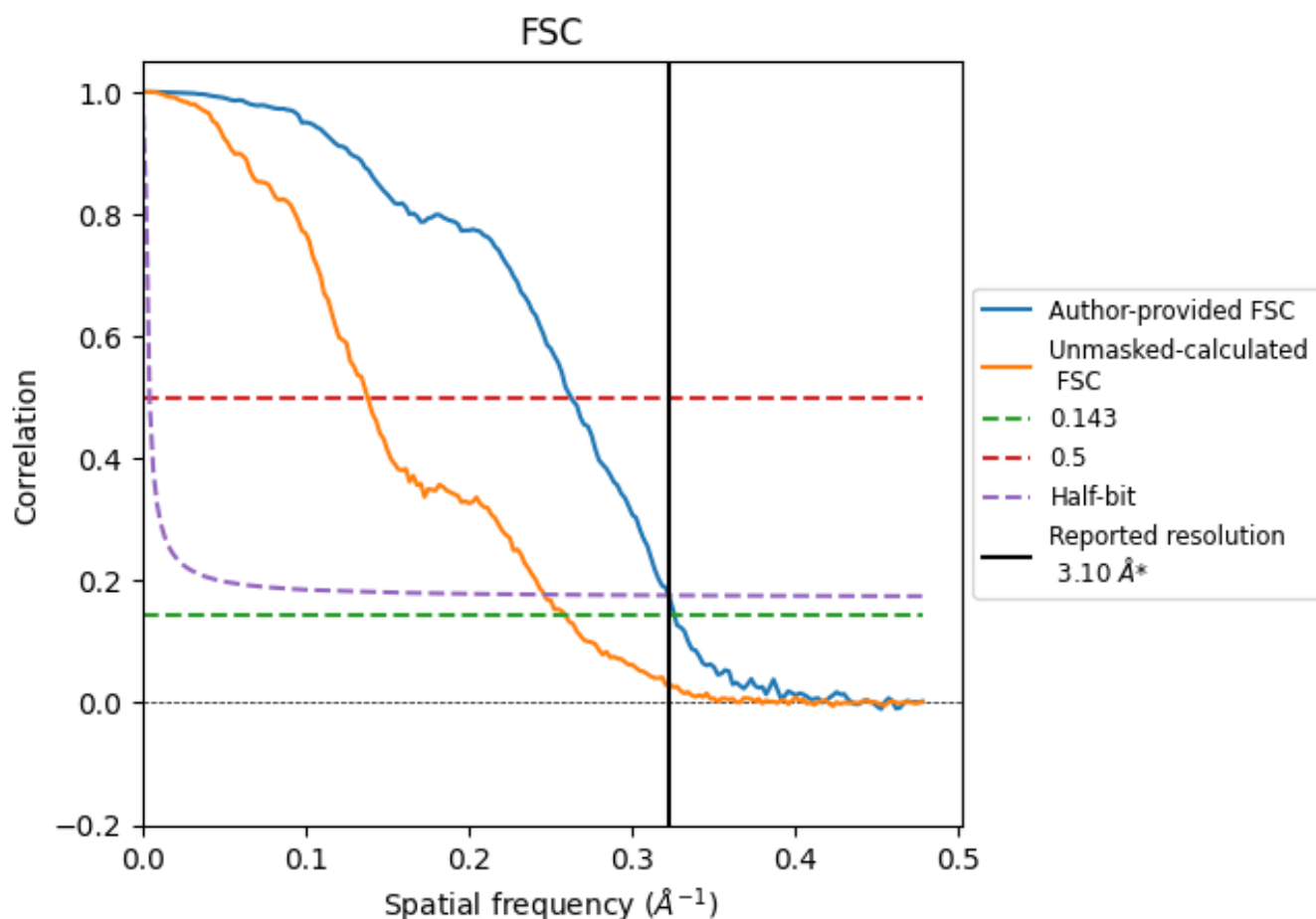


*Reported resolution corresponds to spatial frequency of $0.323 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

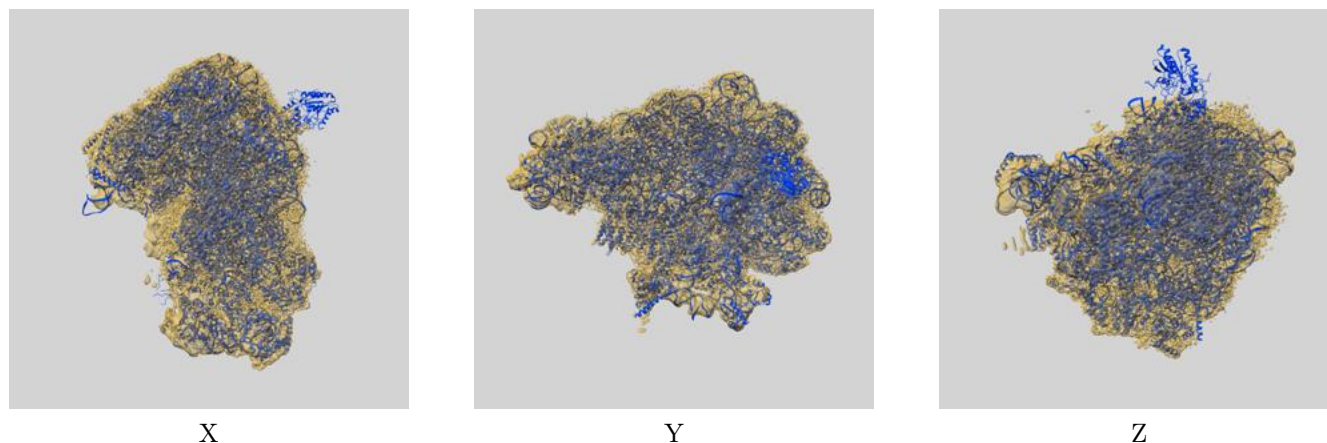
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.06	3.80	3.10
Unmasked-calculated*	3.85	7.23	4.05

*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 3.85 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

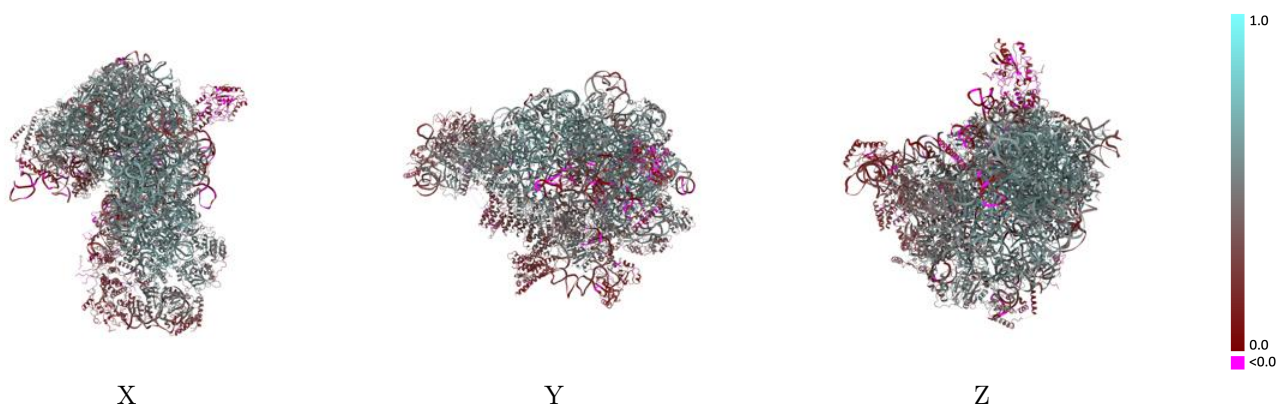
This section contains information regarding the fit between EMDB map EMD-35286 and PDB model 8I9W. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



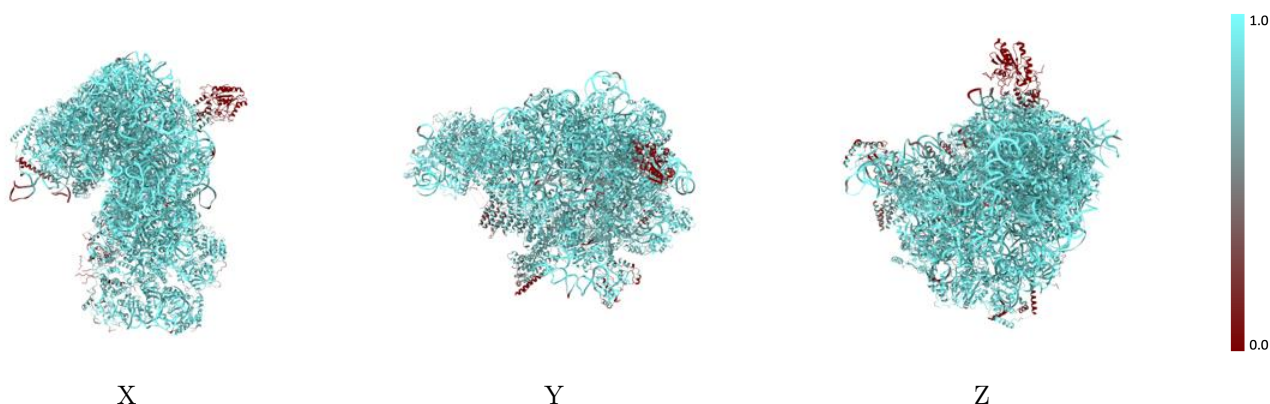
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



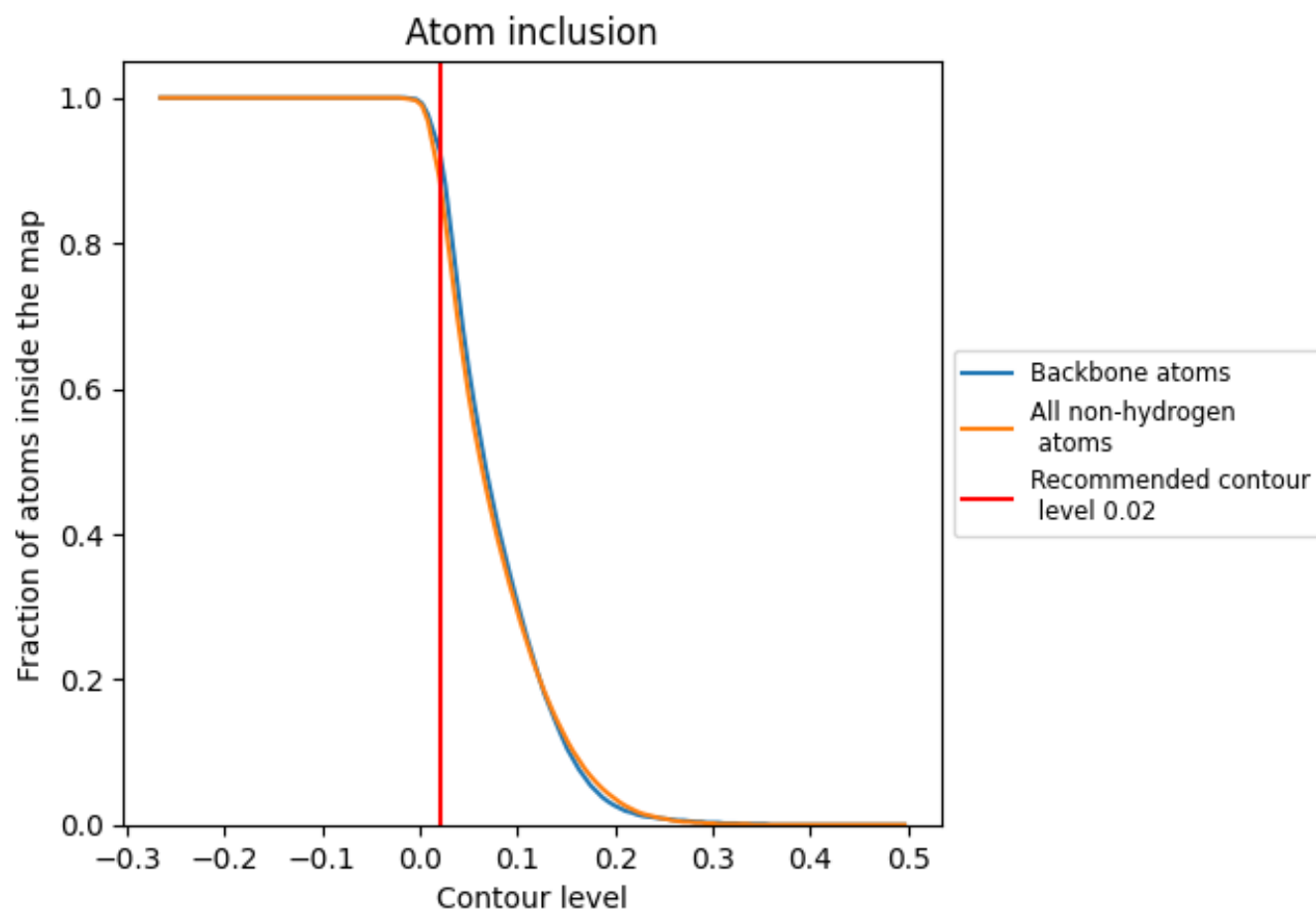
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 89% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8890	 0.4410
C1	 0.9440	 0.4660
C2	 0.9490	 0.4500
CA	 0.9510	 0.5300
CB	 0.8570	 0.3860
CC	 0.8170	 0.3860
CE	 0.8850	 0.4780
CF	 0.8860	 0.4300
CG	 0.9290	 0.4430
CH	 0.8650	 0.4490
CI	 0.8710	 0.4080
CJ	 0.8090	 0.2690
CK	 0.9230	 0.4750
CL	 0.3220	 0.1720
CM	 0.7400	 0.2780
CN	 0.9180	 0.4870
CO	 0.9670	 0.5290
CP	 0.9200	 0.4450
CQ	 0.8820	 0.4350
CR	 0.9400	 0.5290
CS	 0.7260	 0.3300
CT	 0.6890	 0.2780
CU	 0.9090	 0.4630
CV	 0.9460	 0.5250
CX	 0.8400	 0.4060
CY	 0.6120	 0.2110
Cb	 0.8170	 0.3210
Cz	 0.7220	 0.2600
LB	 0.9550	 0.5380
LC	 0.9610	 0.5660
LE	 0.9160	 0.5060
LF	 0.9420	 0.5390
LG	 0.9330	 0.5310
LH	 0.9440	 0.5380
LK	 0.8240	 0.3220



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
LL	 0.9720	 0.5770
LM	 0.9590	 0.5440
LN	 0.9730	 0.5910
LO	 0.9600	 0.5680
LP	 0.9540	 0.5160
LQ	 0.9520	 0.5200
LS	 0.9500	 0.5400
LT	 0.8320	 0.2950
LV	 0.9330	 0.4830
LX	 0.8390	 0.3900
LY	 0.9330	 0.5340
Ld	 0.8300	 0.3610
Le	 0.9600	 0.5730
Lf	 0.9770	 0.5930
Lh	 0.9070	 0.4800
Li	 0.9370	 0.5200
Lj	 0.9680	 0.5690
Lq	 0.6320	 0.1540