



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 09:10 AM UTC

PDB ID : 8EVS / pdb_00008evs
EMDB ID : EMD-28635
Title : Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), eEF2 and GDP, Structure II
Authors : Zhao, Y.; Rai, J.; Li, H.
Deposited on : 2022-10-20
Resolution : 2.62 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

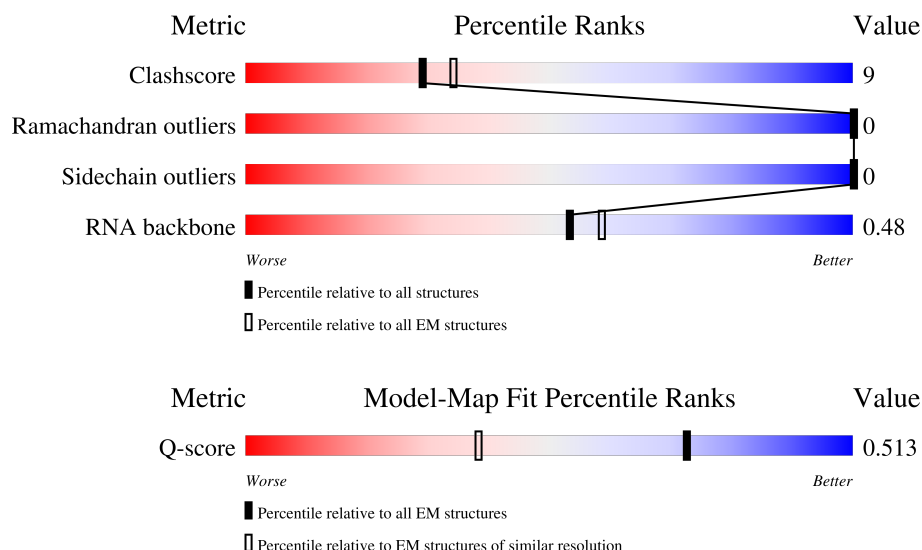
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.62 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	8810 (2.12 - 3.12)

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	 8% 62% 19% 11%
2	BB	255	 8% 59% 25% 8%
3	BC	254	 8% 62% 22% 10%

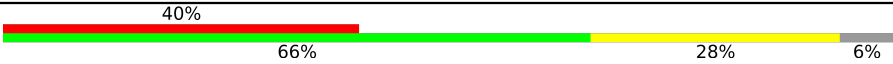
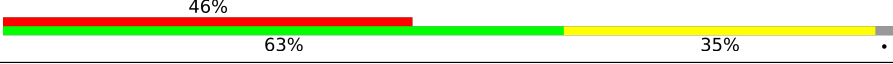
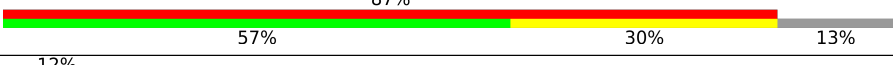
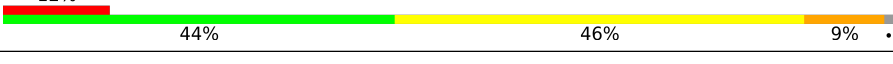
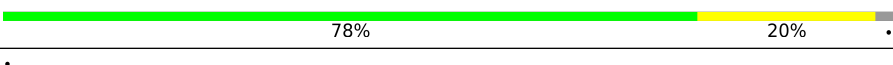
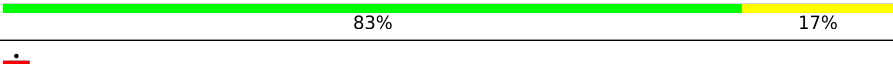
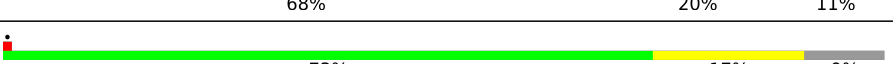
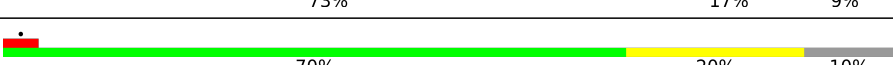
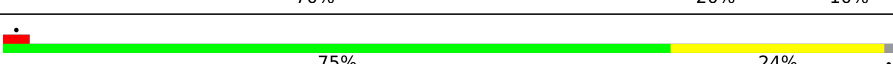
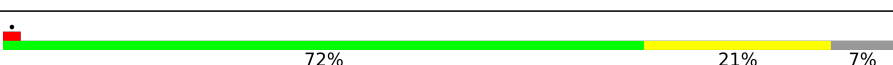
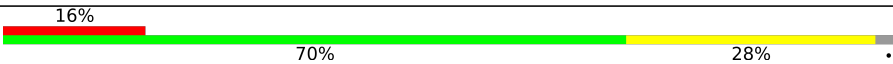
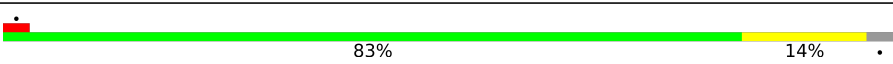
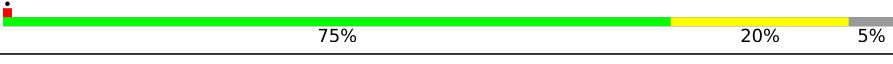
Continued on next page...

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	Bf	152	
33	BM	143	
34	B5	1798	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3199	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	221	
47	AJ	174	
48	AL	199	
49	AM	138	
50	AN	204	
51	AO	199	
52	AP	184	
53	AQ	186	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	AR	189	
55	AS	178	
56	AT	160	
57	AU	121	
58	AV	137	
59	AW	155	
60	AX	142	
61	AY	127	
62	AZ	136	
63	Aa	149	
64	Ab	59	
65	Ac	105	
66	Ad	113	
67	Ae	130	
68	Af	107	
69	Ag	121	
70	Ah	120	
71	Ai	100	
72	Aj	88	
73	Ak	78	
74	Al	51	
75	Am	128	
76	An	25	
77	Ao	106	
78	Ap	92	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	E	217	99% 65% 35%
80	DC	842	35% 64% 33%
81	V	312	30% 34% 26% 39%
82	EC	202	91% 21% 50% 25%

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 214019 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	S	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	121	Total	C	N	O	S	0	0
			975	611	183	179	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 protein called Ubiquitin-40S ribosomal protein S31.

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

- Molecule 33 is a protein called 40S ribosomal protein S12.

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

- Molecule 34 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	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 35 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	386	Total	C	N	O	S	0	0
			3080	1955	584	533	8		

- Molecule 37 is a protein called RPL4A isoform 1.

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

- Molecule 38 is a RNA chain called 25S rRNA.

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

- Molecule 39 is a RNA chain called 5s rRNA.

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

- Molecule 40 is a RNA chain called 5.8 S rRNA.

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

- Molecule 41 is a protein called RPL5 isoform 1.

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

- Molecule 42 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 46 is a protein called RPL10 isoform 1.

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

- Molecule 47 is a protein called RPL11A isoform 1.

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

- Molecule 48 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L20.

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

- Molecule 56 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 59 is a protein called RPL24A isoform 1.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 62 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L28.

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

- Molecule 64 is a protein called RPL29 isoform 1.

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

- Molecule 65 is a protein called 60S ribosomal protein L30.

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

- Molecule 66 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 67 is a protein called RPL32 isoform 1.

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

- Molecule 68 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 73 is a protein called RPL38 isoform 1.

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

- Molecule 74 is a protein called 60S ribosomal protein L39.

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

- Molecule 75 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 76 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ao	102	Total	C	N	O	S	0	0
			819	514	166	134	5		

- Molecule 78 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 79 is a protein called RPL1A isoform 1.

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

- Molecule 80 is a protein called Elongation factor 2.

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

- Molecule 81 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 82 is a RNA chain called TSV IRES.

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

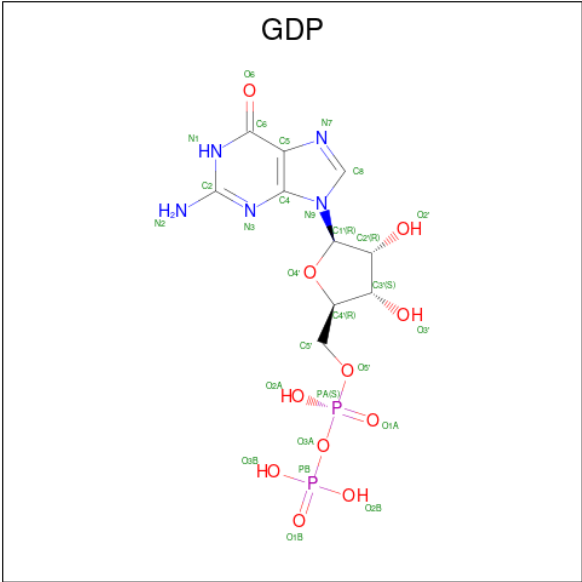
- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	BJ	1	Total 1	Mg 1	0
83	Ba	1	Total 1	Mg 1	0
83	B5	62	Total 62	Mg 62	0
83	A1	174	Total 174	Mg 174	0
83	A3	2	Total 2	Mg 2	0
83	A4	6	Total 6	Mg 6	0
83	AI	1	Total 1	Mg 1	0
83	AL	1	Total 1	Mg 1	0
83	AN	1	Total 1	Mg 1	0
83	AP	1	Total 1	Mg 1	0
83	AR	1	Total 1	Mg 1	0
83	Ae	2	Total 2	Mg 2	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).

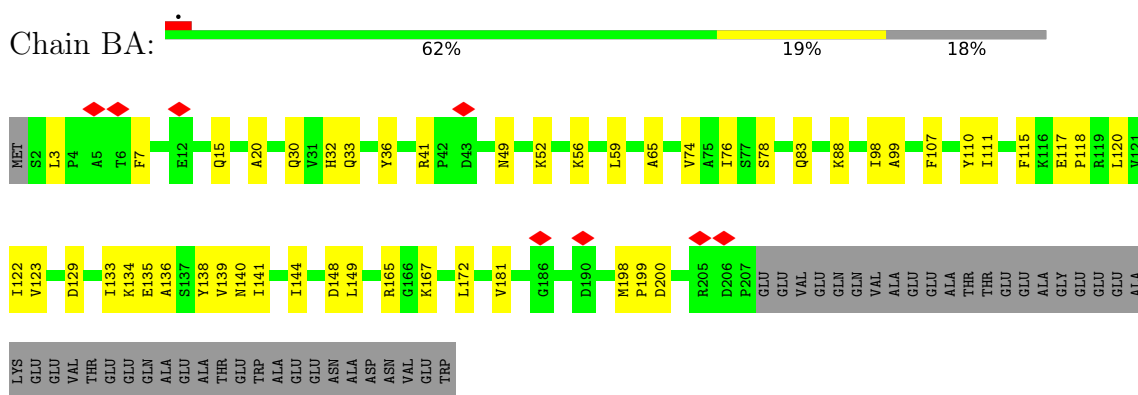


Mol	Chain	Residues	Atoms					AltConf
85	DC	1	Total	C	N	O	P	0
			28	10	5	11	2	

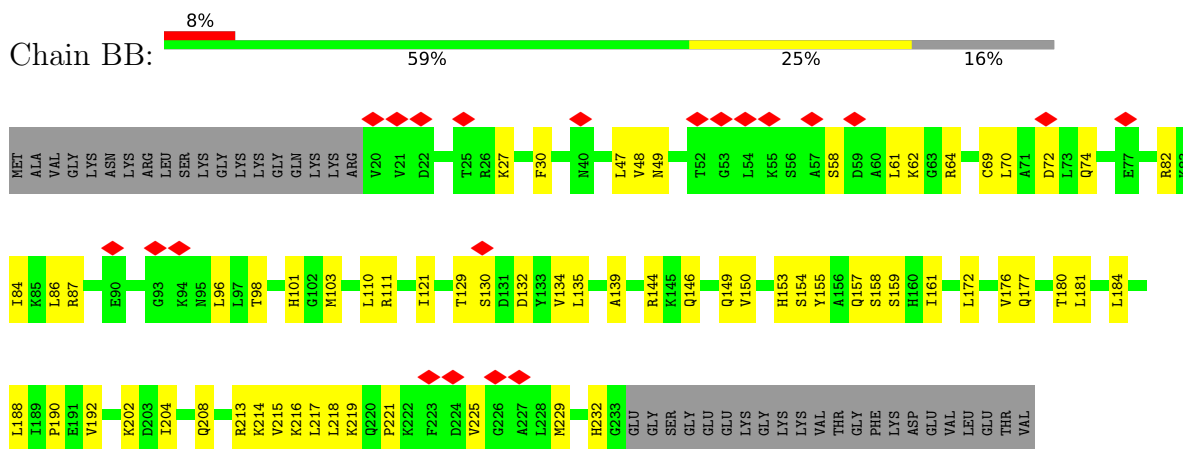
3 Residue-property plots

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.

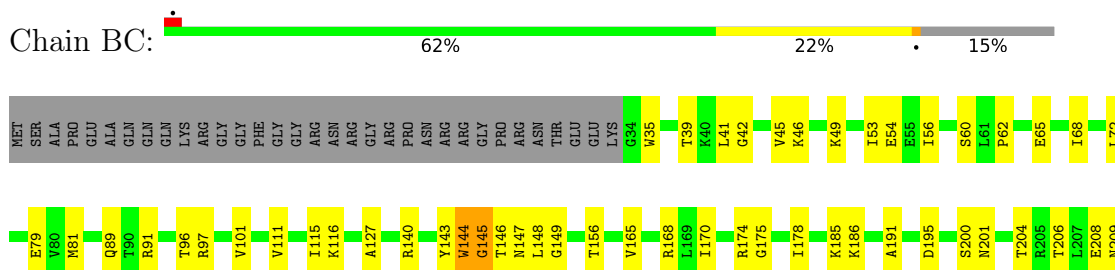
• Molecule 1: 40S ribosomal protein S0-A

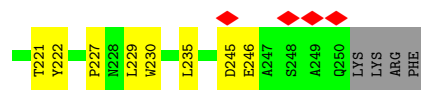


• Molecule 2: RPS1A isoform 1

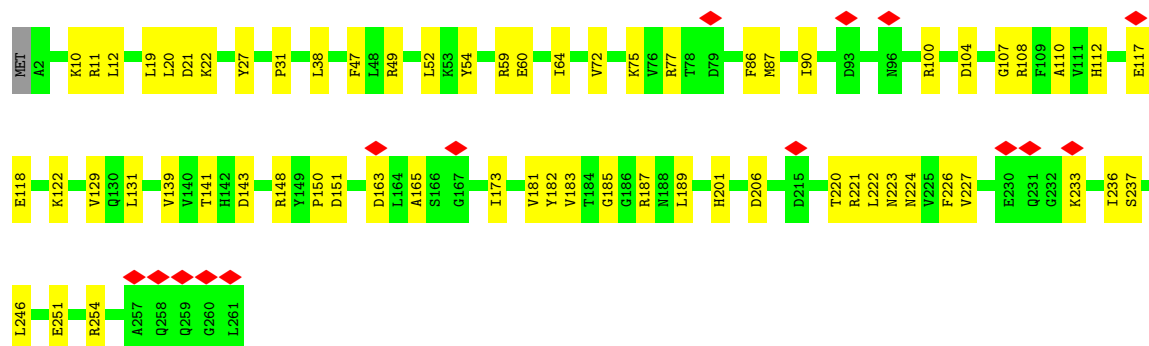
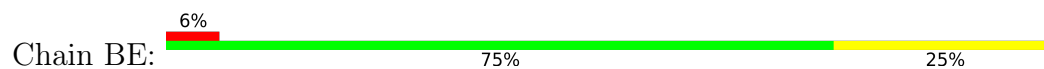


• Molecule 3: RPS2 isoform 1

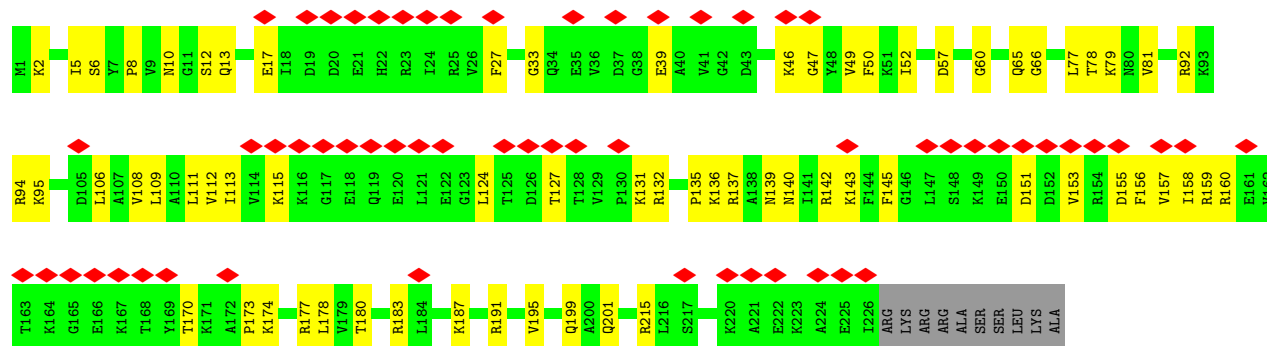




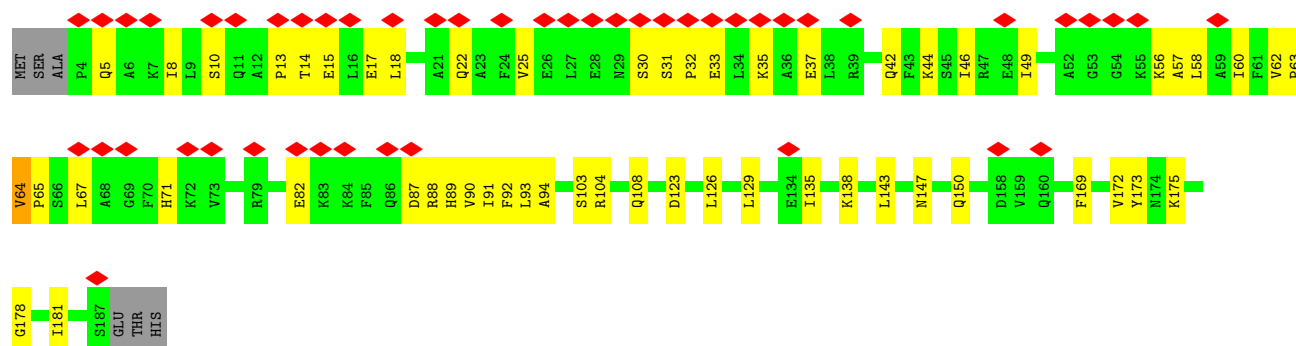
• Molecule 4: 40S ribosomal protein S4-A



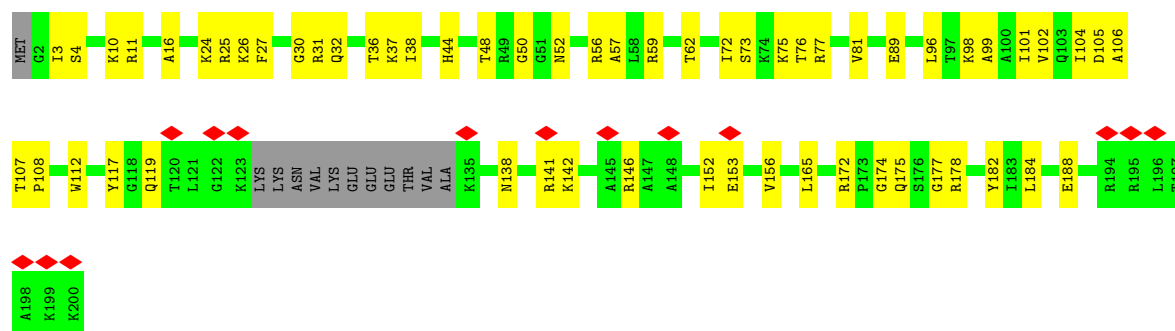
• Molecule 5: 40S ribosomal protein S6-A



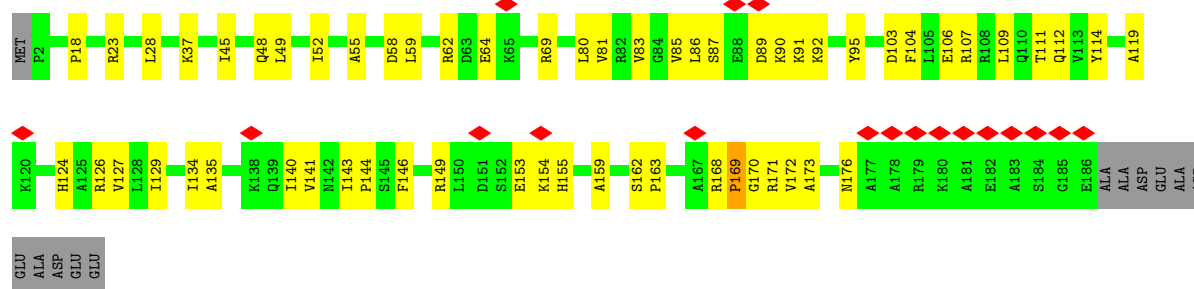
• Molecule 6: 40S ribosomal protein S7-A



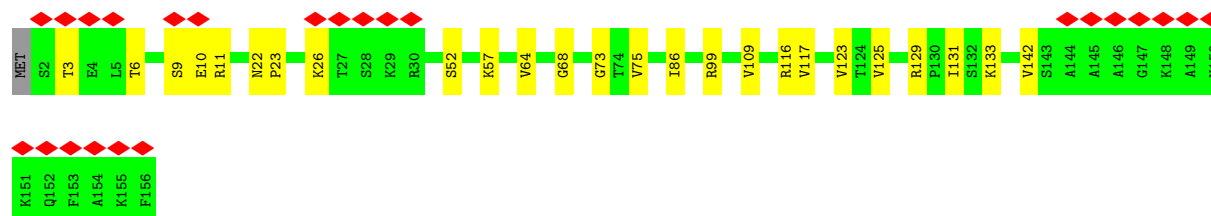
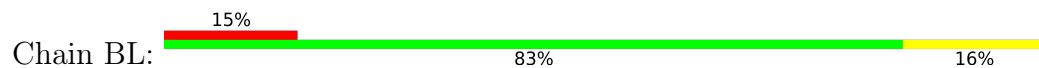
• Molecule 7: 40S ribosomal protein S8-A



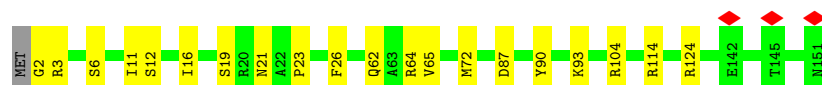
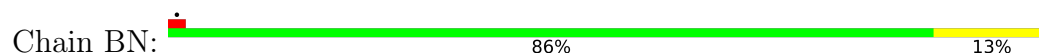
• Molecule 8: 40S ribosomal protein S9-A



• Molecule 9: 40S ribosomal protein S11-A

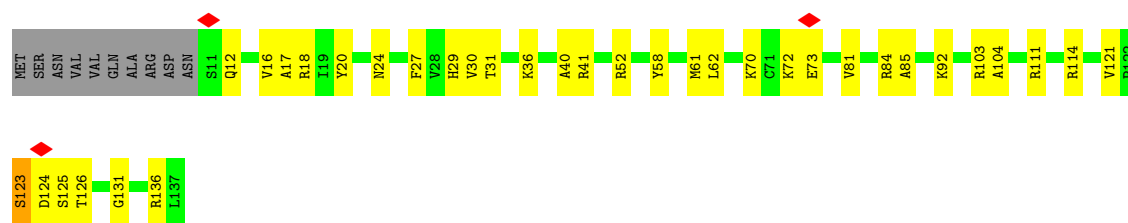


• Molecule 10: 40S ribosomal protein S13

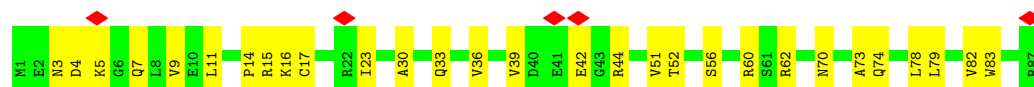


• Molecule 11: 40S ribosomal protein S14-A

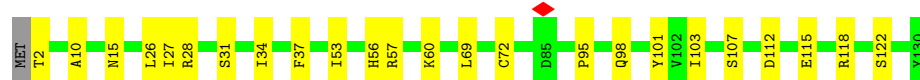
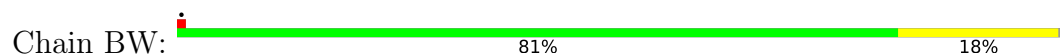




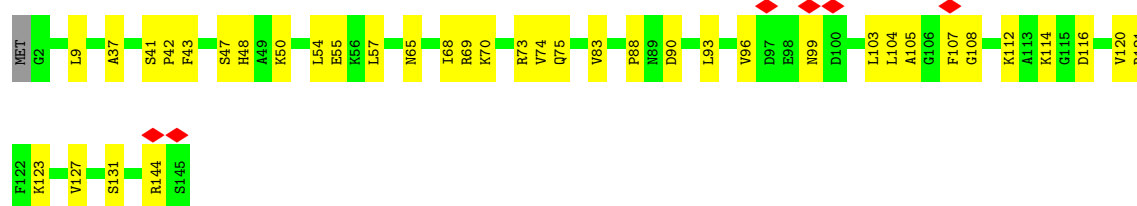
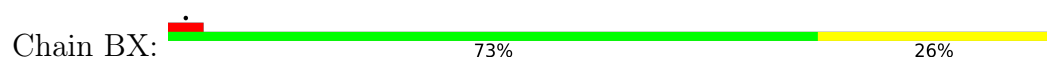
- Molecule 12: 40S ribosomal protein S21-A



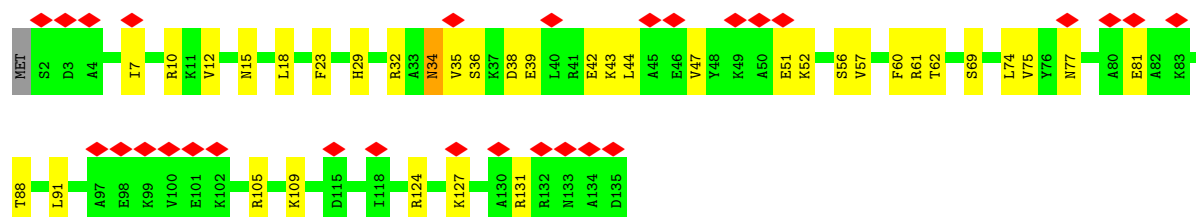
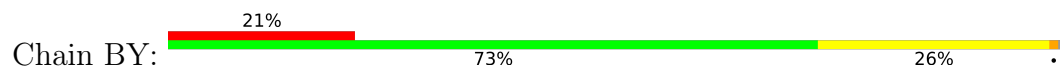
- Molecule 13: RPS22A isoform 1



- Molecule 14: 40S ribosomal protein S23-A

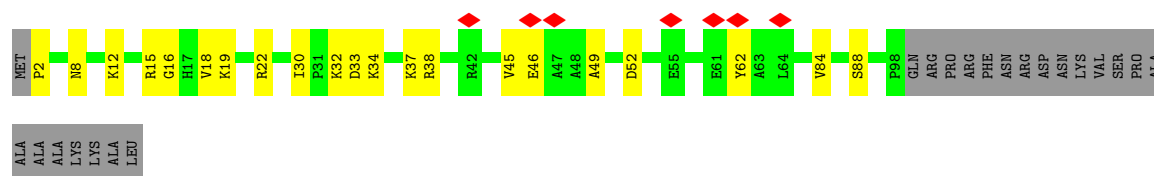


- Molecule 15: 40S ribosomal protein S24-A

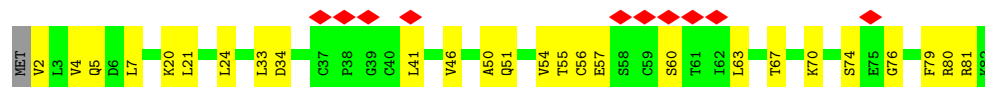


- Molecule 16: RPS26B isoform 1

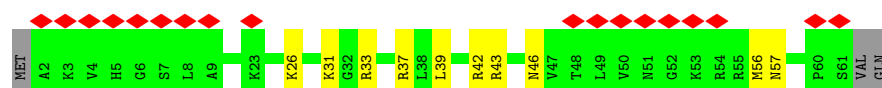
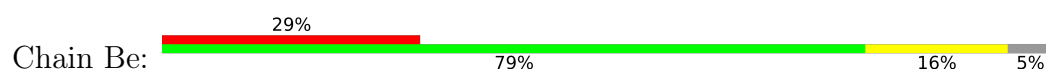




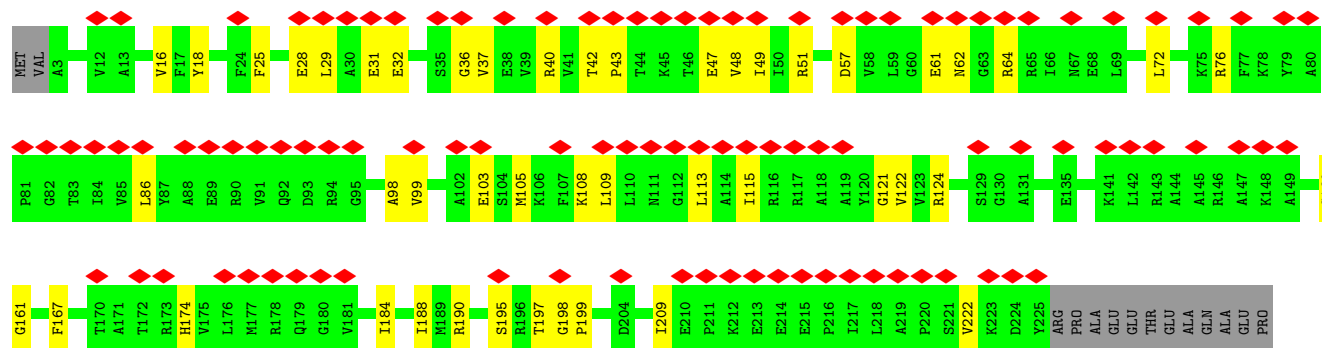
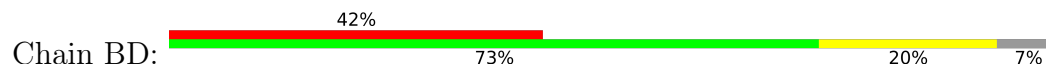
- Molecule 17: 40S ribosomal protein S27-A



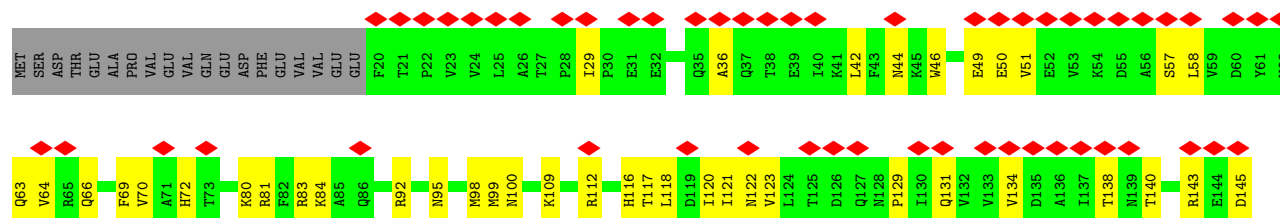
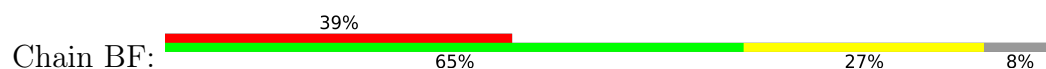
- Molecule 18: 40S ribosomal protein S30-A

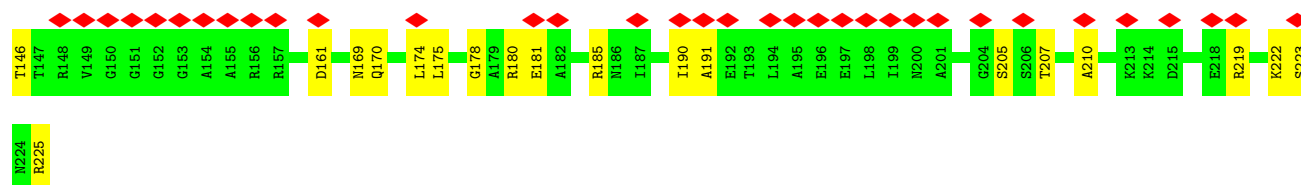


- Molecule 19: RPS3 isoform 1

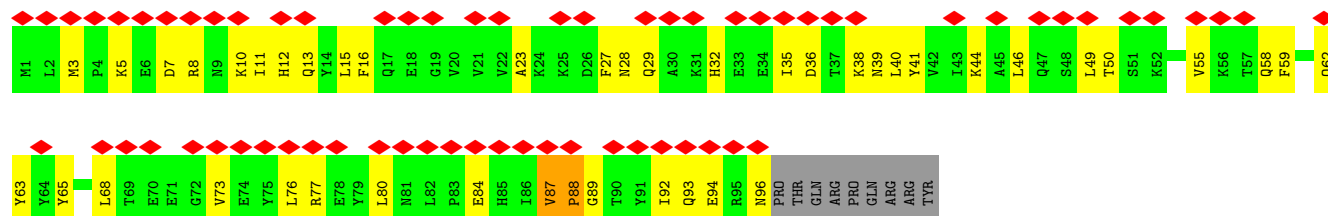


- Molecule 20: Rps5p





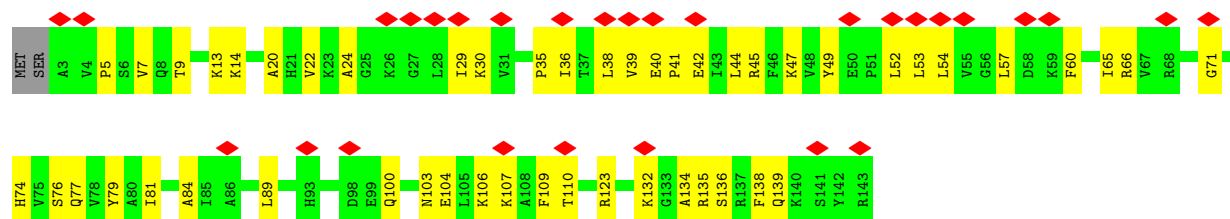
• Molecule 21: 40S ribosomal protein S10-A



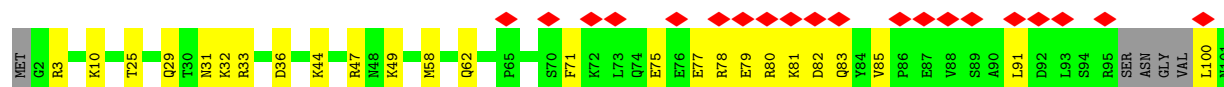
• Molecule 22: RPS15 isoform 1



• Molecule 23: 40S ribosomal protein S16-A

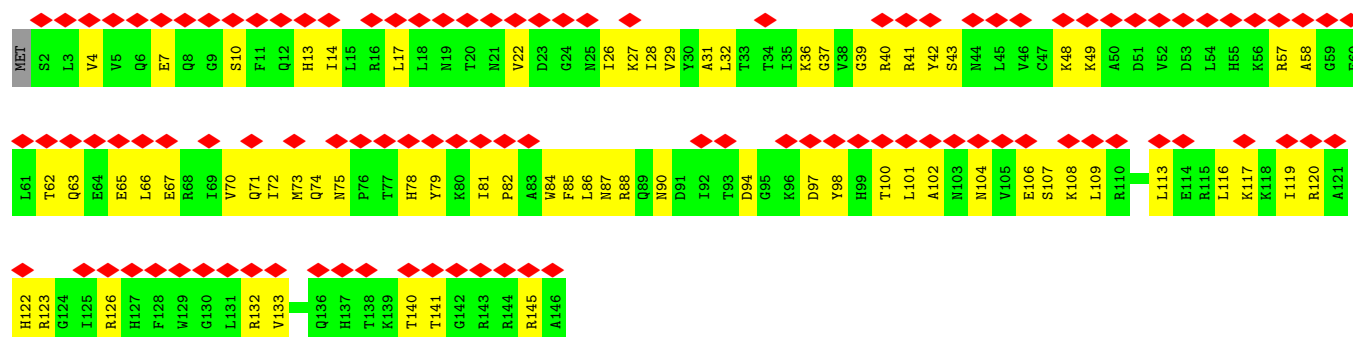
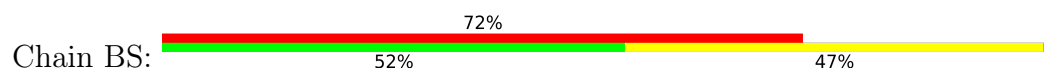


• Molecule 24: 40S ribosomal protein S17-A

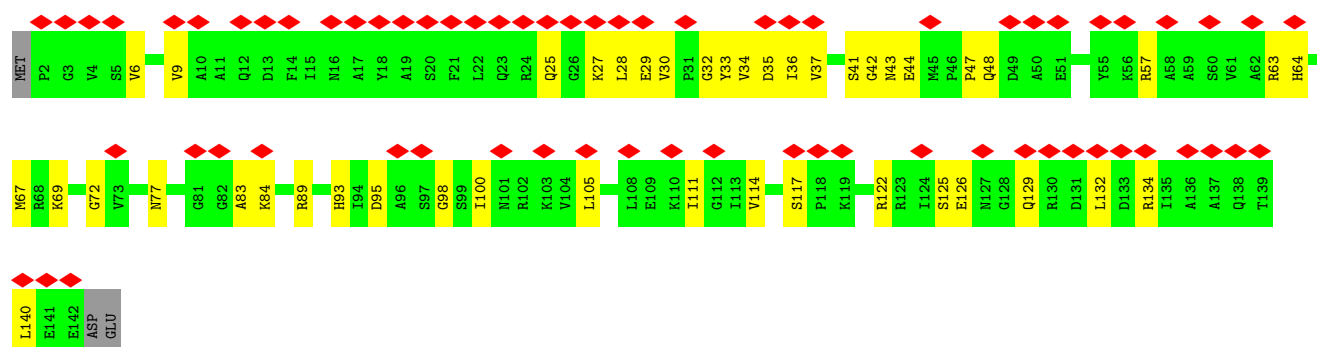




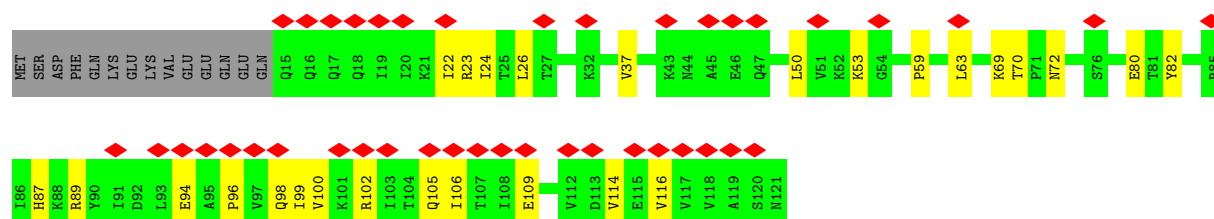
• Molecule 25: 40S ribosomal protein S18-A



• Molecule 26: 40S ribosomal protein S19-A



• Molecule 27: RPS20 isoform 1

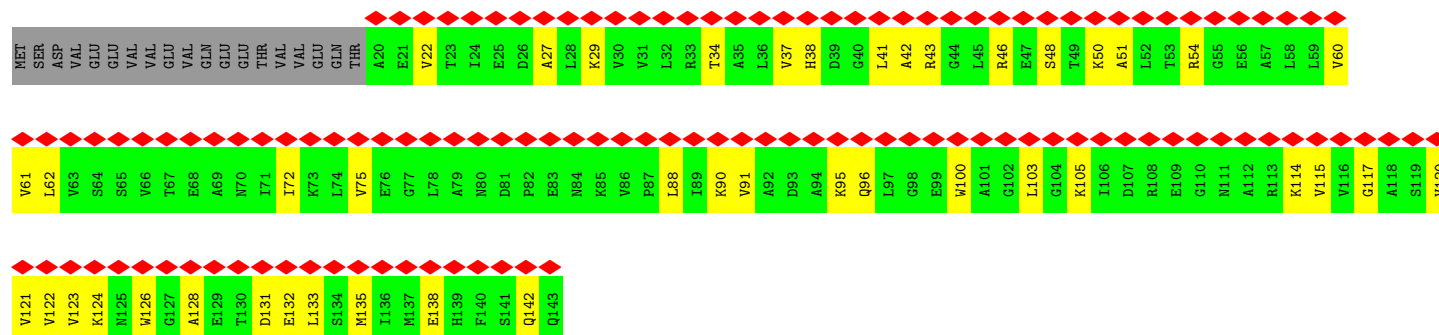
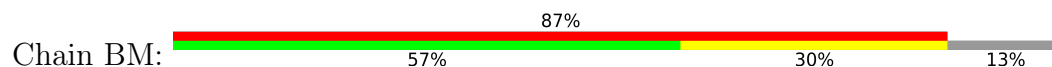


• Molecule 28: RPS25A isoform 1

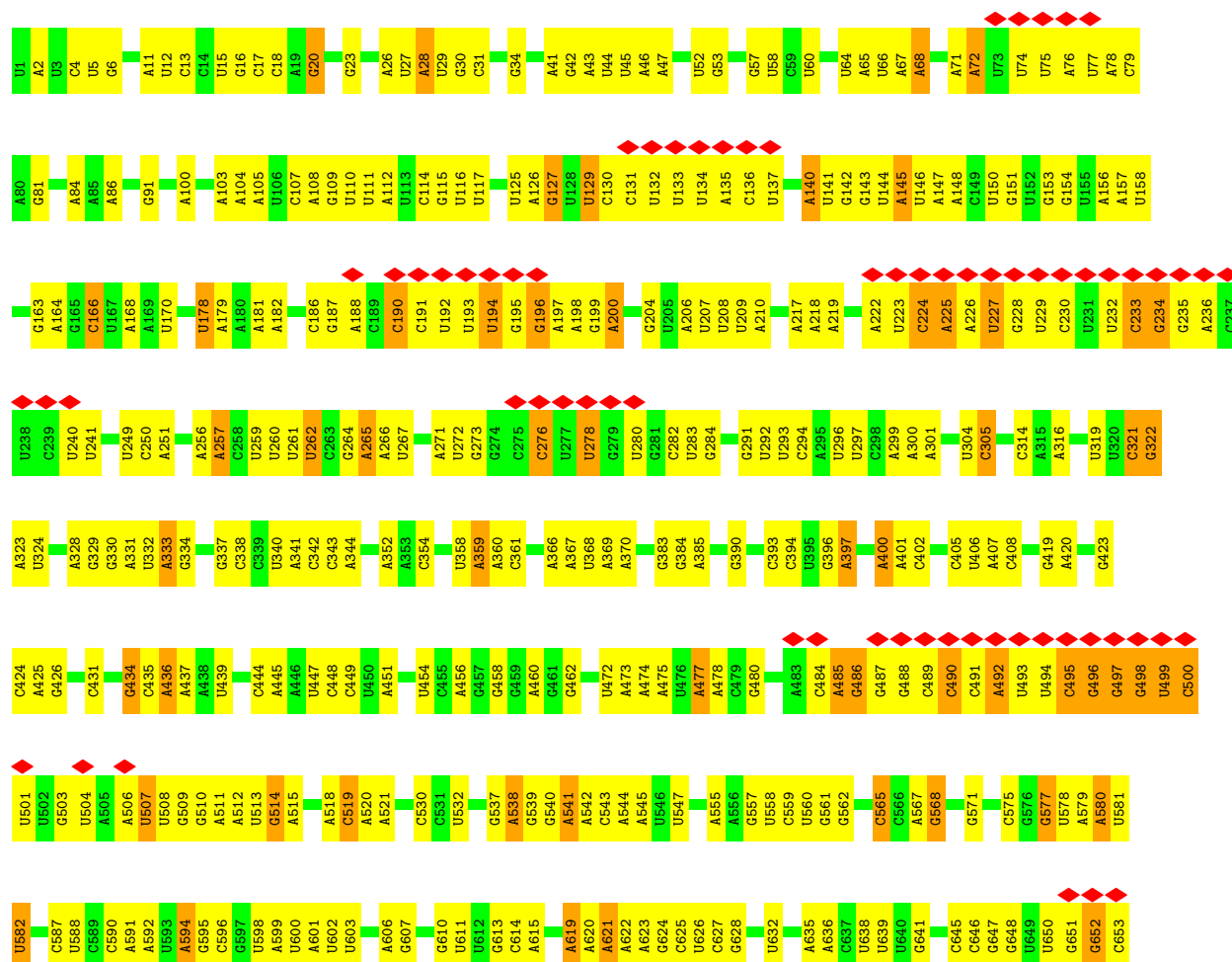
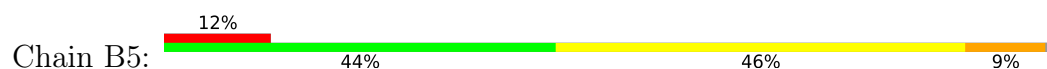


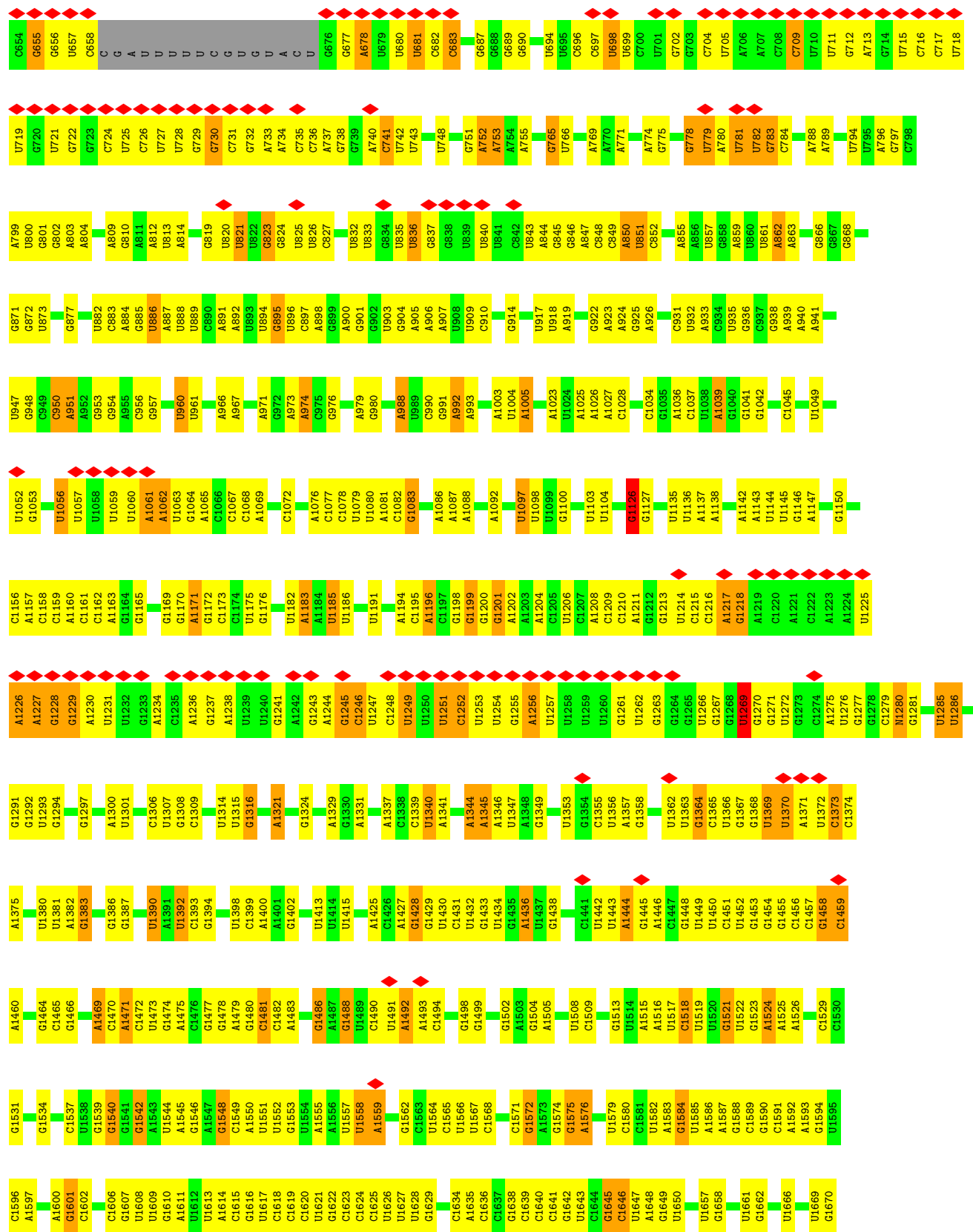


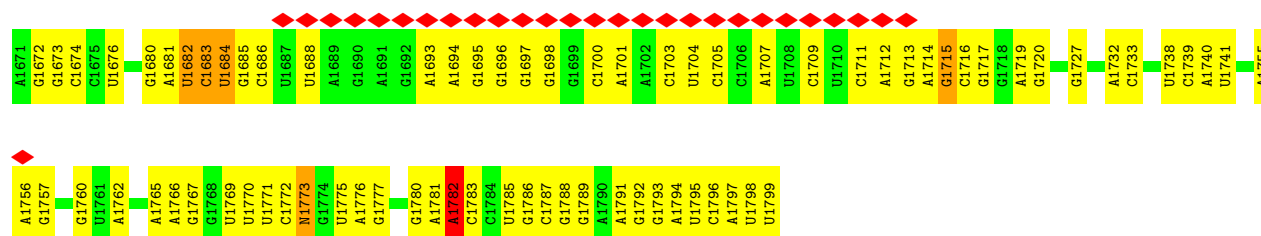
• Molecule 33: 40S ribosomal protein S12



• Molecule 34: 18S rRNA

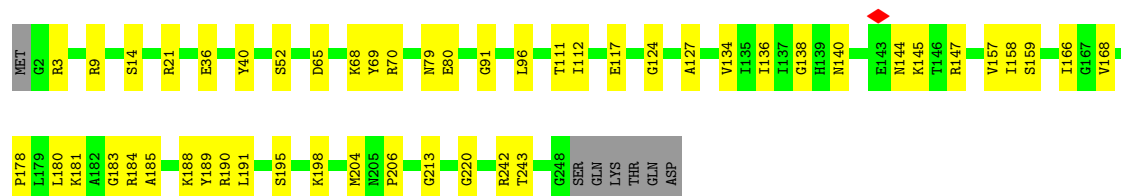






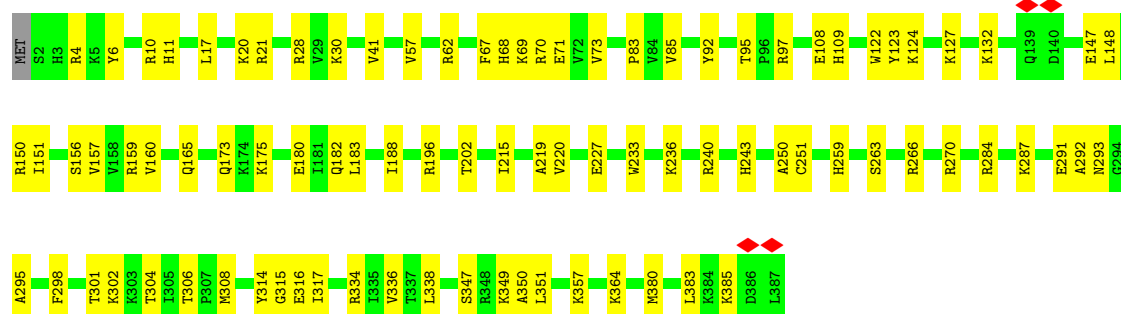
• Molecule 35: 60S ribosomal protein L2-A

Chain AA: 78% 20%



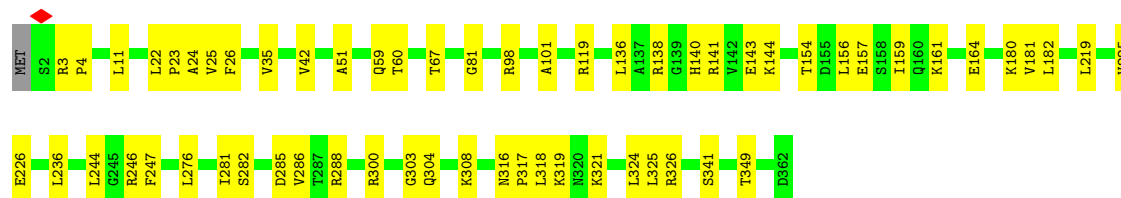
• Molecule 36: 60S ribosomal protein L3

Chain AB: 77% 23%



• Molecule 37: RPL4A isoform 1

Chain AC: 83% 17%



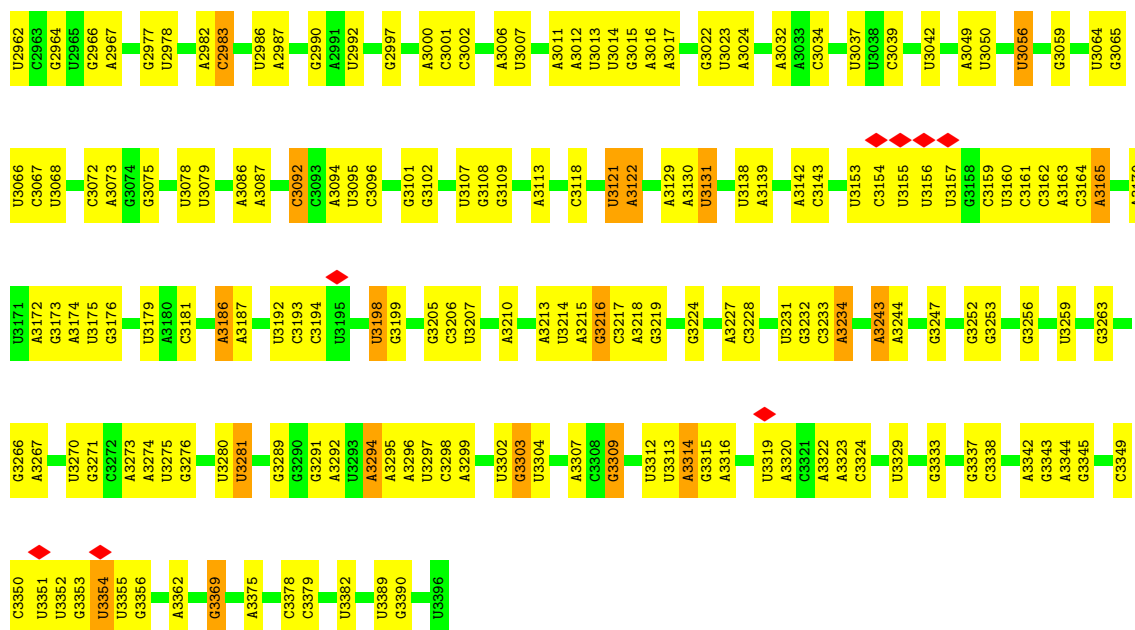
• Molecule 38: 25S rRNA

Chain A1: 56% 37% 7%



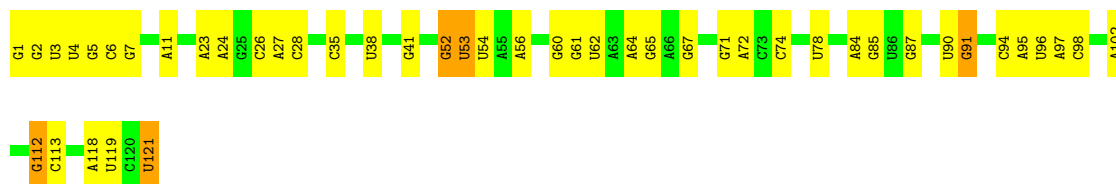


U2865	C2764	G2677	U2565	A2484	U2423	A2345	A2232	U2140	A1886	U1785	C1671	A1583	A1467
U2868	A2678	A2679	C2566	A2485	A2424	C2346	A2233	U2141	A1887	A1786	A1679	A1587	A1468
U2869	U2767	A2680	C2568	A2486	U2426	U2347	A2234	A2142	U1888	A1787	U1682	A1588	U1470
C2870	U2768	U2681	A2569	U2487	U2427	G2353	U2241	A2143	U1889	C1791	U1682	A1589	U1471
C2871	A2769	C2682	U2570	C2488	U2428	G2354	A2242	A2144	U1890	C1792	U1686	G1590	
A2872	C2772	U2683	U2571	C2489	U2429	C2355	C2245	U2148	A1893	C1793	U1687	G1591	A1477
U2875	C2773	C2685	C2572	C2490	A2430	A2356	G2249	A2149	U1899	U1688	U1687	G1592	
C2876	U2774	A2686	C2573	C2492	C2431	A2357	G2249	C2151	A1899	U1689	U1688	A1593	A1481
U2880	G2777	U2687	U2585	U2493	U2434	A2358	U2254	A2152	G1906	A1798	U1694	C1596	A1482
C2881	U2778	C2688	U2586	A2494	G2435	A2359	U2255	U2153	C1907	A1799	U1695	C1597	G1483
U2882	G2791	G2689	U2587	C2495	A2436	A2360	A2256	U2158	A1913	U1800	A1696	G1598	G1486
U2883	A2792	U2690	U2588	C2496	U2438	C2366	A2257	A2159	A1914	C1802	A1697	A1602	G1492
A2887	G2793	A2691	U2589	U2497	A2439	A2367	A2259	U2160	G1914	C1805	C1709	A1605	U1495
C2895	C2796	U2692	U2592	U2498	g	A2368	U2260	U2161	A1914	A1806	C1710	A1605	U1496
A2896	U2697	A2593	C2594	U2499	A2441	G2369	G2261	G2161	A1921	A1807	U1717	A1613	C1497
C2897	G2699	A2595	U2596	A2500	G2442	G2370	A2262	G2169	A1922	G1808	U1717	C1614	A1498
U2898	G2700	U2596	U2597	U2501	A2443	A2373	C2263	U2176	A1932	A1809	U1718	G1615	A1506
G2901	A2704	U2597	U2597	U2502	C2444	C2374	C2267	U2176	A1932	A1810	G1719	U1616	G1507
U2909	A2705	G2606	G2606	U2504	U2446	G2375	U2268	G2180	G1940	G1811	U1720	U1617	C1508
A2910	C2706	G2607	G2607	U2505	A2447	G2376	U2269	C2181	U1942	A1812	U1721	G1618	
C2916	C2707	U2606	U2611	A2449	G2448	C2377	A2270	G2185	U1946	A1813	U1722	A1619	
U2921	A2811	U2607	U2612	A2450	A2449	G2378	A2271	G2185	A1946	A1814	U1723	U1620	U1522
C2922	C2812	C2708	U2613	C2507	G2450	U2379	G2272	U2188	G1947	A1815	U1724	A1621	U1523
U2923	G2813	C2709	G2614	U2508	G2451	U2380	G2273	A2189	G1948	G1817	C1725	G1623	C1527
C2927	U2814	C2710	U2618	U2509	G2452	C2383	C2278	U2189	G1952	U1820	A1729	C1628	A1534
C2928	A2714	U2514	G2619	U2453	U2453	A2379	A2279	U2193	G1953	U1821	G1736	U1629	A1535
U2929	A2715	A2515	C2619	G2454	G2454	U2388	A2280	G2194	U1954	A1828	U1737	U1630	
C2930	U2719	U2520	U2634	U2455	U2455	C2389	A2281	C2197	U1955	G1829	U1740	C1631	A1539
C2931	U2722	U2521	U2635	A2456	A2456	G2391	G2283	G2201	A2093	U1830	A1741	G1635	U1555
U2932	U2723	G2522	U2636	G2457	U2457	C2392	C2284	G2202	C2094	U1831	U1742	U1556	C1556
A2933	U2724	A2523	U2637	U2458	A2458	G2393	C2285	U2203	A2106	C1832	G1747	A1638	G1560
C2934	U2725	G2524	C2638	U2459	A2459	G2394	G2286	U2204	G2110	A1835	G1748	C1639	G1561
U2935	A2726	U2525	G2639	U2460	U2460	A2397	G2305	U2205	U2112	C1836	A1749	A1642	C1562
A2936	C2727	C2526	U2640	A2461	A2461	U2402	C2306	G2206	A2113	U1750	G1751	A1643	C1563
C2937	U2728	U2527	U2641	G2462	U2462	G2403	G2307	A2207	G2114	A1842	U1752	U1644	U1564
U2938	U2729	G2530	A2642	G2463	G2463	A2404	C2308	A2208	G2115	C1846	C1759	U1645	G1565
C2939	A2737	U2536	G2651	U2464	U2464	C2405	A2309	U2209	G2120	C1846	U1760	G1646	A1566
C2940	U2742	U2537	U2652	G2465	G2465	C2406	U2310	A2213	G2121	C1849	C1761	U1567	U1567
C2941	A2743	U2538	A2656	G2466	G2466	C2407	A2313	A2214	U2112	A1850	U1762	U1651	U1568
C2942	U2744	C2539	U2660	G2467	G2467	U2408	G2314	G2218	A2113	U1569	U1763	C1657	U1570
A2946	G2745	A2540	G2661	A2468	A2468	U2411	G2315	A2219	G2114	C1856	U1764	G1658	A1571
C2947	U2746	U2541	G2662	G2469	G2469	G2412	U2334	A2220	G2121	C1857	U1765	U1659	U1572
C2948	A2747	U2542	G2663	C2470	C2470	A2413	U2336	G2221	G2122	A1864	G1766	C1660	G1573
U2949	U2748	U2543	U2664	U2471	U2471	G2414	U2337	A2222	U2129	A1865	C1771	G1662	C1574
C2953	G2749	U2544	C2666	U2472	U2472	U2417	C2338	A2224	G2130	C1866	U1772	A1575	A1576
U2954	U2750	G2549	A2673	G2473	G2473	G2418	G2339	C2227	A2131	A1867	G1775	G1666	C1579
U2955	C2751	U2551	A2674	G2474	G2474	A2419	U2340	U2344	U2133	C1878	G1780	A1667	C1580
C2960	U2752	C2552	A2675	G2475	G2475	C2420	U2344	C2227	C2131	A1879	G1780	G1668	C1581
U2961	U2861	C2755	U2676	C2477	C2477	U2421	U2344	A2229	U2133	U1880			C1582



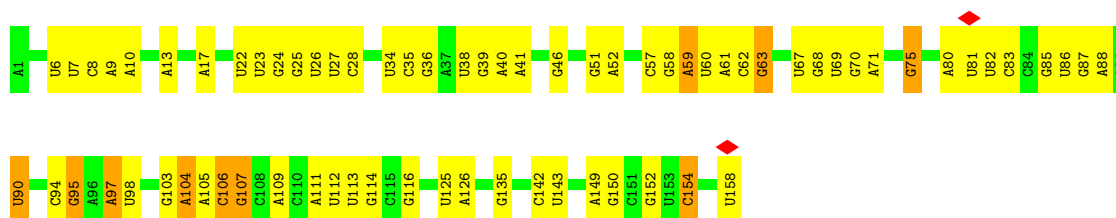
• Molecule 39: 5s rRNA

Chain A3: 62% 34% .



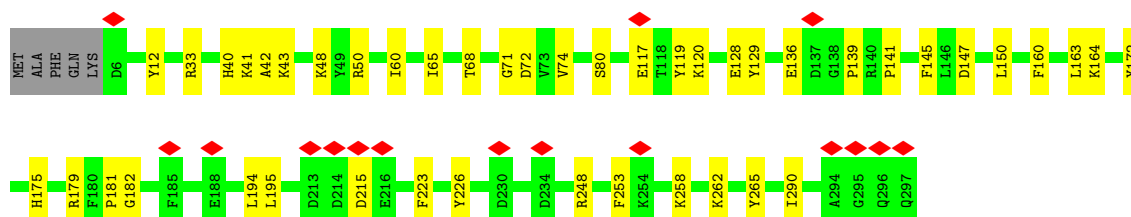
• Molecule 40: 5.8 S rRNA

Chain A4: 55% 39% 6% .

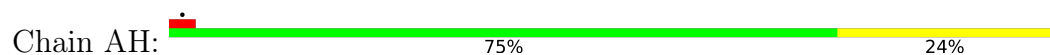
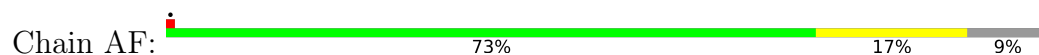


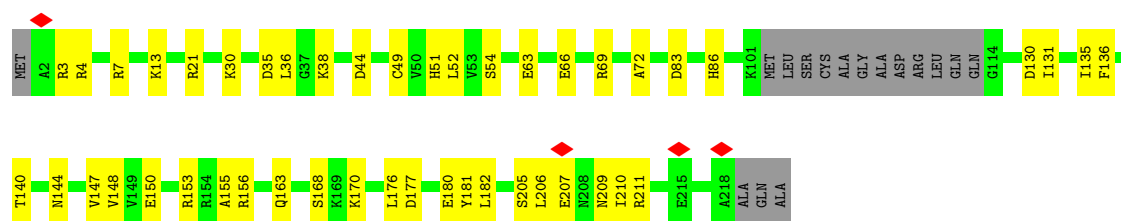
• Molecule 41: RPL5 isoform 1

Chain AD: 5% 83% 15% .

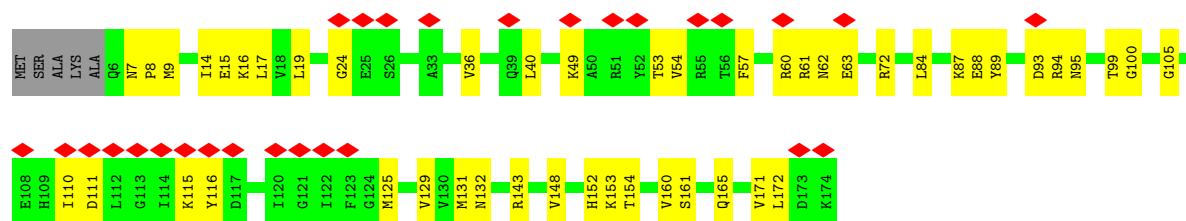


Chain AE: 68% 20% 11%

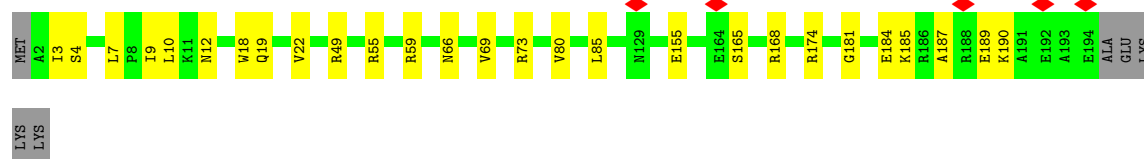
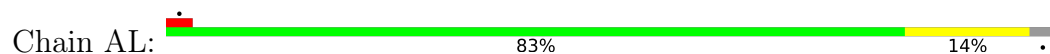




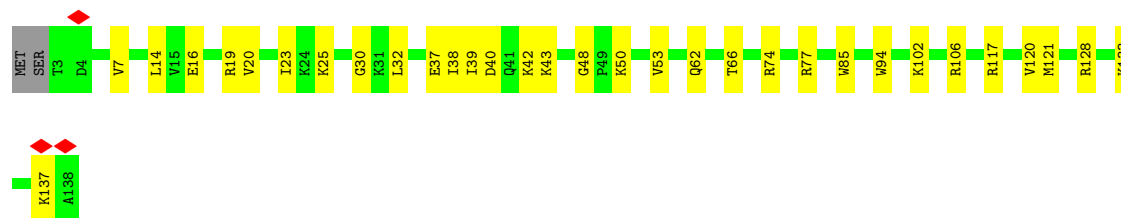
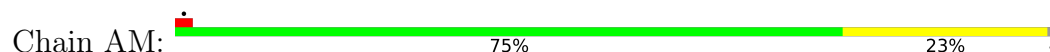
• Molecule 47: RPL11A isoform 1



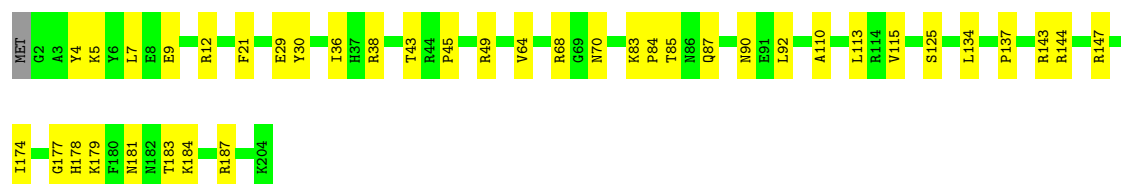
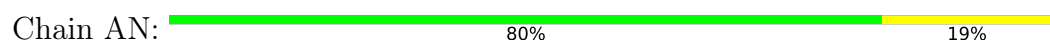
• Molecule 48: 60S ribosomal protein L13-A



• Molecule 49: 60S ribosomal protein L14-A

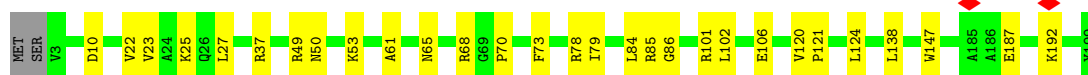


• Molecule 50: 60S ribosomal protein L15-A



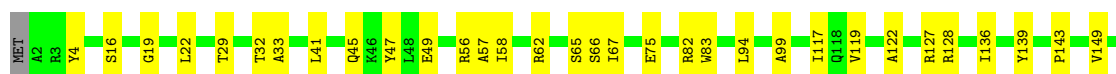
- Molecule 51: 60S ribosomal protein L16-A

Chain AO:  84% 15% .



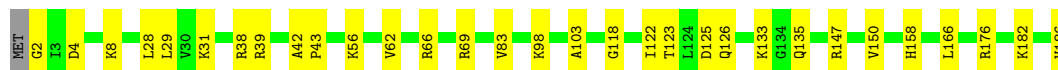
- Molecule 52: 60S ribosomal protein L17-A

Chain AP:  75% 20% 5% .



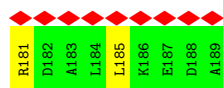
- Molecule 53: 60S ribosomal protein L18-A

Chain AQ:  83% 17% .



- Molecule 54: 60S ribosomal protein L19-A

Chain AR:  10% 81% 19% .



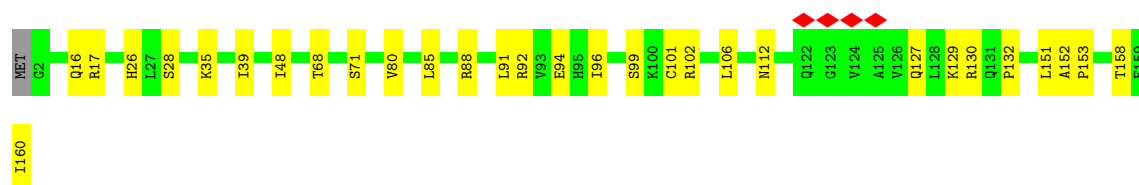
- Molecule 55: 60S ribosomal protein L20

Chain AS:  78% 19% .

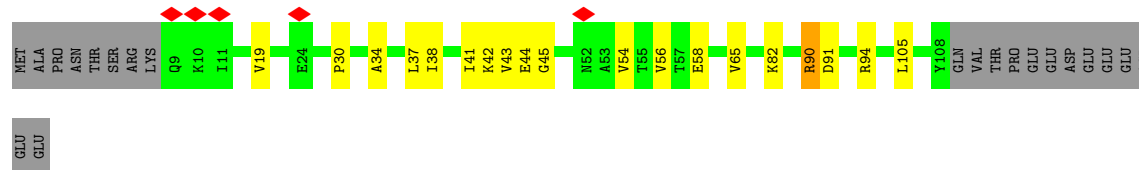


- Molecule 56: 60S ribosomal protein L21-A

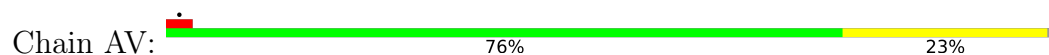
Chain AT:  81% 19% .



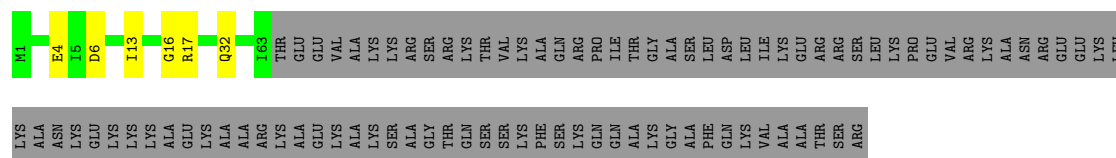
- Molecule 57: 60S ribosomal protein L22-A



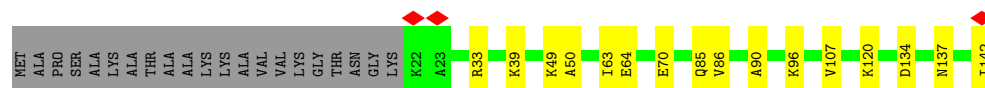
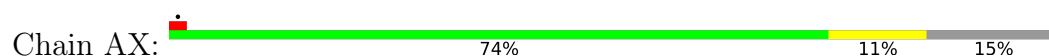
- Molecule 58: 60S ribosomal protein L23-A



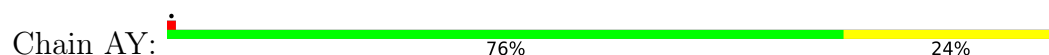
- Molecule 59: RPL24A isoform 1



- Molecule 60: 60S ribosomal protein L25

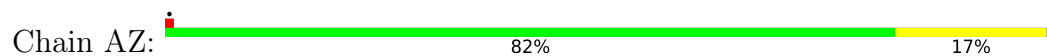


- Molecule 61: 60S ribosomal protein L26-A

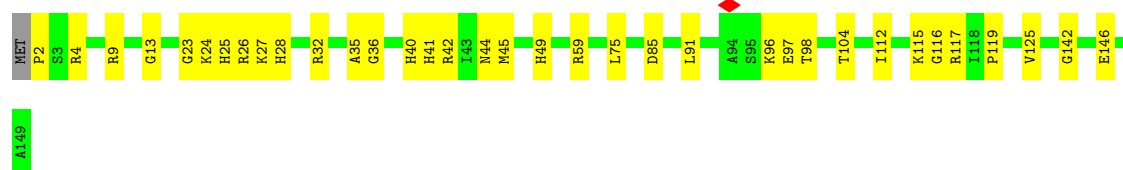
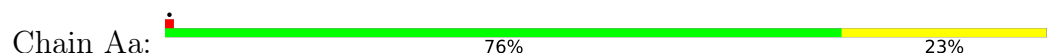




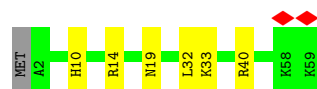
- Molecule 62: 60S ribosomal protein L27-A



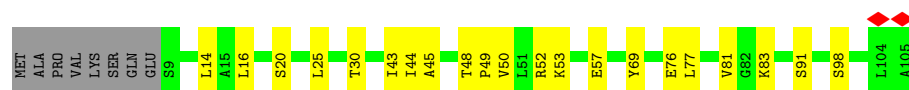
- Molecule 63: 60S ribosomal protein L28



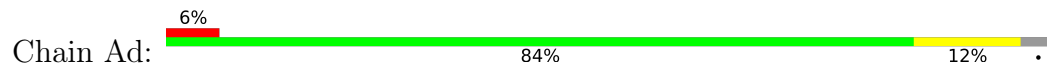
- Molecule 64: RPL29 isoform 1



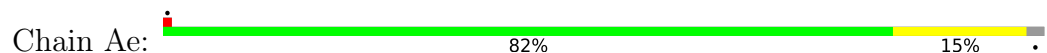
- Molecule 65: 60S ribosomal protein L30



- Molecule 66: 60S ribosomal protein L31-A

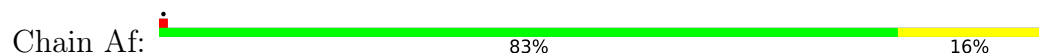


- Molecule 67: RPL32 isoform 1

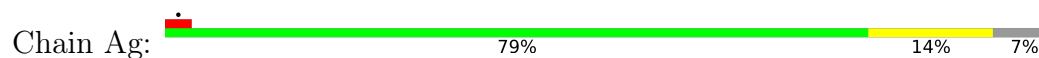




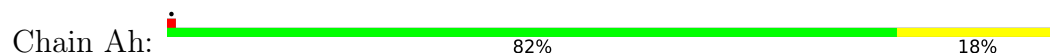
- Molecule 68: 60S ribosomal protein L33-A



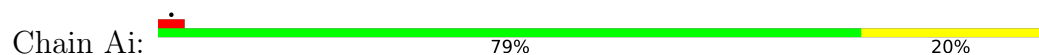
- Molecule 69: 60S ribosomal protein L34-A



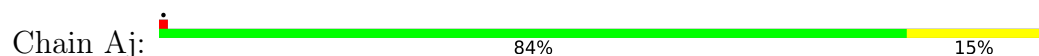
- Molecule 70: 60S ribosomal protein L35-A



- Molecule 71: 60S ribosomal protein L36-A



- Molecule 72: 60S ribosomal protein L37-A



- Molecule 73: RPL38 isoform 1



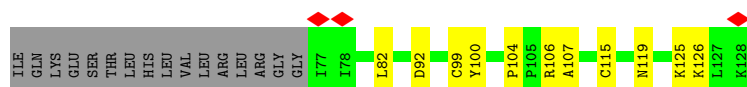
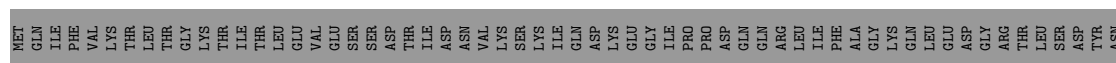
- Molecule 74: 60S ribosomal protein L39

Chain Al:  78% 20% .



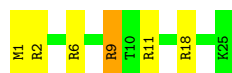
- Molecule 75: Ubiquitin-60S ribosomal protein L40

Chain Am:  32% 9% 59%



- Molecule 76: 60S ribosomal protein L41-A

Chain An:  76% 20% .



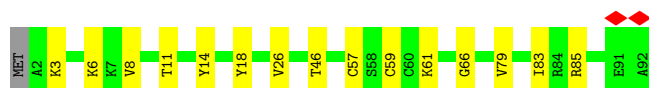
- Molecule 77: 60S ribosomal protein L42-A

Chain Ao:  5% 79% 17% .

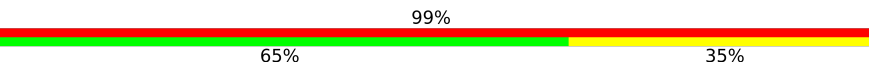


- Molecule 78: 60S ribosomal protein L43-A

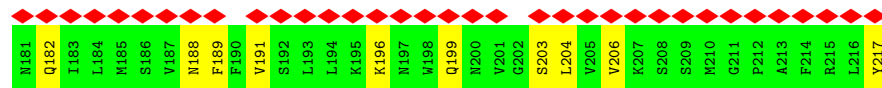
Chain Ap:  83% 16% .



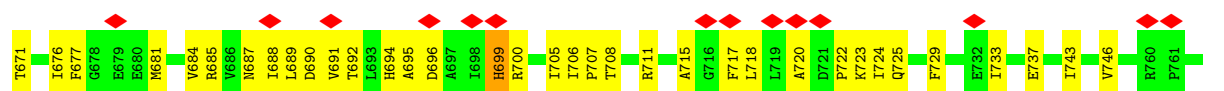
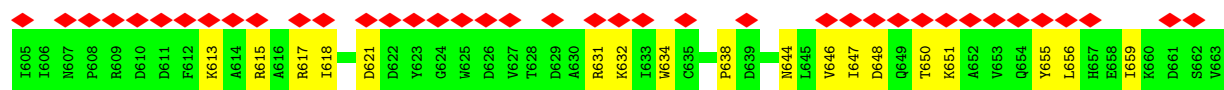
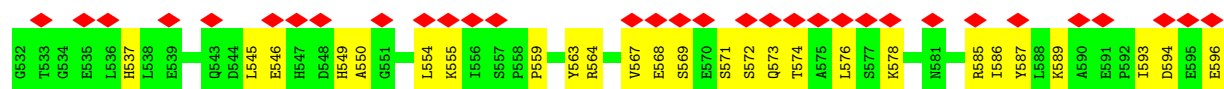
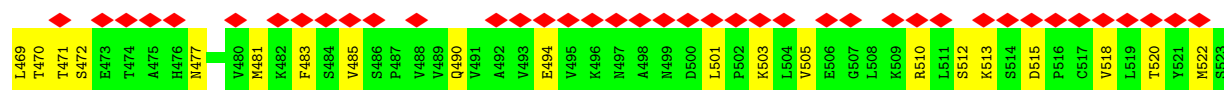
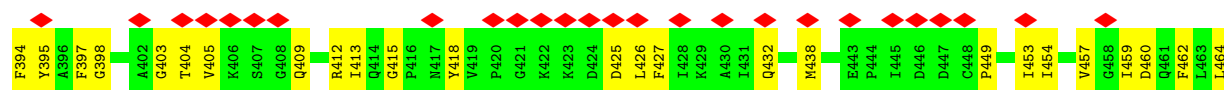
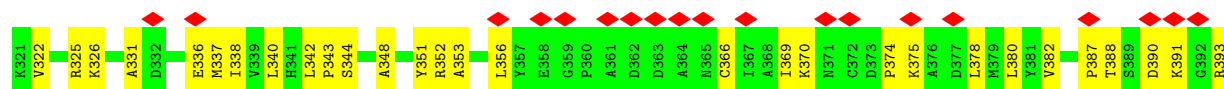
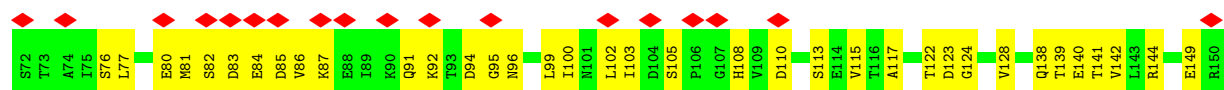
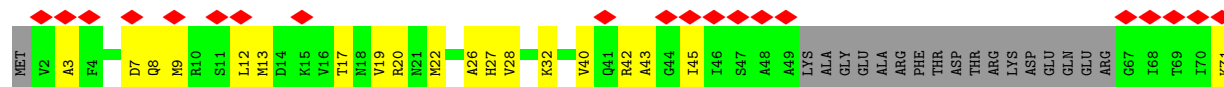
- Molecule 79: RPL1A isoform 1

Chain E:  65% 35% 99%

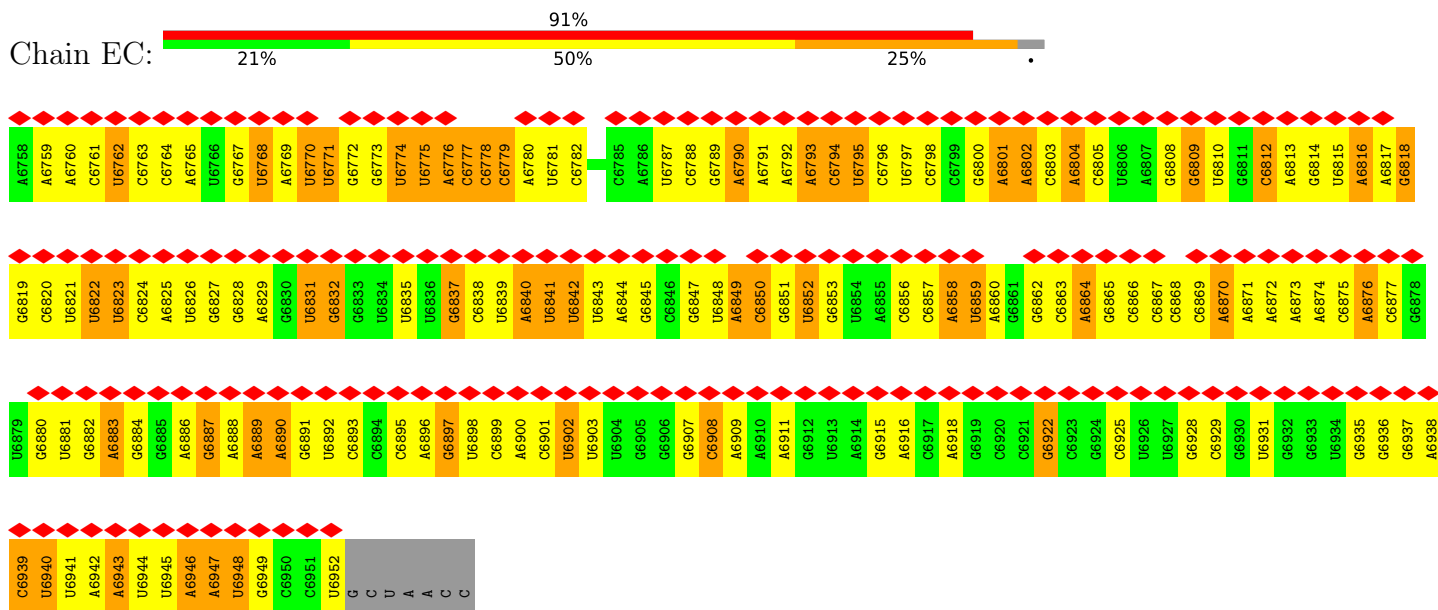
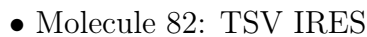




• Molecule 80: Elongation factor 2



Chain V: 30% 34% 26% 39%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	65607	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	0.6	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: 4AC, OMU, GDP, ZN, OMC, MG, OMG, UR3, 5MC, 1MA, 7MG, MA6, DDE, XSX, A2M, HIC

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	0.13	0/1653	0.33	0/2261
2	BB	0.14	0/1735	0.40	0/2335
3	BC	0.14	0/1665	0.31	0/2263
4	BE	0.13	0/2109	0.35	0/2839
5	BG	0.10	0/1844	0.28	0/2464
6	BH	0.15	0/1506	0.41	0/2028
7	BI	0.13	0/1514	0.36	0/2021
8	BJ	0.24	1/1519 (0.1%)	0.45	3/2035 (0.1%)
9	BL	0.14	0/1272	0.29	0/1712
10	BN	0.14	0/1215	0.36	0/1638
11	BO	0.15	0/952	0.39	0/1279
12	BV	0.15	0/693	0.38	0/935
13	BW	0.14	0/1038	0.31	0/1395
14	BX	0.14	0/1139	0.37	0/1518
15	BY	0.12	0/1087	0.32	0/1449
16	Ba	0.15	0/782	0.42	0/1047
17	Bb	0.12	0/620	0.36	0/838
18	Be	0.10	0/483	0.32	0/643
19	BD	0.13	0/1759	0.37	0/2368
20	BF	0.11	0/1629	0.33	0/2202
21	BK	0.74	2/837 (0.2%)	1.18	5/1131 (0.4%)
22	BP	0.15	0/1012	0.37	0/1356
23	BQ	0.12	0/1125	0.33	0/1510
24	BR	0.12	0/984	0.34	0/1318
25	BS	0.14	0/1211	0.39	0/1628
26	BT	0.16	0/1113	0.42	0/1494
27	BU	0.11	0/865	0.32	0/1169
28	BZ	0.10	0/566	0.29	0/761
29	Bc	0.13	0/499	0.39	0/670
30	Bd	0.20	0/452	0.44	1/600 (0.2%)
31	Bg	0.10	0/2454	0.31	0/3340
32	Bf	0.11	0/616	0.51	0/817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.14	0/943	0.49	0/1274
34	B5	0.16	1/41880 (0.0%)	0.29	1/65248 (0.0%)
35	AA	0.18	0/1912	0.33	0/2569
36	AB	0.16	0/3138	0.32	0/4217
37	AC	0.17	0/2800	0.35	0/3790
38	A1	0.20	0/75561	0.31	0/117806
39	A3	0.16	0/2883	0.27	0/4491
40	A4	0.20	0/3746	0.31	0/5832
41	AD	0.13	0/2390	0.29	0/3225
42	AE	0.15	0/1260	0.33	0/1694
43	AF	0.16	0/1821	0.31	0/2451
44	AG	0.15	0/1830	0.34	0/2469
45	AH	0.16	0/1531	0.34	0/2062
46	AI	0.14	0/1708	0.29	0/2290
47	AJ	0.13	0/1374	0.40	0/1842
48	AL	0.16	0/1568	0.32	0/2106
49	AM	0.14	0/1068	0.27	0/1438
50	AN	0.19	0/1757	0.34	0/2354
51	AO	0.16	0/1585	0.30	0/2128
52	AP	0.16	0/1410	0.28	0/1893
53	AQ	0.17	0/1465	0.31	0/1965
54	AR	0.16	0/1538	0.31	0/2050
55	AS	0.17	0/1481	0.37	0/1990
56	AT	0.15	0/1300	0.29	0/1743
57	AU	0.19	0/812	0.51	2/1099 (0.2%)
58	AV	0.17	0/1018	0.35	0/1369
59	AW	0.16	0/533	0.31	0/707
60	AX	0.16	0/983	0.30	0/1325
61	AY	0.18	0/1004	0.33	0/1341
62	AZ	0.16	0/1118	0.34	0/1497
63	Aa	0.20	0/1204	0.34	0/1612
64	Ab	0.14	0/473	0.30	0/629
65	Ac	0.16	0/751	0.27	0/1008
66	Ad	0.15	0/904	0.25	0/1213
67	Ae	0.17	0/1041	0.31	0/1394
68	Af	0.17	0/868	0.30	0/1168
69	Ag	0.17	0/890	0.34	0/1189
70	Ah	0.17	0/978	0.26	0/1301
71	Ai	0.17	0/778	0.35	0/1034
72	Aj	0.18	0/696	0.33	0/923
73	Ak	0.16	0/618	0.34	0/826
74	Al	0.18	0/443	0.32	0/588
75	Am	0.14	0/423	0.29	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.27	0/234	0.82	1/300 (0.3%)
77	Ao	0.15	0/831	0.29	0/1097
78	Ap	0.17	0/701	0.38	0/934
79	E	0.15	0/1745	0.44	0/2342
80	DC	0.13	0/6521	0.38	0/8830
81	V	0.17	0/1498	0.49	0/2025
82	EC	0.12	0/4613	0.33	0/7182
All	All	0.18	4/227575 (0.0%)	0.33	13/333486 (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
3	BC	0	2
6	BH	0	1
11	BO	0	1
14	BX	0	1
15	BY	0	1
38	A1	0	1
43	AF	0	1
44	AG	0	3
76	An	0	1
All	All	0	12

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	BK	88	PRO	CB-CG	16.11	2.30	1.49
21	BK	88	PRO	CG-CD	-12.22	1.09	1.50
8	BJ	169	PRO	CG-CD	-5.88	1.30	1.50
34	B5	1269	OMU	O3'-P	5.00	1.61	1.56

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	BK	88	PRO	CB-CG-CD	-24.30	28.33	106.10
21	BK	88	PRO	CA-N-CD	-21.00	82.59	112.00
21	BK	88	PRO	N-CD-CG	13.19	122.98	103.20
8	BJ	169	PRO	N-CD-CG	-8.82	89.97	103.20
21	BK	88	PRO	N-CA-CB	-8.78	95.08	103.51

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1575	7MG	O3'-P-O5'	7.23	114.85	104.00
21	BK	87	VAL	C-N-CD	7.21	154.54	125.00
8	BJ	169	PRO	CA-CB-CG	-6.81	91.56	104.50
57	AU	90	ARG	CA-C-N	6.80	135.66	124.31
57	AU	90	ARG	C-N-CA	6.80	135.66	124.31
30	Bd	33	LYS	CB-CG-CD	-6.46	96.44	111.30
8	BJ	169	PRO	N-CA-CB	-6.21	97.30	103.20
76	An	9	ARG	CA-CB-CG	5.29	124.68	114.10

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
38	A1	2459	A	Sidechain
43	AF	232	ARG	Peptide
44	AG	121	SER	Peptide
44	AG	30	THR	Peptide
44	AG	76	ALA	Peptide
76	An	9	ARG	Sidechain
3	BC	144	TRP	Peptide
3	BC	145	GLY	Peptide
6	BH	64	VAL	Peptide
11	BO	123	SER	Peptide
14	BX	88	PRO	Peptide
15	BY	34	ASN	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	41	0
2	BB	1709	0	1784	48	0
3	BC	1635	0	1723	42	0
4	BE	2068	0	2154	49	0
5	BG	1820	0	1918	57	0
6	BH	1481	0	1572	45	0
7	BI	1489	0	1525	48	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	BJ	1494	0	1573	46	0
9	BL	1244	0	1314	17	0
10	BN	1192	0	1255	15	0
11	BO	941	0	979	31	0
12	BV	684	0	672	21	0
13	BW	1021	0	1060	22	0
14	BX	1121	0	1196	31	0
15	BY	1073	0	1132	31	0
16	Ba	769	0	818	19	0
17	Bb	610	0	633	18	0
18	Be	475	0	525	10	0
19	BD	1734	0	1817	37	0
20	BF	1609	0	1675	55	0
21	BK	817	0	804	35	0
22	BP	991	0	1035	39	0
23	BQ	1105	0	1166	40	0
24	BR	975	0	1039	25	0
25	BS	1192	0	1222	54	0
26	BT	1095	0	1114	35	0
27	BU	855	0	917	26	0
28	BZ	558	0	598	16	0
29	Bc	497	0	535	14	0
30	Bd	442	0	432	22	0
31	Bg	2401	0	2356	80	0
32	Bf	605	0	654	25	0
33	BM	935	0	975	35	0
34	B5	38004	0	19142	720	0
35	AA	1878	0	1946	37	0
36	AB	3080	0	3158	65	0
37	AC	2748	0	2859	50	0
38	A1	68445	0	34457	835	0
39	A3	2579	0	1304	38	0
40	A4	3353	0	1695	43	0
41	AD	2341	0	2290	31	0
42	AE	1239	0	1326	29	0
43	AF	1784	0	1862	29	0
44	AG	1798	0	1894	31	0
45	AH	1510	0	1576	31	0
46	AI	1672	0	1711	34	0
47	AJ	1353	0	1383	33	0
48	AL	1543	0	1608	23	0
49	AM	1053	0	1149	22	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	AN	1720	0	1779	31	0
51	AO	1555	0	1659	18	0
52	AP	1388	0	1423	24	0
53	AQ	1441	0	1543	28	0
54	AR	1521	0	1617	26	0
55	AS	1445	0	1487	24	0
56	AT	1276	0	1323	24	0
57	AU	796	0	812	13	0
58	AV	1003	0	1048	24	0
59	AW	521	0	551	4	0
60	AX	968	0	1036	11	0
61	AY	993	0	1081	21	0
62	AZ	1092	0	1155	20	0
63	Aa	1173	0	1215	32	0
64	Ab	462	0	491	6	0
65	Ac	743	0	797	14	0
66	Ad	890	0	938	9	0
67	Ae	1020	0	1089	15	0
68	Af	850	0	880	11	0
69	Ag	880	0	945	13	0
70	Ah	969	0	1078	16	0
71	Ai	771	0	849	17	0
72	Aj	681	0	687	12	0
73	Ak	612	0	682	20	0
74	Al	436	0	475	8	0
75	Am	417	0	459	9	0
76	An	233	0	280	10	0
77	Ao	819	0	886	13	0
78	Ap	694	0	738	13	0
79	E	1718	0	1811	54	0
80	DC	6419	0	6493	200	0
81	V	1473	0	1514	63	0
82	EC	4128	0	2082	76	0
83	A1	174	0	0	0	0
83	A3	2	0	0	0	0
83	A4	6	0	0	0	0
83	AI	1	0	0	0	0
83	AL	1	0	0	0	0
83	AN	1	0	0	0	0
83	AP	1	0	0	0	0
83	AR	1	0	0	0	0
83	Ae	2	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	Aj	1	0	0	0	0
83	B5	62	0	0	0	0
83	BJ	1	0	0	0	0
83	Ba	1	0	0	0	0
84	Ao	1	0	0	0	0
85	DC	28	0	12	0	0
All	All	214019	0	160070	3398	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 9.

All (3398) 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)
38:A1:1572:U:HO2'	38:A1:1573:G:H8	1.07	0.98
79:E:89:ASP:O	79:E:93:LEU:HB2	1.65	0.96
34:B5:1542:G:H1	34:B5:1568:C:HO2'	1.18	0.92
34:B5:1588:G:H1	34:B5:1608:U:H3	0.94	0.92
34:B5:1202:A:HO2'	34:B5:1206:U:H3	1.09	0.92
38:A1:2465:G:H1	38:A1:2491:A:N6	1.68	0.91
34:B5:1697:G:H1	34:B5:1704:U:H3	1.01	0.91
6:BH:17:GLU:HB3	6:BH:46:ILE:HG13	1.54	0.90
30:Bd:33:LYS:NZ	34:B5:1594:G:OP1	2.05	0.89
34:B5:1499:G:H1	34:B5:1508:U:H3	0.90	0.87
34:B5:976:G:H1	34:B5:1023:A:HO2'	1.20	0.87
2:BB:27:LYS:HD3	2:BB:47:LEU:HD13	1.56	0.87
38:A1:2465:G:N1	38:A1:2491:A:N6	2.22	0.86
38:A1:171:G:H1	38:A1:246:U:H3	1.21	0.85
31:Bg:89:LEU:HB2	31:Bg:103:PHE:HB2	1.59	0.85
14:BX:121:ARG:NH2	34:B5:1135:U:OP2	2.09	0.83
34:B5:1488:G:N1	34:B5:1518:C:N3	2.23	0.83
34:B5:1370:U:H3	34:B5:1374:C:H41	1.26	0.82
38:A1:2673:A:H5''	47:AJ:95:ASN:HD22	1.42	0.82
38:A1:2480:A:OP1	79:E:98:LYS:NZ	2.11	0.81
58:AV:81:GLN:O	58:AV:98:ASN:ND2	2.13	0.81
35:AA:117:GLU:HG2	35:AA:124:GLY:H	1.46	0.81
34:B5:126:A:H62	34:B5:291:G:H21	1.25	0.81
7:BI:172:ARG:HE	7:BI:175:GLN:HG3	1.45	0.81
33:BM:132:GLU:HB2	33:BM:135:MET:HE2	1.62	0.80
70:Ah:102:GLU:OE2	70:Ah:105:ARG:NH2	2.11	0.80
80:DC:338:ILE:HG23	80:DC:342:LEU:HD12	1.62	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1488:G:N2	34:B5:1518:C:O2	2.15	0.80
3:BC:79:GLU:HG2	3:BC:186:LYS:HD3	1.63	0.80
80:DC:418:TYR:HB3	80:DC:477:ASN:HD22	1.47	0.80
34:B5:1208:A:H8	34:B5:1269:OMU:H6	1.47	0.79
2:BB:132:ASP:HB2	2:BB:221:PRO:HB3	1.64	0.79
5:BG:13:GLN:NE2	34:B5:151:G:N3	2.31	0.79
34:B5:1339:C:O2'	34:B5:1341:A:N7	2.16	0.79
33:BM:27:ALA:HB2	33:BM:135:MET:HE3	1.63	0.79
79:E:8:GLN:HG3	79:E:11:GLU:HB3	1.65	0.79
22:BP:81:ARG:NH2	22:BP:97:TYR:O	2.16	0.78
22:BP:100:LYS:HD3	34:B5:1211:A:H4'	1.64	0.78
25:BS:17:LEU:HD21	25:BS:66:LEU:HD11	1.66	0.78
51:AO:27[A]:LEU:HD21	51:AO:102[A]:LEU:HB2	1.66	0.78
3:BC:148:LEU:HA	12:BV:4:ASP:HB3	1.66	0.78
19:BD:76:ARG:NH2	21:BK:63:TYR:O	2.16	0.78
57:AU:43:VAL:HG12	57:AU:44:GLU:OE1	1.85	0.77
30:Bd:33:LYS:HZ3	34:B5:1594:G:P	2.07	0.77
20:BF:80:LYS:HB2	20:BF:83:ARG:HG3	1.66	0.77
31:Bg:10:ARG:NH1	31:Bg:314:GLN:OE1	2.16	0.77
34:B5:992:A:O2'	34:B5:1785:U:O2	2.02	0.77
32:Bf:132:LEU:HB3	32:Bf:141:CYS:HA	1.67	0.77
38:A1:845:G:H21	38:A1:848:A:H2	1.30	0.77
37:AC:98:ARG:NH2	38:A1:804:C:OP1	2.18	0.76
34:B5:1773:4AC:H5	76:An:2:ARG:HH22	1.49	0.76
82:EC:6788:C:N4	82:EC:6805:C:OP2	2.19	0.76
8:BJ:59:LEU:HD12	8:BJ:69:ARG:HA	1.68	0.76
14:BX:70:LYS:NZ	34:B5:567:A:OP1	2.19	0.76
34:B5:680:U:O2	34:B5:682:C:N4	2.19	0.76
34:B5:868:G:H1	34:B5:960:U:H3	1.33	0.76
37:AC:319:LYS:NZ	38:A1:506:U:OP2	2.19	0.76
4:BE:246:LEU:HD21	4:BE:254:ARG:HH21	1.50	0.75
38:A1:1412:G:OP1	67:Ae:105:ARG:NH2	2.18	0.75
20:BF:72:HIS:NE2	34:B5:1610:G:OP1	2.19	0.75
38:A1:1257:C:O2	81:V:39:HIS:NE2	2.19	0.75
14:BX:74:VAL:HG21	14:BX:104:LEU:HD11	1.68	0.75
34:B5:126:A:H62	34:B5:291:G:N2	1.84	0.75
28:BZ:56:THR:HA	28:BZ:103:ARG:HE	1.50	0.75
33:BM:103:LEU:HD13	34:B5:1227:A:C4	2.22	0.75
50:AN:183:THR:HG22	50:AN:187:ARG:HB3	1.67	0.75
34:B5:1183:A:N3	34:B5:1210:C:O2'	2.20	0.74
38:A1:175:C:H2'	38:A1:176:G:C8	2.22	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:AL:174:ARG:HB3	71:AI:9:ILE:HD12	1.68	0.74
23:BQ:52:LEU:HA	23:BQ:60:PHE:HE2	1.53	0.74
82:EC:6922:G:H1	82:EC:6931:U:H3	1.34	0.74
5:BG:39:GLU:HG3	5:BG:46:LYS:HD3	1.70	0.74
3:BC:39:THR:HG23	3:BC:42:GLY:H	1.53	0.73
1:BA:15:GLN:HA	24:BR:100:LEU:HD11	1.69	0.73
3:BC:81:MET:HB2	3:BC:101:VAL:HG23	1.70	0.73
38:A1:175:C:H2'	38:A1:176:G:H8	1.52	0.73
47:AJ:14:ILE:HG12	47:AJ:131:MET:HE1	1.70	0.73
38:A1:1258:U:H4'	81:V:42:ARG:HH21	1.51	0.73
14:BX:144:ARG:HD2	80:DC:464:LEU:HB2	1.69	0.73
34:B5:1213:G:H1	34:B5:1450:U:H3	1.36	0.73
73:AK:7:ASP:HB3	73:AK:10:GLN:HG2	1.69	0.73
5:BG:2:LYS:HB2	5:BG:108:VAL:HG22	1.71	0.73
58:AV:10:LYS:HD3	58:AV:125:LEU:HD11	1.70	0.73
82:EC:6767:G:H21	82:EC:6768:U:H3	1.37	0.73
45:AH:21:LYS:HG3	45:AH:22:SER:H	1.52	0.73
33:BM:41:LEU:HD12	33:BM:123:VAL:HA	1.70	0.72
58:AV:54:LEU:HD21	58:AV:119:GLY:HA3	1.71	0.72
33:BM:50:LYS:HE2	33:BM:54:ARG:HH12	1.54	0.72
38:A1:1591:G:OP1	69:AG:16:ARG:NH1	2.22	0.72
32:Bf:138:ARG:HD3	32:Bf:147:VAL:HG13	1.71	0.72
31:Bg:260:ILE:HB	31:Bg:274:LEU:HB2	1.71	0.72
34:B5:163:G:OP2	34:B5:163:G:N2	2.20	0.72
15:BY:7:ILE:HG13	15:BY:43:LYS:HG2	1.72	0.72
16:Ba:18:VAL:HG23	16:Ba:19:LYS:H	1.55	0.72
78:Ap:46:THR:OG1	78:Ap:57:CYS:SG	2.47	0.72
38:A1:165:A:HO2'	38:A1:166:C:H6	1.35	0.71
38:A1:1132:C:H2'	38:A1:1133:A2M:H8	1.71	0.71
80:DC:113:SER:HB3	80:DC:483:PHE:HD1	1.55	0.71
10:BN:11:ILE:HG13	10:BN:12:SER:H	1.55	0.71
81:V:189:GLN:NE2	81:V:190:VAL:O	2.23	0.71
38:A1:2767:U:O2'	77:Ao:30:ALA:O	2.07	0.71
80:DC:785:ARG:NH1	80:DC:792:ALA:O	2.24	0.71
20:BF:99:MET:HG2	20:BF:100:ASN:H	1.55	0.71
15:BY:36:SER:OG	15:BY:39:GLU:OE1	2.09	0.71
24:BR:36:ASP:OD1	24:BR:47:ARG:NH1	2.23	0.70
35:AA:9:ARG:NH2	38:A1:912:G:OP2	2.24	0.70
46:AI:36:LEU:HD21	46:AI:69:ARG:HH11	1.54	0.70
7:BI:104:ILE:HG13	7:BI:105:ASP:H	1.55	0.70
81:V:53:MET:SD	81:V:54:GLY:N	2.63	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3302:U:H3	38:A1:3312:U:H3	1.39	0.70
80:DC:247:ASP:OD1	80:DC:271:ARG:NH1	2.24	0.70
8:BJ:109:LEU:HB2	8:BJ:146:PHE:HB3	1.73	0.70
33:BM:43:ARG:HH22	34:B5:1255:G:H3'	1.55	0.70
34:B5:321:C:H42	34:B5:1666:U:H5''	1.54	0.70
38:A1:715:A:H8	63:Aa:115:LYS:HD3	1.56	0.70
38:A1:2478:C:OP2	38:A1:2480:A:N6	2.24	0.70
71:Ai:51:SER:HB3	71:Ai:54:GLU:HG3	1.72	0.70
81:V:123:ALA:HA	81:V:152:ILE:HB	1.72	0.70
26:BT:122:ARG:NH1	34:B5:1499:G:OP1	2.25	0.70
34:B5:224:C:N4	34:B5:837:G:O6	2.23	0.70
81:V:142:PRO:HB2	81:V:153:VAL:HB	1.74	0.70
37:AC:318:LEU:H	37:AC:324:LEU:HD12	1.57	0.70
81:V:38:MET:HE1	81:V:185:LEU:HD13	1.72	0.70
25:BS:71:GLN:HA	25:BS:74:GLN:OE1	1.91	0.69
80:DC:388:THR:HB	80:DC:395:TYR:HE2	1.58	0.69
33:BM:62:LEU:HD11	33:BM:88:LEU:HD22	1.72	0.69
26:BT:42:GLY:HA2	26:BT:84:LYS:HD2	1.74	0.69
33:BM:62:LEU:HB2	33:BM:90:LYS:HG3	1.74	0.69
44:AG:98:ARG:NH2	44:AG:188:THR:O	2.25	0.69
31:Bg:205:SER:OG	31:Bg:207:ASP:OD1	2.11	0.69
38:A1:1661:G:H2'	38:A1:1662:G:C8	2.28	0.69
80:DC:634:TRP:HB2	80:DC:646:VAL:HG23	1.74	0.69
34:B5:17:C:O2'	34:B5:1137:A:N1	2.25	0.69
34:B5:1291:G:H22	34:B5:1324:G:H22	1.40	0.69
35:AA:36:GLU:HG3	35:AA:91:GLY:HA2	1.73	0.69
5:BG:66:GLY:HA2	34:B5:1681:A:H1'	1.74	0.69
23:BQ:20:ALA:HB1	23:BQ:65:ILE:HD11	1.73	0.69
54:AR:181:ARG:HA	54:AR:185:LEU:HB3	1.75	0.69
47:AJ:93:ASP:HB2	47:AJ:172:LEU:HD12	1.75	0.69
79:E:124:LEU:HD12	79:E:128:LEU:HB2	1.74	0.69
10:BN:23:PRO:HD2	10:BN:26:PHE:HB2	1.74	0.68
38:A1:121:A:O2'	44:AG:105:LYS:NZ	2.27	0.68
76:An:1:MET:HE3	76:An:6:ARG:HD2	1.73	0.68
34:B5:702:G:O6	34:B5:737:A:N6	2.25	0.68
81:V:112:GLY:H	81:V:165:VAL:HG13	1.57	0.68
2:BB:130:SER:HB2	2:BB:180:THR:HG22	1.74	0.68
34:B5:1227:A:H61	34:B5:1256:A:H5''	1.58	0.68
69:Ag:58:ARG:HB2	69:Ag:61:GLN:HG2	1.76	0.68
2:BB:149:GLN:HE22	2:BB:154:SER:HB2	1.57	0.68
19:BD:161:GLY:HA3	34:B5:1331:A:H61	1.58	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Bf:140:TYR:OH	34:B5:1234:A:O2'	2.10	0.68
36:AB:291:GLU:HG2	36:AB:302:LYS:NZ	2.09	0.68
6:BH:150:GLN:HB3	6:BH:181:ILE:HG22	1.76	0.68
23:BQ:100:GLN:NE2	31:Bg:57:PRO:O	2.26	0.68
38:A1:2464:U:OP1	38:A1:2485:A:O2'	2.11	0.68
82:EC:6776:A:N3	82:EC:6818:G:N2	2.42	0.68
38:A1:1310:G:HO2'	38:A1:2380:U:HO2'	1.41	0.68
32:Bf:94:LYS:NZ	34:B5:1231:U:OP1	2.27	0.68
80:DC:20:ARG:HB2	80:DC:100:ILE:HG13	1.76	0.68
81:V:97:LYS:HE2	81:V:187:VAL:HG21	1.75	0.68
38:A1:2901:G:O2'	38:A1:3024:A:N1	2.26	0.67
75:Am:92:ASP:OD1	75:Am:126:LYS:NZ	2.26	0.67
1:BA:83:GLN:HG2	1:BA:99:ALA:HB1	1.76	0.67
38:A1:3092:C:O2'	38:A1:3094:A:OP2	2.12	0.67
55:AS:8:GLN:HB3	55:AS:64:ILE:HD11	1.75	0.67
65:Ac:30:THR:HG23	65:Ac:91:SER:HB2	1.76	0.67
80:DC:546:GLU:HG2	80:DC:554:LEU:HD23	1.75	0.67
4:BE:151:ASP:OD1	5:BG:215:ARG:NH1	2.27	0.67
7:BI:152:ILE:HG13	7:BI:153:GLU:H	1.59	0.67
29:Bc:63:ALA:O	29:Bc:64:ARG:NE	2.21	0.67
1:BA:117:GLU:OE2	3:BC:39:THR:OG1	2.12	0.67
13:BW:57:ARG:HG2	34:B5:862:A:H4'	1.76	0.67
36:AB:308:MET:HE2	38:A1:3329:U:H5''	1.77	0.67
38:A1:176:G:HO2'	38:A1:177:U:H6	1.42	0.67
38:A1:1639:C:OP2	69:Ag:74:ARG:NH2	2.27	0.67
67:Ae:83:GLU:OE2	67:Ae:111:ARG:NH1	2.28	0.67
5:BG:180:THR:HG23	5:BG:183:ARG:H	1.58	0.67
76:An:1:MET:HE3	76:An:6:ARG:CD	2.25	0.67
25:BS:87:ASN:OD1	34:B5:1546:G:N2	2.28	0.67
1:BA:148:ASP:OD2	1:BA:165:ARG:NH1	2.27	0.67
38:A1:2474:G:N2	38:A1:2475:G:O6	2.28	0.67
77:Ao:6:LYS:HG3	77:Ao:94:GLY:HA3	1.77	0.67
34:B5:1773:4AC:H5	76:An:2:ARG:NH2	2.10	0.67
80:DC:77:LEU:HB2	80:DC:100:ILE:HG22	1.77	0.67
2:BB:61:LEU:HD22	2:BB:96:LEU:HD21	1.76	0.66
24:BR:117:LEU:HD12	24:BR:118:PRO:HD2	1.77	0.66
32:Bf:119:ARG:HH22	32:Bf:150:VAL:HA	1.59	0.66
35:AA:21:ARG:HD3	38:A1:824:C:H5''	1.78	0.66
38:A1:1186:G:OP2	49:AM:42:LYS:NZ	2.25	0.66
38:A1:1863:G:N1	38:A1:1866:C:OP2	2.22	0.66
46:AI:30:LYS:HG3	46:AI:63:GLU:HG3	1.78	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BJ:85:VAL:HG13	8:BJ:103:ASP:HB3	1.76	0.66
38:A1:284:A:OP2	77:Ao:41:ARG:NH1	2.28	0.66
41:AD:50:ARG:HG2	41:AD:147:ASP:HB2	1.78	0.66
16:Ba:45:VAL:HG23	16:Ba:46:GLU:H	1.59	0.66
19:BD:62:ASN:ND2	21:BK:96:ASN:OD1	2.25	0.66
38:A1:358:G:N2	38:A1:361:A:OP2	2.26	0.66
82:EC:6793:A:H2'	82:EC:6795:U:H5'	1.76	0.66
62:AZ:14:VAL:HB	69:Ag:86:LYS:HG3	1.76	0.66
80:DC:515:ASP:HB3	80:DC:518:VAL:HG12	1.76	0.66
38:A1:3234:A:H61	38:A1:3253:G:H1	1.43	0.66
6:BH:49:ILE:HD12	6:BH:175:LYS:HG2	1.76	0.66
34:B5:900:A:H3'	34:B5:901:G:H21	1.59	0.66
34:B5:1171:A:H2'	34:B5:1172:G:C8	2.30	0.66
36:AB:124:LYS:NZ	38:A1:3297:U:O4	2.29	0.66
80:DC:564:ARG:HB2	80:DC:725:GLN:HB2	1.77	0.66
23:BQ:13:LYS:HG3	23:BQ:14:LYS:H	1.60	0.66
38:A1:937:G:N2	38:A1:961:C:OP1	2.29	0.66
38:A1:3042:U:OP2	38:A1:3092:C:N4	2.25	0.66
73:Ak:5:ILE:HG23	73:Ak:10:GLN:HE21	1.61	0.66
62:AZ:70:PRO:HG3	62:AZ:115:LYS:HB2	1.78	0.66
3:BC:201:ASN:ND2	34:B5:1097:U:O4	2.29	0.65
15:BY:35:VAL:HG23	15:BY:36:SER:H	1.59	0.65
34:B5:871:G:H2'	34:B5:872:G:C8	2.31	0.65
38:A1:1846:C:OP1	38:A1:1849:C:N4	2.27	0.65
38:A1:2227:C:OP1	77:Ao:32:LYS:NZ	2.29	0.65
47:AJ:53:THR:HG23	47:AJ:60:ARG:HA	1.78	0.65
80:DC:464:LEU:HG	80:DC:465:LYS:H	1.61	0.65
16:Ba:8:ASN:HB3	34:B5:1791:A:H3'	1.77	0.65
31:Bg:239:GLU:O	31:Bg:257:ALA:N	2.29	0.65
34:B5:1591:C:H2'	34:B5:1592:A:H8	1.62	0.65
38:A1:1152:G:N2	38:A1:1152:G:OP2	2.26	0.65
38:A1:2588:U:OP1	44:AG:241:LYS:NZ	2.29	0.65
39:A3:64:A:N7	46:AI:209:ASN:ND2	2.43	0.65
16:Ba:30:ILE:HD11	16:Ba:34:LYS:HD3	1.78	0.65
34:B5:71:A:N6	34:B5:72:A:N3	2.44	0.65
45:AH:41:ILE:HG21	45:AH:71:VAL:HG21	1.78	0.65
10:BN:3:ARG:HB3	10:BN:6:SER:HB3	1.78	0.65
31:Bg:200:ASN:ND2	31:Bg:240:VAL:O	2.26	0.65
34:B5:813:U:O2'	54:AR:167:ARG:NH1	2.28	0.65
38:A1:178:U:H2'	38:A1:179:C:H6	1.60	0.65
7:BI:81:VAL:HG12	7:BI:102:VAL:HG12	1.78	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:BV:62:ARG:HH22	34:B5:1039:A:H4'	1.62	0.65
21:BK:46:LEU:O	21:BK:50:THR:HG23	1.96	0.65
34:B5:509:G:H2'	34:B5:510:G:C8	2.32	0.65
34:B5:1357:A:H2'	34:B5:1358:G:H8	1.61	0.65
5:BG:10:ASN:ND2	5:BG:127:THR:O	2.30	0.65
34:B5:655:G:N2	34:B5:657:U:O4	2.30	0.65
34:B5:1575:7MG:O2'	34:B5:1576:A:H5'	1.97	0.65
38:A1:353:G:O6	72:Aj:55:ARG:NH2	2.30	0.65
38:A1:2895:G:O2'	75:Am:100:TYR:O	2.15	0.65
3:BC:143:TYR:HB3	3:BC:145:GLY:HA3	1.79	0.65
19:BD:72:LEU:HD12	21:BK:65:TYR:HD1	1.61	0.65
80:DC:415:GLY:O	80:DC:477:ASN:ND2	2.28	0.65
82:EC:6853:G:N1	82:EC:6876:A:C2	2.64	0.65
11:BO:103:ARG:NH1	16:Ba:52:ASP:OD2	2.28	0.65
38:A1:714:G:HO2'	38:A1:753:C:HO2'	1.45	0.65
20:BF:57:SER:HA	29:Bc:53:ILE:HG13	1.78	0.65
38:A1:655:C:H2'	38:A1:656:A:H8	1.61	0.65
81:V:130:PRO:HA	81:V:150:ILE:HD11	1.78	0.65
38:A1:3016:A:H2'	38:A1:3017:A:C8	2.32	0.65
38:A1:3227:A:O2'	49:AM:133:LYS:NZ	2.30	0.65
54:AR:178:ALA:HA	54:AR:181:ARG:HG2	1.79	0.65
58:AV:104:ASN:HD21	58:AV:108:GLU:HB3	1.62	0.65
1:BA:36:TYR:OH	12:BV:70:ASN:ND2	2.25	0.64
5:BG:27:PHE:HE1	5:BG:111:LEU:HD11	1.62	0.64
34:B5:1171:A:H2'	34:B5:1172:G:H8	1.61	0.64
54:AR:21:LYS:HE3	54:AR:55:VAL:HA	1.80	0.64
19:BD:174:HIS:HE1	34:B5:1277:G:H21	1.45	0.64
26:BT:89:ARG:NH1	34:B5:1562:G:OP1	2.30	0.64
38:A1:2465:G:N1	38:A1:2491:A:C6	2.60	0.64
79:E:109:ALA:HA	79:E:133:LYS:HG2	1.80	0.64
38:A1:1566:A:H8	38:A1:1566:A:O5'	1.80	0.64
39:A3:23:A:HO2'	39:A3:121:U:HO3'	1.46	0.64
2:BB:103:MET:HE3	2:BB:215:VAL:HG23	1.78	0.64
31:Bg:153:GLN:HE21	31:Bg:155:ARG:HH21	1.45	0.64
38:A1:297:G:O6	50:AN:12:ARG:NH1	2.31	0.64
38:A1:1015:U:O2	38:A1:1035:G:O6	2.16	0.64
57:AU:19:VAL:HG23	57:AU:105:LEU:HD12	1.78	0.64
11:BO:18:ARG:NH1	11:BO:31:THR:OG1	2.30	0.64
27:BU:70:THR:OG1	27:BU:72:ASN:OD1	2.15	0.64
34:B5:1201:G:N2	34:B5:1600:A:O5'	2.31	0.64
38:A1:715:A:C8	63:Aa:115:LYS:HD3	2.32	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:AE:172:HIS:CD2	42:AE:173:MET:HG2	2.32	0.64
80:DC:725:GLN:HG2	80:DC:803:THR:HB	1.79	0.64
4:BE:185:GLY:H	4:BE:224:ASN:HB3	1.63	0.64
5:BG:160:ARG:NH2	34:B5:68:A:OP1	2.30	0.64
20:BF:99:MET:SD	34:B5:1165:G:H5''	2.38	0.64
34:B5:514:G:H1	34:B5:543:C:H5	1.43	0.64
34:B5:947:U:H2'	34:B5:948:G:H8	1.61	0.64
34:B5:1170:G:N2	34:B5:1571:C:O2'	2.31	0.64
36:AB:240:ARG:NH2	38:A1:1907:C:O2	2.30	0.64
25:BS:7:GLU:OE2	25:BS:10:SER:OG	2.14	0.64
51:AO:61[A]:ALA:HA	51:AO:70[A]:PRO:HD2	1.78	0.64
57:AU:37:LEU:O	57:AU:41:ILE:HG12	1.98	0.64
80:DC:694:HIS:NE2	80:DC:699:DDE:HD2	2.12	0.64
13:BW:15:ASN:ND2	13:BW:72:CYS:O	2.31	0.64
17:Bb:2:VAL:HG21	17:Bb:5:GLN:HB2	1.79	0.64
41:AD:129:TYR:OH	41:AD:175:HIS:O	2.14	0.64
80:DC:353:ALA:HB3	80:DC:370:LYS:HG2	1.79	0.64
33:BM:22:VAL:HB	33:BM:135:MET:SD	2.38	0.64
34:B5:1466:G:O2'	34:B5:1602:C:OP1	2.14	0.64
38:A1:591:G:O2'	42:AE:17:ALA:O	2.15	0.64
38:A1:1277:C:H2'	38:A1:1278:A:H8	1.62	0.64
23:BQ:40:GLU:OE2	23:BQ:45:ARG:NH2	2.31	0.64
25:BS:75:ASN:OD1	25:BS:78:HIS:ND1	2.23	0.64
34:B5:1169:G:N1	34:B5:1575:7MG:OP2	2.27	0.64
36:AB:219:ALA:HB2	36:AB:336:VAL:HG23	1.80	0.64
3:BC:45:VAL:HG21	3:BC:68:ILE:HG23	1.80	0.63
4:BE:59:ARG:NH1	4:BE:60:GLU:OE2	2.31	0.63
31:Bg:102:ARG:NH2	34:B5:1341:A:O2'	2.31	0.63
38:A1:1213:G:H4'	55:AS:90:MET:HG3	1.80	0.63
38:A1:2700:G:H5''	56:AT:17:ARG:HG2	1.80	0.63
38:A1:2796:G:N7	77:Ao:63:LYS:NZ	2.46	0.63
51:AO:22[A]:VAL:HG21	51:AO:120[A]:VAL:HG11	1.80	0.63
3:BC:146:THR:HG23	3:BC:148:LEU:H	1.63	0.63
4:BE:87:MET:HE1	4:BE:236:ILE:HD13	1.78	0.63
47:AJ:115:LYS:HG3	47:AJ:116:TYR:H	1.63	0.63
80:DC:694:HIS:CD2	80:DC:699:DDE:HB3	2.33	0.63
27:BU:53:LYS:HD2	34:B5:1345:A:H5'	1.81	0.63
22:BP:104:GLN:NE2	22:BP:105:VAL:O	2.32	0.63
34:B5:647:G:H21	34:B5:687:G:H1	1.44	0.63
7:BI:16:ALA:HB2	34:B5:354:C:H5''	1.81	0.63
21:BK:87:VAL:HG22	21:BK:89:GLY:H	1.64	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:239:GLU:HB3	31:Bg:257:ALA:HB2	1.81	0.63
37:AC:35:VAL:HG21	37:AC:244:LEU:HD21	1.79	0.63
38:A1:2875:U:O2'	38:A1:2876:C:O5'	2.15	0.63
38:A1:3231:U:H2'	38:A1:3232:G:H8	1.63	0.63
79:E:20:SER:HA	79:E:24:LYS:HE3	1.78	0.63
3:BC:101:VAL:HG12	3:BC:115:ILE:HD12	1.80	0.63
36:AB:215:ILE:HD12	36:AB:338:LEU:HB3	1.81	0.63
29:Bc:9:LEU:HB3	29:Bc:33:LEU:HD12	1.78	0.63
80:DC:164:LEU:HD21	80:DC:174:LEU:HD22	1.80	0.63
10:BN:104:ARG:NH2	34:B5:951:A:OP1	2.31	0.63
26:BT:64:HIS:NE2	34:B5:1480:G:OP1	2.30	0.63
26:BT:105:LEU:HD13	26:BT:122:ARG:HD3	1.81	0.63
37:AC:156:LEU:HD12	37:AC:159:ILE:HD12	1.79	0.63
38:A1:1729:A:O4'	65:Ac:52:ARG:NH1	2.31	0.63
80:DC:40:VAL:HG12	80:DC:77:LEU:HD11	1.81	0.63
4:BE:206:ASP:HB2	4:BE:222:LEU:HD22	1.81	0.63
23:BQ:22:VAL:HG22	23:BQ:65:ILE:HD13	1.81	0.63
31:Bg:127:ARG:HA	31:Bg:150:TRP:HB2	1.81	0.63
34:B5:273:G:O6	34:B5:283:U:O2	2.17	0.63
40:A4:143:U:OP1	50:AN:38:ARG:NH2	2.29	0.63
2:BB:214:LYS:NZ	34:B5:886:U:OP1	2.31	0.62
22:BP:78:THR:HA	34:B5:1241:G:H4'	1.81	0.62
38:A1:1448:U:H2'	38:A1:1449:A2M:H8	1.81	0.62
43:AF:178:ILE:HG23	43:AF:183:ASP:HB3	1.81	0.62
19:BD:76:ARG:HH22	21:BK:23:ALA:H	1.47	0.62
20:BF:84:LYS:NZ	34:B5:1614:A:OP2	2.32	0.62
38:A1:3252:G:H2'	38:A1:3253:G:C8	2.34	0.62
40:A4:94:C:OP1	72:Aj:75:LYS:NZ	2.32	0.62
82:EC:6812:C:H2'	82:EC:6813:A:C8	2.34	0.62
5:BG:92:ARG:NH1	34:B5:1674:C:OP1	2.32	0.62
61:AY:56:VAL:HG21	61:AY:104:LEU:HD13	1.80	0.62
1:BA:30:GLN:HE22	1:BA:32:HIS:HB2	1.64	0.62
1:BA:107:PHE:HB2	1:BA:135:GLU:HG2	1.81	0.62
6:BH:135:ILE:HG21	6:BH:138:LYS:HE3	1.80	0.62
14:BX:99:ASN:HD21	80:DC:505:VAL:HB	1.64	0.62
34:B5:1027:A:OP1	34:B5:1789:G:O2'	2.15	0.62
34:B5:1266:U:H2'	34:B5:1267:G:H8	1.65	0.62
34:B5:1785:U:H2'	34:B5:1786:G:H8	1.65	0.62
60:AX:50:ALA:HB1	70:Ah:66:VAL:HG11	1.82	0.62
82:EC:6852:U:H2'	82:EC:6853:G:C8	2.34	0.62
34:B5:1575:7MG:H2'	34:B5:1576:A:C8	2.34	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2467:G:H21	38:A1:2488:A:H62	1.47	0.62
47:AJ:19:LEU:HD22	47:AJ:125:MET:HE2	1.82	0.62
80:DC:594:ASP:OD2	80:DC:596:GLU:HG3	1.99	0.62
34:B5:973:A:H2'	34:B5:974:A2M:H8	1.82	0.62
38:A1:1049:C:OP1	46:AI:21:ARG:NH2	2.32	0.62
20:BF:140:THR:HG23	20:BF:210:ALA:HB1	1.81	0.62
34:B5:800:U:H2'	34:B5:801:G:H8	1.65	0.62
38:A1:173:G:H1	38:A1:244:G:H22	1.47	0.62
38:A1:664:U:H2'	38:A1:665:A:C8	2.34	0.62
45:AH:30:PRO:HD2	45:AH:83:THR:HG22	1.81	0.62
51:AO:187[A]:GLU:O	51:AO:192[A]:LYS:NZ	2.33	0.62
6:BH:108:GLN:OE1	34:B5:810:G:N2	2.32	0.62
27:BU:59:PRO:HG3	34:B5:1381:U:H4'	1.82	0.62
34:B5:1672:G:H2'	34:B5:1673:G:C8	2.35	0.62
37:AC:136:LEU:HD21	37:AC:143:GLU:HG3	1.81	0.62
38:A1:655:C:H2'	38:A1:656:A:C8	2.34	0.62
80:DC:353:ALA:HA	80:DC:356:LEU:HB3	1.81	0.62
3:BC:35:TRP:O	3:BC:46:LYS:NZ	2.33	0.61
14:BX:121:ARG:HH22	34:B5:1135:U:P	2.23	0.61
19:BD:16:VAL:HG11	30:Bd:22:ARG:HH11	1.65	0.61
42:AE:92:SER:OG	42:AE:148:GLU:OE1	2.18	0.61
58:AV:38:ALA:HB3	58:AV:59:MET:HB2	1.82	0.61
80:DC:718:LEU:HG	80:DC:722:PRO:HG2	1.82	0.61
30:Bd:16:LYS:O	30:Bd:27:HIS:ND1	2.33	0.61
32:Bf:118:ARG:HH21	32:Bf:139:LEU:HD13	1.64	0.61
38:A1:799:G:O2'	48:AL:18:TRP:NE1	2.33	0.61
38:A1:1194:G:H2'	38:A1:1195:A:C8	2.36	0.61
38:A1:1506:A:OP2	52:AP:127:ARG:NH1	2.31	0.61
38:A1:2768:U:H2'	38:A1:2769:A:H8	1.64	0.61
2:BB:64:ARG:NH2	11:BO:36:LYS:HD2	2.15	0.61
2:BB:144:ARG:HB2	2:BB:208:GLN:HB3	1.81	0.61
11:BO:41:ARG:NH2	34:B5:896:U:O2	2.34	0.61
32:Bf:142:GLY:HA3	34:B5:1252:C:H1'	1.83	0.61
38:A1:2854:U:OP2	46:AI:3:ARG:NH2	2.32	0.61
8:BJ:114:TYR:HA	8:BJ:119:ALA:HB3	1.81	0.61
8:BJ:119:ALA:O	8:BJ:124:HIS:ND1	2.26	0.61
16:Ba:32:LYS:NZ	34:B5:932:U:O2	2.32	0.61
23:BQ:41:PRO:HD2	23:BQ:44:LEU:HB2	1.82	0.61
33:BM:43:ARG:HD2	33:BM:103:LEU:HD21	1.82	0.61
34:B5:1291:G:H22	34:B5:1324:G:N2	1.98	0.61
34:B5:1483:A:H2	34:B5:1607:G:H1'	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:90:C:OP1	63:Aa:59:ARG:NH1	2.33	0.61
38:A1:126:U:OP1	50:AN:144:ARG:NH1	2.33	0.61
38:A1:1333:C:OP1	53:AQ:2:GLY:N	2.33	0.61
63:Aa:24:LYS:O	63:Aa:26:ARG:HG2	2.00	0.61
79:E:54:LYS:NZ	79:E:150:ASP:O	2.33	0.61
7:BI:27:PHE:HB2	34:B5:333:A:H62	1.64	0.61
24:BR:79:GLU:O	24:BR:83:GLN:NE2	2.33	0.61
80:DC:723:LYS:HG2	80:DC:808:PRO:HD3	1.83	0.61
3:BC:41:LEU:HD21	3:BC:56:ILE:HD13	1.81	0.61
4:BE:131:LEU:HD12	34:B5:251:A:H2	1.65	0.61
5:BG:2:LYS:NZ	34:B5:154:G:OP1	2.34	0.61
38:A1:2508:U:H2'	38:A1:2509:U:C6	2.36	0.61
2:BB:134:VAL:HG12	2:BB:219:LYS:HG2	1.80	0.61
11:BO:18:ARG:HD3	34:B5:918:U:H4'	1.83	0.61
32:Bf:107:LYS:HB2	32:Bf:117:LEU:HD11	1.83	0.61
34:B5:1502:G:N2	34:B5:1505:A:OP2	2.24	0.61
43:AF:92:ILE:HG23	53:AQ:4:ASP:HB3	1.81	0.61
80:DC:19:VAL:HG22	80:DC:99:LEU:HD21	1.81	0.61
4:BE:19:LEU:HD11	4:BE:108:ARG:HD2	1.83	0.61
25:BS:67:GLU:HA	25:BS:70:VAL:HG22	1.83	0.61
38:A1:649:A2M:OP2	38:A1:2868:U:O2'	2.17	0.61
38:A1:728:G:H5''	53:AQ:43:PRO:HB2	1.83	0.61
38:A1:1477:A:OP1	38:A1:3075:G:O2'	2.16	0.61
1:BA:111:ILE:HD11	34:B5:1292:G:H21	1.65	0.61
3:BC:148:LEU:O	3:BC:174:ARG:NH2	2.34	0.61
14:BX:41:SER:OG	14:BX:43:PHE:O	2.17	0.61
22:BP:40:ARG:NH1	34:B5:1553:G:O6	2.34	0.61
23:BQ:71:GLY:HA2	34:B5:1483:A:H4'	1.83	0.61
34:B5:752:A:H2	34:B5:797:G:H1	1.47	0.61
34:B5:1575:7MG:O2'	34:B5:1576:A:O4'	2.18	0.61
68:Af:56:SER:O	68:Af:63:LYS:NZ	2.34	0.61
38:A1:2284:C:N4	38:A1:2308:C:OP2	2.32	0.61
44:AG:115:ALA:O	44:AG:120:LYS:N	2.34	0.61
73:Ak:20:VAL:HG11	73:Ak:45:VAL:HG13	1.81	0.61
34:B5:560:U:H2'	34:B5:561:G:H8	1.66	0.60
38:A1:178:U:H2'	38:A1:179:C:C6	2.36	0.60
81:V:143:THR:HG23	81:V:150:ILE:HG23	1.83	0.60
82:EC:6759:A:H2'	82:EC:6760:A:C8	2.36	0.60
25:BS:100:THR:HG23	25:BS:104:ASN:HB3	1.83	0.60
34:B5:851:U:OP2	54:AR:173:ARG:NH2	2.21	0.60
38:A1:2213:A:H2'	38:A1:2214:A:C8	2.36	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BJ:81:VAL:HG21	8:BJ:91:LYS:HE3	1.83	0.60
14:BX:48:HIS:HB3	14:BX:103:LEU:HD11	1.83	0.60
20:BF:95:ASN:O	34:B5:1611:A:O2'	2.19	0.60
42:AE:8:LYS:HG3	42:AE:9:TRP:CD1	2.36	0.60
63:Aa:104:THR:HG21	63:Aa:112:ILE:HD11	1.82	0.60
34:B5:882:U:H5''	78:Ap:85:ARG:HH11	1.66	0.60
34:B5:1443:U:H5''	34:B5:1444:A:H5'	1.83	0.60
38:A1:375:A:OP2	61:AY:89:LYS:NZ	2.34	0.60
80:DC:382:VAL:HA	80:DC:398:GLY:HA3	1.82	0.60
81:V:120:TRP:HB3	81:V:157:LYS:HD3	1.82	0.60
34:B5:44:U:OP2	34:B5:437:A:N6	2.34	0.60
46:AI:49:CYS:HB3	46:AI:168:SER:HB3	1.84	0.60
58:AV:68:GLU:O	58:AV:72:LYS:NZ	2.27	0.60
67:Ae:89:THR:HG22	67:Ae:117:ILE:HD13	1.82	0.60
33:BM:95:LYS:NZ	33:BM:115:VAL:O	2.34	0.60
38:A1:1264:G:N2	38:A1:1265:U:O4	2.35	0.60
39:A3:23:A:H2'	39:A3:24:A:C8	2.37	0.60
54:AR:169:ALA:O	54:AR:173:ARG:NE	2.35	0.60
2:BB:48:VAL:HG23	2:BB:49:ASN:H	1.67	0.60
13:BW:2:THR:N	34:B5:1034:C:HO2'	1.98	0.60
34:B5:651:G:N2	34:B5:652:G:O2'	2.34	0.60
34:B5:1683:C:O2'	34:B5:1684:U:O5'	2.20	0.60
38:A1:407:A:C2	40:A4:17:A:H1'	2.37	0.60
38:A1:1447:G:H3'	52:AP:67:ILE:HD11	1.82	0.60
38:A1:2960:C:H2'	38:A1:2961:G:C8	2.37	0.60
80:DC:289:MET:HE3	80:DC:320:LEU:HD22	1.82	0.60
2:BB:82:ARG:NH1	2:BB:188:LEU:O	2.32	0.60
12:BV:74:GLN:HG3	12:BV:83:TRP:HB3	1.83	0.60
34:B5:591:A:H2'	34:B5:592:A:C8	2.37	0.60
38:A1:1221:A:C5	81:V:5:ARG:HD2	2.37	0.60
38:A1:2836:C:H5	38:A1:2852:C:H42	1.49	0.60
1:BA:3:LEU:HD23	12:BV:39:VAL:HG11	1.84	0.60
32:Bf:81:LYS:HG3	80:DC:651:LYS:HE3	1.84	0.60
36:AB:220:VAL:O	36:AB:334:ARG:NH1	2.34	0.60
36:AB:315:GLY:HA2	38:A1:3379:C:H4'	1.83	0.60
38:A1:904:A:OP2	72:Aj:30:GLN:NE2	2.33	0.60
79:E:90:LEU:HD23	79:E:93:LEU:HD13	1.84	0.60
32:Bf:138:ARG:HD2	32:Bf:139:LEU:N	2.16	0.60
33:BM:34:THR:HA	33:BM:37:VAL:HG22	1.83	0.60
34:B5:924:A:H2'	34:B5:925:G:C8	2.37	0.60
34:B5:1196:A:N6	34:B5:1601:G:O2'	2.35	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2468:A:N3	38:A1:2477:G:N2	2.43	0.60
8:BJ:168:ARG:NH1	34:B5:513:U:OP1	2.35	0.59
16:Ba:46:GLU:HG3	16:Ba:49:ALA:H	1.67	0.59
31:Bg:81:LEU:HD21	31:Bg:122:ILE:HG23	1.83	0.59
31:Bg:180:ALA:HB3	31:Bg:190:ALA:HB3	1.83	0.59
34:B5:233:C:O2'	34:B5:234:G:N2	2.29	0.59
34:B5:1585:U:H3	34:B5:1611:A:H2	1.50	0.59
34:B5:1593:A:H2'	34:B5:1594:G:H8	1.67	0.59
38:A1:784:A:OP2	53:AQ:69:ARG:NH1	2.35	0.59
46:AI:140:THR:HG21	46:AI:148:VAL:HG21	1.84	0.59
57:AU:34:ALA:O	57:AU:38:ILE:HD12	2.01	0.59
58:AV:18:PRO:HA	58:AV:51:ALA:HA	1.83	0.59
75:Am:104:PRO:HG2	75:Am:107:ALA:HB2	1.82	0.59
2:BB:134:VAL:HG13	2:BB:218:LEU:HB2	1.84	0.59
22:BP:118:GLU:O	25:BS:122:HIS:N	2.35	0.59
34:B5:110:U:OP1	34:B5:753:A:O2'	2.20	0.59
56:AT:68:THR:HG1	56:AT:71:SER:HG	1.50	0.59
5:BG:77:LEU:HD12	5:BG:95:LYS:HD3	1.84	0.59
9:BL:3:THR:HA	9:BL:52:SER:HB3	1.85	0.59
11:BO:20:TYR:HB3	11:BO:27:PHE:HB2	1.85	0.59
12:BV:4:ASP:OD1	12:BV:5:LYS:N	2.34	0.59
34:B5:538:A:H5'	34:B5:543:C:H42	1.68	0.59
55:AS:77:VAL:HG11	55:AS:106:LEU:HD22	1.82	0.59
1:BA:118:PRO:HG2	1:BA:141:ILE:HD13	1.85	0.59
21:BK:15:LEU:HD11	21:BK:46:LEU:HD11	1.82	0.59
22:BP:18:ARG:NH1	34:B5:1548:G:OP1	2.30	0.59
34:B5:1202:A:H62	34:B5:1456:C:H3'	1.68	0.59
38:A1:3271:G:O2'	42:AE:108:LYS:HD3	2.02	0.59
80:DC:124:GLY:HA3	80:DC:342:LEU:HD22	1.84	0.59
34:B5:628:G:H21	34:B5:971:A:H62	1.48	0.59
38:A1:874:U:N3	38:A1:2978:U:OP1	2.26	0.59
51:AO:65[A]:ASN:HB3	51:AO:68[A]:ARG:HG2	1.84	0.59
54:AR:68:GLN:NE2	54:AR:72:GLU:OE2	2.35	0.59
22:BP:127:ARG:NH1	22:BP:131:ALA:O	2.35	0.59
34:B5:709:C:N4	34:B5:730:G:O2'	2.34	0.59
34:B5:1267:G:HO2'	34:B5:1448:G:HO2'	1.50	0.59
80:DC:545:LEU:HA	80:DC:549:HIS:HB3	1.85	0.59
4:BE:100:ARG:NH2	4:BE:118:GLU:OE2	2.36	0.59
30:Bd:18:SER:OG	30:Bd:19:ARG:NH1	2.36	0.59
35:AA:80:GLU:HG3	78:Ap:66:GLY:HA2	1.84	0.59
44:AG:162:LEU:HD23	50:AN:7:LEU:HD11	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:11:GLY:HA2	31:Bg:52:GLN:HA	1.83	0.59
38:A1:1270:A:N6	80:DC:737:GLU:OE2	2.36	0.59
40:A4:75:G:OP2	61:AY:74:TYR:OH	2.20	0.59
41:AD:128:GLU:O	41:AD:164:LYS:NZ	2.33	0.59
45:AH:57:VAL:HG23	45:AH:68:LEU:HD13	1.83	0.59
2:BB:72:ASP:OD1	11:BO:114:ARG:NH1	2.35	0.59
5:BG:160:ARG:NH1	34:B5:66:U:O2	2.36	0.59
29:Bc:58:GLU:OE2	29:Bc:60:GLU:HG3	2.03	0.59
30:Bd:10:HIS:ND1	34:B5:1452:U:OP1	2.36	0.59
38:A1:251:G:OP2	38:A1:251:G:H2'	2.02	0.59
5:BG:92:ARG:O	34:B5:405:C:O2'	2.18	0.59
36:AB:291:GLU:HG2	36:AB:302:LYS:HZ2	1.68	0.59
38:A1:177:U:H3	38:A1:239:G:H22	1.49	0.59
38:A1:238:A:H2'	38:A1:239:G:O4'	2.03	0.59
38:A1:3067:C:H3'	54:AR:62:ARG:HH22	1.67	0.59
80:DC:568:GLU:HG3	80:DC:723:LYS:HE3	1.83	0.59
3:BC:165:VAL:HG13	3:BC:204:THR:HG22	1.85	0.58
11:BO:12:GLN:HE22	11:BO:111:ARG:HG3	1.67	0.58
23:BQ:29:ILE:HG22	23:BQ:65:ILE:HG22	1.85	0.58
34:B5:1575:7MG:H2'	34:B5:1576:A:H8	1.68	0.58
34:B5:1588:G:O6	34:B5:1608:U:O4	2.21	0.58
38:A1:662:U:H2'	38:A1:663:OMC:C6	2.38	0.58
43:AF:239:LEU:HG	43:AF:243:MET:HE2	1.85	0.58
79:E:99:LEU:HA	79:E:102:LYS:HE3	1.84	0.58
5:BG:174:LYS:HG2	34:B5:79:C:H1'	1.84	0.58
20:BF:95:ASN:ND2	34:B5:1611:A:OP1	2.36	0.58
34:B5:486:G:N2	34:B5:487:G:O6	2.36	0.58
38:A1:775:A:O2'	38:A1:777:U:OP2	2.20	0.58
38:A1:1259:A:OP1	81:V:53:MET:N	2.26	0.58
38:A1:1348:U:OP1	53:AQ:39:ARG:NH1	2.35	0.58
7:BI:4:SER:HB2	7:BI:24:LYS:HD3	1.86	0.58
20:BF:99:MET:HB3	20:BF:180:ARG:HH12	1.68	0.58
29:Bc:66:LEU:HD23	29:Bc:67:ARG:HG2	1.85	0.58
38:A1:283:G:OP2	77:Ao:45:ARG:NH1	2.35	0.58
38:A1:2185:G:O2'	38:A1:2314:U:OP2	2.16	0.58
38:A1:2568:C:O2'	38:A1:2569:A:O4'	2.18	0.58
80:DC:26:ALA:HB2	80:DC:128:VAL:HB	1.85	0.58
6:BH:14:THR:OG1	6:BH:15:GLU:OE1	2.21	0.58
37:AC:308:LYS:NZ	38:A1:609:G:N7	2.51	0.58
38:A1:1940:G:H21	38:A1:3362:A:H8	1.50	0.58
50:AN:137:PRO:O	50:AN:143:ARG:NH1	2.37	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:512:SER:HB2	80:DC:520:THR:HG22	1.85	0.58
27:BU:87:HIS:ND1	34:B5:1383:G:OP1	2.37	0.58
53:AQ:122:ILE:HG23	53:AQ:126:GLN:HB2	1.85	0.58
8:BJ:18:PRO:O	8:BJ:23:ARG:NH2	2.37	0.58
26:BT:114:VAL:HG21	26:BT:122:ARG:HB3	1.84	0.58
57:AU:56:VAL:HG12	57:AU:65:VAL:HG22	1.86	0.58
80:DC:574:THR:HA	80:DC:589:LYS:HD3	1.84	0.58
25:BS:13:HIS:CD2	25:BS:14:ILE:H	2.21	0.58
31:Bg:178:VAL:HB	31:Bg:192:PHE:HB2	1.85	0.58
34:B5:1266:U:H2'	34:B5:1267:G:C8	2.39	0.58
34:B5:1628:U:H2'	34:B5:1629:G:C8	2.38	0.58
38:A1:3266:G:OP2	42:AE:70:LYS:NZ	2.36	0.58
40:A4:57:C:H4'	40:A4:63:G:N7	2.19	0.58
80:DC:203:TYR:O	80:DC:208:THR:OG1	2.21	0.58
4:BE:72:VAL:HG12	4:BE:90:ILE:HG13	1.84	0.58
12:BV:79:LEU:HD13	12:BV:82:VAL:HG11	1.86	0.58
22:BP:98:ASN:ND2	22:BP:121:ILE:O	2.33	0.58
38:A1:1621:A:H2'	38:A1:1622:U:C6	2.39	0.58
38:A1:2438:A:H2'	38:A1:2439:A:H8	1.69	0.58
38:A1:3280:U:O2'	38:A1:3281:U:O5'	2.20	0.58
1:BA:76:ILE:HB	1:BA:123:VAL:HG12	1.84	0.58
5:BG:94:ARG:NH2	34:B5:406:U:O2'	2.36	0.58
34:B5:65:A:H2	34:B5:84:A:H62	1.52	0.58
34:B5:1594:G:OP2	34:B5:1596:C:N4	2.37	0.58
38:A1:1114:U:OP1	63:Aa:23:GLY:N	2.34	0.58
38:A1:3319:U:H5'	38:A1:3320:A:H5'	1.86	0.58
49:AM:48:GLY:HA3	49:AM:53:VAL:HB	1.86	0.58
65:Ac:14:LEU:HD11	65:Ac:43:ILE:HD12	1.86	0.58
2:BB:48:VAL:HG12	2:BB:64:ARG:NH2	2.19	0.58
14:BX:48:HIS:CD2	14:BX:105:ALA:HB2	2.39	0.58
34:B5:1373:C:H2'	34:B5:1374:C:C6	2.39	0.58
40:A4:135:G:H5''	60:AX:49:LYS:HD2	1.86	0.58
63:Aa:96:LYS:O	63:Aa:97:GLU:HG2	2.03	0.58
71:Ai:70:ARG:HH21	71:Ai:84:LYS:HG2	1.67	0.58
2:BB:110:LEU:HD11	2:BB:213:ARG:HD2	1.85	0.57
17:Bb:56:CYS:O	17:Bb:60:SER:OG	2.16	0.57
38:A1:412:G:OP1	52:AP:62:ARG:NH1	2.37	0.57
38:A1:900:G:H1'	38:A1:1589:A:N6	2.19	0.57
38:A1:1597:C:H5'	38:A1:1696:A:H1'	1.86	0.57
73:Ak:8:ILE:HD11	73:Ak:65:LEU:HD21	1.86	0.57
1:BA:74:VAL:HG23	1:BA:118:PRO:HB3	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:BY:23:PHE:HZ	15:BY:75:VAL:HG23	1.69	0.57
32:Bf:139:LEU:HD23	32:Bf:148:TYR:HB2	1.86	0.57
34:B5:272:U:H5'	34:B5:273:G:H5'	1.86	0.57
38:A1:1596:C:H2'	38:A1:1597:C:C6	2.40	0.57
42:AE:45:GLY:O	42:AE:48:ARG:NH1	2.37	0.57
10:BN:124:ARG:NH2	34:B5:967:A:OP2	2.34	0.57
32:Bf:80:ARG:NH2	34:B5:1270:G:OP2	2.38	0.57
34:B5:1591:C:H2'	34:B5:1592:A:C8	2.39	0.57
38:A1:1492:G:O2'	74:A1:48:LYS:NZ	2.37	0.57
38:A1:2448:G:H1	38:A1:2498:U:H3	1.52	0.57
38:A1:2697:A:H2'	38:A1:2698:G:C8	2.38	0.57
45:AH:41:ILE:HG22	45:AH:43:VAL:HG13	1.86	0.57
4:BE:60:GLU:O	4:BE:64:ILE:HD12	2.04	0.57
4:BE:104:ASP:HB3	4:BE:110:ALA:HB2	1.86	0.57
5:BG:136:LYS:NZ	5:BG:174:LYS:O	2.34	0.57
22:BP:61:ARG:HA	22:BP:64:LYS:HG2	1.86	0.57
38:A1:656:A:H2'	38:A1:657:A:C8	2.40	0.57
38:A1:2107:A:H2	38:A1:3344:A:H8	1.52	0.57
82:EC:6869:C:O2'	82:EC:6870:A:O4'	2.22	0.57
3:BC:116:LYS:HG2	3:BC:127:ALA:HB3	1.85	0.57
25:BS:86:LEU:HD13	25:BS:98:TYR:O	2.04	0.57
34:B5:1208:A:C8	34:B5:1269:OMU:H6	2.33	0.57
34:B5:1458:G:O2'	34:B5:1459:C:OP1	2.21	0.57
36:AB:147:GLU:OE1	36:AB:150:ARG:NH2	2.38	0.57
45:AH:10:ILE:HG13	45:AH:72:LYS:HG2	1.86	0.57
68:Af:16:TYR:OH	68:Af:89:LEU:O	2.17	0.57
30:Bd:36:LEU:HD12	30:Bd:38:ILE:HD12	1.86	0.57
34:B5:1127:G:OP1	76:An:11:ARG:NH2	2.37	0.57
38:A1:1092:C:O2'	38:A1:1093:A:OP1	2.23	0.57
41:AD:68:THR:OG1	41:AD:71:GLY:O	2.21	0.57
48:AL:49:ARG:HH11	70:Ah:115:LYS:HZ1	1.49	0.57
54:AR:174:ALA:HA	54:AR:177:VAL:HG22	1.86	0.57
61:AY:11:ASP:HB3	61:AY:14:LYS:HB2	1.84	0.57
78:Ap:3:LYS:HE2	78:Ap:6:LYS:HA	1.87	0.57
20:BF:145:ASP:OD1	20:BF:146:THR:N	2.35	0.57
27:BU:69:LYS:HE3	34:B5:1280:4AC:H5''	1.87	0.57
34:B5:1146:G:H2'	34:B5:1147:A:C8	2.40	0.57
38:A1:110:G:OP2	48:AL:73:ARG:NH2	2.35	0.57
38:A1:1564:U:H3	38:A1:1575:A:H61	1.51	0.57
38:A1:1580:A:H2	60:AX:33:ARG:HH11	1.52	0.57
81:V:67:LEU:HD21	81:V:74:GLU:HB3	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:EC:6787:U:OP2	82:EC:6804:A:N6	2.38	0.57
82:EC:6812:C:H2'	82:EC:6813:A:H8	1.70	0.57
6:BH:64:VAL:HB	6:BH:94:ALA:HB1	1.86	0.57
22:BP:57:MET:O	22:BP:61:ARG:HG2	2.05	0.57
33:BM:117:GLY:O	34:B5:1228:G:N2	2.37	0.57
38:A1:627:U:H2'	38:A1:628:A:C8	2.40	0.57
38:A1:643:U:O2'	38:A1:1153:A:N1	2.32	0.57
38:A1:1203:A:H2'	38:A1:1204:A:C8	2.40	0.57
38:A1:1259:A:C5	81:V:53:MET:HE1	2.40	0.57
38:A1:1322:U:O2	55:AS:108:GLN:NE2	2.35	0.57
38:A1:1646:G:O2'	38:A1:1808:G:N2	2.33	0.57
38:A1:1747:G:H21	73:Ak:2:ALA:HB3	1.70	0.57
44:AG:62:LYS:HD3	50:AN:29:GLU:HG3	1.87	0.57
60:AX:64:GLU:OE1	60:AX:85:GLN:NE2	2.34	0.57
80:DC:563:TYR:HB2	80:DC:677:PHE:HZ	1.68	0.57
82:EC:6813:A:H2'	82:EC:6814:G:C8	2.39	0.57
5:BG:2:LYS:HG2	5:BG:17:GLU:HG3	1.85	0.57
5:BG:131:LYS:HD2	34:B5:166:C:H4'	1.86	0.57
36:AB:85:VAL:HG22	36:AB:202:THR:HG22	1.87	0.57
38:A1:163:C:H2'	38:A1:164:A:H5'	1.87	0.57
38:A1:2369:G:H2'	38:A1:2370:G:C8	2.40	0.57
80:DC:613:LYS:HD2	80:DC:631:ARG:HD3	1.86	0.57
21:BK:27:PHE:HB3	21:BK:40:LEU:HD12	1.85	0.57
34:B5:12:U:H2'	34:B5:13:C:C6	2.40	0.57
34:B5:276:C:O2'	34:B5:278:U:OP2	2.23	0.57
38:A1:815:G:OP2	72:Aj:31:LYS:NZ	2.36	0.57
38:A1:1259:A:N6	38:A1:1260:A:N1	2.52	0.57
81:V:27:VAL:HB	81:V:189:GLN:HB3	1.87	0.57
81:V:89:THR:HG21	81:V:96:ILE:HD13	1.87	0.57
1:BA:30:GLN:HE21	1:BA:33:GLN:HG2	1.70	0.56
38:A1:2424:A:OP1	50:AN:90:ASN:ND2	2.37	0.56
38:A1:3023:U:O3'	80:DC:162:ARG:NH2	2.38	0.56
38:A1:3295:A:H2'	38:A1:3296:A:C8	2.39	0.56
65:Ac:16:LEU:HB3	65:Ac:98:SER:HB3	1.87	0.56
82:EC:6788:C:H3'	82:EC:6805:C:H41	1.69	0.56
15:BY:131:ARG:NH1	34:B5:153:G:OP2	2.38	0.56
26:BT:48:GLN:OE1	34:B5:1531:G:N2	2.35	0.56
26:BT:72:GLY:HA3	34:B5:1498:G:H5''	1.87	0.56
28:BZ:83:LEU:HG	28:BZ:88:ILE:HD11	1.87	0.56
38:A1:1631:C:OP2	62:AZ:48:ARG:NH2	2.38	0.56
56:AT:127:GLN:NE2	56:AT:129:LYS:O	2.38	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:222:LYS:HA	20:BF:225:ARG:HE	1.71	0.56
25:BS:116:LEU:HA	25:BS:119:ILE:HG22	1.87	0.56
30:Bd:33:LYS:NZ	34:B5:1594:G:P	2.77	0.56
34:B5:891:A:H2'	34:B5:892:A:C8	2.40	0.56
34:B5:895:G:H1	34:B5:917:U:H3	1.53	0.56
34:B5:1182:U:N3	34:B5:1185:U:OP2	2.35	0.56
38:A1:359:U:O3'	72:Aj:25:ARG:NH2	2.38	0.56
38:A1:417:A:H2'	38:A1:418:A:C8	2.40	0.56
38:A1:1717:U:H2'	38:A1:1718:G:C8	2.41	0.56
38:A1:2438:A:H2'	38:A1:2439:A:C8	2.40	0.56
69:Ag:3:GLN:HE22	69:Ag:29:ILE:HB	1.70	0.56
73:Ak:30:LYS:HD2	73:Ak:40:GLN:OE1	2.05	0.56
25:BS:104:ASN:OD1	25:BS:107:SER:OG	2.23	0.56
34:B5:882:U:OP1	78:Ap:85:ARG:NH1	2.39	0.56
38:A1:1805:C:H2'	38:A1:1806:A:H8	1.70	0.56
79:E:100:ILE:HG13	79:E:127:GLN:HG2	1.86	0.56
3:BC:140:ARG:HB3	3:BC:221:THR:HB	1.87	0.56
3:BC:229:LEU:O	12:BV:16:LYS:NZ	2.38	0.56
7:BI:48:THR:OG1	7:BI:52:ASN:O	2.23	0.56
12:BV:30:ALA:O	12:BV:60:ARG:NE	2.32	0.56
13:BW:101:TYR:HB3	13:BW:112:ASP:HB2	1.87	0.56
14:BX:55:GLU:HG3	14:BX:57:LEU:HD21	1.88	0.56
15:BY:36:SER:OG	15:BY:38:ASP:OD1	2.24	0.56
29:Bc:15:VAL:HA	29:Bc:28:VAL:HG12	1.87	0.56
34:B5:1572:OMG:H5''	34:B5:1574:G:H21	1.71	0.56
47:AJ:160:VAL:HG13	47:AJ:171:VAL:HG21	1.86	0.56
79:E:14:LYS:HA	79:E:17:LEU:HG	1.87	0.56
81:V:119:ILE:HG12	81:V:180:PRO:HG2	1.88	0.56
23:BQ:60:PHE:HE1	23:BQ:89:LEU:HD13	1.70	0.56
33:BM:114:LYS:NZ	34:B5:1225:U:OP2	2.39	0.56
34:B5:1366:U:H2'	34:B5:1367:G:H8	1.71	0.56
38:A1:2960:C:H2'	38:A1:2961:G:H8	1.70	0.56
45:AH:20:ILE:HD12	45:AH:25:VAL:HG22	1.88	0.56
48:AL:187:ALA:HA	48:AL:190:LYS:NZ	2.20	0.56
66:Ad:6:ASP:HB3	66:Ad:89:LEU:HD11	1.87	0.56
80:DC:182:VAL:HG11	80:DC:204:PRO:HD3	1.87	0.56
82:EC:6893:C:H5'	82:EC:6943:A:H61	1.69	0.56
25:BS:122:HIS:HE2	25:BS:126:ARG:HH21	1.53	0.56
33:BM:46:ARG:NH2	34:B5:1253:U:OP1	2.39	0.56
35:AA:178:PRO:HG2	78:Ap:26:VAL:HG23	1.87	0.56
38:A1:1899:G:O2'	38:A1:2334:U:O4	2.19	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2160:G:H2'	38:A1:2161:G:H8	1.69	0.56
38:A1:3322:A:H2'	38:A1:3323:A:C8	2.41	0.56
1:BA:30:GLN:NE2	1:BA:33:GLN:HG2	2.20	0.56
9:BL:73:GLY:HA3	9:BL:86:ILE:HD12	1.88	0.56
34:B5:1041:G:H2'	34:B5:1042:G:C8	2.41	0.56
37:AC:317:PRO:C	37:AC:319:LYS:H	2.12	0.56
38:A1:1242:G:H2'	38:A1:1243:G:C8	2.41	0.56
38:A1:1679:A:OP1	57:AU:94:ARG:NH1	2.36	0.56
38:A1:2356:A:H61	38:A1:2983:C:H5	1.52	0.56
38:A1:3050:U:O2'	59:AW:16:GLY:O	2.23	0.56
66:Ad:51:LEU:HB3	66:Ad:55:LEU:HD23	1.86	0.56
15:BY:57:VAL:HB	15:BY:60:PHE:HE2	1.71	0.56
34:B5:1159:C:N4	34:B5:1285:U:OP1	2.38	0.56
34:B5:1695:G:H2'	34:B5:1696:G:C8	2.41	0.56
38:A1:129:U:H2'	38:A1:130:A:C8	2.40	0.56
38:A1:1336:U:H2'	38:A1:1337:A:H8	1.71	0.56
38:A1:1729:A:C6	65:Ac:49:PRO:HD3	2.41	0.56
27:BU:96:PRO:HD2	27:BU:99:ILE:HD11	1.88	0.56
30:Bd:15:GLY:HA3	34:B5:1204:A:H61	1.71	0.56
34:B5:1218:G:N2	34:B5:1444:A:OP2	2.28	0.56
37:AC:154:THR:OG1	37:AC:157:GLU:OE1	2.23	0.56
38:A1:19:U:H2'	38:A1:20:A:C8	2.41	0.56
38:A1:1635:G:N2	38:A1:1638:A:OP2	2.35	0.56
40:A4:46:G:OP1	74:Al:18:LYS:NZ	2.27	0.56
42:AE:40:LEU:HD13	42:AE:84:VAL:HG11	1.88	0.56
45:AH:90:MET:HG2	45:AH:181:VAL:HA	1.86	0.56
56:AT:48:ILE:HG13	56:AT:94:GLU:HG2	1.87	0.56
1:BA:41:ARG:CZ	24:BR:105:GLN:HE22	2.19	0.55
1:BA:107:PHE:HB3	1:BA:139:VAL:HG11	1.88	0.55
8:BJ:106:GLU:O	8:BJ:112:GLN:NE2	2.39	0.55
13:BW:56:HIS:O	34:B5:861:U:O2'	2.24	0.55
32:Bf:132:LEU:HD22	32:Bf:141:CYS:SG	2.46	0.55
34:B5:751:G:H2'	34:B5:752:A:H8	1.70	0.55
34:B5:1738:U:H2'	34:B5:1739:C:C6	2.41	0.55
38:A1:251:G:H5'	38:A1:251:G:H8	1.71	0.55
46:AI:130:ASP:OD1	46:AI:131:ILE:N	2.40	0.55
63:Aa:36:GLY:HA3	63:Aa:40:HIS:CE1	2.40	0.55
80:DC:617:ARG:NE	80:DC:621:ASP:OD2	2.34	0.55
4:BE:251:GLU:O	4:BE:254:ARG:HG2	2.06	0.55
5:BG:139:ASN:ND2	34:B5:143:G:OP2	2.38	0.55
16:Ba:38:ARG:NH2	34:B5:1798:U:OP2	2.38	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:156:VAL:HA	31:Bg:169:ILE:HG22	1.87	0.55
34:B5:29:U:H2'	34:B5:30:G:H8	1.70	0.55
34:B5:209:U:H2'	34:B5:210:A:C8	2.41	0.55
34:B5:1291:G:N2	34:B5:1324:G:H22	2.03	0.55
38:A1:117:U:O4	44:AG:147:LYS:NZ	2.37	0.55
38:A1:618:C:OP1	52:AP:173:ARG:NH2	2.40	0.55
77:Ao:71:ARG:HD3	77:Ao:80:ARG:HD3	1.87	0.55
79:E:126:PRO:HA	82:EC:6774:U:H5''	1.89	0.55
80:DC:378:LEU:H	80:DC:471:THR:HG22	1.71	0.55
21:BK:93:GLN:OE1	21:BK:93:GLN:N	2.39	0.55
22:BP:81:ARG:NH1	34:B5:1453:G:O3'	2.40	0.55
34:B5:1469:A:O2'	34:B5:1540:G:N2	2.35	0.55
34:B5:1471:A:H2	34:B5:1474:G:N3	2.03	0.55
38:A1:165:A:O2'	38:A1:166:C:H6	1.88	0.55
50:AN:9:GLU:HB3	71:Ai:44:VAL:HG21	1.89	0.55
62:AZ:41:ALA:HB2	62:AZ:77:TYR:HE1	1.71	0.55
7:BI:182:TYR:OH	7:BI:188:GLU:OE2	2.21	0.55
34:B5:891:A:H2'	34:B5:892:A:H8	1.71	0.55
34:B5:1483:A:C2	34:B5:1607:G:H1'	2.42	0.55
38:A1:177:U:H3	38:A1:239:G:N2	2.05	0.55
38:A1:966:U:H2'	38:A1:967:A:C8	2.42	0.55
39:A3:1:G:O6	41:AD:262:LYS:NZ	2.39	0.55
25:BS:17:LEU:HD12	25:BS:22:VAL:HB	1.88	0.55
25:BS:86:LEU:HD21	25:BS:97:ASP:HB3	1.88	0.55
34:B5:206:A:H1'	34:B5:262:U:C2	2.41	0.55
34:B5:835:U:H2'	34:B5:836:U:H5	1.71	0.55
34:B5:1280:4AC:H2'	34:B5:1281:G:H8	1.72	0.55
38:A1:426:G:H5'	67:Ae:50:ILE:HG22	1.88	0.55
38:A1:3016:A:H2'	38:A1:3017:A:H8	1.69	0.55
80:DC:380:LEU:HB3	80:DC:469:LEU:HB2	1.89	0.55
80:DC:394:PHE:CE2	80:DC:513:LYS:HB3	2.41	0.55
12:BV:42:GLU:O	12:BV:44:ARG:NH1	2.39	0.55
34:B5:513:U:H2'	34:B5:514:G:C8	2.42	0.55
38:A1:651:G:O2'	38:A1:1435:A:OP1	2.25	0.55
38:A1:1448:U:H5''	52:AP:66:SER:HB2	1.88	0.55
40:A4:103:G:OP2	40:A4:105:A:O2'	2.23	0.55
41:AD:60:ILE:HB	41:AD:80:SER:HB2	1.87	0.55
54:AR:98:ARG:NH2	54:AR:130:ASN:OD1	2.40	0.55
80:DC:225:PHE:CD2	80:DC:277:ILE:HG13	2.42	0.55
31:Bg:68:VAL:HG12	31:Bg:84:SER:HB2	1.88	0.55
34:B5:272:U:O2'	34:B5:284:G:N2	2.40	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1640:C:N4	82:EC:6952:U:OP1	2.39	0.55
37:AC:285:ASP:OD2	37:AC:288:ARG:NH1	2.39	0.55
38:A1:546:C:O2'	38:A1:548:G:OP1	2.22	0.55
38:A1:1290:A:H2'	38:A1:1291:A:C8	2.42	0.55
38:A1:2727:A:OP2	38:A1:2728:G:N2	2.39	0.55
61:AY:55:GLU:HG2	61:AY:108:LYS:HB3	1.87	0.55
71:AI:9:ILE:HA	71:AI:13:LYS:HD2	1.89	0.55
71:AI:74:LYS:HD2	71:AI:80:PHE:HD1	1.72	0.55
73:AK:64:LYS:HD3	73:AK:67:GLN:HE21	1.72	0.55
6:BH:60:ILE:HD11	6:BH:92:PHE:CE1	2.41	0.55
11:BO:125:SER:HB3	34:B5:926:A:H2	1.71	0.55
34:B5:780:A:H4'	34:B5:781:U:H5''	1.88	0.55
61:AY:43:TYR:O	61:AY:125:LYS:N	2.37	0.55
32:Bf:118:ARG:NE	32:Bf:134:ASN:HB3	2.21	0.55
34:B5:5:U:H2'	34:B5:6:G:H8	1.70	0.55
34:B5:1294:G:O2'	34:B5:1321:A:N1	2.30	0.55
38:A1:68:C:OP2	38:A1:301:G:N2	2.38	0.55
80:DC:656:LEU:HA	80:DC:659:ILE:HD12	1.89	0.55
81:V:45:LEU:HD13	81:V:49:ALA:HB3	1.89	0.55
18:Be:42:ARG:NH2	34:B5:590:C:OP2	2.40	0.55
19:BD:25:PHE:O	19:BD:29:LEU:HB2	2.07	0.55
34:B5:655:G:N2	34:B5:678:A:OP2	2.33	0.55
36:AB:67:PHE:HA	36:AB:70:ARG:HD3	1.88	0.55
38:A1:115:A:H8	38:A1:266:A:H5'	1.72	0.55
80:DC:688:ILE:HD11	80:DC:691:VAL:HB	1.88	0.55
4:BE:112:HIS:NE2	4:BE:237:SER:O	2.40	0.54
9:BL:129:ARG:HD3	34:B5:115:G:H5'	1.89	0.54
32:Bf:118:ARG:NH2	32:Bf:139:LEU:HD13	2.22	0.54
79:E:203:SER:O	79:E:204:LEU:HD22	2.07	0.54
19:BD:98:ALA:HA	19:BD:188:ILE:HD12	1.90	0.54
34:B5:436:A2M:H8	34:B5:436:A2M:O5'	2.08	0.54
38:A1:797:U:O2	48:AL:12:ASN:ND2	2.40	0.54
38:A1:1688:U:H2'	38:A1:1689:U:C6	2.42	0.54
38:A1:1694:U:H5	38:A1:1752:A:N1	2.04	0.54
81:V:38:MET:O	81:V:42:ARG:HG2	2.06	0.54
4:BE:131:LEU:HD12	34:B5:251:A:C2	2.42	0.54
8:BJ:173:ALA:HB2	34:B5:511:A:H5'	1.90	0.54
32:Bf:122:SER:HB2	32:Bf:148:TYR:CE2	2.42	0.54
34:B5:1356:U:H2'	34:B5:1357:A:C8	2.42	0.54
38:A1:2768:U:H2'	38:A1:2769:A:C8	2.42	0.54
38:A1:3228:C:H5'	49:AM:137:LYS:HZ1	1.71	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:A3:121:U:OP2	41:AD:265:TYR:OH	2.16	0.54
44:AG:41:GLN:OE1	44:AG:44:ARG:NH2	2.30	0.54
6:BH:143:LEU:HB2	6:BH:147:ASN:HB2	1.88	0.54
15:BY:61:ARG:NH1	34:B5:530:C:O2	2.35	0.54
27:BU:80:GLU:OE1	30:Bd:44:ARG:NH1	2.40	0.54
33:BM:42:ALA:HB3	33:BM:122:VAL:HB	1.89	0.54
34:B5:343:C:H2'	34:B5:344:A:H8	1.72	0.54
34:B5:923:A:H2'	34:B5:924:A:C8	2.42	0.54
34:B5:1357:A:H2'	34:B5:1358:G:C8	2.43	0.54
38:A1:2484:A:O2'	82:EC:6775:U:O2	2.21	0.54
38:A1:3066:U:H2'	38:A1:3067:C:C6	2.43	0.54
38:A1:3162:C:H2'	38:A1:3163:A:H8	1.73	0.54
45:AH:92:TYR:HB2	45:AH:142:ASP:HB3	1.88	0.54
51:AO:79[A]:ILE:HG21	51:AO:138[A]:LEU:HD11	1.90	0.54
80:DC:490:GLN:HG3	80:DC:531:ALA:HB2	1.89	0.54
2:BB:190:PRO:HB2	2:BB:192:VAL:HG13	1.88	0.54
27:BU:59:PRO:HA	34:B5:1382:A:H5'	1.89	0.54
31:Bg:83:ALA:HB2	31:Bg:113:VAL:HB	1.90	0.54
34:B5:590:C:H2'	34:B5:591:A:H8	1.71	0.54
34:B5:947:U:H2'	34:B5:948:G:C8	2.42	0.54
36:AB:287:LYS:O	36:AB:293:ASN:ND2	2.36	0.54
38:A1:173:G:H1	38:A1:244:G:N2	2.06	0.54
38:A1:874:U:OP2	38:A1:1907:C:O2'	2.19	0.54
41:AD:290:ILE:HD11	46:Al:206:LEU:HD11	1.88	0.54
57:AU:90:ARG:O	57:AU:91:ASP:OD1	2.25	0.54
58:AV:40:LYS:HD3	58:AV:59:MET:HE3	1.89	0.54
80:DC:117:ALA:HA	80:DC:481:MET:HE1	1.89	0.54
6:BH:87:ASP:OD2	6:BH:88:ARG:NH1	2.41	0.54
8:BJ:154:LYS:HG3	8:BJ:155:HIS:CD2	2.43	0.54
34:B5:1196:A:OP2	34:B5:1464:G:N2	2.35	0.54
38:A1:307:A:H2'	38:A1:308:A:C8	2.42	0.54
38:A1:508:U:OP1	43:AF:211:SER:OG	2.22	0.54
38:A1:1659:U:H2'	38:A1:1660:C:C6	2.43	0.54
39:A3:52:G:O2'	39:A3:53:U:OP1	2.25	0.54
14:BX:37:ALA:O	14:BX:41:SER:OG	2.26	0.54
20:BF:58:LEU:HD12	20:BF:138:THR:HG22	1.90	0.54
27:BU:98:GLN:HE22	27:BU:102:ARG:HH11	1.56	0.54
34:B5:1272:U:O2	34:B5:1438:G:O6	2.26	0.54
34:B5:1369:U:O2'	34:B5:1370:U:OP1	2.26	0.54
34:B5:1482:C:O5'	34:B5:1521:G:N2	2.39	0.54
38:A1:1020:G:H3'	38:A1:1021:G:H8	1.72	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1147:G:OP1	67:Ae:47:ARG:NH1	2.39	0.54
81:V:129:GLU:HG2	81:V:131:GLY:H	1.73	0.54
82:EC:6849:A:O2'	82:EC:6850:C:O4'	2.25	0.54
8:BJ:106:GLU:HA	8:BJ:111:THR:HG21	1.90	0.54
13:BW:112:ASP:OD1	13:BW:115:GLU:HG2	2.07	0.54
15:BY:62:THR:HA	15:BY:69:SER:HA	1.90	0.54
16:Ba:32:LYS:O	16:Ba:37:LYS:NZ	2.40	0.54
18:Be:57:ASN:ND2	34:B5:588:U:O2	2.41	0.54
22:BP:53:PRO:HB3	22:BP:83:MET:HE1	1.90	0.54
23:BQ:39:VAL:O	23:BQ:45:ARG:NH1	2.40	0.54
29:Bc:22:ARG:HD3	34:B5:1162:C:H5'	1.88	0.54
34:B5:752:A:H2'	34:B5:753:A:C8	2.43	0.54
35:AA:183:GLY:HA2	38:A1:896:A:H5''	1.90	0.54
31:Bg:70:ASP:HB3	31:Bg:113:VAL:HG12	1.89	0.54
31:Bg:195:HIS:NE2	31:Bg:213:SER:OG	2.31	0.54
34:B5:209:U:H2'	34:B5:210:A:H8	1.73	0.54
34:B5:778:G:H2'	34:B5:779:U:H2'	1.90	0.54
34:B5:823:G:C6	34:B5:850:A:N6	2.76	0.54
34:B5:843:U:H2'	34:B5:844:A:H8	1.73	0.54
35:AA:168:VAL:HG13	78:Ap:79:VAL:HG21	1.88	0.54
38:A1:1139:G:OP2	64:Ab:14:ARG:NH2	2.41	0.54
38:A1:1282:G:N2	38:A1:1282:G:OP2	2.40	0.54
38:A1:2700:G:O2'	38:A1:2705:A:N1	2.40	0.54
44:AG:214:LEU:O	44:AG:218:ILE:HG12	2.07	0.54
62:AZ:48:ARG:HB2	62:AZ:69:LYS:HB3	1.90	0.54
81:V:40:GLU:OE2	81:V:103:ASN:ND2	2.41	0.54
8:BJ:48:GLN:O	8:BJ:52:ILE:HG12	2.08	0.54
19:BD:121:GLY:HA2	19:BD:124:ARG:HE	1.72	0.54
20:BF:178:GLY:HA2	20:BF:181:GLU:HG2	1.90	0.54
22:BP:40:ARG:NH2	34:B5:1551:U:O4	2.41	0.54
34:B5:1482:C:P	34:B5:1521:G:H22	2.30	0.54
34:B5:1564:U:H2'	34:B5:1565:C:C6	2.43	0.54
38:A1:2800:G:O6	63:Aa:42:ARG:NH2	2.39	0.54
42:AE:40:LEU:HB3	42:AE:84:VAL:HG13	1.90	0.54
50:AN:143:ARG:NH2	70:Ah:90:ARG:O	2.41	0.54
53:AQ:133:LYS:HB2	53:AQ:135:GLN:HE21	1.73	0.54
2:BB:70:LEU:HD12	2:BB:84:ILE:HD11	1.90	0.53
6:BH:22:GLN:O	6:BH:25:VAL:HG22	2.08	0.53
32:Bf:143:LYS:HD2	34:B5:1253:U:H4'	1.90	0.53
34:B5:681:U:O2'	34:B5:683:C:OP2	2.20	0.53
38:A1:1279:C:H2'	38:A1:1280:C:C6	2.42	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2481:G:OP1	79:E:98:LYS:HE2	2.08	0.53
38:A1:2611:U:H2'	38:A1:2612:U:C6	2.43	0.53
44:AG:82:LEU:HD13	44:AG:222:PHE:HE2	1.73	0.53
50:AN:115:VAL:HA	50:AN:134:LEU:HD23	1.90	0.53
62:AZ:33:SER:OG	62:AZ:35:SER:O	2.23	0.53
17:Bb:34:ASP:OD2	17:Bb:80:ARG:NH1	2.41	0.53
28:BZ:73:GLY:H	34:B5:1534:G:H2'	1.72	0.53
34:B5:1450:U:H2'	34:B5:1451:C:C6	2.43	0.53
38:A1:243:G:H2'	38:A1:244:G:C8	2.42	0.53
45:AH:89:LYS:HG2	45:AH:145:VAL:HG22	1.90	0.53
65:Ac:45:ALA:HB2	65:Ac:77:LEU:HD12	1.89	0.53
4:BE:187:ARG:N	34:B5:753:A:OP2	2.39	0.53
28:BZ:90:LYS:NZ	28:BZ:103:ARG:O	2.38	0.53
34:B5:1062:A:H3'	34:B5:1063:U:C6	2.43	0.53
36:AB:17:LEU:HD21	36:AB:233:TRP:HH2	1.71	0.53
37:AC:316:ASN:HD22	37:AC:319:LYS:HE3	1.74	0.53
38:A1:118:U:O2	38:A1:121:A:H4'	2.08	0.53
38:A1:2232:A:H2'	38:A1:2233:A:C8	2.42	0.53
38:A1:2714:G:OP1	77:Ao:20:HIS:NE2	2.41	0.53
38:A1:3233:C:H2'	38:A1:3234:A:C8	2.44	0.53
80:DC:76:SER:OG	80:DC:438:MET:SD	2.60	0.53
4:BE:54:TYR:O	15:BY:15:ASN:ND2	2.41	0.53
5:BG:112:VAL:HG11	34:B5:164:A:H5'	1.90	0.53
7:BI:98:LYS:HB3	34:B5:329:G:H5''	1.90	0.53
13:BW:115:GLU:HA	13:BW:118:ARG:HG2	1.89	0.53
16:Ba:12:LYS:HZ3	16:Ba:16:GLY:H	1.55	0.53
23:BQ:42:GLU:HA	23:BQ:45:ARG:HG3	1.91	0.53
23:BQ:77:GLN:O	23:BQ:81:ILE:HG12	2.08	0.53
31:Bg:108:SER:HB3	31:Bg:127:ARG:HB3	1.89	0.53
34:B5:108:A:H2'	34:B5:109:G:C8	2.43	0.53
34:B5:939:A:H2'	34:B5:940:A:C8	2.44	0.53
55:AS:13:ARG:HD2	55:AS:51:VAL:HG23	1.89	0.53
55:AS:73:LYS:NZ	55:AS:97:VAL:O	2.39	0.53
25:BS:82:PRO:HB2	25:BS:84:TRP:CD1	2.44	0.53
31:Bg:229:LYS:HZ1	31:Bg:231:MET:HG2	1.73	0.53
34:B5:127:G:H21	34:B5:178:U:H2'	1.74	0.53
34:B5:1488:G:H3'	34:B5:1515:A:H61	1.74	0.53
38:A1:2407:C:H2'	38:A1:2408:U:H6	1.74	0.53
38:A1:2471:U:H3	38:A1:2474:G:H22	1.56	0.53
42:AE:66:SER:HB2	42:AE:76:LEU:HG	1.90	0.53
45:AH:101:VAL:HG22	45:AH:114:VAL:HG22	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:178:GLY:HA3	34:B5:641:G:H21	1.73	0.53
7:BI:76:THR:HG21	7:BI:104:ILE:HD12	1.91	0.53
49:AM:50:LYS:HG3	49:AM:85:TRP:CD1	2.43	0.53
5:BG:159:ARG:NH1	5:BG:170:THR:OG1	2.42	0.53
8:BJ:37:LYS:NZ	34:B5:594:A:OP2	2.38	0.53
14:BX:99:ASN:ND2	80:DC:505:VAL:HB	2.23	0.53
20:BF:63:GLN:NE2	20:BF:66:GLN:OE1	2.42	0.53
24:BR:107:SER:HA	24:BR:110:VAL:HG12	1.89	0.53
25:BS:48:LYS:NZ	26:BT:34:VAL:O	2.41	0.53
31:Bg:32:LEU:HD22	31:Bg:73:LEU:HD21	1.90	0.53
33:BM:29:LYS:HA	33:BM:100:TRP:CE2	2.44	0.53
38:A1:952:A:H4'	38:A1:968:G:N2	2.24	0.53
38:A1:1798:A:H2'	38:A1:1799:A:C8	2.44	0.53
38:A1:3034:C:H5	45:AH:121:LYS:H	1.57	0.53
80:DC:20:ARG:NH1	80:DC:342:LEU:O	2.42	0.53
82:EC:6858:A:H4'	82:EC:6859:U:N3	2.24	0.53
5:BG:201:GLN:NE2	34:B5:125:U:OP1	2.42	0.53
26:BT:83:ALA:HA	26:BT:93:HIS:HA	1.91	0.53
27:BU:26:LEU:HG	27:BU:114:VAL:HG12	1.91	0.53
29:Bc:18:ARG:HG3	34:B5:1616:G:H4'	1.90	0.53
38:A1:91:G:OP2	38:A1:93:C:N4	2.36	0.53
38:A1:674:G:O6	53:AQ:56:LYS:NZ	2.42	0.53
38:A1:1119:C:H2'	38:A1:1120:A:H8	1.73	0.53
38:A1:2467:G:N2	38:A1:2488:A:H62	2.06	0.53
5:BG:39:GLU:OE2	5:BG:47:GLY:N	2.29	0.53
14:BX:144:ARG:NH2	80:DC:425:ASP:OD1	2.42	0.53
20:BF:122:ASN:OD1	20:BF:123:VAL:N	2.42	0.53
34:B5:1374:C:H2'	34:B5:1375:A:H8	1.74	0.53
38:A1:1292:C:O2'	38:A1:1293:U:OP1	2.22	0.53
38:A1:1392:G:H3'	67:Ae:125:ARG:HH12	1.74	0.53
38:A1:2129:U:H2'	38:A1:2130:G:C8	2.44	0.53
42:AE:171:PRO:HA	42:AE:174:LEU:HB2	1.90	0.53
52:AP:122:ALA:HB3	52:AP:143:PRO:HB2	1.91	0.53
61:AY:120:GLN:HE22	61:AY:126:LEU:HD13	1.72	0.53
82:EC:6804:A:O2'	82:EC:6808:G:N2	2.40	0.53
13:BW:37:PHE:CE1	13:BW:103:ILE:HG13	2.44	0.53
15:BY:29:HIS:NE2	15:BY:69:SER:OG	2.39	0.53
79:E:158:GLN:OE1	79:E:160:LYS:NZ	2.34	0.53
80:DC:172:GLU:OE2	80:DC:271:ARG:NH2	2.41	0.53
80:DC:694:HIS:CD2	80:DC:696:ASP:H	2.26	0.53
7:BI:25:ARG:HA	34:B5:400:A:H5''	1.89	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BJ:58:ASP:O	8:BJ:62:ARG:NH1	2.41	0.52
25:BS:123:ARG:NH2	34:B5:1546:G:OP1	2.38	0.52
34:B5:1697:G:O6	34:B5:1704:U:O4	2.27	0.52
36:AB:292:ALA:HB1	36:AB:295:ALA:HB3	1.91	0.52
38:A1:296:A:N3	38:A1:299:G:O2'	2.41	0.52
38:A1:3214:U:OP2	49:AM:128:ARG:NH1	2.39	0.52
62:AZ:50:PRO:HD3	62:AZ:68:ILE:HG12	1.91	0.52
80:DC:578:LYS:HD3	80:DC:585:ARG:NH1	2.25	0.52
1:BA:76:ILE:HD13	1:BA:98:ILE:HB	1.91	0.52
5:BG:142:ARG:NH2	5:BG:151:ASP:O	2.35	0.52
6:BH:129:LEU:HD21	6:BH:169:PHE:HB3	1.91	0.52
9:BL:133:LYS:NZ	34:B5:324:U:OP1	2.28	0.52
10:BN:19:SER:OG	10:BN:21:ASN:O	2.26	0.52
14:BX:57:LEU:HD11	14:BX:73:ARG:HB2	1.91	0.52
23:BQ:107:LYS:HA	23:BQ:110:THR:HG22	1.91	0.52
31:Bg:123:ILE:HD13	31:Bg:169:ILE:HD13	1.92	0.52
31:Bg:131:ILE:HB	31:Bg:144:LEU:HB2	1.91	0.52
36:AB:160:VAL:HB	36:AB:183:LEU:HD21	1.91	0.52
38:A1:633:C:O2'	68:Af:21:ARG:O	2.22	0.52
38:A1:831:G:O2'	38:A1:1864:A:N3	2.35	0.52
38:A1:1836:C:H41	74:Al:3:ALA:HB2	1.74	0.52
39:A3:112:G:H2'	39:A3:113:C:C6	2.44	0.52
42:AE:43:LEU:HD11	42:AE:85:ILE:HG12	1.92	0.52
79:E:34:LEU:HD12	79:E:169:VAL:HG11	1.91	0.52
3:BC:35:TRP:NE1	3:BC:65:GLU:OE2	2.25	0.52
5:BG:52:ILE:HG23	5:BG:109:LEU:HD21	1.91	0.52
21:BK:12:HIS:HB3	21:BK:80:LEU:HD21	1.92	0.52
31:Bg:16:HIS:NE2	31:Bg:35:SER:OG	2.34	0.52
31:Bg:133:VAL:HB	31:Bg:142:ALA:HB3	1.91	0.52
37:AC:181:VAL:O	37:AC:182:LEU:HG	2.10	0.52
38:A1:821:U:H2'	38:A1:822:G:H8	1.73	0.52
38:A1:993:G:N3	38:A1:2637:A:H2'	2.25	0.52
38:A1:2197:OMC:N4	38:A1:2241:U:H2'	2.25	0.52
52:AP:56:ARG:NH2	52:AP:75:GLU:OE2	2.28	0.52
77:Ao:25:VAL:HG22	77:Ao:72:LEU:HD22	1.90	0.52
80:DC:183:GLU:O	80:DC:187:VAL:HG23	2.10	0.52
81:V:96:ILE:HA	81:V:99:VAL:HG12	1.91	0.52
3:BC:143:TYR:OH	3:BC:149:GLY:O	2.26	0.52
34:B5:1469:A:H2'	34:B5:1470:C:C6	2.45	0.52
36:AB:92:TYR:HB2	36:AB:157:VAL:HB	1.91	0.52
38:A1:12:A:H2'	38:A1:13:A:C8	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:406:G:OP1	38:A1:1415:U:O2'	2.27	0.52
38:A1:1582:C:H5''	38:A1:1583:A:OP1	2.09	0.52
38:A1:1592:G:OP2	69:Ag:37:LYS:NZ	2.43	0.52
38:A1:2526:C:H2'	38:A1:2527:G:H8	1.75	0.52
38:A1:3324:C:OP1	66:Ad:19:ARG:NH1	2.36	0.52
39:A3:38:U:N3	39:A3:41:G:OP2	2.36	0.52
41:AD:48:LYS:HG2	41:AD:145:PHE:HE2	1.73	0.52
54:AR:109:TYR:HB3	54:AR:115:ILE:HG12	1.92	0.52
65:Ac:49:PRO:HG2	65:Ac:52:ARG:HB3	1.91	0.52
79:E:42:ASP:HB3	79:E:45:ARG:HB2	1.92	0.52
8:BJ:163:PRO:HD3	8:BJ:168:ARG:HD3	1.90	0.52
9:BL:109:VAL:HG21	9:BL:125:VAL:HG11	1.92	0.52
34:B5:632:U:O2'	34:B5:1103:U:OP1	2.25	0.52
35:AA:206:PRO:HG3	35:AA:213:GLY:HA3	1.92	0.52
36:AB:250:ALA:HB3	38:A1:2880:U:H1'	1.92	0.52
38:A1:179:C:H2'	38:A1:180:C:C6	2.44	0.52
38:A1:2344:U:H2'	38:A1:2345:A:C8	2.45	0.52
38:A1:3234:A:N6	38:A1:3253:G:H1	2.07	0.52
38:A1:3267:A:H2'	42:AE:69:PHE:CZ	2.45	0.52
58:AV:80:ARG:NH1	58:AV:117:PRO:O	2.33	0.52
7:BI:57:ALA:HB2	7:BI:177:GLY:HA2	1.92	0.52
11:BO:123:SER:HB2	34:B5:885:G:H21	1.73	0.52
16:Ba:2:PRO:HB3	34:B5:1142:A:H5''	1.90	0.52
20:BF:42:LEU:O	20:BF:44:ASN:N	2.37	0.52
31:Bg:288:HIS:CE1	31:Bg:306:THR:HG21	2.45	0.52
34:B5:520:A:H2'	34:B5:521:A:C8	2.44	0.52
38:A1:2207:A:N6	38:A1:2233:A:OP2	2.42	0.52
38:A1:2697:A:H2'	38:A1:2698:G:H8	1.73	0.52
43:AF:168:ILE:O	43:AF:172:ASN:ND2	2.41	0.52
44:AG:171:LYS:NZ	44:AG:227:ASP:OD1	2.43	0.52
81:V:141:VAL:HG22	81:V:156:VAL:HG11	1.91	0.52
6:BH:17:GLU:HB3	6:BH:46:ILE:CG1	2.34	0.52
6:BH:46:ILE:HD13	6:BH:60:ILE:HG22	1.92	0.52
7:BI:56:ARG:HH22	34:B5:332:U:P	2.32	0.52
11:BO:126:THR:HG21	34:B5:888:U:H1'	1.91	0.52
15:BY:56:SER:O	15:BY:74:LEU:N	2.39	0.52
23:BQ:132:LYS:HG2	23:BQ:138:PHE:HE1	1.74	0.52
38:A1:1259:A:C6	81:V:53:MET:HE1	2.45	0.52
38:A1:1497:C:O2'	38:A1:1602:A:N3	2.39	0.52
38:A1:2898:G:OP2	45:AH:173:ARG:NH1	2.37	0.52
52:AP:128:ARG:HD2	52:AP:136:ILE:HD13	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:AY:70:ILE:HD13	61:AY:82:VAL:HG22	1.92	0.52
80:DC:80:GLU:OE2	80:DC:96:ASN:ND2	2.43	0.52
5:BG:33:GLY:N	5:BG:52:ILE:O	2.36	0.52
11:BO:121:VAL:O	34:B5:886:U:O2'	2.26	0.52
20:BF:161:ASP:HB3	29:Bc:44:VAL:HG22	1.92	0.52
31:Bg:93:ASP:HB2	31:Bg:100:TYR:CE2	2.45	0.52
34:B5:1161:C:H2'	34:B5:1162:C:H6	1.75	0.52
34:B5:1621:U:H2'	34:B5:1622:G:C8	2.44	0.52
38:A1:787:G:H2'	38:A1:788:C:C6	2.45	0.52
46:AI:35:ASP:OD1	46:AI:86:HIS:NE2	2.41	0.52
48:AL:59:ARG:NH2	48:AL:66:ASN:O	2.36	0.52
48:AL:165:SER:O	48:AL:168:ARG:N	2.43	0.52
53:AQ:123:THR:OG1	53:AQ:125:ASP:OD1	2.22	0.52
80:DC:460:ASP:N	80:DC:460:ASP:OD1	2.42	0.52
7:BI:27:PHE:HB2	34:B5:333:A:N6	2.25	0.52
7:BI:138:ASN:HD21	34:B5:187:G:H2'	1.74	0.52
10:BN:64:ARG:NH2	34:B5:861:U:OP1	2.32	0.52
11:BO:114:ARG:HH21	16:Ba:62:TYR:HE1	1.58	0.52
11:BO:136:ARG:NH2	34:B5:1785:U:OP1	2.35	0.52
27:BU:22:ILE:HG21	27:BU:100:VAL:HG21	1.92	0.52
28:BZ:49:ARG:HA	28:BZ:52:LYS:HG2	1.92	0.52
34:B5:393:C:H2'	34:B5:394:C:C6	2.45	0.52
34:B5:407:A:H2'	34:B5:408:C:C6	2.45	0.52
34:B5:445:A:H61	34:B5:462:G:H1'	1.74	0.52
34:B5:1176:G:N3	34:B5:1195:C:O2'	2.35	0.52
34:B5:1267:G:O2'	34:B5:1448:G:O2'	2.21	0.52
38:A1:1176:C:H2'	38:A1:1177:G:N2	2.25	0.52
38:A1:3216:G:OP2	68:Af:2:ALA:N	2.43	0.52
1:BA:123:VAL:HG21	1:BA:133:ILE:HD11	1.92	0.52
13:BW:31:SER:H	13:BW:34:ILE:HD12	1.74	0.52
34:B5:126:A:N6	34:B5:291:G:H21	2.02	0.52
34:B5:194:U:C4	34:B5:227:U:H5'	2.45	0.52
34:B5:1695:G:H2'	34:B5:1696:G:H8	1.74	0.52
38:A1:845:G:O2'	38:A1:847:A:N1	2.33	0.52
38:A1:1580:A:H4'	38:A1:1581:C:C6	2.45	0.52
38:A1:1722:U:OP2	54:AR:103:ARG:NH1	2.41	0.52
38:A1:2680:A:C2	47:AJ:57:PHE:HB3	2.45	0.52
80:DC:378:LEU:HD22	80:DC:403:GLY:HA3	1.92	0.52
82:EC:6831:U:H1'	82:EC:6832:G:C8	2.45	0.52
2:BB:69:CYS:HB3	11:BO:114:ARG:HH11	1.75	0.51
6:BH:44:LYS:NZ	6:BH:63:PRO:HB3	2.24	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BO:136:ARG:HD3	11:BO:136:ARG:H	1.74	0.51
20:BF:223:SER:HA	82:EC:6840:A:C6	2.45	0.51
22:BP:31:GLU:O	22:BP:35:LYS:HG2	2.11	0.51
25:BS:42:TYR:HA	25:BS:85:PHE:HE2	1.74	0.51
34:B5:809:A:H2'	34:B5:810:G:C8	2.45	0.51
34:B5:953:G:H2'	34:B5:954:G:C8	2.44	0.51
34:B5:960:U:H2'	34:B5:961:U:H6	1.75	0.51
38:A1:531:G:H2'	38:A1:532:A:C8	2.46	0.51
49:AM:39:ILE:HB	49:AM:43:LYS:HB3	1.93	0.51
58:AV:87:ARG:HH22	58:AV:137:VAL:HG22	1.74	0.51
21:BK:7:ASP:O	21:BK:11:ILE:HG12	2.10	0.51
24:BR:103:ASP:HB3	24:BR:105:GLN:OE1	2.11	0.51
25:BS:48:LYS:NZ	26:BT:35:ASP:HB2	2.25	0.51
38:A1:2526:C:H2'	38:A1:2527:G:C8	2.45	0.51
38:A1:2673:A:OP2	47:AJ:94:ARG:NH2	2.43	0.51
38:A1:3291:G:H2'	38:A1:3292:A:H8	1.76	0.51
39:A3:119:U:OP2	41:AD:258:LYS:NZ	2.31	0.51
47:AJ:161:SER:O	47:AJ:165:GLN:HG2	2.10	0.51
48:AL:10:LEU:HD23	53:AQ:166:LEU:HD11	1.92	0.51
4:BE:19:LEU:HD13	34:B5:788:A:C6	2.45	0.51
7:BI:101:ILE:HD12	7:BI:184:LEU:HD11	1.90	0.51
7:BI:152:ILE:HG13	7:BI:153:GLU:N	2.25	0.51
19:BD:105:MET:HE1	19:BD:184:ILE:HB	1.91	0.51
27:BU:69:LYS:NZ	27:BU:80:GLU:OE2	2.42	0.51
38:A1:422:A:C2	38:A1:2363:A:H4'	2.45	0.51
38:A1:1110:U:H2'	38:A1:1111:U:C6	2.45	0.51
38:A1:1282:G:H2'	38:A1:1283:C:O4'	2.10	0.51
38:A1:2406:C:H2'	38:A1:2407:C:C6	2.44	0.51
38:A1:3023:U:H2'	38:A1:3024:A:H8	1.75	0.51
38:A1:3296:A:H2'	38:A1:3297:U:H6	1.76	0.51
39:A3:23:A:O2'	39:A3:121:U:O3'	2.18	0.51
40:A4:59:A:H5''	40:A4:61:A:C8	2.45	0.51
40:A4:154:C:H5''	44:AG:181:LYS:HG2	1.92	0.51
4:BE:27:TYR:O	34:B5:447:U:O2'	2.27	0.51
4:BE:31:PRO:HD2	4:BE:38:LEU:HG	1.93	0.51
11:BO:61:MET:HG3	11:BO:104:ALA:HB2	1.93	0.51
24:BR:10:LYS:NZ	34:B5:1316:G:O2'	2.42	0.51
34:B5:741:C:H4'	34:B5:742:U:H5'	1.93	0.51
34:B5:821:U:O4	34:B5:852:C:N3	2.43	0.51
36:AB:30:LYS:HD2	38:A1:3138:U:OP2	2.10	0.51
38:A1:656:A:H2'	38:A1:657:A:H8	1.76	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1760:A:N6	38:A1:1766:G:O6	2.43	0.51
38:A1:1786:G:H2'	38:A1:1787:A:C8	2.46	0.51
38:A1:2597:U:O2	50:AN:125:SER:OG	2.21	0.51
47:AJ:53:THR:OG1	47:AJ:61:ARG:N	2.43	0.51
51:AO:84[A]:LEU:HD13	51:AO:102[A]:LEU:HD22	1.91	0.51
58:AV:104:ASN:ND2	58:AV:108:GLU:HB3	2.23	0.51
79:E:188:ASN:HA	79:E:191:VAL:HG22	1.93	0.51
80:DC:123:ASP:HA	80:DC:352:ARG:NH1	2.25	0.51
12:BV:7:GLN:O	12:BV:9:VAL:HG13	2.10	0.51
16:Ba:84:VAL:O	34:B5:1797:A:N6	2.37	0.51
19:BD:62:ASN:HD21	21:BK:92:ILE:HD13	1.76	0.51
19:BD:222:VAL:HG11	31:Bg:229:LYS:HA	1.93	0.51
20:BF:36:ALA:HB1	20:BF:69:PHE:CZ	2.45	0.51
26:BT:77:ASN:HB3	26:BT:95:ASP:HB3	1.92	0.51
34:B5:144:U:HO2'	34:B5:145:A:H8	1.57	0.51
35:AA:184:ARG:NH2	78:Ap:14:TYR:OH	2.42	0.51
37:AC:325:LEU:HD23	38:A1:598:A:H4'	1.93	0.51
38:A1:650:OMC:H2'	38:A1:651:G:C8	2.46	0.51
38:A1:2413:A:H2'	38:A1:2414:G:H8	1.76	0.51
39:A3:7:G:OP1	41:AD:33:ARG:NH1	2.43	0.51
40:A4:109:A:O2'	40:A4:112:U:O4	2.27	0.51
48:AL:59:ARG:HD2	48:AL:69:VAL:HG12	1.92	0.51
55:AS:66:GLU:OE2	55:AS:73:LYS:HE3	2.10	0.51
80:DC:336:GLU:O	80:DC:340:LEU:HG	2.10	0.51
81:V:77:LEU:HB3	81:V:78:PRO:HD3	1.92	0.51
81:V:130:PRO:O	81:V:133:THR:OG1	2.28	0.51
15:BY:12:VAL:HG22	15:BY:23:PHE:HB3	1.93	0.51
24:BR:49:LYS:NZ	34:B5:1390:U:OP1	2.27	0.51
27:BU:24:ILE:HG22	27:BU:116:VAL:HG22	1.93	0.51
34:B5:17:C:H2'	34:B5:18:C:C6	2.45	0.51
34:B5:1062:A:H3'	34:B5:1063:U:H6	1.76	0.51
35:AA:111:THR:HB	35:AA:136:ILE:HD13	1.92	0.51
38:A1:532:A:H2'	38:A1:533:A:C8	2.45	0.51
38:A1:2927:C:H2'	38:A1:2928:C:C6	2.45	0.51
44:AG:178:ALA:HB2	44:AG:218:ILE:HG23	1.92	0.51
45:AH:130:ASP:OD1	45:AH:130:ASP:N	2.43	0.51
14:BX:96:VAL:HA	14:BX:127:VAL:HG21	1.93	0.51
18:Be:26:LYS:NZ	34:B5:587:C:OP1	2.43	0.51
31:Bg:59:ARG:CZ	31:Bg:96:THR:HA	2.41	0.51
34:B5:824:G:H2'	34:B5:825:U:C6	2.46	0.51
34:B5:1280:4AC:H2'	34:B5:1281:G:C8	2.46	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1776:A:H2'	34:B5:1777:G:C8	2.46	0.51
38:A1:86:G:O2'	38:A1:98:G:O6	2.27	0.51
38:A1:2160:G:H2'	38:A1:2161:G:C8	2.45	0.51
38:A1:2453:U:O2	38:A1:2454:G:O2'	2.26	0.51
38:A1:2812:C:H2'	38:A1:2813:A:C8	2.46	0.51
42:AE:59:GLU:OE1	42:AE:59:GLU:N	2.28	0.51
56:AT:91:LEU:HD12	56:AT:96:ILE:HD11	1.93	0.51
80:DC:432:GLN:HB2	80:DC:457:VAL:HG23	1.92	0.51
2:BB:188:LEU:HD11	2:BB:215:VAL:HG21	1.91	0.51
7:BI:32:GLN:OE1	34:B5:1727:G:N2	2.34	0.51
24:BR:29:GLN:HA	24:BR:32:LYS:HE3	1.91	0.51
30:Bd:33:LYS:HZ3	34:B5:1594:G:C5'	2.23	0.51
31:Bg:80:ALA:HB3	31:Bg:92:TRP:HB2	1.93	0.51
34:B5:1297:G:N2	34:B5:1300:A:OP2	2.33	0.51
34:B5:1374:C:H2'	34:B5:1375:A:C8	2.46	0.51
38:A1:176:G:O2'	38:A1:177:U:O4'	2.28	0.51
38:A1:716:A:C6	63:Aa:117:ARG:HG3	2.45	0.51
38:A1:2406:C:H2'	38:A1:2407:C:H6	1.75	0.51
80:DC:576:LEU:HD23	80:DC:839:TYR:HE1	1.75	0.51
8:BJ:129:ILE:HG13	8:BJ:134:ILE:HD13	1.92	0.51
9:BL:6:THR:HB	9:BL:9:SER:HB2	1.92	0.51
14:BX:131:SER:HB2	34:B5:30:G:H4'	1.92	0.51
15:BY:23:PHE:CZ	15:BY:75:VAL:HG23	2.46	0.51
20:BF:118:LEU:HA	20:BF:121:ILE:HG12	1.92	0.51
21:BK:38:LYS:HG3	21:BK:41:TYR:H	1.76	0.51
34:B5:146:U:H2'	34:B5:147:A:H8	1.76	0.51
34:B5:1488:G:C8	34:B5:1515:A:C6	2.99	0.51
37:AC:23:PRO:HD2	37:AC:26:PHE:CD2	2.45	0.51
38:A1:69:C:OP1	50:AN:178:HIS:ND1	2.33	0.51
38:A1:1618:G:O2'	40:A4:126:A:N1	2.44	0.51
53:AQ:133:LYS:H	53:AQ:135:GLN:NE2	2.09	0.51
79:E:163:LEU:HD23	79:E:163:LEU:H	1.76	0.51
80:DC:664:VAL:O	80:DC:668:GLN:HG2	2.11	0.51
3:BC:156:THR:HG23	13:BW:95:PRO:HB2	1.93	0.51
4:BE:108:ARG:NH2	34:B5:788:A:OP2	2.38	0.51
6:BH:5:GLN:HE22	6:BH:18:LEU:HB3	1.76	0.51
22:BP:126:VAL:HG11	34:B5:1458:G:H21	1.76	0.51
34:B5:406:U:H2'	34:B5:407:A:H8	1.76	0.51
38:A1:1667:A:H2'	38:A1:1668:G:C8	2.46	0.51
40:A4:106:C:H4'	40:A4:107:G:H5''	1.92	0.51
44:AG:78:PHE:C	44:AG:80:TYR:H	2.18	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:AM:37:GLU:OE2	49:AM:74:ARG:HG2	2.11	0.51
81:V:41:VAL:HG22	81:V:103:ASN:HD21	1.74	0.51
8:BJ:64:GLU:OE2	8:BJ:69:ARG:NH2	2.44	0.50
13:BW:69:LEU:HD11	13:BW:72:CYS:HB3	1.92	0.50
23:BQ:5:PRO:HG2	23:BQ:24:ALA:HB2	1.92	0.50
23:BQ:135:ARG:NH1	34:B5:1583:A:OP1	2.41	0.50
26:BT:30:VAL:HG12	26:BT:32:GLY:H	1.74	0.50
31:Bg:23:LEU:HG	31:Bg:33:LEU:HD11	1.92	0.50
36:AB:123:TYR:CZ	36:AB:124:LYS:HG3	2.46	0.50
38:A1:252:U:H4'	38:A1:253:A:C8	2.46	0.50
38:A1:1657:C:O2'	38:A1:1797:A:OP2	2.19	0.50
38:A1:2666:C:OP2	38:A1:2687:G:N1	2.36	0.50
45:AH:91:ARG:NH2	45:AH:141:LYS:O	2.45	0.50
73:Ak:62:ALA:O	73:Ak:66:ILE:HG13	2.11	0.50
7:BI:56:ARG:NH1	7:BI:174:GLY:O	2.40	0.50
11:BO:29:HIS:HA	11:BO:41:ARG:HA	1.93	0.50
11:BO:131:GLY:O	16:Ba:22:ARG:NH2	2.44	0.50
18:Be:33:ARG:NH2	34:B5:477:A:O3'	2.44	0.50
21:BK:16:PHE:HB2	21:BK:76:LEU:HD23	1.92	0.50
23:BQ:139:GLN:HB3	34:B5:1465:C:H5''	1.93	0.50
30:Bd:19:ARG:NH2	34:B5:1597:A:OP2	2.44	0.50
31:Bg:19:TRP:HB2	31:Bg:38:ARG:HG3	1.92	0.50
34:B5:698:U:O4	34:B5:741:C:N3	2.44	0.50
38:A1:29:C:H4'	38:A1:62:A:H4'	1.93	0.50
38:A1:528:U:H2'	38:A1:529:A:C8	2.46	0.50
38:A1:631:U:H2'	38:A1:632:G:C8	2.46	0.50
47:AJ:49:LYS:HE3	47:AJ:62:ASN:HA	1.93	0.50
5:BG:178:LEU:HD21	34:B5:78:A:C6	2.45	0.50
34:B5:406:U:H2'	34:B5:407:A:C8	2.47	0.50
34:B5:1542:G:N1	34:B5:1568:C:O2'	2.26	0.50
38:A1:1222:G:H5''	81:V:57:THR:HB	1.94	0.50
38:A1:1256:G:H2'	38:A1:1257:C:C6	2.45	0.50
38:A1:1311:G:N2	51:AO:86[A]:GLY:O	2.29	0.50
38:A1:1836:C:O2'	38:A1:1842:A:N1	2.39	0.50
38:A1:3192:U:H2'	38:A1:3193:C:C6	2.46	0.50
38:A1:3214:U:C4	49:AM:121:MET:HG3	2.46	0.50
49:AM:102:LYS:HG2	49:AM:106:ARG:HH21	1.76	0.50
50:AN:36:ILE:HG12	50:AN:64:VAL:HG23	1.93	0.50
67:Ae:60:ASN:HB3	67:Ae:63:THR:HG22	1.93	0.50
80:DC:217:GLY:HA3	80:DC:325:ARG:HD3	1.94	0.50
80:DC:404:THR:HG22	80:DC:449:PRO:HA	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BP:40:ARG:O	22:BP:44:ARG:HG2	2.10	0.50
31:Bg:21:THR:N	31:Bg:36:ALA:O	2.44	0.50
34:B5:250:C:H2'	34:B5:251:A:H8	1.77	0.50
34:B5:264:G:H5''	34:B5:265:A:H5'	1.93	0.50
34:B5:626:U:H2'	34:B5:627:C:H6	1.75	0.50
35:AA:181:LYS:HB2	38:A1:860:G:C5	2.47	0.50
38:A1:251:G:H5'	38:A1:251:G:C8	2.46	0.50
38:A1:2464:U:H1'	79:E:162:VAL:HG21	1.93	0.50
38:A1:3291:G:H2'	38:A1:3292:A:C8	2.46	0.50
55:AS:46:GLN:OE1	55:AS:52:LYS:HB3	2.11	0.50
66:Ad:46:THR:OG1	66:Ad:91:SER:OG	2.20	0.50
79:E:120:VAL:O	79:E:125:GLY:N	2.45	0.50
11:BO:72:LYS:O	11:BO:73:GLU:HG3	2.12	0.50
34:B5:925:G:H2'	34:B5:926:A:C8	2.47	0.50
38:A1:1446:A:H5''	52:AP:65:SER:HB2	1.94	0.50
38:A1:1534:A:H2'	38:A1:1535:A:C8	2.47	0.50
80:DC:632:LYS:HG3	80:DC:648:ASP:OD1	2.12	0.50
80:DC:695:ALA:O	80:DC:700:ARG:NH1	2.45	0.50
81:V:25:LEU:O	81:V:191:TYR:HB3	2.12	0.50
5:BG:187:LYS:O	5:BG:191:ARG:HG2	2.10	0.50
18:Be:37:ARG:NH1	34:B5:478:A:OP1	2.38	0.50
34:B5:752:A:O2'	34:B5:753:A:OP1	2.27	0.50
34:B5:1202:A:N6	34:B5:1457:C:OP1	2.44	0.50
34:B5:1552:U:O2'	34:B5:1597:A:N3	2.38	0.50
38:A1:179:C:H2'	38:A1:180:C:H6	1.75	0.50
38:A1:792:G:H5''	63:Aa:2:PRO:HD2	1.94	0.50
38:A1:1404:G:N2	38:A1:1407:A:OP2	2.33	0.50
38:A1:2565:U:H2'	38:A1:2566:C:H6	1.77	0.50
47:AJ:17:LEU:HB2	47:AJ:129:VAL:HG12	1.94	0.50
58:AV:106:LYS:NZ	58:AV:128:ARG:HH12	2.09	0.50
61:AY:55:GLU:HA	61:AY:69:LYS:HA	1.92	0.50
80:DC:572:SER:OG	80:DC:573:GLN:OE1	2.29	0.50
1:BA:3:LEU:HD22	1:BA:7:PHE:CD2	2.47	0.50
3:BC:144:TRP:O	13:BW:98:GLN:NE2	2.44	0.50
11:BO:29:HIS:CD2	11:BO:41:ARG:HB2	2.47	0.50
14:BX:107:PHE:CG	14:BX:114:LYS:HD3	2.46	0.50
23:BQ:136:SER:HB3	34:B5:1586:A:H5''	1.94	0.50
27:BU:82:TYR:HB3	30:Bd:52:PHE:HB3	1.94	0.50
31:Bg:51:ASP:OD1	31:Bg:53:LYS:HG2	2.11	0.50
34:B5:1488:G:O2'	34:B5:1494:C:O2	2.21	0.50
35:AA:190:ARG:HG3	35:AA:191:LEU:HD22	1.92	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:10:ARG:NH1	36:AB:11:HIS:O	2.45	0.50
38:A1:1193:A:OP1	51:AO:49[A]:ARG:NH2	2.40	0.50
38:A1:2477:G:H5'	38:A1:2487:U:C2	2.46	0.50
39:A3:87:G:OP1	43:AF:218:ARG:NE	2.45	0.50
55:AS:152:LEU:HB2	55:AS:172:TYR:CE2	2.47	0.50
56:AT:158:THR:HG22	56:AT:160:ILE:HB	1.93	0.50
80:DC:394:PHE:HE2	80:DC:513:LYS:HB3	1.75	0.50
15:BY:34:ASN:O	34:B5:521:A:O2'	2.26	0.50
18:Be:31:LYS:HE2	34:B5:545:A:H2'	1.93	0.50
34:B5:507:U:H5''	34:B5:508:U:H5	1.76	0.50
34:B5:689:G:H2'	34:B5:690:G:H8	1.77	0.50
34:B5:844:A:H2'	34:B5:845:G:C8	2.47	0.50
34:B5:848:C:H2'	34:B5:849:C:C6	2.47	0.50
34:B5:1344:A:H4'	34:B5:1345:A:OP1	2.11	0.50
38:A1:792:G:H2'	38:A1:793:C:C6	2.47	0.50
38:A1:1062:A:N3	56:AT:130:ARG:NH2	2.52	0.50
38:A1:1334:U:H5''	43:AF:206:LYS:HB3	1.93	0.50
38:A1:2219:A:H2'	38:A1:2220:A2M:C8	2.42	0.50
38:A1:2673:A:H5''	47:AJ:95:ASN:ND2	2.18	0.50
80:DC:717:PHE:HB3	80:DC:718:LEU:HD12	1.94	0.50
10:BN:62:GLN:HB2	10:BN:65:VAL:HG12	1.94	0.50
19:BD:18:TYR:HE1	19:BD:37:VAL:HG13	1.76	0.50
19:BD:72:LEU:HD12	21:BK:65:TYR:CD1	2.44	0.50
25:BS:132:ARG:NH1	34:B5:1544:U:H4'	2.27	0.50
26:BT:63:ARG:O	26:BT:67:MET:HG2	2.12	0.50
31:Bg:196:ASN:N	31:Bg:219:GLU:OE2	2.41	0.50
32:Bf:102:VAL:HG23	32:Bf:103:LEU:HD22	1.93	0.50
34:B5:1063:U:H2'	34:B5:1064:G:C8	2.47	0.50
34:B5:1458:G:H2'	34:B5:1458:G:N3	2.26	0.50
36:AB:250:ALA:HB1	38:A1:2947:G:N3	2.27	0.50
38:A1:1037:C:H2'	38:A1:1038:C:C6	2.47	0.50
38:A1:1751:G:H5'	73:Ak:26:LYS:HE2	1.94	0.50
38:A1:2193:U:H5''	38:A1:2194:G:H5'	1.94	0.50
39:A3:11:A:N1	39:A3:67:G:O2'	2.40	0.50
41:AD:120:LYS:O	41:AD:248:ARG:NH1	2.44	0.50
58:AV:75:PRO:HG2	58:AV:105:PRO:HD3	1.94	0.50
68:Af:14:LEU:HD11	68:Af:31:LYS:HB2	1.94	0.50
80:DC:71:LYS:HG2	80:DC:387:PRO:HD2	1.94	0.50
80:DC:285:PHE:CD1	80:DC:320:LEU:HD11	2.46	0.50
80:DC:522:MET:HE3	80:DC:526:GLY:HA2	1.94	0.50
82:EC:6901:C:O2'	82:EC:6902:U:H5'	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:52:LEU:HD22	4:BE:54:TYR:CZ	2.47	0.49
7:BI:142:LYS:O	7:BI:146:ARG:HD3	2.12	0.49
8:BJ:144:PRO:HD2	34:B5:474:A:H5'	1.94	0.49
16:Ba:12:LYS:HB2	16:Ba:33:ASP:OD2	2.12	0.49
32:Bf:96:LYS:NZ	34:B5:1251:U:OP2	2.45	0.49
34:B5:590:C:H2'	34:B5:591:A:C8	2.47	0.49
34:B5:1713:G:H2'	34:B5:1714:A:C8	2.46	0.49
34:B5:1772:C:H3'	76:An:2:ARG:NH2	2.27	0.49
36:AB:284:ARG:NH1	36:AB:293:ASN:O	2.44	0.49
37:AC:11:LEU:HD21	37:AC:156:LEU:HB2	1.94	0.49
38:A1:253:A:O5'	38:A1:253:A:H8	1.95	0.49
38:A1:761:A:C2	38:A1:771:A:H1'	2.47	0.49
38:A1:1144:U:OP1	38:A1:1367:G:O2'	2.27	0.49
38:A1:2428:U:H2'	38:A1:2429:G:H8	1.76	0.49
38:A1:2465:G:C6	38:A1:2491:A:N6	2.79	0.49
46:AI:54:SER:HB3	46:AI:135:ILE:HD11	1.94	0.49
70:Ah:77:PRO:HD2	70:Ah:80:LEU:HD12	1.93	0.49
80:DC:17:THR:OG1	80:DC:92:LYS:O	2.22	0.49
8:BJ:149:ARG:HG2	34:B5:765:G:O6	2.12	0.49
16:Ba:15:ARG:HG2	34:B5:936:G:O6	2.12	0.49
21:BK:46:LEU:HD13	21:BK:49:LEU:HD21	1.94	0.49
26:BT:57:ARG:NE	34:B5:1479:A:OP1	2.40	0.49
31:Bg:83:ALA:HB1	31:Bg:110:VAL:HG12	1.93	0.49
34:B5:116:U:H2'	34:B5:117:U:C6	2.47	0.49
34:B5:140:A:H61	34:B5:282:C:P	2.36	0.49
34:B5:485:A:H62	34:B5:486:G:N2	2.10	0.49
34:B5:1429:G:H2'	34:B5:1430:U:C6	2.47	0.49
38:A1:3066:U:H2'	38:A1:3067:C:H6	1.77	0.49
38:A1:3205:G:O2'	55:AS:171:PHE:HZ	1.95	0.49
62:AZ:16:GLY:C	62:AZ:18:TYR:H	2.20	0.49
68:Af:45:LEU:HD11	68:Af:73:ARG:HA	1.94	0.49
80:DC:221:THR:HG23	80:DC:224:GLN:H	1.76	0.49
80:DC:587:TYR:HB2	80:DC:690:ASP:O	2.12	0.49
25:BS:17:LEU:HD21	25:BS:66:LEU:CD1	2.37	0.49
34:B5:190:C:P	34:B5:196:G:H22	2.35	0.49
36:AB:156:SER:HA	36:AB:188:ILE:HG13	1.94	0.49
37:AC:67:THR:HG21	38:A1:2402:A:H2'	1.93	0.49
38:A1:671:U:H2'	38:A1:672:A:H8	1.78	0.49
40:A4:9:A:H2'	40:A4:10:A:C8	2.47	0.49
41:AD:136:GLU:OE1	41:AD:136:GLU:N	2.42	0.49
46:AI:156:ARG:HG3	46:AI:163:GLN:HB2	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:729:PHE:CE2	80:DC:774:VAL:HG13	2.47	0.49
13:BW:107:SER:HA	34:B5:804:A:C8	2.47	0.49
15:BY:39:GLU:HA	15:BY:42:GLU:HG3	1.95	0.49
19:BD:108:LYS:HB3	19:BD:113:LEU:HD22	1.95	0.49
34:B5:1218:G:H22	34:B5:1444:A:P	2.34	0.49
34:B5:1579:U:H2'	34:B5:1580:C:C6	2.47	0.49
35:AA:204:MET:HG2	38:A1:914:A:C2	2.47	0.49
38:A1:1097:G:H8	56:AT:112:ASN:HD22	1.60	0.49
38:A1:1389:G:H5''	67:Ae:101:SER:HB3	1.94	0.49
38:A1:2228:A:H2'	38:A1:2229:A:C8	2.47	0.49
38:A1:3095:U:H2'	38:A1:3096:C:C6	2.48	0.49
43:AF:66:LYS:HE2	43:AF:78:GLU:OE2	2.11	0.49
47:AJ:40:LEU:HD22	47:AJ:125:MET:HE1	1.93	0.49
79:E:19:TYR:O	79:E:23:THR:OG1	2.28	0.49
4:BE:181:VAL:HG12	4:BE:227:VAL:HG22	1.95	0.49
5:BG:135:PRO:HD2	5:BG:158:ILE:HD13	1.95	0.49
9:BL:99:ARG:HG2	14:BX:9:LEU:HA	1.94	0.49
34:B5:1499:G:O6	34:B5:1508:U:O4	2.30	0.49
34:B5:1550:A:H2'	34:B5:1551:U:C6	2.46	0.49
38:A1:2469:G:HO2'	38:A1:2470:C:H6	1.60	0.49
38:A1:2747:A:H2'	38:A1:2748:A:C8	2.48	0.49
38:A1:3298:C:C2	38:A1:3299:A:C8	3.00	0.49
53:AQ:133:LYS:H	53:AQ:135:GLN:HE22	1.58	0.49
82:EC:6777:C:H5'	82:EC:6778:C:H2'	1.95	0.49
3:BC:147:ASN:ND2	12:BV:3:ASN:O	2.45	0.49
5:BG:195:VAL:O	5:BG:199:GLN:HG2	2.11	0.49
7:BI:117:TYR:HB3	7:BI:119:GLN:OE1	2.13	0.49
9:BL:68:GLY:HA2	34:B5:112:A:H5'	1.95	0.49
19:BD:167:PHE:HD1	19:BD:190:ARG:HH12	1.59	0.49
30:Bd:32:ARG:NH1	34:B5:1596:C:OP2	2.45	0.49
31:Bg:125:GLY:HA2	31:Bg:131:ILE:HA	1.94	0.49
32:Bf:141:CYS:SG	32:Bf:144:CYS:N	2.70	0.49
37:AC:341:SER:OG	38:A1:514:G:N3	2.42	0.49
38:A1:1686:U:OP1	57:AU:42:LYS:NZ	2.32	0.49
71:Ai:70:ARG:HH21	71:Ai:84:LYS:CG	2.26	0.49
80:DC:563:TYR:O	80:DC:564:ARG:NH1	2.45	0.49
8:BJ:86:LEU:HD21	8:BJ:91:LYS:HA	1.95	0.49
18:Be:42:ARG:HA	18:Be:46:ASN:OD1	2.13	0.49
31:Bg:68:VAL:HA	31:Bg:84:SER:HA	1.95	0.49
34:B5:64:U:O2'	34:B5:168:A:N3	2.38	0.49
34:B5:1254:U:H3'	34:B5:1255:G:H8	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:96:LEU:HG	78:Ap:83:ILE:HG23	1.93	0.49
38:A1:2213:A:H2'	38:A1:2214:A:H8	1.76	0.49
40:A4:26:U:H2'	40:A4:27:U:C6	2.48	0.49
56:AT:152:ALA:HB1	56:AT:153:PRO:HD2	1.95	0.49
79:E:34:LEU:HD23	79:E:206:VAL:HB	1.94	0.49
80:DC:288:ILE:HG22	80:DC:289:MET:HE2	1.95	0.49
80:DC:813:SER:OG	80:DC:814:LYS:N	2.46	0.49
2:BB:216:LYS:NZ	34:B5:885:G:OP1	2.28	0.49
4:BE:11:ARG:NH1	4:BE:21:ASP:O	2.42	0.49
19:BD:36:GLY:HA3	19:BD:51:ARG:CZ	2.43	0.49
20:BF:219:ARG:HH21	82:EC:6842:U:H5'	1.78	0.49
22:BP:17:TYR:O	22:BP:20:VAL:HG12	2.13	0.49
22:BP:96:ILE:HG12	22:BP:116:LEU:HB3	1.94	0.49
23:BQ:76:SER:N	34:B5:1609:U:OP1	2.44	0.49
24:BR:71:PHE:O	24:BR:75:GLU:HG2	2.12	0.49
34:B5:625:C:H2'	34:B5:626:U:C6	2.48	0.49
34:B5:1234:A:OP2	34:B5:1245:G:O2'	2.25	0.49
34:B5:1434:U:H2'	34:B5:1436:A:H5'	1.94	0.49
34:B5:1504:G:H22	34:B5:1549:C:H1'	1.78	0.49
38:A1:916:G:H5'	38:A1:917:A:OP1	2.12	0.49
38:A1:1250:G:H2'	38:A1:1251:A:C8	2.48	0.49
38:A1:2688:U:OP1	41:AD:12:TYR:OH	2.28	0.49
72:Aj:27:PHE:HA	72:Aj:34:CYS:HA	1.95	0.49
78:Ap:59:CYS:C	78:Ap:61:LYS:H	2.21	0.49
80:DC:576:LEU:HD23	80:DC:839:TYR:CE1	2.47	0.49
4:BE:64:ILE:HD11	15:BY:18:LEU:HG	1.94	0.49
6:BH:10:SER:HB3	6:BH:42:GLN:NE2	2.28	0.49
7:BI:36:THR:OG1	7:BI:57:ALA:O	2.27	0.49
9:BL:10:GLU:HG2	9:BL:11:ARG:H	1.77	0.49
13:BW:103:ILE:HA	13:BW:112:ASP:HA	1.95	0.49
25:BS:13:HIS:CG	25:BS:14:ILE:H	2.30	0.49
33:BM:122:VAL:HG12	33:BM:124:LYS:H	1.76	0.49
34:B5:52:U:H2'	34:B5:53:G:C8	2.48	0.49
36:AB:159:ARG:HG2	36:AB:182:GLN:HA	1.95	0.49
38:A1:36:C:OP2	50:AN:83:LYS:NZ	2.44	0.49
38:A1:292:U:OP2	50:AN:68:ARG:NH2	2.44	0.49
38:A1:970:A:OP2	64:Ab:19:ASN:ND2	2.45	0.49
38:A1:1799:A:H2'	38:A1:1800:A:C8	2.47	0.49
38:A1:2150:G:O2'	38:A1:2189:U:OP1	2.28	0.49
38:A1:2683:U:H2'	38:A1:2684:C:C6	2.48	0.49
42:AE:142:ASP:O	42:AE:146:ILE:HD12	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:AM:117:ARG:HA	49:AM:120:VAL:HG12	1.94	0.49
80:DC:20:ARG:HH22	80:DC:344:SER:HB3	1.76	0.49
80:DC:288:ILE:HG21	80:DC:320:LEU:HB2	1.95	0.49
81:V:23:LYS:HG2	81:V:90:ASN:OD1	2.13	0.49
82:EC:6892:U:O3'	82:EC:6943:A:N6	2.46	0.49
5:BG:155:ASP:N	5:BG:155:ASP:OD1	2.46	0.49
11:BO:84:ARG:HG2	11:BO:85:ALA:O	2.12	0.49
23:BQ:100:GLN:NE2	31:Bq:56:VAL:HB	2.27	0.49
24:BR:77:GLU:OE1	24:BR:80:ARG:NH2	2.46	0.49
26:BT:37:VAL:HG21	26:BT:100:ILE:HD11	1.95	0.49
34:B5:31:C:O2'	34:B5:547:U:OP1	2.31	0.49
35:AA:117:GLU:HG2	35:AA:124:GLY:N	2.20	0.49
38:A1:394:G:N1	38:A1:397:A:OP2	2.44	0.49
38:A1:792:G:H2'	38:A1:793:C:H6	1.78	0.49
38:A1:1108:U:H2'	38:A1:1109:U:C6	2.48	0.49
38:A1:1435:A:H5''	38:A1:1436:U:H5''	1.95	0.49
38:A1:2936:A:H2'	38:A1:2937:G:C8	2.47	0.49
40:A4:69:U:H2'	40:A4:70:G:O4'	2.13	0.49
46:AI:72:ALA:HB2	46:AI:155:ALA:HB2	1.94	0.49
46:AI:144:ASN:HB2	46:AI:147:VAL:HB	1.95	0.49
60:AX:137:ASN:ND2	60:AX:142:ILE:O	2.46	0.49
79:E:96:ASN:HD21	79:E:98:LYS:HE3	1.77	0.49
79:E:104:SER:HA	79:E:110:PHE:CE2	2.48	0.49
80:DC:374:PRO:O	80:DC:375:LYS:HE2	2.13	0.49
17:Bb:41:LEU:HD23	17:Bb:41:LEU:H	1.78	0.48
23:BQ:36:ILE:HG13	23:BQ:49:TYR:HE1	1.78	0.48
28:BZ:44:GLN:HG2	28:BZ:45:GLU:N	2.28	0.48
32:Bf:99:LYS:NZ	34:B5:1229:G:OP1	2.41	0.48
34:B5:698:U:H2'	34:B5:699:U:C6	2.48	0.48
34:B5:1225:U:O4	34:B5:1256:A:N6	2.41	0.48
34:B5:1226:A:C6	34:B5:1230:A:H1'	2.48	0.48
34:B5:1392:U:H2'	34:B5:1393:C:C6	2.48	0.48
38:A1:966:U:OP1	63:Aa:44:ASN:ND2	2.44	0.48
44:AG:148:ALA:HA	44:AG:201:THR:HG22	1.95	0.48
49:AM:32:LEU:HD11	49:AM:94:TRP:CG	2.48	0.48
56:AT:151:LEU:HG	56:AT:152:ALA:H	1.77	0.48
62:AZ:87:LEU:HD11	62:AZ:121:ARG:HD3	1.94	0.48
80:DC:42:ARG:HE	80:DC:331:ALA:HB3	1.79	0.48
81:V:12:PHE:CD1	81:V:62:ALA:HB2	2.48	0.48
81:V:45:LEU:O	81:V:45:LEU:HD12	2.13	0.48
4:BE:47:PHE:HE2	4:BE:90:ILE:HG21	1.78	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BO:52:ARG:HH11	34:B5:905:A:H4'	1.77	0.48
21:BK:11:ILE:O	21:BK:15:LEU:HD23	2.13	0.48
27:BU:89:ARG:HH22	34:B5:1383:G:P	2.35	0.48
27:BU:105:GLN:HG3	27:BU:106:ILE:HG23	1.95	0.48
32:Bf:138:ARG:HD2	32:Bf:139:LEU:H	1.79	0.48
33:BM:62:LEU:O	33:BM:91:VAL:HG12	2.13	0.48
34:B5:885:G:H2'	34:B5:886:U:C6	2.47	0.48
38:A1:163:C:C2'	38:A1:164:A:H5'	2.43	0.48
38:A1:2367:A:H2'	38:A1:2368:A:C8	2.48	0.48
38:A1:2440:G:H2'	38:A1:2441:A:C8	2.48	0.48
38:A1:2458:A:N7	38:A1:2481:G:N1	2.58	0.48
46:AI:66:GLU:CD	46:AI:69:ARG:HH21	2.19	0.48
51:AO:27[A]:LEU:O	51:AO:101[A]:ARG:NH1	2.42	0.48
52:AP:29:THR:HG22	52:AP:119:VAL:HG21	1.95	0.48
52:AP:47:TYR:OH	52:AP:57:ALA:O	2.26	0.48
79:E:21:ASN:OD1	79:E:22:GLU:N	2.46	0.48
80:DC:9:MET:HE1	80:DC:45:ILE:HD12	1.95	0.48
80:DC:394:PHE:O	80:DC:460:ASP:HB3	2.12	0.48
82:EC:6826:U:H2'	82:EC:6827:G:C8	2.48	0.48
82:EC:6858:A:H4'	82:EC:6859:U:H3	1.78	0.48
4:BE:10:LYS:HA	4:BE:27:TYR:HA	1.95	0.48
5:BG:49:VAL:HG12	5:BG:115:LYS:HB3	1.95	0.48
11:BO:16:VAL:O	11:BO:30:VAL:HA	2.13	0.48
22:BP:52:LYS:HB3	22:BP:53:PRO:HD3	1.95	0.48
31:Bg:278:PHE:CD1	31:Bg:287:PRO:HG2	2.48	0.48
33:BM:51:ALA:HB2	33:BM:124:LYS:HE2	1.95	0.48
34:B5:86:A:H4'	34:B5:148:A:H4'	1.95	0.48
34:B5:823:G:O6	34:B5:850:A:N6	2.47	0.48
34:B5:1548:G:N1	34:B5:1564:U:O4	2.47	0.48
35:AA:40:TYR:HA	35:AA:91:GLY:HA3	1.96	0.48
36:AB:175:LYS:HB2	38:A1:3314:A:OP1	2.14	0.48
38:A1:273:A:H2'	38:A1:274:G:C8	2.48	0.48
38:A1:2964:G:N2	38:A1:2967:A:OP2	2.31	0.48
38:A1:3164:C:O2'	38:A1:3165:A:H8	1.97	0.48
66:Ad:84:ASP:OD1	66:Ad:84:ASP:N	2.45	0.48
1:BA:41:ARG:NE	24:BR:105:GLN:HE22	2.11	0.48
6:BH:63:PRO:C	6:BH:65:PRO:HD3	2.39	0.48
7:BI:50:GLY:HA2	34:B5:397:A:H4'	1.94	0.48
8:BJ:85:VAL:HG11	8:BJ:104:PHE:HE1	1.77	0.48
13:BW:31:SER:HB2	34:B5:636:A:H5''	1.94	0.48
22:BP:47:ARG:NH2	34:B5:1553:G:OP2	2.37	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:207:U:H2'	34:B5:208:U:C6	2.49	0.48
34:B5:1586:A:H1'	34:B5:1611:A:N6	2.28	0.48
34:B5:1622:G:H2'	34:B5:1623:C:H6	1.79	0.48
34:B5:1645:G:H2'	34:B5:1646:C:H6	1.78	0.48
38:A1:66:A:N6	38:A1:76:G:H1'	2.29	0.48
38:A1:806:A:N3	38:A1:2812:C:O2'	2.40	0.48
38:A1:1120:A:H2'	38:A1:1121:U:H6	1.77	0.48
39:A3:84:A:H2'	39:A3:85:G:C8	2.49	0.48
47:AJ:7:ASN:OD1	47:AJ:8:PRO:HD2	2.13	0.48
80:DC:27:HIS:ND1	80:DC:138:GLN:HB2	2.28	0.48
80:DC:149:GLU:OE2	80:DC:352:ARG:NH2	2.47	0.48
80:DC:413:ILE:HB	80:DC:427:PHE:HD2	1.79	0.48
8:BJ:90:LYS:HE2	8:BJ:95:TYR:CD1	2.48	0.48
11:BO:40:ALA:HB2	11:BO:70:LYS:HD2	1.94	0.48
31:Bg:295:SER:OG	31:Bg:297:ASP:OD1	2.32	0.48
34:B5:5:U:H2'	34:B5:6:G:C8	2.48	0.48
34:B5:107:C:OP1	34:B5:383:G:O2'	2.30	0.48
34:B5:1740:A:H2'	34:B5:1741:U:C6	2.48	0.48
38:A1:128:G:OP1	70:Ah:75:TYR:OH	2.23	0.48
38:A1:524:U:OP1	49:AM:77:ARG:NH2	2.45	0.48
38:A1:1234:G:H1	38:A1:1255:C:H42	1.61	0.48
38:A1:1620:U:H2'	38:A1:1621:A:C8	2.49	0.48
38:A1:2566:C:H2'	38:A1:2567:C:H6	1.79	0.48
38:A1:2930:A:H2'	38:A1:2931:C:C6	2.48	0.48
81:V:34:SER:OG	81:V:35:SER:N	2.46	0.48
3:BC:91:ARG:HH11	34:B5:1147:A:H5''	1.79	0.48
34:B5:1236:A:N6	34:B5:1237:G:O6	2.47	0.48
34:B5:1364:G:H2'	34:B5:1365:C:C6	2.48	0.48
34:B5:1622:G:H2'	34:B5:1623:C:C6	2.49	0.48
38:A1:1621:A:H2'	38:A1:1622:U:H6	1.78	0.48
38:A1:2357:A:H2'	38:A1:2358:A:C8	2.48	0.48
38:A1:2357:A:H2'	38:A1:2358:A:H8	1.78	0.48
38:A1:2742:C:H2'	38:A1:2743:A:H8	1.78	0.48
38:A1:2772:C:H4'	38:A1:2773:C:H5'	1.96	0.48
48:AL:3:ILE:HG21	63:Aa:45:MET:HE3	1.95	0.48
56:AT:88:ARG:NH1	64:Ab:33:LYS:O	2.47	0.48
80:DC:272:ALA:HA	80:DC:275:MET:HG2	1.94	0.48
4:BE:173:ILE:HD12	4:BE:227:VAL:HG12	1.96	0.48
31:Bg:200:ASN:H	31:Bg:215:GLY:HA2	1.79	0.48
34:B5:225:A:N6	34:B5:835:U:O4	2.46	0.48
34:B5:472:U:O2'	34:B5:769:A:N3	2.41	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:600:U:H2'	34:B5:601:A:C8	2.49	0.48
35:AA:127:ALA:HB2	35:AA:134:VAL:HG23	1.95	0.48
38:A1:219:A:O2'	38:A1:220:G:N2	2.40	0.48
38:A1:1035:G:H2'	38:A1:1036:A:C8	2.48	0.48
40:A4:85:G:OP2	61:AY:113:LYS:NZ	2.35	0.48
41:AD:160:PHE:HA	41:AD:163:LEU:HB3	1.94	0.48
1:BA:59:LEU:HB2	12:BV:79:LEU:HD21	1.96	0.48
6:BH:60:ILE:HD11	6:BH:92:PHE:CD1	2.49	0.48
7:BI:26:LYS:HE3	34:B5:396:G:O6	2.12	0.48
7:BI:106:ALA:HB2	7:BI:165:LEU:HG	1.95	0.48
20:BF:42:LEU:HB3	20:BF:46:TRP:HB2	1.95	0.48
34:B5:647:G:N2	34:B5:648:G:O6	2.47	0.48
38:A1:400:G:H4'	38:A1:401:U:H5''	1.94	0.48
38:A1:589:A:H1'	38:A1:1337:A:H5''	1.95	0.48
38:A1:1596:C:O2'	38:A1:1696:A:N3	2.46	0.48
38:A1:2465:G:H2'	38:A1:2466:G:C8	2.49	0.48
38:A1:2684:C:H2'	38:A1:2685:C:H6	1.79	0.48
38:A1:3000:A:H2'	38:A1:3001:C:C6	2.49	0.48
38:A1:3271:G:C4	42:AE:108:LYS:HE3	2.48	0.48
40:A4:63:G:H22	40:A4:97:A:H2	1.61	0.48
44:AG:108:ARG:O	44:AG:112:GLU:HG3	2.14	0.48
63:Aa:96:LYS:HE2	63:Aa:142:GLY:O	2.14	0.48
80:DC:77:LEU:HB2	80:DC:100:ILE:CG2	2.43	0.48
82:EC:6771:U:O2'	82:EC:6777:C:N3	2.37	0.48
5:BG:57:ASP:HA	5:BG:106:LEU:HA	1.94	0.48
7:BI:3:ILE:O	7:BI:30:GLY:N	2.47	0.48
8:BJ:141:VAL:HG12	8:BJ:143:ILE:H	1.79	0.48
14:BX:68:ILE:HG22	14:BX:70:LYS:HD2	1.95	0.48
24:BR:109:LEU:O	24:BR:109:LEU:HD23	2.13	0.48
29:Bc:27:GLN:NE2	29:Bc:65:ARG:O	2.47	0.48
34:B5:16:G:H2'	34:B5:17:C:C6	2.48	0.48
38:A1:945:C:H2'	38:A1:946:U:C6	2.48	0.48
38:A1:1831:U:O2'	40:A4:114:G:OP1	2.23	0.48
38:A1:2223:A:H2'	38:A1:2224:A:C8	2.48	0.48
38:A1:2592:G:H4'	38:A1:2594:C:C2	2.49	0.48
38:A1:2715:A:O2'	77:Ao:8:ARG:NH2	2.42	0.48
38:A1:3296:A:H2'	38:A1:3297:U:C6	2.48	0.48
42:AE:93:VAL:O	42:AE:95:GLY:N	2.41	0.48
67:Ae:79:VAL:HG13	67:Ae:111:ARG:HG2	1.95	0.48
79:E:148:VAL:HA	79:E:151:VAL:HG12	1.95	0.48
80:DC:110:ASP:HB3	80:DC:537:HIS:HB2	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:733:ILE:HD13	80:DC:743:ILE:HD11	1.95	0.48
81:V:57:THR:HG23	81:V:60:ARG:HD2	1.95	0.48
81:V:176:LEU:HB3	81:V:178:ILE:CD1	2.44	0.48
3:BC:235:LEU:HD23	12:BV:52:THR:HG23	1.96	0.48
9:BL:57:LYS:HG2	9:BL:131:ILE:HD12	1.96	0.48
11:BO:24:ASN:ND2	34:B5:903:U:OP2	2.35	0.48
20:BF:81:ARG:NH2	34:B5:1615:C:OP1	2.46	0.48
21:BK:29:GLN:HB3	21:BK:39:ASN:HB2	1.95	0.48
23:BQ:54:LEU:HD23	23:BQ:109:PHE:HD1	1.78	0.48
36:AB:180:GLU:OE2	38:A1:3002:C:O2'	2.29	0.48
37:AC:321:LYS:NZ	37:AC:324:LEU:HD13	2.29	0.48
38:A1:68:C:O3'	50:AN:177:GLY:HA2	2.14	0.48
38:A1:411:U:H2'	38:A1:412:G:H8	1.79	0.48
38:A1:1643:A:H2'	38:A1:1644:C:C2	2.49	0.48
38:A1:2684:C:H1'	47:AJ:99:THR:HG21	1.95	0.48
38:A1:3160:U:H2'	38:A1:3161:C:C6	2.49	0.48
39:A3:118:A:H5''	41:AD:253:PHE:CZ	2.48	0.48
43:AF:156:ILE:HD12	43:AF:161:VAL:HB	1.95	0.48
80:DC:115:VAL:HG11	80:DC:142:VAL:HG23	1.96	0.48
5:BG:6:SER:OG	5:BG:112:VAL:HG12	2.14	0.47
28:BZ:95:HIS:HE2	34:B5:1529:C:P	2.36	0.47
34:B5:15:U:H2'	34:B5:16:G:O4'	2.13	0.47
38:A1:1242:G:O2'	38:A1:1243:G:OP1	2.25	0.47
38:A1:1351:U:H1'	38:A1:1355:A:H62	1.79	0.47
38:A1:1724:U:H1'	38:A1:1725:C:C6	2.49	0.47
38:A1:2462:A:H2'	38:A1:2463:G:H8	1.78	0.47
41:AD:117:GLU:OE1	41:AD:117:GLU:N	2.34	0.47
46:AI:150:GLU:HA	46:AI:153:ARG:HG2	1.95	0.47
56:AT:39:ILE:HD12	56:AT:102:ARG:HD3	1.96	0.47
60:AX:134:ASP:HA	60:AX:137:ASN:HB2	1.96	0.47
79:E:196:LYS:HB3	79:E:199:GLN:HB3	1.96	0.47
81:V:30:VAL:O	81:V:83:ASN:HB3	2.14	0.47
13:BW:37:PHE:HE1	13:BW:103:ILE:HG13	1.78	0.47
20:BF:92:ARG:NH2	34:B5:1613:U:OP1	2.47	0.47
20:BF:143:ARG:HD2	29:Bc:57:MET:HE2	1.97	0.47
22:BP:56:PHE:CD1	22:BP:78:THR:HG21	2.49	0.47
28:BZ:91:PRO:HG3	28:BZ:94:LYS:HE3	1.96	0.47
31:Bg:26:SER:HB3	31:Bg:29:GLN:HB2	1.94	0.47
34:B5:41:A:O2'	34:B5:437:A:O2'	2.20	0.47
34:B5:1261:G:H2'	34:B5:1262:U:C6	2.49	0.47
34:B5:1592:A:H2'	34:B5:1593:A:H8	1.79	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:180:LEU:HD22	78:Ap:18:TYR:HB3	1.96	0.47
38:A1:169:U:H5	38:A1:253:A:N1	2.12	0.47
38:A1:501:A:H2'	38:A1:502:U:C6	2.49	0.47
38:A1:2465:G:N2	38:A1:2491:A:N1	2.57	0.47
38:A1:2469:G:O2'	38:A1:2470:C:O4'	2.31	0.47
38:A1:2594:C:H2'	38:A1:2595:A:O4'	2.13	0.47
38:A1:2660:G:O3'	38:A1:2749:G:N2	2.47	0.47
39:A3:3:U:H2'	39:A3:4:U:C6	2.50	0.47
40:A4:142:C:H2'	40:A4:143:U:C6	2.50	0.47
46:AI:176:LEU:HD22	46:AI:180:GLU:HG2	1.97	0.47
52:AP:16:SER:HB3	52:AP:149:VAL:HG22	1.96	0.47
55:AS:77:VAL:HG13	55:AS:126:VAL:HG22	1.96	0.47
80:DC:387:PRO:HB3	80:DC:394:PHE:HE1	1.79	0.47
82:EC:6899:C:H2'	82:EC:6900:A:H8	1.79	0.47
4:BE:12:LEU:HD21	4:BE:22:LYS:HG2	1.95	0.47
5:BG:60:GLY:O	34:B5:154:G:N2	2.35	0.47
17:Bb:56:CYS:HB2	17:Bb:63:LEU:HD21	1.97	0.47
20:BF:185:ARG:N	34:B5:1472:C:OP2	2.36	0.47
34:B5:20:G:H5'	34:B5:571:G:C4	2.49	0.47
34:B5:58:U:OP1	34:B5:456:A:O2'	2.32	0.47
38:A1:26:A:N3	38:A1:328:U:O2'	2.44	0.47
38:A1:121:A:C8	38:A1:121:A:OP1	2.67	0.47
38:A1:339:C:OP1	38:A1:1380:G:O2'	2.30	0.47
38:A1:532:A:H2'	38:A1:533:A:H8	1.80	0.47
38:A1:1222:G:O2'	38:A1:1285:G:N2	2.47	0.47
40:A4:39:G:H1'	40:A4:104:A:N6	2.29	0.47
51:AO:106[A]:GLU:HG2	51:AO:147[A]:TRP:CZ2	2.49	0.47
60:AX:90:ALA:O	60:AX:120:LYS:NZ	2.44	0.47
71:Ai:95:ALA:HA	71:Ai:98:ARG:HG2	1.95	0.47
79:E:157:PHE:HE2	79:E:189:PHE:HD2	1.63	0.47
3:BC:54:GLU:OE2	12:BV:11:LEU:C	2.57	0.47
23:BQ:74:HIS:CE1	34:B5:1526:A:H61	2.32	0.47
31:Bg:53:LYS:HG3	31:Bg:54:PHE:H	1.78	0.47
34:B5:894:U:H2'	34:B5:895:G:C8	2.49	0.47
34:B5:1474:G:H2'	34:B5:1475:A:C8	2.49	0.47
35:AA:188:LYS:NZ	38:A1:1793:C:O2	2.46	0.47
36:AB:20:LYS:HD3	38:A1:3139:A:H4'	1.96	0.47
38:A1:273:A:H2'	38:A1:274:G:H8	1.78	0.47
38:A1:1211:U:H2'	38:A1:1212:A:C8	2.49	0.47
38:A1:2662:G:H2'	38:A1:2663:G:C8	2.48	0.47
38:A1:3215:A:H5''	68:Af:2:ALA:HB2	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Ae:23:ASP:OD1	67:Ae:24:ARG:N	2.47	0.47
4:BE:100:ARG:HH12	4:BE:122:LYS:HA	1.78	0.47
4:BE:246:LEU:HD21	4:BE:254:ARG:NH2	2.25	0.47
8:BJ:176:ASN:ND2	34:B5:511:A:OP2	2.48	0.47
11:BO:124:ASP:N	11:BO:124:ASP:OD1	2.45	0.47
31:Bg:199:ILE:HA	31:Bg:215:GLY:HA2	1.95	0.47
34:B5:58:U:O2'	34:B5:451:A:N3	2.45	0.47
34:B5:1782:MA6:H5'	76:An:1:MET:SD	2.55	0.47
38:A1:821:U:H2'	38:A1:822:G:C8	2.49	0.47
38:A1:1486:G:H21	69:Ag:6:THR:HG22	1.80	0.47
38:A1:1572:U:O2'	38:A1:1573:G:O5'	2.33	0.47
38:A1:2383:C:OP2	51:AO:85[A]:ARG:NH2	2.37	0.47
38:A1:3056:U:O2	66:Ad:28:ARG:NH2	2.47	0.47
38:A1:3294:A:H2'	38:A1:3295:A:O4'	2.15	0.47
39:A3:94:C:H2'	39:A3:95:A:C8	2.50	0.47
45:AH:43:VAL:HG12	45:AH:57:VAL:HG22	1.96	0.47
46:AI:170:LYS:HA	46:AI:177:ASP:HA	1.96	0.47
58:AV:10:LYS:HB2	58:AV:125:LEU:HD21	1.95	0.47
62:AZ:42:LEU:HD23	62:AZ:74:VAL:HG22	1.97	0.47
80:DC:32:LYS:NZ	80:DC:105:SER:O	2.34	0.47
81:V:22:TYR:CG	81:V:88:PHE:HB3	2.50	0.47
3:BC:91:ARG:NH1	34:B5:1147:A:H5''	2.29	0.47
4:BE:148:ARG:HD2	34:B5:125:U:H5'	1.97	0.47
30:Bd:22:ARG:NE	30:Bd:36:LEU:O	2.47	0.47
34:B5:580:A:O2'	34:B5:582:U:OP1	2.27	0.47
34:B5:1508:U:H2'	34:B5:1509:C:C6	2.49	0.47
38:A1:8:C:H2'	38:A1:9:U:C6	2.48	0.47
38:A1:165:A:H62	38:A1:257:U:H3	1.63	0.47
38:A1:1084:A:H2'	38:A1:1085:A:C8	2.49	0.47
38:A1:1245:A:N7	38:A1:1271:A:O2'	2.44	0.47
38:A1:2723:U:H2'	38:A1:2724:OMU:H6	1.97	0.47
43:AF:48:ASN:ND2	43:AF:182:ASP:OD2	2.47	0.47
53:AQ:42:ALA:HB2	53:AQ:133:LYS:HB3	1.97	0.47
54:AR:171:ASP:OD1	54:AR:172:ARG:N	2.47	0.47
81:V:30:VAL:HG23	81:V:33:VAL:CG2	2.44	0.47
2:BB:202:LYS:NZ	34:B5:1056:U:O2	2.45	0.47
4:BE:201:HIS:CE1	34:B5:799:A:H4'	2.50	0.47
6:BH:14:THR:OG1	6:BH:15:GLU:N	2.47	0.47
8:BJ:62:ARG:O	8:BJ:69:ARG:NH1	2.47	0.47
8:BJ:90:LYS:HB2	8:BJ:95:TYR:CG	2.49	0.47
10:BN:11:ILE:HG13	10:BN:12:SER:N	2.27	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:32:GLU:HG3	19:BD:57:ASP:HB3	1.96	0.47
21:BK:10:LYS:NZ	21:BK:36:ASP:HB3	2.29	0.47
25:BS:133:VAL:HG12	34:B5:1545:A:H5''	1.95	0.47
34:B5:225:A:C8	34:B5:226:A:N7	2.82	0.47
34:B5:752:A:H2'	34:B5:753:A:H8	1.78	0.47
34:B5:1486:G:N2	34:B5:1522:U:O4	2.47	0.47
34:B5:1641:C:H2'	34:B5:1642:G:C8	2.50	0.47
34:B5:1770:U:H2'	34:B5:1771:U:C6	2.50	0.47
35:AA:69:TYR:OH	38:A1:2557:A:OP1	2.26	0.47
36:AB:173:GLN:HG2	36:AB:175:LYS:H	1.79	0.47
36:AB:291:GLU:HG2	36:AB:302:LYS:HZ3	1.80	0.47
38:A1:148:G:OP2	50:AN:4:TYR:OH	2.20	0.47
38:A1:307:A:H2'	38:A1:308:A:H8	1.79	0.47
38:A1:1037:C:H2'	38:A1:1038:C:H6	1.79	0.47
38:A1:1046:A:H2'	38:A1:1049:C:C5	2.49	0.47
39:A3:71:G:H2'	39:A3:72:A:C8	2.50	0.47
40:A4:97:A:OP1	70:Ah:63:ARG:NE	2.47	0.47
54:AR:175:GLN:HA	54:AR:179:GLU:HB2	1.96	0.47
63:Aa:28:HIS:CD2	63:Aa:32:ARG:HG2	2.50	0.47
79:E:53:LEU:HD23	79:E:53:LEU:H	1.80	0.47
80:DC:99:LEU:H	80:DC:99:LEU:HD23	1.80	0.47
80:DC:501:LEU:O	80:DC:505:VAL:HG22	2.15	0.47
80:DC:587:TYR:HB3	80:DC:689:LEU:HG	1.96	0.47
80:DC:650:THR:HG22	80:DC:690:ASP:HA	1.96	0.47
80:DC:707:PRO:O	80:DC:711:ARG:NE	2.45	0.47
82:EC:6853:G:O6	82:EC:6876:A:N1	2.48	0.47
6:BH:104:ARG:HG3	34:B5:803:A:C4	2.50	0.47
25:BS:106:GLU:HA	25:BS:109:LEU:HG	1.97	0.47
26:BT:25:GLN:HE22	26:BT:27:LYS:HD3	1.80	0.47
26:BT:33:TYR:O	26:BT:36:ILE:HG12	2.15	0.47
31:Bg:216:LYS:HA	31:Bg:239:GLU:OE1	2.15	0.47
34:B5:340:U:H2'	34:B5:341:A:C8	2.50	0.47
34:B5:847:A:H2'	34:B5:848:C:C6	2.50	0.47
34:B5:925:G:H2'	34:B5:926:A:H8	1.79	0.47
34:B5:1694:A:H61	34:B5:1707:A:H62	1.63	0.47
38:A1:229:G:H5''	61:AY:4:GLN:HB2	1.96	0.47
38:A1:341:G:O2'	40:A4:22:U:O4	2.31	0.47
38:A1:1128:U:OP1	46:AI:4:ARG:NH1	2.37	0.47
38:A1:1615:C:H2'	38:A1:1616:U:C6	2.50	0.47
38:A1:1682:U:O2	57:AU:82:LYS:HD2	2.14	0.47
38:A1:2947:G:OP1	38:A1:2982:A:N6	2.45	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:86:VAL:HG23	80:DC:87:LYS:HD3	1.97	0.47
5:BG:50:PHE:CB	5:BG:111:LEU:HD12	2.44	0.47
17:Bb:55:THR:HA	17:Bb:63:LEU:HD13	1.97	0.47
21:BK:28:ASN:HD21	34:B5:1217:A:H2	1.63	0.47
27:BU:63:LEU:HD22	30:Bd:34:TYR:CE1	2.50	0.47
31:Bg:240:VAL:HA	31:Bg:256:THR:HA	1.97	0.47
34:B5:1079:U:H2'	34:B5:1080:U:C6	2.50	0.47
36:AB:10:ARG:NH2	36:AB:263:SER:O	2.47	0.47
37:AC:81:GLY:O	38:A1:356:C:O2'	2.17	0.47
38:A1:2219:A:H2'	38:A1:2220:A2M:H8	1.96	0.47
38:A1:2434:U:H5	38:A1:2594:C:OP2	1.97	0.47
54:AR:98:ARG:HD2	54:AR:133:LYS:O	2.14	0.47
69:Ag:67:LYS:O	69:Ag:71:THR:HG22	2.15	0.47
80:DC:638:PRO:HG3	80:DC:671:THR:HB	1.97	0.47
82:EC:6886:A:H2'	82:EC:6887:G:H8	1.80	0.47
82:EC:6889:A:H4'	82:EC:6890:A:OP1	2.14	0.47
1:BA:198:MET:HG2	1:BA:200:ASP:H	1.79	0.47
4:BE:221:ARG:HG2	4:BE:223:ASN:H	1.80	0.47
7:BI:10:LYS:NZ	34:B5:322:G:O2'	2.48	0.47
14:BX:70:LYS:HG2	14:BX:93:LEU:HD22	1.95	0.47
20:BF:205:SER:HB3	20:BF:207:THR:HG22	1.97	0.47
33:BM:46:ARG:HB3	34:B5:1229:G:C6	2.50	0.47
38:A1:249:U:H1'	38:A1:251:G:OP1	2.15	0.47
38:A1:435:C:H2'	38:A1:436:A:C8	2.50	0.47
38:A1:975:C:H2'	38:A1:976:U:C6	2.50	0.47
38:A1:2152:A:H2'	38:A1:2153:U:H6	1.80	0.47
38:A1:2407:C:H2'	38:A1:2408:U:C6	2.50	0.47
38:A1:3017:A:N1	38:A1:3037:U:H5	2.13	0.47
38:A1:3273:A:H2'	38:A1:3274:A:C8	2.49	0.47
39:A3:6:C:O2'	41:AD:72:ASP:OD2	2.29	0.47
41:AD:182:GLY:HA2	41:AD:194:LEU:HD23	1.96	0.47
43:AF:47:ARG:NH1	43:AF:177:GLY:O	2.46	0.47
46:AI:52:LEU:HB3	46:AI:136:PHE:HB2	1.96	0.47
48:AL:185:LYS:O	48:AL:189:GLU:HG2	2.15	0.47
54:AR:170:ARG:NH1	54:AR:174:ALA:HB3	2.30	0.47
66:Ad:13:THR:OG1	66:Ad:72:ARG:NH1	2.37	0.47
80:DC:139:THR:HA	80:DC:142:VAL:HG12	1.96	0.47
81:V:122:ARG:NH1	81:V:124:VAL:O	2.47	0.47
12:BV:17:CYS:HB2	12:BV:56:SER:HB3	1.97	0.46
22:BP:22:LEU:HD12	22:BP:25:LEU:HD21	1.97	0.46
26:BT:43:ASN:ND2	34:B5:1477:G:OP1	2.48	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Bd:38:ILE:HG22	30:Bd:39:CYS:O	2.15	0.46
34:B5:1524:A:N3	34:B5:1590:G:O2'	2.39	0.46
34:B5:1575:7MG:H2'	34:B5:1576:A:OP2	2.14	0.46
38:A1:93:C:OP2	38:A1:2764:C:O2'	2.27	0.46
38:A1:1828:A:H2'	38:A1:1829:G:C8	2.50	0.46
38:A1:2344:U:H2'	38:A1:2345:A:H8	1.80	0.46
38:A1:2506:U:H2'	38:A1:2507:C:C6	2.50	0.46
38:A1:2801:A:O2'	38:A1:2802:A:H2'	2.14	0.46
45:AH:79:ILE:HA	45:AH:82:VAL:HG12	1.96	0.46
59:AW:6:ASP:OD2	59:AW:32:GLN:N	2.34	0.46
62:AZ:42:LEU:HD22	62:AZ:101:PHE:CE2	2.50	0.46
66:Ad:79:ARG:HA	66:Ad:89:LEU:HD23	1.95	0.46
80:DC:671:THR:HG22	80:DC:681:MET:HG3	1.97	0.46
81:V:60:ARG:HG2	81:V:80:VAL:HG21	1.96	0.46
6:BH:58:LEU:HD12	6:BH:90:VAL:HG12	1.97	0.46
13:BW:26:LEU:HB2	17:Bb:7:LEU:HD13	1.96	0.46
14:BX:42:PRO:HB3	14:BX:83:VAL:HG11	1.97	0.46
19:BD:31:GLU:OE1	19:BD:31:GLU:N	2.34	0.46
34:B5:319:U:H4'	34:B5:323:A:C8	2.50	0.46
34:B5:960:U:H2'	34:B5:961:U:C6	2.50	0.46
34:B5:1732:A:H2'	34:B5:1733:C:C6	2.49	0.46
36:AB:306:THR:HG21	36:AB:316:GLU:HG2	1.97	0.46
38:A1:1021:G:N2	38:A1:1032:C:OP2	2.48	0.46
38:A1:1336:U:H2'	38:A1:1337:A:C8	2.50	0.46
38:A1:2439:A:H2'	38:A1:2440:G:C8	2.50	0.46
38:A1:2565:U:H2'	38:A1:2566:C:C6	2.50	0.46
38:A1:2961:G:H2'	38:A1:2962:U:C6	2.50	0.46
38:A1:3121:U:H1'	38:A1:3122:A:H5''	1.97	0.46
38:A1:3295:A:H2'	38:A1:3296:A:H8	1.81	0.46
45:AH:20:ILE:HG22	49:AM:7:VAL:HG22	1.96	0.46
70:Ah:41:LEU:O	70:Ah:44:ILE:HG22	2.16	0.46
79:E:113:SER:OG	79:E:115:VAL:HG22	2.16	0.46
80:DC:397:PHE:HE1	80:DC:453:ILE:HB	1.80	0.46
80:DC:412:ARG:NH1	80:DC:472:SER:O	2.48	0.46
4:BE:151:ASP:CG	5:BG:215:ARG:HH12	2.21	0.46
17:Bb:67:THR:OG1	17:Bb:70:LYS:O	2.34	0.46
20:BF:109:LYS:HE2	20:BF:109:LYS:HB2	1.67	0.46
25:BS:39:GLY:N	34:B5:1566:U:H5''	2.30	0.46
33:BM:126:TRP:CE3	33:BM:133:LEU:HD22	2.51	0.46
34:B5:78:A:H2'	34:B5:79:C:C6	2.51	0.46
34:B5:538:A:N3	34:B5:538:A:H2'	2.29	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1087:A:H2'	34:B5:1088:A:C8	2.50	0.46
34:B5:1202:A:N6	34:B5:1456:C:H3'	2.29	0.46
34:B5:1262:U:H2'	34:B5:1263:G:C8	2.50	0.46
38:A1:176:G:O2'	38:A1:177:U:O5'	2.33	0.46
38:A1:428:A:H2'	38:A1:429:U:C6	2.50	0.46
38:A1:1119:C:H2'	38:A1:1120:A:C8	2.50	0.46
38:A1:3186:A:N3	45:AH:44:THR:OG1	2.43	0.46
39:A3:96:U:H2'	39:A3:97:A:H8	1.79	0.46
41:AD:141:PRO:HB2	41:AD:172:TYR:HB2	1.97	0.46
63:Aa:91:LEU:HD11	63:Aa:119:PRO:HG3	1.98	0.46
65:Ac:44:ILE:HG22	65:Ac:48:THR:HG21	1.98	0.46
34:B5:751:G:H2'	34:B5:752:A:C8	2.48	0.46
34:B5:979:A:H4'	34:B5:1786:G:N2	2.30	0.46
35:AA:14:SER:OG	38:A1:911:C:OP1	2.33	0.46
38:A1:1497:C:H2'	38:A1:1498:A:H8	1.80	0.46
38:A1:1597:C:H2'	38:A1:1598:G:C8	2.51	0.46
38:A1:2352:A:H5''	52:AP:83:TRP:O	2.15	0.46
79:E:204:LEU:HD23	79:E:217:TYR:HD2	1.81	0.46
80:DC:297:PRO:HA	80:DC:300:LEU:HD12	1.98	0.46
81:V:120:TRP:CB	81:V:157:LYS:HD3	2.46	0.46
1:BA:199:PRO:HG2	24:BR:91:LEU:HD21	1.97	0.46
16:Ba:33:ASP:OD1	16:Ba:33:ASP:N	2.47	0.46
19:BD:76:ARG:HH22	21:BK:23:ALA:N	2.11	0.46
27:BU:96:PRO:HG2	27:BU:99:ILE:HG12	1.98	0.46
37:AC:119:ARG:NH2	38:A1:696:C:OP2	2.47	0.46
38:A1:264:G:OP1	71:Ai:34:SER:HB2	2.16	0.46
38:A1:1230:G:H4'	81:V:34:SER:HA	1.97	0.46
46:AI:66:GLU:OE2	46:AI:69:ARG:NH2	2.40	0.46
62:AZ:27:LYS:HB2	62:AZ:42:LEU:HD12	1.96	0.46
82:EC:6838:C:H2'	82:EC:6839:U:O4'	2.16	0.46
2:BB:135:LEU:HB3	2:BB:217:LEU:HD23	1.96	0.46
16:Ba:18:VAL:HG23	16:Ba:19:LYS:N	2.28	0.46
21:BK:55:VAL:HG22	21:BK:68:LEU:HA	1.98	0.46
25:BS:28:ILE:HA	25:BS:58:ALA:HB2	1.97	0.46
34:B5:492:A:H2'	34:B5:495:C:H5'	1.97	0.46
38:A1:196:G:N1	38:A1:199:A:OP2	2.47	0.46
38:A1:1470:U:H2'	38:A1:1471:U:C6	2.50	0.46
38:A1:2218:G:H2'	38:A1:2219:A:H8	1.81	0.46
38:A1:2455:U:H3	38:A1:2483:G:HO2'	1.63	0.46
38:A1:2676:A:H5'	38:A1:2677:G:C8	2.50	0.46
40:A4:58:G:O6	72:Aj:63:ARG:NH1	2.48	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AF:83:LEU:HD11	43:AF:116:PHE:HB3	1.97	0.46
59:AW:4:GLU:HB2	59:AW:13:ILE:HB	1.98	0.46
62:AZ:27:LYS:HB2	62:AZ:42:LEU:HB2	1.96	0.46
73:AK:42:LYS:HG2	73:AK:55:VAL:HG22	1.98	0.46
80:DC:43:ALA:O	80:DC:77:LEU:HD12	2.16	0.46
80:DC:696:ASP:O	80:DC:700:ARG:HG2	2.16	0.46
80:DC:705:ILE:HA	80:DC:708:THR:HG22	1.98	0.46
5:BG:132:ARG:NH1	34:B5:150:U:O4'	2.49	0.46
8:BJ:92:LYS:HB2	8:BJ:95:TYR:HD2	1.81	0.46
10:BN:90:TYR:HA	10:BN:93:LYS:HG2	1.98	0.46
15:BY:29:HIS:ND1	15:BY:32:ARG:O	2.48	0.46
19:BD:61:GLU:H	19:BD:64:ARG:HB2	1.80	0.46
23:BQ:7:VAL:HG23	23:BQ:22:VAL:HB	1.98	0.46
31:Bg:210:LEU:HD11	31:Bg:222:LEU:HD12	1.98	0.46
34:B5:17:C:H2'	34:B5:18:C:H6	1.81	0.46
34:B5:71:A:H2'	34:B5:72:A:H4'	1.97	0.46
34:B5:333:A:H2'	34:B5:334:G:C8	2.50	0.46
34:B5:980:G:H4'	34:B5:1776:A:H4'	1.96	0.46
34:B5:1272:U:O4	34:B5:1431:C:O2'	2.24	0.46
38:A1:576:C:OP1	43:AF:241:LYS:NZ	2.47	0.46
38:A1:985:U:H2'	38:A1:986:U:H6	1.81	0.46
38:A1:1201:C:H42	38:A1:2857:C:H5''	1.80	0.46
38:A1:1495:U:H5	38:A1:1835:A:N1	2.14	0.46
38:A1:1560:G:O2'	38:A1:1561:G:O4'	2.31	0.46
38:A1:1593:A:N3	38:A1:1615:C:O2'	2.47	0.46
38:A1:1749:A:H5''	38:A1:1751:G:N7	2.31	0.46
38:A1:2674:A:H5''	47:AJ:105:GLY:HA3	1.98	0.46
38:A1:3349:C:H2'	38:A1:3350:C:C6	2.51	0.46
49:AM:23:ILE:O	49:AM:30:GLY:N	2.40	0.46
55:AS:5:LYS:NZ	55:AS:32:SER:O	2.48	0.46
61:AY:119:ILE:HG23	61:AY:124:GLY:HA3	1.98	0.46
80:DC:7:ASP:OD1	80:DC:7:ASP:N	2.49	0.46
80:DC:82:SER:OG	80:DC:84:GLU:HG2	2.15	0.46
80:DC:293:LYS:HA	80:DC:296:ILE:HG12	1.96	0.46
80:DC:694:HIS:HE1	82:EC:6907:G:H4'	1.80	0.46
1:BA:41:ARG:NH2	24:BR:105:GLN:HE22	2.14	0.46
7:BI:37:LYS:C	7:BI:59:ARG:HA	2.40	0.46
13:BW:107:SER:HB2	34:B5:802:G:H21	1.81	0.46
19:BD:40:ARG:NH1	19:BD:49:ILE:HG13	2.31	0.46
22:BP:94:VAL:N	22:BP:104:GLN:HE22	2.13	0.46
25:BS:29:VAL:HG13	25:BS:43:SER:HB3	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BT:64:HIS:HE2	34:B5:1480:G:P	2.39	0.46
27:BU:23:ARG:NH2	34:B5:1347:U:OP1	2.41	0.46
31:Bg:149:ASP:OD1	31:Bg:150:TRP:N	2.48	0.46
34:B5:328:A:H2'	34:B5:329:G:C8	2.51	0.46
34:B5:1081:A:H2	34:B5:1082:C:H42	1.62	0.46
35:AA:65:ASP:HB3	35:AA:68:LYS:O	2.16	0.46
38:A1:13:A:H4'	60:AX:39:LYS:HD3	1.97	0.46
38:A1:1914:G:O2'	54:AR:82:LYS:O	2.30	0.46
38:A1:2254:U:H2'	38:A1:2261:G:N2	2.31	0.46
38:A1:2662:G:H2'	38:A1:2663:G:H8	1.80	0.46
38:A1:2842:U:OP1	38:A1:2844:C:N4	2.46	0.46
38:A1:3193:C:H2'	38:A1:3194:C:C6	2.50	0.46
42:AE:148:GLU:OE2	42:AE:151:LYS:HD2	2.16	0.46
51:AO:50[A]:ASN:HA	51:AO:53[A]:LYS:HG2	1.96	0.46
77:Ao:26:THR:HA	77:Ao:93:LEU:HD21	1.97	0.46
80:DC:270:GLU:HG3	80:DC:275:MET:HB3	1.97	0.46
8:BJ:135:ALA:HA	8:BJ:140:ILE:HA	1.97	0.46
14:BX:47:SER:OG	34:B5:600:U:H1'	2.16	0.46
25:BS:32:LEU:HD22	25:BS:73:MET:HE1	1.97	0.46
34:B5:1524:A:H2'	34:B5:1525:A:C8	2.50	0.46
34:B5:1545:A:N6	34:B5:1567:U:O4	2.49	0.46
34:B5:1624:C:H2'	34:B5:1625:C:H6	1.80	0.46
35:AA:112:ILE:HG13	78:Ap:79:VAL:HG22	1.98	0.46
35:AA:145:LYS:HD2	35:AA:157:VAL:HG12	1.98	0.46
38:A1:175:C:N3	38:A1:242:C:N4	2.64	0.46
38:A1:1207:G:OP1	75:Am:119:ASN:ND2	2.49	0.46
38:A1:2953:U:H2'	38:A1:2954:U:H2'	1.97	0.46
43:AF:169:ILE:HD12	43:AF:181:ILE:HD13	1.98	0.46
47:AJ:36:VAL:HG21	47:AJ:110:ILE:HD12	1.98	0.46
80:DC:576:LEU:HA	80:DC:586:ILE:O	2.16	0.46
80:DC:638:PRO:HA	80:DC:668:GLN:NE2	2.30	0.46
2:BB:155:TYR:OH	34:B5:932:U:OP2	2.24	0.46
8:BJ:85:VAL:HG11	8:BJ:104:PHE:CE1	2.50	0.46
25:BS:49:LYS:HG3	25:BS:81:ILE:HD11	1.98	0.46
34:B5:689:G:H2'	34:B5:690:G:C8	2.51	0.46
34:B5:1126:OMG:OP2	76:An:18:ARG:NH2	2.40	0.46
34:B5:1450:U:H2'	34:B5:1451:C:H6	1.80	0.46
34:B5:1685:G:H2'	34:B5:1686:C:O4'	2.15	0.46
34:B5:1772:C:H3'	76:An:2:ARG:HH21	1.80	0.46
36:AB:57:VAL:HG22	36:AB:73:VAL:HG22	1.98	0.46
37:AC:25:VAL:HA	37:AC:276:LEU:HD21	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:AC:141:ARG:CZ	37:AC:180:LYS:HD3	2.46	0.46
38:A1:221:A:O2'	38:A1:223:U:OP2	2.26	0.46
38:A1:1015:U:C2	38:A1:1035:G:O6	2.69	0.46
38:A1:2305:G:OP2	38:A1:2305:G:N2	2.34	0.46
38:A1:2448:G:H2'	38:A1:2449:A:C8	2.51	0.46
38:A1:3337:G:H2'	38:A1:3338:C:C6	2.51	0.46
43:AF:120:THR:HB	56:AT:132:PRO:HB2	1.97	0.46
47:AJ:87:LYS:O	47:AJ:88:GLU:HG3	2.16	0.46
50:AN:45:PRO:O	50:AN:49:ARG:HG3	2.16	0.46
52:AP:33:ALA:HB1	52:AP:117:ILE:HG12	1.98	0.46
80:DC:378:LEU:O	80:DC:470:THR:HA	2.16	0.46
82:EC:6788:C:O5'	82:EC:6805:C:N4	2.49	0.46
2:BB:150:VAL:H	34:B5:1067:C:H5''	1.81	0.45
4:BE:141:THR:OG1	4:BE:143:ASP:OD1	2.25	0.45
4:BE:163:ASP:C	4:BE:165:ALA:H	2.24	0.45
27:BU:37:VAL:HB	27:BU:109:GLU:OE2	2.16	0.45
34:B5:1209:C:N3	34:B5:1455:G:N2	2.63	0.45
34:B5:1215:C:H2'	34:B5:1216:C:C6	2.51	0.45
34:B5:1552:U:H2'	34:B5:1553:G:C8	2.51	0.45
34:B5:1624:C:H2'	34:B5:1625:C:C6	2.52	0.45
36:AB:122:TRP:CE2	36:AB:127:LYS:HE3	2.51	0.45
37:AC:286:VAL:HG21	53:AQ:28:LEU:HB2	1.97	0.45
38:A1:190:U:H2'	61:AY:60:ARG:HH22	1.81	0.45
38:A1:314:U:H2'	38:A1:315:C:C6	2.51	0.45
38:A1:1696:A:H2'	38:A1:1697:A:C8	2.52	0.45
38:A1:1722:U:O4'	54:AR:96:ILE:HG12	2.16	0.45
38:A1:1791:C:H2'	38:A1:1792:C:C6	2.51	0.45
38:A1:2148:U:H2'	38:A1:2149:A:C8	2.52	0.45
38:A1:2684:C:H2'	38:A1:2685:C:C6	2.51	0.45
38:A1:2767:U:H2'	38:A1:2768:U:C6	2.51	0.45
38:A1:2986:U:H2'	38:A1:2987:A:H8	1.80	0.45
45:AH:93:VAL:HG22	75:Am:82:LEU:HB3	1.98	0.45
63:Aa:96:LYS:C	63:Aa:98:THR:H	2.24	0.45
70:Ah:86:ARG:O	70:Ah:90:ARG:HG2	2.15	0.45
80:DC:9:MET:SD	80:DC:12:LEU:HD12	2.56	0.45
81:V:75:LYS:HD2	81:V:191:TYR:CD1	2.51	0.45
2:BB:150:VAL:HG23	34:B5:1067:C:H5''	1.97	0.45
3:BC:49:LYS:HE2	3:BC:246:GLU:HG3	1.99	0.45
22:BP:39:ALA:N	34:B5:1549:C:OP2	2.50	0.45
23:BQ:104:GLU:HA	23:BQ:107:LYS:HE2	1.97	0.45
28:BZ:95:HIS:NE2	34:B5:1529:C:OP1	2.48	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BM:62:LEU:HD13	33:BM:90:LYS:HE3	1.98	0.45
34:B5:779:U:O2'	34:B5:780:A:H5'	2.16	0.45
34:B5:1163:A:N3	34:B5:1613:U:O2'	2.44	0.45
34:B5:1548:G:H2'	34:B5:1549:C:C6	2.51	0.45
38:A1:2881:C:H2'	38:A1:2882:U:C6	2.52	0.45
46:AI:36:LEU:HD11	46:AI:69:ARG:HD2	1.98	0.45
53:AQ:83:VAL:O	53:AQ:103:ALA:HA	2.16	0.45
57:AU:41:ILE:HG21	57:AU:54:VAL:HG11	1.99	0.45
62:AZ:9:LYS:HB3	62:AZ:25:ILE:HD12	1.98	0.45
80:DC:201:GLN:NE2	80:DC:203:TYR:OH	2.49	0.45
7:BI:104:ILE:HG13	7:BI:105:ASP:N	2.27	0.45
11:BO:16:VAL:HG12	11:BO:18:ARG:HG3	1.98	0.45
33:BM:61:VAL:HG22	33:BM:121:VAL:O	2.16	0.45
34:B5:144:U:O2'	34:B5:145:A:H8	2.00	0.45
34:B5:800:U:H2'	34:B5:801:G:C8	2.48	0.45
36:AB:266:ARG:NH2	38:A1:2392:C:H1'	2.31	0.45
38:A1:1222:G:OP1	81:V:58:MET:HE2	2.16	0.45
38:A1:1721:U:O2'	38:A1:1723:A:N7	2.43	0.45
38:A1:2680:A:C2	47:AJ:24:GLY:HA2	2.52	0.45
38:A1:2848:G:OP1	75:Am:100:TYR:OH	2.26	0.45
38:A1:3015:G:H2'	38:A1:3016:A:H8	1.81	0.45
38:A1:3017:A:O2'	58:AV:8:GLY:HA2	2.15	0.45
48:AL:19:GLN:HA	48:AL:22:VAL:HG23	1.98	0.45
82:EC:6868:C:N4	82:EC:6869:C:H41	2.13	0.45
2:BB:70:LEU:HB2	2:BB:82:ARG:O	2.17	0.45
3:BC:111:VAL:HG13	3:BC:191:ALA:HA	1.99	0.45
15:BY:12:VAL:N	34:B5:783:G:N7	2.62	0.45
22:BP:56:PHE:HE2	22:BP:89:MET:SD	2.39	0.45
22:BP:75:PRO:HA	22:BP:93:VAL:HG12	1.97	0.45
23:BQ:123:ARG:HD3	34:B5:1337:A:H4'	1.99	0.45
24:BR:58:MET:O	24:BR:62:GLN:HG2	2.17	0.45
25:BS:4:VAL:HG23	28:BZ:78:ILE:HG22	1.99	0.45
25:BS:72:ILE:HG12	25:BS:79:TYR:CD2	2.51	0.45
34:B5:156:A:H2'	34:B5:157:A:O4'	2.16	0.45
34:B5:343:C:H2'	34:B5:344:A:C8	2.51	0.45
34:B5:447:U:H2'	34:B5:448:C:O4'	2.16	0.45
34:B5:1517:U:OP2	34:B5:1518:C:N4	2.35	0.45
34:B5:1592:A:H2'	34:B5:1593:A:C8	2.52	0.45
35:AA:52:SER:HB3	35:AA:191:LEU:HD12	1.98	0.45
38:A1:1188:U:OP1	38:A1:1210:U:O2'	2.15	0.45
38:A1:1284:C:H2'	38:A1:1285:G:C8	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1378:U:H2'	38:A1:1379:G:H8	1.81	0.45
38:A1:2552:C:OP1	69:Ag:102:LYS:NZ	2.39	0.45
38:A1:2724:OMU:OP2	38:A1:2726:C:N4	2.49	0.45
38:A1:2935:U:O4	58:AV:44:SER:OG	2.33	0.45
38:A1:3013:U:H2'	38:A1:3014:U:C6	2.51	0.45
41:AD:119:TYR:OH	41:AD:139:PRO:O	2.31	0.45
42:AE:80:ASN:HB3	42:AE:83:TYR:HD1	1.79	0.45
53:AQ:158:HIS:H	53:AQ:186:VAL:CG1	2.30	0.45
79:E:96:ASN:ND2	79:E:98:LYS:HE3	2.31	0.45
80:DC:3:ALA:HB2	80:DC:45:ILE:HG23	1.97	0.45
80:DC:71:LYS:HD3	80:DC:71:LYS:HA	1.74	0.45
80:DC:83:ASP:O	80:DC:87:LYS:NZ	2.35	0.45
80:DC:287:ALA:HB2	80:DC:292:LYS:HE2	1.98	0.45
2:BB:153:HIS:NE2	34:B5:1045:C:OP1	2.45	0.45
4:BE:11:ARG:NH1	4:BE:20:LEU:HB3	2.32	0.45
6:BH:67:LEU:HD12	6:BH:71:HIS:NE2	2.31	0.45
12:BV:36:VAL:HB	12:BV:51:VAL:HG23	1.98	0.45
19:BD:40:ARG:HB2	19:BD:47:GLU:HG2	1.98	0.45
23:BQ:47:LYS:HD2	23:BQ:47:LYS:HA	1.84	0.45
25:BS:101:LEU:HD23	25:BS:101:LEU:H	1.81	0.45
33:BM:38:HIS:CD2	33:BM:128:ALA:HB2	2.51	0.45
34:B5:103:A:H4'	34:B5:105:A:C8	2.52	0.45
34:B5:607:G:H5'	34:B5:613:G:N2	2.32	0.45
34:B5:979:A:N3	34:B5:1775:U:O2'	2.49	0.45
34:B5:1234:A:H3'	34:B5:1245:G:C8	2.51	0.45
38:A1:286:U:O2'	50:AN:179:LYS:O	2.34	0.45
38:A1:396:A:O2'	38:A1:399:A:OP1	2.27	0.45
38:A1:2205:U:H2'	38:A1:2206:G:C8	2.52	0.45
46:AI:38:LYS:HD3	46:AI:83:ASP:HB2	1.98	0.45
52:AP:67:ILE:HD12	52:AP:82:ARG:CZ	2.46	0.45
1:BA:49:ASN:HB3	1:BA:52:LYS:HB2	1.97	0.45
6:BH:31:SER:OG	6:BH:32:PRO:HD3	2.17	0.45
7:BI:62:THR:HG22	7:BI:77:ARG:HG2	1.99	0.45
8:BJ:107:ARG:NH2	8:BJ:153:GLU:OE2	2.48	0.45
23:BQ:13:LYS:HG2	23:BQ:76:SER:HA	1.99	0.45
23:BQ:20:ALA:HB2	23:BQ:84:ALA:HB1	1.98	0.45
31:Bg:131:ILE:HG12	31:Bg:151:VAL:HG11	1.98	0.45
34:B5:565:C:O2'	34:B5:577:G:N2	2.39	0.45
38:A1:712:G:H5'	48:AL:174:ARG:NH1	2.32	0.45
38:A1:1234:G:H2'	38:A1:1235:U:C5	2.51	0.45
38:A1:1236:G:H22	38:A1:1244:A:P	2.40	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1666:G:H2'	38:A1:1667:A:H8	1.82	0.45
39:A3:1:G:H2'	39:A3:2:G:H8	1.81	0.45
39:A3:4:U:H2'	39:A3:5:G:C8	2.52	0.45
53:AQ:28:LEU:HA	53:AQ:31:LYS:HG2	1.99	0.45
55:AS:17:GLU:HG2	55:AS:18:SER:N	2.32	0.45
82:EC:6795:U:H2'	82:EC:6796:C:H6	1.81	0.45
6:BH:126:LEU:HG	6:BH:173:TYR:CE1	2.52	0.45
14:BX:50:LYS:HE3	34:B5:435:C:H5''	1.98	0.45
20:BF:100:ASN:ND2	20:BF:180:ARG:HD3	2.31	0.45
23:BQ:52:LEU:HD13	23:BQ:60:PHE:CE2	2.51	0.45
28:BZ:42:LEU:HD23	28:BZ:46:LYS:HB3	1.99	0.45
31:Bg:260:ILE:O	31:Bg:274:LEU:N	2.46	0.45
34:B5:107:C:H2'	34:B5:108:A:H8	1.82	0.45
34:B5:328:A:H2'	34:B5:329:G:H8	1.80	0.45
34:B5:512:A:H2'	34:B5:513:U:C6	2.51	0.45
34:B5:918:U:H2'	34:B5:919:A:C8	2.52	0.45
34:B5:1548:G:H2'	34:B5:1549:C:H6	1.82	0.45
37:AC:138:ARG:NH1	38:A1:1383:G:O2'	2.50	0.45
38:A1:433:A:OP2	68:Af:57:LYS:NZ	2.44	0.45
38:A1:2445:A:H4'	71:Ai:62:ARG:HD2	1.97	0.45
60:AX:70:GLU:H	60:AX:70:GLU:CD	2.24	0.45
71:Ai:34:SER:H	71:Ai:37:THR:HG22	1.82	0.45
80:DC:8:GLN:O	80:DC:12:LEU:HG	2.16	0.45
80:DC:138:GLN:HA	80:DC:141:THR:HG22	1.97	0.45
80:DC:676:ILE:HG21	80:DC:724:ILE:HD11	1.99	0.45
3:BC:227:PRO:HA	3:BC:230:TRP:CE2	2.52	0.45
5:BG:39:GLU:OE1	5:BG:39:GLU:N	2.49	0.45
20:BF:92:ARG:NH2	20:BF:169:ASN:OD1	2.34	0.45
27:BU:22:ILE:HD11	27:BU:116:VAL:HG12	1.99	0.45
31:Bg:274:LEU:HD22	31:Bg:313:TRP:CZ3	2.51	0.45
34:B5:645:C:H2'	34:B5:646:C:H6	1.81	0.45
34:B5:1160:A:H2'	34:B5:1161:C:C6	2.51	0.45
34:B5:1161:C:H1'	34:B5:1619:C:H42	1.82	0.45
34:B5:1253:U:H2'	34:B5:1254:U:H6	1.81	0.45
34:B5:1292:G:H2'	34:B5:1293:U:C6	2.52	0.45
34:B5:1589:C:H2'	34:B5:1590:G:C8	2.52	0.45
38:A1:585:A:H2'	38:A1:586:C:C6	2.52	0.45
38:A1:595:G:H5''	43:AF:33:ARG:HH12	1.81	0.45
38:A1:2283:G:H1'	38:A1:2285:C:N4	2.32	0.45
38:A1:2373:A:N3	38:A1:2824:G:O2'	2.36	0.45
38:A1:2423:U:H2'	38:A1:2424:A:C8	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2471:U:H3	38:A1:2474:G:N2	2.14	0.45
38:A1:2520:A:H2'	38:A1:2521:U:C6	2.51	0.45
38:A1:3065:G:H2'	38:A1:3066:U:C6	2.52	0.45
38:A1:3333:G:N2	38:A1:3369:G:O2'	2.49	0.45
41:AD:150:LEU:HD12	47:AJ:143:ARG:HG3	1.98	0.45
43:AF:84:VAL:HG23	43:AF:117:VAL:HB	1.99	0.45
47:AJ:100:GLY:HA3	47:AJ:154:THR:HG22	1.99	0.45
49:AM:16:GLU:OE1	55:AS:149:LYS:HE3	2.17	0.45
60:AX:63:ILE:HD13	60:AX:86:VAL:HG12	1.98	0.45
62:AZ:25:ILE:HG23	62:AZ:41:ALA:HB1	1.98	0.45
63:Aa:75:LEU:HB2	63:Aa:116:GLY:H	1.81	0.45
8:BJ:49:LEU:HD22	8:BJ:104:PHE:CE2	2.52	0.45
9:BL:116:ARG:HH12	54:AR:151:ARG:HD3	1.82	0.45
17:Bb:50:ALA:O	17:Bb:51:GLN:HG2	2.17	0.45
30:Bd:33:LYS:HD3	30:Bd:33:LYS:HA	1.61	0.45
31:Bg:14:GLU:HG3	31:Bg:309:VAL:HG22	1.98	0.45
34:B5:600:U:H2'	34:B5:601:A:H8	1.80	0.45
34:B5:1156:C:H2'	34:B5:1157:A:C8	2.52	0.45
34:B5:1606:C:H2'	34:B5:1607:G:C8	2.52	0.45
35:AA:220:GLY:O	38:A1:2245:C:O2'	2.35	0.45
37:AC:60:THR:HG23	38:A1:364:G:OP1	2.17	0.45
37:AC:282:SER:OG	53:AQ:125:ASP:OD2	2.30	0.45
38:A1:971:G:OP1	53:AQ:8:LYS:NZ	2.41	0.45
38:A1:2376:G:H2'	38:A1:2377:G:C8	2.52	0.45
38:A1:2660:G:OP1	38:A1:2750:U:O2'	2.35	0.45
46:AI:30:LYS:HA	46:AI:30:LYS:HD3	1.87	0.45
58:AV:108:GLU:OE1	58:AV:128:ARG:HG2	2.16	0.45
65:Ac:57:GLU:OE2	65:Ac:69:TYR:OH	2.30	0.45
2:BB:204:ILE:O	34:B5:1064:G:O2'	2.34	0.45
2:BB:225:VAL:O	2:BB:229:MET:HG2	2.16	0.45
5:BG:78:THR:OG1	5:BG:79:LYS:N	2.50	0.45
8:BJ:45:ILE:HG23	8:BJ:104:PHE:HD2	1.82	0.45
20:BF:222:LYS:HA	20:BF:225:ARG:NE	2.30	0.45
22:BP:44:ARG:NH2	34:B5:1553:G:O6	2.50	0.45
27:BU:69:LYS:HZ2	27:BU:80:GLU:CD	2.24	0.45
34:B5:855:A:C2	34:B5:857:U:H1'	2.52	0.45
34:B5:1285:U:H4'	34:B5:1286:U:O5'	2.17	0.45
34:B5:1345:A:N1	34:B5:1380:U:H5	2.15	0.45
36:AB:227:GLU:HG2	36:AB:270:ARG:HE	1.82	0.45
38:A1:44:U:OP1	50:AN:85:THR:HG23	2.16	0.45
38:A1:631:U:H2'	38:A1:632:G:H8	1.81	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1629:U:O2'	38:A1:1630:U:OP1	2.31	0.45
38:A1:2810:C:OP2	38:A1:2955:U:O2'	2.34	0.45
38:A1:3206:C:H4'	55:AS:157:GLN:NE2	2.32	0.45
47:AJ:148:VAL:O	47:AJ:153:LYS:NZ	2.43	0.45
48:AL:7:LEU:O	63:Aa:49:HIS:NE2	2.46	0.45
48:AL:187:ALA:HA	48:AL:190:LYS:HZ3	1.81	0.45
56:AT:102:ARG:O	56:AT:106:LEU:HG	2.17	0.45
68:Af:67:MET:HE1	68:Af:90:PRO:HD3	1.98	0.45
68:Af:75:HIS:HB2	68:Af:82:ARG:HG3	1.99	0.45
80:DC:666:ALA:HB2	80:DC:706:ILE:HA	1.99	0.45
82:EC:6939:C:H4'	82:EC:6940:U:OP2	2.14	0.45
1:BA:56:LYS:HA	1:BA:56:LYS:HD2	1.81	0.44
2:BB:202:LYS:NZ	34:B5:1057:U:O4'	2.49	0.44
7:BI:153:GLU:HB3	7:BI:156:VAL:HG22	1.99	0.44
20:BF:58:LEU:HD23	20:BF:58:LEU:HA	1.80	0.44
22:BP:119:PHE:O	25:BS:120:ARG:NH1	2.49	0.44
26:BT:6:VAL:HG21	26:BT:132:LEU:HB3	1.99	0.44
28:BZ:68:ARG:HH21	82:EC:6863:C:N4	2.16	0.44
34:B5:431:C:OP1	80:DC:391:LYS:HD2	2.17	0.44
34:B5:950:C:O2'	34:B5:951:A:OP1	2.29	0.44
34:B5:1144:U:H2'	34:B5:1145:U:C6	2.52	0.44
34:B5:1382:A:O2'	34:B5:1383:G:H8	1.99	0.44
38:A1:94:G:H2'	38:A1:95:A:C8	2.52	0.44
38:A1:266:A:H2'	71:Ai:30:LYS:HE3	1.98	0.44
38:A1:671:U:H2'	38:A1:672:A:C8	2.52	0.44
38:A1:715:A:N1	38:A1:781:G:O2'	2.47	0.44
38:A1:943:U:H3'	63:Aa:13:GLY:HA2	1.98	0.44
38:A1:2428:U:H2'	38:A1:2429:G:C8	2.51	0.44
38:A1:2465:G:H21	79:E:166:ALA:HB3	1.82	0.44
38:A1:3006:A:H2'	38:A1:3007:U:O4'	2.18	0.44
39:A3:71:G:H2'	39:A3:72:A:H8	1.82	0.44
43:AF:92:ILE:HD11	43:AF:110:ARG:HA	1.98	0.44
47:AJ:111:ASP:OD1	47:AJ:111:ASP:N	2.47	0.44
49:AM:40:ASP:OD1	49:AM:43:LYS:N	2.50	0.44
54:AR:175:GLN:OE1	54:AR:179:GLU:HG3	2.17	0.44
64:Ab:32:LEU:HB3	64:Ab:40:ARG:HE	1.82	0.44
76:An:1:MET:HE3	76:An:6:ARG:HD3	1.99	0.44
80:DC:28:VAL:HG12	80:DC:108:HIS:HA	1.99	0.44
80:DC:157:ILE:HD12	80:DC:211:PHE:HE1	1.82	0.44
3:BC:140:ARG:HB2	3:BC:222:TYR:CD1	2.52	0.44
4:BE:117:GLU:OE1	4:BE:117:GLU:N	2.45	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:48:VAL:HB	19:BD:86:LEU:HD22	1.99	0.44
23:BQ:134:ALA:HB3	34:B5:1585:U:H5''	1.98	0.44
34:B5:1252:C:H2'	34:B5:1253:U:O4'	2.17	0.44
34:B5:1518:C:H2'	34:B5:1519:U:C6	2.52	0.44
34:B5:1551:U:H2'	34:B5:1552:U:C6	2.52	0.44
38:A1:640:U:H2'	38:A1:641:C:C6	2.51	0.44
38:A1:1566:A:H5''	38:A1:1567:U:OP2	2.17	0.44
38:A1:1737:U:O2	69:Ag:52:GLN:NE2	2.51	0.44
44:AG:176:PRO:HG3	44:AG:215:VAL:HG13	1.99	0.44
48:AL:80:VAL:HG12	48:AL:85:LEU:O	2.17	0.44
70:Ah:5:LYS:O	70:Ah:8:GLU:HG2	2.17	0.44
79:E:101:LYS:O	79:E:105:LYS:HG3	2.18	0.44
80:DC:322:VAL:HG22	80:DC:326:LYS:NZ	2.32	0.44
80:DC:823:ARG:HH12	80:DC:832:VAL:HA	1.81	0.44
81:V:113:ALA:O	81:V:165:VAL:HG12	2.18	0.44
3:BC:89:GLN:O	34:B5:1145:U:O2'	2.26	0.44
6:BH:8:ILE:O	6:BH:42:GLN:HG3	2.17	0.44
8:BJ:28:LEU:HD11	18:Be:39:LEU:HB3	2.00	0.44
8:BJ:87:SER:OG	8:BJ:89:ASP:OD1	2.33	0.44
10:BN:2:GLY:HA2	34:B5:866:G:H5''	1.98	0.44
20:BF:99:MET:HE2	20:BF:180:ARG:NH1	2.32	0.44
20:BF:131:GLN:HA	20:BF:134:VAL:HG12	1.99	0.44
25:BS:17:LEU:CD2	25:BS:66:LEU:HD11	2.42	0.44
26:BT:25:GLN:OE1	26:BT:27:LYS:HG2	2.16	0.44
26:BT:44:GLU:OE1	26:BT:44:GLU:N	2.50	0.44
31:Bg:10:ARG:HG3	31:Bg:314:GLN:HB2	1.99	0.44
34:B5:52:U:H2'	34:B5:53:G:H8	1.82	0.44
34:B5:225:A:C6	34:B5:837:G:C6	3.05	0.44
34:B5:300:A:H2'	34:B5:301:A:C8	2.52	0.44
34:B5:1234:A:H5''	34:B5:1245:G:H2'	2.00	0.44
36:AB:95:THR:HG23	38:A1:3243:A:H4'	2.00	0.44
36:AB:295:ALA:HB2	36:AB:301:THR:O	2.16	0.44
38:A1:1134:G:O2'	38:A1:2642:A:N3	2.42	0.44
40:A4:95:G:O2'	72:Aj:81:GLY:O	2.28	0.44
43:AF:35:ALA:O	43:AF:39:GLU:HG2	2.16	0.44
53:AQ:176:ARG:HA	53:AQ:182:LYS:O	2.18	0.44
56:AT:26:HIS:CE1	56:AT:28:SER:HB2	2.52	0.44
69:Ag:19:LYS:HD3	69:Ag:19:LYS:HA	1.75	0.44
70:Ah:85:THR:HG22	70:Ah:87:ALA:H	1.82	0.44
72:Aj:54:LYS:O	72:Aj:58:THR:HB	2.17	0.44
80:DC:263:ASP:OD1	80:DC:267:LYS:N	2.50	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:729:PHE:HE2	80:DC:774:VAL:HG13	1.82	0.44
81:V:128:MET:O	81:V:149:THR:HG23	2.18	0.44
82:EC:6790:A:N6	82:EC:6798:C:OP2	2.50	0.44
82:EC:6822:U:H2'	82:EC:6823:U:H5''	1.99	0.44
2:BB:121:ILE:HG12	2:BB:161:ILE:HG23	1.99	0.44
3:BC:53:ILE:HA	3:BC:72:LEU:HD13	1.98	0.44
6:BH:123:ASP:OD1	6:BH:138:LYS:NZ	2.37	0.44
7:BI:99:ALA:HB3	34:B5:329:G:H5'	1.99	0.44
22:BP:98:ASN:HD21	22:BP:122:THR:HA	1.82	0.44
31:Bg:246:SER:HB2	31:Bg:251:TRP:HB2	1.99	0.44
34:B5:938:G:N2	34:B5:941:A:OP2	2.43	0.44
36:AB:251:CYS:SG	38:A1:2943:G:N2	2.91	0.44
38:A1:172:G:H2'	38:A1:173:G:C8	2.53	0.44
38:A1:293:C:H2'	38:A1:294:U:O4'	2.17	0.44
38:A1:616:G:H2'	38:A1:617:G:C8	2.52	0.44
38:A1:673:U:H2'	38:A1:674:G:C8	2.53	0.44
38:A1:1658:G:H2'	38:A1:1659:U:C6	2.52	0.44
38:A1:2180:G:H2'	38:A1:2181:C:C6	2.52	0.44
38:A1:2683:U:H2'	38:A1:2684:C:H6	1.82	0.44
38:A1:2812:C:H2'	38:A1:2813:A:H8	1.83	0.44
38:A1:2966:G:H2'	38:A1:2967:A:C8	2.52	0.44
40:A4:71:A:O2'	61:AY:52:ARG:NH1	2.50	0.44
41:AD:40:HIS:HB3	41:AD:43:LYS:HD2	2.00	0.44
45:AH:6:THR:HG21	45:AH:65:VAL:HG13	2.00	0.44
45:AH:90:MET:HE2	45:AH:146:LEU:HD11	1.99	0.44
50:AN:110:ALA:HB1	50:AN:113:LEU:HD12	1.99	0.44
52:AP:45:GLN:O	52:AP:49:GLU:HG2	2.18	0.44
79:E:104:SER:HA	79:E:110:PHE:CZ	2.52	0.44
2:BB:58:SER:O	2:BB:62:LYS:HG2	2.18	0.44
2:BB:87:ARG:HB2	2:BB:101:HIS:HB2	2.00	0.44
8:BJ:124:HIS:HA	8:BJ:127:VAL:HG22	1.99	0.44
15:BY:10:ARG:NH1	34:B5:778:G:H22	2.16	0.44
19:BD:195:SER:O	19:BD:197:THR:HG22	2.18	0.44
21:BK:10:LYS:HA	21:BK:13:GLN:OE1	2.17	0.44
22:BP:105:VAL:HA	25:BS:120:ARG:HH22	1.83	0.44
24:BR:33:ARG:HD3	24:BR:33:ARG:HA	1.83	0.44
32:Bf:80:ARG:NH1	34:B5:1209:C:OP1	2.49	0.44
34:B5:488:G:N2	34:B5:500:C:OP1	2.51	0.44
34:B5:824:G:H2'	34:B5:825:U:H6	1.83	0.44
34:B5:1483:A:OP2	34:B5:1521:G:N2	2.51	0.44
37:AC:3:ARG:HB3	37:AC:22:LEU:H	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:970:A:H2'	38:A1:971:G:C8	2.53	0.44
38:A1:1497:C:H2'	38:A1:1498:A:C8	2.53	0.44
38:A1:2203:U:H2'	38:A1:2204:C:C6	2.52	0.44
38:A1:2828:G:OP2	46:AI:7:ARG:NH2	2.51	0.44
39:A3:56:A:H4'	47:AJ:152:HIS:HB2	1.99	0.44
39:A3:61:G:H2'	39:A3:62:U:H6	1.82	0.44
41:AD:181:PRO:HD2	41:AD:195:LEU:HD13	2.00	0.44
52:AP:19:GLY:HA3	52:AP:22:LEU:HD11	1.99	0.44
59:AW:17:ARG:HA	59:AW:17:ARG:HD2	1.87	0.44
65:Ac:76:GLU:N	65:Ac:76:GLU:OE1	2.51	0.44
67:Ae:66:LEU:HD23	67:Ae:72:LYS:HG3	1.99	0.44
67:Ae:96:ILE:HG21	67:Ae:105:ARG:HG2	1.99	0.44
82:EC:6764:C:H2'	82:EC:6765:A:C8	2.53	0.44
82:EC:6837:G:H2'	82:EC:6838:C:C6	2.53	0.44
3:BC:245:ASP:OD1	3:BC:245:ASP:N	2.49	0.44
4:BE:86:PHE:CZ	4:BE:87:MET:HE3	2.53	0.44
5:BG:12:SER:OG	5:BG:124:LEU:O	2.29	0.44
13:BW:28:ARG:HG2	13:BW:60:LYS:HG2	2.00	0.44
15:BY:77:ASN:N	15:BY:81:GLU:OE2	2.51	0.44
19:BD:105:MET:HB2	19:BD:122:VAL:HG21	1.99	0.44
21:BK:93:GLN:HG2	21:BK:94:GLU:HG3	2.00	0.44
23:BQ:47:LYS:HE2	23:BQ:79:TYR:CZ	2.53	0.44
31:Bg:207:ASP:OD1	31:Bg:208:GLY:N	2.51	0.44
34:B5:29:U:H2'	34:B5:30:G:C8	2.50	0.44
34:B5:296:U:H2'	34:B5:297:U:C6	2.52	0.44
34:B5:490:C:N4	34:B5:492:A:O4'	2.41	0.44
34:B5:950:C:H2'	34:B5:951:A:C8	2.52	0.44
34:B5:1593:A:H2'	34:B5:1594:G:C8	2.49	0.44
38:A1:833:G:OP1	54:AR:86:GLU:HB3	2.17	0.44
38:A1:1771:C:H2'	38:A1:1772:U:O4'	2.17	0.44
46:AI:206:LEU:O	46:AI:210:ILE:HG12	2.18	0.44
51:AO:121[A]:PRO:HA	51:AO:124[A]:LEU:HD12	2.00	0.44
52:AP:176:ILE:HG22	52:AP:180:LYS:HE2	1.99	0.44
82:EC:6815:U:H3'	82:EC:6816:A:H5''	2.00	0.44
5:BG:65:GLN:NE2	34:B5:1682:U:H4'	2.32	0.44
14:BX:90:ASP:HA	34:B5:568:G:H4'	2.00	0.44
20:BF:46:TRP:HH2	20:BF:122:ASN:HD22	1.64	0.44
27:BU:69:LYS:HA	30:Bd:44:ARG:NH1	2.33	0.44
31:Bg:19:TRP:NE1	31:Bg:306:THR:HB	2.32	0.44
31:Bg:288:HIS:O	31:Bg:306:THR:HG23	2.18	0.44
31:Bg:294:TRP:CZ3	31:Bg:301:LEU:HB2	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:198:A:H3'	34:B5:199:G:H8	1.82	0.44
34:B5:1135:U:H2'	34:B5:1136:U:C6	2.52	0.44
35:AA:68:LYS:HD3	35:AA:70:ARG:CZ	2.47	0.44
36:AB:83:PRO:O	36:AB:165:GLN:NE2	2.45	0.44
36:AB:108:GLU:OE1	36:AB:109:HIS:ND1	2.51	0.44
38:A1:247:C:H3'	38:A1:248:U:C5'	2.48	0.44
38:A1:1856:C:H2'	38:A1:1857:C:H6	1.83	0.44
38:A1:1913:A:N3	38:A1:2120:A:H2'	2.32	0.44
38:A1:3118:C:H4'	75:Am:106:ARG:NH2	2.32	0.44
58:AV:106:LYS:HZ2	58:AV:128:ARG:HH12	1.66	0.44
82:EC:6794:C:O2'	82:EC:6890:A:N6	2.46	0.44
4:BE:139:VAL:HG13	4:BE:150:PRO:HG3	1.99	0.44
6:BH:13:PRO:HA	6:BH:14:THR:HA	1.82	0.44
6:BH:57:ALA:HA	6:BH:89:HIS:H	1.82	0.44
14:BX:65:ASN:ND2	14:BX:116:ASP:OD2	2.30	0.44
25:BS:145:ARG:HH21	34:B5:1172:G:H4'	1.82	0.44
34:B5:1642:G:H2'	34:B5:1643:U:H6	1.82	0.44
35:AA:185:ALA:O	35:AA:189:TYR:HD1	2.01	0.44
38:A1:432:G:H2'	38:A1:433:A:C8	2.52	0.44
38:A1:629:U:H2'	38:A1:630:A:C8	2.53	0.44
38:A1:979:U:H4'	38:A1:980:A:O4'	2.18	0.44
38:A1:1292:C:HO2'	38:A1:1293:U:P	2.38	0.44
38:A1:1799:A:H2'	38:A1:1800:A:H8	1.81	0.44
38:A1:1829:G:H5''	38:A1:1830:G:H5'	1.99	0.44
38:A1:1941:C:H2'	38:A1:1942:U:C6	2.53	0.44
38:A1:2427:U:H2'	38:A1:2428:U:C6	2.53	0.44
38:A1:2486:A:O2'	38:A1:2487:U:H5'	2.18	0.44
38:A1:2639:G:H2'	38:A1:2640:A2M:H8	1.98	0.44
38:A1:3192:U:H2'	38:A1:3193:C:H6	1.81	0.44
39:A3:60:G:H2'	39:A3:61:G:H8	1.82	0.44
52:AP:41:LEU:HD21	52:AP:99:ALA:HB2	1.99	0.44
80:DC:22:MET:SD	80:DC:102:LEU:HD13	2.57	0.44
80:DC:585:ARG:HB2	80:DC:692:THR:OG1	2.18	0.44
81:V:37:GLN:HA	81:V:40:GLU:HG3	1.99	0.44
82:EC:6801:A:H8	82:EC:6883:A:N7	2.15	0.44
5:BG:173:PRO:HG3	34:B5:66:U:C5	2.53	0.44
15:BY:44:LEU:HA	15:BY:47:VAL:HB	2.00	0.44
19:BD:64:ARG:HD3	19:BD:64:ARG:HA	1.88	0.44
36:AB:250:ALA:HB1	38:A1:2947:G:C2	2.53	0.44
38:A1:270:U:H2'	38:A1:271:C:H6	1.83	0.44
38:A1:748:U:H2'	38:A1:749:C:C6	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1482:A:H5''	38:A1:1858:A:C6	2.53	0.44
38:A1:3113:A:H4'	45:AH:69:ARG:HG3	1.98	0.44
44:AG:101:THR:HG22	44:AG:104:GLU:CD	2.42	0.44
48:AL:55:ARG:NH1	48:AL:73:ARG:O	2.44	0.44
61:AY:115:ARG:HA	61:AY:115:ARG:HD2	1.88	0.44
68:Af:49:ILE:HG23	68:Af:100:ILE:HD13	1.99	0.44
77:Ao:12:CYS:HB2	77:Ao:23:HIS:CE1	2.53	0.44
81:V:42:ARG:O	81:V:46:ARG:HG2	2.18	0.44
1:BA:134:LYS:O	1:BA:138:TYR:HD1	2.01	0.43
2:BB:98:THR:H	2:BB:232:HIS:CE1	2.37	0.43
14:BX:107:PHE:HD1	14:BX:123:LYS:HD3	1.82	0.43
15:BY:34:ASN:ND2	34:B5:532:U:O2	2.46	0.43
15:BY:105:ARG:NH2	34:B5:458:G:OP2	2.51	0.43
17:Bb:33:LEU:HD23	17:Bb:81:ARG:HA	1.99	0.43
25:BS:27:LYS:HA	25:BS:57:ARG:HA	2.00	0.43
34:B5:27:U:H2'	34:B5:28:A2M:H8	1.99	0.43
34:B5:78:A:H2'	34:B5:79:C:H6	1.83	0.43
34:B5:1211:A:C6	34:B5:1453:G:C6	3.06	0.43
34:B5:1582:U:C2	34:B5:1614:A:C6	3.06	0.43
37:AC:22:LEU:HA	37:AC:23:PRO:HD3	1.82	0.43
38:A1:551:A:HO2'	38:A1:552:G:H8	1.66	0.43
38:A1:1249:G:H2'	38:A1:1250:G:H8	1.83	0.43
38:A1:2464:U:H2'	38:A1:2465:G:N7	2.33	0.43
39:A3:27:A:H2'	39:A3:28:C:C6	2.52	0.43
40:A4:8:C:H2'	40:A4:9:A:C8	2.52	0.43
1:BA:198:MET:SD	24:BR:85:VAL:HG21	2.58	0.43
8:BJ:89:ASP:O	8:BJ:90:LYS:HG2	2.18	0.43
17:Bb:56:CYS:SG	17:Bb:57:GLU:N	2.91	0.43
26:BT:117:SER:O	26:BT:117:SER:OG	2.30	0.43
34:B5:153:G:H2'	34:B5:154:G:H8	1.83	0.43
34:B5:956:C:OP1	34:B5:1072:C:O2'	2.35	0.43
34:B5:1586:A:H1'	34:B5:1611:A:H61	1.83	0.43
34:B5:1704:U:H2'	34:B5:1705:C:C6	2.53	0.43
34:B5:1732:A:H2'	34:B5:1733:C:H6	1.83	0.43
36:AB:147:GLU:O	36:AB:151:ILE:HG13	2.18	0.43
36:AB:291:GLU:HG3	36:AB:292:ALA:H	1.83	0.43
38:A1:84:U:O2'	38:A1:101:G:O6	2.27	0.43
38:A1:209:A:O2'	38:A1:211:A:OP2	2.24	0.43
38:A1:389:A:OP1	52:AP:4:TYR:OH	2.34	0.43
38:A1:567:G:H2'	38:A1:568:G:C8	2.52	0.43
38:A1:1095:U:H3	56:AT:127:GLN:HG2	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1354:G:H1'	42:AE:9:TRP:NE1	2.33	0.43
38:A1:1801:U:H2'	38:A1:1802:C:C6	2.53	0.43
38:A1:2457:G:O2'	38:A1:2481:G:N7	2.46	0.43
38:A1:2566:C:H2'	38:A1:2567:C:C6	2.53	0.43
43:AF:77:VAL:HG11	55:AS:57:GLU:OE2	2.17	0.43
45:AH:37:ASN:HD21	45:AH:39:LYS:HB2	1.83	0.43
48:AL:174:ARG:NH2	71:AI:9:ILE:HD13	2.33	0.43
82:EC:6886:A:H2'	82:EC:6887:G:C8	2.53	0.43
1:BA:59:LEU:HD22	12:BV:79:LEU:HD11	2.00	0.43
1:BA:140:ASN:ND2	3:BC:60:SER:O	2.51	0.43
19:BD:209:ILE:HD12	19:BD:209:ILE:HA	1.90	0.43
22:BP:105:VAL:HG12	25:BS:120:ARG:HH22	1.83	0.43
23:BQ:103:ASN:HA	23:BQ:106:LYS:HG2	2.01	0.43
25:BS:94:ASP:OD1	25:BS:94:ASP:N	2.51	0.43
34:B5:330:G:H2'	34:B5:331:A:C8	2.54	0.43
34:B5:384:G:H2'	34:B5:385:A:C8	2.53	0.43
36:AB:108:GLU:OE1	36:AB:109:HIS:CE1	2.71	0.43
37:AC:281:ILE:HD12	53:AQ:29:LEU:HG	1.99	0.43
38:A1:20:A:H2'	38:A1:21:G:C8	2.53	0.43
38:A1:1464:G:N2	38:A1:1467:A:OP2	2.51	0.43
38:A1:1740:U:H1'	38:A1:1741:A:H2	1.83	0.43
38:A1:1760:A:N6	38:A1:1766:G:C6	2.86	0.43
38:A1:2374:C:OP1	38:A1:2823:G:O2'	2.34	0.43
38:A1:2709:C:H2'	38:A1:2710:C:C6	2.53	0.43
38:A1:2897:A:H5''	75:Am:125:LYS:HD2	2.00	0.43
39:A3:90:U:H2'	39:A3:91:G:O4'	2.18	0.43
46:AI:63:GLU:H	46:AI:63:GLU:CD	2.26	0.43
71:AI:58:ILE:HD11	71:AI:93:ILE:HD11	2.00	0.43
79:E:93:LEU:HG	79:E:99:LEU:HD22	1.99	0.43
80:DC:122:THR:O	80:DC:352:ARG:NH1	2.38	0.43
80:DC:569:SER:O	80:DC:569:SER:OG	2.31	0.43
80:DC:725:GLN:HA	80:DC:803:THR:HB	2.00	0.43
7:BI:38:ILE:HG12	7:BI:96:LEU:HD11	1.99	0.43
8:BJ:169:PRO:HG2	8:BJ:170:GLY:N	2.32	0.43
14:BX:114:LYS:NZ	14:BX:120:VAL:HG12	2.33	0.43
17:Bb:20:LYS:HG3	17:Bb:21:LEU:HD22	2.00	0.43
22:BP:72:LYS:HG3	22:BP:93:VAL:CG2	2.48	0.43
23:BQ:30:LYS:HD3	23:BQ:35:PRO:HA	2.00	0.43
34:B5:186:C:H2'	34:B5:187:G:O4'	2.19	0.43
34:B5:1062:A:H2'	34:B5:1063:U:O4'	2.18	0.43
34:B5:1209:C:C4	34:B5:1455:G:N2	2.86	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:AC:3:ARG:HH12	37:AC:24:ALA:HB2	1.84	0.43
38:A1:518:G:OP2	38:A1:518:G:N2	2.29	0.43
38:A1:563:U:H2'	38:A1:564:G:H8	1.84	0.43
38:A1:1241:U:N3	38:A1:1244:A:OP2	2.37	0.43
38:A1:2413:A:H2'	38:A1:2414:G:C8	2.51	0.43
38:A1:3160:U:H2'	38:A1:3161:C:H6	1.84	0.43
38:A1:3302:U:H2'	38:A1:3303:G:C8	2.53	0.43
38:A1:3322:A:H2'	38:A1:3323:A:H8	1.81	0.43
40:A4:7:U:H2'	40:A4:8:C:C6	2.54	0.43
40:A4:149:A:H2'	40:A4:150:G:C8	2.53	0.43
48:AL:155:GLU:CD	48:AL:155:GLU:H	2.26	0.43
54:AR:105:LEU:HD23	54:AR:138:LEU:HD23	2.01	0.43
63:Aa:85:ASP:N	63:Aa:85:ASP:OD1	2.51	0.43
4:BE:49:ARG:HE	4:BE:49:ARG:HB3	1.64	0.43
5:BG:8:PRO:HB3	34:B5:164:A:O3'	2.18	0.43
6:BH:104:ARG:HG3	34:B5:803:A:C5	2.53	0.43
20:BF:70:VAL:HG13	20:BF:72:HIS:H	1.84	0.43
21:BK:32:HIS:HD1	21:BK:35:ILE:HG22	1.84	0.43
29:Bc:22:ARG:HG2	34:B5:1619:C:C2	2.53	0.43
34:B5:560:U:H2'	34:B5:561:G:C8	2.49	0.43
34:B5:1077:C:H2'	34:B5:1078:C:H6	1.83	0.43
34:B5:1234:A:H3'	34:B5:1245:G:H8	1.83	0.43
36:AB:314:TYR:HE2	36:AB:317:ILE:HG22	1.84	0.43
38:A1:381:U:H2'	38:A1:382:U:C6	2.53	0.43
38:A1:432:G:H2'	38:A1:433:A:H8	1.83	0.43
38:A1:627:U:H4'	38:A1:1399:A:H1'	2.00	0.43
38:A1:682:U:H5''	38:A1:683:U:H5	1.82	0.43
38:A1:1130:A:H8	38:A1:1130:A:OP2	2.01	0.43
38:A1:1139:G:O6	64:Ab:10:HIS:NE2	2.51	0.43
38:A1:1213:G:H4'	55:AS:90:MET:CG	2.46	0.43
38:A1:1242:G:HO2'	38:A1:1243:G:P	2.39	0.43
38:A1:2618:G:O2'	38:A1:2865:U:OP1	2.23	0.43
38:A1:3162:C:H2'	38:A1:3163:A:C8	2.51	0.43
39:A3:52:G:N2	47:AJ:9:MET:SD	2.90	0.43
43:AF:98:LYS:HB3	43:AF:99:PRO:HD3	1.98	0.43
45:AH:151:VAL:O	45:AH:155:SER:OG	2.27	0.43
70:Ah:102:GLU:CD	70:Ah:105:ARG:HH21	2.18	0.43
80:DC:94:ASP:OD1	80:DC:95:GLY:N	2.51	0.43
80:DC:140:GLU:O	80:DC:144:ARG:HG3	2.18	0.43
80:DC:563:TYR:HB2	80:DC:677:PHE:CZ	2.52	0.43
80:DC:647:ILE:O	80:DC:687:ASN:HA	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:746:VAL:HG21	80:DC:783:GLU:HB3	1.99	0.43
81:V:7:LYS:HA	81:V:10:GLU:OE2	2.18	0.43
82:EC:6947:A:O2'	82:EC:6948:U:H3'	2.19	0.43
2:BB:158:SER:HA	2:BB:161:ILE:HD12	2.01	0.43
5:BG:142:ARG:HE	5:BG:151:ASP:H	1.66	0.43
15:BY:43:LYS:O	15:BY:47:VAL:HG23	2.19	0.43
24:BR:78:ARG:O	24:BR:82:ASP:HB2	2.17	0.43
26:BT:77:ASN:HD21	26:BT:98:GLY:HA2	1.84	0.43
28:BZ:68:ARG:HH12	82:EC:6862:G:H21	1.65	0.43
34:B5:645:C:H2'	34:B5:646:C:C6	2.54	0.43
34:B5:752:A:HO2'	34:B5:753:A:P	2.39	0.43
34:B5:1160:A:H2'	34:B5:1161:C:H6	1.83	0.43
34:B5:1237:G:H2'	34:B5:1238:A:H8	1.83	0.43
34:B5:1477:G:H2'	34:B5:1478:G:H8	1.82	0.43
38:A1:21:G:H3'	38:A1:22:G:H8	1.84	0.43
38:A1:2097:U:H2'	38:A1:2098:C:C6	2.53	0.43
38:A1:2742:C:H2'	38:A1:2743:A:C8	2.53	0.43
48:AL:181:GLY:HA2	48:AL:184:GLU:HG2	2.00	0.43
51:AO:23[A]:VAL:O	51:AO:27[A]:LEU:HD13	2.18	0.43
80:DC:144:ARG:HD2	80:DC:765:LEU:HD11	2.00	0.43
80:DC:576:LEU:HD13	80:DC:586:ILE:O	2.18	0.43
82:EC:6858:A:O2'	82:EC:6859:U:O4	2.34	0.43
14:BX:69:ARG:HA	14:BX:69:ARG:HD3	1.80	0.43
22:BP:20:VAL:HG23	22:BP:24:LYS:HZ2	1.84	0.43
22:BP:44:ARG:NH1	34:B5:1555:A:OP1	2.51	0.43
22:BP:122:THR:HG21	34:B5:1454:G:O3'	2.18	0.43
31:Bg:292:LEU:HA	31:Bg:303:ALA:HA	2.01	0.43
33:BM:138:GLU:O	33:BM:142:GLN:HG3	2.19	0.43
34:B5:142:G:P	34:B5:142:G:H21	2.42	0.43
34:B5:497:G:OP1	34:B5:498:G:N2	2.51	0.43
34:B5:953:G:H2'	34:B5:954:G:H8	1.84	0.43
34:B5:1061:A:H5''	34:B5:1062:A:C2	2.53	0.43
34:B5:1080:U:H2'	34:B5:1081:A:C8	2.54	0.43
34:B5:1636:C:O2	34:B5:1765:A:N6	2.52	0.43
35:AA:79:ASN:ND2	35:AA:166:ILE:O	2.52	0.43
37:AC:138:ARG:HD2	37:AC:140:HIS:CD2	2.53	0.43
38:A1:1068:C:H2'	38:A1:1069:C:H6	1.84	0.43
38:A1:2699:G:H5''	56:AT:16:GLN:NE2	2.34	0.43
44:AG:96:LYS:NZ	44:AG:207:ASP:OD2	2.36	0.43
80:DC:418:TYR:HB3	80:DC:477:ASN:ND2	2.23	0.43
80:DC:593:ILE:HG12	80:DC:685:ARG:HB2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:86:LEU:HB3	2:BB:98:THR:CG2	2.49	0.43
2:BB:181:LEU:HD12	2:BB:184:LEU:HD23	2.01	0.43
5:BG:5:ILE:HG12	5:BG:111:LEU:HB2	2.00	0.43
7:BI:141:ARG:NH2	34:B5:196:G:O6	2.52	0.43
9:BL:23:PRO:HA	9:BL:26:LYS:NZ	2.34	0.43
9:BL:64:VAL:HG11	9:BL:131:ILE:HD11	2.01	0.43
20:BF:112:ARG:NE	34:B5:1529:C:OP1	2.52	0.43
20:BF:118:LEU:HG	20:BF:129:PRO:HB2	2.01	0.43
26:BT:27:LYS:NZ	26:BT:111:ILE:HG23	2.34	0.43
33:BM:132:GLU:O	33:BM:135:MET:HG2	2.18	0.43
34:B5:250:C:H2'	34:B5:251:A:C8	2.53	0.43
34:B5:366:A:H2'	34:B5:367:A:C8	2.53	0.43
34:B5:545:A:O4'	34:B5:594:A:N6	2.51	0.43
34:B5:896:U:H2'	34:B5:897:C:C6	2.54	0.43
34:B5:1237:G:N1	34:B5:1249:U:O4	2.52	0.43
37:AC:219:LEU:HD22	37:AC:225:VAL:HG11	2.01	0.43
38:A1:289:A:H2'	38:A1:290:G:H8	1.84	0.43
38:A1:516:A:H2'	38:A1:517:G:C8	2.54	0.43
38:A1:1083:G:H2'	38:A1:1084:A:C8	2.54	0.43
38:A1:2909:U:H2'	38:A1:2910:A:O4'	2.19	0.43
40:A4:36:G:C5	70:Ah:86:ARG:HD3	2.53	0.43
40:A4:58:G:H5''	40:A4:98:U:O2	2.19	0.43
58:AV:57:MET:HE3	58:AV:126:TRP:CH2	2.54	0.43
65:Ac:81:VAL:HG23	65:Ac:83:LYS:HG2	2.01	0.43
80:DC:155:VAL:O	80:DC:209:VAL:HA	2.19	0.43
80:DC:460:ASP:O	80:DC:513:LYS:NZ	2.43	0.43
82:EC:6778:C:P	82:EC:6779:C:H41	2.41	0.43
1:BA:78:SER:OG	1:BA:129:ASP:OD1	2.27	0.43
5:BG:78:THR:O	5:BG:81:VAL:HG22	2.18	0.43
6:BH:56:LYS:O	6:BH:88:ARG:HA	2.18	0.43
19:BD:28:GLU:HG3	21:BK:58:GLN:HG2	2.01	0.43
20:BF:29:ILE:HD13	23:BQ:57:LEU:HD11	2.00	0.43
25:BS:62:THR:HB	25:BS:65:GLU:HG3	2.00	0.43
27:BU:69:LYS:HG2	27:BU:80:GLU:HG3	2.00	0.43
28:BZ:68:ARG:NH1	82:EC:6864:A:H61	2.17	0.43
32:Bf:132:LEU:HB2	32:Bf:139:LEU:HD11	2.01	0.43
34:B5:170:U:OP2	34:B5:267:U:H4'	2.19	0.43
34:B5:472:U:H2'	34:B5:473:A:H8	1.83	0.43
34:B5:835:U:H2'	34:B5:836:U:C5	2.51	0.43
34:B5:886:U:C2	34:B5:887:A:C8	3.07	0.43
34:B5:888:U:H2'	34:B5:889:U:C6	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:132:LYS:NZ	38:A1:3292:A:H4'	2.34	0.43
38:A1:159:A:H2'	38:A1:160:G:H8	1.83	0.43
38:A1:297:G:OP2	38:A1:297:G:N2	2.35	0.43
38:A1:308:A:H1'	38:A1:2222:A:N3	2.33	0.43
38:A1:1460:A:H2'	38:A1:1461:A:C8	2.53	0.43
38:A1:2722:U:OP1	64:Ab:33:LYS:NZ	2.45	0.43
38:A1:3107:U:H2'	38:A1:3108:G:C8	2.53	0.43
39:A3:4:U:H2'	39:A3:5:G:H8	1.84	0.43
40:A4:40:A:OP2	40:A4:103:G:N1	2.43	0.43
50:AN:5:LYS:HG3	71:Ai:40:VAL:HG11	2.01	0.43
56:AT:99:SER:OG	56:AT:101:CYS:SG	2.71	0.43
67:Ae:111:ARG:HA	67:Ae:111:ARG:HD2	1.83	0.43
79:E:143:ASP:OD1	79:E:143:ASP:N	2.49	0.43
2:BB:139:ALA:HB2	2:BB:172:LEU:HD11	2.01	0.43
2:BB:176:VAL:HG12	2:BB:177:GLN:H	1.84	0.43
13:BW:122:SER:O	34:B5:748:U:O2'	2.30	0.43
20:BF:51:VAL:HG11	20:BF:64:VAL:HG21	2.00	0.43
24:BR:25:THR:O	24:BR:31:ASN:ND2	2.39	0.43
31:Bg:111:MET:HE1	31:Bg:127:ARG:N	2.33	0.43
34:B5:1003:A:O2'	34:B5:1005:A:N7	2.41	0.43
34:B5:1036:A:H2'	34:B5:1037:C:C6	2.54	0.43
34:B5:1480:G:H2'	34:B5:1481:C:O4'	2.19	0.43
36:AB:68:HIS:NE2	36:AB:69:LYS:HE3	2.34	0.43
38:A1:760:G:N2	38:A1:770:G:N3	2.67	0.43
38:A1:873:C:H3'	38:A1:874:U:H4'	2.01	0.43
38:A1:1427:U:OP2	63:Aa:4:ARG:NH1	2.37	0.43
44:AG:195:SER:OG	44:AG:197:VAL:O	2.36	0.43
58:AV:7:GLN:HE21	58:AV:127:PRO:HG3	1.84	0.43
65:Ac:16:LEU:O	65:Ac:20:SER:OG	2.32	0.43
73:Ak:8:ILE:HD11	73:Ak:65:LEU:HD11	2.01	0.43
73:Ak:30:LYS:HD3	73:Ak:38:PHE:CZ	2.54	0.43
80:DC:483:PHE:O	80:DC:485:VAL:N	2.52	0.43
80:DC:644:ASN:HD22	80:DC:684:VAL:H	1.67	0.43
5:BG:135:PRO:HB3	5:BG:140:ASN:HB3	2.01	0.42
6:BH:62:VAL:HG22	6:BH:93:LEU:O	2.19	0.42
13:BW:10:ALA:HB1	13:BW:27:ILE:HD13	2.00	0.42
17:Bb:33:LEU:HD22	17:Bb:79:PHE:HD2	1.84	0.42
31:Bg:81:LEU:HD12	31:Bg:81:LEU:HA	1.88	0.42
34:B5:518:A:O2'	34:B5:519:C:H5'	2.18	0.42
34:B5:844:A:H2'	34:B5:845:G:H8	1.84	0.42
34:B5:1081:A:O2'	34:B5:1083:G:N7	2.47	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:AC:281:ILE:HD13	53:AQ:28:LEU:HD12	2.00	0.42
38:A1:63:A:H5''	50:AN:174:ILE:HG21	2.01	0.42
38:A1:897:U:H2'	38:A1:898:OMU:H6	2.01	0.42
38:A1:1184:A:H2'	38:A1:1185:C:C6	2.53	0.42
38:A1:2430:A:H2'	38:A1:2431:C:C6	2.54	0.42
38:A1:3299:A:H2	38:A1:3315:G:H22	1.67	0.42
43:AF:89:ILE:HD11	43:AF:229:PHE:HB3	2.00	0.42
44:AG:101:THR:HG23	44:AG:103:ALA:H	1.83	0.42
45:AH:85:GLY:HA3	45:AH:187:ILE:HD12	1.99	0.42
70:Ah:28:LEU:HD22	70:Ah:51:ILE:HD12	2.01	0.42
71:Ai:33:ALA:HB1	71:Ai:38:LYS:HG3	2.00	0.42
80:DC:503:LYS:HD3	80:DC:550:ALA:O	2.19	0.42
80:DC:715:ALA:HB2	80:DC:838:TYR:HB3	2.01	0.42
80:DC:829:LYS:C	80:DC:831:GLU:H	2.27	0.42
82:EC:6761:C:H2'	82:EC:6762:U:C6	2.54	0.42
6:BH:30:SER:HB2	6:BH:33:GLU:HG3	2.01	0.42
6:BH:49:ILE:HG13	6:BH:172:VAL:HG23	2.00	0.42
7:BI:31:ARG:HH11	34:B5:332:U:H5''	1.82	0.42
8:BJ:89:ASP:OD1	8:BJ:89:ASP:N	2.46	0.42
12:BV:73:ALA:HB1	12:BV:78:LEU:HB2	2.01	0.42
15:BY:124:ARG:HA	15:BY:127:LYS:HE2	2.02	0.42
21:BK:88:PRO:HG2	21:BK:92:ILE:O	2.19	0.42
25:BS:88:ARG:NH1	25:BS:108:LYS:HD3	2.34	0.42
26:BT:28:LEU:O	26:BT:29:GLU:HG3	2.19	0.42
31:Bg:195:HIS:CE1	31:Bg:221:MET:HG2	2.54	0.42
31:Bg:304:GLY:HA2	31:Bg:310:ILE:HA	2.01	0.42
34:B5:23:G:O2'	34:B5:368:U:OP1	2.37	0.42
34:B5:1246:C:H2'	34:B5:1247:U:C6	2.53	0.42
34:B5:1272:U:O2'	34:B5:1275:A:OP2	2.34	0.42
34:B5:1308:G:H2'	34:B5:1309:C:C6	2.54	0.42
34:B5:1488:G:O6	34:B5:1518:C:N4	2.26	0.42
35:AA:138:GLY:HA3	35:AA:147:ARG:NH2	2.34	0.42
38:A1:226:C:H2'	38:A1:227:G:O4'	2.20	0.42
38:A1:1394:A:H4'	38:A1:1420:C:H4'	2.01	0.42
38:A1:1629:U:H1'	62:AZ:115:LYS:CD	2.49	0.42
38:A1:1785:U:H2'	38:A1:1786:G:C8	2.54	0.42
38:A1:2882:U:H2'	38:A1:2883:U:C6	2.54	0.42
39:A3:3:U:H2'	39:A3:4:U:H6	1.83	0.42
43:AF:232:ARG:O	43:AF:235:PHE:N	2.51	0.42
45:AH:48:VAL:HG21	45:AH:54:LYS:HE2	2.01	0.42
49:AM:20:VAL:O	49:AM:66:THR:OG1	2.33	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AN:147:ARG:HG3	70:Ah:101:THR:HG21	2.01	0.42
74:Al:44:TRP:CE2	74:Al:45:ARG:HG3	2.53	0.42
82:EC:6859:U:H6	82:EC:6859:U:H2'	1.68	0.42
1:BA:148:ASP:OD1	1:BA:149:LEU:N	2.48	0.42
3:BC:200:SER:HB3	3:BC:204:THR:HG21	2.01	0.42
4:BE:183:VAL:HG13	4:BE:220:THR:HG21	2.00	0.42
8:BJ:171:ARG:HD2	34:B5:537:G:N7	2.34	0.42
11:BO:17:ALA:HB3	11:BO:81:VAL:HA	2.01	0.42
16:Ba:88:SER:HA	34:B5:1628:U:H5'	2.02	0.42
24:BR:110:VAL:HG23	24:BR:115:LEU:HD12	2.01	0.42
25:BS:40:ARG:HE	34:B5:1539:G:H5''	1.85	0.42
25:BS:141:THR:HG21	34:B5:1173:C:H3'	2.01	0.42
31:Bg:305:TYR:HB2	31:Bg:311:ARG:NH1	2.34	0.42
34:B5:291:G:H2'	34:B5:292:U:C5	2.54	0.42
34:B5:448:C:H2'	34:B5:449:C:H6	1.85	0.42
34:B5:1061:A:H5''	34:B5:1062:A:N3	2.35	0.42
34:B5:1225:U:O2	34:B5:1230:A:O2'	2.35	0.42
34:B5:1617:U:H2'	34:B5:1618:C:C6	2.54	0.42
36:AB:21:ARG:NH1	38:A1:3309:G:O6	2.50	0.42
38:A1:177:U:C2	38:A1:178:U:C5	3.07	0.42
38:A1:349:A:C4	40:A4:24:G:H1'	2.54	0.42
38:A1:1321:G:N2	55:AS:112:ALA:HB2	2.34	0.42
38:A1:1952:G:N1	38:A1:2094:C:O2'	2.29	0.42
38:A1:3095:U:H2'	38:A1:3096:C:H6	1.85	0.42
39:A3:26:C:H2'	39:A3:27:A:O4'	2.18	0.42
41:AD:41:LYS:HB2	56:AT:68:THR:O	2.19	0.42
42:AE:174:LEU:HD13	49:AM:117:ARG:HH12	1.83	0.42
49:AM:25:LYS:HB2	49:AM:62:GLN:HB2	2.02	0.42
79:E:59:PRO:HD3	79:E:153:SER:HA	2.01	0.42
79:E:127:GLN:NE2	82:EC:6774:U:O4	2.52	0.42
80:DC:366:CYS:O	80:DC:369:ILE:HG22	2.19	0.42
80:DC:393:ARG:NH1	80:DC:510:ARG:HH11	2.17	0.42
80:DC:733:ILE:HG13	80:DC:794:PRO:HA	2.01	0.42
82:EC:6809:G:O2'	82:EC:6810:U:O4'	2.15	0.42
4:BE:87:MET:O	4:BE:122:LYS:HE3	2.19	0.42
6:BH:14:THR:O	6:BH:17:GLU:HG2	2.20	0.42
10:BN:72:MET:HE2	10:BN:72:MET:HB3	1.94	0.42
21:BK:44:LYS:HG3	34:B5:1217:A:H5''	2.01	0.42
23:BQ:38:LEU:C	23:BQ:45:ARG:HH12	2.27	0.42
34:B5:615:A:O2'	34:B5:621:A:N1	2.41	0.42
34:B5:1103:U:H2'	34:B5:1104:U:H6	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:140:ASN:O	35:AA:144:ASN:HA	2.20	0.42
37:AC:304:GLN:NE2	38:A1:594:U:O4	2.47	0.42
38:A1:172:G:H2'	38:A1:173:G:H8	1.85	0.42
38:A1:1431:G:N7	63:Aa:9:ARG:NH2	2.66	0.42
38:A1:1666:G:H2'	38:A1:1667:A:C8	2.54	0.42
45:AH:138:THR:C	45:AH:140:VAL:H	2.27	0.42
53:AQ:62:VAL:HG13	53:AQ:66:ARG:HD2	2.01	0.42
53:AQ:147:ARG:HB3	53:AQ:150:VAL:HG23	2.00	0.42
65:Ac:25:LEU:HD11	65:Ac:83:LYS:HE3	2.00	0.42
79:E:9:VAL:HG12	79:E:180:VAL:HG13	2.01	0.42
80:DC:615:ARG:HA	80:DC:618:ILE:HG12	2.01	0.42
81:V:22:TYR:CD2	81:V:88:PHE:HB3	2.54	0.42
2:BB:86:LEU:HB3	2:BB:98:THR:HG21	2.01	0.42
3:BC:175:GLY:N	3:BC:195:ASP:OD2	2.52	0.42
5:BG:137:ARG:HD3	5:BG:177:ARG:HD2	2.01	0.42
7:BI:31:ARG:NH1	34:B5:332:U:OP1	2.52	0.42
22:BP:30:THR:O	22:BP:34:VAL:HG23	2.19	0.42
25:BS:26:ILE:HG23	25:BS:31:ALA:HB2	2.01	0.42
25:BS:36:LYS:HB3	25:BS:102:ALA:HA	2.02	0.42
31:Bg:255:ALA:HB2	31:Bg:292:LEU:HD23	2.01	0.42
34:B5:407:A:H2'	34:B5:408:C:H6	1.84	0.42
34:B5:1712:A:H2'	34:B5:1713:G:O4'	2.19	0.42
37:AC:349:THR:HG23	43:AF:71:ALA:HB2	2.01	0.42
38:A1:718:G:OP1	63:Aa:117:ARG:NH2	2.48	0.42
38:A1:1092:C:HO2'	38:A1:1093:A:P	2.42	0.42
38:A1:1740:U:H4'	38:A1:1741:A:H5'	2.02	0.42
38:A1:2204:C:H2'	38:A1:2205:U:C6	2.54	0.42
38:A1:2426:U:H2'	38:A1:2427:U:C6	2.54	0.42
38:A1:3068:U:OP2	54:AR:62:ARG:NH2	2.48	0.42
46:AI:44:ASP:OD1	46:AI:181:TYR:OH	2.26	0.42
60:AX:96:LYS:HG3	60:AX:107:VAL:HB	2.01	0.42
74:Al:5:LYS:HE2	74:Al:13:MET:HE1	2.01	0.42
79:E:55:LEU:HD22	79:E:182:GLN:HG2	2.01	0.42
6:BH:33:GLU:O	6:BH:37:GLU:HB2	2.20	0.42
14:BX:112:LYS:NZ	34:B5:1136:U:O4	2.30	0.42
15:BY:88:THR:HA	15:BY:91:LEU:HD23	2.02	0.42
22:BP:98:ASN:OD1	22:BP:122:THR:HA	2.19	0.42
23:BQ:49:TYR:O	23:BQ:53:LEU:N	2.49	0.42
24:BR:81:LYS:O	24:BR:81:LYS:HG2	2.19	0.42
29:Bc:13:ILE:O	29:Bc:14:LYS:HE2	2.19	0.42
33:BM:48:SER:HB2	33:BM:122:VAL:HG23	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:208:U:H2'	34:B5:209:U:C6	2.54	0.42
34:B5:234:G:C2	34:B5:235:G:H1'	2.55	0.42
34:B5:1198:G:OP1	34:B5:1199:G:O2'	2.22	0.42
34:B5:1211:A:N6	34:B5:1453:G:O6	2.52	0.42
34:B5:1393:C:H2'	34:B5:1394:G:H8	1.84	0.42
37:AC:42:VAL:HG23	37:AC:236:LEU:HD21	2.02	0.42
37:AC:300:ARG:NH1	38:A1:1347:U:OP1	2.51	0.42
38:A1:213:A:H1'	61:AY:3:LYS:HB2	2.02	0.42
38:A1:978:G:N2	38:A1:979:U:O4	2.26	0.42
38:A1:1095:U:N3	56:AT:127:GLN:HG2	2.33	0.42
38:A1:1120:A:H2'	38:A1:1121:U:C6	2.54	0.42
38:A1:1203:A:H2'	38:A1:1204:A:H8	1.81	0.42
41:AD:223:PHE:HA	41:AD:226:TYR:HD2	1.84	0.42
44:AG:136:LEU:HD11	44:AG:162:LEU:HB3	2.00	0.42
52:AP:179:GLN:HA	52:AP:182:ILE:HG22	2.01	0.42
53:AQ:98:LYS:HE2	53:AQ:118:GLY:O	2.19	0.42
61:AY:17:LYS:O	61:AY:21:THR:OG1	2.30	0.42
73:AK:60:GLY:O	73:AK:64:LYS:HG2	2.19	0.42
3:BC:96:THR:O	3:BC:97:ARG:HD2	2.20	0.42
7:BI:31:ARG:HB2	34:B5:331:A:O3'	2.20	0.42
8:BJ:126:ARG:HD3	18:Be:33:ARG:HD3	2.01	0.42
17:Bb:46:VAL:HG12	17:Bb:54:VAL:HG11	2.02	0.42
20:BF:95:ASN:HA	20:BF:98:MET:HE2	2.01	0.42
20:BF:140:THR:HG21	20:BF:175:LEU:HG	2.01	0.42
23:BQ:9:THR:HA	34:B5:1340:U:O4	2.20	0.42
24:BR:3:ARG:HD2	34:B5:1390:U:C6	2.54	0.42
31:Bg:205:SER:OG	31:Bg:210:LEU:HB3	2.20	0.42
34:B5:826:U:H2'	34:B5:827:C:C6	2.55	0.42
34:B5:904:G:N2	82:EC:6946:A:O4'	2.53	0.42
34:B5:1575:7MG:O2'	34:B5:1576:A:C5'	2.65	0.42
38:A1:176:G:O2'	38:A1:177:U:H6	2.02	0.42
38:A1:955:U:H2'	38:A1:956:U:C6	2.54	0.42
38:A1:1221:A:H5'	81:V:61:ARG:HG3	2.02	0.42
38:A1:1616:U:H2'	38:A1:1617:G:C8	2.55	0.42
38:A1:1856:C:H2'	38:A1:1857:C:C6	2.54	0.42
38:A1:2218:G:H2'	38:A1:2219:A:C8	2.54	0.42
38:A1:2267:C:H2'	38:A1:2268:U:O4'	2.19	0.42
38:A1:2508:U:H2'	38:A1:2509:U:H6	1.82	0.42
38:A1:2696:A:H2'	38:A1:2697:A:C8	2.55	0.42
42:AE:142:ASP:HA	42:AE:145:LEU:HB2	2.01	0.42
51:AO:73[A]:PHE:HB3	51:AO:78[A]:ARG:HB3	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AS:12:ARG:HB3	55:AS:24:LEU:HD23	2.02	0.42
62:AZ:68:ILE:O	62:AZ:115:LYS:HG3	2.19	0.42
65:Ac:50:VAL:HA	65:Ac:53:LYS:HE3	2.02	0.42
72:Aj:18:LEU:HD13	74:Al:12:LYS:HE3	2.02	0.42
79:E:122:ARG:NH2	82:EC:6770:U:OP2	2.51	0.42
80:DC:201:GLN:OE1	81:V:145:ILE:HB	2.19	0.42
80:DC:638:PRO:HA	80:DC:668:GLN:HE22	1.85	0.42
2:BB:146:GLN:NE2	34:B5:1065:A:N3	2.63	0.42
3:BC:208:GLU:OE1	3:BC:208:GLU:N	2.38	0.42
7:BI:107:THR:HB	7:BI:108:PRO:HD3	2.02	0.42
8:BJ:159:ALA:HB3	8:BJ:162:SER:HB3	2.01	0.42
20:BF:117:THR:HG22	20:BF:191:ALA:O	2.19	0.42
21:BK:59:PHE:CE2	21:BK:62:GLN:HG3	2.55	0.42
30:Bd:33:LYS:O	30:Bd:36:LEU:HD23	2.20	0.42
31:Bg:22:SER:OG	31:Bg:70:ASP:HA	2.19	0.42
31:Bg:53:LYS:HG3	31:Bg:54:PHE:N	2.35	0.42
33:BM:50:LYS:HE2	33:BM:54:ARG:NH1	2.30	0.42
34:B5:329:G:H2'	34:B5:330:G:H8	1.85	0.42
34:B5:496:G:H5'	34:B5:499:U:C4	2.55	0.42
34:B5:884:A:H2'	34:B5:885:G:C8	2.55	0.42
34:B5:1146:G:H2'	34:B5:1147:A:H8	1.83	0.42
34:B5:1226:A:C2	34:B5:1227:A:C5	3.07	0.42
38:A1:268:A:N1	38:A1:295:A:H5'	2.35	0.42
38:A1:1718:G:H2'	38:A1:1719:G:C8	2.55	0.42
38:A1:1718:G:H2'	38:A1:1719:G:H8	1.83	0.42
38:A1:2835:U:H2'	38:A1:2836:C:O2	2.20	0.42
46:AI:51:HIS:CD2	46:AI:168:SER:HB2	2.54	0.42
47:AJ:115:LYS:HG3	47:AJ:116:TYR:N	2.34	0.42
61:AY:120:GLN:NE2	61:AY:126:LEU:HD13	2.33	0.42
79:E:33:GLU:O	79:E:206:VAL:HA	2.20	0.42
80:DC:394:PHE:CZ	80:DC:510:ARG:HG3	2.55	0.42
80:DC:494:GLU:O	80:DC:555:LYS:N	2.53	0.42
1:BA:122:ILE:HA	1:BA:144:ILE:O	2.20	0.42
1:BA:140:ASN:HD22	3:BC:62:PRO:HD3	1.84	0.42
4:BE:233:LYS:O	4:BE:233:LYS:HD2	2.20	0.42
19:BD:167:PHE:HD1	19:BD:190:ARG:NH1	2.17	0.42
25:BS:90:ASN:HB3	34:B5:1548:G:H5'	2.01	0.42
34:B5:888:U:O2	34:B5:988:A:O2'	2.38	0.42
34:B5:1078:C:H2'	34:B5:1079:U:C6	2.54	0.42
36:AB:41:VAL:HG12	36:AB:183:LEU:HD12	2.01	0.42
38:A1:120:G:H4'	38:A1:121:A:OP1	2.08	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:824:C:O2'	38:A1:1534:A:N3	2.49	0.42
38:A1:876:A2M:H5''	38:A1:1890:U:H5''	2.01	0.42
38:A1:1213:G:OP1	55:AS:139:TYR:OH	2.37	0.42
39:A3:64:A:H62	46:AI:209:ASN:ND2	2.17	0.42
39:A3:98:C:OP1	55:AS:39:SER:OG	2.30	0.42
42:AE:40:LEU:HD11	42:AE:54:TYR:HB2	2.02	0.42
44:AG:33:ASN:O	44:AG:39:ALA:HB3	2.20	0.42
44:AG:185:ARG:O	44:AG:188:THR:OG1	2.37	0.42
46:AI:13:LYS:HE2	46:AI:13:LYS:HB3	1.94	0.42
49:AM:14:LEU:H	49:AM:19:ARG:NH2	2.18	0.42
54:AR:95:TRP:CZ2	54:AR:99:LEU:HD22	2.54	0.42
73:AK:27:ILE:HD12	73:AK:78:LEU:HD21	2.01	0.42
75:AM:99:CYS:HB3	75:AM:115:CYS:HB3	2.01	0.42
80:DC:459:ILE:HD12	80:DC:462:PHE:CD2	2.55	0.42
81:V:104:ARG:HA	81:V:184:GLY:HA3	2.01	0.42
81:V:139:LEU:HD21	81:V:169:GLU:HB3	2.01	0.42
81:V:176:LEU:HB3	81:V:178:ILE:HD12	2.02	0.42
82:EC:6788:C:N4	82:EC:6808:G:H21	2.18	0.42
5:BG:143:LYS:HB3	5:BG:143:LYS:HE3	1.83	0.42
13:BW:53:ILE:HD13	17:Bb:24:LEU:HD11	2.01	0.42
17:Bb:70:LYS:HG3	34:B5:1049:U:H5''	2.01	0.42
20:BF:225:ARG:HH22	29:Bc:57:MET:HG3	1.85	0.42
25:BS:48:LYS:HZ2	26:BT:35:ASP:HB2	1.84	0.42
31:Bg:307:ASP:O	31:Bg:309:VAL:HG23	2.19	0.42
33:BM:91:VAL:HG11	33:BM:96:GLN:HE22	1.84	0.42
34:B5:293:U:H2'	34:B5:294:C:C6	2.55	0.42
34:B5:341:A:H2'	34:B5:342:C:C6	2.55	0.42
34:B5:434:G:N1	34:B5:437:A:OP2	2.40	0.42
34:B5:1063:U:H2'	34:B5:1064:G:H8	1.84	0.42
34:B5:1474:G:H2'	34:B5:1475:A:H8	1.84	0.42
36:AB:350:ALA:O	36:AB:351:LEU:HG	2.20	0.42
37:AC:326:ARG:NH2	38:A1:608:A:O3'	2.53	0.42
38:A1:166:C:H2'	38:A1:167:U:H6	1.84	0.42
38:A1:291:C:OP1	50:AN:68:ARG:NE	2.43	0.42
38:A1:791:A:H2'	38:A1:792:G:C8	2.55	0.42
38:A1:1084:A:H5''	56:AT:35:LYS:HE3	2.01	0.42
38:A1:1260:A:H2'	38:A1:1261:G:C4	2.55	0.42
38:A1:1348:U:OP2	53:AQ:38:ARG:NH2	2.53	0.42
38:A1:2456:A:H2	38:A1:2457:G:C6	2.38	0.42
38:A1:2722:U:O2'	56:AT:88:ARG:O	2.32	0.42
40:A4:142:C:H2'	40:A4:143:U:H6	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:AG:140:VAL:HG22	44:AG:166:LEU:HD21	2.01	0.42
47:AJ:16:LYS:HD3	47:AJ:72:ARG:CZ	2.50	0.42
63:Aa:35:ALA:O	63:Aa:41:HIS:ND1	2.53	0.42
73:Ak:32:ASN:OD1	73:Ak:36:LYS:N	2.33	0.42
78:Ap:8:VAL:O	78:Ap:11:THR:OG1	2.34	0.42
79:E:100:ILE:HA	79:E:103:LEU:HG	2.02	0.42
80:DC:194:ASP:OD1	80:DC:194:ASP:N	2.53	0.42
80:DC:571:SER:HB3	80:DC:720:ALA:HB2	2.02	0.42
80:DC:780:PHE:O	80:DC:784:LEU:HD23	2.20	0.42
80:DC:809:LEU:HD12	80:DC:810:ASP:N	2.35	0.42
80:DC:823:ARG:HE	80:DC:828:MET:HB2	1.85	0.42
4:BE:129:VAL:HG22	4:BE:139:VAL:HG12	2.02	0.41
5:BG:153:VAL:O	5:BG:157:VAL:HG23	2.19	0.41
6:BH:14:THR:H	6:BH:17:GLU:CD	2.28	0.41
7:BI:11:ARG:O	9:BL:133:LYS:NZ	2.45	0.41
7:BI:89:GLU:OE1	38:A1:2106:A:O2'	2.37	0.41
8:BJ:172:VAL:O	8:BJ:176:ASN:ND2	2.52	0.41
17:Bb:2:VAL:C	17:Bb:4:VAL:H	2.27	0.41
26:BT:69:LYS:HG2	34:B5:1367:G:H5''	2.02	0.41
34:B5:956:C:H2'	34:B5:957:G:H8	1.84	0.41
34:B5:1170:G:C2	34:B5:1171:A:C8	3.08	0.41
38:A1:2467:G:H1'	38:A1:2468:A:N7	2.34	0.41
39:A3:96:U:H2'	39:A3:97:A:C8	2.55	0.41
40:A4:41:A:H4'	72:Aj:59:THR:HG23	2.01	0.41
40:A4:67:U:H2'	40:A4:68:G:H8	1.85	0.41
43:AF:169:ILE:CD1	43:AF:181:ILE:HD13	2.49	0.41
45:AH:90:MET:HB2	45:AH:144:ILE:HG23	2.02	0.41
55:AS:6:GLU:OE2	55:AS:28:ARG:NE	2.42	0.41
79:E:28:PHE:HD2	79:E:29:LEU:HG	1.84	0.41
79:E:94:ASN:HD22	79:E:123:LEU:HD22	1.84	0.41
80:DC:412:ARG:HD2	80:DC:426:LEU:HD22	2.01	0.41
81:V:55:LYS:HD3	81:V:84:VAL:HG12	2.02	0.41
81:V:96:ILE:HG13	81:V:97:LYS:N	2.34	0.41
82:EC:6809:G:H2'	82:EC:6810:U:C6	2.55	0.41
1:BA:110:TYR:HA	1:BA:115:PHE:CG	2.55	0.41
2:BB:30:PHE:HB3	2:BB:96:LEU:HD13	2.01	0.41
2:BB:157:GLN:C	2:BB:159:SER:H	2.28	0.41
5:BG:159:ARG:HH12	5:BG:170:THR:HG21	1.85	0.41
6:BH:103:SER:OG	6:BH:104:ARG:N	2.53	0.41
7:BI:72:ILE:HD13	7:BI:112:TRP:CD2	2.55	0.41
19:BD:42:THR:OG1	19:BD:43:PRO:HD2	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BR:44:LYS:NZ	34:B5:1387:G:N7	2.56	0.41
25:BS:37:GLY:C	34:B5:1566:U:H4'	2.44	0.41
31:Bg:66:HIS:HD2	34:B5:1386:G:O2'	2.03	0.41
34:B5:199:G:H2'	34:B5:200:A:C8	2.55	0.41
34:B5:256:A:H2'	34:B5:257:A:O4'	2.20	0.41
34:B5:602:U:H2'	34:B5:603:U:C6	2.56	0.41
34:B5:653:C:OP2	34:B5:682:C:N4	2.48	0.41
36:AB:291:GLU:OE2	36:AB:304:THR:HG23	2.19	0.41
38:A1:434:U:H2'	38:A1:435:C:C6	2.55	0.41
38:A1:1464:G:O2'	38:A1:1466:G:N7	2.49	0.41
38:A1:2389:C:H2'	38:A1:2390:A:H8	1.85	0.41
38:A1:2536:A:C2	38:A1:2538:U:H2'	2.54	0.41
38:A1:2881:C:H2'	38:A1:2882:U:H6	1.85	0.41
40:A4:63:G:OP1	40:A4:90:U:H5''	2.19	0.41
80:DC:405:VAL:HA	80:DC:409:GLN:OE1	2.20	0.41
81:V:155:ASP:OD1	81:V:155:ASP:N	2.47	0.41
7:BI:73:SER:OG	34:B5:257:A:H1'	2.20	0.41
9:BL:123:VAL:HG12	9:BL:142:VAL:HG12	2.01	0.41
19:BD:109:LEU:HD22	19:BD:115:ILE:HG12	2.02	0.41
21:BK:73:VAL:HG22	21:BK:77:ARG:HH12	1.86	0.41
34:B5:143:G:H2'	34:B5:144:U:C6	2.55	0.41
35:AA:3:ARG:HD3	38:A1:911:C:H42	1.85	0.41
36:AB:4:ARG:C	36:AB:6:TYR:H	2.28	0.41
38:A1:158:G:H2'	38:A1:159:A:H8	1.85	0.41
38:A1:1143:A:H5'	38:A1:1368:U:H1'	2.03	0.41
38:A1:2429:G:H2'	38:A1:2430:A:C8	2.55	0.41
38:A1:2523:A:H2'	44:AG:49:TYR:O	2.20	0.41
38:A1:3129:A:C6	38:A1:3131:U:H1'	2.56	0.41
38:A1:3215:A:C2	42:AE:157:GLN:HB3	2.56	0.41
38:A1:3232:G:C6	38:A1:3256:G:C6	3.08	0.41
38:A1:3343:G:H2'	38:A1:3344:A:C2	2.55	0.41
51:AO:10[A]:ASP:OD2	51:AO:37[A]:ARG:NH2	2.28	0.41
52:AP:94:LEU:HD23	52:AP:94:LEU:HA	1.93	0.41
61:AY:87:LYS:HB2	61:AY:97:ILE:HD11	2.03	0.41
82:EC:6831:U:H4'	82:EC:6832:G:OP1	2.20	0.41
7:BI:77:ARG:HD3	38:A1:3354:U:O4	2.20	0.41
8:BJ:55:ALA:O	8:BJ:59:LEU:HD23	2.20	0.41
11:BO:92:LYS:HD2	11:BO:121:VAL:HG22	2.02	0.41
19:BD:99:VAL:O	19:BD:103:GLU:HG2	2.20	0.41
19:BD:105:MET:HA	19:BD:108:LYS:HD2	2.02	0.41
21:BK:16:PHE:CE1	21:BK:73:VAL:HG23	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BS:41:ARG:NE	34:B5:1565:C:OP1	2.29	0.41
26:BT:9:VAL:HG12	26:BT:140:LEU:HG	2.02	0.41
31:Bg:153:GLN:OE1	31:Bg:202:LEU:N	2.39	0.41
34:B5:222:A:H2'	34:B5:223:U:C6	2.55	0.41
34:B5:736:C:N4	34:B5:737:A:H62	2.19	0.41
34:B5:1086:A:H2'	34:B5:1087:A:C8	2.56	0.41
36:AB:148:LEU:HD12	36:AB:196:ARG:HH11	1.84	0.41
37:AC:144:LYS:HB2	37:AC:144:LYS:HE3	1.88	0.41
37:AC:303:GLY:H	38:A1:1347:U:H5''	1.85	0.41
38:A1:138:U:H2'	38:A1:139:G:C8	2.54	0.41
38:A1:184:U:H2'	38:A1:185:C:C6	2.54	0.41
38:A1:244:G:N3	38:A1:244:G:H2'	2.34	0.41
38:A1:718:G:C2	38:A1:721:G:H1'	2.55	0.41
38:A1:1622:U:H2'	38:A1:1623:G:H8	1.86	0.41
38:A1:1747:G:N2	73:Ak:2:ALA:HB3	2.34	0.41
38:A1:2115:G:H22	38:A1:2120:A:H1'	1.86	0.41
38:A1:2506:U:H4'	38:A1:2507:C:OP1	2.19	0.41
42:AE:20:LYS:HA	42:AE:20:LYS:HD3	1.80	0.41
44:AG:60:ARG:O	44:AG:64:ILE:HG12	2.20	0.41
44:AG:71:VAL:HG12	50:AN:21:PHE:CE1	2.55	0.41
80:DC:311:GLU:OE1	80:DC:326:LYS:NZ	2.50	0.41
81:V:35:SER:O	81:V:39:HIS:ND1	2.54	0.41
1:BA:65:ALA:HB2	1:BA:181:VAL:HG23	2.03	0.41
10:BN:16:ILE:HD11	34:B5:862:A:O5'	2.21	0.41
10:BN:87:ASP:OD1	10:BN:87:ASP:N	2.53	0.41
27:BU:50:LEU:HD12	27:BU:94:GLU:O	2.20	0.41
34:B5:607:G:H21	34:B5:614:C:H5''	1.85	0.41
34:B5:781:U:H4'	34:B5:782:U:C6	2.55	0.41
34:B5:1600:A:O2'	34:B5:1602:C:N4	2.54	0.41
34:B5:1661:U:H2'	34:B5:1662:G:C8	2.55	0.41
34:B5:1719:A:H2'	34:B5:1720:G:O4'	2.20	0.41
36:AB:385:LYS:HE2	36:AB:385:LYS:HB2	1.83	0.41
37:AC:51:ALA:O	40:A4:26:U:O2'	2.36	0.41
38:A1:426:G:H2'	38:A1:427:C:C6	2.55	0.41
38:A1:716:A:N6	63:Aa:117:ARG:HG3	2.35	0.41
38:A1:1017:C:O2'	38:A1:1035:G:N2	2.54	0.41
38:A1:2440:G:H2'	38:A1:2441:A:H8	1.85	0.41
38:A1:2611:U:H2'	38:A1:2612:U:H6	1.85	0.41
38:A1:2931:C:H5''	58:AV:40:LYS:HD2	2.02	0.41
38:A1:3000:A:H2'	38:A1:3001:C:H6	1.85	0.41
38:A1:3072:C:H2'	38:A1:3073:A:O4'	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:A4:8:C:H2'	40:A4:9:A:H8	1.86	0.41
42:AE:133:GLU:HA	42:AE:136:GLU:OE2	2.21	0.41
56:AT:80:VAL:HG21	56:AT:85:LEU:HD12	2.02	0.41
79:E:65:ILE:HA	79:E:109:ALA:HB3	2.03	0.41
80:DC:102:LEU:HD12	80:DC:103:ILE:H	1.85	0.41
1:BA:167:LYS:HE3	1:BA:167:LYS:HB3	1.88	0.41
2:BB:111:ARG:HE	2:BB:111:ARG:HB3	1.76	0.41
3:BC:168:ARG:HD3	3:BC:170:ILE:HD11	2.03	0.41
4:BE:182:TYR:N	4:BE:226:PHE:O	2.43	0.41
21:BK:3:MET:SD	21:BK:8:ARG:HG2	2.61	0.41
26:BT:125:SER:O	26:BT:129:GLN:HG3	2.21	0.41
26:BT:134:ARG:HA	26:BT:134:ARG:HD3	1.90	0.41
28:BZ:97:LYS:HD2	34:B5:1474:G:O6	2.20	0.41
31:Bg:137:LYS:HA	31:Bg:137:LYS:HD3	1.88	0.41
31:Bg:270:LEU:HD21	31:Bg:273:ASP:HB2	2.03	0.41
33:BM:72:ILE:HA	33:BM:75:VAL:HG22	2.02	0.41
33:BM:131:ASP:OD1	33:BM:131:ASP:N	2.52	0.41
34:B5:11:A:N1	34:B5:1143:A:H2	2.18	0.41
34:B5:628:G:N2	34:B5:971:A:H62	2.17	0.41
34:B5:821:U:N3	34:B5:852:C:O2	2.43	0.41
34:B5:1513:G:H1'	34:B5:1518:C:C2	2.55	0.41
34:B5:1576:A:H8	34:B5:1576:A:OP2	2.04	0.41
34:B5:1647:U:H2'	34:B5:1648:A:C8	2.56	0.41
35:AA:158:ILE:HG22	35:AA:159:SER:N	2.35	0.41
35:AA:242:ARG:NH2	35:AA:243:THR:O	2.54	0.41
36:AB:95:THR:HG22	36:AB:97:ARG:H	1.84	0.41
38:A1:412:G:H2'	38:A1:413:U:C6	2.56	0.41
38:A1:541:U:H3	38:A1:550:A:N6	2.18	0.41
38:A1:679:U:O2'	38:A1:788:C:O2	2.36	0.41
38:A1:1659:U:H2'	38:A1:1660:C:H6	1.84	0.41
38:A1:1687:U:O4	57:AU:45:GLY:N	2.50	0.41
38:A1:2152:A:H2'	38:A1:2153:U:C6	2.54	0.41
38:A1:3271:G:C5	42:AE:108:LYS:HE3	2.56	0.41
40:A4:6:U:H2'	40:A4:7:U:C6	2.55	0.41
46:AI:207:GLU:O	46:AI:211:ARG:HG3	2.20	0.41
47:AJ:15:GLU:CD	47:AJ:132:ASN:ND2	2.79	0.41
47:AJ:60:ARG:N	47:AJ:63:GLU:OE2	2.41	0.41
52:AP:32:THR:HA	52:AP:58:ILE:HD12	2.03	0.41
57:AU:30:PRO:HB2	57:AU:58:GLU:OE2	2.21	0.41
61:AY:106:ILE:HG21	61:AY:109:LEU:HD23	2.02	0.41
77:Ao:72:LEU:HD11	77:Ao:83:LEU:HD12	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:810:ASP:N	80:DC:810:ASP:OD1	2.53	0.41
82:EC:6763:C:H2'	82:EC:6764:C:C6	2.56	0.41
82:EC:6797:U:H2'	82:EC:6798:C:C6	2.55	0.41
82:EC:6801:A:C6	82:EC:6802:A:H1'	2.55	0.41
82:EC:6853:G:C6	82:EC:6876:A:N1	2.89	0.41
82:EC:6897:G:H2'	82:EC:6898:U:H6	1.84	0.41
5:BG:50:PHE:CE1	5:BG:113:ILE:HG12	2.56	0.41
7:BI:178:ARG:NH2	34:B5:207:U:O2	2.54	0.41
21:BK:5:LYS:HD3	21:BK:8:ARG:HB2	2.02	0.41
21:BK:15:LEU:HB3	21:BK:76:LEU:HD21	2.01	0.41
25:BS:140:THR:HG21	34:B5:1175:U:O4	2.20	0.41
26:BT:41:SER:HB2	34:B5:1504:G:H4'	2.03	0.41
34:B5:496:G:H3'	34:B5:497:G:C8	2.56	0.41
34:B5:1142:A:H2'	34:B5:1143:A:C8	2.55	0.41
34:B5:1279:C:H2'	34:B5:1280:4AC:H6	2.01	0.41
34:B5:1483:A:N3	34:B5:1607:G:O2'	2.43	0.41
37:AC:140:HIS:CD2	37:AC:247:PHE:H	2.39	0.41
38:A1:216:G:OP1	61:AY:16:ARG:NH1	2.53	0.41
38:A1:503:C:H2'	38:A1:504:A:H8	1.85	0.41
38:A1:1709:C:H2'	38:A1:1710:C:H6	1.86	0.41
38:A1:2465:G:H2'	38:A1:2466:G:H8	1.85	0.41
50:AN:181:ASN:HA	50:AN:184:LYS:HE2	2.02	0.41
70:Ah:6:ALA:O	70:Ah:10:ARG:HG3	2.21	0.41
80:DC:810:ASP:HA	80:DC:811:PRO:HD3	1.85	0.41
3:BC:206:THR:HG21	3:BC:209:ASN:HD22	1.85	0.41
6:BH:35:LYS:HA	6:BH:35:LYS:HD3	1.93	0.41
8:BJ:85:VAL:HG21	8:BJ:104:PHE:CD1	2.55	0.41
20:BF:219:ARG:NH2	82:EC:6841:U:O2'	2.54	0.41
25:BS:62:THR:HG22	25:BS:63:GLN:N	2.36	0.41
34:B5:1449:U:H2'	34:B5:1450:U:H6	1.85	0.41
34:B5:1787:C:H2'	34:B5:1788:G:C8	2.55	0.41
36:AB:28:ARG:H	36:AB:28:ARG:HG2	1.64	0.41
36:AB:62:ARG:NH1	38:A1:3039:C:OP1	2.48	0.41
37:AC:226:GLU:OE1	37:AC:246:ARG:NH2	2.51	0.41
38:A1:107:A:H1'	38:A1:325:A:N3	2.36	0.41
38:A1:604:G:H2'	38:A1:605:U:C6	2.55	0.41
38:A1:691:A:N1	40:A4:28:C:O2'	2.43	0.41
38:A1:1351:U:H1'	38:A1:1355:A:N6	2.36	0.41
38:A1:1483:G:O6	69:Ag:4:ARG:NH2	2.54	0.41
38:A1:2467:G:H8	79:E:105:LYS:HB3	1.86	0.41
38:A1:2515:A:N1	38:A1:2594:C:N4	2.63	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:A3:61:G:H2'	39:A3:62:U:C6	2.56	0.41
39:A3:118:A:H5''	41:AD:253:PHE:HZ	1.85	0.41
41:AD:40:HIS:CE1	41:AD:42:ALA:HB3	2.56	0.41
58:AV:59:MET:HE1	58:AV:75:PRO:HG3	2.02	0.41
63:Aa:24:LYS:O	63:Aa:25:HIS:C	2.64	0.41
63:Aa:27:LYS:HB3	63:Aa:27:LYS:HE2	1.92	0.41
79:E:160:LYS:HE3	79:E:160:LYS:HB3	1.77	0.41
2:BB:70:LEU:HD23	2:BB:74:GLN:HB2	2.03	0.41
3:BC:178:ILE:O	3:BC:185:LYS:HD2	2.21	0.41
4:BE:107:GLY:HA2	4:BE:189:LEU:HG	2.02	0.41
5:BG:50:PHE:HB2	5:BG:111:LEU:HD12	2.03	0.41
7:BI:44:HIS:ND1	34:B5:1676:U:OP1	2.53	0.41
7:BI:75:LYS:NZ	34:B5:259:U:OP1	2.32	0.41
8:BJ:80:LEU:HA	8:BJ:83:VAL:HG12	2.03	0.41
12:BV:14:PRO:HB2	12:BV:23:ILE:HG23	2.03	0.41
15:BY:109:LYS:HE2	34:B5:458:G:OP1	2.21	0.41
18:Be:43:ARG:HG2	18:Be:56:MET:HE1	2.03	0.41
19:BD:198:GLY:HA3	19:BD:199:PRO:HD3	1.91	0.41
20:BF:36:ALA:HB1	20:BF:69:PHE:HZ	1.84	0.41
20:BF:99:MET:HG2	20:BF:100:ASN:N	2.31	0.41
20:BF:219:ARG:NH2	82:EC:6842:U:H5'	2.35	0.41
21:BK:77:ARG:HD3	21:BK:84:GLU:HA	2.03	0.41
26:BT:126:GLU:OE1	34:B5:1358:G:H4'	2.20	0.41
33:BM:75:VAL:HG11	33:BM:120:VAL:HG11	2.02	0.41
34:B5:304:U:H2'	34:B5:305:C:C6	2.56	0.41
34:B5:368:U:H2'	34:B5:369:A:O4'	2.21	0.41
34:B5:882:U:H2'	34:B5:883:C:C6	2.56	0.41
34:B5:909:U:H2'	34:B5:910:C:C6	2.56	0.41
34:B5:990:C:H2'	34:B5:991:G:O4'	2.21	0.41
34:B5:1584:G:O2'	34:B5:1610:G:O6	2.37	0.41
35:AA:144:ASN:OD1	35:AA:144:ASN:N	2.52	0.41
36:AB:236:LYS:NZ	38:A1:2338:C:OP1	2.30	0.41
36:AB:364:LYS:HG2	38:A1:3049:A:H5''	2.02	0.41
37:AC:59:GLN:NE2	38:A1:347:G:OP1	2.54	0.41
37:AC:161:LYS:HB2	37:AC:164:GLU:OE1	2.21	0.41
38:A1:142:C:H2'	38:A1:143:G:O4'	2.21	0.41
38:A1:165:A:H1'	38:A1:166:C:O5'	2.21	0.41
38:A1:209:A:H4'	38:A1:211:A:C8	2.55	0.41
38:A1:520:U:OP2	43:AF:70:LYS:NZ	2.49	0.41
38:A1:589:A:H8	38:A1:590:G:C8	2.39	0.41
38:A1:594:U:H2'	38:A1:609:G:O6	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:673:U:H2'	38:A1:674:G:H8	1.86	0.41
38:A1:899:U:H2'	38:A1:900:G:H8	1.86	0.41
38:A1:966:U:H2'	38:A1:967:A:H8	1.83	0.41
38:A1:1240:A:H2	38:A1:1248:C:H41	1.69	0.41
38:A1:1619:A:H2'	38:A1:1620:U:O4'	2.20	0.41
38:A1:2986:U:H2'	38:A1:2987:A:C8	2.55	0.41
38:A1:3064:U:H2'	38:A1:3065:G:H8	1.86	0.41
38:A1:3101:G:H2'	38:A1:3102:G:C8	2.56	0.41
38:A1:3198:U:O4	45:AH:26:LYS:HB2	2.21	0.41
40:A4:27:U:H2'	40:A4:28:C:H6	1.86	0.41
40:A4:40:A:H2'	40:A4:41:A:C8	2.55	0.41
44:AG:121:SER:OG	44:AG:122:LYS:N	2.52	0.41
44:AG:247:ASP:OD1	44:AG:248:LYS:N	2.53	0.41
46:AI:205:SER:OG	46:AI:207:GLU:OE1	2.38	0.41
47:AJ:54:VAL:HG21	47:AJ:57:PHE:CD2	2.55	0.41
72:Aj:25:ARG:HD3	74:Al:50:ASN:O	2.20	0.41
79:E:55:LEU:HA	79:E:56:PRO:HD3	1.94	0.41
80:DC:189:VAL:HG11	80:DC:201:GLN:HA	2.03	0.41
80:DC:342:LEU:HA	80:DC:343:PRO:HD3	1.90	0.41
80:DC:388:THR:HG22	80:DC:390:ASP:H	1.86	0.41
80:DC:454:ILE:HD12	80:DC:454:ILE:HA	1.89	0.41
80:DC:559:PRO:HD2	80:DC:778:PHE:HE2	1.85	0.41
80:DC:567:VAL:CG2	80:DC:720:ALA:HB3	2.50	0.41
81:V:26:PHE:CE2	81:V:100:ILE:HD11	2.56	0.41
82:EC:6828:G:H2'	82:EC:6829:A:C8	2.56	0.41
82:EC:6839:U:O5'	82:EC:6839:U:H6	2.04	0.41
82:EC:6937:G:H2'	82:EC:6937:G:N3	2.35	0.41
5:BG:173:PRO:HG3	34:B5:66:U:C6	2.56	0.41
6:BH:14:THR:O	6:BH:18:LEU:HG	2.21	0.41
6:BH:60:ILE:HD11	6:BH:92:PHE:HE1	1.85	0.41
9:BL:22:ASN:HA	9:BL:23:PRO:HD3	1.98	0.41
22:BP:34:VAL:HG13	22:BP:42:ARG:HA	2.03	0.41
25:BS:126:ARG:HD3	25:BS:132:ARG:O	2.21	0.41
33:BM:60:VAL:O	33:BM:60:VAL:HG12	2.21	0.41
33:BM:105:LYS:HD2	34:B5:1256:A:C6	2.56	0.41
34:B5:340:U:H2'	34:B5:341:A:H8	1.86	0.41
34:B5:547:U:H1'	34:B5:596:C:H1'	2.02	0.41
34:B5:1208:A:O2'	34:B5:1270:G:OP2	2.31	0.41
34:B5:1471:A:N3	34:B5:1471:A:H2'	2.36	0.41
34:B5:1586:A:H2'	34:B5:1587:A:O4'	2.21	0.41
36:AB:71:GLU:OE2	36:AB:357:LYS:NZ	2.41	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:380:MET:HE2	36:AB:383:LEU:HD21	2.02	0.41
37:AC:4:PRO:HD2	37:AC:22:LEU:HB2	2.02	0.41
37:AC:281:ILE:HG13	53:AQ:125:ASP:CG	2.46	0.41
38:A1:92:G:H5'	38:A1:94:G:N7	2.36	0.41
38:A1:528:U:H2'	38:A1:529:A:H8	1.86	0.41
38:A1:598:A:H2'	38:A1:599:C:C6	2.56	0.41
38:A1:1334:U:H2'	38:A1:1335:C:C6	2.56	0.41
38:A1:1759:C:N4	38:A1:1760:A:H62	2.19	0.41
38:A1:1948:G:C2	38:A1:2099:A:C2	3.09	0.41
38:A1:2144:A:H1'	38:A1:2281:A2M:N6	2.36	0.41
38:A1:2419:A:H2'	38:A1:2420:C:C6	2.56	0.41
38:A1:2481:G:OP1	79:E:98:LYS:HG3	2.21	0.41
38:A1:2744:U:H2'	38:A1:2745:G:C8	2.56	0.41
41:AD:179:ARG:HA	41:AD:179:ARG:HD3	1.83	0.41
41:AD:215:ASP:OD1	41:AD:215:ASP:N	2.54	0.41
42:AE:36:PRO:HB2	42:AE:93:VAL:HG21	2.02	0.41
43:AF:85:PHE:CZ	43:AF:147:LEU:HD21	2.56	0.41
43:AF:180:SER:H	43:AF:183:ASP:HB2	1.85	0.41
45:AH:138:THR:O	45:AH:140:VAL:N	2.54	0.41
50:AN:30:TYR:OH	50:AN:43:THR:HG21	2.21	0.41
57:AU:82:LYS:HE3	57:AU:82:LYS:HB3	1.81	0.41
62:AZ:24:VAL:HG21	62:AZ:87:LEU:HB3	2.03	0.41
67:Ae:32:TRP:CZ2	67:Ae:53:PRO:HD2	2.56	0.41
73:Ak:28:ASN:HB2	73:Ak:40:GLN:HB3	2.03	0.41
80:DC:13:MET:HG2	80:DC:13:MET:O	2.21	0.41
80:DC:91:GLN:HE22	80:DC:343:PRO:HA	1.86	0.41
80:DC:124:GLY:HA2	80:DC:151:ILE:HG23	2.03	0.41
80:DC:261:ASP:OD1	80:DC:261:ASP:N	2.49	0.41
1:BA:20:ALA:HB2	1:BA:172:LEU:HD13	2.03	0.40
2:BB:129:THR:HG22	2:BB:176:VAL:HG13	2.03	0.40
6:BH:82:GLU:OE2	6:BH:90:VAL:HG22	2.21	0.40
12:BV:15:ARG:NH1	12:BV:33:GLN:OE1	2.54	0.40
17:Bb:74:SER:O	17:Bb:76:GLY:N	2.54	0.40
31:Bg:44:SER:OG	31:Bg:59:ARG:HB3	2.20	0.40
34:B5:1442:U:OP1	80:DC:631:ARG:NH1	2.54	0.40
34:B5:1638:G:H2'	34:B5:1639:OMC:O4'	2.20	0.40
34:B5:1669:U:H2'	34:B5:1670:G:O4'	2.20	0.40
34:B5:1714:A:H2'	34:B5:1715:G:C8	2.56	0.40
37:AC:281:ILE:HD13	53:AQ:28:LEU:CD1	2.51	0.40
38:A1:247:C:H3'	38:A1:248:U:H5''	2.03	0.40
38:A1:563:U:H2'	38:A1:564:G:C8	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:800:G:H2'	38:A1:801:A:N7	2.35	0.40
38:A1:1128:U:H2'	38:A1:1129:A:O4'	2.21	0.40
38:A1:1233:G:N1	38:A1:1256:G:C6	2.90	0.40
38:A1:2442:G:H2'	38:A1:2443:A:C8	2.56	0.40
38:A1:2707:C:H2'	38:A1:2708:C:C6	2.56	0.40
38:A1:2916:U:H2'	38:A1:2917:G:H8	1.86	0.40
39:A3:95:A:N3	55:AS:119:ARG:HD2	2.35	0.40
44:AG:109:LEU:HD23	44:AG:109:LEU:HA	1.93	0.40
46:AI:182:LEU:HA	46:AI:182:LEU:HD23	1.88	0.40
49:AM:38:ILE:HG21	55:AS:150:PHE:HE1	1.85	0.40
58:AV:13:ILE:HG23	58:AV:85:TRP:CG	2.55	0.40
58:AV:15:LEU:HD23	58:AV:51:ALA:HB3	2.02	0.40
62:AZ:42:LEU:CD2	62:AZ:74:VAL:HG22	2.51	0.40
73:AK:17:ARG:C	73:AK:19:ASP:H	2.28	0.40
73:AK:40:GLN:HE21	73:AK:55:VAL:CG1	2.34	0.40
74:AI:30:ARG:HE	74:AI:30:ARG:HB2	1.75	0.40
80:DC:210:ALA:HB2	80:DC:337:MET:HE2	2.02	0.40
80:DC:576:LEU:H	80:DC:839:TYR:HD1	1.70	0.40
6:BH:91:ILE:HG12	6:BH:169:PHE:HE1	1.86	0.40
10:BN:114:ARG:HA	10:BN:114:ARG:HD3	1.91	0.40
15:BY:51:GLU:HG2	15:BY:52:LYS:N	2.36	0.40
19:BD:160:SER:OG	34:B5:1329:A:OP2	2.24	0.40
20:BF:49:GLU:O	20:BF:50:GLU:HG2	2.21	0.40
20:BF:116:HIS:O	20:BF:120:ILE:HG13	2.21	0.40
20:BF:170:GLN:O	20:BF:174:LEU:HD13	2.21	0.40
20:BF:190:ILE:HG22	34:B5:1473:U:OP2	2.22	0.40
30:Bd:54:LYS:HE3	30:Bd:54:LYS:HB3	1.98	0.40
34:B5:226:A:H2'	34:B5:227:U:O3'	2.21	0.40
34:B5:973:A:H4'	38:A1:848:A:C8	2.56	0.40
34:B5:1490:C:H1'	34:B5:1492:A:C6	2.56	0.40
36:AB:259:HIS:NE2	38:A1:2366:C:OP1	2.53	0.40
36:AB:298:PHE:CD2	36:AB:357:LYS:HE3	2.56	0.40
38:A1:573:C:H2'	38:A1:574:U:C6	2.56	0.40
38:A1:759:U:H2'	38:A1:760:G:O4'	2.22	0.40
38:A1:1129:A:H2'	38:A1:1130:A:C8	2.55	0.40
38:A1:1507:G:H1'	52:AP:139:TYR:CE2	2.56	0.40
38:A1:1810:A:H2'	38:A1:1811:G:C8	2.56	0.40
38:A1:1831:U:H2'	38:A1:1832:C:C6	2.56	0.40
38:A1:2354:C:H2'	38:A1:2355:G:O4'	2.21	0.40
38:A1:2379:U:H2'	38:A1:2380:U:C6	2.56	0.40
38:A1:2564:G:H2'	38:A1:2565:U:C6	2.57	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:AJ:84:LEU:HD12	47:AJ:89:TYR:HA	2.03	0.40
48:AL:9:ILE:HD11	63:Aa:45:MET:HE1	2.03	0.40
50:AN:70:ASN:HB3	50:AN:92:LEU:O	2.21	0.40
66:Ad:44:MET:SD	66:Ad:77:ARG:HB2	2.61	0.40
79:E:53:LEU:O	79:E:154:THR:OG1	2.24	0.40
79:E:77:ALA:HB3	79:E:84:ALA:HB2	2.02	0.40
80:DC:81:MET:HE1	80:DC:85:ASP:HB3	2.03	0.40
80:DC:212:GLY:HA3	80:DC:219:ALA:HA	2.03	0.40
80:DC:655:TYR:O	80:DC:659:ILE:HG13	2.21	0.40
1:BA:120:LEU:HD11	1:BA:144:ILE:HG13	2.03	0.40
1:BA:136:ALA:HB1	1:BA:141:ILE:HB	2.04	0.40
6:BH:173:TYR:CD2	6:BH:181:ILE:HD13	2.57	0.40
7:BI:138:ASN:ND2	34:B5:187:G:H2'	2.37	0.40
9:BL:75:VAL:HG21	9:BL:117:VAL:HG13	2.02	0.40
14:BX:108:GLY:HA2	34:B5:600:U:OP2	2.22	0.40
15:BY:32:ARG:HG2	15:BY:35:VAL:HG12	2.04	0.40
15:BY:127:LYS:NZ	34:B5:151:G:OP2	2.50	0.40
26:BT:47:PRO:HA	34:B5:1477:G:H4'	2.03	0.40
30:Bd:11:PRO:HB3	30:Bd:13:ARG:CZ	2.52	0.40
34:B5:91:G:OP1	34:B5:397:A:N6	2.53	0.40
34:B5:129:U:O4'	34:B5:264:G:N1	2.54	0.40
34:B5:358:U:H5''	34:B5:359:A:C2	2.56	0.40
34:B5:366:A:H2'	34:B5:367:A:H8	1.86	0.40
34:B5:598:U:H2'	34:B5:599:A:C8	2.55	0.40
34:B5:887:A:H2'	34:B5:888:U:H6	1.87	0.40
34:B5:1068:C:H2'	34:B5:1069:A:C8	2.57	0.40
34:B5:1558:U:H3'	34:B5:1559:A:H4'	2.02	0.40
34:B5:1626:U:H2'	34:B5:1627:U:C6	2.57	0.40
37:AC:23:PRO:HD2	37:AC:26:PHE:HD2	1.83	0.40
38:A1:36:C:H4'	38:A1:808:A:C2	2.56	0.40
38:A1:500:C:H2'	38:A1:501:A:C8	2.56	0.40
38:A1:632:G:H2'	38:A1:633:C:C6	2.55	0.40
38:A1:861:C:OP1	38:A1:2133:U:O2'	2.25	0.40
38:A1:1137:C:H2'	38:A1:1138:U:O4'	2.22	0.40
38:A1:1157:G:H2'	38:A1:1158:A:O4'	2.22	0.40
38:A1:1671:C:OP1	54:AR:60:LYS:HE2	2.22	0.40
38:A1:2722:U:H2'	38:A1:2723:U:C6	2.56	0.40
41:AD:65:ILE:HG12	41:AD:74:VAL:HG22	2.03	0.40
42:AE:93:VAL:O	42:AE:96:VAL:HG22	2.20	0.40
48:AL:4:SER:O	63:Aa:44:ASN:ND2	2.54	0.40
54:AR:66:HIS:O	54:AR:70:LYS:HG2	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:AT:92:ARG:HB3	56:AT:94:GLU:OE1	2.21	0.40
80:DC:393:ARG:HD2	80:DC:510:ARG:NH1	2.36	0.40
81:V:130:PRO:HB3	81:V:145:ILE:HD12	2.02	0.40
1:BA:88:LYS:HA	1:BA:88:LYS:HD3	1.82	0.40
2:BB:48:VAL:HG11	2:BB:61:LEU:HG	2.03	0.40
4:BE:75:LYS:HD2	4:BE:77:ARG:NH2	2.36	0.40
5:BG:145:PHE:CD2	5:BG:156:PHE:HB3	2.56	0.40
23:BQ:66:ARG:NH2	34:B5:1364:G:H5''	2.35	0.40
25:BS:113:LEU:HB3	25:BS:117:LYS:HZ2	1.85	0.40
27:BU:99:ILE:HA	27:BU:102:ARG:HG2	2.04	0.40
31:Bg:12:THR:OG1	31:Bg:14:GLU:OE2	2.24	0.40
31:Bg:18:GLY:HA3	31:Bg:38:ARG:HB2	2.03	0.40
32:Bf:122:SER:HB2	32:Bf:148:TYR:CZ	2.56	0.40
34:B5:228:G:C4	34:B5:835:U:H1'	2.57	0.40
34:B5:1619:C:C2	34:B5:1620:C:C5	3.10	0.40
34:B5:1642:G:H2'	34:B5:1643:U:C6	2.57	0.40
36:AB:347:SER:C	36:AB:349:LYS:H	2.30	0.40
37:AC:101:ALA:HA	38:A1:800:G:H22	1.86	0.40
38:A1:39:A:H5''	63:Aa:35:ALA:HB2	2.02	0.40
38:A1:87:U:H2'	38:A1:88:A:C8	2.57	0.40
38:A1:507:U:H2'	38:A1:508:U:C6	2.57	0.40
38:A1:1354:G:O2'	38:A1:1355:A:OP1	2.34	0.40
38:A1:1650:G:H2'	38:A1:1651:U:C6	2.56	0.40
38:A1:2453:U:H3'	38:A1:2462:A:OP1	2.22	0.40
38:A1:2493:U:O2'	38:A1:2494:A:H8	2.05	0.40
38:A1:3159:C:H2'	38:A1:3160:U:H6	1.86	0.40
51:AO:25[A]:LYS:HD2	51:AO:25[A]:LYS:HA	1.84	0.40
71:Ai:34:SER:H	71:Ai:37:THR:CG2	2.35	0.40
73:Ak:40:GLN:HE21	73:Ak:55:VAL:HG13	1.87	0.40
80:DC:348:ALA:HA	80:DC:351:TYR:CZ	2.56	0.40
82:EC:6908:C:C2	82:EC:6909:A:C8	3.09	0.40
11:BO:58:TYR:CZ	11:BO:62:LEU:HD11	2.56	0.40
14:BX:54:LEU:HD11	14:BX:75:GLN:HB2	2.03	0.40
20:BF:219:ARG:CZ	82:EC:6841:U:H1'	2.51	0.40
20:BF:219:ARG:HG2	82:EC:6841:U:H4'	2.03	0.40
28:BZ:60:VAL:HG12	28:BZ:80:LEU:HD21	2.03	0.40
31:Bg:74:THR:HG22	31:Bg:115:ILE:HG12	2.03	0.40
34:B5:1649:G:H2'	34:B5:1650:U:C6	2.57	0.40
35:AA:195:SER:O	35:AA:198:LYS:NZ	2.50	0.40
38:A1:393:U:H2'	38:A1:394:G:O4'	2.21	0.40
38:A1:649:A2M:H2'	38:A1:650:OMC:C6	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:727:G:O6	38:A1:742:G:O2'	2.37	0.40
38:A1:1448:U:H2'	38:A1:1449:A2M:C8	2.50	0.40
38:A1:1921:A:H2'	38:A1:1922:A:C8	2.56	0.40
43:AF:132:PRO:HA	43:AF:229:PHE:CD1	2.57	0.40
50:AN:84:PRO:HA	50:AN:87:GLN:HG3	2.03	0.40
62:AZ:115:LYS:HE3	62:AZ:119:GLU:OE2	2.21	0.40
63:Aa:125:VAL:O	63:Aa:146:GLU:N	2.50	0.40
67:Ae:4:LEU:HD23	67:Ae:4:LEU:HA	1.98	0.40
69:Ag:54:ILE:HD11	69:Ag:78:GLY:HA2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	187 (92%)	17 (8%)	0	100	100
2	BB	212/255 (83%)	187 (88%)	25 (12%)	0	100	100
3	BC	215/254 (85%)	206 (96%)	9 (4%)	0	100	100
4	BE	258/261 (99%)	246 (95%)	12 (5%)	0	100	100
5	BG	224/236 (95%)	214 (96%)	10 (4%)	0	100	100
6	BH	182/190 (96%)	168 (92%)	14 (8%)	0	100	100
7	BI	184/200 (92%)	167 (91%)	17 (9%)	0	100	100
8	BJ	183/197 (93%)	170 (93%)	13 (7%)	0	100	100
9	BL	153/156 (98%)	141 (92%)	12 (8%)	0	100	100
10	BN	148/151 (98%)	140 (95%)	8 (5%)	0	100	100
11	BO	125/137 (91%)	111 (89%)	14 (11%)	0	100	100
12	BV	85/87 (98%)	74 (87%)	11 (13%)	0	100	100
13	BW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	BX	142/145 (98%)	131 (92%)	11 (8%)	0	100	100
15	BY	132/135 (98%)	125 (95%)	7 (5%)	0	100	100
16	Ba	95/119 (80%)	82 (86%)	13 (14%)	0	100	100
17	Bb	79/82 (96%)	68 (86%)	11 (14%)	0	100	100
18	Be	58/63 (92%)	49 (84%)	9 (16%)	0	100	100
19	BD	221/240 (92%)	210 (95%)	11 (5%)	0	100	100
20	BF	204/225 (91%)	183 (90%)	21 (10%)	0	100	100
21	BK	94/105 (90%)	82 (87%)	12 (13%)	0	100	100
22	BP	122/142 (86%)	113 (93%)	9 (7%)	0	100	100
23	BQ	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
24	BR	117/136 (86%)	112 (96%)	5 (4%)	0	100	100
25	BS	143/146 (98%)	131 (92%)	12 (8%)	0	100	100
26	BT	139/144 (96%)	130 (94%)	9 (6%)	0	100	100
27	BU	105/121 (87%)	97 (92%)	8 (8%)	0	100	100
28	BZ	67/108 (62%)	63 (94%)	4 (6%)	0	100	100
29	Bc	61/67 (91%)	54 (88%)	7 (12%)	0	100	100
30	Bd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
31	Bg	310/319 (97%)	276 (89%)	34 (11%)	0	100	100
32	Bf	73/152 (48%)	64 (88%)	9 (12%)	0	100	100
33	BM	122/143 (85%)	111 (91%)	11 (9%)	0	100	100
35	AA	245/254 (96%)	232 (95%)	13 (5%)	0	100	100
36	AB	383/387 (99%)	365 (95%)	18 (5%)	0	100	100
37	AC	359/362 (99%)	334 (93%)	25 (7%)	0	100	100
41	AD	290/297 (98%)	276 (95%)	14 (5%)	0	100	100
42	AE	152/176 (86%)	141 (93%)	11 (7%)	0	100	100
43	AF	220/244 (90%)	212 (96%)	8 (4%)	0	100	100
44	AG	228/256 (89%)	211 (92%)	17 (8%)	0	100	100
45	AH	188/191 (98%)	174 (93%)	14 (7%)	0	100	100
46	AI	201/221 (91%)	193 (96%)	8 (4%)	0	100	100
47	AJ	167/174 (96%)	147 (88%)	20 (12%)	0	100	100
48	AL	191/199 (96%)	179 (94%)	12 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	AM	134/138 (97%)	128 (96%)	6 (4%)	0	100	100
50	AN	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
51	AO	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
52	AP	171/184 (93%)	167 (98%)	4 (2%)	0	100	100
53	AQ	183/186 (98%)	180 (98%)	3 (2%)	0	100	100
54	AR	186/189 (98%)	179 (96%)	7 (4%)	0	100	100
55	AS	170/178 (96%)	163 (96%)	7 (4%)	0	100	100
56	AT	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
57	AU	98/121 (81%)	94 (96%)	4 (4%)	0	100	100
58	AV	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
59	AW	61/155 (39%)	61 (100%)	0	0	100	100
60	AX	119/142 (84%)	113 (95%)	6 (5%)	0	100	100
61	AY	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
62	AZ	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
63	Aa	146/149 (98%)	137 (94%)	9 (6%)	0	100	100
64	Ab	56/59 (95%)	49 (88%)	7 (12%)	0	100	100
65	Ac	95/105 (90%)	93 (98%)	2 (2%)	0	100	100
66	Ad	107/113 (95%)	103 (96%)	4 (4%)	0	100	100
67	Ae	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
68	Af	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
69	Ag	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
70	Ah	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
71	Ai	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
72	Aj	85/88 (97%)	83 (98%)	2 (2%)	0	100	100
73	Ak	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
74	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
75	Am	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	100/106 (94%)	93 (93%)	7 (7%)	0	100	100
78	Ap	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
79	E	215/217 (99%)	204 (95%)	11 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
80	DC	819/842 (97%)	768 (94%)	51 (6%)	0	100	100
81	V	187/312 (60%)	176 (94%)	11 (6%)	0	100	100
All	All	12112/13257 (91%)	11374 (94%)	738 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	110/124 (89%)	110 (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
32	Bf	66/135 (49%)	66 (100%)	0	100	100
33	BM	100/119 (84%)	100 (100%)	0	100	100
35	AA	189/196 (96%)	189 (100%)	0	100	100
36	AB	321/322 (100%)	321 (100%)	0	100	100
37	AC	288/289 (100%)	288 (100%)	0	100	100
41	AD	241/245 (98%)	241 (100%)	0	100	100
42	AE	134/153 (88%)	134 (100%)	0	100	100
43	AF	186/205 (91%)	186 (100%)	0	100	100
44	AG	189/208 (91%)	189 (100%)	0	100	100
45	AH	170/171 (99%)	170 (100%)	0	100	100
46	AI	176/187 (94%)	176 (100%)	0	100	100
47	AJ	147/150 (98%)	147 (100%)	0	100	100
48	AL	154/159 (97%)	154 (100%)	0	100	100
49	AM	107/109 (98%)	107 (100%)	0	100	100
50	AN	175/176 (99%)	175 (100%)	0	100	100
51	AO	160/162 (99%)	160 (100%)	0	100	100
52	AP	141/146 (97%)	141 (100%)	0	100	100
53	AQ	150/151 (99%)	150 (100%)	0	100	100
54	AR	153/154 (99%)	153 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	AS	156/162 (96%)	156 (100%)	0	100	100
56	AT	136/137 (99%)	136 (100%)	0	100	100
57	AU	87/107 (81%)	87 (100%)	0	100	100
58	AV	104/105 (99%)	104 (100%)	0	100	100
59	AW	55/129 (43%)	55 (100%)	0	100	100
60	AX	105/118 (89%)	105 (100%)	0	100	100
61	AY	109/110 (99%)	109 (100%)	0	100	100
62	AZ	115/116 (99%)	115 (100%)	0	100	100
63	Aa	118/119 (99%)	118 (100%)	0	100	100
64	Ab	46/47 (98%)	46 (100%)	0	100	100
65	Ac	81/88 (92%)	81 (100%)	0	100	100
66	Ad	96/97 (99%)	96 (100%)	0	100	100
67	Ae	109/111 (98%)	109 (100%)	0	100	100
68	Af	90/91 (99%)	90 (100%)	0	100	100
69	Ag	95/103 (92%)	95 (100%)	0	100	100
70	Ah	104/105 (99%)	104 (100%)	0	100	100
71	Ai	81/82 (99%)	81 (100%)	0	100	100
72	Aj	70/71 (99%)	70 (100%)	0	100	100
73	Ak	68/69 (99%)	68 (100%)	0	100	100
74	Al	45/46 (98%)	45 (100%)	0	100	100
75	Am	47/116 (40%)	47 (100%)	0	100	100
76	An	23/23 (100%)	23 (100%)	0	100	100
77	Ao	87/91 (96%)	87 (100%)	0	100	100
78	Ap	71/72 (99%)	71 (100%)	0	100	100
79	E	198/198 (100%)	198 (100%)	0	100	100
80	DC	699/714 (98%)	699 (100%)	0	100	100
81	V	160/254 (63%)	160 (100%)	0	100	100
All	All	10343/11154 (93%)	10343 (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 (142) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	30	GLN
1	BA	39	ASN
2	BB	42	ASN
2	BB	74	GLN
2	BB	199	ASN
2	BB	209	ASN
2	BB	211	HIS
2	BB	220	GLN
3	BC	233	GLN
4	BE	67	GLN
4	BE	153	ASN
4	BE	157	ASN
6	BH	161	GLN
7	BI	103	GLN
8	BJ	38	ASN
8	BJ	155	HIS
8	BJ	176	ASN
9	BL	14	GLN
9	BL	92	HIS
10	BN	21	ASN
10	BN	62	GLN
10	BN	78	ASN
12	BV	70	ASN
15	BY	22	GLN
15	BY	107	GLN
18	Be	17	GLN
19	BD	162	GLN
19	BD	165	ASN
19	BD	174	HIS
20	BF	35	GLN
20	BF	63	GLN
21	BK	28	ASN
22	BP	104	GLN
23	BQ	100	GLN
23	BQ	139	GLN
24	BR	62	GLN
24	BR	83	GLN
25	BS	13	HIS
25	BS	21	ASN
25	BS	44	ASN
26	BT	101	ASN
27	BU	36	ASN
27	BU	98	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	Bd	5	ASN
31	Bg	29	GLN
31	Bg	174	ASN
31	Bg	184	ASN
31	Bg	288	HIS
33	BM	38	HIS
33	BM	96	GLN
35	AA	47	GLN
35	AA	97	ASN
35	AA	215	ASN
36	AB	182	GLN
37	AC	5	GLN
37	AC	213	ASN
37	AC	291	ASN
37	AC	361	HIS
41	AD	32	GLN
41	AD	151	GLN
41	AD	178	ASN
41	AD	206	GLN
42	AE	97	ASN
44	AG	61	GLN
45	AH	9	GLN
45	AH	50	ASN
45	AH	51	GLN
45	AH	58	HIS
45	AH	100	ASN
45	AH	125	ASN
46	AI	59	GLN
47	AJ	95	ASN
47	AJ	150	ASN
49	AM	27	GLN
49	AM	119	GLN
50	AN	32	GLN
51	AO	31[A]	GLN
51	AO	193[A]	GLN
52	AP	97	ASN
52	AP	133	HIS
53	AQ	58	ASN
53	AQ	135	GLN
53	AQ	158	HIS
54	AR	144	GLN
54	AR	166	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
55	AS	46	GLN
55	AS	62	ASN
55	AS	68	HIS
55	AS	157	GLN
56	AT	134	GLN
56	AT	149	GLN
57	AU	40	HIS
57	AU	49	ASN
58	AV	7	GLN
58	AV	28	ASN
58	AV	98	ASN
60	AX	137	ASN
62	AZ	36	HIS
62	AZ	106	GLN
62	AZ	127	ASN
63	Aa	65	GLN
64	Ab	6	ASN
65	Ac	36	GLN
66	Ad	21	HIS
66	Ad	57	GLN
66	Ad	80	ASN
66	Ad	87	ASN
67	Ae	20	HIS
67	Ae	52	GLN
68	Af	17	GLN
68	Af	24	ASN
68	Af	26	ASN
68	Af	87	ASN
68	Af	106	ASN
69	Ag	3	GLN
69	Ag	61	GLN
69	Ag	69	HIS
69	Ag	108	GLN
70	Ah	76	GLN
70	Ah	99	GLN
71	Ai	63	ASN
72	Aj	69	HIS
73	Ak	10	GLN
73	Ak	40	GLN
73	Ak	67	GLN
74	Al	11	GLN
75	Am	117	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
77	Ao	90	HIS
77	Ao	102	GLN
79	E	35	GLN
79	E	44	GLN
79	E	94	ASN
80	DC	30	HIS
80	DC	259	ASN
80	DC	341	HIS
80	DC	477	ASN
80	DC	543	GLN
80	DC	694	HIS
80	DC	786	GLN
81	V	32	ASN
81	V	103	ASN
81	V	163	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1780/1798 (98%)	408 (22%)	10 (0%)
38	A1	3194/3199 (99%)	592 (18%)	25 (0%)
39	A3	120/121 (99%)	10 (8%)	1 (0%)
40	A4	157/158 (99%)	33 (21%)	0
82	EC	191/202 (94%)	108 (56%)	7 (3%)
All	All	5442/5478 (99%)	1151 (21%)	43 (0%)

All (1151) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	2	A
34	B5	4	C
34	B5	20	G
34	B5	26	A
34	B5	34	G
34	B5	42	G
34	B5	43	A
34	B5	45	U
34	B5	46	A
34	B5	47	A
34	B5	57	G
34	B5	60	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B5	67	A
34	B5	68	A
34	B5	72	A
34	B5	74	U
34	B5	75	U
34	B5	76	A
34	B5	77	U
34	B5	81	G
34	B5	104	A
34	B5	111	U
34	B5	114	C
34	B5	127	G
34	B5	129	U
34	B5	130	C
34	B5	131	C
34	B5	132	U
34	B5	133	U
34	B5	134	U
34	B5	135	A
34	B5	136	C
34	B5	137	U
34	B5	140	A
34	B5	141	U
34	B5	145	A
34	B5	158	U
34	B5	166	C
34	B5	178	U
34	B5	179	A
34	B5	181	A
34	B5	182	A
34	B5	188	A
34	B5	190	C
34	B5	191	C
34	B5	192	U
34	B5	193	U
34	B5	194	U
34	B5	195	G
34	B5	196	G
34	B5	197	A
34	B5	200	A
34	B5	204	G
34	B5	217	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B5	218	A
34	B5	219	A
34	B5	224	C
34	B5	225	A
34	B5	227	U
34	B5	229	U
34	B5	230	C
34	B5	232	U
34	B5	233	C
34	B5	234	G
34	B5	236	A
34	B5	240	U
34	B5	241	U
34	B5	249	U
34	B5	257	A
34	B5	260	U
34	B5	261	U
34	B5	262	U
34	B5	265	A
34	B5	266	A
34	B5	271	A
34	B5	276	C
34	B5	278	U
34	B5	280	U
34	B5	299	A
34	B5	305	C
34	B5	314	C
34	B5	316	A
34	B5	321	C
34	B5	322	G
34	B5	333	A
34	B5	337	G
34	B5	338	C
34	B5	352	A
34	B5	359	A
34	B5	360	A
34	B5	361	C
34	B5	370	A
34	B5	390	G
34	B5	397	A
34	B5	400	A
34	B5	401	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B5	402	C
34	B5	419	G
34	B5	423	G
34	B5	424	C
34	B5	425	A
34	B5	426	G
34	B5	434	G
34	B5	439	U
34	B5	444	C
34	B5	454	U
34	B5	460	A
34	B5	475	A
34	B5	477	A
34	B5	480	G
34	B5	484	C
34	B5	485	A
34	B5	486	G
34	B5	489	C
34	B5	490	C
34	B5	491	C
34	B5	492	A
34	B5	493	U
34	B5	494	U
34	B5	495	C
34	B5	496	G
34	B5	497	G
34	B5	498	G
34	B5	499	U
34	B5	500	C
34	B5	501	U
34	B5	503	G
34	B5	504	U
34	B5	506	A
34	B5	507	U
34	B5	514	G
34	B5	515	A
34	B5	519	C
34	B5	538	A
34	B5	539	G
34	B5	540	G
34	B5	541	A2M
34	B5	542	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B5	544	A
34	B5	555	A
34	B5	557	G
34	B5	558	U
34	B5	559	C
34	B5	565	C
34	B5	568	G
34	B5	575	C
34	B5	577	G
34	B5	579	A
34	B5	580	A
34	B5	581	U
34	B5	582	U
34	B5	594	A
34	B5	595	G
34	B5	606	A
34	B5	610	G
34	B5	611	U
34	B5	619	A2M
34	B5	620	A
34	B5	621	A
34	B5	622	A
34	B5	623	A
34	B5	624	G
34	B5	635	A
34	B5	638	U
34	B5	639	U
34	B5	650	U
34	B5	652	G
34	B5	655	G
34	B5	656	G
34	B5	658	C
34	B5	677	G
34	B5	678	A
34	B5	681	U
34	B5	683	C
34	B5	694	U
34	B5	696	C
34	B5	697	C
34	B5	698	U
34	B5	704	C
34	B5	705	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B5	709	C
34	B5	711	U
34	B5	712	G
34	B5	713	A
34	B5	715	U
34	B5	716	C
34	B5	717	C
34	B5	718	U
34	B5	719	U
34	B5	721	U
34	B5	722	G
34	B5	724	C
34	B5	725	U
34	B5	726	C
34	B5	727	U
34	B5	728	U
34	B5	729	G
34	B5	730	G
34	B5	731	C
34	B5	732	G
34	B5	733	A
34	B5	734	A
34	B5	735	C
34	B5	738	G
34	B5	740	A
34	B5	741	C
34	B5	743	U
34	B5	753	A
34	B5	755	A
34	B5	765	G
34	B5	766	U
34	B5	771	A
34	B5	774	A
34	B5	775	G
34	B5	778	G
34	B5	779	U
34	B5	781	U
34	B5	782	U
34	B5	783	G
34	B5	784	C
34	B5	789	A
34	B5	794	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B5	812	A
34	B5	814	A
34	B5	820	U
34	B5	821	U
34	B5	823	G
34	B5	832	U
34	B5	833	U
34	B5	836	U
34	B5	840	U
34	B5	846	G
34	B5	850	A
34	B5	851	U
34	B5	859	A
34	B5	863	A
34	B5	873	U
34	B5	877	G
34	B5	886	U
34	B5	895	G
34	B5	898	A
34	B5	906	A
34	B5	907	A
34	B5	914	G
34	B5	922	G
34	B5	931	C
34	B5	933	A
34	B5	935	U
34	B5	951	A
34	B5	960	U
34	B5	966	A
34	B5	988	A
34	B5	992	A
34	B5	993	A
34	B5	1004	U
34	B5	1005	A
34	B5	1025	A
34	B5	1026	A
34	B5	1028	C
34	B5	1039	A
34	B5	1052	U
34	B5	1053	G
34	B5	1056	U
34	B5	1059	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B5	1060	U
34	B5	1061	A
34	B5	1062	A
34	B5	1076	A
34	B5	1083	G
34	B5	1092	A
34	B5	1097	U
34	B5	1098	U
34	B5	1100	G
34	B5	1126	OMG
34	B5	1138	A
34	B5	1150	G
34	B5	1158	C
34	B5	1171	A
34	B5	1183	A
34	B5	1185	U
34	B5	1186	U
34	B5	1194	A
34	B5	1196	A
34	B5	1199	G
34	B5	1200	G
34	B5	1201	G
34	B5	1214	U
34	B5	1217	A
34	B5	1218	G
34	B5	1226	A
34	B5	1227	A
34	B5	1228	G
34	B5	1229	G
34	B5	1243	G
34	B5	1244	A
34	B5	1245	G
34	B5	1246	C
34	B5	1248	C
34	B5	1249	U
34	B5	1251	U
34	B5	1252	C
34	B5	1256	A
34	B5	1257	U
34	B5	1269	OMU
34	B5	1276	U
34	B5	1286	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B5	1301	U
34	B5	1306	C
34	B5	1307	U
34	B5	1314	U
34	B5	1315	U
34	B5	1316	G
34	B5	1321	A
34	B5	1340	U
34	B5	1344	A
34	B5	1345	A
34	B5	1346	A
34	B5	1349	G
34	B5	1353	U
34	B5	1355	C
34	B5	1362	U
34	B5	1363	U
34	B5	1364	G
34	B5	1368	G
34	B5	1370	U
34	B5	1371	A
34	B5	1372	U
34	B5	1373	C
34	B5	1383	G
34	B5	1390	U
34	B5	1392	U
34	B5	1398	U
34	B5	1399	C
34	B5	1400	A
34	B5	1402	G
34	B5	1413	U
34	B5	1415	U
34	B5	1425	A
34	B5	1427	A
34	B5	1428	OMG
34	B5	1432	U
34	B5	1433	G
34	B5	1436	A
34	B5	1444	A
34	B5	1445	G
34	B5	1446	A
34	B5	1459	C
34	B5	1460	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B5	1469	A
34	B5	1471	A
34	B5	1481	C
34	B5	1486	G
34	B5	1488	G
34	B5	1491	U
34	B5	1492	A
34	B5	1493	A
34	B5	1516	A
34	B5	1518	C
34	B5	1521	G
34	B5	1523	G
34	B5	1524	A
34	B5	1537	C
34	B5	1540	G
34	B5	1542	G
34	B5	1548	G
34	B5	1557	U
34	B5	1558	U
34	B5	1559	A
34	B5	1576	A
34	B5	1584	G
34	B5	1601	G
34	B5	1634	C
34	B5	1635	A
34	B5	1646	C
34	B5	1657	U
34	B5	1658	G
34	B5	1680	G
34	B5	1682	U
34	B5	1683	C
34	B5	1684	U
34	B5	1688	U
34	B5	1693	A
34	B5	1698	G
34	B5	1700	C
34	B5	1701	A
34	B5	1703	C
34	B5	1709	C
34	B5	1711	C
34	B5	1715	G
34	B5	1716	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B5	1717	G
34	B5	1755	A
34	B5	1756[A]	A
34	B5	1757	G
34	B5	1760	G
34	B5	1762	A
34	B5	1766	A
34	B5	1767	G
34	B5	1769	U
34	B5	1780	G
34	B5	1782	MA6
34	B5	1783	C
34	B5	1792	G
34	B5	1793	G
34	B5	1794	A
34	B5	1795	U
34	B5	1796	C
34	B5	1799	U
38	A1	26	A
38	A1	34	A
38	A1	40	A
38	A1	43	A
38	A1	49	A
38	A1	59	G
38	A1	60	A
38	A1	65	A
38	A1	66	A
38	A1	77	A
38	A1	92	G
38	A1	99	A
38	A1	109	A
38	A1	110	G
38	A1	111	C
38	A1	116	A
38	A1	120	G
38	A1	121	A
38	A1	122	A
38	A1	134	U
38	A1	135	C
38	A1	136	G
38	A1	147	U
38	A1	156	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	157	A
38	A1	164	A
38	A1	165	A
38	A1	166	C
38	A1	169	U
38	A1	170	G
38	A1	173	G
38	A1	174	C
38	A1	175	C
38	A1	176	G
38	A1	177	U
38	A1	187	A
38	A1	190	U
38	A1	191	U
38	A1	200	C
38	A1	210	U
38	A1	211	A
38	A1	219	A
38	A1	234	G
38	A1	237	G
38	A1	240	U
38	A1	241	G
38	A1	242	C
38	A1	243	G
38	A1	244	G
38	A1	245	U
38	A1	246	U
38	A1	248	U
38	A1	249	U
38	A1	250	U
38	A1	251	G
38	A1	252	U
38	A1	253	A
38	A1	269	G
38	A1	286	U
38	A1	295	A
38	A1	296	A
38	A1	298	U
38	A1	305	U
38	A1	315	C
38	A1	329	U
38	A1	339	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	352	A
38	A1	372	A
38	A1	373	A
38	A1	376	G
38	A1	387	A
38	A1	398	A
38	A1	399	A
38	A1	401	U
38	A1	402	A
38	A1	403	C
38	A1	420	G
38	A1	421	G
38	A1	422	A
38	A1	438	A
38	A1	440	A
38	A1	495	G
38	A1	503	C
38	A1	521	A
38	A1	523	A
38	A1	535	G
38	A1	538	G
38	A1	540	U
38	A1	542	G
38	A1	545	U
38	A1	547	G
38	A1	548	G
38	A1	549	U
38	A1	552	G
38	A1	557	A
38	A1	558	U
38	A1	559	A
38	A1	560	G
38	A1	578	A
38	A1	579	G
38	A1	589	A
38	A1	604	G
38	A1	611	A
38	A1	612	U
38	A1	620	U
38	A1	621	A
38	A1	636	C
38	A1	649	A2M

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	660	A
38	A1	677	A
38	A1	681	U
38	A1	690	A
38	A1	705	A
38	A1	715	A
38	A1	725	G
38	A1	758	C
38	A1	763	G
38	A1	765	C
38	A1	766	U
38	A1	767	U
38	A1	774	G
38	A1	777	U
38	A1	781	G
38	A1	785	G
38	A1	786	A
38	A1	799	G
38	A1	801	A
38	A1	806	A
38	A1	813	G
38	A1	817	A2M
38	A1	830	A
38	A1	837	A
38	A1	849	C
38	A1	857	G
38	A1	861	C
38	A1	874	U
38	A1	879	U
38	A1	896	A
38	A1	897	U
38	A1	907	G
38	A1	908	OMG
38	A1	914	A
38	A1	916	G
38	A1	917	A
38	A1	921	A
38	A1	923	C
38	A1	924	G
38	A1	925	A
38	A1	934	G
38	A1	937	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	943	U
38	A1	944	C
38	A1	953	G
38	A1	959	C
38	A1	961	C
38	A1	964	G
38	A1	980	A
38	A1	981	U
38	A1	983	A
38	A1	995	U
38	A1	1002	A
38	A1	1010	G
38	A1	1014	U
38	A1	1016	C
38	A1	1017	C
38	A1	1018	G
38	A1	1019	G
38	A1	1021	G
38	A1	1022	U
38	A1	1032	C
38	A1	1033	U
38	A1	1034	U
38	A1	1035	G
38	A1	1036	A
38	A1	1041	U
38	A1	1047	A
38	A1	1064	A
38	A1	1072	G
38	A1	1081	U
38	A1	1082	U
38	A1	1093	A
38	A1	1094	U
38	A1	1095	U
38	A1	1096	U
38	A1	1097	G
38	A1	1098	A
38	A1	1103	A
38	A1	1104	G
38	A1	1117	G
38	A1	1130	A
38	A1	1131	G
38	A1	1144	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	1153	A
38	A1	1159	A
38	A1	1160	C
38	A1	1179	A
38	A1	1180	A
38	A1	1181	U
38	A1	1182	A
38	A1	1186	G
38	A1	1192	C
38	A1	1193	A
38	A1	1201	C
38	A1	1206	G
38	A1	1208	U
38	A1	1219	C
38	A1	1222	G
38	A1	1223	A
38	A1	1226	G
38	A1	1228	C
38	A1	1231	A
38	A1	1232	C
38	A1	1235	U
38	A1	1236	G
38	A1	1237	G
38	A1	1242	G
38	A1	1243	G
38	A1	1244	A
38	A1	1245	A
38	A1	1246	G
38	A1	1249	G
38	A1	1256	G
38	A1	1258	U
38	A1	1259	A
38	A1	1263	A
38	A1	1265	U
38	A1	1269	U
38	A1	1272	C
38	A1	1279	C
38	A1	1281	G
38	A1	1282	G
38	A1	1283	C
38	A1	1284	C
38	A1	1285	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	1286	A
38	A1	1287	A
38	A1	1292	C
38	A1	1293	U
38	A1	1305	U
38	A1	1307	G
38	A1	1309	U
38	A1	1317	A
38	A1	1330	A
38	A1	1331	U
38	A1	1348	U
38	A1	1349	G
38	A1	1350	A
38	A1	1351	U
38	A1	1352	A
38	A1	1353	U
38	A1	1354	G
38	A1	1355	A
38	A1	1356	U
38	A1	1357	G
38	A1	1386	A
38	A1	1392	G
38	A1	1399	A
38	A1	1400	G
38	A1	1419	A
38	A1	1431	G
38	A1	1434	G
38	A1	1436	U
38	A1	1437	OMC
38	A1	1443	G
38	A1	1446	A
38	A1	1448	U
38	A1	1455	U
38	A1	1469	C
38	A1	1481	A
38	A1	1482	A
38	A1	1496	C
38	A1	1508	C
38	A1	1522	U
38	A1	1523	U
38	A1	1527	C
38	A1	1539	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	1555	U
38	A1	1556	C
38	A1	1562	C
38	A1	1564	U
38	A1	1565	G
38	A1	1566	A
38	A1	1567	U
38	A1	1568	U
38	A1	1569	U
38	A1	1572	U
38	A1	1573	G
38	A1	1574	C
38	A1	1575	A
38	A1	1576	G
38	A1	1579	C
38	A1	1583	A
38	A1	1587	A
38	A1	1589	A
38	A1	1591	G
38	A1	1593	A
38	A1	1605	A
38	A1	1613	A
38	A1	1628	C
38	A1	1629	U
38	A1	1630	U
38	A1	1642	A
38	A1	1643	A
38	A1	1657	C
38	A1	1724	U
38	A1	1736	G
38	A1	1741	A
38	A1	1750	A
38	A1	1751	G
38	A1	1762	C
38	A1	1763	U
38	A1	1764	U
38	A1	1765	U
38	A1	1766	G
38	A1	1775	G
38	A1	1780	G
38	A1	1797	A
38	A1	1808	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	1813	A
38	A1	1815	U
38	A1	1817	G
38	A1	1820	U
38	A1	1821	U
38	A1	1842	A
38	A1	1846	C
38	A1	1849	C
38	A1	1850	A
38	A1	1866	C
38	A1	1878	G
38	A1	1880	U
38	A1	1886	A
38	A1	1893	A
38	A1	1899	G
38	A1	1906	G
38	A1	1932	A
38	A1	1946	A
38	A1	1953	G
38	A1	1954	G
38	A1	1955	U
38	A1	2110	G
38	A1	2112	U
38	A1	2114	C
38	A1	2122	G
38	A1	2131	A
38	A1	2140	U
38	A1	2144	A
38	A1	2158	A
38	A1	2169	G
38	A1	2176	U
38	A1	2188	A
38	A1	2197	OMC
38	A1	2201	G
38	A1	2206	G
38	A1	2207	A
38	A1	2209	U
38	A1	2242	A
38	A1	2249	G
38	A1	2259	A
38	A1	2260	U
38	A1	2263	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	2269	U
38	A1	2270	A
38	A1	2272	G
38	A1	2273	G
38	A1	2280	A2M
38	A1	2281	A2M
38	A1	2282	U
38	A1	2284	C
38	A1	2307	G
38	A1	2308	C
38	A1	2310	U
38	A1	2313	A
38	A1	2314	U
38	A1	2315	G
38	A1	2334	U
38	A1	2335	G
38	A1	2336	U
38	A1	2340	U
38	A1	2373	A
38	A1	2374	C
38	A1	2375	G
38	A1	2376	G
38	A1	2383	C
38	A1	2388	U
38	A1	2393	G
38	A1	2394	G
38	A1	2397	A
38	A1	2402	A
38	A1	2403	G
38	A1	2404	A
38	A1	2411	U
38	A1	2418	G
38	A1	2435	G
38	A1	2447	A
38	A1	2448	G
38	A1	2450	G
38	A1	2451	G
38	A1	2452	G
38	A1	2453	U
38	A1	2454	G
38	A1	2455	U
38	A1	2458	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	2459	A
38	A1	2460	U
38	A1	2461	A
38	A1	2462	A
38	A1	2463	G
38	A1	2467	G
38	A1	2468	A
38	A1	2469	G
38	A1	2470	C
38	A1	2473	C
38	A1	2474	G
38	A1	2475	G
38	A1	2477	G
38	A1	2479	C
38	A1	2480	A
38	A1	2485	A
38	A1	2486	A
38	A1	2487	U
38	A1	2489	C
38	A1	2490	C
38	A1	2492	C
38	A1	2493	U
38	A1	2495	C
38	A1	2497	U
38	A1	2498	U
38	A1	2499	U
38	A1	2502	A
38	A1	2504	U
38	A1	2505	U
38	A1	2506	U
38	A1	2507	C
38	A1	2514	U
38	A1	2522	G
38	A1	2523	A
38	A1	2524	A
38	A1	2530	G
38	A1	2537	U
38	A1	2538	U
38	A1	2539	C
38	A1	2540	A
38	A1	2541	U
38	A1	2542	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	2544	U
38	A1	2549	G
38	A1	2552	C
38	A1	2561	A
38	A1	2569	A
38	A1	2571	U
38	A1	2572	C
38	A1	2573	G
38	A1	2585	G
38	A1	2586	G
38	A1	2593	A
38	A1	2606	G
38	A1	2607	G
38	A1	2614	G
38	A1	2629	U
38	A1	2642	A
38	A1	2651	G
38	A1	2652	U
38	A1	2656	A
38	A1	2674	A
38	A1	2677	G
38	A1	2678	A
38	A1	2681	U
38	A1	2688	U
38	A1	2689	A
38	A1	2691	A
38	A1	2704	A
38	A1	2705	A
38	A1	2714	G
38	A1	2719	U
38	A1	2728	G
38	A1	2729	OMU
38	A1	2737	C
38	A1	2749	G
38	A1	2752	U
38	A1	2753	G
38	A1	2755	C
38	A1	2772	C
38	A1	2777	G
38	A1	2778	G
38	A1	2796	G
38	A1	2799	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	2800	G
38	A1	2801	A
38	A1	2803	A
38	A1	2810	C
38	A1	2814	G
38	A1	2817	A
38	A1	2822	U
38	A1	2842	U
38	A1	2844	C
38	A1	2845	A
38	A1	2849	C
38	A1	2860	U
38	A1	2861	U
38	A1	2871	G
38	A1	2872	A
38	A1	2875	U
38	A1	2876	C
38	A1	2887	A
38	A1	2898	G
38	A1	2923	U
38	A1	2933	A
38	A1	2935	U
38	A1	2936	A
38	A1	2942	C
38	A1	2947	G
38	A1	2977	G
38	A1	2983	C
38	A1	2990	G
38	A1	2992	U
38	A1	2997	G
38	A1	3011	A
38	A1	3012	A
38	A1	3022	G
38	A1	3032	A
38	A1	3056	U
38	A1	3059	G
38	A1	3078	U
38	A1	3079	U
38	A1	3086	A
38	A1	3087	A
38	A1	3092	C
38	A1	3109	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	3122	A
38	A1	3130	A
38	A1	3131	U
38	A1	3142	A
38	A1	3143	C
38	A1	3153	U
38	A1	3154	C
38	A1	3155	U
38	A1	3156	U
38	A1	3157	U
38	A1	3165	A
38	A1	3170	A
38	A1	3172	A
38	A1	3173	G
38	A1	3174	A
38	A1	3175	U
38	A1	3176	G
38	A1	3179	U
38	A1	3181	C
38	A1	3186	A
38	A1	3187	A
38	A1	3198	U
38	A1	3199	G
38	A1	3207	U
38	A1	3210	A
38	A1	3213	A
38	A1	3216	G
38	A1	3217	C
38	A1	3218	A
38	A1	3219	G
38	A1	3224	G
38	A1	3234	A
38	A1	3243	A
38	A1	3244	A
38	A1	3247	G
38	A1	3259	U
38	A1	3263	G
38	A1	3270	U
38	A1	3275	U
38	A1	3276	G
38	A1	3281	U
38	A1	3289	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	3294	A
38	A1	3303	G
38	A1	3304	U
38	A1	3307	A
38	A1	3309	G
38	A1	3313	U
38	A1	3314	A
38	A1	3316	A
38	A1	3342	A
38	A1	3345	G
38	A1	3351	U
38	A1	3352	U
38	A1	3353	G
38	A1	3354	U
38	A1	3355	U
38	A1	3356	G
38	A1	3369	G
38	A1	3375	A
38	A1	3378	C
38	A1	3382	U
38	A1	3389	U
38	A1	3390	G
39	A3	35	C
39	A3	53	U
39	A3	54	U
39	A3	65	G
39	A3	74	C
39	A3	78	U
39	A3	91	G
39	A3	102	A
39	A3	112	G
39	A3	121	U
40	A4	13	A
40	A4	23	U
40	A4	25	G
40	A4	34	U
40	A4	35	C
40	A4	38	U
40	A4	51	G
40	A4	52	A
40	A4	59	A
40	A4	60	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
40	A4	62	C
40	A4	63	G
40	A4	75	G
40	A4	80	A
40	A4	81	U
40	A4	82	U
40	A4	83	C
40	A4	86	U
40	A4	87	G
40	A4	88	A
40	A4	90	U
40	A4	95	G
40	A4	97	A
40	A4	104	A
40	A4	106	C
40	A4	107	G
40	A4	111	A
40	A4	113	U
40	A4	116	G
40	A4	125	U
40	A4	152	G
40	A4	154	C
40	A4	158	U
82	EC	6762	U
82	EC	6768	U
82	EC	6769	A
82	EC	6770	U
82	EC	6771	U
82	EC	6772	G
82	EC	6773	G
82	EC	6774	U
82	EC	6775	U
82	EC	6776	A
82	EC	6777	C
82	EC	6778	C
82	EC	6779	C
82	EC	6780	A
82	EC	6781	U
82	EC	6782	C
82	EC	6789	G
82	EC	6790	A
82	EC	6791	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	EC	6792	A
82	EC	6793	A
82	EC	6794	C
82	EC	6795	U
82	EC	6800	G
82	EC	6801	A
82	EC	6802	A
82	EC	6803	C
82	EC	6804	A
82	EC	6809	G
82	EC	6812	C
82	EC	6816	A
82	EC	6817	A
82	EC	6818	G
82	EC	6819	G
82	EC	6820	C
82	EC	6821	U
82	EC	6822	U
82	EC	6823	U
82	EC	6824	C
82	EC	6825	A
82	EC	6831	U
82	EC	6832	G
82	EC	6835	U
82	EC	6837	G
82	EC	6840	A
82	EC	6841	U
82	EC	6842	U
82	EC	6843	U
82	EC	6844	A
82	EC	6845	G
82	EC	6847	G
82	EC	6848	U
82	EC	6849	A
82	EC	6850	C
82	EC	6852	U
82	EC	6856	C
82	EC	6857	C
82	EC	6858	A
82	EC	6859	U
82	EC	6860	A
82	EC	6864	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	EC	6865	G
82	EC	6866	C
82	EC	6867	C
82	EC	6870	A
82	EC	6871	A
82	EC	6872	A
82	EC	6873	A
82	EC	6874	A
82	EC	6875	C
82	EC	6877	C
82	EC	6880	G
82	EC	6881	U
82	EC	6882	G
82	EC	6883	A
82	EC	6884	G
82	EC	6887	G
82	EC	6888	A
82	EC	6890	A
82	EC	6891	G
82	EC	6895	C
82	EC	6896	A
82	EC	6897	G
82	EC	6902	U
82	EC	6903	U
82	EC	6908	C
82	EC	6911	A
82	EC	6915	G
82	EC	6916	A
82	EC	6918	A
82	EC	6922	G
82	EC	6925	C
82	EC	6928	G
82	EC	6929	C
82	EC	6935	G
82	EC	6936	G
82	EC	6938	A
82	EC	6939	C
82	EC	6940	U
82	EC	6941	U
82	EC	6942	A
82	EC	6943	A
82	EC	6944	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	EC	6945	U
82	EC	6946	A
82	EC	6947	A
82	EC	6948	U
82	EC	6949	G

All (43) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	B5	752	A
34	B5	819	G
34	B5	850	A
34	B5	862	A
34	B5	950	C
34	B5	1285	U
34	B5	1344	A
34	B5	1369	U
34	B5	1458	G
34	B5	1645	G
38	A1	120	G
38	A1	121	A
38	A1	122	A
38	A1	165	A
38	A1	176	G
38	A1	241	G
38	A1	245	U
38	A1	873	C
38	A1	916	G
38	A1	1092	C
38	A1	1218	U
38	A1	1227	C
38	A1	1242	G
38	A1	1280	C
38	A1	1282	G
38	A1	1292	C
38	A1	1354	G
38	A1	1572	U
38	A1	1629	U
38	A1	2241	U
38	A1	2469	G
38	A1	2506	U
38	A1	2801	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	A1	2875	U
38	A1	3121	U
39	A3	52	G
82	EC	6789	G
82	EC	6831	U
82	EC	6851	G
82	EC	6876	A
82	EC	6889	A
82	EC	6939	C
82	EC	6943	A

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

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$
38	A2M	A1	807	38	22,25,26	1.47	4 (18%)	30,36,39	2.12	8 (26%)
38	OMU	A1	898	38	19,22,23	1.25	3 (15%)	25,31,34	1.82	5 (20%)
38	OMG	A1	908	38	23,26,27	1.21	3 (13%)	32,38,41	2.03	6 (18%)
38	OMU	A1	2417	38	19,22,23	1.23	3 (15%)	25,31,34	1.80	5 (20%)
80	DDE	DC	699	80	18,20,21	1.02	1 (5%)	17,28,30	0.86	1 (5%)
34	OMC	B5	1639	34	19,22,23	0.78	0	25,31,34	0.76	0
38	1MA	A1	645	38,83	21,25,26	1.36	4 (19%)	30,37,40	1.71	5 (16%)
38	1MA	A1	2142	38,83	21,25,26	1.35	4 (19%)	30,37,40	1.72	4 (13%)
38	A2M	A1	2280	38	22,25,26	1.46	4 (18%)	30,36,39	2.07	8 (26%)
38	A2M	A1	2256	38,83	22,25,26	1.50	4 (18%)	30,36,39	2.07	9 (30%)
38	OMU	A1	2729	38	19,22,23	1.28	3 (15%)	25,31,34	1.79	5 (20%)
38	OMC	A1	2959	38	19,22,23	0.79	0	25,31,34	0.83	0
34	OMG	B5	562	34	23,26,27	1.20	3 (13%)	32,38,41	1.98	6 (18%)
34	XSX	B5	1191	34	24,28,29	1.03	1 (4%)	30,40,43	1.43	3 (10%)
38	OMC	A1	2197	38	19,22,23	0.78	0	25,31,34	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	OMG	A1	2619	38	23,26,27	1.19	3 (13%)	32,38,41	1.99	6 (18%)
34	OMU	B5	1269	34	19,22,23	1.26	4 (21%)	25,31,34	1.82	5 (20%)
34	OMG	B5	1572	34	23,26,27	1.18	3 (13%)	32,38,41	1.95	6 (18%)
38	OMU	A1	2724	38	19,22,23	1.25	3 (15%)	25,31,34	1.80	6 (24%)
38	A2M	A1	1449	38,83	22,25,26	1.48	4 (18%)	30,36,39	2.01	8 (26%)
34	A2M	B5	28	83,34	22,25,26	1.49	4 (18%)	30,36,39	2.07	9 (30%)
34	OMG	B5	1126	34	23,26,27	1.19	3 (13%)	32,38,41	2.00	6 (18%)
38	OMU	A1	2921	38	19,22,23	1.24	3 (15%)	25,31,34	1.83	5 (20%)
34	A2M	B5	436	34	22,25,26	1.51	4 (18%)	30,36,39	2.05	8 (26%)
38	OMU	A1	1888	38	19,22,23	1.29	3 (15%)	25,31,34	1.82	4 (16%)
36	HIC	AB	243	36	10,11,12	1.47	1 (10%)	9,14,16	1.37	2 (22%)
34	A2M	B5	541	34	22,25,26	1.52	4 (18%)	30,36,39	2.12	7 (23%)
38	OMG	A1	805	38	23,26,27	1.18	3 (13%)	32,38,41	2.00	6 (18%)
38	A2M	A1	817	38,83	22,25,26	1.49	5 (22%)	30,36,39	2.02	8 (26%)
38	OMG	A1	1450	38	23,26,27	1.20	3 (13%)	32,38,41	1.96	6 (18%)
38	OMG	A1	2793	38	23,26,27	1.18	3 (13%)	32,38,41	1.97	6 (18%)
38	OMU	A1	2347	38	19,22,23	1.27	3 (15%)	25,31,34	1.84	5 (20%)
34	MA6	B5	1782	34	23,26,27	1.53	3 (13%)	33,38,41	2.30	10 (30%)
38	OMC	A1	2337	38	19,22,23	0.78	0	25,31,34	0.80	0
38	5MC	A1	2870	38	19,22,23	1.54	3 (15%)	26,32,35	1.22	3 (11%)
34	OMC	B5	414	34	19,22,23	0.79	0	25,31,34	0.81	0
38	OMG	A1	2791	38	23,26,27	1.19	3 (13%)	32,38,41	2.02	6 (18%)
38	OMG	A1	2288	38	23,26,27	1.20	3 (13%)	32,38,41	2.00	6 (18%)
38	A2M	A1	2640	38	22,25,26	1.48	4 (18%)	30,36,39	2.03	8 (26%)
38	A2M	A1	649	38,83	22,25,26	1.49	5 (22%)	30,36,39	2.01	7 (23%)
38	A2M	A1	1133	38	22,25,26	1.48	4 (18%)	30,36,39	2.16	10 (33%)
34	OMG	B5	1271	34	23,26,27	1.18	2 (8%)	32,38,41	1.98	6 (18%)
38	5MC	A1	2278	38,83	19,22,23	1.58	3 (15%)	26,32,35	1.18	3 (11%)
38	A2M	A1	2946	38,83	22,25,26	1.47	4 (18%)	30,36,39	2.13	9 (30%)
38	OMG	A1	867	38	23,26,27	1.18	3 (13%)	32,38,41	1.99	6 (18%)
38	OMG	A1	2815	38	23,26,27	1.19	3 (13%)	32,38,41	2.02	6 (18%)
34	OMG	B5	1428	34	23,26,27	1.19	3 (13%)	32,38,41	1.96	6 (18%)
34	OMU	B5	578	34	19,22,23	1.22	3 (15%)	25,31,34	1.82	5 (20%)
34	A2M	B5	420	34	22,25,26	1.51	4 (18%)	30,36,39	2.04	8 (26%)
34	MA6	B5	1781	34	23,26,27	1.46	5 (21%)	33,38,41	2.21	11 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	A2M	A1	876	38	22,25,26	1.48	5 (22%)	30,36,39	2.02	7 (23%)
38	A2M	A1	2220	38	22,25,26	1.48	4 (18%)	30,36,39	2.05	9 (30%)
34	4AC	B5	1280	34	21,24,25	1.07	1 (4%)	28,34,37	1.08	2 (7%)
38	OMG	A1	2922	38	23,26,27	1.18	3 (13%)	32,38,41	1.98	6 (18%)
34	A2M	B5	796	34	22,25,26	1.49	4 (18%)	30,36,39	2.23	9 (30%)
38	UR3	A1	2634	38,83	19,22,23	0.95	0	26,32,35	1.77	2 (7%)
34	4AC	B5	1773	34	21,24,25	1.03	2 (9%)	28,34,37	2.31	6 (21%)
38	OMC	A1	650	38,83	19,22,23	0.80	1 (5%)	25,31,34	0.91	1 (4%)
34	A2M	B5	974	34	22,25,26	1.49	4 (18%)	30,36,39	2.05	7 (23%)
38	OMU	A1	2421	38	19,22,23	1.29	3 (15%)	25,31,34	1.80	4 (16%)
34	7MG	B5	1575	34	23,26,27	1.59	5 (21%)	27,39,42	2.60	9 (33%)
38	OMC	A1	663	38	19,22,23	0.79	0	25,31,34	0.77	0
38	OMC	A1	2948	38	19,22,23	0.77	0	25,31,34	0.88	1 (4%)
34	A2M	B5	100	83,34	22,25,26	1.51	4 (18%)	30,36,39	2.11	9 (30%)
38	A2M	A1	2281	38	22,25,26	1.44	5 (22%)	30,36,39	2.28	11 (36%)
34	A2M	B5	619	83,34	22,25,26	1.49	4 (18%)	30,36,39	2.09	9 (30%)
34	OMC	B5	1007	34	19,22,23	0.79	0	25,31,34	0.88	0
38	OMC	A1	1437	38	19,22,23	0.77	0	25,31,34	0.96	2 (8%)

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
38	A2M	A1	807	38	-	2/9/27/28	0/3/3/3
38	OMU	A1	898	38	-	0/9/27/28	0/2/2/2
38	OMG	A1	908	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2417	38	-	0/9/27/28	0/2/2/2
80	DDE	DC	699	80	-	5/20/21/23	0/1/1/1
34	OMC	B5	1639	34	-	0/9/27/28	0/2/2/2
38	1MA	A1	645	38,83	-	2/7/25/26	0/3/3/3
38	1MA	A1	2142	38,83	-	1/7/25/26	0/3/3/3
38	A2M	A1	2280	38	-	2/9/27/28	0/3/3/3
38	A2M	A1	2256	38,83	-	1/9/27/28	0/3/3/3
38	OMU	A1	2729	38	-	2/9/27/28	0/2/2/2
38	OMC	A1	2959	38	-	0/9/27/28	0/2/2/2
34	OMG	B5	562	34	-	0/9/27/28	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	XSX	B5	1191	34	-	3/16/34/35	0/2/2/2
38	OMC	A1	2197	38	-	6/9/27/28	0/2/2/2
38	OMG	A1	2619	38	-	1/9/27/28	0/3/3/3
34	OMU	B5	1269	34	-	4/9/27/28	0/2/2/2
34	OMG	B5	1572	34	-	0/9/27/28	0/3/3/3
38	OMU	A1	2724	38	-	1/9/27/28	0/2/2/2
38	A2M	A1	1449	38,83	-	0/9/27/28	0/3/3/3
34	A2M	B5	28	83,34	-	0/9/27/28	0/3/3/3
34	OMG	B5	1126	34	-	2/9/27/28	0/3/3/3
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
34	A2M	B5	436	34	-	0/9/27/28	0/3/3/3
38	OMU	A1	1888	38	-	0/9/27/28	0/2/2/2
36	HIC	AB	243	36	-	2/5/6/8	0/1/1/1
34	A2M	B5	541	34	-	4/9/27/28	0/3/3/3
38	OMG	A1	805	38	-	0/9/27/28	0/3/3/3
38	A2M	A1	817	38,83	-	1/9/27/28	0/3/3/3
38	OMG	A1	1450	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	2793	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2347	38	-	2/9/27/28	0/2/2/2
34	MA6	B5	1782	34	-	6/11/29/30	0/3/3/3
38	OMC	A1	2337	38	-	0/9/27/28	0/2/2/2
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
34	OMC	B5	414	34	-	0/9/27/28	0/2/2/2
38	OMG	A1	2791	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	2288	38	-	0/9/27/28	0/3/3/3
38	A2M	A1	2640	38	-	0/9/27/28	0/3/3/3
38	A2M	A1	649	38,83	-	1/9/27/28	0/3/3/3
38	A2M	A1	1133	38	-	0/9/27/28	0/3/3/3
34	OMG	B5	1271	34	-	0/9/27/28	0/3/3/3
38	5MC	A1	2278	38,83	-	0/7/25/26	0/2/2/2
38	A2M	A1	2946	38,83	-	0/9/27/28	0/3/3/3
38	OMG	A1	867	38	-	1/9/27/28	0/3/3/3
38	OMG	A1	2815	38	-	0/9/27/28	0/3/3/3
34	OMG	B5	1428	34	-	3/9/27/28	0/3/3/3
34	OMU	B5	578	34	-	0/9/27/28	0/2/2/2
34	A2M	B5	420	34	-	1/9/27/28	0/3/3/3
34	MA6	B5	1781	34	-	2/11/29/30	0/3/3/3
38	A2M	A1	876	38	-	0/9/27/28	0/3/3/3
38	A2M	A1	2220	38	-	0/9/27/28	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	4AC	B5	1280	34	-	2/11/29/30	0/2/2/2
38	OMG	A1	2922	38	-	2/9/27/28	0/3/3/3
34	A2M	B5	796	34	-	0/9/27/28	0/3/3/3
38	UR3	A1	2634	38,83	-	0/7/25/26	0/2/2/2
34	4AC	B5	1773	34	-	4/11/29/30	0/2/2/2
38	OMC	A1	650	38,83	-	0/9/27/28	0/2/2/2
34	A2M	B5	974	34	-	0/9/27/28	0/3/3/3
38	OMU	A1	2421	38	-	0/9/27/28	0/2/2/2
34	7MG	B5	1575	34	-	0/7/37/38	0/3/3/3
38	OMC	A1	663	38	-	0/9/27/28	0/2/2/2
38	OMC	A1	2948	38	-	0/9/27/28	0/2/2/2
34	A2M	B5	100	83,34	-	1/9/27/28	0/3/3/3
38	A2M	A1	2281	38	-	2/9/27/28	0/3/3/3
34	A2M	B5	619	83,34	-	4/9/27/28	0/3/3/3
34	OMC	B5	1007	34	-	0/9/27/28	0/2/2/2
38	OMC	A1	1437	38	-	4/9/27/28	0/2/2/2

All (193) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2278	5MC	C5-C4	5.65	1.48	1.44
38	A1	2870	5MC	C5-C4	5.23	1.48	1.44
34	B5	541	A2M	C5-C4	4.80	1.47	1.39
34	B5	436	A2M	C5-C4	4.72	1.47	1.39
34	B5	1782	MA6	C5-C4	4.62	1.47	1.39
34	B5	420	A2M	C5-C4	4.61	1.47	1.39
34	B5	100	A2M	C5-C4	4.60	1.47	1.39
38	A1	2256	A2M	C5-C4	4.59	1.47	1.39
34	B5	974	A2M	C5-C4	4.56	1.47	1.39
34	B5	796	A2M	C5-C4	4.54	1.47	1.39
34	B5	28	A2M	C5-C4	4.54	1.47	1.39
34	B5	619	A2M	C5-C4	4.53	1.47	1.39
38	A1	2220	A2M	C5-C4	4.51	1.47	1.39
34	B5	1781	MA6	C5-C4	4.51	1.47	1.39
38	A1	649	A2M	C5-C4	4.49	1.47	1.39
38	A1	1133	A2M	C5-C4	4.47	1.47	1.39
38	A1	2640	A2M	C5-C4	4.45	1.47	1.39
38	A1	2280	A2M	C5-C4	4.45	1.47	1.39
38	A1	1449	A2M	C5-C4	4.44	1.47	1.39
38	A1	807	A2M	C5-C4	4.43	1.47	1.39
38	A1	2946	A2M	C5-C4	4.42	1.47	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	876	A2M	C5-C4	4.42	1.47	1.39
38	A1	817	A2M	C5-C4	4.39	1.46	1.39
38	A1	2281	A2M	C5-C4	4.29	1.46	1.39
34	B5	1782	MA6	C5-C6	3.24	1.49	1.41
38	A1	645	1MA	C6-N6	3.20	1.35	1.28
34	B5	1428	OMG	C5-C4	3.14	1.47	1.38
34	B5	1575	7MG	C4-N9	-3.14	1.34	1.37
34	B5	562	OMG	C5-C4	3.12	1.47	1.38
34	B5	1572	OMG	C5-C4	3.11	1.47	1.38
34	B5	1271	OMG	C5-C4	3.11	1.47	1.38
38	A1	2142	1MA	C5-C4	3.10	1.47	1.38
38	A1	908	OMG	C5-C4	3.08	1.47	1.38
38	A1	2791	OMG	C5-C4	3.08	1.47	1.38
34	B5	1280	4AC	C4-N4	-3.07	1.35	1.39
38	A1	2815	OMG	C5-C4	3.02	1.47	1.38
38	A1	2619	OMG	C5-C4	3.02	1.47	1.38
38	A1	2288	OMG	C5-C4	3.01	1.47	1.38
34	B5	1126	OMG	C5-C4	3.01	1.47	1.38
38	A1	1450	OMG	C5-C4	3.01	1.47	1.38
38	A1	645	1MA	C5-C4	3.01	1.47	1.38
38	A1	867	OMG	C5-C4	2.99	1.47	1.38
38	A1	2922	OMG	C5-C4	2.97	1.46	1.38
38	A1	2142	1MA	C6-N6	2.97	1.35	1.28
38	A1	2793	OMG	C5-C4	2.95	1.46	1.38
38	A1	2729	OMU	C4-N3	-2.92	1.33	1.38
38	A1	2421	OMU	C4-N3	-2.91	1.33	1.38
38	A1	1888	OMU	C4-N3	-2.91	1.33	1.38
34	B5	1781	MA6	C5-C6	2.89	1.48	1.41
36	AB	243	HIC	CD2-CG	2.88	1.41	1.36
34	B5	1575	7MG	C2'-C3'	-2.87	1.45	1.53
38	A1	805	OMG	C5-C4	2.86	1.46	1.38
38	A1	2347	OMU	C4-N3	-2.85	1.33	1.38
38	A1	898	OMU	C4-N3	-2.83	1.33	1.38
38	A1	2870	5MC	C6-C5	2.81	1.39	1.34
38	A1	2417	OMU	C4-N3	-2.80	1.33	1.38
34	B5	1575	7MG	C5-C4	2.79	1.46	1.37
38	A1	2815	OMG	C6-N1	-2.75	1.33	1.38
38	A1	2724	OMU	C4-N3	-2.72	1.33	1.38
34	B5	28	A2M	C5-C6	2.72	1.48	1.41
38	A1	2921	OMU	C4-N3	-2.72	1.34	1.38
34	B5	1269	OMU	C4-N3	-2.72	1.34	1.38
34	B5	436	A2M	C5-C6	2.71	1.48	1.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	420	A2M	C5-C6	2.70	1.48	1.41
38	A1	1450	OMG	C6-N1	-2.70	1.33	1.38
34	B5	619	A2M	C5-C6	2.69	1.48	1.41
34	B5	796	A2M	C5-C6	2.69	1.48	1.41
38	A1	2256	A2M	C5-C6	2.69	1.48	1.41
34	B5	541	A2M	C5-C6	2.68	1.48	1.41
38	A1	2278	5MC	C6-C5	2.68	1.39	1.34
34	B5	100	A2M	C5-C6	2.67	1.48	1.41
38	A1	2288	OMG	C6-N1	-2.65	1.33	1.38
38	A1	817	A2M	C5-C6	2.65	1.48	1.41
34	B5	974	A2M	C5-C6	2.63	1.48	1.41
38	A1	867	OMG	C6-N1	-2.62	1.33	1.38
38	A1	908	OMG	C6-N1	-2.62	1.33	1.38
38	A1	1449	A2M	C5-C6	2.61	1.48	1.41
38	A1	2791	OMG	C6-N1	-2.61	1.34	1.38
38	A1	2640	A2M	C5-C6	2.60	1.48	1.41
38	A1	2220	A2M	C5-C6	2.60	1.48	1.41
34	B5	1126	OMG	C6-N1	-2.60	1.34	1.38
38	A1	2793	OMG	C6-N1	-2.59	1.34	1.38
38	A1	2619	OMG	C6-N1	-2.59	1.34	1.38
38	A1	649	A2M	C5-C6	2.59	1.48	1.41
38	A1	1133	A2M	C5-C6	2.58	1.48	1.41
38	A1	2280	A2M	C5-C6	2.58	1.48	1.41
34	B5	578	OMU	C4-N3	-2.57	1.34	1.38
38	A1	2946	A2M	C5-C6	2.57	1.48	1.41
38	A1	807	A2M	C5-N7	-2.57	1.34	1.39
38	A1	876	A2M	C5-N7	-2.56	1.34	1.39
38	A1	649	A2M	C5-N7	-2.56	1.34	1.39
38	A1	807	A2M	C5-C6	2.55	1.48	1.41
38	A1	805	OMG	C6-N1	-2.55	1.34	1.38
34	B5	1575	7MG	C6-N1	-2.54	1.34	1.38
38	A1	2281	A2M	C5-C6	2.53	1.48	1.41
38	A1	876	A2M	C5-C6	2.53	1.48	1.41
80	DC	699	DDE	CD2-CG	2.53	1.41	1.36
34	B5	1428	OMG	C6-N1	-2.52	1.34	1.38
34	B5	562	OMG	C6-N1	-2.52	1.34	1.38
38	A1	2922	OMG	C6-N1	-2.51	1.34	1.38
38	A1	1449	A2M	C5-N7	-2.50	1.34	1.39
38	A1	2421	OMU	C2-N3	-2.48	1.33	1.38
34	B5	1271	OMG	C6-N1	-2.45	1.34	1.38
38	A1	2640	A2M	C5-N7	-2.45	1.34	1.39
34	B5	436	A2M	C5-N7	-2.43	1.34	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1572	OMG	C6-N1	-2.42	1.34	1.38
34	B5	100	A2M	C5-N7	-2.42	1.34	1.39
38	A1	817	A2M	C5-N7	-2.42	1.34	1.39
38	A1	1133	A2M	C5-N7	-2.41	1.34	1.39
38	A1	2281	A2M	C5-N7	-2.41	1.34	1.39
34	B5	541	A2M	C5-N7	-2.40	1.34	1.39
38	A1	2280	A2M	C5-N7	-2.40	1.34	1.39
38	A1	1888	OMU	C2-N3	-2.40	1.33	1.38
38	A1	2220	A2M	C5-N7	-2.40	1.34	1.39
38	A1	2946	A2M	C5-N7	-2.39	1.34	1.39
38	A1	2347	OMU	C2-N3	-2.38	1.33	1.38
38	A1	908	OMG	C5-N7	-2.38	1.34	1.39
38	A1	2278	5MC	C6-N1	-2.36	1.34	1.38
34	B5	1773	4AC	C4-N4	-2.36	1.36	1.39
38	A1	2256	A2M	C5-N7	-2.36	1.34	1.39
38	A1	2729	OMU	C2-N3	-2.35	1.33	1.38
38	A1	2724	OMU	C2-N3	-2.34	1.33	1.38
34	B5	796	A2M	C5-N7	-2.34	1.34	1.39
34	B5	974	A2M	C5-N7	-2.34	1.34	1.39
34	B5	1781	MA6	C8-N7	2.34	1.36	1.31
38	A1	2256	A2M	C8-N7	2.33	1.36	1.31
38	A1	898	OMU	C2-N3	-2.33	1.33	1.38
38	A1	2142	1MA	C5-N7	-2.32	1.34	1.39
34	B5	420	A2M	C8-N7	2.32	1.36	1.31
34	B5	420	A2M	C5-N7	-2.31	1.34	1.39
38	A1	2921	OMU	C2-N3	-2.31	1.33	1.38
38	A1	2870	5MC	C6-N1	-2.31	1.34	1.38
34	B5	619	A2M	C8-N7	2.31	1.36	1.31
34	B5	796	A2M	C8-N7	2.31	1.36	1.31
38	A1	2724	OMU	C5-C4	-2.31	1.38	1.43
34	B5	28	A2M	C8-N7	2.30	1.36	1.31
38	A1	2142	1MA	C2-N3	2.29	1.34	1.30
38	A1	2619	OMG	C5-N7	-2.28	1.34	1.39
34	B5	28	A2M	C5-N7	-2.28	1.34	1.39
34	B5	619	A2M	C5-N7	-2.28	1.34	1.39
38	A1	645	1MA	C5-N7	-2.28	1.34	1.39
34	B5	1269	OMU	C2-N1	2.28	1.42	1.38
34	B5	1575	7MG	C5-N7	-2.27	1.32	1.35
38	A1	2417	OMU	C2-N3	-2.26	1.34	1.38
38	A1	898	OMU	C5-C4	-2.25	1.38	1.43
34	B5	100	A2M	C8-N7	2.25	1.36	1.31
38	A1	2347	OMU	C5-C4	-2.25	1.38	1.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2288	OMG	C5-N7	-2.25	1.34	1.39
38	A1	2946	A2M	C8-N7	2.24	1.36	1.31
38	A1	2729	OMU	C5-C4	-2.24	1.38	1.43
34	B5	541	A2M	C8-N7	2.22	1.35	1.31
34	B5	974	A2M	C8-N7	2.21	1.35	1.31
34	B5	436	A2M	C8-N7	2.21	1.35	1.31
38	A1	1450	OMG	C5-N7	-2.20	1.34	1.39
38	A1	2922	OMG	C5-N7	-2.20	1.34	1.39
38	A1	2921	OMU	C5-C4	-2.20	1.38	1.43
34	B5	1126	OMG	C5-N7	-2.19	1.34	1.39
38	A1	1888	OMU	C5-C4	-2.19	1.38	1.43
38	A1	817	A2M	C8-N7	2.18	1.35	1.31
38	A1	2815	OMG	C5-N7	-2.18	1.34	1.39
38	A1	2281	A2M	C8-N7	2.18	1.35	1.31
38	A1	817	A2M	C4-N9	-2.18	1.33	1.37
38	A1	2417	OMU	C5-C4	-2.17	1.39	1.43
38	A1	2421	OMU	C5-C4	-2.17	1.39	1.43
34	B5	1773	4AC	C6-N1	-2.17	1.32	1.38
38	A1	2791	OMG	C5-N7	-2.17	1.34	1.39
34	B5	578	OMU	C2-N3	-2.16	1.34	1.38
38	A1	2280	A2M	C8-N7	2.16	1.35	1.31
38	A1	867	OMG	C5-N7	-2.15	1.34	1.39
38	A1	2220	A2M	C8-N7	2.14	1.35	1.31
34	B5	1269	OMU	C2-N3	-2.14	1.34	1.38
38	A1	645	1MA	C2-N3	2.13	1.34	1.30
38	A1	2640	A2M	C8-N7	2.12	1.35	1.31
34	B5	562	OMG	C5-N7	-2.12	1.34	1.39
34	B5	1191	XSX	C2-N1	2.12	1.41	1.38
38	A1	2793	OMG	C5-N7	-2.11	1.34	1.39
38	A1	805	OMG	C5-N7	-2.10	1.34	1.39
38	A1	1133	A2M	C8-N7	2.10	1.35	1.31
38	A1	2281	A2M	C4-N9	-2.09	1.33	1.37
38	A1	649	A2M	C4-N9	-2.09	1.33	1.37
34	B5	1428	OMG	C5-N7	-2.08	1.34	1.39
34	B5	1781	MA6	C5-N7	-2.08	1.35	1.39
34	B5	1269	OMU	C5-C4	-2.07	1.39	1.43
38	A1	876	A2M	C8-N7	2.07	1.35	1.31
38	A1	1449	A2M	C8-N7	2.07	1.35	1.31
38	A1	807	A2M	C8-N7	2.07	1.35	1.31
34	B5	578	OMU	C5-C4	-2.07	1.39	1.43
34	B5	1572	OMG	C5-N7	-2.04	1.35	1.39
34	B5	1781	MA6	C4-N9	-2.04	1.33	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1782	MA6	C4-N9	-2.03	1.33	1.37
38	A1	876	A2M	C4-N9	-2.03	1.33	1.37
38	A1	649	A2M	C8-N7	2.01	1.35	1.31
38	A1	650	OMC	C6-N1	-2.01	1.33	1.38

All (372) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1773	4AC	N4-C4-N3	8.41	127.53	113.87
38	A1	2634	UR3	C4-N3-C2	-7.21	118.78	124.58
34	B5	1575	7MG	N9-C4-N3	6.67	135.24	125.46
38	A1	908	OMG	C5-C4-N3	-6.43	118.15	128.39
38	A1	2791	OMG	C5-C4-N3	-6.38	118.24	128.39
38	A1	2815	OMG	C5-C4-N3	-6.37	118.25	128.39
38	A1	2619	OMG	C5-C4-N3	-6.37	118.26	128.39
38	A1	2288	OMG	C5-C4-N3	-6.34	118.30	128.39
34	B5	541	A2M	C5-C4-N3	-6.28	118.06	126.72
34	B5	562	OMG	C5-C4-N3	-6.27	118.41	128.39
38	A1	867	OMG	C5-C4-N3	-6.20	118.52	128.39
38	A1	1450	OMG	C5-C4-N3	-6.20	118.53	128.39
34	B5	1271	OMG	C5-C4-N3	-6.19	118.53	128.39
38	A1	2922	OMG	C5-C4-N3	-6.12	118.65	128.39
34	B5	1126	OMG	C5-C4-N3	-6.11	118.66	128.39
34	B5	1428	OMG	C5-C4-N3	-6.09	118.70	128.39
38	A1	807	A2M	C5-C4-N3	-6.08	118.34	126.72
34	B5	796	A2M	C5-C4-N3	-6.00	118.45	126.72
34	B5	100	A2M	C5-C4-N3	-5.98	118.49	126.72
34	B5	436	A2M	C5-C4-N3	-5.96	118.51	126.72
34	B5	974	A2M	C5-C4-N3	-5.94	118.53	126.72
38	A1	649	A2M	C5-C4-N3	-5.92	118.56	126.72
38	A1	876	A2M	C5-C4-N3	-5.91	118.58	126.72
34	B5	1572	OMG	C5-C4-N3	-5.90	119.00	128.39
38	A1	2640	A2M	C5-C4-N3	-5.89	118.61	126.72
34	B5	28	A2M	C5-C4-N3	-5.85	118.66	126.72
38	A1	1449	A2M	C5-C4-N3	-5.84	118.67	126.72
38	A1	2793	OMG	C5-C4-N3	-5.83	119.11	128.39
34	B5	420	A2M	C5-C4-N3	-5.83	118.70	126.72
38	A1	2946	A2M	C5-C4-N3	-5.82	118.70	126.72
38	A1	1133	A2M	C5-C4-N3	-5.82	118.70	126.72
34	B5	619	A2M	C5-C4-N3	-5.80	118.73	126.72
38	A1	2280	A2M	C5-C4-N3	-5.74	118.82	126.72
38	A1	2256	A2M	C5-C4-N3	-5.71	118.85	126.72

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	805	OMG	C5-C4-N3	-5.69	119.33	128.39
38	A1	2220	A2M	C5-C4-N3	-5.61	119.00	126.72
38	A1	2281	A2M	C5-C4-N3	-5.61	119.00	126.72
38	A1	817	A2M	C5-C4-N3	-5.57	119.04	126.72
38	A1	2142	1MA	C5-C4-N3	-5.54	119.11	127.27
38	A1	645	1MA	C5-C4-N3	-5.51	119.16	127.27
34	B5	1781	MA6	C5-C4-N3	-5.32	119.39	126.72
34	B5	1191	XSX	C4-N3-C2	-5.32	118.42	124.66
34	B5	1575	7MG	N9-C8-N7	-5.31	95.86	103.37
34	B5	1773	4AC	C5-C4-N4	-5.23	114.14	122.94
38	A1	2791	OMG	C2-N3-C4	5.20	121.25	112.30
34	B5	1782	MA6	C4-N9-C8	5.17	111.16	105.74
38	A1	2288	OMG	C2-N3-C4	5.16	121.18	112.30
38	A1	2815	OMG	C2-N3-C4	5.15	121.17	112.30
38	A1	867	OMG	C2-N3-C4	5.10	121.08	112.30
34	B5	1271	OMG	C2-N3-C4	5.08	121.05	112.30
34	B5	541	A2M	N3-C4-N9	5.08	135.80	127.17
38	A1	2619	OMG	C2-N3-C4	5.07	121.02	112.30
38	A1	1450	OMG	C2-N3-C4	5.05	121.00	112.30
38	A1	908	OMG	C2-N3-C4	5.05	121.00	112.30
34	B5	562	OMG	C2-N3-C4	5.04	120.99	112.30
38	A1	2922	OMG	C2-N3-C4	5.02	120.95	112.30
34	B5	1575	7MG	C5-C4-N3	-5.01	118.73	128.13
34	B5	1782	MA6	C5-C4-N3	-4.99	119.84	126.72
34	B5	1126	OMG	C2-N3-C4	4.98	120.87	112.30
34	B5	1428	OMG	C2-N3-C4	4.97	120.86	112.30
38	A1	805	OMG	C2-N3-C4	4.96	120.85	112.30
38	A1	2793	OMG	C2-N3-C4	4.94	120.81	112.30
34	B5	1572	OMG	C2-N3-C4	4.93	120.79	112.30
38	A1	908	OMG	N9-C4-N3	4.92	135.79	125.95
34	B5	1782	MA6	N3-C4-N9	4.88	135.47	127.17
38	A1	2288	OMG	N9-C4-N3	4.85	135.65	125.95
38	A1	2921	OMU	C4-N3-C2	-4.84	120.60	126.61
34	B5	1781	MA6	C4-C5-N7	-4.82	105.07	110.58
38	A1	807	A2M	N3-C4-N9	4.82	135.36	127.17
34	B5	578	OMU	C4-N3-C2	-4.81	120.64	126.61
38	A1	2421	OMU	C4-N3-C2	-4.77	120.69	126.61
38	A1	1888	OMU	C4-N3-C2	-4.77	120.69	126.61
38	A1	2815	OMG	N9-C4-N3	4.77	135.49	125.95
38	A1	2791	OMG	N9-C4-N3	4.76	135.47	125.95
38	A1	898	OMU	C4-N3-C2	-4.74	120.72	126.61
38	A1	876	A2M	N3-C4-N9	4.72	135.20	127.17

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2619	OMG	N9-C4-N3	4.72	135.39	125.95
34	B5	974	A2M	N3-C4-N9	4.72	135.19	127.17
38	A1	2417	OMU	C4-N3-C2	-4.72	120.76	126.61
38	A1	649	A2M	N3-C4-N9	4.69	135.15	127.17
34	B5	100	A2M	N3-C4-N9	4.68	135.13	127.17
34	B5	1575	7MG	C2-N3-C4	4.68	120.35	112.30
38	A1	1133	A2M	N3-C4-N9	4.67	135.11	127.17
34	B5	796	A2M	N3-C4-N9	4.66	135.10	127.17
38	A1	2347	OMU	C4-N3-C2	-4.66	120.83	126.61
34	B5	1782	MA6	C2-N1-C6	4.65	123.19	111.83
38	A1	2640	A2M	N3-C4-N9	4.64	135.06	127.17
34	B5	1126	OMG	N9-C4-N3	4.63	135.21	125.95
38	A1	2729	OMU	C4-N3-C2	-4.62	120.88	126.61
34	B5	562	OMG	N9-C4-N3	4.62	135.18	125.95
38	A1	1449	A2M	N3-C4-N9	4.62	135.02	127.17
34	B5	28	A2M	N3-C4-N9	4.61	135.00	127.17
34	B5	436	A2M	N3-C4-N9	4.61	135.00	127.17
38	A1	1450	OMG	N9-C4-N3	4.59	135.14	125.95
34	B5	1271	OMG	N9-C4-N3	4.58	135.12	125.95
38	A1	2922	OMG	N9-C4-N3	4.58	135.12	125.95
34	B5	420	A2M	N3-C4-N9	4.56	134.93	127.17
38	A1	2280	A2M	N3-C4-N9	4.56	134.93	127.17
34	B5	1428	OMG	N9-C4-N3	4.56	135.07	125.95
38	A1	2724	OMU	C4-N3-C2	-4.55	120.96	126.61
38	A1	645	1MA	C2-N3-C4	4.55	121.46	112.53
38	A1	2142	1MA	C2-N3-C4	4.55	121.46	112.53
38	A1	867	OMG	N9-C4-N3	4.55	135.05	125.95
38	A1	2281	A2M	N3-C4-N9	4.53	134.88	127.17
38	A1	2946	A2M	N3-C4-N9	4.52	134.85	127.17
34	B5	619	A2M	N3-C4-N9	4.50	134.81	127.17
34	B5	1269	OMU	C4-N3-C2	-4.49	121.03	126.61
38	A1	2220	A2M	N3-C4-N9	4.49	134.80	127.17
38	A1	2256	A2M	N3-C4-N9	4.46	134.75	127.17
38	A1	2793	OMG	N9-C4-N3	4.36	134.66	125.95
34	B5	1781	MA6	C2-N1-C6	4.34	122.42	111.83
38	A1	817	A2M	N3-C4-N9	4.31	134.50	127.17
38	A1	2417	OMU	N3-C2-N1	4.28	120.46	114.89
34	B5	1572	OMG	N9-C4-N3	4.25	134.45	125.95
38	A1	2421	OMU	N3-C2-N1	4.25	120.42	114.89
38	A1	2921	OMU	N3-C2-N1	4.22	120.38	114.89
34	B5	1269	OMU	N3-C2-N1	4.21	120.37	114.89
38	A1	805	OMG	N9-C4-N3	4.16	134.28	125.95

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	796	A2M	C2'-C1'-N9	-4.13	106.95	113.75
38	A1	2347	OMU	N3-C2-N1	4.12	120.26	114.89
38	A1	1888	OMU	N3-C2-N1	4.11	120.24	114.89
38	A1	898	OMU	N3-C2-N1	4.09	120.21	114.89
38	A1	2729	OMU	N3-C2-N1	4.06	120.18	114.89
34	B5	578	OMU	N3-C2-N1	4.05	120.16	114.89
38	A1	2724	OMU	N3-C2-N1	4.01	120.11	114.89
38	A1	2921	OMU	C5-C4-N3	3.97	120.36	114.80
34	B5	1773	4AC	C6-C5-C4	3.95	121.76	117.00
38	A1	898	OMU	C5-C4-N3	3.94	120.32	114.80
38	A1	2724	OMU	C5-C4-N3	3.93	120.30	114.80
34	B5	578	OMU	C5-C4-N3	3.93	120.30	114.80
38	A1	1888	OMU	C5-C4-N3	3.90	120.26	114.80
38	A1	2870	5MC	C5-C6-N1	-3.87	119.11	123.31
38	A1	2729	OMU	C5-C4-N3	3.85	120.19	114.80
38	A1	2347	OMU	C5-C4-N3	3.84	120.18	114.80
38	A1	2417	OMU	C5-C4-N3	3.82	120.15	114.80
38	A1	2421	OMU	C5-C4-N3	3.81	120.14	114.80
34	B5	1575	7MG	O2'-C2'-C3'	3.81	124.02	111.82
34	B5	796	A2M	C2-N3-C4	3.78	121.06	111.83
34	B5	541	A2M	C2-N3-C4	3.77	121.03	111.83
34	B5	28	A2M	C2-N3-C4	3.76	121.01	111.83
38	A1	2281	A2M	O4'-C1'-N9	3.76	115.31	108.09
38	A1	2142	1MA	N9-C4-N3	3.76	135.46	126.90
38	A1	1449	A2M	C2-N3-C4	3.73	120.94	111.83
38	A1	876	A2M	C2-N3-C4	3.73	120.94	111.83
34	B5	1575	7MG	O3'-C3'-C4'	3.73	121.79	111.08
38	A1	2640	A2M	C2-N3-C4	3.72	120.92	111.83
38	A1	649	A2M	C2-N3-C4	3.72	120.91	111.83
34	B5	100	A2M	C2-N3-C4	3.71	120.90	111.83
34	B5	1269	OMU	C5-C4-N3	3.71	120.00	114.80
38	A1	817	A2M	C2-N3-C4	3.71	120.90	111.83
38	A1	2281	A2M	C2-N3-C4	3.70	120.88	111.83
34	B5	974	A2M	C2-N3-C4	3.70	120.86	111.83
34	B5	436	A2M	C2-N3-C4	3.70	120.86	111.83
34	B5	1781	MA6	C2-N3-C4	3.69	120.85	111.83
38	A1	2256	A2M	C2-N3-C4	3.69	120.85	111.83
38	A1	2280	A2M	C2-N3-C4	3.69	120.84	111.83
38	A1	2946	A2M	C2-N3-C4	3.69	120.83	111.83
38	A1	1133	A2M	C2-N3-C4	3.68	120.83	111.83
34	B5	619	A2M	C4-C5-N7	-3.67	106.38	110.58
34	B5	1781	MA6	N3-C4-N9	3.67	133.41	127.17

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	619	A2M	C2-N3-C4	3.67	120.78	111.83
38	A1	807	A2M	C2-N3-C4	3.66	120.78	111.83
34	B5	420	A2M	C2-N3-C4	3.66	120.78	111.83
34	B5	100	A2M	C4-C5-N7	-3.65	106.40	110.58
34	B5	1280	4AC	N4-C4-N3	3.65	119.79	113.87
38	A1	2220	A2M	C2-N3-C4	3.63	120.70	111.83
34	B5	796	A2M	C4-C5-N7	-3.60	106.46	110.58
38	A1	805	OMG	C6-C5-N7	3.60	136.84	130.29
34	B5	420	A2M	C4-C5-N7	-3.55	106.52	110.58
38	A1	1133	A2M	C4-C5-N7	-3.52	106.55	110.58
34	B5	1781	MA6	N1-C2-N3	-3.51	123.28	128.58
38	A1	2946	A2M	C4-C5-N7	-3.50	106.58	110.58
34	B5	1782	MA6	N1-C2-N3	-3.49	123.30	128.58
34	B5	436	A2M	C4-C5-N7	-3.49	106.59	110.58
34	B5	28	A2M	C4-C5-N7	-3.48	106.60	110.58
38	A1	817	A2M	C4-C5-N7	-3.48	106.60	110.58
38	A1	2256	A2M	C4-C5-N7	-3.48	106.60	110.58
34	B5	1572	OMG	C6-C5-N7	3.47	136.60	130.29
38	A1	1133	A2M	C2'-C1'-N9	-3.45	108.07	113.75
38	A1	645	1MA	N9-C4-N3	3.44	134.75	126.90
34	B5	1782	MA6	N9-C8-N7	-3.44	109.05	113.94
38	A1	807	A2M	C4-C5-N7	-3.44	106.65	110.58
38	A1	2634	UR3	C5-C4-N3	3.44	119.56	115.04
38	A1	2220	A2M	N3-C2-N1	-3.43	123.39	128.58
34	B5	1782	MA6	C2-N3-C4	3.42	120.18	111.83
38	A1	2793	OMG	C6-C5-N7	3.41	136.50	130.29
34	B5	1781	MA6	C5-N7-C8	3.40	108.80	103.45
38	A1	2280	A2M	C4-C5-N7	-3.40	106.69	110.58
38	A1	2640	A2M	C4-C5-N7	-3.39	106.70	110.58
38	A1	649	A2M	C4-C5-N7	-3.39	106.71	110.58
34	B5	974	A2M	C4-C5-N7	-3.39	106.71	110.58
34	B5	1782	MA6	C4-C5-N7	-3.38	106.72	110.58
38	A1	817	A2M	N3-C2-N1	-3.37	123.48	128.58
38	A1	1449	A2M	C4-C5-N7	-3.36	106.74	110.58
38	A1	2281	A2M	N3-C2-N1	-3.35	123.51	128.58
38	A1	2281	A2M	C4-C5-N7	-3.35	106.75	110.58
38	A1	2280	A2M	N3-C2-N1	-3.33	123.54	128.58
34	B5	541	A2M	C4-C5-N7	-3.31	106.80	110.58
38	A1	2256	A2M	N3-C2-N1	-3.28	123.62	128.58
38	A1	2220	A2M	C4-C5-N7	-3.27	106.84	110.58
38	A1	876	A2M	N3-C2-N1	-3.27	123.63	128.58
38	A1	867	OMG	C6-C5-N7	3.27	136.24	130.29

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	28	A2M	N3-C2-N1	-3.26	123.65	128.58
38	A1	1449	A2M	N3-C2-N1	-3.25	123.66	128.58
38	A1	876	A2M	C4-C5-N7	-3.24	106.88	110.58
34	B5	796	A2M	N3-C2-N1	-3.24	123.68	128.58
38	A1	1133	A2M	N3-C2-N1	-3.24	123.68	128.58
34	B5	1271	OMG	C6-C5-N7	3.21	136.14	130.29
38	A1	2946	A2M	N3-C2-N1	-3.20	123.73	128.58
38	A1	649	A2M	N3-C2-N1	-3.19	123.75	128.58
34	B5	974	A2M	N3-C2-N1	-3.18	123.76	128.58
38	A1	2815	OMG	C6-C5-N7	3.18	136.08	130.29
34	B5	1428	OMG	C6-C5-N7	3.18	136.08	130.29
38	A1	1450	OMG	C6-C5-N7	3.18	136.08	130.29
38	A1	2640	A2M	N3-C2-N1	-3.18	123.77	128.58
38	A1	2347	OMU	O4-C4-C5	-3.18	119.68	125.16
38	A1	2724	OMU	O4-C4-C5	-3.16	119.70	125.16
38	A1	2791	OMG	C6-C5-N7	3.16	136.05	130.29
38	A1	2922	OMG	C6-C5-N7	3.16	136.04	130.29
34	B5	1126	OMG	C6-C5-N7	3.16	136.03	130.29
38	A1	2278	5MC	C5-C6-N1	-3.15	119.90	123.31
34	B5	420	A2M	N3-C2-N1	-3.14	123.83	128.58
34	B5	1782	MA6	C5-N7-C8	3.14	108.39	103.45
34	B5	100	A2M	N3-C2-N1	-3.14	123.83	128.58
34	B5	578	OMU	O4-C4-C5	-3.13	119.77	125.16
38	A1	898	OMU	O4-C4-C5	-3.12	119.78	125.16
34	B5	562	OMG	C6-C5-N7	3.12	135.97	130.29
38	A1	2921	OMU	O4-C4-C5	-3.12	119.78	125.16
34	B5	436	A2M	N3-C2-N1	-3.12	123.87	128.58
34	B5	619	A2M	N3-C2-N1	-3.11	123.87	128.58
34	B5	541	A2M	N3-C2-N1	-3.07	123.93	128.58
38	A1	2417	OMU	O4-C4-C5	-3.06	119.88	125.16
38	A1	2281	A2M	C2'-C1'-N9	-3.05	108.73	113.75
38	A1	1888	OMU	O4-C4-C5	-3.03	119.93	125.16
38	A1	2619	OMG	C6-C5-N7	3.03	135.80	130.29
38	A1	2281	A2M	C4-N9-C8	3.02	108.91	105.74
38	A1	2729	OMU	O4-C4-C5	-2.99	120.01	125.16
34	B5	1269	OMU	O4-C4-C5	-2.99	120.01	125.16
36	AB	243	HIC	NE2-CE1-ND1	-2.98	111.52	112.66
34	B5	1575	7MG	C3'-C2'-C1'	2.97	107.08	101.46
38	A1	807	A2M	N3-C2-N1	-2.97	124.08	128.58
38	A1	2288	OMG	C6-C5-N7	2.95	135.66	130.29
34	B5	1781	MA6	C6-C5-N7	2.95	138.14	133.43
38	A1	2421	OMU	O4-C4-C5	-2.94	120.09	125.16

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1781	MA6	C4-N9-C8	2.93	108.81	105.74
34	B5	1191	XSX	C5-C4-N3	2.92	119.67	115.64
38	A1	908	OMG	C6-C5-N7	2.85	135.48	130.29
34	B5	1773	4AC	CM7-C7-N4	2.84	119.86	115.27
38	A1	2870	5MC	C5-C4-N3	-2.82	118.86	121.75
38	A1	2347	OMU	C1'-N1-C2	2.81	122.65	117.59
38	A1	1133	A2M	C4-N9-C8	2.78	108.66	105.74
34	B5	1269	OMU	C1'-N1-C2	2.74	122.51	117.59
34	B5	1773	4AC	C5-C4-N3	-2.72	118.34	122.60
38	A1	2278	5MC	C5-C4-N3	-2.72	118.97	121.75
34	B5	619	A2M	C4-N9-C8	2.71	108.58	105.74
34	B5	1781	MA6	N9-C8-N7	-2.70	110.11	113.94
38	A1	2946	A2M	C2'-C1'-N9	-2.69	109.32	113.75
34	B5	100	A2M	C4-N9-C8	2.69	108.56	105.74
34	B5	100	A2M	C5-N7-C8	2.69	107.68	103.45
34	B5	1572	OMG	C4-C5-N7	-2.68	106.43	110.67
34	B5	619	A2M	C5-N7-C8	2.66	107.64	103.45
34	B5	28	A2M	C4-N9-C8	2.66	108.53	105.74
34	B5	420	A2M	C4-N9-C8	2.64	108.51	105.74
38	A1	2280	A2M	C4-N9-C8	2.64	108.51	105.74
38	A1	805	OMG	C4-C5-N7	-2.63	106.50	110.67
34	B5	1575	7MG	C5-C6-N1	2.63	115.57	110.94
38	A1	867	OMG	C4-C5-N7	-2.63	106.50	110.67
38	A1	2256	A2M	C4-N9-C8	2.63	108.50	105.74
34	B5	1575	7MG	C6-C5-N7	2.62	136.00	131.93
38	A1	1133	A2M	C5-N7-C8	2.61	107.55	103.45
38	A1	817	A2M	C4-N9-C8	2.60	108.47	105.74
38	A1	2278	5MC	O2-C2-N3	-2.58	118.26	122.33
34	B5	796	A2M	C5-N7-C8	2.58	107.51	103.45
38	A1	2220	A2M	C4-N9-C8	2.58	108.45	105.74
38	A1	2946	A2M	C4-N9-C8	2.57	108.44	105.74
38	A1	2281	A2M	C5-N7-C8	2.57	107.48	103.45
34	B5	1271	OMG	C4-C5-N7	-2.57	106.60	110.67
34	B5	420	A2M	C5-N7-C8	2.56	107.47	103.45
80	DC	699	DDE	CAU-CBW-CBI	-2.56	106.21	111.22
38	A1	807	A2M	C5-N7-C8	2.55	107.46	103.45
34	B5	562	OMG	C4-C5-N7	-2.55	106.63	110.67
34	B5	796	A2M	C4-N9-C8	2.55	108.41	105.74
38	A1	2619	OMG	C4-C5-N7	-2.55	106.63	110.67
34	B5	28	A2M	C5-N7-C8	2.54	107.45	103.45
38	A1	2256	A2M	C5-N7-C8	2.54	107.44	103.45
38	A1	2815	OMG	C4-C5-N7	-2.53	106.65	110.67

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2280	A2M	C5-N7-C8	2.53	107.43	103.45
38	A1	2793	OMG	C4-C5-N7	-2.53	106.66	110.67
34	B5	1773	4AC	C1'-N1-C2	2.53	124.02	118.44
34	B5	974	A2M	C4-N9-C8	2.52	108.38	105.74
38	A1	2791	OMG	C4-C5-N7	-2.52	106.68	110.67
38	A1	2724	OMU	C1'-N1-C2	2.51	122.11	117.59
38	A1	2946	A2M	C5-N7-C8	2.51	107.40	103.45
38	A1	2922	OMG	C4-C5-N7	-2.51	106.70	110.67
38	A1	1450	OMG	C4-C5-N7	-2.50	106.71	110.67
34	B5	1428	OMG	C4-C5-N7	-2.50	106.71	110.67
38	A1	2640	A2M	C4-N9-C8	2.49	108.36	105.74
38	A1	876	A2M	C4-N9-C8	2.48	108.34	105.74
38	A1	1437	OMC	O2-C2-N3	-2.47	118.44	122.33
34	B5	1126	OMG	C4-C5-N7	-2.47	106.76	110.67
38	A1	807	A2M	C4-N9-C8	2.47	108.33	105.74
38	A1	645	1MA	C4-C5-N7	-2.46	106.77	110.67
34	B5	541	A2M	C5-N7-C8	2.45	107.29	103.45
38	A1	1449	A2M	C4-N9-C8	2.44	108.30	105.74
38	A1	649	A2M	C4-N9-C8	2.44	108.30	105.74
38	A1	2640	A2M	C5-N7-C8	2.43	107.28	103.45
34	B5	436	A2M	C5-N7-C8	2.43	107.27	103.45
34	B5	974	A2M	C5-N7-C8	2.42	107.25	103.45
38	A1	817	A2M	C5-N7-C8	2.41	107.24	103.45
38	A1	908	OMG	C4-C5-N7	-2.40	106.86	110.67
38	A1	1449	A2M	C5-N7-C8	2.40	107.22	103.45
34	B5	1191	XSX	C1-N3-C4	2.39	121.72	117.10
38	A1	2417	OMU	O2-C2-N1	-2.38	119.69	122.80
38	A1	649	A2M	C5-N7-C8	2.38	107.19	103.45
38	A1	2220	A2M	C5-N7-C8	2.36	107.16	103.45
38	A1	876	A2M	C5-N7-C8	2.35	107.14	103.45
38	A1	1437	OMC	C1'-N1-C2	2.34	123.60	118.44
34	B5	541	A2M	C4-N9-C8	2.33	108.18	105.74
38	A1	2288	OMG	C4-C5-N7	-2.32	106.99	110.67
34	B5	1280	4AC	C6-C5-C4	2.32	119.79	117.00
38	A1	817	A2M	C6-C5-N7	2.31	136.53	132.09
34	B5	1781	MA6	N1-C6-N6	2.30	119.66	116.86
38	A1	2281	A2M	N9-C8-N7	-2.25	110.74	113.94
38	A1	2288	OMG	O6-C6-C5	-2.24	120.62	126.53
38	A1	2948	OMC	O2-C2-N3	-2.21	118.84	122.33
34	B5	619	A2M	C6-C5-N7	2.21	136.36	132.09
34	B5	1126	OMG	O6-C6-C5	-2.21	120.70	126.53
34	B5	1782	MA6	N1-C6-N6	2.20	119.54	116.86

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2281	A2M	C6-C5-N7	2.20	136.32	132.09
38	A1	908	OMG	O6-C6-C5	-2.19	120.75	126.53
38	A1	2619	OMG	O6-C6-C5	-2.18	120.79	126.53
38	A1	2220	A2M	C2-N1-C6	2.17	122.29	118.73
38	A1	2729	OMU	C1'-N1-C2	2.17	121.49	117.59
38	A1	2921	OMU	O2-C2-N1	-2.17	119.98	122.80
34	B5	796	A2M	C6-C5-N7	2.16	136.25	132.09
34	B5	28	A2M	C6-C5-N7	2.16	136.25	132.09
38	A1	2256	A2M	C6-C5-N7	2.16	136.25	132.09
38	A1	2922	OMG	O6-C6-C5	-2.16	120.84	126.53
34	B5	436	A2M	C4-N9-C8	2.14	107.98	105.74
38	A1	805	OMG	O6-C6-C5	-2.14	120.89	126.53
36	AB	243	HIC	CB-CG-CD2	-2.13	124.82	129.96
34	B5	1428	OMG	O6-C6-C5	-2.13	120.92	126.53
34	B5	578	OMU	O2-C2-N1	-2.12	120.04	122.80
34	B5	1271	OMG	O6-C6-C5	-2.12	120.95	126.53
38	A1	1133	A2M	C6-C5-N7	2.11	136.16	132.09
34	B5	619	A2M	N9-C8-N7	-2.11	110.94	113.94
34	B5	562	OMG	O6-C6-C5	-2.10	121.00	126.53
38	A1	2280	A2M	C6-C5-N7	2.09	136.13	132.09
34	B5	100	A2M	N9-C8-N7	-2.09	110.97	113.94
38	A1	898	OMU	C1'-N1-C2	2.08	121.33	117.59
34	B5	100	A2M	C6-C5-N7	2.08	136.10	132.09
38	A1	2815	OMG	O6-C6-C5	-2.08	121.04	126.53
38	A1	2793	OMG	O6-C6-C5	-2.08	121.04	126.53
38	A1	650	OMC	O2-C2-N3	-2.08	119.06	122.33
38	A1	2946	A2M	C6-C5-N7	2.07	136.08	132.09
34	B5	420	A2M	C6-C5-N7	2.07	136.07	132.09
38	A1	2142	1MA	C4-C5-N7	-2.06	107.41	110.67
34	B5	1572	OMG	O6-C6-C5	-2.05	121.11	126.53
38	A1	807	A2M	O4'-C1'-N9	2.05	112.03	108.09
38	A1	1133	A2M	N9-C8-N7	-2.05	111.03	113.94
38	A1	2791	OMG	O6-C6-C5	-2.04	121.15	126.53
38	A1	1450	OMG	O6-C6-C5	-2.03	121.17	126.53
38	A1	2640	A2M	C6-C5-N7	2.03	136.00	132.09
38	A1	2256	A2M	N9-C8-N7	-2.03	111.06	113.94
38	A1	645	1MA	C6-C5-N7	2.02	135.73	132.16
38	A1	2220	A2M	C6-C5-N7	2.02	135.98	132.09
38	A1	2724	OMU	O2-C2-N1	-2.02	120.17	122.80
38	A1	2870	5MC	O2-C2-N3	-2.02	119.15	122.33
38	A1	867	OMG	O6-C6-C5	-2.01	121.22	126.53
38	A1	1449	A2M	C6-C5-N7	2.01	135.97	132.09

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	28	A2M	N9-C8-N7	-2.01	111.08	113.94
34	B5	436	A2M	C6-C5-N7	2.00	135.95	132.09

There are no chirality outliers.

All (78) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B5	420	A2M	C1'-C2'-O2'-CM'
34	B5	1782	MA6	O4'-C4'-C5'-O5'
34	B5	1782	MA6	C5-C6-N6-C9
34	B5	1280	4AC	N3-C4-N4-C7
34	B5	1280	4AC	C5-C4-N4-C7
34	B5	1773	4AC	N3-C4-N4-C7
34	B5	1773	4AC	C5-C4-N4-C7
34	B5	1773	4AC	O7-C7-N4-C4
34	B5	1773	4AC	CM7-C7-N4-C4
38	A1	1437	OMC	C1'-C2'-O2'-CM2
38	A1	2197	OMC	C2'-C1'-N1-C2
38	A1	2197	OMC	C2'-C1'-N1-C6
38	A1	2724	OMU	C1'-C2'-O2'-CM2
38	A1	2729	OMU	C3'-C4'-C5'-O5'
34	B5	1782	MA6	C3'-C4'-C5'-O5'
38	A1	2197	OMC	O4'-C4'-C5'-O5'
34	B5	619	A2M	O4'-C4'-C5'-O5'
38	A1	1437	OMC	O4'-C4'-C5'-O5'
38	A1	2197	OMC	C3'-C4'-C5'-O5'
38	A1	2347	OMU	C3'-C4'-C5'-O5'
38	A1	2729	OMU	O4'-C4'-C5'-O5'
34	B5	1191	XSX	N4-C7-C9-O10
34	B5	1782	MA6	N1-C6-N6-C9
34	B5	541	A2M	C3'-C4'-C5'-O5'
34	B5	541	A2M	O4'-C4'-C5'-O5'
34	B5	619	A2M	C3'-C4'-C5'-O5'
38	A1	1437	OMC	C3'-C4'-C5'-O5'
36	AB	243	HIC	CA-CB-CG-ND1
80	DC	699	DDE	CA-CB-CG-ND1
34	B5	1781	MA6	C5-C6-N6-C9
38	A1	2870	5MC	C2'-C1'-N1-C6
34	B5	1428	OMG	O4'-C4'-C5'-O5'
38	A1	2347	OMU	O4'-C4'-C5'-O5'
34	B5	1191	XSX	N4-C7-C9-O11
80	DC	699	DDE	NAD-CBI-CBW-NCB

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
34	B5	619	A2M	C2'-C1'-N9-C8
34	B5	1269	OMU	O4'-C1'-N1-C6
38	A1	2280	A2M	C3'-C4'-C5'-O5'
38	A1	2870	5MC	O4'-C1'-N1-C6
34	B5	541	A2M	C4'-C5'-O5'-P
38	A1	817	A2M	C4'-C5'-O5'-P
38	A1	2280	A2M	O4'-C4'-C5'-O5'
38	A1	2281	A2M	O4'-C4'-C5'-O5'
38	A1	807	A2M	C3'-C2'-O2'-CM'
36	AB	243	HIC	CA-CB-CG-CD2
34	B5	1269	OMU	O4'-C1'-N1-C2
34	B5	1126	OMG	C3'-C4'-C5'-O5'
80	DC	699	DDE	CAT-CAU-CBW-CBI
38	A1	649	A2M	C4'-C5'-O5'-P
34	B5	1782	MA6	C5-C6-N6-C10
80	DC	699	DDE	N-CA-CB-CG
80	DC	699	DDE	CA-CB-CG-CD2
38	A1	2870	5MC	O4'-C1'-N1-C2
38	A1	2197	OMC	O4'-C1'-N1-C6
38	A1	2922	OMG	C3'-C2'-O2'-CM2
34	B5	1126	OMG	C4'-C5'-O5'-P
38	A1	2870	5MC	C2'-C1'-N1-C2
34	B5	1428	OMG	C4'-C5'-O5'-P
34	B5	1782	MA6	C4'-C5'-O5'-P
34	B5	1428	OMG	C1'-C2'-O2'-CM2
38	A1	2619	OMG	C1'-C2'-O2'-CM2
38	A1	2922	OMG	C1'-C2'-O2'-CM2
38	A1	867	OMG	O4'-C4'-C5'-O5'
38	A1	2142	1MA	O4'-C4'-C5'-O5'
34	B5	1191	XSX	C3-C7-C9-O11
34	B5	541	A2M	O4'-C1'-N9-C8
34	B5	619	A2M	O4'-C1'-N9-C8
38	A1	2256	A2M	C4'-C5'-O5'-P
34	B5	1781	MA6	N1-C6-N6-C9
38	A1	2197	OMC	O4'-C1'-N1-C2
38	A1	645	1MA	C2'-C1'-N9-C8
38	A1	2281	A2M	C3'-C4'-C5'-O5'
34	B5	100	A2M	O4'-C4'-C5'-O5'
38	A1	807	A2M	O4'-C1'-N9-C8
38	A1	1437	OMC	C2'-C1'-N1-C2
34	B5	1269	OMU	C4'-C5'-O5'-P
34	B5	1269	OMU	C2'-C1'-N1-C2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
38	A1	645	1MA	C2'-C1'-N9-C4

There are no ring outliers.

24 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	898	OMU	1	0
80	DC	699	DDE	2	0
34	B5	1639	OMC	1	0
38	A1	2197	OMC	1	0
34	B5	1269	OMU	2	0
34	B5	1572	OMG	1	0
38	A1	2724	OMU	2	0
38	A1	1449	A2M	2	0
34	B5	28	A2M	1	0
34	B5	1126	OMG	1	0
34	B5	436	A2M	1	0
34	B5	1782	MA6	1	0
38	A1	2640	A2M	1	0
38	A1	649	A2M	2	0
38	A1	1133	A2M	1	0
38	A1	876	A2M	1	0
38	A1	2220	A2M	2	0
34	B5	1280	4AC	4	0
34	B5	1773	4AC	2	0
38	A1	650	OMC	2	0
34	B5	974	A2M	1	0
34	B5	1575	7MG	7	0
38	A1	663	OMC	1	0
38	A1	2281	A2M	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 256 ligands modelled in this entry, 255 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	1.16	3 (10%)	45,47,47	1.76	7 (15%)

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	3.12	1.47	1.38
85	DC	901	GDP	C6-N1	-2.51	1.34	1.38
85	DC	901	GDP	C5-N7	-2.10	1.34	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	DC	901	GDP	C5-C4-N3	-6.10	118.68	128.39
85	DC	901	GDP	C2-N3-C4	5.00	120.92	112.30
85	DC	901	GDP	N9-C4-N3	4.59	135.12	125.95
85	DC	901	GDP	C6-C5-N7	3.15	136.03	130.29
85	DC	901	GDP	C4-C5-N7	-2.46	106.78	110.67
85	DC	901	GDP	O6-C6-C5	-2.22	120.67	126.53
85	DC	901	GDP	C3'-C2'-C1'	2.19	105.60	101.46

There are no chirality outliers.

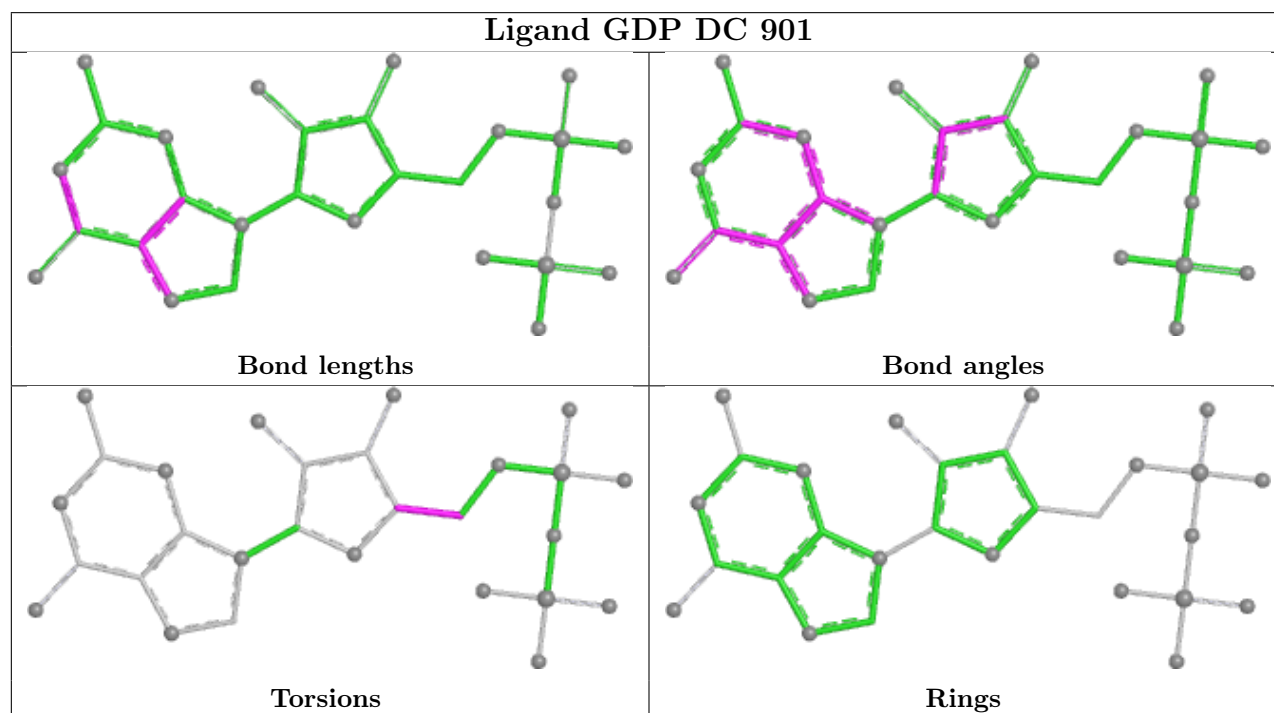
All (2) torsion outliers are listed below:

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.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
38	A1	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	1955:U	O3'	2093:A	P	21.31
1	A1	1023:C	O3'	1030:A	P	14.80
1	A1	440:A	O3'	494:G	P	8.27

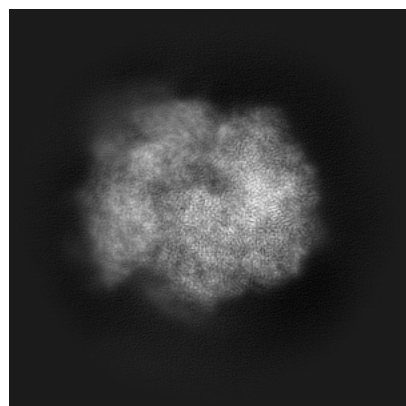
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28635. These allow visual inspection of the internal detail of the map and identification of artifacts.

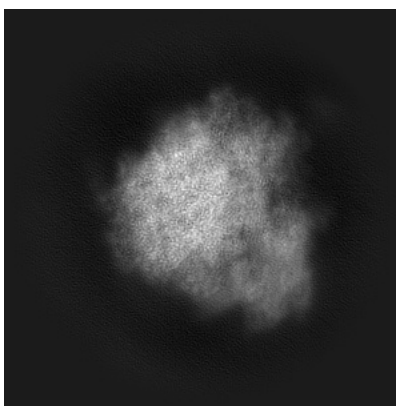
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

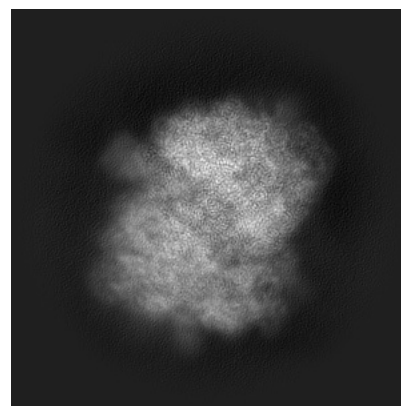
6.1.1 Primary map



X

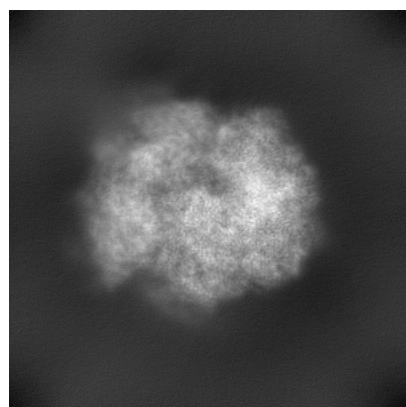


Y

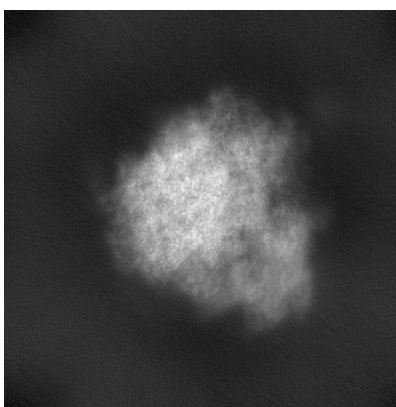


Z

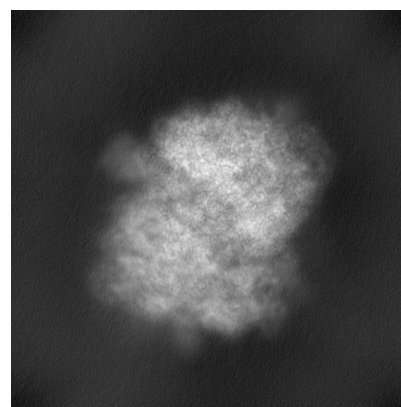
6.1.2 Raw map



X



Y

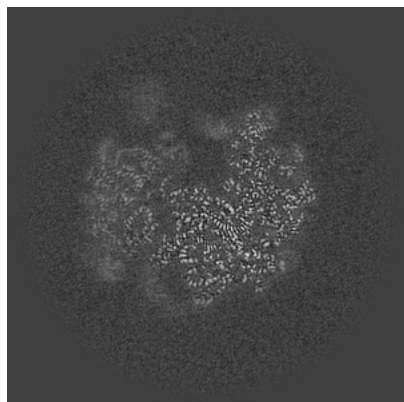


Z

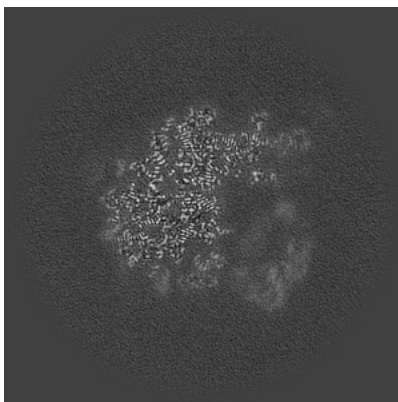
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

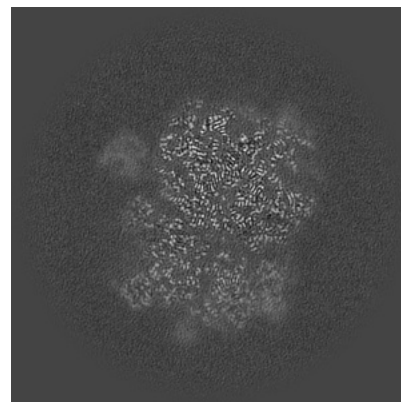
6.2.1 Primary map



X Index: 200

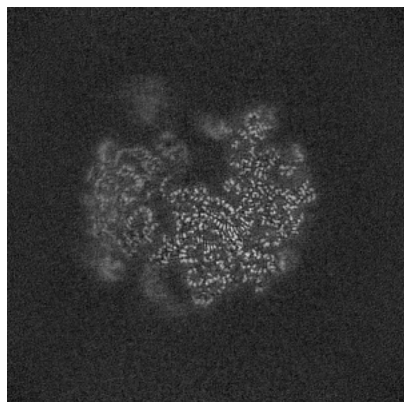


Y Index: 200

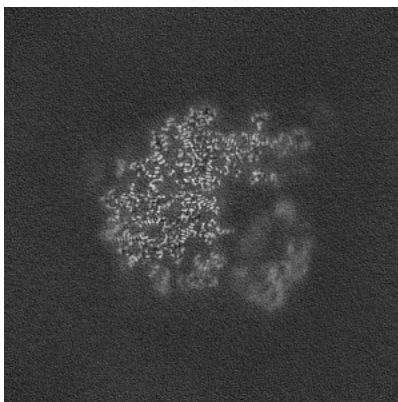


Z Index: 200

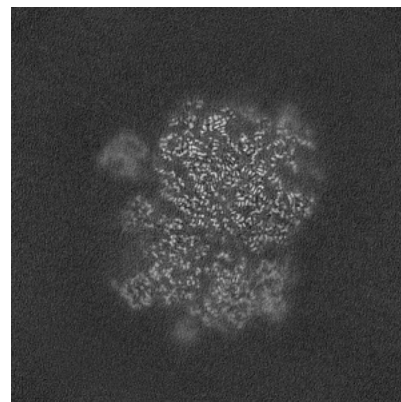
6.2.2 Raw map



X Index: 200



Y Index: 200

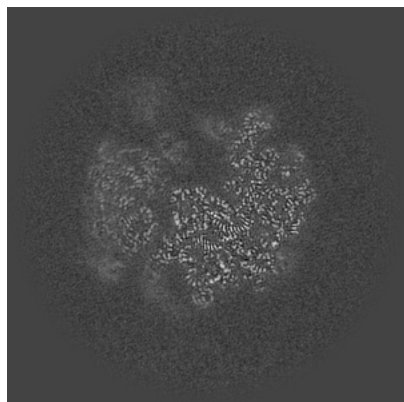


Z Index: 200

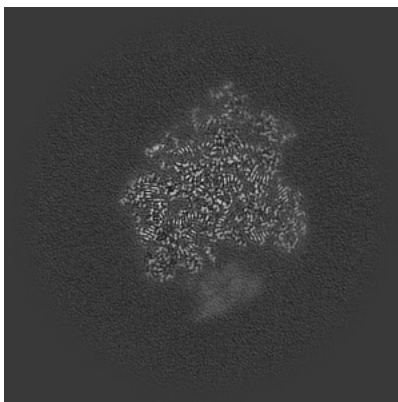
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

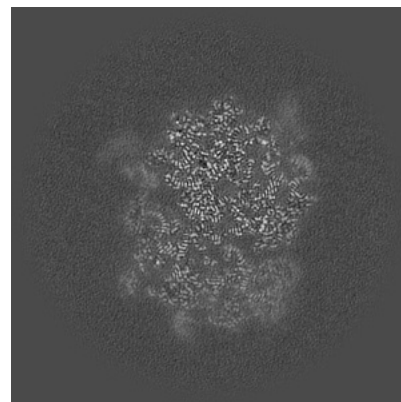
6.3.1 Primary map



X Index: 201

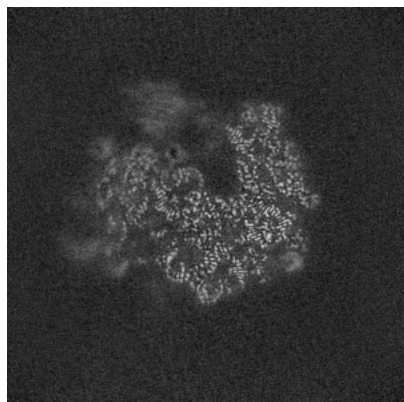


Y Index: 246

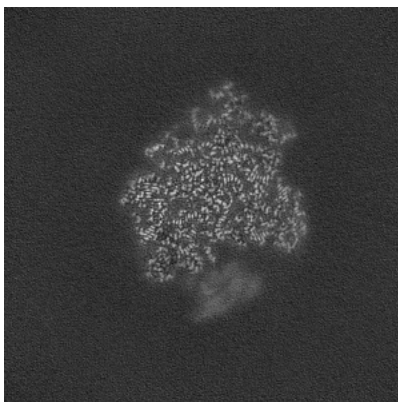


Z Index: 190

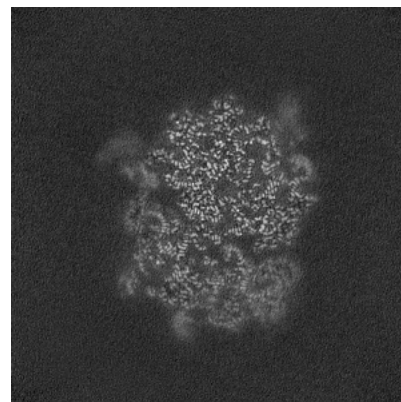
6.3.2 Raw map



X Index: 186



Y Index: 246

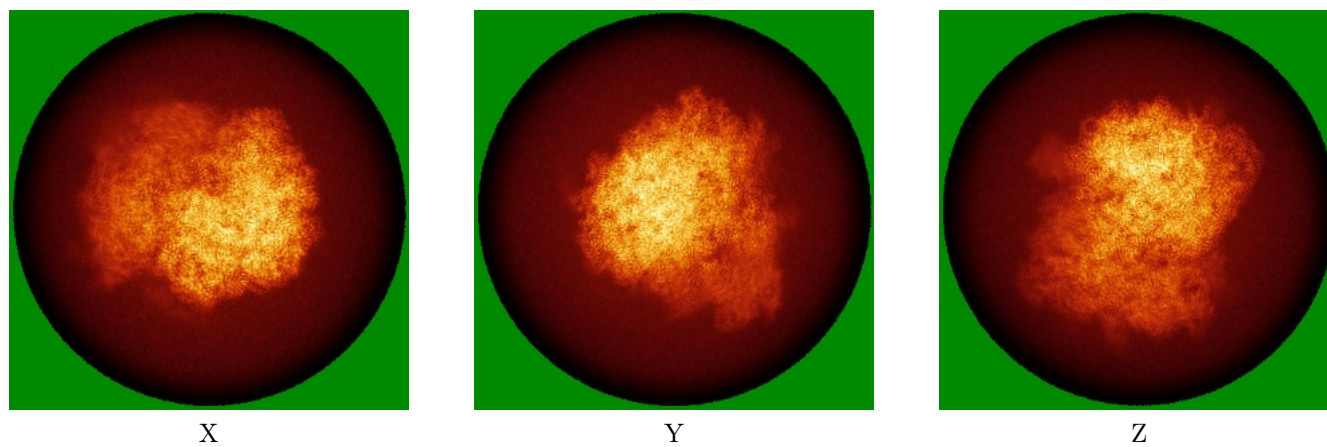


Z Index: 190

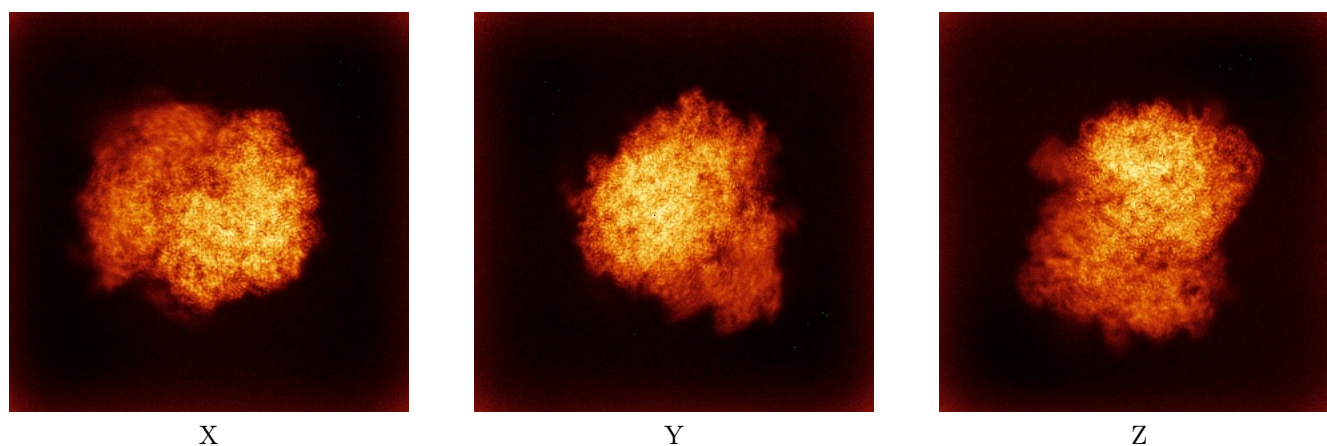
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

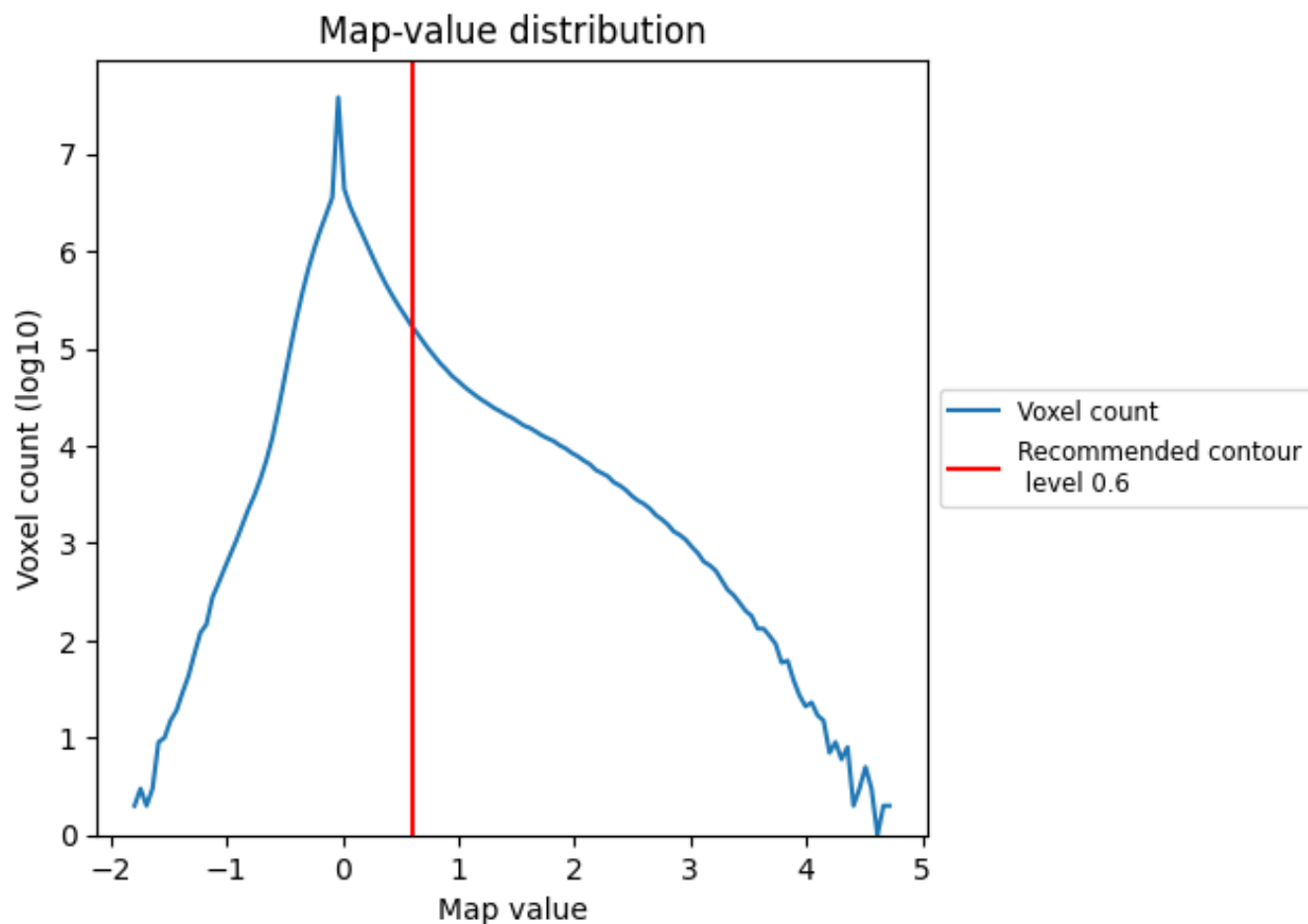
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

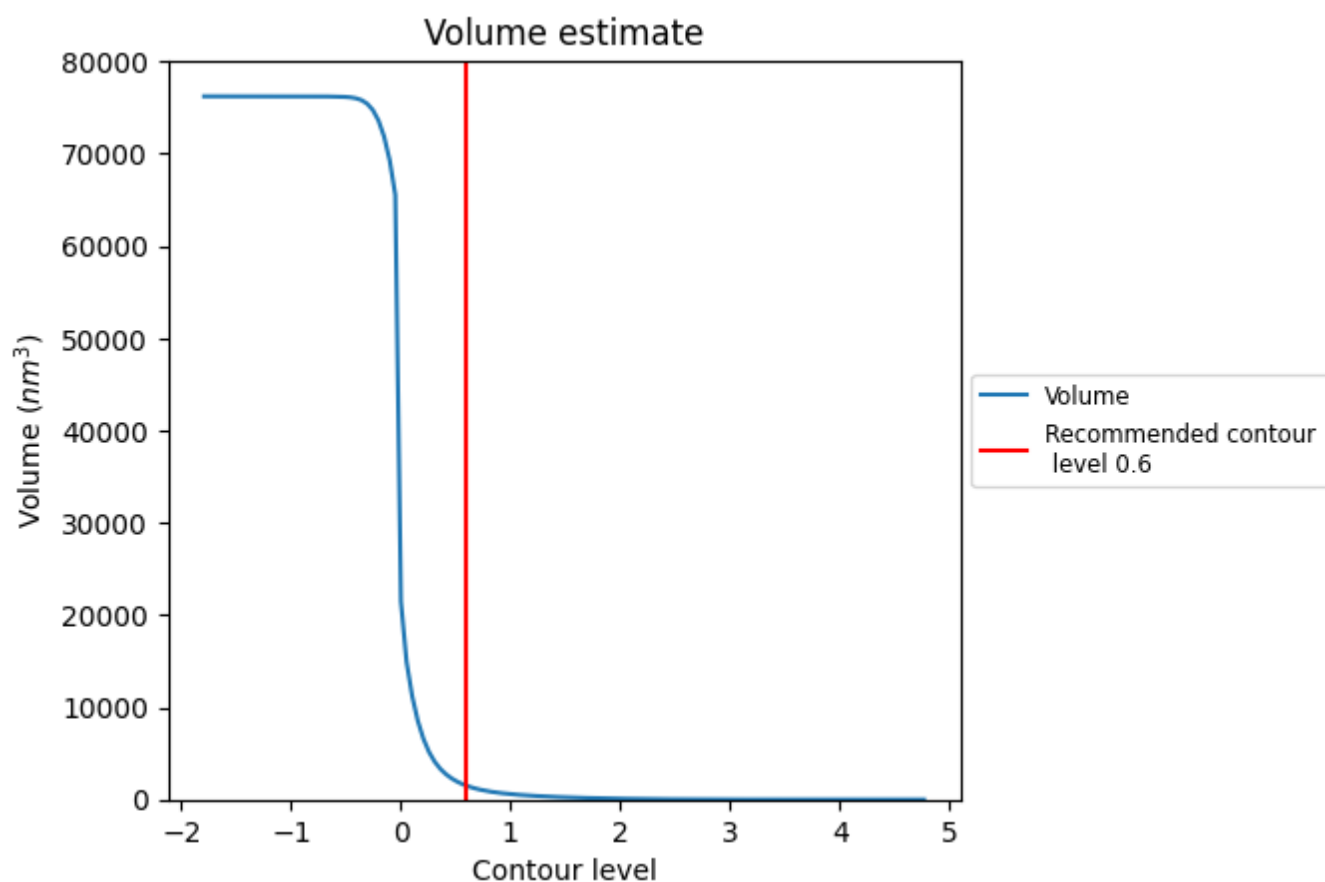
This section contains the results of statistical analysis of the map.

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.

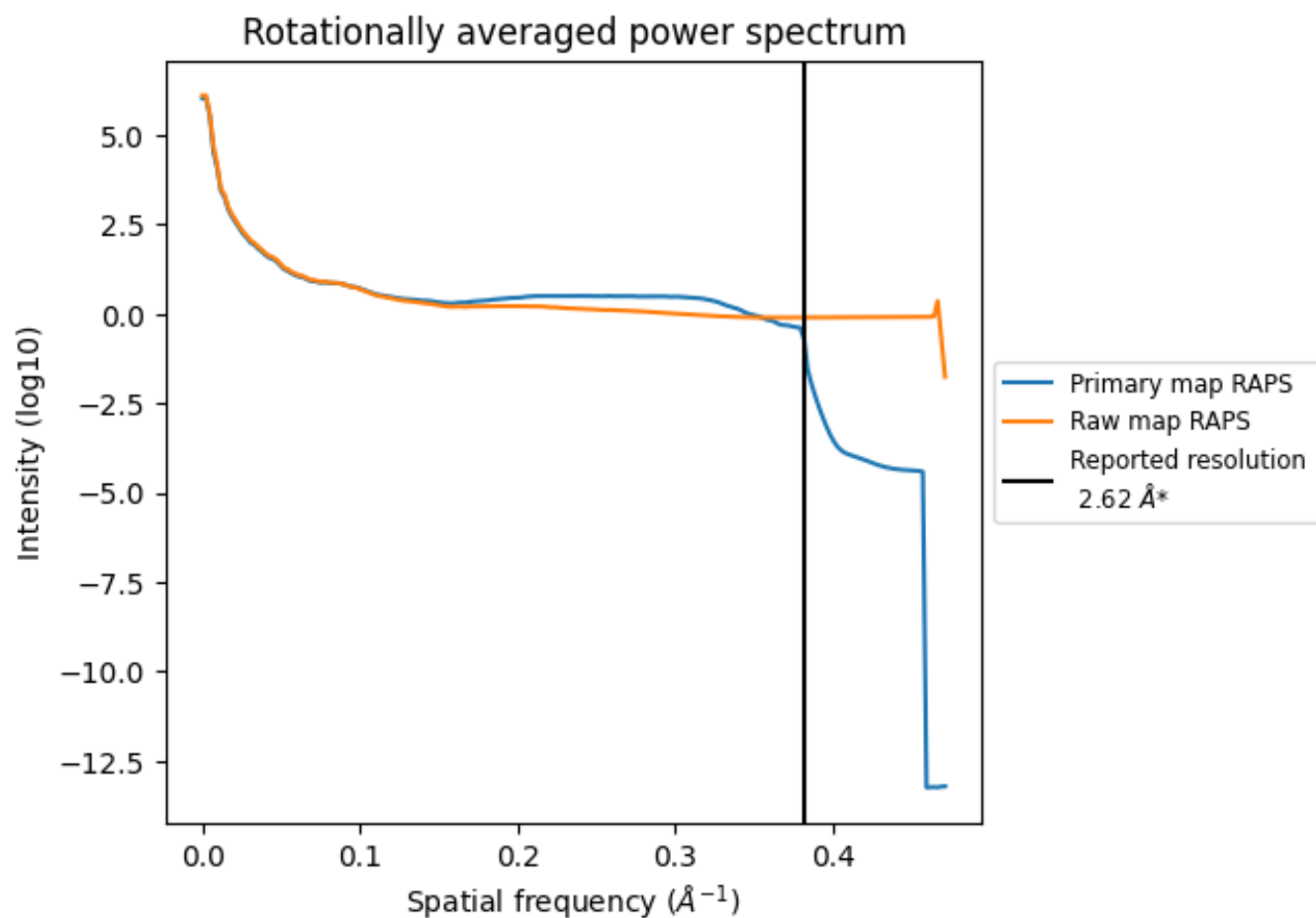
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1503 nm³; this corresponds to an approximate mass of 1358 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 ⓘ

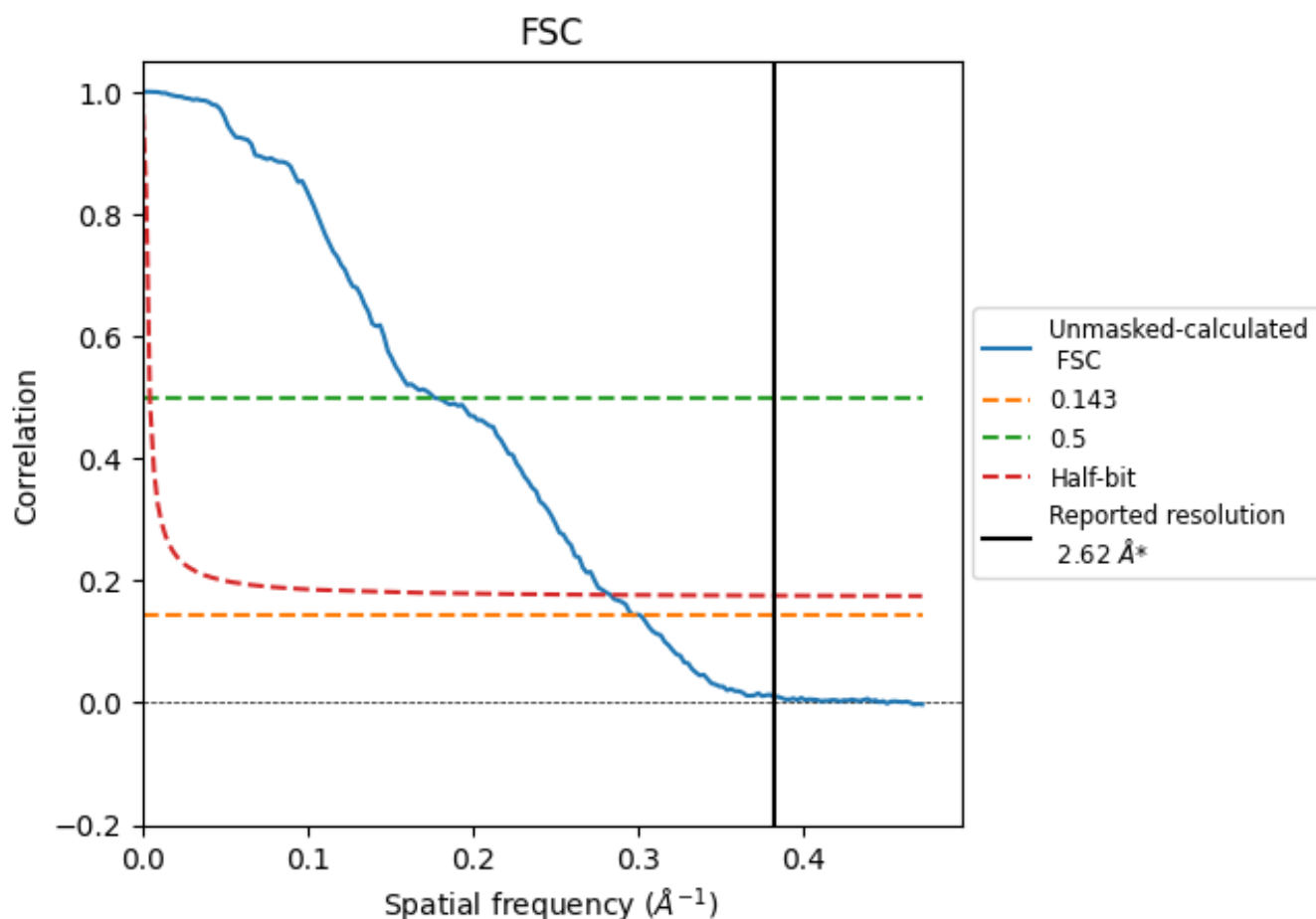


*Reported resolution corresponds to spatial frequency of 0.382 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.382 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

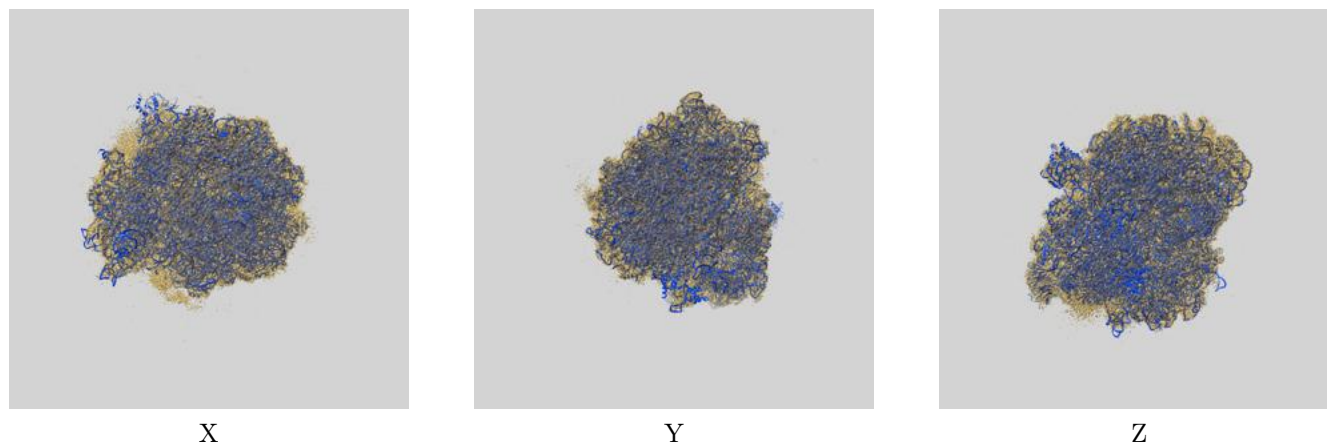
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.62	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.37	5.67	3.53

*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 2.62 by more than 10 %

9 Map-model fit [i](#)

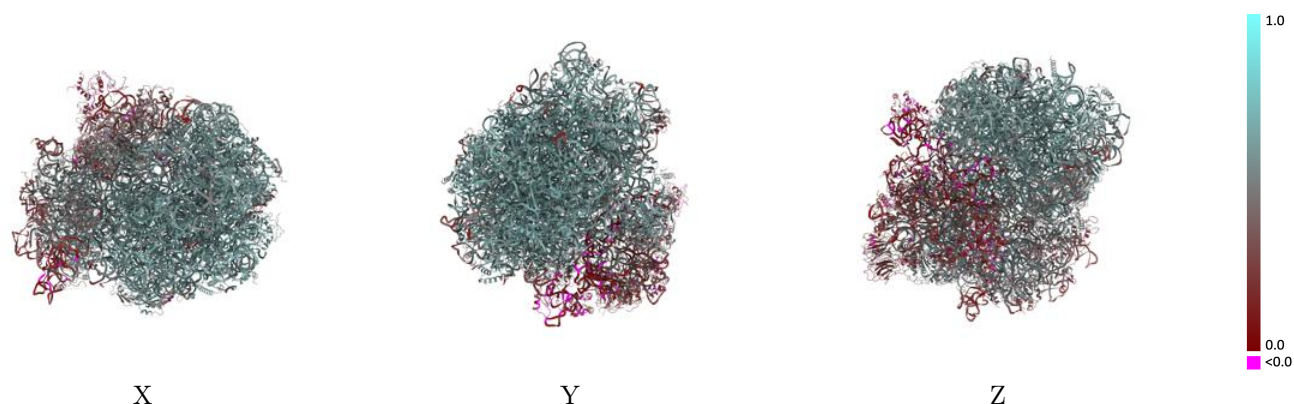
This section contains information regarding the fit between EMDB map EMD-28635 and PDB model 8EVS. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



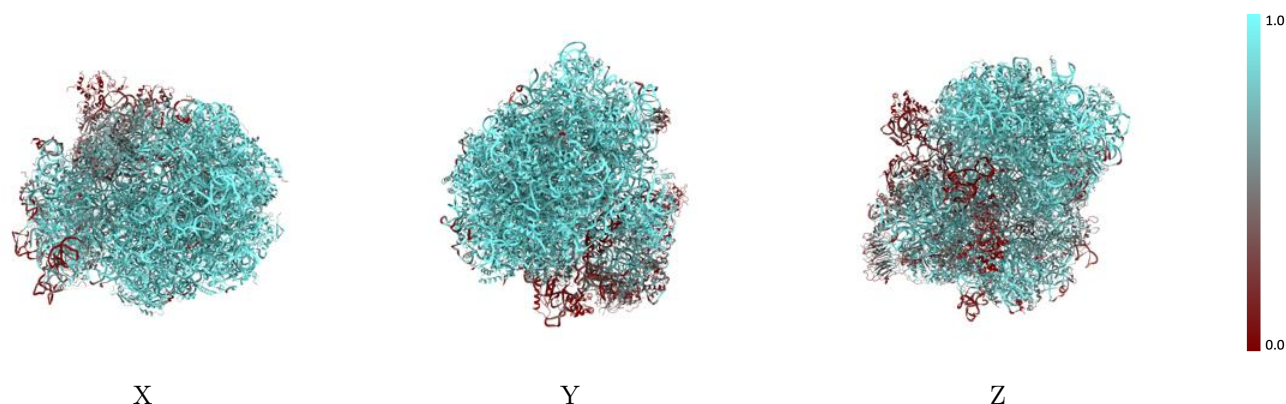
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



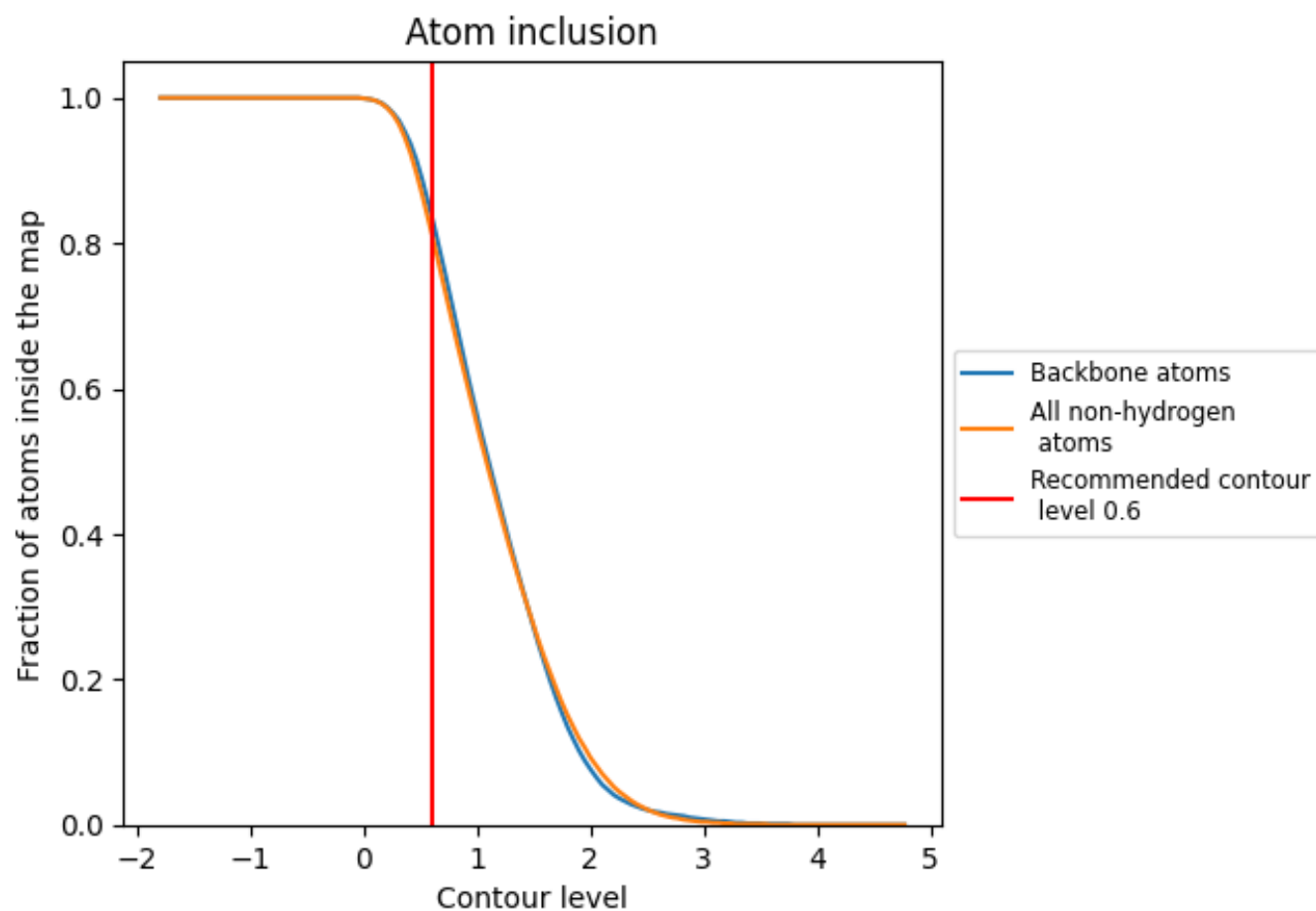
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 81% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8130	 0.5130
A1	 0.9460	 0.5920
A3	 0.9710	 0.5900
A4	 0.9760	 0.6190
AA	 0.9700	 0.6370
AB	 0.9230	 0.6040
AC	 0.9420	 0.6150
AD	 0.8400	 0.5450
AE	 0.8730	 0.5700
AF	 0.9390	 0.6140
AG	 0.8730	 0.5680
AH	 0.8550	 0.5650
AI	 0.8890	 0.5890
AJ	 0.6580	 0.4550
AL	 0.9280	 0.6040
AM	 0.8890	 0.5660
AN	 0.9770	 0.6370
AO	 0.9350	 0.6090
AP	 0.9400	 0.6210
AQ	 0.9630	 0.6280
AR	 0.8340	 0.5590
AS	 0.9140	 0.5900
AT	 0.9030	 0.5920
AU	 0.7970	 0.5230
AV	 0.9060	 0.6080
AW	 0.9210	 0.6070
AX	 0.9280	 0.6070
AY	 0.9260	 0.6020
AZ	 0.8940	 0.5790
Aa	 0.9520	 0.6190
Ab	 0.8940	 0.5640
Ac	 0.8910	 0.5940
Ad	 0.8670	 0.5840
Ae	 0.9660	 0.6310
Af	 0.9780	 0.6280



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Ag	 0.9220	 0.6100
Ah	 0.9260	 0.6040
Ai	 0.8890	 0.5670
Aj	 0.9760	 0.6380
Ak	 0.7810	 0.5290
Al	 0.9590	 0.6240
Am	 0.8780	 0.5830
An	 0.8680	 0.5690
Ao	 0.8930	 0.6040
Ap	 0.9180	 0.6090
B5	 0.8050	 0.4460
BA	 0.7880	 0.5070
BB	 0.7310	 0.5050
BC	 0.8360	 0.5350
BD	 0.4400	 0.2910
BE	 0.7690	 0.4920
BF	 0.4750	 0.3080
BG	 0.5900	 0.3950
BH	 0.6130	 0.4340
BI	 0.8120	 0.5220
BJ	 0.7340	 0.4680
BK	 0.3010	 0.2230
BL	 0.7730	 0.5290
BM	 0.0110	 0.1630
BN	 0.8530	 0.5590
BO	 0.8220	 0.5330
BP	 0.2240	 0.2340
BQ	 0.5920	 0.3400
BR	 0.5680	 0.3590
BS	 0.3000	 0.2430
BT	 0.4390	 0.2700
BU	 0.4810	 0.3050
BV	 0.7790	 0.5190
BW	 0.8960	 0.5730
BX	 0.8200	 0.5410
BY	 0.6040	 0.4150
BZ	 0.3040	 0.2360
Ba	 0.8280	 0.5410
Bb	 0.7550	 0.5140
Bc	 0.5010	 0.3790
Bd	 0.6290	 0.3250
Be	 0.5930	 0.4300

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bf	 0.0440	 0.1900
Bg	 0.4350	 0.2770
DC	 0.5070	 0.3800
E	 0.0790	 0.1620
EC	 0.1610	 0.1170
V	 0.4090	 0.3880