



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 05:54 AM UTC

PDB ID : 8EUB / pdb_00008eub
EMDB ID : EMD-28610
Title : Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), eEF2 and GDP, Structure I
Authors : Zhao, Y.; Rai, J.; Li, H.
Deposited on : 2022-10-18
Resolution : 2.52 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

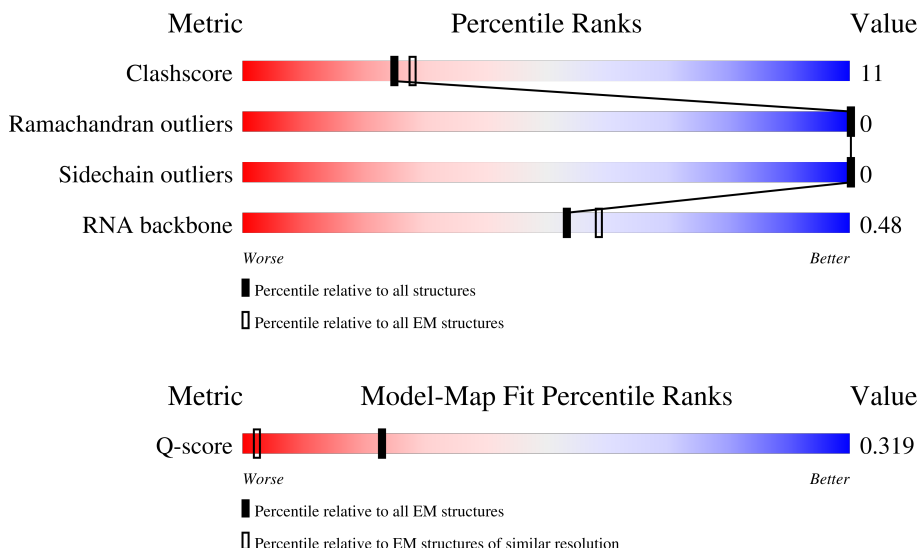
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.52 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.



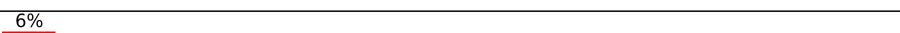
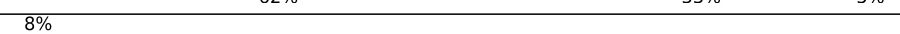
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7226 (2.02 - 3.02)

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	BA	252	
2	BB	255	
3	BC	254	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	BE	261	
5	BG	236	
6	BH	190	
7	BI	200	
8	BJ	197	
9	BL	156	
10	BN	151	
11	BO	137	
12	BV	87	
13	BW	130	
14	BX	145	
15	BY	135	
16	Ba	119	
17	Bb	82	
18	Be	63	
19	BD	240	
20	BF	225	
21	BK	105	
22	BP	142	
23	BQ	143	
24	BR	136	
25	BS	146	
26	BT	144	
27	BU	121	
28	BZ	108	

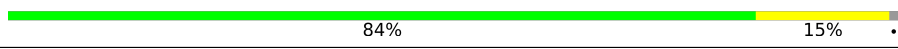
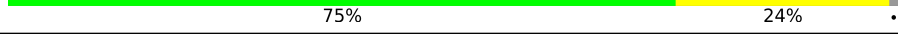
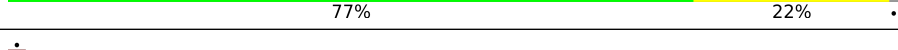
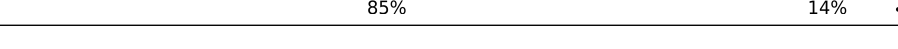
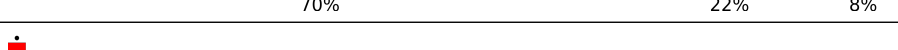
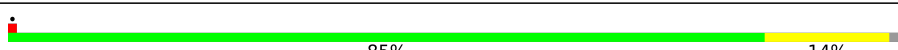
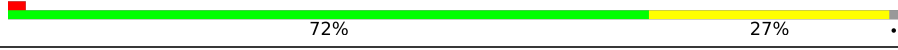
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	B5	1798	
33	AA	254	
34	AB	387	
35	AC	362	
36	A1	3360	
37	A3	121	
38	A4	158	
39	AD	297	
40	AE	176	
41	AF	244	
42	AG	256	
43	AH	191	
44	AI	221	
45	AJ	174	
46	AL	199	
47	AM	138	
48	AN	204	
49	AO	199	
50	AP	184	
51	AQ	186	
52	AR	189	
53	AS	178	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	AT	160	
55	AU	121	
56	AV	137	
57	AW	155	
58	AX	142	
59	AY	127	
60	AZ	136	
61	Aa	149	
62	Ab	59	
63	Ac	105	
64	Ad	113	
65	Ae	130	
66	Af	107	
67	Ag	121	
68	Ah	120	
69	Ai	100	
70	Aj	88	
71	Ak	78	
72	Al	51	
73	Am	128	
74	An	25	
75	Ao	106	
76	Ap	92	
77	E	217	
78	EC	201	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	DC	842	
80	Bf	152	
81	BM	143	
82	VA	312	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 214074 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	BA	206	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 2 is a protein called RPS1A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	BB	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 3 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BC	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 4 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	BE	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 5 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 6 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	BH	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 7 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BI	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 8 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 9 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BL	155	Total	C	N	O	S	0	0
			1244	798	235	208	3		

- Molecule 10 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 11 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BO	127	Total	C	N	O	S	0	0
			941	578	186	174	3		

- Molecule 12 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 13 is a protein called RPS22A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 14 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 15 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BY	134	Total	C	N	O	S	0	0
			1073	676	208	189			

- Molecule 16 is a protein called RPS26B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Ba	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 17 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Bb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 18 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Be	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 19 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BD	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 20 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BF	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 21 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BK	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 22 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BP	124	Total	C	N	O	S	0	0
			991	631	187	166	7		

- Molecule 23 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	BQ	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 24 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BR	125	Total	C	N	O	S	0	0
			1000	625	188	185	2		

- Molecule 25 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 26 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BT	141	Total	C	N	O	S	0	0
			1095	685	206	202	2		

- Molecule 27 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BU	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 28 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	BZ	69	Total	C	N	O	0	0
			558	357	103	98		

- Molecule 29 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Bc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 30 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Bd	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 31 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bg	312	Total	C	N	O	S	0	0
			2401	1522	410	461	8		

- Molecule 32 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B5	1782	Total	C	N	O	P	1	0
			38004	17005	6718	12499	1782		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B5	1280	4AC	C	conflict	GB 1329886537
B5	1773	4AC	C	conflict	GB 1329886537

- Molecule 33 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AA	247	Total	C	N	O	S	0	0
			1878	1170	381	326	1		

- Molecule 34 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AB	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 35 is a protein called RPL4A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 36 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	A1	3198	Total	C	N	O	P	0	0
			68445	30596	12331	22320	3198		

- Molecule 37 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	A3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 38 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 39 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AD	292	Total	C	N	O	S	0	0
			2341	1478	408	453	2		

- Molecule 40 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AE	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 41 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AF	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 42 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AG	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 43 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AH	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 44 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AI	205	Total	C	N	O	S	0	0
			1672	1063	316	288	5		

- Molecule 45 is a protein called RPL11A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AJ	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 46 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	AL	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 47 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 48 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 49 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	AO	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 50 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AP	175	Total	C	N	O	S	0	0
			1388	862	277	249			

- Molecule 51 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 52 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AR	188	Total	C	N	O	S	0	0
			1521	935	326	260			

- Molecule 53 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AS	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 54 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 55 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	AU	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 56 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AV	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 57 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AW	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 58 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AX	121	Total	C	N	O	S	0	0
			968	623	170	173	2		

- Molecule 59 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	AY	126	Total	C	N	O	0	0
			993	625	192	176		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
60	AZ	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 61 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Aa	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 62 is a protein called RPL29 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	Ab	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 63 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Ac	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 64 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Ad	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 65 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ae	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 66 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Af	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 67 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ag	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 68 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ah	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 69 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Ai	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 70 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Aj	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 71 is a protein called RPL38 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ak	77	Total	C	N	O	S	0	0
			612	391	115	106			

- Molecule 72 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Al	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 73 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Am	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 74 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	An	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 75 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ao	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 76 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ap	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 77 is a protein called RPL1A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	E	217	Total	C	N	O	S	0	0
			1718	1097	299	312	10		

- Molecule 78 is a RNA chain called Taura syndrome virus (TSV) internal ribosome entry site (IRES) RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	EC	195	Total	C	N	O	P	0	0
			4128	1843	731	1359	195		

- Molecule 79 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	DC	824	Total	C	N	O	S	0	0
			6419	4085	1096	1208	30		

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Bf	75	Total	C	N	O	S	0	0
			605	386	116	99	4		

- Molecule 81 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BM	124	Total	C	N	O	S	0	0
			935	587	165	181	2		

- Molecule 82 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	VA	189	Total	C	N	O	S	0	0
			1473	942	257	270	4		

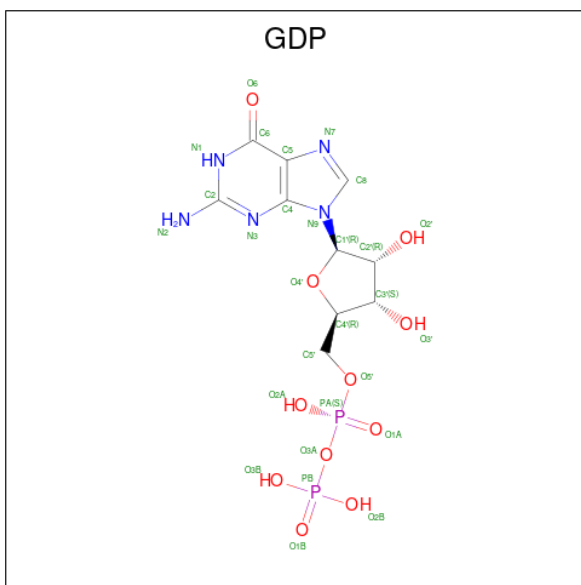
- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	B5	51	Total 51	Mg 51	0
83	AB	1	Total 1	Mg 1	0
83	A1	187	Total 187	Mg 187	0
83	A3	2	Total 2	Mg 2	0
83	A4	5	Total 5	Mg 5	0
83	AG	1	Total 1	Mg 1	0
83	AN	3	Total 3	Mg 3	0
83	AO	2	Total 2	Mg 2	0
83	AP	1	Total 1	Mg 1	0
83	Af	1	Total 1	Mg 1	0
83	Aj	1	Total 1	Mg 1	0

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
84	Ao	1	Total 1	Zn 1	0

- Molecule 85 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂) (labeled as "Ligand of Interest" by depositor).

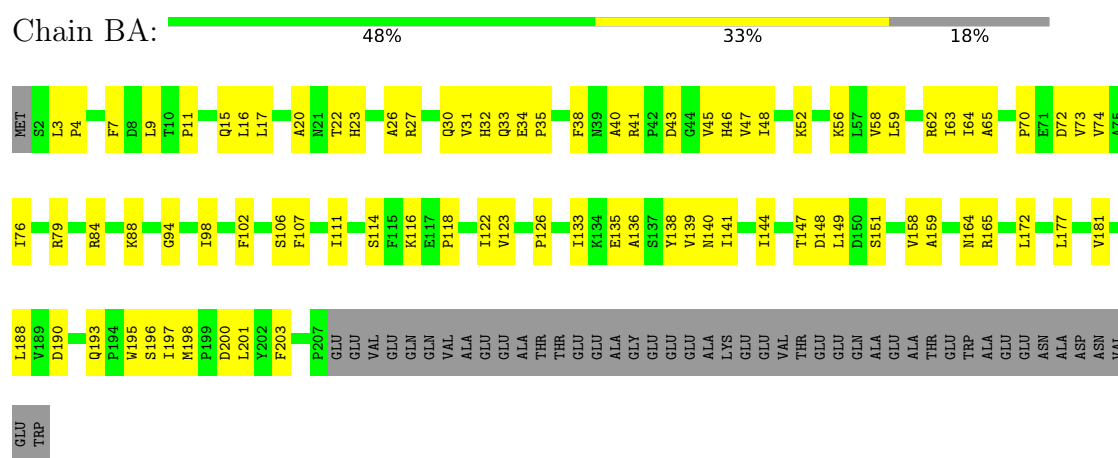


Mol	Chain	Residues	Atoms					AltConf
85	DC	1	Total	C	N	O	P	0
			28	10	5	11	2	

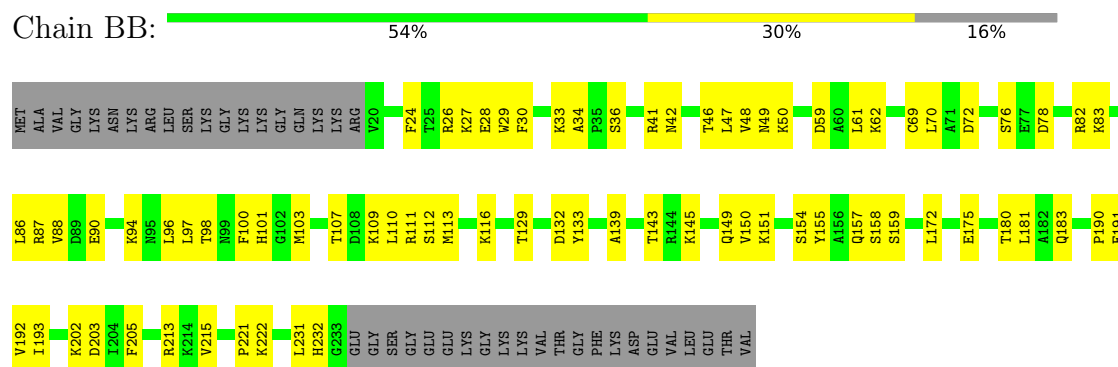
3 Residue-property plots

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.

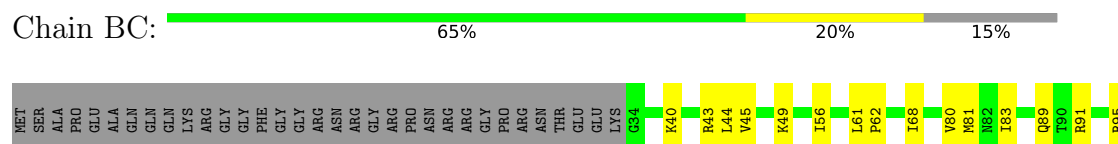
• Molecule 1: 40S ribosomal protein S0-A



• Molecule 2: RPS1A isoform 1

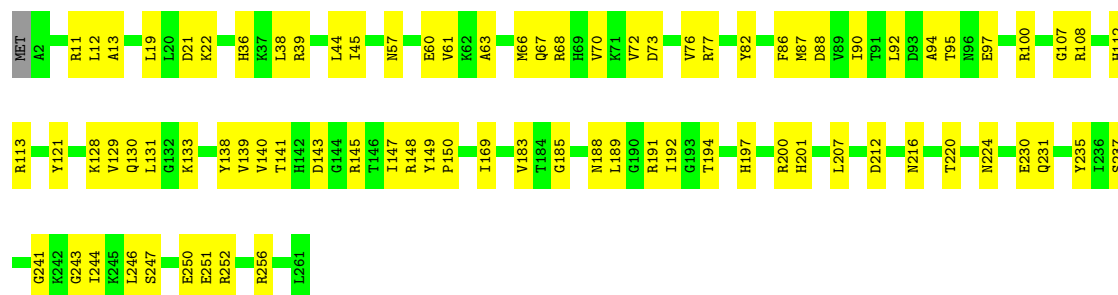


• Molecule 3: RPS2 isoform 1

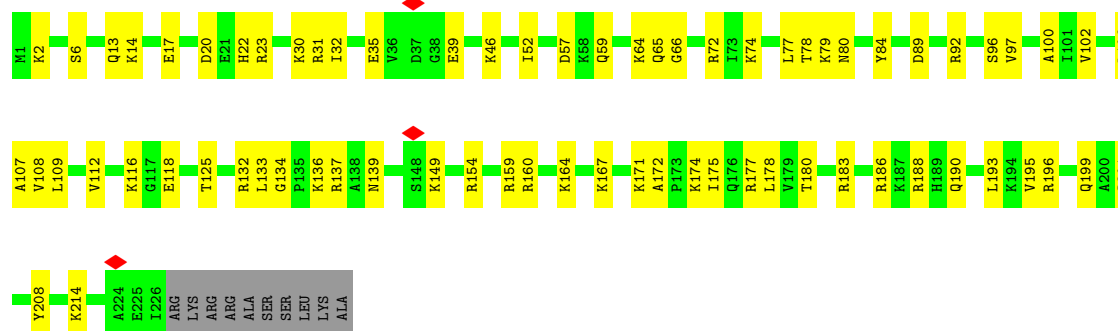




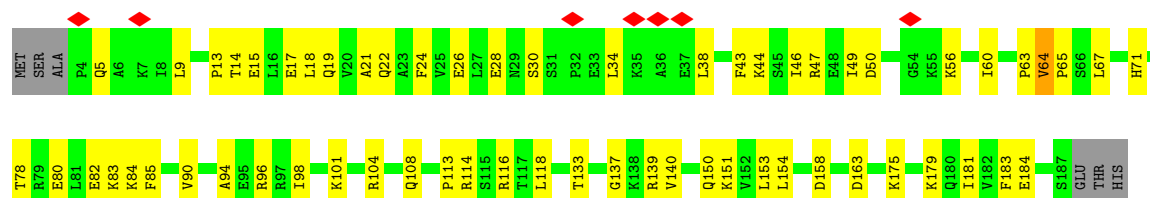
• Molecule 4: 40S ribosomal protein S4-A



• Molecule 5: 40S ribosomal protein S6-A

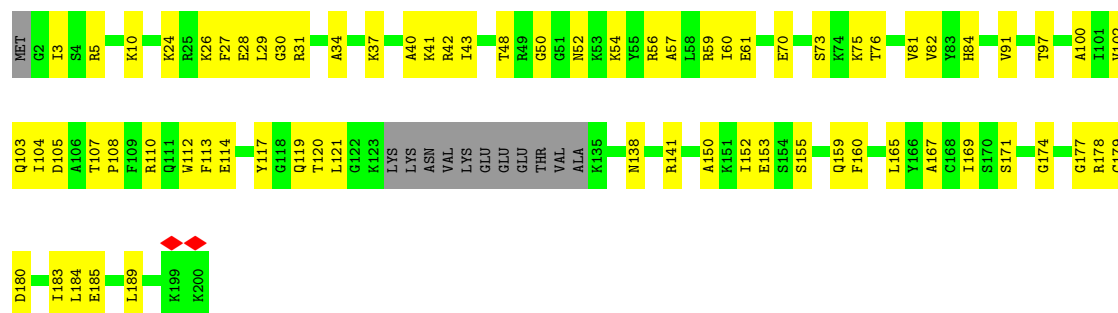


• Molecule 6: 40S ribosomal protein S7-A

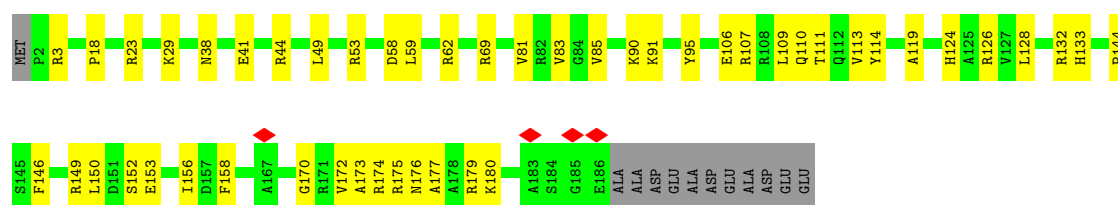


• Molecule 7: 40S ribosomal protein S8-A

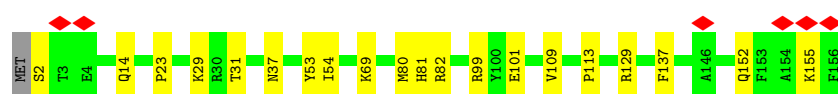
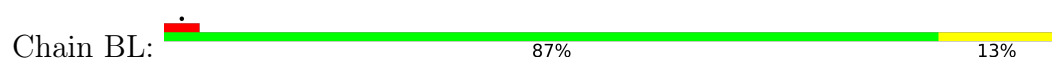




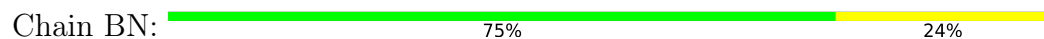
- Molecule 8: 40S ribosomal protein S9-A



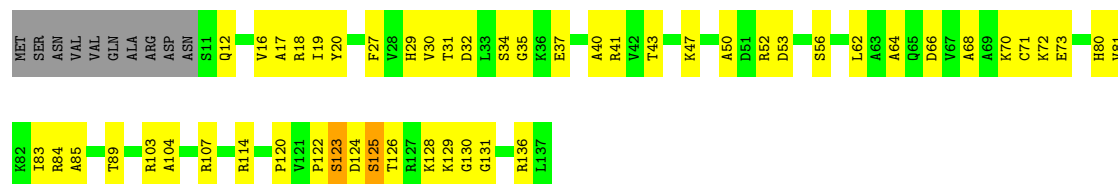
- Molecule 9: 40S ribosomal protein S11-A



- Molecule 10: 40S ribosomal protein S13



- Molecule 11: 40S ribosomal protein S14-A



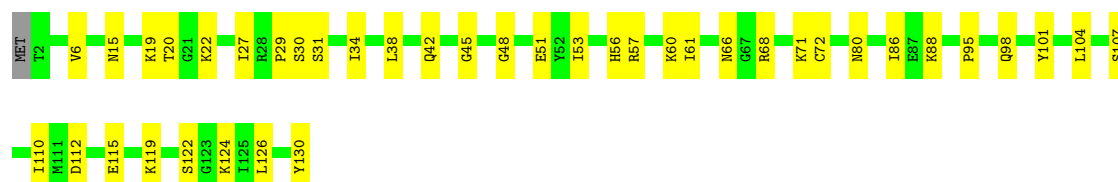
- Molecule 12: 40S ribosomal protein S21-A

Chain BV:  67% 33%



• Molecule 13: RPS22A isoform 1

Chain BW:  68% 31%



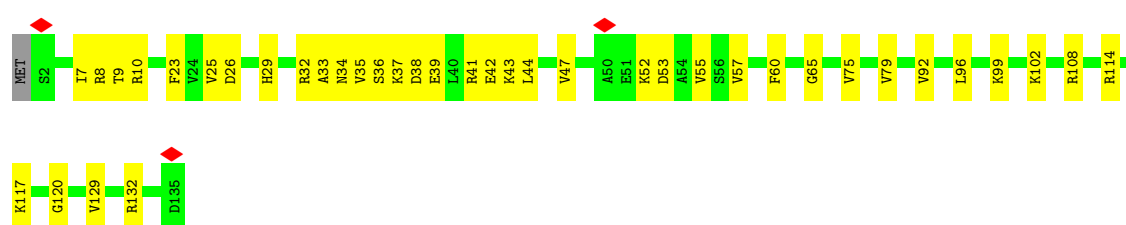
• Molecule 14: 40S ribosomal protein S23-A

Chain BX:  69% 30%



• Molecule 15: 40S ribosomal protein S24-A

Chain BY:  70% 29%



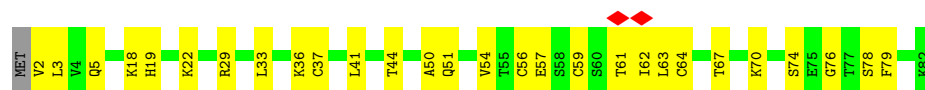
• Molecule 16: RPS26B isoform 1

Chain Ba:  54% 28% 18%



• Molecule 17: 40S ribosomal protein S27-A

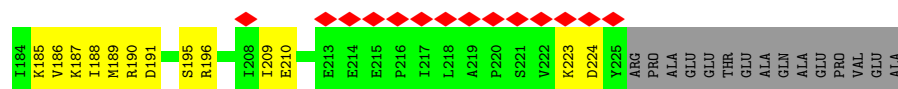
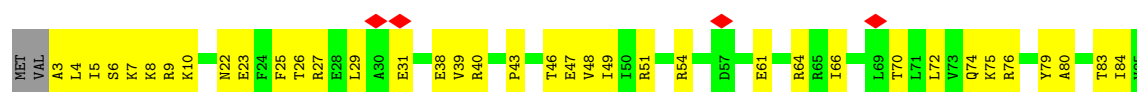
Chain Bb:  65% 34%



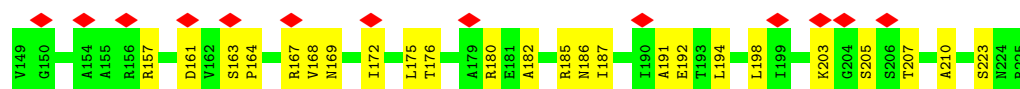
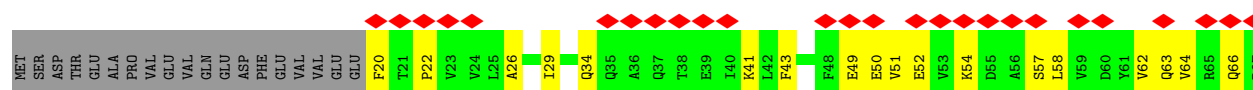
- Molecule 18: 40S ribosomal protein S30-A



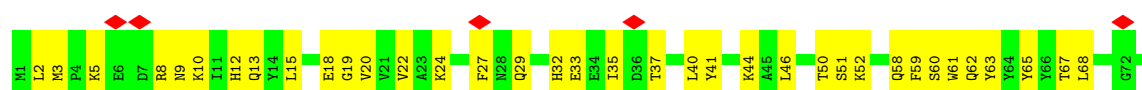
- Molecule 19: RPS3 isoform 1

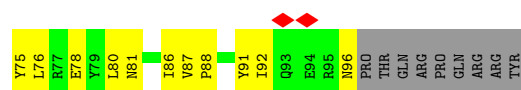


- Molecule 20: Rps5p

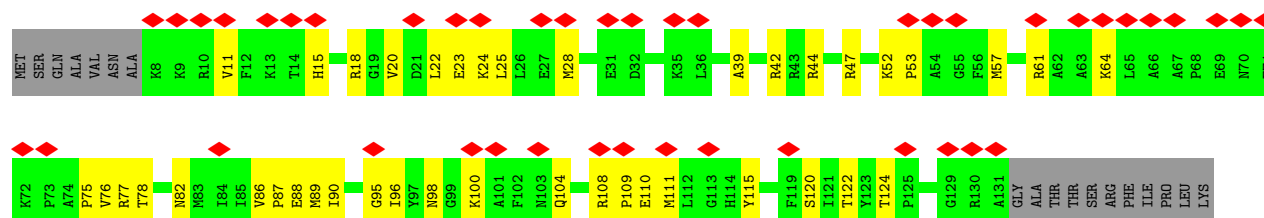


- Molecule 21: 40S ribosomal protein S10-A

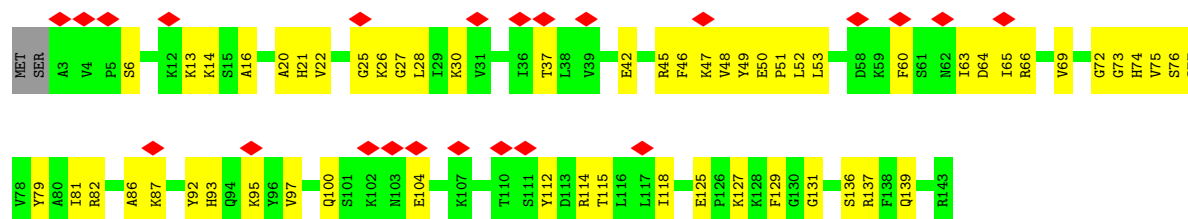




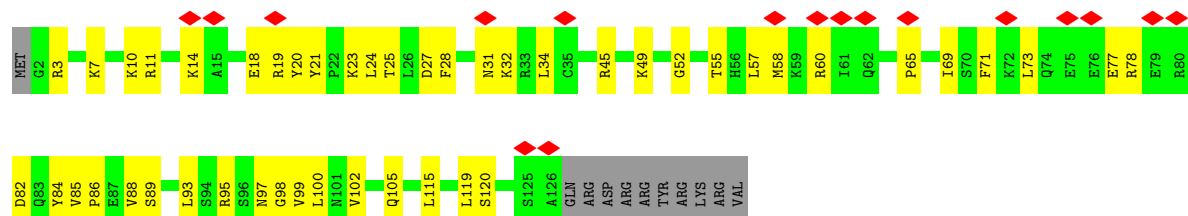
• Molecule 22: RPS15 isoform 1



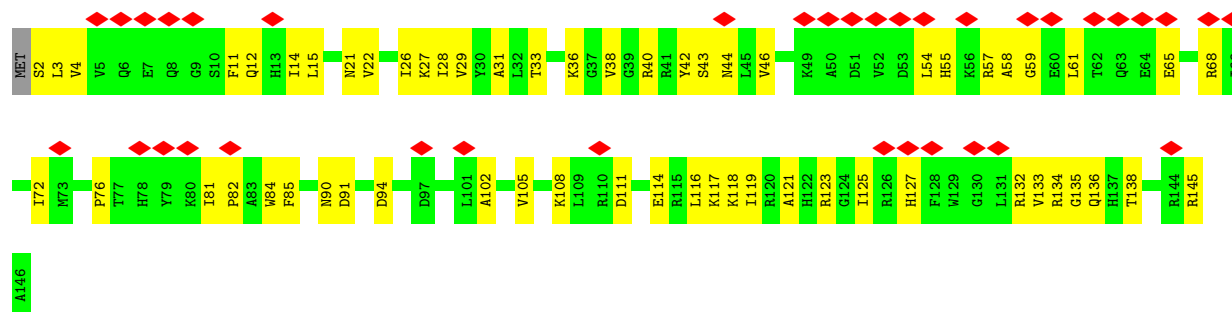
• Molecule 23: 40S ribosomal protein S16-A



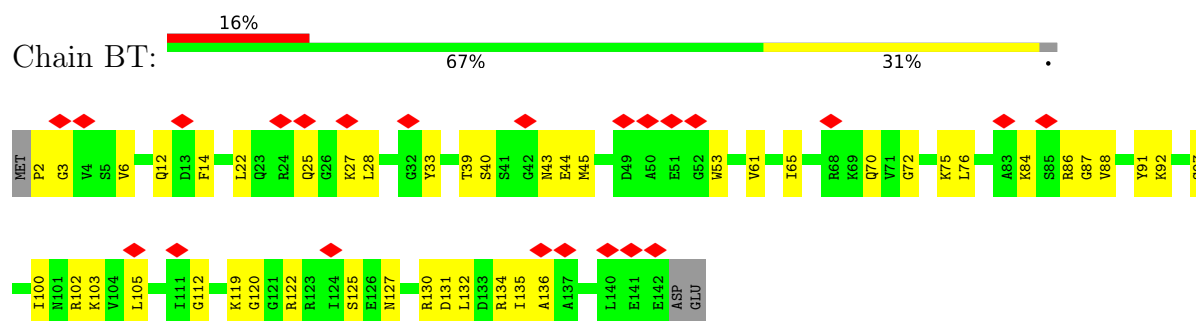
• Molecule 24: 40S ribosomal protein S17-A



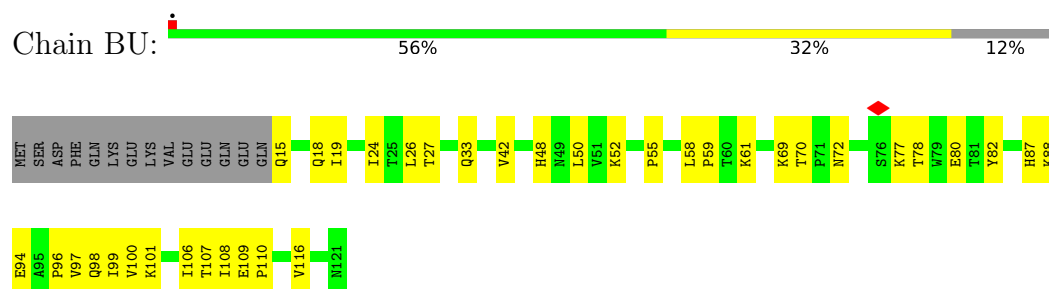
• Molecule 25: 40S ribosomal protein S18-A



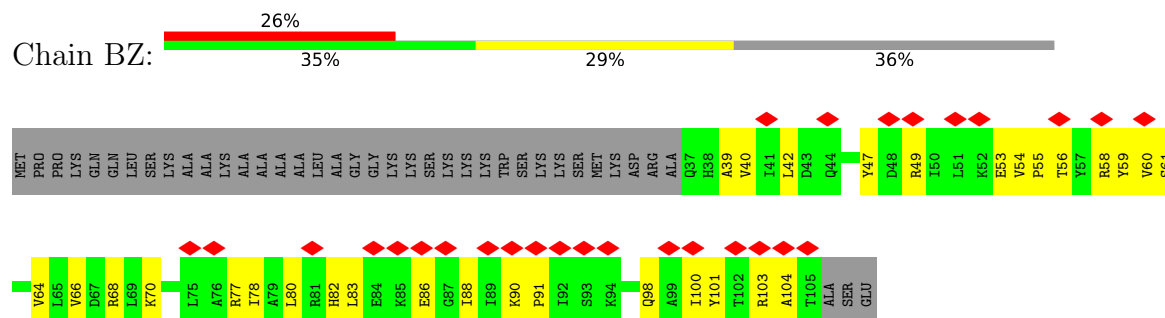
- Molecule 26: 40S ribosomal protein S19-A



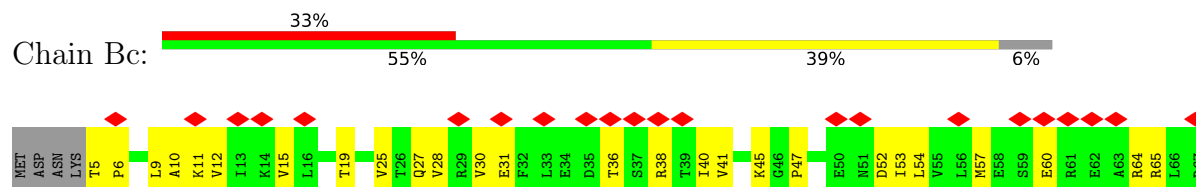
- Molecule 27: RPS20 isoform 1



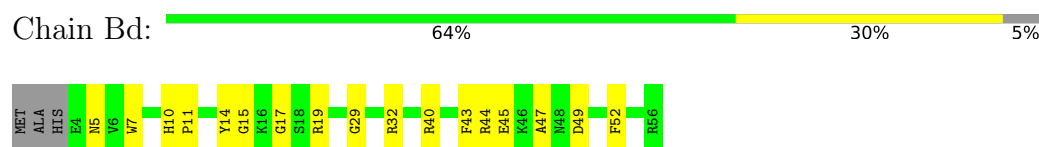
- Molecule 28: RPS25A isoform 1



- Molecule 29: RPS28A isoform 1

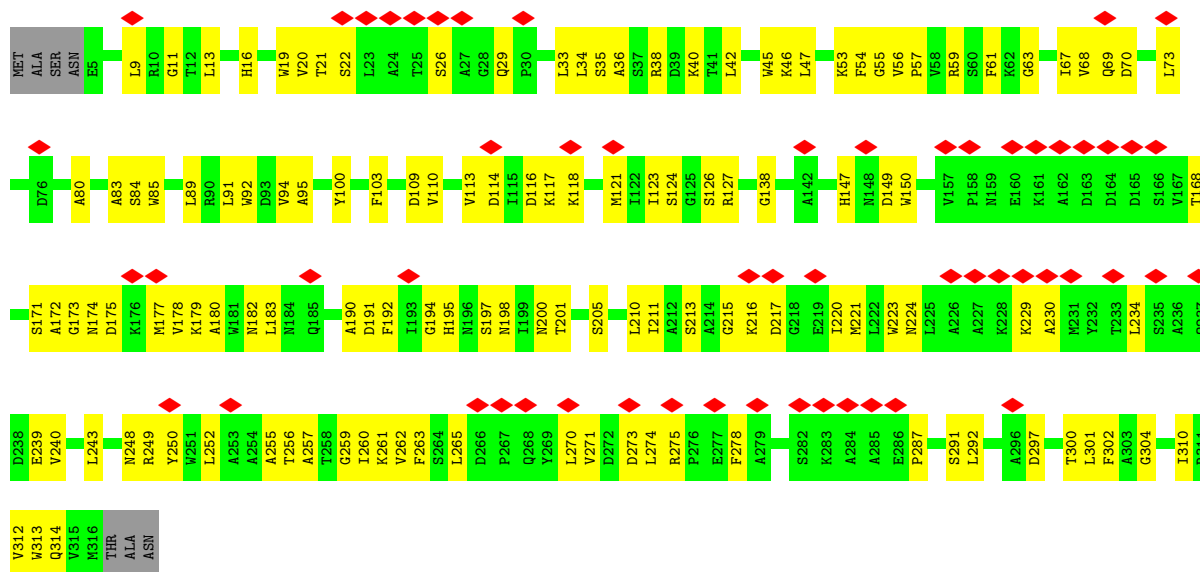


- Molecule 30: RPS29A isoform 1

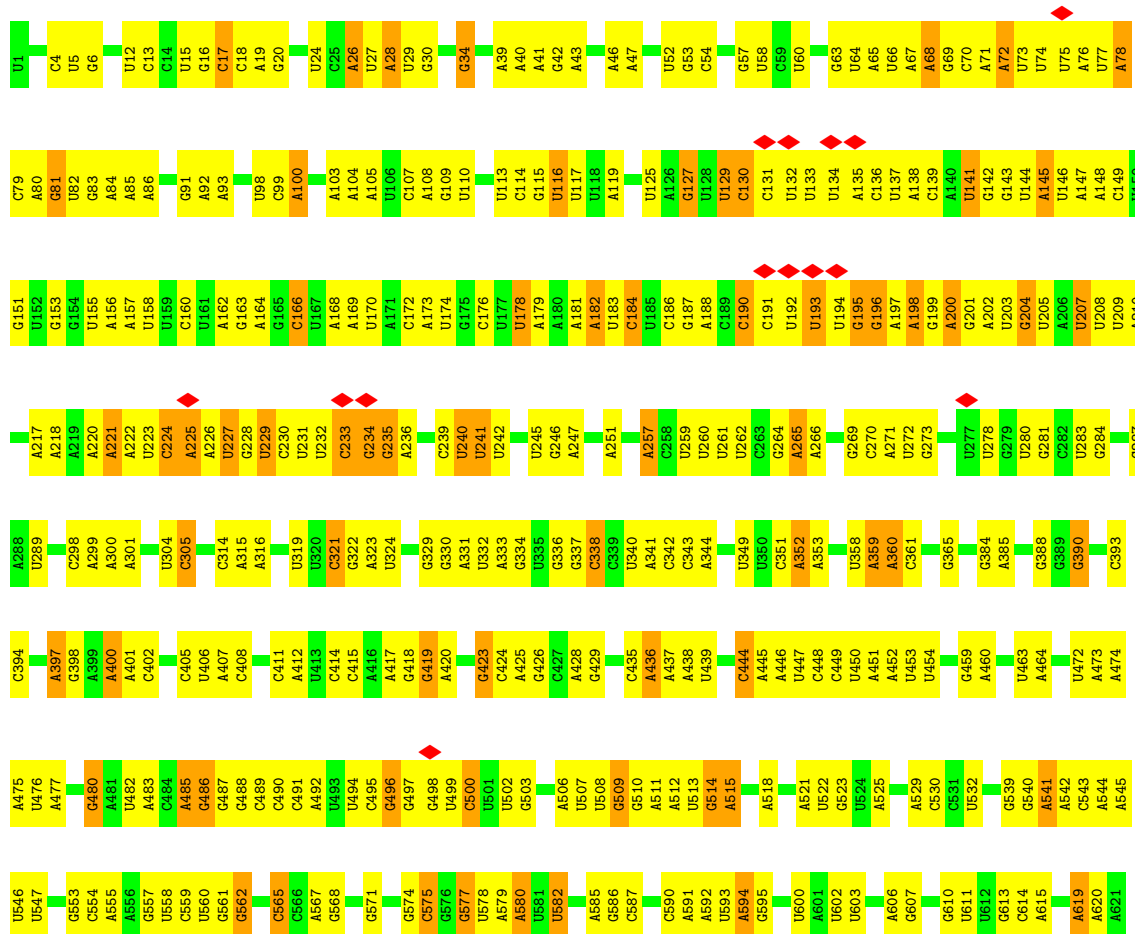


- Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein

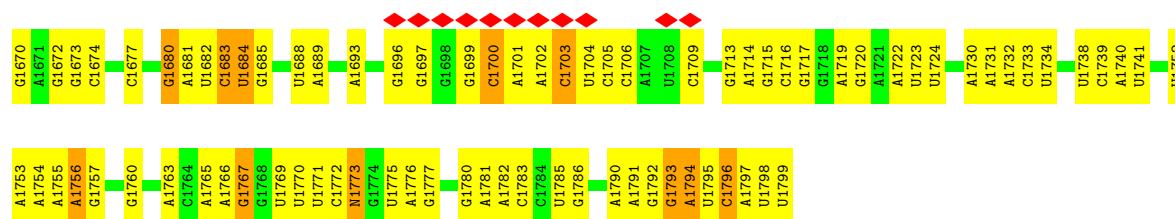




• Molecule 32: 18S rRNA

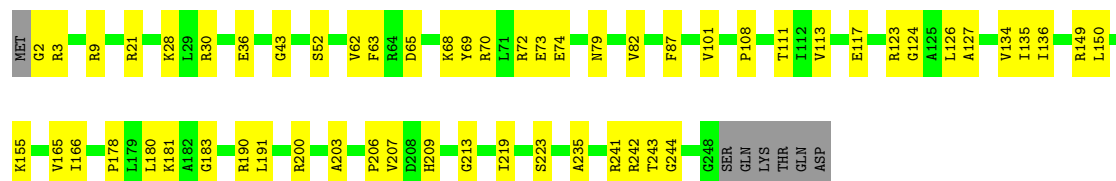


C1589	C1590	C1591	A1592	A1593	G1594	G1595	C1596	A1600	G1601	C1602	C1606	G1607	G1608	G1609	G1610	A1611	C1615	G1616	G1617	G1618	G1619	C1620	C1623	C1624	A1625	A1626	G1627	G1628	G1629	A1635	G1636	G1637	G1638	G1639	C1640	C1641	G1642	G1643	C1644	G1645	C1646	G1647	A1648	G1649	A1651	G1656	G1657	G1658	G1659							
G1522	G1523	A1524	A1525	A1526	G1527	G1528	C1529	C1530	G1531	G1532	C1533	C1537	G1538	G1539	G1540	G1541	G1542	A1545	G1546	G1547	G1549	U1552	G1553	G1554	A1555	A1556	U1557	U1558	A1559	U1560	G1561	G1562	G1563	U1564	G1565	G1566	U1567	C1568	A1569	G1570	A1571	G1572	A1573	G1574	A1575	A1576	U1579	C1580	C1581	G1584	U1585	A1586	A1587	G1588		
C1373	C1374	G1308	C1309	A1310	U1311	U1312	U1313	U1314	G1315	G1316	A1321	A1322	C1323	G1324	A1325	A1326	G1327	G1328	A1329	G1330	A1331	C1332	C1333	U1334	C1338	C1339	A1340	A1341	A1344	A1345	U1347	A1348	G1349	U1350	G1351	G1352	U1353	C1354	C1355	U1356	A1357	G1358	C1359	A1360	U1361	U1362	U1363	G1364	C1365	G1366	G1367	G1368	U1369	U1370	A1371	U1372
A1238	U1239	U1240	G1241	A1242	G1243	A1244	G1245	C1246	U1247	G1248	U1249	U1250	U1251	C1252	U1253	U1254	G1255	A1256	U1257	U1258	U1259	U1260	G1261	U1262	G1263	G1264	U1265	U1266	G1267	U1268	U1269	G1270	G1271	U1272	A1275	U1276	G1277	G1278	C1279	U1280	G1281	C1284	U1285	U1286	U1290	G1291	G1292	U1293	G1294	G1295	A1296	G1297	U1298	G1299	A1300	U1301
G1165	A1166	G1167	G1170	A1171	G1172	C1173	C1174	U1175	G1176	U1182	A1183	U1184	U1185	U1191	A1194	C1195	A1196	C1197	G1198	G1199	G1200	G1201	A1202	C1205	U1206	C1207	A1208	C1209	A1210	A1211	G1212	G1213	U1214	C1215	C1216	A1217	G1218	U1219	C1220	A1221	U1224	U1225	A1226	A1227	G1228	G1229	A1230	U1231	U1232	G1233	A1234	G1237				
C1072	A1076	C1077	C1078	U1079	U1080	A1081	C1082	G1083	A1086	A1087	A1088	A1091	A1092	U1097	U1098	G1100	U1103	U1104	G1107	G1108	G1114	U1115	A1116	A1124	A1125	G1126	G1130	A1137	A1138	A1142	A1143	U1144	U1145	G1146	A1147	G1150	G1153	C1156	A1157	C1158	C1159	C1161	U1071													
U989	C990	G991	A992	A993	C1000	A1001	G1002	A1003	U1004	A1005	C1006	U1017	U1018	G958	A1020	A933	C934	U935	A939	A940	U945	U946	U947	G948	C949	C950	A951	A952	G953	G954	G957	U960	U961	C962	A963	A966	A967	U968	C969	U983	U984	G985	G986	U987	A971	G972	A973	A974	C975	G976	A977	A978	A979	G980	A988	
G838	U839	U840	G846	A847	C848	C849	A850	U851	C852	G853	U854	A855	A856	U857	U781	A859	U860	U861	A862	U864	G867	G868	G871	G872	U873	C874	G875	G876	G877	U882	C883	A884	G885	U886	A887	U888	U889	C890	A891	A892	U893	U894	G895	U896	C897	A898	G899	A900	G901	A905	A906	A907	U908			
U759	A760	G761	G765	A766	G769	A769	A770	A774	G775	G778	U779	A780	U781	U782	G783	C784	A788	A789	U794	U795	A796	U800	G801	G802	A803	A804	U805	U808	A809	U727	U728	G729	U730	C731	G732	U733	A734	U735	U821	U822	G823	G824	U825	U828	A829	A900	U832	U833	G834	U835	U836	G837				
C692	U693	U694	U695	C696	C697	U698	U699	C700	U705	A706	A707	C708	C709	U710	U711	G712	A713	G714	U715	C716	C717	U718	U719	G720	U721	G722	G723	C724	U725	G726	U727	U728	G729	U730	C731	G732	U733	A734	U735	U821	U822	G823	G824	U825	U828	A829	A900	U832	U833	G834	U835	U836	G837			
A622	A623	G624	C625	U626	U629	A630	G631	U632	A636	C637	U638	U639	U640	C645	C646	G647	U650	G651	G652	C653	C654	G655	G656	U657	C658	C	A	U	U	U	U	U	U	C	U	G676	G677	A678	U679	U680	U681	C682	C683	G687	G688	G689	G690	C691								



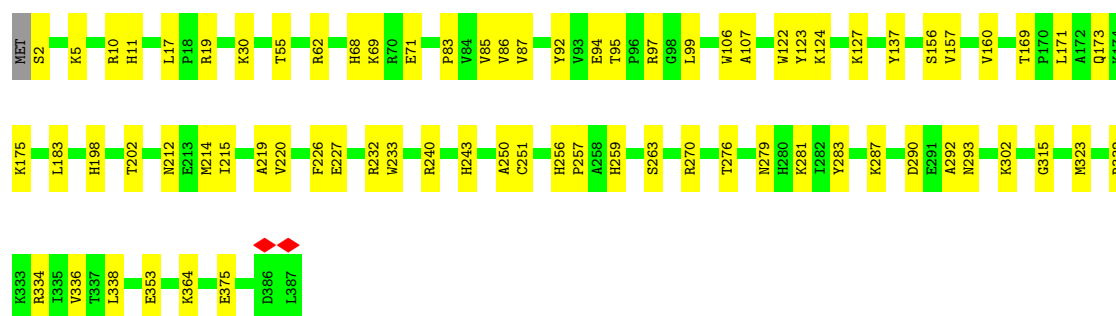
• Molecule 33: 60S ribosomal protein L2-A

Chain AA: 75% 22%



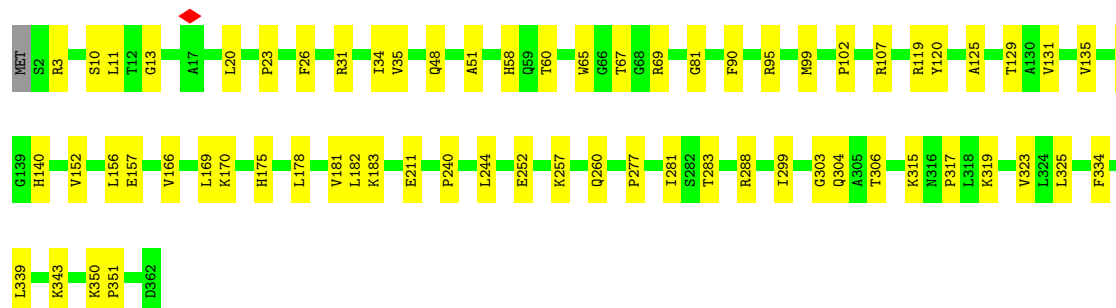
• Molecule 34: 60S ribosomal protein L3

Chain AB: 81% 19%



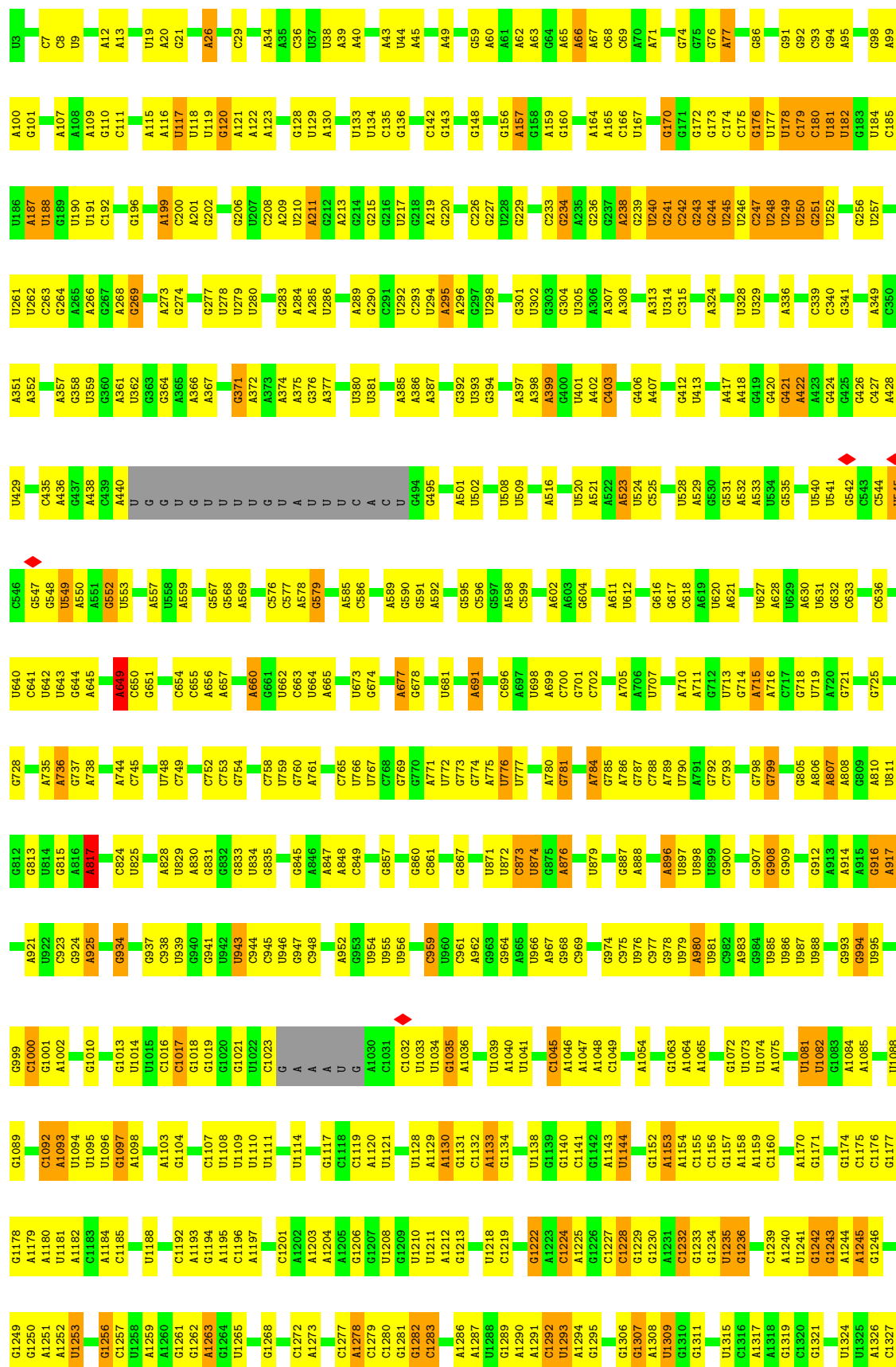
• Molecule 35: RPL4A isoform 1

Chain AC: 81% 18%

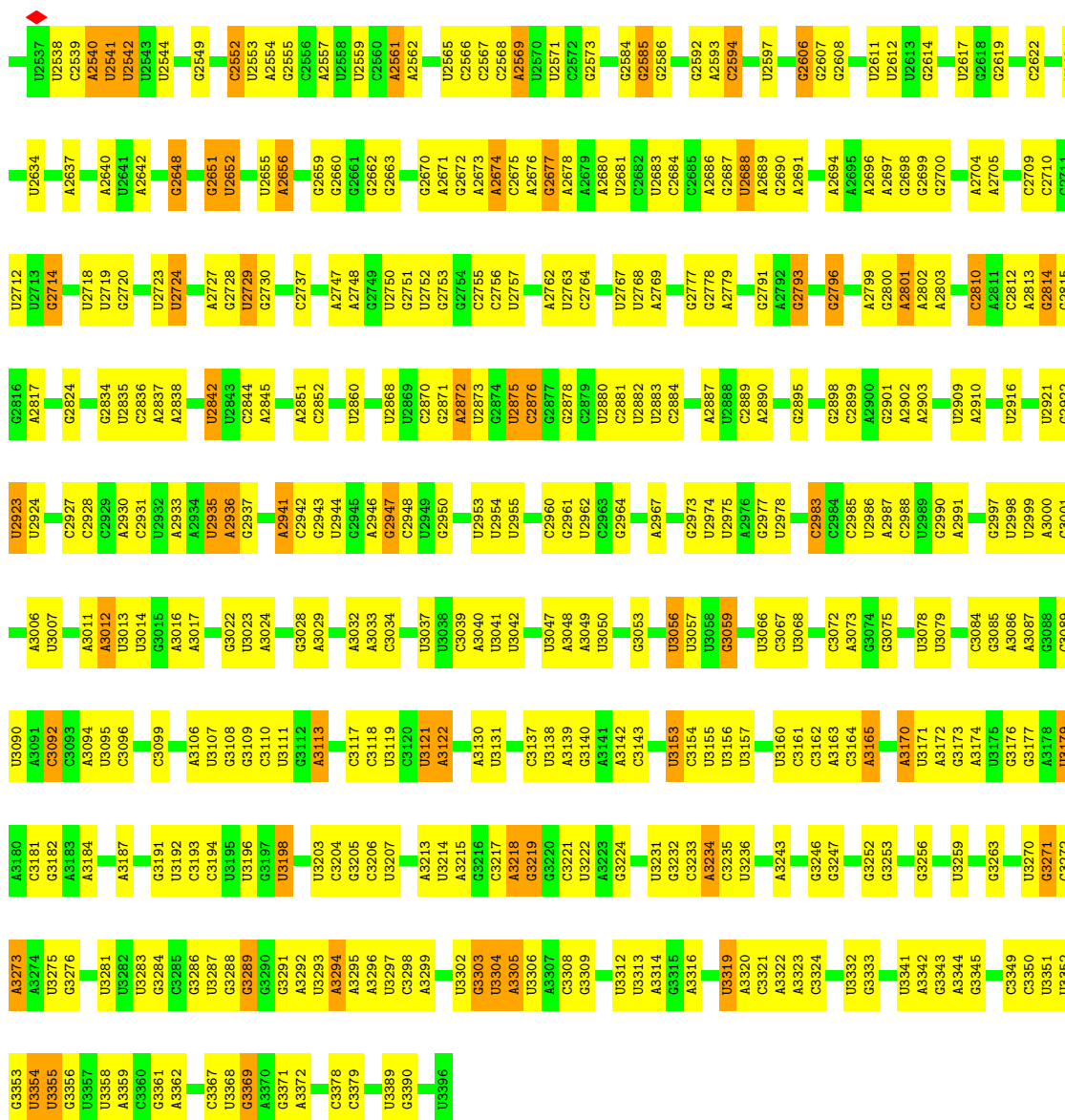


• Molecule 36: 28S rRNA

Chain A1: 49% 38% 7% 5%

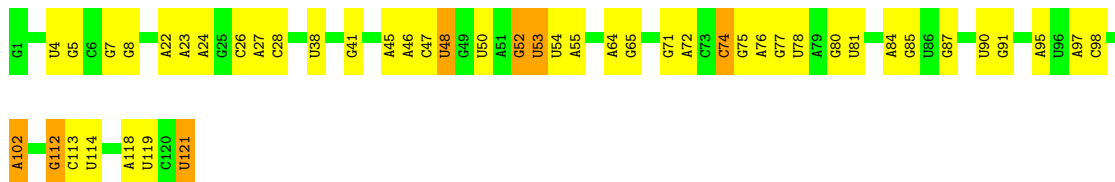


G2467	A2397	G2307	A2213	G2110	G	G	A1911	A1806	U1721	U1622	U1553	A1330
A2466	A2402	C2308	A2214	G2111	U	U	U1912	G1807	U1722	G1623	U1554	U1331
G2469	G2403	A2309	G	A2112	A	G	A1913	G1812	U1723	C1628	U1555	A1435
C2470	A2404	U2310	G	G2113	G	C	G1914	A1813	U1724	U1629	U1556	C1333
U2471	C2405	G2311	C	C2114	A	U	A1915	A1814	C1725	U1630	A1557	U1334
U2472	C2406	A2312	G	G2115	C	U	U1916	U1815	G1728	C1631	A1558	C1335
C2473	C2407	A2313	U	A2120	G	U	A1921	A1816	A1729	G1634	A1559	U1336
U2408	U2408	G2314	G	G2121	C	G	A1922	G1817	G	U1635	U1560	U1337
G2475	G2410	U2315	C	G2122	U	A	C1923	U1820	G1734	U1636	C1562	G1340
C2476	U2411	A2223	G	U2129	U	C	G1927	U1821	G1735	A1637	U1563	U1341
G2477	G2412	A2224	U	G2130	C	U	A1932	G1829	U1737	A1638	U1564	C1342
C2478	A2413	U2225	G	A2131	G	C	U1936	U1830	C1738	C1639	G1565	U1455
A2480	G2414	A2228	U	G	C	U	A1937	U1831	U1739	G1640	A1566	U1347
G2483	U2417	A2229	G	A2138	A	U	U1940	U1832	U1740	A1642	U1567	U1348
A2484	G2418	C2230	U	U2140	U	U	G1941	A1842	A1741	A1643	U1568	A1349
A2485	A2419	C2231	G	G2141	G	U	U1942	C1846	G1744	C1644	U1569	A1462
A2486	C2420	A2232	U	U2142	C	U	C1943	U1849	C1745	G	A1571	U1351
U2487	U2421	A2233	G	A2143	U	G	G1947	A1850	U1749	A1648	U1572	U1352
A2488	G2424	U2241	U	A2144	C	U	G1948	C1856	A1750	U1649	G1573	G1354
C2489	U2425	A2242	U	A2145	U	G	G1949	C1857	G1751	C1657	C1574	A1355
A2490	G2426	A2243	G	U2146	U	C	U1950	G1867	A1752	U1659	A1575	U1356
C2491	U2427	G2249	C	A2147	G	U	C1951	U1868	U1757	G1660	G1576	G1357
C2492	U2428	G2250	U	U2148	U	U	G1952	G1869	A1758	C1662	G1577	C1358
U2493	G2429	G2251	G	A2152	A	G	U1953	G1863	C1762	U1661	C1579	G1367
A2494	A2356	A2255	C	U2153	C	U	G1954	A1864	U1763	A1661	A1580	U1368
A2495	C2357	U2256	C	U2154	C	U	U1955	C1866	U1764	G1666	G1581	A1481
C2496	C2431	G2257	G	G2155	U	C	A	A1867	U1765	A1667	C1582	U1378
U2497	A2438	U2258	U	A2158	C	G	U	U1871	G1770	G1668	A1583	G1379
U2498	A2439	A2259	C	U2159	C	U	U	C1872	C1771	C1669	A1587	U1384
U2499	G	U2260	A	G2160	C	U	A	U1873	U1772	G1680	C1588	C1385
A2500	G2442	U2261	U	G2161	U	G	G	G1878	G1775	U1681	A1589	G1387
U2501	C2443	U2262	C	A2167	G	C	G	U1880	G1778	A1683	G1592	U1388
A2502	C2444	C2265	G	U2168	C	C	C	A1886	U1782	U1686	A1593	G1389
G2503	A2445	U2266	U	G2169	C	C	G	A1887	G1783	U1687	A1594	C1391
U2504	U2446	C2267	C	A2169	C	C	U	U1888	U1784	C1688	U1596	A1498
U2505	G2447	U2268	C	U2170	U	C	A	G1889	U1785	U1689	C1597	G1392
U2506	U2448	U2269	C	G2180	A	C	U	U1890	G1786	U1694	C1598	A1393
C2507	A2449	A2270	U	C2181	C	C	U	A1893	A1787	A1695	A1602	A1394
U2508	G2450	C2271	A	G2185	C	U	A	U1894	U1696	A1696	A1605	A1399
U2509	G2451	G2272	G	A2186	A	U	G	A1895	C1791	A1697	U1606	G1404
U2510	C2374	G2273	C	G2188	U	U	C	U1896	C1792	C1698	U1607	G1507
G2452	U2453	C2278	U	A2188	A	U	C	G1899	C1793	G1708	C1508	A1407
G2454	U2454	C2279	G	C2189	C	C	A	G1906	G1796	C1709	A1613	U1415
U2455	A2456	A2280	C	A2190	C	C	G	C1907	A1797	G1717	C1614	A1418
G2457	A2457	A2281	U	U2103	C	C	U	A1908	A1798	G1718	C1615	A1419
A2458	G2458	U2282	G	G2205	U	C	G	A1909	A1799	G1719	U1616	C1420
A2459	C2459	C2283	C	G2206	U	C	C	A1910	A1800	U1720	A1621	U1427
U2524	U2460	C2284	C	A2207	U	G	A	G1906	A1805			
G2525	A2461	U2285	C	G2208	U	C	C	C1907				
C2526	G2462	G2286	C	A2209	U	C	C	A1908				
G2527	G2463	U2292	U	A2210	U	G	C	A1909				
C2531	U2464		G	A2211	U	U	C	A1910				
U2532	G2465		U	U2212	U	U	C					
G2533	G2466											



• Molecule 37: 5S rRNA

Chain A3: 61% 33% 6%



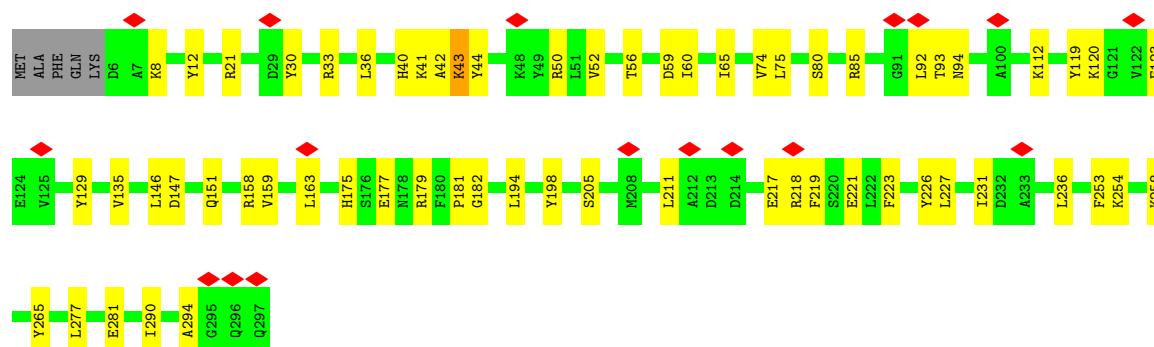
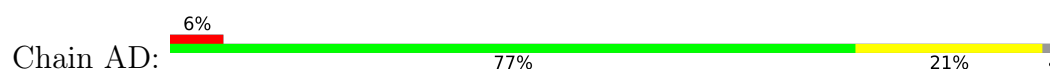
• Molecule 38: 5.8S rRNA

Chain A4: 53% 41% 6%

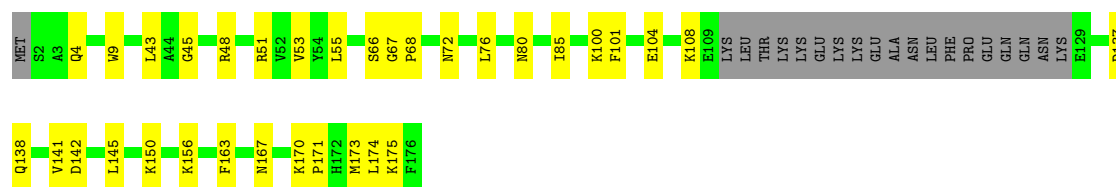




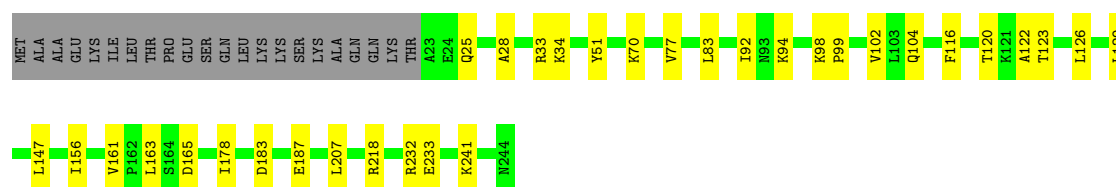
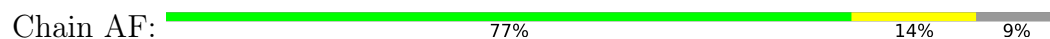
• Molecule 39: RPL5 isoform 1



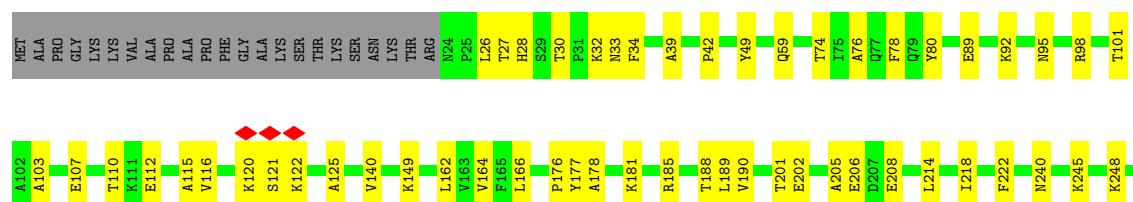
• Molecule 40: 60S ribosomal protein L6-A



• Molecule 41: 60S ribosomal protein L7-A



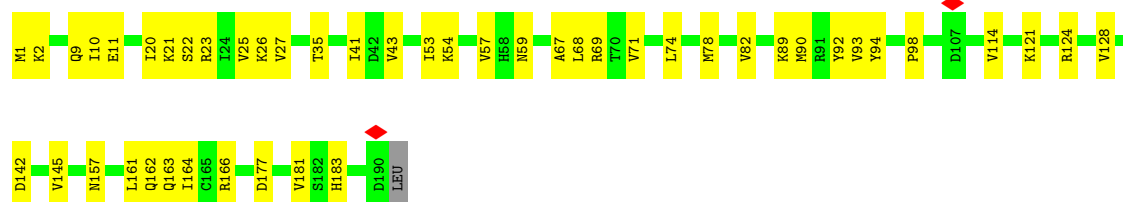
• Molecule 42: 60S ribosomal protein L8-A





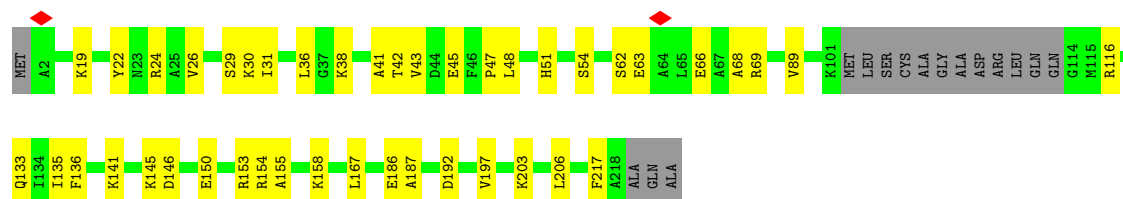
- Molecule 43: 60S ribosomal protein L9-A

Chain AH: 75% 25%



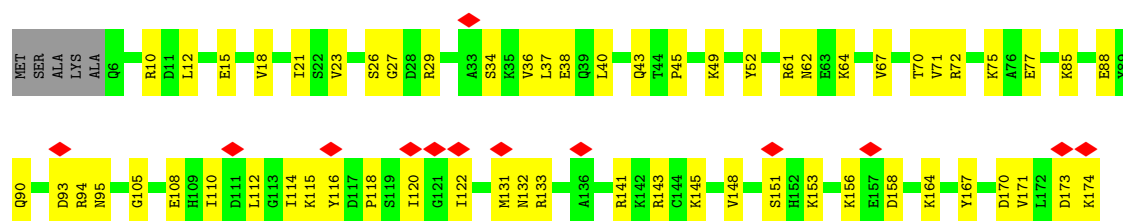
- Molecule 44: RPL10 isoform 1

Chain AI: 73% 19% 7%



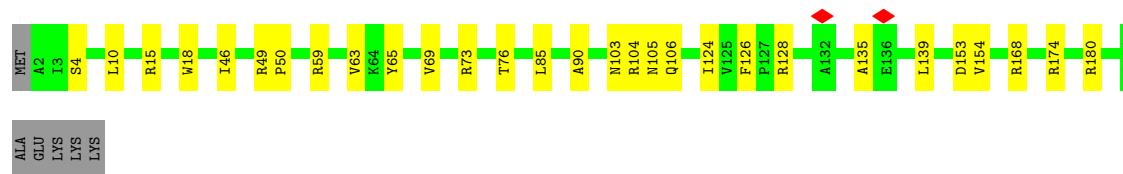
- Molecule 45: RPL11A isoform 1

Chain AJ: 7% 63% 34%



- Molecule 46: 60S ribosomal protein L13-A

Chain AL: 82% 15%



- Molecule 47: 60S ribosomal protein L14-A

Chain AM: 73% 25%



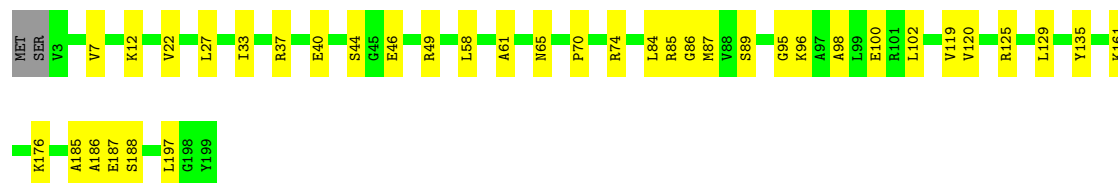
- Molecule 48: 60S ribosomal protein L15-A

Chain AN: 78% 22%



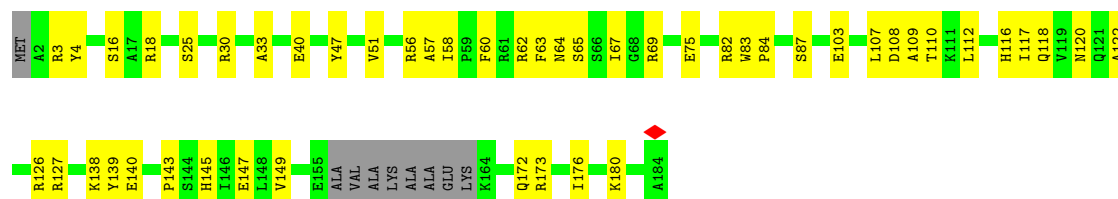
- Molecule 49: 60S ribosomal protein L16-A

Chain AO: 80% 19%



- Molecule 50: 60S ribosomal protein L17-A

Chain AP: 68% 27% 5%



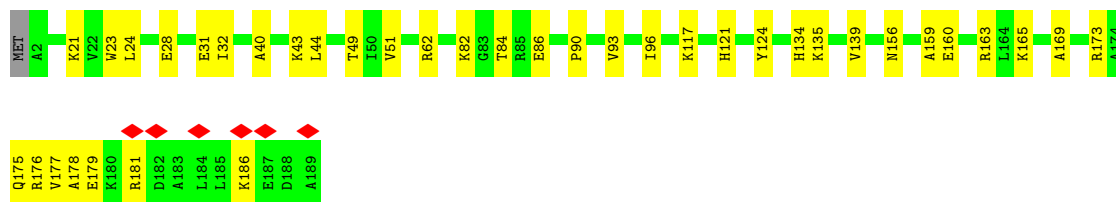
- Molecule 51: 60S ribosomal protein L18-A

Chain AQ: 77% 22%



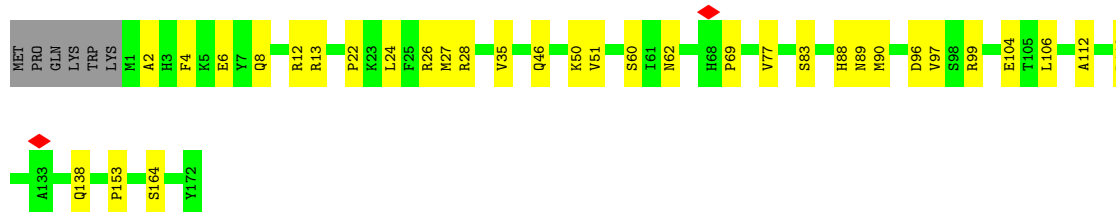
- Molecule 52: 60S ribosomal protein L19-A

Chain AR:  79% 20%



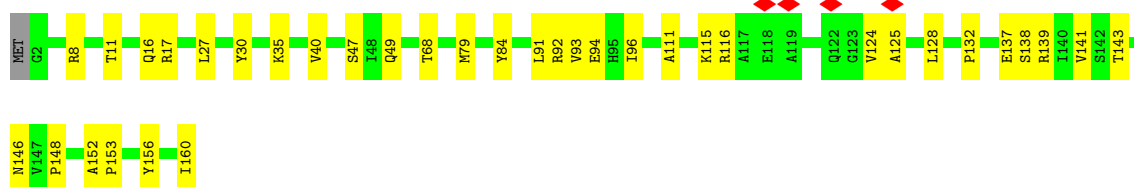
- Molecule 53: 60S ribosomal protein L20

Chain AS:  78% 19%



- Molecule 54: 60S ribosomal protein L21-A

Chain AT:  77% 22%



- Molecule 55: 60S ribosomal protein L22-A

Chain AU:  71% 12% 17%



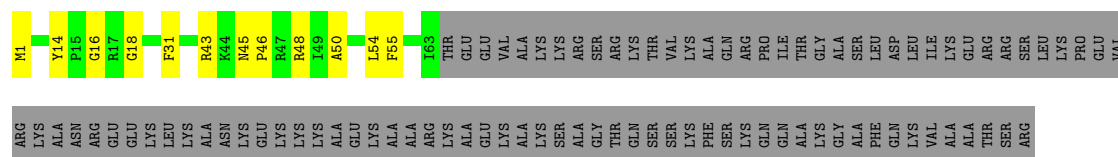
- Molecule 56: 60S ribosomal protein L23-A

Chain AV:  84% 15%



- Molecule 57: RPL24A isoform 1

Chain AW:  33% 8% 59%



- Molecule 58: 60S ribosomal protein L25

Chain AX: 75% 10% 15%



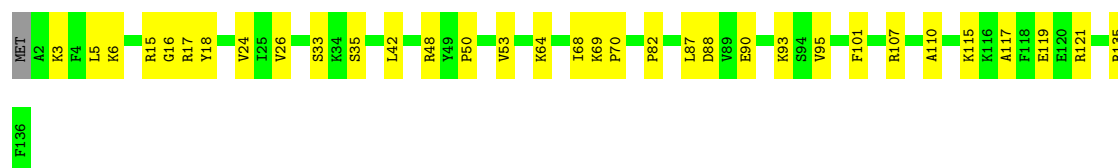
- Molecule 59: 60S ribosomal protein L26-A

Chain AY: 80% 19%



- Molecule 60: 60S ribosomal protein L27-A

Chain AZ: 75% 24%



- Molecule 61: 60S ribosomal protein L28

Chain Aa: 77% 22%



- Molecule 62: RPL29 isoform 1

Chain Ab: 85% 14%



- Molecule 63: 60S ribosomal protein L30

Chain Ac: 70% 22% 8%



- Molecule 64: 60S ribosomal protein L31-A

Chain Ad:  83% 13%



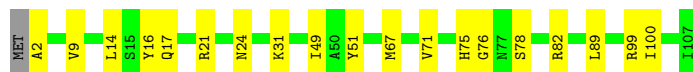
- Molecule 65: RPL32 isoform 1

Chain Ae:  85% 12%



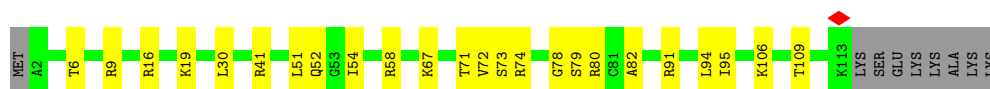
- Molecule 66: 60S ribosomal protein L33-A

Chain Af:  81% 18%



- Molecule 67: 60S ribosomal protein L34-A

Chain Ag:  73% 20% 7%



- Molecule 68: 60S ribosomal protein L35-A

Chain Ah:  79% 20%



- Molecule 69: 60S ribosomal protein L36-A

Chain Ai:  85% 14%

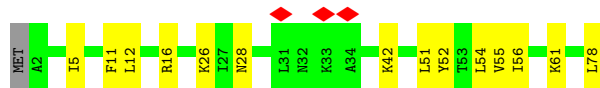


- Molecule 70: 60S ribosomal protein L37-A

Chain Aj:  77% 22%



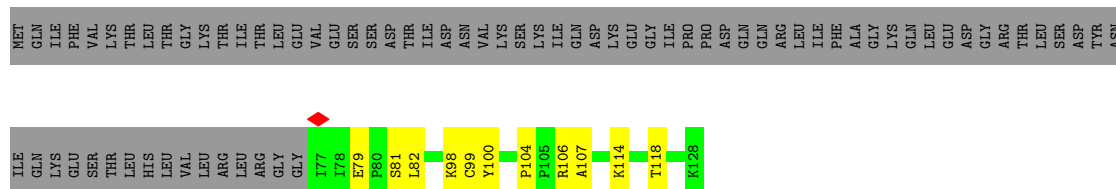
• Molecule 71: RPL38 isoform 1

Chain Ak:  81% 18%

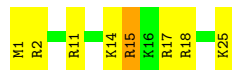
• Molecule 72: 60S ribosomal protein L39

Chain Al:  78% 20%

• Molecule 73: Ubiquitin-60S ribosomal protein L40

Chain Am:  32% 9% 59%

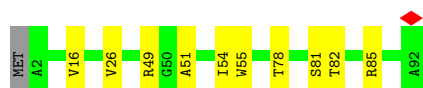
• Molecule 74: 60S ribosomal protein L41-A

Chain An:  68% 28%

• Molecule 75: 60S ribosomal protein L42-A

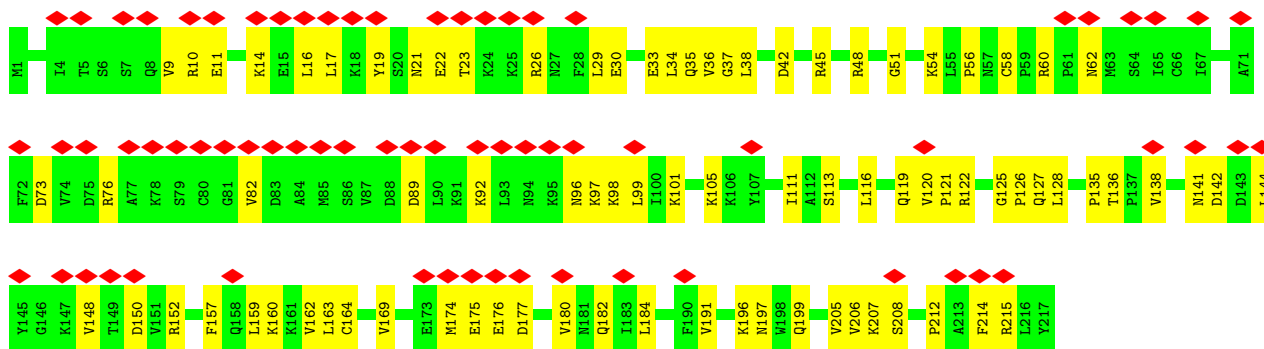
Chain Ao:  72% 27%

• Molecule 76: 60S ribosomal protein L43-A

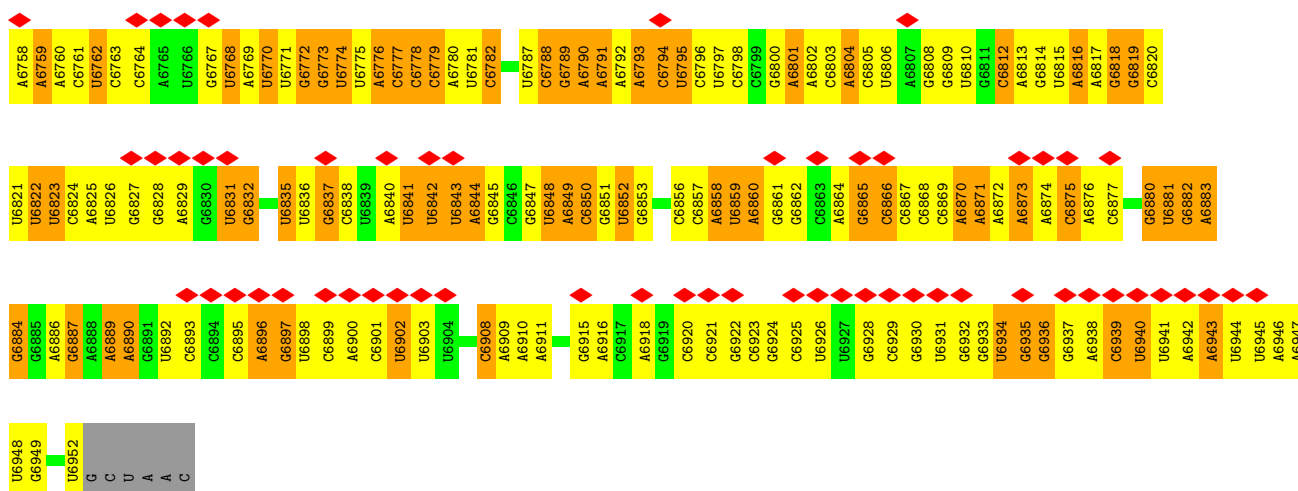
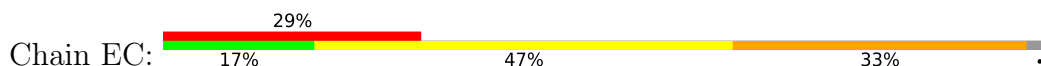
Chain Ap:  88% 11%

• Molecule 77: RPL1A isoform 1

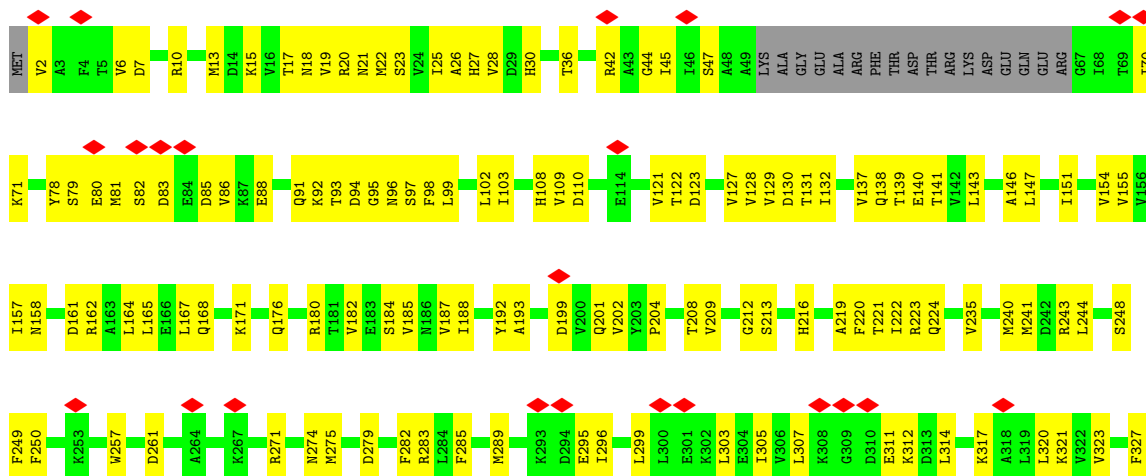
Chain E:  32% 61% 39%

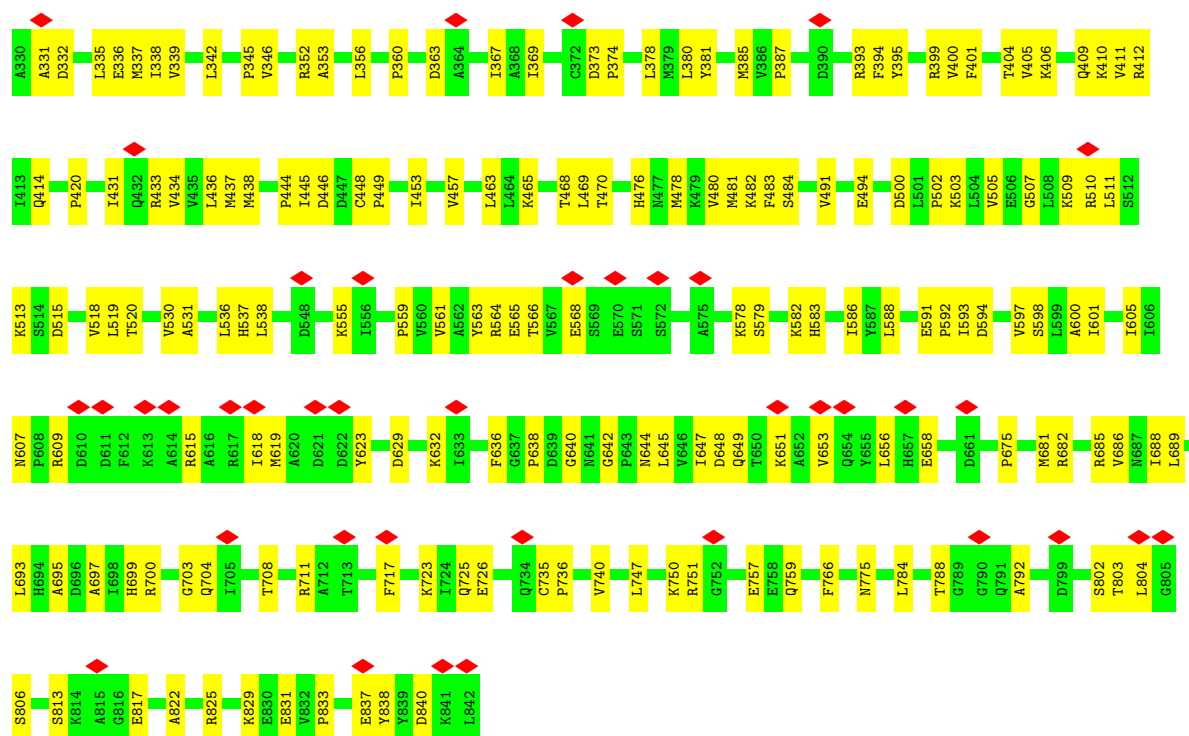


• Molecule 78: Taura syndrome virus (TSV) internal ribosome entry site (IRES) RNA

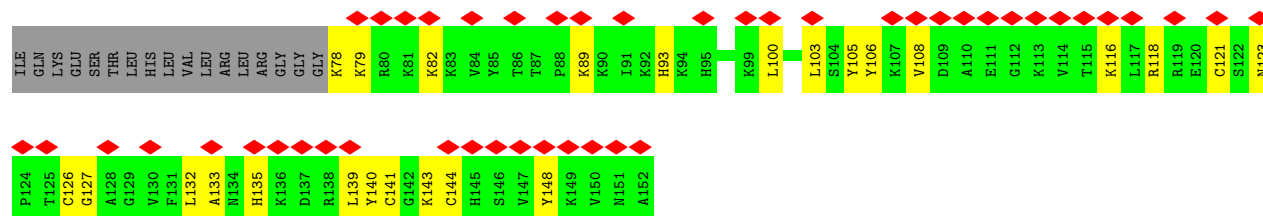
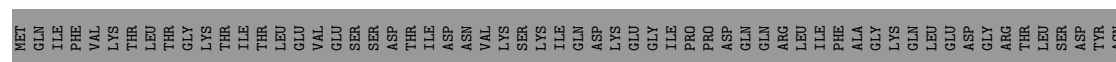
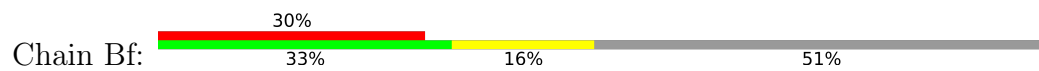


• Molecule 79: Elongation factor 2

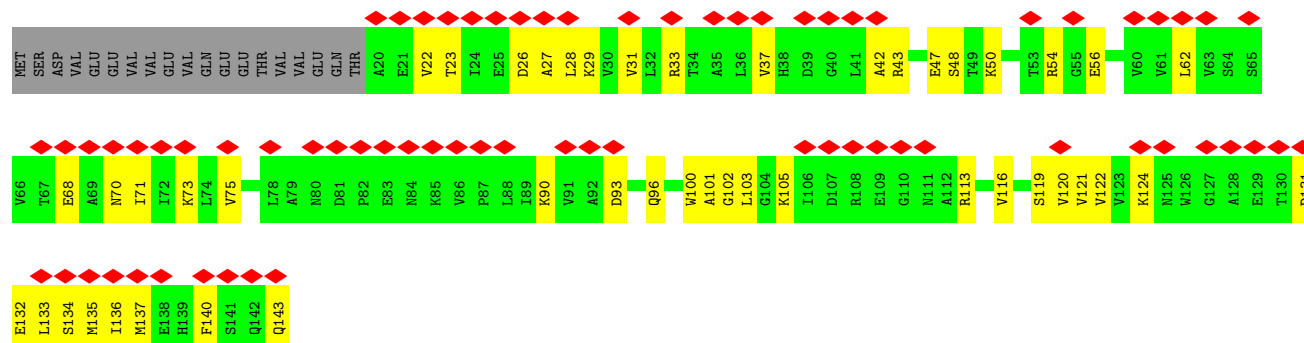




- Molecule 80: Ubiquitin-40S ribosomal protein S31



- Molecule 81: 40S ribosomal protein S12



Chain VA:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	96683	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	4.770	Depositor
Minimum map value	-1.793	Depositor
Average map value	0.035	Depositor
Map value standard deviation	0.202	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 1MA, A2M, ZN, OMC, UR3, G7M, 4AC, OMG, HIC, 5MC, DDE, MG, OMU, MA6, GDP, XSX

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	BA	0.15	0/1653	0.38	0/2261
2	BB	0.16	0/1735	0.41	0/2335
3	BC	0.12	0/1665	0.26	0/2263
4	BE	0.12	0/2109	0.33	0/2839
5	BG	0.11	0/1844	0.30	0/2464
6	BH	0.13	0/1506	0.37	0/2028
7	BI	0.13	0/1514	0.35	0/2021
8	BJ	0.11	0/1519	0.28	0/2035
9	BL	0.13	0/1272	0.29	0/1712
10	BN	0.13	0/1215	0.33	0/1638
11	BO	0.18	0/952	0.56	2/1279 (0.2%)
12	BV	0.15	0/693	0.39	0/935
13	BW	0.14	0/1038	0.31	0/1395
14	BX	0.15	0/1139	0.38	0/1518
15	BY	0.12	0/1087	0.34	0/1449
16	Ba	0.17	0/782	0.45	0/1047
17	Bb	0.13	0/620	0.38	0/838
18	Be	0.09	0/483	0.29	0/643
19	BD	0.11	0/1759	0.28	0/2368
20	BF	0.12	0/1629	0.31	0/2202
21	BK	0.11	0/837	0.42	0/1131
22	BP	0.14	0/1012	0.39	0/1356
23	BQ	0.14	0/1125	0.32	0/1510
24	BR	0.14	0/1010	0.38	0/1355
25	BS	0.12	0/1211	0.35	0/1628
26	BT	0.13	0/1113	0.35	0/1494
27	BU	0.13	0/865	0.36	0/1169
28	BZ	0.12	0/566	0.33	0/761
29	Bc	0.14	0/499	0.35	0/670
30	Bd	0.13	0/452	0.34	0/600
31	Bg	0.11	0/2454	0.32	0/3340
32	B5	0.16	1/41880 (0.0%)	0.29	0/65248

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AA	0.20	0/1912	0.36	0/2569
34	AB	0.17	0/3139	0.32	0/4219
35	AC	0.17	0/2800	0.36	0/3790
36	A1	0.21	0/75561	0.32	0/117806
37	A3	0.17	0/2883	0.28	0/4491
38	A4	0.21	0/3746	0.31	0/5832
39	AD	0.14	0/2390	0.31	0/3225
40	AE	0.15	0/1260	0.33	0/1694
41	AF	0.17	0/1821	0.30	0/2451
42	AG	0.16	0/1830	0.34	0/2469
43	AH	0.15	0/1531	0.34	0/2062
44	AI	0.14	0/1708	0.27	0/2290
45	AJ	0.13	0/1374	0.36	0/1842
46	AL	0.16	0/1568	0.30	0/2106
47	AM	0.15	0/1068	0.28	0/1438
48	AN	0.20	0/1757	0.33	0/2354
49	AO	0.17	0/1585	0.29	0/2128
50	AP	0.17	0/1410	0.31	0/1893
51	AQ	0.17	0/1465	0.32	0/1965
52	AR	0.17	0/1538	0.33	0/2050
53	AS	0.17	0/1481	0.34	0/1990
54	AT	0.16	0/1300	0.30	0/1743
55	AU	0.17	0/812	0.45	0/1099
56	AV	0.15	0/1018	0.31	0/1369
57	AW	0.15	0/533	0.28	0/707
58	AX	0.17	0/983	0.30	0/1325
59	AY	0.17	0/1004	0.29	0/1341
60	AZ	0.16	0/1118	0.34	0/1497
61	Aa	0.20	0/1204	0.32	0/1612
62	Ab	0.15	0/473	0.30	0/629
63	Ac	0.17	0/751	0.30	0/1008
64	Ad	0.16	0/904	0.29	0/1213
65	Ae	0.17	0/1041	0.31	0/1394
66	Af	0.19	0/868	0.31	0/1168
67	Ag	0.18	0/890	0.34	0/1189
68	Ah	0.16	0/978	0.28	0/1301
69	Ai	0.16	0/778	0.32	0/1034
70	Aj	0.18	0/696	0.34	0/923
71	Ak	0.15	0/618	0.29	0/826
72	Al	0.17	0/443	0.29	0/588
73	Am	0.15	0/423	0.33	0/562
74	An	0.26	0/234	0.97	4/300 (1.3%)
75	Ao	0.16	0/860	0.31	0/1136

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Ap	0.16	0/701	0.33	0/934
77	E	0.12	0/1745	0.33	0/2342
78	EC	0.13	0/4613	0.32	0/7182
79	DC	0.12	0/6521	0.34	0/8830
80	Bf	0.11	0/616	0.31	0/817
81	BM	0.11	0/943	0.33	0/1274
82	VA	0.15	0/1498	0.42	0/2025
All	All	0.18	1/227631 (0.0%)	0.32	6/333564 (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
6	BH	0	1
11	BO	0	1
14	BX	0	1
39	AD	0	1
41	AF	0	1
42	AG	0	2
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	B5	1575	G7M	O3'-P	5.72	1.61	1.56

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
74	An	15	ARG	CB-CG-CD	-8.89	90.86	111.30
11	BO	125	SER	CA-C-N	6.33	129.70	120.71
11	BO	125	SER	C-N-CA	6.33	129.70	120.71
74	An	15	ARG	CA-CB-CG	6.08	126.26	114.10
74	An	15	ARG	CG-CD-NE	5.59	124.30	112.00
74	An	15	ARG	N-CA-CB	-5.10	102.09	110.40

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
39	AD	43	LYS	Peptide
41	AF	232	ARG	Peptide
42	AG	30	THR	Peptide
42	AG	76	ALA	Peptide
6	BH	64	VAL	Peptide
11	BO	123	SER	Peptide
14	BX	88	PRO	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BA	1612	0	1623	69	0
2	BB	1709	0	1784	64	0
3	BC	1635	0	1723	33	0
4	BE	2068	0	2154	55	0
5	BG	1820	0	1918	69	0
6	BH	1481	0	1572	48	0
7	BI	1489	0	1525	54	0
8	BJ	1494	0	1573	37	0
9	BL	1244	0	1314	17	0
10	BN	1192	0	1255	27	0
11	BO	941	0	979	41	0
12	BV	684	0	672	22	0
13	BW	1021	0	1060	31	0
14	BX	1121	0	1196	39	0
15	BY	1073	0	1132	32	0
16	Ba	769	0	818	33	0
17	Bb	610	0	633	19	0
18	Be	475	0	525	18	0
19	BD	1734	0	1817	64	0
20	BF	1609	0	1675	65	0
21	BK	817	0	804	34	0
22	BP	991	0	1035	37	0
23	BQ	1105	0	1166	48	0
24	BR	1000	0	1063	40	0
25	BS	1192	0	1222	51	0
26	BT	1095	0	1114	40	0
27	BU	855	0	917	32	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	BZ	558	0	598	26	0
29	Bc	497	0	535	25	0
30	Bd	442	0	432	13	0
31	Bg	2401	0	2356	92	0
32	B5	38004	0	19142	811	0
33	AA	1878	0	1946	48	0
34	AB	3081	0	3162	54	0
35	AC	2748	0	2859	51	0
36	A1	68445	0	34455	957	0
37	A3	2579	0	1304	33	0
38	A4	3353	0	1695	46	0
39	AD	2341	0	2290	47	0
40	AE	1239	0	1326	25	0
41	AF	1784	0	1862	24	0
42	AG	1798	0	1894	33	0
43	AH	1510	0	1576	35	0
44	AI	1672	0	1711	32	0
45	AJ	1353	0	1383	40	0
46	AL	1543	0	1608	23	0
47	AM	1053	0	1149	25	0
48	AN	1720	0	1779	34	0
49	AO	1555	0	1659	29	0
50	AP	1388	0	1423	37	0
51	AQ	1441	0	1543	35	0
52	AR	1521	0	1617	31	0
53	AS	1445	0	1487	24	0
54	AT	1276	0	1323	28	0
55	AU	796	0	812	10	0
56	AV	1003	0	1048	14	0
57	AW	521	0	551	8	0
58	AX	968	0	1036	15	0
59	AY	993	0	1081	17	0
60	AZ	1092	0	1155	26	0
61	Aa	1173	0	1215	32	0
62	Ab	462	0	491	7	0
63	Ac	743	0	797	17	0
64	Ad	890	0	938	11	0
65	Ae	1020	0	1089	15	0
66	Af	850	0	880	12	0
67	Ag	880	0	945	21	0
68	Ah	969	0	1078	23	0
69	Ai	771	0	849	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	Aj	681	0	687	15	0
71	Ak	612	0	682	10	0
72	Al	436	0	475	8	0
73	Am	417	0	459	8	0
74	An	233	0	283	10	0
75	Ao	847	0	914	23	0
76	Ap	694	0	738	8	0
77	E	1718	0	1811	83	0
78	EC	4128	0	2082	104	0
79	DC	6419	0	6493	227	0
80	Bf	605	0	654	23	0
81	BM	935	0	975	36	0
82	VA	1473	0	1514	48	0
83	A1	187	0	0	0	0
83	A3	2	0	0	0	0
83	A4	5	0	0	0	0
83	AB	1	0	0	0	0
83	AG	1	0	0	0	0
83	AN	3	0	0	0	0
83	AO	2	0	0	0	0
83	AP	1	0	0	0	0
83	Af	1	0	0	0	0
83	Aj	1	0	0	0	0
83	B5	51	0	0	0	0
84	Ao	1	0	0	0	0
85	DC	28	0	12	1	0
All	All	214074	0	160127	3877	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 11.

All (3877) 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)
32:B5:1697:G:H1	32:B5:1704:U:H3	1.01	1.00
32:B5:1588:G:H1	32:B5:1608:U:H3	1.02	0.94
36:A1:170:G:H5''	68:Ah:109:ILE:HD12	1.51	0.92
32:B5:69:G:H1	32:B5:82:U:H3	1.18	0.92
36:A1:3234:A:H61	36:A1:3253:G:H1	1.11	0.92
37:A3:23:A:HO2'	37:A3:121:U:HO3'	1.15	0.92
11:BO:12:GLN:HE22	16:Ba:58:VAL:HG11	1.36	0.91

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:2492:C:OP1	77:E:215:ARG:NH2	2.03	0.90
36:A1:2673:A:H5''	45:AJ:95:ASN:HD22	1.36	0.90
1:BA:16:LEU:HB3	1:BA:172:LEU:HD11	1.56	0.88
17:Bb:44:THR:HG21	17:Bb:63:LEU:HD21	1.55	0.86
20:BF:63:GLN:HE22	20:BF:66:GLN:H	1.23	0.86
28:BZ:42:LEU:HD21	28:BZ:47:TYR:HB2	1.58	0.86
79:DC:311:GLU:HA	79:DC:314:LEU:HD13	1.59	0.83
5:BG:160:ARG:HH21	5:BG:171:LYS:HD2	1.43	0.82
53:AS:13:ARG:NH1	53:AS:50:LYS:O	2.12	0.82
32:B5:1585:U:H3	32:B5:1611:A:H2	1.26	0.82
32:B5:833:U:H5'	32:B5:834:G:H5''	1.61	0.82
81:BM:43:ARG:HH22	81:BM:101:ALA:HB1	1.43	0.81
14:BX:114:LYS:HE3	32:B5:571:G:H5''	1.61	0.81
32:B5:1575:G7M:O2'	32:B5:1576:A:O4'	1.99	0.81
36:A1:3354:U:H5'	36:A1:3355:U:H5'	1.64	0.80
77:E:76:ARG:HH21	77:E:144:LEU:H	1.29	0.80
56:AV:81:GLN:O	56:AV:98:ASN:ND2	2.14	0.80
78:EC:6842:U:H4'	78:EC:6843:U:H5''	1.62	0.80
6:BH:139:ARG:HB2	6:BH:151:LYS:HB3	1.63	0.79
19:BD:51:ARG:HH21	19:BD:92:GLN:H	1.31	0.79
31:Bg:42:LEU:HB2	31:Bg:61:PHE:HB2	1.65	0.79
32:B5:1542:G:H1	32:B5:1568:C:HO2'	1.27	0.79
36:A1:1282:G:O2'	36:A1:1283:C:O5'	2.00	0.79
32:B5:1773:4AC:H5	74:An:2:ARG:NH2	1.96	0.78
58:AX:50:ALA:HB1	68:Ah:66:VAL:HG11	1.65	0.78
36:A1:595:G:OP1	41:AF:33:ARG:NH2	2.16	0.78
36:A1:2465:G:N1	36:A1:2491:A:C6	2.51	0.78
36:A1:3028:G:H5'	79:DC:28:VAL:HG11	1.66	0.78
23:BQ:13:LYS:HG3	23:BQ:14:LYS:H	1.47	0.78
49:AO:58[A]:LEU:HD21	49:AO:74[A]:ARG:HH12	1.49	0.78
32:B5:1773:4AC:H5	74:An:2:ARG:HH22	1.48	0.78
20:BF:187:ILE:HG12	28:BZ:66:VAL:HG11	1.66	0.78
11:BO:126:THR:HG1	32:B5:989:U:HO2'	1.31	0.77
32:B5:992:A:O2'	32:B5:1785:U:O2	2.02	0.77
32:B5:1213:G:H1	32:B5:1450:U:H3	1.32	0.77
36:A1:3092:C:O2'	36:A1:3094:A:OP2	2.01	0.77
77:E:116:LEU:HD12	77:E:119:GLN:HB3	1.65	0.77
14:BX:70:LYS:NZ	32:B5:567:A:OP1	2.17	0.77
5:BG:31:ARG:NH1	32:B5:1681:A:O2'	2.17	0.77
36:A1:845:G:H21	36:A1:848:A:H2	1.29	0.77
80:Bf:127:GLY:HA3	81:BM:54:ARG:HH12	1.49	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:9:LEU:HD21	6:BH:21:ALA:HB2	1.65	0.77
23:BQ:100:GLN:NE2	31:Bg:57:PRO:O	2.18	0.76
19:BD:106:LYS:HG3	19:BD:175:VAL:HG22	1.64	0.76
48:AN:183:THR:HG22	48:AN:187:ARG:HB3	1.67	0.76
32:B5:65:A:H2	32:B5:84:A:H62	1.34	0.76
36:A1:2466:G:H4'	77:E:60:ARG:HH12	1.50	0.76
11:BO:122:PRO:HB3	11:BO:125:SER:HB2	1.65	0.76
32:B5:1672:G:H2'	32:B5:1673:G:C8	2.21	0.76
5:BG:154:ARG:HG3	32:B5:78:A:H8	1.52	0.75
31:Bg:211:ILE:HB	31:Bg:223:TRP:HB2	1.67	0.75
1:BA:98:ILE:HD11	1:BA:116:LYS:HE3	1.68	0.75
26:BT:105:LEU:HD13	26:BT:122:ARG:HD3	1.66	0.75
6:BH:14:THR:HG22	6:BH:15:GLU:H	1.51	0.75
36:A1:3234:A:N6	36:A1:3253:G:H1	1.85	0.75
79:DC:10:ARG:NH2	79:DC:444:PRO:O	2.20	0.75
23:BQ:20:ALA:HB1	23:BQ:65:ILE:HD11	1.68	0.74
26:BT:25:GLN:HG3	26:BT:27:LYS:HG2	1.69	0.74
29:Bc:64:ARG:HG3	29:Bc:65:ARG:H	1.53	0.74
36:A1:2138:A:HO2'	70:Aj:2:GLY:N	1.84	0.74
4:BE:129:VAL:HG12	4:BE:139:VAL:HG12	1.68	0.74
36:A1:1174:G:N2	49:AO:87[A]:MET:SD	2.60	0.74
49:AO:84[A]:LEU:HD13	49:AO:102[A]:LEU:HD21	1.69	0.74
78:EC:6812:C:H2'	78:EC:6813:A:H8	1.51	0.74
31:Bg:255:ALA:HB2	31:Bg:292:LEU:HD22	1.69	0.74
32:B5:1339:C:O2'	32:B5:1341:A:N7	2.20	0.74
79:DC:23:SER:HB3	79:DC:122:THR:HG21	1.69	0.74
32:B5:868:G:H1	32:B5:960:U:H3	1.33	0.74
43:AH:92:TYR:HB2	43:AH:142:ASP:HB3	1.68	0.74
36:A1:1235:U:H4'	36:A1:1236:G:H5'	1.67	0.74
13:BW:80:ASN:OD1	13:BW:124:LYS:NZ	2.21	0.73
19:BD:51:ARG:HG3	19:BD:91:VAL:HG12	1.68	0.73
36:A1:176:G:H2'	36:A1:177:U:H6	1.53	0.73
5:BG:78:THR:HG22	5:BG:79:LYS:H	1.53	0.73
13:BW:31:SER:HB3	32:B5:636:A:H5''	1.70	0.73
43:AH:89:LYS:HG2	43:AH:145:VAL:HG22	1.69	0.73
36:A1:2465:G:N1	36:A1:2491:A:N6	2.37	0.73
5:BG:2:LYS:HB2	5:BG:108:VAL:HG22	1.69	0.73
19:BD:38:GLU:HB3	19:BD:49:ILE:HB	1.71	0.73
32:B5:1291:G:H1	32:B5:1324:G:H22	1.36	0.73
17:Bb:51:GLN:OE1	32:B5:957:G:N2	2.21	0.73
74:An:15:ARG:HA	74:An:18:ARG:HG2	1.70	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:201:LEU:HB3	24:BR:85:VAL:HG12	1.71	0.73
8:BJ:59:LEU:HD11	8:BJ:69:ARG:HA	1.70	0.73
27:BU:106:ILE:HG22	27:BU:107:THR:H	1.54	0.72
33:AA:21:ARG:HD3	36:A1:824:C:H5''	1.70	0.72
32:B5:821:U:O4	32:B5:852:C:N3	2.22	0.72
32:B5:1594:G:OP2	32:B5:1596:C:N4	2.23	0.72
38:A4:150:G:OP1	58:AX:27:ARG:NH2	2.22	0.72
31:Bg:200:ASN:H	31:Bg:215:GLY:HA2	1.53	0.72
32:B5:1237:G:N1	32:B5:1249:U:O4	2.22	0.72
78:EC:6777:C:H5'	78:EC:6778:C:H2'	1.71	0.72
32:B5:1227:A:N6	32:B5:1256:A:OP2	2.21	0.72
82:VA:130:PRO:O	82:VA:133:THR:OG1	2.08	0.72
5:BG:154:ARG:HG3	32:B5:78:A:C8	2.25	0.72
79:DC:649:GLN:HB2	79:DC:689:LEU:HA	1.71	0.72
7:BI:41:LYS:HA	7:BI:60:ILE:HA	1.72	0.71
22:BP:90:ILE:HD12	22:BP:109:PRO:HA	1.72	0.71
14:BX:22:ASN:HD22	32:B5:1108:G:H1	1.36	0.71
36:A1:1807:G:H5''	60:AZ:135:ARG:HH12	1.54	0.71
1:BA:30:GLN:HE22	1:BA:32:HIS:HB2	1.54	0.71
36:A1:2464:U:OP1	36:A1:2485:A:O2'	2.07	0.71
45:AJ:49:LYS:HB3	45:AJ:62:ASN:HA	1.72	0.71
4:BE:36:HIS:NE2	4:BE:88:ASP:OD2	2.23	0.71
12:BV:3:ASN:ND2	12:BV:7:GLN:OE1	2.24	0.71
23:BQ:22:VAL:HG11	23:BQ:92:TYR:HB2	1.71	0.71
26:BT:134:ARG:NH2	32:B5:1360:A:OP1	2.23	0.71
35:AC:350:LYS:HD3	35:AC:351:PRO:HD2	1.72	0.71
43:AH:21:LYS:HG3	43:AH:22:SER:H	1.54	0.71
79:DC:81:MET:HE1	79:DC:86:VAL:HG22	1.71	0.71
32:B5:225:A:N7	32:B5:837:G:N2	2.39	0.71
2:BB:28:GLU:HB3	2:BB:94:LYS:HE3	1.70	0.71
36:A1:178:U:H2'	36:A1:179:C:H6	1.55	0.71
63:Ac:55:GLU:HB2	67:Ag:94:LEU:HD11	1.73	0.71
6:BH:34:LEU:HA	6:BH:38:LEU:HD12	1.71	0.71
20:BF:112:ARG:NH2	23:BQ:42:GLU:OE2	2.24	0.71
40:AE:175:LYS:O	47:AM:117:ARG:NH2	2.23	0.71
45:AJ:52:TYR:HA	45:AJ:61:ARG:HG2	1.71	0.71
49:AO:27[A]:LEU:HD21	49:AO:102[A]:LEU:HB2	1.73	0.71
34:AB:160:VAL:HB	34:AB:183:LEU:HD21	1.72	0.70
79:DC:353:ALA:HA	79:DC:356:LEU:HG	1.73	0.70
9:BL:152:GLN:HB3	10:BN:136:PRO:HA	1.72	0.70
78:EC:6774:U:OP1	78:EC:6818:G:O2'	2.08	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:EC:6828:G:H2'	78:EC:6829:A:H8	1.57	0.70
81:BM:23:THR:HG21	81:BM:26:ASP:HB2	1.72	0.70
32:B5:900:A:H3'	32:B5:901:G:H21	1.55	0.70
4:BE:130:GLN:NE2	32:B5:251:A:O2'	2.21	0.70
32:B5:871:G:H2'	32:B5:872:G:C8	2.26	0.70
36:A1:2541:U:H4'	36:A1:2542:U:H5'	1.74	0.70
36:A1:2960:C:H2'	36:A1:2961:G:C8	2.26	0.70
4:BE:212:ASP:HB2	4:BE:216:ASN:HB2	1.72	0.70
6:BH:154:LEU:HD11	6:BH:183:PHE:HD2	1.56	0.70
36:A1:3291:G:H2'	36:A1:3292:A:H8	1.56	0.70
9:BL:69:LYS:NZ	32:B5:304:U:O2	2.24	0.70
36:A1:1017:C:O2	36:A1:1035:G:N2	2.19	0.70
32:B5:1310:U:HO2'	32:B5:1402:G:HO2'	1.36	0.70
33:AA:9:ARG:NH2	36:A1:912:G:OP2	2.25	0.70
15:BY:34:ASN:O	32:B5:521:A:O2'	2.08	0.70
36:A1:1661:G:H2'	36:A1:1662:G:C8	2.27	0.70
68:Ah:101:THR:OG1	68:Ah:104:GLN:NE2	2.25	0.70
34:AB:315:GLY:HA2	36:A1:3379:C:H4'	1.74	0.69
36:A1:952:A:OP1	62:Ab:18:ARG:NH2	2.24	0.69
32:B5:1640:C:N4	78:EC:6952:U:OP1	2.24	0.69
34:AB:220:VAL:O	34:AB:334:ARG:NH1	2.25	0.69
79:DC:110:ASP:HB3	79:DC:537:HIS:HB2	1.73	0.69
73:Am:104:PRO:HG2	73:Am:107:ALA:HB2	1.73	0.69
79:DC:122:THR:O	79:DC:352:ARG:NH1	2.25	0.69
9:BL:129:ARG:HD3	32:B5:115:G:H5'	1.74	0.69
15:BY:55:VAL:HG22	15:BY:75:VAL:HG12	1.75	0.69
22:BP:77:ARG:NH2	32:B5:1241:G:OP2	2.26	0.69
80:Bf:121:CYS:SG	80:Bf:123:ASN:ND2	2.66	0.69
10:BN:11:ILE:HG13	10:BN:12:SER:H	1.56	0.69
36:A1:283:G:OP2	75:Ao:45:ARG:NH1	2.25	0.69
7:BI:60:ILE:HD11	7:BI:179:CYS:HB2	1.75	0.69
27:BU:69:LYS:HE3	32:B5:1280:4AC:H5''	1.75	0.69
30:Bd:14:TYR:OH	32:B5:1553:G:O2'	2.07	0.69
32:B5:1693:A:N1	32:B5:1709:C:N4	2.41	0.69
36:A1:3344:A:C2	36:A1:3361:G:N2	2.56	0.69
78:EC:6770:U:H3	78:EC:6772:G:H21	1.38	0.69
19:BD:31:GLU:O	19:BD:54:ARG:NH2	2.26	0.69
79:DC:723:LYS:NZ	79:DC:803:THR:OG1	2.24	0.69
14:BX:50:LYS:HG2	14:BX:101:GLU:OE2	1.93	0.69
2:BB:86:LEU:HB3	2:BB:98:THR:HG21	1.75	0.68
4:BE:112:HIS:NE2	4:BE:237:SER:O	2.27	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BU:87:HIS:ND1	32:B5:1383:G:OP1	2.27	0.68
34:AB:95:THR:HG22	34:AB:97:ARG:H	1.58	0.68
36:A1:1631:C:OP2	60:AZ:48:ARG:NH2	2.25	0.68
13:BW:86:ILE:HD11	13:BW:104:LEU:HD21	1.75	0.68
19:BD:164:VAL:HA	19:BD:168:ILE:HD12	1.74	0.68
36:A1:68:C:OP2	36:A1:301:G:N2	2.26	0.68
36:A1:180:C:H2'	36:A1:181:U:C6	2.28	0.68
36:A1:3016:A:H2'	36:A1:3017:A:C8	2.28	0.68
49:AO:22[A]:VAL:HG21	49:AO:120[A]:VAL:HG11	1.74	0.68
36:A1:2568:C:O2'	36:A1:2569:A:O4'	2.11	0.68
7:BI:184:LEU:HB3	7:BI:189:LEU:HB2	1.74	0.68
35:AC:11:LEU:HD21	35:AC:156:LEU:HB2	1.75	0.68
77:E:38:LEU:HB2	77:E:163:LEU:HB2	1.75	0.68
40:AE:66:SER:HB2	40:AE:76:LEU:HD23	1.75	0.68
36:A1:2842:U:OP1	36:A1:2844:C:N4	2.26	0.68
32:B5:851:U:OP2	52:AR:173:ARG:NH2	2.27	0.68
32:B5:1260:U:H2'	32:B5:1261:G:H8	1.58	0.68
46:AL:4:SER:O	61:Aa:44:ASN:ND2	2.26	0.68
7:BI:104:ILE:HG13	7:BI:105:ASP:H	1.58	0.68
34:AB:10:ARG:NH1	34:AB:11:HIS:O	2.27	0.68
21:BK:12:HIS:HB3	21:BK:80:LEU:HD11	1.76	0.68
25:BS:145:ARG:HH21	32:B5:1172:G:H4'	1.59	0.68
32:B5:1198:G:OP1	32:B5:1199:G:O2'	2.09	0.68
36:A1:714:G:HO2'	36:A1:753:C:HO2'	1.40	0.68
1:BA:88:LYS:HE2	1:BA:201:LEU:HD13	1.76	0.68
5:BG:65:GLN:HE22	32:B5:1681:A:H8	1.41	0.68
6:BH:15:GLU:HA	6:BH:18:LEU:HD12	1.76	0.68
19:BD:136:VAL:HG22	19:BD:186:VAL:HG22	1.75	0.68
36:A1:2895:G:O2'	73:Am:100:TYR:O	2.12	0.68
2:BB:59:ASP:HA	2:BB:62:LYS:HG2	1.75	0.67
23:BQ:136:SER:HB3	32:B5:1586:A:H5''	1.76	0.67
80:Bf:121:CYS:HB2	80:Bf:132:LEU:HD21	1.75	0.67
27:BU:82:TYR:HB3	30:Bd:52:PHE:HB3	1.76	0.67
61:Aa:24:LYS:O	61:Aa:26:ARG:HG2	1.93	0.67
2:BB:82:ARG:NH2	2:BB:191:GLU:OE1	2.22	0.67
36:A1:655:C:H2'	36:A1:656:A:H8	1.59	0.67
36:A1:2356:A:H61	36:A1:2983:C:H5	1.40	0.67
1:BA:140:ASN:HD22	3:BC:62:PRO:HD3	1.59	0.67
32:B5:233:C:HO2'	32:B5:234:G:H21	1.41	0.67
36:A1:2213:A:H2'	36:A1:2214:A:C8	2.29	0.67
44:AI:66:GLU:OE2	44:AI:69:ARG:NH2	2.28	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:68:VAL:HA	31:Bg:84:SER:HA	1.76	0.67
31:Bg:83:ALA:HB2	31:Bg:113:VAL:HG13	1.76	0.67
36:A1:2465:G:H21	77:E:33:GLU:HG3	1.59	0.67
24:BR:23:LYS:HD2	31:Bg:198:ASN:HD21	1.58	0.67
31:Bg:178:VAL:HB	31:Bg:192:PHE:HB2	1.76	0.67
36:A1:576:C:OP1	41:AF:241:LYS:NZ	2.27	0.67
39:AD:181:PRO:HG3	39:AD:198:TYR:CD2	2.30	0.67
79:DC:27:HIS:HB3	79:DC:30:HIS:CD2	2.30	0.67
32:B5:780:A:H4'	32:B5:781:U:H5''	1.77	0.67
36:A1:831:G:O2'	36:A1:1864:A:N3	2.27	0.67
39:AD:60:ILE:HB	39:AD:80:SER:HB2	1.77	0.67
64:Ad:55:LEU:HB2	64:Ad:95:PRO:HD3	1.77	0.67
7:BI:152:ILE:HG13	7:BI:153:GLU:H	1.60	0.67
34:AB:10:ARG:NH2	34:AB:263:SER:O	2.28	0.67
3:BC:156:THR:HG23	13:BW:95:PRO:HB2	1.77	0.67
27:BU:42:VAL:O	27:BU:52:LYS:NZ	2.28	0.67
79:DC:409:GLN:NE2	79:DC:410:LYS:O	2.28	0.67
29:Bc:19:THR:HG23	29:Bc:25:VAL:HG13	1.75	0.66
33:AA:101:VAL:HG22	33:AA:165:VAL:HG22	1.77	0.66
42:AG:101:THR:HG23	42:AG:103:ALA:H	1.59	0.66
34:AB:5:LYS:HE2	36:A1:2878:G:H5''	1.77	0.66
36:A1:2219:A:H2'	36:A1:2220:A2M:H8	1.76	0.66
18:Be:2:ALA:N	32:B5:1754:A:HO2'	1.93	0.66
32:B5:1502:G:N2	32:B5:1505:A:OP2	2.29	0.66
32:B5:1756[A]:A:H1'	79:DC:703:GLY:HA3	1.76	0.66
79:DC:636:PHE:O	79:DC:642:GLY:N	2.25	0.66
16:Ba:44:ILE:HG23	16:Ba:45:VAL:HG23	1.78	0.66
8:BJ:41:GLU:OE1	8:BJ:44:ARG:NH2	2.27	0.66
32:B5:1474:G:H2'	32:B5:1475:A:H8	1.60	0.66
1:BA:198:MET:HE1	24:BR:89:SER:HB2	1.78	0.66
5:BG:180:THR:HG23	5:BG:183:ARG:H	1.60	0.66
7:BI:48:THR:OG1	7:BI:52:ASN:O	2.14	0.66
32:B5:71:A:N6	32:B5:72:A:N3	2.43	0.66
36:A1:1152:G:N2	36:A1:1152:G:OP2	2.28	0.66
52:AR:178:ALA:HA	52:AR:181:ARG:HB3	1.77	0.66
8:BJ:126:ARG:HB3	18:Be:33:ARG:HH12	1.59	0.66
21:BK:75:TYR:HD1	21:BK:76:LEU:HD12	1.61	0.66
32:B5:924:A:H2'	32:B5:925:G:C8	2.31	0.66
36:A1:417:A:H2'	36:A1:418:A:C8	2.30	0.66
36:A1:2185:G:O2'	36:A1:2314:U:OP2	2.12	0.66
81:BM:42:ALA:HB3	81:BM:122:VAL:HB	1.76	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:VA:28:VAL:HG11	82:VA:185:LEU:HG	1.77	0.66
36:A1:2474:G:N2	36:A1:2475:G:O6	2.29	0.66
82:VA:26:PHE:HE2	82:VA:100:ILE:HD11	1.61	0.66
10:BN:107:LYS:NZ	32:B5:1018:U:OP1	2.29	0.66
36:A1:2697:A:H2'	36:A1:2698:G:C8	2.30	0.66
36:A1:3291:G:H2'	36:A1:3292:A:C8	2.30	0.66
77:E:205:VAL:HG22	77:E:215:ARG:HH22	1.59	0.66
8:BJ:107:ARG:NH2	8:BJ:153:GLU:OE2	2.26	0.66
33:AA:70:ARG:HH21	33:AA:72:ARG:HH22	1.43	0.66
82:VA:48:ARG:HH12	82:VA:96:ILE:HG13	1.60	0.66
5:BG:92:ARG:O	32:B5:405:C:O2'	2.13	0.65
32:B5:591:A:H2'	32:B5:592:A:C8	2.31	0.65
36:A1:1351:U:O2'	36:A1:1355:A:N6	2.28	0.65
36:A1:1762:C:H3'	36:A1:1763:U:H4'	1.77	0.65
36:A1:3252:G:H2'	36:A1:3253:G:C8	2.32	0.65
51:AQ:123:THR:OG1	51:AQ:125:ASP:OD1	2.13	0.65
79:DC:222:ILE:HD11	79:DC:244:LEU:HB2	1.78	0.65
32:B5:1297:G:N2	32:B5:1300:A:OP2	2.21	0.65
32:B5:1358:G:H2'	32:B5:1359:C:C6	2.30	0.65
36:A1:2493:U:O2'	36:A1:2494:A:OP1	2.14	0.65
45:AJ:18:VAL:HG22	45:AJ:70:THR:HG22	1.77	0.65
20:BF:51:VAL:O	20:BF:131:GLN:NE2	2.28	0.65
26:BT:70:GLN:HG3	26:BT:120:GLY:HA3	1.77	0.65
36:A1:1696:A:H2'	36:A1:1697:A:C8	2.32	0.65
45:AJ:77:GLU:OE2	45:AJ:167:TYR:OH	2.15	0.65
79:DC:519:LEU:HB3	79:DC:531:ALA:HB3	1.79	0.65
6:BH:150:GLN:HB3	6:BH:181:ILE:HG22	1.78	0.65
8:BJ:83:VAL:HA	8:BJ:149:ARG:HA	1.78	0.65
20:BF:72:HIS:NE2	32:B5:1610:G:OP1	2.29	0.65
32:B5:1234:A:OP2	32:B5:1245:G:O2'	2.11	0.65
36:A1:178:U:H2'	36:A1:179:C:C6	2.31	0.65
51:AQ:122:ILE:HG23	51:AQ:126:GLN:HB2	1.79	0.65
6:BH:108:GLN:OE1	32:B5:810:G:N2	2.29	0.65
26:BT:70:GLN:NE2	26:BT:119:LYS:O	2.30	0.65
32:B5:12:U:H2'	32:B5:13:C:C6	2.32	0.65
32:B5:407:A:H2'	32:B5:408:C:H6	1.62	0.65
82:VA:56:ASN:OD1	82:VA:60:ARG:NH2	2.30	0.65
8:BJ:133:HIS:NE2	32:B5:512:A:O2'	2.23	0.65
9:BL:101:GLU:OE2	14:BX:13:ARG:NH2	2.30	0.65
31:Bg:22:SER:OG	31:Bg:70:ASP:OD1	2.14	0.65
36:A1:1574:C:H3'	36:A1:1575:A:H5''	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:38:LEU:HD22	32:B5:298:C:H5''	1.77	0.65
8:BJ:119:ALA:O	8:BJ:124:HIS:ND1	2.19	0.65
32:B5:1041:G:H2'	32:B5:1042:G:C8	2.31	0.65
72:Al:25:GLN:OE1	72:Al:28:ARG:NH1	2.30	0.65
77:E:174:MET:SD	77:E:175:GLU:N	2.69	0.65
6:BH:114:ARG:NH1	32:B5:637:C:O2	2.30	0.65
36:A1:209:A:O2'	36:A1:211:A:OP2	2.13	0.65
36:A1:544:C:H5''	36:A1:545:U:H5''	1.78	0.65
46:AL:126:PHE:HZ	46:AL:135:ALA:HB2	1.62	0.65
78:EC:6815:U:H3'	78:EC:6816:A:H5''	1.78	0.64
22:BP:18:ARG:NH1	25:BS:90:ASN:OD1	2.26	0.64
23:BQ:69:VAL:HG11	23:BQ:81:ILE:HD11	1.77	0.64
32:B5:1291:G:H22	32:B5:1324:G:N2	1.96	0.64
45:AJ:49:LYS:HE3	45:AJ:64:LYS:HE3	1.79	0.64
78:EC:6908:C:OP1	79:DC:583:HIS:NE2	2.30	0.64
20:BF:58:LEU:HD22	20:BF:168:VAL:HG13	1.80	0.64
8:BJ:132:ARG:NH2	32:B5:532:U:OP1	2.29	0.64
31:Bg:270:LEU:HD11	31:Bg:273:ASP:HB2	1.79	0.64
32:B5:849:C:H2'	32:B5:850:A:H8	1.62	0.64
34:AB:276:THR:HG21	36:A1:3137:C:H5''	1.78	0.64
42:AG:245:LYS:HA	42:AG:248:LYS:HE3	1.78	0.64
79:DC:338:ILE:HG23	79:DC:342:LEU:HD12	1.79	0.64
4:BE:247:SER:OG	4:BE:250:GLU:OE1	2.15	0.64
5:BG:174:LYS:HD2	32:B5:79:C:H1'	1.80	0.64
32:B5:233:C:O2'	32:B5:234:G:N2	2.26	0.64
32:B5:1225:U:O4	81:BM:113:ARG:NH2	2.30	0.64
23:BQ:6:SER:OG	23:BQ:22:VAL:O	2.13	0.64
79:DC:360:PRO:HB2	79:DC:363:ASP:HB2	1.78	0.64
32:B5:1566:U:C4	32:B5:1567:U:O4	2.51	0.64
36:A1:1757:A:OP1	55:AU:94:ARG:NH2	2.29	0.64
50:AP:108:ASP:OD2	50:AP:110:THR:OG1	2.15	0.64
68:Ah:31:LEU:HB3	68:Ah:44:ILE:HG22	1.79	0.64
82:VA:55:LYS:HE3	82:VA:83:ASN:HA	1.79	0.64
3:BC:49:LYS:NZ	3:BC:246:GLU:OE2	2.27	0.64
30:Bd:32:ARG:NH2	32:B5:1596:C:O2	2.30	0.64
36:A1:655:C:H2'	36:A1:656:A:C8	2.33	0.64
36:A1:1729:A:O4'	63:Ac:52:ARG:NH1	2.28	0.64
71:Ak:56:ILE:HD12	71:Ak:61:LYS:HE3	1.79	0.64
79:DC:369:ILE:HG13	79:DC:401:PHE:HB3	1.79	0.64
81:BM:131:ASP:O	81:BM:134:SER:OG	2.15	0.64
24:BR:102:VAL:HG21	24:BR:119:LEU:HD22	1.80	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:680:U:O2	32:B5:682:C:N4	2.29	0.64
36:A1:1717:U:H2'	36:A1:1718:G:C8	2.33	0.64
11:BO:89:THR:HG22	11:BO:128:LYS:HG3	1.79	0.64
31:Bg:248:ASN:OD1	31:Bg:249:ARG:N	2.31	0.64
36:A1:2836:C:H5	36:A1:2852:C:H42	1.44	0.64
79:DC:436:LEU:HD23	79:DC:445:ILE:HD13	1.79	0.64
20:BF:57:SER:OG	20:BF:167:ARG:NH2	2.31	0.63
30:Bd:45:GLU:OE1	32:B5:1433:G:N2	2.29	0.63
36:A1:1576:G:H2'	36:A1:1577:G:O4'	1.98	0.63
13:BW:15:ASN:ND2	13:BW:72:CYS:O	2.28	0.63
32:B5:509:G:H2'	32:B5:510:G:C8	2.33	0.63
32:B5:647:G:H21	32:B5:687:G:H1	1.46	0.63
36:A1:900:G:H1'	36:A1:1589:A:N6	2.13	0.63
79:DC:17:THR:O	79:DC:91:GLN:NE2	2.31	0.63
82:VA:26:PHE:HB3	82:VA:87:VAL:HB	1.81	0.63
32:B5:343:C:H2'	32:B5:344:A:H8	1.62	0.63
32:B5:699:U:O4	32:B5:741:C:N4	2.30	0.63
32:B5:1488:G:H3'	32:B5:1515:A:H61	1.64	0.63
32:B5:1683:C:O2'	32:B5:1684:U:O5'	2.15	0.63
36:A1:268:A:C4	48:AN:12:ARG:HG2	2.33	0.63
36:A1:799:G:O2'	46:AL:18:TRP:NE1	2.31	0.63
23:BQ:77:GLN:O	23:BQ:81:ILE:HD12	1.99	0.63
32:B5:130:C:O2'	32:B5:133:U:OP1	2.14	0.63
79:DC:7:ASP:HA	79:DC:10:ARG:HD3	1.80	0.63
79:DC:80:GLU:OE1	79:DC:96:ASN:ND2	2.32	0.63
25:BS:136:GLN:NE2	32:B5:1545:A:OP2	2.29	0.63
27:BU:69:LYS:HG2	27:BU:80:GLU:HG3	1.81	0.63
36:A1:3319:U:H5'	36:A1:3320:A:H5'	1.80	0.63
78:EC:6899:C:H2'	78:EC:6900:A:H8	1.64	0.63
2:BB:72:ASP:OD1	16:Ba:59:TYR:OH	2.16	0.63
31:Bg:172:ALA:HB2	31:Bg:178:VAL:HG13	1.78	0.63
32:B5:321:C:H41	32:B5:1666:U:H5''	1.62	0.63
32:B5:1358:G:H2'	32:B5:1359:C:H6	1.64	0.63
77:E:101:LYS:HE3	77:E:105:LYS:HZ2	1.63	0.63
79:DC:568:GLU:HA	79:DC:592:PRO:HG3	1.81	0.63
25:BS:26:ILE:HG13	25:BS:31:ALA:HB2	1.81	0.63
32:B5:1591:C:H2'	32:B5:1592:A:H8	1.62	0.63
23:BQ:14:LYS:NZ	32:B5:1610:G:N7	2.47	0.63
24:BR:84:TYR:CE2	24:BR:86:PRO:HG3	2.33	0.63
31:Bg:248:ASN:ND2	31:Bg:297:ASP:O	2.32	0.63
36:A1:2697:A:H2'	36:A1:2698:G:H8	1.62	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AJ:148:VAL:O	45:AJ:153:LYS:NZ	2.28	0.63
52:AR:160:GLU:HA	52:AR:163:ARG:HG2	1.78	0.63
68:Ah:38:ARG:HH11	68:Ah:38:ARG:HG3	1.64	0.63
6:BH:64:VAL:HB	6:BH:94:ALA:HB1	1.80	0.63
32:B5:196:G:HO2'	32:B5:197:A:H8	1.47	0.63
32:B5:240:U:H3'	32:B5:241:U:H5''	1.79	0.63
32:B5:653:C:OP2	32:B5:682:C:N4	2.32	0.63
32:B5:795:U:H2'	32:B5:796:A2M:H8	1.81	0.63
32:B5:1224:A:OP2	81:BM:113:ARG:NH1	2.32	0.63
36:A1:1786:G:H2'	36:A1:1787:A:C8	2.34	0.62
3:BC:209:ASN:HD21	32:B5:1298:U:H1'	1.64	0.62
32:B5:1477:G:H2'	32:B5:1478:G:H8	1.63	0.62
79:DC:352:ARG:HG2	79:DC:356:LEU:HD23	1.80	0.62
79:DC:632:LYS:HB3	79:DC:648:ASP:OD1	1.99	0.62
15:BY:108:ARG:NH2	32:B5:444:C:OP2	2.31	0.62
33:AA:52:SER:HB3	33:AA:191:LEU:HD12	1.81	0.62
36:A1:2383:C:OP2	49:AO:85[A]:ARG:NH2	2.31	0.62
36:A1:2453:U:O2	36:A1:2454:G:O2'	2.14	0.62
36:A1:3016:A:H2'	36:A1:3017:A:H8	1.62	0.62
36:A1:3275:U:O2'	66:Af:99:ARG:NH1	2.33	0.62
82:VA:51:VAL:HG22	82:VA:87:VAL:HG22	1.80	0.62
7:BI:138:ASN:HA	7:BI:141:ARG:HD2	1.81	0.62
15:BY:92:VAL:HG21	15:BY:99:LYS:HE3	1.81	0.62
20:BF:52:GLU:OE1	20:BF:54:LYS:NZ	2.32	0.62
32:B5:163:G:OP2	32:B5:163:G:N2	2.29	0.62
36:A1:196:G:N1	36:A1:199:A:OP2	2.31	0.62
36:A1:1694:U:H5	36:A1:1752:A:N1	1.98	0.62
79:DC:385:MET:HE1	79:DC:465:LYS:HA	1.80	0.62
1:BA:200:ASP:HB2	24:BR:89:SER:HB2	1.81	0.62
6:BH:26:GLU:OE2	6:BH:84:LYS:NZ	2.33	0.62
29:Bc:38:ARG:HG3	29:Bc:38:ARG:O	1.99	0.62
32:B5:187:G:H21	32:B5:198:A:H62	1.47	0.62
32:B5:1511:U:H2'	32:B5:1512:G:H8	1.65	0.62
1:BA:30:GLN:HE21	1:BA:33:GLN:HG2	1.64	0.62
36:A1:245:U:H2'	36:A1:246:U:C6	2.34	0.62
36:A1:1596:C:H2'	36:A1:1597:C:C6	2.35	0.62
11:BO:52:ARG:HD3	32:B5:905:A:H5''	1.80	0.62
33:AA:30:ARG:HD2	33:AA:63:PHE:CE2	2.35	0.62
49:AO:61[A]:ALA:HA	49:AO:70[A]:PRO:HD2	1.81	0.62
79:DC:22:MET:SD	79:DC:102:LEU:HD12	2.40	0.62
4:BE:185:GLY:H	4:BE:224:ASN:HB3	1.64	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BO:131:GLY:O	16:Ba:22:ARG:NH2	2.33	0.62
31:Bg:54:PHE:HE2	31:Bg:312:VAL:HG11	1.64	0.62
39:AD:75:LEU:O	39:AD:112:LYS:NZ	2.32	0.62
82:VA:123:ALA:HA	82:VA:152:ILE:HB	1.82	0.62
33:AA:2:GLY:HA2	36:A1:2608:G:OP1	2.00	0.62
36:A1:1354:G:O2'	36:A1:1355:A:OP1	2.18	0.62
36:A1:1666:G:H2'	36:A1:1667:A:H8	1.65	0.62
36:A1:1873:U:OP1	52:AR:21:LYS:NZ	2.32	0.62
45:AJ:141:ARG:O	45:AJ:145:LYS:NZ	2.33	0.62
78:EC:6934:U:H5''	78:EC:6935:G:H4'	1.82	0.62
79:DC:2:VAL:N	79:DC:44:GLY:O	2.33	0.62
20:BF:182:ALA:O	20:BF:186:ASN:ND2	2.32	0.61
32:B5:1525:A:H2'	32:B5:1526:A:C8	2.35	0.61
32:B5:1595:U:H3	32:B5:1600:A:H2	1.48	0.61
36:A1:1448:U:H2'	36:A1:1449:A2M:H8	1.82	0.61
78:EC:6896:A:H2	78:EC:6935:G:H22	1.48	0.61
9:BL:109:VAL:HG12	9:BL:137:PHE:HB2	1.81	0.61
32:B5:1071:U:H2'	32:B5:1072:C:C6	2.35	0.61
36:A1:1831:U:O2'	38:A4:114:G:OP1	2.16	0.61
77:E:42:ASP:OD2	77:E:45:ARG:NE	2.30	0.61
32:B5:651:G:H1	32:B5:683:C:H42	1.48	0.61
32:B5:1237:G:H2'	32:B5:1238:A:H8	1.64	0.61
34:AB:169:THR:HG22	34:AB:171:LEU:HD13	1.82	0.61
71:Ak:42:LYS:HG2	71:Ak:55:VAL:HG22	1.83	0.61
77:E:128:LEU:HD21	77:E:135:PRO:HD3	1.81	0.61
6:BH:24:PHE:O	6:BH:28:GLU:N	2.34	0.61
31:Bg:80:ALA:HB3	31:Bg:92:TRP:HB2	1.82	0.61
36:A1:2459:A:N7	36:A1:2461:A:N6	2.49	0.61
37:A3:77:G:N2	37:A3:102:A:OP2	2.27	0.61
52:AR:40:ALA:HA	52:AR:43:LYS:HE3	1.81	0.61
77:E:96:ASN:HB3	77:E:99:LEU:HD13	1.80	0.61
79:DC:648:ASP:HA	79:DC:688:ILE:HG13	1.82	0.61
1:BA:38:PHE:HB3	1:BA:47:VAL:HG13	1.82	0.61
32:B5:1146:G:H2'	32:B5:1147:A:C8	2.35	0.61
36:A1:1311:G:N2	49:AO:86[A]:GLY:O	2.26	0.61
36:A1:1404:G:N2	36:A1:1407:A:OP2	2.32	0.61
50:AP:138:LYS:HD2	50:AP:140:GLU:OE2	2.00	0.61
23:BQ:28:LEU:HD21	23:BQ:30:LYS:HG2	1.83	0.61
39:AD:151:GLN:HG2	39:AD:159:VAL:HG11	1.82	0.61
7:BI:178:ARG:NH1	32:B5:207:U:O2	2.34	0.61
27:BU:100:VAL:HG13	27:BU:101:LYS:HD2	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:AA:69:TYR:OH	36:A1:2557:A:OP1	2.19	0.61
36:A1:2960:C:H2'	36:A1:2961:G:H8	1.66	0.61
43:AH:11:GLU:N	43:AH:11:GLU:OE1	2.33	0.61
77:E:16:LEU:HD13	77:E:214:PHE:HE2	1.63	0.61
77:E:174:MET:SD	77:E:175:GLU:HG3	2.41	0.61
13:BW:30:SER:HB2	13:BW:61:ILE:HG13	1.83	0.61
36:A1:662:U:H2'	36:A1:663:OMC:C6	2.36	0.61
36:A1:1940:G:H21	36:A1:3362:A:H8	1.46	0.61
78:EC:6788:C:N4	78:EC:6805:C:OP2	2.33	0.61
3:BC:142:GLY:N	3:BC:153:SER:O	2.22	0.61
32:B5:1252:C:H5'	80:Bf:105:TYR:HE1	1.64	0.61
36:A1:173:G:H1	36:A1:244:G:N2	1.99	0.61
81:BM:93:ASP:HB3	81:BM:96:GLN:HB2	1.83	0.61
4:BE:141:THR:OG1	4:BE:143:ASP:OD1	2.16	0.61
5:BG:102:VAL:HG13	5:BG:106:LEU:HD12	1.81	0.61
32:B5:138:A:H8	32:B5:141:U:H4'	1.65	0.61
36:A1:307:A:H2'	36:A1:308:A:C8	2.34	0.61
36:A1:2467:G:OP1	77:E:62:ASN:ND2	2.34	0.61
36:A1:3042:U:OP2	36:A1:3092:C:N4	2.25	0.61
63:Ac:43:ILE:HG13	63:Ac:68:TYR:HB3	1.82	0.61
3:BC:45:VAL:HG21	3:BC:68:ILE:HG23	1.81	0.60
20:BF:134:VAL:HA	20:BF:137:ILE:HD12	1.83	0.60
23:BQ:37:THR:O	23:BQ:45:ARG:NH1	2.34	0.60
25:BS:28:ILE:HA	25:BS:58:ALA:HB2	1.83	0.60
38:A4:142:C:OP1	48:AN:38:ARG:NH1	2.32	0.60
63:Ac:13:LYS:HE2	63:Ac:103:THR:HG21	1.83	0.60
80:Bf:108:VAL:HB	81:BM:73:LYS:HE2	1.83	0.60
2:BB:48:VAL:HG13	2:BB:49:ASN:H	1.66	0.60
30:Bd:44:ARG:NH2	32:B5:1280:4AC:OP1	2.33	0.60
32:B5:1488:G:O2'	32:B5:1494:C:O2	2.14	0.60
36:A1:528:U:H2'	36:A1:529:A:C8	2.36	0.60
53:AS:22:PRO:O	54:AT:146:ASN:ND2	2.31	0.60
81:BM:43:ARG:HH21	81:BM:121:VAL:HG11	1.64	0.60
8:BJ:109:LEU:HB2	8:BJ:146:PHE:HB3	1.84	0.60
17:Bb:18:LYS:O	17:Bb:29:ARG:NH2	2.33	0.60
19:BD:76:ARG:HB2	21:BK:22:VAL:HG11	1.83	0.60
26:BT:22:LEU:HD12	26:BT:28:LEU:HD21	1.82	0.60
28:BZ:56:THR:O	28:BZ:103:ARG:NH2	2.33	0.60
36:A1:1657:C:O2'	36:A1:1797:A:OP2	2.17	0.60
36:A1:2768:U:H2'	36:A1:2769:A:H8	1.66	0.60
47:AM:24:LYS:NZ	47:AM:61:GLY:O	2.28	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:BM:134:SER:HA	81:BM:137:MET:HE3	1.81	0.60
7:BI:76:THR:HG21	7:BI:104:ILE:HD12	1.82	0.60
14:BX:54:LEU:HD21	79:DC:502:PRO:HG3	1.83	0.60
14:BX:59:ILE:HG12	18:Be:4:VAL:HG23	1.83	0.60
14:BX:107:PHE:HE1	14:BX:123:LYS:HB3	1.65	0.60
32:B5:1171:A:H2'	32:B5:1172:G:C8	2.37	0.60
32:B5:1772:C:H3'	74:An:2:ARG:HH21	1.67	0.60
11:BO:20:TYR:HB3	11:BO:27:PHE:HB2	1.83	0.60
19:BD:22:ASN:O	19:BD:26:THR:OG1	2.15	0.60
22:BP:108:ARG:H	22:BP:111:MET:HE3	1.65	0.60
36:A1:2107:A:H2	36:A1:3344:A:H8	1.49	0.60
36:A1:2796:G:N7	75:Ao:63:LYS:NZ	2.47	0.60
53:AS:96:ASP:OD1	53:AS:97:VAL:N	2.33	0.60
78:EC:6812:C:H2'	78:EC:6813:A:C8	2.35	0.60
25:BS:27:LYS:NZ	32:B5:1532:U:O2'	2.35	0.60
38:A4:63:G:H22	38:A4:97:A:H2	1.49	0.60
41:AF:156:ILE:HD12	41:AF:161:VAL:HB	1.84	0.60
60:AZ:50:PRO:HD3	60:AZ:68:ILE:HG12	1.83	0.60
1:BA:79:ARG:NH2	1:BA:164:ASN:O	2.35	0.60
32:B5:1697:G:O6	32:B5:1704:U:O4	2.19	0.60
36:A1:1119:C:H2'	36:A1:1120:A:H8	1.67	0.60
36:A1:1580:A:C2	58:AX:33:ARG:HD3	2.36	0.60
36:A1:2555:G:C5	67:Ag:95:ILE:HD11	2.37	0.60
36:A1:2700:G:H5''	54:AT:17:ARG:HG2	1.83	0.60
78:EC:6790:A:N6	78:EC:6798:C:OP2	2.34	0.60
1:BA:114:SER:O	1:BA:116:LYS:NZ	2.35	0.60
33:AA:43:GLY:HA3	33:AA:63:PHE:CE1	2.36	0.60
36:A1:1156:C:OP2	41:AF:94:LYS:NZ	2.33	0.60
36:A1:1580:A:H2	58:AX:33:ARG:HD3	1.67	0.60
36:A1:1724:U:H1'	36:A1:1725:C:C6	2.37	0.60
79:DC:507:GLY:HA2	79:DC:510:ARG:HB2	1.83	0.60
5:BG:160:ARG:NH2	32:B5:68:A:OP1	2.35	0.60
5:BG:195:VAL:O	5:BG:199:GLN:NE2	2.35	0.60
9:BL:29:LYS:HG3	9:BL:31:THR:H	1.67	0.60
27:BU:24:ILE:HG13	27:BU:116:VAL:HG13	1.81	0.60
36:A1:1097:G:N7	54:AT:116:ARG:NH2	2.50	0.60
36:A1:1805:C:H2'	36:A1:1806:A:H8	1.67	0.60
36:A1:2219:A:H2'	36:A1:2220:A2M:C8	2.31	0.60
36:A1:3050:U:O2'	57:AW:16:GLY:O	2.19	0.60
47:AM:20:VAL:O	47:AM:66:THR:OG1	2.17	0.60
79:DC:658:GLU:OE2	79:DC:700:ARG:NE	2.35	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Bb:67:THR:OG1	17:Bb:70:LYS:O	2.20	0.60
31:Bg:89:LEU:HB2	31:Bg:103:PHE:HB2	1.84	0.60
35:AC:166:VAL:O	35:AC:170:LYS:HG2	2.02	0.60
35:AC:317:PRO:C	35:AC:319:LYS:H	2.08	0.60
36:A1:1259:A:N3	36:A1:1280:C:O2'	2.29	0.60
45:AJ:15:GLU:OE2	45:AJ:72:ARG:NH1	2.35	0.60
77:E:10:ARG:NH2	77:E:177:ASP:O	2.35	0.60
23:BQ:25:GLY:HA3	23:BQ:64:ASP:HB2	1.83	0.59
31:Bg:46:LYS:HB3	31:Bg:56:VAL:HG13	1.84	0.59
33:AA:183:GLY:HA2	36:A1:896:A:H5''	1.83	0.59
79:DC:21:ASN:O	79:DC:123:ASP:N	2.31	0.59
79:DC:30:HIS:ND1	79:DC:130:ASP:HB2	2.17	0.59
4:BE:63:ALA:O	4:BE:67:GLN:HG2	2.02	0.59
16:Ba:89:ARG:NH2	32:B5:1088:A:O3'	2.34	0.59
31:Bg:168:THR:HG22	31:Bg:182:ASN:HB3	1.84	0.59
32:B5:1466:G:O2'	32:B5:1602:C:OP1	2.19	0.59
36:A1:129:U:H2'	36:A1:130:A:C8	2.36	0.59
36:A1:249:U:H4'	36:A1:250:U:OP1	2.02	0.59
77:E:125:GLY:H	77:E:126:PRO:HD2	1.67	0.59
79:DC:695:ALA:O	79:DC:700:ARG:NH1	2.35	0.59
5:BG:139:ASN:ND2	32:B5:143:G:OP2	2.30	0.59
7:BI:102:VAL:O	7:BI:167:ALA:N	2.30	0.59
7:BI:184:LEU:HD23	7:BI:189:LEU:HA	1.84	0.59
32:B5:273:G:O6	32:B5:283:U:O2	2.19	0.59
32:B5:947:U:H2'	32:B5:948:G:H8	1.66	0.59
36:A1:238:A:H8	36:A1:238:A:OP2	1.85	0.59
20:BF:117:THR:HG21	20:BF:194:LEU:HD23	1.83	0.59
32:B5:1208:A:H8	32:B5:1269:OMU:H6	1.67	0.59
33:AA:62:VAL:HG22	33:AA:73:GLU:HG2	1.85	0.59
34:AB:240:ARG:NH2	36:A1:1907:C:O2	2.33	0.59
34:AB:287:LYS:O	34:AB:293:ASN:ND2	2.34	0.59
36:A1:664:U:H2'	36:A1:665:A:C8	2.36	0.59
9:BL:2:SER:HB3	9:BL:53:TYR:HB3	1.85	0.59
31:Bg:239:GLU:HB3	31:Bg:257:ALA:HB2	1.83	0.59
32:B5:1230:A:H61	32:B5:1255:G:H1'	1.66	0.59
32:B5:1354:G:O6	32:B5:1369:U:N3	2.34	0.59
32:B5:1511:U:H2'	32:B5:1512:G:C8	2.37	0.59
33:AA:43:GLY:HA3	33:AA:63:PHE:CD1	2.38	0.59
33:AA:180:LEU:HD11	76:Ap:26:VAL:HG21	1.85	0.59
36:A1:2478:C:OP2	36:A1:2480:A:N6	2.35	0.59
50:AP:126:ARG:HG2	50:AP:140:GLU:HG2	1.85	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:EC:6922:G:H1	78:EC:6931:U:H3	1.50	0.59
1:BA:138:TYR:OH	32:B5:1296:A:OP1	2.18	0.59
4:BE:250:GLU:OE1	4:BE:250:GLU:N	2.36	0.59
5:BG:30:LYS:NZ	5:BG:35:GLU:O	2.36	0.59
7:BI:42:ARG:NH1	32:B5:1677:C:OP1	2.35	0.59
21:BK:32:HIS:N	21:BK:37:THR:O	2.33	0.59
32:B5:565:C:O2'	32:B5:577:G:N2	2.36	0.59
36:A1:1666:G:H2'	36:A1:1667:A:C8	2.37	0.59
36:A1:3068:U:OP2	52:AR:62:ARG:NH2	2.32	0.59
53:AS:60:SER:OG	53:AS:62:ASN:ND2	2.31	0.59
75:Ao:24:LYS:HB2	75:Ao:73:GLU:HB3	1.83	0.59
77:E:14:LYS:HA	77:E:17:LEU:HG	1.84	0.59
78:EC:6759:A:H2'	78:EC:6760:A:C8	2.38	0.59
5:BG:188:ARG:NH2	32:B5:284:G:O6	2.35	0.59
22:BP:25:LEU:HD23	22:BP:28:MET:SD	2.43	0.59
26:BT:97:SER:OG	32:B5:1504:G:OP1	2.16	0.59
29:Bc:38:ARG:NH2	29:Bc:60:GLU:OE2	2.36	0.59
32:B5:574:G:H2'	32:B5:575:C:H5''	1.85	0.59
32:B5:1346:A:N6	32:B5:1369:U:O3'	2.35	0.59
79:DC:629:ASP:HB3	79:DC:647:ILE:HD13	1.82	0.59
10:BN:5:HIS:HB3	10:BN:117:LEU:HD23	1.84	0.59
16:Ba:38:ARG:HH21	32:B5:1798:U:H2'	1.68	0.59
32:B5:108:A:H2'	32:B5:109:G:C8	2.37	0.59
32:B5:209:U:H2'	32:B5:210:A:H8	1.67	0.59
36:A1:1203:A:H2'	36:A1:1204:A:C8	2.38	0.59
36:A1:1560:G:O2'	36:A1:1561:G:O4'	2.21	0.59
37:A3:5:G:OP1	45:AJ:143:ARG:NH2	2.35	0.59
36:A1:1348:U:OP1	51:AQ:39:ARG:NH1	2.36	0.59
69:Ai:84:LYS:O	69:Ai:88:GLU:HG2	2.02	0.59
78:EC:6794:C:N4	78:EC:6940:U:O2'	2.36	0.59
3:BC:101:VAL:HG12	3:BC:115:ILE:HD12	1.84	0.59
13:BW:57:ARG:HG2	32:B5:862:A:H4'	1.84	0.59
16:Ba:8:ASN:HB3	32:B5:1791:A:H3'	1.85	0.59
23:BQ:139:GLN:OE1	32:B5:1167:G:N2	2.35	0.59
32:B5:1575:G7M:H2'	32:B5:1576:A:C8	2.38	0.59
36:A1:19:U:H2'	36:A1:20:A:C8	2.38	0.59
81:BM:27:ALA:HB1	81:BM:132:GLU:HB3	1.85	0.59
12:BV:74:GLN:HE21	12:BV:82:VAL:H	1.52	0.58
32:B5:407:A:H2'	32:B5:408:C:C6	2.37	0.58
36:A1:1277:C:H2'	36:A1:1278:A:H8	1.68	0.58
36:A1:1477:A:OP1	36:A1:3075:G:O2'	2.16	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1621:A:H2'	36:A1:1622:U:C6	2.38	0.58
46:AL:76:THR:OG1	46:AL:103:ASN:ND2	2.35	0.58
75:Ao:26:THR:HA	75:Ao:93:LEU:HD21	1.84	0.58
78:EC:6881:U:H2'	78:EC:6882:G:H4'	1.84	0.58
79:DC:578:LYS:HG2	79:DC:582:LYS:HA	1.85	0.58
23:BQ:49:TYR:HA	23:BQ:52:LEU:HD12	1.85	0.58
31:Bg:13:LEU:HB2	31:Bg:310:ILE:HB	1.84	0.58
32:B5:1533:C:H4'	32:B5:1539:G:C6	2.37	0.58
36:A1:3344:A:H2	36:A1:3361:G:H21	1.42	0.58
56:AV:14:SER:O	56:AV:81:GLN:NE2	2.36	0.58
78:EC:6822:U:H2'	78:EC:6823:U:H5''	1.85	0.58
1:BA:27:ARG:NH1	1:BA:43:ASP:O	2.35	0.58
17:Bb:19:HIS:HB3	17:Bb:22:LYS:HB2	1.84	0.58
32:B5:170:U:N3	32:B5:289:U:O2'	2.35	0.58
36:A1:710:A:H2'	36:A1:711:A:C8	2.38	0.58
36:A1:1613:A:OP1	71:Ak:51:LEU:N	2.30	0.58
36:A1:2424:A:OP1	48:AN:90:ASN:ND2	2.28	0.58
36:A1:3322:A:H2'	36:A1:3323:A:C8	2.38	0.58
78:EC:6923:C:H2'	78:EC:6924:G:C8	2.38	0.58
82:VA:30:VAL:HG21	82:VA:185:LEU:HD12	1.85	0.58
4:BE:121:TYR:OH	4:BE:235:TYR:O	2.20	0.58
7:BI:138:ASN:HD21	32:B5:187:G:H2'	1.68	0.58
13:BW:122:SER:O	32:B5:748:U:O2'	2.19	0.58
32:B5:950:C:O2'	32:B5:951:A:OP1	2.21	0.58
36:A1:173:G:H1	36:A1:244:G:H22	1.49	0.58
36:A1:284:A:OP2	75:Ao:41:ARG:NH1	2.37	0.58
36:A1:407:A:C2	38:A4:17:A:H1'	2.39	0.58
36:A1:1571:A:H2'	36:A1:1572:U:O4'	2.03	0.58
36:A1:2555:G:N7	67:Ag:95:ILE:HD11	2.18	0.58
42:AG:95:ASN:OD1	42:AG:98:ARG:NH2	2.36	0.58
26:BT:39:THR:HA	26:BT:100:ILE:HD13	1.85	0.58
36:A1:1268:G:H21	36:A1:1273:A:H62	1.49	0.58
37:A3:4:U:H2'	37:A3:5:G:H8	1.68	0.58
82:VA:25:LEU:HB3	82:VA:191:TYR:HB3	1.86	0.58
5:BG:190:GLN:HA	5:BG:193:LEU:HD12	1.85	0.58
11:BO:120:PRO:HB2	32:B5:887:A:H5''	1.84	0.58
12:BV:32:VAL:HG22	12:BV:60:ARG:HD2	1.85	0.58
25:BS:36:LYS:HB2	25:BS:102:ALA:HA	1.86	0.58
32:B5:1483:A:H2'	32:B5:1484:G:C8	2.38	0.58
46:AL:59:ARG:HD2	46:AL:69:VAL:HG12	1.85	0.58
57:AW:46:PRO:HB2	57:AW:54:LEU:HD23	1.84	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:DC:216:HIS:CD2	79:DC:321:LYS:HG2	2.38	0.58
79:DC:307:LEU:HD13	79:DC:312:LYS:HA	1.85	0.58
79:DC:723:LYS:HZ2	79:DC:804:LEU:H	1.52	0.58
4:BE:147:ILE:HG21	4:BE:169:ILE:HG23	1.85	0.58
34:AB:124:LYS:NZ	36:A1:3297:U:O4	2.37	0.58
36:A1:525:C:H5''	47:AM:79:ALA:HB2	1.86	0.58
36:A1:979:U:H4'	36:A1:980:A:O4'	2.03	0.58
36:A1:1534:A:H2'	36:A1:1535:A:C8	2.39	0.58
36:A1:1659:U:H2'	36:A1:1660:C:C6	2.38	0.58
36:A1:2232:A:H2'	36:A1:2233:A:C8	2.38	0.58
51:AQ:158:HIS:H	51:AQ:186:VAL:HG22	1.69	0.58
77:E:97:LYS:HE3	77:E:126:PRO:HG3	1.85	0.58
78:EC:6835:U:H4'	78:EC:6873:A:H2	1.68	0.58
11:BO:35:GLY:O	32:B5:918:U:O2'	2.19	0.58
22:BP:108:ARG:NH2	25:BS:118:LYS:O	2.37	0.58
27:BU:77:LYS:NZ	32:B5:1195:C:OP1	2.25	0.58
36:A1:2553:U:C4	67:Ag:95:ILE:HG22	2.39	0.58
77:E:34:LEU:HG	77:E:169:VAL:HG11	1.85	0.58
78:EC:6852:U:H2'	78:EC:6853:G:C8	2.38	0.58
8:BJ:106:GLU:HA	8:BJ:111:THR:HG21	1.86	0.58
32:B5:739:G:N2	32:B5:739:G:OP2	2.35	0.58
35:AC:334:PHE:HA	35:AC:339:LEU:HD12	1.85	0.58
46:AL:174:ARG:HB2	69:Ai:9:ILE:HD12	1.86	0.58
61:Aa:104:THR:HG21	61:Aa:112:ILE:HD11	1.85	0.58
11:BO:126:THR:OG1	32:B5:989:U:O2'	2.09	0.58
14:BX:56:LYS:HD3	14:BX:93:LEU:HG	1.86	0.58
31:Bg:147:HIS:CE1	31:Bg:173:GLY:H	2.22	0.58
32:B5:1628:U:H2'	32:B5:1629:G:C8	2.38	0.58
36:A1:2406:C:H2'	36:A1:2407:C:C6	2.39	0.58
52:AR:175:GLN:HG2	52:AR:176:ARG:HD2	1.86	0.58
8:BJ:83:VAL:HG13	8:BJ:85:VAL:HG23	1.86	0.57
32:B5:590:C:H2'	32:B5:591:A:H8	1.69	0.57
36:A1:627:U:H2'	36:A1:628:A:C8	2.39	0.57
36:A1:718:G:OP1	61:Aa:117:ARG:NH2	2.36	0.57
36:A1:3023:U:H2'	36:A1:3024:A:H8	1.69	0.57
63:Ac:16:LEU:HB3	63:Ac:98:SER:HB3	1.85	0.57
2:BB:24:PHE:HA	2:BB:27:LYS:HD2	1.85	0.57
32:B5:209:U:H2'	32:B5:210:A:C8	2.39	0.57
32:B5:1196:A:OP2	32:B5:1464:G:N2	2.31	0.57
36:A1:728:G:H5''	51:AQ:43:PRO:HB2	1.86	0.57
36:A1:1923:C:H5''	74:An:25:LYS:HE2	1.84	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AJ:93:ASP:O	45:AJ:156:LYS:NZ	2.37	0.57
53:AS:4:PHE:HD2	53:AS:104:GLU:HG3	1.67	0.57
4:BE:73:ASP:OD2	4:BE:145:ARG:NH2	2.30	0.57
6:BH:63:PRO:C	6:BH:65:PRO:HD3	2.29	0.57
21:BK:19:GLY:HA2	21:BK:68:LEU:HD12	1.86	0.57
36:A1:1176:C:H2'	36:A1:1177:G:N2	2.19	0.57
36:A1:2180:G:H2'	36:A1:2181:C:C6	2.39	0.57
6:BH:17:GLU:HB2	6:BH:43:PHE:HE2	1.69	0.57
14:BX:90:ASP:O	14:BX:136:TRP:NE1	2.36	0.57
19:BD:27:ARG:NH2	32:B5:1436:A:OP2	2.36	0.57
25:BS:76:PRO:HB3	25:BS:81:ILE:HD12	1.85	0.57
31:Bg:273:ASP:OD1	31:Bg:275:ARG:NH1	2.36	0.57
32:B5:1087:A:H2'	32:B5:1088:A:C8	2.38	0.57
56:AV:23:MET:HE3	56:AV:100:GLY:HA3	1.85	0.57
2:BB:202:LYS:NZ	32:B5:1056:U:O2	2.35	0.57
28:BZ:83:LEU:HD23	28:BZ:88:ILE:HD11	1.87	0.57
32:B5:1357:A:H2'	32:B5:1358:G:H8	1.69	0.57
36:A1:1447:G:H3'	50:AP:67:ILE:HD11	1.87	0.57
45:AJ:37:LEU:HD22	45:AJ:67:VAL:HG12	1.85	0.57
45:AJ:115:LYS:HG3	45:AJ:116:TYR:H	1.69	0.57
7:BI:54:LYS:NZ	32:B5:333:A:OP2	2.37	0.57
10:BN:124:ARG:NH2	32:B5:967:A:OP2	2.36	0.57
23:BQ:47:LYS:HE3	23:BQ:50:GLU:OE2	2.05	0.57
32:B5:1641:C:H2'	32:B5:1642:G:C8	2.40	0.57
36:A1:176:G:H2'	36:A1:177:U:C6	2.35	0.57
41:AF:25:GLN:HB3	41:AF:28:ALA:HB3	1.84	0.57
56:AV:87:ARG:HH22	56:AV:137:VAL:HG21	1.69	0.57
78:EC:6809:G:H2'	78:EC:6810:U:C6	2.39	0.57
13:BW:110:ILE:HD12	13:BW:126:LEU:HD11	1.85	0.57
26:BT:53:TRP:CH2	26:BT:100:ILE:HD11	2.40	0.57
35:AC:138:ARG:NH1	36:A1:1384:U:H5'	2.20	0.57
36:A1:1157:G:H2'	36:A1:1158:A:O4'	2.05	0.57
36:A1:2683:U:H2'	36:A1:2684:C:C6	2.39	0.57
36:A1:3017:A:N1	36:A1:3037:U:H5	2.02	0.57
43:AH:128:VAL:HA	43:AH:157:ASN:HD21	1.70	0.57
1:BA:88:LYS:NZ	24:BR:82:ASP:O	2.33	0.57
3:BC:165:VAL:HG11	3:BC:210:THR:HA	1.85	0.57
19:BD:135:GLU:HB3	19:BD:187:LYS:HB3	1.87	0.57
31:Bg:180:ALA:HB3	31:Bg:190:ALA:HB3	1.85	0.57
35:AC:281:ILE:HD13	51:AQ:28:LEU:HD12	1.85	0.57
36:A1:1138:U:OP1	62:Ab:13:THR:HG21	2.05	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1194:G:H2'	36:A1:1195:A:C8	2.39	0.57
36:A1:2507:C:H2'	36:A1:2508:U:C6	2.39	0.57
55:AU:32:SER:HA	55:AU:35:LYS:HG2	1.86	0.57
79:DC:436:LEU:HD13	79:DC:438:MET:HG2	1.87	0.57
80:Bf:123:ASN:OD1	80:Bf:148:TYR:OH	2.22	0.57
4:BE:148:ARG:NH1	5:BG:201:GLN:OE1	2.38	0.57
10:BN:60:VAL:HG23	10:BN:66:ILE:HD12	1.85	0.57
12:BV:74:GLN:HG3	12:BV:83:TRP:HB3	1.87	0.57
13:BW:101:TYR:HB3	13:BW:112:ASP:HB2	1.86	0.57
32:B5:939:A:H2'	32:B5:940:A:C8	2.39	0.57
36:A1:2457:G:H21	36:A1:2483:G:H1'	1.70	0.57
51:AQ:40:THR:HG22	51:AQ:42:ALA:H	1.70	0.57
52:AR:169:ALA:HB1	52:AR:173:ARG:HH12	1.70	0.57
75:Ao:61:LYS:NZ	75:Ao:63:LYS:O	2.33	0.57
77:E:160:LYS:HE2	77:E:162:VAL:HB	1.86	0.57
11:BO:125:SER:OG	11:BO:126:THR:N	2.38	0.57
20:BF:72:HIS:HD2	20:BF:107:LYS:HD2	1.70	0.57
21:BK:59:PHE:CZ	21:BK:62:GLN:HG3	2.40	0.57
32:B5:778:G:H2'	32:B5:779:U:H2'	1.87	0.57
32:B5:1474:G:H2'	32:B5:1475:A:C8	2.38	0.57
49:AO:125[A]:ARG:HG3	49:AO:129[A]:LEU:HD12	1.87	0.57
67:Ag:54:ILE:HD11	67:Ag:78:GLY:HA2	1.86	0.57
78:EC:6835:U:H4'	78:EC:6873:A:C2	2.40	0.57
82:VA:69:ASP:OD1	82:VA:70:LEU:N	2.38	0.57
10:BN:129:TYR:HA	10:BN:132:VAL:HG12	1.87	0.56
14:BX:57:LEU:HD22	18:Be:4:VAL:HG22	1.87	0.56
19:BD:49:ILE:HD13	19:BD:87:TYR:HB2	1.87	0.56
32:B5:800:U:H2'	32:B5:801:G:H8	1.69	0.56
36:A1:1669:C:H5'	67:Ag:30:LEU:HD11	1.88	0.56
36:A1:2207:A:H5'	36:A1:2208:A:H2	1.70	0.56
36:A1:2448:G:H2'	36:A1:2449:A:C8	2.40	0.56
66:Af:14:LEU:HD11	66:Af:31:LYS:HB2	1.87	0.56
78:EC:6828:G:H2'	78:EC:6829:A:C8	2.39	0.56
79:DC:387:PRO:HA	79:DC:394:PHE:HB3	1.87	0.56
7:BI:155:SER:O	7:BI:159:GLN:NE2	2.38	0.56
9:BL:152:GLN:HE21	10:BN:133:ALA:HA	1.70	0.56
10:BN:62:GLN:HB2	10:BN:65:VAL:HG22	1.86	0.56
21:BK:27:PHE:HB3	21:BK:40:LEU:HD12	1.85	0.56
32:B5:766:U:H3	32:B5:770:A:H62	1.51	0.56
32:B5:895:G:H2'	32:B5:896:U:C6	2.40	0.56
35:AC:48:GLN:NE2	36:A1:336:A:O2'	2.38	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1213:G:H4'	53:AS:90:MET:HE3	1.87	0.56
47:AM:55:ARG:NH1	47:AM:76:ALA:O	2.29	0.56
24:BR:18:GLU:OE2	24:BR:19:ARG:NE	2.35	0.56
29:Bc:11:LYS:O	29:Bc:31:GLU:N	2.37	0.56
32:B5:319:U:H4'	32:B5:323:A:C8	2.41	0.56
32:B5:590:C:H2'	32:B5:591:A:C8	2.41	0.56
32:B5:1253:U:H4'	80:Bf:143:LYS:HB2	1.88	0.56
32:B5:1524:A:H2'	32:B5:1525:A:C8	2.40	0.56
36:A1:93:C:OP2	36:A1:2764:C:O2'	2.20	0.56
36:A1:1107:C:OP2	62:Ab:22:LYS:NZ	2.36	0.56
36:A1:1914:G:O2'	52:AR:82:LYS:O	2.23	0.56
36:A1:2228:A:H2'	36:A1:2229:A:C8	2.40	0.56
36:A1:2720:G:OP1	51:AQ:180:ARG:NH2	2.37	0.56
36:A1:2916:U:H1'	56:AV:44:SER:HB2	1.88	0.56
61:Aa:36:GLY:HA3	61:Aa:40:HIS:CE1	2.40	0.56
79:DC:147:LEU:HD22	79:DC:193:ALA:HB2	1.86	0.56
79:DC:406:LYS:HB2	79:DC:409:GLN:HB2	1.87	0.56
2:BB:111:ARG:NH2	32:B5:930:A:O2'	2.39	0.56
6:BH:104:ARG:NH2	32:B5:805:U:O4	2.37	0.56
7:BI:31:ARG:NH1	32:B5:332:U:OP1	2.39	0.56
24:BR:31:ASN:ND2	24:BR:55:THR:OG1	2.38	0.56
32:B5:358:U:O2'	32:B5:360:A:OP1	2.23	0.56
32:B5:1144:U:H2'	32:B5:1145:U:C6	2.40	0.56
36:A1:2344:U:H2'	36:A1:2345:A:C8	2.41	0.56
60:AZ:90:GLU:HA	60:AZ:93:LYS:HB2	1.88	0.56
11:BO:32:ASP:OD2	11:BO:34:SER:OG	2.22	0.56
14:BX:69:ARG:HG3	14:BX:117:ILE:HG12	1.86	0.56
14:BX:73:ARG:HH12	14:BX:82:LYS:C	2.14	0.56
19:BD:223:LYS:NZ	19:BD:224:ASP:O	2.36	0.56
32:B5:145:A:HO2'	32:B5:146:U:H6	1.54	0.56
32:B5:406:U:H2'	32:B5:407:A:H8	1.70	0.56
32:B5:1490:C:H1'	32:B5:1492:A:N1	2.21	0.56
36:A1:238:A:H2'	36:A1:239:G:O4'	2.05	0.56
36:A1:1233:G:H2'	36:A1:1234:G:C8	2.41	0.56
36:A1:1721:U:O2'	36:A1:1723:A:N7	2.38	0.56
36:A1:2875:U:O2'	36:A1:2876:C:O5'	2.19	0.56
36:A1:3056:U:O2	64:Ad:28:ARG:NH2	2.39	0.56
81:BM:103:LEU:HD21	81:BM:116:VAL:HB	1.88	0.56
82:VA:104:ARG:O	82:VA:182:THR:HG22	2.06	0.56
18:Be:31:LYS:HD3	32:B5:545:A:H2'	1.87	0.56
21:BK:3:MET:HG3	21:BK:8:ARG:HG2	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1134:G:O2'	36:A1:2642:A:N3	2.38	0.56
36:A1:2223:A:H2'	36:A1:2224:A:C8	2.40	0.56
36:A1:3295:A:H2'	36:A1:3296:A:C8	2.40	0.56
41:AF:98:LYS:HG2	41:AF:129:LEU:HD21	1.87	0.56
78:EC:6801:A:C8	78:EC:6884:G:H1'	2.39	0.56
4:BE:200:ARG:NH1	32:B5:737:A:OP1	2.39	0.56
13:BW:115:GLU:OE2	13:BW:119:LYS:NZ	2.37	0.56
20:BF:63:GLN:NE2	20:BF:66:GLN:H	1.98	0.56
25:BS:2:SER:O	28:BZ:82:HIS:ND1	2.38	0.56
32:B5:1477:G:H2'	32:B5:1478:G:C8	2.40	0.56
33:AA:70:ARG:HH21	33:AA:72:ARG:NH2	2.03	0.56
37:A3:50:U:O2'	39:AD:221:GLU:O	2.19	0.56
79:DC:36:THR:HG23	79:DC:102:LEU:HD21	1.88	0.56
5:BG:167:LYS:HD3	32:B5:72:A:H8	1.70	0.56
19:BD:161:GLY:HA3	32:B5:1331:A:H61	1.70	0.56
22:BP:78:THR:HA	32:B5:1241:G:H4'	1.88	0.56
32:B5:698:U:C4	32:B5:741:C:C4	2.93	0.56
34:AB:85:VAL:HG22	34:AB:202:THR:HG22	1.87	0.56
36:A1:640:U:OP1	61:Aa:21:ARG:NH1	2.34	0.56
36:A1:1188:U:OP1	36:A1:1210:U:O2'	2.17	0.56
77:E:9:VAL:HG21	77:E:184:LEU:HD12	1.87	0.56
82:VA:139:LEU:HD11	82:VA:169:GLU:HA	1.87	0.56
14:BX:75:GLN:HG2	79:DC:502:PRO:HG2	1.88	0.56
18:Be:15:LYS:NZ	32:B5:585:A:OP1	2.39	0.56
28:BZ:77:ARG:NH2	32:B5:1533:C:OP2	2.34	0.56
31:Bg:9:LEU:HA	31:Bg:313:TRP:CD1	2.40	0.56
32:B5:918:U:H2'	32:B5:919:A:C8	2.41	0.56
32:B5:1252:C:H5'	80:Bf:105:TYR:CE1	2.40	0.56
36:A1:959:C:O2'	36:A1:2410:U:N3	2.36	0.56
36:A1:1110:U:H2'	36:A1:1111:U:C6	2.41	0.56
37:A3:84:A:H2'	37:A3:85:G:C8	2.41	0.56
37:A3:112:G:H2'	37:A3:113:C:C6	2.41	0.56
38:A4:58:G:O6	70:Aj:63:ARG:NH1	2.37	0.56
44:AI:30:LYS:HE2	44:AI:63:GLU:HA	1.88	0.56
45:AJ:133:ARG:NH2	45:AJ:158:ASP:OD2	2.38	0.56
78:EC:6849:A:O2'	78:EC:6850:C:O4'	2.20	0.56
1:BA:38:PHE:O	24:BR:105:GLN:NE2	2.39	0.56
32:B5:1445:G:O5'	80:Bf:89:LYS:NZ	2.35	0.56
36:A1:994:G:N2	36:A1:995:U:O4	2.27	0.56
36:A1:1175:C:O2	49:AO:87[A]:MET:HG2	2.06	0.56
15:BY:39:GLU:HA	15:BY:42:GLU:HG2	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:BK:5:LYS:O	21:BK:9:ASN:ND2	2.39	0.55
25:BS:123:ARG:NH1	32:B5:1546:G:OP1	2.33	0.55
32:B5:1000:C:N4	32:B5:1003:A:OP2	2.30	0.55
32:B5:1579:U:H2'	32:B5:1580:C:C6	2.41	0.55
36:A1:2673:A:H5''	45:AJ:95:ASN:ND2	2.16	0.55
53:AS:77:VAL:HG11	53:AS:106:LEU:HD22	1.88	0.55
77:E:11:GLU:HA	77:E:14:LYS:HG2	1.88	0.55
5:BG:2:LYS:HG2	5:BG:17:GLU:HG3	1.86	0.55
6:BH:34:LEU:HD12	6:BH:38:LEU:HB2	1.88	0.55
31:Bg:20:VAL:O	31:Bg:291:SER:OG	2.22	0.55
36:A1:250:U:H2'	36:A1:251:G:H5'	1.87	0.55
36:A1:1092:C:O2'	36:A1:1093:A:OP1	2.22	0.55
36:A1:3121:U:H1'	36:A1:3122:A:H5''	1.88	0.55
43:AH:93:VAL:HG13	43:AH:177:ASP:HA	1.87	0.55
77:E:111:ILE:HB	77:E:136:THR:HG22	1.89	0.55
4:BE:97:GLU:HG3	4:BE:113:ARG:HD3	1.89	0.55
5:BG:66:GLY:HA2	32:B5:1681:A:H1'	1.87	0.55
20:BF:223:SER:HB3	78:EC:6841:U:H5''	1.87	0.55
22:BP:20:VAL:HG11	22:BP:25:LEU:HD21	1.88	0.55
32:B5:741:C:H4'	32:B5:742:U:H5'	1.89	0.55
34:AB:212:ASN:ND2	34:AB:353:GLU:OE1	2.40	0.55
36:A1:1667:A:H2'	36:A1:1668:G:C8	2.42	0.55
36:A1:2880:U:OP1	56:AV:47:ASN:ND2	2.32	0.55
82:VA:31:ASP:OD1	82:VA:83:ASN:ND2	2.35	0.55
32:B5:688:G:H2'	32:B5:689:G:H8	1.72	0.55
36:A1:394:G:N1	36:A1:397:A:OP2	2.39	0.55
36:A1:1686:U:OP1	55:AU:42:LYS:NZ	2.27	0.55
36:A1:2463:G:H1'	77:E:162:VAL:HG21	1.88	0.55
43:AH:1:MET:HE1	53:AS:138:GLN:HB3	1.86	0.55
2:BB:116:LYS:HG3	32:B5:931:C:H5''	1.88	0.55
11:BO:80:HIS:HD1	11:BO:114:ARG:HB2	1.72	0.55
31:Bg:292:LEU:HD12	31:Bg:301:LEU:HD11	1.88	0.55
32:B5:1220:C:H2'	32:B5:1221:A:H8	1.71	0.55
36:A1:8:C:H2'	36:A1:9:U:C6	2.42	0.55
42:AG:107:GLU:HA	42:AG:110:THR:HG22	1.89	0.55
65:Ae:89:THR:HG22	65:Ae:117:ILE:HG13	1.89	0.55
1:BA:65:ALA:HB2	1:BA:181:VAL:HG23	1.89	0.55
3:BC:148:LEU:HD21	8:BJ:95:TYR:CZ	2.41	0.55
22:BP:115:TYR:OH	32:B5:1556:A:OP1	2.21	0.55
32:B5:193:U:O2'	32:B5:195:G:OP2	2.23	0.55
32:B5:1575:G7M:O5'	32:B5:1575:G7M:H8	2.07	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1236:G:N2	36:A1:1244:A:OP1	2.39	0.55
36:A1:1388:U:O2'	65:Ae:99:ASN:O	2.24	0.55
36:A1:3040:A:H5''	56:AV:12:ARG:HB2	1.89	0.55
39:AD:85:ARG:HH12	39:AD:254:LYS:H	1.52	0.55
79:DC:27:HIS:HB3	79:DC:30:HIS:NE2	2.22	0.55
32:B5:1208:A:O2'	32:B5:1270:G:OP2	2.15	0.55
32:B5:1398:U:H2'	32:B5:1400:A:C5	2.42	0.55
34:AB:250:ALA:HB1	36:A1:2947:G:N3	2.21	0.55
36:A1:591:G:N2	36:A1:612:U:OP1	2.33	0.55
36:A1:1846:C:OP1	36:A1:1849:C:N4	2.36	0.55
38:A4:9:A:H2'	38:A4:10:A:C8	2.42	0.55
61:Aa:85:ASP:OD1	61:Aa:86:LYS:N	2.39	0.55
79:DC:81:MET:SD	79:DC:85:ASP:HB3	2.47	0.55
32:B5:946:U:H2'	32:B5:947:U:C6	2.42	0.55
32:B5:1291:G:H22	32:B5:1324:G:H22	1.54	0.55
35:AC:20:LEU:HD11	35:AC:252:GLU:HG3	1.89	0.55
36:A1:307:A:H2'	36:A1:308:A:H8	1.71	0.55
36:A1:2376:G:H2'	36:A1:2377:G:C8	2.42	0.55
36:A1:2961:G:H2'	36:A1:2962:U:C6	2.41	0.55
78:EC:6804:A:O2'	78:EC:6808:G:N2	2.34	0.55
2:BB:98:THR:H	2:BB:232:HIS:CE1	2.25	0.55
8:BJ:152:SER:O	8:BJ:156:ILE:HD12	2.06	0.55
17:Bb:54:VAL:HG13	17:Bb:63:LEU:HB3	1.89	0.55
24:BR:21:TYR:CD1	24:BR:58:MET:HE1	2.42	0.55
25:BS:114:GLU:HA	25:BS:117:LYS:HD3	1.89	0.55
32:B5:145:A:O2'	32:B5:146:U:H5''	2.07	0.55
32:B5:1081:A:H2	32:B5:1082:C:H42	1.54	0.55
32:B5:1234:A:O2'	80:Bf:140:TYR:OH	2.15	0.55
32:B5:1684:U:H2'	32:B5:1685:G:C8	2.42	0.55
32:B5:1732:A:H2'	32:B5:1733:C:C6	2.42	0.55
36:A1:69:C:OP1	48:AN:178:HIS:ND1	2.31	0.55
36:A1:2438:A:H2'	36:A1:2439:A:C8	2.41	0.55
78:EC:6776:A:N3	78:EC:6818:G:N2	2.53	0.55
79:DC:20:ARG:NH2	79:DC:339:VAL:O	2.40	0.55
79:DC:187:VAL:HG23	82:VA:130:PRO:HB2	1.88	0.55
4:BE:12:LEU:HD21	4:BE:22:LYS:HG2	1.89	0.55
4:BE:230:GLU:HG2	4:BE:231:GLN:H	1.72	0.55
13:BW:22:LYS:HD3	17:Bb:3:LEU:HA	1.89	0.55
21:BK:46:LEU:O	21:BK:50:THR:OG1	2.21	0.55
33:AA:149:ARG:NH1	33:AA:155:LYS:HE3	2.21	0.55
36:A1:2584:G:H1'	42:AG:240:ASN:ND2	2.22	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A4:57:C:H4'	38:A4:63:G:N7	2.22	0.55
46:AL:46:ILE:HD12	46:AL:49:ARG:HB2	1.89	0.55
47:AM:48:GLY:HA3	47:AM:53:VAL:HB	1.88	0.55
51:AQ:120:GLU:HG3	51:AQ:122:ILE:HG12	1.89	0.55
79:DC:201:GLN:HE22	82:VA:145:ILE:HB	1.72	0.55
7:BI:165:LEU:HD13	7:BI:183:ILE:HD13	1.89	0.54
32:B5:69:G:O6	32:B5:82:U:O4	2.26	0.54
32:B5:1648:A:H2'	32:B5:1649:G:C8	2.42	0.54
35:AC:99:MET:HE3	35:AC:102:PRO:HA	1.88	0.54
36:A1:12:A:H2'	36:A1:13:A:C8	2.43	0.54
36:A1:1222:G:OP1	82:VA:8:LYS:NZ	2.36	0.54
36:A1:1253:U:O2'	36:A1:1263:A:OP1	2.25	0.54
60:AZ:70:PRO:HG3	60:AZ:115:LYS:HB2	1.90	0.54
78:EC:6935:G:O2'	78:EC:6936:G:H8	1.90	0.54
79:DC:155:VAL:HG23	79:DC:202:VAL:HG11	1.88	0.54
2:BB:100:PHE:HB3	2:BB:181:LEU:HD21	1.90	0.54
13:BW:56:HIS:O	32:B5:861:U:O2'	2.25	0.54
21:BK:13:GLN:HA	21:BK:80:LEU:HD21	1.88	0.54
23:BQ:52:LEU:HD23	23:BQ:60:PHE:CD2	2.42	0.54
32:B5:240:U:H2'	32:B5:241:U:C6	2.42	0.54
32:B5:472:U:H2'	32:B5:473:A:H8	1.71	0.54
35:AC:65:TRP:HB3	35:AC:69:ARG:HD3	1.89	0.54
35:AC:169:LEU:HD23	35:AC:178:LEU:HD11	1.88	0.54
36:A1:1129:A:H2'	36:A1:1130:A:C8	2.41	0.54
36:A1:3034:C:H5	43:AH:121:LYS:HB2	1.73	0.54
77:E:120:VAL:HG12	78:EC:6773:G:H22	1.72	0.54
78:EC:6889:A:H4'	78:EC:6890:A:OP1	2.07	0.54
79:DC:6:VAL:HG12	79:DC:47:SER:HB3	1.89	0.54
79:DC:45:ILE:HD11	79:DC:78:TYR:HB3	1.89	0.54
19:BD:160:SER:OG	32:B5:1329:A:OP2	2.19	0.54
25:BS:57:ARG:HH11	28:BZ:40:VAL:HG21	1.72	0.54
32:B5:821:U:N3	32:B5:852:C:O2	2.34	0.54
32:B5:950:C:H2'	32:B5:951:A:C8	2.42	0.54
33:AA:111:THR:HB	33:AA:136:ILE:HD13	1.88	0.54
36:A1:524:U:OP1	47:AM:77:ARG:NH2	2.30	0.54
36:A1:1292:C:O2'	36:A1:1293:U:OP1	2.23	0.54
36:A1:1340:G:OP2	65:Ae:61:LYS:NZ	2.34	0.54
36:A1:1798:A:H2'	36:A1:1799:A:C8	2.43	0.54
36:A1:2213:A:H2'	36:A1:2214:A:H8	1.71	0.54
36:A1:3162:C:H2'	36:A1:3163:A:H8	1.72	0.54
36:A1:3193:C:H2'	36:A1:3194:C:C6	2.41	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AR:159:ALA:HB1	52:AR:163:ARG:HH21	1.73	0.54
3:BC:83:ILE:HD11	3:BC:125:ILE:HD11	1.89	0.54
3:BC:170:ILE:HB	3:BC:197:TYR:HB2	1.89	0.54
17:Bb:50:ALA:O	17:Bb:51:GLN:HG2	2.07	0.54
32:B5:58:U:O2'	32:B5:451:A:N3	2.37	0.54
32:B5:837:G:H2'	32:B5:838:G:C8	2.42	0.54
36:A1:1480:G:O2'	36:A1:1871:U:O4	2.23	0.54
36:A1:1523:U:OP1	36:A1:1607:U:N3	2.41	0.54
36:A1:1765:U:H2'	36:A1:1766:G:H4'	1.88	0.54
79:DC:615:ARG:HA	79:DC:618:ILE:HG12	1.89	0.54
19:BD:8:LYS:HE3	27:BU:61:LYS:HD2	1.90	0.54
20:BF:96:SER:O	20:BF:180:ARG:NH2	2.39	0.54
32:B5:52:U:H2'	32:B5:53:G:C8	2.42	0.54
32:B5:480:G:O6	32:B5:508:U:O2	2.23	0.54
32:B5:705:U:H2'	32:B5:730:G:H1	1.72	0.54
32:B5:812:A:H62	32:B5:859:A:H5'	1.71	0.54
32:B5:894:U:H2'	32:B5:895:G:C8	2.43	0.54
32:B5:1252:C:OP1	80:Bf:118:ARG:NH1	2.36	0.54
33:AA:126:LEU:HD13	33:AA:150:LEU:HD21	1.89	0.54
35:AC:303:GLY:H	36:A1:1347:U:H5''	1.73	0.54
36:A1:358:G:N2	36:A1:361:A:OP2	2.35	0.54
36:A1:1737:U:O2	67:Ag:52:GLN:NE2	2.40	0.54
36:A1:3006:A:H2'	36:A1:3007:U:O4'	2.08	0.54
43:AH:57:VAL:HG23	43:AH:68:LEU:HD13	1.88	0.54
51:AQ:22:ASP:HA	51:AQ:27:LYS:HE2	1.89	0.54
77:E:33:GLU:O	77:E:206:VAL:HA	2.08	0.54
6:BH:151:LYS:HE2	6:BH:184:GLU:HG2	1.89	0.54
12:BV:17:CYS:HB2	12:BV:56:SER:HB3	1.90	0.54
19:BD:75:LYS:HZ1	21:BK:18:GLU:HB3	1.73	0.54
32:B5:546:U:H2'	32:B5:547:U:C6	2.43	0.54
33:AA:135:ILE:HD12	33:AA:149:ARG:HD2	1.90	0.54
36:A1:707:U:OP1	36:A1:780:A:O2'	2.19	0.54
36:A1:939:U:O2'	36:A1:2402:A:N1	2.37	0.54
36:A1:1389:G:H5''	65:Ae:101:SER:HB3	1.88	0.54
36:A1:2160:G:H2'	36:A1:2161:G:H8	1.72	0.54
36:A1:2465:G:N2	36:A1:2491:A:N1	2.55	0.54
36:A1:3302:U:H3	36:A1:3312:U:H3	1.55	0.54
54:AT:111:ALA:O	54:AT:115:LYS:HG2	2.08	0.54
78:EC:6835:U:H2'	78:EC:6848:U:O2'	2.07	0.54
26:BT:130:ARG:NH2	32:B5:1359:C:OP1	2.40	0.54
36:A1:792:G:H2'	36:A1:793:C:C6	2.43	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:23:HIS:O	1:BA:48:ILE:N	2.30	0.54
16:Ba:70:LYS:NZ	32:B5:933:A:OP1	2.36	0.54
19:BD:40:ARG:NE	19:BD:47:GLU:OE2	2.37	0.54
36:A1:737:G:H2'	36:A1:738:A:C8	2.43	0.54
36:A1:1629:U:O2'	36:A1:1630:U:OP1	2.25	0.54
37:A3:4:U:H2'	37:A3:5:G:C8	2.42	0.54
79:DC:82:SER:OG	79:DC:83:ASP:N	2.40	0.54
25:BS:36:LYS:HE3	32:B5:1567:U:H4'	1.89	0.54
36:A1:649:A2M:OP2	36:A1:2868:U:O2'	2.26	0.54
36:A1:1721:U:OP2	52:AR:124:TYR:OH	2.18	0.54
77:E:48:ARG:HE	77:E:159:LEU:HD23	1.72	0.54
2:BB:139:ALA:HB2	2:BB:172:LEU:HD11	1.90	0.54
23:BQ:22:VAL:HG13	23:BQ:63:ILE:HD11	1.89	0.54
32:B5:521:A:H2'	32:B5:522:U:C6	2.42	0.54
32:B5:580:A:O2'	32:B5:582:U:OP1	2.26	0.54
32:B5:698:U:N3	32:B5:741:C:C5	2.76	0.54
36:A1:1290:A:H2'	36:A1:1291:A:C8	2.43	0.54
36:A1:1367:G:OP1	65:Ae:45:ARG:NH2	2.41	0.54
36:A1:1575:A:H2'	36:A1:1576:G:H5''	1.89	0.54
36:A1:2413:A:H2'	36:A1:2414:G:H8	1.73	0.54
36:A1:3033:A:H2'	36:A1:3034:C:O2	2.08	0.54
20:BF:91:GLU:O	20:BF:95:ASN:ND2	2.41	0.53
21:BK:91:TYR:CD1	21:BK:92:ILE:HG12	2.44	0.53
31:Bg:53:LYS:HD2	31:Bg:55:GLY:H	1.73	0.53
31:Bg:300:THR:HA	31:Bg:314:GLN:HG3	1.90	0.53
35:AC:35:VAL:HG21	35:AC:244:LEU:HD21	1.89	0.53
35:AC:107:ARG:HA	36:A1:664:U:H5'	1.89	0.53
36:A1:2459:A:H62	36:A1:2461:A:H61	1.55	0.53
36:A1:2890:A:O2'	36:A1:2933:A:N3	2.39	0.53
42:AG:27:THR:O	42:AG:28:HIS:ND1	2.42	0.53
79:DC:129:VAL:O	79:DC:158:ASN:N	2.32	0.53
79:DC:598:SER:HA	79:DC:601:ILE:HD12	1.89	0.53
2:BB:150:VAL:H	32:B5:1067:C:H5''	1.72	0.53
27:BU:89:ARG:NH2	32:B5:1383:G:O5'	2.37	0.53
32:B5:183:U:H2'	32:B5:184:C:C6	2.44	0.53
32:B5:846:G:H2'	32:B5:847:A:C8	2.43	0.53
32:B5:1086:A:H2'	32:B5:1087:A:C8	2.43	0.53
36:A1:643:U:O2'	36:A1:1153:A:N1	2.33	0.53
36:A1:993:G:N3	36:A1:2637:A:H2'	2.23	0.53
36:A1:1222:G:OP2	82:VA:57:THR:OG1	2.27	0.53
36:A1:2449:A:H2'	36:A1:2450:G:C8	2.43	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:BM:22:VAL:HG11	81:BM:135:MET:HB3	1.90	0.53
82:VA:142:PRO:HG2	82:VA:154:SER:HB3	1.89	0.53
11:BO:68:ALA:HA	11:BO:71:CYS:HB2	1.90	0.53
24:BR:84:TYR:CZ	24:BR:86:PRO:HG3	2.43	0.53
33:AA:149:ARG:HH12	33:AA:155:LYS:HE3	1.74	0.53
36:A1:421:G:O6	36:A1:2383:C:O2'	2.21	0.53
36:A1:2901:G:O2'	36:A1:3024:A:N1	2.41	0.53
37:A3:8:G:O6	39:AD:21:ARG:NH2	2.38	0.53
42:AG:185:ARG:O	42:AG:188:THR:HG22	2.08	0.53
42:AG:189:LEU:HD12	42:AG:190:VAL:HG13	1.90	0.53
5:BG:57:ASP:HA	5:BG:106:LEU:HA	1.90	0.53
32:B5:923:A:H2'	32:B5:924:A:C8	2.44	0.53
32:B5:1160:A:H2'	32:B5:1161:C:C6	2.43	0.53
36:A1:952:A:H4'	36:A1:968:G:N2	2.24	0.53
36:A1:1119:C:H2'	36:A1:1120:A:C8	2.43	0.53
36:A1:2526:C:H2'	36:A1:2527:G:C8	2.43	0.53
50:AP:33:ALA:HB1	50:AP:117:ILE:HG12	1.91	0.53
79:DC:220:PHE:HB3	79:DC:328:LEU:HD13	1.89	0.53
5:BG:32:ILE:HG12	5:BG:100:ALA:HB1	1.90	0.53
11:BO:29:HIS:CD2	11:BO:41:ARG:HB2	2.43	0.53
11:BO:136:ARG:NH2	32:B5:1785:U:OP1	2.35	0.53
14:BX:68:ILE:HG22	14:BX:70:LYS:HD2	1.90	0.53
20:BF:175:LEU:HD22	20:BF:198:LEU:HD23	1.91	0.53
32:B5:333:A:H2'	32:B5:334:G:C8	2.42	0.53
32:B5:646:C:H2'	32:B5:647:G:O4'	2.09	0.53
35:AC:181:VAL:O	35:AC:182:LEU:HG	2.08	0.53
36:A1:585:A:H2'	36:A1:586:C:C6	2.43	0.53
36:A1:2526:C:H2'	36:A1:2527:G:H8	1.74	0.53
56:AV:59:MET:HE3	56:AV:73:VAL:HG12	1.89	0.53
72:Al:5:LYS:HE2	72:Al:13:MET:HE1	1.90	0.53
79:DC:121:VAL:HA	79:DC:399:ARG:HD2	1.91	0.53
79:DC:223:ARG:HB2	79:DC:241:MET:HE3	1.91	0.53
2:BB:26:ARG:HA	2:BB:50:LYS:HE2	1.91	0.53
19:BD:190:ARG:HH12	19:BD:195:SER:HB2	1.72	0.53
25:BS:134:ARG:NH2	32:B5:1546:G:N7	2.57	0.53
29:Bc:10:ALA:HB1	29:Bc:30:VAL:HB	1.90	0.53
32:B5:406:U:H2'	32:B5:407:A:C8	2.44	0.53
36:A1:1282:G:O2'	36:A1:1283:C:H6	1.91	0.53
36:A1:3119:U:H4'	73:Am:104:PRO:HG3	1.91	0.53
50:AP:122:ALA:HB3	50:AP:143:PRO:HB2	1.91	0.53
11:BO:136:ARG:HD3	11:BO:136:ARG:H	1.73	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:195:HIS:NE2	31:Bg:213:SER:OG	2.37	0.53
32:B5:751:G:H2'	32:B5:752:A:H8	1.74	0.53
36:A1:807:A2M:H62	36:A1:934:G:H22	1.57	0.53
36:A1:1232:C:O2'	82:VA:36:GLN:OE1	2.22	0.53
36:A1:2152:A:H2'	36:A1:2153:U:H6	1.73	0.53
36:A1:2622:C:H42	44:AI:116:ARG:HH12	1.57	0.53
36:A1:2793:OMG:H5''	75:Ao:66:LYS:HG2	1.90	0.53
43:AH:94:TYR:HA	43:AH:177:ASP:HB3	1.91	0.53
52:AR:23:TRP:HB3	52:AR:51:VAL:HG22	1.90	0.53
65:Ae:66:LEU:HD23	65:Ae:72:LYS:HG3	1.91	0.53
76:Ap:81:SER:O	76:Ap:85:ARG:HG3	2.09	0.53
1:BA:126:PRO:HG2	1:BA:151:SER:HB2	1.89	0.53
6:BH:64:VAL:HA	6:BH:67:LEU:HD23	1.91	0.53
25:BS:11:PHE:CZ	25:BS:59:GLY:HA3	2.44	0.53
31:Bg:224:ASN:HB3	31:Bg:229:LYS:H	1.73	0.53
32:B5:207:U:H2'	32:B5:208:U:C6	2.44	0.53
32:B5:208:U:H2'	32:B5:209:U:C6	2.44	0.53
32:B5:486:G:N2	32:B5:488:G:O6	2.42	0.53
32:B5:1770:U:H2'	32:B5:1771:U:C6	2.44	0.53
35:AC:67:THR:HG21	36:A1:2402:A:H2'	1.91	0.53
36:A1:115:A:H8	36:A1:266:A:H5'	1.73	0.53
36:A1:302:U:H5''	48:AN:179:LYS:HE3	1.91	0.53
36:A1:1250:G:H2'	36:A1:1251:A:H8	1.74	0.53
49:AO:96[A]:LYS:O	49:AO:100[A]:GLU:HG3	2.08	0.53
60:AZ:24:VAL:HG11	60:AZ:87:LEU:HD23	1.90	0.53
68:Ah:83:LYS:O	70:Aj:73:ARG:NH2	2.41	0.53
77:E:16:LEU:HA	77:E:19:TYR:HB3	1.90	0.53
77:E:38:LEU:HD11	77:E:159:LEU:HD11	1.90	0.53
79:DC:13:MET:HE1	79:DC:449:PRO:HD2	1.90	0.53
3:BC:120:GLU:HG2	3:BC:123:GLY:H	1.74	0.53
7:BI:57:ALA:HB2	7:BI:177:GLY:HA2	1.91	0.53
32:B5:1338:C:H1'	32:B5:1410:A:C4	2.44	0.53
36:A1:2389:C:H2'	36:A1:2390:A:C8	2.44	0.53
42:AG:78:PHE:C	42:AG:80:TYR:H	2.17	0.53
46:AL:153:ASP:OD1	46:AL:154:VAL:N	2.41	0.53
51:AQ:83:VAL:O	51:AQ:103:ALA:HA	2.09	0.53
1:BA:26:ALA:HB3	1:BA:149:LEU:HB2	1.91	0.53
5:BG:132:ARG:NH1	32:B5:149:C:O2'	2.35	0.53
20:BF:140:THR:HG23	20:BF:210:ALA:HB1	1.91	0.53
20:BF:185:ARG:NH1	32:B5:1572:OMG:O2'	2.41	0.53
32:B5:1229:G:N3	32:B5:1255:G:N2	2.56	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:1351:G:H2'	32:B5:1352:G:C8	2.44	0.53
34:AB:106:TRP:O	34:AB:137:TYR:OH	2.27	0.53
36:A1:1389:G:OP1	65:Ae:104:ASN:ND2	2.39	0.53
36:A1:1391:C:C2	65:Ae:103:LYS:HD3	2.44	0.53
38:A4:103:G:OP2	38:A4:105:A:O2'	2.26	0.53
45:AJ:164:LYS:HE3	45:AJ:171:VAL:HG22	1.91	0.53
60:AZ:33:SER:OG	60:AZ:35:SER:O	2.22	0.53
78:EC:6859:U:H1'	78:EC:6860:A:N7	2.24	0.53
23:BQ:48:VAL:HA	23:BQ:82:ARG:HB3	1.91	0.52
36:A1:351:A:N6	72:Al:37:TYR:O	2.41	0.52
36:A1:787:G:H2'	36:A1:788:C:C6	2.44	0.52
55:AU:90:ARG:C	55:AU:92:TRP:H	2.17	0.52
78:EC:6831:U:H4'	78:EC:6832:G:OP1	2.09	0.52
79:DC:161:ASP:HB3	85:DC:901:GDP:HN1	1.74	0.52
79:DC:405:VAL:HG12	79:DC:448:CYS:HB3	1.90	0.52
1:BA:35:PRO:O	1:BA:52:LYS:NZ	2.43	0.52
3:BC:143:TYR:OH	3:BC:149:GLY:O	2.21	0.52
13:BW:107:SER:HA	32:B5:804:A:C8	2.45	0.52
20:BF:26:ALA:N	23:BQ:27:GLY:O	2.41	0.52
22:BP:61:ARG:HA	22:BP:64:LYS:HZ3	1.73	0.52
32:B5:849:C:H2'	32:B5:850:A:C8	2.41	0.52
32:B5:989:U:H2'	32:B5:990:C:C6	2.44	0.52
36:A1:2197:OMC:N4	36:A1:2241:U:H2'	2.23	0.52
36:A1:2930:A:H2'	36:A1:2931:C:C6	2.44	0.52
36:A1:3205:G:OP2	36:A1:3206:C:N4	2.35	0.52
77:E:207:LYS:NZ	77:E:208:SER:O	2.30	0.52
5:BG:178:LEU:HD21	32:B5:78:A:C6	2.45	0.52
19:BD:141:LYS:NZ	32:B5:1275:A:N3	2.42	0.52
32:B5:29:U:H2'	32:B5:30:G:H8	1.74	0.52
32:B5:625:C:H2'	32:B5:626:U:C6	2.44	0.52
34:AB:2:SER:OG	36:A1:2943:G:OP2	2.26	0.52
36:A1:67:A:O2'	36:A1:315:C:O2	2.27	0.52
36:A1:577:C:O2'	36:A1:579:G:OP1	2.27	0.52
36:A1:1658:G:H2'	36:A1:1659:U:C6	2.45	0.52
36:A1:2427:U:H2'	36:A1:2428:U:C6	2.44	0.52
36:A1:2768:U:H2'	36:A1:2769:A:C8	2.45	0.52
44:AI:145:LYS:NZ	44:AI:146:ASP:OD1	2.42	0.52
82:VA:120:TRP:CZ3	82:VA:122:ARG:HA	2.44	0.52
82:VA:130:PRO:HB3	82:VA:145:ILE:HD12	1.91	0.52
1:BA:62:ARG:NH2	12:BV:37:ALA:O	2.36	0.52
4:BE:72:VAL:HG22	4:BE:90:ILE:HG12	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BW:107:SER:HB2	32:B5:802:G:H21	1.74	0.52
15:BY:29:HIS:ND1	15:BY:32:ARG:O	2.42	0.52
16:Ba:84:VAL:O	32:B5:1797:A:N6	2.42	0.52
19:BD:210:GLU:OE2	24:BR:19:ARG:NH1	2.43	0.52
24:BR:49:LYS:NZ	32:B5:1390:U:OP2	2.35	0.52
32:B5:1606:C:H2'	32:B5:1607:G:C8	2.44	0.52
36:A1:1460:A:H5'	64:Ad:51:LEU:O	2.10	0.52
38:A4:26:U:H2'	38:A4:27:U:C6	2.44	0.52
79:DC:511:LEU:HD23	79:DC:518:VAL:HG11	1.91	0.52
79:DC:593:ILE:HD13	79:DC:645:LEU:HD23	1.92	0.52
81:BM:133:LEU:HA	81:BM:136:ILE:HD12	1.92	0.52
1:BA:148:ASP:OD2	1:BA:165:ARG:NH1	2.39	0.52
4:BE:68:ARG:HD3	4:BE:76:VAL:HG11	1.92	0.52
5:BG:92:ARG:NH1	32:B5:1674:C:OP1	2.40	0.52
10:BN:38:VAL:O	10:BN:42:ARG:HG2	2.09	0.52
19:BD:157:LEU:HD21	19:BD:187:LYS:HD2	1.91	0.52
31:Bg:109:ASP:O	31:Bg:127:ARG:N	2.35	0.52
32:B5:823:G:C6	32:B5:850:A:N6	2.78	0.52
32:B5:1284:C:H4'	32:B5:1285:U:H5'	1.92	0.52
36:A1:226:C:H2'	36:A1:227:G:O4'	2.09	0.52
36:A1:618:C:OP1	50:AP:173:ARG:NH2	2.42	0.52
36:A1:1791:C:H2'	36:A1:1792:C:C6	2.44	0.52
36:A1:2369:G:H2'	36:A1:2370:G:C8	2.45	0.52
36:A1:3013:U:H2'	36:A1:3014:U:C6	2.44	0.52
38:A4:46:G:OP1	72:Al:18:LYS:NZ	2.29	0.52
39:AD:294:ALA:HB2	44:Al:217:PHE:HB3	1.92	0.52
79:DC:78:TYR:HE1	79:DC:97:SER:HA	1.74	0.52
79:DC:202:VAL:HG13	79:DC:208:THR:HG22	1.92	0.52
80:Bf:100:LEU:HD22	80:Bf:103:LEU:HB2	1.90	0.52
14:BX:47:SER:HB3	32:B5:600:U:H1'	1.92	0.52
15:BY:37:LYS:O	15:BY:41:ARG:N	2.40	0.52
18:Be:41:THR:HA	18:Be:45:VAL:HB	1.91	0.52
20:BF:26:ALA:HB2	23:BQ:26:LYS:HG3	1.92	0.52
21:BK:3:MET:HE1	21:BK:41:TYR:CD1	2.45	0.52
22:BP:15:HIS:HB3	22:BP:22:LEU:HB2	1.91	0.52
27:BU:70:THR:OG1	27:BU:72:ASN:OD1	2.27	0.52
32:B5:1494:C:H2'	32:B5:1495:C:C6	2.45	0.52
36:A1:428:A:H2'	36:A1:429:U:C6	2.45	0.52
36:A1:1592:G:OP1	67:Ag:58:ARG:NH2	2.41	0.52
36:A1:2467:G:H5''	77:E:29:LEU:HD11	1.91	0.52
36:A1:2585:G:C6	58:AX:24:LEU:HD21	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:2611:U:H2'	36:A1:2612:U:C6	2.45	0.52
37:A3:71:G:H2'	37:A3:72:A:C8	2.45	0.52
45:AJ:36:VAL:HG21	45:AJ:110:ILE:HD12	1.92	0.52
55:AU:90:ARG:O	55:AU:91:ASP:OD1	2.27	0.52
59:AY:55:GLU:HB2	59:AY:108:LYS:HB3	1.90	0.52
81:BM:48:SER:OG	81:BM:120:VAL:O	2.28	0.52
1:BA:20:ALA:HB2	1:BA:172:LEU:HD13	1.92	0.52
8:BJ:150:LEU:HA	8:BJ:153:GLU:OE2	2.09	0.52
11:BO:18:ARG:NH1	11:BO:31:THR:OG1	2.42	0.52
22:BP:124:THR:HB	32:B5:1182:U:H4'	1.91	0.52
26:BT:102:ARG:NH2	32:B5:1502:G:N7	2.57	0.52
32:B5:487:G:H1	32:B5:500:C:H5'	1.75	0.52
32:B5:653:C:OP1	32:B5:679:U:N3	2.37	0.52
36:A1:1046:A:H2'	36:A1:1049:C:C5	2.45	0.52
36:A1:1128:U:H2'	36:A1:1129:A:O4'	2.09	0.52
36:A1:2468:A:N3	36:A1:2477:G:N2	2.49	0.52
36:A1:2801:A:O2'	36:A1:2802:A:H2'	2.09	0.52
37:A3:113:C:H2'	37:A3:114:U:O4'	2.10	0.52
38:A4:85:G:OP2	59:AY:113:LYS:NZ	2.41	0.52
43:AH:163:GLN:O	43:AH:166:ARG:NE	2.42	0.52
49:AO:125[A]:ARG:HD2	49:AO:135[A]:TYR:CD2	2.45	0.52
19:BD:94:ARG:O	19:BD:101:GLN:NE2	2.42	0.52
25:BS:127:HIS:CD2	25:BS:133:VAL:HG11	2.45	0.52
32:B5:1591:C:H2'	32:B5:1592:A:C8	2.44	0.52
36:A1:250:U:H2'	36:A1:251:G:C8	2.44	0.52
36:A1:1229:G:OP1	82:VA:110:ARG:NH2	2.43	0.52
36:A1:1634:G:N7	60:AZ:17:ARG:NH1	2.58	0.52
36:A1:2357:A:H2'	36:A1:2358:A:C8	2.45	0.52
36:A1:2389:C:H2'	36:A1:2390:A:H8	1.75	0.52
36:A1:2699:G:H5''	54:AT:16:GLN:NE2	2.25	0.52
50:AP:60:PHE:O	50:AP:64:ASN:ND2	2.36	0.52
51:AQ:94:PHE:CE2	61:Aa:119:PRO:HD3	2.45	0.52
79:DC:806:SER:OG	79:DC:813:SER:HB3	2.10	0.52
5:BG:201:GLN:NE2	32:B5:125:U:OP1	2.42	0.52
25:BS:40:ARG:CZ	32:B5:1539:G:H4'	2.39	0.52
27:BU:15:GLN:N	27:BU:18:GLN:O	2.43	0.52
32:B5:1055:U:H2'	32:B5:1056:U:C6	2.45	0.52
32:B5:1702:A:H3'	32:B5:1703:C:H6	1.73	0.52
36:A1:1256:G:H2'	36:A1:1257:C:C6	2.45	0.52
36:A1:3218:A:H5''	36:A1:3219:G:C5	2.44	0.52
41:AF:77:VAL:HB	54:AT:139:ARG:HG2	1.90	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Ac:103:THR:HG22	63:Ac:105:ALA:H	1.75	0.52
67:Ag:79:SER:OG	67:Ag:80:ARG:NH1	2.42	0.52
79:DC:103:ILE:HD11	79:DC:453:ILE:HD13	1.92	0.52
30:Bd:44:ARG:HH22	32:B5:1280:4AC:P	2.33	0.52
32:B5:158:U:O2'	32:B5:160:C:OP2	2.20	0.52
32:B5:1656:U:HO2'	36:A1:2292:U:HO2'	1.57	0.52
34:AB:62:ARG:NH1	36:A1:3039:C:OP1	2.38	0.52
36:A1:2367:A:H2'	36:A1:2368:A:C8	2.45	0.52
36:A1:2656:A:H4'	75:Ao:98:LYS:HD2	1.92	0.52
78:EC:6893:C:H5'	78:EC:6943:A:H61	1.75	0.52
2:BB:48:VAL:HG13	2:BB:49:ASN:N	2.25	0.51
15:BY:9:THR:HG22	15:BY:25:VAL:HG22	1.92	0.51
15:BY:53:ASP:OD1	15:BY:96:LEU:HD11	2.09	0.51
23:BQ:16:ALA:HB2	23:BQ:72:GLY:HA3	1.92	0.51
26:BT:6:VAL:HG22	26:BT:136:ALA:HB2	1.92	0.51
32:B5:264:G:H5''	32:B5:265:A:H5'	1.92	0.51
32:B5:1230:A:N6	32:B5:1255:G:H1'	2.25	0.51
32:B5:1619:C:H2'	32:B5:1620:C:H6	1.75	0.51
36:A1:1084:A:OP1	54:AT:35:LYS:NZ	2.40	0.51
36:A1:1863:G:N1	36:A1:1866:C:OP2	2.31	0.51
38:A4:149:A:H2'	38:A4:150:G:C8	2.45	0.51
71:Ak:26:LYS:HD2	71:Ak:78:LEU:HD13	1.91	0.51
77:E:73:ASP:OD2	77:E:113:SER:OG	2.18	0.51
77:E:76:ARG:NH2	77:E:142:ASP:O	2.43	0.51
15:BY:10:ARG:HG2	32:B5:778:G:H1	1.74	0.51
15:BY:38:ASP:OD1	15:BY:39:GLU:N	2.42	0.51
20:BF:143:ARG:HE	29:Bc:57:MET:HE1	1.75	0.51
24:BR:25:THR:O	24:BR:31:ASN:ND2	2.40	0.51
24:BR:97:ASN:HB2	24:BR:99:VAL:HG12	1.92	0.51
31:Bg:177:MET:HE1	31:Bg:179:LYS:NZ	2.25	0.51
32:B5:17:C:H2'	32:B5:18:C:C6	2.45	0.51
32:B5:824:G:H2'	32:B5:825:U:H6	1.76	0.51
35:AC:34:ILE:HD12	35:AC:120:TYR:CE2	2.45	0.51
36:A1:1132:C:H2'	36:A1:1133:A2M:H8	1.92	0.51
36:A1:1717:U:H2'	36:A1:1718:G:H8	1.74	0.51
36:A1:3162:C:H2'	36:A1:3163:A:C8	2.46	0.51
36:A1:3233:C:H2'	36:A1:3234:A:C8	2.45	0.51
40:AE:171:PRO:HA	40:AE:174:LEU:HB2	1.92	0.51
48:AN:159:ARG:HG2	48:AN:164:LEU:HB2	1.93	0.51
55:AU:13:LYS:HE2	55:AU:101:ASN:HD21	1.75	0.51
79:DC:385:MET:HE2	79:DC:513:LYS:HD2	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Bf:139:LEU:N	80:Bf:148:TYR:O	2.40	0.51
12:BV:73:ALA:HB1	12:BV:78:LEU:HB2	1.93	0.51
20:BF:143:ARG:HE	29:Bc:57:MET:CE	2.23	0.51
32:B5:850:A:H4'	52:AR:165:LYS:HG2	1.93	0.51
32:B5:1170:G:C2	32:B5:1171:A:C8	2.99	0.51
33:AA:190:ARG:HG3	33:AA:191:LEU:HD22	1.92	0.51
35:AC:31:ARG:HG3	35:AC:120:TYR:OH	2.10	0.51
36:A1:549:U:H2'	36:A1:550:A:H8	1.75	0.51
36:A1:674:G:O6	51:AQ:56:LYS:NZ	2.43	0.51
36:A1:3000:A:H2'	36:A1:3001:C:C6	2.45	0.51
40:AE:55:LEU:HD11	40:AE:66:SER:HB3	1.91	0.51
60:AZ:24:VAL:HG21	60:AZ:87:LEU:HB3	1.92	0.51
78:EC:6853:G:H22	78:EC:6875:C:H42	1.59	0.51
79:DC:829:LYS:O	79:DC:831:GLU:N	2.43	0.51
4:BE:11:ARG:HD3	4:BE:21:ASP:O	2.10	0.51
17:Bb:36:LYS:HB3	17:Bb:78:SER:HB3	1.93	0.51
28:BZ:60:VAL:HG12	28:BZ:80:LEU:HD11	1.92	0.51
32:B5:1241:G:OP1	32:B5:1241:G:N2	2.38	0.51
32:B5:1260:U:H2'	32:B5:1261:G:C8	2.44	0.51
36:A1:967:A:OP1	61:Aa:47:LYS:NZ	2.40	0.51
36:A1:3164:C:O2'	36:A1:3165:A:H8	1.93	0.51
38:A4:4:C:H2'	38:A4:5:U:O2	2.11	0.51
43:AH:89:LYS:HE2	43:AH:183:HIS:HB3	1.93	0.51
48:AN:52:GLY:O	48:AN:148:TYR:OH	2.27	0.51
64:Ad:96:VAL:HG12	64:Ad:98:VAL:HG13	1.90	0.51
1:BA:72:ASP:HB2	1:BA:118:PRO:HA	1.92	0.51
7:BI:82:VAL:HG11	7:BI:103:GLN:HE21	1.74	0.51
19:BD:74:GLN:HB2	19:BD:84:ILE:HG21	1.93	0.51
23:BQ:76:SER:N	32:B5:1609:U:OP1	2.42	0.51
31:Bg:33:LEU:O	31:Bg:45:TRP:N	2.42	0.51
32:B5:156:A:H2'	32:B5:157:A:O4'	2.09	0.51
32:B5:698:U:N3	32:B5:741:C:C4	2.78	0.51
32:B5:1220:C:H2'	32:B5:1221:A:C8	2.44	0.51
32:B5:1504:G:N3	32:B5:1563:C:O2'	2.43	0.51
36:A1:1228:C:H2'	36:A1:1229:G:H8	1.76	0.51
38:A4:25:G:N7	59:AY:13:ARG:NH1	2.52	0.51
41:AF:147:LEU:HD11	41:AF:207:LEU:HD21	1.93	0.51
48:AN:110:ALA:HB1	48:AN:113:LEU:HD12	1.91	0.51
50:AP:47:TYR:OH	50:AP:57:ALA:O	2.25	0.51
77:E:196:LYS:HB3	77:E:199:GLN:HB2	1.93	0.51
2:BB:155:TYR:OH	32:B5:932:U:OP2	2.20	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:94:ALA:O	4:BE:95:THR:OG1	2.29	0.51
32:B5:17:C:O2'	32:B5:1137:A:N1	2.38	0.51
32:B5:510:G:H2'	32:B5:511:A:H8	1.76	0.51
32:B5:976:G:N1	32:B5:1023:A:O2'	2.35	0.51
36:A1:1947:G:H5''	52:AR:134:HIS:CB	2.41	0.51
36:A1:2115:G:H22	36:A1:2120:A:H1'	1.76	0.51
36:A1:2426:U:H2'	36:A1:2427:U:C6	2.46	0.51
38:A4:6:U:H2'	38:A4:7:U:C6	2.44	0.51
50:AP:4:TYR:OH	50:AP:18:ARG:HG3	2.11	0.51
78:EC:6791:A:H3'	78:EC:6793:A:H8	1.75	0.51
79:DC:305:ILE:HG21	79:DC:323:VAL:HG23	1.92	0.51
3:BC:226:THR:OG1	3:BC:228:ASN:OD1	2.23	0.51
17:Bb:70:LYS:NZ	32:B5:1050:G:OP1	2.34	0.51
19:BD:185:LYS:NZ	32:B5:1279:C:OP2	2.37	0.51
29:Bc:64:ARG:HG3	29:Bc:65:ARG:N	2.22	0.51
31:Bg:127:ARG:HD2	31:Bg:150:TRP:CG	2.45	0.51
32:B5:1058:U:H3'	32:B5:1059:U:C5'	2.41	0.51
32:B5:1521:G:O2'	32:B5:1523:G:OP2	2.24	0.51
34:AB:92:TYR:HB2	34:AB:157:VAL:HB	1.92	0.51
36:A1:1093:A:H5'	36:A1:1096:U:O4	2.11	0.51
36:A1:1108:U:H2'	36:A1:1109:U:C6	2.46	0.51
36:A1:1621:A:H2'	36:A1:1622:U:H6	1.75	0.51
37:A3:23:A:H2'	37:A3:24:A:C8	2.45	0.51
37:A3:118:A:H5''	39:AD:253:PHE:CZ	2.46	0.51
79:DC:27:HIS:HB2	79:DC:139:THR:H	1.75	0.51
79:DC:431:ILE:HG21	79:DC:434:VAL:HG22	1.93	0.51
15:BY:53:ASP:HB3	15:BY:79:VAL:HG22	1.93	0.51
16:Ba:8:ASN:ND2	32:B5:1030:A:OP2	2.44	0.51
19:BD:6:SER:HB3	19:BD:9:ARG:HD3	1.93	0.51
22:BP:11:VAL:HG13	22:BP:23:GLU:OE2	2.10	0.51
31:Bg:262:VAL:HB	31:Bg:271:VAL:HB	1.93	0.51
31:Bg:291:SER:O	31:Bg:304:GLY:N	2.34	0.51
32:B5:1592:A:H2'	32:B5:1593:A:H8	1.76	0.51
34:AB:219:ALA:HB2	34:AB:336:VAL:HG23	1.92	0.51
36:A1:2406:C:H2'	36:A1:2407:C:H6	1.76	0.51
36:A1:3204:C:H2'	36:A1:3205:G:C8	2.45	0.51
48:AN:45:PRO:O	48:AN:49:ARG:HG3	2.10	0.51
67:Ag:41:ARG:NH2	67:Ag:51:LEU:O	2.44	0.51
78:EC:6763:C:H2'	78:EC:6764:C:C6	2.46	0.51
78:EC:6813:A:H2'	78:EC:6814:G:C8	2.45	0.51
79:DC:723:LYS:NZ	79:DC:804:LEU:H	2.08	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:1469:A:H2'	32:B5:1470:C:C6	2.46	0.51
34:AB:17:LEU:HD21	34:AB:233:TRP:HH2	1.76	0.51
36:A1:656:A:H2'	36:A1:657:A:C8	2.46	0.51
36:A1:945:C:H2'	36:A1:946:U:C6	2.46	0.51
36:A1:3191:G:OP1	49:AO:176[A]:LYS:NZ	2.36	0.51
41:AF:51:TYR:OH	41:AF:183:ASP:OD1	2.25	0.51
60:AZ:117:ALA:O	60:AZ:121:ARG:HG3	2.11	0.51
78:EC:6897:G:H2'	78:EC:6898:U:C6	2.46	0.51
1:BA:31:VAL:HA	1:BA:34:GLU:OE2	2.11	0.51
2:BB:149:GLN:HE21	2:BB:151:LYS:HB3	1.75	0.51
20:BF:26:ALA:HB3	23:BQ:28:LEU:HB2	1.91	0.51
31:Bg:240:VAL:HA	31:Bg:256:THR:HA	1.92	0.51
32:B5:1471:A:C8	32:B5:1540:G:H1'	2.46	0.51
33:AA:117:GLU:HG2	33:AA:124:GLY:H	1.76	0.51
36:A1:1915:A:H2'	36:A1:1916:U:C6	2.46	0.51
38:A4:154:C:H5''	42:AG:181:LYS:HG2	1.93	0.51
44:AI:38:LYS:NZ	44:AI:45:GLU:OE1	2.43	0.51
45:AJ:170:ASP:OD1	45:AJ:170:ASP:N	2.44	0.51
47:AM:39:ILE:HB	47:AM:43:LYS:HB3	1.93	0.51
78:EC:6892:U:H2'	78:EC:6893:C:C5	2.46	0.51
2:BB:61:LEU:HD22	2:BB:96:LEU:HD21	1.93	0.50
2:BB:112:SER:HA	16:Ba:68:TYR:CE2	2.46	0.50
2:BB:133:TYR:HD2	2:BB:181:LEU:HB2	1.75	0.50
23:BQ:125:GLU:N	32:B5:1585:U:OP1	2.29	0.50
23:BQ:137:ARG:HB2	32:B5:1580:C:H4'	1.93	0.50
24:BR:10:LYS:O	24:BR:14:LYS:HG2	2.10	0.50
32:B5:148:A:N6	32:B5:166:C:O2	2.44	0.50
32:B5:1757:G:HO2'	36:A1:2255:A:HO2'	1.58	0.50
35:AC:257:LYS:HA	35:AC:260:GLN:NE2	2.25	0.50
36:A1:1114:U:OP1	61:Aa:23:GLY:N	2.33	0.50
36:A1:1336:U:H2'	36:A1:1337:A:H8	1.76	0.50
36:A1:1447:G:O2'	36:A1:2355:G:O6	2.25	0.50
36:A1:2404:A:N7	36:A1:2872:A:N6	2.59	0.50
36:A1:2652:U:OP1	75:Ao:65:THR:OG1	2.23	0.50
37:A3:95:A:N3	53:AS:119:ARG:HD2	2.27	0.50
38:A4:69:U:H2'	38:A4:70:G:O4'	2.11	0.50
60:AZ:16:GLY:C	60:AZ:18:TYR:H	2.19	0.50
79:DC:414:GLN:HB2	79:DC:468:THR:HB	1.94	0.50
3:BC:229:LEU:O	12:BV:16:LYS:NZ	2.44	0.50
8:BJ:18:PRO:O	8:BJ:23:ARG:NH2	2.44	0.50
12:BV:30:ALA:O	12:BV:60:ARG:HD3	2.11	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BX:128:SER:OG	14:BX:142:LYS:NZ	2.44	0.50
25:BS:42:TYR:O	25:BS:46:VAL:HG23	2.11	0.50
32:B5:5:U:H2'	32:B5:6:G:H8	1.75	0.50
32:B5:1285:U:H4'	32:B5:1286:U:O5'	2.10	0.50
32:B5:1592:A:H2'	32:B5:1593:A:C8	2.46	0.50
36:A1:1120:A:H2'	36:A1:1121:U:H6	1.76	0.50
36:A1:2852:C:N3	44:AI:158:LYS:NZ	2.58	0.50
2:BB:145:LYS:HG3	2:BB:154:SER:HB2	1.94	0.50
5:BG:78:THR:HG22	5:BG:79:LYS:N	2.25	0.50
6:BH:64:VAL:HG11	6:BH:96:ARG:HG2	1.94	0.50
10:BN:55:ARG:HH22	17:Bb:51:GLN:NE2	2.08	0.50
11:BO:43:THR:OG1	32:B5:900:A:OP1	2.28	0.50
26:BT:53:TRP:HH2	26:BT:100:ILE:HD11	1.75	0.50
31:Bg:61:PHE:HZ	31:Bg:94:VAL:HA	1.76	0.50
32:B5:947:U:H2'	32:B5:948:G:C8	2.46	0.50
36:A1:769:G:HO2'	46:AL:168:ARG:HH12	1.59	0.50
36:A1:966:U:H2'	36:A1:967:A:C8	2.46	0.50
36:A1:1799:A:H2'	36:A1:1800:A:C8	2.47	0.50
36:A1:1915:A:H5''	52:AR:84:THR:HG22	1.92	0.50
40:AE:76:LEU:HD13	40:AE:101:PHE:CE1	2.46	0.50
44:AI:36:LEU:HD11	44:AI:69:ARG:HD2	1.93	0.50
64:Ad:9:THR:HG23	64:Ad:76:SER:HB3	1.93	0.50
79:DC:468:THR:HG23	79:DC:478:MET:HE1	1.93	0.50
5:BG:31:ARG:NH2	32:B5:1682:U:OP1	2.45	0.50
14:BX:108:GLY:HA2	32:B5:600:U:OP2	2.12	0.50
16:Ba:19:LYS:HD3	16:Ba:20:PRO:HD2	1.93	0.50
16:Ba:79:ILE:HD13	32:B5:1794:A:H1'	1.93	0.50
32:B5:231:U:N3	32:B5:233:C:O4'	2.44	0.50
32:B5:522:U:H2'	32:B5:523:G:O4'	2.10	0.50
32:B5:1589:C:H2'	32:B5:1590:G:C8	2.47	0.50
33:AA:181:LYS:HB2	36:A1:860:G:C5	2.47	0.50
36:A1:1566:A:H8	36:A1:1566:A:O5'	1.94	0.50
36:A1:2747:A:H2'	36:A1:2748:A:C8	2.47	0.50
37:A3:121:U:H5''	39:AD:265:TYR:HE1	1.77	0.50
56:AV:18:PRO:HA	56:AV:51:ALA:HA	1.94	0.50
78:EC:6868:C:N4	78:EC:6869:C:H41	2.09	0.50
1:BA:30:GLN:NE2	1:BA:33:GLN:HG2	2.26	0.50
11:BO:17:ALA:N	11:BO:80:HIS:O	2.27	0.50
19:BD:3:ALA:C	19:BD:4:LEU:HD23	2.36	0.50
19:BD:169:ASP:N	19:BD:169:ASP:OD1	2.45	0.50
20:BF:108:LEU:HD21	23:BQ:75:VAL:HG21	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:229:U:O4	32:B5:236:A:N6	2.45	0.50
32:B5:891:A:H2'	32:B5:892:A:C8	2.46	0.50
32:B5:1350:U:H2'	32:B5:1351:G:C8	2.46	0.50
34:AB:250:ALA:HB3	36:A1:2880:U:H1'	1.93	0.50
35:AC:34:ILE:HG21	35:AC:120:TYR:HD2	1.76	0.50
36:A1:181:U:H2'	36:A1:182:U:O4'	2.11	0.50
36:A1:501:A:H2'	36:A1:502:U:C6	2.46	0.50
36:A1:1497:C:O2'	36:A1:1602:A:N3	2.42	0.50
36:A1:1641:U:O2'	36:A1:1642:A:H3'	2.11	0.50
36:A1:2469:G:H4'	77:E:26:ARG:HE	1.76	0.50
51:AQ:125:ASP:OD1	51:AQ:126:GLN:N	2.44	0.50
64:Ad:84:ASP:N	64:Ad:84:ASP:OD1	2.44	0.50
78:EC:6767:G:H21	78:EC:6768:U:H3	1.59	0.50
78:EC:6898:U:H2'	78:EC:6899:C:H6	1.77	0.50
4:BE:131:LEU:HD12	32:B5:251:A:C2	2.46	0.50
15:BY:35:VAL:HG23	15:BY:36:SER:H	1.75	0.50
19:BD:22:ASN:ND2	30:Bd:49:ASP:OD2	2.43	0.50
27:BU:19:ILE:HD12	27:BU:94:GLU:HB3	1.93	0.50
31:Bg:109:ASP:O	31:Bg:126:SER:OG	2.17	0.50
36:A1:148:G:OP2	48:AN:4:TYR:OH	2.14	0.50
36:A1:716:A:C6	61:Aa:117:ARG:HG3	2.45	0.50
36:A1:1039:U:H2'	36:A1:1040:A:C8	2.46	0.50
36:A1:1606:U:O4	67:Ag:9:ARG:NE	2.45	0.50
36:A1:2266:U:H2'	36:A1:2267:C:C6	2.47	0.50
42:AG:178:ALA:HB2	42:AG:218:ILE:HG23	1.92	0.50
79:DC:757:GLU:N	79:DC:757:GLU:OE1	2.44	0.50
1:BA:64:ILE:HD12	1:BA:177:LEU:HD11	1.94	0.50
9:BL:37:ASN:O	32:B5:247:A:O2'	2.20	0.50
14:BX:99:ASN:ND2	79:DC:505:VAL:HG13	2.27	0.50
21:BK:88:PRO:HB3	21:BK:91:TYR:CZ	2.47	0.50
32:B5:514:G:H1	32:B5:543:C:H5	1.58	0.50
32:B5:1648:A:H2'	32:B5:1649:G:H8	1.75	0.50
36:A1:2688:U:OP1	39:AD:12:TYR:OH	2.28	0.50
39:AD:217:GLU:OE2	39:AD:218:ARG:HG3	2.11	0.50
68:Ah:86:ARG:O	68:Ah:90:ARG:HG2	2.11	0.50
77:E:215:ARG:NE	77:E:215:ARG:HA	2.26	0.50
78:EC:6789:G:H4'	78:EC:6790:A:OP1	2.11	0.50
78:EC:6862:G:O6	78:EC:6869:C:N4	2.45	0.50
79:DC:176:GLN:O	79:DC:180:ARG:HG2	2.12	0.50
6:BH:113:PRO:HG2	6:BH:116:ARG:HD3	1.93	0.50
13:BW:20:THR:HG23	13:BW:22:LYS:HG2	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BW:45:GLY:O	13:BW:66:ASN:ND2	2.34	0.50
31:Bg:263:PHE:HE1	31:Bg:270:LEU:HB2	1.76	0.50
32:B5:1713:G:H2'	32:B5:1714:A:C8	2.47	0.50
36:A1:1084:A:H2'	36:A1:1085:A:C8	2.46	0.50
36:A1:1378:U:H2'	36:A1:1379:G:H8	1.77	0.50
36:A1:1751:G:H5'	71:Ak:26:LYS:HE2	1.93	0.50
36:A1:3231:U:H2'	36:A1:3232:G:H8	1.76	0.50
41:AF:233:GLU:OE1	53:AS:35:VAL:HG22	2.11	0.50
77:E:54:LYS:HE3	77:E:150:ASP:HB3	1.94	0.50
81:BM:96:GLN:O	81:BM:100:TRP:NE1	2.44	0.50
5:BG:57:ASP:HA	5:BG:107:ALA:H	1.77	0.50
7:BI:81:VAL:HG12	7:BI:91:VAL:HG22	1.94	0.50
7:BI:113:PHE:HE2	7:BI:119:GLN:HB2	1.76	0.50
13:BW:42:GLN:NE2	13:BW:48:GLY:O	2.28	0.50
22:BP:110:GLU:OE1	25:BS:119:ILE:HG12	2.12	0.50
32:B5:906:A:H2'	32:B5:907:A:C8	2.47	0.50
34:AB:281:LYS:HD2	34:AB:283:TYR:HE1	1.77	0.50
36:A1:596:C:OP2	41:AF:34:LYS:NZ	2.45	0.50
36:A1:2565:U:H2'	36:A1:2566:C:H6	1.77	0.50
77:E:82:VAL:HG11	77:E:148:VAL:HG11	1.94	0.50
79:DC:289:MET:HE2	79:DC:320:LEU:HD13	1.94	0.50
79:DC:586:ILE:HD12	79:DC:708:THR:HG23	1.92	0.50
4:BE:57:ASN:HB2	4:BE:60:GLU:OE1	2.12	0.49
7:BI:37:LYS:HB2	7:BI:59:ARG:HB3	1.93	0.49
13:BW:6:VAL:HB	13:BW:29:PRO:HD2	1.94	0.49
21:BK:59:PHE:HZ	21:BK:62:GLN:HG3	1.76	0.49
26:BT:61:VAL:O	26:BT:65:ILE:HG12	2.12	0.49
31:Bg:250:TYR:HB3	31:Bg:265:LEU:HD21	1.94	0.49
32:B5:698:U:O4	32:B5:741:C:N3	2.45	0.49
32:B5:1705:C:H2'	32:B5:1706:C:H6	1.77	0.49
37:A3:52:G:O2'	37:A3:53:U:OP1	2.30	0.49
39:AD:50:ARG:HG2	39:AD:147:ASP:HB2	1.94	0.49
41:AF:178:ILE:HG23	41:AF:183:ASP:HB3	1.94	0.49
45:AJ:10:ARG:NH2	45:AJ:151:SER:O	2.45	0.49
79:DC:491:VAL:HA	79:DC:559:PRO:HD3	1.95	0.49
79:DC:747:LEU:HA	79:DC:750:LYS:HB2	1.93	0.49
1:BA:190:ASP:HB2	1:BA:193:GLN:HB2	1.93	0.49
2:BB:203:ASP:OD1	2:BB:203:ASP:N	2.45	0.49
14:BX:31:LYS:HG3	14:BX:36:THR:HB	1.93	0.49
30:Bd:43:PHE:O	30:Bd:47:ALA:N	2.46	0.49
32:B5:1355:C:H2'	32:B5:1356:U:C6	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:1772:C:H2'	32:B5:1773:4AC:H6	1.94	0.49
36:A1:184:U:H2'	36:A1:185:C:C6	2.47	0.49
36:A1:289:A:H2'	36:A1:290:G:H8	1.76	0.49
36:A1:943:U:H3'	61:Aa:13:GLY:HA2	1.94	0.49
36:A1:3192:U:H2'	36:A1:3193:C:C6	2.47	0.49
36:A1:3333:G:N2	36:A1:3369:G:O2'	2.45	0.49
44:AI:29:SER:OG	44:AI:31:ILE:O	2.29	0.49
53:AS:24:LEU:HD21	54:AT:141:VAL:HG11	1.94	0.49
59:AY:48:LEU:HD13	59:AY:115:ARG:HH21	1.77	0.49
79:DC:131:THR:HG22	79:DC:157:ILE:HG22	1.93	0.49
79:DC:249:PHE:CE2	79:DC:261:ASP:HA	2.48	0.49
79:DC:399:ARG:HD3	79:DC:401:PHE:HE1	1.78	0.49
1:BA:102:PHE:HE2	1:BA:135:GLU:HG3	1.77	0.49
5:BG:186:ARG:O	5:BG:190:GLN:HG2	2.12	0.49
6:BH:104:ARG:HG3	32:B5:803:A:C4	2.46	0.49
15:BY:114:ARG:HA	15:BY:117:LYS:HE2	1.93	0.49
26:BT:112:GLY:O	26:BT:125:SER:OG	2.29	0.49
28:BZ:83:LEU:HA	28:BZ:86:GLU:HG2	1.94	0.49
31:Bg:89:LEU:HD11	31:Bg:110:VAL:HG11	1.94	0.49
32:B5:1553:G:N2	32:B5:1555:A:H3'	2.27	0.49
32:B5:1625:C:H2'	32:B5:1626:U:C6	2.47	0.49
36:A1:26:A:N3	36:A1:328:U:O2'	2.36	0.49
36:A1:359:U:H4'	36:A1:817:A2M:N6	2.27	0.49
36:A1:1227:C:O2'	36:A1:1228:C:O5'	2.24	0.49
36:A1:1390:A:N6	36:A1:1418:A:O2'	2.45	0.49
36:A1:2457:G:N1	36:A1:2461:A:N7	2.60	0.49
38:A4:113:U:H5''	72:Al:7:PHE:HB3	1.93	0.49
43:AH:90:MET:HE3	43:AH:181:VAL:HG23	1.94	0.49
77:E:51:GLY:H	77:E:157:PHE:HB2	1.77	0.49
81:BM:75:VAL:HG21	81:BM:120:VAL:HG21	1.93	0.49
20:BF:49:GLU:O	20:BF:50:GLU:HG3	2.12	0.49
23:BQ:74:HIS:NE2	32:B5:1481:C:O2'	2.44	0.49
25:BS:4:VAL:HG12	28:BZ:82:HIS:CG	2.48	0.49
32:B5:602:U:H2'	32:B5:603:U:C6	2.48	0.49
32:B5:1116:A:OP1	74:An:14:LYS:HG2	2.13	0.49
33:AA:113:VAL:HG12	33:AA:166:ILE:HD13	1.95	0.49
33:AA:200:ARG:NH2	36:A1:2147:A:OP2	2.42	0.49
36:A1:1807:G:O2'	36:A1:2559:U:O4	2.27	0.49
46:AL:106:GLN:HB3	69:Al:18:THR:HB	1.94	0.49
52:AR:24:LEU:HB3	52:AR:32:ILE:HD13	1.94	0.49
78:EC:6899:C:C2	78:EC:6900:A:C8	3.01	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:DC:42:ARG:HH21	79:DC:331:ALA:HB3	1.76	0.49
5:BG:57:ASP:HB3	5:BG:106:LEU:HD23	1.95	0.49
6:BH:46:ILE:HG12	6:BH:60:ILE:HG22	1.95	0.49
6:BH:101:LYS:HE2	32:B5:638:U:O2'	2.13	0.49
8:BJ:29:LYS:HD3	18:Be:40:TYR:HE1	1.77	0.49
11:BO:40:ALA:HB2	11:BO:70:LYS:HG2	1.93	0.49
14:BX:99:ASN:OD1	79:DC:509:LYS:HE2	2.12	0.49
26:BT:86:ARG:NH2	32:B5:1601:G:OP1	2.44	0.49
32:B5:146:U:H2'	32:B5:147:A:H8	1.77	0.49
32:B5:329:G:H2'	32:B5:330:G:H8	1.78	0.49
32:B5:1160:A:H2'	32:B5:1161:C:H6	1.78	0.49
32:B5:1776:A:H2'	32:B5:1777:G:C8	2.48	0.49
35:AC:34:ILE:HG21	35:AC:120:TYR:CD2	2.48	0.49
40:AE:43:LEU:HD11	40:AE:85:ILE:HG13	1.95	0.49
57:AW:45:ASN:HB3	57:AW:48:ARG:HG3	1.95	0.49
77:E:126:PRO:HA	78:EC:6773:G:H4'	1.94	0.49
79:DC:445:ILE:HG13	79:DC:446:ASP:H	1.77	0.49
79:DC:813:SER:O	79:DC:817:GLU:N	2.44	0.49
2:BB:28:GLU:OE2	2:BB:50:LYS:HD3	2.12	0.49
2:BB:30:PHE:N	2:BB:46:THR:O	2.46	0.49
4:BE:192:ILE:H	4:BE:243:GLY:HA3	1.77	0.49
20:BF:29:ILE:O	20:BF:34:GLN:NE2	2.45	0.49
31:Bg:171:SER:O	31:Bg:179:LYS:N	2.36	0.49
32:B5:78:A:H2'	32:B5:79:C:C6	2.47	0.49
32:B5:1081:A:O2'	32:B5:1083:G:N7	2.40	0.49
32:B5:1369:U:O2'	32:B5:1370:U:OP1	2.23	0.49
36:A1:987:U:H2'	36:A1:988:U:C6	2.48	0.49
36:A1:2160:G:H2'	36:A1:2161:G:C8	2.48	0.49
36:A1:2357:A:H2'	36:A1:2358:A:H8	1.77	0.49
36:A1:3215:A:H5''	66:Af:2:ALA:HB2	1.94	0.49
36:A1:3273:A:H5''	40:AE:45:GLY:CA	2.42	0.49
47:AM:112:LEU:HD11	49:AO:197[A]:LEU:HB3	1.93	0.49
48:AN:147:ARG:HG3	68:Ah:101:THR:HG21	1.94	0.49
63:Ac:81:VAL:HG23	63:Ac:83:LYS:HG2	1.93	0.49
79:DC:132:ILE:HG13	79:DC:162:ARG:HH11	1.77	0.49
79:DC:494:GLU:HB3	79:DC:555:LYS:HE3	1.95	0.49
1:BA:135:GLU:OE2	32:B5:1321:A:N6	2.45	0.49
5:BG:167:LYS:HD3	32:B5:72:A:C8	2.47	0.49
7:BI:3:ILE:O	7:BI:30:GLY:N	2.45	0.49
8:BJ:3:ARG:NH2	32:B5:39:A:OP1	2.43	0.49
8:BJ:132:ARG:HH21	15:BY:65:GLY:HA2	1.78	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:72:LEU:HD22	21:BK:65:TYR:HD2	1.77	0.49
22:BP:76:VAL:O	22:BP:95:GLY:N	2.39	0.49
23:BQ:73:GLY:H	23:BQ:76:SER:HG	1.60	0.49
32:B5:1044:U:H2'	32:B5:1045:C:C6	2.47	0.49
36:A1:531:G:H2'	36:A1:532:A:C8	2.48	0.49
36:A1:1694:U:O2'	36:A1:1695:U:H5'	2.13	0.49
37:A3:7:G:OP1	39:AD:33:ARG:HD2	2.13	0.49
42:AG:112:GLU:O	42:AG:116:VAL:HG23	2.12	0.49
51:AQ:92:ARG:HG3	61:Aa:76:ASP:HB2	1.94	0.49
78:EC:6882:G:H2'	78:EC:6883:A:C8	2.48	0.49
79:DC:296:ILE:HA	79:DC:299:LEU:HD13	1.95	0.49
6:BH:133:THR:HG22	6:BH:158:ASP:HB3	1.94	0.49
31:Bg:16:HIS:NE2	31:Bg:35:SER:OG	2.38	0.49
32:B5:632:U:O2'	32:B5:1103:U:OP1	2.26	0.49
32:B5:1542:G:H22	32:B5:1568:C:H1'	1.78	0.49
32:B5:1772:C:H3'	74:An:2:ARG:NH2	2.27	0.49
34:AB:68:HIS:CE1	34:AB:69:LYS:HE3	2.47	0.49
36:A1:178:U:O2'	36:A1:179:C:OP1	2.27	0.49
36:A1:422:A:C2	36:A1:2363:A:H4'	2.48	0.49
36:A1:1807:G:C5'	60:AZ:135:ARG:HH12	2.23	0.49
36:A1:2266:U:O2'	36:A1:2267:C:H5'	2.13	0.49
36:A1:2455:U:H3	36:A1:2483:G:HO2'	1.60	0.49
39:AD:93:THR:O	39:AD:158:ARG:NH1	2.42	0.49
40:AE:51:ARG:O	40:AE:72:ASN:ND2	2.46	0.49
58:AX:90:ALA:O	58:AX:120:LYS:NZ	2.43	0.49
77:E:214:PHE:O	77:E:215:ARG:NE	2.34	0.49
78:EC:6831:U:H1'	78:EC:6832:G:C8	2.48	0.49
79:DC:600:ALA:HB1	79:DC:605:ILE:HB	1.94	0.49
15:BY:102:LYS:NZ	32:B5:444:C:OP1	2.36	0.49
25:BS:38:VAL:HG23	25:BS:42:TYR:HB3	1.93	0.49
28:BZ:91:PRO:HB3	28:BZ:101:TYR:CE2	2.48	0.49
32:B5:315:A:N1	32:B5:349:U:O2'	2.39	0.49
32:B5:882:U:H2'	32:B5:883:C:C6	2.48	0.49
36:A1:520:U:OP2	41:AF:70:LYS:NZ	2.42	0.49
36:A1:528:U:H2'	36:A1:529:A:H8	1.75	0.49
36:A1:3182:G:H4'	49:AO:161[A]:LYS:HG2	1.94	0.49
39:AD:177:GLU:OE1	39:AD:177:GLU:N	2.39	0.49
79:DC:70:ILE:HG13	79:DC:71:LYS:HE2	1.95	0.49
79:DC:784:LEU:O	79:DC:788:THR:OG1	2.25	0.49
2:BB:132:ASP:O	2:BB:221:PRO:HD3	2.13	0.49
3:BC:144:TRP:CE2	3:BC:173:PRO:HG3	2.48	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:107:GLY:HA2	4:BE:189:LEU:HG	1.95	0.49
18:Be:14:VAL:HA	18:Be:17:GLN:HE21	1.77	0.49
24:BR:88:VAL:HG23	24:BR:95:ARG:HH12	1.78	0.49
31:Bg:67:ILE:O	31:Bg:85:TRP:N	2.41	0.49
32:B5:513:U:H2'	32:B5:514:G:C8	2.48	0.49
32:B5:782:U:H4'	32:B5:783:G:H5''	1.95	0.49
32:B5:888:U:H2'	32:B5:889:U:C6	2.48	0.49
32:B5:891:A:H2'	32:B5:892:A:H8	1.77	0.49
32:B5:1077:C:H2'	32:B5:1078:C:H6	1.77	0.49
32:B5:1174:C:O2'	32:B5:1196:A:N6	2.45	0.49
36:A1:815:G:OP2	70:Aj:31:LYS:NZ	2.37	0.49
36:A1:916:G:H5'	36:A1:917:A:OP1	2.13	0.49
36:A1:1680:G:H2'	36:A1:1681:U:H6	1.78	0.49
36:A1:2561:A:O4'	42:AG:32:LYS:NZ	2.41	0.49
36:A1:2617:U:H3'	62:Ab:3:LYS:HD2	1.95	0.49
39:AD:290:ILE:HG13	44:AI:206:LEU:HD21	1.95	0.49
42:AG:206:GLU:OE1	42:AG:206:GLU:N	2.42	0.49
61:Aa:19:LYS:HB3	61:Aa:25:HIS:HB2	1.95	0.49
79:DC:385:MET:N	79:DC:385:MET:SD	2.86	0.49
27:BU:26:LEU:N	27:BU:89:ARG:O	2.33	0.48
28:BZ:39:ALA:N	28:BZ:70:LYS:O	2.37	0.48
32:B5:1349:G:H2'	32:B5:1350:U:H6	1.78	0.48
32:B5:1556:A:H1'	32:B5:1560:U:OP2	2.12	0.48
32:B5:1564:U:H2'	32:B5:1565:C:C6	2.48	0.48
36:A1:172:G:H2'	36:A1:173:G:H8	1.76	0.48
36:A1:375:A:H1'	59:AY:87:LYS:HE2	1.95	0.48
36:A1:1250:G:H2'	36:A1:1251:A:C8	2.48	0.48
36:A1:1695:U:O2'	36:A1:1749:A:N1	2.41	0.48
36:A1:2430:A:H2'	36:A1:2431:C:C6	2.48	0.48
36:A1:3294:A:H2'	36:A1:3295:A:O4'	2.13	0.48
79:DC:71:LYS:HD2	79:DC:387:PRO:HD2	1.94	0.48
12:BV:22:ARG:NH2	13:BW:19:LYS:O	2.46	0.48
20:BF:43:PHE:HE1	20:BF:70:VAL:HG23	1.78	0.48
32:B5:304:U:H2'	32:B5:305:C:C6	2.49	0.48
35:AC:325:LEU:HD23	36:A1:598:A:H4'	1.94	0.48
36:A1:1141:C:O2'	36:A1:1153:A:N3	2.42	0.48
36:A1:1227:C:O2'	36:A1:1228:C:O4'	2.30	0.48
36:A1:2352:A:H5''	50:AP:83:TRP:O	2.12	0.48
38:A4:135:G:H5''	58:AX:49:LYS:HD2	1.94	0.48
45:AJ:26:SER:OG	45:AJ:27:GLY:N	2.47	0.48
66:Af:16:TYR:OH	66:Af:89:LEU:O	2.26	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:DC:188:ILE:HG13	79:DC:192:TYR:CD2	2.48	0.48
79:DC:329:PRO:HG2	79:DC:332:ASP:HB2	1.95	0.48
79:DC:566:THR:HG22	79:DC:682:ARG:O	2.14	0.48
2:BB:109:LYS:HE3	2:BB:113:MET:HE2	1.95	0.48
4:BE:45:ILE:HA	4:BE:61:VAL:HG11	1.95	0.48
5:BG:116:LYS:HE3	5:BG:125:THR:HG21	1.94	0.48
7:BI:27:PHE:CD1	7:BI:28:GLU:HG3	2.48	0.48
10:BN:142:GLU:HB2	10:BN:145:THR:HB	1.94	0.48
20:BF:62:VAL:HG12	20:BF:89:ILE:HD13	1.94	0.48
24:BR:77:GLU:O	24:BR:81:LYS:HG2	2.14	0.48
33:AA:108:PRO:O	33:AA:111:THR:OG1	2.27	0.48
35:AC:58:HIS:HA	35:AC:90:PHE:HE1	1.78	0.48
36:A1:616:G:H2'	36:A1:617:G:C8	2.48	0.48
36:A1:650:OMC:H2'	36:A1:651:G:C8	2.47	0.48
36:A1:1230:G:H4'	82:VA:33:VAL:O	2.14	0.48
44:AI:48:LEU:HD11	44:AI:167:LEU:HD12	1.96	0.48
48:AN:116:LEU:O	48:AN:159:ARG:NH2	2.46	0.48
50:AP:172:GLN:O	50:AP:176:ILE:HG13	2.12	0.48
70:Aj:39:TYR:CD1	70:Aj:40:PRO:HA	2.47	0.48
2:BB:33:LYS:NZ	2:BB:42:ASN:OD1	2.46	0.48
4:BE:194:THR:HG21	4:BE:231:GLN:HE22	1.78	0.48
6:BH:5:GLN:HE22	6:BH:22:GLN:HB3	1.79	0.48
12:BV:41:GLU:O	12:BV:42:GLU:HG3	2.13	0.48
14:BX:92:CYS:HG	14:BX:136:TRP:CD1	2.30	0.48
32:B5:1294:G:O2'	32:B5:1321:A:N1	2.40	0.48
36:A1:45:A:OP2	48:AN:85:THR:HG21	2.14	0.48
36:A1:589:A:H8	36:A1:590:G:C8	2.32	0.48
36:A1:873:C:H5''	36:A1:874:U:O5'	2.14	0.48
36:A1:1073:U:H2'	36:A1:1074:U:C6	2.48	0.48
36:A1:3286:G:H2'	36:A1:3287:U:C6	2.48	0.48
38:A4:8:C:H2'	38:A4:9:A:C8	2.48	0.48
59:AY:74:TYR:CE2	59:AY:77:LYS:HG3	2.48	0.48
78:EC:6781:U:O2'	78:EC:6782:C:O5'	2.30	0.48
78:EC:6897:G:H2'	78:EC:6898:U:H6	1.77	0.48
79:DC:283:ARG:NH2	79:DC:299:LEU:HG	2.29	0.48
79:DC:363:ASP:O	79:DC:367:ILE:HG12	2.14	0.48
4:BE:108:ARG:NH2	32:B5:789:A:OP1	2.46	0.48
5:BG:159:ARG:HG2	5:BG:172:ALA:HB2	1.95	0.48
20:BF:148:ARG:HA	20:BF:157:ARG:HA	1.95	0.48
32:B5:64:U:O2'	32:B5:168:A:N3	2.46	0.48
32:B5:1017:U:H2'	32:B5:1018:U:C6	2.49	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:1233:G:H2'	32:B5:1234:A:O4'	2.13	0.48
32:B5:1397:U:O2'	32:B5:1400:A:N6	2.46	0.48
36:A1:215:G:OP1	59:AY:12:ARG:NH1	2.38	0.48
36:A1:248:U:H2'	36:A1:249:U:H4'	1.94	0.48
41:AF:92:ILE:HD12	51:AQ:4:ASP:HB2	1.96	0.48
47:AM:32:LEU:HD11	47:AM:94:TRP:CG	2.48	0.48
51:AQ:177:GLY:O	51:AQ:186:VAL:N	2.43	0.48
78:EC:6935:G:HO2'	78:EC:6936:G:H8	1.61	0.48
79:DC:500:ASP:HA	79:DC:503:LYS:HD3	1.96	0.48
79:DC:566:THR:HG21	79:DC:725:GLN:OE1	2.13	0.48
4:BE:131:LEU:HD12	32:B5:251:A:H2	1.79	0.48
4:BE:188:ASN:OD1	4:BE:191:ARG:NH1	2.45	0.48
9:BL:80:MET:SD	32:B5:324:U:O2'	2.70	0.48
25:BS:82:PRO:HB2	25:BS:84:TRP:NE1	2.28	0.48
32:B5:343:C:H2'	32:B5:344:A:C8	2.47	0.48
32:B5:1214:U:H2'	32:B5:1215:C:C6	2.49	0.48
32:B5:1738:U:H2'	32:B5:1739:C:C6	2.49	0.48
36:A1:2584:G:H1'	42:AG:240:ASN:HD22	1.78	0.48
36:A1:2779:A:O2'	46:AL:180:ARG:NH2	2.47	0.48
36:A1:2835:U:H2'	36:A1:2836:C:O2	2.13	0.48
38:A4:19:C:H2'	38:A4:20:U:C6	2.48	0.48
38:A4:97:A:OP1	68:Ah:63:ARG:NE	2.47	0.48
41:AF:102:VAL:HG21	41:AF:129:LEU:HD23	1.95	0.48
46:AL:10:LEU:HD23	51:AQ:166:LEU:HD11	1.94	0.48
47:AM:72:LEU:HD12	47:AM:73:PRO:HD2	1.94	0.48
50:AP:118:GLN:HB3	50:AP:147:GLU:HG2	1.95	0.48
59:AY:69:LYS:HD2	59:AY:70:ILE:O	2.14	0.48
79:DC:725:GLN:HA	79:DC:803:THR:HB	1.95	0.48
79:DC:740:VAL:HG21	79:DC:766:PHE:CD2	2.48	0.48
4:BE:66:MET:HE2	4:BE:66:MET:HA	1.96	0.48
5:BG:193:LEU:HD23	5:BG:196:ARG:HH22	1.79	0.48
7:BI:40:ALA:N	7:BI:61:GLU:OE2	2.25	0.48
23:BQ:115:THR:HA	23:BQ:118:ILE:O	2.14	0.48
28:BZ:90:LYS:HD3	28:BZ:104:ALA:HA	1.95	0.48
31:Bg:229:LYS:NZ	31:Bg:230:ALA:O	2.42	0.48
32:B5:85:A:N3	32:B5:148:A:O2'	2.42	0.48
32:B5:1214:U:H2'	32:B5:1215:C:H6	1.79	0.48
32:B5:1352:G:H2'	32:B5:1353:U:O4'	2.12	0.48
32:B5:1482:C:O5'	32:B5:1521:G:N2	2.38	0.48
36:A1:38:U:H4'	61:Aa:32:ARG:HD2	1.96	0.48
36:A1:1093:A:H5'	36:A1:1096:U:C4	2.49	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1615:C:H2'	36:A1:1616:U:C6	2.49	0.48
36:A1:2103:U:H2'	36:A1:2104:A:C8	2.48	0.48
36:A1:2356:A:H5'	50:AP:138:LYS:HZ2	1.78	0.48
36:A1:2471:U:H3	36:A1:2474:G:H22	1.62	0.48
36:A1:2506:U:O2'	36:A1:2507:C:OP1	2.27	0.48
36:A1:2660:G:OP1	36:A1:2750:U:O2'	2.30	0.48
36:A1:2882:U:H2'	36:A1:2883:U:C6	2.49	0.48
66:Af:17:GLN:HE21	66:Af:24:ASN:HD22	1.62	0.48
79:DC:697:ALA:HA	79:DC:700:ARG:HG2	1.96	0.48
82:VA:104:ARG:CZ	82:VA:184:GLY:HA3	2.43	0.48
3:BC:40:LYS:HE3	3:BC:248:SER:HB2	1.95	0.48
8:BJ:172:VAL:O	8:BJ:176:ASN:ND2	2.41	0.48
19:BD:120:TYR:HB3	19:BD:124:ARG:HH21	1.79	0.48
23:BQ:21:HIS:HB2	23:BQ:66:ARG:HB2	1.95	0.48
32:B5:1252:C:H2'	32:B5:1253:U:O4'	2.13	0.48
32:B5:1254:U:H3'	32:B5:1255:G:C8	2.49	0.48
32:B5:1524:A:N3	32:B5:1590:G:O2'	2.38	0.48
32:B5:1533:C:H4'	32:B5:1539:G:N1	2.28	0.48
32:B5:1682:U:O2'	32:B5:1683:C:O5'	2.30	0.48
34:AB:169:THR:CG2	34:AB:171:LEU:HD13	2.43	0.48
36:A1:3047:U:O2'	36:A1:3048:A:H5'	2.12	0.48
36:A1:3344:A:H2	36:A1:3361:G:N2	2.04	0.48
41:AF:120:THR:HB	54:AT:132:PRO:HB2	1.95	0.48
44:AI:186:GLU:HG2	44:AI:187:ALA:N	2.29	0.48
51:AQ:62:VAL:HG13	51:AQ:66:ARG:HD2	1.96	0.48
54:AT:30:TYR:HE1	54:AT:94:GLU:OE2	1.96	0.48
4:BE:86:PHE:CZ	4:BE:87:MET:HE2	2.48	0.48
5:BG:17:GLU:OE1	5:BG:17:GLU:N	2.47	0.48
5:BG:133:LEU:HD23	5:BG:134:GLY:O	2.14	0.48
14:BX:8:GLY:O	14:BX:11:SER:OG	2.26	0.48
15:BY:60:PHE:O	32:B5:522:U:O2'	2.31	0.48
19:BD:23:GLU:OE1	21:BK:61:TRP:NE1	2.30	0.48
32:B5:221:A:H5''	32:B5:833:U:O2'	2.12	0.48
32:B5:688:G:H2'	32:B5:689:G:C8	2.48	0.48
35:AC:138:ARG:HH21	35:AC:240:PRO:HG2	1.79	0.48
35:AC:281:ILE:HD13	51:AQ:28:LEU:CD1	2.44	0.48
39:AD:41:LYS:HB2	54:AT:68:THR:O	2.13	0.48
41:AF:178:ILE:HD11	41:AF:187:GLU:HG3	1.95	0.48
68:Ah:45:LYS:O	68:Ah:49:LYS:HG2	2.14	0.48
79:DC:7:ASP:OD1	79:DC:10:ARG:NH1	2.46	0.48
79:DC:591:GLU:OE2	79:DC:685:ARG:HD3	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:185:ARG:NH2	32:B5:1573:A:N7	2.62	0.48
22:BP:75:PRO:HB3	22:BP:104:GLN:NE2	2.28	0.48
32:B5:174:U:H3	32:B5:266:A:H62	1.62	0.48
32:B5:1250:U:H1'	80:Bf:135:HIS:CE1	2.48	0.48
32:B5:1272:U:O2'	32:B5:1275:A:OP2	2.22	0.48
32:B5:1471:A:H2'	32:B5:1471:A:N3	2.27	0.48
32:B5:1542:G:N2	32:B5:1568:C:H1'	2.29	0.48
32:B5:1645:G:H2'	32:B5:1646:C:H6	1.79	0.48
34:AB:92:TYR:HB3	34:AB:99:LEU:HG	1.95	0.48
36:A1:178:U:HO2'	36:A1:179:C:P	2.35	0.48
36:A1:277:G:H2'	36:A1:278:U:C6	2.49	0.48
36:A1:748:U:H2'	36:A1:749:C:C6	2.49	0.48
36:A1:955:U:H2'	36:A1:956:U:C6	2.48	0.48
36:A1:2106:A:H2'	36:A1:2107:A:C8	2.48	0.48
36:A1:2230:C:H2'	36:A1:2231:C:O4'	2.14	0.48
38:A4:59:A:H5''	38:A4:61:A:C8	2.49	0.48
39:AD:129:TYR:OH	39:AD:175:HIS:O	2.19	0.48
79:DC:199:ASP:OD1	79:DC:199:ASP:N	2.46	0.48
81:BM:26:ASP:O	81:BM:29:LYS:HB3	2.14	0.48
81:BM:71:ILE:HD11	81:BM:119:SER:HB3	1.95	0.48
1:BA:107:PHE:HB3	1:BA:139:VAL:HG21	1.96	0.47
4:BE:100:ARG:NH2	4:BE:121:TYR:O	2.45	0.47
11:BO:123:SER:OG	32:B5:886:U:H1'	2.13	0.47
19:BD:61:GLU:H	19:BD:64:ARG:HB2	1.78	0.47
21:BK:15:LEU:HD23	21:BK:76:LEU:HD21	1.95	0.47
31:Bg:47:LEU:HD12	31:Bg:54:PHE:CZ	2.49	0.47
32:B5:199:G:H2'	32:B5:200:A:C8	2.49	0.47
32:B5:1215:C:H2'	32:B5:1216:C:C6	2.49	0.47
32:B5:1254:U:H3'	32:B5:1255:G:H8	1.78	0.47
34:AB:250:ALA:HB1	36:A1:2947:G:C2	2.49	0.47
36:A1:129:U:H2'	36:A1:130:A:H8	1.77	0.47
36:A1:246:U:H3'	36:A1:247:C:H4'	1.96	0.47
36:A1:435:C:H2'	36:A1:436:A:C8	2.48	0.47
36:A1:2465:G:H1	36:A1:2491:A:N6	2.00	0.47
38:A4:23:U:OP1	59:AY:16:ARG:NH2	2.44	0.47
48:AN:8:GLU:HB2	48:AN:50:ARG:HH22	1.79	0.47
77:E:16:LEU:HD13	77:E:214:PHE:CE2	2.47	0.47
79:DC:180:ARG:HE	82:VA:140:GLY:HA2	1.79	0.47
79:DC:491:VAL:HG22	79:DC:538:LEU:HD11	1.96	0.47
79:DC:615:ARG:O	79:DC:619:MET:HG3	2.14	0.47
1:BA:17:LEU:O	1:BA:22:THR:OG1	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:59:LEU:HD22	12:BV:79:LEU:HD21	1.95	0.47
1:BA:118:PRO:HG2	1:BA:141:ILE:HD13	1.96	0.47
4:BE:77:ARG:HA	4:BE:77:ARG:HD3	1.66	0.47
6:BH:84:LYS:HG3	6:BH:85:PHE:HD1	1.78	0.47
7:BI:84:HIS:HE2	7:BI:97:THR:HG1	1.53	0.47
16:Ba:37:LYS:HB3	16:Ba:70:LYS:HE2	1.95	0.47
21:BK:58:GLN:HB3	21:BK:65:TYR:HB2	1.96	0.47
28:BZ:49:ARG:HH21	78:EC:6866:C:H5	1.61	0.47
31:Bg:127:ARG:HA	31:Bg:150:TRP:HB2	1.95	0.47
32:B5:142:G:P	32:B5:142:G:H21	2.36	0.47
32:B5:561:G:H2'	32:B5:562:OMG:H8	1.79	0.47
32:B5:885:G:H2'	32:B5:886:U:C6	2.49	0.47
32:B5:1352:G:C2	32:B5:1353:U:H1'	2.49	0.47
32:B5:1559:A:H5'	32:B5:1560:U:H5''	1.96	0.47
35:AC:157:GLU:OE2	35:AC:211:GLU:N	2.22	0.47
36:A1:874:U:H5''	36:A1:2950:G:OP1	2.14	0.47
36:A1:1211:U:H2'	36:A1:1212:A:C8	2.49	0.47
36:A1:1242:G:O2'	36:A1:1243:G:OP1	2.26	0.47
36:A1:1793:C:OP2	76:Ap:49:ARG:NH2	2.39	0.47
36:A1:2148:U:H2'	36:A1:2149:A:C8	2.49	0.47
36:A1:2469:G:O3'	77:E:26:ARG:HG2	2.14	0.47
43:AH:9:GLN:HE22	43:AH:54:LYS:HE2	1.79	0.47
43:AH:41:ILE:HG21	43:AH:71:VAL:HG21	1.95	0.47
77:E:205:VAL:HG22	77:E:215:ARG:NH2	2.27	0.47
82:VA:53:MET:HE3	82:VA:55:LYS:NZ	2.29	0.47
5:BG:175:ILE:HB	5:BG:178:LEU:HD23	1.96	0.47
22:BP:88:GLU:OE2	22:BP:89:MET:HE3	2.14	0.47
22:BP:122:THR:HG21	32:B5:1454:G:H4'	1.94	0.47
25:BS:28:ILE:HD12	25:BS:28:ILE:H	1.78	0.47
32:B5:341:A:H2'	32:B5:342:C:C6	2.50	0.47
32:B5:884:A:H2'	32:B5:885:G:C8	2.50	0.47
32:B5:1063:U:C2	32:B5:1064:G:C8	3.03	0.47
36:A1:393:U:H2'	36:A1:394:G:O4'	2.15	0.47
36:A1:2419:A:H2'	36:A1:2420:C:C6	2.49	0.47
36:A1:2961:G:H2'	36:A1:2962:U:H6	1.80	0.47
39:AD:85:ARG:NH1	39:AD:254:LYS:H	2.11	0.47
72:Al:44:TRP:CE2	72:Al:45:ARG:HG3	2.49	0.47
78:EC:6758:A:H5'	78:EC:6759:A:OP2	2.14	0.47
78:EC:6788:C:H3'	78:EC:6805:C:N4	2.29	0.47
2:BB:157:GLN:C	2:BB:159:SER:H	2.23	0.47
7:BI:5:ARG:NH2	32:B5:334:G:O6	2.47	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BN:136:PRO:HG2	10:BN:139:TRP:HB2	1.96	0.47
15:BY:8:ARG:HE	15:BY:10:ARG:HH21	1.63	0.47
20:BF:120:ILE:HD13	20:BF:192:GLU:HB3	1.95	0.47
25:BS:42:TYR:HD1	25:BS:85:PHE:CE2	2.31	0.47
31:Bg:149:ASP:HB2	31:Bg:175:ASP:HB3	1.97	0.47
32:B5:52:U:H2'	32:B5:53:G:H8	1.80	0.47
32:B5:1091:A:H4'	32:B5:1092:A:O4'	2.14	0.47
32:B5:1732:A:H2'	32:B5:1733:C:H6	1.78	0.47
36:A1:29:C:H4'	36:A1:62:A:H4'	1.97	0.47
36:A1:264:G:OP1	69:Ai:34:SER:HB2	2.14	0.47
36:A1:2264:U:H2'	36:A1:2265:C:C6	2.49	0.47
36:A1:2683:U:H2'	36:A1:2684:C:H6	1.78	0.47
36:A1:2852:C:O2'	44:AI:30:LYS:NZ	2.46	0.47
36:A1:3198:U:O4	43:AH:26:LYS:HB2	2.14	0.47
44:AI:19:LYS:HD3	44:AI:26:VAL:HB	1.96	0.47
49:AO:44[A]:SER:HB3	49:AO:129[A]:LEU:HD21	1.95	0.47
50:AP:60:PHE:HB3	50:AP:64:ASN:HB3	1.97	0.47
79:DC:180:ARG:NH2	82:VA:140:GLY:O	2.47	0.47
2:BB:47:LEU:HD11	11:BO:37:GLU:HG2	1.97	0.47
10:BN:87:ASP:HB3	32:B5:867:G:H21	1.79	0.47
19:BD:142:LEU:O	19:BD:143:ARG:HG2	2.13	0.47
24:BR:52:GLY:HA3	32:B5:1389:C:O2'	2.14	0.47
33:AA:30:ARG:NH1	33:AA:36:GLU:OE2	2.33	0.47
36:A1:118:U:O2	36:A1:121:A:H5''	2.14	0.47
36:A1:633:C:O2'	66:Af:21:ARG:O	2.28	0.47
36:A1:1639:C:HO2'	36:A1:1737:U:HO2'	1.60	0.47
36:A1:2909:U:H2'	36:A1:2910:A:O4'	2.13	0.47
36:A1:3095:U:H2'	36:A1:3096:C:C6	2.50	0.47
36:A1:3358:U:H2'	36:A1:3359:A:H8	1.78	0.47
45:AJ:118:PRO:O	45:AJ:120:ILE:N	2.45	0.47
50:AP:40:GLU:OE1	50:AP:40:GLU:N	2.47	0.47
73:Am:79:GLU:O	73:Am:82:LEU:N	2.44	0.47
2:BB:27:LYS:HB3	2:BB:47:LEU:HB2	1.95	0.47
5:BG:52:ILE:HD12	5:BG:109:LEU:HD21	1.96	0.47
9:BL:81:HIS:CE1	9:BL:82:ARG:HD2	2.50	0.47
18:Be:54:ARG:NH2	18:Be:56:MET:SD	2.86	0.47
27:BU:50:LEU:HD12	27:BU:94:GLU:O	2.13	0.47
32:B5:1719:A:H2'	32:B5:1720:G:O4'	2.14	0.47
33:AA:242:ARG:NH2	33:AA:243:THR:O	2.48	0.47
36:A1:632:G:H2'	36:A1:633:C:C6	2.49	0.47
36:A1:1222:G:C8	82:VA:57:THR:HG21	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1498:A:H2'	36:A1:1499:C:C6	2.49	0.47
36:A1:1553:U:H4'	36:A1:1554:U:H5'	1.94	0.47
36:A1:2273:G:O2'	36:A1:2311:G:O6	2.29	0.47
36:A1:2748:A:H1'	39:AD:36:LEU:HD23	1.96	0.47
36:A1:3163:A:H2'	36:A1:3164:C:C6	2.50	0.47
51:AQ:176:ARG:HA	51:AQ:182:LYS:O	2.15	0.47
77:E:125:GLY:N	77:E:126:PRO:HD2	2.29	0.47
79:DC:92:LYS:HE3	79:DC:346:VAL:HG21	1.96	0.47
79:DC:515:ASP:OD2	79:DC:537:HIS:NE2	2.47	0.47
7:BI:110:ARG:HG3	7:BI:121:LEU:HB2	1.96	0.47
10:BN:99:ARG:NH2	10:BN:119:GLU:OE2	2.47	0.47
16:Ba:46:GLU:HB3	16:Ba:48:ALA:H	1.80	0.47
18:Be:55:ARG:HG2	18:Be:58:PRO:HB3	1.96	0.47
19:BD:7:LYS:HD2	27:BU:27:THR:HG21	1.96	0.47
19:BD:195:SER:O	19:BD:196:ARG:HG2	2.15	0.47
20:BF:96:SER:OG	20:BF:176:THR:HG21	2.15	0.47
22:BP:42:ARG:NH2	32:B5:1549:C:OP1	2.43	0.47
22:BP:57:MET:HB3	22:BP:61:ARG:HH21	1.79	0.47
24:BR:71:PHE:CE2	24:BR:73:LEU:HB3	2.49	0.47
25:BS:27:LYS:HZ3	32:B5:1539:G:H1	1.63	0.47
30:Bd:17:GLY:N	32:B5:1205:C:O2	2.42	0.47
32:B5:629:U:H2'	32:B5:630:A:H8	1.80	0.47
32:B5:743:U:H2'	32:B5:744:U:C6	2.50	0.47
32:B5:1699:G:N2	32:B5:1700:C:H1'	2.29	0.47
34:AB:226:PHE:O	36:A1:1886:A:O2'	2.31	0.47
35:AC:10:SER:OG	35:AC:13:GLY:O	2.31	0.47
36:A1:142:C:H2'	36:A1:143:G:O4'	2.14	0.47
36:A1:238:A:OP2	36:A1:238:A:C8	2.68	0.47
36:A1:700:C:OP1	46:AL:65:TYR:OH	2.24	0.47
36:A1:828:A:H2'	36:A1:829:U:C6	2.50	0.47
36:A1:1184:A:H2'	36:A1:1185:C:C6	2.49	0.47
36:A1:1525:G:H5'	36:A1:1830:G:OP2	2.13	0.47
36:A1:1620:U:H2'	36:A1:1621:A:C8	2.50	0.47
36:A1:1763:U:H3'	36:A1:1765:U:C4	2.50	0.47
36:A1:2492:C:OP1	77:E:215:ARG:CZ	2.62	0.47
36:A1:2520:A:H2'	36:A1:2521:U:C6	2.49	0.47
36:A1:2565:U:H2'	36:A1:2566:C:C6	2.50	0.47
37:A3:74:C:H2'	37:A3:75:G:C8	2.50	0.47
37:A3:121:U:OP2	39:AD:265:TYR:OH	2.23	0.47
38:A4:12:A:P	50:AP:3:ARG:HH21	2.37	0.47
43:AH:41:ILE:HG21	43:AH:71:VAL:CG2	2.44	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AH:98:PRO:HG2	79:DC:168:GLN:HB2	1.95	0.47
44:AI:68:ALA:HB1	44:AI:155:ALA:HB1	1.95	0.47
45:AJ:23:VAL:HG12	45:AJ:29:ARG:HH21	1.80	0.47
52:AR:28:GLU:HB3	52:AR:31:GLU:HB3	1.95	0.47
60:AZ:115:LYS:HE3	60:AZ:119:GLU:OE2	2.15	0.47
78:EC:6761:C:H2'	78:EC:6762:U:C6	2.50	0.47
78:EC:6835:U:H5''	78:EC:6848:U:C2	2.50	0.47
79:DC:437:MET:O	79:DC:438:MET:HE2	2.15	0.47
79:DC:597:VAL:HG22	79:DC:623:TYR:HB3	1.97	0.47
82:VA:96:ILE:O	82:VA:100:ILE:HG12	2.15	0.47
3:BC:89:GLN:O	32:B5:1145:U:O2'	2.28	0.47
11:BO:103:ARG:HD2	16:Ba:49:ALA:HB2	1.97	0.47
17:Bb:41:LEU:HD23	17:Bb:41:LEU:H	1.80	0.47
20:BF:84:LYS:HE3	20:BF:169:ASN:HD21	1.80	0.47
25:BS:135:GLY:HA3	32:B5:1559:A:O5'	2.14	0.47
30:Bd:5:ASN:OD1	30:Bd:7:TRP:NE1	2.48	0.47
32:B5:34:G:O2'	32:B5:515:A:O2'	2.32	0.47
32:B5:1207:C:H4'	32:B5:1208:A:O4'	2.15	0.47
36:A1:191:U:H2'	36:A1:192:C:C6	2.50	0.47
36:A1:364:G:OP2	70:Aj:52:LYS:NZ	2.28	0.47
36:A1:999:G:H2'	36:A1:1000:C:C6	2.50	0.47
36:A1:1574:C:C3'	36:A1:1575:A:H5''	2.44	0.47
46:AL:124:ILE:HD13	68:Ah:119:LYS:HD2	1.97	0.47
47:AM:37:GLU:HB2	47:AM:45:LEU:HB3	1.97	0.47
77:E:37:GLY:HA2	77:E:164:CYS:SG	2.55	0.47
79:DC:201:GLN:NE2	82:VA:145:ILE:HB	2.29	0.47
79:DC:651:LYS:HE3	80:Bf:82:LYS:HE2	1.96	0.47
79:DC:822:ALA:HA	79:DC:825:ARG:HG2	1.97	0.47
82:VA:26:PHE:CD1	82:VA:190:VAL:HG12	2.50	0.47
2:BB:222:LYS:HA	2:BB:222:LYS:HD2	1.63	0.47
8:BJ:90:LYS:HB2	8:BJ:95:TYR:CD2	2.49	0.47
10:BN:84:ILE:HG22	10:BN:135:LEU:HD21	1.97	0.47
11:BO:84:ARG:HG2	11:BO:85:ALA:O	2.14	0.47
23:BQ:93:HIS:HA	23:BQ:97:VAL:HB	1.95	0.47
25:BS:14:ILE:HD12	25:BS:22:VAL:C	2.40	0.47
31:Bg:91:LEU:HB3	31:Bg:100:TYR:HB2	1.97	0.47
32:B5:233:C:HO2'	32:B5:234:G:N2	2.07	0.47
32:B5:751:G:H2'	32:B5:752:A:C8	2.50	0.47
35:AC:315:LYS:HB2	35:AC:323:VAL:HG21	1.97	0.47
36:A1:876:A2M:H5''	36:A1:1890:U:H5''	1.95	0.47
36:A1:1240:A:H1'	36:A1:1249:G:N2	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1740:U:H1'	36:A1:1741:A:H2	1.80	0.47
36:A1:2264:U:H2'	36:A1:2265:C:H6	1.80	0.47
36:A1:2354:C:H2'	36:A1:2355:G:O4'	2.15	0.47
37:A3:48:U:OP1	39:AD:94:ASN:ND2	2.48	0.47
40:AE:100:LYS:NZ	40:AE:137:ASP:OD2	2.40	0.47
60:AZ:42:LEU:HD22	60:AZ:101:PHE:CE2	2.49	0.47
78:EC:6892:U:H2'	78:EC:6893:C:H5	1.80	0.47
79:DC:140:GLU:HG2	79:DC:188:ILE:HD12	1.97	0.47
79:DC:154:VAL:HG12	79:DC:337:MET:HE2	1.97	0.47
79:DC:520:THR:HG22	79:DC:530:VAL:HG22	1.97	0.47
19:BD:209:ILE:O	24:BR:20:TYR:OH	2.30	0.47
22:BP:47:ARG:NE	32:B5:1555:A:OP1	2.38	0.47
22:BP:87:PRO:HA	22:BP:90:ILE:HG12	1.96	0.47
31:Bg:220:ILE:HB	31:Bg:234:LEU:HB2	1.97	0.47
32:B5:778:G:N1	32:B5:780:A:N7	2.63	0.47
32:B5:1315:U:OP1	32:B5:1328:G:N2	2.32	0.47
32:B5:1349:G:H2'	32:B5:1350:U:C6	2.49	0.47
32:B5:1528:U:H2'	32:B5:1529:C:C6	2.50	0.47
36:A1:159:A:H2'	36:A1:160:G:H8	1.79	0.47
36:A1:256:G:H2'	36:A1:257:U:C6	2.49	0.47
36:A1:1597:C:H5'	36:A1:1696:A:H1'	1.97	0.47
36:A1:1784:G:H2'	36:A1:1785:U:O4'	2.15	0.47
36:A1:2459:A:H62	36:A1:2461:A:N6	2.13	0.47
36:A1:2477:G:H5'	36:A1:2487:U:C2	2.50	0.47
38:A4:47:C:H1'	38:A4:61:A:H2'	1.96	0.47
40:AE:45:GLY:O	40:AE:48:ARG:NH1	2.48	0.47
44:AI:42:THR:HG23	44:AI:192:ASP:OD1	2.15	0.47
64:Ad:44:MET:O	64:Ad:77:ARG:NH1	2.47	0.47
77:E:21:ASN:OD1	77:E:22:GLU:N	2.48	0.47
77:E:141:ASN:OD1	77:E:142:ASP:N	2.48	0.47
79:DC:221:THR:HG23	79:DC:224:GLN:H	1.80	0.47
81:BM:70:ASN:O	81:BM:73:LYS:HG2	2.15	0.47
1:BA:88:LYS:HD3	24:BR:82:ASP:OD2	2.15	0.46
11:BO:107:ARG:HE	11:BO:107:ARG:HB3	1.55	0.46
23:BQ:42:GLU:HB3	23:BQ:45:ARG:HH21	1.80	0.46
25:BS:29:VAL:O	25:BS:33:THR:HG23	2.15	0.46
31:Bg:256:THR:OG1	31:Bg:259:GLY:O	2.19	0.46
32:B5:823:G:H2'	32:B5:824:G:O4'	2.14	0.46
32:B5:1237:G:H2'	32:B5:1238:A:C8	2.49	0.46
32:B5:1315:U:H2'	32:B5:1316:G:O4'	2.15	0.46
32:B5:1705:C:H2'	32:B5:1706:C:C6	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AC:125:ALA:O	35:AC:129:THR:HG23	2.15	0.46
36:A1:947:G:H5'	65:Ae:55:ILE:HB	1.96	0.46
36:A1:1081:U:H4'	36:A1:1082:U:H5'	1.97	0.46
36:A1:1460:A:H2'	36:A1:1461:A:C8	2.49	0.46
36:A1:1643:A:H2'	36:A1:1644:C:C2	2.50	0.46
36:A1:2144:A:H1'	36:A1:2281:A2M:N6	2.30	0.46
36:A1:3066:U:H2'	36:A1:3067:C:C6	2.50	0.46
43:AH:10:ILE:HB	43:AH:53:ILE:HB	1.97	0.46
46:AL:50:PRO:HD2	68:Ah:116:TYR:CE2	2.51	0.46
78:EC:6923:C:H2'	78:EC:6924:G:H8	1.78	0.46
81:BM:56:GLU:O	81:BM:124:LYS:HA	2.15	0.46
7:BI:185:GLU:HG3	9:BL:23:PRO:HG2	1.97	0.46
16:Ba:95:ARG:NH1	32:B5:1796:C:O2'	2.46	0.46
19:BD:5:ILE:HG23	19:BD:10:LYS:HB2	1.96	0.46
27:BU:98:GLN:HG2	27:BU:99:ILE:HG23	1.97	0.46
28:BZ:61:SER:H	28:BZ:64:VAL:HG22	1.80	0.46
31:Bg:54:PHE:CE2	31:Bg:312:VAL:HG11	2.46	0.46
32:B5:15:U:H2'	32:B5:16:G:O4'	2.15	0.46
33:AA:178:PRO:HG2	76:Ap:26:VAL:HG23	1.97	0.46
36:A1:660:A:N1	36:A1:941:G:O2'	2.47	0.46
36:A1:1688:U:H2'	36:A1:1689:U:C6	2.50	0.46
36:A1:2881:C:H2'	36:A1:2882:U:C6	2.51	0.46
36:A1:3235:C:H2'	36:A1:3236:U:O4'	2.15	0.46
38:A4:40:A:H2'	38:A4:41:A:C8	2.50	0.46
53:AS:12:ARG:HB2	53:AS:22:PRO:HB2	1.97	0.46
57:AW:43:ARG:HD3	57:AW:43:ARG:HA	1.75	0.46
66:Af:9:VAL:HG23	66:Af:100:ILE:HB	1.98	0.46
78:EC:6793:A:N6	78:EC:6880:G:O2'	2.48	0.46
79:DC:303:LEU:HD12	79:DC:327:PHE:CE1	2.50	0.46
79:DC:675:PRO:HD3	79:DC:681:MET:HE2	1.97	0.46
82:VA:40:GLU:O	82:VA:44:GLU:HG2	2.15	0.46
4:BE:60:GLU:OE1	4:BE:60:GLU:N	2.46	0.46
11:BO:17:ALA:HB3	11:BO:81:VAL:HA	1.96	0.46
15:BY:37:LYS:HG2	15:BY:57:VAL:HG23	1.97	0.46
18:Be:38:LEU:HA	18:Be:41:THR:HG22	1.96	0.46
21:BK:29:GLN:NE2	21:BK:33:GLU:OE2	2.47	0.46
24:BR:3:ARG:HD2	32:B5:1390:U:C6	2.50	0.46
25:BS:138:THR:HG23	32:B5:1459:C:H2'	1.97	0.46
27:BU:96:PRO:HD2	27:BU:99:ILE:HD11	1.98	0.46
36:A1:567:G:H2'	36:A1:568:G:C8	2.49	0.46
36:A1:715:A:N1	36:A1:781:G:O2'	2.45	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:718:G:C2	36:A1:721:G:H1'	2.50	0.46
36:A1:784:A:OP2	51:AQ:69:ARG:NH1	2.27	0.46
36:A1:1120:A:H2'	36:A1:1121:U:C6	2.51	0.46
36:A1:1289:G:H2'	36:A1:1290:A:C8	2.50	0.46
36:A1:1355:A:H4'	36:A1:1356:U:H5''	1.97	0.46
36:A1:2344:U:H2'	36:A1:2345:A:H8	1.80	0.46
36:A1:2356:A:H5'	50:AP:138:LYS:NZ	2.30	0.46
36:A1:2991:A:O2'	36:A1:3309:G:N7	2.48	0.46
45:AJ:34:SER:HA	45:AJ:67:VAL:HG11	1.97	0.46
50:AP:58:ILE:HD12	50:AP:84:PRO:HD2	1.98	0.46
76:Ap:49:ARG:HB2	76:Ap:55:TRP:CZ3	2.50	0.46
77:E:58:CYS:HB3	77:E:152:ARG:HH21	1.81	0.46
77:E:119:GLN:OE1	77:E:122:ARG:NH1	2.47	0.46
2:BB:76:SER:OG	2:BB:78:ASP:OD1	2.23	0.46
4:BE:246:LEU:HG	4:BE:251:GLU:HG3	1.97	0.46
5:BG:112:VAL:HG11	32:B5:164:A:H5'	1.96	0.46
20:BF:121:ILE:HD11	20:BF:198:LEU:HD12	1.96	0.46
28:BZ:53:GLU:OE1	78:EC:6865:G:N2	2.37	0.46
32:B5:240:U:H3'	32:B5:241:U:C5'	2.43	0.46
32:B5:819:G:N7	32:B5:853:G:N1	2.62	0.46
32:B5:1208:A:O2'	80:Bf:78:LYS:NZ	2.48	0.46
32:B5:1569:A:H2'	32:B5:1570:A:C8	2.51	0.46
32:B5:1696:G:H2'	32:B5:1697:G:H8	1.80	0.46
36:A1:62:A:H5''	48:AN:164:LEU:HD21	1.97	0.46
36:A1:292:U:OP2	48:AN:68:ARG:NH2	2.45	0.46
36:A1:362:U:O4	70:Aj:24:ARG:NH2	2.47	0.46
36:A1:1446:A:H5''	50:AP:65:SER:HB3	1.98	0.46
36:A1:1951:C:H2'	36:A1:1952:G:O4'	2.16	0.46
60:AZ:88:ASP:HB3	60:AZ:121:ARG:NH2	2.31	0.46
67:Ag:74:ARG:NH2	67:Ag:82:ALA:HB2	2.31	0.46
71:Ak:26:LYS:NZ	71:Ak:28:ASN:OD1	2.44	0.46
77:E:58:CYS:SG	77:E:152:ARG:NE	2.86	0.46
77:E:76:ARG:HE	77:E:144:LEU:HB2	1.81	0.46
77:E:127:GLN:O	77:E:127:GLN:NE2	2.48	0.46
78:EC:6886:A:H2'	78:EC:6887:G:C8	2.50	0.46
81:BM:28:LEU:HA	81:BM:31:VAL:HG22	1.96	0.46
3:BC:43:ARG:HH11	3:BC:248:SER:H	1.63	0.46
7:BI:10:LYS:NZ	32:B5:322:G:O2'	2.48	0.46
7:BI:119:GLN:HG3	7:BI:150:ALA:CB	2.45	0.46
7:BI:160:PHE:CZ	7:BI:165:LEU:HD11	2.50	0.46
10:BN:64:ARG:NH2	32:B5:862:A:OP2	2.48	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Ba:45:VAL:O	16:Ba:46:GLU:HG2	2.16	0.46
25:BS:91:ASP:HB3	25:BS:94:ASP:OD1	2.16	0.46
28:BZ:59:TYR:CE1	28:BZ:100:ILE:HG23	2.50	0.46
31:Bg:256:THR:HG21	31:Bg:261:LYS:HD2	1.98	0.46
32:B5:16:G:H2'	32:B5:17:C:C6	2.49	0.46
32:B5:1058:U:H3'	32:B5:1059:U:H5'	1.98	0.46
35:AC:120:TYR:HE1	35:AC:277:PRO:HB3	1.80	0.46
36:A1:86:G:O2'	36:A1:98:G:O6	2.29	0.46
36:A1:180:C:O2'	36:A1:181:U:H5'	2.15	0.46
36:A1:241:G:H1'	36:A1:242:C:OP1	2.16	0.46
36:A1:1045:C:OP1	44:AI:133:GLN:NE2	2.48	0.46
39:AD:119:TYR:CE1	39:AD:135:VAL:HG13	2.51	0.46
43:AH:94:TYR:HA	43:AH:177:ASP:CB	2.45	0.46
67:Ag:91:ARG:O	67:Ag:95:ILE:HG12	2.16	0.46
79:DC:19:VAL:HG12	79:DC:99:LEU:HB3	1.98	0.46
79:DC:594:ASP:HB3	79:DC:597:VAL:HG23	1.97	0.46
82:VA:159:VAL:HG11	82:VA:165:VAL:HG12	1.97	0.46
3:BC:81:MET:HE1	3:BC:186:LYS:HB2	1.98	0.46
3:BC:204:THR:OG1	32:B5:5:U:OP2	2.27	0.46
15:BY:120:GLY:HA2	32:B5:86:A:H5'	1.97	0.46
19:BD:39:VAL:HG12	19:BD:48:VAL:HG22	1.97	0.46
23:BQ:46:PHE:HA	23:BQ:49:TYR:HB2	1.97	0.46
27:BU:33:GLN:HB3	27:BU:109:GLU:OE2	2.16	0.46
31:Bg:11:GLY:HA3	31:Bg:312:VAL:HB	1.98	0.46
31:Bg:274:LEU:HB3	31:Bg:313:TRP:CZ3	2.51	0.46
32:B5:968:U:H2'	32:B5:969:C:O4'	2.16	0.46
32:B5:1171:A:H2'	32:B5:1172:G:H8	1.78	0.46
36:A1:1378:U:H2'	36:A1:1379:G:C8	2.51	0.46
36:A1:2533:G:H2'	36:A1:2534:G:H8	1.80	0.46
36:A1:2953:U:H2'	36:A1:2954:U:H2'	1.97	0.46
47:AM:17:VAL:HG11	47:AM:74:ARG:HA	1.98	0.46
50:AP:176:ILE:O	50:AP:180:LYS:HG3	2.14	0.46
55:AU:53:ALA:HB1	55:AU:69:ALA:HB2	1.97	0.46
58:AX:46:TYR:HD1	68:Ah:75:TYR:HB3	1.79	0.46
59:AY:116:LYS:HB3	59:AY:126:LEU:HD21	1.97	0.46
78:EC:6778:C:P	78:EC:6779:C:H41	2.37	0.46
78:EC:6791:A:H2'	78:EC:6793:A:H5''	1.97	0.46
78:EC:6853:G:N2	78:EC:6875:C:H42	2.14	0.46
1:BA:56:LYS:HA	1:BA:56:LYS:HD2	1.73	0.46
3:BC:220:ASN:OD1	12:BV:25:LYS:NZ	2.49	0.46
5:BG:13:GLN:NE2	32:B5:151:G:N3	2.64	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:98:ILE:HD12	6:BH:118:LEU:HA	1.97	0.46
7:BI:117:TYR:CD2	7:BI:150:ALA:HA	2.51	0.46
22:BP:75:PRO:HB3	22:BP:104:GLN:HE22	1.80	0.46
24:BR:45:ARG:NH1	32:B5:1332:C:OP2	2.49	0.46
25:BS:36:LYS:HB3	25:BS:105:VAL:HG21	1.97	0.46
32:B5:592:A:H2'	32:B5:593:U:O4'	2.16	0.46
32:B5:698:U:H2'	32:B5:699:U:C6	2.51	0.46
36:A1:246:U:H3'	36:A1:247:C:C4'	2.46	0.46
36:A1:2631:U:OP1	36:A1:2757:U:O2'	2.31	0.46
45:AJ:38:GLU:HB3	45:AJ:45:PRO:HD3	1.98	0.46
79:DC:17:THR:OG1	79:DC:91:GLN:NE2	2.32	0.46
2:BB:133:TYR:CD2	2:BB:181:LEU:HB2	2.51	0.46
5:BG:137:ARG:HD3	5:BG:177:ARG:HD2	1.98	0.46
15:BY:57:VAL:HB	15:BY:60:PHE:CE2	2.51	0.46
27:BU:55:PRO:HA	27:BU:91:ILE:HG13	1.98	0.46
31:Bg:103:PHE:CE2	31:Bg:138:GLY:HA2	2.51	0.46
32:B5:182:A:H2'	32:B5:183:U:C6	2.51	0.46
32:B5:482:U:H2'	32:B5:483:A:N3	2.31	0.46
32:B5:560:U:H2'	32:B5:561:G:H8	1.81	0.46
32:B5:1124:A:H2'	32:B5:1125:A:O4'	2.16	0.46
32:B5:1785:U:H2'	32:B5:1786:G:H8	1.80	0.46
36:A1:74:G:OP1	46:AL:105:ASN:HB2	2.16	0.46
36:A1:77:A:OP2	46:AL:73:ARG:NH1	2.48	0.46
36:A1:239:G:H2'	36:A1:240:U:O2	2.16	0.46
36:A1:242:C:C2	36:A1:243:G:C8	3.04	0.46
36:A1:250:U:C2'	36:A1:251:G:H5'	2.46	0.46
36:A1:2838:A:OP1	44:AI:154:ARG:NH2	2.49	0.46
36:A1:3298:C:C2	36:A1:3299:A:C8	3.04	0.46
45:AJ:173:ASP:OD1	45:AJ:173:ASP:N	2.42	0.46
76:Ap:78:THR:O	76:Ap:82:THR:HG23	2.15	0.46
79:DC:146:ALA:O	79:DC:151:ILE:HG22	2.16	0.46
79:DC:381:TYR:HB2	79:DC:478:MET:HE3	1.98	0.46
79:DC:588:LEU:HD12	79:DC:686:VAL:HG13	1.97	0.46
3:BC:145:GLY:O	13:BW:98:GLN:NE2	2.47	0.46
19:BD:80:ALA:O	19:BD:83:THR:HG22	2.16	0.46
20:BF:20:PHE:CE2	20:BF:22:PRO:HG3	2.51	0.46
20:BF:72:HIS:CD2	20:BF:107:LYS:HD2	2.50	0.46
24:BR:28:PHE:CE2	24:BR:32:LYS:HD3	2.50	0.46
26:BT:33:TYR:CE2	26:BT:103:LYS:HD2	2.51	0.46
26:BT:87:GLY:C	32:B5:1542:G:H5''	2.41	0.46
32:B5:962:C:H2'	32:B5:963:A:O4'	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AB:30:LYS:HD2	36:A1:3138:U:OP2	2.16	0.46
36:A1:968:G:H2'	36:A1:969:C:H6	1.81	0.46
36:A1:1144:U:OP1	36:A1:1367:G:O2'	2.27	0.46
36:A1:1718:G:H4'	52:AR:117:LYS:HD2	1.98	0.46
36:A1:1921:A:H2'	36:A1:1922:A:C8	2.51	0.46
36:A1:2407:C:H2'	36:A1:2408:U:H6	1.80	0.46
36:A1:2662:G:H2'	36:A1:2663:G:C8	2.51	0.46
36:A1:3084:C:H2'	36:A1:3085:G:O4'	2.16	0.46
36:A1:3113:A:O2'	43:AH:69:ARG:HB3	2.15	0.46
36:A1:3283:U:H2'	36:A1:3284:G:H8	1.81	0.46
41:AF:163:LEU:O	41:AF:165:ASP:N	2.49	0.46
45:AJ:21:ILE:HG22	45:AJ:23:VAL:HG13	1.98	0.46
51:AQ:116:LYS:HB3	51:AQ:116:LYS:HE2	1.68	0.46
56:AV:54:LEU:HD21	56:AV:119:GLY:HA3	1.98	0.46
79:DC:165:LEU:HD13	79:DC:317:LYS:HE2	1.98	0.46
79:DC:295:GLU:O	79:DC:299:LEU:HD12	2.16	0.46
79:DC:434:VAL:HB	79:DC:445:ILE:HG22	1.98	0.46
5:BG:20:ASP:O	5:BG:23:ARG:HG2	2.16	0.46
5:BG:39:GLU:OE1	5:BG:39:GLU:N	2.47	0.46
7:BI:34:ALA:HB2	7:BI:56:ARG:HD2	1.98	0.46
9:BL:14:GLN:HB3	9:BL:54:ILE:HG13	1.98	0.46
16:Ba:75:VAL:HB	32:B5:1793:G:N1	2.31	0.46
18:Be:26:LYS:HD2	18:Be:27:PRO:O	2.16	0.46
20:BF:164:PRO:HG3	29:Bc:52:ASP:HB3	1.97	0.46
21:BK:2:LEU:HA	32:B5:1257:U:H2'	1.97	0.46
26:BT:22:LEU:HB3	26:BT:28:LEU:HD11	1.96	0.46
32:B5:142:G:N2	32:B5:142:G:OP2	2.48	0.46
32:B5:223:U:H2'	32:B5:224:C:O4'	2.16	0.46
32:B5:948:G:H2'	32:B5:949:C:H6	1.80	0.46
32:B5:1356:U:H2'	32:B5:1357:A:C8	2.51	0.46
32:B5:1441:C:H2'	32:B5:1442:U:C6	2.51	0.46
35:AC:135:VAL:HG12	35:AC:140:HIS:HB2	1.98	0.46
35:AC:283:THR:HG21	35:AC:288:ARG:HH22	1.81	0.46
36:A1:119:U:H4'	36:A1:120:G:H3'	1.98	0.46
36:A1:3094:A:H2'	36:A1:3095:U:C6	2.51	0.46
42:AG:74:THR:HG22	42:AG:164:VAL:HG22	1.97	0.46
43:AH:22:SER:O	43:AH:23:ARG:HD3	2.16	0.46
48:AN:9:GLU:HG3	69:Ai:44:VAL:HG11	1.97	0.46
48:AN:157:LYS:O	48:AN:162:ARG:NH2	2.38	0.46
67:Ag:67:LYS:O	67:Ag:71:THR:HG22	2.16	0.46
77:E:35:GLN:HB3	77:E:205:VAL:HB	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:DC:271:ARG:HB2	79:DC:274:ASN:H	1.81	0.46
79:DC:482:LYS:C	79:DC:484:SER:H	2.24	0.46
6:BH:80:GLU:HA	6:BH:83:LYS:HG2	1.98	0.45
7:BI:84:HIS:HB2	7:BI:91:VAL:HG23	1.98	0.45
20:BF:168:VAL:O	20:BF:172:ILE:HG12	2.15	0.45
29:Bc:15:VAL:HG12	29:Bc:28:VAL:HG12	1.98	0.45
32:B5:113:U:O2'	32:B5:115:G:O2'	2.30	0.45
32:B5:485:A:H62	32:B5:486:G:N2	2.13	0.45
32:B5:828:U:H2'	32:B5:829:A:O4'	2.16	0.45
32:B5:876:G:H2'	32:B5:936:G:N2	2.31	0.45
32:B5:1452:U:H2'	32:B5:1453:G:H8	1.80	0.45
32:B5:1562:G:H2'	32:B5:1563:C:O4'	2.16	0.45
33:AA:219:ILE:HD13	33:AA:223:SER:OG	2.16	0.45
34:AB:87:VAL:O	34:AB:107:ALA:N	2.45	0.45
36:A1:314:U:H2'	36:A1:315:C:C6	2.51	0.45
36:A1:1327:C:O2'	66:Af:76:GLY:HA2	2.17	0.45
36:A1:1593:A:N3	36:A1:1615:C:O2'	2.46	0.45
36:A1:2152:A:H2'	36:A1:2153:U:C6	2.50	0.45
36:A1:2220:A2M:H8	36:A1:2220:A2M:O5'	2.16	0.45
36:A1:2407:C:H2'	36:A1:2408:U:C6	2.51	0.45
36:A1:2836:C:H5	36:A1:2852:C:N4	2.11	0.45
36:A1:2927:C:H2'	36:A1:2928:C:C6	2.51	0.45
40:AE:170:LYS:HB2	40:AE:173:MET:HG2	1.98	0.45
54:AT:40:VAL:HB	54:AT:96:ILE:HG23	1.98	0.45
54:AT:143:THR:HG23	54:AT:148:PRO:HD3	1.99	0.45
58:AX:46:TYR:CD1	68:Ah:75:TYR:HB3	2.51	0.45
71:Ak:12:LEU:HB3	71:Ak:16:ARG:HH12	1.81	0.45
75:Ao:99:GLN:HB3	75:Ao:102:GLN:HG3	1.98	0.45
79:DC:127:VAL:HG11	79:DC:143:LEU:HD13	1.98	0.45
79:DC:243:ARG:O	79:DC:248:SER:OG	2.35	0.45
79:DC:803:THR:OG1	79:DC:804:LEU:N	2.49	0.45
82:VA:41:VAL:HG11	82:VA:185:LEU:HD22	1.96	0.45
1:BA:84:ARG:HD3	1:BA:203:PHE:O	2.16	0.45
8:BJ:38:ASN:ND2	32:B5:594:A:OP2	2.47	0.45
12:BV:38:LYS:HG3	12:BV:49:GLU:HG3	1.98	0.45
14:BX:99:ASN:HD21	79:DC:505:VAL:HG13	1.82	0.45
19:BD:115:ILE:H	19:BD:115:ILE:HD12	1.80	0.45
20:BF:72:HIS:ND1	23:BQ:79:TYR:OH	2.39	0.45
22:BP:39:ALA:N	32:B5:1549:C:OP2	2.44	0.45
25:BS:55:HIS:CG	25:BS:55:HIS:O	2.70	0.45
27:BU:87:HIS:HB3	27:BU:89:ARG:NH1	2.31	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:358:U:H5''	32:B5:359:A:C2	2.52	0.45
32:B5:1357:A:H2'	32:B5:1358:G:C8	2.50	0.45
33:AA:127:ALA:HB2	33:AA:134:VAL:HG23	1.98	0.45
34:AB:259:HIS:HB3	36:A1:2987:A:O2'	2.16	0.45
36:A1:273:A:H2'	36:A1:274:G:C8	2.50	0.45
36:A1:523:A:O2'	53:AS:69:PRO:HD2	2.17	0.45
36:A1:1478:C:H2'	36:A1:1479:U:C6	2.51	0.45
36:A1:2203:U:H2'	36:A1:2204:C:C6	2.51	0.45
36:A1:2674:A:H5''	45:AJ:105:GLY:HA3	1.96	0.45
36:A1:2714:G:OP1	75:Ao:20:HIS:NE2	2.44	0.45
36:A1:2762:A:H2'	36:A1:2763:U:H6	1.81	0.45
36:A1:2964:G:N2	36:A1:2967:A:OP2	2.34	0.45
36:A1:3160:U:H2'	36:A1:3161:C:C6	2.51	0.45
49:AO:186[A]:ALA:O	49:AO:187[A]:GLU:HG2	2.16	0.45
50:AP:56:ARG:NH2	50:AP:75:GLU:OE2	2.46	0.45
82:VA:139:LEU:HD21	82:VA:169:GLU:HG2	1.98	0.45
1:BA:123:VAL:HG21	1:BA:133:ILE:HD11	1.98	0.45
17:Bb:33:LEU:HD22	17:Bb:79:PHE:HB2	1.97	0.45
19:BD:51:ARG:HD2	19:BD:89:GLU:OE2	2.16	0.45
21:BK:5:LYS:HA	21:BK:5:LYS:HD3	1.73	0.45
24:BR:24:LEU:HD23	24:BR:34:LEU:HD11	1.97	0.45
36:A1:107:A:O2'	36:A1:324:A:N3	2.41	0.45
36:A1:2197:OMC:H5''	36:A1:2242:A:H61	1.82	0.45
36:A1:2974:U:H2'	36:A1:2975:U:C6	2.50	0.45
39:AD:277:LEU:HD12	39:AD:281:GLU:HB3	1.98	0.45
40:AE:4:GLN:HG3	65:Ae:75:LEU:HB3	1.98	0.45
45:AJ:36:VAL:HG13	45:AJ:37:LEU:HD12	1.98	0.45
45:AJ:43:GLN:OE1	45:AJ:75:LYS:NZ	2.40	0.45
50:AP:30:ARG:HD2	50:AP:63:PHE:HE2	1.81	0.45
79:DC:164:LEU:HD13	79:DC:282:PHE:HE1	1.82	0.45
3:BC:116:LYS:HG2	3:BC:127:ALA:HB3	1.98	0.45
8:BJ:144:PRO:HD2	32:B5:474:A:H5''	1.98	0.45
19:BD:40:ARG:HG2	27:BU:110:PRO:HG3	1.99	0.45
19:BD:61:GLU:O	19:BD:64:ARG:HG2	2.16	0.45
31:Bg:194:GLY:HA3	31:Bg:221:MET:HE1	1.98	0.45
31:Bg:197:SER:OG	31:Bg:217:ASP:N	2.43	0.45
32:B5:142:G:H2'	32:B5:143:G:C8	2.51	0.45
32:B5:655:G:H4'	32:B5:656:G:H8	1.82	0.45
32:B5:1553:G:N1	32:B5:1556:A:OP2	2.47	0.45
34:AB:71:GLU:OE1	57:AW:1:MET:N	2.47	0.45
36:A1:1170:A:H2'	36:A1:1171:G:O4'	2.15	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1497:C:H2'	36:A1:1498:A:H8	1.81	0.45
36:A1:1597:C:H2'	36:A1:1598:G:C8	2.51	0.45
36:A1:2492:C:H1'	77:E:164:CYS:SG	2.56	0.45
36:A1:2506:U:HO2'	36:A1:2507:C:P	2.39	0.45
36:A1:3029:A:H5'	79:DC:536:LEU:HD21	1.99	0.45
43:AH:21:LYS:CG	43:AH:22:SER:H	2.25	0.45
53:AS:46:GLN:HG2	53:AS:51:VAL:O	2.16	0.45
54:AT:79:MET:HB2	54:AT:84:TYR:CE1	2.51	0.45
69:AI:34:SER:H	69:AI:37:THR:HG22	1.81	0.45
77:E:212:PRO:HG2	77:E:214:PHE:CE1	2.51	0.45
78:EC:6936:G:N2	78:EC:6937:G:H1'	2.31	0.45
79:DC:21:ASN:ND2	79:DC:345:PRO:HG3	2.31	0.45
79:DC:243:ARG:HD3	79:DC:257:TRP:CD2	2.52	0.45
79:DC:336:GLU:HA	79:DC:339:VAL:HG22	1.97	0.45
12:BV:44:ARG:HA	12:BV:44:ARG:HD3	1.83	0.45
21:BK:78:GLU:O	21:BK:81:ASN:ND2	2.50	0.45
24:BR:21:TYR:HD1	24:BR:58:MET:HE1	1.80	0.45
27:BU:89:ARG:HH22	32:B5:1383:G:P	2.40	0.45
32:B5:201:G:H2'	32:B5:202:A:C8	2.50	0.45
32:B5:202:A:H2'	32:B5:203:U:C6	2.50	0.45
32:B5:1702:A:H3'	32:B5:1703:C:C6	2.50	0.45
36:A1:209:A:H4'	36:A1:211:A:C8	2.51	0.45
36:A1:377:A:H1'	36:A1:392:G:N2	2.32	0.45
36:A1:789:A:H2'	36:A1:790:U:C6	2.52	0.45
36:A1:968:G:H2'	36:A1:969:C:C6	2.51	0.45
36:A1:1307:G:O2'	36:A1:1308:A:N7	2.46	0.45
36:A1:1629:U:HO2'	36:A1:1630:U:P	2.40	0.45
36:A1:2566:C:H2'	36:A1:2567:C:C6	2.52	0.45
37:A3:87:G:OP1	41:AF:218:ARG:NE	2.49	0.45
77:E:36:VAL:HG22	77:E:37:GLY:H	1.82	0.45
77:E:116:LEU:O	77:E:120:VAL:HG23	2.17	0.45
78:EC:6892:U:O3'	78:EC:6943:A:N6	2.49	0.45
1:BA:63:ILE:HD13	1:BA:158:VAL:HG21	1.98	0.45
1:BA:102:PHE:CE2	1:BA:135:GLU:HG3	2.51	0.45
2:BB:86:LEU:HB3	2:BB:98:THR:CG2	2.45	0.45
7:BI:24:LYS:O	32:B5:400:A:H5''	2.16	0.45
7:BI:171:SER:HB2	7:BI:180:ASP:HB2	1.99	0.45
29:Bc:19:THR:OG1	29:Bc:65:ARG:O	2.29	0.45
32:B5:393:C:H2'	32:B5:394:C:C6	2.52	0.45
32:B5:512:A:H2'	32:B5:513:U:C6	2.51	0.45
32:B5:1452:U:H2'	32:B5:1453:G:C8	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:1515:A:H4'	32:B5:1517:U:H5	1.80	0.45
33:AA:209:HIS:CE1	33:AA:235:ALA:HB1	2.52	0.45
34:AB:123:TYR:CZ	34:AB:124:LYS:HG3	2.51	0.45
34:AB:292:ALA:HB2	34:AB:302:LYS:HD3	1.98	0.45
36:A1:1324:U:H5'	53:AS:2:ALA:H	1.81	0.45
36:A1:3302:U:O2'	36:A1:3303:G:H5'	2.16	0.45
39:AD:33:ARG:HG2	54:AT:27:LEU:HD21	1.98	0.45
49:AO:27[A]:LEU:HB3	49:AO:98[A]:ALA:HB1	1.98	0.45
67:Ag:106:LYS:HA	67:Ag:109:THR:HG22	1.97	0.45
77:E:101:LYS:O	77:E:105:LYS:NZ	2.46	0.45
77:E:120:VAL:HB	77:E:121:PRO:HD3	1.99	0.45
78:EC:6870:A:O2'	78:EC:6871:A:O5'	2.25	0.45
78:EC:6883:A:H2'	78:EC:6884:G:H4'	1.97	0.45
79:DC:94:ASP:OD1	79:DC:95:GLY:N	2.49	0.45
79:DC:579:SER:HB2	79:DC:704:GLN:HB3	1.99	0.45
79:DC:693:LEU:HD12	79:DC:700:ARG:HB2	1.98	0.45
4:BE:13:ALA:O	4:BE:39:ARG:NH1	2.43	0.45
15:BY:44:LEU:HA	15:BY:47:VAL:HG12	1.99	0.45
15:BY:117:LYS:HE3	15:BY:117:LYS:HB2	1.68	0.45
16:Ba:85:ARG:HD3	32:B5:1153:G:H5'	1.97	0.45
20:BF:117:THR:HG22	20:BF:191:ALA:O	2.16	0.45
22:BP:24:LYS:O	22:BP:28:MET:HG3	2.16	0.45
22:BP:44:ARG:NH1	22:BP:82:ASN:O	2.49	0.45
26:BT:122:ARG:NH1	32:B5:1499:G:OP1	2.49	0.45
32:B5:70:C:H2'	32:B5:71:A:C8	2.52	0.45
32:B5:1484:G:H2'	32:B5:1485:C:H6	1.82	0.45
32:B5:1740:A:H2'	32:B5:1741:U:C6	2.51	0.45
36:A1:44:U:OP1	48:AN:85:THR:HG23	2.17	0.45
36:A1:1229:G:O2'	82:VA:31:ASP:O	2.34	0.45
36:A1:2540:A:H4'	36:A1:2541:U:H2'	1.98	0.45
38:A4:142:C:H2'	38:A4:143:U:C6	2.52	0.45
40:AE:76:LEU:HD21	40:AE:141:VAL:HG11	1.98	0.45
43:AH:74:LEU:O	43:AH:78:MET:HG3	2.16	0.45
78:EC:6804:A:H4'	78:EC:6805:C:H5'	1.99	0.45
79:DC:235:VAL:HG21	79:DC:240:MET:HE3	1.99	0.45
1:BA:31:VAL:HG11	32:B5:1040:G:H5'	1.98	0.45
2:BB:69:CYS:HA	2:BB:83:LYS:HA	1.99	0.45
2:BB:158:SER:HB3	32:B5:875:G:OP1	2.17	0.45
2:BB:180:THR:O	2:BB:183:GLN:N	2.50	0.45
4:BE:149:TYR:HB3	5:BG:208:TYR:HB2	1.99	0.45
6:BH:179:LYS:NZ	32:B5:640:U:O2	2.29	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:BL:155:LYS:HD3	10:BN:83:GLU:HA	1.98	0.45
18:Be:2:ALA:N	32:B5:1754:A:O2'	2.49	0.45
20:BF:133:VAL:HG23	20:BF:198:LEU:HD13	1.98	0.45
21:BK:44:LYS:HA	21:BK:44:LYS:HD3	1.66	0.45
26:BT:12:GLN:NE2	32:B5:1530:C:O4'	2.50	0.45
28:BZ:53:GLU:CD	78:EC:6865:G:H1	2.25	0.45
32:B5:1355:C:H2'	32:B5:1356:U:H6	1.82	0.45
32:B5:1357:A:O2'	32:B5:1358:G:H5'	2.17	0.45
32:B5:1377:U:O2	32:B5:1379:C:N4	2.50	0.45
32:B5:1638:G:H2'	32:B5:1639:OMC:O4'	2.17	0.45
32:B5:1696:G:H2'	32:B5:1697:G:C8	2.52	0.45
36:A1:1682:U:O2	55:AU:82:LYS:HD2	2.17	0.45
36:A1:1899:G:O2'	36:A1:2334:U:O4	2.30	0.45
36:A1:2468:A:O2'	36:A1:2478:C:O2	2.29	0.45
36:A1:2522:G:H2'	36:A1:2522:G:N3	2.32	0.45
36:A1:3094:A:OP1	56:AV:14:SER:OG	2.26	0.45
36:A1:3177:G:N7	40:AE:167:ASN:ND2	2.62	0.45
37:A3:26:C:H2'	37:A3:27:A:O4'	2.17	0.45
42:AG:116:VAL:HA	42:AG:120:LYS:HG3	1.99	0.45
51:AQ:63:SER:OG	51:AQ:90:ASP:HB2	2.16	0.45
63:Ac:43:ILE:HB	63:Ac:90:VAL:HG22	1.98	0.45
65:Ae:115:LEU:HB2	65:Ae:117:ILE:HD12	1.99	0.45
71:Ak:11:PHE:HB2	71:Ak:54:LEU:HD13	1.99	0.45
78:EC:6763:C:H2'	78:EC:6764:C:H6	1.80	0.45
79:DC:563:TYR:O	79:DC:564:ARG:NH1	2.39	0.45
4:BE:241:GLY:O	4:BE:244:ILE:HG12	2.17	0.45
4:BE:252:ARG:HB2	4:BE:256:ARG:NH1	2.32	0.45
10:BN:151:ASN:HB3	63:Ac:79:THR:O	2.17	0.45
12:BV:74:GLN:NE2	12:BV:82:VAL:H	2.15	0.45
20:BF:41:LYS:O	20:BF:69:PHE:HA	2.16	0.45
32:B5:204:G:H2'	32:B5:205:U:O4'	2.17	0.45
32:B5:231:U:O2	32:B5:235:G:N2	2.50	0.45
32:B5:1250:U:H2'	32:B5:1251:U:C4	2.52	0.45
36:A1:71:A:P	61:Aa:67:HIS:HE2	2.40	0.45
36:A1:1572:U:O2'	36:A1:1573:G:H8	2.00	0.45
36:A1:2988:C:OP1	49:AO:65[A]:ASN:ND2	2.36	0.45
36:A1:3322:A:H2'	36:A1:3323:A:H8	1.82	0.45
38:A4:18:U:H2'	38:A4:19:C:C6	2.52	0.45
42:AG:121:SER:OG	42:AG:122:LYS:N	2.48	0.45
48:AN:6:TYR:HE2	69:Ai:43:LEU:HD23	1.82	0.45
54:AT:91:LEU:HD12	54:AT:96:ILE:HD11	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:DC:840:ASP:N	79:DC:840:ASP:OD1	2.48	0.45
5:BG:149:LYS:HD2	5:BG:149:LYS:HA	1.72	0.45
8:BJ:175:ARG:HE	8:BJ:179:ARG:NH2	2.15	0.45
14:BX:96:VAL:HG13	14:BX:97:ASP:N	2.31	0.45
16:Ba:2:PRO:HB3	32:B5:1142:A:H5'	1.98	0.45
23:BQ:100:GLN:O	23:BQ:104:GLU:N	2.38	0.45
30:Bd:15:GLY:O	30:Bd:19:ARG:NE	2.47	0.45
32:B5:116:U:H2'	32:B5:117:U:C6	2.52	0.45
32:B5:330:G:H2'	32:B5:331:A:C8	2.52	0.45
32:B5:450:U:H2'	32:B5:451:A:C8	2.51	0.45
32:B5:824:G:H2'	32:B5:825:U:C6	2.51	0.45
32:B5:1308:G:H2'	32:B5:1309:C:C6	2.52	0.45
32:B5:1767:G:OP1	32:B5:1770:U:H4'	2.17	0.45
33:AA:79:ASN:O	33:AA:82:VAL:HG22	2.16	0.45
36:A1:157:A:N7	69:Ai:26:ILE:HG12	2.31	0.45
36:A1:179:C:H2'	36:A1:180:C:C6	2.52	0.45
36:A1:435:C:H2'	36:A1:436:A:H8	1.82	0.45
36:A1:737:G:H2'	36:A1:738:A:H8	1.80	0.45
36:A1:1290:A:H2'	36:A1:1291:A:H8	1.82	0.45
36:A1:2509:U:H2'	36:A1:2510:U:O4'	2.17	0.45
36:A1:3153:U:H5	36:A1:3293:U:H3	1.63	0.45
42:AG:140:VAL:HG22	42:AG:166:LEU:HD21	1.99	0.45
50:AP:84:PRO:HB2	50:AP:87:SER:HB2	1.98	0.45
73:Am:98:LYS:HD3	73:Am:118:THR:HG21	1.98	0.45
78:EC:6795:U:H2'	78:EC:6796:C:H6	1.81	0.45
78:EC:6901:C:O2'	78:EC:6902:U:H5'	2.17	0.45
81:BM:62:LEU:HD22	81:BM:90:LYS:HE2	1.99	0.45
82:VA:53:MET:HE3	82:VA:55:LYS:HZ1	1.82	0.45
5:BG:118:GLU:OE1	5:BG:118:GLU:N	2.36	0.44
19:BD:123:VAL:HG13	19:BD:134:CYS:HB3	1.99	0.44
19:BD:141:LYS:HA	19:BD:147:ALA:HA	1.99	0.44
32:B5:27:U:H2'	32:B5:28:A2M:H8	2.00	0.44
32:B5:1280:4AC:H2'	32:B5:1281:G:C8	2.52	0.44
32:B5:1330:G:H2'	32:B5:1331:A:O4'	2.17	0.44
32:B5:1352:G:N2	32:B5:1374:C:O2	2.50	0.44
36:A1:94:G:H2'	36:A1:95:A:C8	2.52	0.44
36:A1:426:G:H2'	36:A1:427:C:C6	2.52	0.44
36:A1:1196:C:OP1	36:A1:1309:U:O2'	2.28	0.44
36:A1:1927:G:C8	76:Ap:16:VAL:HG12	2.53	0.44
36:A1:3000:A:H2'	36:A1:3001:C:H6	1.82	0.44
47:AM:12:TRP:CZ3	53:AS:153:PRO:HG3	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:AM:37:GLU:OE2	47:AM:74:ARG:HG2	2.17	0.44
47:AM:50:LYS:HG3	47:AM:85:TRP:CD1	2.51	0.44
52:AR:44:LEU:HD22	52:AR:49:THR:HG21	1.98	0.44
82:VA:91:GLU:HB3	82:VA:92:PRO:CD	2.47	0.44
2:BB:87:ARG:C	2:BB:98:THR:HG23	2.42	0.44
2:BB:111:ARG:HB3	16:Ba:68:TYR:HB2	1.98	0.44
4:BE:70:VAL:HG22	4:BE:92:LEU:HD22	1.99	0.44
5:BG:77:LEU:HD13	5:BG:84:TYR:HB2	2.00	0.44
5:BG:167:LYS:HE3	32:B5:72:A:H2'	1.99	0.44
6:BH:9:LEU:HD22	6:BH:17:GLU:HG3	2.00	0.44
7:BI:56:ARG:HH22	32:B5:332:U:P	2.40	0.44
8:BJ:128:LEU:HD21	8:BJ:158:PHE:HE1	1.82	0.44
10:BN:54:LEU:HB3	10:BN:60:VAL:CG1	2.47	0.44
11:BO:16:VAL:O	11:BO:30:VAL:HA	2.18	0.44
14:BX:14:LYS:NZ	32:B5:1104:U:OP1	2.46	0.44
14:BX:50:LYS:NZ	32:B5:436:A2M:OP1	2.50	0.44
15:BY:10:ARG:NE	15:BY:26:ASP:OD2	2.50	0.44
15:BY:23:PHE:HE2	15:BY:75:VAL:HG22	1.83	0.44
16:Ba:89:ARG:HH22	32:B5:1088:A:H4'	1.82	0.44
23:BQ:114:ARG:NH1	32:B5:1411:A:OP1	2.47	0.44
31:Bg:33:LEU:HD22	31:Bg:302:PHE:CD1	2.52	0.44
32:B5:329:G:H2'	32:B5:330:G:C8	2.52	0.44
32:B5:448:C:H2'	32:B5:449:C:H6	1.82	0.44
32:B5:607:G:H5'	32:B5:613:G:N2	2.32	0.44
32:B5:705:U:O2'	32:B5:732:G:O2'	2.31	0.44
32:B5:1639:OMC:H2'	32:B5:1640:C:O4'	2.17	0.44
32:B5:1680:G:H1'	32:B5:1681:A:H2	1.82	0.44
34:AB:215:ILE:HD12	34:AB:338:LEU:HB3	1.99	0.44
34:AB:256:HIS:HA	34:AB:257:PRO:C	2.42	0.44
34:AB:287:LYS:HB2	34:AB:290:ASP:HB3	1.99	0.44
36:A1:91:G:OP2	36:A1:93:C:N4	2.37	0.44
36:A1:128:G:OP1	68:Ah:75:TYR:OH	2.30	0.44
36:A1:874:U:N3	36:A1:2978:U:OP1	2.44	0.44
36:A1:1486:G:H21	67:Ag:6:THR:HG22	1.81	0.44
36:A1:1867:A:H2'	36:A1:1868:G:C8	2.52	0.44
38:A4:37:A:H5''	38:A4:39:G:O4'	2.17	0.44
40:AE:142:ASP:HA	40:AE:145:LEU:HB2	1.98	0.44
78:EC:6939:C:H4'	78:EC:6940:U:OP2	2.16	0.44
79:DC:20:ARG:NE	79:DC:342:LEU:O	2.33	0.44
79:DC:27:HIS:HB3	79:DC:30:HIS:HE2	1.79	0.44
79:DC:648:ASP:OD1	79:DC:648:ASP:N	2.41	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:11:PRO:O	1:BA:15:GLN:HG2	2.18	0.44
7:BI:37:LYS:C	7:BI:59:ARG:HA	2.42	0.44
8:BJ:49:LEU:HD13	8:BJ:53:ARG:HH22	1.82	0.44
8:BJ:177:ALA:O	8:BJ:180:LYS:HG3	2.17	0.44
12:BV:39:VAL:HA	12:BV:44:ARG:O	2.17	0.44
22:BP:86:VAL:HG23	22:BP:88:GLU:HG3	1.99	0.44
24:BR:7:LYS:HD2	24:BR:11:ARG:HH12	1.82	0.44
32:B5:129:U:H3'	32:B5:130:C:H5'	1.99	0.44
32:B5:485:A:H62	32:B5:486:G:H21	1.64	0.44
32:B5:1552:U:H2'	32:B5:1553:G:O4'	2.17	0.44
32:B5:1617:U:H2'	32:B5:1618:C:C6	2.52	0.44
32:B5:1642:G:H2'	32:B5:1643:U:H6	1.83	0.44
35:AC:3:ARG:HA	35:AC:3:ARG:HD2	1.83	0.44
36:A1:38:U:H2'	36:A1:39:A:O4'	2.16	0.44
36:A1:715:A:HO2'	36:A1:752:C:HO2'	1.62	0.44
36:A1:1268:G:N2	36:A1:1273:A:H62	2.13	0.44
36:A1:1341:U:H2'	36:A1:1342:C:C6	2.52	0.44
36:A1:1357:G:H2'	36:A1:1358:C:C6	2.53	0.44
36:A1:1506:A:OP2	50:AP:127:ARG:NH1	2.47	0.44
36:A1:2566:C:H2'	36:A1:2567:C:H6	1.82	0.44
44:AI:36:LEU:HD21	44:AI:69:ARG:NH1	2.32	0.44
53:AS:6:GLU:OE2	53:AS:28:ARG:NH1	2.46	0.44
70:Aj:43:LYS:HB2	70:Aj:43:LYS:HE3	1.75	0.44
78:EC:6797:U:H2'	78:EC:6798:C:H6	1.83	0.44
78:EC:6808:G:O2'	78:EC:6809:G:O4'	2.32	0.44
79:DC:829:LYS:HE3	79:DC:829:LYS:HB3	1.71	0.44
3:BC:56:ILE:HG23	3:BC:61:LEU:HB2	1.98	0.44
7:BI:114:GLU:OE2	7:BI:120:THR:HA	2.16	0.44
17:Bb:37:CYS:HB2	17:Bb:59:CYS:HB2	1.99	0.44
19:BD:43:PRO:HD3	27:BU:108:ILE:HD12	1.99	0.44
32:B5:1266:U:H2'	32:B5:1267:G:C8	2.52	0.44
36:A1:673:U:H2'	36:A1:674:G:C8	2.52	0.44
36:A1:761:A:C2	36:A1:771:A:H1'	2.52	0.44
36:A1:938:C:OP2	61:Aa:26:ARG:NH1	2.51	0.44
36:A1:1565:G:HO2'	36:A1:1566:A:P	2.41	0.44
36:A1:1593:A:H2'	36:A1:1594:A:C8	2.53	0.44
36:A1:2413:A:H2'	36:A1:2414:G:C8	2.52	0.44
36:A1:2655:U:H4'	36:A1:2656:A:O4'	2.17	0.44
36:A1:2941:A:O5'	36:A1:2943:G:H4'	2.17	0.44
36:A1:3041:U:H2'	36:A1:3042:U:C6	2.53	0.44
36:A1:3177:G:O2'	36:A1:3179:U:OP1	2.28	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:3193:C:H2'	36:A1:3194:C:H6	1.81	0.44
36:A1:3198:U:O2	43:AH:21:LYS:N	2.51	0.44
36:A1:3288:G:O2'	36:A1:3289:G:H8	2.00	0.44
36:A1:3324:C:H4'	64:Ad:13:THR:HG23	1.98	0.44
70:Aj:21:ARG:HD3	70:Aj:39:TYR:CD1	2.53	0.44
71:Ak:5:ILE:HD11	71:Ak:52:TYR:HB3	1.99	0.44
75:Ao:4:VAL:O	75:Ao:94:GLY:N	2.50	0.44
75:Ao:14:GLY:C	75:Ao:16:THR:H	2.25	0.44
78:EC:6797:U:H2'	78:EC:6798:C:C6	2.52	0.44
78:EC:6924:G:H2'	78:EC:6926:U:OP2	2.17	0.44
79:DC:833:PRO:HB3	79:DC:837:GLU:OE1	2.18	0.44
81:BM:105:LYS:NZ	81:BM:113:ARG:HE	2.15	0.44
7:BI:50:GLY:HA2	32:B5:397:A:H4'	2.00	0.44
15:BY:42:GLU:HB3	15:BY:52:LYS:HE2	2.00	0.44
26:BT:91:TYR:HB2	32:B5:1590:G:OP1	2.18	0.44
31:Bg:201:THR:HG23	31:Bg:243:LEU:HD12	2.00	0.44
32:B5:245:U:O2'	32:B5:247:A:N7	2.42	0.44
32:B5:269:G:H2'	32:B5:270:C:C6	2.53	0.44
32:B5:384:G:H2'	32:B5:385:A:C8	2.52	0.44
32:B5:411:C:H2'	32:B5:412:A:O4'	2.17	0.44
32:B5:463:U:H2'	32:B5:464:A:C8	2.52	0.44
32:B5:1156:C:H2'	32:B5:1157:A:C8	2.52	0.44
32:B5:1345:A:H2'	32:B5:1348:A:H62	1.82	0.44
32:B5:1516:A:O2'	32:B5:1517:U:H5'	2.18	0.44
36:A1:117:U:O2'	36:A1:119:U:OP2	2.30	0.44
36:A1:263:C:H2'	36:A1:264:G:O4'	2.18	0.44
36:A1:2115:G:O2'	52:AR:82:LYS:HE2	2.18	0.44
37:A3:119:U:P	39:AD:258:LYS:HZ1	2.40	0.44
38:A4:63:G:OP1	38:A4:90:U:H5''	2.17	0.44
39:AD:146:LEU:HD22	39:AD:163:LEU:HD13	1.99	0.44
44:AI:38:LYS:CG	44:AI:41:ALA:HB2	2.48	0.44
45:AJ:40:LEU:HD13	45:AJ:112:LEU:HD11	1.99	0.44
48:AN:43:THR:OG1	48:AN:131:GLU:OE2	2.29	0.44
48:AN:60:VAL:HG23	48:AN:134:LEU:HB2	2.00	0.44
79:DC:132:ILE:HD12	79:DC:167:LEU:HD22	2.00	0.44
79:DC:468:THR:HG22	79:DC:470:THR:HG23	1.99	0.44
1:BA:9:LEU:HG	24:BR:115:LEU:HD11	1.99	0.44
2:BB:175:GLU:HG3	2:BB:193:ILE:HG23	2.00	0.44
4:BE:133:LYS:HE3	4:BE:133:LYS:HB3	1.84	0.44
6:BH:67:LEU:HD12	6:BH:71:HIS:NE2	2.33	0.44
7:BI:43:ILE:HG12	32:B5:260:U:C5	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Bb:54:VAL:HG12	17:Bb:64:CYS:SG	2.58	0.44
18:Be:29:LYS:O	18:Be:31:LYS:NZ	2.47	0.44
20:BF:51:VAL:HG11	20:BF:64:VAL:HG11	2.00	0.44
25:BS:132:ARG:NH2	32:B5:1173:C:OP1	2.37	0.44
32:B5:1263:G:H2'	32:B5:1264:G:O4'	2.17	0.44
32:B5:1375:A:H2'	32:B5:1376:C:O4'	2.18	0.44
36:A1:874:U:OP2	36:A1:1907:C:O2'	2.29	0.44
36:A1:1315:U:OP2	49:AO:44[A]:SER:OG	2.28	0.44
36:A1:1340:G:H2'	36:A1:1341:U:C6	2.53	0.44
36:A1:1895:A:O2'	36:A1:3053:G:H4'	2.17	0.44
36:A1:2723:U:H2'	36:A1:2724:OMU:H6	2.00	0.44
36:A1:3106:A:H2'	36:A1:3107:U:O4'	2.18	0.44
37:A3:90:U:H2'	37:A3:91:G:O4'	2.17	0.44
52:AR:175:GLN:HA	52:AR:179:GLU:HB2	1.99	0.44
63:Ac:24:THR:HG22	63:Ac:91:SER:HB3	1.99	0.44
75:Ao:15:LYS:HA	75:Ao:18:ARG:HE	1.82	0.44
79:DC:289:MET:HE1	79:DC:317:LYS:HA	1.99	0.44
81:BM:47:GLU:HA	81:BM:50:LYS:HE2	1.99	0.44
1:BA:70:PRO:HB2	1:BA:94:GLY:HA3	1.99	0.44
2:BB:110:LEU:HD11	2:BB:213:ARG:HD2	2.00	0.44
5:BG:39:GLU:HA	5:BG:46:LYS:HD2	1.99	0.44
20:BF:191:ALA:HB3	28:BZ:98:GLN:NE2	2.32	0.44
23:BQ:87:LYS:HE2	23:BQ:87:LYS:HB3	1.74	0.44
25:BS:58:ALA:HA	25:BS:61:LEU:HD23	2.00	0.44
26:BT:72:GLY:HA3	32:B5:1498:G:H5''	1.98	0.44
26:BT:125:SER:OG	26:BT:127:ASN:OD1	2.36	0.44
31:Bg:21:THR:N	31:Bg:36:ALA:O	2.50	0.44
31:Bg:260:ILE:O	31:Bg:273:ASP:HA	2.18	0.44
32:B5:41:A:H2'	32:B5:438:A:N7	2.32	0.44
32:B5:236:A:OP2	32:B5:834:G:H5'	2.18	0.44
32:B5:1114:G:O2'	32:B5:1130:G:O6	2.34	0.44
34:AB:94:GLU:OE1	34:AB:156:SER:OG	2.36	0.44
35:AC:299:ILE:HB	51:AQ:39:ARG:HB3	2.00	0.44
36:A1:261:U:H2'	36:A1:262:U:C6	2.53	0.44
36:A1:1354:G:H1'	40:AE:9:TRP:NE1	2.33	0.44
36:A1:1565:G:O2'	36:A1:1566:A:OP1	2.33	0.44
36:A1:1635:G:OP2	60:AZ:107:ARG:NH2	2.46	0.44
36:A1:1719:G:H2'	36:A1:1720:U:O4'	2.18	0.44
36:A1:1921:A:H2'	36:A1:1922:A:H8	1.82	0.44
37:A3:47:C:OP2	39:AD:158:ARG:HD3	2.18	0.44
38:A4:65:A:H2'	38:A4:66:A:H8	1.83	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A4:117:C:H2'	38:A4:118:C:H6	1.82	0.44
41:AF:98:LYS:HB3	41:AF:99:PRO:HD3	1.99	0.44
44:AI:203:LYS:HB2	44:AI:203:LYS:HE2	1.71	0.44
50:AP:107:LEU:HD23	50:AP:112:LEU:HD21	2.00	0.44
54:AT:137:GLU:HG3	54:AT:138:SER:H	1.83	0.44
61:Aa:70:LYS:HG2	61:Aa:110:GLY:HA3	1.99	0.44
71:Ak:12:LEU:HB3	71:Ak:16:ARG:NH1	2.32	0.44
77:E:101:LYS:HA	77:E:127:GLN:HG2	2.00	0.44
78:EC:6837:G:H2'	78:EC:6838:C:C6	2.53	0.44
1:BA:15:GLN:OE1	24:BR:100:LEU:HD11	2.18	0.44
3:BC:80:VAL:HG21	3:BC:125:ILE:HD12	1.98	0.44
12:BV:3:ASN:HD21	12:BV:7:GLN:HB3	1.82	0.44
22:BP:100:LYS:HD2	32:B5:1183:A:C4	2.52	0.44
26:BT:84:LYS:HE3	26:BT:86:ARG:HG2	2.00	0.44
32:B5:1252:C:O4'	80:Bf:133:ALA:HB2	2.17	0.44
32:B5:1291:G:N2	32:B5:1324:G:H22	2.14	0.44
32:B5:1450:U:H2'	32:B5:1451:C:C6	2.53	0.44
34:AB:55:THR:HG23	36:A1:3049:A:O2'	2.17	0.44
34:AB:122:TRP:O	34:AB:127:LYS:NZ	2.51	0.44
35:AC:23:PRO:HD2	35:AC:26:PHE:CD2	2.53	0.44
36:A1:2592:G:H4'	36:A1:2594:C:C2	2.53	0.44
36:A1:2597:U:O2	48:AN:125:SER:OG	2.27	0.44
39:AD:52:VAL:HG21	39:AD:65:ILE:HD12	2.00	0.44
43:AH:41:ILE:HG22	43:AH:43:VAL:HG13	1.99	0.44
44:AI:135:ILE:HG22	44:AI:136:PHE:CD1	2.53	0.44
50:AP:67:ILE:HD12	50:AP:82:ARG:CZ	2.47	0.44
50:AP:116:HIS:HB3	50:AP:149:VAL:HB	1.99	0.44
61:Aa:103:ASP:HB2	61:Aa:126:LYS:HE3	1.99	0.44
69:Ai:67:LYS:HA	69:Ai:70:ARG:HD3	2.00	0.44
70:Aj:87:SER:OG	70:Aj:88:ALA:N	2.51	0.44
77:E:191:VAL:O	77:E:197:ASN:HA	2.18	0.44
79:DC:18:ASN:HB3	79:DC:98:PHE:HA	2.00	0.44
79:DC:184:SER:O	79:DC:187:VAL:HG12	2.16	0.44
80:Bf:121:CYS:HB3	80:Bf:126:CYS:HB3	1.52	0.44
6:BH:47:ARG:HH21	6:BH:49:ILE:HD11	1.83	0.44
10:BN:42:ARG:HB3	63:Ac:97:ASP:OD2	2.18	0.44
12:BV:14:PRO:HB2	12:BV:23:ILE:HG23	1.99	0.44
14:BX:99:ASN:ND2	79:DC:505:VAL:HG22	2.33	0.44
19:BD:8:LYS:NZ	32:B5:1487:A:OP2	2.33	0.44
20:BF:93:LEU:HD13	20:BF:172:ILE:HG23	1.98	0.44
31:Bg:114:ASP:OD1	31:Bg:123:ILE:HB	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:103:A:H4'	32:B5:105:A:C8	2.53	0.44
32:B5:973:A:H2'	32:B5:974:A2M:H8	2.00	0.44
32:B5:1107:G:O2'	32:B5:1108:G:H5'	2.17	0.44
32:B5:1752:U:H2'	32:B5:1753:A:H8	1.83	0.44
36:A1:1782:U:H2'	36:A1:1783:U:O4'	2.18	0.44
36:A1:2523:A:H2'	42:AG:49:TYR:O	2.18	0.44
36:A1:2727:A:C2	61:Aa:43:ILE:HG23	2.53	0.44
44:AI:29:SER:HB2	44:AI:62:SER:HB2	1.99	0.44
57:AW:18:GLY:HA3	57:AW:31:PHE:O	2.18	0.44
77:E:105:LYS:HB2	77:E:105:LYS:HE2	1.67	0.44
78:EC:6788:C:H3'	78:EC:6805:C:H41	1.82	0.44
79:DC:285:PHE:CD1	79:DC:320:LEU:HD11	2.52	0.44
1:BA:190:ASP:OD1	1:BA:190:ASP:N	2.51	0.43
5:BG:6:SER:HB3	5:BG:112:VAL:HG12	1.99	0.43
6:BH:80:GLU:O	6:BH:84:LYS:HG2	2.18	0.43
14:BX:90:ASP:HA	32:B5:568:G:H4'	1.99	0.43
16:Ba:57:SER:OG	16:Ba:58:VAL:O	2.32	0.43
19:BD:126:VAL:HG11	19:BD:188:ILE:HG12	1.99	0.43
23:BQ:127:LYS:HE2	23:BQ:131:GLY:O	2.18	0.43
29:Bc:9:LEU:HD13	29:Bc:53:ILE:HG21	1.99	0.43
31:Bg:34:LEU:HD13	31:Bg:73:LEU:HD11	2.00	0.43
31:Bg:117:LYS:O	31:Bg:118:LYS:HG2	2.18	0.43
32:B5:972:G:O2'	36:A1:847:A:N6	2.48	0.43
32:B5:1480:G:H2'	32:B5:1481:C:O4'	2.18	0.43
32:B5:1513:G:H1'	32:B5:1518:C:O2	2.18	0.43
33:AA:203:ALA:HB1	36:A1:2146:C:H5''	2.00	0.43
34:AB:251:CYS:SG	36:A1:2944:U:H1'	2.58	0.43
35:AC:181:VAL:C	35:AC:183:LYS:H	2.26	0.43
36:A1:7:C:H2'	36:A1:8:C:C6	2.53	0.43
36:A1:349:A:C4	38:A4:24:G:H1'	2.52	0.43
36:A1:385:A:H2'	36:A1:386:A:C8	2.53	0.43
36:A1:718:G:N2	36:A1:721:G:O2'	2.51	0.43
36:A1:1143:A:H5'	36:A1:1368:U:H1'	1.98	0.43
36:A1:1232:C:H5	36:A1:1261:G:H2'	1.82	0.43
36:A1:1293:U:O2'	36:A1:1294:A:H5'	2.18	0.43
36:A1:1744:G:H2'	36:A1:1745:C:C6	2.53	0.43
36:A1:2180:G:H2'	36:A1:2181:C:H6	1.81	0.43
36:A1:3203:U:H2'	36:A1:3204:C:C6	2.53	0.43
36:A1:3367:C:OP2	36:A1:3368:U:O2'	2.29	0.43
39:AD:92:LEU:HD23	39:AD:92:LEU:HA	1.87	0.43
62:Ab:5:LYS:HE3	62:Ab:8:THR:HB	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:E:56:PRO:HD2	77:E:182:GLN:HG2	2.00	0.43
79:DC:15:LYS:HA	79:DC:15:LYS:HD2	1.86	0.43
79:DC:140:GLU:HG2	79:DC:188:ILE:CD1	2.48	0.43
79:DC:735:CYS:HB3	79:DC:792:ALA:HA	2.00	0.43
7:BI:70:GLU:HB3	7:BI:112:TRP:CH2	2.53	0.43
10:BN:3:ARG:HB3	10:BN:6:SER:HB3	2.00	0.43
16:Ba:33:ASP:OD1	16:Ba:33:ASP:N	2.48	0.43
20:BF:124:LEU:O	20:BF:125:THR:C	2.60	0.43
22:BP:15:HIS:O	22:BP:22:LEU:N	2.51	0.43
26:BT:131:ASP:O	26:BT:135:ILE:HG12	2.18	0.43
27:BU:106:ILE:HG22	27:BU:107:THR:N	2.28	0.43
28:BZ:59:TYR:HE1	28:BZ:100:ILE:HG23	1.84	0.43
31:Bg:63:GLY:HA2	32:B5:1341:A:OP1	2.18	0.43
32:B5:110:U:OP1	32:B5:753:A:O2'	2.35	0.43
32:B5:388:G:OP1	32:B5:423:G:O2'	2.36	0.43
32:B5:892:A:H2'	32:B5:893:U:H6	1.83	0.43
32:B5:980:G:H4'	32:B5:1776:A:H4'	2.00	0.43
32:B5:1039:A:O2'	32:B5:1040:G:H8	2.00	0.43
32:B5:1392:U:H2'	32:B5:1393:C:C6	2.53	0.43
35:AC:119:ARG:NH2	36:A1:696:C:OP2	2.50	0.43
36:A1:1392:G:H1'	36:A1:1418:A:N6	2.34	0.43
36:A1:1482:A:H4'	36:A1:1483:G:OP2	2.18	0.43
36:A1:2686:A:H2'	36:A1:2687:G:O4'	2.18	0.43
36:A1:2916:U:H5	36:A1:2935:U:HO2'	1.63	0.43
36:A1:2936:A:H2'	36:A1:2937:G:C8	2.52	0.43
36:A1:3296:A:H2'	36:A1:3297:U:H6	1.84	0.43
44:AI:43:VAL:HG21	44:AI:197:VAL:HG13	1.98	0.43
45:AJ:90:GLN:NE2	45:AJ:174:LYS:O	2.44	0.43
49:AO:185[A]:ALA:O	49:AO:188[A]:SER:OG	2.32	0.43
64:Ad:26:LYS:HD3	64:Ad:26:LYS:HA	1.83	0.43
73:Am:99:CYS:HB2	73:Am:114:LYS:HE3	2.00	0.43
76:Ap:51:ALA:HB3	76:Ap:54:ILE:HD12	1.99	0.43
79:DC:380:LEU:HG	79:DC:469:LEU:HB2	2.00	0.43
79:DC:607:ASN:ND2	79:DC:609:ARG:HB2	2.34	0.43
2:BB:190:PRO:HB2	2:BB:192:VAL:HG23	1.99	0.43
6:BH:139:ARG:HB3	13:BW:51:GLU:OE2	2.17	0.43
11:BO:80:HIS:ND1	11:BO:114:ARG:HB2	2.33	0.43
19:BD:46:THR:HG21	19:BD:79:TYR:CE2	2.53	0.43
19:BD:70:THR:HA	19:BD:86:LEU:HD13	1.99	0.43
20:BF:109:LYS:NZ	32:B5:1474:G:OP2	2.39	0.43
24:BR:65:PRO:HB3	24:BR:78:ARG:HH22	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BS:14:ILE:HD11	25:BS:21:ASN:HB3	1.99	0.43
31:Bg:121:MET:HE1	31:Bg:123:ILE:HD11	2.01	0.43
32:B5:41:A:O2'	32:B5:437:A:O2'	2.21	0.43
32:B5:270:C:H2'	32:B5:271:A:C8	2.53	0.43
32:B5:1333:C:H2'	32:B5:1334:U:H6	1.83	0.43
32:B5:1586:A:H2'	32:B5:1587:A:O4'	2.18	0.43
34:AB:332:ARG:NH2	36:A1:3304:U:OP2	2.46	0.43
36:A1:412:G:OP1	50:AP:62:ARG:NH1	2.50	0.43
36:A1:598:A:H2'	36:A1:599:C:C6	2.53	0.43
36:A1:616:G:H2'	36:A1:617:G:H8	1.83	0.43
36:A1:735:A:H2'	36:A1:736:A:C8	2.53	0.43
36:A1:759:U:H2'	36:A1:760:G:O4'	2.17	0.43
36:A1:2428:U:H2'	36:A1:2429:G:H8	1.83	0.43
36:A1:2469:G:H4'	77:E:26:ARG:NE	2.33	0.43
36:A1:2723:U:H2'	36:A1:2724:OMU:C6	2.48	0.43
36:A1:3072:C:H2'	36:A1:3073:A:O4'	2.18	0.43
36:A1:3349:C:H2'	36:A1:3350:C:C6	2.52	0.43
38:A4:152:G:H5'	42:AG:59:GLN:HG3	2.00	0.43
42:AG:115:ALA:HB3	42:AG:125:ALA:HB2	2.00	0.43
77:E:10:ARG:NH1	77:E:176:GLU:O	2.50	0.43
77:E:98:LYS:HD2	77:E:98:LYS:O	2.18	0.43
77:E:148:VAL:O	77:E:152:ARG:HG2	2.18	0.43
78:EC:6898:U:H2'	78:EC:6899:C:C6	2.53	0.43
79:DC:71:LYS:HA	79:DC:71:LYS:HD3	1.77	0.43
1:BA:139:VAL:HG23	1:BA:141:ILE:HG13	2.01	0.43
2:BB:62:LYS:HD3	2:BB:62:LYS:HA	1.86	0.43
5:BG:133:LEU:HD12	32:B5:66:U:C2	2.53	0.43
6:BH:137:GLY:HA3	6:BH:153:LEU:HD12	2.00	0.43
7:BI:75:LYS:NZ	32:B5:259:U:OP1	2.35	0.43
11:BO:124:ASP:N	32:B5:885:G:H21	2.17	0.43
15:BY:33:ALA:HB1	32:B5:532:U:O2	2.18	0.43
15:BY:34:ASN:ND2	32:B5:521:A:N3	2.66	0.43
19:BD:51:ARG:HE	19:BD:91:VAL:HA	1.83	0.43
32:B5:699:U:O2'	32:B5:740:A:N1	2.41	0.43
32:B5:1259:U:H2'	32:B5:1260:U:C6	2.54	0.43
32:B5:1338:C:H2'	32:B5:1339:C:C6	2.54	0.43
36:A1:187:A:H2'	36:A1:188:U:O4'	2.19	0.43
36:A1:2469:G:O2'	36:A1:2470:C:O4'	2.36	0.43
36:A1:2810:C:OP2	36:A1:2955:U:O2'	2.35	0.43
43:AH:53:ILE:HD12	47:AM:7:VAL:HG21	1.99	0.43
43:AH:114:VAL:HB	43:AH:124:ARG:HB2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:AI:150:GLU:OE2	44:AI:153:ARG:NH1	2.51	0.43
49:AO:58[A]:LEU:HD21	49:AO:74[A]:ARG:NH1	2.27	0.43
51:AQ:175:ALA:C	61:Aa:51:GLY:HA2	2.44	0.43
54:AT:8:ARG:O	54:AT:11:THR:OG1	2.32	0.43
59:AY:109:LEU:HD22	59:AY:115:ARG:NH2	2.34	0.43
79:DC:393:ARG:HH12	79:DC:510:ARG:HG2	1.82	0.43
79:DC:565:GLU:HB3	79:DC:717:PHE:CZ	2.53	0.43
3:BC:178:ILE:HD13	3:BC:196:VAL:HG12	2.00	0.43
6:BH:175:LYS:HD3	6:BH:175:LYS:HA	1.83	0.43
7:BI:103:GLN:HA	7:BI:165:LEU:O	2.19	0.43
19:BD:162:GLN:HB3	32:B5:1332:C:O2'	2.19	0.43
20:BF:77:TYR:HB3	20:BF:84:LYS:HA	2.01	0.43
20:BF:99:MET:HB2	20:BF:180:ARG:CZ	2.48	0.43
20:BF:99:MET:HE1	32:B5:1165:G:H4'	1.99	0.43
20:BF:185:ARG:NH2	32:B5:1471:A:OP1	2.51	0.43
28:BZ:80:LEU:HD12	28:BZ:101:TYR:CD1	2.53	0.43
31:Bg:175:ASP:N	31:Bg:175:ASP:OD1	2.49	0.43
32:B5:909:U:H2'	32:B5:910:C:C6	2.54	0.43
32:B5:925:G:H2'	32:B5:926:A:H8	1.84	0.43
32:B5:1333:C:H2'	32:B5:1334:U:C6	2.54	0.43
32:B5:1586:A:H1'	32:B5:1611:A:N6	2.33	0.43
33:AA:206:PRO:HG3	33:AA:213:GLY:HA3	2.01	0.43
35:AC:51:ALA:O	38:A4:26:U:O2'	2.36	0.43
35:AC:60:THR:HG23	36:A1:364:G:OP1	2.18	0.43
36:A1:649:A2M:H2'	36:A1:650:OMC:C6	2.53	0.43
36:A1:1497:C:H2'	36:A1:1498:A:C8	2.53	0.43
36:A1:1622:U:H2'	36:A1:1623:G:H8	1.84	0.43
36:A1:2677:G:N3	36:A1:2677:G:H2'	2.33	0.43
36:A1:3164:C:HO2'	36:A1:3165:A:H8	1.65	0.43
36:A1:3271:G:C6	40:AE:108:LYS:HE3	2.52	0.43
36:A1:3295:A:H2'	36:A1:3296:A:H8	1.83	0.43
39:AD:120:LYS:HB3	39:AD:123:GLU:OE2	2.19	0.43
44:AI:47:PRO:HD2	44:AI:141:LYS:HA	2.00	0.43
44:AI:54:SER:HB2	44:AI:135:ILE:HD11	1.99	0.43
45:AJ:71:VAL:HG13	45:AJ:75:LYS:HE3	2.00	0.43
70:Aj:85:LYS:HB3	70:Aj:85:LYS:HE3	1.81	0.43
78:EC:6826:U:H2'	78:EC:6827:G:C8	2.53	0.43
79:DC:751:ARG:HH21	79:DC:775:ASN:HD21	1.65	0.43
1:BA:43:ASP:OD1	1:BA:45:VAL:HG12	2.18	0.43
2:BB:107:THR:O	2:BB:111:ARG:HG2	2.19	0.43
3:BC:91:ARG:HG2	32:B5:1147:A:OP1	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BJ:62:ARG:O	8:BJ:69:ARG:NH1	2.51	0.43
8:BJ:114:TYR:HA	8:BJ:119:ALA:HB3	1.99	0.43
23:BQ:30:LYS:HD3	23:BQ:30:LYS:HA	1.70	0.43
26:BT:33:TYR:HE2	26:BT:103:LYS:HD2	1.83	0.43
26:BT:44:GLU:OE2	32:B5:1476:C:H5''	2.18	0.43
28:BZ:54:VAL:N	28:BZ:55:PRO:HD2	2.33	0.43
32:B5:808:U:H2'	32:B5:809:A:C8	2.54	0.43
32:B5:855:A:C2	32:B5:857:U:H1'	2.53	0.43
32:B5:1146:G:H2'	32:B5:1147:A:H8	1.81	0.43
36:A1:776:U:OP1	62:Ab:41:ARG:NH1	2.51	0.43
36:A1:834:U:H2'	36:A1:835:G:O4'	2.19	0.43
36:A1:1203:A:H2'	36:A1:1204:A:H8	1.79	0.43
36:A1:1680:G:H2'	36:A1:1681:U:C6	2.53	0.43
36:A1:1947:G:H5''	52:AR:134:HIS:HB2	2.01	0.43
36:A1:2651:G:H5''	36:A1:2652:U:O4'	2.18	0.43
36:A1:3023:U:H2'	36:A1:3024:A:C8	2.51	0.43
36:A1:3057:U:O2'	36:A1:3059:G:OP1	2.36	0.43
36:A1:3170:A:H2'	36:A1:3171:U:C6	2.53	0.43
39:AD:40:HIS:HB3	39:AD:43:LYS:HG3	2.01	0.43
40:AE:53:VAL:HG23	40:AE:68:PRO:HD3	2.01	0.43
51:AQ:42:ALA:HB2	51:AQ:133:LYS:HB3	2.00	0.43
51:AQ:161:LYS:HA	51:AQ:161:LYS:HD3	1.80	0.43
52:AR:177:VAL:HG23	52:AR:178:ALA:H	1.84	0.43
54:AT:137:GLU:HG3	54:AT:138:SER:N	2.33	0.43
54:AT:152:ALA:HB1	54:AT:153:PRO:HD2	2.01	0.43
58:AX:59:SER:HB3	58:AX:102:LEU:HG	2.00	0.43
60:AZ:5:LEU:HD21	60:AZ:82:PRO:HB3	2.01	0.43
77:E:96:ASN:HD22	77:E:98:LYS:HB3	1.84	0.43
81:BM:33:ARG:O	81:BM:37:VAL:HG23	2.18	0.43
1:BA:111:ILE:HD11	32:B5:1292:G:H21	1.84	0.43
1:BA:195:TRP:CH2	1:BA:197:ILE:HD11	2.54	0.43
2:BB:28:GLU:OE2	2:BB:50:LYS:HA	2.18	0.43
19:BD:132:LYS:N	19:BD:189:MET:O	2.51	0.43
20:BF:110:ALA:O	20:BF:114:ILE:HG12	2.18	0.43
28:BZ:68:ARG:HG2	78:EC:6868:C:H1'	2.01	0.43
29:Bc:31:GLU:OE2	29:Bc:36:THR:HA	2.19	0.43
31:Bg:26:SER:HB3	31:Bg:29:GLN:HB2	2.00	0.43
31:Bg:40:LYS:HE2	31:Bg:40:LYS:HB2	1.79	0.43
32:B5:172:C:H2'	32:B5:173:A:C8	2.54	0.43
32:B5:496:G:H2'	32:B5:496:G:N3	2.33	0.43
32:B5:691:C:OP1	32:B5:697:C:N4	2.51	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:736:C:N4	32:B5:737:A:H62	2.17	0.43
32:B5:1600:A:O2'	32:B5:1602:C:N4	2.52	0.43
36:A1:20:A:H2'	36:A1:21:G:C8	2.53	0.43
36:A1:268:A:C5	48:AN:12:ARG:HG2	2.53	0.43
36:A1:366:A:H2'	36:A1:367:A:O4'	2.18	0.43
36:A1:552:G:H2'	36:A1:553:U:O4'	2.19	0.43
36:A1:799:G:OP2	61:Aa:32:ARG:HD3	2.18	0.43
36:A1:1367:G:P	65:Ae:45:ARG:HH22	2.41	0.43
36:A1:2218:G:H2'	36:A1:2219:A:C8	2.54	0.43
41:AF:104:GLN:HE21	41:AF:104:GLN:HB2	1.63	0.43
41:AF:123:THR:HA	41:AF:126:LEU:HD12	2.01	0.43
53:AS:83:SER:OG	53:AS:88:HIS:HE1	2.01	0.43
66:Af:31:LYS:NZ	66:Af:78:SER:O	2.51	0.43
66:Af:49:ILE:HD11	66:Af:71:VAL:HG22	2.00	0.43
79:DC:480:VAL:O	79:DC:481:MET:HB3	2.19	0.43
80:Bf:133:ALA:O	80:Bf:139:LEU:HD12	2.19	0.43
80:Bf:141:CYS:SG	80:Bf:144:CYS:N	2.83	0.43
1:BA:40:ALA:HB2	1:BA:46:HIS:CG	2.54	0.43
4:BE:77:ARG:HD2	4:BE:82:TYR:CE1	2.53	0.43
11:BO:72:LYS:O	11:BO:73:GLU:HG3	2.18	0.43
16:Ba:10:ARG:HH12	32:B5:1790:A:P	2.42	0.43
21:BK:40:LEU:HD11	32:B5:1217:A:C4	2.54	0.43
23:BQ:51:PRO:HB3	23:BQ:86:ALA:HB2	2.01	0.43
29:Bc:10:ALA:N	29:Bc:54:LEU:O	2.52	0.43
31:Bg:252:LEU:N	31:Bg:263:PHE:O	2.52	0.43
32:B5:82:U:H2'	32:B5:83:G:O4'	2.19	0.43
32:B5:645:C:H2'	32:B5:646:C:C6	2.54	0.43
32:B5:1001:A:H1'	78:EC:6909:A:O2'	2.19	0.43
32:B5:1214:U:H5'	32:B5:1244:A:N7	2.33	0.43
32:B5:1272:U:O4	32:B5:1431:C:O2'	2.36	0.43
32:B5:1733:C:H2'	32:B5:1734:U:C6	2.54	0.43
32:B5:1776:A:H2'	32:B5:1777:G:H8	1.84	0.43
34:AB:173:GLN:HG2	34:AB:175:LYS:H	1.84	0.43
35:AC:23:PRO:HD2	35:AC:26:PHE:CE2	2.54	0.43
36:A1:184:U:H2'	36:A1:185:C:H6	1.84	0.43
36:A1:1447:G:N7	50:AP:25:SER:OG	2.51	0.43
36:A1:1638:A:OP1	67:Ag:74:ARG:NH1	2.48	0.43
36:A1:2471:U:H3	36:A1:2474:G:N2	2.17	0.43
36:A1:2552:C:N4	63:Ac:57:GLU:OE2	2.50	0.43
36:A1:3214:U:C6	47:AM:121:MET:HE2	2.54	0.43
40:AE:150:LYS:HE2	40:AE:156:LYS:HD2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:AT:17:ARG:NH1	54:AT:47:SER:HB2	2.33	0.43
54:AT:124:VAL:HG22	54:AT:125:ALA:H	1.84	0.43
63:Ac:45:ALA:HB2	63:Ac:77:LEU:HD12	1.99	0.43
77:E:89:ASP:OD1	77:E:89:ASP:N	2.52	0.43
78:EC:6773:G:O2'	78:EC:6819:G:H5'	2.19	0.43
79:DC:378:LEU:O	79:DC:470:THR:HA	2.19	0.43
80:Bf:78:LYS:C	80:Bf:79:LYS:HD2	2.44	0.43
1:BA:136:ALA:HB1	1:BA:141:ILE:HB	2.01	0.43
2:BB:29:TRP:CZ2	2:BB:47:LEU:HD23	2.54	0.43
2:BB:82:ARG:HG3	2:BB:103:MET:SD	2.59	0.43
2:BB:100:PHE:CD2	2:BB:181:LEU:HD11	2.54	0.43
3:BC:230:TRP:CD2	13:BW:68:ARG:HD3	2.54	0.43
6:BH:114:ARG:HD3	6:BH:114:ARG:HA	1.86	0.43
11:BO:53:ASP:OD1	11:BO:56:SER:HB2	2.18	0.43
13:BW:27:ILE:N	13:BW:61:ILE:O	2.47	0.43
14:BX:130:VAL:HG11	14:BX:135:LEU:HD21	2.01	0.43
17:Bb:2:VAL:HG11	17:Bb:5:GLN:HB3	2.01	0.43
22:BP:52:LYS:HG3	22:BP:53:PRO:HD3	2.01	0.43
25:BS:132:ARG:HD2	25:BS:136:GLN:OE1	2.19	0.43
32:B5:127:G:H21	32:B5:178:U:H2'	1.82	0.43
32:B5:272:U:O2'	32:B5:284:G:N2	2.50	0.43
32:B5:760:A:H2'	32:B5:761:G:O4'	2.19	0.43
32:B5:895:G:H1	32:B5:917:U:H3	1.67	0.43
32:B5:1290:U:H2'	32:B5:1291:G:C8	2.53	0.43
32:B5:1775:U:OP1	74:An:11:ARG:NH2	2.50	0.43
36:A1:976:U:H2'	36:A1:977:C:O4'	2.18	0.43
36:A1:1619:A:H2'	36:A1:1620:U:O4'	2.18	0.43
36:A1:1648:A:H2'	36:A1:1649:U:O4'	2.19	0.43
36:A1:1912:U:H2'	36:A1:1913:A:O4'	2.19	0.43
37:A3:22:A:H2'	37:A3:23:A:C8	2.53	0.43
38:A4:41:A:H4'	70:Aj:59:THR:HG23	1.99	0.43
39:AD:41:LYS:HD2	54:AT:93:VAL:HG11	2.00	0.43
39:AD:65:ILE:HG12	39:AD:74:VAL:HG22	1.99	0.43
39:AD:179:ARG:HD3	39:AD:179:ARG:HA	1.81	0.43
61:Aa:24:LYS:O	61:Aa:25:HIS:C	2.62	0.43
61:Aa:103:ASP:HA	61:Aa:126:LYS:HB2	2.01	0.43
77:E:96:ASN:ND2	77:E:98:LYS:HB3	2.34	0.43
79:DC:27:HIS:ND1	79:DC:138:GLN:HB2	2.33	0.43
79:DC:85:ASP:HA	79:DC:88:GLU:OE2	2.19	0.43
79:DC:108:HIS:HB3	79:DC:109:VAL:H	1.63	0.43
79:DC:250:PHE:HB2	79:DC:257:TRP:CZ3	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:DC:433:ARG:O	79:DC:457:VAL:HG22	2.18	0.43
1:BA:102:PHE:CZ	1:BA:106:SER:HB2	2.54	0.43
4:BE:19:LEU:HD13	32:B5:788:A:C4	2.54	0.43
8:BJ:58:ASP:OD1	8:BJ:59:LEU:N	2.52	0.43
8:BJ:173:ALA:HB2	32:B5:511:A:H5'	2.01	0.43
29:Bc:12:VAL:N	29:Bc:52:ASP:O	2.42	0.43
30:Bd:10:HIS:ND1	30:Bd:11:PRO:HD2	2.34	0.43
32:B5:681:U:O2'	32:B5:683:C:OP2	2.27	0.43
32:B5:1227:A:N3	32:B5:1229:G:N1	2.67	0.43
32:B5:1254:U:H2'	32:B5:1255:G:O4'	2.18	0.43
32:B5:1474:G:C2	32:B5:1475:A:C5	3.07	0.43
32:B5:1752:U:H2'	32:B5:1753:A:C8	2.53	0.43
33:AA:244:GLY:HA2	36:A1:2243:A:H3'	2.01	0.43
35:AC:152:VAL:HG21	35:AC:156:LEU:HD22	2.01	0.43
36:A1:182:U:H3	36:A1:234:G:H1	1.67	0.43
36:A1:308:A:H1'	36:A1:2222:A:N3	2.33	0.43
36:A1:371:G:N1	36:A1:374:A:OP2	2.41	0.43
36:A1:532:A:H2'	36:A1:533:A:C8	2.53	0.43
36:A1:947:G:H2'	36:A1:948:C:C6	2.53	0.43
36:A1:1232:C:C5	36:A1:1261:G:H2'	2.53	0.43
36:A1:1771:C:H2'	36:A1:1772:U:O4'	2.19	0.43
36:A1:2361:A:H2'	36:A1:2362:C:H6	1.83	0.43
36:A1:2767:U:OP1	75:Ao:34:SER:HB3	2.19	0.43
36:A1:3110:C:H2'	36:A1:3111:U:C6	2.53	0.43
36:A1:3221:C:H2'	36:A1:3222:U:O4'	2.19	0.43
48:AN:53:TYR:HB2	48:AN:133:ILE:HG21	2.00	0.43
51:AQ:67:ILE:HG12	51:AQ:81:VAL:HG11	2.01	0.43
54:AT:92:ARG:HB3	54:AT:94:GLU:OE1	2.19	0.43
68:Ah:26:LYS:HB3	68:Ah:26:LYS:HE3	1.89	0.43
79:DC:171:LYS:HE3	79:DC:171:LYS:HB2	1.70	0.43
79:DC:249:PHE:CE1	79:DC:271:ARG:HA	2.54	0.43
25:BS:68:ARG:O	25:BS:72:ILE:HG13	2.19	0.42
27:BU:97:VAL:HG23	27:BU:101:LYS:HD3	2.01	0.42
31:Bg:56:VAL:HG13	31:Bg:56:VAL:O	2.19	0.42
31:Bg:197:SER:HB2	31:Bg:216:LYS:HB3	2.01	0.42
32:B5:300:A:H2'	32:B5:301:A:C8	2.54	0.42
32:B5:445:A:C2	32:B5:446:A:C8	3.07	0.42
32:B5:953:G:H2'	32:B5:954:G:H8	1.83	0.42
32:B5:1196:A:H4'	32:B5:1197:C:H5''	2.01	0.42
32:B5:1733:C:H2'	32:B5:1734:U:H6	1.83	0.42
33:AA:135:ILE:HB	33:AA:149:ARG:HG2	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:63:A:H5''	48:AN:174:ILE:HG21	2.01	0.42
36:A1:283:G:OP2	36:A1:285:A:O2'	2.33	0.42
36:A1:954:U:H5	36:A1:967:A:N1	2.18	0.42
36:A1:985:U:H2'	36:A1:986:U:H6	1.83	0.42
36:A1:986:U:O2'	41:AF:122:ALA:O	2.33	0.42
36:A1:1155:C:O2'	36:A1:1197:A:N1	2.41	0.42
36:A1:1909:A:H2'	36:A1:1910:A:C8	2.54	0.42
36:A1:2282:U:O2	36:A1:2310:U:H4'	2.19	0.42
36:A1:2696:A:H2'	36:A1:2697:A:C8	2.54	0.42
36:A1:2899:C:O2'	36:A1:2901:G:OP2	2.32	0.42
60:AZ:3:LYS:O	60:AZ:6:LYS:NZ	2.46	0.42
60:AZ:48:ARG:NH2	60:AZ:69:LYS:HD2	2.34	0.42
63:Ac:103:THR:HG22	63:Ac:105:ALA:N	2.34	0.42
68:Ah:21:LEU:HD11	68:Ah:25:LYS:HE3	2.01	0.42
77:E:89:ASP:O	77:E:92:LYS:HG3	2.19	0.42
77:E:160:LYS:NZ	77:E:164:CYS:O	2.48	0.42
79:DC:420:PRO:HG3	79:DC:476:HIS:HD1	1.84	0.42
79:DC:561:VAL:HG13	79:DC:563:TYR:CE2	2.54	0.42
79:DC:736:PRO:O	79:DC:740:VAL:HG23	2.19	0.42
1:BA:74:VAL:HG23	1:BA:118:PRO:HB3	2.00	0.42
9:BL:53:TYR:CG	9:BL:113:PRO:HG2	2.54	0.42
16:Ba:30:ILE:HG13	16:Ba:31:PRO:HD2	2.00	0.42
23:BQ:79:TYR:HA	23:BQ:82:ARG:HD3	2.00	0.42
26:BT:40:SER:HB3	26:BT:43:ASN:OD1	2.19	0.42
32:B5:138:A:C8	32:B5:142:G:H5'	2.54	0.42
32:B5:234:G:C2	32:B5:235:G:H1'	2.54	0.42
32:B5:428:A:H2'	32:B5:429:G:O4'	2.20	0.42
32:B5:1247:U:H5''	80:Bf:93:HIS:N	2.33	0.42
32:B5:1323:C:H2'	32:B5:1324:G:C8	2.54	0.42
36:A1:871:U:H2'	36:A1:872:U:C6	2.54	0.42
36:A1:975:C:H2'	36:A1:976:U:C6	2.54	0.42
36:A1:1498:A:H2'	36:A1:1499:C:H6	1.84	0.42
36:A1:2099:A:H2'	36:A1:2100:A:N3	2.34	0.42
36:A1:2106:A:H2'	36:A1:2107:A:H8	1.85	0.42
36:A1:2258:U:H2'	36:A1:2259:A:O4'	2.19	0.42
37:A3:8:G:OP2	39:AD:30:TYR:OH	2.32	0.42
46:AL:85:LEU:CD1	46:AL:90:ALA:HB2	2.50	0.42
58:AX:113:LEU:HD11	58:AX:121:LYS:HE2	2.02	0.42
70:Aj:60:GLY:HA2	70:Aj:64:MET:HE2	2.00	0.42
78:EC:6789:G:H1'	78:EC:6790:A:O4'	2.19	0.42
79:DC:638:PRO:HD3	79:DC:644:ASN:HD22	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:76:ILE:HB	1:BA:123:VAL:HG12	2.02	0.42
14:BX:96:VAL:HG13	14:BX:97:ASP:H	1.84	0.42
24:BR:100:LEU:O	24:BR:120:SER:N	2.53	0.42
26:BT:130:ARG:O	26:BT:134:ARG:HG2	2.18	0.42
32:B5:340:U:H2'	32:B5:341:A:C8	2.54	0.42
32:B5:973:A:H4'	36:A1:848:A:H8	1.84	0.42
32:B5:1503:A:H2'	32:B5:1504:G:O4'	2.19	0.42
34:AB:83:PRO:HB2	34:AB:202:THR:HB	2.01	0.42
34:AB:86:VAL:HB	34:AB:198:HIS:O	2.20	0.42
35:AC:317:PRO:C	35:AC:319:LYS:N	2.76	0.42
35:AC:343:LYS:HD2	36:A1:516:A:OP1	2.18	0.42
36:A1:93:C:C2	61:Aa:55:LYS:HE2	2.55	0.42
36:A1:241:G:HO2'	36:A1:242:C:C5'	2.33	0.42
36:A1:872:U:H2'	36:A1:873:C:C6	2.53	0.42
36:A1:1321:G:N2	53:AS:112:ALA:HB2	2.34	0.42
36:A1:1562:C:H2'	36:A1:1563:C:H6	1.84	0.42
36:A1:1829:G:H5''	36:A1:1830:G:H5'	2.00	0.42
36:A1:2428:U:H2'	36:A1:2429:G:C8	2.54	0.42
36:A1:2659:G:H4'	36:A1:2751:G:O2'	2.19	0.42
36:A1:2709:C:H2'	36:A1:2710:C:C6	2.55	0.42
36:A1:3184:A:OP2	49:AO:12[A]:LYS:NZ	2.41	0.42
77:E:51:GLY:N	77:E:157:PHE:HB2	2.33	0.42
78:EC:6793:A:H2'	78:EC:6795:U:H5'	2.00	0.42
79:DC:342:LEU:HD23	79:DC:342:LEU:HA	1.77	0.42
79:DC:759:GLN:HB3	79:DC:766:PHE:CD1	2.54	0.42
3:BC:121:VAL:O	3:BC:125:ILE:HG12	2.19	0.42
5:BG:72:ARG:NH2	32:B5:419:G:H5'	2.34	0.42
6:BH:14:THR:HG22	6:BH:15:GLU:N	2.28	0.42
9:BL:152:GLN:CD	10:BN:137:PRO:HD3	2.44	0.42
24:BR:57:LEU:HA	24:BR:60:ARG:HB2	2.01	0.42
26:BT:14:PHE:HZ	26:BT:132:LEU:HD22	1.84	0.42
31:Bg:109:ASP:C	31:Bg:126:SER:HG	2.17	0.42
32:B5:1256:A:C2	81:BM:103:LEU:HD12	2.54	0.42
32:B5:1369:U:O2	32:B5:1372:U:H2'	2.19	0.42
34:AB:364:LYS:HG2	36:A1:3049:A:H5''	2.01	0.42
36:A1:654:C:H2'	36:A1:655:C:C6	2.54	0.42
36:A1:1856:C:C2	36:A1:1857:C:C5	3.06	0.42
36:A1:2148:U:H2'	36:A1:2149:A:C5	2.55	0.42
36:A1:2941:A:H8	36:A1:2941:A:OP2	2.02	0.42
36:A1:3107:U:H2'	36:A1:3108:G:C8	2.54	0.42
39:AD:44:TYR:H	39:AD:44:TYR:HD1	1.65	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:AY:116:LYS:HG2	59:AY:126:LEU:HD11	2.02	0.42
70:Aj:27:PHE:HA	70:Aj:34:CYS:HA	2.01	0.42
10:BN:87:ASP:OD1	10:BN:87:ASP:N	2.52	0.42
13:BW:57:ARG:HB3	32:B5:863:A:H4'	2.00	0.42
14:BX:65:ASN:HD22	14:BX:116:ASP:HB3	1.84	0.42
16:Ba:26:CYS:SG	16:Ba:28:LYS:HB2	2.60	0.42
19:BD:25:PHE:O	19:BD:29:LEU:HB2	2.19	0.42
19:BD:113:LEU:HD22	19:BD:118:ALA:HB2	2.02	0.42
23:BQ:95:LYS:O	31:Bg:59:ARG:NH1	2.52	0.42
26:BT:45:MET:HB3	32:B5:1477:G:H5'	2.00	0.42
31:Bg:278:PHE:CD1	31:Bg:287:PRO:HG2	2.55	0.42
32:B5:54:C:O2'	32:B5:459:G:N7	2.36	0.42
32:B5:948:G:H2'	32:B5:949:C:C6	2.54	0.42
32:B5:1125:A:C5	32:B5:1126:OMG:HI'	2.55	0.42
33:AA:79:ASN:ND2	33:AA:166:ILE:O	2.52	0.42
36:A1:399:A:O2'	36:A1:403:C:O2'	2.29	0.42
36:A1:1699:A:H2'	36:A1:1700:G:C8	2.54	0.42
36:A1:2220:A2M:N1	36:A1:2225:U:H5	2.18	0.42
38:A4:7:U:H2'	38:A4:8:C:C6	2.55	0.42
39:AD:8:LYS:HD3	39:AD:12:TYR:CE1	2.54	0.42
41:AF:83:LEU:HD11	41:AF:116:PHE:HB3	2.01	0.42
42:AG:162:LEU:HD23	48:AN:7:LEU:HD11	2.00	0.42
44:AI:31:ILE:HD11	44:AI:89:VAL:HG21	2.02	0.42
51:AQ:94:PHE:CZ	61:Aa:119:PRO:HD3	2.55	0.42
52:AR:181:ARG:HG3	52:AR:186:LYS:HD2	2.02	0.42
53:AS:6:GLU:OE2	53:AS:99:ARG:NH2	2.45	0.42
60:AZ:26:VAL:HG12	60:AZ:42:LEU:O	2.19	0.42
63:Ac:73:GLY:N	63:Ac:76:GLU:OE1	2.50	0.42
78:EC:6939:C:H1'	78:EC:6940:U:OP1	2.20	0.42
79:DC:320:LEU:HA	79:DC:323:VAL:HG12	2.02	0.42
81:BM:140:PHE:HA	81:BM:143:GLN:HG2	1.99	0.42
6:BH:13:PRO:HA	6:BH:14:THR:HA	1.73	0.42
7:BI:100:ALA:O	7:BI:169:ILE:HG12	2.18	0.42
8:BJ:81:VAL:HG21	8:BJ:91:LYS:HE3	2.01	0.42
14:BX:97:ASP:HB2	14:BX:100:ASP:OD1	2.19	0.42
18:Be:23:LYS:HE3	32:B5:586:G:OP1	2.20	0.42
21:BK:86:ILE:HG13	21:BK:87:VAL:HG13	2.02	0.42
25:BS:40:ARG:NH1	32:B5:1540:G:OP1	2.52	0.42
26:BT:61:VAL:HG22	26:BT:76:LEU:HD22	2.02	0.42
27:BU:58:LEU:HB2	27:BU:88:LYS:HB3	2.02	0.42
32:B5:153:G:C6	32:B5:162:A:C6	3.07	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:990:C:H2'	32:B5:991:G:O4'	2.20	0.42
32:B5:1624:C:H2'	32:B5:1625:C:C6	2.54	0.42
36:A1:273:A:H2'	36:A1:274:G:H8	1.82	0.42
36:A1:1581:C:N4	58:AX:33:ARG:HH12	2.18	0.42
36:A1:2813:A:H2'	36:A1:2814:G:O4'	2.19	0.42
36:A1:2985:C:H2'	36:A1:2986:U:C6	2.55	0.42
36:A1:3332:U:H2'	36:A1:3333:G:O4'	2.18	0.42
38:A4:65:A:O3'	68:Ah:10:ARG:NH2	2.48	0.42
40:AE:104:GLU:OE1	40:AE:104:GLU:N	2.49	0.42
42:AG:33:ASN:O	42:AG:39:ALA:HB3	2.20	0.42
45:AJ:108:GLU:OE1	45:AJ:122:ILE:HA	2.19	0.42
51:AQ:126:GLN:O	51:AQ:130:ARG:HG2	2.19	0.42
78:EC:6806:U:H5''	78:EC:6881:U:C6	2.54	0.42
79:DC:92:LYS:HD2	79:DC:92:LYS:O	2.19	0.42
79:DC:299:LEU:O	79:DC:303:LEU:HB2	2.19	0.42
2:BB:88:VAL:HG21	2:BB:96:LEU:HD23	2.02	0.42
2:BB:143:THR:HB	2:BB:205:PHE:HE2	1.83	0.42
5:BG:214:LYS:HE3	5:BG:214:LYS:HB3	1.87	0.42
6:BH:140:VAL:O	13:BW:51:GLU:HG3	2.20	0.42
12:BV:62:ARG:CZ	32:B5:1082:C:H1'	2.49	0.42
23:BQ:50:GLU:OE1	23:BQ:112:TYR:HE2	2.03	0.42
32:B5:222:A:H2'	32:B5:223:U:C6	2.55	0.42
32:B5:351:C:H3'	32:B5:352:A:H5'	2.01	0.42
32:B5:415:C:H2'	32:B5:417:A:N7	2.33	0.42
32:B5:650:U:H2'	32:B5:651:G:O4'	2.19	0.42
32:B5:1158:C:O2'	32:B5:1581:C:OP2	2.37	0.42
32:B5:1176:G:C6	32:B5:1464:G:C6	3.08	0.42
32:B5:1239:U:H2'	32:B5:1240:U:O4'	2.19	0.42
36:A1:36:C:H4'	36:A1:808:A:C2	2.54	0.42
36:A1:406:G:OP1	36:A1:1415:U:O2'	2.30	0.42
36:A1:713:U:O2	36:A1:754:G:H4'	2.20	0.42
36:A1:772:U:H2'	36:A1:773:G:C8	2.55	0.42
36:A1:938:C:C5	61:Aa:26:ARG:HD2	2.54	0.42
36:A1:1234:G:C8	36:A1:1235:U:H2'	2.54	0.42
36:A1:2902:A:H2'	36:A1:2903:A:O4'	2.19	0.42
37:A3:27:A:H2'	37:A3:28:C:C6	2.54	0.42
37:A3:97:A:H2'	37:A3:98:C:C6	2.55	0.42
40:AE:51:ARG:HE	40:AE:163:PHE:HB2	1.84	0.42
42:AG:214:LEU:O	42:AG:218:ILE:HG12	2.19	0.42
74:An:14:LYS:O	74:An:17:ARG:HB2	2.20	0.42
77:E:10:ARG:HH12	77:E:177:ASP:HA	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:EC:6787:U:H3	78:EC:6809:G:H1	1.67	0.42
78:EC:6858:A:H4'	78:EC:6859:U:N3	2.34	0.42
82:VA:18:TYR:HE2	82:VA:50:VAL:HG11	1.84	0.42
1:BA:122:ILE:HA	1:BA:144:ILE:O	2.20	0.42
6:BH:163:ASP:OD1	6:BH:163:ASP:N	2.52	0.42
17:Bb:56:CYS:SG	17:Bb:57:GLU:N	2.90	0.42
20:BF:205:SER:C	20:BF:207:THR:H	2.27	0.42
21:BK:24:LYS:HA	21:BK:63:TYR:HA	2.01	0.42
22:BP:25:LEU:HA	22:BP:28:MET:SD	2.60	0.42
22:BP:98:ASN:O	22:BP:122:THR:HG23	2.20	0.42
26:BT:86:ARG:HD2	26:BT:92:LYS:HE2	2.00	0.42
27:BU:96:PRO:HB2	27:BU:98:GLN:OE1	2.20	0.42
32:B5:144:U:HO2'	32:B5:145:A:H8	1.67	0.42
32:B5:225:A:N6	32:B5:837:G:C2	2.88	0.42
32:B5:390:G:O2'	32:B5:1731:A:H5''	2.20	0.42
32:B5:692:C:H2'	32:B5:693:U:C6	2.55	0.42
33:AA:183:GLY:CA	36:A1:896:A:H5''	2.48	0.42
36:A1:268:A:N1	36:A1:295:A:H5'	2.35	0.42
36:A1:418:A:N1	38:A4:5:U:H5	2.18	0.42
36:A1:677:A:H4'	36:A1:678:G:O5'	2.20	0.42
36:A1:691:A:N1	38:A4:28:C:O2'	2.48	0.42
36:A1:1242:G:HO2'	36:A1:1243:G:P	2.43	0.42
36:A1:1523:U:O2'	58:AX:111:ASN:ND2	2.53	0.42
36:A1:2283:G:H1'	36:A1:2285:C:N4	2.34	0.42
36:A1:2486:A:O2'	36:A1:2487:U:H5'	2.20	0.42
36:A1:2648:G:OP1	44:AI:24:ARG:NH2	2.48	0.42
36:A1:2676:A:H5'	36:A1:2677:G:C8	2.55	0.42
36:A1:3192:U:H2'	36:A1:3193:C:H6	1.83	0.42
45:AJ:114:ILE:HG13	45:AJ:114:ILE:O	2.20	0.42
50:AP:120:ASN:HB2	50:AP:145:HIS:HB2	2.02	0.42
56:AV:11:PHE:CE1	56:AV:88:ARG:HD3	2.54	0.42
56:AV:75:PRO:HG2	56:AV:105:PRO:HD3	2.02	0.42
78:EC:6795:U:H2'	78:EC:6796:C:C6	2.55	0.42
79:DC:137:VAL:O	79:DC:141:THR:HG23	2.20	0.42
79:DC:380:LEU:HB3	79:DC:400:VAL:HA	2.01	0.42
1:BA:48:ILE:HG12	1:BA:149:LEU:HD21	2.02	0.42
3:BC:108:ASN:ND2	3:BC:141:ARG:HH22	2.18	0.42
5:BG:74:LYS:HA	5:BG:96:SER:HA	2.01	0.42
19:BD:183:GLY:HA3	32:B5:1277:G:O3'	2.20	0.42
20:BF:163:SER:OG	29:Bc:47:PRO:O	2.23	0.42
32:B5:98:U:H2'	32:B5:99:C:C6	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:182:A:H2'	32:B5:183:U:H6	1.84	0.42
32:B5:1005:A:H2'	32:B5:1006:C:C6	2.55	0.42
32:B5:1624:C:H2'	32:B5:1625:C:H6	1.84	0.42
32:B5:1722:A:H2'	32:B5:1723:U:O4'	2.20	0.42
34:AB:17:LEU:HD21	34:AB:233:TRP:CH2	2.55	0.42
36:A1:170:G:OP1	46:AL:128:ARG:NH2	2.53	0.42
36:A1:280:U:H4'	48:AN:182:ASN:HD21	1.84	0.42
36:A1:1463:U:H2'	36:A1:1464:G:O4'	2.20	0.42
36:A1:2495:C:H2'	36:A1:2496:C:C2	2.55	0.42
36:A1:3343:G:H2'	36:A1:3344:A:C2	2.55	0.42
47:AM:109:ARG:HA	47:AM:112:LEU:HD23	2.02	0.42
54:AT:115:LYS:HB2	54:AT:128:LEU:HD21	2.01	0.42
79:DC:374:PRO:O	79:DC:404:THR:HG23	2.20	0.42
79:DC:711:ARG:HG2	79:DC:838:TYR:HD1	1.85	0.42
1:BA:195:TRP:CD1	1:BA:196:SER:H	2.38	0.42
2:BB:90:GLU:HB2	2:BB:97:LEU:HD12	2.02	0.42
7:BI:73:SER:OG	32:B5:257:A:H1'	2.20	0.42
11:BO:125:SER:OG	11:BO:126:THR:HG22	2.20	0.42
13:BW:71:LYS:HB3	13:BW:130:TYR:CE1	2.55	0.42
18:Be:39:LEU:HD23	18:Be:42:ARG:HE	1.85	0.42
19:BD:108:LYS:HE3	19:BD:113:LEU:HD13	2.02	0.42
20:BF:81:ARG:HA	32:B5:1615:C:C5	2.54	0.42
21:BK:10:LYS:HG2	21:BK:35:ILE:HG23	2.02	0.42
31:Bg:59:ARG:NH2	31:Bg:95:ALA:O	2.45	0.42
32:B5:585:A:H2'	32:B5:586:G:H8	1.85	0.42
32:B5:1439:C:H2'	32:B5:1440:C:H6	1.83	0.42
32:B5:1471:A:H2	32:B5:1474:G:N3	2.18	0.42
32:B5:1499:G:O6	32:B5:1509:C:N4	2.53	0.42
32:B5:1504:G:H2'	32:B5:1505:A:C8	2.55	0.42
32:B5:1642:G:H2'	32:B5:1643:U:C6	2.54	0.42
33:AA:43:GLY:O	33:AA:87:PHE:HA	2.19	0.42
33:AA:241:ARG:NH1	36:A1:2155:G:OP1	2.53	0.42
36:A1:242:C:O2'	36:A1:243:G:P	2.78	0.42
36:A1:642:U:OP1	61:Aa:22:ILE:HG23	2.20	0.42
36:A1:1490:A:O2'	70:Aj:12:HIS:O	2.25	0.42
36:A1:1812:G:O6	60:AZ:64:LYS:HE3	2.20	0.42
36:A1:3371:G:H2'	36:A1:3372:A:C8	2.55	0.42
40:AE:67:GLY:O	40:AE:68:PRO:C	2.63	0.42
42:AG:149:LYS:O	42:AG:176:PRO:HG2	2.20	0.42
43:AH:25:VAL:O	43:AH:35:THR:HA	2.20	0.42
45:AJ:12:LEU:HG	45:AJ:131:MET:HE3	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AJ:94:ARG:O	45:AJ:95:ASN:HB2	2.20	0.42
46:AL:139:LEU:HD23	46:AL:139:LEU:HA	1.89	0.42
50:AP:4:TYR:CZ	50:AP:16:SER:HB2	2.55	0.42
78:EC:6920:C:H2'	78:EC:6921:C:C6	2.55	0.42
79:DC:130:ASP:OD1	79:DC:131:THR:N	2.52	0.42
2:BB:36:SER:N	2:BB:231:LEU:O	2.52	0.41
2:BB:129:THR:OG1	2:BB:133:TYR:HB2	2.20	0.41
6:BH:44:LYS:HG3	6:BH:63:PRO:HD3	2.02	0.41
8:BJ:90:LYS:HE2	8:BJ:95:TYR:CD1	2.54	0.41
11:BO:47:LYS:HE3	11:BO:66:ASP:OD2	2.20	0.41
11:BO:64:ALA:HB3	11:BO:104:ALA:HB3	2.02	0.41
16:Ba:51:ARG:CZ	29:Bc:60:GLU:HB2	2.50	0.41
25:BS:2:SER:N	28:BZ:78:ILE:HG23	2.34	0.41
29:Bc:5:THR:HA	29:Bc:6:PRO:HD3	1.80	0.41
32:B5:1636:C:O2	32:B5:1765:A:N6	2.53	0.41
33:AA:3:ARG:HB3	33:AA:207:VAL:O	2.20	0.41
35:AC:81:GLY:HA3	36:A1:357:A:O4'	2.21	0.41
36:A1:177:U:C4	36:A1:178:U:C5	3.08	0.41
36:A1:789:A:H2'	36:A1:790:U:H6	1.84	0.41
36:A1:887:G:H2'	36:A1:888:A:C8	2.54	0.41
36:A1:1289:G:H2'	36:A1:1290:A:H8	1.85	0.41
36:A1:2217:U:H2'	36:A1:2218:G:H8	1.85	0.41
36:A1:2375:G:O2'	36:A1:2377:G:OP2	2.36	0.41
36:A1:2552:C:H2'	63:Ac:50:VAL:HG11	2.01	0.41
36:A1:2670:G:H2'	36:A1:2671:A:C8	2.55	0.41
38:A4:37:A:OP2	68:Ah:86:ARG:HD2	2.20	0.41
39:AD:40:HIS:CE1	39:AD:42:ALA:HB3	2.55	0.41
43:AH:27:VAL:HG12	43:AH:82:VAL:HG11	2.01	0.41
48:AN:115:VAL:HA	48:AN:134:LEU:HD23	2.01	0.41
50:AP:51:VAL:HA	50:AP:56:ARG:O	2.20	0.41
53:AS:89:ASN:ND2	54:AT:156:TYR:O	2.48	0.41
68:Ah:29:ALA:O	68:Ah:33:VAL:HG13	2.20	0.41
73:Am:106:ARG:HG2	73:Am:106:ARG:O	2.19	0.41
77:E:48:ARG:NE	77:E:159:LEU:HD23	2.35	0.41
81:BM:28:LEU:HG	81:BM:100:TRP:CH2	2.55	0.41
1:BA:41:ARG:HE	1:BA:45:VAL:CG1	2.33	0.41
2:BB:29:TRP:CE2	2:BB:47:LEU:HD23	2.55	0.41
3:BC:95:ARG:NH2	32:B5:1301:U:OP1	2.53	0.41
8:BJ:132:ARG:NH2	15:BY:65:GLY:HA2	2.35	0.41
14:BX:86:PHE:HB2	14:BX:107:PHE:HZ	1.84	0.41
27:BU:59:PRO:HA	32:B5:1382:A:H5'	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:1628:U:H2'	32:B5:1629:G:H8	1.83	0.41
35:AC:67:THR:HG22	36:A1:1436:U:O4	2.20	0.41
36:A1:66:A:N6	36:A1:76:G:H1'	2.35	0.41
36:A1:631:U:H2'	36:A1:632:G:C8	2.55	0.41
36:A1:1092:C:HO2'	36:A1:1093:A:P	2.43	0.41
36:A1:1140:G:O6	62:Ab:10:HIS:HE1	2.02	0.41
36:A1:1336:U:H2'	36:A1:1337:A:C8	2.55	0.41
36:A1:1635:G:N2	36:A1:1638:A:OP2	2.37	0.41
43:AH:2:LYS:HB3	43:AH:59:ASN:OD1	2.19	0.41
43:AH:20:ILE:HG23	43:AH:25:VAL:HG22	2.03	0.41
43:AH:67:ALA:O	43:AH:71:VAL:HG23	2.20	0.41
49:AO:37[A]:ARG:HB3	49:AO:40[A]:GLU:OE1	2.20	0.41
56:AV:81:GLN:HG2	56:AV:83:LYS:H	1.84	0.41
79:DC:182:VAL:HA	79:DC:185:VAL:HG22	2.02	0.41
79:DC:653:VAL:HB	79:DC:656:LEU:HB2	2.03	0.41
81:BM:68:GLU:O	81:BM:71:ILE:HG22	2.20	0.41
2:BB:112:SER:HA	16:Ba:68:TYR:HE2	1.84	0.41
5:BG:79:LYS:HG3	5:BG:80:ASN:ND2	2.35	0.41
5:BG:160:ARG:HB2	32:B5:66:U:C4	2.55	0.41
5:BG:164:LYS:HD3	32:B5:72:A:N7	2.35	0.41
6:BH:82:GLU:HG3	6:BH:90:VAL:HG12	2.01	0.41
17:Bb:74:SER:O	17:Bb:76:GLY:N	2.54	0.41
20:BF:57:SER:HB2	29:Bc:53:ILE:O	2.20	0.41
31:Bg:121:MET:HE1	31:Bg:183:LEU:HD22	2.03	0.41
31:Bg:240:VAL:HG12	31:Bg:256:THR:HG22	2.01	0.41
32:B5:340:U:H2'	32:B5:341:A:H8	1.85	0.41
32:B5:529:A:H2'	32:B5:530:C:H6	1.84	0.41
32:B5:896:U:H2'	32:B5:897:C:C6	2.55	0.41
32:B5:925:G:H2'	32:B5:926:A:C8	2.56	0.41
32:B5:1079:U:H2'	32:B5:1080:U:C6	2.55	0.41
32:B5:1558:U:H3'	32:B5:1559:A:H4'	2.02	0.41
32:B5:1640:C:H1'	32:B5:1763:A:N1	2.35	0.41
36:A1:1001:G:N3	36:A1:1041:U:H5'	2.35	0.41
36:A1:1054:A:H5''	36:A1:2637:A:H61	1.84	0.41
36:A1:1394:A:H4'	36:A1:1420:C:H4'	2.01	0.41
36:A1:1915:A:H2'	36:A1:1916:U:H6	1.84	0.41
36:A1:1949:G:OP2	52:AR:135:LYS:NZ	2.42	0.41
36:A1:2444:C:H2'	36:A1:2445:A:O4'	2.20	0.41
36:A1:3213:A:H2'	36:A1:3214:U:O4'	2.20	0.41
49:AO:119[A]:VAL:HG23	53:AS:164:SER:HB3	2.01	0.41
58:AX:36:LYS:HD3	58:AX:36:LYS:HA	1.80	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:AY:50:ILE:HG21	59:AY:80:VAL:HG11	2.01	0.41
68:Ah:41:LEU:HD12	68:Ah:41:LEU:HA	1.82	0.41
79:DC:132:ILE:HG21	79:DC:162:ARG:HH12	1.85	0.41
80:Bf:106:TYR:CE1	80:Bf:116:LYS:HG2	2.55	0.41
81:BM:43:ARG:HD2	81:BM:103:LEU:HD22	2.02	0.41
2:BB:132:ASP:HB2	2:BB:221:PRO:HB3	2.02	0.41
6:BH:78:THR:HG23	6:BH:90:VAL:HG13	2.02	0.41
7:BI:104:ILE:HG13	7:BI:105:ASP:N	2.31	0.41
9:BL:99:ARG:HG2	14:BX:9:LEU:HA	2.03	0.41
10:BN:40:TYR:HB3	10:BN:50:ILE:HG12	2.03	0.41
15:BY:132:ARG:NH1	32:B5:155:U:OP2	2.53	0.41
24:BR:93:LEU:O	24:BR:98:GLY:HA2	2.20	0.41
25:BS:2:SER:OG	25:BS:3:LEU:N	2.52	0.41
25:BS:127:HIS:HE1	32:B5:1545:A:H4'	1.85	0.41
31:Bg:174:ASN:CG	31:Bg:198:ASN:HB3	2.45	0.41
32:B5:107:C:H2'	32:B5:108:A:H8	1.85	0.41
32:B5:447:U:H2'	32:B5:448:C:O4'	2.20	0.41
32:B5:586:G:H2'	32:B5:587:C:C6	2.56	0.41
32:B5:769:A:H2'	32:B5:770:A:C8	2.55	0.41
32:B5:1142:A:H2'	32:B5:1143:A:C8	2.55	0.41
33:AA:28:LYS:HB2	33:AA:123:ARG:HB3	2.02	0.41
34:AB:227:GLU:HG2	34:AB:270:ARG:HD3	2.01	0.41
36:A1:595:G:H2'	36:A1:596:C:C6	2.56	0.41
36:A1:2129:U:H2'	36:A1:2130:G:C8	2.55	0.41
36:A1:2167:A:H2'	36:A1:2168:A:C8	2.55	0.41
36:A1:2203:U:H2'	36:A1:2204:C:H6	1.85	0.41
36:A1:2355:G:H4'	50:AP:139:TYR:CE1	2.56	0.41
36:A1:2465:G:C6	36:A1:2491:A:N6	2.87	0.41
36:A1:3320:A:H2'	36:A1:3321:C:C6	2.55	0.41
37:A3:80:G:H2'	37:A3:81:U:O4'	2.20	0.41
43:AH:161:LEU:O	43:AH:164:ILE:HG22	2.20	0.41
66:Af:75:HIS:HB2	66:Af:82:ARG:HG3	2.02	0.41
67:Ag:95:ILE:HD13	67:Ag:95:ILE:HG21	1.87	0.41
79:DC:176:GLN:OE1	79:DC:180:ARG:NH2	2.53	0.41
79:DC:420:PRO:HG3	79:DC:476:HIS:ND1	2.35	0.41
81:BM:23:THR:HB	81:BM:27:ALA:N	2.36	0.41
82:VA:89:THR:OG1	82:VA:90:ASN:N	2.53	0.41
6:BH:19:GLN:HA	6:BH:22:GLN:HG2	2.01	0.41
7:BI:56:ARG:NH1	7:BI:174:GLY:O	2.53	0.41
11:BO:19:ILE:HB	11:BO:83:ILE:HD13	2.02	0.41
15:BY:7:ILE:HG13	15:BY:43:LYS:HG2	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:120:ILE:HA	20:BF:123:VAL:HG22	2.01	0.41
22:BP:24:LYS:O	22:BP:24:LYS:HD3	2.20	0.41
22:BP:24:LYS:HD3	22:BP:28:MET:SD	2.60	0.41
24:BR:27:ASP:OD2	31:Bg:38:ARG:NH1	2.45	0.41
24:BR:71:PHE:HE2	24:BR:73:LEU:HB3	1.85	0.41
29:Bc:11:LYS:HA	29:Bc:53:ILE:HA	2.02	0.41
32:B5:336:G:H2'	32:B5:338:C:H5	1.85	0.41
32:B5:463:U:H2'	32:B5:464:A:H8	1.85	0.41
32:B5:1280:4AC:H2'	32:B5:1281:G:H8	1.86	0.41
32:B5:1476:C:H2'	32:B5:1477:G:H8	1.85	0.41
32:B5:1680:G:H1'	32:B5:1681:A:C2	2.55	0.41
36:A1:201:A:H2'	36:A1:202:G:H8	1.85	0.41
36:A1:1195:A:H1'	36:A1:1319:G:H4'	2.01	0.41
36:A1:1524:A:O2'	36:A1:1526:U:OP1	2.38	0.41
36:A1:1722:U:O4'	52:AR:96:ILE:HG12	2.20	0.41
36:A1:2674:A:H2'	36:A1:2675:C:C6	2.55	0.41
39:AD:219:PHE:CE2	39:AD:227:LEU:HD21	2.55	0.41
40:AE:76:LEU:N	40:AE:138:GLN:OE1	2.47	0.41
47:AM:20:VAL:HG21	47:AM:90:VAL:HG11	2.03	0.41
51:AQ:133:LYS:HB2	51:AQ:135:GLN:OE1	2.20	0.41
51:AQ:158:HIS:H	51:AQ:186:VAL:CG2	2.32	0.41
55:AU:51:GLY:O	55:AU:52:ASN:OD1	2.38	0.41
79:DC:161:ASP:HB2	79:DC:213:SER:OG	2.20	0.41
79:DC:385:MET:HB2	79:DC:395:TYR:O	2.20	0.41
81:BM:33:ARG:HH22	81:BM:102:GLY:N	2.18	0.41
1:BA:3:LEU:HD12	1:BA:4:PRO:HD2	2.02	0.41
2:BB:70:LEU:HB2	2:BB:82:ARG:O	2.21	0.41
5:BG:72:ARG:NH2	32:B5:418:G:O2'	2.32	0.41
5:BG:136:LYS:NZ	32:B5:66:U:OP2	2.53	0.41
7:BI:107:THR:HB	7:BI:108:PRO:HD3	2.03	0.41
8:BJ:110:GLN:CD	8:BJ:126:ARG:HB2	2.45	0.41
11:BO:62:LEU:HD23	11:BO:62:LEU:HA	1.94	0.41
13:BW:51:GLU:O	13:BW:61:ILE:HA	2.21	0.41
14:BX:42:PRO:HB3	14:BX:83:VAL:HG11	2.01	0.41
14:BX:65:ASN:ND2	14:BX:116:ASP:OD2	2.54	0.41
16:Ba:2:PRO:HG3	32:B5:1143:A:OP2	2.20	0.41
19:BD:158:ILE:HD11	19:BD:163:PRO:HB2	2.03	0.41
21:BK:92:ILE:HG22	21:BK:96:ASN:HA	2.03	0.41
24:BR:93:LEU:HD23	24:BR:93:LEU:HA	1.86	0.41
25:BS:12:GLN:OE1	25:BS:15:LEU:HB3	2.20	0.41
32:B5:19:A:H2'	32:B5:20:G:O4'	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:91:G:H2'	32:B5:92:A:O4'	2.20	0.41
32:B5:872:G:H2'	32:B5:873:U:O4'	2.20	0.41
32:B5:888:U:O2	32:B5:988:A:O2'	2.36	0.41
32:B5:978:A:H2'	32:B5:979:A:O4'	2.20	0.41
32:B5:1229:G:N2	32:B5:1255:G:O2'	2.54	0.41
32:B5:1441:C:H2'	32:B5:1442:U:H6	1.85	0.41
32:B5:1590:G:H2'	32:B5:1591:C:H6	1.85	0.41
32:B5:1650:U:H2'	32:B5:1651:A:C8	2.55	0.41
32:B5:1682:U:HO2'	32:B5:1683:C:P	2.43	0.41
32:B5:1775:U:H2'	32:B5:1776:A:C8	2.56	0.41
35:AC:95:ARG:NH1	36:A1:366:A:OP1	2.51	0.41
36:A1:74:G:H5''	46:AL:104:ARG:HH11	1.85	0.41
36:A1:213:A:H1'	59:AY:3:LYS:HB2	2.02	0.41
36:A1:833:G:OP1	52:AR:86:GLU:HB3	2.21	0.41
36:A1:1494:U:OP1	72:Al:44:TRP:HB3	2.21	0.41
36:A1:2662:G:H2'	36:A1:2663:G:H8	1.85	0.41
36:A1:2718:U:OP1	75:Ao:13:LYS:NZ	2.53	0.41
36:A1:2767:U:O2'	75:Ao:30:ALA:O	2.31	0.41
36:A1:2836:C:H2'	36:A1:2837:A:O4'	2.21	0.41
36:A1:3139:A:H2'	36:A1:3140:G:O4'	2.21	0.41
36:A1:3308:C:O2'	50:AP:69:ARG:O	2.35	0.41
36:A1:3324:C:OP1	64:Ad:19:ARG:NH1	2.49	0.41
75:Ao:11:TYR:HE1	75:Ao:13:LYS:HB3	1.85	0.41
78:EC:6937:G:H2'	78:EC:6937:G:N3	2.35	0.41
79:DC:636:PHE:HB2	79:DC:640:GLY:O	2.21	0.41
5:BG:174:LYS:CD	32:B5:79:C:H1'	2.48	0.41
8:BJ:170:GLY:O	8:BJ:174:ARG:HG3	2.20	0.41
10:BN:11:ILE:HD11	32:B5:1072:C:H4'	2.03	0.41
10:BN:91:LEU:HB3	10:BN:122:ILE:HG12	2.03	0.41
12:BV:36:VAL:HB	12:BV:51:VAL:HG23	2.03	0.41
13:BW:53:ILE:HB	13:BW:60:LYS:HB2	2.02	0.41
15:BY:129:VAL:HA	15:BY:132:ARG:HB2	2.03	0.41
19:BD:66:ILE:HD11	19:BD:86:LEU:HB3	2.01	0.41
20:BF:203:LYS:NZ	78:EC:6862:G:H5''	2.36	0.41
26:BT:22:LEU:HD12	26:BT:28:LEU:HD11	2.02	0.41
26:BT:102:ARG:NH1	32:B5:1502:G:O6	2.37	0.41
31:Bg:19:TRP:HB2	31:Bg:38:ARG:HG3	2.01	0.41
32:B5:227:U:H1'	32:B5:834:G:H22	1.85	0.41
32:B5:1237:G:N3	32:B5:1238:A:C8	2.89	0.41
32:B5:1286:U:O2	32:B5:1286:U:H2'	2.21	0.41
32:B5:1391:A:H2'	32:B5:1392:U:C6	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:1609:U:H2'	32:B5:1610:G:O4'	2.20	0.41
36:A1:283:G:O6	36:A1:304:G:H1'	2.20	0.41
36:A1:824:C:H2'	36:A1:825:U:C6	2.56	0.41
36:A1:1326:A:H2'	36:A1:1327:C:O4'	2.21	0.41
36:A1:1427:U:OP2	61:Aa:4:ARG:NH2	2.48	0.41
36:A1:1555:U:H5'	36:A1:1556:C:OP2	2.21	0.41
36:A1:2103:U:H2'	36:A1:2104:A:H8	1.85	0.41
39:AD:223:PHE:HA	39:AD:226:TYR:HD2	1.85	0.41
42:AG:166:LEU:HD23	42:AG:166:LEU:HA	1.88	0.41
42:AG:177:TYR:CZ	42:AG:222:PHE:HB3	2.55	0.41
48:AN:70:ASN:HB3	48:AN:92:LEU:O	2.21	0.41
67:Ag:16:ARG:HA	67:Ag:19:LYS:HD3	2.03	0.41
79:DC:411:VAL:HG22	79:DC:412:ARG:H	1.85	0.41
82:VA:42:ARG:NH1	82:VA:51:VAL:O	2.35	0.41
1:BA:4:PRO:HG2	1:BA:7:PHE:CE1	2.56	0.41
2:BB:34:ALA:H	2:BB:41:ARG:HB3	1.84	0.41
7:BI:26:LYS:HE2	7:BI:29:LEU:HD21	2.03	0.41
13:BW:34:ILE:O	13:BW:38:LEU:HG	2.21	0.41
18:Be:26:LYS:NZ	18:Be:29:LYS:HE3	2.35	0.41
19:BD:93:ASP:HB3	19:BD:96:LEU:HD13	2.01	0.41
22:BP:86:VAL:HG22	22:BP:89:MET:HE1	2.03	0.41
24:BR:69:ILE:O	24:BR:69:ILE:HG13	2.20	0.41
25:BS:108:LYS:HA	25:BS:111:ASP:HB2	2.02	0.41
28:BZ:55:PRO:HD3	28:BZ:88:ILE:HD12	2.03	0.41
31:Bg:265:LEU:HD23	31:Bg:265:LEU:H	1.86	0.41
32:B5:614:C:C2	32:B5:615:A:C8	3.08	0.41
32:B5:812:A:N6	32:B5:859:A:H5'	2.35	0.41
32:B5:821:U:C4	32:B5:852:C:N3	2.88	0.41
32:B5:1325:A:H2'	32:B5:1326:A:H8	1.85	0.41
32:B5:1344:A:O2'	32:B5:1345:A:OP1	2.33	0.41
33:AA:30:ARG:HG2	33:AA:74:GLU:HG3	2.03	0.41
33:AA:68:LYS:NZ	33:AA:70:ARG:HD3	2.36	0.41
35:AC:170:LYS:HD2	35:AC:175:HIS:ND1	2.35	0.41
35:AC:304:GLN:C	35:AC:306:THR:H	2.28	0.41
36:A1:243:G:H2'	36:A1:244:G:C8	2.56	0.41
36:A1:266:A:H2'	69:Ai:30:LYS:HE3	2.03	0.41
36:A1:380:U:H2'	36:A1:381:U:C6	2.55	0.41
36:A1:412:G:H2'	36:A1:413:U:C6	2.56	0.41
36:A1:508:U:H2'	36:A1:509:U:C6	2.56	0.41
36:A1:627:U:H2'	36:A1:628:A:H8	1.85	0.41
36:A1:1637:A:H4'	60:AZ:15:ARG:HB3	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:2416:U:H2'	36:A1:2417:OMU:C6	2.50	0.41
36:A1:2611:U:H2'	36:A1:2612:U:H6	1.85	0.41
38:A4:51:G:OP2	72:A1:21:ARG:NH1	2.41	0.41
38:A4:145:U:H2'	38:A4:146:U:C6	2.56	0.41
39:AD:56:THR:OG1	39:AD:59:ASP:HB3	2.21	0.41
44:A1:51:HIS:HD2	54:AT:160:ILE:HG21	1.86	0.41
49:AO:46[A]:GLU:HG3	49:AO:49[A]:ARG:H	1.86	0.41
65:Ae:115:LEU:HB2	65:Ae:117:ILE:CD1	2.50	0.41
79:DC:18:ASN:ND2	79:DC:93:THR:OG1	2.52	0.41
79:DC:25:ILE:HG13	79:DC:127:VAL:HG12	2.02	0.41
82:VA:101:VAL:HA	82:VA:104:ARG:HH21	1.86	0.41
1:BA:76:ILE:HB	1:BA:123:VAL:HA	2.01	0.41
1:BA:147:THR:OG1	1:BA:159:ALA:HB1	2.21	0.41
1:BA:188:LEU:HA	1:BA:188:LEU:HD12	1.84	0.41
1:BA:198:MET:HE1	1:BA:200:ASP:HB2	2.02	0.41
2:BB:47:LEU:CD1	11:BO:37:GLU:HG2	2.50	0.41
4:BE:201:HIS:CD2	4:BE:207:LEU:HD12	2.56	0.41
7:BI:56:ARG:NH2	32:B5:331:A:H5''	2.36	0.41
8:BJ:113:VAL:HG22	8:BJ:156:ILE:HG21	2.02	0.41
12:BV:60:ARG:HG2	12:BV:65:SER:OG	2.21	0.41
14:BX:69:ARG:HA	14:BX:69:ARG:HD3	1.86	0.41
17:Bb:61:THR:O	17:Bb:62:ILE:HG23	2.21	0.41
19:BD:148:LYS:HE2	19:BD:148:LYS:HB3	1.83	0.41
20:BF:69:PHE:HZ	23:BQ:53:LEU:HD22	1.85	0.41
20:BF:124:LEU:HA	28:BZ:58:ARG:HH21	1.86	0.41
21:BK:20:VAL:HG12	21:BK:67:THR:HA	2.03	0.41
21:BK:51:SER:HB3	32:B5:1220:C:H5'	2.03	0.41
23:BQ:75:VAL:HB	32:B5:1609:U:H5''	2.02	0.41
26:BT:88:VAL:O	32:B5:1467:C:O2'	2.32	0.41
27:BU:48:HIS:HB3	27:BU:50:LEU:HD23	2.03	0.41
31:Bg:192:PHE:HB3	31:Bg:223:TRP:CE2	2.56	0.41
31:Bg:302:PHE:CD1	31:Bg:312:VAL:HG22	2.56	0.41
32:B5:80:A:H3'	32:B5:81:G:H5'	2.02	0.41
32:B5:227:U:N3	32:B5:233:C:O2	2.54	0.41
32:B5:415:C:O2'	32:B5:418:G:O6	2.26	0.41
32:B5:445:A:H1'	32:B5:525:A:OP1	2.21	0.41
32:B5:446:A:C6	32:B5:447:U:C4	3.09	0.41
32:B5:855:A:O2'	32:B5:856:A:H3'	2.21	0.41
32:B5:886:U:C2	32:B5:887:A:C8	3.08	0.41
32:B5:1036:A:H2'	32:B5:1037:C:C6	2.56	0.41
32:B5:1210:C:H2'	32:B5:1211:A:C8	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B5:1226:A:H5'	32:B5:1230:A:H5'	2.03	0.41
32:B5:1436:A:H2'	32:B5:1437:U:O4'	2.21	0.41
32:B5:1590:G:H2'	32:B5:1591:C:C6	2.56	0.41
32:B5:1669:U:H2'	32:B5:1670:G:O4'	2.20	0.41
34:AB:94:GLU:OE1	34:AB:94:GLU:N	2.54	0.41
34:AB:323:MET:HE3	34:AB:323:MET:HB2	1.79	0.41
35:AC:11:LEU:HD23	35:AC:11:LEU:HA	1.83	0.41
36:A1:277:G:H5'	75:Ao:49:GLY:HA2	2.03	0.41
36:A1:313:A:H2'	36:A1:314:U:C6	2.56	0.41
36:A1:424:G:O2'	65:Ae:23:ASP:OD2	2.32	0.41
36:A1:1245:A:H2'	36:A1:1272:C:OP1	2.20	0.41
36:A1:1596:C:H2'	36:A1:1597:C:H6	1.85	0.41
36:A1:2421:OMU:O2'	75:Ao:52:GLY:HA3	2.21	0.41
36:A1:2467:G:H1'	36:A1:2468:A:C8	2.56	0.41
36:A1:2555:G:C6	67:Ag:95:ILE:HD11	2.54	0.41
36:A1:2883:U:H2'	36:A1:2884:C:C6	2.56	0.41
36:A1:2986:U:H2'	36:A1:2987:A:H8	1.85	0.41
36:A1:3066:U:H2'	36:A1:3067:C:H6	1.86	0.41
36:A1:3117:C:H2'	36:A1:3118:C:O4'	2.21	0.41
37:A3:45:A:H2'	37:A3:46:A:C8	2.55	0.41
39:AD:226:TYR:HD1	39:AD:231:ILE:HB	1.85	0.41
44:AI:206:LEU:HD12	44:AI:206:LEU:HA	1.92	0.41
45:AJ:49:LYS:HA	45:AJ:64:LYS:H	1.86	0.41
47:AM:14:LEU:H	47:AM:19:ARG:NH2	2.17	0.41
47:AM:21:VAL:HG23	47:AM:65:LEU:HA	2.02	0.41
47:AM:112:LEU:HD21	49:AO:197[A]:LEU:O	2.21	0.41
48:AN:105:ARG:HG2	48:AN:108:ARG:HH22	1.85	0.41
49:AO:89[A]:SER:O	49:AO:95[A]:GLY:HA3	2.21	0.41
50:AP:30:ARG:HD2	50:AP:63:PHE:CE2	2.55	0.41
52:AR:156:ASN:O	52:AR:160:GLU:OE1	2.39	0.41
68:Ah:105:ARG:O	68:Ah:109:ILE:HG12	2.21	0.41
77:E:26:ARG:HD2	77:E:30:GLU:OE2	2.20	0.41
78:EC:6924:G:C2	78:EC:6930:G:C2	3.09	0.41
78:EC:6932:G:H2'	78:EC:6933:G:H8	1.86	0.41
79:DC:188:ILE:HG13	79:DC:192:TYR:CE2	2.55	0.41
79:DC:463:LEU:HD23	79:DC:463:LEU:HA	1.94	0.41
79:DC:481:MET:O	79:DC:483:PHE:N	2.54	0.41
79:DC:726:GLU:N	79:DC:802:SER:O	2.46	0.41
2:BB:103:MET:HE3	2:BB:215:VAL:HG23	2.01	0.41
16:Ba:60:PRO:O	16:Ba:61:GLU:HG2	2.21	0.41
20:BF:140:THR:CG2	20:BF:210:ALA:HB1	2.50	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BP:108:ARG:HG3	22:BP:109:PRO:HD2	2.02	0.41
25:BS:116:LEU:HA	25:BS:119:ILE:HD12	2.04	0.41
26:BT:2:PRO:HB2	26:BT:3:GLY:H	1.60	0.41
31:Bg:69:GLN:N	31:Bg:83:ALA:O	2.40	0.41
32:B5:971:A:H2'	32:B5:972:G:O4'	2.20	0.41
32:B5:1439:C:H2'	32:B5:1440:C:C6	2.56	0.41
32:B5:1723:U:H2'	32:B5:1724:U:O4'	2.21	0.41
33:AA:62:VAL:HA	33:AA:72:ARG:O	2.20	0.41
35:AC:131:VAL:O	35:AC:135:VAL:HG23	2.21	0.41
36:A1:269:G:H5''	48:AN:14:LYS:HE2	2.03	0.41
36:A1:279:U:O4	75:Ao:45:ARG:NH2	2.46	0.41
36:A1:289:A:H2'	36:A1:290:G:C8	2.54	0.41
36:A1:698:U:H2'	36:A1:699:A:O4'	2.21	0.41
36:A1:792:G:H5''	61:Aa:2:PRO:HD3	2.02	0.41
36:A1:1224:C:C2	36:A1:1225:A:C8	3.08	0.41
36:A1:1719:G:N7	52:AR:121:HIS:HE1	2.19	0.41
38:A4:57:C:O2'	38:A4:58:G:H5'	2.22	0.41
39:AD:205:SER:HB3	39:AD:236:LEU:HD23	2.02	0.41
40:AE:108:LYS:HE2	40:AE:108:LYS:HB3	1.87	0.41
47:AM:105:GLN:HE22	47:AM:109:ARG:CZ	2.34	0.41
69:Ai:81:THR:HA	69:Ai:84:LYS:HE3	2.02	0.41
79:DC:275:MET:HA	79:DC:279:ASP:OD2	2.20	0.41
82:VA:8:LYS:HG2	82:VA:58:MET:HE3	2.02	0.41
1:BA:58:VAL:O	1:BA:62:ARG:HG3	2.21	0.40
2:BB:205:PHE:CD1	32:B5:1065:A:H4'	2.56	0.40
4:BE:44:LEU:HD23	4:BE:82:TYR:HB3	2.03	0.40
4:BE:149:TYR:N	4:BE:150:PRO:HD3	2.35	0.40
4:BE:183:VAL:HG13	4:BE:220:THR:HG21	2.03	0.40
11:BO:40:ALA:HB2	11:BO:70:LYS:CG	2.51	0.40
11:BO:129:LYS:HG2	11:BO:130:GLY:N	2.36	0.40
16:Ba:18:VAL:O	16:Ba:19:LYS:HB2	2.21	0.40
20:BF:63:GLN:HE22	20:BF:66:GLN:N	2.03	0.40
25:BS:29:VAL:HG23	25:BS:54:LEU:HD12	2.02	0.40
32:B5:24:U:O2'	32:B5:26:A:OP1	2.39	0.40
32:B5:272:U:O3'	32:B5:273:G:H8	2.03	0.40
32:B5:453:U:H2'	32:B5:454:U:H5''	2.03	0.40
32:B5:1494:C:H2'	32:B5:1495:C:H6	1.87	0.40
32:B5:1642:G:H5'	74:An:1:MET:HG2	2.03	0.40
34:AB:214:MET:HG3	34:AB:279:ASN:HA	2.03	0.40
34:AB:276:THR:CG2	36:A1:3137:C:H5''	2.49	0.40
36:A1:340:C:H2'	36:A1:341:G:O4'	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:630:A:H2'	36:A1:631:U:C6	2.57	0.40
36:A1:978:G:N2	36:A1:979:U:O4	2.35	0.40
36:A1:1306:G:O2'	36:A1:1307:G:H5''	2.20	0.40
36:A1:1622:U:H2'	36:A1:1623:G:C8	2.56	0.40
36:A1:2218:G:H2'	36:A1:2219:A:H8	1.87	0.40
36:A1:2465:G:N2	77:E:33:GLU:HG3	2.33	0.40
36:A1:2585:G:N3	36:A1:2585:G:H2'	2.35	0.40
36:A1:2756:C:O4'	54:AT:49:GLN:HG2	2.21	0.40
36:A1:3305:A:H2'	36:A1:3306:U:O4'	2.20	0.40
37:A3:38:U:N3	37:A3:41:G:OP2	2.30	0.40
39:AD:182:GLY:HA2	39:AD:194:LEU:HD23	2.02	0.40
42:AG:34:PHE:CD1	42:AG:42:PRO:HD3	2.55	0.40
42:AG:205:ALA:HA	42:AG:208:GLU:HG2	2.02	0.40
45:AJ:90:GLN:HE21	45:AJ:173:ASP:CG	2.29	0.40
49:AO:7[A]:VAL:HB	49:AO:33[A]:ILE:HD13	2.03	0.40
51:AQ:55:SER:O	51:AQ:59:ARG:HG2	2.20	0.40
53:AS:8:GLN:HG2	53:AS:62:ASN:HB2	2.04	0.40
61:Aa:116:GLY:HA3	61:Aa:137:LYS:NZ	2.36	0.40
64:Ad:28:ARG:HB2	64:Ad:64:VAL:O	2.22	0.40
73:Am:79:GLU:O	73:Am:81:SER:N	2.55	0.40
77:E:19:TYR:O	77:E:23:THR:OG1	2.29	0.40
79:DC:79:SER:HB3	79:DC:335:LEU:HD22	2.02	0.40
1:BA:116:LYS:HE2	1:BA:116:LYS:HB2	1.61	0.40
4:BE:128:LYS:HG2	4:BE:140:VAL:HB	2.02	0.40
4:BE:130:GLN:HB3	4:BE:138:TYR:CZ	2.57	0.40
5:BG:14:LYS:HD3	5:BG:14:LYS:HA	1.93	0.40
5:BG:89:ASP:OD1	5:BG:89:ASP:N	2.54	0.40
5:BG:174:LYS:HE2	32:B5:65:A:H3'	2.03	0.40
6:BH:104:ARG:NH1	32:B5:803:A:O2'	2.53	0.40
7:BI:31:ARG:HH11	32:B5:332:U:H5''	1.87	0.40
14:BX:65:ASN:HD22	14:BX:116:ASP:CG	2.29	0.40
19:BD:223:LYS:HB3	31:Bg:191:ASP:HB3	2.02	0.40
25:BS:11:PHE:CE2	25:BS:59:GLY:HA3	2.56	0.40
26:BT:75:LYS:HG2	32:B5:1498:G:OP1	2.21	0.40
29:Bc:65:ARG:O	29:Bc:65:ARG:HG3	2.21	0.40
32:B5:100:A2M:H8	32:B5:100:A2M:O5'	2.21	0.40
32:B5:220:A:H5''	32:B5:832:U:O2'	2.21	0.40
32:B5:241:U:H2'	32:B5:242:U:C6	2.55	0.40
32:B5:510:G:H2'	32:B5:511:A:C8	2.56	0.40
32:B5:781:U:H4'	32:B5:782:U:C6	2.56	0.40
32:B5:1673:G:H2'	32:B5:1674:C:H6	1.86	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:100:A:H2'	36:A1:101:G:N3	2.36	0.40
36:A1:217:U:H4'	59:AY:100:HIS:CD2	2.56	0.40
36:A1:293:C:H2'	36:A1:294:U:O4'	2.21	0.40
36:A1:798:G:H4'	46:AL:15:ARG:CZ	2.51	0.40
36:A1:810:A:H2'	36:A1:811:U:C6	2.56	0.40
36:A1:1048:A:H2'	44:AI:22:TYR:CZ	2.57	0.40
36:A1:1333:C:C2	36:A1:1334:U:C5	3.09	0.40
36:A1:1770:G:H2'	36:A1:1771:C:C6	2.56	0.40
36:A1:1948:G:C2	36:A1:2099:A:C2	3.09	0.40
36:A1:2364:G:H22	36:A1:2396:G:H1'	1.86	0.40
36:A1:2373:A:N3	36:A1:2824:G:O2'	2.33	0.40
36:A1:2493:U:O2'	36:A1:2494:A:H8	2.05	0.40
42:AG:26:LEU:HB3	60:AZ:53:VAL:HG21	2.03	0.40
46:AL:63:VAL:HG22	61:Aa:128:ARG:NH1	2.37	0.40
59:AY:32:SER:HA	59:AY:49:PRO:HA	2.03	0.40
60:AZ:48:ARG:HB2	60:AZ:69:LYS:HB3	2.04	0.40
75:Ao:8:ARG:O	75:Ao:23:HIS:N	2.49	0.40
78:EC:6843:U:H5'	78:EC:6844:A:C2	2.57	0.40
79:DC:647:ILE:HD11	79:DC:685:ARG:HE	1.85	0.40
2:BB:26:ARG:HB2	2:BB:50:LYS:HG2	2.03	0.40
4:BE:12:LEU:O	32:B5:756:A:H1'	2.22	0.40
5:BG:64:LYS:HB2	5:BG:97:VAL:HB	2.03	0.40
5:BG:160:ARG:NH2	32:B5:66:U:H1'	2.35	0.40
6:BH:50:ASP:HA	6:BH:56:LYS:HA	2.02	0.40
13:BW:88:LYS:HA	13:BW:88:LYS:HD3	1.88	0.40
19:BD:132:LYS:HE2	19:BD:191:ASP:OD1	2.21	0.40
21:BK:60:SER:HB2	21:BK:65:TYR:CE1	2.56	0.40
22:BP:96:ILE:HB	22:BP:120:SER:HB2	2.02	0.40
23:BQ:129:PHE:CE2	27:BU:78:THR:HA	2.56	0.40
25:BS:29:VAL:HA	25:BS:43:SER:OG	2.22	0.40
25:BS:40:ARG:O	25:BS:44:ASN:HB2	2.22	0.40
25:BS:121:ALA:O	25:BS:125:ILE:HD12	2.21	0.40
31:Bg:205:SER:HB3	31:Bg:210:LEU:HD12	2.04	0.40
32:B5:13:C:H4'	32:B5:1298:U:O2	2.21	0.40
32:B5:148:A:N6	32:B5:166:C:C2	2.89	0.40
32:B5:809:A:H2'	32:B5:810:G:C8	2.56	0.40
32:B5:1405:G:H2'	32:B5:1406:A:C8	2.56	0.40
34:AB:19:ARG:HB2	34:AB:232:ARG:NH2	2.37	0.40
34:AB:375:GLU:OE2	57:AW:14:TYR:OH	2.33	0.40
36:A1:744:A:H2'	36:A1:745:C:O4'	2.21	0.40
36:A1:1500:G:H2'	36:A1:1501:U:O4'	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1667:A:H2'	36:A1:1668:G:H8	1.85	0.40
36:A1:1728:G:O2'	63:Ac:87:VAL:HG12	2.21	0.40
36:A1:2730:G:H4'	51:AQ:184:PHE:CG	2.56	0.40
36:A1:2812:C:H2'	36:A1:2813:A:C8	2.56	0.40
36:A1:2923:U:H2'	36:A1:2924:U:C6	2.56	0.40
36:A1:2930:A:H2'	36:A1:2931:C:H6	1.84	0.40
36:A1:2998:U:H2'	36:A1:2999:U:O4'	2.21	0.40
36:A1:3163:A:N6	36:A1:3288:G:O6	2.54	0.40
36:A1:3272:C:O2	40:AE:80:ASN:ND2	2.55	0.40
36:A1:3296:A:H2'	36:A1:3297:U:C6	2.55	0.40
42:AG:201:THR:OG1	42:AG:202:GLU:OE1	2.17	0.40
45:AJ:15:GLU:HB2	45:AJ:132:ASN:OD1	2.20	0.40
45:AJ:85:LYS:C	45:AJ:88:GLU:H	2.29	0.40
47:AM:117:ARG:O	47:AM:120:VAL:HG22	2.21	0.40
52:AR:90:PRO:O	52:AR:93:VAL:HG22	2.22	0.40
57:AW:50:ALA:HA	57:AW:55:PHE:CG	2.57	0.40
67:Ag:72:VAL:HG12	67:Ag:73:SER:N	2.36	0.40
69:Ai:11:LEU:HD23	69:Ai:11:LEU:HA	1.94	0.40
78:EC:6844:A:O2'	78:EC:6845:G:N7	2.47	0.40
79:DC:204:PRO:HA	79:DC:209:VAL:HB	2.04	0.40
79:DC:420:PRO:HG3	79:DC:476:HIS:CE1	2.56	0.40
81:BM:29:LYS:HD2	81:BM:100:TRP:CD2	2.56	0.40
82:VA:16:ARG:HB2	82:VA:66:PHE:CZ	2.56	0.40
3:BC:44:LEU:HD21	3:BC:247:ALA:HB2	2.04	0.40
4:BE:197:HIS:HB2	32:B5:736:C:OP1	2.21	0.40
5:BG:20:ASP:HB3	5:BG:22:HIS:NE2	2.36	0.40
6:BH:30:SER:O	6:BH:34:LEU:N	2.55	0.40
7:BI:141:ARG:HH12	32:B5:190:C:H5	1.69	0.40
11:BO:50:ALA:C	11:BO:52:ARG:H	2.29	0.40
21:BK:52:LYS:HE3	32:B5:1220:C:H5''	2.03	0.40
24:BR:100:LEU:HB3	24:BR:102:VAL:HG13	2.04	0.40
31:Bg:113:VAL:HG12	31:Bg:124:SER:OG	2.20	0.40
31:Bg:116:ASP:HB3	31:Bg:121:MET:H	1.87	0.40
32:B5:93:A:C6	32:B5:398:G:C6	3.10	0.40
32:B5:472:U:H2'	32:B5:473:A:C8	2.55	0.40
32:B5:1623:C:H2'	32:B5:1624:C:C6	2.56	0.40
32:B5:1755:A:H4'	36:A1:2256:A2M:N6	2.37	0.40
33:AA:2:GLY:O	36:A1:925:A:N6	2.36	0.40
33:AA:181:LYS:HB2	36:A1:860:G:C6	2.56	0.40
36:A1:549:U:H2'	36:A1:550:A:C8	2.54	0.40
36:A1:640:U:H2'	36:A1:641:C:C6	2.57	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:641:C:H2'	36:A1:642:U:O4'	2.21	0.40
36:A1:701:G:H2'	36:A1:702:C:C6	2.57	0.40
36:A1:1941:C:H2'	36:A1:1942:U:C6	2.57	0.40
36:A1:2555:G:N2	60:AZ:135:ARG:O	2.30	0.40
36:A1:2834:G:H2'	36:A1:2835:U:H6	1.86	0.40
36:A1:3012:A:OP2	36:A1:3099:C:H5	2.04	0.40
36:A1:3089:C:H2'	36:A1:3090:U:O4'	2.21	0.40
42:AG:89:GLU:HA	42:AG:92:LYS:HE2	2.02	0.40
43:AH:90:MET:HE1	43:AH:162:GLN:HB2	2.04	0.40
58:AX:50:ALA:O	68:Ah:66:VAL:HG21	2.22	0.40
59:AY:51:ARG:HG2	59:AY:52:ARG:H	1.86	0.40
66:Af:51:TYR:HB3	66:Af:67:MET:HB2	2.03	0.40
75:Ao:12:CYS:HB2	75:Ao:23:HIS:CE1	2.57	0.40
77:E:10:ARG:HD3	77:E:180:VAL:HG21	2.03	0.40
79:DC:19:VAL:HA	79:DC:99:LEU:O	2.22	0.40
79:DC:26:ALA:HB2	79:DC:128:VAL:HB	2.03	0.40
79:DC:212:GLY:HA3	79:DC:219:ALA:HA	2.03	0.40
79:DC:373:ASP:OD1	79:DC:373:ASP:N	2.54	0.40
82:VA:101:VAL:O	82:VA:104:ARG:NE	2.53	0.40
1:BA:64:ILE:HG23	1:BA:73:VAL:HG11	2.02	0.40
2:BB:87:ARG:HB2	2:BB:101:HIS:HB2	2.03	0.40
4:BE:66:MET:HB3	32:B5:454:U:C4	2.56	0.40
5:BG:59:GLN:H	32:B5:155:U:H4'	1.87	0.40
8:BJ:49:LEU:O	8:BJ:53:ARG:HB2	2.21	0.40
20:BF:49:GLU:C	20:BF:50:GLU:HG3	2.47	0.40
20:BF:161:ASP:O	29:Bc:45:LYS:N	2.46	0.40
23:BQ:114:ARG:HG3	23:BQ:118:ILE:HD12	2.03	0.40
25:BS:65:GLU:HG2	25:BS:68:ARG:NH2	2.37	0.40
26:BT:122:ARG:HH22	32:B5:1500:C:P	2.45	0.40
29:Bc:19:THR:HG21	29:Bc:27:GLN:HG3	2.03	0.40
29:Bc:40:ILE:HG12	29:Bc:41:VAL:H	1.87	0.40
30:Bd:29:GLY:O	30:Bd:40:ARG:N	2.49	0.40
32:B5:5:U:O2'	32:B5:553:G:H4'	2.21	0.40
32:B5:119:A:H1'	32:B5:397:A:C5	2.56	0.40
32:B5:365:G:H5'	32:B5:758:U:O2	2.22	0.40
32:B5:973:A:H4'	36:A1:848:A:C8	2.56	0.40
32:B5:1044:U:H2'	32:B5:1045:C:H6	1.87	0.40
32:B5:1082:C:H6	32:B5:1082:C:H2'	1.70	0.40
33:AA:65:ASP:HB3	33:AA:68:LYS:O	2.21	0.40
36:A1:644:G:H2'	36:A1:2372:A:N7	2.37	0.40
36:A1:1088:U:C2	36:A1:1089:G:C8	3.10	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1153:A:O2'	36:A1:1154:A:H5'	2.21	0.40
36:A1:1708:C:H2'	36:A1:1709:C:H6	1.87	0.40
36:A1:2282:U:OP1	36:A1:2973:G:O2'	2.30	0.40
36:A1:2606:G:N3	36:A1:2606:G:H2'	2.37	0.40
37:A3:71:G:H2'	37:A3:72:A:H8	1.83	0.40
39:AD:211:LEU:HD23	39:AD:211:LEU:HA	1.87	0.40
48:AN:114:ARG:HG3	48:AN:151:ILE:HG13	2.03	0.40
50:AP:103:GLU:OE2	50:AP:109:ALA:HB2	2.21	0.40
52:AR:135:LYS:O	52:AR:139:VAL:HG23	2.22	0.40
53:AS:26:ARG:HG2	53:AS:27:MET:N	2.35	0.40
55:AU:35:LYS:HE2	55:AU:35:LYS:HB2	1.87	0.40
60:AZ:95:VAL:HG22	60:AZ:110:ALA:HA	2.02	0.40
65:Ae:96:ILE:HG21	65:Ae:105:ARG:HG2	2.03	0.40
77:E:113:SER:HA	77:E:138:VAL:HG12	2.03	0.40
81:BM:119:SER:O	81:BM:121:VAL:HG23	2.21	0.40
82:VA:27:VAL:HB	82:VA:189:GLN:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	177 (87%)	27 (13%)	0	100	100
2	BB	212/255 (83%)	178 (84%)	34 (16%)	0	100	100
3	BC	215/254 (85%)	206 (96%)	9 (4%)	0	100	100
4	BE	258/261 (99%)	243 (94%)	15 (6%)	0	100	100
5	BG	224/236 (95%)	212 (95%)	12 (5%)	0	100	100
6	BH	182/190 (96%)	168 (92%)	14 (8%)	0	100	100
7	BI	184/200 (92%)	163 (89%)	21 (11%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	BJ	183/197 (93%)	172 (94%)	11 (6%)	0	100	100
9	BL	153/156 (98%)	142 (93%)	11 (7%)	0	100	100
10	BN	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
11	BO	125/137 (91%)	114 (91%)	11 (9%)	0	100	100
12	BV	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
13	BW	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
14	BX	142/145 (98%)	123 (87%)	19 (13%)	0	100	100
15	BY	132/135 (98%)	122 (92%)	10 (8%)	0	100	100
16	Ba	95/119 (80%)	78 (82%)	17 (18%)	0	100	100
17	Bb	79/82 (96%)	69 (87%)	10 (13%)	0	100	100
18	Be	58/63 (92%)	50 (86%)	8 (14%)	0	100	100
19	BD	221/240 (92%)	204 (92%)	17 (8%)	0	100	100
20	BF	204/225 (91%)	192 (94%)	12 (6%)	0	100	100
21	BK	94/105 (90%)	85 (90%)	9 (10%)	0	100	100
22	BP	122/142 (86%)	111 (91%)	11 (9%)	0	100	100
23	BQ	139/143 (97%)	133 (96%)	6 (4%)	0	100	100
24	BR	123/136 (90%)	116 (94%)	7 (6%)	0	100	100
25	BS	143/146 (98%)	125 (87%)	18 (13%)	0	100	100
26	BT	139/144 (96%)	129 (93%)	10 (7%)	0	100	100
27	BU	105/121 (87%)	98 (93%)	7 (7%)	0	100	100
28	BZ	67/108 (62%)	62 (92%)	5 (8%)	0	100	100
29	Bc	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
30	Bd	51/56 (91%)	48 (94%)	3 (6%)	0	100	100
31	Bg	310/319 (97%)	277 (89%)	33 (11%)	0	100	100
33	AA	245/254 (96%)	231 (94%)	14 (6%)	0	100	100
34	AB	383/387 (99%)	365 (95%)	18 (5%)	0	100	100
35	AC	359/362 (99%)	332 (92%)	27 (8%)	0	100	100
39	AD	290/297 (98%)	271 (93%)	19 (7%)	0	100	100
40	AE	152/176 (86%)	139 (91%)	13 (9%)	0	100	100
41	AF	220/244 (90%)	212 (96%)	8 (4%)	0	100	100
42	AG	228/256 (89%)	209 (92%)	19 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	AH	188/191 (98%)	174 (93%)	14 (7%)	0	100	100
44	AI	201/221 (91%)	188 (94%)	13 (6%)	0	100	100
45	AJ	167/174 (96%)	150 (90%)	17 (10%)	0	100	100
46	AL	191/199 (96%)	181 (95%)	10 (5%)	0	100	100
47	AM	134/138 (97%)	129 (96%)	5 (4%)	0	100	100
48	AN	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
49	AO	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
50	AP	171/184 (93%)	165 (96%)	6 (4%)	0	100	100
51	AQ	183/186 (98%)	177 (97%)	6 (3%)	0	100	100
52	AR	186/189 (98%)	179 (96%)	7 (4%)	0	100	100
53	AS	170/178 (96%)	162 (95%)	8 (5%)	0	100	100
54	AT	157/160 (98%)	147 (94%)	10 (6%)	0	100	100
55	AU	98/121 (81%)	89 (91%)	9 (9%)	0	100	100
56	AV	134/137 (98%)	131 (98%)	3 (2%)	0	100	100
57	AW	61/155 (39%)	61 (100%)	0	0	100	100
58	AX	119/142 (84%)	116 (98%)	3 (2%)	0	100	100
59	AY	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
60	AZ	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
61	Aa	146/149 (98%)	134 (92%)	12 (8%)	0	100	100
62	Ab	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
63	Ac	95/105 (90%)	95 (100%)	0	0	100	100
64	Ad	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
65	Ae	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
66	Af	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
67	Ag	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
68	Ah	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
69	Ai	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
70	Aj	85/88 (97%)	81 (95%)	4 (5%)	0	100	100
71	Ak	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
72	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
73	Am	50/128 (39%)	48 (96%)	2 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	An	23/25 (92%)	23 (100%)	0	0	100	100
75	Ao	103/106 (97%)	92 (89%)	11 (11%)	0	100	100
76	Ap	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
77	E	215/217 (99%)	197 (92%)	18 (8%)	0	100	100
79	DC	819/842 (97%)	754 (92%)	65 (8%)	0	100	100
80	Bf	73/152 (48%)	67 (92%)	6 (8%)	0	100	100
81	BM	122/143 (85%)	110 (90%)	12 (10%)	0	100	100
82	VA	187/312 (60%)	169 (90%)	18 (10%)	0	100	100
All	All	12121/13257 (91%)	11282 (93%)	839 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	173/210 (82%)	173 (100%)	0	100	100
2	BB	191/224 (85%)	191 (100%)	0	100	100
3	BC	176/205 (86%)	176 (100%)	0	100	100
4	BE	221/222 (100%)	221 (100%)	0	100	100
5	BG	193/201 (96%)	193 (100%)	0	100	100
6	BH	165/170 (97%)	165 (100%)	0	100	100
7	BI	150/161 (93%)	150 (100%)	0	100	100
8	BJ	158/166 (95%)	158 (100%)	0	100	100
9	BL	136/137 (99%)	136 (100%)	0	100	100
10	BN	127/128 (99%)	127 (100%)	0	100	100
11	BO	96/105 (91%)	96 (100%)	0	100	100
12	BV	74/74 (100%)	74 (100%)	0	100	100
13	BW	110/111 (99%)	110 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	BX	119/120 (99%)	119 (100%)	0	100	100
15	BY	112/113 (99%)	112 (100%)	0	100	100
16	Ba	83/100 (83%)	83 (100%)	0	100	100
17	Bb	70/71 (99%)	70 (100%)	0	100	100
18	Be	51/54 (94%)	51 (100%)	0	100	100
19	BD	182/195 (93%)	182 (100%)	0	100	100
20	BF	173/191 (91%)	173 (100%)	0	100	100
21	BK	89/98 (91%)	89 (100%)	0	100	100
22	BP	104/118 (88%)	104 (100%)	0	100	100
23	BQ	117/119 (98%)	117 (100%)	0	100	100
24	BR	113/124 (91%)	113 (100%)	0	100	100
25	BS	128/129 (99%)	128 (100%)	0	100	100
26	BT	113/116 (97%)	113 (100%)	0	100	100
27	BU	100/114 (88%)	100 (100%)	0	100	100
28	BZ	61/89 (68%)	61 (100%)	0	100	100
29	Bc	56/60 (93%)	56 (100%)	0	100	100
30	Bd	47/49 (96%)	47 (100%)	0	100	100
31	Bg	256/262 (98%)	256 (100%)	0	100	100
33	AA	189/196 (96%)	189 (100%)	0	100	100
34	AB	321/322 (100%)	321 (100%)	0	100	100
35	AC	288/289 (100%)	288 (100%)	0	100	100
39	AD	241/245 (98%)	241 (100%)	0	100	100
40	AE	134/153 (88%)	134 (100%)	0	100	100
41	AF	186/205 (91%)	186 (100%)	0	100	100
42	AG	189/208 (91%)	189 (100%)	0	100	100
43	AH	170/171 (99%)	170 (100%)	0	100	100
44	AI	176/187 (94%)	176 (100%)	0	100	100
45	AJ	147/150 (98%)	147 (100%)	0	100	100
46	AL	154/159 (97%)	154 (100%)	0	100	100
47	AM	107/109 (98%)	107 (100%)	0	100	100
48	AN	175/176 (99%)	175 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	AO	160/162 (99%)	160 (100%)	0	100	100
50	AP	141/146 (97%)	141 (100%)	0	100	100
51	AQ	150/151 (99%)	150 (100%)	0	100	100
52	AR	153/154 (99%)	153 (100%)	0	100	100
53	AS	156/162 (96%)	156 (100%)	0	100	100
54	AT	136/137 (99%)	136 (100%)	0	100	100
55	AU	87/107 (81%)	87 (100%)	0	100	100
56	AV	104/105 (99%)	104 (100%)	0	100	100
57	AW	55/129 (43%)	55 (100%)	0	100	100
58	AX	105/118 (89%)	105 (100%)	0	100	100
59	AY	109/110 (99%)	109 (100%)	0	100	100
60	AZ	115/116 (99%)	115 (100%)	0	100	100
61	Aa	118/119 (99%)	118 (100%)	0	100	100
62	Ab	46/47 (98%)	46 (100%)	0	100	100
63	Ac	81/88 (92%)	81 (100%)	0	100	100
64	Ad	96/97 (99%)	96 (100%)	0	100	100
65	Ae	109/111 (98%)	109 (100%)	0	100	100
66	Af	90/91 (99%)	90 (100%)	0	100	100
67	Ag	95/103 (92%)	95 (100%)	0	100	100
68	Ah	104/105 (99%)	104 (100%)	0	100	100
69	Ai	81/82 (99%)	81 (100%)	0	100	100
70	Aj	70/71 (99%)	70 (100%)	0	100	100
71	Ak	68/69 (99%)	68 (100%)	0	100	100
72	Al	45/46 (98%)	45 (100%)	0	100	100
73	Am	47/116 (40%)	47 (100%)	0	100	100
74	An	23/23 (100%)	23 (100%)	0	100	100
75	Ao	90/91 (99%)	90 (100%)	0	100	100
76	Ap	71/72 (99%)	71 (100%)	0	100	100
77	E	198/198 (100%)	198 (100%)	0	100	100
79	DC	699/714 (98%)	699 (100%)	0	100	100
80	Bf	66/135 (49%)	66 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
81	BM	100/119 (84%)	100 (100%)	0	100	100
82	VA	160/254 (63%)	160 (100%)	0	100	100
All	All	10349/11154 (93%)	10349 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (164) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	23	HIS
1	BA	30	GLN
1	BA	131	GLN
1	BA	140	ASN
2	BB	49	ASN
2	BB	74	GLN
2	BB	209	ASN
2	BB	211	HIS
3	BC	108	ASN
3	BC	150	GLN
3	BC	209	ASN
4	BE	67	GLN
4	BE	130	GLN
4	BE	157	ASN
4	BE	231	GLN
5	BG	80	ASN
5	BG	197	ASN
5	BG	199	GLN
6	BH	5	GLN
6	BH	110	GLN
6	BH	161	GLN
6	BH	180	GLN
7	BI	103	GLN
7	BI	111	GLN
7	BI	175	GLN
8	BJ	112	GLN
8	BJ	139	GLN
9	BL	14	GLN
9	BL	81	HIS
9	BL	110	HIS
10	BN	36	GLN
11	BO	12	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	BV	74	GLN
13	BW	92	ASN
14	BX	18	HIS
14	BX	22	ASN
14	BX	27	ASN
14	BX	65	ASN
14	BX	75	GLN
14	BX	99	ASN
15	BY	22	GLN
15	BY	77	ASN
16	Ba	43	ASN
16	Ba	80	HIS
18	Be	17	GLN
19	BD	165	ASN
20	BF	63	GLN
20	BF	103	ASN
20	BF	104	ASN
20	BF	122	ASN
21	BK	81	ASN
22	BP	104	GLN
23	BQ	21	HIS
23	BQ	103	ASN
24	BR	31	ASN
24	BR	74	GLN
25	BS	25	ASN
25	BS	75	ASN
27	BU	40	ASN
28	BZ	44	GLN
28	BZ	98	GLN
30	Bd	37	ASN
31	Bg	147	HIS
31	Bg	148	ASN
31	Bg	153	GLN
33	AA	24	GLN
33	AA	47	GLN
33	AA	97	ASN
33	AA	215	ASN
34	AB	121	ASN
34	AB	182	GLN
34	AB	377	HIS
35	AC	9	HIS
35	AC	48	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
35	AC	260	GLN
35	AC	291	ASN
35	AC	304	GLN
39	AD	264	GLN
40	AE	102	ASN
41	AF	104	GLN
41	AF	194	HIS
41	AF	197	GLN
41	AF	199	ASN
41	AF	200	ASN
42	AG	145	ASN
42	AG	232	HIS
42	AG	243	GLN
43	AH	9	GLN
43	AH	96	HIS
43	AH	125	ASN
43	AH	157	ASN
44	AI	209	ASN
45	AJ	39	GLN
45	AJ	95	ASN
45	AJ	150	ASN
46	AL	103	ASN
46	AL	106	GLN
46	AL	120	GLN
46	AL	129	ASN
47	AM	41	GLN
47	AM	56	GLN
47	AM	105	GLN
47	AM	119	GLN
48	AN	11	GLN
48	AN	15	GLN
48	AN	86	ASN
48	AN	95	GLN
48	AN	182	ASN
49	AO	26[A]	GLN
49	AO	50[A]	ASN
50	AP	45	GLN
50	AP	121	GLN
51	AQ	45	ASN
51	AQ	145	ASN
52	AR	7	GLN
52	AR	39	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	AR	47	ASN
52	AR	150	GLN
53	AS	62	ASN
53	AS	88	HIS
54	AT	5	HIS
54	AT	112	ASN
54	AT	149	GLN
55	AU	87	ASN
55	AU	101	ASN
56	AV	98	ASN
56	AV	132	ASN
57	AW	42	GLN
58	AX	111	ASN
59	AY	26	GLN
59	AY	42	GLN
59	AY	81	GLN
60	AZ	78	ASN
60	AZ	122	HIS
60	AZ	128	GLN
61	Aa	120	ASN
65	Ae	13	HIS
66	Af	17	GLN
66	Af	26	ASN
66	Af	87	ASN
67	Ag	3	GLN
68	Ah	68	GLN
68	Ah	76	GLN
68	Ah	104	GLN
69	Ai	91	ASN
70	Aj	12	HIS
70	Aj	79	GLN
71	Ak	57	ASN
72	Al	4	GLN
72	Al	43	ASN
73	Am	120	GLN
77	E	96	ASN
77	E	200	ASN
79	DC	18	ASN
79	DC	138	GLN
79	DC	216	HIS
79	DC	603	ASN
79	DC	607	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	DC	654	GLN
79	DC	775	ASN
81	BM	84	ASN
82	VA	39	HIS
82	VA	163	ASN
82	VA	174	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	B5	1780/1798 (98%)	399 (22%)	11 (0%)
36	A1	3194/3360 (95%)	616 (19%)	26 (0%)
37	A3	120/121 (99%)	12 (10%)	1 (0%)
38	A4	157/158 (99%)	31 (19%)	0
78	EC	191/201 (95%)	109 (57%)	8 (4%)
All	All	5442/5638 (96%)	1167 (21%)	46 (0%)

All (1167) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
32	B5	4	C
32	B5	17	C
32	B5	26	A
32	B5	34	G
32	B5	40	A
32	B5	42	G
32	B5	43	A
32	B5	46	A
32	B5	47	A
32	B5	57	G
32	B5	60	U
32	B5	63	G
32	B5	67	A
32	B5	68	A
32	B5	72	A
32	B5	73	U
32	B5	74	U
32	B5	75	U
32	B5	76	A
32	B5	77	U
32	B5	78	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B5	81	G
32	B5	104	A
32	B5	114	C
32	B5	116	U
32	B5	127	G
32	B5	129	U
32	B5	130	C
32	B5	131	C
32	B5	132	U
32	B5	134	U
32	B5	135	A
32	B5	136	C
32	B5	137	U
32	B5	139	C
32	B5	141	U
32	B5	145	A
32	B5	166	C
32	B5	169	A
32	B5	176	C
32	B5	178	U
32	B5	179	A
32	B5	181	A
32	B5	182	A
32	B5	184	C
32	B5	186	C
32	B5	188	A
32	B5	190	C
32	B5	191	C
32	B5	192	U
32	B5	193	U
32	B5	194	U
32	B5	195	G
32	B5	196	G
32	B5	198	A
32	B5	200	A
32	B5	204	G
32	B5	207	U
32	B5	217	A
32	B5	218	A
32	B5	221	A
32	B5	224	C
32	B5	225	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B5	226	A
32	B5	227	U
32	B5	228	G
32	B5	229	U
32	B5	230	C
32	B5	232	U
32	B5	233	C
32	B5	234	G
32	B5	235	G
32	B5	239	C
32	B5	240	U
32	B5	241	U
32	B5	246	G
32	B5	257	A
32	B5	261	U
32	B5	262	U
32	B5	265	A
32	B5	278	U
32	B5	280	U
32	B5	281	G
32	B5	287	G
32	B5	299	A
32	B5	305	C
32	B5	314	C
32	B5	316	A
32	B5	321	C
32	B5	337	G
32	B5	338	C
32	B5	352	A
32	B5	353	A
32	B5	359	A
32	B5	360	A
32	B5	361	C
32	B5	390	G
32	B5	397	A
32	B5	400	A
32	B5	401	A
32	B5	402	C
32	B5	419	G
32	B5	423	G
32	B5	424	C
32	B5	425	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B5	426	G
32	B5	435	C
32	B5	439	U
32	B5	444	C
32	B5	452	A
32	B5	460	A
32	B5	475	A
32	B5	476	U
32	B5	477	A
32	B5	480	G
32	B5	485	A
32	B5	486	G
32	B5	489	C
32	B5	490	C
32	B5	491	C
32	B5	492	A
32	B5	494	U
32	B5	495	C
32	B5	496	G
32	B5	497	G
32	B5	498	G
32	B5	499	U
32	B5	500	C
32	B5	502	U
32	B5	503	G
32	B5	506	A
32	B5	507	U
32	B5	509	G
32	B5	514	G
32	B5	515	A
32	B5	518	A
32	B5	539	G
32	B5	540	G
32	B5	541	A2M
32	B5	542	A
32	B5	544	A
32	B5	554	C
32	B5	555	A
32	B5	557	G
32	B5	558	U
32	B5	559	C
32	B5	565	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B5	575	C
32	B5	577	G
32	B5	579	A
32	B5	580	A
32	B5	582	U
32	B5	594	A
32	B5	595	G
32	B5	606	A
32	B5	610	G
32	B5	611	U
32	B5	619	A2M
32	B5	620	A
32	B5	622	A
32	B5	623	A
32	B5	638	U
32	B5	639	U
32	B5	650	U
32	B5	652	G
32	B5	654	C
32	B5	656	G
32	B5	657	U
32	B5	658	C
32	B5	677	G
32	B5	678	A
32	B5	679	U
32	B5	681	U
32	B5	683	C
32	B5	693	U
32	B5	694	U
32	B5	696	C
32	B5	697	C
32	B5	700	C
32	B5	705	U
32	B5	708	C
32	B5	709	C
32	B5	712	G
32	B5	713	A
32	B5	715	U
32	B5	716	C
32	B5	717	C
32	B5	718	U
32	B5	719	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B5	720	G
32	B5	721	U
32	B5	722	G
32	B5	724	C
32	B5	725	U
32	B5	726	C
32	B5	727	U
32	B5	728	U
32	B5	730	G
32	B5	731	C
32	B5	733	A
32	B5	734	A
32	B5	735	C
32	B5	740	A
32	B5	741	C
32	B5	743	U
32	B5	753	A
32	B5	765	G
32	B5	766	U
32	B5	774	A
32	B5	775	G
32	B5	778	G
32	B5	781	U
32	B5	782	U
32	B5	783	G
32	B5	784	C
32	B5	789	A
32	B5	794	U
32	B5	812	A
32	B5	814	A
32	B5	819	G
32	B5	820	U
32	B5	823	G
32	B5	832	U
32	B5	833	U
32	B5	836	U
32	B5	837	G
32	B5	840	U
32	B5	846	G
32	B5	850	A
32	B5	851	U
32	B5	859	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B5	863	A
32	B5	864	U
32	B5	873	U
32	B5	876	G
32	B5	877	G
32	B5	886	U
32	B5	895	G
32	B5	898	A
32	B5	906	A
32	B5	914	G
32	B5	933	A
32	B5	935	U
32	B5	945	U
32	B5	951	A
32	B5	960	U
32	B5	966	A
32	B5	988	A
32	B5	992	A
32	B5	993	A
32	B5	1003	A
32	B5	1004	U
32	B5	1005	A
32	B5	1020	A
32	B5	1021	C
32	B5	1026	A
32	B5	1028	C
32	B5	1032	G
32	B5	1039	A
32	B5	1052	U
32	B5	1056	U
32	B5	1058	U
32	B5	1059	U
32	B5	1060	U
32	B5	1061	A
32	B5	1062	A
32	B5	1063	U
32	B5	1076	A
32	B5	1083	G
32	B5	1092	A
32	B5	1097	U
32	B5	1098	U
32	B5	1100	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B5	1138	A
32	B5	1150	G
32	B5	1158	C
32	B5	1159	C
32	B5	1185	U
32	B5	1194	A
32	B5	1196	A
32	B5	1199	G
32	B5	1200	G
32	B5	1201	G
32	B5	1202	A
32	B5	1217	A
32	B5	1218	G
32	B5	1226	A
32	B5	1227	A
32	B5	1228	G
32	B5	1229	G
32	B5	1231	U
32	B5	1243	G
32	B5	1244	A
32	B5	1245	G
32	B5	1246	C
32	B5	1251	U
32	B5	1256	A
32	B5	1257	U
32	B5	1269	OMU
32	B5	1276	U
32	B5	1286	U
32	B5	1301	U
32	B5	1312	A
32	B5	1314	U
32	B5	1315	U
32	B5	1316	G
32	B5	1321	A
32	B5	1340	U
32	B5	1345	A
32	B5	1346	A
32	B5	1355	C
32	B5	1358	G
32	B5	1362	U
32	B5	1363	U
32	B5	1364	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B5	1366	U
32	B5	1368	G
32	B5	1370	U
32	B5	1372	U
32	B5	1373	C
32	B5	1376	C
32	B5	1383	G
32	B5	1388	A
32	B5	1390	U
32	B5	1398	U
32	B5	1399	C
32	B5	1400	A
32	B5	1402	G
32	B5	1413	U
32	B5	1414	U
32	B5	1415	U
32	B5	1418	G
32	B5	1427	A
32	B5	1428	OMG
32	B5	1436	A
32	B5	1445	G
32	B5	1446	A
32	B5	1459	C
32	B5	1460	A
32	B5	1471	A
32	B5	1481	C
32	B5	1486	G
32	B5	1491	U
32	B5	1492	A
32	B5	1493	A
32	B5	1496	U
32	B5	1506	G
32	B5	1514	U
32	B5	1516	A
32	B5	1521	G
32	B5	1523	G
32	B5	1524	A
32	B5	1537	C
32	B5	1538	U
32	B5	1539	G
32	B5	1540	G
32	B5	1542	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B5	1557	U
32	B5	1559	A
32	B5	1572	OMG
32	B5	1573	A
32	B5	1574	G
32	B5	1575	G7M
32	B5	1576	A
32	B5	1584	G
32	B5	1600	A
32	B5	1601	G
32	B5	1616	G
32	B5	1619	C
32	B5	1635	A
32	B5	1645	G
32	B5	1646	C
32	B5	1657	U
32	B5	1658	G
32	B5	1680	G
32	B5	1683	C
32	B5	1684	U
32	B5	1688	U
32	B5	1689	A
32	B5	1700	C
32	B5	1701	A
32	B5	1703	C
32	B5	1715	G
32	B5	1716	C
32	B5	1717	G
32	B5	1730	A
32	B5	1756[A]	A
32	B5	1760	G
32	B5	1766	A
32	B5	1767	G
32	B5	1769	U
32	B5	1780	G
32	B5	1783	C
32	B5	1792	G
32	B5	1793	G
32	B5	1794	A
32	B5	1795	U
32	B5	1796	C
32	B5	1799	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	26	A
36	A1	34	A
36	A1	40	A
36	A1	43	A
36	A1	49	A
36	A1	59	G
36	A1	60	A
36	A1	65	A
36	A1	66	A
36	A1	77	A
36	A1	92	G
36	A1	99	A
36	A1	109	A
36	A1	110	G
36	A1	111	C
36	A1	116	A
36	A1	117	U
36	A1	120	G
36	A1	122	A
36	A1	123	A
36	A1	133	U
36	A1	134	U
36	A1	135	C
36	A1	136	G
36	A1	156	G
36	A1	157	A
36	A1	164	A
36	A1	165	A
36	A1	166	C
36	A1	167	U
36	A1	170	G
36	A1	174	C
36	A1	175	C
36	A1	176	G
36	A1	178	U
36	A1	179	C
36	A1	180	C
36	A1	181	U
36	A1	182	U
36	A1	187	A
36	A1	188	U
36	A1	190	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	199	A
36	A1	200	C
36	A1	206	G
36	A1	208	C
36	A1	210	U
36	A1	211	A
36	A1	219	A
36	A1	220	G
36	A1	229	G
36	A1	233	C
36	A1	234	G
36	A1	236	G
36	A1	238	A
36	A1	240	U
36	A1	241	G
36	A1	242	C
36	A1	243	G
36	A1	244	G
36	A1	245	U
36	A1	247	C
36	A1	248	U
36	A1	249	U
36	A1	250	U
36	A1	251	G
36	A1	252	U
36	A1	269	G
36	A1	286	U
36	A1	295	A
36	A1	296	A
36	A1	298	U
36	A1	305	U
36	A1	329	U
36	A1	339	C
36	A1	352	A
36	A1	371	G
36	A1	372	A
36	A1	376	G
36	A1	387	A
36	A1	398	A
36	A1	399	A
36	A1	401	U
36	A1	402	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	403	C
36	A1	420	G
36	A1	421	G
36	A1	422	A
36	A1	438	A
36	A1	440	A
36	A1	495	G
36	A1	521	A
36	A1	523	A
36	A1	535	G
36	A1	540	U
36	A1	541	U
36	A1	542	G
36	A1	545	U
36	A1	547	G
36	A1	548	G
36	A1	549	U
36	A1	552	G
36	A1	557	A
36	A1	559	A
36	A1	569	A
36	A1	578	A
36	A1	579	G
36	A1	592	A
36	A1	602	A
36	A1	604	G
36	A1	611	A
36	A1	620	U
36	A1	621	A
36	A1	636	C
36	A1	649	A2M
36	A1	660	A
36	A1	677	A
36	A1	681	U
36	A1	691	A
36	A1	705	A
36	A1	715	A
36	A1	719	U
36	A1	725	G
36	A1	736	A
36	A1	758	C
36	A1	765	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	766	U
36	A1	767	U
36	A1	774	G
36	A1	775	A
36	A1	776	U
36	A1	777	U
36	A1	781	G
36	A1	784	A
36	A1	785	G
36	A1	786	A
36	A1	799	G
36	A1	806	A
36	A1	813	G
36	A1	817	A2M
36	A1	830	A
36	A1	849	C
36	A1	857	G
36	A1	861	C
36	A1	874	U
36	A1	879	U
36	A1	896	A
36	A1	897	U
36	A1	907	G
36	A1	908	OMG
36	A1	909	G
36	A1	914	A
36	A1	916	G
36	A1	917	A
36	A1	921	A
36	A1	923	C
36	A1	924	G
36	A1	925	A
36	A1	934	G
36	A1	937	G
36	A1	943	U
36	A1	944	C
36	A1	959	C
36	A1	961	C
36	A1	962	A
36	A1	964	G
36	A1	974	G
36	A1	980	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	981	U
36	A1	983	A
36	A1	994	G
36	A1	1000	C
36	A1	1002	A
36	A1	1010	G
36	A1	1013	G
36	A1	1014	U
36	A1	1016	C
36	A1	1017	C
36	A1	1018	G
36	A1	1019	G
36	A1	1021	G
36	A1	1023	C
36	A1	1032	C
36	A1	1033	U
36	A1	1034	U
36	A1	1035	G
36	A1	1036	A
36	A1	1045	C
36	A1	1047	A
36	A1	1063	G
36	A1	1064	A
36	A1	1065	A
36	A1	1072	G
36	A1	1075	A
36	A1	1081	U
36	A1	1082	U
36	A1	1093	A
36	A1	1094	U
36	A1	1095	U
36	A1	1097	G
36	A1	1098	A
36	A1	1103	A
36	A1	1104	G
36	A1	1117	G
36	A1	1130	A
36	A1	1131	G
36	A1	1144	U
36	A1	1153	A
36	A1	1159	A
36	A1	1160	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	1178	G
36	A1	1179	A
36	A1	1180	A
36	A1	1181	U
36	A1	1182	A
36	A1	1192	C
36	A1	1193	A
36	A1	1201	C
36	A1	1206	G
36	A1	1208	U
36	A1	1219	C
36	A1	1222	G
36	A1	1224	C
36	A1	1228	C
36	A1	1232	C
36	A1	1235	U
36	A1	1236	G
36	A1	1239	C
36	A1	1241	U
36	A1	1243	G
36	A1	1245	A
36	A1	1246	G
36	A1	1252	A
36	A1	1253	U
36	A1	1256	G
36	A1	1262	G
36	A1	1263	A
36	A1	1265	U
36	A1	1279	C
36	A1	1281	G
36	A1	1282	G
36	A1	1283	C
36	A1	1286	A
36	A1	1287	A
36	A1	1292	C
36	A1	1293	U
36	A1	1295	G
36	A1	1307	G
36	A1	1309	U
36	A1	1317	A
36	A1	1330	A
36	A1	1331	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	1348	U
36	A1	1350	A
36	A1	1351	U
36	A1	1352	A
36	A1	1353	U
36	A1	1354	G
36	A1	1355	A
36	A1	1356	U
36	A1	1357	G
36	A1	1386	A
36	A1	1391	C
36	A1	1393	A
36	A1	1399	A
36	A1	1400	G
36	A1	1419	A
36	A1	1431	G
36	A1	1434	G
36	A1	1437	OMC
36	A1	1446	A
36	A1	1455	U
36	A1	1468	A
36	A1	1475	A
36	A1	1476	G
36	A1	1481	A
36	A1	1502	C
36	A1	1503	A
36	A1	1508	C
36	A1	1523	U
36	A1	1526	U
36	A1	1539	A
36	A1	1555	U
36	A1	1556	C
36	A1	1558	A
36	A1	1562	C
36	A1	1564	U
36	A1	1565	G
36	A1	1566	A
36	A1	1567	U
36	A1	1568	U
36	A1	1569	U
36	A1	1572	U
36	A1	1574	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	1575	A
36	A1	1576	G
36	A1	1579	C
36	A1	1583	A
36	A1	1587	A
36	A1	1589	A
36	A1	1593	A
36	A1	1605	A
36	A1	1608	C
36	A1	1628	C
36	A1	1629	U
36	A1	1630	U
36	A1	1642	A
36	A1	1643	A
36	A1	1683	A
36	A1	1724	U
36	A1	1729	A
36	A1	1734	G
36	A1	1736	G
36	A1	1738	C
36	A1	1739	U
36	A1	1741	A
36	A1	1750	A
36	A1	1751	G
36	A1	1762	C
36	A1	1763	U
36	A1	1764	U
36	A1	1765	U
36	A1	1766	G
36	A1	1775	G
36	A1	1778	G
36	A1	1796	G
36	A1	1797	A
36	A1	1813	A
36	A1	1815	U
36	A1	1816	A
36	A1	1817	G
36	A1	1820	U
36	A1	1821	U
36	A1	1842	A
36	A1	1846	C
36	A1	1849	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	1850	A
36	A1	1866	C
36	A1	1878	G
36	A1	1880	U
36	A1	1886	A
36	A1	1893	A
36	A1	1896	A
36	A1	1899	G
36	A1	1906	G
36	A1	1932	A
36	A1	1936	A
36	A1	1943	C
36	A1	1950	U
36	A1	1951	C
36	A1	1953	G
36	A1	1954	G
36	A1	1955	U
36	A1	2094	C
36	A1	2110	G
36	A1	2111	G
36	A1	2112	U
36	A1	2114	C
36	A1	2122	G
36	A1	2131	A
36	A1	2140	U
36	A1	2144	A
36	A1	2146	C
36	A1	2158	A
36	A1	2169	G
36	A1	2188	A
36	A1	2197	OMC
36	A1	2201	G
36	A1	2206	G
36	A1	2207	A
36	A1	2209	U
36	A1	2242	A
36	A1	2249	G
36	A1	2251	G
36	A1	2255	A
36	A1	2256	A2M
36	A1	2259	A
36	A1	2260	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	2267	C
36	A1	2269	U
36	A1	2270	A
36	A1	2272	G
36	A1	2273	G
36	A1	2280	A2M
36	A1	2281	A2M
36	A1	2282	U
36	A1	2284	C
36	A1	2307	G
36	A1	2308	C
36	A1	2310	U
36	A1	2313	A
36	A1	2314	U
36	A1	2315	G
36	A1	2318	U
36	A1	2334	U
36	A1	2336	U
36	A1	2340	U
36	A1	2366	C
36	A1	2373	A
36	A1	2374	C
36	A1	2375	G
36	A1	2376	G
36	A1	2383	C
36	A1	2388	U
36	A1	2391	G
36	A1	2393	G
36	A1	2397	A
36	A1	2402	A
36	A1	2403	G
36	A1	2404	A
36	A1	2411	U
36	A1	2412	G
36	A1	2418	G
36	A1	2438	A
36	A1	2442	G
36	A1	2445	A
36	A1	2446	U
36	A1	2450	G
36	A1	2451	G
36	A1	2452	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	2453	U
36	A1	2454	G
36	A1	2455	U
36	A1	2458	A
36	A1	2459	A
36	A1	2460	U
36	A1	2461	A
36	A1	2462	A
36	A1	2463	G
36	A1	2467	G
36	A1	2468	A
36	A1	2469	G
36	A1	2470	C
36	A1	2473	C
36	A1	2474	G
36	A1	2475	G
36	A1	2477	G
36	A1	2479	C
36	A1	2480	A
36	A1	2485	A
36	A1	2486	A
36	A1	2487	U
36	A1	2488	A
36	A1	2489	C
36	A1	2490	C
36	A1	2492	C
36	A1	2493	U
36	A1	2494	A
36	A1	2495	C
36	A1	2496	C
36	A1	2497	U
36	A1	2498	U
36	A1	2500	A
36	A1	2502	A
36	A1	2503	G
36	A1	2504	U
36	A1	2505	U
36	A1	2506	U
36	A1	2507	C
36	A1	2511	A
36	A1	2514	U
36	A1	2523	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	2524	A
36	A1	2531	C
36	A1	2538	U
36	A1	2539	C
36	A1	2540	A
36	A1	2541	U
36	A1	2542	U
36	A1	2544	U
36	A1	2549	G
36	A1	2552	C
36	A1	2554	A
36	A1	2561	A
36	A1	2562	A
36	A1	2569	A
36	A1	2571	U
36	A1	2573	G
36	A1	2585	G
36	A1	2586	G
36	A1	2593	A
36	A1	2594	C
36	A1	2606	G
36	A1	2607	G
36	A1	2614	G
36	A1	2648	G
36	A1	2651	G
36	A1	2652	U
36	A1	2656	A
36	A1	2672	G
36	A1	2674	A
36	A1	2677	G
36	A1	2678	A
36	A1	2680	A
36	A1	2681	U
36	A1	2688	U
36	A1	2689	A
36	A1	2690	G
36	A1	2691	A
36	A1	2694	A
36	A1	2704	A
36	A1	2705	A
36	A1	2712	U
36	A1	2714	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	2719	U
36	A1	2728	G
36	A1	2729	OMU
36	A1	2737	C
36	A1	2752	U
36	A1	2753	G
36	A1	2755	C
36	A1	2777	G
36	A1	2778	G
36	A1	2796	G
36	A1	2799	A
36	A1	2800	G
36	A1	2801	A
36	A1	2803	A
36	A1	2810	C
36	A1	2814	G
36	A1	2817	A
36	A1	2842	U
36	A1	2845	A
36	A1	2851	A
36	A1	2860	U
36	A1	2871	G
36	A1	2872	A
36	A1	2873	U
36	A1	2875	U
36	A1	2876	C
36	A1	2887	A
36	A1	2889	C
36	A1	2898	G
36	A1	2923	U
36	A1	2935	U
36	A1	2936	A
36	A1	2941	A
36	A1	2942	C
36	A1	2947	G
36	A1	2977	G
36	A1	2983	C
36	A1	2990	G
36	A1	2997	G
36	A1	3011	A
36	A1	3012	A
36	A1	3022	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	3032	A
36	A1	3056	U
36	A1	3059	G
36	A1	3078	U
36	A1	3079	U
36	A1	3086	A
36	A1	3087	A
36	A1	3092	C
36	A1	3109	G
36	A1	3113	A
36	A1	3122	A
36	A1	3130	A
36	A1	3131	U
36	A1	3142	A
36	A1	3143	C
36	A1	3153	U
36	A1	3154	C
36	A1	3155	U
36	A1	3156	U
36	A1	3157	U
36	A1	3165	A
36	A1	3170	A
36	A1	3172	A
36	A1	3173	G
36	A1	3174	A
36	A1	3176	G
36	A1	3179	U
36	A1	3181	C
36	A1	3187	A
36	A1	3196	U
36	A1	3198	U
36	A1	3207	U
36	A1	3217	C
36	A1	3218	A
36	A1	3219	G
36	A1	3224	G
36	A1	3234	A
36	A1	3243	A
36	A1	3246	G
36	A1	3247	G
36	A1	3256	G
36	A1	3259	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	3263	G
36	A1	3270	U
36	A1	3271	G
36	A1	3273	A
36	A1	3276	G
36	A1	3281	U
36	A1	3289	G
36	A1	3294	A
36	A1	3303	G
36	A1	3304	U
36	A1	3305	A
36	A1	3313	U
36	A1	3314	A
36	A1	3316	A
36	A1	3319	U
36	A1	3341	U
36	A1	3342	A
36	A1	3345	G
36	A1	3351	U
36	A1	3352	U
36	A1	3353	G
36	A1	3354	U
36	A1	3355	U
36	A1	3356	G
36	A1	3369	G
36	A1	3378	C
36	A1	3389	U
36	A1	3390	G
37	A3	48	U
37	A3	53	U
37	A3	54	U
37	A3	55	A
37	A3	64	A
37	A3	65	G
37	A3	74	C
37	A3	76	A
37	A3	78	U
37	A3	102	A
37	A3	112	G
37	A3	121	U
38	A4	23	U
38	A4	34	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A4	35	C
38	A4	46	G
38	A4	51	G
38	A4	52	A
38	A4	53	A
38	A4	58	G
38	A4	59	A
38	A4	60	U
38	A4	62	C
38	A4	63	G
38	A4	75	G
38	A4	76	C
38	A4	81	U
38	A4	83	C
38	A4	86	U
38	A4	87	G
38	A4	88	A
38	A4	90	U
38	A4	95	G
38	A4	104	A
38	A4	106	C
38	A4	107	G
38	A4	111	A
38	A4	112	U
38	A4	113	U
38	A4	116	G
38	A4	125	U
38	A4	152	G
38	A4	158	U
78	EC	6759	A
78	EC	6762	U
78	EC	6768	U
78	EC	6769	A
78	EC	6770	U
78	EC	6771	U
78	EC	6772	G
78	EC	6773	G
78	EC	6774	U
78	EC	6775	U
78	EC	6776	A
78	EC	6777	C
78	EC	6778	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
78	EC	6779	C
78	EC	6780	A
78	EC	6782	C
78	EC	6788	C
78	EC	6789	G
78	EC	6790	A
78	EC	6791	A
78	EC	6792	A
78	EC	6793	A
78	EC	6794	C
78	EC	6795	U
78	EC	6800	G
78	EC	6801	A
78	EC	6802	A
78	EC	6803	C
78	EC	6804	A
78	EC	6812	C
78	EC	6816	A
78	EC	6817	A
78	EC	6818	G
78	EC	6819	G
78	EC	6820	C
78	EC	6821	U
78	EC	6822	U
78	EC	6823	U
78	EC	6824	C
78	EC	6825	A
78	EC	6831	U
78	EC	6832	G
78	EC	6835	U
78	EC	6836	U
78	EC	6837	G
78	EC	6840	A
78	EC	6841	U
78	EC	6842	U
78	EC	6843	U
78	EC	6844	A
78	EC	6847	G
78	EC	6848	U
78	EC	6849	A
78	EC	6850	C
78	EC	6852	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
78	EC	6856	C
78	EC	6857	C
78	EC	6858	A
78	EC	6859	U
78	EC	6860	A
78	EC	6861	G
78	EC	6864	A
78	EC	6865	G
78	EC	6866	C
78	EC	6867	C
78	EC	6870	A
78	EC	6871	A
78	EC	6872	A
78	EC	6873	A
78	EC	6874	A
78	EC	6875	C
78	EC	6877	C
78	EC	6880	G
78	EC	6881	U
78	EC	6882	G
78	EC	6883	A
78	EC	6884	G
78	EC	6887	G
78	EC	6889	A
78	EC	6890	A
78	EC	6895	C
78	EC	6896	A
78	EC	6897	G
78	EC	6902	U
78	EC	6903	U
78	EC	6908	C
78	EC	6910	A
78	EC	6911	A
78	EC	6915	G
78	EC	6916	A
78	EC	6918	A
78	EC	6925	C
78	EC	6928	G
78	EC	6929	C
78	EC	6934	U
78	EC	6935	G
78	EC	6936	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
78	EC	6938	A
78	EC	6939	C
78	EC	6940	U
78	EC	6941	U
78	EC	6942	A
78	EC	6943	A
78	EC	6944	U
78	EC	6945	U
78	EC	6946	A
78	EC	6947	A
78	EC	6948	U
78	EC	6949	G

All (46) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
32	B5	240	U
32	B5	752	A
32	B5	819	G
32	B5	862	A
32	B5	950	C
32	B5	1285	U
32	B5	1344	A
32	B5	1369	U
32	B5	1458	G
32	B5	1572	OMG
32	B5	1645	G
36	A1	116	A
36	A1	122	A
36	A1	165	A
36	A1	178	U
36	A1	210	U
36	A1	241	G
36	A1	249	U
36	A1	873	C
36	A1	916	G
36	A1	1092	C
36	A1	1218	U
36	A1	1242	G
36	A1	1278	A
36	A1	1292	C
36	A1	1349	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	A1	1354	G
36	A1	1565	G
36	A1	1629	U
36	A1	2241	U
36	A1	2469	G
36	A1	2493	U
36	A1	2494	A
36	A1	2506	U
36	A1	2801	A
36	A1	2875	U
36	A1	3121	U
37	A3	52	G
78	EC	6789	G
78	EC	6817	A
78	EC	6831	U
78	EC	6851	G
78	EC	6876	A
78	EC	6889	A
78	EC	6939	C
78	EC	6943	A

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

68 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	$\# Z > 2$
36	OMU	A1	2729	36	19,22,23	1.24	3 (15%)	25,31,34	1.79	4 (16%)
36	OMG	A1	1450	36	23,26,27	1.19	3 (13%)	32,38,41	1.92	6 (18%)
36	OMU	A1	2724	36	19,22,23	1.24	3 (15%)	25,31,34	1.83	6 (24%)
36	A2M	A1	2640	36	22,25,26	1.48	4 (18%)	30,36,39	2.04	7 (23%)
32	MA6	B5	1781	32	23,26,27	1.50	4 (17%)	33,38,41	2.07	10 (30%)
36	OMG	A1	2793	36	23,26,27	1.18	3 (13%)	32,38,41	2.01	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	MA6	B5	1782	32	23,26,27	1.48	5 (21%)	33,38,41	2.11	10 (30%)
36	OMC	A1	2197	36	19,22,23	0.79	0	25,31,34	0.88	0
36	A2M	A1	2280	36	22,25,26	1.47	4 (18%)	30,36,39	2.09	9 (30%)
32	OMU	B5	578	32	19,22,23	1.19	3 (15%)	25,31,34	1.81	5 (20%)
32	OMG	B5	1428	32,83	23,26,27	1.19	3 (13%)	32,38,41	1.97	6 (18%)
36	A2M	A1	1133	36	22,25,26	1.46	5 (22%)	30,36,39	2.16	10 (33%)
36	OMC	A1	1437	36,83	19,22,23	0.82	0	25,31,34	1.02	2 (8%)
32	OMG	B5	562	32	23,26,27	1.20	3 (13%)	32,38,41	1.99	5 (15%)
32	4AC	B5	1280	32	21,24,25	1.06	1 (4%)	28,34,37	1.07	2 (7%)
36	OMU	A1	2921	36	19,22,23	1.26	3 (15%)	25,31,34	1.83	4 (16%)
36	OMU	A1	2347	36	19,22,23	1.29	3 (15%)	25,31,34	1.82	5 (20%)
36	OMC	A1	2337	36	19,22,23	0.77	0	25,31,34	0.85	1 (4%)
36	OMG	A1	805	36	23,26,27	1.18	3 (13%)	32,38,41	2.02	7 (21%)
36	OMC	A1	2959	36	19,22,23	0.78	0	25,31,34	0.82	0
32	OMG	B5	1271	32	23,26,27	1.18	3 (13%)	32,38,41	1.95	6 (18%)
36	A2M	A1	2256	36	22,25,26	1.48	4 (18%)	30,36,39	2.09	9 (30%)
36	UR3	A1	2634	36	19,22,23	0.96	0	26,32,35	1.77	2 (7%)
36	A2M	A1	1449	36,83	22,25,26	1.49	3 (13%)	30,36,39	2.04	7 (23%)
32	A2M	B5	420	32	22,25,26	1.50	4 (18%)	30,36,39	2.05	9 (30%)
36	A2M	A1	2281	36	22,25,26	1.43	5 (22%)	30,36,39	2.33	11 (36%)
32	OMC	B5	1007	32	19,22,23	0.77	0	25,31,34	0.81	0
36	OMC	A1	2948	36	19,22,23	0.78	0	25,31,34	0.89	1 (4%)
32	OMG	B5	1572	32	23,26,27	1.18	2 (8%)	32,38,41	2.11	7 (21%)
36	A2M	A1	649	36	22,25,26	1.48	4 (18%)	30,36,39	2.02	8 (26%)
36	A2M	A1	807	36	22,25,26	1.48	5 (22%)	30,36,39	2.09	9 (30%)
32	OMG	B5	1126	32	23,26,27	1.13	2 (8%)	32,38,41	2.08	8 (25%)
36	OMG	A1	2815	36	23,26,27	1.19	3 (13%)	32,38,41	1.94	6 (18%)
36	5MC	A1	2278	36,83	19,22,23	1.54	3 (15%)	26,32,35	1.21	3 (11%)
36	A2M	A1	2946	36,83	22,25,26	1.48	4 (18%)	30,36,39	2.20	10 (33%)
32	OMC	B5	414	32	19,22,23	0.79	0	25,31,34	0.80	1 (4%)
36	1MA	A1	645	36,83	21,25,26	1.35	4 (19%)	30,37,40	1.70	6 (20%)
36	OMU	A1	898	36	19,22,23	1.25	3 (15%)	25,31,34	1.81	4 (16%)
32	OMU	B5	1269	32	19,22,23	1.25	4 (21%)	25,31,34	1.85	5 (20%)
36	OMC	A1	663	36	19,22,23	0.81	0	25,31,34	0.74	0
36	OMG	A1	2288	36	23,26,27	1.21	3 (13%)	32,38,41	1.94	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	A2M	B5	28	32	22,25,26	1.50	4 (18%)	30,36,39	2.04	7 (23%)
36	OMG	A1	2791	36	23,26,27	1.18	3 (13%)	32,38,41	1.96	6 (18%)
32	G7M	B5	1575	32	23,26,27	2.54	6 (26%)	34,39,42	3.09	14 (41%)
32	A2M	B5	974	32	22,25,26	1.49	4 (18%)	30,36,39	2.03	8 (26%)
36	OMG	A1	867	36,83	23,26,27	1.20	3 (13%)	32,38,41	1.99	6 (18%)
32	A2M	B5	796	32	22,25,26	1.51	4 (18%)	30,36,39	2.19	9 (30%)
36	OMU	A1	2421	36	19,22,23	1.26	3 (15%)	25,31,34	1.85	5 (20%)
32	A2M	B5	100	32,83	22,25,26	1.48	4 (18%)	30,36,39	2.08	9 (30%)
36	OMU	A1	1888	36	19,22,23	1.28	3 (15%)	25,31,34	1.87	5 (20%)
36	A2M	A1	876	36	22,25,26	1.47	5 (22%)	30,36,39	2.04	7 (23%)
79	DDE	DC	699	79	18,20,21	1.01	1 (5%)	17,28,30	0.76	1 (5%)
36	A2M	A1	2220	36	22,25,26	1.51	5 (22%)	30,36,39	1.94	9 (30%)
36	5MC	A1	2870	36	19,22,23	1.61	3 (15%)	26,32,35	1.23	3 (11%)
32	A2M	B5	436	32	22,25,26	1.49	4 (18%)	30,36,39	2.07	8 (26%)
36	1MA	A1	2142	36,83	21,25,26	1.33	4 (19%)	30,37,40	1.70	3 (10%)
32	OMC	B5	1639	32	19,22,23	0.76	0	25,31,34	0.71	0
36	OMU	A1	2417	36	19,22,23	1.23	3 (15%)	25,31,34	1.82	5 (20%)
36	OMG	A1	2922	36	23,26,27	1.18	3 (13%)	32,38,41	1.96	6 (18%)
34	HIC	AB	243	34	10,11,12	1.46	1 (10%)	9,14,16	1.23	1 (11%)
36	OMC	A1	650	36,83	19,22,23	0.79	0	25,31,34	0.86	0
32	A2M	B5	619	32,83	22,25,26	1.47	4 (18%)	30,36,39	2.04	9 (30%)
36	OMG	A1	908	36	23,26,27	1.23	3 (13%)	32,38,41	2.03	6 (18%)
36	OMG	A1	2619	36	23,26,27	1.20	3 (13%)	32,38,41	1.95	6 (18%)
36	A2M	A1	817	36,83	22,25,26	1.50	5 (22%)	30,36,39	2.03	8 (26%)
32	XSX	B5	1191	32	24,28,29	1.00	1 (4%)	30,40,43	3.70	5 (16%)
32	A2M	B5	541	32	22,25,26	1.51	4 (18%)	30,36,39	2.09	7 (23%)
32	4AC	B5	1773	32	21,24,25	1.05	2 (9%)	28,34,37	2.58	7 (25%)

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
36	OMU	A1	2729	36	-	3/9/27/28	0/2/2/2
36	OMG	A1	1450	36	-	1/9/27/28	0/3/3/3
36	OMU	A1	2724	36	-	1/9/27/28	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	A2M	A1	2640	36	-	0/9/27/28	0/3/3/3
32	MA6	B5	1781	32	-	0/11/29/30	0/3/3/3
36	OMG	A1	2793	36	-	1/9/27/28	0/3/3/3
32	MA6	B5	1782	32	-	2/11/29/30	0/3/3/3
36	OMC	A1	2197	36	-	6/9/27/28	0/2/2/2
36	A2M	A1	2280	36	-	2/9/27/28	0/3/3/3
32	OMU	B5	578	32	-	0/9/27/28	0/2/2/2
32	OMG	B5	1428	32,83	-	2/9/27/28	0/3/3/3
36	A2M	A1	1133	36	-	0/9/27/28	0/3/3/3
36	OMC	A1	1437	36,83	-	4/9/27/28	0/2/2/2
32	OMG	B5	562	32	-	1/9/27/28	0/3/3/3
32	4AC	B5	1280	32	-	4/11/29/30	0/2/2/2
36	OMU	A1	2921	36	-	0/9/27/28	0/2/2/2
36	OMU	A1	2347	36	-	0/9/27/28	0/2/2/2
36	OMC	A1	2337	36	-	1/9/27/28	0/2/2/2
36	OMG	A1	805	36	-	0/9/27/28	0/3/3/3
36	OMC	A1	2959	36	-	0/9/27/28	0/2/2/2
32	OMG	B5	1271	32	-	1/9/27/28	0/3/3/3
36	A2M	A1	2256	36	-	3/9/27/28	0/3/3/3
36	UR3	A1	2634	36	-	0/7/25/26	0/2/2/2
36	A2M	A1	1449	36,83	-	0/9/27/28	0/3/3/3
32	A2M	B5	420	32	-	1/9/27/28	0/3/3/3
36	A2M	A1	2281	36	-	2/9/27/28	0/3/3/3
32	OMC	B5	1007	32	-	0/9/27/28	0/2/2/2
36	OMC	A1	2948	36	-	0/9/27/28	0/2/2/2
32	OMG	B5	1572	32	-	2/9/27/28	0/3/3/3
36	A2M	A1	649	36	-	0/9/27/28	0/3/3/3
36	A2M	A1	807	36	-	1/9/27/28	0/3/3/3
32	OMG	B5	1126	32	-	1/9/27/28	0/3/3/3
36	OMG	A1	2815	36	-	0/9/27/28	0/3/3/3
36	5MC	A1	2278	36,83	-	1/7/25/26	0/2/2/2
36	A2M	A1	2946	36,83	-	0/9/27/28	0/3/3/3
32	OMC	B5	414	32	-	1/9/27/28	0/2/2/2
36	1MA	A1	645	36,83	-	2/7/25/26	0/3/3/3
36	OMU	A1	898	36	-	0/9/27/28	0/2/2/2
32	OMU	B5	1269	32	-	4/9/27/28	0/2/2/2
36	OMC	A1	663	36	-	1/9/27/28	0/2/2/2
36	OMG	A1	2288	36	-	0/9/27/28	0/3/3/3
32	A2M	B5	28	32	-	0/9/27/28	0/3/3/3
36	OMG	A1	2791	36	-	1/9/27/28	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	G7M	B5	1575	32	-	0/7/25/26	0/3/3/3
32	A2M	B5	974	32	-	0/9/27/28	0/3/3/3
36	OMG	A1	867	36,83	-	0/9/27/28	0/3/3/3
32	A2M	B5	796	32	-	0/9/27/28	0/3/3/3
36	OMU	A1	2421	36	-	1/9/27/28	0/2/2/2
32	A2M	B5	100	32,83	-	0/9/27/28	0/3/3/3
36	OMU	A1	1888	36	-	1/9/27/28	0/2/2/2
36	A2M	A1	876	36	-	0/9/27/28	0/3/3/3
79	DDE	DC	699	79	-	7/20/21/23	0/1/1/1
36	A2M	A1	2220	36	-	1/9/27/28	0/3/3/3
36	5MC	A1	2870	36	-	4/7/25/26	0/2/2/2
32	A2M	B5	436	32	-	0/9/27/28	0/3/3/3
36	1MA	A1	2142	36,83	-	0/7/25/26	0/3/3/3
32	OMC	B5	1639	32	-	0/9/27/28	0/2/2/2
36	OMU	A1	2417	36	-	1/9/27/28	0/2/2/2
36	OMG	A1	2922	36	-	1/9/27/28	0/3/3/3
34	HIC	AB	243	34	-	0/5/6/8	0/1/1/1
36	OMC	A1	650	36,83	-	0/9/27/28	0/2/2/2
32	A2M	B5	619	32,83	-	4/9/27/28	0/3/3/3
36	OMG	A1	908	36	-	0/9/27/28	0/3/3/3
36	OMG	A1	2619	36	-	1/9/27/28	0/3/3/3
36	A2M	A1	817	36,83	-	1/9/27/28	0/3/3/3
32	XSX	B5	1191	32	-	6/16/34/35	0/2/2/2
32	A2M	B5	541	32	-	5/9/27/28	0/3/3/3
32	4AC	B5	1773	32	-	4/11/29/30	0/2/2/2

All (194) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	B5	1575	G7M	C8-N7	7.65	1.46	1.33
36	A1	2870	5MC	C5-C4	5.60	1.48	1.44
36	A1	2278	5MC	C5-C4	5.39	1.48	1.44
32	B5	1575	G7M	C5-N7	-4.94	1.33	1.39
32	B5	541	A2M	C5-C4	4.74	1.47	1.39
32	B5	1781	MA6	C5-C4	4.70	1.47	1.39
32	B5	436	A2M	C5-C4	4.62	1.47	1.39
32	B5	28	A2M	C5-C4	4.62	1.47	1.39
32	B5	420	A2M	C5-C4	4.60	1.47	1.39
32	B5	796	A2M	C5-C4	4.58	1.47	1.39
36	A1	2220	A2M	C5-C4	4.58	1.47	1.39
32	B5	974	A2M	C5-C4	4.55	1.47	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	B5	1782	MA6	C5-C4	4.54	1.47	1.39
36	A1	1449	A2M	C5-C4	4.53	1.47	1.39
36	A1	2256	A2M	C5-C4	4.53	1.47	1.39
32	B5	100	A2M	C5-C4	4.53	1.47	1.39
36	A1	649	A2M	C5-C4	4.51	1.47	1.39
36	A1	817	A2M	C5-C4	4.50	1.47	1.39
36	A1	2280	A2M	C5-C4	4.48	1.47	1.39
36	A1	807	A2M	C5-C4	4.46	1.47	1.39
36	A1	2946	A2M	C5-C4	4.46	1.47	1.39
36	A1	2640	A2M	C5-C4	4.45	1.47	1.39
36	A1	876	A2M	C5-C4	4.44	1.47	1.39
32	B5	619	A2M	C5-C4	4.42	1.47	1.39
36	A1	1133	A2M	C5-C4	4.36	1.46	1.39
36	A1	2281	A2M	C5-C4	4.26	1.46	1.39
32	B5	1575	G7M	C8-N9	4.09	1.46	1.35
32	B5	1575	G7M	C5-C4	3.69	1.47	1.38
36	A1	645	1MA	C6-N6	3.14	1.35	1.28
36	A1	908	OMG	C5-C4	3.13	1.47	1.38
32	B5	1428	OMG	C5-C4	3.12	1.47	1.38
32	B5	562	OMG	C5-C4	3.12	1.47	1.38
32	B5	1271	OMG	C5-C4	3.10	1.47	1.38
36	A1	2288	OMG	C5-C4	3.05	1.47	1.38
32	B5	1572	OMG	C5-C4	3.04	1.47	1.38
36	A1	2791	OMG	C5-C4	3.03	1.47	1.38
36	A1	2142	1MA	C5-C4	3.02	1.47	1.38
36	A1	2922	OMG	C5-C4	3.01	1.47	1.38
32	B5	1782	MA6	C5-C6	3.01	1.49	1.41
32	B5	1280	4AC	C4-N4	-2.98	1.35	1.39
36	A1	867	OMG	C5-C4	2.97	1.46	1.38
36	A1	1888	OMU	C4-N3	-2.95	1.33	1.38
36	A1	2815	OMG	C5-C4	2.95	1.46	1.38
36	A1	1450	OMG	C5-C4	2.94	1.46	1.38
36	A1	2619	OMG	C5-C4	2.94	1.46	1.38
36	A1	2793	OMG	C5-C4	2.93	1.46	1.38
36	A1	645	1MA	C5-C4	2.92	1.46	1.38
36	A1	2870	5MC	C6-C5	2.91	1.39	1.34
32	B5	1781	MA6	C5-C6	2.90	1.48	1.41
32	B5	1126	OMG	C5-C4	2.89	1.46	1.38
36	A1	805	OMG	C5-C4	2.89	1.46	1.38
36	A1	2142	1MA	C6-N6	2.88	1.34	1.28
36	A1	2347	OMU	C4-N3	-2.88	1.33	1.38
36	A1	2921	OMU	C4-N3	-2.87	1.33	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	A1	2417	OMU	C4-N3	-2.85	1.33	1.38
34	AB	243	HIC	CD2-CG	2.85	1.41	1.36
36	A1	898	OMU	C4-N3	-2.84	1.33	1.38
36	A1	2421	OMU	C4-N3	-2.83	1.33	1.38
36	A1	2724	OMU	C4-N3	-2.79	1.33	1.38
36	A1	2729	OMU	C4-N3	-2.78	1.33	1.38
36	A1	2278	5MC	C6-C5	2.76	1.39	1.34
32	B5	796	A2M	C5-C6	2.73	1.48	1.41
36	A1	2815	OMG	C6-N1	-2.72	1.33	1.38
36	A1	867	OMG	C6-N1	-2.72	1.33	1.38
32	B5	541	A2M	C5-C6	2.71	1.48	1.41
36	A1	817	A2M	C5-C6	2.71	1.48	1.41
36	A1	2256	A2M	C5-C6	2.70	1.48	1.41
32	B5	420	A2M	C5-C6	2.70	1.48	1.41
32	B5	436	A2M	C5-C6	2.70	1.48	1.41
32	B5	1269	OMU	C4-N3	-2.70	1.34	1.38
36	A1	908	OMG	C6-N1	-2.68	1.33	1.38
36	A1	1450	OMG	C6-N1	-2.68	1.33	1.38
36	A1	2619	OMG	C6-N1	-2.68	1.33	1.38
36	A1	1449	A2M	C5-N7	-2.67	1.34	1.39
36	A1	2288	OMG	C6-N1	-2.67	1.33	1.38
32	B5	28	A2M	C5-C6	2.66	1.48	1.41
32	B5	974	A2M	C5-C6	2.65	1.48	1.41
32	B5	619	A2M	C5-C6	2.64	1.48	1.41
36	A1	2640	A2M	C5-C6	2.60	1.48	1.41
36	A1	807	A2M	C5-C6	2.60	1.48	1.41
36	A1	2280	A2M	C5-C6	2.60	1.48	1.41
36	A1	2946	A2M	C5-C6	2.60	1.48	1.41
36	A1	2791	OMG	C6-N1	-2.60	1.34	1.38
32	B5	100	A2M	C5-C6	2.60	1.48	1.41
36	A1	805	OMG	C6-N1	-2.59	1.34	1.38
36	A1	2793	OMG	C6-N1	-2.58	1.34	1.38
36	A1	649	A2M	C5-C6	2.58	1.48	1.41
36	A1	2640	A2M	C5-N7	-2.56	1.34	1.39
36	A1	2220	A2M	C5-C6	2.56	1.48	1.41
36	A1	2922	OMG	C6-N1	-2.56	1.34	1.38
36	A1	1449	A2M	C5-C6	2.56	1.48	1.41
79	DC	699	DDE	CD2-CG	2.55	1.41	1.36
32	B5	562	OMG	C6-N1	-2.54	1.34	1.38
32	B5	1428	OMG	C6-N1	-2.54	1.34	1.38
36	A1	649	A2M	C5-N7	-2.53	1.34	1.39
32	B5	578	OMU	C4-N3	-2.52	1.34	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	A1	876	A2M	C5-N7	-2.52	1.34	1.39
36	A1	876	A2M	C5-C6	2.50	1.47	1.41
32	B5	1271	OMG	C6-N1	-2.50	1.34	1.38
36	A1	1133	A2M	C5-C6	2.50	1.47	1.41
36	A1	2347	OMU	C2-N3	-2.47	1.33	1.38
36	A1	2946	A2M	C5-N7	-2.47	1.34	1.39
36	A1	2220	A2M	C5-N7	-2.46	1.34	1.39
36	A1	2421	OMU	C2-N3	-2.46	1.33	1.38
36	A1	2281	A2M	C5-C6	2.45	1.47	1.41
32	B5	1575	G7M	C2'-C3'	-2.45	1.46	1.53
36	A1	817	A2M	C5-N7	-2.45	1.34	1.39
36	A1	807	A2M	C5-N7	-2.44	1.34	1.39
36	A1	2921	OMU	C2-N3	-2.44	1.33	1.38
32	B5	1126	OMG	C6-N1	-2.43	1.34	1.38
36	A1	2280	A2M	C5-N7	-2.42	1.34	1.39
36	A1	908	OMG	C5-N7	-2.42	1.34	1.39
32	B5	100	A2M	C5-N7	-2.41	1.34	1.39
36	A1	1888	OMU	C2-N3	-2.40	1.33	1.38
32	B5	1572	OMG	C6-N1	-2.40	1.34	1.38
36	A1	1133	A2M	C5-N7	-2.40	1.34	1.39
32	B5	1575	G7M	C6-N1	-2.39	1.34	1.38
36	A1	2729	OMU	C2-N3	-2.39	1.33	1.38
36	A1	2281	A2M	C5-N7	-2.39	1.34	1.39
32	B5	974	A2M	C5-N7	-2.38	1.34	1.39
36	A1	898	OMU	C2-N3	-2.38	1.33	1.38
36	A1	2724	OMU	C2-N3	-2.37	1.33	1.38
36	A1	2417	OMU	C2-N3	-2.37	1.33	1.38
32	B5	28	A2M	C5-N7	-2.37	1.34	1.39
32	B5	436	A2M	C5-N7	-2.35	1.34	1.39
32	B5	541	A2M	C5-N7	-2.35	1.34	1.39
36	A1	2142	1MA	C5-N7	-2.35	1.34	1.39
32	B5	796	A2M	C5-N7	-2.33	1.34	1.39
32	B5	1781	MA6	C5-N7	-2.32	1.34	1.39
32	B5	619	A2M	C5-N7	-2.32	1.34	1.39
36	A1	2256	A2M	C8-N7	2.31	1.36	1.31
32	B5	420	A2M	C5-N7	-2.30	1.34	1.39
32	B5	436	A2M	C8-N7	2.30	1.36	1.31
32	B5	420	A2M	C8-N7	2.30	1.36	1.31
36	A1	2288	OMG	C5-N7	-2.30	1.34	1.39
32	B5	796	A2M	C8-N7	2.29	1.36	1.31
32	B5	1773	4AC	C4-N4	-2.29	1.36	1.39
36	A1	2729	OMU	C5-C4	-2.27	1.38	1.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	A1	645	1MA	C5-N7	-2.26	1.34	1.39
36	A1	2619	OMG	C5-N7	-2.26	1.34	1.39
32	B5	619	A2M	C8-N7	2.26	1.36	1.31
32	B5	1773	4AC	C6-N1	-2.25	1.32	1.38
36	A1	2724	OMU	C5-C4	-2.25	1.38	1.43
36	A1	2870	5MC	C6-N1	-2.24	1.34	1.38
36	A1	1450	OMG	C5-N7	-2.24	1.34	1.39
36	A1	2142	1MA	C2-N3	2.24	1.34	1.30
36	A1	2278	5MC	C6-N1	-2.24	1.34	1.38
32	B5	1269	OMU	C2-N3	-2.23	1.34	1.38
32	B5	28	A2M	C8-N7	2.23	1.36	1.31
36	A1	2256	A2M	C5-N7	-2.23	1.35	1.39
32	B5	974	A2M	C8-N7	2.23	1.36	1.31
32	B5	100	A2M	C8-N7	2.22	1.36	1.31
36	A1	2347	OMU	C5-C4	-2.22	1.38	1.43
32	B5	1269	OMU	C2-N1	2.22	1.41	1.38
32	B5	1782	MA6	C5-N7	-2.21	1.35	1.39
32	B5	541	A2M	C8-N7	2.21	1.35	1.31
32	B5	1782	MA6	C8-N7	2.21	1.35	1.31
36	A1	2417	OMU	C5-C4	-2.20	1.38	1.43
36	A1	867	OMG	C5-N7	-2.19	1.34	1.39
36	A1	2220	A2M	C4-N9	-2.18	1.33	1.37
36	A1	2922	OMG	C5-N7	-2.18	1.34	1.39
36	A1	2946	A2M	C8-N7	2.17	1.35	1.31
36	A1	1133	A2M	C8-N7	2.16	1.35	1.31
36	A1	2815	OMG	C5-N7	-2.16	1.34	1.39
36	A1	2791	OMG	C5-N7	-2.16	1.34	1.39
32	B5	1428	OMG	C5-N7	-2.14	1.34	1.39
32	B5	578	OMU	C2-N3	-2.14	1.34	1.38
36	A1	805	OMG	C5-N7	-2.14	1.34	1.39
36	A1	2220	A2M	C8-N7	2.13	1.35	1.31
36	A1	2281	A2M	C4-N9	-2.13	1.33	1.37
36	A1	817	A2M	C8-N7	2.13	1.35	1.31
36	A1	2421	OMU	C5-C4	-2.13	1.39	1.43
36	A1	2281	A2M	C8-N7	2.12	1.35	1.31
36	A1	807	A2M	C4-N9	-2.12	1.33	1.37
32	B5	1271	OMG	C5-N7	-2.11	1.34	1.39
32	B5	562	OMG	C5-N7	-2.11	1.34	1.39
36	A1	898	OMU	C5-C4	-2.10	1.39	1.43
36	A1	2280	A2M	C8-N7	2.10	1.35	1.31
36	A1	2921	OMU	C5-C4	-2.09	1.39	1.43
36	A1	2793	OMG	C5-N7	-2.07	1.34	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	A1	2640	A2M	C8-N7	2.07	1.35	1.31
36	A1	817	A2M	C4-N9	-2.07	1.33	1.37
36	A1	807	A2M	C8-N7	2.06	1.35	1.31
36	A1	876	A2M	C4-N9	-2.06	1.33	1.37
36	A1	876	A2M	C8-N7	2.06	1.35	1.31
32	B5	1782	MA6	C4-N9	-2.04	1.33	1.37
32	B5	1191	XSX	C2-N1	2.04	1.41	1.38
36	A1	1133	A2M	C4-N9	-2.04	1.33	1.37
32	B5	1269	OMU	C5-C4	-2.04	1.39	1.43
32	B5	1781	MA6	C4-N9	-2.04	1.33	1.37
36	A1	649	A2M	C8-N7	2.02	1.35	1.31
32	B5	578	OMU	C5-C4	-2.01	1.39	1.43
36	A1	1888	OMU	C5-C4	-2.01	1.39	1.43
36	A1	645	1MA	C2-N3	2.00	1.34	1.30

All (383) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	B5	1191	XSX	C3-C1-N3	18.82	145.05	112.16
32	B5	1773	4AC	N4-C4-N3	9.43	129.18	113.87
32	B5	1575	G7M	CN7-N7-C8	-7.75	113.05	124.79
36	A1	2634	UR3	C4-N3-C2	-7.12	118.85	124.58
36	A1	908	OMG	C5-C4-N3	-6.46	118.11	128.39
32	B5	1575	G7M	N9-C8-N7	-6.46	96.81	112.48
32	B5	562	OMG	C5-C4-N3	-6.30	118.37	128.39
32	B5	1575	G7M	C8-N7-C5	6.29	115.65	107.78
36	A1	867	OMG	C5-C4-N3	-6.25	118.44	128.39
32	B5	541	A2M	C5-C4-N3	-6.24	118.13	126.72
32	B5	1428	OMG	C5-C4-N3	-6.23	118.48	128.39
36	A1	2288	OMG	C5-C4-N3	-6.15	118.61	128.39
36	A1	1449	A2M	C5-C4-N3	-6.11	118.30	126.72
32	B5	1271	OMG	C5-C4-N3	-6.09	118.69	128.39
36	A1	2922	OMG	C5-C4-N3	-6.07	118.72	128.39
36	A1	2619	OMG	C5-C4-N3	-6.05	118.76	128.39
32	B5	1773	4AC	C5-C4-N4	-6.04	112.76	122.94
36	A1	2791	OMG	C5-C4-N3	-6.03	118.80	128.39
32	B5	1572	OMG	C5-C4-N3	-6.01	118.83	128.39
36	A1	2815	OMG	C5-C4-N3	-6.00	118.84	128.39
36	A1	2793	OMG	C5-C4-N3	-6.00	118.84	128.39
32	B5	436	A2M	C5-C4-N3	-5.97	118.49	126.72
36	A1	876	A2M	C5-C4-N3	-5.96	118.51	126.72
36	A1	1450	OMG	C5-C4-N3	-5.93	118.96	128.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	2640	A2M	C5-C4-N3	-5.91	118.58	126.72
32	B5	1126	OMG	C5-C4-N3	-5.90	119.00	128.39
36	A1	2946	A2M	C5-C4-N3	-5.89	118.61	126.72
32	B5	1575	G7M	N9-C4-N3	5.88	137.72	125.95
32	B5	28	A2M	C5-C4-N3	-5.88	118.62	126.72
32	B5	100	A2M	C5-C4-N3	-5.87	118.64	126.72
32	B5	796	A2M	C5-C4-N3	-5.85	118.66	126.72
36	A1	2280	A2M	C5-C4-N3	-5.84	118.67	126.72
36	A1	2256	A2M	C5-C4-N3	-5.81	118.72	126.72
32	B5	974	A2M	C5-C4-N3	-5.81	118.72	126.72
36	A1	805	OMG	C5-C4-N3	-5.79	119.18	128.39
36	A1	817	A2M	C5-C4-N3	-5.76	118.78	126.72
36	A1	649	A2M	C5-C4-N3	-5.72	118.84	126.72
36	A1	807	A2M	C5-C4-N3	-5.72	118.84	126.72
32	B5	420	A2M	C5-C4-N3	-5.72	118.84	126.72
32	B5	619	A2M	C5-C4-N3	-5.68	118.89	126.72
36	A1	1133	A2M	C5-C4-N3	-5.61	118.99	126.72
36	A1	2281	A2M	C5-C4-N3	-5.61	118.99	126.72
32	B5	1781	MA6	C5-C4-N3	-5.48	119.17	126.72
32	B5	1782	MA6	C5-C4-N3	-5.46	119.19	126.72
32	B5	1575	G7M	C5-C4-N3	-5.45	117.85	128.15
36	A1	2142	1MA	C5-C4-N3	-5.42	119.29	127.27
36	A1	2220	A2M	C5-C4-N3	-5.35	119.36	126.72
36	A1	645	1MA	C5-C4-N3	-5.22	119.58	127.27
32	B5	562	OMG	C2-N3-C4	5.15	121.17	112.30
32	B5	1572	OMG	C2-N3-C4	5.09	121.08	112.30
36	A1	2793	OMG	C2-N3-C4	5.08	121.04	112.30
36	A1	908	OMG	N9-C4-N3	5.07	136.10	125.95
36	A1	2922	OMG	C2-N3-C4	5.07	121.02	112.30
36	A1	805	OMG	C2-N3-C4	5.04	120.99	112.30
32	B5	1126	OMG	C2-N3-C4	5.03	120.96	112.30
36	A1	2619	OMG	C2-N3-C4	5.02	120.94	112.30
32	B5	1428	OMG	C2-N3-C4	5.02	120.94	112.30
36	A1	2421	OMU	C4-N3-C2	-5.01	120.39	126.61
32	B5	541	A2M	N3-C4-N9	5.00	135.68	127.17
36	A1	1888	OMU	C4-N3-C2	-5.00	120.40	126.61
36	A1	867	OMG	C2-N3-C4	4.99	120.89	112.30
36	A1	2791	OMG	C2-N3-C4	4.98	120.87	112.30
36	A1	2815	OMG	C2-N3-C4	4.96	120.85	112.30
32	B5	1271	OMG	C2-N3-C4	4.96	120.84	112.30
36	A1	908	OMG	C2-N3-C4	4.95	120.83	112.30
36	A1	2288	OMG	C2-N3-C4	4.93	120.78	112.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	B5	1191	XSX	C4-N3-C2	-4.91	118.89	124.66
36	A1	2921	OMU	C4-N3-C2	-4.90	120.53	126.61
32	B5	578	OMU	C4-N3-C2	-4.90	120.53	126.61
36	A1	898	OMU	C4-N3-C2	-4.89	120.55	126.61
36	A1	1450	OMG	C2-N3-C4	4.88	120.71	112.30
36	A1	1449	A2M	N3-C4-N9	4.87	135.44	127.17
36	A1	2417	OMU	C4-N3-C2	-4.85	120.59	126.61
36	A1	2724	OMU	C4-N3-C2	-4.77	120.69	126.61
36	A1	2640	A2M	N3-C4-N9	4.76	135.26	127.17
36	A1	2347	OMU	C4-N3-C2	-4.71	120.76	126.61
36	A1	876	A2M	N3-C4-N9	4.71	135.18	127.17
36	A1	867	OMG	N9-C4-N3	4.70	135.36	125.95
36	A1	2729	OMU	C4-N3-C2	-4.70	120.78	126.61
32	B5	100	A2M	N3-C4-N9	4.68	135.13	127.17
32	B5	28	A2M	N3-C4-N9	4.68	135.12	127.17
32	B5	1269	OMU	C4-N3-C2	-4.63	120.86	126.61
32	B5	1428	OMG	N9-C4-N3	4.63	135.22	125.95
36	A1	2280	A2M	N3-C4-N9	4.63	135.04	127.17
36	A1	2281	A2M	N3-C4-N9	4.63	135.04	127.17
36	A1	2288	OMG	N9-C4-N3	4.62	135.19	125.95
36	A1	2256	A2M	N3-C4-N9	4.61	135.02	127.17
36	A1	649	A2M	N3-C4-N9	4.59	134.98	127.17
32	B5	436	A2M	N3-C4-N9	4.59	134.98	127.17
32	B5	1773	4AC	C6-C5-C4	4.57	122.51	117.00
36	A1	2946	A2M	N3-C4-N9	4.57	134.94	127.17
32	B5	974	A2M	N3-C4-N9	4.56	134.91	127.17
36	A1	645	1MA	C2-N3-C4	4.54	121.43	112.53
32	B5	562	OMG	N9-C4-N3	4.53	135.01	125.95
36	A1	2142	1MA	C2-N3-C4	4.53	121.41	112.53
32	B5	1271	OMG	N9-C4-N3	4.53	135.00	125.95
36	A1	1888	OMU	N3-C2-N1	4.52	120.78	114.89
36	A1	2619	OMG	N9-C4-N3	4.51	134.98	125.95
36	A1	2791	OMG	N9-C4-N3	4.51	134.97	125.95
32	B5	1575	G7M	C2-N3-C4	4.50	120.06	112.30
36	A1	817	A2M	N3-C4-N9	4.50	134.82	127.17
36	A1	2922	OMG	N9-C4-N3	4.49	134.93	125.95
36	A1	2793	OMG	N9-C4-N3	4.49	134.93	125.95
32	B5	796	A2M	N3-C4-N9	4.49	134.80	127.17
32	B5	420	A2M	N3-C4-N9	4.47	134.77	127.17
36	A1	807	A2M	N3-C4-N9	4.46	134.75	127.17
36	A1	2815	OMG	N9-C4-N3	4.46	134.87	125.95
32	B5	619	A2M	N3-C4-N9	4.44	134.72	127.17

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	1450	OMG	N9-C4-N3	4.42	134.79	125.95
36	A1	1133	A2M	N3-C4-N9	4.42	134.68	127.17
32	B5	1572	OMG	N9-C4-N3	4.37	134.69	125.95
32	B5	1781	MA6	C2-N1-C6	4.34	122.43	111.83
36	A1	2421	OMU	N3-C2-N1	4.31	120.50	114.89
32	B5	1781	MA6	N3-C4-N9	4.30	134.47	127.17
36	A1	2921	OMU	N3-C2-N1	4.29	120.48	114.89
32	B5	1782	MA6	C2-N1-C6	4.28	122.29	111.83
36	A1	2417	OMU	N3-C2-N1	4.27	120.45	114.89
36	A1	2729	OMU	N3-C2-N1	4.27	120.45	114.89
36	A1	898	OMU	N3-C2-N1	4.26	120.44	114.89
32	B5	1269	OMU	N3-C2-N1	4.24	120.41	114.89
32	B5	1782	MA6	C4-C5-N7	-4.23	105.74	110.58
32	B5	1126	OMG	C6-C5-N7	4.21	137.94	130.29
32	B5	578	OMU	N3-C2-N1	4.15	120.29	114.89
36	A1	2220	A2M	N3-C4-N9	4.14	134.21	127.17
36	A1	805	OMG	N9-C4-N3	4.13	134.21	125.95
36	A1	2724	OMU	N3-C2-N1	4.11	120.24	114.89
36	A1	2347	OMU	N3-C2-N1	4.08	120.21	114.89
36	A1	2421	OMU	C5-C4-N3	4.06	120.49	114.80
36	A1	2347	OMU	C5-C4-N3	4.01	120.42	114.80
32	B5	1782	MA6	N3-C4-N9	4.00	133.97	127.17
36	A1	2921	OMU	C5-C4-N3	4.00	120.40	114.80
32	B5	796	A2M	C2'-C1'-N9	-3.99	107.19	113.75
36	A1	2281	A2M	C2'-C1'-N9	-3.98	107.20	113.75
36	A1	898	OMU	C5-C4-N3	3.96	120.34	114.80
32	B5	1781	MA6	C4-C5-N7	-3.96	106.06	110.58
36	A1	2870	5MC	C5-C6-N1	-3.95	119.03	123.31
36	A1	2417	OMU	C5-C4-N3	3.94	120.33	114.80
36	A1	2724	OMU	C5-C4-N3	3.94	120.32	114.80
36	A1	2946	A2M	C2'-C1'-N9	-3.90	107.33	113.75
36	A1	2729	OMU	C5-C4-N3	3.89	120.25	114.80
36	A1	1888	OMU	C5-C4-N3	3.86	120.20	114.80
32	B5	578	OMU	C5-C4-N3	3.83	120.17	114.80
32	B5	541	A2M	C2-N3-C4	3.83	121.19	111.83
32	B5	1575	G7M	O2'-C2'-C3'	3.83	124.09	111.82
36	A1	2281	A2M	O4'-C1'-N9	3.80	115.38	108.09
36	A1	876	A2M	C2-N3-C4	3.79	121.08	111.83
32	B5	1269	OMU	C5-C4-N3	3.79	120.10	114.80
32	B5	436	A2M	C2-N3-C4	3.77	121.05	111.83
36	A1	1449	A2M	C2-N3-C4	3.77	121.04	111.83
32	B5	1126	OMG	N9-C4-N3	3.76	133.48	125.95

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	B5	1575	G7M	C8-N9-C4	3.76	116.40	107.09
36	A1	2946	A2M	C2-N3-C4	3.75	120.98	111.83
36	A1	2142	1MA	N9-C4-N3	3.74	135.43	126.90
36	A1	2640	A2M	C2-N3-C4	3.74	120.97	111.83
32	B5	796	A2M	C2-N3-C4	3.74	120.96	111.83
36	A1	2256	A2M	C2-N3-C4	3.72	120.92	111.83
32	B5	1782	MA6	C2-N3-C4	3.72	120.92	111.83
32	B5	100	A2M	C2-N3-C4	3.71	120.89	111.83
36	A1	817	A2M	C2-N3-C4	3.71	120.88	111.83
32	B5	28	A2M	C2-N3-C4	3.68	120.83	111.83
36	A1	649	A2M	C2-N3-C4	3.68	120.82	111.83
32	B5	420	A2M	C2-N3-C4	3.68	120.81	111.83
36	A1	2280	A2M	C2-N3-C4	3.67	120.81	111.83
32	B5	796	A2M	C4-C5-N7	-3.67	106.39	110.58
32	B5	974	A2M	C2-N3-C4	3.66	120.78	111.83
36	A1	1133	A2M	C2-N3-C4	3.66	120.77	111.83
32	B5	619	A2M	C2-N3-C4	3.66	120.77	111.83
36	A1	2281	A2M	C2-N3-C4	3.65	120.75	111.83
32	B5	1575	G7M	O3'-C3'-C4'	3.64	121.53	111.08
36	A1	807	A2M	C4-C5-N7	-3.64	106.42	110.58
32	B5	1575	G7M	CN7-N7-C5	3.61	131.30	126.80
36	A1	805	OMG	C6-C5-N7	3.61	136.86	130.29
36	A1	807	A2M	C2-N3-C4	3.61	120.64	111.83
32	B5	619	A2M	C4-C5-N7	-3.59	106.48	110.58
32	B5	1280	4AC	N4-C4-N3	3.57	119.66	113.87
32	B5	436	A2M	C4-C5-N7	-3.57	106.50	110.58
36	A1	817	A2M	C4-C5-N7	-3.55	106.52	110.58
36	A1	2280	A2M	C4-C5-N7	-3.54	106.53	110.58
32	B5	1781	MA6	C2-N3-C4	3.53	120.45	111.83
36	A1	1133	A2M	C4-C5-N7	-3.51	106.57	110.58
36	A1	2220	A2M	C2-N3-C4	3.50	120.38	111.83
32	B5	420	A2M	C4-C5-N7	-3.49	106.59	110.58
36	A1	2946	A2M	C4-C5-N7	-3.49	106.60	110.58
36	A1	2220	A2M	N3-C2-N1	-3.48	123.31	128.58
36	A1	2256	A2M	C4-C5-N7	-3.47	106.62	110.58
32	B5	100	A2M	C4-C5-N7	-3.46	106.62	110.58
32	B5	1572	OMG	C6-C5-N7	3.46	136.59	130.29
36	A1	1133	A2M	C2'-C1'-N9	-3.45	108.08	113.75
32	B5	974	A2M	C4-C5-N7	-3.44	106.64	110.58
36	A1	649	A2M	C4-C5-N7	-3.43	106.66	110.58
32	B5	28	A2M	C4-C5-N7	-3.41	106.69	110.58
32	B5	1782	MA6	N1-C2-N3	-3.40	123.43	128.58

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	2793	OMG	C6-C5-N7	3.40	136.48	130.29
32	B5	1126	OMG	C4-C5-N7	-3.40	105.29	110.67
36	A1	1133	A2M	N3-C2-N1	-3.39	123.45	128.58
36	A1	2640	A2M	C4-C5-N7	-3.38	106.72	110.58
36	A1	649	A2M	N3-C2-N1	-3.33	123.55	128.58
32	B5	541	A2M	C4-C5-N7	-3.32	106.79	110.58
36	A1	2220	A2M	C4-C5-N7	-3.31	106.80	110.58
36	A1	876	A2M	C4-C5-N7	-3.31	106.80	110.58
36	A1	2946	A2M	N3-C2-N1	-3.30	123.58	128.58
36	A1	1449	A2M	C4-C5-N7	-3.30	106.81	110.58
36	A1	2281	A2M	N3-C2-N1	-3.30	123.59	128.58
36	A1	876	A2M	N3-C2-N1	-3.29	123.60	128.58
32	B5	562	OMG	C6-C5-N7	3.28	136.26	130.29
36	A1	2791	OMG	C6-C5-N7	3.26	136.23	130.29
36	A1	645	1MA	N9-C4-N3	3.26	134.32	126.90
32	B5	796	A2M	N3-C2-N1	-3.25	123.66	128.58
36	A1	2640	A2M	N3-C2-N1	-3.25	123.66	128.58
36	A1	2256	A2M	N3-C2-N1	-3.25	123.66	128.58
36	A1	2634	UR3	C5-C4-N3	3.25	119.32	115.04
36	A1	2724	OMU	O4-C4-C5	-3.25	119.56	125.16
32	B5	436	A2M	N3-C2-N1	-3.24	123.67	128.58
36	A1	2815	OMG	C6-C5-N7	3.24	136.19	130.29
36	A1	1449	A2M	N3-C2-N1	-3.24	123.68	128.58
32	B5	1781	MA6	N1-C2-N3	-3.23	123.70	128.58
36	A1	2281	A2M	C4-C5-N7	-3.22	106.90	110.58
36	A1	817	A2M	N3-C2-N1	-3.22	123.71	128.58
32	B5	100	A2M	N3-C2-N1	-3.22	123.71	128.58
36	A1	2619	OMG	C6-C5-N7	3.22	136.15	130.29
36	A1	2922	OMG	C6-C5-N7	3.22	136.14	130.29
32	B5	420	A2M	N3-C2-N1	-3.20	123.73	128.58
36	A1	1450	OMG	C6-C5-N7	3.20	136.11	130.29
32	B5	974	A2M	N3-C2-N1	-3.19	123.75	128.58
32	B5	1271	OMG	C6-C5-N7	3.18	136.09	130.29
32	B5	619	A2M	N3-C2-N1	-3.18	123.77	128.58
36	A1	2280	A2M	N3-C2-N1	-3.18	123.77	128.58
32	B5	541	A2M	N3-C2-N1	-3.17	123.79	128.58
32	B5	28	A2M	N3-C2-N1	-3.15	123.82	128.58
36	A1	867	OMG	C6-C5-N7	3.15	136.02	130.29
36	A1	2417	OMU	O4-C4-C5	-3.14	119.75	125.16
36	A1	2281	A2M	C4-N9-C8	3.11	109.00	105.74
36	A1	2421	OMU	O4-C4-C5	-3.09	119.83	125.16
32	B5	578	OMU	O4-C4-C5	-3.09	119.84	125.16

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	2729	OMU	O4-C4-C5	-3.08	119.85	125.16
32	B5	1773	4AC	CM7-C7-N4	3.07	120.23	115.27
36	A1	2347	OMU	O4-C4-C5	-3.07	119.87	125.16
32	B5	1428	OMG	C6-C5-N7	3.06	135.86	130.29
36	A1	2278	5MC	O2-C2-N3	-3.03	117.55	122.33
36	A1	2288	OMG	C6-C5-N7	3.03	135.80	130.29
32	B5	1269	OMU	O4-C4-C5	-3.02	119.95	125.16
32	B5	1782	MA6	C5-N7-C8	2.98	108.14	103.45
36	A1	807	A2M	N3-C2-N1	-2.98	124.07	128.58
36	A1	898	OMU	O4-C4-C5	-2.97	120.04	125.16
32	B5	1572	OMG	CM2-O2'-C2'	-2.97	106.86	114.47
36	A1	2921	OMU	O4-C4-C5	-2.96	120.06	125.16
36	A1	2278	5MC	C5-C6-N1	-2.93	120.13	123.31
34	AB	243	HIC	NE2-CE1-ND1	-2.90	111.55	112.66
32	B5	1773	4AC	C5-C4-N3	-2.90	118.06	122.60
32	B5	1575	G7M	O2'-C2'-C1'	2.84	119.87	110.10
36	A1	2278	5MC	C5-C4-N3	-2.83	118.85	121.75
32	B5	1781	MA6	C5-N7-C8	2.82	107.88	103.45
36	A1	2256	A2M	C4-N9-C8	2.81	108.69	105.74
32	B5	619	A2M	C4-N9-C8	2.81	108.69	105.74
32	B5	1773	4AC	C1'-N1-C2	2.80	124.63	118.44
36	A1	1437	OMC	O2-C2-N3	-2.80	117.92	122.33
32	B5	1781	MA6	C4-N9-C8	2.79	108.67	105.74
36	A1	1888	OMU	O4-C4-C5	-2.78	120.36	125.16
32	B5	1191	XSX	C5-C4-N3	2.77	119.47	115.64
36	A1	1133	A2M	C4-N9-C8	2.76	108.63	105.74
36	A1	807	A2M	C2'-C1'-N9	-2.75	109.23	113.75
32	B5	1782	MA6	C4-N9-C8	2.72	108.60	105.74
32	B5	100	A2M	C4-N9-C8	2.71	108.59	105.74
32	B5	1269	OMU	C1'-N1-C2	2.71	122.46	117.59
36	A1	2280	A2M	C4-N9-C8	2.70	108.58	105.74
32	B5	562	OMG	C4-C5-N7	-2.68	106.42	110.67
32	B5	1572	OMG	C4-C5-N7	-2.67	106.44	110.67
32	B5	619	A2M	C5-N7-C8	2.66	107.63	103.45
36	A1	807	A2M	C4-N9-C8	2.66	108.53	105.74
36	A1	817	A2M	C4-N9-C8	2.62	108.49	105.74
36	A1	2870	5MC	C5-C4-N3	-2.61	119.08	121.75
32	B5	420	A2M	C4-N9-C8	2.61	108.48	105.74
36	A1	2280	A2M	C5-N7-C8	2.61	107.55	103.45
36	A1	649	A2M	C4-N9-C8	2.61	108.48	105.74
36	A1	805	OMG	C4-C5-N7	-2.60	106.54	110.67
36	A1	867	OMG	C4-C5-N7	-2.60	106.55	110.67

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	B5	1782	MA6	C6-C5-N7	2.60	137.59	133.43
32	B5	100	A2M	C5-N7-C8	2.60	107.54	103.45
36	A1	807	A2M	C5-N7-C8	2.60	107.53	103.45
36	A1	908	OMG	C6-C5-N7	2.59	135.00	130.29
36	A1	1133	A2M	C5-N7-C8	2.58	107.50	103.45
36	A1	817	A2M	C5-N7-C8	2.57	107.49	103.45
36	A1	2793	OMG	C4-C5-N7	-2.57	106.60	110.67
36	A1	2640	A2M	C4-N9-C8	2.57	108.43	105.74
36	A1	2347	OMU	C1'-N1-C2	2.57	122.20	117.59
32	B5	796	A2M	C5-N7-C8	2.57	107.48	103.45
36	A1	2256	A2M	C5-N7-C8	2.57	107.48	103.45
32	B5	436	A2M	C5-N7-C8	2.56	107.47	103.45
32	B5	28	A2M	C4-N9-C8	2.56	108.42	105.74
32	B5	974	A2M	C4-N9-C8	2.54	108.41	105.74
36	A1	2640	A2M	C5-N7-C8	2.53	107.43	103.45
36	A1	649	A2M	C5-N7-C8	2.53	107.43	103.45
32	B5	796	A2M	C4-N9-C8	2.53	108.39	105.74
36	A1	2946	A2M	C5-N7-C8	2.53	107.42	103.45
32	B5	1271	OMG	C4-C5-N7	-2.52	106.67	110.67
32	B5	420	A2M	C5-N7-C8	2.52	107.42	103.45
36	A1	2922	OMG	C4-C5-N7	-2.52	106.68	110.67
32	B5	28	A2M	C5-N7-C8	2.51	107.40	103.45
36	A1	2791	OMG	C4-C5-N7	-2.50	106.71	110.67
36	A1	2619	OMG	C4-C5-N7	-2.49	106.73	110.67
36	A1	2220	A2M	C2-N1-C6	2.48	122.80	118.73
32	B5	1428	OMG	C4-C5-N7	-2.48	106.75	110.67
36	A1	1450	OMG	C4-C5-N7	-2.47	106.75	110.67
32	B5	578	OMU	O2-C2-N1	-2.47	119.58	122.80
36	A1	2281	A2M	C5-N7-C8	2.46	107.32	103.45
32	B5	974	A2M	C5-N7-C8	2.46	107.31	103.45
36	A1	645	1MA	C4-C5-N7	-2.46	106.78	110.67
32	B5	1575	G7M	C1'-N9-C8	-2.45	118.47	126.74
36	A1	2288	OMG	C4-C5-N7	-2.44	106.81	110.67
36	A1	2946	A2M	C4-N9-C8	2.43	108.29	105.74
36	A1	2815	OMG	C4-C5-N7	-2.43	106.82	110.67
32	B5	541	A2M	C5-N7-C8	2.43	107.27	103.45
36	A1	1449	A2M	C5-N7-C8	2.42	107.25	103.45
36	A1	876	A2M	C4-N9-C8	2.40	108.26	105.74
32	B5	1575	G7M	O6-C6-C5	-2.39	122.67	128.01
36	A1	2417	OMU	O2-C2-N1	-2.39	119.68	122.80
32	B5	1126	OMG	C8-N7-C5	2.37	108.48	104.26
32	B5	541	A2M	C4-N9-C8	2.35	108.21	105.74

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	B5	1575	G7M	C3'-C2'-C1'	2.34	105.90	101.46
36	A1	876	A2M	C5-N7-C8	2.34	107.12	103.45
32	B5	1280	4AC	C6-C5-C4	2.32	119.80	117.00
32	B5	436	A2M	C4-N9-C8	2.32	108.17	105.74
36	A1	2220	A2M	C4-N9-C8	2.30	108.15	105.74
32	B5	1782	MA6	N9-C8-N7	-2.29	110.68	113.94
32	B5	619	A2M	C6-C5-N7	2.28	136.49	132.09
36	A1	2948	OMC	O2-C2-N3	-2.28	118.73	122.33
36	A1	645	1MA	C6-C5-N7	2.26	136.16	132.16
36	A1	805	OMG	C2'-C1'-N9	-2.26	109.95	114.24
32	B5	1126	OMG	O6-C6-C5	-2.22	120.66	126.53
36	A1	807	A2M	C6-C5-N7	2.22	136.37	132.09
36	A1	1133	A2M	C6-C5-N7	2.22	136.37	132.09
32	B5	1126	OMG	C2'-C1'-N9	-2.21	110.04	114.24
36	A1	817	A2M	C6-C5-N7	2.21	136.35	132.09
36	A1	2281	A2M	N9-C8-N7	-2.21	110.80	113.94
36	A1	2946	A2M	O4'-C1'-N9	2.21	112.33	108.09
36	A1	908	OMG	O6-C6-C5	-2.20	120.71	126.53
32	B5	619	A2M	N9-C8-N7	-2.20	110.81	113.94
32	B5	796	A2M	C6-C5-N7	2.20	136.33	132.09
36	A1	2256	A2M	C6-C5-N7	2.20	136.33	132.09
32	B5	1191	XSX	C1-N3-C4	2.19	121.34	117.10
32	B5	1773	4AC	C1'-N1-C6	-2.19	116.10	120.78
36	A1	2220	A2M	C5-N7-C8	2.18	106.88	103.45
36	A1	2870	5MC	O2-C2-N3	-2.18	118.89	122.33
36	A1	908	OMG	C4-C5-N7	-2.18	107.22	110.67
32	B5	420	A2M	C2'-C1'-N9	-2.17	110.17	113.75
36	A1	2337	OMC	O2-C2-N3	-2.17	118.92	122.33
32	B5	1428	OMG	O6-C6-C5	-2.16	120.82	126.53
36	A1	2793	OMG	O6-C6-C5	-2.16	120.82	126.53
36	A1	1449	A2M	C4-N9-C8	2.16	108.00	105.74
36	A1	2421	OMU	O2-C2-N1	-2.14	120.01	122.80
32	B5	420	A2M	C6-C5-N7	2.14	136.22	132.09
36	A1	2724	OMU	O2-C2-N1	-2.14	120.01	122.80
36	A1	2791	OMG	O6-C6-C5	-2.14	120.89	126.53
36	A1	2220	A2M	C6-C5-N7	2.13	136.19	132.09
32	B5	1271	OMG	O6-C6-C5	-2.12	120.94	126.53
36	A1	649	A2M	C6-C5-N7	2.11	136.16	132.09
36	A1	2256	A2M	N9-C8-N7	-2.11	110.95	113.94
36	A1	1133	A2M	N9-C8-N7	-2.10	110.96	113.94
32	B5	436	A2M	C6-C5-N7	2.10	136.14	132.09
36	A1	2281	A2M	C6-C5-N7	2.10	136.13	132.09

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	2619	OMG	O6-C6-C5	-2.09	121.01	126.53
32	B5	1572	OMG	O6-C6-C5	-2.09	121.01	126.53
36	A1	2280	A2M	C6-C5-N7	2.09	136.12	132.09
36	A1	1888	OMU	O2-C2-N1	-2.09	120.08	122.80
36	A1	2815	OMG	O6-C6-C5	-2.09	121.03	126.53
36	A1	2288	OMG	O6-C6-C5	-2.08	121.04	126.53
36	A1	2922	OMG	O6-C6-C5	-2.08	121.04	126.53
36	A1	805	OMG	O6-C6-C5	-2.07	121.06	126.53
36	A1	2724	OMU	C1'-N1-C2	2.07	121.31	117.59
36	A1	2946	A2M	C6-C5-N7	2.07	136.08	132.09
32	B5	1191	XSX	C6-N1-C2	-2.06	120.11	121.80
32	B5	974	A2M	C6-C5-N7	2.06	136.05	132.09
32	B5	1781	MA6	C6-C5-N7	2.06	136.71	133.43
32	B5	100	A2M	N9-C8-N7	-2.05	111.02	113.94
79	DC	699	DDE	CAU-CBW-CBI	-2.04	107.22	111.22
32	B5	1781	MA6	N9-C8-N7	-2.04	111.04	113.94
36	A1	1450	OMG	O6-C6-C5	-2.03	121.17	126.53
32	B5	414	OMC	O2-C2-N3	-2.03	119.13	122.33
36	A1	2280	A2M	N9-C8-N7	-2.03	111.06	113.94
32	B5	100	A2M	C6-C5-N7	2.02	135.98	132.09
36	A1	1437	OMC	C1'-N1-C2	2.01	122.88	118.44
36	A1	867	OMG	O6-C6-C5	-2.00	121.24	126.53
36	A1	645	1MA	N1-C2-N3	-2.00	123.62	126.00

There are no chirality outliers.

All (86) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	B5	414	OMC	C1'-C2'-O2'-CM2
32	B5	420	A2M	C1'-C2'-O2'-CM'
32	B5	562	OMG	C1'-C2'-O2'-CM2
32	B5	1191	XSX	C3-C1-N3-C2
32	B5	1191	XSX	C3-C1-N3-C4
32	B5	1191	XSX	N4-C7-C9-O11
32	B5	1269	OMU	O4'-C1'-N1-C2
32	B5	1269	OMU	O4'-C1'-N1-C6
32	B5	1271	OMG	C1'-C2'-O2'-CM2
79	DC	699	DDE	O-C-CA-CB
79	DC	699	DDE	CBI-CBW-NCB-CAB
79	DC	699	DDE	CBI-CBW-NCB-CAC
79	DC	699	DDE	CBI-CBW-NCB-CAA
79	DC	699	DDE	CAU-CBW-NCB-CAB

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
79	DC	699	DDE	CAU-CBW-NCB-CAC
79	DC	699	DDE	CAU-CBW-NCB-CAA
32	B5	1280	4AC	N3-C4-N4-C7
32	B5	1280	4AC	C5-C4-N4-C7
32	B5	1280	4AC	O7-C7-N4-C4
32	B5	1280	4AC	CM7-C7-N4-C4
32	B5	1773	4AC	N3-C4-N4-C7
36	A1	663	OMC	C1'-C2'-O2'-CM2
36	A1	1437	OMC	C1'-C2'-O2'-CM2
36	A1	2197	OMC	C2'-C1'-N1-C2
36	A1	2197	OMC	C2'-C1'-N1-C6
36	A1	2220	A2M	C1'-C2'-O2'-CM'
36	A1	2337	OMC	C1'-C2'-O2'-CM2
36	A1	2421	OMU	C1'-C2'-O2'-CM2
36	A1	2619	OMG	C1'-C2'-O2'-CM2
36	A1	2724	OMU	C1'-C2'-O2'-CM2
36	A1	2729	OMU	O4'-C4'-C5'-O5'
36	A1	2791	OMG	C1'-C2'-O2'-CM2
32	B5	1572	OMG	C3'-C4'-C5'-O5'
32	B5	1782	MA6	O4'-C4'-C5'-O5'
36	A1	2197	OMC	O4'-C4'-C5'-O5'
36	A1	2280	A2M	C3'-C4'-C5'-O5'
36	A1	2729	OMU	C3'-C4'-C5'-O5'
32	B5	1191	XSX	N4-C7-C9-O10
32	B5	541	A2M	O4'-C4'-C5'-O5'
32	B5	1572	OMG	O4'-C4'-C5'-O5'
36	A1	1437	OMC	C3'-C4'-C5'-O5'
36	A1	1437	OMC	O4'-C4'-C5'-O5'
36	A1	2197	OMC	C3'-C4'-C5'-O5'
36	A1	2280	A2M	O4'-C4'-C5'-O5'
32	B5	541	A2M	C3'-C4'-C5'-O5'
32	B5	619	A2M	C3'-C4'-C5'-O5'
32	B5	619	A2M	O4'-C4'-C5'-O5'
32	B5	1782	MA6	C3'-C4'-C5'-O5'
36	A1	2870	5MC	C2'-C1'-N1-C6
32	B5	1428	OMG	O4'-C4'-C5'-O5'
36	A1	2281	A2M	O4'-C4'-C5'-O5'
32	B5	541	A2M	C4'-C5'-O5'-P
36	A1	2256	A2M	O4'-C4'-C5'-O5'
36	A1	2256	A2M	C3'-C4'-C5'-O5'
36	A1	2281	A2M	C3'-C4'-C5'-O5'
32	B5	1773	4AC	O7-C7-N4-C4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
32	B5	1773	4AC	CM7-C7-N4-C4
36	A1	2729	OMU	C1'-C2'-O2'-CM2
36	A1	817	A2M	C4'-C5'-O5'-P
32	B5	619	A2M	C2'-C1'-N9-C8
36	A1	2870	5MC	O4'-C1'-N1-C6
32	B5	1191	XSX	C3-C7-C9-O11
36	A1	2870	5MC	O4'-C1'-N1-C2
36	A1	2922	OMG	C3'-C2'-O2'-CM2
36	A1	2197	OMC	O4'-C1'-N1-C6
36	A1	2870	5MC	C2'-C1'-N1-C2
36	A1	2793	OMG	C3'-C2'-O2'-CM2
32	B5	1428	OMG	C4'-C5'-O5'-P
36	A1	2256	A2M	C4'-C5'-O5'-P
36	A1	645	1MA	C2'-C1'-N9-C8
36	A1	1888	OMU	C3'-C2'-O2'-CM2
32	B5	541	A2M	O4'-C1'-N9-C8
32	B5	619	A2M	O4'-C1'-N9-C8
36	A1	807	A2M	O4'-C1'-N9-C8
36	A1	2197	OMC	O4'-C1'-N1-C2
32	B5	1269	OMU	O4'-C4'-C5'-O5'
32	B5	541	A2M	C2'-C1'-N9-C8
36	A1	645	1MA	C2'-C1'-N9-C4
36	A1	2417	OMU	O4'-C4'-C5'-O5'
32	B5	1773	4AC	C5-C4-N4-C7
32	B5	1191	XSX	C3-C7-C9-O10
36	A1	2278	5MC	O4'-C4'-C5'-O5'
36	A1	1450	OMG	C4'-C5'-O5'-P
32	B5	1126	OMG	C4'-C5'-O5'-P
32	B5	1269	OMU	C4'-C5'-O5'-P
36	A1	1437	OMC	C2'-C1'-N1-C2

There are no ring outliers.

29 monomers are involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	A1	2724	OMU	2	0
36	A1	2793	OMG	1	0
36	A1	2197	OMC	2	0
36	A1	1133	A2M	1	0
32	B5	562	OMG	1	0
32	B5	1280	4AC	5	0
36	A1	2256	A2M	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	A1	1449	A2M	1	0
36	A1	2281	A2M	1	0
32	B5	1572	OMG	1	0
36	A1	649	A2M	2	0
36	A1	807	A2M	1	0
32	B5	1126	OMG	1	0
32	B5	1269	OMU	1	0
36	A1	663	OMC	1	0
32	B5	28	A2M	1	0
32	B5	1575	G7M	3	0
32	B5	974	A2M	1	0
32	B5	796	A2M	1	0
36	A1	2421	OMU	1	0
32	B5	100	A2M	1	0
36	A1	876	A2M	1	0
36	A1	2220	A2M	4	0
32	B5	436	A2M	1	0
32	B5	1639	OMC	2	0
36	A1	2417	OMU	1	0
36	A1	650	OMC	2	0
36	A1	817	A2M	1	0
32	B5	1773	4AC	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 257 ligands modelled in this entry, 256 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	$\# Z > 2$
85	GDP	DC	901	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	6 (13%)

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
85	GDP	DC	901	-	-	2/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	DC	901	GDP	C5-C4	3.05	1.47	1.38
85	DC	901	GDP	C6-N1	-2.43	1.34	1.38
85	DC	901	GDP	C5-N7	-2.06	1.34	1.39

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	DC	901	GDP	C5-C4-N3	-5.90	119.00	128.39
85	DC	901	GDP	C2-N3-C4	4.89	120.72	112.30
85	DC	901	GDP	N9-C4-N3	4.41	134.76	125.95
85	DC	901	GDP	C6-C5-N7	3.31	136.31	130.29
85	DC	901	GDP	C4-C5-N7	-2.56	106.62	110.67
85	DC	901	GDP	O6-C6-C5	-2.08	121.04	126.53

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
85	DC	901	GDP	C3'-C4'-C5'-O5'
85	DC	901	GDP	O4'-C4'-C5'-O5'

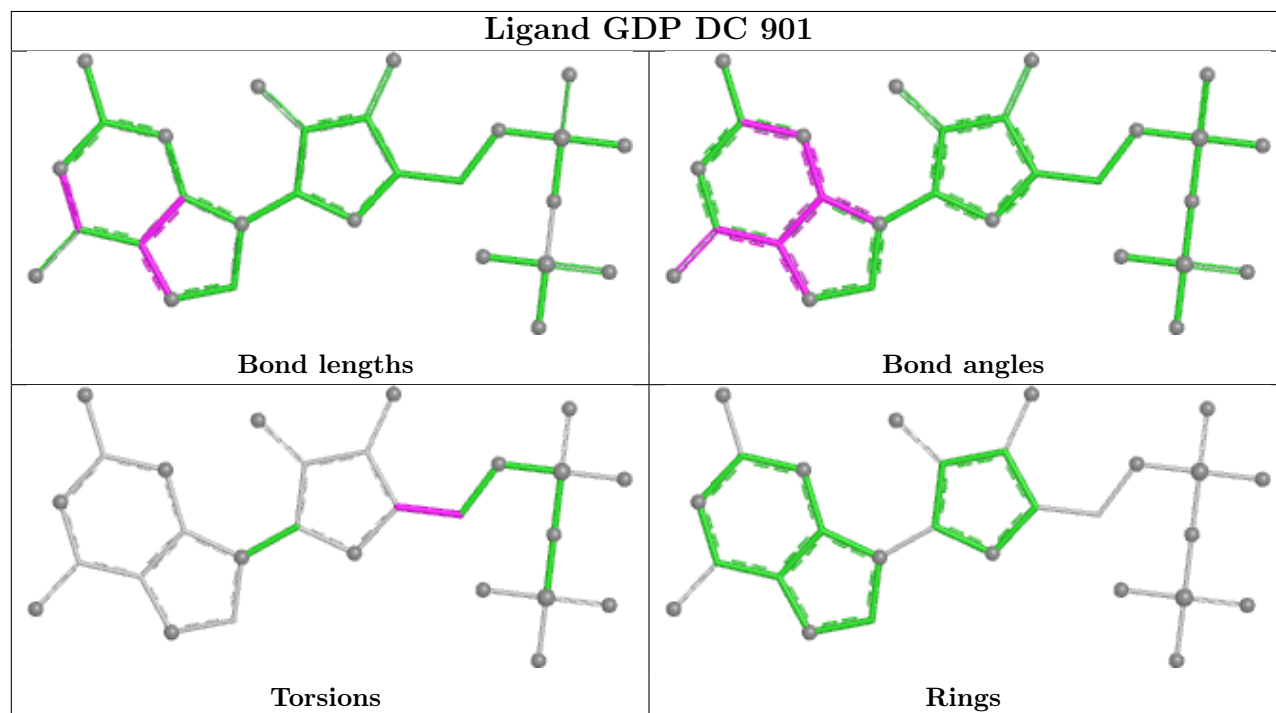
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	DC	901	GDP	1	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.

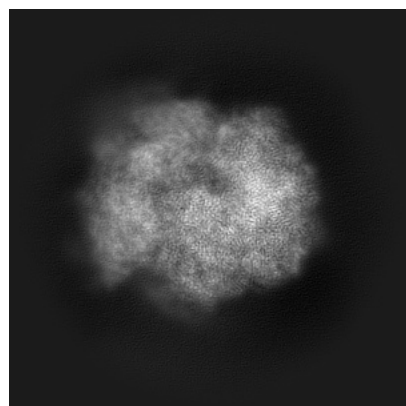
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28610. These allow visual inspection of the internal detail of the map and identification of artifacts.

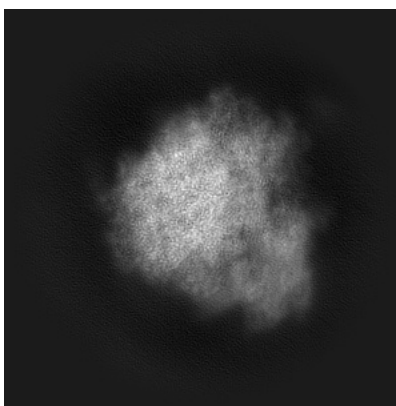
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

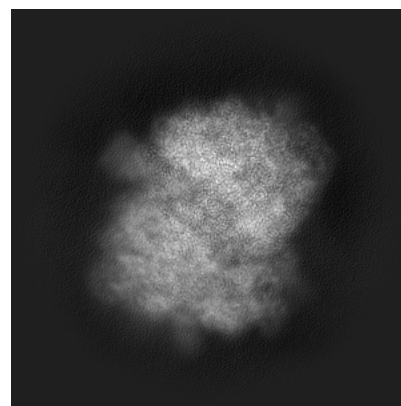
6.1.1 Primary map



X

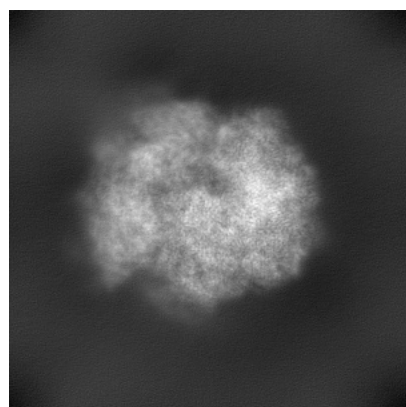


Y

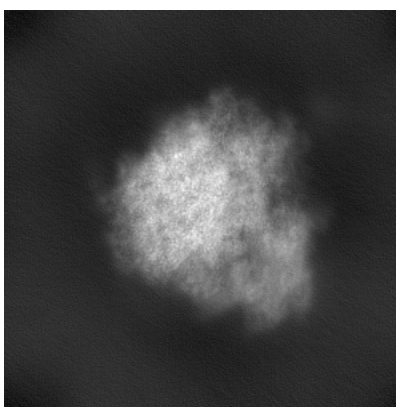


Z

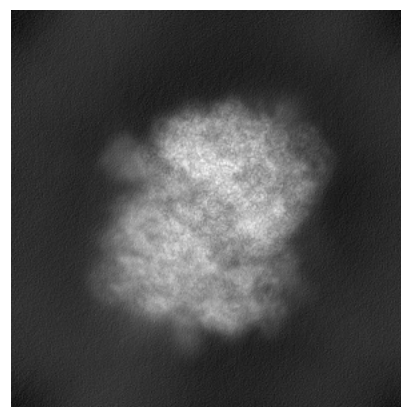
6.1.2 Raw map



X



Y

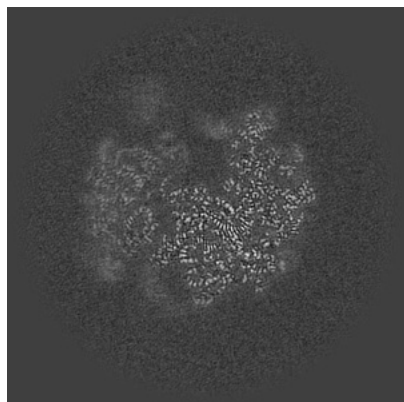


Z

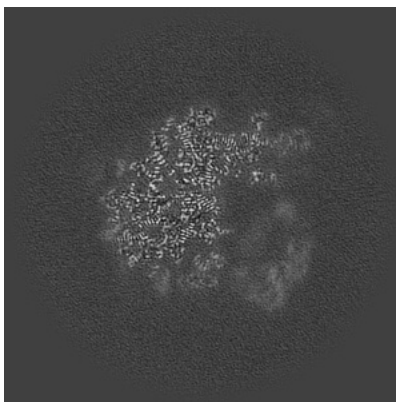
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

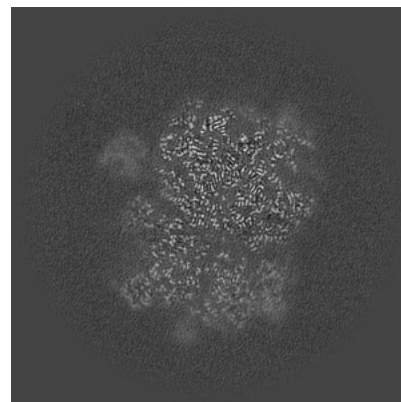
6.2.1 Primary map



X Index: 200

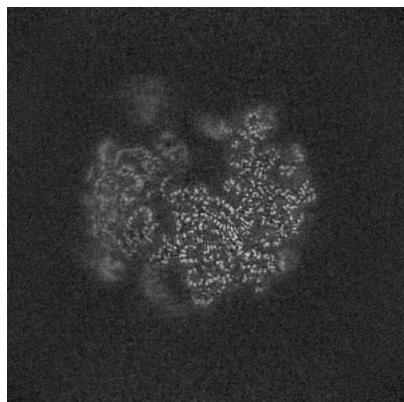


Y Index: 200

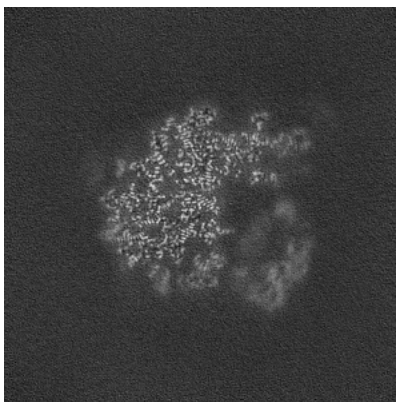


Z Index: 200

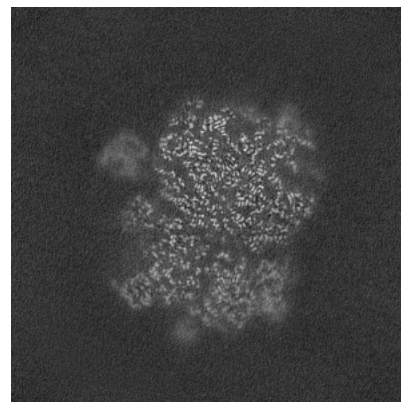
6.2.2 Raw map



X Index: 200



Y Index: 200

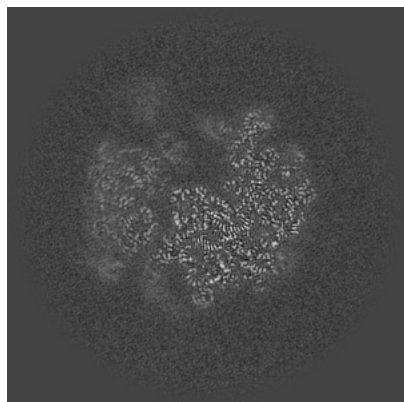


Z Index: 200

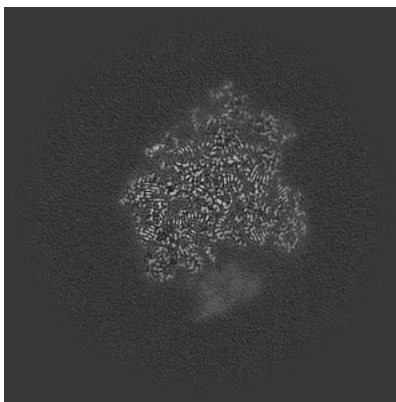
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

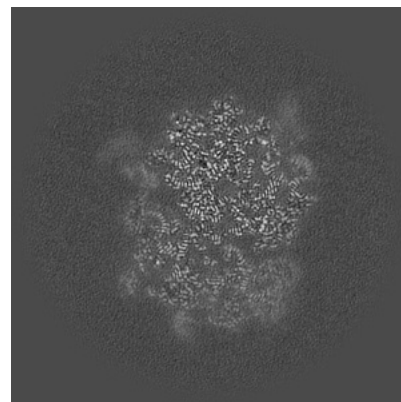
6.3.1 Primary map



X Index: 201

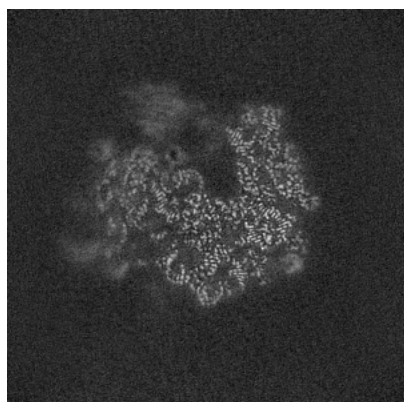


Y Index: 246

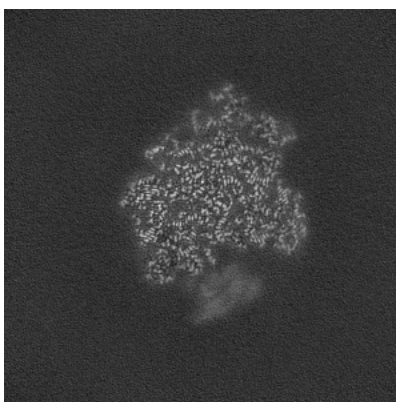


Z Index: 190

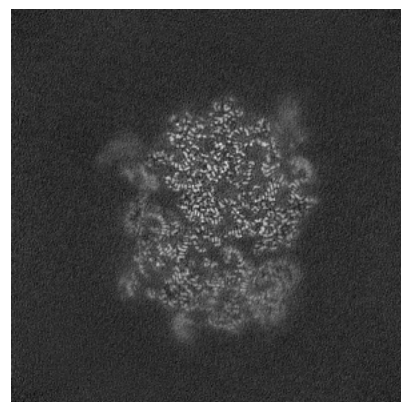
6.3.2 Raw map



X Index: 186



Y Index: 246

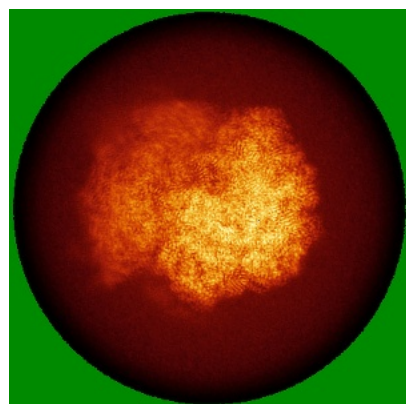


Z Index: 190

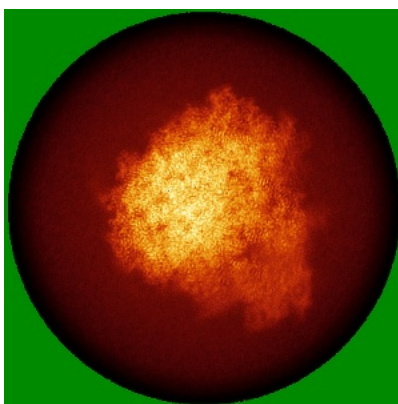
The images above show the largest variance slices of the map in three orthogonal directions.

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

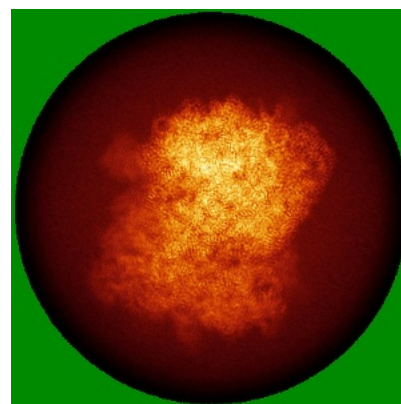
6.4.1 Primary map



X

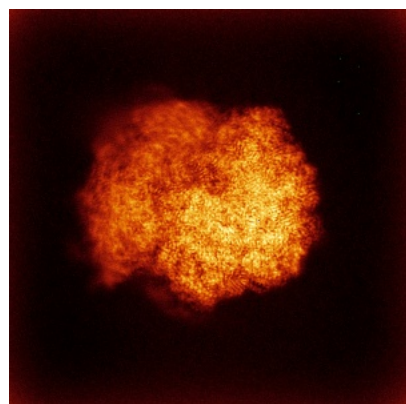


Y

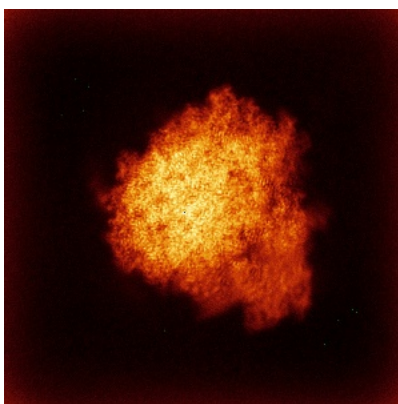


Z

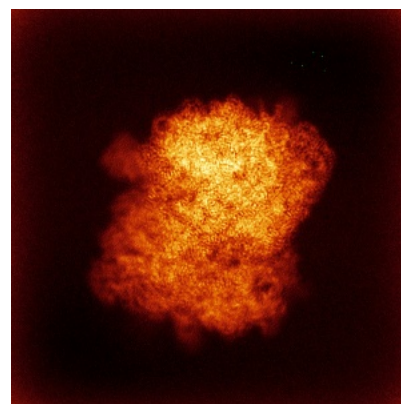
6.4.2 Raw map



X



Y

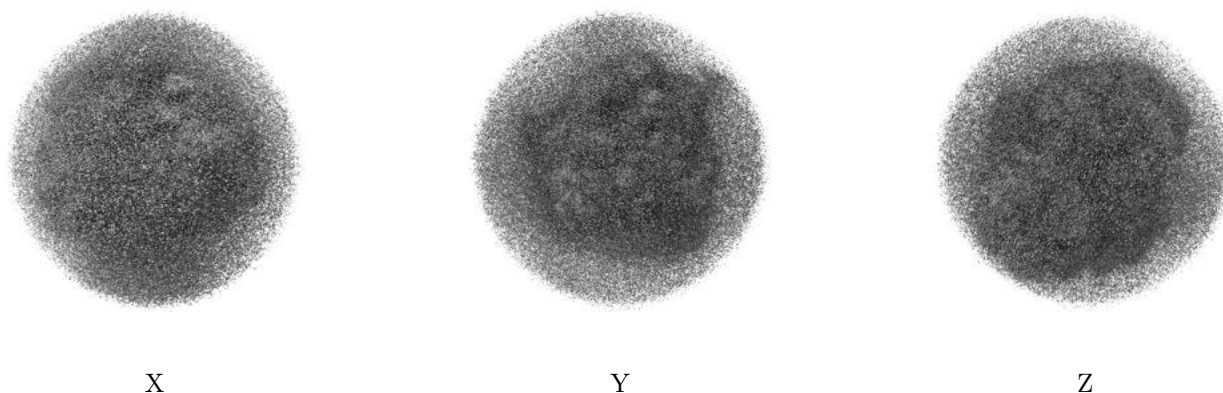


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

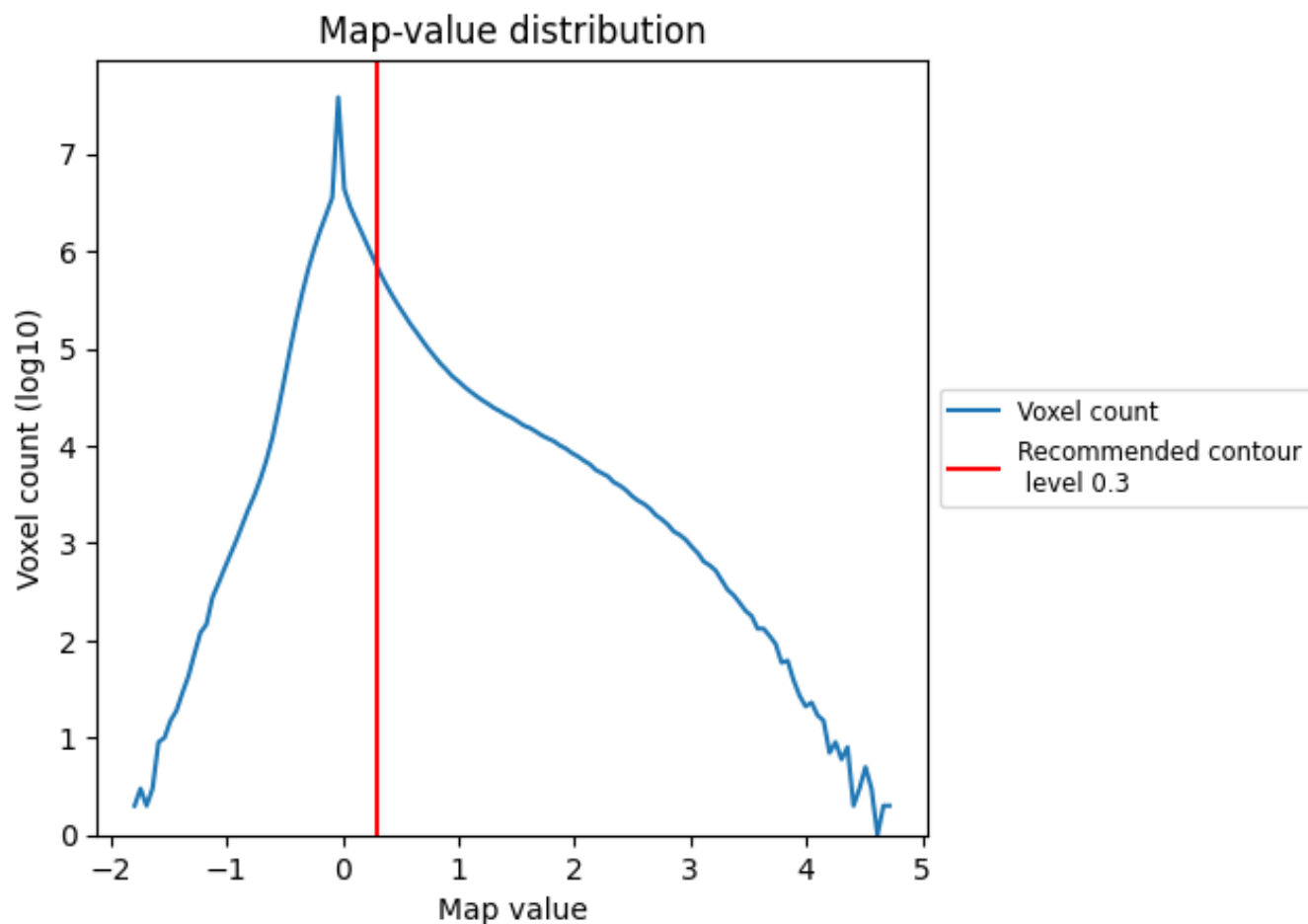
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

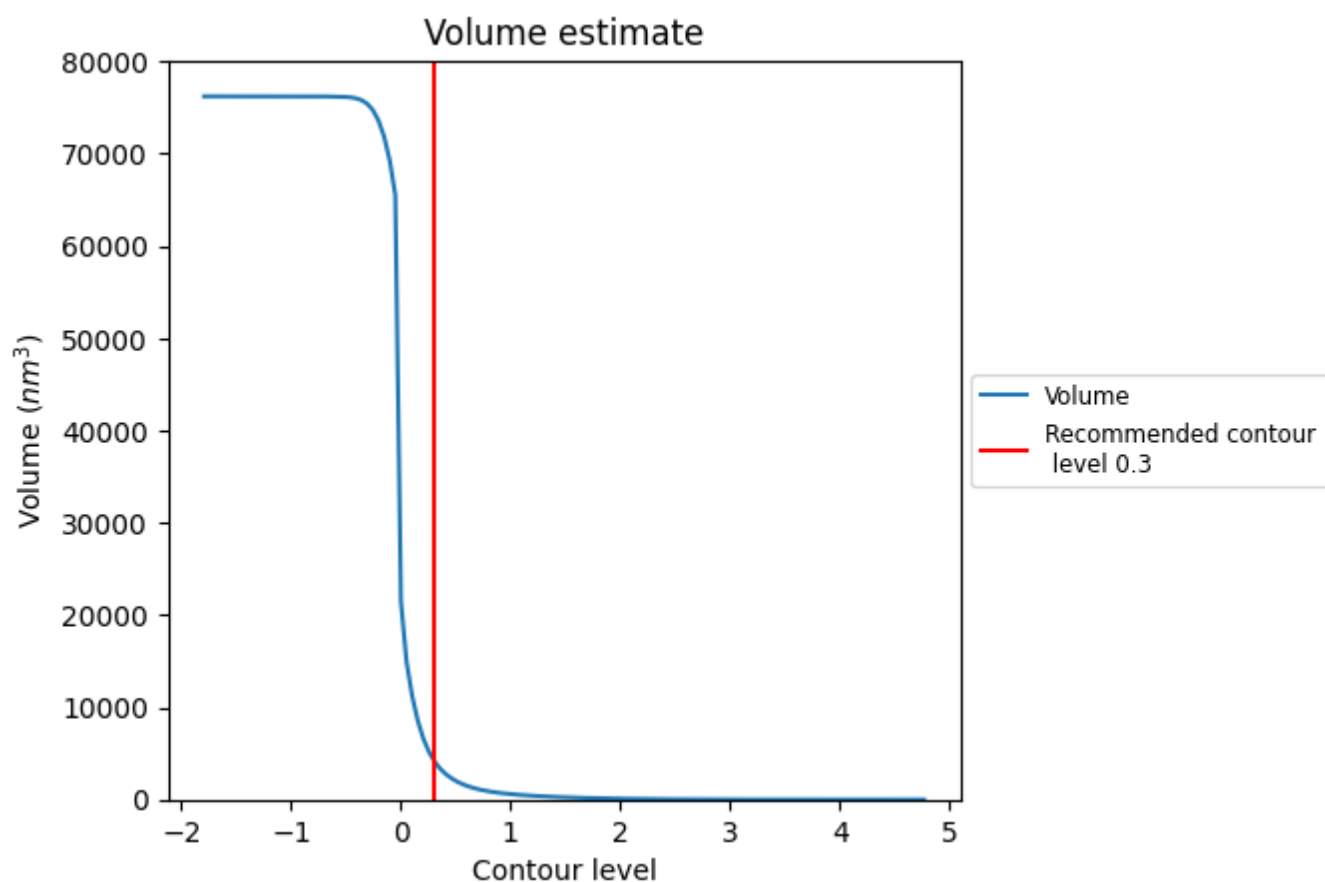
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

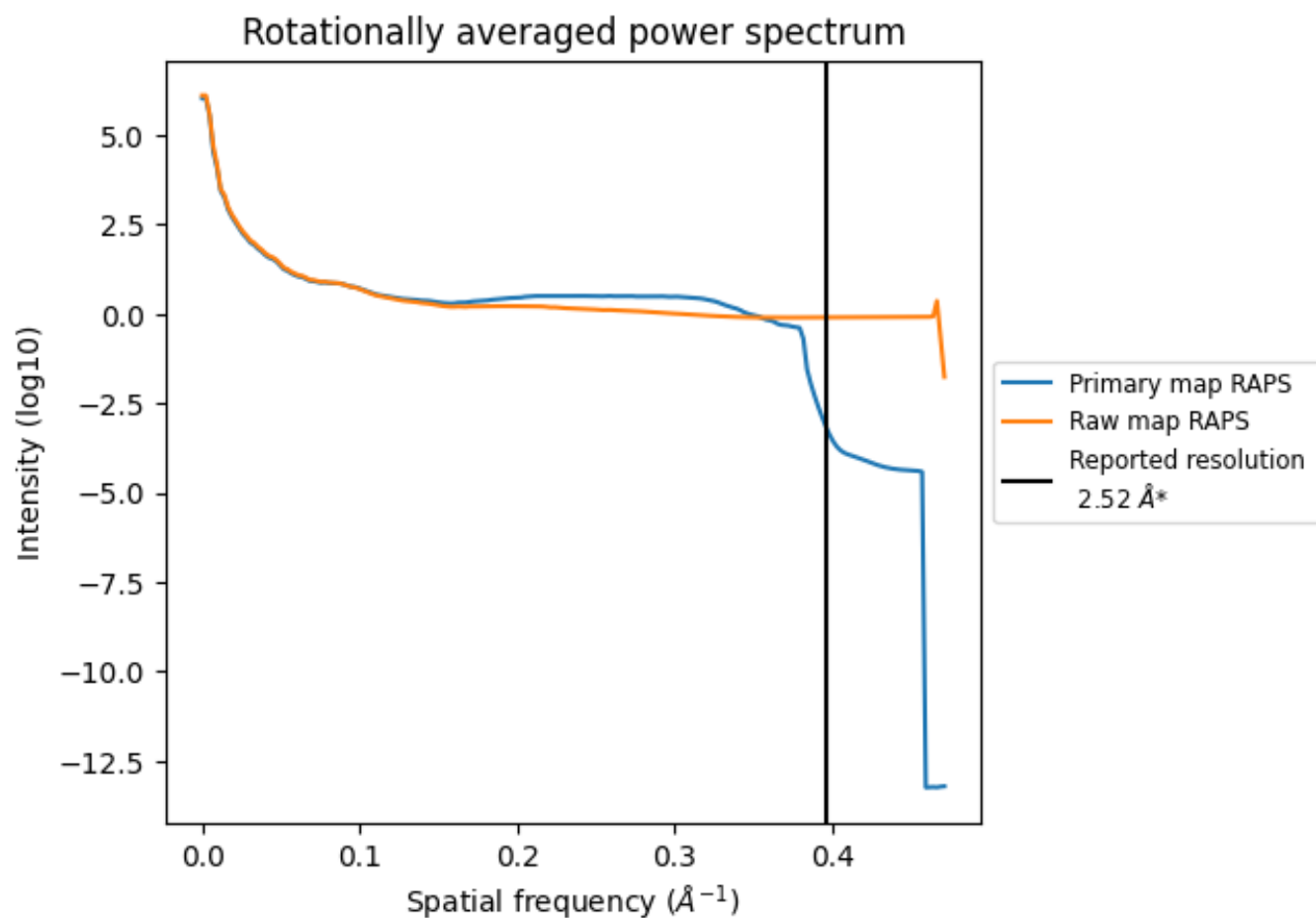
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4289 nm³; this corresponds to an approximate mass of 3874 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 ⓘ

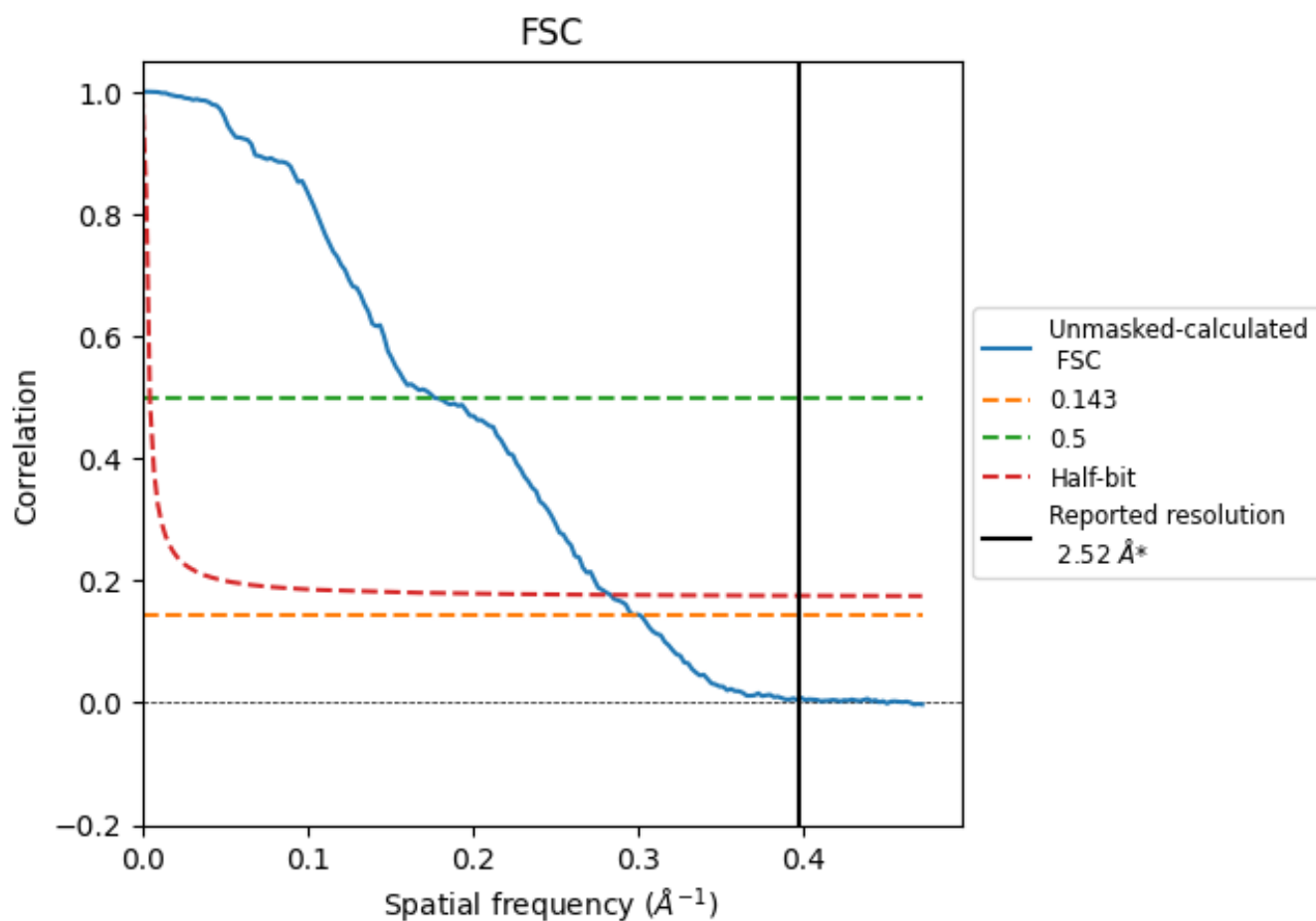


*Reported resolution corresponds to spatial frequency of 0.397 Å⁻¹

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 0.397 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.52	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.37	5.67	3.53

*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 3.37 differs from the reported value 2.52 by more than 10 %

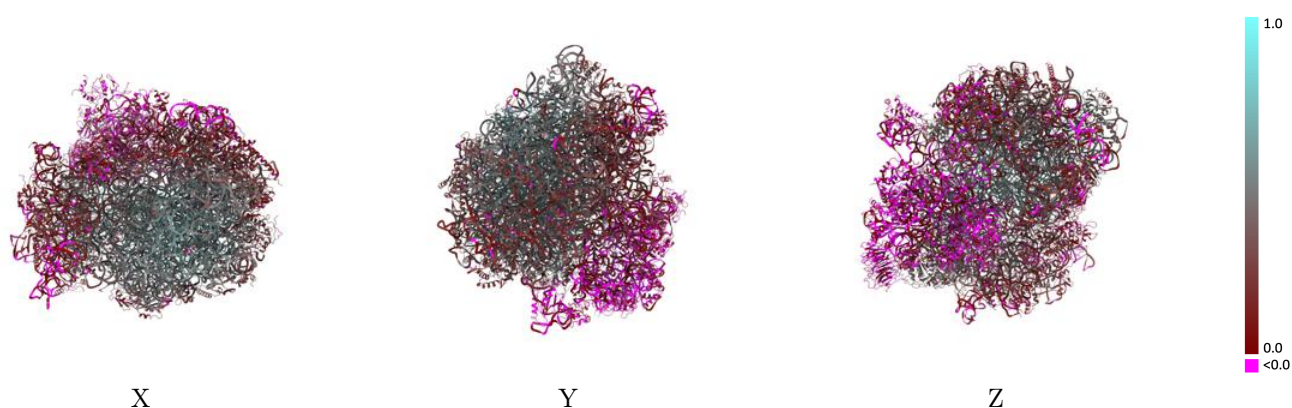
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-28610 and PDB model 8EUB. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

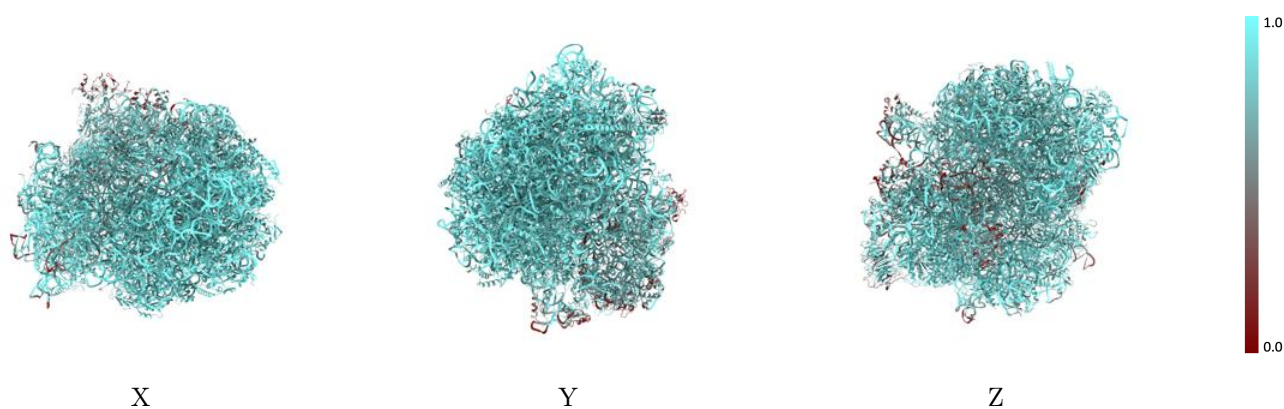
This section was not generated.

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



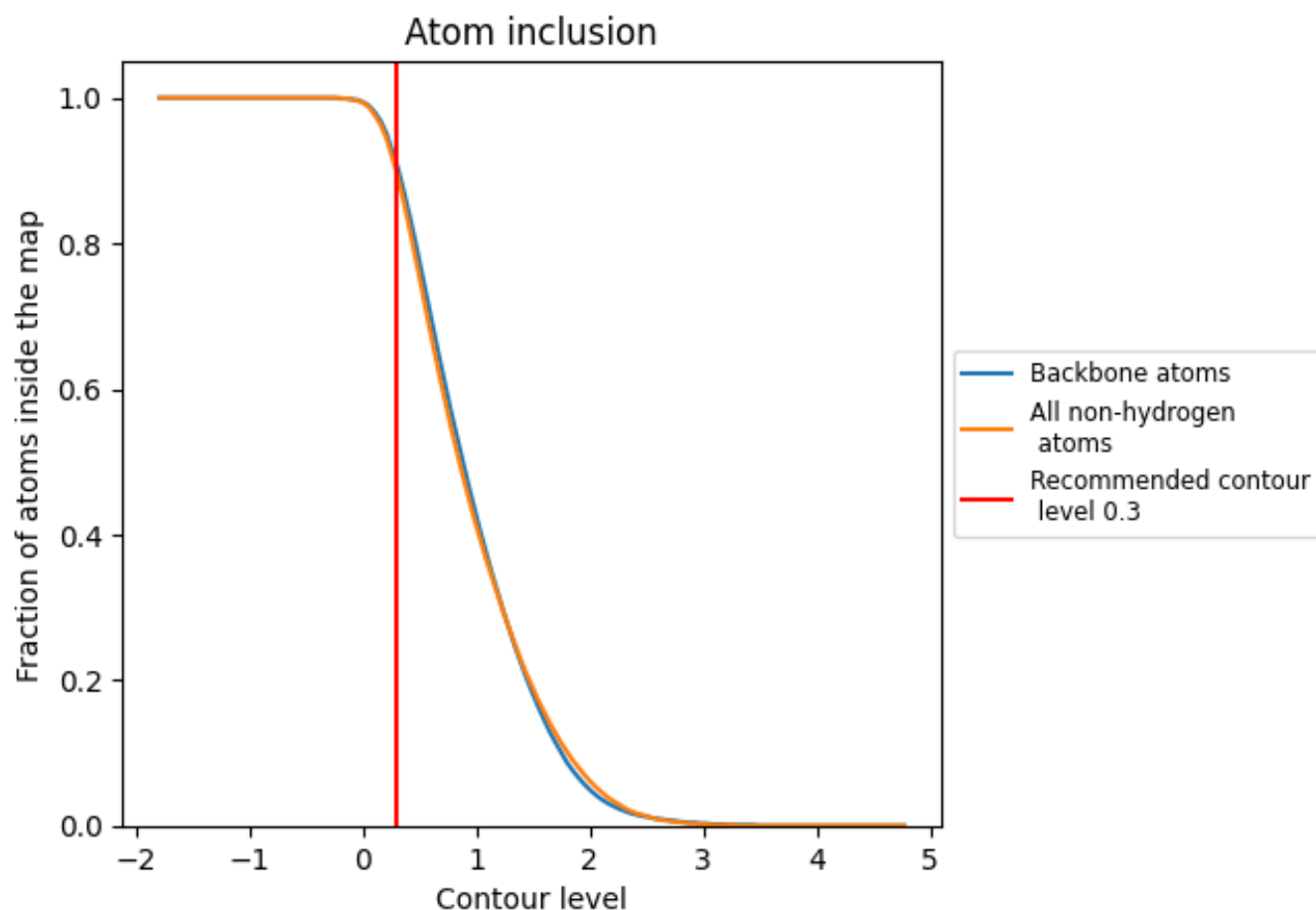
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8960	 0.3190
A1	 0.9640	 0.4260
A3	 0.9010	 0.2260
A4	 0.9740	 0.4720
AA	 0.9870	 0.5900
AB	 0.9600	 0.4810
AC	 0.9080	 0.3380
AD	 0.7540	 0.0920
AE	 0.9300	 0.3710
AF	 0.8930	 0.2610
AG	 0.8840	 0.3370
AH	 0.8490	 0.2560
AI	 0.8640	 0.2530
AJ	 0.7480	 0.1020
AL	 0.8820	 0.2630
AM	 0.8750	 0.2830
AN	 0.9560	 0.4520
AO	 0.9580	 0.4650
AP	 0.9840	 0.5890
AQ	 0.8770	 0.2750
AR	 0.9110	 0.4220
AS	 0.8470	 0.2250
AT	 0.8610	 0.2410
AU	 0.8730	 0.2700
AV	 0.9350	 0.4410
AW	 0.9510	 0.4180
AX	 0.9190	 0.3810
AY	 0.9270	 0.3720
AZ	 0.9190	 0.3610
Aa	 0.8850	 0.3200
Ab	 0.8830	 0.2320
Ac	 0.9450	 0.4620
Ad	 0.9490	 0.4800
Ae	 0.9750	 0.4920
Af	 0.9790	 0.5020



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Ag	 0.9580	 0.4780
Ah	 0.8940	 0.3110
Ai	 0.8910	 0.2990
Aj	 0.9800	 0.5260
Ak	 0.8360	 0.2890
Al	 0.9810	 0.5460
Am	 0.8960	 0.3090
An	 0.9670	 0.4900
Ao	 0.8960	 0.3540
Ap	 0.9760	 0.5740
B5	 0.9140	 0.2600
BA	 0.9550	 0.4160
BB	 0.9180	 0.4220
BC	 0.9390	 0.3920
BD	 0.7680	 0.0650
BE	 0.9050	 0.2300
BF	 0.6140	 -0.0070
BG	 0.8730	 0.1930
BH	 0.8650	 0.3080
BI	 0.9050	 0.3060
BJ	 0.8930	 0.2510
BK	 0.7550	 0.0320
BL	 0.8870	 0.3650
BM	 0.3970	 0.0290
BN	 0.9510	 0.4650
BO	 0.9510	 0.4430
BP	 0.5560	 -0.0090
BQ	 0.7070	 -0.0180
BR	 0.7360	 0.1220
BS	 0.5970	 -0.0140
BT	 0.7040	 -0.0060
BU	 0.8440	 0.0780
BV	 0.9410	 0.3980
BW	 0.9640	 0.4410
BX	 0.9300	 0.3930
BY	 0.8640	 0.1710
BZ	 0.5240	 -0.0250
Ba	 0.9490	 0.4860
Bb	 0.9180	 0.4140
Bc	 0.6060	 0.0420
Bd	 0.8940	 0.0820
Be	 0.8500	 0.2190

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bf	 0.3450	 0.0010
Bg	 0.7110	 -0.0050
DC	 0.7690	 0.1330
E	 0.5780	 0.0160
EC	 0.6050	 0.0380
VA	 0.6510	 0.1170