



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 02:07 AM UTC

PDB ID : 8I9Y / pdb_00008i9y
EMDB ID : EMD-35288
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- Ytm1-2
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:

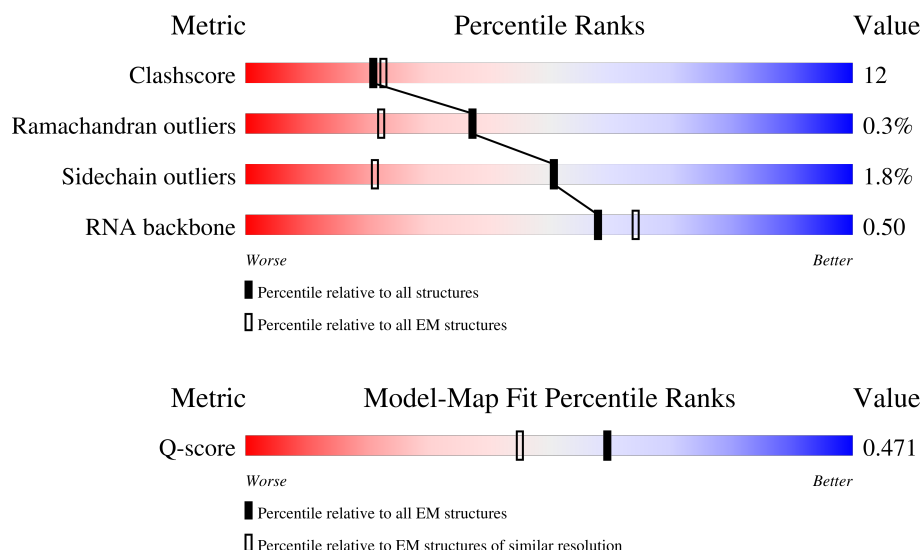
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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.



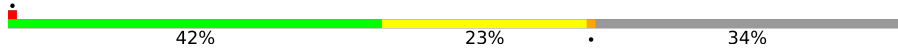
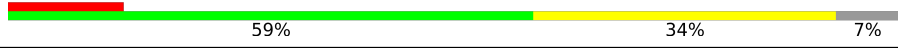
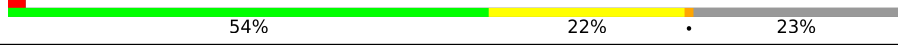
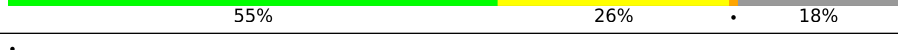
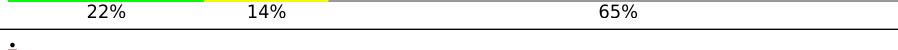
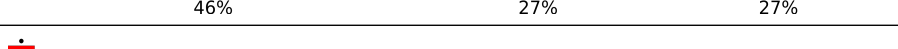
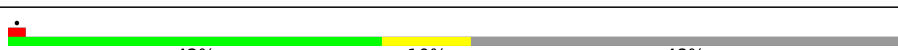
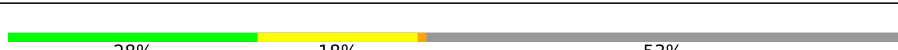
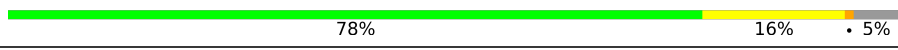
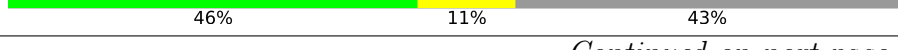
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	

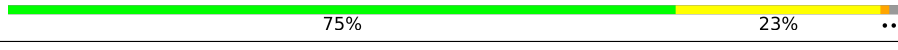
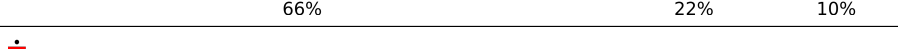
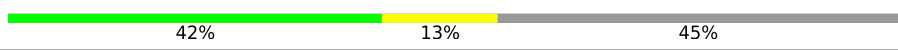
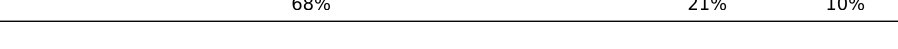
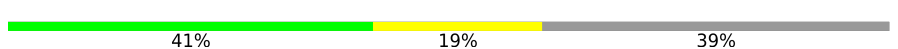
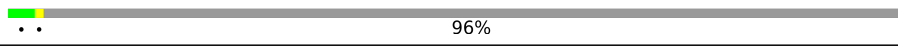
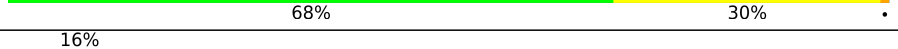
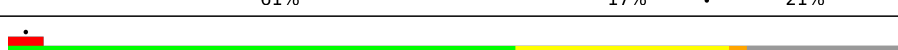
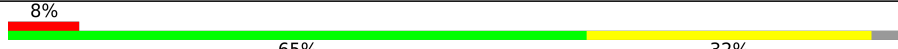
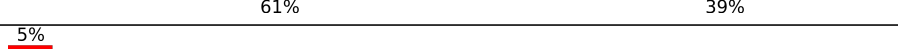
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	CB	391	
5	CC	801	
6	CD	495	
7	CE	598	
8	CF	270	
9	CG	184	
10	CH	661	
11	CI	414	
12	CJ	679	
13	CK	261	
14	CL	558	
15	CM	249	
15	LF	249	
16	CN	246	
17	CO	120	
18	CP	751	
19	CQ	225	
20	CR	237	
21	CS	834	
22	CT	688	
23	CU	451	
24	CV	147	
25	CX	203	
26	CY	788	
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	LR	2898	
41	LS	174	
42	LT	160	
43	LU	127	
44	LV	139	
45	LX	156	
46	LY	138	
47	LZ	135	
48	Lc	108	
49	Ld	120	
50	Le	131	
51	Lf	109	
52	Lg	119	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
53	Lh	935	
54	Li	110	
55	Lj	95	
56	Lk	81	
57	Ll	51	
58	Lq	217	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 156553 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	2609	Total	C	N	O	P	0	0
			55815	24911	10105	18190	2609		

- 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	658	Total	C	N	O	P	S	0	0
			5297	3368	931	983	2	13		

- Molecule 6 is a protein called Ribosome biogenesis protein YTM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CD	460	Total	C	N	O	S	0	0
			3468	2173	610	679	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CD	88	ASP	GLU	conflict	UNP G0SFB5

- Molecule 7 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CE	462	Total	C	N	O	S	0	0
			3669	2350	642	666	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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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 8 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	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 9 is a protein called 60S ribosome subunit biogenesis protein NIP7.

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

- Molecule 10 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CH	542	Total	C	N	O	S	0	0
			4388	2784	770	818	16		

- Molecule 11 is a protein called Putative RNA-binding protein.

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

- Molecule 12 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CJ	494	Total	C	N	O	S	0	0
			4040	2575	719	734	12		

- Molecule 13 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CK	229	Total	C	N	O	S	0	0
			1835	1149	362	320	4		

- Molecule 14 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	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 15 is a protein called 60S ribosomal protein l7-like protein.

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

- Molecule 16 is a protein called Eukaryotic translation initiation factor 6.

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

- Molecule 17 is a protein called DUF2423 domain-containing protein.

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

- Molecule 18 is a protein called RNA methyltransferase nop2-like protein.

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

- Molecule 19 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CQ	179	Total	C	N	O	S	0	0
			1485	926	304	245	10		

- Molecule 20 is a protein called Nucleolar protein 16.

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

- Molecule 21 is a protein called AdoMet-dependent rRNA methyltransferase SPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CS	262	Total	C	N	O	S	0	0
			2105	1322	399	377	7		

- Molecule 22 is a protein called Nucleolar complex-associated protein 3.

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

- Molecule 23 is a protein called rRNA-processing protein EBP2.

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

- Molecule 24 is a protein called Putative 60S ribosomal protein.

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

- Molecule 25 is a protein called 60S ribosomal subunit-like protein.

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

- Molecule 26 is a protein called Putative NOC2 family protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	CY	420	Total	C	N	O	S	0
			3399	2181	616	590	12	0

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
28	LB	356	Total	C	N	O	S	0
			2829	1798	518	501	12	0

- 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
			2752	1738	526	479	9	0

- 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
			1403	898	255	247	3	0

- 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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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	169	Total	C	N	O	S	0	0
			1345	835	273	234	3		

- 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 Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LR	119	Total	C	N	O	S	0	0
			969	610	196	159	4		

- Molecule 41 is a protein called 60S ribosomal protein L20.

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

- Molecule 42 is a protein called 60S ribosomal protein l21-like protein.

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

- Molecule 43 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LU	105	Total	C	N	O	S	0	0
			850	551	147	151	1		

- Molecule 44 is a protein called 60S ribosomal protein l23-like protein.

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

- Molecule 45 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	LX	137	Total	C	N	O		
			1062	678	194	190	0	0

- Molecule 46 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 47 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	LZ	135	Total	C	N	O	S	
			1112	713	207	188	4	0

- Molecule 48 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	Lc	98	Total	C	N	O	S	
			731	463	126	137	5	0

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

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

- Molecule 50 is a protein called 60S ribosomal protein L32-like protein.

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

- Molecule 51 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 52 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Lg	117	Total	C	N	O	S	0	0
			930	578	189	159	4		

- Molecule 53 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 54 is a protein called 60S ribosomal protein L36.

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

- Molecule 55 is a protein called Ribosomal protein L37.

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

- Molecule 56 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Lk	75	Total	C	N	O	S	0	0
			620	394	117	107	2		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lk	?	-	SER	deletion	UNP G0SG89
Lk	?	-	LYS	deletion	UNP G0SG89
Lk	?	-	ILE	deletion	UNP G0SG89
Lk	?	-	LEU	deletion	UNP G0SG89
Lk	?	-	THR	deletion	UNP G0SG89
Lk	?	-	ILE	deletion	UNP G0SG89
Lk	?	-	ALA	deletion	UNP G0SG89
Lk	?	-	PHE	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	LEU	deletion	UNP G0SG89

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
Lk	?	-	THR	deletion	UNP G0SG89

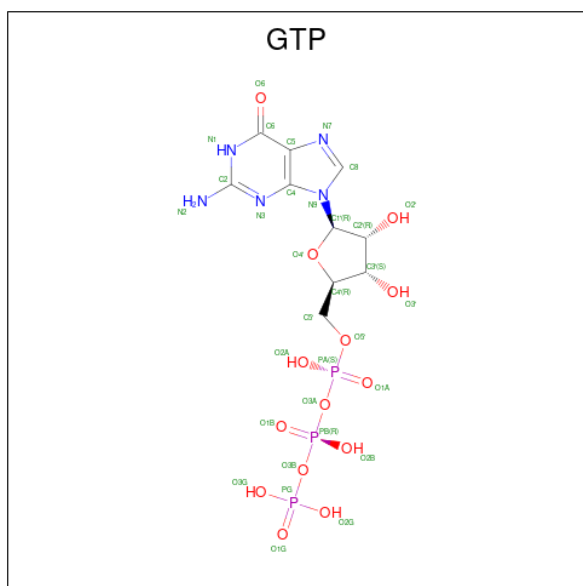
- Molecule 57 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	Ll	38	Total	C	N	O	0	0
			322	204	68	50		

- Molecule 58 is a protein called Ribosomal protein.

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

- Molecule 59 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
59	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	CQ	1	Total	Zn	0
			1	1	

Continued on next page...

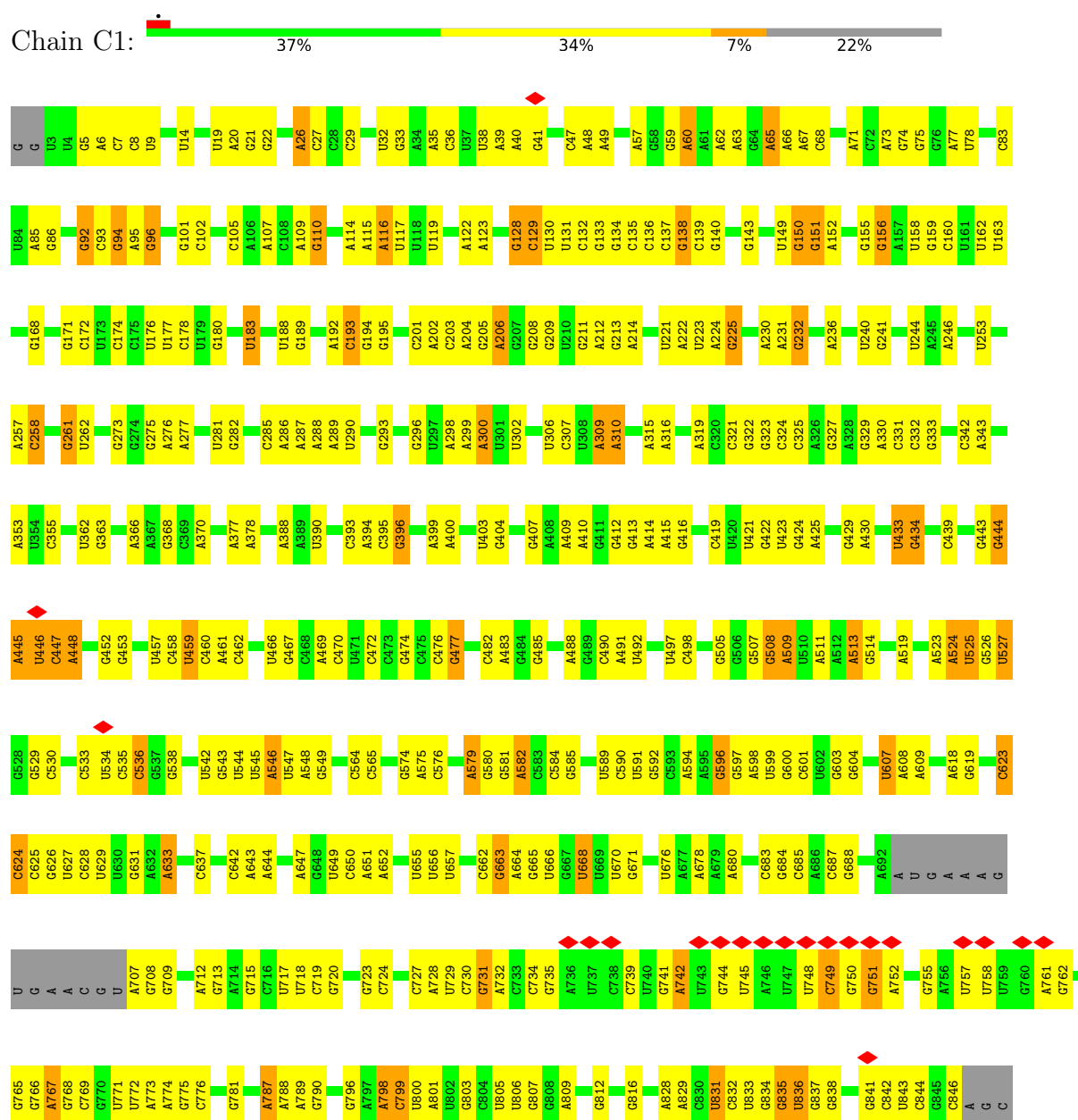
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
60	Lj	1	1	1	0

3 Residue-property plots

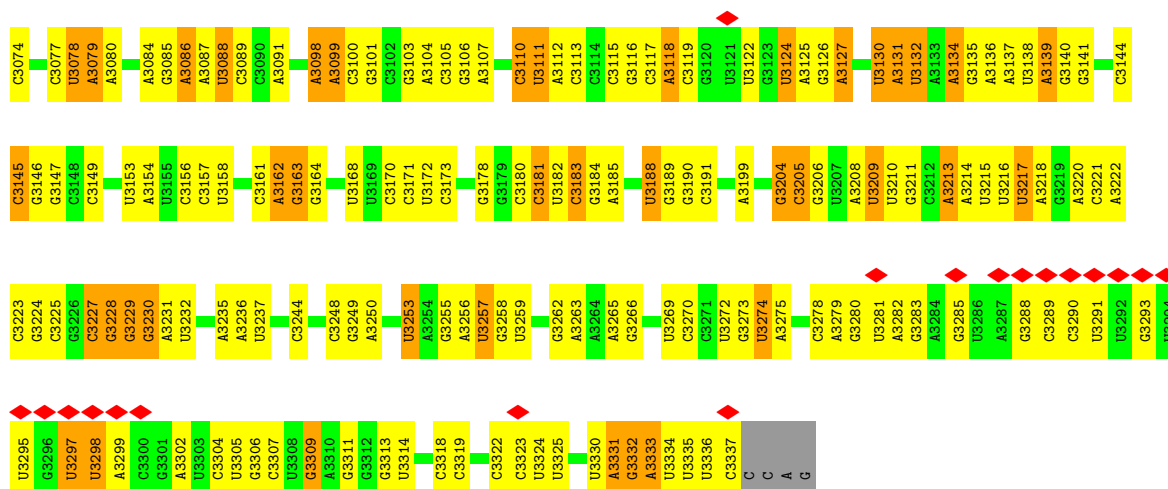
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

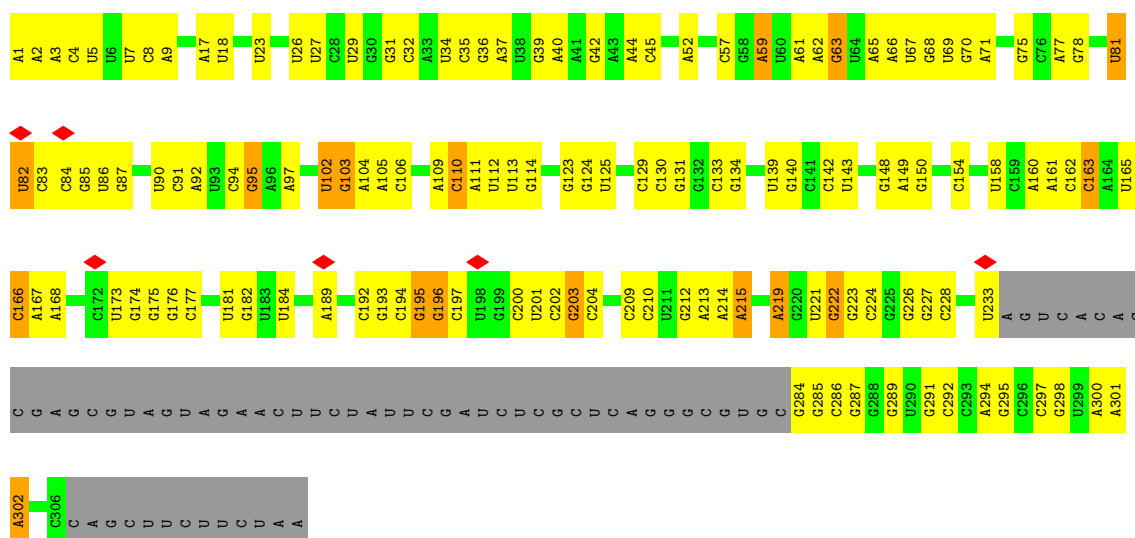




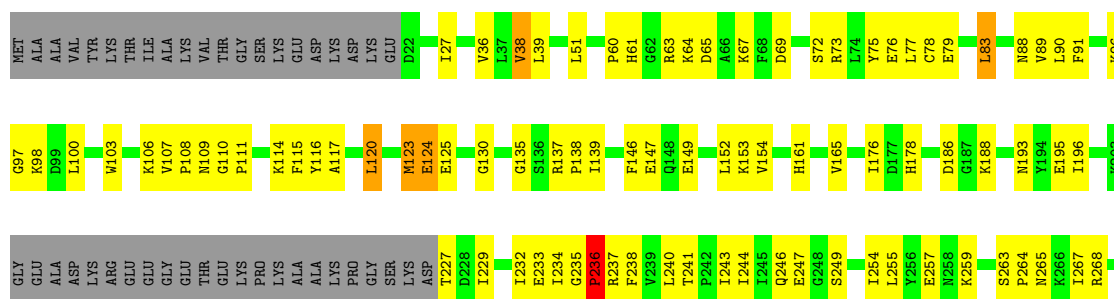


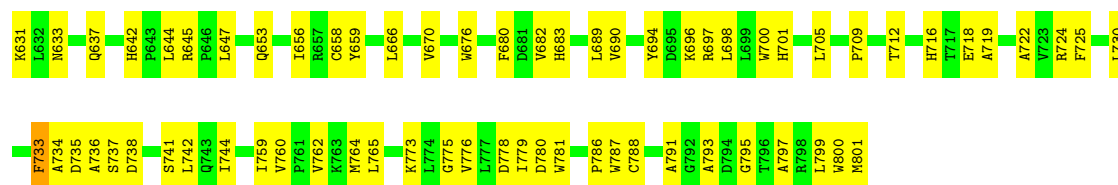


• Molecule 2: RNA (319-MER)

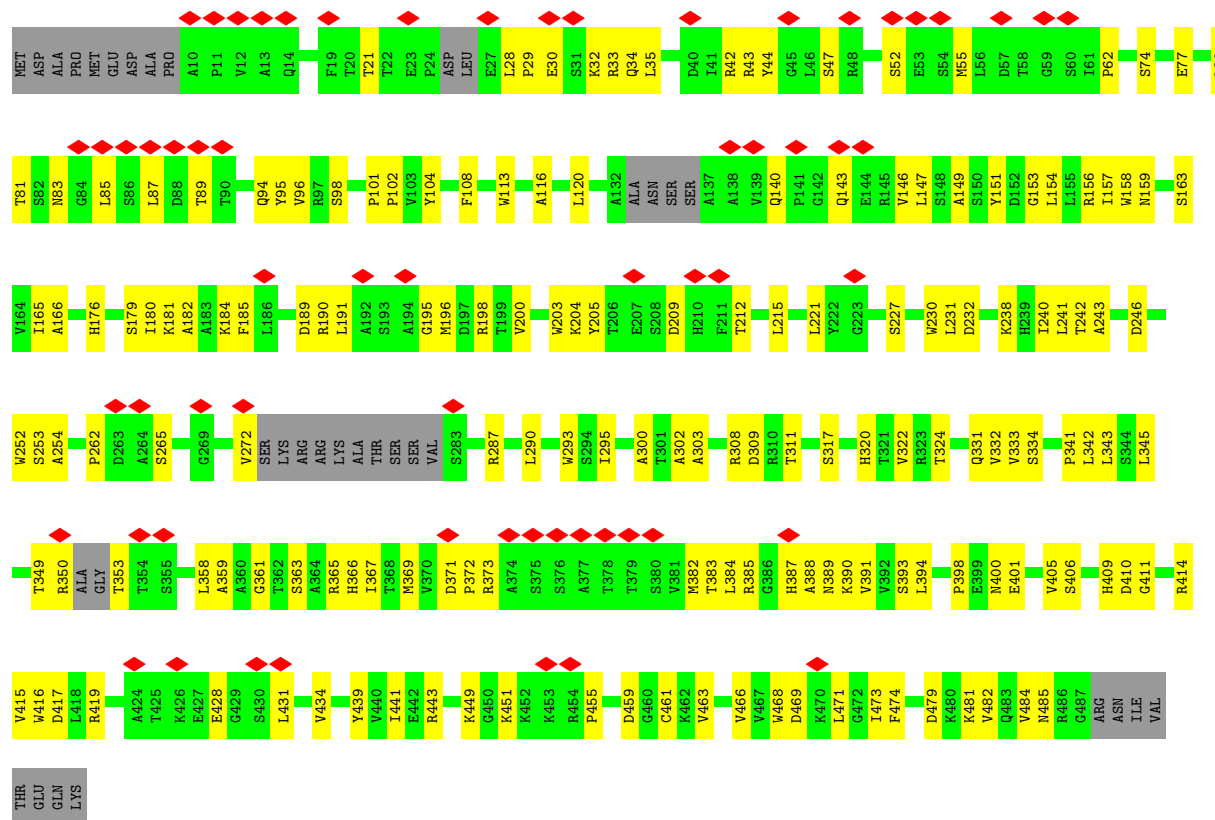


• Molecule 3: Brix domain-containing protein

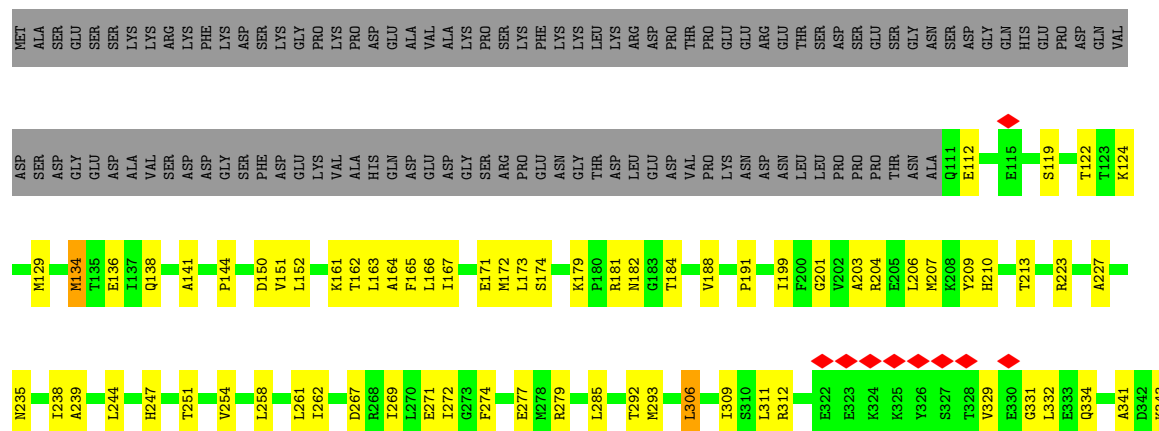


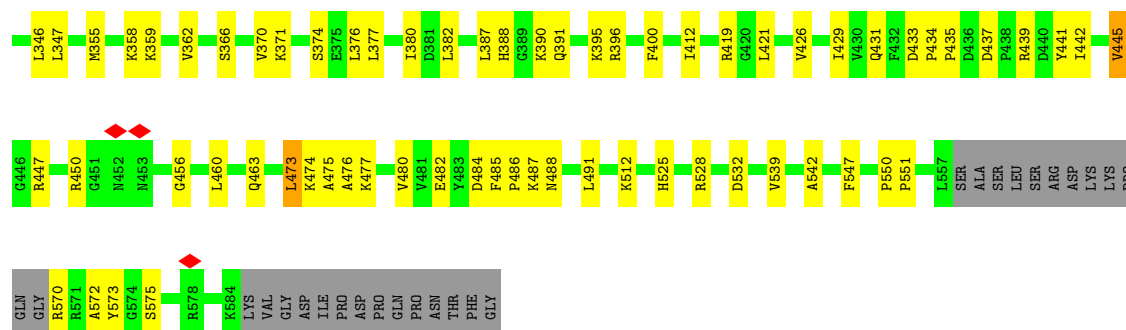


• Molecule 6: Ribosome biogenesis protein YTM1

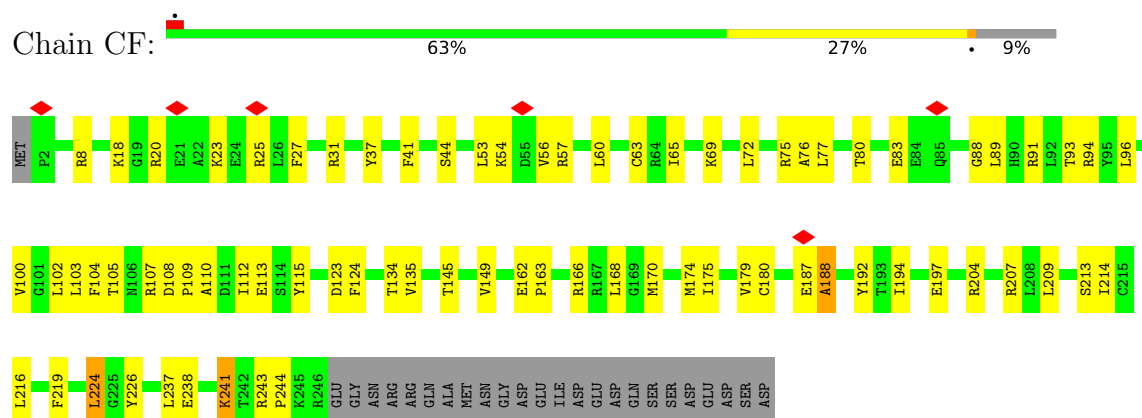


• Molecule 7: RNA helicase

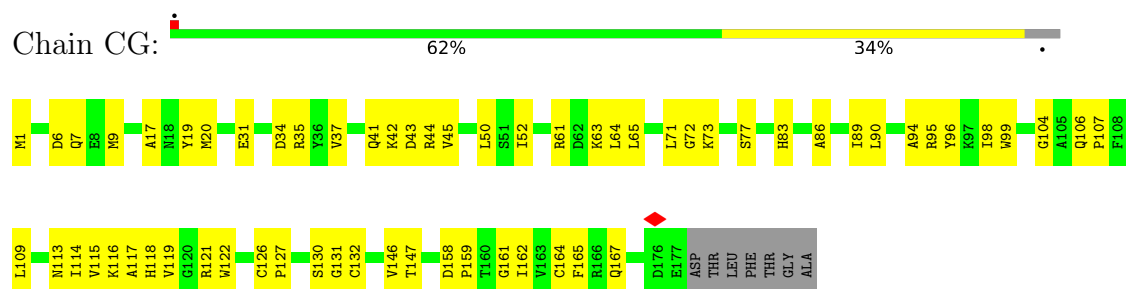




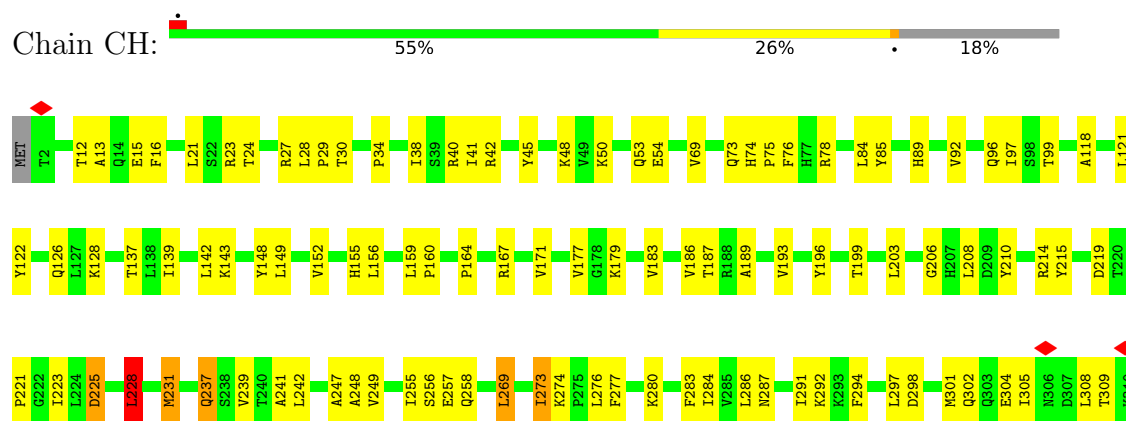
• Molecule 8: Ribosome assembly factor mrt4



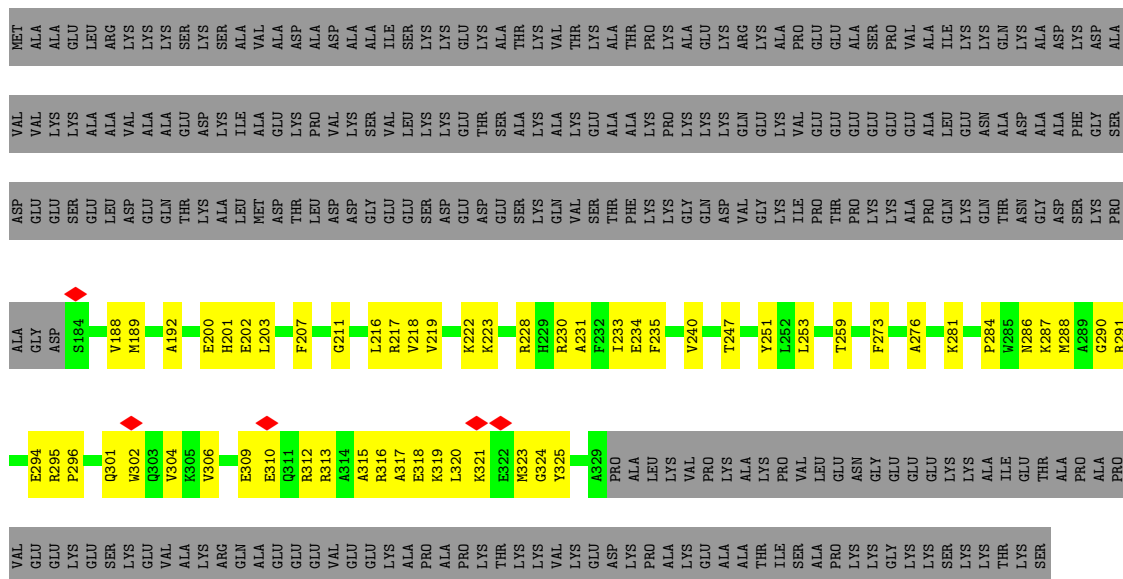
• Molecule 9: 60S ribosome subunit biogenesis protein NIP7



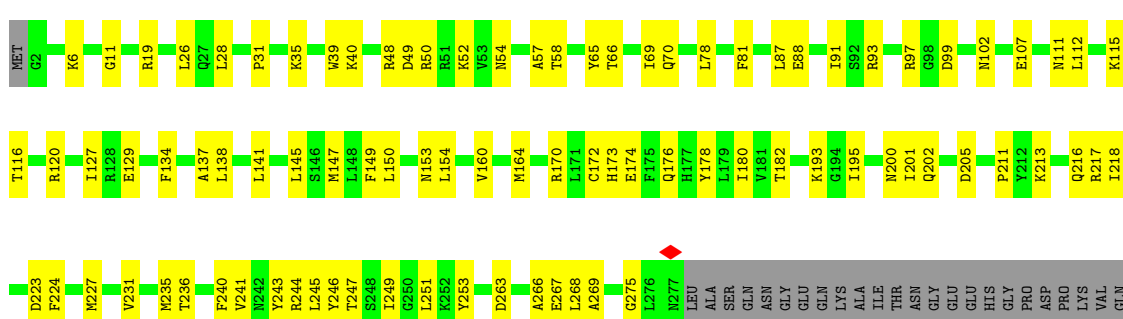
• Molecule 10: Nucleolar GTP-binding protein 1

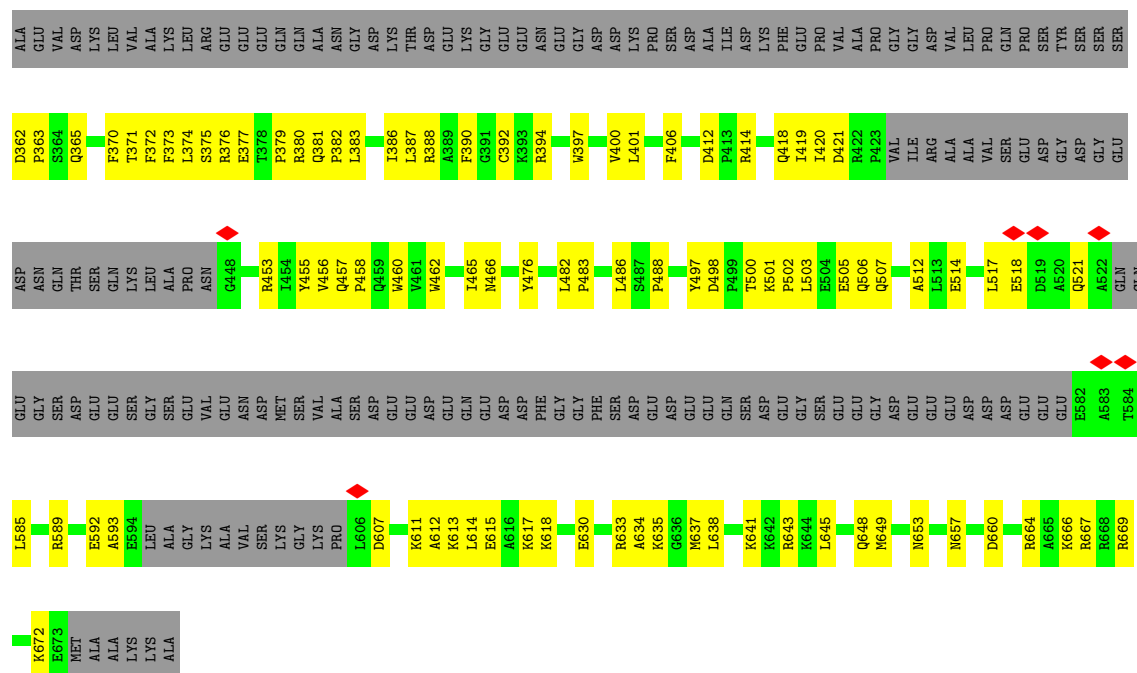


- Molecule 11: Putative RNA-binding protein

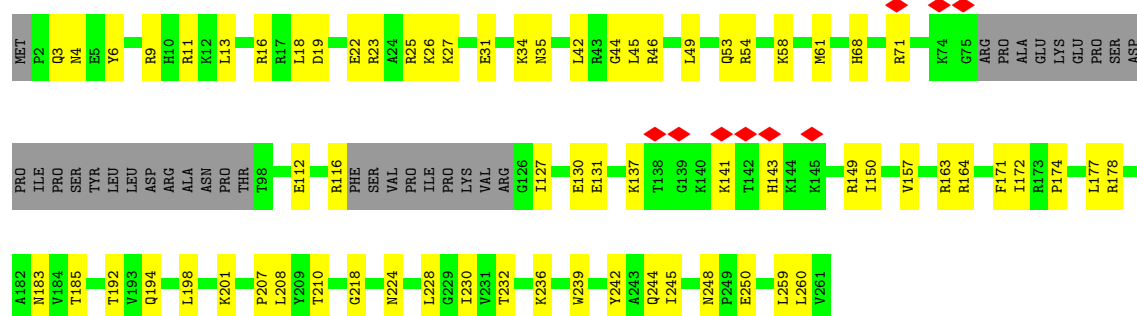


- Molecule 12: Pescadillo homolog

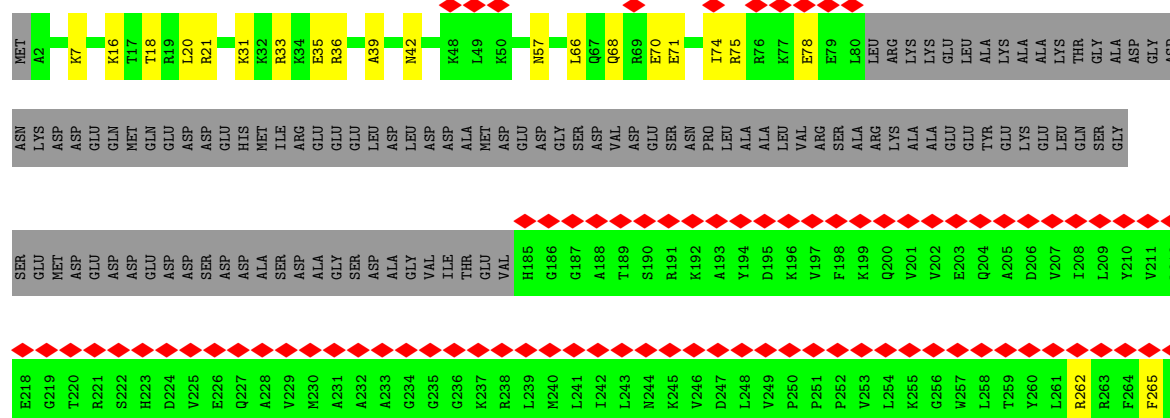


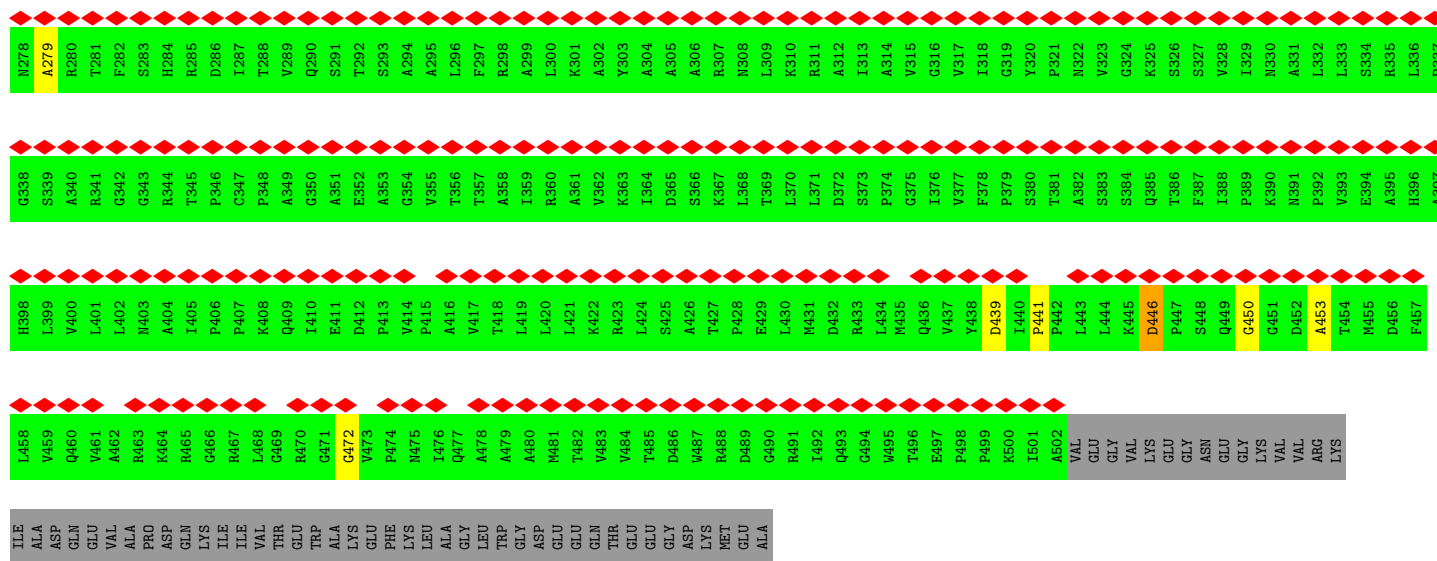


• Molecule 13: Ribosome biogenesis protein NSA2 homolog

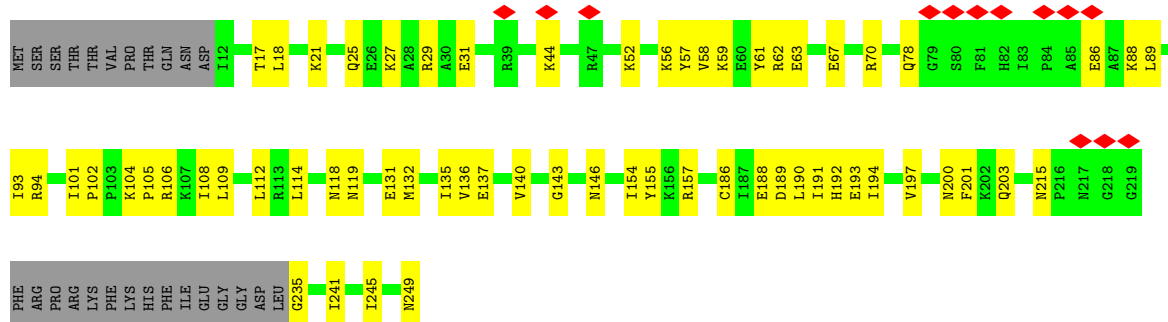


• Molecule 14: Putative GTP binding protein

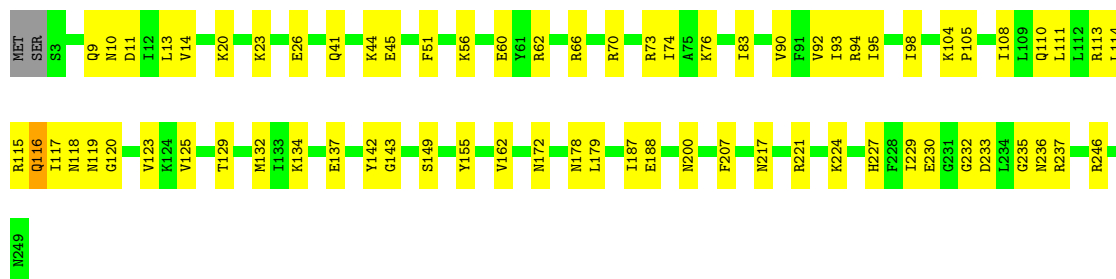




- Molecule 15: 60S ribosomal protein l7-like protein

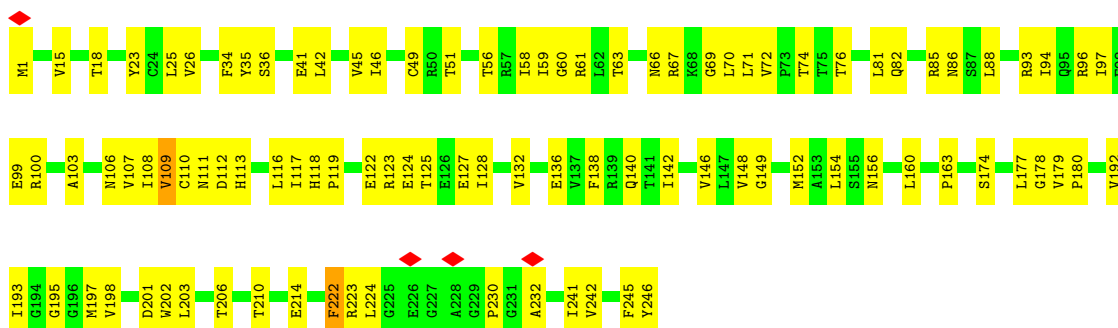


- Molecule 15: 60S ribosomal protein l7-like protein

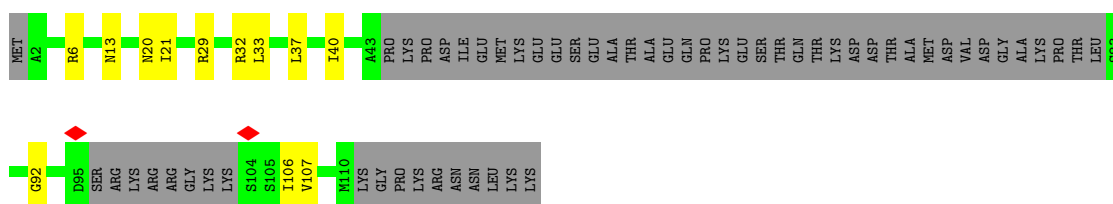


- Molecule 16: Eukaryotic translation initiation factor 6

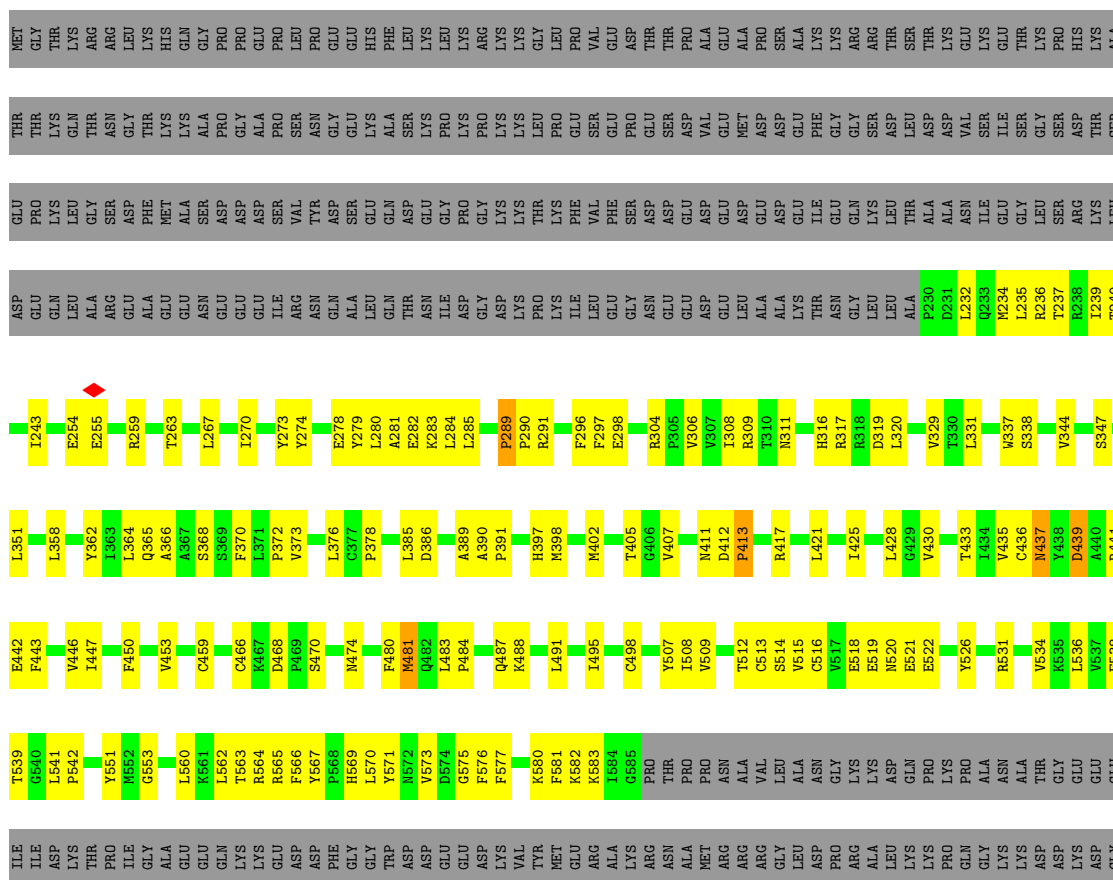
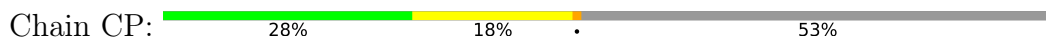




• Molecule 17: DUF2423 domain-containing protein

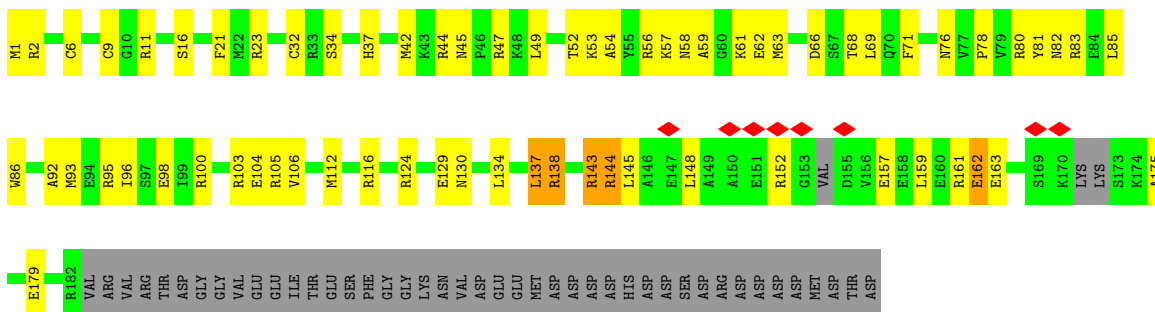


• Molecule 18: RNA methyltransferase nop2-like protein

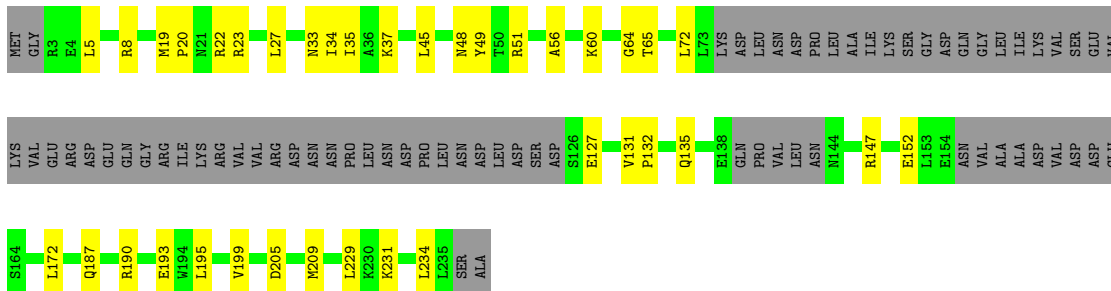


[illegible]

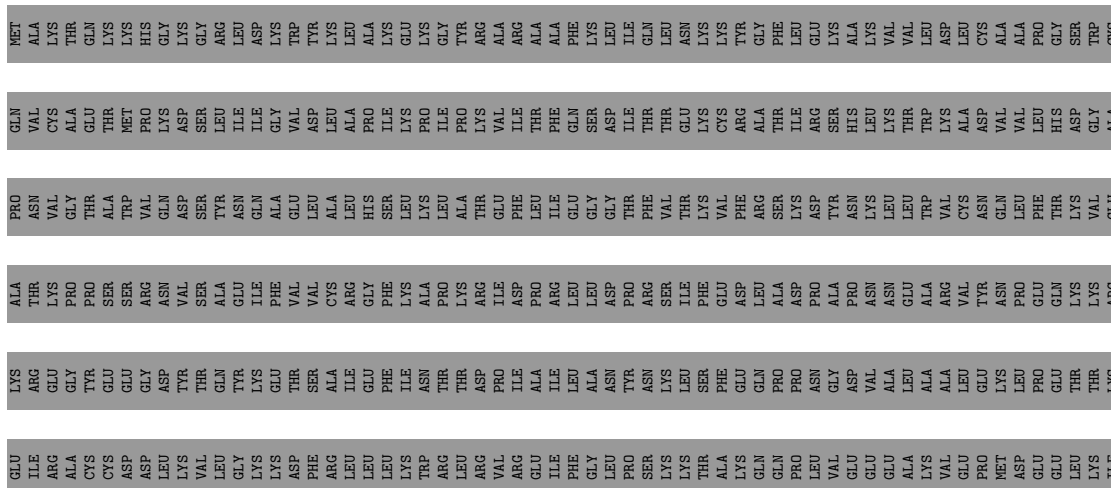
- Molecule 19: Ribosome biogenesis protein RLP24

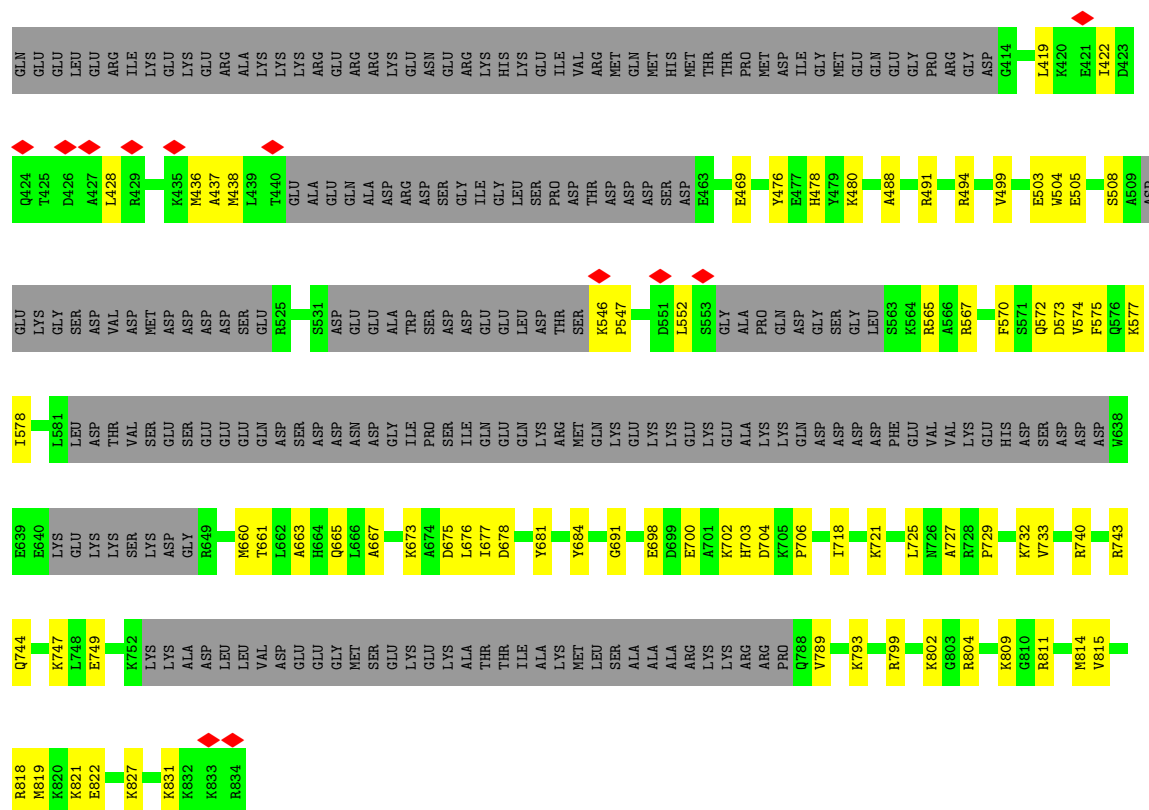


- Molecule 20: Nucleolar protein 16

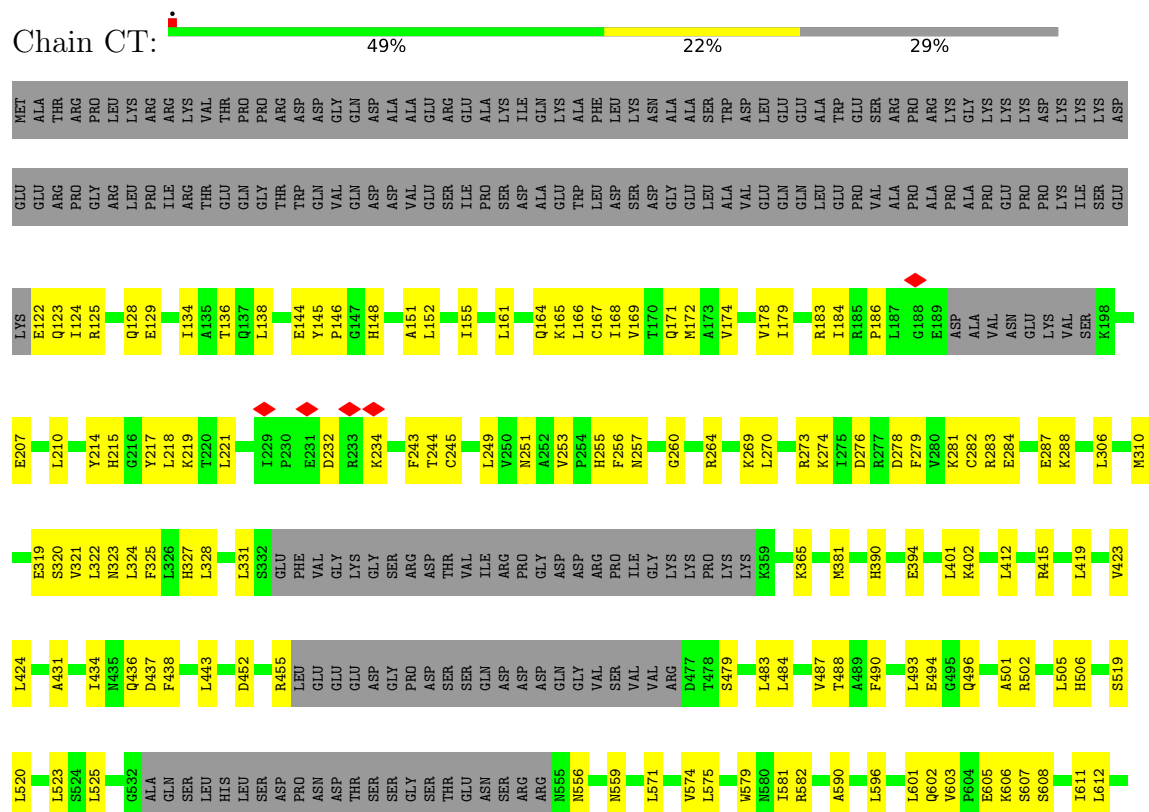


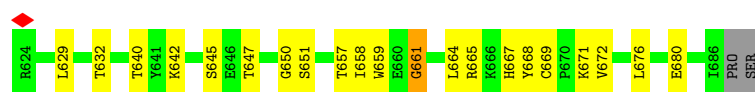
- Molecule 21: AdoMet-dependent rRNA methyltransferase SPB1



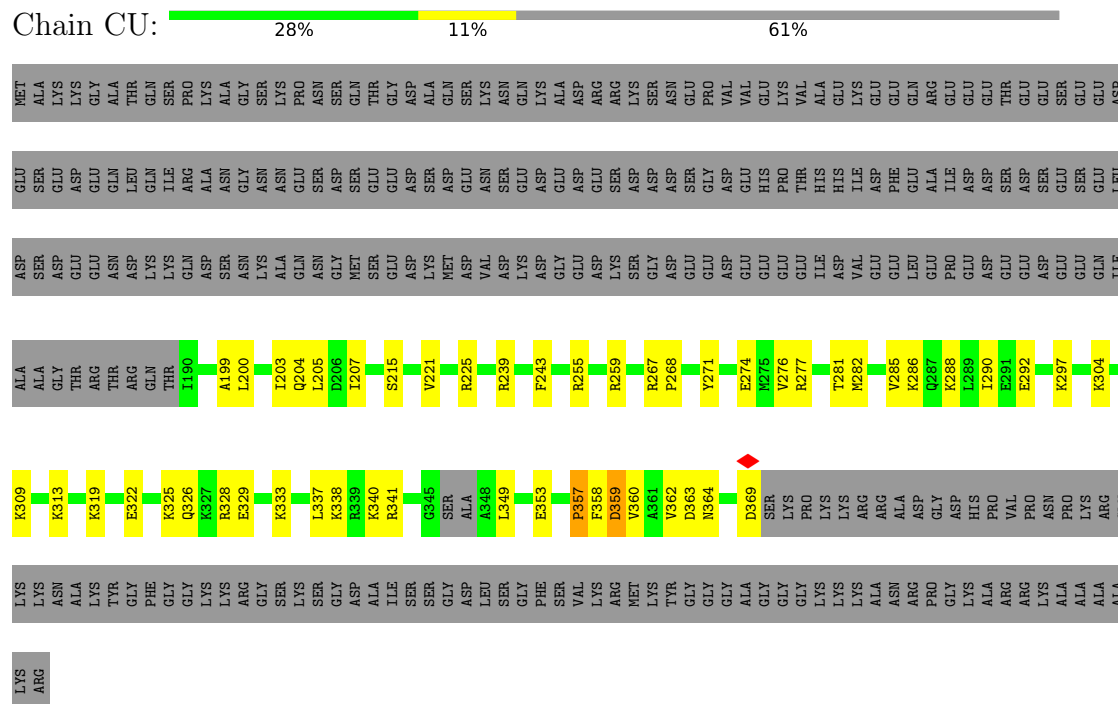


• Molecule 22: Nucleolar complex-associated protein 3

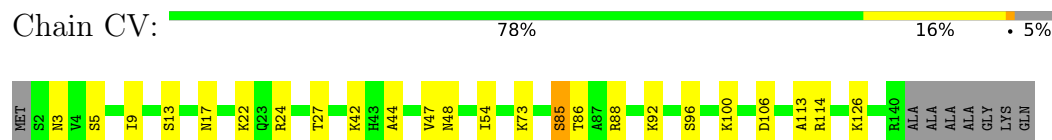




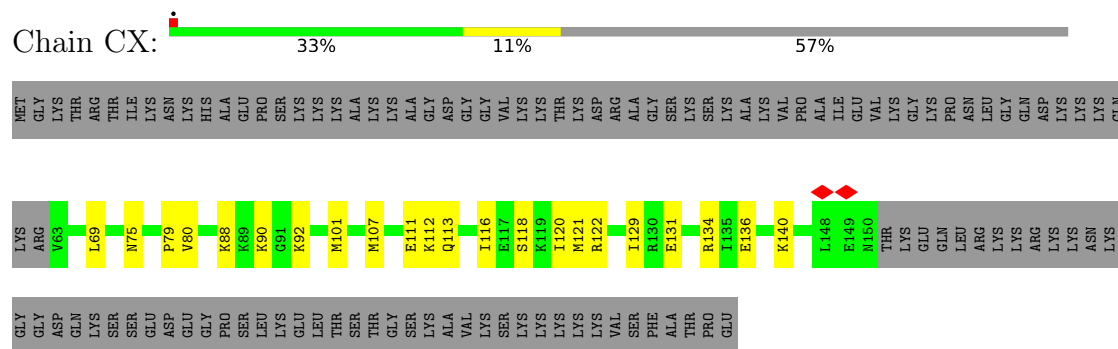
• Molecule 23: rRNA-processing protein EBP2



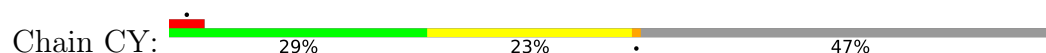
• Molecule 24: Putative 60S ribosomal protein



• Molecule 25: 60S ribosomal subunit-like protein

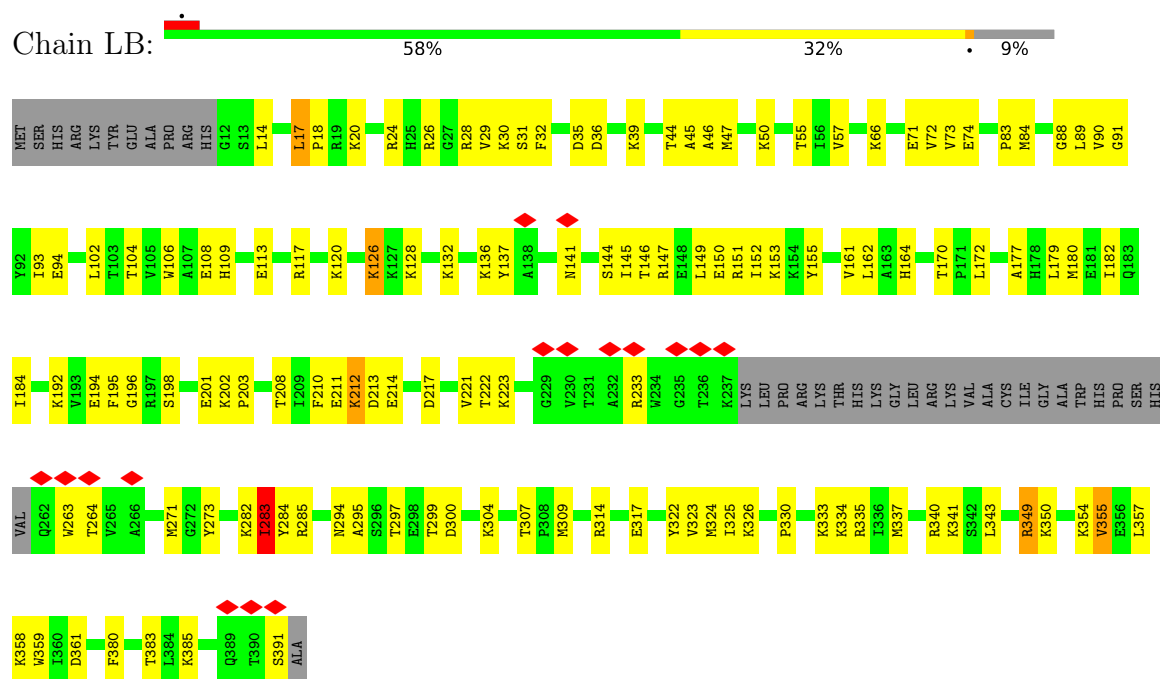


• Molecule 26: Putative NOC2 family protein



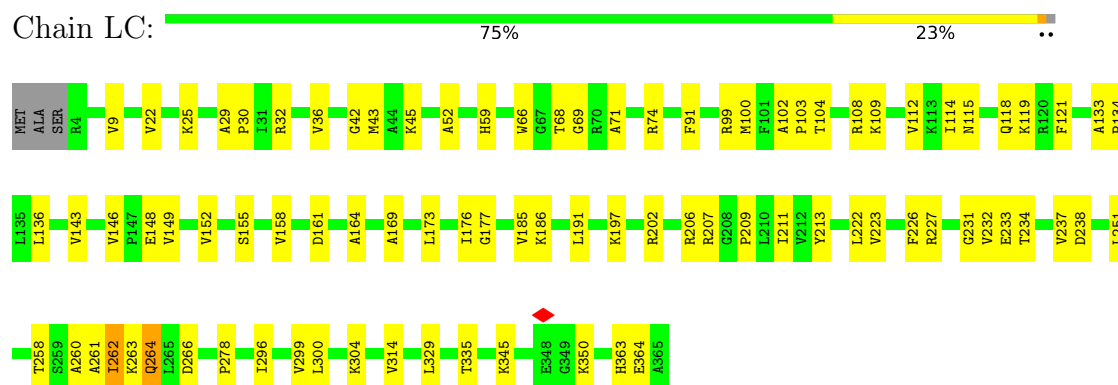
• Molecule 28: 60S ribosomal protein L3-like protein

Chain LB:



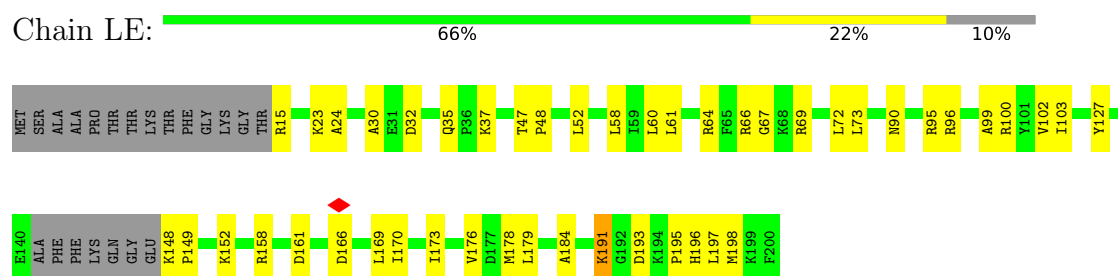
• Molecule 29: 60S ribosomal protein L4-like protein

Chain LC:



• Molecule 30: 60S ribosomal protein L6

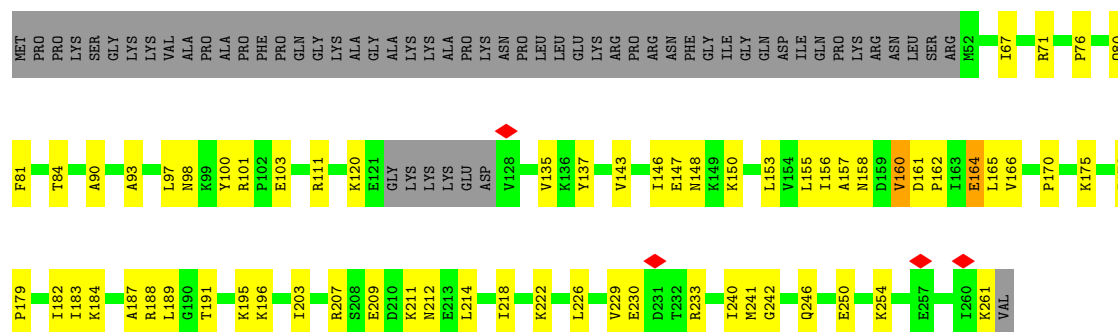
Chain LE:



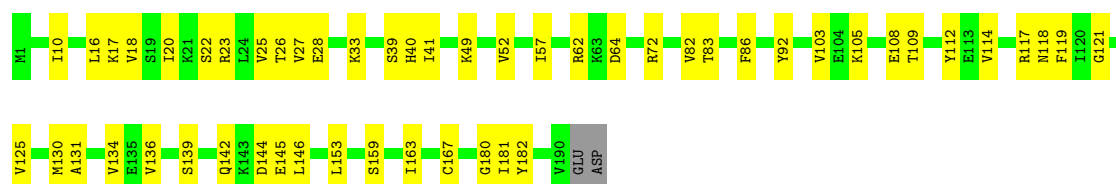
• Molecule 31: 60S ribosomal protein L8

Chain LG:

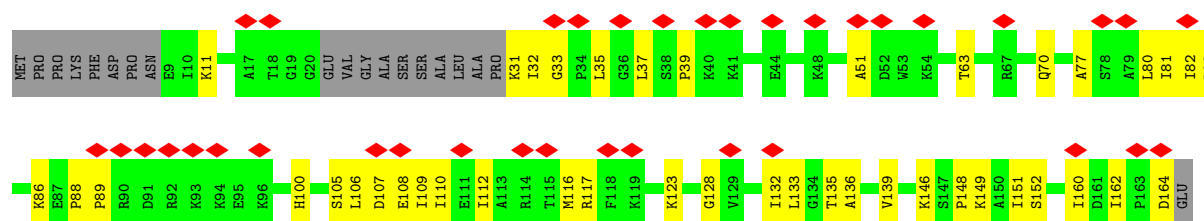




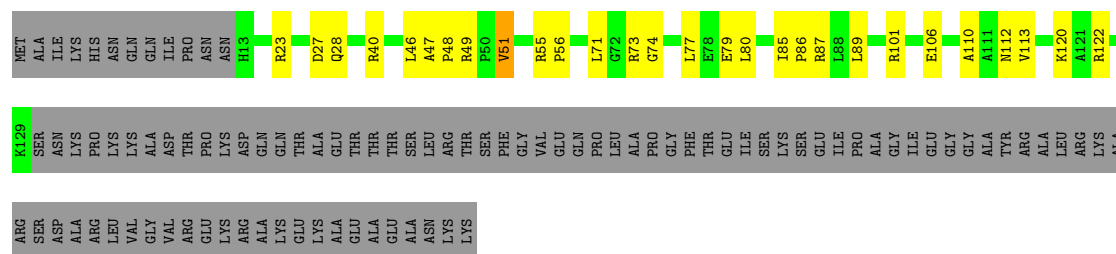
- Molecule 32: 60S ribosomal protein 19-like protein



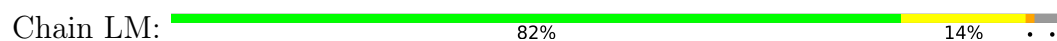
- Molecule 33: 60S ribosomal protein L12-like protein



- Molecule 34: 60S ribosomal protein L13

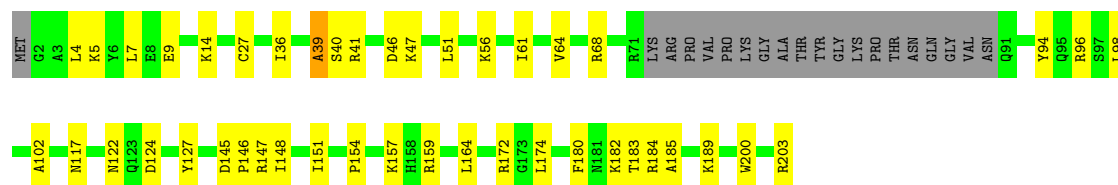


- Molecule 35: 60S ribosomal protein L14-like protein



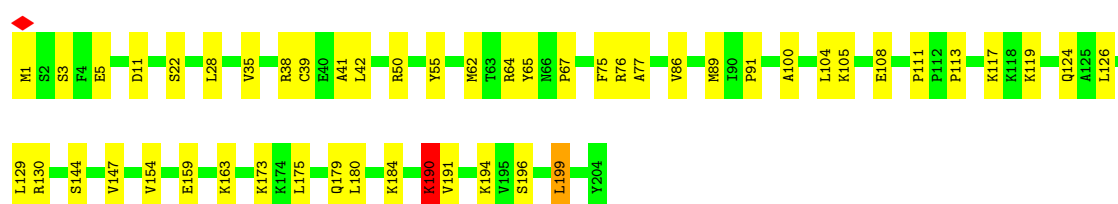
- Molecule 36: Ribosomal protein L15

Chain LN:  68% 21% 10%



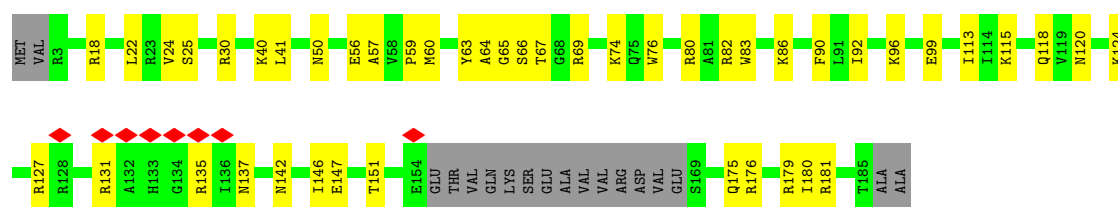
- Molecule 37: 60S ribosomal protein L16-like protein

Chain LO:  75% 24%

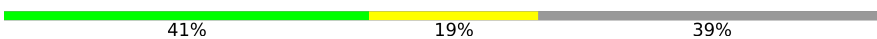


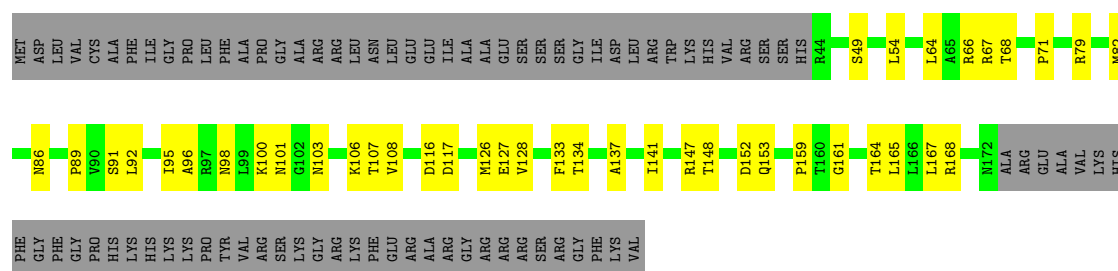
- Molecule 38: 60S ribosomal protein l17-like protein

Chain LP:  66% 25% 10%

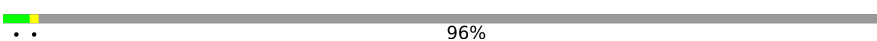


- Molecule 39: Ribosomal protein L18-like protein

Chain LQ:  41% 19% 39%



- Molecule 40: Ribosomal protein L19

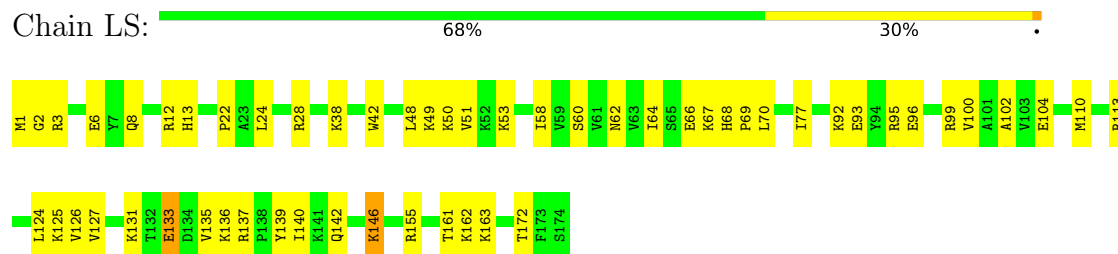
Chain LR:  96%



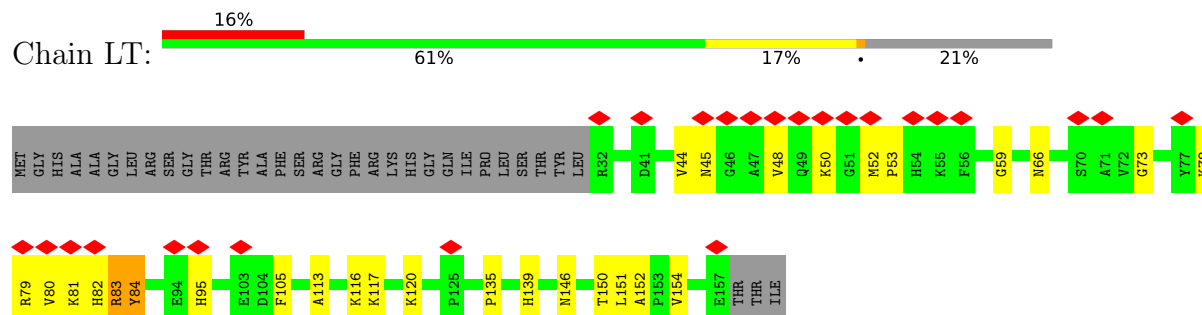




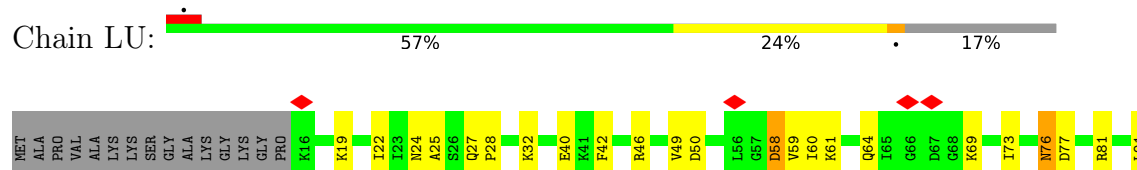
- Molecule 41: 60S ribosomal protein L20

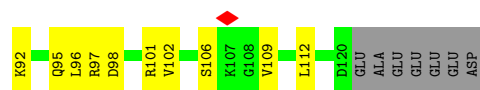


- Molecule 42: 60S ribosomal protein l21-like protein

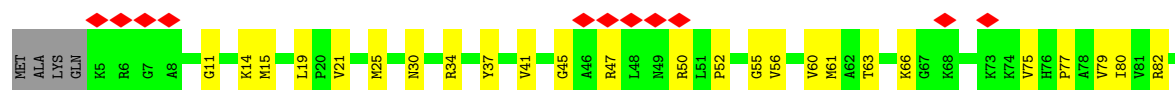


- Molecule 43: 60S ribosomal protein L22-like protein

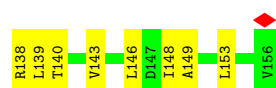
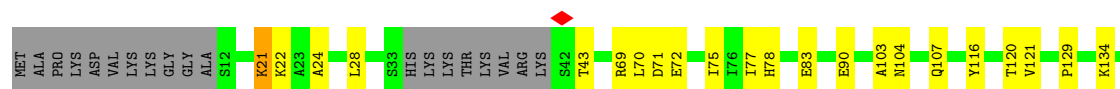




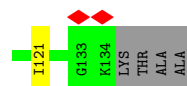
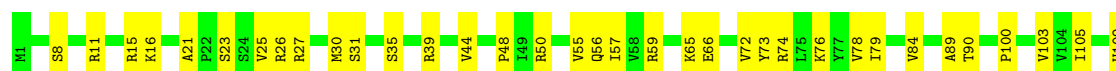
- Molecule 44: 60S ribosomal protein l23-like protein



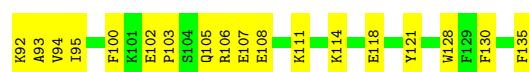
- Molecule 45: 60S ribosomal protein L25-like protein



- Molecule 46: 60S ribosomal protein L26-like protein

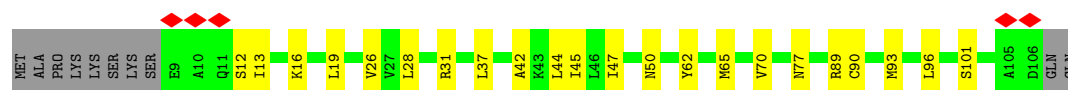


- Molecule 47: 60S ribosomal protein L27

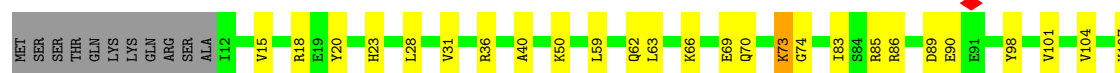


- Molecule 48: 60S ribosomal protein l30-like protein

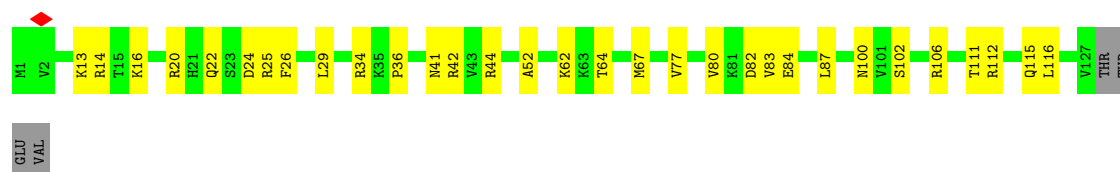
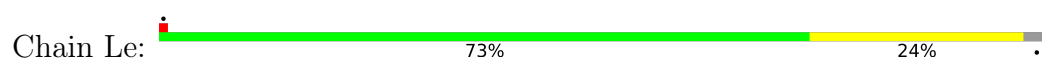




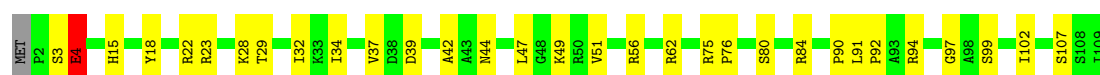
- Molecule 49: Putative 60S ribosomal protein



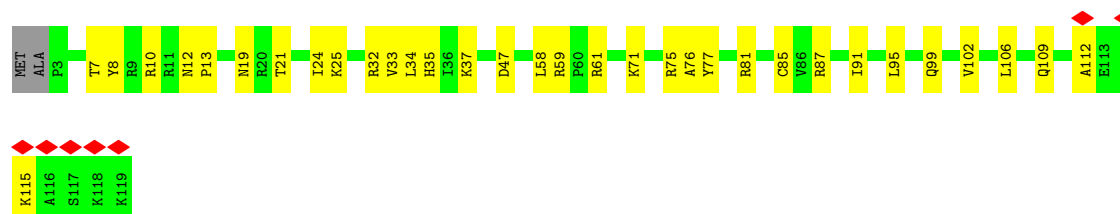
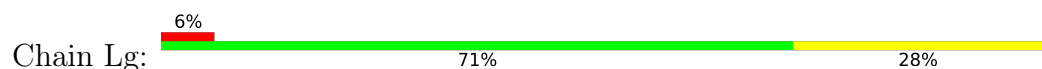
- Molecule 50: 60S ribosomal protein L32-like protein



- Molecule 51: 60S ribosomal protein l33-like protein



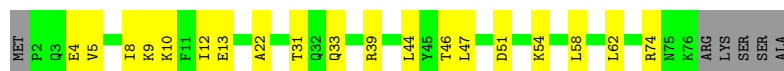
- Molecule 52: Ribosomal protein l34-like protein



- Molecule 53: dolichyl-diphosphooligosaccharide--protein glycotransferase



Chain Lk:  69% 23% 7%



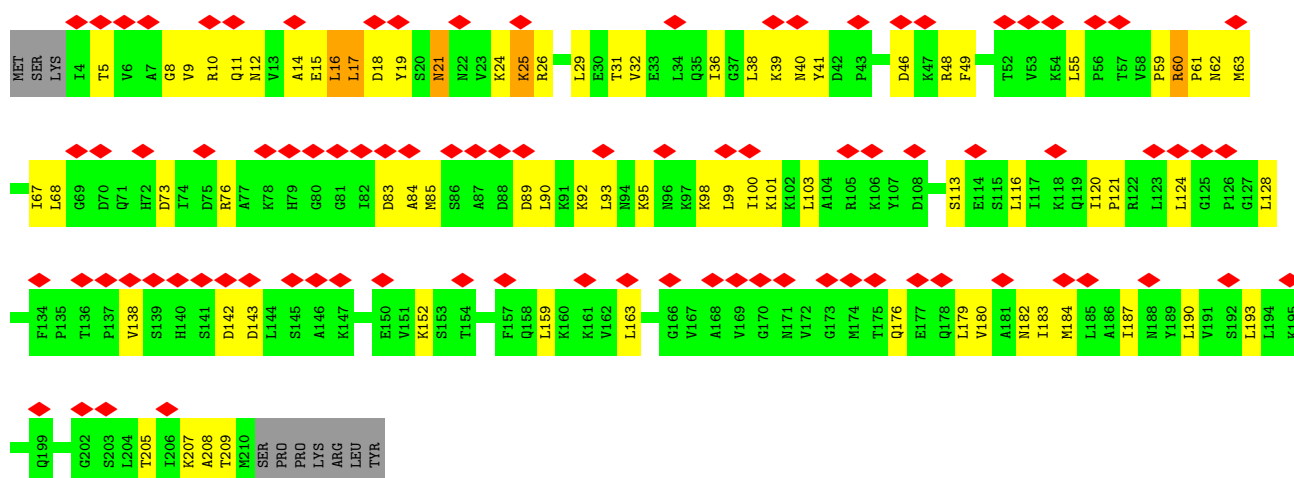
- Molecule 57: 60S ribosomal protein L39

Chain Ll:  57% 18% 25%



- Molecule 58: Ribosomal protein

Chain Lq:  41% 61% 32% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	70516	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	0.520	Depositor
Minimum map value	-0.260	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

5.1 Standard geometry

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

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	0.23	0/62448	0.36	1/97346 (0.0%)
2	C2	0.17	0/6097	0.28	0/9499
3	CA	0.40	0/2115	0.76	5/2840 (0.2%)
4	CB	0.44	0/2109	0.79	1/2866 (0.0%)
5	CC	0.29	0/5423	0.59	2/7380 (0.0%)
6	CD	0.16	0/3543	0.47	0/4824
7	CE	0.37	0/3739	0.67	1/5040 (0.0%)
8	CF	0.26	0/1982	0.55	0/2671
9	CG	0.30	0/1422	0.61	0/1920
10	CH	0.31	0/4468	0.61	1/6029 (0.0%)
11	CI	0.33	0/1225	0.72	0/1645
12	CJ	0.26	0/4125	0.57	0/5548
13	CK	0.19	0/1863	0.46	0/2494
14	CL	0.27	0/2247	0.52	0/3076
15	CM	0.24	0/1851	0.55	0/2481
15	LF	0.29	0/2055	0.56	0/2758
16	CN	0.33	0/1881	0.69	2/2560 (0.1%)
17	CO	0.15	0/470	0.40	0/619
18	CP	0.31	0/2859	0.64	3/3870 (0.1%)
19	CQ	0.33	0/1507	0.70	1/1996 (0.1%)
20	CR	0.21	0/1369	0.49	0/1828
21	CS	0.16	0/2127	0.46	0/2817
22	CT	0.26	0/3974	0.55	0/5357
23	CU	0.30	0/1428	0.66	0/1910
24	CV	0.16	0/1091	0.40	0/1468
25	CX	0.19	0/705	0.46	0/938
26	CY	0.29	0/3454	0.68	3/4637 (0.1%)
27	Cz	0.28	0/598	0.61	0/785
28	LB	0.32	0/2885	0.64	3/3872 (0.1%)
29	LC	0.25	0/2809	0.49	0/3787
30	LE	0.21	0/1428	0.46	0/1921
31	LG	0.29	0/1667	0.56	0/2230

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LH	0.17	0/1516	0.44	0/2038
33	LK	0.16	0/1124	0.41	0/1507
34	LL	0.27	0/983	0.54	0/1318
35	LM	0.34	0/1120	0.65	0/1507
36	LN	0.26	0/1595	0.51	1/2132 (0.0%)
37	LO	0.32	0/1652	0.57	0/2215
38	LP	0.15	0/1367	0.40	0/1838
39	LQ	0.17	0/1033	0.41	0/1391
40	LR	0.16	0/985	0.40	0/1318
41	LS	0.26	0/1468	0.55	2/1975 (0.1%)
42	LT	0.29	0/1033	0.43	0/1389
43	LU	0.38	0/863	0.64	1/1155 (0.1%)
44	LV	0.21	0/1013	0.50	0/1361
45	LX	0.30	0/1078	0.52	0/1451
46	LY	0.16	0/1079	0.39	0/1443
47	LZ	0.29	0/1135	0.58	0/1519
48	Lc	0.41	0/740	0.68	0/995
49	Ld	0.35	0/904	0.58	0/1209
50	Le	0.15	0/1043	0.38	0/1389
51	Lf	0.29	0/883	0.46	0/1187
52	Lg	0.40	0/943	0.64	0/1258
53	Lh	0.15	0/1006	0.32	0/1338
54	Li	0.22	0/738	0.43	0/971
55	Lj	0.37	0/606	0.68	0/803
56	Lk	0.18	0/628	0.52	0/835
57	Ll	0.16	0/329	0.34	0/440
58	Lq	0.29	0/1621	0.65	0/2180
All	All	0.26	0/165449	0.49	27/237174 (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
58	Lq	0	1

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	CC	733	PHE	CA-CB-CG	8.26	122.06	113.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	CA	238	PHE	CA-CB-CG	7.33	121.14	113.80
3	CA	236	PRO	N-CA-CB	-7.31	95.58	103.25
18	CP	289	PRO	CB-CA-C	-7.12	102.23	110.92
36	LN	39	ALA	O-C-N	6.66	131.14	123.29
1	C1	3257	U	C2'-C3'-O3'	6.46	119.19	109.50
28	LB	213	ASP	CA-CB-CG	6.40	119.00	112.60
41	LS	137	ARG	CA-C-N	5.88	125.75	119.28
41	LS	137	ARG	C-N-CA	5.88	125.75	119.28
26	CY	642	PHE	CA-CB-CG	5.74	119.54	113.80
18	CP	413	PRO	CA-C-O	-5.65	117.03	121.38
43	LU	58	ASP	N-CA-C	-5.54	107.10	112.97
5	CC	390	LEU	N-CA-C	-5.45	105.50	111.82
4	CB	263	ILE	N-CA-C	-5.40	105.24	110.42
7	CE	474	LYS	N-CA-C	-5.35	105.45	111.28
10	CH	237	GLN	N-CA-C	-5.34	105.45	111.28
28	LB	283	ILE	N-CA-CB	5.34	116.93	110.95
16	CN	222	PHE	CA-CB-CG	5.32	119.12	113.80
3	CA	61	HIS	N-CA-C	-5.28	106.61	112.57
3	CA	238	PHE	CA-C-N	-5.26	116.25	123.14
3	CA	238	PHE	C-N-CA	-5.26	116.25	123.14
16	CN	198	VAL	CB-CA-C	5.24	117.25	110.12
18	CP	439	ASP	N-CA-C	-5.18	102.61	110.28
26	CY	642	PHE	CA-C-N	-5.18	113.30	122.26
26	CY	642	PHE	C-N-CA	-5.18	113.30	122.26
19	CQ	162	GLU	N-CA-C	-5.08	104.72	112.04
28	LB	18	PRO	N-CA-C	-5.02	102.13	112.47

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
58	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	55815	0	28132	949	0
2	C2	5456	0	2762	103	0
3	CA	2069	0	2109	68	0
4	CB	2063	0	2131	74	0
5	CC	5297	0	5220	175	0
6	CD	3468	0	3428	129	0
7	CE	3669	0	3775	91	0
8	CF	1945	0	1965	54	0
9	CG	1396	0	1420	47	0
10	CH	4388	0	4454	148	0
11	CI	1196	0	1202	50	0
12	CJ	4040	0	4087	135	0
13	CK	1835	0	1935	61	0
14	CL	2239	0	1495	18	0
15	CM	1820	0	1938	49	0
15	LF	2017	0	2130	58	0
16	CN	1856	0	1856	76	0
17	CO	468	0	503	12	0
18	CP	2798	0	2812	105	0
19	CQ	1485	0	1549	68	0
20	CR	1354	0	1400	28	0
21	CS	2105	0	2183	64	0
22	CT	3911	0	4023	110	0
23	CU	1415	0	1457	46	0
24	CV	1073	0	1130	19	0
25	CX	701	0	742	18	0
26	CY	3399	0	3549	157	0
27	Cz	592	0	640	11	0
28	LB	2829	0	2933	101	0
29	LC	2752	0	2878	71	0
30	LE	1403	0	1503	34	0
31	LG	1644	0	1793	50	0
32	LH	1496	0	1575	40	0
33	LK	1112	0	1190	28	0
34	LL	964	0	1041	22	0
35	LM	1101	0	1170	14	0
36	LN	1563	0	1618	31	0
37	LO	1618	0	1714	35	0
38	LP	1345	0	1389	36	0
39	LQ	1021	0	1118	33	0
40	LR	969	0	1027	20	0
41	LS	1433	0	1496	48	0
42	LT	1014	0	1073	20	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	LU	850	0	894	21	0
44	LV	995	0	1055	31	0
45	LX	1062	0	1145	20	0
46	LY	1065	0	1156	32	0
47	LZ	1112	0	1181	44	0
48	Lc	731	0	772	13	0
49	Ld	890	0	940	22	0
50	Le	1025	0	1104	24	0
51	Lf	862	0	891	24	0
52	Lg	930	0	1011	22	0
53	Lh	995	0	1110	17	0
54	Li	731	0	797	16	0
55	Lj	595	0	625	12	0
56	Lk	620	0	680	14	0
57	Ll	322	0	346	8	0
58	Lq	1600	0	1703	54	0
59	CH	32	0	12	3	0
60	CQ	1	0	0	0	0
60	Lj	1	0	0	0	0
All	All	156553	0	128967	3358	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 (3358) 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	1.35	1.22
1:C1:3118:A:N6	1:C1:3225:C:H42	1.36	1.19
1:C1:2848:A:N6	1:C1:2871:C:H42	1.51	1.09
1:C1:2848:A:H61	1:C1:2871:C:N4	1.48	1.08
12:CJ:660:ASP:HB3	12:CJ:664:ARG:HH12	1.26	0.99
1:C1:1464:A:N3	26:CY:16:LYS:NZ	2.13	0.97
1:C1:856:G:N1	1:C1:875:A:N6	2.13	0.96
1:C1:1046:A:N6	1:C1:1074:C:C2	2.35	0.93
1:C1:891:G:H1	1:C1:898:A:N6	1.66	0.92
1:C1:1156:G:H21	1:C1:1157:C:H41	1.10	0.92
6:CD:369:MET:HB2	6:CD:382:MET:HB2	1.51	0.91
2:C2:94:C:H5"	55:Lj:76:ASN:HD21	1.36	0.90
1:C1:2404:G:H1	1:C1:2467:U:H3	1.12	0.90
32:LH:23:ARG:HD2	32:LH:39:SER:HA	1.52	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:258:GLN:HE22	33:LK:33:GLY:HA3	1.37	0.88
32:LH:92:TYR:HB3	32:LH:181:ILE:HG22	1.54	0.88
1:C1:891:G:H1	1:C1:898:A:H61	1.12	0.87
21:CS:488:ALA:HA	21:CS:491:ARG:HG2	1.57	0.87
11:CI:309:GLU:OE1	11:CI:313:ARG:NH1	2.07	0.86
1:C1:670:U:O4	1:C1:684:G:O6	1.94	0.86
10:CH:541:THR:H	19:CQ:143:ARG:HH12	1.24	0.86
6:CD:405:VAL:HG12	6:CD:415:VAL:HG12	1.56	0.85
2:C2:219:A:N6	11:CI:218:VAL:O	2.09	0.85
49:Ld:18:ARG:NH1	49:Ld:20:TYR:OH	2.09	0.85
1:C1:3288:G:H1	1:C1:3297:U:H3	1.26	0.84
1:C1:856:G:H1	1:C1:875:A:N6	1.73	0.84
49:Ld:83:ILE:HG12	49:Ld:101:VAL:HG22	1.60	0.83
3:CA:114:LYS:HB3	3:CA:244:ILE:HG22	1.60	0.83
6:CD:398:PRO:HG2	6:CD:469:ASP:HA	1.61	0.83
6:CD:367:ILE:HB	6:CD:384:LEU:HB2	1.59	0.82
29:LC:109:LYS:HE3	36:LN:203:ARG:HB2	1.62	0.82
6:CD:238:LYS:HD2	6:CD:254:ALA:HB3	1.62	0.82
26:CY:583:GLU:HG3	26:CY:610:ARG:HH21	1.44	0.82
1:C1:1464:A:H1'	26:CY:16:LYS:HZ3	1.44	0.81
1:C1:2433:U:O2	1:C1:2436:G:O6	1.96	0.81
42:LT:79:ARG:HA	42:LT:84:TYR:HA	1.60	0.81
1:C1:874:C:N3	1:C1:875:A:N6	2.28	0.81
29:LC:136:LEU:HD23	29:LC:143:VAL:HG21	1.61	0.81
15:LF:149:SER:HA	15:LF:246:ARG:HH22	1.46	0.81
1:C1:3118:A:N1	1:C1:3225:C:N3	2.29	0.81
22:CT:424:LEU:HB3	22:CT:488:THR:HG21	1.63	0.81
24:CV:88:ARG:HD3	30:LE:24:ALA:HB3	1.64	0.80
5:CC:446:GLN:HE22	6:CD:389:ASN:HA	1.45	0.80
31:LG:229:VAL:O	31:LG:233:ARG:HB3	1.81	0.80
49:Ld:15:VAL:HG22	49:Ld:86:ARG:HA	1.63	0.80
1:C1:1045:G:H21	1:C1:1048:G:H21	1.28	0.80
8:CF:91:ARG:HG3	8:CF:94:ARG:HH22	1.46	0.80
8:CF:107:ARG:HG2	8:CF:108:ASP:H	1.47	0.80
18:CP:487:GLN:NE2	18:CP:519:GLU:OE1	2.15	0.80
15:LF:116:GLN:H	15:LF:119:ASN:HD22	1.26	0.80
1:C1:3164:G:C6	1:C1:3206:G:N1	2.51	0.79
16:CN:41:GLU:HB3	16:CN:203:LEU:HD11	1.64	0.79
1:C1:213:G:C6	1:C1:1371:G:C2	2.71	0.79
3:CA:283:MET:HB3	3:CA:287:ARG:HH12	1.46	0.79
4:CB:176:THR:HG23	4:CB:177:LYS:HG3	1.64	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Lf:44:ASN:HA	51:Lf:47:LEU:HD13	1.61	0.79
22:CT:283:ARG:HD2	22:CT:320:SER:HB3	1.65	0.79
41:LS:6:GLU:HB2	41:LS:64:ILE:O	1.83	0.79
26:CY:31:LYS:HE3	26:CY:35:ARG:HE	1.48	0.79
1:C1:3208:A:OP1	30:LE:64:ARG:NH2	2.12	0.78
1:C1:2848:A:N1	1:C1:2871:C:N3	2.31	0.78
25:CX:116:ILE:O	25:CX:122:ARG:NH1	2.16	0.78
2:C2:83:C:N3	46:LY:50:ARG:NH2	2.32	0.78
4:CB:99:LEU:HB3	4:CB:127:VAL:HG12	1.66	0.78
10:CH:379:ARG:NH2	16:CN:177:LEU:O	2.17	0.78
1:C1:1618:C:OP2	52:Lg:75:ARG:NH2	2.17	0.77
16:CN:82:GLN:O	16:CN:86:ASN:ND2	2.17	0.77
35:LM:59:LEU:O	41:LS:155:ARG:NH2	2.17	0.77
6:CD:159:ASN:ND2	6:CD:163:SER:OG	2.17	0.77
16:CN:70:LEU:HB3	16:CN:94:ILE:HG12	1.65	0.77
37:LO:28:LEU:HD11	37:LO:104:LEU:HB2	1.65	0.77
19:CQ:157:GLU:HB3	19:CQ:161:ARG:HH22	1.49	0.77
1:C1:2760:A:H5'	25:CX:90:LYS:HG2	1.67	0.77
1:C1:1157:C:N4	37:LO:89:MET:SD	2.58	0.77
10:CH:69:VAL:O	10:CH:73:GLN:NE2	2.18	0.77
28:LB:91:GLY:HA3	28:LB:152:ILE:HD12	1.67	0.77
1:C1:1046:A:N1	1:C1:1074:C:C4	2.53	0.76
1:C1:2992:C:H5''	17:CO:13:ASN:HD21	1.48	0.76
39:LQ:127:GLU:OE2	39:LQ:147:ARG:NH1	2.19	0.76
8:CF:63:CYS:SG	8:CF:107:ARG:NH2	2.59	0.76
13:CK:18:LEU:HB2	32:LH:182:TYR:HD2	1.51	0.76
40:LR:105:LEU:HD23	40:LR:138:LEU:HD23	1.68	0.76
42:LT:117:LYS:HA	42:LT:120:LYS:HZ3	1.50	0.76
5:CC:364:LYS:NZ	5:CC:368:GLU:OE2	2.15	0.75
31:LG:156:ILE:HD11	31:LG:166:VAL:HB	1.66	0.75
1:C1:835:G:O2'	40:LR:130:ASN:ND2	2.20	0.75
6:CD:410:ASP:OD2	6:CD:414:ARG:NH2	2.20	0.75
37:LO:39:CYS:HA	37:LO:42:LEU:HD13	1.69	0.75
40:LR:105:LEU:HD22	40:LR:135:LYS:HG3	1.67	0.75
1:C1:1549:U:OP1	5:CC:411:TYR:OH	2.05	0.75
15:LF:123:VAL:HG11	15:LF:129:THR:HG21	1.68	0.75
16:CN:66:ASN:HD21	16:CN:110:CYS:HB2	1.50	0.75
1:C1:2369:C:OP1	23:CU:319:LYS:NZ	2.19	0.75
10:CH:315:GLU:OE2	10:CH:337:ARG:NH1	2.19	0.75
12:CJ:506:GLN:HE22	12:CJ:664:ARG:HG2	1.51	0.75
5:CC:787:TRP:CD1	5:CC:801:MET:HG3	2.22	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CI:200:GLU:HG2	11:CI:201:HIS:HD2	1.50	0.74
12:CJ:267:GLU:HG2	12:CJ:268:LEU:H	1.50	0.74
1:C1:1156:G:H21	1:C1:1157:C:N4	1.85	0.74
1:C1:1156:G:N2	1:C1:1157:C:H41	1.84	0.74
1:C1:1203:U:H5'	8:CF:75:ARG:HH21	1.51	0.74
9:CG:161:GLY:HA2	13:CK:141:LYS:HE3	1.70	0.74
1:C1:1239:C:O3'	8:CF:57:ARG:NH1	2.20	0.74
10:CH:183:VAL:HG21	10:CH:219:ASP:HB2	1.68	0.74
19:CQ:47:ARG:HE	19:CQ:58:ASN:HD22	1.35	0.74
2:C2:215:A:O2'	11:CI:230:ARG:NH1	2.20	0.74
29:LC:115:ASN:HB2	29:LC:118:GLN:HG3	1.68	0.74
1:C1:1263:U:H2'	1:C1:1264:G:H8	1.52	0.74
12:CJ:40:LYS:NZ	12:CJ:129:GLU:OE2	2.20	0.73
19:CQ:157:GLU:OE1	19:CQ:161:ARG:NH1	2.17	0.73
1:C1:298:A:OP2	3:CA:265:ASN:ND2	2.22	0.73
44:LV:14:LYS:NZ	44:LV:15:MET:O	2.21	0.73
1:C1:974:G:O6	1:C1:1038:U:O4	2.05	0.73
26:CY:457:GLN:HG2	26:CY:458:ASN:H	1.51	0.73
46:LY:72:VAL:HG23	46:LY:79:ILE:HG22	1.70	0.73
1:C1:1045:G:O2'	1:C1:1079:G:N2	2.21	0.73
1:C1:864:A:OP1	22:CT:582:ARG:NH2	2.22	0.73
3:CA:51:LEU:HD13	3:CA:120:LEU:HD11	1.69	0.73
10:CH:76:PHE:HE1	10:CH:241:ALA:HA	1.53	0.73
21:CS:740:ARG:O	21:CS:744:GLN:NE2	2.22	0.73
35:LM:54:ARG:NH2	35:LM:76:ALA:O	2.21	0.73
6:CD:30:GLU:HA	6:CD:33:ARG:HG2	1.71	0.73
46:LY:100:PRO:HA	46:LY:103:VAL:HG22	1.71	0.73
12:CJ:458:PRO:HB2	12:CJ:462:TRP:HZ3	1.53	0.73
28:LB:66:LYS:NZ	44:LV:11:GLY:O	2.22	0.73
1:C1:1198:C:OP2	14:CL:57:ASN:ND2	2.22	0.73
1:C1:65:A:H1'	1:C1:77:A:H1'	1.71	0.72
1:C1:745:U:O2	1:C1:749:C:N3	2.22	0.72
1:C1:1201:C:OP1	8:CF:20:ARG:NH1	2.22	0.72
26:CY:485:GLN:HB3	26:CY:488:ARG:HB2	1.72	0.72
5:CC:598:ARG:HH12	5:CC:644:LEU:HA	1.55	0.72
9:CG:19:TYR:OH	9:CG:167:GLN:OE1	2.06	0.72
1:C1:2361:A:N6	1:C1:2900:C:C4	2.58	0.72
1:C1:68:C:OP2	1:C1:293:G:N2	2.22	0.72
1:C1:230:A:H2'	1:C1:231:A:C8	2.25	0.72
1:C1:3269:U:H5''	28:LB:309:MET:HE2	1.72	0.72
22:CT:647:THR:HG23	22:CT:650:GLY:H	1.55	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:LN:46:ASP:OD1	36:LN:47:LYS:N	2.22	0.72
12:CJ:377:GLU:OE2	12:CJ:421:ASP:N	2.18	0.72
12:CJ:507:GLN:HG3	12:CJ:512:ALA:HB2	1.72	0.72
2:C2:297:C:H1'	2:C2:301:A:H61	1.55	0.72
46:LY:56:GLN:HG3	46:LY:66:GLU:HG2	1.72	0.71
5:CC:270:PRO:HB3	31:LG:148:ASN:HA	1.72	0.71
12:CJ:518:GLU:OE2	12:CJ:521:GLN:NE2	2.23	0.71
41:LS:77:ILE:HG12	41:LS:126:VAL:HG22	1.72	0.71
1:C1:1394:G:OP1	50:Le:106:ARG:NH2	2.23	0.71
26:CY:457:GLN:O	26:CY:461:TYR:N	2.23	0.71
15:LF:233:ASP:O	15:LF:237:ARG:NH2	2.23	0.71
41:LS:93:GLU:HB3	41:LS:140:ILE:HD12	1.70	0.71
3:CA:38:VAL:HG13	3:CA:90:LEU:HD23	1.72	0.71
5:CC:531:VAL:HA	5:CC:535:LEU:HD23	1.72	0.71
22:CT:179:ILE:HG21	22:CT:253:VAL:HG21	1.72	0.71
26:CY:588:PRO:HD3	26:CY:664:ASN:HB2	1.73	0.71
15:LF:233:ASP:OD1	15:LF:237:ARG:NH2	2.22	0.71
6:CD:80:LEU:O	6:CD:83:ASN:O	2.08	0.71
1:C1:319:A:OP1	34:LL:23:ARG:NH2	2.24	0.71
1:C1:505:G:H5''	29:LC:345:LYS:HE3	1.73	0.71
1:C1:1071:G:H2'	1:C1:1072:G:C8	2.26	0.71
1:C1:3283:G:O2'	1:C1:3302:A:N6	2.21	0.71
22:CT:321:VAL:HA	22:CT:324:LEU:HD13	1.73	0.71
33:LK:105:SER:OG	33:LK:108:GLU:OE1	2.09	0.71
41:LS:124:LEU:HD11	42:LT:154:VAL:HG22	1.70	0.71
11:CI:295:ARG:NH1	11:CI:296:PRO:O	2.23	0.71
31:LG:103:GLU:OE1	31:LG:111:ARG:NH1	2.22	0.71
55:Lj:15:THR:O	55:Lj:28:HIS:HA	1.91	0.70
19:CQ:53:LYS:NZ	19:CQ:62:GLU:OE2	2.24	0.70
18:CP:385:LEU:HB3	18:CP:453:VAL:HG12	1.73	0.70
4:CB:139:ALA:HB2	31:LG:212:ASN:HD22	1.56	0.70
46:LY:31:SER:HA	46:LY:48:PRO:HA	1.74	0.70
10:CH:97:ILE:HD13	10:CH:142:LEU:HD23	1.74	0.70
47:LZ:74:ILE:HG23	47:LZ:79:LEU:HD11	1.74	0.70
10:CH:160:PRO:HB3	13:CK:3:GLN:HB2	1.72	0.70
58:Lq:98:LYS:HD3	58:Lq:101:LYS:NZ	2.06	0.70
1:C1:2816:U:OP2	1:C1:2817:U:O2'	2.10	0.70
16:CN:85:ARG:HD2	16:CN:94:ILE:HD12	1.74	0.70
26:CY:413:LYS:HA	26:CY:416:ARG:HD2	1.74	0.70
10:CH:257:GLU:HB3	33:LK:39:PRO:HG2	1.73	0.69
16:CN:15:VAL:HA	16:CN:61:ARG:HG2	1.73	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:663:G:O2'	1:C1:665:G:O2'	2.10	0.69
5:CC:532:THR:HA	6:CD:198:ARG:HH12	1.56	0.69
4:CB:215:ARG:NH1	4:CB:219:GLU:OE1	2.25	0.69
13:CK:174:PRO:HG2	13:CK:177:LEU:HB2	1.74	0.69
23:CU:337:LEU:HD22	23:CU:362:VAL:HG13	1.74	0.69
26:CY:420:LEU:HD11	26:CY:463:THR:HG21	1.74	0.69
1:C1:1233:A:H2'	1:C1:1234:A:C8	2.27	0.69
8:CF:69:LYS:HD2	8:CF:72:LEU:HG	1.74	0.69
8:CF:209:LEU:HD13	8:CF:216:LEU:HD13	1.74	0.69
28:LB:50:LYS:HB2	28:LB:337:MET:HE2	1.73	0.69
47:LZ:71:ILE:HD12	47:LZ:100:PHE:HE1	1.56	0.69
1:C1:1330:A:OP2	39:LQ:66:ARG:NH2	2.25	0.69
19:CQ:92:ALA:O	19:CQ:96:ILE:HG13	1.92	0.69
25:CX:131:GLU:OE1	25:CX:134:ARG:NH2	2.25	0.69
1:C1:1214:C:O2	8:CF:54:LYS:NZ	2.24	0.69
1:C1:3184:G:O6	28:LB:151:ARG:NH1	2.25	0.69
1:C1:3205:C:N4	1:C1:3206:G:O6	2.26	0.69
12:CJ:503:LEU:HD23	12:CJ:506:GLN:HE21	1.56	0.69
33:LK:81:ILE:HG21	33:LK:139:VAL:HG21	1.74	0.69
36:LN:36:ILE:HG12	36:LN:64:VAL:HG23	1.74	0.69
1:C1:2433:U:O2	1:C1:2436:G:C6	2.46	0.69
18:CP:304:ARG:NH1	18:CP:466:CYS:SG	2.65	0.69
22:CT:556:ASN:HD21	22:CT:559:ASN:HB3	1.56	0.69
29:LC:42:GLY:HA3	29:LC:114:ILE:HD11	1.74	0.69
9:CG:17:ALA:O	9:CG:95:ARG:NH2	2.26	0.69
12:CJ:374:LEU:HD11	12:CJ:383:LEU:HD13	1.74	0.69
26:CY:579:LEU:HG	26:CY:653:TRP:CZ3	2.28	0.69
58:Lq:59:PRO:C	58:Lq:61:PRO:HD3	2.18	0.68
26:CY:378:MET:HG3	26:CY:381:LYS:HE3	1.75	0.68
31:LG:98:ASN:HA	31:LG:101:ARG:HG3	1.74	0.68
1:C1:3313:G:OP2	49:Ld:110:LYS:NZ	2.26	0.68
5:CC:432:LEU:HD12	5:CC:760:VAL:HG23	1.74	0.68
1:C1:1791:G:OP1	15:CM:21:LYS:NZ	2.25	0.68
18:CP:376:LEU:HB2	18:CP:509:VAL:HG21	1.75	0.68
3:CA:39:LEU:HD12	3:CA:65:ASP:HB3	1.76	0.68
21:CS:729:PRO:HD2	21:CS:732:LYS:HD3	1.74	0.68
26:CY:500:ASP:OD2	26:CY:560:ARG:NH1	2.25	0.68
11:CI:203:LEU:HD23	11:CI:216:LEU:HD11	1.74	0.68
1:C1:2773:G:O3'	23:CU:309:LYS:NZ	2.27	0.68
28:LB:297:THR:OG1	28:LB:300:ASP:OD1	2.10	0.68
26:CY:738:GLU:HA	26:CY:741:ARG:HD2	1.76	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LB:45:ALA:H	28:LB:182:ILE:HG23	1.58	0.68
10:CH:386:ALA:O	10:CH:390:LEU:HB2	1.94	0.68
19:CQ:9:CYS:SG	19:CQ:11:ARG:HG3	2.33	0.68
28:LB:106:TRP:O	28:LB:137:TYR:OH	2.11	0.68
36:LN:172:ARG:O	36:LN:183:THR:OG1	2.11	0.68
57:Ll:27:ILE:O	57:Ll:33:ASN:ND2	2.27	0.68
5:CC:456:VAL:HG12	5:CC:791:ALA:HB1	1.75	0.68
1:C1:447:C:N4	1:C1:467:G:O2'	2.25	0.67
1:C1:717:U:O2'	1:C1:720:G:O6	2.12	0.67
1:C1:935:U:OP1	1:C1:1098:G:N2	2.26	0.67
7:CE:292:THR:HG23	7:CE:311:LEU:HD23	1.76	0.67
8:CF:166:ARG:NH1	13:CK:18:LEU:O	2.27	0.67
5:CC:528:HIS:ND1	5:CC:529:PRO:HD2	2.08	0.67
15:CM:86:GLU:OE1	15:CM:88:LYS:NZ	2.27	0.67
18:CP:329:VAL:HG23	18:CP:331:LEU:HD11	1.76	0.67
19:CQ:157:GLU:HB3	19:CQ:161:ARG:NH2	2.10	0.67
35:LM:32:GLU:OE2	41:LS:95:ARG:NH2	2.27	0.67
54:Li:67:ILE:HD11	54:Li:99:LEU:HD22	1.76	0.67
1:C1:434:G:OP1	24:CV:126:LYS:NZ	2.27	0.67
1:C1:1045:G:N2	1:C1:1048:G:H21	1.92	0.67
1:C1:2725:U:H3	1:C1:2749:G:H1	1.43	0.67
15:CM:118:ASN:ND2	15:CM:215:ASN:OD1	2.27	0.67
1:C1:580:G:H21	30:LE:37:LYS:HD2	1.59	0.67
18:CP:566:PHE:O	18:CP:575:GLY:HA2	1.94	0.67
22:CT:483:LEU:HD21	22:CT:523:LEU:HD11	1.74	0.67
1:C1:1748:G:N7	56:Lk:74:ARG:NH2	2.42	0.67
1:C1:1549:U:O2'	12:CJ:223:ASP:OD2	2.12	0.67
26:CY:468:ILE:HA	26:CY:471:LEU:HD12	1.76	0.67
58:Lq:180:VAL:HA	58:Lq:183:ILE:HG12	1.76	0.67
1:C1:445:A:H4'	1:C1:446:U:OP1	1.94	0.67
58:Lq:32:VAL:HG23	58:Lq:208:ALA:HA	1.77	0.67
58:Lq:60:ARG:HH22	58:Lq:63:MET:HB3	1.59	0.67
1:C1:353:A:OP1	55:Lj:24:ARG:NH1	2.27	0.67
1:C1:1869:U:H2'	1:C1:1870:A:H8	1.59	0.67
41:LS:28:ARG:HH12	41:LS:99:ARG:HH12	1.42	0.67
1:C1:2999:U:H5''	44:LV:47:ARG:HD2	1.77	0.67
12:CJ:93:ARG:HE	12:CJ:97:ARG:HD3	1.60	0.67
1:C1:3117:C:HO2'	1:C1:3118:A:H8	1.42	0.66
18:CP:520:ASN:O	18:CP:521:GLU:HG2	1.94	0.66
44:LV:15:MET:HE1	44:LV:56:VAL:HG22	1.77	0.66
1:C1:1242:A:OP1	8:CF:25:ARG:NH2	2.28	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LG:161:ASP:HB2	31:LG:162:PRO:HD3	1.76	0.66
6:CD:308:ARG:NH2	6:CD:353:THR:O	2.28	0.66
3:CA:283:MET:HB3	3:CA:287:ARG:NH1	2.08	0.66
22:CT:122:GLU:HB2	22:CT:124:ILE:HG12	1.76	0.66
8:CF:96:LEU:HD11	8:CF:102:LEU:HD21	1.77	0.66
15:CM:25:GLN:O	15:CM:29:ARG:HG3	1.96	0.66
10:CH:30:THR:HG22	10:CH:48:LYS:HZ1	1.60	0.66
1:C1:789:A:H2'	1:C1:790:G:C8	2.31	0.66
5:CC:637:GLN:HE21	5:CC:653:GLN:HG3	1.61	0.66
1:C1:2307:A:H2'	1:C1:2308:C:C6	2.31	0.66
2:C2:154:C:H5''	31:LG:184:LYS:HE3	1.78	0.66
18:CP:320:LEU:HD11	18:CP:362:TYR:HD1	1.61	0.66
26:CY:588:PRO:HB3	26:CY:615:GLN:HG3	1.77	0.66
1:C1:327:G:OP1	46:LY:8:SER:OG	2.13	0.66
9:CG:71:LEU:HA	9:CG:86:ALA:HB2	1.78	0.66
10:CH:215:TYR:CE2	10:CH:335:CYS:HB3	2.31	0.65
11:CI:219:VAL:HG23	11:CI:228:ARG:HB2	1.77	0.65
4:CB:61:PRO:HD2	4:CB:286:PRO:HG3	1.77	0.65
18:CP:509:VAL:HG22	18:CP:580:LYS:HG2	1.78	0.65
20:CR:127:GLU:OE2	20:CR:135:GLN:NE2	2.29	0.65
41:LS:38:LYS:HD2	41:LS:58:ILE:HG13	1.78	0.65
1:C1:1046:A:C6	1:C1:1074:C:C2	2.84	0.65
1:C1:1791:G:OP2	47:LZ:60:ARG:NH2	2.29	0.65
3:CA:276:ALA:O	3:CA:280:HIS:ND1	2.28	0.65
6:CD:253:SER:HB2	6:CD:290:LEU:HD11	1.76	0.65
12:CJ:266:ALA:HB1	12:CJ:269:ALA:HB3	1.78	0.65
1:C1:3216:U:O2'	1:C1:3218:A:N6	2.24	0.65
18:CP:296:PHE:HB2	18:CP:569:HIS:HD2	1.61	0.65
20:CR:187:GLN:HG2	20:CR:231:LYS:HE2	1.78	0.65
32:LH:139:SER:OG	32:LH:145:GLU:OE2	2.13	0.65
37:LO:11:ASP:HB2	37:LO:119:LYS:HB3	1.78	0.65
4:CB:183:VAL:O	4:CB:215:ARG:NH2	2.26	0.65
1:C1:1765:G:H2'	1:C1:1766:A:C8	2.32	0.65
1:C1:2814:G:H21	13:CK:192:THR:HG21	1.61	0.65
12:CJ:376:ARG:HH12	15:CM:189:ASP:HA	1.61	0.65
17:CO:37:LEU:HD12	17:CO:40:ILE:HD11	1.78	0.65
58:Lq:92:LYS:HA	58:Lq:95:LYS:HE2	1.78	0.65
5:CC:477:VAL:HG11	5:CC:524:MET:HE1	1.78	0.65
2:C2:219:A:OP1	11:CI:222:LYS:NZ	2.30	0.65
5:CC:180:TYR:O	5:CC:197:ARG:NH2	2.30	0.65
17:CO:32:ARG:NH2	28:LB:211:GLU:OE2	2.29	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:CY:653:TRP:NE1	26:CY:657:MET:HG3	2.12	0.65
1:C1:603:G:H2'	1:C1:604:G:C8	2.32	0.65
1:C1:890:G:H2'	1:C1:891:G:C8	2.31	0.65
5:CC:705:LEU:HD23	56:Lk:9:LYS:HB3	1.78	0.65
7:CE:377:LEU:HD22	7:CE:382:LEU:HD21	1.78	0.65
28:LB:14:LEU:HD13	28:LB:17:LEU:HD13	1.78	0.65
5:CC:737:SER:OG	5:CC:741:SER:OG	2.14	0.65
8:CF:77:LEU:HB3	8:CF:89:LEU:HG	1.79	0.64
29:LC:161:ASP:HA	29:LC:164:ALA:HB3	1.78	0.64
30:LE:127:TYR:OH	30:LE:161:ASP:OD2	2.11	0.64
39:LQ:108:VAL:HG12	39:LQ:165:LEU:HB3	1.79	0.64
1:C1:3249:G:H1'	38:LP:69:ARG:HD2	1.78	0.64
26:CY:446:LYS:HG3	26:CY:501:PHE:HD1	1.61	0.64
58:Lq:98:LYS:HD3	58:Lq:101:LYS:HZ1	1.60	0.64
1:C1:724:C:N3	39:LQ:168:ARG:NH2	2.44	0.64
37:LO:55:TYR:OH	37:LO:75:PHE:O	2.14	0.64
1:C1:2736:A:H2'	1:C1:2737:A:C8	2.32	0.64
3:CA:100:LEU:HB3	3:CA:117:ALA:HB3	1.78	0.64
6:CD:190:ARG:NH2	6:CD:204:LYS:HG2	2.12	0.64
15:CM:157:ARG:NH1	15:CM:249:ASN:OD1	2.30	0.64
28:LB:222:THR:HG22	28:LB:330:PRO:HB3	1.78	0.64
50:Le:36:PRO:HB2	50:Le:41:ASN:ND2	2.13	0.64
28:LB:233:ARG:HG3	28:LB:271:MET:HB2	1.80	0.64
31:LG:155:LEU:HD22	31:LG:183:ILE:HD11	1.79	0.64
1:C1:536:C:H42	32:LH:49:LYS:HG2	1.61	0.64
26:CY:635:ARG:HH21	26:CY:713:TRP:HB3	1.62	0.64
15:LF:94:ARG:HB2	15:LF:114:LEU:HB3	1.79	0.64
35:LM:19:VAL:O	35:LM:65:THR:OG1	2.16	0.64
1:C1:231:A:H2'	1:C1:232:G:C8	2.33	0.64
3:CA:137:ARG:NH2	23:CU:215:SER:O	2.30	0.64
13:CK:236:LYS:NZ	18:CP:474:ASN:O	2.31	0.64
16:CN:197:MET:HG2	16:CN:206:THR:HG22	1.79	0.64
8:CF:145:THR:HG21	8:CF:149:VAL:H	1.62	0.64
1:C1:461:A:OP1	24:CV:92:LYS:NZ	2.31	0.64
1:C1:1171:C:N3	1:C1:1297:U:O2	2.31	0.64
1:C1:1240:U:H4'	8:CF:57:ARG:HH12	1.63	0.64
29:LC:100:MET:HE3	29:LC:103:PRO:HA	1.79	0.64
1:C1:642:C:H2'	1:C1:643:A:H8	1.62	0.63
1:C1:781:G:H1	29:LC:103:PRO:HD2	1.62	0.63
1:C1:3237:U:O3'	38:LP:74:LYS:NZ	2.29	0.63
4:CB:159:ILE:HG22	4:CB:163:LEU:HD12	1.79	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:373:PHE:HD2	12:CJ:418:GLN:HE21	1.46	0.63
12:CJ:418:GLN:HB2	12:CJ:453:ARG:HD2	1.80	0.63
26:CY:386:PHE:O	26:CY:397:ARG:NH2	2.31	0.63
43:LU:92:LYS:HB2	43:LU:97:ARG:HB2	1.79	0.63
3:CA:146:PHE:HA	3:CA:152:LEU:HB3	1.80	0.63
18:CP:425:ILE:HG23	18:CP:430:VAL:HB	1.80	0.63
36:LN:56:LYS:NZ	36:LN:145:ASP:OD2	2.31	0.63
10:CH:215:TYR:HE2	10:CH:335:CYS:HB3	1.63	0.63
1:C1:897:G:H2'	1:C1:898:A:H8	1.63	0.63
1:C1:1868:G:H2'	1:C1:1869:U:C6	2.34	0.63
5:CC:627:ILE:O	5:CC:630:ARG:NH1	2.31	0.63
16:CN:96:ARG:HG3	19:CQ:76:ASN:ND2	2.13	0.63
17:CO:33:LEU:HD21	28:LB:211:GLU:HB3	1.80	0.63
22:CT:320:SER:HA	22:CT:323:ASN:HD22	1.64	0.63
1:C1:2813:C:H2'	1:C1:2814:G:H8	1.62	0.63
13:CK:218:GLY:N	13:CK:245:ILE:O	2.30	0.63
15:CM:137:GLU:OE2	15:CM:235:GLY:N	2.32	0.63
21:CS:827:LYS:HG2	21:CS:831:LYS:HE2	1.81	0.63
58:Lq:39:LYS:HD2	58:Lq:40:ASN:HB2	1.79	0.63
1:C1:1386:G:N2	1:C1:1389:A:OP2	2.25	0.63
1:C1:2320:A:H5'	38:LP:135:ARG:HH12	1.64	0.63
1:C1:2414:G:H3'	1:C1:2415:U:H5'	1.81	0.63
10:CH:541:THR:H	19:CQ:143:ARG:NH1	1.94	0.63
22:CT:490:PHE:O	22:CT:494:GLU:HG2	1.99	0.63
6:CD:400:ASN:OD1	6:CD:401:GLU:N	2.29	0.63
9:CG:96:TYR:HB2	9:CG:131:GLY:O	1.99	0.63
12:CJ:376:ARG:NH2	15:CM:189:ASP:OD1	2.31	0.63
12:CJ:476:TYR:HE1	12:CJ:483:PRO:HG2	1.63	0.63
12:CJ:386:ILE:HG23	12:CJ:465:ILE:HD12	1.79	0.63
32:LH:57:ILE:HD13	32:LH:64:ASP:HB3	1.79	0.63
1:C1:972:G:N2	42:LT:59:GLY:O	2.32	0.63
10:CH:435:ASP:OD1	19:CQ:83:ARG:NH1	2.32	0.63
13:CK:198:LEU:HD21	13:CK:224:ASN:HB2	1.80	0.63
15:CM:101:ILE:O	15:CM:106:ARG:NH2	2.32	0.63
22:CT:124:ILE:O	22:CT:128:GLN:HG2	1.98	0.63
1:C1:623:C:OP1	50:Le:42:ARG:NH1	2.32	0.62
1:C1:2456:A:H2'	1:C1:2457:C:C6	2.33	0.62
4:CB:123:LYS:HE2	4:CB:228:ILE:HG21	1.81	0.62
5:CC:459:VAL:HB	5:CC:791:ALA:HB2	1.80	0.62
10:CH:446:VAL:HG22	19:CQ:93:MET:HE1	1.81	0.62
16:CN:56:THR:HG23	44:LV:126:GLU:HG2	1.80	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CQ:68:THR:HG21	19:CQ:100:ARG:HB2	1.81	0.62
58:Lq:85:MET:HE1	58:Lq:90:LEU:HD22	1.81	0.62
3:CA:103:TRP:CZ2	3:CA:114:LYS:HD2	2.34	0.62
5:CC:716:HIS:HE1	5:CC:764:MET:HE1	1.62	0.62
16:CN:118:HIS:HD2	16:CN:119:PRO:HD2	1.64	0.62
1:C1:95:A:C5	1:C1:96:G:H1'	2.34	0.62
1:C1:887:G:H2'	1:C1:888:G:C8	2.34	0.62
28:LB:146:THR:O	28:LB:150:GLU:HG2	1.99	0.62
47:LZ:73:VAL:HG23	47:LZ:100:PHE:CD2	2.34	0.62
1:C1:3164:G:C6	1:C1:3206:G:C2	2.87	0.62
7:CE:179:LYS:N	7:CE:182:ASN:OD1	2.32	0.62
5:CC:121:PHE:HZ	7:CE:473:LEU:HD13	1.64	0.62
10:CH:187:THR:HG21	10:CH:206:GLY:HA3	1.81	0.62
12:CJ:180:ILE:HD12	12:CJ:388:ARG:HB3	1.80	0.62
26:CY:653:TRP:HE1	26:CY:657:MET:HG3	1.65	0.62
28:LB:307:THR:HG21	28:LB:317:GLU:HG3	1.80	0.62
46:LY:65:LYS:HD2	46:LY:84:VAL:HG12	1.79	0.62
1:C1:281:U:H2'	1:C1:282:G:H8	1.63	0.62
1:C1:861:G:OP1	1:C1:862:C:N4	2.30	0.62
1:C1:1757:G:O2'	1:C1:1759:G:OP2	2.15	0.62
2:C2:75:G:OP2	46:LY:73:TYR:OH	2.16	0.62
12:CJ:634:ALA:O	12:CJ:637:MET:N	2.33	0.62
1:C1:1275:U:H2'	1:C1:1276:A:H8	1.64	0.62
1:C1:1784:C:H2'	1:C1:1785:G:H8	1.65	0.62
5:CC:117:ILE:HD12	7:CE:475:ALA:HB2	1.82	0.62
3:CA:149:GLU:HB2	3:CA:152:LEU:HD12	1.81	0.62
19:CQ:129:GLU:O	19:CQ:130:ASN:ND2	2.33	0.62
28:LB:217:ASP:OD2	28:LB:340:ARG:NH1	2.32	0.62
55:Lj:54:LYS:O	55:Lj:58:VAL:HB	1.99	0.62
3:CA:79:GLU:HG3	7:CE:573:TYR:HB3	1.81	0.62
5:CC:587:VAL:HG21	5:CC:591:ILE:HD11	1.80	0.62
16:CN:82:GLN:HG3	16:CN:86:ASN:HD21	1.64	0.62
31:LG:222:LYS:O	31:LG:226:LEU:HB2	1.98	0.62
1:C1:370:A:H4'	46:LY:90:THR:HG22	1.81	0.62
1:C1:676:U:H3	29:LC:234:THR:HG23	1.65	0.62
1:C1:1842:G:N1	1:C1:1845:C:OP2	2.28	0.62
4:CB:175:THR:HG23	4:CB:178:ARG:NH1	2.15	0.61
6:CD:189:ASP:OD2	6:CD:190:ARG:NH1	2.33	0.61
6:CD:324:THR:HG22	6:CD:334:SER:HB3	1.82	0.61
18:CP:468:ASP:OD2	18:CP:470:SER:OG	2.18	0.61
22:CT:431:ALA:HA	22:CT:434:ILE:HG12	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:CY:488:ARG:HH21	26:CY:547:TYR:HE2	1.47	0.61
28:LB:90:VAL:HG13	28:LB:104:THR:HG22	1.82	0.61
58:Lq:60:ARG:O	58:Lq:62:ASN:N	2.33	0.61
13:CK:127:ILE:HD12	13:CK:131:GLU:HB2	1.82	0.61
34:LL:86:PRO:HG2	34:LL:89:LEU:HB3	1.82	0.61
44:LV:111:MET:HE1	44:LV:134:ASN:HB2	1.83	0.61
1:C1:83:C:HO2'	1:C1:687:C:HO2'	1.43	0.61
1:C1:213:G:C6	1:C1:1371:G:N2	2.68	0.61
1:C1:2847:C:H5'	10:CH:27:ARG:HH12	1.65	0.61
1:C1:3125:A:OP1	51:Lf:94:ARG:NH2	2.32	0.61
6:CD:184:LYS:NZ	6:CD:231:LEU:O	2.27	0.61
14:CL:472:GLY:O	15:LF:200:ASN:ND2	2.33	0.61
19:CQ:44:ARG:HD3	19:CQ:49:LEU:HD21	1.83	0.61
22:CT:659:TRP:HB3	26:CY:637:ILE:HG23	1.81	0.61
28:LB:24:ARG:NH1	28:LB:26:ARG:HB3	2.16	0.61
5:CC:501:THR:HG22	5:CC:516:ALA:HB3	1.82	0.61
8:CF:80:THR:OG1	8:CF:83:GLU:OE1	2.19	0.61
10:CH:444:LYS:HD2	10:CH:449:TYR:HE2	1.65	0.61
22:CT:322:LEU:HD12	22:CT:419:LEU:HD22	1.83	0.61
22:CT:501:ALA:HB1	22:CT:505:LEU:HD13	1.82	0.61
22:CT:506:HIS:HD2	25:CX:113:GLN:HE21	1.49	0.61
28:LB:24:ARG:HH11	28:LB:26:ARG:HB3	1.66	0.61
1:C1:910:A:O2'	55:Lj:49:TRP:O	2.19	0.61
1:C1:1841:U:O2'	1:C1:3023:U:OP1	2.10	0.61
4:CB:98:CYS:HB2	4:CB:150:HIS:CD2	2.35	0.61
6:CD:181:LYS:H	6:CD:195:GLY:HA2	1.66	0.61
12:CJ:397:TRP:HB2	12:CJ:401:LEU:HD12	1.82	0.61
26:CY:387:TRP:HE1	26:CY:404:ILE:HG13	1.64	0.61
44:LV:105:VAL:HG12	44:LV:111:MET:HG2	1.83	0.61
1:C1:63:A:N3	1:C1:78:U:O2'	2.31	0.61
1:C1:1430:U:H5''	38:LP:66:SER:HB2	1.83	0.61
18:CP:337:TRP:HB2	18:CP:542:PRO:HG2	1.81	0.61
28:LB:14:LEU:HD11	28:LB:264:THR:HG22	1.83	0.61
29:LC:296:ILE:O	29:LC:300:LEU:HG	2.01	0.61
43:LU:24:ASN:HA	43:LU:69:LYS:HG2	1.80	0.61
54:Li:35:PRO:HA	54:Li:38:ARG:HB2	1.82	0.61
1:C1:1464:A:H1'	26:CY:16:LYS:NZ	2.15	0.61
8:CF:88:GLY:HA2	8:CF:91:ARG:HD3	1.80	0.61
12:CJ:87:LEU:O	12:CJ:91:ILE:HD12	2.00	0.61
15:LF:62:ARG:O	15:LF:66:ARG:HG2	2.01	0.61
6:CD:262:PRO:HG3	6:CD:287:ARG:HA	1.83	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:428:GLU:OE2	6:CD:431:LEU:N	2.23	0.61
1:C1:643:A:H2'	1:C1:644:A:H8	1.64	0.61
1:C1:662:C:O2'	1:C1:666:U:OP1	2.19	0.61
9:CG:119:VAL:HG11	9:CG:122:TRP:CE2	2.36	0.61
16:CN:116:LEU:HD22	16:CN:148:VAL:HG21	1.82	0.61
28:LB:47:MET:HE2	28:LB:180:MET:HG2	1.82	0.61
47:LZ:71:ILE:HD11	47:LZ:106:ARG:HB2	1.82	0.61
1:C1:1674:U:O2'	1:C1:1728:A:N1	2.29	0.61
1:C1:3164:G:C5	1:C1:3206:G:N2	2.68	0.61
10:CH:461:LEU:O	10:CH:465:GLU:HG2	2.01	0.61
21:CS:660:MET:HB2	21:CS:718:ILE:HD11	1.83	0.61
58:Lq:73:ASP:OD1	58:Lq:76:ARG:NH2	2.34	0.61
5:CC:494:ASN:HB2	5:CC:497:GLU:HB2	1.83	0.60
6:CD:29:PRO:HG2	6:CD:32:LYS:HG2	1.81	0.60
8:CF:77:LEU:HD22	8:CF:89:LEU:HD21	1.83	0.60
13:CK:44:GLY:C	13:CK:46:ARG:H	2.09	0.60
26:CY:616:ASP:HA	26:CY:669:LEU:HD11	1.83	0.60
7:CE:387:LEU:HG	7:CE:396:ARG:HG3	1.83	0.60
19:CQ:179:GLU:OE1	49:Ld:86:ARG:NH1	2.34	0.60
1:C1:1072:G:H2'	1:C1:1073:G:C8	2.36	0.60
1:C1:2456:A:H2'	1:C1:2457:C:H6	1.66	0.60
5:CC:136:ASN:HD22	7:CE:570:ARG:HE	1.48	0.60
5:CC:505:ARG:HD2	5:CC:512:ILE:HD12	1.83	0.60
10:CH:403:LEU:HD21	16:CN:36:SER:HB2	1.83	0.60
16:CN:81:LEU:HG	19:CQ:78:PRO:HG3	1.82	0.60
17:CO:92:GLY:O	28:LB:151:ARG:NH2	2.33	0.60
22:CT:325:PHE:HA	22:CT:328:LEU:HD13	1.82	0.60
22:CT:574:VAL:HG23	22:CT:575:LEU:HG	1.82	0.60
15:LF:41:GLN:HA	15:LF:44:LYS:NZ	2.17	0.60
34:LL:55:ARG:HB2	34:LL:71:LEU:HD22	1.82	0.60
1:C1:2375:A:OP2	9:CG:73:LYS:NZ	2.33	0.60
11:CI:301:GLN:HA	11:CI:304:VAL:HG22	1.83	0.60
45:LX:90:GLU:HG3	45:LX:146:LEU:HD21	1.82	0.60
1:C1:729:U:H2'	1:C1:730:C:C6	2.37	0.60
1:C1:1468:G:H21	52:Lg:7:THR:HG22	1.67	0.60
1:C1:2319:A:H2'	1:C1:2320:A:H8	1.65	0.60
42:LT:52:MET:HE3	42:LT:53:PRO:O	2.01	0.60
58:Lq:15:GLU:HA	58:Lq:19:TYR:HB3	1.83	0.60
1:C1:812:G:H4'	1:C1:1845:C:H42	1.65	0.60
1:C1:1097:G:H4'	1:C1:1098:G:H5''	1.84	0.60
12:CJ:412:ASP:OD2	12:CJ:414:ARG:HG2	2.01	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CT:571:LEU:HD22	22:CT:596:LEU:HD11	1.82	0.60
26:CY:651:LYS:HA	26:CY:654:MET:HE2	1.84	0.60
1:C1:231:A:H2'	1:C1:232:G:H8	1.67	0.60
1:C1:643:A:H2'	1:C1:644:A:C8	2.36	0.60
1:C1:2780:U:H4'	10:CH:34:PRO:HB2	1.83	0.60
10:CH:525:LYS:NZ	43:LU:98:ASP:O	2.31	0.60
16:CN:107:VAL:HG23	16:CN:108:ILE:HG13	1.83	0.60
18:CP:565:ARG:NE	18:CP:567:TYR:OH	2.34	0.60
1:C1:1594:C:H2'	1:C1:1595:U:C6	2.37	0.60
1:C1:3209:U:H1'	30:LE:152:LYS:HE3	1.83	0.60
4:CB:97:VAL:HG22	4:CB:124:ILE:HA	1.83	0.60
17:CO:37:LEU:HG	28:LB:195:PHE:HZ	1.67	0.60
1:C1:507:G:OP1	15:LF:73:ARG:NH2	2.26	0.60
1:C1:974:G:H1	1:C1:1038:U:H3	0.71	0.60
1:C1:1218:G:N2	1:C1:1226:A:OP1	2.32	0.60
2:C2:29:U:H5''	34:LL:27:ASP:HB3	1.84	0.60
3:CA:78:CYS:SG	3:CA:249:SER:OG	2.51	0.60
4:CB:206:ARG:HH22	4:CB:212:ALA:HA	1.67	0.60
15:LF:83:ILE:HD11	42:LT:139:HIS:CE1	2.37	0.60
1:C1:193:C:OP2	46:LY:59:ARG:NH1	2.35	0.60
1:C1:1666:U:H5''	1:C1:1667:U:H5'	1.82	0.60
1:C1:1696:C:H2'	1:C1:1697:A:H8	1.67	0.60
1:C1:2337:G:N2	1:C1:2337:G:OP2	2.34	0.60
12:CJ:99:ASP:OD2	12:CJ:102:ASN:ND2	2.35	0.60
23:CU:200:LEU:O	23:CU:204:GLN:HB2	2.02	0.60
28:LB:24:ARG:HH22	28:LB:28:ARG:HB3	1.66	0.60
1:C1:155:G:H2'	1:C1:156:G:C8	2.37	0.59
1:C1:1429:G:N7	38:LP:25:SER:OG	2.34	0.59
12:CJ:498:ASP:OD2	12:CJ:500:THR:OG1	2.18	0.59
23:CU:340:LYS:NZ	23:CU:369:ASP:OD1	2.34	0.59
26:CY:498:SER:O	26:CY:502:TRP:HD1	1.84	0.59
32:LH:159:SER:O	32:LH:163:ILE:HG13	2.01	0.59
1:C1:1633:A:OP2	22:CT:365:LYS:NZ	2.35	0.59
19:CQ:56:ARG:NH1	19:CQ:62:GLU:OE2	2.35	0.59
30:LE:60:LEU:O	30:LE:67:GLY:N	2.35	0.59
1:C1:1605:U:O4	12:CJ:641:LYS:NZ	2.35	0.59
19:CQ:105:ARG:NH2	28:LB:391:SER:OG	2.35	0.59
41:LS:8:GLN:HB3	41:LS:64:ILE:HD11	1.84	0.59
1:C1:1094:A:H2'	1:C1:1095:G:C8	2.37	0.59
2:C2:161:A:H2'	2:C2:162:C:O4'	2.02	0.59
2:C2:182:G:C6	4:CB:78:LEU:HD23	2.37	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:447:THR:HB	5:CC:799:LEU:HB3	1.83	0.59
10:CH:84:LEU:HD21	10:CH:155:HIS:CE1	2.37	0.59
13:CK:9:ARG:HE	13:CK:13:LEU:HD21	1.67	0.59
21:CS:476:TYR:CE2	21:CS:480:LYS:HD2	2.38	0.59
24:CV:96:SER:HA	24:CV:100:LYS:HG3	1.84	0.59
5:CC:591:ILE:HD13	5:CC:607:SER:HB3	1.83	0.59
16:CN:222:PHE:HB2	16:CN:224:LEU:HD23	1.85	0.59
18:CP:488:LYS:HD3	18:CP:526:TYR:CG	2.37	0.59
22:CT:601:LEU:HA	22:CT:664:LEU:HD21	1.84	0.59
28:LB:57:VAL:HG12	28:LB:73:VAL:HG22	1.84	0.59
1:C1:894:A:C6	21:CS:727:ALA:HB1	2.37	0.59
2:C2:71:A:C6	2:C2:85:G:N2	2.70	0.59
6:CD:85:LEU:HD23	6:CD:89:THR:HB	1.84	0.59
10:CH:42:ARG:NH1	10:CH:118:ALA:O	2.34	0.59
19:CQ:42:MET:HE3	19:CQ:44:ARG:HH12	1.68	0.59
22:CT:183:ARG:NE	22:CT:257:ASN:OD1	2.35	0.59
22:CT:640:THR:OG1	22:CT:642:LYS:NZ	2.36	0.59
15:LF:142:TYR:CZ	15:LF:236:ASN:HB2	2.38	0.59
38:LP:175:GLN:HB3	38:LP:179:ARG:HH12	1.66	0.59
38:LP:179:ARG:HH11	38:LP:179:ARG:HG3	1.68	0.59
1:C1:983:A:N1	1:C1:1032:U:O2'	2.35	0.59
21:CS:572:GLN:HB3	21:CS:575:PHE:HD2	1.66	0.59
21:CS:819:MET:HA	21:CS:822:GLU:HB2	1.84	0.59
26:CY:545:ALA:HA	26:CY:548:PHE:CE2	2.36	0.59
1:C1:789:A:H2'	1:C1:790:G:H8	1.68	0.59
1:C1:1550:C:OP2	15:CM:29:ARG:NH2	2.35	0.59
1:C1:2373:U:H2'	1:C1:2374:G:H8	1.68	0.59
1:C1:3262:G:O2'	49:Ld:50:LYS:NZ	2.34	0.59
7:CE:239:ALA:HB1	7:CE:244:LEU:HB2	1.84	0.59
8:CF:109:PRO:HA	8:CF:112:ILE:HG22	1.83	0.59
9:CG:113:ASN:ND2	9:CG:165:PHE:HA	2.17	0.59
10:CH:534:LEU:HD22	10:CH:539:VAL:HG21	1.83	0.59
10:CH:541:THR:HG23	19:CQ:143:ARG:HH12	1.68	0.59
15:CM:93:ILE:HA	15:CM:119:ASN:O	2.02	0.59
26:CY:449:ALA:HA	26:CY:452:LEU:HD13	1.84	0.59
31:LG:71:ARG:NH1	31:LG:240:ILE:O	2.35	0.59
32:LH:18:VAL:HG22	32:LH:27:VAL:HG12	1.84	0.59
1:C1:663:G:N2	1:C1:767:A:C2	2.71	0.59
1:C1:1646:G:H5'	1:C1:1722:G:H4'	1.85	0.59
13:CK:18:LEU:HB2	32:LH:182:TYR:CD2	2.36	0.59
1:C1:933:A:N3	1:C1:1096:U:O2'	2.35	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3110:C:N4	1:C1:3337:C:OP2	2.34	0.58
6:CD:191:LEU:HB2	6:CD:203:TRP:HB2	1.85	0.58
50:Le:77:VAL:HG13	50:Le:82:ASP:HB2	1.84	0.58
1:C1:119:U:OP1	5:CC:280:ARG:NE	2.36	0.58
2:C2:222:G:O6	11:CI:281:LYS:NZ	2.32	0.58
22:CT:581:ILE:HG23	22:CT:582:ARG:HG3	1.84	0.58
15:LF:41:GLN:HA	15:LF:44:LYS:HZ2	1.68	0.58
39:LQ:107:THR:HA	39:LQ:127:GLU:HB3	1.85	0.58
58:Lq:48:ARG:NH2	58:Lq:159:LEU:O	2.37	0.58
1:C1:2936:U:O2	21:CS:793:LYS:NZ	2.35	0.58
4:CB:135:ALA:HB1	31:LG:209:GLU:HG3	1.85	0.58
7:CE:539:VAL:HA	7:CE:550:PRO:HG3	1.84	0.58
1:C1:476:C:H2'	1:C1:477:G:C8	2.37	0.58
1:C1:855:U:H2'	1:C1:856:G:C8	2.38	0.58
1:C1:1336:G:N2	1:C1:1338:U:O2'	2.31	0.58
1:C1:3045:G:OP1	28:LB:314:ARG:NH2	2.35	0.58
4:CB:87:HIS:CE1	4:CB:254:LYS:HG3	2.39	0.58
13:CK:150:ILE:HG22	13:CK:172:ILE:HB	1.86	0.58
26:CY:635:ARG:HH22	26:CY:713:TRP:HE3	1.50	0.58
28:LB:144:SER:O	28:LB:147:ARG:HG2	2.04	0.58
49:Ld:86:ARG:NH1	49:Ld:98:TYR:OH	2.36	0.58
1:C1:261:G:H5''	36:LN:14:LYS:HE2	1.84	0.58
16:CN:103:ALA:HB1	16:CN:106:ASN:HD22	1.68	0.58
15:LF:23:LYS:HA	15:LF:26:GLU:HG2	1.86	0.58
51:Lf:15:HIS:O	51:Lf:97:GLY:N	2.36	0.58
1:C1:1305:C:H4'	41:LS:2:GLY:H	1.69	0.58
1:C1:3265:A:H2'	1:C1:3266:G:H8	1.69	0.58
1:C1:3307:C:H5''	19:CQ:112:MET:SD	2.42	0.58
5:CC:459:VAL:HG12	5:CC:778:ASP:HB3	1.86	0.58
6:CD:62:PRO:HB2	6:CD:98:SER:HB2	1.84	0.58
7:CE:182:ASN:HD22	20:CR:131:VAL:HG11	1.67	0.58
22:CT:667:HIS:HA	26:CY:568:TYR:HB3	1.85	0.58
1:C1:3188:U:H2'	1:C1:3189:G:C8	2.39	0.58
3:CA:91:PHE:HB3	3:CA:103:TRP:HB2	1.86	0.58
10:CH:284:ILE:HB	10:CH:316:ILE:HD13	1.84	0.58
34:LL:46:LEU:HD22	34:LL:49:ARG:HD2	1.85	0.58
40:LR:106:LEU:HD12	40:LR:138:LEU:HD21	1.86	0.58
1:C1:115:A:N6	1:C1:149:U:C2	2.72	0.58
5:CC:242:VAL:HG21	21:CS:676:LEU:HD12	1.84	0.58
7:CE:199:ILE:HG22	7:CE:238:ILE:HD13	1.86	0.58
7:CE:431:GLN:NE2	7:CE:433:ASP:O	2.37	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:CY:559:LEU:HD21	26:CY:629:PHE:HD1	1.69	0.58
26:CY:666:ASN:ND2	26:CY:669:LEU:HD13	2.19	0.58
32:LH:27:VAL:HG23	32:LH:82:VAL:HG21	1.84	0.58
33:LK:117:ARG:HH11	33:LK:117:ARG:HA	1.68	0.58
43:LU:32:LYS:O	43:LU:32:LYS:HD2	2.04	0.58
58:Lq:14:ALA:HA	58:Lq:18:ASP:OD1	2.04	0.58
1:C1:749:C:H2'	1:C1:750:G:C8	2.39	0.58
1:C1:2472:U:H2'	1:C1:2473:A:H8	1.67	0.58
3:CA:109:ASN:HD21	5:CC:151:TYR:H	1.52	0.58
30:LE:173:ILE:HG23	30:LE:179:LEU:HD23	1.84	0.58
31:LG:143:VAL:O	31:LG:147:GLU:HG3	2.04	0.58
1:C1:1696:C:H2'	1:C1:1697:A:C8	2.39	0.58
19:CQ:58:ASN:OD1	19:CQ:59:ALA:N	2.37	0.58
20:CR:35:ILE:HG21	34:LL:47:ALA:HB1	1.84	0.58
58:Lq:38:LEU:HD23	58:Lq:39:LYS:N	2.17	0.58
1:C1:773:A:H2'	1:C1:774:A:H8	1.69	0.57
1:C1:1108:G:O3'	23:CU:328:ARG:NH1	2.30	0.57
1:C1:1817:C:H5''	1:C1:1818:A:H5'	1.85	0.57
1:C1:2735:G:H1	1:C1:2741:U:H3	1.52	0.57
9:CG:109:LEU:O	13:CK:163:ARG:NH1	2.37	0.57
16:CN:88:LEU:HD12	16:CN:94:ILE:HD11	1.85	0.57
16:CN:109:VAL:HG13	16:CN:149:GLY:HA2	1.86	0.57
1:C1:976:U:O2	1:C1:1036:A:N7	2.37	0.57
1:C1:3274:U:H4'	1:C1:3275:A:H5'	1.87	0.57
19:CQ:47:ARG:HD2	19:CQ:54:ALA:HB1	1.85	0.57
1:C1:979:A:H2'	1:C1:980:G:C8	2.39	0.57
1:C1:3305:U:H2'	1:C1:3306:G:C8	2.39	0.57
12:CJ:153:ASN:HD22	12:CJ:211:PRO:HG2	1.69	0.57
18:CP:267:LEU:HD21	18:CP:278:GLU:HG2	1.86	0.57
21:CS:673:LYS:O	21:CS:677:ILE:HD12	2.05	0.57
1:C1:116:A:OP1	54:Li:45:ARG:NH1	2.37	0.57
5:CC:529:PRO:HG3	6:CD:196:MET:HG3	1.86	0.57
38:LP:124:LYS:HD2	38:LP:142:ASN:HA	1.85	0.57
1:C1:584:C:P	1:C1:596:G:H1	2.28	0.57
1:C1:978:A:N6	1:C1:1032:U:O4	2.36	0.57
1:C1:1640:G:H2'	1:C1:1641:G:C8	2.39	0.57
9:CG:109:LEU:HD13	18:CP:358:LEU:HD12	1.87	0.57
10:CH:386:ALA:HB3	16:CN:45:VAL:HG23	1.85	0.57
11:CI:288:MET:HG2	11:CI:291:ARG:HH12	1.69	0.57
12:CJ:458:PRO:HB2	12:CJ:462:TRP:CZ3	2.38	0.57
29:LC:59:HIS:CE1	29:LC:99:ARG:HD3	2.40	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LG:100:TYR:OH	31:LG:207:ARG:N	2.24	0.57
32:LH:130:MET:HE1	32:LH:163:ILE:HD11	1.87	0.57
39:LQ:126:MET:HG3	39:LQ:128:VAL:HG23	1.86	0.57
58:Lq:205:THR:HG23	58:Lq:207:LYS:HD3	1.86	0.57
1:C1:1046:A:C6	1:C1:1074:C:N3	2.72	0.57
1:C1:3319:C:O2'	28:LB:317:GLU:OE2	2.21	0.57
2:C2:166:C:OP2	4:CB:213:ASN:ND2	2.36	0.57
3:CA:36:VAL:HG22	3:CA:88:ASN:HB2	1.86	0.57
5:CC:258:THR:HG23	31:LG:76:PRO:HG2	1.86	0.57
6:CD:200:VAL:HB	6:CD:221:LEU:HB2	1.86	0.57
12:CJ:112:LEU:H	12:CJ:115:LYS:HZ3	1.52	0.57
20:CR:209:MET:HE1	20:CR:229:LEU:HD11	1.85	0.57
26:CY:15:GLU:HA	26:CY:19:LEU:HB2	1.85	0.57
41:LS:6:GLU:HB2	41:LS:64:ILE:HB	1.87	0.57
1:C1:2778:A:H2'	1:C1:2779:C:O4'	2.04	0.57
2:C2:160:A:H2'	2:C2:161:A:C8	2.40	0.57
3:CA:76:GLU:HA	3:CA:79:GLU:OE1	2.05	0.57
15:CM:59:LYS:NZ	15:CM:63:GLU:OE2	2.33	0.57
16:CN:59:ILE:O	16:CN:63:THR:OG1	2.17	0.57
16:CN:192:VAL:HG22	16:CN:195:GLY:H	1.69	0.57
28:LB:170:THR:HG22	28:LB:172:LEU:HD13	1.87	0.57
32:LH:142:GLN:HB2	32:LH:145:GLU:HG2	1.87	0.57
55:Lj:45:ARG:O	55:Lj:57:LYS:NZ	2.28	0.57
1:C1:3331:A:H3'	1:C1:3332:G:H8	1.70	0.57
5:CC:170:ASN:ND2	5:CC:186:ILE:O	2.36	0.57
15:CM:102:PRO:HB2	15:CM:105:PRO:HD2	1.87	0.57
44:LV:82:ARG:HD2	44:LV:119:PRO:HD2	1.87	0.57
1:C1:1046:A:N1	1:C1:1074:C:N3	2.52	0.57
1:C1:1196:U:H2'	1:C1:1197:A:C8	2.40	0.57
1:C1:1360:U:H2'	1:C1:1361:G:H8	1.70	0.57
6:CD:157:ILE:HB	6:CD:166:ALA:HB3	1.87	0.57
7:CE:441:TYR:HA	7:CE:445:VAL:HG13	1.87	0.57
22:CT:319:GLU:O	22:CT:323:ASN:ND2	2.37	0.57
31:LG:226:LEU:HA	31:LG:229:VAL:HG22	1.87	0.57
46:LY:30:MET:HE1	46:LY:74:ARG:HA	1.87	0.57
1:C1:890:G:OP1	21:CS:743:ARG:NH2	2.38	0.57
1:C1:1573:A:OP2	52:Lg:37:LYS:NZ	2.37	0.57
6:CD:209:ASP:OD1	6:CD:212:THR:N	2.37	0.57
8:CF:107:ARG:HG2	8:CF:108:ASP:N	2.18	0.57
10:CH:526:PRO:HD2	10:CH:529:GLN:HG3	1.87	0.57
30:LE:64:ARG:NH2	38:LP:181:ARG:HH21	2.02	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LK:106:LEU:HA	33:LK:109:ILE:HD12	1.87	0.57
1:C1:476:C:H2'	1:C1:477:G:H8	1.70	0.56
1:C1:642:C:H2'	1:C1:643:A:C8	2.40	0.56
1:C1:1661:U:H3'	43:LU:92:LYS:HZ1	1.70	0.56
1:C1:1869:U:H2'	1:C1:1870:A:C8	2.39	0.56
1:C1:3288:G:O6	1:C1:3297:U:O4	2.23	0.56
5:CC:531:VAL:O	6:CD:198:ARG:NH1	2.38	0.56
6:CD:367:ILE:HD12	6:CD:394:LEU:HD21	1.86	0.56
23:CU:239:ARG:HG2	23:CU:243:PHE:CE2	2.40	0.56
37:LO:55:TYR:CD2	37:LO:147:VAL:HG21	2.40	0.56
1:C1:1483:U:H2'	1:C1:1484:G:C8	2.40	0.56
2:C2:63:G:H22	2:C2:97:A:H2	1.52	0.56
5:CC:541:ASP:O	5:CC:545:ALA:HB2	2.05	0.56
12:CJ:383:LEU:O	12:CJ:387:LEU:HG	2.04	0.56
22:CT:270:LEU:HD21	22:CT:282:CYS:HB2	1.86	0.56
32:LH:103:VAL:HG12	32:LH:114:VAL:HG12	1.87	0.56
1:C1:723:G:OP1	39:LQ:101:ASN:ND2	2.37	0.56
1:C1:920:U:O2	21:CS:818:ARG:NH2	2.37	0.56
1:C1:1196:U:H2'	1:C1:1197:A:H8	1.70	0.56
1:C1:1458:G:N7	10:CH:515:ARG:NH2	2.53	0.56
1:C1:2907:U:H2'	1:C1:2908:G:C8	2.40	0.56
1:C1:2952:A:O2'	2:C2:1:A:N1	2.36	0.56
1:C1:2973:A:H2'	1:C1:2974:G:H8	1.69	0.56
1:C1:3263:A:H5'	49:Ld:50:LYS:HZ1	1.70	0.56
3:CA:73:ARG:HB2	3:CA:76:GLU:HG3	1.86	0.56
3:CA:130:GLY:O	23:CU:277:ARG:NH1	2.36	0.56
5:CC:716:HIS:CE1	5:CC:764:MET:HE1	2.40	0.56
6:CD:230:TRP:HB3	6:CD:243:ALA:HB3	1.88	0.56
7:CE:435:PRO:O	7:CE:525:HIS:NE2	2.38	0.56
18:CP:243:ILE:HG21	18:CP:291:ARG:HH21	1.71	0.56
26:CY:432:ARG:HG2	26:CY:494:GLN:HG2	1.87	0.56
28:LB:57:VAL:HG13	28:LB:359:TRP:HE1	1.70	0.56
30:LE:73:LEU:HD21	30:LE:169:LEU:HD11	1.88	0.56
31:LG:146:ILE:HG23	31:LG:178:ILE:HD12	1.87	0.56
36:LN:159:ARG:HB3	36:LN:164:LEU:HB2	1.87	0.56
37:LO:126:LEU:HD12	37:LO:129:LEU:HD22	1.87	0.56
43:LU:40:GLU:OE1	43:LU:64:GLN:NE2	2.33	0.56
5:CC:539:SER:O	5:CC:543:LEU:HG	2.04	0.56
13:CK:19:ASP:O	13:CK:23:ARG:HG2	2.05	0.56
43:LU:22:ILE:HB	43:LU:109:VAL:HG22	1.87	0.56
1:C1:115:A:H2'	1:C1:257:A:H2'	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:891:G:N2	1:C1:898:A:N1	2.41	0.56
1:C1:975:G:H22	1:C1:1035:A:H2'	1.71	0.56
1:C1:3127:A:OP1	51:Lf:99:SER:OG	2.23	0.56
1:C1:3248:C:N3	38:LP:69:ARG:NH1	2.54	0.56
22:CT:260:GLY:O	22:CT:264:ARG:HG3	2.05	0.56
26:CY:734:ARG:NH2	26:CY:737:GLU:OE1	2.38	0.56
1:C1:150:G:H1'	54:Li:35:PRO:HB2	1.87	0.56
2:C2:194:C:OP1	11:CI:312:ARG:NH2	2.39	0.56
7:CE:203:ALA:O	7:CE:207:MET:HG2	2.05	0.56
23:CU:276:VAL:HG23	23:CU:277:ARG:HG3	1.87	0.56
1:C1:107:A:O2'	1:C1:316:A:N3	2.38	0.56
10:CH:23:ARG:HH11	10:CH:27:ARG:HE	1.52	0.56
10:CH:186:VAL:HG22	10:CH:208:LEU:HD21	1.88	0.56
10:CH:373:PRO:HB3	16:CN:178:GLY:HA2	1.87	0.56
16:CN:76:THR:O	16:CN:96:ARG:NH2	2.39	0.56
18:CP:331:LEU:HD23	18:CP:344:VAL:HG22	1.88	0.56
18:CP:398:MET:O	18:CP:402:MET:HG3	2.05	0.56
18:CP:512:THR:HG22	18:CP:514:SER:H	1.70	0.56
22:CT:125:ARG:NH2	22:CT:129:GLU:OE2	2.32	0.56
22:CT:632:THR:HG21	26:CY:695:ASP:HA	1.88	0.56
22:CT:668:TYR:HE1	26:CY:570:PRO:HD2	1.71	0.56
22:CT:669:CYS:HB3	22:CT:672:VAL:HG12	1.88	0.56
26:CY:666:ASN:HD21	26:CY:669:LEU:HD13	1.71	0.56
47:LZ:3:PHE:O	47:LZ:8:ARG:NH1	2.39	0.56
1:C1:38:U:H2'	1:C1:39:A:C8	2.41	0.56
1:C1:713:G:C6	1:C1:723:G:C2	2.94	0.56
1:C1:1576:C:H2'	1:C1:1577:G:C8	2.41	0.56
1:C1:2408:U:H2'	1:C1:2409:A:C8	2.41	0.56
1:C1:3118:A:H2'	1:C1:3119:C:O4'	2.06	0.56
9:CG:162:ILE:HD11	13:CK:141:LYS:H	1.70	0.56
10:CH:305:ILE:O	10:CH:309:THR:HG23	2.05	0.56
10:CH:541:THR:N	19:CQ:143:ARG:HH12	1.99	0.56
14:CL:70:GLU:O	14:CL:74:ILE:HD12	2.06	0.56
18:CP:447:ILE:HD13	18:CP:450:PHE:HZ	1.70	0.56
23:CU:277:ARG:HB2	23:CU:282:MET:HE3	1.87	0.56
24:CV:13:SER:O	24:CV:17:ASN:ND2	2.39	0.56
1:C1:734:C:H2'	1:C1:735:G:H8	1.71	0.56
1:C1:835:G:O2'	1:C1:836:U:OP1	2.24	0.56
1:C1:978:A:H2'	1:C1:979:A:C8	2.41	0.56
3:CA:139:ILE:HG12	3:CA:176:ILE:HD11	1.86	0.56
13:CK:232:THR:OG1	13:CK:236:LYS:HB2	2.06	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CP:373:VAL:HG21	18:CP:397:HIS:ND1	2.20	0.56
27:Cz:42:THR:HG23	27:Cz:45:LEU:HD12	1.87	0.56
51:Lf:34:ILE:HB	51:Lf:37:VAL:HB	1.88	0.56
1:C1:631:G:H5'	1:C1:1099:G:H1'	1.87	0.56
1:C1:1692:G:H22	1:C1:1709:G:H1'	1.70	0.56
1:C1:2993:G:P	17:CO:13:ASN:HD22	2.28	0.56
3:CA:264:PRO:O	3:CA:268:ARG:HG3	2.06	0.56
28:LB:214:GLU:O	28:LB:283:ILE:HG23	2.06	0.56
51:Lf:18:TYR:OH	51:Lf:91:LEU:O	2.24	0.56
1:C1:151:G:OP2	54:Li:35:PRO:HG2	2.06	0.55
1:C1:1286:A:H8	1:C1:2899:A:H61	1.53	0.55
3:CA:106:LYS:HB2	3:CA:110:GLY:HA3	1.87	0.55
12:CJ:176:GLN:O	12:CJ:180:ILE:HG12	2.06	0.55
26:CY:467:SER:O	26:CY:470:GLN:HG3	2.05	0.55
58:Lq:76:ARG:NH1	58:Lq:142:ASP:O	2.21	0.55
1:C1:424:G:H2'	1:C1:425:A:C8	2.41	0.55
1:C1:1777:A:H2'	1:C1:1778:A:C8	2.41	0.55
1:C1:2407:A:H2'	1:C1:2408:U:H6	1.70	0.55
5:CC:521:ILE:HB	5:CC:585:ILE:HB	1.87	0.55
6:CD:449:LYS:HB3	6:CD:451:LYS:NZ	2.20	0.55
31:LG:90:ALA:HB1	31:LG:188:ARG:HH12	1.71	0.55
36:LN:148:ILE:O	36:LN:151:ILE:HG22	2.06	0.55
38:LP:30:ARG:HD3	38:LP:63:TYR:HE1	1.71	0.55
46:LY:55:VAL:HG12	46:LY:105:ILE:HA	1.88	0.55
1:C1:1372:A:N6	1:C1:1400:A:O2'	2.39	0.55
1:C1:3072:C:OP2	32:LH:62:ARG:NH2	2.35	0.55
1:C1:3227:C:N4	1:C1:3228:G:O6	2.39	0.55
2:C2:63:G:O2'	53:Lh:54:LYS:NZ	2.38	0.55
2:C2:219:A:H5''	11:CI:222:LYS:HZ1	1.71	0.55
4:CB:78:LEU:HD12	4:CB:172:TYR:CD1	2.40	0.55
5:CC:449:PHE:HB2	5:CC:797:ALA:HB3	1.88	0.55
6:CD:331:GLN:NE2	6:CD:332:VAL:O	2.40	0.55
15:CM:94:ARG:HB2	15:CM:114:LEU:HB3	1.87	0.55
38:LP:40:LYS:HD2	38:LP:113:ILE:HG22	1.89	0.55
1:C1:831:U:H2'	1:C1:832:C:C6	2.42	0.55
1:C1:1090:C:H2'	1:C1:1091:A:H8	1.71	0.55
1:C1:2407:A:H2'	1:C1:2408:U:C6	2.42	0.55
1:C1:3046:C:OP1	28:LB:223:LYS:NZ	2.39	0.55
10:CH:199:THR:OG1	59:CH:1001:GTP:O3G	2.22	0.55
12:CJ:231:VAL:O	12:CJ:235:MET:HG3	2.06	0.55
18:CP:411:ASN:HB2	18:CP:443:PHE:HZ	1.72	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LB:297:THR:OG1	28:LB:358:LYS:O	2.25	0.55
15:LF:20:LYS:HG2	15:LF:23:LYS:HE2	1.88	0.55
15:LF:56:LYS:O	15:LF:60:GLU:HG3	2.06	0.55
35:LM:27:LEU:HD12	35:LM:50:LEU:HD23	1.89	0.55
42:LT:113:ALA:HA	42:LT:116:LYS:NZ	2.22	0.55
1:C1:2777:A:H4'	1:C1:2778:A:OP1	2.06	0.55
12:CJ:611:LYS:HA	12:CJ:614:LEU:HG	1.87	0.55
16:CN:25:LEU:HD13	16:CN:49:CYS:HB3	1.89	0.55
37:LO:159:GLU:O	37:LO:163:LYS:HG2	2.06	0.55
47:LZ:28:VAL:HG12	47:LZ:31:GLY:H	1.72	0.55
48:Lc:19:LEU:HD22	48:Lc:101:SER:HB2	1.88	0.55
49:Ld:59:LEU:HB3	49:Ld:63:LEU:HD23	1.89	0.55
1:C1:966:U:H2'	1:C1:967:U:C6	2.42	0.55
1:C1:1636:C:O2'	1:C1:1775:G:O2'	2.25	0.55
1:C1:1842:G:H21	1:C1:1846:A:H62	1.54	0.55
2:C2:166:C:H2'	2:C2:167:A:H8	1.70	0.55
5:CC:260:GLU:OE2	31:LG:233:ARG:NH2	2.38	0.55
12:CJ:497:TYR:OH	12:CJ:667:ARG:HD3	2.06	0.55
28:LB:136:LYS:O	28:LB:141:ASN:HB2	2.06	0.55
1:C1:668:U:O2	1:C1:683:C:N4	2.24	0.55
6:CD:80:LEU:HD11	6:CD:85:LEU:HB2	1.87	0.55
6:CD:179:SER:H	6:CD:196:MET:HE2	1.72	0.55
6:CD:189:ASP:O	6:CD:190:ARG:NH2	2.40	0.55
40:LR:13:SER:OG	40:LR:38:ARG:NH2	2.40	0.55
41:LS:162:LYS:HE3	51:Lf:80:SER:HA	1.88	0.55
1:C1:446:U:H4'	1:C1:447:C:OP2	2.07	0.55
1:C1:1227:A:H2'	1:C1:1254:C:OP1	2.07	0.55
1:C1:1332:A:O2'	1:C1:1334:A:OP1	2.24	0.55
1:C1:2955:U:H2'	1:C1:2956:C:C6	2.42	0.55
1:C1:3314:U:OP1	49:Ld:23:HIS:NE2	2.35	0.55
10:CH:28:LEU:HD21	10:CH:48:LYS:HG2	1.88	0.55
12:CJ:506:GLN:NE2	12:CJ:664:ARG:HG2	2.21	0.55
28:LB:295:ALA:HB3	28:LB:304:LYS:HG3	1.89	0.55
39:LQ:79:ARG:HA	39:LQ:82:MET:HG2	1.89	0.55
58:Lq:67:ILE:HD11	58:Lq:84:ALA:HA	1.88	0.55
3:CA:123:MET:HE3	3:CA:236:PRO:HD2	1.88	0.55
9:CG:96:TYR:O	9:CG:132:CYS:HA	2.07	0.55
12:CJ:49:ASP:OD2	12:CJ:52:LYS:HG2	2.06	0.55
19:CQ:81:TYR:HA	19:CQ:86:TRP:HE1	1.72	0.55
26:CY:488:ARG:NH2	26:CY:547:TYR:HE2	2.04	0.55
31:LG:84:THR:HG21	31:LG:158:ASN:HD22	1.71	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LG:214:LEU:O	31:LG:218:ILE:HG12	2.06	0.55
32:LH:163:ILE:HG22	32:LH:181:ILE:HD11	1.89	0.55
47:LZ:40:ALA:HB2	47:LZ:76:TYR:HE1	1.72	0.55
1:C1:3304:C:H2'	1:C1:3305:U:C6	2.41	0.55
2:C2:226:G:H2'	2:C2:227:G:H8	1.72	0.55
22:CT:525:LEU:HD21	26:CY:645:PRO:HB2	1.88	0.55
39:LQ:64:LEU:O	39:LQ:68:THR:OG1	2.18	0.55
1:C1:781:G:H22	29:LC:102:ALA:HA	1.72	0.54
1:C1:1178:C:H41	1:C1:1302:C:H5''	1.73	0.54
1:C1:1268:A:OP1	27:Cz:40:ARG:NH2	2.40	0.54
4:CB:174:THR:HG22	4:CB:176:THR:HG22	1.89	0.54
6:CD:108:PHE:HE1	6:CD:158:TRP:HB3	1.71	0.54
10:CH:454:ILE:HG12	10:CH:458:LEU:HD23	1.89	0.54
11:CI:188:VAL:HG22	11:CI:234:GLU:HG3	1.89	0.54
12:CJ:630:GLU:OE1	12:CJ:633:ARG:NH1	2.40	0.54
21:CS:725:LEU:HD23	22:CT:401:LEU:HB3	1.88	0.54
27:Cz:61:MET:HE2	27:Cz:61:MET:HA	1.90	0.54
28:LB:294:ASN:HB3	28:LB:322:TYR:HE1	1.72	0.54
50:Le:80:VAL:HA	50:Le:83:VAL:HG22	1.89	0.54
1:C1:895:A:O2'	1:C1:896:A:O5'	2.25	0.54
1:C1:1765:G:H2'	1:C1:1766:A:H8	1.72	0.54
1:C1:3273:G:N2	1:C1:3309:G:O2'	2.39	0.54
10:CH:255:ILE:HD11	10:CH:286:LEU:HD23	1.89	0.54
26:CY:548:PHE:CE1	26:CY:578:VAL:HG13	2.43	0.54
41:LS:60:SER:OG	41:LS:62:ASN:OD1	2.25	0.54
1:C1:712:A:H3'	1:C1:713:G:H8	1.73	0.54
4:CB:215:ARG:HG3	4:CB:220:ILE:HD11	1.89	0.54
7:CE:262:ILE:HG13	7:CE:293:MET:HB2	1.89	0.54
12:CJ:200:ASN:ND2	12:CJ:205:ASP:OD1	2.40	0.54
22:CT:184:ILE:HD13	22:CT:207:GLU:HB3	1.88	0.54
22:CT:310:MET:HE2	22:CT:321:VAL:HG23	1.89	0.54
29:LC:237:VAL:HG21	29:LC:261:ALA:HA	1.88	0.54
33:LK:31:LYS:HG3	33:LK:32:ILE:HG12	1.89	0.54
36:LN:68:ARG:HD2	36:LN:127:TYR:O	2.08	0.54
1:C1:979:A:H5'	41:LS:50:LYS:HE2	1.89	0.54
4:CB:77:ARG:HD2	4:CB:235:LEU:HD22	1.89	0.54
7:CE:258:LEU:HD13	7:CE:285:LEU:HD22	1.88	0.54
7:CE:376:LEU:O	7:CE:380:ILE:HG13	2.07	0.54
7:CE:542:ALA:HB1	7:CE:547:PHE:HB2	1.89	0.54
8:CF:135:VAL:HG23	8:CF:194:ILE:HB	1.90	0.54
9:CG:146:VAL:HG13	9:CG:165:PHE:HD2	1.71	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CS:488:ALA:HB1	22:CT:381:MET:HE1	1.89	0.54
43:LU:91:LEU:HD21	43:LU:112:LEU:HD23	1.89	0.54
7:CE:213:THR:HG23	7:CE:235:ASN:H	1.73	0.54
21:CS:469:GLU:HG2	31:LG:67:ILE:HD12	1.89	0.54
22:CT:328:LEU:HD23	22:CT:331:LEU:HD13	1.88	0.54
22:CT:415:ARG:NH2	22:CT:452:ASP:OD2	2.40	0.54
28:LB:24:ARG:NH2	28:LB:28:ARG:HB3	2.23	0.54
1:C1:1272:U:H2'	1:C1:1273:A:C8	2.42	0.54
1:C1:2361:A:C6	1:C1:2900:C:N3	2.76	0.54
1:C1:3139:A:H3'	32:LH:23:ARG:HH21	1.73	0.54
1:C1:3149:C:OP1	35:LM:98:ASN:ND2	2.40	0.54
2:C2:298:G:O2'	11:CI:291:ARG:NH1	2.41	0.54
5:CC:521:ILE:HD11	5:CC:591:ILE:HG13	1.88	0.54
8:CF:166:ARG:HD3	13:CK:18:LEU:HD22	1.87	0.54
11:CI:200:GLU:HG2	11:CI:201:HIS:CD2	2.38	0.54
16:CN:118:HIS:CD2	16:CN:119:PRO:HD2	2.43	0.54
20:CR:65:THR:HG22	20:CR:72:LEU:HD12	1.90	0.54
15:LF:92:VAL:HG23	15:LF:142:TYR:HB3	1.89	0.54
36:LN:146:PRO:O	36:LN:147:ARG:HG2	2.07	0.54
47:LZ:103:PRO:HA	47:LZ:106:ARG:HD3	1.88	0.54
49:Ld:89:ASP:OD1	49:Ld:90:GLU:N	2.33	0.54
54:Li:99:LEU:O	54:Li:103:ILE:HG13	2.07	0.54
1:C1:117:U:O4	31:LG:150:LYS:NZ	2.31	0.54
4:CB:104:PRO:HD3	4:CB:208:PRO:HB3	1.90	0.54
5:CC:500:ASN:N	5:CC:516:ALA:O	2.41	0.54
6:CD:300:ALA:HA	6:CD:317:SER:HB2	1.90	0.54
18:CP:308:ILE:HD11	18:CP:351:LEU:HD13	1.90	0.54
18:CP:513:CYS:HA	18:CP:576:PHE:CD1	2.43	0.54
39:LQ:107:THR:HA	39:LQ:127:GLU:O	2.07	0.54
1:C1:1151:A:H4'	15:LF:224:LYS:HD3	1.90	0.54
6:CD:411:GLY:HA2	6:CD:463:VAL:HG13	1.89	0.54
11:CI:234:GLU:HB2	11:CI:273:PHE:CE1	2.43	0.54
15:CM:112:LEU:HD21	15:CM:132:MET:HG2	1.89	0.54
46:LY:73:TYR:CD2	46:LY:76:LYS:HG2	2.43	0.54
1:C1:772:U:H2'	1:C1:773:A:H8	1.72	0.54
6:CD:43:ARG:HH12	6:CD:47:SER:HB2	1.72	0.54
10:CH:522:ALA:HB1	40:LR:51:ILE:HD13	1.90	0.54
11:CI:251:TYR:HE2	11:CI:253:LEU:HD13	1.73	0.54
16:CN:136:GLU:HG3	16:CN:138:PHE:HE1	1.73	0.54
26:CY:584:MET:HA	26:CY:584:MET:HE3	1.89	0.54
41:LS:110:MET:HA	41:LS:110:MET:HE2	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:LV:61:MET:HE3	44:LV:75:VAL:HG22	1.88	0.54
44:LV:86:PRO:HA	44:LV:96:TYR:HB3	1.89	0.54
1:C1:649:U:H2'	1:C1:650:C:C6	2.43	0.54
1:C1:1157:C:N3	37:LO:22:SER:HA	2.22	0.54
47:LZ:21:LYS:NZ	47:LZ:128:TRP:O	2.28	0.54
1:C1:403:U:H2'	1:C1:404:G:H8	1.73	0.53
1:C1:798:A:O2'	1:C1:799:C:O5'	2.25	0.53
1:C1:909:C:H2'	1:C1:910:A:C8	2.42	0.53
1:C1:975:G:N2	1:C1:976:U:O4	2.41	0.53
1:C1:2480:C:H2'	1:C1:2481:A:H8	1.74	0.53
7:CE:188:VAL:HG13	7:CE:238:ILE:HG23	1.91	0.53
8:CF:175:ILE:HD12	8:CF:180:CYS:HB2	1.89	0.53
9:CG:45:VAL:HG23	9:CG:71:LEU:HB2	1.89	0.53
12:CJ:111:ASN:OD1	12:CJ:116:THR:HG21	2.08	0.53
17:CO:29:ARG:HG3	28:LB:211:GLU:OE2	2.07	0.53
18:CP:270:ILE:HD11	18:CP:297:PHE:CD2	2.43	0.53
26:CY:631:VAL:HA	26:CY:634:SER:HB2	1.90	0.53
15:LF:115:ARG:H	15:LF:119:ASN:ND2	2.06	0.53
15:LF:134:LYS:HA	15:LF:137:GLU:HG2	1.89	0.53
31:LG:230:GLU:HA	31:LG:233:ARG:HG2	1.89	0.53
58:Lq:60:ARG:NH2	58:Lq:61:PRO:HA	2.23	0.53
1:C1:663:G:H2'	1:C1:767:A:H61	1.73	0.53
1:C1:1673:U:O3'	52:Lg:25:LYS:NZ	2.42	0.53
1:C1:2919:G:H2'	1:C1:2920:U:C6	2.44	0.53
1:C1:3265:A:H2'	1:C1:3266:G:C8	2.42	0.53
10:CH:242:LEU:HD22	10:CH:277:PHE:CE1	2.43	0.53
10:CH:255:ILE:HD12	10:CH:297:LEU:HD11	1.90	0.53
12:CJ:660:ASP:HB3	12:CJ:664:ARG:NH1	2.10	0.53
26:CY:691:ARG:O	26:CY:692:ALA:C	2.51	0.53
38:LP:18:ARG:NH2	38:LP:147:GLU:OE1	2.41	0.53
47:LZ:69:PRO:HG3	47:LZ:114:LYS:HB2	1.91	0.53
1:C1:1176:G:H2'	1:C1:1177:A:C8	2.43	0.53
1:C1:1239:C:OP1	33:LK:123:LYS:NZ	2.41	0.53
1:C1:3250:A:OP1	38:LP:74:LYS:HE2	2.08	0.53
5:CC:276:GLU:OE2	5:CC:280:ARG:NH1	2.41	0.53
8:CF:187:GLU:CD	8:CF:188:ALA:H	2.17	0.53
10:CH:344:SER:O	10:CH:348:LYS:HG3	2.08	0.53
13:CK:260:LEU:HG	23:CU:338:LYS:HG2	1.90	0.53
16:CN:66:ASN:ND2	16:CN:110:CYS:HB2	2.20	0.53
23:CU:255:ARG:HE	23:CU:259:ARG:NH1	2.06	0.53
1:C1:745:U:H3	1:C1:749:C:N4	2.06	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1622:A:H5'	1:C1:1801:C:H5'	1.91	0.53
1:C1:1697:A:H2'	1:C1:1698:G:H8	1.73	0.53
1:C1:2858:A:OP1	13:CK:6:TYR:OH	2.27	0.53
2:C2:57:C:H4'	2:C2:63:G:N7	2.24	0.53
2:C2:163:C:H42	4:CB:165:LYS:HG3	1.73	0.53
18:CP:365:GLN:HG2	18:CP:366:ALA:H	1.73	0.53
22:CT:214:TYR:CE2	22:CT:218:LEU:HD11	2.43	0.53
22:CT:244:THR:OG1	22:CT:281:LYS:NZ	2.35	0.53
15:LF:179:LEU:HD11	15:LF:207:PHE:CD2	2.44	0.53
39:LQ:161:GLY:O	39:LQ:164:THR:OG1	2.24	0.53
1:C1:2455:U:O2'	1:C1:2456:A:H5'	2.09	0.53
3:CA:27:ILE:HD11	5:CC:190:ILE:HD11	1.91	0.53
5:CC:516:ALA:HB2	5:CC:594:ILE:HD11	1.91	0.53
1:C1:514:G:H5'	41:LS:70:LEU:HD12	1.90	0.53
1:C1:707:A:H5''	1:C1:708:G:H5'	1.90	0.53
1:C1:3220:A:H2'	1:C1:3221:C:C6	2.44	0.53
1:C1:3223:C:H2'	1:C1:3224:G:H8	1.72	0.53
2:C2:23:U:O3'	46:LY:16:LYS:NZ	2.42	0.53
3:CA:229:ILE:HG12	23:CU:255:ARG:NH1	2.24	0.53
16:CN:25:LEU:HD12	16:CN:51:THR:HG21	1.91	0.53
16:CN:123:ARG:HD2	16:CN:124:GLU:N	2.23	0.53
22:CT:232:ASP:OD2	22:CT:234:LYS:NZ	2.32	0.53
25:CX:118:SER:HB2	25:CX:121:MET:HG3	1.90	0.53
15:LF:227:HIS:HB3	15:LF:230:GLU:OE1	2.08	0.53
36:LN:68:ARG:HA	36:LN:98:LEU:HD21	1.90	0.53
41:LS:100:VAL:O	41:LS:104:GLU:HG2	2.08	0.53
1:C1:1066:A:H2'	1:C1:1067:A:C8	2.44	0.53
5:CC:173:GLY:HA3	23:CU:274:GLU:HB2	1.89	0.53
1:C1:585:G:H1	1:C1:596:G:H5''	1.74	0.53
1:C1:2959:C:OP1	28:LB:26:ARG:NH1	2.42	0.53
1:C1:3297:U:O2'	1:C1:3298:U:OP1	2.24	0.53
2:C2:71:A:C5	2:C2:85:G:N2	2.76	0.53
2:C2:194:C:H2'	2:C2:195:G:H8	1.72	0.53
3:CA:39:LEU:HD22	3:CA:77:LEU:HD13	1.91	0.53
9:CG:72:GLY:HA2	9:CG:83:HIS:ND1	2.24	0.53
10:CH:167:ARG:HD2	10:CH:215:TYR:CE1	2.43	0.53
22:CT:253:VAL:HG23	22:CT:255:HIS:CE1	2.44	0.53
26:CY:706:ALA:O	26:CY:707:PHE:C	2.51	0.53
28:LB:94:GLU:OE2	37:LO:154:VAL:HG22	2.09	0.53
29:LC:36:VAL:HG21	29:LC:251:LEU:HD21	1.89	0.53
29:LC:155:SER:HA	29:LC:158:VAL:HG12	1.91	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LF:123:VAL:CG1	15:LF:129:THR:HG21	2.38	0.53
32:LH:23:ARG:NH1	32:LH:39:SER:O	2.41	0.53
40:LR:44:LEU:HD22	40:LR:49:LEU:HD12	1.90	0.53
57:LI:21:ARG:HG2	57:LI:22:PRO:HD2	1.89	0.53
1:C1:2841:U:H2'	1:C1:2842:C:H6	1.74	0.53
2:C2:202:C:H2'	2:C2:203:G:H8	1.72	0.53
5:CC:645:ARG:HG2	5:CC:647:LEU:HD13	1.89	0.53
5:CC:780:ASP:OD1	5:CC:781:TRP:N	2.42	0.53
6:CD:116:ALA:HB2	6:CD:182:ALA:HA	1.91	0.53
7:CE:150:ASP:OD2	7:CE:312:ARG:NE	2.42	0.53
13:CK:22:GLU:OE2	13:CK:25:ARG:NH2	2.42	0.53
13:CK:58:LYS:HA	13:CK:61:MET:HG2	1.91	0.53
18:CP:254:GLU:HG3	18:CP:255:GLU:H	1.73	0.53
20:CR:33:ASN:O	20:CR:37:LYS:HG3	2.09	0.53
24:CV:54:ILE:HB	24:CV:114:ARG:HG2	1.91	0.53
26:CY:631:VAL:HB	26:CY:722:VAL:HG21	1.91	0.53
15:LF:94:ARG:O	15:LF:118:ASN:N	2.41	0.53
50:Le:80:VAL:HG13	50:Le:112:ARG:HG2	1.91	0.53
2:C2:45:C:O2'	57:LI:11:GLN:OE1	2.22	0.53
4:CB:260:GLU:HA	4:CB:263:ILE:HG12	1.91	0.53
5:CC:390:LEU:O	5:CC:393:VAL:HG12	2.09	0.53
10:CH:429:ASN:HB3	10:CH:432:TRP:CD2	2.44	0.53
10:CH:461:LEU:HD13	19:CQ:71:PHE:HE2	1.74	0.53
12:CJ:88:GLU:OE2	12:CJ:120:ARG:NH2	2.42	0.53
13:CK:236:LYS:HZ1	18:CP:474:ASN:HB3	1.74	0.53
26:CY:469:ARG:O	26:CY:473:ILE:HD12	2.09	0.53
26:CY:543:PRO:HB3	26:CY:551:ARG:HH22	1.73	0.53
28:LB:93:ILE:HG23	28:LB:102:LEU:HB2	1.90	0.53
41:LS:49:LYS:HG3	41:LS:51:VAL:HG23	1.90	0.53
51:Lf:51:VAL:HG23	51:Lf:102:ILE:HG12	1.90	0.53
58:Lq:16:LEU:HD13	58:Lq:32:VAL:HG21	1.89	0.53
1:C1:68:C:N4	1:C1:306:U:O2'	2.42	0.52
1:C1:1576:C:H2'	1:C1:1577:G:H8	1.73	0.52
3:CA:111:PRO:HD2	23:CU:203:ILE:HD12	1.91	0.52
6:CD:406:SER:OG	6:CD:416:TRP:NE1	2.26	0.52
12:CJ:178:TYR:O	12:CJ:182:THR:HG22	2.09	0.52
13:CK:164:ARG:NH2	13:CK:171:PHE:O	2.20	0.52
18:CP:515:VAL:O	18:CP:565:ARG:NH2	2.42	0.52
22:CT:632:THR:HG21	26:CY:696:PHE:H	1.74	0.52
28:LB:113:GLU:HB2	28:LB:177:ALA:HB2	1.89	0.52
44:LV:41:VAL:HG12	44:LV:60:VAL:HG12	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:423:U:H2'	1:C1:424:G:C8	2.44	0.52
1:C1:1725:C:O2'	56:Lk:4:GLU:OE1	2.26	0.52
1:C1:3115:C:H2'	1:C1:3116:G:C8	2.44	0.52
1:C1:3184:G:OP2	28:LB:155:TYR:OH	2.23	0.52
3:CA:138:PRO:HB3	3:CA:178:HIS:NE2	2.23	0.52
4:CB:118:GLU:OE2	4:CB:121:ARG:NH1	2.41	0.52
5:CC:231:LEU:HD11	21:CS:663:ALA:HB1	1.91	0.52
5:CC:500:ASN:ND2	5:CC:591:ILE:O	2.35	0.52
5:CC:742:LEU:HB2	5:CC:765:LEU:HB2	1.91	0.52
6:CD:102:PRO:HG2	6:CD:441:ILE:HD11	1.92	0.52
6:CD:293:TRP:HB3	6:CD:295:ILE:HG23	1.91	0.52
19:CQ:82:ASN:HB3	19:CQ:85:LEU:HB3	1.91	0.52
28:LB:57:VAL:HG22	28:LB:359:TRP:HD1	1.74	0.52
29:LC:169:ALA:HB1	29:LC:226:PHE:CE1	2.45	0.52
30:LE:90:ASN:HB3	30:LE:184:ALA:HA	1.91	0.52
35:LM:94:TRP:O	35:LM:97:THR:HG22	2.09	0.52
45:LX:149:ALA:HA	45:LX:153:LEU:HB2	1.91	0.52
57:LI:21:ARG:HH12	57:LI:24:PRO:HG3	1.74	0.52
1:C1:881:G:H2'	1:C1:882:A:H8	1.74	0.52
5:CC:432:LEU:HD21	12:CJ:637:MET:HG2	1.91	0.52
19:CQ:95:ARG:NE	19:CQ:98:GLU:OE2	2.42	0.52
50:Le:64:THR:HA	50:Le:67:MET:SD	2.49	0.52
1:C1:67:A:O2'	1:C1:307:C:O2	2.26	0.52
1:C1:947:U:C2	1:C1:948:A:C8	2.98	0.52
1:C1:2817:U:H4'	1:C1:2818:U:O5'	2.09	0.52
1:C1:2891:A:C2	1:C1:2971:U:H4'	2.45	0.52
6:CD:203:TRP:HB3	6:CD:215:LEU:HD11	1.90	0.52
19:CQ:37:HIS:NE2	44:LV:96:TYR:OH	2.34	0.52
26:CY:589:LYS:N	26:CY:610:ARG:O	2.37	0.52
28:LB:222:THR:O	28:LB:273:TYR:HA	2.09	0.52
31:LG:242:GLY:O	31:LG:246:GLN:HG3	2.10	0.52
32:LH:117:ARG:HG2	32:LH:125:VAL:HG23	1.91	0.52
33:LK:80:LEU:HD13	33:LK:112:ILE:HD13	1.92	0.52
51:Lf:47:LEU:HD11	51:Lf:76:PRO:HD3	1.92	0.52
1:C1:5:G:H2'	1:C1:6:A:H8	1.75	0.52
1:C1:1076:U:O2'	1:C1:1078:C:OP1	2.22	0.52
1:C1:1303:G:H2'	1:C1:1304:U:C6	2.45	0.52
1:C1:1453:U:H2'	1:C1:1454:G:H8	1.74	0.52
1:C1:1547:A:OP2	12:CJ:19:ARG:NH2	2.40	0.52
1:C1:2461:U:H2'	1:C1:2462:A:C8	2.44	0.52
1:C1:3180:C:H2'	1:C1:3181:C:O4'	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CA:186:ASP:C	3:CA:188:LYS:H	2.18	0.52
5:CC:524:MET:HG2	5:CC:581:VAL:HG13	1.92	0.52
6:CD:474:PHE:HE1	6:CD:484:VAL:HG13	1.74	0.52
13:CK:9:ARG:HH21	13:CK:13:LEU:HD21	1.73	0.52
30:LE:69:ARG:O	30:LE:90:ASN:ND2	2.41	0.52
38:LP:176:ARG:O	38:LP:180:ILE:HG12	2.10	0.52
54:Li:63:GLU:O	54:Li:67:ILE:HG12	2.09	0.52
1:C1:663:G:O6	39:LQ:89:PRO:HB3	2.10	0.52
1:C1:897:G:H2'	1:C1:898:A:C8	2.43	0.52
1:C1:1046:A:N6	1:C1:1074:C:O2	2.42	0.52
1:C1:3298:U:H2'	1:C1:3299:A:H8	1.74	0.52
12:CJ:380:ARG:HD2	12:CJ:401:LEU:HB3	1.91	0.52
18:CP:308:ILE:CG2	18:CP:362:TYR:HB2	2.40	0.52
20:CR:8:ARG:HH21	55:Lj:63:ARG:HA	1.72	0.52
22:CT:138:LEU:HD21	22:CT:148:HIS:HB2	1.92	0.52
24:CV:5:SER:O	24:CV:9:ILE:HG12	2.09	0.52
30:LE:95:ARG:HG2	30:LE:96:ARG:N	2.24	0.52
37:LO:144:SER:HA	37:LO:147:VAL:HG12	1.92	0.52
39:LQ:116:ASP:OD1	39:LQ:117:ASP:N	2.42	0.52
41:LS:42:TRP:CD1	41:LS:53:LYS:HG3	2.44	0.52
49:Ld:63:LEU:HD22	49:Ld:101:VAL:HG12	1.91	0.52
53:Lh:34:LEU:O	53:Lh:38:LYS:HB2	2.10	0.52
1:C1:975:G:H4'	1:C1:976:U:H5'	1.91	0.52
1:C1:1150:U:H2'	1:C1:1151:A:H8	1.74	0.52
1:C1:1321:C:OP1	50:Le:62:LYS:HG3	2.09	0.52
1:C1:1764:C:H2'	1:C1:1765:G:H8	1.73	0.52
1:C1:3080:A:O2'	32:LH:40:HIS:ND1	2.41	0.52
3:CA:60:PRO:HG3	3:CA:135:GLY:HA2	1.91	0.52
4:CB:159:ILE:HG23	4:CB:162:ARG:HB2	1.92	0.52
5:CC:263:THR:HG22	31:LG:175:LYS:HB2	1.92	0.52
5:CC:398:ASN:O	5:CC:402:GLU:HG3	2.10	0.52
6:CD:417:ASP:OD2	6:CD:419:ARG:NH2	2.43	0.52
14:CL:277:PRO:O	14:CL:279:ALA:N	2.42	0.52
21:CS:814:MET:HB2	29:LC:69:GLY:HA3	1.91	0.52
21:CS:815:VAL:HA	21:CS:819:MET:SD	2.48	0.52
29:LC:223:VAL:HG13	29:LC:234:THR:HG21	1.92	0.52
34:LL:47:ALA:HB3	34:LL:48:PRO:HD3	1.92	0.52
38:LP:67:THR:HA	38:LP:82:ARG:HH21	1.75	0.52
47:LZ:13:THR:HB	52:Lg:87:ARG:HG3	1.92	0.52
1:C1:110:G:OP2	34:LL:73:ARG:NH2	2.42	0.52
1:C1:488:A:O2'	1:C1:3213:A:N1	2.39	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3309:G:OP2	19:CQ:61:LYS:NZ	2.31	0.52
8:CF:145:THR:O	8:CF:214:ILE:HD11	2.10	0.52
12:CJ:227:MET:O	12:CJ:231:VAL:HG23	2.10	0.52
12:CJ:635:LYS:HG2	12:CJ:643:ARG:HE	1.74	0.52
12:CJ:653:ASN:O	12:CJ:657:ASN:ND2	2.41	0.52
15:CM:154:ILE:HG21	15:CM:191:ILE:HG12	1.91	0.52
33:LK:117:ARG:HA	33:LK:117:ARG:NH1	2.24	0.52
1:C1:1217:U:H4'	1:C1:1218:G:H5'	1.91	0.52
1:C1:1275:U:H2'	1:C1:1276:A:C8	2.43	0.52
1:C1:1569:G:O2'	1:C1:1776:A:N6	2.42	0.52
1:C1:1810:U:O2'	2:C2:114:G:OP1	2.26	0.52
1:C1:3021:U:H2'	1:C1:3022:G:H8	1.74	0.52
1:C1:3086:A:C6	1:C1:3088:U:H1'	2.45	0.52
1:C1:3278:C:H2'	1:C1:3279:A:C8	2.45	0.52
5:CC:725:PHE:CD1	5:CC:733:PHE:HB3	2.45	0.52
10:CH:28:LEU:HD12	10:CH:29:PRO:HD2	1.90	0.52
18:CP:518:GLU:HA	18:CP:522:GLU:OE1	2.10	0.52
41:LS:66:GLU:HB2	41:LS:69:PRO:HG3	1.92	0.52
1:C1:377:A:H2'	1:C1:378:A:C8	2.45	0.52
1:C1:1481:U:H2'	1:C1:1482:G:H8	1.75	0.52
1:C1:1516:A:H2'	1:C1:1517:A:C8	2.44	0.52
1:C1:3332:G:O2'	1:C1:3333:A:H8	1.92	0.52
4:CB:133:LEU:HD21	4:CB:167:LEU:HD21	1.91	0.52
5:CC:683:HIS:HA	5:CC:725:PHE:CD2	2.45	0.52
6:CD:367:ILE:HG12	6:CD:387:HIS:NE2	2.25	0.52
33:LK:11:LYS:HD3	33:LK:35:LEU:HD11	1.92	0.52
56:Lk:5:VAL:HG12	56:Lk:47:LEU:HD13	1.92	0.52
1:C1:745:U:N3	1:C1:749:C:N4	2.58	0.51
5:CC:738:ASP:HB2	5:CC:775:GLY:H	1.75	0.51
6:CD:153:GLY:HA2	6:CD:180:ILE:HG13	1.92	0.51
6:CD:361:GLY:HA2	6:CD:367:ILE:HD13	1.90	0.51
17:CO:40:ILE:HD13	28:LB:208:THR:HG21	1.92	0.51
32:LH:40:HIS:HD1	32:LH:41:ILE:HG13	1.75	0.51
39:LQ:79:ARG:HA	39:LQ:82:MET:HE3	1.92	0.51
41:LS:12:ARG:HG3	41:LS:13:HIS:O	2.11	0.51
47:LZ:22:VAL:HG12	47:LZ:44:GLY:HA3	1.92	0.51
1:C1:213:G:O6	1:C1:1371:G:C2	2.63	0.51
1:C1:246:A:OP1	5:CC:289:LYS:NZ	2.42	0.51
1:C1:1044:A:H4'	42:LT:105:PHE:CE1	2.45	0.51
1:C1:1171:C:N3	1:C1:1297:U:C2	2.78	0.51
1:C1:1840:G:OP1	40:LR:60:ARG:NH2	2.42	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2957:G:H5''	28:LB:120:LYS:HE2	1.93	0.51
2:C2:129:C:OP1	12:CJ:11:GLY:N	2.34	0.51
6:CD:366:HIS:HA	6:CD:387:HIS:HD2	1.75	0.51
6:CD:468:TRP:CD1	6:CD:473:ILE:HG13	2.45	0.51
7:CE:184:THR:OG1	7:CE:254:VAL:O	2.27	0.51
9:CG:34:ASP:OD1	9:CG:35:ARG:N	2.43	0.51
16:CN:93:ARG:NH2	16:CN:132:VAL:HA	2.25	0.51
26:CY:438:THR:O	26:CY:442:ILE:HG12	2.09	0.51
41:LS:12:ARG:HD2	41:LS:22:PRO:HD2	1.91	0.51
45:LX:104:ASN:OD1	45:LX:107:GLN:HG3	2.10	0.51
1:C1:1778:A:H2'	1:C1:1779:A:H8	1.74	0.51
1:C1:2385:U:H2'	1:C1:2386:A:H8	1.75	0.51
5:CC:460:ALA:O	5:CC:468:LEU:HD12	2.10	0.51
9:CG:126:CYS:SG	9:CG:130:SER:OG	2.67	0.51
26:CY:580:GLN:HA	26:CY:585:LYS:NZ	2.24	0.51
31:LG:135:VAL:HG22	31:LG:203:ILE:HD11	1.91	0.51
31:LG:165:LEU:HA	36:LN:7:LEU:HD11	1.93	0.51
1:C1:2319:A:H2'	1:C1:2320:A:C8	2.46	0.51
7:CE:388:HIS:CD2	7:CE:391:GLN:HE21	2.28	0.51
21:CS:469:GLU:OE1	31:LG:71:ARG:NE	2.43	0.51
1:C1:1870:A:H2'	1:C1:1871:G:C8	2.44	0.51
2:C2:44:A:H2'	2:C2:45:C:C6	2.45	0.51
4:CB:24:LEU:HG	4:CB:28:LYS:NZ	2.25	0.51
5:CC:631:LYS:NZ	5:CC:633:ASN:OD1	2.43	0.51
6:CD:230:TRP:CG	6:CD:302:ALA:HA	2.46	0.51
6:CD:324:THR:HG23	6:CD:333:VAL:HG23	1.92	0.51
6:CD:345:LEU:HA	6:CD:359:ALA:O	2.10	0.51
7:CE:366:SER:O	7:CE:370:VAL:HG23	2.10	0.51
9:CG:116:LYS:HB3	9:CG:159:PRO:HA	1.93	0.51
10:CH:461:LEU:HD13	19:CQ:71:PHE:CE2	2.45	0.51
18:CP:296:PHE:HB2	18:CP:569:HIS:CD2	2.44	0.51
46:LY:21:ALA:HB1	46:LY:25:VAL:HB	1.91	0.51
1:C1:773:A:H2'	1:C1:774:A:C8	2.45	0.51
1:C1:3131:A:O2'	1:C1:3132:U:OP1	2.28	0.51
2:C2:69:U:H2'	2:C2:70:G:O4'	2.11	0.51
5:CC:348:PRO:HB3	5:CC:352:LEU:HD12	1.92	0.51
6:CD:320:HIS:HE1	6:CD:341:PRO:HD3	1.75	0.51
10:CH:440:ILE:HB	28:LB:300:ASP:HB3	1.93	0.51
21:CS:505:GLU:OE2	31:LG:254:LYS:NZ	2.30	0.51
23:CU:341:ARG:NH2	23:CU:349:LEU:HD21	2.26	0.51
37:LO:111:PRO:HB2	37:LO:113:PRO:HD2	1.92	0.51

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	2.31	0.51
1:C1:423:U:H2'	1:C1:424:G:H8	1.75	0.51
1:C1:966:U:O2'	15:LF:108:ILE:HD11	2.10	0.51
1:C1:2341:U:C2'	1:C1:2342:U:H5'	2.41	0.51
6:CD:80:LEU:O	6:CD:83:ASN:C	2.53	0.51
10:CH:167:ARG:HD2	10:CH:215:TYR:HE1	1.74	0.51
10:CH:248:ALA:HB2	10:CH:338:LEU:HD21	1.92	0.51
11:CI:316:ARG:HA	11:CI:319:LYS:HG2	1.92	0.51
19:CQ:47:ARG:NE	19:CQ:58:ASN:HD22	2.04	0.51
19:CQ:82:ASN:O	19:CQ:86:TRP:HD1	1.93	0.51
29:LC:185:VAL:HG11	29:LC:231:GLY:HA3	1.91	0.51
33:LK:106:LEU:O	33:LK:110:ILE:HG12	2.10	0.51
37:LO:11:ASP:OD2	37:LO:38:ARG:NH2	2.40	0.51
46:LY:30:MET:HG2	46:LY:100:PRO:HG2	1.93	0.51
1:C1:1263:U:H2'	1:C1:1264:G:C8	2.39	0.51
1:C1:2304:U:H2'	1:C1:2305:C:C6	2.46	0.51
1:C1:2874:U:C5	1:C1:2893:U:H2'	2.46	0.51
1:C1:3130:U:O2'	1:C1:3131:A:OP1	2.26	0.51
3:CA:39:LEU:HD23	3:CA:91:PHE:CD1	2.46	0.51
3:CA:137:ARG:HD2	3:CA:165:VAL:O	2.11	0.51
4:CB:109:LYS:HA	4:CB:112:VAL:HG12	1.93	0.51
8:CF:53:LEU:HA	8:CF:56:VAL:HG12	1.92	0.51
10:CH:149:LEU:HA	10:CH:152:VAL:HG22	1.92	0.51
10:CH:448:ASP:CG	19:CQ:2:ARG:HH12	2.19	0.51
16:CN:26:VAL:HG11	16:CN:35:TYR:HD1	1.76	0.51
24:CV:92:LYS:HE2	15:LF:11:ASP:OD2	2.11	0.51
28:LB:172:LEU:HD21	28:LB:334:LYS:HB2	1.92	0.51
31:LG:97:LEU:HD11	31:LG:155:LEU:HD12	1.93	0.51
1:C1:168:G:O2'	1:C1:236:A:N6	2.44	0.51
1:C1:2371:G:H2'	1:C1:2372:U:C6	2.46	0.51
1:C1:2566:G:H2'	1:C1:2567:A:H8	1.76	0.51
4:CB:67:THR:HG22	4:CB:279:ARG:HB3	1.91	0.51
5:CC:722:ALA:HB3	5:CC:736:ALA:HB3	1.93	0.51
11:CI:211:GLY:HA3	11:CI:240:VAL:HG11	1.93	0.51
11:CI:320:LEU:O	11:CI:324:GLY:N	2.33	0.51
12:CJ:387:LEU:HB3	12:CJ:392:CYS:HB3	1.93	0.51
16:CN:42:LEU:HD13	16:CN:46:ILE:HD11	1.93	0.51
18:CP:378:PRO:HB2	18:CP:402:MET:HG2	1.93	0.51
23:CU:322:GLU:HA	23:CU:325:LYS:HE3	1.93	0.51
26:CY:424:TYR:O	26:CY:428:VAL:HG23	2.10	0.51
38:LP:118:GLN:NE2	38:LP:120:ASN:OD1	2.43	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:Lk:10:LYS:O	56:Lk:13:GLU:HG3	2.11	0.51
1:C1:1675:A:H2'	1:C1:1676:A:C8	2.46	0.51
1:C1:3080:A:HO2'	32:LH:40:HIS:HD1	1.56	0.51
10:CH:74:HIS:ND1	10:CH:75:PRO:HD2	2.25	0.51
10:CH:474:TYR:CD1	19:CQ:106:VAL:HG21	2.45	0.51
15:LF:104:LYS:HB3	15:LF:105:PRO:HD3	1.93	0.51
31:LG:80:GLN:HE22	31:LG:170:PRO:HG2	1.76	0.51
39:LQ:92:LEU:HD13	39:LQ:116:ASP:HA	1.93	0.51
52:Lg:8:TYR:HE1	52:Lg:21:THR:HG21	1.75	0.51
1:C1:603:G:H2'	1:C1:604:G:H8	1.75	0.50
1:C1:1375:A:N6	1:C1:1399:G:H1'	2.25	0.50
1:C1:3026:G:C2	1:C1:3027:A:C8	2.99	0.50
1:C1:3223:C:H2'	1:C1:3224:G:C8	2.45	0.50
2:C2:68:G:H2'	2:C2:69:U:H6	1.76	0.50
4:CB:20:PRO:HA	4:CB:23:THR:HG22	1.93	0.50
5:CC:159:ASP:O	5:CC:161:ASP:N	2.44	0.50
6:CD:21:THR:HB	6:CD:95:TYR:CZ	2.46	0.50
10:CH:28:LEU:HD21	10:CH:48:LYS:HA	1.93	0.50
16:CN:23:TYR:OH	16:CN:69:GLY:O	2.26	0.50
1:C1:2361:A:C6	1:C1:2900:C:C4	3.00	0.50
1:C1:3221:C:H2'	1:C1:3222:A:H8	1.75	0.50
1:C1:3283:G:H21	1:C1:3302:A:H2	1.57	0.50
4:CB:116:PHE:HD2	4:CB:121:ARG:HG3	1.76	0.50
4:CB:147:PHE:CE1	4:CB:177:LYS:HD3	2.46	0.50
5:CC:182:SER:HB2	25:CX:129:ILE:HG21	1.93	0.50
5:CC:246:LEU:HG	5:CC:247:ILE:HG13	1.93	0.50
10:CH:403:LEU:HD23	10:CH:405:ARG:H	1.76	0.50
10:CH:432:TRP:HB3	19:CQ:81:TYR:HE2	1.75	0.50
15:CM:193:GLU:O	15:CM:197:VAL:HA	2.11	0.50
19:CQ:63:MET:HE1	19:CQ:104:GLU:HG2	1.94	0.50
21:CS:436:MET:HE3	47:LZ:128:TRP:HB3	1.93	0.50
22:CT:164:GLN:O	22:CT:168:ILE:HG12	2.11	0.50
22:CT:437:ASP:OD1	22:CT:438:PHE:N	2.45	0.50
22:CT:496:GLN:HG2	22:CT:579:TRP:HZ2	1.75	0.50
26:CY:487:TYR:HE1	26:CY:488:ARG:HH12	1.58	0.50
26:CY:563:ARG:HG3	26:CY:632:LEU:HD12	1.93	0.50
26:CY:728:LEU:O	26:CY:731:GLU:HG3	2.11	0.50
50:Le:87:LEU:HA	50:Le:116:LEU:HD23	1.92	0.50
1:C1:1158:C:H4'	37:LO:91:PRO:HD3	1.93	0.50
1:C1:1377:G:O2'	2:C2:18:U:O2	2.29	0.50
1:C1:2557:U:H2'	1:C1:2558:C:C6	2.47	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3127:A:H4'	1:C1:3130:U:C4	2.46	0.50
1:C1:3229:G:H2'	1:C1:3230:G:H8	1.76	0.50
2:C2:59:A:N7	45:LX:69:ARG:NH2	2.59	0.50
7:CE:388:HIS:CE1	7:CE:390:LYS:HB2	2.46	0.50
11:CI:317:ALA:O	11:CI:321:LYS:HG2	2.11	0.50
12:CJ:263:ASP:HB3	15:CM:146:ASN:HD22	1.76	0.50
12:CJ:585:LEU:HD23	12:CJ:589:ARG:HE	1.76	0.50
22:CT:602:GLN:HG3	26:CY:645:PRO:HG3	1.92	0.50
1:C1:1581:A:N6	45:LX:83:GLU:OE2	2.43	0.50
3:CA:123:MET:C	3:CA:125:GLU:N	2.69	0.50
7:CE:165:PHE:CD2	7:CE:262:ILE:HG21	2.46	0.50
12:CJ:466:ASN:CG	12:CJ:488:PRO:HG3	2.36	0.50
23:CU:360:VAL:HG12	23:CU:364:ASN:HD21	1.76	0.50
26:CY:8:LEU:HD23	26:CY:12:LYS:HE2	1.93	0.50
32:LH:26:THR:HG21	32:LH:33:LYS:HE3	1.93	0.50
1:C1:833:U:H2'	1:C1:834:G:H8	1.76	0.50
3:CA:116:TYR:HB3	3:CA:241:THR:OG1	2.12	0.50
5:CC:698:LEU:HD22	5:CC:735:ASP:OD2	2.12	0.50
10:CH:177:VAL:O	10:CH:287:ASN:ND2	2.39	0.50
13:CK:27:LYS:O	13:CK:31:GLU:HG2	2.11	0.50
15:CM:104:LYS:O	15:CM:108:ILE:HG12	2.11	0.50
21:CS:436:MET:CE	47:LZ:128:TRP:HB3	2.41	0.50
26:CY:555:ILE:HG23	26:CY:571:LEU:HD13	1.94	0.50
28:LB:137:TYR:CE1	28:LB:145:ILE:HG13	2.46	0.50
45:LX:72:GLU:HA	45:LX:75:ILE:HD12	1.92	0.50
1:C1:498:C:OP1	15:LF:217:ASN:ND2	2.38	0.50
1:C1:2555:U:H2'	1:C1:2556:G:H8	1.77	0.50
1:C1:3091:A:OP1	37:LO:76:ARG:NH1	2.44	0.50
5:CC:244:GLN:N	5:CC:244:GLN:OE1	2.44	0.50
15:CM:58:VAL:O	15:CM:62:ARG:HG3	2.10	0.50
18:CP:539:THR:HA	18:CP:580:LYS:HD3	1.93	0.50
21:CS:504:TRP:NE1	22:CT:186:PRO:HD3	2.27	0.50
28:LB:164:HIS:HB3	28:LB:179:LEU:HD23	1.93	0.50
53:Lh:24:LEU:HA	53:Lh:27:LEU:HD12	1.93	0.50
1:C1:663:G:N2	1:C1:767:A:N3	2.60	0.50
1:C1:1119:C:H5''	42:LT:79:ARG:HD2	1.94	0.50
1:C1:2356:G:H5''	1:C1:2904:A:H4'	1.92	0.50
1:C1:2373:U:H2'	1:C1:2374:G:C8	2.45	0.50
1:C1:2404:G:H2'	1:C1:2405:A:C8	2.47	0.50
1:C1:3217:U:O4	38:LP:179:ARG:NH2	2.45	0.50
1:C1:3334:U:H2'	1:C1:3335:U:C6	2.46	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:370:TRP:CE2	5:CC:378:ARG:HD3	2.47	0.50
10:CH:85:TYR:O	10:CH:148:TYR:OH	2.27	0.50
12:CJ:141:LEU:HD11	12:CJ:241:VAL:HG11	1.92	0.50
13:CK:11:ARG:CZ	13:CK:16:ARG:HH22	2.25	0.50
28:LB:36:ASP:OD1	28:LB:39:LYS:HD2	2.11	0.50
44:LV:56:VAL:HA	44:LV:80:ILE:HG13	1.93	0.50
1:C1:508:G:H3'	1:C1:509:A:H3'	1.93	0.50
1:C1:1305:C:H4'	41:LS:2:GLY:N	2.27	0.50
1:C1:2768:C:H2'	1:C1:2769:A:C8	2.46	0.50
10:CH:75:PRO:HA	10:CH:78:ARG:HB3	1.94	0.50
11:CI:189:MET:HE3	11:CI:233:ILE:HD12	1.94	0.50
12:CJ:91:ILE:HG21	12:CJ:107:GLU:OE2	2.11	0.50
13:CK:130:GLU:OE2	13:CK:174:PRO:HA	2.12	0.50
19:CQ:144:ARG:HD2	19:CQ:148:LEU:HD13	1.94	0.50
21:CS:565:ARG:HG3	22:CT:136:THR:HG21	1.92	0.50
21:CS:799:ARG:HG3	29:LC:71:ALA:HB3	1.93	0.50
30:LE:99:ALA:HA	30:LE:102:VAL:HG22	1.94	0.50
15:LF:230:GLU:OE1	15:LF:230:GLU:N	2.44	0.50
44:LV:47:ARG:HD3	44:LV:50:ARG:HD2	1.93	0.50
48:Lc:42:ALA:HA	48:Lc:96:LEU:HD13	1.94	0.50
1:C1:137:C:H2'	1:C1:138:G:O4'	2.10	0.50
1:C1:273:G:N7	36:LN:182:LYS:NZ	2.58	0.50
1:C1:288:A:H4'	54:Li:94:ARG:HD2	1.94	0.50
1:C1:926:C:H2'	1:C1:927:C:C6	2.46	0.50
2:C2:26:U:H2'	2:C2:27:U:C6	2.47	0.50
3:CA:75:TYR:HA	3:CA:78:CYS:SG	2.52	0.50
7:CE:122:THR:HG21	7:CE:171:GLU:OE2	2.11	0.50
7:CE:122:THR:HB	7:CE:210:HIS:HE2	1.77	0.50
7:CE:274:PHE:HD1	7:CE:277:GLU:HG3	1.76	0.50
13:CK:112:GLU:OE1	18:CP:232:LEU:HD12	2.11	0.50
18:CP:569:HIS:ND1	18:CP:570:LEU:HG	2.27	0.50
28:LB:71:GLU:OE2	28:LB:358:LYS:NZ	2.45	0.50
29:LC:114:ILE:HB	29:LC:119:LYS:HE3	1.93	0.50
31:LG:153:LEU:HB2	31:LG:218:ILE:HD11	1.94	0.50
1:C1:63:A:H5''	36:LN:174:LEU:HD13	1.94	0.49
1:C1:977:A:C2	1:C1:1036:A:H1'	2.47	0.49
1:C1:1591:C:H5''	56:Lk:44:LEU:HD22	1.92	0.49
1:C1:2747:U:O4	1:C1:2748:A:N6	2.45	0.49
1:C1:3124:U:O4	51:Lf:56:ARG:NH1	2.45	0.49
7:CE:433:ASP:HB3	7:CE:434:PRO:HD2	1.94	0.49
10:CH:242:LEU:HD22	10:CH:277:PHE:HE1	1.76	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CP:316:HIS:NE2	18:CP:319:ASP:OD2	2.44	0.49
18:CP:569:HIS:CE1	18:CP:570:LEU:HG	2.47	0.49
28:LB:137:TYR:CD1	28:LB:145:ILE:HG13	2.47	0.49
29:LC:197:LYS:HB3	29:LC:202:ARG:HD2	1.94	0.49
44:LV:77:PRO:HG2	44:LV:107:PRO:HD3	1.93	0.49
58:Lq:68:LEU:C	58:Lq:116:LEU:HD22	2.37	0.49
1:C1:1201:C:N3	1:C1:1269:A:N1	2.60	0.49
5:CC:473:ASP:C	5:CC:475:GLY:H	2.19	0.49
5:CC:593:ALA:HB3	5:CC:606:VAL:HB	1.94	0.49
6:CD:108:PHE:HB2	6:CD:482:VAL:HB	1.95	0.49
21:CS:438:MET:HE3	47:LZ:128:TRP:HB2	1.93	0.49
22:CT:484:LEU:O	22:CT:488:THR:HG23	2.12	0.49
24:CV:22:LYS:HB3	24:CV:27:THR:HG23	1.94	0.49
33:LK:162:ILE:HG22	33:LK:164:ASP:H	1.77	0.49
41:LS:28:ARG:HH12	41:LS:99:ARG:NH1	2.09	0.49
1:C1:976:U:C2	1:C1:1036:A:N7	2.80	0.49
1:C1:1171:C:C4	1:C1:1297:U:O2	2.64	0.49
1:C1:1795:A:H2'	1:C1:1796:A:C8	2.47	0.49
1:C1:2404:G:O6	1:C1:2467:U:O4	2.30	0.49
1:C1:2764:U:O2'	1:C1:2765:U:H5'	2.12	0.49
3:CA:83:LEU:HD21	54:Li:79:ARG:HB3	1.93	0.49
3:CA:178:HIS:HD2	3:CA:193:ASN:HD21	1.58	0.49
4:CB:160:ILE:HA	4:CB:163:LEU:HD13	1.94	0.49
10:CH:50:LYS:O	10:CH:53:GLN:N	2.45	0.49
16:CN:142:ILE:HD13	16:CN:148:VAL:HG23	1.94	0.49
28:LB:24:ARG:HH11	28:LB:24:ARG:HG2	1.77	0.49
1:C1:370:A:H1'	46:LY:89:ALA:O	2.12	0.49
1:C1:433:U:H2'	1:C1:434:G:C8	2.47	0.49
1:C1:1193:U:O2'	41:LS:113:ARG:NH1	2.46	0.49
1:C1:1607:U:C2	1:C1:1793:A:N6	2.80	0.49
4:CB:139:ALA:HB1	4:CB:141:GLU:HG3	1.94	0.49
6:CD:108:PHE:O	6:CD:481:LYS:HA	2.11	0.49
6:CD:230:TRP:CD1	6:CD:303:ALA:H	2.30	0.49
10:CH:89:HIS:HA	10:CH:92:VAL:HG12	1.95	0.49
10:CH:379:ARG:HH21	16:CN:178:GLY:HA3	1.76	0.49
10:CH:420:ASP:OD1	10:CH:434:TYR:OH	2.18	0.49
14:CL:262:ARG:HA	14:CL:265:PHE:O	2.12	0.49
18:CP:309:ARG:HH11	18:CP:397:HIS:HB2	1.77	0.49
18:CP:311:ASN:HD21	18:CP:428:LEU:HG	1.77	0.49
19:CQ:6:CYS:HB2	19:CQ:32:CYS:HB3	1.94	0.49
20:CR:132:PRO:HG2	34:LL:106:GLU:HB3	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CV:44:ALA:O	24:CV:48:ASN:ND2	2.45	0.49
26:CY:545:ALA:HA	26:CY:548:PHE:CD2	2.47	0.49
29:LC:45:LYS:HE2	29:LC:112:VAL:HG21	1.94	0.49
29:LC:227:ARG:HD2	29:LC:227:ARG:O	2.11	0.49
32:LH:163:ILE:HG22	32:LH:181:ILE:CD1	2.42	0.49
58:Lq:113:SER:HA	58:Lq:138:VAL:HG22	1.93	0.49
1:C1:497:U:H2'	1:C1:498:C:C6	2.48	0.49
1:C1:676:U:O4	29:LC:213:TYR:OH	2.29	0.49
1:C1:857:A:H4'	21:CS:749:GLU:OE2	2.13	0.49
1:C1:1575:C:H2'	1:C1:1576:C:C6	2.48	0.49
2:C2:194:C:H2'	2:C2:195:G:C8	2.47	0.49
5:CC:598:ARG:NH1	5:CC:644:LEU:HA	2.23	0.49
5:CC:725:PHE:HD1	5:CC:733:PHE:HB3	1.77	0.49
10:CH:187:THR:HG23	10:CH:189:ALA:H	1.76	0.49
1:C1:288:A:H2'	1:C1:289:A:C8	2.48	0.49
1:C1:424:G:H2'	1:C1:425:A:H8	1.77	0.49
1:C1:835:G:HO2'	1:C1:836:U:P	2.36	0.49
1:C1:2385:U:H2'	1:C1:2386:A:C8	2.47	0.49
2:C2:175:G:H2'	2:C2:176:G:C8	2.47	0.49
2:C2:192:C:H2'	2:C2:193:G:H8	1.77	0.49
5:CC:212:GLU:HG2	5:CC:212:GLU:O	2.13	0.49
8:CF:60:LEU:HD11	8:CF:115:TYR:CE2	2.48	0.49
10:CH:256:SER:HB2	10:CH:292:LYS:HD3	1.95	0.49
21:CS:681:TYR:CE2	54:Li:65:ARG:HD3	2.46	0.49
26:CY:593:LEU:HD12	26:CY:594:LYS:H	1.77	0.49
28:LB:72:VAL:HG12	44:LV:90:PHE:HD2	1.78	0.49
1:C1:651:A:H2'	1:C1:652:A:C8	2.47	0.49
1:C1:750:G:H2'	1:C1:751:G:C4	2.47	0.49
1:C1:1429:G:O2'	1:C1:2317:G:O6	2.30	0.49
1:C1:1452:U:H2'	1:C1:1453:U:H6	1.77	0.49
2:C2:202:C:H2'	2:C2:203:G:C8	2.46	0.49
4:CB:115:GLU:O	4:CB:115:GLU:HG2	2.12	0.49
5:CC:229:LEU:HD23	21:CS:667:ALA:HB1	1.94	0.49
5:CC:724:ARG:HG2	5:CC:724:ARG:HH11	1.78	0.49
8:CF:238:GLU:HA	8:CF:241:LYS:HE3	1.94	0.49
9:CG:114:ILE:HB	9:CG:164:CYS:HB3	1.95	0.49
18:CP:232:LEU:HB3	18:CP:273:TYR:CD1	2.47	0.49
19:CQ:66:ASP:O	19:CQ:69:LEU:N	2.40	0.49
21:CS:804:ARG:NH1	21:CS:809:LYS:O	2.44	0.49
15:LF:155:TYR:OH	15:LF:188:GLU:OE2	2.29	0.49
38:LP:24:VAL:HG12	38:LP:86:LYS:CD	2.43	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LS:6:GLU:CB	41:LS:64:ILE:HB	2.42	0.49
47:LZ:94:VAL:HG23	47:LZ:95:ILE:HG23	1.95	0.49
50:Le:24:ASP:OD2	50:Le:25:ARG:HD3	2.12	0.49
58:Lq:10:ARG:HH22	58:Lq:184:MET:HE3	1.78	0.49
1:C1:363:G:O2'	1:C1:388:A:N6	2.44	0.49
1:C1:2360:A:H2'	1:C1:2901:G:H1	1.78	0.49
1:C1:2797:G:C6	1:C1:2808:G:C2	3.00	0.49
1:C1:2970:U:H2'	1:C1:2971:U:C6	2.47	0.49
1:C1:3204:G:H2'	1:C1:3205:C:C6	2.47	0.49
2:C2:95:G:O2'	55:Lj:81:GLY:O	2.28	0.49
5:CC:788:CYS:SG	5:CC:800:TRP:HB2	2.52	0.49
14:CL:66:LEU:HD23	27:Cz:64:LYS:NZ	2.28	0.49
16:CN:25:LEU:HB3	16:CN:59:ILE:HD12	1.95	0.49
26:CY:540:ARG:NH1	26:CY:577:GLU:OE2	2.46	0.49
1:C1:2419:G:H2'	1:C1:2421:A:H62	1.77	0.49
3:CA:235:GLY:O	3:CA:236:PRO:C	2.56	0.49
4:CB:98:CYS:HB2	4:CB:150:HIS:HD2	1.78	0.49
18:CP:560:LEU:O	18:CP:560:LEU:HD23	2.13	0.49
19:CQ:44:ARG:NH1	19:CQ:44:ARG:HB2	2.28	0.49
26:CY:405:ARG:HH11	26:CY:405:ARG:HG3	1.77	0.49
48:Lc:44:LEU:HD12	48:Lc:45:ILE:H	1.78	0.49
1:C1:2351:C:H2'	1:C1:2352:A:H8	1.78	0.49
1:C1:2788:G:H2'	1:C1:2789:G:C8	2.47	0.49
1:C1:3138:U:HO2'	41:LS:172:THR:HG1	1.58	0.49
1:C1:3253:U:OP1	28:LB:117:ARG:NH2	2.44	0.49
6:CD:358:LEU:HD11	6:CD:372:PRO:HG3	1.94	0.49
16:CN:112:ASP:HB2	16:CN:156:ASN:HD21	1.78	0.49
16:CN:125:THR:HA	16:CN:128:ILE:HG12	1.95	0.49
18:CP:421:LEU:O	18:CP:425:ILE:HG13	2.13	0.49
18:CP:521:GLU:HB2	18:CP:560:LEU:HD21	1.95	0.49
24:CV:73:LYS:HA	29:LC:148:GLU:H	1.78	0.49
29:LC:258:THR:H	29:LC:261:ALA:HB3	1.78	0.49
30:LE:23:LYS:O	15:LF:9:GLN:NE2	2.46	0.49
34:LL:101:ARG:HH22	34:LL:112:ASN:ND2	2.11	0.49
40:LR:134:HIS:CE1	40:LR:136:ARG:HB2	2.48	0.49
1:C1:448:A:H62	1:C1:467:G:H1'	1.78	0.48
1:C1:1206:C:O2'	8:CF:8:ARG:NH2	2.46	0.48
1:C1:1782:C:O3'	52:Lg:71:LYS:NZ	2.36	0.48
1:C1:2468:U:H2'	1:C1:2469:U:H6	1.78	0.48
1:C1:3305:U:H2'	1:C1:3306:G:H8	1.78	0.48
5:CC:367:ARG:HH22	5:CC:385:THR:HA	1.77	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:418:LYS:HB3	15:CM:18:LEU:HD13	1.94	0.48
6:CD:469:ASP:OD2	6:CD:471:LEU:N	2.40	0.48
16:CN:99:GLU:OE1	16:CN:125:THR:OG1	2.20	0.48
18:CP:309:ARG:HB2	18:CP:370:PHE:CE1	2.48	0.48
21:CS:700:GLU:O	21:CS:704:ASP:HB2	2.13	0.48
22:CT:152:LEU:HA	22:CT:155:ILE:HG22	1.95	0.48
24:CV:9:ILE:HB	24:CV:47:VAL:HG13	1.95	0.48
25:CX:75:ASN:HA	25:CX:80:VAL:HG23	1.94	0.48
26:CY:31:LYS:O	26:CY:35:ARG:HG3	2.13	0.48
26:CY:371:SER:O	26:CY:375:LEU:HD13	2.13	0.48
26:CY:387:TRP:HA	26:CY:397:ARG:NH2	2.28	0.48
26:CY:461:TYR:HE1	26:CY:527:LEU:HB2	1.78	0.48
28:LB:263:TRP:CD1	28:LB:263:TRP:H	2.30	0.48
15:LF:162:VAL:HG13	15:LF:178:ASN:HD21	1.78	0.48
38:LP:92:ILE:O	38:LP:96:LYS:HG2	2.13	0.48
38:LP:124:LYS:HE2	38:LP:142:ASN:OD1	2.13	0.48
44:LV:79:VAL:HG21	44:LV:128:TRP:NE1	2.27	0.48
1:C1:399:A:C2	2:C2:17:A:H1'	2.47	0.48
1:C1:978:A:H2'	1:C1:979:A:H8	1.77	0.48
1:C1:2779:C:H2'	1:C1:2780:U:C6	2.48	0.48
1:C1:3042:G:OP1	19:CQ:34:SER:OG	2.25	0.48
1:C1:3078:U:H1'	1:C1:3079:A:H5''	1.94	0.48
1:C1:3231:A:H2'	1:C1:3232:U:C6	2.48	0.48
6:CD:320:HIS:CE1	6:CD:341:PRO:HD3	2.48	0.48
6:CD:343:LEU:HD13	6:CD:363:SER:HB3	1.95	0.48
7:CE:162:THR:HA	7:CE:165:PHE:CE1	2.48	0.48
10:CH:210:TYR:HB3	10:CH:215:TYR:CE2	2.48	0.48
21:CS:419:LEU:HD12	21:CS:422:ILE:HD11	1.94	0.48
21:CS:422:ILE:O	21:CS:428:LEU:HB2	2.13	0.48
21:CS:437:ALA:O	21:CS:438:MET:HE2	2.12	0.48
28:LB:221:VAL:O	28:LB:335:ARG:NH1	2.38	0.48
36:LN:4:LEU:HD12	36:LN:46:ASP:HA	1.95	0.48
42:LT:66:ASN:HB3	42:LT:73:GLY:HA3	1.95	0.48
44:LV:85:LYS:HD2	44:LV:86:PRO:HD2	1.95	0.48
46:LY:57:ILE:HG12	46:LY:103:VAL:HG12	1.95	0.48
58:Lq:8:GLY:O	58:Lq:11:GLN:HG3	2.13	0.48
58:Lq:128:LEU:O	58:Lq:128:LEU:HD23	2.13	0.48
1:C1:57:A:H5'	36:LN:157:LYS:HE3	1.94	0.48
1:C1:574:G:H2'	1:C1:575:A:H8	1.77	0.48
1:C1:1283:A:C2	13:CK:45:LEU:HB2	2.48	0.48
1:C1:2371:G:H2'	1:C1:2372:U:H6	1.78	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2477:A:N1	1:C1:2552:C:N4	2.59	0.48
1:C1:2727:A:H2'	1:C1:2728:G:C8	2.48	0.48
1:C1:3190:G:H2'	1:C1:3191:C:C6	2.47	0.48
4:CB:68:THR:HG21	4:CB:72:ILE:HD11	1.95	0.48
5:CC:448:ILE:HG12	5:CC:450:ARG:NH2	2.29	0.48
6:CD:384:LEU:HD23	6:CD:416:TRP:CD2	2.49	0.48
9:CG:42:LYS:O	9:CG:44:ARG:HG2	2.14	0.48
11:CI:309:GLU:O	11:CI:313:ARG:HD3	2.14	0.48
13:CK:218:GLY:CA	13:CK:245:ILE:O	2.61	0.48
26:CY:429:GLN:HA	26:CY:432:ARG:HG3	1.95	0.48
28:LB:146:THR:HA	28:LB:149:LEU:HD12	1.95	0.48
15:LF:13:LEU:HD12	15:LF:13:LEU:O	2.12	0.48
31:LG:229:VAL:O	31:LG:233:ARG:CB	2.57	0.48
32:LH:105:LYS:HD2	32:LH:112:TYR:CZ	2.48	0.48
51:Lf:28:LYS:HG3	51:Lf:29:THR:HG23	1.94	0.48
1:C1:713:G:C5	1:C1:723:G:C2	3.02	0.48
1:C1:1715:G:OP1	5:CC:612:ARG:HB2	2.14	0.48
1:C1:3221:C:H2'	1:C1:3222:A:C8	2.48	0.48
4:CB:80:PRO:HB3	4:CB:234:HIS:CD2	2.48	0.48
10:CH:291:ILE:C	10:CH:292:LYS:HD2	2.38	0.48
12:CJ:418:GLN:OE1	12:CJ:420:ILE:HG23	2.13	0.48
22:CT:667:HIS:ND1	22:CT:672:VAL:HG11	2.27	0.48
28:LB:89:LEU:HD13	28:LB:196:GLY:HA3	1.96	0.48
44:LV:89:ARG:O	44:LV:92:GLY:N	2.46	0.48
1:C1:1315:C:H2'	1:C1:1316:C:H6	1.79	0.48
1:C1:1606:U:O2'	1:C1:1791:G:N2	2.34	0.48
9:CG:37:VAL:HG11	9:CG:50:LEU:HD13	1.96	0.48
12:CJ:374:LEU:HD21	12:CJ:380:ARG:HA	1.95	0.48
13:CK:116:ARG:NE	13:CK:116:ARG:HA	2.28	0.48
16:CN:61:ARG:NH1	16:CN:149:GLY:O	2.35	0.48
19:CQ:66:ASP:OD2	19:CQ:103:ARG:NH1	2.39	0.48
26:CY:413:LYS:HA	26:CY:416:ARG:CD	2.42	0.48
15:LF:221:ARG:NH1	15:LF:232:GLY:O	2.46	0.48
53:Lh:119:ARG:HH11	53:Lh:119:ARG:HG3	1.78	0.48
1:C1:20:A:H2'	1:C1:21:G:C8	2.49	0.48
1:C1:155:G:H2'	1:C1:156:G:H8	1.77	0.48
1:C1:663:G:N2	1:C1:768:G:C5	2.82	0.48
1:C1:1083:G:H1'	15:LF:111:LEU:HD22	1.95	0.48
1:C1:1761:U:H2'	1:C1:1762:C:C6	2.49	0.48
2:C2:83:C:O2	46:LY:109:HIS:NE2	2.44	0.48
4:CB:26:ALA:HB2	11:CI:325:TYR:CE2	2.49	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CB:154:LEU:HD23	4:CB:180:ILE:HB	1.96	0.48
5:CC:439:LYS:N	5:CC:440:PRO:HD3	2.28	0.48
5:CC:642:HIS:HB3	5:CC:645:ARG:O	2.13	0.48
9:CG:65:LEU:HD11	18:CP:437:ASN:HB2	1.96	0.48
10:CH:361:LEU:HA	10:CH:364:VAL:HG22	1.95	0.48
16:CN:138:PHE:HB3	16:CN:140:GLN:HE22	1.79	0.48
18:CP:280:LEU:O	18:CP:284:LEU:HG	2.14	0.48
18:CP:498:CYS:O	18:CP:583:LYS:NZ	2.39	0.48
21:CS:508:SER:HB2	22:CT:215:HIS:CE1	2.48	0.48
26:CY:487:TYR:HD1	26:CY:488:ARG:NH2	2.12	0.48
38:LP:50:ASN:HB3	38:LP:56:GLU:HG3	1.95	0.48
1:C1:433:U:H2'	1:C1:434:G:H8	1.76	0.48
1:C1:651:A:H2'	1:C1:652:A:H8	1.78	0.48
1:C1:934:G:H3'	1:C1:1098:G:N2	2.28	0.48
1:C1:1446:G:N2	1:C1:1449:A:OP2	2.45	0.48
1:C1:1588:C:H2'	1:C1:1589:G:H8	1.78	0.48
1:C1:1598:A:N1	1:C1:1805:C:N3	2.61	0.48
1:C1:3136:A:H2	1:C1:3141:G:H4'	1.78	0.48
1:C1:3272:U:H2'	1:C1:3273:G:O4'	2.14	0.48
4:CB:135:ALA:O	4:CB:138:LYS:NZ	2.47	0.48
6:CD:43:ARG:NH1	6:CD:47:SER:HB2	2.29	0.48
10:CH:446:VAL:HG22	19:CQ:93:MET:CE	2.44	0.48
11:CI:288:MET:HA	11:CI:291:ARG:NH1	2.29	0.48
18:CP:459:CYS:SG	18:CP:513:CYS:HB3	2.54	0.48
25:CX:136:GLU:OE2	25:CX:140:LYS:NZ	2.43	0.48
27:Cz:30:GLN:HG2	27:Cz:32:TRP:CZ2	2.48	0.48
35:LM:44:PRO:HB2	35:LM:82:LYS:HG2	1.95	0.48
1:C1:205:G:N7	29:LC:186:LYS:HE2	2.29	0.48
1:C1:421:U:O2'	51:Lf:90:PRO:O	2.27	0.48
1:C1:525:U:H1'	41:LS:146:LYS:HG2	1.96	0.48
1:C1:631:G:H5''	1:C1:1098:G:C8	2.49	0.48
1:C1:831:U:H2'	1:C1:832:C:H6	1.77	0.48
1:C1:861:G:H1'	1:C1:869:A:N6	2.28	0.48
1:C1:1156:G:N2	37:LO:89:MET:HE2	2.28	0.48
1:C1:1242:A:H2'	1:C1:1243:G:C4	2.49	0.48
1:C1:2300:C:H2'	1:C1:2301:C:H6	1.78	0.48
6:CD:240:ILE:HB	6:CD:252:TRP:HB2	1.96	0.48
6:CD:474:PHE:CE1	6:CD:484:VAL:HG13	2.49	0.48
7:CE:346:LEU:HD12	7:CE:491:LEU:O	2.14	0.48
12:CJ:31:PRO:O	12:CJ:35:LYS:HG3	2.13	0.48
16:CN:118:HIS:CD2	16:CN:146:VAL:HB	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CT:590:ALA:HA	22:CT:629:LEU:HD11	1.96	0.48
39:LQ:133:PHE:CE2	39:LQ:148:THR:HG23	2.49	0.48
1:C1:856:G:N1	1:C1:875:A:C6	2.79	0.48
1:C1:920:U:H2'	1:C1:921:G:C8	2.49	0.48
1:C1:1090:C:H2'	1:C1:1091:A:C8	2.49	0.48
1:C1:2457:C:C2	1:C1:2458:U:C5	3.02	0.48
1:C1:3164:G:C5	1:C1:3206:G:C2	3.01	0.48
2:C2:192:C:H2'	2:C2:193:G:C8	2.49	0.48
3:CA:263:SER:O	3:CA:267:ILE:HD12	2.14	0.48
9:CG:1:MET:HE3	9:CG:1:MET:HB2	1.76	0.48
12:CJ:249:ILE:HG23	12:CJ:251:LEU:H	1.78	0.48
47:LZ:107:GLU:OE2	47:LZ:111:LYS:NZ	2.46	0.48
50:Le:14:ARG:HH12	50:Le:52:ALA:HB3	1.77	0.48
50:Le:80:VAL:O	50:Le:84:GLU:HG3	2.14	0.48
1:C1:174:C:N4	1:C1:230:A:H61	2.12	0.48
1:C1:1576:C:OP1	52:Lg:32:ARG:HD2	2.14	0.48
1:C1:2933:U:H2'	1:C1:2934:A:H8	1.79	0.48
1:C1:3041:C:H2'	1:C1:3042:G:O4'	2.14	0.48
2:C2:68:G:H2'	2:C2:69:U:C6	2.49	0.48
4:CB:30:LEU:HB2	4:CB:291:LEU:HD11	1.95	0.48
10:CH:301:MET:HA	10:CH:304:GLU:OE2	2.13	0.48
43:LU:49:VAL:HG22	43:LU:60:ILE:HD12	1.95	0.48
49:Ld:66:LYS:HA	49:Ld:69:GLU:HG3	1.95	0.48
56:Lk:8:ILE:O	56:Lk:12:ILE:HG12	2.14	0.48
1:C1:1600:G:H2'	1:C1:1601:U:C6	2.48	0.47
1:C1:1870:A:H2'	1:C1:1871:G:H8	1.79	0.47
1:C1:2302:U:C2	1:C1:2303:A:C8	3.02	0.47
1:C1:2774:G:H2'	1:C1:2775:A:C8	2.49	0.47
1:C1:3182:U:H3	1:C1:3188:U:H3	1.61	0.47
2:C2:196:G:H1	2:C2:201:U:H3	1.62	0.47
5:CC:479:VAL:HB	5:CC:489:TRP:HB3	1.96	0.47
6:CD:190:ARG:HH21	6:CD:204:LYS:HA	1.79	0.47
6:CD:322:VAL:HB	6:CD:342:LEU:HD11	1.96	0.47
7:CE:572:ALA:HB3	7:CE:575:SER:HB3	1.96	0.47
10:CH:12:THR:HG23	10:CH:15:GLU:H	1.78	0.47
10:CH:193:VAL:HG13	59:CH:1001:GTP:H5''	1.96	0.47
20:CR:190:ARG:HA	20:CR:193:GLU:HG2	1.95	0.47
25:CX:136:GLU:HG2	25:CX:140:LYS:HZ2	1.78	0.47
26:CY:379:LEU:O	26:CY:382:THR:HG22	2.14	0.47
26:CY:499:LEU:HD11	26:CY:534:VAL:HG23	1.96	0.47
29:LC:296:ILE:HD12	39:LQ:64:LEU:HD21	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LC:329:LEU:HD13	15:LF:187:ILE:HG13	1.94	0.47
40:LR:135:LYS:O	40:LR:139:VAL:HG23	2.14	0.47
44:LV:82:ARG:HG2	44:LV:97:PHE:CD1	2.49	0.47
46:LY:35:SER:O	46:LY:39:ARG:HG3	2.13	0.47
51:Lf:15:HIS:HA	51:Lf:32:ILE:HD13	1.96	0.47
58:Lq:93:LEU:HG	58:Lq:100:ILE:HG22	1.96	0.47
58:Lq:183:ILE:O	58:Lq:187:ILE:HG12	2.14	0.47
1:C1:415:A:H3'	1:C1:416:G:H8	1.79	0.47
1:C1:844:C:N4	26:CY:26:ARG:HH12	2.11	0.47
1:C1:1443:A:H2'	1:C1:1444:A:H8	1.79	0.47
1:C1:3262:G:H2'	1:C1:3263:A:H8	1.78	0.47
2:C2:201:U:H2'	2:C2:202:C:C6	2.50	0.47
3:CA:111:PRO:HG3	23:CU:199:ALA:HB1	1.95	0.47
4:CB:85:LEU:HD12	4:CB:86:PRO:HD2	1.96	0.47
5:CC:452:HIS:CE1	5:CC:478:ARG:HD2	2.48	0.47
8:CF:89:LEU:O	8:CF:93:THR:HG23	2.14	0.47
9:CG:19:TYR:HB3	9:CG:90:LEU:HD22	1.95	0.47
13:CK:137:LYS:HE2	13:CK:143:HIS:CG	2.49	0.47
26:CY:416:ARG:HA	26:CY:419:VAL:HG22	1.97	0.47
30:LE:61:LEU:HD21	30:LE:103:ILE:HD12	1.96	0.47
33:LK:107:ASP:OD1	33:LK:107:ASP:N	2.46	0.47
37:LO:35:VAL:HG22	37:LO:105:LYS:HB2	1.96	0.47
38:LP:41:LEU:HD21	38:LP:99:GLU:HB2	1.96	0.47
45:LX:116:TYR:CE1	53:Lh:36:ILE:HG13	2.49	0.47
51:Lf:39:ASP:N	51:Lf:39:ASP:OD1	2.47	0.47
1:C1:7:C:H5''	31:LG:196:LYS:HG2	1.95	0.47
1:C1:772:U:H2'	1:C1:773:A:C8	2.48	0.47
1:C1:835:G:H2'	1:C1:836:U:H6	1.79	0.47
1:C1:856:G:C2	1:C1:875:A:N1	2.82	0.47
1:C1:2764:U:H2'	1:C1:2765:U:C6	2.49	0.47
5:CC:189:ASP:OD1	5:CC:193:LYS:N	2.42	0.47
5:CC:263:THR:HG23	54:Li:55:GLU:OE1	2.14	0.47
7:CE:391:GLN:OE1	7:CE:395:LYS:NZ	2.47	0.47
11:CI:290:GLY:O	11:CI:294:GLU:HG3	2.15	0.47
12:CJ:150:LEU:O	12:CJ:154:LEU:HG	2.14	0.47
12:CJ:380:ARG:HB2	12:CJ:401:LEU:HD13	1.97	0.47
26:CY:657:MET:SD	26:CY:663:GLY:HA3	2.55	0.47
35:LM:121:MET:HE3	35:LM:121:MET:HB2	1.80	0.47
52:Lg:87:ARG:O	52:Lg:91:ILE:HG12	2.15	0.47
1:C1:671:G:OP2	34:LL:28:GLN:NE2	2.44	0.47
1:C1:2470:U:H2'	1:C1:2471:U:C6	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CA:107:VAL:HB	3:CA:108:PRO:HD3	1.95	0.47
5:CC:493:LEU:HB3	5:CC:522:PHE:HE1	1.78	0.47
6:CD:28:LEU:HB3	6:CD:33:ARG:CZ	2.44	0.47
6:CD:372:PRO:HD2	6:CD:373:ARG:HH12	1.79	0.47
7:CE:119:SER:HB3	7:CE:122:THR:HG22	1.97	0.47
12:CJ:514:GLU:O	12:CJ:517:LEU:HG	2.14	0.47
16:CN:61:ARG:HD3	16:CN:106:ASN:OD1	2.14	0.47
18:CP:425:ILE:HD13	18:CP:433:THR:HG21	1.95	0.47
49:Ld:73:LYS:HE3	49:Ld:73:LYS:HB2	1.58	0.47
3:CA:196:ILE:HG23	3:CA:229:ILE:HD12	1.97	0.47
4:CB:175:THR:HG23	4:CB:178:ARG:HH12	1.79	0.47
6:CD:80:LEU:HD21	6:CD:87:LEU:HA	1.96	0.47
6:CD:265:SER:HB2	6:CD:272:VAL:HG11	1.96	0.47
7:CE:450:ARG:HG3	7:CE:456:GLY:H	1.79	0.47
9:CG:158:ASP:OD1	9:CG:159:PRO:HD2	2.15	0.47
10:CH:520:ARG:HA	10:CH:523:VAL:HG12	1.96	0.47
12:CJ:517:LEU:O	12:CJ:521:GLN:HG2	2.14	0.47
13:CK:174:PRO:O	13:CK:178:ARG:HG2	2.13	0.47
18:CP:274:TYR:OH	18:CP:298:GLU:OE2	2.32	0.47
25:CX:134:ARG:HG2	25:CX:134:ARG:HH11	1.78	0.47
38:LP:115:LYS:HB2	38:LP:151:THR:HG22	1.97	0.47
41:LS:3:ARG:HH21	41:LS:100:VAL:HG12	1.79	0.47
41:LS:48:LEU:HD13	42:LT:151:LEU:HD23	1.96	0.47
1:C1:128:G:OP1	53:Lh:80:TYR:OH	2.21	0.47
1:C1:1075:A:H5'	1:C1:1078:C:C5	2.50	0.47
1:C1:1697:A:H2'	1:C1:1698:G:C8	2.50	0.47
1:C1:2797:G:C6	1:C1:2808:G:N2	2.82	0.47
1:C1:3262:G:H2'	1:C1:3263:A:C8	2.49	0.47
3:CA:247:GLU:HB2	3:CA:255:LEU:HD11	1.95	0.47
4:CB:25:LYS:HA	4:CB:28:LYS:HG2	1.96	0.47
6:CD:387:HIS:HA	6:CD:414:ARG:NH1	2.30	0.47
7:CE:267:ASP:N	7:CE:267:ASP:OD1	2.47	0.47
12:CJ:669:ARG:HA	12:CJ:672:LYS:HG2	1.96	0.47
21:CS:570:PHE:HE2	22:CT:128:GLN:HA	1.79	0.47
26:CY:31:LYS:HE3	26:CY:35:ARG:NE	2.23	0.47
31:LG:137:TYR:OH	31:LG:195:LYS:NZ	2.47	0.47
33:LK:105:SER:OG	33:LK:107:ASP:OD1	2.33	0.47
58:Lq:124:LEU:HD23	58:Lq:124:LEU:H	1.79	0.47
1:C1:466:U:H2'	1:C1:467:G:O4'	2.14	0.47
1:C1:628:C:H2'	1:C1:629:U:C6	2.49	0.47
1:C1:637:C:H1'	21:CS:821:LYS:HE3	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:715:G:H5''	39:LQ:71:PRO:HB2	1.96	0.47
1:C1:745:U:C2	1:C1:749:C:N3	2.82	0.47
1:C1:1575:C:H2'	1:C1:1576:C:H6	1.80	0.47
1:C1:1780:U:H2'	1:C1:1781:C:C6	2.50	0.47
1:C1:2340:C:H2'	1:C1:2341:U:H6	1.79	0.47
1:C1:2380:G:H5''	1:C1:2381:A:H5'	1.97	0.47
1:C1:2815:C:O2'	13:CK:183:ASN:OD1	2.30	0.47
1:C1:3215:U:N3	1:C1:3217:U:H5'	2.30	0.47
1:C1:3289:C:C4	1:C1:3290:C:N4	2.82	0.47
2:C2:66:A:H2'	2:C2:67:U:H6	1.80	0.47
2:C2:71:A:N6	2:C2:85:G:N2	2.63	0.47
2:C2:301:A:H2'	2:C2:302:A:O4'	2.15	0.47
5:CC:363:THR:HG23	5:CC:366:GLU:H	1.80	0.47
5:CC:429:LEU:HD22	12:CJ:634:ALA:HB1	1.95	0.47
5:CC:627:ILE:HG13	5:CC:630:ARG:NH1	2.29	0.47
8:CF:37:TYR:HD2	8:CF:104:PHE:HB3	1.80	0.47
8:CF:41:PHE:CD2	8:CF:226:TYR:HB3	2.49	0.47
8:CF:170:MET:HG2	8:CF:192:TYR:CE2	2.50	0.47
9:CG:147:THR:HA	9:CG:164:CYS:HA	1.96	0.47
10:CH:371:ALA:HB1	16:CN:174:SER:HB3	1.97	0.47
14:CL:450:GLY:HA2	14:CL:453:ALA:HB3	1.96	0.47
20:CR:19:MET:HE1	55:Lj:75:LYS:HB2	1.96	0.47
26:CY:493:TRP:CE2	26:CY:602:TYR:HB3	2.50	0.47
28:LB:32:PHE:HD1	28:LB:44:THR:HG21	1.80	0.47
28:LB:333:LYS:O	28:LB:334:LYS:HG2	2.15	0.47
15:LF:125:VAL:HG12	42:LT:135:PRO:HG3	1.97	0.47
41:LS:125:LYS:HG3	41:LS:127:VAL:HG13	1.97	0.47
43:LU:102:VAL:HG22	43:LU:112:LEU:HG	1.96	0.47
45:LX:121:VAL:HG23	45:LX:140:THR:HA	1.96	0.47
53:Lh:43:GLY:O	53:Lh:46:LEU:N	2.48	0.47
58:Lq:16:LEU:O	58:Lq:17:LEU:C	2.57	0.47
1:C1:47:C:OP2	1:C1:48:A:O2'	2.31	0.47
1:C1:461:A:H2'	1:C1:462:C:C6	2.49	0.47
1:C1:781:G:N1	29:LC:103:PRO:HD2	2.29	0.47
1:C1:1171:C:H42	1:C1:1297:U:H1'	1.80	0.47
1:C1:1567:A:C6	57:Ll:4:HIS:HB3	2.50	0.47
3:CA:195:GLU:HB3	3:CA:234:ILE:HD11	1.96	0.47
5:CC:340:ILE:HG12	5:CC:417:ARG:NH2	2.30	0.47
7:CE:419:ARG:NH2	7:CE:437:ASP:HB3	2.29	0.47
13:CK:201:LYS:HE3	13:CK:242:TYR:HE1	1.79	0.47
22:CT:144:GLU:C	22:CT:146:PRO:HD3	2.40	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CT:571:LEU:HA	22:CT:574:VAL:HG22	1.96	0.47
26:CY:593:LEU:HG	26:CY:608:TYR:OH	2.15	0.47
26:CY:618:VAL:O	26:CY:622:VAL:HG23	2.14	0.47
36:LN:64:VAL:HG11	36:LN:102:ALA:HB1	1.96	0.47
58:Lq:31:THR:O	58:Lq:209:THR:OG1	2.32	0.47
1:C1:933:A:H4'	1:C1:949:G:H21	1.80	0.47
1:C1:1448:G:N2	1:C1:1492:G:H5''	2.30	0.47
1:C1:3070:A:H2'	1:C1:3071:A:O4'	2.14	0.47
2:C2:142:C:H2'	2:C2:143:U:C6	2.50	0.47
5:CC:407:CYS:SG	12:CJ:147:MET:HE1	2.55	0.47
5:CC:653:GLN:HG2	5:CC:676:TRP:CD1	2.49	0.47
12:CJ:666:LYS:HG2	12:CJ:669:ARG:HE	1.80	0.47
16:CN:1:MET:N	16:CN:224:LEU:HD12	2.30	0.47
23:CU:268:PRO:HG2	23:CU:271:TYR:HB2	1.97	0.47
26:CY:380:ILE:HD12	26:CY:419:VAL:HG12	1.97	0.47
42:LT:66:ASN:O	42:LT:73:GLY:N	2.41	0.47
46:LY:27:ARG:HG2	46:LY:48:PRO:HB3	1.97	0.47
58:Lq:60:ARG:NH2	58:Lq:63:MET:HB3	2.28	0.47
1:C1:868:G:H2'	1:C1:869:A:H8	1.80	0.47
1:C1:1533:C:H2'	1:C1:1534:G:O4'	2.15	0.47
2:C2:66:A:H2'	2:C2:67:U:C6	2.50	0.47
2:C2:197:C:O2'	2:C2:200:C:N4	2.48	0.47
4:CB:19:ASP:OD1	4:CB:22:GLN:HG3	2.15	0.47
5:CC:696:LYS:HG2	5:CC:718:GLU:C	2.40	0.47
6:CD:77:GLU:O	6:CD:81:THR:HG23	2.15	0.47
10:CH:402:VAL:O	10:CH:406:ASP:HB2	2.15	0.47
11:CI:234:GLU:HB2	11:CI:273:PHE:HE1	1.78	0.47
12:CJ:394:ARG:HB2	12:CJ:406:PHE:CD2	2.50	0.47
12:CJ:615:GLU:HA	12:CJ:618:LYS:HG2	1.97	0.47
18:CP:390:ALA:HB1	18:CP:417:ARG:NH1	2.29	0.47
26:CY:453:TRP:HE1	26:CY:501:PHE:HZ	1.62	0.47
29:LC:213:TYR:O	29:LC:237:VAL:HG23	2.15	0.47
43:LU:106:SER:HB3	43:LU:109:VAL:HB	1.96	0.47
48:Lc:77:ASN:HD21	48:Lc:89:ARG:HD2	1.80	0.47
53:Lh:34:LEU:O	53:Lh:38:LYS:CB	2.63	0.47
54:Li:60:ALA:HB3	54:Li:63:GLU:HG3	1.97	0.47
1:C1:204:A:OP1	29:LC:227:ARG:NE	2.44	0.46
1:C1:213:G:N1	1:C1:1371:G:N2	2.63	0.46
1:C1:745:U:O2	1:C1:749:C:C4	2.68	0.46
1:C1:875:A:H5''	1:C1:877:A:H62	1.80	0.46
1:C1:2971:U:H2'	1:C1:2972:C:C6	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:438:LEU:H	5:CC:438:LEU:HG	1.28	0.46
5:CC:683:HIS:HA	5:CC:725:PHE:HD2	1.80	0.46
6:CD:101:PRO:HG3	12:CJ:593:ALA:HB1	1.96	0.46
6:CD:221:LEU:HD12	6:CD:252:TRP:CE3	2.50	0.46
10:CH:196:TYR:CZ	10:CH:199:THR:HG22	2.50	0.46
11:CI:288:MET:HG2	11:CI:291:ARG:NH1	2.30	0.46
12:CJ:371:THR:HA	12:CJ:394:ARG:HG3	1.97	0.46
13:CK:242:TYR:CZ	23:CU:353:GLU:HG2	2.50	0.46
19:CQ:138:ARG:HE	19:CQ:138:ARG:HB2	1.54	0.46
22:CT:183:ARG:HH21	22:CT:257:ASN:HA	1.80	0.46
22:CT:661:GLY:HA2	22:CT:676:LEU:HD11	1.97	0.46
26:CY:456:ASP:OD1	26:CY:460:GLY:HA3	2.15	0.46
29:LC:108:ARG:O	29:LC:108:ARG:HG2	2.15	0.46
32:LH:136:VAL:HG12	32:LH:146:LEU:HD11	1.96	0.46
38:LP:131:ARG:HB2	38:LP:137:ASN:OD1	2.15	0.46
58:Lq:99:LEU:HD23	58:Lq:103:LEU:HD23	1.97	0.46
1:C1:917:A:H2'	1:C1:919:C:C5	2.50	0.46
1:C1:1548:C:C2	5:CC:408:MET:HE1	2.51	0.46
3:CA:244:ILE:HD11	3:CA:254:ILE:HG23	1.96	0.46
8:CF:162:GLU:HB3	8:CF:163:PRO:HD3	1.98	0.46
10:CH:203:LEU:HD11	10:CH:237:GLN:HB3	1.97	0.46
15:CM:200:ASN:HD22	15:CM:203:GLN:HE21	1.64	0.46
22:CT:215:HIS:HE1	22:CT:219:LYS:HD2	1.80	0.46
34:LL:80:LEU:HD22	34:LL:85:ILE:HB	1.97	0.46
1:C1:1576:C:H5'	1:C1:1675:A:H1'	1.97	0.46
1:C1:1668:U:H2'	1:C1:1669:C:C6	2.50	0.46
1:C1:2918:C:H2'	1:C1:2919:G:H8	1.81	0.46
3:CA:116:TYR:HB2	3:CA:243:ILE:HD11	1.96	0.46
5:CC:238:LEU:HD11	21:CS:673:LYS:HG3	1.96	0.46
5:CC:528:HIS:HD1	5:CC:529:PRO:HD2	1.80	0.46
5:CC:694:TYR:HA	5:CC:719:ALA:HB1	1.98	0.46
5:CC:701:HIS:NE2	5:CC:709:PRO:HG3	2.30	0.46
7:CE:151:VAL:CG1	7:CE:293:MET:HG2	2.45	0.46
9:CG:162:ILE:HG13	13:CK:141:LYS:HD2	1.97	0.46
10:CH:350:GLY:HA3	10:CH:361:LEU:HD21	1.97	0.46
14:CL:39:ALA:O	14:CL:42:ASN:HB2	2.16	0.46
16:CN:118:HIS:NE2	16:CN:146:VAL:HB	2.31	0.46
20:CR:23:ARG:HH11	20:CR:27:LEU:HD21	1.79	0.46
21:CS:573:ASP:O	21:CS:577:LYS:HG2	2.16	0.46
22:CT:172:MET:SD	22:CT:245:CYS:HA	2.55	0.46
22:CT:319:GLU:OE2	22:CT:559:ASN:ND2	2.44	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LC:364:GLU:OE1	42:LT:150:THR:OG1	2.33	0.46
34:LL:46:LEU:HB3	34:LL:49:ARG:HB2	1.97	0.46
51:Lf:47:LEU:HD21	51:Lf:76:PRO:HD3	1.97	0.46
58:Lq:25:LYS:HD3	58:Lq:25:LYS:HA	1.48	0.46
1:C1:1234:A:H2'	1:C1:1235:U:O4'	2.15	0.46
1:C1:1241:A:H2'	1:C1:1242:A:C8	2.51	0.46
1:C1:1690:U:OP2	48:Lc:31:ARG:NH2	2.48	0.46
1:C1:2314:A:H2'	1:C1:2315:G:C8	2.50	0.46
1:C1:3041:C:O2'	1:C1:3272:U:OP1	2.25	0.46
4:CB:147:PHE:HZ	4:CB:174:THR:HG21	1.80	0.46
4:CB:263:ILE:O	4:CB:267:VAL:HG12	2.16	0.46
9:CG:90:LEU:O	9:CG:94:ALA:HB2	2.16	0.46
10:CH:484:GLU:OE2	19:CQ:124:ARG:NH2	2.48	0.46
15:CM:155:TYR:OH	15:CM:188:GLU:OE2	2.18	0.46
16:CN:192:VAL:HG21	44:LV:133:SER:HB2	1.97	0.46
18:CP:306:VAL:HB	18:CP:344:VAL:O	2.15	0.46
18:CP:531:ARG:O	18:CP:534:VAL:HG12	2.16	0.46
22:CT:123:GLN:H	22:CT:123:GLN:CD	2.23	0.46
22:CT:607:SER:O	22:CT:611:ILE:HG12	2.16	0.46
28:LB:126:LYS:HB3	28:LB:128:LYS:HE3	1.97	0.46
36:LN:146:PRO:C	36:LN:148:ILE:H	2.23	0.46
1:C1:105:C:H5'	1:C1:684:G:N2	2.31	0.46
1:C1:213:G:C6	1:C1:1371:G:N1	2.83	0.46
1:C1:452:G:H2'	1:C1:453:G:C8	2.50	0.46
1:C1:809:A:N1	1:C1:879:C:N4	2.63	0.46
1:C1:1231:G:C2	1:C1:1232:G:N7	2.83	0.46
1:C1:2395:U:H2'	1:C1:2396:U:H2'	1.97	0.46
1:C1:2898:A:OP2	1:C1:2902:U:O2'	2.25	0.46
2:C2:175:G:H2'	2:C2:176:G:H8	1.79	0.46
4:CB:97:VAL:HG12	4:CB:152:VAL:CG2	2.45	0.46
5:CC:429:LEU:HD23	12:CJ:638:LEU:HD21	1.98	0.46
12:CJ:462:TRP:HA	12:CJ:465:ILE:HG22	1.98	0.46
16:CN:179:VAL:HG22	16:CN:180:PRO:HD2	1.97	0.46
18:CP:520:ASN:ND2	18:CP:577:PHE:HB2	2.31	0.46
22:CT:608:SER:O	22:CT:612:LEU:HD23	2.16	0.46
23:CU:281:THR:O	23:CU:285:VAL:HG23	2.15	0.46
30:LE:193:ASP:HB3	30:LE:198:MET:HE1	1.98	0.46
15:LF:93:ILE:HA	15:LF:120:GLY:HA2	1.97	0.46
31:LG:81:PHE:CD1	31:LG:182:ILE:HD13	2.51	0.46
31:LG:179:PRO:HG2	31:LG:218:ILE:HG23	1.97	0.46
32:LH:16:LEU:HD11	32:LH:83:THR:HG23	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LH:17:LYS:HE3	32:LH:28:GLU:HB2	1.97	0.46
38:LP:24:VAL:HG12	38:LP:86:LYS:HD3	1.97	0.46
43:LU:95:GLN:O	43:LU:96:LEU:HD23	2.16	0.46
1:C1:1398:C:H2'	1:C1:1399:G:C4	2.50	0.46
1:C1:1792:A:O2'	1:C1:1795:A:N3	2.41	0.46
5:CC:279:ARG:HA	5:CC:282:ILE:HG12	1.98	0.46
13:CK:248:ASN:ND2	13:CK:250:GLU:OE2	2.48	0.46
15:CM:136:VAL:HG12	15:CM:136:VAL:O	2.15	0.46
15:CM:186:CYS:SG	15:CM:189:ASP:N	2.88	0.46
28:LB:55:THR:H	28:LB:361:ASP:HB3	1.81	0.46
28:LB:108:GLU:HB3	28:LB:109:HIS:ND1	2.31	0.46
29:LC:191:LEU:HD12	29:LC:202:ARG:O	2.16	0.46
29:LC:213:TYR:CD2	29:LC:222:LEU:HD21	2.50	0.46
47:LZ:121:TYR:HD1	47:LZ:130:PHE:CD2	2.34	0.46
56:Lk:58:LEU:O	56:Lk:62:LEU:HG	2.15	0.46
1:C1:1202:U:H2'	27:Cz:48:TRP:HE1	1.81	0.46
1:C1:1636:C:HO2'	1:C1:1775:G:HO2'	1.58	0.46
1:C1:3103:G:H2'	1:C1:3104:A:H8	1.79	0.46
2:C2:204:C:OP1	11:CI:223:LYS:HD2	2.16	0.46
3:CA:115:PHE:HB3	3:CA:240:LEU:HB3	1.98	0.46
7:CE:261:LEU:O	7:CE:292:THR:HA	2.14	0.46
10:CH:16:PHE:CD2	10:CH:139:ILE:HD13	2.50	0.46
10:CH:34:PRO:HA	10:CH:121:LEU:HD13	1.98	0.46
13:CK:207:PRO:HA	13:CK:210:THR:HG22	1.97	0.46
14:CL:68:GLN:O	14:CL:71:GLU:HG3	2.16	0.46
16:CN:26:VAL:HG23	16:CN:34:PHE:HD2	1.80	0.46
18:CP:571:TYR:O	18:CP:573:VAL:N	2.48	0.46
23:CU:297:LYS:HE2	25:CX:69:LEU:HD21	1.98	0.46
26:CY:413:LYS:O	26:CY:416:ARG:N	2.48	0.46
28:LB:198:SER:O	28:LB:202:LYS:HE2	2.16	0.46
28:LB:324:MET:HE1	28:LB:357:LEU:HD11	1.97	0.46
29:LC:300:LEU:HD22	39:LQ:67:ARG:HB2	1.96	0.46
32:LH:167:CYS:HB2	32:LH:181:ILE:HG12	1.98	0.46
36:LN:94:TYR:CZ	36:LN:96:ARG:HB2	2.51	0.46
52:Lg:24:ILE:HD13	52:Lg:34:LEU:HG	1.98	0.46
52:Lg:75:ARG:HG2	52:Lg:76:ALA:N	2.30	0.46
1:C1:833:U:H2'	1:C1:834:G:C8	2.50	0.46
1:C1:856:G:C2	1:C1:875:A:C6	3.04	0.46
1:C1:1157:C:O2'	1:C1:1158:C:O5'	2.30	0.46
1:C1:3211:G:H21	30:LE:158:ARG:HH22	1.63	0.46
5:CC:773:LYS:HG3	5:CC:773:LYS:O	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:200:VAL:HG21	6:CD:242:THR:HG21	1.97	0.46
10:CH:387:VAL:HG23	16:CN:45:VAL:HG21	1.98	0.46
11:CI:207:PHE:HB3	11:CI:235:PHE:HZ	1.79	0.46
12:CJ:39:TRP:HZ3	12:CJ:81:PHE:HZ	1.63	0.46
28:LB:29:VAL:HG12	28:LB:31:SER:H	1.81	0.46
45:LX:71:ASP:O	45:LX:75:ILE:HG13	2.15	0.46
53:Lh:89:LEU:O	55:Lj:73:ARG:NH2	2.49	0.46
1:C1:597:G:C5	29:LC:314:VAL:HB	2.51	0.46
1:C1:1328:G:H5'	29:LC:304:LYS:HB2	1.98	0.46
1:C1:2409:A:H2'	1:C1:2410:G:O4'	2.16	0.46
1:C1:3067:C:H2'	1:C1:3068:U:C6	2.51	0.46
5:CC:493:LEU:HD12	5:CC:499:VAL:HG22	1.98	0.46
7:CE:182:ASN:ND2	20:CR:131:VAL:HG11	2.31	0.46
7:CE:355:MET:HG3	7:CE:358:LYS:NZ	2.31	0.46
7:CE:512:LYS:HE3	7:CE:551:PRO:HB3	1.96	0.46
10:CH:269:LEU:HD23	10:CH:269:LEU:HA	1.75	0.46
10:CH:534:LEU:HB3	10:CH:539:VAL:HB	1.98	0.46
22:CT:390:HIS:NE2	22:CT:394:GLU:OE2	2.49	0.46
26:CY:679:LYS:HG3	26:CY:721:TYR:CG	2.51	0.46
30:LE:32:ASP:OD1	30:LE:32:ASP:N	2.48	0.46
32:LH:118:ASN:OD1	32:LH:121:GLY:HA2	2.16	0.46
37:LO:130:ARG:HA	37:LO:130:ARG:HD2	1.76	0.46
39:LQ:49:SER:HB2	39:LQ:54:LEU:HD23	1.98	0.46
40:LR:139:VAL:HG12	40:LR:143:HIS:CE1	2.51	0.46
45:LX:21:LYS:HD2	45:LX:21:LYS:HA	1.69	0.46
1:C1:768:G:H2'	1:C1:769:C:C6	2.51	0.46
1:C1:1083:G:H5'	15:LF:113:ARG:HD2	1.98	0.46
1:C1:1088:G:H2'	1:C1:1089:A:H8	1.80	0.46
1:C1:2569:U:H2'	1:C1:2570:U:C6	2.51	0.46
1:C1:2957:G:H2'	1:C1:2958:U:C6	2.51	0.46
2:C2:133:C:H2'	2:C2:134:G:H8	1.81	0.46
2:C2:182:G:N1	4:CB:78:LEU:HD23	2.31	0.46
10:CH:532:ASP:O	10:CH:536:GLN:HG3	2.16	0.46
15:CM:94:ARG:HA	15:CM:140:VAL:HG12	1.97	0.46
16:CN:67:ARG:HG2	16:CN:112:ASP:HB3	1.98	0.46
16:CN:74:THR:O	16:CN:96:ARG:NH2	2.48	0.46
18:CP:237:THR:O	18:CP:240:THR:OG1	2.28	0.46
21:CS:814:MET:HE3	21:CS:814:MET:HB3	1.89	0.46
23:CU:286:LYS:O	23:CU:290:ILE:HG13	2.15	0.46
26:CY:13:LYS:HE3	26:CY:13:LYS:HB2	1.72	0.46
29:LC:133:ALA:HB2	29:LC:149:VAL:HG21	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LE:61:LEU:HD11	30:LE:103:ILE:HG13	1.98	0.46
35:LM:44:PRO:HG3	35:LM:81:VAL:HG13	1.98	0.46
36:LN:27:CYS:HB2	36:LN:122:ASN:ND2	2.31	0.46
40:LR:24:LEU:HD23	40:LR:50:ILE:HG12	1.97	0.46
41:LS:49:LYS:HE2	41:LS:49:LYS:HB3	1.78	0.46
44:LV:55:GLY:C	44:LV:80:ILE:HD11	2.41	0.46
47:LZ:4:LEU:HD23	47:LZ:76:TYR:CZ	2.51	0.46
56:Lk:8:ILE:HG23	56:Lk:58:LEU:HD13	1.97	0.46
58:Lq:89:ASP:O	58:Lq:92:LYS:HG3	2.15	0.46
1:C1:36:C:O2'	1:C1:915:G:N3	2.43	0.45
1:C1:188:U:H2'	1:C1:189:G:O4'	2.16	0.45
1:C1:452:G:H2'	1:C1:453:G:H8	1.81	0.45
1:C1:624:C:C2	1:C1:625:C:C5	3.04	0.45
1:C1:663:G:H5''	39:LQ:134:THR:HB	1.98	0.45
1:C1:1299:A:O2'	1:C1:1300:A:H3'	2.16	0.45
5:CC:486:ARG:NH2	6:CD:113:TRP:HB2	2.31	0.45
7:CE:166:LEU:HD11	7:CE:199:ILE:HG23	1.98	0.45
10:CH:74:HIS:CE1	10:CH:75:PRO:HD2	2.51	0.45
18:CP:483:LEU:HB2	18:CP:484:PRO:HD3	1.97	0.45
21:CS:491:ARG:HA	21:CS:494:ARG:HG2	1.97	0.45
21:CS:684:TYR:CE2	21:CS:706:PRO:HB3	2.50	0.45
33:LK:82:ILE:HG12	33:LK:100:HIS:NE2	2.31	0.45
49:Ld:70:GLN:HB2	49:Ld:74:GLY:O	2.16	0.45
52:Lg:106:LEU:O	52:Lg:109:GLN:HG3	2.16	0.45
1:C1:834:G:H2'	1:C1:835:G:O4'	2.16	0.45
1:C1:890:G:H2'	1:C1:891:G:H8	1.79	0.45
1:C1:1303:G:H2'	1:C1:1304:U:H6	1.81	0.45
1:C1:2433:U:H1'	1:C1:2436:G:H1	1.82	0.45
1:C1:3235:A:H2'	1:C1:3236:A:C8	2.51	0.45
3:CA:147:GLU:HB2	23:CU:221:VAL:HG11	1.98	0.45
6:CD:146:VAL:HG23	6:CD:158:TRP:HB2	1.98	0.45
8:CF:109:PRO:O	8:CF:112:ILE:HG22	2.17	0.45
11:CI:284:PRO:HB2	11:CI:287:LYS:HB2	1.99	0.45
26:CY:559:LEU:HD23	26:CY:559:LEU:HA	1.76	0.45
28:LB:323:VAL:HG12	28:LB:325:ILE:HG13	1.98	0.45
51:Lf:49:LYS:NZ	51:Lf:107:SER:HA	2.31	0.45
52:Lg:12:ASN:O	52:Lg:19:ASN:ND2	2.49	0.45
1:C1:607:U:O2	51:Lf:62:ARG:NH2	2.50	0.45
1:C1:684:G:H2'	1:C1:685:C:C6	2.52	0.45
1:C1:709:G:H1	1:C1:729:U:H3	1.64	0.45
1:C1:1228:G:N2	1:C1:1246:C:O2'	2.50	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1332:A:H2'	1:C1:1334:A:C8	2.51	0.45
1:C1:2374:G:OP1	9:CG:77:SER:OG	2.31	0.45
1:C1:3089:C:OP1	14:CL:7:LYS:NZ	2.50	0.45
7:CE:167:ILE:O	7:CE:171:GLU:HG2	2.16	0.45
7:CE:341:ALA:HB2	7:CE:463:GLN:NE2	2.31	0.45
10:CH:439:GLU:OE2	19:CQ:1:MET:HB3	2.17	0.45
12:CJ:93:ARG:NE	12:CJ:97:ARG:HD3	2.29	0.45
29:LC:133:ALA:HB3	29:LC:134:PRO:HD3	1.98	0.45
30:LE:176:VAL:HG23	30:LE:179:LEU:HB2	1.99	0.45
34:LL:77:LEU:HD22	34:LL:87:ARG:HG3	1.98	0.45
37:LO:124:GLN:NE2	41:LS:161:THR:O	2.49	0.45
47:LZ:20:LYS:HD3	47:LZ:20:LYS:HA	1.70	0.45
58:Lq:55:LEU:HD21	58:Lq:182:ASN:HB3	1.99	0.45
1:C1:29:C:H4'	1:C1:62:A:H4'	1.99	0.45
1:C1:728:A:H2'	1:C1:729:U:C6	2.52	0.45
1:C1:1618:C:H2'	1:C1:1619:G:H8	1.82	0.45
1:C1:2847:C:H5'	10:CH:27:ARG:NH1	2.30	0.45
1:C1:3069:G:O6	1:C1:3077:C:H5''	2.16	0.45
1:C1:3204:G:O2'	1:C1:3205:C:OP1	2.34	0.45
1:C1:3215:U:C2	1:C1:3217:U:H5'	2.50	0.45
2:C2:284:G:H2'	2:C2:285:G:C8	2.52	0.45
4:CB:115:GLU:HG2	4:CB:217:ILE:HG21	1.97	0.45
5:CC:462:ASP:CG	5:CC:467:ALA:H	2.25	0.45
5:CC:700:TRP:CD2	5:CC:759:ILE:HD11	2.51	0.45
6:CD:140:GLN:CD	6:CD:143:GLN:H	2.19	0.45
12:CJ:112:LEU:H	12:CJ:115:LYS:NZ	2.14	0.45
19:CQ:45:ASN:OD1	19:CQ:47:ARG:HB2	2.15	0.45
20:CR:48:ASN:OD1	20:CR:51:ARG:NH2	2.44	0.45
21:CS:702:LYS:HZ1	21:CS:703:HIS:CE1	2.33	0.45
21:CS:733:VAL:HG11	22:CT:436:GLN:OE1	2.15	0.45
26:CY:453:TRP:H	26:CY:453:TRP:CD1	2.33	0.45
26:CY:589:LYS:HA	26:CY:589:LYS:HD2	1.81	0.45
40:LR:24:LEU:HD22	40:LR:32:ILE:HD13	1.97	0.45
47:LZ:73:VAL:HG23	47:LZ:100:PHE:CE2	2.52	0.45
53:Lh:37:GLN:O	53:Lh:45:LYS:NZ	2.30	0.45
58:Lq:205:THR:HG22	58:Lq:207:LYS:H	1.82	0.45
1:C1:158:U:H2'	1:C1:159:G:C8	2.52	0.45
1:C1:355:C:OP2	55:Lj:56:ARG:NH2	2.42	0.45
1:C1:886:U:H2'	1:C1:887:G:C8	2.52	0.45
1:C1:981:C:H5''	1:C1:982:G:H5'	1.98	0.45
1:C1:1232:G:C2	1:C1:1233:A:C5	3.04	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2973:A:H2'	1:C1:2974:G:C8	2.49	0.45
1:C1:3311:G:OP1	28:LB:385:LYS:NZ	2.49	0.45
4:CB:216:PRO:O	4:CB:220:ILE:HG12	2.17	0.45
5:CC:575:ARG:NH1	5:CC:576:LEU:HD22	2.30	0.45
8:CF:109:PRO:O	8:CF:112:ILE:N	2.50	0.45
10:CH:249:VAL:HG11	10:CH:277:PHE:CZ	2.51	0.45
10:CH:533:HIS:HD2	10:CH:537:LEU:HD13	1.81	0.45
11:CI:202:GLU:HB3	15:CM:57:TYR:HB3	1.99	0.45
13:CK:9:ARG:O	13:CK:13:LEU:HG	2.16	0.45
15:CM:101:ILE:CG2	15:CM:105:PRO:HB2	2.47	0.45
15:CM:143:GLY:C	15:CM:241:ILE:HG21	2.42	0.45
18:CP:376:LEU:HB2	18:CP:509:VAL:CG2	2.45	0.45
21:CS:476:TYR:OH	21:CS:698:GLU:OE1	2.28	0.45
22:CT:243:PHE:CZ	22:CT:269:LYS:HD3	2.52	0.45
27:Cz:68:MET:O	27:Cz:71:GLU:HG3	2.17	0.45
15:LF:227:HIS:ND1	15:LF:229:ILE:HG12	2.32	0.45
41:LS:8:GLN:HE21	41:LS:62:ASN:HB2	1.81	0.45
45:LX:143:VAL:HB	45:LX:148:ILE:HD11	1.97	0.45
1:C1:409:A:H2'	1:C1:410:A:H8	1.82	0.45
1:C1:731:G:C2	1:C1:732:A:C8	3.05	0.45
1:C1:1116:G:H5''	23:CU:313:LYS:HE3	1.99	0.45
1:C1:1272:U:H2'	1:C1:1273:A:H8	1.82	0.45
1:C1:1370:U:O2'	50:Le:100:ASN:O	2.30	0.45
1:C1:1722:G:C2	1:C1:1723:G:N7	2.85	0.45
1:C1:3110:C:H5''	1:C1:3111:U:H5	1.82	0.45
4:CB:139:ALA:HB2	31:LG:212:ASN:ND2	2.28	0.45
5:CC:528:HIS:O	5:CC:531:VAL:HG12	2.17	0.45
5:CC:532:THR:HA	6:CD:198:ARG:NH1	2.27	0.45
15:CM:241:ILE:O	15:CM:245:ILE:HG12	2.16	0.45
18:CP:232:LEU:O	18:CP:236:ARG:HG3	2.17	0.45
18:CP:536:LEU:HD12	18:CP:580:LYS:O	2.16	0.45
20:CR:56:ALA:O	34:LL:51:VAL:HG12	2.17	0.45
26:CY:401:PHE:CD1	26:CY:448:SER:HB2	2.52	0.45
26:CY:685:LYS:HA	26:CY:685:LYS:HD2	1.84	0.45
29:LC:209:PRO:HG2	29:LC:232:VAL:HG22	1.98	0.45
41:LS:135:VAL:HG11	41:LS:140:ILE:HG22	1.98	0.45
58:Lq:163:LEU:HD12	58:Lq:163:LEU:HA	1.83	0.45
1:C1:322:G:C2	1:C1:323:G:C8	3.05	0.45
1:C1:655:U:H2'	1:C1:656:U:C6	2.52	0.45
1:C1:857:A:H2'	1:C1:858:C:O4'	2.16	0.45
1:C1:972:G:O6	1:C1:1040:U:O2	2.35	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1046:A:O2'	1:C1:1075:A:N6	2.49	0.45
1:C1:1658:A:OP1	43:LU:101:ARG:NH2	2.50	0.45
1:C1:1762:C:H2'	1:C1:1763:U:C6	2.52	0.45
1:C1:1812:G:O2'	57:L1:3:SER:O	2.35	0.45
1:C1:2726:U:H2'	1:C1:2727:A:C8	2.52	0.45
1:C1:3144:C:H3'	1:C1:3145:C:H6	1.81	0.45
4:CB:215:ARG:HG3	4:CB:220:ILE:CD1	2.47	0.45
7:CE:150:ASP:OD1	7:CE:292:THR:N	2.24	0.45
10:CH:74:HIS:CE1	10:CH:164:PRO:HB3	2.52	0.45
10:CH:485:GLU:HG3	19:CQ:116:ARG:HH22	1.80	0.45
11:CI:217:ARG:HH12	11:CI:219:VAL:HG12	1.81	0.45
12:CJ:170:ARG:O	12:CJ:174:GLU:HG3	2.17	0.45
20:CR:34:ILE:HD12	20:CR:172:LEU:HD23	1.98	0.45
21:CS:675:ASP:O	21:CS:678:ASP:N	2.49	0.45
22:CT:645:SER:OG	22:CT:651:SER:HB3	2.16	0.45
26:CY:378:MET:HA	26:CY:381:LYS:HG2	1.99	0.45
26:CY:635:ARG:NH1	26:CY:711:LEU:O	2.49	0.45
47:LZ:73:VAL:HG23	47:LZ:100:PHE:HD2	1.81	0.45
48:Lc:12:SER:O	48:Lc:16:LYS:HG3	2.16	0.45
49:Ld:31:VAL:HG23	49:Ld:36:ARG:HG2	1.98	0.45
1:C1:687:C:H2'	1:C1:688:G:H8	1.80	0.45
1:C1:829:A:O5'	1:C1:829:A:H8	2.00	0.45
1:C1:1719:A:H1'	1:C1:1720:A:C8	2.51	0.45
2:C2:37:A:OP2	53:Lh:91:ARG:HD2	2.17	0.45
3:CA:149:GLU:O	3:CA:153:LYS:HG3	2.17	0.45
3:CA:161:HIS:HE2	23:CU:205:LEU:HD22	1.82	0.45
5:CC:781:TRP:CZ3	5:CC:788:CYS:HB3	2.52	0.45
5:CC:793:ALA:C	5:CC:795:GLY:H	2.24	0.45
7:CE:134:MET:HE2	7:CE:138:GLN:HB3	1.98	0.45
7:CE:165:PHE:CE2	7:CE:188:VAL:HG21	2.52	0.45
9:CG:115:VAL:HG12	9:CG:117:ALA:H	1.81	0.45
10:CH:214:ARG:HH11	10:CH:214:ARG:HG3	1.82	0.45
11:CI:273:PHE:HB3	11:CI:276:ALA:HB2	1.97	0.45
15:CM:67:GLU:HA	15:CM:70:ARG:HG2	1.98	0.45
15:CM:89:LEU:HD23	15:CM:89:LEU:H	1.82	0.45
26:CY:594:LYS:O	26:CY:608:TYR:OH	2.28	0.45
26:CY:649:ALA:HA	26:CY:652:ARG:HE	1.82	0.45
31:LG:246:GLN:O	31:LG:250:GLU:OE1	2.34	0.45
37:LO:28:LEU:HB3	37:LO:100:ALA:HB1	1.98	0.45
42:LT:48:VAL:HG12	42:LT:50:LYS:H	1.82	0.45
47:LZ:63:LYS:HA	47:LZ:66:LYS:HG2	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1126:U:H6	1:C1:1142:C:H41	1.65	0.45
1:C1:1259:C:H2'	1:C1:1260:A:H8	1.82	0.45
1:C1:2751:G:H2'	1:C1:2752:G:C8	2.52	0.45
1:C1:2840:U:H2'	1:C1:2841:U:C6	2.52	0.45
1:C1:2898:A:O2'	1:C1:2899:A:OP2	2.29	0.45
1:C1:3173:C:H5'	35:LM:132:ARG:HD3	1.98	0.45
5:CC:736:ALA:HB1	5:CC:776:VAL:HG13	1.99	0.45
7:CE:362:VAL:HB	7:CE:412:ILE:HG22	1.99	0.45
9:CG:96:TYR:CE2	9:CG:127:PRO:HD2	2.52	0.45
13:CK:4:ASN:O	13:CK:6:TYR:N	2.49	0.45
14:CL:16:LYS:HE3	14:CL:16:LYS:HA	1.98	0.45
18:CP:551:TYR:O	18:CP:553:GLY:N	2.50	0.45
29:LC:207:ARG:NH1	29:LC:233:GLU:OE2	2.50	0.45
38:LP:22:LEU:HD23	38:LP:90:PHE:CD2	2.52	0.45
45:LX:77:ILE:HG22	45:LX:78:HIS:HD2	1.81	0.45
1:C1:400:A:N3	1:C1:642:C:O2'	2.46	0.45
1:C1:409:A:H2'	1:C1:410:A:C8	2.51	0.45
1:C1:575:A:H2'	1:C1:576:C:C6	2.51	0.45
1:C1:623:C:H5''	50:Le:42:ARG:NH1	2.31	0.45
1:C1:727:C:H2'	1:C1:728:A:H8	1.82	0.45
1:C1:806:U:O2	1:C1:881:G:O6	2.35	0.45
1:C1:1175:A:OP1	37:LO:50:ARG:NH2	2.50	0.45
1:C1:1588:C:H2'	1:C1:1589:G:C8	2.51	0.45
1:C1:2314:A:H2'	1:C1:2315:G:H8	1.82	0.45
1:C1:2418:A:H2'	1:C1:2419:G:O4'	2.17	0.45
1:C1:2841:U:H2'	1:C1:2842:C:C6	2.51	0.45
1:C1:3053:C:H2'	1:C1:3054:U:C6	2.52	0.45
2:C2:26:U:O2'	29:LC:52:ALA:O	2.33	0.45
2:C2:52:A:N6	57:Ll:27:ILE:HG21	2.32	0.45
5:CC:235:GLU:O	5:CC:239:ILE:HG12	2.17	0.45
5:CC:462:ASP:OD2	5:CC:464:THR:OG1	2.35	0.45
6:CD:409:HIS:C	6:CD:411:GLY:H	2.25	0.45
7:CE:181:ARG:HH12	20:CR:131:VAL:HB	1.83	0.45
7:CE:329:VAL:C	7:CE:331:GLY:H	2.25	0.45
8:CF:31:ARG:HH12	8:CF:76:ALA:HA	1.82	0.45
12:CJ:172:CYS:O	12:CJ:176:GLN:HG3	2.17	0.45
13:CK:35:ASN:HD21	13:CK:54:ARG:NH1	2.15	0.45
13:CK:42:LEU:HD22	13:CK:46:ARG:NH1	2.32	0.45
26:CY:529:TYR:HB3	26:CY:530:PRO:HD3	1.98	0.45
26:CY:574:ALA:O	26:CY:578:VAL:HG23	2.17	0.45
28:LB:285:ARG:HB3	28:LB:324:MET:HE2	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LF:92:VAL:O	15:LF:120:GLY:HA2	2.17	0.45
45:LX:129:PRO:O	57:Ll:14:ALA:HB2	2.17	0.45
53:Lh:42:SER:HB2	53:Lh:46:LEU:HD21	1.98	0.45
1:C1:8:C:H2'	1:C1:9:U:C6	2.52	0.44
1:C1:490:C:H5''	30:LE:100:ARG:HG3	1.98	0.44
1:C1:881:G:H1'	1:C1:1568:A:N6	2.31	0.44
1:C1:1045:G:H21	1:C1:1048:G:N2	2.06	0.44
1:C1:1322:C:H2'	1:C1:1323:U:C6	2.52	0.44
1:C1:2741:U:H2'	1:C1:2742:G:C8	2.52	0.44
1:C1:2859:G:N2	1:C1:2987:G:O2'	2.51	0.44
4:CB:26:ALA:HB1	4:CB:291:LEU:HD13	1.98	0.44
5:CC:575:ARG:HH12	5:CC:576:LEU:HD22	1.81	0.44
8:CF:44:SER:HB2	8:CF:100:VAL:HG12	2.00	0.44
10:CH:308:LEU:O	10:CH:311:SER:OG	2.29	0.44
11:CI:217:ARG:HG2	11:CI:217:ARG:HH11	1.82	0.44
12:CJ:645:LEU:O	12:CJ:649:MET:HG3	2.16	0.44
18:CP:365:GLN:HG2	18:CP:366:ALA:N	2.31	0.44
26:CY:378:MET:HA	26:CY:381:LYS:HE3	1.98	0.44
26:CY:394:ASP:OD1	26:CY:395:SER:N	2.48	0.44
28:LB:28:ARG:HG3	28:LB:30:LYS:HG2	1.99	0.44
15:LF:10:ASN:O	15:LF:14:VAL:HA	2.17	0.44
38:LP:22:LEU:HD22	38:LP:146:ILE:HD12	1.98	0.44
43:LU:92:LYS:HE2	43:LU:92:LYS:HB3	1.59	0.44
45:LX:120:THR:HA	45:LX:139:LEU:HA	1.99	0.44
47:LZ:32:THR:OG1	47:LZ:34:SER:O	2.29	0.44
51:Lf:37:VAL:HG13	51:Lf:42:ALA:HB3	1.99	0.44
1:C1:407:G:H21	1:C1:1381:A:H61	1.65	0.44
1:C1:1054:G:H2'	1:C1:1055:U:C6	2.52	0.44
1:C1:1429:G:H5'	38:LP:65:GLY:H	1.81	0.44
1:C1:1657:G:O6	43:LU:81:ARG:NH2	2.50	0.44
1:C1:2340:C:H2'	1:C1:2341:U:C6	2.52	0.44
1:C1:2440:C:H2'	1:C1:2441:C:O4'	2.17	0.44
1:C1:2762:A:H2'	1:C1:2763:G:H8	1.81	0.44
1:C1:2794:C:H2'	1:C1:2795:A:O4'	2.17	0.44
1:C1:2990:A:H2'	1:C1:2991:C:H6	1.82	0.44
4:CB:103:ASP:HB3	4:CB:104:PRO:HD2	1.98	0.44
5:CC:209:ASP:O	5:CC:213:VAL:HA	2.17	0.44
8:CF:20:ARG:HE	8:CF:23:LYS:HD2	1.83	0.44
8:CF:224:LEU:HD21	8:CF:243:ARG:HG2	1.99	0.44
19:CQ:53:LYS:HE2	28:LB:380:PHE:CZ	2.53	0.44
19:CQ:145:LEU:HD22	19:CQ:159:LEU:HG	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CT:134:ILE:HG23	22:CT:148:HIS:HB3	1.99	0.44
22:CT:452:ASP:HA	22:CT:455:ARG:HG2	1.99	0.44
28:LB:83:PRO:HB2	28:LB:203:PRO:HB2	1.99	0.44
15:LF:70:ARG:O	15:LF:74:ILE:HG12	2.17	0.44
41:LS:67:LYS:HB3	41:LS:68:HIS:CE1	2.52	0.44
43:LU:42:PHE:O	43:LU:46:ARG:HG2	2.17	0.44
46:LY:76:LYS:HG3	46:LY:78:VAL:HG22	1.99	0.44
1:C1:491:A:H2'	1:C1:492:U:C6	2.52	0.44
1:C1:1158:C:OP2	1:C1:1159:G:H3'	2.16	0.44
1:C1:1232:G:H2'	1:C1:1233:A:H8	1.82	0.44
1:C1:1458:G:H5''	10:CH:512:LEU:HD12	2.00	0.44
1:C1:1592:A:OP2	56:Lk:39:ARG:NH1	2.34	0.44
1:C1:3003:A:H4'	28:LB:222:THR:HG21	1.99	0.44
7:CE:152:LEU:HB2	7:CE:311:LEU:HD11	1.98	0.44
8:CF:65:ILE:HD12	8:CF:103:LEU:HD12	1.98	0.44
9:CG:99:TRP:CE3	9:CG:121:ARG:HB3	2.52	0.44
10:CH:342:ARG:O	10:CH:345:GLN:HG2	2.16	0.44
12:CJ:419:ILE:HG12	12:CJ:456:VAL:HG23	1.98	0.44
16:CN:56:THR:CG2	16:CN:58:ILE:HG12	2.47	0.44
16:CN:192:VAL:HG13	16:CN:192:VAL:O	2.17	0.44
18:CP:239:ILE:O	18:CP:243:ILE:HG13	2.17	0.44
26:CY:421:LYS:O	26:CY:425:GLN:OE1	2.35	0.44
26:CY:616:ASP:O	26:CY:620:GLU:HG3	2.18	0.44
29:LC:68:THR:HG22	29:LC:74:ARG:HD3	1.99	0.44
41:LS:48:LEU:HD11	42:LT:152:ALA:O	2.18	0.44
1:C1:209:G:OP1	46:LY:15:ARG:NH1	2.48	0.44
1:C1:1371:G:H5''	50:Le:102:SER:HB3	2.00	0.44
2:C2:2:A:C4	2:C2:3:A:C8	3.06	0.44
2:C2:176:G:H2'	2:C2:177:C:H6	1.83	0.44
2:C2:222:G:H2'	2:C2:223:G:O4'	2.18	0.44
4:CB:159:ILE:O	4:CB:162:ARG:N	2.45	0.44
5:CC:744:ILE:O	5:CC:762:VAL:HG22	2.17	0.44
6:CD:190:ARG:HH21	6:CD:205:TYR:H	1.66	0.44
7:CE:247:HIS:O	7:CE:251:THR:HG22	2.17	0.44
10:CH:309:THR:HG22	10:CH:316:ILE:HG13	2.00	0.44
12:CJ:141:LEU:HD21	12:CJ:241:VAL:HG21	2.00	0.44
12:CJ:251:LEU:HA	12:CJ:275:GLY:HA2	2.00	0.44
15:CM:104:LYS:HB3	15:CM:105:PRO:HD3	1.98	0.44
23:CU:277:ARG:NH1	23:CU:282:MET:HE1	2.32	0.44
26:CY:549:PRO:HA	26:CY:552:PHE:HB2	1.99	0.44
27:Cz:50:LEU:HD11	41:LS:133:GLU:HB2	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LC:223:VAL:O	29:LC:226:PHE:C	2.61	0.44
58:Lq:90:LEU:HA	58:Lq:93:LEU:HB2	1.98	0.44
1:C1:208:G:H5'	46:LY:11:ARG:HG3	1.99	0.44
1:C1:741:G:O2'	1:C1:742:A:OP2	2.33	0.44
1:C1:1233:A:C6	1:C1:1234:A:C6	3.06	0.44
1:C1:1453:U:H2'	1:C1:1454:G:C8	2.53	0.44
1:C1:1594:C:H2'	1:C1:1595:U:H6	1.78	0.44
1:C1:1595:U:H2'	1:C1:1596:G:C8	2.53	0.44
1:C1:2361:A:N6	1:C1:2900:C:C5	2.85	0.44
1:C1:3064:U:OP1	13:CK:34:LYS:NZ	2.35	0.44
1:C1:3135:G:H4'	37:LO:163:LYS:HD2	2.00	0.44
1:C1:3304:C:H2'	1:C1:3305:U:H6	1.79	0.44
2:C2:4:C:C2	2:C2:5:U:C5	3.05	0.44
3:CA:67:LYS:HE2	3:CA:67:LYS:HB3	1.84	0.44
3:CA:137:ARG:O	3:CA:176:ILE:HG13	2.18	0.44
5:CC:730:LEU:HD13	5:CC:786:PRO:HB3	1.99	0.44
7:CE:395:LYS:HB2	7:CE:395:LYS:HE2	1.79	0.44
8:CF:134:THR:OG1	8:CF:197:GLU:N	2.45	0.44
13:CK:137:LYS:HD2	13:CK:137:LYS:HA	1.77	0.44
15:CM:200:ASN:HD22	15:CM:203:GLN:NE2	2.15	0.44
21:CS:691:GLY:HA2	31:LG:241:MET:HE3	1.98	0.44
25:CX:107:MET:O	25:CX:111:GLU:OE1	2.36	0.44
26:CY:26:ARG:HA	26:CY:29:VAL:HG12	2.00	0.44
26:CY:679:LYS:HA	26:CY:679:LYS:HD3	1.79	0.44
28:LB:47:MET:HE3	28:LB:84:MET:SD	2.58	0.44
31:LG:93:ALA:O	31:LG:97:LEU:HG	2.17	0.44
33:LK:133:LEU:HD21	33:LK:148:PRO:O	2.17	0.44
39:LQ:107:THR:O	39:LQ:164:THR:HA	2.17	0.44
1:C1:19:U:H2'	1:C1:20:A:C8	2.52	0.44
1:C1:775:G:H2'	1:C1:776:C:H6	1.83	0.44
1:C1:920:U:H2'	1:C1:921:G:H8	1.83	0.44
1:C1:1381:A:H5'	2:C2:9:A:H5'	2.00	0.44
1:C1:1599:U:OP2	12:CJ:48:ARG:HD3	2.17	0.44
1:C1:1673:U:O2'	1:C1:1674:U:H5'	2.18	0.44
1:C1:2867:U:H2'	1:C1:2868:A:O4'	2.18	0.44
1:C1:3134:A:OP2	37:LO:173:LYS:NZ	2.50	0.44
3:CA:227:THR:O	23:CU:255:ARG:NH2	2.51	0.44
4:CB:215:ARG:HH11	4:CB:219:GLU:CD	2.25	0.44
5:CC:121:PHE:CZ	7:CE:473:LEU:HD13	2.49	0.44
5:CC:307:LYS:HE2	5:CC:307:LYS:HB3	1.67	0.44
5:CC:358:PRO:HA	5:CC:361:LEU:HD23	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:523:LEU:HB2	5:CC:583:LEU:HB3	1.99	0.44
10:CH:255:ILE:HG23	10:CH:297:LEU:HD11	1.99	0.44
10:CH:287:ASN:HA	10:CH:319:ALA:O	2.18	0.44
18:CP:234:MET:O	18:CP:237:THR:OG1	2.31	0.44
18:CP:235:LEU:O	18:CP:239:ILE:HG13	2.17	0.44
23:CU:207:ILE:HG22	23:CU:207:ILE:O	2.17	0.44
23:CU:225:ARG:HH11	23:CU:225:ARG:HG3	1.82	0.44
26:CY:619:GLY:HA3	26:CY:669:LEU:HD21	2.00	0.44
29:LC:296:ILE:HD13	39:LQ:159:PRO:HB3	1.99	0.44
30:LE:58:LEU:HD11	30:LE:72:LEU:HB2	1.99	0.44
33:LK:77:ALA:HB1	33:LK:135:THR:HG21	1.99	0.44
33:LK:83:ARG:O	33:LK:86:LYS:HG3	2.17	0.44
33:LK:88:PRO:HA	33:LK:89:PRO:HD3	1.91	0.44
40:LR:98:ARG:HH21	40:LR:133:LYS:HA	1.82	0.44
58:Lq:176:GLN:HA	58:Lq:179:LEU:HG	1.98	0.44
1:C1:955:U:H5'	39:LQ:86:ASN:ND2	2.32	0.44
1:C1:1172:A:N3	1:C1:1172:A:H2'	2.33	0.44
1:C1:1582:A:OP1	40:LR:38:ARG:NH1	2.50	0.44
1:C1:1599:U:H2'	1:C1:1600:G:C8	2.52	0.44
1:C1:1795:A:H2'	1:C1:1796:A:H8	1.81	0.44
6:CD:104:TYR:HA	6:CD:484:VAL:O	2.18	0.44
7:CE:306:LEU:HA	7:CE:309:ILE:HG22	1.99	0.44
12:CJ:50:ARG:NH1	12:CJ:58:THR:O	2.50	0.44
12:CJ:243:TYR:O	12:CJ:247:THR:HG22	2.18	0.44
15:CM:27:LYS:O	15:CM:31:GLU:OE1	2.36	0.44
15:CM:78:GLN:NE2	15:CM:131:GLU:OE2	2.43	0.44
16:CN:63:THR:HG22	16:CN:72:VAL:HG12	1.99	0.44
18:CP:279:TYR:HE2	18:CP:480:PHE:CD1	2.36	0.44
26:CY:612:ARG:NH2	26:CY:665:LYS:O	2.51	0.44
1:C1:729:U:H2'	1:C1:730:C:H6	1.81	0.44
1:C1:1322:C:H2'	1:C1:1323:U:H6	1.81	0.44
1:C1:3216:U:H5'	30:LE:66:ARG:NH2	2.33	0.44
1:C1:3333:A:H2'	1:C1:3334:U:H6	1.83	0.44
8:CF:88:GLY:O	8:CF:91:ARG:HB2	2.17	0.44
10:CH:13:ALA:HB2	10:CH:143:LYS:HA	1.99	0.44
16:CN:71:LEU:HD11	16:CN:97:ILE:CG2	2.47	0.44
18:CP:536:LEU:HD21	18:CP:563:THR:HG23	1.99	0.44
18:CP:539:THR:HG21	18:CP:564:ARG:HG3	1.99	0.44
22:CT:125:ARG:HA	22:CT:125:ARG:HD2	1.87	0.44
22:CT:269:LYS:HE2	22:CT:278:ASP:HB2	2.00	0.44
32:LH:49:LYS:HB2	32:LH:52:VAL:HG12	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LK:148:PRO:HD2	33:LK:149:LYS:H	1.82	0.44
36:LN:154:PRO:O	36:LN:157:LYS:HG3	2.18	0.44
37:LO:190:LYS:HB2	37:LO:190:LYS:HE3	1.79	0.44
39:LQ:98:ASN:ND2	39:LQ:167:LEU:HD22	2.33	0.44
44:LV:19:LEU:HD21	44:LV:100:ASN:HB3	1.98	0.44
56:Lk:51:ASP:HB3	56:Lk:54:LYS:HE2	1.99	0.44
1:C1:189:G:N1	1:C1:192:A:OP2	2.46	0.44
1:C1:363:G:N1	1:C1:366:A:OP2	2.40	0.44
1:C1:1780:U:H5''	12:CJ:6:LYS:NZ	2.33	0.44
1:C1:2299:C:H2'	1:C1:2300:C:H6	1.83	0.44
1:C1:2427:G:H2'	1:C1:2428:G:C8	2.53	0.44
1:C1:2451:C:N4	1:C1:2452:C:N4	2.65	0.44
1:C1:2458:U:C2	1:C1:2459:C:C5	3.06	0.44
2:C2:284:G:H2'	2:C2:285:G:H8	1.82	0.44
6:CD:52:SER:HB2	6:CD:55:MET:HE2	1.99	0.44
10:CH:291:ILE:O	10:CH:292:LYS:HD2	2.17	0.44
10:CH:444:LYS:HD2	10:CH:449:TYR:CE2	2.48	0.44
10:CH:465:GLU:OE2	19:CQ:103:ARG:NH2	2.51	0.44
19:CQ:137:LEU:HB3	19:CQ:138:ARG:H	1.43	0.44
21:CS:552:LEU:HB2	48:Lc:13:ILE:HD11	2.00	0.44
22:CT:556:ASN:ND2	22:CT:559:ASN:O	2.51	0.44
26:CY:476:ARG:O	26:CY:480:ILE:HG12	2.18	0.44
26:CY:493:TRP:NE1	26:CY:602:TYR:HB3	2.33	0.44
1:C1:323:G:H5''	20:CR:5:LEU:HD23	2.00	0.43
1:C1:968:U:H2'	1:C1:969:U:C6	2.53	0.43
1:C1:2458:U:H2'	1:C1:2459:C:H6	1.83	0.43
1:C1:3214:A:H5''	1:C1:3216:U:OP2	2.18	0.43
5:CC:591:ILE:HD12	5:CC:605:THR:OG1	2.18	0.43
6:CD:140:GLN:OE1	6:CD:143:GLN:N	2.34	0.43
6:CD:309:ASP:OD2	6:CD:311:THR:N	2.42	0.43
6:CD:350:ARG:HG3	6:CD:401:GLU:OE1	2.18	0.43
10:CH:23:ARG:NH1	10:CH:27:ARG:HE	2.16	0.43
18:CP:508:ILE:HB	18:CP:581:PHE:HB2	2.00	0.43
26:CY:69:LYS:HD3	26:CY:72:GLU:OE2	2.18	0.43
26:CY:487:TYR:CD1	26:CY:488:ARG:NH2	2.86	0.43
28:LB:161:VAL:HG23	28:LB:184:ILE:HD11	1.99	0.43
31:LG:157:ALA:HB2	31:LG:189:LEU:HD12	1.99	0.43
39:LQ:101:ASN:C	39:LQ:103:ASN:H	2.26	0.43
46:LY:44:VAL:HG13	46:LY:121:ILE:HG21	2.00	0.43
58:Lq:17:LEU:HB2	58:Lq:176:GLN:NE2	2.33	0.43
1:C1:94:G:H2'	1:C1:95:A:C8	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:599:U:C2	1:C1:600:G:C8	3.06	0.43
1:C1:656:U:H2'	1:C1:657:U:C6	2.54	0.43
1:C1:731:G:H2'	1:C1:731:G:N3	2.32	0.43
1:C1:1490:C:OP1	38:LP:127:ARG:NH1	2.33	0.43
1:C1:1504:U:OP2	45:LX:134:LYS:NZ	2.50	0.43
1:C1:1787:G:OP2	1:C1:1787:G:N2	2.51	0.43
1:C1:2366:A:H5''	13:CK:149:ARG:HH12	1.83	0.43
1:C1:2767:C:H5''	13:CK:208:LEU:HD12	2.00	0.43
1:C1:3333:A:H2'	1:C1:3334:U:C6	2.53	0.43
2:C2:39:G:O2'	2:C2:105:A:N1	2.48	0.43
2:C2:40:A:OP2	2:C2:103:G:N1	2.50	0.43
6:CD:469:ASP:OD2	6:CD:469:ASP:C	2.61	0.43
10:CH:497:GLU:HG2	49:Ld:107:LYS:HD3	2.00	0.43
12:CJ:178:TYR:CE2	12:CJ:245:LEU:HD13	2.53	0.43
13:CK:9:ARG:HA	13:CK:9:ARG:HD2	1.79	0.43
13:CK:22:GLU:O	13:CK:26:LYS:HG3	2.18	0.43
16:CN:163:PRO:HD3	16:CN:193:ILE:HD11	1.99	0.43
28:LB:340:ARG:NH1	28:LB:343:LEU:HG	2.33	0.43
29:LC:146:VAL:HG12	29:LC:177:GLY:HA3	2.01	0.43
31:LG:160:VAL:HG11	31:LG:166:VAL:HG11	1.99	0.43
33:LK:128:GLY:O	33:LK:132:ILE:HD12	2.17	0.43
36:LN:47:LYS:HE3	36:LN:51:LEU:HD11	2.00	0.43
51:Lf:22:ARG:HG3	51:Lf:23:ARG:HH11	1.83	0.43
1:C1:114:A:H2'	1:C1:115:A:O4'	2.18	0.43
1:C1:309:A:H2'	1:C1:310:A:C8	2.53	0.43
1:C1:324:C:O2'	20:CR:19:MET:HE3	2.18	0.43
1:C1:429:G:C4	1:C1:430:A:C8	3.06	0.43
1:C1:600:G:H2'	1:C1:601:C:C6	2.54	0.43
1:C1:1529:G:H2'	1:C1:1530:U:C6	2.53	0.43
1:C1:1561:U:H5'	1:C1:1562:G:H8	1.82	0.43
1:C1:2404:G:H2'	1:C1:2405:A:H8	1.83	0.43
1:C1:2884:A:H4'	10:CH:54:GLU:HG2	2.00	0.43
1:C1:2898:A:H2'	1:C1:2903:G:O4'	2.18	0.43
1:C1:3162:A:H4'	1:C1:3163:G:O5'	2.18	0.43
6:CD:367:ILE:HD11	6:CD:391:VAL:HG21	2.00	0.43
10:CH:541:THR:HG23	19:CQ:143:ARG:NH1	2.32	0.43
11:CI:217:ARG:HG2	11:CI:217:ARG:NH1	2.33	0.43
12:CJ:381:GLN:HB2	12:CJ:382:PRO:HD3	2.00	0.43
16:CN:108:ILE:HG12	16:CN:117:ILE:HG22	1.99	0.43
17:CO:106:ILE:HG23	17:CO:107:VAL:HG13	2.00	0.43
18:CP:442:GLU:O	18:CP:446:VAL:HG23	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CR:49:TYR:OH	34:LL:47:ALA:O	2.27	0.43
22:CT:443:LEU:HD11	22:CT:493:LEU:HD21	2.00	0.43
26:CY:433:VAL:HG12	26:CY:434:THR:HG22	2.00	0.43
28:LB:74:GLU:OE2	28:LB:326:LYS:HG3	2.18	0.43
30:LE:48:PRO:HB3	30:LE:52:LEU:HD11	2.00	0.43
33:LK:77:ALA:N	33:LK:116:MET:HE1	2.33	0.43
37:LO:180:LEU:HG	37:LO:184:LYS:HE2	2.01	0.43
41:LS:139:TYR:O	41:LS:142:GLN:HG2	2.18	0.43
43:LU:92:LYS:O	43:LU:92:LYS:HG2	2.18	0.43
47:LZ:66:LYS:HA	47:LZ:66:LYS:HE2	1.99	0.43
58:Lq:60:ARG:NE	58:Lq:152:LYS:HD2	2.33	0.43
1:C1:85:A:H4'	1:C1:86:G:H4'	2.01	0.43
1:C1:1234:A:OP2	1:C1:1234:A:H8	2.01	0.43
1:C1:1431:A:H2'	1:C1:1432:G:O4'	2.18	0.43
1:C1:1455:A:H5''	40:LR:23:TRP:CD1	2.53	0.43
1:C1:3278:C:H2'	1:C1:3279:A:H8	1.83	0.43
1:C1:3297:U:HO2'	1:C1:3298:U:P	2.39	0.43
2:C2:223:G:H21	2:C2:301:A:N6	2.17	0.43
2:C2:226:G:H2'	2:C2:227:G:C8	2.52	0.43
4:CB:30:LEU:O	4:CB:34:ILE:HG12	2.18	0.43
4:CB:217:ILE:H	4:CB:217:ILE:HD12	1.83	0.43
5:CC:359:GLU:HG2	12:CJ:667:ARG:HD2	1.99	0.43
5:CC:787:TRP:NE1	5:CC:801:MET:HG3	2.34	0.43
7:CE:359:LYS:HB3	7:CE:426:VAL:HG23	2.00	0.43
10:CH:301:MET:O	10:CH:305:ILE:HG13	2.18	0.43
12:CJ:134:PHE:CD1	12:CJ:244:ARG:HD3	2.53	0.43
12:CJ:370:PHE:HD2	12:CJ:372:PHE:HE1	1.65	0.43
12:CJ:371:THR:HG23	12:CJ:394:ARG:HD3	2.00	0.43
12:CJ:400:VAL:HG21	15:CM:192:HIS:ND1	2.34	0.43
13:CK:242:TYR:O	13:CK:259:LEU:HD12	2.18	0.43
14:CL:75:ARG:HA	14:CL:78:GLU:HG2	2.00	0.43
15:CM:131:GLU:O	15:CM:135:ILE:HG12	2.19	0.43
16:CN:210:THR:HG23	16:CN:214:GLU:HG3	1.99	0.43
18:CP:373:VAL:O	18:CP:376:LEU:C	2.61	0.43
18:CP:390:ALA:HB3	18:CP:391:PRO:HD3	2.00	0.43
18:CP:453:VAL:HG22	18:CP:498:CYS:SG	2.58	0.43
18:CP:481:MET:HE3	18:CP:481:MET:HB3	1.75	0.43
26:CY:653:TRP:CD1	26:CY:653:TRP:C	2.96	0.43
32:LH:20:ILE:HG13	32:LH:25:VAL:HG22	2.01	0.43
58:Lq:143:ASP:OD1	58:Lq:143:ASP:N	2.51	0.43
1:C1:1199:A:N6	1:C1:1271:G:O6	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1215:G:C6	1:C1:1238:G:C6	3.07	0.43
1:C1:2942:C:H2'	1:C1:2943:C:C6	2.54	0.43
1:C1:3162:A:H5''	1:C1:3163:G:C5	2.54	0.43
2:C2:286:C:H2'	2:C2:287:G:H8	1.84	0.43
3:CA:27:ILE:HG13	3:CA:27:ILE:O	2.18	0.43
7:CE:434:PRO:HA	7:CE:435:PRO:HD3	1.89	0.43
10:CH:84:LEU:HD21	10:CH:155:HIS:HE1	1.79	0.43
10:CH:214:ARG:HG3	10:CH:214:ARG:NH1	2.32	0.43
10:CH:465:GLU:O	10:CH:468:LEU:N	2.50	0.43
11:CI:302:TRP:O	11:CI:306:VAL:HG23	2.18	0.43
17:CO:20:ASN:HB2	17:CO:21:ILE:HD12	2.00	0.43
20:CR:147:ARG:HD3	20:CR:152:GLU:HG3	2.01	0.43
22:CT:251:ASN:ND2	22:CT:288:LYS:HD3	2.33	0.43
22:CT:273:ARG:C	22:CT:274:LYS:HD3	2.44	0.43
22:CT:603:VAL:HG12	22:CT:607:SER:OG	2.19	0.43
26:CY:552:PHE:CE1	26:CY:578:VAL:HG11	2.54	0.43
38:LP:64:ALA:HB1	38:LP:80:ARG:HD2	2.00	0.43
44:LV:34:ARG:HB3	44:LV:66:LYS:HG3	2.01	0.43
47:LZ:69:PRO:HD3	47:LZ:114:LYS:HG3	1.98	0.43
52:Lg:112:ALA:O	52:Lg:115:LYS:HG3	2.18	0.43
1:C1:581:G:O2'	30:LE:35:GLN:O	2.32	0.43
1:C1:1661:U:H4'	1:C1:1663:U:O4	2.19	0.43
1:C1:3230:G:H2'	1:C1:3231:A:H8	1.82	0.43
3:CA:123:MET:C	3:CA:125:GLU:H	2.24	0.43
5:CC:421:LEU:HD23	5:CC:421:LEU:H	1.83	0.43
5:CC:450:ARG:NH2	6:CD:459:ASP:OD1	2.38	0.43
8:CF:27:PHE:HD2	8:CF:31:ARG:NH1	2.16	0.43
9:CG:42:LYS:HE3	9:CG:42:LYS:HB3	1.90	0.43
13:CK:239:TRP:NE1	18:CP:474:ASN:HD21	2.16	0.43
22:CT:166:LEU:HA	22:CT:169:VAL:HG12	2.00	0.43
26:CY:501:PHE:O	26:CY:505:VAL:HG23	2.19	0.43
26:CY:539:MET:HE1	26:CY:558:LEU:HD12	2.01	0.43
26:CY:617:GLY:O	26:CY:621:GLN:OE1	2.35	0.43
28:LB:144:SER:HA	28:LB:147:ARG:HE	1.83	0.43
29:LC:262:ILE:HD13	29:LC:262:ILE:HA	1.76	0.43
36:LN:5:LYS:NZ	54:Li:46:THR:HG23	2.34	0.43
36:LN:200:TRP:O	36:LN:203:ARG:NH1	2.52	0.43
37:LO:28:LEU:CD1	37:LO:104:LEU:HB2	2.43	0.43
37:LO:199:LEU:HD12	37:LO:199:LEU:HA	1.79	0.43
45:LX:121:VAL:N	45:LX:138:ARG:O	2.52	0.43
49:Ld:15:VAL:HA	49:Ld:85:ARG:O	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:159:G:H2'	1:C1:160:C:C6	2.54	0.43
1:C1:183:U:O2'	46:LY:59:ARG:NH2	2.50	0.43
1:C1:422:G:H2'	1:C1:423:U:C6	2.54	0.43
1:C1:527:U:H3	1:C1:546:A:H2	1.65	0.43
1:C1:1288:G:O2'	1:C1:1289:G:H5''	2.19	0.43
1:C1:1758:C:H2'	26:CY:4:ALA:HB2	2.01	0.43
1:C1:2783:C:O2'	1:C1:2784:U:O4'	2.34	0.43
2:C2:223:G:H2'	2:C2:224:C:C6	2.54	0.43
5:CC:209:ASP:HB2	5:CC:214:PRO:HD3	2.01	0.43
5:CC:445:GLN:HB3	5:CC:800:TRP:CZ3	2.53	0.43
6:CD:365:ARG:O	6:CD:387:HIS:HB2	2.18	0.43
8:CF:109:PRO:O	8:CF:110:ALA:C	2.60	0.43
9:CG:95:ARG:HH11	9:CG:95:ARG:HG3	1.83	0.43
11:CI:200:GLU:HG2	11:CI:201:HIS:N	2.34	0.43
12:CJ:28:LEU:HD11	12:CJ:78:LEU:HD11	2.01	0.43
12:CJ:362:ASP:HB3	12:CJ:363:PRO:HD3	1.99	0.43
12:CJ:379:PRO:HB2	12:CJ:382:PRO:HD2	2.00	0.43
12:CJ:390:PHE:CE2	12:CJ:465:ILE:HG13	2.54	0.43
16:CN:230:PRO:HG2	16:CN:232:ALA:HB3	2.00	0.43
18:CP:514:SER:O	18:CP:520:ASN:ND2	2.48	0.43
21:CS:546:LYS:HD3	21:CS:547:PRO:HD2	2.01	0.43
23:CU:200:LEU:HA	23:CU:203:ILE:HG22	2.00	0.43
39:LQ:92:LEU:HA	39:LQ:95:ILE:HG12	2.00	0.43
44:LV:37:TYR:N	44:LV:63:THR:O	2.49	0.43
45:LX:72:GLU:CD	45:LX:72:GLU:H	2.27	0.43
1:C1:582:A:H5'	30:LE:35:GLN:O	2.19	0.43
1:C1:917:A:O2'	1:C1:918:G:H2'	2.19	0.43
1:C1:1366:U:OP2	29:LC:206:ARG:HA	2.18	0.43
1:C1:2336:C:H2'	1:C1:2337:G:C2	2.54	0.43
2:C2:133:C:H2'	2:C2:134:G:C8	2.53	0.43
9:CG:114:ILE:HD13	9:CG:164:CYS:HB3	2.01	0.43
12:CJ:137:ALA:O	12:CJ:141:LEU:HG	2.18	0.43
12:CJ:218:ILE:HD13	12:CJ:224:PHE:HZ	1.82	0.43
14:CL:16:LYS:HB3	14:CL:21:ARG:HD3	2.01	0.43
14:CL:446:ASP:N	15:LF:45:GLU:OE2	2.52	0.43
19:CQ:175:ALA:HA	49:Ld:104:VAL:HA	1.99	0.43
26:CY:15:GLU:HG2	26:CY:19:LEU:HD22	2.00	0.43
43:LU:25:ALA:C	43:LU:28:PRO:HD2	2.43	0.43
52:Lg:47:ASP:HB2	52:Lg:85:CYS:SG	2.59	0.43
1:C1:123:A:H4'	5:CC:290:GLN:NE2	2.33	0.43
1:C1:513:A:O2'	41:LS:69:PRO:HD2	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:680:A:H5''	29:LC:43:MET:HE3	2.00	0.43
1:C1:1426:G:H2'	1:C1:1427:U:O4'	2.18	0.43
1:C1:2779:C:H2'	1:C1:2780:U:C5	2.53	0.43
1:C1:3064:U:H2'	1:C1:3065:G:H8	1.83	0.43
3:CA:89:VAL:HG23	3:CA:107:VAL:HG22	2.01	0.43
4:CB:147:PHE:CZ	4:CB:177:LYS:HD3	2.54	0.43
5:CC:171:THR:O	5:CC:171:THR:HG22	2.19	0.43
5:CC:206:ASN:HD22	25:CX:120:ILE:HG12	1.84	0.43
5:CC:213:VAL:HG21	21:CS:721:LYS:HE2	2.01	0.43
6:CD:147:LEU:HD22	6:CD:191:LEU:HD12	2.00	0.43
6:CD:415:VAL:CG2	6:CD:439:TYR:HB3	2.48	0.43
7:CE:174:SER:OG	7:CE:210:HIS:ND1	2.38	0.43
8:CF:238:GLU:O	8:CF:241:LYS:HB2	2.19	0.43
9:CG:52:ILE:HG12	18:CP:407:VAL:HG22	2.01	0.43
9:CG:106:GLN:HB3	9:CG:107:PRO:HD3	2.00	0.43
12:CJ:66:THR:O	12:CJ:70:GLN:HG2	2.19	0.43
13:CK:68:HIS:HA	13:CK:71:ARG:HG2	2.01	0.43
19:CQ:53:LYS:C	19:CQ:57:LYS:HZ2	2.26	0.43
26:CY:393:THR:O	26:CY:397:ARG:HG2	2.19	0.43
26:CY:714:GLU:HG3	26:CY:723:VAL:HG11	2.01	0.43
30:LE:166:ASP:O	30:LE:170:ILE:HD12	2.18	0.43
32:LH:10:ILE:HG12	32:LH:72:ARG:HG2	2.00	0.43
45:LX:70:LEU:HD21	45:LX:103:ALA:HB2	2.00	0.43
47:LZ:3:PHE:HB2	47:LZ:8:ARG:HH12	1.84	0.43
51:Lf:22:ARG:HG3	51:Lf:23:ARG:HD2	2.01	0.43
1:C1:206:A:N6	1:C1:221:U:O4'	2.52	0.43
1:C1:490:C:H2'	1:C1:491:A:H8	1.84	0.43
1:C1:662:C:H2'	1:C1:663:G:O4'	2.19	0.43
1:C1:2963:A:C2	1:C1:3098:A:C4	3.07	0.43
1:C1:3040:G:H2'	1:C1:3041:C:C6	2.53	0.43
1:C1:3117:C:O2'	1:C1:3118:A:H8	2.01	0.43
1:C1:3164:G:O6	1:C1:3206:G:N1	2.51	0.43
1:C1:3298:U:H2'	1:C1:3299:A:C8	2.54	0.43
2:C2:31:G:H2'	2:C2:32:C:O4'	2.19	0.43
2:C2:297:C:H2'	2:C2:298:G:C8	2.54	0.43
3:CA:69:ASP:O	3:CA:72:SER:OG	2.27	0.43
5:CC:694:TYR:CZ	47:LZ:103:PRO:HG2	2.54	0.43
7:CE:347:LEU:HA	7:CE:347:LEU:HD23	1.74	0.43
7:CE:476:ALA:O	7:CE:477:LYS:HG3	2.19	0.43
19:CQ:52:THR:O	19:CQ:56:ARG:HG2	2.19	0.43
22:CT:412:LEU:HG	22:CT:423:VAL:HG11	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CV:113:ALA:HB1	30:LE:30:ALA:HA	2.01	0.43
26:CY:548:PHE:CD1	26:CY:578:VAL:HG13	2.54	0.43
32:LH:72:ARG:HD2	32:LH:72:ARG:C	2.44	0.43
35:LM:112:LEU:HD12	35:LM:112:LEU:HA	1.73	0.43
37:LO:77:ALA:HB1	37:LO:108:GLU:OE1	2.19	0.43
44:LV:30:ASN:OD1	44:LV:114:SER:N	2.45	0.43
1:C1:683:C:H1'	20:CR:64:GLY:HA3	2.01	0.42
1:C1:1050:C:H3'	1:C1:1051:C:H6	1.83	0.42
1:C1:2883:C:H2'	1:C1:2884:A:H8	1.84	0.42
2:C2:139:U:H2'	2:C2:140:G:H8	1.84	0.42
6:CD:43:ARG:HE	12:CJ:592:GLU:CD	2.27	0.42
10:CH:122:TYR:O	10:CH:126:GLN:HG2	2.19	0.42
15:CM:190:LEU:O	15:CM:194:ILE:HG12	2.19	0.42
21:CS:565:ARG:HD2	22:CT:136:THR:OG1	2.19	0.42
22:CT:519:SER:O	22:CT:523:LEU:HG	2.19	0.42
26:CY:453:TRP:HA	26:CY:456:ASP:OD2	2.18	0.42
26:CY:536:LEU:HA	26:CY:539:MET:HG2	2.00	0.42
26:CY:583:GLU:CG	26:CY:610:ARG:HH21	2.23	0.42
26:CY:646:THR:O	26:CY:650:LEU:HG	2.19	0.42
26:CY:653:TRP:O	26:CY:653:TRP:HD1	2.02	0.42
27:Cz:45:LEU:HD23	27:Cz:45:LEU:HA	1.80	0.42
15:LF:76:LYS:HB2	15:LF:76:LYS:HE3	1.67	0.42
39:LQ:137:ALA:O	39:LQ:141:ILE:HG12	2.19	0.42
44:LV:25:MET:SD	44:LV:80:ILE:HG22	2.59	0.42
58:Lq:46:ASP:OD1	58:Lq:46:ASP:N	2.50	0.42
1:C1:332:C:H2'	1:C1:333:G:O4'	2.19	0.42
1:C1:796:G:H1	1:C1:906:A:N6	2.17	0.42
2:C2:65:A:OP1	53:Lh:58:ARG:NH1	2.48	0.42
4:CB:42:ARG:HH22	4:CB:48:ASN:HB2	1.84	0.42
5:CC:326:LEU:HD22	12:CJ:240:PHE:HD2	1.84	0.42
6:CD:80:LEU:HA	6:CD:83:ASN:OD1	2.19	0.42
9:CG:65:LEU:HD12	18:CP:435:VAL:HG12	2.01	0.42
10:CH:23:ARG:NH1	10:CH:27:ARG:HH21	2.17	0.42
11:CI:286:ASN:OD1	11:CI:287:LYS:N	2.52	0.42
12:CJ:635:LYS:HA	12:CJ:638:LEU:HD23	2.02	0.42
16:CN:18:THR:OG1	16:CN:60:GLY:HA2	2.19	0.42
16:CN:241:ILE:HG23	16:CN:245:PHE:HD2	1.84	0.42
18:CP:337:TRP:CE3	18:CP:338:SER:HB3	2.54	0.42
18:CP:516:CYS:O	18:CP:520:ASN:HB2	2.20	0.42
22:CT:161:LEU:HG	22:CT:165:LYS:NZ	2.34	0.42
22:CT:479:SER:O	22:CT:483:LEU:HD23	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:CY:405:ARG:O	26:CY:409:VAL:HG22	2.19	0.42
28:LB:57:VAL:HG22	28:LB:359:TRP:CD1	2.53	0.42
28:LB:330:PRO:O	28:LB:337:MET:HE1	2.19	0.42
32:LH:22:SER:OG	32:LH:23:ARG:N	2.50	0.42
32:LH:119:PHE:HE2	32:LH:180:GLY:HA2	1.84	0.42
34:LL:122:ARG:HE	34:LL:122:ARG:HB2	1.71	0.42
46:LY:79:ILE:HD11	46:LY:103:VAL:HG11	2.01	0.42
47:LZ:92:LYS:HD2	47:LZ:93:ALA:N	2.34	0.42
52:Lg:59:ARG:HD2	52:Lg:59:ARG:HA	1.73	0.42
58:Lq:98:LYS:O	58:Lq:101:LYS:HG2	2.18	0.42
1:C1:159:G:H2'	1:C1:160:C:H6	1.85	0.42
1:C1:202:A:H4'	1:C1:204:A:N7	2.33	0.42
1:C1:1162:G:C4	1:C1:1164:G:C8	3.08	0.42
1:C1:1375:A:H62	1:C1:1399:G:H1'	1.83	0.42
1:C1:1776:A:H2'	1:C1:1777:A:C8	2.54	0.42
4:CB:167:LEU:HD12	4:CB:171:PHE:CE1	2.53	0.42
5:CC:119:GLU:HB2	5:CC:122:VAL:HG22	2.01	0.42
5:CC:448:ILE:HG12	5:CC:450:ARG:HH21	1.84	0.42
8:CF:63:CYS:SG	8:CF:105:THR:HG22	2.59	0.42
8:CF:174:MET:SD	8:CF:179:VAL:HG22	2.59	0.42
10:CH:155:HIS:O	10:CH:159:LEU:HG	2.19	0.42
12:CJ:462:TRP:O	12:CJ:465:ILE:HG22	2.19	0.42
15:CM:109:LEU:HD12	15:CM:114:LEU:O	2.20	0.42
21:CS:574:VAL:O	21:CS:578:ILE:HD12	2.19	0.42
22:CT:306:LEU:O	22:CT:310:MET:HG3	2.19	0.42
22:CT:424:LEU:HB3	22:CT:488:THR:CG2	2.40	0.42
28:LB:17:LEU:HD22	28:LB:263:TRP:HE3	1.82	0.42
28:LB:210:PHE:HE1	28:LB:341:LYS:HG2	1.83	0.42
28:LB:282:LYS:HB3	28:LB:284:TYR:CE1	2.54	0.42
47:LZ:103:PRO:O	47:LZ:106:ARG:HG2	2.19	0.42
58:Lq:5:THR:O	58:Lq:9:VAL:HG23	2.18	0.42
1:C1:129:C:H2'	1:C1:130:U:O4'	2.19	0.42
1:C1:447:C:H42	30:LE:15:ARG:HH21	1.67	0.42
1:C1:1202:U:H2'	27:Cz:48:TRP:NE1	2.34	0.42
1:C1:1615:C:H5''	47:LZ:72:LYS:NZ	2.34	0.42
1:C1:2882:U:H2'	1:C1:2883:C:C6	2.54	0.42
1:C1:3136:A:H2'	1:C1:3137:A:H8	1.84	0.42
2:C2:227:G:H2'	2:C2:228:C:C6	2.55	0.42
4:CB:21:ASP:N	4:CB:21:ASP:OD1	2.51	0.42
5:CC:680:PHE:HA	5:CC:690:VAL:O	2.20	0.42
6:CD:383:THR:O	6:CD:434:VAL:HA	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CG:31:GLU:HG3	22:CT:642:LYS:HD2	2.00	0.42
12:CJ:611:LYS:O	12:CJ:614:LEU:N	2.53	0.42
22:CT:669:CYS:SG	22:CT:671:LYS:HB2	2.59	0.42
23:CU:309:LYS:HE2	23:CU:309:LYS:HB2	1.69	0.42
27:Cz:45:LEU:HD21	41:LS:142:GLN:HA	2.00	0.42
28:LB:26:ARG:NH1	28:LB:179:LEU:O	2.53	0.42
29:LC:59:HIS:HA	29:LC:91:PHE:HE1	1.84	0.42
36:LN:9:GLU:HG3	54:Li:49:VAL:HG12	2.01	0.42
39:LQ:152:ASP:OD1	39:LQ:153:GLN:N	2.52	0.42
1:C1:579:A:H1'	1:C1:1319:G:H5''	2.01	0.42
1:C1:889:G:H1	1:C1:900:U:H3	1.66	0.42
1:C1:1242:A:O3'	8:CF:18:LYS:NZ	2.52	0.42
1:C1:1293:G:H1'	1:C1:2343:G:OP1	2.20	0.42
1:C1:1690:U:H2'	1:C1:1691:G:O4'	2.18	0.42
1:C1:2400:A:H2'	1:C1:2401:A:H8	1.85	0.42
1:C1:2807:C:H2'	1:C1:2808:G:O4'	2.19	0.42
6:CD:34:GLN:C	6:CD:35:LEU:HD12	2.45	0.42
7:CE:124:LYS:HE3	7:CE:209:TYR:CE1	2.55	0.42
8:CF:168:LEU:O	8:CF:204:ARG:HD2	2.19	0.42
9:CG:6:ASP:OD1	9:CG:7:GLN:N	2.52	0.42
10:CH:485:GLU:HG2	10:CH:486:GLU:N	2.34	0.42
15:CM:197:VAL:HG23	15:CM:201:PHE:CD2	2.54	0.42
18:CP:317:ARG:NH2	18:CP:338:SER:O	2.40	0.42
19:CQ:16:SER:HB3	28:LB:73:VAL:HG11	2.01	0.42
20:CR:195:LEU:HD22	20:CR:229:LEU:HD23	2.00	0.42
22:CT:179:ILE:CG2	22:CT:253:VAL:HG21	2.46	0.42
22:CT:520:LEU:HD23	22:CT:520:LEU:HA	1.85	0.42
23:CU:288:LYS:O	23:CU:292:GLU:OE1	2.38	0.42
23:CU:326:GLN:HA	23:CU:329:GLU:CD	2.45	0.42
24:CV:13:SER:HB2	24:CV:17:ASN:OD1	2.20	0.42
15:LF:94:ARG:HH22	15:LF:98:ILE:HB	1.85	0.42
15:LF:95:ILE:C	15:LF:117:ILE:HG23	2.44	0.42
44:LV:21:VAL:HG23	44:LV:52:PRO:O	2.18	0.42
52:Lg:10:ARG:HG3	52:Lg:35:HIS:CD2	2.54	0.42
1:C1:174:C:N3	1:C1:230:A:N1	2.67	0.42
1:C1:977:A:C2	1:C1:978:A:H1'	2.55	0.42
1:C1:1258:U:OP1	8:CF:207:ARG:NH1	2.52	0.42
1:C1:1548:C:C4	5:CC:408:MET:HE1	2.55	0.42
1:C1:2468:U:H2'	1:C1:2469:U:C6	2.54	0.42
1:C1:3105:C:H2'	1:C1:3106:G:H8	1.84	0.42
5:CC:453:GLU:HB2	5:CC:474:ASP:HB3	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CE:485:PHE:HA	7:CE:486:PRO:HD3	1.86	0.42
10:CH:45:TYR:HD1	10:CH:128:LYS:HB2	1.83	0.42
10:CH:508:MET:HE1	49:Ld:62:GLN:O	2.20	0.42
12:CJ:460:TRP:HA	12:CJ:476:TYR:CD2	2.54	0.42
13:CK:181:LYS:HG2	13:CK:194:GLN:HG2	2.01	0.42
15:CM:44:LYS:HA	15:CM:44:LYS:HD2	1.68	0.42
16:CN:56:THR:HG22	16:CN:58:ILE:HG12	2.01	0.42
19:CQ:47:ARG:HE	19:CQ:58:ASN:ND2	2.11	0.42
19:CQ:148:LEU:O	19:CQ:152:ARG:HG3	2.18	0.42
22:CT:402:LYS:HB2	22:CT:402:LYS:HE2	1.88	0.42
26:CY:731:GLU:O	26:CY:735:LEU:HG	2.19	0.42
28:LB:299:THR:HG21	28:LB:358:LYS:HD3	2.01	0.42
30:LE:47:THR:HG23	30:LE:47:THR:O	2.19	0.42
33:LK:136:ALA:HA	33:LK:139:VAL:HG22	2.01	0.42
50:Le:20:ARG:NH1	50:Le:29:LEU:HD22	2.34	0.42
1:C1:362:U:H4'	1:C1:396:G:H5'	2.01	0.42
1:C1:1149:U:P	51:Lf:75:ARG:HH22	2.43	0.42
1:C1:1316:C:C2	1:C1:1317:C:C5	3.08	0.42
1:C1:2936:U:H1'	21:CS:793:LYS:NZ	2.34	0.42
4:CB:33:HIS:HB2	11:CI:323:MET:HE3	2.02	0.42
5:CC:734:ALA:HB3	5:CC:779:ILE:HD12	2.01	0.42
6:CD:455:PRO:HG2	6:CD:461:CYS:SG	2.60	0.42
10:CH:442:ASP:HB2	10:CH:444:LYS:HZ3	1.84	0.42
12:CJ:65:TYR:O	12:CJ:69:ILE:HG12	2.20	0.42
22:CT:145:TYR:N	22:CT:146:PRO:HD3	2.35	0.42
26:CY:387:TRP:NE1	26:CY:404:ILE:HG13	2.34	0.42
29:LC:350:LYS:HD2	29:LC:350:LYS:HA	1.86	0.42
15:LF:137:GLU:OE1	15:LF:235:GLY:HA2	2.20	0.42
34:LL:85:ILE:HG12	34:LL:120:LYS:HD3	2.02	0.42
40:LR:139:VAL:HG12	40:LR:143:HIS:HE1	1.85	0.42
44:LV:41:VAL:HA	44:LV:60:VAL:HA	2.02	0.42
47:LZ:76:TYR:C	47:LZ:78:HIS:H	2.25	0.42
1:C1:105:C:OP1	20:CR:60:LYS:HE3	2.20	0.42
1:C1:421:U:C2	1:C1:422:G:C8	3.08	0.42
1:C1:579:A:H8	1:C1:580:G:C8	2.37	0.42
1:C1:625:C:C2	1:C1:626:G:C8	3.08	0.42
1:C1:909:C:H2'	1:C1:910:A:H8	1.83	0.42
1:C1:1793:A:N3	12:CJ:648:GLN:HA	2.35	0.42
1:C1:2957:G:H2'	1:C1:2958:U:H6	1.84	0.42
3:CA:229:ILE:HG12	23:CU:255:ARG:HH11	1.85	0.42
5:CC:327:TRP:HB3	5:CC:330:GLU:HB2	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:42:ARG:HD3	6:CD:43:ARG:H	1.84	0.42
6:CD:443:ARG:NH2	6:CD:479:ASP:OD2	2.43	0.42
7:CE:129:MET:HE2	7:CE:206:LEU:HA	2.02	0.42
8:CF:123:ASP:OD2	8:CF:219:PHE:HB2	2.19	0.42
10:CH:375:ASP:OD1	10:CH:376:GLY:N	2.52	0.42
20:CR:199:VAL:HG21	20:CR:234:LEU:CD1	2.49	0.42
23:CU:267:ARG:HE	25:CX:79:PRO:HG3	1.84	0.42
24:CV:42:LYS:NZ	24:CV:106:ASP:HB2	2.33	0.42
26:CY:379:LEU:O	26:CY:383:VAL:HG23	2.20	0.42
26:CY:693:LYS:H	26:CY:693:LYS:HG3	1.49	0.42
28:LB:46:ALA:HA	28:LB:84:MET:HE1	2.01	0.42
29:LC:299:VAL:HG21	39:LQ:159:PRO:HG2	2.02	0.42
34:LL:56:PRO:HG3	34:LL:74:GLY:O	2.20	0.42
47:LZ:57:SER:O	47:LZ:61:ILE:HG12	2.20	0.42
58:Lq:39:LYS:HD2	58:Lq:40:ASN:N	2.35	0.42
1:C1:35:A:H2'	1:C1:36:C:H6	1.85	0.42
1:C1:194:G:H2'	1:C1:195:G:H8	1.83	0.42
1:C1:422:G:H2'	1:C1:423:U:H6	1.85	0.42
1:C1:787:A:H2'	1:C1:788:A:C2	2.55	0.42
1:C1:1655:C:H2'	1:C1:1656:A:C8	2.54	0.42
1:C1:2340:C:C2	1:C1:2341:U:C5	3.08	0.42
1:C1:2919:G:H2'	1:C1:2920:U:H6	1.84	0.42
3:CA:97:GLY:O	3:CA:98:LYS:HE2	2.19	0.42
9:CG:41:GLN:HE22	9:CG:61:ARG:HG2	1.85	0.42
10:CH:171:VAL:HG13	10:CH:219:ASP:HA	2.02	0.42
10:CH:179:LYS:HB2	10:CH:179:LYS:HE2	1.80	0.42
10:CH:379:ARG:HD3	16:CN:113:HIS:CB	2.50	0.42
16:CN:123:ARG:O	16:CN:127:GLU:OE1	2.37	0.42
18:CP:283:LYS:NZ	18:CP:518:GLU:OE2	2.31	0.42
18:CP:491:LEU:O	18:CP:495:ILE:HG12	2.20	0.42
18:CP:538:GLU:HG3	18:CP:562:LEU:HD22	2.01	0.42
21:CS:789:VAL:HG23	21:CS:811:ARG:HG3	2.02	0.42
24:CV:100:LYS:HE3	24:CV:100:LYS:HB3	1.84	0.42
30:LE:178:MET:HE3	35:LM:119:LYS:HG2	2.02	0.42
30:LE:195:PRO:HA	30:LE:198:MET:HG2	2.01	0.42
34:LL:110:ALA:HA	34:LL:113:VAL:HG22	2.01	0.42
35:LM:20:LEU:HD23	35:LM:30:ILE:HD11	2.01	0.42
37:LO:86:VAL:HG11	37:LO:104:LEU:HD22	2.02	0.42
37:LO:117:LYS:HB3	37:LO:117:LYS:HE3	1.86	0.42
42:LT:83:ARG:HA	42:LT:83:ARG:HD3	1.73	0.42
47:LZ:8:ARG:HD3	47:LZ:9:VAL:N	2.35	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:LZ:49:PRO:HD3	47:LZ:67:ILE:HG12	2.01	0.42
47:LZ:135:PHE:O	52:Lg:77:TYR:OH	2.34	0.42
51:Lf:92:PRO:C	51:Lf:94:ARG:H	2.28	0.42
58:Lq:120:ILE:N	58:Lq:121:PRO:HD3	2.34	0.42
1:C1:39:A:H2'	1:C1:40:A:C8	2.54	0.42
1:C1:222:A:H2'	1:C1:223:U:C6	2.54	0.42
1:C1:285:C:H2'	1:C1:286:A:O4'	2.20	0.42
1:C1:2470:U:H2'	1:C1:2471:U:H6	1.84	0.42
1:C1:3158:U:H5''	51:Lf:4:GLU:HG2	2.01	0.42
2:C2:149:A:H2'	2:C2:150:G:C8	2.55	0.42
3:CA:154:VAL:HA	23:CU:200:LEU:HD13	2.02	0.42
6:CD:372:PRO:HD2	6:CD:373:ARG:NH1	2.35	0.42
7:CE:172:MET:SD	7:CE:173:LEU:N	2.93	0.42
7:CE:528:ARG:O	7:CE:532:ASP:HB3	2.19	0.42
10:CH:21:LEU:HA	10:CH:24:THR:HG22	2.01	0.42
10:CH:96:GLN:HA	10:CH:99:THR:HG22	2.02	0.42
10:CH:298:ASP:O	10:CH:302:GLN:HG2	2.20	0.42
12:CJ:476:TYR:CE1	12:CJ:483:PRO:HG2	2.49	0.42
18:CP:386:ASP:CG	18:CP:389:ALA:HB2	2.44	0.42
21:CS:499:VAL:HB	21:CS:503:GLU:OE2	2.20	0.42
22:CT:256:PHE:CG	22:CT:257:ASN:N	2.87	0.42
15:LF:116:GLN:H	15:LF:119:ASN:ND2	2.05	0.42
33:LK:133:LEU:HD21	33:LK:152:SER:HB2	2.01	0.42
37:LO:1:MET:N	41:LS:163:LYS:HD2	2.35	0.42
45:LX:116:TYR:HE1	53:Lh:36:ILE:HG13	1.84	0.42
1:C1:139:C:H2'	1:C1:140:G:O4'	2.20	0.41
1:C1:224:A:H2'	1:C1:225:G:O4'	2.20	0.41
1:C1:378:A:H8	1:C1:378:A:O5'	2.02	0.41
1:C1:459:U:O2'	1:C1:460:C:H5''	2.20	0.41
1:C1:482:C:H2'	1:C1:483:A:C8	2.55	0.41
1:C1:497:U:H2'	1:C1:498:C:H6	1.84	0.41
1:C1:627:U:H2'	1:C1:628:C:C6	2.55	0.41
1:C1:886:U:O2'	1:C1:887:G:OP1	2.30	0.41
1:C1:1199:A:C6	1:C1:1271:G:C6	3.08	0.41
1:C1:1795:A:OP2	5:CC:418:LYS:NZ	2.53	0.41
1:C1:2408:U:H2'	1:C1:2409:A:H8	1.85	0.41
1:C1:2444:U:H2'	1:C1:2445:G:O4'	2.20	0.41
1:C1:2797:G:C5	1:C1:2808:G:N2	2.88	0.41
1:C1:2875:G:C6	1:C1:2888:A:C6	3.08	0.41
1:C1:2923:U:H4'	1:C1:2925:A:C6	2.55	0.41
1:C1:3084:A:H2'	1:C1:3085:G:O4'	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3334:U:H2'	1:C1:3335:U:H6	1.85	0.41
2:C2:110:C:H41	55:Lj:19:CYS:HA	1.85	0.41
5:CC:240:ARG:HE	31:LG:261:LYS:HE2	1.84	0.41
5:CC:486:ARG:HH22	6:CD:151:TYR:HB2	1.84	0.41
5:CC:647:LEU:HD23	5:CC:658:CYS:SG	2.59	0.41
6:CD:189:ASP:OD1	6:CD:189:ASP:N	2.53	0.41
7:CE:141:ALA:O	7:CE:144:PRO:HD2	2.20	0.41
10:CH:228:LEU:HA	10:CH:231:MET:HG3	2.01	0.41
11:CI:247:THR:HG21	45:LX:24:ALA:CB	2.50	0.41
12:CJ:613:LYS:O	12:CJ:617:LYS:HG2	2.20	0.41
14:CL:33:ARG:O	14:CL:36:ARG:HG2	2.20	0.41
18:CP:507:TYR:CE1	18:CP:582:LYS:HD3	2.55	0.41
21:CS:802:LYS:HD3	29:LC:66:TRP:CE2	2.55	0.41
23:CU:358:PHE:O	23:CU:362:VAL:HG23	2.19	0.41
26:CY:29:VAL:HG22	26:CY:33:LYS:HG2	2.02	0.41
29:LC:100:MET:HE1	29:LC:104:THR:HG23	2.01	0.41
32:LH:86:PHE:CE2	32:LH:153:LEU:HB2	2.55	0.41
38:LP:59:PRO:HD3	38:LP:76:TRP:CE2	2.55	0.41
38:LP:60:MET:O	38:LP:80:ARG:NE	2.53	0.41
41:LS:92:LYS:HE2	41:LS:110:MET:HE3	2.01	0.41
41:LS:95:ARG:HH11	41:LS:95:ARG:HG3	1.85	0.41
47:LZ:102:GLU:HB2	47:LZ:105:GLN:HB2	2.02	0.41
52:Lg:77:TYR:HB3	52:Lg:81:ARG:HB2	2.01	0.41
1:C1:1305:C:H5'	41:LS:1:MET:HB2	2.01	0.41
1:C1:1430:U:H2'	1:C1:1431:A:H8	1.85	0.41
1:C1:1458:G:OP1	10:CH:512:LEU:N	2.40	0.41
1:C1:1659:G:H2'	1:C1:1660:U:H6	1.84	0.41
1:C1:1750:G:H2'	1:C1:1751:U:O4'	2.20	0.41
1:C1:3156:C:H2'	1:C1:3157:C:O4'	2.20	0.41
4:CB:215:ARG:NH1	4:CB:220:ILE:HD13	2.36	0.41
5:CC:298:ILE:HG22	31:LG:120:LYS:HE3	2.02	0.41
5:CC:503:ARG:O	5:CC:513:LEU:HD12	2.20	0.41
5:CC:576:LEU:HB3	5:CC:581:VAL:HB	2.02	0.41
6:CD:371:ASP:OD1	6:CD:373:ARG:NH1	2.53	0.41
7:CE:486:PRO:C	7:CE:488:ASN:N	2.76	0.41
10:CH:321:CYS:N	59:CH:1001:GTP:O6	2.53	0.41
12:CJ:246:TYR:HA	12:CJ:249:ILE:HG22	2.01	0.41
12:CJ:502:PRO:HG2	12:CJ:505:GLU:OE1	2.19	0.41
12:CJ:607:ASP:O	12:CJ:611:LYS:HD3	2.21	0.41
16:CN:202:TRP:C	16:CN:224:LEU:HD11	2.44	0.41
16:CN:242:VAL:O	16:CN:246:TYR:HB2	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CP:329:VAL:HG12	18:CP:347:SER:HB2	2.01	0.41
21:CS:661:THR:O	21:CS:665:GLN:HG2	2.20	0.41
22:CT:245:CYS:O	22:CT:249:LEU:HD23	2.20	0.41
23:CU:341:ARG:NH2	23:CU:353:GLU:OE1	2.47	0.41
25:CX:88:LYS:HD3	25:CX:88:LYS:HA	1.79	0.41
26:CY:469:ARG:O	26:CY:472:ALA:N	2.54	0.41
26:CY:469:ARG:HE	26:CY:473:ILE:HD11	1.86	0.41
26:CY:583:GLU:HG2	26:CY:615:GLN:OE1	2.20	0.41
26:CY:589:LYS:HB2	26:CY:610:ARG:HB2	2.03	0.41
15:LF:83:ILE:HG13	15:LF:83:ILE:O	2.20	0.41
42:LT:113:ALA:HA	42:LT:116:LYS:HZ2	1.84	0.41
44:LV:99:ASP:OD1	44:LV:99:ASP:N	2.52	0.41
47:LZ:60:ARG:O	47:LZ:64:ARG:HG3	2.20	0.41
58:Lq:17:LEU:O	58:Lq:21:ASN:ND2	2.29	0.41
1:C1:59:G:H4'	1:C1:60:A:H4'	2.02	0.41
1:C1:772:U:C2	1:C1:773:A:C8	3.08	0.41
1:C1:832:C:H2'	1:C1:833:U:C6	2.55	0.41
1:C1:968:U:H2'	1:C1:969:U:H6	1.85	0.41
1:C1:1232:G:H2'	1:C1:1233:A:C8	2.55	0.41
1:C1:1598:A:C2	1:C1:1805:C:C2	3.09	0.41
1:C1:2314:A:OP1	38:LP:82:ARG:HG2	2.20	0.41
1:C1:2994:C:H5''	28:LB:349:ARG:HD3	2.01	0.41
1:C1:3263:A:H5'	49:Ld:50:LYS:NZ	2.36	0.41
6:CD:116:ALA:HB3	6:CD:149:ALA:HB3	2.01	0.41
11:CI:192:ALA:HB3	11:CI:259:THR:OG1	2.20	0.41
11:CI:315:ALA:HA	11:CI:318:GLU:HG2	2.01	0.41
12:CJ:637:MET:HE2	12:CJ:637:MET:HB2	1.82	0.41
15:CM:105:PRO:O	15:CM:109:LEU:HD23	2.20	0.41
16:CN:124:GLU:O	16:CN:128:ILE:HG12	2.20	0.41
18:CP:539:THR:HG23	18:CP:541:LEU:H	1.85	0.41
19:CQ:145:LEU:HD21	19:CQ:163:GLU:HG2	2.03	0.41
22:CT:287:GLU:HG2	22:CT:327:HIS:ND1	2.35	0.41
15:LF:179:LEU:HD11	15:LF:207:PHE:CG	2.54	0.41
36:LN:39:ALA:HB3	36:LN:61:ILE:HB	2.02	0.41
36:LN:180:PHE:O	36:LN:184:ARG:HG2	2.20	0.41
37:LO:3:SER:OG	37:LO:5:GLU:OE2	2.29	0.41
47:LZ:114:LYS:HE3	47:LZ:118:GLU:OE2	2.21	0.41
48:Lc:28:LEU:HD12	48:Lc:90:CYS:HB3	2.02	0.41
48:Lc:37:LEU:HD21	48:Lc:45:ILE:HG13	2.02	0.41
52:Lg:99:GLN:HA	52:Lg:102:VAL:HG12	2.03	0.41
1:C1:1787:G:H1'	1:C1:1788:A:C8	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2399:G:H2'	1:C1:2400:A:C8	2.55	0.41
1:C1:3088:U:OP1	17:CO:6:ARG:NH2	2.53	0.41
2:C2:42:G:H1	2:C2:102:U:H3	1.68	0.41
2:C2:97:A:OP1	53:Lh:72:ARG:NH2	2.53	0.41
2:C2:210:C:OP1	7:CE:488:ASN:ND2	2.53	0.41
4:CB:22:GLN:OE1	11:CI:325:TYR:OH	2.38	0.41
4:CB:69:LYS:HB2	4:CB:69:LYS:HE3	1.75	0.41
4:CB:180:ILE:HA	4:CB:181:PRO:HD3	1.95	0.41
5:CC:627:ILE:HG13	5:CC:630:ARG:HH12	1.86	0.41
6:CD:42:ARG:HH12	6:CD:74:SER:C	2.28	0.41
6:CD:154:LEU:HB2	6:CD:156:ARG:HH21	1.85	0.41
6:CD:388:ALA:H	6:CD:414:ARG:HH22	1.68	0.41
7:CE:201:GLY:O	7:CE:204:ARG:HG2	2.20	0.41
7:CE:355:MET:HG3	7:CE:358:LYS:HZ2	1.84	0.41
7:CE:371:LYS:HB2	7:CE:371:LYS:HE3	1.80	0.41
7:CE:388:HIS:HE1	7:CE:390:LYS:HB2	1.85	0.41
9:CG:20:MET:O	9:CG:95:ARG:NH2	2.53	0.41
11:CI:310:GLU:HA	11:CI:313:ARG:CZ	2.50	0.41
15:CM:94:ARG:O	15:CM:118:ASN:N	2.52	0.41
18:CP:534:VAL:CG2	18:CP:581:PHE:HB3	2.49	0.41
19:CQ:21:PHE:HE2	19:CQ:23:ARG:HG2	1.85	0.41
21:CS:478:HIS:ND1	21:CS:478:HIS:C	2.78	0.41
22:CT:281:LYS:HA	22:CT:284:GLU:OE1	2.20	0.41
24:CV:3:ASN:ND2	29:LC:29:ALA:O	2.52	0.41
26:CY:405:ARG:NH1	26:CY:409:VAL:HG21	2.36	0.41
26:CY:486:ALA:O	26:CY:489:ASN:OD1	2.38	0.41
31:LG:164:GLU:H	31:LG:164:GLU:HG3	1.38	0.41
33:LK:63:THR:HB	33:LK:70:GLN:HE21	1.86	0.41
37:LO:62:MET:HE2	37:LO:67:PRO:HB3	2.01	0.41
43:LU:27:GLN:HB3	43:LU:28:PRO:HD3	2.01	0.41
1:C1:837:G:OP2	40:LR:92:GLN:NE2	2.54	0.41
1:C1:862:C:H4'	1:C1:863:A:O5'	2.20	0.41
1:C1:1323:U:H2'	1:C1:1324:C:C6	2.56	0.41
1:C1:1479:C:H2'	1:C1:1480:A:C8	2.55	0.41
1:C1:2389:U:H2'	1:C1:2390:U:C6	2.56	0.41
1:C1:2553:A:H3'	1:C1:2554:U:H6	1.85	0.41
1:C1:3110:C:H5''	1:C1:3111:U:C5	2.55	0.41
1:C1:3183:C:H5'	1:C1:3184:G:OP2	2.20	0.41
2:C2:209:C:H5''	7:CE:488:ASN:OD1	2.21	0.41
3:CA:244:ILE:HD11	3:CA:254:ILE:HD12	2.02	0.41
5:CC:446:GLN:HG3	5:CC:801:MET:HB2	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:637:GLN:OE1	5:CC:637:GLN:HA	2.20	0.41
8:CF:124:PHE:HE2	8:CF:213:SER:HA	1.85	0.41
10:CH:383:ILE:HD11	16:CN:201:ASP:HB3	2.03	0.41
12:CJ:615:GLU:HG3	12:CJ:618:LYS:HZ3	1.86	0.41
16:CN:25:LEU:HD12	16:CN:51:THR:CG2	2.50	0.41
16:CN:100:ARG:NH1	16:CN:122:GLU:OE2	2.53	0.41
18:CP:243:ILE:HG21	18:CP:291:ARG:HE	1.85	0.41
18:CP:412:ASP:HA	18:CP:413:PRO:HD3	1.90	0.41
19:CQ:105:ARG:HH11	28:LB:383:THR:HG21	1.85	0.41
21:CS:546:LYS:HB2	21:CS:546:LYS:HE2	1.80	0.41
26:CY:461:TYR:CD1	26:CY:524:LEU:HA	2.56	0.41
28:LB:88:GLY:HA3	28:LB:162:LEU:HD12	2.02	0.41
42:LT:45:ASN:H	42:LT:95:HIS:CD2	2.39	0.41
47:LZ:55:ARG:HG2	47:LZ:55:ARG:O	2.21	0.41
50:Le:20:ARG:HE	50:Le:34:ARG:HB2	1.85	0.41
52:Lg:21:THR:HB	52:Lg:33:VAL:HG13	2.02	0.41
58:Lq:29:LEU:HD23	58:Lq:62:ASN:HB2	2.02	0.41
1:C1:21:G:OP2	2:C2:36:G:N2	2.52	0.41
1:C1:969:U:H2'	1:C1:970:A:H8	1.85	0.41
1:C1:976:U:N3	1:C1:1036:A:C8	2.86	0.41
1:C1:1207:A:H2'	1:C1:1208:G:O4'	2.21	0.41
1:C1:1311:C:OP1	51:Lf:84:ARG:NH2	2.54	0.41
1:C1:1514:C:H2'	1:C1:1515:U:C6	2.55	0.41
1:C1:2566:G:H2'	1:C1:2567:A:C8	2.53	0.41
2:C2:91:C:H2'	2:C2:92:A:C8	2.56	0.41
2:C2:160:A:H8	2:C2:160:A:OP2	2.03	0.41
2:C2:166:C:H2'	2:C2:167:A:C8	2.53	0.41
3:CA:257:GLU:HG2	3:CA:259:LYS:HG2	2.01	0.41
5:CC:463:PRO:O	5:CC:508:LYS:NZ	2.54	0.41
5:CC:682:VAL:HG12	5:CC:689:LEU:CD2	2.51	0.41
6:CD:42:ARG:HG3	6:CD:44:TYR:H	1.86	0.41
6:CD:120:LEU:HB2	6:CD:185:PHE:CE2	2.56	0.41
6:CD:159:ASN:HB3	6:CD:165:ILE:HD11	2.03	0.41
6:CD:232:ASP:OD1	6:CD:241:LEU:HB2	2.21	0.41
13:CK:44:GLY:C	13:CK:46:ARG:N	2.77	0.41
15:CM:108:ILE:CG2	15:CM:132:MET:HG3	2.51	0.41
19:CQ:42:MET:HE3	19:CQ:44:ARG:NH1	2.34	0.41
29:LC:30:PRO:HD2	29:LC:278:PRO:HG2	2.03	0.41
29:LC:211:ILE:HD13	29:LC:226:PHE:CE2	2.55	0.41
29:LC:335:THR:HG21	15:LF:51:PHE:HZ	1.86	0.41
36:LN:185:ALA:O	36:LN:189:LYS:HE2	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:LQ:106:LYS:HE3	39:LQ:106:LYS:HB3	1.74	0.41
48:Lc:50:ASN:HD21	48:Lc:77:ASN:CG	2.29	0.41
49:Ld:28:LEU:HD11	49:Ld:40:ALA:HB2	2.02	0.41
1:C1:258:C:N4	54:Li:39:LYS:HA	2.35	0.41
1:C1:618:A:H2'	1:C1:619:G:C8	2.55	0.41
1:C1:927:C:H2'	1:C1:928:G:H8	1.86	0.41
1:C1:2399:G:H2'	1:C1:2400:A:H8	1.84	0.41
1:C1:2998:U:O2'	44:LV:45:GLY:HA3	2.21	0.41
2:C2:184:U:C6	4:CB:169:LYS:HD3	2.56	0.41
5:CC:343:PRO:HD3	15:CM:17:THR:HG22	2.03	0.41
5:CC:483:LEU:HD12	6:CD:343:LEU:HD21	2.03	0.41
5:CC:504:TRP:CZ3	5:CC:513:LEU:HB2	2.55	0.41
7:CE:400:PHE:CD2	7:CE:421:LEU:HD23	2.55	0.41
10:CH:283:PHE:CE2	10:CH:334:VAL:HG13	2.55	0.41
10:CH:294:PHE:HE1	10:CH:305:ILE:HD12	1.86	0.41
18:CP:368:SER:O	18:CP:372:PRO:HD3	2.20	0.41
22:CT:148:HIS:HA	22:CT:151:ALA:HB3	2.02	0.41
22:CT:217:TYR:CE2	22:CT:221:LEU:HD11	2.56	0.41
22:CT:676:LEU:O	22:CT:680:GLU:HG3	2.21	0.41
26:CY:417:GLU:OE2	26:CY:459:LEU:HD22	2.20	0.41
26:CY:628:GLU:HA	26:CY:631:VAL:HG12	2.03	0.41
26:CY:738:GLU:O	26:CY:742:GLU:OE1	2.39	0.41
29:LC:173:LEU:HA	29:LC:176:ILE:HG12	2.02	0.41
30:LE:196:HIS:CE1	30:LE:197:LEU:HG	2.56	0.41
36:LN:27:CYS:SG	36:LN:124:ASP:HB2	2.61	0.41
39:LQ:96:ALA:O	39:LQ:100:LYS:HG2	2.21	0.41
50:Le:111:THR:O	50:Le:115:GLN:HG3	2.20	0.41
58:Lq:49:PHE:HB2	58:Lq:193:LEU:HG	2.03	0.41
1:C1:419:C:OP1	50:Le:16:LYS:HD3	2.20	0.41
1:C1:633:A:H1'	1:C1:2334:A:C2	2.56	0.41
1:C1:650:C:H2'	1:C1:651:A:H8	1.86	0.41
1:C1:1055:U:H2'	1:C1:1056:U:C6	2.55	0.41
1:C1:1189:G:OP1	13:CK:54:ARG:NH1	2.54	0.41
1:C1:1318:C:H2'	1:C1:1319:G:H8	1.84	0.41
1:C1:1401:A:N7	29:LC:191:LEU:HD23	2.35	0.41
1:C1:1452:U:H2'	1:C1:1453:U:C6	2.55	0.41
1:C1:1680:U:H2'	1:C1:1681:C:C6	2.56	0.41
1:C1:2400:A:H2'	1:C1:2401:A:C8	2.55	0.41
1:C1:2451:C:H2'	1:C1:2452:C:O4'	2.20	0.41
1:C1:2759:A:O3'	25:CX:92:LYS:NZ	2.53	0.41
5:CC:724:ARG:HG2	5:CC:724:ARG:NH1	2.36	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:176:HIS:CD2	6:CD:180:ILE:HG12	2.55	0.41
6:CD:349:THR:O	6:CD:353:THR:N	2.53	0.41
6:CD:393:SER:HB3	6:CD:466:VAL:HG12	2.01	0.41
9:CG:9:MET:HE1	25:CX:101:MET:HE2	2.03	0.41
10:CH:473:PHE:CE2	19:CQ:106:VAL:HG11	2.56	0.41
12:CJ:498:ASP:HB3	12:CJ:501:LYS:HE3	2.03	0.41
18:CP:267:LEU:HD11	18:CP:282:GLU:HB2	2.02	0.41
21:CS:572:GLN:HG3	21:CS:573:ASP:N	2.36	0.41
22:CT:167:CYS:O	22:CT:171:GLN:HG3	2.21	0.41
22:CT:605:GLU:HG3	22:CT:606:LYS:HG3	2.03	0.41
26:CY:542:ILE:HG23	26:CY:542:ILE:O	2.20	0.41
29:LC:36:VAL:HG11	29:LC:251:LEU:HD21	2.03	0.41
1:C1:177:U:H2'	1:C1:178:C:C6	2.56	0.41
1:C1:508:G:OP2	15:LF:73:ARG:NH2	2.39	0.41
1:C1:564:C:H2'	1:C1:565:C:C6	2.55	0.41
1:C1:805:U:H2'	1:C1:806:U:O4'	2.21	0.41
1:C1:942:C:H6	1:C1:942:C:H2'	1.74	0.41
1:C1:984:A:N6	1:C1:1032:U:H1'	2.36	0.41
1:C1:1070:U:H2'	1:C1:1071:G:H8	1.85	0.41
1:C1:1089:A:H2'	1:C1:1090:C:H6	1.86	0.41
1:C1:1151:A:H2'	1:C1:1152:A:C8	2.56	0.41
1:C1:1385:C:O2	24:CV:24:ARG:NH2	2.52	0.41
1:C1:1531:U:H2'	1:C1:1532:C:C6	2.55	0.41
1:C1:1573:A:H1'	1:C1:1594:C:H1'	2.01	0.41
1:C1:1574:G:C4	1:C1:1575:C:C5	3.09	0.41
1:C1:1607:U:N3	1:C1:1793:A:C6	2.89	0.41
1:C1:1767:C:H2'	1:C1:1768:G:H8	1.85	0.41
1:C1:2305:C:H2'	1:C1:2306:U:C6	2.56	0.41
1:C1:2732:C:H2'	1:C1:2733:U:C6	2.56	0.41
1:C1:2990:A:H2'	1:C1:2991:C:C6	2.56	0.41
1:C1:3058:G:H2'	1:C1:3059:G:C8	2.56	0.41
1:C1:3335:U:H2'	1:C1:3336:U:C6	2.55	0.41
2:C2:130:C:H2'	2:C2:131:G:C8	2.55	0.41
3:CA:39:LEU:HD22	3:CA:77:LEU:CD1	2.51	0.41
3:CA:246:GLN:HG2	3:CA:254:ILE:HD13	2.02	0.41
5:CC:444:VAL:HG23	5:CC:446:GLN:OE1	2.20	0.41
6:CD:94:GLN:HE22	6:CD:96:VAL:HG22	1.86	0.41
6:CD:383:THR:HG21	6:CD:385:ARG:HE	1.86	0.41
7:CE:150:ASP:OD1	7:CE:292:THR:HG22	2.20	0.41
7:CE:161:LYS:HA	7:CE:164:ALA:HB3	2.03	0.41
7:CE:162:THR:HG23	7:CE:163:LEU:H	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CE:191:PRO:HB3	7:CE:269:ILE:HG12	2.03	0.41
7:CE:271:GLU:O	7:CE:272:ILE:C	2.63	0.41
10:CH:437:ILE:HG22	19:CQ:81:TYR:CE1	2.56	0.41
11:CI:218:VAL:HG12	11:CI:231:ALA:HB2	2.02	0.41
11:CI:315:ALA:O	11:CI:318:GLU:HG2	2.21	0.41
12:CJ:127:ILE:HD11	12:CJ:236:THR:HB	2.03	0.41
12:CJ:160:VAL:HG13	12:CJ:164:MET:HE3	2.02	0.41
12:CJ:201:ILE:HG22	12:CJ:202:GLN:HG3	2.03	0.41
12:CJ:482:LEU:HA	12:CJ:483:PRO:HD3	1.98	0.41
12:CJ:611:LYS:O	12:CJ:614:LEU:HG	2.21	0.41
13:CK:157:VAL:HG21	13:CK:178:ARG:NH1	2.36	0.41
13:CK:185:THR:HG22	13:CK:192:THR:OG1	2.21	0.41
14:CL:441:PRO:HA	15:LF:56:LYS:NZ	2.35	0.41
15:CM:101:ILE:HG23	15:CM:105:PRO:HB2	2.01	0.41
16:CN:1:MET:H2	16:CN:224:LEU:HB3	1.86	0.41
16:CN:88:LEU:O	19:CQ:80:ARG:NH2	2.54	0.41
18:CP:259:ARG:O	18:CP:263:THR:HG22	2.21	0.41
18:CP:308:ILE:HG12	18:CP:364:LEU:HD23	2.03	0.41
18:CP:385:LEU:HB2	18:CP:450:PHE:CD1	2.56	0.41
21:CS:567:ARG:NH1	22:CT:125:ARG:HH22	2.19	0.41
22:CT:169:VAL:HG23	22:CT:172:MET:HE2	2.02	0.41
25:CX:112:LYS:HE2	25:CX:112:LYS:HB2	1.78	0.41
26:CY:31:LYS:O	26:CY:31:LYS:HD2	2.20	0.41
26:CY:417:GLU:HG3	26:CY:459:LEU:HD13	2.02	0.41
26:CY:429:GLN:O	26:CY:433:VAL:HG23	2.21	0.41
26:CY:624:GLU:O	26:CY:627:SER:N	2.53	0.41
26:CY:635:ARG:NH2	26:CY:713:TRP:HE3	2.16	0.41
28:LB:108:GLU:HB2	28:LB:201:GLU:OE2	2.21	0.41
28:LB:151:ARG:HE	28:LB:151:ARG:HB2	1.63	0.41
29:LC:32:ARG:HG3	29:LC:121:PHE:CE2	2.56	0.41
32:LH:131:ALA:O	32:LH:134:VAL:HG22	2.20	0.41
38:LP:57:ALA:HB2	38:LP:83:TRP:CE2	2.56	0.41
39:LQ:91:SER:OG	39:LQ:117:ASP:HB2	2.21	0.41
40:LR:3:ASN:OD1	40:LR:5:ARG:HG3	2.21	0.41
41:LS:96:GLU:HG3	41:LS:102:ALA:HA	2.03	0.41
47:LZ:108:GLU:HA	47:LZ:111:LYS:HG2	2.03	0.41
48:Lc:26:VAL:HG21	48:Lc:93:MET:HE3	2.02	0.41
53:Lh:119:ARG:HG3	53:Lh:119:ARG:NH1	2.36	0.41
58:Lq:36:ILE:HG21	58:Lq:190:LEU:HD21	2.03	0.41
1:C1:300:A:H2'	1:C1:300:A:N3	2.35	0.41
1:C1:1481:U:H2'	1:C1:1482:G:C8	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2425:G:H2'	1:C1:2426:U:C6	2.56	0.41
1:C1:2746:C:H2'	1:C1:2747:U:C6	2.56	0.41
1:C1:2821:G:H1	10:CH:69:VAL:HA	1.85	0.41
1:C1:3172:U:H2'	1:C1:3173:C:C6	2.57	0.41
2:C2:139:U:H2'	2:C2:140:G:C8	2.56	0.41
4:CB:164:PRO:HA	4:CB:172:TYR:CE2	2.56	0.41
5:CC:172:ILE:HD11	23:CU:271:TYR:HE1	1.86	0.41
5:CC:473:ASP:C	5:CC:475:GLY:N	2.79	0.41
6:CD:390:LYS:HB2	6:CD:409:HIS:CG	2.55	0.41
7:CE:141:ALA:C	7:CE:144:PRO:HD2	2.46	0.41
7:CE:285:LEU:HD23	7:CE:285:LEU:HA	1.81	0.41
7:CE:473:LEU:HD12	7:CE:473:LEU:HA	1.90	0.41
10:CH:38:ILE:O	10:CH:42:ARG:HG3	2.21	0.41
12:CJ:173:HIS:CE1	12:CJ:267:GLU:HB2	2.56	0.41
12:CJ:178:TYR:CE1	12:CJ:245:LEU:HB3	2.56	0.41
12:CJ:611:LYS:O	12:CJ:612:ALA:C	2.61	0.41
12:CJ:666:LYS:HA	12:CJ:669:ARG:HG3	2.02	0.41
13:CK:244:GLN:HB2	13:CK:260:LEU:HD11	2.03	0.41
14:CL:31:LYS:O	14:CL:35:GLU:HG3	2.21	0.41
15:CM:56:LYS:O	15:CM:57:TYR:C	2.63	0.41
16:CN:71:LEU:HD11	16:CN:97:ILE:HG23	2.03	0.41
18:CP:281:ALA:O	18:CP:285:LEU:HG	2.21	0.41
18:CP:488:LYS:HD3	18:CP:526:TYR:CD2	2.56	0.41
22:CT:496:GLN:HG2	22:CT:579:TRP:CZ2	2.54	0.41
29:LC:238:ASP:N	29:LC:238:ASP:OD1	2.51	0.41
29:LC:329:LEU:HA	15:LF:172:ASN:HD21	1.86	0.41
31:LG:187:ALA:O	31:LG:191:THR:HG23	2.20	0.41
36:LN:164:LEU:HD23	36:LN:172:ARG:HH12	1.86	0.41
37:LO:175:LEU:O	37:LO:179:GLN:HG3	2.21	0.41
50:Le:22:GLN:HG2	50:Le:25:ARG:HH21	1.86	0.41
50:Le:34:ARG:HD3	50:Le:34:ARG:HA	1.91	0.41
56:Lk:22:ALA:HB3	56:Lk:39:ARG:HB3	2.02	0.41
1:C1:40:A:O2'	1:C1:92:G:N2	2.54	0.40
1:C1:171:G:H2'	1:C1:172:C:H6	1.85	0.40
1:C1:1320:C:O2	50:Le:13:LYS:NZ	2.53	0.40
1:C1:1323:U:H2'	1:C1:1324:C:H6	1.84	0.40
1:C1:1669:C:H2'	1:C1:1670:U:C6	2.56	0.40
1:C1:1834:C:O2'	52:Lg:13:PRO:O	2.24	0.40
1:C1:3107:A:OP1	28:LB:132:LYS:HB2	2.21	0.40
2:C2:123:G:H2'	2:C2:124:G:C8	2.55	0.40
5:CC:360:TYR:O	5:CC:384:PRO:HG2	2.20	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:656:ILE:HB	5:CC:670:VAL:CG2	2.51	0.40
7:CE:343:LYS:HE2	7:CE:487:LYS:NZ	2.36	0.40
9:CG:117:ALA:N	9:CG:159:PRO:O	2.54	0.40
10:CH:69:VAL:C	10:CH:73:GLN:HE22	2.22	0.40
10:CH:525:LYS:HA	10:CH:526:PRO:HD3	1.83	0.40
20:CR:45:LEU:HD12	34:LL:40:ARG:HA	2.03	0.40
21:CS:743:ARG:NH1	21:CS:747:LYS:HB2	2.35	0.40
22:CT:665:ARG:HB2	22:CT:665:ARG:NH1	2.36	0.40
29:LC:191:LEU:HD11	29:LC:197:LYS:HD2	2.03	0.40
30:LE:148:LYS:N	30:LE:149:PRO:HD2	2.36	0.40
15:LF:90:VAL:HA	15:LF:143:GLY:O	2.21	0.40
32:LH:92:TYR:CZ	32:LH:144:ASP:HA	2.56	0.40
33:LK:35:LEU:HD22	33:LK:37:LEU:HD23	2.03	0.40
37:LO:38:ARG:HB3	37:LO:41:ALA:HB3	2.04	0.40
43:LU:60:ILE:HD11	43:LU:76:ASN:HD21	1.86	0.40
46:LY:26:ARG:HD3	46:LY:74:ARG:O	2.21	0.40
46:LY:30:MET:HE1	46:LY:74:ARG:HG2	2.03	0.40
54:Li:83:LYS:HE3	54:Li:89:PHE:CE1	2.56	0.40
1:C1:772:U:C2	1:C1:773:A:N7	2.89	0.40
1:C1:1046:A:H61	1:C1:1074:C:H2'	1.86	0.40
1:C1:1046:A:C2	1:C1:1074:C:C4	3.09	0.40
1:C1:1049:C:H5'	1:C1:1050:C:OP2	2.22	0.40
1:C1:1067:A:H2'	1:C1:1068:C:C6	2.56	0.40
1:C1:1657:G:H2'	1:C1:1658:A:C8	2.56	0.40
1:C1:1675:A:H2'	1:C1:1676:A:H8	1.87	0.40
1:C1:2458:U:H2'	1:C1:2459:C:C6	2.57	0.40
2:C2:4:C:H2'	2:C2:5:U:H6	1.87	0.40
2:C2:7:U:H2'	2:C2:8:C:C6	2.57	0.40
2:C2:44:A:H2'	2:C2:45:C:H6	1.86	0.40
2:C2:77:A:H2'	2:C2:78:G:C8	2.56	0.40
2:C2:227:G:H2'	2:C2:228:C:H6	1.86	0.40
5:CC:240:ARG:HE	31:LG:261:LYS:CE	2.34	0.40
5:CC:659:TYR:HD2	5:CC:666:LEU:HA	1.87	0.40
5:CC:697:ARG:HH21	5:CC:712:THR:HG22	1.86	0.40
6:CD:102:PRO:HB2	6:CD:485:ASN:HB3	2.03	0.40
6:CD:384:LEU:HB3	6:CD:416:TRP:CZ3	2.56	0.40
7:CE:223:ARG:NH1	7:CE:227:ALA:HB2	2.37	0.40
10:CH:85:TYR:CZ	10:CH:156:LEU:HD12	2.55	0.40
11:CI:202:GLU:OE2	15:CM:61:TYR:HD1	2.04	0.40
12:CJ:243:TYR:HD1	12:CJ:253:TYR:CD2	2.38	0.40
12:CJ:362:ASP:HA	12:CJ:365:GLN:NE2	2.36	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:453:ARG:HG2	12:CJ:455:TYR:CZ	2.56	0.40
23:CU:358:PHE:O	23:CU:359:ASP:C	2.64	0.40
26:CY:400:ALA:HA	26:CY:403:VAL:HG22	2.02	0.40
26:CY:611:THR:HB	26:CY:613:VAL:HG12	2.03	0.40
26:CY:638:ALA:O	26:CY:639:PHE:C	2.63	0.40
29:LC:9:VAL:HG13	29:LC:152:VAL:HG12	2.03	0.40
15:LF:108:ILE:HD12	15:LF:132:MET:SD	2.61	0.40
33:LK:146:LYS:HD3	33:LK:151:ILE:HD11	2.02	0.40
34:LL:79:GLU:CD	34:LL:112:ASN:HD22	2.29	0.40
38:LP:60:MET:HA	38:LP:60:MET:HE2	2.02	0.40
47:LZ:81:PRO:HG2	48:Lc:65:MET:HE3	2.02	0.40
50:Le:41:ASN:OD1	50:Le:44:ARG:HB3	2.21	0.40
56:Lk:31:THR:HG23	56:Lk:33:GLN:HB2	2.03	0.40
1:C1:443:G:H2'	1:C1:444:G:O4'	2.21	0.40
1:C1:836:U:C2	1:C1:837:G:C8	3.09	0.40
1:C1:974:G:N2	1:C1:1038:U:O2	2.35	0.40
1:C1:1321:C:H2'	1:C1:1322:C:C6	2.57	0.40
1:C1:1726:G:O3'	56:Lk:46:THR:HG21	2.22	0.40
1:C1:2365:G:C2	1:C1:2366:A:H1'	2.57	0.40
1:C1:2431:G:C6	1:C1:2439:G:C5	3.09	0.40
4:CB:153:PHE:HE1	4:CB:177:LYS:HE3	1.86	0.40
5:CC:350:TYR:HE2	12:CJ:486:LEU:HD12	1.86	0.40
7:CE:163:LEU:O	7:CE:167:ILE:HG12	2.21	0.40
7:CE:306:LEU:HA	7:CE:306:LEU:HD23	1.91	0.40
10:CH:247:ALA:H	10:CH:280:LYS:HG3	1.86	0.40
12:CJ:54:ASN:HB3	12:CJ:57:ALA:HB2	2.03	0.40
12:CJ:138:LEU:HA	12:CJ:141:LEU:HD12	2.04	0.40
12:CJ:145:LEU:HD12	12:CJ:149:PHE:CE2	2.56	0.40
13:CK:228:LEU:HD23	13:CK:230:ILE:HD11	2.03	0.40
18:CP:402:MET:HE2	18:CP:405:THR:O	2.21	0.40
18:CP:498:CYS:SG	18:CP:508:ILE:HG13	2.60	0.40
20:CR:20:PRO:HG2	20:CR:22:ARG:HE	1.86	0.40
22:CT:276:ASP:H	22:CT:279:PHE:HB3	1.86	0.40
23:CU:281:THR:HG22	23:CU:282:MET:HE2	2.04	0.40
26:CY:375:LEU:HA	26:CY:378:MET:HE2	2.02	0.40
26:CY:493:TRP:HE3	26:CY:497:HIS:NE2	2.19	0.40
26:CY:506:LEU:HD21	26:CY:527:LEU:HB3	2.04	0.40
28:LB:35:ASP:OD2	28:LB:192:LYS:NZ	2.54	0.40
28:LB:126:LYS:HB2	28:LB:126:LYS:HE2	1.81	0.40
28:LB:153:LYS:HZ2	28:LB:194:GLU:HG2	1.86	0.40
29:LC:363:HIS:CG	41:LS:67:LYS:NZ	2.90	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LH:181:ILE:C	32:LH:182:TYR:CD1	2.99	0.40
46:LY:57:ILE:HD12	46:LY:84:VAL:HG11	2.04	0.40
47:LZ:24:ILE:HG12	47:LZ:42:VAL:HG12	2.02	0.40
53:Lh:107:GLU:H	53:Lh:107:GLU:CD	2.28	0.40
58:Lq:83:ASP:OD1	58:Lq:83:ASP:N	2.54	0.40
1:C1:21:G:P	2:C2:36:G:H22	2.44	0.40
1:C1:26:A:H2'	1:C1:27:C:H6	1.86	0.40
1:C1:32:U:H2'	1:C1:33:G:O4'	2.20	0.40
1:C1:101:G:H2'	1:C1:102:C:O4'	2.22	0.40
1:C1:201:C:H2'	1:C1:202:A:O4'	2.22	0.40
1:C1:523:A:H2'	1:C1:524:A:C8	2.56	0.40
1:C1:1436:A:N6	1:C1:1858:A:O2'	2.54	0.40
1:C1:1561:U:H5'	1:C1:1562:G:C8	2.56	0.40
1:C1:1662:C:C5	10:CH:503:ARG:HD3	2.57	0.40
1:C1:1712:A:H2'	1:C1:1713:G:H8	1.86	0.40
1:C1:2303:A:H2'	1:C1:2304:U:C6	2.57	0.40
1:C1:2370:U:H2'	1:C1:2371:G:H8	1.86	0.40
2:C2:81:U:O2	2:C2:82:U:O2'	2.40	0.40
2:C2:233:U:H3	2:C2:284:G:H1	1.68	0.40
4:CB:24:LEU:HG	4:CB:28:LYS:HZ2	1.86	0.40
4:CB:163:LEU:N	4:CB:164:PRO:HD2	2.37	0.40
5:CC:529:PRO:HB2	6:CD:227:SER:HB2	2.02	0.40
5:CC:618:HIS:CD2	5:CC:618:HIS:N	2.89	0.40
7:CE:374:SER:OG	7:CE:412:ILE:HD11	2.22	0.40
9:CG:104:GLY:HA3	9:CG:118:HIS:HB3	2.03	0.40
10:CH:38:ILE:HA	10:CH:41:ILE:HD12	2.03	0.40
11:CI:288:MET:HG2	11:CI:291:ARG:HH22	1.86	0.40
12:CJ:375:SER:HB2	12:CJ:419:ILE:O	2.22	0.40
14:CL:441:PRO:HA	15:LF:56:LYS:HD3	2.04	0.40
20:CR:205:ASP:O	20:CR:209:MET:HG3	2.20	0.40
22:CT:483:LEU:O	22:CT:487:VAL:HG23	2.22	0.40
23:CU:333:LYS:HG2	23:CU:362:VAL:HG11	2.03	0.40
24:CV:85:SER:OG	24:CV:86:THR:N	2.49	0.40
26:CY:614:TYR:O	26:CY:618:VAL:HG22	2.22	0.40
31:LG:207:ARG:O	31:LG:211:LYS:HG3	2.22	0.40
32:LH:108:GLU:O	32:LH:109:THR:OG1	2.32	0.40
36:LN:51:LEU:HD22	36:LN:117:ASN:ND2	2.37	0.40
40:LR:132:PHE:CE1	40:LR:138:LEU:HD12	2.55	0.40
46:LY:73:TYR:CE2	46:LY:76:LYS:HE3	2.56	0.40
50:Le:26:PHE:HB2	50:Le:29:LEU:HD12	2.03	0.40
1:C1:771:U:H2'	1:C1:772:U:H6	1.86	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1050:C:H3'	1:C1:1051:C:C6	2.55	0.40
1:C1:1358:C:C2	1:C1:1359:G:C8	3.10	0.40
1:C1:1639:C:H2'	1:C1:1640:G:H8	1.86	0.40
1:C1:3098:A:H3'	1:C1:3099:A:H4'	2.02	0.40
3:CA:279:HIS:CE1	3:CA:283:MET:HE3	2.56	0.40
6:CD:246:ASP:N	6:CD:246:ASP:OD1	2.53	0.40
6:CD:332:VAL:O	6:CD:332:VAL:HG13	2.22	0.40
8:CF:109:PRO:O	8:CF:113:GLU:OE1	2.40	0.40
9:CG:20:MET:HE1	9:CG:89:ILE:HG22	2.03	0.40
9:CG:98:ILE:HD11	9:CG:119:VAL:HG22	2.03	0.40
10:CH:40:ARG:HH11	10:CH:40:ARG:HG2	1.86	0.40
10:CH:273:ILE:O	10:CH:276:LEU:HB2	2.22	0.40
12:CJ:26:LEU:HB3	12:CJ:28:LEU:HD13	2.04	0.40
18:CP:411:ASN:HB2	18:CP:443:PHE:CZ	2.54	0.40
23:CU:325:LYS:O	23:CU:329:GLU:OE1	2.40	0.40
28:LB:212:LYS:HE2	28:LB:355:VAL:HG23	2.04	0.40
29:LC:260:ALA:O	29:LC:264:GLN:HB2	2.21	0.40
41:LS:24:LEU:HD13	42:LT:146:ASN:OD1	2.22	0.40
43:LU:92:LYS:C	43:LU:95:GLN:H	2.30	0.40
46:LY:23:SER:HB2	46:LY:74:ARG:HH11	1.86	0.40
48:Lc:89:ARG:HE	48:Lc:89:ARG:HB2	1.72	0.40
58:Lq:38:LEU:HD22	58:Lq:41:TYR:H	1.86	0.40
58:Lq:100:ILE:O	58:Lq:103:LEU:HG	2.22	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%)	228 (92%)	16 (6%)	3 (1%)	10 37
4	CB	256/391 (66%)	228 (89%)	28 (11%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	CC	648/801 (81%)	606 (94%)	38 (6%)	4 (1%)	21	52
6	CD	450/495 (91%)	416 (92%)	34 (8%)	0	100	100
7	CE	458/598 (77%)	428 (93%)	30 (7%)	0	100	100
8	CF	243/270 (90%)	227 (93%)	14 (6%)	2 (1%)	16	47
9	CG	175/184 (95%)	163 (93%)	11 (6%)	1 (1%)	21	52
10	CH	538/661 (81%)	511 (95%)	25 (5%)	2 (0%)	30	61
11	CI	144/414 (35%)	135 (94%)	9 (6%)	0	100	100
12	CJ	484/679 (71%)	462 (96%)	21 (4%)	1 (0%)	43	73
13	CK	223/261 (85%)	212 (95%)	11 (5%)	0	100	100
14	CL	393/558 (70%)	366 (93%)	25 (6%)	2 (0%)	24	57
15	CM	219/249 (88%)	210 (96%)	9 (4%)	0	100	100
15	LF	245/249 (98%)	238 (97%)	7 (3%)	0	100	100
16	CN	244/246 (99%)	227 (93%)	17 (7%)	0	100	100
17	CO	56/120 (47%)	56 (100%)	0	0	100	100
18	CP	354/751 (47%)	330 (93%)	24 (7%)	0	100	100
19	CQ	173/225 (77%)	165 (95%)	8 (5%)	0	100	100
20	CR	159/237 (67%)	157 (99%)	2 (1%)	0	100	100
21	CS	246/834 (30%)	238 (97%)	8 (3%)	0	100	100
22	CT	478/688 (70%)	452 (95%)	24 (5%)	2 (0%)	30	61
23	CU	174/451 (39%)	170 (98%)	3 (2%)	1 (1%)	21	52
24	CV	137/147 (93%)	135 (98%)	1 (1%)	1 (1%)	18	49
25	CX	86/203 (42%)	84 (98%)	2 (2%)	0	100	100
26	CY	406/788 (52%)	371 (91%)	33 (8%)	2 (0%)	24	57
27	Cz	68/123 (55%)	64 (94%)	4 (6%)	0	100	100
28	LB	352/392 (90%)	333 (95%)	19 (5%)	0	100	100
29	LC	360/365 (99%)	344 (96%)	16 (4%)	0	100	100
30	LE	175/200 (88%)	163 (93%)	11 (6%)	1 (1%)	21	52
31	LG	200/262 (76%)	189 (94%)	11 (6%)	0	100	100
32	LH	188/192 (98%)	180 (96%)	8 (4%)	0	100	100
33	LK	142/165 (86%)	129 (91%)	11 (8%)	2 (1%)	9	34
34	LL	115/213 (54%)	107 (93%)	7 (6%)	1 (1%)	14	44

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	LM	135/142 (95%)	129 (96%)	6 (4%)	0	100	100
36	LN	179/203 (88%)	170 (95%)	9 (5%)	0	100	100
37	LO	202/204 (99%)	190 (94%)	9 (4%)	3 (2%)	8	32
38	LP	165/187 (88%)	160 (97%)	5 (3%)	0	100	100
39	LQ	127/213 (60%)	121 (95%)	6 (5%)	0	100	100
40	LR	115/2898 (4%)	115 (100%)	0	0	100	100
41	LS	172/174 (99%)	160 (93%)	12 (7%)	0	100	100
42	LT	124/160 (78%)	117 (94%)	6 (5%)	1 (1%)	16	47
43	LU	103/127 (81%)	96 (93%)	7 (7%)	0	100	100
44	LV	133/139 (96%)	128 (96%)	5 (4%)	0	100	100
45	LX	133/156 (85%)	129 (97%)	4 (3%)	0	100	100
46	LY	132/138 (96%)	130 (98%)	2 (2%)	0	100	100
47	LZ	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
48	Lc	96/108 (89%)	93 (97%)	3 (3%)	0	100	100
49	Ld	107/120 (89%)	101 (94%)	6 (6%)	0	100	100
50	Le	125/131 (95%)	123 (98%)	2 (2%)	0	100	100
51	Lf	106/109 (97%)	99 (93%)	5 (5%)	2 (2%)	6	27
52	Lg	115/119 (97%)	113 (98%)	2 (2%)	0	100	100
53	Lh	119/935 (13%)	113 (95%)	6 (5%)	0	100	100
54	Li	86/110 (78%)	84 (98%)	2 (2%)	0	100	100
55	Lj	72/95 (76%)	71 (99%)	1 (1%)	0	100	100
56	Lk	73/81 (90%)	67 (92%)	6 (8%)	0	100	100
57	Ll	36/51 (71%)	33 (92%)	3 (8%)	0	100	100
58	Lq	205/217 (94%)	179 (87%)	25 (12%)	1 (0%)	24	57
All	All	11829/19680 (60%)	11173 (94%)	624 (5%)	32 (0%)	37	67

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	CA	236	PRO
5	CC	161	ASP
22	CT	502	ARG
26	CY	692	ALA
26	CY	707	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	LL	51	VAL
9	CG	43	ASP
5	CC	440	PRO
10	CH	225	ASP
10	CH	228	LEU
14	CL	439	ASP
22	CT	661	GLY
24	CV	85	SER
30	LE	191	LYS
33	LK	51	ALA
37	LO	190	LYS
3	CA	123	MET
3	CA	124	GLU
8	CF	188	ALA
37	LO	191	VAL
58	Lq	16	LEU
14	CL	446	ASP
33	LK	160	ILE
51	Lf	3	SER
51	Lf	4	GLU
12	CJ	216	GLN
37	LO	65	TYR
42	LT	44	VAL
8	CF	244	PRO
5	CC	120	PRO
23	CU	357	PRO
5	CC	567	GLY

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%)	213 (96%)	10 (4%)	24	56
4	CB	222/329 (68%)	210 (95%)	12 (5%)	20	50
5	CC	578/708 (82%)	566 (98%)	12 (2%)	47	71

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	CD	381/410 (93%)	381 (100%)	0	100	100
7	CE	398/517 (77%)	381 (96%)	17 (4%)	26	57
8	CF	214/236 (91%)	211 (99%)	3 (1%)	59	76
9	CG	150/155 (97%)	148 (99%)	2 (1%)	61	77
10	CH	481/575 (84%)	471 (98%)	10 (2%)	47	71
11	CI	121/336 (36%)	121 (100%)	0	100	100
12	CJ	428/579 (74%)	423 (99%)	5 (1%)	63	78
13	CK	195/225 (87%)	193 (99%)	2 (1%)	68	79
14	CL	72/458 (16%)	70 (97%)	2 (3%)	38	66
15	CM	191/215 (89%)	190 (100%)	1 (0%)	81	85
15	LF	213/215 (99%)	211 (99%)	2 (1%)	70	80
16	CN	206/206 (100%)	200 (97%)	6 (3%)	37	66
17	CO	48/99 (48%)	48 (100%)	0	100	100
18	CP	302/632 (48%)	295 (98%)	7 (2%)	44	70
19	CQ	150/192 (78%)	144 (96%)	6 (4%)	28	60
20	CR	144/206 (70%)	144 (100%)	0	100	100
21	CS	209/716 (29%)	209 (100%)	0	100	100
22	CT	427/600 (71%)	422 (99%)	5 (1%)	63	78
23	CU	149/376 (40%)	145 (97%)	4 (3%)	39	67
24	CV	109/112 (97%)	109 (100%)	0	100	100
25	CX	76/172 (44%)	76 (100%)	0	100	100
26	CY	364/686 (53%)	358 (98%)	6 (2%)	55	75
27	Cz	60/107 (56%)	58 (97%)	2 (3%)	33	63
28	LB	301/331 (91%)	292 (97%)	9 (3%)	36	65
29	LC	283/285 (99%)	277 (98%)	6 (2%)	47	71
30	LE	151/166 (91%)	150 (99%)	1 (1%)	76	82
31	LG	175/222 (79%)	173 (99%)	2 (1%)	65	78
32	LH	167/169 (99%)	167 (100%)	0	100	100
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%)	113 (98%)	2 (2%)	53	74

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	LN	164/180 (91%)	162 (99%)	2 (1%)	63	78
37	LO	163/163 (100%)	158 (97%)	5 (3%)	35	64
38	LP	137/152 (90%)	137 (100%)	0	100	100
39	LQ	110/178 (62%)	110 (100%)	0	100	100
40	LR	104/2396 (4%)	104 (100%)	0	100	100
41	LS	154/154 (100%)	150 (97%)	4 (3%)	40	68
42	LT	109/135 (81%)	103 (94%)	6 (6%)	19	50
43	LU	93/108 (86%)	85 (91%)	8 (9%)	10	34
44	LV	99/102 (97%)	98 (99%)	1 (1%)	68	79
45	LX	114/129 (88%)	110 (96%)	4 (4%)	32	62
46	LY	117/119 (98%)	117 (100%)	0	100	100
47	LZ	121/121 (100%)	120 (99%)	1 (1%)	73	81
48	Lc	79/88 (90%)	76 (96%)	3 (4%)	29	60
49	Ld	95/105 (90%)	94 (99%)	1 (1%)	65	78
50	Le	110/114 (96%)	110 (100%)	0	100	100
51	Lf	89/90 (99%)	88 (99%)	1 (1%)	65	78
52	Lg	101/102 (99%)	98 (97%)	3 (3%)	36	65
53	Lh	108/781 (14%)	108 (100%)	0	100	100
54	Li	75/93 (81%)	74 (99%)	1 (1%)	61	77
55	Lj	61/78 (78%)	60 (98%)	1 (2%)	55	75
56	Lk	71/76 (93%)	71 (100%)	0	100	100
57	Ll	34/46 (74%)	34 (100%)	0	100	100
58	Lq	179/189 (95%)	173 (97%)	6 (3%)	32	63
All	All	10010/16639 (60%)	9829 (98%)	181 (2%)	51	73

All (181) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	CA	38	VAL
3	CA	63	ARG
3	CA	64	LYS
3	CA	83	LEU
3	CA	120	LEU
3	CA	124	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	CA	232	ILE
3	CA	233	GLU
3	CA	236	PRO
3	CA	237	ARG
4	CB	46	LYS
4	CB	47	GLN
4	CB	65	THR
4	CB	67	THR
4	CB	69	LYS
4	CB	245	VAL
4	CB	274	LYS
4	CB	279	ARG
4	CB	281	PHE
4	CB	283	VAL
4	CB	293	ILE
4	CB	295	GLN
5	CC	122	VAL
5	CC	161	ASP
5	CC	164	ASP
5	CC	353	SER
5	CC	388	ASP
5	CC	390	LEU
5	CC	391	ARG
5	CC	437	GLU
5	CC	438	LEU
5	CC	439	LYS
5	CC	564	GLU
5	CC	626	GLN
7	CE	112	GLU
7	CE	134	MET
7	CE	136	GLU
7	CE	279	ARG
7	CE	306	LEU
7	CE	332	LEU
7	CE	334	GLN
7	CE	429	ILE
7	CE	439	ARG
7	CE	442	ILE
7	CE	445	VAL
7	CE	447	ARG
7	CE	460	LEU
7	CE	473	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	CE	480	VAL
7	CE	482	GLU
7	CE	484	ASP
8	CF	224	LEU
8	CF	237	LEU
8	CF	241	LYS
9	CG	63	LYS
9	CG	64	LEU
10	CH	137	THR
10	CH	221	PRO
10	CH	223	ILE
10	CH	225	ASP
10	CH	228	LEU
10	CH	231	MET
10	CH	239	VAL
10	CH	269	LEU
10	CH	273	ILE
10	CH	274	LYS
12	CJ	193	LYS
12	CJ	195	ILE
12	CJ	213	LYS
12	CJ	217	ARG
12	CJ	457	GLN
13	CK	49	LEU
13	CK	53	GLN
14	CL	18	THR
14	CL	20	LEU
15	CM	52	LYS
16	CN	109	VAL
16	CN	111	ASN
16	CN	152	MET
16	CN	154	LEU
16	CN	160	LEU
16	CN	223	ARG
18	CP	289	PRO
18	CP	290	PRO
18	CP	436	CYS
18	CP	437	ASN
18	CP	439	ASP
18	CP	441	ARG
18	CP	481	MET
19	CQ	134	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
19	CQ	137	LEU
19	CQ	138	ARG
19	CQ	143	ARG
19	CQ	144	ARG
19	CQ	162	GLU
22	CT	174	VAL
22	CT	178	VAL
22	CT	210	LEU
22	CT	657	THR
22	CT	658	ILE
23	CU	304	LYS
23	CU	357	PRO
23	CU	359	ASP
23	CU	363	ASP
26	CY	636	ASN
26	CY	637	ILE
26	CY	640	PRO
26	CY	690	ARG
26	CY	693	LYS
26	CY	708	LEU
27	Cz	52	VAL
27	Cz	53	LYS
28	LB	17	LEU
28	LB	20	LYS
28	LB	126	LYS
28	LB	212	LYS
28	LB	283	ILE
28	LB	349	ARG
28	LB	350	LYS
28	LB	354	LYS
28	LB	355	VAL
29	LC	22	VAL
29	LC	25	LYS
29	LC	262	ILE
29	LC	263	LYS
29	LC	264	GLN
29	LC	266	ASP
30	LE	191	LYS
15	LF	110	GLN
15	LF	116	GLN
31	LG	160	VAL
31	LG	164	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
35	LM	112	LEU
35	LM	122	ARG
36	LN	40	SER
36	LN	41	ARG
37	LO	64	ARG
37	LO	190	LYS
37	LO	194	LYS
37	LO	196	SER
37	LO	199	LEU
41	LS	131	LYS
41	LS	133	GLU
41	LS	136	LYS
41	LS	146	LYS
42	LT	78	LYS
42	LT	80	VAL
42	LT	81	LYS
42	LT	82	HIS
42	LT	83	ARG
42	LT	84	TYR
43	LU	19	LYS
43	LU	50	ASP
43	LU	58	ASP
43	LU	59	VAL
43	LU	61	LYS
43	LU	73	ILE
43	LU	76	ASN
43	LU	77	ASP
44	LV	95	LEU
45	LX	21	LYS
45	LX	22	LYS
45	LX	28	LEU
45	LX	43	THR
47	LZ	11	LEU
48	Lc	47	ILE
48	Lc	62	TYR
48	Lc	70	VAL
49	Ld	73	LYS
51	Lf	4	GLU
52	Lg	58	LEU
52	Lg	61	ARG
52	Lg	95	LEU
54	Li	25	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
55	Lj	18	LEU
58	Lq	12	ASN
58	Lq	17	LEU
58	Lq	21	ASN
58	Lq	24	LYS
58	Lq	25	LYS
58	Lq	26	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (115) such sidechains are listed below:

Mol	Chain	Res	Type
3	CA	34	GLN
3	CA	88	ASN
3	CA	109	ASN
3	CA	127	HIS
3	CA	178	HIS
3	CA	246	GLN
3	CA	295	GLN
4	CB	47	GLN
4	CB	105	GLN
4	CB	277	ASN
4	CB	280	ASN
5	CC	136	ASN
5	CC	166	ASN
5	CC	205	GLN
5	CC	290	GLN
5	CC	446	GLN
5	CC	626	GLN
5	CC	637	GLN
5	CC	716	HIS
5	CC	753	GLN
6	CD	94	GLN
6	CD	331	GLN
7	CE	299	GLN
7	CE	334	GLN
7	CE	463	GLN
8	CF	118	ASN
8	CF	121	GLN
9	CG	41	GLN
9	CG	113	ASN
10	CH	25	GLN
10	CH	237	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	CH	258	GLN
10	CH	328	GLN
10	CH	369	HIS
11	CI	185	GLN
12	CJ	102	ASN
12	CJ	153	ASN
12	CJ	177	HIS
12	CJ	485	HIS
12	CJ	506	GLN
13	CK	53	GLN
14	CL	6	ASN
15	CM	25	GLN
15	CM	48	GLN
15	CM	200	ASN
15	CM	217	ASN
16	CN	82	GLN
16	CN	86	ASN
16	CN	113	HIS
16	CN	118	HIS
17	CO	13	ASN
18	CP	265	GLN
18	CP	322	GLN
18	CP	326	ASN
18	CP	482	GLN
18	CP	485	HIS
18	CP	489	GLN
19	CQ	24	ASN
19	CQ	39	ASN
19	CQ	130	ASN
20	CR	202	HIS
21	CS	651	ASN
21	CS	744	GLN
22	CT	137	GLN
22	CT	208	GLN
22	CT	215	HIS
22	CT	323	ASN
22	CT	436	GLN
23	CU	364	ASN
24	CV	23	GLN
24	CV	43	HIS
25	CX	113	GLN
26	CY	34	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
26	CY	509	HIS
26	CY	533	GLN
26	CY	636	ASN
27	Cz	58	GLN
28	LB	68	HIS
28	LB	275	HIS
28	LB	320	ASN
29	LC	59	HIS
29	LC	88	GLN
29	LC	111	HIS
29	LC	292	ASN
30	LE	98	ASN
15	LF	10	ASN
15	LF	119	ASN
15	LF	165	GLN
15	LF	178	ASN
31	LG	62	GLN
31	LG	158	ASN
31	LG	212	ASN
32	LH	151	ASN
36	LN	95	GLN
36	LN	138	ASN
38	LP	118	GLN
38	LP	120	ASN
39	LQ	86	ASN
39	LQ	122	GLN
40	LR	39	GLN
40	LR	141	HIS
42	LT	127	GLN
42	LT	139	HIS
43	LU	75	HIS
43	LU	76	ASN
44	LV	134	ASN
45	LX	73	HIS
48	Lc	72	HIS
50	Le	50	ASN
54	Li	47	GLN
55	Lj	48	ASN
55	Lj	76	ASN
56	Lk	33	GLN
57	Ll	20	ASN
58	Lq	40	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2594/3341 (77%)	574 (22%)	40 (1%)
2	C2	254/319 (79%)	49 (19%)	1 (0%)
All	All	2848/3660 (77%)	623 (21%)	41 (1%)

All (623) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	14	U
1	C1	22	G
1	C1	26	A
1	C1	41	G
1	C1	49	A
1	C1	60	A
1	C1	65	A
1	C1	66	A
1	C1	71	A
1	C1	73	A
1	C1	74	G
1	C1	75	G
1	C1	92	G
1	C1	93	C
1	C1	94	G
1	C1	96	G
1	C1	109	A
1	C1	110	G
1	C1	116	A
1	C1	122	A
1	C1	128	G
1	C1	129	C
1	C1	131	U
1	C1	132	C
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	162	U
1	C1	163	U
1	C1	176	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	214	A
1	C1	225	G
1	C1	232	G
1	C1	240	U
1	C1	241	G
1	C1	244	U
1	C1	253	U
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	290	U
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	329	G
1	C1	330	A
1	C1	331	C
1	C1	342	C
1	C1	343	A
1	C1	368	G
1	C1	390	U
1	C1	393	C
1	C1	394	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	395	C
1	C1	396	G
1	C1	412	G
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	445	A
1	C1	446	U
1	C1	447	C
1	C1	448	A
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	485	G
1	C1	508	G
1	C1	509	A
1	C1	511	A
1	C1	513	A
1	C1	519	A
1	C1	524	A
1	C1	525	U
1	C1	526	G
1	C1	527	U
1	C1	529	G
1	C1	530	C
1	C1	533	C
1	C1	534	U
1	C1	535	C
1	C1	536	C
1	C1	538	G
1	C1	542	U
1	C1	543	G
1	C1	544	U
1	C1	545	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	546	A
1	C1	547	U
1	C1	548	A
1	C1	549	G
1	C1	579	A
1	C1	582	A
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	623	C
1	C1	624	C
1	C1	633	A
1	C1	647	A
1	C1	663	G
1	C1	664	A
1	C1	668	U
1	C1	678	A
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	765	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	803	G
1	C1	807	G
1	C1	816	G
1	C1	828	A
1	C1	831	U
1	C1	835	G
1	C1	836	U
1	C1	838	G
1	C1	841	G
1	C1	842	C
1	C1	843	U
1	C1	846	C
1	C1	858	C
1	C1	862	C
1	C1	863	A
1	C1	871	C
1	C1	876	A
1	C1	877	A
1	C1	878	U
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	964	A
1	C1	965	G
1	C1	974	G
1	C1	975	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	1072	G
1	C1	1073	G
1	C1	1074	C
1	C1	1076	U
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	1099	G
1	C1	1114	C
1	C1	1124	G
1	C1	1125	A
1	C1	1126	U
1	C1	1134	G
1	C1	1135	A
1	C1	1141	A
1	C1	1142	C
1	C1	1157	C
1	C1	1158	C
1	C1	1159	G
1	C1	1160	G
1	C1	1163	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	1164	G
1	C1	1167	C
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	1185	A
1	C1	1186	A
1	C1	1187	A
1	C1	1189	G
1	C1	1190	C
1	C1	1191	G
1	C1	1203	U
1	C1	1204	G
1	C1	1214	C
1	C1	1218	G
1	C1	1227	A
1	C1	1228	G
1	C1	1234	A
1	C1	1236	C
1	C1	1240	U
1	C1	1245	A
1	C1	1247	U
1	C1	1254	C
1	C1	1267	G
1	C1	1268	A
1	C1	1269	A
1	C1	1271	G
1	C1	1272	U
1	C1	1286	A
1	C1	1287	U
1	C1	1289	G
1	C1	1291	U
1	C1	1295	G
1	C1	1312	A
1	C1	1314	A
1	C1	1331	G
1	C1	1332	A
1	C1	1333	A
1	C1	1334	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	1335	C
1	C1	1336	G
1	C1	1337	A
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	1417	A
1	C1	1419	C
1	C1	1434	A
1	C1	1437	U
1	C1	1438	A
1	C1	1452	U
1	C1	1465	G
1	C1	1478	C
1	C1	1490	C
1	C1	1496	G
1	C1	1535	U
1	C1	1537	U
1	C1	1538	C
1	C1	1541	A
1	C1	1543	G
1	C1	1548	C
1	C1	1549	U
1	C1	1551	G
1	C1	1552	U
1	C1	1553	G
1	C1	1556	C
1	C1	1557	C
1	C1	1560	G
1	C1	1561	U
1	C1	1562	G
1	C1	1566	A
1	C1	1567	A
1	C1	1568	A
1	C1	1575	C
1	C1	1584	A
1	C1	1607	U
1	C1	1608	U
1	C1	1609	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	1610	C
1	C1	1618	C
1	C1	1621	A
1	C1	1622	A
1	C1	1623	C
1	C1	1624	U
1	C1	1637	G
1	C1	1662	C
1	C1	1695	A
1	C1	1696	C
1	C1	1703	U
1	C1	1722	G
1	C1	1729	A
1	C1	1730	G
1	C1	1739	A
1	C1	1741	U
1	C1	1742	U
1	C1	1744	U
1	C1	1749	G
1	C1	1759	G
1	C1	1760	C
1	C1	1774	U
1	C1	1775	G
1	C1	1776	A
1	C1	1794	U
1	C1	1795	A
1	C1	1798	U
1	C1	1799	C
1	C1	1800	U
1	C1	1818	A
1	C1	1819	U
1	C1	1820	A
1	C1	1821	A
1	C1	1825	C
1	C1	1828	C
1	C1	1829	A
1	C1	1837	A
1	C1	1842	G
1	C1	1843	A
1	C1	1845	C
1	C1	1857	G
1	C1	1858	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	1859	U
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	2297	G
1	C1	2298	U
1	C1	2302	U
1	C1	2310	A
1	C1	2311	U
1	C1	2325	A
1	C1	2327	C
1	C1	2334	A
1	C1	2335	A
1	C1	2338	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	2384	C
1	C1	2396	U
1	C1	2397	G
1	C1	2399	G
1	C1	2407	A
1	C1	2409	A
1	C1	2410	G
1	C1	2413	G
1	C1	2414	G
1	C1	2415	U
1	C1	2422	U
1	C1	2424	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	2425	G
1	C1	2428	G
1	C1	2430	A
1	C1	2434	U
1	C1	2435	C
1	C1	2436	G
1	C1	2437	G
1	C1	2438	C
1	C1	2439	G
1	C1	2442	A
1	C1	2443	G
1	C1	2444	U
1	C1	2449	U
1	C1	2453	A
1	C1	2456	A
1	C1	2464	U
1	C1	2465	G
1	C1	2466	U
1	C1	2467	U
1	C1	2484	G
1	C1	2551	A
1	C1	2553	A
1	C1	2558	C
1	C1	2560	G
1	C1	2564	G
1	C1	2730	C
1	C1	2735	G
1	C1	2736	A
1	C1	2738	A
1	C1	2739	U
1	C1	2740	U
1	C1	2749	G
1	C1	2759	A
1	C1	2760	A
1	C1	2761	A
1	C1	2765	U
1	C1	2775	A
1	C1	2777	A
1	C1	2778	A
1	C1	2782	G
1	C1	2783	C
1	C1	2784	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	2786	G
1	C1	2806	G
1	C1	2818	U
1	C1	2819	U
1	C1	2820	U
1	C1	2845	A
1	C1	2846	U
1	C1	2847	C
1	C1	2856	G
1	C1	2857	C
1	C1	2862	U
1	C1	2869	A
1	C1	2874	U
1	C1	2889	C
1	C1	2893	U
1	C1	2894	A
1	C1	2899	A
1	C1	2901	G
1	C1	2902	U
1	C1	2917	C
1	C1	2922	G
1	C1	2923	U
1	C1	2926	G
1	C1	2935	G
1	C1	2936	U
1	C1	2942	C
1	C1	2948	G
1	C1	2950	U
1	C1	2954	C
1	C1	2955	U
1	C1	2956	C
1	C1	2969	A
1	C1	3006	A
1	C1	3014	U
1	C1	3015	U
1	C1	3016	G
1	C1	3035	G
1	C1	3036	U
1	C1	3037	G
1	C1	3043	A
1	C1	3049	C
1	C1	3050	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	3110	C
1	C1	3111	U
1	C1	3112	A
1	C1	3113	C
1	C1	3118	A
1	C1	3122	U
1	C1	3124	U
1	C1	3126	G
1	C1	3127	A
1	C1	3130	U
1	C1	3131	A
1	C1	3132	U
1	C1	3134	A
1	C1	3139	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	3168	U
1	C1	3170	C
1	C1	3171	C
1	C1	3178	G
1	C1	3181	C
1	C1	3183	C
1	C1	3185	A
1	C1	3188	U
1	C1	3199	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	3205	C
1	C1	3209	U
1	C1	3210	U
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	3259	U
1	C1	3270	C
1	C1	3274	U
1	C1	3280	G
1	C1	3281	U
1	C1	3282	A
1	C1	3285	G
1	C1	3291	U
1	C1	3293	G
1	C1	3295	U
1	C1	3298	U
1	C1	3309	G
1	C1	3318	C
1	C1	3322	C
1	C1	3323	C
1	C1	3324	U
1	C1	3325	U
1	C1	3330	U
1	C1	3331	A
1	C1	3332	G
1	C1	3333	A
2	C2	34	U
2	C2	35	C
2	C2	59	A
2	C2	61	A
2	C2	62	A
2	C2	63	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	C2	81	U
2	C2	82	U
2	C2	84	C
2	C2	86	U
2	C2	87	G
2	C2	90	U
2	C2	95	G
2	C2	103	G
2	C2	104	A
2	C2	106	C
2	C2	109	A
2	C2	110	C
2	C2	111	A
2	C2	112	U
2	C2	113	U
2	C2	125	U
2	C2	148	G
2	C2	158	U
2	C2	163	C
2	C2	165	U
2	C2	166	C
2	C2	168	A
2	C2	173	U
2	C2	174	G
2	C2	181	U
2	C2	189	A
2	C2	195	G
2	C2	196	G
2	C2	203	G
2	C2	212	G
2	C2	213	A
2	C2	214	A
2	C2	215	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	294	A
2	C2	295	G
2	C2	300	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	C2	302	A

All (41) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	132	C
1	C1	150	G
1	C1	412	G
1	C1	445	A
1	C1	446	U
1	C1	524	A
1	C1	526	G
1	C1	543	G
1	C1	590	C
1	C1	835	G
1	C1	862	C
1	C1	870	U
1	C1	886	U
1	C1	897	G
1	C1	959	C
1	C1	964	A
1	C1	1063	C
1	C1	1134	G
1	C1	1136	A
1	C1	2301	C
1	C1	2333	G
1	C1	2360	A
1	C1	2759	A
1	C1	2777	A
1	C1	2785	U
1	C1	2817	U
1	C1	2898	A
1	C1	2925	A
1	C1	3013	U
1	C1	3014	U
1	C1	3078	U
1	C1	3131	A
1	C1	3162	A
1	C1	3204	G
1	C1	3209	U
1	C1	3229	G
1	C1	3255	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	3257	U
1	C1	3297	U
1	C1	3330	U
2	C2	102	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	TPO	CC	163	5	8,10,11	0.78	0	10,14,16	1.38	2 (20%)
5	SEP	CC	160	5	8,9,10	1.60	1 (12%)	7,12,14	1.22	1 (14%)

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	TPO	CC	163	5	-	7/9/11/13	-
5	SEP	CC	160	5	-	0/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	CC	160	SEP	P-O1P	3.53	1.61	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	CC	163	TPO	O-C-CA	-2.85	117.44	124.77
5	CC	160	SEP	OG-CB-CA	2.61	110.68	108.14

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	CC	163	TPO	P-OG1-CB	2.43	129.94	123.33

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	CC	163	TPO	N-CA-CB-OG1
5	CC	163	TPO	C-CA-CB-CG2
5	CC	163	TPO	O-C-CA-CB
5	CC	163	TPO	CG2-CB-OG1-P
5	CC	163	TPO	CB-OG1-P-O1P
5	CC	163	TPO	CB-OG1-P-O2P
5	CC	163	TPO	N-CA-CB-CG2

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	$\# Z > 2$
59	GTP	CH	1001	-	33,34,34	0.97	2 (6%)	50,54,54	1.60	8 (16%)

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
59	GTP	CH	1001	-	-	3/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	CH	1001	GTP	PB-O3A	2.17	1.61	1.59
59	CH	1001	GTP	C2-N3	2.11	1.38	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	CH	1001	GTP	C5-C4-N3	-5.04	120.37	128.39
59	CH	1001	GTP	C2-N3-C4	4.67	120.34	112.30
59	CH	1001	GTP	N9-C4-N3	3.14	132.24	125.95
59	CH	1001	GTP	C2-N1-C6	-2.90	119.85	125.11
59	CH	1001	GTP	N9-C8-N7	-2.69	108.40	113.40
59	CH	1001	GTP	C8-N7-C5	2.58	108.85	104.26
59	CH	1001	GTP	C5-C6-N1	2.51	119.63	113.25
59	CH	1001	GTP	O6-C6-C5	-2.31	120.44	126.53

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	CH	1001	GTP	C5'-O5'-PA-O3A
59	CH	1001	GTP	PB-O3A-PA-O2A
59	CH	1001	GTP	C4'-C5'-O5'-PA

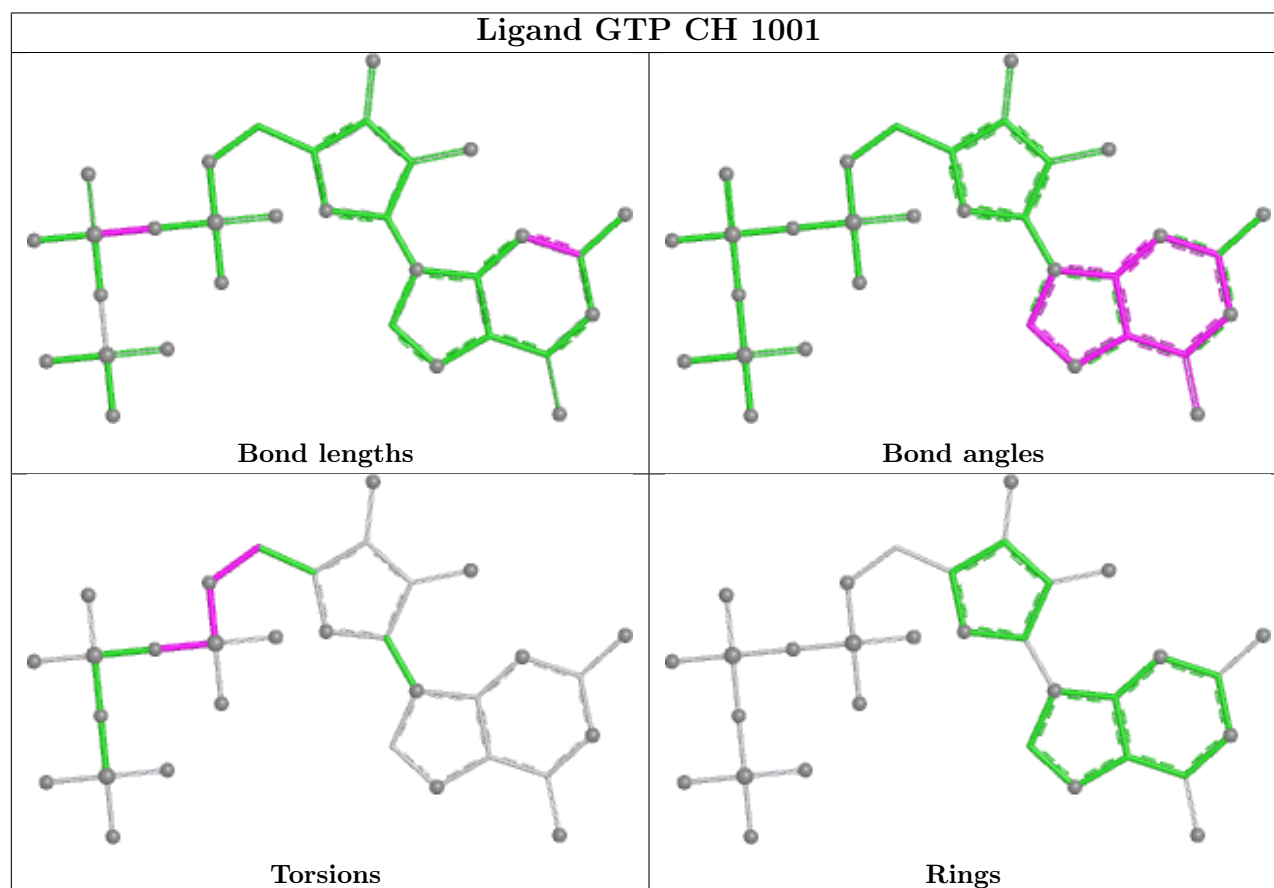
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	CH	1001	GTP	3	0

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

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

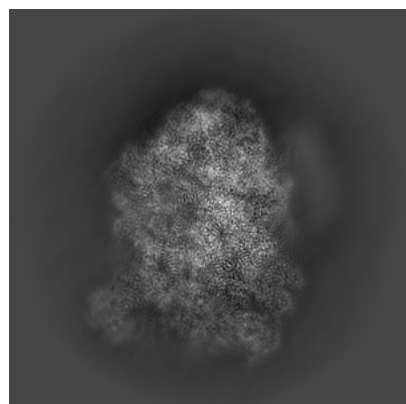
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35288. These allow visual inspection of the internal detail of the map and identification of artifacts.

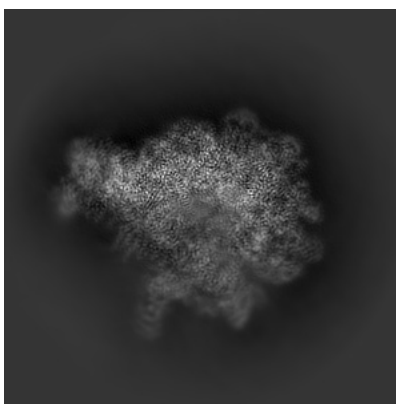
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

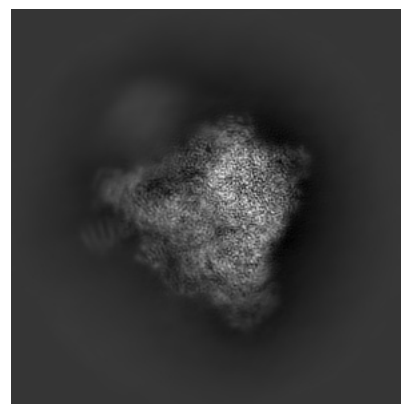
6.1.1 Primary map



X

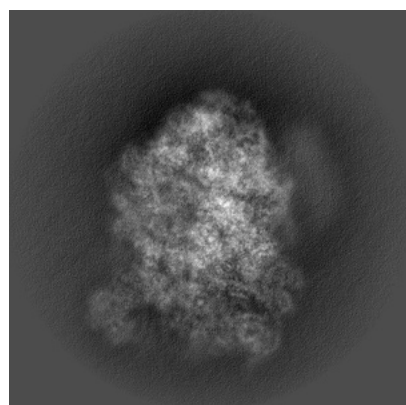


Y

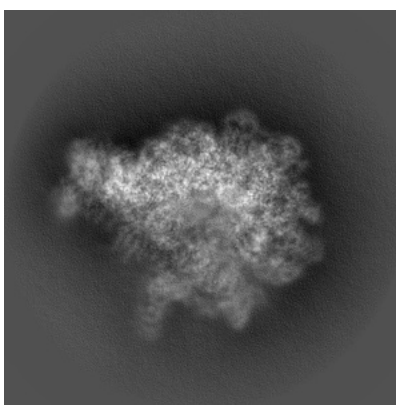


Z

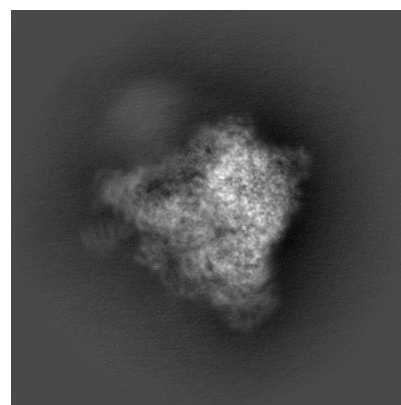
6.1.2 Raw map



X



Y

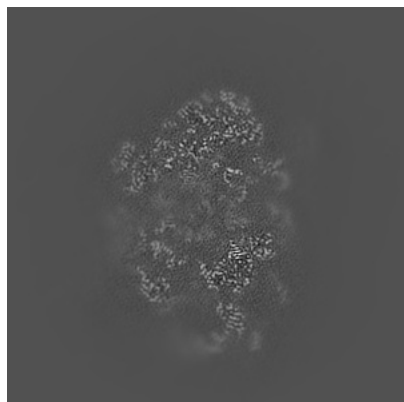


Z

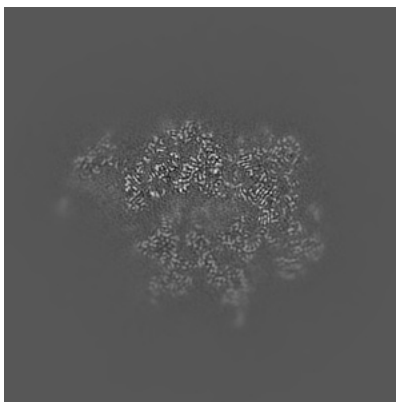
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

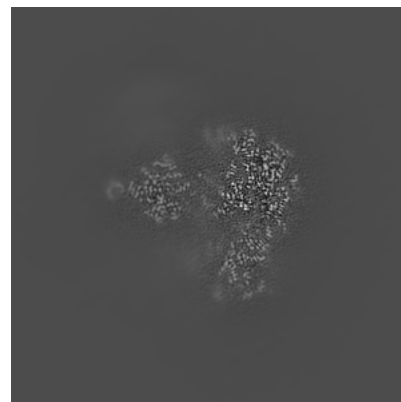
6.2.1 Primary map



X Index: 210

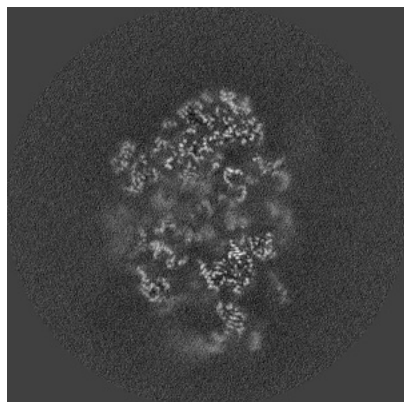


Y Index: 210

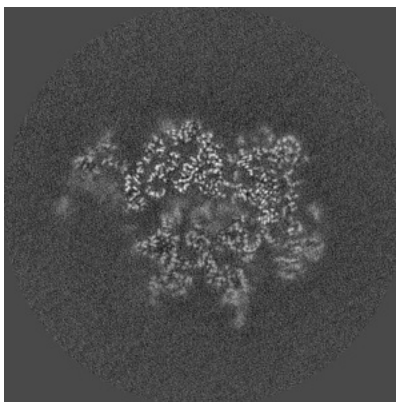


Z Index: 210

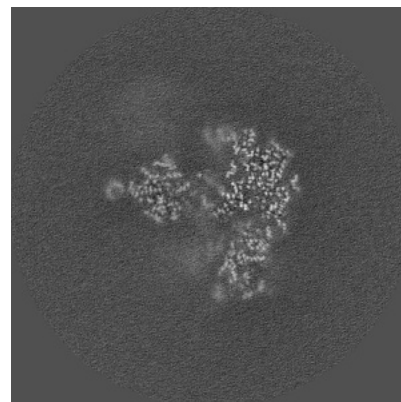
6.2.2 Raw map



X Index: 210



Y Index: 210

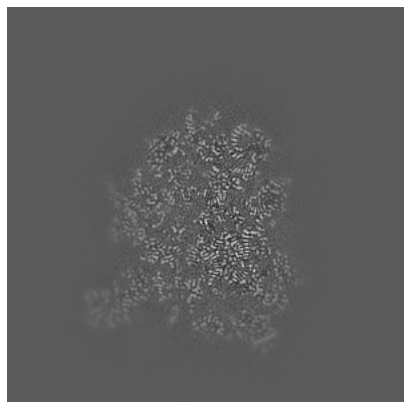


Z Index: 210

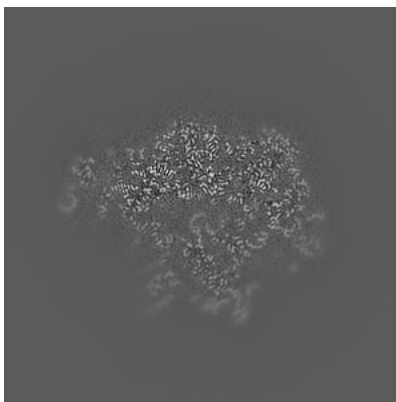
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

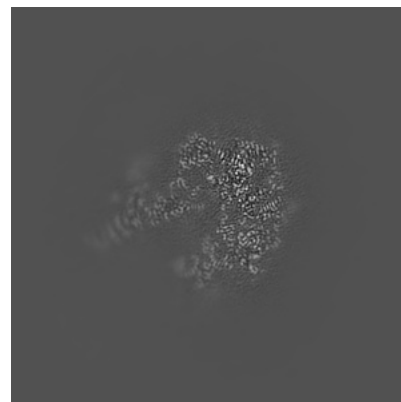
6.3.1 Primary map



X Index: 244

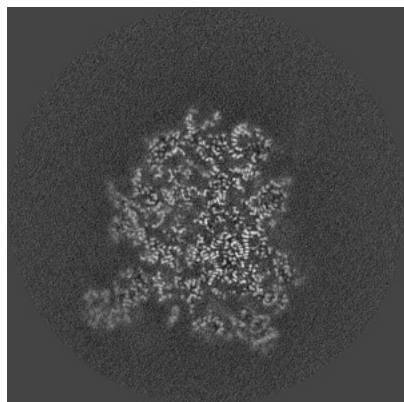


Y Index: 221

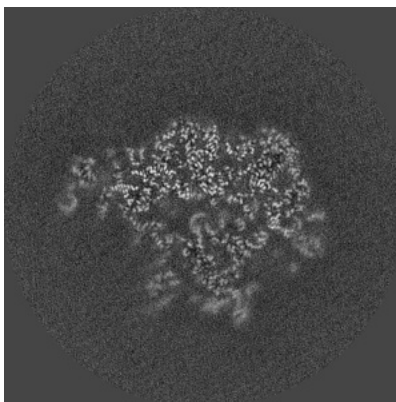


Z Index: 166

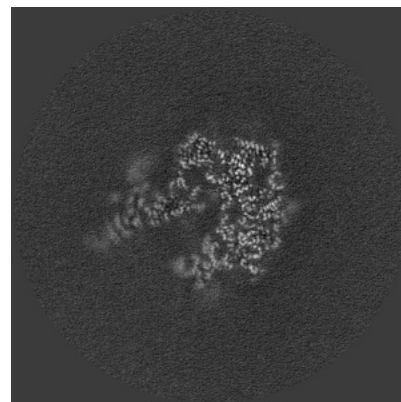
6.3.2 Raw map



X Index: 244



Y Index: 221

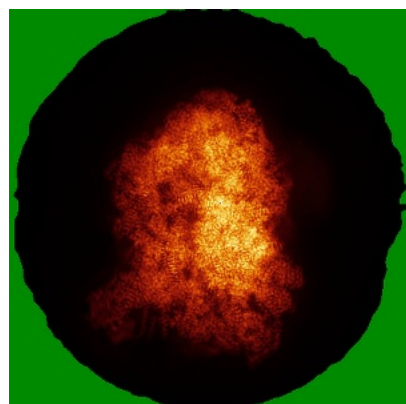


Z Index: 166

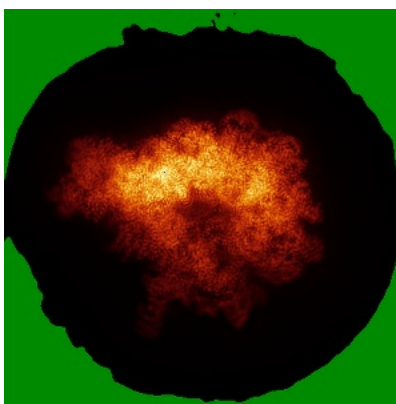
The images above show the largest variance slices of the map in three orthogonal directions.

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

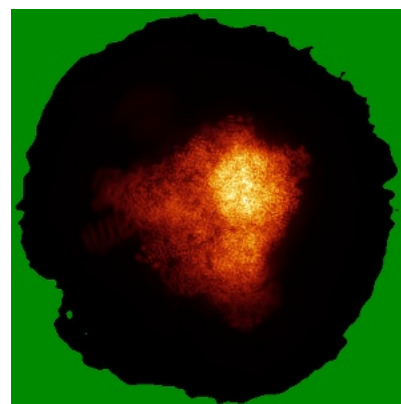
6.4.1 Primary map



X

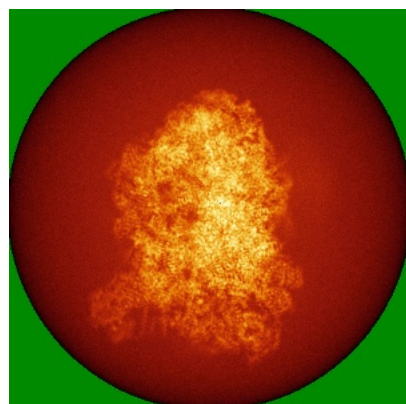


Y

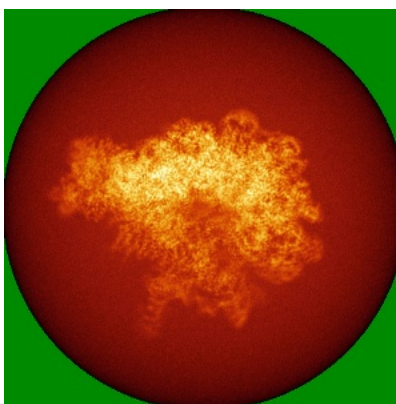


Z

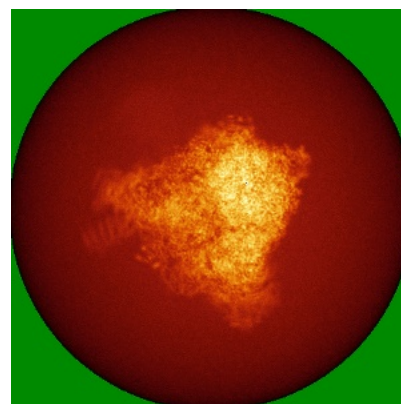
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



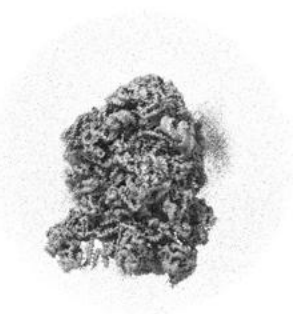
Y



Z

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

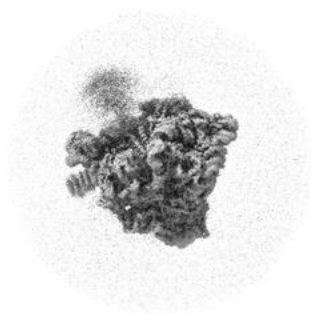
6.5.2 Raw map



X



Y



Z

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

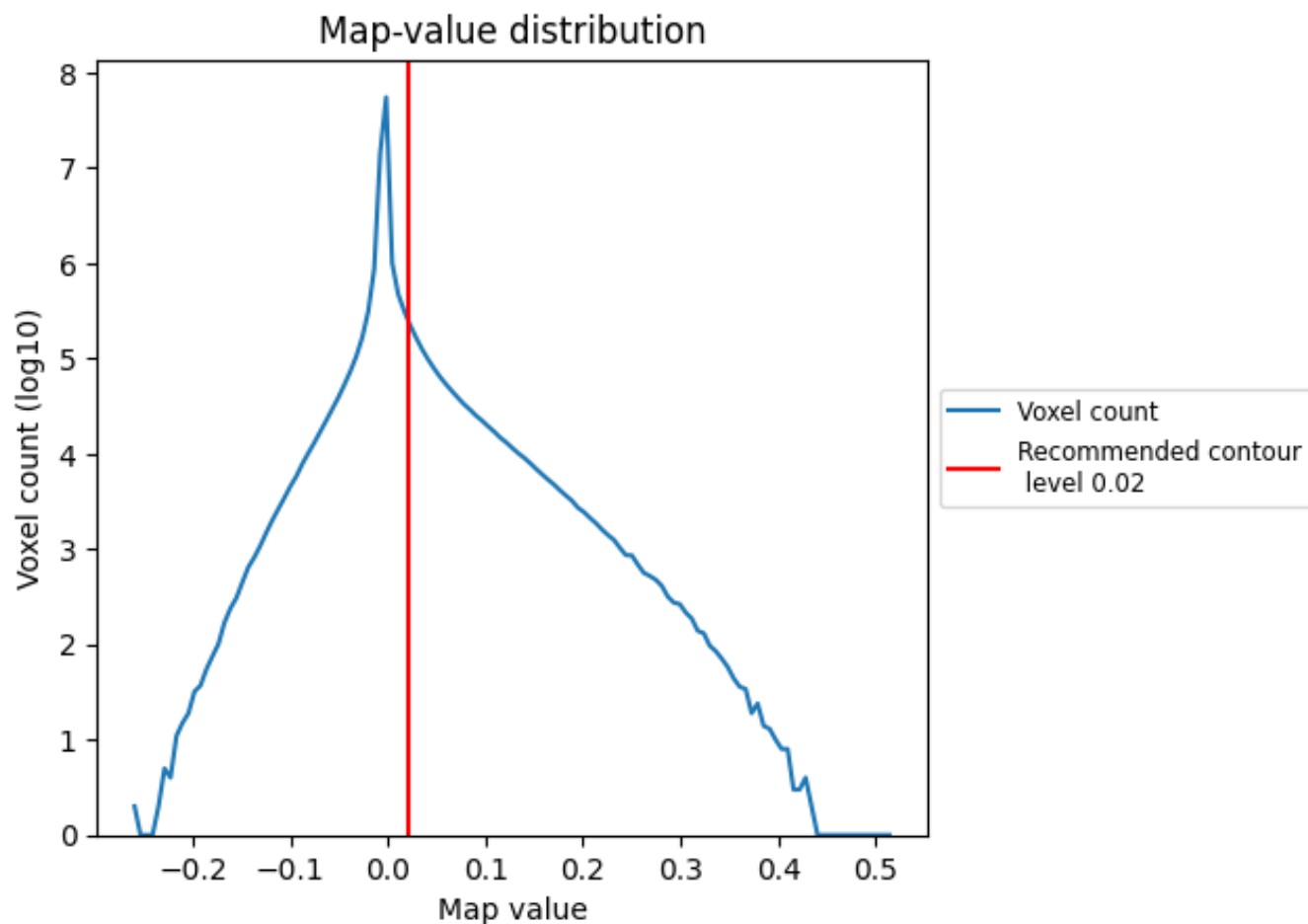
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

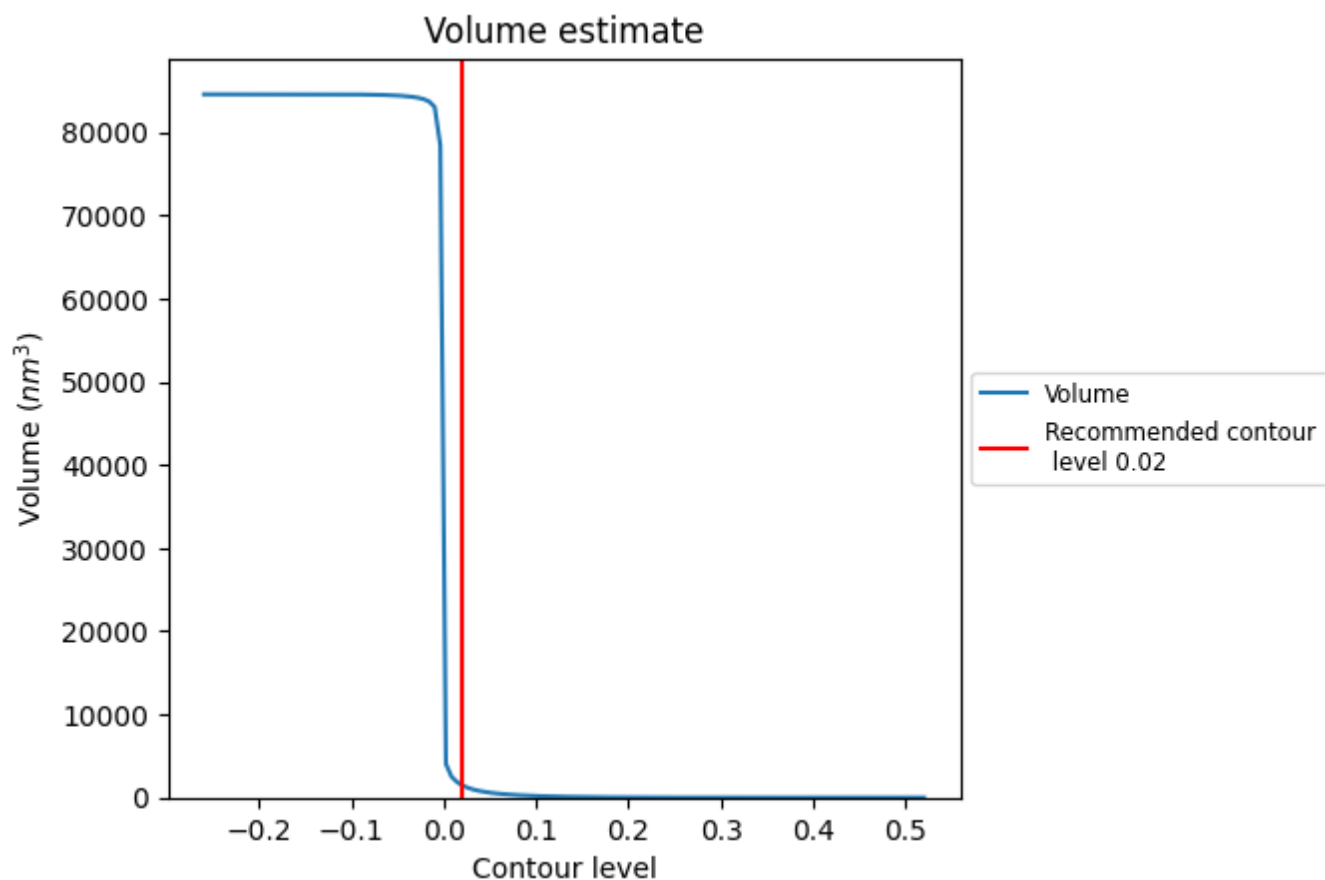
This section contains the results of statistical analysis of the map.

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.

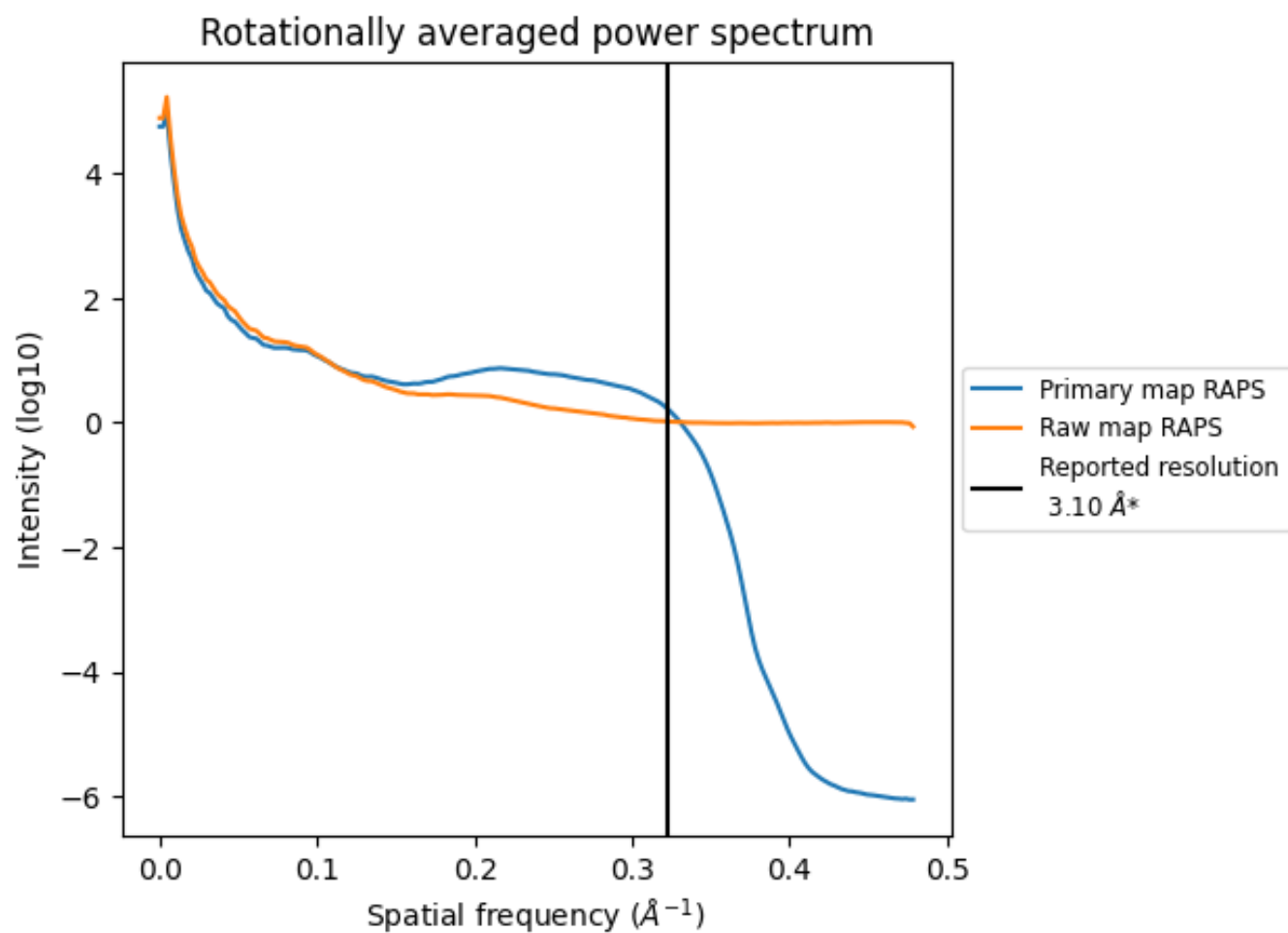
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1474 nm^3 ; this corresponds to an approximate mass of 1331 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 ⓘ

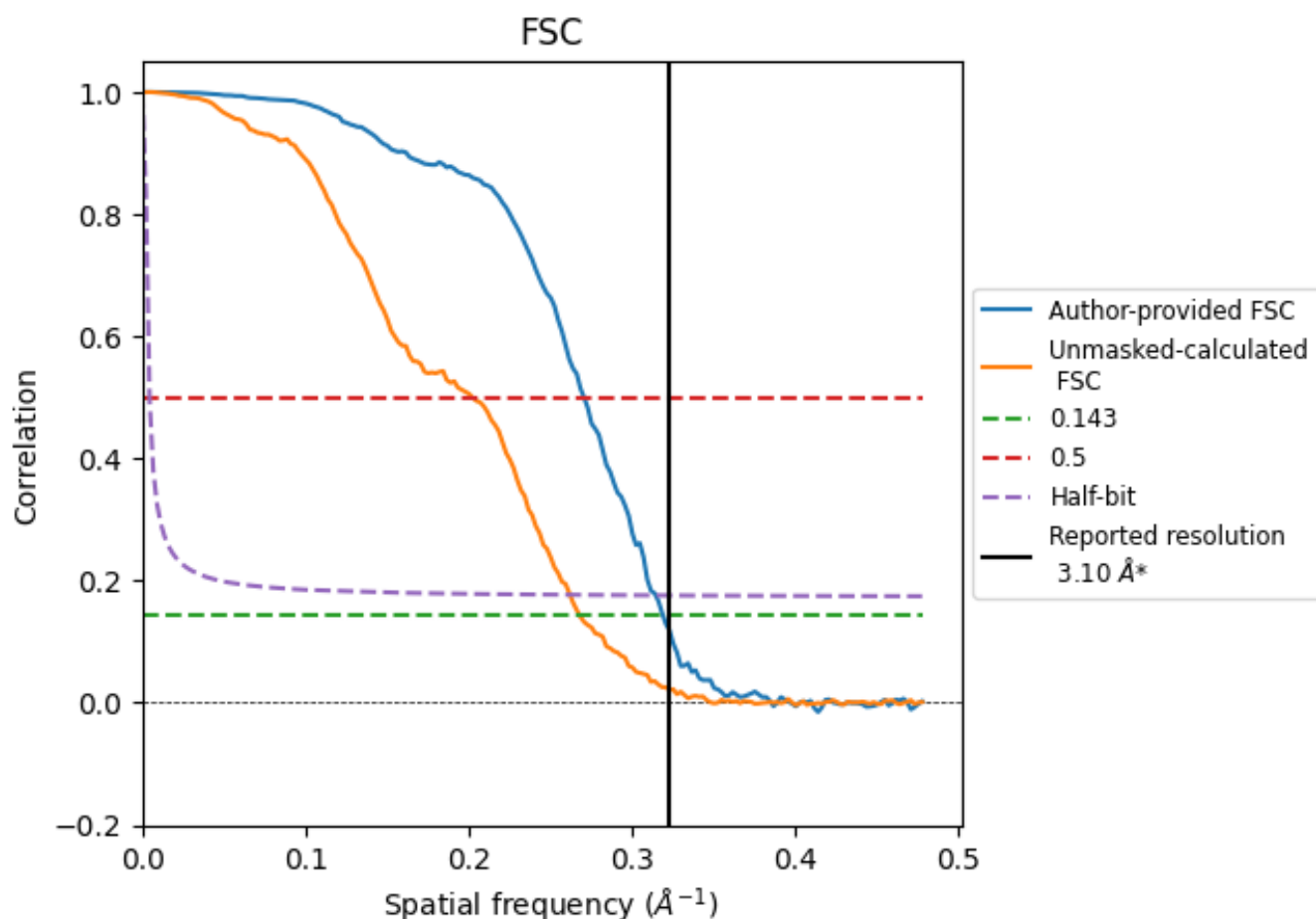


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

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](#)

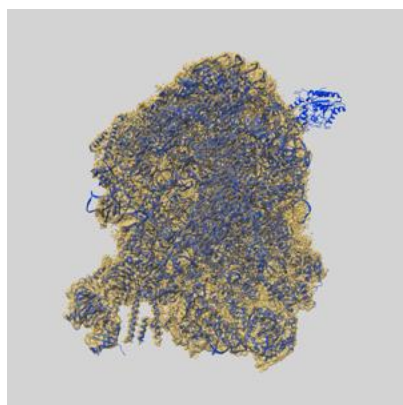
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.13	3.69	3.17
Unmasked-calculated*	3.73	4.94	3.81

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

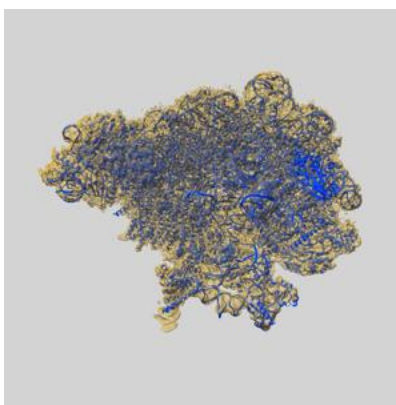
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35288 and PDB model 8I9Y. Per-residue inclusion information can be found in section 3 on page 19.

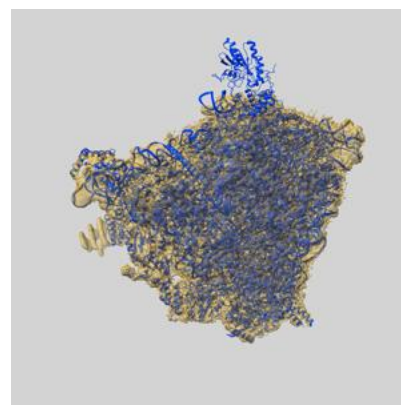
9.1 Map-model overlay [i](#)



X



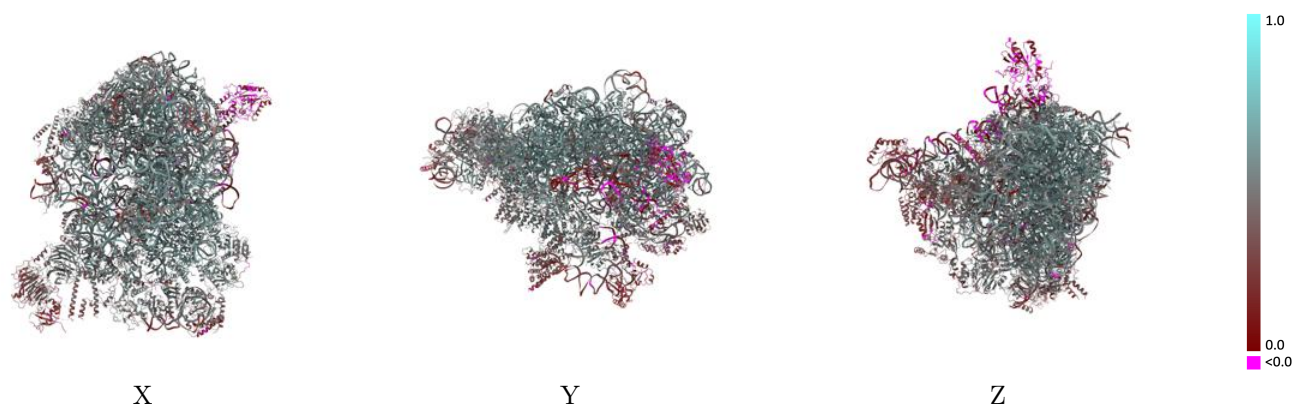
Y



Z

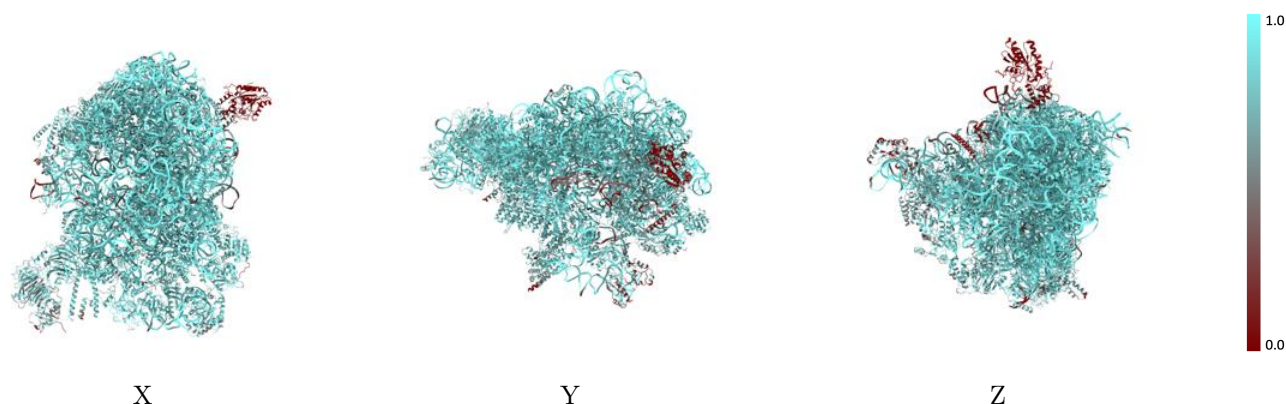
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



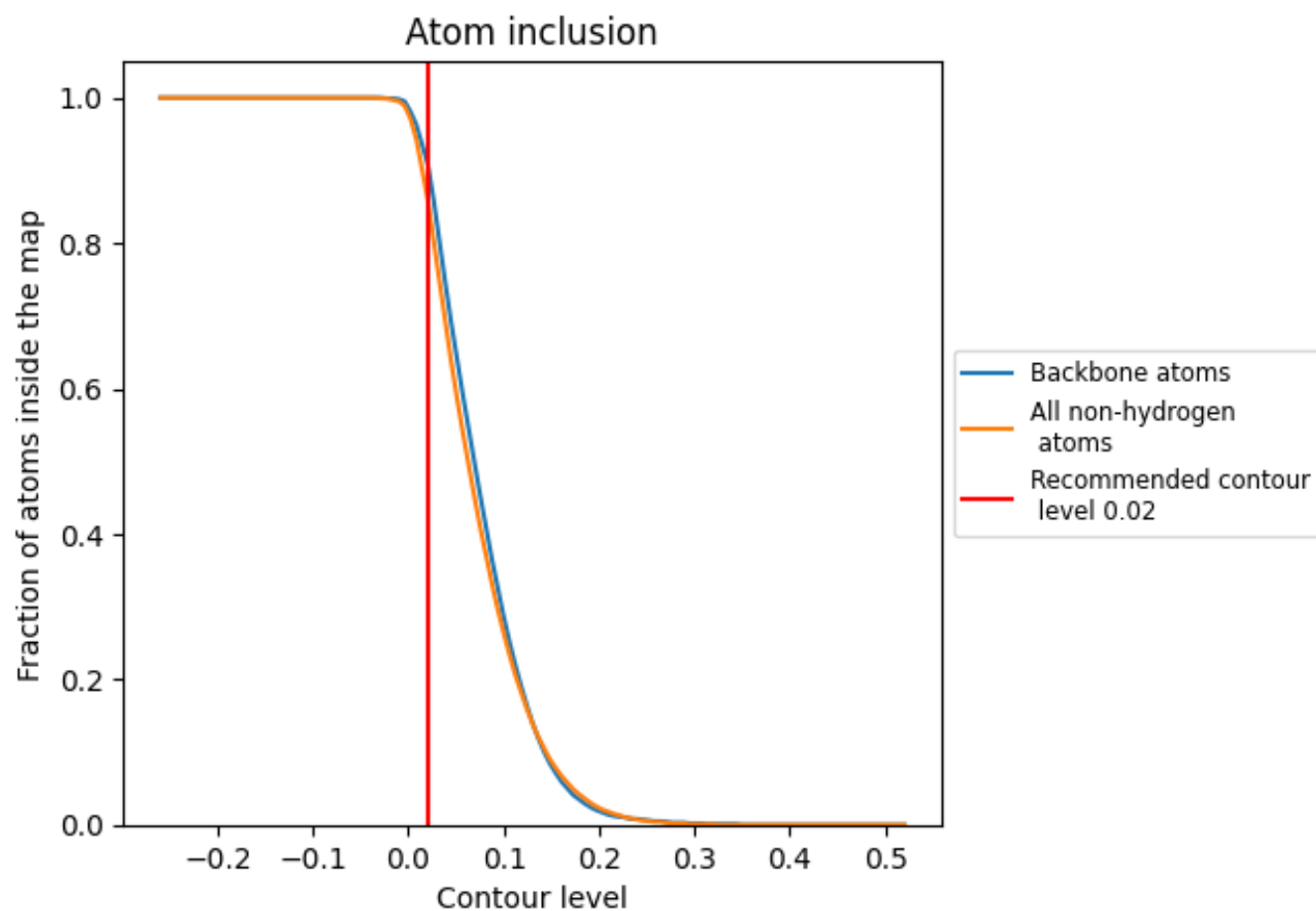
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 ⓘ



At the recommended contour level, 91% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8630	 0.4710
C1	 0.9200	 0.4890
C2	 0.9280	 0.4950
CA	 0.9200	 0.5400
CB	 0.8170	 0.4190
CC	 0.8580	 0.4760
CD	 0.6650	 0.3030
CE	 0.8630	 0.4880
CF	 0.8060	 0.4020
CG	 0.8790	 0.5030
CH	 0.8140	 0.4370
CI	 0.8340	 0.4300
CJ	 0.8530	 0.4660
CK	 0.8520	 0.4740
CL	 0.2330	 0.1480
CM	 0.8200	 0.4370
CN	 0.7850	 0.4530
CO	 0.8440	 0.4870
CP	 0.8640	 0.4730
CQ	 0.8070	 0.4290
CR	 0.9080	 0.5300
CS	 0.8090	 0.4480
CT	 0.8600	 0.4680
CU	 0.8710	 0.5000
CV	 0.9380	 0.5550
CX	 0.8250	 0.4730
CY	 0.6990	 0.3240
Cz	 0.4860	 0.2640
LB	 0.8780	 0.5090
LC	 0.9420	 0.5620
LE	 0.8940	 0.4990
LF	 0.9040	 0.5260
LG	 0.9110	 0.5450
LH	 0.8790	 0.4970
LK	 0.6180	 0.2110



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
LL	 0.9480	 0.5740
LM	 0.9220	 0.5360
LN	 0.9660	 0.5990
LO	 0.9300	 0.5520
LP	 0.8900	 0.5050
LQ	 0.9050	 0.5240
LR	 0.8530	 0.4610
LS	 0.9120	 0.5260
LT	 0.6510	 0.3180
LU	 0.8060	 0.4510
LV	 0.7440	 0.4470
LX	 0.8830	 0.5100
LY	 0.9060	 0.5260
LZ	 0.8660	 0.4930
Lc	 0.7930	 0.4320
Ld	 0.8810	 0.5280
Le	 0.9180	 0.5490
Lf	 0.9470	 0.5740
Lg	 0.8690	 0.5130
Lh	 0.8860	 0.5060
Li	 0.8960	 0.5190
Lj	 0.9520	 0.5840
Lk	 0.8350	 0.4490
Ll	 0.8480	 0.4330
Lq	 0.4710	 0.1900