



Full wwPDB EM Validation Report ⓘ

Jun 26, 2026 – 04:44 AM EDT

PDB ID : 9P78 / pdb_00009p78
EMDB ID : EMD-71334
Title : In situ human Hibernating rotate 3 with E-site tRNA state 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2025-06-20
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

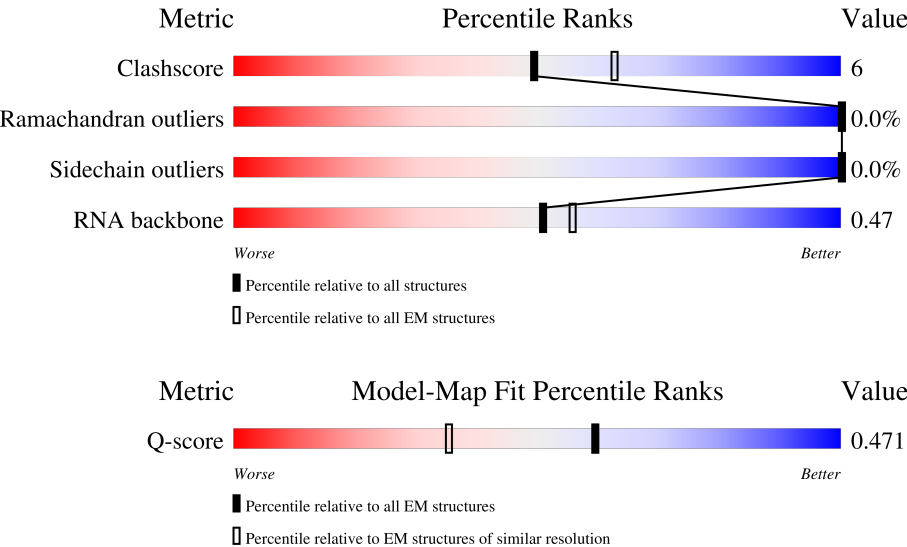
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.



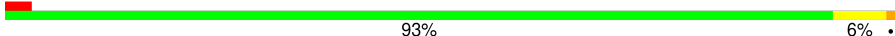
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	CD	408	11% 87%
2	CI	31	13% 97%
3	L5	5070	44% 24% 28%

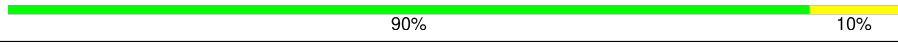
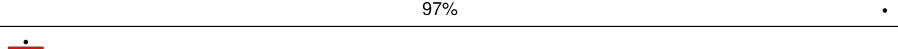
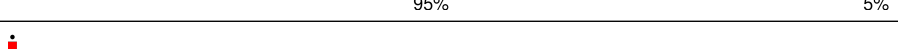
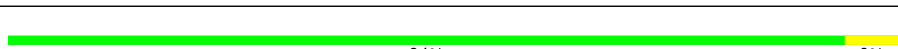
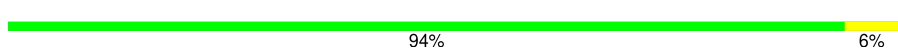
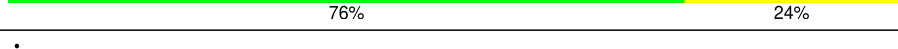
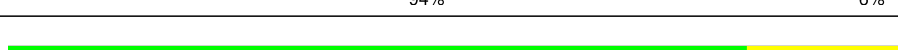
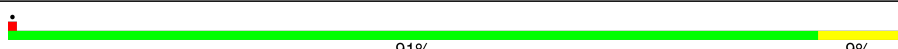
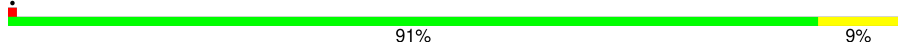
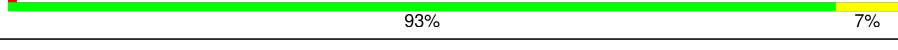
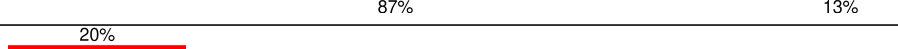
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Mol	Chain	Length	Quality of chain
4	L7	120	
5	L8	156	
6	LA	248	
7	LB	402	
8	LC	368	
9	LD	293	
10	LE	250	
11	LF	225	
12	LG	241	
13	LH	190	
14	LI	213	
15	LJ	176	
16	LL	210	
17	LM	139	
18	LN	203	
19	LO	201	
20	LP	153	
21	LQ	187	
22	LR	187	
23	LS	175	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

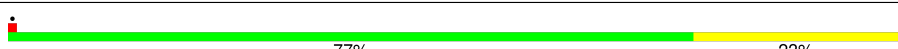
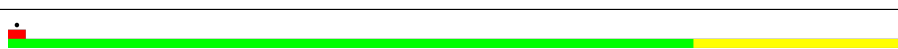
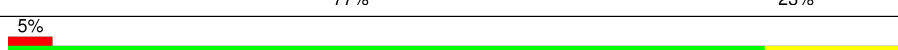
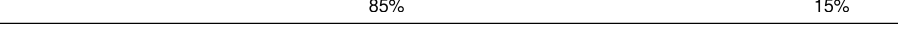
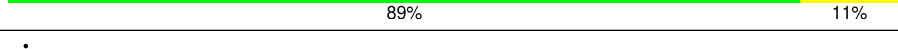
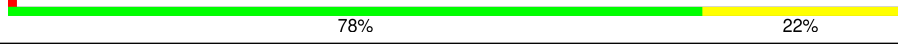
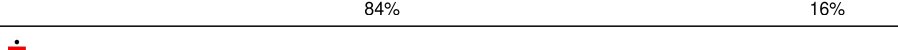
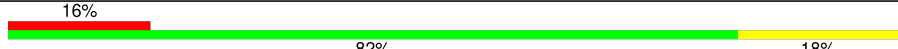
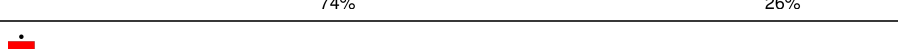
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Mol	Chain	Length	Quality of chain
29	LY	134	
30	LZ	135	
31	La	147	
32	Lb	121	
33	Lc	98	
34	Ld	107	
35	Le	128	
36	Lf	109	
37	Lg	114	
38	Lh	122	
39	Li	102	
40	Lj	86	
41	Lk	69	
42	Ll	50	
43	Lm	52	
44	Ln	24	
45	Lo	105	
46	Lp	91	
47	Lr	125	
48	Ls	196	
49	Lt	157	
50	SA	221	
51	SB	214	
52	SC	222	
53	SE	262	

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Mol	Chain	Length	Quality of chain
54	SG	237	
55	SH	189	
56	SI	206	
57	SJ	185	
58	SL	153	
59	SN	150	
60	SO	140	
61	SV	83	
62	SW	129	
63	SX	141	
64	SY	131	
65	Sa	102	
66	Sb	83	
67	Se	58	
68	S2	1740	
69	SR	135	
70	SD	227	
71	SF	189	
72	SK	98	
73	SM	122	
74	SP	121	
75	SQ	144	
76	SS	145	
77	ST	143	
78	SU	104	

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Mol	Chain	Length	Quality of chain
79	SZ	75	
80	Sc	64	
81	Sd	55	
82	Sf	67	
83	Sg	313	
84	Et	75	
85	CB	856	
86	CA	356	

2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 228149 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 SERPINE1 mRNA-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	CD	55	Total	C	N	O	0	0
			440	263	87	90		

- Molecule 2 is a protein called Transcription factor BTF3.

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

- 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	205	Total	C	N	O	S	0	0
			1658	1052	318	274	14		

- 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 40S ribosomal protein SA.

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

- Molecule 51 is a protein called 40S ribosomal protein S3a.

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

- Molecule 52 is a protein called 40S ribosomal protein S2.

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

- Molecule 53 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 54 is a protein called 40S ribosomal protein S6.

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

- Molecule 55 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 56 is a protein called 40S ribosomal protein S8.

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

- Molecule 57 is a protein called 40S ribosomal protein S9.

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

- Molecule 58 is a protein called 40S ribosomal protein S11.

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

- Molecule 59 is a protein called 40S ribosomal protein S13.

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

- Molecule 60 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 61 is a protein called Small ribosomal subunit protein eS21.

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

- Molecule 62 is a protein called 40S ribosomal protein S15a.

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

- Molecule 63 is a protein called 40S ribosomal protein S23.

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

- Molecule 64 is a protein called 40S ribosomal protein S24.

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

- Molecule 65 is a protein called 40S ribosomal protein S26.

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

- Molecule 66 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 67 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 68 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	S2	1740	Total	C	N	O	P	0	0
			36952	16508	6600	12105	1739		

- Molecule 69 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 70 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 71 is a protein called 40S ribosomal protein S5.

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

- Molecule 72 is a protein called 40S ribosomal protein S10.

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

- Molecule 73 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 74 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 75 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 76 is a protein called 40S ribosomal protein S18.

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

- Molecule 77 is a protein called 40S ribosomal protein S19.

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

- Molecule 78 is a protein called 40S ribosomal protein S20.

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

- Molecule 79 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 80 is a protein called 40S ribosomal protein S28.

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

- Molecule 81 is a protein called 40S ribosomal protein S29.

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

- Molecule 82 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 83 is a protein called Receptor of activated protein C kinase 1.

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

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

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

- Molecule 85 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	CB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

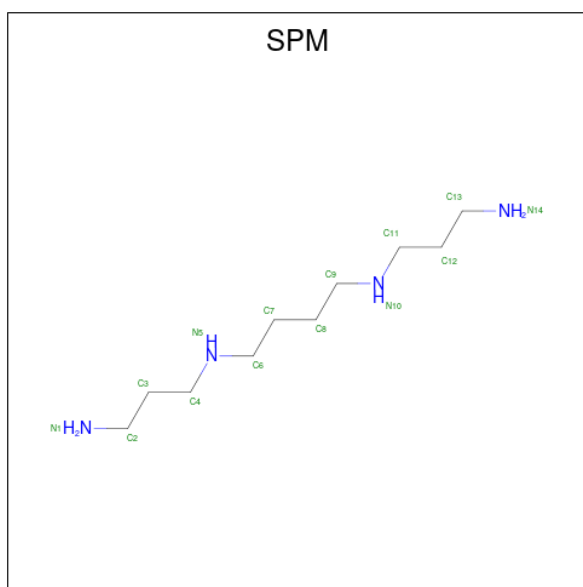
- Molecule 86 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	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	178	Total	Mg	0
			178	178	
87	L7	3	Total	Mg	0
			3	3	
87	L8	5	Total	Mg	0
			5	5	
87	LA	1	Total	Mg	0
			1	1	
87	LP	1	Total	Mg	0
			1	1	
87	LV	1	Total	Mg	0
			1	1	
87	Le	1	Total	Mg	0
			1	1	
87	Lj	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: C₁₀H₂₆N₄) (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	

- Molecule 89 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃) (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	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
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

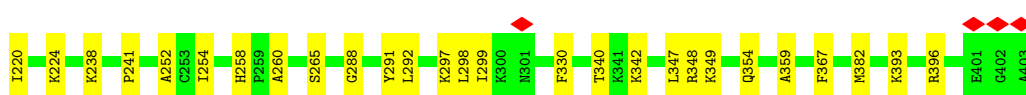
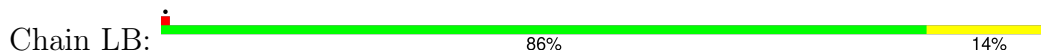




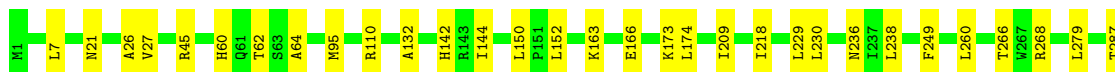




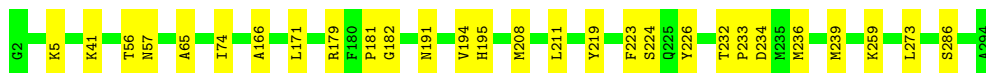
- Molecule 7: Large ribosomal subunit protein uL3



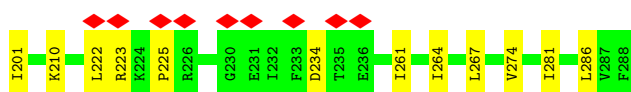
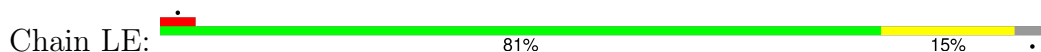
- Molecule 8: 60S ribosomal protein L4



- Molecule 9: Large ribosomal subunit protein uL18



- Molecule 10: Large ribosomal subunit protein eL6

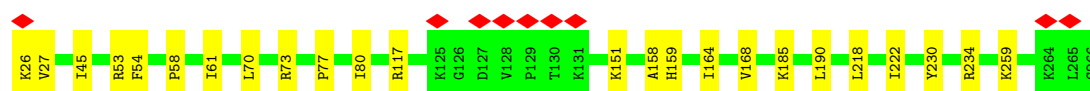


- Molecule 11: 60S ribosomal protein L7



- Molecule 12: 60S ribosomal protein L7a

Chain LG:  90% 10%



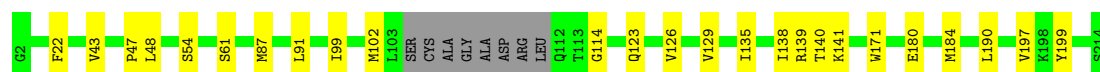
- Molecule 13: 60S ribosomal protein L9

Chain LH:  88% 12%



- Molecule 14: Ribosomal protein uL16-like

Chain LI:  85% 12%



- Molecule 15: 60S ribosomal protein L11

Chain LJ:  85% 11%



- Molecule 16: Large ribosomal subunit protein eL13

Chain LL:  93% 6%



- Molecule 17: 60S ribosomal protein L14

Chain LM:  90% 9%



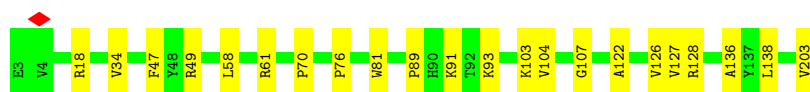
- Molecule 18: 60S ribosomal protein L15

Chain LN:  91% 9%



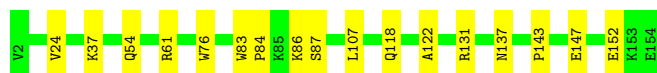
- Molecule 19: 60S ribosomal protein L13a

Chain LO:  89% 11%



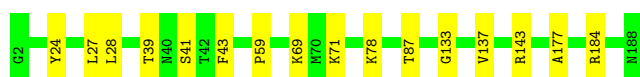
- Molecule 20: 60S ribosomal protein L17

Chain LP:  89% 11%



- Molecule 21: 60S ribosomal protein L18

Chain LQ:  91% 9%



- Molecule 22: 60S ribosomal protein L19

Chain LR:  5% 90% 10%



- Molecule 23: 60S ribosomal protein L18a

Chain LS:  89% 11%



- Molecule 24: 60S ribosomal protein L21

Chain LT:  92% 8%



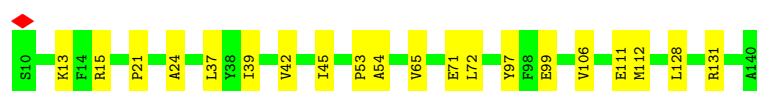
- Molecule 25: Heparin-binding protein HBp15

Chain LU:  88% 12%



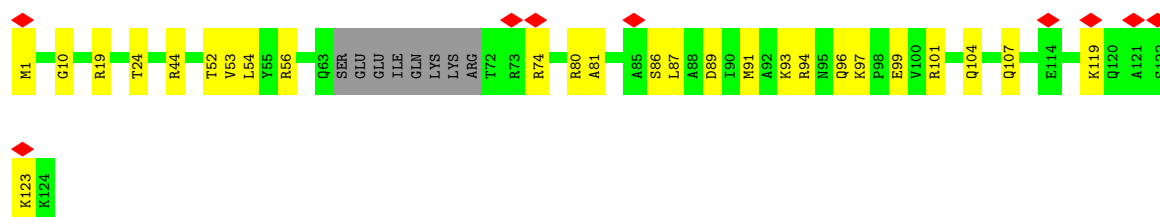
- Molecule 26: 60S ribosomal protein L23

Chain LV:  85% 15%



- Molecule 27: Ribosomal protein L24

Chain LW:  7% 73% 21% 6%



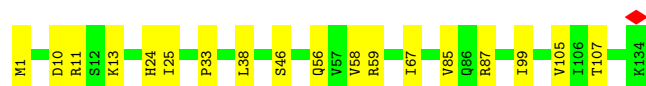
- Molecule 28: 60S ribosomal protein L23a

Chain LX:  92% 8%



- Molecule 29: 60S ribosomal protein L26

Chain LY:  87% 13%

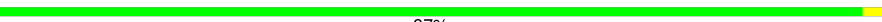


- Molecule 30: 60S ribosomal protein L27

Chain LZ:  90% 10%



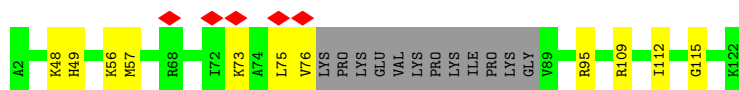
- Molecule 31: 60S ribosomal protein L27a

Chain La:  97%

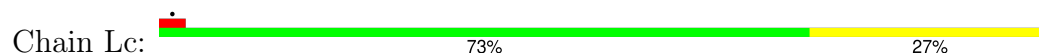


- Molecule 32: Large ribosomal subunit protein eL29

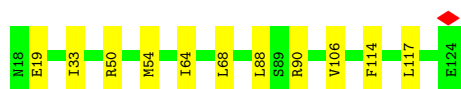
Chain Lb:  81% 9% 10%



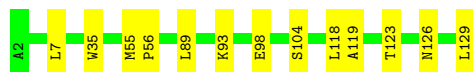
- Molecule 33: 60S ribosomal protein L30



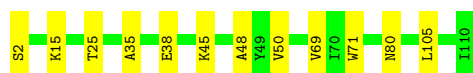
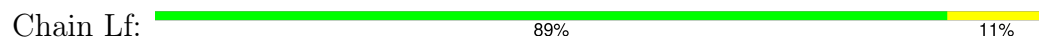
- Molecule 34: 60S ribosomal protein L31



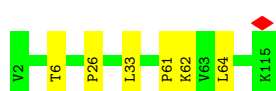
- Molecule 35: 60S ribosomal protein L32



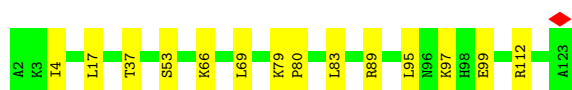
- Molecule 36: 60S ribosomal protein L35a



- Molecule 37: 60S ribosomal protein L34



- Molecule 38: 60S ribosomal protein L35



- Molecule 39: 60S ribosomal protein L36

Chain Li:  94% 6%



- Molecule 40: 60S ribosomal protein L37

Chain Lj:  94% 6%



- Molecule 41: 60S ribosomal protein L38

Chain Lk:  88% 12%



- Molecule 42: 60S ribosomal protein L39

Chain Ll:  76% 24%



- Molecule 43: Large ribosomal subunit protein eL40

Chain Lm:  94% 6%



- Molecule 44: 60S ribosomal protein L41

Chain Ln:  83% 17%



- Molecule 45: 60S ribosomal protein L36a

Chain Lo:  91% 9%



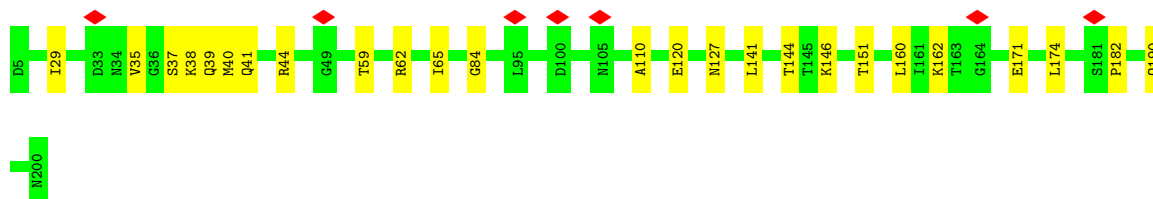
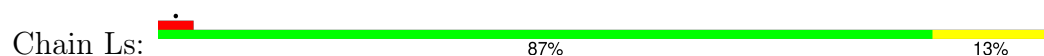
- Molecule 46: 60S ribosomal protein L37a



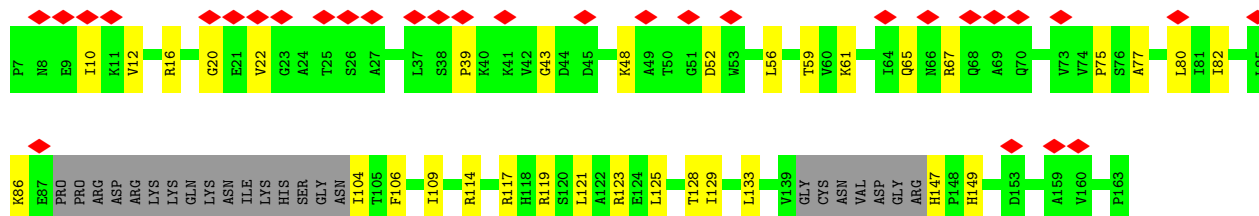
- Molecule 47: 60S ribosomal protein L28



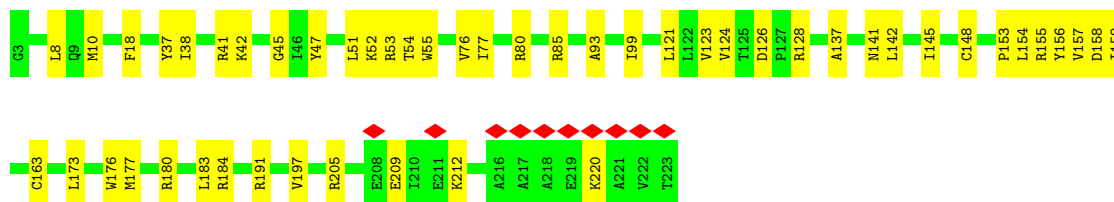
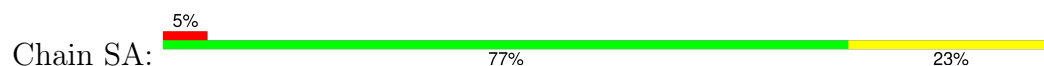
- Molecule 48: 60S acidic ribosomal protein P0



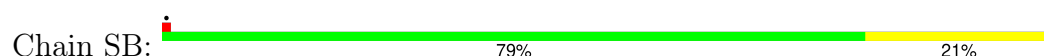
- Molecule 49: Large ribosomal subunit protein uL11

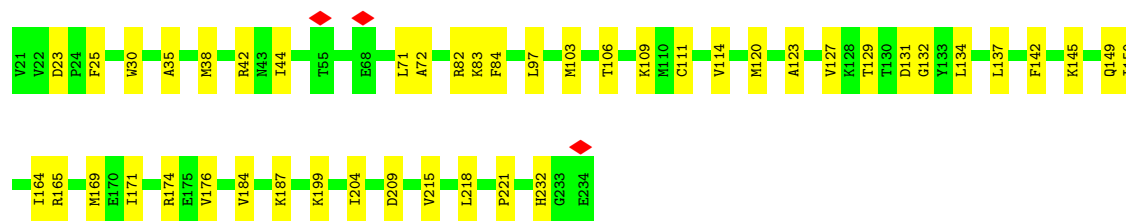


- Molecule 50: 40S ribosomal protein SA



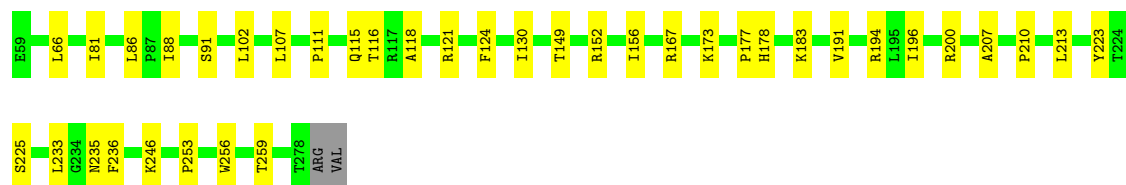
- Molecule 51: 40S ribosomal protein S3a





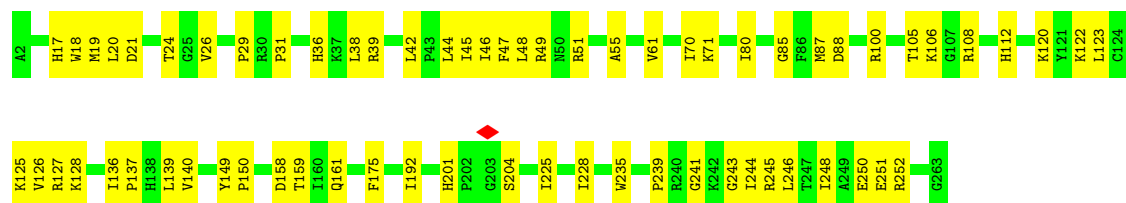
- Molecule 52: 40S ribosomal protein S2

Chain SC: 82% 17%



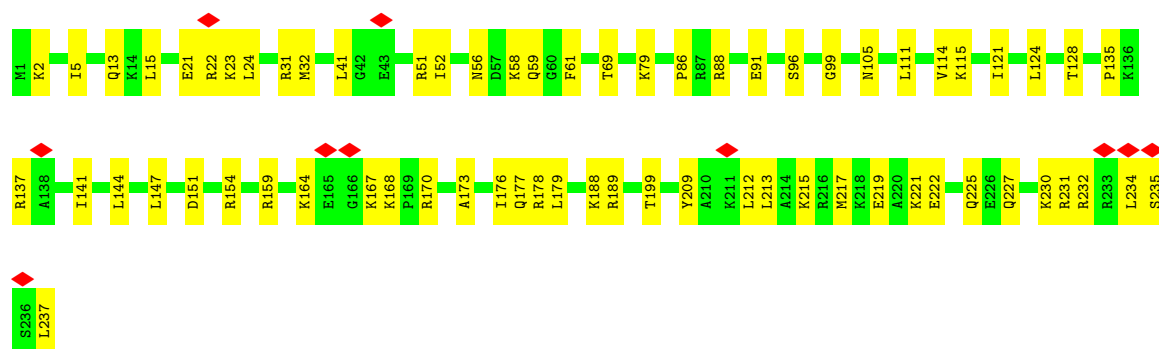
- Molecule 53: Small ribosomal subunit protein eS4, X isoform

Chain SE: 75% 25%



- Molecule 54: 40S ribosomal protein S6

Chain SG: 72% 28%



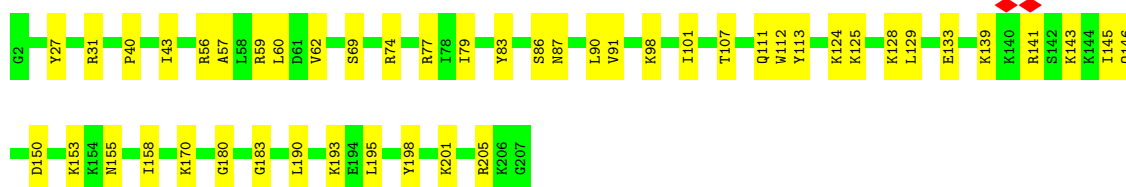
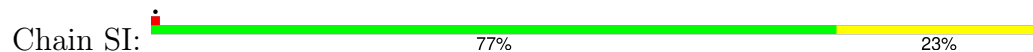
- Molecule 55: Small ribosomal subunit protein eS7

Chain SH: 5% 75% 24%

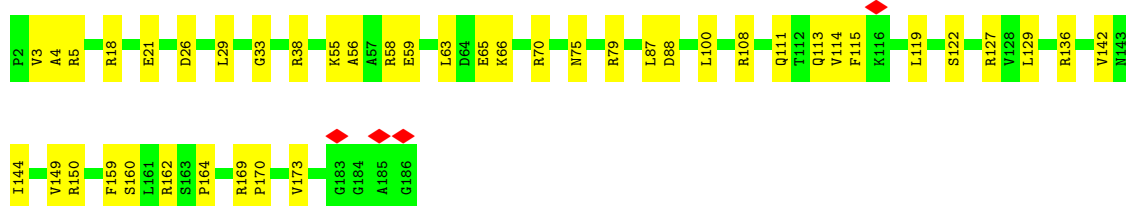




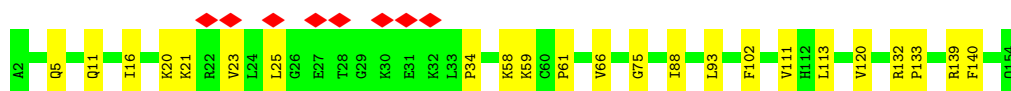
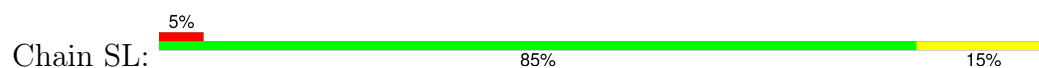
- Molecule 56: 40S ribosomal protein S8



- Molecule 57: 40S ribosomal protein S9



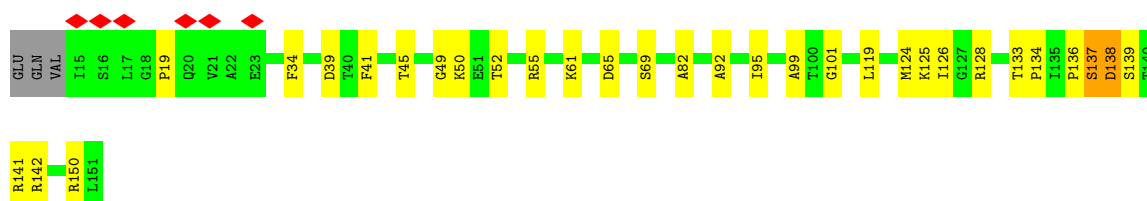
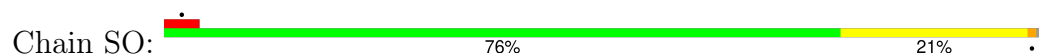
- Molecule 58: 40S ribosomal protein S11



- Molecule 59: 40S ribosomal protein S13



- Molecule 60: Small ribosomal subunit protein uS11



- Molecule 61: Small ribosomal subunit protein eS21

Chain SV:  78% 22%



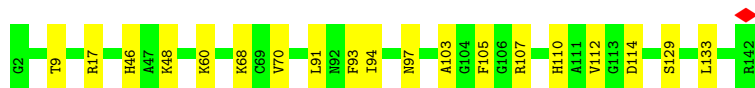
- Molecule 62: 40S ribosomal protein S15a

Chain SW:  88% 12%



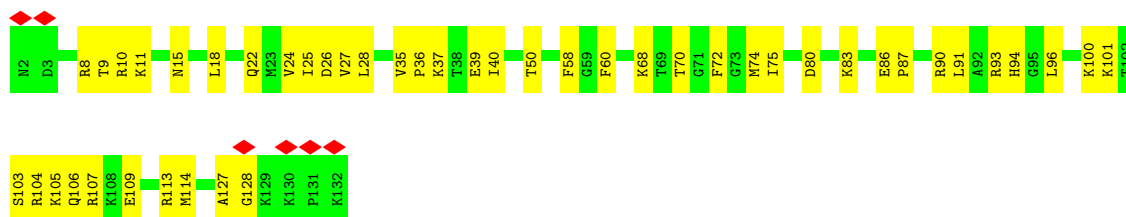
- Molecule 63: 40S ribosomal protein S23

Chain SX:  87% 13%



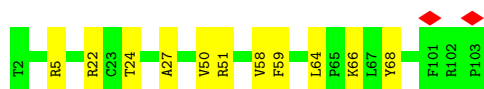
- Molecule 64: 40S ribosomal protein S24

Chain SY:  5% 65% 35%



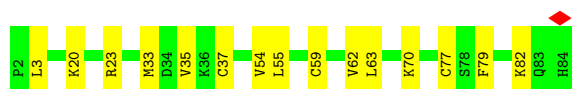
- Molecule 65: 40S ribosomal protein S26

Chain Sa:  89% 11%

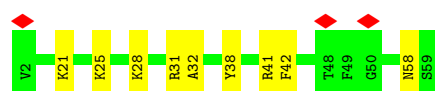
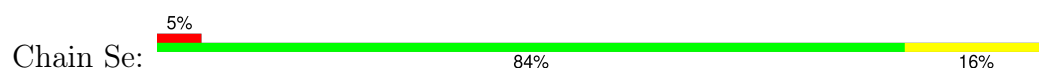


- Molecule 66: Small ribosomal subunit protein eS27

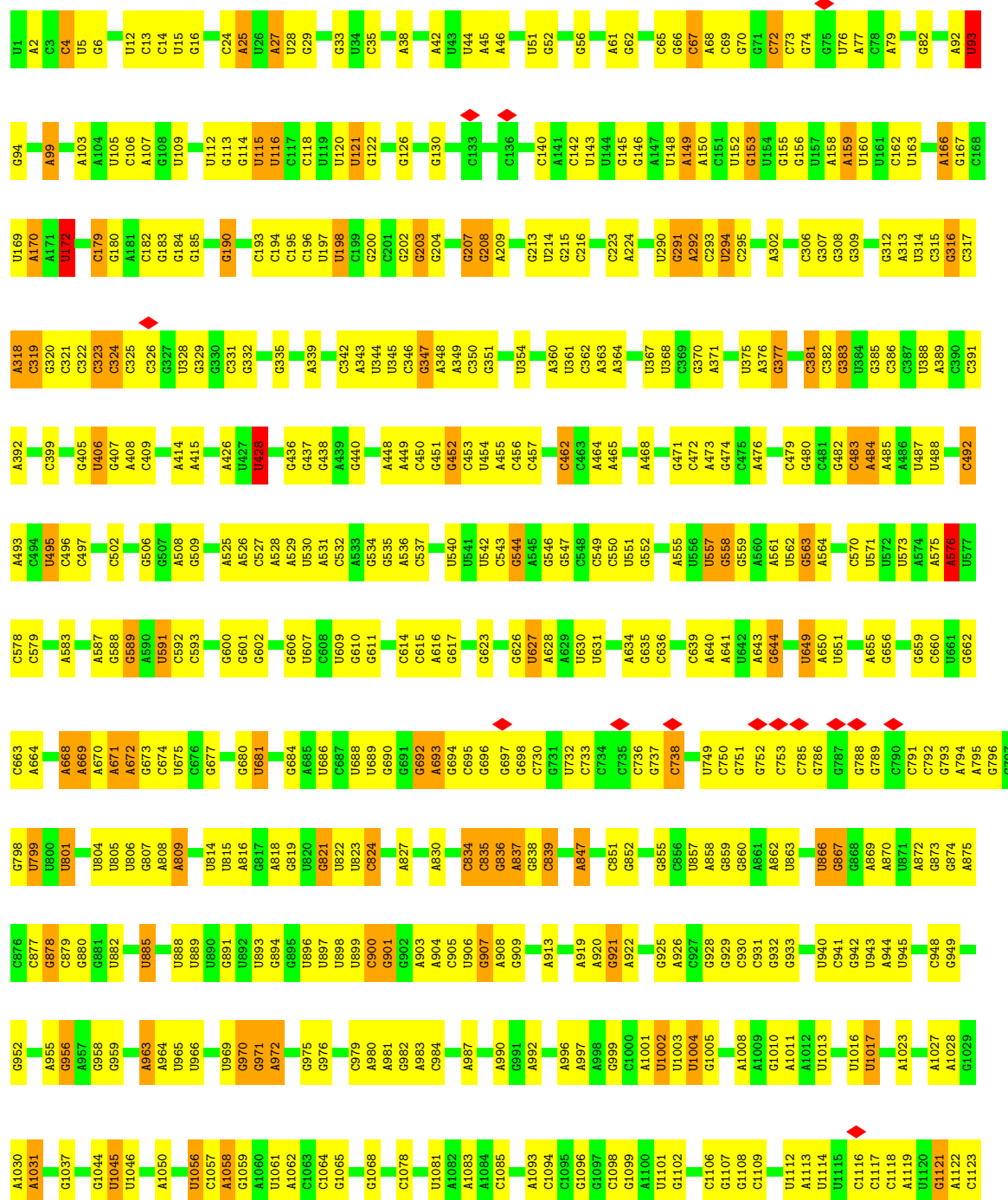
Chain Sb:  82% 18%

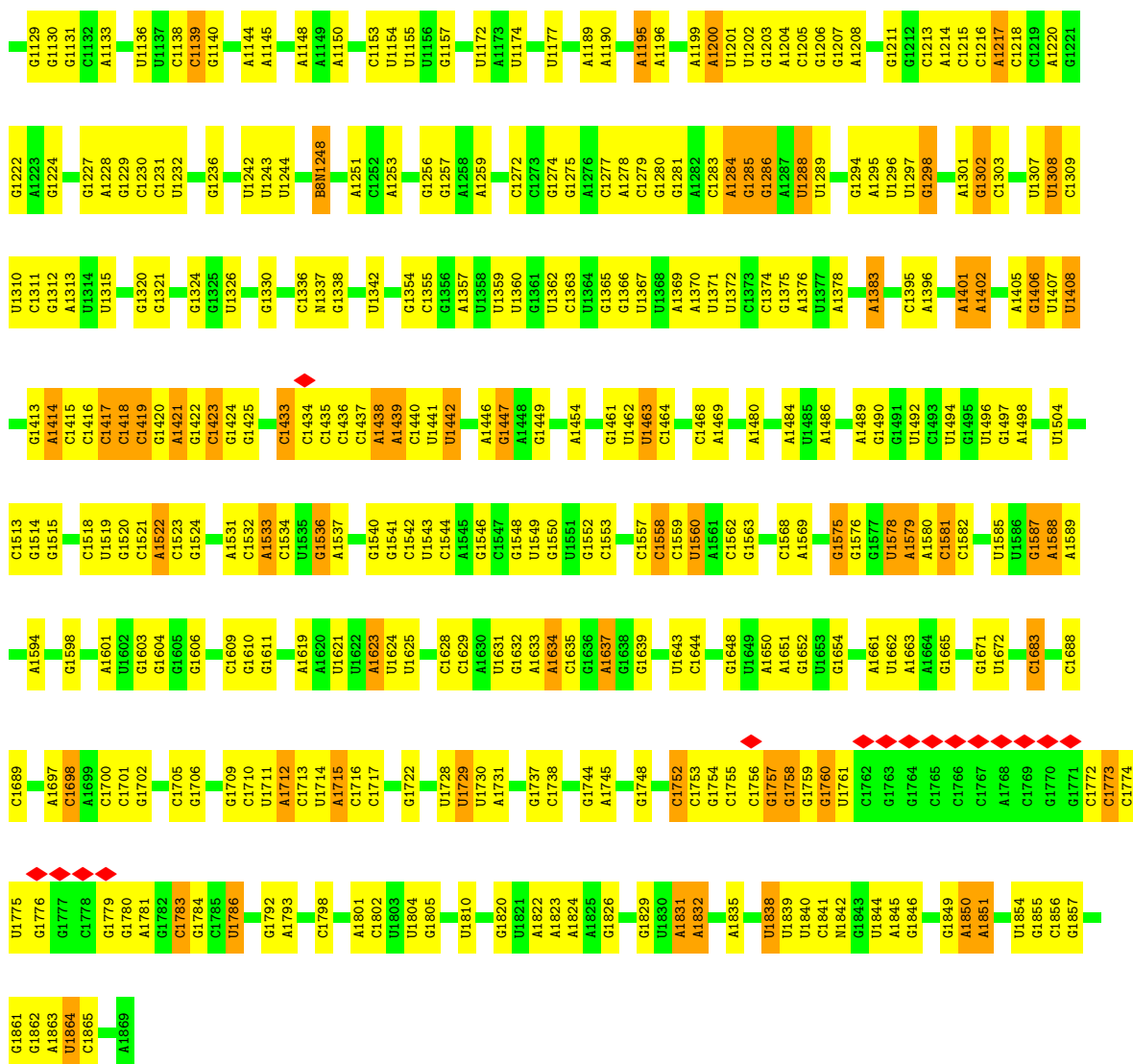


- Molecule 67: Small ribosomal subunit protein eS30

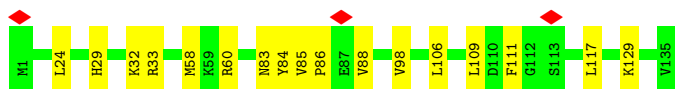


• Molecule 68: 18S rRNA

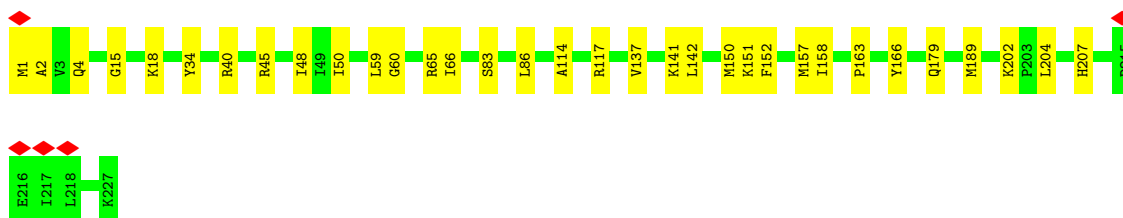
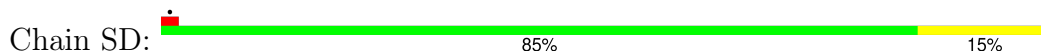




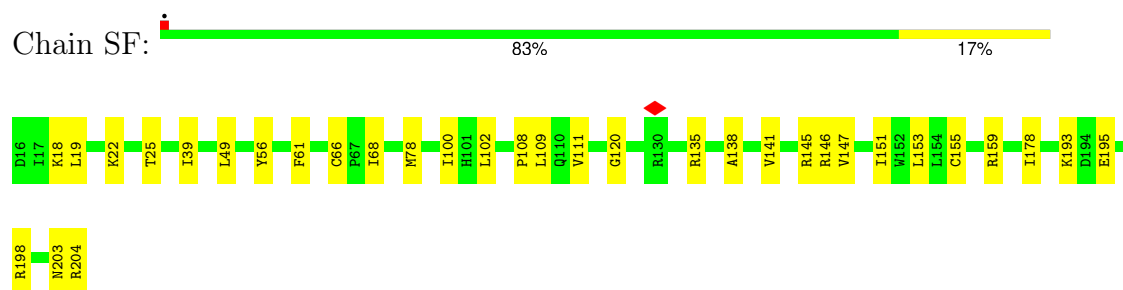
- Molecule 69: Small ribosomal subunit protein eS17



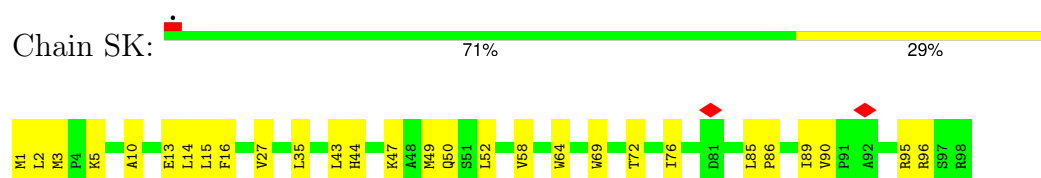
- Molecule 70: Small ribosomal subunit protein uS3



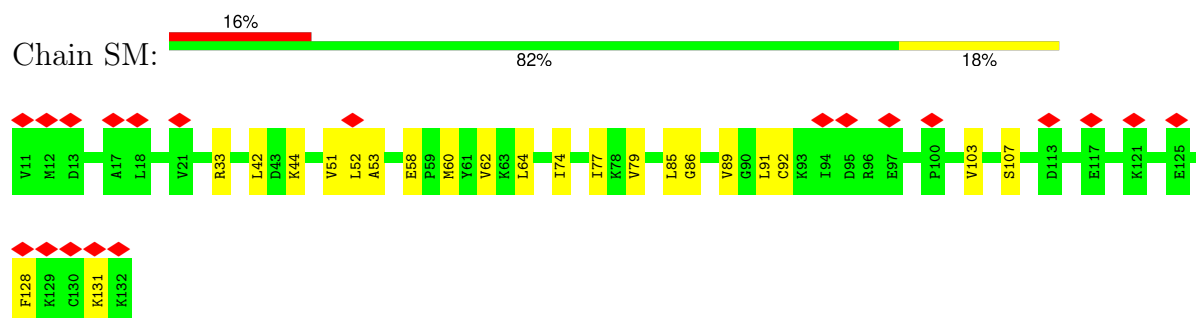
- Molecule 71: 40S ribosomal protein S5



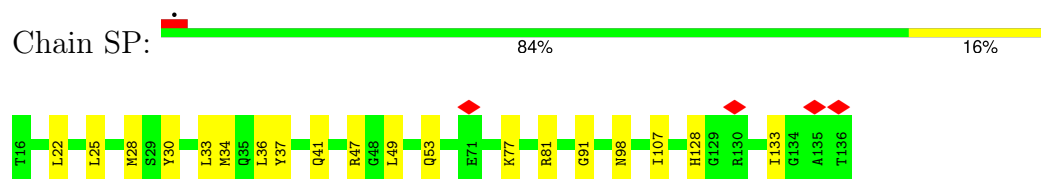
- Molecule 72: 40S ribosomal protein S10



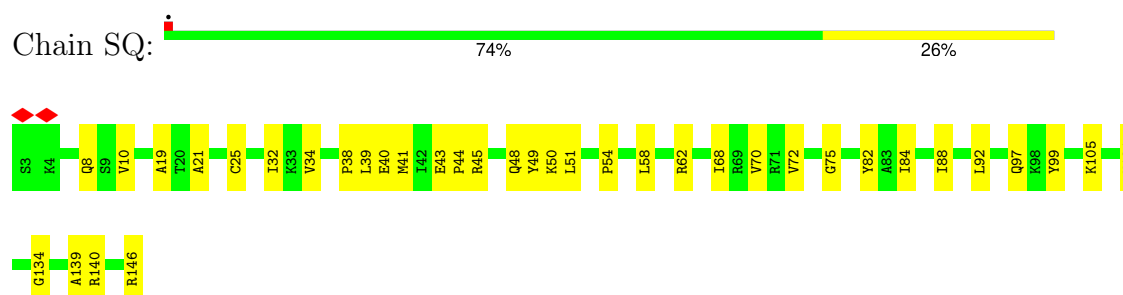
- Molecule 73: Small ribosomal subunit protein eS12



- Molecule 74: Small ribosomal subunit protein uS19

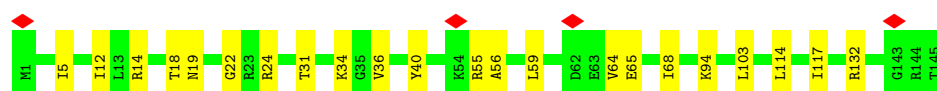


- Molecule 75: Small ribosomal subunit protein uS9



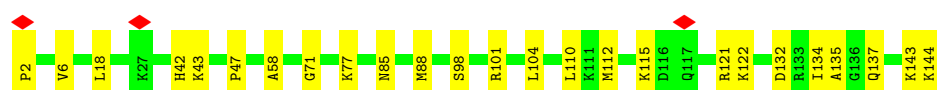
- Molecule 76: 40S ribosomal protein S18

Chain SS:  85% 15%



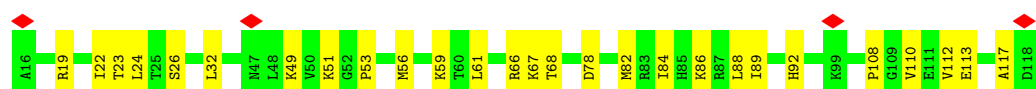
- Molecule 77: 40S ribosomal protein S19

Chain ST:  83% 17%



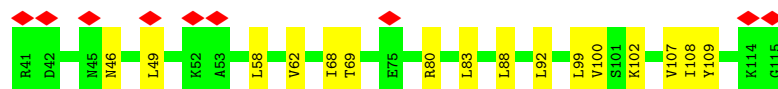
- Molecule 78: 40S ribosomal protein S20

Chain SU:  74% 26%



- Molecule 79: Small ribosomal subunit protein eS25

Chain SZ:  12% 79% 21%



- Molecule 80: 40S ribosomal protein S28

Chain Sc:  77% 23%



- Molecule 81: 40S ribosomal protein S29

Chain Sd:  84% 16%

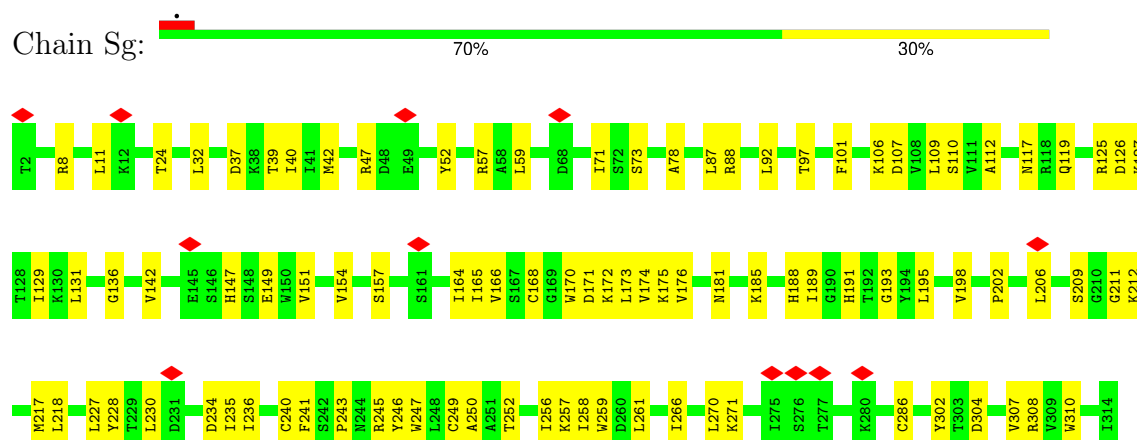


- Molecule 82: Ubiquitin-40S ribosomal protein S27a

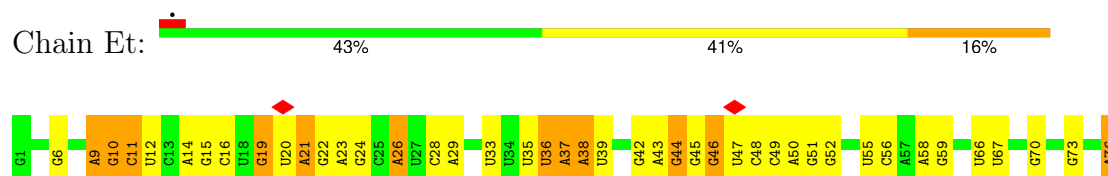
Chain Sf:  10% 64% 36%



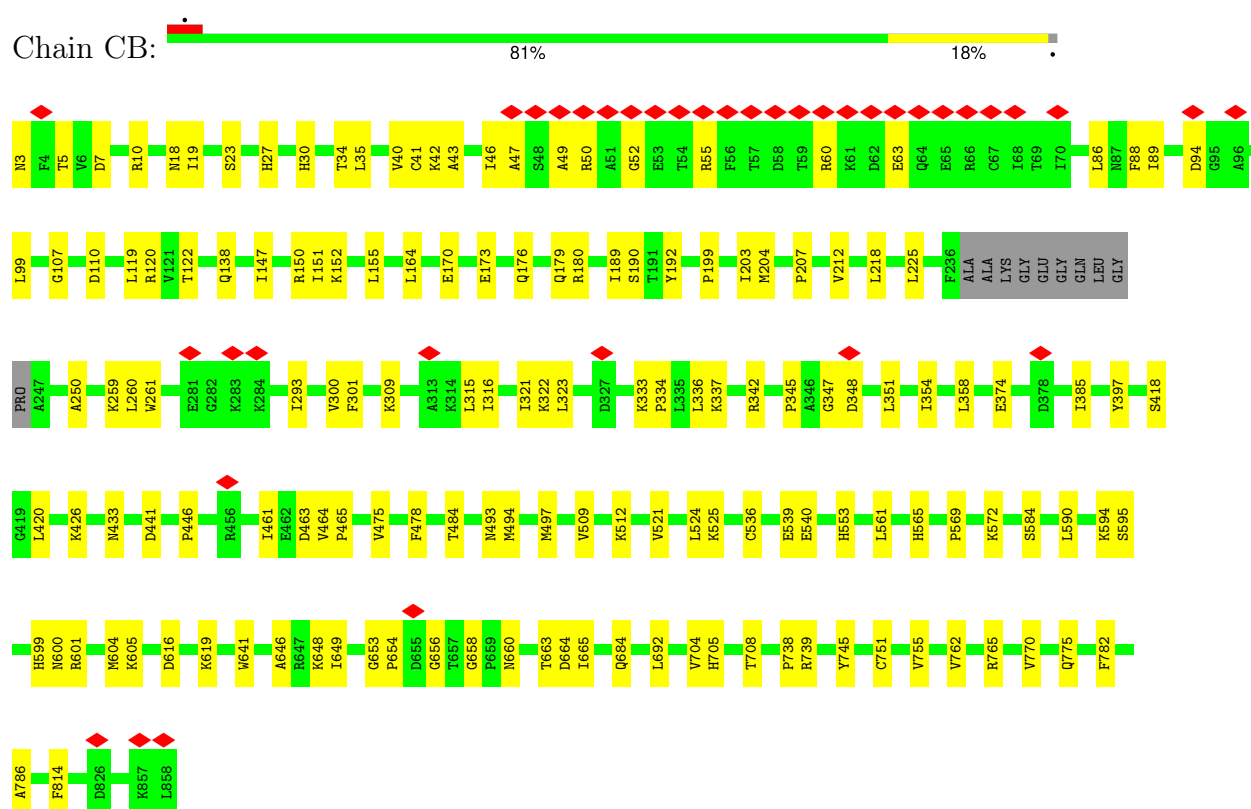
- Molecule 83: Receptor of activated protein C kinase 1



- Molecule 84: E site tRNA

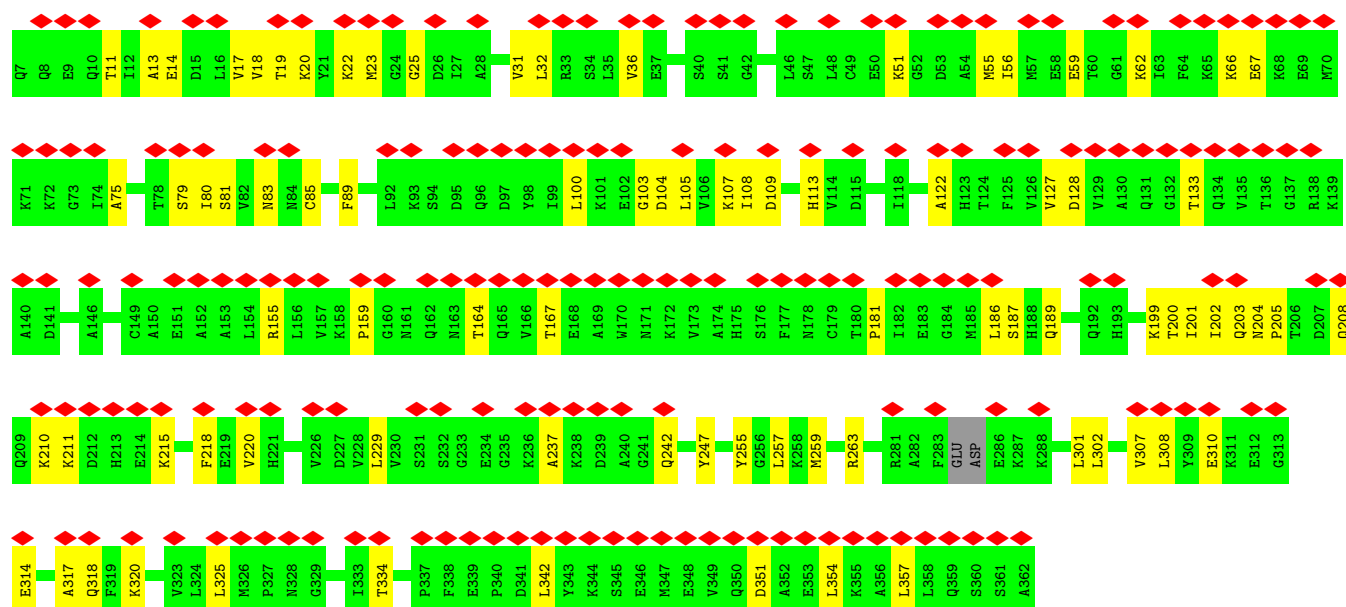


- Molecule 85: Elongation factor 2



- Molecule 86: Proliferation-associated protein 2G4

Chain CA: 53% 76% 23% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	28219	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	0.138	Depositor
Minimum map value	-0.048	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0145	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: MG, G7M, OMU, PSU, 5MC, 1MA, OMC, 6MZ, MA6, B8N, UY1, A2M, UR3, SPD, ZN, OMG, 4AC, SPM

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	CD	0.17	0/447	0.33	0/592
2	CI	0.19	0/247	0.33	0/323
3	L5	0.43	0/85098	0.36	0/132762
4	L7	0.42	0/2861	0.32	0/4459
5	L8	0.43	0/3631	0.33	0/5657
6	LA	0.42	0/1936	0.39	0/2596
7	LB	0.39	0/3306	0.39	0/4424
8	LC	0.41	0/2981	0.39	0/4002
9	LD	0.32	0/2428	0.35	0/3252
10	LE	0.31	0/1973	0.37	0/2645
11	LF	0.41	0/1905	0.34	0/2539
12	LG	0.34	0/1960	0.36	0/2637
13	LH	0.36	0/1537	0.36	0/2066
14	LI	0.35	0/1697	0.32	0/2266
15	LJ	0.29	0/1385	0.35	0/1852
16	LL	0.37	0/1732	0.36	0/2315
17	LM	0.37	0/1161	0.35	0/1554
18	LN	0.44	0/1746	0.38	0/2338
19	LO	0.42	0/1682	0.36	0/2250
20	LP	0.41	0/1268	0.41	0/1701
21	LQ	0.41	0/1537	0.39	0/2052
22	LR	0.34	0/1582	0.34	0/2091
23	LS	0.41	0/1493	0.37	0/2003
24	LT	0.39	0/1326	0.33	0/1770
25	LU	0.28	0/839	0.35	0/1126
26	LV	0.39	0/993	0.40	0/1332
27	LW	0.29	0/959	0.35	0/1270
28	LX	0.37	0/1002	0.35	0/1345
29	LY	0.38	0/1132	0.35	0/1504
30	LZ	0.34	0/1130	0.36	0/1507
31	La	0.42	0/1191	0.35	0/1591

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Lb	0.32	0/889	0.41	0/1175
33	Lc	0.35	0/774	0.34	0/1038
34	Ld	0.38	0/903	0.37	0/1216
35	Le	0.41	0/1071	0.36	0/1429
36	Lf	0.43	0/895	0.39	0/1198
37	Lg	0.38	0/916	0.37	0/1220
38	Lh	0.34	0/1023	0.37	0/1351
39	Li	0.32	0/843	0.33	0/1115
40	Lj	0.43	0/720	0.44	0/952
41	Lk	0.31	0/575	0.32	0/761
42	Ll	0.41	0/454	0.36	0/599
43	Lm	0.36	0/435	0.38	0/575
44	Ln	0.32	0/231	0.27	0/294
45	Lo	0.37	0/876	0.37	0/1156
46	Lp	0.38	0/718	0.34	0/953
47	Lr	0.39	0/1017	0.37	0/1364
48	Ls	0.20	0/1519	0.34	0/2052
49	Lt	0.18	0/1009	0.47	0/1363
50	SA	0.25	0/1778	0.40	0/2416
51	SB	0.23	0/1765	0.35	0/2362
52	SC	0.26	0/1744	0.37	0/2357
53	SE	0.21	0/2118	0.34	0/2849
54	SG	0.20	0/1946	0.40	0/2590
55	SH	0.20	0/1519	0.42	0/2033
56	SI	0.25	0/1715	0.37	0/2287
57	SJ	0.22	0/1550	0.35	0/2069
58	SL	0.25	0/1268	0.35	0/1696
59	SN	0.24	0/1232	0.35	0/1656
60	SO	0.31	0/1037	0.49	1/1391 (0.1%)
61	SV	0.22	0/643	0.34	0/860
62	SW	0.27	0/1051	0.35	0/1406
63	SX	0.27	0/1116	0.39	0/1490
64	SY	0.20	0/1083	0.36	0/1438
65	Sa	0.29	0/836	0.39	0/1121
66	Sb	0.24	0/665	0.36	0/891
67	Se	0.20	0/465	0.34	0/612
68	S2	0.31	0/39756	0.34	0/61939
69	SR	0.22	0/1105	0.41	0/1484
70	SD	0.23	0/1793	0.34	0/2414
71	SF	0.21	0/1516	0.35	0/2037
72	SK	0.22	0/851	0.39	0/1147
73	SM	0.17	0/950	0.43	0/1275
74	SP	0.22	0/1003	0.34	0/1342

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	SQ	0.23	0/1160	0.39	0/1553
76	SS	0.20	0/1216	0.33	0/1628
77	ST	0.25	0/1131	0.41	0/1515
78	SU	0.26	0/831	0.37	0/1115
79	SZ	0.20	0/604	0.38	0/810
80	Sc	0.20	0/508	0.34	0/680
81	Sd	0.25	0/470	0.36	0/623
82	Sf	0.20	0/560	0.47	0/745
83	Sg	0.19	0/2493	0.38	0/3394
84	Et	0.22	0/1778	0.38	0/2767
85	CB	0.22	0/6734	0.37	1/9094 (0.0%)
86	CA	0.17	0/2810	0.38	0/3780
All	All	0.36	0/239833	0.36	2/350498 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	SO	137	SER	N-CA-C	-5.24	105.69	111.71
85	CB	293	ILE	N-CA-C	-5.03	107.65	111.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CD	440	0	402	7	0
2	CI	247	0	283	1	0
3	L5	78444	0	39719	600	0
4	L7	2561	0	1295	8	0
5	L8	3315	0	1685	24	0
6	LA	1898	0	1993	21	0
7	LB	3238	0	3376	41	0
8	LC	2927	0	3104	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	LD	2382	0	2410	20	0
10	LE	1935	0	2096	25	0
11	LF	1870	0	1996	12	0
12	LG	1927	0	2074	16	0
13	LH	1518	0	1601	13	0
14	LI	1658	0	1697	13	0
15	LJ	1362	0	1399	11	0
16	LL	1701	0	1818	11	0
17	LM	1138	0	1204	8	0
18	LN	1701	0	1749	15	0
19	LO	1650	0	1794	19	0
20	LP	1242	0	1269	11	0
21	LQ	1513	0	1628	11	0
22	LR	1566	0	1729	17	0
23	LS	1453	0	1490	13	0
24	LT	1298	0	1366	10	0
25	LU	825	0	850	6	0
26	LV	979	0	1039	12	0
27	LW	945	0	1003	18	0
28	LX	985	0	1066	8	0
29	LY	1115	0	1205	13	0
30	LZ	1107	0	1182	9	0
31	La	1162	0	1213	4	0
32	Lb	876	0	948	9	0
33	Lc	764	0	804	16	0
34	Ld	888	0	930	7	0
35	Le	1053	0	1147	8	0
36	Lf	876	0	912	7	0
37	Lg	906	0	998	5	0
38	Lh	1015	0	1148	13	0
39	Li	832	0	917	7	0
40	Lj	705	0	737	4	0
41	Lk	569	0	637	4	0
42	Ll	444	0	483	10	0
43	Lm	429	0	465	2	0
44	Ln	230	0	276	4	0
45	Lo	862	0	929	5	0
46	Lp	708	0	756	7	0
47	Lr	1002	0	1068	7	0
48	Ls	1496	0	1540	16	0
49	Lt	998	0	1032	25	0
50	SA	1741	0	1744	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	SB	1738	0	1809	30	0
52	SC	1707	0	1791	29	0
53	SE	2076	0	2177	43	0
54	SG	1923	0	2088	56	0
55	SH	1497	0	1590	29	0
56	SI	1686	0	1772	31	0
57	SJ	1525	0	1640	33	0
58	SL	1247	0	1323	15	0
59	SN	1208	0	1294	11	0
60	SO	1024	0	1050	29	0
61	SV	636	0	637	11	0
62	SW	1034	0	1080	14	0
63	SX	1098	0	1167	14	0
64	SY	1065	0	1142	34	0
65	Sa	821	0	870	11	0
66	Sb	651	0	669	10	0
67	Se	459	0	503	9	0
68	S2	36952	0	18676	485	0
69	SR	1090	0	1149	16	0
70	SD	1765	0	1865	22	0
71	SF	1495	0	1549	23	0
72	SK	827	0	854	19	0
73	SM	940	0	965	16	0
74	SP	985	0	1031	13	0
75	SQ	1142	0	1213	29	0
76	SS	1198	0	1261	14	0
77	ST	1112	0	1146	15	0
78	SU	821	0	883	16	0
79	SZ	598	0	656	13	0
80	Sc	506	0	536	10	0
81	Sd	459	0	449	7	0
82	Sf	548	0	551	20	0
83	Sg	2436	0	2389	62	0
84	Et	1593	0	810	28	0
85	CB	6605	0	6679	93	0
86	CA	2764	0	2779	50	0
87	L5	178	0	0	0	0
87	L7	3	0	0	0	0
87	L8	5	0	0	0	0
87	LA	1	0	0	0	0
87	LP	1	0	0	0	0
87	LV	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	Le	1	0	0	0	0
87	Lj	1	0	0	0	0
87	S2	26	0	0	0	0
87	SG	1	0	0	0	0
88	L5	98	0	182	5	0
89	L5	90	0	171	1	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	228149	0	172621	2293	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 6.

All (2293) 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)
84:Et:26:A:H62	84:Et:44:G:N2	1.66	0.93
3:L5:1177:U:H3	3:L5:1183:C:H42	1.20	0.89
68:S2:1748:G:H1	68:S2:1786:U:H3	0.96	0.89
3:L5:505:G:H1	3:L5:653:U:H3	1.20	0.86
3:L5:512:U:H3	3:L5:647:G:H1	1.23	0.84
3:L5:4775:C:H41	3:L5:4859:C:H42	1.25	0.84
68:S2:588:G:H4'	68:S2:589:G:H5'	1.60	0.83
68:S2:1298:G:H5'	74:SP:77:LYS:HB2	1.62	0.81
49:Lt:117:ARG:HE	49:Lt:119:ARG:H	1.29	0.80
49:Lt:123:ARG:HD2	49:Lt:129:ILE:HD11	1.64	0.80
68:S2:639:C:H2'	68:S2:640:A:H8	1.45	0.80
76:SS:34:LYS:HG3	76:SS:103:LEU:HD23	1.63	0.80
84:Et:21:A:H61	84:Et:46:G:H2'	1.46	0.79
26:LV:13:LYS:HD2	26:LV:128:LEU:HD11	1.64	0.78
84:Et:6:G:H1	84:Et:67:U:H3	1.31	0.77
68:S2:834:C:H42	68:S2:839:C:H42	1.33	0.77
3:L5:2709:C:H42	86:CA:257:LEU:H	1.32	0.77
85:CB:18:ASN:HD21	85:CB:94:ASP:HB3	1.50	0.76
83:Sg:32:LEU:HD21	83:Sg:71:ILE:HD11	1.68	0.76
3:L5:2611:A:H5'	3:L5:2688:G:H4'	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:SS:5:ILE:HG13	79:SZ:49:LEU:HB2	1.67	0.75
76:SS:12:ILE:HD11	76:SS:19:ASN:HB2	1.67	0.75
53:SE:38:LEU:HD22	68:S2:346:C:H5''	1.68	0.75
84:Et:26:A:N6	84:Et:44:G:H21	1.82	0.75
49:Lt:65:GLN:HG3	49:Lt:67:ARG:H	1.51	0.74
84:Et:26:A:N6	84:Et:44:G:N2	2.33	0.74
3:L5:1366:G:H5''	16:LL:36:ARG:HH12	1.51	0.74
68:S2:120:U:H2'	68:S2:121:OMU:H6	1.68	0.74
68:S2:166:A2M:H2'	68:S2:167:G:H8	1.53	0.73
3:L5:2303:C:H5''	35:Le:104:SER:HB3	1.69	0.73
77:ST:18:LEU:HD22	77:ST:58:ALA:HA	1.71	0.73
26:LV:111:GLU:HG3	26:LV:131:ARG:HD3	1.71	0.72
68:S2:1550:G:H3'	68:S2:1579:A:H61	1.52	0.72
70:SD:60:GLY:HA3	70:SD:65:ARG:H	1.53	0.72
68:S2:140:C:H42	68:S2:313:A:H61	1.35	0.72
68:S2:70:G:N2	68:S2:79:A:H62	1.87	0.72
3:L5:2458:C:H5''	18:LN:67:ARG:HD2	1.70	0.72
27:LW:119:LYS:HG2	27:LW:123:LYS:HE3	1.71	0.72
85:CB:42:LYS:HG2	85:CB:347:GLY:HA3	1.72	0.72
68:S2:70:G:H21	68:S2:79:A:H62	1.38	0.71
51:SB:127:VAL:HG11	51:SB:176:VAL:HG13	1.72	0.71
83:Sg:107:ASP:HB2	83:Sg:125:ARG:HD2	1.71	0.71
86:CA:122:ALA:HB2	86:CA:320:LYS:HE3	1.72	0.71
60:SO:52:THR:HG21	68:S2:952:G:H21	1.54	0.71
3:L5:4910:G:H4'	7:LB:95:THR:HG22	1.72	0.71
3:L5:4251:A:H5''	15:LJ:108:GLY:HA3	1.73	0.71
68:S2:1286:G:H21	68:S2:1313:A:H62	1.39	0.71
78:SU:24:LEU:HB3	78:SU:32:LEU:HD11	1.73	0.70
68:S2:155:G:H2'	68:S2:156:G:H8	1.56	0.70
6:LA:104:VAL:HA	6:LA:107:MET:HE2	1.73	0.70
76:SS:36:VAL:HG23	76:SS:40:TYR:HB3	1.74	0.70
3:L5:1177:U:H3	3:L5:1183:C:N4	1.89	0.69
3:L5:137:G:H2'	3:L5:138:G:H8	1.58	0.69
64:SY:87:PRO:HG2	64:SY:90:ARG:HG3	1.74	0.69
68:S2:528:A:H61	68:S2:557:U:H3	1.40	0.69
86:CA:79:SER:HB3	86:CA:109:ASP:HB2	1.74	0.69
52:SC:207:ALA:HB2	68:S2:4:C:H4'	1.74	0.69
58:SL:58:LYS:HE3	58:SL:59:LYS:HE3	1.75	0.69
54:SG:137:ARG:HH21	68:S2:170:A:H5'	1.58	0.69
64:SY:9:THR:H	68:S2:837:A:H61	1.41	0.69
86:CA:80:ILE:HG12	86:CA:108:ILE:HG12	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:3944:G:H1	3:L5:4069:U:H3	1.39	0.69
75:SQ:58:LEU:HB2	75:SQ:62:ARG:HH11	1.58	0.69
3:L5:1942:A:H2'	3:L5:1943:A:C8	2.28	0.68
48:Ls:110:ALA:HA	48:Ls:182:PRO:HG2	1.75	0.68
68:S2:149:A:N7	68:S2:169:U:O2	2.26	0.68
68:S2:851:C:H5''	68:S2:852:G:H5'	1.74	0.68
84:Et:37:A:H3'	84:Et:38:A:H8	1.59	0.68
3:L5:2351:OMC:HM22	8:LC:95:MET:HG3	1.74	0.68
86:CA:159:PRO:HD3	86:CA:325:LEU:HD22	1.75	0.68
7:LB:92:TYR:HB2	7:LB:159:VAL:HB	1.76	0.68
85:CB:334:PRO:HA	85:CB:337:LYS:HD2	1.75	0.68
3:L5:3954:A:H1'	3:L5:4058:U:H5'	1.75	0.68
68:S2:1421:A:H3'	68:S2:1422:G:C8	2.28	0.68
56:SI:87:ASN:HB3	56:SI:90:LEU:HD13	1.76	0.67
3:L5:1100:U:N3	3:L5:1195:G:N1	2.42	0.67
68:S2:1010:G:H2'	68:S2:1011:A:H8	1.59	0.67
68:S2:1752:C:H42	68:S2:1755:C:H41	1.38	0.67
27:LW:80:ARG:HH21	54:SG:128:THR:HG23	1.59	0.67
72:SK:49:MET:HA	72:SK:52:LEU:HD12	1.75	0.67
85:CB:745:TYR:HB2	85:CB:814:PHE:HA	1.77	0.67
57:SJ:63:LEU:HD23	57:SJ:70:ARG:HB2	1.77	0.67
83:Sg:202:PRO:HG2	83:Sg:243:PRO:HA	1.76	0.67
83:Sg:247:TRP:HB3	83:Sg:258:ILE:HD11	1.76	0.67
3:L5:1095:A:N1	3:L5:1200:G:O6	2.28	0.67
3:L5:4594:U:H2'	3:L5:4595:G:H8	1.60	0.67
85:CB:354:ILE:HG23	85:CB:358:LEU:HD12	1.75	0.67
83:Sg:259:TRP:HB3	83:Sg:266:ILE:HA	1.77	0.67
86:CA:203:GLN:HE22	86:CA:229:LEU:H	1.43	0.67
3:L5:2517:A:H5'	37:Lg:62:LYS:HD3	1.78	0.66
7:LB:107:ALA:HB2	7:LB:201:LEU:HD22	1.76	0.66
30:LZ:95:VAL:HG11	30:LZ:113:GLU:HG3	1.77	0.66
83:Sg:87:LEU:HB2	83:Sg:101:PHE:HB2	1.77	0.66
3:L5:2362:U:H2'	3:L5:2363:A2M:H8	1.78	0.66
49:Lt:106:PHE:HB2	49:Lt:109:ILE:HG12	1.76	0.66
3:L5:3868:G:H22	3:L5:3900:G:H1'	1.59	0.66
63:SX:129:SER:HB2	68:S2:29:G:H4'	1.78	0.66
3:L5:502:C:H3'	3:L5:503:C:H3'	1.78	0.66
3:L5:3717:A:H2'	3:L5:3718:A2M:H8	1.77	0.66
68:S2:885:U:O2	68:S2:901:G:O6	2.13	0.66
78:SU:22:ILE:HD11	78:SU:112:VAL:HB	1.77	0.66
83:Sg:157:SER:HB3	83:Sg:164:ILE:HG12	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:4126:C:H5''	3:L5:4127:A:H5''	1.77	0.66
8:LC:230:LEU:HD21	8:LC:236:ASN:H	1.61	0.66
53:SE:31:PRO:HG2	53:SE:38:LEU:HB2	1.76	0.66
86:CA:75:ALA:HB2	86:CA:113:HIS:HB3	1.78	0.66
54:SG:176:ILE:HG23	54:SG:179:LEU:HD11	1.78	0.65
68:S2:557:U:H2'	68:S2:558:G:C8	2.30	0.65
3:L5:1100:U:O2	3:L5:1195:G:N2	2.29	0.65
55:SH:87:PHE:HB3	55:SH:90:LYS:HD2	1.78	0.65
68:S2:640:A:H2'	68:S2:641:A:C8	2.31	0.65
68:S2:955:A:H62	68:S2:971:G:N2	1.94	0.65
53:SE:87:MET:HG2	53:SE:100:ARG:HH11	1.60	0.65
68:S2:1854:U:H2'	68:S2:1855:G:H8	1.62	0.65
12:LG:58:PRO:HD2	12:LG:61:ILE:HD12	1.79	0.65
68:S2:1759:G:H21	68:S2:1773:C:H4'	1.62	0.65
57:SJ:164:PRO:HB3	57:SJ:170:PRO:HA	1.78	0.65
3:L5:497:G:H1	3:L5:657:C:H42	1.44	0.65
50:SA:156:TYR:HB3	61:SV:60:ARG:HH21	1.62	0.65
11:LF:105:VAL:HG13	11:LF:136:VAL:HG12	1.78	0.65
68:S2:600:G:H2'	68:S2:601:OMG:H8	1.61	0.65
68:S2:1560:U:O2	68:S2:1575:G:O6	2.14	0.65
68:S2:166:A2M:H2'	68:S2:167:G:C8	2.31	0.64
21:LQ:39:THR:HG22	21:LQ:41:SER:H	1.62	0.64
85:CB:10:ARG:HH22	85:CB:420:LEU:HD11	1.61	0.64
3:L5:696:C:H1'	10:LE:225:PRO:HB3	1.80	0.64
51:SB:72:ALA:HB3	60:SO:128:ARG:HH22	1.62	0.64
78:SU:61:LEU:HB2	78:SU:82:MET:HB3	1.79	0.64
83:Sg:8:ARG:HH12	83:Sg:47:ARG:HA	1.63	0.64
85:CB:86:LEU:HD12	85:CB:89:ILE:HD12	1.79	0.64
68:S2:106:C:H2'	68:S2:107:A:H8	1.63	0.64
84:Et:44:G:H2'	84:Et:45:G:C8	2.33	0.64
3:L5:3946:G:N2	3:L5:4067:U:O2	2.23	0.64
14:LI:43:VAL:HG21	14:LI:197:VAL:HG13	1.80	0.64
68:S2:116:OMU:HN3	68:S2:347:G:H1	1.45	0.64
68:S2:1203:G:H2'	68:S2:1204:A:C8	2.32	0.64
85:CB:561:LEU:HA	85:CB:565:HIS:HB2	1.79	0.64
52:SC:196:ILE:HB	52:SC:223:TYR:HB2	1.79	0.63
3:L5:3697:U:H5''	3:L5:3698:G:H5'	1.80	0.63
3:L5:4967:A:H2'	3:L5:4968:A:H8	1.63	0.63
3:L5:3937:C:H1'	18:LN:125:SER:HB3	1.80	0.63
11:LF:88:LYS:HE2	11:LF:197:VAL:H	1.64	0.63
3:L5:1175:A:H2	3:L5:1185:G:H1	1.46	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LB:205:VAL:HG13	7:LB:209:GLN:HE21	1.63	0.63
54:SG:167:LYS:HE2	54:SG:170:ARG:NH1	2.14	0.63
72:SK:14:LEU:HD22	72:SK:35:LEU:HD23	1.80	0.63
25:LU:28:PRO:HB2	25:LU:34:MET:HB3	1.81	0.63
85:CB:654:PRO:HD2	85:CB:658:GLY:HA3	1.81	0.63
3:L5:3615:G:H1'	27:LW:44:ARG:HD2	1.80	0.63
19:LO:126:VAL:HG13	19:LO:127:VAL:HG13	1.81	0.63
22:LR:172:ARG:HH22	68:S2:908:A:H5''	1.64	0.63
27:LW:97:LYS:HG3	27:LW:99:GLU:H	1.64	0.63
3:L5:1992:U:H4'	3:L5:1993:C:H5''	1.79	0.63
60:SO:99:ALA:H	60:SO:133:THR:HG22	1.62	0.62
68:S2:70:G:H21	68:S2:79:A:N6	1.97	0.62
3:L5:691:C:H2'	3:L5:692:A:C8	2.34	0.62
3:L5:2708:U:H3	86:CA:257:LEU:HD23	1.64	0.62
10:LE:223:ARG:HH11	10:LE:234:ASP:HB3	1.64	0.62
33:Lc:44:LYS:HB3	33:Lc:104:ILE:HD13	1.80	0.62
68:S2:1562:C:H2'	68:S2:1563:G:H8	1.64	0.62
68:S2:1598:G:H3'	79:SZ:80:ARG:HD2	1.80	0.62
84:Et:37:A:H3'	84:Et:38:A:C8	2.34	0.62
68:S2:928:G:H1	68:S2:1013:U:H3	1.47	0.62
72:SK:85:LEU:HD12	72:SK:89:ILE:HG13	1.81	0.62
52:SC:173:LYS:HD3	61:SV:3:ASN:HA	1.81	0.62
68:S2:543:C:H3'	68:S2:544:G:H8	1.63	0.62
68:S2:1277:C:H2'	68:S2:1278:A:H8	1.65	0.62
86:CA:310:GLU:HG3	86:CA:314:GLU:HB2	1.80	0.62
68:S2:692:G:H22	68:S2:738:C:H2'	1.62	0.62
85:CB:43:ALA:HB2	85:CB:351:LEU:HD21	1.81	0.62
51:SB:164:ILE:HD11	51:SB:204:ILE:HB	1.82	0.62
68:S2:1711:U:H2'	68:S2:1712:A:H8	1.65	0.62
71:SF:18:LYS:HD3	71:SF:22:LYS:HA	1.82	0.62
64:SY:10:ARG:HA	68:S2:839:C:H41	1.63	0.62
68:S2:1461:G:H3'	68:S2:1463:U:H3	1.64	0.62
34:Ld:50:ARG:HG2	34:Ld:54:MET:HE3	1.82	0.62
3:L5:4887:C:H42	3:L5:4932:U:H3	1.46	0.61
49:Lt:61:LYS:HA	49:Lt:75:PRO:HD2	1.82	0.61
7:LB:354:GLN:HB3	7:LB:359:ALA:HB1	1.80	0.61
55:SH:100:ILE:HD12	55:SH:122:LEU:HA	1.82	0.61
68:S2:1101:U:H2'	68:S2:1102:G:H8	1.65	0.61
3:L5:2554:U:O2	3:L5:2764:A:N7	2.33	0.61
7:LB:14:LEU:HD22	7:LB:17:LEU:HD11	1.82	0.61
22:LR:32:ILE:HD13	22:LR:44:LEU:HD13	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lf:15:LYS:HB3	36:Lf:25:THR:HG23	1.83	0.61
68:S2:1438:A:H2'	68:S2:1439:A:C8	2.35	0.61
80:Sc:10:LYS:HZ1	80:Sc:61:SER:HB2	1.65	0.61
85:CB:385:ILE:HG22	85:CB:418:SER:HB2	1.81	0.61
3:L5:2706:G:H22	3:L5:2709:C:H5''	1.65	0.61
63:SX:9:THR:HG22	68:S2:681:PSU:H4'	1.82	0.61
9:LD:65:ALA:HB2	9:LD:74:ILE:HD13	1.82	0.61
68:S2:1228:A:H2'	68:S2:1229:G:H8	1.66	0.61
8:LC:287:THR:HG21	47:Lr:5:LEU:HD12	1.81	0.61
9:LD:223:PHE:HB3	9:LD:226:TYR:HB2	1.83	0.61
51:SB:71:LEU:HD12	51:SB:84:PHE:HE1	1.66	0.61
68:S2:1030:A:H2'	68:S2:1031:A2M:H8	1.82	0.61
42:Ll:38:ASN:HB3	42:Ll:41:ARG:HG2	1.82	0.61
52:SC:81:ILE:HG23	52:SC:86:LEU:HB2	1.83	0.61
56:Sl:83:TYR:HB3	56:Sl:101:ILE:HD12	1.83	0.61
50:SA:137:ALA:HB1	50:SA:142:LEU:HB3	1.83	0.60
68:S2:1711:U:H2'	68:S2:1712:A:C8	2.36	0.60
88:L5:5292:SPM:H112	19:LO:91:LYS:HD3	1.83	0.60
53:SE:139:LEU:HD22	53:SE:150:PRO:HB3	1.81	0.60
58:SL:113:LEU:HD21	58:SL:120:VAL:HG11	1.84	0.60
68:S2:1228:A:H2'	68:S2:1229:G:C8	2.35	0.60
3:L5:1620:U:H5''	40:Lj:30:GLN:HE21	1.66	0.60
83:Sg:195:LEU:HA	83:Sg:211:GLY:HA3	1.83	0.60
52:SC:116:THR:HG21	52:SC:121:ARG:HE	1.65	0.60
55:SH:83:LEU:HB3	55:SH:92:VAL:HG11	1.83	0.60
3:L5:432:U:H1'	88:L5:5292:SPM:H82	1.84	0.60
3:L5:2101:C:H2'	3:L5:2102:G:H2'	1.82	0.60
57:SJ:111:GLN:HE22	57:SJ:127:ARG:HD2	1.65	0.60
85:CB:110:ASP:HB3	85:CB:553:HIS:HB2	1.84	0.60
85:CB:316:ILE:HG23	85:CB:321:ILE:HB	1.81	0.60
3:L5:1994:C:H2'	3:L5:1995:G:C8	2.36	0.60
64:SY:27:VAL:HG21	64:SY:35:VAL:HG21	1.83	0.60
3:L5:512:U:O4	3:L5:647:G:O6	2.20	0.60
45:Lo:33:LEU:HA	45:Lo:38:LYS:HG2	1.84	0.60
58:SL:16:ILE:HG23	58:SL:34:PRO:HG2	1.82	0.60
64:SY:36:PRO:HG2	64:SY:39:GLU:HB2	1.84	0.60
75:SQ:58:LEU:HD12	75:SQ:62:ARG:HD2	1.84	0.60
83:Sg:24:THR:HB	83:Sg:71:ILE:HG21	1.84	0.60
85:CB:23:SER:HB3	85:CB:122:THR:HG21	1.83	0.60
3:L5:2495:U:H2'	3:L5:2496:G:H8	1.66	0.60
20:LP:107:LEU:HD12	20:LP:152:GLU:HG3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S2:145:G:H2'	68:S2:146:G:C8	2.37	0.60
8:LC:110:ARG:HB2	18:LN:204:ARG:HH21	1.66	0.59
70:SD:59:LEU:HD23	70:SD:66:ILE:HG13	1.84	0.59
82:Sf:108:VAL:HB	82:Sf:112:GLY:HA2	1.84	0.59
58:SL:111:VAL:HG12	58:SL:140:PHE:HB2	1.84	0.59
68:S2:677:G:H21	68:S2:1028:A:H62	1.49	0.59
34:Ld:64:ILE:HG23	34:Ld:68:LEU:HD23	1.84	0.59
50:SA:205:ARG:HH22	69:SR:84:TYR:H	1.49	0.59
60:SO:101:GLY:HA3	60:SO:134:PRO:HD2	1.84	0.59
68:S2:5:U:H2'	68:S2:6:G:H8	1.66	0.59
68:S2:1775:U:H2'	68:S2:1776:G:H8	1.67	0.59
7:LB:367:PHE:HB2	27:LW:1:MET:HG3	1.85	0.59
38:Lh:80:PRO:HD2	38:Lh:83:LEU:HD12	1.85	0.59
81:Sd:6:LEU:HA	81:Sd:9:SER:HB3	1.85	0.59
83:Sg:149:GLU:HB2	83:Sg:171:ASP:HB3	1.83	0.59
28:LX:61:PRO:HG2	38:Lh:80:PRO:HG3	1.85	0.59
85:CB:345:PRO:HG2	85:CB:348:ASP:HB2	1.84	0.59
3:L5:2709:C:H5'	22:LR:43:LYS:HD2	1.85	0.59
52:SC:259:THR:HG21	61:SV:16:LYS:H	1.68	0.59
23:LS:15:ARG:HB3	23:LS:27:LEU:HD23	1.84	0.59
54:SG:56:ASN:HD21	68:S2:155:G:H21	1.50	0.59
54:SG:213:LEU:HD22	54:SG:217:MET:HG2	1.83	0.59
68:S2:115:U:H2'	68:S2:116:OMU:H6	1.85	0.59
68:S2:388:U:H2'	68:S2:389:A:H8	1.67	0.59
68:S2:925:G:H1	68:S2:1017:U:H3	1.50	0.59
3:L5:1339:U:H2'	3:L5:1340:OMC:C6	2.38	0.58
56:SI:62:VAL:HA	56:SI:77:ARG:HA	1.83	0.58
57:SJ:38:ARG:HA	67:Se:31:ARG:HB3	1.83	0.58
68:S2:149:A:H3'	68:S2:150:A:H8	1.67	0.58
68:S2:527:C:H2'	68:S2:528:A:H8	1.67	0.58
3:L5:1942:A:H2'	3:L5:1943:A:H8	1.68	0.58
69:SR:109:LEU:HG	69:SR:111:PHE:HD2	1.68	0.58
3:L5:964:A:H2'	3:L5:965:G:H4'	1.85	0.58
54:SG:135:PRO:HG2	54:SG:141:ILE:HG22	1.86	0.58
63:SX:46:HIS:CD2	63:SX:103:ALA:HB2	2.39	0.58
66:Sb:70:LYS:HD2	68:S2:1106:C:H5''	1.85	0.58
51:SB:132:GLY:HA3	51:SB:221:PRO:HB3	1.85	0.58
56:SI:155:ASN:HB2	58:SL:23:VAL:HB	1.85	0.58
71:SF:49:LEU:HD12	75:SQ:50:LYS:HG3	1.86	0.58
9:LD:182:GLY:HA2	9:LD:194:VAL:HG23	1.85	0.58
3:L5:4967:A:H2'	3:L5:4968:A:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LZ:77:TYR:HD2	33:Lc:39:ARG:HD3	1.69	0.58
68:S2:1416:C:H4'	77:ST:132:ASP:HB3	1.84	0.58
68:S2:1562:C:H2'	68:S2:1563:G:C8	2.39	0.58
68:S2:1588:A:H2'	68:S2:1589:A:C8	2.39	0.58
85:CB:461:ILE:HG21	85:CB:464:VAL:HG23	1.86	0.58
60:SO:134:PRO:HB3	68:S2:944:A:H5''	1.86	0.58
68:S2:940:U:H3	68:S2:1002:U:H3	1.51	0.58
68:S2:943:U:H2'	68:S2:944:A:H8	1.69	0.58
68:S2:1581:C:H5'	68:S2:1582:C:H5	1.69	0.58
75:SQ:68:ILE:HD12	75:SQ:88:ILE:HD12	1.85	0.57
60:SO:136:PRO:HG2	60:SO:139:SER:HB3	1.85	0.57
83:Sg:40:ILE:HD11	83:Sg:59:LEU:HD12	1.86	0.57
21:LQ:59:PRO:HG3	21:LQ:143:ARG:HA	1.85	0.57
27:LW:96:GLN:HB2	27:LW:101:ARG:HE	1.69	0.57
56:SI:91:VAL:HG11	56:SI:205:ARG:HH22	1.70	0.57
66:Sb:33:MET:HB2	66:Sb:79:PHE:HB2	1.86	0.57
68:S2:24:C:HO2'	68:S2:25:A:H8	1.51	0.57
68:S2:342:C:H2'	68:S2:343:A:C8	2.39	0.57
68:S2:1523:C:H2'	68:S2:1524:G:H8	1.69	0.57
75:SQ:19:ALA:HB2	75:SQ:75:GLY:HA3	1.86	0.57
68:S2:319:C:H2'	68:S2:320:G:H8	1.68	0.57
76:SS:31:THR:HA	76:SS:36:VAL:HG13	1.86	0.57
64:SY:104:ARG:HH12	68:S2:492:C:H5	1.52	0.57
85:CB:512:LYS:HD3	85:CB:569:PRO:HB2	1.86	0.57
9:LD:232:THR:HG22	9:LD:234:ASP:H	1.68	0.57
83:Sg:234:ASP:H	83:Sg:252:THR:HB	1.70	0.57
56:SI:125:LYS:H	56:SI:128:LYS:HZ1	1.52	0.57
58:SL:93:LEU:HB3	58:SL:102:PHE:HB3	1.86	0.57
68:S2:508:A:H3'	68:S2:509:OMG:H8	1.69	0.57
75:SQ:34:VAL:HG12	75:SQ:70:VAL:HB	1.87	0.57
8:LC:218:ILE:HA	8:LC:229:LEU:HD13	1.85	0.57
68:S2:639:C:H2'	68:S2:640:A:C8	2.34	0.57
3:L5:1778:C:H5''	9:LD:5:LYS:HG3	1.86	0.57
7:LB:224:LYS:HG2	7:LB:340:THR:HG22	1.86	0.57
22:LR:172:ARG:HD2	22:LR:176:ARG:HH12	1.68	0.57
30:LZ:92:ASP:HB3	30:LZ:95:VAL:HG12	1.86	0.57
68:S2:562:U:H2'	68:S2:563:G:C8	2.40	0.57
68:S2:1050:A:H62	68:S2:1068:G:H21	1.52	0.57
86:CA:159:PRO:HA	86:CA:218:PHE:HB2	1.86	0.57
3:L5:137:G:H2'	3:L5:138:G:C8	2.38	0.57
3:L5:3641:U:H5	3:L5:3646:A:N7	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:4162:C:H5	12:LG:73:ARG:HH12	1.50	0.57
3:L5:5054:C:H4'	3:L5:5055:G:H8	1.70	0.57
3:L5:173:C:H1'	38:Lh:112:ARG:HD2	1.87	0.56
57:SJ:87:LEU:HD12	57:SJ:100:LEU:HD11	1.86	0.56
68:S2:342:C:H2'	68:S2:343:A:H8	1.70	0.56
68:S2:543:C:H3'	68:S2:544:G:C8	2.40	0.56
68:S2:996:A:H2'	68:S2:997:A:C8	2.40	0.56
3:L5:498:C:C2	3:L5:499:G:H1'	2.40	0.56
3:L5:699:C:H2'	3:L5:700:G:H8	1.70	0.56
52:SC:81:ILE:HG21	52:SC:88:ILE:HD11	1.87	0.56
68:S2:609:U:H2'	68:S2:610:G:H8	1.69	0.56
3:L5:1500:A:H5''	3:L5:1501:C:H5''	1.87	0.56
3:L5:3748:A:H5''	6:LA:243:THR:HB	1.86	0.56
3:L5:3911:C:H2'	3:L5:3912:U:H6	1.71	0.56
7:LB:10:ARG:HH12	7:LB:265:SER:HB2	1.69	0.56
26:LV:24:ALA:HB3	26:LV:39:ILE:HD12	1.88	0.56
49:Lt:22:VAL:HA	49:Lt:48:LYS:HG2	1.87	0.56
68:S2:112:U:H3	68:S2:349:A:H61	1.54	0.56
68:S2:649:PSU:H2'	68:S2:650:A:H8	1.70	0.56
3:L5:3946:G:O6	3:L5:4067:U:O4	2.23	0.56
68:S2:1804:U:H2'	68:S2:1805:G:C8	2.41	0.56
83:Sg:256:ILE:HB	83:Sg:270:LEU:HB2	1.86	0.56
85:CB:50:ARG:HG2	85:CB:52:GLY:H	1.70	0.56
3:L5:947:C:H5''	10:LE:51:VAL:HG21	1.88	0.56
3:L5:3736:A:H2'	3:L5:3737:A:C8	2.40	0.56
3:L5:3880:G:H2'	3:L5:3881:G:C8	2.41	0.56
57:SJ:3:VAL:HB	57:SJ:5:ARG:HD3	1.87	0.56
68:S2:1422:G:H4'	68:S2:1423:C:H3'	1.88	0.56
54:SG:199:THR:HG21	68:S2:126:G:C8	2.41	0.56
68:S2:28:U:H2'	68:S2:29:G:H8	1.70	0.56
3:L5:233:U:O2'	3:L5:234:G:H2'	2.05	0.56
3:L5:1405:C:H2'	3:L5:1406:G:H8	1.70	0.56
68:S2:808:A:H2	68:S2:855:G:H22	1.53	0.56
83:Sg:227:LEU:HD23	83:Sg:228:TYR:HB2	1.87	0.56
3:L5:513:U:H3'	3:L5:514:U:H4'	1.88	0.56
10:LE:261:ILE:HG23	10:LE:267:LEU:HD23	1.87	0.56
11:LF:127:LYS:HB2	24:LT:133:ALA:HB3	1.87	0.56
74:SP:49:LEU:HD12	74:SP:53:GLN:HG2	1.88	0.56
3:L5:2400:G:H21	37:Lg:6:THR:HG22	1.71	0.56
3:L5:4260:U:H2'	3:L5:4261:C:C6	2.41	0.56
55:SH:101:LEU:HD12	55:SH:116:ARG:HG3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S2:454:U:H2'	68:S2:455:A:H8	1.71	0.56
74:SP:22:LEU:HA	74:SP:25:LEU:HB2	1.86	0.56
77:ST:98:SER:HA	77:ST:101:ARG:HE	1.71	0.56
77:ST:104:LEU:HD23	77:ST:121:ARG:HE	1.70	0.56
83:Sg:110:SER:HB2	83:Sg:154:VAL:HG12	1.87	0.56
54:SG:231:ARG:HG3	54:SG:232:ARG:HG2	1.88	0.56
68:S2:692:G:H2'	68:S2:693:A:C8	2.41	0.56
86:CA:103:GLY:H	86:CA:128:ASP:HB2	1.71	0.56
68:S2:874:G:H2'	68:S2:875:A:H8	1.70	0.55
84:Et:26:A:N6	84:Et:44:G:C2	2.73	0.55
3:L5:908:G:H2'	3:L5:909:A:H8	1.71	0.55
3:L5:4601:U:H2'	3:L5:4602:A:H8	1.70	0.55
55:SH:39:GLN:HG3	55:SH:75:ILE:HG12	1.87	0.55
3:L5:1503:A:H62	21:LQ:87:THR:HG21	1.72	0.55
3:L5:1932:A:OP1	19:LO:49:ARG:NH2	2.25	0.55
3:L5:3910:C:H2'	3:L5:3911:C:C6	2.42	0.55
10:LE:114:ARG:HH21	47:Lr:87:ARG:HH12	1.54	0.55
56:SI:31:ARG:HD2	56:SI:56:ARG:HH22	1.72	0.55
63:SX:17:ARG:HH12	68:S2:659:G:H21	1.53	0.55
3:L5:1725:U:H2'	3:L5:1726:U:H6	1.71	0.55
3:L5:4618:OMG:H5'	26:LV:15:ARG:HB2	1.88	0.55
13:LH:106:GLN:HB2	13:LH:111:LEU:HB3	1.87	0.55
68:S2:1101:U:H2'	68:S2:1102:G:C8	2.41	0.55
85:CB:604:MET:HE2	85:CB:704:VAL:HG22	1.89	0.55
3:L5:3717:A:H2'	3:L5:3718:A2M:C8	2.36	0.55
14:LI:91:LEU:HD21	14:LI:129:VAL:HB	1.89	0.55
16:LL:80:GLU:HG3	16:LL:110:LEU:HD12	1.89	0.55
48:Ls:35:VAL:HG21	48:Ls:40:MET:HE3	1.87	0.55
50:SA:41:ARG:HE	50:SA:45:GLY:HA2	1.72	0.55
57:SJ:142:VAL:HG12	57:SJ:144:ILE:H	1.72	0.55
85:CB:5:THR:HG23	85:CB:7:ASP:H	1.72	0.55
3:L5:907:C:H2'	3:L5:908:G:H8	1.71	0.55
3:L5:4965:U:H4'	3:L5:4966:A:H5'	1.89	0.55
68:S2:1337:4AC:H2'	68:S2:1338:G:H8	1.72	0.55
3:L5:71:C:H1'	16:LL:62:PRO:O	2.06	0.55
3:L5:138:G:H2'	3:L5:139:G:H8	1.71	0.55
3:L5:3952:A:H2'	3:L5:3953:G:C4	2.42	0.55
6:LA:108:PRO:HB2	46:Lp:86:LEU:HD22	1.88	0.55
49:Lt:121:LEU:HD22	49:Lt:129:ILE:HG23	1.89	0.55
77:ST:85:ASN:HB3	77:ST:88:MET:HB2	1.89	0.55
3:L5:4699:U:H1'	3:L5:4700:A:H5''	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SO:92:ALA:HA	60:SO:125:LYS:HB2	1.87	0.55
68:S2:1540:G:H5'	77:ST:47:PRO:HB3	1.89	0.55
78:SU:56:MET:HB2	78:SU:86:LYS:HB3	1.87	0.55
3:L5:257:C:H2'	3:L5:258:G:C8	2.42	0.55
3:L5:4088:C:H2'	3:L5:4089:G:C8	2.42	0.55
11:LF:223:LYS:HA	11:LF:232:ASP:HB2	1.89	0.55
15:LJ:57:VAL:HG12	15:LJ:60:PHE:H	1.72	0.55
41:Lk:26:LYS:HB2	41:Lk:69:LEU:HD12	1.89	0.55
49:Lt:12:VAL:HG11	49:Lt:65:GLN:H	1.70	0.55
68:S2:1532:C:H3'	68:S2:1637:A:H62	1.72	0.55
78:SU:19:ARG:HG3	78:SU:117:ALA:HB3	1.88	0.55
86:CA:255:TYR:HB3	86:CA:301:LEU:HD11	1.88	0.55
3:L5:1974:U:H3	3:L5:2002:A:H8	1.54	0.54
50:SA:141:ASN:HD22	52:SC:86:LEU:HD23	1.73	0.54
68:S2:172:OMU:H6	68:S2:314:U:H1'	1.88	0.54
68:S2:436:OMG:HM22	68:S2:437:G:H5'	1.88	0.54
3:L5:256:G:H2'	3:L5:257:C:C6	2.41	0.54
3:L5:1972:G:H5'	48:Ls:38:LYS:HE2	1.89	0.54
3:L5:2745:A:H2'	3:L5:2746:A:H8	1.72	0.54
68:S2:1730:U:H2'	68:S2:1731:A:C8	2.41	0.54
74:SP:37:TYR:HB3	74:SP:41:GLN:HB2	1.90	0.54
3:L5:444:G:H2'	3:L5:445:U:C6	2.43	0.54
3:L5:1197:C:H2'	3:L5:1198:G:C8	2.42	0.54
54:SG:13:GLN:NE2	68:S2:153:G:H21	2.06	0.54
68:S2:391:C:H2'	68:S2:392:A:H8	1.71	0.54
68:S2:980:A:H2'	68:S2:981:A:C8	2.42	0.54
68:S2:982:G:H2'	68:S2:983:A:H8	1.72	0.54
85:CB:120:ARG:HG3	85:CB:497:MET:HG2	1.89	0.54
3:L5:659:G:H2'	3:L5:660:A:H8	1.71	0.54
3:L5:967:C:H5'	3:L5:969:C:H5	1.72	0.54
3:L5:1933:G:H2'	3:L5:1934:A:C8	2.43	0.54
68:S2:5:U:H2'	68:S2:6:G:C8	2.42	0.54
68:S2:941:C:H2'	68:S2:942:G:C8	2.42	0.54
32:Lb:75:LEU:HD23	32:Lb:76:VAL:HG22	1.89	0.54
44:Ln:1:MET:HB2	68:S2:1706:G:H5'	1.89	0.54
68:S2:1748:G:O6	68:S2:1786:U:O4	2.24	0.54
86:CA:189:GLN:HB2	86:CA:199:LYS:HB3	1.89	0.54
1:CD:220:THR:HG23	1:CD:222:LYS:H	1.73	0.54
54:SG:232:ARG:HH12	68:S2:785:C:H5'	1.73	0.54
56:SI:69:SER:HB2	58:SL:21:LYS:HB2	1.89	0.54
58:SL:75:GLY:HA3	58:SL:88:ILE:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:Sg:129:ILE:HB	83:Sg:142:VAL:HB	1.89	0.54
3:L5:4543:G:H2'	3:L5:4544:A:C8	2.42	0.54
56:SI:124:LYS:HD3	56:SI:128:LYS:HE3	1.90	0.54
83:Sg:236:ILE:HG13	83:Sg:252:THR:HG22	1.89	0.54
3:L5:505:G:O6	3:L5:653:U:O4	2.26	0.54
3:L5:1593:A:H5''	3:L5:2839:PSU:H5'	1.90	0.54
3:L5:4537:C:H2'	3:L5:4538:G:H8	1.72	0.54
8:LC:209:ILE:HB	8:LC:229:LEU:HD23	1.88	0.54
26:LV:42:VAL:HB	26:LV:45:ILE:HG13	1.89	0.54
35:Le:7:LEU:HB2	35:Le:93:LYS:HB3	1.89	0.54
56:SI:143:LYS:HD3	56:SI:146:GLN:HB2	1.90	0.54
72:SK:16:PHE:HE1	72:SK:76:ILE:HG23	1.72	0.54
86:CA:31:VAL:HG21	86:CA:56:ILE:HD11	1.89	0.54
3:L5:1332:C:H2'	3:L5:1333:A:H8	1.73	0.54
50:SA:85:ARG:HH22	69:SR:83:ASN:HA	1.73	0.54
55:SH:10:LYS:HE2	55:SH:47:ALA:HA	1.89	0.54
68:S2:291:G:H2'	68:S2:292:A:C8	2.43	0.54
68:S2:1405:A:H2'	68:S2:1406:G:O4'	2.08	0.54
85:CB:40:VAL:HG13	85:CB:47:ALA:HB1	1.89	0.54
3:L5:4736:C:H2'	3:L5:4737:G:H8	1.73	0.54
85:CB:594:LYS:HG2	85:CB:601:ARG:HG2	1.90	0.54
85:CB:616:ASP:HA	85:CB:619:LYS:HE2	1.90	0.54
50:SA:158:ASP:HB2	50:SA:159:ILE:HD12	1.90	0.53
68:S2:1286:G:N2	68:S2:1313:A:H62	2.06	0.53
68:S2:1661:A:H8	81:Sd:14:PHE:HB2	1.73	0.53
68:S2:1671:G:H2'	68:S2:1672:U:H6	1.72	0.53
68:S2:1752:C:N4	68:S2:1755:C:H41	2.05	0.53
3:L5:3607:U:H2'	3:L5:3608:A:C8	2.43	0.53
56:SI:190:LEU:HB3	56:SI:195:LEU:HB2	1.90	0.53
86:CA:237:ALA:HB1	86:CA:308:LEU:HD12	1.89	0.53
42:Ll:12:PHE:CE2	42:Ll:51:LEU:HD22	2.44	0.53
57:SJ:162:ARG:HH21	57:SJ:169:ARG:HG2	1.72	0.53
68:S2:1536:G:H2'	68:S2:1537:A:C8	2.43	0.53
79:SZ:99:LEU:HD11	79:SZ:102:LYS:HB2	1.90	0.53
85:CB:147:ILE:HG21	85:CB:189:ILE:HG22	1.90	0.53
86:CA:59:GLU:HA	86:CA:62:LYS:HE3	1.90	0.53
3:L5:1097:C:H2'	3:L5:1098:G:C8	2.43	0.53
3:L5:2544:G:H22	5:L8:124:U:H4'	1.74	0.53
53:SE:105:THR:HG23	53:SE:245:ARG:HA	1.90	0.53
68:S2:1759:G:H2'	68:S2:1760:G:H8	1.73	0.53
3:L5:956:A:H1'	3:L5:2076:G:H5''	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:1333:A:H2'	3:L5:1334:A:C8	2.44	0.53
3:L5:4239:A:H2'	3:L5:4240:G:C8	2.44	0.53
21:LQ:78:LYS:HD2	21:LQ:137:VAL:HG23	1.91	0.53
26:LV:106:VAL:HG12	26:LV:112:MET:HA	1.90	0.53
54:SG:115:LYS:HE2	68:S2:1779:G:H5''	1.90	0.53
61:SV:59:ILE:HA	61:SV:62:MET:HG2	1.90	0.53
68:S2:589:G:H8	68:S2:591:U:H2'	1.73	0.53
3:L5:3599:A:H2'	3:L5:3600:G:C8	2.44	0.53
14:LI:54:SER:HB3	14:LI:135:ILE:HD11	1.91	0.53
85:CB:3:ASN:HA	85:CB:46:ILE:HA	1.91	0.53
3:L5:2744:A:H2'	3:L5:2745:A:C8	2.43	0.53
50:SA:209:GLU:HA	50:SA:212:LYS:HG2	1.89	0.53
54:SG:167:LYS:HE2	54:SG:170:ARG:HH11	1.71	0.53
64:SY:37:LYS:HA	64:SY:40:ILE:HG22	1.91	0.53
68:S2:835:C:H5'	68:S2:836:G:H5'	1.90	0.53
76:SS:22:GLY:HA2	76:SS:56:ALA:HB3	1.90	0.53
48:Ls:141:LEU:HD22	48:Ls:174:LEU:HD13	1.90	0.53
68:S2:414:A:H2'	68:S2:415:A:H8	1.74	0.53
3:L5:4173:G:H2'	3:L5:4174:U:H6	1.74	0.53
18:LN:159:ARG:HB3	18:LN:164:LEU:HB2	1.90	0.53
86:CA:354:LEU:HD23	86:CA:357:LEU:HD21	1.90	0.53
3:L5:5029:C:HO2'	3:L5:5030:U:H6	1.56	0.53
25:LU:63:ILE:HG13	25:LU:72:VAL:HG22	1.91	0.53
25:LU:100:LEU:HD13	25:LU:112:LEU:HD23	1.90	0.53
54:SG:227:GLN:HA	54:SG:230:LYS:HD3	1.90	0.53
60:SO:55:ARG:HH22	68:S2:972:A:H61	1.57	0.53
68:S2:317:C:H2'	68:S2:318:A:C4	2.43	0.53
3:L5:2640:G:H2'	3:L5:2641:A:C8	2.44	0.52
3:L5:4537:C:H2'	3:L5:4538:G:C8	2.44	0.52
3:L5:4992:G:H2'	3:L5:4993:G:C8	2.44	0.52
62:SW:28:ARG:HD2	68:S2:921:G:C6	2.43	0.52
68:S2:454:U:H2'	68:S2:455:A:C8	2.43	0.52
71:SF:19:LEU:HD23	71:SF:109:LEU:HD11	1.91	0.52
76:SS:114:LEU:HD23	76:SS:117:ILE:HD11	1.91	0.52
80:Sc:12:ALA:HB1	80:Sc:32:VAL:HB	1.91	0.52
3:L5:1270:A:H8	3:L5:2106:G:H21	1.56	0.52
3:L5:1695:U:H2'	3:L5:1696:C:C6	2.44	0.52
68:S2:834:C:N4	68:S2:839:C:H42	2.03	0.52
68:S2:1420:G:H21	68:S2:1421:A:H1'	1.74	0.52
3:L5:433:A:C2	3:L5:3867:A2M:H4'	2.45	0.52
68:S2:671:A:H4'	68:S2:672:A:H5''	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S2:904:A:H8	68:S2:905:C:C5	2.27	0.52
72:SK:90:VAL:HG21	72:SK:95:ARG:HB2	1.90	0.52
3:L5:5006:U:H4'	3:L5:5007:A:H5'	1.91	0.52
68:S2:610:G:H2'	68:S2:611:G:H8	1.73	0.52
68:S2:1058:A:H2'	68:S2:1059:G:C8	2.45	0.52
68:S2:1320:G:H2'	68:S2:1321:G:O4'	2.09	0.52
69:SR:106:LEU:HD13	69:SR:109:LEU:HD23	1.92	0.52
3:L5:1458:C:H5''	21:LQ:69:LYS:HD2	1.92	0.52
3:L5:2870:A:H2'	3:L5:2871:A:C8	2.45	0.52
75:SQ:40:GLU:HA	75:SQ:48:GLN:HE21	1.74	0.52
85:CB:420:LEU:HD12	85:CB:465:PRO:HB3	1.92	0.52
20:LP:122:ALA:HB3	20:LP:143:PRO:HG2	1.91	0.52
68:S2:1230:C:H2'	68:S2:1231:C:H6	1.75	0.52
73:SM:128:PHE:HA	73:SM:131:LYS:HG2	1.90	0.52
3:L5:1082:C:HO2'	3:L5:1083:U:H6	1.56	0.52
3:L5:4163:U:H5'	3:L5:4164:C:H5''	1.92	0.52
17:LM:100:ARG:HA	17:LM:103:LYS:HG2	1.91	0.52
47:Lr:90:LEU:HD22	47:Lr:111:ILE:HG23	1.92	0.52
54:SG:88:ARG:HB3	54:SG:91:GLU:HB2	1.91	0.52
65:Sa:66:LYS:HB2	65:Sa:68:TYR:CZ	2.45	0.52
84:Et:21:A:N6	84:Et:46:G:H2'	2.20	0.52
85:CB:119:LEU:HD22	85:CB:151:ILE:HG13	1.91	0.52
86:CA:247:TYR:HB3	86:CA:302:LEU:HB3	1.90	0.52
3:L5:2480:G:H2'	3:L5:2481:G:H8	1.74	0.52
7:LB:258:HIS:HA	7:LB:260:ALA:N	2.24	0.52
16:LL:64:VAL:HA	16:LL:67:HIS:CD2	2.44	0.52
29:LY:33:PRO:HG2	29:LY:105:VAL:HG12	1.91	0.52
68:S2:1650:A:H5''	75:SQ:139:ALA:HB2	1.92	0.52
78:SU:59:LYS:HB2	78:SU:84:ILE:HB	1.91	0.52
85:CB:539:GLU:HG2	85:CB:540:GLU:H	1.74	0.52
3:L5:280:G:H5''	18:LN:14:LYS:HE2	1.90	0.52
3:L5:1300:G:H2'	3:L5:1301:C:C2	2.45	0.52
3:L5:1772:C:H2'	3:L5:1773:U:H6	1.74	0.52
3:L5:2745:A:H2'	3:L5:2746:A:C8	2.45	0.52
3:L5:4069:U:H2'	3:L5:4070:U:H6	1.74	0.52
68:S2:1728:U:H2'	68:S2:1729:U:O4'	2.09	0.52
85:CB:207:PRO:HG2	85:CB:261:TRP:CE2	2.45	0.52
3:L5:93:G:H2'	3:L5:94:A:C8	2.45	0.52
51:SB:71:LEU:HD12	51:SB:84:PHE:CE1	2.45	0.52
68:S2:28:U:H2'	68:S2:29:G:C8	2.45	0.52
68:S2:367:U:H4'	68:S2:371:A:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:1994:C:H2'	3:L5:1995:G:H8	1.74	0.51
3:L5:2109:G:H2'	3:L5:2110:C:C6	2.45	0.51
3:L5:3861:A:H2'	3:L5:3862:A:C8	2.45	0.51
4:L7:63:C:H5'	4:L7:64:G:H5''	1.92	0.51
44:Ln:10:MET:HE2	68:S2:1172:U:H4'	1.92	0.51
52:SC:102:LEU:HD12	52:SC:130:ILE:HG12	1.91	0.51
68:S2:207:G:H3'	68:S2:208:G:H8	1.75	0.51
75:SQ:38:PRO:HG2	75:SQ:41:MET:HG2	1.92	0.51
7:LB:297:LYS:HG3	7:LB:299:ILE:HG23	1.92	0.51
7:LB:393:LYS:HG3	7:LB:396:ARG:HH21	1.75	0.51
23:LS:161:ARG:HE	23:LS:164:LYS:HB2	1.76	0.51
68:S2:1424:G:H2'	68:S2:1425:G:H8	1.75	0.51
85:CB:762:VAL:HA	85:CB:765:ARG:HH21	1.75	0.51
41:Lk:24:LYS:HG2	41:Lk:67:LYS:HB3	1.92	0.51
48:Ls:144:THR:HG22	85:CB:179:GLN:HG2	1.93	0.51
49:Lt:10:ILE:HD13	49:Lt:65:GLN:HG2	1.92	0.51
50:SA:52:LYS:HB2	69:SR:109:LEU:HD13	1.92	0.51
54:SG:137:ARG:HG3	54:SG:178:ARG:HD3	1.93	0.51
55:SH:95:ILE:HD11	55:SH:133:LEU:HB2	1.91	0.51
68:S2:349:A:H2'	68:S2:350:C:C6	2.45	0.51
71:SF:100:ILE:HG22	71:SF:178:ILE:HD11	1.92	0.51
3:L5:3867:A2M:H8	3:L5:3867:A2M:H5''	1.92	0.51
7:LB:136:LYS:HB2	7:LB:142:GLY:HA3	1.92	0.51
10:LE:178:PRO:HD2	10:LE:181:LEU:HD12	1.92	0.51
14:LI:61:SER:HA	14:LI:126:VAL:HG12	1.93	0.51
53:SE:126:VAL:HG22	53:SE:158:ASP:H	1.75	0.51
68:S2:399:C:H5	68:S2:680:G:H5''	1.76	0.51
3:L5:253:G:H2'	3:L5:254:G:C8	2.46	0.51
3:L5:3720:G:H22	3:L5:3733:A:H2	1.58	0.51
3:L5:3946:G:H1	3:L5:4067:U:H3	0.72	0.51
27:LW:91:MET:HA	27:LW:94:ARG:HG2	1.92	0.51
54:SG:147:LEU:HD22	54:SG:151:ASP:HB2	1.93	0.51
68:S2:508:A:H3'	68:S2:509:OMG:C8	2.45	0.51
68:S2:656:G:H5'	68:S2:662:G:N2	2.26	0.51
68:S2:1421:A:H3'	68:S2:1422:G:H8	1.72	0.51
53:SE:137:PRO:HG2	53:SE:150:PRO:HD2	1.92	0.51
54:SG:135:PRO:HG3	54:SG:144:LEU:HD13	1.91	0.51
68:S2:1288:OMU:HM21	68:S2:1315:U:H1'	1.93	0.51
82:Sf:94:LYS:HG3	82:Sf:96:LYS:HE3	1.91	0.51
3:L5:1207:C:H2'	3:L5:1208:G:H8	1.75	0.51
13:LH:102:ASN:HB2	13:LH:115:ARG:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SO:128:ARG:HD3	65:Sa:59:PHE:CZ	2.46	0.51
68:S2:525:A:H2'	68:S2:526:A:H8	1.75	0.51
68:S2:1010:G:H2'	68:S2:1011:A:C8	2.43	0.51
68:S2:1093:A:H2'	68:S2:1094:C:C6	2.45	0.51
68:S2:1562:C:H5''	77:ST:71:GLY:HA3	1.93	0.51
68:S2:1775:U:H2'	68:S2:1776:G:C8	2.46	0.51
68:S2:1844:U:H2'	68:S2:1845:A:C8	2.45	0.51
85:CB:646:ALA:HA	85:CB:649:ILE:HG12	1.93	0.51
3:L5:702:U:H2'	3:L5:703:G:O4'	2.11	0.51
5:L8:8:U:H2'	5:L8:9:A:C8	2.46	0.51
29:LY:56:GLN:HB3	29:LY:67:ILE:HD13	1.93	0.51
33:Lc:45:LEU:HD23	33:Lc:96:ILE:HD12	1.91	0.51
54:SG:154:ARG:HD2	68:S2:77:A:C5	2.46	0.51
67:Se:28:LYS:HE2	67:Se:32:ALA:HB1	1.93	0.51
68:S2:388:U:H2'	68:S2:389:A:C8	2.45	0.51
68:S2:882:U:H1'	68:S2:905:C:C2	2.45	0.51
68:S2:1568:C:H2'	68:S2:1569:A:C8	2.46	0.51
68:S2:1792:G:H2'	68:S2:1793:A:H8	1.75	0.51
70:SD:137:VAL:HG22	70:SD:151:LYS:HG3	1.92	0.51
3:L5:1333:A:H2'	3:L5:1334:A:H8	1.76	0.51
3:L5:2091:C:H1'	3:L5:2094:G:H8	1.76	0.51
11:LF:199:LYS:HG3	11:LF:200:ARG:HG2	1.92	0.51
62:SW:28:ARG:HD2	68:S2:921:G:C5	2.46	0.51
68:S2:375:U:H2'	68:S2:376:A:C8	2.46	0.51
68:S2:549:C:H2'	68:S2:550:C:C6	2.45	0.51
3:L5:701:G:H2'	3:L5:702:U:C6	2.46	0.51
3:L5:1804:A:H61	3:L5:1833:G:H5''	1.74	0.51
3:L5:4991:U:H2'	3:L5:4992:G:C8	2.46	0.51
6:LA:137:ILE:HD11	6:LA:149:LYS:HB2	1.93	0.51
51:SB:103:MET:HB3	51:SB:215:VAL:HG22	1.93	0.51
64:SY:10:ARG:HA	68:S2:839:C:N4	2.26	0.51
68:S2:1801:A:H2'	68:S2:1802:C:C6	2.46	0.51
70:SD:48:ILE:HB	70:SD:86:LEU:HD12	1.93	0.51
70:SD:163:PRO:HA	70:SD:166:TYR:CZ	2.46	0.51
80:Sc:11:LEU:HD23	80:Sc:57:THR:HA	1.93	0.51
86:CA:187:SER:HB2	86:CA:201:ILE:HB	1.93	0.51
3:L5:4459:U:H2'	3:L5:4460:U:C6	2.45	0.50
49:Lt:10:ILE:HG21	49:Lt:65:GLN:HB3	1.92	0.50
68:S2:955:A:N3	68:S2:956:G:H1'	2.26	0.50
83:Sg:106:LYS:HE3	83:Sg:125:ARG:HB3	1.93	0.50
3:L5:1251:C:H2'	3:L5:1252:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:2611:A:H2'	3:L5:2612:G:C8	2.47	0.50
6:LA:114:CYS:HB3	6:LA:165:VAL:HB	1.92	0.50
53:SE:19:MET:HB2	53:SE:51:ARG:HH22	1.77	0.50
54:SG:31:ARG:HH22	68:S2:1745:A:H4'	1.76	0.50
54:SG:159:ARG:HG3	54:SG:173:ALA:HB2	1.93	0.50
68:S2:1101:U:H3	68:S2:1131:G:H1	1.58	0.50
68:S2:1144:A:H2'	68:S2:1145:A:C8	2.46	0.50
68:S2:1801:A:H2'	68:S2:1802:C:H6	1.75	0.50
82:Sf:116:ARG:HG2	82:Sf:131:PHE:HE2	1.76	0.50
83:Sg:256:ILE:HG13	83:Sg:310:TRP:HZ3	1.75	0.50
3:L5:1629:G:H1	6:LA:208:GLU:HG2	1.77	0.50
5:L8:67:U:H2'	5:L8:68:G:H8	1.77	0.50
78:SU:66:ARG:HG2	78:SU:68:THR:HG22	1.92	0.50
83:Sg:250:ALA:HB3	83:Sg:257:LYS:HB2	1.93	0.50
86:CA:208:GLN:HA	86:CA:211:LYS:HE3	1.92	0.50
3:L5:4594:U:H2'	3:L5:4595:G:C8	2.43	0.50
8:LC:330:PRO:HB3	11:LF:47:ARG:HH21	1.76	0.50
51:SB:111:CYS:HB3	65:Sa:68:TYR:HB2	1.93	0.50
68:S2:496:C:H2'	68:S2:497:C:C6	2.46	0.50
68:S2:527:C:H2'	68:S2:528:A:C8	2.45	0.50
68:S2:1365:G:H2'	68:S2:1366:G:H8	1.76	0.50
68:S2:1513:C:H2'	68:S2:1514:G:H8	1.76	0.50
75:SQ:58:LEU:HD11	75:SQ:92:LEU:HD21	1.93	0.50
75:SQ:97:GLN:HG3	75:SQ:105:LYS:HE2	1.93	0.50
50:SA:205:ARG:HH22	69:SR:84:TYR:N	2.10	0.50
51:SB:35:ALA:HB2	51:SB:44:ILE:HD11	1.93	0.50
53:SE:26:VAL:HG22	57:SJ:4:ALA:HB2	1.93	0.50
61:SV:1:MET:HB3	61:SV:10:ASP:HB3	1.92	0.50
66:Sb:54:VAL:HG23	66:Sb:63:LEU:HB2	1.94	0.50
68:S2:550:C:H2'	68:S2:551:U:C6	2.46	0.50
68:S2:1217:A:H2'	68:S2:1218:C:C6	2.47	0.50
78:SU:26:SER:HB2	78:SU:110:VAL:HG23	1.94	0.50
3:L5:1172:C:HO2'	3:L5:1173:G:H8	1.60	0.50
3:L5:2090:U:H4'	3:L5:2091:C:H3'	1.94	0.50
3:L5:3848:U:H2'	3:L5:3849:A:C8	2.47	0.50
64:SY:104:ARG:HA	64:SY:107:ARG:HE	1.76	0.50
68:S2:13:C:H4'	68:S2:1355:C:H5	1.75	0.50
70:SD:66:ILE:HG23	70:SD:86:LEU:HD23	1.94	0.50
81:Sd:22:ARG:HH21	81:Sd:37:ASN:HB2	1.77	0.50
85:CB:316:ILE:HA	85:CB:321:ILE:HD12	1.92	0.50
3:L5:261:G:H2'	3:L5:262:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:3861:A:H2'	3:L5:3862:A:H8	1.76	0.50
3:L5:4274:A:H2'	3:L5:4275:G:C8	2.46	0.50
19:LO:61:ARG:HA	19:LO:70:PRO:HD2	1.92	0.50
50:SA:10:MET:HE3	50:SA:55:TRP:HB2	1.94	0.50
51:SB:106:THR:HG23	51:SB:109:LYS:H	1.76	0.50
56:SI:98:LYS:HB3	68:S2:377:G:H5'	1.93	0.50
63:SX:17:ARG:HH12	68:S2:659:G:N2	2.10	0.50
63:SX:97:ASN:HB3	85:CB:521:VAL:HG21	1.94	0.50
86:CA:107:LYS:HD2	86:CA:318:GLN:OE1	2.11	0.50
3:L5:1812:C:H1'	32:Lb:57:MET:HE2	1.93	0.50
3:L5:3760:A:H4'	3:L5:3761:C:H5''	1.92	0.50
3:L5:4069:U:H2'	3:L5:4070:U:C6	2.47	0.50
3:L5:4697:U:H4'	43:Lm:104:HIS:CE1	2.46	0.50
48:Ls:59:THR:HG22	48:Ls:62:ARG:HH22	1.76	0.50
53:SE:18:TRP:HB3	53:SE:20:LEU:HD13	1.94	0.50
68:S2:1059:G:N2	68:S2:1829:G:H4'	2.25	0.50
75:SQ:131:LYS:HB2	75:SQ:140:ARG:HH22	1.76	0.50
83:Sg:11:LEU:HB2	83:Sg:307:VAL:HB	1.94	0.50
85:CB:656:GLY:HA2	85:CB:684:GLN:HE22	1.77	0.50
3:L5:268:G:H2'	3:L5:269:G:H8	1.77	0.50
3:L5:1178:G:H2'	9:LD:286:SER:HB3	1.93	0.50
3:L5:1932:A:P	19:LO:49:ARG:HH12	2.35	0.50
10:LE:136:HIS:HB2	10:LE:138:ARG:HH12	1.75	0.50
29:LY:10:ASP:HB3	29:LY:13:LYS:HB2	1.94	0.50
53:SE:44:LEU:HD21	53:SE:70:ILE:HD11	1.93	0.50
54:SG:32:MET:HA	54:SG:52:ILE:HB	1.94	0.50
68:S2:15:U:H2'	68:S2:16:G:O4'	2.11	0.50
68:S2:223:C:H2'	68:S2:224:A:C8	2.46	0.50
83:Sg:230:LEU:HD22	83:Sg:259:TRP:CE2	2.46	0.50
85:CB:604:MET:HG2	85:CB:704:VAL:HA	1.92	0.50
35:Le:126:ASN:HA	35:Le:129:LEU:HD21	1.93	0.49
52:SC:253:PRO:HA	52:SC:256:TRP:CE2	2.47	0.49
55:SH:82:GLU:HA	55:SH:85:LYS:HZ3	1.77	0.49
84:Et:11:C:H2'	84:Et:12:U:H6	1.77	0.49
3:L5:3770:U:H2'	3:L5:3771:C:C6	2.47	0.49
56:SI:56:ARG:HA	56:SI:180:GLY:HA2	1.94	0.49
68:S2:1093:A:H2'	68:S2:1094:C:H6	1.77	0.49
72:SK:15:LEU:HD22	72:SK:49:MET:HE2	1.93	0.49
74:SP:91:GLY:H	74:SP:107:ILE:HB	1.76	0.49
84:Et:11:C:H2'	84:Et:12:U:C6	2.48	0.49
3:L5:162:A:H2'	3:L5:163:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:1503:A:H4'	3:L5:1504:G:H5'	1.94	0.49
3:L5:2654:C:H2'	3:L5:2655:C:H6	1.77	0.49
3:L5:2676:A:OP2	3:L5:2676:A:H8	1.96	0.49
5:L8:144:U:H2'	5:L8:145:C:C6	2.47	0.49
68:S2:12:U:H2'	68:S2:13:C:C6	2.47	0.49
68:S2:928:G:H2'	68:S2:929:G:C8	2.47	0.49
68:S2:1205:C:H2'	68:S2:1206:G:H8	1.77	0.49
68:S2:1284:A:C4	73:SM:91:LEU:HD21	2.47	0.49
70:SD:204:LEU:HB2	70:SD:207:HIS:HB2	1.94	0.49
84:Et:28:C:H2'	84:Et:29:A:H8	1.77	0.49
86:CA:18:VAL:HG12	86:CA:22:LYS:HE2	1.93	0.49
3:L5:1176:C:H42	3:L5:1184:A:H61	1.60	0.49
3:L5:2732:G:H2'	3:L5:2733:C:H6	1.78	0.49
3:L5:3684:G:H2'	3:L5:3685:C:C6	2.47	0.49
3:L5:3758:U:H2'	3:L5:3765:G:N2	2.26	0.49
3:L5:4238:G:H2'	3:L5:4239:A:C8	2.47	0.49
7:LB:258:HIS:HA	7:LB:260:ALA:H	1.76	0.49
13:LH:26:ILE:HG13	13:LH:35:ARG:HG3	1.94	0.49
19:LO:18:ARG:CZ	19:LO:128:ARG:HH21	2.25	0.49
19:LO:76:PRO:HB3	19:LO:138:LEU:HG	1.93	0.49
25:LU:80:LYS:HZ1	25:LU:109:SER:H	1.59	0.49
68:S2:483:C:H2'	68:S2:484:A2M:H8	1.94	0.49
68:S2:943:U:H2'	68:S2:944:A:C8	2.47	0.49
83:Sg:206:LEU:HD11	83:Sg:218:LEU:HD23	1.92	0.49
85:CB:641:TRP:HZ3	85:CB:649:ILE:HD11	1.77	0.49
3:L5:2095:A:H1'	3:L5:2096:G:N2	2.27	0.49
3:L5:4260:U:H2'	3:L5:4261:C:H6	1.77	0.49
7:LB:133:TYR:O	7:LB:136:LYS:HG2	2.13	0.49
8:LC:163:LYS:HB2	8:LC:166:GLU:HG2	1.94	0.49
32:Lb:109:ARG:HA	32:Lb:112:ILE:HG12	1.94	0.49
35:Le:89:LEU:HD13	35:Le:118:LEU:HD22	1.93	0.49
53:SE:112:HIS:HB2	53:SE:239:PRO:HB3	1.93	0.49
56:SI:129:LEU:O	56:SI:133:GLU:HG2	2.13	0.49
63:SX:17:ARG:HH22	68:S2:659:G:H21	1.59	0.49
68:S2:13:C:H4'	68:S2:1355:C:C5	2.47	0.49
68:S2:155:G:H2'	68:S2:156:G:C8	2.41	0.49
68:S2:344:U:H2'	68:S2:345:U:H6	1.77	0.49
68:S2:955:A:H62	68:S2:971:G:H21	1.60	0.49
83:Sg:149:GLU:O	83:Sg:170:TRP:HB2	2.12	0.49
85:CB:147:ILE:HD11	85:CB:192:TYR:HB2	1.95	0.49
3:L5:173:C:H5''	16:LL:129:ARG:NH1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LB:292:LEU:HB2	7:LB:298:LEU:HB2	1.95	0.49
51:SB:114:VAL:HG11	68:S2:987:A:H2'	1.95	0.49
68:S2:106:C:H2'	68:S2:107:A:C8	2.46	0.49
68:S2:1289:U:C5	82:Sf:97:LYS:HE2	2.48	0.49
71:SF:61:PHE:HB3	80:Sc:51:ARG:HH21	1.78	0.49
79:SZ:102:LYS:HA	79:SZ:107:VAL:HG12	1.94	0.49
3:L5:4173:G:H2'	3:L5:4174:U:C6	2.48	0.49
15:LJ:146:ARG:HG2	15:LJ:147:ARG:HG3	1.93	0.49
25:LU:111:GLU:CD	25:LU:113:ARG:HE	2.20	0.49
27:LW:52:THR:O	27:LW:56:ARG:HG2	2.12	0.49
45:Lo:75:PRO:HA	45:Lo:78:ARG:HE	1.77	0.49
51:SB:145:LYS:HB2	51:SB:149:GLN:HG2	1.93	0.49
55:SH:10:LYS:HE3	55:SH:20:GLU:HG2	1.95	0.49
68:S2:877:C:H2'	68:S2:878:G:C8	2.48	0.49
68:S2:931:C:H2'	68:S2:932:G:C8	2.48	0.49
68:S2:1496:U:H4'	81:Sd:24:CYS:HB2	1.93	0.49
85:CB:107:GLY:O	85:CB:138:GLN:HG2	2.12	0.49
3:L5:989:U:H1'	3:L5:1065:G:N2	2.28	0.49
3:L5:4457:PSU:H1'	7:LB:252:ALA:HB3	1.95	0.49
48:Ls:29:ILE:HG13	48:Ls:190:GLN:HB2	1.95	0.49
53:SE:175:PHE:HE1	53:SE:225:ILE:HG21	1.76	0.49
68:S2:979:C:H2'	68:S2:980:A:C8	2.48	0.49
78:SU:67:LYS:HG2	78:SU:78:ASP:HB2	1.94	0.49
3:L5:172:C:H4'	3:L5:173:C:H5'	1.95	0.49
3:L5:179:G:H2'	3:L5:180:C:C6	2.48	0.49
3:L5:737:C:C4	3:L5:739:G:H5''	2.48	0.49
3:L5:1806:G:H2'	3:L5:1807:C:H6	1.78	0.49
68:S2:1407:U:H2'	68:S2:1408:U:C6	2.48	0.49
71:SF:39:ILE:HG23	71:SF:68:ILE:HG21	1.94	0.49
75:SQ:45:ARG:HA	75:SQ:48:GLN:HB2	1.93	0.49
3:L5:3736:A:H2'	3:L5:3737:A:H8	1.78	0.49
3:L5:3785:A2M:H2	3:L5:4551:U:O2	2.12	0.49
8:LC:27:VAL:HG11	8:LC:260:LEU:HD22	1.95	0.49
52:SC:235:ASN:HD21	68:S2:1355:C:H6	1.61	0.49
68:S2:1716:C:H2'	68:S2:1717:C:H6	1.78	0.49
68:S2:1829:G:H1'	68:S2:1850:MA6:H2	1.95	0.49
76:SS:59:LEU:HD23	76:SS:64:VAL:HG22	1.94	0.49
78:SU:49:LYS:HG3	78:SU:92:HIS:HB2	1.95	0.49
3:L5:454:U:H2'	3:L5:455:C:O4'	2.13	0.48
3:L5:1100:U:C2	3:L5:1195:G:N1	2.81	0.48
3:L5:1700:G:H5'	3:L5:1702:C:OP2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:1831:G:H2'	3:L5:1832:C:O4'	2.13	0.48
3:L5:2481:G:H2'	3:L5:2482:C:C6	2.48	0.48
3:L5:2870:A:H2'	3:L5:2871:A:H8	1.78	0.48
3:L5:4067:U:H2'	3:L5:4068:U:C6	2.48	0.48
29:LY:67:ILE:HD12	29:LY:107:THR:HG21	1.95	0.48
30:LZ:41:ALA:HB2	30:LZ:77:TYR:HE1	1.78	0.48
68:S2:1518:C:H5''	68:S2:1519:U:H5''	1.95	0.48
68:S2:1705:C:H2'	68:S2:1706:G:C8	2.48	0.48
83:Sg:129:ILE:HD11	83:Sg:151:VAL:HG11	1.94	0.48
15:LJ:24:ILE:HG12	15:LJ:128:LEU:HB3	1.95	0.48
26:LV:45:ILE:HG21	26:LV:53:PRO:HB3	1.94	0.48
27:LW:81:ALA:HB2	27:LW:87:LEU:HD13	1.93	0.48
33:Lc:38:ILE:HG21	33:Lc:63:TYR:HB3	1.94	0.48
53:SE:125:LYS:HA	53:SE:159:THR:HA	1.95	0.48
55:SH:31:GLU:CD	55:SH:37:LYS:HE2	2.38	0.48
61:SV:15:ARG:HH21	61:SV:24:ILE:HG21	1.78	0.48
68:S2:975:G:H2'	68:S2:976:G:H8	1.76	0.48
85:CB:521:VAL:O	85:CB:525:LYS:HG2	2.12	0.48
3:L5:138:G:H2'	3:L5:139:G:C8	2.48	0.48
3:L5:4591:U:H2'	3:L5:4592:C:C6	2.48	0.48
3:L5:4991:U:H2'	3:L5:4992:G:H8	1.78	0.48
7:LB:117:ARG:HA	7:LB:177:LYS:HD2	1.96	0.48
49:Lt:114:ARG:CZ	49:Lt:133:LEU:HD12	2.43	0.48
64:SY:50:THR:HG21	64:SY:75:ILE:HD11	1.95	0.48
68:S2:1628:C:H2'	68:S2:1629:C:C6	2.48	0.48
3:L5:158:A:H5''	3:L5:159:C:H2'	1.94	0.48
3:L5:711:A:H2'	3:L5:712:C:C6	2.49	0.48
3:L5:1563:A:H2'	3:L5:1564:A:C8	2.48	0.48
3:L5:1577:G:O2'	3:L5:1612:G:H4'	2.13	0.48
9:LD:56:THR:HG22	9:LD:57:ASN:H	1.78	0.48
53:SE:45:ILE:HB	53:SE:80:ILE:HG22	1.95	0.48
68:S2:1468:C:H2'	68:S2:1469:A:H8	1.77	0.48
68:S2:1845:A:H2'	68:S2:1846:G:H8	1.78	0.48
73:SM:42:LEU:HD12	73:SM:74:ILE:HG13	1.95	0.48
78:SU:23:THR:HB	78:SU:113:GLU:HG2	1.95	0.48
5:L8:45:C:H4'	42:L1:11:ARG:HE	1.78	0.48
18:LN:116:LEU:HD22	18:LN:135:ILE:HD11	1.95	0.48
33:Lc:48:LEU:HD23	33:Lc:57:LYS:HG2	1.96	0.48
49:Lt:12:VAL:HG11	49:Lt:65:GLN:N	2.28	0.48
68:S2:382:C:H2'	68:S2:383:G:C8	2.48	0.48
68:S2:1401:A:H2'	68:S2:1402:A:C8	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S2:1438:A:H2'	68:S2:1439:A:H8	1.77	0.48
83:Sg:240:CYS:H	83:Sg:249:CYS:HB2	1.78	0.48
1:CD:220:THR:H	1:CD:223:ASP:HB2	1.78	0.48
3:L5:135:G:H5''	38:Lh:97:LYS:H	1.79	0.48
3:L5:1995:G:H2'	3:L5:1996:C:C6	2.48	0.48
18:LN:140:LYS:HD3	18:LN:140:LYS:HA	1.62	0.48
50:SA:10:MET:HE1	50:SA:51:LEU:HG	1.95	0.48
68:S2:1845:A:H2'	68:S2:1846:G:C8	2.49	0.48
86:CA:351:ASP:HB3	86:CA:354:LEU:HB2	1.96	0.48
3:L5:1308:C:H2'	3:L5:1309:C:C6	2.49	0.48
7:LB:217:ILE:HD12	7:LB:347:LEU:HB3	1.96	0.48
13:LH:18:ILE:HG12	13:LH:27:VAL:HG22	1.96	0.48
13:LH:89:ARG:HG3	13:LH:145:ILE:HG23	1.96	0.48
50:SA:8:LEU:HD12	50:SA:191:ARG:HH12	1.78	0.48
53:SE:19:MET:HE3	53:SE:108:ARG:HD3	1.96	0.48
60:SO:34:PHE:HB3	60:SO:41:PHE:HB2	1.95	0.48
64:SY:105:LYS:O	64:SY:109:GLU:HG2	2.14	0.48
68:S2:525:A:H2'	68:S2:526:A:C8	2.49	0.48
68:S2:1324:G:H1	68:S2:1504:U:H3	1.62	0.48
1:CD:183:ASP:HB2	85:CB:599:HIS:NE2	2.29	0.48
3:L5:690:C:H2'	3:L5:691:C:H6	1.79	0.48
3:L5:1617:G:H1'	3:L5:2513:A:N6	2.28	0.48
3:L5:3873:G:H2'	3:L5:3874:G:C8	2.49	0.48
3:L5:4392:OMG:HM21	3:L5:4394:A:H2'	1.96	0.48
3:L5:4612:C:C2	13:LH:120:GLU:HB2	2.48	0.48
3:L5:4739:C:H2'	3:L5:4740:G:H5'	1.95	0.48
3:L5:4942:C:H4'	10:LE:154:THR:HG22	1.96	0.48
6:LA:114:CYS:SG	6:LA:169:VAL:HG22	2.54	0.48
17:LM:65:PRO:HG2	17:LM:68:ALA:HB2	1.96	0.48
52:SC:118:ALA:HB2	68:S2:1486:A:H4'	1.96	0.48
54:SG:227:GLN:O	54:SG:230:LYS:HG2	2.14	0.48
56:SI:57:ALA:HB2	56:SI:183:GLY:HA2	1.96	0.48
57:SJ:113:GLN:HG2	57:SJ:149:VAL:HG21	1.95	0.48
85:CB:41:CYS:HA	85:CB:49:ALA:HA	1.96	0.48
3:L5:398:A2M:O5'	3:L5:398:A2M:H8	2.14	0.48
3:L5:1812:C:H5''	32:Lb:56:LYS:HE3	1.95	0.48
22:LR:66:ASN:HB3	22:LR:70:ARG:HH12	1.78	0.48
61:SV:14:PRO:HG2	61:SV:23:ILE:HD12	1.95	0.48
68:S2:1098:C:H2'	68:S2:1099:G:C8	2.48	0.48
69:SR:83:ASN:HB3	69:SR:85:VAL:HG13	1.94	0.48
3:L5:19:G:H2'	3:L5:20:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:411:G:H4'	3:L5:412:G:H5''	1.95	0.48
3:L5:1857:C:H2'	3:L5:1858:A:H8	1.79	0.48
3:L5:4913:G:H4'	3:L5:4914:C:O5'	2.13	0.48
14:LI:99:ILE:HG22	14:LI:123:GLN:HB2	1.96	0.48
48:Ls:120:GLU:HG2	48:Ls:162:LYS:HA	1.96	0.48
51:SB:150:ILE:HD13	69:SR:129:LYS:HB2	1.95	0.48
54:SG:177:GLN:HG3	54:SG:178:ARG:H	1.78	0.48
56:SI:113:TYR:CZ	56:SI:158:ILE:HD11	2.49	0.48
68:S2:198:U:H1'	68:S2:203:G:H22	1.78	0.48
68:S2:929:G:H2'	68:S2:930:C:O4'	2.14	0.48
68:S2:1359:U:H2'	68:S2:1360:U:H6	1.79	0.48
68:S2:1369:A:H2'	68:S2:1370:A:C8	2.48	0.48
70:SD:158:ILE:HG23	70:SD:189:MET:HE1	1.95	0.48
85:CB:88:PHE:HE1	85:CB:250:ALA:HA	1.79	0.48
85:CB:649:ILE:HD13	85:CB:663:THR:HB	1.96	0.48
3:L5:261:G:H2'	3:L5:262:G:H8	1.78	0.47
3:L5:4371:G:H5'	84:Et:76:A:H62	1.79	0.47
9:LD:181:PRO:HD2	9:LD:195:HIS:CD2	2.49	0.47
23:LS:96:GLU:HG3	23:LS:139:ARG:HG2	1.96	0.47
68:S2:414:A:H2'	68:S2:415:A:C8	2.50	0.47
68:S2:1004:PSU:H2'	68:S2:1005:G:H8	1.78	0.47
68:S2:1523:C:H2'	68:S2:1524:G:C8	2.49	0.47
75:SQ:72:VAL:HG21	75:SQ:84:ILE:HD11	1.96	0.47
83:Sg:37:ASP:HB3	83:Sg:39:THR:HG22	1.95	0.47
3:L5:325:U:H2'	3:L5:326:C:C6	2.50	0.47
3:L5:1207:C:H2'	3:L5:1208:G:C8	2.49	0.47
3:L5:1431:C:H2'	3:L5:1432:G:O4'	2.14	0.47
3:L5:4291:G:H4'	3:L5:4292:A:H5''	1.95	0.47
3:L5:4401:G:H2'	3:L5:4402:C:H6	1.78	0.47
3:L5:4910:G:H22	19:LO:107:GLY:HA3	1.78	0.47
10:LE:91:THR:HG22	10:LE:108:LYS:HA	1.96	0.47
14:LI:87:MET:HG2	14:LI:138:ILE:HG12	1.95	0.47
51:SB:142:PHE:HD1	51:SB:209:ASP:HB3	1.79	0.47
64:SY:103:SER:H	64:SY:106:GLN:HE22	1.63	0.47
68:S2:859:G:O6	68:S2:860:G:O6	2.31	0.47
68:S2:1310:U:H2'	68:S2:1311:C:C6	2.49	0.47
68:S2:1359:U:H2'	68:S2:1360:U:C6	2.49	0.47
77:ST:143:LYS:HE2	77:ST:144:LYS:HG2	1.97	0.47
3:L5:490:C:H2'	3:L5:491:G:C8	2.50	0.47
3:L5:2664:G:H4'	3:L5:2677:G:H4'	1.96	0.47
3:L5:2890:C:H2'	3:L5:2891:U:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LJ:39:VAL:HG21	15:LJ:126:TYR:HD2	1.79	0.47
23:LS:140:PRO:HA	23:LS:143:LYS:HB2	1.96	0.47
51:SB:71:LEU:HB2	51:SB:82:ARG:HB3	1.95	0.47
54:SG:234:LEU:HD11	54:SG:237:LEU:HB3	1.96	0.47
60:SO:138:ASP:OD2	68:S2:984:C:O2'	2.32	0.47
64:SY:22:GLN:HB2	64:SY:72:PHE:CZ	2.49	0.47
68:S2:677:G:N2	68:S2:1028:A:H62	2.13	0.47
68:S2:750:C:H42	68:S2:793:G:H1'	1.79	0.47
68:S2:804:U:H2'	68:S2:805:U:C6	2.49	0.47
68:S2:1619:A:OP1	74:SP:47:ARG:HD3	2.14	0.47
85:CB:665:ILE:HD11	85:CB:705:HIS:CD2	2.49	0.47
86:CA:242:GLN:HB3	86:CA:307:VAL:HG11	1.97	0.47
7:LB:29:VAL:HG12	7:LB:31:SER:H	1.79	0.47
60:SO:136:PRO:HB3	68:S2:944:A:H1'	1.96	0.47
64:SY:114:MET:HE1	64:SY:127:ALA:HB3	1.96	0.47
65:Sa:5:ARG:HH21	68:S2:1864:U:H3'	1.79	0.47
68:S2:1514:G:H2'	68:S2:1515:G:H8	1.78	0.47
68:S2:1531:A:H2'	68:S2:1532:C:C6	2.49	0.47
68:S2:1780:G:H2'	68:S2:1781:A:O4'	2.14	0.47
71:SF:135:ARG:HH12	71:SF:203:ASN:HB2	1.80	0.47
86:CA:81:SER:OG	86:CA:107:LYS:HE2	2.15	0.47
3:L5:1509:C:H5''	31:La:2:PRO:HD3	1.96	0.47
3:L5:2610:G:H2'	3:L5:2611:A:C8	2.49	0.47
23:LS:76:LYS:HB2	23:LS:131:GLU:OE1	2.14	0.47
52:SC:210:PRO:HD3	52:SC:236:PHE:CE2	2.50	0.47
53:SE:192:ILE:HG23	53:SE:228:ILE:HD11	1.97	0.47
65:Sa:51:ARG:HB3	80:Sc:63:ARG:HH22	1.79	0.47
68:S2:1757:G:H3'	68:S2:1758:G:H4'	1.96	0.47
82:Sf:121:CYS:HB3	82:Sf:141:CYS:HB2	1.45	0.47
85:CB:654:PRO:HD3	85:CB:660:ASN:HD22	1.80	0.47
3:L5:2480:G:H2'	3:L5:2481:G:C8	2.49	0.47
3:L5:4088:C:H2'	3:L5:4089:G:H8	1.80	0.47
10:LE:165:LEU:HD11	10:LE:176:THR:HB	1.96	0.47
12:LG:158:ALA:HB2	12:LG:190:LEU:HD12	1.97	0.47
37:Lg:61:PRO:HA	37:Lg:64:LEU:HD12	1.96	0.47
55:SH:5:SER:HB3	55:SH:21:SER:HB2	1.96	0.47
68:S2:1688:C:H2'	68:S2:1689:C:H6	1.79	0.47
72:SK:64:TRP:HB3	81:Sd:23:VAL:HA	1.96	0.47
85:CB:653:GLY:HA2	85:CB:660:ASN:HB2	1.97	0.47
3:L5:300:A:H2'	3:L5:301:G:H8	1.79	0.47
3:L5:455:C:O2'	3:L5:456:C:H5'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:924:C:H2'	3:L5:925:C:O4'	2.15	0.47
3:L5:1084:C:H2'	3:L5:1085:C:H6	1.78	0.47
3:L5:1084:C:H2'	3:L5:1085:C:C6	2.49	0.47
3:L5:1097:C:H2'	3:L5:1098:G:H8	1.80	0.47
3:L5:1415:G:H2'	3:L5:1416:G:H8	1.79	0.47
3:L5:2732:G:H2'	3:L5:2733:C:C6	2.50	0.47
3:L5:2845:A:H61	3:L5:3843:C:H42	1.63	0.47
3:L5:3919:C:OP1	6:LA:2:GLY:HA3	2.15	0.47
3:L5:4274:A:H2'	3:L5:4275:G:H8	1.78	0.47
3:L5:4392:OMG:H2'	3:L5:4447:5MC:HM51	1.95	0.47
3:L5:4584:A:H2'	3:L5:4585:U:O4'	2.14	0.47
18:LN:6:TYR:CZ	39:Li:40:VAL:HG22	2.49	0.47
34:Ld:88:LEU:HD22	34:Ld:106:VAL:HG22	1.95	0.47
48:Ls:146:LYS:HE3	48:Ls:146:LYS:HB2	1.74	0.47
50:SA:128:ARG:HG2	50:SA:153:PRO:HD3	1.97	0.47
54:SG:188:LYS:HE3	54:SG:188:LYS:HB3	1.76	0.47
60:SO:50:LYS:HE2	68:S2:976:G:H21	1.80	0.47
68:S2:51:U:H2'	68:S2:52:G:C8	2.50	0.47
68:S2:1688:C:H2'	68:S2:1689:C:C6	2.49	0.47
77:ST:110:LEU:HD22	77:ST:112:MET:HE2	1.96	0.47
83:Sg:101:PHE:CE2	83:Sg:136:GLY:HA2	2.48	0.47
83:Sg:147:HIS:HA	83:Sg:175:LYS:HE3	1.96	0.47
83:Sg:246:TYR:HB3	83:Sg:261:LEU:HG	1.95	0.47
85:CB:155:LEU:HB3	85:CB:212:VAL:HG23	1.95	0.47
85:CB:300:VAL:HG12	85:CB:315:LEU:HD13	1.96	0.47
3:L5:269:G:H2'	3:L5:270:U:C6	2.50	0.47
3:L5:3607:U:H2'	3:L5:3608:A:H8	1.79	0.47
3:L5:3718:A2M:H2'	3:L5:3719:A:O4'	2.14	0.47
51:SB:23:ASP:HB2	51:SB:25:PHE:HD2	1.80	0.47
52:SC:178:HIS:HB3	52:SC:200:ARG:HH21	1.80	0.47
52:SC:191:VAL:HG11	52:SC:236:PHE:HA	1.96	0.47
57:SJ:33:GLY:HA3	67:Se:38:TYR:CG	2.50	0.47
58:SL:132:ARG:HD3	68:S2:114:G:H5'	1.96	0.47
82:Sf:121:CYS:HB2	82:Sf:145:CYS:HB3	1.80	0.47
82:Sf:135:HIS:NE2	82:Sf:140:TYR:HB3	2.30	0.47
3:L5:1359:G:H4'	18:LN:203:TYR:HB2	1.97	0.47
3:L5:2539:C:H2'	3:L5:2540:C:C6	2.50	0.47
3:L5:4067:U:H2'	3:L5:4068:U:H6	1.80	0.47
20:LP:24:VAL:HG12	20:LP:86:LYS:HG2	1.96	0.47
24:LT:14:MET:HE1	24:LT:55:LYS:HB2	1.97	0.47
47:Lr:63:VAL:HG12	47:Lr:79:ARG:HG2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SC:152:ARG:O	52:SC:156:ILE:HG12	2.15	0.47
57:SJ:115:PHE:HZ	57:SJ:122:SER:C	2.23	0.47
68:S2:942:G:H2'	68:S2:943:U:C6	2.50	0.47
68:S2:1844:U:H2'	68:S2:1845:A:H8	1.80	0.47
79:SZ:69:THR:HG22	79:SZ:108:ILE:HG23	1.96	0.47
82:Sf:103:LEU:HG	82:Sf:104:LYS:H	1.78	0.47
83:Sg:195:LEU:HD13	83:Sg:209:SER:HB2	1.96	0.47
86:CA:17:VAL:HA	86:CA:20:LYS:HE3	1.97	0.47
86:CA:159:PRO:HG2	86:CA:220:VAL:HG12	1.97	0.47
3:L5:1199:G:H2'	3:L5:1200:G:C8	2.50	0.47
3:L5:1461:C:H2'	3:L5:1462:A:C8	2.50	0.47
3:L5:3723:A:H2'	3:L5:3724:A:C8	2.49	0.47
3:L5:4887:C:N4	3:L5:4932:U:H3	2.13	0.47
5:L8:67:U:H2'	5:L8:68:G:C8	2.50	0.47
6:LA:180:LEU:HD22	46:Lp:18:TYR:HB3	1.97	0.47
8:LC:173:LYS:HD3	8:LC:173:LYS:HA	1.71	0.47
60:SO:128:ARG:HA	60:SO:128:ARG:HD2	1.81	0.47
64:SY:86:GLU:HB3	64:SY:91:LEU:HD11	1.97	0.47
68:S2:807:G:H2'	68:S2:808:A:H8	1.80	0.47
73:SM:79:VAL:HG11	73:SM:85:LEU:HB3	1.97	0.47
76:SS:65:GLU:HA	76:SS:68:ILE:HG12	1.97	0.47
83:Sg:88:ARG:HE	83:Sg:97:THR:HG21	1.79	0.47
3:L5:318:A:H2'	3:L5:319:A:C8	2.49	0.46
3:L5:2663:G:H4'	22:LR:117:ARG:HH11	1.79	0.46
3:L5:4113:U:H4'	3:L5:4115:G:C6	2.50	0.46
8:LC:62:THR:HG22	8:LC:64:ALA:H	1.81	0.46
10:LE:274:VAL:HG21	36:Lf:2:SER:HB2	1.97	0.46
19:LO:34:VAL:HG22	19:LO:103:LYS:HB2	1.97	0.46
20:LP:131:ARG:HG3	20:LP:137:ASN:OD1	2.15	0.46
52:SC:246:LYS:HB3	52:SC:246:LYS:HE2	1.66	0.46
68:S2:1365:G:H2'	68:S2:1366:G:C8	2.50	0.46
83:Sg:206:LEU:HD22	83:Sg:241:PHE:HZ	1.79	0.46
3:L5:491:G:H2'	3:L5:492:U:C6	2.51	0.46
3:L5:2611:A:H2'	3:L5:2612:G:H8	1.78	0.46
3:L5:2859:G:H2'	3:L5:2860:C:H6	1.80	0.46
3:L5:4458:C:H2'	3:L5:4459:U:C6	2.49	0.46
3:L5:4771:C:H2'	3:L5:4772:C:C6	2.50	0.46
53:SE:123:LEU:HD23	53:SE:161:GLN:HA	1.97	0.46
54:SG:215:LYS:O	54:SG:219:GLU:HB2	2.15	0.46
58:SL:23:VAL:HG23	58:SL:25:LEU:HG	1.96	0.46
64:SY:101:LYS:HD2	64:SY:101:LYS:HA	1.66	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:Sb:55:LEU:HD11	66:Sb:62:VAL:HG12	1.97	0.46
68:S2:610:G:H2'	68:S2:611:G:C8	2.50	0.46
68:S2:1336:C:H2'	68:S2:1337:4AC:H6	1.98	0.46
68:S2:1839:U:H2'	68:S2:1840:U:C6	2.50	0.46
84:Et:51:G:H2'	84:Et:52:G:H8	1.80	0.46
3:L5:267:G:H2'	3:L5:268:G:H8	1.80	0.46
3:L5:907:C:H2'	3:L5:908:G:C8	2.49	0.46
3:L5:1551:C:H2'	3:L5:1552:G:O4'	2.16	0.46
3:L5:2751:G:H2'	3:L5:2752:G:H8	1.80	0.46
3:L5:4239:A:H2'	3:L5:4240:G:H8	1.80	0.46
3:L5:4601:U:H2'	3:L5:4602:A:C8	2.50	0.46
7:LB:92:TYR:HB3	7:LB:99:LEU:HD22	1.97	0.46
33:Lc:20:LEU:HD23	33:Lc:101:ASP:HB2	1.97	0.46
55:SH:43:LEU:HD11	55:SH:71:SER:HB3	1.97	0.46
56:SI:139:LYS:HE2	56:SI:139:LYS:HB2	1.75	0.46
68:S2:1541:G:H2'	68:S2:1542:C:C6	2.50	0.46
68:S2:1631:U:H2'	68:S2:1632:G:O4'	2.16	0.46
3:L5:1278:C:H2'	3:L5:1279:A:O4'	2.15	0.46
3:L5:2411:C:H2'	3:L5:2412:A:H8	1.80	0.46
3:L5:3923:A:H2'	3:L5:3924:C:C6	2.50	0.46
22:LR:66:ASN:HB3	22:LR:70:ARG:NH1	2.30	0.46
35:Le:98:GLU:HG2	35:Le:123:THR:OG1	2.16	0.46
68:S2:35:C:H5''	68:S2:579:C:H5''	1.97	0.46
68:S2:948:C:H2'	68:S2:949:G:H8	1.80	0.46
68:S2:1229:G:H2'	68:S2:1230:C:C6	2.50	0.46
70:SD:202:LYS:HA	70:SD:202:LYS:HD2	1.74	0.46
1:CD:218:TRP:CE2	70:SD:142:LEU:HB2	2.51	0.46
3:L5:979:C:OP2	10:LE:66:LYS:HD3	2.15	0.46
3:L5:1914:C:H4'	19:LO:89:PRO:HD3	1.96	0.46
7:LB:161:ARG:HG2	7:LB:184:GLN:HA	1.98	0.46
9:LD:208:MET:HB2	9:LD:233:PRO:HG3	1.97	0.46
24:LT:44:GLY:HA2	24:LT:95:HIS:HB3	1.96	0.46
28:LX:64:SER:HB2	38:Lh:69:LEU:HD13	1.96	0.46
36:Lf:50:VAL:HG22	36:Lf:69:VAL:HG23	1.98	0.46
44:Ln:7:LYS:HE2	44:Ln:11:ARG:NH2	2.31	0.46
53:SE:246:LEU:HD22	53:SE:250:GLU:HG3	1.98	0.46
58:SL:61:PRO:HA	58:SL:66:VAL:HG23	1.97	0.46
62:SW:69:LEU:HD21	62:SW:72:CYS:HB3	1.97	0.46
63:SX:60:LYS:H	63:SX:114:ASP:HB2	1.81	0.46
64:SY:10:ARG:HG2	64:SY:11:LYS:HG3	1.97	0.46
68:S2:194:C:H2'	68:S2:195:C:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S2:375:U:H2'	68:S2:376:A:H8	1.81	0.46
85:CB:150:ARG:HH12	85:CB:199:PRO:HD2	1.81	0.46
3:L5:133:C:H42	38:Lh:79:LYS:NZ	2.14	0.46
3:L5:1683:PSU:H2'	3:L5:1684:A:C8	2.50	0.46
3:L5:2413:U:H2'	3:L5:2414:G:H8	1.81	0.46
3:L5:5004:C:H2'	3:L5:5005:G:O4'	2.15	0.46
5:L8:5:U:H2'	5:L8:6:C:H6	1.80	0.46
20:LP:54:GLN:HA	20:LP:83:TRP:CD1	2.50	0.46
21:LQ:27:LEU:HD23	21:LQ:27:LEU:HA	1.82	0.46
48:Ls:37:SER:O	48:Ls:41:GLN:HG2	2.16	0.46
50:SA:76:VAL:HG12	50:SA:123:VAL:HB	1.98	0.46
56:SI:145:ILE:HG21	68:S2:190:G:H5'	1.97	0.46
60:SO:137:SER:HB2	68:S2:942:G:H21	1.81	0.46
68:S2:1199:A:H2'	68:S2:1200:A:C8	2.50	0.46
68:S2:1279:C:H2'	68:S2:1280:G:H8	1.79	0.46
75:SQ:21:ALA:HB2	75:SQ:72:VAL:HG13	1.98	0.46
83:Sg:42:MET:HG2	83:Sg:57:ARG:HB3	1.97	0.46
85:CB:595:SER:HB2	85:CB:600:ASN:HB2	1.98	0.46
3:L5:1534:A2M:N3	40:Lj:11:ARG:HB2	2.30	0.46
3:L5:4920:C:H2'	3:L5:4921:C:C6	2.50	0.46
4:L7:26:C:H5''	9:LD:56:THR:HG21	1.98	0.46
6:LA:133:TYR:HB3	6:LA:168:VAL:HG12	1.97	0.46
8:LC:110:ARG:HG3	18:LN:204:ARG:HE	1.80	0.46
13:LH:45:LEU:HD23	13:LH:57:VAL:HG22	1.98	0.46
68:S2:980:A:H2'	68:S2:981:A:H8	1.80	0.46
68:S2:1414:A:H2'	68:S2:1415:C:C6	2.50	0.46
70:SD:114:ALA:HB3	70:SD:117:ARG:HB2	1.98	0.46
73:SM:92:CYS:HB3	73:SM:103:VAL:HG12	1.97	0.46
85:CB:27:HIS:HB3	85:CB:30:HIS:CD2	2.51	0.46
85:CB:170:GLU:HG2	85:CB:173:GLU:HG2	1.98	0.46
3:L5:982:U:H2'	3:L5:983:C:C6	2.51	0.46
3:L5:1788:A:H2'	14:LI:22:PHE:CZ	2.51	0.46
3:L5:4238:G:H2'	3:L5:4239:A:H8	1.81	0.46
18:LN:98:LEU:HD12	18:LN:128:LYS:HD2	1.98	0.46
62:SW:36:ARG:HA	62:SW:39:THR:HG22	1.98	0.46
68:S2:1514:G:H2'	68:S2:1515:G:C8	2.51	0.46
71:SF:138:ALA:HB3	71:SF:204:ARG:HA	1.97	0.46
83:Sg:166:VAL:HG22	83:Sg:176:VAL:HG22	1.97	0.46
3:L5:422:C:H2'	3:L5:423:G:H8	1.81	0.46
3:L5:462:G:H2'	3:L5:463:A:C8	2.51	0.46
3:L5:1191:C:H2'	3:L5:1192:C:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:4063:U:H2'	3:L5:4064:C:C2	2.51	0.46
19:LO:81:TRP:HB2	19:LO:104:VAL:HG21	1.98	0.46
22:LR:99:MET:HE1	22:LR:127:VAL:HG12	1.98	0.46
33:Lc:48:LEU:HD11	33:Lc:60:ILE:HG21	1.98	0.46
44:Ln:7:LYS:HE2	44:Ln:11:ARG:HH21	1.81	0.46
50:SA:220:LYS:HD3	50:SA:220:LYS:HA	1.74	0.46
52:SC:149:THR:HG22	52:SC:152:ARG:HH21	1.81	0.46
54:SG:61:PHE:CE2	54:SG:96:SER:HB2	2.51	0.46
54:SG:219:GLU:HA	54:SG:222:GLU:HB2	1.98	0.46
55:SH:65:PRO:HB2	55:SH:68:GLN:HG3	1.98	0.46
68:S2:1117:C:H2'	68:S2:1118:C:C6	2.51	0.46
68:S2:1277:C:H2'	68:S2:1278:A:C8	2.46	0.46
84:Et:28:C:H2'	84:Et:29:A:C8	2.50	0.46
1:CD:210:ARG:HB3	1:CD:213:SER:HB3	1.98	0.46
3:L5:3932:U:H2'	3:L5:3933:G:H8	1.81	0.46
7:LB:128:LYS:HA	7:LB:128:LYS:HD2	1.83	0.46
14:LI:47:PRO:HB3	14:LI:171:TRP:CZ2	2.50	0.46
27:LW:86:SER:HB3	27:LW:89:ASP:HB3	1.98	0.46
49:Lt:20:GLY:HA2	49:Lt:56:LEU:HG	1.98	0.46
54:SG:21:GLU:HA	54:SG:24:LEU:HB2	1.98	0.46
55:SH:17:ASP:HB2	55:SH:20:GLU:HB3	1.97	0.46
56:SI:107:THR:HG22	56:SI:111:GLN:HE22	1.80	0.46
66:Sb:37:CYS:HB3	66:Sb:59:CYS:HB3	1.55	0.46
68:S2:121:OMU:H2'	68:S2:122:G:H8	1.81	0.46
68:S2:455:A:H2'	68:S2:456:C:C6	2.51	0.46
68:S2:1214:A:H2'	68:S2:1217:A:N7	2.31	0.46
68:S2:1533:A:H2	68:S2:1536:G:N3	2.14	0.46
86:CA:164:THR:HG21	86:CA:215[A]:LYS:HE2	1.97	0.46
3:L5:667:A:H5''	3:L5:668:C:H5''	1.98	0.45
3:L5:1662:C:H2'	3:L5:1663:C:C6	2.51	0.45
3:L5:2292:C:H2'	3:L5:2293:U:C6	2.52	0.45
3:L5:2765:A:H2'	3:L5:2766:A:C8	2.51	0.45
3:L5:4174:U:H2'	3:L5:4175:G:H8	1.81	0.45
3:L5:4508:C:N3	3:L5:4512:U:H5	2.13	0.45
3:L5:4524:G:C2	7:LB:252:ALA:HB1	2.51	0.45
8:LC:152:LEU:HD21	8:LC:174:LEU:HD22	1.98	0.45
35:Le:35:TRP:CZ2	35:Le:56:PRO:HD2	2.50	0.45
46:Lp:28:LYS:HB3	46:Lp:28:LYS:HE3	1.72	0.45
63:SX:107:ARG:HG3	63:SX:110:HIS:HB3	1.98	0.45
64:SY:104:ARG:HA	64:SY:107:ARG:HH21	1.81	0.45
66:Sb:35:VAL:HG13	66:Sb:77:CYS:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Se:21:LYS:HG2	68:S2:635:G:H5''	1.97	0.45
68:S2:1308:U:H2'	68:S2:1309:C:H6	1.81	0.45
68:S2:1536:G:H2'	68:S2:1537:A:H8	1.81	0.45
68:S2:1543:U:H4'	75:SQ:43:GLU:CD	2.41	0.45
75:SQ:50:LYS:HE2	75:SQ:82:TYR:CZ	2.50	0.45
77:ST:42:HIS:CD2	77:ST:43:LYS:HE3	2.52	0.45
79:SZ:92:LEU:HD22	79:SZ:109:TYR:HE2	1.81	0.45
80:Sc:7:GLN:HG2	80:Sc:8:PRO:HD2	1.97	0.45
3:L5:2385:U:H2'	3:L5:2386:U:C6	2.50	0.45
3:L5:2656:U:H5''	30:LZ:38:TYR:HB3	1.98	0.45
3:L5:4467:A:H61	3:L5:4490:C:H42	1.64	0.45
47:Lr:45:HIS:CG	47:Lr:103:ARG:HH22	2.34	0.45
51:SB:199:LYS:HD3	51:SB:199:LYS:HA	1.71	0.45
54:SG:135:PRO:HA	68:S2:169:U:H5''	1.98	0.45
55:SH:76:GLN:O	55:SH:80:VAL:HG13	2.16	0.45
68:S2:1217:A:H2'	68:S2:1218:C:H6	1.80	0.45
68:S2:1716:C:H2'	68:S2:1717:C:C6	2.51	0.45
86:CA:186:LEU:HD12	86:CA:200:THR:OG1	2.16	0.45
3:L5:182:G:C5	3:L5:183:C:H1'	2.51	0.45
3:L5:208:A:C2	3:L5:233:U:H5''	2.50	0.45
3:L5:229:G:H5''	29:LY:11:ARG:HG3	1.96	0.45
3:L5:1259:G:H2'	3:L5:1260:G:H8	1.80	0.45
3:L5:1857:C:H2'	3:L5:1858:A:C8	2.50	0.45
3:L5:1952:G:P	23:LS:139:ARG:HE	2.39	0.45
49:Lt:114:ARG:HD3	49:Lt:129:ILE:HG22	1.97	0.45
51:SB:30:TRP:CD2	60:SO:19:PRO:HG3	2.51	0.45
54:SG:164:LYS:HD3	54:SG:164:LYS:HA	1.82	0.45
68:S2:121:OMU:H1'	68:S2:121:OMU:HM23	1.78	0.45
68:S2:462:OMC:HM23	68:S2:462:OMC:H1'	1.63	0.45
68:S2:484:A2M:HM'2	68:S2:485:A:C5	2.52	0.45
68:S2:576:A2M:H1'	68:S2:576:A2M:HM'3	1.62	0.45
68:S2:885:U:C2	68:S2:901:G:O6	2.70	0.45
68:S2:1230:C:H2'	68:S2:1231:C:C6	2.51	0.45
70:SD:34:TYR:HE1	70:SD:50:ILE:HG23	1.82	0.45
71:SF:49:LEU:HD11	75:SQ:49:TYR:HB2	1.99	0.45
3:L5:683:C:H2'	3:L5:684:G:O4'	2.16	0.45
3:L5:1197:C:H2'	3:L5:1198:G:H8	1.80	0.45
3:L5:1301:C:H2'	3:L5:1303:A:N6	2.31	0.45
3:L5:2079:G:H2'	3:L5:2080:U:C6	2.51	0.45
3:L5:2485:U:H3	3:L5:2491:C:H41	1.65	0.45
3:L5:4096:C:C4	3:L5:4097:G:H1'	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L7:49:A:H5''	9:LD:224:SER:HB3	1.98	0.45
13:LH:94:SER:OG	13:LH:142:ASP:HB3	2.16	0.45
15:LJ:15:LEU:HD12	15:LJ:165:TRP:HB2	1.98	0.45
19:LO:47:PHE:HA	19:LO:136:ALA:HB2	1.97	0.45
63:SX:68:LYS:HG2	63:SX:91:LEU:HD22	1.98	0.45
68:S2:1418:C:H4'	68:S2:1419:C:H5	1.81	0.45
69:SR:98:VAL:HG21	69:SR:117:LEU:HB2	1.99	0.45
75:SQ:43:GLU:HB2	75:SQ:44:PRO:HD3	1.99	0.45
2:CI:50:MET:HE2	2:CI:50:MET:HB3	1.85	0.45
3:L5:937:U:C6	17:LM:46:ARG:HD2	2.51	0.45
3:L5:2714:G:H2'	3:L5:2715:G:H8	1.81	0.45
3:L5:3707:U:H2'	3:L5:3708:C:C6	2.51	0.45
3:L5:3928:A:H2'	3:L5:3929:G:O4'	2.16	0.45
3:L5:4139:G:H21	3:L5:4140:C:H41	1.62	0.45
18:LN:200:LEU:HA	18:LN:200:LEU:HD23	1.79	0.45
54:SG:79:LYS:HD3	54:SG:86:PRO:HG2	1.97	0.45
56:SI:139:LYS:O	56:SI:141:ARG:HG2	2.15	0.45
64:SY:80:ASP:HA	64:SY:83:LYS:NZ	2.32	0.45
68:S2:115:U:H2'	68:S2:116:OMU:C6	2.46	0.45
74:SP:30:TYR:HA	74:SP:33:LEU:HB2	1.99	0.45
78:SU:56:MET:HE3	78:SU:88:LEU:HD23	1.99	0.45
83:Sg:212:LYS:HD2	83:Sg:235:ILE:HG12	1.97	0.45
3:L5:1327:C:H2'	3:L5:1328:G:C8	2.52	0.45
3:L5:2436:U:C4	28:LX:130:PRO:HG3	2.52	0.45
3:L5:3856:A:H5''	20:LP:83:TRP:O	2.17	0.45
3:L5:4063:U:H2'	3:L5:4064:C:N3	2.32	0.45
50:SA:173:LEU:HD23	50:SA:177:MET:HE1	1.98	0.45
54:SG:168:LYS:HG2	68:S2:72:C:H5	1.81	0.45
54:SG:221:LYS:O	54:SG:225:GLN:HG2	2.16	0.45
61:SV:64:GLU:HG3	66:Sb:3:LEU:HG	1.98	0.45
68:S2:1112:U:O2	68:S2:1121:G:O6	2.34	0.45
68:S2:1634:A:H2'	68:S2:1635:C:O4'	2.16	0.45
73:SM:44:LYS:HE2	82:Sf:128:ALA:H	1.81	0.45
80:Sc:60:GLU:OE1	80:Sc:63:ARG:HG3	2.16	0.45
83:Sg:78:ALA:HB2	83:Sg:92:LEU:HD11	1.98	0.45
85:CB:35:LEU:HD23	85:CB:35:LEU:HA	1.80	0.45
85:CB:433:ASN:HB2	85:CB:441:ASP:OD2	2.17	0.45
86:CA:107:LYS:HD3	86:CA:317:ALA:HA	1.99	0.45
3:L5:208:A:H2	3:L5:233:U:H5''	1.81	0.45
3:L5:4350:C:H2'	3:L5:4351:U:H6	1.82	0.45
4:L7:110:G:H2'	4:L7:111:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L8:8:U:H2'	5:L8:9:A:H8	1.80	0.45
5:L8:96:C:H5''	38:Lh:66:LYS:HG2	1.99	0.45
9:LD:211:LEU:HB3	9:LD:219:TYR:HB2	1.98	0.45
15:LJ:19:LYS:HE3	15:LJ:133:VAL:HG21	1.99	0.45
19:LO:58:LEU:HD23	19:LO:58:LEU:HA	1.76	0.45
21:LQ:71:LYS:HE2	21:LQ:71:LYS:HB3	1.79	0.45
27:LW:10:GLY:HA3	27:LW:53:VAL:HB	1.99	0.45
34:Ld:114:PHE:HA	34:Ld:117:LEU:HD12	1.99	0.45
52:SC:115:GLN:HG2	68:S2:1697:A:H2	1.81	0.45
68:S2:1096:G:H1	68:S2:1136:U:H3	1.64	0.45
68:S2:1302:G:H1	68:S2:1307:U:H3	1.63	0.45
68:S2:1603:G:N2	76:SS:24:ARG:HH21	2.15	0.45
3:L5:1772:C:H2'	3:L5:1773:U:C6	2.51	0.45
3:L5:1993:C:H2'	3:L5:1994:C:H6	1.81	0.45
3:L5:3690:U:H2'	3:L5:3691:G:O4'	2.17	0.45
17:LM:36:ALA:HB2	17:LM:52:PHE:CZ	2.51	0.45
53:SE:88:ASP:HA	53:SE:122:LYS:HD2	1.98	0.45
64:SY:8:ARG:HB3	68:S2:835:C:N4	2.32	0.45
68:S2:1468:C:H2'	68:S2:1469:A:C8	2.50	0.45
71:SF:102:LEU:HD21	79:SZ:100:VAL:HG21	1.99	0.45
3:L5:518:G:H22	3:L5:643:C:H2'	1.82	0.45
3:L5:701:G:H2'	3:L5:702:U:H6	1.81	0.45
3:L5:1244:G:H2'	3:L5:1245:C:H6	1.81	0.45
3:L5:1274:A:O2'	3:L5:1275:G:H8	2.00	0.45
3:L5:4146:G:H2'	3:L5:4147:G:H8	1.80	0.45
3:L5:4965:U:H5''	7:LB:128:LYS:HZ1	1.82	0.45
3:L5:5062:G:C2	3:L5:5063:G:C8	3.04	0.45
4:L7:23:A:H2'	4:L7:24:C:C6	2.51	0.45
9:LD:191:ASN:HB3	9:LD:194:VAL:HG22	1.98	0.45
11:LF:182:TYR:HB3	11:LF:200:ARG:HG3	1.98	0.45
17:LM:36:ALA:HB3	17:LM:55:MET:HE1	1.99	0.45
50:SA:51:LEU:HA	50:SA:54:THR:HG22	1.99	0.45
68:S2:1752:C:H42	68:S2:1755:C:N4	2.12	0.45
68:S2:1781:A:H5''	68:S2:1783:C:N4	2.32	0.45
83:Sg:245:ARG:HD2	83:Sg:247:TRP:CE2	2.52	0.45
84:Et:48:C:C4	84:Et:59:G:C8	3.05	0.45
15:LJ:50:PHE:HB2	15:LJ:67:LYS:HD2	1.99	0.45
48:Ls:160:LEU:HD21	48:Ls:171:GLU:HB3	1.98	0.45
49:Lt:16:ARG:HB3	49:Lt:61:LYS:HZ3	1.82	0.45
52:SC:183:LYS:HD3	52:SC:194:ARG:NH2	2.32	0.45
52:SC:191:VAL:HG11	52:SC:236:PHE:HD1	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SE:39:ARG:HD2	53:SE:39:ARG:HA	1.78	0.45
53:SE:248:ILE:HA	53:SE:251:GLU:HB3	1.99	0.45
54:SG:227:GLN:HB3	54:SG:231:ARG:NH2	2.31	0.45
68:S2:635:G:H2'	68:S2:636:C:H6	1.82	0.45
68:S2:948:C:H2'	68:S2:949:G:C8	2.52	0.45
68:S2:1129:G:H2'	68:S2:1130:G:N3	2.32	0.45
70:SD:40:ARG:HB2	78:SU:108:PRO:HG3	1.98	0.45
72:SK:47:LYS:HA	72:SK:50:GLN:HG2	1.98	0.45
82:Sf:119:ARG:HB3	82:Sf:132:MET:HB2	1.99	0.45
3:L5:1725:U:H2'	3:L5:1726:U:C6	2.52	0.44
3:L5:1932:A:OP2	19:LO:49:ARG:NH1	2.38	0.44
3:L5:2654:C:H2'	3:L5:2655:C:C6	2.52	0.44
3:L5:2789:A:H1'	42:LI:45:ARG:HH22	1.81	0.44
3:L5:4093:G:H3'	3:L5:4094:G:C8	2.52	0.44
8:LC:7:LEU:HG	8:LC:21:ASN:HB3	1.99	0.44
10:LE:281:ILE:HG23	10:LE:286:LEU:HD21	1.98	0.44
30:LZ:100:VAL:HG12	30:LZ:106:LEU:HB3	1.99	0.44
34:Ld:33:ILE:HD13	34:Ld:33:ILE:HA	1.80	0.44
48:Ls:127:ASN:HD21	48:Ls:151:THR:HG23	1.82	0.44
53:SE:47:PHE:HD2	53:SE:48:LEU:HD12	1.82	0.44
59:SN:114:ARG:HA	59:SN:114:ARG:HD3	1.88	0.44
70:SD:1:MET:HB3	70:SD:4:GLN:HB2	1.98	0.44
85:CB:27:HIS:HA	85:CB:138:GLN:HB3	2.00	0.44
86:CA:20:LYS:HA	86:CA:23:MET:HG2	1.99	0.44
3:L5:223:G:H4'	3:L5:225:G:N7	2.32	0.44
3:L5:1326:A2M:H2'	3:L5:1327:C:C6	2.51	0.44
3:L5:1733:G:N3	3:L5:4214:A:H2'	2.32	0.44
3:L5:1741:G:N3	3:L5:1781:PSU:H5''	2.32	0.44
3:L5:2250:C:H2'	3:L5:2251:G:C8	2.51	0.44
3:L5:2478:C:H2'	3:L5:2479:G:H5'	1.99	0.44
3:L5:3600:G:H2'	3:L5:3601:C:C6	2.52	0.44
9:LD:166:ALA:HB1	9:LD:171:LEU:HD12	1.99	0.44
39:Li:94:LEU:HD23	39:Li:94:LEU:HA	1.82	0.44
51:SB:137:LEU:HG	51:SB:215:VAL:HG12	1.99	0.44
54:SG:2:LYS:HB3	54:SG:15:LEU:HD22	1.98	0.44
59:SN:88:LEU:HD11	59:SN:122:ILE:HG23	1.98	0.44
59:SN:102:LEU:O	59:SN:106:ARG:HD2	2.17	0.44
64:SY:9:THR:HG22	64:SY:25:ILE:HG22	1.99	0.44
67:Se:32:ALA:HB2	68:S2:525:A:H5''	1.99	0.44
68:S2:479:C:H2'	68:S2:480:G:C8	2.53	0.44
68:S2:815:U:H2'	68:S2:816:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S2:964:A:H2'	68:S2:965:U:H6	1.82	0.44
68:S2:1284:A:C8	73:SM:33:ARG:HG3	2.52	0.44
74:SP:28:MET:HE1	74:SP:36:LEU:HG	1.99	0.44
79:SZ:99:LEU:HD21	79:SZ:102:LYS:HB2	1.98	0.44
83:Sg:127:LYS:HD2	83:Sg:149:GLU:H	1.82	0.44
3:L5:106:A:H2'	3:L5:107:G:O4'	2.18	0.44
3:L5:1300:G:H2'	3:L5:1301:C:N1	2.32	0.44
3:L5:1318:C:H42	3:L5:1322:1MA:H8	1.64	0.44
3:L5:2521:G:H4'	37:Lg:26:PRO:HD2	1.98	0.44
3:L5:2861:OMC:HM23	3:L5:2861:OMC:H1'	1.74	0.44
3:L5:4139:G:N2	3:L5:4140:C:H41	2.16	0.44
6:LA:36:GLU:HG3	6:LA:91:GLY:HA2	1.98	0.44
8:LC:45:ARG:HG3	8:LC:238:LEU:HD22	2.00	0.44
22:LR:172:ARG:NH2	68:S2:908:A:H5''	2.31	0.44
30:LZ:30:ASP:HA	30:LZ:39:SER:OG	2.18	0.44
51:SB:129:THR:HG22	51:SB:131:ASP:H	1.82	0.44
54:SG:58:LYS:HE2	54:SG:105:ASN:HA	1.99	0.44
54:SG:167:LYS:HD3	68:S2:67:C:H41	1.82	0.44
64:SY:58:PHE:HE1	64:SY:74:MET:HE2	1.82	0.44
68:S2:121:OMU:H2'	68:S2:122:G:C8	2.53	0.44
68:S2:644:OMG:HM23	68:S2:644:OMG:H1'	1.77	0.44
68:S2:900:C:H5'	68:S2:901:G:N7	2.31	0.44
68:S2:1330:G:N7	68:S2:1492:U:H3'	2.32	0.44
68:S2:1713:C:H2'	68:S2:1714:U:C6	2.52	0.44
76:SS:14:ARG:HD2	76:SS:18:THR:C	2.42	0.44
84:Et:22:G:N7	84:Et:46:G:O6	2.50	0.44
3:L5:2021:G:H4'	48:Ls:84:GLY:C	2.42	0.44
3:L5:2496:G:H2'	3:L5:2497:C:H6	1.82	0.44
3:L5:4192:A:H2'	3:L5:4193:C:H6	1.82	0.44
12:LG:259:LYS:HE3	12:LG:259:LYS:HB3	1.87	0.44
14:LI:190:LEU:HD23	14:LI:199:TYR:HA	1.97	0.44
16:LL:139:SER:HB3	16:LL:142:GLU:HB2	1.98	0.44
22:LR:139:MET:HG2	22:LR:143:HIS:NE2	2.33	0.44
26:LV:99:GLU:HB3	27:LW:24:THR:HG23	1.99	0.44
34:Ld:19:GLU:HA	34:Ld:90:ARG:HH11	1.82	0.44
53:SE:45:ILE:HG13	53:SE:61:VAL:HG11	1.98	0.44
68:S2:61:A:H1'	68:S2:316:G:H1'	2.00	0.44
68:S2:692:G:H2'	68:S2:693:A:H8	1.80	0.44
69:SR:33:ARG:HD3	69:SR:33:ARG:HA	1.77	0.44
71:SF:25:THR:HG22	71:SF:109:LEU:HD22	1.99	0.44
3:L5:239:C:OP1	29:LY:46:SER:HB3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:2385:U:H2'	3:L5:2386:U:H6	1.82	0.44
3:L5:4653:C:H2'	3:L5:4654:C:C6	2.52	0.44
5:L8:78:G:H2'	5:L8:79:G:C8	2.53	0.44
22:LR:110:ARG:HE	22:LR:110:ARG:HB3	1.67	0.44
36:Lf:48:ALA:HB2	36:Lf:71:TRP:CZ3	2.52	0.44
62:SW:107:SER:HA	68:S2:862:A:C8	2.52	0.44
68:S2:1139:C:H2'	68:S2:1140:G:O4'	2.18	0.44
68:S2:1195:A:H2'	68:S2:1196:A:H8	1.83	0.44
68:S2:1203:G:H2'	68:S2:1204:A:H8	1.77	0.44
68:S2:1417:C:H3'	68:S2:1418:C:O4'	2.18	0.44
3:L5:243:A:H5'	29:LY:1:MET:O	2.17	0.44
3:L5:457:G:H2'	3:L5:458:C:C6	2.53	0.44
3:L5:739:G:H22	3:L5:926:G:H1'	1.83	0.44
3:L5:1294:A:H1'	3:L5:1296:G:N1	2.32	0.44
3:L5:1309:C:H2'	3:L5:1310:C:C6	2.52	0.44
3:L5:2073:C:OP1	11:LF:212:LYS:HE3	2.18	0.44
3:L5:2376:A:H2'	3:L5:2377:C:C6	2.53	0.44
3:L5:2465:C:H2'	3:L5:2466:G:O4'	2.18	0.44
3:L5:4600:G:H4'	3:L5:4601:U:O5'	2.18	0.44
3:L5:4619:U:H2'	3:L5:4620:OMU:H6	2.00	0.44
10:LE:190:HIS:HB3	10:LE:193:PHE:HD1	1.82	0.44
11:LF:216:PRO:HD3	11:LF:247:MET:HE2	1.98	0.44
23:LS:127:MET:HB3	24:LT:153:PRO:HG2	1.99	0.44
24:LT:4:THR:OG1	24:LT:9:ARG:HD3	2.17	0.44
39:Li:76:ARG:HD3	39:Li:76:ARG:HA	1.66	0.44
54:SG:189:ARG:HH21	68:S2:331:C:H5''	1.82	0.44
60:SO:150:ARG:HB3	68:S2:1838:U:H1'	2.00	0.44
64:SY:113:ARG:NE	64:SY:128:GLY:HA2	2.32	0.44
66:Sb:20:LYS:HA	66:Sb:23:ARG:NH1	2.33	0.44
68:S2:194:C:H2'	68:S2:195:C:C6	2.52	0.44
68:S2:557:U:H3'	68:S2:558:G:H2'	1.99	0.44
68:S2:1374:C:H2'	68:S2:1375:G:O4'	2.17	0.44
73:SM:52:LEU:HD21	73:SM:62:VAL:HG13	2.00	0.44
80:Sc:35:MET:HE3	80:Sc:35:MET:HB3	1.76	0.44
85:CB:164:LEU:HD12	85:CB:301:PHE:CE2	2.52	0.44
1:CD:205:LYS:HG3	68:S2:1698:C:H5'	2.00	0.44
3:L5:162:A:H2'	3:L5:163:A:C8	2.53	0.44
3:L5:518:G:N2	3:L5:643:C:H2'	2.32	0.44
3:L5:1332:C:H2'	3:L5:1333:A:C8	2.53	0.44
3:L5:2293:U:H2'	3:L5:2294:G:C8	2.53	0.44
3:L5:4113:U:H4'	3:L5:4115:G:C2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:5056:A:H2'	3:L5:5057:C:C6	2.53	0.44
53:SE:29:PRO:HG3	68:S2:496:C:OP1	2.17	0.44
55:SH:170:VAL:HG13	55:SH:187:PHE:HB2	1.99	0.44
68:S2:496:C:H2'	68:S2:497:C:H6	1.82	0.44
68:S2:674:C:H2'	68:S2:675:U:C6	2.52	0.44
68:S2:919:A:H8	68:S2:919:A:OP2	2.01	0.44
83:Sg:106:LYS:HD3	83:Sg:126:ASP:HA	1.99	0.44
84:Et:10:G:H2'	84:Et:11:C:C6	2.52	0.44
86:CA:342:LEU:HD23	86:CA:342:LEU:H	1.83	0.44
3:L5:1175:A:H2	3:L5:1185:G:H22	1.64	0.44
3:L5:1802:A:H5''	3:L5:1803:G:H5'	1.99	0.44
3:L5:1846:G:H2'	3:L5:1847:C:C6	2.53	0.44
3:L5:2029:A:H2'	3:L5:2030:A:C8	2.52	0.44
3:L5:3808:OMC:HM23	3:L5:3808:OMC:H1'	1.80	0.44
3:L5:3867:A2M:HM'3	3:L5:3867:A2M:H1'	1.48	0.44
12:LG:230:TYR:CZ	12:LG:234:ARG:HD3	2.53	0.44
25:LU:79:SER:HB2	25:LU:82:TYR:HB2	2.00	0.44
26:LV:97:TYR:CE1	27:LW:19:ARG:HD3	2.53	0.44
29:LY:58:VAL:HG23	29:LY:59:ARG:HG2	1.99	0.44
33:Lc:11:LEU:HD13	33:Lc:75:SER:HB2	1.98	0.44
38:Lh:17:LEU:HD23	38:Lh:17:LEU:HA	1.88	0.44
48:Ls:35:VAL:HB	48:Ls:39:GLN:HG2	1.98	0.44
53:SE:127:ARG:HB2	53:SE:140:VAL:HG23	1.99	0.44
57:SJ:5:ARG:HG3	68:S2:38:A:OP1	2.18	0.44
57:SJ:129:LEU:HD12	57:SJ:129:LEU:HA	1.75	0.44
62:SW:36:ARG:HA	62:SW:36:ARG:HD3	1.84	0.44
68:S2:405:G:H2'	68:S2:406:PSU:C6	2.53	0.44
68:S2:867:OMG:H8	68:S2:867:OMG:H5''	1.83	0.44
80:Sc:31:ARG:HD2	80:Sc:41:SER:HB2	2.00	0.44
84:Et:51:G:H2'	84:Et:52:G:C8	2.52	0.44
85:CB:10:ARG:NH1	85:CB:465:PRO:HD3	2.33	0.44
85:CB:484:THR:HG21	85:CB:494:MET:HB2	2.00	0.44
3:L5:1095:A:N1	3:L5:1200:G:C6	2.86	0.44
3:L5:2413:U:H2'	3:L5:2414:G:C8	2.53	0.44
3:L5:2559:G:H2'	3:L5:2560:C:O4'	2.18	0.44
3:L5:3932:U:H2'	3:L5:3933:G:C8	2.52	0.44
3:L5:4363:A:H5''	45:Lo:36:GLN:HG2	1.99	0.44
3:L5:4957:C:H2'	3:L5:4958:C:C6	2.52	0.44
12:LG:117:ARG:HA	12:LG:117:ARG:HD2	1.89	0.44
17:LM:25:VAL:HB	17:LM:38:VAL:HG13	2.00	0.44
23:LS:47:PHE:HE1	23:LS:125:GLN:HG3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lo:35:ALA:O	45:Lo:39:ARG:HG3	2.18	0.44
50:SA:154:LEU:HD22	50:SA:157:VAL:HG21	2.00	0.44
51:SB:134:LEU:HG	51:SB:218:LEU:HD12	1.99	0.44
55:SH:147:LYS:HE3	55:SH:153:LEU:HD23	2.00	0.44
61:SV:22:ARG:NH2	61:SV:58:ALA:HB3	2.33	0.44
62:SW:3:ARG:HH22	68:S2:1093:A:H4'	1.83	0.44
67:Se:58:ASN:C	67:Se:58:ASN:HD22	2.24	0.44
68:S2:159:A2M:O5'	68:S2:159:A2M:H8	2.18	0.44
68:S2:344:U:H2'	68:S2:345:U:C6	2.52	0.44
68:S2:1279:C:H2'	68:S2:1280:G:C8	2.53	0.44
75:SQ:134:GLY:HA3	75:SQ:140:ARG:HA	2.00	0.44
83:Sg:286:CYS:HA	83:Sg:302:TYR:HD1	1.83	0.44
3:L5:1323:A2M:H2'	3:L5:1324:A:O4'	2.17	0.43
3:L5:1405:C:H2'	3:L5:1406:G:C8	2.52	0.43
12:LG:164:ILE:O	12:LG:168:VAL:HG13	2.17	0.43
23:LS:28:TYR:CD2	23:LS:54:MET:HE1	2.53	0.43
24:LT:102:ARG:HA	24:LT:102:ARG:HD2	1.86	0.43
24:LT:130:ARG:HE	24:LT:130:ARG:HB2	1.60	0.43
30:LZ:50:PRO:HD3	30:LZ:68:ILE:HG12	1.99	0.43
31:La:100:ILE:HG21	31:La:125:LYS:HE2	1.99	0.43
32:Lb:73:LYS:HA	32:Lb:73:LYS:HD3	1.77	0.43
40:Lj:67:LEU:HD23	40:Lj:67:LEU:HA	1.86	0.43
55:SH:58:LYS:HG3	55:SH:90:LYS:HG2	2.00	0.43
68:S2:635:G:H2'	68:S2:636:C:C6	2.52	0.43
68:S2:958:G:H2'	68:S2:959:G:C8	2.52	0.43
68:S2:1201:U:H2'	68:S2:1202:U:C6	2.53	0.43
82:Sf:106:TYR:HB3	82:Sf:116:ARG:HG3	2.00	0.43
83:Sg:119:GLN:HB3	83:Sg:131:LEU:HD11	1.99	0.43
3:L5:7:C:H2'	3:L5:8:U:C6	2.53	0.43
3:L5:1693:U:H2'	3:L5:1694:C:O4'	2.17	0.43
55:SH:65:PRO:HA	55:SH:97:GLN:HE22	1.83	0.43
57:SJ:55:LYS:HB2	57:SJ:55:LYS:HE3	1.68	0.43
68:S2:24:C:O2'	68:S2:25:A:H8	2.00	0.43
68:S2:1831:A:H2'	68:S2:1832:6MZ:H8	1.99	0.43
71:SF:141:VAL:HG13	71:SF:145:ARG:HB3	2.00	0.43
74:SP:81:ARG:HH11	74:SP:98:ASN:HA	1.83	0.43
84:Et:14:A:H2'	84:Et:15:G:O4'	2.18	0.43
3:L5:693:C:H2'	3:L5:694:C:C6	2.53	0.43
3:L5:1096:C:H2'	3:L5:1097:C:C6	2.54	0.43
3:L5:1811:G:H2'	3:L5:1812:C:H6	1.83	0.43
3:L5:2903:G:H1'	3:L5:2904:U:C5	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:4188:U:H2'	3:L5:4189:U:C6	2.54	0.43
89:L5:5290:SPD:H52	8:LC:60:HIS:O	2.19	0.43
8:LC:318:PRO:C	8:LC:320:LYS:H	2.26	0.43
20:LP:84:PRO:HB2	20:LP:87:SER:HB2	2.01	0.43
22:LR:19:LYS:HB2	22:LR:19:LYS:HE2	1.80	0.43
38:Lh:4:ILE:HD12	38:Lh:53:SER:HB3	2.00	0.43
53:SE:17:HIS:HA	53:SE:19:MET:HE2	2.00	0.43
56:SI:43:ILE:HD11	56:SI:60:LEU:HD21	2.00	0.43
57:SJ:87:LEU:HD23	57:SJ:88:ASP:O	2.18	0.43
57:SJ:150:ARG:HG3	68:S2:821:G:C6	2.53	0.43
68:S2:179:C:H3'	68:S2:180:G:C8	2.54	0.43
68:S2:534:G:H2'	68:S2:535:G:H8	1.84	0.43
68:S2:1064:C:H2'	68:S2:1065:G:H8	1.83	0.43
68:S2:1709:G:H2'	68:S2:1710:C:H6	1.81	0.43
73:SM:86:GLY:HA2	73:SM:89:VAL:HG12	2.00	0.43
77:ST:6:VAL:HG12	77:ST:135:ALA:HB2	1.99	0.43
83:Sg:147:HIS:HD1	83:Sg:175:LYS:HD2	1.84	0.43
83:Sg:302:TYR:HE2	83:Sg:308:ARG:HD2	1.83	0.43
85:CB:301:PHE:CD1	85:CB:336:LEU:HD21	2.53	0.43
3:L5:173:C:H2'	3:L5:174:C:H6	1.84	0.43
3:L5:1100:U:O2	3:L5:1195:G:C2	2.72	0.43
3:L5:1350:C:H2'	3:L5:1351:G:C8	2.53	0.43
3:L5:1702:C:H4'	8:LC:308:LYS:HD2	2.01	0.43
3:L5:2489:C:H4'	3:L5:2491:C:H42	1.83	0.43
3:L5:2496:G:H2'	3:L5:2497:C:C6	2.54	0.43
6:LA:27:ALA:HB1	6:LA:77:ILE:HG13	1.99	0.43
6:LA:132:ASN:O	6:LA:169:VAL:HG23	2.18	0.43
7:LB:173:LEU:HD22	7:LB:342:LYS:HD2	2.00	0.43
11:LF:187:MET:HE3	11:LF:187:MET:HB2	1.84	0.43
41:Lk:7:GLU:HB3	41:Lk:10:ASP:HB2	2.00	0.43
42:Ll:27:ILE:HD13	42:Ll:30:LYS:HD2	2.01	0.43
46:Lp:62:LYS:HE2	46:Lp:62:LYS:HB2	1.87	0.43
49:Lt:48:LYS:HE3	49:Lt:52:ASP:OD1	2.17	0.43
53:SE:241:GLY:O	53:SE:244:ILE:HG12	2.18	0.43
55:SH:33:ASN:CG	55:SH:36:LEU:HB2	2.44	0.43
59:SN:25:TRP:CD2	66:Sb:82:LYS:HD3	2.54	0.43
59:SN:48:SER:HB3	68:S2:926:A:H1'	1.99	0.43
64:SY:60:PHE:HA	64:SY:70:THR:O	2.18	0.43
75:SQ:32:ILE:HG21	75:SQ:39:LEU:HD23	1.99	0.43
85:CB:189:ILE:HD11	85:CB:204:MET:HA	2.00	0.43
85:CB:590:LEU:HD12	85:CB:605:LYS:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:CA:51:LYS:HD2	86:CA:55:MET:HE2	1.99	0.43
3:L5:1326:A2M:H1'	3:L5:1326:A2M:HM'3	1.63	0.43
3:L5:2683:C:H2'	3:L5:2684:C:C6	2.54	0.43
3:L5:3757:G:H2'	3:L5:3758:U:O4'	2.19	0.43
3:L5:3911:C:H2'	3:L5:3912:U:C6	2.52	0.43
3:L5:4132:C:H2'	3:L5:4133:C:O4'	2.18	0.43
3:L5:4364:G:H2'	3:L5:4365:C:H6	1.82	0.43
8:LC:279:LEU:HD23	8:LC:279:LEU:HA	1.84	0.43
19:LO:93:LYS:HA	19:LO:93:LYS:HD3	1.76	0.43
45:Lo:32:SER:C	45:Lo:34:TYR:H	2.27	0.43
49:Lt:125:LEU:HB2	49:Lt:128:THR:HG23	2.01	0.43
53:SE:136:ILE:HG23	53:SE:149:TYR:CE1	2.53	0.43
57:SJ:55:LYS:HA	57:SJ:58:ARG:HE	1.83	0.43
65:Sa:50:VAL:HG23	65:Sa:64:LEU:HD12	2.00	0.43
68:S2:27:A2M:HM'3	68:S2:27:A2M:H1'	1.56	0.43
68:S2:66:G:H2'	68:S2:67:C:H4'	1.98	0.43
68:S2:149:A:N7	68:S2:169:U:C2	2.86	0.43
68:S2:609:U:H2'	68:S2:610:G:C8	2.52	0.43
68:S2:649:PSU:H2'	68:S2:650:A:C8	2.52	0.43
68:S2:1003:U:H2'	68:S2:1004:PSU:C6	2.53	0.43
68:S2:1337:4AC:H2'	68:S2:1338:G:C8	2.52	0.43
72:SK:96:ARG:O	72:SK:96:ARG:HD2	2.19	0.43
83:Sg:109:LEU:HD11	83:Sg:125:ARG:CZ	2.49	0.43
85:CB:397:TYR:HD1	85:CB:484:THR:HG22	1.83	0.43
85:CB:524:LEU:HD12	85:CB:536:CYS:HB3	2.00	0.43
3:L5:750:U:H2'	3:L5:751:G:C8	2.54	0.43
3:L5:1266:G:N7	32:Lb:95:ARG:HB3	2.33	0.43
3:L5:3711:A:C4	68:S2:970:G:C6	3.07	0.43
10:LE:155:GLY:O	10:LE:158:ARG:HG3	2.18	0.43
10:LE:210:LYS:HA	10:LE:210:LYS:HD3	1.78	0.43
36:Lf:35:ALA:HB3	36:Lf:38:GLU:HG3	2.00	0.43
37:Lg:33:LEU:HD23	37:Lg:33:LEU:HA	1.78	0.43
50:SA:18:PHE:HD2	50:SA:51:LEU:HD11	1.83	0.43
50:SA:77:ILE:HG12	50:SA:99:ILE:HB	2.01	0.43
57:SJ:18:ARG:HB3	57:SJ:21:GLU:OE2	2.18	0.43
64:SY:15:ASN:HD21	64:SY:18:LEU:HB2	1.82	0.43
66:Sb:55:LEU:HG	66:Sb:62:VAL:HA	1.99	0.43
68:S2:1195:A:H2'	68:S2:1196:A:C8	2.52	0.43
68:S2:1856:C:H2'	68:S2:1857:G:C8	2.54	0.43
69:SR:84:TYR:HD2	69:SR:86:PRO:HG3	1.84	0.43
3:L5:2372:U:H2'	3:L5:2373:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:2390:G:H22	3:L5:2825:A:H2	1.66	0.43
5:L8:154:G:H2'	5:L8:155:C:C6	2.53	0.43
26:LV:21:PRO:HA	26:LV:54:ALA:HA	2.00	0.43
27:LW:74:ARG:HG3	54:SG:114:VAL:HG21	2.01	0.43
42:L1:9:ILE:HD12	42:L1:51:LEU:HD12	2.01	0.43
49:Lt:104:ILE:HG13	49:Lt:106:PHE:CD2	2.53	0.43
50:SA:121:LEU:HD21	50:SA:145:ILE:HD12	1.99	0.43
51:SB:165:ARG:O	51:SB:169:MET:HG2	2.19	0.43
55:SH:168:HIS:CE1	55:SH:169:LYS:HG3	2.54	0.43
56:SI:124:LYS:C	56:SI:125:LYS:HZ2	2.26	0.43
60:SO:61:LYS:HA	60:SO:61:LYS:HD3	1.76	0.43
68:S2:456:C:H2'	68:S2:457:C:C6	2.54	0.43
68:S2:558:G:H1'	68:S2:559:G:C8	2.54	0.43
68:S2:806:U:H2'	68:S2:807:G:H8	1.84	0.43
69:SR:117:LEU:HD23	69:SR:117:LEU:H	1.83	0.43
70:SD:59:LEU:HA	70:SD:66:ILE:HG12	2.01	0.43
71:SF:147:VAL:O	71:SF:151:ILE:HG22	2.19	0.43
82:Sf:132:MET:HA	82:Sf:141:CYS:HA	2.00	0.43
83:Sg:302:TYR:HB2	83:Sg:304:ASP:OD1	2.18	0.43
3:L5:173:C:H2'	3:L5:174:C:C6	2.54	0.43
3:L5:457:G:H2'	3:L5:458:C:H6	1.84	0.43
3:L5:754:U:H2'	3:L5:755:C:C6	2.54	0.43
3:L5:1096:C:H2'	3:L5:1097:C:H6	1.84	0.43
3:L5:1204:C:H2'	3:L5:1205:G:H8	1.83	0.43
3:L5:1345:A:H2'	3:L5:1346:C:C6	2.54	0.43
3:L5:2411:C:H2'	3:L5:2412:A:C8	2.53	0.43
3:L5:3765:G:H21	3:L5:3766:A:N6	2.16	0.43
3:L5:4130:C:H2'	3:L5:4131:G:H8	1.84	0.43
3:L5:4169:G:H4'	3:L5:4171:C:C2	2.54	0.43
3:L5:4903:G:H2'	3:L5:4904:G:H8	1.84	0.43
7:LB:86:VAL:HG12	7:LB:201:LEU:HD23	1.99	0.43
12:LG:159:HIS:ND1	12:LG:185:LYS:HA	2.34	0.43
20:LP:61:ARG:HH22	20:LP:76:TRP:HB3	1.83	0.43
50:SA:155:ARG:HG2	50:SA:156:TYR:CD2	2.53	0.43
53:SE:252:ARG:NH1	57:SJ:75:ASN:HD22	2.17	0.43
54:SG:177:GLN:HG3	54:SG:178:ARG:N	2.34	0.43
56:SI:201:LYS:HA	56:SI:201:LYS:HD3	1.77	0.43
57:SJ:65:GLU:O	57:SJ:66:LYS:HG2	2.19	0.43
62:SW:36:ARG:HB3	62:SW:110:ILE:HD12	2.01	0.43
62:SW:106:THR:HG21	62:SW:121:THR:HG23	2.00	0.43
68:S2:319:C:H2'	68:S2:320:G:C8	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S2:1278:A:H2'	68:S2:1279:C:C6	2.53	0.43
68:S2:1671:G:H2'	68:S2:1672:U:C6	2.52	0.43
68:S2:1850:MA6:H8	68:S2:1850:MA6:O5'	2.18	0.43
3:L5:262:G:H2'	3:L5:263:G:C8	2.54	0.43
3:L5:4504:C:H2'	3:L5:4505:C:C6	2.54	0.43
41:Lk:35:LYS:HB3	41:Lk:42:LEU:HD11	2.01	0.43
50:SA:176:TRP:HE1	50:SA:197:VAL:HG12	1.83	0.43
52:SC:194:ARG:HG2	52:SC:225:SER:HB3	2.00	0.43
53:SE:36:HIS:CD2	53:SE:85:GLY:HA3	2.54	0.43
53:SE:100:ARG:HH12	53:SE:122:LYS:HG3	1.83	0.43
68:S2:857:U:H2'	68:S2:858:A:C8	2.53	0.43
83:Sg:8:ARG:HD3	83:Sg:52:TYR:HE1	1.84	0.43
83:Sg:172:LYS:HG2	83:Sg:193:GLY:C	2.44	0.43
84:Et:16:C:H1'	84:Et:19:G:OP2	2.18	0.43
85:CB:475:VAL:HA	85:CB:478:PHE:CD2	2.54	0.43
86:CA:155:ARG:HD3	86:CA:357:LEU:HB2	2.01	0.43
3:L5:690:C:H2'	3:L5:691:C:C6	2.53	0.43
3:L5:958:G:N2	10:LE:124:LYS:HB3	2.34	0.43
3:L5:1806:G:H2'	3:L5:1807:C:C6	2.54	0.43
3:L5:3723:A:H2'	3:L5:3724:A:H8	1.83	0.43
3:L5:4954:G:H2'	3:L5:4955:A:C8	2.53	0.43
7:LB:18:PRO:HG2	7:LB:20:LYS:HG2	2.01	0.43
12:LG:151:LYS:HB3	12:LG:151:LYS:HE2	1.77	0.43
17:LM:24:LEU:H	17:LM:43:THR:HG21	1.84	0.43
27:LW:104:GLN:O	27:LW:107:GLN:HG3	2.19	0.43
28:LX:96:LEU:HD12	28:LX:140:LEU:HD11	2.01	0.43
49:Lt:59:THR:HG23	49:Lt:80:LEU:HD21	2.01	0.43
50:SA:93:ALA:HB1	50:SA:183:LEU:HD11	2.01	0.43
53:SE:192:ILE:HG12	53:SE:243:GLY:HA3	2.00	0.43
54:SG:69:THR:O	54:SG:99:GLY:HA3	2.19	0.43
54:SG:235:SER:HB2	68:S2:786:G:C5	2.54	0.43
68:S2:1050:A:H62	68:S2:1068:G:N2	2.17	0.43
68:S2:1548:G:H2'	68:S2:1549:U:C6	2.54	0.43
70:SD:15:GLY:HA2	70:SD:18:LYS:HE3	2.00	0.43
71:SF:49:LEU:HD21	75:SQ:49:TYR:HD2	1.83	0.43
71:SF:108:PRO:HA	71:SF:111:VAL:HG12	2.01	0.43
71:SF:120:GLY:HA3	71:SF:146:ARG:HE	1.84	0.43
71:SF:195:GLU:N	71:SF:198:ARG:HH21	2.17	0.43
86:CA:100:LEU:HD11	86:CA:127:VAL:HG11	2.00	0.43
3:L5:267:G:H2'	3:L5:268:G:C8	2.53	0.42
3:L5:650:C:H2'	3:L5:651:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:2610:G:H2'	3:L5:2611:A:H8	1.84	0.42
3:L5:3841:OMC:HM23	3:L5:3841:OMC:H1'	1.84	0.42
3:L5:3848:U:H2'	3:L5:3849:A:H8	1.84	0.42
3:L5:4088:C:C5	12:LG:54:PHE:HZ	2.37	0.42
3:L5:4258:C:H2'	3:L5:4259:C:H6	1.84	0.42
3:L5:4460:U:H2'	3:L5:4461:C:H6	1.83	0.42
3:L5:4695:C:H2'	3:L5:4696:C:O4'	2.19	0.42
88:L5:5292:SPM:H132	19:LO:91:LYS:HB3	2.00	0.42
5:L8:66:A:H2'	5:L8:67:U:C6	2.54	0.42
10:LE:201:ILE:HG22	10:LE:264:ILE:HD12	2.01	0.42
12:LG:70:LEU:HD23	12:LG:70:LEU:HA	1.82	0.42
55:SH:58:LYS:HD2	55:SH:90:LYS:HE3	2.00	0.42
57:SJ:173:VAL:HG21	68:S2:561:A:N7	2.33	0.42
64:SY:100:LYS:HD3	64:SY:107:ARG:NH1	2.33	0.42
68:S2:981:A:H2'	68:S2:982:G:C8	2.54	0.42
68:S2:1189:A:H2'	68:S2:1190:A:H8	1.84	0.42
3:L5:404:U:H4'	29:LY:87:ARG:HH22	1.84	0.42
3:L5:497:G:N2	3:L5:498:C:H41	2.17	0.42
3:L5:1318:C:H2'	3:L5:1319:U:O4'	2.20	0.42
3:L5:2570:U:H2'	3:L5:2571:C:C6	2.54	0.42
3:L5:4125:C:H5'	12:LG:45:ILE:HD12	2.00	0.42
3:L5:4196:OMG:HM23	3:L5:4196:OMG:H1'	1.62	0.42
3:L5:4935:C:H2'	3:L5:4936:G:C8	2.54	0.42
5:L8:88:A:H2'	5:L8:89:U:O4'	2.20	0.42
5:L8:122:G:C6	5:L8:123:U:H1'	2.54	0.42
7:LB:238:LYS:HB2	7:LB:238:LYS:HE2	1.76	0.42
9:LD:179:ARG:HD3	9:LD:179:ARG:HA	1.78	0.42
26:LV:37:LEU:HD23	26:LV:65:VAL:HG12	2.01	0.42
28:LX:149:VAL:HA	28:LX:152:LYS:HG2	2.01	0.42
33:Lc:36:LYS:HG2	33:Lc:37:MET:HE2	2.00	0.42
42:Ll:5:LYS:HB3	42:Ll:5:LYS:HE3	1.87	0.42
50:SA:38:ILE:HD12	50:SA:47:TYR:HB3	2.00	0.42
51:SB:123:ALA:HB2	51:SB:165:ARG:HG3	2.00	0.42
54:SG:121:ILE:HG23	54:SG:124:LEU:HB3	2.01	0.42
55:SH:126:HIS:HA	55:SH:129:ILE:HG12	2.01	0.42
56:SI:150:ASP:HA	56:SI:153:LYS:HD3	2.01	0.42
63:SX:93:PHE:CD2	63:SX:133:LEU:HB3	2.54	0.42
68:S2:149:A:H3'	68:S2:150:A:C8	2.52	0.42
79:SZ:58:LEU:HG	79:SZ:62:VAL:HG21	2.00	0.42
82:Sf:123:SER:HB3	82:Sf:126:CYS:SG	2.59	0.42
83:Sg:173:LEU:HD13	83:Sg:189:ILE:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:CB:322:LYS:HD2	85:CB:322:LYS:HA	1.71	0.42
86:CA:14:GLU:O	86:CA:18:VAL:HG23	2.19	0.42
1:CD:286:TRP:CZ3	72:SK:86:PRO:HG3	2.54	0.42
3:L5:181:C:C4	3:L5:256:G:C2	3.08	0.42
3:L5:2554:U:H3	3:L5:2764:A:H8	1.63	0.42
3:L5:3920:PSU:H2'	3:L5:3921:U:C6	2.54	0.42
3:L5:4500:PSU:H2'	3:L5:4501:U:C6	2.55	0.42
3:L5:4920:C:H2'	3:L5:4921:C:H6	1.83	0.42
5:L8:37:A:OP2	38:Lh:89:ARG:HD2	2.19	0.42
8:LC:132:ALA:C	8:LC:150:LEU:HD23	2.45	0.42
8:LC:298:ILE:O	8:LC:302:LEU:HG	2.20	0.42
20:LP:118:GLN:HG2	20:LP:147:GLU:HG2	2.00	0.42
21:LQ:24:TYR:O	21:LQ:28:LEU:HD23	2.19	0.42
27:LW:93:LYS:HA	27:LW:96:GLN:HG3	2.02	0.42
53:SE:42:LEU:HG	53:SE:46:ILE:HD11	2.01	0.42
60:SO:82:ALA:HB2	60:SO:119:LEU:HD23	2.01	0.42
60:SO:142:ARG:NE	65:Sa:27:ALA:HB2	2.34	0.42
63:SX:70:VAL:HG11	63:SX:94:ILE:HG21	2.00	0.42
68:S2:69:C:H2'	68:S2:70:G:O4'	2.19	0.42
68:S2:452:G:H2'	68:S2:453:C:C6	2.54	0.42
68:S2:529:A:H61	68:S2:555:A:H61	1.66	0.42
68:S2:1395:C:H2'	68:S2:1396:A:O4'	2.19	0.42
68:S2:1610:G:H2'	68:S2:1611:G:C8	2.54	0.42
68:S2:1643:U:H2'	68:S2:1644:C:H6	1.84	0.42
68:S2:1737:G:H2'	68:S2:1738:C:C6	2.54	0.42
72:SK:5:LYS:HB3	72:SK:5:LYS:HE2	1.83	0.42
79:SZ:46:ASN:HB3	79:SZ:80:ARG:HA	2.01	0.42
83:Sg:217:MET:HE3	83:Sg:217:MET:HB2	1.96	0.42
85:CB:770:VAL:HA	85:CB:786:ALA:HA	2.02	0.42
3:L5:1878:G:H2'	3:L5:1879:C:C6	2.54	0.42
3:L5:2060:G:N2	23:LS:115:ALA:HB2	2.35	0.42
3:L5:2365:OMC:HM23	3:L5:2365:OMC:H1'	1.82	0.42
3:L5:2448:G:H2'	3:L5:2449:A:C8	2.54	0.42
3:L5:4146:G:H2'	3:L5:4147:G:C8	2.54	0.42
3:L5:4343:U:H2'	3:L5:4344:U:C6	2.54	0.42
3:L5:4938:A:P	10:LE:183:ARG:HH21	2.42	0.42
3:L5:5057:C:H2'	3:L5:5058:A:C8	2.55	0.42
6:LA:115:CYS:SG	6:LA:124:GLY:HA3	2.59	0.42
9:LD:259:LYS:HE2	9:LD:259:LYS:HB2	1.84	0.42
13:LH:5:LEU:HB2	13:LH:60:TRP:CE3	2.55	0.42
14:LI:140:THR:HG23	14:LI:141:LYS:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LL:56:ARG:HB2	16:LL:72:ALA:HB1	2.01	0.42
36:Lf:45:LYS:HD2	36:Lf:105:LEU:HA	2.01	0.42
51:SB:171:ILE:HA	51:SB:174:ARG:HD3	2.01	0.42
52:SC:66:LEU:HD23	52:SC:66:LEU:HA	1.87	0.42
57:SJ:144:ILE:HG21	68:S2:824:C:H1'	2.01	0.42
68:S2:428:OMU:H2'	68:S2:428:OMU:H6	1.82	0.42
68:S2:1417:C:H42	68:S2:1422:G:H22	1.65	0.42
73:SM:64:LEU:HD13	82:Sf:104:LYS:NZ	2.34	0.42
75:SQ:146:ARG:HH21	84:Et:35:U:P	2.42	0.42
77:ST:122:LYS:HE2	77:ST:122:LYS:HB2	1.87	0.42
79:SZ:49:LEU:HA	79:SZ:83:LEU:HD13	2.01	0.42
84:Et:9:A:O4'	84:Et:46:G:H1'	2.18	0.42
85:CB:60:ARG:HB2	85:CB:63:GLU:HB2	2.00	0.42
85:CB:426:LYS:HZ2	85:CB:446:PRO:HD3	1.84	0.42
3:L5:693:C:H2'	3:L5:694:C:H6	1.84	0.42
3:L5:737:C:C5	3:L5:739:G:H5''	2.53	0.42
3:L5:4530:UR3:H2'	3:L5:4531:U:H2'	2.02	0.42
3:L5:4936:G:C5	10:LE:183:ARG:HD3	2.54	0.42
10:LE:67:ALA:HA	10:LE:69:TYR:CE2	2.54	0.42
49:Lt:48:LYS:HA	49:Lt:48:LYS:HD2	1.85	0.42
49:Lt:147:HIS:ND1	49:Lt:149:HIS:HB3	2.35	0.42
52:SC:256:TRP:CD2	62:SW:68:ARG:HD3	2.55	0.42
58:SL:133:PRO:HB3	58:SL:139:ARG:NH1	2.34	0.42
68:S2:166:A2M:HM'3	68:S2:166:A2M:H1'	1.56	0.42
68:S2:1213:C:H2'	68:S2:1214:A:C8	2.54	0.42
68:S2:1383:A2M:H1'	68:S2:1383:A2M:HM'3	1.54	0.42
68:S2:1587:G:H21	77:ST:77:LYS:NZ	2.18	0.42
68:S2:1609:C:H2'	68:S2:1610:G:H8	1.84	0.42
84:Et:36:U:H5''	84:Et:37:A:H2	1.83	0.42
85:CB:34:THR:HG21	85:CB:218:LEU:HA	2.02	0.42
3:L5:276:C:H2'	39:Li:29:ARG:NH2	2.35	0.42
3:L5:423:G:H2'	3:L5:424:U:C6	2.55	0.42
3:L5:676:C:H2'	3:L5:677:G:H8	1.85	0.42
3:L5:1304:C:H2'	3:L5:1305:C:C6	2.54	0.42
3:L5:1846:G:H2'	3:L5:1847:C:H6	1.83	0.42
3:L5:4080:C:H2'	3:L5:4081:G:H8	1.84	0.42
3:L5:4456:OMC:HM21	7:LB:241:PRO:HD3	2.02	0.42
3:L5:4585:U:H2'	3:L5:4586:G:H8	1.84	0.42
3:L5:5000:G:O2'	7:LB:382:MET:HE1	2.19	0.42
8:LC:26:ALA:HB3	8:LC:266:THR:HA	2.00	0.42
15:LJ:55:TYR:HD1	15:LJ:64:ARG:HH12	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LX:103:LYS:HE3	28:LX:103:LYS:HB2	1.93	0.42
33:Lc:46:VAL:HB	33:Lc:71:VAL:HG22	2.02	0.42
34:Ld:117:LEU:HD23	34:Ld:117:LEU:HA	1.74	0.42
51:SB:184:VAL:HA	51:SB:187:LYS:HD2	2.02	0.42
57:SJ:26:ASP:HB2	67:Se:42:PHE:HZ	1.84	0.42
62:SW:43:LYS:HE2	62:SW:43:LYS:HB3	1.71	0.42
63:SX:48:LYS:HD2	68:S2:483:C:H5''	2.01	0.42
68:S2:93:PSU:H2'	68:S2:94:G:O4'	2.20	0.42
68:S2:959:G:H22	68:S2:963:A:H5''	1.84	0.42
68:S2:1056:PSU:H2'	68:S2:1057:C:O4'	2.19	0.42
68:S2:1222:G:H5''	71:SF:78:MET:HE1	2.01	0.42
68:S2:1540:G:H2'	68:S2:1541:G:H8	1.85	0.42
68:S2:1558:C:H2'	68:S2:1559:C:C6	2.55	0.42
68:S2:1578:U:N3	70:SD:2:ALA:HA	2.34	0.42
68:S2:1842:4AC:O5'	68:S2:1842:4AC:H6	2.20	0.42
75:SQ:88:ILE:HD13	75:SQ:88:ILE:HA	1.92	0.42
80:Sc:44:ARG:HD3	80:Sc:44:ARG:HA	1.89	0.42
81:Sd:20:SER:HB3	81:Sd:27:ARG:NH1	2.34	0.42
85:CB:19:ILE:HD12	85:CB:99:LEU:HD23	2.01	0.42
86:CA:11:THR:HG23	86:CA:13:ALA:H	1.84	0.42
3:L5:1266:G:C5	32:Lb:95:ARG:HB3	2.54	0.42
3:L5:4563:U:H2'	3:L5:4564:A:H8	1.85	0.42
3:L5:4585:U:H2'	3:L5:4586:G:C8	2.54	0.42
3:L5:5030:U:H2'	3:L5:5031:G:H8	1.84	0.42
5:L8:56:G:H21	5:L8:62:A:H5''	1.85	0.42
6:LA:3:ARG:HB2	6:LA:207:VAL:HG22	2.01	0.42
7:LB:206:PRO:HD2	7:LB:209:GLN:NE2	2.34	0.42
8:LC:230:LEU:HD12	8:LC:230:LEU:HA	1.87	0.42
15:LJ:35:ARG:HE	15:LJ:123:ILE:HA	1.85	0.42
22:LR:172:ARG:HD2	22:LR:176:ARG:NH1	2.33	0.42
32:Lb:48:LYS:HE3	32:Lb:49:HIS:CE1	2.54	0.42
46:Lp:51:ALA:HB3	46:Lp:54:ILE:HD12	2.01	0.42
54:SG:23:LYS:HE2	54:SG:41:LEU:HA	2.01	0.42
55:SH:168:HIS:CD2	55:SH:168:HIS:H	2.37	0.42
60:SO:95:ILE:HD12	60:SO:126:ILE:HG23	2.02	0.42
68:S2:575:A:C2	68:S2:576:A2M:H1'	2.55	0.42
68:S2:578:C:H2'	68:S2:579:C:H6	1.85	0.42
68:S2:615:C:H2'	68:S2:616:A:O4'	2.20	0.42
68:S2:634:A:H2'	68:S2:635:G:H8	1.85	0.42
74:SP:30:TYR:O	74:SP:34:MET:HG2	2.20	0.42
85:CB:584:SER:HB3	85:CB:739:ARG:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:262:G:H2'	3:L5:263:G:H8	1.84	0.42
3:L5:1341:U:H2'	3:L5:1342:A:C8	2.54	0.42
3:L5:1812:C:H2'	3:L5:1813:U:C6	2.55	0.42
3:L5:2422:OMC:HM23	3:L5:2422:OMC:H1'	1.72	0.42
3:L5:2521:G:H5'	3:L5:2640:G:H1'	2.01	0.42
3:L5:2640:G:H2'	3:L5:2641:A:H8	1.83	0.42
6:LA:180:LEU:HD21	46:Lp:22:LEU:HB3	2.01	0.42
12:LG:77:PRO:HD2	12:LG:80:ILE:HD12	2.02	0.42
18:LN:94:PHE:CE2	18:LN:96:ARG:HB2	2.54	0.42
47:Lr:103:ARG:HA	47:Lr:103:ARG:HD3	1.72	0.42
54:SG:5:ILE:HD12	54:SG:124:LEU:HD22	2.02	0.42
54:SG:52:ILE:HA	54:SG:111:LEU:HD13	2.02	0.42
56:SI:79:ILE:HG13	56:SI:170:LYS:HD2	2.02	0.42
57:SJ:144:ILE:HG13	68:S2:824:C:C6	2.55	0.42
60:SO:65:ASP:HB3	68:S2:963:A:OP1	2.20	0.42
60:SO:142:ARG:HH12	65:Sa:24:THR:HA	1.84	0.42
64:SY:25:ILE:HD11	64:SY:60:PHE:HZ	1.84	0.42
64:SY:100:LYS:HD3	64:SY:107:ARG:HH11	1.84	0.42
68:S2:570:C:H2'	68:S2:571:U:O4'	2.20	0.42
68:S2:944:A:H2'	68:S2:945:U:C6	2.55	0.42
83:Sg:8:ARG:HD3	83:Sg:52:TYR:CE1	2.54	0.42
83:Sg:154:VAL:HG22	83:Sg:165:ILE:HD11	2.01	0.42
85:CB:692:LEU:HD11	85:CB:738:PRO:HB2	2.02	0.42
86:CA:25:GLY:HA2	86:CA:334:THR:HG22	2.02	0.42
86:CA:83:ASN:HD21	86:CA:104:ASP:HB3	1.85	0.42
3:L5:716:C:OP1	8:LC:317:ASN:HB2	2.20	0.42
3:L5:1400:G:H2'	3:L5:1401:C:C6	2.55	0.42
3:L5:1973:G:H3'	3:L5:1974:U:H2'	2.01	0.42
3:L5:1998:A:H2'	3:L5:1999:A:C8	2.55	0.42
3:L5:4161:G:N2	12:LG:53:ARG:HH21	2.18	0.42
3:L5:4600:G:H1'	3:L5:4609:G:O6	2.19	0.42
3:L5:4688:C:H2'	3:L5:4689:PSU:C6	2.55	0.42
5:L8:76:C:H2'	5:L8:77:A:O4'	2.20	0.42
7:LB:288:GLY:HA3	7:LB:330:PHE:CE1	2.55	0.42
28:LX:155:ILE:HA	38:Lh:37:THR:HG21	2.02	0.42
33:Lc:47:ILE:HB	33:Lc:94:LEU:HG	2.01	0.42
57:SJ:29:LEU:HD23	67:Se:41:ARG:HD2	2.02	0.42
57:SJ:56:ALA:HA	57:SJ:59:GLU:HG2	2.02	0.42
68:S2:5:U:O2'	68:S2:602:G:H4'	2.19	0.42
68:S2:145:G:H2'	68:S2:146:G:H8	1.82	0.42
68:S2:215:G:H2'	68:S2:216:C:H6	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S2:495:U:H2'	68:S2:496:C:O4'	2.20	0.42
68:S2:1285:G:N2	73:SM:58:GLU:HB2	2.35	0.42
68:S2:1822:A:H2'	68:S2:1823:A:C8	2.55	0.42
73:SM:60:MET:HE2	73:SM:60:MET:HB3	1.92	0.42
3:L5:99:A:H2'	3:L5:100:C:O2	2.19	0.42
3:L5:481:G:H2'	3:L5:482:G:C8	2.55	0.42
3:L5:1194:G:H2'	3:L5:1195:G:C8	2.54	0.42
3:L5:1503:A:N6	21:LQ:87:THR:HG21	2.35	0.42
3:L5:1883:G:O6	3:L5:1896:A:H2	2.03	0.42
3:L5:4236:G:H4'	3:L5:4328:G:O2'	2.20	0.42
7:LB:198:ARG:HE	7:LB:198:ARG:HB3	1.76	0.42
7:LB:291:TYR:CE1	7:LB:299:ILE:HG22	2.55	0.42
13:LH:88:PHE:CE2	13:LH:151:ILE:HB	2.55	0.42
14:LI:48:LEU:O	14:LI:139:ARG:HA	2.19	0.42
51:SB:97:LEU:HG	51:SB:232:HIS:CE1	2.55	0.42
57:SJ:111:GLN:O	57:SJ:114:VAL:HG12	2.20	0.42
57:SJ:136:ARG:HD3	57:SJ:160:SER:HA	2.01	0.42
64:SY:90:ARG:HE	64:SY:93:ARG:NH1	2.18	0.42
68:S2:27:A2M:H2'	68:S2:28:U:C6	2.55	0.42
68:S2:376:A:H2'	68:S2:377:G:O4'	2.20	0.42
68:S2:818:A:C8	68:S2:847:A:C6	3.07	0.42
68:S2:1280:G:H2'	68:S2:1281:G:H8	1.85	0.42
68:S2:1446:A:O2'	68:S2:1447:G:H5''	2.20	0.42
68:S2:1522:A:N7	74:SP:128:HIS:HB3	2.35	0.42
72:SK:16:PHE:HE2	72:SK:89:ILE:HG22	1.84	0.42
75:SQ:40:GLU:HA	75:SQ:48:GLN:NE2	2.35	0.42
78:SU:51:LYS:HD3	78:SU:51:LYS:HA	1.58	0.42
79:SZ:80:ARG:HA	79:SZ:80:ARG:HD3	1.83	0.42
3:L5:269:G:H2'	3:L5:270:U:H6	1.84	0.41
3:L5:650:C:H2'	3:L5:651:C:H6	1.85	0.41
3:L5:717:U:H2'	3:L5:718:C:C6	2.55	0.41
3:L5:1504:G:H2'	3:L5:1505:C:C6	2.55	0.41
3:L5:2364:OMG:HM23	3:L5:2364:OMG:H1'	1.66	0.41
3:L5:2864:A:H2'	3:L5:2865:U:C6	2.55	0.41
3:L5:3771:C:H2'	3:L5:3772:U:O4'	2.19	0.41
3:L5:3910:C:H2'	3:L5:3911:C:H6	1.83	0.41
3:L5:3925:OMU:HM23	3:L5:3925:OMU:H1'	1.77	0.41
3:L5:4460:U:H2'	3:L5:4461:C:C6	2.55	0.41
3:L5:4623:OMG:HM23	3:L5:4623:OMG:H1'	1.84	0.41
3:L5:5002:U:H2'	3:L5:5003:U:C6	2.55	0.41
7:LB:348:ARG:HG2	7:LB:349:LYS:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LH:40:HIS:CD2	13:LH:40:HIS:H	2.37	0.41
48:Ls:65:ILE:HD13	48:Ls:65:ILE:HA	1.94	0.41
49:Lt:114:ARG:NE	49:Lt:133:LEU:HD12	2.35	0.41
50:SA:124:VAL:HG12	50:SA:126:ASP:H	1.85	0.41
52:SC:107:LEU:HB3	52:SC:233:LEU:HD21	2.01	0.41
56:SI:193:LYS:HD3	56:SI:193:LYS:HA	1.86	0.41
68:S2:193:C:H2'	68:S2:194:C:C6	2.55	0.41
68:S2:793:G:H2'	68:S2:794:A:H8	1.84	0.41
68:S2:1854:U:H2'	68:S2:1855:G:C8	2.50	0.41
69:SR:24:LEU:HB2	69:SR:58:MET:HE3	2.02	0.41
70:SD:157:MET:HE3	70:SD:157:MET:HB3	1.87	0.41
85:CB:572:LYS:HE2	85:CB:572:LYS:HB2	1.87	0.41
85:CB:601:ARG:HB2	85:CB:708:THR:OG1	2.20	0.41
85:CB:648:LYS:HB3	85:CB:664:ASP:OD1	2.20	0.41
3:L5:37:U:H2'	3:L5:38:A:O4'	2.20	0.41
3:L5:734:G:C2	3:L5:735:G:C8	3.08	0.41
8:LC:142:HIS:CD2	8:LC:249:PHE:H	2.38	0.41
9:LD:56:THR:HG22	9:LD:57:ASN:N	2.35	0.41
10:LE:145:THR:OG1	10:LE:200:LYS:HE3	2.20	0.41
14:LI:180:GLU:O	14:LI:184:MET:HB2	2.20	0.41
35:Le:35:TRP:HH2	35:Le:55:MET:HG2	1.86	0.41
49:Lt:82:ILE:HG22	49:Lt:86:LYS:HE2	2.02	0.41
50:SA:177:MET:HE2	50:SA:177:MET:HB2	1.62	0.41
51:SB:83:LYS:HE2	51:SB:106:THR:HA	2.02	0.41
51:SB:120:MET:HE1	68:S2:987:A:C6	2.55	0.41
52:SC:91:SER:HB2	52:SC:156:ILE:HG23	2.02	0.41
52:SC:210:PRO:HA	52:SC:213:LEU:HB2	2.02	0.41
53:SE:71:LYS:HB3	53:SE:71:LYS:HE2	1.86	0.41
59:SN:20:ARG:HH21	62:SW:56:HIS:HB3	1.85	0.41
68:S2:152:U:H2'	68:S2:153:G:C8	2.55	0.41
68:S2:323:C:H5'	68:S2:324:C:OP1	2.19	0.41
68:S2:982:G:H2'	68:S2:983:A:C8	2.55	0.41
68:S2:1309:C:H1'	82:Sf:133:ALA:HB2	2.02	0.41
69:SR:29:HIS:HA	69:SR:32:LYS:HG2	2.03	0.41
71:SF:193:LYS:HB3	71:SF:193:LYS:HE3	1.81	0.41
73:SM:91:LEU:HD12	73:SM:91:LEU:HA	1.85	0.41
79:SZ:68:ILE:HG22	79:SZ:88:LEU:HD11	2.02	0.41
83:Sg:206:LEU:HD21	83:Sg:218:LEU:HG	2.01	0.41
83:Sg:271:LYS:HD2	83:Sg:271:LYS:HA	1.94	0.41
84:Et:36:U:H5''	84:Et:37:A:C2	2.55	0.41
84:Et:66:U:H2'	84:Et:67:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:CB:152:LYS:HG3	85:CB:203:ILE:HD11	2.01	0.41
3:L5:276:C:H2'	39:Li:29:ARG:HH22	1.85	0.41
3:L5:1613:A:H5''	6:LA:183:GLY:CA	2.51	0.41
3:L5:2520:C:H2'	3:L5:2521:G:H8	1.85	0.41
3:L5:4071:U:H2'	3:L5:4072:C:C6	2.56	0.41
3:L5:4872:G:C2	19:LO:203:VAL:HG23	2.55	0.41
3:L5:4938:A:N3	10:LE:185:PRO:HB3	2.35	0.41
6:LA:130:SER:HB2	6:LA:171:GLY:HA3	2.02	0.41
7:LB:165:HIS:HA	7:LB:179:HIS:O	2.20	0.41
9:LD:41:LYS:HD2	24:LT:93:ILE:HD13	2.02	0.41
10:LE:92:VAL:HG22	10:LE:109:LEU:HD11	2.02	0.41
14:LI:102:MET:HE1	14:LI:114:GLY:H	1.84	0.41
17:LM:96:GLU:O	17:LM:100:ARG:HG2	2.21	0.41
22:LR:105:LEU:HD23	22:LR:138:LEU:HD23	2.01	0.41
29:LY:24:HIS:CE1	29:LY:25:ILE:HG23	2.55	0.41
31:La:7:LYS:HB3	31:La:7:LYS:HE2	1.73	0.41
33:Lc:28:VAL:HG12	33:Lc:95:ALA:HB3	2.02	0.41
56:SI:190:LEU:HD21	56:SI:198:TYR:HD2	1.85	0.41
57:SJ:79:ARG:HH22	68:S2:819:G:H5''	1.85	0.41
59:SN:35:GLU:HA	59:SN:38:TYR:CD2	2.54	0.41
68:S2:348:A:H2'	68:S2:349:A:C8	2.55	0.41
68:S2:958:G:C6	68:S2:959:G:C6	3.08	0.41
68:S2:1296:U:H2'	68:S2:1297:U:C6	2.55	0.41
68:S2:1623:A:N6	76:SS:132:ARG:HD3	2.36	0.41
77:ST:134:ILE:HA	77:ST:137:GLN:HG2	2.02	0.41
85:CB:775:GLN:HA	85:CB:782:PHE:HD1	1.84	0.41
86:CA:66:LYS:HG3	86:CA:67:GLU:CD	2.45	0.41
3:L5:1403:G:N2	3:L5:1415:G:C4	2.88	0.41
3:L5:1662:C:H2'	3:L5:1663:C:H6	1.86	0.41
3:L5:1820:C:H2'	3:L5:1822:U:H5'	2.01	0.41
3:L5:1997:U:H4'	48:Ls:44:ARG:NH1	2.35	0.41
16:LL:110:LEU:O	16:LL:114:VAL:HG13	2.20	0.41
31:La:145:VAL:HG12	39:Li:5:TYR:CZ	2.55	0.41
68:S2:451:G:O5'	68:S2:451:G:H8	2.03	0.41
68:S2:1440:C:H2'	68:S2:1441:U:C6	2.55	0.41
71:SF:56:TYR:CG	71:SF:66:CYS:HB2	2.55	0.41
75:SQ:10:VAL:HG22	75:SQ:25:CYS:HB3	2.02	0.41
83:Sg:73:SER:HB3	83:Sg:117:ASN:HD21	1.85	0.41
84:Et:23:A:H2'	84:Et:24:G:C8	2.56	0.41
85:CB:333:LYS:HG3	85:CB:334:PRO:HD3	2.02	0.41
85:CB:342:ARG:HA	85:CB:342:ARG:HD3	1.75	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:674:G:H2'	3:L5:675:C:C6	2.56	0.41
3:L5:1301:C:H2'	3:L5:1303:A:H62	1.84	0.41
3:L5:1380:G:H4'	3:L5:1381:U:H6	1.85	0.41
3:L5:2065:G:H21	36:Lf:80:ASN:ND2	2.18	0.41
3:L5:2107:C:H2'	3:L5:2108:G:H8	1.85	0.41
3:L5:2481:G:H2'	3:L5:2482:C:H6	1.85	0.41
3:L5:2709:C:H2'	86:CA:263:ARG:NE	2.36	0.41
3:L5:4203:A:C4	3:L5:4221:C:H5'	2.54	0.41
20:LP:107:LEU:HD23	20:LP:107:LEU:H	1.85	0.41
21:LQ:177:ALA:O	21:LQ:184:ARG:HB2	2.21	0.41
33:Lc:29:LEU:HD13	33:Lc:91:VAL:HG21	2.03	0.41
38:Lh:95:LEU:HD22	38:Lh:99:GLU:HG3	2.02	0.41
53:SE:201:HIS:HB3	53:SE:204:SER:HB3	2.03	0.41
59:SN:54:LEU:HB3	59:SN:60:VAL:CG2	2.51	0.41
60:SO:39:ASP:N	60:SO:69:SER:HB3	2.36	0.41
68:S2:1713:C:H2'	68:S2:1714:U:H6	1.86	0.41
71:SF:155:CYS:HB3	71:SF:159:ARG:NH2	2.36	0.41
83:Sg:174:VAL:HB	83:Sg:188:HIS:HB2	2.01	0.41
86:CA:19:THR:HA	86:CA:22:LYS:HE3	2.03	0.41
86:CA:85:CYS:SG	86:CA:89:PHE:HB2	2.60	0.41
86:CA:167:THR:HB	86:CA:202:ILE:O	2.20	0.41
3:L5:18:C:H4'	18:LN:138:PHE:CD1	2.56	0.41
3:L5:1346:C:H2'	3:L5:1347:G:H8	1.85	0.41
3:L5:3656:A:H5''	6:LA:245:ARG:CZ	2.51	0.41
3:L5:3718:A2M:H2	3:L5:3934:G:H1'	2.02	0.41
3:L5:4306:OMU:H1'	3:L5:4306:OMU:HM23	1.69	0.41
3:L5:4743:G:H2'	3:L5:4744:A:C8	2.56	0.41
3:L5:4859:C:H2'	3:L5:4860:G:C8	2.55	0.41
27:LW:54:LEU:HD23	27:LW:54:LEU:HA	1.90	0.41
33:Lc:20:LEU:HD12	33:Lc:20:LEU:HA	1.86	0.41
39:Li:44:ILE:HD13	39:Li:44:ILE:HA	1.96	0.41
50:SA:37:TYR:HA	50:SA:53:ARG:HD3	2.01	0.41
50:SA:42:LYS:HB3	50:SA:42:LYS:HE2	1.85	0.41
52:SC:111:PRO:HB3	52:SC:124:PHE:CE1	2.56	0.41
54:SG:51:ARG:HE	54:SG:51:ARG:HB3	1.70	0.41
54:SG:59:GLN:HB2	54:SG:61:PHE:CD1	2.56	0.41
54:SG:235:SER:HB2	68:S2:786:G:C6	2.55	0.41
55:SH:53:VAL:HG12	55:SH:175:GLY:HA3	2.01	0.41
60:SO:125:LYS:HB3	65:Sa:58:VAL:HG13	2.02	0.41
68:S2:1236:G:H4'	74:SP:133:ILE:HB	2.01	0.41
68:S2:1643:U:H2'	68:S2:1644:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:SK:3:MET:HG3	72:SK:44:HIS:ND1	2.35	0.41
73:SM:51:VAL:HG22	73:SM:77:ILE:HB	2.03	0.41
83:Sg:71:ILE:HD13	83:Sg:71:ILE:HA	1.93	0.41
3:L5:1346:C:H2'	3:L5:1347:G:C8	2.56	0.41
3:L5:2554:U:C2	3:L5:2764:A:N7	2.88	0.41
3:L5:2638:G:N1	3:L5:2718:U:H2'	2.36	0.41
3:L5:4095:G:H2'	3:L5:4096:C:C5	2.56	0.41
3:L5:4770:U:H2'	3:L5:4771:C:C6	2.56	0.41
3:L5:4872:G:N2	19:LO:203:VAL:HG23	2.36	0.41
23:LS:157:ARG:HD2	23:LS:157:ARG:HA	1.88	0.41
24:LT:151:LEU:HD23	24:LT:151:LEU:HA	1.90	0.41
35:Le:119:ALA:HB2	47:Lr:119:ARG:NH1	2.35	0.41
53:SE:120:LYS:HA	53:SE:120:LYS:HD2	1.95	0.41
54:SG:209:TYR:CE1	54:SG:212:LEU:HD22	2.55	0.41
56:SI:74:ARG:NH2	56:SI:112:TRP:HD1	2.19	0.41
56:SI:86:SER:O	68:S2:389:A:H1'	2.21	0.41
58:SL:5:GLN:HE22	58:SL:11:GLN:HB2	1.84	0.41
64:SY:28:LEU:HG	64:SY:68:LYS:HD2	2.01	0.41
68:S2:601:OMG:HM23	68:S2:601:OMG:H1'	1.55	0.41
68:S2:795:A:H2'	68:S2:796:G:C8	2.56	0.41
68:S2:815:U:H2'	68:S2:816:A:C8	2.56	0.41
68:S2:1004:PSU:H2'	68:S2:1005:G:C8	2.55	0.41
68:S2:1433:C:H42	78:SU:92:HIS:CD2	2.39	0.41
68:S2:1651:A:H2'	68:S2:1652:G:H8	1.85	0.41
68:S2:1841:C:H2'	68:S2:1842:4AC:H6	2.01	0.41
70:SD:150:MET:HB3	70:SD:152:PHE:CE1	2.56	0.41
3:L5:646:G:H2'	3:L5:647:G:O4'	2.20	0.41
3:L5:965:G:O2'	3:L5:966:A:H5''	2.21	0.41
5:L8:69:PSU:H2'	5:L8:70:G:O4'	2.21	0.41
5:L8:130:C:H2'	5:L8:131:G:C8	2.56	0.41
8:LC:268:ARG:H	8:LC:268:ARG:HG2	1.71	0.41
16:LL:211:LYS:HE3	16:LL:211:LYS:HB3	1.91	0.41
18:LN:44:ARG:HD3	18:LN:119:TYR:CD2	2.56	0.41
23:LS:156:HIS:CE1	23:LS:174:THR:HG21	2.56	0.41
53:SE:123:LEU:HD21	53:SE:235:TRP:HE3	1.85	0.41
57:SJ:108:ARG:HD2	57:SJ:108:ARG:HA	1.87	0.41
58:SL:21:LYS:HA	58:SL:21:LYS:HD3	1.84	0.41
64:SY:22:GLN:HB2	64:SY:72:PHE:HZ	1.84	0.41
68:S2:440:G:H5''	68:S2:1798:C:O2'	2.21	0.41
68:S2:808:A:H2'	68:S2:809:A:C8	2.56	0.41
68:S2:1218:C:H1'	68:S2:1683:C:H42	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S2:1714:U:H2'	68:S2:1715:A:C8	2.55	0.41
68:S2:1757:G:H5'	68:S2:1758:G:OP2	2.21	0.41
69:SR:86:PRO:HB2	69:SR:88:VAL:O	2.21	0.41
70:SD:45:ARG:HA	70:SD:83:SER:HB3	2.03	0.41
70:SD:141:LYS:HE3	70:SD:179:GLN:HB3	2.03	0.41
72:SK:64:TRP:CE3	81:Sd:23:VAL:HG22	2.56	0.41
74:SP:30:TYR:HD1	74:SP:33:LEU:HD12	1.85	0.41
82:Sf:103:LEU:HD12	82:Sf:105:TYR:CZ	2.56	0.41
82:Sf:107:LYS:HE2	82:Sf:107:LYS:HB2	1.90	0.41
85:CB:374:GLU:HB2	85:CB:493:ASN:O	2.20	0.41
85:CB:420:LEU:HD21	85:CB:463:ASP:HB2	2.03	0.41
86:CA:83:ASN:OD1	86:CA:105:LEU:HG	2.21	0.41
86:CA:133:THR:O	86:CA:342:LEU:HB2	2.20	0.41
3:L5:268:G:H2'	3:L5:269:G:C8	2.54	0.41
3:L5:399:G:H2'	3:L5:400:A2M:H8	2.03	0.41
3:L5:696:C:C5	10:LE:222:LEU:HD12	2.56	0.41
3:L5:705:G:H2'	3:L5:706:C:C6	2.56	0.41
3:L5:750:U:H2'	3:L5:751:G:H8	1.86	0.41
3:L5:1241:C:O2	32:Lb:115:GLY:HA2	2.20	0.41
3:L5:1284:G:O2'	3:L5:1285:U:H5''	2.21	0.41
3:L5:1468:C:H2'	3:L5:1469:C:C6	2.55	0.41
3:L5:3770:U:H2'	3:L5:3771:C:H6	1.85	0.41
3:L5:4412:C:H2'	3:L5:4413:C:H6	1.85	0.41
3:L5:4578:G:H2'	3:L5:4579:PSU:C6	2.55	0.41
4:L7:108:G:OP1	9:LD:273:LEU:HB2	2.20	0.41
4:L7:111:C:H2'	4:L7:112:U:O4'	2.21	0.41
6:LA:171:GLY:O	46:Lp:68:ALA:HB2	2.20	0.41
12:LG:26:LYS:HB3	12:LG:27:VAL:H	1.55	0.41
29:LY:38:LEU:HD23	29:LY:38:LEU:HA	1.86	0.41
30:LZ:12:LEU:HD22	30:LZ:134:LEU:HD22	2.02	0.41
33:Lc:77:ASN:OD1	33:Lc:80:GLU:HG2	2.21	0.41
42:Ll:41:ARG:HA	42:Ll:41:ARG:HD2	1.72	0.41
43:Lm:80:PRO:O	43:Lm:84:GLN:HG2	2.21	0.41
50:SA:80:ARG:HH21	50:SA:126:ASP:HB2	1.86	0.41
53:SE:49:ARG:HG3	53:SE:55:ALA:O	2.21	0.41
53:SE:149:TYR:HB3	54:SG:209:TYR:CE1	2.56	0.41
55:SH:63:PHE:HA	55:SH:95:ILE:O	2.21	0.41
62:SW:42:MET:HE2	62:SW:42:MET:HB3	1.86	0.41
63:SX:105:PHE:HB3	63:SX:112:VAL:HG21	2.03	0.41
64:SY:8:ARG:HB2	64:SY:26:ASP:OD1	2.21	0.41
64:SY:24:VAL:HG22	64:SY:72:PHE:HD1	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S2:184:G:H2'	68:S2:185:G:C8	2.56	0.41
68:S2:314:U:H2'	68:S2:315:C:C6	2.56	0.41
68:S2:591:U:H4'	68:S2:592:C:H5''	2.02	0.41
68:S2:879:C:H3'	68:S2:880:G:H21	1.85	0.41
68:S2:1037:G:H4'	68:S2:1845:A:H4'	2.03	0.41
68:S2:1362:U:H5''	68:S2:1363:C:C5	2.56	0.41
68:S2:1729:U:H3	68:S2:1805:G:H1	1.68	0.41
68:S2:1737:G:H2'	68:S2:1738:C:H6	1.86	0.41
72:SK:27:VAL:HB	72:SK:43:LEU:HD12	2.01	0.41
73:SM:53:ALA:HB3	73:SM:107:SER:HB2	2.03	0.41
76:SS:24:ARG:C	76:SS:55:ARG:HD2	2.46	0.41
76:SS:94:LYS:HA	76:SS:94:LYS:HD3	1.81	0.41
78:SU:53:PRO:HB3	78:SU:89:ILE:HG13	2.03	0.41
82:Sf:116:ARG:HG2	82:Sf:131:PHE:CE2	2.55	0.41
83:Sg:168:CYS:HB3	83:Sg:198:VAL:HB	2.03	0.41
85:CB:225:LEU:HD12	85:CB:260:LEU:HB3	2.02	0.41
3:L5:31:U:H2'	3:L5:32:G:O4'	2.21	0.41
3:L5:677:G:H2'	3:L5:678:C:C6	2.57	0.41
3:L5:1730:U:H4'	24:LT:100:LYS:HB2	2.03	0.41
3:L5:3898:G:H5'	7:LB:254:ILE:HG13	2.02	0.41
3:L5:4637:OMG:HM23	3:L5:4637:OMG:H1'	1.70	0.41
88:L5:5263:SPM:HN41	88:L5:5263:SPM:H111	1.64	0.41
4:L7:92:C:H2'	4:L7:93:G:H8	1.86	0.41
5:L8:29:G:H5''	16:LL:27:ASN:HB3	2.03	0.41
5:L8:36:G:C5	38:Lh:89:ARG:HD3	2.56	0.41
7:LB:29:VAL:HA	7:LB:220:ILE:HD13	2.03	0.41
12:LG:218:LEU:O	12:LG:222:ILE:HG12	2.21	0.41
21:LQ:43:PHE:CD2	21:LQ:133:GLY:HA3	2.56	0.41
40:Lj:19:CYS:SG	40:Lj:34:CYS:HB2	2.60	0.41
51:SB:42:ARG:HH21	51:SB:232:HIS:HD1	1.69	0.41
59:SN:49:GLN:HA	59:SN:52:VAL:HG22	2.03	0.41
61:SV:17:CYS:HB2	61:SV:56:CYS:HB2	2.03	0.41
61:SV:67:ASP:HA	61:SV:70:LEU:HB3	2.02	0.41
62:SW:105:THR:HB	62:SW:110:ILE:HG12	2.02	0.41
68:S2:184:G:H2'	68:S2:185:G:H8	1.86	0.41
68:S2:293:C:O2'	68:S2:294:U:H3'	2.20	0.41
68:S2:321:C:H2'	68:S2:322:C:C6	2.56	0.41
68:S2:694:G:H5''	68:S2:730:C:C5	2.56	0.41
68:S2:737:G:H3'	68:S2:738:C:H4'	2.03	0.41
68:S2:1285:G:H21	73:SM:58:GLU:HB2	1.86	0.41
68:S2:1308:U:H2'	68:S2:1309:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SF:153:LEU:HA	71:SF:153:LEU:HD23	1.80	0.41
85:CB:50:ARG:HH21	85:CB:55:ARG:HA	1.85	0.41
85:CB:190:SER:HB2	85:CB:204:MET:HE2	2.03	0.41
3:L5:473:C:H2'	3:L5:474:C:H6	1.86	0.40
3:L5:500:G:O2'	3:L5:504:G:H3'	2.21	0.40
3:L5:718:C:OP1	11:LF:217:ARG:HD3	2.21	0.40
3:L5:1188:C:H2'	3:L5:1189:G:C8	2.57	0.40
3:L5:1760:G:O3'	3:L5:1761:G:H2'	2.21	0.40
3:L5:1811:G:H2'	3:L5:1812:C:C6	2.56	0.40
3:L5:3619:G:H4'	22:LR:79:GLY:O	2.21	0.40
3:L5:4618:OMG:HM23	3:L5:4618:OMG:H1'	1.74	0.40
88:L5:5288:SPM:H82	88:L5:5288:SPM:H22	2.03	0.40
5:L8:130:C:H2'	5:L8:131:G:H8	1.85	0.40
5:L8:141:C:H2'	5:L8:142:U:C6	2.55	0.40
9:LD:236:MET:O	9:LD:239:MET:HG3	2.21	0.40
20:LP:37:LYS:HB3	20:LP:37:LYS:HE2	1.78	0.40
26:LV:71:GLU:HG2	26:LV:72:LEU:HG	2.04	0.40
50:SA:38:ILE:HG21	50:SA:47:TYR:HD2	1.86	0.40
50:SA:148:CYS:SG	50:SA:163:CYS:N	2.94	0.40
54:SG:59:GLN:HB2	54:SG:61:PHE:HD1	1.86	0.40
54:SG:230:LYS:HG3	68:S2:786:G:H5'	2.02	0.40
55:SH:33:ASN:ND2	55:SH:36:LEU:HB2	2.37	0.40
56:SI:27:TYR:HB2	68:S2:381:C:N4	2.36	0.40
57:SJ:111:GLN:HE21	57:SJ:111:GLN:HB2	1.62	0.40
57:SJ:119:LEU:HD23	57:SJ:159:PHE:CE1	2.56	0.40
58:SL:20:LYS:HD2	58:SL:20:LYS:HA	1.92	0.40
59:SN:132:LYS:HD3	59:SN:132:LYS:HA	1.89	0.40
60:SO:45:THR:OG1	60:SO:49:GLY:HA2	2.21	0.40
68:S2:159:A2M:H1'	68:S2:159:A2M:HM'3	1.50	0.40
68:S2:190:G:C6	68:S2:208:G:C6	3.08	0.40
68:S2:941:C:H2'	68:S2:942:G:H8	1.84	0.40
68:S2:944:A:H2'	68:S2:945:U:H6	1.86	0.40
68:S2:1121:G:C6	68:S2:1122:A:C5	3.09	0.40
68:S2:1205:C:H2'	68:S2:1206:G:C8	2.56	0.40
68:S2:1563:G:H4'	77:ST:115:LYS:NZ	2.36	0.40
71:SF:141:VAL:HG12	71:SF:146:ARG:HG2	2.02	0.40
75:SQ:51:LEU:O	75:SQ:54:PRO:HD2	2.21	0.40
82:Sf:123:SER:HB3	82:Sf:126:CYS:HB2	2.03	0.40
85:CB:512:LYS:HE3	85:CB:512:LYS:HB3	1.88	0.40
86:CA:32:LEU:O	86:CA:36:VAL:HG13	2.20	0.40
3:L5:74:G:H5'	16:LL:59:VAL:HG13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:377:A:H2'	3:L5:378:A:O4'	2.21	0.40
3:L5:398:A2M:HM'3	3:L5:398:A2M:H1'	1.51	0.40
3:L5:1392:A:H2'	3:L5:1393:G:C8	2.55	0.40
3:L5:1404:G:N7	3:L5:1408:G:N2	2.69	0.40
3:L5:1633:G:H5'	3:L5:1634:A:OP1	2.21	0.40
3:L5:1840:G:H1'	11:LF:111:LEU:HD23	2.03	0.40
3:L5:2267:U:C6	3:L5:2270:G:H4'	2.56	0.40
3:L5:2730:U:H2'	3:L5:2731:C:C6	2.56	0.40
3:L5:3732:A:H2'	3:L5:3733:A:H8	1.86	0.40
3:L5:3851:PSU:H2'	3:L5:3852:A:O4'	2.21	0.40
3:L5:4273:A:H2'	3:L5:4274:A:C8	2.56	0.40
13:LH:52:LYS:HD2	13:LH:52:LYS:HA	1.84	0.40
13:LH:91:LYS:HG2	13:LH:145:ILE:HG13	2.01	0.40
15:LJ:37:ALA:HB2	15:LJ:50:PHE:HE1	1.87	0.40
27:LW:74:ARG:HD3	27:LW:74:ARG:HA	1.83	0.40
29:LY:1:MET:HB2	29:LY:1:MET:HE3	1.74	0.40
53:SE:106:LYS:HB3	53:SE:108:ARG:NH2	2.35	0.40
53:SE:128:LYS:HG2	53:SE:140:VAL:HG22	2.03	0.40
56:SI:40:PRO:HD2	56:SI:59:ARG:NH1	2.36	0.40
64:SY:94:HIS:HB3	64:SY:96:LEU:HD13	2.03	0.40
68:S2:183:G:C2	68:S2:184:G:C8	3.09	0.40
68:S2:866:PSU:H2'	68:S2:867:OMG:C8	2.56	0.40
68:S2:1533:A:N3	68:S2:1533:A:H2'	2.35	0.40
68:S2:1610:G:H2'	68:S2:1611:G:H8	1.85	0.40
68:S2:1624:U:H2'	68:S2:1625:U:O4'	2.21	0.40
75:SQ:8:GLN:HG3	75:SQ:99:TYR:CD1	2.56	0.40
85:CB:259:LYS:H	85:CB:259:LYS:HG2	1.65	0.40
85:CB:309:LYS:HE3	85:CB:309:LYS:HB3	1.91	0.40
3:L5:60:G:H2'	3:L5:61:A:C8	2.57	0.40
3:L5:1307:A:H2'	3:L5:1308:C:C6	2.56	0.40
3:L5:1445:U:H5'	3:L5:1446:C:OP2	2.21	0.40
3:L5:1824:G:H2'	3:L5:1825:A:C8	2.56	0.40
3:L5:2045:G:O2'	3:L5:2046:G:H5''	2.21	0.40
3:L5:2431:A:OP1	42:Ll:22:PRO:HG3	2.22	0.40
3:L5:3729:U:H2'	3:L5:3730:U:C6	2.57	0.40
3:L5:4947:U:H2'	3:L5:4948:C:C6	2.57	0.40
3:L5:4965:U:H5''	7:LB:128:LYS:NZ	2.36	0.40
3:L5:4970:C:C2	3:L5:4971:A:C8	3.09	0.40
6:LA:7:GLY:HA2	6:LA:10:LYS:HG3	2.04	0.40
22:LR:135:LYS:HE2	22:LR:135:LYS:HB3	1.89	0.40
28:LX:88:LYS:HG3	86:CA:259:MET:SD	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Ll:26:TRP:CD1	42:Ll:26:TRP:H	2.38	0.40
50:SA:145:ILE:HG12	50:SA:159:ILE:HD13	2.04	0.40
51:SB:38:MET:HE2	51:SB:38:MET:HB2	1.96	0.40
55:SH:75:ILE:HG23	55:SH:79:LEU:HD23	2.03	0.40
59:SN:15:ALA:O	68:S2:1016:U:H5'	2.21	0.40
60:SO:124:MET:HG3	60:SO:125:LYS:H	1.86	0.40
68:S2:14:C:H2'	68:S2:15:U:C6	2.56	0.40
68:S2:1464:C:H4'	69:SR:60:ARG:NH2	2.36	0.40
70:SD:59:LEU:HD23	70:SD:66:ILE:CG1	2.51	0.40
72:SK:1:MET:HB2	72:SK:2:LEU:H	1.71	0.40
72:SK:10:ALA:O	72:SK:13:GLU:HG2	2.21	0.40
72:SK:72:THR:O	72:SK:76:ILE:HG12	2.20	0.40
82:Sf:108:VAL:HA	82:Sf:113:LYS:O	2.21	0.40
85:CB:509:VAL:HG12	85:CB:572:LYS:HG3	2.02	0.40
85:CB:751:CYS:SG	85:CB:755:VAL:HG23	2.60	0.40
3:L5:182:G:H2'	3:L5:183:C:H4'	2.03	0.40
3:L5:424:U:H2'	3:L5:425:U:C6	2.56	0.40
3:L5:461:G:H2'	3:L5:462:G:H8	1.85	0.40
3:L5:473:C:H2'	3:L5:474:C:C6	2.57	0.40
3:L5:1340:OMC:HM23	3:L5:1340:OMC:H1'	1.85	0.40
3:L5:2506:G:H2'	3:L5:2506:G:N3	2.36	0.40
3:L5:2520:C:H2'	3:L5:2521:G:C8	2.57	0.40
3:L5:4573:G:H2'	3:L5:4574:U:C6	2.56	0.40
3:L5:4578:G:H2'	3:L5:4579:PSU:H6	1.87	0.40
5:L8:19:C:H2'	5:L8:20:A:C8	2.56	0.40
8:LC:144:ILE:O	8:LC:144:ILE:HG13	2.21	0.40
29:LY:85:VAL:HG11	29:LY:99:ILE:HD11	2.03	0.40
33:Lc:80:GLU:HG2	33:Lc:80:GLU:H	1.66	0.40
53:SE:21:ASP:OD1	53:SE:24:THR:HG22	2.22	0.40
60:SO:142:ARG:HB3	65:Sa:22:ARG:HD3	2.04	0.40
67:Se:25:LYS:HD3	67:Se:25:LYS:HA	1.91	0.40
68:S2:573:U:O2	68:S2:576:A2M:H8	2.22	0.40
68:S2:907:G:H2'	68:S2:908:A:C8	2.55	0.40
83:Sg:112:ALA:HB2	83:Sg:154:VAL:HG13	2.02	0.40
83:Sg:181:ASN:HD21	83:Sg:185:LYS:NZ	2.19	0.40
3:L5:385:A:N3	3:L5:387:G:H5''	2.37	0.40
3:L5:1194:G:H2'	3:L5:1195:G:H8	1.85	0.40
3:L5:1974:U:OP1	49:Lt:77:ALA:HA	2.21	0.40
3:L5:2844:A:O2'	3:L5:4631:G:H4'	2.21	0.40
3:L5:4112:C:H2'	3:L5:4113:U:O4'	2.21	0.40
3:L5:4524:G:N3	7:LB:252:ALA:HB1	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L5:4736:C:H2'	3:L5:4737:G:C8	2.55	0.40
3:L5:4957:C:H2'	3:L5:4958:C:H6	1.87	0.40
19:LO:122:ALA:HA	23:LS:162:GLN:HB3	2.03	0.40
22:LR:65:LYS:HB3	22:LR:65:LYS:HE2	1.80	0.40
49:Lt:39:PRO:HB2	49:Lt:43:GLY:HA3	2.03	0.40
50:SA:180:ARG:O	50:SA:184:ARG:HB2	2.21	0.40
52:SC:167:ARG:HB3	52:SC:177:PRO:HB2	2.03	0.40
54:SG:22:ARG:H	54:SG:22:ARG:HD2	1.87	0.40
55:SH:160:LYS:HE3	55:SH:160:LYS:HB3	1.79	0.40
60:SO:141:ARG:CZ	65:Sa:22:ARG:HH21	2.34	0.40
68:S2:669:A:H2'	68:S2:670:A:C8	2.56	0.40
72:SK:58:VAL:HG21	72:SK:69:TRP:HB3	2.03	0.40
75:SQ:8:GLN:HA	75:SQ:99:TYR:CZ	2.56	0.40
83:Sg:191:HIS:CD2	83:Sg:195:LEU:HD11	2.57	0.40
85:CB:176:GLN:O	85:CB:180:ARG:HG2	2.21	0.40
85:CB:323:LEU:HD12	85:CB:323:LEU:HA	1.88	0.40
86:CA:181:PRO:HB2	86:CA:204:ASN:HB2	2.04	0.40
86:CA:205:PRO:HB2	86:CA:210:LYS:HE2	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	CD	51/408 (12%)	50 (98%)	1 (2%)	0	100	100
2	CI	29/31 (94%)	28 (97%)	1 (3%)	0	100	100
6	LA	246/248 (99%)	234 (95%)	12 (5%)	0	100	100
7	LB	400/402 (100%)	385 (96%)	15 (4%)	0	100	100
8	LC	366/368 (100%)	351 (96%)	15 (4%)	0	100	100
9	LD	291/293 (99%)	283 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	LE	236/250 (94%)	221 (94%)	15 (6%)	0	100	100
11	LF	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
12	LG	239/241 (99%)	229 (96%)	10 (4%)	0	100	100
13	LH	188/190 (99%)	176 (94%)	12 (6%)	0	100	100
14	LI	201/213 (94%)	198 (98%)	3 (2%)	0	100	100
15	LJ	168/176 (96%)	163 (97%)	4 (2%)	1 (1%)	21	51
16	LL	208/210 (99%)	200 (96%)	7 (3%)	1 (0%)	24	54
17	LM	137/139 (99%)	133 (97%)	4 (3%)	0	100	100
18	LN	201/203 (99%)	197 (98%)	4 (2%)	0	100	100
19	LO	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
20	LP	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
21	LQ	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
22	LR	185/187 (99%)	181 (98%)	4 (2%)	0	100	100
23	LS	173/175 (99%)	168 (97%)	5 (3%)	0	100	100
24	LT	157/159 (99%)	154 (98%)	3 (2%)	0	100	100
25	LU	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
26	LV	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
27	LW	112/124 (90%)	109 (97%)	3 (3%)	0	100	100
28	LX	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
29	LY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
30	LZ	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
31	La	145/147 (99%)	139 (96%)	6 (4%)	0	100	100
32	Lb	105/121 (87%)	99 (94%)	6 (6%)	0	100	100
33	Lc	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
34	Ld	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
35	Le	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
36	Lf	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
37	Lg	112/114 (98%)	112 (100%)	0	0	100	100
38	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
39	Li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
40	Lj	84/86 (98%)	82 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	Lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
42	Ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
43	Lm	50/52 (96%)	50 (100%)	0	0	100	100
44	Ln	22/24 (92%)	22 (100%)	0	0	100	100
45	Lo	103/105 (98%)	98 (95%)	5 (5%)	0	100	100
46	Lp	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
47	Lr	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
48	Ls	194/196 (99%)	183 (94%)	11 (6%)	0	100	100
49	Lt	128/157 (82%)	104 (81%)	24 (19%)	0	100	100
50	SA	219/221 (99%)	207 (94%)	12 (6%)	0	100	100
51	SB	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
52	SC	218/222 (98%)	207 (95%)	11 (5%)	0	100	100
53	SE	260/262 (99%)	246 (95%)	14 (5%)	0	100	100
54	SG	235/237 (99%)	218 (93%)	17 (7%)	0	100	100
55	SH	182/189 (96%)	166 (91%)	16 (9%)	0	100	100
56	SI	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
57	SJ	183/185 (99%)	173 (94%)	10 (6%)	0	100	100
58	SL	151/153 (99%)	143 (95%)	8 (5%)	0	100	100
59	SN	148/150 (99%)	146 (99%)	2 (1%)	0	100	100
60	SO	135/140 (96%)	122 (90%)	13 (10%)	0	100	100
61	SV	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
62	SW	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
63	SX	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
64	SY	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
65	Sa	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
66	Sb	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
67	Se	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
69	SR	133/135 (98%)	129 (97%)	4 (3%)	0	100	100
70	SD	225/227 (99%)	219 (97%)	6 (3%)	0	100	100
71	SF	187/189 (99%)	177 (95%)	10 (5%)	0	100	100
72	SK	96/98 (98%)	90 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	SM	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
74	SP	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
75	SQ	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
76	SS	143/145 (99%)	133 (93%)	10 (7%)	0	100	100
77	ST	141/143 (99%)	139 (99%)	2 (1%)	0	100	100
78	SU	102/104 (98%)	97 (95%)	5 (5%)	0	100	100
79	SZ	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
80	Sc	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
81	Sd	53/55 (96%)	53 (100%)	0	0	100	100
82	Sf	65/67 (97%)	59 (91%)	6 (9%)	0	100	100
83	Sg	311/313 (99%)	283 (91%)	28 (9%)	0	100	100
85	CB	842/856 (98%)	807 (96%)	35 (4%)	0	100	100
86	CA	350/356 (98%)	329 (94%)	21 (6%)	0	100	100
All	All	12905/13527 (95%)	12310 (95%)	593 (5%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	LJ	123	ILE
16	LL	62	PRO

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	CD	46/328 (14%)	46 (100%)	0	100	100
2	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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
12	LG	203/205 (99%)	203 (100%)	0	100	100
13	LH	169/169 (100%)	169 (100%)	0	100	100
14	LI	175/180 (97%)	175 (100%)	0	100	100
15	LJ	143/148 (97%)	143 (100%)	0	100	100
16	LL	176/176 (100%)	175 (99%)	1 (1%)	78	93
17	LM	118/118 (100%)	116 (98%)	2 (2%)	53	82
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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	SA	183/183 (100%)	183 (100%)	0	100	100
51	SB	195/195 (100%)	195 (100%)	0	100	100
52	SC	186/188 (99%)	186 (100%)	0	100	100
53	SE	224/224 (100%)	224 (100%)	0	100	100
54	SG	207/207 (100%)	207 (100%)	0	100	100
55	SH	166/169 (98%)	166 (100%)	0	100	100
56	SI	178/178 (100%)	178 (100%)	0	100	100
57	SJ	161/161 (100%)	161 (100%)	0	100	100
58	SL	137/137 (100%)	137 (100%)	0	100	100
59	SN	130/130 (100%)	130 (100%)	0	100	100
60	SO	107/110 (97%)	106 (99%)	1 (1%)	70	90
61	SV	67/67 (100%)	67 (100%)	0	100	100
62	SW	112/112 (100%)	112 (100%)	0	100	100
63	SX	113/113 (100%)	113 (100%)	0	100	100
64	SY	113/113 (100%)	113 (100%)	0	100	100
65	Sa	89/89 (100%)	89 (100%)	0	100	100
66	Sb	75/75 (100%)	75 (100%)	0	100	100
67	Se	47/47 (100%)	47 (100%)	0	100	100
69	SR	122/122 (100%)	122 (100%)	0	100	100
70	SD	190/190 (100%)	190 (100%)	0	100	100
71	SF	159/159 (100%)	159 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	SK	89/89 (100%)	89 (100%)	0	100	100
73	SM	102/104 (98%)	102 (100%)	0	100	100
74	SP	107/107 (100%)	107 (100%)	0	100	100
75	SQ	119/119 (100%)	119 (100%)	0	100	100
76	SS	126/126 (100%)	126 (100%)	0	100	100
77	ST	113/113 (100%)	112 (99%)	1 (1%)	70	90
78	SU	94/94 (100%)	94 (100%)	0	100	100
79	SZ	66/66 (100%)	66 (100%)	0	100	100
80	Sc	57/57 (100%)	57 (100%)	0	100	100
81	Sd	48/48 (100%)	48 (100%)	0	100	100
82	Sf	60/60 (100%)	60 (100%)	0	100	100
83	Sg	272/272 (100%)	272 (100%)	0	100	100
85	CB	722/728 (99%)	722 (100%)	0	100	100
86	CA	303/305 (99%)	303 (100%)	0	100	100
All	All	11213/11582 (97%)	11208 (100%)	5 (0%)	100	100

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	LL	59	VAL
17	LM	31	ILE
17	LM	38	VAL
60	SO	138	ASP
77	ST	2	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (75) such sidechains are listed below:

Mol	Chain	Res	Type
6	LA	97	ASN
7	LB	184	GLN
7	LB	209	GLN
8	LC	43	ASN
8	LC	347	HIS
9	LD	111	ASN
9	LD	191	ASN
10	LE	228	GLN

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Mol	Chain	Res	Type
13	LH	102	ASN
14	LI	59	GLN
14	LI	73	ASN
16	LL	19	GLN
16	LL	104	ASN
17	LM	20	HIS
17	LM	34	ASN
17	LM	48	GLN
17	LM	125	ASN
20	LP	25	HIS
20	LP	97	ASN
21	LQ	21	GLN
21	LQ	162	HIS
23	LS	91	HIS
24	LT	66	ASN
24	LT	131	GLN
25	LU	38	ASN
26	LV	50	ASN
28	LX	125	ASN
30	LZ	78	ASN
30	LZ	127	ASN
31	La	28	HIS
32	Lb	60	ASN
34	Ld	121	ASN
35	Le	92	ASN
35	Le	107	ASN
36	Lf	21	GLN
36	Lf	80	ASN
37	Lg	100	GLN
37	Lg	114	GLN
38	Lh	20	GLN
38	Lh	62	ASN
39	Li	15	HIS
40	Lj	66	HIS
45	Lo	25	GLN
48	Ls	68	HIS
48	Ls	71	ASN
48	Ls	127	ASN
49	Lt	66	ASN
50	SA	50	ASN
51	SB	75	GLN
52	SC	172	ASN

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Mol	Chain	Res	Type
53	SE	214	ASN
54	SG	56	ASN
55	SH	97	GLN
56	SI	52	ASN
57	SJ	75	ASN
57	SJ	111	GLN
58	SL	18	GLN
58	SL	106	HIS
61	SV	47	ASN
62	SW	98	GLN
63	SX	16	HIS
64	SY	112	ASN
70	SD	74	GLN
70	SD	226	GLN
71	SF	114	ASN
74	SP	35	GLN
75	SQ	11	GLN
75	SQ	48	GLN
78	SU	81	GLN
82	Sf	151	ASN
83	Sg	181	ASN
83	Sg	196	ASN
85	CB	18	ASN
85	CB	803	ASN
86	CA	203	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	L5	3643/5070 (71%)	776 (21%)	15 (0%)
4	L7	119/120 (99%)	10 (8%)	0
5	L8	155/156 (99%)	26 (16%)	0
68	S2	1715/1740 (98%)	409 (23%)	4 (0%)
84	Et	73/75 (97%)	25 (34%)	0
All	All	5705/7161 (79%)	1246 (21%)	19 (0%)

All (1246) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	L5	21	G
3	L5	25	A

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Mol	Chain	Res	Type
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
3	L5	65	A
3	L5	73	A
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	127	G
3	L5	128	C
3	L5	132	G
3	L5	133	C
3	L5	135	G
3	L5	136	C
3	L5	140	G
3	L5	144	G
3	L5	146	G
3	L5	151	G
3	L5	159	C
3	L5	165	A
3	L5	182	G
3	L5	183	C
3	L5	184	U
3	L5	185	C
3	L5	186	G
3	L5	187	U
3	L5	188	G
3	L5	189	G
3	L5	200	U
3	L5	209	U
3	L5	216	C
3	L5	218	A
3	L5	220	C
3	L5	237	G

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Mol	Chain	Res	Type
3	L5	255	C
3	L5	256	G
3	L5	261	G
3	L5	265	C
3	L5	266	C
3	L5	267	G
3	L5	275	C
3	L5	276	C
3	L5	280	G
3	L5	292	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	440	U
3	L5	449	C
3	L5	450	G
3	L5	452	A
3	L5	453	G
3	L5	454	U
3	L5	456	C
3	L5	457	G
3	L5	464	G
3	L5	465	G
3	L5	467	U
3	L5	468	U
3	L5	472	C
3	L5	484	U
3	L5	485	C

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Mol	Chain	Res	Type
3	L5	486	C
3	L5	489	C
3	L5	493	G
3	L5	494	U
3	L5	496	G
3	L5	497	G
3	L5	498	C
3	L5	499	G
3	L5	502	C
3	L5	503	C
3	L5	504	G
3	L5	505	G
3	L5	507	G
3	L5	509	A
3	L5	510	U
3	L5	512	U
3	L5	513	U
3	L5	514	U
3	L5	516	C
3	L5	517	C
3	L5	518	G
3	L5	519	C
3	L5	643	C
3	L5	644	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	686	A
3	L5	687	U
3	L5	696	C
3	L5	704	C
3	L5	708	G
3	L5	729	G
3	L5	730	G
3	L5	731	G

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Mol	Chain	Res	Type
3	L5	738	C
3	L5	739	G
3	L5	742	G
3	L5	746	A
3	L5	750	U
3	L5	758	G
3	L5	904	C
3	L5	905	C
3	L5	906	C
3	L5	913	U
3	L5	914	U
3	L5	915	A
3	L5	916	C
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
3	L5	943	A
3	L5	945	U
3	L5	946	C
3	L5	956	A
3	L5	958	G
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	968	C
3	L5	969	C
3	L5	970	G
3	L5	971	U
3	L5	982	U
3	L5	985	C
3	L5	986	C
3	L5	989	U
3	L5	1070	G

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Mol	Chain	Res	Type
3	L5	1071	C
3	L5	1075	G
3	L5	1076	C
3	L5	1082	C
3	L5	1083	U
3	L5	1095	A
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	1189	G
3	L5	1200	G
3	L5	1202	C
3	L5	1203	G
3	L5	1206	C
3	L5	1210	C
3	L5	1211	G
3	L5	1214	C
3	L5	1218	G
3	L5	1219	G
3	L5	1222	A
3	L5	1242	G
3	L5	1246	G
3	L5	1253	G
3	L5	1254	A
3	L5	1255	A
3	L5	1257	A
3	L5	1262	G
3	L5	1266	G
3	L5	1267	C
3	L5	1269	G
3	L5	1270	A
3	L5	1271	G
3	L5	1272	C
3	L5	1273	G
3	L5	1275	G

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Mol	Chain	Res	Type
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	1314	C
3	L5	1326	A2M
3	L5	1337	A
3	L5	1354	A
3	L5	1359	G
3	L5	1365	C
3	L5	1366	G
3	L5	1367	C
3	L5	1378	C
3	L5	1379	C
3	L5	1387	A
3	L5	1394	G
3	L5	1397	A
3	L5	1398	A
3	L5	1404	G
3	L5	1407	C
3	L5	1409	C
3	L5	1410	U
3	L5	1411	C
3	L5	1415	G
3	L5	1416	G
3	L5	1417	C
3	L5	1418	C
3	L5	1420	A
3	L5	1421	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

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Mol	Chain	Res	Type
3	L5	1480	C
3	L5	1483	C
3	L5	1497	A
3	L5	1498	G
3	L5	1501	C
3	L5	1502	G
3	L5	1516	G
3	L5	1517	G
3	L5	1524	A2M
3	L5	1534	A2M
3	L5	1535	C
3	L5	1537	A
3	L5	1547	A
3	L5	1564	A
3	L5	1566	C
3	L5	1574	G
3	L5	1578	U
3	L5	1586	G
3	L5	1591	U
3	L5	1596	U
3	L5	1612	G
3	L5	1624	G
3	L5	1625	OMG
3	L5	1626	G
3	L5	1631	A
3	L5	1633	G
3	L5	1634	A
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	1694	C
3	L5	1697	G
3	L5	1700	G
3	L5	1701	A
3	L5	1703	C
3	L5	1704	C
3	L5	1705	G
3	L5	1706	A
3	L5	1718	C

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Mol	Chain	Res	Type
3	L5	1719	A
3	L5	1721	G
3	L5	1731	C
3	L5	1740	C
3	L5	1741	G
3	L5	1742	A
3	L5	1756	U
3	L5	1757	U
3	L5	1758	G
3	L5	1760	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	1770	A
3	L5	1787	A
3	L5	1804	A
3	L5	1810	G
3	L5	1821	G
3	L5	1833	G
3	L5	1836	G
3	L5	1837	A
3	L5	1842	G
3	L5	1855	G
3	L5	1869	G
3	L5	1882	U
3	L5	1892	A
3	L5	1897	A
3	L5	1916	G
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

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Mol	Chain	Res	Type
3	L5	1936	C
3	L5	1948	G
3	L5	1961	G
3	L5	1962	A
3	L5	1971	C
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	1989	G
3	L5	1991	A
3	L5	1992	U
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	2005	G
3	L5	2009	A
3	L5	2011	C
3	L5	2024	G
3	L5	2025	A
3	L5	2026	A
3	L5	2044	U
3	L5	2046	G
3	L5	2048	U
3	L5	2055	G
3	L5	2056	G
3	L5	2069	A
3	L5	2084	C
3	L5	2092	G
3	L5	2093	A
3	L5	2095	A
3	L5	2096	G
3	L5	2097	U
3	L5	2098	G

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Mol	Chain	Res	Type
3	L5	2099	G
3	L5	2100	A
3	L5	2101	C
3	L5	2107	C
3	L5	2112	G
3	L5	2252	G
3	L5	2253	A
3	L5	2256	C
3	L5	2259	G
3	L5	2260	C
3	L5	2269	C
3	L5	2289	C
3	L5	2300	A
3	L5	2301	G
3	L5	2313	A
3	L5	2332	A
3	L5	2333	G
3	L5	2348	G
3	L5	2351	OMC
3	L5	2360	A
3	L5	2364	OMG
3	L5	2389	A
3	L5	2395	A
3	L5	2397	G
3	L5	2398	U
3	L5	2401	A2M
3	L5	2411	C
3	L5	2412	A
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
3	L5	2484	A
3	L5	2485	U

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Mol	Chain	Res	Type
3	L5	2487	G
3	L5	2488	C
3	L5	2489	C
3	L5	2490	U
3	L5	2491	C
3	L5	2493	G
3	L5	2504	C
3	L5	2511	A
3	L5	2513	A
3	L5	2519	U
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	2559	G
3	L5	2560	C
3	L5	2565	A
3	L5	2573	A
3	L5	2583	C
3	L5	2586	G
3	L5	2587	A
3	L5	2589	C
3	L5	2627	C
3	L5	2653	C
3	L5	2662	G
3	L5	2669	C
3	L5	2673	G
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	2702	C
3	L5	2703	G
3	L5	2707	U
3	L5	2708	U
3	L5	2709	C
3	L5	2710	C

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Mol	Chain	Res	Type
3	L5	2711	G
3	L5	2712	G
3	L5	2719	C
3	L5	2721	G
3	L5	2724	G
3	L5	2726	G
3	L5	2738	C
3	L5	2739	C
3	L5	2742	G
3	L5	2743	A
3	L5	2746	A
3	L5	2761	U
3	L5	2763	U
3	L5	2764	A
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	2848	G
3	L5	2855	G
3	L5	2867	C
3	L5	2877	G
3	L5	2892	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	3592	G
3	L5	3594	C
3	L5	3595	U
3	L5	3596	A

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Mol	Chain	Res	Type
3	L5	3597	G
3	L5	3599	A
3	L5	3603	G
3	L5	3605	C
3	L5	3615	G
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	3691	G
3	L5	3692	A
3	L5	3701	OMC
3	L5	3710	G
3	L5	3711	A
3	L5	3713	U
3	L5	3727	A
3	L5	3736	A
3	L5	3748	A
3	L5	3760	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	3813	A
3	L5	3814	U
3	L5	3817	A
3	L5	3819	G
3	L5	3824	A
3	L5	3838	U
3	L5	3839	G

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Mol	Chain	Res	Type
3	L5	3840	U
3	L5	3867	A2M
3	L5	3877	A
3	L5	3878	C
3	L5	3879	G
3	L5	3885	G
3	L5	3890	A
3	L5	3892	U
3	L5	3897	G
3	L5	3898	G
3	L5	3899	OMG
3	L5	3901	A
3	L5	3906	A
3	L5	3907	G
3	L5	3908	A
3	L5	3915	U
3	L5	3930	U
3	L5	3938	G
3	L5	3942	A
3	L5	3943	A
3	L5	3944	G
3	L5	3947	A
3	L5	3949	A
3	L5	3950	U
3	L5	3951	G
3	L5	3952	A
3	L5	3953	G
3	L5	4057	C
3	L5	4058	U
3	L5	4059	C
3	L5	4060	U
3	L5	4061	G
3	L5	4062	A
3	L5	4064	C
3	L5	4069	U
3	L5	4076	G
3	L5	4084	G
3	L5	4097	G
3	L5	4099	G
3	L5	4104	G
3	L5	4105	A
3	L5	4107	G

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Mol	Chain	Res	Type
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	4121	G
3	L5	4122	G
3	L5	4127	A
3	L5	4138	C
3	L5	4140	C
3	L5	4141	G
3	L5	4142	C
3	L5	4143	G
3	L5	4144	C
3	L5	4146	G
3	L5	4156	G
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	4201	G
3	L5	4203	A
3	L5	4212	A
3	L5	4220	6MZ
3	L5	4222	G
3	L5	4225	G
3	L5	4228	OMG
3	L5	4229	U
3	L5	4232	U
3	L5	4233	A
3	L5	4234	A
3	L5	4243	C
3	L5	4251	A
3	L5	4254	G
3	L5	4256	A
3	L5	4257	A
3	L5	4258	C
3	L5	4265	U
3	L5	4268	A

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Mol	Chain	Res	Type
3	L5	4273	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	4321	U
3	L5	4326	G
3	L5	4329	G
3	L5	4330	G
3	L5	4332	C
3	L5	4349	C
3	L5	4364	G
3	L5	4373	G
3	L5	4376	A
3	L5	4377	G
3	L5	4378	A
3	L5	4379	A
3	L5	4382	G
3	L5	4387	C
3	L5	4391	G
3	L5	4394	A
3	L5	4405	G
3	L5	4421	C
3	L5	4422	A
3	L5	4428	A
3	L5	4438	U
3	L5	4442	PSU
3	L5	4448	G
3	L5	4449	A
3	L5	4452	U
3	L5	4464	A
3	L5	4466	C
3	L5	4488	A
3	L5	4500	PSU
3	L5	4512	U
3	L5	4513	A
3	L5	4515	G
3	L5	4519	C
3	L5	4524	G

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Mol	Chain	Res	Type
3	L5	4525	C
3	L5	4529	G
3	L5	4545	G
3	L5	4548	A
3	L5	4549	G
3	L5	4560	C
3	L5	4567	G
3	L5	4569	U
3	L5	4575	G
3	L5	4589	A
3	L5	4590	A2M
3	L5	4600	G
3	L5	4601	U
3	L5	4635	A
3	L5	4636	PSU
3	L5	4637	OMG
3	L5	4652	G
3	L5	4656	A
3	L5	4657	U
3	L5	4670	C
3	L5	4672	A
3	L5	4679	G
3	L5	4694	G
3	L5	4695	C
3	L5	4700	A
3	L5	4708	A
3	L5	4709	U
3	L5	4719	G
3	L5	4733	C
3	L5	4734	A
3	L5	4740	G
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

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Mol	Chain	Res	Type
3	L5	4775	C
3	L5	4859	C
3	L5	4863	G
3	L5	4864	U
3	L5	4867	G
3	L5	4870	G
3	L5	4871	C
3	L5	4875	G
3	L5	4882	U
3	L5	4883	C
3	L5	4889	G
3	L5	4895	C
3	L5	4896	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	4923	C
3	L5	4925	U
3	L5	4926	C
3	L5	4927	G
3	L5	4928	C
3	L5	4931	G
3	L5	4934	A
3	L5	4940	C
3	L5	4941	G
3	L5	4943	A
3	L5	4944	C
3	L5	4945	G
3	L5	4951	G
3	L5	4960	G
3	L5	4975	G
3	L5	4976	U
3	L5	4979	A
3	L5	4985	U
3	L5	4988	U
3	L5	4990	C
3	L5	4991	U
3	L5	5006	U
3	L5	5007	A

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Mol	Chain	Res	Type
3	L5	5013	C
3	L5	5014	A
3	L5	5017	G
3	L5	5020	G
3	L5	5022	U
3	L5	5023	C
3	L5	5024	C
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	5058	A
3	L5	5060	A
3	L5	5061	A
3	L5	5062	G
3	L5	5069	U
4	L7	2	U
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	100	A
4	L7	110	G
5	L8	23	C
5	L8	25	G
5	L8	34	U
5	L8	35	C
5	L8	38	U
5	L8	59	A
5	L8	62	A
5	L8	63	U
5	L8	80	A
5	L8	82	A
5	L8	83	C
5	L8	84	A
5	L8	85	U
5	L8	87	G

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Mol	Chain	Res	Type
5	L8	94	G
5	L8	103	A
5	L8	105	C
5	L8	111	U
5	L8	114	G
5	L8	123	U
5	L8	124	U
5	L8	125	C
5	L8	126	C
5	L8	127	U
5	L8	147	G
5	L8	151	G
68	S2	2	A
68	S2	4	C
68	S2	25	A
68	S2	33	G
68	S2	42	A
68	S2	44	U
68	S2	45	A
68	S2	46	A
68	S2	56	G
68	S2	62	G
68	S2	65	C
68	S2	67	C
68	S2	68	A
68	S2	72	C
68	S2	73	C
68	S2	74	G
68	S2	76	U
68	S2	82	G
68	S2	92	A
68	S2	93	PSU
68	S2	99	A2M
68	S2	103	A
68	S2	113	G
68	S2	115	U
68	S2	118	C
68	S2	130	G
68	S2	142	C
68	S2	143	U
68	S2	148	U
68	S2	149	A

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Mol	Chain	Res	Type
68	S2	153	G
68	S2	158	A
68	S2	160	U
68	S2	162	C
68	S2	163	U
68	S2	170	A
68	S2	172	OMU
68	S2	179	C
68	S2	182	C
68	S2	190	G
68	S2	196	C
68	S2	197	U
68	S2	198	U
68	S2	200	G
68	S2	202	G
68	S2	203	G
68	S2	204	G
68	S2	207	G
68	S2	208	G
68	S2	209	A
68	S2	213	G
68	S2	214	U
68	S2	290	U
68	S2	291	G
68	S2	292	A
68	S2	294	U
68	S2	295	C
68	S2	302	A
68	S2	306	C
68	S2	307	G
68	S2	308	G
68	S2	309	G
68	S2	312	G
68	S2	316	G
68	S2	318	A
68	S2	319	C
68	S2	323	C
68	S2	324	C
68	S2	325	C
68	S2	326	C
68	S2	328	U
68	S2	329	G

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Mol	Chain	Res	Type
68	S2	332	G
68	S2	335	G
68	S2	339	A
68	S2	347	G
68	S2	351	G
68	S2	360	A
68	S2	361	U
68	S2	362	C
68	S2	363	A
68	S2	364	A
68	S2	368	U
68	S2	370	G
68	S2	377	G
68	S2	381	C
68	S2	383	G
68	S2	385	G
68	S2	386	C
68	S2	407	G
68	S2	408	A
68	S2	409	C
68	S2	426	A
68	S2	428	OMU
68	S2	438	G
68	S2	448	A
68	S2	449	A
68	S2	450	C
68	S2	452	G
68	S2	464	A
68	S2	465	A
68	S2	471	G
68	S2	472	C
68	S2	473	A
68	S2	474	G
68	S2	476	A
68	S2	482	G
68	S2	483	C
68	S2	487	U
68	S2	488	U
68	S2	492	C
68	S2	493	A
68	S2	495	U
68	S2	502	C

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Mol	Chain	Res	Type
68	S2	506	G
68	S2	530	U
68	S2	531	A
68	S2	532	C
68	S2	536	A
68	S2	537	C
68	S2	540	U
68	S2	542	U
68	S2	544	G
68	S2	546	G
68	S2	547	G
68	S2	552	G
68	S2	557	U
68	S2	558	G
68	S2	563	G
68	S2	564	A
68	S2	576	A2M
68	S2	583	A
68	S2	587	A
68	S2	589	G
68	S2	591	U
68	S2	593	C
68	S2	606	G
68	S2	607	U
68	S2	614	C
68	S2	617	G
68	S2	623	G
68	S2	626	G
68	S2	627	OMU
68	S2	628	A
68	S2	630	U
68	S2	631	U
68	S2	643	A
68	S2	644	OMG
68	S2	655	A
68	S2	660	C
68	S2	663	C
68	S2	664	A
68	S2	668	A2M
68	S2	669	A
68	S2	671	A
68	S2	672	A

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Mol	Chain	Res	Type
68	S2	673	G
68	S2	684	G
68	S2	688	U
68	S2	689	U
68	S2	690	G
68	S2	692	G
68	S2	693	A
68	S2	695	C
68	S2	696	G
68	S2	697	G
68	S2	698	G
68	S2	732	U
68	S2	733	C
68	S2	736	C
68	S2	738	C
68	S2	749	U
68	S2	751	G
68	S2	752	G
68	S2	753	C
68	S2	788	G
68	S2	789	G
68	S2	791	C
68	S2	792	C
68	S2	798	G
68	S2	799	OMU
68	S2	801	PSU
68	S2	809	A
68	S2	821	G
68	S2	822	U
68	S2	823	U
68	S2	824	C
68	S2	827	A
68	S2	830	A
68	S2	834	C
68	S2	835	C
68	S2	836	G
68	S2	837	A
68	S2	838	G
68	S2	839	C
68	S2	847	A
68	S2	867	OMG
68	S2	869	A

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Mol	Chain	Res	Type
68	S2	870	A
68	S2	872	A
68	S2	873	G
68	S2	878	G
68	S2	885	U
68	S2	888	U
68	S2	889	U
68	S2	891	G
68	S2	893	U
68	S2	894	G
68	S2	896	U
68	S2	897	U
68	S2	898	U
68	S2	899	U
68	S2	900	C
68	S2	901	G
68	S2	903	A
68	S2	906	U
68	S2	907	G
68	S2	909	G
68	S2	913	A
68	S2	920	A
68	S2	921	G
68	S2	922	A
68	S2	933	G
68	S2	956	G
68	S2	963	A
68	S2	969	U
68	S2	970	G
68	S2	971	G
68	S2	972	A
68	S2	990	A
68	S2	992	A
68	S2	999	G
68	S2	1001	A
68	S2	1002	U
68	S2	1008	A
68	S2	1017	U
68	S2	1023	A
68	S2	1027	A
68	S2	1044	G
68	S2	1045	PSU

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Mol	Chain	Res	Type
68	S2	1058	A
68	S2	1061	U
68	S2	1062	A
68	S2	1078	C
68	S2	1083	A
68	S2	1085	C
68	S2	1107	G
68	S2	1108	G
68	S2	1109	C
68	S2	1113	A
68	S2	1114	U
68	S2	1116	C
68	S2	1119	A
68	S2	1121	G
68	S2	1123	C
68	S2	1133	A
68	S2	1138	C
68	S2	1139	C
68	S2	1148	A
68	S2	1150	A
68	S2	1153	C
68	S2	1154	U
68	S2	1155	U
68	S2	1157	G
68	S2	1195	A
68	S2	1200	A
68	S2	1207	G
68	S2	1208	A
68	S2	1211	G
68	S2	1215	C
68	S2	1216	C
68	S2	1217	A
68	S2	1220	A
68	S2	1224	G
68	S2	1227	G
68	S2	1242	U
68	S2	1243	U
68	S2	1248	B8N
68	S2	1251	A
68	S2	1253	A
68	S2	1256	G
68	S2	1257	G

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Mol	Chain	Res	Type
68	S2	1259	A
68	S2	1274	G
68	S2	1275	G
68	S2	1283	C
68	S2	1284	A
68	S2	1285	G
68	S2	1286	G
68	S2	1294	G
68	S2	1295	A
68	S2	1298	G
68	S2	1301	A
68	S2	1302	G
68	S2	1303	C
68	S2	1308	U
68	S2	1312	G
68	S2	1342	U
68	S2	1354	G
68	S2	1357	A
68	S2	1371	U
68	S2	1372	U
68	S2	1376	A
68	S2	1378	A
68	S2	1401	A
68	S2	1402	A
68	S2	1406	G
68	S2	1408	U
68	S2	1413	G
68	S2	1414	A
68	S2	1417	C
68	S2	1418	C
68	S2	1419	C
68	S2	1421	A
68	S2	1423	C
68	S2	1433	C
68	S2	1434	C
68	S2	1435	C
68	S2	1436	C
68	S2	1437	C
68	S2	1438	A
68	S2	1439	A
68	S2	1442	OMU
68	S2	1447	G

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Mol	Chain	Res	Type
68	S2	1449	G
68	S2	1454	A
68	S2	1462	U
68	S2	1463	U
68	S2	1480	A
68	S2	1484	A
68	S2	1489	A
68	S2	1490	OMG
68	S2	1494	U
68	S2	1497	G
68	S2	1498	A
68	S2	1520	G
68	S2	1521	C
68	S2	1522	A
68	S2	1533	A
68	S2	1534	C
68	S2	1536	G
68	S2	1544	C
68	S2	1546	G
68	S2	1552	G
68	S2	1553	C
68	S2	1557	C
68	S2	1558	C
68	S2	1560	U
68	S2	1575	G
68	S2	1576	G
68	S2	1578	U
68	S2	1579	A
68	S2	1580	A
68	S2	1581	C
68	S2	1585	U
68	S2	1587	G
68	S2	1588	A
68	S2	1594	A
68	S2	1601	A
68	S2	1604	G
68	S2	1606	G
68	S2	1621	U
68	S2	1623	A
68	S2	1633	A
68	S2	1634	A
68	S2	1637	A

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Mol	Chain	Res	Type
68	S2	1648	G
68	S2	1654	G
68	S2	1662	U
68	S2	1663	A
68	S2	1665	G
68	S2	1683	C
68	S2	1698	C
68	S2	1700	C
68	S2	1701	C
68	S2	1702	G
68	S2	1712	A
68	S2	1715	A
68	S2	1722	G
68	S2	1729	U
68	S2	1744	G
68	S2	1752	C
68	S2	1753	C
68	S2	1754	G
68	S2	1756	C
68	S2	1757	G
68	S2	1758	G
68	S2	1760	G
68	S2	1761	U
68	S2	1772	C
68	S2	1773	C
68	S2	1774	C
68	S2	1783	C
68	S2	1784	G
68	S2	1786	U
68	S2	1810	U
68	S2	1820	G
68	S2	1824	A
68	S2	1826	G
68	S2	1831	A
68	S2	1835	A
68	S2	1838	U
68	S2	1849	G
68	S2	1851	MA6
68	S2	1861	G
68	S2	1862	G
68	S2	1863	A
68	S2	1864	U

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Mol	Chain	Res	Type
68	S2	1865	C
84	Et	9	A
84	Et	10	G
84	Et	11	C
84	Et	19	G
84	Et	20	U
84	Et	21	A
84	Et	26	A
84	Et	33	U
84	Et	36	U
84	Et	37	A
84	Et	38	A
84	Et	39	U
84	Et	42	G
84	Et	43	A
84	Et	44	G
84	Et	46	G
84	Et	47	U
84	Et	49	C
84	Et	50	A
84	Et	55	U
84	Et	56	C
84	Et	58	A
84	Et	70	G
84	Et	73	G
84	Et	76	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	L5	406	C
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	2763	U
3	L5	3673	C
3	L5	4061	G

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Mol	Chain	Res	Type
3	L5	4600	G
3	L5	4699	U
3	L5	4913	G
68	S2	291	G
68	S2	531	A
68	S2	563	G
68	S2	688	U

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

178 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	A2M	L5	1323	3	22,25,26	1.38	3 (13%)	30,36,39	1.63	9 (30%)
3	OMC	L5	3869	3	19,22,23	0.78	1 (5%)	25,31,34	0.64	0
68	PSU	S2	863	68	18,21,22	1.15	2 (11%)	21,30,33	1.84	4 (19%)
3	A2M	L5	1534	87,3	22,25,26	1.32	2 (9%)	30,36,39	1.50	10 (33%)
5	PSU	L8	69	5	18,21,22	1.11	2 (11%)	21,30,33	2.07	5 (23%)
3	A2M	L5	398	3	22,25,26	1.27	3 (13%)	30,36,39	1.55	7 (23%)
3	OMC	L5	2365	3	19,22,23	0.72	0	25,31,34	0.50	0
3	PSU	L5	3884	3	18,21,22	1.12	2 (11%)	21,30,33	1.99	4 (19%)
68	OMU	S2	172	68	19,22,23	3.30	7 (36%)	25,31,34	1.84	5 (20%)
3	OMG	L5	1316	3	23,26,27	0.78	0	32,38,41	0.62	0
3	PSU	L5	4442	3	18,21,22	1.06	2 (11%)	21,30,33	1.98	4 (19%)
68	OMG	S2	601	68	23,26,27	0.64	0	32,38,41	0.66	0
3	A2M	L5	1326	3	22,25,26	1.32	2 (9%)	30,36,39	1.48	9 (30%)
3	PSU	L5	4353	3	18,21,22	1.06	2 (11%)	21,30,33	2.09	5 (23%)
3	PSU	L5	1677	3	18,21,22	1.21	3 (16%)	21,30,33	2.00	5 (23%)
3	OMG	L5	2364	87,3	23,26,27	0.66	0	32,38,41	0.40	0
3	PSU	L5	4972	3	18,21,22	1.05	2 (11%)	21,30,33	1.99	4 (19%)
3	OMG	L5	4637	3	23,26,27	0.64	0	32,38,41	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	OMC	L5	3808	3	19,22,23	0.81	1 (5%)	25,31,34	0.97	2 (8%)
68	PSU	S2	1045	68	18,21,22	1.11	1 (5%)	21,30,33	2.00	5 (23%)
3	PSU	L5	1744	87,3	18,21,22	1.07	2 (11%)	21,30,33	1.99	4 (19%)
3	OMG	L5	4392	3	23,26,27	0.66	0	32,38,41	0.48	0
68	OMU	S2	354	68	19,22,23	3.19	7 (36%)	25,31,34	1.81	5 (20%)
68	A2M	S2	1031	68	22,25,26	1.21	2 (9%)	30,36,39	1.51	7 (23%)
68	4AC	S2	1337	68	21,24,25	0.42	0	28,34,37	0.57	0
3	PSU	L5	2839	3	18,21,22	1.10	2 (11%)	21,30,33	1.86	4 (19%)
3	PSU	L5	4312	3	18,21,22	1.10	2 (11%)	21,30,33	2.06	5 (23%)
68	OMU	S2	627	68	19,22,23	3.34	7 (36%)	25,31,34	1.79	4 (16%)
3	OMC	L5	2351	87,3	19,22,23	0.79	1 (5%)	25,31,34	0.68	0
68	PSU	S2	686	68	18,21,22	1.04	2 (11%)	21,30,33	1.96	4 (19%)
68	OMG	S2	436	68	23,26,27	0.55	0	32,38,41	0.60	0
68	OMU	S2	116	68	19,22,23	3.27	7 (36%)	25,31,34	1.65	5 (20%)
68	A2M	S2	576	68	22,25,26	1.16	1 (4%)	30,36,39	1.50	8 (26%)
68	OMC	S2	462	68	19,22,23	0.57	0	25,31,34	0.76	1 (4%)
5	OMG	L8	75	5	23,26,27	0.64	0	32,38,41	0.51	0
3	PSU	L5	4628	3	18,21,22	1.12	2 (11%)	21,30,33	2.00	4 (19%)
3	OMC	L5	3841	3	19,22,23	0.84	1 (5%)	25,31,34	0.52	0
68	6MZ	S2	1832	68,87	22,25,26	3.09	5 (22%)	29,36,39	2.26	9 (31%)
3	OMG	L5	2424	3	23,26,27	0.66	0	32,38,41	0.52	0
68	PSU	S2	1174	68	18,21,22	1.10	2 (11%)	21,30,33	1.94	4 (19%)
3	OMC	L5	2804	3	19,22,23	0.71	0	25,31,34	0.55	0
3	OMG	L5	3792	3	23,26,27	0.66	0	32,38,41	0.61	0
3	PSU	L5	2632	3	18,21,22	1.07	2 (11%)	21,30,33	1.96	5 (23%)
3	OMG	L5	4499	3	23,26,27	0.58	0	32,38,41	0.51	0
68	A2M	S2	484	68	22,25,26	1.20	2 (9%)	30,36,39	1.48	7 (23%)
3	OMU	L5	4227	3	19,22,23	3.10	7 (36%)	25,31,34	1.93	5 (20%)
3	OMC	L5	3701	3	19,22,23	0.75	0	25,31,34	0.66	0
3	A2M	L5	4523	87,3	22,25,26	1.38	3 (13%)	30,36,39	1.58	8 (26%)
5	PSU	L8	55	5	18,21,22	1.07	2 (11%)	21,30,33	1.94	4 (19%)
68	PSU	S2	649	68	18,21,22	1.16	2 (11%)	21,30,33	1.78	4 (19%)
3	PSU	L5	1792	3	18,21,22	1.10	2 (11%)	21,30,33	1.93	4 (19%)
68	A2M	S2	668	68,87	22,25,26	1.38	2 (9%)	30,36,39	1.58	8 (26%)
3	OMC	L5	2824	3	19,22,23	0.70	0	25,31,34	0.58	0
3	OMG	L5	4196	3	23,26,27	0.61	0	32,38,41	0.45	0
3	PSU	L5	4299	3	18,21,22	1.07	2 (11%)	21,30,33	1.92	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	A2M	L5	3867	3	22,25,26	1.35	2 (9%)	30,36,39	1.57	9 (30%)
3	PSU	L5	4457	3	18,21,22	1.10	2 (11%)	21,30,33	2.07	4 (19%)
68	PSU	S2	1244	68	18,21,22	1.06	2 (11%)	21,30,33	1.92	4 (19%)
68	OMC	S2	174	68	19,22,23	0.54	0	25,31,34	0.66	0
3	OMG	L5	2876	3	23,26,27	0.64	0	32,38,41	0.55	0
3	OMC	L5	1340	3	19,22,23	0.75	0	25,31,34	0.77	0
3	OMC	L5	4456	3	19,22,23	0.88	1 (5%)	25,31,34	0.81	1 (4%)
3	A2M	L5	1871	87,3	22,25,26	1.59	3 (13%)	30,36,39	1.70	6 (20%)
3	1MA	L5	1322	87,3	21,25,26	0.77	0	30,37,40	0.76	1 (3%)
3	6MZ	L5	4220	3	22,25,26	2.95	6 (27%)	29,36,39	2.43	10 (34%)
3	A2M	L5	3785	87,3	22,25,26	1.16	1 (4%)	30,36,39	1.60	9 (30%)
3	PSU	L5	4532	3	18,21,22	1.08	3 (16%)	21,30,33	1.95	5 (23%)
3	PSU	L5	4579	3	18,21,22	1.05	2 (11%)	21,30,33	1.90	4 (19%)
3	PSU	L5	3822	3	18,21,22	1.08	3 (16%)	21,30,33	2.03	6 (28%)
3	PSU	L5	4296	3	18,21,22	1.10	2 (11%)	21,30,33	2.12	5 (23%)
3	PSU	L5	5001	3	18,21,22	1.14	2 (11%)	21,30,33	1.99	4 (19%)
3	A2M	L5	2815	3	22,25,26	1.26	2 (9%)	30,36,39	1.52	9 (30%)
3	A2M	L5	3718	3	22,25,26	1.31	3 (13%)	30,36,39	1.60	6 (20%)
68	PSU	S2	1232	68	18,21,22	1.06	2 (11%)	21,30,33	2.05	5 (23%)
3	PSU	L5	1860	3	18,21,22	1.14	2 (11%)	21,30,33	1.85	4 (19%)
3	PSU	L5	1536	3	18,21,22	1.17	2 (11%)	21,30,33	2.07	4 (19%)
3	PSU	L5	3920	87,3	18,21,22	1.12	3 (16%)	21,30,33	1.92	5 (23%)
68	OMU	S2	1288	68	19,22,23	3.28	7 (36%)	25,31,34	1.90	5 (20%)
68	OMC	S2	1272	68	19,22,23	0.59	0	25,31,34	0.94	2 (8%)
3	A2M	L5	2787	87,3	22,25,26	1.20	2 (9%)	30,36,39	1.52	9 (30%)
3	A2M	L5	1524	3	22,25,26	1.44	3 (13%)	30,36,39	1.58	7 (23%)
68	OMG	S2	644	68	23,26,27	0.51	0	32,38,41	0.55	0
3	PSU	L5	1781	3	18,21,22	1.06	2 (11%)	21,30,33	1.84	4 (19%)
3	OMG	L5	3627	3	23,26,27	0.64	0	32,38,41	0.66	0
3	OMG	L5	1625	3	23,26,27	0.67	0	32,38,41	0.45	0
3	A2M	L5	3825	3	22,25,26	1.33	3 (13%)	30,36,39	1.62	7 (23%)
3	PSU	L5	3844	3	18,21,22	1.10	2 (11%)	21,30,33	1.96	4 (19%)
3	PSU	L5	1683	3	18,21,22	1.07	2 (11%)	21,30,33	2.15	4 (19%)
3	OMG	L5	4494	3	23,26,27	0.66	0	32,38,41	0.57	0
68	PSU	S2	1081	68	18,21,22	1.05	2 (11%)	21,30,33	1.99	6 (28%)
68	OMG	S2	1490	68	23,26,27	0.53	0	32,38,41	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PSU	L5	4493	3	18,21,22	0.98	2 (11%)	21,30,33	1.68	2 (9%)
3	A2M	L5	400	3	22,25,26	1.32	3 (13%)	30,36,39	1.58	8 (26%)
68	OMG	S2	867	68	23,26,27	0.50	0	32,38,41	0.53	0
3	PSU	L5	4576	3	18,21,22	1.05	2 (11%)	21,30,33	1.87	4 (19%)
3	PSU	L5	1782	3	18,21,22	1.07	2 (11%)	21,30,33	1.88	4 (19%)
3	PSU	L5	4552	3	18,21,22	1.13	2 (11%)	21,30,33	2.07	5 (23%)
68	PSU	S2	681	68	18,21,22	1.04	2 (11%)	21,30,33	1.93	4 (19%)
3	OMU	L5	4306	3	19,22,23	3.07	7 (36%)	25,31,34	1.73	4 (16%)
3	A2M	L5	4590	3	22,25,26	1.32	3 (13%)	30,36,39	1.60	6 (20%)
3	A2M	L5	4571	3	22,25,26	1.46	3 (13%)	30,36,39	1.56	9 (30%)
68	A2M	S2	166	68	22,25,26	1.21	1 (4%)	30,36,39	1.62	7 (23%)
68	A2M	S2	468	68	22,25,26	1.29	1 (4%)	30,36,39	1.73	7 (23%)
3	OMG	L5	3744	3	23,26,27	0.66	0	32,38,41	0.46	0
68	OMU	S2	1326	68	19,22,23	3.31	7 (36%)	25,31,34	1.87	5 (20%)
3	PSU	L5	4293	3	18,21,22	1.11	2 (11%)	21,30,33	2.00	4 (19%)
3	OMG	L5	4228	3	23,26,27	0.67	0	32,38,41	0.71	0
3	PSU	L5	3637	3	18,21,22	1.11	2 (11%)	21,30,33	2.17	5 (23%)
3	PSU	L5	4673	3	18,21,22	1.09	3 (16%)	21,30,33	1.80	4 (19%)
68	OMC	S2	1703	68	19,22,23	0.63	0	25,31,34	0.66	0
3	PSU	L5	1862	3	18,21,22	1.09	2 (11%)	21,30,33	2.07	4 (19%)
68	A2M	S2	27	68	22,25,26	1.28	3 (13%)	30,36,39	1.57	7 (23%)
3	OMC	L5	2422	87,3	19,22,23	0.76	1 (5%)	25,31,34	0.68	0
3	A2M	L5	2363	87,3	22,25,26	1.41	3 (13%)	30,36,39	1.60	8 (26%)
3	OMC	L5	4536	3	19,22,23	0.83	1 (5%)	25,31,34	0.65	0
3	5MC	L5	3782	87,3	19,22,23	0.83	0	26,32,35	0.69	0
3	OMG	L5	1522	3	23,26,27	0.71	0	32,38,41	0.64	1 (3%)
3	UR3	L5	4530	3	19,22,23	2.50	6 (31%)	26,32,35	1.56	2 (7%)
3	PSU	L5	3695	3	18,21,22	1.03	2 (11%)	21,30,33	1.99	5 (23%)
68	PSU	S2	406	68	18,21,22	1.07	2 (11%)	21,30,33	1.84	4 (19%)
68	PSU	S2	651	68	18,21,22	1.00	1 (5%)	21,30,33	1.91	5 (23%)
3	OMG	L5	3899	3	23,26,27	0.75	0	32,38,41	0.56	0
3	PSU	L5	4471	3	18,21,22	1.11	2 (11%)	21,30,33	1.96	4 (19%)
3	PSU	L5	1582	3	18,21,22	1.13	2 (11%)	21,30,33	1.90	4 (19%)
68	4AC	S2	1842	68	21,24,25	0.44	0	28,34,37	0.44	0
68	PSU	S2	1046	68	18,21,22	1.06	2 (11%)	21,30,33	1.90	4 (19%)
3	OMC	L5	2861	3	19,22,23	0.69	0	25,31,34	0.75	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	OMC	L5	3887	3	19,22,23	0.70	0	25,31,34	0.63	0
68	OMG	S2	683	68	23,26,27	0.59	0	32,38,41	0.53	0
3	PSU	L5	4500	3	18,21,22	1.12	3 (16%)	21,30,33	2.05	5 (23%)
68	OMU	S2	799	68	19,22,23	3.37	7 (36%)	25,31,34	1.85	5 (20%)
68	OMC	S2	1391	68	19,22,23	0.63	0	25,31,34	0.74	0
3	OMU	L5	2837	3	19,22,23	3.16	7 (36%)	25,31,34	1.92	5 (20%)
3	PSU	L5	3853	87,3	18,21,22	1.04	2 (11%)	21,30,33	1.92	4 (19%)
68	A2M	S2	159	68	22,25,26	1.12	1 (4%)	30,36,39	1.53	7 (23%)
3	PSU	L5	4521	87,3	18,21,22	1.06	2 (11%)	21,30,33	2.05	5 (23%)
68	PSU	S2	866	68	18,21,22	1.10	1 (5%)	21,30,33	1.93	5 (23%)
3	PSU	L5	4403	3	18,21,22	1.06	2 (11%)	21,30,33	2.10	6 (28%)
3	A2M	L5	3830	3	22,25,26	1.25	1 (4%)	30,36,39	1.56	8 (26%)
68	PSU	S2	1177	68	18,21,22	1.03	2 (11%)	21,30,33	2.00	5 (23%)
3	PSU	L5	4431	3	18,21,22	1.05	2 (11%)	21,30,33	1.81	4 (19%)
3	OMU	L5	4498	3	19,22,23	3.15	7 (36%)	25,31,34	1.87	5 (20%)
3	PSU	L5	4689	3	18,21,22	1.15	2 (11%)	21,30,33	2.05	4 (19%)
68	OMU	S2	1442	68	19,22,23	3.38	7 (36%)	25,31,34	1.84	5 (20%)
68	OMG	S2	1328	68	23,26,27	0.55	0	32,38,41	0.54	0
68	PSU	S2	814	68	18,21,22	1.10	1 (5%)	21,30,33	2.01	5 (23%)
68	MA6	S2	1850	68	23,26,27	1.36	4 (17%)	33,38,41	3.27	12 (36%)
3	OMG	L5	4623	3	23,26,27	0.68	0	32,38,41	0.52	0
3	OMU	L5	4620	3	19,22,23	3.09	7 (36%)	25,31,34	1.82	5 (20%)
68	OMG	S2	509	68	23,26,27	0.53	0	32,38,41	0.55	0
68	OMU	S2	121	68	19,22,23	3.13	7 (36%)	25,31,34	1.53	4 (16%)
68	PSU	S2	105	68	18,21,22	1.17	1 (5%)	21,30,33	2.06	4 (19%)
68	PSU	S2	801	68	18,21,22	1.14	1 (5%)	21,30,33	1.74	4 (19%)
3	PSU	L5	5010	3	18,21,22	1.07	2 (11%)	21,30,33	2.01	4 (19%)
3	PSU	L5	4636	3	18,21,22	1.10	2 (11%)	21,30,33	2.23	6 (28%)
3	OMG	L5	4370	3	23,26,27	0.63	0	32,38,41	0.55	0
68	OMC	S2	517	68	19,22,23	0.60	0	25,31,34	0.63	0
68	A2M	S2	99	68,87	22,25,26	1.20	2 (9%)	30,36,39	1.65	8 (26%)
3	PSU	L5	4973	3	18,21,22	1.03	2 (11%)	21,30,33	2.06	5 (23%)
68	MA6	S2	1851	68	23,26,27	1.31	4 (17%)	33,38,41	3.40	12 (36%)
3	PSU	L5	4361	3	18,21,22	1.06	2 (11%)	21,30,33	1.85	4 (19%)
68	PSU	S2	1056	68	18,21,22	1.08	2 (11%)	21,30,33	1.90	4 (19%)
68	PSU	S2	1367	68	18,21,22	1.04	1 (5%)	21,30,33	1.95	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	A2M	L5	2401	3	22,25,26	1.38	2 (9%)	30,36,39	1.59	6 (20%)
3	5MC	L5	4447	3	19,22,23	1.16	2 (10%)	26,32,35	0.93	0
68	B8N	S2	1248	68	25,29,30	3.22	7 (28%)	28,42,45	2.01	7 (25%)
3	PSU	L5	3639	3	18,21,22	1.17	3 (16%)	21,30,33	1.92	4 (19%)
68	PSU	S2	966	68,87	18,21,22	1.05	1 (5%)	21,30,33	1.91	4 (19%)
3	PSU	L5	3851	3	18,21,22	1.03	2 (11%)	21,30,33	2.00	4 (19%)
68	A2M	S2	1383	68	22,25,26	1.24	1 (4%)	30,36,39	1.67	6 (20%)
68	PSU	S2	109	68	18,21,22	1.06	1 (5%)	21,30,33	1.96	5 (23%)
68	OMU	S2	428	68	19,22,23	3.36	7 (36%)	25,31,34	1.89	5 (20%)
3	OMG	L5	4618	3	23,26,27	0.65	0	32,38,41	0.49	0
68	PSU	S2	93	68	18,21,22	1.06	1 (5%)	21,30,33	1.78	4 (19%)
3	OMU	L5	3925	3	19,22,23	3.06	7 (36%)	25,31,34	1.91	5 (20%)
68	PSU	S2	1004	68	18,21,22	1.07	2 (11%)	21,30,33	1.93	4 (19%)
3	UY1	L5	3818	3	19,22,23	4.73	9 (47%)	21,31,34	1.94	5 (23%)
68	G7M	S2	1639	68,84	23,26,27	2.69	9 (39%)	34,39,42	2.59	11 (32%)

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	A2M	L5	1323	3	-	1/9/27/28	0/3/3/3
3	OMC	L5	3869	3	-	1/9/27/28	0/2/2/2
68	PSU	S2	863	68	-	0/7/25/26	0/2/2/2
3	A2M	L5	1534	87,3	-	1/9/27/28	0/3/3/3
5	PSU	L8	69	5	-	0/7/25/26	0/2/2/2
3	A2M	L5	398	3	-	1/9/27/28	0/3/3/3
3	OMC	L5	2365	3	-	0/9/27/28	0/2/2/2
3	PSU	L5	3884	3	-	0/7/25/26	0/2/2/2
68	OMU	S2	172	68	-	3/9/27/28	0/2/2/2
3	OMG	L5	1316	3	-	0/9/27/28	0/3/3/3
3	PSU	L5	4442	3	-	0/7/25/26	0/2/2/2
68	OMG	S2	601	68	-	1/9/27/28	0/3/3/3
3	A2M	L5	1326	3	-	3/9/27/28	0/3/3/3
3	PSU	L5	4353	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	1677	3	-	1/7/25/26	0/2/2/2
3	OMG	L5	2364	87,3	-	3/9/27/28	0/3/3/3
3	PSU	L5	4972	3	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OMG	L5	4637	3	-	3/9/27/28	0/3/3/3
3	OMC	L5	3808	3	-	1/9/27/28	0/2/2/2
68	PSU	S2	1045	68	-	2/7/25/26	0/2/2/2
3	PSU	L5	1744	87,3	-	0/7/25/26	0/2/2/2
3	OMG	L5	4392	3	-	0/9/27/28	0/3/3/3
68	OMU	S2	354	68	-	1/9/27/28	0/2/2/2
68	A2M	S2	1031	68	-	0/9/27/28	0/3/3/3
68	4AC	S2	1337	68	-	0/11/29/30	0/2/2/2
3	PSU	L5	2839	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	4312	3	-	0/7/25/26	0/2/2/2
68	OMU	S2	627	68	-	2/9/27/28	0/2/2/2
3	OMC	L5	2351	87,3	-	1/9/27/28	0/2/2/2
68	PSU	S2	686	68	-	0/7/25/26	0/2/2/2
68	OMG	S2	436	68	-	1/9/27/28	0/3/3/3
68	OMU	S2	116	68	-	0/9/27/28	0/2/2/2
68	A2M	S2	576	68	-	4/9/27/28	0/3/3/3
68	OMC	S2	462	68	-	1/9/27/28	0/2/2/2
5	OMG	L8	75	5	-	0/9/27/28	0/3/3/3
3	PSU	L5	4628	3	-	0/7/25/26	0/2/2/2
3	OMC	L5	3841	3	-	0/9/27/28	0/2/2/2
68	6MZ	S2	1832	68,87	-	2/9/27/28	0/3/3/3
3	OMG	L5	2424	3	-	0/9/27/28	0/3/3/3
68	PSU	S2	1174	68	-	0/7/25/26	0/2/2/2
3	OMC	L5	2804	3	-	0/9/27/28	0/2/2/2
3	OMG	L5	3792	3	-	2/9/27/28	0/3/3/3
3	PSU	L5	2632	3	-	2/7/25/26	0/2/2/2
3	OMG	L5	4499	3	-	0/9/27/28	0/3/3/3
68	A2M	S2	484	68	-	0/9/27/28	0/3/3/3
3	OMU	L5	4227	3	-	1/9/27/28	0/2/2/2
3	OMC	L5	3701	3	-	6/9/27/28	0/2/2/2
3	A2M	L5	4523	87,3	-	0/9/27/28	0/3/3/3
5	PSU	L8	55	5	-	0/7/25/26	0/2/2/2
68	PSU	S2	649	68	-	0/7/25/26	0/2/2/2
3	PSU	L5	1792	3	-	1/7/25/26	0/2/2/2
68	A2M	S2	668	68,87	-	2/9/27/28	0/3/3/3
3	OMC	L5	2824	3	-	0/9/27/28	0/2/2/2
3	OMG	L5	4196	3	-	1/9/27/28	0/3/3/3
3	PSU	L5	4299	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	4457	3	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
68	PSU	S2	1244	68	-	0/7/25/26	0/2/2/2
68	OMC	S2	174	68	-	0/9/27/28	0/2/2/2
3	OMG	L5	2876	3	-	0/9/27/28	0/3/3/3
3	OMC	L5	1340	3	-	0/9/27/28	0/2/2/2
3	OMC	L5	4456	3	-	0/9/27/28	0/2/2/2
3	A2M	L5	1871	87,3	-	0/9/27/28	0/3/3/3
3	1MA	L5	1322	87,3	-	2/7/25/26	0/3/3/3
3	6MZ	L5	4220	3	-	2/9/27/28	0/3/3/3
3	A2M	L5	3785	87,3	-	3/9/27/28	0/3/3/3
3	PSU	L5	4532	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	4579	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	3822	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	4296	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	2815	3	-	2/9/27/28	0/3/3/3
3	A2M	L5	3718	3	-	0/9/27/28	0/3/3/3
68	PSU	S2	1232	68	-	0/7/25/26	0/2/2/2
3	PSU	L5	1860	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	1536	3	-	2/7/25/26	0/2/2/2
3	PSU	L5	3920	87,3	-	0/7/25/26	0/2/2/2
68	OMU	S2	1288	68	-	1/9/27/28	0/2/2/2
68	OMC	S2	1272	68	-	0/9/27/28	0/2/2/2
3	A2M	L5	2787	87,3	-	6/9/27/28	0/3/3/3
3	A2M	L5	1524	3	-	3/9/27/28	0/3/3/3
68	OMG	S2	644	68	-	4/9/27/28	0/3/3/3
3	PSU	L5	1781	3	-	1/7/25/26	0/2/2/2
3	OMG	L5	3627	3	-	0/9/27/28	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
3	PSU	L5	3844	3	-	1/7/25/26	0/2/2/2
3	PSU	L5	1683	3	-	0/7/25/26	0/2/2/2
3	OMG	L5	4494	3	-	1/9/27/28	0/3/3/3
68	PSU	S2	1081	68	-	1/7/25/26	0/2/2/2
68	OMG	S2	1490	68	-	1/9/27/28	0/3/3/3
3	PSU	L5	4493	3	-	0/7/25/26	0/2/2/2
3	A2M	L5	400	3	-	0/9/27/28	0/3/3/3
68	OMG	S2	867	68	-	0/9/27/28	0/3/3/3
3	PSU	L5	4576	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	1782	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	4552	3	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
68	PSU	S2	681	68	-	0/7/25/26	0/2/2/2
3	OMU	L5	4306	3	-	1/9/27/28	0/2/2/2
3	A2M	L5	4590	3	-	3/9/27/28	0/3/3/3
3	A2M	L5	4571	3	-	0/9/27/28	0/3/3/3
68	A2M	S2	166	68	-	1/9/27/28	0/3/3/3
68	A2M	S2	468	68	-	0/9/27/28	0/3/3/3
3	OMG	L5	3744	3	-	0/9/27/28	0/3/3/3
68	OMU	S2	1326	68	-	0/9/27/28	0/2/2/2
3	PSU	L5	4293	3	-	0/7/25/26	0/2/2/2
3	OMG	L5	4228	3	-	2/9/27/28	0/3/3/3
3	PSU	L5	3637	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	4673	3	-	0/7/25/26	0/2/2/2
68	OMC	S2	1703	68	-	2/9/27/28	0/2/2/2
3	PSU	L5	1862	3	-	0/7/25/26	0/2/2/2
68	A2M	S2	27	68	-	1/9/27/28	0/3/3/3
3	OMC	L5	2422	87,3	-	3/9/27/28	0/2/2/2
3	A2M	L5	2363	87,3	-	0/9/27/28	0/3/3/3
3	OMC	L5	4536	3	-	0/9/27/28	0/2/2/2
3	5MC	L5	3782	87,3	-	0/7/25/26	0/2/2/2
3	OMG	L5	1522	3	-	0/9/27/28	0/3/3/3
3	UR3	L5	4530	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	3695	3	-	0/7/25/26	0/2/2/2
68	PSU	S2	406	68	-	0/7/25/26	0/2/2/2
68	PSU	S2	651	68	-	0/7/25/26	0/2/2/2
3	OMG	L5	3899	3	-	2/9/27/28	0/3/3/3
3	PSU	L5	4471	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	1582	3	-	2/7/25/26	0/2/2/2
68	4AC	S2	1842	68	-	0/11/29/30	0/2/2/2
68	PSU	S2	1046	68	-	0/7/25/26	0/2/2/2
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
68	OMG	S2	683	68	-	1/9/27/28	0/3/3/3
3	PSU	L5	4500	3	-	3/7/25/26	0/2/2/2
68	OMU	S2	799	68	-	0/9/27/28	0/2/2/2
68	OMC	S2	1391	68	-	0/9/27/28	0/2/2/2
3	OMU	L5	2837	3	-	0/9/27/28	0/2/2/2
3	PSU	L5	3853	87,3	-	0/7/25/26	0/2/2/2
68	A2M	S2	159	68	-	1/9/27/28	0/3/3/3
3	PSU	L5	4521	87,3	-	0/7/25/26	0/2/2/2
68	PSU	S2	866	68	-	1/7/25/26	0/2/2/2
3	PSU	L5	4403	3	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	A2M	L5	3830	3	-	2/9/27/28	0/3/3/3
68	PSU	S2	1177	68	-	0/7/25/26	0/2/2/2
3	PSU	L5	4431	3	-	0/7/25/26	0/2/2/2
3	OMU	L5	4498	3	-	0/9/27/28	0/2/2/2
3	PSU	L5	4689	3	-	0/7/25/26	0/2/2/2
68	OMU	S2	1442	68	-	2/9/27/28	0/2/2/2
68	OMG	S2	1328	68	-	1/9/27/28	0/3/3/3
68	PSU	S2	814	68	-	0/7/25/26	0/2/2/2
68	MA6	S2	1850	68	-	0/11/29/30	0/3/3/3
3	OMG	L5	4623	3	-	0/9/27/28	0/3/3/3
3	OMU	L5	4620	3	-	0/9/27/28	0/2/2/2
68	OMG	S2	509	68	-	0/9/27/28	0/3/3/3
68	OMU	S2	121	68	-	1/9/27/28	0/2/2/2
68	PSU	S2	105	68	-	0/7/25/26	0/2/2/2
68	PSU	S2	801	68	-	3/7/25/26	0/2/2/2
3	PSU	L5	5010	3	-	0/7/25/26	0/2/2/2
3	PSU	L5	4636	3	-	2/7/25/26	0/2/2/2
3	OMG	L5	4370	3	-	0/9/27/28	0/3/3/3
68	OMC	S2	517	68	-	0/9/27/28	0/2/2/2
68	A2M	S2	99	68,87	-	2/9/27/28	0/3/3/3
3	PSU	L5	4973	3	-	0/7/25/26	0/2/2/2
68	MA6	S2	1851	68	-	1/11/29/30	0/3/3/3
3	PSU	L5	4361	3	-	0/7/25/26	0/2/2/2
68	PSU	S2	1056	68	-	0/7/25/26	0/2/2/2
68	PSU	S2	1367	68	-	0/7/25/26	0/2/2/2
3	A2M	L5	2401	3	-	2/9/27/28	0/3/3/3
3	5MC	L5	4447	3	-	4/7/25/26	0/2/2/2
68	B8N	S2	1248	68	-	5/16/34/35	0/2/2/2
3	PSU	L5	3639	3	-	0/7/25/26	0/2/2/2
68	PSU	S2	966	68,87	-	0/7/25/26	0/2/2/2
3	PSU	L5	3851	3	-	0/7/25/26	0/2/2/2
68	A2M	S2	1383	68	-	1/9/27/28	0/3/3/3
68	PSU	S2	109	68	-	0/7/25/26	0/2/2/2
68	OMU	S2	428	68	-	6/9/27/28	0/2/2/2
3	OMG	L5	4618	3	-	3/9/27/28	0/3/3/3
68	PSU	S2	93	68	-	2/7/25/26	0/2/2/2
3	OMU	L5	3925	3	-	0/9/27/28	0/2/2/2
68	PSU	S2	1004	68	-	0/7/25/26	0/2/2/2
3	UY1	L5	3818	3	-	1/9/27/28	0/2/2/2
68	G7M	S2	1639	68,84	-	0/7/25/26	0/3/3/3

All (375) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
68	S2	1832	6MZ	C6-N6	12.76	1.48	1.34
3	L5	3818	UY1	C6-C5	12.15	1.48	1.35
3	L5	4220	6MZ	C6-N6	11.60	1.47	1.34
3	L5	3818	UY1	C2-N1	11.43	1.51	1.36
68	S2	799	OMU	C2-N1	8.43	1.51	1.38
68	S2	1442	OMU	C2-N1	8.31	1.51	1.38
68	S2	172	OMU	C2-N1	8.18	1.51	1.38
68	S2	428	OMU	C2-N1	8.12	1.51	1.38
68	S2	627	OMU	C2-N1	8.10	1.51	1.38
68	S2	1326	OMU	C2-N1	8.03	1.51	1.38
68	S2	1288	OMU	C2-N1	8.01	1.51	1.38
68	S2	1248	B8N	C4-N3	-8.00	1.26	1.40
68	S2	116	OMU	C2-N1	7.98	1.51	1.38
68	S2	1248	B8N	C6-N1	7.71	1.55	1.36
68	S2	121	OMU	C2-N1	7.61	1.50	1.38
68	S2	354	OMU	C2-N1	7.60	1.50	1.38
3	L5	2837	OMU	C2-N1	7.57	1.50	1.38
3	L5	3818	UY1	C2-N3	7.57	1.49	1.37
3	L5	4227	OMU	C2-N1	7.38	1.50	1.38
3	L5	4498	OMU	C2-N1	7.33	1.49	1.38
3	L5	4306	OMU	C2-N1	7.32	1.49	1.38
3	L5	4620	OMU	C2-N1	7.30	1.49	1.38
3	L5	3925	OMU	C2-N1	7.03	1.49	1.38
68	S2	428	OMU	C2-N3	6.93	1.50	1.38
68	S2	627	OMU	C2-N3	6.89	1.50	1.38
68	S2	799	OMU	C2-N3	6.84	1.49	1.38
68	S2	1442	OMU	C2-N3	6.84	1.49	1.38
68	S2	1248	B8N	C4-C5	6.79	1.62	1.47
68	S2	1326	OMU	C2-N3	6.74	1.49	1.38
68	S2	172	OMU	C2-N3	6.73	1.49	1.38
68	S2	116	OMU	C2-N3	6.70	1.49	1.38
68	S2	1288	OMU	C2-N3	6.60	1.49	1.38
68	S2	1639	G7M	C4-N3	6.48	1.49	1.34
3	L5	4498	OMU	C2-N3	6.42	1.49	1.38
3	L5	2837	OMU	C2-N3	6.42	1.49	1.38
68	S2	354	OMU	C2-N3	6.40	1.49	1.38
3	L5	4227	OMU	C2-N3	6.30	1.48	1.38
3	L5	4620	OMU	C2-N3	6.28	1.48	1.38
3	L5	4530	UR3	C6-C5	6.27	1.49	1.35
3	L5	3925	OMU	C2-N3	6.16	1.48	1.38
68	S2	121	OMU	C2-N3	6.10	1.48	1.38
3	L5	4306	OMU	C2-N3	6.03	1.48	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
68	S2	428	OMU	C6-C5	5.91	1.48	1.35
68	S2	627	OMU	C6-C5	5.85	1.48	1.35
68	S2	1442	OMU	C6-C5	5.82	1.48	1.35
68	S2	1326	OMU	C6-C5	5.79	1.48	1.35
3	L5	2837	OMU	O4-C4	-5.77	1.13	1.24
68	S2	116	OMU	C6-C5	5.77	1.48	1.35
3	L5	3925	OMU	O4-C4	-5.76	1.13	1.24
68	S2	799	OMU	O4-C4	-5.73	1.13	1.24
68	S2	354	OMU	C6-C5	5.73	1.48	1.35
68	S2	428	OMU	O4-C4	-5.72	1.13	1.24
68	S2	121	OMU	C6-C5	5.71	1.48	1.35
68	S2	172	OMU	C6-C5	5.71	1.48	1.35
3	L5	4306	OMU	O4-C4	-5.70	1.13	1.24
68	S2	1248	B8N	C2-N1	5.69	1.55	1.39
3	L5	4227	OMU	O4-C4	-5.68	1.13	1.24
68	S2	799	OMU	C6-C5	5.67	1.48	1.35
3	L5	4620	OMU	O4-C4	-5.66	1.13	1.24
68	S2	1288	OMU	C6-C5	5.65	1.48	1.35
68	S2	121	OMU	O4-C4	-5.63	1.13	1.24
3	L5	4498	OMU	C6-C5	5.62	1.48	1.35
68	S2	1442	OMU	O4-C4	-5.62	1.13	1.24
68	S2	116	OMU	O4-C4	-5.58	1.13	1.24
68	S2	354	OMU	O4-C4	-5.57	1.13	1.24
3	L5	4498	OMU	O4-C4	-5.57	1.13	1.24
68	S2	1288	OMU	O4-C4	-5.57	1.13	1.24
3	L5	4306	OMU	C6-C5	5.54	1.47	1.35
3	L5	3925	OMU	C6-C5	5.51	1.47	1.35
3	L5	2837	OMU	C6-C5	5.49	1.47	1.35
68	S2	1326	OMU	O4-C4	-5.49	1.13	1.24
68	S2	1639	G7M	C2-N3	5.49	1.46	1.33
3	L5	4620	OMU	C6-C5	5.45	1.47	1.35
68	S2	627	OMU	O4-C4	-5.45	1.13	1.24
3	L5	4227	OMU	C6-C5	5.41	1.47	1.35
68	S2	172	OMU	O4-C4	-5.39	1.14	1.24
3	L5	4530	UR3	C2-N3	5.30	1.49	1.39
68	S2	1639	G7M	C5-N7	-5.22	1.33	1.39
68	S2	1248	B8N	C6-C5	5.19	1.42	1.35
3	L5	3818	UY1	C6-N1	5.15	1.44	1.36
3	L5	4530	UR3	C2-N1	4.96	1.45	1.38
68	S2	1639	G7M	C2-N2	4.87	1.45	1.34
68	S2	627	OMU	C4-N3	4.46	1.46	1.38
68	S2	1442	OMU	C4-N3	4.33	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
68	S2	1326	OMU	C4-N3	4.30	1.46	1.38
68	S2	172	OMU	C4-N3	4.25	1.45	1.38
68	S2	1288	OMU	C4-N3	4.23	1.45	1.38
68	S2	428	OMU	C4-N3	4.21	1.45	1.38
3	L5	3818	UY1	C4-N3	4.20	1.46	1.38
68	S2	799	OMU	C4-N3	4.19	1.45	1.38
68	S2	116	OMU	C4-N3	4.06	1.45	1.38
3	L5	1871	A2M	O5'-C5'	-3.99	1.32	1.44
3	L5	4498	OMU	C4-N3	3.99	1.45	1.38
68	S2	354	OMU	C4-N3	3.91	1.45	1.38
68	S2	1639	G7M	C5-C6	3.87	1.54	1.43
3	L5	4220	6MZ	C5-C4	-3.85	1.32	1.39
3	L5	3825	A2M	O5'-C5'	-3.83	1.33	1.44
3	L5	3818	UY1	O4-C4	-3.77	1.16	1.23
3	L5	400	A2M	O5'-C5'	-3.75	1.33	1.44
3	L5	2837	OMU	C4-N3	3.75	1.45	1.38
3	L5	2787	A2M	O5'-C5'	-3.71	1.33	1.44
68	S2	649	PSU	C6-C5	3.71	1.39	1.35
3	L5	4620	OMU	C4-N3	3.71	1.45	1.38
3	L5	4227	OMU	C4-N3	3.68	1.44	1.38
68	S2	801	PSU	C6-C5	3.68	1.39	1.35
3	L5	1524	A2M	O5'-C5'	-3.63	1.33	1.44
3	L5	3925	OMU	C4-N3	3.63	1.44	1.38
68	S2	105	PSU	C6-C5	3.62	1.39	1.35
3	L5	4571	A2M	O5'-C5'	-3.61	1.33	1.44
68	S2	863	PSU	C6-C5	3.60	1.39	1.35
68	S2	121	OMU	C4-N3	3.60	1.44	1.38
3	L5	1677	PSU	C6-C5	3.60	1.39	1.35
68	S2	668	A2M	O5'-C5'	-3.58	1.33	1.44
3	L5	2815	A2M	O5'-C5'	-3.58	1.33	1.44
3	L5	3718	A2M	O5'-C5'	-3.55	1.33	1.44
3	L5	2401	A2M	O5'-C5'	-3.54	1.33	1.44
3	L5	1326	A2M	O5'-C5'	-3.53	1.33	1.44
3	L5	3830	A2M	O5'-C5'	-3.52	1.33	1.44
68	S2	484	A2M	O5'-C5'	-3.52	1.33	1.44
3	L5	1323	A2M	O5'-C5'	-3.51	1.34	1.44
68	S2	1383	A2M	O5'-C5'	-3.50	1.34	1.44
3	L5	4220	6MZ	C5-N7	-3.49	1.32	1.39
68	S2	814	PSU	C6-C5	3.47	1.39	1.35
3	L5	2363	A2M	O5'-C5'	-3.47	1.34	1.44
68	S2	468	A2M	O5'-C5'	-3.46	1.34	1.44
68	S2	1031	A2M	O5'-C5'	-3.46	1.34	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L5	1534	A2M	O5'-C5'	-3.44	1.34	1.44
3	L5	4523	A2M	O5'-C5'	-3.44	1.34	1.44
3	L5	3867	A2M	O5'-C5'	-3.40	1.34	1.44
3	L5	4306	OMU	C4-N3	3.39	1.44	1.38
68	S2	27	A2M	O5'-C5'	-3.39	1.34	1.44
3	L5	4590	A2M	O5'-C5'	-3.39	1.34	1.44
68	S2	99	A2M	O5'-C5'	-3.38	1.34	1.44
68	S2	93	PSU	C6-C5	3.37	1.39	1.35
68	S2	966	PSU	C6-C5	3.37	1.39	1.35
3	L5	398	A2M	O5'-C5'	-3.33	1.34	1.44
68	S2	1045	PSU	C6-C5	3.33	1.39	1.35
68	S2	866	PSU	C6-C5	3.32	1.39	1.35
68	S2	576	A2M	O5'-C5'	-3.32	1.34	1.44
3	L5	3785	A2M	O5'-C5'	-3.32	1.34	1.44
68	S2	1248	B8N	C1'-C5	3.31	1.57	1.50
68	S2	166	A2M	O5'-C5'	-3.30	1.34	1.44
3	L5	1871	A2M	O4'-C4'	-3.30	1.37	1.45
68	S2	109	PSU	C6-C5	3.29	1.38	1.35
68	S2	1832	6MZ	C5-N7	-3.26	1.33	1.39
68	S2	1056	PSU	C6-C5	3.24	1.38	1.35
68	S2	1832	6MZ	C5-C4	-3.23	1.33	1.39
68	S2	1244	PSU	C6-C5	3.19	1.38	1.35
68	S2	159	A2M	O5'-C5'	-3.17	1.34	1.44
3	L5	4220	6MZ	C8-N9	-3.17	1.32	1.37
3	L5	3818	UY1	O2-C2	-3.15	1.16	1.23
3	L5	2363	A2M	O4'-C4'	-3.14	1.38	1.45
3	L5	1862	PSU	C6-C5	3.14	1.38	1.35
68	S2	686	PSU	C6-C5	3.12	1.38	1.35
3	L5	4628	PSU	C6-C5	3.12	1.38	1.35
68	S2	1046	PSU	C6-C5	3.12	1.38	1.35
68	S2	1174	PSU	C6-C5	3.08	1.38	1.35
3	L5	1582	PSU	C6-C5	3.08	1.38	1.35
68	S2	1832	6MZ	C8-N9	-3.07	1.32	1.37
68	S2	668	A2M	O4'-C4'	-3.07	1.38	1.45
3	L5	1781	PSU	C6-C5	3.07	1.38	1.35
3	L5	1323	A2M	O4'-C4'	-3.06	1.38	1.45
3	L5	1524	A2M	O4'-C4'	-3.06	1.38	1.45
3	L5	4571	A2M	O4'-C4'	-3.06	1.38	1.45
5	L8	55	PSU	C6-C5	3.05	1.38	1.35
3	L5	5001	PSU	C6-C5	3.05	1.38	1.35
3	L5	4312	PSU	C6-C5	3.05	1.38	1.35
3	L5	4471	PSU	C6-C5	3.05	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L5	1534	A2M	O4'-C4'	-3.04	1.38	1.45
3	L5	2632	PSU	C6-C5	3.03	1.38	1.35
3	L5	1860	PSU	C6-C5	3.00	1.38	1.35
68	S2	1367	PSU	C6-C5	3.00	1.38	1.35
68	S2	1004	PSU	C6-C5	3.00	1.38	1.35
3	L5	1326	A2M	O4'-C4'	-2.99	1.38	1.45
68	S2	1850	MA6	C6-N6	2.99	1.45	1.36
5	L8	69	PSU	C6-C5	2.98	1.38	1.35
3	L5	1782	PSU	C6-C5	2.98	1.38	1.35
3	L5	4636	PSU	C6-C5	2.97	1.38	1.35
3	L5	5010	PSU	C6-C5	2.96	1.38	1.35
3	L5	4530	UR3	O2-C2	-2.95	1.17	1.22
68	S2	1851	MA6	C6-N6	2.95	1.44	1.36
68	S2	406	PSU	C6-C5	2.94	1.38	1.35
3	L5	4296	PSU	C6-C5	2.94	1.38	1.35
3	L5	4500	PSU	C6-C5	2.94	1.38	1.35
68	S2	1081	PSU	C6-C5	2.92	1.38	1.35
3	L5	4689	PSU	C6-C5	2.92	1.38	1.35
3	L5	4576	PSU	C6-C5	2.91	1.38	1.35
3	L5	1792	PSU	C6-C5	2.91	1.38	1.35
3	L5	1536	PSU	C6-C5	2.90	1.38	1.35
3	L5	3818	UY1	C1'-C5	2.89	1.56	1.50
3	L5	2839	PSU	C6-C5	2.88	1.38	1.35
3	L5	4972	PSU	C6-C5	2.84	1.38	1.35
68	S2	1639	G7M	C2-N1	2.83	1.44	1.37
3	L5	4532	PSU	C6-C5	2.83	1.38	1.35
68	S2	651	PSU	C6-C5	2.83	1.38	1.35
3	L5	3822	PSU	C6-C5	2.83	1.38	1.35
68	S2	1232	PSU	C6-C5	2.83	1.38	1.35
68	S2	1326	OMU	C5-C4	2.82	1.49	1.43
3	L5	3844	PSU	C6-C5	2.81	1.38	1.35
68	S2	1177	PSU	C6-C5	2.80	1.38	1.35
68	S2	627	OMU	C5-C4	2.79	1.49	1.43
3	L5	4523	A2M	O4'-C4'	-2.79	1.38	1.45
3	L5	4220	6MZ	C6-N1	-2.78	1.30	1.35
68	S2	1850	MA6	C5-C4	-2.76	1.34	1.39
68	S2	1288	OMU	C5-C4	2.76	1.49	1.43
68	S2	681	PSU	C6-C5	2.76	1.38	1.35
68	S2	1442	OMU	C5-C4	2.75	1.49	1.43
3	L5	4293	PSU	C6-C5	2.75	1.38	1.35
3	L5	4299	PSU	C6-C5	2.74	1.38	1.35
3	L5	4457	PSU	C6-C5	2.74	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
68	S2	428	OMU	C5-C4	2.74	1.49	1.43
3	L5	3825	A2M	O4'-C4'	-2.71	1.39	1.45
3	L5	4361	PSU	C6-C5	2.71	1.38	1.35
3	L5	1744	PSU	C6-C5	2.70	1.38	1.35
3	L5	3818	UY1	O4'-C1'	-2.70	1.40	1.43
68	S2	1442	OMU	C6-N1	2.70	1.44	1.38
3	L5	3637	PSU	C6-C5	2.69	1.38	1.35
68	S2	799	OMU	C6-N1	2.68	1.44	1.38
3	L5	2815	A2M	O4'-C4'	-2.64	1.39	1.45
3	L5	4447	5MC	C4-N3	-2.64	1.29	1.34
3	L5	3639	PSU	C6-C5	2.64	1.38	1.35
3	L5	3853	PSU	C6-C5	2.63	1.38	1.35
3	L5	4521	PSU	C6-C5	2.63	1.38	1.35
3	L5	4431	PSU	C6-C5	2.63	1.38	1.35
3	L5	4498	OMU	C5-C4	2.63	1.49	1.43
68	S2	1851	MA6	C5-C4	-2.63	1.34	1.39
3	L5	4442	PSU	C6-C5	2.62	1.38	1.35
3	L5	3695	PSU	C6-C5	2.62	1.38	1.35
3	L5	4973	PSU	C6-C5	2.62	1.38	1.35
68	S2	799	OMU	C5-C4	2.61	1.49	1.43
68	S2	1326	OMU	C6-N1	2.61	1.44	1.38
68	S2	172	OMU	C5-C4	2.61	1.49	1.43
3	L5	4403	PSU	C6-C5	2.61	1.38	1.35
3	L5	3867	A2M	O4'-C4'	-2.60	1.39	1.45
68	S2	354	OMU	C5-C4	2.60	1.49	1.43
3	L5	4552	PSU	C6-C5	2.60	1.38	1.35
3	L5	2401	A2M	O4'-C4'	-2.59	1.39	1.45
68	S2	27	A2M	O4'-C4'	-2.58	1.39	1.45
3	L5	1683	PSU	C6-C5	2.58	1.38	1.35
3	L5	4673	PSU	C6-C5	2.57	1.38	1.35
68	S2	1639	G7M	O6-C6	-2.57	1.18	1.23
3	L5	4353	PSU	C6-C5	2.57	1.38	1.35
3	L5	3884	PSU	C6-C5	2.56	1.38	1.35
3	L5	4447	5MC	C5-C4	-2.56	1.42	1.44
3	L5	3920	PSU	C6-C5	2.55	1.38	1.35
3	L5	4493	PSU	C6-C5	2.54	1.38	1.35
3	L5	3639	PSU	C4-C5	-2.54	1.37	1.44
3	L5	3884	PSU	C4-C5	-2.53	1.37	1.44
68	S2	428	OMU	C6-N1	2.53	1.44	1.38
68	S2	627	OMU	C6-N1	2.52	1.44	1.38
68	S2	116	OMU	C5-C4	2.49	1.49	1.43
3	L5	4673	PSU	C4-C5	-2.48	1.37	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L5	3851	PSU	C6-C5	2.48	1.38	1.35
3	L5	3920	PSU	C4-C5	-2.47	1.37	1.44
68	S2	1288	OMU	C6-N1	2.47	1.44	1.38
3	L5	1323	A2M	O3'-C3'	-2.47	1.36	1.43
3	L5	3925	OMU	C5-C4	2.46	1.49	1.43
68	S2	1832	6MZ	C6-N1	-2.45	1.31	1.35
3	L5	2363	A2M	O3'-C3'	-2.45	1.36	1.43
68	S2	1639	G7M	C6-N1	2.45	1.43	1.38
68	S2	121	OMU	C5-C4	2.44	1.49	1.43
3	L5	4227	OMU	C5-C4	2.43	1.49	1.43
68	S2	172	OMU	C6-N1	2.43	1.43	1.38
68	S2	116	OMU	C6-N1	2.41	1.43	1.38
3	L5	4590	A2M	O3'-C3'	-2.40	1.37	1.43
3	L5	4552	PSU	C4-C5	-2.40	1.37	1.44
3	L5	4353	PSU	C4-C5	-2.40	1.37	1.44
68	S2	354	OMU	C6-N1	2.39	1.43	1.38
3	L5	4293	PSU	C4-C5	-2.39	1.37	1.44
3	L5	4523	A2M	O3'-C3'	-2.39	1.37	1.43
68	S2	121	OMU	C6-N1	2.38	1.43	1.38
3	L5	3718	A2M	O4'-C4'	-2.38	1.39	1.45
3	L5	398	A2M	O4'-C4'	-2.38	1.39	1.45
3	L5	1536	PSU	C4-C5	-2.37	1.37	1.44
3	L5	4571	A2M	O3'-C3'	-2.36	1.37	1.43
3	L5	4689	PSU	C4-C5	-2.36	1.37	1.44
3	L5	400	A2M	O4'-C4'	-2.35	1.39	1.45
3	L5	2837	OMU	C6-N1	2.35	1.43	1.38
3	L5	4306	OMU	C5-C4	2.34	1.48	1.43
3	L5	4306	OMU	C6-N1	2.34	1.43	1.38
3	L5	1871	A2M	O3'-C3'	-2.34	1.37	1.43
68	S2	1248	B8N	O4'-C1'	-2.34	1.40	1.43
3	L5	1860	PSU	C4-C5	-2.34	1.37	1.44
3	L5	4620	OMU	C5-C4	2.32	1.48	1.43
3	L5	4498	OMU	C6-N1	2.32	1.43	1.38
3	L5	4312	PSU	C4-C5	-2.31	1.37	1.44
3	L5	2837	OMU	C5-C4	2.31	1.48	1.43
3	L5	4521	PSU	C4-C5	-2.31	1.37	1.44
3	L5	4579	PSU	C6-C5	2.31	1.37	1.35
3	L5	3695	PSU	C4-C5	-2.30	1.38	1.44
3	L5	1744	PSU	C4-C5	-2.30	1.38	1.44
3	L5	4579	PSU	C4-C5	-2.30	1.38	1.44
68	S2	1850	MA6	C4-N9	-2.29	1.32	1.37
3	L5	3844	PSU	C4-C5	-2.29	1.38	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L8	69	PSU	C4-C5	-2.28	1.38	1.44
3	L5	2839	PSU	C4-C5	-2.28	1.38	1.44
3	L5	5001	PSU	C4-C5	-2.27	1.38	1.44
3	L5	4500	PSU	C4-C5	-2.26	1.38	1.44
3	L5	3639	PSU	O4'-C1'	-2.26	1.40	1.43
3	L5	4457	PSU	C4-C5	-2.26	1.38	1.44
3	L5	4296	PSU	C4-C5	-2.25	1.38	1.44
3	L5	4972	PSU	C4-C5	-2.24	1.38	1.44
3	L5	4530	UR3	C6-N1	2.24	1.43	1.38
3	L5	4403	PSU	C4-C5	-2.24	1.38	1.44
3	L5	4431	PSU	C4-C5	-2.24	1.38	1.44
3	L5	1782	PSU	C4-C5	-2.24	1.38	1.44
3	L5	4456	OMC	C4-N3	-2.22	1.30	1.34
3	L5	1792	PSU	C4-C5	-2.22	1.38	1.44
3	L5	4590	A2M	O4'-C4'	-2.21	1.40	1.45
3	L5	400	A2M	O3'-C3'	-2.21	1.37	1.43
3	L5	4442	PSU	C4-C5	-2.21	1.38	1.44
3	L5	4628	PSU	C4-C5	-2.21	1.38	1.44
68	S2	1850	MA6	C5-N7	-2.21	1.35	1.39
3	L5	2351	OMC	C4-N3	-2.21	1.30	1.34
3	L5	3841	OMC	C4-N3	-2.20	1.30	1.34
68	S2	1639	G7M	C4-N9	-2.20	1.32	1.38
3	L5	398	A2M	O3'-C3'	-2.20	1.37	1.43
3	L5	1582	PSU	C4-C5	-2.20	1.38	1.44
68	S2	1174	PSU	C4-C5	-2.20	1.38	1.44
3	L5	2632	PSU	C4-C5	-2.19	1.38	1.44
3	L5	4220	6MZ	C4-N9	-2.19	1.33	1.37
3	L5	3718	A2M	O3'-C3'	-2.19	1.37	1.43
3	L5	1683	PSU	C4-C5	-2.19	1.38	1.44
3	L5	4532	PSU	C4-C5	-2.19	1.38	1.44
3	L5	4500	PSU	O4'-C1'	-2.19	1.40	1.43
3	L5	3822	PSU	C4-C5	-2.17	1.38	1.44
3	L5	4530	UR3	C5-C4	2.17	1.49	1.43
68	S2	406	PSU	C4-C5	-2.17	1.38	1.44
3	L5	1524	A2M	O3'-C3'	-2.16	1.37	1.43
3	L5	4620	OMU	C6-N1	2.16	1.43	1.38
3	L5	4536	OMC	C4-N3	-2.15	1.30	1.34
3	L5	1677	PSU	O4'-C1'	-2.15	1.40	1.43
68	S2	1232	PSU	C4-C5	-2.15	1.38	1.44
3	L5	4471	PSU	C4-C5	-2.15	1.38	1.44
3	L5	2787	A2M	O4'-C4'	-2.15	1.40	1.45
3	L5	3637	PSU	C4-C5	-2.15	1.38	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L5	4227	OMU	C6-N1	2.14	1.43	1.38
3	L5	4361	PSU	C4-C5	-2.14	1.38	1.44
3	L5	3869	OMC	C4-N3	-2.14	1.30	1.34
3	L5	3925	OMU	C6-N1	2.13	1.43	1.38
68	S2	1031	A2M	O4'-C4'	-2.13	1.40	1.45
3	L5	3822	PSU	O4'-C1'	-2.12	1.40	1.43
3	L5	4299	PSU	C4-C5	-2.12	1.38	1.44
3	L5	3920	PSU	O4'-C1'	-2.12	1.40	1.43
3	L5	4576	PSU	C4-C5	-2.12	1.38	1.44
3	L5	1781	PSU	C4-C5	-2.12	1.38	1.44
3	L5	4973	PSU	C4-C5	-2.11	1.38	1.44
3	L5	3851	PSU	C4-C5	-2.11	1.38	1.44
68	S2	1177	PSU	C4-C5	-2.11	1.38	1.44
68	S2	484	A2M	O4'-C4'	-2.10	1.40	1.45
3	L5	3808	OMC	C4-N3	-2.10	1.30	1.34
68	S2	1851	MA6	C5-N7	-2.10	1.35	1.39
68	S2	1004	PSU	C4-C5	-2.09	1.38	1.44
3	L5	1677	PSU	C4-C5	-2.09	1.38	1.44
3	L5	5010	PSU	C4-C5	-2.08	1.38	1.44
68	S2	1081	PSU	C4-C5	-2.08	1.38	1.44
3	L5	2422	OMC	C4-N3	-2.08	1.30	1.34
68	S2	27	A2M	O3'-C3'	-2.07	1.37	1.43
3	L5	1862	PSU	C4-C5	-2.06	1.38	1.44
5	L8	55	PSU	C4-C5	-2.06	1.38	1.44
68	S2	863	PSU	C4-C5	-2.04	1.38	1.44
68	S2	681	PSU	C4-C5	-2.03	1.38	1.44
3	L5	4493	PSU	C4-C5	-2.03	1.38	1.44
3	L5	4673	PSU	O4'-C1'	-2.03	1.41	1.43
3	L5	4532	PSU	O4'-C1'	-2.02	1.41	1.43
3	L5	4636	PSU	C4-C5	-2.02	1.38	1.44
3	L5	3825	A2M	O3'-C3'	-2.02	1.37	1.43
68	S2	99	A2M	O4'-C4'	-2.01	1.40	1.45
68	S2	1056	PSU	C4-C5	-2.01	1.38	1.44
68	S2	1244	PSU	C4-C5	-2.01	1.38	1.44
68	S2	649	PSU	C4-C5	-2.01	1.38	1.44
68	S2	1851	MA6	C4-N9	-2.01	1.33	1.37
3	L5	3853	PSU	O4'-C1'	-2.01	1.41	1.43
68	S2	686	PSU	C4-C5	-2.01	1.38	1.44
68	S2	1046	PSU	O4'-C1'	-2.00	1.41	1.43

All (691) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	1851	MA6	N1-C6-N6	-12.19	102.01	116.86
68	S2	1850	MA6	N1-C6-N6	-11.48	102.87	116.86
68	S2	1851	MA6	C5-C6-N6	7.96	137.92	125.33
68	S2	1850	MA6	C5-C6-N6	7.74	137.59	125.33
68	S2	1639	G7M	C1'-N9-C4	7.51	148.69	126.49
68	S2	1639	G7M	C1'-N9-C8	-7.47	101.53	126.74
3	L5	4227	OMU	C4-N3-C2	-6.07	119.07	126.61
68	S2	1851	MA6	N1-C2-N3	-5.94	119.60	128.58
68	S2	1288	OMU	C4-N3-C2	-5.90	119.29	126.61
3	L5	4498	OMU	C4-N3-C2	-5.88	119.32	126.61
3	L5	3925	OMU	C4-N3-C2	-5.85	119.35	126.61
3	L5	4220	6MZ	N1-C2-N3	-5.84	119.74	128.58
3	L5	2837	OMU	C4-N3-C2	-5.83	119.37	126.61
68	S2	428	OMU	C4-N3-C2	-5.82	119.38	126.61
68	S2	1326	OMU	C4-N3-C2	-5.82	119.39	126.61
3	L5	3637	PSU	N1-C2-N3	5.79	121.27	115.17
68	S2	1832	6MZ	N1-C2-N3	-5.71	119.93	128.58
3	L5	4530	UR3	C4-N3-C2	-5.69	120.00	124.58
3	L5	4636	PSU	C4-N3-C2	-5.66	118.58	126.37
68	S2	172	OMU	C4-N3-C2	-5.64	119.61	126.61
68	S2	354	OMU	C4-N3-C2	-5.63	119.62	126.61
68	S2	799	OMU	C4-N3-C2	-5.63	119.62	126.61
68	S2	1442	OMU	C4-N3-C2	-5.59	119.67	126.61
68	S2	627	OMU	C4-N3-C2	-5.58	119.68	126.61
68	S2	1850	MA6	N1-C2-N3	-5.52	120.23	128.58
3	L5	4620	OMU	C4-N3-C2	-5.47	119.83	126.61
68	S2	105	PSU	N1-C2-N3	5.45	120.91	115.17
68	S2	1851	MA6	N9-C8-N7	-5.44	106.22	113.94
3	L5	1683	PSU	N1-C2-N3	5.38	120.84	115.17
3	L5	4636	PSU	N1-C2-N3	5.38	120.84	115.17
3	L5	4457	PSU	C4-N3-C2	-5.37	118.97	126.37
3	L5	4689	PSU	N1-C2-N3	5.35	120.81	115.17
68	S2	1850	MA6	N9-C8-N7	-5.34	106.36	113.94
3	L5	1862	PSU	N1-C2-N3	5.34	120.80	115.17
3	L5	4312	PSU	N1-C2-N3	5.32	120.78	115.17
3	L5	4552	PSU	C4-N3-C2	-5.32	119.05	126.37
3	L5	1683	PSU	C4-N3-C2	-5.30	119.08	126.37
3	L5	1536	PSU	N1-C2-N3	5.29	120.74	115.17
3	L5	1862	PSU	C4-N3-C2	-5.27	119.11	126.37
3	L5	3637	PSU	C4-N3-C2	-5.26	119.13	126.37
3	L5	4353	PSU	C4-N3-C2	-5.25	119.15	126.37
3	L5	4296	PSU	N1-C2-N3	5.24	120.69	115.17
3	L5	4306	OMU	C4-N3-C2	-5.23	120.12	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	4552	PSU	N1-C2-N3	5.21	120.67	115.17
3	L5	4403	PSU	N1-C2-N3	5.21	120.66	115.17
3	L5	4973	PSU	C4-N3-C2	-5.20	119.22	126.37
68	S2	1177	PSU	C4-N3-C2	-5.19	119.22	126.37
3	L5	4973	PSU	N1-C2-N3	5.19	120.64	115.17
3	L5	5010	PSU	N1-C2-N3	5.19	120.64	115.17
3	L5	4220	6MZ	C9-N6-C6	-5.17	118.05	122.85
3	L5	4457	PSU	N1-C2-N3	5.17	120.62	115.17
5	L8	69	PSU	N1-C2-N3	5.16	120.61	115.17
3	L5	4220	6MZ	N9-C8-N7	-5.16	106.61	113.94
3	L5	4293	PSU	C4-N3-C2	-5.15	119.27	126.37
3	L5	4628	PSU	N1-C2-N3	5.15	120.60	115.17
3	L5	4403	PSU	C4-N3-C2	-5.15	119.27	126.37
68	S2	814	PSU	C4-N3-C2	-5.15	119.27	126.37
3	L5	3851	PSU	N1-C2-N3	5.15	120.60	115.17
5	L8	69	PSU	C4-N3-C2	-5.15	119.28	126.37
68	S2	1232	PSU	C4-N3-C2	-5.12	119.32	126.37
3	L5	4972	PSU	N1-C2-N3	5.11	120.56	115.17
68	S2	1248	B8N	C5-C4-N3	5.10	125.42	116.15
3	L5	3822	PSU	N1-C2-N3	5.10	120.55	115.17
68	S2	1045	PSU	C4-N3-C2	-5.09	119.36	126.37
68	S2	814	PSU	N1-C2-N3	5.09	120.54	115.17
3	L5	4353	PSU	N1-C2-N3	5.08	120.53	115.17
3	L5	3851	PSU	C4-N3-C2	-5.08	119.38	126.37
3	L5	4521	PSU	C4-N3-C2	-5.08	119.38	126.37
3	L5	1744	PSU	C4-N3-C2	-5.07	119.38	126.37
3	L5	4296	PSU	C4-N3-C2	-5.06	119.40	126.37
3	L5	3884	PSU	N1-C2-N3	5.06	120.50	115.17
68	S2	1244	PSU	C4-N3-C2	-5.04	119.42	126.37
68	S2	105	PSU	C4-N3-C2	-5.04	119.43	126.37
68	S2	681	PSU	C4-N3-C2	-5.04	119.43	126.37
5	L8	55	PSU	N1-C2-N3	5.03	120.48	115.17
3	L5	4521	PSU	N1-C2-N3	5.03	120.47	115.17
3	L5	4442	PSU	C4-N3-C2	-5.02	119.46	126.37
3	L5	4471	PSU	N1-C2-N3	5.02	120.46	115.17
68	S2	1232	PSU	N1-C2-N3	5.01	120.45	115.17
68	S2	651	PSU	C4-N3-C2	-5.00	119.48	126.37
3	L5	3822	PSU	C4-N3-C2	-5.00	119.49	126.37
68	S2	1367	PSU	C4-N3-C2	-4.99	119.49	126.37
3	L5	5001	PSU	N1-C2-N3	4.99	120.43	115.17
3	L5	2632	PSU	N1-C2-N3	4.98	120.42	115.17
3	L5	4299	PSU	N1-C2-N3	4.97	120.42	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	1045	PSU	N1-C2-N3	4.97	120.41	115.17
3	L5	4312	PSU	C4-N3-C2	-4.97	119.53	126.37
3	L5	4500	PSU	C4-N3-C2	-4.96	119.53	126.37
3	L5	1582	PSU	N1-C2-N3	4.96	120.40	115.17
68	S2	1081	PSU	N1-C2-N3	4.96	120.40	115.17
3	L5	3853	PSU	C4-N3-C2	-4.96	119.54	126.37
68	S2	109	PSU	N1-C2-N3	4.95	120.38	115.17
3	L5	3884	PSU	C4-N3-C2	-4.94	119.56	126.37
68	S2	1081	PSU	C4-N3-C2	-4.94	119.56	126.37
3	L5	5010	PSU	C4-N3-C2	-4.94	119.57	126.37
68	S2	686	PSU	N1-C2-N3	4.93	120.36	115.17
3	L5	1792	PSU	N1-C2-N3	4.92	120.36	115.17
3	L5	1744	PSU	N1-C2-N3	4.92	120.35	115.17
3	L5	4361	PSU	C4-N3-C2	-4.91	119.60	126.37
3	L5	3695	PSU	N1-C2-N3	4.91	120.35	115.17
3	L5	1677	PSU	N1-C2-N3	4.91	120.35	115.17
68	S2	1177	PSU	N1-C2-N3	4.91	120.35	115.17
3	L5	3844	PSU	N1-C2-N3	4.91	120.34	115.17
3	L5	4442	PSU	N1-C2-N3	4.90	120.34	115.17
68	S2	681	PSU	N1-C2-N3	4.90	120.33	115.17
3	L5	3844	PSU	C4-N3-C2	-4.89	119.63	126.37
68	S2	1174	PSU	C4-N3-C2	-4.89	119.64	126.37
3	L5	4972	PSU	C4-N3-C2	-4.89	119.64	126.37
68	S2	1174	PSU	N1-C2-N3	4.88	120.32	115.17
3	L5	4500	PSU	N1-C2-N3	4.88	120.32	115.17
3	L5	3920	PSU	C4-N3-C2	-4.88	119.65	126.37
68	S2	1004	PSU	N1-C2-N3	4.88	120.31	115.17
3	L5	3818	UY1	C4-N3-C2	-4.88	119.66	126.37
3	L5	4293	PSU	N1-C2-N3	4.87	120.31	115.17
3	L5	3695	PSU	C4-N3-C2	-4.87	119.67	126.37
3	L5	4299	PSU	C4-N3-C2	-4.87	119.67	126.37
68	S2	109	PSU	C4-N3-C2	-4.85	119.69	126.37
68	S2	1367	PSU	N1-C2-N3	4.84	120.27	115.17
68	S2	1056	PSU	N1-C2-N3	4.84	120.27	115.17
68	S2	966	PSU	N1-C2-N3	4.83	120.27	115.17
3	L5	4576	PSU	C4-N3-C2	-4.83	119.71	126.37
3	L5	4628	PSU	C4-N3-C2	-4.83	119.72	126.37
68	S2	686	PSU	C4-N3-C2	-4.83	119.72	126.37
3	L5	5001	PSU	C4-N3-C2	-4.83	119.72	126.37
68	S2	1046	PSU	N1-C2-N3	4.83	120.26	115.17
3	L5	1582	PSU	C4-N3-C2	-4.83	119.72	126.37
3	L5	4532	PSU	N1-C2-N3	4.82	120.25	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	1004	PSU	C4-N3-C2	-4.81	119.75	126.37
3	L5	3853	PSU	N1-C2-N3	4.81	120.24	115.17
68	S2	1832	6MZ	N9-C8-N7	-4.80	107.12	113.94
3	L5	1792	PSU	C4-N3-C2	-4.80	119.76	126.37
5	L8	55	PSU	C4-N3-C2	-4.79	119.77	126.37
3	L5	1782	PSU	C4-N3-C2	-4.79	119.77	126.37
68	S2	866	PSU	C4-N3-C2	-4.78	119.78	126.37
3	L5	1860	PSU	N1-C2-N3	4.77	120.20	115.17
3	L5	4431	PSU	C4-N3-C2	-4.77	119.81	126.37
3	L5	4579	PSU	C4-N3-C2	-4.77	119.81	126.37
3	L5	4532	PSU	C4-N3-C2	-4.75	119.82	126.37
3	L5	1677	PSU	C4-N3-C2	-4.75	119.83	126.37
3	L5	4579	PSU	N1-C2-N3	4.75	120.18	115.17
68	S2	93	PSU	C4-N3-C2	-4.75	119.83	126.37
3	L5	1536	PSU	C4-N3-C2	-4.75	119.83	126.37
3	L5	3639	PSU	N1-C2-N3	4.73	120.16	115.17
3	L5	3920	PSU	N1-C2-N3	4.73	120.16	115.17
68	S2	1248	B8N	C4-N3-C2	-4.72	119.82	125.62
3	L5	4471	PSU	C4-N3-C2	-4.71	119.89	126.37
3	L5	2632	PSU	C4-N3-C2	-4.70	119.89	126.37
3	L5	1781	PSU	C4-N3-C2	-4.70	119.90	126.37
68	S2	1046	PSU	C4-N3-C2	-4.69	119.90	126.37
3	L5	4493	PSU	C4-N3-C2	-4.69	119.91	126.37
68	S2	863	PSU	N1-C2-N3	4.69	120.11	115.17
68	S2	651	PSU	N1-C2-N3	4.69	120.11	115.17
68	S2	1244	PSU	N1-C2-N3	4.68	120.11	115.17
68	S2	1832	6MZ	C5-C4-N3	-4.67	120.29	126.72
3	L5	4673	PSU	C4-N3-C2	-4.67	119.94	126.37
68	S2	116	OMU	C4-N3-C2	-4.66	120.82	126.61
68	S2	866	PSU	N1-C2-N3	4.66	120.08	115.17
68	S2	406	PSU	C4-N3-C2	-4.64	119.98	126.37
68	S2	1056	PSU	C4-N3-C2	-4.64	119.98	126.37
3	L5	4576	PSU	N1-C2-N3	4.64	120.06	115.17
68	S2	801	PSU	N1-C2-N3	4.62	120.04	115.17
68	S2	966	PSU	C4-N3-C2	-4.62	120.01	126.37
3	L5	3639	PSU	C4-N3-C2	-4.61	120.02	126.37
3	L5	1781	PSU	N1-C2-N3	4.60	120.02	115.17
68	S2	863	PSU	C4-N3-C2	-4.55	120.10	126.37
68	S2	406	PSU	N1-C2-N3	4.53	119.95	115.17
3	L5	4689	PSU	C4-N3-C2	-4.52	120.14	126.37
3	L5	1782	PSU	N1-C2-N3	4.52	119.93	115.17
68	S2	1639	G7M	C2-N3-C4	4.52	120.08	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	649	PSU	N1-C2-N3	4.51	119.92	115.17
3	L5	2839	PSU	N1-C2-N3	4.50	119.92	115.17
3	L5	1860	PSU	C4-N3-C2	-4.49	120.19	126.37
3	L5	4361	PSU	N1-C2-N3	4.48	119.90	115.17
68	S2	649	PSU	C4-N3-C2	-4.47	120.21	126.37
3	L5	2839	PSU	C4-N3-C2	-4.46	120.23	126.37
3	L5	3830	A2M	C3'-C2'-C1'	-4.40	94.38	102.81
68	S2	1850	MA6	C4-N9-C8	4.40	110.36	105.74
68	S2	93	PSU	N1-C2-N3	4.39	119.80	115.17
68	S2	121	OMU	C4-N3-C2	-4.36	121.20	126.61
3	L5	4673	PSU	N1-C2-N3	4.34	119.75	115.17
3	L5	2363	A2M	C2'-C1'-N9	4.34	120.90	113.75
68	S2	468	A2M	C3'-C2'-C1'	-4.34	94.51	102.81
3	L5	3925	OMU	N3-C2-N1	4.33	120.53	114.89
3	L5	4431	PSU	N1-C2-N3	4.32	119.73	115.17
68	S2	1851	MA6	C5-C4-N3	-4.32	120.77	126.72
3	L5	1871	A2M	C3'-C2'-C1'	-4.28	94.61	102.81
3	L5	4220	6MZ	C5-C4-N3	-4.23	120.89	126.72
68	S2	1851	MA6	C4-N9-C8	4.22	110.16	105.74
3	L5	4498	OMU	N3-C2-N1	4.17	120.32	114.89
68	S2	428	OMU	N3-C2-N1	4.11	120.25	114.89
68	S2	354	OMU	N3-C2-N1	4.11	120.24	114.89
68	S2	1639	G7M	C5-C4-N3	-4.09	120.41	128.15
3	L5	4620	OMU	N3-C2-N1	4.08	120.20	114.89
3	L5	4689	PSU	C6-N1-C2	-4.07	118.91	122.69
68	S2	1850	MA6	C5-C4-N3	-4.06	121.13	126.72
3	L5	3818	UY1	N1-C2-N3	4.05	119.44	115.17
3	L5	4227	OMU	N3-C2-N1	4.05	120.16	114.89
3	L5	2837	OMU	N3-C2-N1	4.04	120.15	114.89
68	S2	801	PSU	C4-N3-C2	-4.00	120.86	126.37
68	S2	1639	G7M	C5-C6-N1	3.95	120.01	111.84
68	S2	1383	A2M	C3'-C2'-C1'	-3.95	95.24	102.81
68	S2	172	OMU	N3-C2-N1	3.94	120.02	114.89
68	S2	799	OMU	C5-C4-N3	3.94	120.32	114.80
3	L5	4493	PSU	N1-C2-N3	3.93	119.32	115.17
68	S2	1288	OMU	C5-C4-N3	3.90	120.26	114.80
68	S2	1248	B8N	C1'-C5-C4	3.88	123.50	117.61
68	S2	1326	OMU	C5-C4-N3	3.86	120.21	114.80
3	L5	2837	OMU	C5-C4-N3	3.85	120.19	114.80
3	L5	4227	OMU	C5-C4-N3	3.85	120.19	114.80
68	S2	1326	OMU	N3-C2-N1	3.84	119.89	114.89
68	S2	1442	OMU	C5-C4-N3	3.84	120.17	114.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	4306	OMU	N3-C2-N1	3.83	119.88	114.89
68	S2	1288	OMU	N3-C2-N1	3.83	119.87	114.89
3	L5	4220	6MZ	C4-N9-C8	3.81	109.73	105.74
68	S2	627	OMU	C5-C4-N3	3.77	120.09	114.80
68	S2	1442	OMU	N3-C2-N1	3.76	119.78	114.89
3	L5	1683	PSU	O2-C2-N1	-3.76	118.92	122.79
68	S2	799	OMU	N3-C2-N1	3.73	119.75	114.89
68	S2	1383	A2M	O3'-C3'-C2'	3.71	121.58	111.19
3	L5	1536	PSU	O2-C2-N1	-3.70	118.97	122.79
3	L5	3818	UY1	C6-C5-C4	3.69	120.67	118.17
68	S2	1850	MA6	C4-C5-C6	3.65	119.68	115.91
68	S2	1248	B8N	N3-C2-N1	3.64	121.17	116.72
3	L5	3825	A2M	C3'-C2'-C1'	-3.64	95.84	102.81
3	L5	398	A2M	C3'-C2'-C1'	-3.60	95.91	102.81
3	L5	4498	OMU	C5-C4-N3	3.60	119.85	114.80
3	L5	3925	OMU	C5-C4-N3	3.60	119.84	114.80
3	L5	4523	A2M	C3'-C2'-C1'	-3.60	95.92	102.81
68	S2	1851	MA6	C2-N1-C6	3.57	120.54	111.83
68	S2	428	OMU	C5-C4-N3	3.56	119.79	114.80
68	S2	1850	MA6	C2-N1-C6	3.54	120.47	111.83
3	L5	4306	OMU	C5-C4-N3	3.51	119.72	114.80
3	L5	3718	A2M	C3'-C2'-C1'	-3.51	96.10	102.81
68	S2	354	OMU	C5-C4-N3	3.50	119.71	114.80
3	L5	4590	A2M	C3'-C2'-C1'	-3.50	96.11	102.81
68	S2	172	OMU	C5-C4-N3	3.49	119.69	114.80
68	S2	966	PSU	O2-C2-N1	-3.48	119.20	122.79
68	S2	1832	6MZ	C2-N3-C4	3.47	120.31	111.83
3	L5	4530	UR3	C5-C4-N3	3.47	119.61	115.04
68	S2	99	A2M	O3'-C3'-C2'	3.47	120.89	111.19
68	S2	99	A2M	C3'-C2'-C1'	-3.45	96.19	102.81
68	S2	468	A2M	O3'-C3'-C2'	3.45	120.84	111.19
68	S2	1832	6MZ	C5-N7-C8	3.44	108.86	103.45
68	S2	116	OMU	N3-C2-N1	3.44	119.37	114.89
3	L5	4296	PSU	O2-C2-N1	-3.42	119.26	122.79
3	L5	4620	OMU	C5-C4-N3	3.41	119.58	114.80
68	S2	627	OMU	N3-C2-N1	3.40	119.32	114.89
3	L5	3718	A2M	O3'-C3'-C2'	3.36	120.59	111.19
68	S2	1031	A2M	C3'-C2'-C1'	-3.35	96.38	102.81
3	L5	4636	PSU	C6-C5-C4	3.35	120.44	118.17
3	L5	5010	PSU	O2-C2-N1	-3.33	119.36	122.79
3	L5	1536	PSU	C6-N1-C2	-3.32	119.61	122.69
68	S2	1639	G7M	O6-C6-C5	-3.31	120.62	128.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	1046	PSU	O2-C2-N1	-3.31	119.38	122.79
68	S2	468	A2M	C4-N9-C1'	-3.28	118.96	126.63
68	S2	121	OMU	N3-C2-N1	3.28	119.16	114.89
68	S2	1639	G7M	N9-C4-N3	3.28	132.51	125.95
68	S2	1851	MA6	C2-N3-C4	3.28	119.84	111.83
3	L5	1323	A2M	C2'-C1'-N9	3.27	119.13	113.75
68	S2	121	OMU	C5-C4-N3	3.26	119.36	114.80
68	S2	1288	OMU	O4-C4-C5	-3.26	119.55	125.16
3	L5	4220	6MZ	C2-N3-C4	3.26	119.78	111.83
68	S2	159	A2M	O3'-C3'-C2'	3.25	120.28	111.19
3	L5	400	A2M	C2'-C1'-N9	3.24	119.08	113.75
68	S2	166	A2M	C4-N9-C1'	-3.23	119.09	126.63
68	S2	99	A2M	C4-N9-C1'	-3.22	119.11	126.63
3	L5	4471	PSU	O2-C2-N1	-3.22	119.47	122.79
68	S2	801	PSU	C6-N1-C2	-3.20	119.72	122.69
68	S2	1851	MA6	N3-C4-N9	3.20	132.61	127.17
68	S2	799	OMU	O4-C4-C5	-3.19	119.66	125.16
3	L5	4403	PSU	O2-C2-N1	-3.19	119.50	122.79
3	L5	4628	PSU	C6-N1-C2	-3.18	119.74	122.69
3	L5	1871	A2M	C4-N9-C1'	-3.18	119.20	126.63
68	S2	166	A2M	C3'-C2'-C1'	-3.17	96.73	102.81
3	L5	1677	PSU	O2-C2-N1	-3.17	119.52	122.79
68	S2	1851	MA6	C4-C5-C6	3.16	119.18	115.91
3	L5	3695	PSU	O2-C2-N1	-3.16	119.53	122.79
3	L5	4523	A2M	C4-N9-C1'	-3.15	119.26	126.63
3	L5	4532	PSU	O2-C2-N1	-3.15	119.54	122.79
68	S2	627	OMU	O4-C4-C5	-3.15	119.74	125.16
3	L5	3808	OMC	C1'-N1-C2	3.15	125.39	118.44
3	L5	2837	OMU	O4-C4-C5	-3.14	119.74	125.16
3	L5	3830	A2M	O3'-C3'-C2'	3.14	119.98	111.19
68	S2	116	OMU	C5-C4-N3	3.14	119.20	114.80
68	S2	576	A2M	O3'-C3'-C2'	3.13	119.95	111.19
68	S2	1850	MA6	N3-C4-N9	3.13	132.49	127.17
68	S2	1851	MA6	C5-N7-C8	3.13	108.36	103.45
68	S2	1639	G7M	C2-N1-C6	-3.12	119.45	125.11
3	L5	3825	A2M	O3'-C3'-C2'	3.12	119.91	111.19
3	L5	1524	A2M	O3'-C3'-C2'	3.11	119.90	111.19
5	L8	69	PSU	O2-C2-N1	-3.11	119.58	122.79
3	L5	4590	A2M	C4-N9-C1'	-3.10	119.38	126.63
3	L5	3785	A2M	O3'-C3'-C2'	3.10	119.86	111.19
68	S2	1326	OMU	O4-C4-C5	-3.10	119.82	125.16
68	S2	1383	A2M	C4-N9-C1'	-3.09	119.40	126.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	4500	PSU	O2-C2-N1	-3.09	119.60	122.79
3	L5	4521	PSU	O2-C2-N1	-3.09	119.61	122.79
3	L5	4689	PSU	O2-C2-N1	-3.09	119.61	122.79
3	L5	2401	A2M	C4-N9-C1'	-3.08	119.42	126.63
3	L5	4220	6MZ	N3-C4-N9	3.07	132.39	127.17
68	S2	1056	PSU	O2-C2-N1	-3.07	119.62	122.79
3	L5	400	A2M	C3'-C2'-C1'	-3.07	96.92	102.81
68	S2	166	A2M	O3'-C3'-C2'	3.07	119.78	111.19
3	L5	1677	PSU	C6-N1-C2	-3.07	119.84	122.69
3	L5	4471	PSU	C6-N1-C2	-3.07	119.84	122.69
68	S2	428	OMU	O4-C4-C5	-3.06	119.89	125.16
68	S2	1442	OMU	O4-C4-C5	-3.06	119.89	125.16
68	S2	105	PSU	C6-N1-C2	-3.05	119.86	122.69
3	L5	5001	PSU	O2-C2-N1	-3.04	119.65	122.79
3	L5	398	A2M	O3'-C3'-C2'	3.04	119.69	111.19
3	L5	1323	A2M	O3'-C3'-C2'	3.03	119.67	111.19
3	L5	4293	PSU	O2-C2-N1	-3.02	119.67	122.79
3	L5	1871	A2M	O3'-C3'-C2'	3.02	119.64	111.19
3	L5	3867	A2M	C4-N9-C1'	-3.02	119.57	126.63
3	L5	4312	PSU	C6-N1-C2	-3.02	119.89	122.69
3	L5	4220	6MZ	C5-N7-C8	3.00	108.17	103.45
3	L5	1534	A2M	C3'-C2'-C1'	-2.99	97.08	102.81
68	S2	668	A2M	C4-N9-C1'	-2.99	119.65	126.63
3	L5	2815	A2M	C2'-C1'-N9	2.99	118.67	113.75
3	L5	4227	OMU	O4-C4-C5	-2.98	120.03	125.16
3	L5	2401	A2M	C1'-N9-C8	2.97	133.69	127.09
3	L5	1323	A2M	C3'-C2'-C1'	-2.97	97.12	102.81
3	L5	2839	PSU	O2-C2-N1	-2.97	119.72	122.79
3	L5	1860	PSU	C6-N1-C2	-2.97	119.94	122.69
3	L5	4973	PSU	O2-C2-N1	-2.97	119.73	122.79
3	L5	3639	PSU	C6-N1-C2	-2.97	119.94	122.69
68	S2	1850	MA6	C5-N7-C8	2.96	108.11	103.45
3	L5	4972	PSU	C6-N1-C2	-2.96	119.94	122.69
3	L5	2363	A2M	C3'-C2'-C1'	-2.95	97.15	102.81
3	L5	1524	A2M	C4'-O4'-C1'	-2.95	102.95	109.47
68	S2	686	PSU	O2-C2-N1	-2.94	119.75	122.79
3	L5	2632	PSU	O2-C2-N1	-2.94	119.75	122.79
68	S2	27	A2M	C4-N9-C1'	-2.93	119.79	126.63
68	S2	172	OMU	O4-C4-C5	-2.92	120.12	125.16
3	L5	3825	A2M	C4-N9-C1'	-2.92	119.79	126.63
68	S2	116	OMU	O4-C4-C5	-2.92	120.12	125.16
3	L5	3844	PSU	O2-C2-N1	-2.92	119.78	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	1004	PSU	O2-C2-N1	-2.92	119.78	122.79
68	S2	484	A2M	O3'-C3'-C2'	2.92	119.36	111.19
68	S2	1850	MA6	C2-N3-C4	2.92	118.96	111.83
3	L5	2787	A2M	O3'-C3'-C2'	2.91	119.34	111.19
3	L5	4457	PSU	O2-C2-N1	-2.91	119.78	122.79
3	L5	4498	OMU	O4-C4-C5	-2.91	120.14	125.16
3	L5	1871	A2M	C1'-N9-C8	2.91	133.55	127.09
68	S2	99	A2M	C1'-N9-C8	2.91	133.55	127.09
68	S2	1367	PSU	O2-C2-N1	-2.90	119.79	122.79
3	L5	4628	PSU	O2-C2-N1	-2.90	119.80	122.79
3	L5	3718	A2M	C1'-N9-C8	2.90	133.53	127.09
68	S2	166	A2M	C1'-N9-C8	2.90	133.53	127.09
5	L8	55	PSU	C6-N1-C2	-2.89	120.00	122.69
3	L5	5001	PSU	C6-N1-C2	-2.89	120.01	122.69
68	S2	1177	PSU	O2-C2-N1	-2.88	119.82	122.79
68	S2	1232	PSU	O2-C2-N1	-2.87	119.82	122.79
3	L5	4442	PSU	O2-C2-N1	-2.87	119.83	122.79
3	L5	4353	PSU	C6-C5-C4	2.87	120.11	118.17
3	L5	4500	PSU	C6-C5-C4	2.87	120.11	118.17
68	S2	1174	PSU	O2-C2-N1	-2.87	119.83	122.79
3	L5	2401	A2M	C3'-C2'-C1'	-2.87	97.31	102.81
68	S2	1056	PSU	C6-N1-C2	-2.87	120.03	122.69
3	L5	1792	PSU	C6-N1-C2	-2.87	120.03	122.69
3	L5	3853	PSU	O2-C2-N1	-2.86	119.83	122.79
3	L5	1782	PSU	O2-C2-N1	-2.86	119.84	122.79
3	L5	3639	PSU	O2-C2-N1	-2.86	119.84	122.79
68	S2	27	A2M	C3'-C2'-C1'	-2.86	97.33	102.81
3	L5	4523	A2M	C1'-N9-C8	2.86	133.43	127.09
68	S2	468	A2M	C1'-N9-C8	2.85	133.42	127.09
3	L5	1792	PSU	O2-C2-N1	-2.85	119.85	122.79
3	L5	4312	PSU	O2-C2-N1	-2.85	119.85	122.79
3	L5	3718	A2M	C4-N9-C1'	-2.84	119.98	126.63
3	L5	4571	A2M	C3'-C2'-C1'	-2.84	97.36	102.81
3	L5	4296	PSU	C6-N1-C2	-2.84	120.06	122.69
68	S2	1004	PSU	C6-N1-C2	-2.84	120.06	122.69
3	L5	3925	OMU	O4-C4-C5	-2.84	120.27	125.16
3	L5	2839	PSU	C6-N1-C2	-2.83	120.06	122.69
3	L5	2632	PSU	C6-N1-C2	-2.82	120.08	122.69
3	L5	3884	PSU	C6-N1-C2	-2.81	120.08	122.69
68	S2	1832	6MZ	C4-N9-C8	2.81	108.69	105.74
3	L5	1744	PSU	O2-C2-N1	-2.81	119.89	122.79
68	S2	1832	6MZ	C4-C5-N7	-2.81	107.37	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	1832	6MZ	C4-C5-C6	2.80	119.11	116.78
68	S2	668	A2M	O3'-C3'-C2'	2.80	119.03	111.19
3	L5	3822	PSU	O2-C2-N1	-2.80	119.90	122.79
3	L5	3695	PSU	C6-N1-C2	-2.80	120.09	122.69
3	L5	4590	A2M	C1'-N9-C8	2.80	133.31	127.09
68	S2	1174	PSU	C6-N1-C2	-2.80	120.10	122.69
3	L5	2815	A2M	O3'-C3'-C2'	2.79	119.01	111.19
3	L5	400	A2M	O3'-C3'-C2'	2.79	119.00	111.19
3	L5	4590	A2M	O3'-C3'-C2'	2.79	119.00	111.19
3	L5	2401	A2M	O3'-C3'-C2'	2.79	118.99	111.19
68	S2	1639	G7M	CN7-N7-C5	2.79	130.27	126.80
3	L5	5010	PSU	C6-N1-C2	-2.79	120.11	122.69
3	L5	3637	PSU	C6-N1-C2	-2.78	120.11	122.69
68	S2	1232	PSU	C6-C5-C4	2.78	120.05	118.17
68	S2	686	PSU	C6-N1-C2	-2.78	120.11	122.69
3	L5	398	A2M	C4-N9-C1'	-2.78	120.13	126.63
68	S2	866	PSU	O2-C2-N1	-2.78	119.93	122.79
3	L5	3851	PSU	O2-C2-N1	-2.77	119.93	122.79
68	S2	1383	A2M	C1'-N9-C8	2.77	133.24	127.09
3	L5	1781	PSU	O2-C2-N1	-2.77	119.94	122.79
3	L5	398	A2M	C1'-N9-C8	2.76	133.23	127.09
3	L5	3867	A2M	C1'-N9-C8	2.76	133.23	127.09
5	L8	69	PSU	C6-N1-C2	-2.76	120.13	122.69
68	S2	1031	A2M	O3'-C3'-C2'	2.75	118.89	111.19
3	L5	1582	PSU	C6-N1-C2	-2.75	120.14	122.69
3	L5	4353	PSU	O2-C2-N1	-2.75	119.95	122.79
3	L5	4571	A2M	O3'-C3'-C2'	2.74	118.87	111.19
3	L5	1683	PSU	C6-N1-C2	-2.74	120.15	122.69
68	S2	1272	OMC	C1'-N1-C2	2.74	124.48	118.44
3	L5	4403	PSU	C6-N1-C2	-2.74	120.15	122.69
3	L5	3884	PSU	O2-C2-N1	-2.73	119.97	122.79
3	L5	3844	PSU	C6-N1-C2	-2.73	120.16	122.69
3	L5	3637	PSU	C6-C5-C4	2.72	120.01	118.17
68	S2	1045	PSU	O2-C2-N1	-2.72	119.98	122.79
68	S2	27	A2M	O3'-C3'-C2'	2.72	118.80	111.19
68	S2	406	PSU	O2-C2-N1	-2.70	120.00	122.79
3	L5	4620	OMU	O4-C4-C5	-2.70	120.50	125.16
68	S2	1832	6MZ	N3-C4-N9	2.70	131.76	127.17
68	S2	649	PSU	C6-N1-C2	-2.70	120.19	122.69
68	S2	668	A2M	C1'-N9-C8	2.70	133.08	127.09
68	S2	668	A2M	O4'-C1'-C2'	2.69	111.22	106.59
68	S2	159	A2M	C3'-C2'-C1'	-2.69	97.66	102.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	4361	PSU	O2-C2-N1	-2.69	120.02	122.79
3	L5	1862	PSU	O2-C2-N1	-2.68	120.02	122.79
3	L5	4576	PSU	O2-C2-N1	-2.68	120.02	122.79
3	L5	3785	A2M	C3'-C2'-C1'	-2.68	97.67	102.81
68	S2	406	PSU	C6-N1-C2	-2.68	120.20	122.69
3	L5	4521	PSU	C6-N1-C2	-2.68	120.21	122.69
5	L8	55	PSU	O2-C2-N1	-2.68	120.03	122.79
3	L5	3785	A2M	C4-N9-C1'	-2.67	120.38	126.63
68	S2	1031	A2M	C4-N9-C1'	-2.67	120.39	126.63
3	L5	4972	PSU	O2-C2-N1	-2.67	120.04	122.79
3	L5	3867	A2M	O3'-C3'-C2'	2.66	118.64	111.19
3	L5	1524	A2M	C4-N9-C1'	-2.66	120.41	126.63
68	S2	814	PSU	O2-C2-N1	-2.66	120.04	122.79
3	L5	4571	A2M	C4-N9-C1'	-2.66	120.41	126.63
3	L5	3825	A2M	C1'-N9-C8	2.66	132.99	127.09
68	S2	105	PSU	O2-C2-N1	-2.66	120.05	122.79
68	S2	1081	PSU	O2-C2-N1	-2.65	120.05	122.79
3	L5	4579	PSU	O2-C2-N1	-2.65	120.06	122.79
68	S2	863	PSU	C6-N1-C2	-2.65	120.23	122.69
68	S2	109	PSU	O2-C2-N1	-2.65	120.06	122.79
68	S2	576	A2M	C4-N9-C1'	-2.64	120.46	126.63
68	S2	966	PSU	C6-N1-C2	-2.64	120.24	122.69
68	S2	1046	PSU	C6-N1-C2	-2.63	120.25	122.69
3	L5	3925	OMU	O2-C2-N1	-2.62	119.38	122.80
3	L5	4220	6MZ	C5-C6-N1	2.62	120.96	118.15
3	L5	3822	PSU	C6-N1-C2	-2.62	120.26	122.69
68	S2	1248	B8N	O4-C4-N3	-2.62	115.74	119.99
68	S2	27	A2M	C1'-N9-C8	2.61	132.88	127.09
3	L5	4523	A2M	O3'-C3'-C2'	2.61	118.48	111.19
3	L5	4306	OMU	O4-C4-C5	-2.60	120.67	125.16
3	L5	1326	A2M	O3'-C3'-C2'	2.60	118.48	111.19
68	S2	484	A2M	C2'-C1'-N9	2.59	118.02	113.75
68	S2	109	PSU	C6-N1-C2	-2.59	120.29	122.69
3	L5	1323	A2M	O4'-C1'-C2'	2.59	111.04	106.59
3	L5	4636	PSU	O2-C2-N1	-2.58	120.12	122.79
3	L5	3808	OMC	C1'-N1-C6	-2.58	115.27	120.78
68	S2	27	A2M	O4'-C1'-C2'	2.58	111.03	106.59
3	L5	3785	A2M	C1'-N9-C8	2.57	132.80	127.09
3	L5	4299	PSU	C6-N1-C2	-2.56	120.31	122.69
3	L5	2787	A2M	C4-N9-C1'	-2.54	120.69	126.63
3	L5	4579	PSU	C6-N1-C2	-2.54	120.33	122.69
3	L5	1534	A2M	C4-N9-C1'	-2.54	120.70	126.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	1081	PSU	C6-N1-C2	-2.53	120.34	122.69
3	L5	4296	PSU	C6-C5-C4	2.53	119.88	118.17
68	S2	1031	A2M	C1'-N9-C8	2.53	132.71	127.09
3	L5	1781	PSU	C6-N1-C2	-2.53	120.34	122.69
3	L5	3818	UY1	C6-N1-C2	-2.52	120.35	122.69
3	L5	4442	PSU	C6-N1-C2	-2.52	120.35	122.69
68	S2	1639	G7M	CN7-N7-C8	-2.52	120.98	124.79
68	S2	866	PSU	C6-N1-C2	-2.52	120.36	122.69
68	S2	159	A2M	C1'-N9-C8	2.51	132.67	127.09
3	L5	1862	PSU	C6-N1-C2	-2.51	120.36	122.69
68	S2	159	A2M	C4-N9-C1'	-2.51	120.77	126.63
68	S2	354	OMU	O4-C4-C5	-2.51	120.84	125.16
68	S2	1244	PSU	O2-C2-N1	-2.50	120.21	122.79
68	S2	866	PSU	C6-C5-C4	2.50	119.86	118.17
68	S2	681	PSU	C6-N1-C2	-2.50	120.37	122.69
3	L5	4532	PSU	C6-N1-C2	-2.50	120.37	122.69
68	S2	484	A2M	C1'-N9-C8	2.50	132.64	127.09
3	L5	4498	OMU	O2-C2-N1	-2.49	119.55	122.80
3	L5	4973	PSU	C6-N1-C2	-2.49	120.38	122.69
3	L5	3851	PSU	C6-N1-C2	-2.49	120.38	122.69
68	S2	166	A2M	C6-C5-C4	-2.48	113.79	117.18
3	L5	3818	UY1	O2-C2-N1	-2.48	120.23	122.79
3	L5	1524	A2M	O4'-C1'-C2'	2.47	110.84	106.59
3	L5	1323	A2M	C4-N9-C1'	-2.47	120.86	126.63
3	L5	2787	A2M	C1'-N9-C8	2.46	132.56	127.09
3	L5	1534	A2M	C1'-N9-C8	2.46	132.55	127.09
3	L5	4220	6MZ	C4-C5-C6	2.46	118.82	116.78
68	S2	576	A2M	C1'-N9-C8	2.45	132.53	127.09
3	L5	2401	A2M	C6-C5-C4	-2.45	113.83	117.18
3	L5	1744	PSU	C6-N1-C2	-2.45	120.42	122.69
3	L5	4500	PSU	C6-N1-C2	-2.44	120.42	122.69
3	L5	3920	PSU	C6-N1-C2	-2.44	120.42	122.69
3	L5	1524	A2M	C1'-N9-C8	2.44	132.51	127.09
68	S2	1639	G7M	N9-C8-N7	-2.43	106.58	112.48
3	L5	4431	PSU	O2-C2-N1	-2.43	120.28	122.79
3	L5	2815	A2M	C3'-C2'-C1'	-2.43	98.16	102.81
68	S2	1248	B8N	O4'-C1'-C2'	2.43	108.51	105.15
3	L5	2837	OMU	O2-C2-N1	-2.42	119.64	122.80
3	L5	2787	A2M	O4'-C1'-C2'	2.42	110.76	106.59
68	S2	27	A2M	C6-C5-C4	-2.42	113.87	117.18
3	L5	4457	PSU	C6-N1-C2	-2.42	120.45	122.69
68	S2	1851	MA6	C1'-N9-C8	-2.42	121.73	127.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	576	A2M	C3'-C2'-C1'	-2.41	98.18	102.81
3	L5	1782	PSU	C6-N1-C2	-2.41	120.45	122.69
68	S2	484	A2M	C4-N9-C1'	-2.41	121.00	126.63
3	L5	2363	A2M	O3'-C3'-C2'	2.41	117.92	111.19
68	S2	484	A2M	O4'-C1'-C2'	2.40	110.73	106.59
3	L5	4590	A2M	C6-C5-C4	-2.40	113.90	117.18
3	L5	3920	PSU	O2-C2-N1	-2.40	120.31	122.79
68	S2	484	A2M	O4'-C4'-C3'	2.40	109.91	105.15
3	L5	4636	PSU	C5-C6-N1	-2.40	118.81	122.14
3	L5	4571	A2M	C1'-N9-C8	2.39	132.40	127.09
3	L5	1326	A2M	O4'-C1'-C2'	2.39	110.70	106.59
68	S2	121	OMU	O4-C4-C5	-2.38	121.06	125.16
68	S2	1045	PSU	C6-C5-C4	2.38	119.78	118.17
3	L5	1323	A2M	C1'-N9-C8	2.38	132.38	127.09
3	L5	4571	A2M	O3'-C3'-C4'	-2.38	104.25	111.08
3	L5	4673	PSU	C6-N1-C2	-2.38	120.48	122.69
3	L5	4620	OMU	O2-C2-N1	-2.37	119.70	122.80
3	L5	3637	PSU	O2-C2-N1	-2.37	120.34	122.79
68	S2	1326	OMU	O2-C2-N1	-2.37	119.71	122.80
3	L5	3830	A2M	C1'-N9-C8	2.37	132.35	127.09
68	S2	166	A2M	O4'-C1'-C2'	2.37	110.66	106.59
3	L5	3867	A2M	C2'-C1'-N9	2.37	117.65	113.75
3	L5	1871	A2M	C6-C5-C4	-2.37	113.95	117.18
68	S2	116	OMU	C1'-N1-C2	2.37	121.84	117.59
3	L5	4521	PSU	C6-C5-C4	2.36	119.77	118.17
3	L5	4552	PSU	O2-C2-N1	-2.36	120.35	122.79
3	L5	4293	PSU	C6-N1-C2	-2.36	120.50	122.69
3	L5	4227	OMU	O2-C2-N1	-2.35	119.74	122.80
3	L5	4552	PSU	C6-N1-C2	-2.35	120.51	122.69
3	L5	3830	A2M	C4-N9-C1'	-2.34	121.15	126.63
68	S2	468	A2M	C4'-O4'-C1'	-2.34	104.30	109.47
3	L5	1871	A2M	C4'-O4'-C1'	-2.34	104.30	109.47
3	L5	1326	A2M	C2'-C1'-N9	2.34	117.60	113.75
68	S2	1232	PSU	C6-N1-C2	-2.34	120.52	122.69
3	L5	2861	OMC	C1'-N1-C2	2.34	123.60	118.44
3	L5	4523	A2M	C6-C5-C4	-2.33	114.00	117.18
3	L5	3867	A2M	C6-C5-C4	-2.32	114.01	117.18
3	L5	1326	A2M	C4-N9-C1'	-2.31	121.22	126.63
68	S2	354	OMU	O2-C2-N1	-2.31	119.78	122.80
3	L5	4532	PSU	C6-C5-C4	2.31	119.73	118.17
68	S2	801	PSU	O2-C2-N1	-2.31	120.41	122.79
68	S2	681	PSU	O2-C2-N1	-2.30	120.42	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L5	400	A2M	C1'-N9-C8	2.30	132.19	127.09
68	S2	1850	MA6	C1'-N9-C8	-2.30	122.00	127.09
3	L5	400	A2M	C4-N9-C1'	-2.29	121.27	126.63
68	S2	468	A2M	C6-C5-C4	-2.29	114.05	117.18
3	L5	4456	OMC	C1'-N1-C2	2.29	123.50	118.44
3	L5	3785	A2M	C2-N1-C6	-2.29	114.97	118.73
3	L5	1524	A2M	C6-C5-C4	-2.29	114.06	117.18
3	L5	1534	A2M	O4'-C1'-C2'	2.29	110.52	106.59
3	L5	3830	A2M	C2-N1-C6	-2.28	114.98	118.73
68	S2	1272	OMC	C1'-N1-C6	-2.28	115.91	120.78
3	L5	1326	A2M	C2-N1-C6	-2.28	114.99	118.73
3	L5	2815	A2M	C4-N9-C1'	-2.27	121.32	126.63
3	L5	3867	A2M	C3'-C2'-C1'	-2.27	98.45	102.81
3	L5	4431	PSU	C6-N1-C2	-2.27	120.58	122.69
3	L5	3825	A2M	C6-C5-C4	-2.27	114.08	117.18
3	L5	4403	PSU	C6-C5-C4	2.27	119.71	118.17
68	S2	93	PSU	O2-C2-N1	-2.27	120.45	122.79
68	S2	159	A2M	C2'-C1'-N9	2.27	117.48	113.75
68	S2	668	A2M	O3'-C3'-C4'	-2.27	104.57	111.08
3	L5	2363	A2M	C1'-N9-C8	2.27	132.12	127.09
3	L5	400	A2M	O3'-C3'-C4'	-2.26	104.58	111.08
3	L5	4571	A2M	O4'-C1'-C2'	2.26	110.48	106.59
3	L5	4299	PSU	O2-C2-N1	-2.25	120.47	122.79
3	L5	2815	A2M	C1'-N9-C8	2.25	132.09	127.09
68	S2	1383	A2M	C6-C5-C4	-2.25	114.11	117.18
68	S2	462	OMC	C1'-N1-C2	2.25	123.40	118.44
68	S2	651	PSU	O2-C2-N1	-2.24	120.48	122.79
3	L5	1323	A2M	C2-N1-C6	-2.24	115.06	118.73
3	L5	2815	A2M	O4'-C1'-C2'	2.24	110.44	106.59
68	S2	1367	PSU	C6-N1-C2	-2.23	120.62	122.69
3	L5	4353	PSU	C6-N1-C2	-2.23	120.62	122.69
3	L5	1326	A2M	C1'-N9-C8	2.23	132.04	127.09
3	L5	1860	PSU	O2-C2-N1	-2.23	120.49	122.79
3	L5	3822	PSU	C6-C5-C4	2.22	119.67	118.17
68	S2	1081	PSU	O4'-C1'-C2'	2.22	108.22	105.15
3	L5	4673	PSU	O2-C2-N1	-2.22	120.50	122.79
3	L5	3785	A2M	C6-C5-C4	-2.22	114.15	117.18
3	L5	3785	A2M	O4'-C4'-C3'	2.21	109.55	105.15
68	S2	668	A2M	C6-C5-C4	-2.21	114.16	117.18
3	L5	4973	PSU	C6-C5-C4	2.21	119.67	118.17
68	S2	159	A2M	C2-N1-C6	-2.21	115.10	118.73
3	L5	3867	A2M	C2-N1-C6	-2.20	115.11	118.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	863	PSU	O2-C2-N1	-2.20	120.52	122.79
3	L5	2787	A2M	C3'-C2'-C1'	-2.20	98.60	102.81
3	L5	2363	A2M	C2-N1-C6	-2.20	115.12	118.73
3	L5	4576	PSU	C6-N1-C2	-2.19	120.66	122.69
68	S2	468	A2M	O4'-C1'-C2'	2.19	110.36	106.59
3	L5	4552	PSU	C6-C5-C4	2.19	119.65	118.17
3	L5	1323	A2M	C5-C6-N1	2.19	123.06	117.51
68	S2	1177	PSU	C6-N1-C2	-2.18	120.66	122.69
3	L5	1326	A2M	C3'-C2'-C1'	-2.18	98.63	102.81
68	S2	99	A2M	C6-C5-C4	-2.18	114.20	117.18
3	L5	1326	A2M	C5-C6-N1	2.18	123.05	117.51
3	L5	3825	A2M	C5-C6-N1	2.17	123.02	117.51
3	L5	3825	A2M	C2-N1-C6	-2.17	115.17	118.73
3	L5	1534	A2M	C2-N1-C6	-2.17	115.17	118.73
68	S2	109	PSU	C6-C5-C4	2.17	119.64	118.17
68	S2	1248	B8N	O4-C4-C5	-2.16	118.83	122.58
68	S2	172	OMU	O2-C2-N1	-2.16	119.98	122.80
68	S2	428	OMU	O2-C2-N1	-2.16	119.98	122.80
68	S2	99	A2M	O4'-C1'-C2'	2.16	110.31	106.59
3	L5	3830	A2M	C5-C6-N1	2.16	123.00	117.51
3	L5	3785	A2M	C4'-O4'-C1'	-2.16	104.69	109.47
3	L5	3718	A2M	C6-C5-C4	-2.16	114.23	117.18
68	S2	576	A2M	C2-N1-C6	-2.16	115.18	118.73
68	S2	1442	OMU	C1'-N1-C2	2.16	121.47	117.59
3	L5	1534	A2M	O3'-C3'-C2'	2.16	117.23	111.19
3	L5	400	A2M	C2-N1-C6	-2.16	115.18	118.73
3	L5	4403	PSU	O4'-C1'-C2'	2.16	108.14	105.15
3	L5	2787	A2M	C6-C5-C4	-2.16	114.23	117.18
68	S2	814	PSU	C6-N1-C2	-2.15	120.69	122.69
3	L5	1534	A2M	C5-C6-N1	2.15	122.98	117.51
3	L5	3822	PSU	O4'-C1'-C2'	2.15	108.13	105.15
3	L5	1534	A2M	C6-C5-C4	-2.15	114.24	117.18
3	L5	3785	A2M	C5-C6-N1	2.15	122.97	117.51
68	S2	27	A2M	C5-C6-N1	2.15	122.97	117.51
68	S2	1081	PSU	C6-C5-C4	2.15	119.62	118.17
3	L5	1534	A2M	O3'-C3'-C4'	-2.14	104.92	111.08
68	S2	93	PSU	C6-N1-C2	-2.14	120.70	122.69
3	L5	3853	PSU	C6-N1-C2	-2.14	120.70	122.69
68	S2	1045	PSU	C6-N1-C2	-2.14	120.70	122.69
68	S2	99	A2M	C2-N1-C6	-2.14	115.22	118.73
68	S2	99	A2M	C5-C6-N1	2.13	122.93	117.51
68	S2	576	A2M	C5-C6-N1	2.13	122.93	117.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	799	OMU	C1'-N1-C2	2.13	121.42	117.59
3	L5	2815	A2M	C5-C6-N1	2.13	122.91	117.51
3	L5	1323	A2M	C6-C5-C4	-2.13	114.27	117.18
68	S2	651	PSU	C6-C5-C4	2.13	119.61	118.17
5	L8	69	PSU	O4'-C1'-C2'	2.12	108.09	105.15
3	L5	4571	A2M	C2-N1-C6	-2.12	115.25	118.73
3	L5	400	A2M	C5-C6-N1	2.12	122.88	117.51
3	L5	2363	A2M	C5-C6-N1	2.11	122.88	117.51
3	L5	2632	PSU	C6-C5-C4	2.11	119.60	118.17
68	S2	1031	A2M	O4'-C1'-C2'	2.11	110.22	106.59
3	L5	2787	A2M	C5-C6-N1	2.11	122.87	117.51
68	S2	1177	PSU	C6-C5-C4	2.11	119.60	118.17
68	S2	1244	PSU	C6-N1-C2	-2.11	120.74	122.69
68	S2	576	A2M	C6-C5-C4	-2.10	114.31	117.18
3	L5	398	A2M	C5-C6-N1	2.10	122.85	117.51
3	L5	2787	A2M	C2-N1-C6	-2.10	115.28	118.73
3	L5	3867	A2M	O4'-C1'-C2'	2.10	110.20	106.59
68	S2	576	A2M	O4'-C4'-C3'	2.10	109.32	105.15
68	S2	1031	A2M	C2-N1-C6	-2.10	115.28	118.73
3	L5	1677	PSU	O4'-C1'-C2'	2.09	108.04	105.15
3	L5	1326	A2M	C6-C5-C4	-2.09	114.32	117.18
68	S2	1383	A2M	C5-C6-N1	2.09	122.82	117.51
3	L5	4312	PSU	C6-C5-C4	2.09	119.58	118.17
3	L5	2363	A2M	C4-N9-C1'	-2.09	121.75	126.63
3	L5	4636	PSU	O4'-C1'-C2'	2.09	108.04	105.15
3	L5	3920	PSU	O4'-C1'-C2'	2.08	108.03	105.15
3	L5	2815	A2M	C2-N1-C6	-2.08	115.31	118.73
3	L5	4523	A2M	C5-C6-N1	2.08	122.79	117.51
68	S2	166	A2M	C5-C6-N1	2.07	122.78	117.51
3	L5	398	A2M	C6-C5-C4	-2.07	114.35	117.18
68	S2	668	A2M	C5-C6-N1	2.07	122.77	117.51
3	L5	1322	1MA	N1-C6-N6	2.07	124.91	119.71
3	L5	4523	A2M	C2-N1-C6	-2.07	115.34	118.73
68	S2	651	PSU	C6-N1-C2	-2.07	120.77	122.69
68	S2	484	A2M	C2-N1-C6	-2.07	115.34	118.73
3	L5	1534	A2M	C2'-C1'-N9	2.06	117.15	113.75
3	L5	2815	A2M	C6-C5-C4	-2.06	114.36	117.18
3	L5	398	A2M	C2-N1-C6	-2.06	115.34	118.73
3	L5	1522	OMG	C2'-C1'-N9	-2.06	110.33	114.24
3	L5	3718	A2M	C2-N1-C6	-2.06	115.34	118.73
3	L5	4590	A2M	C5-C6-N1	2.06	122.74	117.51
68	S2	1288	OMU	O2-C2-N1	-2.06	120.12	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	S2	668	A2M	C2-N1-C6	-2.06	115.35	118.73
68	S2	649	PSU	O2-C2-N1	-2.06	120.67	122.79
3	L5	3695	PSU	O4'-C1'-C2'	2.05	107.99	105.15
3	L5	4571	A2M	C5-C6-N1	2.05	122.72	117.51
3	L5	1582	PSU	O2-C2-N1	-2.05	120.68	122.79
3	L5	1524	A2M	CM'-O2'-C2'	-2.04	109.25	114.47
3	L5	3867	A2M	C5-C6-N1	2.03	122.68	117.51
3	L5	2787	A2M	O2'-C2'-C1'	2.03	112.85	108.99
68	S2	814	PSU	C6-C5-C4	2.03	119.55	118.17
3	L5	2401	A2M	C5-C6-N1	2.03	122.67	117.51
68	S2	159	A2M	C5-C6-N1	2.03	122.66	117.51
3	L5	4361	PSU	C6-N1-C2	-2.03	120.81	122.69
68	S2	1031	A2M	C6-C5-C4	-2.02	114.42	117.18
3	L5	3830	A2M	C4'-O4'-C1'	-2.02	105.01	109.47
3	L5	4571	A2M	C2'-C1'-N9	2.01	117.06	113.75
3	L5	3830	A2M	C6-C5-C4	-2.00	114.44	117.18
3	L5	2363	A2M	O4'-C1'-C2'	2.00	110.04	106.59
3	L5	4523	A2M	O4'-C1'-C2'	2.00	110.04	106.59

There are no chirality outliers.

All (146) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L5	398	A2M	C1'-C2'-O2'-CM'
3	L5	1326	A2M	O4'-C4'-C5'-O5'
3	L5	1625	OMG	O4'-C4'-C5'-O5'
3	L5	2351	OMC	C1'-C2'-O2'-CM2
3	L5	2364	OMG	O4'-C4'-C5'-O5'
3	L5	2364	OMG	C1'-C2'-O2'-CM2
3	L5	2401	A2M	C3'-C4'-C5'-O5'
3	L5	2422	OMC	C1'-C2'-O2'-CM2
3	L5	2787	A2M	C1'-C2'-O2'-CM'
3	L5	2861	OMC	C1'-C2'-O2'-CM2
3	L5	3701	OMC	C2'-C1'-N1-C6
3	L5	3701	OMC	O4'-C4'-C5'-O5'
3	L5	3785	A2M	C3'-C4'-C5'-O5'
3	L5	3792	OMG	O4'-C4'-C5'-O5'
3	L5	3808	OMC	C1'-C2'-O2'-CM2
3	L5	3867	A2M	C1'-C2'-O2'-CM'
3	L5	4196	OMG	C1'-C2'-O2'-CM2
3	L5	4227	OMU	C1'-C2'-O2'-CM2
3	L5	4306	OMU	C1'-C2'-O2'-CM2

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Mol	Chain	Res	Type	Atoms
3	L5	4500	PSU	C3'-C4'-C5'-O5'
3	L5	4500	PSU	O4'-C4'-C5'-O5'
3	L5	4590	A2M	C3'-C4'-C5'-O5'
3	L5	4618	OMG	C1'-C2'-O2'-CM2
3	L5	4636	PSU	C2'-C1'-C5-C4
3	L5	4637	OMG	C1'-C2'-O2'-CM2
68	S2	27	A2M	C1'-C2'-O2'-CM'
68	S2	159	A2M	C1'-C2'-O2'-CM'
68	S2	166	A2M	C1'-C2'-O2'-CM'
68	S2	354	OMU	C1'-C2'-O2'-CM2
68	S2	428	OMU	C2'-C1'-N1-C2
68	S2	428	OMU	C2'-C1'-N1-C6
68	S2	462	OMC	C1'-C2'-O2'-CM2
68	S2	576	A2M	C1'-C2'-O2'-CM'
68	S2	601	OMG	C1'-C2'-O2'-CM2
68	S2	627	OMU	C3'-C4'-C5'-O5'
68	S2	627	OMU	O4'-C4'-C5'-O5'
68	S2	644	OMG	O4'-C4'-C5'-O5'
68	S2	1045	PSU	O4'-C4'-C5'-O5'
68	S2	1383	A2M	C1'-C2'-O2'-CM'
68	S2	1832	6MZ	N1-C6-N6-C9
3	L5	3701	OMC	C2'-C1'-N1-C2
3	L5	1326	A2M	C3'-C4'-C5'-O5'
3	L5	1536	PSU	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	3899	OMG	O4'-C4'-C5'-O5'
3	L5	3899	OMG	C3'-C4'-C5'-O5'
3	L5	4637	OMG	O4'-C4'-C5'-O5'
68	S2	99	A2M	O4'-C4'-C5'-O5'
68	S2	801	PSU	C3'-C4'-C5'-O5'
3	L5	1625	OMG	C3'-C4'-C5'-O5'
3	L5	2401	A2M	O4'-C4'-C5'-O5'
3	L5	2815	A2M	O4'-C4'-C5'-O5'
3	L5	3785	A2M	O4'-C4'-C5'-O5'
3	L5	3867	A2M	O4'-C4'-C5'-O5'
3	L5	4220	6MZ	C3'-C4'-C5'-O5'
3	L5	4590	A2M	O4'-C4'-C5'-O5'
3	L5	4618	OMG	O4'-C4'-C5'-O5'
3	L5	4618	OMG	C3'-C4'-C5'-O5'
68	S2	172	OMU	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
68	S2	172	OMU	O4'-C4'-C5'-O5'
68	S2	428	OMU	C3'-C4'-C5'-O5'
68	S2	428	OMU	O4'-C4'-C5'-O5'
68	S2	576	A2M	O4'-C4'-C5'-O5'
68	S2	644	OMG	C3'-C4'-C5'-O5'
68	S2	801	PSU	O4'-C4'-C5'-O5'
68	S2	1045	PSU	C3'-C4'-C5'-O5'
68	S2	1248	B8N	O4'-C4'-C5'-O5'
68	S2	1442	OMU	O4'-C4'-C5'-O5'
68	S2	1703	OMC	O4'-C4'-C5'-O5'
3	L5	3792	OMG	C3'-C4'-C5'-O5'
3	L5	2364	OMG	C3'-C4'-C5'-O5'
3	L5	2787	A2M	C3'-C4'-C5'-O5'
3	L5	4220	6MZ	O4'-C4'-C5'-O5'
68	S2	576	A2M	C3'-C4'-C5'-O5'
68	S2	668	A2M	O4'-C4'-C5'-O5'
68	S2	668	A2M	C3'-C4'-C5'-O5'
3	L5	1524	A2M	O4'-C4'-C5'-O5'
3	L5	4228	OMG	O4'-C4'-C5'-O5'
3	L5	4637	OMG	C3'-C4'-C5'-O5'
68	S2	93	PSU	O4'-C4'-C5'-O5'
3	L5	4590	A2M	C4'-C5'-O5'-P
3	L5	2422	OMC	C3'-C4'-C5'-O5'
3	L5	2422	OMC	O4'-C4'-C5'-O5'
68	S2	93	PSU	C3'-C4'-C5'-O5'
68	S2	683	OMG	C3'-C4'-C5'-O5'
68	S2	1442	OMU	C3'-C4'-C5'-O5'
3	L5	2787	A2M	C2'-C1'-N9-C8
3	L5	1524	A2M	C3'-C4'-C5'-O5'
3	L5	4228	OMG	C3'-C4'-C5'-O5'
68	S2	99	A2M	C3'-C4'-C5'-O5'
3	L5	2815	A2M	C3'-C4'-C5'-O5'
3	L5	3830	A2M	O4'-C4'-C5'-O5'
68	S2	1248	B8N	C3'-C4'-C5'-O5'
68	S2	1248	B8N	N34-C33-C34-O36
68	S2	121	OMU	C1'-C2'-O2'-CM2
3	L5	4447	5MC	C2'-C1'-N1-C6
3	L5	1781	PSU	C3'-C4'-C5'-O5'
3	L5	2632	PSU	C3'-C4'-C5'-O5'
3	L5	2632	PSU	O4'-C4'-C5'-O5'
3	L5	3830	A2M	C3'-C4'-C5'-O5'
68	S2	866	PSU	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
3	L5	1582	PSU	C3'-C4'-C5'-O5'
68	S2	1832	6MZ	C5-C6-N6-C9
3	L5	4447	5MC	O4'-C1'-N1-C6
68	S2	436	OMG	O4'-C4'-C5'-O5'
3	L5	4500	PSU	C4'-C5'-O5'-P
68	S2	1703	OMC	C3'-C4'-C5'-O5'
3	L5	3701	OMC	O4'-C1'-N1-C2
3	L5	1524	A2M	C3'-C2'-O2'-CM'
3	L5	1534	A2M	C4'-C5'-O5'-P
3	L5	3818	UY1	C4'-C5'-O5'-P
68	S2	644	OMG	C4'-C5'-O5'-P
68	S2	1851	MA6	C4'-C5'-O5'-P
3	L5	4636	PSU	O4'-C1'-C5-C4
68	S2	1248	B8N	O4'-C1'-C5-C4
3	L5	2787	A2M	C2'-C1'-N9-C4
3	L5	1326	A2M	C4'-C5'-O5'-P
3	L5	3701	OMC	O4'-C1'-N1-C6
68	S2	1081	PSU	C4'-C5'-O5'-P
68	S2	428	OMU	O4'-C1'-N1-C6
3	L5	3785	A2M	C3'-C2'-O2'-CM'
68	S2	576	A2M	C4'-C5'-O5'-P
68	S2	1490	OMG	C4'-C5'-O5'-P
3	L5	4447	5MC	O4'-C1'-N1-C2
3	L5	3844	PSU	C4'-C5'-O5'-P
68	S2	1288	OMU	C4'-C5'-O5'-P
3	L5	1792	PSU	O4'-C4'-C5'-O5'
68	S2	644	OMG	C1'-C2'-O2'-CM2
68	S2	1328	OMG	C1'-C2'-O2'-CM2
3	L5	1677	PSU	O4'-C1'-C5-C6
3	L5	3869	OMC	C3'-C2'-O2'-CM2
3	L5	4494	OMG	C3'-C2'-O2'-CM2
3	L5	1322	1MA	C2'-C1'-N9-C8
68	S2	428	OMU	O4'-C1'-N1-C2
3	L5	1323	A2M	O4'-C4'-C5'-O5'
3	L5	1582	PSU	O4'-C4'-C5'-O5'
3	L5	3887	OMC	C4'-C5'-O5'-P
68	S2	172	OMU	C4'-C5'-O5'-P
3	L5	2787	A2M	O4'-C4'-C5'-O5'
3	L5	2787	A2M	O4'-C1'-N9-C8
3	L5	4447	5MC	C2'-C1'-N1-C2
68	S2	1248	B8N	N3-C31-C32-C33
68	S2	801	PSU	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
3	L5	1322	1MA	C2'-C1'-N9-C4

There are no ring outliers.

68 monomers are involved in 99 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L5	1323	A2M	1	0
3	L5	1534	A2M	1	0
5	L8	69	PSU	1	0
3	L5	398	A2M	2	0
3	L5	2365	OMC	1	0
68	S2	172	OMU	1	0
68	S2	601	OMG	2	0
3	L5	1326	A2M	2	0
3	L5	2364	OMG	1	0
3	L5	4637	OMG	1	0
3	L5	3808	OMC	1	0
3	L5	4392	OMG	2	0
68	S2	1031	A2M	1	0
68	S2	1337	4AC	3	0
3	L5	2839	PSU	1	0
3	L5	2351	OMC	1	0
68	S2	436	OMG	1	0
68	S2	116	OMU	3	0
68	S2	576	A2M	3	0
68	S2	462	OMC	1	0
3	L5	3841	OMC	1	0
68	S2	1832	6MZ	1	0
68	S2	484	A2M	2	0
68	S2	649	PSU	2	0
3	L5	4196	OMG	1	0
3	L5	3867	A2M	3	0
3	L5	4457	PSU	1	0
3	L5	1340	OMC	2	0
3	L5	4456	OMC	1	0
3	L5	1322	1MA	1	0
3	L5	3785	A2M	1	0
3	L5	4579	PSU	2	0
3	L5	3718	A2M	4	0
3	L5	3920	PSU	1	0
68	S2	1288	OMU	1	0
68	S2	644	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L5	1781	PSU	1	0
3	L5	1683	PSU	1	0
3	L5	400	A2M	1	0
68	S2	867	OMG	2	0
68	S2	681	PSU	1	0
3	L5	4306	OMU	1	0
68	S2	166	A2M	3	0
68	S2	27	A2M	2	0
3	L5	2422	OMC	1	0
3	L5	2363	A2M	1	0
3	L5	4530	UR3	1	0
68	S2	406	PSU	1	0
68	S2	1842	4AC	2	0
3	L5	2861	OMC	1	0
3	L5	4500	PSU	1	0
68	S2	159	A2M	2	0
68	S2	866	PSU	1	0
3	L5	4689	PSU	1	0
68	S2	1850	MA6	2	0
3	L5	4623	OMG	1	0
3	L5	4620	OMU	1	0
68	S2	509	OMG	2	0
68	S2	121	OMU	4	0
68	S2	1056	PSU	1	0
3	L5	4447	5MC	1	0
3	L5	3851	PSU	1	0
68	S2	1383	A2M	1	0
68	S2	428	OMU	1	0
3	L5	4618	OMG	2	0
68	S2	93	PSU	1	0
3	L5	3925	OMU	1	0
68	S2	1004	PSU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 241 ligands modelled in this entry, 224 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	5261	-	9,9,9	0.36	0	8,8,8	1.08	0
88	SPM	L5	5292	-	13,13,13	0.37	0	12,12,12	0.84	0
89	SPD	L5	5282	-	9,9,9	0.30	0	8,8,8	0.80	0
89	SPD	L5	5283	-	9,9,9	0.33	0	8,8,8	0.97	0
89	SPD	L5	5285	-	9,9,9	0.35	0	8,8,8	0.77	0
89	SPD	L5	5286	-	9,9,9	0.33	0	8,8,8	0.89	0
88	SPM	L5	5288	-	13,13,13	0.38	0	12,12,12	0.83	0
89	SPD	L5	5287	-	9,9,9	0.32	0	8,8,8	0.81	0
88	SPM	L5	5267	-	13,13,13	0.37	0	12,12,12	0.99	0
88	SPM	L5	5259	-	13,13,13	0.35	0	12,12,12	1.03	0
88	SPM	L5	5291	-	13,13,13	0.33	0	12,12,12	0.88	0
89	SPD	L5	5289	-	9,9,9	0.33	0	8,8,8	0.93	0
89	SPD	L5	5290	-	9,9,9	0.32	0	8,8,8	0.90	0
89	SPD	L5	5284	-	9,9,9	0.31	0	8,8,8	0.87	0
89	SPD	LN	301	-	9,9,9	0.35	0	8,8,8	0.97	0
88	SPM	L5	5264	-	13,13,13	0.39	0	12,12,12	1.15	0
88	SPM	L5	5263	-	13,13,13	0.36	0	12,12,12	1.00	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	5261	-	-	1/7/7/7	-
88	SPM	L5	5292	-	-	2/11/11/11	-
89	SPD	L5	5282	-	-	1/7/7/7	-
89	SPD	L5	5283	-	-	2/7/7/7	-
89	SPD	L5	5285	-	-	3/7/7/7	-
89	SPD	L5	5286	-	-	1/7/7/7	-
88	SPM	L5	5288	-	-	6/11/11/11	-
89	SPD	L5	5287	-	-	1/7/7/7	-
88	SPM	L5	5267	-	-	2/11/11/11	-
88	SPM	L5	5259	-	-	2/11/11/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	SPM	L5	5291	-	-	6/11/11/11	-
89	SPD	L5	5289	-	-	0/7/7/7	-
89	SPD	L5	5290	-	-	3/7/7/7	-
89	SPD	L5	5284	-	-	3/7/7/7	-
89	SPD	LN	301	-	-	1/7/7/7	-
88	SPM	L5	5264	-	-	3/11/11/11	-
88	SPM	L5	5263	-	-	1/11/11/11	-

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
88	L5	5264	SPM	C2-C3-C4-N5
88	L5	5259	SPM	N5-C6-C7-C8
89	L5	5286	SPD	C3-C4-C5-N6
88	L5	5291	SPM	C7-C8-C9-N10
88	L5	5288	SPM	C3-C4-N5-C6
89	L5	5285	SPD	N6-C7-C8-C9
88	L5	5292	SPM	C8-C9-N10-C11
89	L5	5283	SPD	C8-C7-N6-C5
88	L5	5288	SPM	C8-C9-N10-C11
89	L5	5287	SPD	C8-C7-N6-C5
89	L5	5284	SPD	C3-C4-C5-N6
89	L5	5284	SPD	C2-C3-C4-C5
88	L5	5259	SPM	C6-C7-C8-C9
89	LN	301	SPD	C4-C5-N6-C7
89	L5	5290	SPD	C2-C3-C4-C5
89	L5	5282	SPD	C2-C3-C4-C5
88	L5	5264	SPM	C6-C7-C8-C9
88	L5	5292	SPM	C6-C7-C8-C9
89	L5	5290	SPD	N6-C7-C8-C9
88	L5	5264	SPM	N1-C2-C3-C4
88	L5	5291	SPM	C6-C7-C8-C9
88	L5	5288	SPM	C7-C6-N5-C4
89	L5	5261	SPD	C4-C5-N6-C7
88	L5	5291	SPM	C7-C6-N5-C4
88	L5	5291	SPM	C8-C9-N10-C11
88	L5	5263	SPM	C11-C12-C13-N14

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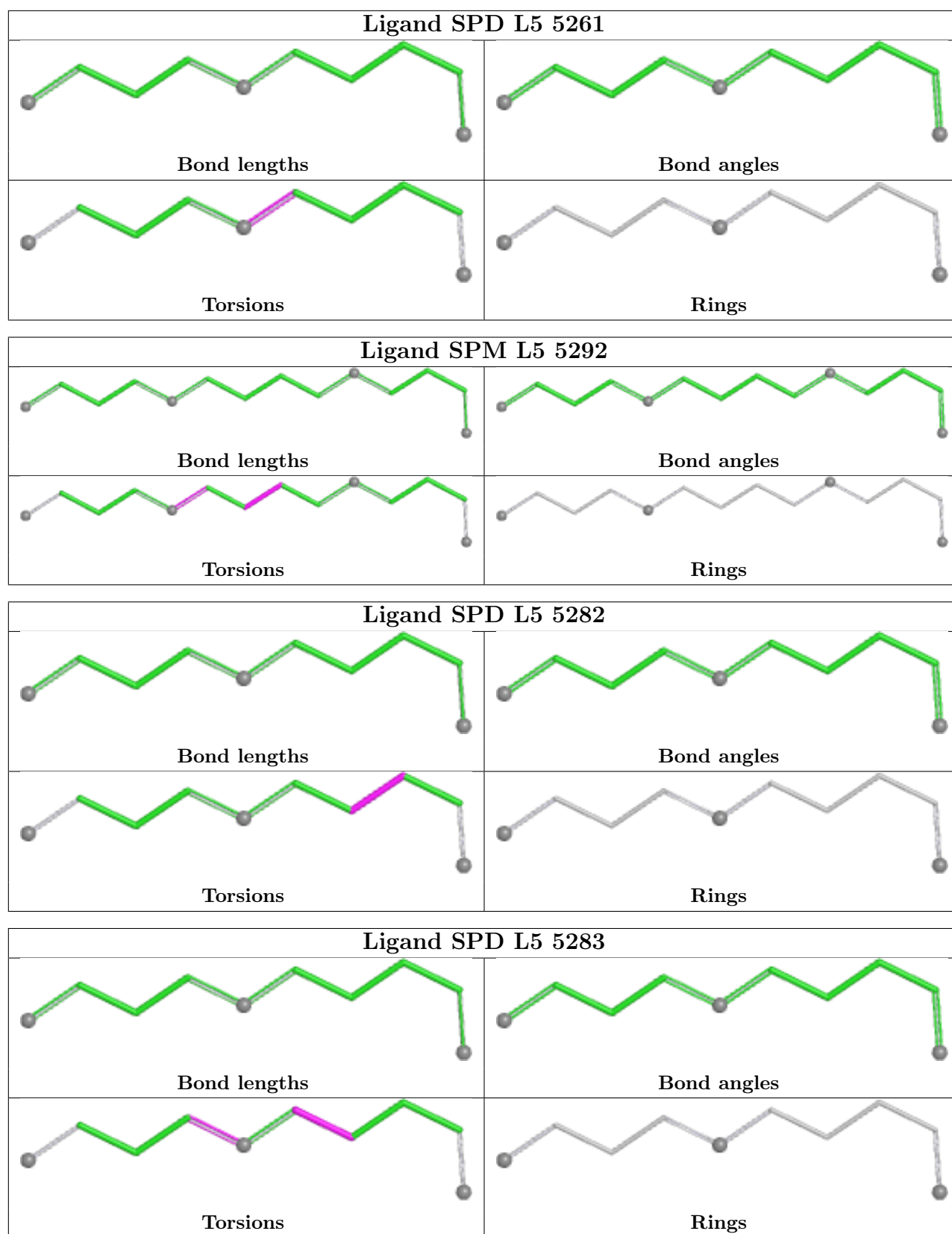
Mol	Chain	Res	Type	Atoms
88	L5	5267	SPM	C8-C9-N10-C11
88	L5	5288	SPM	N5-C6-C7-C8
89	L5	5290	SPD	C8-C7-N6-C5
88	L5	5291	SPM	C3-C4-N5-C6
89	L5	5285	SPD	C2-C3-C4-C5
89	L5	5284	SPD	N6-C7-C8-C9
88	L5	5288	SPM	C12-C11-N10-C9
89	L5	5285	SPD	C4-C5-N6-C7
88	L5	5288	SPM	C11-C12-C13-N14
88	L5	5267	SPM	C2-C3-C4-N5
89	L5	5283	SPD	C3-C4-C5-N6
88	L5	5291	SPM	C2-C3-C4-N5

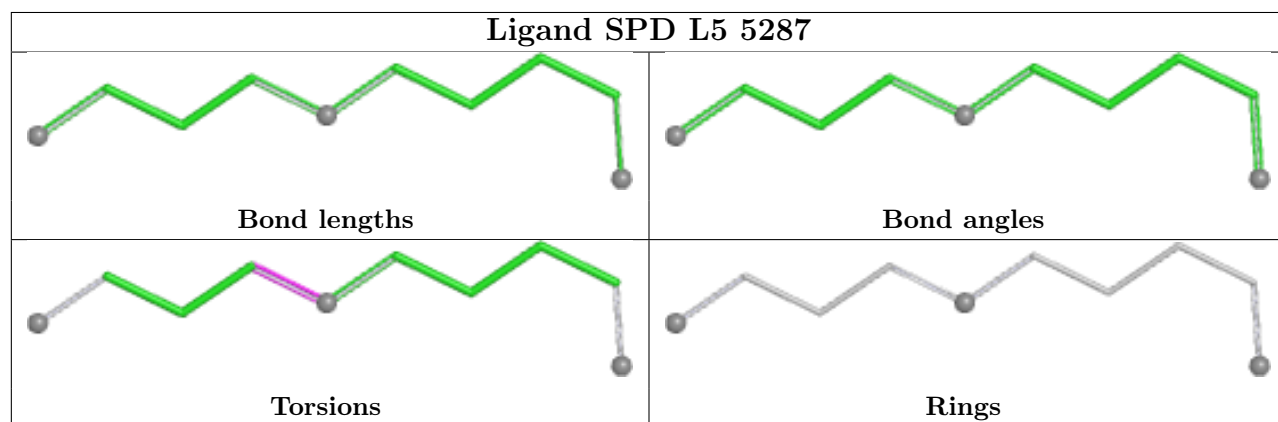
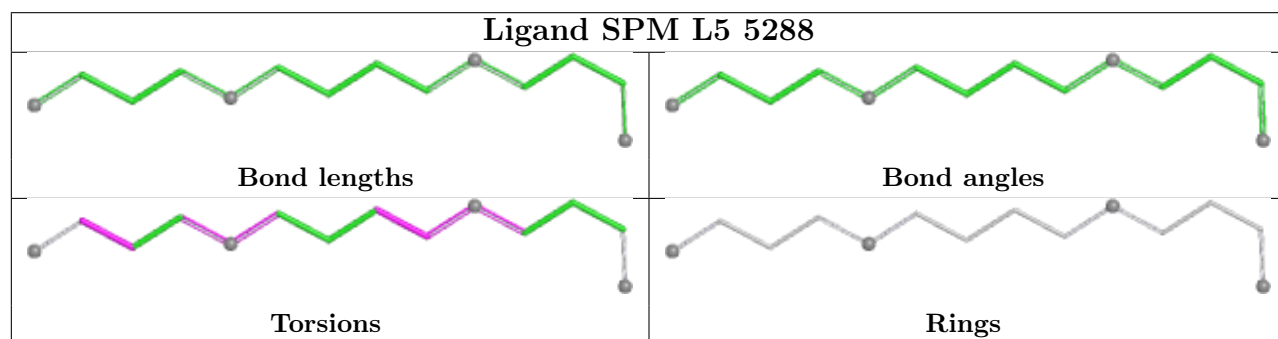
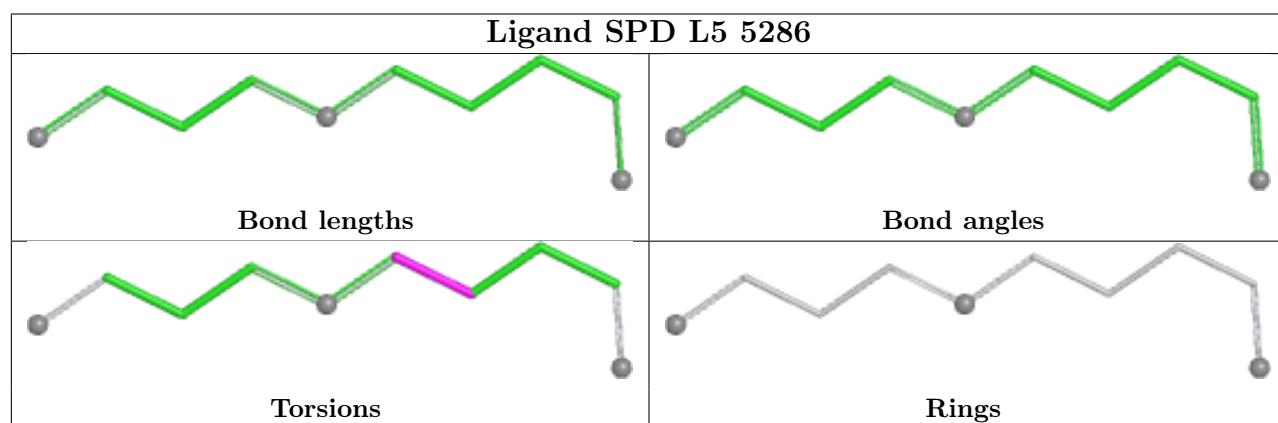
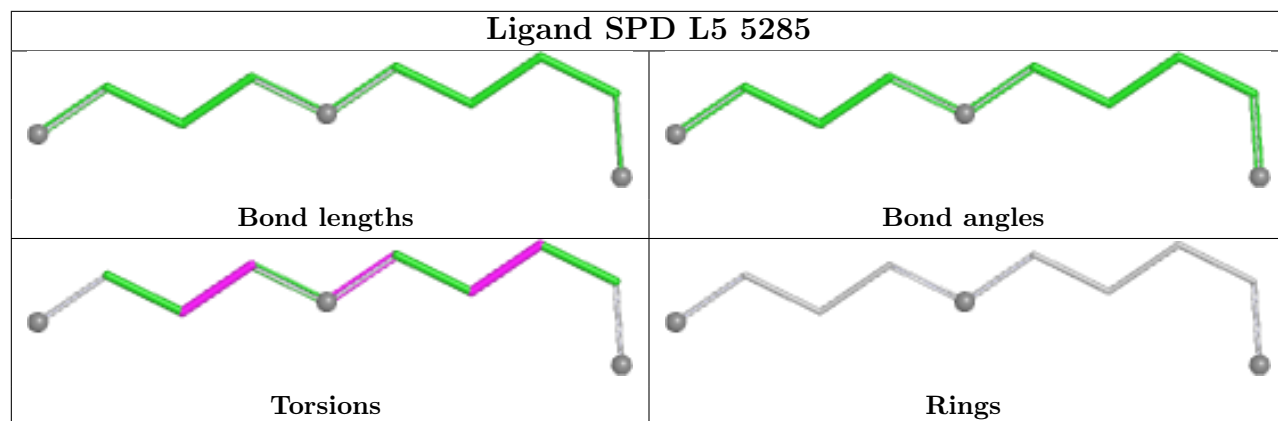
There are no ring outliers.

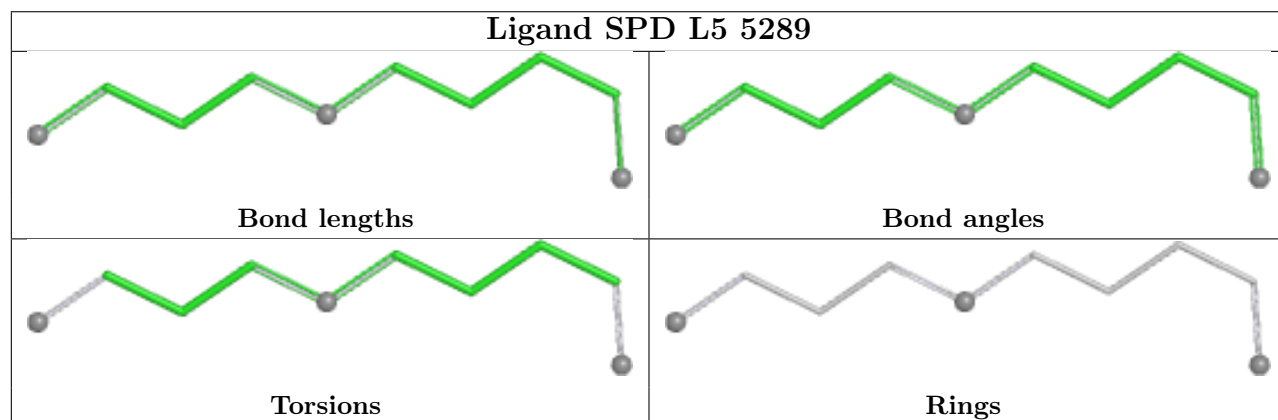
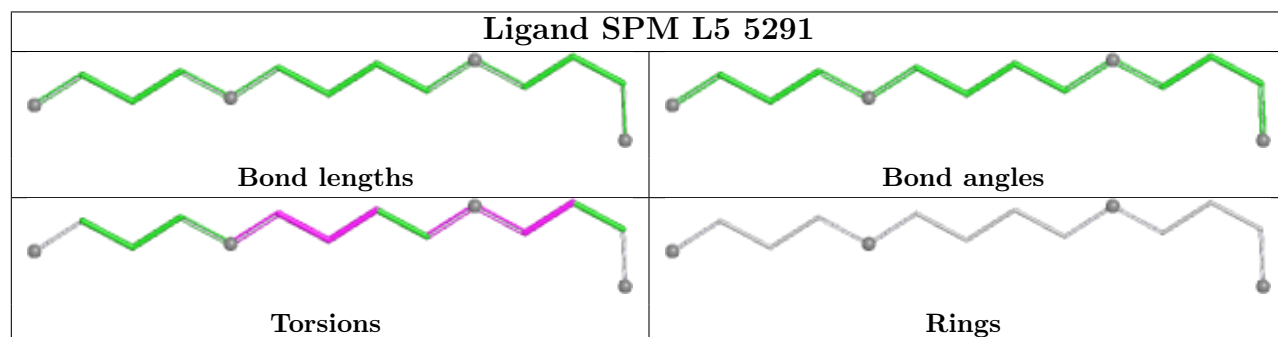
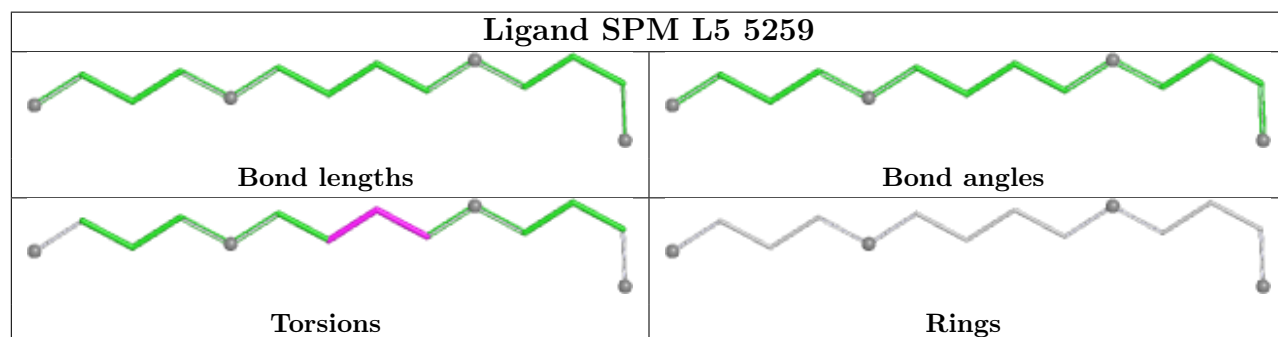
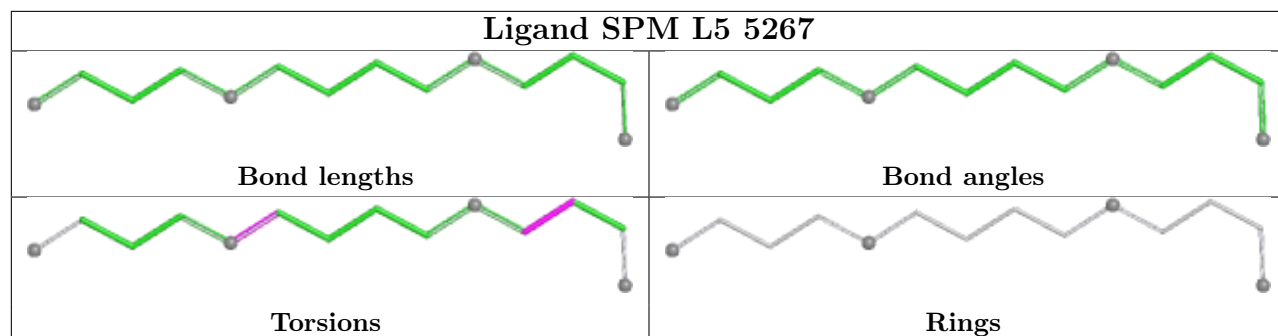
4 monomers are involved in 6 short contacts:

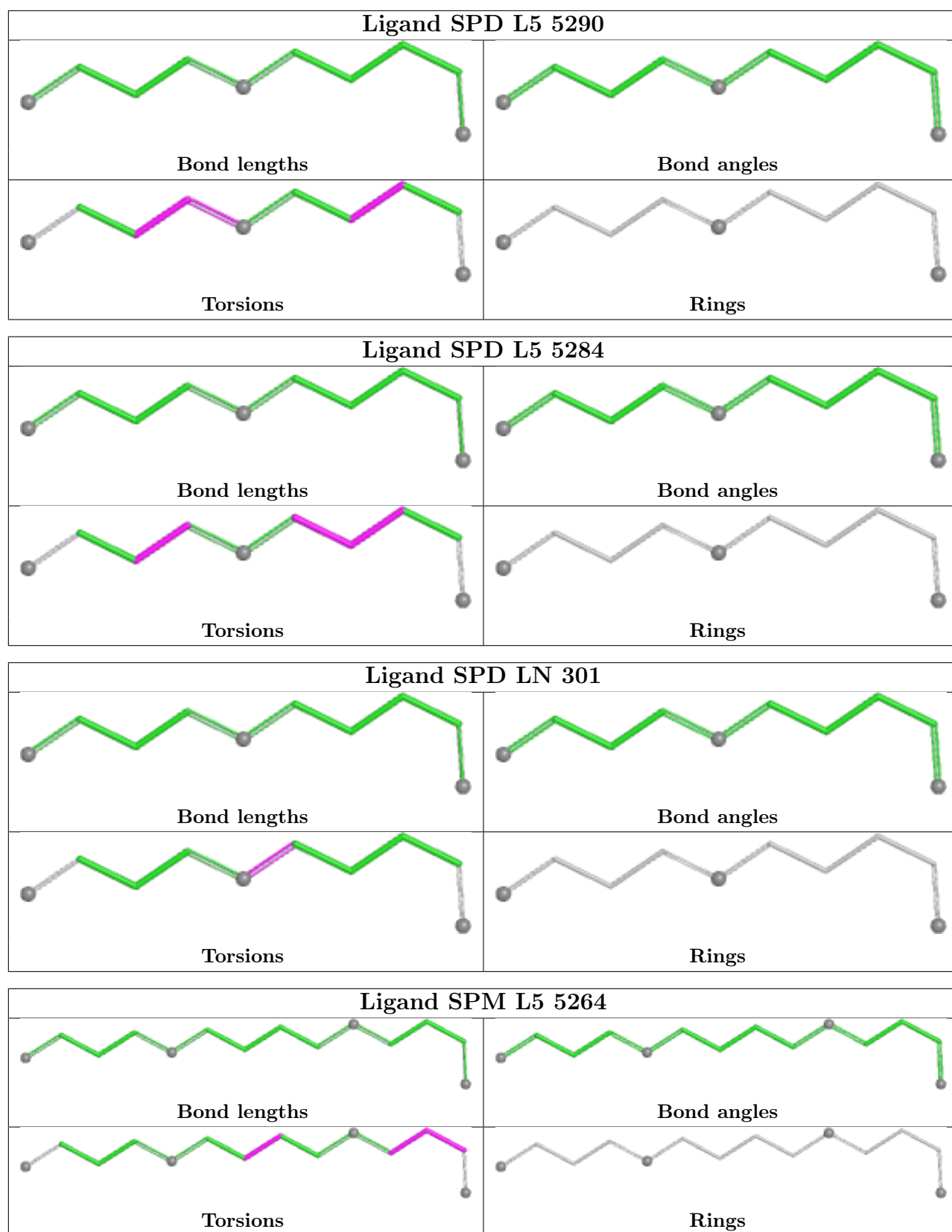
Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	L5	5292	SPM	3	0
88	L5	5288	SPM	1	0
89	L5	5290	SPD	1	0
88	L5	5263	SPM	1	0

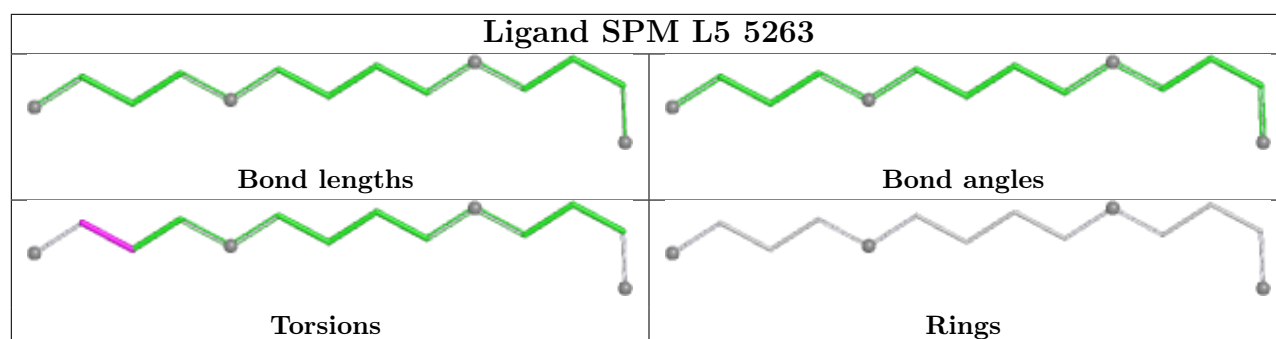
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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
68	S2	4
84	Et	1
3	L5	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	29.18
1	S2	698:G	O3'	730:C	P	14.27
1	S2	739:C	O3'	746:C	P	13.75
1	Et	16:C	O3'	18:U	P	7.68
1	S2	225:G	O3'	287:U	P	6.39
1	L5	3818:UY1	O3'	3819:G	P	3.31

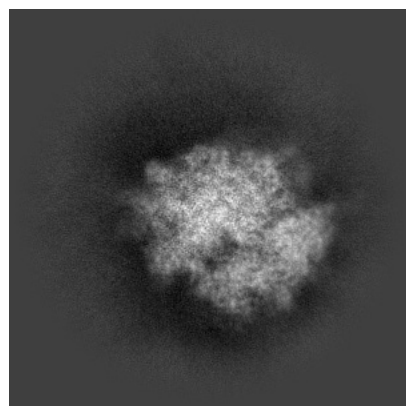
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71334. These allow visual inspection of the internal detail of the map and identification of artifacts.

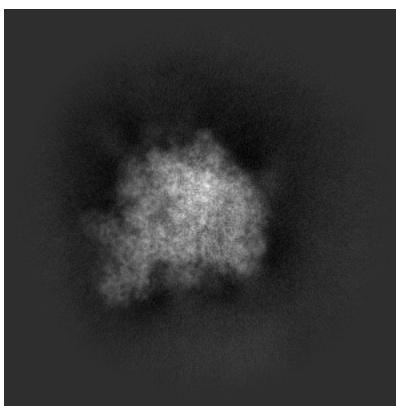
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

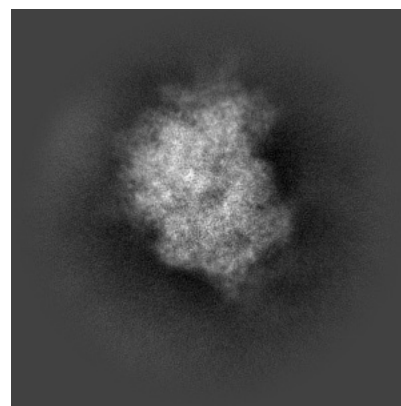
6.1.1 Primary map



X

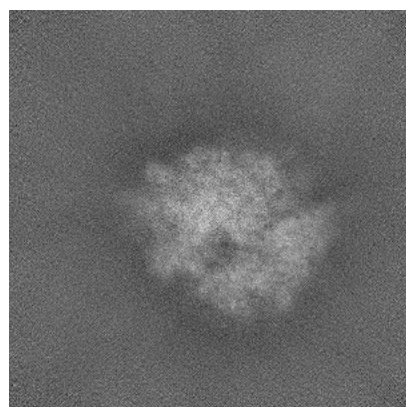


Y

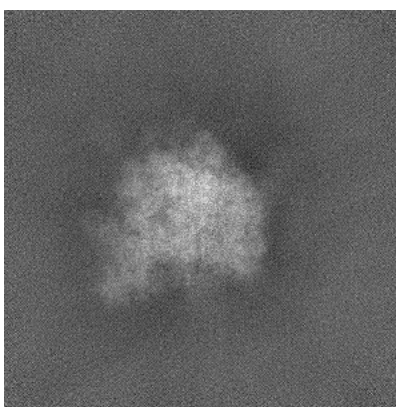


Z

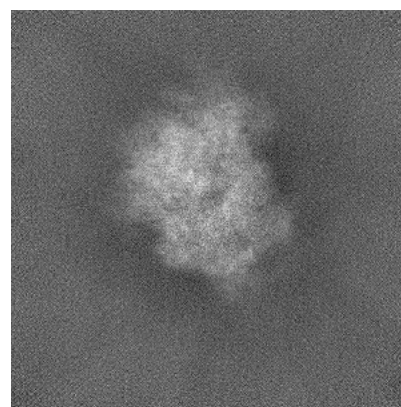
6.1.2 Raw map



X



Y

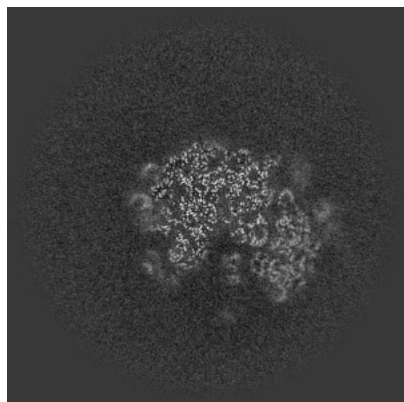


Z

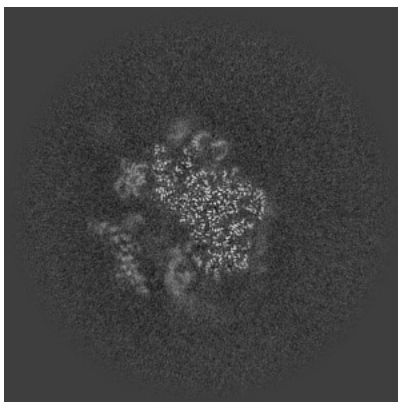
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

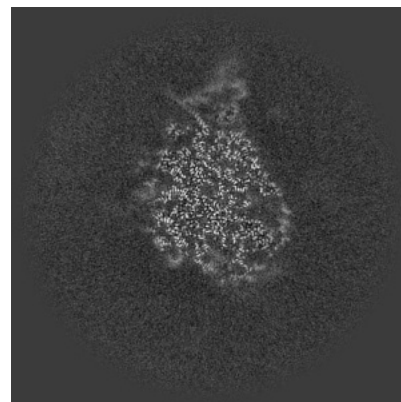
6.2.1 Primary map



X Index: 256

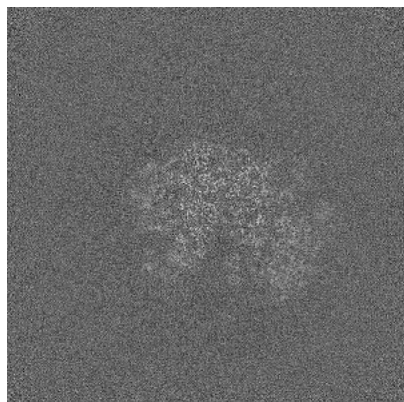


Y Index: 256

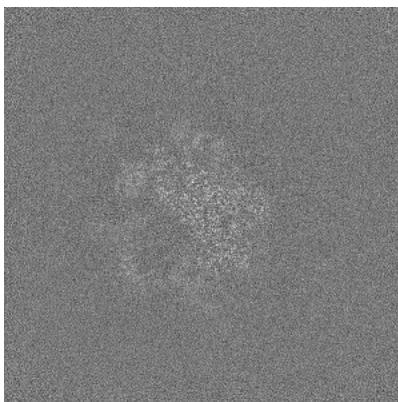


Z Index: 256

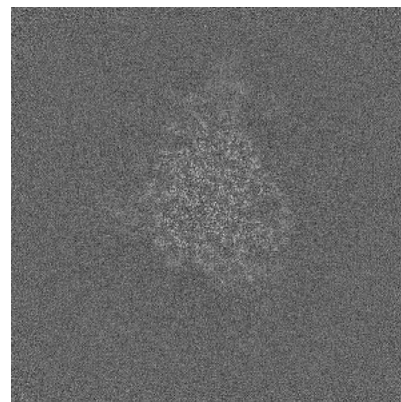
6.2.2 Raw map



X Index: 256



Y Index: 256

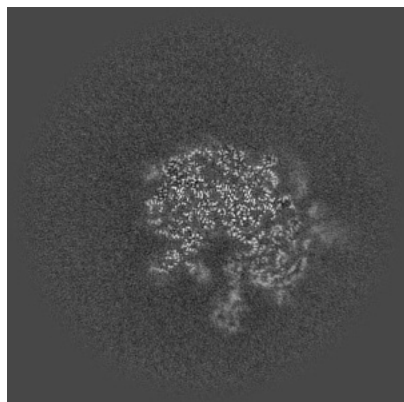


Z Index: 256

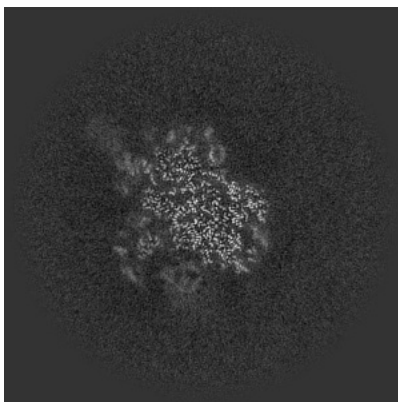
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

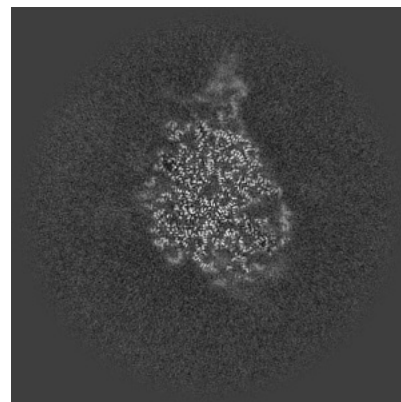
6.3.1 Primary map



X Index: 243

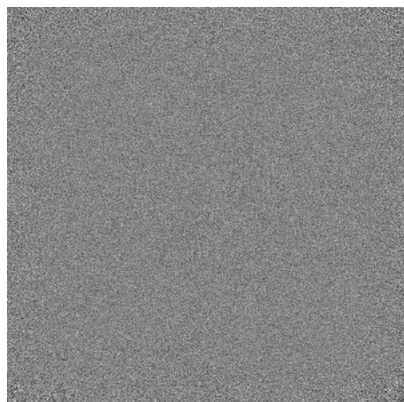


Y Index: 243

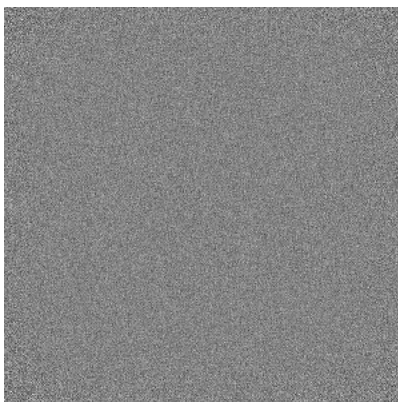


Z Index: 258

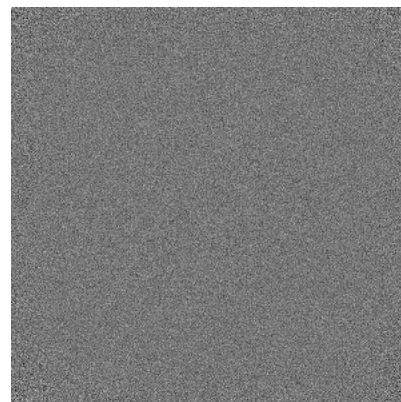
6.3.2 Raw map



X Index: 0



Y Index: 0

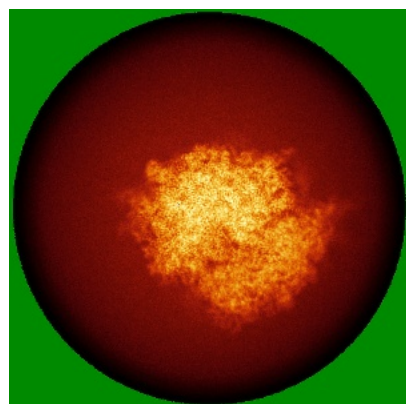


Z Index: 0

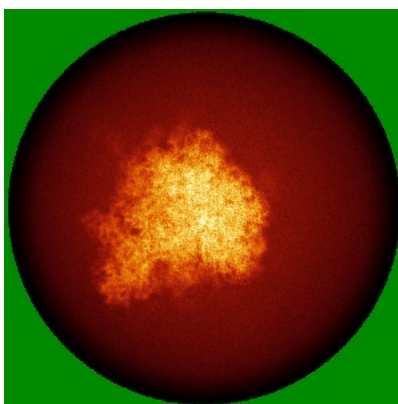
The images above show the largest variance slices of the map in three orthogonal directions.

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

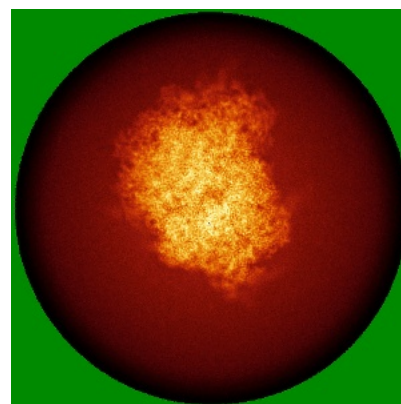
6.4.1 Primary map



X

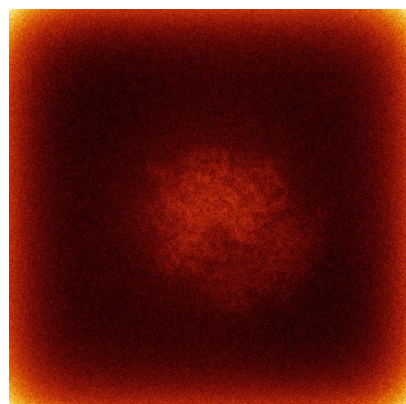


Y

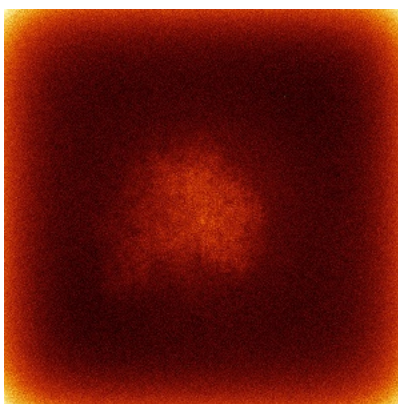


Z

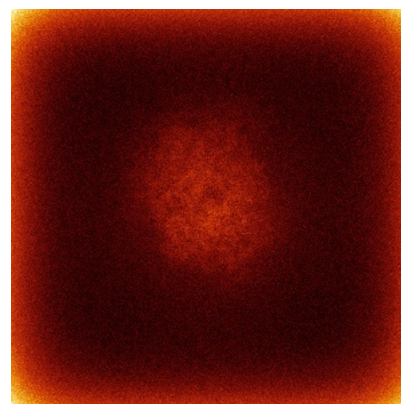
6.4.2 Raw map



X



Y

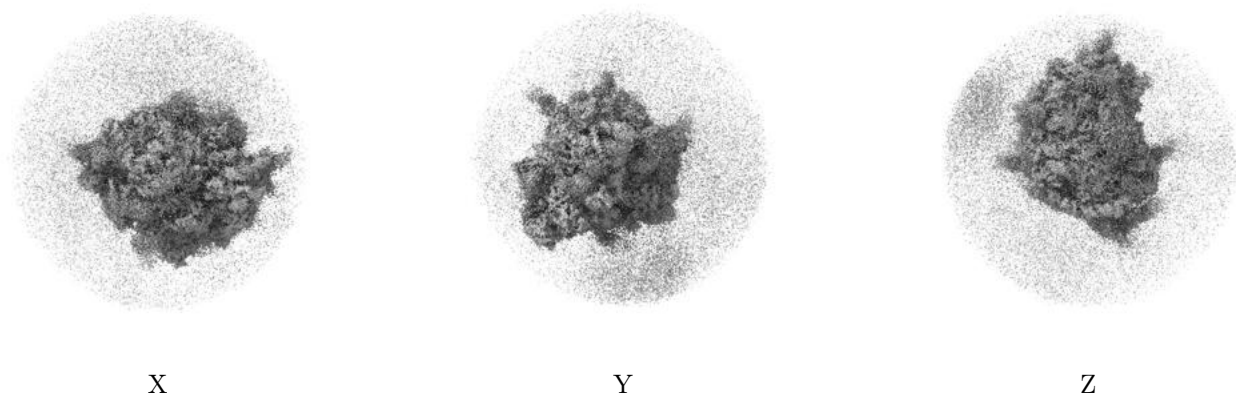


Z

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.

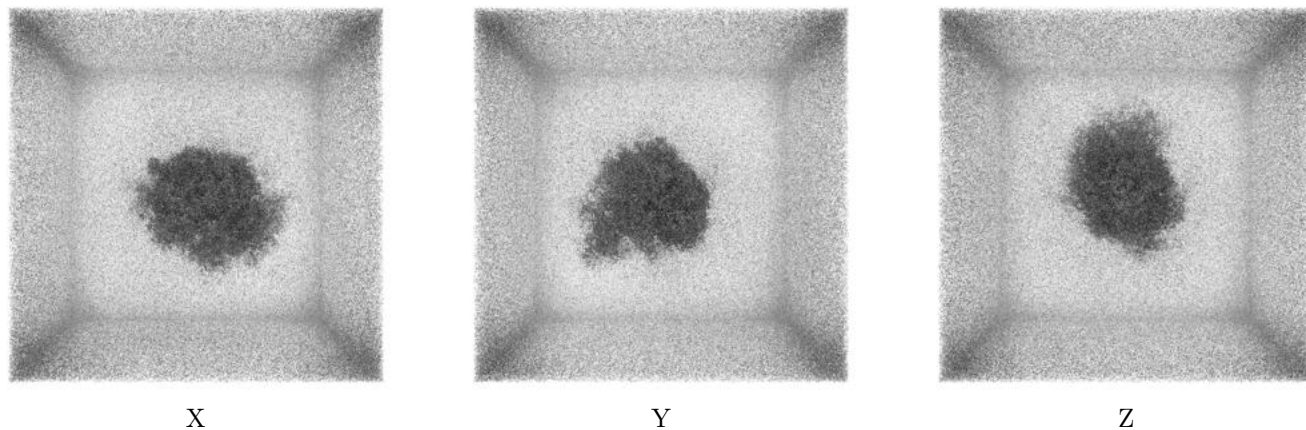
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0145. 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.

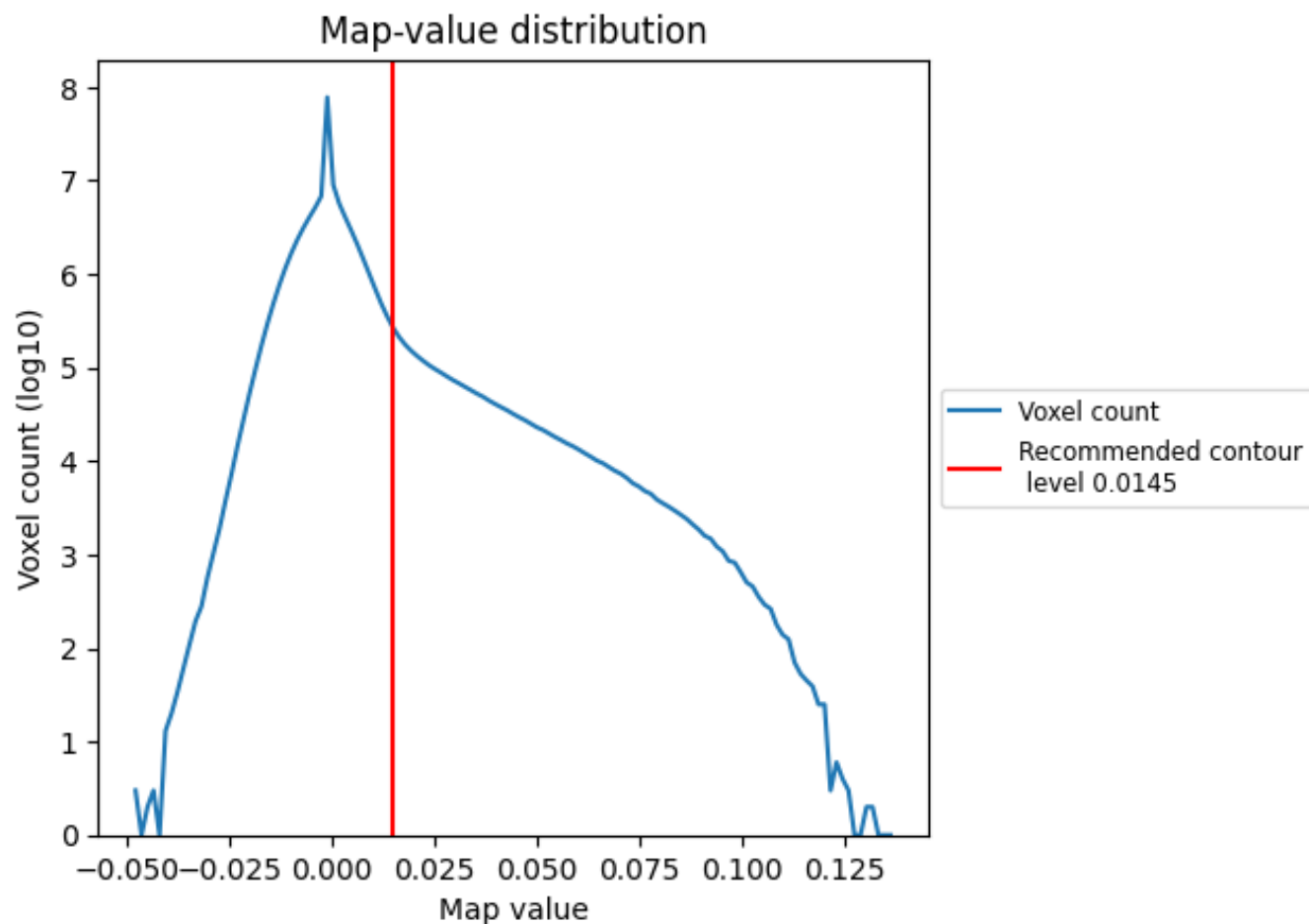
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

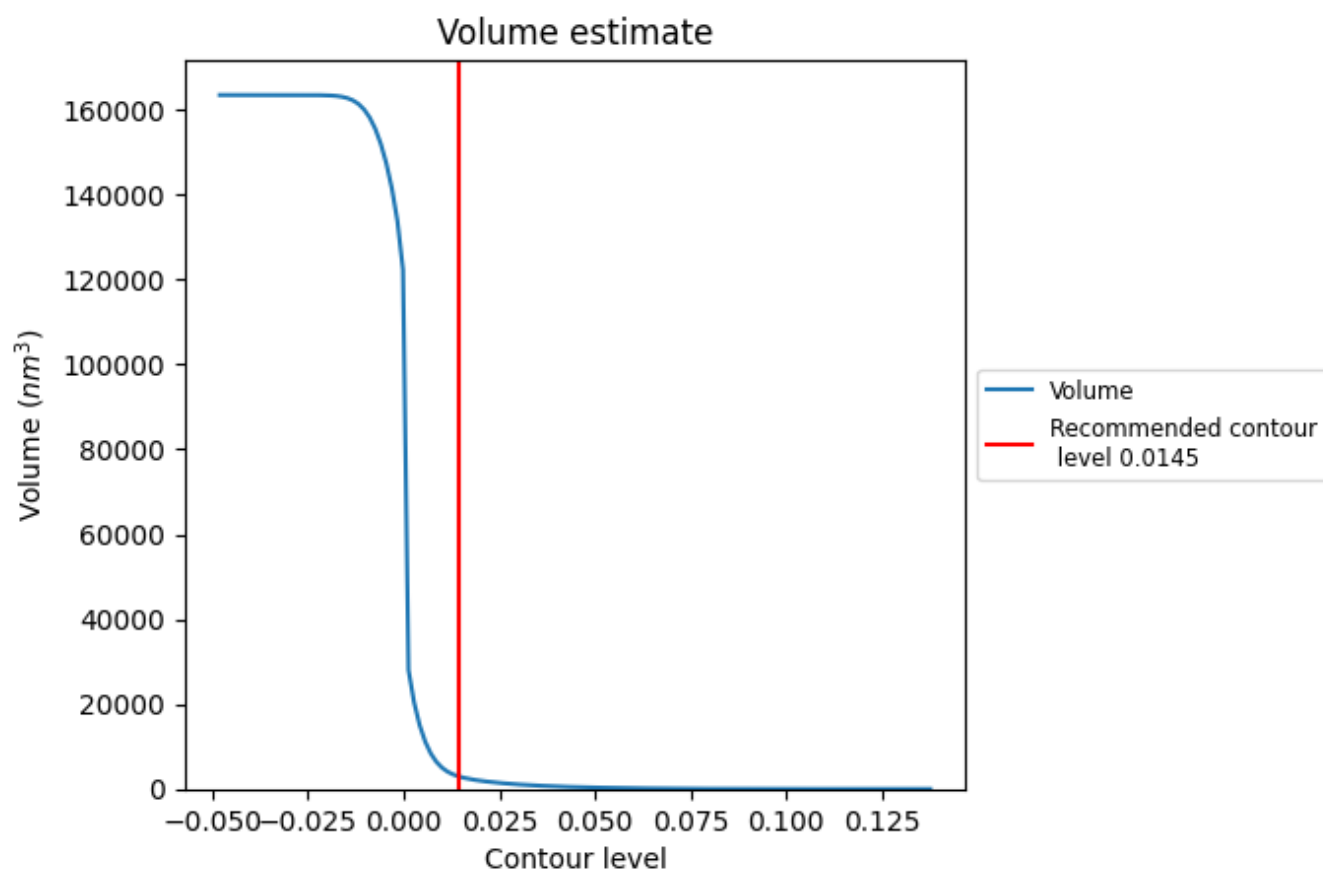
This section contains the results of statistical analysis of the map.

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.

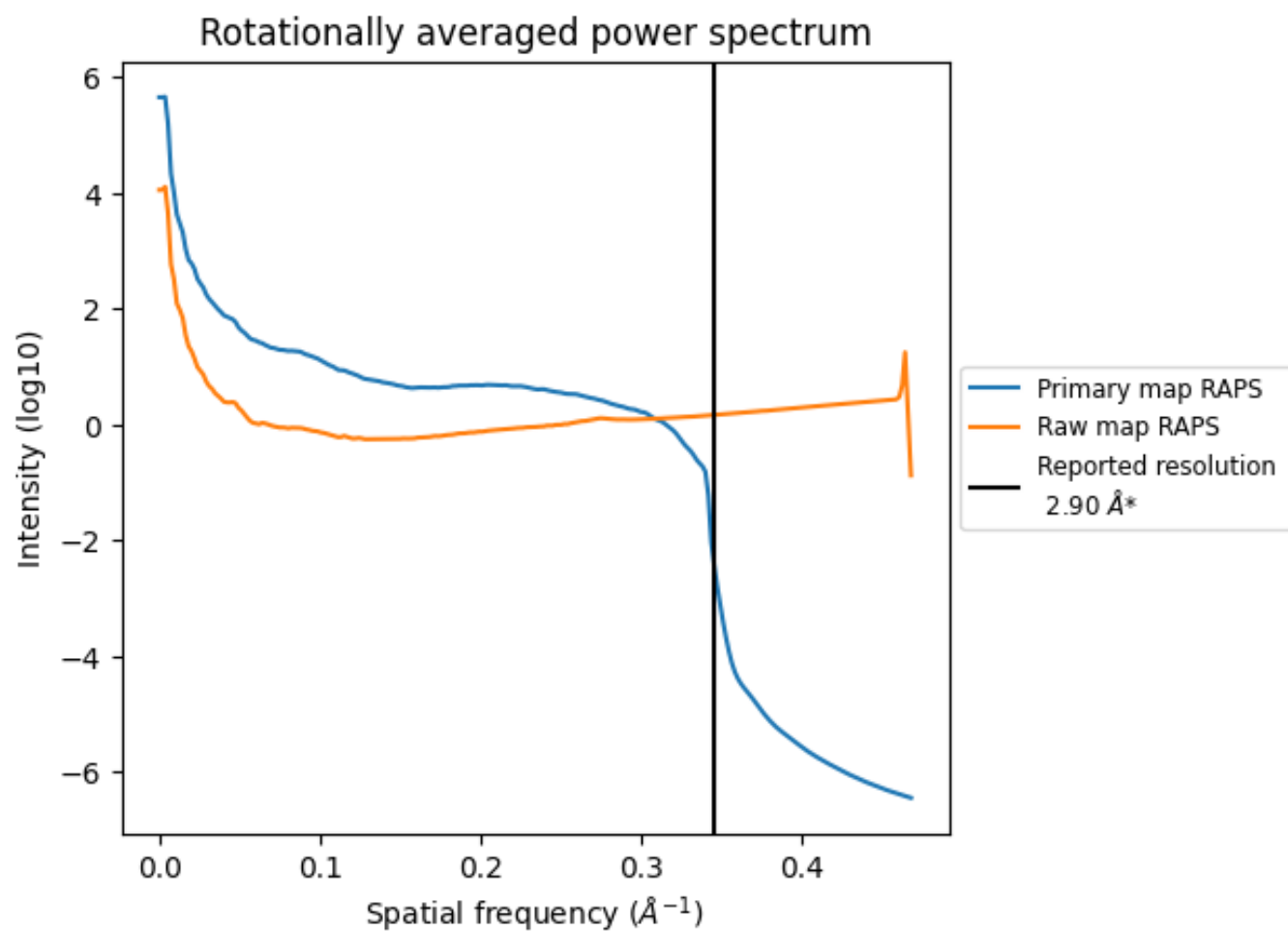
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2931 nm³; this corresponds to an approximate mass of 2648 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 ⓘ

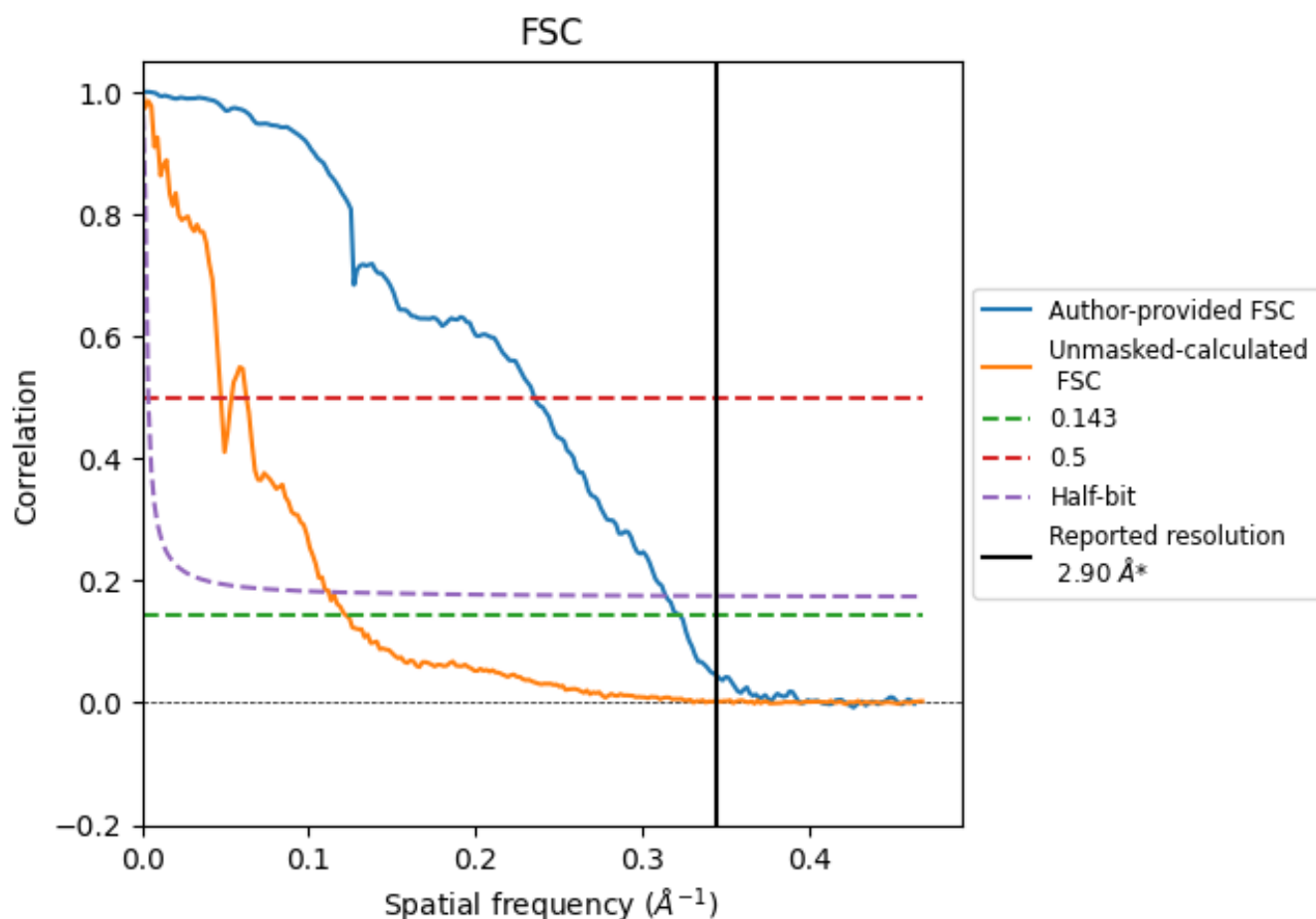


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

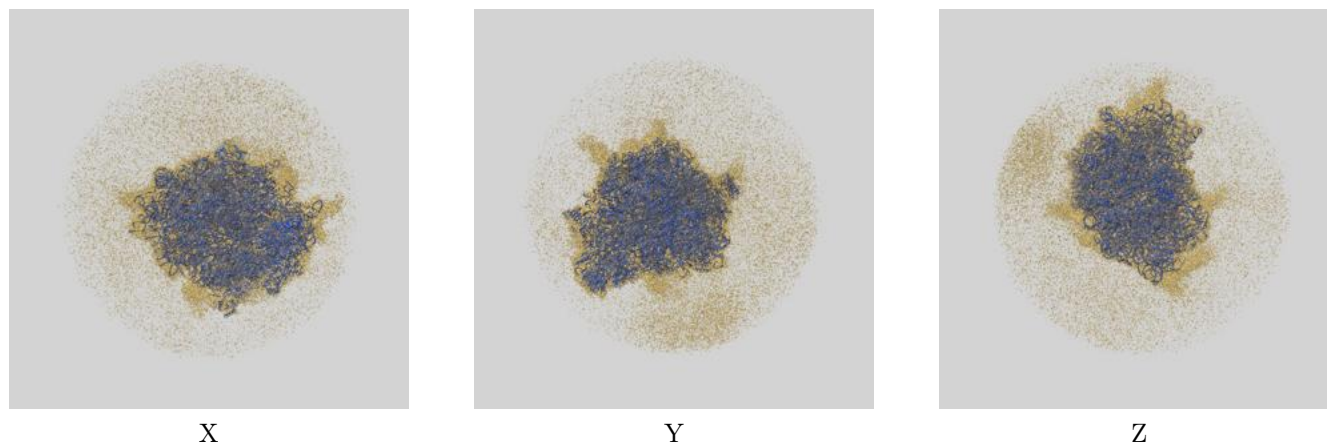
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	3.10	4.25	3.18
Unmasked-calculated*	8.18	21.23	8.94

*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 8.18 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

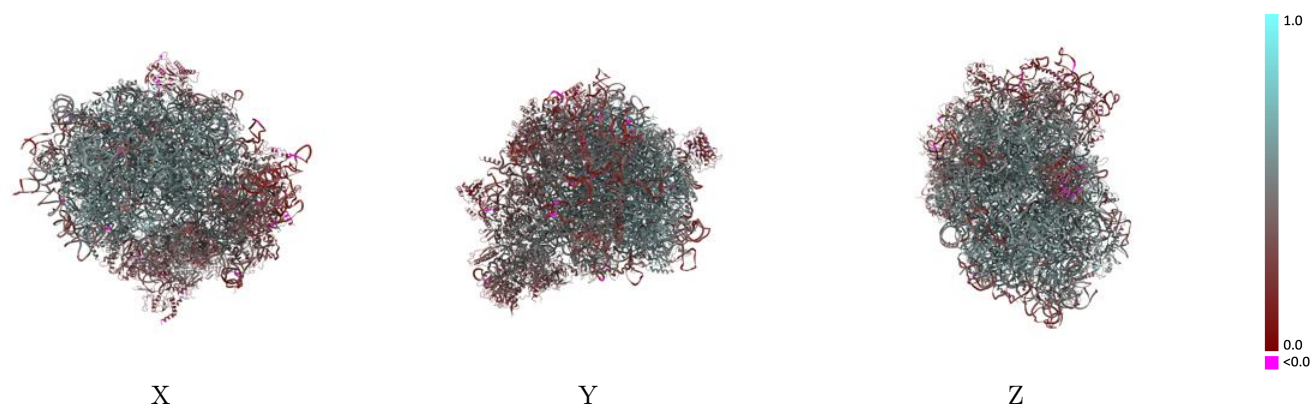
This section contains information regarding the fit between EMDB map EMD-71334 and PDB model 9P78. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



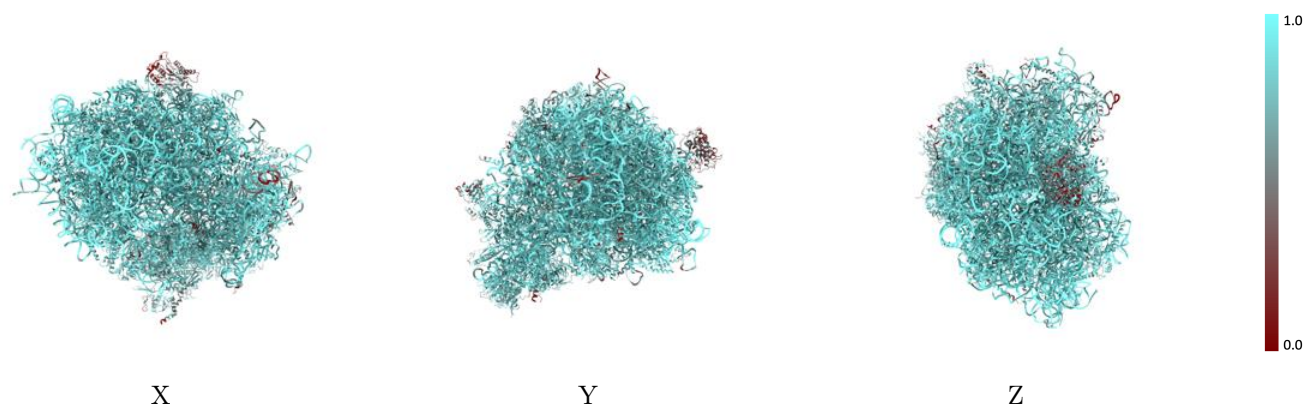
The images above show the 3D surface view of the map at the recommended contour level 0.0145 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



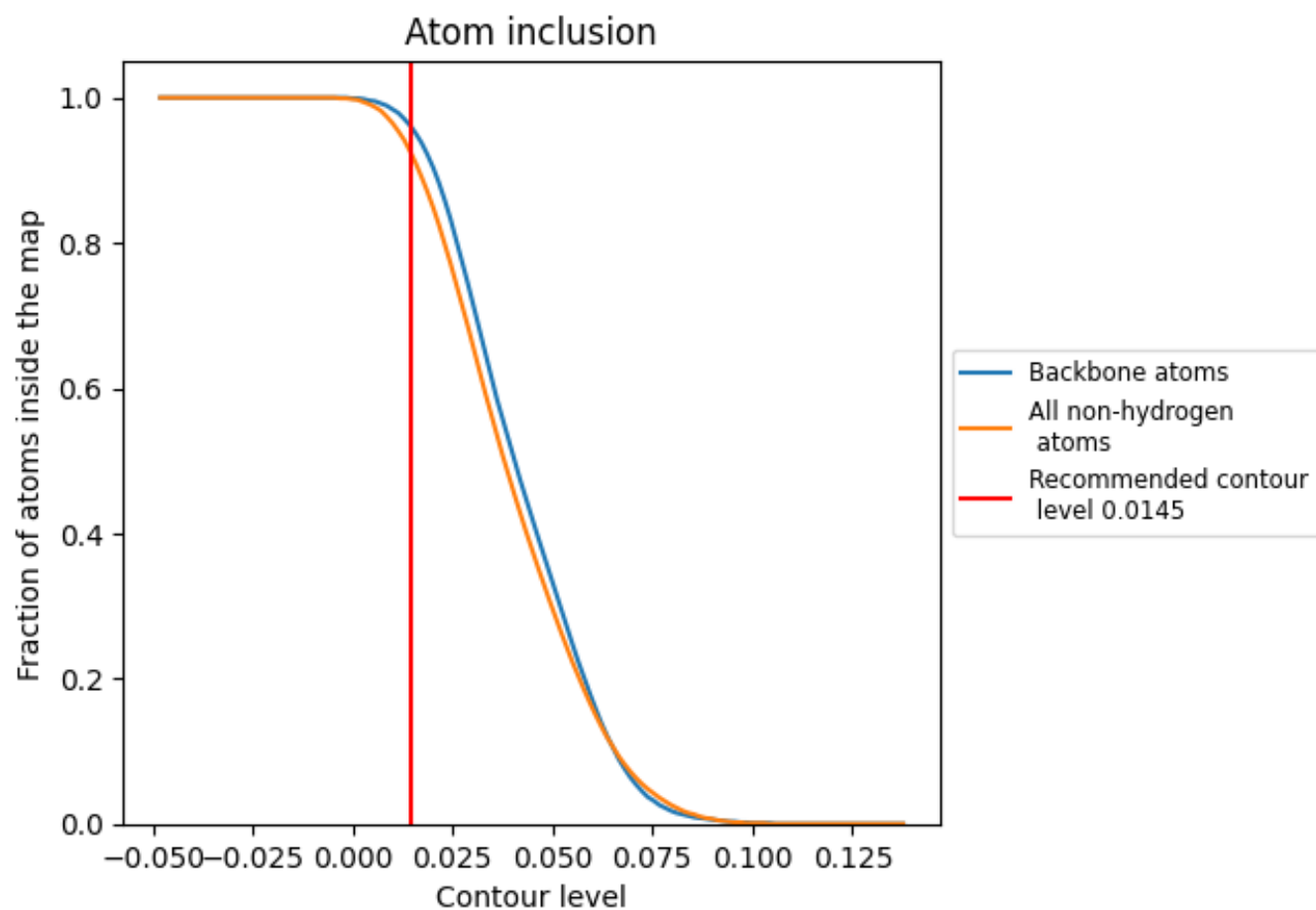
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0145).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 92% 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 (0.0145) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9250	 0.4710
CA	 0.3910	 0.2530
CB	 0.7830	 0.3760
CD	 0.6990	 0.2770
CI	 0.7030	 0.4020
Et	 0.9080	 0.3150
L5	 0.9770	 0.5150
L7	 0.9950	 0.5510
L8	 0.9830	 0.5350
LA	 0.9680	 0.5810
LB	 0.9430	 0.5560
LC	 0.9460	 0.5570
LD	 0.9320	 0.5190
LE	 0.9000	 0.4990
LF	 0.9640	 0.5580
LG	 0.8910	 0.5060
LH	 0.9370	 0.5440
LI	 0.9470	 0.5570
LJ	 0.8990	 0.4840
LL	 0.9140	 0.5330
LM	 0.9560	 0.5440
LN	 0.9820	 0.5880
LO	 0.9490	 0.5580
LP	 0.9570	 0.5660
LQ	 0.9660	 0.5740
LR	 0.9050	 0.5000
LS	 0.9670	 0.5710
LT	 0.9410	 0.5450
LU	 0.8870	 0.4740
LV	 0.9510	 0.5610
LW	 0.8240	 0.3860
LX	 0.9440	 0.5370
LY	 0.9300	 0.5340
LZ	 0.9580	 0.5290
La	 0.9660	 0.5820



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Chain	Atom inclusion	Q-score
Lb	 0.8870	 0.4750
Lc	 0.9050	 0.5070
Ld	 0.9390	 0.5470
Le	 0.9750	 0.5740
Lf	 0.9800	 0.5850
Lg	 0.9450	 0.5440
Lh	 0.9270	 0.5400
Li	 0.9410	 0.5390
Lj	 0.9720	 0.5760
Lk	 0.8900	 0.4840
Ll	 0.9570	 0.5520
Lm	 0.9400	 0.5630
Ln	 0.9520	 0.5370
Lo	 0.9250	 0.5490
Lp	 0.9380	 0.5480
Lr	 0.9590	 0.5590
Ls	 0.8030	 0.3490
Lt	 0.6270	 0.2480
S2	 0.9620	 0.4170
SA	 0.8390	 0.4120
SB	 0.8520	 0.4140
SC	 0.9230	 0.4720
SD	 0.8330	 0.3870
SE	 0.8790	 0.3680
SF	 0.8320	 0.3740
SG	 0.7880	 0.2880
SH	 0.7840	 0.3440
SI	 0.8690	 0.3950
SJ	 0.8440	 0.3610
SK	 0.8160	 0.3430
SL	 0.8490	 0.4420
SM	 0.6290	 0.2270
SN	 0.8860	 0.4520
SO	 0.8470	 0.4260
SP	 0.8170	 0.3810
SQ	 0.8540	 0.3870
SR	 0.8330	 0.3790
SS	 0.8040	 0.3480
ST	 0.8360	 0.3670
SU	 0.8070	 0.3680
SV	 0.8680	 0.4220
SW	 0.9280	 0.4670

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Chain	Atom inclusion	Q-score
SX	 0.8800	 0.4610
SY	 0.8140	 0.2980
SZ	 0.7220	 0.3440
Sa	 0.9070	 0.4690
Sb	 0.8610	 0.4200
Sc	 0.8020	 0.3900
Sd	 0.9090	 0.4290
Se	 0.8200	 0.3620
Sf	 0.7170	 0.2470
Sg	 0.7930	 0.3230