



Full wwPDB EM Validation Report ⓘ

Jun 23, 2026 – 10:28 PM EDT

PDB ID : 9P8I / pdb_00009p8i
EMDB ID : EMD-71378
Title : In situ HHT and CHX treated human P-Z state 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2025-06-23
Resolution : 3.89 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

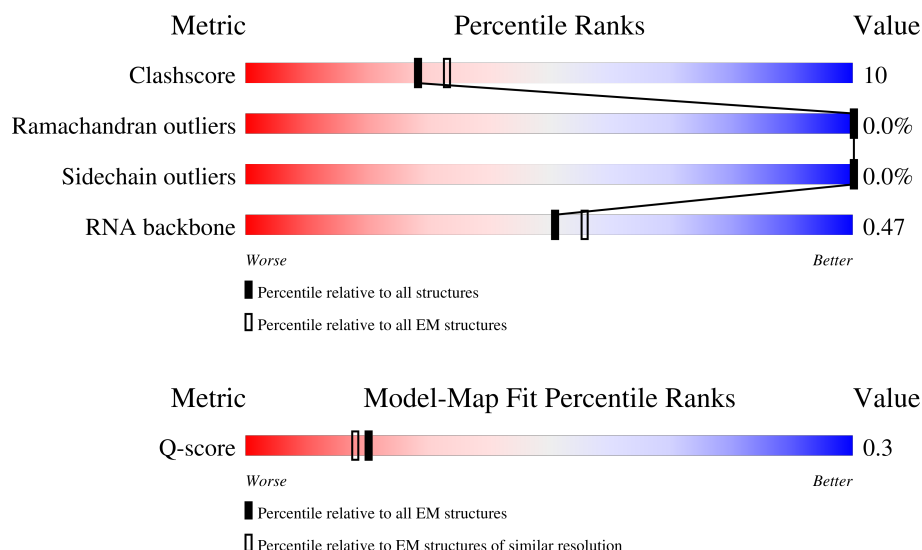
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.89 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.



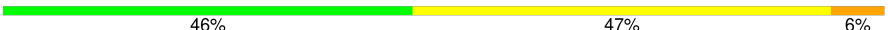
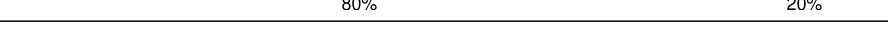
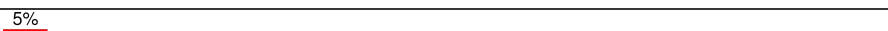
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8712 (3.39 - 4.39)

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	Pt	74	
2	L5	3655	
3	L7	120	

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Mol	Chain	Length	Quality of chain
4	L8	156	
5	LA	248	
6	LB	402	
7	LC	368	
8	LD	293	
9	LE	250	
10	LF	225	
11	LG	241	
12	LH	190	
13	LI	213	
14	LJ	176	
15	LL	210	
16	LM	139	
17	LN	203	
18	LO	201	
19	LP	153	
20	LQ	187	
21	LR	187	
22	LS	175	
23	LT	159	
24	LU	101	
25	LV	131	
26	LW	124	
27	LX	120	
28	LY	134	

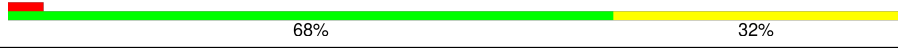
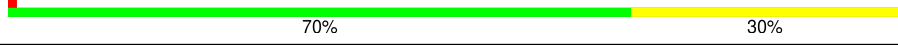
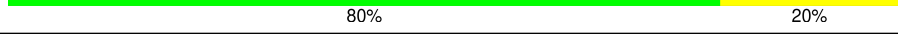
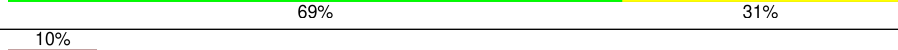
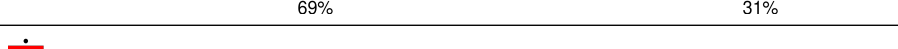
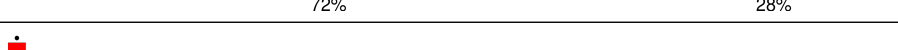
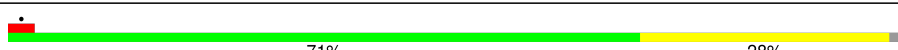
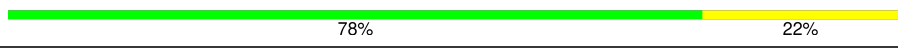
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Mol	Chain	Length	Quality of chain
29	LZ	135	
30	La	147	
31	Lb	121	
32	Lc	98	
33	Ld	107	
34	Le	128	
35	Lf	109	
36	Lg	114	
37	Lh	122	
38	Li	102	
39	Lj	86	
40	Lk	69	
41	Ll	50	
42	Lm	52	
43	Ln	24	
44	Lo	105	
45	Lp	91	
46	Lr	125	
47	Ls	196	
48	Lt	157	
49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

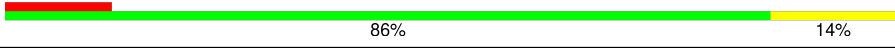
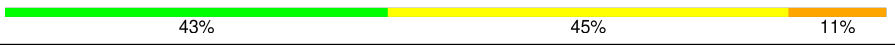
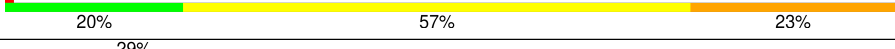
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Mol	Chain	Length	Quality of chain
54	SQ	144	
55	SR	135	
56	SS	145	
57	ST	143	
58	SU	104	
59	SZ	75	
60	Sc	64	
61	Sd	55	
62	Sf	67	
63	Sg	313	
64	SA	221	
65	SB	214	
66	SC	222	
67	SE	262	
68	SG	237	
69	SH	189	
70	SI	206	
71	SJ	185	
72	SL	153	
73	SN	150	
74	SO	140	
75	SV	83	
76	SW	129	
77	SX	141	
78	SY	131	

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Mol	Chain	Length	Quality of chain
79	Sa	102	 85% 15%
80	Sb	83	 76% 24%
81	Se	58	 12% 86% 14%
82	S2	1740	 43% 45% 11%
83	Zt	75	 20% 57% 23%
84	CI	31	 29% 68% 32%

2 Entry composition [i](#)

There are 90 unique types of molecules in this entry. The entry contains 220030 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called P site tRNA [Homo sapiens].

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

- Molecule 2 is a RNA chain called 28S rRNA [Homo sapiens].

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

- Molecule 3 is a RNA chain called 5S rRNA [Homo sapiens].

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

- Molecule 4 is a RNA chain called 5.8S rRNA [Homo sapiens].

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

- Molecule 5 is a protein called 60S ribosomal protein L8.

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

- Molecule 6 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 7 is a protein called 60S ribosomal protein L4.

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

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 9 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 10 is a protein called 60S ribosomal protein L7.

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

- Molecule 11 is a protein called 60S ribosomal protein L7a.

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

- Molecule 12 is a protein called 60S ribosomal protein L9.

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

- Molecule 13 is a protein called Ribosomal protein uL16-like.

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

- Molecule 14 is a protein called 60S ribosomal protein L11.

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

- Molecule 15 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 16 is a protein called 60S ribosomal protein L14.

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

- Molecule 17 is a protein called 60S ribosomal protein L15.

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

- Molecule 18 is a protein called 60S ribosomal protein L13a.

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

- Molecule 19 is a protein called 60S ribosomal protein L17.

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

- Molecule 20 is a protein called 60S ribosomal protein L18.

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

- Molecule 21 is a protein called 60S ribosomal protein L19.

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

- Molecule 22 is a protein called 60S ribosomal protein L18a.

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

- Molecule 23 is a protein called 60S ribosomal protein L21.

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

- Molecule 24 is a protein called Heparin-binding protein HBp15.

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

- Molecule 25 is a protein called 60S ribosomal protein L23.

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

- Molecule 26 is a protein called Ribosomal protein L24.

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

- Molecule 27 is a protein called 60S ribosomal protein L23a.

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

- Molecule 28 is a protein called 60S ribosomal protein L26.

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

- Molecule 29 is a protein called 60S ribosomal protein L27.

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

- Molecule 30 is a protein called 60S ribosomal protein L27a.

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

- Molecule 31 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 32 is a protein called 60S ribosomal protein L30.

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

- Molecule 33 is a protein called 60S ribosomal protein L31.

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

- Molecule 34 is a protein called 60S ribosomal protein L32.

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

- Molecule 35 is a protein called 60S ribosomal protein L35a.

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

- Molecule 36 is a protein called 60S ribosomal protein L34.

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

- Molecule 37 is a protein called 60S ribosomal protein L35.

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

- Molecule 38 is a protein called 60S ribosomal protein L36.

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

- Molecule 39 is a protein called 60S ribosomal protein L37.

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

- Molecule 40 is a protein called 60S ribosomal protein L38.

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

- Molecule 41 is a protein called 60S ribosomal protein L39.

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

- Molecule 42 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 43 is a protein called 60S ribosomal protein L41.

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

- Molecule 44 is a protein called 60S ribosomal protein L36a.

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

- Molecule 45 is a protein called 60S ribosomal protein L37a.

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

- Molecule 46 is a protein called 60S ribosomal protein L28.

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

- Molecule 47 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 48 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 49 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 50 is a protein called 40S ribosomal protein S5.

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

- Molecule 51 is a protein called 40S ribosomal protein S10.

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

- Molecule 52 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 54 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 55 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 56 is a protein called 40S ribosomal protein S18.

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

- Molecule 57 is a protein called 40S ribosomal protein S19.

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

- Molecule 58 is a protein called 40S ribosomal protein S20.

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

- Molecule 59 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 60 is a protein called 40S ribosomal protein S28.

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

- Molecule 61 is a protein called 40S ribosomal protein S29.

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

- Molecule 62 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 63 is a protein called Receptor of activated protein C kinase 1.

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

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

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

- Molecule 65 is a protein called 40S ribosomal protein S3a.

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

- Molecule 66 is a protein called 40S ribosomal protein S2.

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

- Molecule 67 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 68 is a protein called 40S ribosomal protein S6.

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

- Molecule 69 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 70 is a protein called 40S ribosomal protein S8.

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

- Molecule 71 is a protein called 40S ribosomal protein S9.

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

- Molecule 72 is a protein called 40S ribosomal protein S11.

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

- Molecule 73 is a protein called 40S ribosomal protein S13.

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

- Molecule 74 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 75 is a protein called Small ribosomal subunit protein eS21.

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

- Molecule 76 is a protein called 40S ribosomal protein S15a.

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

- Molecule 77 is a protein called 40S ribosomal protein S23.

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

- Molecule 78 is a protein called 40S ribosomal protein S24.

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

- Molecule 79 is a protein called 40S ribosomal protein S26.

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

- Molecule 80 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 81 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 82 is a RNA chain called 18S rRNA [Homo sapiens].

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

- Molecule 83 is a RNA chain called Z site tRNA [Homo sapiens].

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

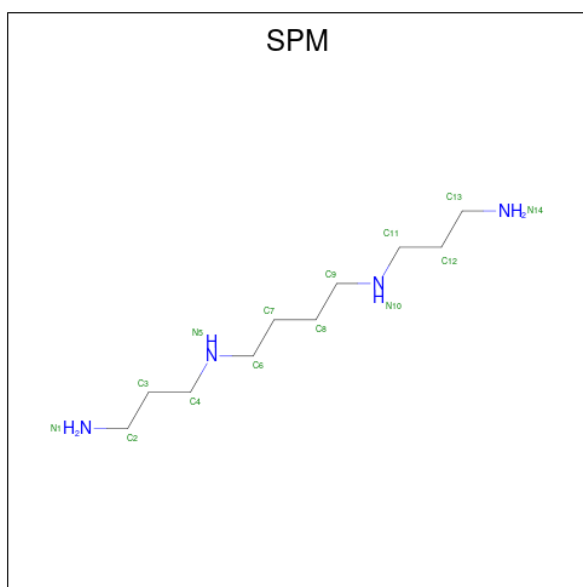
- Molecule 84 is a protein called Transcription factor BTF3.

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

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

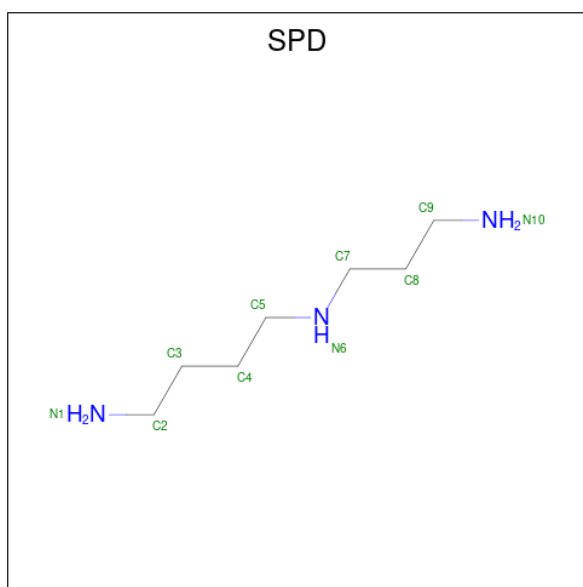
Mol	Chain	Residues	Atoms		AltConf
85	L5	179	Total	Mg	0
			179	179	
85	L7	3	Total	Mg	0
			3	3	
85	L8	4	Total	Mg	0
			4	4	
85	LA	1	Total	Mg	0
			1	1	
85	LP	1	Total	Mg	0
			1	1	
85	LV	1	Total	Mg	0
			1	1	
85	Le	1	Total	Mg	0
			1	1	
85	Lj	1	Total	Mg	0
			1	1	
85	SS	1	Total	Mg	0
			1	1	
85	S2	27	Total	Mg	0
			27	27	

- Molecule 86 is SPERMINE (CCD ID: SPM) (formula: C₁₀H₂₆N₄) (labeled as "Ligand of Interest" by depositor).



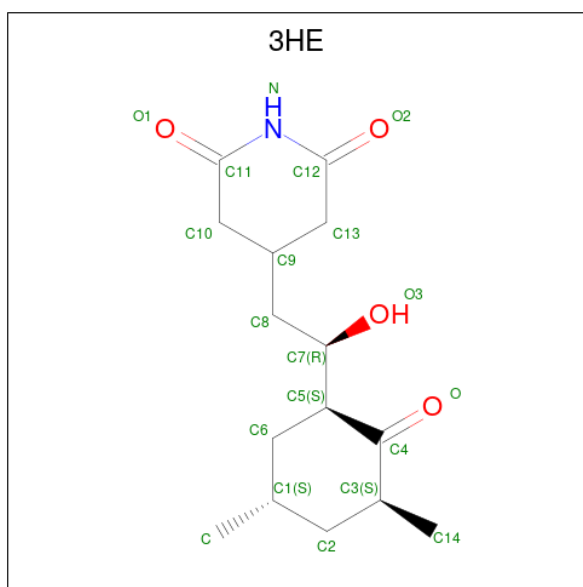
Mol	Chain	Residues	Atoms			AltConf
86	L5	1	Total	C	N	0
			14	10	4	
86	L5	1	Total	C	N	0
			14	10	4	
86	L5	1	Total	C	N	0
			14	10	4	
86	L5	1	Total	C	N	0
			14	10	4	
86	L5	1	Total	C	N	0
			14	10	4	
86	L5	1	Total	C	N	0
			14	10	4	

- Molecule 87 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$) (labeled as "Ligand of Interest" by depositor).



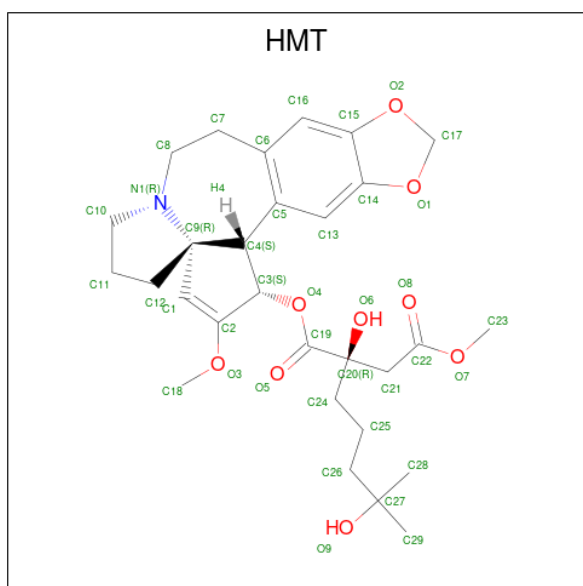
Mol	Chain	Residues	Atoms			AltConf
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	LN	1	Total	C	N	0
			10	7	3	

- Molecule 88 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: C₁₅H₂₃NO₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
88	L5	1	Total	C	N	O	0
			20	15	1	4	

- Molecule 89 is (3beta)-O 3 -[(2R)-2,6-dihydroxy-2-(2-methoxy-2-oxoethyl)-6-methylheptan oyl]cephalotaxine (CCD ID: HMT) (formula: $C_{29}H_{39}NO_9$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
89	L5	1	Total	C	N	O	0
			39	29	1	9	

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

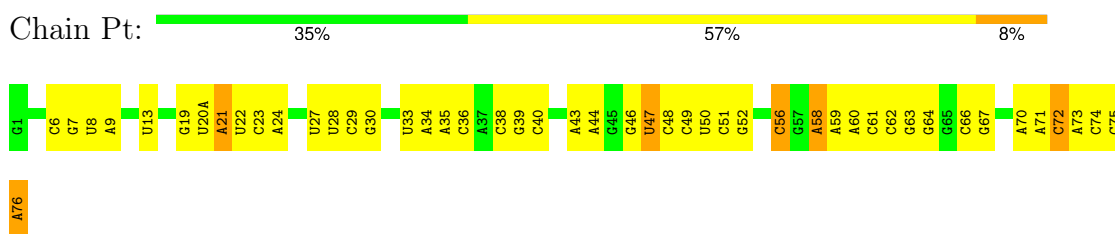
depositor).

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

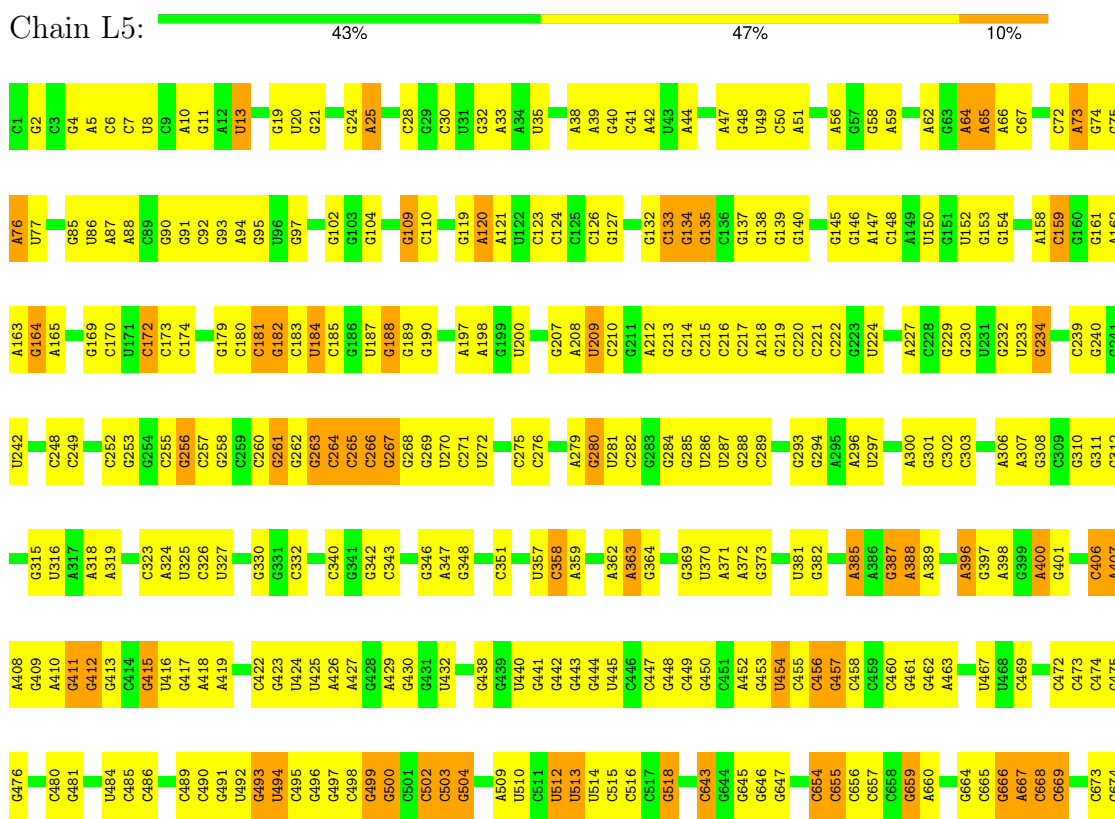
3 Residue-property plots

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

- Molecule 1: P site tRNA [Homo sapiens]

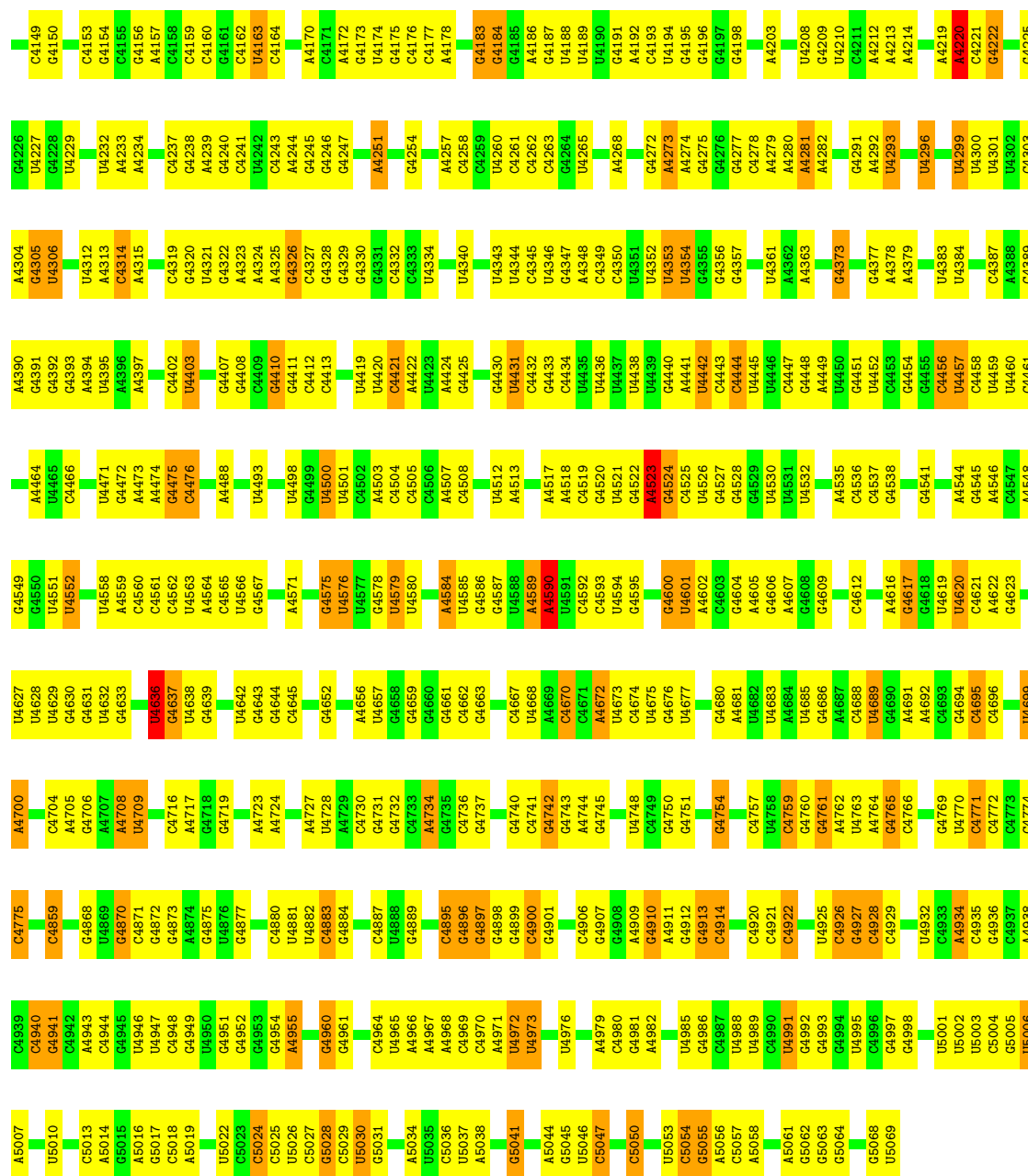


- Molecule 2: 28S rRNA [Homo sapiens]



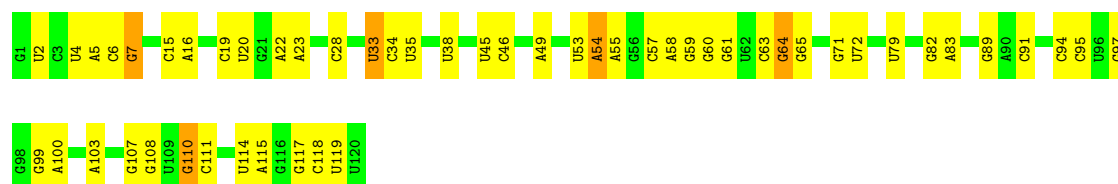
A1991	G1915	A1837	G1761	C1637	C1590	U1513	C1417	A1343	C1278	C1183	C962	G748	C675
U1992	G1916	G1842	C1762	C1678	C1591	U1514	C1418	C1344	C1279	A1184	G963	G749	C676
C1993	U1917	G1843	C1763	A1679	C1594	A1515	C1419	A1345	C1280	U1186	A964	U750	G677
G1994	U1918	G1844	C1764	A1680	C1595	A1516	A1420	A1346	C1281	G1187	G965	G751	C678
G1995	G1919	A1765	A1765	U1683	G1596	A1518	G1425	G1347	G1282	C1188	A966	G752	C679
G1996	G1920	U1845	A1766	U1684	G1597	A1519	G1426	G1348	G1283	C1189	C967	G755	G680
C1921	G1921	G1846	A1767	A1684	G1597	C1520	G1426	C1350	G1284	C1190	C968	G756	
U1997	G1922	C1847	C1768	A1687	A1601	C1520	C1431	C1350	U1285	C1191	C969		
A1998	C1925	C1848	C1769	G1688	A1602	A1523	C1432	C1351	U1286		C970		
A1999	C1926	U1849	A1770	G1689	G1612	A1524	G1433	C1352	C1287	G1194	U971	G759	
G2000	U1927	A1850	U1771	G1691	A1613	A1525	G1434	C1353	G1287	G1195	C972		
A2002	C1931	G1851	C1772	G1692	A1614		C1435	A1354	G1288	G1196	C973		
G2003	U1932	G1852	U1773	G1693	C1615	G1532	C1436	U1355	G1289	C904	C974		
U2004	C1933	G1853	U1774	G1694	U1616	A1533	C1437	U1356	G1290	C905			
G2005	U1934	C1854	U1775	G1695	G1617	A1534	C1438	C1357	C1291	C906			
C2006	A1934	C1855	U1776	G1696	G1618	C1535	C1439	C1358	G1292	C907			
G2007	U1935	C1856	U1777	G1697	U1619	C1536	C1440	G1359	G1293	G908			
U2008	C1936	C1857	U1778	G1698	G1620	A1537	A1441	A1443	A1294	G909			
A2009	G1940	C1858	U1779	G1699	U1621	A1538	G1442	U1360	C1295	G910			
A2010	A1941	C1859	C1780	G1700	U1622	U1539	A1443	C1361	G1296	G911			
C2011	A1942	C1860	C1781	G1701	A1623	C1540	G1444	U1362	U1297	G912			
A2012	A1943	U1861	U1782	G1702	U1624	C1541	G1445	C1363	C1298	G913			
		C1862	U1783	G1703	G1625	C1542	U1446	U1364	C1299	G914			
		U1863	U1784	G1704	U1626	C1543	C1447	U1365	G1300	G915			
		C1864	U1785	G1705	G1627	G1545	G1448	C1366	C1301	G916			
		A1865	C1786	G1706	G1628	C1546	C1449	C1367	U1302	G917			
		U1866	U1787	G1707	C1629	A1547	C1450	U1368	C1303	G918			
		C1867	U1788	G1708	U1630	A1548	C1451	C1369	C1304	G919			
		A1868	U1789	G1709	A1631	G1549	C1452	C1370	C1305	G920			
		C1869	U1790	G1710	U1632	G1550	C1453	C1371	C1306	G921			
		U1870	U1791	G1711	A1633	C1551	C1454	C1372	A1307	G922			
		C1871	U1792	G1712	A1634	C1552	C1455	C1373	C1308	G923			
		U1872	U1793	G1713	U1635	A1553	C1456	C1374	C1309	G924			
		A1873	U1794	G1714	A1636	A1554	C1457	C1375	C1310	G925			
		C1874	U1795	G1715	U1637	C1555	C1458	C1376	C1311	G926			
		U1875	U1796	G1716	U1638	A1556	C1459	C1377	C1312	G927			
		C1876	U1797	G1717	U1639	C1557	C1460	C1378	C1313	G928			
		A1877	U1798	G1718	U1640	A1558	C1461	C1379	C1314	G929			
		C1878	U1799	G1719	U1641	C1559	C1462	C1380	C1315	G930			
		U1879	U1800	G1720	U1642	C1560	C1463	C1381	C1316	G931			
		C1880	U1801	G1721	U1643	A1561	C1464	C1382	C1317	G932			
		A1881	U1802	G1722	U1644	C1562	C1465	C1383	C1318	G933			
		C1882	U1803	G1723	U1645	A1563	C1466	C1384	C1319	G934			
		U1883	U1804	G1724	U1646	C1564	C1467	C1385	C1320	G935			
		C1884	U1805	G1725	U1647	A1565	C1468	C1386	C1321	G936			
		A1885	U1806	G1726	U1648	C1566	C1469	C1387	C1322	G937			
		C1886	U1807	G1727	U1649	A1567	C1470	C1388	C1323	G938			
		U1887	U1808	G1728	U1650	C1568	C1471	C1389	C1324	G939			
		C1888	U1809	G1729	U1651	C1569	C1472	C1390	C1325	G940			
		A1889	U1810	G1730	U1652	C1570	C1473	C1391	C1326	G941			
		C1890	U1811	G1731	U1653	C1571	C1474	C1392	C1327	G942			
		U1891	U1812	G1732	U1654	C1572	C1475	C1393	C1328	G943			
		C1892	U1813	G1733	U1655	C1573	C1476	C1394	C1329	G944			
		A1893	U1814	G1734	U1656	C1574	C1477	C1395	C1330	G945			
		C1894	U1815	G1735	U1657	C1575	C1478	C1396	C1331	G946			
		U1895	U1816	G1736	U1658	C1576	C1479	C1397	C1332	G947			
		C1896	U1817	G1737	U1659	C1577	C1480	C1398	C1333	G948			
		A1897	U1818	G1738	U1660	C1578	C1481	C1399	C1334	G949			
		C1898	U1819	G1739	U1661	C1579	C1482	C1400	C1335	G950			
		U1899	U1820	G1740	U1662	C1580	C1483	C1401	C1336	G951			
		A1899	U1821	G1741	U1663	C1581	C1484	C1402	C1337	G952			
		C1899	U1822	G1742	U1664	C1582	C1485	C1403	C1338	G953			
		U1900	U1823	G1743	U1665	C1583	C1486	C1404	C1339	G954			
		A1900	U1824	G1744	U1666	C1584	C1487	C1405	C1340	G955			
		C1900	U1825	G1745	U1667	C1585	C1488	C1406	C1341	G956			
		U1901	U1826	G1746	U1668	C1586	C1489	C1407	C1342	G957			
		A1901	U1827	G1747	U1669	C1587	C1490	C1408	C1343	G958			
		C1901	U1828	G1748	U1670	C1588	C1491	C1409	C1344	G959			
		U1902	U1829	G1749	U1671	C1589	C1492	C1410	C1345	G960			
		A1902	U1830	G1750	U1672	C1590	C1493	C1411	C1346	G961			
		C1902	U1831	G1751	U1673	C1591	C1494	C1412	C1347	G962			
		U1903	U1832	G1752	U1674	C1592	C1495	C1413	C1348	G963			
		A1903	U1833	G1753	U1675	C1593	C1496	C1414	C1349	G964			
		C1903	U1834	G1754	U1676	C1594	C1497	C1415	C1350	G965			
		U1904	U1835	G1755	U1677	C1595	C1498	C1416	C1351	G966			
		A1904	U1836	G1756	U1678	C1596	C1499	C1417	C1352	G967			
		C1904	U1837	G1757	U1679	C1597	C1500	C1418	C1353	G968			
		U1905	U1838	G1758	U1680	C1598	C1501	C1419	C1354	G969			
		A1905	U1839	G1759	U1681	C1599	C1502	C1420	C1355	G970			
		C1905	U1840	G1760	U1682	C1600	C1503	C1421	C1356	G971			
		U1906	U1841	G1761	U1683	C1601	C1504	C1422	C1357	G972			
		A1906	U1842	G1762	U1684	C1602	C1505	C1423	C1358	G973			
		C1906	U1843	G1763	U1685	C1603	C1506	C1424	C1359	G974			
		U1907	U1844	G1764	U1686	C1604	C1507	C1425	C1360	G975			
		A1907	U1845	G1765	U1687	C1605	C1508	C1426	C1361	G976			
		C1907	U1846	G1766	U1688	C1606	C1509	C1427	C1362	G977			
		U1908	U1847	G1767	U1689	C1607	C1510	C1428	C1363	G978			
		A1908	U1848	G1768	U1690	C1608	C1511	C1429	C1364	G979			
		C1908	U1849	G1769	U1691	C1609	C1512	C1430	C1365	G980			
		U1909	U1850	G1770	U1692	C1610	C1513	C1431	C1366	G981			
		A1909	U1851	G1771	U1693	C1611	C1514	C1432	C1367	G982			
		C1909	U1852	G1772	U1694	C1612	C1515	C1433	C1368	G983			
		U1910	U1853	G1773	U1695	C1613	C1516	C1434	C1369	G984			
		A1910	U1854	G1774	U1696	C1614	C1517	C1435	C1370	G985			
		C1910	U1855	G1775	U1697	C1615	C1518	C1436	C1371	G986			
		U1911	U1856	G1776	U1698	C1616	C1519	C1437	C1372	G987			
		A1911	U1857	G1777	U1699	C1617	C1520	C1438	C1373	G988			
		C1911	U1858	G1778	U1700	C1618	C1521	C1439	C1374	G989			
		U1912	U1859	G1779	U1701	C1619	C1522	C1440	C1375	G990			
		A1912	U1860	G1780	U1702	C1620	C1523	C1441	C1376	G991			
		C1912	U1861	G1781	U1703	C1621	C1524	C1442	C1377	G992			
		U1913	U1862	G1782	U1704	C1622	C1525	C1443	C1378	G993			
		A1913	U1863	G1783	U1705	C1623	C1526	C1444	C1379	G994			
		C1913	U1864	G1784	U1706	C1624	C1527	C1445	C1380	G995			
		U1914	U1865	G1785	U1707	C1625	C1528	C1446	C1381	G996			
		A1914	U1866	G1786	U1708	C1626	C1529	C1447	C1382	G997			
		C1914	U1867	G1787	U1709	C1627	C1530	C1448	C1383	G998			
		U1915	U1868	G1788	U1710	C1628	C1531	C1449	C1384	G999			
		A1915	U1869	G1789	U1711	C1629	C1532	C1450	C1385	G1000			
		C1915	U1870	G1790	U1712	C1630	C1533	C1451	C1386	G1001			
		U1916	U1871	G1791	U1713	C1631	C1534	C1452	C1387	G1002			
		A1916	U1872	G1792	U1714	C1632	C1535	C1453	C1388	G1003			
		C1916											

C4072	G3907	C3826	A3748	C3666	G3592	G2847	C2772	G2700	G2622	C2539	G2459	G2384	C2078
G4075	A3908	A3830	G3753	C3667	C3593	G2848	G2773	U2701	A2623	C2540	A2460	G2289	G2079
G4076	C3911	G3831	G3754	C3668	C3594	A2849	G2777	G2702	G2524	G2542	C2461	G2289	U2080
C4080	U3912	C3832	C3755	G3669	U3595	G2855	G2778	G2703	C2627	A2543	C2462	C2296	C2081
G4081	G3913	C3833	U3758	C3670	G3597	G2856	G2779	G2706	U2631	G2544	C2463	C2296	C2082
G4082	U3914	C3834	A3759	G3671	C3598	A2857	G2780	U2707	U2632	U2545	C2464	C2297	C2083
U4083	U3915	C3834	A3760	G3672	A3599	A2858	G2781	G2708	U2633	G2546	C2465	U2298	C2084
G4084	G3916	U3838	G3764	G3673	G3600	C2861	G2782	C2709	U2634	G2547	C2469	G2299	C2087
A4085	A3917	G3839	G3765	G3674	C3601	C2862	G2785	C2710	U2635	G2554	C2470	A2300	U2090
G4086	G3918	U3840	A3766	G3675	A3604	G2863	C2786	G2711	U2636	U2554	C2471	G2301	U2091
G4087	C3919	C3841	C3767	C3676	C3605	G2864	A2788	G2715	U2637	G2555	G2474	C2302	G2092
C4088	U3920	G3842	G3767	A3687	U3606	U2865	G2788	G2718	G2638	G2556	G2475	C2303	A2093
G4089	G3921	C3843	G3770	G3687	U3607	C2866	G2789	U2718	U2639	G2557	G2478	G2306	G2094
G4090	A3922	U3844	U3770	G3688	A3608	C2867	U2790	C2719	G2640	C2558	C2478	A2307	G2095
G4091	C3923	G3845	C3771	G3689	G3609	U2868	G2791	G2720	A2641	C2560	G2479	A2308	G2096
U4092	G3924	U3846	G3774	U3695	A3610	U2869	C2794	G2721	A2642	G2565	G2483	U2311	U2097
G4093	U3925	U3847	A3775	C3696	A3611	A2870	G2799	U2722	G2647	G2566	G2484	U2312	G2098
G4094	C3926	C3849	A3776	C3697	G3615	C2875	G2799	G2723	U2648	G2567	U2485	U2313	G2099
A4095	U3927	G3850	G3776	U3698	U3616	G2876	G2800	U2724	G2649	G2568	G2486	A2313	C2101
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G4103	G3938	G3862	G3787	U3709	G3627	G2884	G2809	C2739	G2658	G2576	U2494	G2324	G2109
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	U4070	A3824	A3824	A3746	G3664	G3590	A2845	G2770	G2698	G2620	A2537	C2458	A2283
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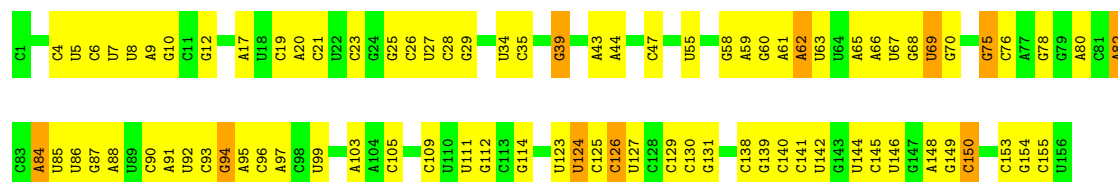
• Molecule 3: 5S rRNA [Homo sapiens]

Chain L7: 57% 39%



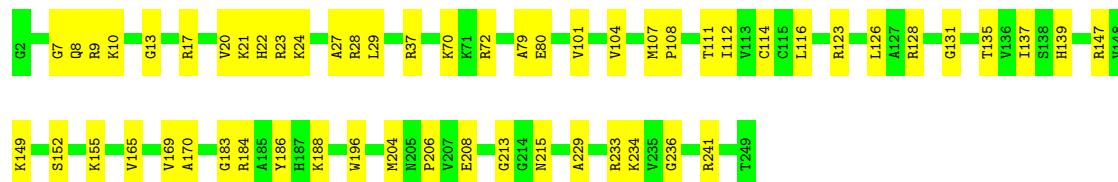
• Molecule 4: 5.8S rRNA [Homo sapiens]

Chain L8: 46% 47% 6%



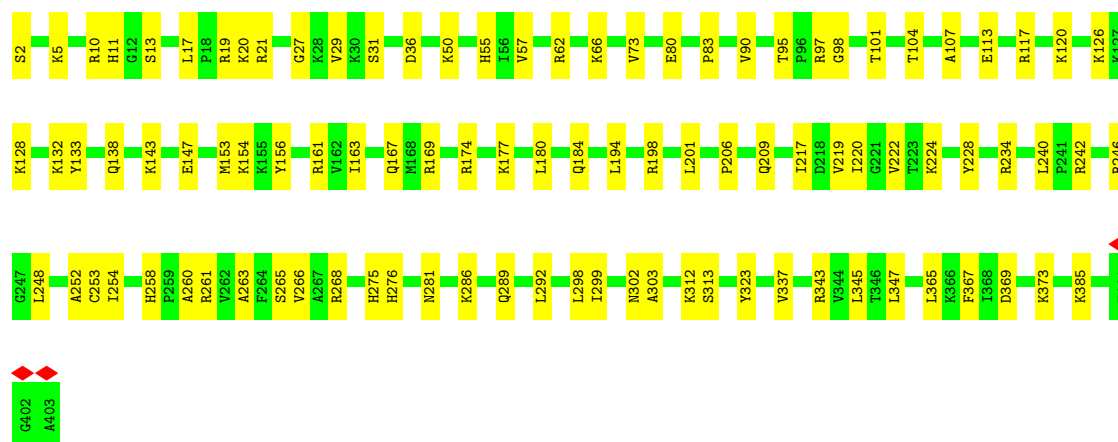
- Molecule 5: 60S ribosomal protein L8

Chain LA: 77% 23%



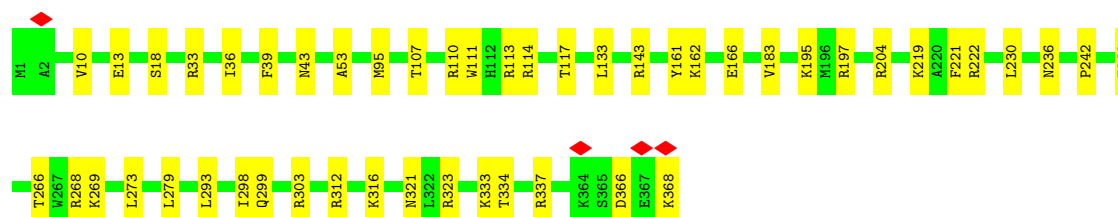
- Molecule 6: Large ribosomal subunit protein uL3

Chain LB: 76% 24%



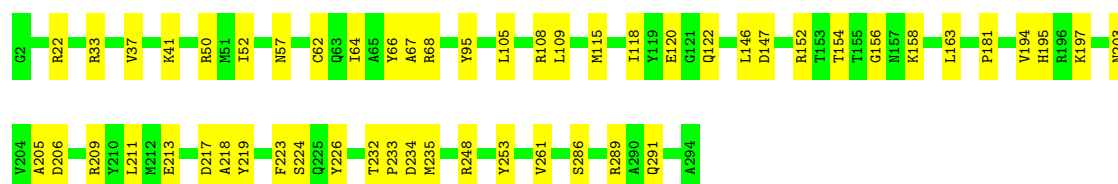
- Molecule 7: 60S ribosomal protein L4

Chain LC: 87% 13%

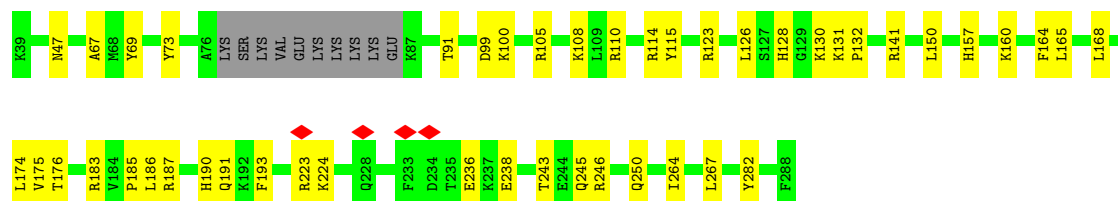
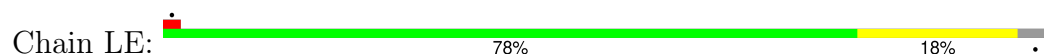


- Molecule 8: Large ribosomal subunit protein uL18

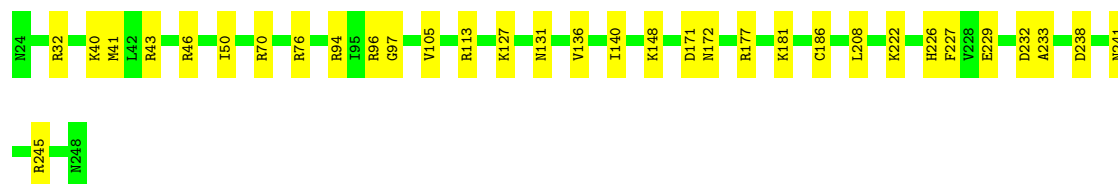
Chain LD: 82% 18%



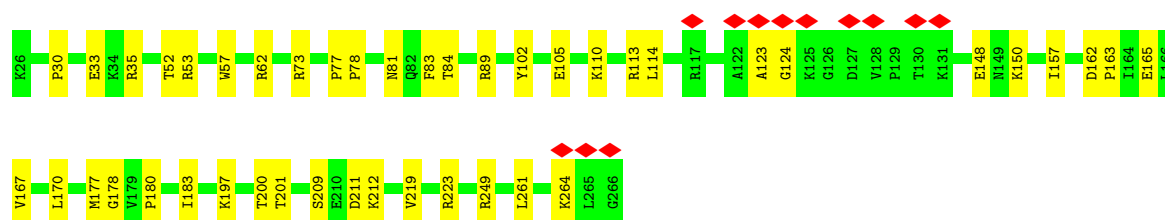
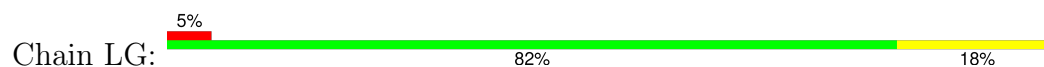
- Molecule 9: Large ribosomal subunit protein eL6



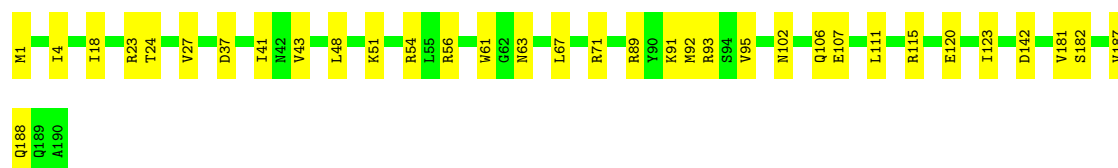
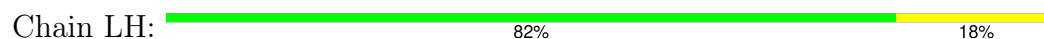
- Molecule 10: 60S ribosomal protein L7



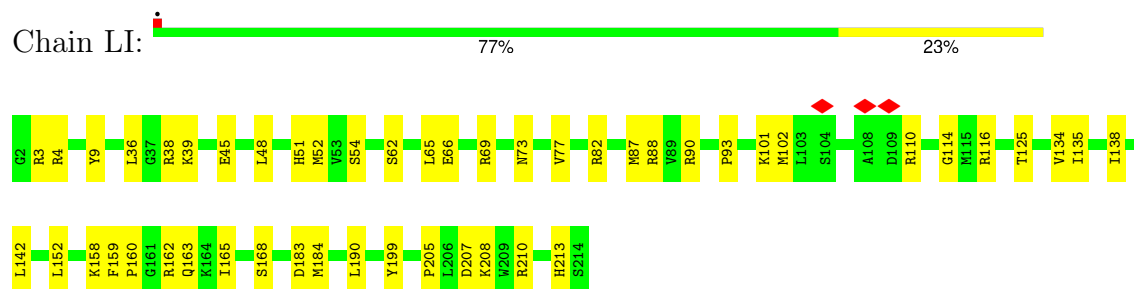
- Molecule 11: 60S ribosomal protein L7a



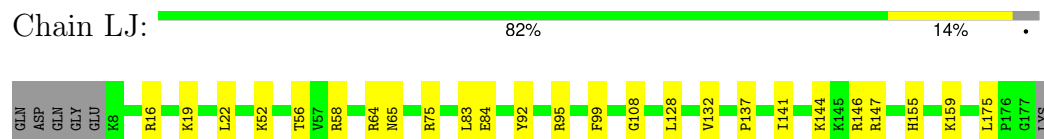
- Molecule 12: 60S ribosomal protein L9



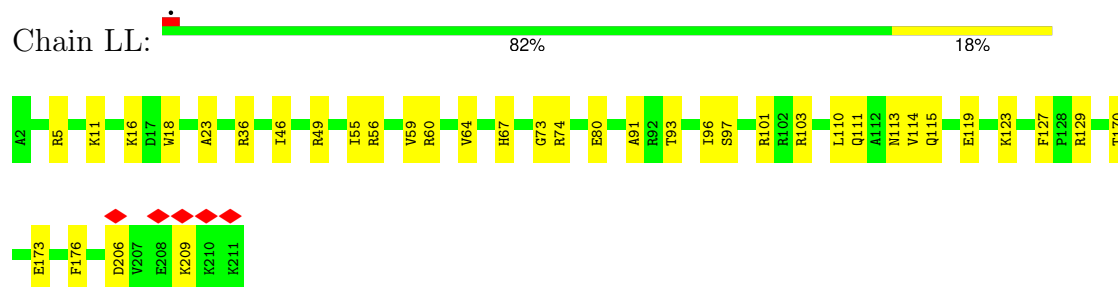
- Molecule 13: Ribosomal protein uL16-like



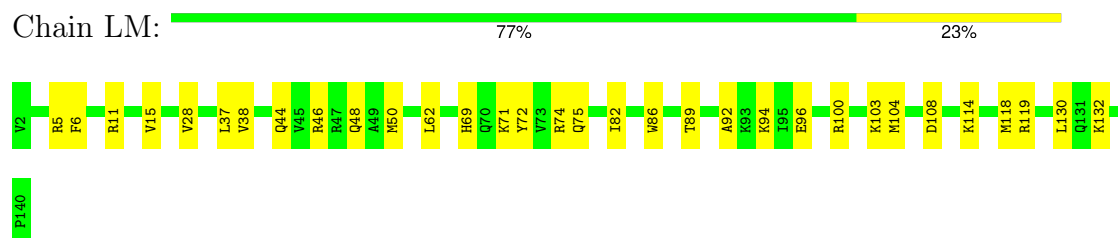
- Molecule 14: 60S ribosomal protein L11



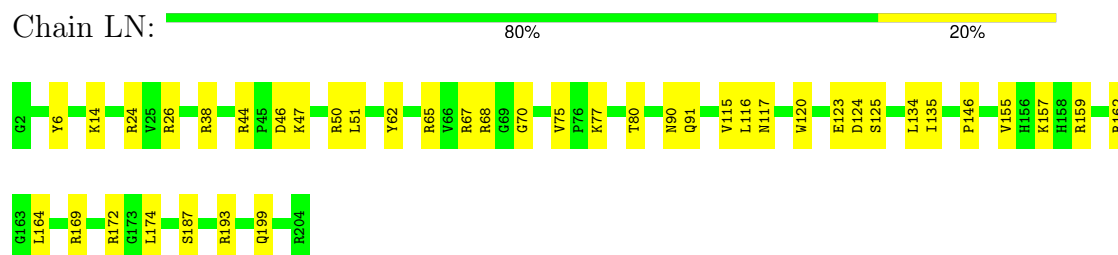
- Molecule 15: Large ribosomal subunit protein eL13



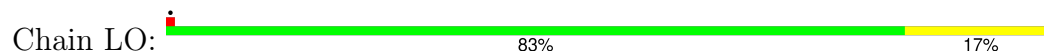
- Molecule 16: 60S ribosomal protein L14

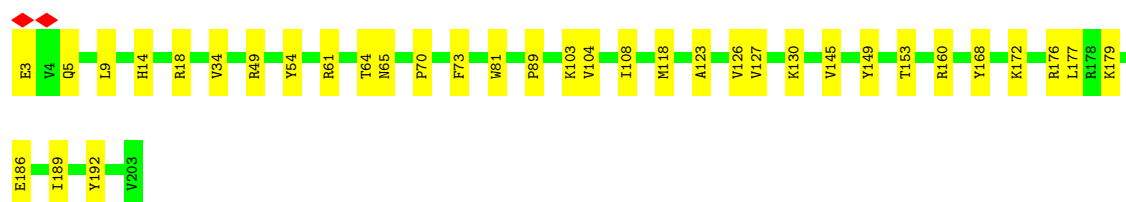


- Molecule 17: 60S ribosomal protein L15



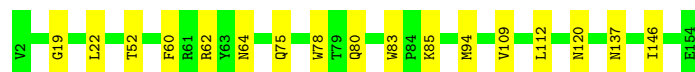
- Molecule 18: 60S ribosomal protein L13a





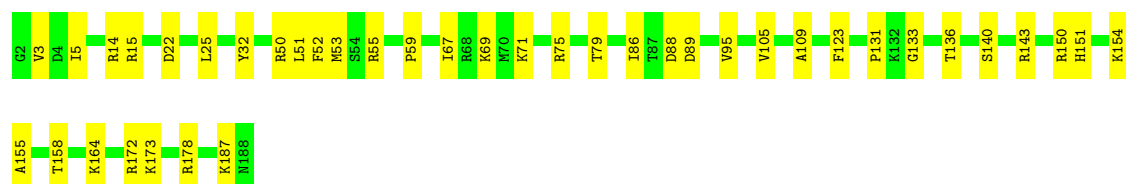
- Molecule 19: 60S ribosomal protein L17

Chain LP: 89% 11%



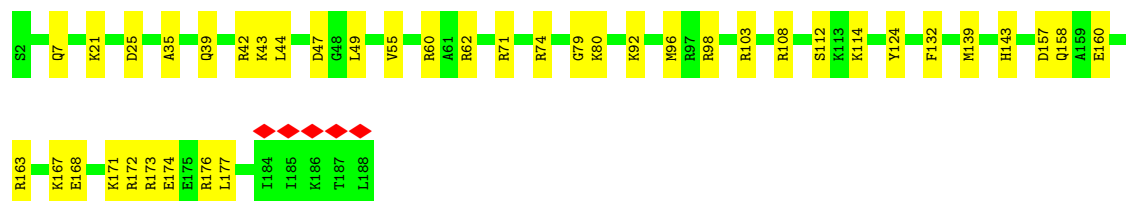
- Molecule 20: 60S ribosomal protein L18

Chain LQ: 79% 21%



- Molecule 21: 60S ribosomal protein L19

Chain LR: 79% 21%



- Molecule 22: 60S ribosomal protein L18a

Chain LS: 89% 11%



- Molecule 23: 60S ribosomal protein L21

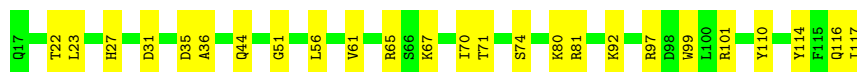
Chain LT: 78% 22%





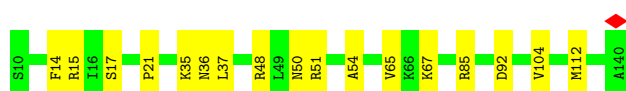
- Molecule 24: Heparin-binding protein HBp15

Chain LU: 75% 25%



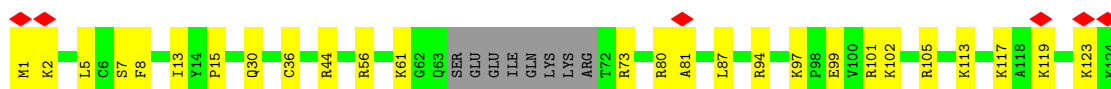
- Molecule 25: 60S ribosomal protein L23

Chain LV: 87% 13%



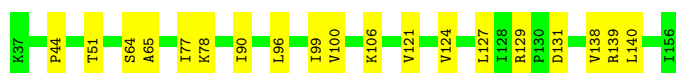
- Molecule 26: Ribosomal protein L24

Chain LW: 5% 73% 21% 6%



- Molecule 27: 60S ribosomal protein L23a

Chain LX: 84% 16%



- Molecule 28: 60S ribosomal protein L26

Chain LY: 90% 10%



- Molecule 29: 60S ribosomal protein L27

Chain LZ: 82% 18%

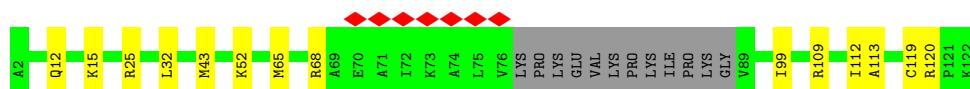
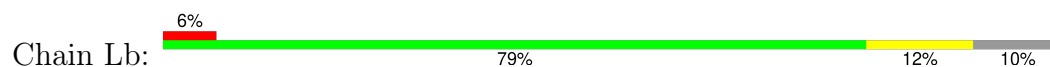


- Molecule 30: 60S ribosomal protein L27a

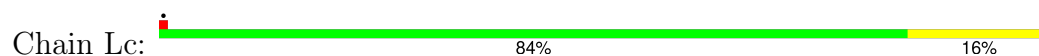
Chain La: 87% 13%



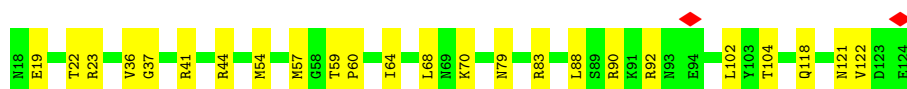
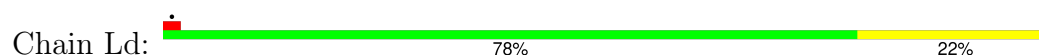
- Molecule 31: Large ribosomal subunit protein eL29



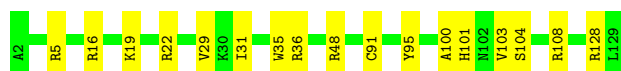
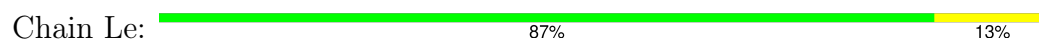
- Molecule 32: 60S ribosomal protein L30



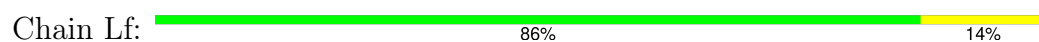
- Molecule 33: 60S ribosomal protein L31



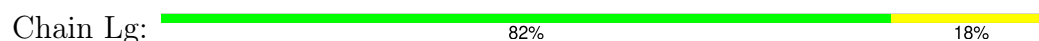
- Molecule 34: 60S ribosomal protein L32



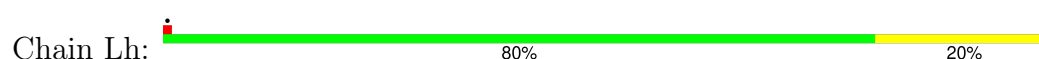
- Molecule 35: 60S ribosomal protein L35a



- Molecule 36: 60S ribosomal protein L34



- Molecule 37: 60S ribosomal protein L35





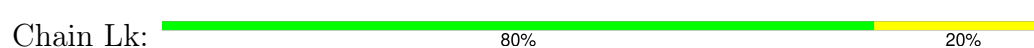
- Molecule 38: 60S ribosomal protein L36



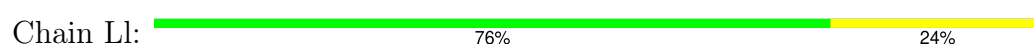
- Molecule 39: 60S ribosomal protein L37



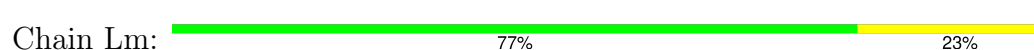
- Molecule 40: 60S ribosomal protein L38



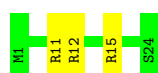
- Molecule 41: 60S ribosomal protein L39



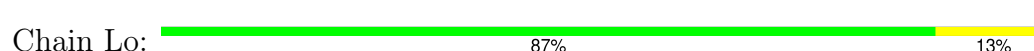
- Molecule 42: Large ribosomal subunit protein eL40



- Molecule 43: 60S ribosomal protein L41

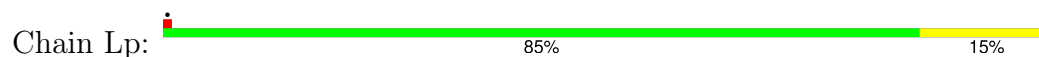


- Molecule 44: 60S ribosomal protein L36a





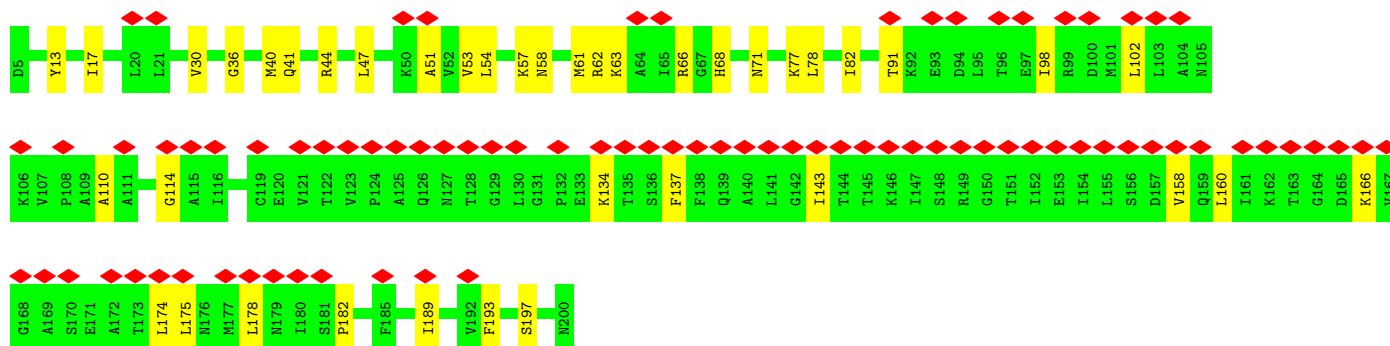
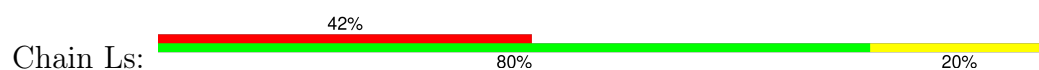
- Molecule 45: 60S ribosomal protein L37a



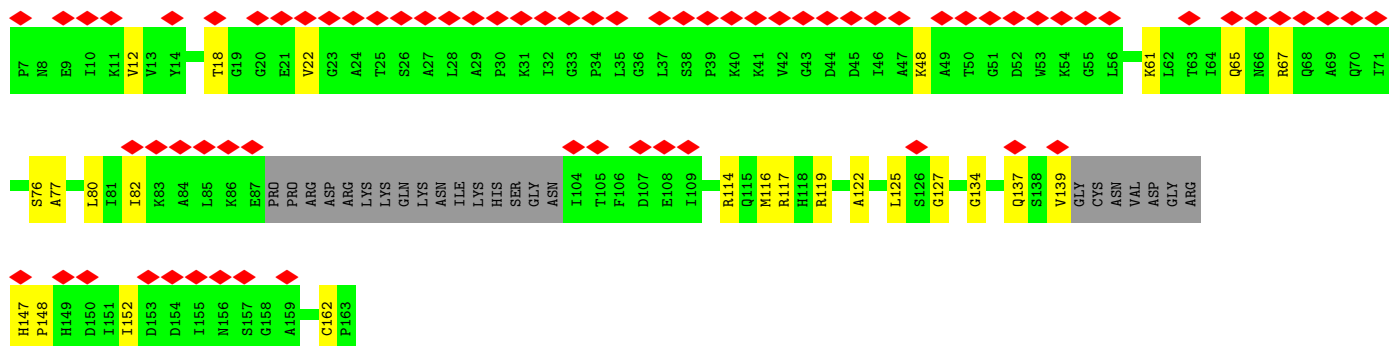
- Molecule 46: 60S ribosomal protein L28



- Molecule 47: 60S acidic ribosomal protein P0



- Molecule 48: Large ribosomal subunit protein uL11



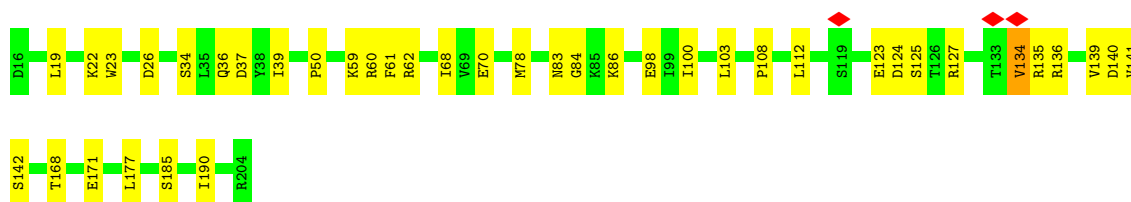
- Molecule 49: Small ribosomal subunit protein uS3

Chain SD:  81% 19%



- Molecule 50: 40S ribosomal protein S5

Chain SF:  79% 21%



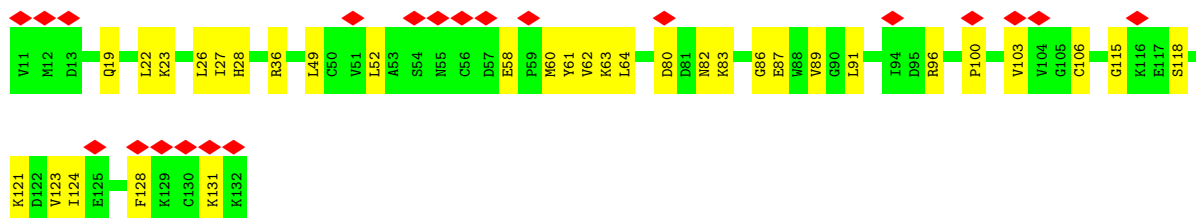
- Molecule 51: 40S ribosomal protein S10

Chain SK:  68% 32%



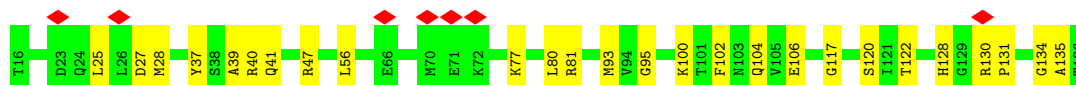
- Molecule 52: Small ribosomal subunit protein eS12

Chain SM:  17% 73% 27%



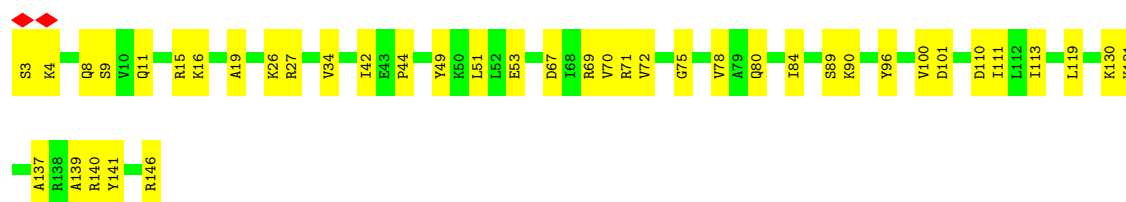
- Molecule 53: Small ribosomal subunit protein uS19

Chain SP:  6% 79% 21%

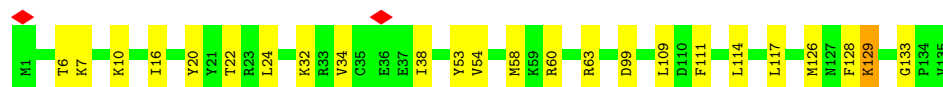
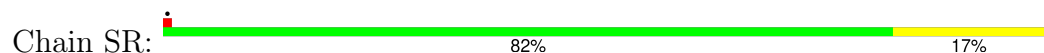


- Molecule 54: Small ribosomal subunit protein uS9

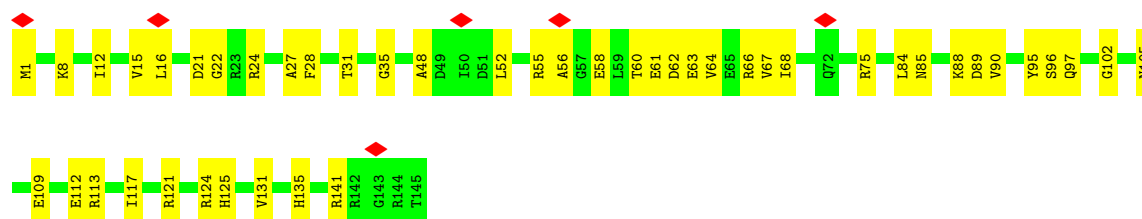
Chain SQ:  72% 28%



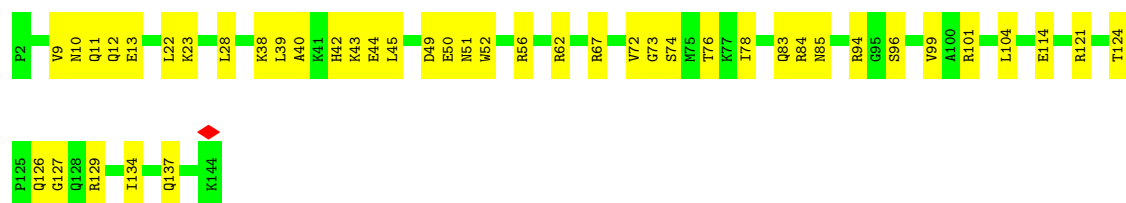
- Molecule 55: Small ribosomal subunit protein eS17



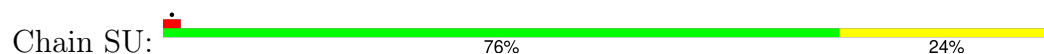
- Molecule 56: 40S ribosomal protein S18



- Molecule 57: 40S ribosomal protein S19

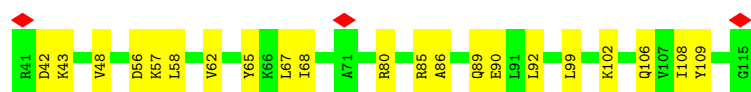


- Molecule 58: 40S ribosomal protein S20

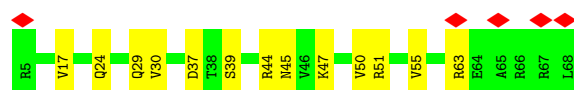
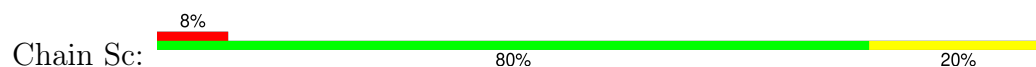


- Molecule 59: Small ribosomal subunit protein eS25





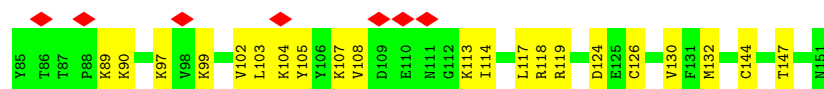
- Molecule 60: 40S ribosomal protein S28



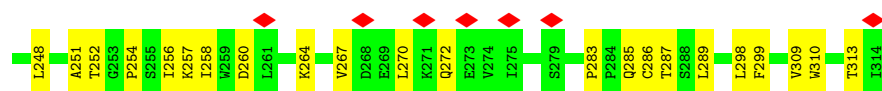
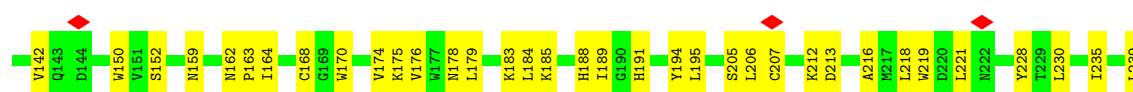
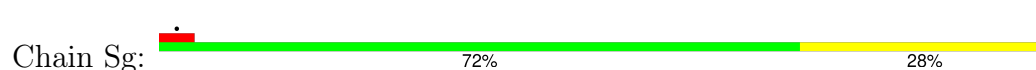
- Molecule 61: 40S ribosomal protein S29



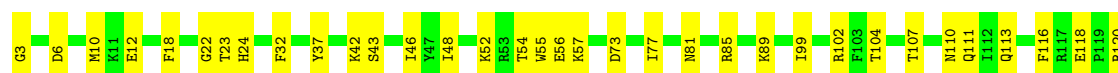
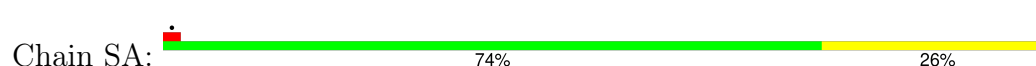
- Molecule 62: Ubiquitin-40S ribosomal protein S27a



- Molecule 63: Receptor of activated protein C kinase 1

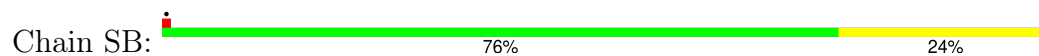


- Molecule 64: 40S ribosomal protein SA

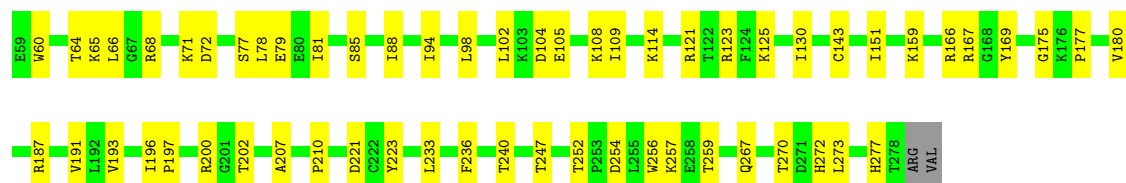




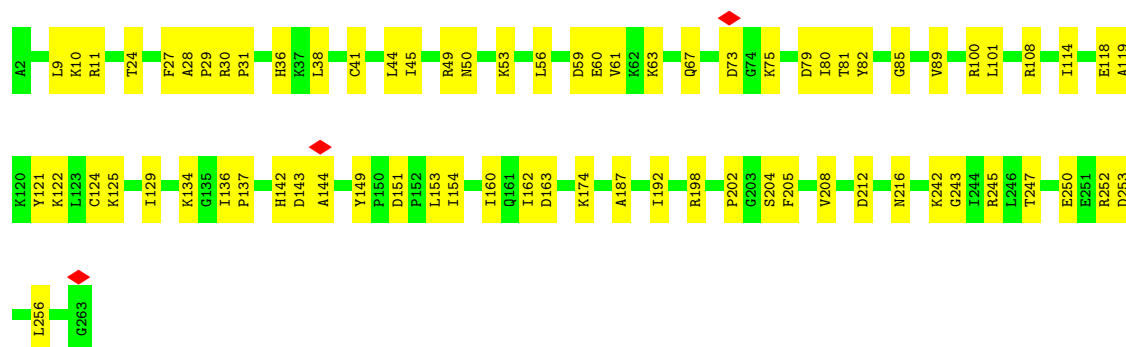
- Molecule 65: 40S ribosomal protein S3a



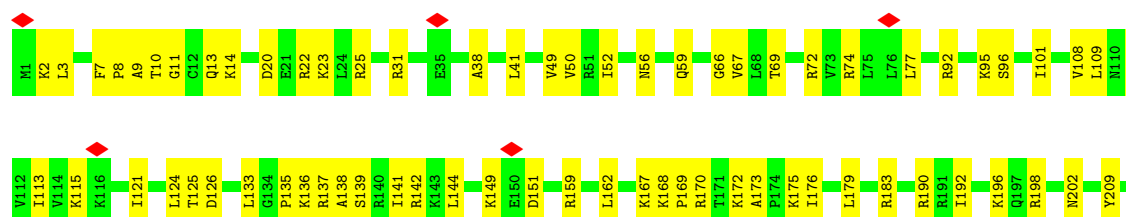
- Molecule 66: 40S ribosomal protein S2



- Molecule 67: Small ribosomal subunit protein eS4, X isoform



- Molecule 68: 40S ribosomal protein S6





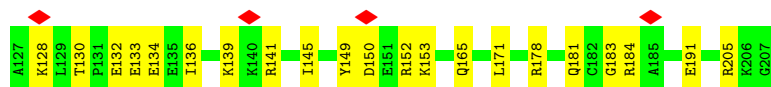
- Molecule 69: Small ribosomal subunit protein eS7

Chain SH: 71% 28%



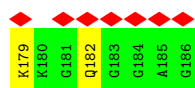
- Molecule 70: 40S ribosomal protein S8

Chain SI: 73% 27%



- Molecule 71: 40S ribosomal protein S9

Chain SJ: 5% 83% 17%



- Molecule 72: 40S ribosomal protein S11

Chain SL: 5% 79% 21%

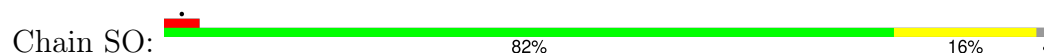


- Molecule 73: 40S ribosomal protein S13

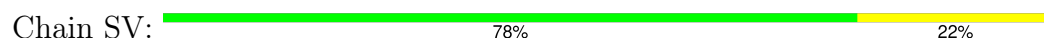
Chain SN: 88% 12%



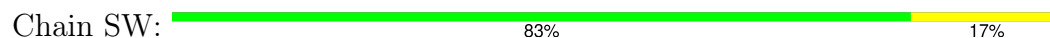
- Molecule 74: Small ribosomal subunit protein uS11



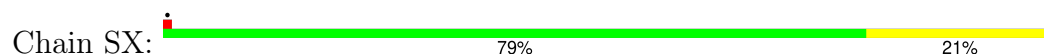
- Molecule 75: Small ribosomal subunit protein eS21



- Molecule 76: 40S ribosomal protein S15a



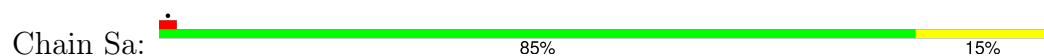
- Molecule 77: 40S ribosomal protein S23

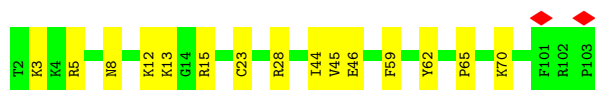


- Molecule 78: 40S ribosomal protein S24

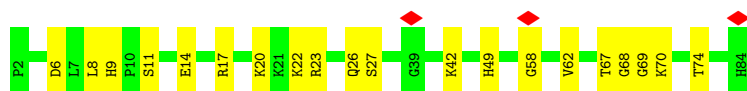
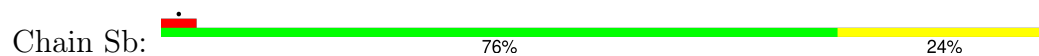


- Molecule 79: 40S ribosomal protein S26

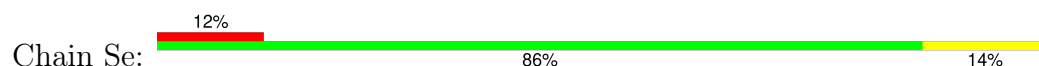




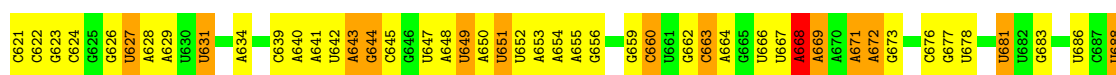
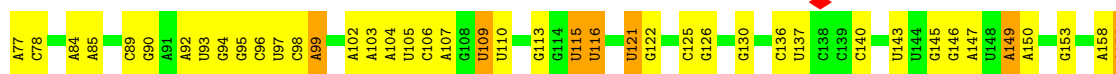
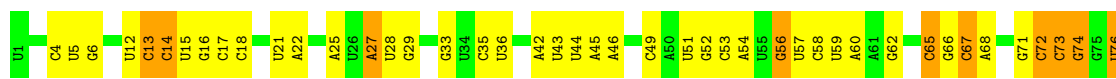
- Molecule 80: Small ribosomal subunit protein eS27



- Molecule 81: Small ribosomal subunit protein eS30



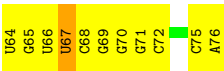
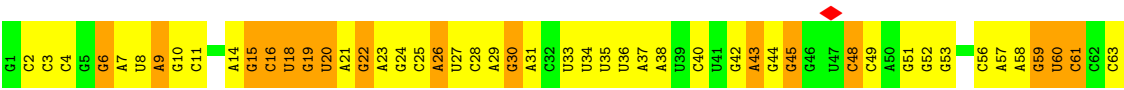
- Molecule 82: 18S rRNA [Homo sapiens]



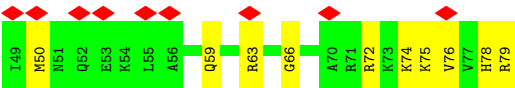
C1767	U1692	U1621	A1545	C1464	U1390	U1156	A1084	A1001	G921	G836	U689
C1772	G1693	U1622	G1546	C1468	C1391	U1160	C1085	U1002	G925	A837	G692
C1773	U1694	A1623	C1547	A1469	G1393	U1239	U1030	U1004	G838	G839	G839
C1774	A1695	C1628	U1549	G1475	A1396	U1241	C1091	G1005	G828	G840	G695
U1775	A1699	C1629	U1551	A1476	U1397	A1243	G1092	A1008	G929	G841	G696
G1776	C1700	U1631	U1551	U1477	G1398	U1244	A1093	A1009	G930	C842	G697
C1777	C1701	G1632	C1553	C1482	A1402	U1245	G1097	A1010	G933	G843	G698
C1778	C1702	A1633	C1553	C1482	A1402	U1245	G1098	A1011	G934	G845	C732
C1779	C1703	A1633	C1553	C1482	A1402	U1245	G1099	A1012	U940	G846	U733
C1780	C1704	A1634	A1556	A1489	G1405	B8N1248	G1099	A1013	G941	A847	C736
U1781	C1705	A1637	C1557	A1489	A1406	A1251	G1100	U1014	G942	C851	C737
C1782	G1706	G1638	C1558	G1491	U1407	C1252	U1101	U1015	G943	G852	C738
C1783	G1706	G1638	C1558	G1491	U1407	C1252	G1102	U1016	U944		
G1784	G1706	G1638	C1558	U1492	U1408	C1253	G1103	U1017	U945		
U1711	U1711	A1640	A1561	C1493	A1409	C1254	G1104	U1018	U946		
U1712	C1712	U1494	G1562	U1494	C1410	C1255	G1107	U1019	G947		
C1713	C1713	G1563	G1563	G1495	G1411	G1256	G1108	A1020	G948		
U1714	C1644	C1644	G1566	U1496	C1412	G1257	C1109	A1023	G949		
A1715	C1645	C1645	G1567	C1497	G1413	A1258	C1109	U1024	C953		
U1719	G1648	G1648	G1567	A1498	A1413	A1259	C1110	U1025	G952		
U1720	A1569	A1569	C1568	C1415	C1416	A1189	C1111	U1026	C954		
U1721	A1569	A1569	C1568	C1415	C1416	A1189	C1111	A1027	U954		
G1722	A1650	A1650	C1502	C1503	C1417	C1264	U1112	A1028			
U1729	A1651	A1651	C1503	C1418	C1418	C1264	U1113	A1029			
G1726	G1652	G1652	U1504	U1504	C1419	C1267	U1115	A1030	G959		
U1733	G1655	G1655	U1505	U1505	G1420	C1268	C1116	A1031	U960		
G1734	G1657	G1657	A1585	U1510	A1421	G1270	C1117	A1032	G961		
U1808	U1659	U1659	U1586	U1511	G1422	C1271	G1121	C1033	A962		
A1809	G1736	G1660	G1587	C1512	C1423	C1272	A963	A1034	A964		
U1810	G1737	A1661	A1588	G1513	G1425	C1273	A964	A1035	U965		
C1811	C1738	U1662	A1589	G1514	U1426	C1274	U966	G1037	U966		
U1812	U1662	U1662	A1589	G1515	C1427	C1276	C1125		G970		
A1813	A1663	A1663	G1593	G1516	G1428	A1278	G1126	U1045	G971		
A1814	A1664	A1664	C1593	C1433	C1433	C1279	G1129	U1046	A972		
A1815	G1665	G1665	C1593	C1434	C1434	G1280	G1130	C1047			
G1744	C1666	C1666	C1597	C1435	C1435	G1281	A1133	G1048	G976		
A1745	U1667	U1667	G1598	C1437	C1437	C1283	C1215	A1049	G977		
U1821	U1668	U1668	G1600	C1521	A1438	C1283	C1216	A1050	G978		
A1822	G1669	G1669	G1600	C1521	A1438	C1283	C1217	U1056	G979		
A1825	C1670	C1670	G1603	G1524	U1442	A1287	C1218	C1057	A981		
G1829	G1671	G1671	G1604	G1528	C1443	U1288	C1219	A1058	G982		
A1830	U1672	U1672	G1605	G1528	U1444	G1289	G1140	U1061	G985		
C1833	U1673	U1673	G1606	A1531	G1447	A1291	A1143	U1062	G986		
A1834	U1677	U1677	C1609	A1532	G1448	C1292	A1144	A1062	G987		
A1835	A1678	A1678	C1609	A1533	G1449	A1293	A1145	C1063	G988		
G1836	G1679	G1679	G1612	G1536	A1452	G1294	C1146	G1068	G989		
G1837	G1680	G1680	G1613	A1537	C1453	A1295	C1147	U1069	G990		
A1838	C1682	C1682	A1614	C1538	A1454	C1301	A1148	A1070	G991		
G1839	C1683	C1683	U1615	U1539	A1455	G1302	A1149	A1070	G992		
U1761	G1686	G1686	U1616	G1540	C1456	C1303	A1150	C1079	G996		
C1762	G1687	C1687	G1617	G1541	U1304	G1304	A1151	A1080	A997		
U1840	C1688	C1688	U1618	U1542	C1384	C1305	U1152	A1081	A998		
	C1689	C1689	A1620	C1544	U1306	G1307	C1153	U1082	A999		
					U1307		U1155	A1083	C1000		



• Molecule 83: Z site tRNA [Homo sapiens]



• Molecule 84: Transcription factor BTF3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7312	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	0.519	Depositor
Minimum map value	-0.244	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.0717	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: MA6, UY1, SPD, 5MC, 4AC, HMT, 6MZ, SPM, A2M, OMU, B8N, PSU, OMC, 3HE, MG, OMG, G7M, ZN, 1MA, UR3

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	Pt	0.12	0/1761	0.27	0/2741
2	L5	0.17	0/85098	0.28	0/132762
3	L7	0.14	0/2861	0.23	0/4459
4	L8	0.16	0/3631	0.29	0/5657
5	LA	0.16	0/1936	0.36	0/2596
6	LB	0.15	0/3306	0.35	0/4424
7	LC	0.15	0/2981	0.34	0/4002
8	LD	0.14	0/2428	0.32	0/3252
9	LE	0.15	0/1973	0.39	0/2645
10	LF	0.15	0/1905	0.30	0/2539
11	LG	0.16	0/1960	0.34	0/2637
12	LH	0.14	0/1537	0.30	0/2066
13	LI	0.14	0/1751	0.34	0/2340
14	LJ	0.14	0/1385	0.35	0/1852
15	LL	0.14	0/1732	0.30	0/2315
16	LM	0.16	0/1161	0.34	0/1554
17	LN	0.15	0/1746	0.30	0/2338
18	LO	0.15	0/1682	0.32	0/2250
19	LP	0.15	0/1268	0.35	0/1701
20	LQ	0.15	0/1537	0.32	0/2052
21	LR	0.15	0/1582	0.36	0/2091
22	LS	0.15	0/1493	0.33	0/2003
23	LT	0.14	0/1326	0.29	0/1770
24	LU	0.17	0/839	0.42	0/1126
25	LV	0.15	0/993	0.34	0/1332
26	LW	0.21	0/959	0.41	0/1270
27	LX	0.14	0/1002	0.32	0/1345
28	LY	0.14	0/1132	0.35	0/1504
29	LZ	0.15	0/1130	0.34	0/1507
30	La	0.14	0/1191	0.31	0/1591
31	Lb	0.14	0/889	0.35	0/1175

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Lc	0.14	0/774	0.32	0/1038
33	Ld	0.15	0/903	0.33	0/1216
34	Le	0.15	0/1071	0.30	0/1429
35	Lf	0.15	0/895	0.30	0/1198
36	Lg	0.14	0/916	0.32	0/1220
37	Lh	0.13	0/1023	0.30	0/1351
38	Li	0.14	0/843	0.29	0/1115
39	Lj	0.14	0/720	0.32	0/952
40	Lk	0.14	0/575	0.32	0/761
41	Ll	0.13	0/454	0.26	0/599
42	Lm	0.14	0/435	0.37	0/575
43	Ln	0.14	0/231	0.32	0/294
44	Lo	0.15	0/876	0.33	0/1156
45	Lp	0.15	0/718	0.31	0/953
46	Lr	0.15	0/1017	0.34	0/1364
47	Ls	0.13	0/1519	0.34	0/2052
48	Lt	0.16	0/1009	0.50	0/1363
49	SD	0.12	0/1793	0.30	0/2414
50	SF	0.14	0/1516	0.37	1/2037 (0.0%)
51	SK	0.16	0/851	0.44	0/1147
52	SM	0.13	0/950	0.38	0/1275
53	SP	0.13	0/1003	0.37	0/1342
54	SQ	0.19	0/1160	0.42	0/1553
55	SR	0.16	0/1105	0.43	0/1484
56	SS	0.14	0/1216	0.36	0/1628
57	ST	0.15	0/1131	0.41	0/1515
58	SU	0.16	0/831	0.43	0/1115
59	SZ	0.16	0/604	0.48	0/810
60	Sc	0.14	0/508	0.33	0/680
61	Sd	0.13	0/470	0.32	0/623
62	Sf	0.15	0/560	0.45	0/745
63	Sg	0.16	0/2493	0.36	0/3394
64	SA	0.15	0/1778	0.36	0/2416
65	SB	0.15	0/1765	0.36	0/2362
66	SC	0.15	0/1744	0.35	0/2357
67	SE	0.14	0/2118	0.36	0/2849
68	SG	0.14	0/1946	0.36	0/2590
69	SH	0.17	0/1519	0.42	0/2033
70	SI	0.14	0/1715	0.35	0/2287
71	SJ	0.13	0/1550	0.32	0/2069
72	SL	0.14	0/1268	0.34	0/1696
73	SN	0.13	0/1232	0.31	0/1656
74	SO	0.17	0/1037	0.38	0/1391

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	SV	0.14	0/643	0.35	0/860
76	SW	0.16	0/1051	0.34	0/1406
77	SX	0.13	0/1116	0.34	0/1490
78	SY	0.14	0/1083	0.35	0/1438
79	Sa	0.15	0/836	0.36	0/1121
80	Sb	0.15	0/665	0.33	0/891
81	Se	0.14	0/465	0.39	0/612
82	S2	0.18	2/39756 (0.0%)	0.28	0/61939
83	Zt	0.14	0/1779	0.35	0/2771
84	CI	0.16	0/247	0.30	0/323
All	All	0.16	2/231658 (0.0%)	0.31	1/339851 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	S2	668	A2M	O3'-P	5.01	1.61	1.56
82	S2	99	A2M	O3'-P	5.00	1.61	1.56

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	SF	134	VAL	N-CA-C	-5.36	107.39	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	Pt	1576	0	803	30	0
2	L5	78444	0	39714	1490	0
3	L7	2561	0	1295	38	0
4	L8	3315	0	1685	68	0
5	LA	1898	0	1993	45	0
6	LB	3238	0	3376	76	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	LC	2927	0	3104	36	0
8	LD	2382	0	2410	38	0
9	LE	1935	0	2096	37	0
10	LF	1870	0	1996	24	0
11	LG	1927	0	2074	29	0
12	LH	1518	0	1601	21	0
13	LI	1711	0	1749	31	0
14	LJ	1362	0	1399	15	0
15	LL	1701	0	1818	31	0
16	LM	1138	0	1204	25	0
17	LN	1701	0	1749	34	0
18	LO	1650	0	1794	28	0
19	LP	1242	0	1269	12	0
20	LQ	1513	0	1628	31	0
21	LR	1566	0	1729	29	0
22	LS	1453	0	1490	15	0
23	LT	1298	0	1366	30	0
24	LU	825	0	850	23	0
25	LV	979	0	1039	13	0
26	LW	945	0	1003	19	0
27	LX	985	0	1066	13	0
28	LY	1115	0	1205	11	0
29	LZ	1107	0	1182	18	0
30	La	1162	0	1213	14	0
31	Lb	876	0	948	12	0
32	Lc	764	0	804	11	0
33	Ld	888	0	930	17	0
34	Le	1053	0	1147	15	0
35	Lf	876	0	912	12	0
36	Lg	906	0	998	17	0
37	Lh	1015	0	1148	22	0
38	Li	832	0	917	9	0
39	Lj	705	0	737	21	0
40	Lk	569	0	637	11	0
41	Ll	444	0	483	10	0
42	Lm	429	0	465	10	0
43	Ln	230	0	276	2	0
44	Lo	862	0	929	11	0
45	Lp	708	0	756	12	0
46	Lr	1002	0	1068	12	0
47	Ls	1496	0	1540	28	0
48	Lt	998	0	1032	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	SD	1765	0	1865	28	0
50	SF	1495	0	1549	31	0
51	SK	827	0	854	25	0
52	SM	940	0	965	20	0
53	SP	985	0	1031	20	0
54	SQ	1142	0	1213	37	0
55	SR	1090	0	1149	20	0
56	SS	1198	0	1261	32	0
57	ST	1112	0	1146	31	0
58	SU	821	0	883	20	0
59	SZ	598	0	656	16	0
60	Sc	506	0	536	10	0
61	Sd	459	0	452	15	0
62	Sf	548	0	551	16	0
63	Sg	2436	0	2393	55	0
64	SA	1741	0	1746	41	0
65	SB	1738	0	1809	34	0
66	SC	1707	0	1791	41	0
67	SE	2076	0	2177	50	0
68	SG	1923	0	2089	61	0
69	SH	1497	0	1590	37	0
70	SI	1686	0	1772	40	0
71	SJ	1525	0	1640	25	0
72	SL	1247	0	1323	23	0
73	SN	1208	0	1294	12	0
74	SO	1024	0	1050	17	0
75	SV	636	0	637	14	0
76	SW	1034	0	1080	19	0
77	SX	1098	0	1167	24	0
78	SY	1065	0	1142	32	0
79	Sa	821	0	870	14	0
80	Sb	651	0	672	15	0
81	Se	459	0	503	9	0
82	S2	36953	0	18679	697	0
83	Zt	1593	0	809	37	0
84	CI	247	0	282	23	0
85	L5	179	0	0	0	0
85	L7	3	0	0	0	0
85	L8	4	0	0	0	0
85	LA	1	0	0	0	0
85	LP	1	0	0	0	0
85	LV	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	Le	1	0	0	0	0
85	Lj	1	0	0	0	0
85	S2	27	0	0	0	0
85	SS	1	0	0	0	0
86	L5	98	0	182	8	0
87	L5	90	0	171	10	0
87	LN	10	0	19	2	0
88	L5	20	0	23	2	0
89	L5	39	0	36	8	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	220030	0	163684	3540	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 10.

All (3540) 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)
89:L5:5297:HMT:C6	89:L5:5297:HMT:C7	1.77	1.60
89:L5:5297:HMT:C7	89:L5:5297:HMT:C8	1.79	1.58
2:L5:2706:G:N7	84:CI:78:HIS:NE2	1.64	1.38
24:LU:117:ILE:C	84:CI:75:LYS:H	1.36	1.32
2:L5:2706:G:N7	84:CI:78:HIS:CD2	2.10	1.19
2:L5:2706:G:C8	84:CI:78:HIS:NE2	2.19	1.10
24:LU:116:GLN:O	84:CI:74:LYS:HA	1.56	1.04
24:LU:117:ILE:C	84:CI:75:LYS:N	2.18	1.01
2:L5:2557:G:H1	2:L5:2570:U:H3	1.05	0.98
2:L5:1996:C:N4	2:L5:2000:G:H22	1.61	0.97
2:L5:4887:C:N4	2:L5:4932:U:H3	1.63	0.97
82:S2:1351:G:H1	82:S2:1360:U:H3	1.12	0.96
83:Zt:26:A:N6	83:Zt:44:G:H1	1.62	0.96
2:L5:3944:G:H1	2:L5:4069:U:H3	1.13	0.95
2:L5:1996:C:H42	2:L5:2000:G:N2	1.63	0.94
2:L5:1996:C:H42	2:L5:2000:G:H22	0.95	0.94
82:S2:1033:G:H1	82:S2:1080:A:HO2'	1.10	0.94
83:Zt:26:A:H61	83:Zt:44:G:H1	0.96	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1656:G:H1	82:S2:1668:U:H3	1.07	0.93
82:S2:1324:G:H1	82:S2:1504:U:H3	1.03	0.92
2:L5:4946:U:HO2'	35:Lf:2:SER:N	1.71	0.88
83:Zt:6:G:H1	83:Zt:67:U:H3	0.92	0.88
2:L5:4887:C:H42	2:L5:4932:U:H3	0.92	0.87
2:L5:4775:C:H41	2:L5:4859:C:H42	1.21	0.87
82:S2:1737:G:H1	82:S2:1797:U:H3	1.22	0.87
76:SW:2:VAL:N	82:S2:1091:C:HO2'	1.73	0.87
82:S2:110:U:H3	82:S2:351:G:H1	1.20	0.86
2:L5:2706:G:C5	84:CI:78:HIS:NE2	2.45	0.85
82:S2:1417:C:N4	82:S2:1422:G:H22	1.75	0.84
82:S2:1748:G:H1	82:S2:1786:U:H3	0.85	0.84
2:L5:2706:G:C5	84:CI:78:HIS:CD2	2.66	0.83
2:L5:1100:U:H3	2:L5:1194:G:H1	1.22	0.83
82:S2:1417:C:H42	82:S2:1422:G:N2	1.76	0.82
82:S2:1776:G:N2	82:S2:1777:G:N7	2.27	0.82
2:L5:2007:G:H21	2:L5:2012:A:H62	1.27	0.82
2:L5:4763:U:HO2'	22:LS:174:THR:HG1	1.27	0.81
82:S2:1417:C:H42	82:S2:1422:G:H22	1.27	0.81
33:Ld:70:LYS:NZ	84:CI:66:GLY:HA3	1.95	0.81
24:LU:116:GLN:O	84:CI:74:LYS:CA	2.29	0.80
82:S2:1606:G:H1	82:S2:1632:G:HO2'	1.27	0.80
2:L5:4098:A:H2'	2:L5:4099:G:H4'	1.64	0.80
2:L5:2520:C:O2	2:L5:2640:G:N2	2.15	0.79
62:Sf:126:CYS:SG	62:Sf:144:CYS:N	2.53	0.79
1:Pt:50:U:H3	1:Pt:64:G:H1	0.81	0.79
82:S2:925:G:H1	82:S2:1017:U:H3	1.31	0.78
2:L5:1095:A:H2	2:L5:1200:G:H1	1.32	0.78
2:L5:5024:C:H41	2:L5:5028:G:H21	1.31	0.76
2:L5:3954:A:H1'	2:L5:4058:U:H5'	1.67	0.76
2:L5:4774:C:O2'	2:L5:4775:C:O2	2.03	0.76
26:LW:119:LYS:O	26:LW:123:LYS:HB2	1.86	0.75
2:L5:1870:C:H2'	2:L5:1871:A2M:H8	1.69	0.74
2:L5:2845:A:H61	2:L5:3843:C:H42	1.32	0.74
54:SQ:72:VAL:HG11	54:SQ:80:GLN:HG3	1.68	0.74
54:SQ:4:LYS:HE3	82:S2:1423:C:H41	1.52	0.74
82:S2:1417:C:N3	82:S2:1422:G:N1	2.35	0.73
26:LW:80:ARG:NH2	68:SG:8:PRO:O	2.21	0.73
57:ST:12:GLN:NE2	82:S2:1593:C:O2	2.21	0.73
82:S2:1729:U:H3	82:S2:1805:G:H1	1.36	0.73
82:S2:106:C:H2'	82:S2:107:A:H8	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1743:A:N1	2:L5:1789:C:O2'	2.23	0.72
2:L5:3641:U:OP2	2:L5:3646:A:N6	2.23	0.72
68:SG:11:GLY:HA2	82:S2:166:A2M:HM'1	1.72	0.72
2:L5:518:G:H1	2:L5:643:C:H2'	1.54	0.72
2:L5:664:G:N2	2:L5:666:G:O6	2.23	0.72
2:L5:4546:A:N7	5:LA:215:ASN:ND2	2.37	0.72
63:Sg:206:LEU:HD12	63:Sg:218:LEU:HD12	1.70	0.72
2:L5:2495:U:H2'	2:L5:2496:G:H8	1.55	0.72
50:SF:127:ARG:HG2	50:SF:136:ARG:HE	1.55	0.72
2:L5:4638:U:H3	2:L5:4661:G:H1	1.35	0.72
2:L5:381:U:H4'	2:L5:415:G:H5'	1.71	0.71
2:L5:2362:U:H2'	2:L5:2363:A2M:H8	1.72	0.71
2:L5:1563:A:N6	82:S2:1028:A:N1	2.39	0.71
2:L5:1971:C:O2	47:Ls:41:GLN:NE2	2.23	0.71
63:Sg:152:SER:HG	63:Sg:168:CYS:HG	1.37	0.71
2:L5:512:U:H3	2:L5:647:G:H1	1.38	0.70
82:S2:94:G:HO2'	82:S2:508:A:HO2'	1.34	0.70
2:L5:4896:G:H21	2:L5:4926:C:H42	1.40	0.70
2:L5:184:U:O2	2:L5:253:G:N2	2.23	0.70
2:L5:1414:C:H2'	2:L5:1415:G:H8	1.57	0.70
2:L5:4910:G:H4'	6:LB:95:THR:HG22	1.72	0.70
2:L5:3823:G:N2	2:L5:3823:G:OP2	2.23	0.70
2:L5:4102:C:H1'	2:L5:4108:G:H1	1.56	0.70
54:SQ:140:ARG:HB2	82:S2:1644:C:H4'	1.73	0.70
76:SW:107:SER:HB2	82:S2:860:G:H21	1.55	0.70
32:Lc:78:ASN:HD21	45:Lp:43:GLY:HA3	1.57	0.70
68:SG:168:LYS:NZ	82:S2:74:G:O6	2.23	0.70
82:S2:110:U:O2	82:S2:351:G:N2	2.23	0.70
65:SB:40:ASN:HD21	65:SB:76:ASN:HB2	1.57	0.69
2:L5:3594:C:O2	2:L5:3597:G:N2	2.25	0.69
65:SB:122:GLU:HG2	65:SB:140:VAL:HG12	1.74	0.69
2:L5:2611:A:H5'	2:L5:2688:G:H4'	1.75	0.69
6:LB:10:ARG:NH1	6:LB:11:HIS:O	2.24	0.69
82:S2:1581:C:H5'	82:S2:1582:C:H5	1.58	0.69
2:L5:1408:G:O2'	2:L5:1411:C:N4	2.25	0.69
5:LA:107:MET:HB3	5:LA:111:THR:HG21	1.75	0.69
2:L5:935:A:N7	16:LM:46:ARG:NH2	2.41	0.68
2:L5:4541:G:N2	2:L5:4544:A:OP2	2.26	0.68
2:L5:267:G:H2'	2:L5:268:G:H8	1.58	0.68
2:L5:2601:A:N6	2:L5:2744:A:OP2	2.25	0.68
82:S2:1422:G:H4'	82:S2:1423:C:H3'	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:388:U:H2'	82:S2:389:A:H8	1.57	0.68
2:L5:2702:C:OP1	24:LU:101:ARG:NH2	2.25	0.68
2:L5:4126:C:H5''	2:L5:4127:A:H5''	1.76	0.68
57:ST:126:GLN:HB2	57:ST:129:ARG:HH21	1.59	0.68
66:SC:210:PRO:HB3	66:SC:240:THR:HG21	1.75	0.68
81:Se:41:ARG:NH2	82:S2:639:C:OP1	2.27	0.68
2:L5:24:G:N7	39:Lj:46:LYS:NZ	2.42	0.68
2:L5:2622:G:O6	24:LU:81:ARG:NH2	2.27	0.68
33:Ld:90:ARG:HD3	33:Ld:102:LEU:HD13	1.75	0.67
63:Sg:63:SER:HB2	82:S2:1398:G:H1'	1.76	0.67
2:L5:327:U:O2'	38:Li:30:ARG:NH1	2.27	0.67
82:S2:1658:G:OP2	82:S2:1660:C:N4	2.28	0.67
31:Lb:109:ARG:HA	31:Lb:112:ILE:HG12	1.76	0.67
83:Zt:15:G:N2	83:Zt:20:U:OP1	2.28	0.67
7:LC:39:PHE:O	7:LC:43:ASN:ND2	2.26	0.67
72:SL:35:ARG:NH2	72:SL:55:TYR:O	2.27	0.67
77:SX:107:ARG:HG3	77:SX:110:HIS:HB3	1.77	0.67
66:SC:200:ARG:O	71:SJ:54:ARG:NH2	2.26	0.67
82:S2:454:U:H2'	82:S2:455:A:H8	1.60	0.67
82:S2:508:A:H3'	82:S2:509:OMG:H8	1.58	0.67
45:Lp:38:THR:HA	45:Lp:45:THR:HA	1.76	0.67
68:SG:198:ARG:NH1	82:S2:126:G:OP2	2.28	0.67
21:LR:176:ARG:NH2	82:S2:910:G:OP1	2.28	0.67
59:SZ:58:LEU:HD12	59:SZ:62:VAL:HG21	1.77	0.67
73:SN:14:SER:HB3	82:S2:1016:U:H5''	1.75	0.67
83:Zt:15:G:H22	83:Zt:48:C:H42	1.43	0.67
2:L5:2092:G:O2'	2:L5:2262:G:N2	2.28	0.67
2:L5:2780:C:H2'	2:L5:2781:G:H8	1.58	0.67
2:L5:3697:U:H5''	2:L5:3698:G:H5'	1.77	0.67
64:SA:89:LYS:HD2	64:SA:201:LEU:HG	1.77	0.67
2:L5:323:C:H2'	2:L5:324:A:H8	1.60	0.66
2:L5:2400:G:H21	36:Lg:6:THR:HG22	1.60	0.66
40:Lk:68:GLU:HG3	40:Lk:70:LYS:H	1.58	0.66
2:L5:308:G:OP2	2:L5:308:G:N2	2.23	0.66
2:L5:1499:C:OP1	20:LQ:150:ARG:NH2	2.28	0.66
7:LC:230:LEU:HD21	7:LC:236:ASN:H	1.59	0.66
2:L5:1818:G:OP2	2:L5:1818:G:N2	2.23	0.66
17:LN:146:PRO:HB2	37:Lh:104:THR:HG23	1.77	0.66
68:SG:66:GLY:HA2	82:S2:1745:A:H1'	1.76	0.66
2:L5:369:G:N2	2:L5:372:A:OP2	2.26	0.66
12:LH:102:ASN:HB2	12:LH:115:ARG:HB2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:3937:C:H1'	17:LN:125:SER:HB3	1.76	0.66
54:SQ:131:LYS:HB2	54:SQ:140:ARG:HH22	1.61	0.66
2:L5:2845:A:H61	2:L5:3843:C:N4	1.94	0.66
63:Sg:252:THR:HG21	63:Sg:257:LYS:HD2	1.78	0.66
68:SG:135:PRO:HG2	68:SG:141:ILE:HG22	1.76	0.66
82:S2:140:C:H42	82:S2:313:A:H61	1.43	0.66
82:S2:557:U:H2'	82:S2:558:G:C8	2.30	0.66
2:L5:2484:A:H62	2:L5:2494:U:H3	1.44	0.66
4:L8:94:G:H21	39:Lj:82:THR:HB	1.60	0.66
24:LU:65:ARG:HG2	24:LU:67:LYS:H	1.61	0.66
53:SP:37:TYR:O	56:SS:88:LYS:NZ	2.28	0.66
74:SO:104:ARG:NH2	82:S2:959:G:OP1	2.29	0.66
82:S2:482:G:N1	82:S2:485:A:OP2	2.28	0.66
82:S2:587:A:H5'	82:S2:592:C:H41	1.60	0.66
2:L5:513:U:N3	2:L5:516:C:OP2	2.29	0.66
2:L5:1982:G:N2	2:L5:2009:A:O2'	2.29	0.65
2:L5:2103:G:N7	2:L5:2104:G:N2	2.43	0.65
82:S2:928:G:H2'	82:S2:929:G:C8	2.31	0.65
82:S2:1130:G:N2	82:S2:1130:G:OP2	2.29	0.65
24:LU:116:GLN:O	84:CI:74:LYS:CB	2.44	0.65
30:La:103:VAL:HB	30:La:108:TYR:HB2	1.78	0.65
71:SJ:124:HIS:HD2	81:Se:31:ARG:HE	1.43	0.65
73:SN:70:LYS:NZ	82:S2:1020:A:N7	2.43	0.65
2:L5:1704:C:O3'	10:LF:46:ARG:NH1	2.29	0.65
12:LH:106:GLN:HB2	12:LH:111:LEU:HB3	1.78	0.65
52:SM:96:ARG:NH2	52:SM:100:PRO:O	2.29	0.65
82:S2:1562:C:H2'	82:S2:1563:G:H8	1.59	0.65
2:L5:2059:C:H2'	2:L5:2060:G:H8	1.61	0.65
2:L5:1670:G:OP1	31:Lb:12:GLN:NE2	2.28	0.65
89:L5:5297:HMT:C7	89:L5:5297:HMT:C16	2.69	0.65
65:SB:26:SER:O	65:SB:51:ARG:NH2	2.30	0.65
65:SB:103:MET:HG3	65:SB:215:VAL:HG12	1.79	0.65
83:Zt:19:G:O2'	83:Zt:48:C:N4	2.26	0.65
2:L5:4601:U:H2'	2:L5:4602:A:H8	1.61	0.65
6:LB:90:VAL:HG23	6:LB:163:ILE:HD11	1.78	0.65
82:S2:613:G:N1	82:S2:629:A:OP2	2.27	0.65
70:SI:70:GLU:OE2	72:SL:21:LYS:NZ	2.29	0.65
2:L5:4094:G:N2	2:L5:4115:G:OP2	2.30	0.64
2:L5:4098:A:N1	2:L5:4112:C:N4	2.45	0.64
51:SK:25:LYS:NZ	82:S2:1497:G:N7	2.40	0.64
60:Sc:29:GLN:HA	60:Sc:45:ASN:HA	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2020:U:H2'	2:L5:2021:G:H8	1.61	0.64
71:SJ:136:ARG:NH1	71:SJ:159:PHE:O	2.30	0.64
82:S2:830:A:OP2	82:S2:846:G:N2	2.30	0.64
52:SM:49:LEU:HD21	52:SM:123:VAL:HG11	1.79	0.64
82:S2:300:U:H2'	82:S2:301:A:H8	1.62	0.64
2:L5:2007:G:N2	2:L5:2012:A:H62	1.95	0.64
2:L5:4457:PSU:OP1	25:LV:50:ASN:ND2	2.27	0.64
2:L5:2351:OMC:HM22	7:LC:95:MET:HG3	1.80	0.64
5:LA:137:ILE:HD11	5:LA:149:LYS:HB2	1.80	0.64
68:SG:176:ILE:HG12	68:SG:179:LEU:HD11	1.78	0.64
63:Sg:40:ILE:HB	63:Sg:59:LEU:HB2	1.78	0.64
2:L5:1095:A:N1	2:L5:1200:G:O6	2.31	0.64
2:L5:1996:C:O3'	47:Ls:44:ARG:NH1	2.30	0.64
63:Sg:258:ILE:HG23	63:Sg:267:VAL:HG23	1.80	0.64
2:L5:262:G:H2'	2:L5:263:G:H8	1.62	0.64
11:LG:150:LYS:NZ	11:LG:177:MET:O	2.31	0.64
47:Ls:62:ARG:HB3	47:Ls:66:ARG:HH12	1.63	0.64
55:SR:22:THR:O	63:Sg:212:LYS:NZ	2.30	0.64
61:Sd:17:GLY:O	61:Sd:27:ARG:NH1	2.31	0.64
2:L5:4443:C:O2	2:L5:4444:C:N4	2.31	0.64
5:LA:104:VAL:HA	5:LA:107:MET:HE3	1.80	0.64
47:Ls:68:HIS:O	47:Ls:71:ASN:ND2	2.30	0.64
54:SQ:139:ALA:HB2	82:S2:1650:A:H5''	1.80	0.64
67:SE:153:LEU:O	67:SE:174:LYS:NZ	2.30	0.64
82:S2:149:A:H3'	82:S2:150:A:H8	1.62	0.64
18:LO:34:VAL:HG22	18:LO:103:LYS:HB2	1.80	0.63
82:S2:1396:A:N7	82:S2:1449:G:O6	2.30	0.63
2:L5:460:C:H2'	2:L5:461:G:H8	1.64	0.63
2:L5:4403:PSU:HN3	2:L5:4440:G:H1	1.44	0.63
68:SG:169:PRO:O	82:S2:72:C:N4	2.32	0.63
2:L5:2034:G:O2'	22:LS:118:ARG:NH1	2.30	0.63
21:LR:172:ARG:NH1	82:S2:909:G:OP1	2.30	0.63
53:SP:135:ALA:HB2	82:S2:1235:G:H21	1.64	0.63
82:S2:1808:U:H2'	82:S2:1809:A:H8	1.63	0.63
57:ST:101:ARG:NH2	82:S2:1566:G:N7	2.47	0.63
76:SW:111:MET:HE1	76:SW:119:LYS:HD2	1.81	0.63
82:S2:747:U:N3	82:S2:796:G:N1	2.46	0.63
1:Pt:73:A:N3	13:LI:110:ARG:NH1	2.47	0.63
2:L5:4431:PSU:OP2	13:LI:3:ARG:NH2	2.31	0.63
82:S2:1228:A:H2'	82:S2:1229:G:H8	1.64	0.63
2:L5:25:A:H61	2:L5:58:G:H1	1.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2295:C:H2'	2:L5:2296:G:H8	1.63	0.63
2:L5:4522:G:O2'	2:L5:4525:C:OP2	2.17	0.63
69:SH:105:THR:HG23	69:SH:107:LYS:H	1.62	0.63
2:L5:2093:A:N3	2:L5:2094:G:N1	2.46	0.63
4:L8:67:U:H2'	4:L8:68:G:H8	1.63	0.63
52:SM:58:GLU:HB3	52:SM:61:TYR:HB2	1.81	0.63
67:SE:31:PRO:HA	67:SE:81:THR:HB	1.80	0.63
2:L5:2758:G:O2'	2:L5:2765:A:N3	2.30	0.63
8:LD:232:THR:OG1	8:LD:234:ASP:OD1	2.16	0.63
10:LF:105:VAL:HG13	10:LF:136:VAL:HG12	1.81	0.63
65:SB:144:LYS:HD3	65:SB:208:HIS:HB3	1.79	0.63
82:S2:1513:C:H2'	82:S2:1514:G:H8	1.63	0.63
2:L5:4594:U:H2'	2:L5:4595:G:H8	1.64	0.62
12:LH:51:LYS:HE2	12:LH:54:ARG:HH12	1.64	0.62
42:Lm:99:CYS:HB2	42:Lm:114:LYS:HE3	1.79	0.62
61:Sd:2:GLY:N	82:S2:1271:C:O2	2.31	0.62
82:S2:1030:A:H2'	82:S2:1031:A2M:H8	1.80	0.62
83:Zt:6:G:O6	83:Zt:67:U:O4	2.16	0.62
2:L5:3619:G:H22	2:L5:3624:A:H1'	1.64	0.62
82:S2:1228:A:H2'	82:S2:1229:G:C8	2.33	0.62
82:S2:1243:U:OP2	82:S2:1518:C:O2'	2.15	0.62
82:S2:1277:C:H2'	82:S2:1278:A:H8	1.64	0.62
2:L5:1332:C:H2'	2:L5:1333:A:H8	1.63	0.62
2:L5:3726:A:H2'	2:L5:3727:A:C8	2.35	0.62
2:L5:4566:U:O2'	6:LB:234:ARG:NH1	2.32	0.62
82:S2:165:G:OP2	82:S2:165:G:N2	2.32	0.62
7:LC:107:THR:O	7:LC:111:TRP:NE1	2.30	0.62
2:L5:1100:U:O3'	2:L5:1167:C:N4	2.32	0.62
2:L5:4305:G:N7	23:LT:87:LYS:NZ	2.42	0.62
9:LE:164:PHE:HA	9:LE:175:VAL:HG12	1.81	0.62
48:Lt:65:GLN:HG3	48:Lt:67:ARG:H	1.63	0.62
2:L5:3870:C:H2'	2:L5:3871:A:H8	1.64	0.62
4:L8:155:C:OP1	11:LG:89:ARG:NH1	2.32	0.62
5:LA:29:LEU:O	5:LA:123:ARG:NH1	2.33	0.62
16:LM:15:VAL:HG22	16:LM:50:MET:HE1	1.82	0.62
2:L5:5002:U:OP2	6:LB:385:LYS:NZ	2.31	0.62
6:LB:83:PRO:O	6:LB:167:GLN:NE2	2.33	0.62
25:LV:35:LYS:HB2	25:LV:67:LYS:HG3	1.82	0.62
65:SB:205:TYR:CD1	82:S2:1122:A:H4'	2.34	0.62
82:S2:1748:G:O6	82:S2:1786:U:O4	2.17	0.62
83:Zt:22:G:H2'	83:Zt:23:A:H8	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:184:U:O2'	2:L5:189:G:O4'	2.17	0.62
2:L5:2599:G:N2	2:L5:2747:U:O4	2.32	0.62
2:L5:2764:A:H2'	2:L5:2765:A:H8	1.65	0.62
2:L5:3717:A:H2'	2:L5:3718:A2M:H8	1.82	0.62
14:LJ:141:ILE:HA	14:LJ:144:LYS:HD2	1.81	0.62
57:ST:124:THR:HG23	57:ST:127:GLY:H	1.64	0.62
82:S2:350:C:HO2'	82:S2:383:G:H1	1.43	0.62
2:L5:73:A:N7	15:LL:103:ARG:NH2	2.47	0.62
50:SF:134:VAL:HG12	50:SF:135:ARG:HG2	1.81	0.62
79:Sa:12:LYS:NZ	82:S2:1086:G:OP2	2.29	0.62
82:S2:1605:G:N2	82:S2:1633:A:OP2	2.32	0.62
22:LS:76:LYS:NZ	22:LS:100:LEU:O	2.33	0.62
78:SY:124:ASN:HD22	82:S2:84:A:H5''	1.64	0.62
2:L5:1354:A:N6	2:L5:1503:A:O4'	2.33	0.61
2:L5:4129:G:O6	2:L5:4156:G:N2	2.33	0.61
24:LU:44:GLN:HB2	24:LU:56:LEU:HD21	1.82	0.61
26:LW:7:SER:HB2	26:LW:13:ILE:HD11	1.80	0.61
33:Ld:36:VAL:HG21	33:Ld:44:ARG:HG2	1.81	0.61
82:S2:1004:PSU:H2'	82:S2:1005:G:H8	1.65	0.61
83:Zt:68:C:H2'	83:Zt:69:G:C8	2.35	0.61
2:L5:4301:U:OP2	2:L5:4303:C:N4	2.33	0.61
2:L5:4413:C:O2	13:LI:158:LYS:NZ	2.32	0.61
69:SH:191:GLU:O	69:SH:193:GLN:NE2	2.27	0.61
77:SX:48:LYS:HB3	77:SX:75:ILE:HD12	1.83	0.61
2:L5:330:G:N7	87:L5:5284:SPD:N1	2.48	0.61
2:L5:3661:G:H4'	2:L5:3662:A:H5'	1.82	0.61
2:L5:4474:A:OP2	2:L5:4476:C:N4	2.33	0.61
2:L5:300:A:H2'	2:L5:301:G:H8	1.65	0.61
73:SN:64:ARG:HD3	73:SN:70:LYS:HG2	1.81	0.61
78:SY:111:LYS:NZ	82:S2:54:A:OP1	2.28	0.61
82:S2:889:U:OP2	82:S2:896:U:N3	2.33	0.61
2:L5:4277:G:H5''	23:LT:17:ARG:HG2	1.83	0.61
82:S2:588:G:H4'	82:S2:589:G:H5'	1.82	0.61
2:L5:364:G:O6	39:Lj:55:ARG:NH2	2.33	0.61
2:L5:3589:G:N2	2:L5:3590:G:O6	2.33	0.61
4:L8:150:C:N4	11:LG:52:THR:O	2.34	0.61
40:Lk:8:ILE:HD11	40:Lk:56:LEU:HD13	1.82	0.61
66:SC:191:VAL:HG11	66:SC:236:PHE:HA	1.82	0.61
67:SE:79:ASP:HB3	67:SE:82:TYR:HB2	1.83	0.61
2:L5:1326:A2M:H2'	2:L5:1327:C:C6	2.36	0.61
2:L5:1396:G:HO2'	2:L5:1468:C:HO2'	1.46	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2520:C:H2'	2:L5:2521:G:H8	1.66	0.61
2:L5:3672:G:OP2	2:L5:3672:G:N2	2.32	0.61
2:L5:3824:A:H3'	2:L5:3825:A2M:H8	1.81	0.61
39:Lj:19:CYS:SG	39:Lj:34:CYS:HB2	2.41	0.61
58:SU:116:ILE:HG13	58:SU:119:ALA:H	1.66	0.61
66:SC:167:ARG:HB3	66:SC:177:PRO:HB2	1.83	0.61
2:L5:4458:C:OP1	6:LB:11:HIS:NE2	2.31	0.61
21:LR:98:ARG:NH1	21:LR:132:PHE:O	2.34	0.61
82:S2:874:G:H2'	82:S2:875:A:H8	1.65	0.61
2:L5:4873:G:N7	18:LO:179:LYS:NZ	2.48	0.61
89:L5:5297:HMT:C7	89:L5:5297:HMT:N1	2.61	0.61
11:LG:81:ASN:O	11:LG:84:THR:OG1	2.19	0.61
82:S2:1179:G:N2	82:S2:1182:A:OP2	2.30	0.61
2:L5:382:G:N1	2:L5:385:A:OP2	2.34	0.60
2:L5:2444:U:HO2'	4:L8:112:G:HO2'	1.46	0.60
18:LO:126:VAL:HG13	18:LO:127:VAL:HG13	1.83	0.60
82:S2:136:C:H5''	82:S2:137:U:H5''	1.82	0.60
2:L5:1979:A:N6	2:L5:1984:A:OP1	2.27	0.60
15:LL:80:GLU:OE2	15:LL:113:ASN:ND2	2.34	0.60
40:Lk:24:LYS:HD3	40:Lk:69:LEU:HD21	1.83	0.60
66:SC:267:GLN:OE1	75:SV:35:ASN:ND2	2.34	0.60
68:SG:202:ASN:ND2	82:S2:125:C:OP1	2.33	0.60
2:L5:1626:G:OP2	17:LN:77:LYS:NZ	2.33	0.60
2:L5:2893:U:O2'	70:SI:88:ASN:ND2	2.33	0.60
2:L5:3668:C:OP1	5:LA:8:GLN:NE2	2.30	0.60
53:SP:130:ARG:HD3	53:SP:131:PRO:HD2	1.82	0.60
54:SQ:89:SER:OG	54:SQ:119:LEU:O	2.19	0.60
64:SA:22:GLY:O	64:SA:24:HIS:ND1	2.34	0.60
67:SE:27:PHE:O	82:S2:495:U:O2'	2.19	0.60
69:SH:142:LYS:HB3	76:SW:54:ASP:HB3	1.82	0.60
82:S2:1337:4AC:H2'	82:S2:1338:G:H8	1.65	0.60
2:L5:1982:G:H1'	2:L5:2010:A:H4'	1.83	0.60
2:L5:2554:U:O2	2:L5:2764:A:N7	2.34	0.60
2:L5:3880:G:H2'	2:L5:3881:G:C8	2.36	0.60
2:L5:4525:C:OP1	6:LB:246:ARG:NH2	2.29	0.60
50:SF:19:LEU:HD11	50:SF:50:PRO:HD3	1.82	0.60
66:SC:257:LYS:O	75:SV:16:LYS:NZ	2.34	0.60
82:S2:90:G:OP1	82:S2:445:A:N6	2.30	0.60
2:L5:3938:G:O6	2:L5:4172:A:N6	2.33	0.60
49:SD:99:ILE:HG23	49:SD:173:ARG:HH21	1.66	0.60
66:SC:68:ARG:HG2	66:SC:277:HIS:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1829:G:H1'	82:S2:1850:MA6:H2	1.83	0.60
2:L5:332:C:OP2	87:L5:5284:SPD:N10	2.34	0.60
2:L5:1933:G:H2'	2:L5:1934:A:C8	2.37	0.60
2:L5:2835:A:O2'	6:LB:228:TYR:O	2.18	0.60
22:LS:15:ARG:HD2	22:LS:25:PRO:HG2	1.83	0.60
2:L5:2856:C:O2	6:LB:242:ARG:NH2	2.33	0.60
2:L5:4670:C:O2'	2:L5:4672:A:OP2	2.18	0.60
50:SF:124:ASP:OD1	50:SF:125:SER:N	2.30	0.60
51:SK:14:LEU:HD22	51:SK:35:LEU:HD23	1.83	0.60
51:SK:85:LEU:HD21	51:SK:89:ILE:HB	1.84	0.60
54:SQ:49:TYR:O	54:SQ:53:GLU:HB2	2.01	0.60
67:SE:144:ALA:HB3	82:S2:121:OMU:HM23	1.84	0.60
82:S2:1759:G:N2	82:S2:1760:G:O6	2.34	0.60
2:L5:1739:G:N3	2:L5:1742:A:N6	2.49	0.60
2:L5:3917:A:H2'	2:L5:3918:G:H8	1.67	0.60
78:SY:74:MET:SD	78:SY:90:ARG:NH1	2.75	0.60
2:L5:2577:C:OP1	29:LZ:111:ARG:NH2	2.35	0.60
5:LA:114:CYS:HB3	5:LA:165:VAL:HB	1.84	0.60
66:SC:193:VAL:HG11	66:SC:240:THR:HG22	1.83	0.60
68:SG:92:ARG:O	82:S2:453:C:O2'	2.18	0.60
70:SI:133:GLU:HA	70:SI:136:ILE:HG12	1.83	0.60
78:SY:111:LYS:NZ	82:S2:56:G:OP1	2.30	0.60
2:L5:1700:G:H5''	2:L5:1704:C:H42	1.66	0.60
2:L5:1906:U:H2'	2:L5:1907:A:H8	1.67	0.60
2:L5:2298:U:OP1	7:LC:204:ARG:NE	2.34	0.60
74:SO:134:PRO:HB3	82:S2:944:A:H5''	1.84	0.60
82:S2:941:C:H2'	82:S2:942:G:H8	1.67	0.60
2:L5:4563:U:H2'	2:L5:4564:A:H8	1.65	0.59
6:LB:292:LEU:HB2	6:LB:298:LEU:HD12	1.84	0.59
51:SK:8:ARG:NH2	82:S2:1314:U:O2'	2.34	0.59
68:SG:2:LYS:HB2	68:SG:108:VAL:HG12	1.83	0.59
82:S2:1652:G:H1	82:S2:1672:U:H3	1.49	0.59
2:L5:1532:G:OP2	39:Lj:31:LYS:NZ	2.33	0.59
2:L5:1994:C:H2'	2:L5:1995:G:C8	2.36	0.59
53:SP:40:ARG:NH2	82:S2:1615:U:O4	2.35	0.59
60:Sc:17:VAL:HA	60:Sc:30:VAL:HG12	1.84	0.59
71:SJ:162:ARG:NH1	82:S2:582:U:OP1	2.34	0.59
83:Zt:68:C:H2'	83:Zt:69:G:H8	1.65	0.59
2:L5:1969:G:H4'	47:Ls:36:GLY:HA2	1.84	0.59
2:L5:2448:G:O2'	5:LA:21:LYS:NZ	2.30	0.59
8:LD:52:ILE:HA	8:LD:147:ASP:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SS:141:ARG:NH1	82:S2:1524:G:OP2	2.33	0.59
58:SU:20:ILE:HG22	58:SU:116:ILE:HG22	1.84	0.59
64:SA:155:ARG:NH2	82:S2:1137:U:O2'	2.35	0.59
4:L8:21:C:OP1	7:LC:195:LYS:NZ	2.35	0.59
19:LP:109:VAL:HA	19:LP:112:LEU:HD13	1.84	0.59
22:LS:147:ASP:HB3	22:LS:150:ILE:HB	1.82	0.59
50:SF:168:THR:OG1	50:SF:171:GLU:OE1	2.19	0.59
68:SG:77:LEU:HD12	68:SG:95:LYS:HD3	1.83	0.59
74:SO:55:ARG:NH2	82:S2:954:U:O2	2.35	0.59
2:L5:4239:A:H2'	2:L5:4240:G:C8	2.37	0.59
4:L8:19:C:H2'	4:L8:20:A:H8	1.66	0.59
82:S2:1528:G:O2'	82:S2:1666:C:OP1	2.19	0.59
2:L5:1100:U:O4	2:L5:1194:G:O6	2.21	0.59
2:L5:1457:G:O2'	20:LQ:75:ARG:NH2	2.36	0.59
2:L5:4163:U:OP2	11:LG:53:ARG:NH2	2.35	0.59
2:L5:4699:U:H1'	2:L5:4700:A:H5''	1.84	0.59
21:LR:39:GLN:OE1	21:LR:42:ARG:NH1	2.36	0.59
40:Lk:26:LYS:HB2	40:Lk:69:LEU:HD12	1.84	0.59
40:Lk:54:GLU:OE2	40:Lk:58:GLN:NE2	2.26	0.59
67:SE:11:ARG:NH1	67:SE:24:THR:OG1	2.36	0.59
68:SG:135:PRO:HA	82:S2:169:U:H5''	1.84	0.59
83:Zt:30:G:H2'	83:Zt:31:A:H8	1.67	0.59
9:LE:91:THR:HA	9:LE:108:LYS:HA	1.83	0.59
44:Lo:78:ARG:O	44:Lo:80:LYS:NZ	2.36	0.59
76:SW:3:ARG:HH22	76:SW:28:ARG:HH21	1.49	0.59
82:S2:300:U:H2'	82:S2:301:A:C8	2.37	0.59
2:L5:441:G:H2'	2:L5:442:G:H8	1.68	0.59
2:L5:512:U:O4	2:L5:647:G:O6	2.21	0.59
2:L5:1927:U:OP1	2:L5:1949:U:O2'	2.15	0.59
2:L5:2845:A:N6	2:L5:3843:C:H42	2.01	0.59
18:LO:9:LEU:HD23	18:LO:118:MET:HB2	1.85	0.59
32:Lc:48:LEU:HD13	32:Lc:57:LYS:HG3	1.83	0.59
56:SS:8:LYS:HZ1	56:SS:60:THR:HA	1.68	0.59
64:SA:73:ASP:HB3	64:SA:120:ARG:HB2	1.85	0.59
78:SY:36:PRO:HG3	82:S2:570:C:H4'	1.83	0.59
2:L5:40:G:N7	87:L5:5262:SPD:N1	2.51	0.59
2:L5:1844:G:H5''	31:Lb:25:ARG:HH22	1.68	0.59
2:L5:2770:C:H2'	2:L5:2771:G:H8	1.67	0.59
2:L5:4728:U:OP1	6:LB:132:LYS:NZ	2.32	0.59
7:LC:293:LEU:O	7:LC:299:GLN:NE2	2.33	0.59
2:L5:1253:G:H2'	2:L5:1256:G:H5'	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1932:A:OP1	18:LO:49:ARG:NH2	2.28	0.59
2:L5:2899:C:OP1	21:LR:108:ARG:NH2	2.34	0.59
2:L5:3787:G:H1'	2:L5:3789:C:H41	1.68	0.59
2:L5:4075:U:OP1	11:LG:249:ARG:NH2	2.36	0.59
2:L5:4097:G:O6	2:L5:4098:A:N6	2.36	0.59
2:L5:4363:A:H5''	44:Lo:36:GLN:HG2	1.84	0.59
3:L7:7:G:OP1	8:LD:33:ARG:NH1	2.35	0.59
77:SX:90:CYS:HB3	77:SX:130:LEU:HD22	1.85	0.59
82:S2:60:A:N3	82:S2:316:G:O2'	2.35	0.59
82:S2:463:C:O2'	82:S2:466:G:O6	2.17	0.59
50:SF:60:ARG:HD2	82:S2:1679:A:H2'	1.85	0.58
54:SQ:19:ALA:HB2	54:SQ:75:GLY:HA3	1.85	0.58
82:S2:795:A:H2'	82:S2:796:G:C8	2.38	0.58
2:L5:62:A:N3	2:L5:77:U:O2'	2.33	0.58
2:L5:2386:U:H2'	2:L5:2387:G:H8	1.67	0.58
6:LB:10:ARG:NH2	6:LB:265:SER:O	2.36	0.58
40:Lk:24:LYS:HB2	40:Lk:35:LYS:HB2	1.83	0.58
57:ST:73:GLY:O	57:ST:94:ARG:NH2	2.36	0.58
82:S2:145:G:H2'	82:S2:146:G:C8	2.38	0.58
2:L5:2613:C:OP1	36:Lg:24:ARG:NH2	2.36	0.58
2:L5:2870:A:OP2	2:L5:2879:A:N6	2.33	0.58
2:L5:3633:C:OP1	86:L5:5292:SPM:N10	2.37	0.58
2:L5:4304:A:OP2	2:L5:4305:G:N2	2.35	0.58
48:Lt:77:ALA:HB3	48:Lt:80:LEU:HB2	1.84	0.58
70:SI:22:HIS:HB3	82:S2:433:A:H5''	1.83	0.58
82:S2:71:G:N2	82:S2:73:C:OP1	2.36	0.58
82:S2:1841:C:H2'	82:S2:1842:4AC:H6	1.86	0.58
2:L5:1849:U:H3'	15:LL:5:ARG:HH12	1.67	0.58
2:L5:4239:A:H2'	2:L5:4240:G:H8	1.68	0.58
2:L5:4868:G:O2'	2:L5:4872:G:OP1	2.21	0.58
4:L8:39:G:OP1	37:Lh:86:LYS:NZ	2.35	0.58
17:LN:159:ARG:HB3	17:LN:164:LEU:HB2	1.85	0.58
62:Sf:97:LYS:NZ	82:S2:1289:U:OP2	2.30	0.58
2:L5:423:G:OP1	19:LP:62:ARG:NH1	2.36	0.58
2:L5:3796:U:HO2'	82:S2:1720:U:HO2'	1.49	0.58
2:L5:4992:G:H2'	2:L5:4993:G:C8	2.38	0.58
3:L7:28:C:OP2	8:LD:57:ASN:ND2	2.36	0.58
56:SS:85:ASN:OD1	56:SS:97:GLN:NE2	2.36	0.58
68:SG:31:ARG:NH1	82:S2:1745:A:O3'	2.35	0.58
2:L5:417:G:OP1	2:L5:2329:U:O2'	2.22	0.58
6:LB:95:THR:OG1	6:LB:98:GLY:O	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LB:138:GLN:O	6:LB:143:LYS:NZ	2.37	0.58
11:LG:180:PRO:HG3	11:LG:219:VAL:HG13	1.85	0.58
12:LH:187:VAL:HG12	12:LH:188:GLN:HG3	1.86	0.58
39:Lj:2:THR:HG22	39:Lj:4:GLY:H	1.69	0.58
49:SD:32:ASP:OD2	49:SD:65:ARG:NH1	2.36	0.58
51:SK:31:LYS:HZ3	51:SK:40:VAL:H	1.49	0.58
2:L5:3689:G:O2'	2:L5:3818:UY1:OP2	2.20	0.58
2:L5:3868:G:H22	2:L5:3900:G:H1'	1.69	0.58
2:L5:4676:G:OP1	6:LB:281:ASN:ND2	2.37	0.58
17:LN:157:LYS:O	17:LN:162:ARG:NH1	2.37	0.58
63:Sg:57:ARG:NH2	63:Sg:94:THR:O	2.36	0.58
68:SG:183:ARG:NH2	82:S2:316:G:OP2	2.36	0.58
2:L5:1563:A:H2'	2:L5:1564:A:C8	2.38	0.58
63:Sg:129:ILE:HB	63:Sg:142:VAL:HB	1.85	0.58
82:S2:629:A:O2'	82:S2:631:U:OP1	2.21	0.58
2:L5:67:C:N4	2:L5:325:U:O2'	2.36	0.58
2:L5:3928:A:OP1	17:LN:90:ASN:ND2	2.36	0.58
2:L5:4683:U:OP2	2:L5:4706:G:N1	2.35	0.58
20:LQ:50:ARG:HH21	20:LQ:140:SER:HB2	1.69	0.58
62:Sf:119:ARG:HB3	62:Sf:132:MET:HB2	1.85	0.58
82:S2:1536:G:H2'	82:S2:1537:A:H8	1.69	0.58
82:S2:1550:G:O2'	82:S2:1558:C:O2	2.22	0.58
2:L5:4993:G:H22	2:L5:5058:A:H2	1.52	0.58
15:LL:64:VAL:HA	15:LL:67:HIS:HD2	1.69	0.58
51:SK:27:VAL:HB	51:SK:43:LEU:HD12	1.85	0.58
52:SM:63:LYS:HD3	52:SM:64:LEU:HD22	1.85	0.58
54:SQ:8:GLN:HG3	54:SQ:27:ARG:HE	1.69	0.58
82:S2:851:C:H5''	82:S2:852:G:H5'	1.86	0.58
82:S2:1831:A:O2'	82:S2:1832:6MZ:H8	2.04	0.58
2:L5:325:U:H2'	2:L5:326:C:C6	2.39	0.57
6:LB:117:ARG:HA	6:LB:177:LYS:HD2	1.86	0.57
20:LQ:79:THR:HB	20:LQ:136:THR:HG22	1.86	0.57
56:SS:55:ARG:N	56:SS:58:GLU:OE2	2.34	0.57
57:ST:40:ALA:HB3	57:ST:43:LYS:HG2	1.84	0.57
1:Pt:76:A:H2'	2:L5:4397:A:H1'	1.85	0.57
2:L5:2397:G:O6	36:Lg:4:ARG:NH2	2.31	0.57
49:SD:40:ARG:NH2	58:SU:106:ILE:O	2.38	0.57
59:SZ:85:ARG:NH2	82:S2:1597:C:OP2	2.35	0.57
74:SO:142:ARG:NH1	79:Sa:23:CYS:O	2.37	0.57
76:SW:71:LYS:NZ	82:S2:1156:U:OP1	2.37	0.57
2:L5:500:G:OP1	2:L5:504:G:N2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:4212:A:N1	23:LT:3:ASN:ND2	2.45	0.57
2:L5:4620:OMU:OP2	2:L5:4670:C:N4	2.37	0.57
63:Sg:176:VAL:HG23	63:Sg:185:LYS:HB2	1.86	0.57
77:SX:51:VAL:HA	77:SX:72:VAL:HG22	1.86	0.57
78:SY:34:THR:O	82:S2:570:C:O2'	2.21	0.57
82:S2:1144:A:H2'	82:S2:1145:A:C8	2.38	0.57
2:L5:1094:G:O6	2:L5:1201:U:O2	2.22	0.57
2:L5:1270:A:H8	2:L5:2106:G:H21	1.52	0.57
2:L5:2335:C:H2'	2:L5:2336:G:H8	1.69	0.57
2:L5:1326:A2M:OP2	2:L5:4445:U:O2'	2.22	0.57
2:L5:1461:C:H2'	2:L5:1462:A:H8	1.69	0.57
2:L5:2017:A:O2'	2:L5:2018:C:O5'	2.21	0.57
2:L5:4472:G:O2'	42:Lm:100:TYR:O	2.22	0.57
14:LJ:146:ARG:HG2	14:LJ:147:ARG:HG3	1.87	0.57
49:SD:40:ARG:HA	58:SU:108:PRO:HB3	1.85	0.57
59:SZ:80:ARG:O	82:S2:1598:G:O2'	2.19	0.57
82:S2:388:U:H2'	82:S2:389:A:C8	2.38	0.57
82:S2:468:A2M:H2'	82:S2:469:A:C8	2.38	0.57
82:S2:600:G:H2'	82:S2:601:OMG:H8	1.68	0.57
82:S2:639:C:H2'	82:S2:640:A:H8	1.69	0.57
82:S2:808:A:H2	82:S2:855:G:H22	1.51	0.57
1:Pt:33:U:H3'	54:SQ:146:ARG:HH22	1.70	0.57
2:L5:4896:G:H2'	2:L5:4897:G:C8	2.40	0.57
13:LI:38:ARG:NH1	13:LI:45:GLU:OE1	2.31	0.57
20:LQ:86:ILE:HD12	20:LQ:105:VAL:HG22	1.87	0.57
51:SK:2:LEU:HD21	82:S2:1289:U:H4'	1.86	0.57
82:S2:981:A:H2'	82:S2:982:G:C8	2.39	0.57
2:L5:1502:G:H1	20:LQ:89:ASP:HA	1.70	0.57
2:L5:4274:A:H2'	2:L5:4275:G:H8	1.69	0.57
68:SG:136:LYS:HB2	82:S2:65:C:H41	1.70	0.57
2:L5:1279:A:OP1	9:LE:131:LYS:NZ	2.37	0.57
2:L5:2083:C:OP2	20:LQ:14:ARG:NH2	2.37	0.57
2:L5:2517:A:H5'	36:Lg:62:LYS:HD3	1.87	0.57
2:L5:4951:G:H2'	2:L5:4952:G:H8	1.70	0.57
10:LF:40:LYS:HA	10:LF:43:ARG:HE	1.70	0.57
2:L5:950:G:H2'	2:L5:951:G:H8	1.70	0.57
2:L5:3666:C:OP1	5:LA:234:LYS:NZ	2.27	0.57
86:L5:5289:SPM:H21	87:L5:5290:SPD:H102	1.70	0.57
2:L5:121:A:OP1	11:LG:110:LYS:NZ	2.35	0.57
2:L5:1346:C:H2'	2:L5:1347:G:H8	1.68	0.57
2:L5:3695:PSU:HN3	2:L5:3820:G:H1	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:4184:G:H5'	5:LA:233:ARG:HB2	1.85	0.57
2:L5:4627:U:O2'	6:LB:55:HIS:ND1	2.34	0.57
55:SR:7:LYS:NZ	82:S2:1373:C:OP1	2.36	0.57
58:SU:85:HIS:ND1	82:S2:1447:G:OP1	2.38	0.57
82:S2:223:C:H2'	82:S2:224:A:C8	2.40	0.57
82:S2:1692:U:H2'	82:S2:1693:G:C8	2.40	0.57
2:L5:137:G:H2'	2:L5:138:G:H8	1.69	0.56
2:L5:3855:C:H2'	2:L5:3856:A:H8	1.70	0.56
2:L5:4177:C:H2'	2:L5:4178:A:H8	1.70	0.56
2:L5:4314:C:OP1	23:LT:70:HIS:ND1	2.37	0.56
20:LQ:15:ARG:NH1	20:LQ:52:PHE:O	2.34	0.56
24:LU:99:TRP:HE1	84:CI:59:GLN:HB2	1.69	0.56
36:Lg:45:ALA:HB3	36:Lg:82:MET:HE2	1.86	0.56
58:SU:51:LYS:HB3	58:SU:90:ASP:HB2	1.87	0.56
63:Sg:107:ASP:HB2	63:Sg:125:ARG:HG3	1.87	0.56
66:SC:196:ILE:HB	66:SC:223:TYR:HB2	1.86	0.56
67:SE:100:ARG:HB2	67:SE:114:ILE:HD13	1.86	0.56
82:S2:1560:U:O2	82:S2:1575:G:O6	2.23	0.56
1:Pt:23:C:H2'	1:Pt:24:A:C8	2.40	0.56
39:Lj:14:LYS:NZ	41:Ll:51:LEU:OXT	2.38	0.56
67:SE:45:ILE:HG13	67:SE:61:VAL:HG11	1.85	0.56
69:SH:154:ILE:HB	69:SH:185:VAL:HG22	1.87	0.56
78:SY:102:THR:OG1	78:SY:106:GLN:OE1	2.23	0.56
80:Sb:14:GLU:HA	80:Sb:17:ARG:HG2	1.85	0.56
83:Zt:48:C:H2'	83:Zt:59:G:H1'	1.86	0.56
2:L5:13:U:OP2	87:L5:5287:SPD:N10	2.38	0.56
2:L5:705:G:OP1	34:Le:5:ARG:NH2	2.39	0.56
2:L5:1332:C:H2'	2:L5:1333:A:C8	2.40	0.56
2:L5:1646:A:O2'	39:Lj:49:TRP:O	2.22	0.56
2:L5:1867:A:H2'	2:L5:1868:A:C8	2.40	0.56
2:L5:3615:G:H1'	26:LW:44:ARG:HD3	1.87	0.56
2:L5:4238:G:H2'	2:L5:4239:A:H8	1.69	0.56
2:L5:4954:G:H2'	2:L5:4955:A:H8	1.70	0.56
2:L5:5064:G:H21	19:LP:75:GLN:HE22	1.54	0.56
13:LI:54:SER:HB3	13:LI:135:ILE:HD11	1.86	0.56
15:LL:46:ILE:HB	15:LL:49:ARG:HB2	1.87	0.56
53:SP:81:ARG:NH2	53:SP:117:GLY:O	2.38	0.56
59:SZ:65:TYR:HB3	83:Zt:34:U:H5'	1.87	0.56
74:SO:45:THR:HA	74:SO:52:THR:HA	1.86	0.56
78:SY:119:GLY:HA2	82:S2:85:A:H5'	1.87	0.56
82:S2:737:G:H8	82:S2:738:C:H4'	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:495:C:H2'	2:L5:496:G:C8	2.41	0.56
2:L5:665:C:H4'	2:L5:666:G:H5'	1.87	0.56
2:L5:1667:G:N1	2:L5:2281:U:OP2	2.29	0.56
2:L5:1759:G:N2	2:L5:1773:U:O2	2.37	0.56
2:L5:4389:C:H2'	2:L5:4390:A:H8	1.69	0.56
2:L5:4667:C:OP1	6:LB:224:LYS:NZ	2.32	0.56
7:LC:110:ARG:O	7:LC:113:ARG:NH1	2.37	0.56
68:SG:162:LEU:HG	68:SG:167:LYS:HE3	1.86	0.56
70:SI:141:ARG:HD3	70:SI:145:ILE:HG21	1.87	0.56
82:S2:28:U:H2'	82:S2:29:G:H8	1.70	0.56
82:S2:907:G:H2'	82:S2:908:A:C8	2.40	0.56
1:Pt:40:C:HO2'	82:S2:1640:A:HO2'	1.47	0.56
2:L5:267:G:H2'	2:L5:268:G:C8	2.40	0.56
2:L5:268:G:H2'	2:L5:269:G:H8	1.69	0.56
2:L5:1655:C:OP2	30:La:26:ARG:NH1	2.38	0.56
2:L5:2846:G:OP1	25:LV:85:ARG:NH2	2.36	0.56
2:L5:2846:G:H2'	2:L5:2847:G:H8	1.70	0.56
2:L5:4315:A:OP1	23:LT:69:GLN:NE2	2.39	0.56
2:L5:4523:A2M:H5''	2:L5:4524:G:H5'	1.86	0.56
82:S2:323:C:H2'	82:S2:327:G:H1	1.70	0.56
82:S2:1174:PSU:H2'	82:S2:1175:G:H8	1.71	0.56
82:S2:1360:U:O2'	82:S2:1379:A:OP2	2.22	0.56
2:L5:153:G:H2'	2:L5:154:G:H8	1.71	0.56
2:L5:419:A:N3	2:L5:1332:C:O2'	2.36	0.56
2:L5:2706:G:C6	84:CI:78:HIS:CD2	2.92	0.56
2:L5:2706:G:O6	84:CI:78:HIS:HD2	1.89	0.56
2:L5:4565:C:OP1	18:LO:65:ASN:ND2	2.34	0.56
58:SU:19:ARG:HH11	58:SU:92:HIS:HB3	1.69	0.56
65:SB:136:ARG:HB2	65:SB:218:LEU:HD11	1.86	0.56
2:L5:2539:C:H2'	2:L5:2540:C:C6	2.41	0.56
2:L5:4657:U:O2'	2:L5:4659:G:OP2	2.24	0.56
4:L8:142:U:OP1	17:LN:38:ARG:NH2	2.39	0.56
6:LB:161:ARG:HG2	6:LB:184:GLN:HA	1.88	0.56
33:Ld:64:ILE:HG23	33:Ld:68:LEU:HD23	1.88	0.56
67:SE:192:ILE:HG12	67:SE:243:GLY:HA3	1.87	0.56
82:S2:223:C:H2'	82:S2:224:A:H8	1.70	0.56
2:L5:1327:C:H2'	2:L5:1328:G:C8	2.41	0.56
10:LF:227:PHE:N	10:LF:233:ALA:O	2.39	0.56
34:Le:108:ARG:HD2	34:Le:128:ARG:HB2	1.86	0.56
82:S2:49:C:OP1	82:S2:471:G:N2	2.39	0.56
1:Pt:33:U:OP2	54:SQ:146:ARG:NH1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L8:96:C:H2'	4:L8:97:A:C8	2.40	0.56
51:SK:55:ARG:NH1	51:SK:78:TYR:OH	2.38	0.56
65:SB:146:ARG:HH21	82:S2:1122:A:H1'	1.70	0.56
67:SE:49:ARG:NH1	82:S2:495:U:OP1	2.39	0.56
72:SL:33:LEU:HD12	72:SL:34:PRO:HD2	1.87	0.56
2:L5:120:A:N1	2:L5:148:C:O2'	2.34	0.56
2:L5:150:U:OP2	11:LG:200:THR:OG1	2.20	0.56
2:L5:4419:U:OP1	2:L5:4475:G:N2	2.39	0.56
2:L5:5030:U:H2'	2:L5:5031:G:H8	1.71	0.56
40:Lk:26:LYS:NZ	40:Lk:28:ASN:OD1	2.38	0.56
56:SS:109:GLU:HA	56:SS:112:GLU:HG2	1.88	0.56
64:SA:37:TYR:OH	75:SV:66:ASP:OD2	2.18	0.56
82:S2:520:A:O2'	82:S2:825:A:N3	2.38	0.56
1:Pt:35:A:OP2	54:SQ:146:ARG:NH2	2.38	0.55
2:L5:462:G:H2'	2:L5:463:A:C8	2.41	0.55
2:L5:968:C:OP2	9:LE:110:ARG:NH2	2.39	0.55
2:L5:2533:C:OP1	27:LX:139:ARG:NH1	2.39	0.55
2:L5:4645:C:OP2	21:LR:62:ARG:NH1	2.40	0.55
2:L5:4870:G:OP2	16:LM:5:ARG:NH1	2.29	0.55
4:L8:62:A:OP1	37:Lh:52:LYS:NZ	2.37	0.55
11:LG:209:SER:HA	11:LG:212:LYS:HG3	1.88	0.55
12:LH:93:ARG:NE	12:LH:142:ASP:O	2.35	0.55
33:Ld:70:LYS:HZ2	84:CI:66:GLY:HA3	1.70	0.55
56:SS:27:ALA:HB2	56:SS:52:LEU:HD12	1.88	0.55
56:SS:48:ALA:O	56:SS:66:ARG:NH2	2.40	0.55
82:S2:472:C:O2	82:S2:475:C:N4	2.39	0.55
82:S2:640:A:H2'	82:S2:641:A:C8	2.41	0.55
2:L5:1514:U:H2'	2:L5:1515:A:C8	2.41	0.55
2:L5:4076:G:OP1	11:LG:73:ARG:NE	2.38	0.55
2:L5:4088:C:H2'	2:L5:4089:G:H8	1.71	0.55
2:L5:4220:6MZ:H8	2:L5:4220:6MZ:OP2	2.06	0.55
4:L8:5:U:H2'	4:L8:6:C:H6	1.71	0.55
33:Ld:70:LYS:HZ1	84:CI:66:GLY:HA3	1.71	0.55
54:SQ:110:ASP:N	54:SQ:110:ASP:OD1	2.33	0.55
67:SE:50:ASN:O	67:SE:53:LYS:NZ	2.33	0.55
2:L5:2576:G:OP1	29:LZ:48:ARG:NH2	2.39	0.55
2:L5:4537:C:H2'	2:L5:4538:G:H8	1.71	0.55
2:L5:4742:G:OP1	2:L5:4900:C:N4	2.36	0.55
82:S2:432:G:H2'	82:S2:433:A:C8	2.41	0.55
2:L5:1982:G:H2'	2:L5:1983:A:O4'	2.07	0.55
2:L5:2624:G:OP2	24:LU:97:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L8:153:C:H2'	4:L8:154:G:H8	1.71	0.55
51:SK:50:GLN:HE22	82:S2:1276:A:H1'	1.71	0.55
69:SH:145:ARG:HE	76:SW:51:GLU:HB2	1.72	0.55
79:Sa:12:LYS:HG3	79:Sa:15:ARG:HB2	1.89	0.55
2:L5:109:G:OP2	15:LL:74:ARG:NH2	2.40	0.55
2:L5:691:C:H2'	2:L5:692:A:C8	2.41	0.55
2:L5:1333:A:H2'	2:L5:1334:A:H8	1.72	0.55
2:L5:2848:G:O2'	2:L5:3838:U:O4	2.23	0.55
8:LD:62:CYS:HB3	8:LD:105:LEU:HD22	1.88	0.55
13:LI:62:SER:HA	13:LI:65:LEU:HD12	1.86	0.55
33:Ld:54:MET:HE3	33:Ld:60:PRO:HA	1.86	0.55
49:SD:8:LYS:HG2	58:SU:61:LEU:HD11	1.87	0.55
50:SF:84:GLY:O	82:S2:1673:U:O2'	2.18	0.55
82:S2:941:C:H2'	82:S2:942:G:C8	2.42	0.55
2:L5:714:G:H2'	2:L5:715:G:H8	1.72	0.55
2:L5:1727:U:OP1	10:LF:131:ASN:ND2	2.39	0.55
2:L5:1983:A:H4'	2:L5:1984:A:C8	2.41	0.55
2:L5:4272:G:OP2	2:L5:4272:G:N2	2.28	0.55
2:L5:4274:A:H2'	2:L5:4275:G:C8	2.42	0.55
3:L7:23:A:N3	3:L7:118:C:O2'	2.32	0.55
47:Ls:174:LEU:O	47:Ls:178:LEU:HB2	2.07	0.55
49:SD:15:GLY:HA3	61:Sd:50:ILE:HG23	1.88	0.55
54:SQ:78:VAL:HG12	82:S2:1673:U:H5''	1.89	0.55
65:SB:150:ILE:HG12	82:S2:1124:C:H5''	1.87	0.55
66:SC:94:ILE:O	66:SC:98:LEU:N	2.37	0.55
66:SC:121:ARG:HH12	66:SC:123:ARG:HE	1.53	0.55
2:L5:1346:C:H2'	2:L5:1347:G:C8	2.41	0.55
2:L5:4139:G:H21	2:L5:4140:C:H41	1.53	0.55
2:L5:4587:G:OP1	18:LO:61:ARG:NH1	2.37	0.55
62:Sf:89:LYS:NZ	62:Sf:90:LYS:O	2.35	0.55
64:SA:77:ILE:HG13	64:SA:99:ILE:HB	1.88	0.55
67:SE:73:ASP:OD2	67:SE:122:LYS:NZ	2.39	0.55
82:S2:639:C:H2'	82:S2:640:A:C8	2.42	0.55
82:S2:1215:C:H42	82:S2:1220:A:H61	1.54	0.55
82:S2:1461:G:H3'	82:S2:1463:U:H3	1.72	0.55
2:L5:678:C:OP1	46:Lr:95:HIS:ND1	2.34	0.55
2:L5:4088:C:OP1	5:LA:37:ARG:NH1	2.39	0.55
4:L8:123:U:H2'	4:L8:126:C:H42	1.72	0.55
8:LD:223:PHE:HB3	8:LD:226:TYR:HB2	1.89	0.55
33:Ld:23:ARG:HG2	33:Ld:121:ASN:HA	1.88	0.55
50:SF:36:GLN:NE2	50:SF:37:ASP:OD1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SZ:42:ASP:OD1	59:SZ:43:LYS:N	2.39	0.55
63:Sg:87:LEU:HB2	63:Sg:101:PHE:HB2	1.88	0.55
78:SY:90:ARG:HA	78:SY:93:ARG:HD2	1.87	0.55
82:S2:1240:A:N3	82:S2:1267:C:O2'	2.33	0.55
2:L5:279:A:OP1	17:LN:50:ARG:NH1	2.40	0.55
2:L5:3944:G:O6	2:L5:4069:U:O4	2.24	0.55
2:L5:4389:C:H2'	2:L5:4390:A:C8	2.42	0.55
2:L5:4473:A:O2'	42:Lm:122:ARG:NH2	2.40	0.55
10:LF:127:LYS:HB2	23:LT:133:ALA:HB3	1.87	0.55
13:LI:152:LEU:HB3	13:LI:165:ILE:HD12	1.88	0.55
26:LW:2:LYS:HE3	26:LW:15:PRO:HB3	1.89	0.55
66:SC:77:SER:OG	66:SC:79:GLU:OE1	2.25	0.55
68:SG:3:LEU:HD23	68:SG:109:LEU:HB3	1.89	0.55
68:SG:59:GLN:OE1	68:SG:72:ARG:NH2	2.40	0.55
70:SI:88:ASN:OD1	70:SI:205:ARG:NH2	2.40	0.55
81:Se:56:ASN:HB3	82:S2:606:G:H5''	1.88	0.55
2:L5:4347:G:H2'	2:L5:4348:A:C8	2.42	0.55
2:L5:4586:G:O6	2:L5:4717:A:N6	2.40	0.55
3:L7:63:C:H5'	3:L7:64:G:H5''	1.89	0.55
4:L8:96:C:H5''	37:Lh:66:LYS:HG2	1.89	0.55
14:LJ:95:ARG:HD3	14:LJ:175:LEU:HB2	1.89	0.55
56:SS:15:VAL:HG12	56:SS:16:LEU:HG	1.89	0.55
63:Sg:260:ASP:O	63:Sg:264:LYS:N	2.39	0.55
82:S2:1275:G:N2	82:S2:1506:A:OP2	2.37	0.55
2:L5:137:G:H2'	2:L5:138:G:C8	2.42	0.54
2:L5:148:C:OP2	11:LG:197:LYS:NZ	2.31	0.54
2:L5:2017:A:O2'	2:L5:2018:C:H6	1.90	0.54
2:L5:3893:C:H2'	2:L5:3894:A:H8	1.73	0.54
8:LD:37:VAL:HG12	8:LD:50:ARG:HD3	1.89	0.54
23:LT:119:ALA:HA	23:LT:122:LYS:HE3	1.88	0.54
70:SI:84:ASN:HD22	70:SI:100:CYS:HB3	1.72	0.54
82:S2:1337:4AC:H2'	82:S2:1338:G:C8	2.42	0.54
82:S2:1348:G:H2'	82:S2:1349:G:H8	1.72	0.54
2:L5:2407:G:N2	2:L5:2407:G:OP2	2.40	0.54
2:L5:3599:A:H2'	2:L5:3600:G:C8	2.41	0.54
5:LA:80:GLU:HB2	5:LA:170:ALA:HA	1.88	0.54
9:LE:165:LEU:HD11	9:LE:176:THR:HG22	1.89	0.54
22:LS:83:ARG:HG3	22:LS:125:GLN:HB2	1.89	0.54
54:SQ:141:TYR:OH	82:S2:1668:U:OP2	2.25	0.54
82:S2:602:G:H3'	82:S2:603:C:H2'	1.89	0.54
2:L5:135:G:H22	37:Lh:94:ARG:HG2	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:172:C:H4'	2:L5:173:C:H5'	1.88	0.54
2:L5:429:A:H2'	2:L5:430:G:H8	1.71	0.54
2:L5:469:C:O2	9:LE:105:ARG:NE	2.36	0.54
2:L5:1683:PSU:OP1	30:La:44:ASN:ND2	2.39	0.54
42:Lm:79:GLU:OE2	42:Lm:81:SER:OG	2.20	0.54
70:SI:81:VAL:HG22	70:SI:102:VAL:HG12	1.90	0.54
70:SI:98:LYS:HG3	70:SI:178:ARG:HG2	1.89	0.54
70:SI:106:SER:HB3	70:SI:171:LEU:HG	1.89	0.54
1:Pt:38:C:O2'	82:S2:1058:A:OP1	2.22	0.54
2:L5:444:G:H2'	2:L5:445:U:H6	1.71	0.54
2:L5:1091:C:H2'	2:L5:1092:G:H8	1.72	0.54
2:L5:1327:C:H2'	2:L5:1328:G:H8	1.72	0.54
2:L5:1334:A:H2'	2:L5:1335:G:H8	1.72	0.54
2:L5:2486:G:O6	2:L5:2493:G:O6	2.25	0.54
2:L5:4736:C:H2'	2:L5:4737:G:H8	1.72	0.54
6:LB:29:VAL:HG12	6:LB:31:SER:H	1.73	0.54
8:LD:64:ILE:HD13	8:LD:109:LEU:HD22	1.88	0.54
54:SQ:42:ILE:HG23	54:SQ:44:PRO:HD2	1.89	0.54
82:S2:695:C:N4	82:S2:736:C:O2'	2.40	0.54
82:S2:980:A:H2'	82:S2:981:A:C8	2.42	0.54
82:S2:1217:A:H2'	82:S2:1218:C:C6	2.43	0.54
2:L5:438:G:OP1	34:Le:16:ARG:NH1	2.36	0.54
2:L5:1795:A:N3	3:L7:79:U:O2'	2.41	0.54
2:L5:2647:A:H3'	2:L5:2648:G:H8	1.72	0.54
2:L5:4723:A:O2'	6:LB:101:THR:O	2.25	0.54
11:LG:83:PHE:HA	11:LG:183:ILE:HD13	1.88	0.54
14:LJ:22:LEU:HD22	14:LJ:128:LEU:HD12	1.89	0.54
67:SE:44:LEU:HD23	67:SE:82:TYR:HB3	1.90	0.54
82:S2:323:C:H2'	82:S2:327:G:H22	1.72	0.54
82:S2:1417:C:O2	82:S2:1422:G:O6	2.26	0.54
82:S2:1719:A:N6	82:S2:1814:G:O2'	2.40	0.54
2:L5:429:A:H2'	2:L5:430:G:C8	2.43	0.54
2:L5:667:A:H5''	2:L5:668:C:H5''	1.89	0.54
2:L5:1872:G:O2'	2:L5:4219:A:N3	2.36	0.54
2:L5:3664:G:H2'	2:L5:3665:G:H8	1.73	0.54
2:L5:4594:U:H2'	2:L5:4595:G:C8	2.43	0.54
4:L8:43:A:H2'	4:L8:44:A:H8	1.72	0.54
16:LM:100:ARG:HA	16:LM:103:LYS:HG2	1.89	0.54
58:SU:80:PHE:HB3	61:Sd:52:PHE:HB3	1.88	0.54
63:Sg:22:ALA:HB1	63:Sg:71:ILE:HG23	1.89	0.54
66:SC:72:ASP:OD2	66:SC:272:HIS:NE2	2.32	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SE:80:ILE:HG23	67:SE:81:THR:HG23	1.89	0.54
80:Sb:42:LYS:HE3	80:Sb:58:GLY:H	1.71	0.54
82:S2:420:G:O2'	82:S2:660:C:N3	2.39	0.54
2:L5:262:G:H2'	2:L5:263:G:C8	2.41	0.54
2:L5:1802:A:N3	23:LT:130:ARG:NH2	2.55	0.54
2:L5:2756:G:O6	29:LZ:51:ARG:NH2	2.38	0.54
4:L8:67:U:H2'	4:L8:68:G:C8	2.42	0.54
28:LY:83:GLU:OE1	28:LY:84:ARG:NH1	2.41	0.54
46:Lr:28:GLU:OE2	46:Lr:31:ASN:ND2	2.38	0.54
65:SB:186:ASN:HA	65:SB:189:ILE:HD12	1.90	0.54
77:SX:28:LYS:HE2	77:SX:32:LEU:HD22	1.90	0.54
82:S2:1845:A:H2'	82:S2:1846:G:C8	2.43	0.54
2:L5:426:A:H2'	2:L5:427:A:H8	1.73	0.54
2:L5:502:C:H3'	2:L5:503:C:H3'	1.90	0.54
2:L5:748:G:O6	22:LS:98:ARG:NH2	2.41	0.54
2:L5:2406:G:O6	2:L5:2785:C:N4	2.41	0.54
2:L5:2777:G:H5''	2:L5:2778:G:H5'	1.89	0.54
3:L7:6:C:O2'	8:LD:50:ARG:NH2	2.40	0.54
3:L7:119:U:C2	8:LD:261:VAL:HG11	2.42	0.54
8:LD:122:GLN:O	8:LD:248:ARG:NH2	2.41	0.54
26:LW:105:ARG:NH2	68:SG:149:LYS:O	2.40	0.54
50:SF:100:ILE:HD11	50:SF:108:PRO:HB3	1.90	0.54
55:SR:60:ARG:HA	55:SR:63:ARG:HG2	1.90	0.54
63:Sg:32:LEU:HA	63:Sg:42:MET:HA	1.90	0.54
63:Sg:254:PRO:O	63:Sg:272:GLN:NE2	2.41	0.54
79:Sa:23:CYS:HB3	79:Sa:28:ARG:H	1.72	0.54
83:Zt:64:U:H2'	83:Zt:65:G:H8	1.72	0.54
2:L5:515:C:H41	2:L5:647:G:H21	1.53	0.54
2:L5:2318:G:N2	2:L5:2321:G:OP2	2.29	0.54
2:L5:2495:U:H2'	2:L5:2496:G:C8	2.40	0.54
2:L5:4174:U:H2'	2:L5:4175:G:H8	1.73	0.54
4:L8:47:C:H1'	4:L8:61:A:H2'	1.90	0.54
5:LA:20:VAL:HA	5:LA:23:ARG:HG3	1.89	0.54
6:LB:258:HIS:HA	6:LB:260:ALA:H	1.73	0.54
11:LG:167:VAL:HG12	11:LG:170:LEU:HD12	1.90	0.54
57:ST:56:ARG:NE	82:S2:1541:G:OP1	2.34	0.54
82:S2:1259:A:H62	82:S2:1518:C:H3'	1.73	0.54
2:L5:1890:G:OP2	2:L5:1890:G:N2	2.32	0.54
2:L5:2572:C:O2'	29:LZ:112:ARG:NH2	2.40	0.54
2:L5:4954:G:H2'	2:L5:4955:A:C8	2.43	0.54
6:LB:222:VAL:O	6:LB:343:ARG:NH1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SH:100:ILE:HG21	69:SH:122:LEU:HD12	1.90	0.54
82:S2:1244:PSU:H2'	82:S2:1245:G:H8	1.73	0.54
82:S2:1568:C:H2'	82:S2:1569:A:C8	2.43	0.54
83:Zt:15:G:N2	83:Zt:48:C:H42	2.06	0.54
2:L5:2275:G:H2'	2:L5:2276:A:C8	2.43	0.53
2:L5:2640:G:H2'	2:L5:2641:A:C8	2.43	0.53
2:L5:4238:G:H2'	2:L5:4239:A:C8	2.43	0.53
2:L5:4420:U:H5''	2:L5:4421:C:H5	1.72	0.53
2:L5:4604:G:N2	2:L5:4607:A:OP2	2.36	0.53
3:L7:99:G:OP2	22:LS:55:LYS:NZ	2.31	0.53
28:LY:67:ILE:O	28:LY:84:ARG:NH2	2.38	0.53
56:SS:60:THR:OG1	56:SS:62:ASP:OD1	2.22	0.53
73:SN:15:ALA:HB2	80:Sb:20:LYS:HD3	1.89	0.53
78:SY:11:LYS:NZ	82:S2:832:G:O6	2.41	0.53
79:Sa:5:ARG:HH21	82:S2:1864:U:H3'	1.72	0.53
83:Zt:16:C:H1'	83:Zt:18:U:H5''	1.90	0.53
2:L5:85:G:O2'	2:L5:97:G:O6	2.22	0.53
2:L5:1281:G:H5'	7:LC:323:ARG:HB2	1.90	0.53
2:L5:2460:A:OP2	87:LN:301:SPD:N10	2.42	0.53
8:LD:211:LEU:HB3	8:LD:219:TYR:HB2	1.90	0.53
50:SF:124:ASP:O	50:SF:139:VAL:N	2.38	0.53
66:SC:65:LYS:HD2	66:SC:273:LEU:HD13	1.89	0.53
71:SJ:149:VAL:HG11	71:SJ:157:ILE:HD11	1.90	0.53
74:SO:113:GLN:OE1	79:Sa:46:GLU:N	2.41	0.53
78:SY:41:ARG:NH2	78:SY:52:PRO:O	2.41	0.53
82:S2:1726:G:H1	82:S2:1808:U:H3	1.55	0.53
82:S2:1845:A:H2'	82:S2:1846:G:H8	1.72	0.53
2:L5:1511:U:H2'	2:L5:1512:G:H8	1.73	0.53
2:L5:3610:A:H2'	2:L5:3611:A:H8	1.72	0.53
2:L5:3796:U:O2'	82:S2:1720:U:O2'	2.21	0.53
30:La:36:GLY:HA3	30:La:40:HIS:CE1	2.43	0.53
63:Sg:18:VAL:O	63:Sg:287:THR:OG1	2.25	0.53
63:Sg:89:LEU:HB3	63:Sg:99:ARG:HB3	1.90	0.53
82:S2:888:U:H4'	82:S2:889:U:H5'	1.89	0.53
2:L5:287:U:H2'	2:L5:288:G:C8	2.44	0.53
2:L5:2475:G:N1	27:LX:51:THR:O	2.28	0.53
2:L5:3774:A:H2'	2:L5:3775:A:C8	2.43	0.53
2:L5:4107:G:N2	2:L5:4108:G:O6	2.41	0.53
2:L5:4716:C:H2'	2:L5:4717:A:H8	1.72	0.53
2:L5:4997:G:H1	2:L5:5053:U:H3	1.57	0.53
16:LM:119:ARG:HG3	18:LO:189:ILE:HG23	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LP:64:ASN:ND2	19:LP:80:GLN:OE1	2.39	0.53
20:LQ:151:HIS:ND1	20:LQ:164:LYS:O	2.38	0.53
29:LZ:9:LYS:NZ	29:LZ:83:THR:O	2.34	0.53
64:SA:102:ARG:HH12	82:S2:1377:U:H3'	1.73	0.53
82:S2:454:U:H2'	82:S2:455:A:C8	2.42	0.53
82:S2:1656:G:O6	82:S2:1668:U:O4	2.27	0.53
82:S2:1744:G:O2'	82:S2:1789:G:N2	2.29	0.53
2:L5:2519:U:O2'	2:L5:2530:U:O2	2.21	0.53
2:L5:3870:C:H2'	2:L5:3871:A:C8	2.43	0.53
2:L5:3873:G:H2'	2:L5:3874:G:C8	2.43	0.53
2:L5:4897:G:H2'	2:L5:4898:G:H8	1.74	0.53
3:L7:64:G:H2'	3:L7:65:G:C8	2.44	0.53
5:LA:79:ALA:HA	5:LA:169:VAL:HA	1.89	0.53
18:LO:186:GLU:OE1	18:LO:186:GLU:N	2.41	0.53
50:SF:59:LYS:HB3	50:SF:62:ARG:HG3	1.90	0.53
54:SQ:130:LYS:NZ	54:SQ:131:LYS:O	2.41	0.53
63:Sg:106:LYS:HB3	63:Sg:125:ARG:HB2	1.91	0.53
71:SJ:109:ARG:NH2	71:SJ:111:GLN:OE1	2.41	0.53
71:SJ:145:PRO:HD2	82:S2:522:A:H5''	1.90	0.53
82:S2:1172:U:H2'	82:S2:1173:A:H8	1.74	0.53
82:S2:1536:G:H2'	82:S2:1537:A:C8	2.42	0.53
2:L5:1983:A:H4'	2:L5:1984:A:H8	1.74	0.53
2:L5:2295:C:H2'	2:L5:2296:G:C8	2.42	0.53
2:L5:2884:G:H2'	2:L5:2885:A:H8	1.73	0.53
2:L5:4520:G:N2	6:LB:253:CYS:SG	2.82	0.53
3:L7:28:C:H1'	3:L7:54:A:H61	1.74	0.53
3:L7:64:G:H2'	3:L7:65:G:H8	1.73	0.53
6:LB:217:ILE:HD12	6:LB:347:LEU:HB3	1.91	0.53
23:LT:43:LYS:O	23:LT:58:HIS:ND1	2.42	0.53
25:LV:21:PRO:HA	25:LV:54:ALA:HA	1.90	0.53
50:SF:127:ARG:H	50:SF:135:ARG:HD2	1.73	0.53
64:SA:118:GLU:HG3	66:SC:65:LYS:HE2	1.90	0.53
69:SH:165:ASN:O	69:SH:169:LYS:NZ	2.37	0.53
1:Pt:50:U:O2	1:Pt:64:G:N2	2.23	0.53
2:L5:959:G:O2'	2:L5:2263:A:N6	2.41	0.53
17:LN:70:GLY:O	87:LN:301:SPD:N6	2.41	0.53
51:SK:31:LYS:NZ	51:SK:40:VAL:H	2.05	0.53
54:SQ:67:ASP:OD2	54:SQ:69:ARG:NH1	2.42	0.53
69:SH:31:GLU:HA	69:SH:37:LYS:HG3	1.91	0.53
76:SW:6:VAL:HG13	76:SW:29:PRO:HB2	1.90	0.53
82:S2:291:G:H2'	82:S2:292:A:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1115:U:O2'	82:S2:1117:C:OP2	2.27	0.53
2:L5:293:G:OP1	86:L5:5265:SPM:N1	2.38	0.53
2:L5:1241:C:H1'	31:Lb:119:CYS:HA	1.90	0.53
2:L5:1820:C:H2'	2:L5:1822:U:H5'	1.90	0.53
2:L5:2296:G:O2'	7:LC:242:PRO:O	2.23	0.53
5:LA:229:ALA:HB3	5:LA:234:LYS:HB3	1.91	0.53
9:LE:190:HIS:HB3	9:LE:193:PHE:HD2	1.73	0.53
27:LX:121:VAL:HA	27:LX:140:LEU:HA	1.91	0.53
50:SF:78:MET:HE3	82:S2:1222:G:H5''	1.89	0.53
52:SM:91:LEU:HD12	52:SM:106:CYS:HB2	1.91	0.53
56:SS:88:LYS:H	56:SS:95:TYR:HD1	1.57	0.53
63:Sg:164:ILE:HG22	63:Sg:178:ASN:HA	1.91	0.53
74:SO:38:ASN:ND2	82:S2:960:U:OP2	2.39	0.53
77:SX:68:LYS:HB3	77:SX:91:LEU:HD13	1.90	0.53
82:S2:329:G:H2'	82:S2:330:G:C8	2.44	0.53
2:L5:370:U:HO2'	39:Lj:16:HIS:HD1	1.57	0.53
2:L5:4373:G:N7	44:Lo:61:LYS:NZ	2.48	0.53
2:L5:4730:C:H2'	2:L5:4731:G:C8	2.44	0.53
6:LB:219:VAL:HG11	6:LB:337:VAL:HG13	1.89	0.53
46:Lr:26:SER:OG	46:Lr:28:GLU:OE1	2.21	0.53
68:SG:133:LEU:HB2	82:S2:65:C:C2	2.43	0.53
82:S2:525:A:H2'	82:S2:526:A:H8	1.72	0.53
82:S2:979:C:H2'	82:S2:980:A:H8	1.74	0.53
2:L5:121:A:H62	2:L5:152:U:H3	1.57	0.53
2:L5:1243:C:H2'	2:L5:1244:G:H8	1.74	0.53
2:L5:1366:G:H5''	15:LL:36:ARG:HH12	1.73	0.53
2:L5:3807:A:HO2'	82:S2:1816:G:HO2'	1.57	0.53
2:L5:4906:C:H2'	2:L5:4907:G:H8	1.74	0.53
2:L5:5057:C:H2'	2:L5:5058:A:C8	2.44	0.53
12:LH:89:ARG:HD3	12:LH:91:LYS:HE3	1.91	0.53
34:Le:101:HIS:O	34:Le:128:ARG:NH2	2.42	0.53
47:Ls:143:ILE:HD12	47:Ls:158:VAL:HG11	1.90	0.53
53:SP:81:ARG:NH1	53:SP:120:SER:OG	2.41	0.53
64:SA:198:MET:HG2	64:SA:200:ASP:H	1.74	0.53
68:SG:20:ASP:HB3	68:SG:23:LYS:HB2	1.89	0.53
68:SG:23:LYS:HE3	68:SG:41:LEU:HA	1.90	0.53
80:Sb:68:GLY:O	82:S2:928:G:N2	2.37	0.53
82:S2:527:C:H2'	82:S2:528:A:C8	2.43	0.53
2:L5:1207:C:H2'	2:L5:1208:G:H8	1.73	0.52
4:L8:130:C:H2'	4:L8:131:G:H8	1.73	0.52
20:LQ:155:ALA:O	20:LQ:158:THR:OG1	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SM:83:LYS:NZ	52:SM:103:VAL:O	2.42	0.52
67:SE:108:ARG:NH1	82:S2:847:A:OP1	2.42	0.52
68:SG:22:ARG:HG3	68:SG:25:ARG:HH12	1.74	0.52
78:SY:119:GLY:O	82:S2:84:A:O2'	2.25	0.52
82:S2:996:A:H2'	82:S2:997:A:C8	2.44	0.52
2:L5:441:G:H2'	2:L5:442:G:C8	2.44	0.52
2:L5:1351:G:O6	20:LQ:55:ARG:NH1	2.42	0.52
2:L5:1655:C:OP1	2:L5:1679:A:O2'	2.22	0.52
2:L5:1697:G:H22	2:L5:2084:C:P	2.32	0.52
2:L5:1998:A:N6	47:Ls:40:MET:SD	2.82	0.52
2:L5:2101:C:H2'	2:L5:2102:G:C8	2.44	0.52
2:L5:2389:A:H4'	33:Ld:70:LYS:HG3	1.91	0.52
2:L5:3723:A:H2'	2:L5:3724:A:H8	1.74	0.52
13:LI:4:ARG:NH1	13:LI:9:TYR:OH	2.40	0.52
16:LM:104:MET:HG3	16:LM:108:ASP:HB2	1.91	0.52
56:SS:12:ILE:HG22	56:SS:21:ASP:HA	1.91	0.52
66:SC:78:LEU:HD12	66:SC:81:ILE:HD12	1.91	0.52
77:SX:20:GLN:OE1	82:S2:1165:G:N1	2.40	0.52
78:SY:41:ARG:HA	78:SY:55:ILE:HG21	1.91	0.52
2:L5:280:G:OP2	17:LN:44:ARG:NH1	2.41	0.52
2:L5:1197:C:H2'	2:L5:1198:G:H8	1.74	0.52
3:L7:49:A:H5''	8:LD:224:SER:HB2	1.90	0.52
15:LL:111:GLN:O	15:LL:115:GLN:HG2	2.09	0.52
56:SS:121:ARG:HG3	56:SS:131:VAL:HB	1.90	0.52
68:SG:170:ARG:NH1	82:S2:72:C:O2	2.42	0.52
69:SH:164:ASN:OD1	69:SH:165:ASN:ND2	2.43	0.52
82:S2:98:C:OP2	82:S2:426:A:O2'	2.24	0.52
2:L5:1826:G:H4'	31:Lb:43:MET:HE3	1.92	0.52
2:L5:4088:C:H2'	2:L5:4089:G:C8	2.44	0.52
2:L5:4281:A:H2'	2:L5:4282:A:H2'	1.91	0.52
2:L5:4584:A:H2'	2:L5:4585:U:O4'	2.09	0.52
15:LL:59:VAL:HG21	15:LL:73:GLY:HA3	1.91	0.52
43:Ln:11:ARG:NH2	82:S2:1844:U:OP1	2.42	0.52
46:Lr:32:LEU:HD21	46:Lr:50:GLY:HA2	1.90	0.52
60:Sc:24:GLN:NE2	82:S2:1218:C:O2'	2.42	0.52
75:SV:17:CYS:HB3	75:SV:22:ARG:H	1.73	0.52
77:SX:28:LYS:NZ	82:S2:1189:A:OP1	2.36	0.52
82:S2:1754:G:N7	82:S2:1779:G:N2	2.57	0.52
2:L5:32:G:H21	2:L5:50:C:H5	1.56	0.52
2:L5:38:A:H61	2:L5:41:C:H3'	1.75	0.52
2:L5:1984:A:N6	2:L5:2010:A:O2'	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2079:G:H2'	2:L5:2080:U:C6	2.45	0.52
2:L5:2620:G:H1	2:L5:2636:U:H3	1.57	0.52
2:L5:4353:PSU:H5'	2:L5:4354:U:H5'	1.89	0.52
2:L5:4622:A:H2'	2:L5:4623:OMG:C8	2.45	0.52
2:L5:4966:A:H5''	6:LB:128:LYS:HG3	1.91	0.52
67:SE:134:LYS:N	82:S2:298:G:OP1	2.38	0.52
68:SG:7:PHE:HD1	68:SG:113:ILE:HB	1.72	0.52
82:S2:1588:A:H2'	82:S2:1589:A:C8	2.44	0.52
2:L5:64:A:H1'	2:L5:76:A:H1'	1.90	0.52
2:L5:447:C:H2'	2:L5:448:G:H8	1.73	0.52
2:L5:2080:U:H2'	2:L5:2081:C:C6	2.44	0.52
2:L5:3816:A:OP1	2:L5:3818:UY1:N1	2.43	0.52
2:L5:3893:C:H2'	2:L5:3894:A:C8	2.45	0.52
36:Lg:41:ALA:O	36:Lg:52:ARG:NH1	2.37	0.52
67:SE:125:LYS:O	67:SE:142:HIS:N	2.43	0.52
75:SV:15:ARG:NH1	75:SV:33:GLN:OE1	2.43	0.52
78:SY:41:ARG:HH21	78:SY:53:ASP:HA	1.74	0.52
82:S2:329:G:H2'	82:S2:330:G:H8	1.75	0.52
82:S2:1208:A:H2'	82:S2:1209:A:H8	1.75	0.52
2:L5:86:U:H2'	2:L5:87:A:H8	1.74	0.52
2:L5:1258:G:H2'	2:L5:1259:G:C8	2.44	0.52
2:L5:3933:G:H2'	2:L5:3934:G:H8	1.74	0.52
2:L5:4327:C:OP1	23:LT:70:HIS:NE2	2.43	0.52
2:L5:4872:G:OP2	16:LM:94:LYS:NZ	2.40	0.52
6:LB:206:PRO:HG2	6:LB:209:GLN:HG3	1.91	0.52
32:Lc:38:ILE:HD11	32:Lc:46:VAL:HG21	1.90	0.52
49:SD:45:ARG:NH1	49:SD:85:GLU:OE1	2.42	0.52
51:SK:51:SER:OG	82:S2:1277:C:OP1	2.28	0.52
65:SB:99:ASN:OD1	65:SB:100:PHE:N	2.39	0.52
69:SH:58:LYS:HB2	69:SH:90:LYS:HG2	1.90	0.52
71:SJ:45:ARG:NH2	82:S2:522:A:OP2	2.39	0.52
82:S2:601:OMG:H2'	82:S2:602:G:C8	2.45	0.52
1:Pt:43:A:H2'	1:Pt:44:A:C8	2.45	0.52
2:L5:418:A:H4'	2:L5:2311:C:H5'	1.92	0.52
2:L5:1876:U:H2'	2:L5:1877:G:C8	2.45	0.52
2:L5:1895:G:OP1	10:LF:96:ARG:NH2	2.41	0.52
2:L5:2375:A:H2'	2:L5:2376:A:H8	1.73	0.52
2:L5:4981:G:H3'	2:L5:4982:A:H8	1.75	0.52
9:LE:223:ARG:NH2	9:LE:236:GLU:O	2.43	0.52
39:Lj:2:THR:O	39:Lj:7:SER:OG	2.25	0.52
49:SD:23:GLU:OE2	49:SD:27:ARG:NE	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:Sd:7:TYR:OH	82:S2:1274:G:N7	2.32	0.52
77:SX:54:LYS:NZ	77:SX:94:ILE:O	2.41	0.52
82:S2:516:A:N1	82:S2:643:A:O2'	2.38	0.52
82:S2:929:G:H2'	82:S2:930:C:O4'	2.09	0.52
2:L5:1194:G:H2'	2:L5:1195:G:H8	1.73	0.52
2:L5:1411:C:H2'	2:L5:1412:G:C8	2.44	0.52
2:L5:1618:G:OP1	39:Lj:13:ASN:ND2	2.35	0.52
2:L5:3722:G:H2'	2:L5:3723:A:H8	1.74	0.52
4:L8:60:G:O6	4:L8:96:C:O2'	2.27	0.52
6:LB:29:VAL:HA	6:LB:220:ILE:HD13	1.92	0.52
21:LR:21:LYS:HE3	21:LR:55:VAL:HA	1.92	0.52
29:LZ:100:VAL:HG23	29:LZ:106:LEU:HB3	1.92	0.52
47:Ls:114:GLY:HA2	47:Ls:166:LYS:HD2	1.92	0.52
70:SI:25:ARG:HA	82:S2:448:A:H5''	1.91	0.52
82:S2:1220:A:N3	82:S2:1677:U:O2'	2.41	0.52
2:L5:418:A:C2	4:L8:17:A:H1'	2.45	0.52
2:L5:2274:C:H2'	2:L5:2275:G:C8	2.45	0.52
2:L5:3633:C:H2'	2:L5:3634:G:C8	2.44	0.52
2:L5:4188:U:H2'	2:L5:4189:U:C6	2.45	0.52
2:L5:4232:U:H5'	44:Lo:3:ASN:HB3	1.92	0.52
2:L5:4688:C:H2'	2:L5:4689:PSU:C6	2.44	0.52
2:L5:4887:C:N3	2:L5:4932:U:O2	2.43	0.52
3:L7:57:C:H2'	3:L7:58:A:H8	1.75	0.52
7:LC:13:GLU:OE1	7:LC:161:TYR:OH	2.25	0.52
63:Sg:68:ASP:HB3	63:Sg:111:VAL:HG22	1.92	0.52
68:SG:136:LYS:NZ	68:SG:175:LYS:O	2.35	0.52
82:S2:655:A:H4'	82:S2:656:G:H3'	1.92	0.52
82:S2:656:G:N2	82:S2:663:C:H5''	2.24	0.52
82:S2:672:A:N6	82:S2:1027:A:OP1	2.35	0.52
2:L5:1461:C:H2'	2:L5:1462:A:C8	2.46	0.51
2:L5:1787:A:O5'	86:L5:5259:SPM:N14	2.42	0.51
2:L5:1971:C:H2'	2:L5:1972:G:C8	2.45	0.51
2:L5:3723:A:H2'	2:L5:3724:A:C8	2.45	0.51
2:L5:3787:G:N3	2:L5:3789:C:N4	2.58	0.51
2:L5:4064:C:N4	2:L5:4065:G:O6	2.43	0.51
2:L5:4340:U:N3	88:L5:5296:3HE:O1	2.43	0.51
2:L5:4622:A:H2'	2:L5:4623:OMG:H8	1.75	0.51
4:L8:90:C:HO2'	28:LY:24:HIS:HD1	1.58	0.51
82:S2:467:G:H2'	82:S2:468:A2M:H8	1.92	0.51
82:S2:1201:U:H2'	82:S2:1202:U:C6	2.45	0.51
2:L5:2457:G:OP1	17:LN:65:ARG:NH2	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2809:G:O2'	2:L5:4644:G:OP1	2.28	0.51
2:L5:3805:U:H2'	2:L5:3806:G:H8	1.75	0.51
2:L5:4321:U:H2'	2:L5:4322:G:C8	2.45	0.51
2:L5:4759:C:H2'	2:L5:4760:G:C8	2.45	0.51
3:L7:34:C:N3	3:L7:46:C:O2'	2.40	0.51
6:LB:107:ALA:HB2	6:LB:201:LEU:HD22	1.92	0.51
8:LD:146:LEU:HB2	8:LD:163:LEU:HD12	1.93	0.51
11:LG:157:ILE:HA	11:LG:201:THR:HG22	1.92	0.51
82:S2:1206:G:O2'	82:S2:1208:A:OP1	2.23	0.51
2:L5:161:G:H2'	2:L5:162:A:H8	1.76	0.51
2:L5:1095:A:C2	2:L5:1200:G:N1	2.68	0.51
2:L5:1390:G:N2	2:L5:1393:G:OP2	2.33	0.51
2:L5:1824:G:H2'	2:L5:1825:A:C8	2.45	0.51
2:L5:3819:G:H2'	2:L5:3820:G:H8	1.75	0.51
26:LW:7:SER:OG	26:LW:8:PHE:N	2.43	0.51
82:S2:603:C:N4	82:S2:620:G:O6	2.43	0.51
2:L5:93:G:H2'	2:L5:94:A:C8	2.46	0.51
2:L5:752:G:O6	2:L5:912:G:N2	2.43	0.51
2:L5:1172:C:HO2'	2:L5:1173:G:H8	1.58	0.51
2:L5:3661:G:N7	5:LA:152:SER:OG	2.36	0.51
49:SD:66:ILE:HD11	49:SD:86:LEU:HB3	1.92	0.51
69:SH:20:GLU:HG2	69:SH:48:ALA:HB3	1.92	0.51
70:SI:3:ILE:O	70:SI:30:GLY:N	2.41	0.51
1:Pt:33:U:N3	1:Pt:36:C:OP2	2.43	0.51
2:L5:1253:G:O2'	2:L5:1257:A:N7	2.43	0.51
2:L5:1345:A:H2'	2:L5:1346:C:C6	2.46	0.51
2:L5:1787:A:N3	2:L5:4210:U:O2'	2.43	0.51
2:L5:1825:A:H2'	2:L5:1826:G:C8	2.46	0.51
2:L5:2706:G:C6	84:CI:78:HIS:HD2	2.28	0.51
15:LL:206:ASP:HA	15:LL:209:LYS:HD3	1.93	0.51
64:SA:111:GLN:HA	64:SA:116:PHE:CG	2.45	0.51
65:SB:98:THR:O	65:SB:232:HIS:NE2	2.44	0.51
78:SY:80:ASP:OD1	78:SY:81:TYR:N	2.43	0.51
82:S2:1777:G:H2'	82:S2:1778:C:H6	1.75	0.51
2:L5:444:G:OP2	35:Lf:55:ASN:ND2	2.40	0.51
2:L5:942:G:H3'	10:LF:148:LYS:HD2	1.93	0.51
2:L5:3718:A2M:H2'	2:L5:3719:A:O4'	2.10	0.51
2:L5:3848:U:H2'	2:L5:3849:A:C8	2.45	0.51
8:LD:181:PRO:HD2	8:LD:195:HIS:CD2	2.46	0.51
21:LR:160:GLU:OE1	21:LR:163:ARG:NH2	2.41	0.51
23:LT:119:ALA:O	23:LT:123:GLY:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Ls:110:ALA:HA	47:Ls:182:PRO:HG2	1.92	0.51
48:Lt:76:SER:OG	48:Lt:116:MET:SD	2.64	0.51
54:SQ:3:SER:OG	54:SQ:4:LYS:N	2.44	0.51
63:Sg:175:LYS:HB3	63:Sg:184:LEU:HD11	1.92	0.51
63:Sg:191:HIS:CG	63:Sg:195:LEU:HD21	2.46	0.51
68:SG:92:ARG:NH1	82:S2:1738:C:OP1	2.37	0.51
68:SG:135:PRO:HG3	68:SG:144:LEU:HD13	1.93	0.51
82:S2:1277:C:H2'	82:S2:1278:A:C8	2.44	0.51
82:S2:1657:G:H1	82:S2:1667:U:H3	1.57	0.51
2:L5:359:A:N3	2:L5:363:A:O2'	2.42	0.51
2:L5:4459:U:H2'	2:L5:4460:U:C6	2.45	0.51
2:L5:4504:C:H2'	2:L5:4505:C:H6	1.75	0.51
2:L5:5055:G:N2	33:Ld:118:GLN:OE1	2.38	0.51
11:LG:30:PRO:HG2	29:LZ:124:THR:HA	1.93	0.51
46:Lr:54:ALA:HA	46:Lr:61:VAL:HG23	1.92	0.51
49:SD:42:THR:OG1	49:SD:45:ARG:O	2.26	0.51
2:L5:1283:G:N1	2:L5:2076:G:OP1	2.24	0.51
2:L5:1328:G:O2'	2:L5:2349:A:OP1	2.29	0.51
2:L5:2751:G:H2'	2:L5:2752:G:H8	1.75	0.51
2:L5:2910:G:N2	2:L5:3585:G:O2'	2.44	0.51
5:LA:184:ARG:NH2	45:Lp:14:TYR:OH	2.40	0.51
14:LJ:83:LEU:HD22	14:LJ:132:VAL:HG11	1.93	0.51
62:Sf:103:LEU:HB2	62:Sf:105:TYR:CE2	2.45	0.51
66:SC:108:LYS:HD2	66:SC:233:LEU:HD13	1.93	0.51
69:SH:111:LYS:HE3	82:S2:796:G:H21	1.74	0.51
82:S2:1304:U:H2'	82:S2:1305:C:C6	2.46	0.51
82:S2:1808:U:H2'	82:S2:1809:A:C8	2.46	0.51
2:L5:1503:A:H4'	2:L5:1504:G:H5'	1.93	0.51
2:L5:1631:A:H2	5:LA:208:GLU:HG3	1.75	0.51
2:L5:1992:U:H4'	2:L5:1993:C:H5''	1.93	0.51
2:L5:2007:G:H21	2:L5:2012:A:N6	2.04	0.51
2:L5:2671:C:H2'	2:L5:2672:C:C6	2.45	0.51
2:L5:4111:U:H2'	2:L5:4112:C:H5	1.75	0.51
4:L8:148:A:H2'	4:L8:149:G:C8	2.46	0.51
29:LZ:11:VAL:HG12	29:LZ:82:PRO:HA	1.93	0.51
37:Lh:88:THR:HB	37:Lh:91:MET:HB2	1.93	0.51
52:SM:86:GLY:HA2	52:SM:89:VAL:HG12	1.93	0.51
68:SG:50:VAL:HA	68:SG:113:ILE:HA	1.92	0.51
70:SI:114:GLU:HB3	70:SI:136:ILE:HD12	1.93	0.51
73:SN:66:VAL:HG13	73:SN:67:THR:HG23	1.92	0.51
82:S2:528:A:H2'	82:S2:529:A:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1511:U:H2'	2:L5:1512:G:C8	2.46	0.51
2:L5:1733:G:N3	2:L5:4214:A:H2'	2.26	0.51
2:L5:2588:C:OP1	2:L5:2768:C:O2'	2.27	0.51
2:L5:3610:A:H2'	2:L5:3611:A:C8	2.46	0.51
2:L5:4089:G:H2'	2:L5:4090:G:H8	1.75	0.51
2:L5:4695:C:O2	42:Lm:106:ARG:NH2	2.43	0.51
2:L5:4997:G:H2'	2:L5:4998:G:H8	1.76	0.51
8:LD:67:ALA:HB1	23:LT:31:MET:HE2	1.92	0.51
12:LH:1:MET:HE1	22:LS:140:PRO:HB2	1.92	0.51
47:Ls:13:TYR:O	47:Ls:17:ILE:HG12	2.11	0.51
82:S2:109:PSU:H2'	82:S2:110:U:C6	2.46	0.51
82:S2:543:C:H3'	82:S2:544:G:H8	1.76	0.51
2:L5:256:G:H2'	2:L5:257:C:C6	2.46	0.50
2:L5:426:A:H2'	2:L5:427:A:C8	2.46	0.50
2:L5:659:G:H2'	2:L5:660:A:H8	1.75	0.50
2:L5:2272:C:H2'	2:L5:2273:G:H8	1.76	0.50
2:L5:2503:G:O6	5:LA:72:ARG:NH1	2.38	0.50
2:L5:3848:U:H2'	2:L5:3849:A:H8	1.76	0.50
2:L5:4095:G:H22	2:L5:4099:G:H22	1.58	0.50
2:L5:4156:G:H5''	2:L5:4157:A:H2'	1.93	0.50
4:L8:8:U:H2'	4:L8:9:A:C8	2.45	0.50
6:LB:299:ILE:HB	6:LB:313:SER:HB3	1.92	0.50
19:LP:94:MET:HE1	19:LP:146:ILE:HB	1.93	0.50
20:LQ:67:ILE:HD11	20:LQ:95:VAL:HG13	1.93	0.50
26:LW:56:ARG:HE	26:LW:61:LYS:HB2	1.77	0.50
63:Sg:205:SER:HA	63:Sg:221:LEU:HB2	1.93	0.50
77:SX:52:LEU:HD11	77:SX:73:GLN:HB2	1.92	0.50
78:SY:10:ARG:HA	82:S2:839:C:H41	1.76	0.50
82:S2:432:G:H2'	82:S2:433:A:H8	1.76	0.50
82:S2:1831:A:O2'	82:S2:1832:6MZ:O5'	2.23	0.50
1:Pt:47:U:O2'	1:Pt:50:U:OP1	2.27	0.50
2:L5:7:C:H2'	2:L5:8:U:C6	2.47	0.50
2:L5:268:G:H2'	2:L5:269:G:C8	2.46	0.50
2:L5:2764:A:H2'	2:L5:2765:A:C8	2.45	0.50
2:L5:3809:G:OP2	2:L5:3809:G:N2	2.33	0.50
2:L5:4612:C:C2	12:LH:120:GLU:HB2	2.46	0.50
5:LA:206:PRO:HG3	5:LA:213:GLY:HA3	1.93	0.50
7:LC:262:GLU:HB3	7:LC:273:LEU:HD13	1.93	0.50
8:LD:120:GLU:O	8:LD:248:ARG:NH1	2.44	0.50
49:SD:32:ASP:OD1	49:SD:57:ASN:ND2	2.44	0.50
49:SD:175:VAL:HB	49:SD:182:LEU:HB3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SB:171:ILE:HG22	65:SB:174:ARG:HE	1.77	0.50
68:SG:67:VAL:HG12	68:SG:69:THR:HG22	1.93	0.50
74:SO:147:ARG:HH22	82:S2:1854:U:P	2.34	0.50
77:SX:63:ASN:OD1	82:S2:624:C:N4	2.42	0.50
82:S2:17:C:H2'	82:S2:18:C:C6	2.46	0.50
82:S2:1797:U:H2'	82:S2:1798:C:C6	2.47	0.50
2:L5:65:A:H61	2:L5:75:G:H1'	1.76	0.50
2:L5:425:U:H2'	2:L5:426:A:H8	1.76	0.50
2:L5:1197:C:H2'	2:L5:1198:G:C8	2.46	0.50
2:L5:1305:C:OP1	4:L8:7:U:O2'	2.29	0.50
2:L5:2404:A:O2'	39:Lj:12:ARG:O	2.29	0.50
2:L5:3785:A2M:H2	2:L5:4551:U:O2	2.11	0.50
13:LI:87:MET:HG2	13:LI:138:ILE:HG12	1.92	0.50
18:LO:168:TYR:CE2	18:LO:172:LYS:HD2	2.46	0.50
57:ST:84:ARG:NH1	82:S2:1605:G:OP1	2.36	0.50
63:Sg:124:SER:OG	63:Sg:125:ARG:N	2.45	0.50
66:SC:94:ILE:HD11	66:SC:159:LYS:HG2	1.93	0.50
68:SG:136:LYS:O	68:SG:176:ILE:HG13	2.11	0.50
70:SI:130:THR:O	70:SI:134:GLU:HB2	2.12	0.50
82:S2:751:G:H1'	82:S2:793:G:H21	1.75	0.50
82:S2:1203:G:H2'	82:S2:1204:A:C8	2.47	0.50
82:S2:1447:G:H2'	82:S2:1448:A:C8	2.47	0.50
2:L5:1176:C:H42	2:L5:1184:A:H61	1.57	0.50
2:L5:1309:C:H2'	2:L5:1310:C:C6	2.47	0.50
2:L5:1613:A:H5''	5:LA:183:GLY:HA2	1.93	0.50
2:L5:2008:U:N3	2:L5:2011:C:OP2	2.29	0.50
2:L5:3727:A:H2'	2:L5:3728:A:C8	2.46	0.50
2:L5:4092:G:N7	2:L5:4114:C:N4	2.59	0.50
5:LA:13:GLY:O	5:LA:17:ARG:HG3	2.11	0.50
12:LH:115:ARG:HD3	12:LH:123:ILE:HD12	1.94	0.50
38:Li:55:ARG:O	38:Li:59:GLU:HG2	2.11	0.50
57:ST:62:ARG:NH2	82:S2:1543:U:OP2	2.38	0.50
61:Sd:19:ARG:NH2	82:S2:1661:A:OP1	2.40	0.50
69:SH:10:LYS:HE3	69:SH:17:ASP:HB3	1.94	0.50
72:SL:133:PRO:O	82:S2:383:G:O2'	2.29	0.50
82:S2:1410:C:H2'	82:S2:1411:G:H8	1.76	0.50
2:L5:86:U:H2'	2:L5:87:A:C8	2.46	0.50
2:L5:1601:A:OP1	39:Lj:5:THR:OG1	2.25	0.50
2:L5:3684:G:H2'	2:L5:3685:C:C6	2.46	0.50
2:L5:4501:U:OP1	6:LB:5:LYS:NZ	2.44	0.50
2:L5:4909:A:OP2	6:LB:156:TYR:OH	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LJ:84:GLU:OE2	14:LJ:92:TYR:OH	2.22	0.50
19:LP:60:PHE:O	19:LP:78:TRP:NE1	2.44	0.50
21:LR:92:LYS:HG2	21:LR:96:MET:HE3	1.94	0.50
30:La:84:GLU:OE1	30:La:87:ARG:NH2	2.44	0.50
64:SA:85:ARG:NH1	64:SA:203:PHE:O	2.44	0.50
64:SA:147:LEU:HD13	64:SA:161:ILE:HB	1.94	0.50
82:S2:1010:G:H2'	82:S2:1011:A:H8	1.77	0.50
2:L5:422:C:H2'	2:L5:423:G:H8	1.77	0.50
2:L5:1802:A:H5''	2:L5:1803:G:H5'	1.93	0.50
2:L5:2891:U:OP2	21:LR:74:ARG:NE	2.42	0.50
2:L5:4246:G:H2'	2:L5:4247:G:H8	1.76	0.50
2:L5:4575:G:H2'	2:L5:4576:PSU:H6	1.77	0.50
4:L8:65:A:OP1	37:Lh:56:ARG:NE	2.41	0.50
5:LA:116:LEU:HB3	5:LA:126:LEU:HB2	1.92	0.50
26:LW:8:PHE:HB3	26:LW:36:CYS:HB3	1.94	0.50
68:SG:121:ILE:HB	68:SG:125:THR:HG23	1.94	0.50
78:SY:5:VAL:HG12	78:SY:43:LYS:HE3	1.93	0.50
80:Sb:26:GLN:NE2	82:S2:921:G:OP2	2.44	0.50
82:S2:317:C:H2'	82:S2:318:A:C4	2.46	0.50
82:S2:1753:C:H5'	82:S2:1780:G:H22	1.77	0.50
82:S2:1801:A:H2'	82:S2:1802:C:C6	2.47	0.50
83:Zt:64:U:H2'	83:Zt:65:G:C8	2.47	0.50
2:L5:1687:U:H2'	2:L5:1688:G:C8	2.45	0.50
2:L5:1942:A:N3	2:L5:4432:C:O2'	2.32	0.50
2:L5:1995:G:O2'	48:Lt:122:ALA:O	2.24	0.50
2:L5:2386:U:H2'	2:L5:2387:G:C8	2.47	0.50
2:L5:4680:G:H2'	2:L5:4681:A:C8	2.46	0.50
4:L8:12:G:N2	19:LP:120:ASN:OD1	2.35	0.50
8:LD:108:ARG:CZ	8:LD:253:TYR:HB2	2.41	0.50
8:LD:194:VAL:HA	8:LD:197:LYS:HD2	1.94	0.50
13:LI:88:ARG:HG2	13:LI:90:ARG:HD2	1.93	0.50
15:LL:91:ALA:HB1	15:LL:96:ILE:HB	1.92	0.50
49:SD:28:GLU:OE2	49:SD:65:ARG:NH2	2.44	0.50
67:SE:10:LYS:NZ	82:S2:95:G:OP1	2.34	0.50
82:S2:649:PSU:H2'	82:S2:650:A:H8	1.77	0.50
82:S2:979:C:H2'	82:S2:980:A:C8	2.47	0.50
82:S2:1598:G:N2	82:S2:1599:U:O4	2.36	0.50
1:Pt:34:A:OP2	54:SQ:146:ARG:NH2	2.44	0.50
2:L5:654:C:H2'	2:L5:655:C:C6	2.47	0.50
2:L5:1741:G:O6	3:L7:103:A:O2'	2.21	0.50
2:L5:2745:A:H2'	2:L5:2746:A:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:4291:G:H4'	2:L5:4292:A:H5''	1.93	0.50
6:LB:113:GLU:OE2	6:LB:169:ARG:NH1	2.45	0.50
10:LF:41:MET:HE2	31:Lb:113:ALA:HB2	1.94	0.50
16:LM:46:ARG:O	16:LM:48:GLN:NE2	2.31	0.50
29:LZ:84:ARG:NH2	29:LZ:85:TYR:OH	2.45	0.50
62:Sf:117:LEU:HD12	62:Sf:118:ARG:HD3	1.94	0.50
67:SE:121:TYR:HA	67:SE:163:ASP:HA	1.94	0.50
82:S2:368:U:H3'	82:S2:369:C:H2'	1.93	0.50
82:S2:1239:U:N3	82:S2:1242:U:OP2	2.35	0.50
82:S2:1858:G:H2'	82:S2:1859:A:H8	1.77	0.50
83:Zt:22:G:H2'	83:Zt:23:A:C8	2.45	0.50
2:L5:94:A:H5''	30:La:34:ASN:HB2	1.92	0.50
2:L5:424:U:H2'	2:L5:425:U:C6	2.47	0.50
2:L5:2407:G:O6	41:Ll:2:SER:N	2.45	0.50
27:LX:78:LYS:HD3	27:LX:99:ILE:HG22	1.94	0.50
50:SF:22:LYS:HG3	50:SF:23:TRP:CD2	2.47	0.50
51:SK:85:LEU:HD12	51:SK:86:PRO:HD2	1.94	0.50
59:SZ:99:LEU:HD21	59:SZ:102:LYS:HB2	1.93	0.50
80:Sb:22:LYS:HE3	82:S2:1129:G:H5''	1.94	0.50
80:Sb:67:THR:OG1	80:Sb:70:LYS:O	2.23	0.50
82:S2:895:G:H2'	82:S2:896:U:H4'	1.94	0.50
82:S2:1398:G:H22	82:S2:1448:A:H2	1.58	0.50
82:S2:1550:G:H3'	82:S2:1579:A:H61	1.77	0.50
82:S2:1657:G:H2'	82:S2:1658:G:H8	1.77	0.50
2:L5:97:G:OP1	15:LL:16:LYS:NZ	2.36	0.49
2:L5:500:G:N2	2:L5:504:G:O2'	2.25	0.49
2:L5:1961:G:O2'	2:L5:2025:A:N6	2.45	0.49
2:L5:1994:C:H2'	2:L5:1995:G:H8	1.76	0.49
2:L5:2000:G:O2'	2:L5:2001:G:N7	2.44	0.49
2:L5:2458:C:H5''	17:LN:67:ARG:HD2	1.93	0.49
2:L5:2570:U:H2'	2:L5:2571:C:C6	2.47	0.49
2:L5:4322:G:N2	2:L5:4325:A:OP2	2.36	0.49
2:L5:4638:U:H3'	2:L5:4639:G:H21	1.77	0.49
2:L5:5005:G:N2	2:L5:5041:G:O2'	2.45	0.49
6:LB:258:HIS:HA	6:LB:260:ALA:N	2.26	0.49
50:SF:26:ASP:N	50:SF:26:ASP:OD1	2.45	0.49
62:Sf:108:VAL:HB	62:Sf:113:LYS:H	1.76	0.49
63:Sg:82:SER:OG	63:Sg:83:TRP:N	2.45	0.49
71:SJ:136:ARG:HA	71:SJ:141:VAL:HA	1.94	0.49
82:S2:940:U:H3	82:S2:1002:U:H3	1.60	0.49
2:L5:180:C:H2'	2:L5:181:C:H6	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:690:C:OP1	46:Lr:87:ARG:NH1	2.45	0.49
2:L5:1308:C:H2'	2:L5:1309:C:C6	2.47	0.49
2:L5:1555:G:O6	45:Lp:4:ARG:NH1	2.41	0.49
2:L5:1669:A:H5''	31:Lb:15:LYS:HD2	1.94	0.49
2:L5:2033:A:OP1	13:LI:162:ARG:NH2	2.35	0.49
2:L5:3777:G:H22	2:L5:3816:A:P	2.36	0.49
2:L5:4527:G:OP2	2:L5:4527:G:N2	2.35	0.49
2:L5:4775:C:N4	2:L5:4859:C:H42	2.00	0.49
18:LO:186:GLU:HA	18:LO:189:ILE:HB	1.93	0.49
52:SM:23:LYS:O	52:SM:27:ILE:HG12	2.12	0.49
72:SL:39:ASN:O	82:S2:292:A:O2'	2.23	0.49
75:SV:30:ALA:O	75:SV:60:ARG:HD3	2.12	0.49
82:S2:807:G:H2'	82:S2:808:A:H8	1.75	0.49
2:L5:713:C:O2	9:LE:130:LYS:NZ	2.41	0.49
2:L5:1392:A:H2'	2:L5:1393:G:C8	2.47	0.49
2:L5:1977:C:O2'	2:L5:1978:C:OP1	2.31	0.49
2:L5:2610:G:H2'	2:L5:2611:A:C8	2.47	0.49
2:L5:3659:G:OP1	5:LA:241:ARG:NH1	2.45	0.49
2:L5:4537:C:H2'	2:L5:4538:G:C8	2.47	0.49
2:L5:4629:U:H2'	2:L5:4630:G:H8	1.76	0.49
2:L5:4940:C:O2'	9:LE:246:ARG:NH2	2.45	0.49
2:L5:4967:A:H2'	2:L5:4968:A:C8	2.46	0.49
2:L5:4991:U:H2'	2:L5:4992:G:H8	1.76	0.49
18:LO:61:ARG:HA	18:LO:70:PRO:HD2	1.95	0.49
41:LI:23:ILE:HG23	41:LI:38:ASN:HB2	1.93	0.49
63:Sg:159:ASN:ND2	63:Sg:162:ASN:OD1	2.43	0.49
66:SC:259:THR:HG21	75:SV:16:LYS:H	1.77	0.49
78:SY:21:LYS:HE2	78:SY:75:ILE:HD11	1.94	0.49
82:S2:1854:U:H2'	82:S2:1855:G:H8	1.76	0.49
2:L5:1578:U:H2'	2:L5:1579:C:C6	2.47	0.49
4:L8:75:OMG:OP2	28:LY:74:TYR:OH	2.25	0.49
5:LA:108:PRO:HB2	45:Lp:86:LEU:HD23	1.94	0.49
27:LX:64:SER:HB2	37:Lh:69:LEU:HD13	1.94	0.49
62:Sf:89:LYS:O	82:S2:1507:G:N2	2.40	0.49
63:Sg:21:ILE:HG21	63:Sg:299:PHE:HB2	1.93	0.49
82:S2:5:U:H2'	82:S2:6:G:C8	2.47	0.49
82:S2:1289:U:H2'	82:S2:1290:G:C8	2.47	0.49
82:S2:1545:A:N3	82:S2:1671:G:O2'	2.31	0.49
83:Zt:67:U:H2'	83:Zt:68:C:C6	2.48	0.49
2:L5:400:A2M:H2'	2:L5:401:G:O4'	2.13	0.49
2:L5:475:G:H2'	2:L5:476:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1857:C:H2'	2:L5:1858:A:C8	2.47	0.49
2:L5:4458:C:H2'	2:L5:4459:U:C6	2.48	0.49
2:L5:4895:C:O2'	16:LM:132:LYS:NZ	2.38	0.49
2:L5:4991:U:H2'	2:L5:4992:G:C8	2.47	0.49
5:LA:114:CYS:N	5:LA:165:VAL:O	2.46	0.49
6:LB:57:VAL:HG22	6:LB:73:VAL:HG22	1.94	0.49
29:LZ:46:ILE:HA	29:LZ:70:SER:HA	1.93	0.49
48:Lt:114:ARG:NH2	48:Lt:162:CYS:SG	2.86	0.49
62:Sf:99:LYS:NZ	82:S2:1287:A:OP1	2.39	0.49
82:S2:1048:G:H21	82:S2:1070:A:H62	1.60	0.49
82:S2:1146:C:O2'	82:S2:1150:A:N1	2.42	0.49
82:S2:1242:U:O2	82:S2:1517:G:O2'	2.27	0.49
82:S2:1515:G:H2'	82:S2:1516:G:C8	2.48	0.49
82:S2:1705:C:H2'	82:S2:1706:G:C8	2.48	0.49
2:L5:264:C:H2'	2:L5:265:C:C4	2.47	0.49
2:L5:310:G:H2'	2:L5:311:G:H8	1.76	0.49
2:L5:444:G:H2'	2:L5:445:U:C6	2.47	0.49
2:L5:474:C:H2'	2:L5:475:G:C8	2.47	0.49
14:LJ:56:THR:OG1	14:LJ:64:ARG:N	2.43	0.49
26:LW:97:LYS:O	26:LW:99:GLU:N	2.43	0.49
51:SK:64:TRP:HB3	61:Sd:23:VAL:HA	1.95	0.49
63:Sg:129:ILE:O	63:Sg:142:VAL:N	2.44	0.49
64:SA:37:TYR:OH	64:SA:57:LYS:NZ	2.45	0.49
73:SN:2:GLY:N	82:S2:1092:G:OP1	2.45	0.49
82:S2:527:C:H2'	82:S2:528:A:H8	1.77	0.49
82:S2:1320:G:H2'	82:S2:1321:G:O4'	2.13	0.49
82:S2:1617:G:N1	82:S2:1620:A:OP2	2.46	0.49
2:L5:62:A:OP1	17:LN:172:ARG:NH1	2.38	0.49
2:L5:1414:C:H2'	2:L5:1415:G:C8	2.43	0.49
2:L5:1942:A:H2'	2:L5:1943:A:C8	2.48	0.49
2:L5:2638:G:N1	2:L5:2718:U:H2'	2.28	0.49
2:L5:2739:C:O2	5:LA:188:LYS:NZ	2.37	0.49
2:L5:2784:C:H2'	2:L5:2785:C:H6	1.78	0.49
2:L5:4911:A:OP1	6:LB:97:ARG:NH2	2.38	0.49
7:LC:298:ILE:HD13	20:LQ:131:PRO:HB3	1.93	0.49
9:LE:141:ARG:NH1	9:LE:191:GLN:O	2.44	0.49
47:Ls:17:ILE:HD12	47:Ls:54:LEU:HD21	1.93	0.49
55:SR:60:ARG:NH1	82:S2:1464:C:O3'	2.46	0.49
58:SU:68:THR:O	61:Sd:40:ARG:NH1	2.45	0.49
68:SG:49:VAL:HB	68:SG:115:LYS:HG2	1.94	0.49
68:SG:227:GLN:HB3	68:SG:231:ARG:HH21	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:207:G:H2'	2:L5:208:A:C8	2.47	0.49
2:L5:325:U:H3'	38:Li:28:ARG:HH21	1.78	0.49
2:L5:1825:A:H2'	2:L5:1826:G:H8	1.78	0.49
2:L5:2749:C:H2'	2:L5:2750:G:C8	2.48	0.49
2:L5:2763:U:H4'	2:L5:2764:A:H5''	1.93	0.49
2:L5:4084:G:O6	5:LA:70:LYS:NZ	2.42	0.49
2:L5:4208:U:H2'	2:L5:4209:G:H8	1.77	0.49
2:L5:4345:C:H2'	2:L5:4346:U:C6	2.48	0.49
2:L5:4941:G:O3'	9:LE:187:ARG:NH2	2.45	0.49
11:LG:165:GLU:OE2	17:LN:26:ARG:NH1	2.45	0.49
19:LP:52:THR:HG23	19:LP:85:LYS:HG3	1.94	0.49
24:LU:114:TYR:CE2	84:CI:50:MET:HG3	2.47	0.49
55:SR:16:ILE:HD11	55:SR:54:VAL:HG21	1.94	0.49
60:Sc:37:ASP:OD1	60:Sc:39:SER:OG	2.25	0.49
79:Sa:44:ILE:HG23	79:Sa:45:VAL:HG13	1.95	0.49
2:L5:965:G:H21	2:L5:2092:G:H1'	1.78	0.49
2:L5:1558:A:H2'	2:L5:1559:G:H8	1.78	0.49
2:L5:2843:U:O2'	2:L5:4632:U:OP1	2.28	0.49
2:L5:3607:U:H2'	2:L5:3608:A:C8	2.48	0.49
2:L5:4630:G:H2'	2:L5:4631:G:H8	1.77	0.49
2:L5:4691:A:O3'	12:LH:71:ARG:HD3	2.13	0.49
4:L8:43:A:H2'	4:L8:44:A:C8	2.47	0.49
20:LQ:15:ARG:HB3	20:LQ:52:PHE:HB3	1.95	0.49
26:LW:105:ARG:NE	68:SG:151:ASP:OD1	2.45	0.49
52:SM:82:ASN:OD1	52:SM:83:LYS:N	2.46	0.49
66:SC:60:TRP:O	66:SC:71:LYS:NZ	2.37	0.49
82:S2:1653:U:H2'	82:S2:1654:G:C8	2.47	0.49
2:L5:181:C:H2'	2:L5:182:G:C8	2.48	0.49
2:L5:224:U:O2	7:LC:219:LYS:NZ	2.41	0.49
2:L5:1584:G:O6	87:L5:5285:SPD:N1	2.46	0.49
2:L5:2701:U:H3	2:L5:2715:G:H1	1.60	0.49
2:L5:4237:C:H2'	2:L5:4238:G:C8	2.47	0.49
2:L5:4260:U:H2'	2:L5:4261:C:H6	1.77	0.49
18:LO:81:TRP:HB2	18:LO:104:VAL:HG21	1.95	0.49
33:Ld:22:THR:HG23	33:Ld:122:VAL:HG13	1.95	0.49
41:Ll:28:ARG:HA	41:Ll:33:ASN:ND2	2.27	0.49
55:SR:109:LEU:HD13	64:SA:52:LYS:HB2	1.94	0.49
57:ST:11:GLN:HB2	82:S2:1542:C:H4'	1.95	0.49
65:SB:97:LEU:HD23	65:SB:232:HIS:CG	2.48	0.49
66:SC:85:SER:OG	75:SV:25:GLY:O	2.26	0.49
82:S2:1468:C:H2'	82:S2:1469:A:H8	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1199:G:H2'	2:L5:1200:G:H8	1.78	0.48
2:L5:1333:A:H2'	2:L5:1334:A:C8	2.47	0.48
2:L5:1480:C:O2'	2:L5:1482:G:OP2	2.30	0.48
2:L5:3939:G:O2'	2:L5:4076:G:N2	2.42	0.48
5:LA:147:ARG:HH21	5:LA:155:LYS:HG3	1.78	0.48
15:LL:23:ALA:HB3	17:LN:199:GLN:HA	1.94	0.48
52:SM:87:GLU:HG3	52:SM:103:VAL:HG11	1.94	0.48
57:ST:121:ARG:HH21	82:S2:1563:G:H5''	1.78	0.48
70:SI:43:ILE:HD13	82:S2:305:U:H1'	1.95	0.48
72:SL:3:ASP:OD1	72:SL:4:ILE:N	2.46	0.48
82:S2:35:C:H5''	82:S2:579:C:H5''	1.95	0.48
82:S2:96:C:H2'	82:S2:97:U:C6	2.48	0.48
82:S2:538:U:H2'	82:S2:539:C:C6	2.48	0.48
82:S2:952:G:H2'	82:S2:953:C:C6	2.47	0.48
82:S2:1199:A:H2'	82:S2:1200:A:C8	2.48	0.48
82:S2:1773:C:H2'	82:S2:1774:C:H5''	1.94	0.48
1:Pt:22:U:H2'	1:Pt:23:C:C6	2.48	0.48
2:L5:248:C:O2	28:LY:121:ARG:NH2	2.41	0.48
2:L5:287:U:H2'	2:L5:288:G:H8	1.79	0.48
2:L5:447:C:H2'	2:L5:448:G:C8	2.48	0.48
2:L5:951:G:H2'	2:L5:952:G:H8	1.79	0.48
2:L5:1194:G:H2'	2:L5:1195:G:C8	2.47	0.48
2:L5:1241:C:O2'	31:Lb:120:ARG:O	2.30	0.48
2:L5:1243:C:H2'	2:L5:1244:G:C8	2.48	0.48
2:L5:1315:C:H2'	2:L5:1316:OMG:H8	1.78	0.48
2:L5:1405:C:H2'	2:L5:1406:G:H8	1.77	0.48
2:L5:4237:C:OP1	2:L5:4327:C:O2'	2.30	0.48
2:L5:4343:U:O2'	44:Lo:31:ASP:OD1	2.30	0.48
2:L5:4643:G:H2'	2:L5:4644:G:H8	1.78	0.48
3:L7:114:U:H2'	3:L7:115:A:H8	1.79	0.48
4:L8:65:A:O2'	37:Lh:10:ARG:NH2	2.47	0.48
12:LH:41:ILE:HG22	12:LH:43:VAL:HG13	1.95	0.48
13:LI:66:GLU:OE2	13:LI:69:ARG:NH2	2.31	0.48
24:LU:36:ALA:HB1	24:LU:70:ILE:HD11	1.95	0.48
50:SF:141:VAL:HG12	60:Sc:47:LYS:HG2	1.94	0.48
55:SR:10:LYS:HG2	55:SR:53:TYR:CE2	2.48	0.48
72:SL:23:VAL:HG23	72:SL:25:LEU:HG	1.95	0.48
80:Sb:62:VAL:HG23	80:Sb:74:THR:HG21	1.94	0.48
82:S2:1419:C:H41	82:S2:1421:A:H2	1.60	0.48
2:L5:358:C:H2'	2:L5:359:A:C8	2.48	0.48
2:L5:475:G:H2'	2:L5:476:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1195:G:H2'	2:L5:1196:G:C8	2.49	0.48
2:L5:1399:G:H2'	2:L5:1400:G:H8	1.78	0.48
2:L5:1669:A:N3	2:L5:1852:U:O2'	2.40	0.48
2:L5:1683:PSU:H2'	2:L5:1684:A:H8	1.78	0.48
2:L5:2011:C:H3'	2:L5:2012:A:H8	1.78	0.48
2:L5:2869:U:O2'	2:L5:2881:A:N7	2.31	0.48
2:L5:4732:G:N2	2:L5:4734:A:N7	2.62	0.48
21:LR:168:GLU:HA	21:LR:171:LYS:HE3	1.95	0.48
64:SA:145:ILE:HG23	64:SA:159:ILE:HB	1.96	0.48
66:SC:125:LYS:HA	66:SC:143:CYS:HA	1.95	0.48
76:SW:6:VAL:HG12	76:SW:34:ILE:HD11	1.93	0.48
78:SY:76:TYR:OH	78:SY:86:GLU:OE1	2.25	0.48
82:S2:1013:U:H2'	82:S2:1014:G:H8	1.79	0.48
2:L5:921:C:H2'	2:L5:922:C:C6	2.49	0.48
2:L5:1824:G:H5''	23:LT:35:LYS:HE2	1.95	0.48
2:L5:2078:C:H2'	2:L5:2079:G:C8	2.48	0.48
2:L5:2084:C:C4	20:LQ:14:ARG:HD2	2.49	0.48
2:L5:2708:U:H1'	84:CI:79:ARG:HH22	1.78	0.48
4:L8:6:C:H2'	4:L8:7:U:C6	2.48	0.48
4:L8:141:C:H2'	4:L8:142:U:C6	2.49	0.48
37:Lh:89:ARG:O	37:Lh:93:ARG:HG2	2.14	0.48
58:SU:40:ILE:O	58:SU:44:LYS:HG2	2.13	0.48
67:SE:36:HIS:NE2	67:SE:143:ASP:OD1	2.46	0.48
82:S2:1215:C:N4	82:S2:1220:A:H61	2.12	0.48
82:S2:1455:A:H2'	82:S2:1456:G:H8	1.78	0.48
82:S2:1713:C:H2'	82:S2:1714:U:C6	2.49	0.48
83:Zt:27:U:H2'	83:Zt:28:C:C6	2.49	0.48
1:Pt:20(A):U:O4'	14:LJ:58:ARG:NH2	2.46	0.48
2:L5:257:C:H2'	2:L5:258:G:C8	2.48	0.48
2:L5:956:A:H1'	2:L5:2076:G:H5''	1.94	0.48
2:L5:2444:U:O2'	4:L8:112:G:O2'	2.22	0.48
2:L5:4642:U:H2'	2:L5:4643:G:H8	1.78	0.48
17:LN:120:TRP:HE1	17:LN:123:GLU:HB3	1.78	0.48
18:LO:14:HIS:HD2	18:LO:123:ALA:HB3	1.78	0.48
40:Lk:5:ILE:HG21	40:Lk:11:PHE:HB2	1.95	0.48
54:SQ:110:ASP:OD1	54:SQ:111:ILE:HD12	2.13	0.48
62:Sf:102:VAL:HG22	62:Sf:104:LYS:HG2	1.96	0.48
64:SA:184:ARG:HE	64:SA:191:ARG:HA	1.78	0.48
2:L5:173:C:H5''	15:LL:129:ARG:HH12	1.77	0.48
2:L5:173:C:H2'	2:L5:174:C:C6	2.49	0.48
2:L5:261:G:H2'	2:L5:262:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:966:A:OP2	2:L5:2092:G:N2	2.44	0.48
2:L5:1876:U:H2'	2:L5:1877:G:H8	1.79	0.48
2:L5:2274:C:H2'	2:L5:2275:G:H8	1.78	0.48
2:L5:2897:G:H2'	2:L5:2898:G:H8	1.78	0.48
6:LB:367:PHE:HB2	26:LW:1:MET:HB2	1.96	0.48
57:ST:44:GLU:HG3	57:ST:45:LEU:HD12	1.96	0.48
57:ST:49:ASP:OD1	57:ST:50:GLU:N	2.47	0.48
58:SU:19:ARG:HB3	58:SU:92:HIS:CE1	2.49	0.48
59:SZ:86:ALA:HA	59:SZ:89:GLN:HE21	1.78	0.48
73:SN:29:THR:OG1	73:SN:31:ASP:OD1	2.28	0.48
78:SY:11:LYS:HB2	78:SY:24:VAL:HG12	1.95	0.48
82:S2:325:C:N3	82:S2:326:C:O2'	2.44	0.48
82:S2:1842:4AC:H2'	82:S2:1843:G:C8	2.49	0.48
2:L5:163:A:H2'	2:L5:164:G:H8	1.79	0.48
2:L5:184:U:H3	2:L5:253:G:H1	1.57	0.48
2:L5:260:C:H2'	2:L5:261:G:C8	2.49	0.48
2:L5:323:C:H2'	2:L5:324:A:C8	2.47	0.48
2:L5:1464:C:H5''	31:Lb:32:LEU:HD12	1.95	0.48
2:L5:1494:U:H2'	2:L5:1495:G:H8	1.78	0.48
2:L5:1847:C:H2'	2:L5:1848:C:C6	2.49	0.48
2:L5:2411:C:H2'	2:L5:2412:A:H8	1.78	0.48
2:L5:2492:C:H2'	2:L5:2493:G:H8	1.77	0.48
2:L5:4251:A:H5''	14:LJ:108:GLY:HA3	1.96	0.48
3:L7:82:G:H2'	3:L7:83:A:C8	2.48	0.48
25:LV:92:ASP:O	26:LW:2:LYS:NZ	2.46	0.48
47:Ls:30:VAL:HA	47:Ls:189:ILE:HA	1.96	0.48
68:SG:172:LYS:NZ	82:S2:67:C:OP2	2.38	0.48
82:S2:610:G:H2'	82:S2:611:G:H8	1.78	0.48
82:S2:1804:U:H2'	82:S2:1805:G:H8	1.79	0.48
83:Zt:60:U:H2'	83:Zt:61:C:H5	1.77	0.48
1:Pt:51:C:H2'	1:Pt:52:G:C8	2.49	0.48
2:L5:1070:G:O2'	2:L5:1071:C:O5'	2.29	0.48
2:L5:1091:C:H2'	2:L5:1092:G:C8	2.49	0.48
2:L5:2769:U:N3	36:Lg:69:LYS:HD3	2.28	0.48
2:L5:2897:G:H2'	2:L5:2898:G:C8	2.48	0.48
2:L5:3867:A2M:H2'	2:L5:3868:G:O4'	2.13	0.48
2:L5:3933:G:H2'	2:L5:3934:G:C8	2.49	0.48
2:L5:4069:U:H2'	2:L5:4070:U:H6	1.79	0.48
2:L5:4452:U:OP2	2:L5:4522:G:N1	2.30	0.48
2:L5:4504:C:H2'	2:L5:4505:C:C6	2.49	0.48
2:L5:4524:G:H2'	2:L5:4525:C:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L8:19:C:H2'	4:L8:20:A:C8	2.48	0.48
16:LM:71:LYS:O	16:LM:75:GLN:HG3	2.13	0.48
29:LZ:51:ARG:HB2	29:LZ:65:ARG:HB3	1.94	0.48
30:La:127:LYS:HD3	38:Li:8:ALA:HB2	1.95	0.48
34:Le:35:TRP:O	34:Le:36:ARG:NH1	2.44	0.48
65:SB:123:ALA:HB2	65:SB:165:ARG:HG2	1.95	0.48
66:SC:166:ARG:HB3	66:SC:247:THR:HB	1.94	0.48
69:SH:49:LYS:NZ	69:SH:50:GLU:O	2.45	0.48
82:S2:1275:G:H22	82:S2:1506:A:P	2.35	0.48
2:L5:294:G:OP2	2:L5:296:A:O2'	2.27	0.48
2:L5:1591:U:OP2	2:L5:2856:C:O2'	2.30	0.48
2:L5:1837:A:OP2	23:LT:130:ARG:NH1	2.47	0.48
2:L5:4122:G:O3'	36:Lg:90:ARG:NH2	2.47	0.48
2:L5:4178:A:OP2	17:LN:91:GLN:NE2	2.35	0.48
2:L5:4643:G:H2'	2:L5:4644:G:C8	2.49	0.48
2:L5:4964:C:H2'	2:L5:4965:U:C6	2.49	0.48
4:L8:138:C:H2'	4:L8:139:G:C8	2.49	0.48
49:SD:51:LEU:HD12	49:SD:91:VAL:HG12	1.95	0.48
57:ST:114:GLU:OE1	57:ST:114:GLU:N	2.46	0.48
61:Sd:13:LYS:HG3	82:S2:1556:A:N7	2.29	0.48
61:Sd:21:CYS:HB3	61:Sd:26:ASN:H	1.79	0.48
68:SG:159:ARG:NH1	82:S2:76:U:O2'	2.47	0.48
82:S2:1842:4AC:H2'	82:S2:1843:G:H8	1.79	0.48
2:L5:1348:U:H2'	2:L5:1349:G:C8	2.49	0.48
2:L5:1478:C:H2'	2:L5:1479:G:H8	1.78	0.48
2:L5:1779:U:H2'	2:L5:1780:A:C8	2.49	0.48
2:L5:2021:G:OP1	47:Ls:58:ASN:N	2.44	0.48
2:L5:2348:G:OP1	2:L5:2351:OMC:N4	2.46	0.48
2:L5:4237:C:H2'	2:L5:4238:G:H8	1.79	0.48
2:L5:4633:G:H22	2:L5:4663:G:H2'	1.79	0.48
2:L5:4685:U:H2'	2:L5:4686:G:C8	2.49	0.48
11:LG:178:GLY:O	11:LG:223:ARG:NH2	2.46	0.48
12:LH:18:ILE:HG12	12:LH:27:VAL:HG22	1.95	0.48
21:LR:157:ASP:OD1	21:LR:158:GLN:N	2.47	0.48
33:Ld:37:GLY:O	33:Ld:41:ARG:HG3	2.14	0.48
54:SQ:100:VAL:HG22	54:SQ:101:ASP:H	1.78	0.48
71:SJ:124:HIS:CD2	81:Se:35:ARG:HD2	2.49	0.48
78:SY:57:VAL:HG12	78:SY:73:GLY:HA2	1.96	0.48
81:Se:56:ASN:ND2	82:S2:606:G:O4'	2.46	0.48
83:Zt:30:G:H2'	83:Zt:31:A:C8	2.48	0.48
83:Zt:75:C:H3'	83:Zt:76:A:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1188:C:H2'	2:L5:1189:G:H8	1.79	0.47
2:L5:1705:G:H5''	10:LF:177:ARG:HG2	1.95	0.47
2:L5:2521:G:H2'	2:L5:2522:G:H8	1.79	0.47
2:L5:2759:G:O2'	2:L5:2760:G:O4'	2.28	0.47
2:L5:4324:A:H2'	2:L5:4325:A:C8	2.49	0.47
2:L5:5037:U:H2'	2:L5:5038:A:C8	2.49	0.47
4:L8:60:G:O6	37:Lh:62:ASN:ND2	2.31	0.47
4:L8:92:U:H2'	4:L8:93:C:O4'	2.14	0.47
6:LB:50:LYS:HB2	6:LB:345:LEU:HD11	1.95	0.47
8:LD:217:ASP:OD1	8:LD:218:ALA:N	2.47	0.47
10:LF:94:ARG:NH2	10:LF:97:GLY:O	2.35	0.47
48:Lt:18:THR:O	48:Lt:61:LYS:NZ	2.46	0.47
48:Lt:117:ARG:HE	48:Lt:119:ARG:H	1.60	0.47
50:SF:60:ARG:HE	82:S2:1679:A:P	2.37	0.47
57:ST:42:HIS:HE2	57:ST:43:LYS:HE3	1.79	0.47
64:SA:110:ASN:HB3	64:SA:113:GLN:HE22	1.79	0.47
68:SG:7:PHE:CE2	68:SG:9:ALA:HB3	2.49	0.47
68:SG:138:ALA:HA	68:SG:176:ILE:HD11	1.95	0.47
82:S2:89:C:H2'	82:S2:90:G:C8	2.49	0.47
82:S2:1103:C:H2'	82:S2:1104:G:C8	2.49	0.47
82:S2:1276:A:C6	82:S2:1322:G:H1'	2.49	0.47
82:S2:1407:U:H2'	82:S2:1408:U:C6	2.48	0.47
2:L5:490:C:H2'	2:L5:491:G:C8	2.48	0.47
2:L5:2654:C:H2'	2:L5:2655:C:H6	1.79	0.47
2:L5:2658:G:O2'	2:L5:2675:G:N2	2.46	0.47
2:L5:3670:C:H2'	2:L5:3671:G:C8	2.49	0.47
2:L5:4080:C:H2'	2:L5:4081:G:H8	1.79	0.47
2:L5:4356:G:H2'	2:L5:4357:G:H8	1.79	0.47
2:L5:4578:G:H2'	2:L5:4579:PSU:H6	1.79	0.47
3:L7:15:C:H2'	3:L7:16:A:H8	1.79	0.47
51:SK:11:ILE:HD11	51:SK:40:VAL:HG11	1.96	0.47
54:SQ:80:GLN:O	54:SQ:84:ILE:HG13	2.14	0.47
67:SE:247:THR:N	67:SE:250:GLU:OE2	2.43	0.47
69:SH:118:ARG:HD3	69:SH:121:THR:HG21	1.96	0.47
78:SY:11:LYS:NZ	82:S2:831:G:O6	2.46	0.47
78:SY:77:ASP:OD1	78:SY:77:ASP:N	2.47	0.47
82:S2:671:A:H4'	82:S2:672:A:H5''	1.95	0.47
82:S2:835:C:H4'	82:S2:836:G:C8	2.49	0.47
82:S2:1142:G:N2	82:S2:1145:A:OP2	2.35	0.47
82:S2:1687:C:H2'	82:S2:1688:C:C6	2.49	0.47
82:S2:1722:G:O6	82:S2:1812:U:O2	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:978:G:OP1	9:LE:47:ASN:ND2	2.42	0.47
2:L5:1419:G:H5''	20:LQ:71:LYS:NZ	2.29	0.47
2:L5:2335:C:H2'	2:L5:2336:G:C8	2.49	0.47
2:L5:2361:G:N2	2:L5:3860:A:OP2	2.42	0.47
50:SF:103:LEU:HD11	59:SZ:67:LEU:HD22	1.95	0.47
50:SF:123:GLU:OE1	60:Sc:63:ARG:NH2	2.46	0.47
52:SM:128:PHE:HA	52:SM:131:LYS:HG2	1.97	0.47
69:SH:91:HIS:ND1	69:SH:169:LYS:HG2	2.29	0.47
74:SO:113:GLN:HE22	79:Sa:45:VAL:HA	1.79	0.47
77:SX:68:LYS:NZ	82:S2:616:A:OP1	2.48	0.47
82:S2:328:U:O2'	82:S2:329:G:O5'	2.31	0.47
82:S2:468:A2M:HM'3	82:S2:468:A2M:H1'	1.53	0.47
82:S2:1172:U:H2'	82:S2:1173:A:C8	2.50	0.47
82:S2:1217:A:H2'	82:S2:1218:C:H6	1.78	0.47
82:S2:1643:U:H2'	82:S2:1644:C:C6	2.50	0.47
2:L5:179:G:H2'	2:L5:180:C:C6	2.48	0.47
2:L5:1179:U:OP2	8:LD:289:ARG:NH2	2.38	0.47
2:L5:1718:C:O2'	10:LF:181:LYS:NZ	2.47	0.47
2:L5:2297:G:H4'	7:LC:242:PRO:HB2	1.97	0.47
2:L5:4095:G:H2'	2:L5:4096:C:C6	2.50	0.47
2:L5:4192:A:H2'	2:L5:4193:C:H6	1.79	0.47
7:LC:162:LYS:N	7:LC:166:GLU:OE2	2.35	0.47
18:LO:3:GLU:OE1	18:LO:5:GLN:NE2	2.41	0.47
39:Lj:2:THR:HB	39:Lj:6:SER:HB2	1.95	0.47
54:SQ:110:ASP:O	54:SQ:113:ILE:N	2.43	0.47
64:SA:177:MET:SD	64:SA:180:ARG:NH2	2.87	0.47
70:SI:31:ARG:NH2	82:S2:381:C:OP1	2.47	0.47
71:SJ:40:LYS:NZ	82:S2:641:A:OP1	2.31	0.47
72:SL:68:ILE:HD11	72:SL:141:ASN:HB2	1.96	0.47
82:S2:5:U:H2'	82:S2:6:G:H8	1.79	0.47
82:S2:1280:G:H2'	82:S2:1281:G:H8	1.79	0.47
82:S2:1800:A:H3'	82:S2:1801:A:H8	1.79	0.47
82:S2:1801:A:H2'	82:S2:1802:C:H6	1.80	0.47
2:L5:1095:A:N1	2:L5:1200:G:C6	2.83	0.47
2:L5:1259:G:H2'	2:L5:1260:G:H8	1.79	0.47
2:L5:2430:C:H2'	2:L5:2431:A:H8	1.79	0.47
2:L5:4968:A:OP1	6:LB:120:LYS:N	2.45	0.47
4:L8:130:C:H2'	4:L8:131:G:C8	2.49	0.47
17:LN:155:VAL:O	17:LN:162:ARG:NH2	2.47	0.47
24:LU:23:LEU:HD23	24:LU:110:TYR:HB2	1.95	0.47
32:Lc:47:ILE:HD12	32:Lc:94:LEU:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Ls:102:LEU:HD23	47:Ls:189:ILE:HG13	1.96	0.47
81:Se:8:ARG:HG2	81:Se:11:LYS:HD3	1.96	0.47
82:S2:1221:G:H2'	82:S2:1222:G:H8	1.80	0.47
82:S2:1539:U:H2'	82:S2:1540:G:C8	2.50	0.47
2:L5:123:C:H2'	2:L5:124:C:H6	1.79	0.47
2:L5:146:G:H2'	2:L5:147:A:H8	1.79	0.47
2:L5:162:A:H2'	2:L5:163:A:H8	1.80	0.47
2:L5:3898:G:H5'	6:LB:254:ILE:HG13	1.97	0.47
2:L5:4070:U:H2'	2:L5:4071:U:H6	1.79	0.47
2:L5:4194:U:O2'	13:LI:116:ARG:NH2	2.46	0.47
2:L5:4967:A:H2'	2:L5:4968:A:H8	1.80	0.47
3:L7:35:U:O2	3:L7:45:U:O2'	2.32	0.47
5:LA:112:ILE:HG22	5:LA:135:THR:HG23	1.97	0.47
50:SF:34:SER:HA	60:Sc:55:VAL:HG23	1.96	0.47
64:SA:18:PHE:HD1	64:SA:23:THR:HG21	1.79	0.47
67:SE:242:LYS:HA	67:SE:242:LYS:HD3	1.76	0.47
70:SI:57:ALA:HB2	70:SI:183:GLY:HA2	1.96	0.47
75:SV:17:CYS:HB2	75:SV:56:CYS:HB3	1.96	0.47
76:SW:62:VAL:HG11	80:Sb:8:LEU:HG	1.96	0.47
82:S2:52:G:H2'	82:S2:53:C:C6	2.50	0.47
82:S2:1644:C:H2'	82:S2:1645:C:C6	2.50	0.47
83:Zt:15:G:N1	83:Zt:48:C:N3	2.63	0.47
2:L5:239:C:H2'	2:L5:240:G:C8	2.49	0.47
2:L5:270:U:H2'	2:L5:271:C:C6	2.49	0.47
2:L5:347:A:H2'	2:L5:348:G:C8	2.49	0.47
2:L5:351:C:OP2	7:LC:197:ARG:NH1	2.32	0.47
2:L5:454:U:H2'	2:L5:455:C:O4'	2.15	0.47
2:L5:1305:C:OP1	87:L5:5288:SPD:N1	2.48	0.47
2:L5:1328:G:H2'	2:L5:1329:G:C8	2.49	0.47
2:L5:1554:A:OP1	45:Lp:5:THR:OG1	2.28	0.47
2:L5:1703:C:OP1	2:L5:1704:C:N4	2.48	0.47
2:L5:1903:G:OP1	35:Lf:87:LYS:NZ	2.43	0.47
2:L5:2257:C:O2'	2:L5:2259:G:OP2	2.27	0.47
2:L5:2520:C:H2'	2:L5:2521:G:C8	2.47	0.47
2:L5:2554:U:C2	2:L5:2764:A:N7	2.83	0.47
2:L5:2581:A:H2'	2:L5:2582:A:C8	2.49	0.47
2:L5:2638:G:H22	2:L5:2719:C:P	2.37	0.47
2:L5:2808:G:O3'	21:LR:60:ARG:NH1	2.47	0.47
2:L5:3744:OMG:HM23	2:L5:3744:OMG:H1'	1.72	0.47
2:L5:4246:G:H2'	2:L5:4247:G:C8	2.49	0.47
2:L5:4621:C:H2'	2:L5:4622:A:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:4727:A:OP1	6:LB:133:TYR:N	2.47	0.47
2:L5:4750:G:H2'	2:L5:4751:G:H8	1.79	0.47
2:L5:5025:C:H2'	2:L5:5028:G:H1'	1.96	0.47
3:L7:110:G:H2'	3:L7:111:C:C6	2.49	0.47
5:LA:107:MET:O	5:LA:139:HIS:NE2	2.47	0.47
10:LF:171:ASP:OD1	10:LF:172:ASN:N	2.47	0.47
17:LN:169:ARG:HG3	17:LN:174:LEU:HD12	1.96	0.47
32:Lc:58:SER:HB3	36:Lg:96:LEU:HD13	1.95	0.47
52:SM:60:MET:HA	52:SM:63:LYS:HB3	1.97	0.47
53:SP:93:MET:HE1	53:SP:106:GLU:OE1	2.15	0.47
57:ST:74:SER:O	57:ST:78:ILE:HD12	2.15	0.47
62:Sf:103:LEU:HD12	62:Sf:105:TYR:CZ	2.50	0.47
63:Sg:216:ALA:N	63:Sg:230:LEU:O	2.43	0.47
64:SA:184:ARG:HG2	64:SA:189:ILE:HB	1.97	0.47
77:SX:9:THR:HG22	82:S2:681:PSU:H4'	1.95	0.47
82:S2:54:A:H3'	82:S2:451:G:H22	1.80	0.47
82:S2:66:G:H2'	82:S2:67:C:H4'	1.97	0.47
82:S2:116:OMU:HM23	82:S2:116:OMU:H1'	1.71	0.47
82:S2:146:G:H2'	82:S2:147:A:C8	2.49	0.47
82:S2:375:U:H2'	82:S2:376:A:C8	2.50	0.47
82:S2:379:C:H2'	82:S2:380:G:C8	2.49	0.47
82:S2:495:U:H2'	82:S2:496:C:O4'	2.13	0.47
82:S2:1424:G:H2'	82:S2:1425:G:H8	1.78	0.47
82:S2:1547:C:H3'	82:S2:1548:G:H8	1.80	0.47
2:L5:669:C:OP1	46:Lr:71:ARG:NH1	2.34	0.47
2:L5:1339:U:H2'	2:L5:1340:OMC:C6	2.50	0.47
2:L5:1756:U:O2'	2:L5:1758:G:OP2	2.27	0.47
2:L5:2568:C:H2'	2:L5:2569:G:C8	2.50	0.47
2:L5:2615:C:H2'	2:L5:2616:C:H6	1.80	0.47
2:L5:4089:G:H2'	2:L5:4090:G:C8	2.50	0.47
2:L5:4139:G:N2	2:L5:4140:C:H41	2.12	0.47
2:L5:4906:C:H2'	2:L5:4907:G:C8	2.50	0.47
2:L5:5027:C:HO2'	2:L5:5028:G:H5''	1.80	0.47
3:L7:94:C:H2'	3:L7:95:C:H6	1.80	0.47
3:L7:114:U:H2'	3:L7:115:A:C8	2.50	0.47
4:L8:144:U:H2'	4:L8:145:C:C6	2.50	0.47
15:LL:60:ARG:NH1	15:LL:67:HIS:O	2.45	0.47
15:LL:176:PHE:O	30:La:138:LYS:NZ	2.44	0.47
17:LN:51:LEU:O	17:LN:117:ASN:ND2	2.45	0.47
31:Lb:65:MET:HG3	31:Lb:68:ARG:HH12	1.80	0.47
51:SK:37:ASP:OD1	51:SK:37:ASP:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:Sf:108:VAL:HG12	62:Sf:114:ILE:HA	1.97	0.47
68:SG:74:ARG:NH1	68:SG:96:SER:OG	2.48	0.47
69:SH:51:ILE:HG21	69:SH:179:LYS:HG2	1.97	0.47
70:SI:10:LYS:O	70:SI:18:ARG:NH1	2.48	0.47
75:SV:74:LYS:NZ	75:SV:83:PHE:HB3	2.30	0.47
82:S2:433:A:H2'	82:S2:434:G:C8	2.49	0.47
82:S2:1491:G:H2'	82:S2:1492:U:C6	2.50	0.47
82:S2:1692:U:H2'	82:S2:1693:G:H8	1.79	0.47
2:L5:214:G:H2'	2:L5:215:C:C6	2.50	0.47
2:L5:458:C:OP2	9:LE:114:ARG:NH2	2.47	0.47
2:L5:494:U:H2'	2:L5:495:C:C6	2.50	0.47
2:L5:1316:OMG:HM23	2:L5:1316:OMG:H1'	1.73	0.47
2:L5:1628:C:OP2	5:LA:9:ARG:HD2	2.15	0.47
2:L5:1884:C:H2'	2:L5:1885:G:H8	1.79	0.47
2:L5:2627:C:OP1	24:LU:92:LYS:NZ	2.41	0.47
2:L5:4163:U:H5'	2:L5:4164:C:H5''	1.96	0.47
8:LD:41:LYS:NZ	23:LT:32:ARG:O	2.41	0.47
26:LW:73:ARG:NH2	82:S2:1749:G:O6	2.41	0.47
65:SB:180:ASP:N	65:SB:183:GLU:OE2	2.36	0.47
80:Sb:11:SER:OG	80:Sb:14:GLU:OE1	2.32	0.47
2:L5:1364:U:OP2	15:LL:36:ARG:NH2	2.31	0.47
2:L5:1578:U:H2'	2:L5:1579:C:H6	1.79	0.47
2:L5:1884:C:H2'	2:L5:1885:G:C8	2.51	0.47
2:L5:1914:C:H4'	18:LO:89:PRO:HD3	1.95	0.47
2:L5:2411:C:H2'	2:L5:2412:A:C8	2.50	0.47
2:L5:2641:A:H2'	2:L5:2642:A:O4'	2.15	0.47
2:L5:3866:C:H2'	2:L5:3867:A2M:O4'	2.15	0.47
2:L5:4441:A:H5''	13:LI:114:GLY:HA2	1.97	0.47
9:LE:243:THR:HG22	9:LE:245:GLN:H	1.80	0.47
27:LX:124:VAL:HG22	27:LX:138:VAL:HG13	1.96	0.47
49:SD:126:ILE:O	49:SD:129:SER:OG	2.28	0.47
71:SJ:136:ARG:HD3	71:SJ:160:SER:HA	1.98	0.47
72:SL:111:VAL:HG12	72:SL:140:PHE:HB2	1.96	0.47
2:L5:461:G:H2'	2:L5:462:G:H8	1.80	0.46
2:L5:1081:C:O2'	2:L5:1082:C:H5'	2.14	0.46
2:L5:1683:PSU:H2'	2:L5:1684:A:C8	2.50	0.46
2:L5:2375:A:H2'	2:L5:2376:A:C8	2.50	0.46
2:L5:2406:G:N7	41:Ll:2:SER:N	2.63	0.46
2:L5:4069:U:H2'	2:L5:4070:U:C6	2.51	0.46
2:L5:4153:C:H2'	2:L5:4154:G:C8	2.50	0.46
2:L5:4475:G:O6	42:Lm:125:LYS:NZ	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:5004:C:H2'	2:L5:5005:G:O4'	2.15	0.46
13:LI:183:ASP:OD1	13:LI:184:MET:N	2.48	0.46
21:LR:103:ARG:HG2	21:LR:124:TYR:CE2	2.50	0.46
48:Lt:82:ILE:HG12	48:Lt:137:GLN:HG2	1.97	0.46
56:SS:124:ARG:NH1	82:S2:1521:C:OP2	2.45	0.46
63:Sg:283:PRO:O	63:Sg:285:GLN:NE2	2.48	0.46
64:SA:10:MET:HE3	64:SA:55:TRP:HB2	1.96	0.46
70:SI:89:GLU:OE1	70:SI:92:ARG:NH2	2.48	0.46
76:SW:52:ILE:HG12	76:SW:61:ILE:HG12	1.96	0.46
82:S2:436:OMG:H2'	82:S2:437:G:H8	1.79	0.46
82:S2:484:A2M:HM'3	82:S2:484:A2M:H1'	1.64	0.46
82:S2:1221:G:H2'	82:S2:1222:G:C8	2.49	0.46
82:S2:1657:G:H2'	82:S2:1658:G:C8	2.49	0.46
2:L5:6:C:H2'	2:L5:7:C:C6	2.50	0.46
2:L5:265:C:H1'	2:L5:266:C:H5''	1.98	0.46
2:L5:425:U:H2'	2:L5:426:A:C8	2.50	0.46
2:L5:702:U:H2'	2:L5:703:G:O4'	2.16	0.46
2:L5:959:G:C8	9:LE:123:ARG:HG2	2.50	0.46
2:L5:1558:A:H2'	2:L5:1559:G:C8	2.50	0.46
2:L5:2709:C:H5''	21:LR:43:LYS:HD2	1.97	0.46
2:L5:3946:G:N2	2:L5:4067:U:O2	2.48	0.46
2:L5:4622:A:H4'	6:LB:13:SER:HB2	1.97	0.46
4:L8:70:G:H1'	4:L8:88:A:H61	1.81	0.46
15:LL:127:PHE:HB2	37:Lh:118:LYS:HB3	1.96	0.46
79:Sa:13:LYS:HD3	79:Sa:13:LYS:HA	1.71	0.46
82:S2:1098:C:H2'	82:S2:1099:G:C8	2.50	0.46
82:S2:1805:G:H2'	82:S2:1806:A:H8	1.80	0.46
2:L5:208:A:N3	2:L5:232:G:O2'	2.46	0.46
2:L5:714:G:H2'	2:L5:715:G:C8	2.50	0.46
2:L5:746:A:H2'	2:L5:747:A:C8	2.51	0.46
2:L5:1410:U:H3	31:Lb:52:LYS:NZ	2.13	0.46
2:L5:3707:U:H2'	2:L5:3708:C:C6	2.51	0.46
2:L5:4196:OMG:HM23	2:L5:4196:OMG:H1'	1.76	0.46
2:L5:4616:A:H2'	2:L5:4617:G:O4'	2.15	0.46
2:L5:4723:A:H2'	2:L5:4724:A:C8	2.51	0.46
2:L5:4743:G:H2'	2:L5:4744:A:C8	2.50	0.46
3:L7:55:A:H4'	14:LJ:155:HIS:HB2	1.96	0.46
6:LB:289:GLN:HE22	6:LB:292:LEU:HD11	1.80	0.46
50:SF:185:SER:H	50:SF:190:ILE:HD11	1.80	0.46
62:Sf:124:ASP:OD1	62:Sf:124:ASP:N	2.45	0.46
65:SB:145:LYS:HB2	65:SB:145:LYS:HE3	1.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SE:122:LYS:N	67:SE:162:ILE:O	2.48	0.46
82:S2:116:OMU:HN3	82:S2:347:G:H1	1.63	0.46
82:S2:382:C:H2'	82:S2:383:G:C8	2.49	0.46
82:S2:807:G:H2'	82:S2:808:A:C8	2.50	0.46
82:S2:1749:G:H2'	82:S2:1750:C:C6	2.50	0.46
2:L5:10:A:H2'	2:L5:11:G:H8	1.81	0.46
2:L5:473:C:H2'	2:L5:474:C:C6	2.50	0.46
2:L5:1878:G:H2'	2:L5:1879:C:C6	2.50	0.46
2:L5:2412:A:H2'	2:L5:2413:U:C6	2.50	0.46
2:L5:2610:G:H2'	2:L5:2611:A:H8	1.80	0.46
2:L5:2787:A2M:HM'2	2:L5:2787:A2M:H1'	1.70	0.46
2:L5:4128:A:O2'	11:LG:33:GLU:O	2.27	0.46
2:L5:4208:U:H2'	2:L5:4209:G:C8	2.51	0.46
2:L5:4410:G:C6	2:L5:4433:G:C6	3.03	0.46
2:L5:4507:A:H2'	2:L5:4508:C:C6	2.51	0.46
2:L5:4704:C:H2'	2:L5:4705:A:C8	2.51	0.46
10:LF:241:ASN:O	10:LF:245:ARG:HG2	2.15	0.46
17:LN:46:ASP:OD1	17:LN:47:LYS:N	2.48	0.46
23:LT:44:GLY:HA2	23:LT:95:HIS:HB3	1.97	0.46
29:LZ:61:LYS:HE3	29:LZ:65:ARG:HD2	1.96	0.46
30:La:72:THR:HG22	30:La:110:LYS:HB3	1.97	0.46
32:Lc:48:LEU:O	32:Lc:74:TYR:N	2.46	0.46
35:Lf:25:THR:HB	35:Lf:87:LYS:HD3	1.97	0.46
56:SS:22:GLY:HA2	56:SS:56:ALA:HB3	1.97	0.46
58:SU:65:THR:O	58:SU:78:ASP:N	2.37	0.46
63:Sg:207:CYS:HB3	63:Sg:221:LEU:HD21	1.98	0.46
66:SC:207:ALA:HB2	82:S2:4:C:H4'	1.97	0.46
82:S2:835:C:H4'	82:S2:836:G:H8	1.80	0.46
82:S2:1562:C:H2'	82:S2:1563:G:C8	2.47	0.46
2:L5:88:A:OP1	20:LQ:172:ARG:NH2	2.46	0.46
2:L5:952:G:H2'	2:L5:953:C:C6	2.50	0.46
2:L5:962:C:H2'	2:L5:1702:C:H41	1.81	0.46
2:L5:1348:U:H2'	2:L5:1349:G:H8	1.79	0.46
2:L5:4524:G:H2'	2:L5:4525:C:C6	2.50	0.46
2:L5:4674:C:H2'	2:L5:4675:U:C6	2.51	0.46
12:LH:48:LEU:HD21	12:LH:56:ARG:HB2	1.96	0.46
29:LZ:50:PRO:HD3	29:LZ:68:ILE:HG12	1.97	0.46
44:Lo:6:LYS:HG3	44:Lo:94:GLY:HA3	1.98	0.46
54:SQ:15:ARG:HH22	82:S2:1444:U:P	2.39	0.46
56:SS:63:GLU:O	56:SS:67:VAL:HG23	2.16	0.46
62:Sf:130:VAL:HB	82:S2:1310:U:H5''	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SA:3:GLY:N	64:SA:56:GLU:OE1	2.48	0.46
64:SA:6:ASP:OD1	64:SA:6:ASP:N	2.48	0.46
82:S2:626:G:H5''	82:S2:627:OMU:H5'	1.97	0.46
82:S2:1380:C:H2'	82:S2:1381:G:C8	2.51	0.46
2:L5:713:C:H2'	2:L5:714:G:C8	2.50	0.46
2:L5:755:C:H2'	2:L5:756:G:H8	1.81	0.46
2:L5:964:A:H2'	2:L5:965:G:H4'	1.98	0.46
2:L5:966:A:H5''	2:L5:2092:G:H22	1.81	0.46
2:L5:1090:G:OP1	23:LT:142:ARG:NE	2.39	0.46
2:L5:1399:G:H2'	2:L5:1400:G:C8	2.50	0.46
2:L5:1541:C:H5''	5:LA:21:LYS:HG2	1.98	0.46
2:L5:1677:PSU:H4'	2:L5:1680:G:C2	2.50	0.46
2:L5:2284:G:OP1	30:La:7:LYS:NZ	2.41	0.46
2:L5:2823:G:H2'	2:L5:2824:OMC:C6	2.51	0.46
2:L5:4561:C:H2'	2:L5:4562:C:C6	2.50	0.46
2:L5:4601:U:OP2	2:L5:4609:G:N1	2.40	0.46
2:L5:4688:C:H2'	2:L5:4689:PSU:H6	1.80	0.46
2:L5:4764:A:OP1	22:LS:156:HIS:ND1	2.36	0.46
8:LD:234:ASP:OD1	8:LD:235:MET:N	2.49	0.46
15:LL:119:GLU:HG2	15:LL:123:LYS:HE2	1.96	0.46
17:LN:75:VAL:HG21	17:LN:80:THR:HG22	1.97	0.46
18:LO:108:ILE:HD12	18:LO:160:ARG:CZ	2.45	0.46
51:SK:80:ARG:HH22	51:SK:90:VAL:HG12	1.81	0.46
53:SP:39:ALA:N	82:S2:1613:G:OP2	2.49	0.46
69:SH:111:LYS:HE3	82:S2:796:G:N2	2.31	0.46
82:S2:293:C:O2'	82:S2:294:U:H3'	2.16	0.46
82:S2:656:G:H21	82:S2:663:C:H5''	1.80	0.46
82:S2:811:A:H2'	82:S2:812:A:H8	1.81	0.46
82:S2:945:U:H2'	82:S2:946:U:C6	2.51	0.46
82:S2:948:C:H2'	82:S2:949:G:H8	1.81	0.46
82:S2:1050:A:H62	82:S2:1068:G:H21	1.62	0.46
82:S2:1255:G:OP1	82:S2:1256:G:O2'	2.24	0.46
82:S2:1278:A:H2'	82:S2:1279:C:C6	2.51	0.46
82:S2:1628:C:H2'	82:S2:1629:C:C6	2.49	0.46
2:L5:50:C:C2	2:L5:51:A:C8	3.03	0.46
2:L5:284:G:H2'	2:L5:285:G:H8	1.80	0.46
2:L5:1089:G:H2'	2:L5:1090:G:H8	1.80	0.46
2:L5:2078:C:H2'	2:L5:2079:G:H8	1.81	0.46
2:L5:2580:U:OP1	29:LZ:36:ARG:NH1	2.34	0.46
2:L5:3660:C:P	5:LA:241:ARG:HH22	2.38	0.46
2:L5:5056:A:H2'	2:L5:5057:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L8:9:A:H2'	4:L8:10:G:H8	1.81	0.46
9:LE:150:LEU:HD11	9:LE:164:PHE:HB2	1.98	0.46
19:LP:19:GLY:HA3	19:LP:22:LEU:HD11	1.98	0.46
53:SP:122:THR:HG1	82:S2:1622:U:H3	1.64	0.46
63:Sg:37:ASP:OD1	63:Sg:39:THR:OG1	2.28	0.46
63:Sg:289:LEU:HD11	63:Sg:298:LEU:HD21	1.97	0.46
67:SE:160:ILE:HD12	67:SE:162:ILE:HD11	1.97	0.46
72:SL:68:ILE:HD13	72:SL:131:CYS:HB3	1.97	0.46
82:S2:1112:U:O2	82:S2:1121:G:O6	2.34	0.46
1:Pt:51:C:H2'	1:Pt:52:G:H8	1.81	0.46
2:L5:33:A:H3'	2:L5:47:A:H61	1.81	0.46
2:L5:88:A:N7	20:LQ:173:LYS:NZ	2.64	0.46
2:L5:1800:U:H2'	2:L5:1801:A:H8	1.80	0.46
2:L5:2394:G:O4'	2:L5:2397:G:N2	2.49	0.46
2:L5:2666:U:OP2	21:LR:124:TYR:OH	2.21	0.46
2:L5:3869:OMC:C2	86:L5:5293:SPM:H32	2.50	0.46
2:L5:3916:G:H2'	2:L5:3917:A:C8	2.51	0.46
2:L5:3917:A:H2'	2:L5:3918:G:C8	2.50	0.46
2:L5:4212:A:N6	2:L5:4219:A:OP2	2.46	0.46
2:L5:4261:C:OP1	14:LJ:19:LYS:NZ	2.45	0.46
2:L5:4742:G:H2'	2:L5:4743:G:C8	2.50	0.46
4:L8:5:U:H2'	4:L8:6:C:C6	2.50	0.46
21:LR:173:ARG:O	21:LR:176:ARG:NH1	2.49	0.46
24:LU:114:TYR:CD2	84:CI:50:MET:HG3	2.51	0.46
53:SP:128:HIS:CE1	82:S2:1521:C:H1'	2.51	0.46
67:SE:56:LEU:N	67:SE:60:GLU:OE1	2.37	0.46
73:SN:93:LYS:HA	73:SN:150:VAL:HG21	1.97	0.46
2:L5:209:U:OP1	28:LY:63:LYS:NZ	2.39	0.46
2:L5:460:C:H2'	2:L5:461:G:C8	2.49	0.46
2:L5:679:C:H2'	2:L5:680:G:C8	2.51	0.46
2:L5:978:G:H2'	2:L5:979:C:C6	2.51	0.46
2:L5:1494:U:H2'	2:L5:1495:G:C8	2.51	0.46
2:L5:1645:C:H2'	2:L5:1646:A:C8	2.50	0.46
2:L5:1725:U:H2'	2:L5:1726:U:H6	1.81	0.46
2:L5:1764:G:H4'	2:L5:1769:G:C6	2.51	0.46
2:L5:2376:A:H2'	2:L5:2377:C:C6	2.51	0.46
2:L5:2633:U:H2'	2:L5:2634:C:H6	1.81	0.46
2:L5:4156:G:H3'	2:L5:4157:A:H8	1.80	0.46
2:L5:4578:G:H2'	2:L5:4579:PSU:C6	2.50	0.46
3:L7:15:C:H2'	3:L7:16:A:C8	2.51	0.46
3:L7:58:A:H2'	3:L7:59:G:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LH:24:THR:HA	12:LH:37:ASP:HA	1.98	0.46
37:Lh:36:VAL:HG13	37:Lh:37:THR:HG23	1.97	0.46
46:Lr:16:PHE:HB3	46:Lr:27:THR:H	1.81	0.46
48:Lt:125:LEU:HG	48:Lt:127:GLY:H	1.81	0.46
65:SB:167:LYS:O	65:SB:171:ILE:HG12	2.15	0.46
66:SC:121:ARG:NH1	66:SC:123:ARG:HE	2.13	0.46
68:SG:13:GLN:NE2	82:S2:153:G:N3	2.59	0.46
70:SI:139:LYS:HB2	70:SI:139:LYS:HE2	1.69	0.46
78:SY:9:THR:H	82:S2:837:A:N6	2.14	0.46
82:S2:429:C:H2'	82:S2:430:C:C6	2.51	0.46
82:S2:525:A:H2'	82:S2:526:A:C8	2.50	0.46
82:S2:1392:U:H2'	82:S2:1393:G:C8	2.51	0.46
2:L5:10:A:H2'	2:L5:11:G:C8	2.51	0.46
2:L5:736:C:OP1	16:LM:74:ARG:NH2	2.41	0.46
2:L5:739:G:HO2'	2:L5:740:G:H8	1.62	0.46
2:L5:1290:G:H2'	2:L5:1291:G:C8	2.51	0.46
2:L5:3600:G:H2'	2:L5:3601:C:C6	2.51	0.46
2:L5:4128:A:H1'	11:LG:35:ARG:HB2	1.97	0.46
2:L5:5046:U:P	33:Ld:83:ARG:HH12	2.39	0.46
6:LB:286:LYS:HB2	6:LB:365:LEU:HD11	1.98	0.46
21:LR:44:LEU:HD22	21:LR:49:LEU:HD12	1.97	0.46
48:Lt:22:VAL:HA	48:Lt:48:LYS:HG2	1.96	0.46
57:ST:22:LEU:HD11	57:ST:28:LEU:HD21	1.98	0.46
64:SA:32:PHE:CG	82:S2:1097:G:H4'	2.51	0.46
69:SH:17:ASP:HB2	69:SH:20:GLU:HB2	1.98	0.46
82:S2:543:C:H3'	82:S2:544:G:C8	2.50	0.46
82:S2:824:C:H2'	82:S2:825:A:C8	2.51	0.46
82:S2:1606:G:O2'	82:S2:1632:G:N2	2.49	0.46
2:L5:666:G:N7	2:L5:668:C:N4	2.65	0.45
2:L5:1186:U:H3'	2:L5:1187:G:H21	1.81	0.45
2:L5:1278:C:H2'	2:L5:1279:A:O4'	2.16	0.45
2:L5:1942:A:H2'	2:L5:1943:A:H8	1.81	0.45
2:L5:3867:A2M:HM'3	2:L5:3867:A2M:H1'	1.59	0.45
2:L5:4981:G:O6	6:LB:21:ARG:NH2	2.48	0.45
8:LD:209:ARG:O	8:LD:213:GLU:HG2	2.16	0.45
11:LG:102:TYR:OH	11:LG:211:ASP:OD2	2.25	0.45
15:LL:56:ARG:NH1	15:LL:74:ARG:O	2.40	0.45
20:LQ:133:GLY:O	20:LQ:136:THR:OG1	2.26	0.45
54:SQ:90:LYS:HB3	54:SQ:90:LYS:HE2	1.79	0.45
58:SU:51:LYS:HD3	82:S2:1433:C:N4	2.31	0.45
58:SU:104:ILE:HB	58:SU:106:ILE:HG12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SE:89:VAL:HG11	67:SE:119:ALA:HB1	1.98	0.45
68:SG:52:ILE:HA	68:SG:111:LEU:HD23	1.98	0.45
72:SL:17:PHE:CG	82:S2:222:U:H5''	2.51	0.45
75:SV:40:ASP:OD1	75:SV:44:GLY:N	2.49	0.45
82:S2:43:U:OP2	82:S2:485:A:N6	2.38	0.45
82:S2:496:C:H2'	82:S2:497:C:H6	1.81	0.45
2:L5:67:C:H41	2:L5:325:U:HO2'	1.62	0.45
2:L5:1413:C:H2'	2:L5:1414:C:C6	2.51	0.45
2:L5:1563:A:OP1	82:S2:678:U:O2'	2.31	0.45
2:L5:1751:A:H2'	2:L5:1752:G:C8	2.50	0.45
2:L5:2041:A:H62	2:L5:4434:C:H1'	1.81	0.45
2:L5:2081:C:H2'	2:L5:2082:G:H8	1.80	0.45
2:L5:2281:U:H2'	2:L5:2282:A:H8	1.81	0.45
2:L5:2857:A:H2'	2:L5:2858:A:O4'	2.16	0.45
2:L5:3732:A:H2'	2:L5:3733:A:H8	1.81	0.45
2:L5:3911:C:H2'	2:L5:3912:U:H6	1.80	0.45
2:L5:4080:C:H2'	2:L5:4081:G:C8	2.51	0.45
2:L5:4986:G:H1'	6:LB:174:ARG:NH2	2.30	0.45
6:LB:147:GLU:OE2	6:LB:198:ARG:NH2	2.31	0.45
16:LM:118:MET:HG2	18:LO:192:TYR:CZ	2.52	0.45
24:LU:27:HIS:HB3	24:LU:114:TYR:HE1	1.82	0.45
26:LW:99:GLU:HB3	26:LW:102:LYS:HE3	1.97	0.45
27:LX:129:ARG:NH2	27:LX:131:ASP:OD2	2.49	0.45
28:LY:55:VAL:HG12	28:LY:106:ILE:HA	1.98	0.45
56:SS:89:ASP:OD1	56:SS:90:VAL:N	2.49	0.45
62:Sf:147:THR:OG1	82:S2:1292:C:O2'	2.27	0.45
70:SI:150:ASP:HA	70:SI:153:LYS:HG2	1.98	0.45
76:SW:2:VAL:N	82:S2:1091:C:O2'	2.42	0.45
82:S2:212:C:H2'	82:S2:213:G:C8	2.51	0.45
82:S2:897:U:H2'	82:S2:898:U:H4'	1.97	0.45
82:S2:1804:U:H2'	82:S2:1805:G:C8	2.51	0.45
2:L5:302:C:H2'	2:L5:303:C:H6	1.82	0.45
2:L5:418:A:H2'	2:L5:419:A:C8	2.50	0.45
2:L5:745:G:H2'	2:L5:746:A:C8	2.51	0.45
2:L5:749:G:C6	2:L5:912:G:C8	3.05	0.45
2:L5:1845:U:H2'	2:L5:1846:G:H8	1.82	0.45
2:L5:2328:G:H2'	2:L5:2329:U:C6	2.52	0.45
2:L5:2608:G:H2'	2:L5:2609:G:H8	1.81	0.45
2:L5:2621:A:H2'	2:L5:2622:G:C8	2.52	0.45
2:L5:2875:C:OP1	45:Lp:23:ARG:NH2	2.45	0.45
2:L5:4765:G:OP1	12:LH:23:ARG:NE	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SQ:113:ILE:HD13	54:SQ:113:ILE:HA	1.78	0.45
63:Sg:178:ASN:HB2	63:Sg:185:LYS:HD3	1.97	0.45
63:Sg:207:CYS:SG	63:Sg:219:TRP:HB2	2.56	0.45
69:SH:51:ILE:HD11	69:SH:176:VAL:HG12	1.99	0.45
72:SL:104:LYS:O	77:SX:11:ARG:NH2	2.46	0.45
82:S2:15:U:H2'	82:S2:16:G:O4'	2.17	0.45
82:S2:1501:C:H2'	82:S2:1502:C:H6	1.81	0.45
82:S2:1817:G:H2'	82:S2:1818:A:C8	2.51	0.45
82:S2:1850:MA6:H8	82:S2:1850:MA6:O5'	2.17	0.45
2:L5:221:C:H2'	2:L5:222:C:C6	2.52	0.45
2:L5:280:G:H5''	17:LN:14:LYS:HE2	1.99	0.45
2:L5:918:G:H5'	16:LM:72:TYR:CZ	2.51	0.45
2:L5:1393:G:O2'	2:L5:4352:U:OP1	2.33	0.45
2:L5:2438:A:OP1	27:LX:106:LYS:NZ	2.42	0.45
2:L5:4411:G:H2'	2:L5:4412:C:H6	1.82	0.45
2:L5:4590:A2M:H1'	2:L5:4590:A2M:HM'3	1.56	0.45
3:L7:19:C:H2'	3:L7:20:U:C6	2.52	0.45
13:LI:39:LYS:HE3	13:LI:39:LYS:HB2	1.75	0.45
16:LM:86:TRP:O	16:LM:89:THR:OG1	2.27	0.45
20:LQ:88:ASP:HB2	20:LQ:109:ALA:HB2	1.97	0.45
65:SB:23:ASP:N	65:SB:23:ASP:OD1	2.48	0.45
65:SB:146:ARG:HB2	65:SB:149:GLN:HB2	1.97	0.45
65:SB:229:MET:O	65:SB:233:GLY:N	2.32	0.45
66:SC:259:THR:HG23	75:SV:16:LYS:HZ3	1.82	0.45
68:SG:190:ARG:NH2	82:S2:334:C:OP2	2.42	0.45
69:SH:126:HIS:CE1	69:SH:181:THR:HG23	2.51	0.45
70:SI:126:GLY:O	70:SI:128:LYS:NZ	2.44	0.45
78:SY:108:LYS:NZ	82:S2:506:G:OP1	2.47	0.45
82:S2:864:A:H2'	82:S2:865:A:H8	1.82	0.45
82:S2:1244:PSU:H2'	82:S2:1245:G:C8	2.50	0.45
82:S2:1779:G:H2'	82:S2:1780:G:C8	2.51	0.45
2:L5:6:C:H2'	2:L5:7:C:H6	1.82	0.45
2:L5:28:C:P	17:LN:193:ARG:HH22	2.39	0.45
2:L5:1178:G:H2'	8:LD:286:SER:HB3	1.97	0.45
2:L5:2365:OMC:HM23	2:L5:2365:OMC:H1'	1.84	0.45
2:L5:2374:A:H2'	2:L5:2375:A:H8	1.81	0.45
2:L5:3667:C:H2'	2:L5:3668:C:H6	1.82	0.45
2:L5:4346:U:O2'	44:Lo:80:LYS:O	2.34	0.45
2:L5:4769:G:H2'	2:L5:4770:U:H6	1.82	0.45
2:L5:5036:C:H2'	2:L5:5037:U:C6	2.52	0.45
5:LA:7:GLY:HA2	5:LA:10:LYS:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LH:107:GLU:N	12:LH:107:GLU:OE1	2.49	0.45
27:LX:77:ILE:HD13	27:LX:100:VAL:HG12	1.98	0.45
50:SF:70:GLU:OE2	50:SF:86:LYS:NZ	2.32	0.45
53:SP:100:LYS:HD3	82:S2:1240:A:C8	2.50	0.45
54:SQ:16:LYS:NZ	82:S2:1648:G:O6	2.36	0.45
56:SS:62:ASP:OD1	56:SS:62:ASP:N	2.48	0.45
65:SB:147:ASN:OD1	65:SB:148:ASN:N	2.50	0.45
66:SC:169:TYR:OH	66:SC:175:GLY:O	2.24	0.45
67:SE:198:ARG:HA	67:SE:208:VAL:HA	1.98	0.45
74:SO:34:PHE:HB3	74:SO:41:PHE:HB2	1.99	0.45
82:S2:16:G:H2'	82:S2:17:C:C6	2.51	0.45
82:S2:57:U:O2'	82:S2:499:G:N3	2.48	0.45
82:S2:644:OMG:H2'	82:S2:645:C:C6	2.51	0.45
82:S2:1426:U:H2'	82:S2:1427:C:C6	2.51	0.45
82:S2:1844:U:H2'	82:S2:1845:A:C8	2.52	0.45
2:L5:318:A:H2'	2:L5:319:A:C8	2.50	0.45
2:L5:974:C:H5''	10:LF:43:ARG:NH1	2.31	0.45
2:L5:977:C:OP1	7:LC:333:LYS:NZ	2.41	0.45
2:L5:1290:G:H2'	2:L5:1291:G:H8	1.82	0.45
2:L5:1323:A2M:H2'	2:L5:1324:A:O4'	2.17	0.45
2:L5:2018:C:H2'	2:L5:2019:C:C6	2.52	0.45
2:L5:2279:A:O2'	34:Le:48:ARG:NH2	2.50	0.45
2:L5:2303:C:H5''	34:Le:104:SER:HB3	1.99	0.45
2:L5:2347:A:OP1	34:Le:22:ARG:NH2	2.32	0.45
2:L5:2634:C:H2'	2:L5:2635:U:H6	1.81	0.45
2:L5:2682:G:H2'	2:L5:2683:C:H6	1.81	0.45
2:L5:3872:A:H2'	2:L5:3873:G:H8	1.81	0.45
3:L7:60:G:H2'	3:L7:61:G:H8	1.81	0.45
10:LF:136:VAL:HG23	10:LF:140:ILE:HD13	1.99	0.45
13:LI:73:ASN:HB2	13:LI:87:MET:HE1	1.99	0.45
47:Ls:77:LYS:HE2	47:Ls:193:PHE:HE1	1.81	0.45
51:SK:31:LYS:HZ3	51:SK:39:ASN:N	2.14	0.45
52:SM:36:ARG:HB3	82:S2:1286:G:O6	2.16	0.45
64:SA:104:THR:O	64:SA:107:THR:OG1	2.34	0.45
82:S2:556:U:H3'	82:S2:557:U:H4'	1.99	0.45
82:S2:1101:U:H2'	82:S2:1102:G:C8	2.51	0.45
1:Pt:50:U:O4	1:Pt:64:G:O6	2.35	0.45
2:L5:1287:G:C2	9:LE:132:PRO:HG3	2.52	0.45
2:L5:1577:G:O2'	2:L5:1612:G:H4'	2.16	0.45
2:L5:1654:G:C6	2:L5:3914:U:H5''	2.52	0.45
2:L5:1759:G:H1	2:L5:1773:U:H3	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1979:A:H1'	2:L5:1988:G:N2	2.31	0.45
2:L5:2694:G:H5'	2:L5:2695:A:C2	2.51	0.45
2:L5:4113:U:H4'	2:L5:4115:G:C5	2.51	0.45
3:L7:2:U:H3	3:L7:117:G:H1	1.64	0.45
4:L8:140:C:H2'	4:L8:141:C:C6	2.51	0.45
6:LB:27:GLY:HA2	6:LB:276:HIS:CD2	2.52	0.45
6:LB:50:LYS:NZ	6:LB:337:VAL:O	2.44	0.45
6:LB:369:ASP:OD1	6:LB:373:LYS:NZ	2.46	0.45
7:LC:33:ARG:HG2	7:LC:36:ILE:HD12	1.99	0.45
9:LE:157:HIS:HA	9:LE:160:LYS:HE3	1.98	0.45
65:SB:63:LYS:HE2	65:SB:90:ASP:HA	1.98	0.45
68:SG:126:ASP:OD1	68:SG:126:ASP:N	2.47	0.45
77:SX:17:ARG:HH22	82:S2:659:G:N2	2.15	0.45
81:Se:41:ARG:HG3	81:Se:42:PHE:CD1	2.52	0.45
82:S2:1269:G:H2'	82:S2:1270:G:H8	1.81	0.45
82:S2:1279:C:H2'	82:S2:1280:G:C8	2.51	0.45
82:S2:1503:C:H2'	82:S2:1504:U:C6	2.52	0.45
2:L5:67:C:OP2	2:L5:312:G:N2	2.50	0.45
2:L5:310:G:H2'	2:L5:311:G:C8	2.52	0.45
2:L5:691:C:H2'	2:L5:692:A:H8	1.81	0.45
2:L5:1199:G:H2'	2:L5:1200:G:C8	2.51	0.45
2:L5:1621:A:H2'	2:L5:1622:U:C6	2.52	0.45
2:L5:2079:G:H2'	2:L5:2080:U:H6	1.82	0.45
2:L5:2394:G:O2'	2:L5:2819:U:O4	2.31	0.45
2:L5:2658:G:N2	2:L5:2676:A:OP2	2.49	0.45
2:L5:4153:C:H2'	2:L5:4154:G:H8	1.82	0.45
2:L5:4383:U:H2'	2:L5:4384:U:C6	2.52	0.45
2:L5:4691:A:H2'	2:L5:4692:A:O4'	2.15	0.45
89:L5:5297:HMT:C7	89:L5:5297:HMT:C9	2.94	0.45
7:LC:183:VAL:HA	7:LC:204:ARG:HB3	1.99	0.45
9:LE:186:LEU:N	9:LE:250:GLN:OE1	2.44	0.45
14:LJ:99:PHE:HB2	14:LJ:159:LYS:HE3	1.98	0.45
20:LQ:22:ASP:HB3	20:LQ:25:LEU:HB3	1.99	0.45
56:SS:75:ARG:NH1	56:SS:95:TYR:HB2	2.32	0.45
63:Sg:239:LEU:HD11	63:Sg:248:LEU:HD21	1.98	0.45
79:Sa:70:LYS:NZ	82:S2:988:C:OP2	2.50	0.45
82:S2:96:C:H2'	82:S2:97:U:H6	1.82	0.45
82:S2:652:U:H2'	82:S2:653:A:C8	2.52	0.45
82:S2:1680:G:H2'	82:S2:1681:U:C6	2.52	0.45
2:L5:499:G:H2'	2:L5:499:G:N3	2.32	0.45
2:L5:1296:G:H2'	2:L5:1297:U:H6	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1382:G:H2'	2:L5:1383:G:H8	1.81	0.45
2:L5:1490:G:H2'	2:L5:1491:A:H8	1.82	0.45
2:L5:1751:A:H2'	2:L5:1752:G:H8	1.80	0.45
2:L5:2568:C:H2'	2:L5:2569:G:H8	1.82	0.45
2:L5:2683:C:H2'	2:L5:2684:C:H6	1.81	0.45
2:L5:2800:G:H1'	39:Lj:9:GLY:HA3	1.98	0.45
3:L7:4:U:H2'	3:L7:5:A:C8	2.52	0.45
4:L8:138:C:H2'	4:L8:139:G:H8	1.82	0.45
6:LB:20:LYS:O	6:LB:275:HIS:ND1	2.49	0.45
13:LI:52:MET:HE3	13:LI:163:GLN:HG2	1.98	0.45
51:SK:64:TRP:CD2	61:Sd:23:VAL:HG22	2.52	0.45
56:SS:125:HIS:CD2	56:SS:131:VAL:HG11	2.52	0.45
66:SC:187:ARG:NH2	82:S2:1142:G:OP1	2.49	0.45
68:SG:192:ILE:HG22	68:SG:196:LYS:HE3	1.98	0.45
82:S2:919:A:O2'	82:S2:1020:A:N1	2.50	0.45
83:Zt:27:U:H2'	83:Zt:28:C:H6	1.82	0.45
2:L5:491:G:H2'	2:L5:492:U:H6	1.81	0.45
2:L5:980:U:H2'	2:L5:981:C:C6	2.52	0.45
2:L5:1567:U:H2'	2:L5:1568:C:H6	1.82	0.45
2:L5:1646:A:H2'	2:L5:1647:U:C6	2.52	0.45
2:L5:2063:G:H2'	2:L5:2064:G:H8	1.82	0.45
2:L5:2323:C:H2'	2:L5:2324:C:C6	2.52	0.45
2:L5:2555:G:H2'	2:L5:2556:G:C8	2.51	0.45
2:L5:3717:A:H2'	2:L5:3718:A2M:C8	2.46	0.45
2:L5:4589:A:N1	2:L5:4621:C:O2'	2.49	0.45
3:L7:107:G:H2'	3:L7:108:G:H8	1.82	0.45
46:Lr:38:PHE:O	46:Lr:45:HIS:NE2	2.33	0.45
47:Ls:58:ASN:C	47:Ls:62:ARG:HE	2.25	0.45
47:Ls:160:LEU:HD11	47:Ls:175:LEU:HD21	1.98	0.45
53:SP:37:TYR:HB3	53:SP:41:GLN:HB2	1.98	0.45
57:ST:39:LEU:HD23	57:ST:39:LEU:HA	1.75	0.45
58:SU:79:ARG:NH2	82:S2:1669:G:OP1	2.50	0.45
64:SA:54:THR:HG21	64:SA:163:CYS:HB3	1.99	0.45
66:SC:180:VAL:HG23	66:SC:197:PRO:HG3	1.99	0.45
80:Sb:68:GLY:C	82:S2:928:G:H21	2.25	0.45
82:S2:35:C:H2'	82:S2:36:U:C6	2.51	0.45
82:S2:212:C:H2'	82:S2:213:G:H8	1.82	0.45
82:S2:373:G:H2'	82:S2:374:G:H8	1.81	0.45
82:S2:1116:C:H2'	82:S2:1117:C:C6	2.52	0.45
82:S2:1208:A:H2'	82:S2:1209:A:C8	2.52	0.45
82:S2:1288:OMU:HN3	82:S2:1311:C:H42	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1720:U:H5''	82:S2:1721:U:H5''	1.98	0.45
82:S2:1736:G:H2'	82:S2:1737:G:H8	1.81	0.45
2:L5:44:A:N3	2:L5:94:A:H2	2.16	0.44
2:L5:162:A:H2'	2:L5:163:A:C8	2.52	0.44
2:L5:270:U:H2'	2:L5:271:C:H6	1.81	0.44
2:L5:1304:C:H2'	2:L5:1305:C:C6	2.52	0.44
2:L5:2649:G:H2'	2:L5:2650:G:C8	2.51	0.44
2:L5:3932:U:H2'	2:L5:3933:G:H8	1.82	0.44
2:L5:4452:U:H5'	89:L5:5297:HMT:H16	1.99	0.44
2:L5:4592:C:H2'	2:L5:4593:C:C6	2.51	0.44
2:L5:5053:U:H5'	2:L5:5054:C:C4	2.52	0.44
7:LC:268:ARG:HH12	7:LC:269:LYS:HE2	1.81	0.44
20:LQ:3:VAL:HG13	20:LQ:5:ILE:HG12	2.00	0.44
56:SS:64:VAL:O	56:SS:68:ILE:HG12	2.16	0.44
67:SE:122:LYS:HE2	67:SE:124:CYS:SG	2.57	0.44
69:SH:65:PRO:HB2	69:SH:67:PRO:HD2	1.99	0.44
82:S2:27:A2M:H1'	82:S2:27:A2M:HM'3	1.51	0.44
82:S2:51:U:H2'	82:S2:52:G:H8	1.82	0.44
82:S2:649:PSU:H2'	82:S2:650:A:C8	2.51	0.44
82:S2:668:A2M:HM'3	82:S2:668:A2M:H1'	1.55	0.44
82:S2:1407:U:H2'	82:S2:1408:U:H6	1.82	0.44
82:S2:1702:G:O6	82:S2:1836:G:N2	2.50	0.44
2:L5:90:G:OP2	2:L5:92:C:N4	2.41	0.44
2:L5:1566:C:H2'	2:L5:1567:U:H6	1.81	0.44
2:L5:2060:G:H4'	22:LS:118:ARG:HG3	1.99	0.44
2:L5:2413:U:H2'	2:L5:2414:G:H8	1.82	0.44
2:L5:3588:C:H2'	2:L5:3589:G:O4'	2.17	0.44
2:L5:3718:A2M:HM'3	2:L5:3718:A2M:H1'	1.57	0.44
2:L5:4210:U:H3	2:L5:4222:G:H1	1.65	0.44
2:L5:4299:PSU:H2'	2:L5:4300:U:C6	2.53	0.44
2:L5:4452:U:H5'	89:L5:5297:HMT:H7	1.98	0.44
11:LG:162:ASP:HB3	11:LG:163:PRO:HD3	1.99	0.44
16:LM:28:VAL:HB	16:LM:37:LEU:HB3	1.99	0.44
21:LR:47:ASP:HB3	84:CI:76:VAL:O	2.18	0.44
23:LT:144:ASN:HB2	23:LT:146:LYS:HE2	1.98	0.44
24:LU:22:THR:HA	24:LU:71:THR:HA	1.99	0.44
36:Lg:64:LEU:HD23	36:Lg:67:LEU:HD12	1.99	0.44
49:SD:142:LEU:HD13	49:SD:150:MET:HE2	1.99	0.44
69:SH:18:GLU:OE1	69:SH:18:GLU:N	2.50	0.44
82:S2:89:C:H2'	82:S2:90:G:H8	1.81	0.44
82:S2:352:U:H2'	82:S2:353:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:747:U:O2	82:S2:796:G:N2	2.51	0.44
82:S2:1242:U:H4'	82:S2:1243:U:H5''	1.99	0.44
2:L5:400:A2M:HM'3	2:L5:400:A2M:H1'	1.52	0.44
2:L5:1534:A2M:H8	2:L5:1637:A:H61	1.81	0.44
2:L5:1768:C:H42	2:L5:1772:C:H41	1.65	0.44
2:L5:2743:A:H2'	2:L5:2744:A:C8	2.52	0.44
2:L5:3708:C:H2'	2:L5:3709:U:C6	2.52	0.44
2:L5:3867:A2M:H2'	2:L5:3868:G:C8	2.53	0.44
2:L5:4345:C:H2'	2:L5:4346:U:H6	1.82	0.44
2:L5:4523:A2M:H1'	2:L5:4558:U:C4	2.51	0.44
2:L5:4913:G:H4'	2:L5:4914:C:O5'	2.17	0.44
2:L5:4929:C:OP1	16:LM:114:LYS:NZ	2.37	0.44
8:LD:156:GLY:HA2	8:LD:181:PRO:HG3	1.99	0.44
11:LG:261:LEU:HA	11:LG:264:LYS:HB3	1.99	0.44
20:LQ:178:ARG:N	30:La:51:GLY:HA2	2.31	0.44
48:Lt:12:VAL:HG11	48:Lt:65:GLN:H	1.82	0.44
63:Sg:183:LYS:HD2	63:Sg:183:LYS:HA	1.82	0.44
66:SC:252:THR:OG1	66:SC:254:ASP:OD1	2.29	0.44
66:SC:256:TRP:CD2	76:SW:68:ARG:HD3	2.52	0.44
77:SX:68:LYS:HG2	77:SX:91:LEU:HD22	1.99	0.44
82:S2:376:A:H2'	82:S2:377:G:O4'	2.18	0.44
82:S2:835:C:N3	82:S2:839:C:N4	2.65	0.44
2:L5:158:A:N1	2:L5:276:C:O2'	2.38	0.44
2:L5:189:G:H2'	2:L5:190:G:H8	1.83	0.44
2:L5:695:G:H3'	2:L5:696:C:H4'	1.99	0.44
2:L5:727:C:H2'	2:L5:728:U:C6	2.52	0.44
2:L5:1195:G:H2'	2:L5:1196:G:H8	1.82	0.44
2:L5:1519:C:H2'	2:L5:1520:C:H6	1.82	0.44
2:L5:1594:C:O2'	2:L5:1597:G:H1'	2.17	0.44
2:L5:2055:G:O5'	18:LO:130:LYS:NZ	2.47	0.44
2:L5:2631:U:O4	24:LU:51:GLY:N	2.51	0.44
2:L5:3687:A:O2'	5:LA:236:GLY:N	2.47	0.44
2:L5:4070:U:H2'	2:L5:4071:U:C6	2.53	0.44
2:L5:4082:G:H2'	2:L5:4083:U:C6	2.53	0.44
6:LB:240:LEU:HB2	6:LB:248:LEU:HA	2.00	0.44
12:LH:95:VAL:HG12	42:Lm:82:LEU:HD13	1.98	0.44
23:LT:102:ARG:O	23:LT:106:LEU:HG	2.17	0.44
30:La:30:GLY:O	30:La:40:HIS:NE2	2.38	0.44
54:SQ:137:ALA:N	82:S2:1650:A:OP1	2.51	0.44
65:SB:29:ASP:OD1	65:SB:29:ASP:N	2.50	0.44
67:SE:9:LEU:HB2	67:SE:30:ARG:HD3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SE:29:PRO:HA	82:S2:496:C:H5'	1.99	0.44
68:SG:7:PHE:HD2	68:SG:10:THR:HG22	1.81	0.44
69:SH:37:LYS:HA	69:SH:40:LEU:HB3	2.00	0.44
82:S2:1605:G:H2'	82:S2:1606:G:C4	2.53	0.44
83:Zt:9:A:O2'	83:Zt:45:G:N3	2.43	0.44
2:L5:717:U:H2'	2:L5:718:C:C6	2.53	0.44
2:L5:951:G:H2'	2:L5:952:G:C8	2.52	0.44
2:L5:982:U:OP1	9:LE:73:TYR:OH	2.20	0.44
2:L5:1332:C:H5''	34:Le:29:VAL:HB	1.97	0.44
2:L5:1637:A:OP1	2:L5:1640:C:N4	2.48	0.44
2:L5:2358:G:H2'	2:L5:2359:U:O4'	2.17	0.44
2:L5:2696:A:H62	40:Lk:35:LYS:NZ	2.15	0.44
2:L5:2699:C:H2'	2:L5:2700:G:C8	2.52	0.44
2:L5:2756:G:H2'	2:L5:2757:A:C8	2.52	0.44
2:L5:3758:U:H2'	2:L5:3765:G:N2	2.32	0.44
2:L5:3922[A]:G:H4'	2:L5:4183:G:H22	1.82	0.44
2:L5:4094:G:H1	2:L5:4114:C:H2'	1.83	0.44
2:L5:4111:U:H2'	2:L5:4112:C:C5	2.53	0.44
2:L5:4587:G:H5''	18:LO:61:ARG:HH12	1.82	0.44
4:L8:78:G:O2'	37:Lh:45:SER:OG	2.31	0.44
8:LD:41:LYS:HG3	23:LT:93:ILE:HG21	1.99	0.44
21:LR:174:GLU:HA	21:LR:177:LEU:HB2	2.00	0.44
30:La:110:LYS:HG3	30:La:128:PHE:HB2	2.00	0.44
47:Ls:47:LEU:HD23	47:Ls:53:VAL:HB	2.00	0.44
49:SD:146:ARG:NH1	82:S2:1489:A:N3	2.64	0.44
54:SQ:111:ILE:HD12	54:SQ:111:ILE:H	1.82	0.44
55:SR:6:THR:HA	82:S2:1373:C:H5'	1.99	0.44
55:SR:111:PHE:HE1	64:SA:12:GLU:HG3	1.83	0.44
57:ST:10:ASN:HB3	57:ST:13:GLU:OE2	2.17	0.44
61:Sd:54:LYS:NZ	82:S2:1482:C:OP1	2.50	0.44
67:SE:187:ALA:O	67:SE:245:ARG:NH1	2.43	0.44
82:S2:159:A2M:HM'3	82:S2:159:A2M:H1'	1.54	0.44
82:S2:354:OMU:HM23	82:S2:354:OMU:H1'	1.71	0.44
82:S2:509:OMG:H2'	82:S2:510:G:H8	1.82	0.44
82:S2:1004:PSU:H2'	82:S2:1005:G:C8	2.48	0.44
82:S2:1093:A:H2'	82:S2:1094:C:C6	2.52	0.44
82:S2:1597:C:H4'	82:S2:1603:G:O6	2.17	0.44
82:S2:1667:U:H2'	82:S2:1668:U:C6	2.53	0.44
83:Zt:67:U:H2'	83:Zt:68:C:H6	1.82	0.44
1:Pt:56:C:N4	44:Lo:104:ILE:HG21	2.33	0.44
2:L5:65:A:N6	2:L5:75:G:H1'	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:133:C:N4	2:L5:134:G:N3	2.66	0.44
2:L5:275:C:H2'	2:L5:276:C:C6	2.53	0.44
2:L5:684:G:H5''	9:LE:100:LYS:HE3	2.00	0.44
2:L5:1296:G:H2'	2:L5:1297:U:C6	2.53	0.44
2:L5:1705:G:OP1	2:L5:1705:G:N2	2.26	0.44
2:L5:1830:G:H2'	2:L5:1831:G:C8	2.53	0.44
2:L5:2087:C:P	7:LC:303:ARG:HH22	2.41	0.44
2:L5:2458:C:O2'	2:L5:3671:G:N3	2.44	0.44
2:L5:4220:6MZ:O2'	2:L5:4222:G:OP1	2.27	0.44
2:L5:4754:G:N1	2:L5:4880:C:N3	2.66	0.44
51:SK:90:VAL:HG21	51:SK:95:ARG:HB2	2.00	0.44
68:SG:170:ARG:NH1	82:S2:71:G:O6	2.50	0.44
70:SI:10:LYS:NZ	82:S2:370:G:O2'	2.51	0.44
76:SW:30:CYS:SG	76:SW:31:SER:N	2.90	0.44
77:SX:129:SER:HB2	82:S2:29:G:H4'	1.99	0.44
80:Sb:23:ARG:NH1	80:Sb:27:SER:O	2.51	0.44
82:S2:92:A:H61	82:S2:444:G:H1'	1.83	0.44
82:S2:1198:G:H2'	82:S2:1199:A:H8	1.82	0.44
82:S2:1345:G:OP1	82:S2:1688:C:O2'	2.35	0.44
82:S2:1405:A:H2'	82:S2:1406:G:O4'	2.17	0.44
82:S2:1744:G:HO2'	82:S2:1789:G:H22	1.60	0.44
82:S2:1856:C:H2'	82:S2:1857:G:C8	2.52	0.44
2:L5:161:G:H2'	2:L5:162:A:C8	2.53	0.44
2:L5:689:U:H2'	2:L5:690:C:C6	2.52	0.44
2:L5:700:G:H2'	2:L5:701:G:C8	2.53	0.44
2:L5:1908:A:H2'	2:L5:1909:G:O4'	2.18	0.44
2:L5:2351:OMC:HM23	2:L5:2351:OMC:H1'	1.71	0.44
2:L5:3607:U:H2'	2:L5:3608:A:H8	1.82	0.44
2:L5:3700:C:H2'	2:L5:3746:A:H61	1.83	0.44
2:L5:3765:G:O2'	2:L5:3767:C:N4	2.51	0.44
2:L5:3787:G:H1'	2:L5:3789:C:N4	2.31	0.44
2:L5:3825:A2M:H2'	2:L5:3826:C:C6	2.53	0.44
2:L5:3927:U:H2'	2:L5:3928:A:C8	2.52	0.44
2:L5:4454:G:H1	2:L5:4526:U:H3	1.65	0.44
2:L5:4523:A2M:H2'	2:L5:4559:A:N7	2.32	0.44
2:L5:4593:C:H2'	2:L5:4594:U:H6	1.83	0.44
2:L5:4667:C:H2'	2:L5:4668:U:O4'	2.18	0.44
4:L8:58:G:N7	39:Lj:63:ARG:NH2	2.49	0.44
22:LS:69:GLU:HG3	22:LS:71:SER:H	1.82	0.44
56:SS:61:GLU:HA	56:SS:64:VAL:HG12	1.99	0.44
59:SZ:48:VAL:HG23	59:SZ:80:ARG:HD2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SA:42:LYS:HD2	64:SA:48:ILE:HD11	1.99	0.44
76:SW:111:MET:HE3	76:SW:116:ALA:HA	1.99	0.44
78:SY:22:GLN:HB2	78:SY:72:PHE:CZ	2.53	0.44
82:S2:28:U:H2'	82:S2:29:G:C8	2.51	0.44
82:S2:106:C:H2'	82:S2:107:A:C8	2.43	0.44
82:S2:1736:G:H2'	82:S2:1737:G:C8	2.53	0.44
82:S2:1737:G:O6	82:S2:1797:U:O4	2.35	0.44
1:Pt:27:U:H2'	1:Pt:28:U:H6	1.83	0.44
2:L5:1716:G:H2'	2:L5:1717:C:C6	2.52	0.44
2:L5:1823:G:H2'	2:L5:1824:G:C8	2.52	0.44
2:L5:2041:A:N7	2:L5:4434:C:O2'	2.50	0.44
2:L5:2081:C:H2'	2:L5:2082:G:C8	2.53	0.44
2:L5:2283:G:H2'	2:L5:2284:G:H8	1.82	0.44
2:L5:2521:G:H2'	2:L5:2522:G:C8	2.53	0.44
2:L5:2699:C:H2'	2:L5:2700:G:H8	1.83	0.44
2:L5:3841:OMC:HM23	2:L5:3841:OMC:H1'	1.80	0.44
2:L5:3844:PSU:H2'	2:L5:3845:A:H8	1.82	0.44
2:L5:3937:C:O2'	17:LN:124:ASP:OD1	2.36	0.44
2:L5:4086:G:C8	27:LX:44:PRO:HG3	2.53	0.44
2:L5:4565:C:H2'	2:L5:4566:U:H6	1.81	0.44
2:L5:4637:OMG:HM23	2:L5:4637:OMG:H1'	1.72	0.44
2:L5:4685:U:H2'	2:L5:4686:G:H8	1.83	0.44
2:L5:5030:U:C2	2:L5:5031:G:C8	3.05	0.44
3:L7:58:A:H2'	3:L7:59:G:C8	2.53	0.44
4:L8:7:U:H2'	4:L8:8:U:C6	2.52	0.44
16:LM:96:GLU:O	16:LM:100:ARG:HG2	2.17	0.44
67:SE:38:LEU:HA	67:SE:41:CYS:SG	2.58	0.44
82:S2:696:G:H8	82:S2:733:C:H41	1.65	0.44
82:S2:1047:C:H2'	82:S2:1048:G:O4'	2.17	0.44
82:S2:1146:C:H2'	82:S2:1147:C:C6	2.52	0.44
82:S2:1198:G:H2'	82:S2:1199:A:C8	2.52	0.44
82:S2:1476:A:H4'	82:S2:1477:U:H5''	2.00	0.44
82:S2:1760:G:N1	82:S2:1774:C:OP1	2.51	0.44
2:L5:75:G:O2'	15:LL:101:ARG:NH1	2.38	0.44
2:L5:95:G:OP2	15:LL:11:LYS:NZ	2.51	0.44
2:L5:406:C:O2'	2:L5:407:A:OP1	2.33	0.44
2:L5:1334:A:H2'	2:L5:1335:G:C8	2.51	0.44
2:L5:1419:G:H5''	20:LQ:71:LYS:HZ2	1.82	0.44
2:L5:1569:U:H2'	2:L5:1570:G:H8	1.83	0.44
2:L5:1802:A:O2'	23:LT:108:ARG:NH2	2.51	0.44
2:L5:2632:PSU:H2'	2:L5:2633:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2649:G:H2'	2:L5:2650:G:H8	1.83	0.44
2:L5:2696:A:OP1	40:Lk:26:LYS:NZ	2.50	0.44
2:L5:2844:A:N6	2:L5:3839:G:O2'	2.51	0.44
2:L5:2884:G:H2'	2:L5:2885:A:C8	2.53	0.44
2:L5:2903:G:H1'	2:L5:2904:U:C5	2.53	0.44
2:L5:3611:A:H2	2:L5:5016:A:H8	1.66	0.44
2:L5:3736:A:H2'	2:L5:3737:A:C8	2.52	0.44
2:L5:4517:A:OP2	6:LB:2:SER:N	2.51	0.44
2:L5:4695:C:H2'	2:L5:4696:C:O4'	2.17	0.44
4:L8:90:C:H2'	4:L8:91:A:C8	2.53	0.44
6:LB:17:LEU:O	6:LB:19:ARG:N	2.50	0.44
9:LE:67:ALA:HA	9:LE:69:TYR:CE2	2.52	0.44
58:SU:38:ASP:OD1	58:SU:39:LEU:N	2.51	0.44
64:SA:42:LYS:HD3	64:SA:46:ILE:HB	2.00	0.44
67:SE:59:ASP:O	67:SE:63:LYS:HG3	2.18	0.44
69:SH:43:LEU:HB3	69:SH:72:PHE:CE1	2.53	0.44
69:SH:165:ASN:HA	69:SH:168:HIS:HE1	1.83	0.44
70:SI:141:ARG:HA	70:SI:141:ARG:CZ	2.48	0.44
74:SO:44:VAL:HG12	74:SO:53:ILE:HB	2.00	0.44
82:S2:526:A:H2'	82:S2:527:C:C6	2.53	0.44
82:S2:605:A:N3	82:S2:639:C:H1'	2.33	0.44
82:S2:1688:C:H2'	82:S2:1689:C:H6	1.81	0.44
82:S2:1700:C:O2	82:S2:1834:A:N6	2.50	0.44
2:L5:184:U:O2	2:L5:253:G:C2	2.71	0.43
2:L5:443:G:OP1	35:Lf:68:ARG:NH2	2.51	0.43
2:L5:457:G:H2'	2:L5:458:C:C6	2.53	0.43
2:L5:457:G:OP1	9:LE:115:TYR:HB3	2.17	0.43
2:L5:2063:G:H2'	2:L5:2064:G:C8	2.53	0.43
2:L5:2109:G:H2'	2:L5:2110:C:C6	2.52	0.43
2:L5:2250:C:H2'	2:L5:2251:G:C8	2.53	0.43
2:L5:2347:A:C4	34:Le:31:ILE:HD11	2.52	0.43
2:L5:2692:U:H2'	2:L5:2693:G:O4'	2.18	0.43
2:L5:4319:C:H2'	2:L5:4320:G:H8	1.82	0.43
2:L5:4402:C:N3	2:L5:4403:PSU:N1	2.65	0.43
2:L5:4617:G:OP1	6:LB:62:ARG:NH1	2.50	0.43
2:L5:4717:A:H4'	6:LB:20:LYS:HD3	2.00	0.43
6:LB:153:MET:HB3	6:LB:194:LEU:HD11	2.00	0.43
10:LF:238:ASP:O	10:LF:241:ASN:ND2	2.49	0.43
13:LI:205:PRO:HD2	13:LI:208:LYS:HE2	2.01	0.43
50:SF:140:ASP:OD1	50:SF:140:ASP:N	2.51	0.43
55:SR:24:LEU:HB2	55:SR:58:MET:HE1	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:ST:96:SER:HB3	57:ST:99:VAL:HB	1.99	0.43
59:SZ:106:GLN:HG3	59:SZ:108:ILE:HD11	2.00	0.43
62:Sf:107:LYS:NZ	62:Sf:108:VAL:O	2.45	0.43
63:Sg:251:ALA:HA	63:Sg:256:ILE:HD13	2.00	0.43
65:SB:33:VAL:HA	65:SB:96:CYS:HB2	2.00	0.43
65:SB:40:ASN:OD1	65:SB:41:ILE:HD12	2.18	0.43
66:SC:114:LYS:HD2	82:S2:1358:U:H5'	2.00	0.43
68:SG:56:ASN:HB2	68:SG:108:VAL:HG22	1.99	0.43
82:S2:644:OMG:HM23	82:S2:644:OMG:H1'	1.70	0.43
82:S2:688:U:H1'	82:S2:689:U:OP2	2.18	0.43
2:L5:715:G:OP1	7:LC:321:ASN:ND2	2.46	0.43
2:L5:919:C:OP1	16:LM:69:HIS:ND1	2.26	0.43
2:L5:1298:C:H2'	2:L5:1299:G:H8	1.82	0.43
2:L5:1354:A:H62	2:L5:1502:G:HO2'	1.62	0.43
2:L5:1503:A:H1'	2:L5:1504:G:C8	2.53	0.43
2:L5:1548:G:O2'	2:L5:2812:A:N3	2.47	0.43
2:L5:2102:G:N2	2:L5:2104:G:H1	2.15	0.43
2:L5:2389:A:H2'	2:L5:2390:G:C8	2.53	0.43
2:L5:2459:G:N2	2:L5:2462:C:OP2	2.45	0.43
2:L5:2861:OMC:HM23	2:L5:2861:OMC:H1'	1.70	0.43
2:L5:2877:G:H2'	2:L5:2878:G:O4'	2.18	0.43
2:L5:3619:G:H4'	21:LR:79:GLY:O	2.19	0.43
2:L5:3701:OMC:H4'	2:L5:3702:A:H5''	1.99	0.43
2:L5:3825:A2M:H1'	2:L5:3825:A2M:HM'3	1.51	0.43
2:L5:4174:U:H2'	2:L5:4175:G:C8	2.52	0.43
2:L5:4551:U:H2'	2:L5:4552:PSU:C6	2.53	0.43
5:LA:27:ALA:HB3	5:LA:128:ARG:HH22	1.82	0.43
6:LB:36:ASP:OD1	6:LB:36:ASP:N	2.50	0.43
11:LG:57:TRP:O	11:LG:62:ARG:NH1	2.51	0.43
14:LJ:52:LYS:HB3	14:LJ:65:ASN:HA	1.99	0.43
42:Lm:93:LYS:HD3	42:Lm:102:ARG:HG2	1.98	0.43
50:SF:142:SER:HB3	60:Sc:50:VAL:HG22	2.00	0.43
58:SU:61:LEU:HB2	58:SU:82:MET:HB3	2.00	0.43
64:SA:215:GLN:O	64:SA:219:GLU:HG2	2.17	0.43
70:SI:165:GLN:HB3	70:SI:171:LEU:HD23	2.00	0.43
72:SL:98:LYS:HD3	72:SL:99:TYR:CZ	2.53	0.43
74:SO:42:VAL:HG11	74:SO:78:ALA:HA	2.01	0.43
78:SY:105:LYS:O	78:SY:109:GLU:HG2	2.18	0.43
82:S2:323:C:H5'	82:S2:324:C:OP1	2.18	0.43
82:S2:563:G:O2'	82:S2:564:A:OP1	2.34	0.43
82:S2:944:A:H2'	82:S2:945:U:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1174:PSU:H2'	82:S2:1175:G:C8	2.51	0.43
82:S2:1846:G:H2'	82:S2:1847:G:C8	2.53	0.43
2:L5:907:C:H2'	2:L5:908:G:C8	2.53	0.43
2:L5:1095:A:H2	2:L5:1200:G:N1	2.09	0.43
2:L5:1281:G:C6	9:LE:128:HIS:HB2	2.53	0.43
2:L5:1358:G:OP1	7:LC:117:THR:N	2.39	0.43
2:L5:1468:C:H2'	2:L5:1469:C:H6	1.83	0.43
2:L5:1647:U:H5''	87:L5:5291:SPD:H72	1.99	0.43
2:L5:1850:A:N3	2:L5:2283:G:O2'	2.46	0.43
2:L5:2557:G:N2	2:L5:2570:U:O2	2.32	0.43
2:L5:2578:G:N7	29:LZ:17:ARG:NH2	2.62	0.43
2:L5:2831:G:H2'	2:L5:2832:A:H8	1.84	0.43
2:L5:3627:OMG:HM23	2:L5:3627:OMG:H1'	1.83	0.43
2:L5:3736:A:H2'	2:L5:3737:A:H8	1.83	0.43
2:L5:3788:C:N4	2:L5:3812:C:O4'	2.51	0.43
2:L5:3936:A:N6	2:L5:4175:G:O6	2.51	0.43
2:L5:3949:A:OP1	2:L5:4065:G:N2	2.52	0.43
2:L5:5062:G:H2'	2:L5:5063:G:H8	1.82	0.43
32:Lc:82:GLY:HA2	32:Lc:91:VAL:HG12	2.00	0.43
44:Lo:63:THR:O	44:Lo:87:ARG:NH1	2.51	0.43
57:ST:134:ILE:HA	57:ST:137:GLN:HG2	2.00	0.43
64:SA:140:VAL:HG13	64:SA:142:LEU:HB2	2.00	0.43
66:SC:202:THR:OG1	66:SC:221:ASP:HB3	2.18	0.43
66:SC:202:THR:HG1	66:SC:221:ASP:HB3	1.83	0.43
68:SG:31:ARG:HG3	68:SG:101:ILE:HG13	2.00	0.43
72:SL:126:VAL:HG12	72:SL:145:VAL:HG22	2.00	0.43
76:SW:125:ILE:HD12	76:SW:125:ILE:HA	1.85	0.43
78:SY:89:HIS:CE1	78:SY:90:ARG:HG3	2.53	0.43
82:S2:77:A:H2'	82:S2:78:C:C6	2.53	0.43
82:S2:102:A:H4'	82:S2:104:A:C8	2.53	0.43
82:S2:1189:A:H2'	82:S2:1190:A:H8	1.83	0.43
1:Pt:27:U:H2'	1:Pt:28:U:C6	2.53	0.43
2:L5:19:G:P	37:Lh:93:ARG:HE	2.42	0.43
2:L5:49:U:H2'	2:L5:50:C:H6	1.82	0.43
2:L5:126:C:H2'	2:L5:127:G:H8	1.84	0.43
2:L5:271:C:H2'	2:L5:272:U:H6	1.82	0.43
2:L5:2028:C:H2'	2:L5:2029:A:H8	1.83	0.43
2:L5:2436:U:H3'	27:LX:127:LEU:HD22	2.00	0.43
2:L5:2654:C:H2'	2:L5:2655:C:C6	2.53	0.43
2:L5:3722:G:H2'	2:L5:3723:A:C8	2.52	0.43
2:L5:3830:A2M:H1'	2:L5:3830:A2M:HM'3	1.63	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LE:99:ASP:OD1	9:LE:99:ASP:N	2.51	0.43
23:LT:112:ASN:HB3	23:LT:128:LEU:HD23	2.00	0.43
46:Lr:28:GLU:HG2	46:Lr:31:ASN:HB2	2.01	0.43
47:Ls:134:LYS:HD2	47:Ls:137:PHE:HE2	1.84	0.43
52:SM:28:HIS:CE1	52:SM:115:GLY:HA3	2.54	0.43
55:SR:128:PHE:CD2	55:SR:129:LYS:HG3	2.54	0.43
64:SA:164:ASN:OD1	64:SA:165:ASN:N	2.51	0.43
67:SE:202:PRO:HB2	72:SL:42:LEU:HD23	1.99	0.43
72:SL:128:VAL:HG12	72:SL:142:VAL:HA	2.00	0.43
73:SN:37:ILE:HG23	73:SN:50:ILE:HG21	2.00	0.43
80:Sb:49:HIS:ND1	80:Sb:69:GLY:O	2.51	0.43
82:S2:344:U:H2'	82:S2:345:U:C6	2.54	0.43
82:S2:512:A:H4'	82:S2:576:A2M:H2	2.00	0.43
82:S2:653:A:H2'	82:S2:654:A:O4'	2.18	0.43
82:S2:959:G:H1'	82:S2:964:A:H61	1.83	0.43
82:S2:1091:C:N4	82:S2:1092:G:O6	2.51	0.43
82:S2:1093:A:H2'	82:S2:1094:C:H6	1.82	0.43
2:L5:73:A:N6	15:LL:103:ARG:HH22	2.16	0.43
2:L5:227:A:N6	2:L5:242:U:O4'	2.51	0.43
2:L5:963:G:N2	10:LF:32:ARG:HH22	2.17	0.43
2:L5:1426:G:N1	2:L5:1458:C:OP2	2.46	0.43
2:L5:1875:C:H2'	2:L5:1876:U:C6	2.54	0.43
2:L5:2890:C:H2'	2:L5:2891:U:C6	2.53	0.43
2:L5:3609:G:H2'	2:L5:3610:A:H8	1.82	0.43
2:L5:4299:PSU:H2'	2:L5:4300:U:H6	1.84	0.43
2:L5:4305:G:O5'	23:LT:83:LYS:NZ	2.51	0.43
2:L5:4424:A:C4	2:L5:4425:G:C8	3.07	0.43
2:L5:4672:A:OP1	25:LV:17:SER:OG	2.33	0.43
7:LC:366:ASP:HB3	7:LC:368:LYS:HE2	2.01	0.43
55:SR:133:GLY:HA3	65:SB:152:LYS:HD3	1.99	0.43
64:SA:126:ASP:OD1	64:SA:165:ASN:ND2	2.51	0.43
64:SA:184:ARG:NE	64:SA:191:ARG:HD3	2.33	0.43
71:SJ:64:ASP:OD1	71:SJ:65:GLU:N	2.52	0.43
78:SY:104:ARG:HG2	78:SY:108:LYS:HE2	1.99	0.43
82:S2:207:G:H3'	82:S2:208:G:H8	1.82	0.43
82:S2:1215:C:H42	82:S2:1220:A:N6	2.16	0.43
82:S2:1269:G:H2'	82:S2:1270:G:C8	2.53	0.43
82:S2:1390:U:H2'	82:S2:1391:OMC:C6	2.53	0.43
82:S2:1531:A:H2'	82:S2:1532:C:C6	2.54	0.43
82:S2:1538:C:H2'	82:S2:1539:U:C6	2.53	0.43
82:S2:1540:G:H2'	82:S2:1541:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:Zt:26:A:N1	83:Zt:44:G:N2	2.54	0.43
2:L5:158:A:H5''	2:L5:159:C:H2'	2.00	0.43
2:L5:416:U:H2'	2:L5:417:G:O4'	2.19	0.43
2:L5:1617:G:H1'	2:L5:2513:A:N6	2.33	0.43
2:L5:1949:U:H2'	2:L5:1950:U:C6	2.53	0.43
2:L5:2323:C:H2'	2:L5:2324:C:H6	1.83	0.43
2:L5:2543:A:H2	2:L5:2773:G:H22	1.66	0.43
2:L5:4244:A:H2'	2:L5:4245:G:O4'	2.18	0.43
2:L5:4619:U:H2'	2:L5:4620:OMU:H6	2.00	0.43
2:L5:4972:PSU:H2'	2:L5:4973:PSU:C6	2.53	0.43
10:LF:113:ARG:NH1	10:LF:208:LEU:O	2.39	0.43
13:LI:101:LYS:NZ	13:LI:102:MET:O	2.48	0.43
15:LL:123:LYS:HA	37:Lh:122:LYS:HE3	2.00	0.43
18:LO:54:TYR:OH	18:LO:73:PHE:O	2.36	0.43
29:LZ:84:ARG:NH2	36:Lg:102:ILE:HG21	2.33	0.43
36:Lg:33:LEU:HD23	36:Lg:33:LEU:HA	1.88	0.43
66:SC:270:THR:HA	66:SC:273:LEU:HB2	1.99	0.43
70:SI:36:THR:HG22	70:SI:96:LEU:HD12	2.01	0.43
70:SI:47:ARG:HH22	82:S2:446:G:P	2.41	0.43
71:SJ:179:LYS:HA	71:SJ:182:GLN:HG3	2.01	0.43
79:Sa:3:LYS:HA	82:S2:1861:G:H5''	2.01	0.43
82:S2:52:G:H2'	82:S2:53:C:H6	1.83	0.43
82:S2:811:A:H2'	82:S2:812:A:C8	2.53	0.43
82:S2:1177:PSU:H2'	82:S2:1178:U:C6	2.53	0.43
82:S2:1373:C:H2'	82:S2:1374:C:H6	1.83	0.43
83:Zt:75:C:H3'	83:Zt:76:A:C8	2.53	0.43
2:L5:138:G:H2'	2:L5:139:G:H8	1.82	0.43
2:L5:318:A:H2'	2:L5:319:A:H8	1.83	0.43
2:L5:711:A:H2'	2:L5:712:C:C6	2.54	0.43
2:L5:908:G:H2'	2:L5:909:A:H8	1.83	0.43
2:L5:909:A:H2'	2:L5:910:G:H8	1.83	0.43
2:L5:2683:C:H2'	2:L5:2684:C:C6	2.53	0.43
2:L5:4503:A:H2'	2:L5:4504:C:C6	2.53	0.43
2:L5:4636:PSU:N1	33:Ld:79:ASN:OD1	2.51	0.43
2:L5:4736:C:H4'	2:L5:5068:G:C4	2.53	0.43
2:L5:4927:G:H5''	2:L5:4928:C:H5	1.83	0.43
4:L8:140:C:H2'	4:L8:141:C:H6	1.83	0.43
9:LE:168:LEU:HD11	9:LE:174:LEU:HB2	2.00	0.43
11:LG:105:GLU:OE2	11:LG:113:ARG:NH1	2.52	0.43
16:LM:6:PHE:H	16:LM:11:ARG:NH2	2.16	0.43
51:SK:5:LYS:O	51:SK:8:ARG:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SP:95:GLY:HA2	53:SP:104:GLN:HA	1.99	0.43
56:SS:28:PHE:O	56:SS:31:THR:OG1	2.30	0.43
58:SU:31:SER:O	58:SU:34:LYS:HG3	2.18	0.43
64:SA:81:ASN:ND2	64:SA:204:TYR:OH	2.51	0.43
64:SA:220:LYS:HA	64:SA:220:LYS:HD3	1.81	0.43
66:SC:66:LEU:HD21	66:SC:88:ILE:HD13	2.00	0.43
70:SI:44:HIS:ND1	82:S2:1740:C:OP1	2.41	0.43
72:SL:112:HIS:HB3	72:SL:141:ASN:OD1	2.19	0.43
82:S2:174:OMC:HM23	82:S2:174:OMC:H1'	1.82	0.43
83:Zt:2:C:H2'	83:Zt:3:C:C6	2.53	0.43
2:L5:303:C:OP2	17:LN:68:ARG:NH2	2.38	0.43
2:L5:674:G:H2'	2:L5:675:C:C6	2.53	0.43
2:L5:1341:U:H2'	2:L5:1342:A:C8	2.54	0.43
2:L5:1567:U:H2'	2:L5:1568:C:C6	2.53	0.43
2:L5:1656:U:H2'	2:L5:1657:G:H8	1.84	0.43
2:L5:1952:G:OP1	22:LS:139:ARG:NE	2.52	0.43
2:L5:2368:A:N6	2:L5:2827:G:O2'	2.51	0.43
2:L5:2407:G:H2'	41:L1:13:LEU:HD22	2.01	0.43
2:L5:2674:A:C6	45:Lp:42:CYS:HA	2.54	0.43
2:L5:3896:C:O2'	6:LB:268:ARG:NH2	2.49	0.43
2:L5:3951:G:H1'	2:L5:4062:A:H61	1.83	0.43
2:L5:4291:G:H5'	2:L5:4293:PSU:C6	2.54	0.43
2:L5:4600:G:N2	2:L5:4601:U:O4	2.52	0.43
4:L8:28:C:H2'	4:L8:29:G:C8	2.54	0.43
6:LB:117:ARG:HG2	6:LB:180:LEU:HD12	2.01	0.43
8:LD:95:TYR:HA	8:LD:158:LYS:HG2	2.00	0.43
24:LU:35:ASP:OD1	24:LU:35:ASP:N	2.51	0.43
49:SD:223:ILE:HD11	63:Sg:189:ILE:HD12	2.01	0.43
50:SF:185:SER:O	50:SF:185:SER:OG	2.36	0.43
67:SE:136:ILE:HD12	67:SE:149:TYR:CE1	2.54	0.43
67:SE:212:ASP:OD1	67:SE:216:ASN:N	2.51	0.43
77:SX:32:LEU:HD12	77:SX:32:LEU:HA	1.88	0.43
82:S2:1226:G:N1	82:S2:1639:G7M:OP2	2.46	0.43
82:S2:1711:U:H2'	82:S2:1712:A:C8	2.54	0.43
2:L5:755:C:H2'	2:L5:756:G:C8	2.54	0.43
2:L5:1317:U:H2'	2:L5:1318:C:C6	2.54	0.43
2:L5:2634:C:H2'	2:L5:2635:U:C6	2.54	0.43
2:L5:2642:A:C2	40:Lk:2:PRO:HD2	2.54	0.43
2:L5:2695:A:H1'	2:L5:2697:A:N7	2.34	0.43
2:L5:3659:G:H2'	2:L5:3660:C:C6	2.54	0.43
2:L5:3932:U:H2'	2:L5:3933:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:4277:G:H2'	2:L5:4278:C:C6	2.53	0.43
2:L5:4579:PSU:H2'	2:L5:4580:U:C6	2.54	0.43
2:L5:4761:G:N2	2:L5:4766:C:O3'	2.52	0.43
2:L5:4910:G:N1	18:LO:108:ILE:O	2.52	0.43
21:LR:139:MET:HG2	21:LR:143:HIS:CE1	2.54	0.43
49:SD:106:ARG:HG3	49:SD:175:VAL:HG22	2.01	0.43
49:SD:211:VAL:O	55:SR:20:TYR:OH	2.29	0.43
51:SK:61:GLN:HB3	51:SK:68:TYR:HB2	2.00	0.43
54:SQ:110:ASP:CG	54:SQ:111:ILE:HD12	2.44	0.43
57:ST:23:LYS:HD3	57:ST:51:ASN:HD22	1.84	0.43
57:ST:104:LEU:HD22	57:ST:121:ARG:HD2	2.01	0.43
67:SE:45:ILE:HD12	67:SE:80:ILE:HD11	2.00	0.43
75:SV:42:VAL:HG23	75:SV:43:THR:HG23	1.99	0.43
82:S2:107:A:H61	82:S2:354:OMU:C4	2.32	0.43
82:S2:496:C:H2'	82:S2:497:C:C6	2.53	0.43
82:S2:1204:A:H2'	82:S2:1205:C:C6	2.53	0.43
82:S2:1558:C:H2'	82:S2:1559:C:C6	2.53	0.43
2:L5:396:A:H2'	2:L5:397:G:C8	2.54	0.43
2:L5:455:C:O2'	2:L5:456:C:H5'	2.18	0.43
2:L5:1960:A:C8	47:Ls:63:LYS:HE2	2.53	0.43
2:L5:1996:C:N4	2:L5:2000:G:N2	2.39	0.43
2:L5:2090:U:H4'	2:L5:2091:C:H3'	2.01	0.43
2:L5:2744:A:H2'	2:L5:2745:A:C8	2.54	0.43
2:L5:2837:OMU:HM23	2:L5:2837:OMU:H1'	1.86	0.43
2:L5:3721:U:H2'	2:L5:3722:G:H8	1.84	0.43
2:L5:3754:G:O6	2:L5:3771:C:N4	2.51	0.43
2:L5:3927:U:H2'	2:L5:3928:A:H8	1.83	0.43
2:L5:4883:C:H2'	2:L5:4884:G:C8	2.54	0.43
2:L5:4921:C:H2'	2:L5:4922:C:H6	1.84	0.43
4:L8:26:C:O2'	7:LC:53:ALA:O	2.35	0.43
12:LH:63:ASN:O	12:LH:67:LEU:HG	2.18	0.43
23:LT:68:THR:OG1	23:LT:71:ALA:O	2.35	0.43
54:SQ:96:TYR:HA	54:SQ:100:VAL:HG12	2.01	0.43
56:SS:35:GLY:HA2	82:S2:1630:A:O2'	2.19	0.43
56:SS:102:GLY:HA2	56:SS:105:ASN:HD21	1.84	0.43
65:SB:167:LYS:HB2	65:SB:167:LYS:HE2	1.87	0.43
69:SH:76:GLN:O	69:SH:80:VAL:HG23	2.19	0.43
82:S2:160:U:O2'	82:S2:162:C:O5'	2.36	0.43
82:S2:386:C:H2'	82:S2:387:C:C6	2.53	0.43
82:S2:609:U:H2'	82:S2:610:G:H8	1.84	0.43
82:S2:1010:G:H2'	82:S2:1011:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1025:U:H2'	82:S2:1026:C:O4'	2.19	0.43
2:L5:233:U:O2'	2:L5:234:G:H8	2.02	0.42
2:L5:474:C:H2'	2:L5:475:G:H8	1.84	0.42
2:L5:2689:C:H2'	2:L5:2690:C:C6	2.53	0.42
2:L5:3911:C:H2'	2:L5:3912:U:C6	2.54	0.42
2:L5:4186:A:H2'	2:L5:4187:G:H8	1.84	0.42
2:L5:4934:A:H2'	2:L5:4935:C:C6	2.53	0.42
4:L8:95:A:N3	37:Lh:63:GLN:NE2	2.66	0.42
21:LR:80:LYS:HA	21:LR:80:LYS:HD2	1.82	0.42
26:LW:5:LEU:HD12	26:LW:30:GLN:NE2	2.34	0.42
35:Lf:45:LYS:HA	35:Lf:107:PRO:HD2	2.01	0.42
47:Ls:62:ARG:HB3	47:Ls:66:ARG:NH1	2.32	0.42
63:Sg:131:LEU:O	63:Sg:139:LYS:N	2.51	0.42
67:SE:75:LYS:NZ	82:S2:122:G:OP1	2.39	0.42
82:S2:12:U:H2'	82:S2:13:C:C6	2.53	0.42
82:S2:12:U:H2'	82:S2:13:C:H6	1.83	0.42
82:S2:181:A:OP2	82:S2:182:C:O2'	2.33	0.42
82:S2:1347:U:H3'	82:S2:1348:G:H21	1.84	0.42
2:L5:85:G:H1'	2:L5:86:U:H5	1.84	0.42
2:L5:325:U:P	38:Li:28:ARG:HH22	2.42	0.42
2:L5:480:C:H2'	2:L5:481:G:C8	2.54	0.42
2:L5:705:G:H2'	2:L5:706:C:C6	2.54	0.42
2:L5:1662:C:H2'	2:L5:1663:C:C6	2.54	0.42
2:L5:1662:C:H2'	2:L5:1663:C:H6	1.84	0.42
2:L5:1976:G:H22	48:Lt:139:VAL:HG11	1.83	0.42
2:L5:2039:G:OP2	2:L5:2040:A:O2'	2.35	0.42
2:L5:3716:C:H3'	2:L5:3735:G:H22	1.85	0.42
2:L5:4589:A:OP2	87:L5:5290:SPD:N10	2.52	0.42
2:L5:4592:C:H2'	2:L5:4593:C:H6	1.85	0.42
2:L5:4601:U:H2'	2:L5:4602:A:C8	2.48	0.42
2:L5:4672:A:OP1	25:LV:15:ARG:NH2	2.47	0.42
2:L5:4716:C:H5''	6:LB:276:HIS:O	2.20	0.42
6:LB:302:ASN:HB2	6:LB:313:SER:HA	2.02	0.42
12:LH:92:MET:HG2	12:LH:181:VAL:HG22	2.00	0.42
13:LI:93:PRO:HB2	13:LI:125:THR:HB	2.00	0.42
17:LN:115:VAL:HA	17:LN:134:LEU:HD13	2.01	0.42
32:Lc:30:GLY:O	32:Lc:34:THR:OG1	2.29	0.42
41:Ll:24:PRO:HD2	41:Ll:27:ILE:HG13	2.01	0.42
48:Lt:134:GLY:HA3	48:Lt:152:ILE:HD11	2.01	0.42
56:SS:1:MET:SD	56:SS:1:MET:N	2.91	0.42
69:SH:37:LYS:HD2	69:SH:40:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:484:A2M:H8	82:S2:484:A2M:O5'	2.19	0.42
82:S2:698:G:H2'	82:S2:733:C:C4	2.54	0.42
2:L5:188:G:O2'	2:L5:190:G:OP2	2.32	0.42
2:L5:217:C:OP2	2:L5:219:G:O2'	2.23	0.42
2:L5:408:A:O2'	2:L5:411:G:OP2	2.27	0.42
2:L5:972:C:C6	9:LE:126:LEU:HD13	2.55	0.42
2:L5:1273:G:C5	9:LE:73:TYR:HB2	2.54	0.42
2:L5:1307:A:H2'	2:L5:1308:C:C6	2.53	0.42
2:L5:1519:C:H2'	2:L5:1520:C:C6	2.54	0.42
2:L5:2098:G:H2'	2:L5:2099:G:C8	2.54	0.42
2:L5:2811:G:N2	2:L5:2813:A:H3'	2.33	0.42
2:L5:3920:PSU:H2'	2:L5:3921:U:C6	2.54	0.42
2:L5:4896:G:H2'	2:L5:4897:G:H8	1.83	0.42
8:LD:205:ALA:HB1	8:LD:233:PRO:HB3	2.00	0.42
13:LI:51:HIS:CD2	13:LI:168:SER:HB3	2.53	0.42
25:LV:36:ASN:ND2	25:LV:67:LYS:HG2	2.34	0.42
37:Lh:107:GLN:O	37:Lh:111:GLU:HG3	2.19	0.42
47:Ls:91:THR:HG21	47:Ls:98:ILE:HG13	2.01	0.42
55:SR:32:LYS:NZ	82:S2:1452:A:OP2	2.53	0.42
57:ST:9:VAL:O	57:ST:11:GLN:NE2	2.52	0.42
74:SO:80:ASP:O	74:SO:83:GLN:HG3	2.19	0.42
82:S2:573:U:H1'	82:S2:576:A2M:N7	2.33	0.42
82:S2:943:U:H2'	82:S2:944:A:H8	1.83	0.42
82:S2:1605:G:H1'	82:S2:1634:A:H61	1.85	0.42
82:S2:1803:U:H2'	82:S2:1804:U:C6	2.54	0.42
83:Zt:51:G:H2'	83:Zt:52:G:H8	1.84	0.42
1:Pt:58:A:O2'	1:Pt:60:A:OP2	2.28	0.42
2:L5:269:G:H2'	2:L5:270:U:C6	2.54	0.42
2:L5:1084:C:H2'	2:L5:1085:C:H6	1.84	0.42
2:L5:1516:G:O2'	15:LL:18:TRP:NE1	2.53	0.42
2:L5:1574:G:OP2	21:LR:92:LYS:NZ	2.49	0.42
2:L5:2540:C:H5''	36:Lg:65:MET:HE3	2.02	0.42
2:L5:2616:C:C2	2:L5:2722:G:N2	2.87	0.42
2:L5:2804:OMC:H2'	2:L5:2805:C:H6	1.85	0.42
2:L5:4159:C:H2'	2:L5:4160:C:C6	2.55	0.42
4:L8:129:C:H2'	4:L8:130:C:H6	1.85	0.42
17:LN:116:LEU:HD22	17:LN:135:ILE:HD11	2.01	0.42
26:LW:81:ALA:HB2	26:LW:87:LEU:HG	2.01	0.42
41:Ll:23:ILE:HD11	41:Ll:28:ARG:HE	1.84	0.42
42:Lm:99:CYS:HB3	42:Lm:115:CYS:HB3	2.00	0.42
45:Lp:49:ARG:HG3	45:Lp:55:TRP:CE2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Lr:8:MET:HE3	46:Lr:8:MET:HB3	1.83	0.42
61:Sd:3:HIS:CE1	61:Sd:5:GLN:HB2	2.54	0.42
66:SC:102:LEU:HD22	66:SC:130:ILE:HD12	2.01	0.42
71:SJ:18:ARG:HH22	82:S2:4:C:H1'	1.85	0.42
74:SO:39:ASP:N	74:SO:69:SER:HB3	2.33	0.42
82:S2:14:C:H2'	82:S2:15:U:C6	2.53	0.42
82:S2:115:U:H2'	82:S2:116:OMU:C6	2.49	0.42
82:S2:651:PSU:H2'	82:S2:652:U:C6	2.54	0.42
82:S2:656:G:H5'	82:S2:662:G:N2	2.35	0.42
82:S2:813:A:H2'	82:S2:814:PSU:O4'	2.19	0.42
82:S2:874:G:H2'	82:S2:875:A:C8	2.49	0.42
82:S2:1031:A2M:H2'	82:S2:1032:C:O4'	2.19	0.42
82:S2:1414:A:H2'	82:S2:1415:C:C6	2.55	0.42
82:S2:1428:G:N1	82:S2:1585:U:O4'	2.53	0.42
82:S2:1511:U:H2'	82:S2:1512:C:C6	2.54	0.42
82:S2:1533:A:H2	82:S2:1536:G:N3	2.17	0.42
83:Zt:43:A:H3'	83:Zt:44:G:H8	1.84	0.42
2:L5:197:A:H2'	2:L5:198:A:C8	2.55	0.42
2:L5:325:U:H2'	2:L5:326:C:H6	1.84	0.42
2:L5:1186:U:H2'	2:L5:1187:G:N3	2.34	0.42
2:L5:1207:C:H2'	2:L5:1208:G:C8	2.53	0.42
2:L5:1357:C:O2'	7:LC:114:ARG:NH2	2.45	0.42
2:L5:1703:C:O2'	2:L5:1704:C:O5'	2.33	0.42
2:L5:1981:G:N1	2:L5:1982:G:O6	2.53	0.42
2:L5:2353:U:H2'	2:L5:2354:G:C8	2.54	0.42
2:L5:2730:U:H2'	2:L5:2731:C:C6	2.55	0.42
2:L5:3825:A2M:H2'	2:L5:3826:C:H6	1.84	0.42
2:L5:4300:U:H2'	2:L5:4301:U:C6	2.55	0.42
3:L7:57:C:H2'	3:L7:58:A:C8	2.54	0.42
5:LA:131:GLY:H	5:LA:169:VAL:HG13	1.84	0.42
6:LB:17:LEU:HD23	6:LB:17:LEU:HA	1.89	0.42
13:LI:36:LEU:HD13	13:LI:87:MET:HE3	2.01	0.42
14:LJ:19:LYS:HD3	14:LJ:75:ARG:HH12	1.84	0.42
28:LY:67:ILE:HD12	28:LY:107:THR:HG21	2.01	0.42
32:Lc:78:ASN:OD1	32:Lc:78:ASN:N	2.52	0.42
36:Lg:44:SER:OG	36:Lg:46:CYS:SG	2.60	0.42
54:SQ:34:VAL:HG22	54:SQ:70:VAL:HB	2.02	0.42
55:SR:34:VAL:O	55:SR:38:ILE:HG12	2.20	0.42
71:SJ:39:ASN:HB2	82:S2:642:U:P	2.59	0.42
72:SL:22:ARG:NH1	72:SL:23:VAL:O	2.52	0.42
82:S2:16:G:H5'	82:S2:669:A:H61	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:342:C:H2'	82:S2:343:A:H8	1.84	0.42
82:S2:976:G:H2'	82:S2:977:C:C6	2.54	0.42
82:S2:1018:U:H2'	82:S2:1019:C:C6	2.54	0.42
82:S2:1351:G:O2'	82:S2:1378:A:N1	2.46	0.42
82:S2:1373:C:H2'	82:S2:1374:C:C6	2.53	0.42
82:S2:1733:U:H2'	82:S2:1734:G:O4'	2.19	0.42
82:S2:1803:U:H2'	82:S2:1804:U:H6	1.84	0.42
1:Pt:33:U:H3'	54:SQ:146:ARG:NH2	2.34	0.42
2:L5:73:A:H62	15:LL:103:ARG:HH22	1.68	0.42
2:L5:279:A:H5''	17:LN:47:LYS:NZ	2.35	0.42
2:L5:728:U:OP1	10:LF:76:ARG:NH2	2.46	0.42
2:L5:920:C:H2'	2:L5:921:C:C6	2.54	0.42
2:L5:1273:G:C6	9:LE:73:TYR:HB2	2.54	0.42
2:L5:1368:A:H2'	2:L5:1369:C:O4'	2.20	0.42
2:L5:1717:C:H2'	2:L5:1718:C:C4	2.55	0.42
2:L5:1811:G:H2'	2:L5:1812:C:C6	2.54	0.42
2:L5:2581:A:H1'	2:L5:2654:C:O2'	2.20	0.42
2:L5:2749:C:H2'	2:L5:2750:G:H8	1.84	0.42
2:L5:4208:U:P	23:LT:6:GLY:HA3	2.59	0.42
2:L5:4237:C:O3'	2:L5:4326:G:N2	2.53	0.42
2:L5:4262:C:H2'	2:L5:4263:C:H6	1.84	0.42
2:L5:4947:U:H2'	2:L5:4948:C:C6	2.54	0.42
2:L5:4969:C:H2'	2:L5:4970:C:H6	1.83	0.42
2:L5:4970:C:C2	2:L5:4971:A:C8	3.08	0.42
4:L8:26:C:H2'	4:L8:27:U:C6	2.55	0.42
6:LB:154:LYS:HE2	6:LB:154:LYS:HB2	1.75	0.42
7:LC:221:PHE:O	7:LC:222:ARG:HG2	2.19	0.42
9:LE:223:ARG:HH22	9:LE:238:GLU:HG3	1.85	0.42
12:LH:93:ARG:HG2	12:LH:182:SER:HB3	2.02	0.42
16:LM:62:LEU:HD21	16:LM:82:ILE:HD11	2.00	0.42
16:LM:86:TRP:CE2	16:LM:92:ALA:HB2	2.54	0.42
30:La:76:ASP:OD1	30:La:77:LYS:N	2.52	0.42
35:Lf:36:ARG:O	35:Lf:39:THR:OG1	2.27	0.42
49:SD:77:PHE:HB2	49:SD:79:PHE:CE1	2.55	0.42
51:SK:80:ARG:NH2	51:SK:89:ILE:O	2.38	0.42
53:SP:56:LEU:HD22	53:SP:80:LEU:HD11	2.01	0.42
74:SO:55:ARG:NH1	82:S2:953:C:O2	2.42	0.42
82:S2:468:A2M:H2'	82:S2:469:A:H8	1.81	0.42
82:S2:900:C:H5'	82:S2:901:G:N7	2.34	0.42
82:S2:1031:A2M:H1'	82:S2:1031:A2M:HM'3	1.81	0.42
2:L5:66:A:N6	2:L5:282:C:O2'	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:139:G:H2'	2:L5:140:G:C8	2.55	0.42
2:L5:286:U:H2'	2:L5:287:U:C6	2.54	0.42
2:L5:1187:G:OP2	2:L5:1187:G:N2	2.44	0.42
2:L5:1298:C:H2'	2:L5:1299:G:C8	2.55	0.42
2:L5:1566:C:H2'	2:L5:1567:U:C6	2.54	0.42
2:L5:1721:G:H2'	2:L5:1722:C:C6	2.55	0.42
2:L5:1749:A:H2'	2:L5:1750:G:C8	2.55	0.42
2:L5:2374:A:H2'	2:L5:2375:A:C8	2.55	0.42
2:L5:2539:C:H2'	2:L5:2540:C:H6	1.82	0.42
2:L5:2891:U:H2'	2:L5:2892:C:O4'	2.20	0.42
2:L5:3825:A2M:H2'	2:L5:3826:C:O4'	2.20	0.42
2:L5:3938:G:P	17:LN:24:ARG:HE	2.43	0.42
2:L5:3946:G:H2'	2:L5:3947:A:H5''	2.02	0.42
2:L5:4175:G:H2'	2:L5:4176:C:C6	2.55	0.42
2:L5:4313:A:H2'	2:L5:4314:C:O4'	2.19	0.42
2:L5:5018:C:H2'	2:L5:5019:A:H8	1.85	0.42
7:LC:279:LEU:HD23	7:LC:279:LEU:HA	1.89	0.42
9:LE:264:ILE:HD11	9:LE:267:LEU:HD22	2.02	0.42
10:LF:222:LYS:N	10:LF:232:ASP:OD1	2.41	0.42
16:LM:130:LEU:HB3	18:LO:177:LEU:HD11	2.01	0.42
21:LR:7:GLN:NE2	21:LR:35:ALA:O	2.41	0.42
29:LZ:135:ARG:HA	29:LZ:135:ARG:HD2	1.88	0.42
35:Lf:29:LYS:HG3	35:Lf:83:MET:HE1	2.00	0.42
47:Ls:57:LYS:O	47:Ls:61:MET:HG2	2.20	0.42
49:SD:204:LEU:HB2	49:SD:207:HIS:HB2	2.02	0.42
57:ST:72:VAL:O	57:ST:76:THR:HG23	2.19	0.42
59:SZ:99:LEU:HD11	59:SZ:102:LYS:HB2	2.02	0.42
67:SE:36:HIS:CG	67:SE:85:GLY:HA3	2.54	0.42
68:SG:137:ARG:NE	82:S2:171:A:OP1	2.51	0.42
76:SW:19:LYS:NZ	82:S2:1152:U:O3'	2.53	0.42
77:SX:105:PHE:CE2	77:SX:112:VAL:HB	2.54	0.42
82:S2:867:OMG:H1'	82:S2:867:OMG:HM23	1.83	0.42
82:S2:888:U:O2'	82:S2:898:U:N3	2.52	0.42
82:S2:902:G:O2'	82:S2:903:A:O4'	2.37	0.42
2:L5:4:G:H2'	2:L5:5:A:H8	1.85	0.42
2:L5:20:U:H3'	2:L5:21:G:C8	2.55	0.42
2:L5:1340:OMC:H2'	2:L5:1341:U:C6	2.55	0.42
2:L5:1342:A:H2'	2:L5:1343:A:C8	2.55	0.42
2:L5:1352:C:O2'	2:L5:1356:U:OP1	2.37	0.42
2:L5:1552:G:O2'	2:L5:1574:G:N2	2.52	0.42
2:L5:1580:C:H2'	2:L5:1581:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1666:C:H2'	2:L5:1667:G:O4'	2.19	0.42
2:L5:1846:G:H2'	2:L5:1847:C:C6	2.54	0.42
2:L5:2018:C:H2'	2:L5:2019:C:H6	1.84	0.42
2:L5:2397:G:C8	2:L5:2399:G:C8	3.08	0.42
2:L5:3605:C:OP2	21:LR:71:ARG:NE	2.52	0.42
2:L5:3923:A:H2'	2:L5:3924:C:C6	2.55	0.42
2:L5:4113:U:H4'	2:L5:4115:G:C4	2.54	0.42
2:L5:4551:U:H2'	2:L5:4552:PSU:H6	1.84	0.42
2:L5:4621:C:H2'	2:L5:4622:A:C8	2.55	0.42
2:L5:4736:C:H2'	2:L5:4737:G:C8	2.54	0.42
2:L5:5044:A:H2'	2:L5:5045:G:H8	1.85	0.42
3:L7:33:U:H2'	3:L7:34:C:C6	2.55	0.42
8:LD:206:ASP:HA	8:LD:209:ARG:HG2	2.01	0.42
11:LG:148:GLU:OE2	17:LN:6:TYR:OH	2.29	0.42
12:LH:4:ILE:HG12	12:LH:61:TRP:CH2	2.55	0.42
15:LL:110:LEU:O	15:LL:114:VAL:HG13	2.20	0.42
20:LQ:59:PRO:HG3	20:LQ:143:ARG:HA	2.02	0.42
39:Lj:27:TYR:HA	39:Lj:34:CYS:HA	2.02	0.42
52:SM:52:LEU:HD11	52:SM:62:VAL:HG12	2.01	0.42
56:SS:15:VAL:HG13	56:SS:68:ILE:HD11	2.01	0.42
65:SB:89:GLU:OE2	65:SB:99:ASN:HB3	2.20	0.42
68:SG:14:LYS:HG2	68:SG:124:LEU:HD12	2.02	0.42
68:SG:38:ALA:HB2	68:SG:50:VAL:HG12	2.02	0.42
71:SJ:59:GLU:O	71:SJ:62:THR:OG1	2.37	0.42
79:Sa:8:ASN:ND2	82:S2:1861:G:OP1	2.52	0.42
82:S2:21:U:H2'	82:S2:22:A:H8	1.84	0.42
82:S2:602:G:OP2	82:S2:603:C:O2'	2.30	0.42
82:S2:666:U:H2'	82:S2:667:U:C6	2.54	0.42
82:S2:1215:C:O2'	82:S2:1645:C:OP2	2.30	0.42
82:S2:1539:U:H2'	82:S2:1540:G:H8	1.83	0.42
82:S2:1749:G:H2'	82:S2:1750:C:H6	1.85	0.42
83:Zt:44:G:H3'	83:Zt:45:G:C8	2.55	0.42
2:L5:28:C:OP1	17:LN:187:SER:OG	2.27	0.42
2:L5:44:A:H5''	86:L5:5265:SPM:H81	2.02	0.42
2:L5:288:G:H2'	2:L5:289:C:C6	2.55	0.42
2:L5:423:G:H2'	2:L5:424:U:C6	2.55	0.42
2:L5:1926:C:H2'	2:L5:1927:U:C6	2.55	0.42
2:L5:3715:U:H2'	2:L5:3716:C:O4'	2.19	0.42
2:L5:4208:U:OP1	2:L5:4334:U:O2'	2.26	0.42
2:L5:4705:A:H2'	2:L5:4706:G:O4'	2.20	0.42
2:L5:4748:U:H3	2:L5:4952:G:H1	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:4926:C:H5''	2:L5:4927:G:H21	1.83	0.42
2:L5:4935:C:H2'	2:L5:4936:G:C8	2.54	0.42
4:L8:27:U:H2'	4:L8:28:C:C6	2.54	0.42
20:LQ:32:TYR:HD2	20:LQ:51:LEU:HD11	1.85	0.42
23:LT:127:GLN:NE2	23:LT:129:LYS:O	2.49	0.42
34:Le:19:LYS:HE3	34:Le:19:LYS:HB3	1.87	0.42
36:Lg:60:ARG:HD2	36:Lg:60:ARG:HA	1.79	0.42
44:Lo:74:GLU:HB3	44:Lo:77:CYS:HB3	2.02	0.42
65:SB:94:LYS:HA	65:SB:94:LYS:HD2	1.82	0.42
68:SG:136:LYS:N	82:S2:170:A:OP1	2.43	0.42
72:SL:120:VAL:HG22	72:SL:145:VAL:HG11	2.02	0.42
72:SL:153:LYS:HD3	72:SL:153:LYS:HA	1.82	0.42
82:S2:647:U:H2'	82:S2:648:A:H8	1.85	0.42
82:S2:944:A:H2'	82:S2:945:U:C6	2.55	0.42
82:S2:1129:G:H2'	82:S2:1130:G:N3	2.35	0.42
82:S2:1303:C:H2'	82:S2:1304:U:C6	2.55	0.42
84:CI:63:ARG:HD2	84:CI:63:ARG:HA	1.85	0.42
2:L5:935:A:O2'	16:LM:44:GLN:O	2.29	0.42
2:L5:1495:G:H4'	20:LQ:187:LYS:HE3	2.01	0.42
2:L5:1998:A:O2'	2:L5:2019:C:O2'	2.23	0.42
2:L5:2111:G:N2	2:L5:2252:G:O4'	2.53	0.42
2:L5:2508:U:H2'	2:L5:2509:C:H6	1.85	0.42
2:L5:2558:C:H2'	2:L5:2559:G:C8	2.55	0.42
2:L5:2632:PSU:H2'	2:L5:2633:U:H6	1.85	0.42
2:L5:2682:G:H2'	2:L5:2683:C:C6	2.55	0.42
2:L5:3832:U:H2'	2:L5:3833:C:H6	1.84	0.42
2:L5:3833:C:H2'	2:L5:3834:C:H6	1.85	0.42
2:L5:3852:A:N7	2:L5:3853:PSU:N1	2.67	0.42
2:L5:4177:C:H2'	2:L5:4178:A:C8	2.51	0.42
2:L5:4524:G:N3	6:LB:252:ALA:HB1	2.35	0.42
2:L5:4708:A:N3	2:L5:4709:U:H5'	2.35	0.42
2:L5:4770:U:H2'	2:L5:4771:C:C6	2.55	0.42
2:L5:5047:C:O2'	2:L5:5050:C:OP2	2.28	0.42
4:L8:75:OMG:H2'	4:L8:76:C:C6	2.54	0.42
5:LA:101:VAL:HG22	5:LA:165:VAL:HG22	2.02	0.42
7:LC:266:THR:N	7:LC:269:LYS:O	2.51	0.42
11:LG:114:LEU:HD23	11:LG:114:LEU:HA	1.92	0.42
32:Lc:50:ASN:ND2	32:Lc:76:GLY:O	2.53	0.42
48:Lt:12:VAL:HG11	48:Lt:65:GLN:N	2.35	0.42
54:SQ:11:GLN:OE1	54:SQ:71:ARG:NH2	2.44	0.42
63:Sg:205:SER:C	63:Sg:221:LEU:HD23	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SG:162:LEU:O	68:SG:167:LYS:NZ	2.51	0.42
70:SI:45:THR:HG23	70:SI:53:LYS:HG3	2.02	0.42
77:SX:28:LYS:O	77:SX:32:LEU:HB2	2.19	0.42
82:S2:845:G:H2'	82:S2:846:G:C8	2.55	0.42
82:S2:1139:C:H2'	82:S2:1140:G:O4'	2.20	0.42
82:S2:1384:C:C2	82:S2:1385:G:C8	3.07	0.42
82:S2:1435:C:O2'	82:S2:1436:C:O4'	2.35	0.42
82:S2:1740:C:H2'	82:S2:1741:U:C6	2.54	0.42
82:S2:1777:G:H2'	82:S2:1778:C:C6	2.52	0.42
2:L5:239:C:H5'	28:LY:33:PRO:HD3	2.02	0.41
2:L5:325:U:O5'	38:Li:28:ARG:NH2	2.53	0.41
2:L5:387:G:HO2'	2:L5:412:G:H1	1.66	0.41
2:L5:1403:G:N2	2:L5:1415:G:C4	2.88	0.41
2:L5:1460:C:H2'	2:L5:1461:C:H6	1.84	0.41
2:L5:1672:U:H2'	2:L5:1673:U:C6	2.55	0.41
2:L5:1701:A:C2	2:L5:1702:C:H5	2.38	0.41
2:L5:4291:G:H8	2:L5:4328:G:H2'	1.85	0.41
2:L5:4340:U:H3	88:L5:5296:3HE:C11	2.32	0.41
2:L5:4392:OMG:N2	2:L5:4395:U:O2	2.49	0.41
2:L5:4761:G:H2'	2:L5:4762:A:C8	2.55	0.41
86:L5:5293:SPM:H31	86:L5:5293:SPM:H62	1.82	0.41
4:L8:28:C:H2'	4:L8:29:G:H8	1.84	0.41
13:LI:48:LEU:HB2	13:LI:142:LEU:HA	2.01	0.41
16:LM:38:VAL:HG21	16:LM:50:MET:HB3	2.02	0.41
18:LO:149:TYR:O	18:LO:153:THR:OG1	2.27	0.41
21:LR:167:LYS:HB3	21:LR:167:LYS:HE2	1.80	0.41
22:LS:113:MET:HE3	22:LS:113:MET:HB3	1.86	0.41
34:Le:91:CYS:HB3	34:Le:95:TYR:HD2	1.85	0.41
38:Li:99:LYS:HE2	38:Li:99:LYS:HB2	1.77	0.41
52:SM:19:GLN:O	52:SM:22:LEU:HG	2.19	0.41
60:Sc:44:ARG:NH2	60:Sc:63:ARG:HH11	2.18	0.41
70:SI:83:TYR:HB3	70:SI:101:ILE:HD11	2.02	0.41
78:SY:4:THR:H	78:SY:32:LYS:HZ3	1.67	0.41
78:SY:42:GLU:HA	78:SY:52:PRO:HB3	2.02	0.41
82:S2:14:C:O2	82:S2:668:A2M:H2	2.19	0.41
82:S2:509:OMG:HM23	82:S2:509:OMG:H1'	1.77	0.41
82:S2:1324:G:O6	82:S2:1504:U:O4	2.37	0.41
1:Pt:8:U:O2'	1:Pt:21:A:N1	2.45	0.41
2:L5:362:A:N6	41:Ll:37:TYR:O	2.49	0.41
2:L5:480:C:H2'	2:L5:481:G:H8	1.86	0.41
2:L5:737:C:C5	2:L5:739:G:H5''	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1389:U:OP1	2:L5:1497:A:O2'	2.24	0.41
2:L5:1857:C:H2'	2:L5:1858:A:H8	1.85	0.41
2:L5:2300:A:N7	7:LC:143:ARG:NH1	2.68	0.41
2:L5:2306:G:N2	2:L5:2331:G:O2'	2.52	0.41
2:L5:2364:OMG:HM23	2:L5:2364:OMG:H1'	1.90	0.41
2:L5:2415:U:H2'	2:L5:2416:G:C8	2.55	0.41
2:L5:2544:G:N1	4:L8:124:U:OP1	2.54	0.41
2:L5:3871:A:H2'	2:L5:3872:A:C8	2.55	0.41
2:L5:5064:G:N2	19:LP:75:GLN:HE22	2.18	0.41
3:L7:7:G:H5''	8:LD:22:ARG:HD3	2.01	0.41
4:L8:66:A:H2'	4:L8:67:U:C6	2.55	0.41
6:LB:66:LYS:HB2	25:LV:14:PHE:CE2	2.55	0.41
6:LB:303:ALA:HB3	6:LB:312:LYS:HG3	2.03	0.41
23:LT:50:LYS:HB3	23:LT:50:LYS:HE2	1.80	0.41
27:LX:65:ALA:HB2	37:Lh:69:LEU:HD11	2.02	0.41
48:Lt:147:HIS:HA	48:Lt:148:PRO:HD3	1.89	0.41
51:SK:4:PRO:HD2	51:SK:7:ASN:HD21	1.85	0.41
58:SU:75:LYS:NZ	82:S2:1252:C:OP1	2.46	0.41
67:SE:137:PRO:HG3	68:SG:209:TYR:CZ	2.55	0.41
67:SE:252:ARG:O	67:SE:256:LEU:HG	2.19	0.41
70:SI:116:HIS:O	70:SI:152:ARG:NH2	2.40	0.41
71:SJ:41:ARG:N	82:S2:642:U:OP1	2.52	0.41
72:SL:94:HIS:O	72:SL:103:GLU:N	2.53	0.41
74:SO:71:PRO:HB3	74:SO:114:SER:OG	2.20	0.41
82:S2:445:A:H2'	82:S2:446:G:C8	2.56	0.41
82:S2:1037:G:H4'	82:S2:1845:A:H4'	2.02	0.41
82:S2:1079:C:H4'	82:S2:1182:A:H61	1.85	0.41
82:S2:1614:A:H2'	82:S2:1615:U:C6	2.54	0.41
82:S2:1839:U:H2'	82:S2:1840:U:C6	2.54	0.41
83:Zt:2:C:H2'	83:Zt:3:C:H6	1.85	0.41
2:L5:301:G:H2'	2:L5:302:C:C6	2.55	0.41
2:L5:678:C:H2'	2:L5:679:C:C6	2.55	0.41
2:L5:1210:C:OP1	10:LF:70:ARG:HD3	2.20	0.41
2:L5:1404:G:N7	2:L5:1408:G:N1	2.68	0.41
2:L5:1570:G:O6	45:Lp:2:ALA:N	2.54	0.41
2:L5:2308:A:OP1	34:Le:101:HIS:NE2	2.54	0.41
2:L5:4195:G:O2'	2:L5:4442:PSU:OP1	2.21	0.41
4:L8:67:U:OP1	39:Lj:87:LYS:HG2	2.20	0.41
7:LC:10:VAL:O	7:LC:18:SER:OG	2.30	0.41
7:LC:133:LEU:HD23	7:LC:133:LEU:HA	1.94	0.41
29:LZ:12:LEU:HB2	29:LZ:81:MET:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SF:112:LEU:HD13	50:SF:177:LEU:HD21	2.01	0.41
53:SP:25:LEU:HA	53:SP:28:MET:HB2	2.01	0.41
55:SR:7:LYS:HG3	82:S2:1373:C:OP1	2.20	0.41
56:SS:135:HIS:ND1	82:S2:1232:PSU:OP2	2.53	0.41
61:Sd:14:PHE:HB2	82:S2:1661:A:H8	1.85	0.41
67:SE:100:ARG:NH2	67:SE:118:GLU:OE2	2.53	0.41
70:SI:31:ARG:NE	82:S2:380:G:OP1	2.39	0.41
79:Sa:44:ILE:HG21	79:Sa:65:PRO:HD2	2.01	0.41
82:S2:207:G:H3'	82:S2:208:G:C8	2.55	0.41
82:S2:441:C:H2'	82:S2:442:C:C6	2.55	0.41
82:S2:1062:A:H2'	82:S2:1063:C:C6	2.56	0.41
82:S2:1240:A:H2'	82:S2:1241:A:C8	2.56	0.41
82:S2:1294:G:H3'	82:S2:1295:A:H8	1.86	0.41
82:S2:1337:4AC:O5'	82:S2:1337:4AC:H6	2.20	0.41
82:S2:1518:C:H5''	82:S2:1519:U:H5''	2.03	0.41
82:S2:1805:G:H2'	82:S2:1806:A:C8	2.55	0.41
2:L5:342:G:H2'	2:L5:343:C:C6	2.55	0.41
2:L5:491:G:H2'	2:L5:492:U:C6	2.55	0.41
2:L5:679:C:H2'	2:L5:680:G:H8	1.85	0.41
2:L5:1175:A:H2	2:L5:1185:G:H22	1.69	0.41
2:L5:1625:OMG:P	86:L5:5268:SPM:HN5	2.43	0.41
2:L5:1730:U:H1'	23:LT:101:SER:HB3	2.01	0.41
2:L5:2324:C:H2'	2:L5:2325:C:C6	2.55	0.41
2:L5:2378:G:N2	2:L5:2381:A:OP2	2.53	0.41
2:L5:2864:A:H2'	2:L5:2865:U:C6	2.55	0.41
2:L5:3796:U:H2'	2:L5:3797:C:C6	2.54	0.41
2:L5:4071:U:H2'	2:L5:4072:C:H6	1.86	0.41
2:L5:4620:OMU:H1'	2:L5:4620:OMU:HM23	1.84	0.41
2:L5:4960:G:H2'	2:L5:4961:G:C8	2.55	0.41
2:L5:5006:U:H4'	2:L5:5007:A:H5'	2.02	0.41
4:L8:82:A:N7	4:L8:84:A:H3'	2.35	0.41
26:LW:94:ARG:HA	26:LW:101:ARG:NH2	2.35	0.41
49:SD:29:LEU:HD22	49:SD:58:VAL:HG23	2.02	0.41
49:SD:163:PRO:HA	49:SD:166:TYR:CZ	2.55	0.41
63:Sg:163:PRO:HB2	63:Sg:179:LEU:HB2	2.01	0.41
69:SH:30:LEU:O	69:SH:33:ASN:ND2	2.53	0.41
71:SJ:147:PHE:CE1	82:S2:824:C:H5'	2.55	0.41
72:SL:131:CYS:SG	72:SL:141:ASN:ND2	2.94	0.41
81:Se:32:ALA:HB2	82:S2:525:A:H5''	2.03	0.41
82:S2:458:A:H2'	82:S2:459:C:H6	1.85	0.41
82:S2:544:G:H2'	82:S2:545:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:601:OMG:HM23	82:S2:601:OMG:H1'	1.87	0.41
82:S2:610:G:C6	82:S2:634:A:C6	3.09	0.41
82:S2:676:C:H2'	82:S2:677:G:O4'	2.21	0.41
82:S2:1713:C:H2'	82:S2:1714:U:H6	1.85	0.41
82:S2:1798:C:H2'	82:S2:1799:G:O4'	2.20	0.41
1:Pt:38:C:H2'	1:Pt:39:G:O4'	2.20	0.41
1:Pt:62:C:H2'	1:Pt:63:G:H8	1.86	0.41
2:L5:422:C:H2'	2:L5:423:G:C8	2.55	0.41
2:L5:677:G:H2'	2:L5:678:C:C6	2.55	0.41
2:L5:737:C:C4	2:L5:739:G:H5''	2.56	0.41
2:L5:907:C:H2'	2:L5:908:G:H8	1.86	0.41
2:L5:952:G:H2'	2:L5:953:C:H6	1.85	0.41
2:L5:982:U:H2'	2:L5:983:C:C6	2.56	0.41
2:L5:1190:C:H2'	2:L5:1191:C:C6	2.56	0.41
2:L5:1538:U:H2'	2:L5:1539:G:H8	1.85	0.41
2:L5:1631:A:C2	5:LA:204:MET:HG2	2.55	0.41
2:L5:2633:U:H2'	2:L5:2634:C:C6	2.55	0.41
2:L5:3934:G:H2'	2:L5:3935:C:C6	2.56	0.41
2:L5:4273:A:H2'	2:L5:4274:A:C8	2.56	0.41
2:L5:4313:A:H4'	23:LT:71:ALA:HB3	2.03	0.41
2:L5:4535:A:H2'	2:L5:4536:OMC:H6	1.86	0.41
2:L5:4605:A:H2'	2:L5:4606:G:C8	2.55	0.41
2:L5:4921:C:H2'	2:L5:4922:C:C6	2.55	0.41
2:L5:4967:A:P	6:LB:126:LYS:H	2.44	0.41
8:LD:66:TYR:HE2	8:LD:68:ARG:HE	1.68	0.41
32:Lc:23:LYS:HB3	32:Lc:23:LYS:HE3	1.86	0.41
33:Ld:57:MET:HG2	33:Ld:88:LEU:HD23	2.03	0.41
35:Lf:5:LEU:HA	35:Lf:5:LEU:HD23	1.88	0.41
53:SP:47:ARG:NE	82:S2:1619:A:OP1	2.39	0.41
56:SS:113:ARG:O	56:SS:117:ILE:HG12	2.21	0.41
57:ST:38:LYS:NZ	82:S2:1628:C:OP1	2.44	0.41
63:Sg:125:ARG:HD3	63:Sg:150:TRP:CE2	2.56	0.41
63:Sg:212:LYS:HA	63:Sg:235:ILE:HG13	2.02	0.41
65:SB:57:ILE:HG22	65:SB:59:SER:H	1.85	0.41
69:SH:30:LEU:HG	69:SH:33:ASN:HD22	1.85	0.41
69:SH:83:LEU:HB3	69:SH:92:VAL:HG21	2.03	0.41
70:SI:181:GLN:HE21	82:S2:379:C:P	2.44	0.41
73:SN:4:MET:HG2	73:SN:5:HIS:CD2	2.55	0.41
73:SN:91:LEU:HB3	73:SN:122:ILE:HG12	2.03	0.41
82:S2:1218:C:H2'	82:S2:1219:C:C6	2.56	0.41
82:S2:1567:G:H2'	82:S2:1568:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:72:C:H5	15:LL:67:HIS:HD1	1.68	0.41
2:L5:102:G:O2'	2:L5:1381:U:O2'	2.33	0.41
2:L5:734:G:H22	2:L5:929:A:H2	1.67	0.41
2:L5:4727:A:H2'	2:L5:4728:U:O4'	2.20	0.41
2:L5:5002:U:H2'	2:L5:5003:U:C6	2.55	0.41
8:LD:152:ARG:HG3	8:LD:154:THR:HG23	2.03	0.41
8:LD:203:ASN:OD1	8:LD:203:ASN:N	2.51	0.41
8:LD:211:LEU:HD12	8:LD:223:PHE:HE2	1.85	0.41
9:LE:223:ARG:HB3	9:LE:224:LYS:HB2	2.03	0.41
27:LX:90:ILE:HG12	27:LX:96:LEU:HD23	2.02	0.41
47:Ls:193:PHE:HA	47:Ls:197:SER:O	2.20	0.41
50:SF:22:LYS:NZ	50:SF:98:GLU:OE2	2.42	0.41
50:SF:83:ASN:OD1	82:S2:1651:A:O2'	2.34	0.41
51:SK:32:HIS:CD2	51:SK:45:VAL:HG11	2.55	0.41
56:SS:84:LEU:HD23	56:SS:96:SER:C	2.46	0.41
63:Sg:170:TRP:HA	63:Sg:194:TYR:HB2	2.02	0.41
67:SE:101:LEU:HD12	67:SE:101:LEU:HA	1.89	0.41
70:SI:132:GLU:O	70:SI:136:ILE:HG23	2.20	0.41
74:SO:66:ARG:HG2	82:S2:962:A:H5''	2.03	0.41
77:SX:5:ARG:N	82:S2:1160:U:OP2	2.52	0.41
81:Se:41:ARG:HG3	81:Se:42:PHE:HD1	1.85	0.41
82:S2:145:G:H2'	82:S2:146:G:H8	1.82	0.41
82:S2:839:C:O2'	82:S2:841:G:O4'	2.37	0.41
82:S2:1232:PSU:H2'	82:S2:1233:G:C8	2.55	0.41
82:S2:1802:C:H2'	82:S2:1803:U:H6	1.86	0.41
82:S2:1821:U:O4	82:S2:1822:A:N6	2.53	0.41
2:L5:248:C:H2'	2:L5:249:C:H6	1.86	0.41
2:L5:302:C:H2'	2:L5:303:C:C6	2.55	0.41
2:L5:416:U:H4'	2:L5:2330:G:H4'	2.03	0.41
2:L5:2571:C:H2'	2:L5:2572:C:C6	2.55	0.41
2:L5:2745:A:H2'	2:L5:2746:A:C8	2.55	0.41
2:L5:2824:OMC:HM23	2:L5:2824:OMC:H1'	1.71	0.41
2:L5:2856:C:H2'	2:L5:2857:A:O4'	2.21	0.41
2:L5:2904:U:O2	2:L5:3591:C:H2'	2.19	0.41
2:L5:3650:C:H2'	2:L5:3651:A:C8	2.55	0.41
2:L5:3856:A:H5''	19:LP:83:TRP:O	2.20	0.41
2:L5:4194:U:N3	2:L5:4198:G:OP2	2.53	0.41
2:L5:4407:G:H2'	2:L5:4408:G:C8	2.55	0.41
2:L5:4621:C:OP1	25:LV:48:ARG:NE	2.41	0.41
3:L7:19:C:H2'	3:L7:20:U:H6	1.85	0.41
4:L8:96:C:OP1	37:Lh:70:ARG:NH2	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LD:115:MET:HG2	8:LD:118:ILE:HD11	2.03	0.41
13:LI:36:LEU:HD21	13:LI:69:ARG:NH1	2.36	0.41
13:LI:190:LEU:HD23	13:LI:199:TYR:HA	2.02	0.41
13:LI:207:ASP:OD1	13:LI:210:ARG:NH1	2.54	0.41
15:LL:170:THR:OG1	15:LL:173:GLU:HG3	2.21	0.41
16:LM:100:ARG:HA	16:LM:103:LYS:HE3	2.03	0.41
54:SQ:9:SER:HB3	54:SQ:26:LYS:HG3	2.02	0.41
55:SR:99:ASP:OD2	64:SA:42:LYS:NZ	2.36	0.41
56:SS:24:ARG:H	56:SS:24:ARG:HG2	1.67	0.41
63:Sg:4:GLN:O	63:Sg:313:THR:N	2.47	0.41
65:SB:138:PHE:O	65:SB:213:ARG:N	2.54	0.41
66:SC:256:TRP:CE2	76:SW:68:ARG:HD3	2.56	0.41
67:SE:129:ILE:HD11	67:SE:154:ILE:HG22	2.03	0.41
71:SJ:147:PHE:HE1	82:S2:824:C:H5'	1.85	0.41
82:S2:327:G:H5''	82:S2:328:U:C2	2.56	0.41
82:S2:462:OMC:HM23	82:S2:462:OMC:H1'	1.88	0.41
82:S2:943:U:H2'	82:S2:944:A:C8	2.56	0.41
1:Pt:29:C:H2'	1:Pt:30:G:H8	1.86	0.41
2:L5:153:G:H2'	2:L5:154:G:C8	2.53	0.41
2:L5:492:U:H2'	2:L5:493:G:O4'	2.19	0.41
2:L5:978:G:H2'	2:L5:979:C:H6	1.84	0.41
2:L5:1545:G:H2'	2:L5:1546:C:C6	2.56	0.41
2:L5:1952:G:H2'	2:L5:1953:U:H6	1.85	0.41
2:L5:2102:G:H1'	2:L5:2103:G:C8	2.55	0.41
2:L5:2558:C:H2'	2:L5:2559:G:H8	1.86	0.41
2:L5:2849:A:O2'	2:L5:2855:G:N7	2.50	0.41
2:L5:2893:U:H2'	2:L5:2894:A:C8	2.56	0.41
2:L5:4173:G:H2'	2:L5:4174:U:C6	2.56	0.41
2:L5:4176:C:H2'	2:L5:4177:C:C6	2.56	0.41
2:L5:4344:U:H2'	2:L5:4345:C:C6	2.56	0.41
2:L5:4407:G:H2'	2:L5:4408:G:H8	1.86	0.41
2:L5:4460:U:H2'	2:L5:4461:C:H6	1.85	0.41
2:L5:4524:G:C2	6:LB:252:ALA:HB1	2.56	0.41
6:LB:90:VAL:HG22	6:LB:104:THR:HG23	2.02	0.41
9:LE:150:LEU:HD12	9:LE:175:VAL:HG11	2.02	0.41
20:LQ:50:ARG:HA	20:LQ:53:MET:HE3	2.02	0.41
45:Lp:49:ARG:NH1	45:Lp:68:ALA:O	2.39	0.41
47:Ls:78:LEU:O	47:Ls:82:ILE:HG12	2.20	0.41
49:SD:213:PRO:HB3	55:SR:20:TYR:CE1	2.56	0.41
55:SR:126:MET:HG2	64:SA:43:SER:HB2	2.02	0.41
67:SE:136:ILE:HD12	67:SE:149:TYR:HE1	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SH:25:GLN:O	69:SH:28:LEU:HG	2.21	0.41
75:SV:11:LEU:HD23	75:SV:11:LEU:H	1.86	0.41
82:S2:602:G:N2	82:S2:621:C:N3	2.69	0.41
82:S2:1165:G:OP2	82:S2:1165:G:N2	2.31	0.41
82:S2:1229:G:H2'	82:S2:1230:C:C6	2.56	0.41
82:S2:1329:U:O2'	82:S2:1332:A:OP2	2.29	0.41
1:Pt:71:A:H2'	1:Pt:72:C:C6	2.55	0.41
2:L5:208:A:C2	2:L5:233:U:H5''	2.55	0.41
2:L5:271:C:H2'	2:L5:272:U:C6	2.56	0.41
2:L5:307:A:N3	2:L5:310:G:O2'	2.48	0.41
2:L5:457:G:H2'	2:L5:458:C:H6	1.85	0.41
2:L5:1281:G:OP1	7:LC:316:LYS:NZ	2.46	0.41
2:L5:1431:C:H2'	2:L5:1432:G:O4'	2.21	0.41
2:L5:1512:G:H2'	2:L5:1513:U:C6	2.55	0.41
2:L5:1585:C:N4	87:L5:5285:SPD:HN11	2.19	0.41
2:L5:1806:G:H2'	2:L5:1807:C:H6	1.84	0.41
2:L5:1845:U:H2'	2:L5:1846:G:C8	2.55	0.41
2:L5:1846:G:H2'	2:L5:1847:C:H6	1.86	0.41
2:L5:2413:U:H2'	2:L5:2414:G:C8	2.56	0.41
2:L5:2526:C:H2'	2:L5:2527:A:C8	2.56	0.41
2:L5:2542:G:H2'	2:L5:2543:A:C8	2.55	0.41
2:L5:2589:C:H2'	2:L5:2590:G:O4'	2.21	0.41
2:L5:2728:U:H2'	2:L5:2729:C:C6	2.56	0.41
2:L5:2803:U:H2'	2:L5:2804:OMC:C6	2.56	0.41
2:L5:2878:G:OP2	2:L5:2879:A:O2'	2.33	0.41
2:L5:3660:C:OP1	5:LA:241:ARG:NH2	2.50	0.41
2:L5:3709:U:H2'	2:L5:3710:G:C8	2.56	0.41
2:L5:4638:U:H2'	2:L5:4639:G:N3	2.35	0.41
2:L5:4642:U:H2'	2:L5:4643:G:C8	2.54	0.41
2:L5:4704:C:H2'	2:L5:4705:A:H8	1.86	0.41
2:L5:4769:G:H5''	18:LO:176:ARG:HD3	2.03	0.41
3:L7:110:G:H2'	3:L7:111:C:H6	1.85	0.41
4:L8:69:PSU:H2'	4:L8:70:G:O4'	2.20	0.41
13:LI:51:HIS:HB3	13:LI:134:VAL:HG13	2.02	0.41
21:LR:25:ASP:OD2	84:CI:72:ARG:NH2	2.52	0.41
24:LU:61:VAL:HG22	24:LU:74:SER:HB2	2.03	0.41
26:LW:113:LYS:O	26:LW:117:LYS:HG2	2.21	0.41
33:Ld:59:THR:OG1	33:Ld:104:THR:OG1	2.28	0.41
34:Le:100:ALA:HB3	34:Le:103:VAL:HG23	2.02	0.41
35:Lf:15:LYS:HB3	35:Lf:25:THR:HG23	2.02	0.41
38:Li:59:GLU:HA	38:Li:62:LYS:HE3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:SD:135:GLU:HB3	49:SD:157:MET:HE3	2.02	0.41
52:SM:80:ASP:N	52:SM:80:ASP:OD1	2.53	0.41
52:SM:124:ILE:HD13	52:SM:124:ILE:HA	1.94	0.41
53:SP:27:ASP:OD1	53:SP:27:ASP:N	2.46	0.41
56:SS:125:HIS:HE1	82:S2:1609:C:H4'	1.86	0.41
57:ST:42:HIS:NE2	57:ST:43:LYS:HE3	2.35	0.41
57:ST:67:ARG:HD3	82:S2:1587:G:N7	2.36	0.41
57:ST:129:ARG:HG3	82:S2:1416:C:OP1	2.21	0.41
59:SZ:68:ILE:HB	59:SZ:109:TYR:HB2	2.02	0.41
59:SZ:86:ALA:O	59:SZ:90:GLU:HG2	2.21	0.41
59:SZ:92:LEU:HD11	59:SZ:109:TYR:CE1	2.56	0.41
61:Sd:2:GLY:HA3	61:Sd:6:LEU:HD21	2.02	0.41
63:Sg:8:ARG:HB3	63:Sg:309:VAL:HG13	2.01	0.41
63:Sg:213:ASP:OD1	63:Sg:213:ASP:N	2.53	0.41
63:Sg:289:LEU:HD12	63:Sg:289:LEU:HA	1.93	0.41
65:SB:52:THR:HG23	65:SB:57:ILE:HA	2.02	0.41
67:SE:151:ASP:HA	68:SG:212:LEU:HD21	2.03	0.41
67:SE:253:ASP:OD1	67:SE:253:ASP:N	2.54	0.41
68:SG:173:ALA:HB3	82:S2:78:C:H5'	2.02	0.41
69:SH:7:LYS:HD3	69:SH:10:LYS:HB3	2.03	0.41
70:SI:76:THR:OG1	70:SI:77:ARG:N	2.53	0.41
71:SJ:58:ARG:O	71:SJ:62:THR:HG23	2.21	0.41
77:SX:46:HIS:CD2	77:SX:103:ALA:HB2	2.56	0.41
77:SX:86:PRO:HG3	77:SX:121:LYS:HD2	2.03	0.41
77:SX:90:CYS:HA	77:SX:93:PHE:CD2	2.56	0.41
82:S2:383:G:H2'	82:S2:384:U:C6	2.56	0.41
82:S2:490:C:H2'	82:S2:491:C:C6	2.56	0.41
82:S2:1330:G:N7	82:S2:1492:U:H3'	2.36	0.41
82:S2:1452:A:O2'	82:S2:1475:G:N2	2.54	0.41
82:S2:1515:G:H2'	82:S2:1516:G:H8	1.82	0.41
82:S2:1693:G:H2'	82:S2:1694:U:C6	2.56	0.41
82:S2:1737:G:H2'	82:S2:1738:C:C6	2.56	0.41
2:L5:35:U:H4'	2:L5:1525:A:H2	1.85	0.41
2:L5:135:G:N7	37:Lh:97:LYS:HG3	2.36	0.41
2:L5:221:C:H2'	2:L5:222:C:H6	1.86	0.41
2:L5:266:C:HO2'	2:L5:267:G:H8	1.64	0.41
2:L5:720:G:H2'	2:L5:721:G:H8	1.86	0.41
2:L5:1174:G:H2'	2:L5:1175:A:C8	2.56	0.41
2:L5:2274:C:H5''	7:LC:312:ARG:HB3	2.03	0.41
2:L5:2327:G:H2'	2:L5:2328:G:H8	1.86	0.41
2:L5:2609:G:H2'	2:L5:2610:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2881:A:H3'	2:L5:2882:A:H8	1.86	0.41
2:L5:3600:G:H2'	2:L5:3601:C:H6	1.86	0.41
2:L5:4451:G:H1'	89:L5:5297:HMT:H26	2.03	0.41
2:L5:4920:C:H2'	2:L5:4921:C:H6	1.86	0.41
2:L5:4938:A:P	9:LE:183:ARG:HH21	2.44	0.41
2:L5:5029:C:O2'	2:L5:5030:U:H6	2.04	0.41
3:L7:71:G:H2'	3:L7:72:U:C6	2.56	0.41
6:LB:80:GLU:OE1	6:LB:323:TYR:OH	2.34	0.41
14:LJ:16:ARG:HH21	14:LJ:137:PRO:HA	1.85	0.41
18:LO:54:TYR:CD1	18:LO:145:VAL:HG21	2.56	0.41
24:LU:31:ASP:OD2	24:LU:114:TYR:OH	2.28	0.41
35:Lf:78:HIS:HB3	35:Lf:83:MET:HB3	2.03	0.41
45:Lp:61:MET:HE3	45:Lp:61:MET:HB3	1.88	0.41
47:Ls:44:ARG:HD3	47:Ls:44:ARG:HA	1.93	0.41
53:SP:77:LYS:HB3	53:SP:102:PHE:CD1	2.56	0.41
63:Sg:228:TYR:CE2	63:Sg:264:LYS:HG2	2.56	0.41
63:Sg:270:LEU:HD13	63:Sg:310:TRP:CE3	2.55	0.41
67:SE:204:SER:OG	67:SE:205:PHE:N	2.54	0.41
70:SI:149:TYR:O	70:SI:153:LYS:HG2	2.21	0.41
71:SJ:132:GLN:HB2	71:SJ:134:HIS:CD2	2.56	0.41
76:SW:57:ARG:NH2	80:Sb:26:GLN:HB2	2.36	0.41
82:S2:15:U:O2'	82:S2:669:A:N6	2.50	0.41
82:S2:677:G:N1	82:S2:1027:A:OP2	2.34	0.41
82:S2:1034:A:H3'	82:S2:1035:A:H8	1.86	0.41
83:Zt:23:A:H2'	83:Zt:24:G:C8	2.56	0.41
83:Zt:26:A:N6	83:Zt:44:G:N1	2.32	0.41
1:Pt:6:C:H2'	1:Pt:7:G:C8	2.55	0.40
2:L5:152:U:C2	2:L5:153:G:C8	3.09	0.40
2:L5:1266:G:H5'	31:Lb:99:ILE:HD11	2.04	0.40
2:L5:1269:G:O2'	2:L5:1270:A:O4'	2.34	0.40
2:L5:1748:U:H2'	2:L5:1749:A:C8	2.56	0.40
2:L5:1879:C:H2'	2:L5:1880:G:O4'	2.21	0.40
2:L5:2402:G:H2'	2:L5:2403:A:H8	1.86	0.40
2:L5:2412:A:H2'	2:L5:2413:U:H6	1.86	0.40
2:L5:2544:G:H22	4:L8:124:U:H4'	1.86	0.40
2:L5:2565:A:H3'	2:L5:2566:G:H8	1.85	0.40
2:L5:2862:G:N3	2:L5:3624:A:H2'	2.35	0.40
2:L5:3633:C:H2'	2:L5:3634:G:H8	1.85	0.40
2:L5:4344:U:H2'	2:L5:4345:C:H6	1.86	0.40
3:L7:2:U:O4	3:L7:117:G:O6	2.39	0.40
7:LC:334:THR:HG22	7:LC:337:ARG:HH21	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LD:291:GLN:NE2	13:LI:213:HIS:O	2.39	0.40
10:LF:50:ILE:HD12	10:LF:186:CYS:HB3	2.03	0.40
11:LG:77:PRO:HA	11:LG:78:PRO:HD3	1.94	0.40
15:LL:55:ILE:O	15:LL:97:SER:OG	2.37	0.40
22:LS:27:LEU:HB3	23:LT:148:PRO:HB3	2.03	0.40
28:LY:4:ASN:HB3	28:LY:7:VAL:HG22	2.03	0.40
46:Lr:59:GLY:O	46:Lr:121:GLN:NE2	2.32	0.40
49:SD:75:LYS:NZ	51:SK:18:GLU:HG3	2.36	0.40
52:SM:118:SER:O	52:SM:121:LYS:NZ	2.51	0.40
54:SQ:51:LEU:HD23	54:SQ:51:LEU:HA	1.93	0.40
64:SA:32:PHE:CD1	82:S2:1097:G:H4'	2.56	0.40
65:SB:73:ASP:OD1	65:SB:73:ASP:N	2.54	0.40
66:SC:109:ILE:HD11	66:SC:151:ILE:HD11	2.03	0.40
68:SG:139:SER:HA	68:SG:142:ARG:HB2	2.02	0.40
70:SI:191:GLU:HG3	72:SL:19:ASN:ND2	2.36	0.40
71:SJ:176:LYS:HA	71:SJ:179:LYS:HG2	2.02	0.40
78:SY:129:LYS:HD3	78:SY:129:LYS:HA	1.86	0.40
80:Sb:6:ASP:OD1	80:Sb:9:HIS:N	2.49	0.40
82:S2:864:A:H2'	82:S2:865:A:C8	2.55	0.40
82:S2:1107:G:C6	82:S2:1126:G:C6	3.09	0.40
83:Zt:51:G:H2'	83:Zt:52:G:C8	2.56	0.40
2:L5:123:C:H2'	2:L5:124:C:C6	2.57	0.40
2:L5:1537:A:H2'	2:L5:1538:U:C6	2.56	0.40
2:L5:1814:C:H2'	2:L5:1816:C:H5	1.87	0.40
2:L5:2056:G:H4'	18:LO:18:ARG:HH22	1.86	0.40
2:L5:2277:C:H2'	2:L5:2278:G:C8	2.55	0.40
2:L5:2598:A:H2'	2:L5:2599:G:O4'	2.22	0.40
2:L5:2779:C:H2'	2:L5:2780:C:C6	2.57	0.40
2:L5:3642:A:C8	39:Lj:3:LYS:HE2	2.56	0.40
2:L5:4323:A:C2	8:LD:146:LEU:HD23	2.57	0.40
2:L5:4769:G:H2'	2:L5:4770:U:C6	2.56	0.40
2:L5:4979:A:OP1	6:LB:228:TYR:HB2	2.21	0.40
2:L5:4997:G:H2'	2:L5:4998:G:C8	2.55	0.40
4:L8:4:C:H2'	4:L8:5:U:C6	2.57	0.40
4:L8:109:C:H3'	39:Lj:20:ARG:HH22	1.85	0.40
5:LA:28:ARG:HE	5:LA:28:ARG:HB2	1.74	0.40
5:LA:186:TYR:HB2	5:LA:196:TRP:CZ3	2.57	0.40
6:LB:263:ALA:HB3	6:LB:266:VAL:HG23	2.03	0.40
10:LF:226:HIS:HB3	10:LF:229:GLU:HG2	2.03	0.40
11:LG:123:ALA:HA	11:LG:124:GLY:HA2	1.80	0.40
15:LL:93:THR:HA	37:Lh:116:LEU:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LN:38:ARG:HA	17:LN:62:TYR:HA	2.04	0.40
20:LQ:69:LYS:HD3	20:LQ:69:LYS:HA	1.85	0.40
20:LQ:154:LYS:HB3	20:LQ:154:LYS:HE2	1.83	0.40
24:LU:80:LYS:HG2	24:LU:110:TYR:CE2	2.56	0.40
28:LY:106:ILE:HG21	28:LY:109:LEU:HD23	2.03	0.40
33:Ld:19:GLU:OE2	33:Ld:92:ARG:NH2	2.54	0.40
36:Lg:60:ARG:HB2	36:Lg:63:VAL:HG23	2.03	0.40
36:Lg:61:PRO:HA	36:Lg:64:LEU:HD12	2.02	0.40
50:SF:39:ILE:HG23	50:SF:68:ILE:HD13	2.03	0.40
52:SM:26:LEU:HD11	52:SM:89:VAL:HA	2.03	0.40
53:SP:81:ARG:NH1	53:SP:120:SER:HG	2.18	0.40
55:SR:114:LEU:HD12	55:SR:117:LEU:HD11	2.02	0.40
63:Sg:174:VAL:HG23	63:Sg:188:HIS:HB2	2.02	0.40
67:SE:28:ALA:O	82:S2:496:C:H4'	2.22	0.40
68:SG:133:LEU:HD12	82:S2:65:C:C4	2.57	0.40
69:SH:17:ASP:OD1	69:SH:17:ASP:N	2.53	0.40
70:SI:184:ARG:HD2	82:S2:219:U:H1'	2.02	0.40
71:SJ:28:GLU:OE2	71:SJ:44:TRP:NE1	2.42	0.40
73:SN:29:THR:O	73:SN:33:VAL:HG23	2.21	0.40
82:S2:89:C:O2	82:S2:499:G:H4'	2.21	0.40
82:S2:943:U:C2	82:S2:944:A:C8	3.09	0.40
82:S2:1305:C:H2'	82:S2:1306:U:C6	2.56	0.40
82:S2:1348:G:OP2	82:S2:1348:G:N2	2.51	0.40
2:L5:197:A:N6	2:L5:242:U:H3	2.20	0.40
2:L5:252:C:H2'	2:L5:253:G:C8	2.56	0.40
2:L5:370:U:H2'	2:L5:371:A:C8	2.57	0.40
2:L5:385:A:O2'	2:L5:387:G:H5'	2.21	0.40
2:L5:388:A:H5'	2:L5:389:A:H5'	2.03	0.40
2:L5:965:G:N2	2:L5:2092:G:H1'	2.37	0.40
2:L5:1614:C:H2'	2:L5:1615:C:C6	2.56	0.40
2:L5:1993:C:H2'	2:L5:1994:C:C6	2.57	0.40
2:L5:2325:C:OP1	34:Le:101:HIS:ND1	2.44	0.40
2:L5:2422:OMC:HM23	2:L5:2422:OMC:H1'	1.83	0.40
2:L5:4456:OMC:HM23	2:L5:4456:OMC:H1'	1.90	0.40
2:L5:4524:G:OP1	2:L5:4559:A:N6	2.52	0.40
2:L5:4544:A:H5''	5:LA:213:GLY:HA3	2.03	0.40
2:L5:4662:C:O2'	2:L5:5004:C:OP1	2.38	0.40
2:L5:5027:C:O2'	2:L5:5028:G:H5''	2.21	0.40
5:LA:22:HIS:O	5:LA:24:LYS:NZ	2.53	0.40
13:LI:159:PHE:HA	13:LI:160:PRO:HD3	1.94	0.40
17:LN:120:TRP:HZ2	17:LN:123:GLU:HG2	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LP:137:ASN:HD22	19:LP:137:ASN:HA	1.69	0.40
25:LV:104:VAL:HB	25:LV:112:MET:HE3	2.02	0.40
41:Ll:16:LYS:HD3	41:Ll:19:GLN:HE21	1.86	0.40
49:SD:192:TRP:NE1	49:SD:201:LYS:O	2.47	0.40
50:SF:61:PHE:CD2	60:Sc:51:ARG:HD3	2.56	0.40
50:SF:171:GLU:OE2	59:SZ:106:GLN:NE2	2.54	0.40
63:Sg:133:ASN:HB3	63:Sg:139:LYS:HD2	2.02	0.40
66:SC:104:ASP:OD1	66:SC:105:GLU:N	2.53	0.40
69:SH:33:ASN:ND2	69:SH:36:LEU:HB3	2.35	0.40
70:SI:10:LYS:HD3	82:S2:387:C:P	2.61	0.40
70:SI:117:TYR:HB3	70:SI:119:LEU:HD23	2.02	0.40
71:SJ:111:GLN:HE21	71:SJ:123:ILE:HG13	1.85	0.40
79:Sa:59:PHE:HB2	79:Sa:62:TYR:HB2	2.04	0.40
82:S2:218:U:H2'	82:S2:219:U:C6	2.56	0.40
82:S2:1368:U:O2'	82:S2:1370:A:N7	2.46	0.40
82:S2:1391:OMC:HM23	82:S2:1391:OMC:H1'	1.92	0.40
82:S2:1844:U:H2'	82:S2:1845:A:H8	1.86	0.40
2:L5:212:A:H2'	2:L5:213:G:H8	1.86	0.40
2:L5:229:G:H2'	2:L5:230:G:H8	1.87	0.40
2:L5:326:C:H2'	2:L5:327:U:C6	2.56	0.40
2:L5:1577:G:H5'	2:L5:1578:U:H5''	2.04	0.40
2:L5:1589:C:H2'	2:L5:1590:C:C6	2.57	0.40
2:L5:1973:G:O2'	48:Lt:117:ARG:NH2	2.54	0.40
2:L5:2059:C:H2'	2:L5:2060:G:C8	2.48	0.40
2:L5:2555:G:H2'	2:L5:2556:G:H8	1.87	0.40
2:L5:2574:G:O6	2:L5:2760:G:N2	2.54	0.40
2:L5:2823:G:H2'	2:L5:2824:OMC:H6	1.87	0.40
2:L5:3794:C:H2'	2:L5:3795:A:C8	2.57	0.40
2:L5:3814:U:H2'	2:L5:3815:G:C8	2.56	0.40
2:L5:4186:A:H2'	2:L5:4187:G:C8	2.57	0.40
2:L5:4473:A:P	42:Lm:102:ARG:HH21	2.44	0.40
2:L5:4980:C:H3'	2:L5:4981:G:H21	1.85	0.40
4:L8:123:U:H2'	4:L8:126:C:N4	2.34	0.40
4:L8:145:C:H2'	4:L8:146:U:C6	2.57	0.40
6:LB:261:ARG:HB3	18:LO:64:THR:HG21	2.04	0.40
20:LQ:32:TYR:OH	20:LQ:123:PHE:O	2.36	0.40
21:LR:112:SER:OG	21:LR:114:LYS:HG3	2.21	0.40
39:Lj:67:LEU:HA	39:Lj:67:LEU:HD23	1.82	0.40
43:Ln:12:ARG:HG2	43:Ln:15:ARG:HH21	1.86	0.40
48:Lt:117:ARG:HG3	48:Lt:119:ARG:HG3	2.03	0.40
57:ST:39:LEU:HD21	57:ST:52:TRP:CZ3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SA:73:ASP:O	64:SA:120:ARG:N	2.52	0.40
64:SA:184:ARG:HG3	64:SA:189:ILE:HD12	2.03	0.40
66:SC:64:THR:HG22	66:SC:66:LEU:N	2.36	0.40
68:SG:170:ARG:HG3	82:S2:72:C:N3	2.37	0.40
82:S2:534:G:H2'	82:S2:535:G:C8	2.56	0.40
82:S2:959:G:H1'	82:S2:964:A:N6	2.36	0.40
82:S2:1171:G:O2'	82:S2:1187:G:O6	2.39	0.40
82:S2:1287:A:N6	82:S2:1288:OMU:O2	2.55	0.40
82:S2:1510:G:H2'	82:S2:1511:U:O4'	2.22	0.40
82:S2:1688:C:H2'	82:S2:1689:C:C6	2.57	0.40
2:L5:20:U:H3'	2:L5:21:G:H8	1.85	0.40
2:L5:169:G:O6	2:L5:170:C:N4	2.55	0.40
2:L5:239:C:H2'	2:L5:240:G:H8	1.86	0.40
2:L5:325:U:H3'	38:Li:28:ARG:NH2	2.35	0.40
2:L5:346:G:H2'	2:L5:347:A:C8	2.57	0.40
2:L5:928:C:H2'	2:L5:929:A:C8	2.57	0.40
2:L5:1473:U:H2'	2:L5:1474:C:C6	2.56	0.40
2:L5:1956:A:H2'	2:L5:1957:U:H6	1.85	0.40
2:L5:4203:A:N3	2:L5:4221:C:H5'	2.36	0.40
2:L5:4279:A:H5'	2:L5:4281:A:H1'	2.03	0.40
2:L5:4291:G:OP1	44:Lo:18:HIS:NE2	2.54	0.40
2:L5:4938:A:H1'	9:LE:185:PRO:HG3	2.03	0.40
9:LE:282:TYR:HE1	35:Lf:31:GLU:HG2	1.87	0.40
13:LI:77:VAL:HG22	13:LI:82:ARG:HA	2.03	0.40
25:LV:37:LEU:HD23	25:LV:65:VAL:HG12	2.03	0.40
25:LV:48:ARG:HG2	25:LV:51:ARG:CZ	2.52	0.40
47:Ls:47:LEU:HD11	47:Ls:51:ALA:HB3	2.02	0.40
53:SP:134:GLY:H	82:S2:1236:G:H4'	1.87	0.40
57:ST:83:GLN:NE2	57:ST:85:ASN:OD1	2.54	0.40
59:SZ:56:ASP:OD1	59:SZ:57:LYS:N	2.54	0.40
63:Sg:256:ILE:HD11	63:Sg:286:CYS:SG	2.62	0.40
67:SE:63:LYS:O	67:SE:67:GLN:HG3	2.21	0.40
69:SH:18:GLU:C	69:SH:20:GLU:H	2.29	0.40
69:SH:78:ARG:O	69:SH:81:ARG:HG2	2.20	0.40
82:S2:1328:OMG:H1'	82:S2:1328:OMG:HM23	1.85	0.40
82:S2:1348:G:H2'	82:S2:1349:G:C8	2.56	0.40
82:S2:1612:G:H2'	82:S2:1613:G:H8	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	LA	246/248 (99%)	232 (94%)	14 (6%)	0	100	100
6	LB	400/402 (100%)	380 (95%)	20 (5%)	0	100	100
7	LC	366/368 (100%)	353 (96%)	13 (4%)	0	100	100
8	LD	291/293 (99%)	281 (97%)	10 (3%)	0	100	100
9	LE	236/250 (94%)	223 (94%)	13 (6%)	0	100	100
10	LF	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
11	LG	239/241 (99%)	225 (94%)	14 (6%)	0	100	100
12	LH	188/190 (99%)	182 (97%)	6 (3%)	0	100	100
13	LI	211/213 (99%)	202 (96%)	9 (4%)	0	100	100
14	LJ	168/176 (96%)	162 (96%)	6 (4%)	0	100	100
15	LL	208/210 (99%)	199 (96%)	9 (4%)	0	100	100
16	LM	137/139 (99%)	132 (96%)	5 (4%)	0	100	100
17	LN	201/203 (99%)	197 (98%)	4 (2%)	0	100	100
18	LO	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
19	LP	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
20	LQ	185/187 (99%)	182 (98%)	3 (2%)	0	100	100
21	LR	185/187 (99%)	181 (98%)	4 (2%)	0	100	100
22	LS	173/175 (99%)	168 (97%)	5 (3%)	0	100	100
23	LT	157/159 (99%)	155 (99%)	2 (1%)	0	100	100
24	LU	99/101 (98%)	94 (95%)	5 (5%)	0	100	100
25	LV	129/131 (98%)	127 (98%)	2 (2%)	0	100	100
26	LW	112/124 (90%)	109 (97%)	3 (3%)	0	100	100
27	LX	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
28	LY	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
29	LZ	133/135 (98%)	126 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	La	145/147 (99%)	141 (97%)	4 (3%)	0	100	100
31	Lb	105/121 (87%)	97 (92%)	8 (8%)	0	100	100
32	Lc	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
33	Ld	105/107 (98%)	103 (98%)	2 (2%)	0	100	100
34	Le	126/128 (98%)	125 (99%)	1 (1%)	0	100	100
35	Lf	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
36	Lg	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
37	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
38	Li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
39	Lj	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
40	Lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
41	Ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
42	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
43	Ln	22/24 (92%)	22 (100%)	0	0	100	100
44	Lo	103/105 (98%)	98 (95%)	5 (5%)	0	100	100
45	Lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
46	Lr	123/125 (98%)	119 (97%)	4 (3%)	0	100	100
47	Ls	194/196 (99%)	182 (94%)	12 (6%)	0	100	100
48	Lt	128/157 (82%)	113 (88%)	15 (12%)	0	100	100
49	SD	225/227 (99%)	219 (97%)	6 (3%)	0	100	100
50	SF	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
51	SK	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
52	SM	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
53	SP	119/121 (98%)	117 (98%)	2 (2%)	0	100	100
54	SQ	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
55	SR	133/135 (98%)	124 (93%)	8 (6%)	1 (1%)	16	50
56	SS	143/145 (99%)	135 (94%)	8 (6%)	0	100	100
57	ST	141/143 (99%)	138 (98%)	3 (2%)	0	100	100
58	SU	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
59	SZ	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
60	Sc	62/64 (97%)	60 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	Sd	53/55 (96%)	53 (100%)	0	0	100	100
62	Sf	65/67 (97%)	58 (89%)	7 (11%)	0	100	100
63	Sg	311/313 (99%)	295 (95%)	16 (5%)	0	100	100
64	SA	219/221 (99%)	208 (95%)	11 (5%)	0	100	100
65	SB	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
66	SC	218/222 (98%)	204 (94%)	14 (6%)	0	100	100
67	SE	260/262 (99%)	252 (97%)	8 (3%)	0	100	100
68	SG	235/237 (99%)	223 (95%)	12 (5%)	0	100	100
69	SH	182/189 (96%)	167 (92%)	15 (8%)	0	100	100
70	SI	204/206 (99%)	193 (95%)	11 (5%)	0	100	100
71	SJ	183/185 (99%)	175 (96%)	7 (4%)	1 (0%)	24	59
72	SL	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
73	SN	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
74	SO	135/140 (96%)	127 (94%)	8 (6%)	0	100	100
75	SV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
76	SW	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
77	SX	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
78	SY	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
79	Sa	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
80	Sb	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
81	Se	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
84	CI	29/31 (94%)	29 (100%)	0	0	100	100
All	All	11672/11907 (98%)	11192 (96%)	478 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
71	SJ	138	ARG
55	SR	129	LYS

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	LA	190/190 (100%)	190 (100%)	0	100	100
6	LB	348/348 (100%)	348 (100%)	0	100	100
7	LC	306/306 (100%)	306 (100%)	0	100	100
8	LD	246/247 (100%)	246 (100%)	0	100	100
9	LE	212/222 (96%)	212 (100%)	0	100	100
10	LF	194/194 (100%)	194 (100%)	0	100	100
11	LG	203/205 (99%)	203 (100%)	0	100	100
12	LH	169/169 (100%)	169 (100%)	0	100	100
13	LI	180/180 (100%)	180 (100%)	0	100	100
14	LJ	143/148 (97%)	143 (100%)	0	100	100
15	LL	176/176 (100%)	176 (100%)	0	100	100
16	LM	118/118 (100%)	118 (100%)	0	100	100
17	LN	171/171 (100%)	171 (100%)	0	100	100
18	LO	173/173 (100%)	173 (100%)	0	100	100
19	LP	134/134 (100%)	134 (100%)	0	100	100
20	LQ	164/164 (100%)	164 (100%)	0	100	100
21	LR	166/166 (100%)	166 (100%)	0	100	100
22	LS	156/156 (100%)	156 (100%)	0	100	100
23	LT	139/139 (100%)	139 (100%)	0	100	100
24	LU	91/91 (100%)	91 (100%)	0	100	100
25	LV	101/101 (100%)	101 (100%)	0	100	100
26	LW	95/103 (92%)	95 (100%)	0	100	100
27	LX	108/108 (100%)	108 (100%)	0	100	100
28	LY	124/124 (100%)	124 (100%)	0	100	100
29	LZ	117/117 (100%)	117 (100%)	0	100	100
30	La	120/120 (100%)	120 (100%)	0	100	100
31	Lb	88/101 (87%)	88 (100%)	0	100	100
32	Lc	83/83 (100%)	83 (100%)	0	100	100
33	Ld	98/98 (100%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Le	114/114 (100%)	114 (100%)	0	100	100
35	Lf	88/88 (100%)	88 (100%)	0	100	100
36	Lg	98/98 (100%)	98 (100%)	0	100	100
37	Lh	109/109 (100%)	109 (100%)	0	100	100
38	Li	86/86 (100%)	86 (100%)	0	100	100
39	Lj	73/73 (100%)	73 (100%)	0	100	100
40	Lk	64/64 (100%)	64 (100%)	0	100	100
41	Ll	47/47 (100%)	47 (100%)	0	100	100
42	Lm	48/48 (100%)	48 (100%)	0	100	100
43	Ln	23/23 (100%)	23 (100%)	0	100	100
44	Lo	93/93 (100%)	93 (100%)	0	100	100
45	Lp	74/74 (100%)	74 (100%)	0	100	100
46	Lr	109/109 (100%)	109 (100%)	0	100	100
47	Ls	162/164 (99%)	162 (100%)	0	100	100
48	Lt	107/130 (82%)	107 (100%)	0	100	100
49	SD	190/190 (100%)	190 (100%)	0	100	100
50	SF	159/159 (100%)	159 (100%)	0	100	100
51	SK	89/89 (100%)	89 (100%)	0	100	100
52	SM	102/104 (98%)	102 (100%)	0	100	100
53	SP	107/107 (100%)	107 (100%)	0	100	100
54	SQ	119/119 (100%)	119 (100%)	0	100	100
55	SR	122/122 (100%)	122 (100%)	0	100	100
56	SS	126/126 (100%)	126 (100%)	0	100	100
57	ST	113/113 (100%)	113 (100%)	0	100	100
58	SU	94/94 (100%)	94 (100%)	0	100	100
59	SZ	66/66 (100%)	66 (100%)	0	100	100
60	Sc	57/57 (100%)	57 (100%)	0	100	100
61	Sd	48/48 (100%)	48 (100%)	0	100	100
62	Sf	60/60 (100%)	60 (100%)	0	100	100
63	Sg	272/272 (100%)	272 (100%)	0	100	100
64	SA	183/183 (100%)	183 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
65	SB	195/195 (100%)	195 (100%)	0	100	100
66	SC	186/188 (99%)	186 (100%)	0	100	100
67	SE	224/224 (100%)	224 (100%)	0	100	100
68	SG	207/207 (100%)	207 (100%)	0	100	100
69	SH	166/169 (98%)	165 (99%)	1 (1%)	78	80
70	SI	178/178 (100%)	178 (100%)	0	100	100
71	SJ	161/161 (100%)	161 (100%)	0	100	100
72	SL	137/137 (100%)	137 (100%)	0	100	100
73	SN	130/130 (100%)	130 (100%)	0	100	100
74	SO	107/110 (97%)	107 (100%)	0	100	100
75	SV	67/67 (100%)	67 (100%)	0	100	100
76	SW	112/112 (100%)	112 (100%)	0	100	100
77	SX	113/113 (100%)	113 (100%)	0	100	100
78	SY	113/113 (100%)	113 (100%)	0	100	100
79	Sa	89/89 (100%)	89 (100%)	0	100	100
80	Sb	75/75 (100%)	75 (100%)	0	100	100
81	Se	47/47 (100%)	47 (100%)	0	100	100
84	CI	25/25 (100%)	25 (100%)	0	100	100
All	All	10147/10221 (99%)	10146 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
69	SH	162	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (82) such sidechains are listed below:

Mol	Chain	Res	Type
5	LA	50	HIS
6	LB	68	ASN
6	LB	184	GLN
6	LB	203	GLN
6	LB	289	GLN
7	LC	38	ASN
7	LC	112	HIS

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Mol	Chain	Res	Type
7	LC	329	ASN
7	LC	347	HIS
10	LF	192	HIS
11	LG	64	GLN
11	LG	112	GLN
12	LH	39	ASN
12	LH	78	GLN
12	LH	98	HIS
12	LH	116	ASN
12	LH	138	GLN
13	LI	73	ASN
13	LI	166	HIS
14	LJ	71	HIS
15	LL	19	GLN
15	LL	149	GLN
16	LM	34	ASN
17	LN	32	GLN
17	LN	199	GLN
18	LO	26	GLN
18	LO	180	GLN
19	LP	75	GLN
22	LS	23	HIS
22	LS	108	GLN
22	LS	173	ASN
23	LT	131	GLN
23	LT	144	ASN
24	LU	94	ASN
25	LV	77	HIS
26	LW	79	GLN
28	LY	14	ASN
28	LY	61	HIS
30	La	28	HIS
30	La	34	ASN
35	Lf	99	HIS
41	Ll	19	GLN
46	Lr	4	HIS
46	Lr	21	ASN
46	Lr	31	ASN
48	Lt	65	GLN
49	SD	145	GLN
49	SD	159	HIS
51	SK	32	HIS

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Mol	Chain	Res	Type
51	SK	50	GLN
51	SK	84	HIS
52	SM	19	GLN
52	SM	119	GLN
53	SP	103	ASN
56	SS	11	HIS
56	SS	87	GLN
59	SZ	89	GLN
60	Sc	24	GLN
63	Sg	147	HIS
64	SA	9	GLN
64	SA	84	GLN
64	SA	132	GLN
65	SB	53	GLN
65	SB	75	GLN
65	SB	95	ASN
66	SC	267	GLN
67	SE	50	ASN
67	SE	188	ASN
68	SG	56	ASN
69	SH	76	GLN
69	SH	165	ASN
70	SI	35	ASN
72	SL	19	ASN
72	SL	141	ASN
73	SN	105	ASN
75	SV	35	ASN
76	SW	5	ASN
77	SX	31	HIS
78	SY	89	HIS
78	SY	124	ASN
79	Sa	8	ASN
79	Sa	72	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Pt	72/74 (97%)	19 (26%)	0
2	L5	3643/3655 (99%)	762 (20%)	15 (0%)
3	L7	119/120 (99%)	12 (10%)	0
4	L8	155/156 (99%)	26 (16%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
82	S2	1714/1740 (98%)	391 (22%)	3 (0%)
83	Zt	74/75 (98%)	43 (58%)	0
All	All	5777/5820 (99%)	1253 (21%)	18 (0%)

All (1253) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Pt	9	A
1	Pt	13	U
1	Pt	19	G
1	Pt	21	A
1	Pt	46	G
1	Pt	47	U
1	Pt	48	C
1	Pt	49	C
1	Pt	56	C
1	Pt	58	A
1	Pt	59	A
1	Pt	61	C
1	Pt	66	C
1	Pt	67	G
1	Pt	70	A
1	Pt	72	C
1	Pt	74	C
1	Pt	75	C
1	Pt	76	A
2	L5	2	G
2	L5	13	U
2	L5	25	A
2	L5	30	C
2	L5	39	A
2	L5	42	A
2	L5	48	G
2	L5	56	A
2	L5	59	A
2	L5	64	A
2	L5	65	A
2	L5	73	A
2	L5	74	G
2	L5	76	A
2	L5	91	G
2	L5	104	G

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Mol	Chain	Res	Type
2	L5	109	G
2	L5	110	C
2	L5	119	G
2	L5	120	A
2	L5	132	G
2	L5	133	C
2	L5	134	G
2	L5	135	G
2	L5	145	G
2	L5	159	C
2	L5	164	G
2	L5	165	A
2	L5	172	C
2	L5	181	C
2	L5	182	G
2	L5	183	C
2	L5	184	U
2	L5	185	C
2	L5	187	U
2	L5	188	G
2	L5	200	U
2	L5	209	U
2	L5	210	C
2	L5	216	C
2	L5	218	A
2	L5	220	C
2	L5	234	G
2	L5	255	C
2	L5	256	G
2	L5	261	G
2	L5	263	G
2	L5	264	C
2	L5	265	C
2	L5	266	C
2	L5	267	G
2	L5	280	G
2	L5	281	U
2	L5	297	U
2	L5	306	A
2	L5	315	G
2	L5	316	U
2	L5	340	C

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Mol	Chain	Res	Type
2	L5	357	U
2	L5	358	C
2	L5	363	A
2	L5	373	G
2	L5	385	A
2	L5	387	G
2	L5	388	A
2	L5	396	A
2	L5	406	C
2	L5	407	A
2	L5	409	G
2	L5	410	A
2	L5	411	G
2	L5	412	G
2	L5	413	G
2	L5	415	G
2	L5	432	U
2	L5	440	U
2	L5	449	C
2	L5	450	G
2	L5	452	A
2	L5	453	G
2	L5	454	U
2	L5	456	C
2	L5	457	G
2	L5	467	U
2	L5	472	C
2	L5	484	U
2	L5	485	C
2	L5	486	C
2	L5	489	C
2	L5	493	G
2	L5	494	U
2	L5	497	G
2	L5	498	C
2	L5	499	G
2	L5	500	G
2	L5	502	C
2	L5	503	C
2	L5	504	G
2	L5	509	A
2	L5	510	U

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Mol	Chain	Res	Type
2	L5	512	U
2	L5	513	U
2	L5	514	U
2	L5	518	G
2	L5	643	C
2	L5	645	G
2	L5	646	G
2	L5	654	C
2	L5	655	C
2	L5	656	C
2	L5	657	C
2	L5	659	G
2	L5	666	G
2	L5	667	A
2	L5	668	C
2	L5	669	C
2	L5	673	C
2	L5	685	C
2	L5	686	A
2	L5	687	U
2	L5	696	C
2	L5	700	G
2	L5	704	C
2	L5	708	G
2	L5	731	G
2	L5	738	C
2	L5	739	G
2	L5	742	G
2	L5	750	U
2	L5	759	G
2	L5	904	C
2	L5	905	C
2	L5	906	C
2	L5	910	G
2	L5	913	U
2	L5	914	U
2	L5	915	A
2	L5	917	A
2	L5	923	C
2	L5	924	C
2	L5	926	G
2	L5	932	A

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Mol	Chain	Res	Type
2	L5	933	G
2	L5	935	A
2	L5	936	C
2	L5	941	C
2	L5	943	A
2	L5	944	A
2	L5	945	U
2	L5	956	A
2	L5	959	G
2	L5	960	A
2	L5	961	G
2	L5	962	C
2	L5	965	G
2	L5	966	A
2	L5	967	C
2	L5	969	C
2	L5	970	G
2	L5	982	U
2	L5	985	C
2	L5	1070	G
2	L5	1071	C
2	L5	1072	C
2	L5	1075	G
2	L5	1082	C
2	L5	1083	U
2	L5	1168	G
2	L5	1171	G
2	L5	1172	C
2	L5	1173	G
2	L5	1179	U
2	L5	1180	C
2	L5	1181	C
2	L5	1182	C
2	L5	1183	C
2	L5	1187	G
2	L5	1202	C
2	L5	1203	G
2	L5	1210	C
2	L5	1211	G
2	L5	1214	C
2	L5	1215	C
2	L5	1219	G

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Mol	Chain	Res	Type
2	L5	1222	A
2	L5	1246	G
2	L5	1253	G
2	L5	1254	A
2	L5	1257	A
2	L5	1258	G
2	L5	1266	G
2	L5	1267	C
2	L5	1269	G
2	L5	1271	G
2	L5	1272	C
2	L5	1273	G
2	L5	1275	G
2	L5	1280	C
2	L5	1284	G
2	L5	1285	U
2	L5	1287	G
2	L5	1293	G
2	L5	1294	A
2	L5	1295	C
2	L5	1296	G
2	L5	1301	C
2	L5	1302	U
2	L5	1314	C
2	L5	1326	A2M
2	L5	1337	A
2	L5	1344	C
2	L5	1345	A
2	L5	1354	A
2	L5	1359	G
2	L5	1364	U
2	L5	1365	C
2	L5	1366	G
2	L5	1367	C
2	L5	1379	C
2	L5	1387	A
2	L5	1394	G
2	L5	1397	A
2	L5	1404	G
2	L5	1407	C
2	L5	1409	C
2	L5	1410	U

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Mol	Chain	Res	Type
2	L5	1411	C
2	L5	1414	C
2	L5	1415	G
2	L5	1417	C
2	L5	1420	A
2	L5	1425	G
2	L5	1437	C
2	L5	1439	C
2	L5	1442	C
2	L5	1443	A
2	L5	1444	G
2	L5	1446	C
2	L5	1447	C
2	L5	1457	G
2	L5	1482	G
2	L5	1483	C
2	L5	1497	A
2	L5	1498	G
2	L5	1502	G
2	L5	1504	G
2	L5	1517	G
2	L5	1523	A
2	L5	1524	A2M
2	L5	1534	A2M
2	L5	1537	A
2	L5	1547	A
2	L5	1562	G
2	L5	1564	A
2	L5	1566	C
2	L5	1574	G
2	L5	1578	U
2	L5	1591	U
2	L5	1596	U
2	L5	1624	G
2	L5	1625	OMG
2	L5	1631	A
2	L5	1633	G
2	L5	1634	A
2	L5	1638	A
2	L5	1640	C
2	L5	1654	G
2	L5	1661	C

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Mol	Chain	Res	Type
2	L5	1676	C
2	L5	1677	PSU
2	L5	1678	C
2	L5	1691	G
2	L5	1699	A
2	L5	1700	G
2	L5	1701	A
2	L5	1702	C
2	L5	1704	C
2	L5	1705	G
2	L5	1717	C
2	L5	1718	C
2	L5	1719	A
2	L5	1731	C
2	L5	1734	G
2	L5	1740	C
2	L5	1742	A
2	L5	1750	G
2	L5	1753	G
2	L5	1757	U
2	L5	1758	G
2	L5	1761	G
2	L5	1762	C
2	L5	1763	C
2	L5	1764	G
2	L5	1765	A
2	L5	1766	A
2	L5	1767	A
2	L5	1768	C
2	L5	1770	A
2	L5	1785	C
2	L5	1787	A
2	L5	1803	G
2	L5	1804	A
2	L5	1806	G
2	L5	1810	G
2	L5	1815	G
2	L5	1821	G
2	L5	1822	U
2	L5	1836	G
2	L5	1837	A
2	L5	1842	G

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Mol	Chain	Res	Type
2	L5	1855	G
2	L5	1869	G
2	L5	1882	U
2	L5	1888	A
2	L5	1893	C
2	L5	1897	A
2	L5	1916	G
2	L5	1917	A
2	L5	1918	U
2	L5	1919	G
2	L5	1920	C
2	L5	1921	C
2	L5	1922	G
2	L5	1925	G
2	L5	1931	C
2	L5	1932	A
2	L5	1940	G
2	L5	1948	G
2	L5	1951	G
2	L5	1961	G
2	L5	1962	A
2	L5	1965	G
2	L5	1974	U
2	L5	1975	G
2	L5	1978	C
2	L5	1980	U
2	L5	1981	G
2	L5	1982	G
2	L5	1983	A
2	L5	1984	A
2	L5	1985	G
2	L5	1986	U
2	L5	1991	A
2	L5	1993	C
2	L5	1997	U
2	L5	1999	A
2	L5	2001	G
2	L5	2002	A
2	L5	2003	G
2	L5	2004	U
2	L5	2005	G
2	L5	2011	C

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Mol	Chain	Res	Type
2	L5	2017	A
2	L5	2018	C
2	L5	2024	G
2	L5	2026	A
2	L5	2046	G
2	L5	2048	U
2	L5	2055	G
2	L5	2056	G
2	L5	2069	A
2	L5	2084	C
2	L5	2092	G
2	L5	2093	A
2	L5	2094	G
2	L5	2095	A
2	L5	2096	G
2	L5	2097	U
2	L5	2098	G
2	L5	2099	G
2	L5	2101	C
2	L5	2102	G
2	L5	2103	G
2	L5	2107	C
2	L5	2110	C
2	L5	2112	G
2	L5	2250	C
2	L5	2252	G
2	L5	2256	C
2	L5	2258	C
2	L5	2268	A
2	L5	2289	C
2	L5	2300	A
2	L5	2301	G
2	L5	2313	A
2	L5	2316	G
2	L5	2322	G
2	L5	2331	G
2	L5	2333	G
2	L5	2348	G
2	L5	2349	A
2	L5	2351	OMC
2	L5	2360	A
2	L5	2364	OMG

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Mol	Chain	Res	Type
2	L5	2395	A
2	L5	2397	G
2	L5	2402	G
2	L5	2410	C
2	L5	2417	A
2	L5	2422	OMC
2	L5	2425	U
2	L5	2453	A
2	L5	2464	C
2	L5	2465	C
2	L5	2469	C
2	L5	2471	G
2	L5	2474	G
2	L5	2475	G
2	L5	2478	C
2	L5	2479	G
2	L5	2483	G
2	L5	2484	A
2	L5	2485	U
2	L5	2486	G
2	L5	2487	G
2	L5	2488	C
2	L5	2489	C
2	L5	2490	U
2	L5	2494	U
2	L5	2504	C
2	L5	2505	C
2	L5	2506	G
2	L5	2507	A
2	L5	2513	A
2	L5	2519	U
2	L5	2529	A
2	L5	2537	A
2	L5	2544	G
2	L5	2546	G
2	L5	2547	G
2	L5	2554	U
2	L5	2555	G
2	L5	2556	G
2	L5	2560	C
2	L5	2565	A
2	L5	2567	G

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Mol	Chain	Res	Type
2	L5	2573	A
2	L5	2581	A
2	L5	2583	C
2	L5	2587	A
2	L5	2589	C
2	L5	2600	A
2	L5	2627	C
2	L5	2653	C
2	L5	2662	G
2	L5	2669	C
2	L5	2676	A
2	L5	2687	U
2	L5	2694	G
2	L5	2695	A
2	L5	2696	A
2	L5	2703	G
2	L5	2706	G
2	L5	2707	U
2	L5	2708	U
2	L5	2709	C
2	L5	2710	C
2	L5	2711	G
2	L5	2719	C
2	L5	2721	G
2	L5	2724	G
2	L5	2726	G
2	L5	2739	C
2	L5	2742	G
2	L5	2743	A
2	L5	2754	G
2	L5	2761	U
2	L5	2763	U
2	L5	2769	U
2	L5	2770	C
2	L5	2787	A2M
2	L5	2788	U
2	L5	2790	U
2	L5	2794	C
2	L5	2799	G
2	L5	2802	C
2	L5	2806	A
2	L5	2814	C

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Mol	Chain	Res	Type
2	L5	2826	U
2	L5	2827	G
2	L5	2829	U
2	L5	2835	A
2	L5	2855	G
2	L5	2867	C
2	L5	2877	G
2	L5	2894	A
2	L5	2895	A
2	L5	2899	C
2	L5	2900	U
2	L5	2902	G
2	L5	2903	G
2	L5	2904	U
2	L5	2905	C
2	L5	2907	G
2	L5	2908	U
2	L5	3590	G
2	L5	3591	C
2	L5	3592	G
2	L5	3594	C
2	L5	3595	U
2	L5	3596	A
2	L5	3597	G
2	L5	3604	A
2	L5	3605	C
2	L5	3616	U
2	L5	3617	G
2	L5	3626	G
2	L5	3630	A
2	L5	3635	A
2	L5	3643	A
2	L5	3644	U
2	L5	3646	A
2	L5	3653	A
2	L5	3662	A
2	L5	3664	G
2	L5	3670	C
2	L5	3673	C
2	L5	3674	G
2	L5	3701	OMC
2	L5	3710	G

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Mol	Chain	Res	Type
2	L5	3711	A
2	L5	3713	U
2	L5	3714	G
2	L5	3726	A
2	L5	3727	A
2	L5	3748	A
2	L5	3753	G
2	L5	3760	A
2	L5	3764	U
2	L5	3770	U
2	L5	3774	A
2	L5	3775	A
2	L5	3776	G
2	L5	3777	G
2	L5	3778	U
2	L5	3784	A
2	L5	3785	A2M
2	L5	3786	U
2	L5	3792	OMG
2	L5	3811	G
2	L5	3812	C
2	L5	3814	U
2	L5	3817	A
2	L5	3819	G
2	L5	3824	A
2	L5	3839	G
2	L5	3840	U
2	L5	3876	A
2	L5	3877	A
2	L5	3878	C
2	L5	3879	G
2	L5	3892	U
2	L5	3897	G
2	L5	3898	G
2	L5	3901	A
2	L5	3906	A
2	L5	3907	G
2	L5	3908	A
2	L5	3915	U
2	L5	3923	A
2	L5	3938	G
2	L5	3939	G

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Mol	Chain	Res	Type
2	L5	3942	A
2	L5	3945	A
2	L5	3947	A
2	L5	3949	A
2	L5	3950	U
2	L5	3951	G
2	L5	3952	A
2	L5	3953	G
2	L5	4057	C
2	L5	4058	U
2	L5	4059	C
2	L5	4061	G
2	L5	4062	A
2	L5	4064	C
2	L5	4065	G
2	L5	4067	U
2	L5	4068	U
2	L5	4069	U
2	L5	4076	G
2	L5	4084	G
2	L5	4093	G
2	L5	4095	G
2	L5	4097	G
2	L5	4098	A
2	L5	4099	G
2	L5	4101	C
2	L5	4104	G
2	L5	4108	G
2	L5	4111	U
2	L5	4114	C
2	L5	4115	G
2	L5	4116	C
2	L5	4119	C
2	L5	4122	G
2	L5	4127	A
2	L5	4133	C
2	L5	4141	G
2	L5	4142	C
2	L5	4143	G
2	L5	4144	C
2	L5	4146	G
2	L5	4149	C

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Mol	Chain	Res	Type
2	L5	4150	G
2	L5	4162	C
2	L5	4163	U
2	L5	4170	A
2	L5	4183	G
2	L5	4184	G
2	L5	4191	G
2	L5	4213	A
2	L5	4220	6MZ
2	L5	4222	G
2	L5	4225	G
2	L5	4229	U
2	L5	4233	A
2	L5	4234	A
2	L5	4241	C
2	L5	4243	C
2	L5	4251	A
2	L5	4254	G
2	L5	4257	A
2	L5	4258	C
2	L5	4265	U
2	L5	4268	A
2	L5	4273	A
2	L5	4280	A
2	L5	4281	A
2	L5	4296	PSU
2	L5	4305	G
2	L5	4306	OMU
2	L5	4314	C
2	L5	4326	G
2	L5	4329	G
2	L5	4330	G
2	L5	4332	C
2	L5	4349	C
2	L5	4350	C
2	L5	4354	U
2	L5	4373	G
2	L5	4377	G
2	L5	4378	A
2	L5	4379	A
2	L5	4387	C
2	L5	4391	G

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Mol	Chain	Res	Type
2	L5	4393	G
2	L5	4394	A
2	L5	4410	G
2	L5	4421	C
2	L5	4422	A
2	L5	4430	G
2	L5	4436	U
2	L5	4438	U
2	L5	4444	C
2	L5	4447	5MC
2	L5	4448	G
2	L5	4449	A
2	L5	4464	A
2	L5	4466	C
2	L5	4475	G
2	L5	4476	C
2	L5	4488	A
2	L5	4500	PSU
2	L5	4512	U
2	L5	4513	A
2	L5	4518	A
2	L5	4519	C
2	L5	4523	A2M
2	L5	4524	G
2	L5	4528	G
2	L5	4545	G
2	L5	4548	A
2	L5	4549	G
2	L5	4560	C
2	L5	4567	G
2	L5	4575	G
2	L5	4584	A
2	L5	4589	A
2	L5	4590	A2M
2	L5	4601	U
2	L5	4617	G
2	L5	4636	PSU
2	L5	4637	OMG
2	L5	4652	G
2	L5	4656	A
2	L5	4670	C
2	L5	4672	A

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Mol	Chain	Res	Type
2	L5	4677	U
2	L5	4694	G
2	L5	4695	C
2	L5	4700	A
2	L5	4708	A
2	L5	4709	U
2	L5	4719	G
2	L5	4734	A
2	L5	4740	G
2	L5	4741	C
2	L5	4742	G
2	L5	4745	G
2	L5	4754	G
2	L5	4757	C
2	L5	4759	C
2	L5	4761	G
2	L5	4765	G
2	L5	4771	C
2	L5	4772	C
2	L5	4775	C
2	L5	4859	C
2	L5	4870	G
2	L5	4871	C
2	L5	4875	G
2	L5	4877	G
2	L5	4881	U
2	L5	4882	U
2	L5	4883	C
2	L5	4889	G
2	L5	4895	C
2	L5	4896	G
2	L5	4897	G
2	L5	4899	G
2	L5	4900	C
2	L5	4901	G
2	L5	4910	G
2	L5	4912	G
2	L5	4914	C
2	L5	4922	C
2	L5	4925	U
2	L5	4926	C
2	L5	4927	G

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Mol	Chain	Res	Type
2	L5	4928	C
2	L5	4934	A
2	L5	4940	C
2	L5	4941	G
2	L5	4943	A
2	L5	4944	C
2	L5	4949	G
2	L5	4955	A
2	L5	4960	G
2	L5	4976	U
2	L5	4985	U
2	L5	4988	U
2	L5	4989	U
2	L5	4991	U
2	L5	4995	U
2	L5	5006	U
2	L5	5013	C
2	L5	5014	A
2	L5	5017	G
2	L5	5022	U
2	L5	5024	C
2	L5	5026	U
2	L5	5028	G
2	L5	5030	U
2	L5	5034	A
2	L5	5041	G
2	L5	5047	C
2	L5	5050	C
2	L5	5054	C
2	L5	5055	G
2	L5	5061	A
2	L5	5069	U
3	L7	7	G
3	L7	22	A
3	L7	33	U
3	L7	38	U
3	L7	53	U
3	L7	54	A
3	L7	64	G
3	L7	89	G
3	L7	91	C
3	L7	97	G

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Mol	Chain	Res	Type
3	L7	100	A
3	L7	110	G
4	L8	23	C
4	L8	25	G
4	L8	34	U
4	L8	35	C
4	L8	39	G
4	L8	59	A
4	L8	62	A
4	L8	63	U
4	L8	75	OMG
4	L8	80	A
4	L8	82	A
4	L8	84	A
4	L8	85	U
4	L8	86	U
4	L8	87	G
4	L8	94	G
4	L8	99	U
4	L8	103	A
4	L8	105	C
4	L8	111	U
4	L8	114	G
4	L8	124	U
4	L8	125	C
4	L8	126	C
4	L8	127	U
4	L8	150	C
82	S2	13	C
82	S2	14	C
82	S2	25	A
82	S2	33	G
82	S2	42	A
82	S2	44	U
82	S2	45	A
82	S2	46	A
82	S2	56	G
82	S2	58	C
82	S2	59	U
82	S2	62	G
82	S2	65	C
82	S2	67	C

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Mol	Chain	Res	Type
82	S2	68	A
82	S2	72	C
82	S2	73	C
82	S2	74	G
82	S2	76	U
82	S2	99	A2M
82	S2	103	A
82	S2	113	G
82	S2	115	U
82	S2	130	G
82	S2	143	U
82	S2	149	A
82	S2	158	A
82	S2	160	U
82	S2	162	C
82	S2	168	C
82	S2	170	A
82	S2	171	A
82	S2	175	A
82	S2	190	G
82	S2	191	A
82	S2	196	C
82	S2	197	U
82	S2	198	U
82	S2	200	G
82	S2	203	G
82	S2	204	G
82	S2	206	G
82	S2	207	G
82	S2	208	G
82	S2	209	A
82	S2	211	G
82	S2	212	C
82	S2	214	U
82	S2	220	U
82	S2	291	G
82	S2	292	A
82	S2	295	C
82	S2	302	A
82	S2	303	C
82	S2	305	U
82	S2	306	C

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Mol	Chain	Res	Type
82	S2	307	G
82	S2	308	G
82	S2	309	G
82	S2	311	C
82	S2	312	G
82	S2	313	A
82	S2	318	A
82	S2	319	C
82	S2	323	C
82	S2	324	C
82	S2	325	C
82	S2	326	C
82	S2	328	U
82	S2	329	G
82	S2	332	G
82	S2	335	G
82	S2	339	A
82	S2	340	C
82	S2	347	G
82	S2	351	G
82	S2	360	A
82	S2	362	C
82	S2	364	A
82	S2	368	U
82	S2	370	G
82	S2	381	C
82	S2	383	G
82	S2	385	G
82	S2	386	C
82	S2	407	G
82	S2	408	A
82	S2	409	C
82	S2	426	A
82	S2	438	G
82	S2	448	A
82	S2	449	A
82	S2	450	C
82	S2	452	G
82	S2	464	A
82	S2	465	A
82	S2	471	G
82	S2	472	C

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Mol	Chain	Res	Type
82	S2	473	A
82	S2	474	G
82	S2	476	A
82	S2	482	G
82	S2	487	U
82	S2	488	U
82	S2	492	C
82	S2	493	A
82	S2	502	C
82	S2	516	A
82	S2	517	OMC
82	S2	530	U
82	S2	531	A
82	S2	532	C
82	S2	536	A
82	S2	537	C
82	S2	540	U
82	S2	542	U
82	S2	544	G
82	S2	546	G
82	S2	547	G
82	S2	551	U
82	S2	557	U
82	S2	558	G
82	S2	559	G
82	S2	563	G
82	S2	564	A
82	S2	576	A2M
82	S2	583	A
82	S2	587	A
82	S2	589	G
82	S2	590	A
82	S2	591	U
82	S2	593	C
82	S2	604	A
82	S2	606	G
82	S2	607	U
82	S2	614	C
82	S2	617	G
82	S2	622	C
82	S2	623	G
82	S2	628	A

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Mol	Chain	Res	Type
82	S2	631	U
82	S2	643	A
82	S2	644	OMG
82	S2	660	C
82	S2	663	C
82	S2	664	A
82	S2	668	A2M
82	S2	669	A
82	S2	671	A
82	S2	672	A
82	S2	673	G
82	S2	683	OMG
82	S2	688	U
82	S2	689	U
82	S2	692	G
82	S2	695	C
82	S2	696	G
82	S2	697	G
82	S2	698	G
82	S2	732	U
82	S2	733	C
82	S2	736	C
82	S2	737	G
82	S2	738	C
82	S2	749	U
82	S2	751	G
82	S2	752	G
82	S2	753	C
82	S2	788	G
82	S2	791	C
82	S2	792	C
82	S2	793	G
82	S2	798	G
82	S2	799	OMU
82	S2	801	PSU
82	S2	821	G
82	S2	822	U
82	S2	823	U
82	S2	824	C
82	S2	827	A
82	S2	830	A
82	S2	834	C

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Mol	Chain	Res	Type
82	S2	835	C
82	S2	836	G
82	S2	837	A
82	S2	838	G
82	S2	839	C
82	S2	842	C
82	S2	844	U
82	S2	847	A
82	S2	867	OMG
82	S2	870	A
82	S2	874	G
82	S2	877	C
82	S2	880	G
82	S2	888	U
82	S2	889	U
82	S2	891	G
82	S2	894	G
82	S2	896	U
82	S2	897	U
82	S2	898	U
82	S2	899	U
82	S2	900	C
82	S2	901	G
82	S2	903	A
82	S2	913	A
82	S2	920	A
82	S2	933	G
82	S2	934	G
82	S2	963	A
82	S2	970	G
82	S2	971	G
82	S2	972	A
82	S2	978	G
82	S2	985	G
82	S2	990	A
82	S2	992	A
82	S2	999	G
82	S2	1001	A
82	S2	1002	U
82	S2	1008	A
82	S2	1017	U
82	S2	1023	A

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Mol	Chain	Res	Type
82	S2	1027	A
82	S2	1045	PSU
82	S2	1061	U
82	S2	1062	A
82	S2	1080	A
82	S2	1083	A
82	S2	1085	C
82	S2	1109	C
82	S2	1113	A
82	S2	1116	C
82	S2	1121	G
82	S2	1123	C
82	S2	1126	G
82	S2	1133	A
82	S2	1138	C
82	S2	1139	C
82	S2	1148	A
82	S2	1150	A
82	S2	1153	C
82	S2	1154	U
82	S2	1155	U
82	S2	1170	A
82	S2	1195	A
82	S2	1200	A
82	S2	1207	G
82	S2	1208	A
82	S2	1215	C
82	S2	1217	A
82	S2	1220	A
82	S2	1224	G
82	S2	1227	G
82	S2	1242	U
82	S2	1243	U
82	S2	1248	B8N
82	S2	1251	A
82	S2	1253	A
82	S2	1256	G
82	S2	1257	G
82	S2	1259	A
82	S2	1264	C
82	S2	1271	C
82	S2	1272	OMC

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Mol	Chain	Res	Type
82	S2	1274	G
82	S2	1275	G
82	S2	1281	G
82	S2	1282	A
82	S2	1283	C
82	S2	1286	G
82	S2	1288	OMU
82	S2	1290	G
82	S2	1294	G
82	S2	1295	A
82	S2	1301	A
82	S2	1302	G
82	S2	1303	C
82	S2	1308	U
82	S2	1333	U
82	S2	1342	U
82	S2	1357	A
82	S2	1358	U
82	S2	1371	U
82	S2	1375	G
82	S2	1376	A
82	S2	1378	A
82	S2	1382	A
82	S2	1402	A
82	S2	1406	G
82	S2	1413	G
82	S2	1414	A
82	S2	1418	C
82	S2	1419	C
82	S2	1420	G
82	S2	1421	A
82	S2	1422	G
82	S2	1423	C
82	S2	1433	C
82	S2	1435	C
82	S2	1438	A
82	S2	1442	OMU
82	S2	1449	G
82	S2	1454	A
82	S2	1463	U
82	S2	1489	A
82	S2	1490	OMG

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Mol	Chain	Res	Type
82	S2	1492	U
82	S2	1494	U
82	S2	1495	G
82	S2	1497	G
82	S2	1498	A
82	S2	1507	G
82	S2	1520	G
82	S2	1521	C
82	S2	1531	A
82	S2	1533	A
82	S2	1544	C
82	S2	1546	G
82	S2	1552	G
82	S2	1553	C
82	S2	1556	A
82	S2	1558	C
82	S2	1560	U
82	S2	1575	G
82	S2	1580	A
82	S2	1581	C
82	S2	1582	C
82	S2	1585	U
82	S2	1587	G
82	S2	1588	A
82	S2	1600	G
82	S2	1604	G
82	S2	1606	G
82	S2	1621	U
82	S2	1623	A
82	S2	1630	A
82	S2	1631	U
82	S2	1633	A
82	S2	1634	A
82	S2	1637	A
82	S2	1638	G
82	S2	1648	G
82	S2	1649	U
82	S2	1654	G
82	S2	1663	A
82	S2	1665	G
82	S2	1680	G
82	S2	1683	C

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Mol	Chain	Res	Type
82	S2	1686	G
82	S2	1695	A
82	S2	1699	A
82	S2	1713	C
82	S2	1715	A
82	S2	1721	U
82	S2	1722	G
82	S2	1729	U
82	S2	1744	G
82	S2	1745	A
82	S2	1752	C
82	S2	1753	C
82	S2	1754	G
82	S2	1755	C
82	S2	1756	C
82	S2	1757	G
82	S2	1759	G
82	S2	1761	U
82	S2	1772	C
82	S2	1773	C
82	S2	1774	C
82	S2	1777	G
82	S2	1782	G
82	S2	1783	C
82	S2	1784	G
82	S2	1786	U
82	S2	1798	C
82	S2	1810	U
82	S2	1825	A
82	S2	1829	G
82	S2	1831	A
82	S2	1835	A
82	S2	1838	U
82	S2	1849	G
82	S2	1851	MA6
82	S2	1852	C
82	S2	1861	G
82	S2	1862	G
82	S2	1863	A
82	S2	1864	U
82	S2	1865	C
83	Zt	4	C

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Mol	Chain	Res	Type
83	Zt	6	G
83	Zt	7	A
83	Zt	8	U
83	Zt	9	A
83	Zt	10	G
83	Zt	11	C
83	Zt	14	A
83	Zt	15	G
83	Zt	16	C
83	Zt	18	U
83	Zt	19	G
83	Zt	20	U
83	Zt	21	A
83	Zt	22	G
83	Zt	25	C
83	Zt	26	A
83	Zt	29	A
83	Zt	30	G
83	Zt	33	U
83	Zt	35	U
83	Zt	36	U
83	Zt	37	A
83	Zt	38	A
83	Zt	40	C
83	Zt	42	G
83	Zt	43	A
83	Zt	45	G
83	Zt	48	C
83	Zt	49	C
83	Zt	53	G
83	Zt	56	C
83	Zt	57	A
83	Zt	58	A
83	Zt	59	G
83	Zt	60	U
83	Zt	61	C
83	Zt	63	C
83	Zt	66	U
83	Zt	67	U
83	Zt	70	G
83	Zt	71	G
83	Zt	72	C

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L5	406	C
2	L5	493	G
2	L5	914	U
2	L5	1082	C
2	L5	1633	G
2	L5	1977	C
2	L5	2416	G
2	L5	2485	U
2	L5	2675	G
2	L5	2760	G
2	L5	3673	C
2	L5	4447	5MC
2	L5	4600	G
2	L5	4699	U
2	L5	4913	G
82	S2	291	G
82	S2	563	G
82	S2	688	U

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

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	$\# Z > 2$
82	PSU	S2	1004	82	18,21,22	1.09	1 (5%)	21,30,33	1.84	4 (19%)
2	PSU	L5	4361	2	18,21,22	1.07	1 (5%)	21,30,33	1.83	4 (19%)
2	OMC	L5	2422	2,85	19,22,23	0.54	0	25,31,34	0.69	0
82	OMC	S2	1703	82	19,22,23	0.53	0	25,31,34	0.70	1 (4%)
82	OMU	S2	116	82	19,22,23	3.33	7 (36%)	25,31,34	1.69	5 (20%)
2	OMG	L5	3899	2	23,26,27	0.51	0	32,38,41	0.49	0
82	A2M	S2	1031	82	22,25,26	1.20	1 (4%)	30,36,39	1.55	7 (23%)
2	PSU	L5	1782	2	18,21,22	1.15	1 (5%)	21,30,33	1.91	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	L5	4972	2	18,21,22	1.09	1 (5%)	21,30,33	1.90	6 (28%)
2	OMG	L5	4637	2	23,26,27	0.49	0	32,38,41	0.49	0
2	OMU	L5	4306	2	19,22,23	3.34	7 (36%)	25,31,34	1.77	4 (16%)
2	PSU	L5	1744	2,85	18,21,22	1.08	1 (5%)	21,30,33	1.90	6 (28%)
2	OMG	L5	4228	2	23,26,27	0.49	0	32,38,41	0.58	0
82	PSU	S2	109	82	18,21,22	1.11	1 (5%)	21,30,33	1.89	4 (19%)
82	PSU	S2	1046	82	18,21,22	1.11	1 (5%)	21,30,33	1.80	4 (19%)
2	A2M	L5	3825	2	22,25,26	1.22	1 (4%)	30,36,39	1.57	8 (26%)
2	PSU	L5	4628	2	18,21,22	1.00	1 (5%)	21,30,33	1.85	4 (19%)
2	PSU	L5	1582	2	18,21,22	1.12	1 (5%)	21,30,33	1.75	4 (19%)
2	A2M	L5	1323	2	22,25,26	1.23	2 (9%)	30,36,39	1.62	9 (30%)
4	PSU	L8	69	4	18,21,22	1.09	1 (5%)	21,30,33	1.82	5 (23%)
2	OMC	L5	2351	2,85	19,22,23	0.54	0	25,31,34	0.83	1 (4%)
2	OMG	L5	4499	2	23,26,27	0.45	0	32,38,41	0.49	0
2	OMG	L5	4494	2	23,26,27	0.47	0	32,38,41	0.46	0
82	OMG	S2	509	82	23,26,27	0.47	0	32,38,41	0.47	0
2	PSU	L5	4471	2	18,21,22	1.06	1 (5%)	21,30,33	1.83	4 (19%)
2	OMU	L5	2837	2	19,22,23	3.35	7 (36%)	25,31,34	1.85	5 (20%)
2	A2M	L5	1326	2,85	22,25,26	1.18	1 (4%)	30,36,39	1.54	9 (30%)
2	PSU	L5	3884	2	18,21,22	1.11	1 (5%)	21,30,33	1.89	4 (19%)
82	A2M	S2	576	82	22,25,26	1.18	1 (4%)	30,36,39	1.52	7 (23%)
82	OMU	S2	1442	82	19,22,23	3.40	7 (36%)	25,31,34	1.80	5 (20%)
82	PSU	S2	1177	82	18,21,22	1.11	1 (5%)	21,30,33	1.87	4 (19%)
2	OMG	L5	4618	2	23,26,27	0.48	0	32,38,41	0.55	0
2	OMU	L5	4498	2	19,22,23	3.37	7 (36%)	25,31,34	1.81	5 (20%)
82	OMU	S2	354	82	19,22,23	3.35	7 (36%)	25,31,34	1.82	5 (20%)
2	PSU	L5	3637	2	18,21,22	1.11	1 (5%)	21,30,33	2.04	5 (23%)
82	PSU	S2	1244	82	18,21,22	1.14	1 (5%)	21,30,33	1.88	4 (19%)
82	4AC	S2	1842	82	21,24,25	0.38	0	28,34,37	0.45	0
2	PSU	L5	4296	2	18,21,22	1.10	1 (5%)	21,30,33	1.96	5 (23%)
2	PSU	L5	4636	2	18,21,22	1.11	1 (5%)	21,30,33	2.04	6 (28%)
82	MA6	S2	1850	82	23,26,27	1.28	2 (8%)	33,38,41	3.32	12 (36%)
82	OMC	S2	174	82	19,22,23	0.51	0	25,31,34	0.70	0
2	PSU	L5	2839	2	18,21,22	1.08	1 (5%)	21,30,33	1.93	5 (23%)
2	OMC	L5	4456	2	19,22,23	0.56	0	25,31,34	0.79	1 (4%)
82	PSU	S2	651	82	18,21,22	1.14	1 (5%)	21,30,33	1.89	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	L5	1792	2	18,21,22	1.06	1 (5%)	21,30,33	1.86	4 (19%)
2	PSU	L5	4431	2	18,21,22	1.10	1 (5%)	21,30,33	1.94	5 (23%)
82	A2M	S2	99	82,85	22,25,26	1.19	1 (4%)	30,36,39	1.53	7 (23%)
82	PSU	S2	105	82	18,21,22	1.07	1 (5%)	21,30,33	1.86	4 (19%)
82	4AC	S2	1337	82	21,24,25	0.37	0	28,34,37	0.64	1 (3%)
2	A2M	L5	3785	2,85	22,25,26	1.21	1 (4%)	30,36,39	1.72	9 (30%)
82	PSU	S2	866	82	18,21,22	1.13	1 (5%)	21,30,33	1.92	5 (23%)
82	PSU	S2	1174	82	18,21,22	1.10	1 (5%)	21,30,33	1.86	4 (19%)
2	PSU	L5	1781	2	18,21,22	1.07	1 (5%)	21,30,33	1.81	4 (19%)
2	PSU	L5	5001	2	18,21,22	1.10	1 (5%)	21,30,33	1.82	4 (19%)
82	OMU	S2	121	82	19,22,23	3.39	7 (36%)	25,31,34	1.79	5 (20%)
2	OMG	L5	4196	1,2	23,26,27	0.46	0	32,38,41	0.47	0
4	OMG	L8	75	4	23,26,27	0.46	0	32,38,41	0.51	0
2	OMC	L5	3701	2	19,22,23	0.56	0	25,31,34	0.82	1 (4%)
2	OMC	L5	3869	2	19,22,23	0.51	0	25,31,34	0.64	0
2	OMC	L5	3887	2	19,22,23	0.54	0	25,31,34	0.78	0
2	OMG	L5	2364	2,85	23,26,27	0.48	0	32,38,41	0.47	0
82	G7M	S2	1639	1,82	23,26,27	2.65	9 (39%)	34,39,42	2.63	11 (32%)
82	6MZ	S2	1832	82,85	26,26,26	2.86	5 (19%)	36,39,39	2.04	10 (27%)
2	PSU	L5	3851	2,85	18,21,22	1.08	1 (5%)	21,30,33	1.80	4 (19%)
82	A2M	S2	159	82	22,25,26	1.26	1 (4%)	30,36,39	1.56	8 (26%)
2	PSU	L5	3853	2,85	18,21,22	1.07	1 (5%)	21,30,33	1.78	4 (19%)
2	PSU	L5	4973	2	18,21,22	1.08	1 (5%)	21,30,33	1.87	4 (19%)
2	A2M	L5	1534	2,85	22,25,26	1.20	1 (4%)	30,36,39	1.59	8 (26%)
82	OMC	S2	462	82	19,22,23	0.52	0	25,31,34	0.78	1 (4%)
2	PSU	L5	4579	2	18,21,22	1.07	1 (5%)	21,30,33	1.81	4 (19%)
2	OMC	L5	2824	2	19,22,23	0.54	0	25,31,34	0.81	1 (4%)
2	PSU	L5	4532	2	18,21,22	1.11	1 (5%)	21,30,33	1.89	4 (19%)
2	A2M	L5	4523	2,85	22,25,26	1.27	1 (4%)	30,36,39	1.59	8 (26%)
2	OMC	L5	2861	2	19,22,23	0.56	0	25,31,34	1.00	2 (8%)
2	5MC	L5	3782	2,85	19,22,23	0.52	0	26,32,35	0.80	1 (3%)
2	OMG	L5	1625	2	23,26,27	0.47	0	32,38,41	0.47	0
82	A2M	S2	468	82	22,25,26	1.21	1 (4%)	30,36,39	1.53	7 (23%)
2	OMG	L5	3744	2	23,26,27	0.48	0	32,38,41	0.45	0
2	PSU	L5	5010	2	18,21,22	1.13	1 (5%)	21,30,33	1.91	4 (19%)
2	PSU	L5	4552	2	18,21,22	1.06	1 (5%)	21,30,33	1.86	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
82	PSU	S2	966	82,85	18,21,22	1.05	1 (5%)	21,30,33	1.85	4 (19%)
2	PSU	L5	4299	2	18,21,22	1.10	1 (5%)	21,30,33	1.93	4 (19%)
82	OMU	S2	172	82	19,22,23	3.38	7 (36%)	25,31,34	1.82	5 (20%)
2	PSU	L5	3844	2	18,21,22	1.10	1 (5%)	21,30,33	1.91	4 (19%)
82	OMU	S2	799	82	19,22,23	3.43	7 (36%)	25,31,34	1.78	5 (20%)
2	OMG	L5	3792	2	23,26,27	0.47	0	32,38,41	0.50	0
82	OMC	S2	1391	82	19,22,23	0.51	0	25,31,34	0.67	0
2	PSU	L5	4673	2	18,21,22	1.08	1 (5%)	21,30,33	1.87	4 (19%)
82	PSU	S2	1045	82	18,21,22	1.10	1 (5%)	21,30,33	1.89	4 (19%)
2	OMU	L5	4620	2	19,22,23	3.34	7 (36%)	25,31,34	1.77	4 (16%)
2	OMG	L5	3627	2	23,26,27	0.46	0	32,38,41	0.56	0
82	OMG	S2	644	82	23,26,27	0.45	0	32,38,41	0.48	0
2	OMC	L5	1340	2	19,22,23	0.53	0	25,31,34	0.74	0
2	5MC	L5	4447	2	19,22,23	0.63	0	26,32,35	0.54	0
82	OMG	S2	1490	82	23,26,27	0.50	0	32,38,41	0.46	0
82	PSU	S2	406	82	18,21,22	1.12	1 (5%)	21,30,33	1.84	4 (19%)
82	PSU	S2	93	82	18,21,22	1.10	1 (5%)	21,30,33	1.83	4 (19%)
82	PSU	S2	649	82	18,21,22	1.07	1 (5%)	21,30,33	1.90	4 (19%)
82	A2M	S2	668	82,85	22,25,26	1.26	2 (9%)	30,36,39	1.57	7 (23%)
2	PSU	L5	4312	2	18,21,22	1.08	1 (5%)	21,30,33	1.89	4 (19%)
2	PSU	L5	1536	2	18,21,22	1.11	1 (5%)	21,30,33	1.99	4 (19%)
2	6MZ	L5	4220	2	22,25,26	4.00	11 (50%)	29,36,39	2.44	12 (41%)
82	PSU	S2	863	82	18,21,22	1.10	1 (5%)	21,30,33	1.87	4 (19%)
82	PSU	S2	1367	82	18,21,22	1.12	1 (5%)	21,30,33	1.90	4 (19%)
2	PSU	L5	1683	2	18,21,22	1.10	1 (5%)	21,30,33	1.88	4 (19%)
82	PSU	S2	814	82	18,21,22	1.12	1 (5%)	21,30,33	1.88	4 (19%)
82	OMG	S2	683	82	23,26,27	0.51	0	32,38,41	0.45	0
82	OMG	S2	1328	82	23,26,27	0.45	0	32,38,41	0.44	0
82	OMU	S2	1326	82	19,22,23	3.37	7 (36%)	25,31,34	1.81	5 (20%)
2	OMG	L5	1316	2	23,26,27	0.49	0	32,38,41	0.47	0
2	PSU	L5	4521	2,85	18,21,22	1.11	1 (5%)	21,30,33	1.88	4 (19%)
2	A2M	L5	2401	2	22,25,26	1.20	1 (4%)	30,36,39	1.56	7 (23%)
2	PSU	L5	3920	2,85	18,21,22	1.08	1 (5%)	21,30,33	1.89	5 (23%)
82	OMG	S2	436	82	23,26,27	0.46	0	32,38,41	0.51	0
82	PSU	S2	1232	82	18,21,22	1.13	1 (5%)	21,30,33	1.87	4 (19%)
82	A2M	S2	27	82	22,25,26	1.26	1 (4%)	30,36,39	1.53	7 (23%)
2	UR3	L5	4530	2	19,22,23	2.78	7 (36%)	26,32,35	1.58	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	L5	4493	2	18,21,22	1.08	1 (5%)	21,30,33	1.92	5 (23%)
2	UY1	L5	3818	2	19,22,23	4.96	9 (47%)	21,31,34	2.02	6 (28%)
2	PSU	L5	2632	2	18,21,22	1.09	1 (5%)	21,30,33	1.99	5 (23%)
2	A2M	L5	3867	2	22,25,26	1.25	2 (9%)	30,36,39	1.51	9 (30%)
82	OMC	S2	1272	82	19,22,23	0.53	0	25,31,34	0.82	1 (4%)
2	A2M	L5	398	2	22,25,26	1.22	1 (4%)	30,36,39	1.60	7 (23%)
82	OMU	S2	1288	82	19,22,23	3.38	7 (36%)	25,31,34	1.80	5 (20%)
82	PSU	S2	686	82	18,21,22	1.11	1 (5%)	21,30,33	1.90	5 (23%)
2	OMG	L5	2876	2	23,26,27	0.49	0	32,38,41	0.47	0
2	A2M	L5	1524	2	22,25,26	1.30	2 (9%)	30,36,39	1.54	8 (26%)
2	PSU	L5	3695	2	18,21,22	1.09	1 (5%)	21,30,33	1.88	5 (23%)
2	OMC	L5	2365	2,85	19,22,23	0.53	0	25,31,34	0.63	0
82	PSU	S2	1056	82	18,21,22	1.07	1 (5%)	21,30,33	1.88	5 (23%)
2	PSU	L5	4353	2	18,21,22	1.10	1 (5%)	21,30,33	1.91	5 (23%)
2	OMG	L5	4623	2	23,26,27	0.48	0	32,38,41	0.46	0
2	PSU	L5	1860	2	18,21,22	1.13	1 (5%)	21,30,33	1.90	4 (19%)
2	A2M	L5	2815	2	22,25,26	1.18	1 (4%)	30,36,39	1.44	9 (30%)
2	A2M	L5	3830	2	22,25,26	1.21	1 (4%)	30,36,39	1.60	7 (23%)
2	OMU	L5	3925	2	19,22,23	3.32	7 (36%)	25,31,34	1.87	5 (20%)
2	PSU	L5	4403	2	18,21,22	1.02	1 (5%)	21,30,33	1.84	5 (23%)
2	PSU	L5	4689	2	18,21,22	1.04	1 (5%)	21,30,33	1.88	4 (19%)
2	OMU	L5	4227	2	19,22,23	3.36	7 (36%)	25,31,34	1.83	5 (20%)
2	OMC	L5	3808	2	19,22,23	0.59	0	25,31,34	0.95	2 (8%)
82	OMU	S2	627	82	19,22,23	3.37	7 (36%)	25,31,34	1.80	5 (20%)
2	PSU	L5	4500	2	18,21,22	1.13	1 (5%)	21,30,33	1.95	5 (23%)
82	OMG	S2	867	82	23,26,27	0.48	0	32,38,41	0.47	0
2	PSU	L5	4293	2	18,21,22	1.13	2 (11%)	21,30,33	1.93	4 (19%)
2	OMG	L5	2424	2	23,26,27	0.49	0	32,38,41	0.48	0
2	OMC	L5	2804	2	19,22,23	0.53	0	25,31,34	0.65	0
82	B8N	S2	1248	82	25,29,30	3.29	6 (24%)	28,42,45	1.98	8 (28%)
82	OMC	S2	517	82	19,22,23	0.54	0	25,31,34	0.64	0
82	A2M	S2	484	82	22,25,26	1.21	1 (4%)	30,36,39	1.52	7 (23%)
2	A2M	L5	4571	2	22,25,26	1.23	1 (4%)	30,36,39	1.58	6 (20%)
82	PSU	S2	1081	82	18,21,22	1.13	1 (5%)	21,30,33	1.91	5 (23%)
82	OMU	S2	428	82	19,22,23	3.37	7 (36%)	25,31,34	1.83	5 (20%)
2	PSU	L5	1862	2	18,21,22	1.12	1 (5%)	21,30,33	1.89	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	L5	4576	2	18,21,22	1.08	1 (5%)	21,30,33	1.86	5 (23%)
2	A2M	L5	1871	2,85	22,25,26	1.19	1 (4%)	30,36,39	1.52	7 (23%)
2	PSU	L5	3639	2	18,21,22	1.12	1 (5%)	21,30,33	1.91	4 (19%)
2	PSU	L5	3822	2	18,21,22	1.13	2 (11%)	21,30,33	1.99	6 (28%)
2	A2M	L5	2363	2,85	22,25,26	1.18	1 (4%)	30,36,39	1.51	8 (26%)
82	A2M	S2	166	82	22,25,26	1.27	1 (4%)	30,36,39	1.65	7 (23%)
2	OMG	L5	4370	2	23,26,27	0.46	0	32,38,41	0.45	0
2	A2M	L5	4590	2	22,25,26	1.18	1 (4%)	30,36,39	1.60	7 (23%)
82	OMG	S2	601	82	23,26,27	0.48	0	32,38,41	0.64	0
82	MA6	S2	1851	82	23,26,27	1.28	2 (8%)	33,38,41	3.36	12 (36%)
2	A2M	L5	3718	2	22,25,26	1.19	1 (4%)	30,36,39	1.52	7 (23%)
2	OMG	L5	4392	2	23,26,27	0.47	0	32,38,41	0.45	0
2	OMC	L5	4536	2	19,22,23	0.58	0	25,31,34	0.79	0
82	PSU	S2	681	82	18,21,22	1.07	1 (5%)	21,30,33	1.88	4 (19%)
2	A2M	L5	400	2	22,25,26	1.25	1 (4%)	30,36,39	1.56	9 (30%)
2	OMG	L5	1522	2	23,26,27	0.47	0	32,38,41	0.58	0
2	PSU	L5	1677	2	18,21,22	1.09	2 (11%)	21,30,33	1.95	5 (23%)
82	PSU	S2	801	82	18,21,22	1.11	1 (5%)	21,30,33	1.85	4 (19%)
2	PSU	L5	4442	2	18,21,22	1.13	1 (5%)	21,30,33	2.06	6 (28%)
2	A2M	L5	2787	2	22,25,26	1.19	1 (4%)	30,36,39	1.48	7 (23%)
2	OMC	L5	3841	2	19,22,23	0.51	0	25,31,34	0.70	1 (4%)
2	1MA	L5	1322	2,85	21,25,26	0.47	0	30,37,40	0.75	1 (3%)
4	PSU	L8	55	4	18,21,22	1.13	1 (5%)	21,30,33	1.90	4 (19%)
2	PSU	L5	4457	2	18,21,22	1.10	1 (5%)	21,30,33	1.91	5 (23%)
82	A2M	S2	1383	82	22,25,26	1.26	1 (4%)	30,36,39	1.70	7 (23%)

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
82	PSU	S2	1004	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	4361	2	-	0/7/25/26	0/2/2/2
2	OMC	L5	2422	2,85	-	2/9/27/28	0/2/2/2
82	OMC	S2	1703	82	-	0/9/27/28	0/2/2/2
82	OMU	S2	116	82	-	1/9/27/28	0/2/2/2
2	OMG	L5	3899	2	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	A2M	S2	1031	82	-	0/9/27/28	0/3/3/3
2	PSU	L5	1782	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	4972	2	-	0/7/25/26	0/2/2/2
2	OMG	L5	4637	2	-	1/9/27/28	0/3/3/3
2	OMU	L5	4306	2	-	0/9/27/28	0/2/2/2
2	PSU	L5	1744	2,85	-	0/7/25/26	0/2/2/2
2	OMG	L5	4228	2	-	0/9/27/28	0/3/3/3
82	PSU	S2	109	82	-	0/7/25/26	0/2/2/2
82	PSU	S2	1046	82	-	0/7/25/26	0/2/2/2
2	A2M	L5	3825	2	-	1/9/27/28	0/3/3/3
2	PSU	L5	4628	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	1582	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	1323	2	-	3/9/27/28	0/3/3/3
4	PSU	L8	69	4	-	0/7/25/26	0/2/2/2
2	OMC	L5	2351	2,85	-	2/9/27/28	0/2/2/2
2	OMG	L5	4499	2	-	0/9/27/28	0/3/3/3
2	OMG	L5	4494	2	-	0/9/27/28	0/3/3/3
82	OMG	S2	509	82	-	1/9/27/28	0/3/3/3
2	PSU	L5	4471	2	-	0/7/25/26	0/2/2/2
2	OMU	L5	2837	2	-	0/9/27/28	0/2/2/2
2	A2M	L5	1326	2,85	-	3/9/27/28	0/3/3/3
2	PSU	L5	3884	2	-	0/7/25/26	0/2/2/2
82	A2M	S2	576	82	-	4/9/27/28	0/3/3/3
82	OMU	S2	1442	82	-	2/9/27/28	0/2/2/2
82	PSU	S2	1177	82	-	0/7/25/26	0/2/2/2
2	OMG	L5	4618	2	-	2/9/27/28	0/3/3/3
2	OMU	L5	4498	2	-	0/9/27/28	0/2/2/2
82	OMU	S2	354	82	-	1/9/27/28	0/2/2/2
2	PSU	L5	3637	2	-	0/7/25/26	0/2/2/2
82	PSU	S2	1244	82	-	0/7/25/26	0/2/2/2
82	4AC	S2	1842	82	-	0/11/29/30	0/2/2/2
2	PSU	L5	4296	2	-	2/7/25/26	0/2/2/2
2	PSU	L5	4636	2	-	1/7/25/26	0/2/2/2
82	MA6	S2	1850	82	-	0/11/29/30	0/3/3/3
82	OMC	S2	174	82	-	0/9/27/28	0/2/2/2
2	PSU	L5	2839	2	-	0/7/25/26	0/2/2/2
2	OMC	L5	4456	2	-	0/9/27/28	0/2/2/2
82	PSU	S2	651	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	1792	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	4431	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	A2M	S2	99	82,85	-	2/9/27/28	0/3/3/3
82	PSU	S2	105	82	-	0/7/25/26	0/2/2/2
82	4AC	S2	1337	82	-	1/11/29/30	0/2/2/2
2	A2M	L5	3785	2,85	-	0/9/27/28	0/3/3/3
82	PSU	S2	866	82	-	0/7/25/26	0/2/2/2
82	PSU	S2	1174	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	1781	2	-	1/7/25/26	0/2/2/2
2	PSU	L5	5001	2	-	0/7/25/26	0/2/2/2
82	OMU	S2	121	82	-	0/9/27/28	0/2/2/2
2	OMG	L5	4196	1,2	-	1/9/27/28	0/3/3/3
4	OMG	L8	75	4	-	1/9/27/28	0/3/3/3
2	OMC	L5	3701	2	-	4/9/27/28	0/2/2/2
2	OMC	L5	3869	2	-	0/9/27/28	0/2/2/2
2	OMC	L5	3887	2	-	2/9/27/28	0/2/2/2
2	OMG	L5	2364	2,85	-	2/9/27/28	0/3/3/3
82	G7M	S2	1639	1,82	-	0/7/25/26	0/3/3/3
82	6MZ	S2	1832	82,85	-	7/12/28/28	0/3/3/3
2	PSU	L5	3851	2,85	-	1/7/25/26	0/2/2/2
82	A2M	S2	159	82	-	2/9/27/28	0/3/3/3
2	PSU	L5	3853	2,85	-	0/7/25/26	0/2/2/2
2	PSU	L5	4973	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	1534	2,85	-	2/9/27/28	0/3/3/3
82	OMC	S2	462	82	-	0/9/27/28	0/2/2/2
2	PSU	L5	4579	2	-	0/7/25/26	0/2/2/2
2	OMC	L5	2824	2	-	1/9/27/28	0/2/2/2
2	PSU	L5	4532	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	4523	2,85	-	1/9/27/28	0/3/3/3
2	OMC	L5	2861	2	-	3/9/27/28	0/2/2/2
2	5MC	L5	3782	2,85	-	0/7/25/26	0/2/2/2
2	OMG	L5	1625	2	-	2/9/27/28	0/3/3/3
82	A2M	S2	468	82	-	1/9/27/28	0/3/3/3
2	OMG	L5	3744	2	-	1/9/27/28	0/3/3/3
2	PSU	L5	5010	2	-	2/7/25/26	0/2/2/2
2	PSU	L5	4552	2	-	0/7/25/26	0/2/2/2
82	PSU	S2	966	82,85	-	0/7/25/26	0/2/2/2
2	PSU	L5	4299	2	-	0/7/25/26	0/2/2/2
82	OMU	S2	172	82	-	0/9/27/28	0/2/2/2
2	PSU	L5	3844	2	-	1/7/25/26	0/2/2/2
82	OMU	S2	799	82	-	2/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMG	L5	3792	2	-	2/9/27/28	0/3/3/3
82	OMC	S2	1391	82	-	0/9/27/28	0/2/2/2
2	PSU	L5	4673	2	-	0/7/25/26	0/2/2/2
82	PSU	S2	1045	82	-	2/7/25/26	0/2/2/2
2	OMU	L5	4620	2	-	0/9/27/28	0/2/2/2
2	OMG	L5	3627	2	-	0/9/27/28	0/3/3/3
82	OMG	S2	644	82	-	4/9/27/28	0/3/3/3
2	OMC	L5	1340	2	-	1/9/27/28	0/2/2/2
2	5MC	L5	4447	2	-	5/7/25/26	0/2/2/2
82	OMG	S2	1490	82	-	1/9/27/28	0/3/3/3
82	PSU	S2	406	82	-	0/7/25/26	0/2/2/2
82	PSU	S2	93	82	-	0/7/25/26	0/2/2/2
82	PSU	S2	649	82	-	0/7/25/26	0/2/2/2
82	A2M	S2	668	82,85	-	3/9/27/28	0/3/3/3
2	PSU	L5	4312	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	1536	2	-	2/7/25/26	0/2/2/2
2	6MZ	L5	4220	2	-	4/9/27/28	0/3/3/3
82	PSU	S2	863	82	-	0/7/25/26	0/2/2/2
82	PSU	S2	1367	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	1683	2	-	0/7/25/26	0/2/2/2
82	PSU	S2	814	82	-	0/7/25/26	0/2/2/2
82	OMG	S2	683	82	-	2/9/27/28	0/3/3/3
82	OMG	S2	1328	82	-	0/9/27/28	0/3/3/3
82	OMU	S2	1326	82	-	0/9/27/28	0/2/2/2
2	OMG	L5	1316	2	-	1/9/27/28	0/3/3/3
2	PSU	L5	4521	2,85	-	2/7/25/26	0/2/2/2
2	A2M	L5	2401	2	-	0/9/27/28	0/3/3/3
2	PSU	L5	3920	2,85	-	0/7/25/26	0/2/2/2
82	OMG	S2	436	82	-	0/9/27/28	0/3/3/3
82	PSU	S2	1232	82	-	0/7/25/26	0/2/2/2
82	A2M	S2	27	82	-	1/9/27/28	0/3/3/3
2	UR3	L5	4530	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	4493	2	-	0/7/25/26	0/2/2/2
2	UY1	L5	3818	2	-	1/9/27/28	0/2/2/2
2	PSU	L5	2632	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	3867	2	-	1/9/27/28	0/3/3/3
82	OMC	S2	1272	82	-	2/9/27/28	0/2/2/2
2	A2M	L5	398	2	-	0/9/27/28	0/3/3/3
82	OMU	S2	1288	82	-	2/9/27/28	0/2/2/2
82	PSU	S2	686	82	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMG	L5	2876	2	-	0/9/27/28	0/3/3/3
2	A2M	L5	1524	2	-	4/9/27/28	0/3/3/3
2	PSU	L5	3695	2	-	0/7/25/26	0/2/2/2
2	OMC	L5	2365	2,85	-	0/9/27/28	0/2/2/2
82	PSU	S2	1056	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	4353	2	-	0/7/25/26	0/2/2/2
2	OMG	L5	4623	2	-	1/9/27/28	0/3/3/3
2	PSU	L5	1860	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	2815	2	-	2/9/27/28	0/3/3/3
2	A2M	L5	3830	2	-	1/9/27/28	0/3/3/3
2	OMU	L5	3925	2	-	0/9/27/28	0/2/2/2
2	PSU	L5	4403	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	4689	2	-	0/7/25/26	0/2/2/2
2	OMU	L5	4227	2	-	0/9/27/28	0/2/2/2
2	OMC	L5	3808	2	-	0/9/27/28	0/2/2/2
82	OMU	S2	627	82	-	5/9/27/28	0/2/2/2
2	PSU	L5	4500	2	-	3/7/25/26	0/2/2/2
82	OMG	S2	867	82	-	1/9/27/28	0/3/3/3
2	PSU	L5	4293	2	-	1/7/25/26	0/2/2/2
2	OMG	L5	2424	2	-	0/9/27/28	0/3/3/3
2	OMC	L5	2804	2	-	0/9/27/28	0/2/2/2
82	B8N	S2	1248	82	-	4/16/34/35	0/2/2/2
82	OMC	S2	517	82	-	3/9/27/28	0/2/2/2
82	A2M	S2	484	82	-	1/9/27/28	0/3/3/3
2	A2M	L5	4571	2	-	0/9/27/28	0/3/3/3
82	PSU	S2	1081	82	-	1/7/25/26	0/2/2/2
82	OMU	S2	428	82	-	3/9/27/28	0/2/2/2
2	PSU	L5	1862	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	4576	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	1871	2,85	-	0/9/27/28	0/3/3/3
2	PSU	L5	3639	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	3822	2	-	2/7/25/26	0/2/2/2
2	A2M	L5	2363	2,85	-	0/9/27/28	0/3/3/3
82	A2M	S2	166	82	-	0/9/27/28	0/3/3/3
2	OMG	L5	4370	2	-	0/9/27/28	0/3/3/3
2	A2M	L5	4590	2	-	4/9/27/28	0/3/3/3
82	OMG	S2	601	82	-	0/9/27/28	0/3/3/3
82	MA6	S2	1851	82	-	2/11/29/30	0/3/3/3
2	A2M	L5	3718	2	-	1/9/27/28	0/3/3/3
2	OMG	L5	4392	2	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMC	L5	4536	2	-	0/9/27/28	0/2/2/2
82	PSU	S2	681	82	-	0/7/25/26	0/2/2/2
2	A2M	L5	400	2	-	1/9/27/28	0/3/3/3
2	OMG	L5	1522	2	-	0/9/27/28	0/3/3/3
2	PSU	L5	1677	2	-	2/7/25/26	0/2/2/2
82	PSU	S2	801	82	-	2/7/25/26	0/2/2/2
2	PSU	L5	4442	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	2787	2	-	5/9/27/28	0/3/3/3
2	OMC	L5	3841	2	-	1/9/27/28	0/2/2/2
2	1MA	L5	1322	2,85	-	0/7/25/26	0/3/3/3
4	PSU	L8	55	4	-	0/7/25/26	0/2/2/2
2	PSU	L5	4457	2	-	0/7/25/26	0/2/2/2
82	A2M	S2	1383	82	-	3/9/27/28	0/3/3/3

All (271) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	S2	1832	6MZ	C6-N6	12.93	1.49	1.34
2	L5	3818	UY1	C6-C5	12.90	1.49	1.35
2	L5	4220	6MZ	C6-N6	12.54	1.48	1.34
2	L5	3818	UY1	C2-N1	12.00	1.52	1.36
82	S2	1442	OMU	C2-N1	8.53	1.51	1.38
82	S2	799	OMU	C2-N1	8.51	1.51	1.38
2	L5	4220	6MZ	C3'-C2'	-8.35	1.30	1.53
82	S2	121	OMU	C2-N1	8.28	1.51	1.38
82	S2	627	OMU	C2-N1	8.27	1.51	1.38
82	S2	1288	OMU	C2-N1	8.27	1.51	1.38
82	S2	172	OMU	C2-N1	8.25	1.51	1.38
2	L5	4498	OMU	C2-N1	8.24	1.51	1.38
2	L5	4620	OMU	C2-N1	8.22	1.51	1.38
82	S2	354	OMU	C2-N1	8.19	1.51	1.38
82	S2	428	OMU	C2-N1	8.19	1.51	1.38
2	L5	2837	OMU	C2-N1	8.19	1.51	1.38
2	L5	4306	OMU	C2-N1	8.18	1.51	1.38
82	S2	1326	OMU	C2-N1	8.16	1.51	1.38
2	L5	4227	OMU	C2-N1	8.15	1.51	1.38
2	L5	3925	OMU	C2-N1	8.07	1.51	1.38
82	S2	116	OMU	C2-N1	8.05	1.51	1.38
82	S2	1248	B8N	C6-N1	7.92	1.55	1.36
2	L5	3818	UY1	C2-N3	7.86	1.50	1.37
82	S2	1248	B8N	C4-N3	-7.75	1.26	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	S2	1248	B8N	C4-C5	7.09	1.63	1.47
82	S2	799	OMU	C2-N3	7.07	1.50	1.38
82	S2	172	OMU	C2-N3	7.02	1.50	1.38
82	S2	1326	OMU	C2-N3	6.98	1.50	1.38
82	S2	116	OMU	C2-N3	6.97	1.50	1.38
82	S2	121	OMU	C2-N3	6.97	1.50	1.38
82	S2	428	OMU	C2-N3	6.94	1.50	1.38
2	L5	4498	OMU	C2-N3	6.94	1.50	1.38
82	S2	1288	OMU	C2-N3	6.93	1.50	1.38
82	S2	1442	OMU	C2-N3	6.93	1.50	1.38
82	S2	627	OMU	C2-N3	6.92	1.50	1.38
2	L5	4227	OMU	C2-N3	6.92	1.50	1.38
2	L5	4620	OMU	C2-N3	6.85	1.49	1.38
2	L5	3925	OMU	C2-N3	6.84	1.49	1.38
82	S2	354	OMU	C2-N3	6.83	1.49	1.38
2	L5	2837	OMU	C2-N3	6.81	1.49	1.38
2	L5	4306	OMU	C2-N3	6.80	1.49	1.38
2	L5	4530	UR3	C2-N1	6.63	1.47	1.38
82	S2	1639	G7M	C4-N3	6.54	1.49	1.34
2	L5	4530	UR3	C6-C5	6.31	1.49	1.35
82	S2	1248	B8N	C2-N1	6.00	1.56	1.39
82	S2	428	OMU	C6-C5	5.95	1.48	1.35
82	S2	354	OMU	C6-C5	5.93	1.48	1.35
82	S2	799	OMU	C6-C5	5.91	1.48	1.35
82	S2	1288	OMU	C6-C5	5.91	1.48	1.35
2	L5	4498	OMU	C6-C5	5.91	1.48	1.35
82	S2	121	OMU	C6-C5	5.91	1.48	1.35
2	L5	4530	UR3	C2-N3	5.89	1.50	1.39
2	L5	4227	OMU	C6-C5	5.88	1.48	1.35
82	S2	172	OMU	C6-C5	5.88	1.48	1.35
82	S2	1326	OMU	C6-C5	5.87	1.48	1.35
82	S2	116	OMU	C6-C5	5.85	1.48	1.35
82	S2	627	OMU	C6-C5	5.85	1.48	1.35
2	L5	4620	OMU	C6-C5	5.85	1.48	1.35
2	L5	4306	OMU	C6-C5	5.83	1.48	1.35
82	S2	1442	OMU	C6-C5	5.82	1.48	1.35
2	L5	3925	OMU	C6-C5	5.82	1.48	1.35
2	L5	2837	OMU	C6-C5	5.79	1.48	1.35
2	L5	3818	UY1	C6-N1	5.55	1.45	1.36
82	S2	1248	B8N	C6-C5	5.51	1.42	1.35
2	L5	4306	OMU	O4-C4	-5.50	1.13	1.24
2	L5	3925	OMU	O4-C4	-5.49	1.13	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L5	4620	OMU	O4-C4	-5.48	1.13	1.24
2	L5	2837	OMU	O4-C4	-5.48	1.13	1.24
82	S2	1639	G7M	C2-N3	5.46	1.46	1.33
82	S2	1326	OMU	O4-C4	-5.46	1.13	1.24
2	L5	4227	OMU	O4-C4	-5.42	1.13	1.24
82	S2	121	OMU	O4-C4	-5.42	1.13	1.24
2	L5	4498	OMU	O4-C4	-5.42	1.13	1.24
82	S2	354	OMU	O4-C4	-5.41	1.14	1.24
82	S2	116	OMU	O4-C4	-5.41	1.14	1.24
82	S2	1442	OMU	O4-C4	-5.41	1.14	1.24
82	S2	172	OMU	O4-C4	-5.40	1.14	1.24
82	S2	799	OMU	O4-C4	-5.39	1.14	1.24
82	S2	428	OMU	O4-C4	-5.39	1.14	1.24
82	S2	627	OMU	O4-C4	-5.38	1.14	1.24
82	S2	1288	OMU	O4-C4	-5.35	1.14	1.24
82	S2	1639	G7M	C2-N2	4.93	1.45	1.34
2	L5	4220	6MZ	O4'-C1'	-4.68	1.31	1.42
2	L5	4220	6MZ	O4'-C4'	4.67	1.55	1.45
82	S2	1639	G7M	C5-N7	-4.66	1.33	1.39
2	L5	3818	UY1	C4-N3	4.58	1.47	1.38
82	S2	627	OMU	C4-N3	4.50	1.46	1.38
82	S2	1326	OMU	C4-N3	4.43	1.46	1.38
82	S2	1288	OMU	C4-N3	4.42	1.46	1.38
2	L5	4220	6MZ	C5'-C4'	-4.41	1.38	1.51
82	S2	172	OMU	C4-N3	4.40	1.46	1.38
82	S2	1442	OMU	C4-N3	4.39	1.46	1.38
82	S2	428	OMU	C4-N3	4.38	1.46	1.38
2	L5	4227	OMU	C4-N3	4.38	1.46	1.38
2	L5	2837	OMU	C4-N3	4.38	1.46	1.38
82	S2	799	OMU	C4-N3	4.37	1.46	1.38
82	S2	121	OMU	C4-N3	4.33	1.46	1.38
2	L5	4498	OMU	C4-N3	4.28	1.45	1.38
2	L5	4306	OMU	C4-N3	4.26	1.45	1.38
82	S2	354	OMU	C4-N3	4.25	1.45	1.38
82	S2	116	OMU	C4-N3	4.22	1.45	1.38
2	L5	4620	OMU	C4-N3	4.20	1.45	1.38
2	L5	3925	OMU	C4-N3	4.16	1.45	1.38
82	S2	1639	G7M	C5-C6	3.85	1.54	1.43
2	L5	1582	PSU	C6-C5	3.85	1.39	1.35
2	L5	1782	PSU	C6-C5	3.77	1.39	1.35
82	S2	866	PSU	C6-C5	3.75	1.39	1.35
82	S2	801	PSU	C6-C5	3.74	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	S2	1232	PSU	C6-C5	3.73	1.39	1.35
4	L8	55	PSU	C6-C5	3.73	1.39	1.35
82	S2	1244	PSU	C6-C5	3.73	1.39	1.35
82	S2	93	PSU	C6-C5	3.73	1.39	1.35
82	S2	1177	PSU	C6-C5	3.72	1.39	1.35
82	S2	1046	PSU	C6-C5	3.72	1.39	1.35
2	L5	3637	PSU	C6-C5	3.71	1.39	1.35
82	S2	1367	PSU	C6-C5	3.71	1.39	1.35
82	S2	651	PSU	C6-C5	3.70	1.39	1.35
2	L5	4532	PSU	C6-C5	3.68	1.39	1.35
2	L5	4500	PSU	C6-C5	3.67	1.39	1.35
82	S2	1248	B8N	C1'-C5	3.66	1.58	1.50
82	S2	406	PSU	C6-C5	3.66	1.39	1.35
82	S2	686	PSU	C6-C5	3.66	1.39	1.35
2	L5	1860	PSU	C6-C5	3.64	1.39	1.35
82	S2	109	PSU	C6-C5	3.63	1.39	1.35
82	S2	814	PSU	C6-C5	3.62	1.39	1.35
2	L5	1781	PSU	C6-C5	3.61	1.39	1.35
2	L5	1683	PSU	C6-C5	3.60	1.39	1.35
2	L5	5010	PSU	C6-C5	3.59	1.39	1.35
2	L5	3639	PSU	C6-C5	3.58	1.39	1.35
82	S2	1081	PSU	C6-C5	3.58	1.39	1.35
2	L5	1862	PSU	C6-C5	3.58	1.39	1.35
2	L5	4299	PSU	C6-C5	3.58	1.39	1.35
2	L5	1792	PSU	C6-C5	3.58	1.39	1.35
2	L5	3853	PSU	C6-C5	3.58	1.39	1.35
2	L5	4293	PSU	C6-C5	3.56	1.39	1.35
82	S2	1045	PSU	C6-C5	3.56	1.39	1.35
2	L5	5001	PSU	C6-C5	3.56	1.39	1.35
2	L5	3851	PSU	C6-C5	3.55	1.39	1.35
2	L5	4431	PSU	C6-C5	3.55	1.39	1.35
82	S2	1174	PSU	C6-C5	3.55	1.39	1.35
2	L5	1536	PSU	C6-C5	3.55	1.39	1.35
2	L5	3818	UY1	O4-C4	-3.55	1.16	1.23
2	L5	4471	PSU	C6-C5	3.55	1.39	1.35
82	S2	863	PSU	C6-C5	3.55	1.39	1.35
2	L5	3884	PSU	C6-C5	3.54	1.39	1.35
2	L5	4361	PSU	C6-C5	3.53	1.39	1.35
2	L5	4442	PSU	C6-C5	3.53	1.39	1.35
82	S2	1004	PSU	C6-C5	3.52	1.39	1.35
2	L5	4296	PSU	C6-C5	3.52	1.39	1.35
2	L5	4353	PSU	C6-C5	3.51	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L5	3844	PSU	C6-C5	3.51	1.39	1.35
4	L8	69	PSU	C6-C5	3.50	1.39	1.35
2	L5	2632	PSU	C6-C5	3.49	1.39	1.35
2	L5	4493	PSU	C6-C5	3.49	1.39	1.35
2	L5	4521	PSU	C6-C5	3.49	1.39	1.35
2	L5	4972	PSU	C6-C5	3.49	1.39	1.35
82	S2	105	PSU	C6-C5	3.49	1.39	1.35
2	L5	3695	PSU	C6-C5	3.48	1.39	1.35
2	L5	4636	PSU	C6-C5	3.48	1.39	1.35
2	L5	4579	PSU	C6-C5	3.47	1.39	1.35
2	L5	3822	PSU	C6-C5	3.46	1.39	1.35
2	L5	4457	PSU	C6-C5	3.46	1.39	1.35
2	L5	3920	PSU	C6-C5	3.45	1.39	1.35
82	S2	649	PSU	C6-C5	3.44	1.39	1.35
82	S2	966	PSU	C6-C5	3.44	1.39	1.35
2	L5	4552	PSU	C6-C5	3.43	1.39	1.35
2	L5	4523	A2M	O5'-C5'	-3.42	1.34	1.44
2	L5	398	A2M	O5'-C5'	-3.42	1.34	1.44
2	L5	4312	PSU	C6-C5	3.42	1.39	1.35
2	L5	1744	PSU	C6-C5	3.41	1.39	1.35
2	L5	4673	PSU	C6-C5	3.41	1.39	1.35
82	S2	681	PSU	C6-C5	3.41	1.39	1.35
82	S2	1056	PSU	C6-C5	3.41	1.39	1.35
82	S2	1383	A2M	O5'-C5'	-3.41	1.34	1.44
2	L5	3785	A2M	O5'-C5'	-3.40	1.34	1.44
2	L5	4576	PSU	C6-C5	3.39	1.39	1.35
82	S2	668	A2M	O5'-C5'	-3.39	1.34	1.44
2	L5	4973	PSU	C6-C5	3.36	1.39	1.35
2	L5	3830	A2M	O5'-C5'	-3.35	1.34	1.44
82	S2	166	A2M	O5'-C5'	-3.35	1.34	1.44
2	L5	2839	PSU	C6-C5	3.34	1.39	1.35
82	S2	99	A2M	O5'-C5'	-3.34	1.34	1.44
2	L5	400	A2M	O5'-C5'	-3.33	1.34	1.44
2	L5	4571	A2M	O5'-C5'	-3.33	1.34	1.44
2	L5	2787	A2M	O5'-C5'	-3.33	1.34	1.44
2	L5	1323	A2M	O5'-C5'	-3.33	1.34	1.44
2	L5	4220	6MZ	C2'-C1'	3.33	1.63	1.53
2	L5	3825	A2M	O5'-C5'	-3.32	1.34	1.44
2	L5	1534	A2M	O5'-C5'	-3.31	1.34	1.44
2	L5	3718	A2M	O5'-C5'	-3.31	1.34	1.44
2	L5	3818	UY1	C1'-C5	3.30	1.57	1.50
2	L5	4689	PSU	C6-C5	3.29	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L5	1871	A2M	O5'-C5'	-3.29	1.34	1.44
2	L5	2815	A2M	O5'-C5'	-3.28	1.34	1.44
82	S2	27	A2M	O5'-C5'	-3.28	1.34	1.44
2	L5	1524	A2M	O5'-C5'	-3.27	1.34	1.44
82	S2	576	A2M	O5'-C5'	-3.27	1.34	1.44
82	S2	468	A2M	O5'-C5'	-3.26	1.34	1.44
82	S2	1031	A2M	O5'-C5'	-3.26	1.34	1.44
2	L5	2401	A2M	O5'-C5'	-3.25	1.34	1.44
2	L5	1677	PSU	C6-C5	3.22	1.38	1.35
2	L5	2363	A2M	O5'-C5'	-3.22	1.34	1.44
82	S2	484	A2M	O5'-C5'	-3.20	1.34	1.44
2	L5	3818	UY1	O2-C2	-3.20	1.16	1.23
2	L5	1326	A2M	O5'-C5'	-3.19	1.34	1.44
2	L5	4590	A2M	O5'-C5'	-3.19	1.34	1.44
2	L5	3867	A2M	O5'-C5'	-3.18	1.34	1.44
82	S2	1850	MA6	C6-N6	3.18	1.45	1.36
2	L5	4220	6MZ	C5-N7	-3.17	1.33	1.39
82	S2	1851	MA6	C6-N6	3.16	1.45	1.36
82	S2	1832	6MZ	C5-N7	-3.14	1.33	1.39
2	L5	4403	PSU	C6-C5	3.12	1.38	1.35
2	L5	4628	PSU	C6-C5	3.11	1.38	1.35
2	L5	4220	6MZ	C5-C4	-3.11	1.33	1.39
82	S2	159	A2M	O5'-C5'	-3.08	1.35	1.44
82	S2	1288	OMU	C5-C4	2.93	1.50	1.43
82	S2	1832	6MZ	C5-C4	-2.91	1.33	1.39
82	S2	1832	6MZ	C8-N9	-2.91	1.32	1.37
82	S2	799	OMU	C5-C4	2.89	1.50	1.43
82	S2	627	OMU	C5-C4	2.89	1.50	1.43
82	S2	428	OMU	C5-C4	2.89	1.50	1.43
2	L5	4220	6MZ	C8-N9	-2.89	1.32	1.37
2	L5	3925	OMU	C5-C4	2.88	1.49	1.43
82	S2	354	OMU	C5-C4	2.87	1.49	1.43
82	S2	172	OMU	C5-C4	2.86	1.49	1.43
2	L5	4227	OMU	C5-C4	2.85	1.49	1.43
82	S2	1326	OMU	C5-C4	2.84	1.49	1.43
82	S2	121	OMU	C5-C4	2.82	1.49	1.43
2	L5	4498	OMU	C5-C4	2.82	1.49	1.43
82	S2	1639	G7M	C2-N1	2.81	1.44	1.37
82	S2	1442	OMU	C5-C4	2.80	1.49	1.43
82	S2	121	OMU	C6-N1	2.80	1.44	1.38
2	L5	2837	OMU	C5-C4	2.79	1.49	1.43
2	L5	4306	OMU	C5-C4	2.79	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	S2	116	OMU	C5-C4	2.76	1.49	1.43
82	S2	1288	OMU	C6-N1	2.75	1.44	1.38
82	S2	799	OMU	C6-N1	2.75	1.44	1.38
2	L5	4620	OMU	C5-C4	2.74	1.49	1.43
82	S2	354	OMU	C6-N1	2.71	1.44	1.38
2	L5	4498	OMU	C6-N1	2.71	1.44	1.38
82	S2	1442	OMU	C6-N1	2.70	1.44	1.38
2	L5	2837	OMU	C6-N1	2.68	1.44	1.38
2	L5	4220	6MZ	O3'-C3'	2.67	1.49	1.43
82	S2	627	OMU	C6-N1	2.65	1.44	1.38
2	L5	4306	OMU	C6-N1	2.65	1.44	1.38
82	S2	1326	OMU	C6-N1	2.64	1.44	1.38
82	S2	116	OMU	C6-N1	2.64	1.44	1.38
2	L5	4227	OMU	C6-N1	2.63	1.44	1.38
2	L5	4530	UR3	C6-N1	2.62	1.44	1.38
2	L5	3925	OMU	C6-N1	2.59	1.44	1.38
82	S2	428	OMU	C6-N1	2.59	1.44	1.38
82	S2	172	OMU	C6-N1	2.58	1.44	1.38
2	L5	4620	OMU	C6-N1	2.55	1.44	1.38
2	L5	4530	UR3	O2-C2	-2.54	1.17	1.22
82	S2	1639	G7M	O6-C6	-2.47	1.18	1.23
82	S2	1639	G7M	C6-N1	2.43	1.43	1.38
82	S2	1850	MA6	C5-C4	-2.40	1.34	1.39
82	S2	1851	MA6	C5-C4	-2.37	1.34	1.39
2	L5	4530	UR3	C5-C4	2.29	1.49	1.43
2	L5	4530	UR3	C3U-N3	2.28	1.51	1.47
2	L5	3867	A2M	O4'-C4'	-2.22	1.40	1.45
2	L5	1524	A2M	O4'-C4'	-2.18	1.40	1.45
2	L5	1323	A2M	O4'-C4'	-2.16	1.40	1.45
2	L5	3818	UY1	C4-C5	2.11	1.50	1.44
82	S2	668	A2M	O4'-C4'	-2.10	1.40	1.45
82	S2	1639	G7M	C4-N9	-2.08	1.32	1.38
82	S2	1832	6MZ	C6-N1	-2.05	1.31	1.35
2	L5	1677	PSU	C4-C5	-2.03	1.38	1.44
2	L5	4293	PSU	C4-C5	-2.03	1.38	1.44
2	L5	3822	PSU	O4'-C1'	-2.02	1.41	1.43
2	L5	4220	6MZ	C6-N1	-2.00	1.31	1.35

All (704) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	1851	MA6	N1-C6-N6	-11.73	102.56	116.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	1850	MA6	N1-C6-N6	-11.70	102.59	116.86
82	S2	1850	MA6	C5-C6-N6	7.78	137.64	125.33
82	S2	1639	G7M	C1'-N9-C4	7.75	149.37	126.49
82	S2	1851	MA6	C5-C6-N6	7.71	137.54	125.33
82	S2	1639	G7M	C1'-N9-C8	-7.67	100.85	126.74
2	L5	3925	OMU	C4-N3-C2	-5.89	119.30	126.61
82	S2	428	OMU	C4-N3-C2	-5.70	119.54	126.61
2	L5	4227	OMU	C4-N3-C2	-5.69	119.55	126.61
82	S2	172	OMU	C4-N3-C2	-5.65	119.60	126.61
82	S2	1326	OMU	C4-N3-C2	-5.63	119.62	126.61
2	L5	2837	OMU	C4-N3-C2	-5.62	119.63	126.61
82	S2	627	OMU	C4-N3-C2	-5.62	119.63	126.61
82	S2	354	OMU	C4-N3-C2	-5.60	119.67	126.61
2	L5	4498	OMU	C4-N3-C2	-5.59	119.67	126.61
82	S2	1288	OMU	C4-N3-C2	-5.56	119.70	126.61
82	S2	1832	6MZ	N1-C2-N3	-5.56	120.17	128.58
82	S2	1850	MA6	N1-C2-N3	-5.56	120.17	128.58
82	S2	1851	MA6	N1-C2-N3	-5.52	120.22	128.58
82	S2	1442	OMU	C4-N3-C2	-5.49	119.80	126.61
2	L5	4306	OMU	C4-N3-C2	-5.49	119.80	126.61
82	S2	1851	MA6	N9-C8-N7	-5.48	106.16	113.94
2	L5	4530	UR3	C4-N3-C2	-5.47	120.18	124.58
2	L5	3637	PSU	N1-C2-N3	5.46	120.93	115.17
2	L5	4220	6MZ	N1-C2-N3	-5.44	120.35	128.58
82	S2	1850	MA6	N9-C8-N7	-5.43	106.23	113.94
2	L5	4620	OMU	C4-N3-C2	-5.43	119.88	126.61
82	S2	799	OMU	C4-N3-C2	-5.41	119.89	126.61
82	S2	121	OMU	C4-N3-C2	-5.29	120.05	126.61
82	S2	1248	B8N	C5-C4-N3	5.15	125.50	116.15
2	L5	4636	PSU	C4-N3-C2	-5.15	119.28	126.37
82	S2	116	OMU	C4-N3-C2	-5.11	120.26	126.61
2	L5	4442	PSU	N1-C2-N3	5.03	120.47	115.17
2	L5	4442	PSU	C4-N3-C2	-5.01	119.47	126.37
2	L5	4312	PSU	C4-N3-C2	-5.00	119.48	126.37
2	L5	2632	PSU	C4-N3-C2	-5.00	119.49	126.37
2	L5	5010	PSU	C4-N3-C2	-4.96	119.54	126.37
2	L5	3637	PSU	C4-N3-C2	-4.96	119.54	126.37
2	L5	4296	PSU	C4-N3-C2	-4.95	119.55	126.37
2	L5	1860	PSU	C4-N3-C2	-4.95	119.56	126.37
2	L5	1536	PSU	C4-N3-C2	-4.95	119.56	126.37
82	S2	649	PSU	C4-N3-C2	-4.94	119.56	126.37
2	L5	1536	PSU	N1-C2-N3	4.94	120.38	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	4636	PSU	N1-C2-N3	4.94	120.38	115.17
2	L5	3818	UY1	C4-N3-C2	-4.92	119.59	126.37
2	L5	4521	PSU	C4-N3-C2	-4.91	119.60	126.37
82	S2	863	PSU	C4-N3-C2	-4.91	119.60	126.37
2	L5	4293	PSU	C4-N3-C2	-4.91	119.60	126.37
2	L5	4299	PSU	C4-N3-C2	-4.91	119.61	126.37
2	L5	2632	PSU	N1-C2-N3	4.91	120.34	115.17
2	L5	2839	PSU	C4-N3-C2	-4.90	119.62	126.37
2	L5	4431	PSU	N1-C2-N3	4.89	120.33	115.17
2	L5	1677	PSU	C4-N3-C2	-4.88	119.65	126.37
2	L5	4500	PSU	C4-N3-C2	-4.87	119.66	126.37
82	S2	1174	PSU	C4-N3-C2	-4.86	119.67	126.37
2	L5	3884	PSU	C4-N3-C2	-4.86	119.67	126.37
2	L5	3920	PSU	C4-N3-C2	-4.86	119.67	126.37
82	S2	1056	PSU	C4-N3-C2	-4.86	119.68	126.37
82	S2	814	PSU	C4-N3-C2	-4.85	119.69	126.37
2	L5	4500	PSU	N1-C2-N3	4.85	120.28	115.17
2	L5	3639	PSU	C4-N3-C2	-4.85	119.69	126.37
2	L5	3844	PSU	C4-N3-C2	-4.84	119.70	126.37
2	L5	4457	PSU	C4-N3-C2	-4.84	119.70	126.37
2	L5	4299	PSU	N1-C2-N3	4.84	120.28	115.17
2	L5	3822	PSU	C4-N3-C2	-4.84	119.71	126.37
2	L5	4296	PSU	N1-C2-N3	4.84	120.27	115.17
2	L5	1677	PSU	N1-C2-N3	4.83	120.27	115.17
82	S2	1045	PSU	C4-N3-C2	-4.82	119.73	126.37
82	S2	866	PSU	C4-N3-C2	-4.82	119.73	126.37
2	L5	4353	PSU	C4-N3-C2	-4.81	119.74	126.37
82	S2	1004	PSU	C4-N3-C2	-4.81	119.74	126.37
82	S2	686	PSU	C4-N3-C2	-4.81	119.75	126.37
82	S2	1081	PSU	C4-N3-C2	-4.80	119.75	126.37
2	L5	4532	PSU	N1-C2-N3	4.80	120.23	115.17
2	L5	1744	PSU	C4-N3-C2	-4.80	119.75	126.37
82	S2	109	PSU	C4-N3-C2	-4.80	119.76	126.37
82	S2	651	PSU	C4-N3-C2	-4.80	119.76	126.37
82	S2	866	PSU	N1-C2-N3	4.79	120.22	115.17
82	S2	1832	6MZ	C5-C4-N3	-4.79	120.12	126.72
2	L5	1862	PSU	C4-N3-C2	-4.79	119.77	126.37
4	L8	55	PSU	C4-N3-C2	-4.79	119.78	126.37
4	L8	55	PSU	N1-C2-N3	4.79	120.22	115.17
2	L5	3695	PSU	C4-N3-C2	-4.79	119.78	126.37
2	L5	4431	PSU	C4-N3-C2	-4.79	119.78	126.37
2	L5	4972	PSU	C4-N3-C2	-4.79	119.78	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	1367	PSU	N1-C2-N3	4.78	120.21	115.17
2	L5	1792	PSU	N1-C2-N3	4.78	120.21	115.17
2	L5	4493	PSU	N1-C2-N3	4.78	120.21	115.17
2	L5	4493	PSU	C4-N3-C2	-4.78	119.78	126.37
2	L5	3844	PSU	N1-C2-N3	4.77	120.20	115.17
82	S2	801	PSU	N1-C2-N3	4.77	120.20	115.17
2	L5	4532	PSU	C4-N3-C2	-4.76	119.81	126.37
2	L5	1792	PSU	C4-N3-C2	-4.76	119.82	126.37
2	L5	5001	PSU	C4-N3-C2	-4.76	119.82	126.37
2	L5	1782	PSU	N1-C2-N3	4.76	120.18	115.17
2	L5	3822	PSU	N1-C2-N3	4.76	120.18	115.17
2	L5	3639	PSU	N1-C2-N3	4.75	120.18	115.17
2	L5	4457	PSU	N1-C2-N3	4.75	120.18	115.17
82	S2	651	PSU	N1-C2-N3	4.75	120.18	115.17
2	L5	4220	6MZ	N9-C8-N7	-4.75	107.20	113.94
2	L5	4689	PSU	N1-C2-N3	4.75	120.17	115.17
2	L5	4471	PSU	N1-C2-N3	4.74	120.17	115.17
2	L5	1782	PSU	C4-N3-C2	-4.74	119.84	126.37
2	L5	4361	PSU	C4-N3-C2	-4.74	119.84	126.37
2	L5	4673	PSU	C4-N3-C2	-4.74	119.84	126.37
82	S2	1244	PSU	C4-N3-C2	-4.74	119.84	126.37
82	S2	105	PSU	N1-C2-N3	4.74	120.17	115.17
82	S2	681	PSU	N1-C2-N3	4.74	120.17	115.17
2	L5	1683	PSU	C4-N3-C2	-4.74	119.85	126.37
82	S2	681	PSU	C4-N3-C2	-4.74	119.85	126.37
2	L5	4293	PSU	N1-C2-N3	4.73	120.16	115.17
82	S2	966	PSU	C4-N3-C2	-4.72	119.86	126.37
2	L5	1683	PSU	N1-C2-N3	4.72	120.14	115.17
82	S2	1232	PSU	C4-N3-C2	-4.72	119.87	126.37
82	S2	109	PSU	N1-C2-N3	4.72	120.14	115.17
2	L5	4353	PSU	N1-C2-N3	4.72	120.14	115.17
82	S2	686	PSU	N1-C2-N3	4.71	120.14	115.17
82	S2	1232	PSU	N1-C2-N3	4.71	120.14	115.17
82	S2	1045	PSU	N1-C2-N3	4.71	120.14	115.17
2	L5	2839	PSU	N1-C2-N3	4.71	120.14	115.17
2	L5	4220	6MZ	C5-C4-N3	-4.70	120.24	126.72
2	L5	1862	PSU	N1-C2-N3	4.70	120.12	115.17
2	L5	1860	PSU	N1-C2-N3	4.69	120.12	115.17
82	S2	1081	PSU	N1-C2-N3	4.69	120.11	115.17
2	L5	5010	PSU	N1-C2-N3	4.69	120.11	115.17
82	S2	105	PSU	C4-N3-C2	-4.68	119.92	126.37
2	L5	3920	PSU	N1-C2-N3	4.68	120.11	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	1056	PSU	N1-C2-N3	4.68	120.10	115.17
82	S2	406	PSU	N1-C2-N3	4.68	120.10	115.17
82	S2	1177	PSU	C4-N3-C2	-4.68	119.93	126.37
82	S2	1367	PSU	C4-N3-C2	-4.68	119.93	126.37
82	S2	1244	PSU	N1-C2-N3	4.68	120.10	115.17
82	S2	1177	PSU	N1-C2-N3	4.68	120.10	115.17
2	L5	4552	PSU	C4-N3-C2	-4.67	119.93	126.37
2	L5	4973	PSU	C4-N3-C2	-4.67	119.94	126.37
2	L5	3695	PSU	N1-C2-N3	4.67	120.09	115.17
2	L5	4972	PSU	N1-C2-N3	4.67	120.09	115.17
82	S2	93	PSU	N1-C2-N3	4.67	120.09	115.17
82	S2	649	PSU	N1-C2-N3	4.67	120.09	115.17
2	L5	4552	PSU	N1-C2-N3	4.66	120.09	115.17
2	L5	4628	PSU	C4-N3-C2	-4.66	119.95	126.37
82	S2	801	PSU	C4-N3-C2	-4.66	119.95	126.37
2	L5	1744	PSU	N1-C2-N3	4.66	120.08	115.17
82	S2	814	PSU	N1-C2-N3	4.66	120.08	115.17
2	L5	4579	PSU	C4-N3-C2	-4.66	119.96	126.37
82	S2	93	PSU	C4-N3-C2	-4.66	119.96	126.37
82	S2	1046	PSU	C4-N3-C2	-4.65	119.96	126.37
2	L5	4403	PSU	C4-N3-C2	-4.65	119.97	126.37
2	L5	4576	PSU	N1-C2-N3	4.64	120.07	115.17
2	L5	1781	PSU	C4-N3-C2	-4.64	119.98	126.37
82	S2	966	PSU	N1-C2-N3	4.64	120.06	115.17
2	L5	4312	PSU	N1-C2-N3	4.64	120.06	115.17
82	S2	1851	MA6	C5-C4-N3	-4.63	120.34	126.72
82	S2	863	PSU	N1-C2-N3	4.63	120.05	115.17
2	L5	4673	PSU	N1-C2-N3	4.63	120.05	115.17
2	L5	4628	PSU	N1-C2-N3	4.62	120.05	115.17
2	L5	1781	PSU	N1-C2-N3	4.62	120.04	115.17
4	L8	69	PSU	C4-N3-C2	-4.61	120.02	126.37
2	L5	4576	PSU	C4-N3-C2	-4.61	120.02	126.37
2	L5	1582	PSU	N1-C2-N3	4.61	120.03	115.17
2	L5	4973	PSU	N1-C2-N3	4.59	120.01	115.17
82	S2	1174	PSU	N1-C2-N3	4.59	120.01	115.17
82	S2	406	PSU	C4-N3-C2	-4.58	120.06	126.37
2	L5	3884	PSU	N1-C2-N3	4.58	120.00	115.17
2	L5	3853	PSU	C4-N3-C2	-4.58	120.06	126.37
2	L5	4361	PSU	N1-C2-N3	4.56	119.98	115.17
2	L5	4471	PSU	C4-N3-C2	-4.55	120.10	126.37
82	S2	1046	PSU	N1-C2-N3	4.55	119.97	115.17
2	L5	4521	PSU	N1-C2-N3	4.55	119.97	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	3851	PSU	C4-N3-C2	-4.55	120.10	126.37
2	L5	5001	PSU	N1-C2-N3	4.55	119.96	115.17
2	L5	4579	PSU	N1-C2-N3	4.54	119.96	115.17
4	L8	69	PSU	N1-C2-N3	4.54	119.95	115.17
82	S2	1832	6MZ	N9-C8-N7	-4.53	107.50	113.94
82	S2	1004	PSU	N1-C2-N3	4.53	119.95	115.17
2	L5	3851	PSU	N1-C2-N3	4.53	119.94	115.17
2	L5	3853	PSU	N1-C2-N3	4.52	119.93	115.17
82	S2	1248	B8N	C4-N3-C2	-4.51	120.07	125.62
2	L5	4689	PSU	C4-N3-C2	-4.50	120.18	126.37
82	S2	1639	G7M	C2-N3-C4	4.48	120.01	112.30
2	L5	3818	UY1	N1-C2-N3	4.42	119.83	115.17
82	S2	1850	MA6	C5-C4-N3	-4.41	120.64	126.72
2	L5	4403	PSU	N1-C2-N3	4.40	119.81	115.17
82	S2	1383	A2M	C3'-C2'-C1'	-4.31	94.56	102.81
2	L5	1582	PSU	C4-N3-C2	-4.28	120.48	126.37
82	S2	1850	MA6	C4-N9-C8	4.24	110.19	105.74
82	S2	1851	MA6	C4-N9-C8	4.22	110.17	105.74
2	L5	3925	OMU	N3-C2-N1	4.11	120.24	114.89
82	S2	354	OMU	N3-C2-N1	4.10	120.22	114.89
82	S2	121	OMU	N3-C2-N1	4.04	120.16	114.89
2	L5	4498	OMU	N3-C2-N1	4.02	120.13	114.89
82	S2	1639	G7M	C5-C6-N1	3.97	120.05	111.84
82	S2	1639	G7M	C5-C4-N3	-3.96	120.66	128.15
2	L5	4227	OMU	N3-C2-N1	3.93	120.00	114.89
82	S2	428	OMU	N3-C2-N1	3.91	119.98	114.89
82	S2	799	OMU	N3-C2-N1	3.90	119.96	114.89
2	L5	2837	OMU	N3-C2-N1	3.88	119.95	114.89
82	S2	1288	OMU	N3-C2-N1	3.87	119.93	114.89
82	S2	172	OMU	N3-C2-N1	3.85	119.91	114.89
2	L5	4620	OMU	N3-C2-N1	3.83	119.87	114.89
82	S2	1248	B8N	C1'-C5-C4	3.81	123.39	117.61
2	L5	4306	OMU	N3-C2-N1	3.80	119.83	114.89
82	S2	1442	OMU	N3-C2-N1	3.80	119.83	114.89
82	S2	1326	OMU	N3-C2-N1	3.75	119.77	114.89
82	S2	116	OMU	N3-C2-N1	3.74	119.76	114.89
82	S2	1851	MA6	C4-C5-C6	3.72	119.76	115.91
2	L5	4523	A2M	C3'-C2'-C1'	-3.71	95.70	102.81
2	L5	3925	OMU	C5-C4-N3	3.71	120.00	114.80
82	S2	627	OMU	N3-C2-N1	3.69	119.69	114.89
82	S2	627	OMU	C5-C4-N3	3.68	119.95	114.80
2	L5	398	A2M	C3'-C2'-C1'	-3.64	95.83	102.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	1326	OMU	C5-C4-N3	3.63	119.89	114.80
2	L5	2837	OMU	C5-C4-N3	3.61	119.86	114.80
2	L5	4227	OMU	C5-C4-N3	3.60	119.84	114.80
82	S2	1850	MA6	C4-C5-C6	3.59	119.62	115.91
82	S2	1383	A2M	O3'-C3'-C2'	3.59	121.22	111.19
2	L5	4220	6MZ	C9-N6-C6	-3.58	119.53	122.85
2	L5	4306	OMU	C5-C4-N3	3.57	119.81	114.80
2	L5	4530	UR3	C5-C4-N3	3.53	119.69	115.04
2	L5	4620	OMU	C5-C4-N3	3.53	119.74	114.80
82	S2	1442	OMU	C5-C4-N3	3.53	119.74	114.80
82	S2	1248	B8N	N3-C2-N1	3.52	121.02	116.72
82	S2	428	OMU	C5-C4-N3	3.51	119.71	114.80
82	S2	354	OMU	C5-C4-N3	3.50	119.71	114.80
2	L5	4498	OMU	C5-C4-N3	3.50	119.70	114.80
82	S2	1288	OMU	C5-C4-N3	3.49	119.69	114.80
82	S2	172	OMU	C5-C4-N3	3.49	119.69	114.80
82	S2	1850	MA6	C2-N1-C6	3.48	120.34	111.83
82	S2	799	OMU	C5-C4-N3	3.46	119.65	114.80
82	S2	1851	MA6	N3-C4-N9	3.46	133.05	127.17
2	L5	3830	A2M	C3'-C2'-C1'	-3.46	96.19	102.81
2	L5	3785	A2M	C4'-O4'-C1'	-3.44	101.87	109.47
2	L5	398	A2M	O3'-C3'-C2'	3.44	120.81	111.19
82	S2	166	A2M	O3'-C3'-C2'	3.43	120.79	111.19
82	S2	1851	MA6	C2-N1-C6	3.42	120.18	111.83
2	L5	1534	A2M	C3'-C2'-C1'	-3.39	96.33	102.81
2	L5	3818	UY1	C6-C5-C4	3.37	120.45	118.17
82	S2	1832	6MZ	C2-N3-C4	3.37	120.06	111.83
82	S2	576	A2M	O3'-C3'-C2'	3.36	120.60	111.19
2	L5	1536	PSU	O2-C2-N1	-3.36	119.32	122.79
82	S2	116	OMU	C5-C4-N3	3.33	119.47	114.80
82	S2	121	OMU	C5-C4-N3	3.32	119.45	114.80
82	S2	1639	G7M	O6-C6-C5	-3.32	120.61	128.01
2	L5	4220	6MZ	C2-N3-C4	3.32	119.93	111.83
82	S2	166	A2M	C3'-C2'-C1'	-3.30	96.48	102.81
82	S2	1639	G7M	CN7-N7-C5	3.30	130.91	126.80
82	S2	1851	MA6	C5-N7-C8	3.29	108.63	103.45
2	L5	3825	A2M	O3'-C3'-C2'	3.26	120.32	111.19
2	L5	4571	A2M	O3'-C3'-C2'	3.26	120.31	111.19
82	S2	484	A2M	O3'-C3'-C2'	3.25	120.27	111.19
82	S2	1832	6MZ	C4-C5-C6	3.25	119.48	116.78
2	L5	1524	A2M	O3'-C3'-C2'	3.24	120.26	111.19
2	L5	1323	A2M	C2'-C1'-N9	3.23	119.07	113.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	1850	MA6	N3-C4-N9	3.23	132.66	127.17
82	S2	1031	A2M	C3'-C2'-C1'	-3.22	96.63	102.81
2	L5	2787	A2M	O3'-C3'-C2'	3.22	120.20	111.19
2	L5	3785	A2M	C4-N9-C1'	-3.22	119.11	126.63
2	L5	4220	6MZ	N3-C4-N9	3.21	132.63	127.17
2	L5	4590	A2M	C3'-C2'-C1'	-3.21	96.66	102.81
2	L5	4220	6MZ	C4-N9-C8	3.21	109.11	105.74
82	S2	1832	6MZ	N3-C4-N9	3.21	132.62	127.17
82	S2	1850	MA6	C5-N7-C8	3.20	108.47	103.45
82	S2	166	A2M	C4-N9-C1'	-3.19	119.17	126.63
82	S2	159	A2M	O3'-C3'-C2'	3.19	120.11	111.19
82	S2	1639	G7M	N9-C4-N3	3.19	132.33	125.95
82	S2	1851	MA6	C2-N3-C4	3.18	119.61	111.83
2	L5	2401	A2M	O3'-C3'-C2'	3.18	120.08	111.19
2	L5	4590	A2M	O3'-C3'-C2'	3.17	120.06	111.19
2	L5	3718	A2M	C3'-C2'-C1'	-3.17	96.75	102.81
82	S2	1383	A2M	C4-N9-C1'	-3.16	119.24	126.63
2	L5	4220	6MZ	C4-C5-C6	3.16	119.41	116.78
82	S2	1031	A2M	O3'-C3'-C2'	3.16	120.03	111.19
2	L5	3830	A2M	O3'-C3'-C2'	3.16	120.02	111.19
2	L5	4689	PSU	C6-N1-C2	-3.15	119.77	122.69
2	L5	400	A2M	O3'-C3'-C2'	3.14	119.98	111.19
2	L5	1871	A2M	C3'-C2'-C1'	-3.13	96.82	102.81
82	S2	1850	MA6	C2-N3-C4	3.13	119.47	111.83
2	L5	4590	A2M	C4-N9-C1'	-3.12	119.32	126.63
82	S2	1832	6MZ	C5-N7-C8	3.10	108.32	103.45
82	S2	99	A2M	O3'-C3'-C2'	3.09	119.83	111.19
2	L5	3718	A2M	O3'-C3'-C2'	3.08	119.80	111.19
2	L5	3830	A2M	C4-N9-C1'	-3.07	119.44	126.63
82	S2	468	A2M	O3'-C3'-C2'	3.06	119.75	111.19
2	L5	2861	OMC	C1'-N1-C2	3.05	125.18	118.44
82	S2	99	A2M	C3'-C2'-C1'	-3.05	96.97	102.81
82	S2	576	A2M	C3'-C2'-C1'	-3.04	96.99	102.81
2	L5	2363	A2M	C3'-C2'-C1'	-3.03	97.00	102.81
2	L5	4220	6MZ	C5-N7-C8	3.03	108.21	103.45
2	L5	3818	UY1	C6-N1-C2	-3.03	119.88	122.69
2	L5	1683	PSU	O2-C2-N1	-3.03	119.67	122.79
2	L5	4689	PSU	O2-C2-N1	-3.02	119.67	122.79
2	L5	3808	OMC	C1'-N1-C2	3.01	125.09	118.44
2	L5	2401	A2M	C4-N9-C1'	-3.01	119.60	126.63
82	S2	1442	OMU	O4-C4-C5	-3.01	119.97	125.16
82	S2	627	OMU	O4-C4-C5	-3.01	119.98	125.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	2837	OMU	O4-C4-C5	-3.00	119.99	125.16
2	L5	4571	A2M	C4-N9-C1'	-2.99	119.64	126.63
2	L5	1326	A2M	O3'-C3'-C2'	2.98	119.52	111.19
82	S2	27	A2M	O3'-C3'-C2'	2.98	119.52	111.19
82	S2	668	A2M	O4'-C1'-C2'	2.96	111.69	106.59
82	S2	1326	OMU	O4-C4-C5	-2.96	120.05	125.16
82	S2	1639	G7M	C2-N1-C6	-2.96	119.74	125.11
82	S2	27	A2M	C3'-C2'-C1'	-2.96	97.14	102.81
82	S2	172	OMU	O4-C4-C5	-2.95	120.07	125.16
2	L5	4227	OMU	O4-C4-C5	-2.94	120.09	125.16
82	S2	668	A2M	C4-N9-C1'	-2.94	119.76	126.63
82	S2	428	OMU	O4-C4-C5	-2.93	120.11	125.16
82	S2	1832	6MZ	C4-N9-C8	2.93	108.81	105.74
2	L5	4493	PSU	O2-C2-N1	-2.92	119.78	122.79
2	L5	3822	PSU	O2-C2-N1	-2.92	119.78	122.79
2	L5	1323	A2M	C4-N9-C1'	-2.92	119.80	126.63
2	L5	4523	A2M	C4-N9-C1'	-2.92	119.81	126.63
4	L8	55	PSU	O2-C2-N1	-2.92	119.78	122.79
2	L5	4628	PSU	O2-C2-N1	-2.91	119.79	122.79
82	S2	668	A2M	O3'-C3'-C2'	2.90	119.32	111.19
2	L5	2815	A2M	O3'-C3'-C2'	2.90	119.29	111.19
2	L5	4523	A2M	O3'-C3'-C2'	2.90	119.29	111.19
2	L5	3785	A2M	O3'-C3'-C2'	2.90	119.29	111.19
2	L5	3637	PSU	C6-N1-C2	-2.89	120.00	122.69
82	S2	1031	A2M	C4-N9-C1'	-2.89	119.86	126.63
2	L5	398	A2M	C4-N9-C1'	-2.89	119.87	126.63
2	L5	4442	PSU	O2-C2-N1	-2.89	119.81	122.79
82	S2	166	A2M	C1'-N9-C8	2.89	133.50	127.09
82	S2	159	A2M	C3'-C2'-C1'	-2.88	97.29	102.81
2	L5	2787	A2M	O4'-C1'-C2'	2.88	111.54	106.59
2	L5	1782	PSU	O2-C2-N1	-2.87	119.83	122.79
82	S2	109	PSU	O2-C2-N1	-2.87	119.83	122.79
2	L5	3925	OMU	O4-C4-C5	-2.86	120.23	125.16
82	S2	1177	PSU	O2-C2-N1	-2.86	119.84	122.79
82	S2	27	A2M	C4-N9-C1'	-2.86	119.95	126.63
2	L5	4403	PSU	O2-C2-N1	-2.85	119.84	122.79
2	L5	4590	A2M	C1'-N9-C8	2.85	133.43	127.09
82	S2	1367	PSU	O2-C2-N1	-2.85	119.85	122.79
2	L5	3825	A2M	C3'-C2'-C1'	-2.85	97.36	102.81
2	L5	4673	PSU	O2-C2-N1	-2.85	119.85	122.79
2	L5	1871	A2M	O3'-C3'-C2'	2.84	119.15	111.19
2	L5	1326	A2M	C2'-C1'-N9	2.84	118.43	113.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	1383	A2M	C1'-N9-C8	2.83	133.39	127.09
2	L5	4636	PSU	O2-C2-N1	-2.83	119.87	122.79
82	S2	799	OMU	O4-C4-C5	-2.83	120.28	125.16
2	L5	4431	PSU	O2-C2-N1	-2.83	119.87	122.79
82	S2	866	PSU	O2-C2-N1	-2.83	119.87	122.79
2	L5	1871	A2M	C4-N9-C1'	-2.82	120.03	126.63
2	L5	3718	A2M	C4-N9-C1'	-2.82	120.03	126.63
2	L5	4498	OMU	O4-C4-C5	-2.82	120.30	125.16
2	L5	2401	A2M	C1'-N9-C8	2.82	133.35	127.09
82	S2	1288	OMU	O4-C4-C5	-2.81	120.31	125.16
2	L5	4620	OMU	O4-C4-C5	-2.81	120.31	125.16
82	S2	99	A2M	C4-N9-C1'	-2.81	120.06	126.63
2	L5	4532	PSU	O2-C2-N1	-2.81	119.89	122.79
2	L5	4500	PSU	O2-C2-N1	-2.81	119.89	122.79
2	L5	3785	A2M	C1'-N9-C8	2.81	133.32	127.09
2	L5	3830	A2M	C1'-N9-C8	2.80	133.31	127.09
82	S2	681	PSU	O2-C2-N1	-2.80	119.90	122.79
82	S2	121	OMU	O4-C4-C5	-2.80	120.33	125.16
2	L5	1323	A2M	O4'-C1'-C2'	2.80	111.41	106.59
2	L5	4306	OMU	O4-C4-C5	-2.80	120.34	125.16
82	S2	801	PSU	O2-C2-N1	-2.78	119.92	122.79
2	L5	3825	A2M	C4-N9-C1'	-2.78	120.14	126.63
82	S2	468	A2M	C4-N9-C1'	-2.77	120.14	126.63
2	L5	4353	PSU	O2-C2-N1	-2.77	119.93	122.79
2	L5	3844	PSU	O2-C2-N1	-2.77	119.93	122.79
2	L5	3867	A2M	O3'-C3'-C2'	2.77	118.93	111.19
82	S2	105	PSU	O2-C2-N1	-2.77	119.93	122.79
2	L5	1534	A2M	O3'-C3'-C2'	2.77	118.93	111.19
2	L5	4299	PSU	O2-C2-N1	-2.77	119.94	122.79
2	L5	1677	PSU	O2-C2-N1	-2.76	119.94	122.79
2	L5	1534	A2M	C4-N9-C1'	-2.76	120.17	126.63
2	L5	4576	PSU	O2-C2-N1	-2.76	119.95	122.79
4	L8	69	PSU	O2-C2-N1	-2.75	119.95	122.79
2	L5	4972	PSU	O2-C2-N1	-2.75	119.95	122.79
2	L5	4457	PSU	O2-C2-N1	-2.74	119.96	122.79
2	L5	3884	PSU	O2-C2-N1	-2.74	119.96	122.79
82	S2	354	OMU	O4-C4-C5	-2.74	120.44	125.16
82	S2	406	PSU	O2-C2-N1	-2.74	119.96	122.79
2	L5	3718	A2M	C1'-N9-C8	2.74	133.17	127.09
2	L5	4296	PSU	O2-C2-N1	-2.74	119.97	122.79
2	L5	398	A2M	C1'-N9-C8	2.74	133.17	127.09
82	S2	468	A2M	C3'-C2'-C1'	-2.73	97.57	102.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	3785	A2M	C3'-C2'-C1'	-2.73	97.57	102.81
2	L5	1323	A2M	C1'-N9-C8	2.72	133.14	127.09
82	S2	159	A2M	C4-N9-C1'	-2.72	120.26	126.63
2	L5	4471	PSU	O2-C2-N1	-2.72	119.98	122.79
82	S2	651	PSU	O2-C2-N1	-2.72	119.98	122.79
82	S2	1056	PSU	O2-C2-N1	-2.72	119.98	122.79
2	L5	4571	A2M	C1'-N9-C8	2.72	133.13	127.09
2	L5	4571	A2M	C3'-C2'-C1'	-2.72	97.60	102.81
82	S2	1639	G7M	CN7-N7-C8	-2.72	120.68	124.79
82	S2	1045	PSU	O2-C2-N1	-2.71	119.99	122.79
82	S2	814	PSU	O2-C2-N1	-2.71	119.99	122.79
82	S2	116	OMU	O4-C4-C5	-2.71	120.48	125.16
82	S2	1031	A2M	C1'-N9-C8	2.71	133.11	127.09
2	L5	4521	PSU	O2-C2-N1	-2.71	120.00	122.79
82	S2	966	PSU	O2-C2-N1	-2.70	120.00	122.79
2	L5	4523	A2M	C1'-N9-C8	2.70	133.08	127.09
2	L5	2839	PSU	O2-C2-N1	-2.70	120.01	122.79
2	L5	1524	A2M	O4'-C1'-C2'	2.70	111.23	106.59
82	S2	668	A2M	C1'-N9-C8	2.70	133.08	127.09
82	S2	1248	B8N	O4-C4-N3	-2.69	115.62	119.99
2	L5	2363	A2M	O3'-C3'-C2'	2.69	118.72	111.19
2	L5	4552	PSU	O2-C2-N1	-2.69	120.01	122.79
2	L5	1323	A2M	O3'-C3'-C2'	2.69	118.71	111.19
2	L5	1677	PSU	C6-C5-C4	2.69	119.99	118.17
2	L5	3920	PSU	O2-C2-N1	-2.69	120.02	122.79
2	L5	1860	PSU	O2-C2-N1	-2.68	120.02	122.79
82	S2	1244	PSU	O2-C2-N1	-2.68	120.02	122.79
82	S2	686	PSU	O2-C2-N1	-2.68	120.02	122.79
82	S2	1174	PSU	O2-C2-N1	-2.68	120.02	122.79
2	L5	1582	PSU	C6-N1-C2	-2.68	120.20	122.69
2	L5	4973	PSU	O2-C2-N1	-2.68	120.03	122.79
2	L5	1534	A2M	C1'-N9-C8	2.68	133.03	127.09
2	L5	5010	PSU	O2-C2-N1	-2.66	120.04	122.79
82	S2	99	A2M	C1'-N9-C8	2.66	132.99	127.09
82	S2	576	A2M	C4-N9-C1'	-2.65	120.43	126.63
82	S2	1232	PSU	O2-C2-N1	-2.65	120.05	122.79
2	L5	1862	PSU	O2-C2-N1	-2.65	120.06	122.79
2	L5	1781	PSU	O2-C2-N1	-2.64	120.07	122.79
2	L5	4576	PSU	C6-N1-C2	-2.64	120.24	122.69
2	L5	1744	PSU	O2-C2-N1	-2.64	120.07	122.79
2	L5	400	A2M	C3'-C2'-C1'	-2.64	97.76	102.81
2	L5	3867	A2M	C2'-C1'-N9	2.63	118.08	113.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	406	PSU	C6-N1-C2	-2.63	120.25	122.69
2	L5	2363	A2M	C4-N9-C1'	-2.63	120.49	126.63
2	L5	1871	A2M	C1'-N9-C8	2.63	132.93	127.09
2	L5	4579	PSU	O2-C2-N1	-2.63	120.08	122.79
82	S2	93	PSU	O2-C2-N1	-2.63	120.08	122.79
2	L5	400	A2M	C4-N9-C1'	-2.62	120.49	126.63
2	L5	1582	PSU	O2-C2-N1	-2.62	120.08	122.79
2	L5	4361	PSU	O2-C2-N1	-2.62	120.09	122.79
82	S2	159	A2M	C1'-N9-C8	2.61	132.89	127.09
2	L5	2632	PSU	C6-C5-C4	2.61	119.94	118.17
82	S2	27	A2M	C1'-N9-C8	2.61	132.88	127.09
82	S2	468	A2M	C1'-N9-C8	2.61	132.88	127.09
2	L5	1792	PSU	O2-C2-N1	-2.61	120.10	122.79
82	S2	484	A2M	C4-N9-C1'	-2.60	120.54	126.63
2	L5	3639	PSU	O2-C2-N1	-2.60	120.11	122.79
2	L5	3825	A2M	C1'-N9-C8	2.60	132.86	127.09
2	L5	3637	PSU	O2-C2-N1	-2.59	120.11	122.79
2	L5	3867	A2M	C4-N9-C1'	-2.59	120.57	126.63
2	L5	2632	PSU	O2-C2-N1	-2.59	120.12	122.79
2	L5	4471	PSU	C6-N1-C2	-2.59	120.29	122.69
2	L5	4293	PSU	O2-C2-N1	-2.58	120.13	122.79
2	L5	3853	PSU	O2-C2-N1	-2.58	120.13	122.79
2	L5	4636	PSU	C6-C5-C4	2.57	119.91	118.17
2	L5	4431	PSU	C6-N1-C2	-2.56	120.31	122.69
82	S2	1046	PSU	O2-C2-N1	-2.56	120.15	122.79
82	S2	801	PSU	C6-N1-C2	-2.56	120.32	122.69
82	S2	1367	PSU	C6-N1-C2	-2.55	120.32	122.69
2	L5	1677	PSU	C6-N1-C2	-2.55	120.32	122.69
2	L5	3851	PSU	O2-C2-N1	-2.55	120.16	122.79
82	S2	484	A2M	C1'-N9-C8	2.55	132.74	127.09
82	S2	576	A2M	C1'-N9-C8	2.54	132.74	127.09
82	S2	681	PSU	C6-N1-C2	-2.54	120.33	122.69
2	L5	4628	PSU	C6-N1-C2	-2.54	120.33	122.69
82	S2	1004	PSU	O2-C2-N1	-2.54	120.17	122.79
82	S2	484	A2M	O4'-C4'-C3'	2.53	110.18	105.15
2	L5	2363	A2M	C1'-N9-C8	2.53	132.71	127.09
2	L5	4973	PSU	C6-N1-C2	-2.53	120.34	122.69
2	L5	1782	PSU	C6-N1-C2	-2.52	120.35	122.69
2	L5	4442	PSU	O4'-C1'-C2'	2.52	108.63	105.15
4	L8	55	PSU	C6-N1-C2	-2.52	120.36	122.69
2	L5	1683	PSU	C6-N1-C2	-2.51	120.36	122.69
2	L5	4312	PSU	O2-C2-N1	-2.51	120.20	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	2351	OMC	C1'-N1-C2	2.51	123.98	118.44
2	L5	1536	PSU	C6-N1-C2	-2.50	120.37	122.69
2	L5	4579	PSU	C6-N1-C2	-2.50	120.37	122.69
2	L5	1326	A2M	C4-N9-C1'	-2.49	120.80	126.63
2	L5	4500	PSU	C6-N1-C2	-2.49	120.38	122.69
2	L5	4673	PSU	C6-N1-C2	-2.49	120.38	122.69
2	L5	400	A2M	C1'-N9-C8	2.48	132.61	127.09
2	L5	3818	UY1	O2-C2-N1	-2.48	120.23	122.79
82	S2	484	A2M	O4'-C1'-C2'	2.48	110.86	106.59
82	S2	649	PSU	O2-C2-N1	-2.48	120.23	122.79
82	S2	1177	PSU	C6-N1-C2	-2.48	120.39	122.69
82	S2	1081	PSU	O2-C2-N1	-2.48	120.23	122.79
2	L5	2401	A2M	C3'-C2'-C1'	-2.47	98.07	102.81
2	L5	4442	PSU	C6-N1-C2	-2.47	120.40	122.69
2	L5	1323	A2M	C3'-C2'-C1'	-2.47	98.08	102.81
2	L5	3695	PSU	O2-C2-N1	-2.47	120.24	122.79
2	L5	3822	PSU	O4'-C1'-C2'	2.47	108.57	105.15
2	L5	4552	PSU	C6-N1-C2	-2.47	120.40	122.69
82	S2	1232	PSU	C6-N1-C2	-2.46	120.41	122.69
2	L5	2824	OMC	C1'-N1-C2	2.46	123.87	118.44
82	S2	105	PSU	C6-N1-C2	-2.45	120.42	122.69
4	L8	69	PSU	C6-N1-C2	-2.45	120.42	122.69
2	L5	5001	PSU	O2-C2-N1	-2.44	120.27	122.79
2	L5	4493	PSU	C6-N1-C2	-2.44	120.42	122.69
2	L5	1326	A2M	C1'-N9-C8	2.43	132.49	127.09
2	L5	3867	A2M	C1'-N9-C8	2.43	132.48	127.09
82	S2	1851	MA6	C1'-N9-C8	-2.42	121.72	127.09
2	L5	1326	A2M	O4'-C1'-C2'	2.42	110.75	106.59
82	S2	863	PSU	O2-C2-N1	-2.42	120.30	122.79
2	L5	2787	A2M	C4-N9-C1'	-2.42	120.98	126.63
2	L5	3822	PSU	C6-N1-C2	-2.41	120.45	122.69
2	L5	4457	PSU	C6-N1-C2	-2.41	120.45	122.69
2	L5	4532	PSU	C6-N1-C2	-2.41	120.45	122.69
82	S2	109	PSU	C6-N1-C2	-2.41	120.46	122.69
2	L5	4456	OMC	C1'-N1-C2	2.39	123.73	118.44
82	S2	166	A2M	C6-C5-C4	-2.39	113.92	117.18
2	L5	4353	PSU	C6-N1-C2	-2.38	120.48	122.69
2	L5	1862	PSU	C6-N1-C2	-2.38	120.48	122.69
82	S2	1244	PSU	C6-N1-C2	-2.38	120.48	122.69
2	L5	4571	A2M	O4'-C1'-C2'	2.38	110.68	106.59
2	L5	3844	PSU	C6-N1-C2	-2.38	120.48	122.69
82	S2	651	PSU	C6-N1-C2	-2.38	120.49	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	462	OMC	C1'-N1-C2	2.38	123.69	118.44
2	L5	2787	A2M	O4'-C4'-C3'	2.37	109.86	105.15
2	L5	2787	A2M	C1'-N9-C8	2.37	132.35	127.09
2	L5	4530	UR3	C6-N1-C2	-2.36	119.87	121.80
2	L5	4590	A2M	C6-C5-C4	-2.36	113.96	117.18
2	L5	4293	PSU	C6-N1-C2	-2.36	120.50	122.69
82	S2	1272	OMC	C1'-N1-C2	2.36	123.64	118.44
2	L5	3884	PSU	C6-N1-C2	-2.35	120.51	122.69
2	L5	2401	A2M	O4'-C1'-C2'	2.35	110.63	106.59
2	L5	4220	6MZ	C5-C6-N1	2.35	120.67	118.15
2	L5	4523	A2M	C4'-O4'-C1'	-2.35	104.29	109.47
2	L5	1871	A2M	O4'-C1'-C2'	2.35	110.63	106.59
2	L5	1524	A2M	C4-N9-C1'	-2.34	121.16	126.63
2	L5	1781	PSU	C6-N1-C2	-2.33	120.53	122.69
2	L5	4296	PSU	C6-N1-C2	-2.33	120.53	122.69
2	L5	4442	PSU	C6-C5-C4	2.33	119.75	118.17
2	L5	3851	PSU	C6-N1-C2	-2.33	120.53	122.69
82	S2	428	OMU	O2-C2-N1	-2.33	119.77	122.80
82	S2	1639	G7M	N9-C8-N7	-2.33	106.83	112.48
82	S2	93	PSU	C6-N1-C2	-2.33	120.53	122.69
2	L5	2839	PSU	C6-N1-C2	-2.32	120.54	122.69
82	S2	814	PSU	C6-N1-C2	-2.32	120.54	122.69
82	S2	866	PSU	C6-N1-C2	-2.32	120.54	122.69
2	L5	2861	OMC	C1'-N1-C6	-2.32	115.83	120.78
2	L5	3867	A2M	C3'-C2'-C1'	-2.31	98.37	102.81
2	L5	3808	OMC	C1'-N1-C6	-2.31	115.85	120.78
82	S2	166	A2M	O4'-C1'-C2'	2.31	110.56	106.59
2	L5	2401	A2M	C6-C5-C4	-2.30	114.04	117.18
2	L5	4972	PSU	C6-N1-C2	-2.30	120.56	122.69
2	L5	3695	PSU	C6-N1-C2	-2.30	120.56	122.69
2	L5	3639	PSU	C6-N1-C2	-2.30	120.56	122.69
2	L5	1524	A2M	C1'-N9-C8	2.30	132.19	127.09
82	S2	1045	PSU	C6-N1-C2	-2.30	120.56	122.69
2	L5	4227	OMU	O2-C2-N1	-2.30	119.81	122.80
82	S2	1081	PSU	C6-N1-C2	-2.29	120.56	122.69
82	S2	354	OMU	O2-C2-N1	-2.29	119.81	122.80
82	S2	1056	PSU	C6-N1-C2	-2.29	120.57	122.69
82	S2	1248	B8N	O4'-C1'-C2'	2.29	108.32	105.15
2	L5	4403	PSU	O4'-C1'-C2'	2.29	108.32	105.15
82	S2	1081	PSU	C6-C5-C4	2.28	119.71	118.17
2	L5	4220	6MZ	C3'-C2'-C1'	2.28	105.77	101.46
82	S2	686	PSU	C6-N1-C2	-2.28	120.58	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	27	A2M	O4'-C1'-C2'	2.27	110.50	106.59
2	L5	1744	PSU	C6-N1-C2	-2.27	120.59	122.69
2	L5	4299	PSU	C6-N1-C2	-2.27	120.59	122.69
2	L5	1792	PSU	C6-N1-C2	-2.26	120.59	122.69
2	L5	2632	PSU	C6-N1-C2	-2.26	120.59	122.69
2	L5	3830	A2M	C6-C5-C4	-2.26	114.09	117.18
2	L5	5001	PSU	C6-N1-C2	-2.26	120.59	122.69
2	L5	3785	A2M	C6-C5-C4	-2.26	114.09	117.18
82	S2	1046	PSU	C6-N1-C2	-2.26	120.60	122.69
82	S2	1383	A2M	C6-C5-C4	-2.26	114.10	117.18
82	S2	159	A2M	O3'-C3'-C4'	-2.25	104.61	111.08
2	L5	1534	A2M	C2'-C1'-N9	2.25	117.46	113.75
2	L5	400	A2M	O4'-C1'-C2'	2.24	110.45	106.59
2	L5	4403	PSU	C6-N1-C2	-2.24	120.61	122.69
2	L5	4498	OMU	O2-C2-N1	-2.24	119.88	122.80
82	S2	1004	PSU	C6-N1-C2	-2.24	120.61	122.69
2	L5	2815	A2M	C2'-C1'-N9	2.24	117.43	113.75
2	L5	4590	A2M	O4'-C1'-C2'	2.24	110.44	106.59
2	L5	3825	A2M	O4'-C1'-C2'	2.23	110.43	106.59
2	L5	1323	A2M	C6-C5-C4	-2.23	114.13	117.18
82	S2	468	A2M	O4'-C1'-C2'	2.23	110.42	106.59
2	L5	3925	OMU	O2-C2-N1	-2.22	119.90	122.80
2	L5	4523	A2M	C6-C5-C4	-2.22	114.14	117.18
2	L5	4296	PSU	C6-C5-C4	2.22	119.67	118.17
82	S2	1031	A2M	C6-C5-C4	-2.21	114.16	117.18
2	L5	4636	PSU	C6-N1-C2	-2.21	120.64	122.69
2	L5	1524	A2M	C2'-C1'-N9	2.20	117.38	113.75
2	L5	3920	PSU	C6-N1-C2	-2.20	120.65	122.69
2	L5	1860	PSU	C6-N1-C2	-2.20	120.65	122.69
82	S2	966	PSU	C6-N1-C2	-2.19	120.66	122.69
82	S2	1174	PSU	C6-N1-C2	-2.19	120.66	122.69
2	L5	3782	5MC	C1'-N1-C6	-2.18	117.56	121.15
2	L5	4571	A2M	C6-C5-C4	-2.18	114.20	117.18
2	L5	4431	PSU	C6-C5-C4	2.18	119.64	118.17
2	L5	3825	A2M	C6-C5-C4	-2.17	114.21	117.18
2	L5	1534	A2M	C6-C5-C4	-2.17	114.22	117.18
82	S2	668	A2M	C6-C5-C4	-2.17	114.22	117.18
2	L5	2363	A2M	O4'-C1'-C2'	2.17	110.32	106.59
2	L5	3867	A2M	O4'-C1'-C2'	2.16	110.31	106.59
82	S2	1832	6MZ	C4-C5-N7	-2.16	108.11	110.58
2	L5	1322	1MA	N1-C6-N6	2.16	125.14	119.71
82	S2	121	OMU	O2-C2-N1	-2.16	119.98	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	3822	PSU	C6-C5-C4	2.16	119.63	118.17
2	L5	3785	A2M	O4'-C1'-N9	2.16	112.23	108.09
2	L5	4361	PSU	C6-N1-C2	-2.16	120.69	122.69
2	L5	3830	A2M	O4'-C1'-C2'	2.16	110.30	106.59
2	L5	1744	PSU	O4'-C1'-C2'	2.16	108.13	105.15
2	L5	1871	A2M	C6-C5-C4	-2.15	114.24	117.18
2	L5	3867	A2M	C6-C5-C4	-2.15	114.24	117.18
82	S2	27	A2M	C6-C5-C4	-2.15	114.24	117.18
2	L5	3785	A2M	C2-N1-C6	-2.15	115.20	118.73
2	L5	398	A2M	C6-C5-C4	-2.15	114.24	117.18
2	L5	1524	A2M	C4'-O4'-C1'	-2.15	104.73	109.47
82	S2	668	A2M	O4'-C4'-C3'	2.14	109.41	105.15
82	S2	1326	OMU	O2-C2-N1	-2.14	120.01	122.80
2	L5	3853	PSU	C6-N1-C2	-2.14	120.70	122.69
2	L5	2839	PSU	C6-C5-C4	2.14	119.62	118.17
82	S2	863	PSU	C6-N1-C2	-2.14	120.71	122.69
82	S2	1248	B8N	O4-C4-C5	-2.14	118.88	122.58
2	L5	4457	PSU	O4'-C1'-C2'	2.14	108.11	105.15
2	L5	4576	PSU	O4'-C1'-C2'	2.14	108.11	105.15
2	L5	4523	A2M	O4'-C1'-C2'	2.14	110.26	106.59
2	L5	2815	A2M	C5-C6-N1	2.13	122.93	117.51
82	S2	172	OMU	O2-C2-N1	-2.13	120.02	122.80
82	S2	159	A2M	C6-C5-C4	-2.13	114.27	117.18
2	L5	5010	PSU	C6-N1-C2	-2.13	120.72	122.69
82	S2	99	A2M	C6-C5-C4	-2.13	114.27	117.18
82	S2	468	A2M	C6-C5-C4	-2.13	114.27	117.18
82	S2	799	OMU	C1'-N1-C2	2.12	121.40	117.59
2	L5	400	A2M	C6-C5-C4	-2.12	114.28	117.18
82	S2	1337	4AC	N4-C4-N3	2.12	117.31	113.87
2	L5	1326	A2M	O4'-C4'-C3'	2.12	109.35	105.15
2	L5	4636	PSU	O4'-C1'-C2'	2.11	108.08	105.15
2	L5	1326	A2M	C3'-C2'-C1'	-2.11	98.76	102.81
2	L5	2815	A2M	C4-N9-C1'	-2.11	121.70	126.63
2	L5	400	A2M	C2'-C1'-N9	2.11	117.22	113.75
82	S2	1383	A2M	C4'-O4'-C1'	-2.11	104.81	109.47
4	L8	69	PSU	O4'-C1'-C2'	2.10	108.06	105.15
2	L5	1534	A2M	C2-N1-C6	-2.10	115.28	118.73
2	L5	3701	OMC	C1'-N1-C2	2.10	123.08	118.44
2	L5	1534	A2M	C5-C6-N1	2.10	122.85	117.51
82	S2	649	PSU	C6-N1-C2	-2.10	120.74	122.69
2	L5	3695	PSU	O4'-C1'-C2'	2.09	108.05	105.15
2	L5	4972	PSU	O4'-C1'-C2'	2.09	108.05	105.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	3867	A2M	C2-N1-C6	-2.09	115.29	118.73
2	L5	2837	OMU	O2-C2-N1	-2.09	120.08	122.80
82	S2	866	PSU	C6-C5-C4	2.09	119.58	118.17
82	S2	576	A2M	C6-C5-C4	-2.09	114.33	117.18
2	L5	2815	A2M	C2-N1-C6	-2.09	115.30	118.73
2	L5	1326	A2M	C2-N1-C6	-2.09	115.30	118.73
82	S2	1248	B8N	C31-N3-C4	2.09	120.13	117.18
2	L5	3718	A2M	C6-C5-C4	-2.08	114.33	117.18
2	L5	2363	A2M	C2-N1-C6	-2.08	115.31	118.73
2	L5	3718	A2M	C2-N1-C6	-2.08	115.31	118.73
82	S2	484	A2M	C2-N1-C6	-2.08	115.31	118.73
2	L5	4220	6MZ	C4'-O4'-C1'	-2.08	104.87	109.47
82	S2	1850	MA6	C1'-N9-C8	-2.08	122.48	127.09
82	S2	159	A2M	C5-C6-N1	2.08	122.79	117.51
2	L5	2815	A2M	C1'-N9-C8	2.08	131.70	127.09
82	S2	166	A2M	C5-C6-N1	2.08	122.78	117.51
2	L5	2787	A2M	C2-N1-C6	-2.07	115.32	118.73
2	L5	400	A2M	C5-C6-N1	2.07	122.77	117.51
2	L5	2401	A2M	C5-C6-N1	2.07	122.77	117.51
2	L5	3841	OMC	C1'-N1-C2	2.07	123.01	118.44
82	S2	99	A2M	C5-C6-N1	2.07	122.77	117.51
82	S2	1031	A2M	O4'-C1'-C2'	2.07	110.15	106.59
2	L5	3830	A2M	C5-C6-N1	2.06	122.75	117.51
82	S2	484	A2M	C5-C6-N1	2.06	122.75	117.51
2	L5	3785	A2M	C5-C6-N1	2.06	122.75	117.51
2	L5	1744	PSU	C6-C5-C4	2.06	119.56	118.17
82	S2	1031	A2M	C5-C6-N1	2.06	122.74	117.51
82	S2	99	A2M	C2-N1-C6	-2.06	115.35	118.73
82	S2	116	OMU	O2-C2-N1	-2.06	120.12	122.80
2	L5	4521	PSU	C6-N1-C2	-2.06	120.78	122.69
82	S2	627	OMU	O2-C2-N1	-2.06	120.12	122.80
2	L5	3818	UY1	O4'-C1'-C2'	2.05	108.16	104.56
2	L5	1323	A2M	C5-C6-N1	2.05	122.73	117.51
2	L5	4590	A2M	C5-C6-N1	2.05	122.73	117.51
82	S2	1383	A2M	C5-C6-N1	2.05	122.73	117.51
2	L5	2815	A2M	C3'-C2'-C1'	-2.05	98.88	102.81
2	L5	1524	A2M	C5-C6-N1	2.05	122.72	117.51
2	L5	3825	A2M	C5-C6-N1	2.05	122.72	117.51
2	L5	398	A2M	C5-C6-N1	2.05	122.72	117.51
82	S2	159	A2M	C2-N1-C6	-2.05	115.36	118.73
82	S2	1288	OMU	O2-C2-N1	-2.05	120.13	122.80
2	L5	4500	PSU	C6-C5-C4	2.05	119.55	118.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	27	A2M	C5-C6-N1	2.04	122.70	117.51
2	L5	400	A2M	C2-N1-C6	-2.04	115.37	118.73
2	L5	2363	A2M	C6-C5-C4	-2.04	114.39	117.18
82	S2	1442	OMU	C1'-N1-C2	2.04	121.26	117.59
2	L5	3718	A2M	C5-C6-N1	2.04	122.70	117.51
2	L5	1323	A2M	C2-N1-C6	-2.04	115.38	118.73
2	L5	1871	A2M	C5-C6-N1	2.04	122.69	117.51
2	L5	2363	A2M	C5-C6-N1	2.04	122.69	117.51
2	L5	3920	PSU	O4'-C1'-C2'	2.04	107.97	105.15
2	L5	1524	A2M	C2-N1-C6	-2.03	115.39	118.73
2	L5	3637	PSU	C6-C5-C4	2.03	119.54	118.17
82	S2	1056	PSU	O4'-C1'-C2'	2.03	107.96	105.15
2	L5	3867	A2M	C5-C6-N1	2.03	122.66	117.51
82	S2	576	A2M	C5-C6-N1	2.03	122.66	117.51
2	L5	4523	A2M	C5-C6-N1	2.03	122.66	117.51
82	S2	1832	6MZ	C5-C6-N1	2.03	120.33	118.15
82	S2	1703	OMC	C1'-N1-C2	2.02	122.91	118.44
82	S2	576	A2M	C2-N1-C6	-2.02	115.41	118.73
2	L5	2787	A2M	C5-C6-N1	2.02	122.64	117.51
2	L5	1326	A2M	C5-C6-N1	2.02	122.64	117.51
2	L5	398	A2M	C2-N1-C6	-2.02	115.41	118.73
82	S2	668	A2M	C2-N1-C6	-2.02	115.42	118.73
2	L5	2815	A2M	O4'-C4'-C3'	2.02	109.16	105.15
2	L5	2815	A2M	C6-C5-C4	-2.02	114.43	117.18
2	L5	4312	PSU	C6-N1-C2	-2.01	120.82	122.69
82	S2	686	PSU	C6-C5-C4	2.01	119.53	118.17
82	S2	468	A2M	C5-C6-N1	2.01	122.62	117.51
2	L5	4493	PSU	C6-C5-C4	2.01	119.53	118.17
2	L5	4353	PSU	C6-C5-C4	2.01	119.53	118.17
2	L5	4972	PSU	C6-C5-C4	2.01	119.53	118.17
2	L5	3825	A2M	C2-N1-C6	-2.01	115.44	118.73

There are no chirality outliers.

All (157) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L8	75	OMG	C1'-C2'-O2'-CM2
2	L5	400	A2M	C1'-C2'-O2'-CM'
2	L5	1316	OMG	C1'-C2'-O2'-CM2
2	L5	1323	A2M	C1'-C2'-O2'-CM'
2	L5	1326	A2M	O4'-C4'-C5'-O5'
2	L5	1326	A2M	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	L5	1326	A2M	C1'-C2'-O2'-CM'
2	L5	1340	OMC	C1'-C2'-O2'-CM2
2	L5	1625	OMG	O4'-C4'-C5'-O5'
2	L5	2351	OMC	C1'-C2'-O2'-CM2
2	L5	2364	OMG	O4'-C4'-C5'-O5'
2	L5	2787	A2M	C1'-C2'-O2'-CM'
2	L5	2787	A2M	C2'-C1'-N9-C8
2	L5	2787	A2M	C2'-C1'-N9-C4
2	L5	2824	OMC	C1'-C2'-O2'-CM2
2	L5	2861	OMC	C1'-C2'-O2'-CM2
2	L5	3701	OMC	O4'-C4'-C5'-O5'
2	L5	3718	A2M	C1'-C2'-O2'-CM'
2	L5	3744	OMG	C1'-C2'-O2'-CM2
2	L5	3792	OMG	O4'-C4'-C5'-O5'
2	L5	3825	A2M	C1'-C2'-O2'-CM'
2	L5	3830	A2M	C1'-C2'-O2'-CM'
2	L5	3867	A2M	C1'-C2'-O2'-CM'
2	L5	4196	OMG	C1'-C2'-O2'-CM2
2	L5	4220	6MZ	C5-C6-N6-C9
2	L5	4220	6MZ	N1-C6-N6-C9
2	L5	4220	6MZ	O4'-C4'-C5'-O5'
2	L5	4447	5MC	C2'-C1'-N1-C2
2	L5	4447	5MC	C2'-C1'-N1-C6
2	L5	4500	PSU	O4'-C4'-C5'-O5'
2	L5	4590	A2M	O4'-C4'-C5'-O5'
2	L5	4590	A2M	C1'-C2'-O2'-CM'
2	L5	4637	OMG	C1'-C2'-O2'-CM2
82	S2	27	A2M	C1'-C2'-O2'-CM'
82	S2	116	OMU	C1'-C2'-O2'-CM2
82	S2	159	A2M	C1'-C2'-O2'-CM'
82	S2	354	OMU	C1'-C2'-O2'-CM2
82	S2	468	A2M	C1'-C2'-O2'-CM'
82	S2	484	A2M	C1'-C2'-O2'-CM'
82	S2	644	OMG	O4'-C4'-C5'-O5'
82	S2	644	OMG	C1'-C2'-O2'-CM2
82	S2	668	A2M	C1'-C2'-O2'-CM'
82	S2	683	OMG	C3'-C4'-C5'-O5'
82	S2	1248	B8N	O4'-C4'-C5'-O5'
82	S2	1272	OMC	O4'-C4'-C5'-O5'
82	S2	1288	OMU	O4'-C4'-C5'-O5'
82	S2	1337	4AC	N3-C4-N4-C7
82	S2	1383	A2M	C1'-C2'-O2'-CM'

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Mol	Chain	Res	Type	Atoms
82	S2	1442	OMU	O4'-C4'-C5'-O5'
82	S2	1832	6MZ	C5-C6-N6-C9
82	S2	1832	6MZ	N1-C6-N6-C9
82	S2	1832	6MZ	C5'-O5'-P-OP2
82	S2	1832	6MZ	C5'-O5'-P-OP3
82	S2	1248	B8N	N34-C33-C34-O36
2	L5	1323	A2M	O4'-C4'-C5'-O5'
2	L5	1536	PSU	C3'-C4'-C5'-O5'
2	L5	2787	A2M	C3'-C4'-C5'-O5'
2	L5	3701	OMC	C3'-C4'-C5'-O5'
2	L5	4500	PSU	C3'-C4'-C5'-O5'
2	L5	4590	A2M	C3'-C4'-C5'-O5'
2	L5	4618	OMG	C3'-C4'-C5'-O5'
82	S2	517	OMC	C3'-C4'-C5'-O5'
82	S2	517	OMC	O4'-C4'-C5'-O5'
82	S2	801	PSU	C3'-C4'-C5'-O5'
82	S2	1272	OMC	C3'-C4'-C5'-O5'
82	S2	1288	OMU	C3'-C4'-C5'-O5'
82	S2	1832	6MZ	O4'-C4'-C5'-O5'
2	L5	1524	A2M	C3'-C4'-C5'-O5'
2	L5	1536	PSU	O4'-C4'-C5'-O5'
2	L5	1625	OMG	C3'-C4'-C5'-O5'
2	L5	2422	OMC	C3'-C4'-C5'-O5'
2	L5	3899	OMG	O4'-C4'-C5'-O5'
2	L5	3899	OMG	C3'-C4'-C5'-O5'
2	L5	4618	OMG	O4'-C4'-C5'-O5'
82	S2	576	A2M	O4'-C4'-C5'-O5'
82	S2	683	OMG	O4'-C4'-C5'-O5'
82	S2	1045	PSU	C3'-C4'-C5'-O5'
82	S2	1045	PSU	O4'-C4'-C5'-O5'
82	S2	1442	OMU	C3'-C4'-C5'-O5'
2	L5	3792	OMG	C3'-C4'-C5'-O5'
2	L5	4220	6MZ	C3'-C4'-C5'-O5'
82	S2	1248	B8N	C3'-C4'-C5'-O5'
2	L5	1323	A2M	C3'-C4'-C5'-O5'
2	L5	1524	A2M	O4'-C4'-C5'-O5'
2	L5	2364	OMG	C3'-C4'-C5'-O5'
82	S2	576	A2M	C3'-C4'-C5'-O5'
82	S2	644	OMG	C3'-C4'-C5'-O5'
82	S2	799	OMU	C3'-C4'-C5'-O5'
2	L5	2422	OMC	O4'-C4'-C5'-O5'
2	L5	2787	A2M	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	L5	4296	PSU	O4'-C4'-C5'-O5'
82	S2	99	A2M	O4'-C4'-C5'-O5'
82	S2	799	OMU	O4'-C4'-C5'-O5'
82	S2	627	OMU	C2'-C1'-N1-C6
2	L5	1534	A2M	C3'-C2'-O2'-CM'
2	L5	4296	PSU	C3'-C4'-C5'-O5'
82	S2	668	A2M	O4'-C4'-C5'-O5'
82	S2	801	PSU	O4'-C4'-C5'-O5'
2	L5	4590	A2M	C4'-C5'-O5'-P
82	S2	1832	6MZ	C5'-O5'-P-OP1
82	S2	1832	6MZ	C3'-C4'-C5'-O5'
82	S2	668	A2M	C3'-C4'-C5'-O5'
82	S2	509	OMG	C1'-C2'-O2'-CM2
82	S2	99	A2M	C3'-C4'-C5'-O5'
82	S2	1383	A2M	O4'-C4'-C5'-O5'
2	L5	3701	OMC	O4'-C1'-N1-C6
82	S2	1383	A2M	C3'-C4'-C5'-O5'
2	L5	4447	5MC	O4'-C1'-N1-C6
82	S2	627	OMU	O4'-C1'-N1-C6
2	L5	3701	OMC	O4'-C1'-N1-C2
2	L5	1534	A2M	C4'-C5'-O5'-P
2	L5	4500	PSU	C4'-C5'-O5'-P
82	S2	576	A2M	C4'-C5'-O5'-P
2	L5	3822	PSU	C3'-C4'-C5'-O5'
82	S2	627	OMU	O4'-C4'-C5'-O5'
82	S2	627	OMU	C2'-C1'-N1-C2
2	L5	3844	PSU	C4'-C5'-O5'-P
2	L5	1677	PSU	O4'-C1'-C5-C4
2	L5	4521	PSU	O4'-C1'-C5-C4
2	L5	4636	PSU	O4'-C1'-C5-C4
2	L5	5010	PSU	O4'-C1'-C5-C4
2	L5	3818	UY1	C4'-C5'-O5'-P
2	L5	3887	OMC	C4'-C5'-O5'-P
82	S2	1081	PSU	C4'-C5'-O5'-P
2	L5	4293	PSU	O4'-C4'-C5'-O5'
82	S2	1851	MA6	C5-C6-N6-C10
2	L5	4447	5MC	O4'-C1'-N1-C2
82	S2	1851	MA6	C4'-C5'-O5'-P
2	L5	4523	A2M	O4'-C4'-C5'-O5'
82	S2	627	OMU	O4'-C1'-N1-C2
82	S2	644	OMG	C4'-C5'-O5'-P
2	L5	1781	PSU	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	L5	3841	OMC	C1'-C2'-O2'-CM2
82	S2	576	A2M	C1'-C2'-O2'-CM'
82	S2	1490	OMG	C4'-C5'-O5'-P
82	S2	428	OMU	O4'-C1'-N1-C6
2	L5	2815	A2M	O4'-C4'-C5'-O5'
2	L5	4623	OMG	C3'-C4'-C5'-O5'
2	L5	4521	PSU	O4'-C1'-C5-C6
2	L5	5010	PSU	O4'-C1'-C5-C6
82	S2	428	OMU	C2'-C1'-N1-C6
2	L5	1524	A2M	C3'-C2'-O2'-CM'
2	L5	2351	OMC	O4'-C4'-C5'-O5'
2	L5	3887	OMC	C3'-C4'-C5'-O5'
2	L5	1524	A2M	O4'-C1'-N9-C8
2	L5	3822	PSU	O4'-C4'-C5'-O5'
82	S2	159	A2M	O4'-C4'-C5'-O5'
82	S2	517	OMC	C4'-C5'-O5'-P
2	L5	2815	A2M	C3'-C2'-O2'-CM'
2	L5	1677	PSU	O4'-C4'-C5'-O5'
2	L5	2861	OMC	O4'-C4'-C5'-O5'
2	L5	3851	PSU	C3'-C4'-C5'-O5'
2	L5	4447	5MC	O4'-C4'-C5'-O5'
82	S2	428	OMU	O4'-C4'-C5'-O5'
2	L5	2861	OMC	C2'-C1'-N1-C2
82	S2	867	OMG	C4'-C5'-O5'-P
82	S2	1248	B8N	N34-C33-C34-O35

There are no ring outliers.

99 monomers are involved in 163 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	S2	1004	PSU	2	0
2	L5	2422	OMC	1	0
82	S2	116	OMU	3	0
82	S2	1031	A2M	3	0
2	L5	4972	PSU	1	0
2	L5	4637	OMG	1	0
82	S2	109	PSU	1	0
2	L5	3825	A2M	5	0
2	L5	1323	A2M	1	0
4	L8	69	PSU	1	0
2	L5	2351	OMC	3	0
82	S2	509	OMG	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L5	2837	OMU	1	0
2	L5	1326	A2M	2	0
82	S2	576	A2M	2	0
82	S2	1177	PSU	1	0
82	S2	354	OMU	2	0
82	S2	1244	PSU	2	0
82	S2	1842	4AC	3	0
2	L5	4636	PSU	1	0
82	S2	1850	MA6	2	0
82	S2	174	OMC	1	0
2	L5	4456	OMC	1	0
82	S2	651	PSU	1	0
2	L5	4431	PSU	1	0
82	S2	1337	4AC	3	0
2	L5	3785	A2M	1	0
82	S2	1174	PSU	2	0
82	S2	121	OMU	1	0
2	L5	4196	OMG	1	0
4	L8	75	OMG	2	0
2	L5	3701	OMC	1	0
2	L5	3869	OMC	1	0
2	L5	2364	OMG	1	0
82	S2	1639	G7M	1	0
82	S2	1832	6MZ	2	0
82	S2	159	A2M	1	0
2	L5	3853	PSU	1	0
2	L5	4973	PSU	1	0
2	L5	1534	A2M	1	0
82	S2	462	OMC	1	0
2	L5	4579	PSU	3	0
2	L5	2824	OMC	3	0
2	L5	4523	A2M	3	0
2	L5	2861	OMC	1	0
2	L5	1625	OMG	1	0
82	S2	468	A2M	4	0
2	L5	3744	OMG	1	0
2	L5	4552	PSU	2	0
2	L5	4299	PSU	2	0
2	L5	3844	PSU	1	0
82	S2	1391	OMC	2	0
2	L5	4620	OMU	3	0
2	L5	3627	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	S2	644	OMG	2	0
2	L5	1340	OMC	2	0
82	S2	649	PSU	2	0
82	S2	668	A2M	2	0
2	L5	4220	6MZ	2	0
2	L5	1683	PSU	3	0
82	S2	814	PSU	1	0
82	S2	1328	OMG	1	0
2	L5	1316	OMG	2	0
2	L5	3920	PSU	1	0
82	S2	436	OMG	1	0
82	S2	1232	PSU	2	0
82	S2	27	A2M	1	0
2	L5	3818	UY1	2	0
2	L5	2632	PSU	2	0
2	L5	3867	A2M	4	0
82	S2	1288	OMU	2	0
2	L5	3695	PSU	1	0
2	L5	2365	OMC	1	0
2	L5	4353	PSU	1	0
2	L5	4623	OMG	2	0
2	L5	3830	A2M	1	0
2	L5	4403	PSU	2	0
2	L5	4689	PSU	2	0
82	S2	627	OMU	1	0
82	S2	867	OMG	1	0
2	L5	4293	PSU	1	0
2	L5	2804	OMC	2	0
82	S2	484	A2M	2	0
2	L5	4576	PSU	1	0
2	L5	1871	A2M	1	0
2	L5	2363	A2M	1	0
82	S2	166	A2M	1	0
2	L5	4590	A2M	1	0
82	S2	601	OMG	3	0
2	L5	3718	A2M	4	0
2	L5	4392	OMG	1	0
2	L5	4536	OMC	1	0
82	S2	681	PSU	1	0
2	L5	400	A2M	2	0
2	L5	1677	PSU	1	0
2	L5	4442	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L5	2787	A2M	1	0
2	L5	3841	OMC	1	0
2	L5	4457	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 244 ligands modelled in this entry, 225 are monoatomic - leaving 19 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	$\# Z > 2$
87	SPD	L5	5290	-	9,9,9	0.32	0	8,8,8	0.92	0
86	SPM	L5	5293	-	13,13,13	0.35	0	12,12,12	0.90	0
89	HMT	L5	5297	-	41,43,43	4.55	15 (36%)	43,66,66	2.01	14 (32%)
87	SPD	L5	5262	-	9,9,9	0.33	0	8,8,8	0.95	0
87	SPD	L5	5283	-	9,9,9	0.33	0	8,8,8	0.84	0
86	SPM	L5	5264	-	13,13,13	0.35	0	12,12,12	0.95	0
87	SPD	LN	301	-	9,9,9	0.32	0	8,8,8	0.87	0
86	SPM	L5	5289	-	13,13,13	0.36	0	12,12,12	0.91	0
87	SPD	L5	5288	-	9,9,9	0.32	0	8,8,8	0.86	0
86	SPM	L5	5259	-	13,13,13	0.35	0	12,12,12	0.98	0
86	SPM	L5	5292	-	13,13,13	0.35	0	12,12,12	0.95	0
86	SPM	L5	5265	-	13,13,13	0.35	0	12,12,12	0.99	0
87	SPD	L5	5284	-	9,9,9	0.33	0	8,8,8	0.85	0
87	SPD	L5	5291	-	9,9,9	0.32	0	8,8,8	0.80	0
87	SPD	L5	5285	-	9,9,9	0.33	0	8,8,8	0.83	0
86	SPM	L5	5268	-	13,13,13	0.35	0	12,12,12	1.01	0
87	SPD	L5	5287	-	9,9,9	0.32	0	8,8,8	0.87	0
88	3HE	L5	5296	-	21,21,21	0.41	0	23,30,30	0.93	1 (4%)
87	SPD	L5	5286	-	9,9,9	0.33	0	8,8,8	0.82	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
87	SPD	L5	5290	-	-	2/7/7/7	-
86	SPM	L5	5293	-	-	1/11/11/11	-
89	HMT	L5	5297	-	-	8/27/74/74	0/5/5/5
87	SPD	L5	5262	-	-	1/7/7/7	-
87	SPD	L5	5283	-	-	1/7/7/7	-
86	SPM	L5	5264	-	-	3/11/11/11	-
87	SPD	LN	301	-	-	1/7/7/7	-
86	SPM	L5	5289	-	-	5/11/11/11	-
87	SPD	L5	5288	-	-	2/7/7/7	-
86	SPM	L5	5259	-	-	2/11/11/11	-
86	SPM	L5	5292	-	-	3/11/11/11	-
86	SPM	L5	5265	-	-	5/11/11/11	-
87	SPD	L5	5284	-	-	3/7/7/7	-
87	SPD	L5	5291	-	-	2/7/7/7	-
87	SPD	L5	5285	-	-	2/7/7/7	-
86	SPM	L5	5268	-	-	3/11/11/11	-
87	SPD	L5	5287	-	-	3/7/7/7	-
88	3HE	L5	5296	-	-	1/8/36/36	0/2/2/2
87	SPD	L5	5286	-	-	0/7/7/7	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	L5	5297	HMT	C8-C7	18.29	1.79	1.52
89	L5	5297	HMT	C7-C6	12.08	1.77	1.51
89	L5	5297	HMT	C5-C4	-10.08	1.36	1.51
89	L5	5297	HMT	C10-N1	7.58	1.57	1.47
89	L5	5297	HMT	C1-C2	7.05	1.43	1.32
89	L5	5297	HMT	O4-C19	5.82	1.45	1.34
89	L5	5297	HMT	C9-N1	-4.87	1.34	1.48
89	L5	5297	HMT	O4-C3	-4.42	1.36	1.44
89	L5	5297	HMT	C12-C9	3.62	1.60	1.54
89	L5	5297	HMT	O3-C2	3.20	1.41	1.35
89	L5	5297	HMT	O7-C22	2.65	1.41	1.33
89	L5	5297	HMT	C3-C2	-2.54	1.44	1.50
89	L5	5297	HMT	O2-C15	2.44	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	L5	5297	HMT	O1-C14	2.41	1.42	1.38
89	L5	5297	HMT	C21-C22	2.28	1.55	1.50

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	L5	5297	HMT	O4-C19-C20	5.73	121.75	111.24
89	L5	5297	HMT	O7-C22-C21	5.06	120.05	111.16
89	L5	5297	HMT	C3-O4-C19	-3.88	111.14	117.24
89	L5	5297	HMT	O1-C14-C13	3.29	132.23	127.86
89	L5	5297	HMT	O2-C15-C16	3.04	131.90	127.86
89	L5	5297	HMT	C25-C24-C20	-2.83	108.74	115.34
89	L5	5297	HMT	O4-C19-O5	-2.59	119.37	123.95
89	L5	5297	HMT	C17-O1-C14	2.42	108.55	105.32
89	L5	5297	HMT	O5-C19-C20	-2.32	118.88	124.07
89	L5	5297	HMT	C10-N1-C9	-2.19	101.58	107.65
89	L5	5297	HMT	C18-O3-C2	-2.15	112.97	116.53
89	L5	5297	HMT	C13-C5-C6	-2.12	117.08	119.39
89	L5	5297	HMT	C16-C15-C14	-2.10	119.40	122.03
88	L5	5296	3HE	C9-C13-C12	-2.10	110.94	114.46
89	L5	5297	HMT	C17-O2-C15	2.09	108.12	105.32

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	L5	5297	HMT	C1-C2-O3-C18
89	L5	5297	HMT	C3-C2-O3-C18
89	L5	5297	HMT	C25-C26-C27-O9
86	L5	5292	SPM	C7-C8-C9-N10
89	L5	5297	HMT	C21-C22-O7-C23
86	L5	5265	SPM	N5-C6-C7-C8
87	L5	5288	SPD	N6-C7-C8-C9
86	L5	5268	SPM	N10-C11-C12-C13
86	L5	5289	SPM	N10-C11-C12-C13
89	L5	5297	HMT	O8-C22-O7-C23
86	L5	5264	SPM	C7-C8-C9-N10
86	L5	5265	SPM	C8-C9-N10-C11
86	L5	5265	SPM	C12-C11-N10-C9
86	L5	5289	SPM	C7-C6-N5-C4
87	L5	5291	SPD	C4-C5-N6-C7
87	L5	5285	SPD	C2-C3-C4-C5

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Mol	Chain	Res	Type	Atoms
87	L5	5287	SPD	C3-C4-C5-N6
89	L5	5297	HMT	C25-C26-C27-C28
89	L5	5297	HMT	C25-C26-C27-C29
86	L5	5289	SPM	C7-C8-C9-N10
86	L5	5264	SPM	C6-C7-C8-C9
86	L5	5259	SPM	C6-C7-C8-C9
87	L5	5283	SPD	C2-C3-C4-C5
86	L5	5289	SPM	C6-C7-C8-C9
87	L5	5262	SPD	C2-C3-C4-C5
86	L5	5264	SPM	C11-C12-C13-N14
86	L5	5289	SPM	N1-C2-C3-C4
87	L5	5284	SPD	C7-C8-C9-N10
89	L5	5297	HMT	C20-C24-C25-C26
87	L5	5291	SPD	N6-C7-C8-C9
86	L5	5292	SPM	N10-C11-C12-C13
87	L5	5287	SPD	C4-C5-N6-C7
87	L5	5287	SPD	C2-C3-C4-C5
86	L5	5292	SPM	C8-C9-N10-C11
87	L5	5290	SPD	C7-C8-C9-N10
86	L5	5268	SPM	C8-C9-N10-C11
87	LN	301	SPD	C8-C7-N6-C5
87	L5	5290	SPD	C2-C3-C4-C5
86	L5	5293	SPM	C7-C6-N5-C4
86	L5	5265	SPM	C7-C6-N5-C4
87	L5	5285	SPD	N6-C7-C8-C9
86	L5	5265	SPM	C6-C7-C8-C9
88	L5	5296	3HE	C7-C8-C9-C10
87	L5	5284	SPD	C8-C7-N6-C5
86	L5	5259	SPM	C11-C12-C13-N14
87	L5	5288	SPD	C7-C8-C9-N10
87	L5	5284	SPD	N1-C2-C3-C4
86	L5	5268	SPM	C7-C8-C9-N10

There are no ring outliers.

16 monomers are involved in 29 short contacts:

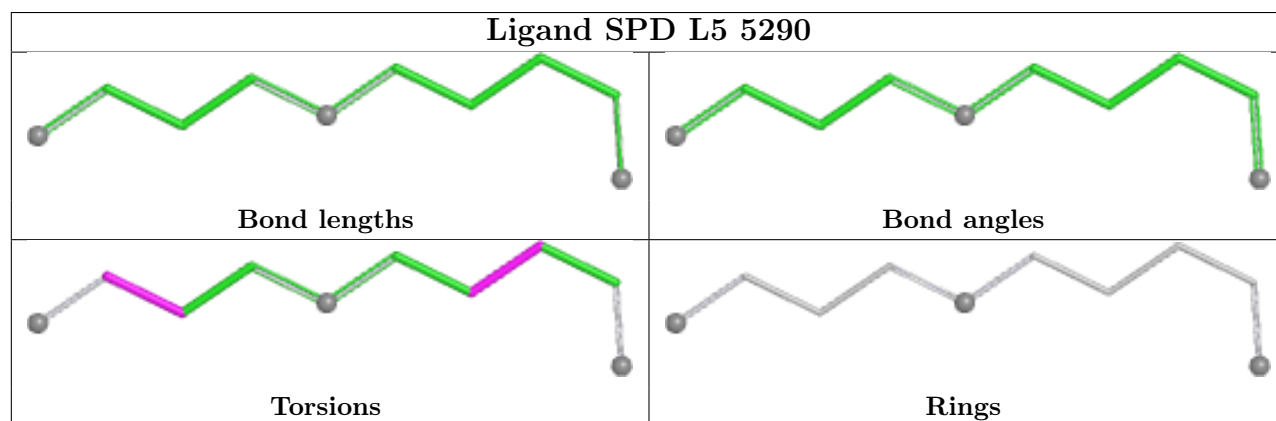
Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	L5	5290	SPD	2	0
86	L5	5293	SPM	2	0
89	L5	5297	HMT	8	0
87	L5	5262	SPD	1	0
87	LN	301	SPD	2	0

Continued on next page...

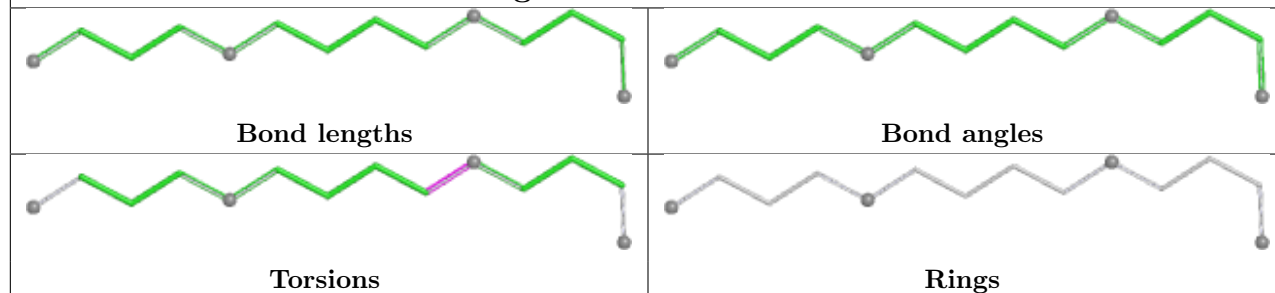
Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	L5	5289	SPM	1	0
87	L5	5288	SPD	1	0
86	L5	5259	SPM	1	0
86	L5	5292	SPM	1	0
86	L5	5265	SPM	2	0
87	L5	5284	SPD	2	0
87	L5	5291	SPD	1	0
87	L5	5285	SPD	2	0
86	L5	5268	SPM	1	0
87	L5	5287	SPD	1	0
88	L5	5296	3HE	2	0

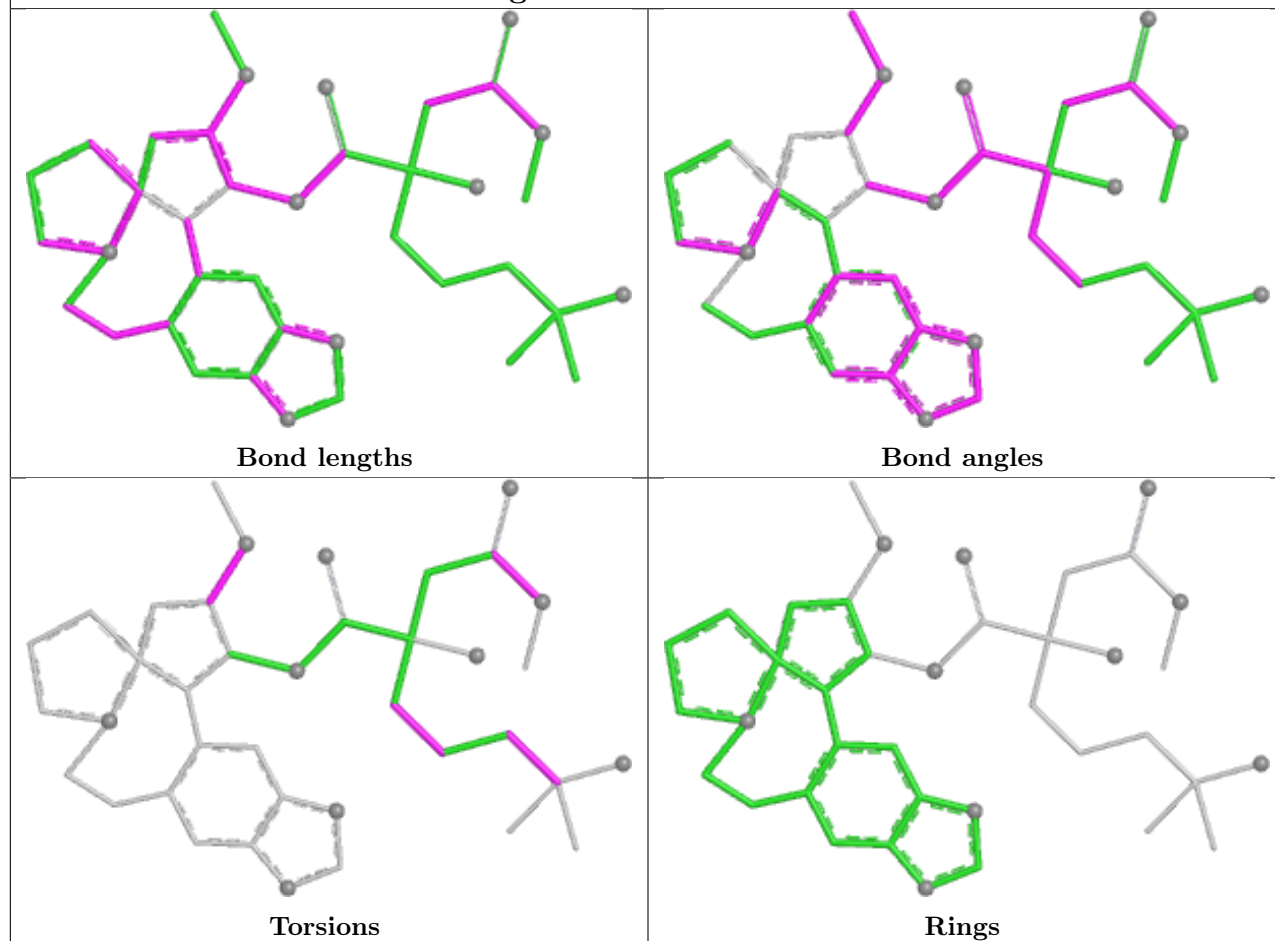
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



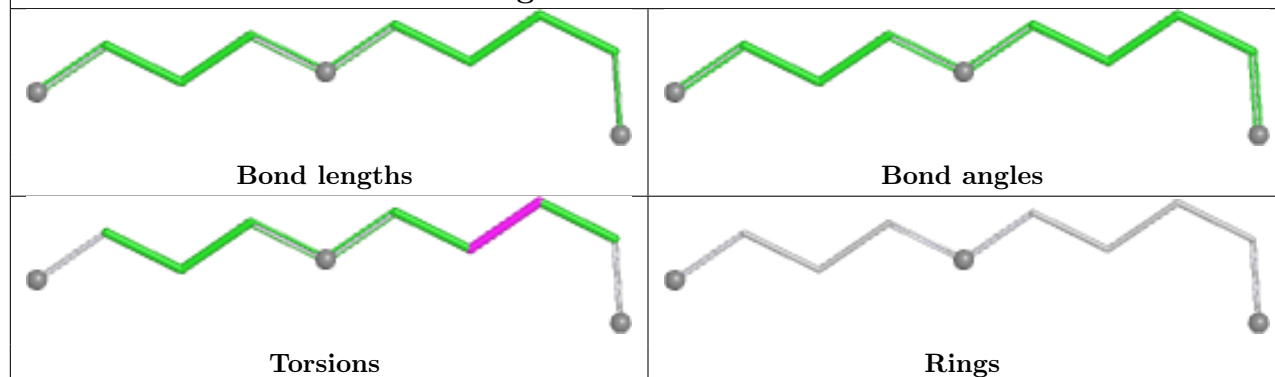
Ligand SPM L5 5293

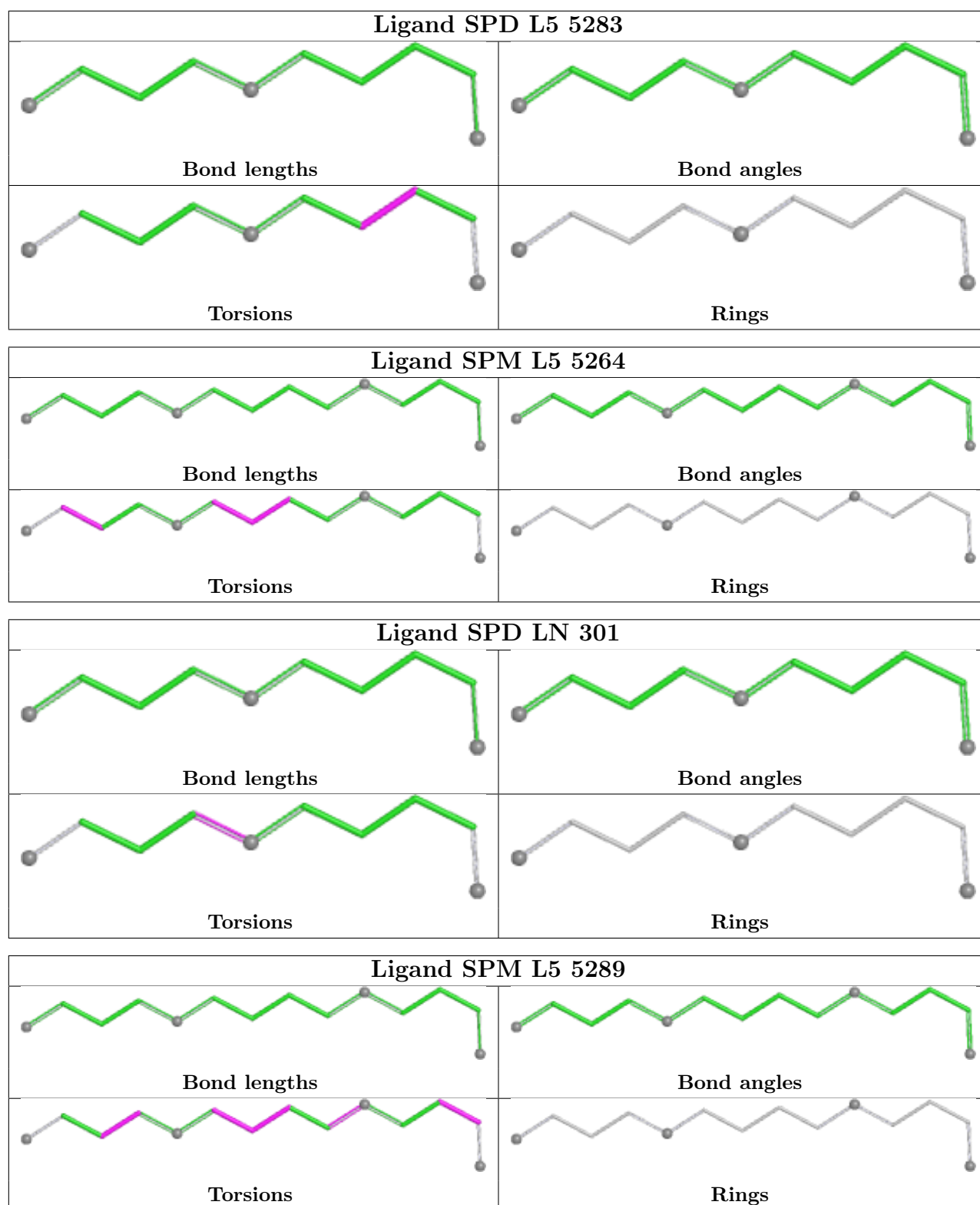


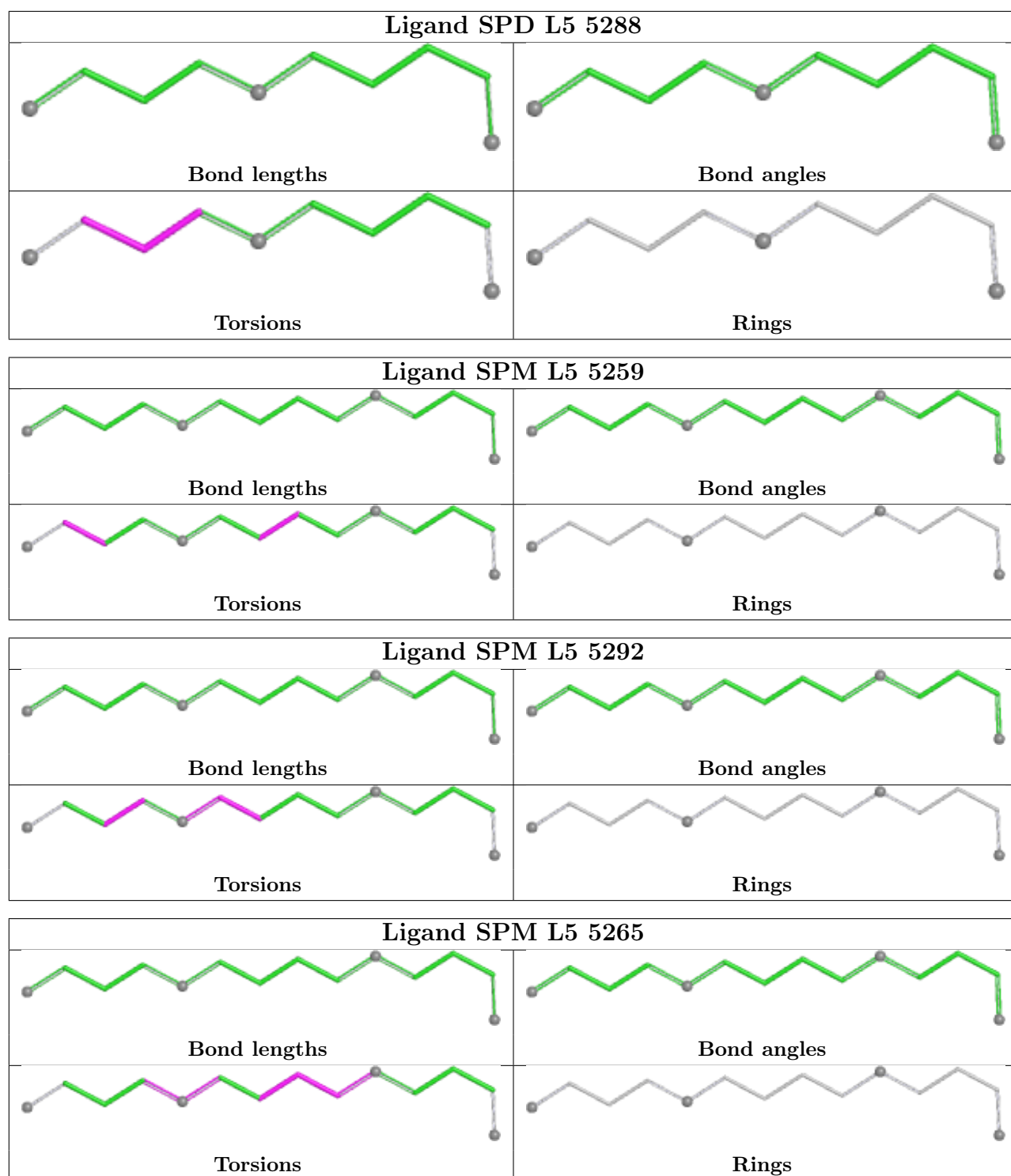
Ligand HMT L5 5297

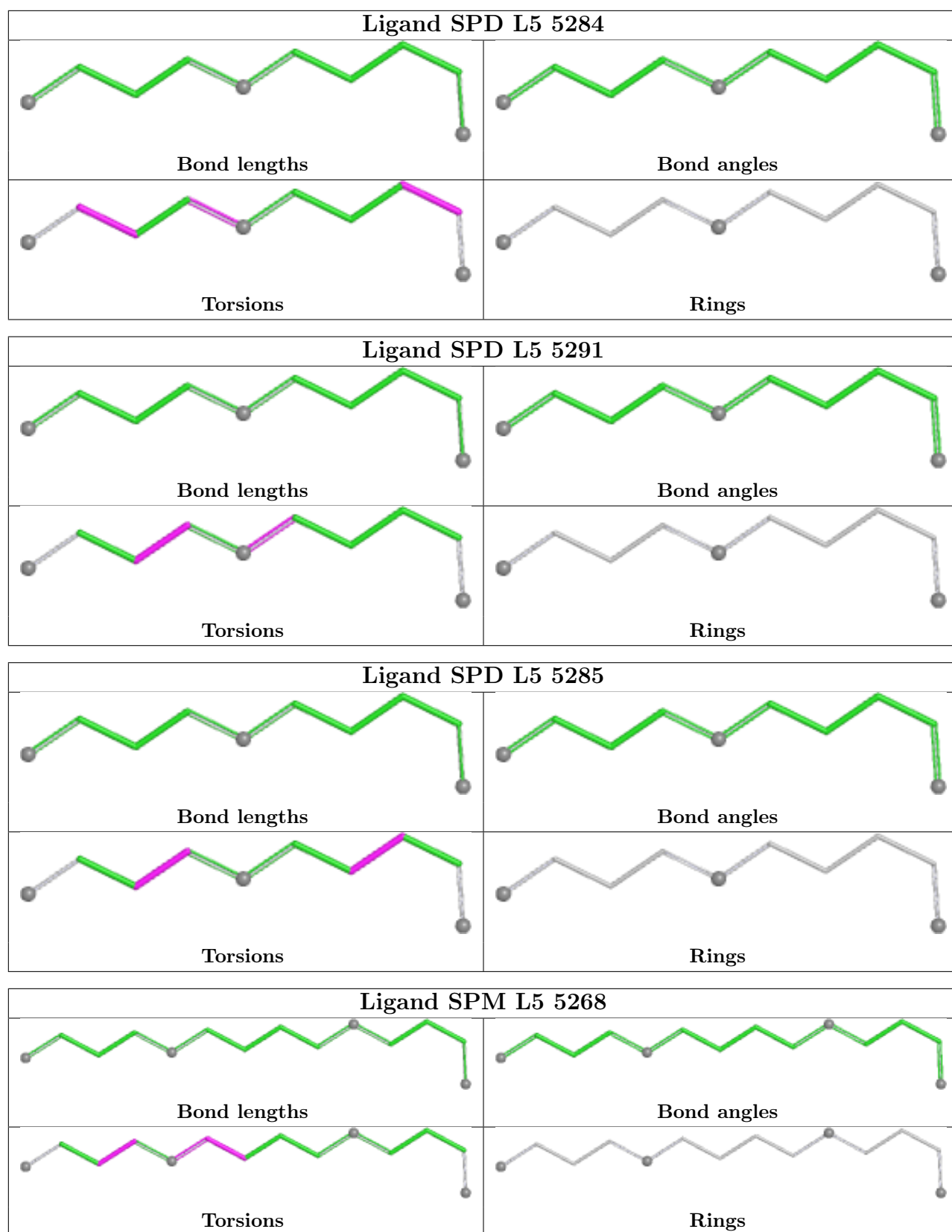


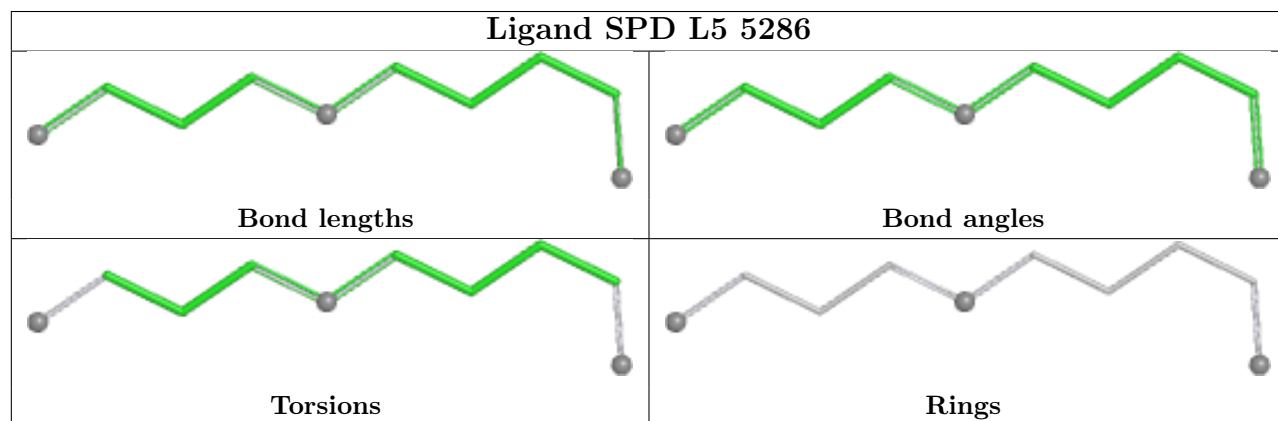
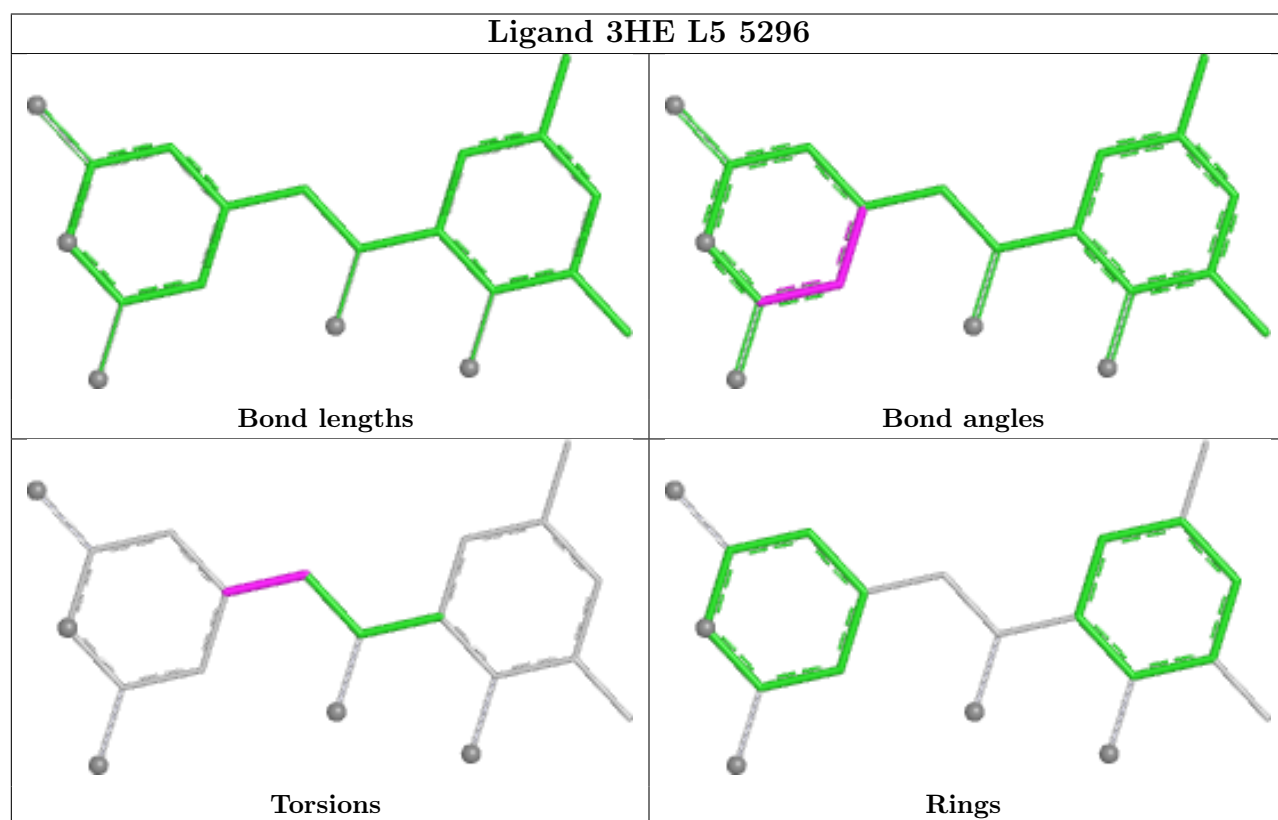
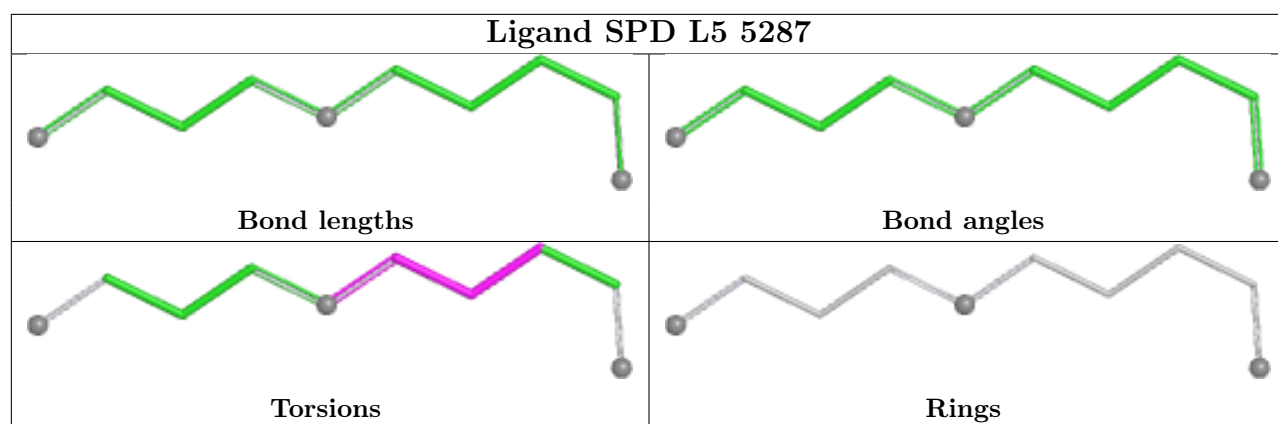
Ligand SPD L5 5262











5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	L5	10
82	S2	5
1	Pt	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	29.10
1	L5	1706:A	O3'	1716:G	P	22.00
1	L5	2910:G	O3'	3584:C	P	21.10
1	L5	760:G	O3'	903:C	P	17.10
1	L5	519:C	O3'	642:G	P	15.85
1	L5	4776:G	O3'	4858:C	P	14.95
1	S2	698:G	O3'	730:C	P	14.89
1	L5	2112:G	O3'	2249:C	P	14.72
1	L5	3954:A	O3'	4056:A	P	13.01
1	S2	739:C	O3'	746:C	P	12.79
1	L5	990:C	O3'	1064:G	P	12.33
1	Pt	15:G	O3'	18:G	P	10.04
1	L5	1222:A	O3'	1234:G	P	9.20
1	S2	225:G	O3'	287:U	P	7.57
1	L5	1100:U	O3'	1167:C	P	7.12
1	S2	1831:A	O3'	1832:6MZ	P	4.22

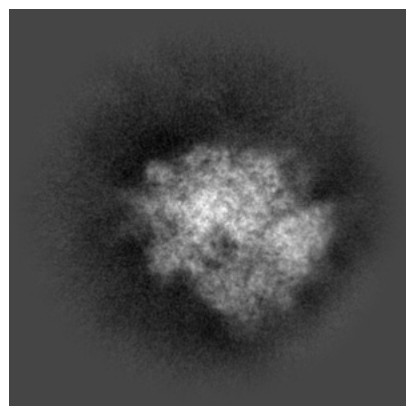
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71378. These allow visual inspection of the internal detail of the map and identification of artifacts.

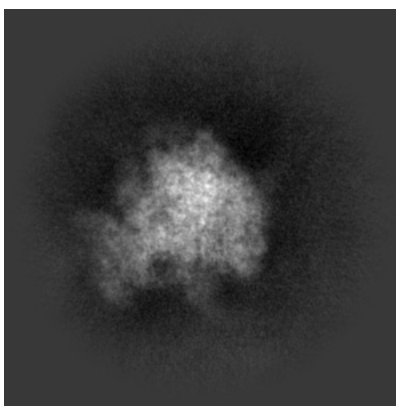
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

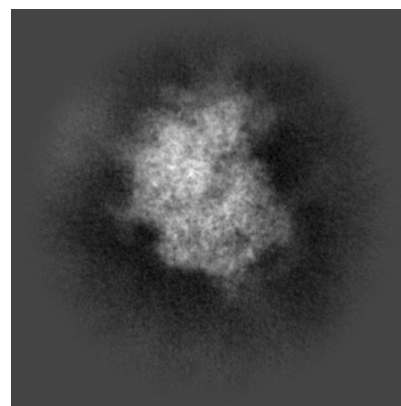
6.1.1 Primary map



X

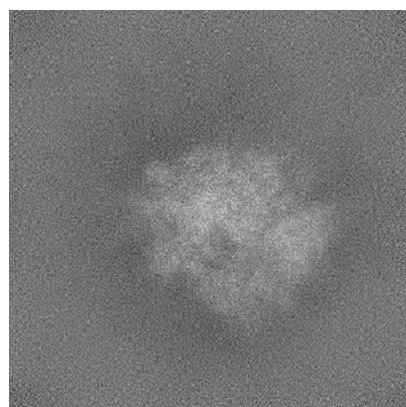


Y

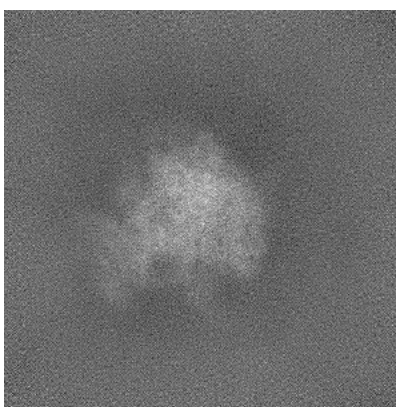


Z

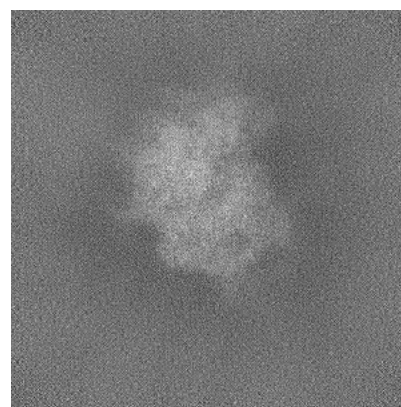
6.1.2 Raw map



X



Y

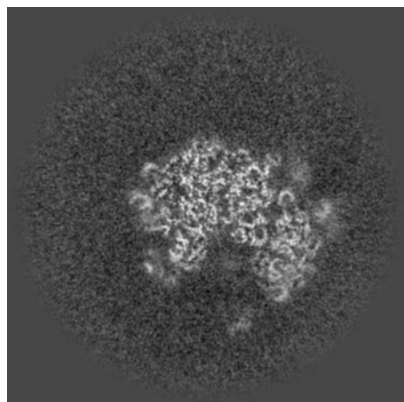


Z

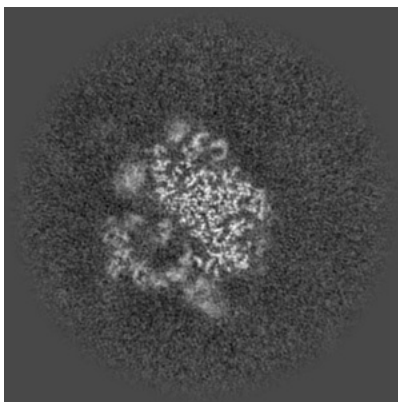
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

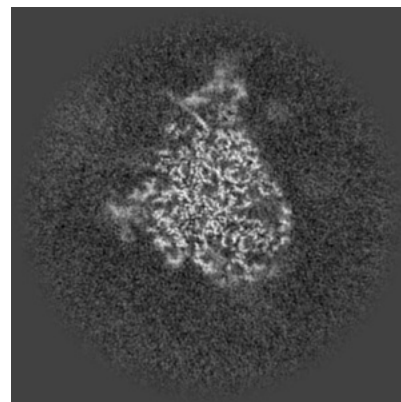
6.2.1 Primary map



X Index: 256

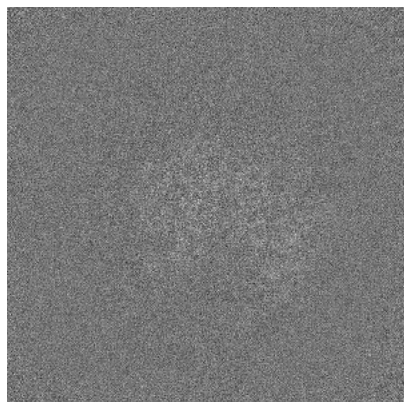


Y Index: 256

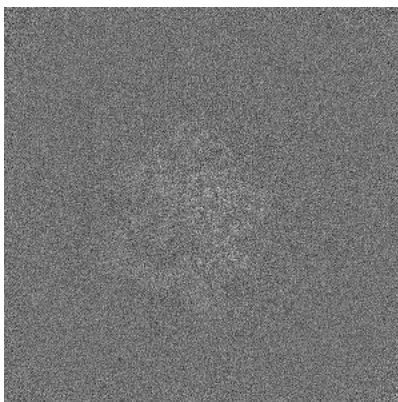


Z Index: 256

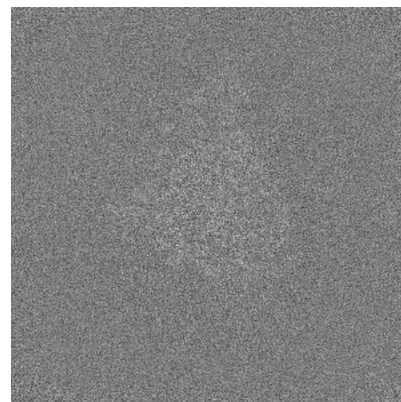
6.2.2 Raw map



X Index: 256



Y Index: 256

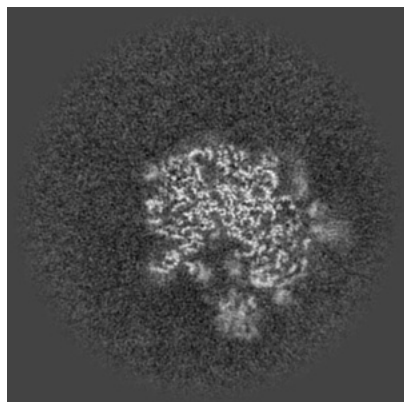


Z Index: 256

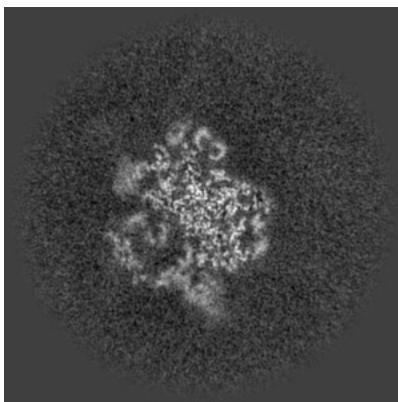
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

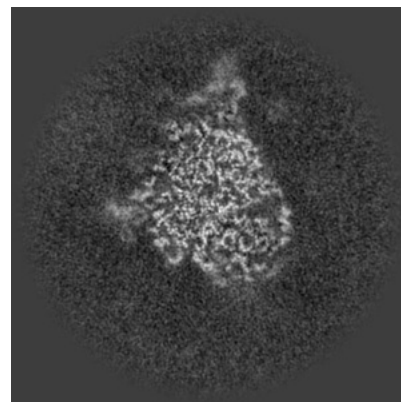
6.3.1 Primary map



X Index: 243

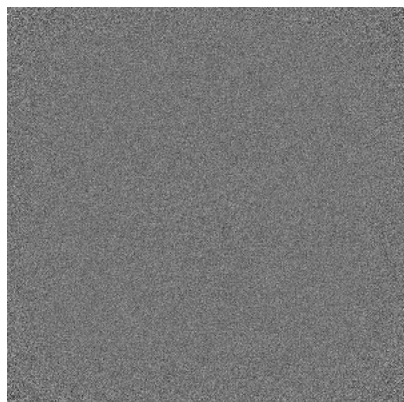


Y Index: 251

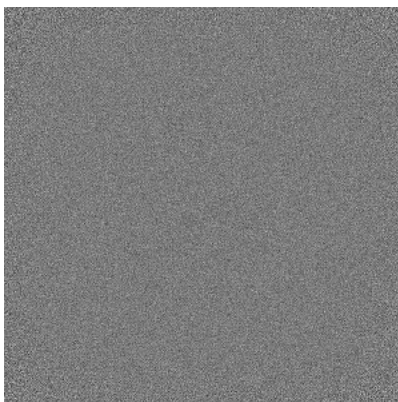


Z Index: 258

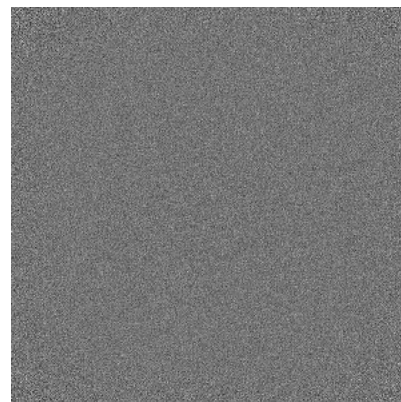
6.3.2 Raw map



X Index: 0



Y Index: 0

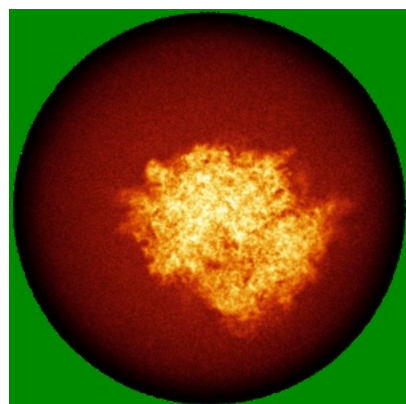


Z Index: 0

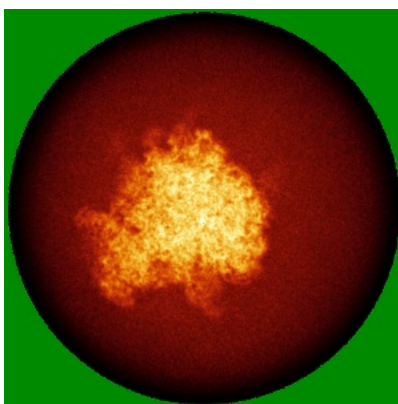
The images above show the largest variance slices of the map in three orthogonal directions.

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

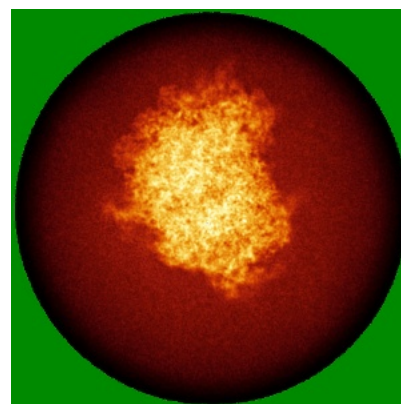
6.4.1 Primary map



X

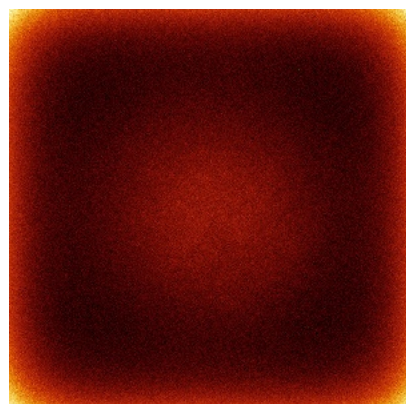


Y

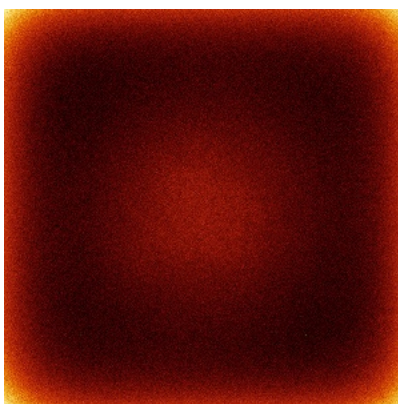


Z

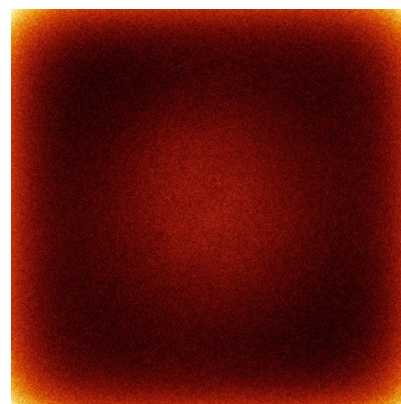
6.4.2 Raw map



X



Y

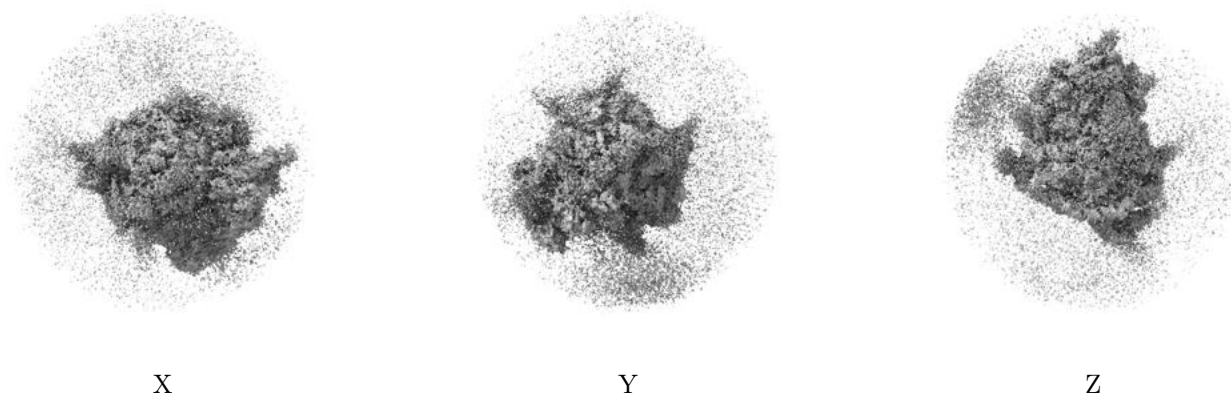


Z

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.

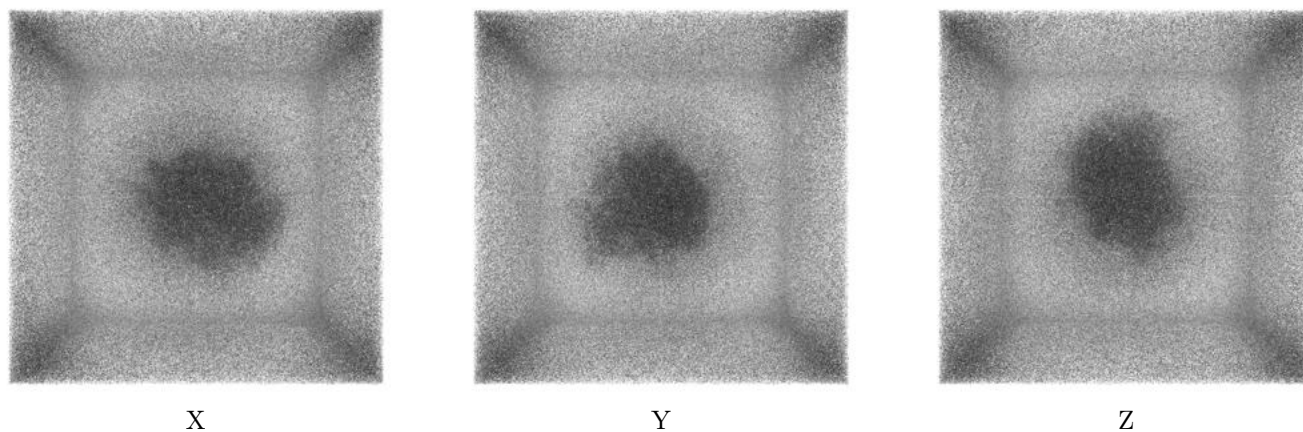
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0717. 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.

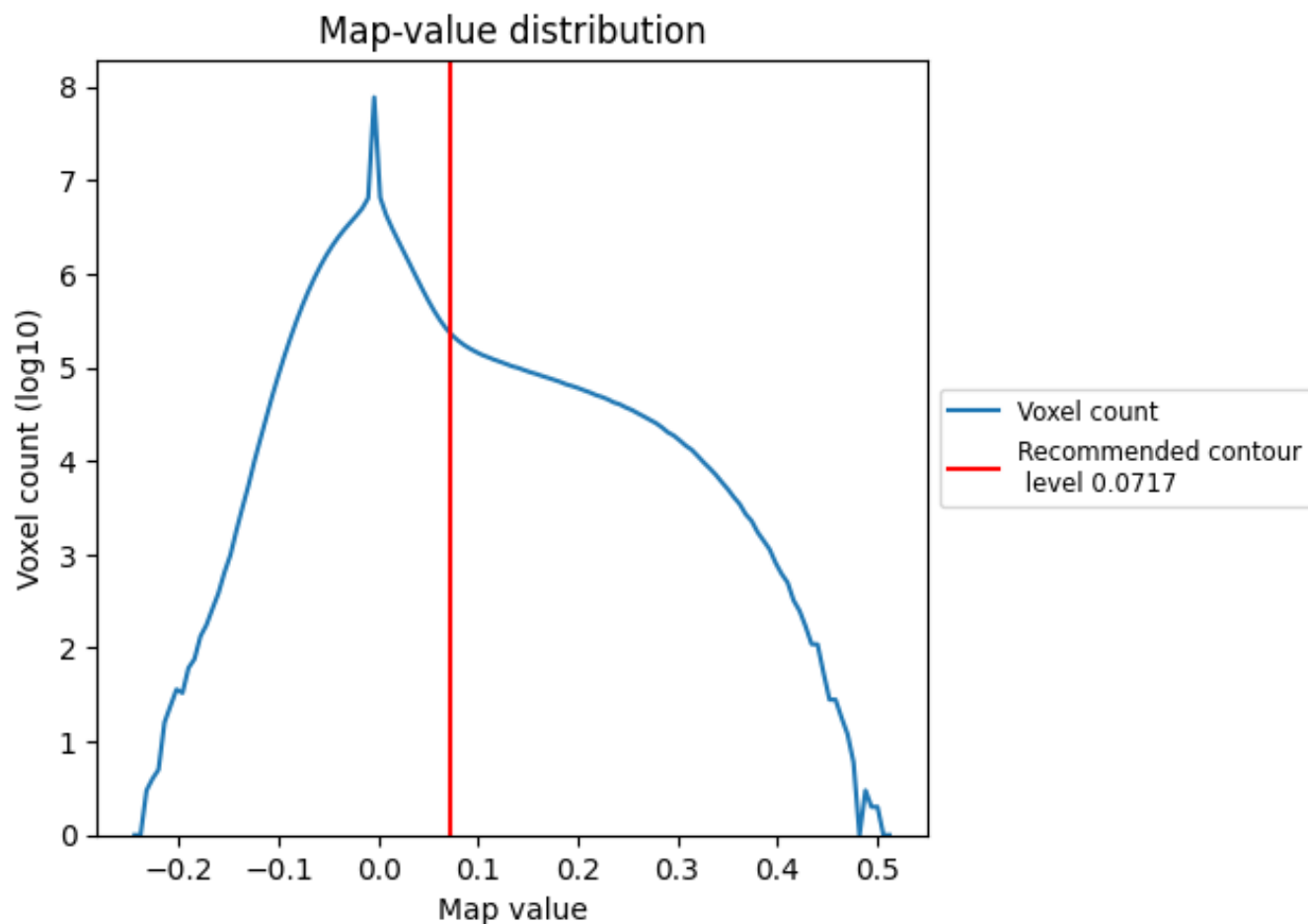
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

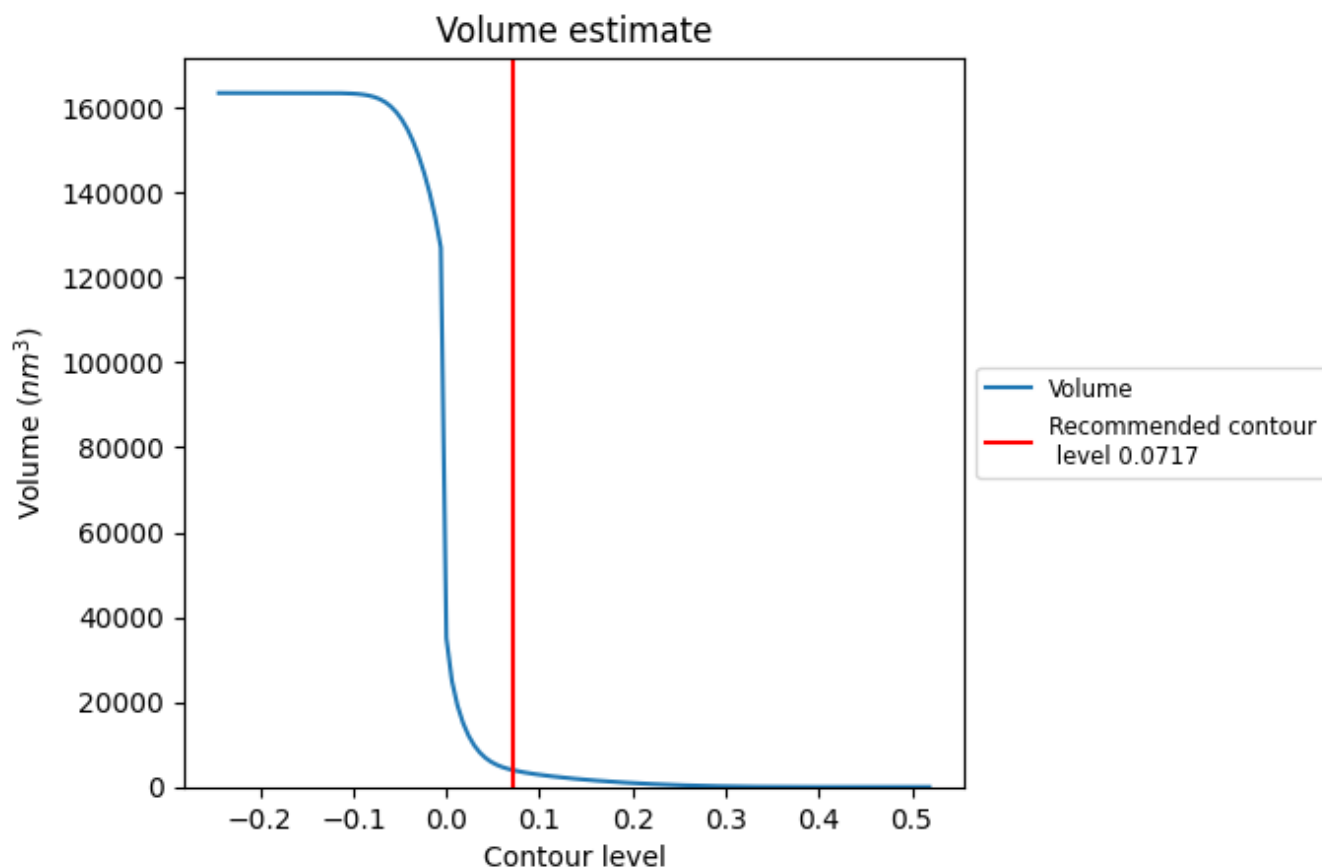
This section contains the results of statistical analysis of the map.

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.

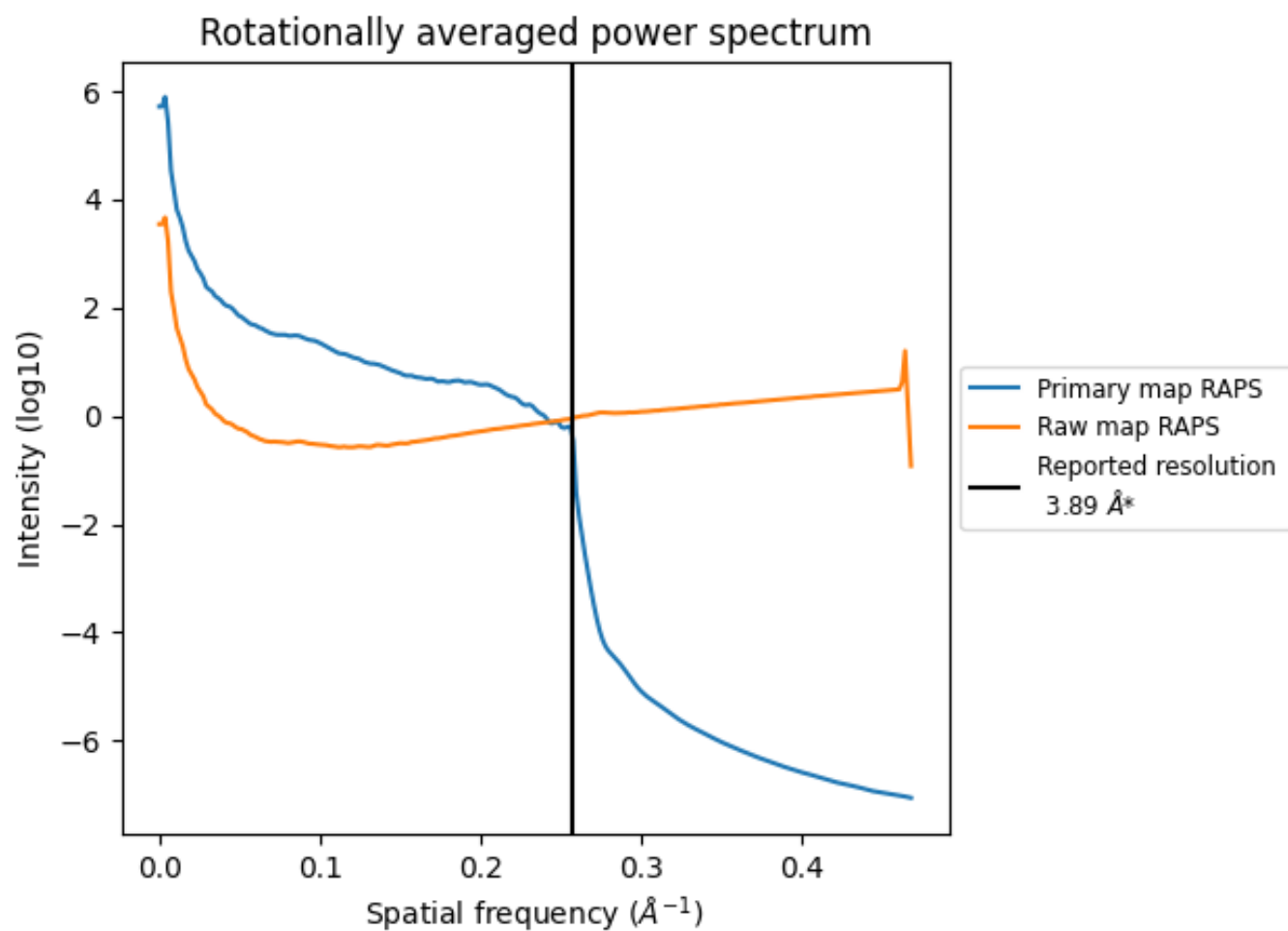
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3963 nm^3 ; this corresponds to an approximate mass of 3580 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 ⓘ

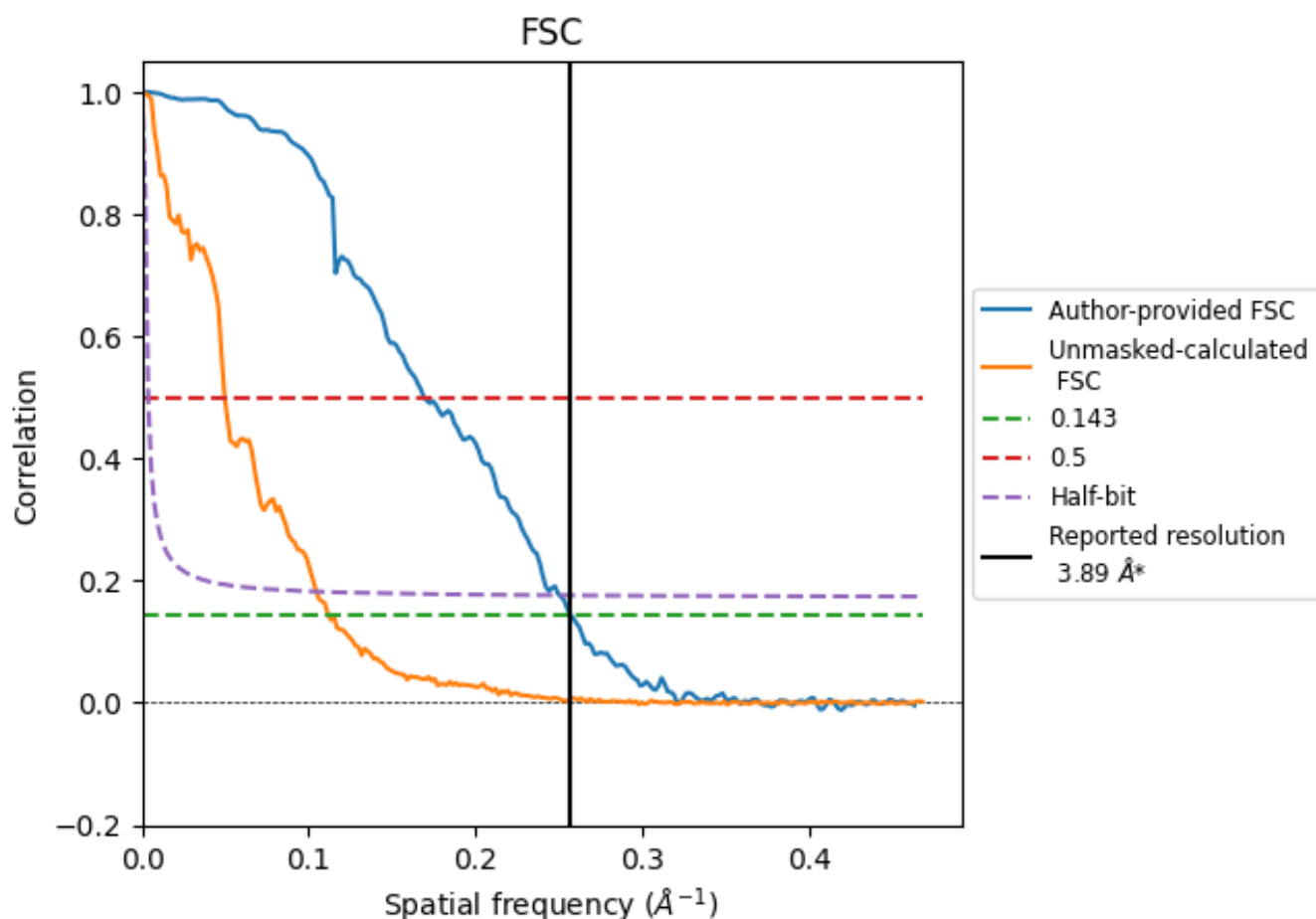


*Reported resolution corresponds to spatial frequency of 0.257 $\text{\AA}^{-1}$

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 0.257 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

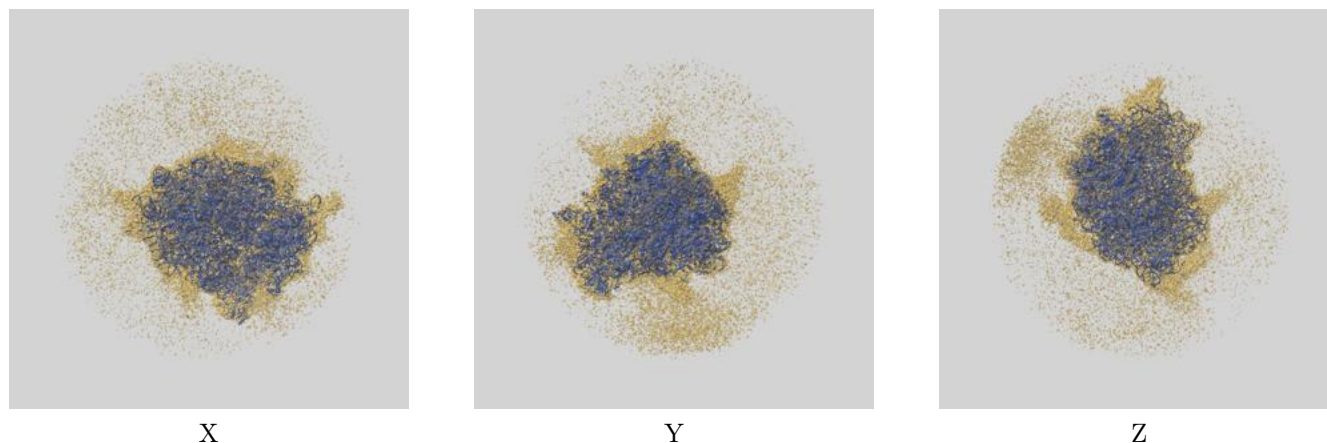
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.89	-	-
Author-provided FSC curve	3.89	5.92	3.99
Unmasked-calculated*	8.95	20.20	9.56

*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 8.95 differs from the reported value 3.89 by more than 10 %

9 Map-model fit [i](#)

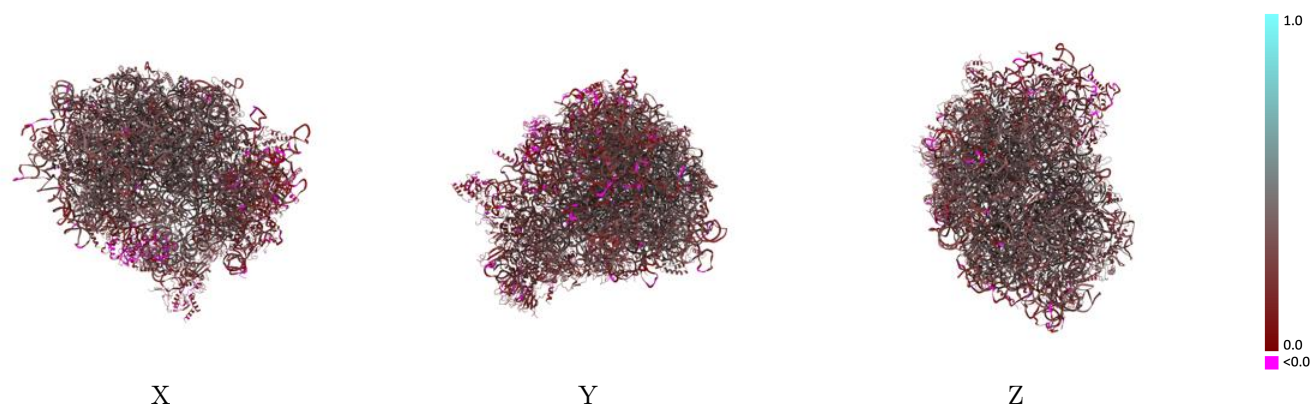
This section contains information regarding the fit between EMDB map EMD-71378 and PDB model 9P8I. Per-residue inclusion information can be found in section [3](#) on page [24](#).

9.1 Map-model overlay [i](#)



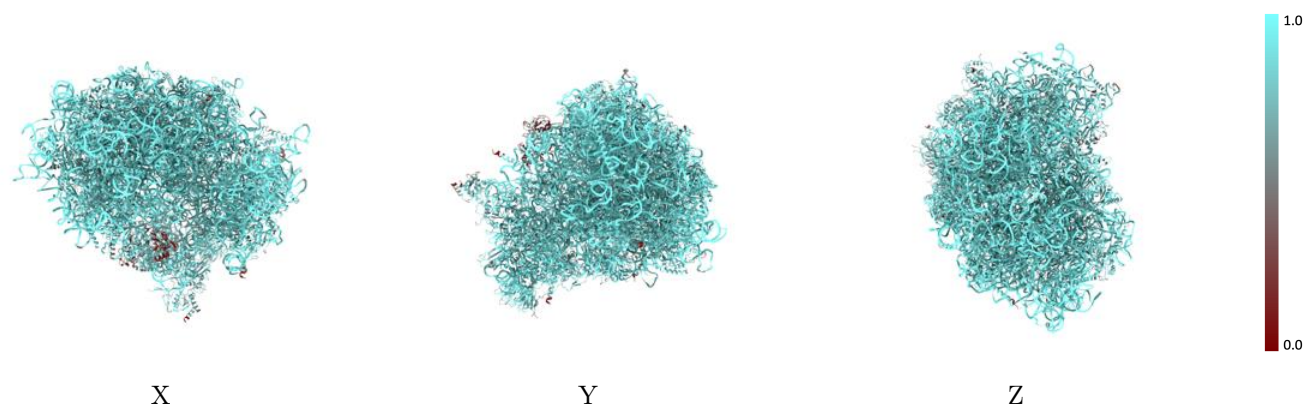
The images above show the 3D surface view of the map at the recommended contour level 0.0717 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



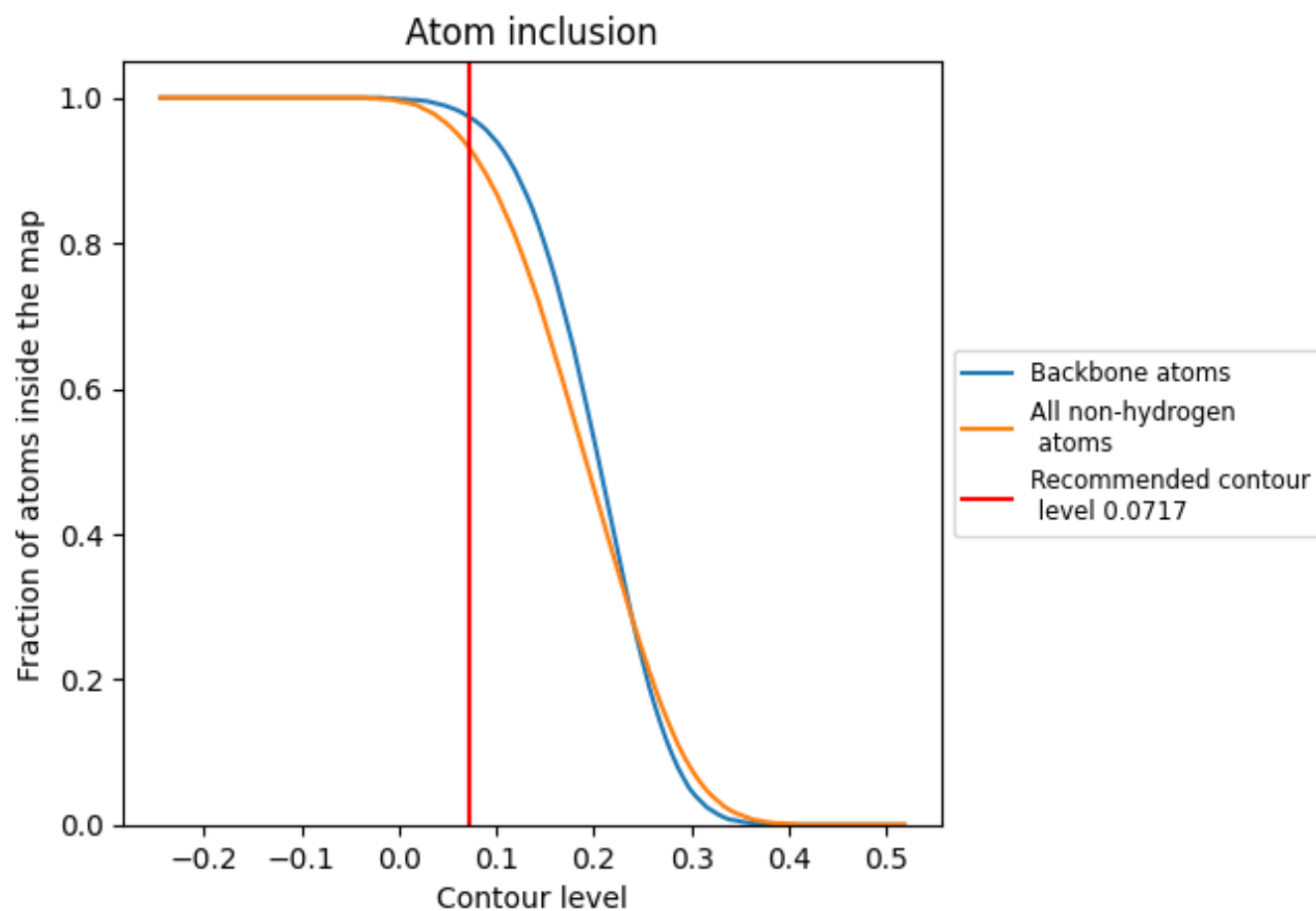
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0717).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 93% 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 (0.0717) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9320	 0.3000
CI	 0.5610	 0.1690
L5	 0.9850	 0.3310
L7	 0.9960	 0.3520
L8	 0.9920	 0.3450
LA	 0.9150	 0.3640
LB	 0.8940	 0.3380
LC	 0.8930	 0.3360
LD	 0.8840	 0.2910
LE	 0.8750	 0.2820
LF	 0.8780	 0.3160
LG	 0.8490	 0.2960
LH	 0.8700	 0.3270
LI	 0.8840	 0.3280
LJ	 0.8620	 0.2790
LL	 0.8860	 0.3170
LM	 0.8860	 0.3100
LN	 0.9230	 0.3540
LO	 0.8880	 0.3320
LP	 0.8810	 0.3320
LQ	 0.8920	 0.3490
LR	 0.8790	 0.2960
LS	 0.9130	 0.3500
LT	 0.9170	 0.3460
LU	 0.8960	 0.2820
LV	 0.8820	 0.3510
LW	 0.8140	 0.2150
LX	 0.9070	 0.3330
LY	 0.9140	 0.3160
LZ	 0.9140	 0.3210
La	 0.9170	 0.3530
Lb	 0.8490	 0.2750
Lc	 0.8730	 0.3220
Ld	 0.9050	 0.3330
Le	 0.8880	 0.3500



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Chain	Atom inclusion	Q-score
Lf	 0.9170	 0.3650
Lg	 0.9240	 0.3480
Lh	 0.8860	 0.3080
Li	 0.8760	 0.3150
Lj	 0.9480	 0.3490
Lk	 0.9010	 0.2920
Ll	 0.9030	 0.3170
Lm	 0.8990	 0.3480
Ln	 0.9230	 0.2810
Lo	 0.8920	 0.3410
Lp	 0.9100	 0.3360
Lr	 0.9090	 0.3410
Ls	 0.5250	 0.0480
Lt	 0.4110	 0.0230
Pt	 0.9520	 0.2660
S2	 0.9830	 0.2870
SA	 0.8740	 0.2910
SB	 0.8600	 0.2960
SC	 0.8750	 0.2940
SD	 0.8760	 0.2390
SE	 0.8780	 0.2050
SF	 0.8320	 0.2320
SG	 0.8670	 0.1770
SH	 0.8250	 0.2380
SI	 0.8520	 0.2450
SJ	 0.8240	 0.1990
SK	 0.8670	 0.1880
SL	 0.8450	 0.2660
SM	 0.6690	 0.0910
SN	 0.8590	 0.3120
SO	 0.8500	 0.3030
SP	 0.8390	 0.2160
SQ	 0.8490	 0.2170
SR	 0.8390	 0.2390
SS	 0.8300	 0.2180
ST	 0.8710	 0.2240
SU	 0.8610	 0.2160
SV	 0.8750	 0.2880
SW	 0.8950	 0.3200
SX	 0.8390	 0.2580
SY	 0.8250	 0.1620
SZ	 0.7980	 0.2200

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Chain	Atom inclusion	Q-score
Sa	 0.8870	 0.3040
Sb	 0.8590	 0.2800
Sc	 0.7920	 0.2430
Sd	 0.9270	 0.2370
Se	 0.8150	 0.1870
Sf	 0.7970	 0.1640
Sg	 0.8430	 0.1890
Zt	 0.9260	 0.1430