



Full wwPDB EM Validation Report ⓘ

Jun 27, 2026 – 11:55 AM EDT

PDB ID : 9P7N / pdb_00009p7n
EMDB ID : EMD-71348
Title : In situ human Post-eEF1A-A/T-P-Z state 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2025-06-20
Resolution : 2.83 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:

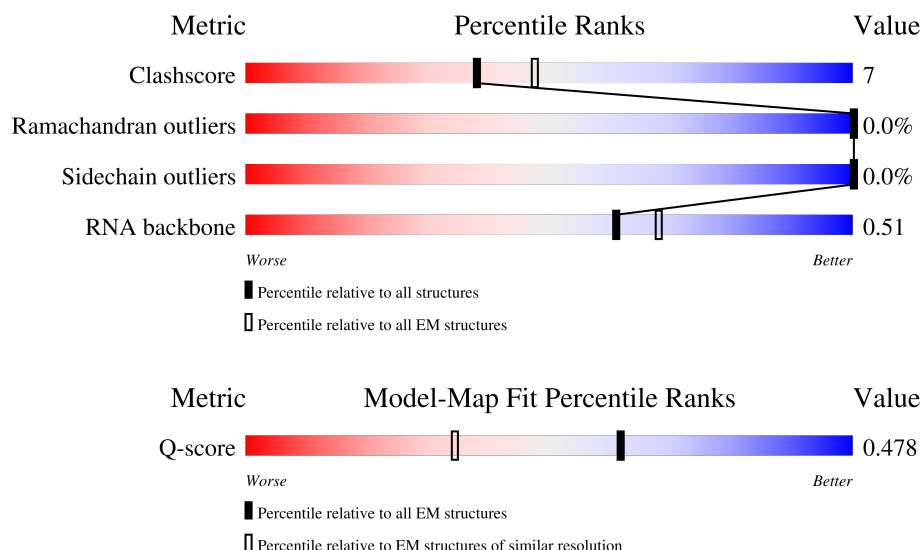
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 2.83 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	11847 (2.33 - 3.33)

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	CI	31	 6% 74% 26%
2	Pt	74	 54% 42% .
3	L5	3655	 57% 36% 7%

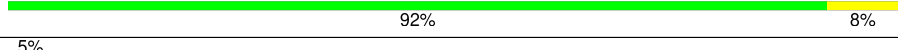
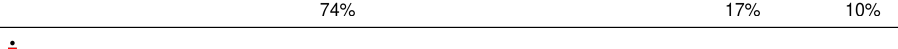
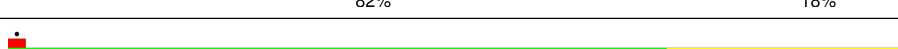
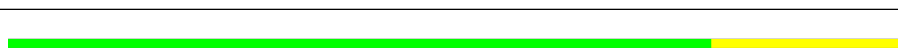
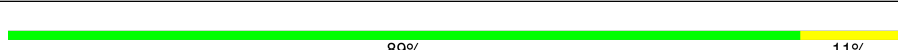
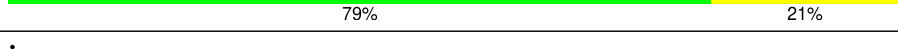
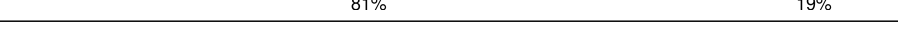
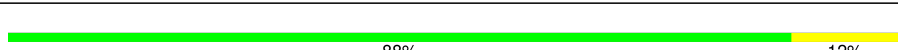
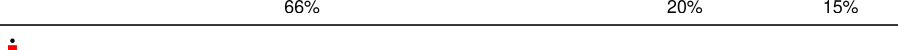
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	L7	120	 74% 22%
5	L8	156	 63% 36%
6	LA	248	 77% 23%
7	LB	402	 79% 21%
8	LC	368	 88% 12%
9	LD	293	 83% 17%
10	LE	250	 81% 15%
11	LF	225	 82% 18%
12	LG	241	 6% 85% 15%
13	LH	190	 87% 13%
14	LI	213	 84% 16%
15	LJ	176	 79% 18%
16	LL	210	 86% 14%
17	LM	139	 82% 18%
18	LN	203	 82% 18%
19	LO	201	 79% 21%
20	LP	153	 85% 15%
21	LQ	187	 86% 14%
22	LR	187	 83% 16%
23	LS	175	 90% 10%
24	LT	159	 81% 19%
25	LU	101	 72% 27%
26	LV	131	 83% 17%
27	LW	124	 75% 19% 6%
28	LX	120	 84% 16%

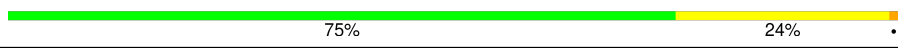
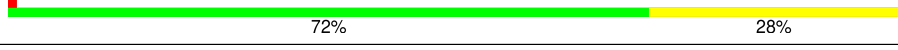
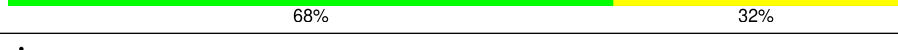
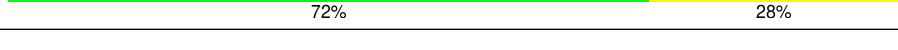
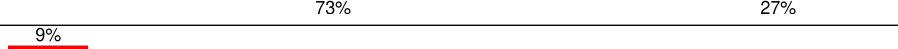
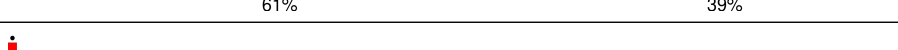
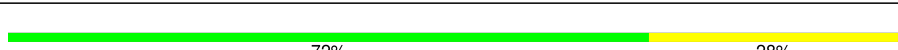
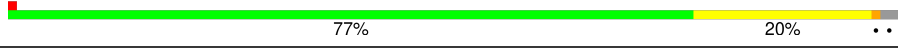
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	LY	134	
30	LZ	135	
31	La	147	
32	Lb	121	
33	Lc	98	
34	Ld	107	
35	Le	128	
36	Lf	109	
37	Lg	114	
38	Lh	122	
39	Li	102	
40	Lj	86	
41	Lk	69	
42	Ll	50	
43	Lm	52	
44	Ln	24	
45	Lo	105	
46	Lp	91	
47	Lr	125	
48	Ls	196	
49	Lt	157	
50	SD	227	
51	SF	189	
52	SK	98	
53	SM	122	

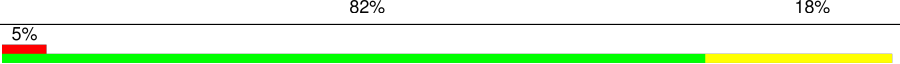
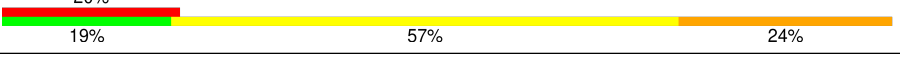
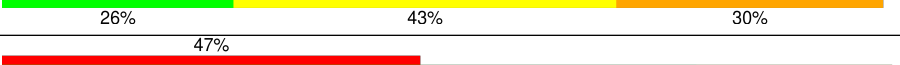
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	SP	121	
55	SQ	144	
56	SR	135	
57	SS	145	
58	ST	143	
59	SU	104	
60	SZ	75	
61	Sc	64	
62	Sd	55	
63	Sf	67	
64	Sg	313	
65	SA	221	
66	SB	214	
67	SC	222	
68	SE	262	
69	SG	237	
70	SH	189	
71	SI	206	
72	SJ	185	
73	SL	153	
74	SN	150	
75	SO	140	
76	SV	83	
77	SW	129	
78	SX	141	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	SY	131	
80	Sa	102	
81	Sb	83	
82	Se	58	
83	S2	1740	
84	Zt	75	
85	AT	76	
86	CF	441	

2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 224970 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 Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CI	31	Total	C	N	O	S	0	0
			247	153	55	38	1		

- Molecule 2 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Pt	74	Total	C	N	O	P	0	0
			1576	705	286	512	73		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Pt	3	C	U	conflict	GB X64278
Pt	?	-	U	deletion	GB X64278
Pt	?	-	G	deletion	GB X64278
Pt	19	G	U	conflict	GB X64278
Pt	50	U	-	insertion	GB X64278
Pt	74	C	-	insertion	GB X64278

- Molecule 3 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L5	3655	Total	C	N	O	P	1	0
			78444	34968	14346	25475	3655		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L8	156	Total	C	N	O	P	0	0
			3315	1481	585	1094	155		

- Molecule 6 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 7 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 8 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 9 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 10 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LE	240	Total	C	N	O	S	0	0
			1935	1242	368	321	4		

- Molecule 11 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 12 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 13 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 14 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 15 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LJ	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 16 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 17 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 18 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 19 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 20 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 21 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 22 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 23 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 24 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 25 is a protein called Heparin-binding protein HBp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 26 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 27 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LW	116	Total	C	N	O	S	0	0
			945	592	193	156	4		

- Molecule 28 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 30 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 31 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 32 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 36 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 37 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 39 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 40 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 41 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 43 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 44 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 45 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 46 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 47 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 48 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 49 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lt	134	Total	C	N	O	S	0	0
			998	626	180	189	3		

- Molecule 50 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 51 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 52 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 53 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 54 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 55 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 56 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 57 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 58 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 59 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 60 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 61 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 62 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 63 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 64 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 65 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 66 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 67 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SC	220	Total	C	N	O	S	0	0
			1707	1104	293	300	10		

- Molecule 68 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 69 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 70 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 71 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 72 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 73 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 74 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 75 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SO	137	Total	C	N	O	S	0	0
			1024	627	200	191	6		

- Molecule 76 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 77 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 78 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 79 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 80 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 81 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 82 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 83 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	S2	1740	Total	C	N	O	P	0	0
			36953	16508	6600	12106	1739		

- Molecule 84 is a RNA chain called Z site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Zt	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 85 is a RNA chain called RNA (76-MER)A/T site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	AT	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 86 is a protein called Elongation factor 1-alpha 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
86	CF	441	Total	C	N	O	P	S	0	0
			3383	2148	581	636	1	17		

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

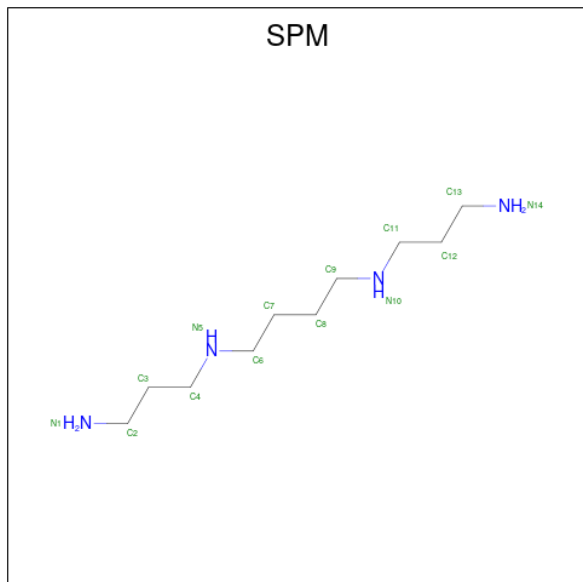
Mol	Chain	Residues	Atoms		AltConf
87	L5	179	Total	Mg	0
			179	179	
87	L7	3	Total	Mg	0
			3	3	
87	L8	4	Total	Mg	0
			4	4	
87	LA	1	Total	Mg	0
			1	1	
87	LI	1	Total	Mg	0
			1	1	
87	LP	1	Total	Mg	0
			1	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
87	LV	1	Total	Mg	0
			1	1	
87	Le	1	Total	Mg	0
			1	1	
87	SS	1	Total	Mg	0
			1	1	
87	SG	1	Total	Mg	0
			1	1	
87	S2	26	Total	Mg	0
			26	26	

- Molecule 88 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$) (labeled as "Ligand of Interest" by depositor).



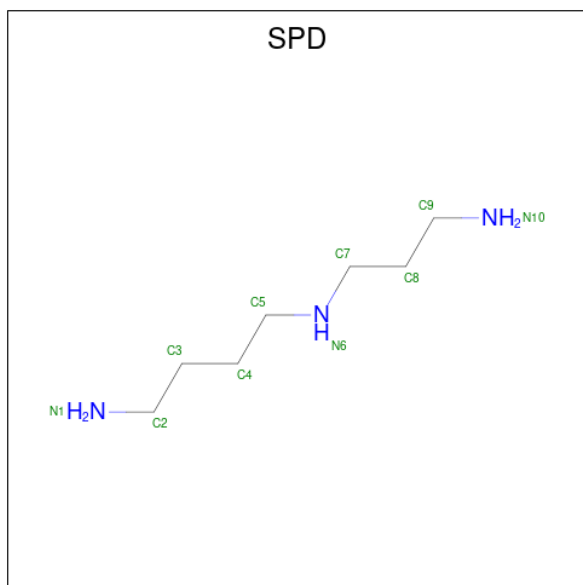
Mol	Chain	Residues	Atoms			AltConf
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			AltConf
88	L5	1	Total	C	N	0
			14	10	4	

- Molecule 89 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	LN	1	Total	C	N	0
			10	7	3	

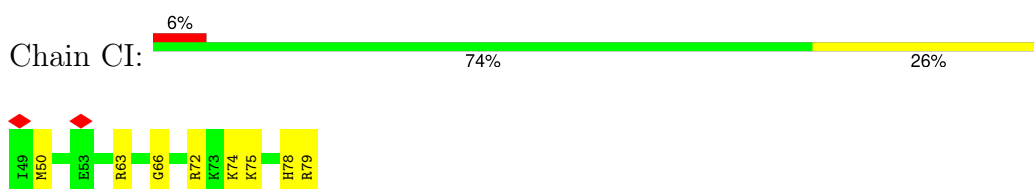
- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
90	Lg	1	Total 1	Zn 1	0
90	Lj	1	Total 1	Zn 1	0
90	Lm	1	Total 1	Zn 1	0
90	Lo	1	Total 1	Zn 1	0
90	Lp	1	Total 1	Zn 1	0
90	Sa	1	Total 1	Zn 1	0

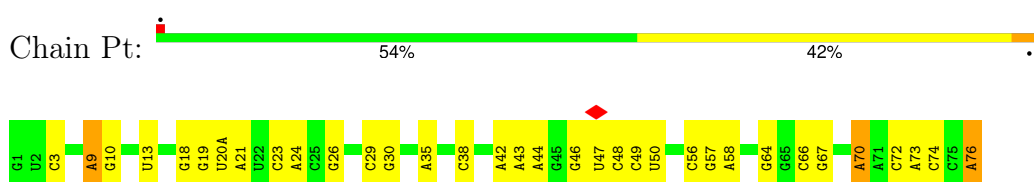
3 Residue-property plots

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

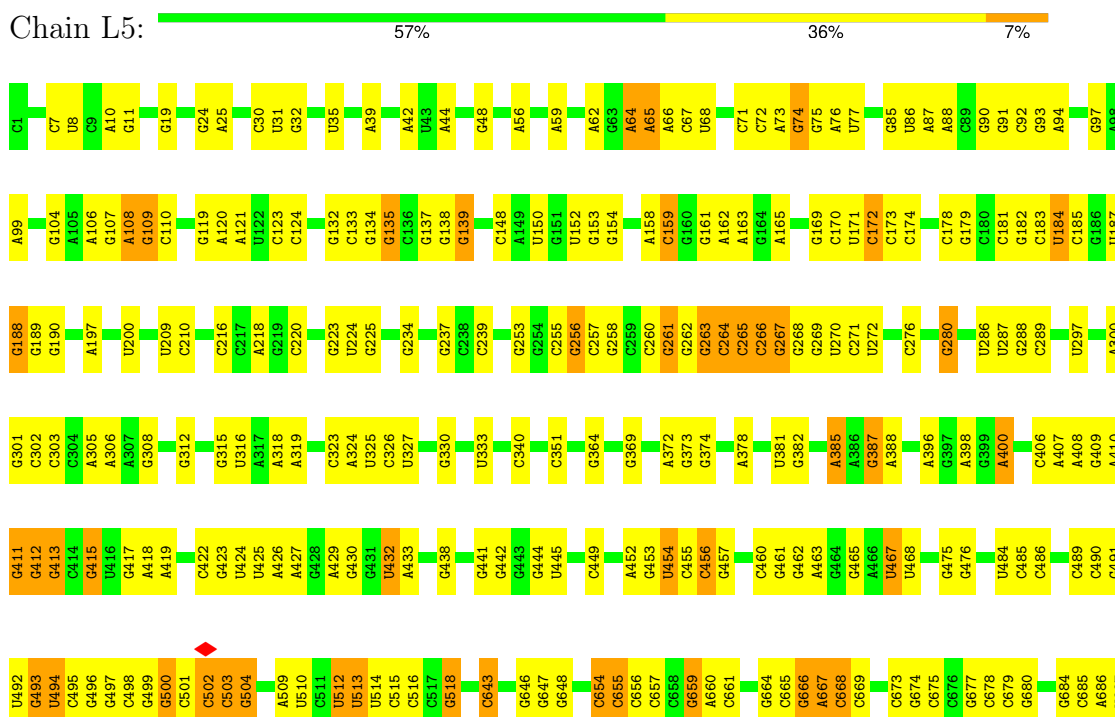
• Molecule 1: Transcription factor BTF3



• Molecule 2: P site tRNA

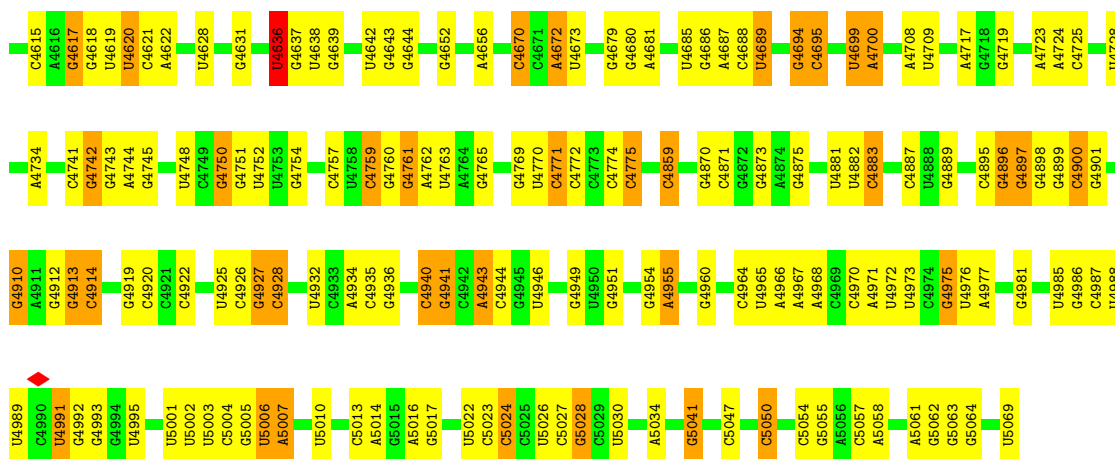


• Molecule 3: 28S rRNA



U2398	G2399	G2400	A2401	A2404	G2407	C2411	C2412	C2415	G2416	A2417	G2421	C2422	A2423	G2424	U2425	U2436	G2448	A2449	A2453	C2458	G2459	C2462	G2463	C2464	C2465	G2466	U2467	U2468	C2469	G2470	G2471	G2474	G2475	C2478	G2479	G2483	A2484	U2485	G2486	G2487	C2488	C2489	U2490	C2491	C2492	C2493					
G2284	G2289	C2289	C2289	C2289	C2292	U2293	G2294	C2295	G2296	G2297	U2298	G2299	A2300	G2301	C2302	C2303	G2306	A2313	G2318	G2321	U2329	G2330	C2331	A2332	G2332	G2333	G2334	C2335	C2336	A2347	G2348	G2349	U2350	C2351	A2360	G2361	U2362	A2363	A2376	C2377	G2380	U2386	G2387	A2388	A2389	G2394	A2395	A2396	G2397		
G2045	G2046	A2047	U2048	G2049	G2052	G2055	G2056	A2057	G2069	G2076	G2079	U2080	C2083	C2084	U2090	C2091	G2092	A2093	G2094	A2095	G2096	U2097	G2098	C2101	G2102	G2103	G2104	A2105	G2106	C2107	G2110	G2111	G2112	C2249	C2250	G2251	G2252	C2256	C2257	G2258	G2259	C2260	G2261	G2262	A2279	G2280	U2281				
C1856	C1857	A1858	C1859	U1860	U1861	U1862	U1866	A1867	C1868	G1869	C1870	A1871	G1872	C1875	U1876	G1877	G1878	G1879	G1880	C1881	U1882	G1890	G1895	G1896	A1897	C1898	G1899	G1912	C1913	C1914	A1917	U1918	G1919	C1920	C1921	G1922	G1925	C1931	A1932	G1933	A1934	A1942	A1943	G1948	G1951	G1952	G1961				
A1962	G1965	G1969	A1970	C1971	G1972	G1973	U1974	G1975	C1976	G1977	C1978	A1979	U1980	G1981	G1982	A1983	A1984	G1985	C1987	G1988	G1989	A1990	A1991	U1992	C1993	G1994	G1995	C1996	U1997	A1998	G1999	G2000	G2001	A2002	G2003	G2007	U2008	A2009	C2011	A2012	C2017	C2018	C2019	U2020	G2021	G2024	A2025	A2026	A2029	A2030	A2041
G2045	G2046	A2047	U2048	G2049	G2052	G2055	G2056	A2057	G2069	G2076	G2079	U2080	C2083	C2084	U2090	C2091	G2092	A2093	G2094	A2095	G2096	U2097	G2098	C2101	G2102	G2103	G2104	A2105	G2106	C2107	G2110	G2111	G2112	C2249	C2250	G2251	G2252	C2256	C2257	G2258	G2259	C2260	G2261	G2262	A2279	G2280	U2281				
G2284	C2289	C2289	C2289	C2289	C2292	U2293	G2294	C2295	G2296	G2297	U2298	G2299	A2300	G2301	C2302	C2303	G2306	A2313	G2318	G2321	U2329	G2330	C2331	A2332	G2332	G2333	G2334	C2335	G2336	A2347	G2348	G2349	U2350	C2351	A2360	G2361	U2362	A2363	A2376	C2377	G2380	U2386	G2387	A2388	A2389	G2394	A2395	A2396	G2397		
U2398	G2399	G2400	A2401	A2404	G2407	C2411	C2412	C2415	G2416	A2417	G2421	C2422	A2423	G2424	U2425	U2436	G2448	A2449	A2453	C2458	G2459	C2462	G2463	C2464	C2465	G2466	U2467	U2468	C2469	G2470	G2471	G2474	G2475	C2478	G2479	G2483	A2484	U2485	G2486	G2487	C2488	C2489	U2490	C2491	C2492	C2493					
C691	A692	U702	C703	C704	C707	G708	A711	C712	C713	G714	G715	C716	U717	C718	G730	G731	G735	C736	C737	C738	G739	G742	A746	A747	G748	G759	C904	C905	G908	A909	G910	U913	U914	A915	C916	A917	G918	C919	C920	C921	C922	C923	A1087	C924	G925	G926	A932				
G933	C934	A935	C936	C941	G942	A943	A944	U945	C946	G952	C953	A956	G959	A960	G961	C962	G965	A966	C967	G968	C969	G970	C979	U982	C985	U989	C990	G1064	G1070	A1071	C1072	G1075	C1076	A1077	C1079	C1080	C1081	C1082	U1083	C1084	C1085	C1086	A1087	C1088	G1094	A1095					
C1096	C1097	C1098	C1099	U1100	C1167	G1168	G1171	C1172	C1173	U1177	G1176	U1179	C1180	C1181	C1182	C1183	G1187	C1188	G1194	G1195	C1196	C1197	G1198	G1199	C1200	U1201	U982	C985	U989	C990	G1064	G1070	A1071	C1072	G1075	C1076	A1077	C1079	C1080	C1081	C1082	U1083	C1084	C1085	C1086	A1087	C1088	G1094	A1095		
G1261	G1262	G1266	C1267	G1268	G1269	A1270	G1271	C1272	G1273	A1274	G1275	G1276	G1277	C1278	A1279	C1280	G1281	G1282	G1283	G1284	U1285	G1286	G1287	G1293	A1294	C1295	G1296	U1297	C1298	G1299	G1300	C1301	C1305	C1308	C1309	C1314	U1317	C1318	A1322	A1323	A1324	C1325	A1326	G1327	G1328	C1332	A1333	A1334	G1338	U1339	
C1340	A1345	C1346	C1347	U1348	G1349	C1350	G1351	C1352	G1353	A1354	G1359	U1364	C1365	C1366	C1367	A1368	G1369	C1379	G1382	A1387	G1390	C1391	A1392	G1393	C1394	G1395	A1396	A1397	G1398	G1400	G1403	A1404	C1407	G1408	C1409	U1410	C1411	G1412	C1413	C1414	G1415	C1416	C1417	A1420	G1425	C1431					
G1432	C1437	U1438	C1439	C1442	A1443	G1444	U1445	C1446	C1447	G1457	C1461	A1462	G1466	C1480	C1481	G1482	C1483	U1494	G1495	G1495	A1497	G1498	C1499	A1500	C1501	G1502	A1503	G1504	C1509	U1514	A1515	A1516	G1517	A1523	A1524	A1525	A1534	C1535	U1536	A1537	U1538	G1539	A1547	G1552	A1558						
G1559	G1562	A1563	U1564	A1565	C1566	G1574	G1577	U1578	C1579	U1582	U1588	C1589	C1590	U1591	U1596	C1597	A1601	G1604	G1605	G1612	A1613	G1617	A1621	G1624	G1625	C1628	A1631	A1632	G1633	A1634	A1638	A1639	C1640	G1641	A1642	A1646	G1654	C1655	C1661	C1662	C1663										
A1669	G1670	C1676	U1677	C1678	A1679	G1680	U1683	G1684	G1685	C1689	U1695	G1696	C1697	G1698	A1699	G1700	A1701	C1702	C1703	G1704	G1705	A1706	G1716	C1717	A1718	A1719	G1720	G1721	U1725	U1726	U1727	C1731	G1732	G1733	G1734	U1735	G1739	C1740	G1741	A1742	U1744	G1750	A1751	G1752	G1753	U1754	U1755	U1756	U1757	G1758	G1759
G1760	G1761	C1762	G1763	G1764	A1765	U1766	A1767	C1768	G1769	A1770	U1773	U1779	A1780	U1781	U1782	C1785	A1786	A1787	U1788	C1789	U1792	A1802	G1803	A1804	A1805	G1806	G1810	G1811	G1815	G1818	G1819	G1820	G1821	U1822	G1823	G1824	A1825	G1826	U1834	G1835	A1836	A1837	G1842	G1846	C1847	C1848	G1855				
C1856	C1857	A1858	C1859	U1860	U1861	U1862	U1866	A1867	C1868	G1869	C1870	A1871	G1872	C1875	U1876	G1877	G1878	G1879	G1880	C1881	U1882	G1890	G1895	G1896	A1897	C1898	G1899	G1912	C1913	C1914	A1917	U1918	G1919	C1920	C1921	G1922	G1925	C1931	A1932	G1933	A1934	A1942	A1943	G1948	G1951	G1952	G1961				
A1962	G1965	G1969	A1970	C1971	G1972	G1973	U1974	G1975	C1976	G1977	C1978	A1979	U1980	G1981	G1982	A1983	A1984	G1985	C1987	G1988	G1989	A1990	A1991	U1992	C1993	G1994	G1995	C1996	U1997	A1998	G1999	G2000	G2001	A2002	G2003	G2007	U2008	A2009	C2011	A2012	C2017	C2018	C2019	U2020	G2021	G2024	A2025	A2026	A2029	A2030	A2041
G2045	G2046	A2047	U2048	G2049	G2052	G2055	G2056	A2057	G2069	G2076	G2079	U2080	C2083	C2084	U2090	C2091	G2092	A2093	G2094	A2095	G2096	U2097	G2098	C2101	G2102	G2103	G2104	A2105	G2106	C2107	G2110	G2111	G2112	C2249	C2250	G2251	G2252	C2256	C2257	G2258	G2259	C2260	G2261	G2262	A2279	G2280	U2281				
G2284	C2289	C2289	C2289	C2289	C2292	U2293	G2294	C2295	G2296	G2297	U2298	G2299	A2300	G2301	C2302	C2303	G2306	A2313	G2318	G2321	U2329	G2330	C2331	A2332	G2332	G2333	G2334	C2335	G2336	A2347	G2348	G2349	U2350	C2351	A2360	G2361	U2362	A2363	A2376	C2377	G2380	U2386	G2387	A2388	A2389	G2394	A2395	A2396	G2397		
U2398	G2399	G2400	A2401	A2404	G2407	C2411	C2412	C2415	G2416	A2417	G2421	C2422	A2423	G2424	U2425	U2436	G2448	A2449	A2453	C2458	G2459	C2462	G2463	C2464	C2465	G2466	U2467	U2468	C2469	G2470	G2471	G2474	G2475	C2478	G2479	G2483	A2484	U2485	G2486	G2487	C2488	A2389	U2489	U2490	C2491	C2492	C2493				





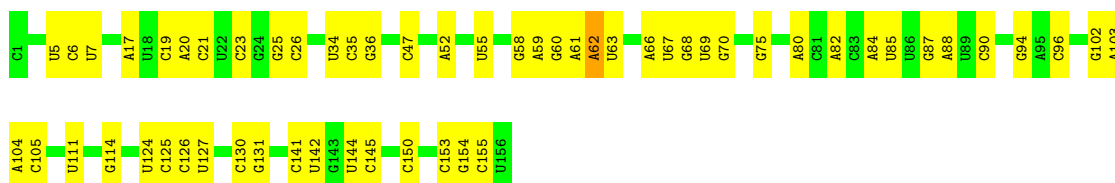
- Molecule 4: 5S rRNA

Chain L7: 74% 22%



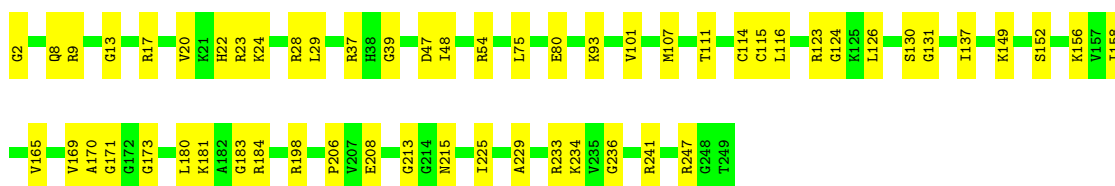
- Molecule 5: 5.8S rRNA

Chain L8: 63% 36%



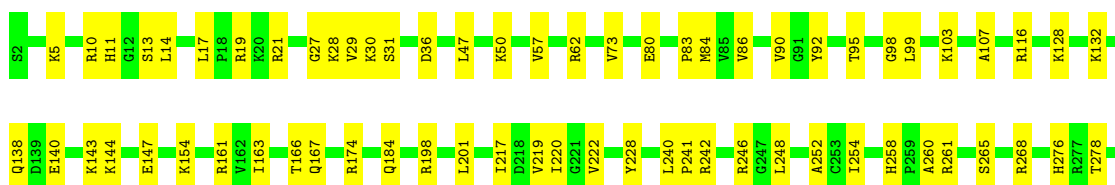
- Molecule 6: 60S ribosomal protein L8

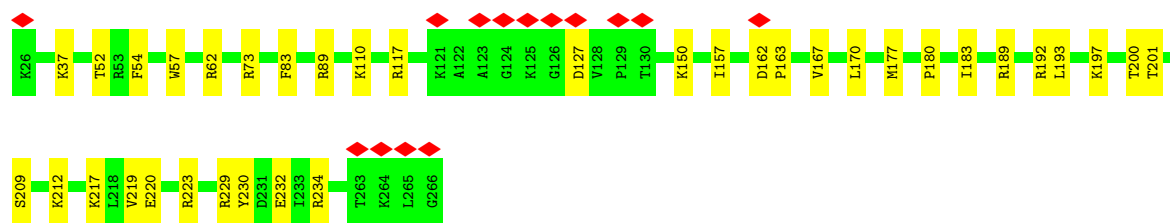
Chain LA: 77% 23%



- Molecule 7: Large ribosomal subunit protein uL3

Chain LB: 79% 21%





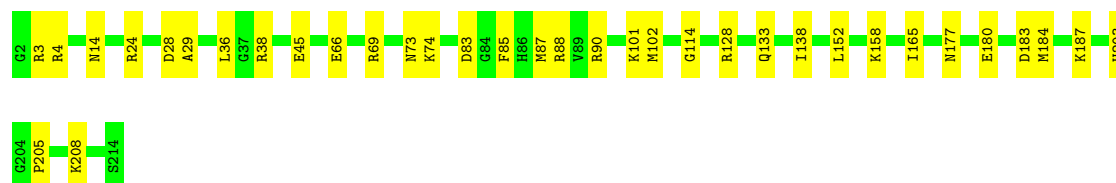
- Molecule 13: 60S ribosomal protein L9

Chain LH: 87% 13%



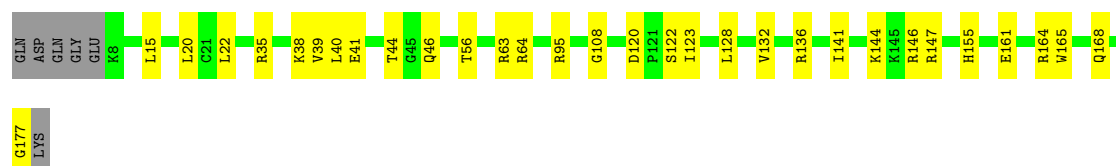
- Molecule 14: Ribosomal protein uL16-like

Chain LI: 84% 16%



- Molecule 15: 60S ribosomal protein L11

Chain LJ: 79% 18% .



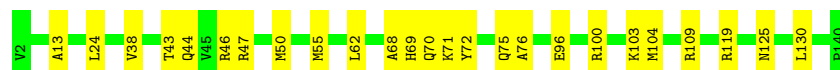
- Molecule 16: Large ribosomal subunit protein eL13

Chain LL: 86% 14%



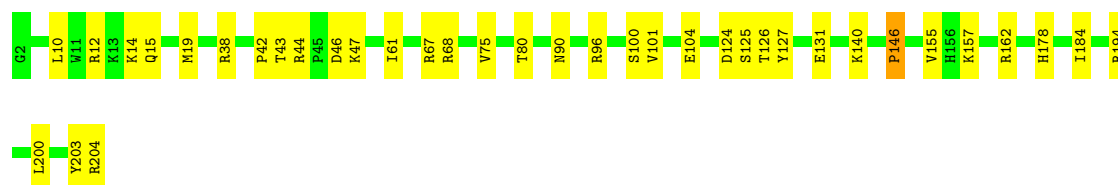
- Molecule 17: 60S ribosomal protein L14

Chain LM: 82% 18%



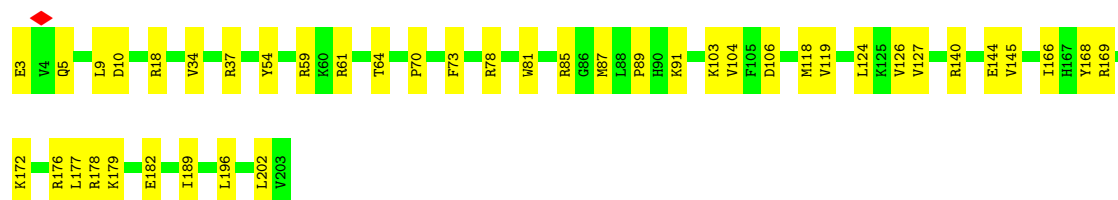
- Molecule 18: 60S ribosomal protein L15

Chain LN:  82% 18%



- Molecule 19: 60S ribosomal protein L13a

Chain LO:  79% 21%



- Molecule 20: 60S ribosomal protein L17

Chain LP:  85% 15%



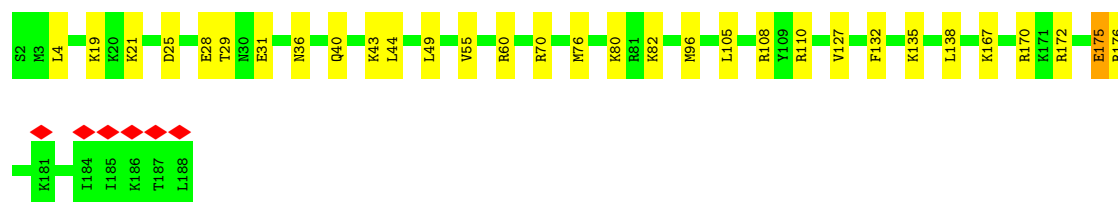
- Molecule 21: 60S ribosomal protein L18

Chain LQ:  86% 14%



- Molecule 22: 60S ribosomal protein L19

Chain LR:  83% 16%



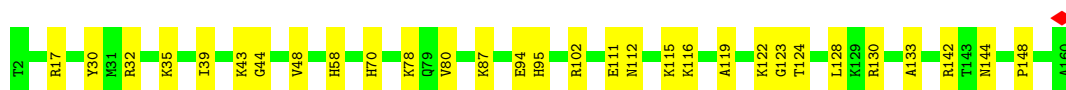
- Molecule 23: 60S ribosomal protein L18a

Chain LS:  90% 10%



- Molecule 24: 60S ribosomal protein L21

Chain LT:  81% 19%



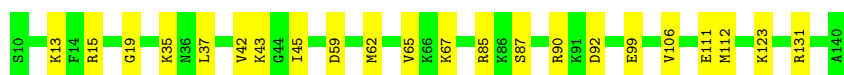
- Molecule 25: Heparin-binding protein HBp15

Chain LU:  72% 27%



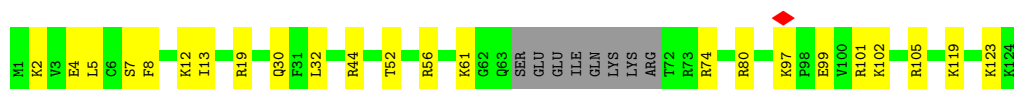
- Molecule 26: 60S ribosomal protein L23

Chain LV:  83% 17%



- Molecule 27: Ribosomal protein L24

Chain LW:  75% 19% 6%



- Molecule 28: 60S ribosomal protein L23a

Chain LX:  84% 16%



- Molecule 29: 60S ribosomal protein L26

Chain LY:  81% 19%



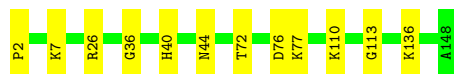
- Molecule 30: 60S ribosomal protein L27

Chain LZ:  81% 19%



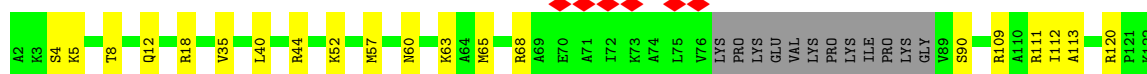
- Molecule 31: 60S ribosomal protein L27a

Chain La:  92% 8%



- Molecule 32: Large ribosomal subunit protein eL29

Chain Lb:  5% 74% 17% 10%



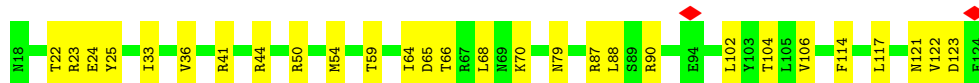
- Molecule 33: 60S ribosomal protein L30

Chain Lc:  82% 18%



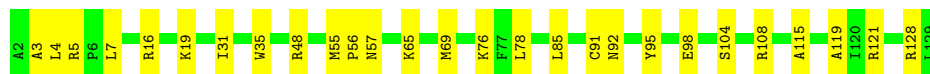
- Molecule 34: 60S ribosomal protein L31

Chain Ld:  74% 26%



- Molecule 35: 60S ribosomal protein L32

Chain Le:  79% 21%



- Molecule 36: 60S ribosomal protein L35a

Chain Lf:  89% 11%



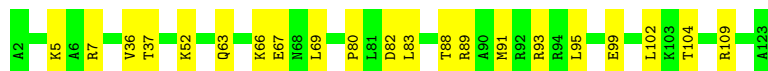
- Molecule 37: 60S ribosomal protein L34

Chain Lg:  90% 10%



- Molecule 38: 60S ribosomal protein L35

Chain Lh: 83% 17%



- Molecule 39: 60S ribosomal protein L36

Chain Li: 82% 18%



- Molecule 40: 60S ribosomal protein L37

Chain Lj: 79% 21%



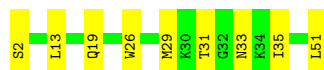
- Molecule 41: 60S ribosomal protein L38

Chain Lk: 81% 19%



- Molecule 42: 60S ribosomal protein L39

Chain Ll: 82% 18%



- Molecule 43: Large ribosomal subunit protein eL40

Chain Lm: 85% 15%



- Molecule 44: 60S ribosomal protein L41

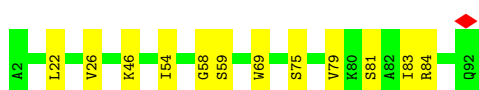
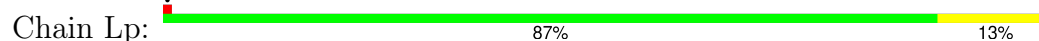
Chain Ln: 88% 12%



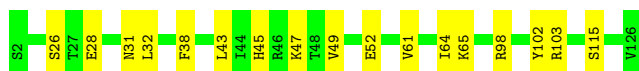
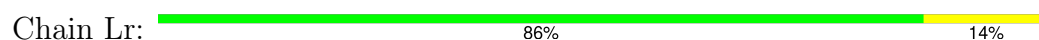
- Molecule 45: 60S ribosomal protein L36a



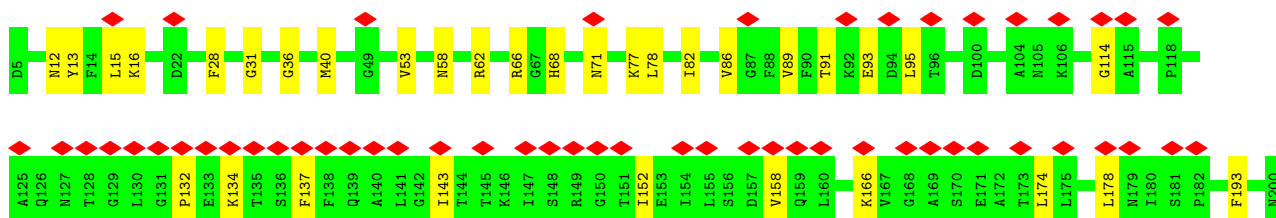
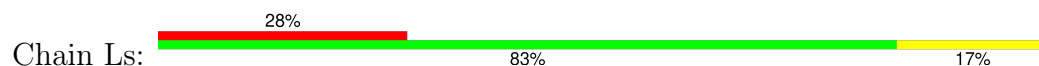
- Molecule 46: 60S ribosomal protein L37a



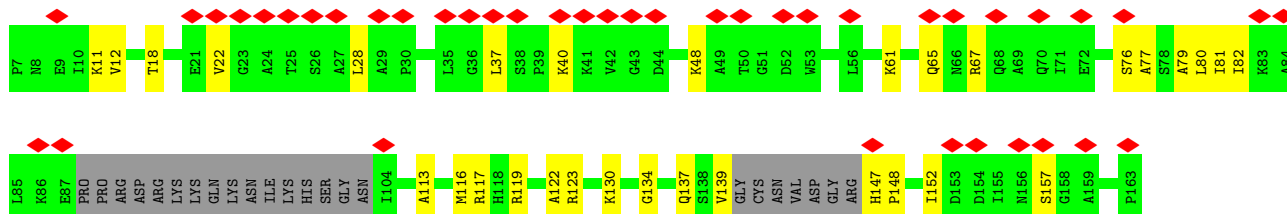
- Molecule 47: 60S ribosomal protein L28



- Molecule 48: 60S acidic ribosomal protein P0

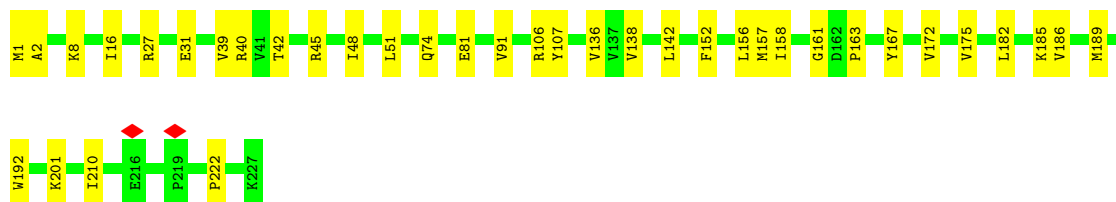


- Molecule 49: Large ribosomal subunit protein uL11



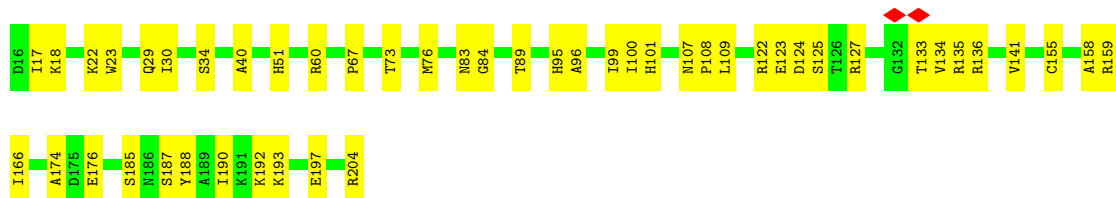
- Molecule 50: Small ribosomal subunit protein uS3

Chain SD:  84% 16%



- Molecule 51: 40S ribosomal protein S5

Chain SF:  75% 25%



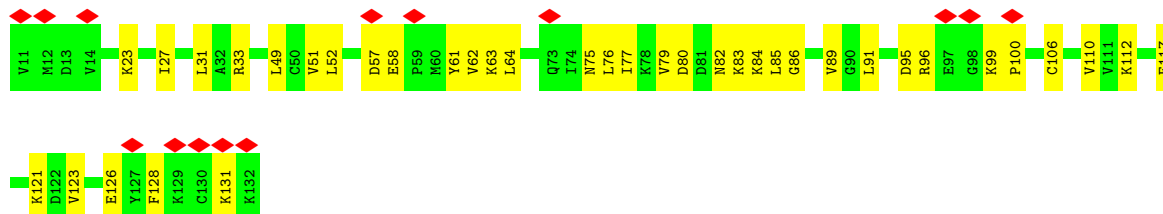
- Molecule 52: 40S ribosomal protein S10

Chain SK:  72% 28%



- Molecule 53: Small ribosomal subunit protein eS12

Chain SM:  11% 69% 31%



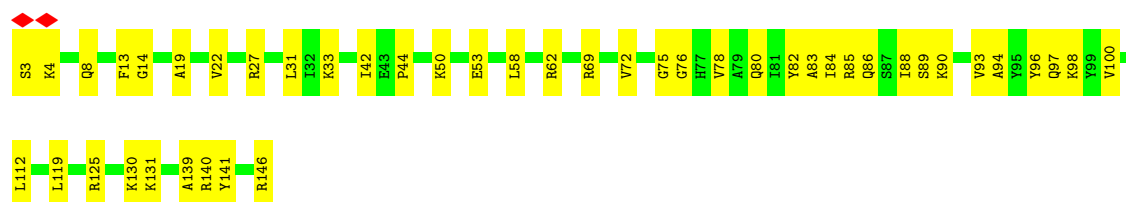
- Molecule 54: Small ribosomal subunit protein uS19

Chain SP:  75% 25%



- Molecule 55: Small ribosomal subunit protein uS9

Chain SQ:  69% 31%



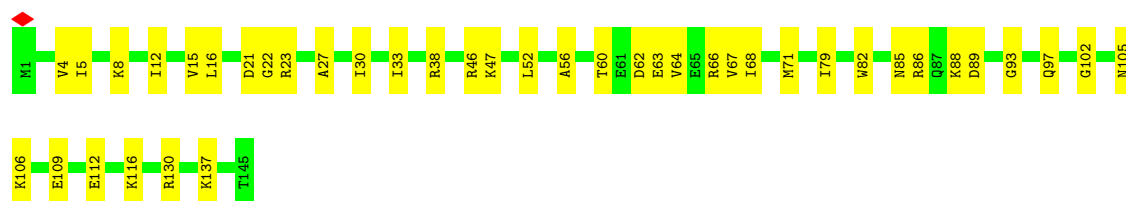
- Molecule 56: Small ribosomal subunit protein eS17

Chain SR: 75% 24%



- Molecule 57: 40S ribosomal protein S18

Chain SS: 72% 28%



- Molecule 58: 40S ribosomal protein S19

Chain ST: 69% 31%



- Molecule 59: 40S ribosomal protein S20

Chain SU: 70% 30%

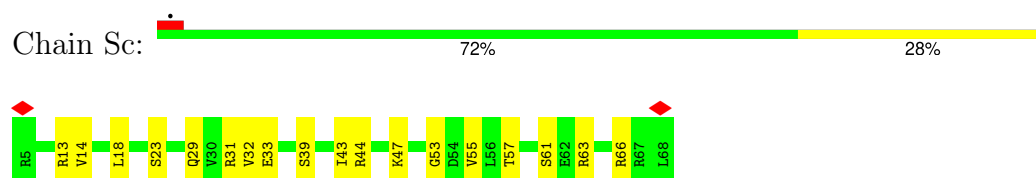


- Molecule 60: Small ribosomal subunit protein eS25

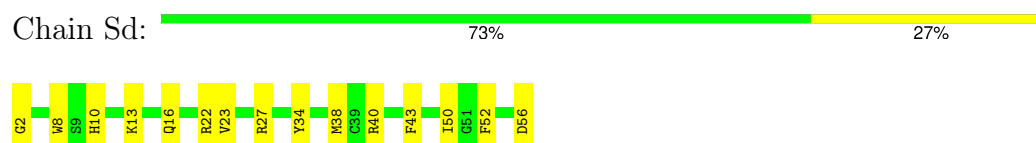
Chain SZ: 68% 32%



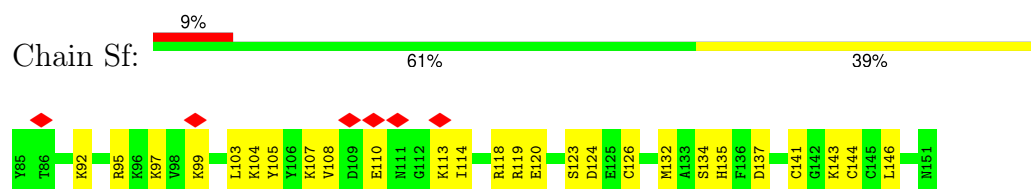
- Molecule 61: 40S ribosomal protein S28



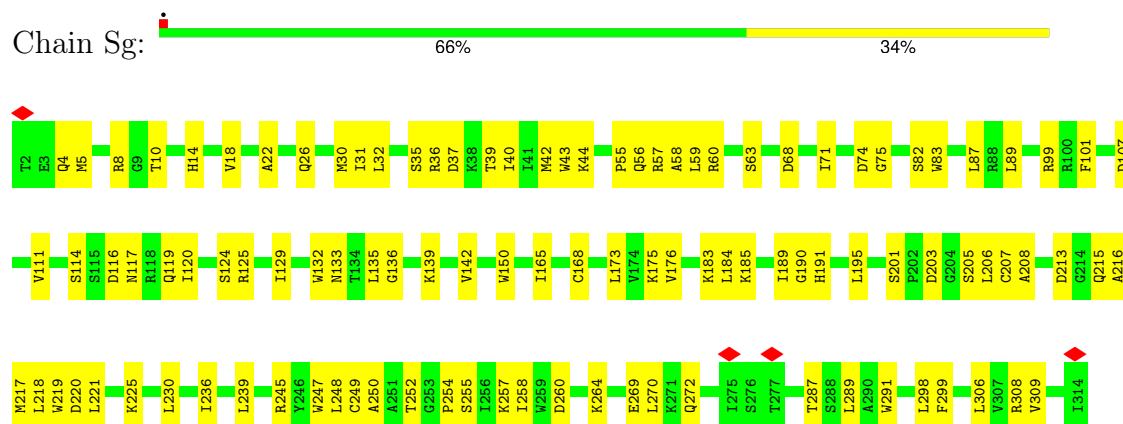
- Molecule 62: 40S ribosomal protein S29



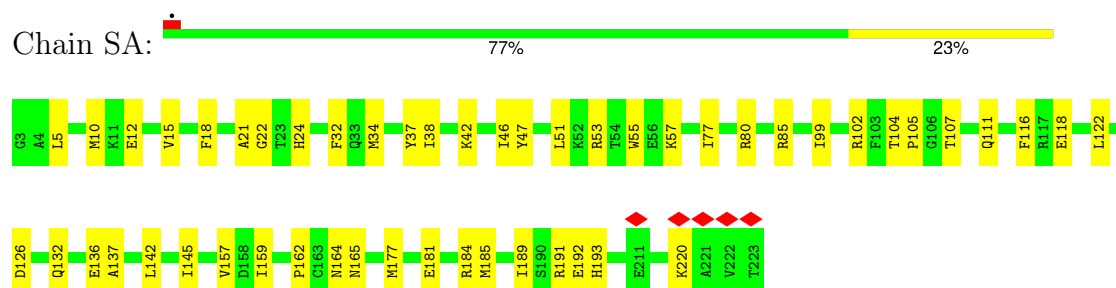
- Molecule 63: Ubiquitin-40S ribosomal protein S27a



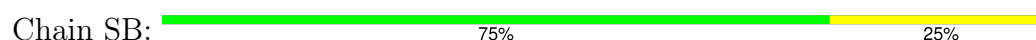
- Molecule 64: Receptor of activated protein C kinase 1

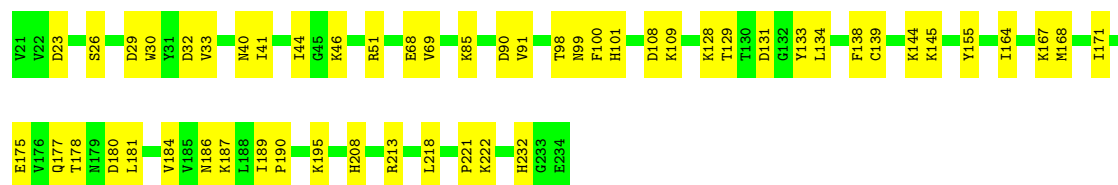


- Molecule 65: 40S ribosomal protein SA



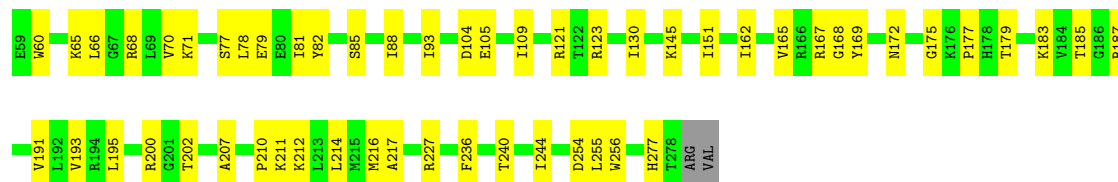
- Molecule 66: 40S ribosomal protein S3a





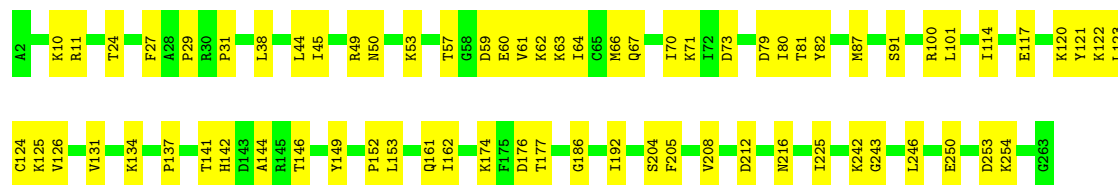
- Molecule 67: 40S ribosomal protein S2

Chain SC: 75% 24%



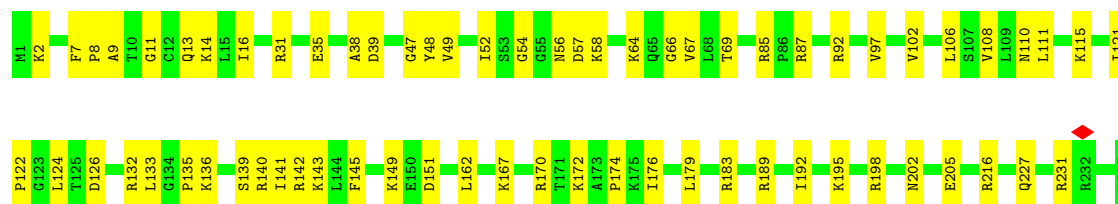
- Molecule 68: Small ribosomal subunit protein eS4, X isoform

Chain SE: 73% 27%



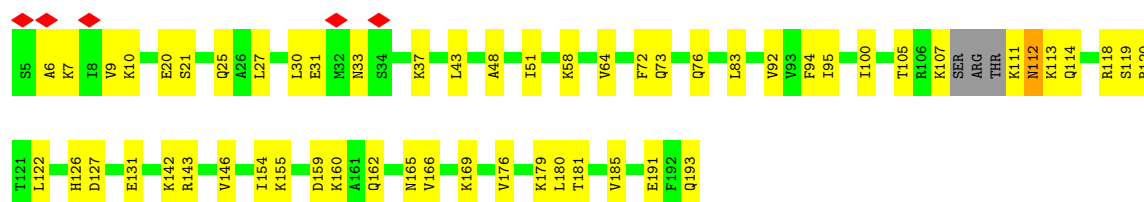
- Molecule 69: 40S ribosomal protein S6

Chain SG: 72% 28%



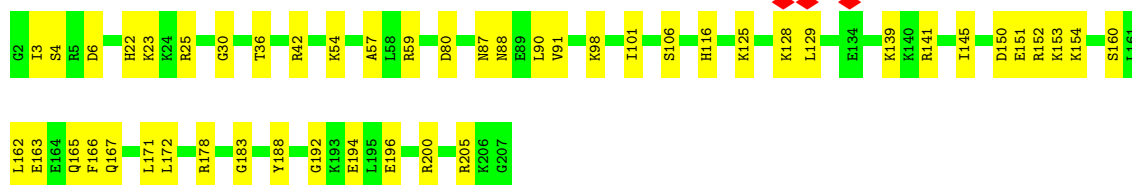
- Molecule 70: Small ribosomal subunit protein eS7

Chain SH: 69% 29%



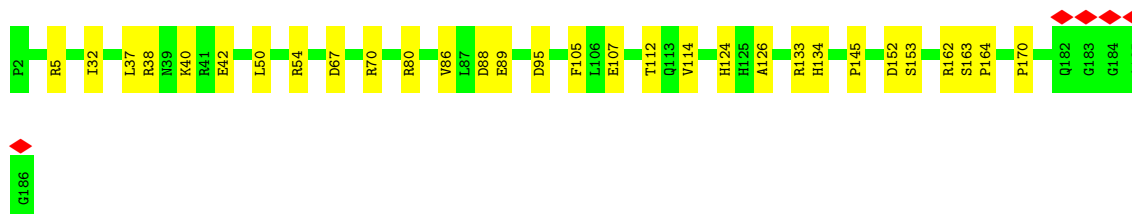
- Molecule 71: 40S ribosomal protein S8

Chain SI:  77% 23%



- Molecule 72: 40S ribosomal protein S9

Chain SJ:  84% 16%



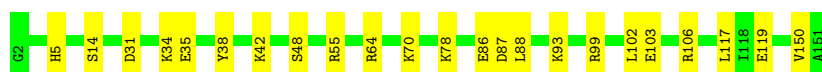
- Molecule 73: 40S ribosomal protein S11

Chain SL:  5% 84% 16%



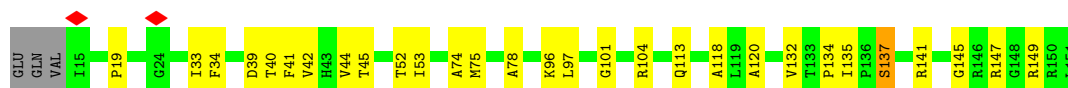
- Molecule 74: 40S ribosomal protein S13

Chain SN:  85% 15%



- Molecule 75: Small ribosomal subunit protein uS11

Chain SO:  77% 20% ..



- Molecule 76: Small ribosomal subunit protein eS21

Chain SV:  73% 27%



- Molecule 77: 40S ribosomal protein S15a

Chain SW:  79% 21%



- Molecule 78: 40S ribosomal protein S23

Chain SX:  80% 20%



- Molecule 79: 40S ribosomal protein S24

Chain SY:  5% 64% 36%



- Molecule 80: 40S ribosomal protein S26

Chain Sa:  84% 16%



- Molecule 81: Small ribosomal subunit protein eS27

Chain Sb:  82% 18%



- Molecule 82: Small ribosomal subunit protein eS30

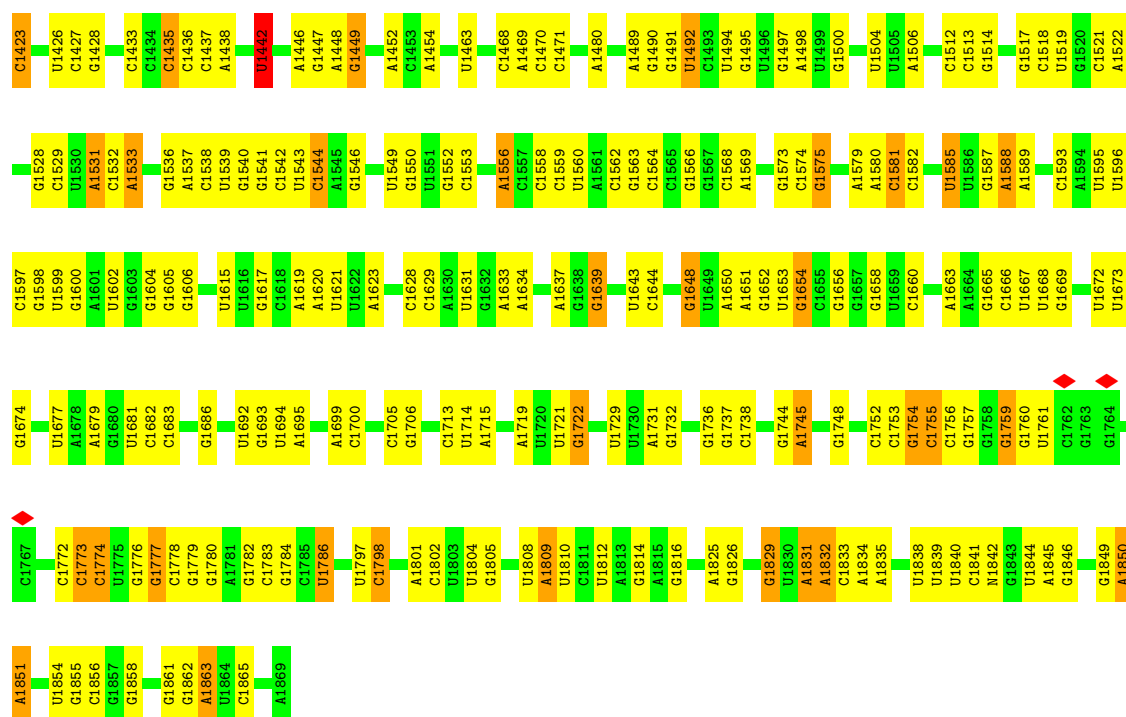
Chain Se:  5% 79% 21%



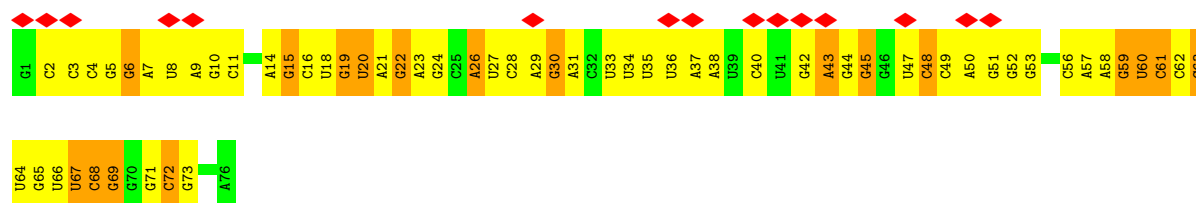
- Molecule 83: 18S rRNA

Chain S2:  51% 41% 8%

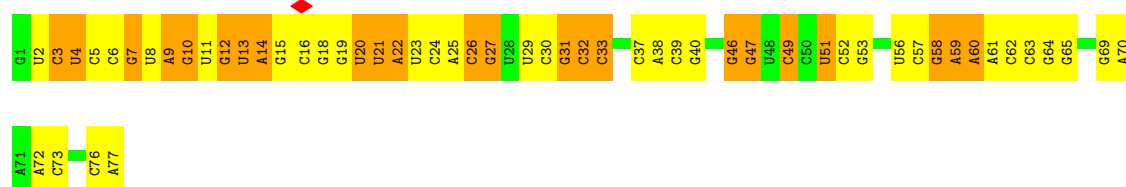
U1	A83	C162	A398	A486	A576	C663	U804	U888	G982	U1081	G1179	G1256	U1342
A2	A84	G165	U406	U487	A576	A604	U805	U889	G985	A1082	A1182	G1257	U1347
C3	A85	A166	G407	U488	C579	A668	U806	U890	G986	A1083	A1183	G1258	U1348
C4	G90	G167	A408	C492	U580	A669	A808	U891	C989	A1084	G1184	A1259	G1349
U6	U83	C168	C409	C493	U581	A670	A809	U892	G990	C1085	G1187	C1262	U1354
C14	G94	U169	A414	C494	U582	A671	U814	U893	G991	C1091	A1188	U1263	G1357
U15	G95	A170	A415	U495	A583	A672	U818	U897	G992	G1092	A1189	C1264	U1358
G16	C96	A171	A416	C496	A587	G674	A818	U898	G993	A1093	A1190	C1267	U1359
C17	U97	U172	G420	C497	A588	U675	U821	U899	A996	A1094	A1191	C1270	U1360
G18	C98	A175	C502	C502	G589	U681	G821	C900	A997	G1095	A1194	C1271	G1365
A25	A99	C186	A426	G507	A590	U682	U822	G901	A998	A1100	A1195	C1272	U1366
U26	A102	G187	U427	A508	U591	G683	U823	G902	G999	U1101	U1201	C1273	U1367
A27	A103	C330	U428	A509	C592	G684	C824	A903	U1002	G1102	U1202	G1274	G1368
U28	A104	G190	G431	A510	C593	U685	U827	G908	U1003	U1103	G1203	A1275	U1371
G29	U105	A191	G432	G510	G600	U686	A827	A909	U1004	G1104	A1204	C1276	U1372
C30	C106	C192	G433	C517	G601	U687	A830	G909	U1005	U1105	G1205	A1277	U1373
G33	A107	C196	G434	G518	A604	U688	A831	G910	A1006	A1113	G1206	C1283	C1372
C35	U109	C197	A435	A522	A605	G690	C834	A913	A1007	U1114	G1207	A1284	C1373
A38	G113	U198	G436	A523	G606	U689	C835	G914	A1008	U1115	A1208	G1285	A1376
G41	U115	C199	G437	A524	G614	U690	C836	A919	A1009	C1116	A1209	G1286	U1377
A42	U116	G200	A438	A525	C615	U691	C837	A920	U1010	C1117	G1215	A1287	A1378
U43	C118	C201	C440	C527	A616	G692	C838	A921	U1011	G1121	C1216	U1288	A1379
U44	G204	G202	C441	A528	G617	G693	C839	G922	A1012	A1122	A1217	U1289	A1382
U45	G205	G203	C442	U530	G623	G694	C840	G923	U1013	U1123	C1218	G1290	A1383
A46	G206	G204	A445	A531	G624	G695	C841	G924	U1014	C1128	C1219	A1291	C1384
G49	U121	G207	A446	A532	G625	G696	C842	G925	A1015	G1129	G1220	G1294	G1385
U51	G122	C208	A447	A533	U627	G697	C843	G926	U1016	G1130	G1221	A1295	A1386
C53	G130	G209	A448	A534	A628	G698	C844	G927	U1017	G1131	A1222	G1387	U1387
A54	C136	A209	A449	A535	A629	G699	C845	G928	A1018	C1132	A1223	A1388	A1388
U55	U137	U214	G451	C537	U630	C734	C851	G929	U1019	G1133	U1224	A1301	G1393
G52	G142	C223	G452	C538	U631	C735	C852	G930	U1020	G1134	U1225	G1302	G1394
U57	U143	A292	U454	A541	U632	C736	C853	G931	U1021	C1135	G1226	C1303	C1395
C58	U144	C293	U455	U542	A634	C737	G855	G932	U1022	C1136	G1227	U1304	A1396
U59	G145	C294	A465	C543	A635	C738	G856	G933	U1023	U1137	A1228	C1305	U1397
A60	G146	C295	G466	C544	G644	C739	U863	G934	G1037	A1143	G1229	U1308	G1398
A64	U149	G298	G467	A554	A648	C740	U864	G935	U1038	A1144	G1230	C1309	A1402
C65	A150	U300	A468	A555	U649	C741	U865	G936	U1039	A1145	G1231	U1310	A1405
G66	C151	A301	G471	U556	U651	C742	U866	G937	U1040	U1146	C1232	C1311	G1406
C67	U152	A302	C472	U557	U652	C743	U867	G938	U1041	A1147	U1233	G1312	U1407
A68	G153	C306	A473	G559	A654	C744	U868	G939	U1042	A1148	U1234	G1320	U1408
G71	U154	C307	C474	G560	A655	C745	U869	G940	U1043	C1153	A1240	G1321	G1413
C72	G155	G307	C475	G561	U656	C746	U870	G941	U1044	U1154	A1241	U1324	A1413
G73	U156	G308	A476	G562	U657	C747	U871	G942	U1045	U1155	U1242	G1325	C1415
C74	U157	A389	G482	G563	U658	C748	U872	G943	U1046	U1156	U1243	U1326	C1416
G75	A158	C390	C483	A564	A656	C749	U873	G944	U1047	G1171	B8N1248	U1329	C1417
U76	U159	G311	U484	C570	G659	C750	U874	G945	U1048	A1172	A1251	A1332	C1418
A77	U161	G312	A485	U571	G660	C751	U875	G946	U1049	U1174	C1252	U1337	G1420
		A313			G662	C752	U876	G947	A1080	U1177	U1253	G1338	G1422



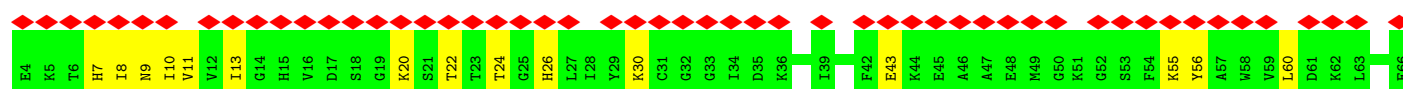
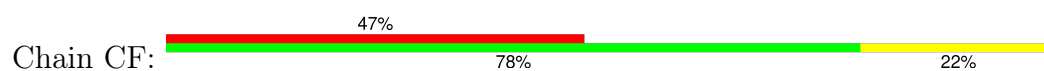
• Molecule 84: Z site tRNA

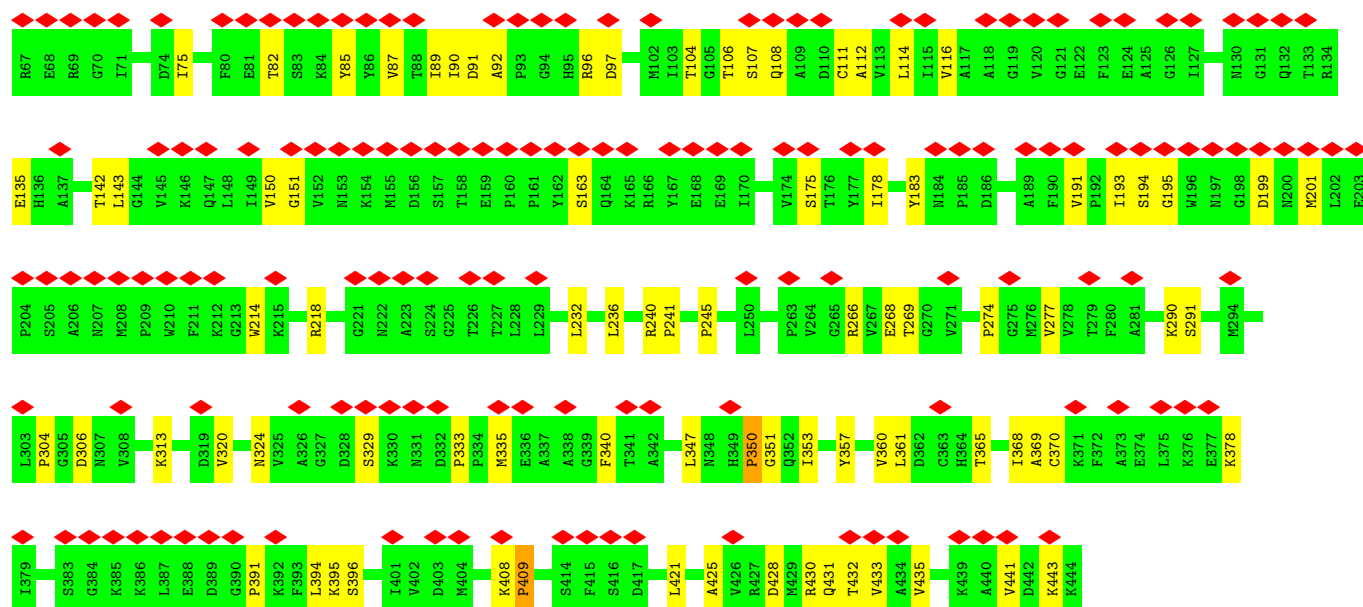


• Molecule 85: RNA (76-MER)A/T site tRNA



• Molecule 86: Elongation factor 1-alpha 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	50321	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.179	Depositor
Minimum map value	-0.055	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0153	Depositor
Map size ($\text{\AA}$)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.068, 1.068, 1.068	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMU, SEP, UR3, SPD, OMG, G7M, MG, 6MZ, SPM, 4AC, UY1, PSU, A2M, 5MC, ZN, B8N, 1MA, OMC, MA6

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	CI	0.16	0/247	0.30	0/323
2	Pt	0.12	0/1761	0.24	0/2741
3	L5	0.18	0/85098	0.28	1/132762 (0.0%)
4	L7	0.16	0/2861	0.23	0/4459
5	L8	0.16	0/3631	0.27	0/5657
6	LA	0.19	0/1936	0.38	0/2596
7	LB	0.17	0/3306	0.37	0/4424
8	LC	0.17	0/2981	0.34	0/4002
9	LD	0.16	0/2428	0.38	0/3252
10	LE	0.17	0/1973	0.42	0/2645
11	LF	0.19	0/1905	0.34	0/2539
12	LG	0.17	0/1960	0.37	0/2637
13	LH	0.16	0/1537	0.33	0/2066
14	LI	0.15	0/1751	0.35	0/2340
15	LJ	0.17	0/1385	0.41	0/1852
16	LL	0.15	0/1732	0.31	0/2315
17	LM	0.18	0/1161	0.40	0/1554
18	LN	0.17	0/1746	0.35	2/2338 (0.1%)
19	LO	0.17	0/1682	0.32	0/2250
20	LP	0.19	0/1268	0.38	0/1701
21	LQ	0.17	0/1537	0.34	0/2052
22	LR	0.19	0/1582	0.48	2/2091 (0.1%)
23	LS	0.17	0/1493	0.34	0/2003
24	LT	0.17	0/1326	0.32	0/1770
25	LU	0.20	0/839	0.49	0/1126
26	LV	0.16	0/993	0.34	0/1332
27	LW	0.16	0/959	0.36	0/1270
28	LX	0.15	0/1002	0.33	0/1345
29	LY	0.16	0/1132	0.37	0/1504
30	LZ	0.16	0/1130	0.36	0/1507
31	La	0.16	0/1191	0.29	0/1591

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Lb	0.15	0/889	0.38	0/1175
33	Lc	0.16	0/774	0.34	0/1038
34	Ld	0.17	0/903	0.33	0/1216
35	Le	0.18	0/1071	0.33	0/1429
36	Lf	0.17	0/895	0.32	0/1198
37	Lg	0.17	0/916	0.35	0/1220
38	Lh	0.17	0/1023	0.37	0/1351
39	Li	0.14	0/843	0.33	0/1115
40	Lj	0.16	0/720	0.33	0/952
41	Lk	0.18	0/575	0.50	0/761
42	Ll	0.15	0/454	0.25	0/599
43	Lm	0.15	0/435	0.32	0/575
44	Ln	0.17	0/231	0.34	0/294
45	Lo	0.16	0/876	0.30	0/1156
46	Lp	0.17	0/718	0.38	0/953
47	Lr	0.18	0/1017	0.34	0/1364
48	Ls	0.14	0/1519	0.38	0/2052
49	Lt	0.16	0/1009	0.47	0/1363
50	SD	0.15	0/1793	0.39	0/2414
51	SF	0.22	0/1516	0.52	0/2037
52	SK	0.21	0/851	0.54	0/1147
53	SM	0.18	0/950	0.46	1/1275 (0.1%)
54	SP	0.20	0/1003	0.49	0/1342
55	SQ	0.18	0/1160	0.42	0/1553
56	SR	0.21	0/1105	0.57	1/1484 (0.1%)
57	SS	0.17	0/1216	0.44	0/1628
58	ST	0.16	0/1131	0.41	0/1515
59	SU	0.19	0/831	0.50	0/1115
60	SZ	0.18	0/604	0.49	0/810
61	Sc	0.17	0/508	0.47	0/680
62	Sd	0.16	0/470	0.39	0/623
63	Sf	0.19	0/560	0.56	0/745
64	Sg	0.14	0/2493	0.39	0/3394
65	SA	0.17	0/1778	0.41	0/2416
66	SB	0.16	0/1765	0.42	1/2362 (0.0%)
67	SC	0.18	0/1744	0.45	0/2357
68	SE	0.15	0/2118	0.40	0/2849
69	SG	0.16	0/1946	0.41	0/2590
70	SH	0.18	0/1519	0.48	0/2033
71	SI	0.16	0/1715	0.39	0/2287
72	SJ	0.14	0/1550	0.37	0/2069
73	SL	0.15	0/1268	0.34	0/1696
74	SN	0.17	0/1232	0.38	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	SO	0.19	0/1037	0.51	2/1391 (0.1%)
76	SV	0.22	0/643	0.49	0/860
77	SW	0.17	0/1051	0.38	0/1406
78	SX	0.17	0/1116	0.44	0/1490
79	SY	0.17	0/1083	0.44	0/1438
80	Sa	0.15	0/836	0.35	0/1121
81	Sb	0.16	0/665	0.41	0/891
82	Se	0.15	0/465	0.43	0/612
83	S2	0.17	0/39756	0.27	0/61939
84	Zt	0.15	0/1779	0.39	0/2771
85	AT	0.13	0/1805	0.34	0/2809
86	CF	0.53	4/3442 (0.1%)	0.83	8/4656 (0.2%)
All	All	0.18	4/236905 (0.0%)	0.34	18/347316 (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
51	SF	0	1
75	SO	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	CF	409	PRO	CG-CD	-22.27	0.75	1.50
86	CF	350	PRO	CG-CD	-13.93	1.03	1.50
86	CF	409	PRO	CB-CG	10.34	2.01	1.49
86	CF	409	PRO	CA-CB	-6.82	1.44	1.53

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	CF	409	PRO	N-CD-CG	-32.47	54.49	103.20
86	CF	409	PRO	CA-CB-CG	-23.06	60.69	104.50
86	CF	350	PRO	N-CD-CG	-17.38	77.14	103.20
86	CF	350	PRO	CA-CB-CG	-10.76	84.06	104.50
86	CF	409	PRO	N-CA-CB	-10.50	92.23	103.25
75	SO	137	SER	CA-C-N	7.81	136.46	121.54
75	SO	137	SER	C-N-CA	7.81	136.46	121.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	CF	350	PRO	CA-N-CD	-7.59	101.37	112.00
86	CF	409	PRO	CA-N-CD	-7.41	101.63	112.00
22	LR	175	GLU	CA-C-N	-6.87	109.12	121.14
22	LR	175	GLU	C-N-CA	-6.87	109.12	121.14
86	CF	350	PRO	CB-CG-CD	6.20	125.95	106.10
18	LN	146	PRO	CA-C-N	5.91	136.61	126.32
18	LN	146	PRO	C-N-CA	5.91	136.61	126.32
3	L5	1703	C	C2'-C3'-O3'	5.26	117.39	109.50
56	SR	65	PRO	CA-N-CD	-5.24	104.67	112.00
53	SM	84	LYS	CA-CB-CG	5.13	124.36	114.10
66	SB	222	LYS	N-CA-CB	-5.02	108.45	114.17

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
51	SF	17	ILE	Peptide
75	SO	137	SER	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	CI	247	0	283	15	0
2	Pt	1576	0	803	16	0
3	L5	78444	0	39718	859	0
4	L7	2561	0	1295	19	0
5	L8	3315	0	1685	33	0
6	LA	1898	0	1993	41	0
7	LB	3238	0	3376	67	0
8	LC	2927	0	3104	37	0
9	LD	2382	0	2410	36	0
10	LE	1935	0	2096	29	0
11	LF	1870	0	1996	29	0
12	LG	1927	0	2074	25	0
13	LH	1518	0	1601	15	0
14	LI	1711	0	1749	26	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	LJ	1362	0	1399	20	0
16	LL	1701	0	1818	25	0
17	LM	1138	0	1204	17	0
18	LN	1701	0	1749	29	0
19	LO	1650	0	1794	32	0
20	LP	1242	0	1269	18	0
21	LQ	1513	0	1628	20	0
22	LR	1566	0	1729	29	0
23	LS	1453	0	1490	12	0
24	LT	1298	0	1366	24	0
25	LU	825	0	850	22	0
26	LV	979	0	1039	14	0
27	LW	945	0	1003	22	0
28	LX	985	0	1066	14	0
29	LY	1115	0	1205	16	0
30	LZ	1107	0	1182	19	0
31	La	1162	0	1213	9	0
32	Lb	876	0	948	15	0
33	Lc	764	0	804	9	0
34	Ld	888	0	930	18	0
35	Le	1053	0	1147	19	0
36	Lf	876	0	912	10	0
37	Lg	906	0	998	11	0
38	Lh	1015	0	1148	19	0
39	Li	832	0	917	11	0
40	Lj	705	0	737	16	0
41	Lk	569	0	637	11	0
42	Ll	444	0	483	8	0
43	Lm	429	0	465	6	0
44	Ln	230	0	276	3	0
45	Lo	862	0	929	9	0
46	Lp	708	0	756	10	0
47	Lr	1002	0	1068	12	0
48	Ls	1496	0	1540	19	0
49	Lt	998	0	1032	20	0
50	SD	1765	0	1865	25	0
51	SF	1495	0	1549	41	0
52	SK	827	0	854	21	0
53	SM	940	0	965	21	0
54	SP	985	0	1031	23	0
55	SQ	1142	0	1213	34	0
56	SR	1090	0	1149	23	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	SS	1198	0	1261	31	0
58	ST	1112	0	1146	34	0
59	SU	821	0	883	23	0
60	SZ	598	0	656	20	0
61	Sc	506	0	536	18	0
62	Sd	459	0	452	15	0
63	Sf	548	0	551	25	0
64	Sg	2436	0	2393	72	0
65	SA	1741	0	1746	37	0
66	SB	1738	0	1809	34	0
67	SC	1707	0	1791	38	0
68	SE	2076	0	2177	49	0
69	SG	1923	0	2089	58	0
70	SH	1497	0	1590	40	0
71	SI	1686	0	1772	35	0
72	SJ	1525	0	1640	22	0
73	SL	1247	0	1323	17	0
74	SN	1208	0	1294	16	0
75	SO	1024	0	1050	21	0
76	SV	636	0	637	16	0
77	SW	1034	0	1080	25	0
78	SX	1098	0	1167	24	0
79	SY	1065	0	1142	39	0
80	Sa	821	0	870	13	0
81	Sb	651	0	672	9	0
82	Se	459	0	503	12	0
83	S2	36953	0	18679	507	0
84	Zt	1593	0	809	34	0
85	AT	1616	0	824	45	0
86	CF	3383	0	3431	63	0
87	L5	179	0	0	0	0
87	L7	3	0	0	0	0
87	L8	4	0	0	0	0
87	LA	1	0	0	0	0
87	LI	1	0	0	0	0
87	LP	1	0	0	0	0
87	LV	1	0	0	0	0
87	Le	1	0	0	0	0
87	S2	26	0	0	0	0
87	SG	1	0	0	0	0
87	SS	1	0	0	0	0
88	L5	98	0	182	5	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	L5	90	0	171	4	0
89	LN	10	0	19	0	0
90	Lg	1	0	0	0	0
90	Lj	1	0	0	0	0
90	Lm	1	0	0	0	0
90	Lo	1	0	0	0	0
90	Lp	1	0	0	0	0
90	Sa	1	0	0	0	0
All	All	224970	0	167885	2831	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 7.

All (2831) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:79:ARG:NH1	3:L5:2708:U:O2'	1.75	1.20
3:L5:1996:C:H42	3:L5:2000:G:N2	1.60	0.98
3:L5:4946:U:HO2'	36:Lf:2:SER:N	1.63	0.95
3:L5:1996:C:N4	3:L5:2000:G:H22	1.64	0.94
1:CI:78:HIS:NE2	3:L5:2706:G:N7	2.16	0.92
2:Pt:50:U:H3	2:Pt:64:G:H1	0.94	0.91
3:L5:1996:C:H42	3:L5:2000:G:H22	0.98	0.89
83:S2:1748:G:H1	83:S2:1786:U:H3	0.96	0.89
1:CI:74:LYS:HA	25:LU:116:GLN:O	1.74	0.87
3:L5:2557:G:H1	3:L5:2570:U:H3	1.20	0.86
83:S2:1033:G:H1	83:S2:1080:A:HO2'	1.25	0.84
3:L5:4775:C:H41	3:L5:4859:C:H42	1.27	0.82
83:S2:487:U:H5'	86:CF:313:LYS:HZ3	1.42	0.82
83:S2:925:G:H1	83:S2:1017:U:H3	1.30	0.79
79:SY:44:LEU:HG	79:SY:47:MET:HE2	1.61	0.79
83:S2:1776:G:N2	83:S2:1777:G:N7	2.31	0.78
1:CI:78:HIS:NE2	3:L5:2706:G:C8	2.50	0.78
1:CI:78:HIS:CD2	3:L5:2706:G:N7	2.53	0.77
7:LB:90:VAL:HG23	7:LB:163:ILE:HD11	1.64	0.77
11:LF:243:LEU:O	11:LF:247:MET:HB2	1.83	0.77
77:SW:2:VAL:N	83:S2:1091:C:HO2'	1.83	0.77
68:SE:62:LYS:HG2	68:SE:66:MET:HE1	1.65	0.77
58:ST:105:GLN:NE2	83:S2:1564:C:OP1	2.18	0.76
3:L5:1702:C:H4'	8:LC:308:LYS:HD2	1.67	0.76
55:SQ:14:GLY:HA3	55:SQ:86:GLN:HE22	1.51	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:2520:C:O2	3:L5:2640:G:N2	2.19	0.75
5:L8:155:C:OP2	12:LG:89:ARG:NH1	2.19	0.75
83:S2:940:U:H3	83:S2:1002:U:H3	1.34	0.75
85:AT:21:U:H5'	85:AT:49:C:H42	1.51	0.75
41:Lk:24:LYS:HB2	41:Lk:35:LYS:HB2	1.68	0.74
3:L5:3937:C:H1'	18:LN:125:SER:HB3	1.67	0.74
60:SZ:94:LYS:HD2	60:SZ:96:LEU:HD22	1.70	0.74
3:L5:2007:G:H21	3:L5:2012:A:H62	1.33	0.74
3:L5:5024:C:H41	3:L5:5028:G:H21	1.35	0.74
70:SH:9:VAL:HG11	70:SH:27:LEU:HD22	1.69	0.74
3:L5:664:G:N2	3:L5:666:G:O6	2.20	0.74
63:Sf:126:CYS:SG	63:Sf:144:CYS:N	2.55	0.73
74:SN:103:GLU:HA	74:SN:106:ARG:HH22	1.54	0.73
83:S2:94:G:HO2'	83:S2:508:A:HO2'	1.37	0.73
85:AT:2:U:H3	85:AT:72:A:H61	1.34	0.73
13:LH:106:GLN:HB2	13:LH:111:LEU:HB3	1.71	0.72
86:CF:96:ARG:NH2	86:CF:430:ARG:O	2.22	0.72
3:L5:184:U:O2	3:L5:253:G:N2	2.21	0.72
81:Sb:14:GLU:HA	81:Sb:17:ARG:HG2	1.71	0.72
69:SG:135:PRO:HG2	69:SG:141:ILE:HG13	1.72	0.71
3:L5:1100:U:H3	3:L5:1194:G:H1	1.37	0.71
3:L5:1836:G:N7	24:LT:116:LYS:NZ	2.32	0.71
56:SR:17:ILE:HG21	56:SR:57:LEU:HD11	1.72	0.71
67:SC:210:PRO:HB3	67:SC:240:THR:HG21	1.71	0.71
3:L5:2611:A:H5'	3:L5:2688:G:H4'	1.72	0.71
88:L5:5294:SPM:H112	19:LO:91:LYS:HD3	1.71	0.71
18:LN:10:LEU:HG	18:LN:19:MET:HE3	1.73	0.71
26:LV:111:GLU:HG3	26:LV:131:ARG:HG3	1.73	0.71
40:Lj:60:GLY:HA2	40:Lj:64:MET:HE2	1.70	0.71
70:SH:154:ILE:HB	70:SH:185:VAL:HG22	1.72	0.70
51:SF:134:VAL:HG12	51:SF:135:ARG:HG2	1.74	0.70
3:L5:3594:C:O2	3:L5:3597:G:N2	2.25	0.70
3:L5:4910:G:H4'	7:LB:95:THR:HG22	1.74	0.70
3:L5:1982:G:N2	3:L5:2009:A:O2'	2.25	0.70
67:SC:172:ASN:ND2	72:SJ:95:ASP:OD1	2.25	0.70
85:AT:18:G:H21	85:AT:59:A:H5'	1.56	0.69
3:L5:3641:U:OP2	3:L5:3646:A:N6	2.25	0.69
7:LB:83:PRO:O	7:LB:167:GLN:NE2	2.25	0.69
55:SQ:58:LEU:HB3	55:SQ:62:ARG:HD2	1.74	0.69
4:L7:6:C:O2'	9:LD:50:ARG:NH2	2.25	0.69
25:LU:41:GLN:OE1	25:LU:44:GLN:NE2	2.25	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:S2:1658:G:OP2	83:S2:1660:C:N4	2.26	0.69
3:L5:2601:A:N6	3:L5:2744:A:OP2	2.26	0.69
39:Li:2:ALA:N	39:Li:5:TYR:HH	1.91	0.69
68:SE:122:LYS:H	68:SE:161:GLN:HE22	1.38	0.69
3:L5:2351:OMC:HM22	8:LC:95:MET:HG3	1.74	0.69
3:L5:2845:A:H61	3:L5:3843:C:H42	1.40	0.69
14:LI:87:MET:HG2	14:LI:138:ILE:HG12	1.74	0.69
35:Le:4:LEU:O	35:Le:121:ARG:NH2	2.24	0.69
67:SC:193:VAL:HG11	67:SC:240:THR:HG22	1.75	0.69
83:S2:1829:G:H1'	83:S2:1850:MA6:H2	1.75	0.69
3:L5:2702:C:OP1	25:LU:101:ARG:NH2	2.24	0.69
85:AT:61:A:OP1	85:AT:63:C:N4	2.26	0.69
52:SK:80:ARG:NH2	52:SK:86:PRO:O	2.26	0.69
84:Zt:26:A:N6	84:Zt:44:G:H1	1.91	0.69
3:L5:184:U:H3	3:L5:253:G:H1	1.39	0.68
84:Zt:6:G:H1	84:Zt:67:U:H3	1.40	0.68
70:SH:143:ARG:HB2	70:SH:155:LYS:HB2	1.74	0.68
3:L5:513:U:N3	3:L5:516:C:OP2	2.27	0.68
83:S2:851:C:H5''	83:S2:852:G:H5'	1.76	0.68
63:Sf:99:LYS:NZ	83:S2:1287:A:OP1	2.25	0.67
68:SE:57:THR:OG1	68:SE:60:GLU:OE1	2.12	0.67
69:SG:66:GLY:HA2	83:S2:1745:A:H1'	1.76	0.67
79:SY:103:SER:OG	79:SY:106:GLN:OE1	2.11	0.67
29:LY:67:ILE:O	29:LY:84:ARG:NH2	2.28	0.67
86:CF:340:PHE:HB3	86:CF:441:VAL:HG23	1.77	0.67
63:Sf:119:ARG:HE	63:Sf:120:GLU:H	1.40	0.67
82:Se:35:ARG:O	82:Se:39:ASN:ND2	2.27	0.67
27:LW:80:ARG:NH2	69:SG:8:PRO:O	2.27	0.67
64:Sg:176:VAL:HG23	64:Sg:185:LYS:HB2	1.75	0.67
68:SE:87:MET:HE1	68:SE:123:LEU:H	1.59	0.67
3:L5:4910:G:N2	19:LO:106:ASP:O	2.27	0.67
64:Sg:31:ILE:HG21	64:Sg:299:PHE:HE1	1.58	0.67
7:LB:10:ARG:NH1	7:LB:11:HIS:O	2.28	0.67
15:LJ:146:ARG:HG2	15:LJ:147:ARG:HG3	1.77	0.67
32:Lb:109:ARG:HA	32:Lb:112:ILE:HG12	1.77	0.67
54:SP:37:TYR:O	57:SS:88:LYS:NZ	2.28	0.67
6:LA:114:CYS:HB3	6:LA:165:VAL:HB	1.77	0.66
70:SH:7:LYS:HD3	70:SH:10:LYS:HB3	1.77	0.66
70:SH:114:GLN:HE22	83:S2:874:G:H21	1.42	0.66
79:SY:36:PRO:HG3	83:S2:570:C:H4'	1.77	0.66
3:L5:387:G:HO2'	3:L5:412:G:H1	1.42	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:170:C:H42	3:L5:266:C:H42	1.44	0.66
15:LJ:164:ARG:O	15:LJ:168:GLN:NE2	2.28	0.66
24:LT:48:VAL:HG21	24:LT:94:GLU:HG2	1.77	0.66
15:LJ:22:LEU:HD12	15:LJ:128:LEU:HD12	1.76	0.66
84:Zt:26:A:N6	84:Zt:44:G:N1	2.43	0.66
3:L5:665:C:H4'	3:L5:666:G:H5'	1.76	0.66
3:L5:4525:C:OP1	7:LB:246:ARG:NH2	2.28	0.66
27:LW:7:SER:HB2	27:LW:13:ILE:HD11	1.77	0.66
49:Lt:65:GLN:HG3	49:Lt:67:ARG:H	1.61	0.66
50:SD:8:LYS:HG2	59:SU:61:LEU:HD11	1.77	0.66
85:AT:24:C:H2'	85:AT:25:A:C8	2.31	0.66
73:SL:82:MET:HE3	73:SL:85:THR:HG23	1.77	0.66
28:LX:64:SER:HB2	38:Lh:69:LEU:HD13	1.78	0.65
3:L5:4094:G:N2	3:L5:4115:G:OP2	2.29	0.65
61:Sc:44:ARG:HH12	61:Sc:63:ARG:HD2	1.61	0.65
64:Sg:247:TRP:HB3	64:Sg:258:ILE:HD11	1.77	0.65
69:SG:13:GLN:HE22	83:S2:153:G:H21	1.42	0.65
83:S2:488:U:OP2	86:CF:290:LYS:NZ	2.30	0.65
69:SG:56:ASN:HD22	83:S2:156:G:H1'	1.61	0.65
83:S2:165:G:OP2	83:S2:165:G:N2	2.29	0.65
6:LA:29:LEU:O	6:LA:123:ARG:NH1	2.29	0.65
75:SO:104:ARG:NH2	83:S2:959:G:OP1	2.29	0.65
64:Sg:63:SER:HB2	83:S2:1398:G:H1'	1.78	0.65
64:Sg:215:GLN:HE22	64:Sg:217:MET:HE3	1.61	0.65
25:LU:52:LYS:NZ	25:LU:55:ASN:OD1	2.30	0.65
69:SG:56:ASN:HD21	83:S2:155:G:H21	1.42	0.65
83:S2:508:A:H3'	83:S2:509:OMG:H8	1.61	0.65
15:LJ:95:ARG:HD2	15:LJ:177:GLY:HA3	1.79	0.65
58:ST:65:TYR:HE1	58:ST:128:GLN:HG3	1.62	0.65
64:Sg:14:HIS:HD2	64:Sg:35:SER:HB2	1.62	0.65
3:L5:1414:C:H2'	3:L5:1415:G:H8	1.61	0.65
3:L5:4546:A:N7	6:LA:215:ASN:ND2	2.44	0.65
76:SV:14:PRO:HG2	76:SV:23:ILE:HD11	1.79	0.65
68:SE:246:LEU:HD13	68:SE:250:GLU:HG2	1.79	0.65
77:SW:107:SER:HB2	83:S2:860:G:H21	1.61	0.65
57:SS:23:ARG:NH2	60:SZ:46:ASN:O	2.31	0.64
83:S2:1417:C:O2	83:S2:1422:G:O6	2.14	0.64
22:LR:4:LEU:HD11	22:LR:29:THR:HG23	1.78	0.64
3:L5:3954:A:H1'	3:L5:4058:U:H5'	1.79	0.64
53:SM:51:VAL:HG12	53:SM:77:ILE:HB	1.78	0.64
67:SC:200:ARG:O	72:SJ:54:ARG:NH2	2.27	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:SN:35:GLU:HA	74:SN:38:TYR:HD1	1.62	0.64
3:L5:1811:G:H21	32:Lb:57:MET:HE3	1.62	0.64
3:L5:4606:G:N2	85:AT:63:C:O2'	2.31	0.64
23:LS:76:LYS:NZ	23:LS:100:LEU:O	2.31	0.64
51:SF:95:HIS:O	51:SF:99:ILE:HG13	1.97	0.64
86:CF:104:THR:HG23	86:CF:365:THR:HG23	1.78	0.64
3:L5:2554:U:O2	3:L5:2764:A:N7	2.31	0.64
3:L5:3946:G:H1	3:L5:4067:U:H3	1.46	0.64
64:Sg:252:THR:HG21	64:Sg:257:LYS:HD2	1.78	0.64
85:AT:21:U:OP1	85:AT:49:C:N4	2.31	0.64
33:Lc:21:VAL:HG11	33:Lc:96:ILE:HD12	1.79	0.64
54:SP:48:GLY:O	54:SP:50:ARG:NH1	2.30	0.64
70:SH:6:ALA:O	70:SH:25:GLN:NE2	2.31	0.64
3:L5:1095:A:H2	3:L5:1200:G:H1	1.45	0.64
3:L5:1095:A:N1	3:L5:1200:G:O6	2.31	0.64
3:L5:1366:G:H5''	16:LL:36:ARG:HH12	1.62	0.64
68:SE:79:ASP:HB3	68:SE:82:TYR:HB2	1.78	0.64
73:SL:133:PRO:HG2	83:S2:383:G:H21	1.63	0.64
84:Zt:30:G:H2'	84:Zt:31:A:H8	1.61	0.64
3:L5:1739:G:N3	3:L5:1742:A:N6	2.46	0.64
3:L5:2020:U:H2'	3:L5:2021:G:H8	1.63	0.64
3:L5:2458:C:H5''	18:LN:67:ARG:HD2	1.79	0.64
7:LB:222:VAL:O	7:LB:343:ARG:NH1	2.30	0.64
3:L5:1270:A:H8	3:L5:2106:G:H21	1.45	0.64
3:L5:4413:C:O2	14:LI:158:LYS:NZ	2.31	0.64
51:SF:185:SER:H	51:SF:190:ILE:HD11	1.63	0.64
62:Sd:13:LYS:HE2	83:S2:1556:A:H1'	1.80	0.64
16:LL:204:GLU:OE1	16:LL:205:GLN:NE2	2.31	0.63
56:SR:90:ALA:O	56:SR:93:GLN:NE2	2.30	0.63
3:L5:267:G:OP1	38:Lh:109:ARG:NH2	2.31	0.63
3:L5:2362:U:H2'	3:L5:2363:A2M:H8	1.80	0.63
9:LD:104:LEU:HB2	9:LD:247:ILE:HD12	1.80	0.63
74:SN:38:TYR:CE2	74:SN:78:LYS:HG3	2.34	0.63
83:S2:1277:C:H2'	83:S2:1278:A:H8	1.62	0.63
68:SE:45:ILE:HG13	68:SE:61:VAL:HG11	1.80	0.63
83:S2:159:A2M:H2	83:S2:467:G:H21	1.63	0.63
3:L5:2083:C:OP2	21:LQ:14:ARG:NH2	2.30	0.63
64:Sg:68:ASP:HB3	64:Sg:111:VAL:HG12	1.80	0.63
84:Zt:26:A:H61	84:Zt:44:G:H1	1.42	0.63
14:LI:85:PHE:HE2	14:LI:87:MET:HE2	1.64	0.63
68:SE:121:TYR:HB2	68:SE:161:GLN:NE2	2.13	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78: SX:107: ARG: HG3	78: SX:110: HIS: HB3	1.81	0.63
83: S2:1536: G: H2'	83: S2:1537: A: H8	1.64	0.63
3: L5:4873: G: N7	19: LO:179: LYS: NZ	2.47	0.63
26: LV:90: ARG: HH12	26: LV:123: LYS: HB3	1.63	0.63
84: Zt:48: C: H2'	84: Zt:59: G: H1'	1.81	0.63
1: CI:66: GLY: HA3	34: Ld:70: LYS: NZ	2.13	0.63
29: LY:43: ASN: ND2	29: LY:127: GLN: OE1	2.32	0.63
51: SF:18: LYS: HE2	51: SF:22: LYS: HA	1.81	0.63
52: SK:1: MET: HE1	83: S2:1274: G: H5''	1.81	0.63
58: ST:126: GLN: HB2	58: ST:129: ARG: HH21	1.64	0.63
83: S2:928: G: H2'	83: S2:929: G: C8	2.34	0.63
3: L5:1332: C: H2'	3: L5:1333: A: H8	1.63	0.62
3: L5:1759: G: H1	3: L5:1773: U: H3	1.45	0.62
53: SM:86: GLY: HA2	53: SM:89: VAL: HG12	1.82	0.62
84: Zt:22: G: H2'	84: Zt:23: A: H8	1.64	0.62
3: L5:3822: PSU: OP1	88: L5:5293: SPM: N5	2.32	0.62
3: L5:500: G: OP1	3: L5:504: G: N2	2.31	0.62
3: L5:2484: A: H62	3: L5:2494: U: H3	1.47	0.62
3: L5:4088: C: OP1	6: LA:37: ARG: NH1	2.32	0.62
3: L5:4472: G: O2'	43: Lm:100: TYR: O	2.17	0.62
18: LN:146: PRO: HB2	38: Lh:104: THR: HG23	1.82	0.62
3: L5:1646: A: O2'	40: Lj:49: TRP: O	2.17	0.62
3: L5:1704: C: O3'	11: LF:46: ARG: NH1	2.33	0.62
34: Ld:90: ARG: HD3	34: Ld:102: LEU: HD13	1.79	0.62
50: SD:74: GLN: NE2	50: SD:81: GLU: OE2	2.33	0.62
3: L5:72: C: H5	16: LL:67: HIS: HD2	1.47	0.62
3: L5:500: G: N2	3: L5:504: G: O2'	2.30	0.62
3: L5:4251: A: H5''	15: LJ:108: GLY: HA3	1.81	0.62
8: LC:110: ARG: O	8: LC:113: ARG: NH1	2.32	0.62
21: LQ:15: ARG: NH1	21: LQ:52: PHE: O	2.33	0.62
47: Lr:26: SER: OG	47: Lr:28: GLU: OE1	2.16	0.62
55: SQ:78: VAL: HG12	83: S2:1673: U: H5''	1.81	0.62
66: SB:144: LYS: HD3	66: SB:208: HIS: HB3	1.81	0.62
3: L5:1961: G: N2	3: L5:2024: G: O2'	2.33	0.62
25: LU:65: ARG: HG2	25: LU:70: ILE: HG12	1.82	0.62
52: SK:49: MET: HE3	52: SK:58: VAL: HG11	1.81	0.62
55: SQ:89: SER: OG	55: SQ:119: LEU: O	2.17	0.62
56: SR:91: LEU: HD11	65: SA:21: ALA: HB2	1.82	0.62
59: SU:79: ARG: NH2	83: S2:1669: G: OP1	2.33	0.62
62: Sd:27: ARG: HD2	83: S2:1263: U: H4'	1.82	0.62
83: S2:1228: A: H2'	83: S2:1229: G: H8	1.63	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:2486:G:O6	3:L5:2493:G:O6	2.18	0.62
24:LT:142:ARG:NH1	24:LT:144:ASN:OD1	2.33	0.62
30:LZ:12:LEU:HB2	30:LZ:81:MET:HB3	1.80	0.62
64:Sg:173:LEU:HD22	64:Sg:189:ILE:HG22	1.82	0.62
86:CF:333:PRO:HG2	86:CF:335:MET:HE3	1.81	0.62
3:L5:2092:G:O2'	3:L5:2262:G:N2	2.33	0.62
3:L5:4098:A:N1	3:L5:4112:C:N4	2.47	0.62
3:L5:1704:C:OP1	11:LF:43:ARG:NH2	2.31	0.61
3:L5:4305:G:N7	24:LT:87:LYS:NZ	2.46	0.61
9:LD:120:GLU:O	9:LD:248:ARG:NH1	2.33	0.61
84:Zt:15:G:N2	84:Zt:20:U:OP1	2.30	0.61
3:L5:3717:A:H2'	3:L5:3718:A2M:H8	1.83	0.61
34:Ld:64:ILE:HG23	34:Ld:68:LEU:HD23	1.81	0.61
67:SC:68:ARG:HG2	67:SC:277:HIS:HB2	1.82	0.61
83:S2:106:C:H2'	83:S2:107:A:H8	1.66	0.61
86:CF:97:ASP:OD1	86:CF:430:ARG:NH2	2.34	0.61
64:Sg:129:ILE:HB	64:Sg:142:VAL:HB	1.82	0.61
83:S2:587:A:H5'	83:S2:592:C:H41	1.66	0.61
61:Sc:29:GLN:NE2	61:Sc:66:ARG:O	2.25	0.61
64:Sg:206:LEU:HD12	64:Sg:218:LEU:HD12	1.80	0.61
3:L5:966:A:H5''	3:L5:2092:G:H22	1.64	0.61
65:SA:22:GLY:O	65:SA:24:HIS:ND1	2.33	0.61
69:SG:140:ARG:HA	69:SG:143:LYS:HZ2	1.66	0.61
69:SG:183:ARG:NH2	83:S2:316:G:OP2	2.33	0.61
70:SH:105:THR:HG23	70:SH:107:LYS:H	1.64	0.61
73:SL:35:ARG:NH2	73:SL:55:TYR:O	2.33	0.61
83:S2:43:U:OP2	83:S2:485:A:N6	2.30	0.61
83:S2:1754:G:N7	83:S2:1779:G:N2	2.47	0.61
3:L5:2049:G:HO2'	3:L5:3884:PSU:HO2'	1.49	0.61
3:L5:2758:G:O2'	3:L5:2765:A:N3	2.29	0.61
3:L5:4620:OMU:OP2	3:L5:4670:C:N4	2.33	0.61
3:L5:4992:G:H2'	3:L5:4993:G:C8	2.36	0.61
20:LP:128:ARG:NH2	20:LP:130:TYR:OH	2.25	0.61
72:SJ:162:ARG:NH1	83:S2:582:U:OP1	2.34	0.61
1:CI:50:MET:HG3	25:LU:114:TYR:CE1	2.35	0.61
3:L5:1480:C:O2'	3:L5:1482:G:OP2	2.19	0.61
3:L5:1895:G:OP1	11:LF:96:ARG:NH2	2.34	0.61
26:LV:35:LYS:HB2	26:LV:67:LYS:HG3	1.81	0.61
66:SB:175:GLU:OE1	66:SB:187:LYS:NZ	2.25	0.61
68:SE:144:ALA:HB3	83:S2:121:OMU:HM23	1.82	0.61
70:SH:112:ASN:O	70:SH:112:ASN:ND2	2.33	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:224:U:O2	8:LC:219:LYS:NZ	2.30	0.61
3:L5:2093:A:N3	3:L5:2094:G:N1	2.48	0.61
3:L5:4098:A:H2'	3:L5:4099:G:H4'	1.82	0.61
3:L5:4242:U:H3	3:L5:4281:A:H2	1.49	0.61
11:LF:50:ILE:HD12	11:LF:186:CYS:HB3	1.83	0.61
26:LV:85:ARG:NH1	26:LV:99:GLU:O	2.33	0.61
55:SQ:42:ILE:HG23	55:SQ:44:PRO:HD2	1.83	0.61
73:SL:33:LEU:HD12	73:SL:34:PRO:HD2	1.83	0.61
78:SX:68:LYS:NZ	83:S2:616:A:OP1	2.34	0.61
83:S2:639:C:H2'	83:S2:640:A:H8	1.66	0.61
85:AT:18:G:H1	85:AT:56:U:H1'	1.64	0.61
3:L5:171:U:H4'	16:LL:135:LYS:HG2	1.83	0.60
11:LF:157:ARG:HE	11:LF:248:ASN:HB2	1.66	0.60
83:S2:1228:A:H2'	83:S2:1229:G:C8	2.35	0.60
1:CI:79:ARG:NH1	3:L5:2708:U:HO2'	1.94	0.60
3:L5:121:A:OP1	12:LG:110:LYS:NZ	2.25	0.60
3:L5:3688:U:OP2	6:LA:198:ARG:NH2	2.34	0.60
30:LZ:5:MET:O	30:LZ:28:ASN:ND2	2.34	0.60
52:SK:55:ARG:NH1	52:SK:78:TYR:OH	2.35	0.60
65:SA:38:ILE:HG21	65:SA:47:TYR:HD2	1.67	0.60
83:S2:888:U:H4'	83:S2:889:U:H5'	1.82	0.60
84:Zt:19:G:O2'	84:Zt:48:C:N4	2.29	0.60
20:LP:39:MET:HG2	20:LP:43:LYS:HD3	1.82	0.60
59:SU:26:SER:HB2	59:SU:110:VAL:HA	1.81	0.60
69:SG:198:ARG:NH1	83:S2:126:G:OP2	2.34	0.60
85:AT:37:C:H3'	85:AT:38:A:H8	1.66	0.60
3:L5:308:G:OP2	3:L5:308:G:N2	2.28	0.60
6:LA:137:ILE:HD11	6:LA:149:LYS:HB2	1.83	0.60
19:LO:196:LEU:HD23	19:LO:202:LEU:HD13	1.82	0.60
22:LR:44:LEU:HD22	22:LR:49:LEU:HD12	1.83	0.60
72:SJ:134:HIS:ND1	72:SJ:163:SER:OG	2.29	0.60
2:Pt:50:U:O2	2:Pt:64:G:N2	2.25	0.60
3:L5:67:C:OP2	3:L5:312:G:N2	2.32	0.60
5:L8:150:C:N4	12:LG:52:THR:O	2.35	0.60
63:Sf:92:LYS:NZ	83:S2:1303:C:O2	2.33	0.60
85:AT:10:G:O6	85:AT:46:G:N2	2.34	0.60
25:LU:65:ARG:HH21	25:LU:67:LYS:HA	1.66	0.60
86:CF:8:ILE:HG12	86:CF:85:TYR:HE2	1.66	0.60
75:SO:39:ASP:OD2	75:SO:40:THR:N	2.34	0.60
3:L5:267:G:H2'	3:L5:268:G:H8	1.67	0.60
3:L5:305:A:OP2	18:LN:15:GLN:NE2	2.27	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:512:U:H3	3:L5:647:G:H1	1.49	0.59
3:L5:3868:G:H22	3:L5:3900:G:H1'	1.67	0.59
49:Lt:77:ALA:HB3	49:Lt:80:LEU:HB2	1.83	0.59
50:SD:40:ARG:NH2	59:SU:106:ILE:O	2.34	0.59
57:SS:130:ARG:NH2	83:S2:1230:C:OP1	2.35	0.59
64:Sg:87:LEU:HB2	64:Sg:101:PHE:HB2	1.83	0.59
77:SW:111:MET:HE3	77:SW:115:GLU:HG2	1.84	0.59
3:L5:327:U:O2'	39:Li:30:ARG:NH1	2.35	0.59
3:L5:4594:U:H2'	3:L5:4595:G:H8	1.67	0.59
23:LS:5:GLY:O	23:LS:111:ARG:NH2	2.35	0.59
67:SC:121:ARG:HH12	67:SC:123:ARG:HE	1.49	0.59
3:L5:109:G:OP2	16:LL:74:ARG:NH2	2.34	0.59
3:L5:2495:U:H2'	3:L5:2496:G:H8	1.67	0.59
24:LT:43:LYS:O	24:LT:58:HIS:ND1	2.35	0.59
59:SU:51:LYS:HB3	59:SU:90:ASP:HB2	1.84	0.59
83:S2:1130:G:OP2	83:S2:1130:G:N2	2.30	0.59
7:LB:107:ALA:HB2	7:LB:201:LEU:HD22	1.85	0.59
9:LD:236:MET:HG2	9:LD:239:MET:HE2	1.83	0.59
41:Lk:8:ILE:HD12	41:Lk:56:LEU:HD21	1.83	0.59
52:SK:29:MET:HB3	52:SK:42:ASN:HD22	1.68	0.59
83:S2:1528:G:O2'	83:S2:1666:C:OP1	2.20	0.59
3:L5:2745:A:H2'	3:L5:2746:A:H8	1.68	0.59
50:SD:156:LEU:O	50:SD:157:MET:HE2	2.02	0.59
51:SF:188:TYR:OH	51:SF:192:LYS:NZ	2.36	0.59
83:S2:1536:G:H2'	83:S2:1537:A:C8	2.37	0.59
83:S2:1562:C:H2'	83:S2:1563:G:H8	1.65	0.59
3:L5:1969:G:H4'	48:Ls:36:GLY:HA2	1.85	0.59
3:L5:2845:A:H61	3:L5:3843:C:N4	2.00	0.59
45:Lo:2:VAL:N	45:Lo:90:HIS:O	2.36	0.59
68:SE:71:LYS:HB3	68:SE:91:SER:HB2	1.84	0.59
75:SO:44:VAL:HG13	75:SO:53:ILE:HB	1.84	0.59
83:S2:747:U:N3	83:S2:796:G:N1	2.51	0.59
2:Pt:38:C:O2'	83:S2:1058:A:OP1	2.20	0.59
3:L5:62:A:N3	3:L5:77:U:O2'	2.31	0.59
3:L5:3619:G:H22	3:L5:3624:A:H1'	1.66	0.59
51:SF:29:GLN:NE2	51:SF:30:ILE:O	2.36	0.59
58:ST:40:ALA:HB3	58:ST:43:LYS:HG2	1.84	0.59
69:SG:135:PRO:HA	83:S2:169:U:H5''	1.85	0.59
78:SX:45:SER:OG	83:S2:648:A:N3	2.33	0.59
83:S2:1354:G:N2	83:S2:1357:A:OP2	2.32	0.59
5:L8:21:C:OP1	8:LC:195:LYS:NZ	2.36	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LF:105:VAL:HG13	11:LF:136:VAL:HG12	1.85	0.59
54:SP:20:VAL:HB	54:SP:24:GLN:HE21	1.68	0.59
59:SU:19:ARG:HD2	59:SU:92:HIS:ND1	2.17	0.59
62:Sd:2:GLY:N	83:S2:1271:C:O2	2.35	0.59
86:CF:24:THR:HG23	86:CF:89:ILE:HD13	1.85	0.59
58:ST:124:THR:HG23	58:ST:127:GLY:H	1.68	0.59
64:Sg:254:PRO:O	64:Sg:272:GLN:NE2	2.36	0.59
71:SI:192:GLY:HA3	73:SL:19:ASN:HD21	1.68	0.59
3:L5:1408:G:O2'	3:L5:1411:C:N4	2.36	0.58
7:LB:10:ARG:NH2	7:LB:265:SER:O	2.35	0.58
3:L5:5002:U:OP2	7:LB:385:LYS:NZ	2.36	0.58
51:SF:34:SER:HA	61:Sc:55:VAL:HG23	1.85	0.58
3:L5:184:U:O2'	3:L5:189:G:O4'	2.21	0.58
3:L5:4097:G:O6	3:L5:4098:A:N6	2.36	0.58
64:Sg:191:HIS:ND1	64:Sg:213:ASP:OD2	2.36	0.58
74:SN:64:ARG:NH2	83:S2:919:A:OP2	2.33	0.58
83:S2:981:A:H2'	83:S2:982:G:C8	2.39	0.58
3:L5:2764:A:H2'	3:L5:2765:A:H8	1.68	0.58
78:SX:28:LYS:HE2	78:SX:32:LEU:HD22	1.84	0.58
9:LD:64:ILE:HD13	9:LD:109:LEU:HD22	1.84	0.58
55:SQ:131:LYS:HB2	55:SQ:140:ARG:HH22	1.68	0.58
3:L5:2613:C:OP1	37:Lg:24:ARG:NH2	2.36	0.58
46:Lp:75:SER:O	46:Lp:79:VAL:HG23	2.03	0.58
57:SS:60:THR:OG1	57:SS:62:ASP:OD1	2.20	0.58
2:Pt:9:A:O2'	2:Pt:10:G:N7	2.34	0.58
3:L5:919:C:OP1	17:LM:69:HIS:ND1	2.27	0.58
3:L5:1756:U:O2'	3:L5:1758:G:OP2	2.18	0.58
4:L7:49:A:H5''	9:LD:224:SER:HB3	1.86	0.58
60:SZ:99:LEU:HD21	60:SZ:102:LYS:HB2	1.86	0.58
69:SG:133:LEU:HD12	83:S2:65:C:C4	2.38	0.58
86:CF:75:ILE:HD11	86:CF:90:ILE:HD12	1.86	0.58
3:L5:1094:G:O6	3:L5:1201:U:O2	2.22	0.58
3:L5:1979:A:N6	3:L5:1984:A:OP1	2.36	0.58
40:Lj:14:LYS:NZ	42:Ll:51:LEU:OXT	2.37	0.58
55:SQ:53:GLU:OE2	55:SQ:85:ARG:NH2	2.29	0.58
68:SE:153:LEU:O	68:SE:174:LYS:NZ	2.36	0.58
3:L5:4752:U:O4	36:Lf:52:LYS:NZ	2.37	0.58
10:LE:274:VAL:HG21	36:Lf:2:SER:HB3	1.85	0.58
28:LX:114:LYS:NZ	28:LX:120:ASP:OD2	2.37	0.58
53:SM:63:LYS:HD3	53:SM:64:LEU:HD22	1.86	0.58
69:SG:11:GLY:HA2	83:S2:166:A2M:HM'1	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:Zt:60:U:H2'	84:Zt:61:C:H5	1.69	0.58
3:L5:172:C:H4'	3:L5:173:C:H5'	1.86	0.58
16:LL:139:SER:OG	16:LL:142:GLU:OE1	2.21	0.58
48:Ls:143:ILE:HD12	48:Ls:158:VAL:HG11	1.85	0.58
50:SD:31:GLU:HA	50:SD:107:TYR:HE2	1.69	0.58
55:SQ:140:ARG:HB2	83:S2:1644:C:H4'	1.85	0.58
59:SU:59:LYS:HB2	59:SU:84:ILE:HB	1.85	0.58
82:Se:41:ARG:NH2	83:S2:639:C:OP1	2.37	0.58
83:S2:628:A:N6	83:S2:1500:G:O2'	2.37	0.58
3:L5:748:G:O6	23:LS:98:ARG:NH2	2.37	0.57
3:L5:1396:G:N7	31:La:110:LYS:NZ	2.46	0.57
4:L7:120:U:H4'	9:LD:262:LYS:HG2	1.85	0.57
19:LO:34:VAL:HG22	19:LO:103:LYS:HB2	1.86	0.57
33:Lc:34:THR:HG23	33:Lc:95:ALA:HB2	1.86	0.57
53:SM:79:VAL:HG11	53:SM:85:LEU:HB2	1.86	0.57
3:L5:2103:G:N7	3:L5:2104:G:N2	2.52	0.57
22:LR:172:ARG:NH1	83:S2:909:G:OP1	2.36	0.57
27:LW:105:ARG:NH2	69:SG:149:LYS:O	2.38	0.57
50:SD:106:ARG:HG3	50:SD:175:VAL:HG22	1.84	0.57
51:SF:127:ARG:HG2	51:SF:136:ARG:HB2	1.85	0.57
66:SB:180:ASP:OD1	66:SB:181:LEU:N	2.37	0.57
85:AT:26:C:H2'	85:AT:27:G:H8	1.70	0.57
3:L5:3946:G:N2	3:L5:4067:U:O2	2.36	0.57
38:Lh:80:PRO:HD2	38:Lh:83:LEU:HD12	1.86	0.57
41:Lk:17:ARG:NH2	41:Lk:19:ASP:OD2	2.38	0.57
44:Ln:1:MET:HG3	83:S2:1706:G:H5'	1.85	0.57
47:Lr:28:GLU:OE2	47:Lr:31:ASN:ND2	2.31	0.57
83:S2:1030:A:H2'	83:S2:1031:A2M:H8	1.86	0.57
51:SF:127:ARG:HG2	51:SF:136:ARG:HE	1.69	0.57
60:SZ:85:ARG:NH2	83:S2:1597:C:OP2	2.35	0.57
70:SH:51:ILE:HG21	70:SH:179:LYS:HG2	1.86	0.57
75:SO:135:ILE:O	83:S2:943:U:O2'	2.23	0.57
83:S2:1759:G:N2	83:S2:1760:G:O6	2.36	0.57
3:L5:158:A:N1	3:L5:276:C:O2'	2.34	0.57
3:L5:1837:A:OP2	24:LT:130:ARG:NH1	2.38	0.57
3:L5:3661:G:N7	6:LA:152:SER:OG	2.36	0.57
22:LR:170:ARG:NH2	83:S2:872:A:OP1	2.37	0.57
56:SR:114:LEU:HB2	56:SR:117:LEU:HD13	1.87	0.57
83:S2:1841:C:H2'	83:S2:1842:4AC:H6	1.86	0.57
3:L5:3701:OMC:H5	3:L5:3748:A:H62	1.51	0.57
15:LJ:38:LYS:HD2	15:LJ:123:ILE:HD11	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lj:2:THR:HB	40:Lj:6:SER:HB2	1.85	0.57
51:SF:127:ARG:HH22	61:Sc:66:ARG:HH22	1.51	0.57
57:SS:67:VAL:HG12	57:SS:71:MET:HE2	1.85	0.57
3:L5:4122:G:O3'	37:Lg:90:ARG:NH2	2.37	0.57
58:ST:42:HIS:ND1	58:ST:93:SER:OG	2.38	0.57
83:S2:557:U:H2'	83:S2:558:G:C8	2.39	0.57
83:S2:1010:G:H2'	83:S2:1011:A:H8	1.70	0.57
86:CF:9:ASN:CG	86:CF:266:ARG:HH12	2.12	0.57
86:CF:22:THR:HG23	86:CF:56:TYR:HB2	1.86	0.57
3:L5:3659:G:OP1	6:LA:241:ARG:NH1	2.38	0.57
3:L5:3697:U:H5''	3:L5:3698:G:H5'	1.86	0.57
81:Sb:67:THR:OG1	81:Sb:70:LYS:O	2.18	0.57
86:CF:378:LYS:HB2	86:CF:391:PRO:HG2	1.86	0.57
3:L5:137:G:H2'	3:L5:138:G:H8	1.70	0.57
27:LW:105:ARG:NE	69:SG:151:ASP:OD1	2.37	0.57
69:SG:14:LYS:HG2	69:SG:124:LEU:HD12	1.87	0.57
71:SI:88:ASN:C	71:SI:88:ASN:HD22	2.11	0.57
74:SN:14:SER:HB3	83:S2:1016:U:H5''	1.87	0.57
83:S2:874:G:H2'	83:S2:875:A:H8	1.70	0.57
3:L5:88:A:N7	21:LQ:173:LYS:NZ	2.52	0.57
3:L5:2516:G:O2'	37:Lg:62:LYS:NZ	2.37	0.57
3:L5:4537:C:H2'	3:L5:4538:G:H8	1.69	0.57
7:LB:299:ILE:HB	7:LB:313:SER:HB3	1.87	0.57
25:LU:27:HIS:HB3	25:LU:114:TYR:HE2	1.70	0.57
34:Ld:22:THR:HG23	34:Ld:122:VAL:HG23	1.87	0.57
57:SS:109:GLU:HA	57:SS:112:GLU:HG2	1.87	0.57
6:LA:101:VAL:HG22	6:LA:165:VAL:HG22	1.85	0.56
43:Lm:79:GLU:OE2	43:Lm:81:SER:OG	2.22	0.56
50:SD:27:ARG:HB3	52:SK:61:GLN:NE2	2.19	0.56
67:SC:191:VAL:HG11	67:SC:236:PHE:HA	1.87	0.56
83:S2:388:U:H2'	83:S2:389:A:H8	1.70	0.56
83:S2:692:G:N7	83:S2:693:A:N6	2.53	0.56
3:L5:502:C:H3'	3:L5:503:C:H3'	1.87	0.56
3:L5:713:C:O2	10:LE:130:LYS:NZ	2.38	0.56
3:L5:1785:C:OP1	14:LI:133:GLN:NE2	2.38	0.56
3:L5:1870:C:H2'	3:L5:1871:A2M:H8	1.86	0.56
3:L5:4363:A:H5''	45:Lo:36:GLN:HG2	1.86	0.56
3:L5:5064:G:H21	20:LP:75:GLN:HE22	1.54	0.56
8:LC:221:PHE:HB2	8:LC:229:LEU:HD11	1.87	0.56
16:LL:56:ARG:NH1	16:LL:74:ARG:O	2.35	0.56
17:LM:71:LYS:O	17:LM:75:GLN:HG3	2.03	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SM:117:GLU:O	53:SM:121:LYS:NZ	2.38	0.56
69:SG:67:VAL:HG12	69:SG:69:THR:HG22	1.87	0.56
83:S2:145:G:H2'	83:S2:146:G:C8	2.40	0.56
3:L5:935:A:O2'	17:LM:44:GLN:O	2.17	0.56
3:L5:1994:C:H2'	3:L5:1995:G:C8	2.40	0.56
3:L5:4279:A:H5'	3:L5:4281:A:H1'	1.86	0.56
3:L5:4769:G:OP1	19:LO:176:ARG:NH1	2.34	0.56
10:LE:66:LYS:HB3	10:LE:68:MET:HE3	1.86	0.56
50:SD:192:TRP:NE1	50:SD:201:LYS:O	2.35	0.56
55:SQ:3:SER:OG	55:SQ:4:LYS:N	2.35	0.56
65:SA:34:MET:HE1	65:SA:162:PRO:HB3	1.86	0.56
65:SA:77:ILE:HG13	65:SA:99:ILE:HB	1.87	0.56
68:SE:29:PRO:HA	83:S2:496:C:H5'	1.87	0.56
70:SH:20:GLU:HG2	70:SH:48:ALA:HB3	1.87	0.56
79:SY:7:ILE:HG23	79:SY:25:ILE:HD11	1.88	0.56
79:SY:19:GLN:HG3	79:SY:81:TYR:CD2	2.40	0.56
79:SY:23:MET:HE1	79:SY:25:ILE:HD13	1.87	0.56
83:S2:525:A:H2'	83:S2:526:A:H8	1.70	0.56
86:CF:60:LEU:HD22	86:CF:91:ASP:HB2	1.86	0.56
3:L5:4774:C:O2'	3:L5:4775:C:O2	2.13	0.56
19:LO:9:LEU:HD23	19:LO:118:MET:HB2	1.88	0.56
36:Lf:43:LEU:O	36:Lf:109:ARG:NH2	2.38	0.56
69:SG:39:ASP:OD1	69:SG:47:GLY:N	2.36	0.56
69:SG:172:LYS:NZ	83:S2:67:C:OP2	2.35	0.56
77:SW:71:LYS:NZ	83:S2:1156:U:OP1	2.39	0.56
86:CF:175:SER:HA	86:CF:178:ILE:HG22	1.87	0.56
3:L5:2017:A:O2'	3:L5:2018:C:O5'	2.21	0.56
51:SF:60:ARG:HD2	83:S2:1679:A:H2'	1.87	0.56
55:SQ:58:LEU:HD11	55:SQ:112:LEU:HD21	1.87	0.56
75:SO:33:ILE:HB	75:SO:97:LEU:HD23	1.87	0.56
86:CF:10:ILE:HG12	86:CF:111:CYS:HB3	1.88	0.56
3:L5:1942:A:H2'	3:L5:1943:A:C8	2.40	0.56
7:LB:220:ILE:HB	7:LB:346:THR:HB	1.88	0.56
33:Lc:51:ASN:HB2	33:Lc:77:ASN:HB2	1.88	0.56
59:SU:26:SER:HB3	59:SU:32:LEU:HD11	1.87	0.56
59:SU:70:CYS:SG	83:S2:1492:U:H1'	2.45	0.56
3:L5:1438:U:H4'	11:LF:31:LYS:HE3	1.88	0.56
9:LD:223:PHE:HB3	9:LD:226:TYR:HB2	1.88	0.56
13:LH:93:ARG:HG2	13:LH:182:SER:HB3	1.88	0.56
63:Sf:108:VAL:HG12	63:Sf:114:ILE:HA	1.86	0.56
64:Sg:8:ARG:HB3	64:Sg:309:VAL:HG13	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:CF:104:THR:O	86:CF:108:GLN:HG2	2.06	0.56
3:L5:2588:C:OP1	3:L5:2768:C:O2'	2.21	0.56
64:Sg:40:ILE:HB	64:Sg:59:LEU:HB2	1.86	0.56
72:SJ:50:LEU:HD13	72:SJ:105:PHE:HE1	1.71	0.56
3:L5:68:U:OP1	18:LN:178:HIS:ND1	2.38	0.56
3:L5:1563:A:N6	83:S2:1028:A:N1	2.54	0.56
3:L5:1992:U:H4'	3:L5:1993:C:H5''	1.87	0.56
3:L5:2007:G:N2	3:L5:2012:A:H62	2.03	0.56
3:L5:2577:C:OP1	30:LZ:111:ARG:NH2	2.39	0.56
3:L5:4107:G:N2	3:L5:4108:G:O6	2.36	0.56
19:LO:10:ASP:OD2	19:LO:37:ARG:NH2	2.38	0.56
51:SF:84:GLY:O	83:S2:1673:U:O2'	2.21	0.56
69:SG:139:SER:HA	69:SG:142:ARG:HE	1.70	0.56
83:S2:1581:C:H5'	83:S2:1582:C:H5	1.71	0.56
3:L5:1283:G:N1	3:L5:2076:G:OP1	2.31	0.56
3:L5:3823:G:OP2	3:L5:3823:G:N2	2.31	0.56
3:L5:4220:6MZ:H2'	3:L5:4222:G:H5''	1.88	0.56
3:L5:4775:C:H41	3:L5:4859:C:N4	2.03	0.56
7:LB:57:VAL:HB	7:LB:367:PHE:HB3	1.87	0.56
9:LD:232:THR:OG1	9:LD:234:ASP:OD1	2.21	0.56
69:SG:13:GLN:HE22	83:S2:153:G:N2	2.04	0.56
83:S2:543:C:H3'	83:S2:544:G:H8	1.71	0.56
83:S2:1550:G:H3'	83:S2:1579:A:H61	1.71	0.56
86:CF:194:SER:HB3	86:CF:199:ASP:HB3	1.88	0.56
16:LL:59:VAL:HG21	16:LL:73:GLY:HA3	1.87	0.55
57:SS:89:ASP:HB2	57:SS:93:GLY:H	1.71	0.55
59:SU:80:PHE:HB3	62:Sd:52:PHE:HB3	1.88	0.55
75:SO:45:THR:HA	75:SO:52:THR:HA	1.87	0.55
83:S2:1422:G:H4'	83:S2:1423:C:H3'	1.87	0.55
83:S2:1010:G:H2'	83:S2:1011:A:C8	2.41	0.55
85:AT:12:G:H22	85:AT:23:U:H3	1.54	0.55
85:AT:29:U:H2'	85:AT:30:C:O4'	2.05	0.55
6:LA:80:GLU:HB2	6:LA:170:ALA:HA	1.87	0.55
26:LV:90:ARG:NH1	26:LV:123:LYS:HB3	2.21	0.55
43:Lm:99:CYS:HB2	43:Lm:114:LYS:HE3	1.89	0.55
57:SS:27:ALA:HB2	57:SS:52:LEU:HD12	1.88	0.55
60:SZ:42:ASP:OD1	60:SZ:43:LYS:N	2.39	0.55
83:S2:795:A:H2'	83:S2:796:G:C8	2.41	0.55
84:Zt:64:U:H2'	84:Zt:65:G:H8	1.71	0.55
86:CF:142:THR:HG23	86:CF:435:VAL:HG13	1.88	0.55
27:LW:119:LYS:O	27:LW:123:LYS:HB2	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SA:118:GLU:HG3	67:SC:65:LYS:HE2	1.87	0.55
68:SE:100:ARG:HB2	68:SE:114:ILE:HD13	1.87	0.55
83:S2:454:U:H2'	83:S2:455:A:H8	1.70	0.55
3:L5:462:G:H2'	3:L5:463:A:C8	2.42	0.55
3:L5:1933:G:H2'	3:L5:1934:A:C8	2.42	0.55
3:L5:4987:C:OP2	7:LB:116:ARG:NH2	2.40	0.55
4:L7:23:A:N3	4:L7:118:C:O2'	2.32	0.55
8:LC:218:ILE:HA	8:LC:229:LEU:HD13	1.88	0.55
10:LE:91:THR:HA	10:LE:108:LYS:HA	1.88	0.55
12:LG:57:TRP:O	12:LG:62:ARG:NH1	2.40	0.55
49:Lt:76:SER:OG	49:Lt:116:MET:SD	2.62	0.55
67:SC:169:TYR:OH	67:SC:175:GLY:O	2.21	0.55
67:SC:207:ALA:HB2	83:S2:4:C:H4'	1.89	0.55
70:SH:165:ASN:O	70:SH:169:LYS:NZ	2.36	0.55
80:Sa:11:ALA:O	80:Sa:15:ARG:NH2	2.40	0.55
82:Se:13:ARG:NH1	83:S2:634:A:OP1	2.38	0.55
3:L5:239:C:OP1	29:LY:46:SER:OG	2.24	0.55
3:L5:1995:G:O2'	49:Lt:122:ALA:O	2.21	0.55
3:L5:3870:C:H2'	3:L5:3871:A:H8	1.71	0.55
9:LD:156:GLY:HA2	9:LD:181:PRO:HG3	1.89	0.55
50:SD:172:VAL:HG22	50:SD:185:LYS:HG2	1.89	0.55
55:SQ:130:LYS:NZ	55:SQ:131:LYS:O	2.40	0.55
64:Sg:18:VAL:O	64:Sg:287:THR:OG1	2.25	0.55
69:SG:92:ARG:O	83:S2:453:C:O2'	2.23	0.55
73:SL:133:PRO:O	83:S2:383:G:O2'	2.25	0.55
77:SW:106:THR:OG1	77:SW:111:MET:SD	2.59	0.55
3:L5:2279:A:O2'	35:Le:48:ARG:NH2	2.40	0.55
3:L5:4563:U:H2'	3:L5:4564:A:H8	1.72	0.55
19:LO:3:GLU:OE1	19:LO:5:GLN:NE2	2.31	0.55
57:SS:4:VAL:HG13	60:SZ:51:ASP:HA	1.88	0.55
70:SH:143:ARG:O	70:SH:155:LYS:N	2.34	0.55
79:SY:43:LYS:O	79:SY:46:LYS:HG3	2.06	0.55
83:S2:71:G:N2	83:S2:73:C:OP1	2.40	0.55
83:S2:1748:G:O6	83:S2:1786:U:O4	2.25	0.55
86:CF:241:PRO:HG2	86:CF:269:THR:HG22	1.89	0.55
3:L5:1172:C:H42	3:L5:1188:C:H42	1.54	0.55
17:LM:104:MET:HE3	17:LM:109:ARG:HG2	1.89	0.55
25:LU:24:ASP:OD1	25:LU:69:LYS:NZ	2.38	0.55
59:SU:56:MET:HG3	59:SU:86:LYS:NZ	2.22	0.55
63:Sf:107:LYS:NZ	63:Sf:108:VAL:O	2.39	0.55
71:SI:98:LYS:HB3	83:S2:377:G:H5'	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:1726:U:H5'	11:LF:135:ILE:HD11	1.89	0.55
3:L5:4431:PSU:OP2	14:LI:3:ARG:NH2	2.39	0.55
3:L5:1241:C:O2'	32:Lb:120:ARG:O	2.25	0.55
3:L5:1669:A:OP1	32:Lb:18:ARG:NH2	2.38	0.55
5:L8:62:A:OP1	38:Lh:52:LYS:NZ	2.36	0.55
7:LB:378:ARG:HE	27:LW:32:LEU:HD21	1.71	0.55
1:CI:72:ARG:NH2	22:LR:25:ASP:OD2	2.40	0.54
3:L5:1390:G:N2	3:L5:1393:G:OP2	2.35	0.54
3:L5:2495:U:H2'	3:L5:2496:G:C8	2.42	0.54
3:L5:4281:A:H2'	3:L5:4282:A:H2'	1.88	0.54
11:LF:96:ARG:HH12	11:LF:224:THR:HG22	1.71	0.54
25:LU:28:PRO:HB2	25:LU:34:MET:HG2	1.89	0.54
27:LW:123:LYS:HD2	83:S2:320:G:H5''	1.89	0.54
53:SM:91:LEU:HD12	53:SM:106:CYS:HB2	1.89	0.54
3:L5:261:G:H2'	3:L5:262:G:C8	2.42	0.54
3:L5:4347:G:H2'	3:L5:4348:A:C8	2.42	0.54
10:LE:261:ILE:HG23	10:LE:267:LEU:HD23	1.89	0.54
30:LZ:46:ILE:HA	30:LZ:70:SER:HA	1.90	0.54
84:Zt:30:G:H2'	84:Zt:31:A:C8	2.40	0.54
3:L5:72:C:C5	16:LL:67:HIS:HD2	2.26	0.54
3:L5:223:G:OP2	8:LC:165:LYS:NZ	2.39	0.54
7:LB:95:THR:OG1	7:LB:98:GLY:O	2.17	0.54
15:LJ:44:THR:HG23	15:LJ:46:GLN:HB3	1.89	0.54
26:LV:92:ASP:O	27:LW:2:LYS:NZ	2.37	0.54
48:Ls:91:THR:OG1	48:Ls:93:GLU:OE1	2.26	0.54
52:SK:64:TRP:HB3	62:Sd:23:VAL:HA	1.89	0.54
63:Sf:110:GLU:HG2	63:Sf:113:LYS:HD3	1.88	0.54
80:Sa:60:ASP:OD1	80:Sa:61:ALA:N	2.38	0.54
83:S2:28:U:H2'	83:S2:29:G:H8	1.72	0.54
86:CF:353:ILE:HB	86:CF:394:LEU:HB2	1.89	0.54
3:L5:268:G:H2'	3:L5:269:G:H8	1.72	0.54
6:LA:107:MET:HB3	6:LA:111:THR:HG21	1.89	0.54
19:LO:54:TYR:OH	19:LO:73:PHE:O	2.25	0.54
64:Sg:107:ASP:HB2	64:Sg:125:ARG:HG3	1.90	0.54
77:SW:3:ARG:HH22	77:SW:28:ARG:HH21	1.54	0.54
83:S2:1652:G:H1	83:S2:1672:U:H3	1.54	0.54
83:S2:1831:A:O2'	83:S2:1832:6MZ:O5'	2.23	0.54
85:AT:57:C:N4	85:AT:58:G:O6	2.40	0.54
3:L5:3611:A:H2	3:L5:5016:A:H8	1.55	0.54
3:L5:3732:A:H2'	3:L5:3733:A:H8	1.73	0.54
3:L5:4694:G:H4'	13:LH:71:ARG:HH12	1.73	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:SY:34:THR:O	83:S2:570:C:O2'	2.22	0.54
3:L5:432:U:H1'	88:L5:5294:SPM:H82	1.90	0.54
3:L5:491:G:H2'	3:L5:492:U:C6	2.42	0.54
3:L5:2411:C:H2'	3:L5:2412:A:C8	2.43	0.54
3:L5:3664:G:H2'	3:L5:3665:G:H8	1.72	0.54
3:L5:4670:C:O2'	3:L5:4672:A:OP2	2.24	0.54
7:LB:50:LYS:HB2	7:LB:345:LEU:HD11	1.90	0.54
18:LN:157:LYS:O	18:LN:162:ARG:NH1	2.41	0.54
22:LR:167:LYS:NZ	83:S2:871:U:O2'	2.41	0.54
69:SG:192:ILE:HD11	83:S2:126:G:C2	2.43	0.54
83:S2:640:A:H2'	83:S2:641:A:C8	2.42	0.54
3:L5:381:U:H4'	3:L5:415:G:H5'	1.88	0.54
3:L5:3689:G:O2'	3:L5:3818:UY1:OP2	2.26	0.54
3:L5:4225:G:OP1	14:LI:24:ARG:NH2	2.34	0.54
55:SQ:8:GLN:HG3	55:SQ:27:ARG:HE	1.72	0.54
83:S2:928:G:H1	83:S2:1013:U:H3	1.53	0.54
83:S2:993:G:OP1	83:S2:1131:G:N2	2.35	0.54
3:L5:3672:G:OP2	3:L5:3672:G:N2	2.37	0.54
4:L7:63:C:H5'	4:L7:64:G:H5''	1.90	0.54
22:LR:172:ARG:HA	22:LR:175:GLU:CD	2.33	0.54
3:L5:2017:A:O2'	3:L5:2018:C:H6	1.90	0.54
8:LC:141:GLY:O	8:LC:204:ARG:NH1	2.26	0.54
11:LF:88:LYS:HE3	11:LF:197:VAL:H	1.72	0.54
48:Ls:31:GLY:HA2	48:Ls:86:VAL:HG12	1.90	0.54
54:SP:86:LEU:HB2	54:SP:89:MET:HE1	1.90	0.54
57:SS:85:ASN:OD1	57:SS:97:GLN:NE2	2.27	0.54
67:SC:212:LYS:O	67:SC:216:MET:HG2	2.07	0.54
83:S2:207:G:H3'	83:S2:208:G:H8	1.72	0.54
83:S2:639:C:H2'	83:S2:640:A:C8	2.42	0.54
84:Zt:68:C:H2'	84:Zt:69:G:C8	2.43	0.54
54:SP:22:LEU:HD21	54:SP:109:PRO:HB3	1.90	0.54
72:SJ:107:GLU:O	72:SJ:112:THR:OG1	2.26	0.54
75:SO:134:PRO:HB3	83:S2:944:A:H5''	1.89	0.54
83:S2:1324:G:H1	83:S2:1504:U:H3	1.56	0.54
86:CF:178:ILE:HG12	86:CF:183:TYR:HB2	1.89	0.54
3:L5:300:A:H2'	3:L5:301:G:H8	1.73	0.53
3:L5:654:C:H2'	3:L5:655:C:C6	2.43	0.53
3:L5:1258:G:H2'	3:L5:1259:G:C8	2.42	0.53
3:L5:1332:C:H2'	3:L5:1333:A:C8	2.42	0.53
3:L5:4541:G:N2	3:L5:4544:A:OP2	2.34	0.53
19:LO:178:ARG:NH1	19:LO:182:GLU:OE2	2.41	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:Zt:15:G:H22	84:Zt:48:C:H42	1.54	0.53
3:L5:24:G:N7	40:Lj:46:LYS:NZ	2.55	0.53
8:LC:293:LEU:O	8:LC:299:GLN:NE2	2.36	0.53
21:LQ:79:THR:HB	21:LQ:136:THR:HG22	1.90	0.53
67:SC:167:ARG:HB3	67:SC:177:PRO:HB2	1.90	0.53
83:S2:1589:A:N3	83:S2:1653:U:O2'	2.41	0.53
86:CF:191:VAL:HG12	86:CF:193:ILE:HG23	1.91	0.53
1:CI:50:MET:HG3	25:LU:114:TYR:CD1	2.43	0.53
3:L5:308:G:O6	18:LN:12:ARG:NH1	2.41	0.53
3:L5:2318:G:N2	3:L5:2321:G:OP2	2.33	0.53
31:La:113:GLY:O	31:La:136:LYS:NZ	2.35	0.53
52:SK:76:ILE:O	52:SK:80:ARG:HG3	2.08	0.53
71:SI:150:ASP:HA	71:SI:153:LYS:HG2	1.91	0.53
83:S2:136:C:H5''	83:S2:137:U:H5''	1.90	0.53
83:S2:941:C:H2'	83:S2:942:G:H8	1.72	0.53
3:L5:461:G:H2'	3:L5:462:G:H8	1.73	0.53
3:L5:2543:A:H2	3:L5:2773:G:H22	1.56	0.53
7:LB:92:TYR:HB3	7:LB:99:LEU:HD22	1.91	0.53
9:LD:243:ALA:O	9:LD:247:ILE:HG12	2.08	0.53
22:LR:176:ARG:NH2	83:S2:910:G:OP1	2.37	0.53
50:SD:42:THR:OG1	50:SD:45:ARG:O	2.19	0.53
67:SC:109:ILE:HD11	67:SC:151:ILE:HD11	1.89	0.53
75:SO:34:PHE:HB3	75:SO:41:PHE:HB2	1.91	0.53
3:L5:438:G:OP1	35:Le:16:ARG:NH1	2.39	0.53
4:L7:7:G:OP1	9:LD:33:ARG:NH1	2.40	0.53
9:LD:62:CYS:HB3	9:LD:105:LEU:HD22	1.90	0.53
21:LQ:151:HIS:ND1	21:LQ:164:LYS:O	2.39	0.53
28:LX:87:MET:O	28:LX:91:GLU:HG2	2.07	0.53
50:SD:175:VAL:HB	50:SD:182:LEU:HB3	1.91	0.53
83:S2:528:A:H2'	83:S2:529:A:C8	2.43	0.53
5:L8:67:U:H2'	5:L8:68:G:H8	1.74	0.53
27:LW:7:SER:OG	27:LW:8:PHE:N	2.42	0.53
50:SD:161:GLY:HA3	83:S2:1388:A:H61	1.73	0.53
85:AT:32:C:H2'	85:AT:33:C:C6	2.43	0.53
3:L5:418:A:C2	5:L8:17:A:H1'	2.43	0.53
3:L5:1100:U:O3'	3:L5:1167:C:N4	2.41	0.53
3:L5:1333:A:H2'	3:L5:1334:A:C8	2.44	0.53
14:LI:205:PRO:HD2	14:LI:208:LYS:HE2	1.90	0.53
50:SD:158:ILE:HG12	50:SD:189:MET:HE2	1.91	0.53
53:SM:96:ARG:NH2	53:SM:100:PRO:O	2.42	0.53
65:SA:102:ARG:HH12	83:S2:1377:U:H3'	1.73	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:Zt:64:U:H2'	84:Zt:65:G:C8	2.44	0.53
3:L5:3951:G:H1'	3:L5:4062:A:H61	1.73	0.53
3:L5:4088:C:H2'	3:L5:4089:G:H8	1.74	0.53
3:L5:4967:A:H2'	3:L5:4968:A:H8	1.73	0.53
20:LP:18:ARG:NH2	20:LP:147:GLU:OE1	2.41	0.53
30:LZ:47:ASP:N	30:LZ:69:LYS:O	2.41	0.53
52:SK:15:LEU:HG	52:SK:71:LEU:HD12	1.90	0.53
59:SU:68:THR:O	62:Sd:40:ARG:NH1	2.42	0.53
60:SZ:88:LEU:HB3	60:SZ:109:TYR:CE1	2.43	0.53
65:SA:5:LEU:HD11	76:SV:41:LYS:HD2	1.91	0.53
73:SL:126:VAL:HG12	73:SL:145:VAL:HG22	1.90	0.53
58:ST:12:GLN:NE2	83:S2:1593:C:O2	2.41	0.53
3:L5:1866:U:OP1	14:LI:4:ARG:NH1	2.33	0.53
3:L5:2296:G:O2'	8:LC:242:PRO:O	2.23	0.53
3:L5:5041:G:C6	7:LB:389:MET:HG2	2.43	0.53
9:LD:233:PRO:HA	9:LD:236:MET:HE2	1.90	0.53
51:SF:123:GLU:OE1	61:Sc:63:ARG:NH2	2.42	0.53
79:SY:21:LYS:HE2	79:SY:75:ILE:HD11	1.90	0.53
83:S2:1845:A:H2'	83:S2:1846:G:C8	2.44	0.53
3:L5:3615:G:H1'	27:LW:44:ARG:HD3	1.91	0.52
55:SQ:98:LYS:O	64:Sg:57:ARG:NH1	2.33	0.52
58:ST:28:LEU:HD12	58:ST:106:ALA:HB1	1.90	0.52
64:Sg:10:THR:HG22	64:Sg:308:ARG:HG2	1.91	0.52
69:SG:49:VAL:HB	69:SG:115:LYS:HG2	1.90	0.52
83:S2:223:C:H2'	83:S2:224:A:C8	2.44	0.52
83:S2:533:A:H61	83:S2:550:C:H42	1.54	0.52
83:S2:889:U:OP2	83:S2:896:U:N3	2.42	0.52
83:S2:1226:G:N1	83:S2:1639:G7M:OP2	2.37	0.52
86:CF:108:GLN:HB2	86:CF:266:ARG:HD2	1.90	0.52
3:L5:93:G:H2'	3:L5:94:A:C8	2.45	0.52
3:L5:3898:G:H5'	7:LB:254:ILE:HG13	1.91	0.52
3:L5:4967:A:H2'	3:L5:4968:A:C8	2.44	0.52
7:LB:138:GLN:O	7:LB:143:LYS:NZ	2.43	0.52
14:LI:66:GLU:OE2	14:LI:69:ARG:NH2	2.30	0.52
22:LR:170:ARG:HH22	83:S2:872:A:H5'	1.75	0.52
62:Sd:38:MET:HE1	62:Sd:50:ILE:HD11	1.90	0.52
65:SA:42:LYS:HD3	65:SA:46:ILE:HB	1.90	0.52
83:S2:1098:C:H2'	83:S2:1099:G:C8	2.44	0.52
83:S2:1348:G:H2'	83:S2:1349:G:H8	1.74	0.52
3:L5:85:G:O2'	3:L5:97:G:O6	2.22	0.52
3:L5:2407:G:OP2	3:L5:2407:G:N2	2.35	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L8:58:G:N7	40:Lj:63:ARG:NH2	2.45	0.52
6:LA:229:ALA:HB3	6:LA:234:LYS:HB3	1.91	0.52
31:La:72:THR:HG22	31:La:110:LYS:HB3	1.91	0.52
55:SQ:139:ALA:HB2	83:S2:1650:A:H5''	1.92	0.52
57:SS:22:GLY:HA2	57:SS:56:ALA:HB3	1.91	0.52
58:ST:140:ALA:HA	58:ST:143:LYS:HE2	1.91	0.52
61:Sc:13:ARG:NH1	61:Sc:53:GLY:O	2.41	0.52
3:L5:1703:C:O2'	3:L5:1704:C:O5'	2.28	0.52
3:L5:2899:C:OP1	22:LR:108:ARG:NH2	2.32	0.52
3:L5:4239:A:H2'	3:L5:4240:G:C8	2.44	0.52
3:L5:4537:C:H2'	3:L5:4538:G:C8	2.44	0.52
11:LF:36:LYS:HD3	11:LF:39:GLN:HE21	1.74	0.52
24:LT:119:ALA:O	24:LT:123:GLY:N	2.42	0.52
27:LW:80:ARG:HH22	83:S2:167:G:H4'	1.74	0.52
80:Sa:87:ARG:NH1	80:Sa:94:ASP:OD2	2.42	0.52
83:S2:325:C:N3	83:S2:326:C:O2'	2.41	0.52
83:S2:1277:C:H2'	83:S2:1278:A:C8	2.43	0.52
3:L5:1591:U:OP2	3:L5:2856:C:O2'	2.20	0.52
3:L5:2411:C:H2'	3:L5:2412:A:H8	1.73	0.52
7:LB:80:GLU:OE1	7:LB:323:TYR:OH	2.25	0.52
41:Lk:27:LYS:O	41:Lk:70:LYS:NZ	2.42	0.52
84:Zt:26:A:N1	84:Zt:44:G:N2	2.56	0.52
7:LB:140:GLU:O	7:LB:144:LYS:HG2	2.10	0.52
20:LP:29:THR:HG21	20:LP:146:ILE:HD11	1.92	0.52
66:SB:33:VAL:HG12	66:SB:44:ILE:HD13	1.91	0.52
72:SJ:145:PRO:HD2	83:S2:522:A:H5''	1.92	0.52
3:L5:1516:G:O2'	16:LL:18:TRP:NE1	2.42	0.52
3:L5:2407:G:O6	42:Ll:2:SER:N	2.43	0.52
3:L5:4162:C:H5	12:LG:73:ARG:HH12	1.58	0.52
15:LJ:141:ILE:HA	15:LJ:144:LYS:HD2	1.91	0.52
34:Ld:23:ARG:HG2	34:Ld:121:ASN:HA	1.92	0.52
56:SR:16:ILE:HD11	56:SR:54:VAL:HG21	1.91	0.52
59:SU:67:LYS:HG2	59:SU:78:ASP:HB2	1.92	0.52
67:SC:255:LEU:O	76:SV:16:LYS:NZ	2.36	0.52
83:S2:902:G:O2'	83:S2:903:A:O4'	2.28	0.52
3:L5:303:C:OP2	18:LN:68:ARG:NH2	2.41	0.52
3:L5:2521:G:H4'	37:Lg:26:PRO:HD2	1.91	0.52
10:LE:264:ILE:HD11	10:LE:267:LEU:HD22	1.91	0.52
21:LQ:50:ARG:HA	21:LQ:53:MET:HE3	1.91	0.52
34:Ld:33:ILE:HD11	34:Ld:41:ARG:HA	1.92	0.52
75:SO:96:LYS:HD3	75:SO:132:VAL:HG11	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:SV:11:LEU:HD12	76:SV:12:TYR:HD1	1.75	0.52
79:SY:41:ARG:HH21	79:SY:53:ASP:HA	1.75	0.52
81:Sb:68:GLY:O	83:S2:928:G:N2	2.39	0.52
3:L5:369:G:N2	3:L5:372:A:OP2	2.37	0.52
3:L5:1494:U:H2'	3:L5:1495:G:H8	1.75	0.52
3:L5:1577:G:O2'	3:L5:1612:G:H4'	2.10	0.52
3:L5:1824:G:H2'	3:L5:1825:A:C8	2.45	0.52
3:L5:2845:A:N6	3:L5:3843:C:H42	2.08	0.52
3:L5:2910:G:N2	3:L5:3585:G:O2'	2.43	0.52
3:L5:3880:G:H2'	3:L5:3881:G:C8	2.45	0.52
3:L5:4260:U:H2'	3:L5:4261:C:C6	2.45	0.52
57:SS:15:VAL:HG12	57:SS:16:LEU:HG	1.92	0.52
68:SE:31:PRO:HA	68:SE:81:THR:HB	1.91	0.52
70:SH:100:ILE:HG21	70:SH:122:LEU:HD12	1.91	0.52
3:L5:1499:C:OP1	21:LQ:150:ARG:NH2	2.43	0.52
3:L5:1734:G:N2	3:L5:1735:U:O4	2.35	0.52
9:LD:217:ASP:OD1	9:LD:218:ALA:N	2.43	0.52
59:SU:20:ILE:HG22	59:SU:116:ILE:HG22	1.92	0.52
65:SA:157:VAL:O	76:SV:65:SER:OG	2.28	0.52
69:SG:170:ARG:HA	83:S2:72:C:H42	1.75	0.52
71:SI:101:ILE:HD12	71:SI:172:LEU:HD12	1.92	0.52
74:SN:55:ARG:HD3	83:S2:1017:U:H5'	1.92	0.52
19:LO:166:ILE:HG12	19:LO:169:ARG:HH21	1.74	0.51
65:SA:104:THR:O	65:SA:107:THR:OG1	2.25	0.51
3:L5:1333:A:H2'	3:L5:1334:A:H8	1.75	0.51
3:L5:1982:G:H2'	3:L5:1983:A:O4'	2.10	0.51
3:L5:2696:A:OP1	41:Lk:26:LYS:NZ	2.42	0.51
3:L5:3736:A:H2'	3:L5:3737:A:C8	2.45	0.51
3:L5:4274:A:H2'	3:L5:4275:G:C8	2.45	0.51
3:L5:4601:U:H2'	3:L5:4602:A:H8	1.75	0.51
7:LB:57:VAL:HG22	7:LB:73:VAL:HG22	1.92	0.51
8:LC:135:ALA:HA	47:Lr:43:LEU:HD23	1.93	0.51
54:SP:40:ARG:NH2	83:S2:1615:U:O4	2.43	0.51
71:SI:22:HIS:HB3	83:S2:433:A:H5''	1.91	0.51
79:SY:105:LYS:NZ	83:S2:507:G:O6	2.42	0.51
83:S2:1203:G:H2'	83:S2:1204:A:C8	2.45	0.51
3:L5:1326:A2M:H2'	3:L5:1327:C:C6	2.45	0.51
3:L5:4322:G:N2	3:L5:4325:A:OP2	2.36	0.51
3:L5:4887:C:H42	3:L5:4932:U:H3	1.58	0.51
11:LF:155:TYR:CE1	11:LF:187:MET:HG2	2.46	0.51
24:LT:112:ASN:HD22	24:LT:128:LEU:HD12	1.74	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Le:108:ARG:HD2	35:Le:128:ARG:HB2	1.92	0.51
51:SF:96:ALA:O	51:SF:100:ILE:HD12	2.10	0.51
57:SS:112:GLU:O	57:SS:116:LYS:HG2	2.11	0.51
63:Sf:135:HIS:CE1	83:S2:1308:U:H1'	2.45	0.51
63:Sf:144:CYS:HB2	63:Sf:146:LEU:HD13	1.91	0.51
71:SI:91:VAL:HG11	71:SI:205:ARG:HH12	1.76	0.51
83:S2:1259:A:N6	83:S2:1519:U:O5'	2.44	0.51
83:S2:1286:G:N2	83:S2:1312:G:O2'	2.44	0.51
3:L5:1346:C:H2'	3:L5:1347:G:H8	1.75	0.51
12:LG:117:ARG:NH1	12:LG:127:ASP:O	2.43	0.51
39:Li:55:ARG:O	39:Li:59:GLU:HG2	2.10	0.51
51:SF:141:VAL:HG12	61:Sc:47:LYS:HG2	1.93	0.51
60:SZ:88:LEU:HB3	60:SZ:109:TYR:HE1	1.76	0.51
64:Sg:26:GLN:NE2	64:Sg:74:ASP:O	2.44	0.51
70:SH:64:VAL:HB	70:SH:72:PHE:HE2	1.76	0.51
74:SN:35:GLU:HA	74:SN:38:TYR:CD1	2.44	0.51
83:S2:1417:C:H42	83:S2:1422:G:H22	1.56	0.51
3:L5:1339:U:H2'	3:L5:1340:OMC:C6	2.45	0.51
3:L5:1727:U:OP1	11:LF:131:ASN:ND2	2.43	0.51
3:L5:2724:G:O2'	3:L5:2726:G:OP2	2.28	0.51
3:L5:4238:G:H2'	3:L5:4239:A:H8	1.76	0.51
3:L5:4260:U:H2'	3:L5:4261:C:H6	1.75	0.51
3:L5:4274:A:H2'	3:L5:4275:G:H8	1.75	0.51
8:LC:177:TRP:CD1	8:LC:181:LYS:HE2	2.45	0.51
10:LE:119:GLU:HG3	35:Le:7:LEU:HD22	1.93	0.51
48:Ls:132:PRO:HA	48:Ls:152:ILE:HD11	1.92	0.51
54:SP:27:ASP:OD1	54:SP:27:ASP:N	2.41	0.51
64:Sg:299:PHE:HE2	64:Sg:309:VAL:HG23	1.74	0.51
68:SE:44:LEU:HD21	68:SE:70:ILE:HG21	1.92	0.51
83:S2:1801:A:H2'	83:S2:1802:C:C6	2.46	0.51
3:L5:490:C:H2'	3:L5:491:G:C8	2.45	0.51
3:L5:1552:G:O2'	3:L5:1574:G:N2	2.32	0.51
6:LA:131:GLY:H	6:LA:169:VAL:HG13	1.76	0.51
17:LM:38:VAL:HG21	17:LM:50:MET:HB3	1.93	0.51
21:LQ:50:ARG:HH21	21:LQ:140:SER:HB2	1.76	0.51
48:Ls:134:LYS:HD2	48:Ls:137:PHE:HE2	1.76	0.51
57:SS:46:ARG:NH1	58:ST:50:GLU:OE2	2.43	0.51
67:SC:214:LEU:HD22	67:SC:244:ILE:HD11	1.92	0.51
3:L5:935:A:N7	17:LM:46:ARG:NH2	2.59	0.51
3:L5:3811:G:O2'	3:L5:3814:U:OP2	2.27	0.51
3:L5:4188:U:H2'	3:L5:4189:U:C6	2.46	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:4940:C:H5'	3:L5:4941:G:H5''	1.92	0.51
3:L5:4954:G:H2'	3:L5:4955:A:C8	2.45	0.51
5:L8:141:C:H2'	5:L8:142:U:C6	2.46	0.51
83:S2:1013:U:OP1	83:S2:1129:G:O2'	2.28	0.51
83:S2:1854:U:H2'	83:S2:1855:G:H8	1.76	0.51
86:CF:108:GLN:HB2	86:CF:266:ARG:NE	2.26	0.51
3:L5:150:U:OP2	12:LG:200:THR:OG1	2.24	0.51
3:L5:1298:C:H2'	3:L5:1299:G:C8	2.46	0.51
3:L5:2298:U:OP1	8:LC:204:ARG:NE	2.44	0.51
3:L5:4304:A:OP2	3:L5:4305:G:N2	2.43	0.51
15:LJ:56:THR:OG1	15:LJ:64:ARG:N	2.44	0.51
16:LL:58:ILE:HD13	16:LL:157:VAL:HG22	1.93	0.51
53:SM:49:LEU:HD21	53:SM:123:VAL:HG11	1.93	0.51
56:SR:6:THR:HA	83:S2:1373:C:H5'	1.91	0.51
64:Sg:255:SER:OG	64:Sg:269:GLU:OE2	2.27	0.51
65:SA:37:TYR:HA	65:SA:53:ARG:HD3	1.93	0.51
3:L5:1669:A:H4'	3:L5:1685:G:N2	2.26	0.51
59:SU:22:ILE:HG23	59:SU:114:VAL:HG22	1.93	0.51
83:S2:941:C:H2'	83:S2:942:G:C8	2.44	0.51
3:L5:659:G:H2'	3:L5:660:A:H8	1.75	0.51
3:L5:2667:C:O4'	22:LR:96:MET:HG2	2.10	0.51
3:L5:4618:OMG:H5'	26:LV:15:ARG:HB2	1.93	0.51
5:L8:102:G:OP2	5:L8:104:A:O2'	2.26	0.51
12:LG:150:LYS:NZ	12:LG:177:MET:O	2.44	0.51
23:LS:173:ASN:ND2	23:LS:175:PHE:O	2.44	0.51
61:Sc:18:LEU:HD12	61:Sc:29:GLN:HG2	1.93	0.51
65:SA:102:ARG:NH1	83:S2:1378:A:OP2	2.44	0.51
67:SC:70:VAL:HG11	67:SC:93:ILE:HG23	1.93	0.51
79:SY:80:ASP:HA	79:SY:83:LYS:HD2	1.92	0.51
83:S2:695:C:N4	83:S2:736:C:O2'	2.44	0.51
3:L5:966:A:OP2	3:L5:2092:G:N2	2.45	0.50
3:L5:2844:A:N6	3:L5:3839:G:O2'	2.44	0.50
3:L5:4419:U:OP1	3:L5:4475:G:N2	2.43	0.50
79:SY:104:ARG:NH1	83:S2:507:G:OP2	2.36	0.50
83:S2:149:A:H3'	83:S2:150:A:H8	1.75	0.50
83:S2:1115:U:O2'	83:S2:1117:C:OP2	2.27	0.50
83:S2:1773:C:H2'	83:S2:1774:C:H5''	1.92	0.50
2:Pt:3:C:H42	2:Pt:70:A:H61	1.59	0.50
3:L5:419:A:N3	3:L5:1332:C:O2'	2.40	0.50
3:L5:1802:A:H5''	3:L5:1803:G:H5'	1.93	0.50
3:L5:2083:C:P	21:LQ:14:ARG:HH22	2.34	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LR:127:VAL:HG12	22:LR:132:PHE:HD2	1.76	0.50
52:SK:1:MET:HG3	52:SK:3:MET:H	1.75	0.50
58:ST:11:GLN:HB2	83:S2:1542:C:H4'	1.93	0.50
67:SC:121:ARG:NH1	67:SC:123:ARG:HE	2.10	0.50
86:CF:82:THR:HG21	86:CF:232:LEU:HD22	1.94	0.50
3:L5:2046:G:OP1	19:LO:59:ARG:NH1	2.44	0.50
16:LL:69:LYS:NZ	16:LL:161:TYR:OH	2.45	0.50
20:LP:109:VAL:HA	20:LP:112:LEU:HD13	1.92	0.50
40:Lj:27:TYR:HA	40:Lj:34:CYS:HA	1.93	0.50
51:SF:23:TRP:CD1	51:SF:108:PRO:HD2	2.46	0.50
66:SB:177:GLN:HG3	66:SB:178:THR:HG23	1.94	0.50
69:SG:202:ASN:ND2	83:S2:125:C:OP1	2.37	0.50
75:SO:141:ARG:NH2	83:S2:1856:C:OP1	2.39	0.50
83:S2:525:A:H2'	83:S2:526:A:C8	2.46	0.50
83:S2:1144:A:H2'	83:S2:1145:A:C8	2.46	0.50
83:S2:1407:U:H2'	83:S2:1408:U:C6	2.45	0.50
83:S2:1595:U:H2'	83:S2:1596:U:C6	2.46	0.50
3:L5:153:G:H2'	3:L5:154:G:H8	1.76	0.50
3:L5:364:G:O6	40:Lj:55:ARG:NH2	2.44	0.50
3:L5:518:G:H1	3:L5:643:C:H2'	1.76	0.50
3:L5:1328:G:O2'	3:L5:2349:A:OP1	2.29	0.50
3:L5:1411:C:H2'	3:L5:1412:G:C8	2.47	0.50
3:L5:3917:A:H2'	3:L5:3918:G:H8	1.77	0.50
3:L5:4504:C:H2'	3:L5:4505:C:C6	2.46	0.50
3:L5:4748:U:H5''	36:Lf:54:LYS:HE3	1.94	0.50
32:Lb:65:MET:HG2	32:Lb:68:ARG:HH12	1.76	0.50
36:Lf:25:THR:HB	36:Lf:87:LYS:HD3	1.93	0.50
57:SS:64:VAL:O	57:SS:68:ILE:HG12	2.11	0.50
61:Sc:39:SER:HB3	80:Sa:51:ARG:HH12	1.76	0.50
66:SB:68:GLU:OE2	75:SO:96:LYS:NZ	2.32	0.50
66:SB:181:LEU:HA	66:SB:184:VAL:HB	1.92	0.50
71:SI:57:ALA:HB2	71:SI:183:GLY:HA2	1.94	0.50
83:S2:1651:A:H2'	83:S2:1652:G:H8	1.75	0.50
85:AT:21:U:C4	85:AT:47:G:H1'	2.45	0.50
3:L5:262:G:H2'	3:L5:263:G:H8	1.76	0.50
3:L5:1683:PSU:OP1	31:La:44:ASN:ND2	2.43	0.50
3:L5:1718:C:O2'	11:LF:181:LYS:NZ	2.44	0.50
3:L5:4594:U:H2'	3:L5:4595:G:C8	2.47	0.50
9:LD:236:MET:HA	9:LD:239:MET:HG2	1.94	0.50
34:Ld:24:GLU:OE2	34:Ld:87:ARG:NH2	2.40	0.50
54:SP:105:VAL:HG21	54:SP:119:PHE:HB3	1.92	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SR:57:LEU:O	56:SR:61:ILE:HG13	2.11	0.50
64:Sg:216:ALA:N	64:Sg:230:LEU:O	2.41	0.50
67:SC:85:SER:OG	76:SV:25:GLY:O	2.29	0.50
67:SC:185:THR:OG1	83:S2:1155:U:OP1	2.24	0.50
69:SG:57:ASP:OD1	69:SG:58:LYS:N	2.41	0.50
69:SG:121:ILE:HD12	69:SG:122:PRO:HD2	1.94	0.50
84:Zt:68:C:H2'	84:Zt:69:G:H8	1.76	0.50
3:L5:382:G:N1	3:L5:385:A:OP2	2.41	0.50
3:L5:444:G:H2'	3:L5:445:U:C6	2.47	0.50
5:L8:19:C:H2'	5:L8:20:A:C8	2.47	0.50
17:LM:119:ARG:HG3	19:LO:189:ILE:HG23	1.93	0.50
41:Lk:26:LYS:HB2	41:Lk:69:LEU:HD12	1.94	0.50
71:SI:116:HIS:O	71:SI:152:ARG:NH2	2.42	0.50
74:SN:87:ASP:OD1	74:SN:88:LEU:N	2.45	0.50
77:SW:6:VAL:HG13	77:SW:29:PRO:HB2	1.93	0.50
83:S2:1513:C:H2'	83:S2:1514:G:H8	1.76	0.50
84:Zt:22:G:H2'	84:Zt:23:A:C8	2.44	0.50
3:L5:3944:G:H1	3:L5:4069:U:H3	1.60	0.50
14:LI:73:ASN:HB2	14:LI:87:MET:HE1	1.94	0.50
16:LL:111:GLN:O	16:LL:115:GLN:HG2	2.12	0.50
29:LY:2:LYS:HD2	29:LY:7:VAL:HG23	1.92	0.50
52:SK:60:GLU:HB2	52:SK:69:TRP:CD1	2.46	0.50
64:Sg:35:SER:OG	64:Sg:36:ARG:N	2.45	0.50
71:SI:3:ILE:O	71:SI:30:GLY:N	2.41	0.50
71:SI:151:GLU:OE2	71:SI:154:LYS:NZ	2.45	0.50
73:SL:103:GLU:HG3	78:SX:11:ARG:HB2	1.93	0.50
77:SW:10:ALA:O	77:SW:14:ILE:HD12	2.12	0.50
83:S2:656:G:H21	83:S2:663:C:H5''	1.77	0.50
3:L5:684:G:H5''	10:LE:100:LYS:HE3	1.94	0.50
3:L5:2568:C:H2'	3:L5:2569:G:H8	1.76	0.50
3:L5:5057:C:H2'	3:L5:5058:A:C8	2.46	0.50
68:SE:64:ILE:HG23	79:SY:17:LEU:HD12	1.94	0.50
69:SG:136:LYS:HB2	83:S2:65:C:H41	1.76	0.50
75:SO:113:GLN:HE22	80:Sa:45:VAL:HA	1.77	0.50
79:SY:80:ASP:OD1	79:SY:81:TYR:N	2.44	0.50
83:S2:5:U:H2'	83:S2:6:G:H8	1.76	0.50
7:LB:147:GLU:OE2	7:LB:198:ARG:NH2	2.36	0.50
9:LD:215:ASP:OD1	9:LD:218:ALA:HB3	2.11	0.50
10:LE:161:ARG:O	10:LE:182:ASN:ND2	2.45	0.50
18:LN:43:THR:OG1	18:LN:131:GLU:OE2	2.28	0.50
58:ST:62:ARG:NH2	83:S2:1543:U:OP2	2.39	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:Sg:37:ASP:OD1	64:Sg:39:THR:OG1	2.27	0.50
64:Sg:165:ILE:O	64:Sg:176:VAL:HA	2.12	0.50
68:SE:125:LYS:O	68:SE:142:HIS:N	2.45	0.50
68:SE:204:SER:OG	68:SE:205:PHE:N	2.38	0.50
69:SG:162:LEU:HG	69:SG:167:LYS:HE3	1.94	0.50
70:SH:76:GLN:HG2	70:SH:94:PHE:HD2	1.77	0.50
83:S2:420:G:O2'	83:S2:660:C:N3	2.39	0.50
83:S2:1468:C:H2'	83:S2:1469:A:H8	1.77	0.50
86:CF:335:MET:HB2	86:CF:443:LYS:HD3	1.93	0.50
3:L5:433:A:C2	3:L5:3867:A2M:H4'	2.46	0.49
3:L5:1670:G:OP1	32:Lb:12:GLN:NE2	2.32	0.49
3:L5:2520:C:H2'	3:L5:2521:G:H8	1.77	0.49
3:L5:4523:A2M:H5''	3:L5:4524:G:H5'	1.94	0.49
3:L5:4761:G:H2'	3:L5:4762:A:C8	2.47	0.49
3:L5:4769:G:H5''	19:LO:176:ARG:HD3	1.94	0.49
3:L5:4897:G:H2'	3:L5:4898:G:H8	1.75	0.49
7:LB:14:LEU:HD22	7:LB:17:LEU:HD11	1.94	0.49
7:LB:17:LEU:O	7:LB:19:ARG:N	2.43	0.49
55:SQ:4:LYS:HE3	83:S2:1423:C:H41	1.75	0.49
55:SQ:19:ALA:HB2	55:SQ:75:GLY:HA3	1.94	0.49
62:Sd:8:TRP:HZ3	83:S2:1512:C:H5''	1.77	0.49
69:SG:13:GLN:NE2	83:S2:153:G:N3	2.60	0.49
83:S2:482:G:N1	83:S2:485:A:OP2	2.43	0.49
3:L5:2808:G:O3'	22:LR:60:ARG:NH1	2.45	0.49
12:LG:180:PRO:HG3	12:LG:219:VAL:HG13	1.95	0.49
22:LR:36:ASN:OD1	22:LR:40:GLN:NE2	2.42	0.49
33:Lc:48:LEU:HD13	33:Lc:57:LYS:HG3	1.94	0.49
51:SF:23:TRP:HE1	51:SF:101:HIS:CG	2.30	0.49
52:SK:53:LYS:NZ	52:SK:60:GLU:HB3	2.27	0.49
64:Sg:39:THR:HG22	64:Sg:60:ARG:HG2	1.94	0.49
64:Sg:114:SER:O	64:Sg:117:ASN:ND2	2.45	0.49
78:SX:105:PHE:HD1	78:SX:121:LYS:HB3	1.76	0.49
80:Sa:59:PHE:HB2	80:Sa:62:TYR:HB2	1.95	0.49
83:S2:1208:A:H2'	83:S2:1209:A:H8	1.77	0.49
83:S2:1705:C:H2'	83:S2:1706:G:C8	2.48	0.49
3:L5:956:A:H1'	3:L5:2076:G:H5''	1.94	0.49
29:LY:31:SER:HA	29:LY:48:PRO:HA	1.93	0.49
49:Lt:130:LYS:NZ	49:Lt:157:SER:O	2.45	0.49
51:SF:22:LYS:HG3	51:SF:23:TRP:CE3	2.47	0.49
51:SF:83:ASN:OD1	83:S2:1651:A:O2'	2.29	0.49
53:SM:23:LYS:O	53:SM:27:ILE:HG12	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:ST:134:ILE:HA	58:ST:137:GLN:HG2	1.94	0.49
65:SA:111:GLN:HA	65:SA:116:PHE:CG	2.47	0.49
66:SB:44:ILE:HG23	66:SB:69:VAL:HG11	1.94	0.49
3:L5:460:C:H2'	3:L5:461:G:H8	1.78	0.49
3:L5:1367:C:O2'	3:L5:1369:C:OP2	2.26	0.49
3:L5:2478:C:N3	3:L5:2591:A:O2'	2.45	0.49
3:L5:2809:G:O2'	3:L5:4644:G:OP1	2.27	0.49
15:LJ:120:ASP:OD2	15:LJ:122:SER:OG	2.27	0.49
83:S2:17:C:H2'	83:S2:18:C:C6	2.47	0.49
83:S2:98:C:OP2	83:S2:426:A:O2'	2.24	0.49
83:S2:388:U:H2'	83:S2:389:A:C8	2.48	0.49
83:S2:472:C:O2	83:S2:475:C:N4	2.44	0.49
83:S2:656:G:N2	83:S2:663:C:H5''	2.27	0.49
83:S2:942:G:H2'	83:S2:943:U:C6	2.48	0.49
83:S2:1831:A:O2'	83:S2:1832:6MZ:H8	2.12	0.49
86:CF:245:PRO:O	86:CF:269:THR:OG1	2.17	0.49
3:L5:417:G:OP1	3:L5:2329:U:O2'	2.27	0.49
3:L5:1942:A:H2'	3:L5:1943:A:H8	1.78	0.49
3:L5:3687:A:O2'	6:LA:236:GLY:N	2.45	0.49
3:L5:4102:C:H1'	3:L5:4108:G:H1	1.77	0.49
4:L7:110:G:H2'	4:L7:111:C:C6	2.47	0.49
15:LJ:15:LEU:HD12	15:LJ:165:TRP:HB2	1.95	0.49
39:Li:59:GLU:HA	39:Li:62:LYS:HE3	1.94	0.49
65:SA:10:MET:HE2	65:SA:18:PHE:HE2	1.77	0.49
69:SG:192:ILE:HD12	69:SG:195:LYS:HD2	1.94	0.49
70:SH:146:VAL:HG12	77:SW:42:MET:HE1	1.94	0.49
83:S2:455:A:H2'	83:S2:456:C:H6	1.78	0.49
83:S2:1405:A:H2'	83:S2:1406:G:O4'	2.12	0.49
3:L5:691:C:H2'	3:L5:692:A:C8	2.47	0.49
3:L5:1509:C:H5''	31:La:2:PRO:HD3	1.94	0.49
33:Lc:47:ILE:HD12	33:Lc:94:LEU:HD11	1.94	0.49
55:SQ:83:ALA:HA	55:SQ:86:GLN:HE21	1.77	0.49
56:SR:105:MET:HE3	65:SA:51:LEU:H	1.77	0.49
64:Sg:32:LEU:HA	64:Sg:42:MET:HA	1.95	0.49
66:SB:98:THR:O	66:SB:232:HIS:NE2	2.45	0.49
67:SC:187:ARG:NH2	83:S2:1143:A:OP2	2.45	0.49
68:SE:131:VAL:HA	68:SE:137:PRO:HA	1.94	0.49
83:S2:1568:C:H2'	83:S2:1569:A:C8	2.47	0.49
3:L5:325:U:H2'	3:L5:326:C:C6	2.47	0.49
3:L5:4238:G:H2'	3:L5:4239:A:C8	2.47	0.49
7:LB:29:VAL:HG12	7:LB:31:SER:H	1.78	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SB:108:ASP:OD1	66:SB:109:LYS:N	2.46	0.49
83:S2:64:A:N6	83:S2:83:A:OP2	2.45	0.49
85:AT:51:U:H2'	85:AT:52:C:C6	2.48	0.49
3:L5:2539:C:H2'	3:L5:2540:C:C6	2.48	0.49
10:LE:161:ARG:NH1	10:LE:273:SER:OG	2.46	0.49
18:LN:184:ILE:O	18:LN:194:ARG:NH1	2.34	0.49
26:LV:42:VAL:HB	26:LV:45:ILE:HG13	1.95	0.49
53:SM:58:GLU:HB3	53:SM:61:TYR:HB2	1.94	0.49
74:SN:102:LEU:O	74:SN:106:ARG:NH2	2.46	0.49
76:SV:59:ILE:HA	76:SV:62:MET:HE3	1.95	0.49
78:SX:9:THR:HG22	83:S2:681:PSU:H4'	1.94	0.49
83:S2:1217:A:H2'	83:S2:1218:C:C6	2.47	0.49
3:L5:702:U:H2'	3:L5:703:G:O4'	2.12	0.49
3:L5:2018:C:H2'	3:L5:2019:C:C6	2.48	0.49
3:L5:2079:G:H2'	3:L5:2080:U:C6	2.48	0.49
3:L5:4088:C:H2'	3:L5:4089:G:C8	2.48	0.49
3:L5:4459:U:H2'	3:L5:4460:U:C6	2.48	0.49
16:LL:91:ALA:HB1	16:LL:96:ILE:HB	1.95	0.49
26:LV:43:LYS:HE2	26:LV:62:MET:HE3	1.95	0.49
78:SX:90:CYS:HA	78:SX:93:PHE:HD2	1.77	0.49
83:S2:5:U:H2'	83:S2:6:G:C8	2.48	0.49
83:S2:1736:G:H2'	83:S2:1737:G:C8	2.48	0.49
3:L5:10:A:H2'	3:L5:11:G:C8	2.48	0.49
3:L5:148:C:OP2	12:LG:197:LYS:NZ	2.42	0.49
3:L5:2491:C:O2'	3:L5:2492:C:O4'	2.26	0.49
3:L5:3855:C:H2'	3:L5:3856:A:H8	1.78	0.49
3:L5:4622:A:H4'	7:LB:13:SER:HB2	1.95	0.49
3:L5:4717:A:OP2	7:LB:30:LYS:NZ	2.33	0.49
6:LA:13:GLY:O	6:LA:17:ARG:HG3	2.12	0.49
8:LC:289:LEU:HD21	21:LQ:31:LEU:HB2	1.95	0.49
15:LJ:38:LYS:HA	15:LJ:41:GLU:HG2	1.94	0.49
17:LM:62:LEU:HD12	17:LM:76:ALA:HB1	1.95	0.49
22:LR:28:GLU:HG3	22:LR:31:GLU:OE2	2.12	0.49
51:SF:40:ALA:HB3	51:SF:67:PRO:HA	1.94	0.49
51:SF:100:ILE:HD11	51:SF:174:ALA:HA	1.95	0.49
64:Sg:129:ILE:O	64:Sg:142:VAL:N	2.37	0.49
65:SA:192:GLU:OE2	65:SA:193:HIS:ND1	2.46	0.49
82:Se:56:ASN:ND2	83:S2:606:G:O4'	2.45	0.49
83:S2:468:A2M:HM'3	83:S2:468:A2M:H1'	1.60	0.49
83:S2:600:G:H2'	83:S2:601:OMG:H8	1.78	0.49
2:Pt:43:A:H2'	2:Pt:44:A:C8	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:351:C:OP2	8:LC:197:ARG:NH1	2.35	0.48
3:L5:1461:C:H2'	3:L5:1462:A:C8	2.48	0.48
3:L5:1683:PSU:H2'	3:L5:1684:A:C8	2.48	0.48
7:LB:258:HIS:HA	7:LB:260:ALA:N	2.27	0.48
27:LW:80:ARG:NH1	83:S2:167:G:O2'	2.45	0.48
60:SZ:62:VAL:HA	60:SZ:65:TYR:CE1	2.48	0.48
66:SB:129:THR:OG1	66:SB:131:ASP:OD1	2.27	0.48
79:SY:40:ILE:HG23	79:SY:44:LEU:HD13	1.95	0.48
79:SY:111:LYS:NZ	83:S2:56:G:OP1	2.39	0.48
83:S2:432:G:H2'	83:S2:433:A:C8	2.48	0.48
86:CF:360:VAL:HA	86:CF:369:ALA:HA	1.94	0.48
3:L5:64:A:H1'	3:L5:76:A:H1'	1.95	0.48
3:L5:1802:A:N3	24:LT:130:ARG:NH2	2.61	0.48
3:L5:2400:G:H21	37:Lg:6:THR:HG22	1.78	0.48
5:L8:90:C:H1'	29:LY:24:HIS:HB3	1.95	0.48
6:LA:20:VAL:HA	6:LA:23:ARG:HG3	1.93	0.48
24:LT:119:ALA:HA	24:LT:122:LYS:HE3	1.94	0.48
48:Ls:12:ASN:HA	48:Ls:15:LEU:HG	1.95	0.48
51:SF:73:THR:O	51:SF:89:THR:HG21	2.13	0.48
53:SM:82:ASN:OD1	53:SM:83:LYS:N	2.47	0.48
56:SR:70:SER:HB2	56:SR:73:LEU:HB2	1.94	0.48
58:ST:121:ARG:HH21	83:S2:1563:G:H5''	1.78	0.48
82:Se:40:ARG:O	82:Se:44:ASN:ND2	2.42	0.48
83:S2:1304:U:H2'	83:S2:1305:C:C6	2.48	0.48
86:CF:142:THR:HG21	86:CF:425:ALA:HB2	1.95	0.48
3:L5:330:G:N7	89:L5:5285:SPD:N1	2.61	0.48
3:L5:1324:A:O2'	3:L5:1326:A2M:OP1	2.29	0.48
3:L5:1461:C:H2'	3:L5:1462:A:H8	1.77	0.48
3:L5:1867:A:H2'	3:L5:1868:A:C8	2.49	0.48
3:L5:1996:C:N4	3:L5:2000:G:N2	2.39	0.48
3:L5:4441:A:H5''	14:LI:114:GLY:HA2	1.95	0.48
3:L5:4589:A:N1	3:L5:4621:C:O2'	2.41	0.48
40:Lj:2:THR:HG22	40:Lj:4:GLY:H	1.79	0.48
69:SG:176:ILE:HG13	69:SG:179:LEU:HD11	1.95	0.48
70:SH:51:ILE:HD11	70:SH:176:VAL:HG12	1.95	0.48
75:SO:145:GLY:O	80:Sa:22:ARG:NH2	2.46	0.48
83:S2:1417:C:N3	83:S2:1422:G:N1	2.58	0.48
84:Zt:44:G:H3'	84:Zt:45:G:H8	1.78	0.48
86:CF:87:VAL:HG11	86:CF:232:LEU:HD21	1.94	0.48
1:CI:74:LYS:CA	25:LU:116:GLN:O	2.55	0.48
3:L5:2744:A:H2'	3:L5:2745:A:C8	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:4761:G:H2'	3:L5:4762:A:H8	1.79	0.48
7:LB:29:VAL:HA	7:LB:220:ILE:HD13	1.94	0.48
18:LN:101:VAL:HA	18:LN:104:GLU:HG2	1.95	0.48
18:LN:155:VAL:O	18:LN:162:ARG:NH2	2.45	0.48
30:LZ:136:PHE:O	37:Lg:78:TYR:OH	2.26	0.48
58:ST:23:LYS:HE2	58:ST:54:TYR:HD2	1.79	0.48
61:Sc:23:SER:O	83:S2:1681:U:O2'	2.31	0.48
61:Sc:39:SER:O	80:Sa:51:ARG:NH1	2.45	0.48
66:SB:190:PRO:O	66:SB:195:LYS:NZ	2.46	0.48
68:SE:50:ASN:O	68:SE:53:LYS:NZ	2.40	0.48
83:S2:730:C:OP2	83:S2:734:C:N4	2.46	0.48
86:CF:353:ILE:HG23	86:CF:357:TYR:HE1	1.78	0.48
3:L5:1070:G:O2'	3:L5:1071:C:O5'	2.27	0.48
3:L5:1195:G:H2'	3:L5:1196:G:C8	2.49	0.48
3:L5:2407:G:H2'	42:Ll:13:LEU:HD22	1.96	0.48
4:L7:38:U:N3	4:L7:41:G:OP2	2.34	0.48
19:LO:126:VAL:HG13	19:LO:127:VAL:HG13	1.95	0.48
52:SK:80:ARG:NH2	52:SK:87:PRO:HA	2.29	0.48
56:SR:17:ILE:HD13	56:SR:57:LEU:HD13	1.94	0.48
64:Sg:120:ILE:HB	64:Sg:132:TRP:HB2	1.96	0.48
66:SB:26:SER:O	66:SB:51:ARG:NH2	2.46	0.48
69:SG:174:PRO:O	83:S2:77:A:O2'	2.26	0.48
70:SH:64:VAL:HB	70:SH:72:PHE:CE2	2.49	0.48
70:SH:162:GLN:HE22	70:SH:166:VAL:HB	1.79	0.48
3:L5:4941:G:OP2	10:LE:188:ARG:NH2	2.38	0.48
3:L5:5064:G:N2	20:LP:75:GLN:HE22	2.11	0.48
39:Li:95:ALA:HA	39:Li:98:ARG:HG2	1.96	0.48
54:SP:20:VAL:HG23	54:SP:25:LEU:HD21	1.95	0.48
58:ST:39:LEU:HD21	58:ST:52:TRP:CZ3	2.48	0.48
68:SE:80:ILE:HG23	68:SE:81:THR:HG23	1.95	0.48
78:SX:50:ILE:HG22	78:SX:73:GLN:HB3	1.96	0.48
83:S2:454:U:H2'	83:S2:455:A:C8	2.48	0.48
86:CF:277:VAL:HG13	86:CF:329:SER:HB3	1.96	0.48
86:CF:350:PRO:HD2	86:CF:351:GLY:H	1.78	0.48
3:L5:99:A:H5''	18:LN:184:ILE:HD12	1.94	0.48
3:L5:3867:A2M:H2'	3:L5:3868:G:O4'	2.14	0.48
3:L5:4612:C:C2	13:LH:120:GLU:HB2	2.49	0.48
17:LM:24:LEU:HB2	17:LM:43:THR:HG21	1.95	0.48
45:Lo:33:LEU:HA	45:Lo:38:LYS:HG2	1.96	0.48
50:SD:51:LEU:HD12	50:SD:91:VAL:HG22	1.96	0.48
51:SF:60:ARG:NH2	83:S2:1679:A:OP1	2.46	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:Sc:31:ARG:HE	61:Sc:43:ILE:HG12	1.78	0.48
62:Sd:56:ASP:OXT	83:S2:1480:A:O2'	2.31	0.48
66:SB:85:LYS:HB2	66:SB:101:HIS:HB3	1.95	0.48
66:SB:186:ASN:HA	66:SB:189:ILE:HD12	1.95	0.48
67:SC:78:LEU:HD12	67:SC:81:ILE:HD12	1.96	0.48
67:SC:165:VAL:HG21	67:SC:217:ALA:HB1	1.95	0.48
68:SE:59:ASP:O	68:SE:63:LYS:HG3	2.14	0.48
78:SX:105:PHE:CD1	78:SX:121:LYS:HB3	2.49	0.48
83:S2:90:G:OP1	83:S2:445:A:N6	2.47	0.48
83:S2:1588:A:H2'	83:S2:1589:A:C8	2.49	0.48
3:L5:735:G:H5''	17:LM:70:GLN:HG3	1.95	0.48
3:L5:979:C:OP2	10:LE:66:LYS:HD3	2.14	0.48
3:L5:1890:G:OP2	3:L5:1890:G:N2	2.37	0.48
3:L5:4743:G:H2'	3:L5:4744:A:C8	2.49	0.48
3:L5:4927:G:H5''	3:L5:4928:C:H5	1.78	0.48
3:L5:4986:G:H1'	7:LB:174:ARG:NH2	2.28	0.48
16:LL:55:ILE:O	16:LL:97:SER:OG	2.28	0.48
50:SD:210:ILE:HD13	56:SR:15:VAL:HG11	1.96	0.48
67:SC:227:ARG:NH2	83:S2:663:C:O2'	2.47	0.48
69:SG:7:PHE:HB2	69:SG:124:LEU:HD21	1.94	0.48
83:S2:51:U:H2'	83:S2:52:G:H8	1.79	0.48
83:S2:1719:A:N6	83:S2:1814:G:O2'	2.46	0.48
85:AT:14:A:H2'	85:AT:15:G:O4'	2.14	0.48
86:CF:240:ARG:HD3	86:CF:304:PRO:HB2	1.95	0.48
3:L5:2568:C:H2'	3:L5:2569:G:C8	2.49	0.48
3:L5:4321:U:H2'	3:L5:4322:G:C8	2.49	0.48
9:LD:41:LYS:NZ	24:LT:32:ARG:O	2.41	0.48
22:LR:70:ARG:HG2	22:LR:76:MET:HE3	1.96	0.48
25:LU:100:LEU:HD13	25:LU:112:LEU:HD13	1.96	0.48
26:LV:13:LYS:NZ	26:LV:59:ASP:OD2	2.47	0.48
29:LY:23:SER:HA	29:LY:26:ARG:HB2	1.95	0.48
47:Lr:65:LYS:O	47:Lr:102:TYR:OH	2.26	0.48
64:Sg:175:LYS:HB3	64:Sg:184:LEU:HD11	1.96	0.48
65:SA:10:MET:HE3	65:SA:55:TRP:HB2	1.95	0.48
66:SB:167:LYS:O	66:SB:171:ILE:HG12	2.14	0.48
70:SH:126:HIS:CE1	70:SH:181:THR:HG23	2.49	0.48
71:SI:141:ARG:HD3	71:SI:145:ILE:HG21	1.96	0.48
72:SJ:5:ARG:HB3	83:S2:38:A:H5''	1.95	0.48
77:SW:6:VAL:HG12	77:SW:34:ILE:HD11	1.95	0.48
79:SY:11:LYS:HB2	79:SY:24:VAL:HG12	1.96	0.48
83:S2:329:G:H2'	83:S2:330:G:C8	2.49	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:138:G:H2'	3:L5:139:G:H8	1.78	0.48
3:L5:654:C:O3'	8:LC:268:ARG:NH1	2.47	0.48
3:L5:1281:G:C6	10:LE:128:HIS:HB2	2.49	0.48
3:L5:2517:A:H5'	37:Lg:62:LYS:HD3	1.95	0.48
3:L5:2835:A:O2'	7:LB:228:TYR:O	2.27	0.48
5:L8:96:C:H5''	38:Lh:66:LYS:HG2	1.96	0.48
9:LD:66:TYR:HE2	9:LD:68:ARG:HE	1.62	0.48
23:LS:84:TYR:HE1	23:LS:93:MET:HE3	1.79	0.48
39:Li:94:LEU:HA	39:Li:97:MET:HG2	1.96	0.48
64:Sg:124:SER:OG	64:Sg:125:ARG:N	2.46	0.48
66:SB:164:ILE:O	66:SB:168:MET:HG2	2.12	0.48
68:SE:146:THR:HG21	83:S2:122:G:H21	1.78	0.48
70:SH:142:LYS:HB3	77:SW:54:ASP:HB3	1.95	0.48
83:S2:107:A:H2'	83:S2:108:G:C8	2.49	0.48
83:S2:367:U:H4'	83:S2:371:A:C8	2.49	0.48
83:S2:693:A:H2'	83:S2:694:G:C8	2.48	0.48
2:Pt:10:G:N2	2:Pt:26:G:H1'	2.29	0.47
3:L5:1084:C:H2'	3:L5:1085:C:C6	2.49	0.47
3:L5:1253:G:H2'	3:L5:1256:G:H5'	1.95	0.47
3:L5:1558:A:H2'	3:L5:1559:G:H8	1.79	0.47
3:L5:3668:C:OP1	6:LA:8:GLN:NE2	2.35	0.47
3:L5:3870:C:H2'	3:L5:3871:A:C8	2.49	0.47
3:L5:3911:C:H2'	3:L5:3912:U:H6	1.78	0.47
3:L5:4389:C:H2'	3:L5:4390:A:C8	2.49	0.47
5:L8:19:C:H2'	5:L8:20:A:H8	1.79	0.47
9:LD:211:LEU:HB3	9:LD:219:TYR:HB2	1.95	0.47
27:LW:56:ARG:HH21	27:LW:61:LYS:HB3	1.79	0.47
38:Lh:89:ARG:O	38:Lh:93:ARG:HG2	2.14	0.47
51:SF:193:LYS:O	51:SF:197:GLU:HG2	2.14	0.47
53:SM:110:VAL:O	53:SM:112:LYS:NZ	2.46	0.47
71:SI:25:ARG:HA	83:S2:448:A:H5''	1.95	0.47
85:AT:64:G:O2'	86:CF:430:ARG:NH1	2.46	0.47
2:Pt:29:C:H2'	2:Pt:30:G:H8	1.78	0.47
3:L5:1399:G:H2'	3:L5:1400:G:C8	2.49	0.47
3:L5:1824:G:H5''	24:LT:35:LYS:HE2	1.95	0.47
3:L5:3937:C:O2'	18:LN:124:ASP:OD2	2.31	0.47
15:LJ:20:LEU:HG	15:LJ:132:VAL:HG12	1.97	0.47
64:Sg:249:CYS:HB3	64:Sg:258:ILE:HD13	1.95	0.47
66:SB:30:TRP:CG	75:SO:19:PRO:HB3	2.49	0.47
72:SJ:164:PRO:HB3	72:SJ:170:PRO:HA	1.95	0.47
85:AT:49:C:H2'	85:AT:60:A:H1'	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:256:G:H2'	3:L5:257:C:C6	2.49	0.47
3:L5:707:C:O2'	3:L5:4943:A:N1	2.43	0.47
3:L5:2638:G:H22	3:L5:2719:C:P	2.38	0.47
3:L5:2656:U:H5''	30:LZ:38:TYR:HB3	1.96	0.47
3:L5:2745:A:H2'	3:L5:2746:A:C8	2.46	0.47
3:L5:4288:C:O2'	3:L5:4321:U:OP1	2.33	0.47
5:L8:102:G:H5''	40:Lj:39:TYR:HE1	1.80	0.47
11:LF:127:LYS:HB2	24:LT:133:ALA:HB3	1.96	0.47
42:Ll:33:ASN:ND2	42:Ll:35:ILE:H	2.13	0.47
66:SB:32:ASP:OD1	66:SB:46:LYS:NZ	2.38	0.47
67:SC:145:LYS:NZ	83:S2:1348:G:H5''	2.29	0.47
71:SI:125:LYS:HB2	71:SI:128:LYS:HZ3	1.78	0.47
73:SL:49:GLU:O	73:SL:53:GLY:N	2.47	0.47
77:SW:115:GLU:HA	77:SW:118:ARG:HB2	1.95	0.47
83:S2:1221:G:H2'	83:S2:1222:G:C8	2.50	0.47
83:S2:1337:4AC:H2'	83:S2:1338:G:H8	1.79	0.47
2:Pt:18:G:HO2'	2:Pt:57:G:H22	1.59	0.47
3:L5:1084:C:H2'	3:L5:1085:C:H6	1.79	0.47
3:L5:1662:C:H2'	3:L5:1663:C:C6	2.48	0.47
3:L5:1700:G:H5''	3:L5:1704:C:N4	2.28	0.47
3:L5:2848:G:O2'	3:L5:3838:U:O4	2.22	0.47
8:LC:154:VAL:HG11	8:LC:174:LEU:HD11	1.96	0.47
8:LC:268:ARG:NH1	8:LC:269:LYS:HE2	2.29	0.47
18:LN:140:LYS:HD3	18:LN:140:LYS:HA	1.71	0.47
28:LX:105:ASN:OD1	28:LX:108:GLN:HG3	2.15	0.47
64:Sg:205:SER:HA	64:Sg:221:LEU:HB2	1.97	0.47
71:SI:98:LYS:HG3	71:SI:178:ARG:HG2	1.96	0.47
74:SN:99:ARG:NH2	74:SN:119:GLU:OE2	2.44	0.47
83:S2:186:C:H2'	83:S2:187:G:H8	1.80	0.47
83:S2:1348:G:OP2	83:S2:1348:G:N2	2.46	0.47
3:L5:1296:G:H2'	3:L5:1297:U:C6	2.50	0.47
3:L5:1410:U:H3	32:Lb:52:LYS:NZ	2.12	0.47
3:L5:3873:G:H2'	3:L5:3874:G:C8	2.50	0.47
3:L5:3932:U:H2'	3:L5:3933:G:H8	1.80	0.47
3:L5:4991:U:H2'	3:L5:4992:G:H8	1.78	0.47
6:LA:247:ARG:HB3	83:S2:1069:U:H4'	1.97	0.47
58:ST:73:GLY:O	58:ST:94:ARG:NH2	2.44	0.47
65:SA:184:ARG:NE	65:SA:191:ARG:HD3	2.29	0.47
68:SE:134:LYS:N	83:S2:298:G:OP1	2.40	0.47
70:SH:119:SER:OG	70:SH:120:ARG:NH1	2.46	0.47
3:L5:108:A:N1	3:L5:333:U:O2'	2.44	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:197:A:N1	3:L5:225:G:O2'	2.42	0.47
3:L5:423:G:OP1	20:LP:62:ARG:NH1	2.43	0.47
3:L5:1818:G:O2'	3:L5:1820:C:OP2	2.24	0.47
3:L5:4420:U:H5''	3:L5:4421:C:H5	1.80	0.47
3:L5:4584:A:H2'	3:L5:4585:U:O4'	2.14	0.47
3:L5:5047:C:O2'	3:L5:5050:C:OP2	2.26	0.47
12:LG:52:THR:HG22	28:LX:41:ARG:HG3	1.96	0.47
15:LJ:63:ARG:HH11	45:Lo:106:PHE:HB2	1.79	0.47
23:LS:99:ASP:OD1	23:LS:100:LEU:N	2.43	0.47
55:SQ:97:GLN:HE22	64:Sg:58:ALA:HB3	1.78	0.47
57:SS:62:ASP:OD1	57:SS:62:ASP:N	2.48	0.47
67:SC:60:TRP:O	67:SC:71:LYS:NZ	2.30	0.47
3:L5:280:G:H5''	18:LN:14:LYS:HE2	1.96	0.47
3:L5:378:A:O2'	3:L5:413:G:N2	2.47	0.47
3:L5:1846:G:H2'	3:L5:1847:C:C6	2.49	0.47
3:L5:1914:C:H4'	19:LO:89:PRO:HD3	1.97	0.47
3:L5:2306:G:H1'	3:L5:2332:A:N6	2.30	0.47
3:L5:4163:U:H5'	3:L5:4164:C:H5''	1.96	0.47
3:L5:4456:OMC:HM21	7:LB:241:PRO:HD3	1.96	0.47
4:L7:15:C:H2'	4:L7:16:A:H8	1.80	0.47
5:L8:67:U:H2'	5:L8:68:G:C8	2.50	0.47
12:LG:162:ASP:HB3	12:LG:163:PRO:HD3	1.96	0.47
13:LH:18:ILE:HG12	13:LH:27:VAL:HG22	1.97	0.47
25:LU:44:GLN:HB2	25:LU:56:LEU:HD21	1.95	0.47
47:Lr:52:GLU:HG3	47:Lr:61:VAL:HB	1.96	0.47
56:SR:32:LYS:NZ	83:S2:1452:A:OP2	2.48	0.47
57:SS:85:ASN:ND2	83:S2:1629:C:O2	2.42	0.47
63:Sf:97:LYS:NZ	83:S2:1289:U:OP2	2.44	0.47
65:SA:12:GLU:HA	65:SA:15:VAL:HG22	1.96	0.47
65:SA:145:ILE:HG23	65:SA:159:ILE:HB	1.96	0.47
70:SH:159:ASP:OD1	70:SH:160:LYS:N	2.47	0.47
72:SJ:38:ARG:N	72:SJ:42:GLU:OE2	2.32	0.47
72:SJ:124:HIS:CD2	82:Se:35:ARG:HD2	2.50	0.47
72:SJ:124:HIS:HD2	82:Se:31:ARG:HE	1.62	0.47
74:SN:38:TYR:O	74:SN:42:LYS:HG2	2.15	0.47
74:SN:70:LYS:NZ	83:S2:1020:A:N7	2.63	0.47
79:SY:9:THR:H	83:S2:837:A:N6	2.13	0.47
83:S2:563:G:HO2'	83:S2:564:A:P	2.36	0.47
83:S2:1220:A:N3	83:S2:1677:U:O2'	2.41	0.47
83:S2:1643:U:H2'	83:S2:1644:C:C6	2.49	0.47
83:S2:1808:U:H2'	83:S2:1809:A:H8	1.80	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:AT:9:A:N6	85:AT:23:U:OP2	2.36	0.47
86:CF:11:VAL:HG11	86:CF:106:THR:HA	1.96	0.47
3:L5:262:G:H2'	3:L5:263:G:C8	2.50	0.47
3:L5:989:U:H3	3:L5:1064:G:H1	1.60	0.47
3:L5:1399:G:H2'	3:L5:1400:G:H8	1.80	0.47
3:L5:3777:G:O2'	3:L5:3815:G:O6	2.30	0.47
3:L5:3910:C:H2'	3:L5:3911:C:H6	1.80	0.47
3:L5:4095:G:H2'	3:L5:4096:C:C6	2.49	0.47
27:LW:5:LEU:HB3	27:LW:30:GLN:HG3	1.96	0.47
29:LY:76:LYS:HE2	42:L1:31:THR:HB	1.97	0.47
54:SP:34:MET:HE3	54:SP:42:ARG:HG3	1.96	0.47
58:ST:65:TYR:CE1	58:ST:128:GLN:HG3	2.46	0.47
79:SY:77:ASP:OD1	79:SY:77:ASP:N	2.47	0.47
83:S2:659:G:HO2'	83:S2:662:G:HO2'	1.55	0.47
83:S2:1777:G:H2'	83:S2:1778:C:H6	1.80	0.47
2:Pt:35:A:OP2	55:SQ:146:ARG:NH2	2.48	0.47
3:L5:170:C:H42	3:L5:266:C:N4	2.10	0.47
3:L5:1696:C:H5'	3:L5:1719:A:H1'	1.97	0.47
3:L5:2021:G:OP1	48:Ls:58:ASN:N	2.40	0.47
3:L5:2846:G:O2'	26:LV:19:GLY:O	2.29	0.47
3:L5:4095:G:N7	3:L5:4096:C:N4	2.63	0.47
3:L5:4301:U:OP2	3:L5:4303:C:N4	2.48	0.47
18:LN:126:THR:HG23	18:LN:127:TYR:CD1	2.50	0.47
34:Ld:65:ASP:OD2	34:Ld:66:THR:N	2.48	0.47
50:SD:136:VAL:HG23	50:SD:152:PHE:HD2	1.79	0.47
63:Sf:132:MET:HG2	63:Sf:141:CYS:HA	1.97	0.47
70:SH:30:LEU:HG	70:SH:33:ASN:HD22	1.80	0.47
79:SY:76:TYR:OH	79:SY:86:GLU:OE1	2.28	0.47
83:S2:1084:A:OP1	83:S2:1858:G:O2'	2.28	0.47
83:S2:1491:G:H2'	83:S2:1492:U:C6	2.50	0.47
83:S2:1560:U:O2	83:S2:1575:G:O6	2.33	0.47
83:S2:1801:A:H2'	83:S2:1802:C:H6	1.80	0.47
83:S2:1850:MA6:H8	83:S2:1850:MA6:O5'	2.15	0.47
3:L5:426:A:H2'	3:L5:427:A:C8	2.50	0.47
3:L5:965:G:H21	3:L5:2092:G:H1'	1.79	0.47
3:L5:1971:C:H2'	3:L5:1972:G:C8	2.50	0.47
3:L5:2257:C:O2'	3:L5:2259:G:OP2	2.28	0.47
3:L5:2284:G:OP1	31:La:7:LYS:NZ	2.44	0.47
3:L5:2580:U:HO2'	30:LZ:79:HIS:HD1	1.60	0.47
3:L5:2749:C:H2'	3:L5:2750:G:C8	2.50	0.47
3:L5:4239:A:H2'	3:L5:4240:G:H8	1.79	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L7:57:C:H2'	4:L7:58:A:H8	1.80	0.47
7:LB:258:HIS:HA	7:LB:260:ALA:H	1.79	0.47
7:LB:302:ASN:HB2	7:LB:313:SER:HA	1.96	0.47
11:LF:46:ARG:O	11:LF:50:ILE:HG12	2.15	0.47
64:Sg:133:ASN:HB3	64:Sg:139:LYS:HD2	1.97	0.47
72:SJ:40:LYS:NZ	83:S2:641:A:OP1	2.39	0.47
79:SY:119:GLY:HA2	83:S2:85:A:H5'	1.96	0.47
83:S2:414:A:H2'	83:S2:415:A:H8	1.80	0.47
83:S2:1201:U:H2'	83:S2:1202:U:C6	2.50	0.47
83:S2:1337:4AC:H2'	83:S2:1338:G:C8	2.50	0.47
83:S2:1694:U:O2'	83:S2:1833:C:O2'	2.29	0.47
85:AT:4:U:H2'	85:AT:5:C:C6	2.50	0.47
3:L5:267:G:H2'	3:L5:268:G:C8	2.48	0.46
3:L5:1617:G:H1'	3:L5:2513:A:N6	2.30	0.46
3:L5:2579:G:N2	3:L5:2582:A:OP2	2.32	0.46
3:L5:2658:G:N2	3:L5:2676:A:OP2	2.47	0.46
3:L5:3910:C:H2'	3:L5:3911:C:C6	2.50	0.46
5:L8:70:G:H1'	5:L8:88:A:H61	1.81	0.46
5:L8:70:G:H1'	5:L8:88:A:N6	2.30	0.46
5:L8:75:OMG:OP2	29:LY:74:TYR:OH	2.28	0.46
19:LO:54:TYR:CD1	19:LO:145:VAL:HG21	2.50	0.46
21:LQ:22:ASP:HB3	21:LQ:25:LEU:HB3	1.97	0.46
21:LQ:133:GLY:O	21:LQ:136:THR:OG1	2.28	0.46
29:LY:56:GLN:HB3	29:LY:67:ILE:HD13	1.95	0.46
38:Lh:5:LYS:HD3	38:Lh:7:ARG:HH21	1.81	0.46
51:SF:51:HIS:NE2	83:S2:1674:G:OP1	2.39	0.46
63:Sf:92:LYS:NZ	83:S2:1271:C:OP1	2.35	0.46
66:SB:138:PHE:O	66:SB:213:ARG:N	2.48	0.46
78:SX:93:PHE:O	78:SX:140:ARG:NH1	2.48	0.46
83:S2:118:C:H1'	83:S2:445:A:C5	2.49	0.46
83:S2:830:A:OP2	83:S2:846:G:N2	2.48	0.46
83:S2:929:G:H2'	83:S2:930:C:O4'	2.15	0.46
83:S2:1845:A:H2'	83:S2:1846:G:H8	1.79	0.46
86:CF:368:ILE:HG23	86:CF:408:LYS:HB2	1.96	0.46
3:L5:90:G:OP2	3:L5:92:C:N4	2.46	0.46
3:L5:715:G:OP1	8:LC:321:ASN:ND2	2.41	0.46
3:L5:1494:U:H2'	3:L5:1495:G:C8	2.50	0.46
3:L5:1725:U:H2'	3:L5:1726:U:H6	1.80	0.46
3:L5:4153:C:H2'	3:L5:4154:G:H8	1.81	0.46
6:LA:114:CYS:N	6:LA:165:VAL:O	2.48	0.46
20:LP:4:TYR:CD1	20:LP:16:LYS:HE3	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lo:11:PHE:O	45:Lo:81:ARG:NH2	2.43	0.46
56:SR:7:LYS:HG3	83:S2:1373:C:OP1	2.16	0.46
56:SR:81:ARG:HH21	65:SA:85:ARG:HA	1.81	0.46
57:SS:5:ILE:N	60:SZ:50:PHE:O	2.41	0.46
63:Sf:137:ASP:N	63:Sf:137:ASP:OD2	2.49	0.46
68:SE:11:ARG:NH1	68:SE:24:THR:OG1	2.49	0.46
70:SH:111:LYS:HE3	83:S2:796:G:H21	1.81	0.46
79:SY:111:LYS:NZ	83:S2:54:A:OP1	2.45	0.46
83:S2:17:C:O2'	83:S2:1194:A:N1	2.39	0.46
83:S2:1128:C:H2'	83:S2:1129:G:C8	2.50	0.46
83:S2:1656:G:H1	83:S2:1668:U:H3	1.61	0.46
3:L5:173:C:OP1	16:LL:129:ARG:NH1	2.48	0.46
3:L5:1298:C:H2'	3:L5:1299:G:H8	1.80	0.46
3:L5:1743:A:N1	3:L5:1789:C:O2'	2.43	0.46
3:L5:2876:OMG:HM22	3:L5:2877:G:H5'	1.97	0.46
3:L5:3707:U:H2'	3:L5:3708:C:C6	2.50	0.46
3:L5:4149:C:OP1	30:LZ:59:LYS:N	2.47	0.46
3:L5:4327:C:OP1	24:LT:70:HIS:NE2	2.49	0.46
3:L5:4591:U:H2'	3:L5:4592:C:C6	2.50	0.46
3:L5:4699:U:H1'	3:L5:4700:A:H5''	1.96	0.46
3:L5:4991:U:H2'	3:L5:4992:G:C8	2.50	0.46
6:LA:116:LEU:HB3	6:LA:126:LEU:HB2	1.97	0.46
19:LO:119:VAL:N	23:LS:168:THR:O	2.45	0.46
29:LY:4:ASN:HB3	29:LY:7:VAL:HG22	1.95	0.46
47:Lr:47:LYS:O	47:Lr:103:ARG:HD2	2.14	0.46
54:SP:56:LEU:HD22	54:SP:80:LEU:HD11	1.97	0.46
64:Sg:5:MET:HB2	64:Sg:270:LEU:HD21	1.97	0.46
64:Sg:31:ILE:HG21	64:Sg:299:PHE:CE1	2.46	0.46
70:SH:21:SER:O	70:SH:25:GLN:HG2	2.16	0.46
83:S2:102:A:H4'	83:S2:104:A:C8	2.50	0.46
83:S2:186:C:H2'	83:S2:187:G:C8	2.51	0.46
3:L5:1079:C:O2	3:L5:1221:G:N2	2.35	0.46
3:L5:3680:U:OP1	6:LA:54:ARG:NH2	2.32	0.46
3:L5:4723:A:H2'	3:L5:4724:A:C8	2.50	0.46
8:LC:298:ILE:HD13	21:LQ:131:PRO:HB3	1.97	0.46
26:LV:87:SER:OG	27:LW:19:ARG:NH1	2.48	0.46
55:SQ:84:ILE:O	55:SQ:88:ILE:HG12	2.15	0.46
66:SB:23:ASP:N	66:SB:23:ASP:OD1	2.48	0.46
68:SE:176:ASP:OD1	68:SE:177:THR:N	2.48	0.46
76:SV:1:MET:HB3	76:SV:10:ASP:CG	2.40	0.46
3:L5:7:C:H2'	3:L5:8:U:C6	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:424:U:H2'	3:L5:425:U:C6	2.51	0.46
3:L5:1733:G:N3	3:L5:4214:A:H2'	2.31	0.46
3:L5:2018:C:H2'	3:L5:2019:C:H6	1.80	0.46
3:L5:2580:U:O2'	30:LZ:79:HIS:ND1	2.46	0.46
3:L5:2693:G:OP1	41:Lk:35:LYS:HE2	2.15	0.46
3:L5:4092:G:N7	3:L5:4114:C:N4	2.63	0.46
7:LB:322:HIS:O	7:LB:342:LYS:NZ	2.41	0.46
11:LF:39:GLN:OE1	11:LF:43:ARG:NH2	2.48	0.46
14:LI:177:ASN:HB2	14:LI:180:GLU:HG2	1.97	0.46
35:Le:3:ALA:HB1	35:Le:121:ARG:NH2	2.31	0.46
37:Lg:45:ALA:HB3	37:Lg:82:MET:HG2	1.97	0.46
48:Ls:68:HIS:O	48:Ls:71:ASN:ND2	2.47	0.46
50:SD:163:PRO:O	50:SD:167:TYR:HB2	2.15	0.46
58:ST:132:ASP:OD2	83:S2:1415:C:O2'	2.30	0.46
78:SX:34:THR:HG21	83:S2:1189:A:H4'	1.97	0.46
83:S2:1779:G:H2'	83:S2:1780:G:C8	2.50	0.46
3:L5:1503:A:H4'	3:L5:1504:G:H5'	1.97	0.46
3:L5:2521:G:H5'	3:L5:2640:G:H1'	1.97	0.46
3:L5:3856:A:H5''	20:LP:83:TRP:O	2.16	0.46
3:L5:4340:U:O2	89:L5:5262:SPD:N10	2.49	0.46
6:LA:180:LEU:HD21	46:Lp:22:LEU:HB3	1.96	0.46
6:LA:206:PRO:HG3	6:LA:213:GLY:HA3	1.96	0.46
7:LB:36:ASP:N	7:LB:36:ASP:OD1	2.49	0.46
17:LM:96:GLU:O	17:LM:100:ARG:HG2	2.15	0.46
19:LO:168:TYR:CE2	19:LO:172:LYS:HD2	2.49	0.46
50:SD:31:GLU:HA	50:SD:107:TYR:CE2	2.50	0.46
60:SZ:99:LEU:HD13	60:SZ:109:TYR:HE2	1.80	0.46
65:SA:55:TRP:HZ3	65:SA:177:MET:HE2	1.81	0.46
66:SB:99:ASN:OD1	66:SB:100:PHE:N	2.49	0.46
69:SG:56:ASN:HD21	83:S2:155:G:N2	2.10	0.46
70:SH:114:GLN:NE2	83:S2:874:G:H21	2.13	0.46
79:SY:41:ARG:HA	79:SY:55:ILE:HG21	1.97	0.46
80:Sa:13:LYS:HD3	80:Sa:13:LYS:HA	1.74	0.46
83:S2:49:C:H2'	83:S2:472:C:H41	1.80	0.46
86:CF:11:VAL:HG12	86:CF:90:ILE:HB	1.98	0.46
3:L5:475:G:H2'	3:L5:476:G:H8	1.80	0.46
3:L5:1677:PSU:H4'	3:L5:1680:G:C2	2.51	0.46
3:L5:2459:G:N2	3:L5:2462:C:OP2	2.43	0.46
3:L5:2637:U:O2'	3:L5:2718:U:O2'	2.29	0.46
3:L5:4069:U:H2'	3:L5:4070:U:H6	1.81	0.46
3:L5:4089:G:H2'	3:L5:4090:G:H8	1.81	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:4277:G:H5''	24:LT:17:ARG:HG2	1.98	0.46
3:L5:4475:G:O6	43:Lm:125:LYS:NZ	2.48	0.46
5:L8:70:G:H2'	29:LY:114:ASP:OD1	2.16	0.46
23:LS:27:LEU:HB3	24:LT:148:PRO:HB3	1.98	0.46
42:L1:26:TRP:HA	42:L1:29:MET:HE2	1.97	0.46
64:Sg:116:ASP:OD2	64:Sg:119:GLN:NE2	2.49	0.46
66:SB:90:ASP:OD1	66:SB:91:VAL:N	2.48	0.46
68:SE:126:VAL:HA	68:SE:141:THR:HA	1.98	0.46
68:SE:212:ASP:OD1	68:SE:216:ASN:N	2.49	0.46
2:Pt:72:C:H3'	2:Pt:73:A:H8	1.81	0.46
3:L5:137:G:H2'	3:L5:138:G:C8	2.50	0.46
3:L5:1281:G:N1	10:LE:128:HIS:HB2	2.31	0.46
3:L5:1500:A:H5''	3:L5:1501:C:H5''	1.98	0.46
3:L5:2386:U:H2'	3:L5:2387:G:H8	1.81	0.46
9:LD:181:PRO:HD2	9:LD:195:HIS:CD2	2.51	0.46
30:LZ:50:PRO:HD3	30:LZ:68:ILE:HG12	1.97	0.46
31:La:76:ASP:OD2	31:La:77:LYS:HG2	2.15	0.46
51:SF:166:ILE:HG13	83:S2:1599:U:C5	2.51	0.46
56:SR:128:PHE:CD2	56:SR:129:LYS:HG3	2.51	0.46
57:SS:8:LYS:NZ	57:SS:60:THR:HG22	2.31	0.46
57:SS:12:ILE:HG22	57:SS:21:ASP:HA	1.98	0.46
62:Sd:16:GLN:NE2	83:S2:1262:C:O2	2.45	0.46
63:Sf:105:TYR:HD2	63:Sf:118:ARG:HG3	1.79	0.46
65:SA:80:ARG:HH21	65:SA:126:ASP:HB2	1.80	0.46
69:SG:87:ARG:HD3	69:SG:87:ARG:HA	1.72	0.46
70:SH:73:GLN:HA	70:SH:76:GLN:HB2	1.97	0.46
70:SH:176:VAL:O	70:SH:180:LEU:HD23	2.15	0.46
74:SN:48:SER:OG	74:SN:86:GLU:OE2	2.34	0.46
79:SY:10:ARG:HA	83:S2:839:C:H41	1.81	0.46
79:SY:119:GLY:O	83:S2:84:A:O2'	2.33	0.46
83:S2:996:A:H2'	83:S2:997:A:C8	2.51	0.46
3:L5:287:U:H2'	3:L5:288:G:C8	2.51	0.46
3:L5:318:A:H2'	3:L5:319:A:C8	2.51	0.46
3:L5:1346:C:H2'	3:L5:1347:G:C8	2.50	0.46
3:L5:2856:C:O2	7:LB:242:ARG:NH2	2.38	0.46
3:L5:3861:A:H2'	3:L5:3862:A:H8	1.81	0.46
3:L5:3886:G:OP1	19:LO:85:ARG:NH2	2.49	0.46
3:L5:4077:A:N1	3:L5:4171:C:N4	2.60	0.46
3:L5:4896:G:H2'	3:L5:4897:G:C8	2.51	0.46
7:LB:161:ARG:HG2	7:LB:184:GLN:HA	1.98	0.46
10:LE:223:ARG:NH2	10:LE:236:GLU:O	2.49	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:La:36:GLY:HA3	31:La:40:HIS:CE1	2.51	0.46
41:Lk:8:ILE:HD13	41:Lk:45:LEU:HD21	1.98	0.46
63:Sf:124:ASP:OD1	63:Sf:124:ASP:N	2.45	0.46
64:Sg:26:GLN:HE21	64:Sg:75:GLY:HA3	1.80	0.46
68:SE:10:LYS:NZ	83:S2:95:G:OP1	2.36	0.46
69:SG:14:LYS:NZ	69:SG:16:ILE:HD11	2.31	0.46
71:SI:188:TYR:OH	71:SI:194:GLU:OE2	2.34	0.46
83:S2:656:G:H5'	83:S2:662:G:N2	2.31	0.46
83:S2:1221:G:H2'	83:S2:1222:G:H8	1.81	0.46
83:S2:1396:A:N7	83:S2:1449:G:O6	2.49	0.46
83:S2:1435:C:O2'	83:S2:1436:C:O4'	2.29	0.46
83:S2:1722:G:O6	83:S2:1812:U:O2	2.34	0.46
86:CF:395:LYS:HD3	86:CF:396:SER:H	1.81	0.46
3:L5:97:G:OP1	16:LL:16:LYS:NZ	2.40	0.46
3:L5:908:G:H2'	3:L5:909:A:H8	1.79	0.46
3:L5:2380:G:N2	3:L5:2424:OMG:H5''	2.31	0.46
3:L5:4578:G:H2'	3:L5:4579:PSU:H6	1.81	0.46
10:LE:190:HIS:HB3	10:LE:193:PHE:HD2	1.81	0.46
12:LG:167:VAL:HG12	12:LG:170:LEU:HD12	1.98	0.46
29:LY:22:PRO:HD2	29:LY:25:ILE:HD11	1.98	0.46
66:SB:145:LYS:HB2	66:SB:145:LYS:HE3	1.73	0.46
71:SI:80:ASP:OD2	71:SI:80:ASP:N	2.48	0.46
77:SW:3:ARG:HD3	77:SW:6:VAL:HG22	1.98	0.46
81:Sb:56:CYS:SG	81:Sb:63:LEU:HD21	2.56	0.46
82:Se:36:MET:HA	82:Se:39:ASN:HD21	1.81	0.46
85:AT:59:A:O2'	85:AT:61:A:OP2	2.32	0.46
3:L5:400:A2M:HM'3	3:L5:400:A2M:H1'	1.55	0.45
3:L5:1199:G:H2'	3:L5:1200:G:C8	2.51	0.45
3:L5:1558:A:H2'	3:L5:1559:G:C8	2.51	0.45
3:L5:4638:U:H2'	3:L5:4639:G:N3	2.32	0.45
3:L5:4750:G:H2'	3:L5:4751:G:H8	1.81	0.45
5:L8:144:U:H2'	5:L8:145:C:C6	2.50	0.45
20:LP:15:CYS:SG	20:LP:150:LEU:HB2	2.56	0.45
27:LW:4:GLU:HG2	27:LW:12:LYS:NZ	2.31	0.45
33:Lc:82:GLY:HA2	33:Lc:91:VAL:HG12	1.96	0.45
44:Ln:17:ARG:NH1	83:S2:1173:A:OP1	2.49	0.45
49:Lt:12:VAL:HG11	49:Lt:65:GLN:H	1.80	0.45
54:SP:135:ALA:HB2	83:S2:1235:G:H21	1.80	0.45
55:SQ:72:VAL:HG11	55:SQ:80:GLN:HG2	1.98	0.45
58:ST:82:ARG:NH1	83:S2:1654:G:OP1	2.49	0.45
69:SG:189:ARG:HA	69:SG:192:ILE:HG22	1.96	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:SO:149:ARG:NH2	83:S2:961:G:OP1	2.48	0.45
83:S2:1393:G:H2'	83:S2:1394:G:C8	2.50	0.45
85:AT:23:U:H2'	85:AT:24:C:C6	2.52	0.45
2:Pt:56:C:O4'	15:LJ:64:ARG:NE	2.45	0.45
3:L5:162:A:H2'	3:L5:163:A:C8	2.52	0.45
3:L5:257:C:H2'	3:L5:258:G:C8	2.51	0.45
3:L5:1194:G:H2'	3:L5:1195:G:H8	1.81	0.45
3:L5:1662:C:H2'	3:L5:1663:C:H6	1.81	0.45
3:L5:1700:G:H5''	3:L5:1704:C:H42	1.81	0.45
3:L5:2640:G:H2'	3:L5:2641:A:C8	2.52	0.45
7:LB:27:GLY:HA2	7:LB:276:HIS:CD2	2.51	0.45
18:LN:90:ASN:O	45:Lo:48:TYR:OH	2.30	0.45
52:SK:64:TRP:CD2	62:Sd:23:VAL:HG22	2.50	0.45
54:SP:24:GLN:O	54:SP:28:MET:HG2	2.15	0.45
55:SQ:76:GLY:O	83:S2:1544:C:O2'	2.34	0.45
56:SR:34:VAL:O	56:SR:38:ILE:HG12	2.16	0.45
60:SZ:99:LEU:HD11	60:SZ:102:LYS:HB2	1.98	0.45
69:SG:7:PHE:CE2	69:SG:9:ALA:HB3	2.51	0.45
69:SG:227:GLN:HB3	69:SG:231:ARG:HH21	1.81	0.45
71:SI:160:SER:HA	71:SI:163:GLU:HG2	1.98	0.45
83:S2:27:A2M:HM'3	83:S2:27:A2M:H1'	1.57	0.45
83:S2:159:A2M:O5'	83:S2:159:A2M:H8	2.17	0.45
83:S2:436:OMG:OP2	83:S2:471:G:O2'	2.28	0.45
83:S2:588:G:H4'	83:S2:589:G:H5'	1.98	0.45
83:S2:1231:C:O2'	83:S2:1253:A:N6	2.49	0.45
83:S2:1273:C:O2'	83:S2:1506:A:N1	2.47	0.45
84:Zt:15:G:N2	84:Zt:48:C:H42	2.14	0.45
84:Zt:27:U:H2'	84:Zt:28:C:C6	2.51	0.45
85:AT:22:A:H2'	85:AT:23:U:C6	2.51	0.45
3:L5:268:G:H2'	3:L5:269:G:C8	2.50	0.45
3:L5:1172:C:O2'	3:L5:1173:G:H8	2.00	0.45
3:L5:1326:A2M:OP2	3:L5:4445:U:O2'	2.29	0.45
3:L5:2029:A:H2'	3:L5:2030:A:C8	2.50	0.45
3:L5:2389:A:H4'	34:Ld:70:LYS:HG3	1.99	0.45
3:L5:4373:G:N7	45:Lo:61:LYS:NZ	2.56	0.45
13:LH:107:GLU:N	13:LH:107:GLU:OE1	2.49	0.45
20:LP:4:TYR:HE2	20:LP:147:GLU:HB2	1.81	0.45
33:Lc:36:LYS:O	33:Lc:40:GLN:HG2	2.16	0.45
47:Lr:28:GLU:HG2	47:Lr:31:ASN:HB2	1.98	0.45
51:SF:127:ARG:NH2	61:Sc:66:ARG:HH22	2.14	0.45
53:SM:91:LEU:HD23	53:SM:91:LEU:HA	1.84	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SP:79:HIS:HD2	83:S2:1298:G:C4	2.34	0.45
55:SQ:14:GLY:CA	55:SQ:86:GLN:HE22	2.25	0.45
66:SB:155:TYR:OH	83:S2:989:C:OP2	2.24	0.45
69:SG:64:LYS:HB2	69:SG:97:VAL:HG21	1.98	0.45
71:SI:54:LYS:NZ	83:S2:381:C:OP2	2.43	0.45
75:SO:101:GLY:HA3	75:SO:134:PRO:HD2	1.98	0.45
77:SW:30:CYS:SG	77:SW:31:SER:N	2.89	0.45
83:S2:1442:OMU:HM23	83:S2:1442:OMU:H1'	1.81	0.45
85:AT:9:A:O2'	85:AT:10:G:N7	2.46	0.45
85:AT:30:C:H2'	85:AT:31:G:C8	2.51	0.45
3:L5:71:C:H1'	16:LL:62:PRO:O	2.17	0.45
3:L5:1751:A:H2'	3:L5:1752:G:C8	2.52	0.45
3:L5:3841:OMC:HM23	3:L5:3841:OMC:H1'	1.79	0.45
5:L8:52:A:H4'	42:LI:19:GLN:HA	1.98	0.45
11:LF:182:TYR:HB3	11:LF:200:ARG:HG3	1.99	0.45
17:LM:130:LEU:HB3	19:LO:177:LEU:HD11	1.98	0.45
28:LX:64:SER:HG	38:Lh:82:ASP:CG	2.23	0.45
33:Lc:31:TYR:OH	33:Lc:59:GLU:OE2	2.31	0.45
55:SQ:31:LEU:HD12	55:SQ:33:LYS:HE2	1.98	0.45
58:ST:114:GLU:OE1	58:ST:114:GLU:N	2.49	0.45
70:SH:191:GLU:O	70:SH:193:GLN:NE2	2.36	0.45
83:S2:84:A:N3	83:S2:150:A:O2'	2.48	0.45
83:S2:433:A:H2'	83:S2:434:G:C8	2.51	0.45
83:S2:1179:G:N2	83:S2:1182:A:OP2	2.43	0.45
84:Zt:15:G:N1	84:Zt:48:C:N3	2.65	0.45
3:L5:10:A:H2'	3:L5:11:G:H8	1.80	0.45
3:L5:934:C:N4	8:LC:350:ARG:HH12	2.15	0.45
3:L5:1095:A:N1	3:L5:1200:G:C6	2.84	0.45
3:L5:1317:U:H2'	3:L5:1318:C:C6	2.51	0.45
3:L5:1340:OMC:HM23	3:L5:1340:OMC:H1'	1.73	0.45
3:L5:2764:A:H2'	3:L5:2765:A:C8	2.51	0.45
3:L5:3722:G:H2'	3:L5:3723:A:H8	1.81	0.45
3:L5:3807:A:O2'	83:S2:1816:G:O2'	2.31	0.45
3:L5:4728:U:OP1	7:LB:132:LYS:NZ	2.50	0.45
12:LG:83:PHE:HA	12:LG:183:ILE:HD13	1.98	0.45
21:LQ:154:LYS:NZ	21:LQ:159:PRO:O	2.42	0.45
49:Lt:22:VAL:HA	49:Lt:48:LYS:HG2	1.97	0.45
65:SA:53:ARG:O	65:SA:57:LYS:HG2	2.16	0.45
83:S2:368:U:H3'	83:S2:369:C:H2'	1.98	0.45
83:S2:629:A:O2'	83:S2:631:U:OP1	2.35	0.45
83:S2:907:G:H2'	83:S2:908:A:C8	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:Zt:51:G:H2'	84:Zt:52:G:C8	2.52	0.45
3:L5:4617:G:OP1	7:LB:62:ARG:NH1	2.41	0.45
3:L5:4642:U:H2'	3:L5:4643:G:H8	1.82	0.45
6:LA:181:LYS:HB2	6:LA:184:ARG:HG3	1.98	0.45
42:LI:33:ASN:ND2	42:LI:35:ILE:O	2.50	0.45
50:SD:222:PRO:HB3	64:Sg:190:GLY:HA3	1.98	0.45
64:Sg:201:SER:OG	64:Sg:203:ASP:OD1	2.32	0.45
67:SC:130:ILE:HG13	67:SC:162:ILE:HD11	1.98	0.45
79:SY:83:LYS:NZ	79:SY:96:LEU:HD11	2.32	0.45
83:S2:327:G:H5''	83:S2:328:U:C2	2.51	0.45
85:AT:18:G:H4'	85:AT:61:A:N1	2.31	0.45
86:CF:7:HIS:CE1	86:CF:306:ASP:HA	2.51	0.45
3:L5:158:A:H5''	3:L5:159:C:H2'	1.99	0.45
3:L5:475:G:H2'	3:L5:476:G:C8	2.52	0.45
3:L5:491:G:H2'	3:L5:492:U:H6	1.80	0.45
3:L5:1876:U:H2'	3:L5:1877:G:C8	2.52	0.45
3:L5:2436:U:H3'	28:LX:127:LEU:HD22	1.98	0.45
3:L5:3726:A:H2'	3:L5:3727:A:C8	2.51	0.45
3:L5:4089:G:H2'	3:L5:4090:G:C8	2.51	0.45
3:L5:4126:C:H5''	3:L5:4127:A:H5''	1.99	0.45
7:LB:84:MET:HE1	7:LB:166:THR:HG22	1.99	0.45
14:LI:14:ASN:O	14:LI:128:ARG:NH2	2.28	0.45
15:LJ:136:ARG:NH2	15:LJ:161:GLU:OE1	2.50	0.45
55:SQ:125:ARG:HB2	83:S2:1648:G:H5''	1.97	0.45
62:Sd:38:MET:HE3	62:Sd:43:PHE:HA	1.99	0.45
66:SB:133:TYR:CE2	66:SB:221:PRO:HD2	2.51	0.45
70:SH:127:ASP:O	70:SH:131:GLU:HG3	2.17	0.45
76:SV:17:CYS:HB2	76:SV:56:CYS:HB3	1.97	0.45
81:Sb:49:HIS:ND1	81:Sb:69:GLY:O	2.50	0.45
83:S2:808:A:H2	83:S2:855:G:H22	1.65	0.45
83:S2:1240:A:N3	83:S2:1267:C:O2'	2.43	0.45
83:S2:1446:A:O2'	83:S2:1447:G:H5''	2.17	0.45
86:CF:353:ILE:HG23	86:CF:357:TYR:CE1	2.52	0.45
3:L5:162:A:H2'	3:L5:163:A:H8	1.81	0.45
3:L5:4126:C:OP1	12:LG:37:LYS:NZ	2.50	0.45
3:L5:4392:OMG:HM21	3:L5:4394:A:H2'	1.98	0.45
3:L5:4507:A:H2'	3:L5:4508:C:C6	2.52	0.45
6:LA:48:ILE:HG22	46:Lp:54:ILE:HG12	1.99	0.45
10:LE:183:ARG:HA	10:LE:183:ARG:HD2	1.84	0.45
11:LF:241:ASN:O	11:LF:245:ARG:HG2	2.17	0.45
21:LQ:15:ARG:HB3	21:LQ:52:PHE:HB3	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LR:105:LEU:HD23	22:LR:138:LEU:HD23	1.97	0.45
25:LU:23:LEU:HD23	25:LU:110:TYR:HB2	1.99	0.45
35:Le:85:LEU:HD21	35:Le:115:ALA:HB2	1.98	0.45
36:Lf:45:LYS:HA	36:Lf:107:PRO:HD2	1.97	0.45
57:SS:137:LYS:NZ	83:S2:1236:G:O6	2.50	0.45
60:SZ:56:ASP:OD1	60:SZ:57:LYS:N	2.50	0.45
60:SZ:68:ILE:HB	60:SZ:109:TYR:HB2	1.98	0.45
74:SN:5:HIS:HB3	74:SN:117:LEU:HD13	1.99	0.45
79:SY:68:LYS:HB3	79:SY:68:LYS:HE2	1.80	0.45
83:S2:1736:G:H2'	83:S2:1737:G:H8	1.81	0.45
83:S2:1755:C:H2'	83:S2:1756:C:C6	2.52	0.45
3:L5:74:G:H1'	16:LL:62:PRO:HG3	1.98	0.45
3:L5:679:C:H2'	3:L5:680:G:H8	1.82	0.45
3:L5:1268:G:N7	32:Lb:111:ARG:NH2	2.60	0.45
3:L5:2492:C:H2'	3:L5:2493:G:H8	1.81	0.45
3:L5:3893:C:H2'	3:L5:3894:A:C8	2.52	0.45
3:L5:4571:A2M:H2'	3:L5:4572:U:H6	1.82	0.45
15:LJ:40:LEU:O	15:LJ:44:THR:HG22	2.17	0.45
19:LO:81:TRP:HB2	19:LO:104:VAL:HG21	1.99	0.45
20:LP:153:LYS:HE3	20:LP:153:LYS:HB3	1.79	0.45
64:Sg:168:CYS:HB2	64:Sg:195:LEU:HD13	1.98	0.45
64:Sg:239:LEU:HD11	64:Sg:248:LEU:HD21	1.99	0.45
72:SJ:152:ASP:OD2	72:SJ:153:SER:N	2.50	0.45
75:SO:75:MET:HG3	75:SO:118:ALA:HB2	1.99	0.45
78:SX:46:HIS:HB3	78:SX:101:LEU:HD21	1.99	0.45
81:Sb:62:VAL:HG23	81:Sb:74:THR:HG21	1.99	0.45
83:S2:1540:G:H2'	83:S2:1541:G:H8	1.82	0.45
3:L5:188:G:N2	3:L5:190:G:O6	2.50	0.45
3:L5:1327:C:H2'	3:L5:1328:G:C8	2.52	0.45
3:L5:2693:G:OP2	41:Lk:33:LYS:NZ	2.47	0.45
3:L5:4070:U:H2'	3:L5:4071:U:C6	2.52	0.45
3:L5:4389:C:H2'	3:L5:4390:A:H8	1.82	0.45
3:L5:4685:U:H2'	3:L5:4686:G:C8	2.52	0.45
3:L5:4688:C:H2'	3:L5:4689:PSU:C6	2.52	0.45
10:LE:47:ASN:HB2	10:LE:62:MET:HE2	1.98	0.45
12:LG:219:VAL:HG12	12:LG:223:ARG:HE	1.82	0.45
22:LR:170:ARG:HH12	83:S2:872:A:H5''	1.81	0.45
28:LX:79:PHE:CD2	38:Lh:36:VAL:HG11	2.52	0.45
32:Lb:5:LYS:HE2	32:Lb:8:THR:HB	1.98	0.45
34:Ld:50:ARG:HG2	34:Ld:54:MET:HE3	1.99	0.45
37:Lg:46:CYS:HB3	37:Lg:82:MET:HE3	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SF:127:ARG:H	51:SF:135:ARG:HD2	1.81	0.45
64:Sg:236:ILE:HD12	64:Sg:250:ALA:HB1	1.98	0.45
83:S2:16:G:H2'	83:S2:17:C:C6	2.51	0.45
83:S2:455:A:H2'	83:S2:456:C:C6	2.52	0.45
83:S2:1372:U:OP1	83:S2:1385:G:N2	2.38	0.45
84:Zt:4:C:H2'	84:Zt:5:G:C8	2.51	0.45
3:L5:1296:G:H2'	3:L5:1297:U:H6	1.82	0.44
3:L5:2111:G:N2	3:L5:2251:G:O2'	2.50	0.44
3:L5:2299:G:OP1	8:LC:182:LYS:NZ	2.45	0.44
3:L5:2777:G:H5''	3:L5:2778:G:H5'	1.98	0.44
3:L5:3708:C:H2'	3:L5:3709:U:C6	2.53	0.44
3:L5:3809:G:OP2	3:L5:3809:G:N2	2.33	0.44
3:L5:3932:U:H2'	3:L5:3933:G:C8	2.52	0.44
3:L5:4291:G:H4'	3:L5:4292:A:H5''	1.99	0.44
3:L5:4770:U:H2'	3:L5:4771:C:C6	2.52	0.44
7:LB:86:VAL:HG12	7:LB:201:LEU:HD23	1.98	0.44
13:LH:95:VAL:HG12	43:Lm:82:LEU:HD13	2.00	0.44
22:LR:172:ARG:HA	22:LR:175:GLU:OE1	2.16	0.44
35:Le:76:LYS:HD2	35:Le:98:GLU:OE2	2.17	0.44
48:Ls:13:TYR:HA	48:Ls:16:LYS:HG2	1.99	0.44
63:Sf:118:ARG:NH1	63:Sf:134:SER:HB2	2.33	0.44
64:Sg:14:HIS:CD2	64:Sg:35:SER:HB2	2.45	0.44
64:Sg:245:ARG:HG3	64:Sg:247:TRP:H	1.81	0.44
83:S2:674:C:H2'	83:S2:675:U:C6	2.52	0.44
83:S2:1562:C:H2'	83:S2:1563:G:C8	2.50	0.44
86:CF:108:GLN:HB2	86:CF:266:ARG:CD	2.46	0.44
3:L5:1194:G:H2'	3:L5:1195:G:C8	2.52	0.44
3:L5:1308:C:H2'	3:L5:1309:C:C6	2.51	0.44
3:L5:2394:G:O2'	3:L5:2819:U:O4	2.33	0.44
3:L5:2695:A:OP1	41:Lk:35:LYS:NZ	2.34	0.44
3:L5:3717:A:H2'	3:L5:3718:A2M:C8	2.46	0.44
3:L5:3717:A:OP2	3:L5:3735:G:N2	2.43	0.44
3:L5:4492:U:O2'	3:L5:4512:U:O2	2.27	0.44
8:LC:334:THR:HG22	8:LC:337:ARG:HH21	1.81	0.44
9:LD:152:ARG:O	9:LD:157:ASN:ND2	2.50	0.44
9:LD:179:ARG:HD3	9:LD:179:ARG:HA	1.71	0.44
57:SS:89:ASP:HB2	57:SS:93:GLY:N	2.31	0.44
57:SS:106:LYS:O	57:SS:109:GLU:HG3	2.17	0.44
63:Sf:95:ARG:HH12	83:S2:1291:A:H62	1.64	0.44
65:SA:55:TRP:CZ3	65:SA:177:MET:HE2	2.51	0.44
65:SA:220:LYS:HA	65:SA:220:LYS:HD3	1.86	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SE:73:ASP:OD2	68:SE:122:LYS:NZ	2.47	0.44
69:SG:174:PRO:HB3	83:S2:65:C:C6	2.52	0.44
71:SI:4:SER:OG	71:SI:6:ASP:OD2	2.23	0.44
83:S2:159:A2M:HM'3	83:S2:159:A2M:H1'	1.61	0.44
3:L5:173:C:H2'	3:L5:174:C:C6	2.53	0.44
3:L5:1100:U:O4	3:L5:1194:G:O6	2.36	0.44
3:L5:1177:U:O2'	9:LD:286:SER:OG	2.23	0.44
3:L5:2468:U:O2'	3:L5:2506:G:N2	2.50	0.44
3:L5:2570:U:H2'	3:L5:2571:C:C6	2.52	0.44
3:L5:2870:A:H2'	3:L5:2871:A:C8	2.52	0.44
7:LB:240:LEU:HB2	7:LB:248:LEU:HA	2.00	0.44
14:LI:101:LYS:NZ	14:LI:102:MET:O	2.49	0.44
20:LP:112:LEU:HD23	20:LP:150:LEU:HD13	1.99	0.44
25:LU:38:ASN:HB3	25:LU:90:TYR:OH	2.17	0.44
54:SP:37:TYR:HB3	54:SP:41:GLN:HB2	1.99	0.44
55:SQ:94:ALA:O	55:SQ:97:GLN:HB3	2.17	0.44
58:ST:108:GLU:HG3	58:ST:113:VAL:O	2.16	0.44
60:SZ:58:LEU:HD12	60:SZ:62:VAL:HG21	1.98	0.44
64:Sg:82:SER:OG	64:Sg:83:TRP:N	2.49	0.44
71:SI:42:ARG:HH21	71:SI:59:ARG:NH1	2.15	0.44
83:S2:835:C:H5'	83:S2:836:G:H5'	1.98	0.44
83:S2:1139:C:H2'	83:S2:1140:G:O4'	2.17	0.44
83:S2:1383:A2M:HM'3	83:S2:1383:A2M:H1'	1.72	0.44
1:CI:79:ARG:HH22	3:L5:2708:U:H1'	1.82	0.44
3:L5:121:A:H62	3:L5:152:U:H3	1.64	0.44
3:L5:455:C:O2'	3:L5:456:C:H5'	2.16	0.44
3:L5:1095:A:C2	3:L5:1200:G:N1	2.77	0.44
3:L5:1414:C:H2'	3:L5:1415:G:C8	2.49	0.44
3:L5:1563:A:H2'	3:L5:1564:A:C8	2.52	0.44
3:L5:2520:C:H2'	3:L5:2521:G:C8	2.53	0.44
3:L5:4069:U:H2'	3:L5:4070:U:C6	2.53	0.44
3:L5:4186:A:H2'	3:L5:4187:G:C8	2.52	0.44
3:L5:4318:C:H4'	45:Lo:17:LYS:HA	1.99	0.44
12:LG:217:LYS:O	12:LG:220:GLU:HG3	2.17	0.44
14:LI:36:LEU:HB2	14:LI:87:MET:HE3	1.99	0.44
21:LQ:35:LEU:O	21:LQ:39:THR:OG1	2.26	0.44
50:SD:1:MET:SD	50:SD:2:ALA:N	2.91	0.44
55:SQ:96:TYR:HA	55:SQ:100:VAL:HG12	1.99	0.44
56:SR:100:PRO:HA	56:SR:103:LYS:HB3	1.99	0.44
63:Sf:105:TYR:CD2	63:Sf:118:ARG:HG3	2.52	0.44
67:SC:66:LEU:HD11	67:SC:81:ILE:HG23	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:SO:40:THR:HG21	75:SO:74:ALA:HB2	1.98	0.44
83:S2:342:C:H2'	83:S2:343:A:H8	1.82	0.44
83:S2:484:A2M:H8	83:S2:484:A2M:O5'	2.16	0.44
83:S2:672:A:N6	83:S2:1027:A:OP1	2.40	0.44
83:S2:1713:C:H2'	83:S2:1714:U:C6	2.52	0.44
84:Zt:50:A:H2'	84:Zt:51:G:C8	2.52	0.44
86:CF:361:LEU:HD13	86:CF:370:CYS:HB2	1.99	0.44
3:L5:422:C:H2'	3:L5:423:G:H8	1.83	0.44
3:L5:1404:G:N7	3:L5:1408:G:N1	2.65	0.44
3:L5:2295:C:H2'	3:L5:2296:G:H8	1.81	0.44
3:L5:2891:U:H2'	3:L5:2892:C:O4'	2.18	0.44
3:L5:3720:G:H22	3:L5:3733:A:H2	1.65	0.44
3:L5:4076:G:OP1	12:LG:73:ARG:NE	2.31	0.44
3:L5:4759:C:H2'	3:L5:4760:G:C8	2.53	0.44
4:L7:64:G:OP1	14:LI:203:HIS:HB2	2.18	0.44
10:LE:99:ASP:OD1	10:LE:99:ASP:N	2.50	0.44
38:Lh:63:GLN:O	38:Lh:67:GLU:HG2	2.18	0.44
59:SU:85:HIS:ND1	83:S2:1447:G:OP1	2.48	0.44
77:SW:111:MET:HE1	77:SW:119:LYS:HD2	1.99	0.44
80:Sa:12:LYS:HG3	80:Sa:15:ARG:HB2	2.00	0.44
83:S2:349:A:H2'	83:S2:350:C:C6	2.52	0.44
83:S2:1653:U:H2'	83:S2:1654:G:C8	2.52	0.44
86:CF:96:ARG:HH22	86:CF:431:GLN:HG2	1.82	0.44
3:L5:1604:G:H2'	3:L5:1605:G:C8	2.52	0.44
3:L5:1847:C:H2'	3:L5:1848:C:C6	2.52	0.44
3:L5:1878:G:H2'	3:L5:1879:C:C6	2.53	0.44
3:L5:2610:G:H2'	3:L5:2611:A:C8	2.53	0.44
3:L5:2824:OMC:H1'	3:L5:2824:OMC:HM23	1.67	0.44
3:L5:4501:U:OP1	7:LB:5:LYS:NZ	2.50	0.44
3:L5:4578:G:H2'	3:L5:4579:PSU:C6	2.52	0.44
3:L5:4883:C:N4	10:LE:181:LEU:O	2.41	0.44
3:L5:5006:U:H4'	3:L5:5007:A:H5'	1.99	0.44
6:LA:173:GLY:O	46:Lp:69:TRP:NE1	2.49	0.44
13:LH:137:SER:HB3	13:LH:143:GLU:HB3	1.98	0.44
24:LT:39:ILE:HG13	24:LT:102:ARG:HE	1.82	0.44
51:SF:124:ASP:OD1	51:SF:125:SER:N	2.44	0.44
57:SS:8:LYS:HZ1	57:SS:60:THR:HG22	1.82	0.44
64:Sg:289:LEU:HD11	64:Sg:298:LEU:HD21	1.98	0.44
69:SG:2:LYS:HB2	69:SG:108:VAL:HG12	1.99	0.44
71:SI:36:THR:OG1	71:SI:57:ALA:O	2.33	0.44
72:SJ:88:ASP:OD1	72:SJ:89:GLU:N	2.50	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:SO:42:VAL:HG11	75:SO:78:ALA:HA	1.98	0.44
75:SO:120:ALA:HB2	80:Sa:53:ILE:HD13	2.00	0.44
83:S2:60:A:N3	83:S2:316:G:O2'	2.45	0.44
83:S2:835:C:H4'	83:S2:836:G:C8	2.53	0.44
83:S2:1217:A:H2'	83:S2:1218:C:H6	1.81	0.44
83:S2:1288:OMU:HN3	83:S2:1311:C:H42	1.64	0.44
83:S2:1337:4AC:O5'	83:S2:1337:4AC:H6	2.17	0.44
83:S2:1540:G:H2'	83:S2:1541:G:C8	2.53	0.44
3:L5:138:G:H2'	3:L5:139:G:C8	2.52	0.44
3:L5:1382:G:OP1	16:LL:66:TYR:OH	2.33	0.44
3:L5:2303:C:H5''	35:Le:104:SER:HB3	2.00	0.44
3:L5:2347:A:C4	35:Le:31:ILE:HD11	2.52	0.44
3:L5:3732:A:H2'	3:L5:3733:A:C8	2.51	0.44
3:L5:4196:OMG:H1'	3:L5:4196:OMG:HM23	1.75	0.44
3:L5:4742:G:OP1	3:L5:4900:C:N4	2.36	0.44
4:L7:55:A:H4'	15:LJ:155:HIS:HB2	1.99	0.44
6:LA:180:LEU:HD11	46:Lp:26:VAL:HG11	2.00	0.44
7:LB:217:ILE:HD12	7:LB:347:LEU:HB3	1.99	0.44
7:LB:219:VAL:HG11	7:LB:337:VAL:HG13	2.00	0.44
8:LC:268:ARG:HH12	8:LC:269:LYS:HE2	1.83	0.44
49:Lt:37:LEU:HA	49:Lt:40:LYS:HE3	2.00	0.44
61:Sc:14:VAL:HA	61:Sc:32:VAL:HA	1.99	0.44
64:Sg:89:LEU:HB3	64:Sg:99:ARG:HB3	2.00	0.44
65:SA:164:ASN:OD1	65:SA:165:ASN:N	2.51	0.44
66:SB:139:CYS:SG	66:SB:168:MET:HE2	2.58	0.44
76:SV:22:ARG:NH2	77:SW:19:LYS:O	2.51	0.44
77:SW:115:GLU:HB2	77:SW:118:ARG:NH2	2.33	0.44
83:S2:1189:A:H2'	83:S2:1190:A:H8	1.83	0.44
83:S2:1406:G:H2'	83:S2:1407:U:C6	2.53	0.44
83:S2:1447:G:H2'	83:S2:1448:A:C8	2.53	0.44
86:CF:114:LEU:HD23	86:CF:150:VAL:HG22	2.00	0.44
3:L5:106:A:H2'	3:L5:107:G:O4'	2.17	0.44
3:L5:374:G:OP2	40:Lj:56:ARG:NH1	2.42	0.44
3:L5:423:G:H2'	3:L5:424:U:C6	2.52	0.44
3:L5:921:C:H2'	3:L5:922:C:C6	2.53	0.44
3:L5:1751:A:H2'	3:L5:1752:G:H8	1.83	0.44
3:L5:1979:A:H1'	3:L5:1988:G:N2	2.33	0.44
3:L5:2045:G:O6	3:L5:3870:C:O2'	2.35	0.44
3:L5:4742:G:H2'	3:L5:4743:G:H8	1.83	0.44
4:L7:4:U:H2'	4:L7:5:A:H8	1.83	0.44
5:L8:130:C:H2'	5:L8:131:G:H8	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LD:152:ARG:HG3	9:LD:154:THR:HG23	2.00	0.44
18:LN:96:ARG:NH2	18:LN:100:SER:OG	2.43	0.44
22:LR:105:LEU:HD13	22:LR:135:LYS:HE3	1.99	0.44
27:LW:52:THR:O	27:LW:56:ARG:HG2	2.18	0.44
27:LW:74:ARG:NH1	69:SG:35:GLU:OE2	2.50	0.44
57:SS:30:ILE:O	57:SS:33:ILE:HG22	2.18	0.44
58:ST:22:LEU:HD11	58:ST:28:LEU:HD21	1.99	0.44
68:SE:122:LYS:N	68:SE:161:GLN:HE22	2.11	0.44
69:SG:170:ARG:HG3	83:S2:72:C:N3	2.32	0.44
73:SL:28:THR:HA	73:SL:29:GLY:HA2	1.70	0.44
83:S2:165:G:H2'	83:S2:166:A2M:H8	2.00	0.44
83:S2:885:U:O2	83:S2:901:G:O6	2.36	0.44
83:S2:1033:G:N2	83:S2:1080:A:HO2'	2.16	0.44
83:S2:1037:G:H4'	83:S2:1845:A:H4'	2.00	0.44
85:AT:5:C:H2'	85:AT:6:C:C6	2.52	0.44
3:L5:271:C:H2'	3:L5:272:U:C6	2.53	0.44
3:L5:1081:C:C2'	3:L5:1082:C:H5'	2.48	0.44
3:L5:1697:G:H22	3:L5:2084:C:P	2.41	0.44
3:L5:3785:A2M:H2	3:L5:4551:U:O2	2.17	0.44
11:LF:26:ALA:HA	11:LF:29:LYS:NZ	2.33	0.44
12:LG:209:SER:HA	12:LG:212:LYS:HG3	2.00	0.44
13:LH:113:GLU:OE1	13:LH:115:ARG:NH2	2.51	0.44
17:LM:100:ARG:HA	17:LM:103:LYS:HG2	2.00	0.44
17:LM:125:ASN:C	17:LM:125:ASN:HD22	2.26	0.44
34:Ld:36:VAL:HG21	34:Ld:44:ARG:HG2	1.98	0.44
36:Lf:41:PHE:HE1	36:Lf:110:ILE:HD13	1.83	0.44
39:Li:73:ILE:O	39:Li:77:VAL:HG22	2.18	0.44
57:SS:63:GLU:HA	57:SS:66:ARG:HG2	2.00	0.44
64:Sg:44:LYS:HG2	64:Sg:56:GLN:HB2	1.99	0.44
68:SE:63:LYS:O	68:SE:67:GLN:HG3	2.18	0.44
79:SY:42:GLU:HA	79:SY:52:PRO:HB3	1.98	0.44
83:S2:943:U:C2	83:S2:944:A:C8	3.06	0.44
83:S2:1275:G:N2	83:S2:1506:A:OP2	2.37	0.44
83:S2:1692:U:H2'	83:S2:1693:G:C8	2.52	0.44
84:Zt:4:C:H2'	84:Zt:5:G:H8	1.83	0.44
85:AT:60:A:H3'	85:AT:61:A:H8	1.83	0.44
86:CF:107:SER:HB3	86:CF:143:LEU:HD13	1.99	0.44
3:L5:461:G:H2'	3:L5:462:G:C8	2.53	0.43
3:L5:2751:G:H2'	3:L5:2752:G:H8	1.83	0.43
3:L5:4301:U:OP1	24:LT:78:LYS:NZ	2.50	0.43
3:L5:4524:G:N3	7:LB:252:ALA:HB1	2.33	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LI:88:ARG:HG2	14:LI:90:ARG:HD2	1.99	0.43
29:LY:42:TYR:CD1	29:LY:119:LEU:HD23	2.52	0.43
35:Le:92:ASN:ND2	35:Le:119:ALA:O	2.36	0.43
48:Ls:114:GLY:HA2	48:Ls:166:LYS:HD2	1.99	0.43
54:SP:21:ASP:O	54:SP:25:LEU:HD23	2.18	0.43
59:SU:28:ASN:O	59:SU:32:LEU:HD13	2.17	0.43
67:SC:81:ILE:HG21	67:SC:88:ILE:HD11	1.99	0.43
79:SY:19:GLN:HE21	79:SY:81:TYR:HB3	1.82	0.43
82:Se:8:ARG:NH1	83:S2:615:C:O3'	2.51	0.43
83:S2:1232:PSU:H2'	83:S2:1233:G:H8	1.83	0.43
3:L5:667:A:H5''	3:L5:668:C:H5''	1.99	0.43
3:L5:716:C:OP1	8:LC:317:ASN:HB2	2.18	0.43
3:L5:1628:C:OP2	6:LA:9:ARG:HD2	2.18	0.43
3:L5:2624:G:OP2	25:LU:97:ARG:NH2	2.51	0.43
3:L5:4353:PSU:H5'	3:L5:4354:U:H5'	1.99	0.43
6:LA:115:CYS:SG	6:LA:124:GLY:HA3	2.58	0.43
9:LD:146:LEU:HB2	9:LD:163:LEU:HD12	2.00	0.43
33:Lc:13:SER:O	33:Lc:17:ARG:HG3	2.18	0.43
63:Sf:103:LEU:HG	63:Sf:104:LYS:H	1.82	0.43
71:SI:141:ARG:NH2	83:S2:192:C:OP2	2.51	0.43
72:SJ:32:ILE:HG12	72:SJ:37:LEU:HB2	1.99	0.43
82:Se:36:MET:SD	82:Se:40:ARG:NH2	2.90	0.43
83:S2:432:G:H2'	83:S2:433:A:H8	1.82	0.43
83:S2:1047:C:H2'	83:S2:1048:G:O4'	2.18	0.43
83:S2:1797:U:H2'	83:S2:1798:C:C6	2.53	0.43
3:L5:280:G:OP2	18:LN:44:ARG:NH1	2.49	0.43
3:L5:2765:A:H2'	3:L5:2766:A:C8	2.53	0.43
3:L5:4742:G:H2'	3:L5:4743:G:C8	2.53	0.43
4:L7:119:U:C2	9:LD:261:VAL:HG21	2.53	0.43
14:LI:152:LEU:HB3	14:LI:165:ILE:HD12	1.99	0.43
27:LW:97:LYS:O	27:LW:99:GLU:N	2.49	0.43
54:SP:24:GLN:HB2	54:SP:28:MET:HE3	2.00	0.43
58:ST:39:LEU:HA	58:ST:39:LEU:HD23	1.71	0.43
58:ST:101:ARG:NH2	83:S2:1566:G:N7	2.65	0.43
66:SB:167:LYS:HB2	66:SB:167:LYS:HE2	1.84	0.43
68:SE:49:ARG:NH2	83:S2:496:C:OP1	2.49	0.43
69:SG:132:ARG:NH2	83:S2:152:U:O4'	2.48	0.43
73:SL:23:VAL:HG23	73:SL:25:LEU:HG	2.00	0.43
78:SX:85:VAL:HA	78:SX:86:PRO:HD3	1.86	0.43
79:SY:22:GLN:HB2	79:SY:74:MET:HE1	2.01	0.43
83:S2:26:U:H2'	83:S2:27:A2M:H8	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:S2:207:G:H3'	83:S2:208:G:C8	2.52	0.43
83:S2:352:U:H2'	83:S2:353:C:C6	2.54	0.43
83:S2:644:OMG:HM23	83:S2:644:OMG:H1'	1.76	0.43
83:S2:750:C:H42	83:S2:793:G:H1'	1.82	0.43
83:S2:804:U:H2'	83:S2:805:U:C6	2.54	0.43
83:S2:1360:U:O2'	83:S2:1379:A:OP2	2.31	0.43
83:S2:1407:U:H2'	83:S2:1408:U:H6	1.84	0.43
83:S2:1421:A:H5''	83:S2:1422:G:H2'	1.99	0.43
3:L5:965:G:N2	3:L5:2092:G:H1'	2.33	0.43
3:L5:1701:A:H5'	8:LC:304:ALA:HB3	2.00	0.43
3:L5:2102:G:H1'	3:L5:2103:G:C8	2.54	0.43
3:L5:2743:A:H2'	3:L5:2744:A:C8	2.54	0.43
3:L5:2903:G:H1'	3:L5:2904:U:H5	1.83	0.43
3:L5:4070:U:H2'	3:L5:4071:U:H6	1.83	0.43
3:L5:4536:OMC:HM22	3:L5:4537:C:O4'	2.18	0.43
3:L5:4965:U:H4'	3:L5:4966:A:H5'	2.01	0.43
5:L8:60:G:O6	5:L8:96:C:O2'	2.34	0.43
5:L8:75:OMG:HM23	5:L8:75:OMG:H1'	1.77	0.43
9:LD:33:ARG:O	9:LD:37:VAL:HG22	2.18	0.43
10:LE:115:TYR:HA	47:Lr:115:SER:OG	2.18	0.43
13:LH:51:LYS:HG3	13:LH:52:LYS:H	1.84	0.43
22:LR:82:LYS:HA	22:LR:82:LYS:HD2	1.87	0.43
34:Ld:25:TYR:CE1	34:Ld:88:LEU:HD12	2.52	0.43
51:SF:133:THR:HG22	51:SF:134:VAL:HG23	2.00	0.43
53:SM:75:ASN:OD1	53:SM:76:LEU:N	2.52	0.43
64:Sg:220:ASP:HB3	64:Sg:225:LYS:H	1.83	0.43
78:SX:17:ARG:HH22	83:S2:659:G:H21	1.65	0.43
83:S2:495:U:H2'	83:S2:496:C:O4'	2.18	0.43
83:S2:562:U:H2'	83:S2:563:G:C8	2.53	0.43
83:S2:1533:A:H62	83:S2:1602:U:H3	1.66	0.43
83:S2:1729:U:H3	83:S2:1805:G:H1	1.65	0.43
3:L5:717:U:H2'	3:L5:718:C:C6	2.53	0.43
3:L5:1392:A:H2'	3:L5:1393:G:C8	2.53	0.43
3:L5:1588:U:H2'	3:L5:1589:C:C6	2.54	0.43
3:L5:1613:A:H5''	6:LA:183:GLY:CA	2.49	0.43
3:L5:1999:A:H62	48:Ls:40:MET:HE2	1.83	0.43
3:L5:2756:G:O6	30:LZ:51:ARG:NH2	2.38	0.43
3:L5:3661:G:H4'	3:L5:3662:A:H5'	2.00	0.43
3:L5:3736:A:H2'	3:L5:3737:A:H8	1.84	0.43
3:L5:4093:G:H1	3:L5:4114:C:H2'	1.84	0.43
7:LB:17:LEU:HA	7:LB:17:LEU:HD23	1.81	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LD:41:LYS:NZ	24:LT:30:TYR:O	2.37	0.43
50:SD:16:ILE:HG21	62:Sd:22:ARG:CZ	2.48	0.43
60:SZ:86:ALA:HA	60:SZ:89:GLN:HE21	1.83	0.43
62:Sd:10:HIS:HB3	83:S2:1513:C:OP1	2.18	0.43
64:Sg:22:ALA:HB1	64:Sg:71:ILE:HG23	1.99	0.43
65:SA:32:PHE:CD1	83:S2:1097:G:H4'	2.54	0.43
66:SB:29:ASP:OD1	66:SB:29:ASP:N	2.51	0.43
66:SB:40:ASN:OD1	66:SB:41:ILE:HD12	2.19	0.43
71:SI:162:LEU:O	71:SI:166:PHE:HD1	2.01	0.43
73:SL:111:VAL:HG11	73:SL:128:VAL:HG11	2.00	0.43
80:Sa:11:ALA:HB3	80:Sa:33:ASP:HB2	2.00	0.43
83:S2:96:C:H2'	83:S2:97:U:C6	2.54	0.43
83:S2:835:C:H4'	83:S2:836:G:H8	1.84	0.43
83:S2:1417:C:O2	83:S2:1422:G:C6	2.71	0.43
83:S2:1428:G:N1	83:S2:1585:U:O4'	2.51	0.43
85:AT:2:U:H2'	85:AT:3:C:C6	2.53	0.43
3:L5:494:U:H2'	3:L5:495:C:C6	2.53	0.43
3:L5:2415:U:H2'	3:L5:2416:G:C8	2.53	0.43
3:L5:4476:C:O2'	3:L5:4478:G:OP2	2.23	0.43
3:L5:4478:G:O2'	3:L5:4602:A:N1	2.46	0.43
10:LE:222:LEU:HB2	10:LE:237:LYS:HD2	2.00	0.43
19:LO:140:ARG:O	19:LO:144:GLU:HG3	2.18	0.43
50:SD:39:VAL:HG12	50:SD:48:ILE:HG13	1.99	0.43
58:ST:10:ASN:HB3	58:ST:13:GLU:OE2	2.19	0.43
64:Sg:4:GLN:NE2	64:Sg:5:MET:O	2.52	0.43
67:SC:104:ASP:OD1	67:SC:105:GLU:N	2.51	0.43
68:SE:186:GLY:HA3	83:S2:809:A:OP1	2.19	0.43
69:SG:52:ILE:HA	69:SG:111:LEU:HD23	2.01	0.43
77:SW:28:ARG:HH22	83:S2:1093:A:H5''	1.82	0.43
78:SX:60:LYS:H	78:SX:114:ASP:HB2	1.84	0.43
83:S2:201:C:H3'	83:S2:202:G:H21	1.84	0.43
83:S2:441:C:H2'	83:S2:442:C:C6	2.53	0.43
83:S2:1550:G:O2'	83:S2:1558:C:O2	2.26	0.43
3:L5:426:A:H2'	3:L5:427:A:H8	1.82	0.43
3:L5:679:C:H2'	3:L5:680:G:C8	2.54	0.43
3:L5:1767:A:H2'	3:L5:1769:G:H5''	2.00	0.43
5:L8:26:C:O2'	8:LC:53:ALA:O	2.30	0.43
9:LD:108:ARG:CZ	9:LD:253:TYR:HB2	2.49	0.43
15:LJ:35:ARG:O	15:LJ:39:VAL:HG23	2.19	0.43
16:LL:110:LEU:O	16:LL:114:VAL:HG13	2.18	0.43
22:LR:25:ASP:HB3	22:LR:28:GLU:HB3	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lf:45:LYS:NZ	36:Lf:108:SER:HA	2.34	0.43
38:Lh:52:LYS:HD3	38:Lh:52:LYS:HA	1.79	0.43
49:Lt:12:VAL:HG11	49:Lt:65:GLN:N	2.34	0.43
49:Lt:18:THR:O	49:Lt:61:LYS:NZ	2.51	0.43
53:SM:128:PHE:HA	53:SM:131:LYS:HG2	2.01	0.43
63:Sf:143:LYS:NZ	83:S2:1310:U:O3'	2.49	0.43
82:Se:11:LYS:O	82:Se:15:GLN:HG3	2.19	0.43
83:S2:1533:A:H2	83:S2:1536:G:N3	2.17	0.43
84:Zt:67:U:H2'	84:Zt:68:C:C6	2.53	0.43
85:AT:12:G:H2'	85:AT:13:U:O4'	2.18	0.43
86:CF:218:ARG:HD3	86:CF:236:LEU:HD11	2.01	0.43
86:CF:428:ASP:HB3	86:CF:433:VAL:HG11	2.00	0.43
3:L5:495:C:H2'	3:L5:496:G:C8	2.53	0.43
3:L5:1345:A:H2'	3:L5:1346:C:C6	2.54	0.43
3:L5:1437:C:H1'	3:L5:2098:G:H3'	2.01	0.43
3:L5:1855:G:OP1	32:Lb:4:SER:HB2	2.19	0.43
3:L5:2422:OMC:HM23	3:L5:2422:OMC:H1'	1.88	0.43
3:L5:4153:C:H2'	3:L5:4154:G:C8	2.54	0.43
3:L5:4636:PSU:N1	34:Ld:79:ASN:OD1	2.51	0.43
3:L5:4935:C:H2'	3:L5:4936:G:C8	2.53	0.43
8:LC:266:THR:HG22	8:LC:267:TRP:H	1.83	0.43
13:LH:102:ASN:HB2	13:LH:115:ARG:HB2	2.01	0.43
27:LW:101:ARG:NH2	69:SG:145:PHE:O	2.44	0.43
37:Lg:33:LEU:HD23	37:Lg:33:LEU:HA	1.85	0.43
51:SF:76:MET:HE2	51:SF:155:CYS:SG	2.59	0.43
64:Sg:14:HIS:CE1	64:Sg:43:TRP:HZ2	2.36	0.43
68:SE:60:GLU:HB3	79:SY:18:LEU:HD21	2.01	0.43
71:SI:196:GLU:O	71:SI:200:ARG:HG2	2.19	0.43
79:SY:47:MET:HE3	79:SY:48:TYR:CZ	2.54	0.43
84:Zt:44:G:H3'	84:Zt:45:G:C8	2.54	0.43
85:AT:2:U:H3	85:AT:72:A:N6	2.09	0.43
3:L5:271:C:H2'	3:L5:272:U:H6	1.84	0.43
3:L5:674:G:H2'	3:L5:675:C:C6	2.54	0.43
3:L5:4080:C:H2'	3:L5:4081:G:H8	1.84	0.43
3:L5:5004:C:H2'	3:L5:5005:G:O4'	2.18	0.43
7:LB:28:LYS:HG3	7:LB:30:LYS:HG3	2.01	0.43
13:LH:4:ILE:HG12	13:LH:61:TRP:CH2	2.54	0.43
14:LI:28:ASP:OD1	14:LI:29:ALA:N	2.52	0.43
18:LN:46:ASP:OD2	18:LN:47:LYS:N	2.51	0.43
46:Lp:79:VAL:O	46:Lp:83:ILE:HG12	2.18	0.43
57:SS:38:ARG:HD2	58:ST:45:LEU:HD11	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:ST:42:HIS:NE2	58:ST:43:LYS:HE3	2.33	0.43
64:Sg:125:ARG:HD3	64:Sg:150:TRP:CE2	2.54	0.43
65:SA:177:MET:HE3	65:SA:181:GLU:HG2	2.00	0.43
68:SE:27:PHE:O	83:S2:495:U:O2'	2.37	0.43
68:SE:117:GLU:HA	68:SE:120:LYS:NZ	2.34	0.43
68:SE:161:GLN:NE2	68:SE:162:ILE:O	2.52	0.43
68:SE:253:ASP:OD1	68:SE:254:LYS:N	2.52	0.43
73:SL:3:ASP:OD1	73:SL:4:ILE:N	2.52	0.43
74:SN:31:ASP:O	74:SN:34:LYS:HB2	2.19	0.43
83:S2:15:U:H2'	83:S2:16:G:O4'	2.18	0.43
83:S2:106:C:OP1	83:S2:431:G:O2'	2.35	0.43
83:S2:496:C:H2'	83:S2:497:C:H6	1.84	0.43
83:S2:554:A:HO2'	83:S2:555:A:H8	1.66	0.43
83:S2:1232:PSU:H2'	83:S2:1233:G:C8	2.54	0.43
3:L5:1431:C:H2'	3:L5:1432:G:O4'	2.19	0.43
3:L5:1503:A:H62	21:LQ:87:THR:HG21	1.83	0.43
3:L5:1912:G:N2	19:LO:87:MET:HE2	2.34	0.43
3:L5:2260:C:OP1	10:LE:108:LYS:NZ	2.51	0.43
3:L5:2540:C:H2'	3:L5:2541:G:H8	1.83	0.43
3:L5:4725:C:OP1	7:LB:103:LYS:NZ	2.49	0.43
88:L5:5294:SPM:H31	88:L5:5294:SPM:H62	1.83	0.43
13:LH:41:ILE:HG22	13:LH:43:VAL:HG13	2.00	0.43
24:LT:122:LYS:NZ	24:LT:124:THR:HB	2.34	0.43
55:SQ:97:GLN:NE2	64:Sg:58:ALA:HB3	2.34	0.43
60:SZ:48:VAL:HG23	60:SZ:80:ARG:HD2	2.00	0.43
65:SA:184:ARG:HG2	65:SA:189:ILE:HB	2.00	0.43
66:SB:134:LEU:HG	66:SB:218:LEU:HD12	2.01	0.43
67:SC:183:LYS:HA	67:SC:195:LEU:O	2.19	0.43
67:SC:211:LYS:HE3	67:SC:211:LYS:HB2	1.88	0.43
69:SG:31:ARG:NH1	83:S2:1745:A:O3'	2.52	0.43
83:S2:115:U:H2'	83:S2:116:OMU:C6	2.49	0.43
84:Zt:72:C:C2	84:Zt:73:G:C8	3.07	0.43
86:CF:191:VAL:HG22	86:CF:214:TRP:CD1	2.54	0.43
3:L5:169:G:O6	3:L5:170:C:N4	2.52	0.42
3:L5:429:A:H2'	3:L5:430:G:C8	2.53	0.42
3:L5:1466:G:OP2	32:Lb:44:ARG:NH2	2.52	0.42
3:L5:1578:U:H2'	3:L5:1579:C:H6	1.83	0.42
3:L5:2041:A:N7	3:L5:4434:C:O2'	2.49	0.42
3:L5:3925:OMU:H1'	3:L5:3925:OMU:HM23	1.79	0.42
6:LA:225:ILE:HG12	6:LA:234:LYS:HA	2.01	0.42
7:LB:47:LEU:H	7:LB:84:MET:HE3	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LI:36:LEU:HD21	14:LI:69:ARG:NH1	2.34	0.42
23:LS:76:LYS:HD3	23:LS:131:GLU:HG3	2.01	0.42
28:LX:145:ASP:HB3	28:LX:148:ASP:OD1	2.19	0.42
40:Lj:67:LEU:HD23	40:Lj:67:LEU:HA	1.88	0.42
48:Ls:58:ASN:C	48:Ls:62:ARG:HE	2.26	0.42
49:Lt:82:ILE:HG12	49:Lt:137:GLN:HG2	2.01	0.42
51:SF:158:ALA:N	51:SF:176:GLU:OE1	2.52	0.42
64:Sg:107:ASP:C	64:Sg:124:SER:HG	2.24	0.42
64:Sg:208:ALA:HB2	64:Sg:218:LEU:HD13	2.01	0.42
68:SE:38:LEU:HD23	83:S2:346:C:H5''	2.01	0.42
76:SV:30:ALA:O	76:SV:60:ARG:HD3	2.18	0.42
82:Se:31:ARG:NH2	83:S2:525:A:O3'	2.53	0.42
83:S2:329:G:H2'	83:S2:330:G:H8	1.84	0.42
1:CI:66:GLY:HA3	34:Ld:70:LYS:HZ1	1.84	0.42
3:L5:161:G:H2'	3:L5:162:A:H8	1.83	0.42
3:L5:737:C:C5	3:L5:739:G:H5''	2.54	0.42
3:L5:1086:C:H2'	3:L5:1087:A:H8	1.83	0.42
3:L5:2611:A:H2'	3:L5:2612:G:C8	2.54	0.42
3:L5:3654:G:O2'	3:L5:3693:U:OP1	2.32	0.42
3:L5:3916:G:H2'	3:L5:3917:A:C8	2.54	0.42
3:L5:4184:G:H5'	6:LA:233:ARG:HB2	2.00	0.42
6:LA:47:ASP:OD1	6:LA:48:ILE:N	2.52	0.42
17:LM:13:ALA:HB1	17:LM:55:MET:HB3	2.02	0.42
19:LO:61:ARG:HA	19:LO:70:PRO:HD2	2.01	0.42
29:LY:54:GLU:HB2	29:LY:108:ARG:HB3	2.01	0.42
52:SK:42:ASN:HA	52:SK:45:VAL:HG12	2.01	0.42
53:SM:57:ASP:OD1	83:S2:1285:G:N1	2.50	0.42
56:SR:41:ILE:HD13	56:SR:47:ARG:HA	2.00	0.42
58:ST:56:ARG:O	58:ST:60:THR:HG23	2.19	0.42
58:ST:84:ARG:HH12	83:S2:1605:G:P	2.41	0.42
64:Sg:213:ASP:OD2	64:Sg:215:GLN:NE2	2.52	0.42
65:SA:137:ALA:HB1	65:SA:142:LEU:HB3	2.01	0.42
70:SH:83:LEU:HB3	70:SH:92:VAL:HG21	2.01	0.42
78:SX:128:VAL:HG23	78:SX:138:LYS:HD2	2.00	0.42
83:S2:389:A:H2'	83:S2:390:C:C6	2.54	0.42
83:S2:689:U:H2'	83:S2:690:G:C4	2.54	0.42
83:S2:1531:A:H2'	83:S2:1532:C:C6	2.54	0.42
83:S2:1832:6MZ:H5'2	83:S2:1840:U:H5''	2.01	0.42
3:L5:35:U:H4'	3:L5:1525:A:C2	2.54	0.42
3:L5:123:C:H2'	3:L5:124:C:H6	1.84	0.42
3:L5:288:G:H2'	3:L5:289:C:C6	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:1514:U:H2'	3:L5:1515:A:C8	2.54	0.42
3:L5:2079:G:H2'	3:L5:2080:U:H6	1.84	0.42
3:L5:4111:U:H2'	3:L5:4112:C:H5	1.84	0.42
3:L5:4680:G:H2'	3:L5:4681:A:C8	2.55	0.42
7:LB:154:LYS:HE2	7:LB:154:LYS:HB2	1.73	0.42
10:LE:157:HIS:HA	10:LE:160:LYS:HE3	2.00	0.42
10:LE:223:ARG:HA	10:LE:224:LYS:HA	1.78	0.42
18:LN:146:PRO:HG3	38:Lh:102:LEU:HD12	2.01	0.42
19:LO:124:LEU:HD23	19:LO:124:LEU:HA	1.88	0.42
28:LX:80:PRO:HA	28:LX:98:PHE:HA	2.00	0.42
37:Lg:60:ARG:HD2	37:Lg:60:ARG:HA	1.80	0.42
38:Lh:95:LEU:HD22	38:Lh:99:GLU:HG3	2.00	0.42
46:Lp:46:LYS:HE3	46:Lp:46:LYS:HB3	1.62	0.42
50:SD:138:VAL:HG12	50:SD:142:LEU:HD11	2.02	0.42
83:S2:28:U:H2'	83:S2:29:G:C8	2.52	0.42
83:S2:945:U:H2'	83:S2:946:U:C6	2.54	0.42
83:S2:1844:U:H2'	83:S2:1845:A:C8	2.54	0.42
85:AT:23:U:H2'	85:AT:24:C:H6	1.83	0.42
85:AT:60:A:C2	85:AT:61:A:H1'	2.54	0.42
3:L5:260:C:H2'	3:L5:261:G:C8	2.54	0.42
3:L5:270:U:H2'	3:L5:271:C:C6	2.54	0.42
3:L5:3824:A:H3'	3:L5:3825:A2M:H8	2.01	0.42
3:L5:4523:A2M:H1'	3:L5:4558:U:C4	2.55	0.42
3:L5:4619:U:H2'	3:L5:4620:OMU:H6	2.00	0.42
89:L5:5285:SPD:H82	89:L5:5285:SPD:H51	1.84	0.42
9:LD:245:ALA:O	9:LD:248:ARG:N	2.53	0.42
10:LE:45:SER:C	10:LE:47:ASN:H	2.28	0.42
11:LF:148:LYS:O	11:LF:152:GLU:HG2	2.20	0.42
11:LF:173:ALA:O	11:LF:177:ARG:HG2	2.19	0.42
14:LI:180:GLU:O	14:LI:184:MET:HE2	2.19	0.42
18:LN:96:ARG:HH12	18:LN:104:GLU:CD	2.27	0.42
23:LS:15:ARG:HD2	23:LS:25:PRO:HG2	2.00	0.42
30:LZ:135:ARG:HD2	30:LZ:135:ARG:HA	1.85	0.42
32:Lb:60:ASN:HA	32:Lb:63:LYS:HG2	2.02	0.42
38:Lh:88:THR:HB	38:Lh:91:MET:HB2	2.01	0.42
47:Lr:49:VAL:HG12	47:Lr:64:ILE:HG22	2.01	0.42
54:SP:103:ASN:HD21	54:SP:120:SER:HA	1.84	0.42
58:ST:44:GLU:HG3	58:ST:45:LEU:HD12	2.01	0.42
64:Sg:207:CYS:SG	64:Sg:219:TRP:HB2	2.60	0.42
68:SE:87:MET:HE2	68:SE:100:ARG:HH11	1.85	0.42
69:SG:85:ARG:O	69:SG:87:ARG:NH1	2.53	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:S2:494:C:N4	83:S2:509:OMG:HN22	2.18	0.42
83:S2:1227:G:C2	83:S2:1228:A:C8	3.07	0.42
83:S2:1804:U:H2'	83:S2:1805:G:C8	2.54	0.42
85:AT:15:G:N2	85:AT:49:C:C2	2.84	0.42
86:CF:26:HIS:CE1	86:CF:30:LYS:HZ1	2.37	0.42
86:CF:111:CYS:SG	86:CF:112:ALA:N	2.93	0.42
3:L5:918:G:H5'	17:LM:72:TYR:CZ	2.54	0.42
3:L5:1088:C:O2	11:LF:74:MET:HE1	2.19	0.42
3:L5:2110:C:N4	3:L5:2111:G:O6	2.53	0.42
3:L5:2376:A:H2'	3:L5:2377:C:C6	2.55	0.42
3:L5:3595:U:H5''	3:L5:3597:G:OP2	2.19	0.42
3:L5:4458:C:H2'	3:L5:4459:U:C6	2.54	0.42
3:L5:4919:G:H2'	3:L5:4920:C:H6	1.84	0.42
4:L7:26:C:O2'	15:LJ:147:ARG:NH1	2.52	0.42
7:LB:261:ARG:HB2	19:LO:64:THR:HG21	2.00	0.42
21:LQ:110:ARG:HG3	21:LQ:120:ILE:HD12	2.00	0.42
22:LR:21:LYS:HE3	22:LR:55:VAL:HA	2.01	0.42
25:LU:28:PRO:HG3	25:LU:112:LEU:HD11	2.02	0.42
25:LU:54:GLY:O	25:LU:56:LEU:N	2.52	0.42
26:LV:106:VAL:HG12	26:LV:112:MET:HG2	2.02	0.42
48:Ls:53:VAL:HA	48:Ls:89:VAL:HA	2.02	0.42
51:SF:51:HIS:O	55:SQ:50:LYS:NZ	2.45	0.42
51:SF:187:SER:OG	51:SF:190:ILE:HG12	2.19	0.42
68:SE:192:ILE:HG12	68:SE:243:GLY:HA3	2.00	0.42
70:SH:30:LEU:O	70:SH:33:ASN:ND2	2.53	0.42
73:SL:49:GLU:OE1	73:SL:116:CYS:HA	2.19	0.42
78:SX:17:ARG:HH12	83:S2:659:G:N2	2.17	0.42
78:SX:129:SER:HB2	83:S2:29:G:H4'	2.02	0.42
83:S2:66:G:H2'	83:S2:67:C:H4'	2.01	0.42
83:S2:649:PSU:H2'	83:S2:650:A:C8	2.54	0.42
83:S2:1347:U:H2'	83:S2:1348:G:N3	2.34	0.42
1:CI:75:LYS:H	25:LU:117:ILE:C	2.28	0.42
3:L5:989:U:O2	3:L5:1064:G:N2	2.43	0.42
3:L5:1350:C:H2'	3:L5:1351:G:C8	2.54	0.42
3:L5:1825:A:H2'	3:L5:1826:G:C8	2.55	0.42
3:L5:2351:OMC:HM23	3:L5:2351:OMC:H1'	1.69	0.42
3:L5:2664:G:H4'	3:L5:2677:G:H4'	2.01	0.42
3:L5:3599:A:H2'	3:L5:3600:G:C8	2.54	0.42
3:L5:3861:A:H2'	3:L5:3862:A:C8	2.54	0.42
3:L5:4113:U:H4'	3:L5:4115:G:C5	2.54	0.42
3:L5:4237:C:H2'	3:L5:4238:G:H8	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:5002:U:H2'	3:L5:5003:U:C6	2.55	0.42
4:L7:82:G:H2'	4:L7:83:A:C8	2.54	0.42
12:LG:157:ILE:HA	12:LG:201:THR:HG22	2.01	0.42
14:LI:83:ASP:OD2	14:LI:83:ASP:N	2.52	0.42
22:LR:80:LYS:HA	22:LR:80:LYS:HD2	1.86	0.42
26:LV:37:LEU:HD23	26:LV:65:VAL:HG12	2.01	0.42
44:Ln:16:LYS:HA	44:Ln:16:LYS:HD2	1.82	0.42
52:SK:61:GLN:O	52:SK:68:TYR:HB2	2.19	0.42
53:SM:95:ASP:HB3	53:SM:99:LYS:HB3	2.00	0.42
57:SS:102:GLY:HA2	57:SS:105:ASN:HD21	1.84	0.42
64:Sg:101:PHE:CE2	64:Sg:136:GLY:HA2	2.54	0.42
64:Sg:135:LEU:HD23	64:Sg:135:LEU:HA	1.89	0.42
65:SA:185:MET:O	76:SV:45:ARG:HD3	2.19	0.42
68:SE:101:LEU:HD12	68:SE:101:LEU:HA	1.91	0.42
68:SE:242:LYS:HD3	68:SE:242:LYS:HA	1.75	0.42
71:SI:106:SER:HB3	71:SI:171:LEU:HG	2.02	0.42
71:SI:192:GLY:O	71:SI:196:GLU:HG3	2.20	0.42
72:SJ:67:ASP:HB3	72:SJ:70:ARG:HB3	2.02	0.42
83:S2:51:U:H2'	83:S2:52:G:C8	2.54	0.42
83:S2:671:A:H4'	83:S2:672:A:H5''	2.01	0.42
83:S2:1839:U:H2'	83:S2:1840:U:C6	2.54	0.42
85:AT:4:U:H2'	85:AT:5:C:H6	1.85	0.42
86:CF:268:GLU:OE2	86:CF:421:LEU:HG	2.20	0.42
3:L5:1899:G:O2'	35:Le:57:ASN:OD1	2.35	0.42
3:L5:2580:U:OP1	30:LZ:36:ARG:NH1	2.39	0.42
3:L5:3866:C:H2'	3:L5:3867:A2M:O4'	2.20	0.42
3:L5:4457:PSU:H1'	7:LB:252:ALA:HB3	2.02	0.42
3:L5:4535:A:H2'	3:L5:4536:OMC:H6	1.85	0.42
3:L5:4611:A:H2'	3:L5:4612:C:H6	1.85	0.42
3:L5:4966:A:H5''	7:LB:128:LYS:HG3	2.01	0.42
8:LC:144:ILE:HG13	8:LC:144:ILE:O	2.20	0.42
27:LW:56:ARG:HE	27:LW:61:LYS:HB2	1.83	0.42
52:SK:43:LEU:HD11	83:S2:1274:G:C5	2.54	0.42
55:SQ:82:TYR:O	55:SQ:86:GLN:HG3	2.20	0.42
60:SZ:62:VAL:HA	60:SZ:65:TYR:HE1	1.84	0.42
63:Sf:97:LYS:HE2	83:S2:1289:U:C5	2.55	0.42
64:Sg:213:ASP:OD1	64:Sg:213:ASP:N	2.52	0.42
79:SY:9:THR:HG23	83:S2:839:C:H5	1.84	0.42
83:S2:440:G:OP1	83:S2:1798:C:O2'	2.37	0.42
85:AT:20:U:O2'	85:AT:22:A:OP1	2.37	0.42
2:Pt:23:C:H2'	2:Pt:24:A:C8	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:1846:G:H2'	3:L5:1847:C:H6	1.84	0.42
3:L5:2676:A:OP2	3:L5:2676:A:H8	2.03	0.42
3:L5:2844:A:O2'	3:L5:4631:G:H4'	2.20	0.42
3:L5:3718:A2M:H2'	3:L5:3719:A:O4'	2.20	0.42
3:L5:4324:A:H2'	3:L5:4325:A:C8	2.55	0.42
3:L5:4964:C:H2'	3:L5:4965:U:C6	2.54	0.42
7:LB:220:ILE:HG12	7:LB:278:THR:HG23	2.01	0.42
8:LC:54:VAL:HG21	8:LC:101:MET:HE3	2.02	0.42
8:LC:150:LEU:O	8:LC:152:LEU:N	2.53	0.42
10:LE:258:LEU:O	10:LE:262:LYS:HG2	2.20	0.42
19:LO:178:ARG:HG2	19:LO:178:ARG:HH11	1.84	0.42
20:LP:61:ARG:HA	20:LP:78:TRP:CZ2	2.55	0.42
22:LR:105:LEU:HD22	22:LR:135:LYS:HG3	2.01	0.42
27:LW:99:GLU:HB3	27:LW:102:LYS:HE3	2.00	0.42
34:Ld:59:THR:OG1	34:Ld:104:THR:OG1	2.33	0.42
35:Le:78:LEU:HD12	35:Le:98:GLU:HB2	2.02	0.42
39:Li:76:ARG:HD3	39:Li:76:ARG:HA	1.76	0.42
56:SR:60:ARG:HA	56:SR:63:ARG:HG2	2.01	0.42
68:SE:149:TYR:CD2	69:SG:205:GLU:HB3	2.55	0.42
76:SV:11:LEU:HD12	76:SV:12:TYR:CD1	2.54	0.42
78:SX:28:LYS:NZ	83:S2:1189:A:OP1	2.40	0.42
83:S2:35:C:H5''	83:S2:579:C:H5''	2.01	0.42
83:S2:964:A:H2'	83:S2:965:U:H6	1.84	0.42
83:S2:1628:C:H2'	83:S2:1629:C:C6	2.54	0.42
83:S2:1667:U:H2'	83:S2:1668:U:C6	2.54	0.42
85:AT:18:G:H4'	85:AT:61:A:C6	2.55	0.42
1:CI:63:ARG:HD2	1:CI:63:ARG:HA	1.85	0.42
3:L5:444:G:H2'	3:L5:445:U:H6	1.84	0.42
3:L5:1538:U:H2'	3:L5:1539:G:H8	1.84	0.42
3:L5:2465:C:H2'	3:L5:2466:G:O4'	2.20	0.42
3:L5:2652:G:N1	46:Lp:58:GLY:O	2.41	0.42
3:L5:3760:A:N7	85:AT:39:C:H5''	2.35	0.42
3:L5:4913:G:H4'	3:L5:4914:C:O5'	2.19	0.42
3:L5:4981:G:O6	7:LB:21:ARG:NH2	2.53	0.42
7:LB:47:LEU:HB2	7:LB:84:MET:HE1	2.01	0.42
13:LH:92:MET:HE2	13:LH:179:ILE:HG22	2.01	0.42
24:LT:44:GLY:HA2	24:LT:95:HIS:HB3	2.01	0.42
55:SQ:141:TYR:OH	83:S2:1668:U:OP2	2.25	0.42
63:Sf:119:ARG:HG3	63:Sf:132:MET:HE3	2.02	0.42
64:Sg:10:THR:HB	64:Sg:306:LEU:HD21	2.02	0.42
86:CF:20:LYS:HD2	86:CF:92:ALA:HB3	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:CF:195:GLY:HA2	86:CF:201:MET:HE3	2.01	0.42
3:L5:323:C:H2'	3:L5:324:A:H8	1.85	0.42
3:L5:408:A:O2'	3:L5:411:G:OP2	2.24	0.42
3:L5:1178:G:H2'	9:LD:286:SER:HB3	2.01	0.42
3:L5:1248:C:H2'	3:L5:1249:C:C6	2.55	0.42
3:L5:1359:G:H4'	18:LN:203:TYR:HB2	2.02	0.42
3:L5:1655:C:OP2	31:La:26:ARG:NH1	2.53	0.42
3:L5:2632:PSU:H2'	3:L5:2633:U:C6	2.54	0.42
3:L5:4192:A:H2'	3:L5:4193:C:H6	1.85	0.42
3:L5:4592:C:H2'	3:L5:4593:C:C6	2.54	0.42
3:L5:4600:G:H4'	3:L5:4601:U:O5'	2.19	0.42
3:L5:4946:U:O2'	36:Lf:2:SER:N	2.38	0.42
9:LD:205:ALA:O	9:LD:209:ARG:HG2	2.19	0.42
16:LL:18:TRP:CD1	16:LL:18:TRP:H	2.38	0.42
48:Ls:77:LYS:HE2	48:Ls:193:PHE:HE1	1.83	0.42
52:SK:91:PRO:HB2	52:SK:94:LEU:HD23	2.02	0.42
67:SC:202:THR:HG23	72:SJ:54:ARG:HH22	1.84	0.42
67:SC:212:LYS:HE2	67:SC:212:LYS:HB3	1.87	0.42
71:SI:141:ARG:HA	71:SI:141:ARG:CZ	2.50	0.42
73:SL:82:MET:SD	83:S2:395:G:H5'	2.60	0.42
77:SW:26:LEU:HB2	81:Sb:7:LEU:HD13	2.01	0.42
77:SW:57:ARG:HD2	83:S2:919:A:H4'	2.02	0.42
77:SW:125:ILE:HD12	77:SW:125:ILE:HA	1.87	0.42
83:S2:1208:A:H2'	83:S2:1209:A:C8	2.55	0.42
83:S2:1558:C:H2'	83:S2:1559:C:C6	2.55	0.42
3:L5:1364:U:OP2	16:LL:36:ARG:NH2	2.32	0.41
3:L5:1683:PSU:H2'	3:L5:1684:A:H8	1.85	0.41
3:L5:1725:U:H2'	3:L5:1726:U:C6	2.55	0.41
3:L5:2292:C:H2'	3:L5:2293:U:C6	2.55	0.41
3:L5:2709:C:H5''	22:LR:43:LYS:HD2	2.02	0.41
3:L5:3641:U:H5	3:L5:3646:A:N7	2.17	0.41
3:L5:4232:U:H5''	45:Lo:3:ASN:O	2.20	0.41
3:L5:4305:G:C6	24:LT:80:VAL:HG21	2.55	0.41
3:L5:4415:A:H4'	14:LI:74:LYS:HD3	2.01	0.41
3:L5:4642:U:H2'	3:L5:4643:G:C8	2.55	0.41
4:L7:15:C:H2'	4:L7:16:A:C8	2.54	0.41
10:LE:250:GLN:HE21	10:LE:254:ASP:CG	2.28	0.41
11:LF:57:TYR:OH	11:LF:189:ASP:OD1	2.29	0.41
54:SP:47:ARG:HE	83:S2:1619:A:P	2.43	0.41
56:SR:99:ASP:OD1	65:SA:42:LYS:HE3	2.20	0.41
58:ST:84:ARG:NH1	83:S2:1605:G:OP1	2.45	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:Sc:13:ARG:O	61:Sc:33:GLU:N	2.34	0.41
69:SG:38:ALA:N	69:SG:48:TYR:O	2.49	0.41
70:SH:113:LYS:HA	70:SH:113:LYS:HD2	1.67	0.41
79:SY:60:PHE:O	83:S2:571:U:O2'	2.30	0.41
83:S2:386:C:H2'	83:S2:387:C:C6	2.55	0.41
83:S2:747:U:C2	83:S2:796:G:N1	2.88	0.41
83:S2:952:G:H2'	83:S2:953:C:C6	2.54	0.41
83:S2:1242:U:O2	83:S2:1517:G:O2'	2.31	0.41
86:CF:43:GLU:HG3	86:CF:55:LYS:HD3	2.02	0.41
3:L5:318:A:H2'	3:L5:319:A:H8	1.84	0.41
3:L5:1857:C:H2'	3:L5:1858:A:C8	2.55	0.41
3:L5:1995:G:H2'	3:L5:1996:C:C6	2.55	0.41
3:L5:2475:G:N1	28:LX:51:THR:O	2.39	0.41
3:L5:2521:G:H2'	3:L5:2522:G:H8	1.85	0.41
3:L5:2694:G:H5'	3:L5:2695:A:C2	2.55	0.41
3:L5:2863:G:O2'	22:LR:82:LYS:O	2.33	0.41
3:L5:3664:G:H2'	3:L5:3665:G:C8	2.53	0.41
3:L5:4927:G:H5''	3:L5:4928:C:C5	2.55	0.41
5:L8:5:U:H2'	5:L8:6:C:H6	1.85	0.41
6:LA:28:ARG:HD2	6:LA:123:ARG:HG3	2.02	0.41
6:LA:75:LEU:HD12	6:LA:75:LEU:HA	1.92	0.41
6:LA:130:SER:HB2	6:LA:171:GLY:HA3	2.01	0.41
22:LR:19:LYS:HB2	22:LR:19:LYS:HE2	1.86	0.41
30:LZ:41:ALA:HB2	30:LZ:77:TYR:HE1	1.85	0.41
41:Lk:60:LEU:HD23	41:Lk:60:LEU:HA	1.92	0.41
55:SQ:69:ARG:HH21	83:S2:1426:U:P	2.43	0.41
63:Sf:108:VAL:HB	63:Sf:113:LYS:H	1.85	0.41
69:SG:92:ARG:NH1	83:S2:1738:C:OP1	2.39	0.41
71:SI:165:GLN:OE1	71:SI:172:LEU:HD23	2.20	0.41
83:S2:1134:G:H2'	83:S2:1135:C:C6	2.55	0.41
83:S2:1183:A:H2'	83:S2:1184:G:H8	1.85	0.41
83:S2:1203:G:H2'	83:S2:1204:A:H8	1.85	0.41
83:S2:1204:A:O2'	83:S2:1700:C:OP2	2.34	0.41
85:AT:6:C:H2'	85:AT:7:G:C8	2.55	0.41
3:L5:178:C:N4	3:L5:179:G:O6	2.53	0.41
3:L5:1278:C:H2'	3:L5:1279:A:O4'	2.20	0.41
3:L5:1305:C:OP1	5:L8:7:U:O2'	2.39	0.41
3:L5:2652:G:N2	46:Lp:59:SER:O	2.51	0.41
3:L5:3871:A:H2'	3:L5:3872:A:C8	2.55	0.41
3:L5:4392:OMG:N3	3:L5:4447:5MC:HM52	2.35	0.41
16:LL:184:MET:HE2	16:LL:184:MET:HB3	1.90	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LP:4:TYR:CE2	20:LP:147:GLU:HB2	2.55	0.41
48:Ls:28:PHE:HZ	48:Ls:95:LEU:HA	1.85	0.41
67:SC:254:ASP:HB2	76:SV:1:MET:SD	2.60	0.41
70:SH:58:LYS:HA	70:SH:58:LYS:HD2	1.82	0.41
74:SN:93:LYS:HA	74:SN:150:VAL:HG21	2.02	0.41
78:SX:105:PHE:CE2	78:SX:112:VAL:HB	2.55	0.41
81:Sb:64:CYS:HB2	81:Sb:71:ALA:HB1	2.02	0.41
83:S2:517:OMC:H2'	83:S2:518:G:O4'	2.21	0.41
83:S2:652:U:H2'	83:S2:653:A:C8	2.55	0.41
83:S2:1617:G:N1	83:S2:1620:A:OP2	2.53	0.41
83:S2:1673:U:H2'	83:S2:1674:G:O4'	2.21	0.41
83:S2:1681:U:H2'	83:S2:1682:C:C6	2.55	0.41
86:CF:320:VAL:HG13	86:CF:324:ASN:HD22	1.85	0.41
3:L5:1097:C:H2'	3:L5:1098:G:C8	2.55	0.41
3:L5:1214:C:N3	32:Lb:90:SER:OG	2.53	0.41
3:L5:2090:U:H4'	3:L5:2091:C:H3'	2.01	0.41
3:L5:3896:C:H1'	7:LB:268:ARG:NH2	2.35	0.41
5:L8:153:C:H2'	5:L8:154:G:H8	1.86	0.41
8:LC:138:MET:HE1	8:LC:145:GLU:OE2	2.20	0.41
13:LH:24:THR:HA	13:LH:37:ASP:HA	2.02	0.41
28:LX:112:ALA:O	28:LX:116:LEU:HG	2.20	0.41
30:LZ:95:VAL:HG12	30:LZ:110:ALA:HA	2.03	0.41
34:Ld:123:ASP:OD1	34:Ld:123:ASP:N	2.51	0.41
35:Le:35:TRP:CZ2	35:Le:56:PRO:HD2	2.55	0.41
49:Lt:134:GLY:HA3	49:Lt:152:ILE:HD11	2.03	0.41
54:SP:56:LEU:HD23	54:SP:83:MET:HE3	2.01	0.41
55:SQ:13:PHE:HA	55:SQ:22:VAL:HA	2.02	0.41
65:SA:122:LEU:HD22	65:SA:137:ALA:HB2	2.01	0.41
66:SB:68:GLU:O	66:SB:68:GLU:HG2	2.20	0.41
71:SI:163:GLU:O	71:SI:167:GLN:HG2	2.20	0.41
78:SX:107:ARG:HG2	78:SX:112:VAL:HG22	2.01	0.41
83:S2:463:C:O2'	83:S2:466:G:O6	2.34	0.41
83:S2:509:OMG:H2'	83:S2:510:G:H8	1.85	0.41
83:S2:1101:U:H2'	83:S2:1102:G:H8	1.86	0.41
83:S2:1731:A:H2'	83:S2:1732:G:C8	2.55	0.41
86:CF:135:GLU:OE2	86:CF:432:THR:OG1	2.38	0.41
2:Pt:29:C:H2'	2:Pt:30:G:C8	2.55	0.41
3:L5:19:G:P	38:Lh:93:ARG:HE	2.43	0.41
3:L5:1338:G:H4'	3:L5:1339:U:C6	2.55	0.41
3:L5:2056:G:H4'	19:LO:18:ARG:HH22	1.85	0.41
3:L5:2335:C:H2'	3:L5:2336:G:H8	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:2424:OMG:HM23	3:L5:2424:OMG:H1'	1.92	0.41
3:L5:2861:OMC:HM23	3:L5:2861:OMC:H1'	1.73	0.41
3:L5:4071:U:H2'	3:L5:4072:C:C6	2.56	0.41
18:LN:42:PRO:HD3	18:LN:61:ILE:HG13	2.02	0.41
48:Ls:78:LEU:O	48:Ls:82:ILE:HG12	2.20	0.41
48:Ls:174:LEU:O	48:Ls:178:LEU:HB2	2.20	0.41
57:SS:47:LYS:HD2	57:SS:79:ILE:HD13	2.02	0.41
66:SB:133:TYR:CD1	66:SB:181:LEU:HD22	2.56	0.41
83:S2:223:C:H2'	83:S2:224:A:H8	1.84	0.41
83:S2:1171:G:O2'	83:S2:1187:G:O6	2.31	0.41
83:S2:1243:U:OP2	83:S2:1518:C:O2'	2.26	0.41
83:S2:1386:A:H2'	83:S2:1387:G:O4'	2.20	0.41
83:S2:1470:C:H2'	83:S2:1471:C:H6	1.85	0.41
2:Pt:76:A:H2'	3:L5:4397:A:H1'	2.03	0.41
3:L5:711:A:H2'	3:L5:712:C:C6	2.55	0.41
3:L5:1601:A:OP1	40:Lj:5:THR:OG1	2.27	0.41
3:L5:1869:G:C6	89:L5:5287:SPD:H32	2.55	0.41
3:L5:1875:C:H2'	3:L5:1876:U:C6	2.55	0.41
3:L5:1952:G:OP1	23:LS:139:ARG:NE	2.54	0.41
3:L5:2540:C:H2'	3:L5:2541:G:C8	2.55	0.41
3:L5:3600:G:H2'	3:L5:3601:C:C6	2.56	0.41
6:LA:22:HIS:O	6:LA:24:LYS:NZ	2.52	0.41
7:LB:288:GLY:HA3	7:LB:330:PHE:CE1	2.56	0.41
11:LF:37:PHE:HZ	32:Lb:113:ALA:HB1	1.86	0.41
20:LP:94:MET:HE1	20:LP:146:ILE:HB	2.02	0.41
35:Le:35:TRP:CH2	35:Le:55:MET:HG2	2.56	0.41
50:SD:136:VAL:HG12	50:SD:186:VAL:HG22	2.02	0.41
54:SP:81:ARG:NH1	54:SP:120:SER:OG	2.53	0.41
55:SQ:90:LYS:HA	55:SQ:93:VAL:HG22	2.01	0.41
64:Sg:30:MET:HE2	64:Sg:42:MET:HE2	2.01	0.41
67:SC:256:TRP:CE2	77:SW:68:ARG:HD3	2.55	0.41
70:SH:31:GLU:HA	70:SH:37:LYS:HG3	2.03	0.41
70:SH:143:ARG:HB3	77:SW:51:GLU:OE1	2.21	0.41
73:SL:135:SER:O	73:SL:139:ARG:NH1	2.47	0.41
83:S2:1204:A:H2'	83:S2:1205:C:C6	2.56	0.41
3:L5:286:U:H2'	3:L5:287:U:C6	2.56	0.41
3:L5:515:C:H41	3:L5:647:G:H21	1.67	0.41
3:L5:1248:C:H2'	3:L5:1249:C:H6	1.85	0.41
3:L5:2448:G:H2'	3:L5:2449:A:C8	2.56	0.41
3:L5:2519:U:H1'	3:L5:2520:C:C6	2.55	0.41
3:L5:2716:C:O3'	25:LU:107:LYS:NZ	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:2884:G:H2'	3:L5:2885:A:H8	1.86	0.41
3:L5:3911:C:H2'	3:L5:3912:U:C6	2.54	0.41
3:L5:4237:C:H2'	3:L5:4238:G:C8	2.55	0.41
3:L5:4761:G:OP2	19:LO:37:ARG:NH1	2.53	0.41
5:L8:142:U:OP1	18:LN:38:ARG:NH2	2.47	0.41
8:LC:10:VAL:O	8:LC:18:SER:OG	2.34	0.41
11:LF:157:ARG:HD2	11:LF:213:LEU:HD23	2.02	0.41
14:LI:36:LEU:HD11	14:LI:69:ARG:HD2	2.03	0.41
18:LN:200:LEU:HD22	18:LN:204:ARG:NH1	2.35	0.41
25:LU:103:VAL:N	25:LU:111:GLU:O	2.30	0.41
47:Lr:38:PHE:O	47:Lr:45:HIS:NE2	2.34	0.41
48:Ls:62:ARG:HB3	48:Ls:66:ARG:HH12	1.85	0.41
50:SD:40:ARG:HE	59:SU:108:PRO:HD3	1.86	0.41
51:SF:60:ARG:HE	83:S2:1679:A:P	2.44	0.41
52:SK:14:LEU:HD22	52:SK:35:LEU:HD23	2.01	0.41
54:SP:86:LEU:HB3	54:SP:88:GLU:OE1	2.20	0.41
56:SR:33:ARG:HA	56:SR:33:ARG:HD3	1.84	0.41
67:SC:168:GLY:N	67:SC:179:THR:O	2.40	0.41
69:SG:14:LYS:HZ2	69:SG:16:ILE:HD11	1.84	0.41
71:SI:87:ASN:HB3	71:SI:90:LEU:HG	2.03	0.41
71:SI:139:LYS:HB2	71:SI:139:LYS:HE2	1.69	0.41
77:SW:94:LEU:HD21	77:SW:102:ILE:HG13	2.03	0.41
83:S2:142:C:N4	83:S2:329:G:H5''	2.35	0.41
83:S2:293:C:O2'	83:S2:294:U:H3'	2.21	0.41
83:S2:527:C:H2'	83:S2:528:A:C8	2.55	0.41
83:S2:649:PSU:H2'	83:S2:650:A:H8	1.86	0.41
83:S2:909:G:H2'	83:S2:910:G:C8	2.55	0.41
83:S2:1528:G:H2'	83:S2:1529:C:C6	2.56	0.41
84:Zt:2:C:H2'	84:Zt:3:C:C6	2.55	0.41
85:AT:49:C:H5''	85:AT:51:U:OP2	2.20	0.41
3:L5:86:U:H2'	3:L5:87:A:H8	1.85	0.41
3:L5:86:U:H2'	3:L5:87:A:C8	2.56	0.41
3:L5:441:G:H2'	3:L5:442:G:H8	1.86	0.41
3:L5:1739:G:H2'	3:L5:1740:C:C6	2.56	0.41
3:L5:3610:A:H2'	3:L5:3611:A:C8	2.55	0.41
3:L5:3610:A:H2'	3:L5:3611:A:H8	1.86	0.41
3:L5:3822:PSU:H3'	3:L5:3823:G:N2	2.36	0.41
3:L5:4088:C:C5	12:LG:54:PHE:HZ	2.39	0.41
5:L8:47:C:H1'	5:L8:61:A:H2'	2.01	0.41
24:LT:111:GLU:O	24:LT:115:LYS:HG3	2.20	0.41
29:LY:86:GLN:HA	29:LY:97:VAL:HG23	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Lb:35:VAL:HB	32:Lb:40:LEU:HD21	2.03	0.41
53:SM:80:ASP:OD1	53:SM:80:ASP:N	2.54	0.41
58:ST:6:VAL:HG12	58:ST:135:ALA:HB2	2.03	0.41
59:SU:33:GLU:OE1	83:S2:1447:G:O2'	2.30	0.41
59:SU:55:ARG:HG2	59:SU:87:ARG:NE	2.35	0.41
59:SU:56:MET:HG3	59:SU:86:LYS:HZ2	1.84	0.41
60:SZ:80:ARG:O	83:S2:1598:G:O2'	2.21	0.41
64:Sg:43:TRP:CZ3	64:Sg:55:PRO:HD3	2.56	0.41
65:SA:105:PRO:HA	65:SA:132:GLN:HE21	1.85	0.41
71:SI:129:LEU:HD12	71:SI:129:LEU:HA	1.93	0.41
72:SJ:86:VAL:HG11	72:SJ:105:PHE:CD2	2.56	0.41
73:SL:153:LYS:HD3	73:SL:153:LYS:HA	1.85	0.41
78:SX:90:CYS:HA	78:SX:93:PHE:CD2	2.54	0.41
83:S2:14:C:H2'	83:S2:15:U:C6	2.55	0.41
83:S2:198:U:H2'	83:S2:199:C:H2'	2.01	0.41
83:S2:496:C:H2'	83:S2:497:C:C6	2.56	0.41
86:CF:116:VAL:N	86:CF:151:GLY:O	2.48	0.41
3:L5:31:U:H2'	3:L5:32:G:O4'	2.21	0.41
3:L5:264:C:H2'	3:L5:265:C:C4	2.56	0.41
3:L5:501:C:O2'	3:L5:648:G:OP1	2.35	0.41
3:L5:659:G:H2'	3:L5:660:A:C8	2.54	0.41
3:L5:1197:C:H2'	3:L5:1198:G:C8	2.54	0.41
3:L5:1348:U:H2'	3:L5:1349:G:H8	1.86	0.41
3:L5:1403:G:N2	3:L5:1415:G:C4	2.88	0.41
3:L5:1631:A:H2	6:LA:208:GLU:HG3	1.86	0.41
3:L5:1872:G:O2'	3:L5:4219:A:N3	2.50	0.41
3:L5:1881:C:H5'	3:L5:2281:U:H1'	2.02	0.41
3:L5:1918:U:O2'	3:L5:1920:C:OP2	2.39	0.41
3:L5:1976:G:H22	49:Lt:139:VAL:HG11	1.86	0.41
3:L5:2404:A:O2'	40:Lj:12:ARG:O	2.35	0.41
3:L5:2542:G:H2'	3:L5:2543:A:C8	2.55	0.41
3:L5:4071:U:H2'	3:L5:4072:C:H6	1.85	0.41
3:L5:4122:G:O2'	30:LZ:136:PHE:OXT	2.38	0.41
3:L5:4345:C:H2'	3:L5:4346:U:C6	2.56	0.41
3:L5:5062:G:H2'	3:L5:5063:G:H8	1.86	0.41
14:LI:38:ARG:NH1	14:LI:45:GLU:OE1	2.43	0.41
19:LO:78:ARG:HD2	19:LO:78:ARG:HA	1.86	0.41
28:LX:82:THR:HG21	38:Lh:37:THR:HG22	2.02	0.41
30:LZ:30:ASP:HA	30:LZ:39:SER:OG	2.20	0.41
30:LZ:51:ARG:HB2	30:LZ:65:ARG:HB3	2.03	0.41
35:Le:19:LYS:HE3	35:Le:19:LYS:HB3	1.89	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Le:91:CYS:HB3	35:Le:95:TYR:HD2	1.86	0.41
47:Lr:32:LEU:HD11	47:Lr:49:VAL:HG23	2.03	0.41
49:Lt:117:ARG:HG3	49:Lt:119:ARG:HG3	2.02	0.41
49:Lt:147:HIS:HA	49:Lt:148:PRO:HD3	1.89	0.41
53:SM:31:LEU:HG	53:SM:33:ARG:HG3	2.02	0.41
53:SM:123:VAL:O	53:SM:126:GLU:HG3	2.20	0.41
56:SR:10:LYS:HG2	56:SR:53:TYR:CE2	2.56	0.41
58:ST:39:LEU:HD13	58:ST:56:ARG:NH2	2.36	0.41
62:Sd:34:TYR:OH	83:S2:1549:U:OP1	2.38	0.41
67:SC:77:SER:OG	67:SC:79:GLU:OE1	2.27	0.41
68:SE:208:VAL:HG11	68:SE:225:ILE:HG13	2.03	0.41
70:SH:43:LEU:HB3	70:SH:72:PHE:HE1	1.86	0.41
70:SH:118:ARG:HA	70:SH:118:ARG:HD3	1.92	0.41
71:SI:141:ARG:NE	83:S2:191:A:OP1	2.54	0.41
75:SO:147:ARG:HH22	83:S2:1854:U:P	2.44	0.41
76:SV:27:LYS:HA	76:SV:27:LYS:HD3	1.85	0.41
76:SV:70:LEU:HD21	76:SV:83:PHE:CE2	2.56	0.41
79:SY:43:LYS:HE3	79:SY:43:LYS:HB2	1.89	0.41
79:SY:120:THR:OG1	79:SY:123:ALA:HB3	2.20	0.41
83:S2:563:G:O2'	83:S2:564:A:OP1	2.32	0.41
83:S2:959:G:H1'	83:S2:964:A:N6	2.35	0.41
83:S2:1320:G:H2'	83:S2:1321:G:O4'	2.20	0.41
83:S2:1408:U:H2'	83:S2:1409:A:C8	2.56	0.41
83:S2:1468:C:H2'	83:S2:1469:A:C8	2.54	0.41
86:CF:347:LEU:O	86:CF:396:SER:OG	2.39	0.41
3:L5:135:G:N2	38:Lh:91:MET:O	2.54	0.41
3:L5:302:C:H2'	3:L5:303:C:H6	1.86	0.41
3:L5:454:U:O2	35:Le:5:ARG:HD2	2.21	0.41
3:L5:1767:A:N1	3:L5:1769:G:O2'	2.49	0.41
3:L5:1989:G:H2'	3:L5:1990:A:C8	2.56	0.41
3:L5:2262:G:OP2	47:Lr:98:ARG:NH2	2.42	0.41
3:L5:2634:C:H2'	3:L5:2635:U:H6	1.86	0.41
3:L5:3848:U:H2'	3:L5:3849:A:H8	1.86	0.41
3:L5:3848:U:H2'	3:L5:3849:A:C8	2.56	0.41
5:L8:58:G:O6	40:Lj:63:ARG:NH1	2.54	0.41
8:LC:221:PHE:O	8:LC:222:ARG:HG2	2.21	0.41
17:LM:47:ARG:NH2	17:LM:68:ALA:O	2.45	0.41
20:LP:27:LYS:O	20:LP:31:GLU:HG2	2.21	0.41
34:Ld:88:LEU:HD23	34:Ld:106:VAL:HG22	2.03	0.41
35:Le:65:LYS:O	35:Le:69:MET:HE3	2.21	0.41
39:Li:26:HIS:CE1	39:Li:29:ARG:HD3	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lj:19:CYS:SG	40:Lj:34:CYS:HB2	2.60	0.41
49:Lt:11:LYS:HD2	49:Lt:11:LYS:HA	1.92	0.41
61:Sc:44:ARG:HH21	61:Sc:61:SER:C	2.29	0.41
63:Sf:103:LEU:HD12	63:Sf:105:TYR:CE1	2.56	0.41
64:Sg:291:TRP:CE2	64:Sg:298:LEU:HD13	2.56	0.41
65:SA:132:GLN:NE2	65:SA:136:GLU:OE2	2.54	0.41
66:SB:128:LYS:NZ	66:SB:129:THR:O	2.54	0.41
69:SG:102:VAL:HG23	69:SG:106:LEU:HD22	2.03	0.41
71:Sl:23:LYS:NZ	83:S2:435:A:OP1	2.51	0.41
79:SY:110:ARG:O	79:SY:114:MET:HG2	2.20	0.41
83:S2:99:A2M:HM'3	83:S2:99:A2M:H1'	1.82	0.41
86:CF:274:PRO:HB3	86:CF:291:SER:HA	2.03	0.41
3:L5:44:A:H5''	88:L5:5265:SPM:H81	2.03	0.40
3:L5:302:C:H2'	3:L5:303:C:C6	2.56	0.40
3:L5:467:U:C4	3:L5:468:U:H1'	2.55	0.40
3:L5:1259:G:H2'	3:L5:1260:G:H8	1.86	0.40
3:L5:1352:C:H2'	3:L5:1353:G:O4'	2.21	0.40
3:L5:1716:G:H2'	3:L5:1717:C:C6	2.56	0.40
3:L5:1982:G:H1'	3:L5:2010:A:H4'	2.03	0.40
3:L5:2007:G:H2'	3:L5:2008:U:C6	2.56	0.40
3:L5:4460:U:H2'	3:L5:4461:C:C6	2.56	0.40
3:L5:4522:G:O2'	3:L5:4525:C:OP2	2.26	0.40
3:L5:4695:C:O2	43:Lm:106:ARG:NH2	2.51	0.40
3:L5:4763:U:O2'	23:LS:174:THR:OG1	2.24	0.40
3:L5:4975:G:O2'	3:L5:4977:A:N6	2.49	0.40
5:L8:36:G:C5	38:Lh:89:ARG:HD3	2.55	0.40
8:LC:177:TRP:HD1	8:LC:181:LYS:HE2	1.86	0.40
9:LD:289:ARG:O	9:LD:292:GLU:HG3	2.21	0.40
11:LF:227:PHE:HA	11:LF:231:GLY:O	2.21	0.40
12:LG:193:LEU:HD23	12:LG:193:LEU:HA	1.93	0.40
14:LI:183:ASP:O	14:LI:187:LYS:HG2	2.21	0.40
51:SF:155:CYS:HB3	51:SF:159:ARG:HH22	1.86	0.40
52:SK:80:ARG:HA	52:SK:85:LEU:HD21	2.03	0.40
56:SR:64:GLY:HA2	56:SR:65:PRO:HD2	1.88	0.40
60:SZ:72:VAL:HA	60:SZ:75:GLU:HG2	2.03	0.40
64:Sg:183:LYS:HD2	64:Sg:183:LYS:HA	1.86	0.40
68:SE:152:PRO:HG2	69:SG:216:ARG:HG3	2.02	0.40
69:SG:126:ASP:OD1	69:SG:126:ASP:N	2.53	0.40
72:SJ:133:ARG:NH1	83:S2:581:U:OP1	2.39	0.40
77:SW:111:MET:CE	77:SW:115:GLU:HG2	2.51	0.40
83:S2:1329:U:O2'	83:S2:1332:A:OP2	2.33	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:S2:1538:C:H2'	83:S2:1539:U:C6	2.56	0.40
84:Zt:43:A:H3'	84:Zt:44:G:H8	1.85	0.40
3:L5:492:U:H2'	3:L5:493:G:O4'	2.21	0.40
3:L5:660:A:H2'	3:L5:661:C:C6	2.56	0.40
3:L5:677:G:H2'	3:L5:678:C:C6	2.56	0.40
3:L5:1642:A:H61	6:LA:2:GLY:C	2.29	0.40
3:L5:2497:C:H2'	3:L5:2498:C:H6	1.86	0.40
3:L5:2683:C:H2'	3:L5:2684:C:C6	2.56	0.40
3:L5:2811:G:N1	3:L5:2814:C:OP2	2.49	0.40
3:L5:3690:U:H2'	3:L5:3691:G:O4'	2.21	0.40
6:LA:39:GLY:HA2	6:LA:93:LYS:HE2	2.02	0.40
12:LG:230:TYR:CE1	12:LG:234:ARG:HD2	2.56	0.40
34:Ld:114:PHE:HA	34:Ld:117:LEU:HD12	2.04	0.40
53:SM:52:LEU:HD21	53:SM:62:VAL:HG13	2.03	0.40
59:SU:26:SER:OG	59:SU:27:ARG:N	2.53	0.40
64:Sg:260:ASP:O	64:Sg:264:LYS:N	2.54	0.40
68:SE:124:CYS:HB3	68:SE:141:THR:HB	2.03	0.40
83:S2:962:A:N1	83:S2:1055:A:O2'	2.52	0.40
85:AT:6:C:H2'	85:AT:7:G:H8	1.86	0.40
3:L5:65:A:N6	3:L5:75:G:H1'	2.37	0.40
3:L5:1077:C:OP1	3:L5:1215:C:O2'	2.29	0.40
3:L5:1195:G:H2'	3:L5:1196:G:H8	1.85	0.40
3:L5:4195:G:OP1	3:L5:4221:C:O2'	2.38	0.40
3:L5:4406:U:C2	3:L5:4407:G:C8	3.09	0.40
3:L5:4615:C:H5''	7:LB:357:ARG:HH11	1.86	0.40
4:L7:58:A:H2'	4:L7:59:G:C8	2.55	0.40
6:LA:156:LYS:HG2	6:LA:158:ILE:HG23	2.02	0.40
7:LB:201:LEU:HD23	7:LB:201:LEU:HA	1.90	0.40
7:LB:289:GLN:HE22	7:LB:292:LEU:HD11	1.85	0.40
9:LD:55:VAL:HG11	9:LD:158:LYS:HE3	2.04	0.40
16:LL:58:ILE:HG12	16:LL:116:ARG:HD2	2.03	0.40
39:Li:90:LEU:HA	39:Li:93:VAL:HG12	2.04	0.40
46:Lp:81:SER:HA	46:Lp:84:ARG:HG2	2.03	0.40
49:Lt:28:LEU:H	49:Lt:28:LEU:HD23	1.86	0.40
49:Lt:119:ARG:NH2	49:Lt:123:ARG:HH12	2.19	0.40
51:SF:204:ARG:HG3	61:Sc:63:ARG:HE	1.85	0.40
52:SK:53:LYS:HZ2	52:SK:60:GLU:HB3	1.86	0.40
59:SU:54:VAL:HG12	83:S2:1402:A:H1'	2.04	0.40
63:Sf:123:SER:HG	63:Sf:126:CYS:H	1.68	0.40
67:SC:82:TYR:OH	67:SC:162:ILE:O	2.30	0.40
68:SE:122:LYS:HE2	68:SE:124:CYS:SG	2.61	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SG:54:GLY:O	69:SG:110:ASN:N	2.54	0.40
70:SH:64:VAL:HG22	70:SH:95:ILE:O	2.22	0.40
83:S2:29:G:H2'	83:S2:30:C:C6	2.57	0.40
83:S2:1128:C:H2'	83:S2:1129:G:H8	1.85	0.40
84:Zt:62:C:H2'	84:Zt:63:C:C6	2.56	0.40
3:L5:952:G:H2'	3:L5:953:C:C6	2.57	0.40
3:L5:1766:A:OP2	3:L5:1768:C:O2'	2.31	0.40
3:L5:1834:U:C2	24:LT:128:LEU:HD23	2.57	0.40
3:L5:1977:C:O2'	3:L5:1978:C:OP1	2.35	0.40
3:L5:2052:G:O2'	3:L5:2057:A:N1	2.50	0.40
3:L5:2421:G:OP2	3:L5:2828:U:H1'	2.21	0.40
3:L5:3893:C:H2'	3:L5:3894:A:H8	1.87	0.40
3:L5:4344:U:H2'	3:L5:4345:C:C6	2.56	0.40
10:LE:243:THR:HG22	10:LE:245:GLN:H	1.87	0.40
12:LG:229:ARG:HB2	12:LG:232:GLU:OE2	2.22	0.40
21:LQ:43:PHE:CD2	21:LQ:133:GLY:HA3	2.56	0.40
49:Lt:79:ALA:HA	49:Lt:82:ILE:HG22	2.03	0.40
51:SF:18:LYS:CE	51:SF:22:LYS:HA	2.51	0.40
51:SF:107:ASN:OD1	51:SF:109:LEU:N	2.52	0.40
51:SF:122:ARG:HG2	61:Sc:57:THR:HG21	2.03	0.40
54:SP:131:PRO:HA	83:S2:1237:C:H5'	2.01	0.40
72:SJ:80:ARG:NH2	83:S2:818:A:OP1	2.48	0.40
78:SX:88:ASP:HA	83:S2:617:G:H4'	2.03	0.40
81:Sb:14:GLU:O	81:Sb:18:LYS:HG3	2.21	0.40
83:S2:27:A2M:H2'	83:S2:28:U:O4'	2.21	0.40
83:S2:300:U:H2'	83:S2:301:A:H8	1.87	0.40
83:S2:1541:G:H2'	83:S2:1542:C:C6	2.57	0.40
85:AT:10:G:H2'	85:AT:11:U:C6	2.57	0.40
86:CF:9:ASN:HB3	86:CF:266:ARG:HH22	1.86	0.40
2:Pt:3:C:H42	2:Pt:70:A:N6	2.20	0.40
3:L5:223:G:H4'	3:L5:225:G:N7	2.37	0.40
3:L5:1779:U:H2'	3:L5:1780:A:C8	2.56	0.40
3:L5:2665:U:OP2	22:LR:110:ARG:NH1	2.47	0.40
3:L5:4153:C:H5''	28:LX:38:LYS:HD2	2.03	0.40
3:L5:4970:C:C2	3:L5:4971:A:C8	3.09	0.40
3:L5:5002:U:H2'	3:L5:5003:U:H6	1.87	0.40
4:L7:7:G:H5''	9:LD:22:ARG:HD3	2.04	0.40
5:L8:66:A:H2'	5:L8:67:U:C6	2.56	0.40
7:LB:337:VAL:HG11	7:LB:345:LEU:HD13	2.02	0.40
8:LC:292:ILE:HG12	21:LQ:128:LEU:HD21	2.02	0.40
11:LF:27:GLU:O	11:LF:31:LYS:HG2	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LG:189:ARG:HG2	12:LG:192:ARG:NH2	2.36	0.40
18:LN:75:VAL:HG21	18:LN:80:THR:HG22	2.03	0.40
39:Li:99:LYS:HB2	39:Li:99:LYS:HE2	1.76	0.40
49:Lt:81:ILE:HD13	49:Lt:113:ALA:HB1	2.02	0.40
51:SF:166:ILE:HD12	51:SF:166:ILE:H	1.85	0.40
57:SS:82:TRP:CD1	57:SS:82:TRP:H	2.40	0.40
57:SS:86:ARG:HG3	57:SS:89:ASP:OD1	2.22	0.40
72:SJ:114:VAL:HG23	72:SJ:126:ALA:HB1	2.03	0.40
79:SY:86:GLU:HB3	79:SY:91:LEU:HD11	2.03	0.40
80:Sa:4:LYS:NZ	83:S2:1863:A:OP2	2.50	0.40
83:S2:737:G:H8	83:S2:738:C:H4'	1.85	0.40
83:S2:1365:G:H2'	83:S2:1366:G:H8	1.86	0.40
83:S2:1426:U:H2'	83:S2:1427:C:C6	2.57	0.40
83:S2:1700:C:O2	83:S2:1834:A:N6	2.55	0.40
84:Zt:27:U:H2'	84:Zt:28:C:H6	1.86	0.40
84:Zt:48:C:C4	84:Zt:59:G:C5	3.10	0.40
85:AT:5:C:H2'	85:AT:6:C:H6	1.86	0.40
86:CF:13:ILE:HG13	86:CF:114:LEU:HA	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	CI	29/31 (94%)	29 (100%)	0	0	100	100
6	LA	246/248 (99%)	231 (94%)	15 (6%)	0	100	100
7	LB	400/402 (100%)	384 (96%)	16 (4%)	0	100	100
8	LC	366/368 (100%)	354 (97%)	12 (3%)	0	100	100
9	LD	291/293 (99%)	281 (97%)	10 (3%)	0	100	100
10	LE	236/250 (94%)	227 (96%)	9 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	LF	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
12	LG	239/241 (99%)	225 (94%)	14 (6%)	0	100	100
13	LH	188/190 (99%)	183 (97%)	5 (3%)	0	100	100
14	LI	211/213 (99%)	204 (97%)	7 (3%)	0	100	100
15	LJ	168/176 (96%)	162 (96%)	6 (4%)	0	100	100
16	LL	208/210 (99%)	200 (96%)	8 (4%)	0	100	100
17	LM	137/139 (99%)	130 (95%)	7 (5%)	0	100	100
18	LN	201/203 (99%)	199 (99%)	2 (1%)	0	100	100
19	LO	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
20	LP	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
21	LQ	185/187 (99%)	181 (98%)	4 (2%)	0	100	100
22	LR	185/187 (99%)	180 (97%)	5 (3%)	0	100	100
23	LS	173/175 (99%)	167 (96%)	6 (4%)	0	100	100
24	LT	157/159 (99%)	153 (98%)	4 (2%)	0	100	100
25	LU	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	12	24
26	LV	129/131 (98%)	125 (97%)	4 (3%)	0	100	100
27	LW	112/124 (90%)	107 (96%)	5 (4%)	0	100	100
28	LX	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
29	LY	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
30	LZ	133/135 (98%)	126 (95%)	7 (5%)	0	100	100
31	La	145/147 (99%)	139 (96%)	6 (4%)	0	100	100
32	Lb	105/121 (87%)	100 (95%)	5 (5%)	0	100	100
33	Lc	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
34	Ld	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
35	Le	126/128 (98%)	126 (100%)	0	0	100	100
36	Lf	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
37	Lg	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
38	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
39	Li	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
40	Lj	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
41	Lk	67/69 (97%)	64 (96%)	3 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	Ll	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
43	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
44	Ln	22/24 (92%)	22 (100%)	0	0	100	100
45	Lo	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
46	Lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
47	Lr	123/125 (98%)	120 (98%)	3 (2%)	0	100	100
48	Ls	194/196 (99%)	183 (94%)	11 (6%)	0	100	100
49	Lt	128/157 (82%)	110 (86%)	18 (14%)	0	100	100
50	SD	225/227 (99%)	219 (97%)	6 (3%)	0	100	100
51	SF	187/189 (99%)	179 (96%)	8 (4%)	0	100	100
52	SK	96/98 (98%)	85 (88%)	11 (12%)	0	100	100
53	SM	120/122 (98%)	108 (90%)	12 (10%)	0	100	100
54	SP	119/121 (98%)	118 (99%)	1 (1%)	0	100	100
55	SQ	142/144 (99%)	133 (94%)	9 (6%)	0	100	100
56	SR	133/135 (98%)	127 (96%)	5 (4%)	1 (1%)	16	31
57	SS	143/145 (99%)	133 (93%)	10 (7%)	0	100	100
58	ST	141/143 (99%)	137 (97%)	4 (3%)	0	100	100
59	SU	102/104 (98%)	95 (93%)	7 (7%)	0	100	100
60	SZ	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
61	Sc	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
62	Sd	53/55 (96%)	53 (100%)	0	0	100	100
63	Sf	65/67 (97%)	56 (86%)	9 (14%)	0	100	100
64	Sg	311/313 (99%)	297 (96%)	14 (4%)	0	100	100
65	SA	219/221 (99%)	206 (94%)	13 (6%)	0	100	100
66	SB	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
67	SC	218/222 (98%)	206 (94%)	12 (6%)	0	100	100
68	SE	260/262 (99%)	250 (96%)	10 (4%)	0	100	100
69	SG	235/237 (99%)	225 (96%)	10 (4%)	0	100	100
70	SH	182/189 (96%)	169 (93%)	13 (7%)	0	100	100
71	SI	204/206 (99%)	196 (96%)	8 (4%)	0	100	100
72	SJ	183/185 (99%)	175 (96%)	8 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	SL	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
74	SN	148/150 (99%)	146 (99%)	2 (1%)	0	100	100
75	SO	135/140 (96%)	127 (94%)	8 (6%)	0	100	100
76	SV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
77	SW	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
78	SX	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
79	SY	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
80	Sa	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
81	Sb	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
82	Se	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
86	CF	438/441 (99%)	431 (98%)	7 (2%)	0	100	100
All	All	12110/12348 (98%)	11625 (96%)	483 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	LU	55	ASN
56	SR	129	LYS

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	CI	25/25 (100%)	25 (100%)	0	100	100
6	LA	190/190 (100%)	190 (100%)	0	100	100
7	LB	348/348 (100%)	348 (100%)	0	100	100
8	LC	306/306 (100%)	306 (100%)	0	100	100
9	LD	246/247 (100%)	246 (100%)	0	100	100
10	LE	212/222 (96%)	212 (100%)	0	100	100
11	LF	194/194 (100%)	194 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	LG	203/205 (99%)	203 (100%)	0	100	100
13	LH	169/169 (100%)	169 (100%)	0	100	100
14	LI	180/180 (100%)	180 (100%)	0	100	100
15	LJ	143/148 (97%)	143 (100%)	0	100	100
16	LL	176/176 (100%)	176 (100%)	0	100	100
17	LM	118/118 (100%)	118 (100%)	0	100	100
18	LN	171/171 (100%)	171 (100%)	0	100	100
19	LO	173/173 (100%)	173 (100%)	0	100	100
20	LP	134/134 (100%)	134 (100%)	0	100	100
21	LQ	164/164 (100%)	164 (100%)	0	100	100
22	LR	166/166 (100%)	166 (100%)	0	100	100
23	LS	156/156 (100%)	156 (100%)	0	100	100
24	LT	139/139 (100%)	139 (100%)	0	100	100
25	LU	91/91 (100%)	91 (100%)	0	100	100
26	LV	101/101 (100%)	101 (100%)	0	100	100
27	LW	95/103 (92%)	95 (100%)	0	100	100
28	LX	108/108 (100%)	108 (100%)	0	100	100
29	LY	124/124 (100%)	124 (100%)	0	100	100
30	LZ	117/117 (100%)	117 (100%)	0	100	100
31	La	120/120 (100%)	120 (100%)	0	100	100
32	Lb	88/101 (87%)	88 (100%)	0	100	100
33	Lc	83/83 (100%)	83 (100%)	0	100	100
34	Ld	98/98 (100%)	98 (100%)	0	100	100
35	Le	114/114 (100%)	114 (100%)	0	100	100
36	Lf	88/88 (100%)	88 (100%)	0	100	100
37	Lg	98/98 (100%)	98 (100%)	0	100	100
38	Lh	109/109 (100%)	109 (100%)	0	100	100
39	Li	86/86 (100%)	86 (100%)	0	100	100
40	Lj	73/73 (100%)	73 (100%)	0	100	100
41	Lk	64/64 (100%)	64 (100%)	0	100	100
42	Ll	47/47 (100%)	47 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	Lm	48/48 (100%)	48 (100%)	0	100	100
44	Ln	23/23 (100%)	23 (100%)	0	100	100
45	Lo	93/93 (100%)	93 (100%)	0	100	100
46	Lp	74/74 (100%)	74 (100%)	0	100	100
47	Lr	109/109 (100%)	109 (100%)	0	100	100
48	Ls	162/164 (99%)	162 (100%)	0	100	100
49	Lt	107/130 (82%)	107 (100%)	0	100	100
50	SD	190/190 (100%)	190 (100%)	0	100	100
51	SF	159/159 (100%)	159 (100%)	0	100	100
52	SK	89/89 (100%)	89 (100%)	0	100	100
53	SM	102/104 (98%)	102 (100%)	0	100	100
54	SP	107/107 (100%)	107 (100%)	0	100	100
55	SQ	119/119 (100%)	119 (100%)	0	100	100
56	SR	122/122 (100%)	122 (100%)	0	100	100
57	SS	126/126 (100%)	126 (100%)	0	100	100
58	ST	113/113 (100%)	113 (100%)	0	100	100
59	SU	94/94 (100%)	94 (100%)	0	100	100
60	SZ	66/66 (100%)	66 (100%)	0	100	100
61	Sc	57/57 (100%)	57 (100%)	0	100	100
62	Sd	48/48 (100%)	48 (100%)	0	100	100
63	Sf	60/60 (100%)	60 (100%)	0	100	100
64	Sg	272/272 (100%)	272 (100%)	0	100	100
65	SA	183/183 (100%)	183 (100%)	0	100	100
66	SB	195/195 (100%)	195 (100%)	0	100	100
67	SC	186/188 (99%)	186 (100%)	0	100	100
68	SE	224/224 (100%)	224 (100%)	0	100	100
69	SG	207/207 (100%)	207 (100%)	0	100	100
70	SH	166/169 (98%)	165 (99%)	1 (1%)	78	89
71	SI	178/178 (100%)	178 (100%)	0	100	100
72	SJ	161/161 (100%)	161 (100%)	0	100	100
73	SL	137/137 (100%)	137 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
74	SN	130/130 (100%)	130 (100%)	0	100	100
75	SO	107/110 (97%)	107 (100%)	0	100	100
76	SV	67/67 (100%)	66 (98%)	1 (2%)	57	77
77	SW	112/112 (100%)	112 (100%)	0	100	100
78	SX	113/113 (100%)	113 (100%)	0	100	100
79	SY	113/113 (100%)	113 (100%)	0	100	100
80	Sa	89/89 (100%)	89 (100%)	0	100	100
81	Sb	75/75 (100%)	75 (100%)	0	100	100
82	Se	47/47 (100%)	47 (100%)	0	100	100
86	CF	365/366 (100%)	364 (100%)	1 (0%)	86	94
All	All	10512/10587 (99%)	10509 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
70	SH	112	ASN
76	SV	49	GLN
86	CF	409	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (100) such sidechains are listed below:

Mol	Chain	Res	Type
6	LA	97	ASN
7	LB	184	GLN
7	LB	203	GLN
7	LB	204	GLN
7	LB	289	GLN
8	LC	329	ASN
8	LC	347	HIS
9	LD	244	HIS
10	LE	228	GLN
10	LE	245	GLN
12	LG	64	GLN
12	LG	90	GLN
12	LG	112	GLN
13	LH	98	HIS
14	LI	59	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
14	LI	73	ASN
14	LI	166	HIS
15	LJ	168	GLN
16	LL	19	GLN
16	LL	67	HIS
16	LL	205	GLN
17	LM	34	ASN
19	LO	50	ASN
20	LP	75	GLN
20	LP	97	ASN
21	LQ	21	GLN
22	LR	118	HIS
22	LR	158	GLN
23	LS	108	GLN
24	LT	112	ASN
26	LV	27	ASN
26	LV	77	HIS
27	LW	50	ASN
27	LW	79	GLN
29	LY	14	ASN
29	LY	40	GLN
29	LY	43	ASN
29	LY	61	HIS
29	LY	127	GLN
31	La	34	ASN
33	Lc	72	HIS
35	Le	52	GLN
35	Le	92	ASN
35	Le	117	GLN
39	Li	26	HIS
40	Lj	66	HIS
42	Ll	33	ASN
46	Lp	33	GLN
47	Lr	21	ASN
47	Lr	30	ASN
49	Lt	65	GLN
51	SF	79	HIS
52	SK	42	ASN
52	SK	61	GLN
52	SK	84	HIS
53	SM	19	GLN
54	SP	103	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	SP	114	HIS
55	SQ	8	GLN
55	SQ	86	GLN
58	ST	105	GLN
64	Sg	14	HIS
64	Sg	26	GLN
64	Sg	215	GLN
64	Sg	285	GLN
65	SA	9	GLN
65	SA	132	GLN
65	SA	169	HIS
66	SB	95	ASN
66	SB	101	HIS
66	SB	158	HIS
68	SE	98	ASN
68	SE	161	GLN
68	SE	188	ASN
69	SG	13	GLN
69	SG	56	ASN
70	SH	25	GLN
70	SH	114	GLN
70	SH	162	GLN
71	SI	35	ASN
71	SI	167	GLN
72	SJ	156	HIS
73	SL	19	ASN
73	SL	39	ASN
74	SN	36	GLN
74	SN	69	ASN
74	SN	105	ASN
76	SV	2	GLN
76	SV	35	ASN
76	SV	47	ASN
76	SV	49	GLN
78	SX	77	ASN
78	SX	92	ASN
79	SY	112	ASN
80	Sa	72	HIS
82	Se	39	ASN
86	CF	147	GLN
86	CF	197	ASN
86	CF	324	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
86	CF	352	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	Pt	72/74 (97%)	16 (22%)	0
3	L5	3643/3655 (99%)	713 (19%)	14 (0%)
4	L7	119/120 (99%)	11 (9%)	0
5	L8	155/156 (99%)	21 (13%)	0
83	S2	1714/1740 (98%)	357 (20%)	3 (0%)
84	Zt	74/75 (98%)	45 (60%)	0
85	AT	74/76 (97%)	34 (45%)	1 (1%)
All	All	5851/5896 (99%)	1197 (20%)	18 (0%)

All (1197) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	Pt	9	A
2	Pt	13	U
2	Pt	19	G
2	Pt	20(A)	U
2	Pt	21	A
2	Pt	42	A
2	Pt	46	G
2	Pt	47	U
2	Pt	48	C
2	Pt	49	C
2	Pt	58	A
2	Pt	66	C
2	Pt	67	G
2	Pt	70	A
2	Pt	74	C
2	Pt	76	A
3	L5	25	A
3	L5	30	C
3	L5	39	A
3	L5	42	A
3	L5	48	G
3	L5	56	A
3	L5	59	A
3	L5	64	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	65	A
3	L5	66	A
3	L5	73	A
3	L5	74	G
3	L5	91	G
3	L5	104	G
3	L5	108	A
3	L5	109	G
3	L5	110	C
3	L5	119	G
3	L5	120	A
3	L5	132	G
3	L5	133	C
3	L5	134	G
3	L5	135	G
3	L5	139	G
3	L5	159	C
3	L5	165	A
3	L5	172	C
3	L5	181	C
3	L5	182	G
3	L5	183	C
3	L5	184	U
3	L5	185	C
3	L5	187	U
3	L5	188	G
3	L5	200	U
3	L5	209	U
3	L5	210	C
3	L5	216	C
3	L5	218	A
3	L5	220	C
3	L5	234	G
3	L5	237	G
3	L5	255	C
3	L5	256	G
3	L5	261	G
3	L5	263	G
3	L5	264	C
3	L5	265	C
3	L5	266	C
3	L5	267	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	280	G
3	L5	297	U
3	L5	306	A
3	L5	315	G
3	L5	316	U
3	L5	340	C
3	L5	373	G
3	L5	385	A
3	L5	387	G
3	L5	388	A
3	L5	396	A
3	L5	407	A
3	L5	409	G
3	L5	410	A
3	L5	411	G
3	L5	412	G
3	L5	413	G
3	L5	415	G
3	L5	432	U
3	L5	449	C
3	L5	452	A
3	L5	453	G
3	L5	454	U
3	L5	456	C
3	L5	457	G
3	L5	465	G
3	L5	467	U
3	L5	484	U
3	L5	485	C
3	L5	486	C
3	L5	489	C
3	L5	493	G
3	L5	494	U
3	L5	497	G
3	L5	498	C
3	L5	499	G
3	L5	500	G
3	L5	502	C
3	L5	503	C
3	L5	504	G
3	L5	509	A
3	L5	510	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	512	U
3	L5	513	U
3	L5	514	U
3	L5	518	G
3	L5	643	C
3	L5	646	G
3	L5	654	C
3	L5	655	C
3	L5	656	C
3	L5	657	C
3	L5	659	G
3	L5	666	G
3	L5	667	A
3	L5	668	C
3	L5	669	C
3	L5	673	C
3	L5	685	C
3	L5	686	A
3	L5	687	U
3	L5	704	C
3	L5	708	G
3	L5	730	G
3	L5	731	G
3	L5	738	C
3	L5	739	G
3	L5	742	G
3	L5	746	A
3	L5	759	G
3	L5	904	C
3	L5	905	C
3	L5	910	G
3	L5	913	U
3	L5	914	U
3	L5	915	A
3	L5	917	A
3	L5	923	C
3	L5	924	C
3	L5	926	G
3	L5	932	A
3	L5	933	G
3	L5	935	A
3	L5	936	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	941	C
3	L5	943	A
3	L5	944	A
3	L5	945	U
3	L5	946	C
3	L5	956	A
3	L5	959	G
3	L5	960	A
3	L5	961	G
3	L5	962	C
3	L5	965	G
3	L5	966	A
3	L5	967	C
3	L5	969	C
3	L5	970	G
3	L5	982	U
3	L5	985	C
3	L5	1070	G
3	L5	1071	C
3	L5	1072	C
3	L5	1075	G
3	L5	1082	C
3	L5	1083	U
3	L5	1168	G
3	L5	1171	G
3	L5	1172	C
3	L5	1173	G
3	L5	1179	U
3	L5	1180	C
3	L5	1181	C
3	L5	1182	C
3	L5	1183	C
3	L5	1187	G
3	L5	1202	C
3	L5	1203	G
3	L5	1210	C
3	L5	1211	G
3	L5	1214	C
3	L5	1215	C
3	L5	1219	G
3	L5	1222	A
3	L5	1246	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	1253	G
3	L5	1254	A
3	L5	1257	A
3	L5	1258	G
3	L5	1262	G
3	L5	1266	G
3	L5	1267	C
3	L5	1269	G
3	L5	1271	G
3	L5	1272	C
3	L5	1273	G
3	L5	1275	G
3	L5	1277	G
3	L5	1280	C
3	L5	1284	G
3	L5	1285	U
3	L5	1287	G
3	L5	1293	G
3	L5	1294	A
3	L5	1295	C
3	L5	1296	G
3	L5	1301	C
3	L5	1314	C
3	L5	1326	A2M
3	L5	1354	A
3	L5	1359	G
3	L5	1365	C
3	L5	1366	G
3	L5	1367	C
3	L5	1379	C
3	L5	1387	A
3	L5	1394	G
3	L5	1397	A
3	L5	1398	A
3	L5	1403	G
3	L5	1404	G
3	L5	1407	C
3	L5	1409	C
3	L5	1410	U
3	L5	1411	C
3	L5	1417	C
3	L5	1420	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	1425	G
3	L5	1437	C
3	L5	1439	C
3	L5	1442	C
3	L5	1443	A
3	L5	1444	G
3	L5	1446	C
3	L5	1447	C
3	L5	1457	G
3	L5	1482	G
3	L5	1483	C
3	L5	1497	A
3	L5	1498	G
3	L5	1502	G
3	L5	1517	G
3	L5	1523	A
3	L5	1524	A2M
3	L5	1534	A2M
3	L5	1537	A
3	L5	1547	A
3	L5	1562	G
3	L5	1566	C
3	L5	1574	G
3	L5	1578	U
3	L5	1591	U
3	L5	1596	U
3	L5	1621	A
3	L5	1624	G
3	L5	1625	OMG
3	L5	1631	A
3	L5	1633	G
3	L5	1634	A
3	L5	1638	A
3	L5	1640	C
3	L5	1641	G
3	L5	1642	A
3	L5	1654	G
3	L5	1661	C
3	L5	1676	C
3	L5	1677	PSU
3	L5	1678	C
3	L5	1694	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	1697	G
3	L5	1699	A
3	L5	1700	G
3	L5	1701	A
3	L5	1702	C
3	L5	1704	C
3	L5	1705	G
3	L5	1706	A
3	L5	1717	C
3	L5	1718	C
3	L5	1719	A
3	L5	1721	G
3	L5	1731	C
3	L5	1734	G
3	L5	1742	A
3	L5	1750	G
3	L5	1753	G
3	L5	1755	C
3	L5	1757	U
3	L5	1758	G
3	L5	1761	G
3	L5	1762	C
3	L5	1763	C
3	L5	1764	G
3	L5	1765	A
3	L5	1766	A
3	L5	1767	A
3	L5	1768	C
3	L5	1769	G
3	L5	1770	A
3	L5	1787	A
3	L5	1804	A
3	L5	1806	G
3	L5	1810	G
3	L5	1815	G
3	L5	1821	G
3	L5	1822	U
3	L5	1834	U
3	L5	1836	G
3	L5	1837	A
3	L5	1842	G
3	L5	1855	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	1869	G
3	L5	1882	U
3	L5	1897	A
3	L5	1917	A
3	L5	1918	U
3	L5	1919	G
3	L5	1920	C
3	L5	1921	C
3	L5	1922	G
3	L5	1925	G
3	L5	1931	C
3	L5	1932	A
3	L5	1948	G
3	L5	1951	G
3	L5	1961	G
3	L5	1962	A
3	L5	1974	U
3	L5	1975	G
3	L5	1978	C
3	L5	1980	U
3	L5	1981	G
3	L5	1982	G
3	L5	1984	A
3	L5	1985	G
3	L5	1986	U
3	L5	1991	A
3	L5	1993	C
3	L5	1997	U
3	L5	1998	A
3	L5	1999	A
3	L5	2001	G
3	L5	2002	A
3	L5	2003	G
3	L5	2004	U
3	L5	2011	C
3	L5	2017	A
3	L5	2018	C
3	L5	2024	G
3	L5	2026	A
3	L5	2046	G
3	L5	2048	U
3	L5	2055	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	2056	G
3	L5	2069	A
3	L5	2084	C
3	L5	2092	G
3	L5	2093	A
3	L5	2094	G
3	L5	2095	A
3	L5	2096	G
3	L5	2097	U
3	L5	2098	G
3	L5	2101	C
3	L5	2102	G
3	L5	2107	C
3	L5	2110	C
3	L5	2112	G
3	L5	2250	C
3	L5	2252	G
3	L5	2256	C
3	L5	2289	C
3	L5	2300	A
3	L5	2301	G
3	L5	2313	A
3	L5	2331	G
3	L5	2333	G
3	L5	2348	G
3	L5	2351	OMC
3	L5	2360	A
3	L5	2395	A
3	L5	2397	G
3	L5	2398	U
3	L5	2417	A
3	L5	2425	U
3	L5	2453	A
3	L5	2464	C
3	L5	2465	C
3	L5	2469	C
3	L5	2471	G
3	L5	2474	G
3	L5	2475	G
3	L5	2478	C
3	L5	2479	G
3	L5	2483	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	2484	A
3	L5	2485	U
3	L5	2487	G
3	L5	2488	C
3	L5	2489	C
3	L5	2490	U
3	L5	2494	U
3	L5	2504	C
3	L5	2505	C
3	L5	2506	G
3	L5	2513	A
3	L5	2519	U
3	L5	2520	C
3	L5	2529	A
3	L5	2537	A
3	L5	2544	G
3	L5	2546	G
3	L5	2547	G
3	L5	2554	U
3	L5	2555	G
3	L5	2556	G
3	L5	2560	C
3	L5	2565	A
3	L5	2567	G
3	L5	2573	A
3	L5	2583	C
3	L5	2586	G
3	L5	2587	A
3	L5	2589	C
3	L5	2601	A
3	L5	2602	G
3	L5	2627	C
3	L5	2653	C
3	L5	2662	G
3	L5	2669	C
3	L5	2675	G
3	L5	2676	A
3	L5	2687	U
3	L5	2694	G
3	L5	2695	A
3	L5	2696	A
3	L5	2706	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	2708	U
3	L5	2709	C
3	L5	2710	C
3	L5	2711	G
3	L5	2712	G
3	L5	2721	G
3	L5	2724	G
3	L5	2726	G
3	L5	2739	C
3	L5	2742	G
3	L5	2743	A
3	L5	2761	U
3	L5	2763	U
3	L5	2769	U
3	L5	2770	C
3	L5	2788	U
3	L5	2790	U
3	L5	2806	A
3	L5	2814	C
3	L5	2826	U
3	L5	2827	G
3	L5	2829	U
3	L5	2855	G
3	L5	2867	C
3	L5	2877	G
3	L5	2899	C
3	L5	2900	U
3	L5	2902	G
3	L5	2903	G
3	L5	2904	U
3	L5	2905	C
3	L5	2907	G
3	L5	2908	U
3	L5	3588	C
3	L5	3590	G
3	L5	3591	C
3	L5	3594	C
3	L5	3595	U
3	L5	3596	A
3	L5	3597	G
3	L5	3604	A
3	L5	3605	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	3616	U
3	L5	3626	G
3	L5	3630	A
3	L5	3635	A
3	L5	3644	U
3	L5	3646	A
3	L5	3648	A
3	L5	3662	A
3	L5	3664	G
3	L5	3670	C
3	L5	3673	C
3	L5	3674	G
3	L5	3701	OMC
3	L5	3710	G
3	L5	3711	A
3	L5	3713	U
3	L5	3726	A
3	L5	3727	A
3	L5	3748	A
3	L5	3753	G
3	L5	3760	A
3	L5	3764	U
3	L5	3770	U
3	L5	3774	A
3	L5	3775	A
3	L5	3776	G
3	L5	3777	G
3	L5	3785	A2M
3	L5	3786	U
3	L5	3792	OMG
3	L5	3811	G
3	L5	3812	C
3	L5	3814	U
3	L5	3817	A
3	L5	3819	G
3	L5	3824	A
3	L5	3838	U
3	L5	3839	G
3	L5	3840	U
3	L5	3867	A2M
3	L5	3877	A
3	L5	3878	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	3879	G
3	L5	3885	G
3	L5	3892	U
3	L5	3897	G
3	L5	3901	A
3	L5	3906	A
3	L5	3907	G
3	L5	3908	A
3	L5	3915	U
3	L5	3923	A
3	L5	3938	G
3	L5	3939	G
3	L5	3942	A
3	L5	3945	A
3	L5	3947	A
3	L5	3949	A
3	L5	3950	U
3	L5	3952	A
3	L5	3953	G
3	L5	4057	C
3	L5	4058	U
3	L5	4059	C
3	L5	4061	G
3	L5	4062	A
3	L5	4064	C
3	L5	4065	G
3	L5	4068	U
3	L5	4076	G
3	L5	4084	G
3	L5	4095	G
3	L5	4097	G
3	L5	4099	G
3	L5	4101	C
3	L5	4104	G
3	L5	4108	G
3	L5	4111	U
3	L5	4114	C
3	L5	4115	G
3	L5	4116	C
3	L5	4119	C
3	L5	4120	U
3	L5	4122	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	4127	A
3	L5	4141	G
3	L5	4142	C
3	L5	4143	G
3	L5	4144	C
3	L5	4146	G
3	L5	4149	C
3	L5	4162	C
3	L5	4163	U
3	L5	4170	A
3	L5	4183	G
3	L5	4184	G
3	L5	4191	G
3	L5	4203	A
3	L5	4212	A
3	L5	4220	6MZ
3	L5	4222	G
3	L5	4225	G
3	L5	4229	U
3	L5	4233	A
3	L5	4251	A
3	L5	4254	G
3	L5	4257	A
3	L5	4258	C
3	L5	4265	U
3	L5	4268	A
3	L5	4273	A
3	L5	4280	A
3	L5	4291	G
3	L5	4295	U
3	L5	4304	A
3	L5	4305	G
3	L5	4306	OMU
3	L5	4314	C
3	L5	4319	C
3	L5	4329	G
3	L5	4330	G
3	L5	4332	C
3	L5	4349	C
3	L5	4350	C
3	L5	4354	U
3	L5	4373	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	4377	G
3	L5	4378	A
3	L5	4379	A
3	L5	4387	C
3	L5	4391	G
3	L5	4394	A
3	L5	4421	C
3	L5	4422	A
3	L5	4448	G
3	L5	4449	A
3	L5	4464	A
3	L5	4466	C
3	L5	4475	G
3	L5	4488	A
3	L5	4500	PSU
3	L5	4510	A
3	L5	4512	U
3	L5	4513	A
3	L5	4519	C
3	L5	4524	G
3	L5	4545	G
3	L5	4548	A
3	L5	4557	U
3	L5	4560	C
3	L5	4567	G
3	L5	4569	U
3	L5	4575	G
3	L5	4584	A
3	L5	4589	A
3	L5	4590	A2M
3	L5	4600	G
3	L5	4601	U
3	L5	4617	G
3	L5	4636	PSU
3	L5	4637	OMG
3	L5	4652	G
3	L5	4656	A
3	L5	4670	C
3	L5	4672	A
3	L5	4679	G
3	L5	4687	A
3	L5	4694	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	4695	C
3	L5	4700	A
3	L5	4708	A
3	L5	4709	U
3	L5	4719	G
3	L5	4734	A
3	L5	4741	C
3	L5	4742	G
3	L5	4745	G
3	L5	4750	G
3	L5	4754	G
3	L5	4757	C
3	L5	4759	C
3	L5	4761	G
3	L5	4765	G
3	L5	4771	C
3	L5	4772	C
3	L5	4775	C
3	L5	4859	C
3	L5	4870	G
3	L5	4871	C
3	L5	4875	G
3	L5	4881	U
3	L5	4882	U
3	L5	4883	C
3	L5	4889	G
3	L5	4895	C
3	L5	4896	G
3	L5	4897	G
3	L5	4899	G
3	L5	4900	C
3	L5	4901	G
3	L5	4910	G
3	L5	4912	G
3	L5	4914	C
3	L5	4922	C
3	L5	4925	U
3	L5	4926	C
3	L5	4927	G
3	L5	4928	C
3	L5	4934	A
3	L5	4940	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	L5	4941	G
3	L5	4943	A
3	L5	4944	C
3	L5	4949	G
3	L5	4951	G
3	L5	4955	A
3	L5	4960	G
3	L5	4975	G
3	L5	4976	U
3	L5	4985	U
3	L5	4988	U
3	L5	4989	U
3	L5	4991	U
3	L5	4995	U
3	L5	5006	U
3	L5	5007	A
3	L5	5013	C
3	L5	5014	A
3	L5	5017	G
3	L5	5022	U
3	L5	5023	C
3	L5	5024	C
3	L5	5026	U
3	L5	5027	C
3	L5	5028	G
3	L5	5030	U
3	L5	5034	A
3	L5	5041	G
3	L5	5050	C
3	L5	5054	C
3	L5	5055	G
3	L5	5061	A
3	L5	5069	U
4	L7	7	G
4	L7	22	A
4	L7	24	C
4	L7	33	U
4	L7	38	U
4	L7	53	U
4	L7	54	A
4	L7	64	G
4	L7	97	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	L7	100	A
4	L7	110	G
5	L8	23	C
5	L8	25	G
5	L8	34	U
5	L8	35	C
5	L8	59	A
5	L8	62	A
5	L8	63	U
5	L8	80	A
5	L8	82	A
5	L8	84	A
5	L8	85	U
5	L8	87	G
5	L8	94	G
5	L8	103	A
5	L8	105	C
5	L8	111	U
5	L8	114	G
5	L8	124	U
5	L8	125	C
5	L8	126	C
5	L8	127	U
83	S2	2	A
83	S2	14	C
83	S2	25	A
83	S2	33	G
83	S2	41	G
83	S2	42	A
83	S2	44	U
83	S2	45	A
83	S2	46	A
83	S2	56	G
83	S2	58	C
83	S2	59	U
83	S2	65	C
83	S2	67	C
83	S2	68	A
83	S2	72	C
83	S2	73	C
83	S2	74	G
83	S2	76	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
83	S2	99	A2M
83	S2	103	A
83	S2	113	G
83	S2	115	U
83	S2	126	G
83	S2	130	G
83	S2	143	U
83	S2	149	A
83	S2	158	A
83	S2	160	U
83	S2	162	C
83	S2	170	A
83	S2	175	A
83	S2	190	G
83	S2	191	A
83	S2	196	C
83	S2	197	U
83	S2	198	U
83	S2	200	G
83	S2	203	G
83	S2	204	G
83	S2	206	G
83	S2	207	G
83	S2	208	G
83	S2	209	A
83	S2	214	U
83	S2	291	G
83	S2	292	A
83	S2	295	C
83	S2	302	A
83	S2	306	C
83	S2	307	G
83	S2	308	G
83	S2	309	G
83	S2	311	C
83	S2	312	G
83	S2	313	A
83	S2	318	A
83	S2	319	C
83	S2	323	C
83	S2	324	C
83	S2	325	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
83	S2	326	C
83	S2	328	U
83	S2	329	G
83	S2	332	G
83	S2	339	A
83	S2	347	G
83	S2	351	G
83	S2	360	A
83	S2	362	C
83	S2	364	A
83	S2	368	U
83	S2	370	G
83	S2	381	C
83	S2	383	G
83	S2	385	G
83	S2	386	C
83	S2	398	A
83	S2	407	G
83	S2	408	A
83	S2	409	C
83	S2	438	G
83	S2	448	A
83	S2	449	A
83	S2	450	C
83	S2	452	G
83	S2	464	A
83	S2	465	A
83	S2	471	G
83	S2	472	C
83	S2	473	A
83	S2	474	G
83	S2	476	A
83	S2	482	G
83	S2	487	U
83	S2	488	U
83	S2	492	C
83	S2	493	A
83	S2	502	C
83	S2	517	OMC
83	S2	531	A
83	S2	532	C
83	S2	536	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
83	S2	537	C
83	S2	540	U
83	S2	542	U
83	S2	544	G
83	S2	546	G
83	S2	547	G
83	S2	557	U
83	S2	558	G
83	S2	559	G
83	S2	563	G
83	S2	564	A
83	S2	576	A2M
83	S2	583	A
83	S2	587	A
83	S2	589	G
83	S2	590	A
83	S2	591	U
83	S2	593	C
83	S2	604	A
83	S2	614	C
83	S2	617	G
83	S2	623	G
83	S2	627	OMU
83	S2	628	A
83	S2	631	U
83	S2	643	A
83	S2	644	OMG
83	S2	655	A
83	S2	660	C
83	S2	664	A
83	S2	668	A2M
83	S2	669	A
83	S2	671	A
83	S2	672	A
83	S2	673	G
83	S2	683	OMG
83	S2	688	U
83	S2	689	U
83	S2	692	G
83	S2	695	C
83	S2	696	G
83	S2	697	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
83	S2	698	G
83	S2	731	G
83	S2	732	U
83	S2	733	C
83	S2	736	C
83	S2	737	G
83	S2	738	C
83	S2	749	U
83	S2	751	G
83	S2	752	G
83	S2	753	C
83	S2	788	G
83	S2	791	C
83	S2	792	C
83	S2	798	G
83	S2	799	OMU
83	S2	801	PSU
83	S2	821	G
83	S2	822	U
83	S2	823	U
83	S2	824	C
83	S2	827	A
83	S2	830	A
83	S2	834	C
83	S2	835	C
83	S2	836	G
83	S2	837	A
83	S2	838	G
83	S2	839	C
83	S2	842	C
83	S2	844	U
83	S2	847	A
83	S2	867	OMG
83	S2	870	A
83	S2	874	G
83	S2	877	C
83	S2	878	G
83	S2	880	G
83	S2	888	U
83	S2	889	U
83	S2	891	G
83	S2	893	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
83	S2	896	U
83	S2	897	U
83	S2	898	U
83	S2	899	U
83	S2	900	C
83	S2	901	G
83	S2	903	A
83	S2	913	A
83	S2	920	A
83	S2	933	G
83	S2	934	G
83	S2	943	U
83	S2	963	A
83	S2	970	G
83	S2	971	G
83	S2	972	A
83	S2	985	G
83	S2	990	A
83	S2	992	A
83	S2	999	G
83	S2	1002	U
83	S2	1008	A
83	S2	1017	U
83	S2	1023	A
83	S2	1027	A
83	S2	1060	A
83	S2	1061	U
83	S2	1062	A
83	S2	1083	A
83	S2	1085	C
83	S2	1109	C
83	S2	1113	A
83	S2	1116	C
83	S2	1121	G
83	S2	1123	C
83	S2	1133	A
83	S2	1138	C
83	S2	1148	A
83	S2	1153	C
83	S2	1154	U
83	S2	1195	A
83	S2	1207	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
83	S2	1208	A
83	S2	1215	C
83	S2	1216	C
83	S2	1217	A
83	S2	1224	G
83	S2	1227	G
83	S2	1242	U
83	S2	1243	U
83	S2	1248	B8N
83	S2	1251	A
83	S2	1253	A
83	S2	1256	G
83	S2	1257	G
83	S2	1259	A
83	S2	1264	C
83	S2	1271	C
83	S2	1272	OMC
83	S2	1274	G
83	S2	1275	G
83	S2	1283	C
83	S2	1286	G
83	S2	1288	OMU
83	S2	1294	G
83	S2	1295	A
83	S2	1301	A
83	S2	1302	G
83	S2	1303	C
83	S2	1308	U
83	S2	1342	U
83	S2	1357	A
83	S2	1358	U
83	S2	1371	U
83	S2	1372	U
83	S2	1376	A
83	S2	1378	A
83	S2	1382	A
83	S2	1402	A
83	S2	1413	G
83	S2	1418	C
83	S2	1419	C
83	S2	1420	G
83	S2	1421	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
83	S2	1422	G
83	S2	1423	C
83	S2	1433	C
83	S2	1435	C
83	S2	1437	C
83	S2	1438	A
83	S2	1442	OMU
83	S2	1449	G
83	S2	1454	A
83	S2	1463	U
83	S2	1489	A
83	S2	1490	OMG
83	S2	1492	U
83	S2	1494	U
83	S2	1495	G
83	S2	1497	G
83	S2	1498	A
83	S2	1521	C
83	S2	1522	A
83	S2	1531	A
83	S2	1533	A
83	S2	1544	C
83	S2	1546	G
83	S2	1552	G
83	S2	1553	C
83	S2	1556	A
83	S2	1573	G
83	S2	1574	C
83	S2	1575	G
83	S2	1580	A
83	S2	1581	C
83	S2	1585	U
83	S2	1587	G
83	S2	1588	A
83	S2	1600	G
83	S2	1604	G
83	S2	1606	G
83	S2	1621	U
83	S2	1623	A
83	S2	1631	U
83	S2	1633	A
83	S2	1634	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
83	S2	1637	A
83	S2	1648	G
83	S2	1654	G
83	S2	1663	A
83	S2	1665	G
83	S2	1683	C
83	S2	1686	G
83	S2	1695	A
83	S2	1699	A
83	S2	1715	A
83	S2	1721	U
83	S2	1722	G
83	S2	1744	G
83	S2	1745	A
83	S2	1752	C
83	S2	1753	C
83	S2	1754	G
83	S2	1755	C
83	S2	1757	G
83	S2	1759	G
83	S2	1761	U
83	S2	1772	C
83	S2	1773	C
83	S2	1774	C
83	S2	1777	G
83	S2	1782	G
83	S2	1783	C
83	S2	1784	G
83	S2	1786	U
83	S2	1798	C
83	S2	1809	A
83	S2	1810	U
83	S2	1825	A
83	S2	1826	G
83	S2	1829	G
83	S2	1831	A
83	S2	1835	A
83	S2	1838	U
83	S2	1849	G
83	S2	1851	MA6
83	S2	1861	G
83	S2	1862	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
83	S2	1863	A
83	S2	1865	C
84	Zt	6	G
84	Zt	7	A
84	Zt	8	U
84	Zt	9	A
84	Zt	10	G
84	Zt	11	C
84	Zt	14	A
84	Zt	15	G
84	Zt	16	C
84	Zt	18	U
84	Zt	19	G
84	Zt	20	U
84	Zt	21	A
84	Zt	22	G
84	Zt	24	G
84	Zt	26	A
84	Zt	29	A
84	Zt	30	G
84	Zt	33	U
84	Zt	34	U
84	Zt	35	U
84	Zt	36	U
84	Zt	37	A
84	Zt	38	A
84	Zt	40	C
84	Zt	42	G
84	Zt	43	A
84	Zt	45	G
84	Zt	47	U
84	Zt	48	C
84	Zt	49	C
84	Zt	53	G
84	Zt	56	C
84	Zt	57	A
84	Zt	58	A
84	Zt	59	G
84	Zt	60	U
84	Zt	61	C
84	Zt	63	C
84	Zt	66	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
84	Zt	67	U
84	Zt	68	C
84	Zt	69	G
84	Zt	71	G
84	Zt	72	C
85	AT	3	C
85	AT	4	U
85	AT	8	U
85	AT	9	A
85	AT	10	G
85	AT	12	G
85	AT	13	U
85	AT	14	A
85	AT	16	C
85	AT	19	G
85	AT	20	U
85	AT	21	U
85	AT	22	A
85	AT	26	C
85	AT	27	G
85	AT	31	G
85	AT	32	C
85	AT	33	C
85	AT	40	G
85	AT	46	G
85	AT	47	G
85	AT	49	C
85	AT	51	U
85	AT	53	G
85	AT	58	G
85	AT	59	A
85	AT	60	A
85	AT	62	C
85	AT	65	G
85	AT	69	G
85	AT	70	A
85	AT	73	C
85	AT	76	C
85	AT	77	A

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	L5	406	C
3	L5	493	G
3	L5	914	U
3	L5	1082	C
3	L5	1633	G
3	L5	1703	C
3	L5	1977	C
3	L5	2416	G
3	L5	2675	G
3	L5	2760	G
3	L5	3673	C
3	L5	4600	G
3	L5	4699	U
3	L5	4913	G
83	S2	291	G
83	S2	563	G
83	S2	688	U
85	AT	7	G

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

179 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$
3	PSU	L5	5010	3	18,21,22	1.11	1 (5%)	21,30,33	1.90	4 (19%)
3	OMG	L5	3792	3	23,26,27	0.49	0	32,38,41	0.49	0
3	PSU	L5	1744	87,3	18,21,22	1.11	1 (5%)	21,30,33	1.91	4 (19%)
83	PSU	S2	651	83	18,21,22	1.15	1 (5%)	21,30,33	1.94	4 (19%)
3	OMC	L5	3869	3	19,22,23	0.56	0	25,31,34	0.71	0
3	OMG	L5	4370	3	23,26,27	0.47	0	32,38,41	0.50	0
3	A2M	L5	4571	3	22,25,26	1.26	1 (4%)	30,36,39	1.56	7 (23%)
83	A2M	S2	1383	83	22,25,26	1.23	1 (4%)	30,36,39	1.66	7 (23%)
3	A2M	L5	3830	3	22,25,26	1.21	1 (4%)	30,36,39	1.60	7 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	OMU	L5	2837	3	19,22,23	3.35	7 (36%)	25,31,34	1.85	5 (20%)
3	PSU	L5	4431	3	18,21,22	1.10	1 (5%)	21,30,33	1.90	4 (19%)
3	A2M	L5	3718	3	22,25,26	1.17	1 (4%)	30,36,39	1.53	7 (23%)
3	PSU	L5	4442	3	18,21,22	1.11	1 (5%)	21,30,33	1.95	6 (28%)
3	OMG	L5	3744	3	23,26,27	0.48	0	32,38,41	0.47	0
3	A2M	L5	4590	3	22,25,26	1.19	1 (4%)	30,36,39	1.55	6 (20%)
3	PSU	L5	4689	3	18,21,22	1.08	1 (5%)	21,30,33	1.94	4 (19%)
3	PSU	L5	3851	3	18,21,22	1.10	1 (5%)	21,30,33	1.90	5 (23%)
3	A2M	L5	1326	3	22,25,26	1.17	1 (4%)	30,36,39	1.54	9 (30%)
3	OMU	L5	4620	3	19,22,23	3.27	7 (36%)	25,31,34	1.68	4 (16%)
3	OMG	L5	1316	3	23,26,27	0.52	0	32,38,41	0.52	0
3	PSU	L5	4576	3	18,21,22	1.09	1 (5%)	21,30,33	1.88	5 (23%)
3	PSU	L5	1582	3	18,21,22	1.06	1 (5%)	21,30,33	1.74	4 (19%)
3	UY1	L5	3818	3	19,22,23	4.95	10 (52%)	21,31,34	1.99	5 (23%)
83	A2M	S2	484	83	22,25,26	1.21	1 (4%)	30,36,39	1.49	6 (20%)
3	PSU	L5	1862	3	18,21,22	1.07	1 (5%)	21,30,33	1.90	4 (19%)
3	PSU	L5	3844	3	18,21,22	1.11	1 (5%)	21,30,33	1.83	4 (19%)
3	OMC	L5	4536	3	19,22,23	0.57	0	25,31,34	0.76	0
5	PSU	L8	69	5	18,21,22	1.09	1 (5%)	21,30,33	1.91	5 (23%)
83	PSU	S2	686	83	18,21,22	1.09	1 (5%)	21,30,33	1.96	5 (23%)
3	PSU	L5	3639	3	18,21,22	1.11	1 (5%)	21,30,33	1.94	5 (23%)
83	OMG	S2	644	83	23,26,27	0.45	0	32,38,41	0.49	0
3	PSU	L5	3853	87,3	18,21,22	1.08	1 (5%)	21,30,33	1.78	4 (19%)
83	OMU	S2	172	83	19,22,23	3.38	7 (36%)	25,31,34	1.84	5 (20%)
3	PSU	L5	4471	3	18,21,22	1.08	1 (5%)	21,30,33	1.81	4 (19%)
3	1MA	L5	1322	87,3	21,25,26	0.53	0	30,37,40	0.78	1 (3%)
83	OMG	S2	601	83	23,26,27	0.47	0	32,38,41	0.48	0
3	PSU	L5	1536	3	18,21,22	1.08	1 (5%)	21,30,33	1.91	4 (19%)
3	OMG	L5	3899	3	23,26,27	0.53	0	32,38,41	0.52	0
3	A2M	L5	398	3	22,25,26	1.21	1 (4%)	30,36,39	1.61	7 (23%)
83	OMU	S2	1288	83	19,22,23	3.39	7 (36%)	25,31,34	1.75	4 (16%)
83	6MZ	S2	1832	83,87	26,26,26	2.84	5 (19%)	36,39,39	2.04	9 (25%)
3	A2M	L5	2787	3	22,25,26	1.21	1 (4%)	30,36,39	1.49	7 (23%)
5	PSU	L8	55	5	18,21,22	1.09	1 (5%)	21,30,33	1.89	4 (19%)
3	PSU	L5	3822	3	18,21,22	1.11	1 (5%)	21,30,33	1.92	5 (23%)
83	MA6	S2	1850	83	23,26,27	1.27	2 (8%)	33,38,41	3.35	12 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
83	PSU	S2	1045	83	18,21,22	1.08	1 (5%)	21,30,33	1.87	4 (19%)
83	PSU	S2	1004	83	18,21,22	1.13	1 (5%)	21,30,33	1.86	4 (19%)
3	A2M	L5	4523	87,3	22,25,26	1.25	1 (4%)	30,36,39	1.58	7 (23%)
3	OMU	L5	4227	3	19,22,23	3.34	7 (36%)	25,31,34	1.81	5 (20%)
3	PSU	L5	3920	87,3	18,21,22	1.08	1 (5%)	21,30,33	1.90	4 (19%)
83	OMU	S2	1326	83	19,22,23	3.37	7 (36%)	25,31,34	1.81	5 (20%)
83	A2M	S2	166	83	22,25,26	1.26	1 (4%)	30,36,39	1.58	7 (23%)
3	OMC	L5	2861	3	19,22,23	0.53	0	25,31,34	0.82	1 (4%)
3	OMC	L5	3887	3	19,22,23	0.54	0	25,31,34	0.74	0
3	PSU	L5	4493	3	18,21,22	1.10	1 (5%)	21,30,33	1.88	4 (19%)
83	PSU	S2	966	83,87	18,21,22	1.08	1 (5%)	21,30,33	1.83	4 (19%)
83	OMG	S2	683	83	23,26,27	0.50	0	32,38,41	0.47	0
83	4AC	S2	1337	83	21,24,25	0.39	0	28,34,37	0.68	1 (3%)
3	OMC	L5	4456	3	19,22,23	0.58	0	25,31,34	0.81	1 (4%)
83	PSU	S2	649	83	18,21,22	1.12	1 (5%)	21,30,33	1.94	5 (23%)
3	PSU	L5	2839	3	18,21,22	1.09	1 (5%)	21,30,33	1.90	4 (19%)
3	PSU	L5	4628	3	18,21,22	1.03	1 (5%)	21,30,33	1.81	4 (19%)
83	4AC	S2	1842	83	21,24,25	0.38	0	28,34,37	0.48	0
83	OMG	S2	509	83	23,26,27	0.45	0	32,38,41	0.49	0
3	PSU	L5	4457	3	18,21,22	1.10	1 (5%)	21,30,33	1.95	6 (28%)
5	OMG	L8	75	5	23,26,27	0.48	0	32,38,41	0.49	0
83	OMC	S2	174	83	19,22,23	0.50	0	25,31,34	0.66	0
3	PSU	L5	3695	3	18,21,22	1.09	1 (5%)	21,30,33	1.96	5 (23%)
3	OMG	L5	4499	3	23,26,27	0.48	0	32,38,41	0.47	0
3	OMG	L5	4637	3	23,26,27	0.49	0	32,38,41	0.48	0
3	OMG	L5	4623	3	23,26,27	0.49	0	32,38,41	0.53	0
83	OMC	S2	1703	83	19,22,23	0.53	0	25,31,34	0.65	0
83	PSU	S2	801	83	18,21,22	1.11	1 (5%)	21,30,33	1.79	4 (19%)
3	PSU	L5	4973	3	18,21,22	1.08	1 (5%)	21,30,33	1.91	4 (19%)
3	PSU	L5	4293	3	18,21,22	1.11	1 (5%)	21,30,33	1.93	4 (19%)
3	A2M	L5	1524	3	22,25,26	1.23	2 (9%)	30,36,39	1.50	6 (20%)
83	PSU	S2	1177	83	18,21,22	1.11	1 (5%)	21,30,33	1.91	4 (19%)
83	MA6	S2	1851	83	23,26,27	1.27	2 (8%)	33,38,41	3.40	12 (36%)
3	A2M	L5	2815	3	22,25,26	1.18	1 (4%)	30,36,39	1.49	9 (30%)
3	OMG	L5	1522	3	23,26,27	0.50	0	32,38,41	0.62	0
3	A2M	L5	1323	3	22,25,26	1.23	2 (9%)	30,36,39	1.60	9 (30%)
3	PSU	L5	1683	3	18,21,22	1.11	1 (5%)	21,30,33	1.91	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	OMC	L5	3841	3	19,22,23	0.55	0	25,31,34	0.71	0
83	OMC	S2	1391	83	19,22,23	0.52	0	25,31,34	0.66	0
3	PSU	L5	1782	3	18,21,22	1.11	1 (5%)	21,30,33	1.91	4 (19%)
3	OMC	L5	2365	87,3	19,22,23	0.54	0	25,31,34	0.58	0
83	OMG	S2	1328	83	23,26,27	0.46	0	32,38,41	0.44	0
3	PSU	L5	1860	3	18,21,22	1.11	1 (5%)	21,30,33	1.94	4 (19%)
3	A2M	L5	3785	87,3	22,25,26	1.15	1 (4%)	30,36,39	1.63	9 (30%)
83	PSU	S2	109	83	18,21,22	1.12	1 (5%)	21,30,33	1.88	4 (19%)
83	OMC	S2	1272	83	19,22,23	0.53	0	25,31,34	0.87	1 (4%)
3	PSU	L5	4532	3	18,21,22	1.09	1 (5%)	21,30,33	1.86	4 (19%)
3	OMU	L5	4306	3	19,22,23	3.31	7 (36%)	25,31,34	1.80	4 (16%)
3	PSU	L5	4552	3	18,21,22	1.09	1 (5%)	21,30,33	1.92	4 (19%)
83	A2M	S2	1031	83	22,25,26	1.21	1 (4%)	30,36,39	1.57	7 (23%)
3	PSU	L5	3637	3	18,21,22	1.09	1 (5%)	21,30,33	2.02	5 (23%)
3	PSU	L5	4636	3	18,21,22	1.09	1 (5%)	21,30,33	2.01	6 (28%)
3	OMU	L5	4498	3	19,22,23	3.35	7 (36%)	25,31,34	1.82	5 (20%)
3	OMG	L5	2364	87,3	23,26,27	0.48	0	32,38,41	0.45	0
86	SEP	CF	163	86	8,9,10	1.62	1 (12%)	7,12,14	1.39	1 (14%)
3	PSU	L5	1792	3	18,21,22	1.06	1 (5%)	21,30,33	1.85	4 (19%)
3	OMG	L5	4228	3	23,26,27	0.48	0	32,38,41	0.57	0
3	A2M	L5	400	3	22,25,26	1.23	1 (4%)	30,36,39	1.58	8 (26%)
83	A2M	S2	668	83,87	22,25,26	1.32	2 (9%)	30,36,39	1.63	6 (20%)
3	OMC	L5	2351	87,3	19,22,23	0.56	0	25,31,34	0.89	1 (4%)
3	PSU	L5	2632	3	18,21,22	1.10	1 (5%)	21,30,33	1.96	5 (23%)
83	PSU	S2	1174	83	18,21,22	1.12	1 (5%)	21,30,33	1.90	4 (19%)
3	OMG	L5	3627	3	23,26,27	0.49	0	32,38,41	0.59	0
3	PSU	L5	4312	3	18,21,22	1.11	1 (5%)	21,30,33	1.90	4 (19%)
83	B8N	S2	1248	83	25,29,30	3.28	6 (24%)	28,42,45	1.99	8 (28%)
3	PSU	L5	4972	3	18,21,22	1.06	1 (5%)	21,30,33	1.90	4 (19%)
83	OMU	S2	428	83	19,22,23	3.38	7 (36%)	25,31,34	1.82	5 (20%)
83	OMG	S2	867	83	23,26,27	0.50	0	32,38,41	0.47	0
83	OMC	S2	517	83	19,22,23	0.51	0	25,31,34	0.66	0
3	PSU	L5	4579	3	18,21,22	1.07	1 (5%)	21,30,33	1.89	4 (19%)
3	PSU	L5	5001	3	18,21,22	1.10	1 (5%)	21,30,33	1.83	4 (19%)
3	A2M	L5	3867	3	22,25,26	1.22	1 (4%)	30,36,39	1.52	8 (26%)
3	PSU	L5	4361	3	18,21,22	1.09	1 (5%)	21,30,33	1.85	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
83	PSU	S2	1056	83	18,21,22	1.09	1 (5%)	21,30,33	1.90	4 (19%)
3	A2M	L5	2363	87,3	22,25,26	1.17	1 (4%)	30,36,39	1.52	9 (30%)
83	PSU	S2	1244	83	18,21,22	1.12	1 (5%)	21,30,33	1.92	5 (23%)
83	PSU	S2	814	83	18,21,22	1.11	1 (5%)	21,30,33	1.82	4 (19%)
83	PSU	S2	105	83	18,21,22	1.09	1 (5%)	21,30,33	1.88	4 (19%)
3	OMG	L5	4392	3	23,26,27	0.50	0	32,38,41	0.49	0
3	A2M	L5	1871	87,3	22,25,26	1.25	1 (4%)	30,36,39	1.59	6 (20%)
3	PSU	L5	4353	3	18,21,22	1.08	1 (5%)	21,30,33	1.93	5 (23%)
3	OMC	L5	2804	3	19,22,23	0.52	0	25,31,34	0.65	0
83	PSU	S2	93	83	18,21,22	1.11	1 (5%)	21,30,33	1.78	4 (19%)
83	OMU	S2	116	83	19,22,23	3.38	7 (36%)	25,31,34	1.72	4 (16%)
83	OMU	S2	121	83	19,22,23	3.39	7 (36%)	25,31,34	1.85	5 (20%)
83	PSU	S2	863	83	18,21,22	1.12	1 (5%)	21,30,33	1.88	4 (19%)
83	OMU	S2	1442	83	19,22,23	3.41	7 (36%)	25,31,34	1.80	5 (20%)
83	A2M	S2	576	83	22,25,26	1.21	1 (4%)	30,36,39	1.51	5 (16%)
3	5MC	L5	3782	87,3	19,22,23	0.56	0	26,32,35	0.76	0
83	PSU	S2	1367	83	18,21,22	1.10	1 (5%)	21,30,33	1.88	4 (19%)
3	PSU	L5	4299	3	18,21,22	1.07	1 (5%)	21,30,33	1.89	4 (19%)
83	OMU	S2	354	83	19,22,23	3.35	7 (36%)	25,31,34	1.84	5 (20%)
3	OMG	L5	2876	3	23,26,27	0.49	0	32,38,41	0.50	0
83	A2M	S2	468	83	22,25,26	1.22	1 (4%)	30,36,39	1.58	7 (23%)
3	PSU	L5	4673	3	18,21,22	1.11	1 (5%)	21,30,33	1.93	4 (19%)
3	PSU	L5	1781	3	18,21,22	1.10	1 (5%)	21,30,33	1.83	4 (19%)
3	OMC	L5	3701	3	19,22,23	0.63	0	25,31,34	1.57	4 (16%)
3	A2M	L5	1534	87,3	22,25,26	1.18	1 (4%)	30,36,39	1.55	9 (30%)
83	PSU	S2	406	83	18,21,22	1.11	1 (5%)	21,30,33	1.95	5 (23%)
83	PSU	S2	1046	83	18,21,22	1.13	1 (5%)	21,30,33	1.85	4 (19%)
83	OMU	S2	627	83	19,22,23	3.39	7 (36%)	25,31,34	1.79	4 (16%)
83	A2M	S2	159	83	22,25,26	1.25	2 (9%)	30,36,39	1.52	8 (26%)
3	PSU	L5	4296	3	18,21,22	1.11	1 (5%)	21,30,33	1.95	5 (23%)
3	UR3	L5	4530	3	19,22,23	2.75	7 (36%)	26,32,35	1.57	3 (11%)
3	5MC	L5	4447	3	19,22,23	0.70	0	26,32,35	0.63	0
3	OMC	L5	1340	3	19,22,23	0.56	0	25,31,34	0.76	0
3	PSU	L5	4403	3	18,21,22	1.05	1 (5%)	21,30,33	1.95	6 (28%)
3	PSU	L5	1677	3	18,21,22	1.08	1 (5%)	21,30,33	1.92	5 (23%)
83	PSU	S2	1232	83	18,21,22	1.12	1 (5%)	21,30,33	1.94	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PSU	L5	4521	87,3	18,21,22	1.09	1 (5%)	21,30,33	1.99	5 (23%)
3	A2M	L5	2401	3	22,25,26	1.19	1 (4%)	30,36,39	1.59	7 (23%)
3	6MZ	L5	4220	3	22,25,26	3.96	11 (50%)	29,36,39	2.44	11 (37%)
83	PSU	S2	1081	83	18,21,22	1.07	1 (5%)	21,30,33	1.86	5 (23%)
83	PSU	S2	681	83	18,21,22	1.05	1 (5%)	21,30,33	1.86	4 (19%)
3	PSU	L5	4500	3	18,21,22	1.14	1 (5%)	21,30,33	1.97	5 (23%)
83	A2M	S2	99	83,87	22,25,26	1.20	1 (4%)	30,36,39	1.55	7 (23%)
3	PSU	L5	3884	3	18,21,22	1.10	1 (5%)	21,30,33	1.92	4 (19%)
83	OMC	S2	462	83	19,22,23	0.52	0	25,31,34	0.77	1 (4%)
83	PSU	S2	866	83	18,21,22	1.12	1 (5%)	21,30,33	1.92	5 (23%)
3	OMC	L5	3808	3	19,22,23	0.60	0	25,31,34	0.85	2 (8%)
83	OMG	S2	1490	83	23,26,27	0.50	0	32,38,41	0.48	0
83	OMU	S2	799	83	19,22,23	3.39	7 (36%)	25,31,34	1.77	5 (20%)
3	OMU	L5	3925	3	19,22,23	3.32	7 (36%)	25,31,34	1.85	5 (20%)
3	OMG	L5	4196	2,3	23,26,27	0.48	0	32,38,41	0.47	0
83	A2M	S2	27	83	22,25,26	1.22	1 (4%)	30,36,39	1.52	7 (23%)
3	OMC	L5	2824	3	19,22,23	0.55	0	25,31,34	0.70	0
83	OMG	S2	436	83	23,26,27	0.47	0	32,38,41	0.51	0
3	OMG	L5	4494	3	23,26,27	0.50	0	32,38,41	0.51	0
3	OMG	L5	2424	3	23,26,27	0.51	0	32,38,41	0.47	0
3	OMC	L5	2422	87,3	19,22,23	0.56	0	25,31,34	0.69	0
3	OMG	L5	4618	3	23,26,27	0.49	0	32,38,41	0.53	0
83	G7M	S2	1639	83,2	23,26,27	2.66	8 (34%)	34,39,42	2.57	11 (32%)
3	OMG	L5	1625	3	23,26,27	0.48	0	32,38,41	0.47	0
3	A2M	L5	3825	3	22,25,26	1.19	1 (4%)	30,36,39	1.57	8 (26%)

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
3	PSU	L5	5010	3	-	0/7/25/26	0/2/2/2
3	OMG	L5	3792	3	-	2/9/27/28	0/3/3/3
3	PSU	L5	1744	87,3	-	0/7/25/26	0/2/2/2
83	PSU	S2	651	83	-	0/7/25/26	0/2/2/2
3	OMC	L5	3869	3	-	0/9/27/28	0/2/2/2
3	OMG	L5	4370	3	-	0/9/27/28	0/3/3/3
3	A2M	L5	4571	3	-	0/9/27/28	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
83	A2M	S2	1383	83	-	3/9/27/28	0/3/3/3
3	A2M	L5	3830	3	-	0/9/27/28	0/3/3/3
3	OMU	L5	2837	3	-	0/9/27/28	0/2/2/2
3	PSU	L5	4431	3	-	0/7/25/26	0/2/2/2
3	A2M	L5	3718	3	-	0/9/27/28	0/3/3/3
3	PSU	L5	4442	3	-	0/7/25/26	0/2/2/2
3	OMG	L5	3744	3	-	0/9/27/28	0/3/3/3
3	A2M	L5	4590	3	-	3/9/27/28	0/3/3/3
3	PSU	L5	4689	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	3851	3	-	0/7/25/26	0/2/2/2
3	A2M	L5	1326	3	-	3/9/27/28	0/3/3/3
3	OMU	L5	4620	3	-	0/9/27/28	0/2/2/2
3	OMG	L5	1316	3	-	0/9/27/28	0/3/3/3
3	PSU	L5	4576	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	1582	3	-	0/7/25/26	0/2/2/2
3	UY1	L5	3818	3	-	2/9/27/28	0/2/2/2
83	A2M	S2	484	83	-	0/9/27/28	0/3/3/3
3	PSU	L5	1862	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	3844	3	-	1/7/25/26	0/2/2/2
3	OMC	L5	4536	3	-	0/9/27/28	0/2/2/2
5	PSU	L8	69	5	-	0/7/25/26	0/2/2/2
83	PSU	S2	686	83	-	0/7/25/26	0/2/2/2
3	PSU	L5	3639	3	-	0/7/25/26	0/2/2/2
83	OMG	S2	644	83	-	4/9/27/28	0/3/3/3
3	PSU	L5	3853	87,3	-	0/7/25/26	0/2/2/2
83	OMU	S2	172	83	-	0/9/27/28	0/2/2/2
3	PSU	L5	4471	3	-	1/7/25/26	0/2/2/2
3	1MA	L5	1322	87,3	-	2/7/25/26	0/3/3/3
83	OMG	S2	601	83	-	1/9/27/28	0/3/3/3
3	PSU	L5	1536	3	-	2/7/25/26	0/2/2/2
3	OMG	L5	3899	3	-	2/9/27/28	0/3/3/3
3	A2M	L5	398	3	-	1/9/27/28	0/3/3/3
83	OMU	S2	1288	83	-	2/9/27/28	0/2/2/2
83	6MZ	S2	1832	83,87	-	3/12/28/28	0/3/3/3
3	A2M	L5	2787	3	-	5/9/27/28	0/3/3/3
5	PSU	L8	55	5	-	0/7/25/26	0/2/2/2
3	PSU	L5	3822	3	-	0/7/25/26	0/2/2/2
83	MA6	S2	1850	83	-	0/11/29/30	0/3/3/3
83	PSU	S2	1045	83	-	2/7/25/26	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
83	PSU	S2	1004	83	-	0/7/25/26	0/2/2/2
3	A2M	L5	4523	87,3	-	0/9/27/28	0/3/3/3
3	OMU	L5	4227	3	-	0/9/27/28	0/2/2/2
3	PSU	L5	3920	87,3	-	0/7/25/26	0/2/2/2
83	OMU	S2	1326	83	-	0/9/27/28	0/2/2/2
83	A2M	S2	166	83	-	0/9/27/28	0/3/3/3
3	OMC	L5	2861	3	-	1/9/27/28	0/2/2/2
3	OMC	L5	3887	3	-	1/9/27/28	0/2/2/2
3	PSU	L5	4493	3	-	0/7/25/26	0/2/2/2
83	PSU	S2	966	83,87	-	0/7/25/26	0/2/2/2
83	OMG	S2	683	83	-	2/9/27/28	0/3/3/3
83	4AC	S2	1337	83	-	1/11/29/30	0/2/2/2
3	OMC	L5	4456	3	-	0/9/27/28	0/2/2/2
83	PSU	S2	649	83	-	0/7/25/26	0/2/2/2
3	PSU	L5	2839	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	4628	3	-	0/7/25/26	0/2/2/2
83	4AC	S2	1842	83	-	0/11/29/30	0/2/2/2
83	OMG	S2	509	83	-	0/9/27/28	0/3/3/3
3	PSU	L5	4457	3	-	0/7/25/26	0/2/2/2
5	OMG	L8	75	5	-	1/9/27/28	0/3/3/3
83	OMC	S2	174	83	-	0/9/27/28	0/2/2/2
3	PSU	L5	3695	3	-	0/7/25/26	0/2/2/2
3	OMG	L5	4499	3	-	1/9/27/28	0/3/3/3
3	OMG	L5	4637	3	-	3/9/27/28	0/3/3/3
3	OMG	L5	4623	3	-	0/9/27/28	0/3/3/3
83	OMC	S2	1703	83	-	1/9/27/28	0/2/2/2
83	PSU	S2	801	83	-	2/7/25/26	0/2/2/2
3	PSU	L5	4973	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	4293	3	-	0/7/25/26	0/2/2/2
3	A2M	L5	1524	3	-	2/9/27/28	0/3/3/3
83	PSU	S2	1177	83	-	0/7/25/26	0/2/2/2
83	MA6	S2	1851	83	-	1/11/29/30	0/3/3/3
3	A2M	L5	2815	3	-	2/9/27/28	0/3/3/3
3	OMG	L5	1522	3	-	0/9/27/28	0/3/3/3
3	A2M	L5	1323	3	-	2/9/27/28	0/3/3/3
3	PSU	L5	1683	3	-	0/7/25/26	0/2/2/2
3	OMC	L5	3841	3	-	0/9/27/28	0/2/2/2
83	OMC	S2	1391	83	-	0/9/27/28	0/2/2/2
3	PSU	L5	1782	3	-	0/7/25/26	0/2/2/2
3	OMC	L5	2365	87,3	-	0/9/27/28	0/2/2/2
83	OMG	S2	1328	83	-	1/9/27/28	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PSU	L5	1860	3	-	0/7/25/26	0/2/2/2
3	A2M	L5	3785	87,3	-	0/9/27/28	0/3/3/3
83	PSU	S2	109	83	-	0/7/25/26	0/2/2/2
83	OMC	S2	1272	83	-	2/9/27/28	0/2/2/2
3	PSU	L5	4532	3	-	0/7/25/26	0/2/2/2
3	OMU	L5	4306	3	-	0/9/27/28	0/2/2/2
3	PSU	L5	4552	3	-	0/7/25/26	0/2/2/2
83	A2M	S2	1031	83	-	0/9/27/28	0/3/3/3
3	PSU	L5	3637	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	4636	3	-	1/7/25/26	0/2/2/2
3	OMU	L5	4498	3	-	0/9/27/28	0/2/2/2
3	OMG	L5	2364	87,3	-	2/9/27/28	0/3/3/3
86	SEP	CF	163	86	-	6/6/8/10	-
3	PSU	L5	1792	3	-	0/7/25/26	0/2/2/2
3	OMG	L5	4228	3	-	0/9/27/28	0/3/3/3
3	A2M	L5	400	3	-	1/9/27/28	0/3/3/3
83	A2M	S2	668	83,87	-	4/9/27/28	0/3/3/3
3	OMC	L5	2351	87,3	-	1/9/27/28	0/2/2/2
3	PSU	L5	2632	3	-	0/7/25/26	0/2/2/2
83	PSU	S2	1174	83	-	0/7/25/26	0/2/2/2
3	OMG	L5	3627	3	-	0/9/27/28	0/3/3/3
3	PSU	L5	4312	3	-	0/7/25/26	0/2/2/2
83	B8N	S2	1248	83	-	4/16/34/35	0/2/2/2
3	PSU	L5	4972	3	-	0/7/25/26	0/2/2/2
83	OMU	S2	428	83	-	6/9/27/28	0/2/2/2
83	OMG	S2	867	83	-	2/9/27/28	0/3/3/3
83	OMC	S2	517	83	-	2/9/27/28	0/2/2/2
3	PSU	L5	4579	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	5001	3	-	0/7/25/26	0/2/2/2
3	A2M	L5	3867	3	-	3/9/27/28	0/3/3/3
3	PSU	L5	4361	3	-	0/7/25/26	0/2/2/2
83	PSU	S2	1056	83	-	0/7/25/26	0/2/2/2
3	A2M	L5	2363	87,3	-	0/9/27/28	0/3/3/3
83	PSU	S2	1244	83	-	0/7/25/26	0/2/2/2
83	PSU	S2	814	83	-	0/7/25/26	0/2/2/2
83	PSU	S2	105	83	-	0/7/25/26	0/2/2/2
3	OMG	L5	4392	3	-	0/9/27/28	0/3/3/3
3	A2M	L5	1871	87,3	-	0/9/27/28	0/3/3/3
3	PSU	L5	4353	3	-	0/7/25/26	0/2/2/2
3	OMC	L5	2804	3	-	0/9/27/28	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
83	PSU	S2	93	83	-	0/7/25/26	0/2/2/2
83	OMU	S2	116	83	-	0/9/27/28	0/2/2/2
83	OMU	S2	121	83	-	0/9/27/28	0/2/2/2
83	PSU	S2	863	83	-	0/7/25/26	0/2/2/2
83	OMU	S2	1442	83	-	2/9/27/28	0/2/2/2
83	A2M	S2	576	83	-	3/9/27/28	0/3/3/3
3	5MC	L5	3782	87,3	-	1/7/25/26	0/2/2/2
83	PSU	S2	1367	83	-	0/7/25/26	0/2/2/2
3	PSU	L5	4299	3	-	0/7/25/26	0/2/2/2
83	OMU	S2	354	83	-	0/9/27/28	0/2/2/2
3	OMG	L5	2876	3	-	0/9/27/28	0/3/3/3
83	A2M	S2	468	83	-	1/9/27/28	0/3/3/3
3	PSU	L5	4673	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	1781	3	-	2/7/25/26	0/2/2/2
3	OMC	L5	3701	3	-	6/9/27/28	0/2/2/2
3	A2M	L5	1534	87,3	-	2/9/27/28	0/3/3/3
83	PSU	S2	406	83	-	0/7/25/26	0/2/2/2
83	PSU	S2	1046	83	-	0/7/25/26	0/2/2/2
83	OMU	S2	627	83	-	3/9/27/28	0/2/2/2
83	A2M	S2	159	83	-	1/9/27/28	0/3/3/3
3	PSU	L5	4296	3	-	0/7/25/26	0/2/2/2
3	UR3	L5	4530	3	-	0/7/25/26	0/2/2/2
3	5MC	L5	4447	3	-	4/7/25/26	0/2/2/2
3	OMC	L5	1340	3	-	1/9/27/28	0/2/2/2
3	PSU	L5	4403	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	1677	3	-	3/7/25/26	0/2/2/2
83	PSU	S2	1232	83	-	0/7/25/26	0/2/2/2
3	PSU	L5	4521	87,3	-	0/7/25/26	0/2/2/2
3	A2M	L5	2401	3	-	1/9/27/28	0/3/3/3
3	6MZ	L5	4220	3	-	2/9/27/28	0/3/3/3
83	PSU	S2	1081	83	-	0/7/25/26	0/2/2/2
83	PSU	S2	681	83	-	0/7/25/26	0/2/2/2
3	PSU	L5	4500	3	-	5/7/25/26	0/2/2/2
83	A2M	S2	99	83,87	-	2/9/27/28	0/3/3/3
3	PSU	L5	3884	3	-	0/7/25/26	0/2/2/2
83	OMC	S2	462	83	-	0/9/27/28	0/2/2/2
83	PSU	S2	866	83	-	0/7/25/26	0/2/2/2
3	OMC	L5	3808	3	-	0/9/27/28	0/2/2/2
83	OMG	S2	1490	83	-	1/9/27/28	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
83	OMU	S2	799	83	-	2/9/27/28	0/2/2/2
3	OMU	L5	3925	3	-	1/9/27/28	0/2/2/2
3	OMG	L5	4196	2,3	-	1/9/27/28	0/3/3/3
83	A2M	S2	27	83	-	1/9/27/28	0/3/3/3
3	OMC	L5	2824	3	-	1/9/27/28	0/2/2/2
83	OMG	S2	436	83	-	0/9/27/28	0/3/3/3
3	OMG	L5	4494	3	-	0/9/27/28	0/3/3/3
3	OMG	L5	2424	3	-	0/9/27/28	0/3/3/3
3	OMC	L5	2422	87,3	-	2/9/27/28	0/2/2/2
3	OMG	L5	4618	3	-	2/9/27/28	0/3/3/3
83	G7M	S2	1639	83,2	-	2/7/25/26	0/3/3/3
3	OMG	L5	1625	3	-	2/9/27/28	0/3/3/3
3	A2M	L5	3825	3	-	0/9/27/28	0/3/3/3

All (269) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L5	3818	UY1	C6-C5	12.92	1.49	1.35
83	S2	1832	6MZ	C6-N6	12.84	1.48	1.34
3	L5	4220	6MZ	C6-N6	12.27	1.48	1.34
3	L5	3818	UY1	C2-N1	11.92	1.52	1.36
83	S2	1442	OMU	C2-N1	8.49	1.51	1.38
83	S2	1288	OMU	C2-N1	8.42	1.51	1.38
83	S2	799	OMU	C2-N1	8.41	1.51	1.38
3	L5	4220	6MZ	C3'-C2'	-8.35	1.30	1.53
83	S2	627	OMU	C2-N1	8.35	1.51	1.38
83	S2	121	OMU	C2-N1	8.34	1.51	1.38
83	S2	428	OMU	C2-N1	8.31	1.51	1.38
83	S2	172	OMU	C2-N1	8.30	1.51	1.38
83	S2	116	OMU	C2-N1	8.25	1.51	1.38
3	L5	2837	OMU	C2-N1	8.25	1.51	1.38
83	S2	354	OMU	C2-N1	8.21	1.51	1.38
3	L5	4498	OMU	C2-N1	8.19	1.51	1.38
3	L5	4227	OMU	C2-N1	8.19	1.51	1.38
83	S2	1326	OMU	C2-N1	8.17	1.51	1.38
3	L5	3925	OMU	C2-N1	8.13	1.51	1.38
3	L5	4306	OMU	C2-N1	8.07	1.51	1.38
3	L5	4620	OMU	C2-N1	7.89	1.50	1.38
83	S2	1248	B8N	C6-N1	7.89	1.55	1.36
3	L5	3818	UY1	C2-N3	7.79	1.50	1.37
83	S2	1248	B8N	C4-N3	-7.72	1.26	1.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	S2	1248	B8N	C4-C5	7.13	1.63	1.47
83	S2	799	OMU	C2-N3	7.03	1.50	1.38
83	S2	116	OMU	C2-N3	7.03	1.50	1.38
83	S2	1326	OMU	C2-N3	7.00	1.50	1.38
83	S2	1442	OMU	C2-N3	6.99	1.50	1.38
83	S2	627	OMU	C2-N3	6.97	1.50	1.38
83	S2	121	OMU	C2-N3	6.95	1.50	1.38
83	S2	172	OMU	C2-N3	6.94	1.50	1.38
83	S2	428	OMU	C2-N3	6.93	1.50	1.38
83	S2	1288	OMU	C2-N3	6.89	1.50	1.38
3	L5	4498	OMU	C2-N3	6.84	1.49	1.38
3	L5	2837	OMU	C2-N3	6.83	1.49	1.38
3	L5	4227	OMU	C2-N3	6.83	1.49	1.38
83	S2	354	OMU	C2-N3	6.79	1.49	1.38
3	L5	3925	OMU	C2-N3	6.78	1.49	1.38
3	L5	4306	OMU	C2-N3	6.75	1.49	1.38
3	L5	4620	OMU	C2-N3	6.66	1.49	1.38
83	S2	1639	G7M	C4-N3	6.66	1.49	1.34
3	L5	4530	UR3	C2-N1	6.52	1.47	1.38
3	L5	4530	UR3	C6-C5	6.27	1.49	1.35
83	S2	1248	B8N	C2-N1	5.93	1.56	1.39
83	S2	121	OMU	C6-C5	5.92	1.48	1.35
83	S2	1326	OMU	C6-C5	5.89	1.48	1.35
83	S2	1288	OMU	C6-C5	5.89	1.48	1.35
83	S2	116	OMU	C6-C5	5.88	1.48	1.35
83	S2	428	OMU	C6-C5	5.88	1.48	1.35
83	S2	172	OMU	C6-C5	5.88	1.48	1.35
83	S2	1442	OMU	C6-C5	5.86	1.48	1.35
83	S2	627	OMU	C6-C5	5.86	1.48	1.35
3	L5	2837	OMU	C6-C5	5.85	1.48	1.35
83	S2	354	OMU	C6-C5	5.84	1.48	1.35
83	S2	799	OMU	C6-C5	5.83	1.48	1.35
3	L5	4227	OMU	C6-C5	5.81	1.48	1.35
3	L5	4498	OMU	C6-C5	5.81	1.48	1.35
3	L5	4620	OMU	C6-C5	5.80	1.48	1.35
3	L5	4530	UR3	C2-N3	5.80	1.50	1.39
3	L5	3925	OMU	C6-C5	5.78	1.48	1.35
3	L5	4306	OMU	C6-C5	5.74	1.48	1.35
83	S2	1639	G7M	C2-N3	5.53	1.46	1.33
3	L5	3818	UY1	C6-N1	5.53	1.45	1.36
3	L5	3925	OMU	O4-C4	-5.51	1.13	1.24
3	L5	4498	OMU	O4-C4	-5.50	1.13	1.24

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L5	4306	OMU	O4-C4	-5.49	1.13	1.24
3	L5	4227	OMU	O4-C4	-5.49	1.13	1.24
83	S2	1248	B8N	C6-C5	5.49	1.42	1.35
3	L5	4620	OMU	O4-C4	-5.48	1.13	1.24
83	S2	354	OMU	O4-C4	-5.48	1.13	1.24
3	L5	2837	OMU	O4-C4	-5.47	1.13	1.24
83	S2	172	OMU	O4-C4	-5.45	1.13	1.24
83	S2	1442	OMU	O4-C4	-5.44	1.13	1.24
83	S2	428	OMU	O4-C4	-5.44	1.13	1.24
83	S2	1326	OMU	O4-C4	-5.43	1.13	1.24
83	S2	121	OMU	O4-C4	-5.41	1.14	1.24
83	S2	116	OMU	O4-C4	-5.40	1.14	1.24
83	S2	627	OMU	O4-C4	-5.40	1.14	1.24
83	S2	1288	OMU	O4-C4	-5.36	1.14	1.24
83	S2	799	OMU	O4-C4	-5.35	1.14	1.24
83	S2	1639	G7M	C2-N2	4.95	1.45	1.34
3	L5	4220	6MZ	O4'-C4'	4.80	1.55	1.45
3	L5	4220	6MZ	O4'-C1'	-4.69	1.31	1.42
83	S2	1639	G7M	C5-N7	-4.57	1.33	1.39
83	S2	627	OMU	C4-N3	4.52	1.46	1.38
3	L5	3818	UY1	C4-N3	4.52	1.47	1.38
83	S2	116	OMU	C4-N3	4.45	1.46	1.38
83	S2	1442	OMU	C4-N3	4.43	1.46	1.38
83	S2	1326	OMU	C4-N3	4.43	1.46	1.38
83	S2	428	OMU	C4-N3	4.43	1.46	1.38
83	S2	1288	OMU	C4-N3	4.42	1.46	1.38
83	S2	172	OMU	C4-N3	4.38	1.46	1.38
3	L5	4220	6MZ	C5'-C4'	-4.37	1.38	1.51
83	S2	799	OMU	C4-N3	4.36	1.46	1.38
83	S2	121	OMU	C4-N3	4.31	1.46	1.38
3	L5	4498	OMU	C4-N3	4.30	1.46	1.38
83	S2	354	OMU	C4-N3	4.30	1.46	1.38
3	L5	4227	OMU	C4-N3	4.30	1.46	1.38
3	L5	2837	OMU	C4-N3	4.29	1.46	1.38
3	L5	4306	OMU	C4-N3	4.22	1.45	1.38
3	L5	3925	OMU	C4-N3	4.20	1.45	1.38
3	L5	4620	OMU	C4-N3	4.06	1.45	1.38
83	S2	1639	G7M	C5-C6	3.90	1.54	1.43
83	S2	651	PSU	C6-C5	3.82	1.39	1.35
83	S2	1248	B8N	C1'-C5	3.77	1.58	1.50
83	S2	93	PSU	C6-C5	3.76	1.39	1.35
83	S2	801	PSU	C6-C5	3.75	1.39	1.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	S2	814	PSU	C6-C5	3.70	1.39	1.35
83	S2	1004	PSU	C6-C5	3.70	1.39	1.35
3	L5	3844	PSU	C6-C5	3.68	1.39	1.35
83	S2	1244	PSU	C6-C5	3.68	1.39	1.35
83	S2	1232	PSU	C6-C5	3.68	1.39	1.35
83	S2	1046	PSU	C6-C5	3.68	1.39	1.35
83	S2	1174	PSU	C6-C5	3.68	1.39	1.35
3	L5	4500	PSU	C6-C5	3.66	1.39	1.35
83	S2	866	PSU	C6-C5	3.66	1.39	1.35
3	L5	5010	PSU	C6-C5	3.65	1.39	1.35
83	S2	1367	PSU	C6-C5	3.65	1.39	1.35
83	S2	863	PSU	C6-C5	3.65	1.39	1.35
3	L5	4493	PSU	C6-C5	3.65	1.39	1.35
3	L5	1781	PSU	C6-C5	3.64	1.39	1.35
3	L5	1683	PSU	C6-C5	3.63	1.39	1.35
83	S2	649	PSU	C6-C5	3.63	1.39	1.35
3	L5	4296	PSU	C6-C5	3.63	1.39	1.35
3	L5	1782	PSU	C6-C5	3.62	1.39	1.35
83	S2	1177	PSU	C6-C5	3.61	1.39	1.35
3	L5	1860	PSU	C6-C5	3.61	1.39	1.35
83	S2	105	PSU	C6-C5	3.61	1.39	1.35
3	L5	3818	UY1	O4-C4	-3.61	1.16	1.23
83	S2	109	PSU	C6-C5	3.61	1.39	1.35
3	L5	1744	PSU	C6-C5	3.61	1.39	1.35
3	L5	4312	PSU	C6-C5	3.61	1.39	1.35
3	L5	5001	PSU	C6-C5	3.59	1.39	1.35
3	L5	3851	PSU	C6-C5	3.59	1.39	1.35
3	L5	4293	PSU	C6-C5	3.59	1.39	1.35
83	S2	406	PSU	C6-C5	3.58	1.39	1.35
3	L5	4361	PSU	C6-C5	3.58	1.39	1.35
3	L5	4471	PSU	C6-C5	3.58	1.39	1.35
83	S2	966	PSU	C6-C5	3.57	1.39	1.35
3	L5	2632	PSU	C6-C5	3.56	1.39	1.35
83	S2	686	PSU	C6-C5	3.56	1.39	1.35
3	L5	3637	PSU	C6-C5	3.55	1.39	1.35
83	S2	1045	PSU	C6-C5	3.55	1.39	1.35
3	L5	4673	PSU	C6-C5	3.55	1.39	1.35
83	S2	1056	PSU	C6-C5	3.54	1.39	1.35
3	L5	3822	PSU	C6-C5	3.54	1.39	1.35
5	L8	55	PSU	C6-C5	3.54	1.39	1.35
86	CF	163	SEP	P-O1P	3.53	1.61	1.50
3	L5	1582	PSU	C6-C5	3.53	1.39	1.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L5	4532	PSU	C6-C5	3.53	1.39	1.35
3	L5	4552	PSU	C6-C5	3.53	1.39	1.35
3	L5	4431	PSU	C6-C5	3.53	1.39	1.35
3	L5	2401	A2M	O5'-C5'	-3.51	1.33	1.44
3	L5	2839	PSU	C6-C5	3.49	1.39	1.35
3	L5	3884	PSU	C6-C5	3.49	1.39	1.35
83	S2	1081	PSU	C6-C5	3.49	1.39	1.35
3	L5	1792	PSU	C6-C5	3.48	1.39	1.35
3	L5	3853	PSU	C6-C5	3.48	1.39	1.35
3	L5	4442	PSU	C6-C5	3.48	1.39	1.35
3	L5	4576	PSU	C6-C5	3.48	1.39	1.35
3	L5	3695	PSU	C6-C5	3.48	1.39	1.35
3	L5	3920	PSU	C6-C5	3.47	1.39	1.35
3	L5	4353	PSU	C6-C5	3.47	1.39	1.35
5	L8	69	PSU	C6-C5	3.45	1.39	1.35
3	L5	1862	PSU	C6-C5	3.45	1.39	1.35
3	L5	4972	PSU	C6-C5	3.45	1.39	1.35
3	L5	4299	PSU	C6-C5	3.43	1.39	1.35
3	L5	1536	PSU	C6-C5	3.43	1.39	1.35
3	L5	4636	PSU	C6-C5	3.43	1.39	1.35
3	L5	4579	PSU	C6-C5	3.43	1.39	1.35
3	L5	4973	PSU	C6-C5	3.42	1.39	1.35
3	L5	4521	PSU	C6-C5	3.42	1.39	1.35
3	L5	3825	A2M	O5'-C5'	-3.41	1.34	1.44
3	L5	3639	PSU	C6-C5	3.40	1.39	1.35
83	S2	668	A2M	O5'-C5'	-3.39	1.34	1.44
3	L5	3785	A2M	O5'-C5'	-3.39	1.34	1.44
3	L5	3830	A2M	O5'-C5'	-3.39	1.34	1.44
3	L5	4457	PSU	C6-C5	3.39	1.39	1.35
83	S2	681	PSU	C6-C5	3.37	1.39	1.35
3	L5	3818	UY1	C1'-C5	3.37	1.57	1.50
3	L5	1323	A2M	O5'-C5'	-3.35	1.34	1.44
3	L5	2787	A2M	O5'-C5'	-3.35	1.34	1.44
3	L5	400	A2M	O5'-C5'	-3.34	1.34	1.44
83	S2	166	A2M	O5'-C5'	-3.34	1.34	1.44
83	S2	99	A2M	O5'-C5'	-3.34	1.34	1.44
3	L5	4571	A2M	O5'-C5'	-3.33	1.34	1.44
3	L5	1871	A2M	O5'-C5'	-3.33	1.34	1.44
83	S2	468	A2M	O5'-C5'	-3.32	1.34	1.44
83	S2	576	A2M	O5'-C5'	-3.32	1.34	1.44
3	L5	1524	A2M	O5'-C5'	-3.30	1.34	1.44
3	L5	2815	A2M	O5'-C5'	-3.30	1.34	1.44

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	S2	1031	A2M	O5'-C5'	-3.30	1.34	1.44
3	L5	4523	A2M	O5'-C5'	-3.30	1.34	1.44
3	L5	4689	PSU	C6-C5	3.29	1.38	1.35
3	L5	3867	A2M	O5'-C5'	-3.29	1.34	1.44
83	S2	27	A2M	O5'-C5'	-3.28	1.34	1.44
3	L5	2363	A2M	O5'-C5'	-3.28	1.34	1.44
3	L5	1677	PSU	C6-C5	3.27	1.38	1.35
3	L5	3718	A2M	O5'-C5'	-3.26	1.34	1.44
3	L5	4628	PSU	C6-C5	3.25	1.38	1.35
3	L5	398	A2M	O5'-C5'	-3.24	1.34	1.44
83	S2	1383	A2M	O5'-C5'	-3.24	1.34	1.44
3	L5	1326	A2M	O5'-C5'	-3.22	1.34	1.44
83	S2	484	A2M	O5'-C5'	-3.21	1.34	1.44
83	S2	1851	MA6	C6-N6	3.21	1.45	1.36
83	S2	1850	MA6	C6-N6	3.19	1.45	1.36
3	L5	4590	A2M	O5'-C5'	-3.18	1.34	1.44
83	S2	1832	6MZ	C5-N7	-3.18	1.33	1.39
3	L5	3818	UY1	O2-C2	-3.17	1.16	1.23
3	L5	4220	6MZ	C5-N7	-3.15	1.33	1.39
3	L5	4220	6MZ	C5-C4	-3.15	1.33	1.39
83	S2	159	A2M	O5'-C5'	-3.14	1.35	1.44
3	L5	4403	PSU	C6-C5	3.14	1.38	1.35
3	L5	4220	6MZ	C2'-C1'	3.13	1.63	1.53
3	L5	1534	A2M	O5'-C5'	-3.07	1.35	1.44
83	S2	1832	6MZ	C5-C4	-2.93	1.33	1.39
83	S2	799	OMU	C5-C4	2.89	1.50	1.43
83	S2	1288	OMU	C5-C4	2.87	1.49	1.43
83	S2	627	OMU	C5-C4	2.86	1.49	1.43
83	S2	1639	G7M	C2-N1	2.86	1.44	1.37
83	S2	354	OMU	C5-C4	2.86	1.49	1.43
83	S2	1326	OMU	C5-C4	2.86	1.49	1.43
83	S2	1442	OMU	C5-C4	2.84	1.49	1.43
83	S2	428	OMU	C5-C4	2.84	1.49	1.43
83	S2	1832	6MZ	C8-N9	-2.84	1.32	1.37
3	L5	3925	OMU	C5-C4	2.82	1.49	1.43
3	L5	4498	OMU	C5-C4	2.81	1.49	1.43
83	S2	172	OMU	C5-C4	2.80	1.49	1.43
3	L5	4220	6MZ	C8-N9	-2.78	1.32	1.37
83	S2	121	OMU	C5-C4	2.77	1.49	1.43
83	S2	121	OMU	C6-N1	2.77	1.44	1.38
83	S2	1288	OMU	C6-N1	2.75	1.44	1.38
3	L5	2837	OMU	C5-C4	2.74	1.49	1.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L5	4227	OMU	C5-C4	2.74	1.49	1.43
83	S2	116	OMU	C5-C4	2.73	1.49	1.43
3	L5	4220	6MZ	O3'-C3'	2.73	1.49	1.43
3	L5	4306	OMU	C5-C4	2.72	1.49	1.43
83	S2	1326	OMU	C6-N1	2.69	1.44	1.38
3	L5	4620	OMU	C5-C4	2.69	1.49	1.43
83	S2	799	OMU	C6-N1	2.69	1.44	1.38
83	S2	1442	OMU	C6-N1	2.68	1.44	1.38
83	S2	627	OMU	C6-N1	2.68	1.44	1.38
83	S2	354	OMU	C6-N1	2.67	1.44	1.38
3	L5	4498	OMU	C6-N1	2.67	1.44	1.38
3	L5	4306	OMU	C6-N1	2.64	1.44	1.38
83	S2	116	OMU	C6-N1	2.64	1.44	1.38
83	S2	428	OMU	C6-N1	2.63	1.44	1.38
3	L5	4227	OMU	C6-N1	2.63	1.44	1.38
83	S2	668	A2M	O4'-C4'	-2.62	1.39	1.45
83	S2	172	OMU	C6-N1	2.61	1.44	1.38
3	L5	2837	OMU	C6-N1	2.60	1.44	1.38
3	L5	4620	OMU	C6-N1	2.59	1.44	1.38
3	L5	4530	UR3	C6-N1	2.57	1.44	1.38
3	L5	4530	UR3	O2-C2	-2.57	1.17	1.22
3	L5	3925	OMU	C6-N1	2.53	1.44	1.38
83	S2	1639	G7M	C6-N1	2.47	1.43	1.38
83	S2	1639	G7M	O6-C6	-2.44	1.18	1.23
83	S2	1851	MA6	C5-C4	-2.35	1.34	1.39
3	L5	4530	UR3	C5-C4	2.33	1.49	1.43
83	S2	1850	MA6	C5-C4	-2.28	1.35	1.39
3	L5	1524	A2M	O4'-C4'	-2.24	1.40	1.45
3	L5	1323	A2M	O4'-C4'	-2.16	1.40	1.45
3	L5	4530	UR3	C3U-N3	2.16	1.50	1.47
3	L5	4220	6MZ	C6-N1	-2.12	1.31	1.35
3	L5	3818	UY1	C4-C5	2.11	1.50	1.44
83	S2	159	A2M	C5-C4	2.11	1.42	1.39
3	L5	3818	UY1	O4'-C1'	-2.08	1.41	1.43
83	S2	1832	6MZ	C6-N1	-2.06	1.31	1.35

All (687) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	1851	MA6	N1-C6-N6	-12.01	102.22	116.86
83	S2	1850	MA6	N1-C6-N6	-11.89	102.36	116.86
83	S2	1850	MA6	C5-C6-N6	7.99	137.98	125.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	1851	MA6	C5-C6-N6	7.92	137.87	125.33
83	S2	1639	G7M	C1'-N9-C4	7.48	148.60	126.49
83	S2	1639	G7M	C1'-N9-C8	-7.35	101.91	126.74
3	L5	3925	OMU	C4-N3-C2	-5.79	119.42	126.61
83	S2	1851	MA6	N1-C2-N3	-5.73	119.90	128.58
83	S2	428	OMU	C4-N3-C2	-5.69	119.54	126.61
3	L5	2837	OMU	C4-N3-C2	-5.66	119.58	126.61
83	S2	1832	6MZ	N1-C2-N3	-5.66	120.02	128.58
83	S2	172	OMU	C4-N3-C2	-5.66	119.59	126.61
83	S2	354	OMU	C4-N3-C2	-5.65	119.59	126.61
3	L5	4220	6MZ	N1-C2-N3	-5.65	120.03	128.58
3	L5	4498	OMU	C4-N3-C2	-5.64	119.61	126.61
83	S2	1326	OMU	C4-N3-C2	-5.63	119.62	126.61
83	S2	627	OMU	C4-N3-C2	-5.60	119.65	126.61
3	L5	4227	OMU	C4-N3-C2	-5.57	119.70	126.61
3	L5	4306	OMU	C4-N3-C2	-5.56	119.71	126.61
83	S2	121	OMU	C4-N3-C2	-5.55	119.72	126.61
3	L5	4530	UR3	C4-N3-C2	-5.52	120.14	124.58
83	S2	1442	OMU	C4-N3-C2	-5.52	119.76	126.61
83	S2	1850	MA6	N1-C2-N3	-5.50	120.26	128.58
83	S2	799	OMU	C4-N3-C2	-5.43	119.87	126.61
83	S2	1851	MA6	N9-C8-N7	-5.41	106.26	113.94
83	S2	1288	OMU	C4-N3-C2	-5.38	119.94	126.61
3	L5	3637	PSU	N1-C2-N3	5.36	120.82	115.17
83	S2	1248	B8N	C5-C4-N3	5.26	125.70	116.15
83	S2	1850	MA6	N9-C8-N7	-5.22	106.54	113.94
83	S2	116	OMU	C4-N3-C2	-5.20	120.15	126.61
3	L5	4636	PSU	C4-N3-C2	-5.09	119.36	126.37
3	L5	4620	OMU	C4-N3-C2	-5.05	120.35	126.61
3	L5	1677	PSU	C4-N3-C2	-5.03	119.44	126.37
3	L5	4521	PSU	C4-N3-C2	-4.97	119.52	126.37
3	L5	4636	PSU	N1-C2-N3	4.96	120.40	115.17
3	L5	4521	PSU	N1-C2-N3	4.95	120.39	115.17
3	L5	4457	PSU	C4-N3-C2	-4.93	119.57	126.37
3	L5	3637	PSU	C4-N3-C2	-4.93	119.58	126.37
83	S2	649	PSU	C4-N3-C2	-4.92	119.59	126.37
3	L5	4296	PSU	C4-N3-C2	-4.91	119.61	126.37
83	S2	651	PSU	C4-N3-C2	-4.91	119.61	126.37
3	L5	4403	PSU	C4-N3-C2	-4.91	119.61	126.37
83	S2	1232	PSU	C4-N3-C2	-4.90	119.62	126.37
3	L5	3695	PSU	N1-C2-N3	4.90	120.34	115.17
3	L5	4500	PSU	C4-N3-C2	-4.90	119.62	126.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	1232	PSU	N1-C2-N3	4.89	120.33	115.17
3	L5	1860	PSU	C4-N3-C2	-4.89	119.64	126.37
3	L5	4973	PSU	C4-N3-C2	-4.88	119.64	126.37
3	L5	1862	PSU	C4-N3-C2	-4.88	119.65	126.37
3	L5	3695	PSU	C4-N3-C2	-4.88	119.65	126.37
3	L5	4500	PSU	N1-C2-N3	4.88	120.31	115.17
83	S2	651	PSU	N1-C2-N3	4.88	120.31	115.17
3	L5	4293	PSU	C4-N3-C2	-4.88	119.66	126.37
3	L5	2632	PSU	N1-C2-N3	4.87	120.31	115.17
83	S2	686	PSU	C4-N3-C2	-4.87	119.66	126.37
3	L5	4296	PSU	N1-C2-N3	4.87	120.31	115.17
83	S2	406	PSU	N1-C2-N3	4.87	120.31	115.17
83	S2	686	PSU	N1-C2-N3	4.87	120.30	115.17
3	L5	4689	PSU	N1-C2-N3	4.87	120.30	115.17
3	L5	1860	PSU	N1-C2-N3	4.86	120.29	115.17
3	L5	3884	PSU	C4-N3-C2	-4.85	119.69	126.37
3	L5	4673	PSU	N1-C2-N3	4.85	120.28	115.17
3	L5	4442	PSU	C4-N3-C2	-4.84	119.70	126.37
3	L5	4293	PSU	N1-C2-N3	4.84	120.28	115.17
3	L5	1677	PSU	N1-C2-N3	4.84	120.27	115.17
83	S2	105	PSU	N1-C2-N3	4.84	120.27	115.17
3	L5	4299	PSU	C4-N3-C2	-4.84	119.70	126.37
3	L5	1683	PSU	N1-C2-N3	4.84	120.27	115.17
3	L5	2632	PSU	C4-N3-C2	-4.83	119.71	126.37
3	L5	4552	PSU	C4-N3-C2	-4.83	119.71	126.37
3	L5	3818	UY1	C4-N3-C2	-4.83	119.71	126.37
3	L5	1536	PSU	N1-C2-N3	4.83	120.26	115.17
83	S2	866	PSU	C4-N3-C2	-4.83	119.72	126.37
83	S2	1174	PSU	C4-N3-C2	-4.82	119.73	126.37
3	L5	3851	PSU	N1-C2-N3	4.82	120.25	115.17
3	L5	4552	PSU	N1-C2-N3	4.82	120.25	115.17
83	S2	406	PSU	C4-N3-C2	-4.82	119.73	126.37
83	S2	649	PSU	N1-C2-N3	4.82	120.25	115.17
3	L5	4353	PSU	N1-C2-N3	4.82	120.25	115.17
3	L5	1782	PSU	N1-C2-N3	4.81	120.24	115.17
3	L5	3639	PSU	C4-N3-C2	-4.81	119.75	126.37
3	L5	4673	PSU	C4-N3-C2	-4.81	119.75	126.37
3	L5	3920	PSU	N1-C2-N3	4.80	120.23	115.17
83	S2	1177	PSU	C4-N3-C2	-4.80	119.75	126.37
3	L5	4442	PSU	N1-C2-N3	4.80	120.23	115.17
3	L5	4353	PSU	C4-N3-C2	-4.80	119.76	126.37
3	L5	4457	PSU	N1-C2-N3	4.80	120.23	115.17

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	1862	PSU	N1-C2-N3	4.80	120.23	115.17
3	L5	3822	PSU	N1-C2-N3	4.80	120.23	115.17
3	L5	3884	PSU	N1-C2-N3	4.79	120.22	115.17
5	L8	55	PSU	N1-C2-N3	4.79	120.22	115.17
3	L5	1744	PSU	N1-C2-N3	4.79	120.22	115.17
3	L5	4579	PSU	C4-N3-C2	-4.78	119.78	126.37
83	S2	1832	6MZ	C5-C4-N3	-4.78	120.13	126.72
3	L5	4972	PSU	C4-N3-C2	-4.78	119.78	126.37
3	L5	1683	PSU	C4-N3-C2	-4.78	119.79	126.37
3	L5	5010	PSU	C4-N3-C2	-4.78	119.79	126.37
83	S2	1244	PSU	N1-C2-N3	4.78	120.21	115.17
3	L5	4493	PSU	C4-N3-C2	-4.77	119.79	126.37
83	S2	1081	PSU	C4-N3-C2	-4.77	119.79	126.37
3	L5	4312	PSU	N1-C2-N3	4.77	120.20	115.17
3	L5	4972	PSU	N1-C2-N3	4.77	120.20	115.17
3	L5	1782	PSU	C4-N3-C2	-4.77	119.80	126.37
83	S2	863	PSU	C4-N3-C2	-4.77	119.80	126.37
3	L5	3701	OMC	C1'-N1-C2	4.77	128.98	118.44
3	L5	4431	PSU	C4-N3-C2	-4.77	119.80	126.37
83	S2	1244	PSU	C4-N3-C2	-4.77	119.80	126.37
83	S2	1177	PSU	N1-C2-N3	4.77	120.20	115.17
83	S2	866	PSU	N1-C2-N3	4.77	120.19	115.17
83	S2	1056	PSU	N1-C2-N3	4.76	120.19	115.17
3	L5	3639	PSU	N1-C2-N3	4.76	120.19	115.17
3	L5	4299	PSU	N1-C2-N3	4.75	120.18	115.17
3	L5	5010	PSU	N1-C2-N3	4.75	120.18	115.17
3	L5	3920	PSU	C4-N3-C2	-4.75	119.83	126.37
83	S2	1045	PSU	C4-N3-C2	-4.75	119.83	126.37
83	S2	1056	PSU	C4-N3-C2	-4.74	119.83	126.37
3	L5	2839	PSU	N1-C2-N3	4.74	120.17	115.17
83	S2	1367	PSU	N1-C2-N3	4.74	120.17	115.17
3	L5	4579	PSU	N1-C2-N3	4.74	120.17	115.17
5	L8	69	PSU	C4-N3-C2	-4.74	119.84	126.37
83	S2	1367	PSU	C4-N3-C2	-4.74	119.84	126.37
5	L8	55	PSU	C4-N3-C2	-4.74	119.84	126.37
5	L8	69	PSU	N1-C2-N3	4.74	120.16	115.17
83	S2	1045	PSU	N1-C2-N3	4.74	120.16	115.17
83	S2	109	PSU	C4-N3-C2	-4.73	119.85	126.37
3	L5	4493	PSU	N1-C2-N3	4.73	120.16	115.17
3	L5	4576	PSU	C4-N3-C2	-4.73	119.86	126.37
3	L5	4532	PSU	C4-N3-C2	-4.73	119.86	126.37
83	S2	1174	PSU	N1-C2-N3	4.72	120.15	115.17

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	4431	PSU	N1-C2-N3	4.72	120.15	115.17
3	L5	1792	PSU	N1-C2-N3	4.72	120.14	115.17
3	L5	1744	PSU	C4-N3-C2	-4.72	119.87	126.37
3	L5	4220	6MZ	N9-C8-N7	-4.71	107.25	113.94
3	L5	1781	PSU	N1-C2-N3	4.71	120.13	115.17
3	L5	4361	PSU	N1-C2-N3	4.71	120.13	115.17
83	S2	681	PSU	N1-C2-N3	4.71	120.13	115.17
3	L5	4312	PSU	C4-N3-C2	-4.70	119.89	126.37
3	L5	4471	PSU	N1-C2-N3	4.70	120.13	115.17
3	L5	4361	PSU	C4-N3-C2	-4.70	119.89	126.37
3	L5	4403	PSU	N1-C2-N3	4.70	120.12	115.17
3	L5	3844	PSU	N1-C2-N3	4.69	120.11	115.17
3	L5	4973	PSU	N1-C2-N3	4.68	120.11	115.17
3	L5	4689	PSU	C4-N3-C2	-4.68	119.92	126.37
3	L5	3822	PSU	C4-N3-C2	-4.68	119.93	126.37
3	L5	1792	PSU	C4-N3-C2	-4.67	119.93	126.37
83	S2	1081	PSU	N1-C2-N3	4.67	120.10	115.17
3	L5	1536	PSU	C4-N3-C2	-4.67	119.94	126.37
3	L5	4576	PSU	N1-C2-N3	4.67	120.09	115.17
83	S2	1004	PSU	C4-N3-C2	-4.66	119.95	126.37
3	L5	3851	PSU	C4-N3-C2	-4.66	119.95	126.37
3	L5	4532	PSU	N1-C2-N3	4.65	120.07	115.17
3	L5	2839	PSU	C4-N3-C2	-4.65	119.96	126.37
83	S2	814	PSU	C4-N3-C2	-4.65	119.96	126.37
83	S2	105	PSU	C4-N3-C2	-4.65	119.97	126.37
3	L5	5001	PSU	N1-C2-N3	4.64	120.06	115.17
83	S2	1046	PSU	N1-C2-N3	4.64	120.06	115.17
83	S2	863	PSU	N1-C2-N3	4.64	120.06	115.17
83	S2	681	PSU	C4-N3-C2	-4.63	119.99	126.37
3	L5	4220	6MZ	C5-C4-N3	-4.62	120.35	126.72
83	S2	966	PSU	N1-C2-N3	4.62	120.04	115.17
3	L5	5001	PSU	C4-N3-C2	-4.62	120.01	126.37
83	S2	1046	PSU	C4-N3-C2	-4.61	120.01	126.37
83	S2	801	PSU	N1-C2-N3	4.61	120.03	115.17
83	S2	1832	6MZ	N9-C8-N7	-4.61	107.40	113.94
83	S2	1248	B8N	C4-N3-C2	-4.61	119.95	125.62
83	S2	966	PSU	C4-N3-C2	-4.60	120.04	126.37
83	S2	1004	PSU	N1-C2-N3	4.60	120.02	115.17
83	S2	1383	A2M	C3'-C2'-C1'	-4.59	94.01	102.81
83	S2	93	PSU	N1-C2-N3	4.59	120.01	115.17
83	S2	109	PSU	N1-C2-N3	4.59	120.01	115.17
83	S2	1851	MA6	C5-C4-N3	-4.59	120.40	126.72

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	93	PSU	C4-N3-C2	-4.58	120.06	126.37
83	S2	814	PSU	N1-C2-N3	4.58	120.00	115.17
3	L5	4628	PSU	N1-C2-N3	4.55	119.96	115.17
83	S2	1850	MA6	C5-C4-N3	-4.53	120.48	126.72
3	L5	1781	PSU	C4-N3-C2	-4.52	120.14	126.37
3	L5	1582	PSU	N1-C2-N3	4.52	119.94	115.17
3	L5	4628	PSU	C4-N3-C2	-4.51	120.16	126.37
3	L5	3844	PSU	C4-N3-C2	-4.50	120.18	126.37
3	L5	3853	PSU	N1-C2-N3	4.48	119.90	115.17
83	S2	801	PSU	C4-N3-C2	-4.47	120.22	126.37
3	L5	3853	PSU	C4-N3-C2	-4.46	120.23	126.37
83	S2	1639	G7M	C2-N3-C4	4.45	119.97	112.30
3	L5	4471	PSU	C4-N3-C2	-4.45	120.24	126.37
3	L5	4220	6MZ	C9-N6-C6	-4.45	118.72	122.85
3	L5	3818	UY1	N1-C2-N3	4.34	119.75	115.17
3	L5	1582	PSU	C4-N3-C2	-4.31	120.44	126.37
83	S2	1851	MA6	C4-N9-C8	4.25	110.20	105.74
3	L5	3830	A2M	C3'-C2'-C1'	-4.21	94.76	102.81
83	S2	121	OMU	N3-C2-N1	4.18	120.33	114.89
83	S2	1850	MA6	C4-N9-C8	4.04	109.98	105.74
3	L5	3925	OMU	N3-C2-N1	4.04	120.15	114.89
83	S2	1639	G7M	C5-C6-N1	4.01	120.12	111.84
83	S2	1639	G7M	C5-C4-N3	-4.01	120.58	128.15
3	L5	4498	OMU	N3-C2-N1	3.99	120.09	114.89
3	L5	4523	A2M	C3'-C2'-C1'	-3.97	95.21	102.81
3	L5	2837	OMU	N3-C2-N1	3.96	120.04	114.89
3	L5	1871	A2M	C3'-C2'-C1'	-3.94	95.27	102.81
83	S2	354	OMU	N3-C2-N1	3.90	119.97	114.89
83	S2	1248	B8N	C1'-C5-C4	3.86	123.47	117.61
83	S2	1326	OMU	N3-C2-N1	3.85	119.90	114.89
3	L5	4306	OMU	N3-C2-N1	3.84	119.89	114.89
83	S2	172	OMU	N3-C2-N1	3.83	119.88	114.89
3	L5	398	A2M	C3'-C2'-C1'	-3.83	95.47	102.81
3	L5	4227	OMU	N3-C2-N1	3.82	119.87	114.89
83	S2	428	OMU	N3-C2-N1	3.78	119.81	114.89
3	L5	3701	OMC	C1'-N1-C6	-3.76	112.75	120.78
83	S2	1442	OMU	N3-C2-N1	3.75	119.77	114.89
83	S2	627	OMU	N3-C2-N1	3.71	119.72	114.89
83	S2	428	OMU	C5-C4-N3	3.70	119.98	114.80
83	S2	1288	OMU	N3-C2-N1	3.69	119.70	114.89
83	S2	1850	MA6	C4-C5-C6	3.68	119.71	115.91
83	S2	799	OMU	N3-C2-N1	3.67	119.67	114.89

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	354	OMU	C5-C4-N3	3.65	119.91	114.80
83	S2	116	OMU	N3-C2-N1	3.64	119.63	114.89
3	L5	4620	OMU	N3-C2-N1	3.64	119.63	114.89
3	L5	3925	OMU	C5-C4-N3	3.64	119.89	114.80
3	L5	4227	OMU	C5-C4-N3	3.63	119.89	114.80
3	L5	4306	OMU	C5-C4-N3	3.62	119.87	114.80
3	L5	4530	UR3	C5-C4-N3	3.61	119.80	115.04
83	S2	627	OMU	C5-C4-N3	3.60	119.85	114.80
3	L5	398	A2M	O3'-C3'-C2'	3.60	121.28	111.19
83	S2	172	OMU	C5-C4-N3	3.60	119.84	114.80
83	S2	1326	OMU	C5-C4-N3	3.59	119.83	114.80
83	S2	799	OMU	C5-C4-N3	3.58	119.82	114.80
83	S2	1442	OMU	C5-C4-N3	3.58	119.82	114.80
3	L5	4498	OMU	C5-C4-N3	3.58	119.82	114.80
3	L5	2837	OMU	C5-C4-N3	3.58	119.82	114.80
3	L5	1534	A2M	C3'-C2'-C1'	-3.58	95.96	102.81
83	S2	1383	A2M	O3'-C3'-C2'	3.56	121.15	111.19
83	S2	1031	A2M	C3'-C2'-C1'	-3.55	96.02	102.81
83	S2	166	A2M	O3'-C3'-C2'	3.54	121.10	111.19
3	L5	2401	A2M	O3'-C3'-C2'	3.53	121.08	111.19
3	L5	1323	A2M	C2'-C1'-N9	3.53	119.56	113.75
83	S2	1851	MA6	C2-N1-C6	3.53	120.44	111.83
83	S2	1288	OMU	C5-C4-N3	3.52	119.73	114.80
83	S2	1850	MA6	C2-N1-C6	3.51	120.41	111.83
83	S2	121	OMU	C5-C4-N3	3.48	119.68	114.80
83	S2	1248	B8N	N3-C2-N1	3.45	120.94	116.72
83	S2	116	OMU	C5-C4-N3	3.45	119.64	114.80
83	S2	1851	MA6	C4-C5-C6	3.43	119.46	115.91
83	S2	576	A2M	O3'-C3'-C2'	3.43	120.78	111.19
83	S2	1851	MA6	N3-C4-N9	3.40	132.96	127.17
83	S2	1832	6MZ	C2-N3-C4	3.40	120.14	111.83
3	L5	3718	A2M	C3'-C2'-C1'	-3.38	96.33	102.81
83	S2	468	A2M	O3'-C3'-C2'	3.38	120.65	111.19
3	L5	4620	OMU	C5-C4-N3	3.37	119.52	114.80
83	S2	468	A2M	C3'-C2'-C1'	-3.35	96.38	102.81
3	L5	4220	6MZ	C2-N3-C4	3.35	120.02	111.83
3	L5	2787	A2M	O3'-C3'-C2'	3.34	120.53	111.19
3	L5	1524	A2M	O3'-C3'-C2'	3.32	120.48	111.19
83	S2	1851	MA6	C2-N3-C4	3.30	119.88	111.83
83	S2	1639	G7M	O6-C6-C5	-3.29	120.66	128.01
83	S2	1850	MA6	N3-C4-N9	3.29	132.75	127.17
83	S2	99	A2M	C3'-C2'-C1'	-3.28	96.52	102.81

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	1639	G7M	CN7-N7-C5	3.26	130.86	126.80
3	L5	3818	UY1	C6-C5-C4	3.25	120.37	118.17
3	L5	4590	A2M	C3'-C2'-C1'	-3.24	96.60	102.81
83	S2	1031	A2M	O3'-C3'-C2'	3.23	120.24	111.19
3	L5	3718	A2M	O3'-C3'-C2'	3.23	120.23	111.19
3	L5	3825	A2M	O3'-C3'-C2'	3.22	120.21	111.19
83	S2	668	A2M	C4-N9-C1'	-3.22	119.09	126.63
83	S2	1851	MA6	C5-N7-C8	3.22	108.52	103.45
83	S2	576	A2M	C3'-C2'-C1'	-3.22	96.64	102.81
83	S2	99	A2M	O3'-C3'-C2'	3.20	120.15	111.19
3	L5	3830	A2M	O3'-C3'-C2'	3.20	120.13	111.19
83	S2	1832	6MZ	C4-C5-C6	3.19	119.43	116.78
3	L5	400	A2M	O3'-C3'-C2'	3.18	120.08	111.19
3	L5	4571	A2M	O3'-C3'-C2'	3.17	120.06	111.19
83	S2	1639	G7M	N9-C4-N3	3.17	132.29	125.95
83	S2	1832	6MZ	N3-C4-N9	3.17	132.55	127.17
83	S2	159	A2M	O3'-C3'-C2'	3.16	120.03	111.19
3	L5	4220	6MZ	C4-N9-C8	3.16	109.05	105.74
83	S2	1832	6MZ	C5-N7-C8	3.15	108.40	103.45
3	L5	3825	A2M	C3'-C2'-C1'	-3.15	96.78	102.81
83	S2	1850	MA6	C2-N3-C4	3.14	119.50	111.83
3	L5	1536	PSU	O2-C2-N1	-3.13	119.56	122.79
3	L5	4220	6MZ	N3-C4-N9	3.13	132.48	127.17
83	S2	1850	MA6	C5-N7-C8	3.12	108.35	103.45
83	S2	166	A2M	C3'-C2'-C1'	-3.10	96.86	102.81
3	L5	2401	A2M	C3'-C2'-C1'	-3.06	96.95	102.81
3	L5	3785	A2M	O3'-C3'-C2'	3.05	119.72	111.19
86	CF	163	SEP	OG-CB-CA	3.03	111.09	108.14
83	S2	1442	OMU	O4-C4-C5	-3.03	119.94	125.16
3	L5	4689	PSU	C6-N1-C2	-3.03	119.88	122.69
83	S2	484	A2M	O3'-C3'-C2'	3.03	119.66	111.19
3	L5	3867	A2M	C2'-C1'-N9	3.02	118.72	113.75
3	L5	4590	A2M	C4-N9-C1'	-3.01	119.59	126.63
3	L5	1871	A2M	C4-N9-C1'	-3.01	119.60	126.63
83	S2	428	OMU	O4-C4-C5	-3.01	119.98	125.16
83	S2	1639	G7M	C2-N1-C6	-3.00	119.67	125.11
3	L5	4523	A2M	O3'-C3'-C2'	3.00	119.58	111.19
3	L5	4689	PSU	O2-C2-N1	-3.00	119.70	122.79
3	L5	2815	A2M	O3'-C3'-C2'	2.99	119.56	111.19
3	L5	1326	A2M	O3'-C3'-C2'	2.99	119.55	111.19
83	S2	668	A2M	O3'-C3'-C2'	2.98	119.53	111.19
3	L5	4312	PSU	O2-C2-N1	-2.98	119.72	122.79

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	1323	A2M	O3'-C3'-C2'	2.98	119.52	111.19
3	L5	3818	UY1	C6-N1-C2	-2.98	119.93	122.69
3	L5	400	A2M	C3'-C2'-C1'	-2.97	97.11	102.81
83	S2	27	A2M	C3'-C2'-C1'	-2.97	97.12	102.81
3	L5	2401	A2M	C4-N9-C1'	-2.97	119.69	126.63
3	L5	4227	OMU	O4-C4-C5	-2.96	120.06	125.16
83	S2	172	OMU	O4-C4-C5	-2.96	120.06	125.16
83	S2	27	A2M	O3'-C3'-C2'	2.96	119.47	111.19
3	L5	1871	A2M	O3'-C3'-C2'	2.95	119.45	111.19
3	L5	2632	PSU	O2-C2-N1	-2.95	119.75	122.79
83	S2	668	A2M	C1'-N9-C8	2.94	133.63	127.09
3	L5	4220	6MZ	C5-N7-C8	2.94	108.07	103.45
83	S2	468	A2M	C4-N9-C1'	-2.93	119.77	126.63
83	S2	627	OMU	O4-C4-C5	-2.93	120.10	125.16
3	L5	3785	A2M	C4'-O4'-C1'	-2.93	102.99	109.47
3	L5	4571	A2M	C3'-C2'-C1'	-2.93	97.20	102.81
3	L5	4579	PSU	O2-C2-N1	-2.92	119.77	122.79
83	S2	686	PSU	O2-C2-N1	-2.92	119.78	122.79
83	S2	116	OMU	O4-C4-C5	-2.92	120.13	125.16
3	L5	4500	PSU	O2-C2-N1	-2.92	119.78	122.79
83	S2	1832	6MZ	C4-N9-C8	2.91	108.80	105.74
83	S2	121	OMU	O4-C4-C5	-2.91	120.15	125.16
3	L5	4306	OMU	O4-C4-C5	-2.90	120.16	125.16
3	L5	2839	PSU	O2-C2-N1	-2.90	119.80	122.79
83	S2	1288	OMU	O4-C4-C5	-2.90	120.16	125.16
83	S2	1326	OMU	O4-C4-C5	-2.89	120.17	125.16
3	L5	4498	OMU	O4-C4-C5	-2.89	120.18	125.16
83	S2	799	OMU	O4-C4-C5	-2.89	120.18	125.16
83	S2	99	A2M	C4-N9-C1'	-2.89	119.88	126.63
83	S2	406	PSU	O2-C2-N1	-2.89	119.81	122.79
3	L5	4521	PSU	O2-C2-N1	-2.89	119.81	122.79
83	S2	668	A2M	O4'-C1'-C2'	2.88	111.55	106.59
3	L5	4220	6MZ	C4-C5-C6	2.88	119.18	116.78
83	S2	354	OMU	O4-C4-C5	-2.88	120.20	125.16
3	L5	2837	OMU	O4-C4-C5	-2.87	120.21	125.16
3	L5	4590	A2M	O3'-C3'-C2'	2.86	119.20	111.19
83	S2	1177	PSU	O2-C2-N1	-2.86	119.83	122.79
83	S2	1031	A2M	C4-N9-C1'	-2.86	119.94	126.63
3	L5	4523	A2M	C4-N9-C1'	-2.86	119.94	126.63
3	L5	2363	A2M	O3'-C3'-C2'	2.86	119.19	111.19
83	S2	1056	PSU	O2-C2-N1	-2.85	119.84	122.79
3	L5	3851	PSU	O2-C2-N1	-2.85	119.85	122.79

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	1174	PSU	O2-C2-N1	-2.84	119.86	122.79
83	S2	1244	PSU	O2-C2-N1	-2.83	119.87	122.79
3	L5	4636	PSU	O2-C2-N1	-2.83	119.87	122.79
3	L5	3925	OMU	O4-C4-C5	-2.83	120.28	125.16
5	L8	69	PSU	O2-C2-N1	-2.83	119.87	122.79
83	S2	1383	A2M	C4-N9-C1'	-2.83	120.02	126.63
3	L5	3639	PSU	O2-C2-N1	-2.83	119.87	122.79
3	L5	4431	PSU	O2-C2-N1	-2.82	119.88	122.79
3	L5	3695	PSU	O2-C2-N1	-2.82	119.88	122.79
3	L5	3785	A2M	C4-N9-C1'	-2.82	120.05	126.63
3	L5	4442	PSU	O2-C2-N1	-2.81	119.89	122.79
3	L5	4673	PSU	O2-C2-N1	-2.81	119.89	122.79
3	L5	3825	A2M	C4-N9-C1'	-2.81	120.06	126.63
3	L5	5010	PSU	O2-C2-N1	-2.81	119.89	122.79
83	S2	1004	PSU	O2-C2-N1	-2.80	119.90	122.79
83	S2	651	PSU	O2-C2-N1	-2.80	119.90	122.79
3	L5	4403	PSU	O2-C2-N1	-2.80	119.90	122.79
3	L5	1683	PSU	O2-C2-N1	-2.79	119.91	122.79
3	L5	3884	PSU	O2-C2-N1	-2.79	119.91	122.79
3	L5	2401	A2M	C1'-N9-C8	2.79	133.28	127.09
83	S2	1248	B8N	O4-C4-N3	-2.79	115.47	119.99
3	L5	4552	PSU	O2-C2-N1	-2.78	119.92	122.79
3	L5	4972	PSU	O2-C2-N1	-2.78	119.92	122.79
3	L5	3822	PSU	O2-C2-N1	-2.77	119.93	122.79
83	S2	1046	PSU	O2-C2-N1	-2.77	119.93	122.79
3	L5	1871	A2M	C1'-N9-C8	2.76	133.23	127.09
3	L5	1677	PSU	O2-C2-N1	-2.76	119.94	122.79
3	L5	1860	PSU	O2-C2-N1	-2.76	119.94	122.79
3	L5	3830	A2M	C4-N9-C1'	-2.76	120.18	126.63
3	L5	1744	PSU	O2-C2-N1	-2.76	119.94	122.79
83	S2	99	A2M	C1'-N9-C8	2.76	133.21	127.09
3	L5	4576	PSU	O2-C2-N1	-2.75	119.95	122.79
3	L5	4590	A2M	C1'-N9-C8	2.75	133.20	127.09
3	L5	1524	A2M	O4'-C1'-C2'	2.75	111.32	106.59
3	L5	3867	A2M	C4-N9-C1'	-2.75	120.20	126.63
3	L5	2839	PSU	C6-N1-C2	-2.75	120.14	122.69
83	S2	27	A2M	C4-N9-C1'	-2.74	120.23	126.63
3	L5	1781	PSU	O2-C2-N1	-2.74	119.97	122.79
3	L5	4973	PSU	O2-C2-N1	-2.73	119.97	122.79
83	S2	159	A2M	C4-N9-C1'	-2.73	120.25	126.63
3	L5	4353	PSU	O2-C2-N1	-2.73	119.98	122.79
3	L5	4493	PSU	O2-C2-N1	-2.72	119.98	122.79

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	398	A2M	C4-N9-C1'	-2.72	120.27	126.63
3	L5	4628	PSU	O2-C2-N1	-2.72	119.98	122.79
83	S2	681	PSU	O2-C2-N1	-2.72	119.99	122.79
3	L5	400	A2M	C4-N9-C1'	-2.71	120.28	126.63
3	L5	2363	A2M	C3'-C2'-C1'	-2.71	97.61	102.81
3	L5	3844	PSU	O2-C2-N1	-2.71	119.99	122.79
3	L5	1782	PSU	O2-C2-N1	-2.70	120.00	122.79
3	L5	3920	PSU	O2-C2-N1	-2.70	120.00	122.79
3	L5	1792	PSU	O2-C2-N1	-2.70	120.01	122.79
3	L5	5001	PSU	O2-C2-N1	-2.70	120.01	122.79
83	S2	166	A2M	C4-N9-C1'	-2.69	120.33	126.63
83	S2	1639	G7M	CN7-N7-C8	-2.69	120.71	124.79
3	L5	4296	PSU	O2-C2-N1	-2.69	120.01	122.79
83	S2	801	PSU	O2-C2-N1	-2.69	120.01	122.79
83	S2	468	A2M	C1'-N9-C8	2.69	133.06	127.09
83	S2	866	PSU	O2-C2-N1	-2.69	120.02	122.79
3	L5	3637	PSU	C6-N1-C2	-2.69	120.20	122.69
3	L5	4571	A2M	C4-N9-C1'	-2.69	120.35	126.63
3	L5	1862	PSU	O2-C2-N1	-2.68	120.02	122.79
3	L5	3825	A2M	C1'-N9-C8	2.68	133.04	127.09
3	L5	4532	PSU	O2-C2-N1	-2.68	120.03	122.79
3	L5	1536	PSU	C6-N1-C2	-2.68	120.21	122.69
3	L5	1326	A2M	C3'-C2'-C1'	-2.67	97.69	102.81
5	L8	55	PSU	O2-C2-N1	-2.67	120.03	122.79
3	L5	2787	A2M	O4'-C1'-C2'	2.67	111.19	106.59
3	L5	398	A2M	C1'-N9-C8	2.67	133.01	127.09
83	S2	966	PSU	O2-C2-N1	-2.66	120.04	122.79
83	S2	159	A2M	C1'-N9-C8	2.66	133.00	127.09
83	S2	109	PSU	O2-C2-N1	-2.66	120.04	122.79
83	S2	1367	PSU	O2-C2-N1	-2.66	120.05	122.79
3	L5	4293	PSU	O2-C2-N1	-2.65	120.05	122.79
83	S2	105	PSU	O2-C2-N1	-2.65	120.05	122.79
3	L5	4361	PSU	O2-C2-N1	-2.65	120.06	122.79
3	L5	3718	A2M	C4-N9-C1'	-2.65	120.44	126.63
3	L5	3853	PSU	O2-C2-N1	-2.64	120.06	122.79
3	L5	4620	OMU	O4-C4-C5	-2.64	120.61	125.16
83	S2	1031	A2M	C1'-N9-C8	2.64	132.95	127.09
3	L5	4471	PSU	O2-C2-N1	-2.64	120.07	122.79
3	L5	3844	PSU	C6-N1-C2	-2.64	120.24	122.69
83	S2	105	PSU	C6-N1-C2	-2.63	120.25	122.69
3	L5	1323	A2M	O4'-C1'-C2'	2.63	111.12	106.59
83	S2	801	PSU	C6-N1-C2	-2.63	120.25	122.69

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	3808	OMC	C1'-N1-C2	2.62	124.23	118.44
3	L5	3718	A2M	C1'-N9-C8	2.62	132.92	127.09
3	L5	1326	A2M	C4-N9-C1'	-2.62	120.50	126.63
3	L5	4523	A2M	C1'-N9-C8	2.62	132.91	127.09
83	S2	1045	PSU	O2-C2-N1	-2.62	120.09	122.79
83	S2	814	PSU	O2-C2-N1	-2.62	120.09	122.79
3	L5	4471	PSU	C6-N1-C2	-2.62	120.26	122.69
3	L5	1582	PSU	O2-C2-N1	-2.62	120.09	122.79
83	S2	863	PSU	O2-C2-N1	-2.61	120.09	122.79
3	L5	2363	A2M	C4-N9-C1'	-2.61	120.53	126.63
3	L5	2351	OMC	C1'-N1-C2	2.61	124.20	118.44
3	L5	3818	UY1	O2-C2-N1	-2.60	120.10	122.79
3	L5	1534	A2M	C2'-C1'-N9	2.60	118.03	113.75
3	L5	3830	A2M	C1'-N9-C8	2.60	132.87	127.09
83	S2	484	A2M	C4-N9-C1'	-2.60	120.55	126.63
3	L5	1781	PSU	C6-N1-C2	-2.60	120.28	122.69
83	S2	1383	A2M	C1'-N9-C8	2.60	132.86	127.09
83	S2	649	PSU	O2-C2-N1	-2.59	120.11	122.79
3	L5	4312	PSU	C6-N1-C2	-2.59	120.29	122.69
83	S2	27	A2M	C1'-N9-C8	2.59	132.84	127.09
3	L5	1326	A2M	C2'-C1'-N9	2.59	118.01	113.75
3	L5	3867	A2M	C1'-N9-C8	2.58	132.83	127.09
3	L5	4628	PSU	C6-N1-C2	-2.58	120.30	122.69
83	S2	1232	PSU	O2-C2-N1	-2.58	120.13	122.79
83	S2	1272	OMC	C1'-N1-C2	2.57	124.12	118.44
3	L5	3822	PSU	C6-N1-C2	-2.57	120.31	122.69
83	S2	681	PSU	C6-N1-C2	-2.57	120.31	122.69
3	L5	3785	A2M	C1'-N9-C8	2.56	132.78	127.09
3	L5	1582	PSU	C6-N1-C2	-2.56	120.32	122.69
83	S2	484	A2M	C1'-N9-C8	2.55	132.76	127.09
3	L5	1323	A2M	C3'-C2'-C1'	-2.55	97.92	102.81
3	L5	2363	A2M	C1'-N9-C8	2.54	132.73	127.09
3	L5	3785	A2M	C3'-C2'-C1'	-2.54	97.94	102.81
3	L5	400	A2M	C1'-N9-C8	2.54	132.73	127.09
83	S2	406	PSU	C6-N1-C2	-2.54	120.33	122.69
3	L5	3695	PSU	C6-N1-C2	-2.54	120.34	122.69
3	L5	4673	PSU	C6-N1-C2	-2.53	120.34	122.69
83	S2	576	A2M	C4-N9-C1'	-2.53	120.72	126.63
83	S2	1046	PSU	C6-N1-C2	-2.53	120.35	122.69
3	L5	4579	PSU	C6-N1-C2	-2.52	120.35	122.69
3	L5	2787	A2M	C4-N9-C1'	-2.52	120.73	126.63
3	L5	4457	PSU	O2-C2-N1	-2.52	120.19	122.79

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	1004	PSU	C6-N1-C2	-2.52	120.35	122.69
3	L5	3851	PSU	C6-N1-C2	-2.52	120.35	122.69
83	S2	166	A2M	C1'-N9-C8	2.52	132.69	127.09
3	L5	5001	PSU	C6-N1-C2	-2.52	120.35	122.69
3	L5	4431	PSU	C6-N1-C2	-2.52	120.36	122.69
3	L5	4500	PSU	C6-N1-C2	-2.51	120.36	122.69
3	L5	3867	A2M	O3'-C3'-C2'	2.51	118.22	111.19
5	L8	55	PSU	C6-N1-C2	-2.51	120.36	122.69
3	L5	2861	OMC	C1'-N1-C2	2.51	123.98	118.44
3	L5	1744	PSU	C6-N1-C2	-2.51	120.36	122.69
3	L5	3701	OMC	O2-C2-N3	-2.51	118.38	122.33
83	S2	1081	PSU	O2-C2-N1	-2.51	120.20	122.79
3	L5	4571	A2M	C1'-N9-C8	2.50	132.64	127.09
3	L5	3884	PSU	C6-N1-C2	-2.50	120.37	122.69
3	L5	2815	A2M	C2'-C1'-N9	2.50	117.86	113.75
83	S2	159	A2M	C3'-C2'-C1'	-2.50	98.03	102.81
3	L5	5010	PSU	C6-N1-C2	-2.49	120.38	122.69
3	L5	2632	PSU	C6-N1-C2	-2.49	120.38	122.69
3	L5	1683	PSU	C6-N1-C2	-2.49	120.38	122.69
3	L5	1792	PSU	C6-N1-C2	-2.49	120.38	122.69
3	L5	4552	PSU	C6-N1-C2	-2.49	120.38	122.69
83	S2	1056	PSU	C6-N1-C2	-2.49	120.38	122.69
3	L5	1860	PSU	C6-N1-C2	-2.48	120.39	122.69
3	L5	1534	A2M	C4-N9-C1'	-2.48	120.83	126.63
83	S2	484	A2M	O4'-C1'-C2'	2.47	110.84	106.59
83	S2	1851	MA6	C1'-N9-C8	-2.47	121.61	127.09
3	L5	1326	A2M	C1'-N9-C8	2.47	132.57	127.09
3	L5	3701	OMC	O2-C2-N1	2.47	123.73	118.90
3	L5	2363	A2M	C2'-C1'-N9	2.46	117.80	113.75
3	L5	4299	PSU	O2-C2-N1	-2.46	120.25	122.79
3	L5	1782	PSU	C6-N1-C2	-2.46	120.41	122.69
3	L5	4293	PSU	C6-N1-C2	-2.45	120.41	122.69
3	L5	3639	PSU	C6-N1-C2	-2.45	120.41	122.69
83	S2	1244	PSU	C6-N1-C2	-2.45	120.42	122.69
83	S2	966	PSU	C6-N1-C2	-2.45	120.42	122.69
83	S2	1177	PSU	C6-N1-C2	-2.45	120.42	122.69
83	S2	651	PSU	C6-N1-C2	-2.44	120.43	122.69
3	L5	4521	PSU	C6-N1-C2	-2.44	120.43	122.69
83	S2	686	PSU	C6-N1-C2	-2.44	120.43	122.69
83	S2	1232	PSU	C6-N1-C2	-2.43	120.44	122.69
3	L5	1534	A2M	O3'-C3'-C2'	2.43	117.99	111.19
3	L5	3920	PSU	C6-N1-C2	-2.43	120.44	122.69

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	1174	PSU	C6-N1-C2	-2.42	120.44	122.69
83	S2	863	PSU	C6-N1-C2	-2.42	120.45	122.69
3	L5	1323	A2M	C4-N9-C1'	-2.42	120.98	126.63
83	S2	93	PSU	O2-C2-N1	-2.42	120.30	122.79
3	L5	1534	A2M	C1'-N9-C8	2.41	132.45	127.09
3	L5	4353	PSU	C6-N1-C2	-2.41	120.45	122.69
3	L5	2787	A2M	C1'-N9-C8	2.41	132.44	127.09
5	L8	69	PSU	C6-N1-C2	-2.41	120.46	122.69
83	S2	1367	PSU	C6-N1-C2	-2.40	120.46	122.69
3	L5	4220	6MZ	C5-C6-N1	2.40	120.73	118.15
3	L5	4361	PSU	C6-N1-C2	-2.40	120.46	122.69
83	S2	576	A2M	C1'-N9-C8	2.40	132.42	127.09
3	L5	4972	PSU	C6-N1-C2	-2.40	120.47	122.69
3	L5	4576	PSU	C6-N1-C2	-2.39	120.47	122.69
3	L5	4442	PSU	C6-N1-C2	-2.39	120.47	122.69
83	S2	1045	PSU	C6-N1-C2	-2.39	120.47	122.69
3	L5	3853	PSU	C6-N1-C2	-2.39	120.48	122.69
3	L5	4403	PSU	O4'-C1'-C2'	2.38	108.45	105.15
3	L5	4457	PSU	C6-N1-C2	-2.38	120.49	122.69
3	L5	2363	A2M	O4'-C1'-C2'	2.37	110.67	106.59
83	S2	1337	4AC	N4-C4-N3	2.37	117.72	113.87
83	S2	93	PSU	C6-N1-C2	-2.36	120.50	122.69
3	L5	4493	PSU	C6-N1-C2	-2.36	120.50	122.69
83	S2	649	PSU	C6-N1-C2	-2.35	120.51	122.69
83	S2	814	PSU	C6-N1-C2	-2.35	120.51	122.69
83	S2	866	PSU	C6-N1-C2	-2.35	120.51	122.69
3	L5	3822	PSU	O4'-C1'-C2'	2.35	108.40	105.15
3	L5	3637	PSU	O2-C2-N1	-2.33	120.38	122.79
3	L5	2815	A2M	C4-N9-C1'	-2.33	121.19	126.63
3	L5	1323	A2M	C1'-N9-C8	2.33	132.26	127.09
83	S2	109	PSU	C6-N1-C2	-2.31	120.54	122.69
3	L5	1326	A2M	O4'-C1'-C2'	2.31	110.57	106.59
3	L5	4299	PSU	C6-N1-C2	-2.31	120.55	122.69
3	L5	1862	PSU	C6-N1-C2	-2.31	120.55	122.69
83	S2	1248	B8N	O4'-C1'-C2'	2.31	108.35	105.15
3	L5	4296	PSU	C6-N1-C2	-2.30	120.56	122.69
83	S2	668	A2M	C6-C5-C4	-2.29	114.05	117.18
3	L5	4636	PSU	C6-C5-C4	2.29	119.72	118.17
3	L5	400	A2M	O4'-C1'-C2'	2.29	110.53	106.59
3	L5	1322	1MA	N1-C6-N6	2.28	125.44	119.71
3	L5	4456	OMC	C1'-N1-C2	2.28	123.48	118.44
3	L5	3637	PSU	C6-C5-C4	2.28	119.71	118.17

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	1081	PSU	C6-N1-C2	-2.28	120.58	122.69
3	L5	2815	A2M	C1'-N9-C8	2.27	132.14	127.09
83	S2	484	A2M	O4'-C4'-C3'	2.27	109.67	105.15
3	L5	4636	PSU	C6-N1-C2	-2.27	120.58	122.69
83	S2	799	OMU	C1'-N1-C2	2.27	121.67	117.59
3	L5	1524	A2M	C4-N9-C1'	-2.27	121.33	126.63
3	L5	4403	PSU	C6-C5-C4	2.26	119.70	118.17
3	L5	1677	PSU	C6-C5-C4	2.26	119.70	118.17
3	L5	4442	PSU	O4'-C1'-C2'	2.26	108.28	105.15
3	L5	3639	PSU	C6-C5-C4	2.26	119.70	118.17
3	L5	4532	PSU	C6-N1-C2	-2.25	120.60	122.69
3	L5	1524	A2M	C4'-O4'-C1'	-2.25	104.49	109.47
3	L5	4530	UR3	C6-N1-C2	-2.25	119.96	121.80
3	L5	400	A2M	C2'-C1'-N9	2.25	117.45	113.75
3	L5	4590	A2M	C6-C5-C4	-2.24	114.11	117.18
3	L5	2815	A2M	C3'-C2'-C1'	-2.24	98.52	102.81
3	L5	4973	PSU	C6-N1-C2	-2.24	120.61	122.69
83	S2	1639	G7M	N9-C8-N7	-2.24	107.05	112.48
3	L5	1871	A2M	C6-C5-C4	-2.24	114.12	117.18
3	L5	3785	A2M	C2-N1-C6	-2.23	115.06	118.73
3	L5	1524	A2M	C1'-N9-C8	2.22	132.02	127.09
83	S2	468	A2M	O4'-C1'-C2'	2.22	110.41	106.59
3	L5	4590	A2M	O4'-C1'-C2'	2.22	110.41	106.59
3	L5	4521	PSU	C6-C5-C4	2.21	119.67	118.17
3	L5	2837	OMU	O2-C2-N1	-2.21	119.92	122.80
3	L5	1534	A2M	O3'-C3'-C4'	-2.20	104.75	111.08
3	L5	2815	A2M	O4'-C1'-C2'	2.20	110.38	106.59
3	L5	4227	OMU	O2-C2-N1	-2.20	119.93	122.80
3	L5	1677	PSU	C6-N1-C2	-2.20	120.65	122.69
3	L5	4498	OMU	O2-C2-N1	-2.20	119.94	122.80
3	L5	2632	PSU	C6-C5-C4	2.20	119.66	118.17
3	L5	4457	PSU	O4'-C1'-C2'	2.19	108.18	105.15
5	L8	69	PSU	O4'-C1'-C2'	2.19	108.18	105.15
83	S2	462	OMC	C1'-N1-C2	2.19	123.27	118.44
3	L5	2401	A2M	C6-C5-C4	-2.19	114.19	117.18
3	L5	3830	A2M	C6-C5-C4	-2.19	114.19	117.18
83	S2	1326	OMU	O2-C2-N1	-2.19	119.95	122.80
83	S2	1832	6MZ	C4-C5-N7	-2.18	108.09	110.58
3	L5	3825	A2M	C6-C5-C4	-2.18	114.20	117.18
3	L5	4571	A2M	C6-C5-C4	-2.17	114.21	117.18
83	S2	27	A2M	C6-C5-C4	-2.17	114.22	117.18
83	S2	1850	MA6	C1'-N9-C8	-2.17	122.29	127.09

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	S2	1383	A2M	C4'-O4'-C1'	-2.17	104.68	109.47
83	S2	1383	A2M	C6-C5-C4	-2.17	114.22	117.18
83	S2	1248	B8N	O4-C4-C5	-2.16	118.84	122.58
83	S2	121	OMU	O2-C2-N1	-2.16	119.98	122.80
83	S2	866	PSU	C6-C5-C4	2.16	119.63	118.17
83	S2	468	A2M	C6-C5-C4	-2.16	114.23	117.18
3	L5	4571	A2M	O4'-C1'-C2'	2.15	110.30	106.59
83	S2	668	A2M	C2'-C1'-N9	2.15	117.30	113.75
83	S2	686	PSU	C6-C5-C4	2.15	119.63	118.17
83	S2	166	A2M	C6-C5-C4	-2.15	114.24	117.18
3	L5	3867	A2M	C6-C5-C4	-2.15	114.25	117.18
3	L5	3785	A2M	C5-C6-N1	2.15	122.96	117.51
83	S2	166	A2M	O4'-C1'-C2'	2.14	110.28	106.59
83	S2	354	OMU	O2-C2-N1	-2.14	120.01	122.80
3	L5	4500	PSU	C6-C5-C4	2.14	119.62	118.17
3	L5	398	A2M	C6-C5-C4	-2.14	114.26	117.18
3	L5	1871	A2M	O4'-C1'-C2'	2.14	110.27	106.59
83	S2	406	PSU	C6-C5-C4	2.14	119.62	118.17
3	L5	400	A2M	C6-C5-C4	-2.14	114.26	117.18
3	L5	4523	A2M	C6-C5-C4	-2.14	114.26	117.18
3	L5	1326	A2M	C6-C5-C4	-2.13	114.26	117.18
83	S2	99	A2M	C6-C5-C4	-2.13	114.27	117.18
3	L5	2787	A2M	C6-C5-C4	-2.13	114.27	117.18
3	L5	4353	PSU	C6-C5-C4	2.13	119.61	118.17
3	L5	4523	A2M	C4'-O4'-C1'	-2.13	104.77	109.47
3	L5	4403	PSU	C6-N1-C2	-2.12	120.72	122.69
3	L5	3785	A2M	C6-C5-C4	-2.12	114.28	117.18
3	L5	3695	PSU	O4'-C1'-C2'	2.12	108.08	105.15
83	S2	1031	A2M	C6-C5-C4	-2.12	114.29	117.18
3	L5	2787	A2M	O4'-C4'-C3'	2.11	109.35	105.15
83	S2	27	A2M	O4'-C1'-C2'	2.11	110.22	106.59
3	L5	3718	A2M	C6-C5-C4	-2.11	114.30	117.18
83	S2	1244	PSU	C6-C5-C4	2.11	119.60	118.17
3	L5	3925	OMU	O2-C2-N1	-2.10	120.06	122.80
83	S2	428	OMU	O2-C2-N1	-2.10	120.06	122.80
83	S2	576	A2M	C6-C5-C4	-2.10	114.31	117.18
3	L5	4636	PSU	O4'-C1'-C2'	2.09	108.05	105.15
83	S2	159	A2M	C6-C5-C4	-2.09	114.32	117.18
83	S2	1031	A2M	O4'-C1'-C2'	2.09	110.18	106.59
3	L5	3785	A2M	O4'-C4'-C3'	2.08	109.28	105.15
83	S2	159	A2M	O4'-C1'-C2'	2.08	110.17	106.59
3	L5	3867	A2M	O4'-C4'-C3'	2.07	109.27	105.15

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	1534	A2M	C6-C5-C4	-2.07	114.35	117.18
3	L5	1534	A2M	C2-N1-C6	-2.07	115.33	118.73
3	L5	3867	A2M	O4'-C1'-C2'	2.07	110.14	106.59
3	L5	4442	PSU	C6-C5-C4	2.07	119.57	118.17
3	L5	3867	A2M	C2-N1-C6	-2.06	115.34	118.73
3	L5	4220	6MZ	C3'-C2'-C1'	2.06	105.37	101.46
3	L5	3825	A2M	O4'-C1'-C2'	2.06	110.14	106.59
3	L5	4296	PSU	C6-C5-C4	2.06	119.56	118.17
3	L5	2815	A2M	C5-C6-N1	2.05	122.72	117.51
3	L5	1326	A2M	C5-C6-N1	2.05	122.72	117.51
3	L5	1534	A2M	C5-C6-N1	2.05	122.72	117.51
83	S2	1442	OMU	C1'-N1-C2	2.05	121.28	117.59
3	L5	3808	OMC	C1'-N1-C6	-2.05	116.40	120.78
3	L5	2401	A2M	O4'-C1'-C2'	2.05	110.12	106.59
83	S2	166	A2M	C5-C6-N1	2.05	122.71	117.51
3	L5	3825	A2M	C2-N1-C6	-2.04	115.38	118.73
83	S2	649	PSU	C6-C5-C4	2.04	119.55	118.17
3	L5	3830	A2M	C4'-O4'-C1'	-2.04	104.96	109.47
3	L5	1323	A2M	C2-N1-C6	-2.04	115.38	118.73
3	L5	1323	A2M	C5-C6-N1	2.04	122.69	117.51
3	L5	3825	A2M	C5-C6-N1	2.04	122.69	117.51
3	L5	1323	A2M	C6-C5-C4	-2.04	114.40	117.18
3	L5	3830	A2M	C5-C6-N1	2.04	122.69	117.51
3	L5	398	A2M	C5-C6-N1	2.04	122.68	117.51
3	L5	1524	A2M	C6-C5-C4	-2.03	114.40	117.18
3	L5	1326	A2M	C2-N1-C6	-2.03	115.39	118.73
3	L5	2815	A2M	C6-C5-C4	-2.03	114.41	117.18
3	L5	2363	A2M	C2-N1-C6	-2.03	115.40	118.73
3	L5	400	A2M	C5-C6-N1	2.03	122.66	117.51
3	L5	4571	A2M	C5-C6-N1	2.03	122.66	117.51
83	S2	27	A2M	C5-C6-N1	2.03	122.66	117.51
83	S2	99	A2M	O4'-C1'-C2'	2.02	110.07	106.59
83	S2	1031	A2M	C5-C6-N1	2.02	122.65	117.51
83	S2	1248	B8N	C31-N3-C4	2.02	120.04	117.18
83	S2	484	A2M	C6-C5-C4	-2.02	114.42	117.18
83	S2	468	A2M	C5-C6-N1	2.02	122.65	117.51
83	S2	1383	A2M	C5-C6-N1	2.02	122.64	117.51
3	L5	2363	A2M	C5-C6-N1	2.02	122.64	117.51
3	L5	3718	A2M	C5-C6-N1	2.02	122.64	117.51
3	L5	4576	PSU	O4'-C1'-C2'	2.02	107.94	105.15
3	L5	398	A2M	C2-N1-C6	-2.02	115.41	118.73
3	L5	2401	A2M	C5-C6-N1	2.02	122.64	117.51

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	2787	A2M	C5-C6-N1	2.02	122.64	117.51
83	S2	99	A2M	C5-C6-N1	2.02	122.63	117.51
3	L5	2363	A2M	C6-C5-C4	-2.01	114.43	117.18
3	L5	3718	A2M	C2-N1-C6	-2.01	115.43	118.73
83	S2	1081	PSU	O4'-C1'-C2'	2.01	107.93	105.15
83	S2	159	A2M	C2-N1-C6	-2.01	115.43	118.73
83	S2	159	A2M	C5-C6-N1	2.01	122.61	117.51
83	S2	172	OMU	O2-C2-N1	-2.01	120.19	122.80
3	L5	2815	A2M	C2-N1-C6	-2.00	115.44	118.73
3	L5	4523	A2M	C5-C6-N1	2.00	122.59	117.51
3	L5	3851	PSU	O4'-C1'-C2'	2.00	107.92	105.15
3	L5	4457	PSU	C6-C5-C4	2.00	119.52	118.17

There are no chirality outliers.

All (148) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	CF	163	SEP	C-CA-CB-OG
86	CF	163	SEP	CB-OG-P-O1P
86	CF	163	SEP	CB-OG-P-O2P
86	CF	163	SEP	CB-OG-P-O3P
3	L5	400	A2M	C1'-C2'-O2'-CM'
3	L5	1326	A2M	O4'-C4'-C5'-O5'
3	L5	1326	A2M	C1'-C2'-O2'-CM'
3	L5	1340	OMC	C1'-C2'-O2'-CM2
3	L5	1625	OMG	O4'-C4'-C5'-O5'
3	L5	2351	OMC	C1'-C2'-O2'-CM2
3	L5	2787	A2M	C1'-C2'-O2'-CM'
3	L5	2824	OMC	C1'-C2'-O2'-CM2
3	L5	2861	OMC	C1'-C2'-O2'-CM2
3	L5	3701	OMC	O4'-C4'-C5'-O5'
3	L5	3792	OMG	O4'-C4'-C5'-O5'
3	L5	3867	A2M	C1'-C2'-O2'-CM'
3	L5	4196	OMG	C1'-C2'-O2'-CM2
3	L5	4220	6MZ	O4'-C4'-C5'-O5'
3	L5	4590	A2M	O4'-C4'-C5'-O5'
3	L5	4636	PSU	C2'-C1'-C5-C4
3	L5	4637	OMG	O4'-C4'-C5'-O5'
3	L5	4637	OMG	C1'-C2'-O2'-CM2
83	S2	27	A2M	C1'-C2'-O2'-CM'
83	S2	159	A2M	C1'-C2'-O2'-CM'
83	S2	468	A2M	C1'-C2'-O2'-CM'

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
83	S2	601	OMG	C1'-C2'-O2'-CM2
83	S2	644	OMG	O4'-C4'-C5'-O5'
83	S2	644	OMG	C1'-C2'-O2'-CM2
83	S2	1248	B8N	O4'-C4'-C5'-O5'
83	S2	1272	OMC	C3'-C4'-C5'-O5'
83	S2	1272	OMC	O4'-C4'-C5'-O5'
83	S2	1288	OMU	O4'-C4'-C5'-O5'
83	S2	1328	OMG	C1'-C2'-O2'-CM2
83	S2	1337	4AC	N3-C4-N4-C7
83	S2	1383	A2M	C1'-C2'-O2'-CM'
83	S2	1442	OMU	O4'-C4'-C5'-O5'
83	S2	1832	6MZ	C5-C6-N6-C9
83	S2	1832	6MZ	N1-C6-N6-C9
3	L5	1323	A2M	O4'-C4'-C5'-O5'
3	L5	1326	A2M	C3'-C4'-C5'-O5'
3	L5	1536	PSU	O4'-C4'-C5'-O5'
3	L5	3701	OMC	C3'-C4'-C5'-O5'
3	L5	3867	A2M	C3'-C4'-C5'-O5'
3	L5	4500	PSU	C3'-C4'-C5'-O5'
3	L5	4500	PSU	O4'-C4'-C5'-O5'
3	L5	4590	A2M	C3'-C4'-C5'-O5'
83	S2	576	A2M	O4'-C4'-C5'-O5'
83	S2	576	A2M	C3'-C4'-C5'-O5'
83	S2	683	OMG	C3'-C4'-C5'-O5'
83	S2	801	PSU	C3'-C4'-C5'-O5'
83	S2	867	OMG	C3'-C4'-C5'-O5'
83	S2	1288	OMU	C3'-C4'-C5'-O5'
3	L5	1536	PSU	C3'-C4'-C5'-O5'
3	L5	2364	OMG	O4'-C4'-C5'-O5'
83	S2	517	OMC	C3'-C4'-C5'-O5'
83	S2	517	OMC	O4'-C4'-C5'-O5'
83	S2	799	OMU	C3'-C4'-C5'-O5'
83	S2	799	OMU	O4'-C4'-C5'-O5'
83	S2	1442	OMU	C3'-C4'-C5'-O5'
3	L5	4447	5MC	C2'-C1'-N1-C6
83	S2	428	OMU	C2'-C1'-N1-C6
3	L5	1625	OMG	C3'-C4'-C5'-O5'
3	L5	3792	OMG	C3'-C4'-C5'-O5'
3	L5	3899	OMG	C3'-C4'-C5'-O5'
83	S2	644	OMG	C3'-C4'-C5'-O5'
83	S2	683	OMG	O4'-C4'-C5'-O5'
3	L5	4447	5MC	C2'-C1'-N1-C2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	L5	4220	6MZ	C3'-C4'-C5'-O5'
3	L5	4637	OMG	C3'-C4'-C5'-O5'
83	S2	1248	B8N	C3'-C4'-C5'-O5'
83	S2	1248	B8N	N34-C33-C34-O36
3	L5	3701	OMC	C2'-C1'-N1-C2
3	L5	1323	A2M	C3'-C4'-C5'-O5'
3	L5	1524	A2M	O4'-C4'-C5'-O5'
3	L5	1677	PSU	O4'-C4'-C5'-O5'
3	L5	3867	A2M	O4'-C4'-C5'-O5'
3	L5	3899	OMG	O4'-C4'-C5'-O5'
83	S2	99	A2M	O4'-C4'-C5'-O5'
83	S2	801	PSU	O4'-C4'-C5'-O5'
83	S2	867	OMG	O4'-C4'-C5'-O5'
83	S2	1045	PSU	C3'-C4'-C5'-O5'
83	S2	1045	PSU	O4'-C4'-C5'-O5'
3	L5	1524	A2M	C3'-C4'-C5'-O5'
3	L5	3701	OMC	C2'-C1'-N1-C6
3	L5	1677	PSU	C3'-C4'-C5'-O5'
3	L5	1781	PSU	C3'-C4'-C5'-O5'
83	S2	668	A2M	O4'-C4'-C5'-O5'
3	L5	4590	A2M	C4'-C5'-O5'-P
3	L5	2364	OMG	C3'-C4'-C5'-O5'
3	L5	2815	A2M	O4'-C4'-C5'-O5'
83	S2	1383	A2M	O4'-C4'-C5'-O5'
3	L5	2787	A2M	C2'-C1'-N9-C8
5	L8	75	OMG	C1'-C2'-O2'-CM2
3	L5	4618	OMG	C3'-C4'-C5'-O5'
83	S2	627	OMU	O4'-C4'-C5'-O5'
83	S2	668	A2M	C3'-C4'-C5'-O5'
3	L5	2422	OMC	C3'-C4'-C5'-O5'
3	L5	2422	OMC	O4'-C4'-C5'-O5'
3	L5	2787	A2M	C3'-C4'-C5'-O5'
83	S2	1383	A2M	C3'-C4'-C5'-O5'
86	CF	163	SEP	CA-CB-OG-P
3	L5	3701	OMC	O4'-C1'-N1-C2
83	S2	428	OMU	C2'-C1'-N1-C2
3	L5	3701	OMC	O4'-C1'-N1-C6
83	S2	428	OMU	O4'-C1'-N1-C6
3	L5	3887	OMC	C3'-C4'-C5'-O5'
83	S2	428	OMU	O4'-C1'-N1-C2
86	CF	163	SEP	N-CA-CB-OG
3	L5	4447	5MC	O4'-C1'-N1-C6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	L5	1534	A2M	C4'-C5'-O5'-P
3	L5	3818	UY1	C4'-C5'-O5'-P
3	L5	4500	PSU	C4'-C5'-O5'-P
83	S2	1851	MA6	C4'-C5'-O5'-P
3	L5	3818	UY1	O4'-C1'-C5-C4
3	L5	4500	PSU	O4'-C1'-C5-C4
3	L5	2787	A2M	C2'-C1'-N9-C4
3	L5	4447	5MC	O4'-C1'-N1-C2
3	L5	2815	A2M	C3'-C4'-C5'-O5'
83	S2	99	A2M	C3'-C4'-C5'-O5'
83	S2	428	OMU	O4'-C4'-C5'-O5'
83	S2	1639	G7M	C3'-C4'-C5'-O5'
83	S2	576	A2M	C4'-C5'-O5'-P
83	S2	644	OMG	C4'-C5'-O5'-P
83	S2	1490	OMG	C4'-C5'-O5'-P
3	L5	3782	5MC	O4'-C4'-C5'-O5'
3	L5	4618	OMG	O4'-C4'-C5'-O5'
83	S2	1832	6MZ	O4'-C4'-C5'-O5'
3	L5	3844	PSU	C4'-C5'-O5'-P
3	L5	3925	OMU	C1'-C2'-O2'-CM2
3	L5	398	A2M	O4'-C4'-C5'-O5'
3	L5	1677	PSU	O4'-C1'-C5-C6
3	L5	4500	PSU	O4'-C1'-C5-C6
3	L5	4471	PSU	C3'-C4'-C5'-O5'
83	S2	627	OMU	C2'-C1'-N1-C6
83	S2	668	A2M	O4'-C1'-N9-C8
3	L5	1322	1MA	C2'-C1'-N9-C8
3	L5	2401	A2M	C3'-C4'-C5'-O5'
83	S2	627	OMU	O4'-C1'-N1-C6
3	L5	1534	A2M	O4'-C4'-C5'-O5'
83	S2	428	OMU	C3'-C4'-C5'-O5'
83	S2	1639	G7M	O4'-C4'-C5'-O5'
3	L5	4499	OMG	C3'-C2'-O2'-CM2
83	S2	1703	OMC	O4'-C4'-C5'-O5'
3	L5	2787	A2M	O4'-C1'-N9-C8
3	L5	1322	1MA	C2'-C1'-N9-C4
83	S2	668	A2M	C2'-C1'-N9-C8
3	L5	1781	PSU	O4'-C4'-C5'-O5'
83	S2	1248	B8N	N34-C33-C34-O35

There are no ring outliers.

66 monomers are involved in 97 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L5	4571	A2M	1	0
83	S2	1383	A2M	1	0
3	L5	4431	PSU	1	0
3	L5	3718	A2M	3	0
3	L5	4689	PSU	1	0
3	L5	1326	A2M	3	0
3	L5	4620	OMU	2	0
3	L5	3818	UY1	1	0
83	S2	484	A2M	1	0
3	L5	4536	OMC	2	0
83	S2	644	OMG	1	0
83	S2	601	OMG	1	0
83	S2	1288	OMU	1	0
83	S2	1832	6MZ	3	0
3	L5	3822	PSU	2	0
83	S2	1850	MA6	2	0
3	L5	4523	A2M	2	0
83	S2	166	A2M	2	0
3	L5	2861	OMC	1	0
83	S2	1337	4AC	3	0
3	L5	4456	OMC	1	0
83	S2	649	PSU	2	0
83	S2	1842	4AC	1	0
83	S2	509	OMG	3	0
3	L5	4457	PSU	1	0
5	L8	75	OMG	2	0
3	L5	1683	PSU	3	0
3	L5	3841	OMC	1	0
3	L5	3785	A2M	1	0
83	S2	1031	A2M	1	0
3	L5	4636	PSU	1	0
3	L5	400	A2M	1	0
3	L5	2351	OMC	2	0
3	L5	2632	PSU	1	0
83	S2	517	OMC	1	0
3	L5	4579	PSU	2	0
3	L5	3867	A2M	3	0
3	L5	2363	A2M	1	0
3	L5	4392	OMG	2	0
3	L5	1871	A2M	1	0
3	L5	4353	PSU	1	0
83	S2	116	OMU	1	0
83	S2	121	OMU	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
83	S2	1442	OMU	1	0
3	L5	2876	OMG	1	0
83	S2	468	A2M	1	0
3	L5	3701	OMC	1	0
83	S2	159	A2M	3	0
3	L5	4447	5MC	1	0
3	L5	1340	OMC	2	0
3	L5	1677	PSU	1	0
83	S2	1232	PSU	2	0
3	L5	4220	6MZ	1	0
83	S2	681	PSU	1	0
83	S2	99	A2M	1	0
3	L5	3884	PSU	1	0
3	L5	3925	OMU	1	0
3	L5	4196	OMG	1	0
83	S2	27	A2M	3	0
3	L5	2824	OMC	1	0
83	S2	436	OMG	1	0
3	L5	2424	OMG	2	0
3	L5	2422	OMC	1	0
3	L5	4618	OMG	1	0
83	S2	1639	G7M	1	0
3	L5	3825	A2M	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 242 ligands modelled in this entry, 225 are monoatomic - leaving 17 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
89	SPD	L5	5289	-	9,9,9	0.33	0	8,8,8	0.83	0
89	SPD	L5	5287	-	9,9,9	0.33	0	8,8,8	0.79	0
89	SPD	L5	5285	-	9,9,9	0.31	0	8,8,8	0.81	0
89	SPD	L5	5262	-	9,9,9	0.32	0	8,8,8	0.92	0
89	SPD	L5	5291	-	9,9,9	0.32	0	8,8,8	0.87	0
89	SPD	L5	5284	-	9,9,9	0.33	0	8,8,8	0.83	0
88	SPM	L5	5265	-	13,13,13	0.35	0	12,12,12	0.98	0
89	SPD	L5	5286	-	9,9,9	0.32	0	8,8,8	0.89	0
89	SPD	L5	5292	-	9,9,9	0.31	0	8,8,8	0.77	0
89	SPD	LN	301	-	9,9,9	0.32	0	8,8,8	0.86	0
89	SPD	L5	5288	-	9,9,9	0.32	0	8,8,8	0.86	0
88	SPM	L5	5294	-	13,13,13	0.35	0	12,12,12	0.85	0
88	SPM	L5	5268	-	13,13,13	0.35	0	12,12,12	0.97	0
88	SPM	L5	5293	-	13,13,13	0.37	0	12,12,12	0.89	0
88	SPM	L5	5290	-	13,13,13	0.36	0	12,12,12	0.98	0
88	SPM	L5	5259	-	13,13,13	0.35	0	12,12,12	0.92	0
88	SPM	L5	5264	-	13,13,13	0.35	0	12,12,12	0.90	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
89	SPD	L5	5289	-	-	1/7/7/7	-
89	SPD	L5	5287	-	-	0/7/7/7	-
89	SPD	L5	5285	-	-	2/7/7/7	-
89	SPD	L5	5262	-	-	0/7/7/7	-
89	SPD	L5	5291	-	-	0/7/7/7	-
89	SPD	L5	5284	-	-	1/7/7/7	-
88	SPM	L5	5265	-	-	2/11/11/11	-
89	SPD	L5	5286	-	-	4/7/7/7	-
89	SPD	L5	5292	-	-	3/7/7/7	-
89	SPD	LN	301	-	-	1/7/7/7	-
89	SPD	L5	5288	-	-	3/7/7/7	-
88	SPM	L5	5294	-	-	4/11/11/11	-
88	SPM	L5	5268	-	-	3/11/11/11	-
88	SPM	L5	5293	-	-	4/11/11/11	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	SPM	L5	5290	-	-	4/11/11/11	-
88	SPM	L5	5259	-	-	2/11/11/11	-
88	SPM	L5	5264	-	-	4/11/11/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	L5	5286	SPD	C3-C4-C5-N6
88	L5	5293	SPM	C7-C8-C9-N10
88	L5	5293	SPM	N10-C11-C12-C13
89	L5	5286	SPD	N6-C7-C8-C9
89	L5	5288	SPD	C3-C4-C5-N6
88	L5	5265	SPM	N5-C6-C7-C8
88	L5	5268	SPM	C2-C3-C4-N5
89	L5	5292	SPD	C4-C5-N6-C7
89	L5	5288	SPD	N6-C7-C8-C9
89	L5	5285	SPD	C3-C4-C5-N6
88	L5	5259	SPM	C3-C4-N5-C6
88	L5	5290	SPM	C7-C6-N5-C4
88	L5	5290	SPM	C12-C11-N10-C9
89	L5	5286	SPD	C2-C3-C4-C5
88	L5	5294	SPM	C8-C9-N10-C11
88	L5	5259	SPM	C6-C7-C8-C9
89	L5	5284	SPD	C2-C3-C4-C5
88	L5	5268	SPM	C6-C7-C8-C9
88	L5	5264	SPM	C11-C12-C13-N14
88	L5	5290	SPM	N1-C2-C3-C4
89	L5	5286	SPD	C4-C5-N6-C7
88	L5	5294	SPM	C6-C7-C8-C9
88	L5	5268	SPM	N10-C11-C12-C13
89	LN	301	SPD	C4-C5-N6-C7
89	L5	5288	SPD	C8-C7-N6-C5
88	L5	5294	SPM	N10-C11-C12-C13
89	L5	5285	SPD	C2-C3-C4-C5
88	L5	5264	SPM	C6-C7-C8-C9
88	L5	5265	SPM	C7-C6-N5-C4
88	L5	5294	SPM	C7-C6-N5-C4

Continued on next page...

Continued from previous page...

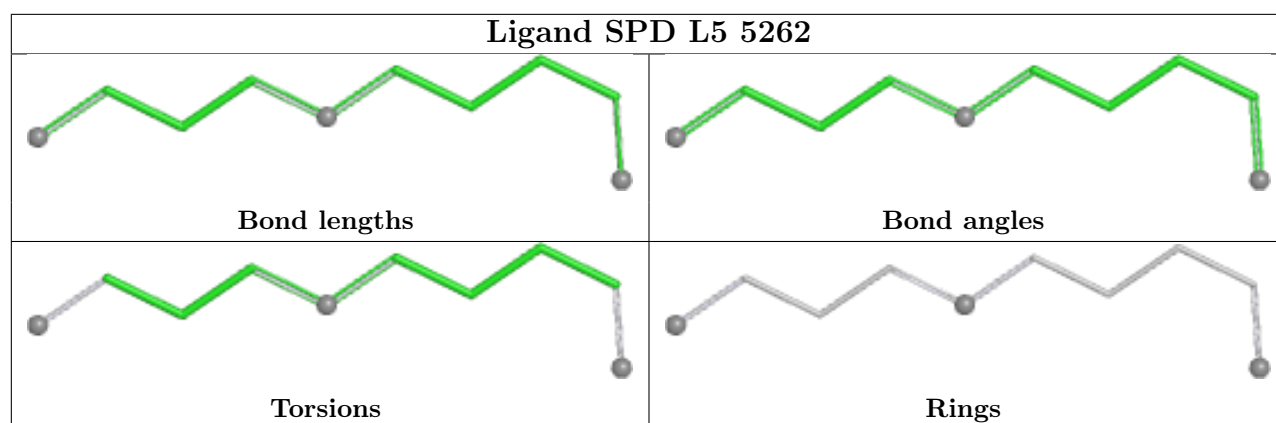
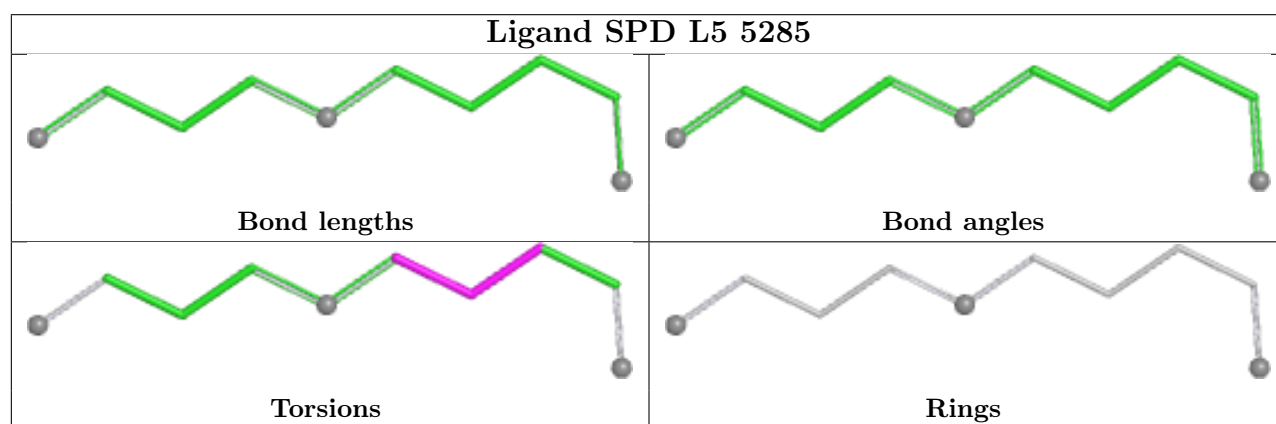
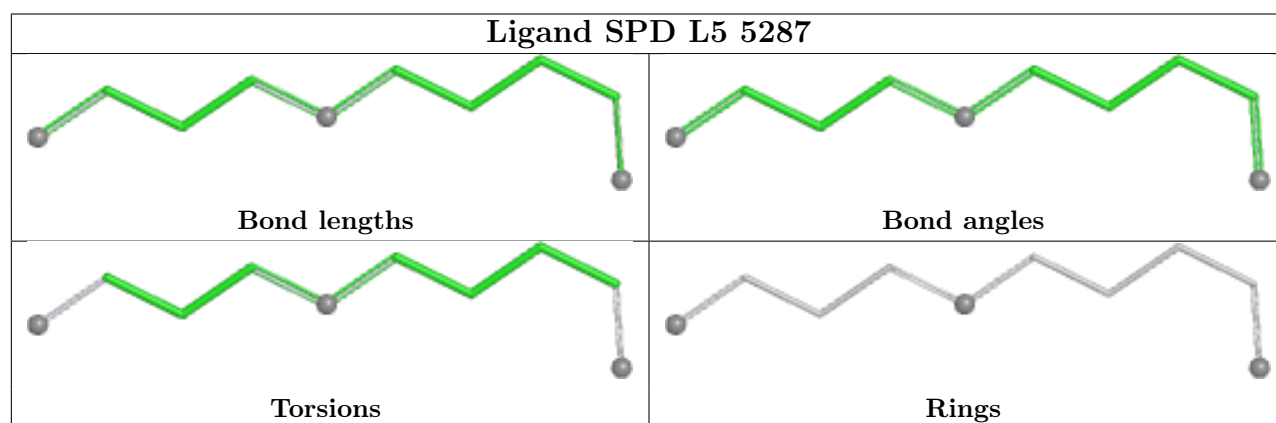
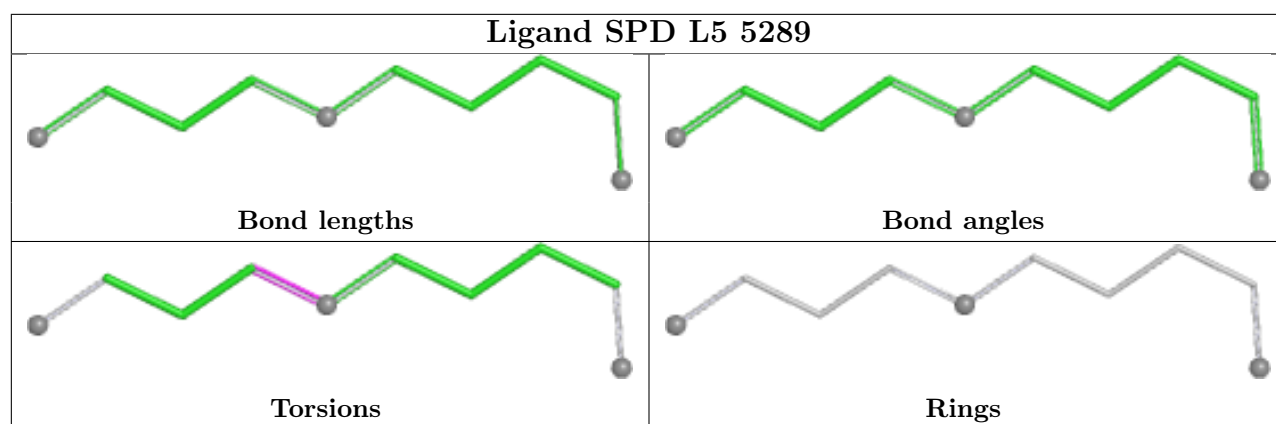
Mol	Chain	Res	Type	Atoms
89	L5	5292	SPD	C8-C7-N6-C5
89	L5	5292	SPD	C3-C4-C5-N6
88	L5	5264	SPM	C7-C6-N5-C4
88	L5	5293	SPM	C7-C6-N5-C4
88	L5	5293	SPM	C8-C9-N10-C11
89	L5	5289	SPD	C8-C7-N6-C5
88	L5	5264	SPM	N10-C11-C12-C13
88	L5	5290	SPM	N10-C11-C12-C13

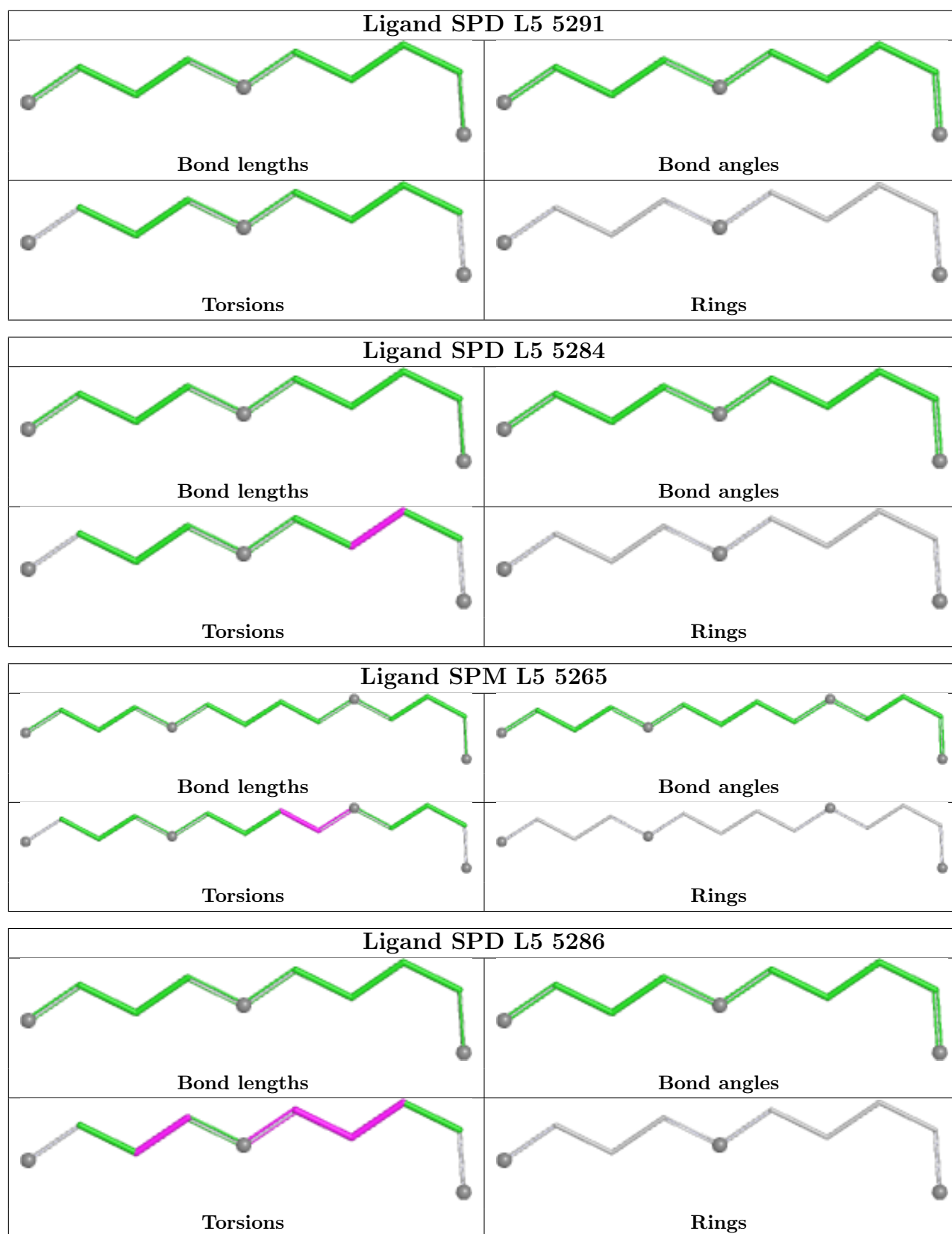
There are no ring outliers.

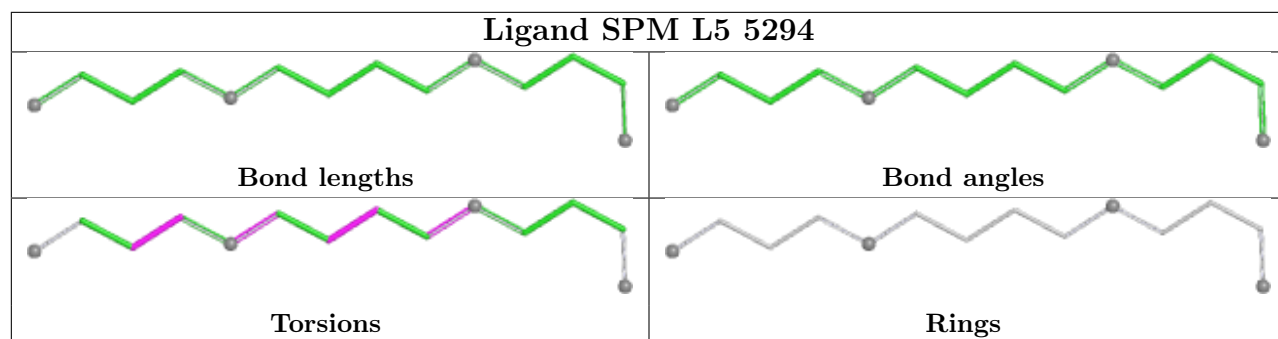
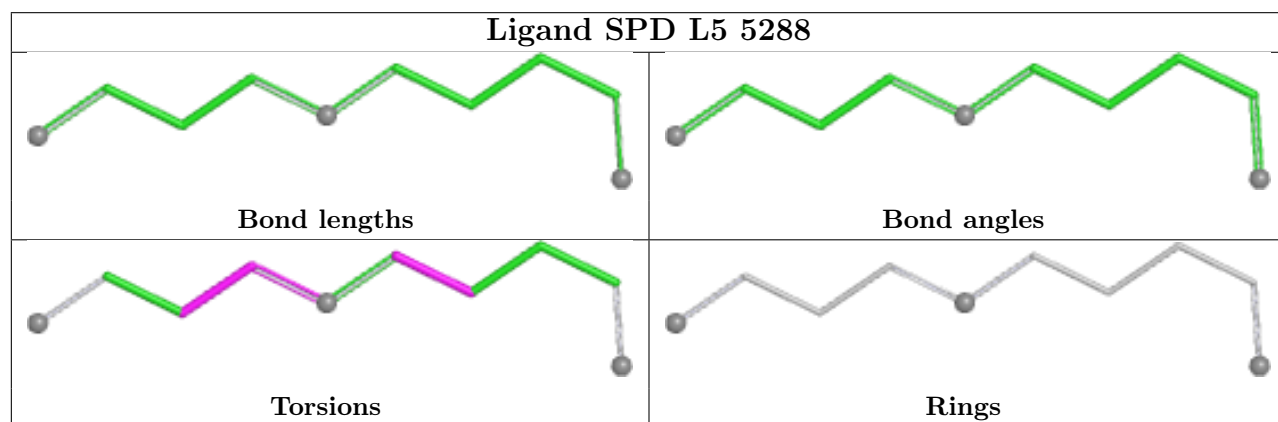
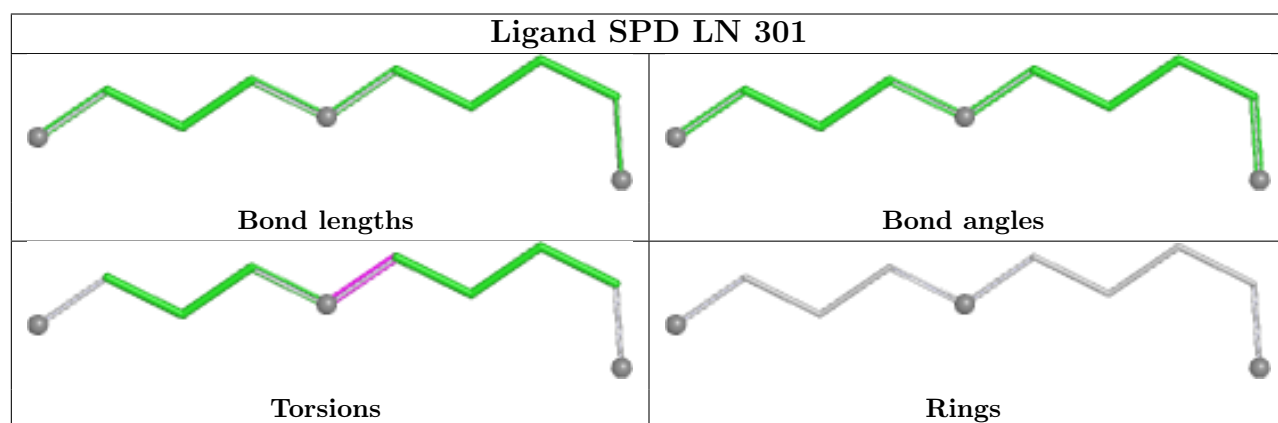
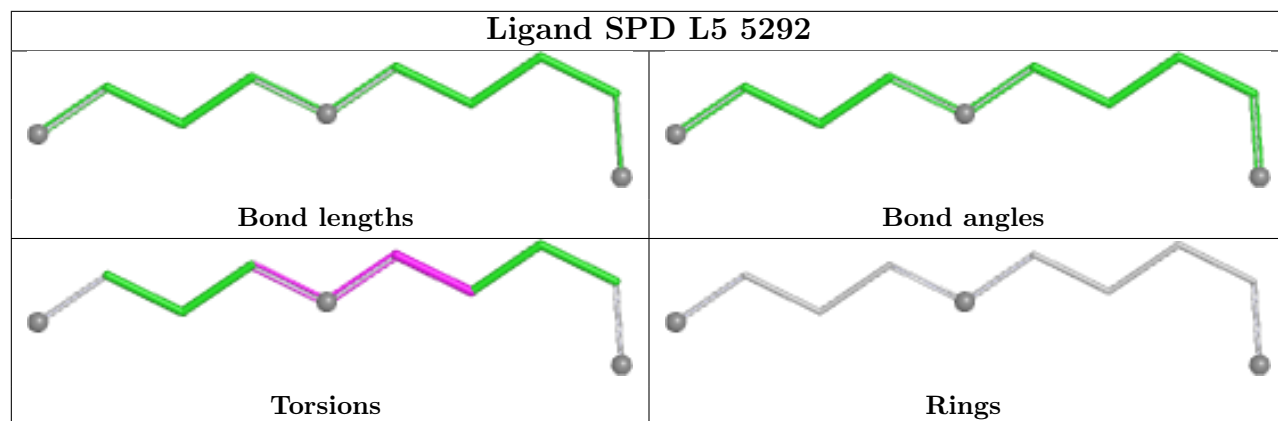
6 monomers are involved in 9 short contacts:

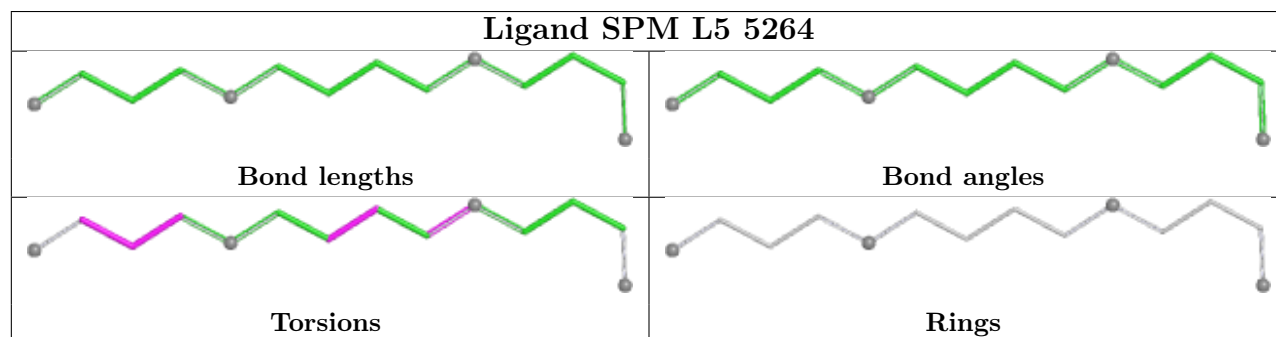
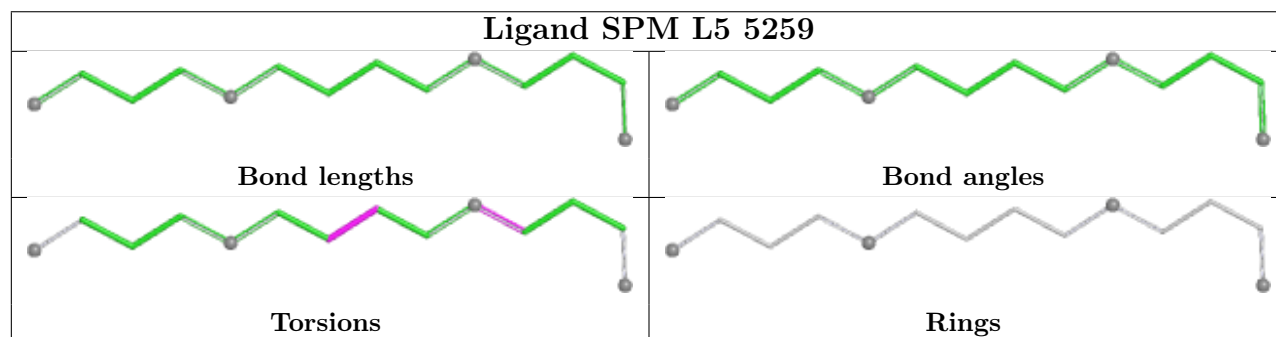
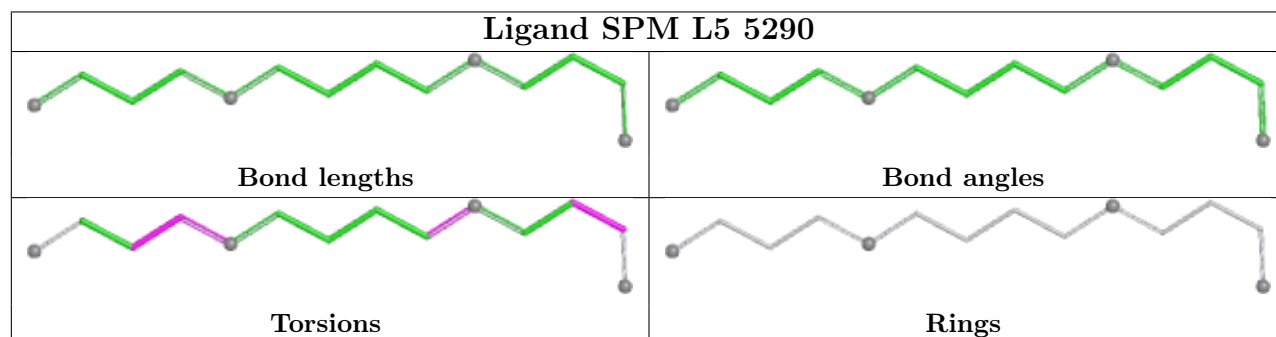
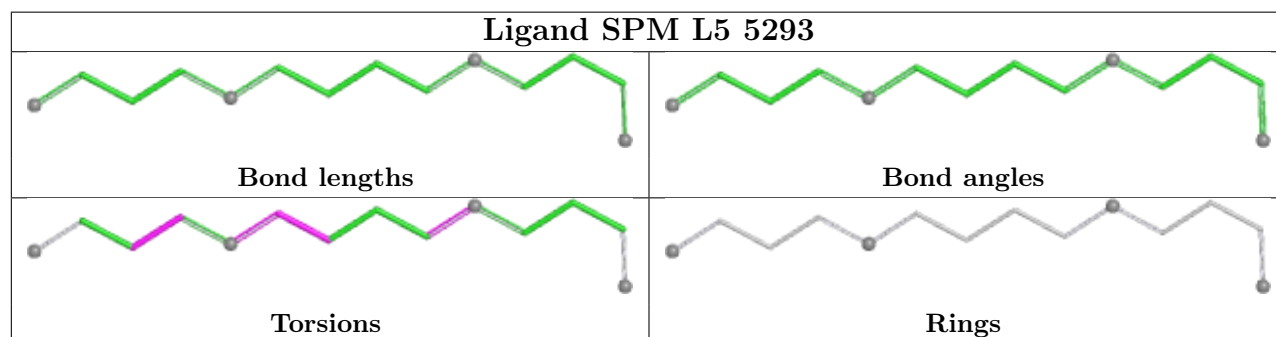
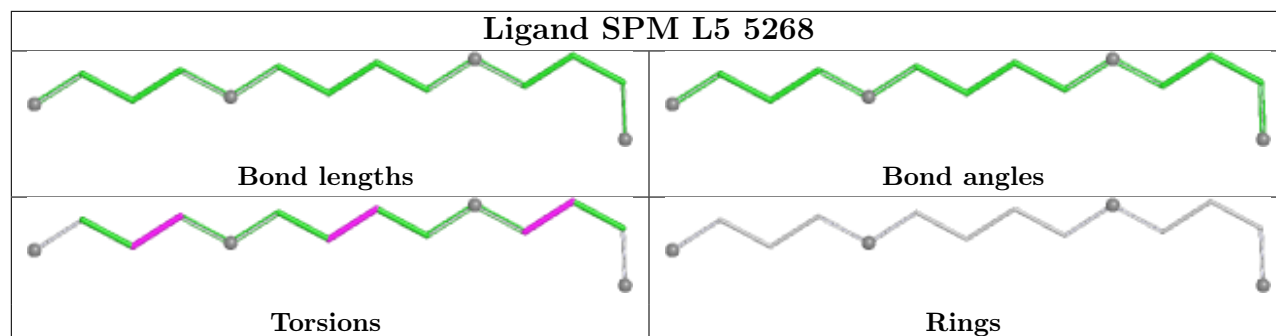
Mol	Chain	Res	Type	Clashes	Symm-Clashes
89	L5	5287	SPD	1	0
89	L5	5285	SPD	2	0
89	L5	5262	SPD	1	0
88	L5	5265	SPM	1	0
88	L5	5294	SPM	3	0
88	L5	5293	SPM	1	0

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









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	L5	10
83	S2	5
2	Pt	1
85	AT	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	753:C	O3'	785:C	P	29.09
1	L5	1706:A	O3'	1716:G	P	21.10
1	L5	2910:G	O3'	3584:C	P	21.05
1	L5	760:G	O3'	903:C	P	17.03
1	L5	519:C	O3'	642:G	P	15.83
1	L5	4776:G	O3'	4858:C	P	15.25
1	S2	698:G	O3'	730:C	P	15.05
1	L5	2112:G	O3'	2249:C	P	14.89
1	L5	3954:A	O3'	4056:A	P	13.14
1	L5	990:C	O3'	1064:G	P	12.67
1	S2	739:C	O3'	746:C	P	12.59
1	L5	1222:A	O3'	1234:G	P	10.39
1	Pt	15:G	O3'	18:G	P	9.83
1	S2	225:G	O3'	287:U	P	7.56
1	L5	1100:U	O3'	1167:C	P	6.79
1	AT	16:C	O3'	18:G	P	5.23
1	S2	1831:A	O3'	1832:6MZ	P	4.22

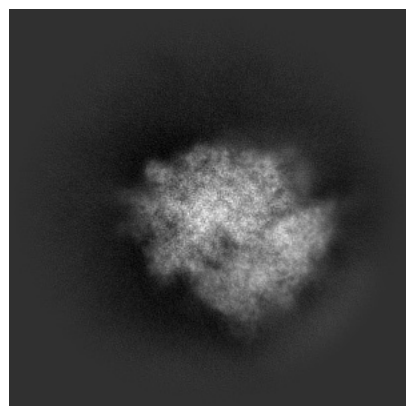
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71348. These allow visual inspection of the internal detail of the map and identification of artifacts.

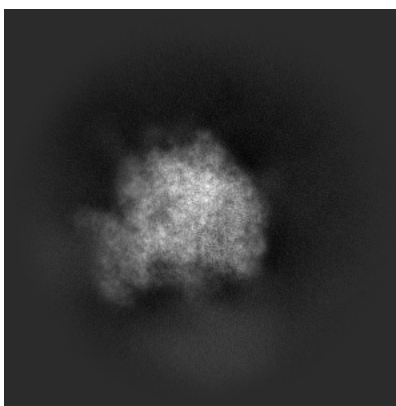
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

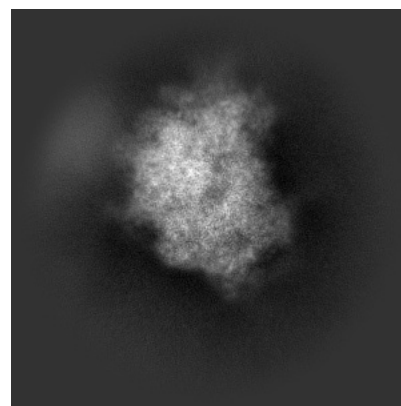
6.1.1 Primary map



X

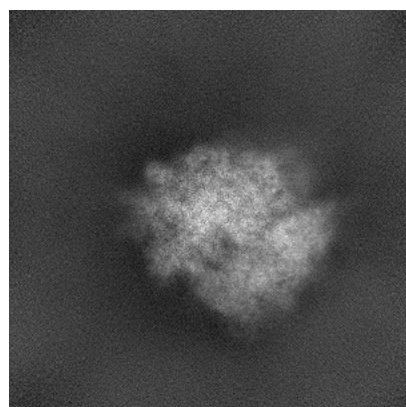


Y

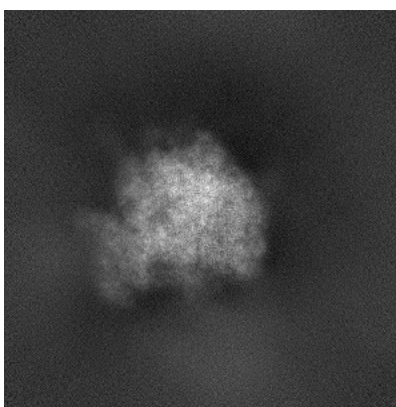


Z

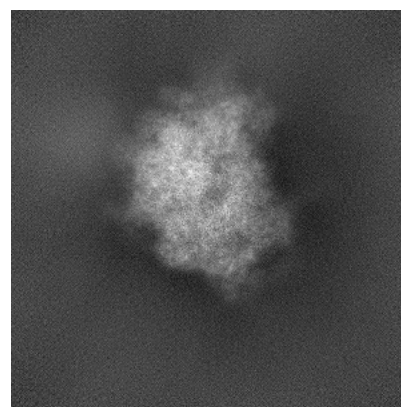
6.1.2 Raw map



X



Y

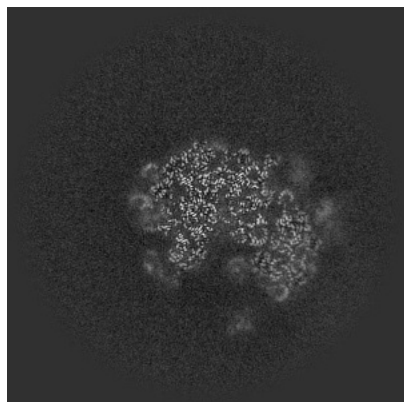


Z

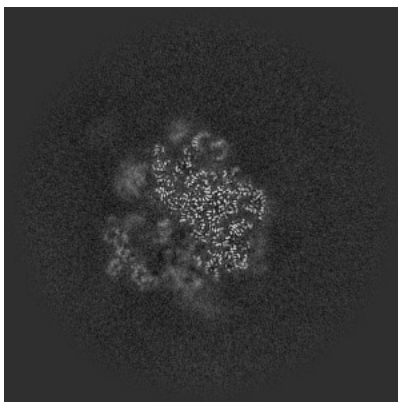
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

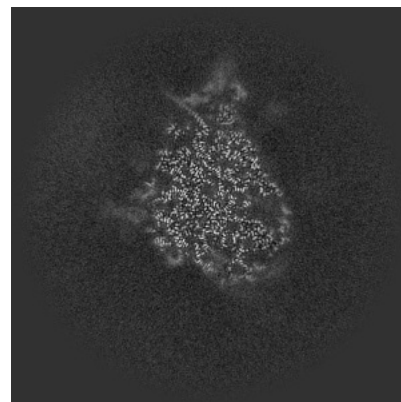
6.2.1 Primary map



X Index: 256

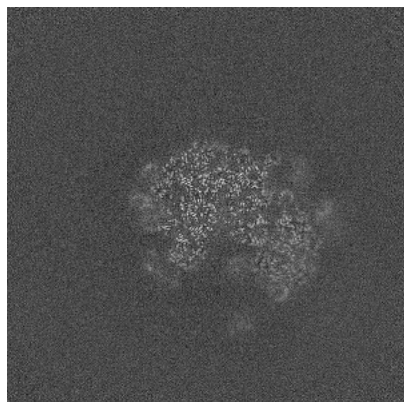


Y Index: 256

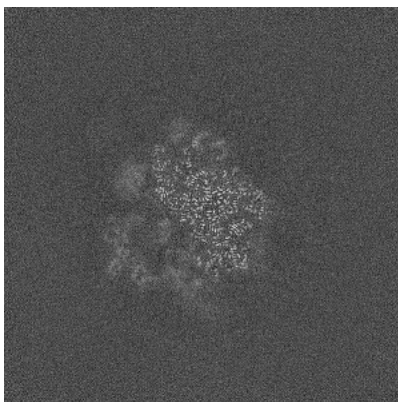


Z Index: 256

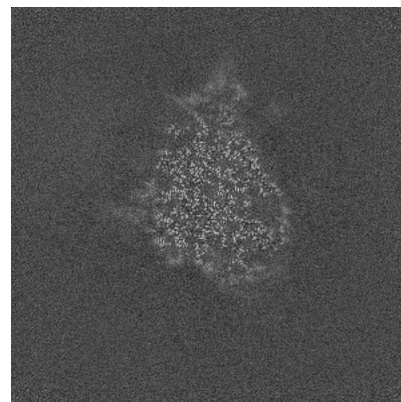
6.2.2 Raw map



X Index: 256



Y Index: 256

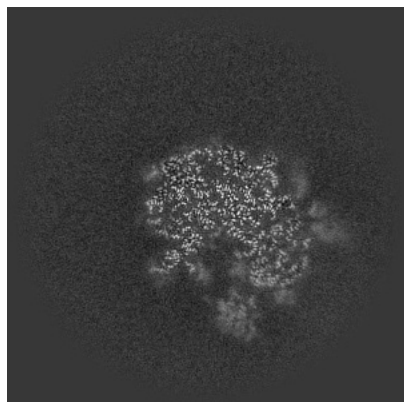


Z Index: 256

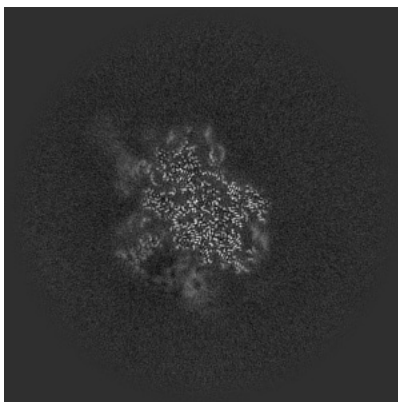
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

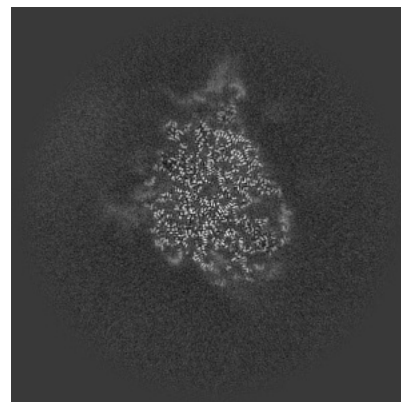
6.3.1 Primary map



X Index: 243

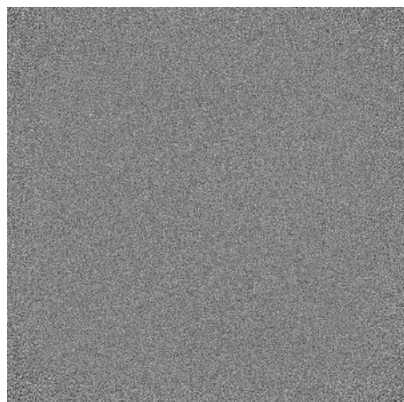


Y Index: 243

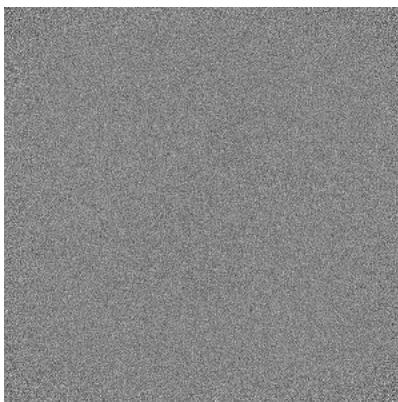


Z Index: 258

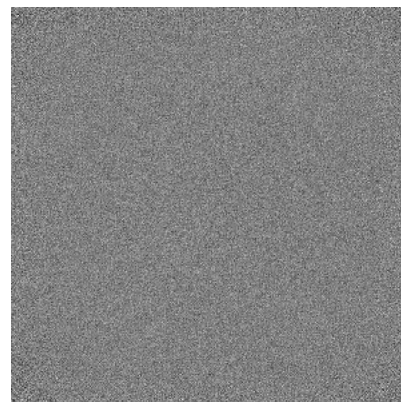
6.3.2 Raw map



X Index: 0



Y Index: 0

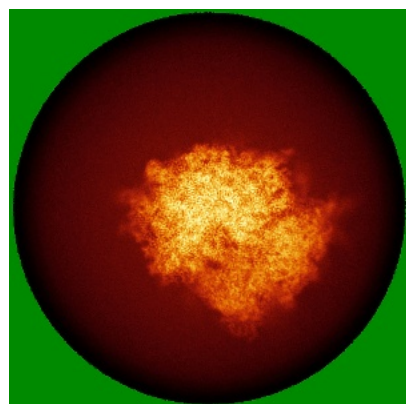


Z Index: 0

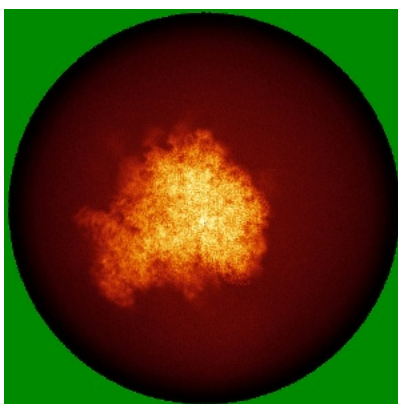
The images above show the largest variance slices of the map in three orthogonal directions.

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

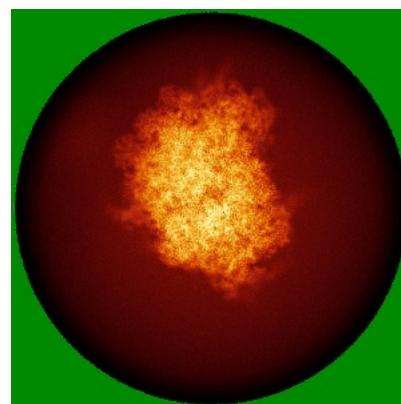
6.4.1 Primary map



X

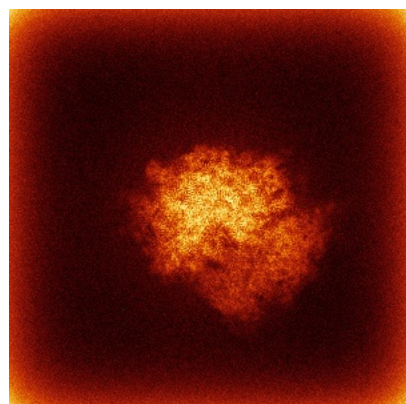


Y

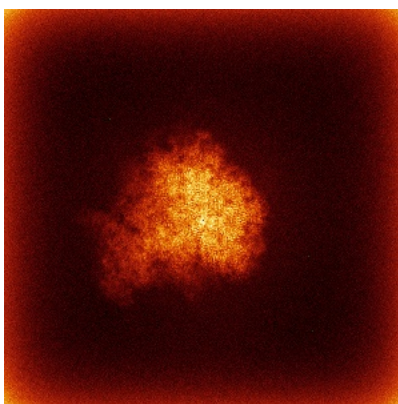


Z

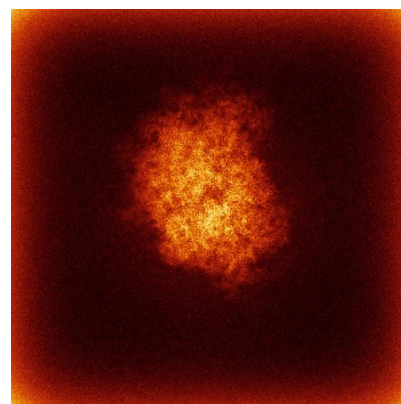
6.4.2 Raw map



X



Y

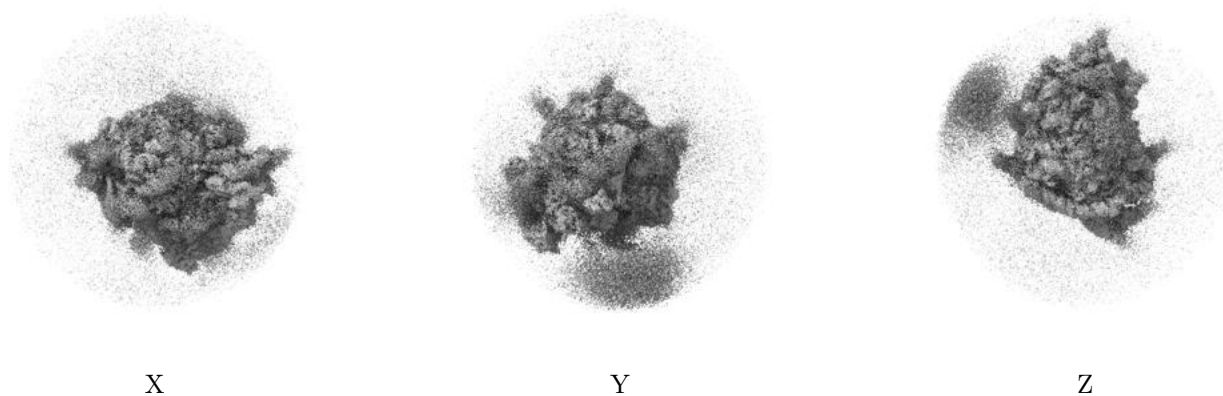


Z

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

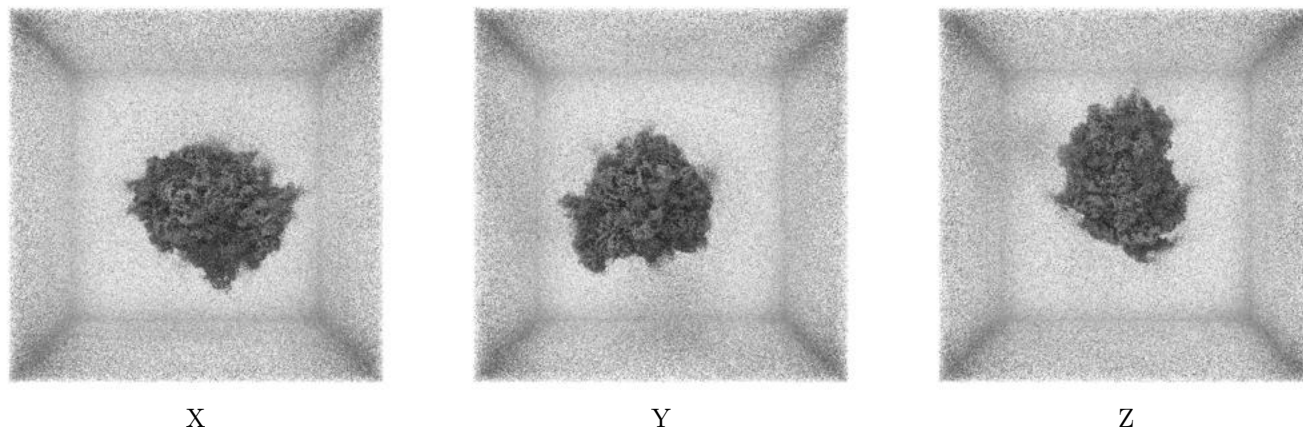
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0153. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

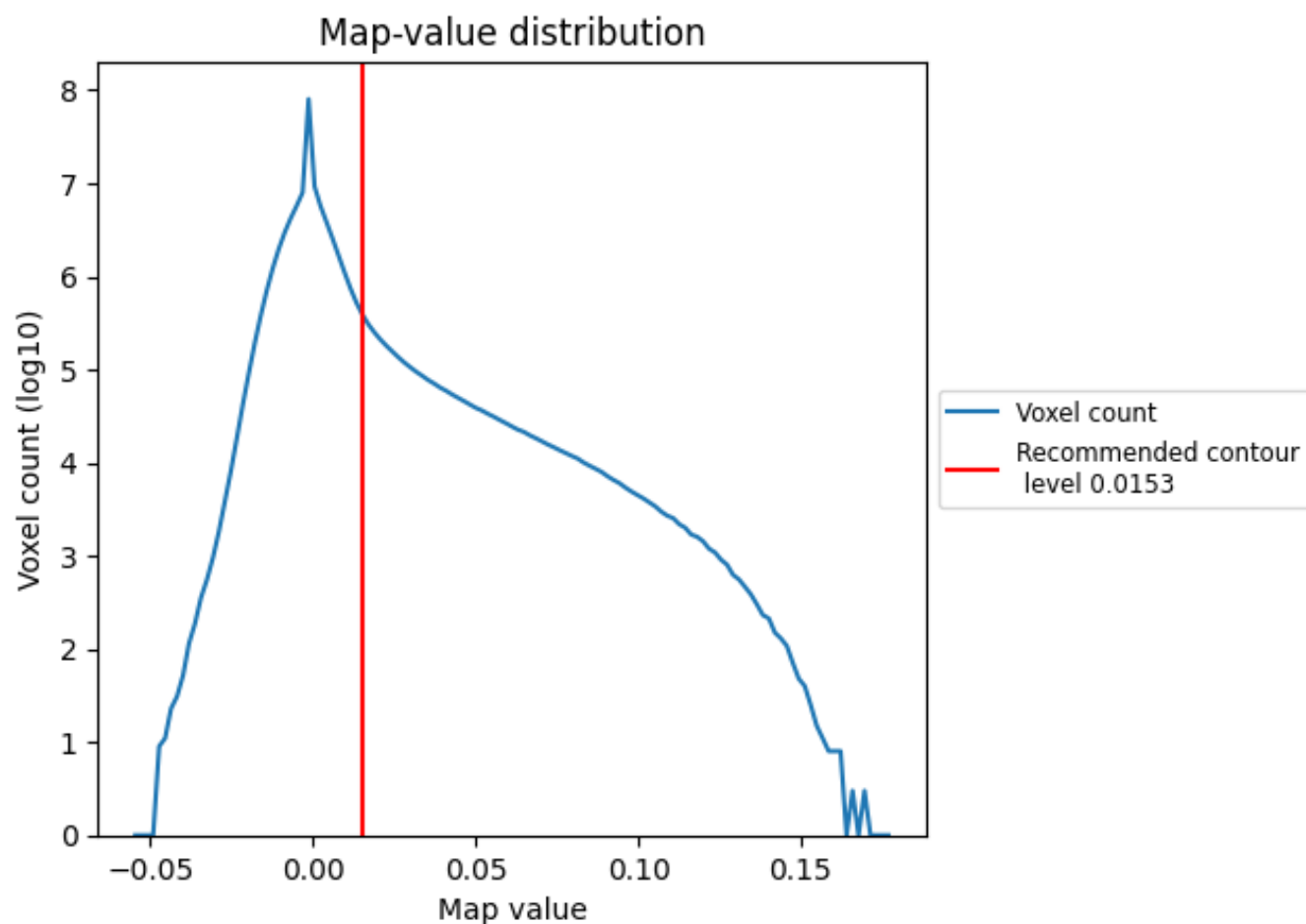
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

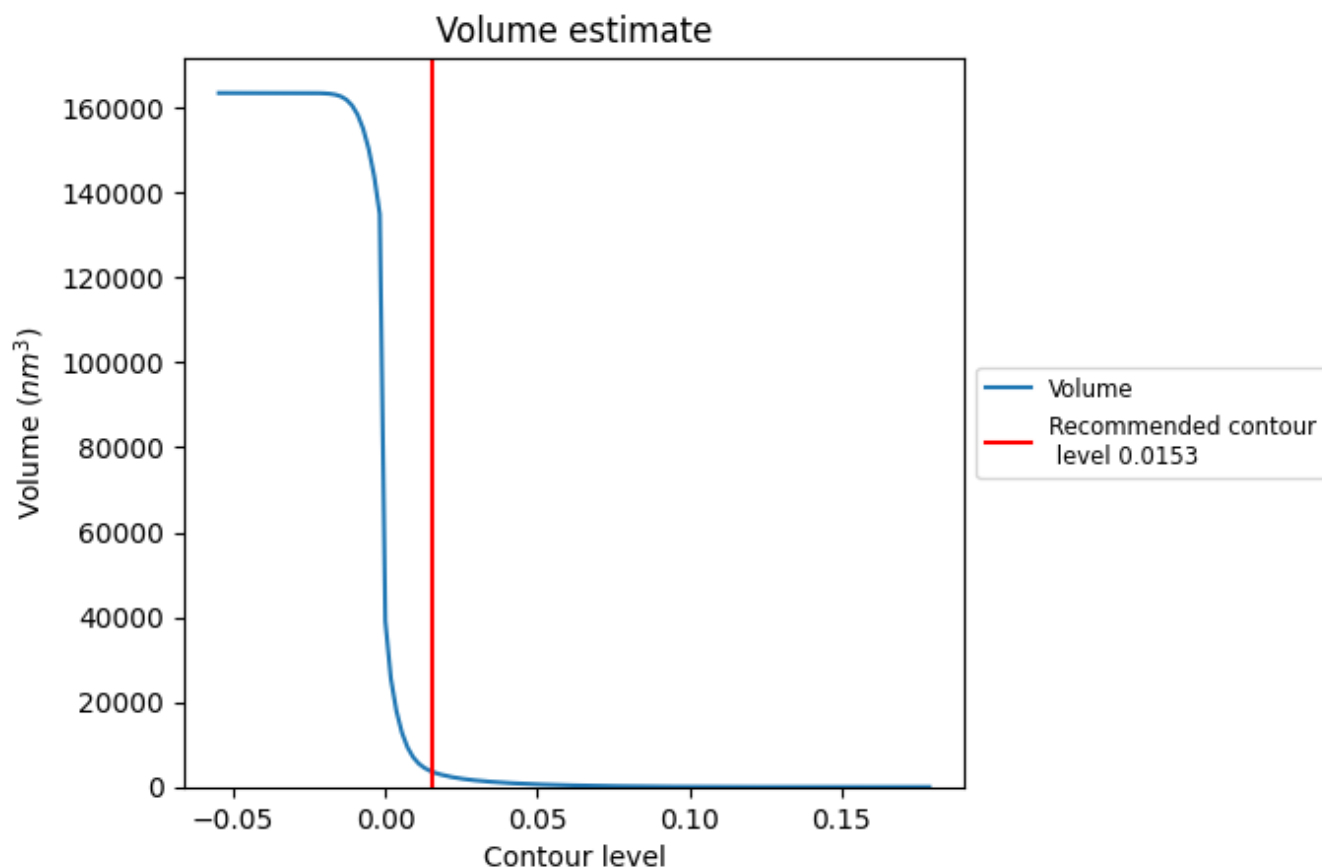
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

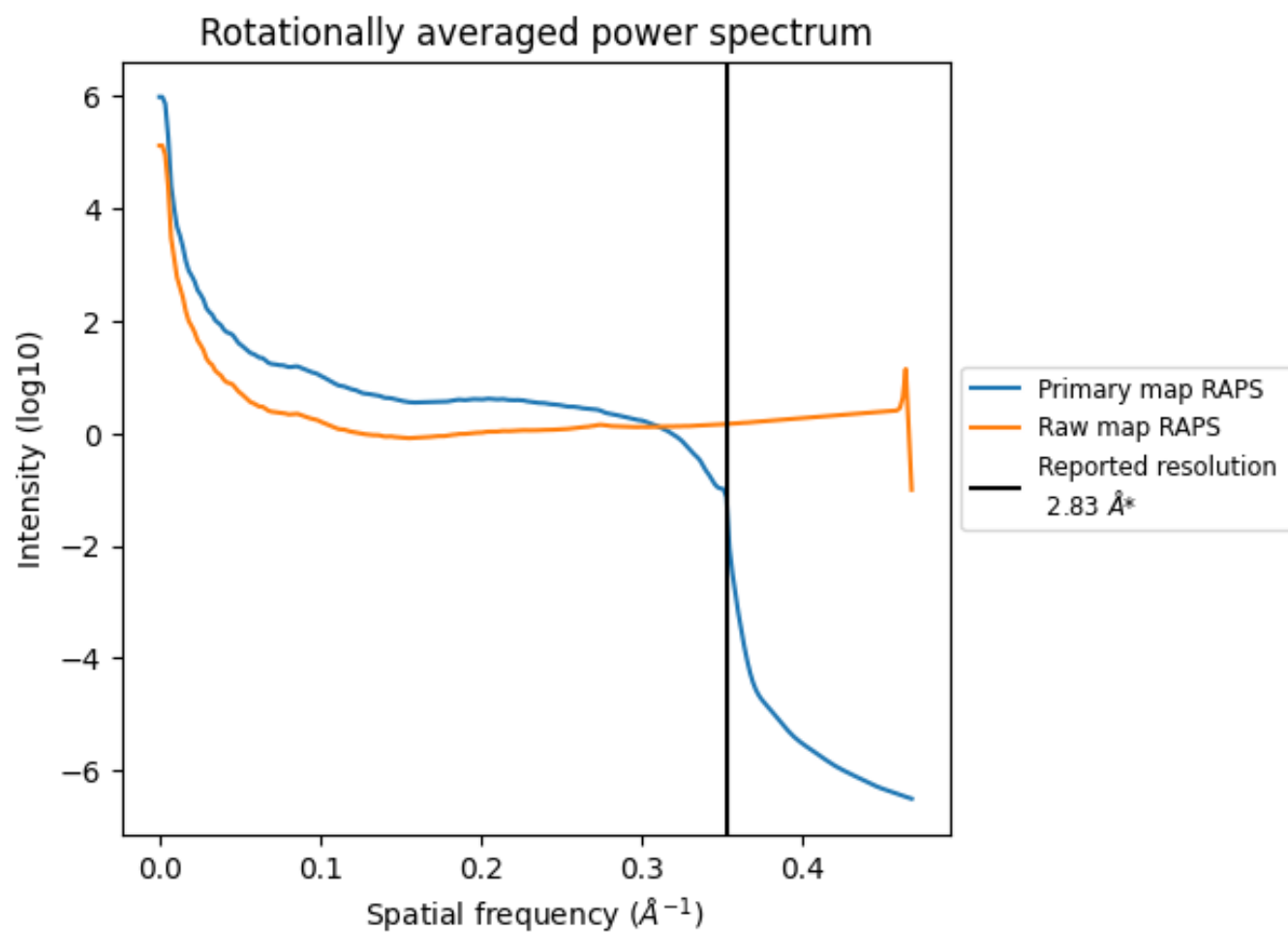
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3647 nm^3 ; this corresponds to an approximate mass of 3294 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 ⓘ

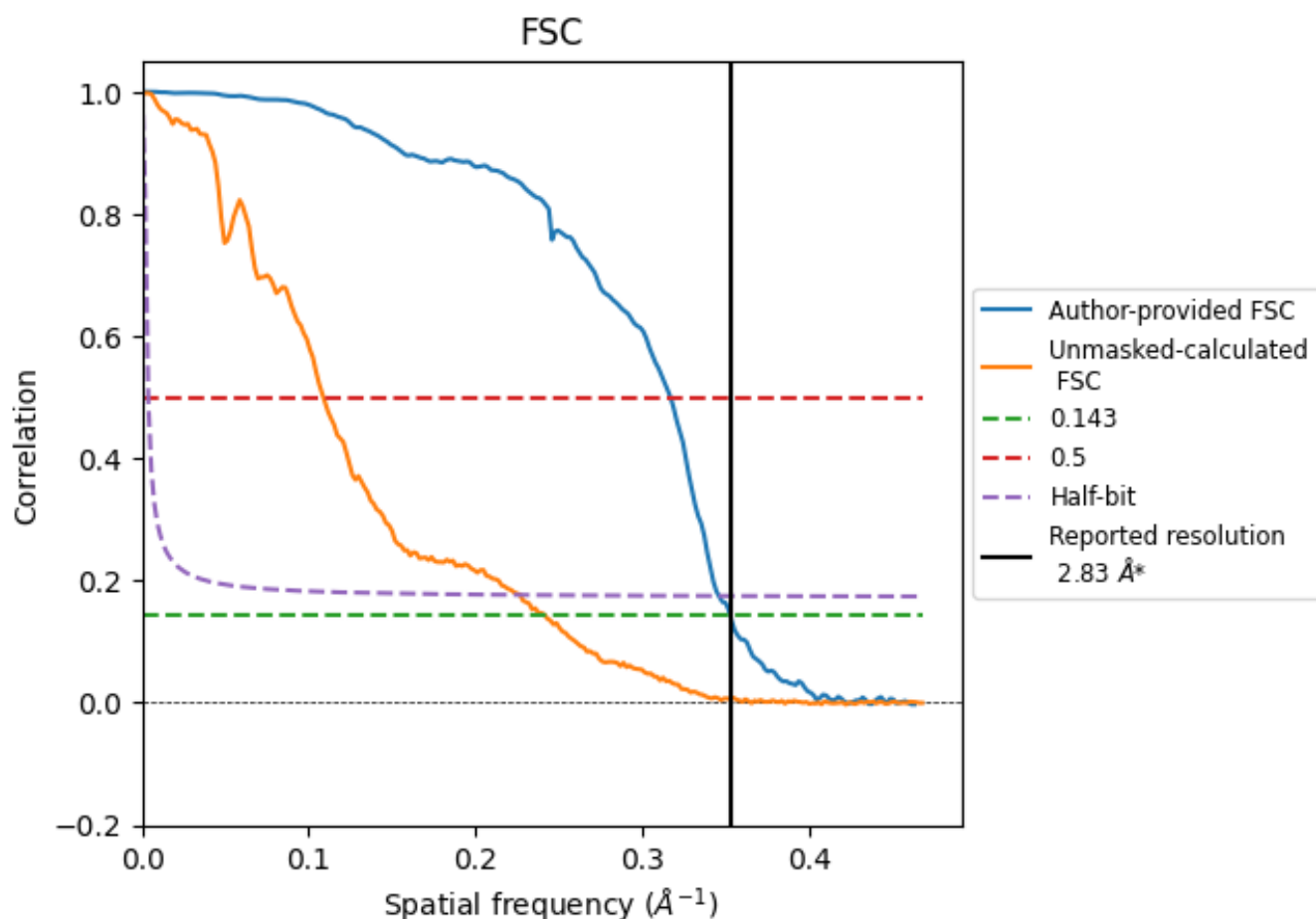


*Reported resolution corresponds to spatial frequency of 0.353 $\text{\AA}^{-1}$

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 0.353 Å⁻¹

8.2 Resolution estimates [i](#)

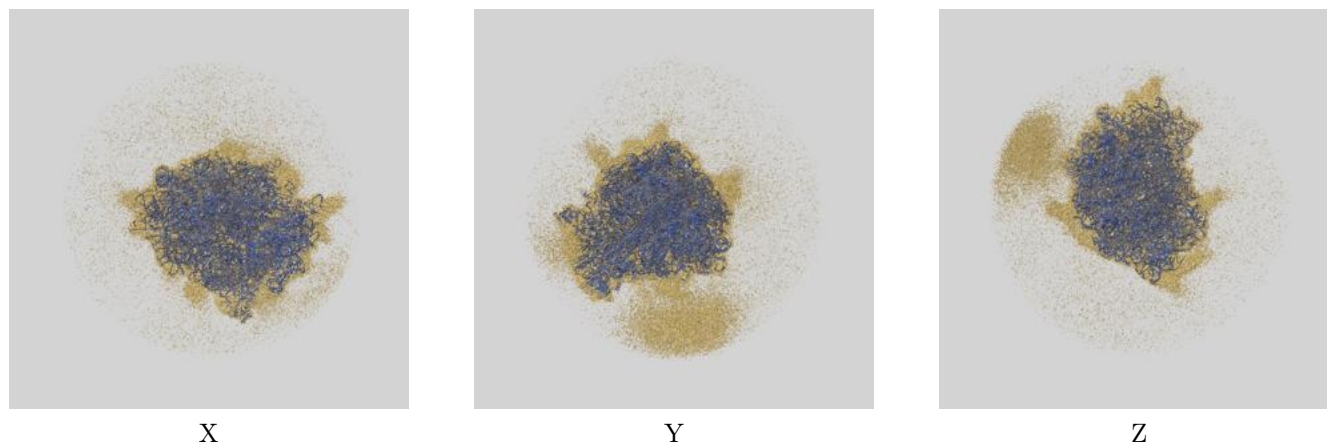
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.83	-	-
Author-provided FSC curve	2.83	3.15	2.89
Unmasked-calculated*	4.14	9.20	4.41

*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 4.14 differs from the reported value 2.83 by more than 10 %

9 Map-model fit [i](#)

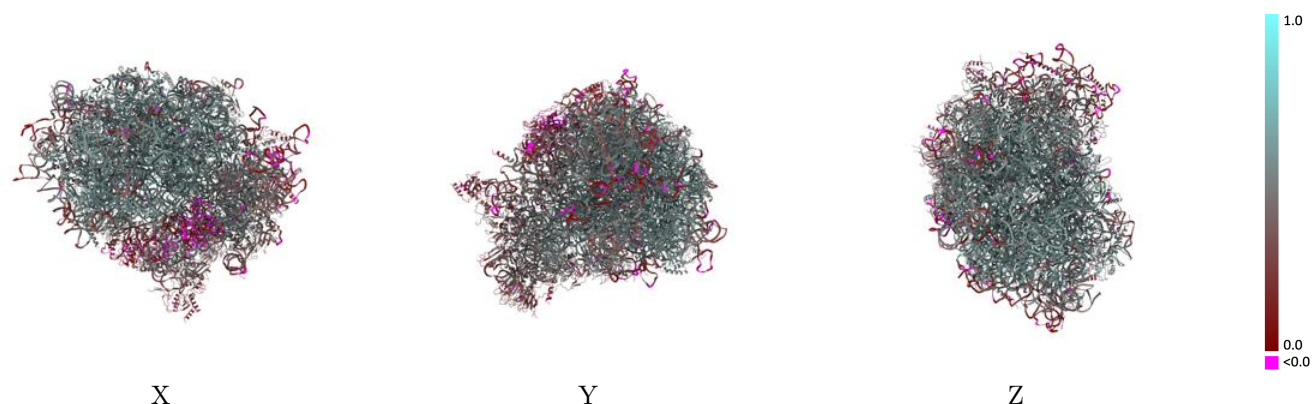
This section contains information regarding the fit between EMDB map EMD-71348 and PDB model 9P7N. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



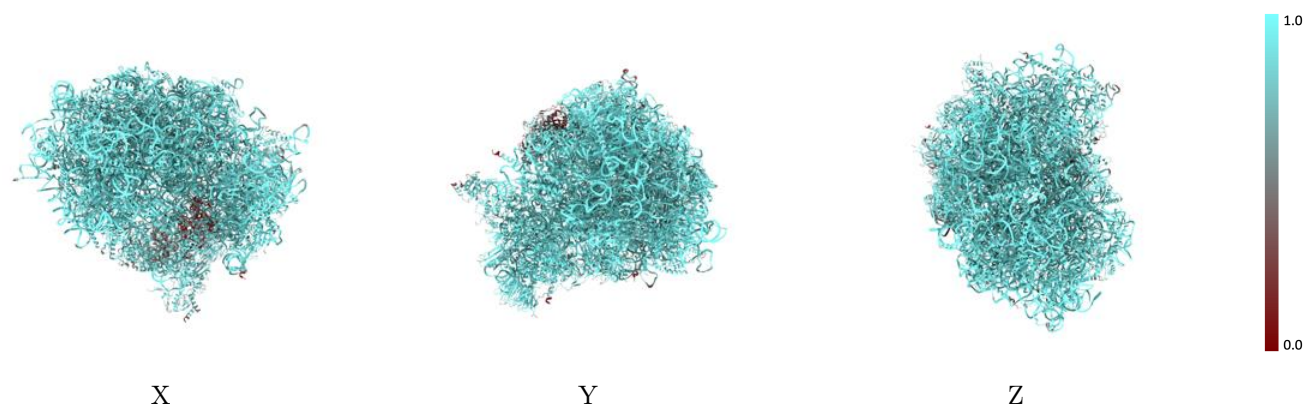
The images above show the 3D surface view of the map at the recommended contour level 0.0153 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



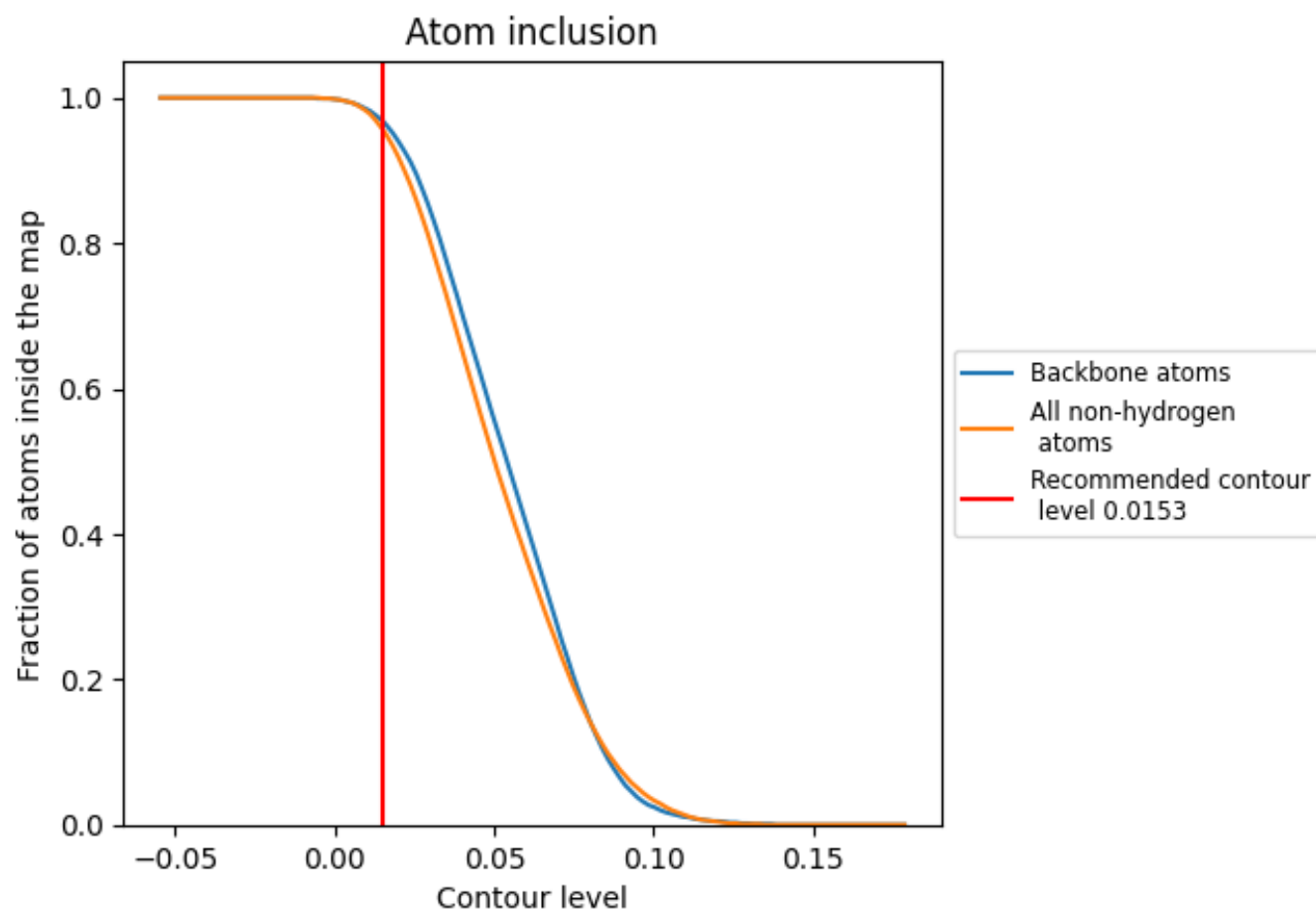
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0153).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% 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 (0.0153) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9550	 0.4780
AT	 0.8820	 0.1490
CF	 0.4680	 0.0580
CI	 0.8290	 0.4170
L5	 0.9850	 0.5150
L7	 0.9980	 0.5660
L8	 0.9900	 0.5410
LA	 0.9880	 0.5830
LB	 0.9670	 0.5660
LC	 0.9700	 0.5590
LD	 0.9560	 0.5200
LE	 0.9280	 0.4910
LF	 0.9780	 0.5640
LG	 0.9080	 0.4940
LH	 0.9660	 0.5420
LI	 0.9730	 0.5530
LJ	 0.9460	 0.4950
LL	 0.9450	 0.5400
LM	 0.9750	 0.5420
LN	 0.9920	 0.5960
LO	 0.9760	 0.5650
LP	 0.9700	 0.5700
LQ	 0.9850	 0.5850
LR	 0.9350	 0.5080
LS	 0.9890	 0.5840
LT	 0.9660	 0.5470
LU	 0.9520	 0.4700
LV	 0.9750	 0.5740
LW	 0.9130	 0.3790
LX	 0.9730	 0.5460
LY	 0.9640	 0.5440
LZ	 0.9730	 0.5380
La	 0.9850	 0.5880
Lb	 0.9220	 0.4870
Lc	 0.9590	 0.5220



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Ld	 0.9640	 0.5400
Le	 0.9910	 0.5790
Lf	 0.9870	 0.5940
Lg	 0.9720	 0.5500
Lh	 0.9620	 0.5370
Li	 0.9640	 0.5370
Lj	 0.9910	 0.5860
Lk	 0.9170	 0.4810
Ll	 0.9930	 0.5720
Lm	 0.9570	 0.5540
Ln	 0.9950	 0.5760
Lo	 0.9790	 0.5610
Lp	 0.9670	 0.5520
Lr	 0.9800	 0.5680
Ls	 0.6400	 0.1610
Lt	 0.5350	 0.0620
Pt	 0.9840	 0.4460
S2	 0.9880	 0.4570
SA	 0.9220	 0.4550
SB	 0.9400	 0.4850
SC	 0.9650	 0.4850
SD	 0.9290	 0.3740
SE	 0.9610	 0.4480
SF	 0.9260	 0.4120
SG	 0.9150	 0.3530
SH	 0.8890	 0.3860
SI	 0.9390	 0.4580
SJ	 0.9400	 0.4230
SK	 0.9190	 0.3260
SL	 0.9210	 0.4860
SM	 0.7250	 0.1820
SN	 0.9640	 0.5250
SO	 0.9560	 0.5060
SP	 0.9070	 0.3760
SQ	 0.9320	 0.4020
SR	 0.9200	 0.4050
SS	 0.8930	 0.3840
ST	 0.9330	 0.3880
SU	 0.9200	 0.3590
SV	 0.9650	 0.4690
SW	 0.9820	 0.5090
SX	 0.9590	 0.4860

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SY	 0.9100	 0.3450
SZ	 0.8660	 0.3640
Sa	 0.9750	 0.5110
Sb	 0.9450	 0.4720
Sc	 0.9070	 0.4000
Sd	 0.9750	 0.4320
Se	 0.8850	 0.3520
Sf	 0.8200	 0.1980
Sg	 0.9020	 0.3110
Zt	 0.6540	 0.0510