



Full wwPDB EM Validation Report ⓘ

Jun 25, 2026 – 10:03 PM EDT

PDB ID : 9P7K / pdb_00009p7k
EMDB ID : EMD-71345
Title : In situ human post eEF1A-A/T-P-E state 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2025-06-20
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

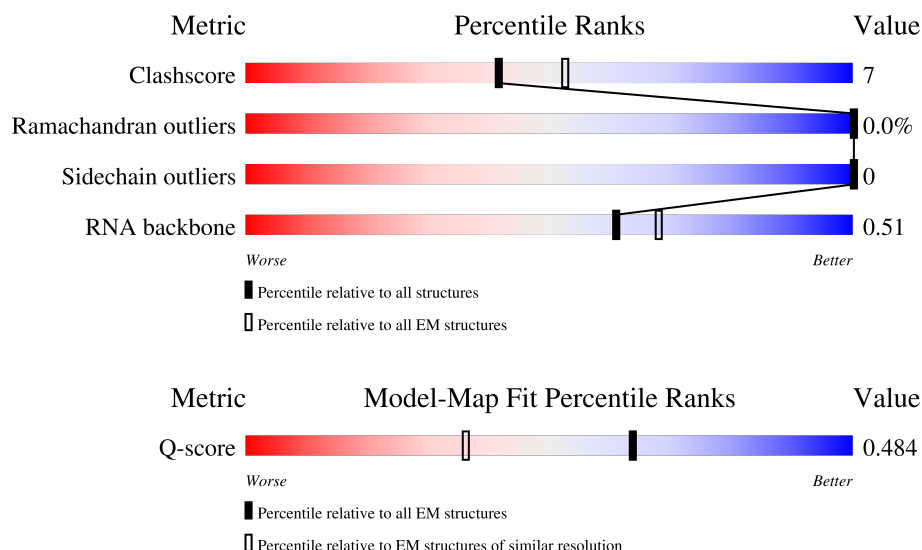
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.



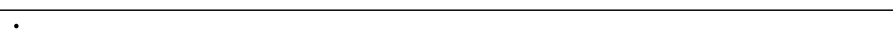
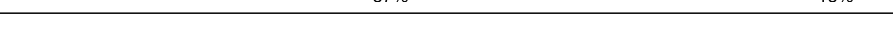
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	CI	31	77% 23%
2	Pt	74	58% 39%
3	Et	75	5% 35% 53% 12%

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Mol	Chain	Length	Quality of chain
4	L5	3655	
5	L7	120	
6	L8	156	
7	LA	248	
8	LB	402	
9	LC	368	
10	LD	293	
11	LE	250	
12	LF	225	
13	LG	241	
14	LH	190	
15	LI	213	
16	LJ	176	
17	LL	210	
18	LM	139	
19	LN	203	
20	LO	201	
21	LP	153	
22	LQ	187	
23	LR	187	
24	LS	175	
25	LT	159	
26	LU	101	
27	LV	131	
28	LW	124	

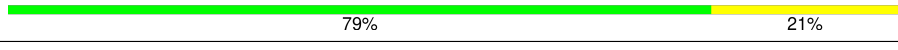
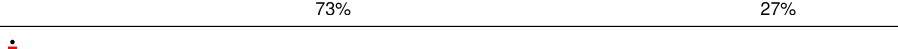
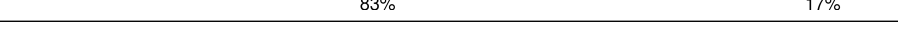
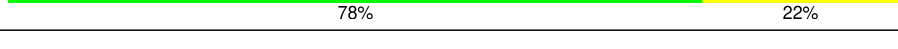
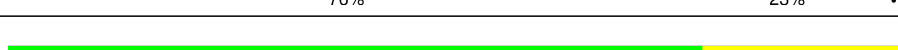
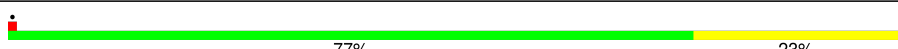
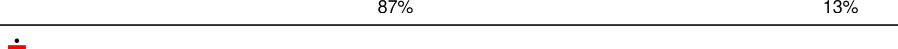
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Mol	Chain	Length	Quality of chain
29	LX	120	
30	LY	134	
31	LZ	135	
32	La	147	
33	Lb	121	
34	Lc	98	
35	Ld	107	
36	Le	128	
37	Lf	109	
38	Lg	114	
39	Lh	122	
40	Li	102	
41	Lj	86	
42	Lk	69	
43	Ll	50	
44	Lm	52	
45	Ln	24	
46	Lo	105	
47	Lp	91	
48	Lr	125	
49	Ls	196	
50	Lt	157	
51	SD	227	
52	SF	189	
53	SK	98	

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Mol	Chain	Length	Quality of chain
54	SM	122	
55	SP	121	
56	SQ	144	
57	SR	135	
58	SS	145	
59	ST	143	
60	SU	104	
61	SZ	75	
62	Sc	64	
63	Sd	55	
64	Sf	67	
65	Sg	313	
66	SA	221	
67	SB	214	
68	SC	222	
69	SE	262	
70	SG	237	
71	SH	189	
72	SI	206	
73	SJ	185	
74	SL	153	
75	SN	150	
76	SO	140	
77	SV	83	
78	SW	129	

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Mol	Chain	Length	Quality of chain
79	SX	141	 79%21%
80	SY	131	 5%78%22%
81	Sa	102	 79%20%
82	Sb	83	 75%25%
83	Se	58	 84%16%
84	S2	1740	 54%38%8%
85	AT	76	 16%49%36%
86	CF	441	 45%73%27%

2 Entry composition [i](#)

There are 90 unique types of molecules in this entry. The entry contains 224970 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Transcription factor BTF3.

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

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

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

There are 6 discrepancies between the modelled and reference sequences:

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

- Molecule 3 is a RNA chain called E site tRNA.

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

- Molecule 4 is a RNA chain called 28S rRNA.

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

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

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

- Molecule 6 is a RNA chain called 5.8S rRNA.

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

- Molecule 7 is a protein called 60S ribosomal protein L8.

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

- Molecule 8 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 9 is a protein called 60S ribosomal protein L4.

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

- Molecule 10 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 11 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 12 is a protein called 60S ribosomal protein L7.

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

- Molecule 13 is a protein called 60S ribosomal protein L7a.

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

- Molecule 14 is a protein called 60S ribosomal protein L9.

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

- Molecule 15 is a protein called Ribosomal protein uL16-like.

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

- Molecule 16 is a protein called 60S ribosomal protein L11.

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

- Molecule 17 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 18 is a protein called 60S ribosomal protein L14.

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

- Molecule 19 is a protein called 60S ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L13a.

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

- Molecule 21 is a protein called 60S ribosomal protein L17.

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

- Molecule 22 is a protein called 60S ribosomal protein L18.

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

- Molecule 23 is a protein called 60S ribosomal protein L19.

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

- Molecule 24 is a protein called 60S ribosomal protein L18a.

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

- Molecule 25 is a protein called 60S ribosomal protein L21.

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

- Molecule 26 is a protein called Heparin-binding protein HBp15.

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

- Molecule 27 is a protein called 60S ribosomal protein L23.

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

- Molecule 28 is a protein called Ribosomal protein L24.

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

- Molecule 29 is a protein called 60S ribosomal protein L23a.

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

- Molecule 30 is a protein called 60S ribosomal protein L26.

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

- Molecule 31 is a protein called 60S ribosomal protein L27.

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

- Molecule 32 is a protein called 60S ribosomal protein L27a.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 34 is a protein called 60S ribosomal protein L30.

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

- Molecule 35 is a protein called 60S ribosomal protein L31.

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

- Molecule 36 is a protein called 60S ribosomal protein L32.

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

- Molecule 37 is a protein called 60S ribosomal protein L35a.

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

- Molecule 38 is a protein called 60S ribosomal protein L34.

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

- Molecule 39 is a protein called 60S ribosomal protein L35.

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

- Molecule 40 is a protein called 60S ribosomal protein L36.

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

- Molecule 41 is a protein called 60S ribosomal protein L37.

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

- Molecule 42 is a protein called 60S ribosomal protein L38.

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

- Molecule 43 is a protein called 60S ribosomal protein L39.

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

- Molecule 44 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 45 is a protein called 60S ribosomal protein L41.

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

- Molecule 46 is a protein called 60S ribosomal protein L36a.

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

- Molecule 47 is a protein called 60S ribosomal protein L37a.

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

- Molecule 48 is a protein called 60S ribosomal protein L28.

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

- Molecule 49 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 50 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 51 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 52 is a protein called 40S ribosomal protein S5.

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

- Molecule 53 is a protein called 40S ribosomal protein S10.

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

- Molecule 54 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 55 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 56 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 57 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 58 is a protein called 40S ribosomal protein S18.

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

- Molecule 59 is a protein called 40S ribosomal protein S19.

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

- Molecule 60 is a protein called 40S ribosomal protein S20.

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

- Molecule 61 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 62 is a protein called 40S ribosomal protein S28.

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

- Molecule 63 is a protein called 40S ribosomal protein S29.

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

- Molecule 64 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 65 is a protein called Receptor of activated protein C kinase 1.

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

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

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

- Molecule 67 is a protein called 40S ribosomal protein S3a.

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

- Molecule 68 is a protein called 40S ribosomal protein S2.

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

- Molecule 69 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 70 is a protein called 40S ribosomal protein S6.

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

- Molecule 71 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 72 is a protein called 40S ribosomal protein S8.

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

- Molecule 73 is a protein called 40S ribosomal protein S9.

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

- Molecule 74 is a protein called 40S ribosomal protein S11.

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

- Molecule 75 is a protein called 40S ribosomal protein S13.

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

- Molecule 76 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 77 is a protein called Small ribosomal subunit protein eS21.

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

- Molecule 78 is a protein called 40S ribosomal protein S15a.

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

- Molecule 79 is a protein called 40S ribosomal protein S23.

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

- Molecule 80 is a protein called 40S ribosomal protein S24.

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

- Molecule 81 is a protein called 40S ribosomal protein S26.

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

- Molecule 82 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 83 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 84 is a RNA chain called 18S rRNA.

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

- Molecule 85 is a RNA chain called A/T site tRNA.

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

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

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

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

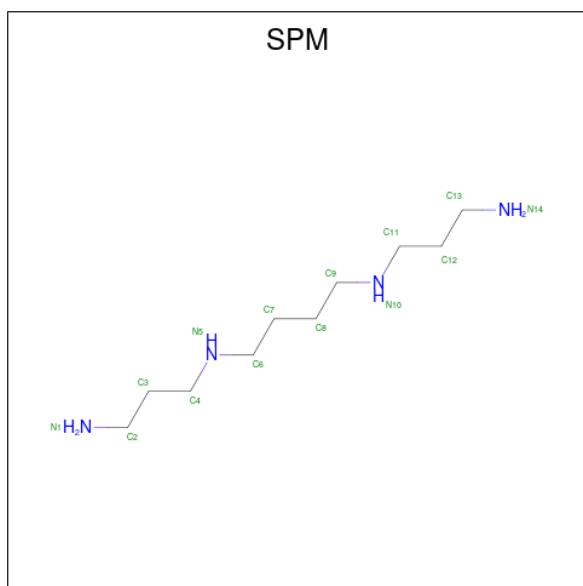
Mol	Chain	Residues	Atoms		AltConf
87	L5	177	Total	Mg	0
			177	177	
87	L7	3	Total	Mg	0
			3	3	
87	L8	5	Total	Mg	0
			5	5	
87	LA	1	Total	Mg	0
			1	1	
87	LB	1	Total	Mg	0
			1	1	
87	LP	1	Total	Mg	0
			1	1	

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

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



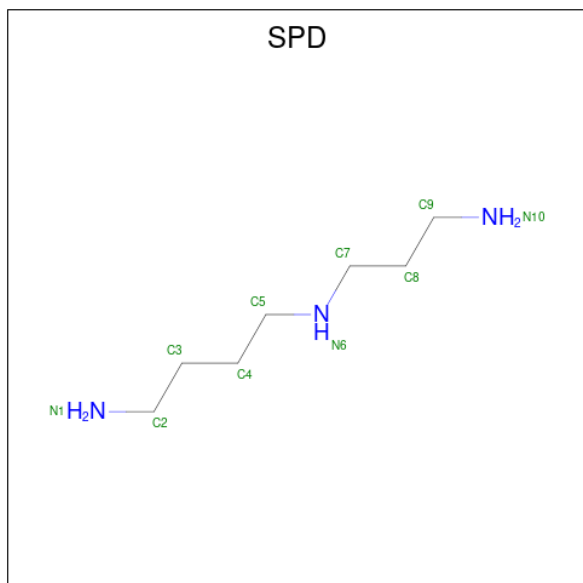
Mol	Chain	Residues	Atoms			AltConf
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	

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

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



Mol	Chain	Residues	Atoms			AltConf
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L8	1	Total	C	N	0
			10	7	3	

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

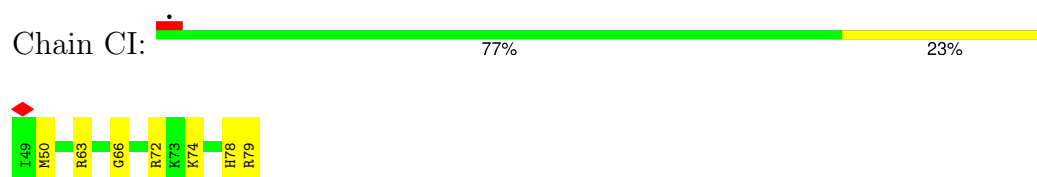
- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

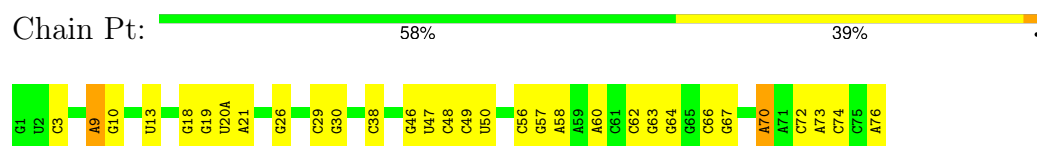
3 Residue-property plots

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

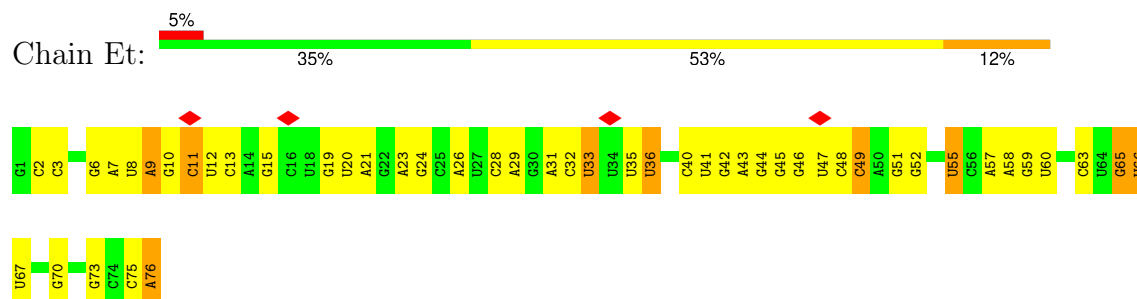
• Molecule 1: Transcription factor BTF3



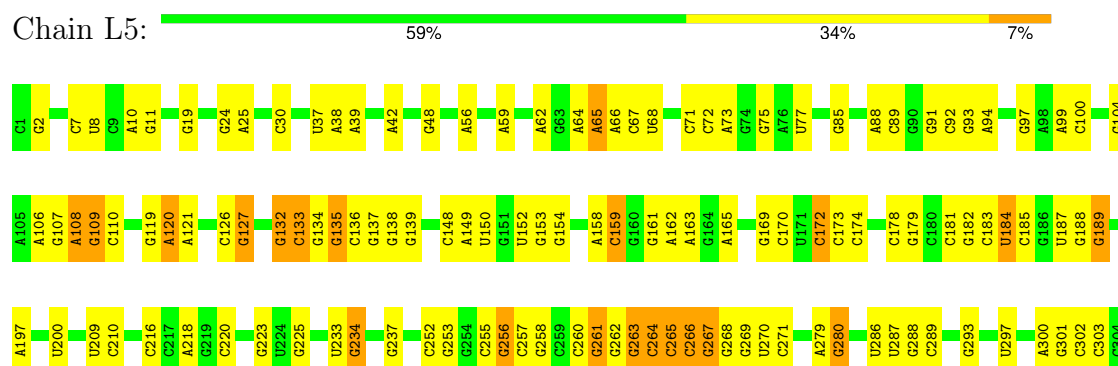
• Molecule 2: P site tRNA



• Molecule 3: E site tRNA

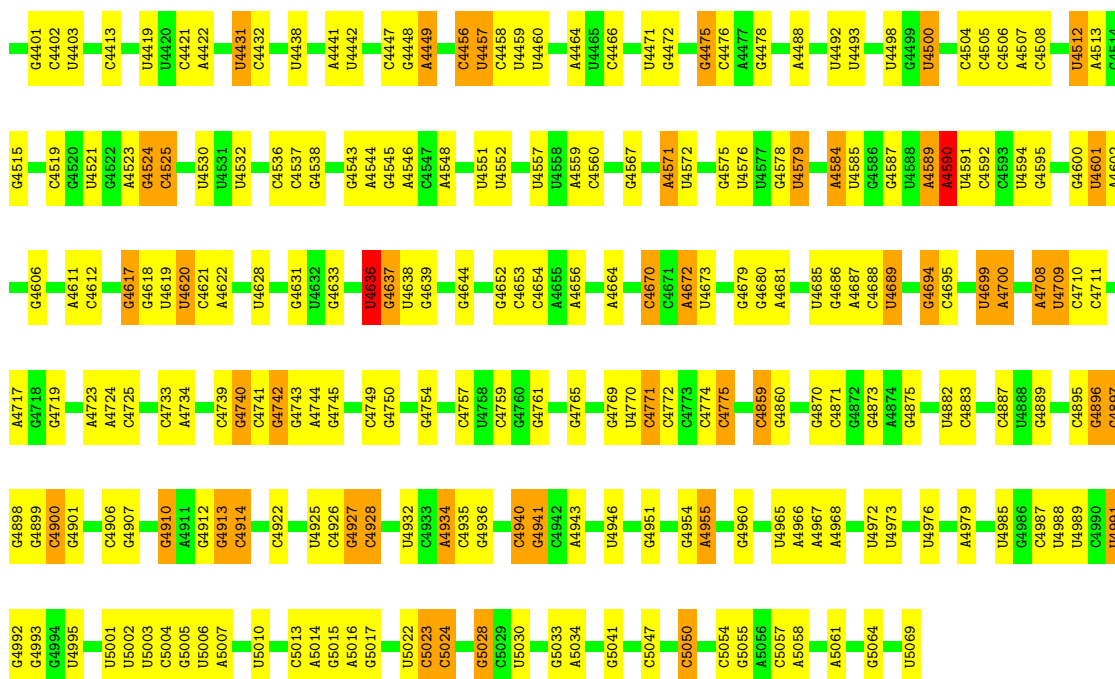


• Molecule 4: 28S rRNA



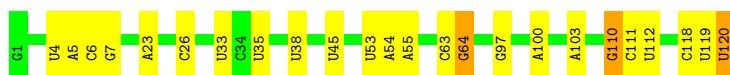
C2019	G1833	U1834	G1739	G1504	C1401	C1308	C1210	C1070	C738	C519	U424	A305
U2020	A1934	G1835	C1740	C1505	C1402	C1309	G1211	G1071	G739	G642	U425	A306
G2021	G1836	G1741	A1742	C1509	G1403	U1317	G1212	C1072	G742	G643	U432	A307
G2024	A1941	A1837	G1743	U1510	G1404	C1318	C1214	C985	G746	G646	A433	G308
A2025	A1942	G1842	U1744	U1511	G1405	U1319	C1215	G1073	A746	G647	G312	G312
A2026	A1943				G1406	U1320	G1219	G1074	A747	G444	G444	
A2029	G1948	G1846	G1760	G1516	C1407	G1321	G1220	C1075	G748	U445	U445	G315
A2030	C1847	C1848	G1752	G1517	C1408	A1322	G1221	C1076	G759	C655	U449	U316
G2033	G1951			A1524	U1410	A1324	A1222	G1077		C657	C449	A317
G2046	A1960	G1855	U1756	A1534	C1411	C1325	C1241	C1078	C904	C658	A452	A319
A2047	G1961	C1856	U1757	G1535	C1412	C1327	G1246	C1079	C905	G453	G453	U325
U2048	A1962	A1857	G1758	U1536	C1413	G1328		C1080	C906	A660	U454	U326
G2049	G1969	A1858	U1759	A1537	C1414	U1332	G1253	C1081	C907	C661	C455	U327
		C1859	G1760	U1538	G1415	C1332	G1254	C1082	G908	C662	C456	G457
G2055	U1860	U1861	G1761	G1539	C1416	A1333	A1254	C1083	A909	G663	G457	G330
G2056	U1862	C1861	C1762	A1669	C1417	A1334	A1255	C1084	G910	G664	C458	
G2060	U1866	U1867	G1763	A1670	C1418		G1256	C1085	U913	C665	U333	
G2069	A1867	A1867	G1764	C1676	C1419	A1337	G1257	C1086	U914	A667	A463	
A2069	A1868	A1868	A1765	U1677	C1420	G1338	A1257	C1087	U915	C668	C340	
C2072	G1869	A1767	G1766	A1678	G1425	U1339	G1258	C1088	C916	U467	U468	C351
C2073	C1870	C1870	G1767	G1680		C1340	G1259	C1089	A917	U469	C469	
G2076	A1871	A1871	A1770		C1431		G1262	C1090	G918	C672		G364
G2079	G1877		U1773	A1563	C1432	C1344		C1091	C919	C673		
U2080	C1881	U1882	U1781	A1564	C1433	A1345	G1266	C1092	C920	C473		G369
C2083	U1882		U1782	A1565	C1437	C1346	C1267	C1093	C921	C474		
G2084	A1891	A1891	G1787	C1566	C1438	G1347	G1268	C1094	C922	C685	U484	A372
G2085	G1895	A1896	A1788	G1577	C1439	C1352	G1269	C1095	C923	A686	C485	G373
A2093	A1897	C1898	U1792	U1578		G1353	A1270	C1096	C924	U687	C486	G374
A2095	G1899	G1899	U1793	U1579	C1442	A1354	G1271	C1097	A932	C691	C489	U381
G2096	A1907	A1907	G1802	U1582	C1443	G1355	C1272	C1098	C933	A692	C490	A385
U2097	A1908	A1908	A1804	U1588	C1444	U1356	G1273	C1099	C934	C696	G491	A386
G2098	G1912	G1806	G1805	C1589	C1445	C1357	A1274	C1100	A935	U492	U492	A387
C2101	C1913	C1807	C1717	C1590	C1446	G1358	G1275	C1101	C936	U702	G493	A388
G2102	G1914	A1719	C1718	U1591	C1447	C1359	C1278	C1102	A943	G703	U494	
G2103	A1917	G1720	A1719	U1596	C1461	C1365	A1279	C1103	A944	C704	C495	A396
A2105	U1918	G1721	G1717	U1597	C1462	G1366	G1280	C1104	U945	G705	G496	A397
G2106	C1919	U1725	C1718	G1612	C1463	C1367	G1281	C1105	C946	G706	G497	A398
C2107	C1920	U1726	A1719	A1613	C1466	A1368	G1282	C1106	A956	C707	C498	A399
G2110	C1921	U1727	C1718	G1624	C1467	C1369	G1283	C1107	C959	G708	G499	A400
G2111	G1922	U1728	C1719	G1625	C1468	C1379	U1285	C1108	A960	A711	C501	C406
G2112	G1925	C1731	C1720	C1628	C1481	G1382	C1286	C1109	A961	C712	C502	C407
C2246	C2011	G1732	G1721	A1631	C1482	U1387	G1287	C1110	C962	G715	G504	A408
G2250	U1930	G1733	U1735	A1632	C1483	A1387	G1293	C1111	C965	G716	G509	G409
G2251	C1931	U1734	G1735	A1633	C1484	G1390	C1295	C1112	A966	U717	U510	A410
G2252	A2017	A1825	A1826	A1634	C1485	G1391	U1296	C1113	C967	C718	C511	G412
						A1392	U1297	C1114	C968	G729	C512	G415
						G1393	C1298	C1115	C969	G730	U513	U416
						G1394	G1299	C1116	G970	G731	U514	G417
						U1395	G1300	C1117			C515	C417
						G1396	C1301	C1118	C977	G735	C516	A418
						A1397	U1302	C1119	C978	C736	C517	A419
						A1398	A1307	C1120	C979	C737	G518	G423

A4304	A4214	C4102	U3920	C3841	A3719	A3635	G2876	C2770	G2677	C2572	G2483	A2382	C2256
G4305	A4219	C4103	A3923	C3842	G3720	C3636	G2877	G2773	C2683	A2573	A2484	A2383	C2261
U4306	A4220	G4104	C3924	U3843	U3721	U3637	G2878	C2774	C2684	C2577	A2485	A2384	G2262
U4312	C4221	G4107	U3925	U3844	A3723	U3638	U2880	A2783	U2687	U2580	A2486	A2395	A2263
C4314	G4222	G4108	A3928	U3845	A3726	U3640	A2881	A2787	C2688	C2583	C2488	C2397	C2254
A4315	U4111	U4112	G3929	C3850	A3727	U3641	A2882	U2788	G2689	C2588	C2489	U2398	G2265
C4318	C4112	C4113	U3932	U3851	A3732	U3644	C2882	A2789	U2689	A2587	A2490	A2400	A2279
C4319	U4113	U4114	G3933	A3852	A3733	A3646	U2883	A2695	C2690	C2588	C2491	G2401	G2280
U4322	G4115	G4116	A3937	U3853	A3734	A3647	A2884	A2696	A2696	U2493	C2492	A2401	U2281
C4325	C4116	C4117	G3938	A3856	A3735	A3648	C2889	C2804	C2702	U2484	C2493	A2404	G2284
A4326	G4122	G4123	G3939	A3861	A3737	A3649	U2900	C2805	U2495	U2495	G2496	G2407	G2284
C4327	A4126	A4127	A3942	A3862	A3748	C3655	G2901	A2806	G2706	G2407	U2496	G2408	C2289
G4328	C4126	C4127	U3946	A3865	G3753	A3656	G2902	A2807	U2707	U2408	G2496	U2409	C2295
C4330	U4127	U4128	G3947	C3866	A3754	U3657	U2904	G2808	C2709	G2503	G2502	G2410	C2296
G4331	C4133	C4134	A3948	A3867	A3755	C3658	C2905	G2809	C2710	C2504	C2503	C2411	C2297
C4332	U4134	U4135	U3949	C3868	G3776	G3659	G2906	U2810	C2711	C2505	C2504	C2412	U2298
U4340	C4140	C4141	A3950	A3871	A3774	C3660	G2907	A2811	G2712	G2506	A2507	U2413	G2299
C4341	G4141	G4142	G3953	C3872	A3775	A3661	U2908	A2812	C2716	A2507	G2414	G2415	G2300
U4344	C4142	C4143	A4056	G3873	A3776	A3662	C2909	C2814	C2719	A2513	G2416	G2417	G2301
C4345	U4143	U4144	C4057	A3874	G3777	C3665	G3585	A2815	C2720	G2516	A2417	C2303	C2302
G4346	C4145	C4146	A4058	A3877	A3778	C3670	G3590	G2822	C2721	G2517	G2421	G2422	G2306
C4347	U4146	U4147	U4059	C3878	C3782	C3673	C3591	U2826	G2724	G2518	G2423	A2424	A2313
A4348	C4147	C4148	A4060	G3879	A3785	G3674	C3592	G2827	A2725	U2519	G2424	G2425	G2318
C4349	U4148	U4149	G4061	C3880	U3786	U3675	C3593	U2828	G2726	G2521	U2425	G2426	G2319
C4350	C4149	C4150	A4062	G3881	U3787	C3676	C3594	U2829	U2730	A2529	G2434	G2435	G2321
U4353	U4151	U4152	A4063	A3882	G3792	C3684	U3595	A2832	C2731	U2537	G2448	G2449	G2326
U4354	C4153	C4154	C4064	C3885	U3796	C3686	G3597	A2835	C2739	U2538	G2450	G2451	U2329
A4355	U4155	U4156	U4065	A3886	A3797	A3687	C3598	U2836	G2742	C2539	A2453	A2454	A2332
U4356	C4157	C4158	G4066	C3887	A3799	U3688	G3600	U2837	A2743	C2540	G2458	G2459	G2333
A4361	U4159	U4160	U4067	A3888	C3808	C3691	A3604	U2838	A2744	G2544	C2468	C2469	C2334
C4362	G4161	G4162	U4068	C3889	U3809	A3692	C3605	U2839	A2745	U2545	G2469	G2470	C2335
A4363	U4163	U4164	A4069	G3890	G3811	U3693	U3606	A2844	A2746	G2546	A2460	A2461	G2336
G4364	C4165	C4166	U4070	C3891	A3812	U3694	U3607	A2845	G2749	G2547	C2462	C2463	A2347
C4365	U4167	U4168	U4071	G3892	A3813	C3695	A3608	G2846	G2750	U2554	G2464	G2465	G2348
U4371	C4169	C4170	G4076	C3893	U3814	C3696	G3609	G2847	G2751	G2555	C2466	C2467	U2350
U4372	U4171	U4172	A4084	G3900	U3815	U3697	A3610	U2848	G2752	G2556	G2468	G2469	A2351
G4373	C4173	C4174	G4084	A3901	A3817	C3698	A3611	G2855	G2753	G2557	U2468	U2469	A2360
A4376	U4175	U4176	C4084	A3902	A3818	C3701	G3615	C2856	G2754	G2558	G2470	G2471	G2362
C4377	C4177	C4178	G4088	G3907	G3819	U3707	U3616	C2861	G2755	G2559	U2471	U2472	A2368
A4378	U4179	U4180	A4089	A3908	U3822	C3708	C3617	U2864	G2756	G2560	G2473	G2474	A2376
C4379	C4181	C4182	G4092	C3909	G3823	U3709	G3618	U2865	G2757	G2561	G2475	G2476	G2377
A4388	U4183	U4184	G4093	C3910	A3824	G3710	C3619	C2866	G2758	G2562	G2477	G2478	A2378
C4389	C4185	C4186	G4094	C3911	A3825	A3711	G3620	U2867	G2759	G2563	G2479	G2480	G2479
A4390	U4187	U4188	C4096	U3912	A3826	A3712	C3621	C2868	G2760	G2564	G2481	G2482	
G4391	C4189	C4190	A4097	C3913	A3827	U3713	G3622	U2869	G2761	G2565	G2483	G2484	
C4392	U4191	U4192	A4098	U3914	A3828	U3714	C3623	C2870	G2762	G2566	G2485	G2486	
A4393	C4193	C4194	G4099	C3915	A3829	U3715	G3624	U2871	G2763	G2567	G2487	G2488	
C4394	U4195	U4196	A4100	C3916	A3830	U3716	C3625	U2872	G2764	G2568	G2489	G2490	
A4395	C4197	C4198	C4101	C3917	U3838	A3717	G3626	C2873	G2765	G2569	G2491	G2492	
G4396	U4199	U4200	C4102	A3918	U3839	A3718	C3627	U2874	G2766	G2570	G2493	G2494	
A4397	C4201	C4202	C4103	C3919	U3840	A3719	A3630	A2875	G2767	G2571	G2495	G2496	



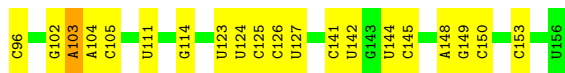
• Molecule 5: 5S rRNA

Chain L7: 80% 18% .



• Molecule 6: 5.8S rRNA

Chain L8: 63% 35% .

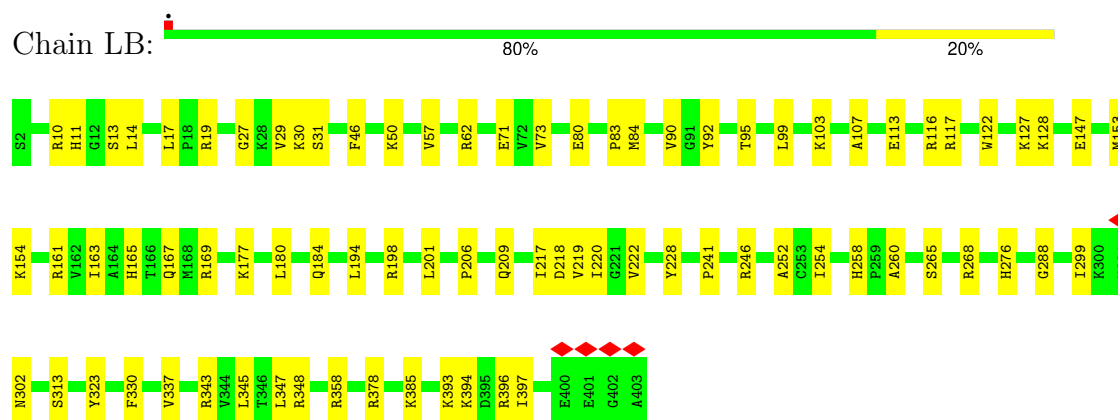


• Molecule 7: 60S ribosomal protein L8

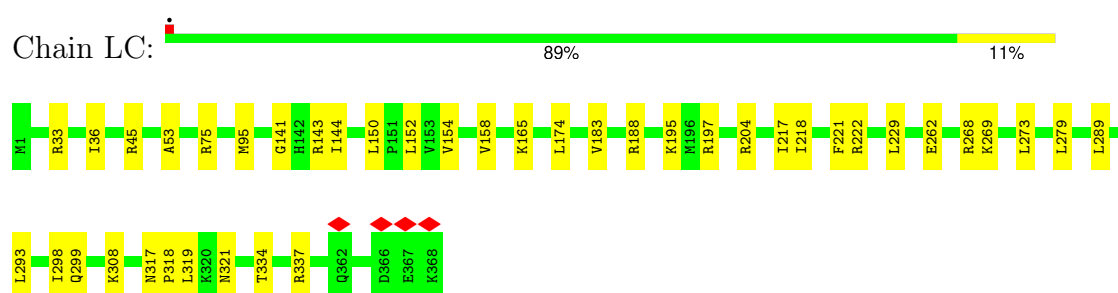
Chain LA: 76% 24%



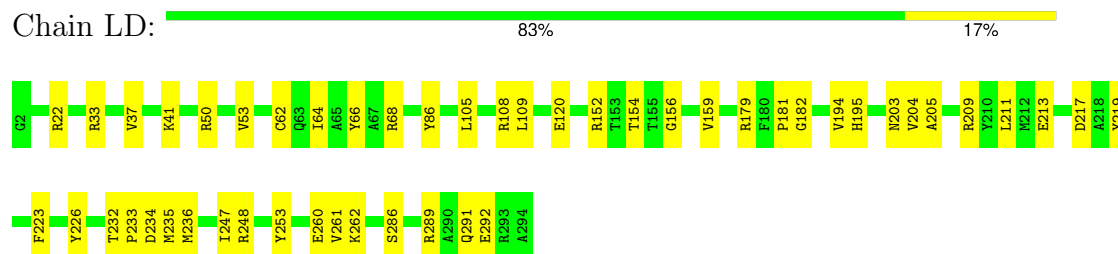
• Molecule 8: Large ribosomal subunit protein uL3



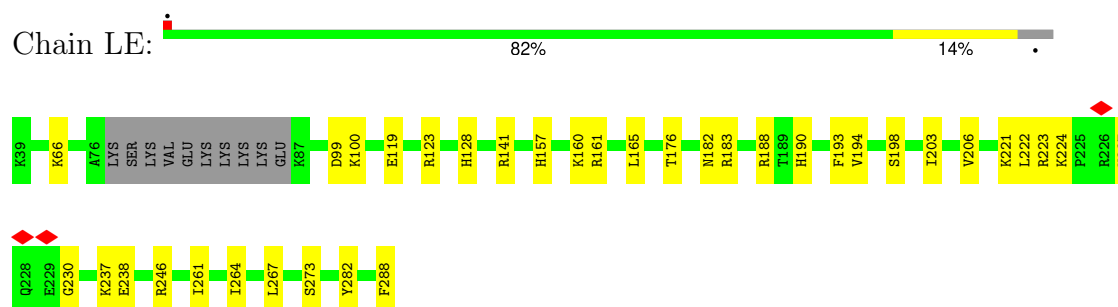
- Molecule 9: 60S ribosomal protein L4



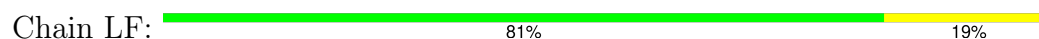
- Molecule 10: Large ribosomal subunit protein uL18

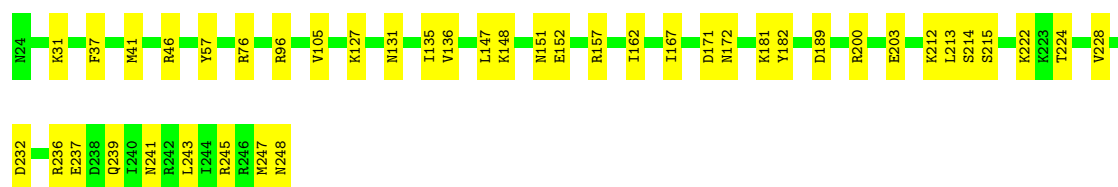


- Molecule 11: Large ribosomal subunit protein eL6



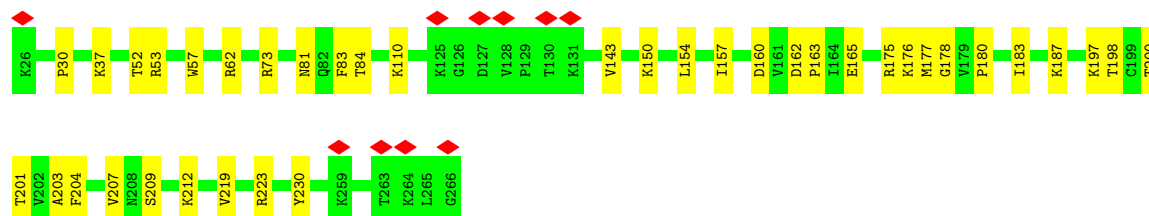
- Molecule 12: 60S ribosomal protein L7





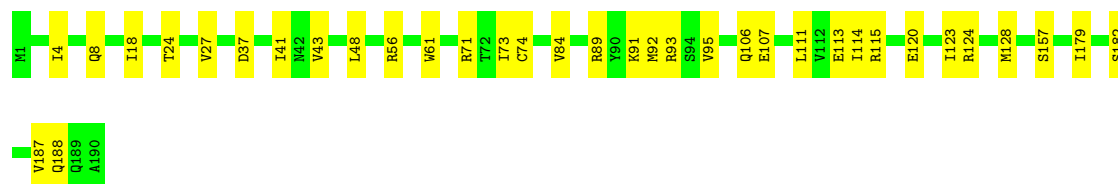
- Molecule 13: 60S ribosomal protein L7a

Chain LG: 84% 16%



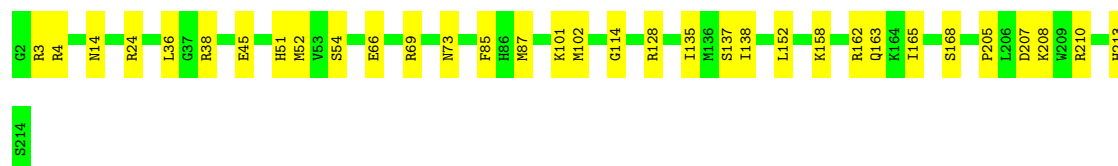
- Molecule 14: 60S ribosomal protein L9

Chain LH: 82% 18%



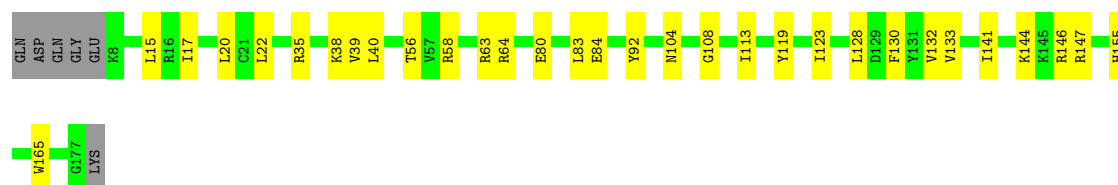
- Molecule 15: Ribosomal protein uL16-like

Chain LI: 85% 15%

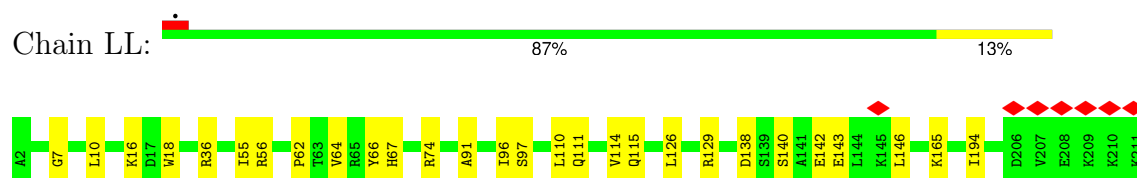


- Molecule 16: 60S ribosomal protein L11

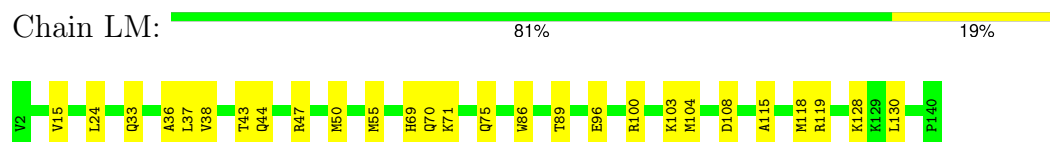
Chain LJ: 79% 18%



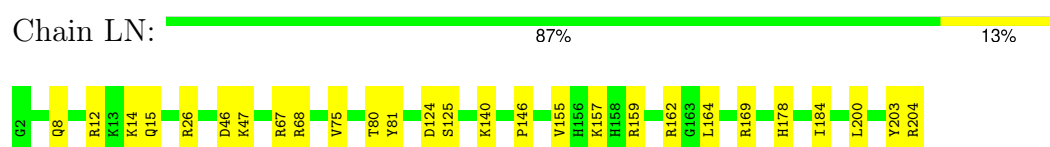
- Molecule 17: Large ribosomal subunit protein eL13



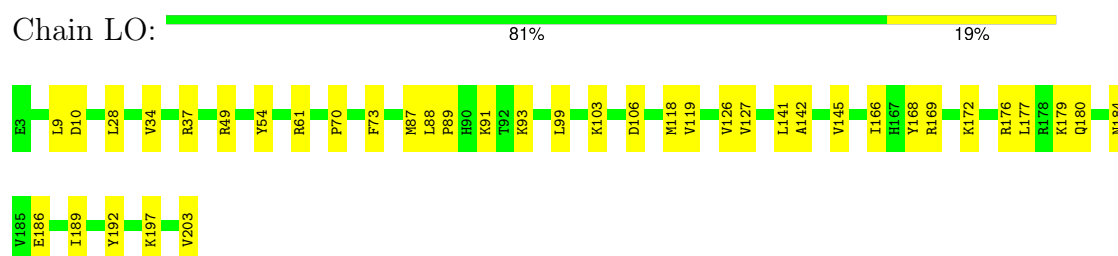
- Molecule 18: 60S ribosomal protein L14



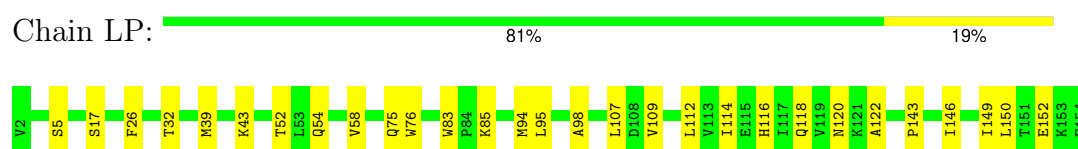
- Molecule 19: 60S ribosomal protein L15



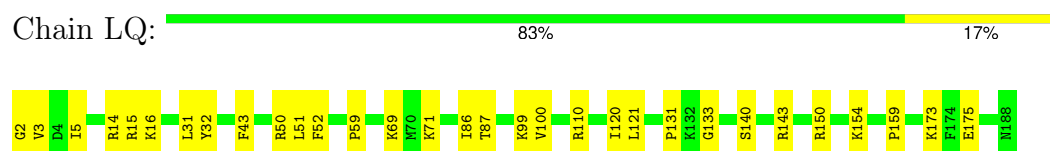
- Molecule 20: 60S ribosomal protein L13a



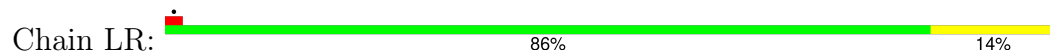
- Molecule 21: 60S ribosomal protein L17



- Molecule 22: 60S ribosomal protein L18

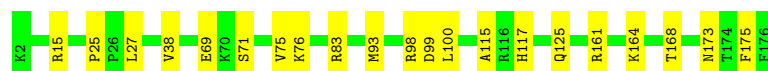
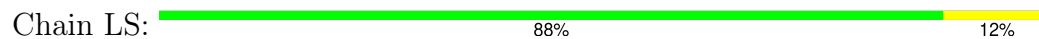


- Molecule 23: 60S ribosomal protein L19

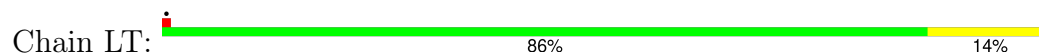




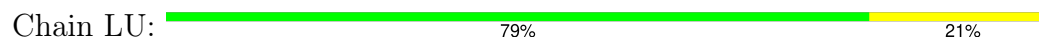
- Molecule 24: 60S ribosomal protein L18a



- Molecule 25: 60S ribosomal protein L21



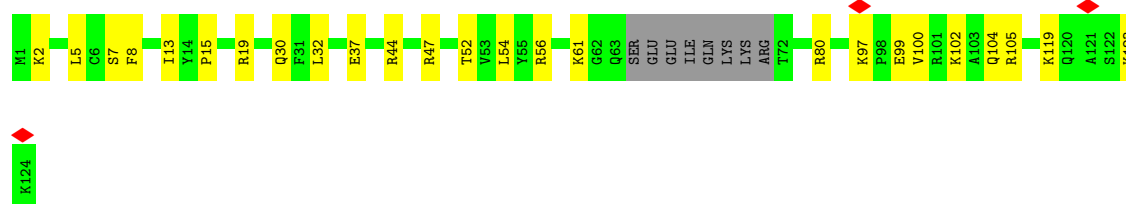
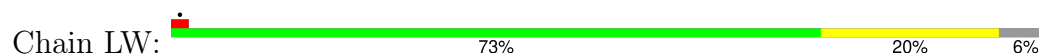
- Molecule 26: Heparin-binding protein HBp15



- Molecule 27: 60S ribosomal protein L23



- Molecule 28: Ribosomal protein L24



- Molecule 29: 60S ribosomal protein L23a



- Molecule 30: 60S ribosomal protein L26

Chain LY:  82% 18%



- Molecule 31: 60S ribosomal protein L27

Chain LZ:  84% 16%



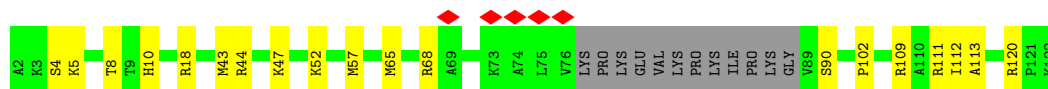
- Molecule 32: 60S ribosomal protein L27a

Chain La:  92% 8%



- Molecule 33: Large ribosomal subunit protein eL29

Chain Lb:  74% 16% 10%



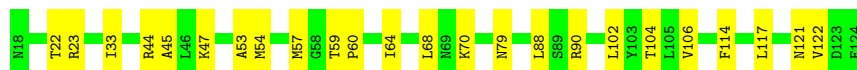
- Molecule 34: 60S ribosomal protein L30

Chain Lc:  85% 15%



- Molecule 35: 60S ribosomal protein L31

Chain Ld:  78% 22%



- Molecule 36: 60S ribosomal protein L32

Chain Le:  83% 17%



- Molecule 37: 60S ribosomal protein L35a

Chain Lf:  89% 11%



- Molecule 38: 60S ribosomal protein L34

Chain Lg:  89% 11%



- Molecule 39: 60S ribosomal protein L35

Chain Lh:  86% 14%



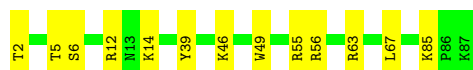
- Molecule 40: 60S ribosomal protein L36

Chain Li:  92% 8%



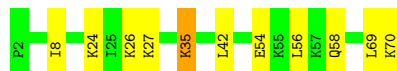
- Molecule 41: 60S ribosomal protein L37

Chain Lj:  85% 15%



- Molecule 42: 60S ribosomal protein L38

Chain Lk:  84% 14%

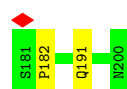
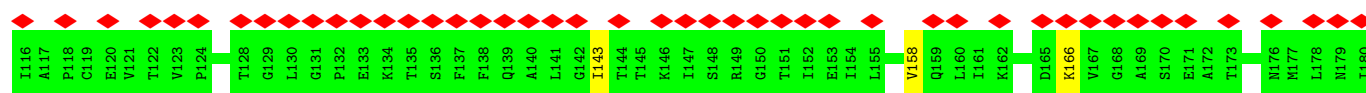
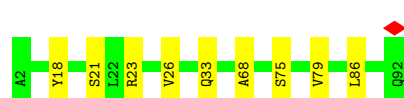
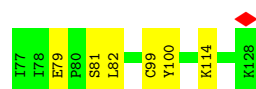


- Molecule 43: 60S ribosomal protein L39

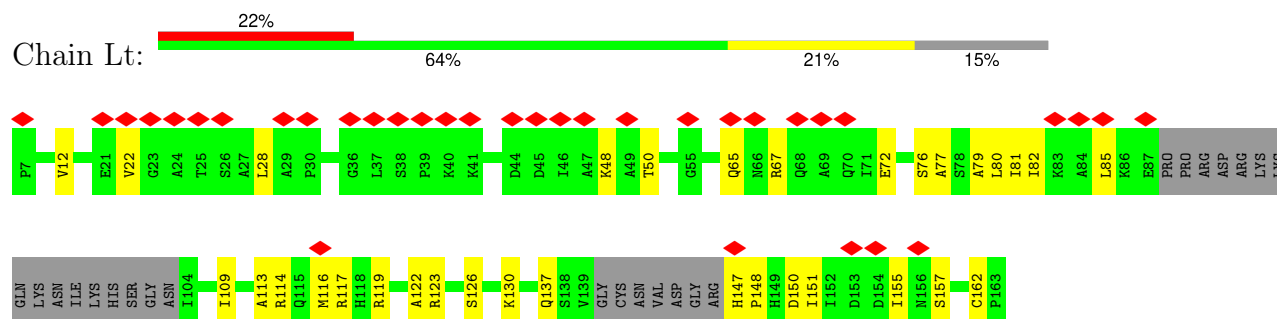
Chain Ll:  86% 14%



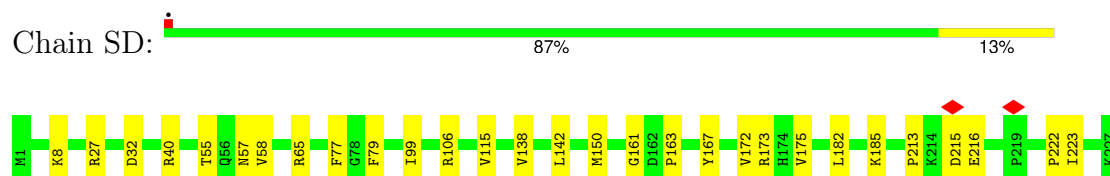
- Molecule 44: Large ribosomal subunit protein eL40



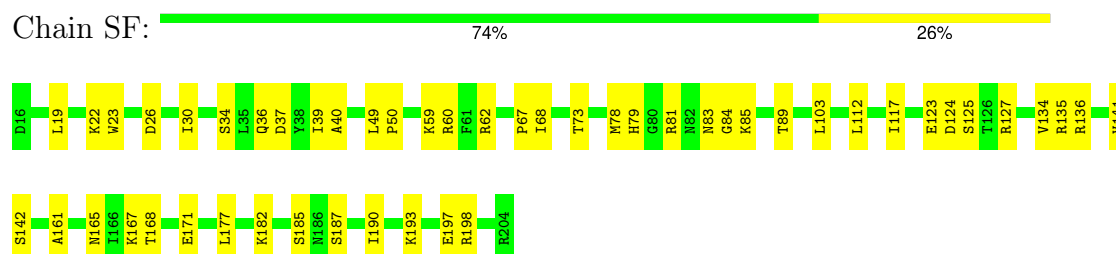
- Molecule 50: Large ribosomal subunit protein uL11



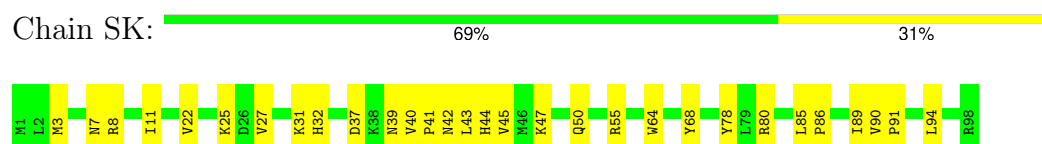
- Molecule 51: Small ribosomal subunit protein uS3



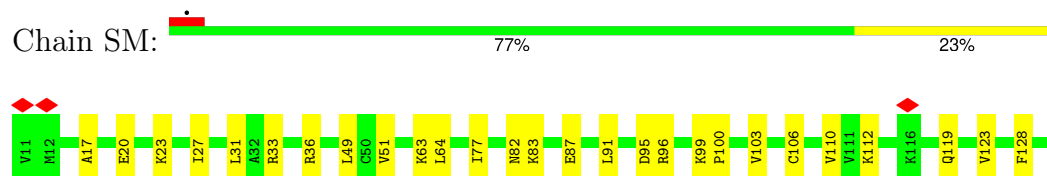
- Molecule 52: 40S ribosomal protein S5



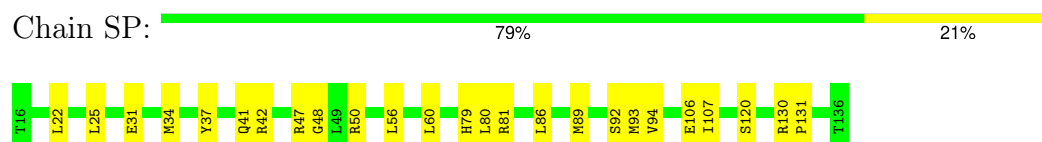
- Molecule 53: 40S ribosomal protein S10



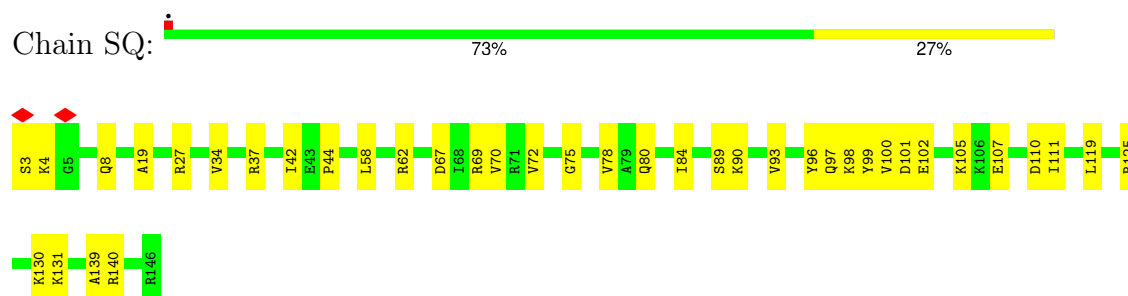
- Molecule 54: Small ribosomal subunit protein eS12



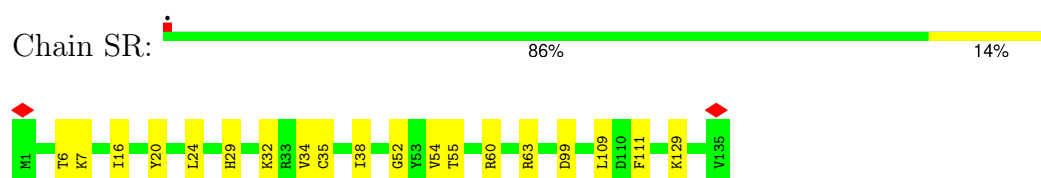
- Molecule 55: Small ribosomal subunit protein uS19



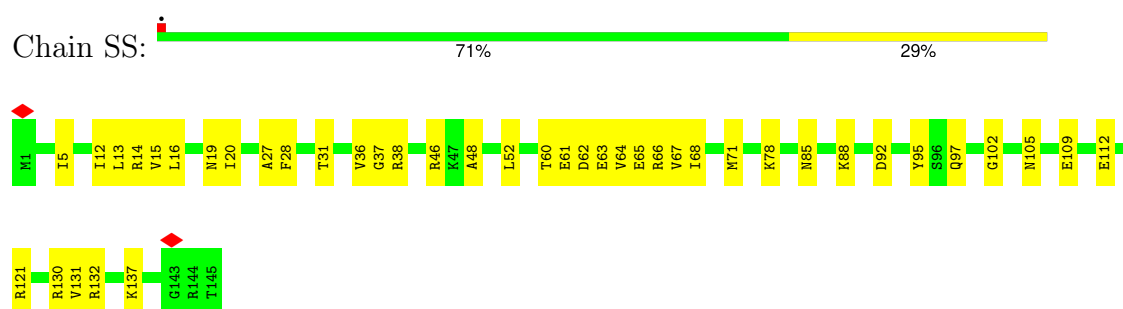
- Molecule 56: Small ribosomal subunit protein uS9



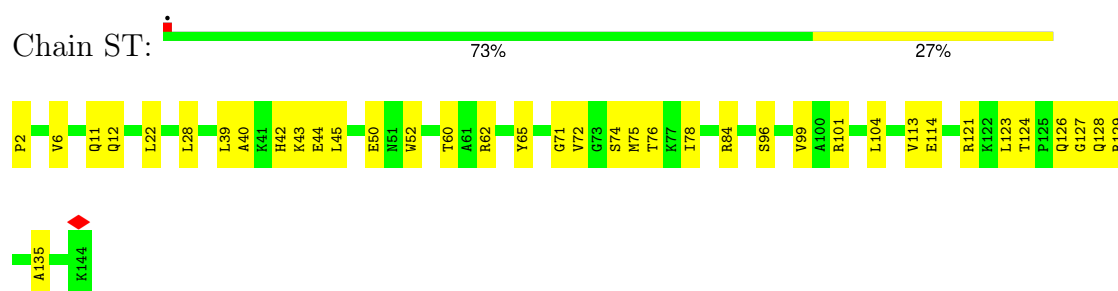
- Molecule 57: Small ribosomal subunit protein eS17



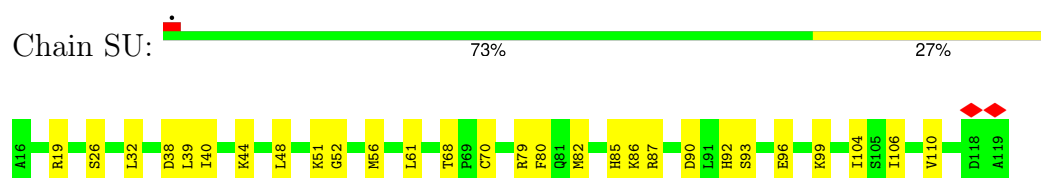
- Molecule 58: 40S ribosomal protein S18



- Molecule 59: 40S ribosomal protein S19

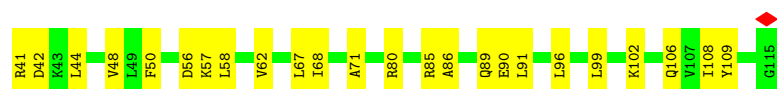


- Molecule 60: 40S ribosomal protein S20



- Molecule 61: Small ribosomal subunit protein eS25

Chain SZ:  68% 32%



- Molecule 62: 40S ribosomal protein S28

Chain Sc:  83% 17%



- Molecule 63: 40S ribosomal protein S29

Chain Sd:  67% 33%



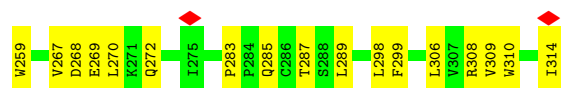
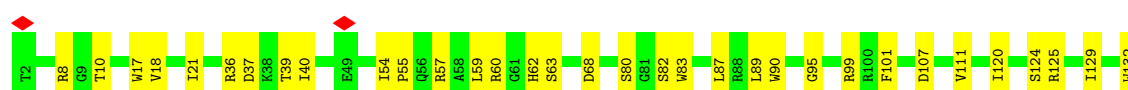
- Molecule 64: Ubiquitin-40S ribosomal protein S27a

Chain Sf:  66% 34%



- Molecule 65: Receptor of activated protein C kinase 1

Chain Sg:  72% 28%



- Molecule 66: 40S ribosomal protein SA

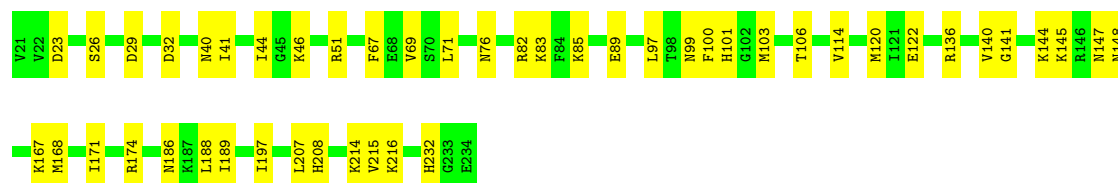
Chain SA:  73% 27%





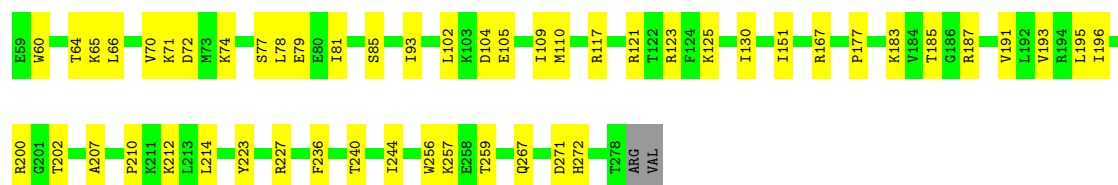
- Molecule 67: 40S ribosomal protein S3a

Chain SB: 78% 22%



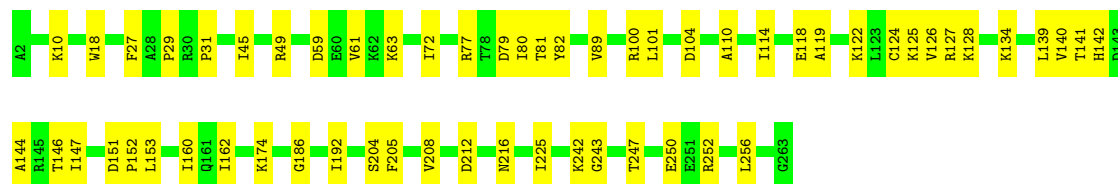
- Molecule 68: 40S ribosomal protein S2

Chain SC: 76% 23%



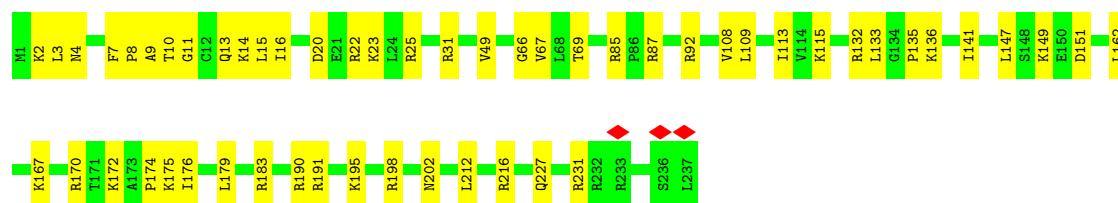
- Molecule 69: Small ribosomal subunit protein eS4, X isoform

Chain SE: 78% 22%



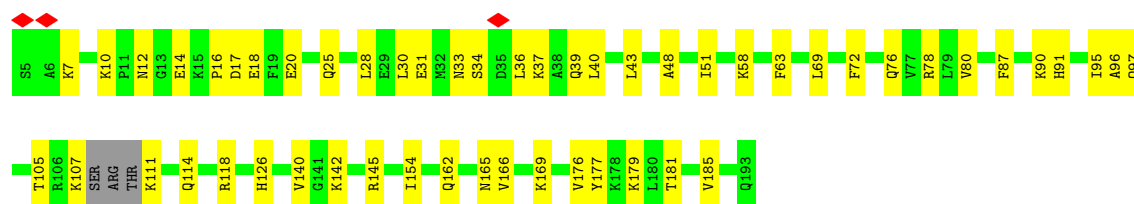
- Molecule 70: 40S ribosomal protein S6

Chain SG: 77% 23%



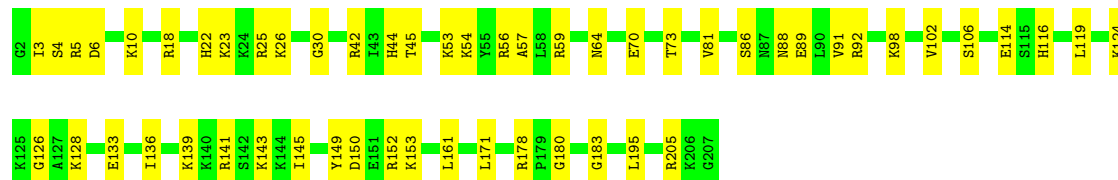
- Molecule 71: Small ribosomal subunit protein eS7

Chain SH: 70% 28%



- Molecule 72: 40S ribosomal protein S8

Chain SI: 74% 26%



- Molecule 73: 40S ribosomal protein S9

Chain SJ: 87% 13%



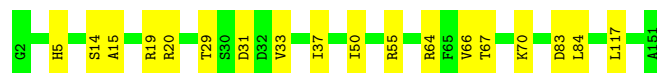
- Molecule 74: 40S ribosomal protein S11

Chain SL: 86% 14%



- Molecule 75: 40S ribosomal protein S13

Chain SN: 88% 12%



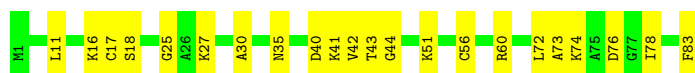
- Molecule 76: Small ribosomal subunit protein uS11

Chain SO: 81% 17%

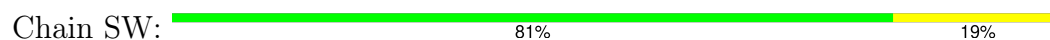


- Molecule 77: Small ribosomal subunit protein eS21

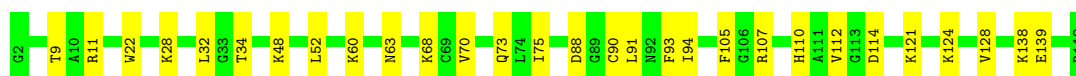
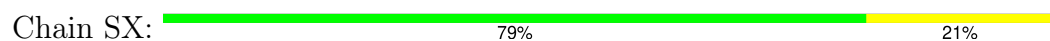
Chain SV: 73% 27%



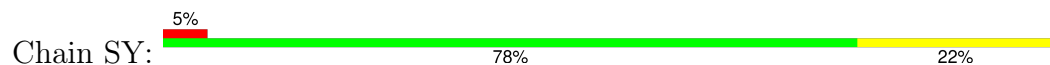
- Molecule 78: 40S ribosomal protein S15a



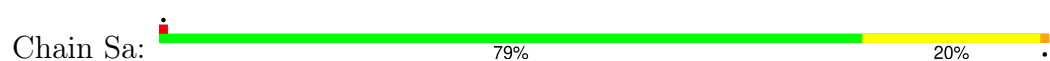
- Molecule 79: 40S ribosomal protein S23



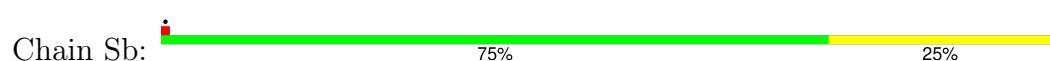
- Molecule 80: 40S ribosomal protein S24



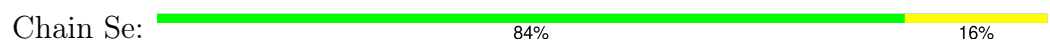
- Molecule 81: 40S ribosomal protein S26



- Molecule 82: Small ribosomal subunit protein eS27



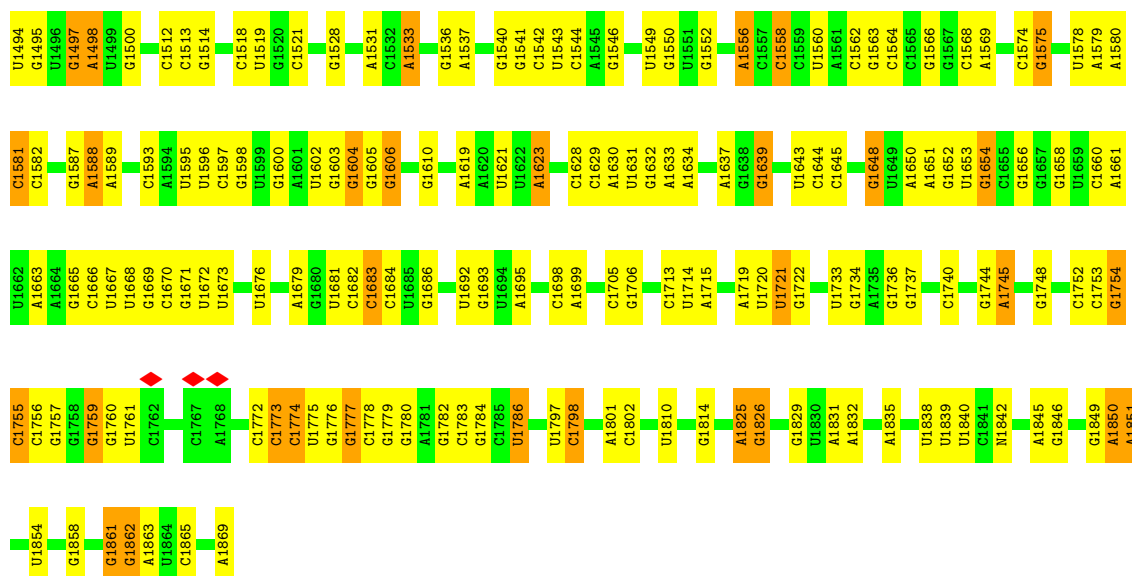
- Molecule 83: Small ribosomal subunit protein eS30



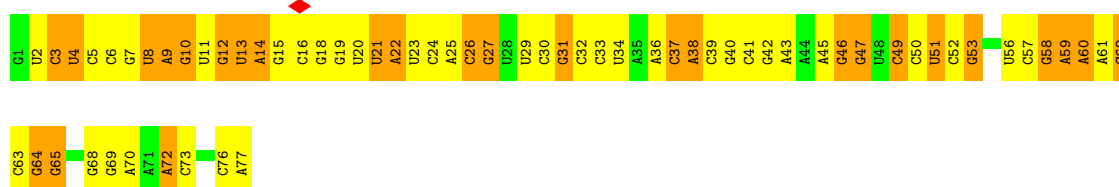
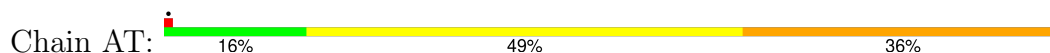
- Molecule 84: 18S rRNA



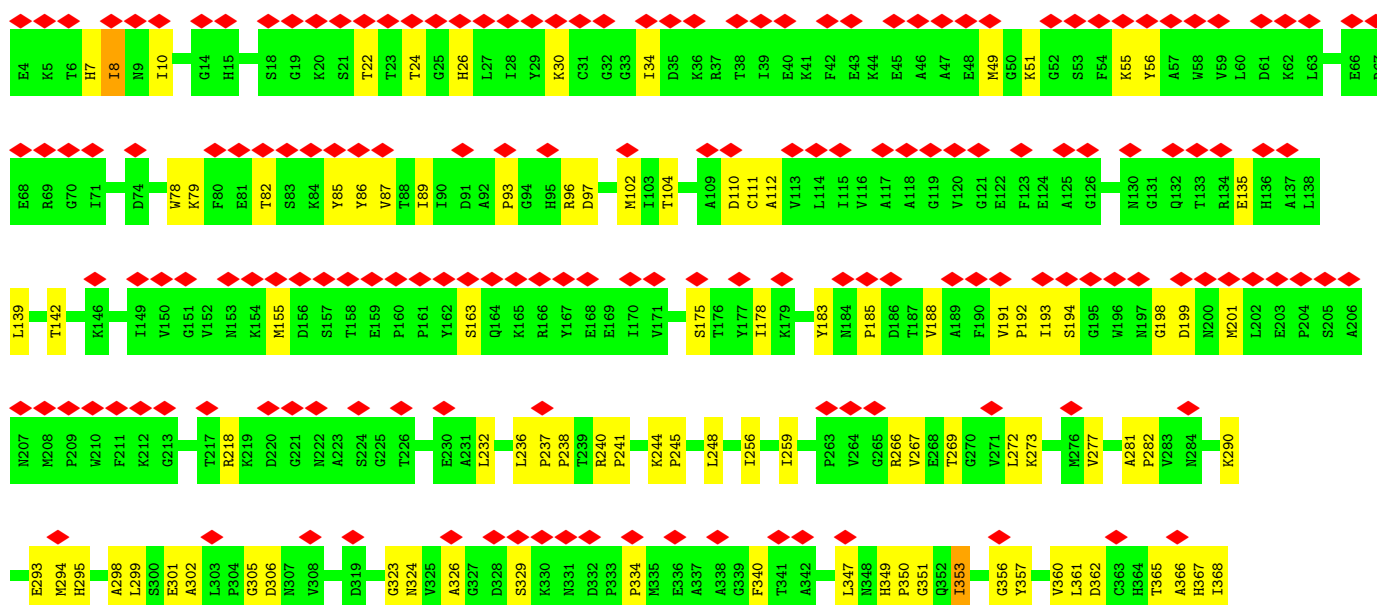
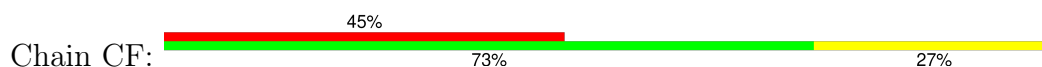
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G1207	A1208	C1215	C1216	A1217	C1218	G1221	G1222	A1223	G1224	U1225	G1226	G1227	A1228	C1229	C1230	C1231	U1232	G1233	G1236	A1240	A1241	U1242	U1243	U1244	B8U1248	U1342	U1347	G1348	C1252	A1253	C1254	G1255	G1256	G1257	C1258	A1259	C1264	C1267	C1271	C1272	G1273	C1274	G1275	A1276	C1277	A1278	C1279	G1280	C1283	U1382	A1383	G1286				
G1102	C1103	C1109	U1112	A1113	U1114	U1115	C1116	C1117	G1121	A1122	C1123	G1129	G1130	A1133	C1138	C1139	G1140	A1143	A1144	A1145	A1148	A1149	A1150	C1153	U1154	U1155	U1156	G1171	U1172	C1173	U1174	U1177	G1187	A1188	A1189	A1190	A1194	A1195	A1199	C1200	U1201	U1202	G1203	A1204												
A1001	U1002	U1003	U1004	A1008	A1009	G1010	A1011	U1012	U1013	U1016	U1017	A1020	A1023	U1024	U1025	C1026	A1027	U1028	U1040	C941	G942	U943	A944	U945	U946	G959	U960	A961	A962	A963	U1056	C1057	A1058	G1059	A1060	U1061	A1062	A1080	U1081	A1082	A1083	A1084	C1085	U1088	C1089	C1090	C1091	C1098	G1099	A1100	U1101					
G902	A903	G907	A908	G909	G910	A913	A919	A920	G925	G928	G929	C930	C931	G932	G933	G934	U940	C941	G942	U943	A944	U945	U946	G959	U960	A961	A962	A963	U964	U965	U966	G970	G971	A972	A981	G982	G985	G986	G987	A990	G991	A992	A996	A997	A998	G999	C1000									
G821	U822	U823	C824	A825	A830	C834	C835	C836	A837	C838	C839	C940	G941	C942	C943	U944	C945	G946	A947	C951	G952	G955	G960	U863	U866	C967	A870	C874	C875	C876	C877	G978	G980	C981	U888	U889	U890	G991	U892	U893	C994	C995	U896	U897	U898	U899	C900	G901								
U675	U681	U682	G683	U686	C687	U688	U689	G692	A693	C694	C695	U696	C697	C698	C700	G701	U702	C703	C736	G737	C738	C739	C746	U747	C748	U749	C750	G751	G752	C753	G758	C791	C792	G793	A794	A795	C796	C797	G798	U799	U800	U801	U804	U805	A808	A809	U814	U815	A816							
C592	C593	A594	U595	G596	G597	G598	G601	A604	A605	G606	U607	C608	A609	G610	C614	C615	G617	G623	C624	U627	A628	A629	C630	U631	C639	A640	A641	U642	A643	G644	U649	A650	U651	A655	G656	G659	C660	U661	G662	C663	A664	A668	A669	A670	A671	A672	C673	C674								
A516	C517	G518	A519	A520	A521	A522	A525	C526	C527	A528	A529	U530	A531	C532	A533	A536	C537	U540	U541	U542	C543	A544	A545	G546	C547	C550	U553	A554	A555	U556	U557	G558	G559	U562	G563	A564	C570	U573	A574	A575	A576	U582	A583	A587	G588	G589	A590	U591								
A433	G434	A435	G436	G437	G438	C441	C442	U443	U444	A445	A448	A449	A450	G451	G452	C453	U454	A455	C456	C463	A464	A465	G466	A467	A468	G471	A472	A473	G474	A475	A476	C482	C483	A484	A485	A486	U487	U488	C492	A493	C494	U495	C496	C497	U406	G407	A408	C409	G420	U428	G509					
U93	G94	G95	A99	A102	A103	A104	U105	C106	A107	G108	U109	G113	G114	U115	U116	G117	C118	U119	G120	U121	G122	C125	G126	U124	G130	G136	U137	C142	C293	U143	U144	G145	G146	A149	C151	U152	G153	U154	A158	A159	U160	U161	C162	G165	A166	G167	C168	U169	A170	A171						
U172	A175	C179	C186	G187	A190	A191	C192	C193	C194	C195	C196	U197	C198	U199	G200	C201	G202	G203	G204	G207	G208	U214	C223	A224	G291	A292	C293	U294	C295	G298	A302	C306	G307	G308	C309	C310	C311	G312	A313	G316	G317	A318	C319	G320	C323	C324										
C325	C326	G327	G328	G329	C331	G332	C333	C334	A339	C340	G347	A348	A349	C350	G351	U352	U353	A360	U361	C362	A363	A364	U367	U368	C369	A370	U372	G373	A376	G377	C379	C381	G382	G383	U384	C385	C386	C387	C388	C389	C390	C392	G393	U394	U406	G407	A408	C409	G420	U428	G509					



• Molecule 85: A/T site tRNA



• Molecule 86: Elongation factor 1-alpha 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48914	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	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	0.310	Depositor
Minimum map value	-0.085	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.0226	Depositor
Map size ($\text{\AA}$)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CI	0.16	0/247	0.30	0/323
2	Pt	0.14	0/1761	0.25	0/2741
3	Et	0.14	0/1778	0.31	0/2767
4	L5	0.23	0/85098	0.30	0/132762
5	L7	0.20	0/2861	0.25	0/4459
6	L8	0.21	0/3631	0.27	0/5657
7	LA	0.24	0/1936	0.40	0/2596
8	LB	0.22	0/3306	0.37	0/4424
9	LC	0.23	0/2981	0.36	0/4002
10	LD	0.19	0/2428	0.31	0/3252
11	LE	0.19	0/1973	0.39	0/2645
12	LF	0.22	0/1905	0.31	0/2539
13	LG	0.20	0/1960	0.37	0/2637
14	LH	0.20	0/1537	0.32	0/2066
15	LI	0.20	0/1751	0.33	0/2340
16	LJ	0.17	0/1385	0.37	0/1852
17	LL	0.19	0/1732	0.30	0/2315
18	LM	0.22	0/1161	0.37	0/1554
19	LN	0.23	0/1746	0.32	0/2338
20	LO	0.23	0/1682	0.36	0/2250
21	LP	0.23	0/1268	0.39	0/1701
22	LQ	0.24	0/1537	0.36	0/2052
23	LR	0.20	0/1582	0.36	0/2091
24	LS	0.22	0/1493	0.33	0/2003
25	LT	0.20	0/1326	0.31	0/1770
26	LU	0.21	0/839	0.48	0/1126
27	LV	0.20	0/993	0.36	0/1332
28	LW	0.20	0/959	0.37	0/1270
29	LX	0.20	0/1002	0.35	0/1345
30	LY	0.22	0/1132	0.35	0/1504
31	LZ	0.19	0/1130	0.34	0/1507

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	La	0.21	0/1191	0.31	0/1591
33	Lb	0.19	0/889	0.38	0/1175
34	Lc	0.21	0/774	0.37	0/1038
35	Ld	0.21	0/903	0.34	0/1216
36	Le	0.22	0/1071	0.33	0/1429
37	Lf	0.23	0/895	0.35	0/1198
38	Lg	0.20	0/916	0.33	0/1220
39	Lh	0.18	0/1023	0.32	0/1351
40	Li	0.17	0/843	0.29	0/1115
41	Lj	0.23	0/720	0.36	0/952
42	Lk	0.31	1/575 (0.2%)	0.47	0/761
43	Ll	0.21	0/454	0.28	0/599
44	Lm	0.19	0/435	0.33	0/575
45	Ln	0.23	0/231	0.33	0/294
46	Lo	0.22	0/876	0.33	0/1156
47	Lp	0.21	0/718	0.33	0/953
48	Lr	0.21	0/1017	0.32	0/1364
49	Ls	0.29	1/1519 (0.1%)	0.38	0/2052
50	Lt	0.19	0/1009	0.49	0/1363
51	SD	0.13	0/1793	0.28	0/2414
52	SF	0.16	0/1516	0.35	0/2037
53	SK	0.16	0/851	0.43	0/1147
54	SM	0.14	0/950	0.38	0/1275
55	SP	0.26	1/1003 (0.1%)	0.40	0/1342
56	SQ	0.16	0/1160	0.38	0/1553
57	SR	0.18	0/1105	0.44	0/1484
58	SS	0.16	0/1216	0.37	0/1628
59	ST	0.15	0/1131	0.37	0/1515
60	SU	0.17	0/831	0.46	0/1115
61	SZ	0.22	0/604	0.47	0/810
62	Sc	0.16	0/508	0.36	0/680
63	Sd	0.17	0/470	0.37	0/623
64	Sf	0.15	0/560	0.44	0/745
65	Sg	0.14	0/2493	0.37	0/3394
66	SA	0.16	0/1778	0.36	0/2416
67	SB	0.16	0/1765	0.35	0/2362
68	SC	0.19	0/1744	0.34	0/2357
69	SE	0.18	0/2118	0.35	0/2849
70	SG	0.14	0/1946	0.34	0/2590
71	SH	0.18	0/1519	0.42	0/2033
72	SI	0.19	0/1715	0.37	0/2287
73	SJ	0.14	0/1550	0.34	1/2069 (0.0%)
74	SL	0.17	0/1268	0.29	0/1696

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	SN	0.17	0/1232	0.26	0/1656
76	SO	0.19	0/1037	0.38	0/1391
77	SV	0.17	0/643	0.38	0/860
78	SW	0.20	0/1051	0.34	0/1406
79	SX	0.16	0/1116	0.35	0/1490
80	SY	0.16	0/1083	0.39	0/1438
81	Sa	0.43	1/836 (0.1%)	0.43	1/1121 (0.1%)
82	Sb	0.18	0/665	0.36	0/891
83	Se	0.14	0/465	0.37	0/612
84	S2	0.20	1/39756 (0.0%)	0.28	0/61939
85	AT	0.26	0/1805	0.44	1/2809 (0.0%)
86	CF	0.48	3/3442 (0.1%)	0.80	7/4656 (0.2%)
All	All	0.22	8/236904 (0.0%)	0.33	10/347312 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
56	SQ	0	1
76	SO	0	1
All	All	0	2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	CF	391	PRO	CB-CG	-11.27	0.93	1.49
81	Sa	98	PRO	CA-C	-10.72	1.46	1.51
86	CF	391	PRO	N-CA	10.18	1.59	1.47
49	Ls	14	PHE	CE1-CZ	8.26	1.63	1.38
86	CF	390	GLY	C-N	-8.16	1.22	1.33
55	SP	94	VAL	C-N	-6.13	1.30	1.33
42	Lk	35	LYS	CB-CG	-5.06	1.37	1.52
84	S2	1288	OMU	O3'-P	5.02	1.61	1.56

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	CF	391	PRO	CB-CG-CD	23.08	179.97	106.10
86	CF	391	PRO	N-CD-CG	-18.19	75.92	103.20
86	CF	391	PRO	CA-CB-CG	-17.07	72.08	104.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	CF	391	PRO	CA-N-CD	-9.43	98.80	112.00
81	Sa	98	PRO	O-C-N	-7.86	117.69	121.31
86	CF	139	LEU	CD1-CG-CD2	-7.02	95.35	110.80
86	CF	353	ILE	CA-CB-CG2	5.65	120.10	110.50
86	CF	8	ILE	CB-CA-C	-5.64	103.45	111.34
85	AT	38	A	N9-C1'-C2'	5.23	119.84	112.00
73	SJ	43	VAL	N-CA-C	-5.17	107.79	112.96

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
76	SO	137	SER	Peptide
56	SQ	107	GLU	Peptide

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	CI	247	0	283	12	0
2	Pt	1576	0	803	14	0
3	Et	1593	0	810	32	0
4	L5	78444	0	39719	812	0
5	L7	2561	0	1295	15	0
6	L8	3315	0	1685	28	0
7	LA	1898	0	1993	45	0
8	LB	3238	0	3375	58	0
9	LC	2927	0	3104	32	0
10	LD	2382	0	2410	36	0
11	LE	1935	0	2096	28	0
12	LF	1870	0	1996	32	0
13	LG	1927	0	2074	27	0
14	LH	1518	0	1601	22	0
15	LI	1711	0	1749	23	0
16	LJ	1362	0	1399	21	0
17	LL	1701	0	1818	24	0
18	LM	1138	0	1204	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	LN	1701	0	1749	22	0
20	LO	1650	0	1794	32	0
21	LP	1242	0	1269	19	0
22	LQ	1513	0	1628	22	0
23	LR	1566	0	1729	22	0
24	LS	1453	0	1490	15	0
25	LT	1298	0	1366	19	0
26	LU	825	0	850	15	0
27	LV	979	0	1039	12	0
28	LW	945	0	1003	24	0
29	LX	985	0	1066	8	0
30	LY	1115	0	1205	16	0
31	LZ	1107	0	1182	15	0
32	La	1162	0	1213	11	0
33	Lb	876	0	948	19	0
34	Lc	764	0	804	9	0
35	Ld	888	0	930	15	0
36	Le	1053	0	1147	15	0
37	Lf	876	0	912	9	0
38	Lg	906	0	998	11	0
39	Lh	1015	0	1148	15	0
40	Li	832	0	917	7	0
41	Lj	705	0	737	13	0
42	Lk	569	0	637	9	0
43	Ll	444	0	483	7	0
44	Lm	429	0	465	4	0
45	Ln	230	0	276	5	0
46	Lo	862	0	929	12	0
47	Lp	708	0	756	8	0
48	Lr	1002	0	1068	6	0
49	Ls	1496	0	1540	21	0
50	Lt	998	0	1032	24	0
51	SD	1765	0	1865	19	0
52	SF	1495	0	1549	40	0
53	SK	827	0	854	23	0
54	SM	940	0	965	16	0
55	SP	985	0	1031	16	0
56	SQ	1142	0	1213	27	0
57	SR	1090	0	1149	16	0
58	SS	1198	0	1261	30	0
59	ST	1112	0	1146	28	0
60	SU	821	0	883	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	SZ	598	0	656	18	0
62	Sc	506	0	536	11	0
63	Sd	459	0	452	16	0
64	Sf	548	0	551	17	0
65	Sg	2436	0	2393	55	0
66	SA	1741	0	1746	41	0
67	SB	1738	0	1809	31	0
68	SC	1707	0	1791	36	0
69	SE	2076	0	2177	38	0
70	SG	1923	0	2089	49	0
71	SH	1497	0	1590	38	0
72	SI	1686	0	1772	40	0
73	SJ	1525	0	1640	16	0
74	SL	1247	0	1323	15	0
75	SN	1208	0	1294	13	0
76	SO	1024	0	1050	17	0
77	SV	636	0	637	16	0
78	SW	1034	0	1080	21	0
79	SX	1098	0	1167	23	0
80	SY	1065	0	1142	24	0
81	Sa	821	0	870	15	0
82	Sb	651	0	672	16	0
83	Se	459	0	503	11	0
84	S2	36953	0	18677	462	0
85	AT	1616	0	824	55	0
86	CF	3383	0	3432	83	0
87	L5	177	0	0	0	0
87	L7	3	0	0	0	0
87	L8	5	0	0	0	0
87	LA	1	0	0	0	0
87	LB	1	0	0	0	0
87	LP	1	0	0	0	0
87	LV	1	0	0	0	0
87	Le	1	0	0	0	0
87	Lj	1	0	0	0	0
87	S2	26	0	0	0	0
87	SG	1	0	0	0	0
87	SS	1	0	0	0	0
88	L5	98	0	182	6	0
89	L5	80	0	152	4	0
89	L8	10	0	19	0	0
89	LN	10	0	19	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
90	Lg	1	0	0	0	0
90	Lj	1	0	0	0	0
90	Lm	1	0	0	0	0
90	Lo	1	0	0	0	0
90	Lp	1	0	0	0	0
90	Sa	1	0	0	0	0
All	All	224970	0	167885	2611	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (2611) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:79:ARG:NH1	4:L5:2708:U:O2'	1.68	1.26
86:CF:362:ASP:HB3	86:CF:367:HIS:CD2	1.74	1.22
80:SY:38:THR:O	80:SY:42:GLU:OE1	1.68	1.10
4:L5:1996:C:H42	4:L5:2000:G:N2	1.55	1.02
3:Et:26:A:H61	3:Et:44:G:H1	1.03	1.00
2:Pt:50:U:H3	2:Pt:64:G:H1	1.10	0.95
4:L5:1996:C:N4	4:L5:2000:G:H22	1.66	0.94
86:CF:362:ASP:HB3	86:CF:367:HIS:HD2	1.24	0.93
3:Et:26:A:N6	3:Et:44:G:H1	1.66	0.92
84:S2:1748:G:H1	84:S2:1786:U:H3	0.99	0.92
4:L5:3946:G:H1	4:L5:4067:U:H3	1.13	0.92
1:CI:74:LYS:HA	26:LU:116:GLN:O	1.71	0.90
4:L5:1996:C:H42	4:L5:2000:G:H22	0.95	0.90
86:CF:362:ASP:CB	86:CF:367:HIS:CD2	2.55	0.89
86:CF:97:ASP:OD1	86:CF:430:ARG:NH2	2.08	0.87
67:SB:103:MET:HG3	67:SB:215:VAL:HG12	1.57	0.86
4:L5:2007:G:H21	4:L5:2012:A:H62	1.22	0.84
17:LL:64:VAL:HA	17:LL:67:HIS:HD2	1.39	0.84
64:Sf:126:CYS:SG	64:Sf:144:CYS:N	2.51	0.83
86:CF:96:ARG:NH2	86:CF:430:ARG:O	2.10	0.83
4:L5:1100:U:H3	4:L5:1194:G:H1	1.27	0.82
84:S2:925:G:H1	84:S2:1017:U:H3	1.29	0.80
28:LW:100:VAL:HG12	28:LW:104:GLN:HE22	1.46	0.79
68:SC:210:PRO:HB3	68:SC:240:THR:HG21	1.64	0.79
84:S2:1776:G:N2	84:S2:1777:G:N7	2.32	0.78
4:L5:1095:A:H2	4:L5:1200:G:H1	1.24	0.77
4:L5:4910:G:H4'	8:LB:95:THR:HG22	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SB:122:GLU:HG2	67:SB:140:VAL:HG12	1.69	0.75
68:SC:193:VAL:HG11	68:SC:240:THR:HG22	1.69	0.75
4:L5:1982:G:H5'	50:Lt:28:LEU:HD13	1.68	0.75
52:SF:134:VAL:HG12	52:SF:135:ARG:HG2	1.67	0.74
4:L5:5024:C:H41	4:L5:5028:G:H21	1.32	0.74
56:SQ:72:VAL:HG11	56:SQ:80:GLN:HG3	1.69	0.74
4:L5:2611:A:H5'	4:L5:2688:G:H4'	1.70	0.74
85:AT:38:A:H2'	85:AT:39:C:C6	2.23	0.73
4:L5:1702:C:H4'	9:LC:308:LYS:HD2	1.71	0.73
86:CF:49:MET:HE3	86:CF:51:LYS:HB2	1.69	0.73
65:Sg:247:TRP:HB3	65:Sg:258:ILE:HD11	1.69	0.73
84:S2:1825:A:N6	85:AT:38:A:N3	2.37	0.73
4:L5:3701:OMC:H5	4:L5:3748:A:H62	1.37	0.72
84:S2:94:G:HO2'	84:S2:508:A:HO2'	1.36	0.72
86:CF:368:ILE:HD12	86:CF:408:LYS:HD3	1.71	0.71
4:L5:664:G:N2	4:L5:666:G:O6	2.24	0.71
35:Ld:90:ARG:HD3	35:Ld:102:LEU:HD13	1.73	0.71
59:ST:12:GLN:NE2	84:S2:1593:C:O2	2.23	0.71
21:LP:109:VAL:HA	21:LP:112:LEU:HD13	1.73	0.71
69:SE:208:VAL:HG11	69:SE:225:ILE:HG13	1.73	0.70
85:AT:18:G:H21	85:AT:59:A:H5'	1.55	0.70
4:L5:3594:C:O2	4:L5:3597:G:N2	2.25	0.70
71:SH:154:ILE:HB	71:SH:185:VAL:HG22	1.72	0.70
4:L5:4546:A:N7	7:LA:215:ASN:ND2	2.40	0.70
86:CF:104:THR:HG23	86:CF:365:THR:HG23	1.74	0.70
18:LM:15:VAL:HG22	18:LM:50:MET:HE1	1.72	0.70
4:L5:387:G:HO2'	4:L5:412:G:H1	1.39	0.70
4:L5:3954:A:H1'	4:L5:4058:U:H5'	1.74	0.70
35:Ld:68:LEU:HD22	35:Ld:106:VAL:HG12	1.72	0.70
70:SG:2:LYS:HB2	70:SG:108:VAL:HG12	1.72	0.70
65:Sg:176:VAL:HG23	65:Sg:185:LYS:HB2	1.72	0.70
7:LA:104:VAL:HA	7:LA:107:MET:HE3	1.74	0.69
4:L5:2702:C:OP1	26:LU:101:ARG:NH2	2.24	0.69
71:SH:105:THR:HG23	71:SH:107:LYS:H	1.57	0.69
4:L5:3937:C:H1'	19:LN:125:SER:HB3	1.73	0.69
84:S2:1658:G:OP2	84:S2:1660:C:N4	2.25	0.69
86:CF:353:ILE:HG23	86:CF:357:TYR:HE1	1.55	0.69
4:L5:2092:G:O2'	4:L5:2262:G:N2	2.26	0.69
4:L5:2484:A:H62	4:L5:2494:U:H3	1.41	0.69
3:Et:9:A:H2'	3:Et:11:C:H41	1.57	0.69
3:Et:32:C:OP1	52:SF:135:ARG:NH2	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4946:U:HO2'	37:Lf:2:SER:N	1.90	0.69
86:CF:93:PRO:HD2	86:CF:102:MET:HB3	1.74	0.69
4:L5:4242:U:H3	4:L5:4281:A:H2	1.39	0.69
28:LW:80:ARG:NH2	70:SG:8:PRO:O	2.26	0.69
4:L5:184:U:O2	4:L5:253:G:N2	2.24	0.68
64:Sf:99:LYS:NZ	84:S2:1287:A:OP1	2.26	0.68
4:L5:1995:G:O2'	50:Lt:122:ALA:O	2.11	0.68
54:SM:51:VAL:HG12	54:SM:77:ILE:HB	1.74	0.68
50:Lt:65:GLN:HG3	50:Lt:67:ARG:H	1.58	0.68
82:Sb:14:GLU:HA	82:Sb:17:ARG:HG2	1.75	0.68
84:S2:940:U:H3	84:S2:1002:U:H3	1.38	0.68
85:AT:21:U:H5'	85:AT:49:C:H42	1.58	0.68
4:L5:748:G:O6	24:LS:98:ARG:NH2	2.26	0.68
65:Sg:87:LEU:HB2	65:Sg:101:PHE:HB2	1.75	0.68
15:LI:205:PRO:HD2	15:LI:208:LYS:HE2	1.76	0.68
4:L5:2520:C:O2	4:L5:2640:G:N2	2.26	0.68
4:L5:2351:OMC:HM22	9:LC:95:MET:HG3	1.75	0.68
4:L5:2554:U:O2	4:L5:2764:A:N7	2.27	0.68
76:SO:104:ARG:NH2	84:S2:959:G:OP1	2.26	0.68
4:L5:665:C:H4'	4:L5:666:G:H5'	1.75	0.67
51:SD:106:ARG:HG3	51:SD:175:VAL:HG22	1.76	0.67
4:L5:1414:C:H2'	4:L5:1415:G:H8	1.59	0.67
85:AT:18:G:H1	85:AT:56:U:H1'	1.58	0.67
7:LA:107:MET:HB3	7:LA:111:THR:HG21	1.74	0.67
8:LB:90:VAL:HG23	8:LB:163:ILE:HD11	1.76	0.67
19:LN:157:LYS:O	19:LN:162:ARG:NH1	2.27	0.67
20:LO:34:VAL:HG22	20:LO:103:LYS:HB2	1.77	0.67
4:L5:1870:C:H2'	4:L5:1871:A2M:H8	1.77	0.67
88:L5:5290:SPM:H112	20:LO:91:LYS:HD3	1.75	0.67
80:SY:39:GLU:HA	80:SY:42:GLU:OE2	1.94	0.67
85:AT:2:U:H3	85:AT:72:A:H61	1.42	0.67
4:L5:2458:C:H5''	19:LN:67:ARG:HD2	1.77	0.67
14:LH:106:GLN:HB2	14:LH:111:LEU:HB3	1.77	0.67
28:LW:56:ARG:HE	28:LW:61:LYS:HB2	1.59	0.67
78:SW:107:SER:HB2	84:S2:860:G:H21	1.58	0.67
86:CF:353:ILE:HG23	86:CF:357:TYR:CE1	2.29	0.67
85:AT:57:C:N4	85:AT:58:G:O6	2.27	0.67
59:ST:124:THR:HG23	59:ST:127:GLY:H	1.61	0.66
70:SG:183:ARG:NH2	84:S2:316:G:OP2	2.27	0.66
3:Et:26:A:N1	3:Et:44:G:N2	2.42	0.66
7:LA:29:LEU:O	7:LA:123:ARG:NH1	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2007:G:N2	4:L5:2012:A:H62	1.93	0.66
27:LV:35:LYS:HB2	27:LV:67:LYS:HG3	1.76	0.66
83:Se:41:ARG:NH2	84:S2:639:C:OP1	2.29	0.66
4:L5:1669:A:OP1	33:Lb:18:ARG:NH2	2.29	0.66
53:SK:50:GLN:HE22	84:S2:1276:A:H1'	1.60	0.66
68:SC:187:ARG:NH2	84:S2:1143:A:OP2	2.29	0.66
86:CF:277:VAL:HG13	86:CF:329:SER:HB3	1.76	0.66
4:L5:1095:A:N1	4:L5:1200:G:O6	2.29	0.66
4:L5:4910:G:N2	20:LO:106:ASP:O	2.28	0.66
8:LB:222:VAL:O	8:LB:343:ARG:NH1	2.29	0.66
84:S2:747:U:N3	84:S2:796:G:N1	2.44	0.66
24:LS:76:LYS:NZ	24:LS:100:LEU:O	2.29	0.66
42:Lk:8:ILE:HD11	42:Lk:56:LEU:HD13	1.77	0.66
84:S2:1536:G:H2'	84:S2:1537:A:H8	1.61	0.66
8:LB:10:ARG:NH1	8:LB:11:HIS:O	2.29	0.65
52:SF:124:ASP:OD1	52:SF:125:SER:N	2.27	0.65
49:Ls:58:ASN:ND2	49:Ls:84:GLY:O	2.23	0.65
70:SG:132:ARG:NH2	84:S2:152:U:O4'	2.29	0.65
85:AT:38:A:H2'	85:AT:39:C:H6	1.60	0.65
86:CF:110:ASP:OD1	86:CF:266:ARG:NH2	2.29	0.65
6:L8:75:OMG:OP2	30:LY:74:TYR:OH	2.15	0.65
85:AT:9:A:N6	85:AT:23:U:OP2	2.30	0.65
1:CI:79:ARG:NH1	4:L5:2708:U:HO2'	1.94	0.65
84:S2:928:G:H2'	84:S2:929:G:C8	2.31	0.65
32:La:84:GLU:OE1	32:La:87:ARG:NH2	2.30	0.65
78:SW:71:LYS:NZ	84:S2:1156:U:OP1	2.30	0.65
78:SW:2:VAL:N	84:S2:1091:C:HO2'	1.95	0.65
23:LR:172:ARG:NH1	84:S2:909:G:OP1	2.29	0.65
85:AT:61:A:OP1	85:AT:63:C:N4	2.29	0.65
86:CF:273:LYS:HE3	86:CF:301:GLU:HG2	1.79	0.65
86:CF:24:THR:HG23	86:CF:89:ILE:HD13	1.78	0.65
4:L5:1079:C:O2	4:L5:1221:G:N2	2.23	0.65
58:SS:85:ASN:OD1	58:SS:97:GLN:NE2	2.30	0.65
84:S2:628:A:N6	84:S2:1500:G:O2'	2.29	0.65
70:SG:135:PRO:HG2	70:SG:141:ILE:HG22	1.78	0.64
84:S2:751:G:H1'	84:S2:793:G:H21	1.61	0.64
1:CI:78:HIS:NE2	4:L5:2706:G:N7	2.44	0.64
4:L5:68:U:OP1	19:LN:178:HIS:ND1	2.31	0.64
25:LT:43:LYS:O	25:LT:58:HIS:ND1	2.30	0.64
84:S2:533:A:H61	84:S2:550:C:H42	1.45	0.64
4:L5:1994:C:H2'	4:L5:1995:G:C8	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Lt:130:LYS:NZ	50:Lt:157:SER:O	2.30	0.64
84:S2:1829:G:H1'	84:S2:1850:MA6:H2	1.78	0.64
4:L5:4525:C:OP1	8:LB:246:ARG:NH2	2.29	0.64
72:SI:98:LYS:HB3	84:S2:377:G:H5'	1.80	0.64
14:LH:106:GLN:NE2	14:LH:113:GLU:OE2	2.30	0.64
52:SF:168:THR:OG1	52:SF:171:GLU:OE1	2.16	0.64
4:L5:67:C:OP2	4:L5:312:G:N2	2.28	0.64
4:L5:3641:U:OP2	4:L5:3646:A:N6	2.31	0.64
21:LP:39:MET:HG2	21:LP:43:LYS:HD3	1.80	0.64
70:SG:7:PHE:HD2	70:SG:10:THR:HG22	1.63	0.64
7:LA:137:ILE:HD11	7:LA:149:LYS:HB2	1.80	0.64
71:SH:114:GLN:HE22	84:S2:874:G:H21	1.45	0.64
4:L5:2601:A:N6	4:L5:2744:A:OP2	2.28	0.64
26:LU:65:ARG:HG2	26:LU:67:LYS:H	1.62	0.64
33:Lb:109:ARG:HA	33:Lb:112:ILE:HG12	1.80	0.63
65:Sg:252:THR:HG21	65:Sg:257:LYS:HD2	1.80	0.63
4:L5:1704:C:O3'	12:LF:46:ARG:NH1	2.31	0.63
42:Lk:54:GLU:OE2	42:Lk:58:GLN:NE2	2.28	0.63
56:SQ:19:ALA:HB2	56:SQ:75:GLY:HA3	1.81	0.63
51:SD:142:LEU:HD13	51:SD:150:MET:HE2	1.81	0.63
61:SZ:99:LEU:HD21	61:SZ:102:LYS:HB2	1.80	0.63
68:SC:259:THR:HG23	77:SV:16:LYS:HZ3	1.63	0.63
66:SA:89:LYS:HD2	66:SA:201:LEU:HG	1.80	0.63
69:SE:153:LEU:O	69:SE:174:LYS:NZ	2.31	0.63
84:S2:106:C:H2'	84:S2:107:A:H8	1.64	0.63
4:L5:2495:U:H2'	4:L5:2496:G:H8	1.64	0.63
16:LJ:146:ARG:HG2	16:LJ:147:ARG:HG3	1.81	0.63
51:SD:40:ARG:NH2	60:SU:106:ILE:O	2.31	0.63
60:SU:51:LYS:HB3	60:SU:90:ASP:HB2	1.80	0.63
48:Lr:26:SER:OG	48:Lr:28:GLU:OE1	2.16	0.63
73:SJ:162:ARG:NH1	84:S2:582:U:OP1	2.30	0.63
4:L5:327:U:O2'	40:Li:30:ARG:NH1	2.32	0.63
4:L5:4281:A:H2'	4:L5:4282:A:H2'	1.80	0.63
52:SF:127:ARG:HG2	52:SF:136:ARG:HE	1.63	0.63
4:L5:4987:C:OP2	8:LB:116:ARG:NH2	2.32	0.63
60:SU:70:CYS:SG	84:S2:1491:G:O2'	2.55	0.63
4:L5:170:C:H42	4:L5:266:C:H42	1.47	0.62
13:LG:209:SER:HA	13:LG:212:LYS:HG3	1.81	0.62
69:SE:79:ASP:HB3	69:SE:82:TYR:HB2	1.81	0.62
4:L5:1982:G:N2	4:L5:2009:A:O2'	2.33	0.62
4:L5:3946:G:N2	4:L5:4067:U:O2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4431:PSU:OP2	15:LI:3:ARG:NH2	2.28	0.62
7:LA:114:CYS:HB3	7:LA:165:VAL:HB	1.82	0.62
42:Lk:26:LYS:HB2	42:Lk:69:LEU:HD12	1.81	0.62
69:SE:45:ILE:HG13	69:SE:61:VAL:HG11	1.80	0.62
70:SG:22:ARG:HG3	70:SG:25:ARG:HH12	1.64	0.62
4:L5:1326:A2M:H2'	4:L5:1327:C:C6	2.33	0.62
4:L5:2899:C:OP1	23:LR:108:ARG:NH2	2.30	0.62
84:S2:1536:G:H2'	84:S2:1537:A:C8	2.34	0.62
28:LW:80:ARG:HH22	84:S2:167:G:H4'	1.64	0.62
53:SK:85:LEU:HD21	53:SK:89:ILE:HB	1.80	0.62
60:SU:80:PHE:HB3	63:Sd:52:PHE:HB3	1.81	0.62
79:SX:105:PHE:HD1	79:SX:121:LYS:HB3	1.65	0.62
4:L5:4992:G:H2'	4:L5:4993:G:C8	2.35	0.62
69:SE:144:ALA:HB3	84:S2:121:OMU:HM23	1.80	0.62
84:S2:587:A:H5'	84:S2:592:C:H41	1.65	0.62
4:L5:1100:U:O3'	4:L5:1167:C:N4	2.32	0.62
4:L5:2362:U:H2'	4:L5:2363:A2M:H8	1.82	0.62
65:Sg:213:ASP:OD2	65:Sg:215:GLN:NE2	2.33	0.62
84:S2:1825:A:N7	85:AT:38:A:H1'	2.15	0.62
4:L5:2758:G:O2'	4:L5:2765:A:N3	2.30	0.62
51:SD:8:LYS:HG2	60:SU:61:LEU:HD11	1.81	0.62
84:S2:554:A:HO2'	84:S2:555:A:H8	1.46	0.62
4:L5:3717:A:H2'	4:L5:3718:A2M:H8	1.81	0.61
60:SU:26:SER:HB3	60:SU:110:VAL:HA	1.82	0.61
84:S2:1417:C:O2	84:S2:1422:G:O6	2.18	0.61
35:Ld:64:ILE:HG23	35:Ld:68:LEU:HD23	1.82	0.61
4:L5:2557:G:H1	4:L5:2570:U:H3	1.47	0.61
4:L5:4092:G:N7	4:L5:4114:C:N4	2.46	0.61
20:LO:180:GLN:NE2	20:LO:184:ASN:OD1	2.34	0.61
49:Ls:17:ILE:HD12	49:Ls:54:LEU:HD21	1.82	0.61
56:SQ:58:LEU:HB3	56:SQ:62:ARG:HD2	1.82	0.61
72:SI:70:GLU:OE2	74:SL:21:LYS:NZ	2.32	0.61
85:AT:12:G:H22	85:AT:23:U:H3	1.48	0.61
85:AT:37:C:H3'	85:AT:38:A:H8	1.65	0.61
16:LJ:141:ILE:HA	16:LJ:144:LYS:HD2	1.83	0.61
84:S2:1228:A:H2'	84:S2:1229:G:C8	2.35	0.61
12:LF:243:LEU:O	12:LF:247:MET:HB2	2.00	0.61
52:SF:84:GLY:O	84:S2:1673:U:O2'	2.16	0.61
54:SM:91:LEU:HD12	54:SM:106:CYS:HB2	1.81	0.61
80:SY:11:LYS:HB2	80:SY:24:VAL:HG12	1.83	0.61
4:L5:1802:A:N3	25:LT:130:ARG:NH2	2.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4618:OMG:H5'	27:LV:15:ARG:HB2	1.83	0.61
52:SF:34:SER:HA	62:Sc:55:VAL:HG23	1.81	0.61
64:Sf:108:VAL:HG12	64:Sf:114:ILE:HA	1.81	0.61
84:S2:1277:C:H2'	84:S2:1278:A:H8	1.65	0.61
84:S2:1422:G:H4'	84:S2:1423:C:H3'	1.82	0.61
4:L5:1499:C:OP1	22:LQ:150:ARG:NH2	2.34	0.61
8:LB:107:ALA:HB2	8:LB:201:LEU:HD22	1.81	0.61
19:LN:155:VAL:O	19:LN:162:ARG:NH2	2.33	0.61
73:SJ:40:LYS:NZ	84:S2:641:A:OP1	2.31	0.61
85:AT:26:C:H2'	85:AT:27:G:H8	1.66	0.61
4:L5:3811:G:O2'	4:L5:3814:U:OP2	2.18	0.61
51:SD:99:ILE:HG23	51:SD:173:ARG:HH21	1.63	0.61
74:SL:85:THR:HG21	84:S2:373:G:H4'	1.83	0.61
86:CF:30:LYS:HE3	86:CF:201:MET:HB3	1.82	0.61
4:L5:4088:C:OP1	7:LA:37:ARG:NH1	2.34	0.60
57:SR:109:LEU:HD13	66:SA:52:LYS:HB2	1.83	0.60
61:SZ:58:LEU:HD12	61:SZ:62:VAL:HG21	1.83	0.60
72:SI:88:ASN:OD1	72:SI:205:ARG:NH2	2.34	0.60
84:S2:838:G:H1	84:S2:840:C:HO2'	1.47	0.60
86:CF:110:ASP:OD2	86:CF:240:ARG:NH2	2.34	0.60
4:L5:1960:A:C8	49:Ls:63:LYS:HE2	2.37	0.60
4:L5:4472:G:O2'	44:Lm:100:TYR:O	2.20	0.60
4:L5:1175:A:H2	4:L5:1185:G:H22	1.49	0.60
4:L5:4153:C:H5''	29:LX:38:LYS:HD2	1.83	0.60
15:LI:87:MET:HG2	15:LI:138:ILE:HG12	1.82	0.60
56:SQ:78:VAL:HG12	84:S2:1673:U:H5''	1.83	0.60
59:ST:22:LEU:HG	59:ST:28:LEU:HD21	1.82	0.60
69:SE:29:PRO:HA	84:S2:496:C:H5'	1.83	0.60
86:CF:245:PRO:O	86:CF:269:THR:OG1	2.19	0.60
4:L5:1739:G:N3	4:L5:1742:A:N6	2.49	0.60
55:SP:130:ARG:HD3	55:SP:131:PRO:HD2	1.83	0.60
74:SL:133:PRO:HG2	84:S2:383:G:H21	1.66	0.60
53:SK:31:LYS:HZ3	53:SK:40:VAL:H	1.50	0.60
63:Sd:54:LYS:NZ	84:S2:1482:C:OP1	2.35	0.60
85:AT:10:G:O6	85:AT:46:G:N2	2.34	0.60
10:LD:223:PHE:HB3	10:LD:226:TYR:HB2	1.84	0.60
53:SK:25:LYS:NZ	84:S2:1497:G:N7	2.45	0.60
68:SC:200:ARG:O	73:SJ:54:ARG:NH2	2.30	0.60
70:SG:66:GLY:HA2	84:S2:1745:A:H1'	1.83	0.60
74:SL:35:ARG:NH2	74:SL:55:TYR:O	2.35	0.60
55:SP:48:GLY:O	55:SP:50:ARG:NH1	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:SX:107:ARG:HG3	79:SX:110:HIS:HB3	1.83	0.60
84:S2:1550:G:H3'	84:S2:1579:A:H61	1.67	0.60
85:AT:49:C:H2'	85:AT:60:A:H1'	1.83	0.60
4:L5:4076:G:OP1	13:LG:73:ARG:NE	2.34	0.60
58:SS:27:ALA:HB2	58:SS:52:LEU:HD12	1.83	0.60
66:SA:118:GLU:HG3	68:SC:65:LYS:HE2	1.83	0.60
80:SY:21:LYS:HE2	80:SY:75:ILE:HD11	1.84	0.60
84:S2:640:A:H2'	84:S2:641:A:C8	2.37	0.60
23:LR:39:GLN:OE1	23:LR:42:ARG:NH1	2.35	0.59
85:AT:24:C:H2'	85:AT:25:A:C8	2.37	0.59
4:L5:1396:G:N7	32:La:110:LYS:NZ	2.48	0.59
4:L5:2658:G:N2	4:L5:2676:A:OP2	2.34	0.59
30:LY:67:ILE:O	30:LY:84:ARG:NH2	2.34	0.59
46:Lo:2:VAL:N	46:Lo:90:HIS:O	2.35	0.59
52:SF:185:SER:H	52:SF:190:ILE:HD11	1.68	0.59
54:SM:63:LYS:HD3	54:SM:64:LEU:HD22	1.84	0.59
58:SS:130:ARG:NH2	84:S2:1230:C:OP1	2.35	0.59
4:L5:3688:U:OP2	7:LA:198:ARG:NH2	2.36	0.59
72:SI:150:ASP:HA	72:SI:153:LYS:HG2	1.84	0.59
84:S2:874:G:H2'	84:S2:875:A:H8	1.67	0.59
86:CF:8:ILE:HG12	86:CF:85:TYR:HE2	1.67	0.59
86:CF:26:HIS:HE1	86:CF:198:GLY:HA3	1.67	0.59
4:L5:1366:G:H5''	17:LL:36:ARG:HH12	1.67	0.59
4:L5:3868:G:H22	4:L5:3900:G:H1'	1.66	0.59
4:L5:4594:U:H2'	4:L5:4595:G:H8	1.67	0.59
28:LW:5:LEU:HD12	28:LW:30:GLN:NE2	2.18	0.59
64:Sf:144:CYS:HB2	64:Sf:146:LEU:HD23	1.84	0.59
80:SY:34:THR:O	84:S2:570:C:O2'	2.19	0.59
86:CF:22:THR:HG23	86:CF:56:TYR:HB2	1.83	0.59
18:LM:100:ARG:HA	18:LM:103:LYS:HG2	1.84	0.59
4:L5:497:G:N2	4:L5:498:C:H41	2.01	0.59
4:L5:500:G:OP1	4:L5:504:G:N2	2.36	0.59
4:L5:513:U:N3	4:L5:516:C:OP2	2.32	0.59
4:L5:1703:C:O2'	4:L5:1704:C:O4'	2.21	0.59
45:Ln:1:MET:HG3	84:S2:1706:G:H5'	1.84	0.59
69:SE:49:ARG:NH2	84:S2:496:C:OP1	2.33	0.59
84:S2:165:G:OP2	84:S2:165:G:N2	2.29	0.59
4:L5:919:C:OP1	18:LM:69:HIS:ND1	2.21	0.59
65:Sg:206:LEU:HD12	65:Sg:218:LEU:HD12	1.84	0.59
68:SC:267:GLN:OE1	77:SV:35:ASN:ND2	2.36	0.59
86:CF:361:LEU:HD13	86:CF:370:CYS:HB2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SH:7:LYS:HD3	71:SH:10:LYS:HB3	1.83	0.59
51:SD:172:VAL:HG22	51:SD:185:LYS:HG2	1.85	0.59
84:S2:488:U:OP2	86:CF:290:LYS:NZ	2.35	0.59
4:L5:62:A:N3	4:L5:77:U:O2'	2.32	0.58
4:L5:659:G:H2'	4:L5:660:A:H8	1.68	0.58
44:Lm:79:GLU:OE2	44:Lm:81:SER:OG	2.19	0.58
4:L5:2093:A:N3	4:L5:2094:G:N1	2.51	0.58
4:L5:2516:G:O2'	38:Lg:62:LYS:NZ	2.36	0.58
26:LU:44:GLN:HB2	26:LU:56:LEU:HD21	1.84	0.58
28:LW:80:ARG:NH1	84:S2:167:G:O2'	2.36	0.58
48:Lr:28:GLU:OE2	48:Lr:31:ASN:ND2	2.30	0.58
65:Sg:68:ASP:HB3	65:Sg:111:VAL:HG22	1.84	0.58
4:L5:3736:A:H2'	4:L5:3737:A:C8	2.38	0.58
10:LD:62:CYS:HB3	10:LD:105:LEU:HD22	1.84	0.58
10:LD:64:ILE:HD13	10:LD:109:LEU:HD22	1.85	0.58
74:SL:33:LEU:HD12	74:SL:34:PRO:HD2	1.85	0.58
76:SO:15:ILE:HG23	76:SO:16:SER:H	1.68	0.58
84:S2:1825:A:N6	85:AT:38:A:C4	2.72	0.58
4:L5:1339:U:H2'	4:L5:1340:OMC:C6	2.38	0.58
8:LB:80:GLU:OE1	8:LB:323:TYR:OH	2.21	0.58
41:Lj:14:LYS:NZ	43:Ll:51:LEU:OXT	2.37	0.58
86:CF:194:SER:HB3	86:CF:199:ASP:HB3	1.85	0.58
86:CF:340:PHE:HB3	86:CF:441:VAL:HG23	1.85	0.58
4:L5:1996:C:O3'	49:Ls:44:ARG:NH1	2.35	0.58
4:L5:4097:G:O6	4:L5:4098:A:N6	2.37	0.58
70:SG:133:LEU:HD12	84:S2:65:C:C4	2.38	0.58
70:SG:176:ILE:HG12	70:SG:179:LEU:HD11	1.85	0.58
4:L5:184:U:O2'	4:L5:189:G:O4'	2.22	0.58
4:L5:2020:U:H2'	4:L5:2021:G:H8	1.68	0.58
44:Lm:99:CYS:HB2	44:Lm:114:LYS:HE3	1.86	0.58
51:SD:32:ASP:OD1	51:SD:57:ASN:ND2	2.36	0.58
59:ST:126:GLN:HB2	59:ST:129:ARG:HH21	1.68	0.58
65:Sg:107:ASP:HB2	65:Sg:125:ARG:HG3	1.86	0.58
85:AT:14:A:H2'	85:AT:15:G:O4'	2.04	0.58
4:L5:1503:A:H62	22:LQ:87:THR:HG21	1.68	0.58
8:LB:165:HIS:HB3	8:LB:180:LEU:HD23	1.86	0.58
56:SQ:125:ARG:HB2	84:S2:1648:G:H5''	1.86	0.58
61:SZ:80:ARG:O	84:S2:1598:G:O2'	2.19	0.58
69:SE:146:THR:HG21	84:S2:122:G:H21	1.67	0.58
4:L5:4887:C:H42	4:L5:4932:U:H3	1.50	0.58
19:LN:164:LEU:O	19:LN:169:ARG:NH2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1332:C:H2'	4:L5:1333:A:H8	1.69	0.58
4:L5:2017:A:O2'	4:L5:2018:C:H6	1.87	0.58
4:L5:2017:A:O2'	4:L5:2018:C:O5'	2.19	0.58
52:SF:81:ARG:O	52:SF:85:LYS:NZ	2.32	0.58
85:AT:21:U:OP1	85:AT:49:C:N4	2.37	0.58
4:L5:1961:G:N2	4:L5:2024:G:O2'	2.37	0.58
4:L5:4107:G:N2	4:L5:4108:G:O6	2.34	0.58
4:L5:5002:U:OP2	8:LB:385:LYS:NZ	2.37	0.58
42:Lk:27:LYS:O	42:Lk:70:LYS:NZ	2.35	0.58
4:L5:2468:U:O2'	4:L5:2506:G:N2	2.37	0.57
4:L5:4873:G:N7	20:LO:179:LYS:NZ	2.49	0.57
10:LD:120:GLU:O	10:LD:248:ARG:NH1	2.36	0.57
72:SI:22:HIS:HB3	84:S2:433:A:H5''	1.84	0.57
85:AT:29:U:H2'	85:AT:30:C:O4'	2.04	0.57
11:LE:165:LEU:HD11	11:LE:176:THR:HG22	1.86	0.57
40:Li:2:ALA:N	40:Li:5:TYR:HH	2.02	0.57
50:Lt:77:ALA:HB3	50:Lt:80:LEU:HB2	1.86	0.57
64:Sf:92:LYS:NZ	84:S2:1271:C:OP1	2.33	0.57
84:S2:508:A:H3'	84:S2:509:OMG:H8	1.69	0.57
84:S2:1228:A:H2'	84:S2:1229:G:H8	1.69	0.57
72:SI:106:SER:HB3	72:SI:171:LEU:HG	1.87	0.57
84:S2:695:C:N4	84:S2:736:C:O2'	2.37	0.57
4:L5:24:G:N7	41:Lj:46:LYS:NZ	2.51	0.57
67:SB:99:ASN:OD1	67:SB:100:PHE:N	2.38	0.57
70:SG:11:GLY:HA2	84:S2:166:A2M:HM'1	1.86	0.57
76:SO:135:ILE:O	84:S2:943:U:O2'	2.21	0.57
4:L5:267:G:OP1	39:Lh:109:ARG:NH2	2.37	0.57
4:L5:1942:A:H2'	4:L5:1943:A:C8	2.38	0.57
4:L5:4537:C:H2'	4:L5:4538:G:H8	1.68	0.57
11:LE:161:ARG:NH1	11:LE:273:SER:OG	2.37	0.57
20:LO:54:TYR:CD1	20:LO:145:VAL:HG21	2.38	0.57
86:CF:241:PRO:HG2	86:CF:269:THR:HG22	1.87	0.57
4:L5:966:A:H5''	4:L5:2092:G:H22	1.68	0.57
4:L5:2295:C:O2'	9:LC:45:ARG:NH2	2.38	0.57
26:LU:28:PRO:HB2	26:LU:34:MET:HG3	1.86	0.57
53:SK:8:ARG:NH2	84:S2:1314:U:O2'	2.37	0.57
4:L5:935:A:O2'	18:LM:44:GLN:O	2.23	0.57
4:L5:1094:G:O6	4:L5:1201:U:O2	2.22	0.57
4:L5:2613:C:OP1	38:Lg:24:ARG:NH2	2.38	0.57
4:L5:4098:A:H2'	4:L5:4099:G:H4'	1.86	0.57
10:LD:41:LYS:NZ	25:LT:32:ARG:O	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:Sg:63:SER:HB2	84:S2:1398:G:H1'	1.86	0.57
70:SG:92:ARG:O	84:S2:453:C:O2'	2.21	0.57
72:SI:133:GLU:HA	72:SI:136:ILE:HG12	1.86	0.57
4:L5:4340:U:O2	89:L5:5260:SPD:N10	2.38	0.57
4:L5:4413:C:O2	15:LI:158:LYS:NZ	2.38	0.57
6:L8:52:A:H5'	43:Ll:21:ARG:HD3	1.87	0.57
84:S2:1354:G:N2	84:S2:1357:A:OP2	2.34	0.57
53:SK:31:LYS:NZ	53:SK:40:VAL:H	2.03	0.57
86:CF:34:ILE:HG23	86:CF:78:TRP:HZ2	1.68	0.57
86:CF:178:ILE:HG12	86:CF:183:TYR:HB2	1.86	0.57
86:CF:350:PRO:O	86:CF:395:LYS:NZ	2.38	0.57
4:L5:1992:U:H4'	4:L5:1993:C:H5''	1.86	0.57
9:LC:298:ILE:HD13	22:LQ:131:PRO:HB3	1.85	0.57
54:SM:36:ARG:NH1	84:S2:1310:U:OP1	2.37	0.57
56:SQ:67:ASP:OD2	56:SQ:69:ARG:NH1	2.38	0.57
65:Sg:254:PRO:O	65:Sg:272:GLN:NE2	2.38	0.57
4:L5:4725:C:OP1	8:LB:103:LYS:NZ	2.36	0.56
49:Ls:68:HIS:O	49:Ls:71:ASN:ND2	2.38	0.56
4:L5:1993:C:H2'	4:L5:1994:C:C6	2.40	0.56
69:SE:100:ARG:HB2	69:SE:114:ILE:HD13	1.86	0.56
4:L5:2083:C:OP2	22:LQ:14:ARG:NH2	2.32	0.56
6:L8:62:A:OP1	39:Lh:52:LYS:NZ	2.35	0.56
18:LM:71:LYS:O	18:LM:75:GLN:HG3	2.06	0.56
23:LR:176:ARG:NH2	84:S2:910:G:OP1	2.38	0.56
43:Ll:28:ARG:HA	43:Ll:33:ASN:HD22	1.70	0.56
58:SS:5:ILE:N	61:SZ:50:PHE:O	2.36	0.56
77:SV:51:LYS:NZ	77:SV:76:ASP:OD1	2.26	0.56
79:SX:68:LYS:HB3	79:SX:91:LEU:HD13	1.86	0.56
86:CF:135:GLU:OE2	86:CF:432:THR:OG1	2.23	0.56
3:Et:33:U:OP1	52:SF:135:ARG:NH1	2.39	0.56
4:L5:2460:A:OP2	89:LN:301:SPD:N10	2.38	0.56
4:L5:2478:C:N3	4:L5:2591:A:O2'	2.38	0.56
5:L7:6:C:O2'	10:LD:50:ARG:NH2	2.38	0.56
8:LB:10:ARG:NH2	8:LB:265:SER:O	2.37	0.56
8:LB:83:PRO:O	8:LB:167:GLN:NE2	2.39	0.56
13:LG:165:GLU:OE2	19:LN:26:ARG:NH1	2.35	0.56
18:LM:36:ALA:HB3	18:LM:55:MET:HE1	1.86	0.56
20:LO:9:LEU:HD23	20:LO:118:MET:HB2	1.88	0.56
21:LP:17:SER:HB2	21:LP:98:ALA:HB2	1.87	0.56
68:SC:109:ILE:HD11	68:SC:151:ILE:HD11	1.86	0.56
76:SO:134:PRO:HB3	84:S2:944:A:H5''	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4094:G:N2	4:L5:4115:G:OP2	2.39	0.56
15:LI:38:ARG:NH1	15:LI:45:GLU:OE1	2.35	0.56
60:SU:85:HIS:ND1	84:S2:1447:G:OP1	2.38	0.56
84:S2:436:OMG:OP2	84:S2:471:G:O2'	2.23	0.56
4:L5:966:A:OP2	4:L5:2092:G:N2	2.39	0.56
4:L5:3760:A:N7	85:AT:39:C:H5''	2.21	0.56
13:LG:180:PRO:HG3	13:LG:219:VAL:HG13	1.86	0.56
52:SF:36:GLN:NE2	52:SF:37:ASP:OD1	2.39	0.56
56:SQ:80:GLN:O	56:SQ:84:ILE:HG13	2.06	0.56
80:SY:80:ASP:OD1	80:SY:81:TYR:N	2.39	0.56
4:L5:1969:G:H4'	49:Ls:36:GLY:HA2	1.88	0.56
10:LD:232:THR:OG1	10:LD:234:ASP:OD1	2.19	0.56
22:LQ:15:ARG:NH1	22:LQ:52:PHE:O	2.37	0.56
70:SG:198:ARG:NH1	84:S2:126:G:OP2	2.38	0.56
71:SH:34:SER:OG	71:SH:78:ARG:NH2	2.37	0.56
86:CF:191:VAL:HG12	86:CF:193:ILE:HG23	1.87	0.56
10:LD:204:VAL:HB	10:LD:236:MET:HE1	1.87	0.56
24:LS:161:ARG:HD2	24:LS:164:LYS:HB2	1.87	0.56
38:Lg:45:ALA:HB3	38:Lg:82:MET:HE2	1.88	0.56
46:Lo:33:LEU:HA	46:Lo:38:LYS:HG2	1.88	0.56
64:Sf:97:LYS:NZ	84:S2:1289:U:OP2	2.37	0.56
80:SY:105:LYS:NZ	84:S2:507:G:O6	2.35	0.56
4:L5:3611:A:H2	4:L5:5016:A:H8	1.52	0.56
4:L5:5023:C:OP2	72:SI:124:LYS:NZ	2.39	0.56
63:Sd:19:ARG:NH2	84:S2:1661:A:OP1	2.38	0.56
65:Sg:129:ILE:HB	65:Sg:142:VAL:HB	1.87	0.56
4:L5:137:G:H2'	4:L5:138:G:H8	1.71	0.56
4:L5:1281:G:N1	11:LE:128:HIS:HB2	2.21	0.56
4:L5:1914:C:H4'	20:LO:89:PRO:HD3	1.87	0.56
4:L5:2318:G:N2	4:L5:2321:G:OP2	2.33	0.56
8:LB:17:LEU:O	8:LB:19:ARG:N	2.38	0.56
50:Lt:50:THR:OG1	50:Lt:72:GLU:OE1	2.23	0.56
74:SL:103:GLU:HG3	79:SX:11:ARG:HB2	1.86	0.56
2:Pt:18:G:O2'	2:Pt:57:G:N2	2.30	0.55
4:L5:1328:G:O2'	4:L5:2349:A:OP1	2.24	0.55
4:L5:2007:G:H21	4:L5:2012:A:N6	2.00	0.55
35:Ld:22:THR:HG23	35:Ld:122:VAL:HG13	1.87	0.55
56:SQ:100:VAL:HG22	56:SQ:101:ASP:H	1.71	0.55
71:SH:12:ASN:ND2	71:SH:14:GLU:OE2	2.40	0.55
75:SN:55:ARG:HD3	84:S2:1017:U:H5'	1.89	0.55
76:SO:34:PHE:HB3	76:SO:41:PHE:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:S2:1226:G:N1	84:S2:1639:G7M:OP2	2.30	0.55
86:CF:293:GLU:HG2	86:CF:298:ALA:HA	1.89	0.55
2:Pt:50:U:O2	2:Pt:64:G:N2	2.29	0.55
4:L5:4279:A:H5'	4:L5:4281:A:H1'	1.87	0.55
15:LI:85:PHE:HE2	15:LI:87:MET:HE2	1.69	0.55
50:Lt:117:ARG:HE	50:Lt:119:ARG:H	1.52	0.55
86:CF:428:ASP:HB3	86:CF:433:VAL:HG11	1.88	0.55
4:L5:184:U:H3	4:L5:253:G:H1	1.55	0.55
4:L5:1759:G:H1	4:L5:1773:U:H3	1.54	0.55
4:L5:2407:G:O6	43:Lt:2:SER:N	2.39	0.55
4:L5:4220:6MZ:H5'2	4:L5:4221:C:P	2.46	0.55
15:LI:152:LEU:HB3	15:LI:165:ILE:HD12	1.88	0.55
84:S2:543:C:H3'	84:S2:544:G:H8	1.71	0.55
84:S2:888:U:H4'	84:S2:889:U:H5'	1.88	0.55
4:L5:1100:U:O4	4:L5:1194:G:O6	2.24	0.55
4:L5:3717:A:H2'	4:L5:3718:A2M:C8	2.36	0.55
22:LQ:99:LYS:HZ2	22:LQ:121:LEU:HD11	1.72	0.55
69:SE:151:ASP:HA	70:SG:212:LEU:HD21	1.88	0.55
1:CI:50:MET:HG3	26:LU:114:TYR:CD2	2.42	0.55
4:L5:4163:U:OP2	13:LG:53:ARG:NH2	2.40	0.55
7:LA:229:ALA:HB3	7:LA:234:LYS:HB3	1.87	0.55
52:SF:171:GLU:OE2	61:SZ:106:GLN:NE2	2.36	0.55
58:SS:48:ALA:O	58:SS:66:ARG:NH2	2.40	0.55
84:S2:1513:C:H2'	84:S2:1514:G:H8	1.71	0.55
4:L5:1591:U:OP2	4:L5:2856:C:O2'	2.18	0.55
4:L5:4098:A:N1	4:L5:4112:C:N4	2.54	0.55
4:L5:4617:G:OP2	8:LB:358:ARG:NH2	2.39	0.55
32:La:87:ARG:HG3	32:La:120:GLN:HE22	1.72	0.55
60:SU:48:LEU:HG	60:SU:93:SER:HB3	1.88	0.55
63:Sd:17:GLY:O	63:Sd:27:ARG:NH1	2.40	0.55
77:SV:42:VAL:HG23	77:SV:43:THR:HG23	1.88	0.55
85:AT:4:U:H2'	85:AT:5:C:C6	2.42	0.55
4:L5:121:A:OP1	13:LG:110:LYS:NZ	2.31	0.55
4:L5:2745:A:H2'	4:L5:2746:A:C8	2.42	0.55
7:LA:101:VAL:HG22	7:LA:165:VAL:HG22	1.88	0.55
8:LB:219:VAL:HG11	8:LB:337:VAL:HG13	1.88	0.55
26:LU:23:LEU:HD23	26:LU:110:TYR:HB2	1.89	0.55
50:Lt:114:ARG:NH2	50:Lt:126:SER:OG	2.40	0.55
71:SH:111:LYS:HE3	84:S2:796:G:H21	1.72	0.55
86:CF:175:SER:HA	86:CF:178:ILE:HG22	1.87	0.55
4:L5:261:G:H2'	4:L5:262:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1726:U:H5'	12:LF:135:ILE:HD11	1.89	0.55
9:LC:262:GLU:HB3	9:LC:273:LEU:HD13	1.89	0.55
24:LS:173:ASN:ND2	24:LS:175:PHE:O	2.40	0.55
56:SQ:4:LYS:HE3	84:S2:1423:C:H41	1.72	0.55
65:Sg:89:LEU:HB3	65:Sg:99:ARG:HB3	1.88	0.55
72:SI:91:VAL:HG11	72:SI:205:ARG:HH12	1.72	0.55
72:SI:143:LYS:NZ	84:S2:202:G:OP1	2.40	0.55
76:SO:33:ILE:HB	76:SO:97:LEU:HD23	1.89	0.55
4:L5:1734:G:N2	4:L5:1735:U:O4	2.33	0.55
17:LL:91:ALA:HB1	17:LL:96:ILE:HB	1.89	0.55
28:LW:105:ARG:NH2	70:SG:149:LYS:O	2.40	0.55
54:SM:96:ARG:NH2	54:SM:100:PRO:O	2.40	0.55
66:SA:22:GLY:O	66:SA:24:HIS:ND1	2.39	0.55
68:SC:72:ASP:OD2	68:SC:272:HIS:NE2	2.39	0.55
84:S2:795:A:H2'	84:S2:796:G:C8	2.42	0.55
84:S2:1203:G:H2'	84:S2:1204:A:C8	2.41	0.55
4:L5:109:G:OP2	17:LL:74:ARG:NH2	2.35	0.55
4:L5:2845:A:H61	4:L5:3843:C:H42	1.53	0.55
58:SS:36:VAL:HG21	58:SS:71:MET:HE3	1.89	0.55
84:S2:553:U:O4	84:S2:554:A:N6	2.39	0.55
7:LA:118:GLU:OE2	7:LA:156:LYS:NZ	2.40	0.54
10:LD:260:GLU:OE1	10:LD:260:GLU:O	2.25	0.54
34:Lc:99:PRO:HG3	34:Lc:104:ILE:HB	1.89	0.54
56:SQ:130:LYS:NZ	56:SQ:131:LYS:O	2.40	0.54
67:SB:144:LYS:HD3	67:SB:208:HIS:HB3	1.88	0.54
84:S2:981:A:H2'	84:S2:982:G:C8	2.42	0.54
4:L5:305:A:OP2	19:LN:15:GLN:NE2	2.36	0.54
4:L5:1756:U:O2'	4:L5:1758:G:OP2	2.24	0.54
4:L5:2745:A:H2'	4:L5:2746:A:H8	1.73	0.54
4:L5:3910:C:H2'	4:L5:3911:C:C6	2.42	0.54
4:L5:4537:C:H2'	4:L5:4538:G:C8	2.41	0.54
7:LA:108:PRO:HB2	47:Lp:86:LEU:HD23	1.89	0.54
30:LY:4:ASN:HB3	30:LY:7:VAL:HG22	1.88	0.54
31:LZ:46:ILE:HA	31:LZ:70:SER:HA	1.88	0.54
49:Ls:110:ALA:HA	49:Ls:182:PRO:HG2	1.89	0.54
52:SF:40:ALA:HB3	52:SF:67:PRO:HA	1.88	0.54
56:SQ:3:SER:OG	56:SQ:4:LYS:N	2.40	0.54
59:ST:65:TYR:HE1	59:ST:128:GLN:HG3	1.72	0.54
65:Sg:258:ILE:HG23	65:Sg:267:VAL:HG23	1.89	0.54
66:SA:126:ASP:OD1	66:SA:165:ASN:ND2	2.39	0.54
71:SH:31:GLU:HA	71:SH:37:LYS:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:Sb:20:LYS:NZ	84:S2:1016:U:OP2	2.39	0.54
84:S2:889:U:OP2	84:S2:896:U:N3	2.40	0.54
4:L5:4571:A2M:H2'	4:L5:4572:U:H6	1.72	0.54
59:ST:62:ARG:NH2	84:S2:1543:U:OP2	2.35	0.54
80:SY:39:GLU:HA	80:SY:42:GLU:CD	2.32	0.54
84:S2:17:C:H2'	84:S2:18:C:C6	2.42	0.54
4:L5:702:U:H2'	4:L5:703:G:O4'	2.07	0.54
4:L5:1333:A:H2'	4:L5:1334:A:C8	2.42	0.54
4:L5:4363:A:H5''	46:Lo:36:GLN:HG2	1.88	0.54
38:Lg:44:SER:OG	38:Lg:46:CYS:SG	2.65	0.54
55:SP:31:GLU:HA	55:SP:34:MET:HE2	1.88	0.54
62:Sc:37:ASP:OD1	62:Sc:39:SER:OG	2.26	0.54
66:SA:18:PHE:HD1	66:SA:23:THR:HG21	1.71	0.54
4:L5:88:A:N7	22:LQ:173:LYS:NZ	2.55	0.54
4:L5:729:G:H5''	12:LF:76:ARG:HD2	1.90	0.54
4:L5:2495:U:H2'	4:L5:2496:G:C8	2.42	0.54
17:LL:64:VAL:HA	17:LL:67:HIS:CD2	2.31	0.54
34:Lc:38:ILE:HD11	34:Lc:46:VAL:HG21	1.90	0.54
50:Lt:82:ILE:HG12	50:Lt:137:GLN:HG2	1.89	0.54
53:SK:27:VAL:HB	53:SK:43:LEU:HD12	1.89	0.54
59:ST:2:PRO:HD2	84:S2:1419:C:H42	1.72	0.54
60:SU:68:THR:O	63:Sd:40:ARG:NH1	2.40	0.54
2:Pt:20(A):U:O4'	16:LJ:58:ARG:NH2	2.41	0.54
3:Et:28:C:H2'	3:Et:29:A:H8	1.73	0.54
4:L5:502:C:H3'	4:L5:503:C:H3'	1.89	0.54
6:L8:58:G:N7	41:Lj:63:ARG:NH2	2.44	0.54
13:LG:57:TRP:O	13:LG:62:ARG:NH1	2.41	0.54
39:Lh:80:PRO:HD2	39:Lh:83:LEU:HD12	1.89	0.54
42:Lk:24:LYS:HD3	42:Lk:69:LEU:HD21	1.90	0.54
66:SA:77:ILE:HG13	66:SA:99:ILE:HB	1.88	0.54
84:S2:851:C:H5''	84:S2:852:G:H5'	1.89	0.54
84:S2:1013:U:OP1	84:S2:1129:G:O2'	2.25	0.54
4:L5:223:G:OP2	9:LC:165:LYS:NZ	2.40	0.54
4:L5:691:C:H2'	4:L5:692:A:C8	2.42	0.54
4:L5:1837:A:OP2	25:LT:130:ARG:NH1	2.37	0.54
4:L5:1933:G:H2'	4:L5:1934:A:C8	2.43	0.54
75:SN:66:VAL:HG13	75:SN:67:THR:HG23	1.89	0.54
4:L5:907:C:H2'	4:L5:908:G:H8	1.73	0.54
21:LP:118:GLN:OE1	21:LP:120:ASN:ND2	2.41	0.54
57:SR:16:ILE:HD11	57:SR:54:VAL:HG21	1.89	0.54
84:S2:942:G:H2'	84:S2:943:U:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:CF:360:VAL:HA	86:CF:369:ALA:HA	1.88	0.54
1:CI:50:MET:HG3	26:LU:114:TYR:CE2	2.42	0.54
4:L5:497:G:H21	4:L5:498:C:H41	1.55	0.54
4:L5:654:C:H2'	4:L5:655:C:C6	2.43	0.54
18:LM:119:ARG:HG3	20:LO:189:ILE:HG23	1.89	0.54
21:LP:116:HIS:HB3	21:LP:149:ILE:HB	1.88	0.54
58:SS:109:GLU:HA	58:SS:112:GLU:HG2	1.90	0.54
59:ST:121:ARG:HH21	84:S2:1563:G:H5''	1.72	0.54
79:SX:70:VAL:HG11	79:SX:94:ILE:HG21	1.88	0.54
83:Se:58:ASN:ND2	84:S2:608:C:O4'	2.40	0.54
1:CI:79:ARG:HH22	4:L5:2708:U:H1'	1.72	0.54
4:L5:4260:U:H2'	4:L5:4261:C:C6	2.43	0.54
4:L5:4717:A:OP2	8:LB:30:LYS:NZ	2.30	0.54
4:L5:4967:A:H2'	4:L5:4968:A:C8	2.42	0.54
16:LJ:84:GLU:OE2	16:LJ:92:TYR:OH	2.25	0.54
52:SF:39:ILE:HG23	52:SF:68:ILE:HD13	1.89	0.54
61:SZ:106:GLN:HG3	61:SZ:108:ILE:HD11	1.88	0.54
64:Sf:110:GLU:HG2	64:Sf:113:LYS:HD3	1.90	0.54
69:SE:125:LYS:O	69:SE:142:HIS:N	2.40	0.54
84:S2:928:G:H1	84:S2:1013:U:H3	1.56	0.54
37:Lf:43:LEU:O	37:Lf:109:ARG:NH2	2.41	0.53
65:Sg:8:ARG:HB3	65:Sg:309:VAL:HG13	1.90	0.53
70:SG:7:PHE:HD1	70:SG:113:ILE:HB	1.73	0.53
74:SL:128:VAL:HG12	74:SL:142:VAL:HA	1.89	0.53
82:Sb:62:VAL:HG23	82:Sb:74:THR:HG21	1.90	0.53
30:LY:2:LYS:HD2	30:LY:7:VAL:HG23	1.88	0.53
71:SH:10:LYS:NZ	71:SH:16:PRO:O	2.41	0.53
84:S2:557:U:H2'	84:S2:558:G:C8	2.43	0.53
2:Pt:38:C:O2'	84:S2:1058:A:OP1	2.26	0.53
4:L5:4694:G:H4'	14:LH:71:ARG:HH12	1.73	0.53
19:LN:146:PRO:HB2	39:Lh:104:THR:HG23	1.91	0.53
41:Lj:2:THR:HB	41:Lj:6:SER:HB2	1.90	0.53
51:SD:161:GLY:HA3	84:S2:1388:A:H61	1.74	0.53
58:SS:88:LYS:H	58:SS:95:TYR:HD1	1.56	0.53
65:Sg:18:VAL:O	65:Sg:287:THR:OG1	2.27	0.53
66:SA:37:TYR:OH	66:SA:57:LYS:NZ	2.38	0.53
84:S2:1610:G:O6	84:S2:1630:A:N6	2.41	0.53
86:CF:413:GLU:CD	86:CF:421:LEU:HD13	2.33	0.53
4:L5:735:G:H5''	18:LM:70:GLN:HG3	1.90	0.53
4:L5:1241:C:O2'	33:Lb:120:ARG:O	2.27	0.53
4:L5:2486:G:O6	4:L5:2493:G:O6	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4941:G:OP2	11:LE:188:ARG:NH2	2.33	0.53
27:LV:92:ASP:O	28:LW:2:LYS:NZ	2.41	0.53
52:SF:30:ILE:HG23	52:SF:117:ILE:HD11	1.90	0.53
56:SQ:131:LYS:HB2	56:SQ:140:ARG:HH22	1.74	0.53
75:SN:70:LYS:NZ	84:S2:1020:A:N7	2.55	0.53
78:SW:111:MET:HE1	78:SW:119:LYS:HD2	1.90	0.53
84:S2:118:C:H1'	84:S2:445:A:C5	2.44	0.53
84:S2:1606:G:N2	84:S2:1632:G:H1'	2.23	0.53
85:AT:21:U:C4	85:AT:47:G:H1'	2.43	0.53
4:L5:4274:A:H2'	4:L5:4275:G:C8	2.43	0.53
51:SD:138:VAL:HG13	51:SD:182:LEU:HD21	1.91	0.53
63:Sd:2:GLY:N	84:S2:1271:C:O2	2.41	0.53
66:SA:10:MET:HE3	66:SA:55:TRP:HB2	1.89	0.53
70:SG:136:LYS:NZ	70:SG:175:LYS:O	2.33	0.53
86:CF:7:HIS:CE1	86:CF:306:ASP:HA	2.44	0.53
4:L5:364:G:O6	41:Lj:55:ARG:NH2	2.42	0.53
4:L5:1994:C:H2'	4:L5:1995:G:H8	1.73	0.53
4:L5:4601:U:H2'	4:L5:4602:A:H8	1.74	0.53
12:LF:96:ARG:HH12	12:LF:224:THR:HG22	1.73	0.53
49:Ls:29:ILE:HG22	49:Ls:88:PHE:HD1	1.72	0.53
55:SP:56:LEU:HD22	55:SP:80:LEU:HD11	1.90	0.53
68:SC:102:LEU:HD22	68:SC:130:ILE:HD12	1.89	0.53
82:Sb:34:ASP:O	82:Sb:79:PHE:HA	2.08	0.53
4:L5:4620:OMU:OP2	4:L5:4670:C:N4	2.34	0.53
20:LO:54:TYR:OH	20:LO:73:PHE:O	2.26	0.53
20:LO:168:TYR:CE2	20:LO:172:LYS:HD2	2.44	0.53
20:LO:186:GLU:OE1	20:LO:186:GLU:N	2.41	0.53
66:SA:106:GLY:N	66:SA:136:GLU:OE2	2.34	0.53
70:SG:13:GLN:NE2	84:S2:153:G:N3	2.57	0.53
76:SO:145:GLY:O	81:Sa:22:ARG:NH2	2.42	0.53
84:S2:1773:C:H2'	84:S2:1774:C:H5''	1.91	0.53
10:LD:156:GLY:HA2	10:LD:181:PRO:HG3	1.91	0.53
53:SK:55:ARG:NH1	53:SK:78:TYR:OH	2.41	0.53
72:SI:10:LYS:O	72:SI:18:ARG:NH1	2.41	0.53
80:SY:119:GLY:HA2	84:S2:85:A:H5'	1.90	0.53
4:L5:2756:G:O6	31:LZ:51:ARG:NH2	2.29	0.53
48:Lr:38:PHE:O	48:Lr:45:HIS:NE2	2.32	0.53
58:SS:15:VAL:HG12	58:SS:16:LEU:HG	1.91	0.53
64:Sf:102:VAL:HG22	64:Sf:104:LYS:HG2	1.90	0.53
84:S2:455:A:H2'	84:S2:456:C:H6	1.74	0.53
84:S2:1581:C:H5'	84:S2:1582:C:H5	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LU:36:ALA:HB1	26:LU:70:ILE:HD11	1.90	0.53
28:LW:123:LYS:HD2	84:S2:320:G:H5''	1.90	0.53
71:SH:20:GLU:HG2	71:SH:48:ALA:HB3	1.90	0.53
74:SL:61:PRO:HG3	74:SL:141:ASN:HB3	1.91	0.53
74:SL:133:PRO:O	84:S2:383:G:O2'	2.25	0.53
75:SN:64:ARG:NH2	84:S2:919:A:OP2	2.40	0.53
84:S2:1130:G:OP2	84:S2:1130:G:N2	2.32	0.53
86:CF:272:LEU:HB3	86:CF:302:ALA:HB3	1.90	0.53
4:L5:268:G:H2'	4:L5:269:G:H8	1.74	0.52
4:L5:3911:C:H2'	4:L5:3912:U:H6	1.73	0.52
16:LJ:104:ASN:HD22	16:LJ:133:VAL:HG13	1.73	0.52
37:Lf:78:HIS:HB3	37:Lf:83:MET:HB3	1.91	0.52
40:Li:55:ARG:O	40:Li:59:GLU:HG2	2.09	0.52
56:SQ:42:ILE:HG23	56:SQ:44:PRO:HD2	1.91	0.52
59:ST:11:GLN:HB2	84:S2:1542:C:H4'	1.92	0.52
60:SU:40:ILE:O	60:SU:44:LYS:HG2	2.08	0.52
69:SE:126:VAL:HA	69:SE:141:THR:HA	1.91	0.52
78:SW:6:VAL:HG13	78:SW:29:PRO:HB2	1.90	0.52
84:S2:367:U:H4'	84:S2:371:A:C8	2.44	0.52
86:CF:30:LYS:HE3	86:CF:201:MET:CB	2.39	0.52
4:L5:71:C:H1'	17:LL:62:PRO:O	2.10	0.52
4:L5:93:G:H2'	4:L5:94:A:C8	2.45	0.52
4:L5:1258:G:H2'	4:L5:1259:G:C8	2.44	0.52
4:L5:1509:C:H5''	32:La:2:PRO:HD3	1.91	0.52
4:L5:3898:G:H5'	8:LB:254:ILE:HG13	1.91	0.52
4:L5:4220:6MZ:O5'	4:L5:4220:6MZ:H8	2.10	0.52
4:L5:5016:A:C2	4:L5:5033:G:N2	2.73	0.52
6:L8:21:C:OP1	9:LC:195:LYS:NZ	2.40	0.52
9:LC:293:LEU:O	9:LC:299:GLN:NE2	2.40	0.52
30:LY:76:LYS:HE2	43:Ll:31:THR:HB	1.90	0.52
68:SC:77:SER:OG	68:SC:79:GLU:OE1	2.27	0.52
68:SC:207:ALA:HB2	84:S2:4:C:H4'	1.92	0.52
79:SX:48:LYS:HB3	79:SX:75:ILE:HD12	1.90	0.52
84:S2:1748:G:O6	84:S2:1786:U:O4	2.27	0.52
4:L5:1718:C:O2'	12:LF:181:LYS:NZ	2.42	0.52
4:L5:2084:C:O2	22:LQ:16:LYS:NZ	2.42	0.52
4:L5:3732:A:H2'	4:L5:3733:A:H8	1.74	0.52
8:LB:57:VAL:HG22	8:LB:73:VAL:HG22	1.91	0.52
62:Sc:66:ARG:HH12	62:Sc:68:LEU:HD23	1.74	0.52
65:Sg:249:CYS:HB3	65:Sg:258:ILE:HD13	1.91	0.52
71:SH:165:ASN:O	71:SH:169:LYS:NZ	2.32	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:SX:139:GLU:HG2	86:CF:444:LYS:NZ	2.25	0.52
4:L5:2624:G:OP2	26:LU:97:ARG:NH2	2.42	0.52
53:SK:3:MET:HE1	53:SK:11:ILE:HD12	1.90	0.52
65:Sg:40:ILE:HB	65:Sg:59:LEU:HB2	1.91	0.52
3:Et:32:C:H5'	52:SF:134:VAL:HG13	1.92	0.52
4:L5:97:G:OP1	17:LL:16:LYS:NZ	2.36	0.52
4:L5:4219:A:H2'	4:L5:4220:6MZ:C8	2.40	0.52
4:L5:4478:G:O2'	4:L5:4602:A:N1	2.42	0.52
20:LO:10:ASP:OD2	20:LO:37:ARG:NH2	2.43	0.52
56:SQ:89:SER:OG	56:SQ:119:LEU:O	2.25	0.52
66:SA:85:ARG:NH1	66:SA:203:PHE:O	2.41	0.52
71:SH:51:ILE:HG21	71:SH:179:LYS:HG2	1.91	0.52
84:S2:1777:G:H2'	84:S2:1778:C:H6	1.73	0.52
4:L5:267:G:H2'	4:L5:268:G:H8	1.74	0.52
4:L5:1214:C:N3	33:Lb:90:SER:OG	2.42	0.52
28:LW:7:SER:OG	28:LW:8:PHE:N	2.43	0.52
54:SM:82:ASN:OD1	54:SM:83:LYS:N	2.43	0.52
55:SP:79:HIS:HD2	84:S2:1298:G:C4	2.28	0.52
67:SB:32:ASP:OD1	67:SB:46:LYS:NZ	2.37	0.52
84:S2:672:A:N6	84:S2:1027:A:OP1	2.40	0.52
84:S2:902:G:O2'	84:S2:903:A:O4'	2.28	0.52
84:S2:1801:A:H2'	84:S2:1802:C:C6	2.45	0.52
4:L5:418:A:C2	6:L8:17:A:H1'	2.45	0.52
56:SQ:140:ARG:HB2	84:S2:1644:C:H4'	1.91	0.52
67:SB:26:SER:O	67:SB:51:ARG:NH2	2.43	0.52
84:S2:525:A:H2'	84:S2:526:A:H8	1.74	0.52
84:S2:1588:A:H2'	84:S2:1589:A:C8	2.45	0.52
4:L5:303:C:OP2	19:LN:68:ARG:NH2	2.42	0.52
33:Lb:102:PRO:O	33:Lb:109:ARG:NH2	2.42	0.52
52:SF:60:ARG:HD2	84:S2:1679:A:H2'	1.92	0.52
84:S2:28:U:H2'	84:S2:29:G:H8	1.75	0.52
84:S2:1405:A:H2'	84:S2:1406:G:O4'	2.10	0.52
6:L8:39:G:OP1	39:Lh:86:LYS:NZ	2.43	0.52
10:LD:291:GLN:NE2	15:LI:213:HIS:O	2.33	0.52
49:Ls:13:TYR:O	49:Ls:17:ILE:HG12	2.10	0.52
69:SE:31:PRO:HA	69:SE:81:THR:HB	1.92	0.52
82:Sb:11:SER:N	82:Sb:14:GLU:OE2	2.43	0.52
4:L5:4967:A:H2'	4:L5:4968:A:H8	1.74	0.52
9:LC:218:ILE:HA	9:LC:229:LEU:HD22	1.91	0.52
12:LF:41:MET:HE2	33:Lb:113:ALA:HB2	1.91	0.52
52:SF:78:MET:HE3	84:S2:1222:G:H5''	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:Sf:103:LEU:HB2	64:Sf:105:TYR:CE2	2.44	0.52
68:SC:191:VAL:HG11	68:SC:236:PHE:HA	1.92	0.52
84:S2:604:A:N3	84:S2:639:C:O2'	2.40	0.52
84:S2:1845:A:H2'	84:S2:1846:G:C8	2.45	0.52
4:L5:1646:A:O2'	41:Lj:49:TRP:O	2.23	0.51
4:L5:2568:C:H2'	4:L5:2569:G:H8	1.74	0.51
50:Lt:117:ARG:HG3	50:Lt:119:ARG:HG3	1.92	0.51
60:SU:96:GLU:OE1	60:SU:99:LYS:N	2.36	0.51
71:SH:162:GLN:HE22	71:SH:166:VAL:HB	1.74	0.51
80:SY:108:LYS:NZ	84:S2:506:G:OP1	2.36	0.51
81:Sa:41:ILE:HD12	81:Sa:68:TYR:HD2	1.75	0.51
66:SA:76:VAL:HG12	66:SA:123:VAL:HB	1.91	0.51
70:SG:191:ARG:HH12	84:S2:312:G:H2'	1.75	0.51
78:SW:6:VAL:HG12	78:SW:34:ILE:HD11	1.93	0.51
84:S2:1010:G:H2'	84:S2:1011:A:C8	2.45	0.51
11:LE:223:ARG:HH22	11:LE:238:GLU:HG3	1.75	0.51
55:SP:37:TYR:O	58:SS:88:LYS:NZ	2.43	0.51
79:SX:124:LYS:NZ	84:S2:29:G:OP1	2.40	0.51
84:S2:57:U:OP1	84:S2:504:G:O2'	2.29	0.51
4:L5:1268:G:N7	33:Lb:111:ARG:NH2	2.52	0.51
4:L5:1270:A:H8	4:L5:2106:G:H21	1.57	0.51
4:L5:1961:G:O2'	4:L5:2025:A:N6	2.44	0.51
4:L5:3664:G:H2'	4:L5:3665:G:H8	1.75	0.51
8:LB:288:GLY:HA3	8:LB:330:PHE:CE1	2.46	0.51
11:LE:264:ILE:HD11	11:LE:267:LEU:HD22	1.93	0.51
17:LL:7:GLY:O	32:La:49:HIS:NE2	2.39	0.51
68:SC:60:TRP:O	68:SC:71:LYS:NZ	2.37	0.51
70:SG:20:ASP:HB3	70:SG:23:LYS:HB2	1.91	0.51
84:S2:964:A:H2'	84:S2:965:U:H6	1.76	0.51
86:CF:294:MET:HE2	86:CF:299:LEU:HD21	1.92	0.51
4:L5:173:C:OP1	17:LL:129:ARG:NH1	2.44	0.51
4:L5:351:C:OP2	9:LC:197:ARG:NH1	2.33	0.51
4:L5:500:G:N2	4:L5:504:G:O2'	2.37	0.51
4:L5:5064:G:N2	21:LP:75:GLN:HE22	2.09	0.51
74:SL:3:ASP:OD1	74:SL:4:ILE:N	2.43	0.51
86:CF:347:LEU:O	86:CF:396:SER:OG	2.29	0.51
3:Et:23:A:H2'	3:Et:24:G:C8	2.45	0.51
4:L5:308:G:OP2	4:L5:308:G:N2	2.35	0.51
4:L5:2809:G:O2'	4:L5:4644:G:OP1	2.26	0.51
4:L5:4239:A:H2'	4:L5:4240:G:C8	2.45	0.51
4:L5:4612:C:C2	14:LH:120:GLU:HB2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LR:92:LYS:HG2	23:LR:96:MET:HE3	1.93	0.51
49:Ls:29:ILE:HG22	49:Ls:88:PHE:CD1	2.45	0.51
78:SW:111:MET:HE3	78:SW:116:ALA:HA	1.93	0.51
84:S2:17:C:O2'	84:S2:1194:A:N1	2.38	0.51
4:L5:1655:C:OP2	32:La:26:ARG:NH1	2.44	0.51
4:L5:2517:A:H5'	38:Lg:62:LYS:HD3	1.92	0.51
9:LC:141:GLY:O	9:LC:204:ARG:NH1	2.33	0.51
50:Lt:85:LEU:HD13	50:Lt:109:ILE:HD12	1.91	0.51
67:SB:40:ASN:HD21	67:SB:76:ASN:HB2	1.76	0.51
73:SJ:136:ARG:NH1	73:SJ:159:PHE:O	2.40	0.51
82:Sb:67:THR:OG1	82:Sb:70:LYS:O	2.20	0.51
84:S2:1589:A:N3	84:S2:1653:U:O2'	2.43	0.51
4:L5:1332:C:H2'	4:L5:1333:A:C8	2.45	0.51
4:L5:1411:C:H2'	4:L5:1412:G:C8	2.46	0.51
4:L5:1548:G:O2'	4:L5:2812:A:N3	2.38	0.51
4:L5:2492:C:H2'	4:L5:2493:G:H8	1.76	0.51
4:L5:3823:G:OP2	4:L5:3823:G:N2	2.37	0.51
4:L5:4459:U:H2'	4:L5:4460:U:C6	2.45	0.51
16:LJ:22:LEU:HD22	16:LJ:128:LEU:HD12	1.93	0.51
52:SF:141:VAL:HG12	62:Sc:47:LYS:HG2	1.91	0.51
65:Sg:57:ARG:HE	65:Sg:95:GLY:HA3	1.76	0.51
68:SC:85:SER:OG	77:SV:25:GLY:O	2.28	0.51
70:SG:3:LEU:HD23	70:SG:109:LEU:HB3	1.92	0.51
72:SI:45:THR:HG23	72:SI:53:LYS:HG3	1.93	0.51
84:S2:107:A:H2'	84:S2:108:G:C8	2.46	0.51
86:CF:185:PRO:HA	86:CF:188:VAL:HB	1.92	0.51
4:L5:3760:A:C8	85:AT:39:C:H5''	2.46	0.51
63:Sd:12:ARG:NH1	84:S2:1513:C:OP1	2.31	0.51
69:SE:204:SER:OG	69:SE:205:PHE:N	2.39	0.51
84:S2:145:G:H2'	84:S2:146:G:C8	2.45	0.51
84:S2:149:A:H3'	84:S2:150:A:H8	1.75	0.51
4:L5:1683:PSU:OP1	32:La:44:ASN:ND2	2.42	0.51
4:L5:1867:A:H2'	4:L5:1868:A:C8	2.46	0.51
4:L5:3659:G:OP1	7:LA:241:ARG:NH1	2.44	0.51
4:L5:4636:PSU:N1	35:Ld:79:ASN:OD1	2.43	0.51
9:LC:154:VAL:HG11	9:LC:174:LEU:HD11	1.93	0.51
20:LO:197:LYS:NZ	20:LO:203:VAL:O	2.43	0.51
53:SK:85:LEU:HD12	53:SK:86:PRO:HD2	1.92	0.51
68:SC:196:ILE:HB	68:SC:223:TYR:HB2	1.92	0.51
70:SG:190:ARG:NH2	84:S2:334:C:OP2	2.39	0.51
4:L5:3707:U:H2'	4:L5:3708:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:3910:C:H2'	4:L5:3911:C:H6	1.76	0.50
49:Ls:99:ARG:HG3	49:Ls:103:LEU:HD13	1.93	0.50
58:SS:14:ARG:HH11	58:SS:19:ASN:HB3	1.76	0.50
86:CF:142:THR:HG23	86:CF:435:VAL:HG13	1.92	0.50
1:CI:78:HIS:NE2	4:L5:2706:G:C8	2.75	0.50
2:Pt:3:C:H42	2:Pt:70:A:H61	1.57	0.50
4:L5:2102:G:H1'	4:L5:2103:G:C8	2.46	0.50
4:L5:3796:U:HO2'	84:S2:1720:U:HO2'	1.53	0.50
8:LB:378:ARG:HE	28:LW:32:LEU:HD21	1.75	0.50
10:LD:182:GLY:HA2	10:LD:194:VAL:HG23	1.93	0.50
15:LI:207:ASP:OD1	15:LI:210:ARG:NH1	2.43	0.50
16:LJ:38:LYS:HD2	16:LJ:123:ILE:HD11	1.94	0.50
61:SZ:41:ARG:HH12	61:SZ:44:LEU:HG	1.76	0.50
71:SH:10:LYS:HE3	71:SH:17:ASP:HB3	1.94	0.50
80:SY:119:GLY:O	84:S2:84:A:O2'	2.26	0.50
4:L5:1070:G:O2'	4:L5:1071:C:O5'	2.27	0.50
4:L5:2835:A:O2'	8:LB:228:TYR:O	2.25	0.50
11:LE:141:ARG:NH2	37:Lf:110:ILE:O	2.44	0.50
84:S2:1033:G:N1	84:S2:1080:A:O2'	2.39	0.50
84:S2:1421:A:H5''	84:S2:1422:G:H2'	1.92	0.50
4:L5:10:A:H2'	4:L5:11:G:C8	2.47	0.50
4:L5:369:G:N2	4:L5:372:A:OP2	2.40	0.50
4:L5:1390:G:N2	4:L5:1393:G:OP2	2.39	0.50
4:L5:1438:U:H4'	12:LF:31:LYS:HE3	1.93	0.50
4:L5:1628:C:OP1	7:LA:14:SER:OG	2.29	0.50
20:LO:141:LEU:O	20:LO:145:VAL:HG12	2.11	0.50
27:LV:87:SER:OG	28:LW:19:ARG:NH1	2.44	0.50
35:Ld:59:THR:OG1	35:Ld:104:THR:OG1	2.26	0.50
52:SF:22:LYS:HG3	52:SF:23:TRP:CD2	2.46	0.50
4:L5:433:A:C2	4:L5:3867:A2M:H4'	2.46	0.50
4:L5:2764:A:H2'	4:L5:2765:A:H8	1.76	0.50
4:L5:3641:U:H5	4:L5:3646:A:N7	2.09	0.50
4:L5:4457:PSU:H1'	8:LB:252:ALA:HB3	1.93	0.50
31:LZ:50:PRO:HD3	31:LZ:68:ILE:HG12	1.94	0.50
60:SU:79:ARG:NH2	84:S2:1669:G:OP1	2.41	0.50
66:SA:137:ALA:HB1	66:SA:142:LEU:HB3	1.94	0.50
72:SI:141:ARG:HD3	72:SI:145:ILE:HG21	1.93	0.50
84:S2:49:C:H2'	84:S2:472:C:H41	1.75	0.50
84:S2:482:G:N1	84:S2:485:A:OP2	2.38	0.50
85:AT:23:U:H2'	85:AT:24:C:C6	2.46	0.50
3:Et:9:A:O2'	3:Et:45:G:N3	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:325:U:H2'	4:L5:326:C:C6	2.46	0.50
4:L5:717:U:H2'	4:L5:718:C:C6	2.46	0.50
4:L5:1480:C:O2'	4:L5:1482:G:OP2	2.30	0.50
4:L5:1802:A:H5''	4:L5:1803:G:H5'	1.94	0.50
4:L5:4188:U:H2'	4:L5:4189:U:C6	2.47	0.50
17:LL:111:GLN:O	17:LL:115:GLN:HG2	2.12	0.50
28:LW:100:VAL:O	28:LW:104:GLN:NE2	2.45	0.50
68:SC:78:LEU:HD12	68:SC:81:ILE:HD12	1.94	0.50
76:SO:45:THR:HA	76:SO:52:THR:HA	1.94	0.50
84:S2:1562:C:H2'	84:S2:1563:G:H8	1.75	0.50
4:L5:387:G:O2'	4:L5:412:G:N1	2.36	0.50
4:L5:1320:U:O2'	4:L5:1891:A:N1	2.44	0.50
4:L5:2018:C:H2'	4:L5:2019:C:C6	2.47	0.50
4:L5:2539:C:H2'	4:L5:2540:C:C6	2.47	0.50
4:L5:3720:G:H22	4:L5:3733:A:H2	1.58	0.50
4:L5:4347:G:H2'	4:L5:4348:A:C8	2.46	0.50
12:LF:171:ASP:OD1	12:LF:172:ASN:N	2.45	0.50
24:LS:27:LEU:HB3	25:LT:148:PRO:HB3	1.93	0.50
28:LW:2:LYS:HE3	28:LW:15:PRO:HB3	1.93	0.50
65:Sg:239:LEU:HD11	65:Sg:248:LEU:HD21	1.94	0.50
68:SC:121:ARG:NH1	68:SC:123:ARG:HE	2.10	0.50
68:SC:183:LYS:HA	68:SC:195:LEU:O	2.11	0.50
70:SG:135:PRO:HA	84:S2:169:U:H5''	1.93	0.50
85:AT:51:U:H2'	85:AT:52:C:C6	2.47	0.50
4:L5:1503:A:H4'	4:L5:1504:G:H5'	1.94	0.50
4:L5:1743:A:N1	4:L5:1789:C:O2'	2.42	0.50
4:L5:3619:G:H22	4:L5:3624:A:H1'	1.75	0.50
4:L5:4591:U:H2'	4:L5:4592:C:C6	2.47	0.50
4:L5:4633:G:N2	4:L5:4664:A:N7	2.59	0.50
4:L5:4699:U:H1'	4:L5:4700:A:H5''	1.93	0.50
8:LB:147:GLU:OE2	8:LB:198:ARG:NH2	2.32	0.50
14:LH:107:GLU:N	14:LH:107:GLU:OE1	2.45	0.50
78:SW:44:HIS:NE2	78:SW:112:ASP:OD2	2.41	0.50
80:SY:51:THR:OG1	80:SY:53:ASP:OD1	2.23	0.50
84:S2:1277:C:H2'	84:S2:1278:A:C8	2.46	0.50
86:CF:248:LEU:HB2	86:CF:326:ALA:HB3	1.94	0.50
4:L5:4896:G:H2'	4:L5:4897:G:C8	2.47	0.50
23:LR:127:VAL:HG12	23:LR:132:PHE:HD2	1.76	0.50
58:SS:46:ARG:NH1	59:ST:50:GLU:OE2	2.45	0.50
69:SE:247:THR:N	69:SE:250:GLU:OE2	2.41	0.50
73:SJ:38:ARG:N	73:SJ:42:GLU:OE2	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:S2:455:A:H2'	84:S2:456:C:C6	2.46	0.50
4:L5:4225:G:OP1	15:LI:24:ARG:NH2	2.37	0.49
8:LB:50:LYS:HB2	8:LB:345:LEU:HD11	1.94	0.49
58:SS:28:PHE:O	58:SS:31:THR:OG1	2.26	0.49
66:SA:184:ARG:HE	66:SA:191:ARG:HA	1.77	0.49
67:SB:167:LYS:O	67:SB:171:ILE:HG12	2.11	0.49
84:S2:1288:OMU:HN3	84:S2:1311:C:H42	1.60	0.49
86:CF:282:PRO:HG2	86:CF:324:ASN:HD22	1.75	0.49
4:L5:1307:A:H2'	4:L5:1308:C:C6	2.47	0.49
4:L5:1617:G:H1'	4:L5:2513:A:N6	2.26	0.49
4:L5:2577:C:OP1	31:LZ:111:ARG:NH2	2.45	0.49
4:L5:3697:U:H5''	4:L5:3698:G:H5'	1.93	0.49
4:L5:4966:A:H5''	8:LB:128:LYS:HG3	1.93	0.49
7:LA:181:LYS:HB2	7:LA:184:ARG:HG3	1.94	0.49
8:LB:394:LYS:HA	8:LB:397:ILE:HG12	1.94	0.49
10:LD:217:ASP:N	10:LD:217:ASP:OD1	2.41	0.49
49:Ls:143:ILE:HD12	49:Ls:158:VAL:HG11	1.94	0.49
59:ST:44:GLU:HG3	59:ST:45:LEU:HD12	1.94	0.49
59:ST:60:THR:HG22	59:ST:75:MET:HE2	1.94	0.49
66:SA:128:ARG:NH2	66:SA:151:ASP:O	2.44	0.49
71:SH:140:VAL:HG12	75:SN:19:ARG:HD3	1.94	0.49
84:S2:159:A2M:O5'	84:S2:159:A2M:H8	2.12	0.49
4:L5:1662:C:H2'	4:L5:1663:C:C6	2.47	0.49
4:L5:2300:A:N7	9:LC:143:ARG:NH1	2.61	0.49
4:L5:2588:C:OP1	4:L5:2768:C:O2'	2.26	0.49
50:Lt:76:SER:OG	50:Lt:116:MET:SD	2.69	0.49
71:SH:63:PHE:HA	71:SH:95:ILE:O	2.12	0.49
81:Sa:41:ILE:HD12	81:Sa:68:TYR:CD2	2.46	0.49
84:S2:1720:U:H5''	84:S2:1721:U:H5''	1.94	0.49
4:L5:1516:G:O2'	17:LL:18:TRP:NE1	2.45	0.49
4:L5:1697:G:H22	4:L5:2084:C:P	2.36	0.49
4:L5:3615:G:H1'	28:LW:44:ARG:HD3	1.94	0.49
8:LB:153:MET:HB3	8:LB:194:LEU:HD11	1.94	0.49
8:LB:217:ILE:HD12	8:LB:347:LEU:HB3	1.95	0.49
19:LN:46:ASP:OD1	19:LN:47:LYS:N	2.45	0.49
52:SF:60:ARG:NH2	84:S2:1679:A:OP1	2.44	0.49
53:SK:64:TRP:HB3	63:Sd:23:VAL:HA	1.95	0.49
59:ST:74:SER:O	59:ST:78:ILE:HD12	2.12	0.49
61:SZ:42:ASP:OD1	61:SZ:42:ASP:N	2.43	0.49
64:Sf:95:ARG:HH12	84:S2:1291:A:H62	1.59	0.49
84:S2:960:U:O2'	84:S2:962:A:N7	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:280:G:H5''	19:LN:14:LYS:HE2	1.93	0.49
4:L5:2284:G:OP1	32:La:7:LYS:NZ	2.41	0.49
4:L5:2739:C:O2	7:LA:188:LYS:NZ	2.43	0.49
4:L5:3732:A:H2'	4:L5:3733:A:C8	2.47	0.49
4:L5:3880:G:H2'	4:L5:3881:G:C8	2.47	0.49
4:L5:4305:G:N7	25:LT:87:LYS:NZ	2.52	0.49
4:L5:4769:G:H5''	20:LO:176:ARG:HD3	1.95	0.49
12:LF:237:GLU:HG2	24:LS:38:VAL:HG22	1.94	0.49
14:LH:48:LEU:HD21	14:LH:56:ARG:HB2	1.93	0.49
47:Lp:75:SER:O	47:Lp:79:VAL:HG23	2.13	0.49
54:SM:49:LEU:HD21	54:SM:123:VAL:HG11	1.94	0.49
57:SR:32:LYS:NZ	84:S2:1452:A:OP2	2.45	0.49
71:SH:87:PHE:HB3	71:SH:90:LYS:HD2	1.95	0.49
81:Sa:8:ASN:ND2	84:S2:1861:G:OP1	2.42	0.49
84:S2:793:G:H2'	84:S2:794:A:H8	1.78	0.49
84:S2:1098:C:H2'	84:S2:1099:G:C8	2.47	0.49
84:S2:1528:G:O2'	84:S2:1666:C:OP1	2.30	0.49
85:AT:8:U:O2'	85:AT:21:U:N3	2.42	0.49
86:CF:82:THR:HG21	86:CF:232:LEU:HD22	1.95	0.49
4:L5:512:U:H3	4:L5:647:G:H1	1.60	0.49
4:L5:1500:A:H5''	4:L5:1501:C:H5''	1.95	0.49
4:L5:2411:C:H2'	4:L5:2412:A:C8	2.47	0.49
4:L5:2491:C:H2'	4:L5:2492:C:C6	2.47	0.49
36:Le:108:ARG:HD2	36:Le:128:ARG:HB2	1.93	0.49
66:SA:134:LEU:HD21	66:SA:144:THR:HG21	1.95	0.49
70:SG:170:ARG:HG3	84:S2:72:C:N3	2.27	0.49
71:SH:126:HIS:CE1	71:SH:181:THR:HG23	2.48	0.49
79:SX:28:LYS:HE2	79:SX:32:LEU:HD22	1.93	0.49
1:CI:78:HIS:CD2	4:L5:2706:G:N7	2.80	0.49
4:L5:121:A:H62	4:L5:152:U:H3	1.61	0.49
4:L5:148:C:OP2	13:LG:197:LYS:NZ	2.42	0.49
4:L5:1283:G:N1	4:L5:2076:G:OP1	2.32	0.49
11:LE:190:HIS:HB3	11:LE:193:PHE:HD2	1.78	0.49
14:LH:41:ILE:HG22	14:LH:43:VAL:HG13	1.94	0.49
35:Ld:23:ARG:HG2	35:Ld:121:ASN:HA	1.95	0.49
52:SF:161:ALA:O	52:SF:165:ASN:ND2	2.39	0.49
58:SS:132:ARG:NH1	84:S2:1623:A:N1	2.60	0.49
78:SW:3:ARG:HH22	78:SW:28:ARG:HH21	1.60	0.49
80:SY:7:ILE:HG12	80:SY:43:LYS:HD3	1.94	0.49
84:S2:84:A:N3	84:S2:150:A:O2'	2.45	0.49
85:AT:10:G:H2'	85:AT:11:U:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:AT:12:G:H2'	85:AT:13:U:O4'	2.13	0.49
3:Et:55:U:H2'	3:Et:57:A:N7	2.28	0.49
4:L5:417:G:OP1	4:L5:2329:U:O2'	2.26	0.49
4:L5:1985:G:N2	4:L5:2003:G:O2'	2.46	0.49
4:L5:2049:G:HO2'	4:L5:3884:PSU:HO2'	1.54	0.49
4:L5:2298:U:OP1	9:LC:204:ARG:NE	2.45	0.49
4:L5:2744:A:H2'	4:L5:2745:A:C8	2.47	0.49
4:L5:4769:G:OP1	20:LO:176:ARG:NH1	2.42	0.49
4:L5:4774:C:O2'	4:L5:4775:C:O2	2.25	0.49
4:L5:4940:C:O2'	11:LE:246:ARG:NH2	2.45	0.49
8:LB:258:HIS:HA	8:LB:260:ALA:N	2.27	0.49
13:LG:157:ILE:HA	13:LG:201:THR:HG22	1.95	0.49
52:SF:142:SER:HB3	62:Sc:50:VAL:HG22	1.93	0.49
79:SX:128:VAL:HG23	79:SX:138:LYS:HD2	1.95	0.49
84:S2:1171:G:O2'	84:S2:1187:G:O6	2.28	0.49
84:S2:1337:4AC:O5'	84:S2:1337:4AC:H6	2.12	0.49
86:CF:26:HIS:CE1	86:CF:198:GLY:HA3	2.47	0.49
86:CF:26:HIS:C	86:CF:30:LYS:HZ3	2.21	0.49
86:CF:86:TYR:OH	86:CF:295:HIS:ND1	2.42	0.49
4:L5:423:G:H21	21:LP:118:GLN:NE2	2.10	0.49
4:L5:1942:A:H2'	4:L5:1943:A:H8	1.77	0.49
11:LE:119:GLU:HG3	36:Le:7:LEU:HD22	1.94	0.49
14:LH:61:TRP:CZ3	18:LM:33:GLN:HG3	2.48	0.49
14:LH:92:MET:HE2	14:LH:179:ILE:HG22	1.94	0.49
17:LL:56:ARG:NH1	17:LL:74:ARG:O	2.40	0.49
45:Ln:12:ARG:HG2	45:Ln:15:ARG:HH21	1.77	0.49
71:SH:69:LEU:HD13	71:SH:96:ALA:HB2	1.95	0.49
75:SN:29:THR:OG1	75:SN:31:ASP:OD1	2.26	0.49
84:S2:207:G:H3'	84:S2:208:G:H8	1.78	0.49
84:S2:454:U:H2'	84:S2:455:A:H8	1.78	0.49
4:L5:308:G:O6	19:LN:12:ARG:NH1	2.46	0.49
4:L5:2411:C:H2'	4:L5:2412:A:H8	1.77	0.49
4:L5:2568:C:H2'	4:L5:2569:G:C8	2.48	0.49
12:LF:157:ARG:HE	12:LF:248:ASN:HB2	1.78	0.49
67:SB:97:LEU:HB3	67:SB:232:HIS:NE2	2.28	0.49
69:SE:104:ASP:HB3	69:SE:110:ALA:HB2	1.93	0.49
72:SI:116:HIS:O	72:SI:152:ARG:NH2	2.38	0.49
73:SJ:60:LEU:HD22	73:SJ:70:ARG:HA	1.95	0.49
83:Se:41:ARG:HG3	83:Se:42:PHE:HD1	1.78	0.49
4:L5:711:A:H2'	4:L5:712:C:C6	2.48	0.48
4:L5:1461:C:H2'	4:L5:1462:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4149:C:OP1	31:LZ:59:LYS:N	2.46	0.48
21:LP:54:GLN:HA	21:LP:83:TRP:CD1	2.47	0.48
36:Le:91:CYS:HB3	36:Le:95:TYR:HD2	1.78	0.48
56:SQ:96:TYR:HA	56:SQ:100:VAL:HG12	1.95	0.48
65:Sg:195:LEU:HA	65:Sg:211:GLY:HA3	1.94	0.48
67:SB:168:MET:HB2	67:SB:197:ILE:HD13	1.95	0.48
67:SB:171:ILE:HG22	67:SB:174:ARG:HE	1.78	0.48
68:SC:227:ARG:NH2	84:S2:663:C:O2'	2.45	0.48
77:SV:73:ALA:HB1	77:SV:78:ILE:HB	1.95	0.48
82:Sb:49:HIS:ND1	82:Sb:69:GLY:O	2.46	0.48
84:S2:5:U:H2'	84:S2:6:G:H8	1.78	0.48
84:S2:1595:U:H2'	84:S2:1596:U:C6	2.48	0.48
4:L5:2101:C:H2'	4:L5:2102:G:C8	2.47	0.48
4:L5:4935:C:H2'	4:L5:4936:G:C8	2.47	0.48
14:LH:18:ILE:HG12	14:LH:27:VAL:HG22	1.95	0.48
20:LO:119:VAL:N	24:LS:168:THR:O	2.45	0.48
28:LW:56:ARG:HE	28:LW:61:LYS:CB	2.26	0.48
68:SC:257:LYS:O	77:SV:16:LYS:NZ	2.40	0.48
70:SG:172:LYS:NZ	84:S2:67:C:OP2	2.35	0.48
72:SI:54:LYS:NZ	84:S2:381:C:OP2	2.44	0.48
84:S2:1407:U:H2'	84:S2:1408:U:C6	2.48	0.48
84:S2:1438:A:H2'	84:S2:1439:A:C8	2.48	0.48
85:AT:2:U:H3	85:AT:72:A:N6	2.10	0.48
4:L5:158:A:H5''	4:L5:159:C:H2'	1.96	0.48
4:L5:667:A:H5''	4:L5:668:C:H5''	1.95	0.48
4:L5:1095:A:N1	4:L5:1200:G:C6	2.81	0.48
4:L5:1344:C:H1'	17:LL:10:LEU:HD11	1.95	0.48
4:L5:1727:U:OP1	12:LF:131:ASN:ND2	2.45	0.48
4:L5:2903:G:H1'	4:L5:2904:U:H5	1.78	0.48
8:LB:218:ASP:OD2	8:LB:348:ARG:NH2	2.34	0.48
33:Lb:5:LYS:HE2	33:Lb:8:THR:HB	1.94	0.48
52:SF:19:LEU:HD11	52:SF:50:PRO:HD3	1.94	0.48
65:Sg:133:ASN:HB3	65:Sg:139:LYS:HD2	1.96	0.48
77:SV:30:ALA:O	77:SV:60:ARG:HD3	2.13	0.48
86:CF:34:ILE:HG23	86:CF:78:TRP:CZ2	2.47	0.48
4:L5:178:C:N4	4:L5:179:G:O6	2.46	0.48
4:L5:500:G:H1'	4:L5:504:G:H3'	1.95	0.48
4:L5:1176:C:H42	4:L5:1184:A:H61	1.60	0.48
4:L5:1866:U:OP1	15:LI:4:ARG:NH1	2.36	0.48
4:L5:2279:A:O2'	36:Le:48:ARG:NH2	2.46	0.48
4:L5:2846:G:OP1	27:LV:85:ARG:NH2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L8:150:C:N4	13:LG:52:THR:O	2.46	0.48
8:LB:299:ILE:HB	8:LB:313:SER:HB3	1.95	0.48
21:LP:107:LEU:HD13	21:LP:152:GLU:HG3	1.95	0.48
67:SB:85:LYS:HB2	67:SB:101:HIS:HB3	1.94	0.48
75:SN:14:SER:HB3	84:S2:1016:U:H5''	1.96	0.48
84:S2:996:A:H2'	84:S2:997:A:C8	2.48	0.48
84:S2:1115:U:O2'	84:S2:1117:C:OP2	2.30	0.48
84:S2:1435:C:O2'	84:S2:1436:C:O4'	2.30	0.48
4:L5:4301:U:OP2	4:L5:4303:C:N4	2.46	0.48
6:L8:141:C:H2'	6:L8:142:U:C6	2.48	0.48
9:LC:144:ILE:HG13	9:LC:144:ILE:O	2.12	0.48
10:LD:66:TYR:HE2	10:LD:68:ARG:HE	1.61	0.48
13:LG:150:LYS:NZ	13:LG:177:MET:O	2.47	0.48
14:LH:89:ARG:HD3	14:LH:91:LYS:HE3	1.95	0.48
42:Lk:35:LYS:HD3	42:Lk:42:LEU:HD21	1.95	0.48
53:SK:22:VAL:HG22	53:SK:68:TYR:HD1	1.78	0.48
54:SM:23:LYS:O	54:SM:27:ILE:HG12	2.13	0.48
70:SG:202:ASN:ND2	84:S2:125:C:OP1	2.39	0.48
75:SN:15:ALA:HB2	82:Sb:20:LYS:HD3	1.95	0.48
85:AT:60:A:C2	85:AT:61:A:H1'	2.49	0.48
86:CF:240:ARG:HH12	86:CF:266:ARG:NH2	2.11	0.48
4:L5:172:C:H4'	4:L5:173:C:H5'	1.96	0.48
4:L5:2029:A:H2'	4:L5:2030:A:C8	2.48	0.48
58:SS:64:VAL:O	58:SS:68:ILE:HG12	2.12	0.48
79:SX:105:PHE:CD1	79:SX:121:LYS:HB3	2.45	0.48
83:Se:41:ARG:HG3	83:Se:42:PHE:CD1	2.49	0.48
4:L5:1097:C:H2'	4:L5:1098:G:C8	2.49	0.48
4:L5:2716:C:O3'	26:LU:107:LYS:NZ	2.46	0.48
4:L5:4345:C:H2'	4:L5:4346:U:C6	2.48	0.48
9:LC:268:ARG:NH1	9:LC:269:LYS:HE2	2.29	0.48
12:LF:127:LYS:HB2	25:LT:133:ALA:HB3	1.96	0.48
25:LT:102:ARG:O	25:LT:106:LEU:HG	2.13	0.48
27:LV:43:LYS:HE2	27:LV:62:MET:HE3	1.95	0.48
54:SM:110:VAL:O	54:SM:112:LYS:NZ	2.44	0.48
69:SE:192:ILE:HG12	69:SE:243:GLY:HA3	1.96	0.48
82:Sb:11:SER:OG	82:Sb:14:GLU:OE1	2.29	0.48
85:AT:12:G:N2	85:AT:23:U:H3	2.10	0.48
4:L5:737:C:C5	4:L5:739:G:H5''	2.48	0.48
4:L5:2640:G:H2'	4:L5:2641:A:C8	2.49	0.48
4:L5:3908:A:N7	4:L5:4449:A:N6	2.62	0.48
4:L5:4220:6MZ:H2'	4:L5:4222:G:H5''	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LB:14:LEU:HD22	8:LB:17:LEU:HD11	1.94	0.48
10:LD:179:ARG:HD3	10:LD:179:ARG:HA	1.72	0.48
10:LD:205:ALA:HB1	10:LD:233:PRO:HB3	1.95	0.48
12:LF:105:VAL:HG13	12:LF:136:VAL:HG12	1.96	0.48
16:LJ:63:ARG:HH11	46:Lo:106:PHE:HB2	1.79	0.48
20:LO:126:VAL:HG13	20:LO:127:VAL:HG13	1.94	0.48
53:SK:41:PRO:HG2	53:SK:44:HIS:CG	2.49	0.48
61:SZ:85:ARG:NH2	84:S2:1597:C:OP2	2.39	0.48
67:SB:171:ILE:HD11	67:SB:197:ILE:HA	1.95	0.48
71:SH:51:ILE:HD11	71:SH:176:VAL:HG12	1.96	0.48
84:S2:106:C:H2'	84:S2:107:A:C8	2.46	0.48
84:S2:907:G:H2'	84:S2:908:A:C8	2.48	0.48
84:S2:1144:A:H2'	84:S2:1145:A:C8	2.49	0.48
84:S2:1736:G:H2'	84:S2:1737:G:C8	2.48	0.48
12:LF:241:ASN:O	12:LF:245:ARG:HG2	2.14	0.48
22:LQ:50:ARG:HH21	22:LQ:140:SER:HB2	1.79	0.48
72:SI:57:ALA:HB2	72:SI:183:GLY:HA2	1.95	0.48
84:S2:223:C:H2'	84:S2:224:A:C8	2.49	0.48
84:S2:1652:G:H1	84:S2:1672:U:H3	1.60	0.48
85:AT:30:C:H2'	85:AT:31:G:C8	2.49	0.48
86:CF:240:ARG:CZ	86:CF:305:GLY:HA3	2.43	0.48
4:L5:138:G:H2'	4:L5:139:G:H8	1.79	0.48
4:L5:233:U:HO2'	4:L5:234:G:H8	1.61	0.48
4:L5:490:C:H2'	4:L5:491:G:C8	2.48	0.48
4:L5:1396:G:HO2'	4:L5:1468:C:HO2'	1.57	0.48
4:L5:3661:G:N7	7:LA:152:SER:OG	2.43	0.48
4:L5:4584:A:H2'	4:L5:4585:U:O4'	2.14	0.48
12:LF:213:LEU:HB3	12:LF:247:MET:HG3	1.96	0.48
13:LG:154:LEU:HB3	13:LG:204:PHE:HB2	1.96	0.48
62:Sc:39:SER:HB2	81:Sa:51:ARG:HH12	1.78	0.48
81:Sa:87:ARG:NH1	81:Sa:94:ASP:OD1	2.47	0.48
84:S2:329:G:H2'	84:S2:330:G:C8	2.49	0.48
84:S2:598:G:O2'	84:S2:605:A:N1	2.45	0.48
84:S2:1568:C:H2'	84:S2:1569:A:C8	2.49	0.48
84:S2:1692:U:H2'	84:S2:1693:G:C8	2.49	0.48
86:CF:395:LYS:HD3	86:CF:396:SER:H	1.79	0.48
4:L5:99:A:H5''	19:LN:184:ILE:HD12	1.95	0.47
4:L5:519:C:H1'	4:L5:643:C:C2	2.49	0.47
4:L5:1095:A:C2	4:L5:1200:G:N1	2.65	0.47
4:L5:1367:C:O2'	4:L5:1369:C:OP2	2.26	0.47
4:L5:1461:C:H2'	4:L5:1462:A:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1877:G:O6	33:Lb:10:HIS:NE2	2.45	0.47
6:L8:75:OMG:HM23	6:L8:75:OMG:H1'	1.70	0.47
52:SF:49:LEU:HD12	52:SF:50:PRO:HD2	1.95	0.47
70:SG:4:ASN:ND2	84:S2:154:U:O2	2.46	0.47
71:SH:30:LEU:O	71:SH:33:ASN:ND2	2.47	0.47
72:SI:3:ILE:O	72:SI:30:GLY:N	2.41	0.47
79:SX:28:LYS:NZ	84:S2:1189:A:OP1	2.39	0.47
79:SX:52:LEU:HD11	79:SX:73:GLN:HB2	1.95	0.47
4:L5:257:C:H2'	4:L5:258:G:C8	2.49	0.47
4:L5:1846:G:H2'	4:L5:1847:C:C6	2.49	0.47
4:L5:1998:A:O2'	4:L5:1999:A:O4'	2.30	0.47
4:L5:2725:A:N6	23:LR:88:ARG:O	2.47	0.47
4:L5:2869:U:O2'	4:L5:2881:A:N7	2.43	0.47
4:L5:4113:U:H4'	4:L5:4115:G:C6	2.49	0.47
6:L8:102:G:OP2	6:L8:104:A:O2'	2.29	0.47
7:LA:180:LEU:HD22	47:Lp:18:TYR:HB3	1.96	0.47
8:LB:27:GLY:HA2	8:LB:276:HIS:CD2	2.49	0.47
35:Ld:53:ALA:HA	35:Ld:88:LEU:HD21	1.96	0.47
57:SR:29:HIS:CD2	65:Sg:36:ARG:HH21	2.33	0.47
72:SI:25:ARG:HA	84:S2:448:A:H5''	1.96	0.47
72:SI:89:GLU:OE1	72:SI:92:ARG:NH2	2.47	0.47
84:S2:1144:A:H5'	84:S2:1355:C:H41	1.79	0.47
4:L5:169:G:O6	4:L5:170:C:N4	2.47	0.47
4:L5:256:G:H2'	4:L5:257:C:C6	2.49	0.47
4:L5:444:G:H2'	4:L5:445:U:C6	2.49	0.47
4:L5:907:C:H2'	4:L5:908:G:C8	2.49	0.47
4:L5:1333:A:H2'	4:L5:1334:A:H8	1.77	0.47
4:L5:2832:A:OP1	35:Ld:47:LYS:NZ	2.30	0.47
4:L5:4606:G:N2	85:AT:63:C:O2'	2.47	0.47
5:L7:23:A:N3	5:L7:118:C:O2'	2.37	0.47
8:LB:29:VAL:HG12	8:LB:31:SER:H	1.79	0.47
21:LP:114:ILE:HA	21:LP:150:LEU:HD23	1.96	0.47
23:LR:157:ASP:OD1	23:LR:158:GLN:N	2.47	0.47
52:SF:83:ASN:OD1	84:S2:1651:A:O2'	2.28	0.47
59:ST:84:ARG:NH1	84:S2:1605:G:OP1	2.40	0.47
65:Sg:124:SER:OG	65:Sg:125:ARG:N	2.46	0.47
65:Sg:207:CYS:HB3	65:Sg:221:LEU:HD21	1.96	0.47
69:SE:127:ARG:HG3	69:SE:142:HIS:HA	1.96	0.47
80:SY:105:LYS:O	80:SY:109:GLU:HG2	2.14	0.47
84:S2:16:G:H2'	84:S2:17:C:C6	2.49	0.47
3:Et:66:U:H2'	3:Et:67:U:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1855:G:OP1	33:Lb:4:SER:HB2	2.14	0.47
4:L5:2021:G:OP1	49:Ls:58:ASN:N	2.43	0.47
4:L5:3799:A:N3	4:L5:4506:C:O2'	2.41	0.47
4:L5:3917:A:H2'	4:L5:3918:G:H8	1.79	0.47
4:L5:4622:A:H4'	8:LB:13:SER:HB2	1.95	0.47
6:L8:19:C:H2'	6:L8:20:A:C8	2.49	0.47
17:LL:110:LEU:O	17:LL:114:VAL:HG13	2.15	0.47
19:LN:140:LYS:HD3	19:LN:140:LYS:HA	1.66	0.47
54:SM:128:PHE:HA	54:SM:131:LYS:HG2	1.97	0.47
58:SS:137:LYS:NZ	84:S2:1236:G:O6	2.47	0.47
65:Sg:39:THR:HG22	65:Sg:60:ARG:HG2	1.96	0.47
84:S2:1383:A2M:HM'3	84:S2:1383:A2M:H1'	1.64	0.47
84:S2:1491:G:H2'	84:S2:1492:U:C6	2.49	0.47
4:L5:300:A:H2'	4:L5:301:G:H8	1.80	0.47
4:L5:1899:G:O2'	36:Le:57:ASN:OD1	2.31	0.47
4:L5:2580:U:OP1	31:LZ:36:ARG:NH1	2.41	0.47
4:L5:2811:G:N1	4:L5:2814:C:OP2	2.42	0.47
4:L5:3923:A:H2'	4:L5:3924:C:C6	2.50	0.47
10:LD:234:ASP:OD1	10:LD:235:MET:N	2.48	0.47
14:LH:114:ILE:HB	14:LH:124:ARG:HB2	1.96	0.47
51:SD:115:VAL:HG21	51:SD:138:VAL:HG11	1.97	0.47
69:SE:247:THR:OG1	69:SE:250:GLU:OE1	2.33	0.47
80:SY:41:ARG:NH2	80:SY:52:PRO:O	2.47	0.47
4:L5:1326:A2M:HM'3	4:L5:1326:A2M:H1'	1.63	0.47
4:L5:1577:G:O2'	4:L5:1612:G:H4'	2.14	0.47
4:L5:2018:C:H2'	4:L5:2019:C:H6	1.79	0.47
4:L5:4251:A:H5''	16:LJ:108:GLY:HA3	1.96	0.47
15:LI:36:LEU:HD11	15:LI:69:ARG:HD2	1.97	0.47
26:LU:63:ILE:HD13	26:LU:72:VAL:HG22	1.97	0.47
59:ST:40:ALA:HB3	59:ST:43:LYS:HG2	1.97	0.47
84:S2:656:G:N2	84:S2:663:C:H5''	2.29	0.47
84:S2:656:G:H5'	84:S2:662:G:N2	2.29	0.47
84:S2:1656:G:H1	84:S2:1668:U:H3	1.62	0.47
86:CF:349:HIS:ND1	86:CF:351:GLY:O	2.48	0.47
3:Et:35:U:H2'	3:Et:36:U:H6	1.79	0.47
4:L5:374:G:OP2	41:Lj:56:ARG:NH1	2.38	0.47
4:L5:467:U:C4	4:L5:468:U:H1'	2.49	0.47
4:L5:1601:A:OP1	41:Lj:5:THR:OG1	2.23	0.47
4:L5:1857:C:H2'	4:L5:1858:A:C8	2.49	0.47
4:L5:1932:A:OP1	20:LO:49:ARG:NH2	2.27	0.47
4:L5:1995:G:H2'	4:L5:1996:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2583:C:OP2	38:Lg:76:ARG:NH1	2.47	0.47
4:L5:4274:A:H2'	4:L5:4275:G:H8	1.79	0.47
4:L5:4742:G:H2'	4:L5:4743:G:H8	1.80	0.47
4:L5:4897:G:OP1	18:LM:128:LYS:NZ	2.45	0.47
10:LD:86:TYR:HE1	10:LD:247:ILE:HG13	1.79	0.47
17:LL:142:GLU:HA	17:LL:146:LEU:HD12	1.96	0.47
21:LP:122:ALA:HB3	21:LP:143:PRO:HG2	1.96	0.47
37:Lf:45:LYS:NZ	37:Lf:108:SER:HA	2.30	0.47
52:SF:26:ASP:N	52:SF:26:ASP:OD1	2.46	0.47
56:SQ:8:GLN:HG3	56:SQ:27:ARG:HE	1.80	0.47
56:SQ:110:ASP:OD1	56:SQ:111:ILE:HD12	2.14	0.47
63:Sd:46:TYR:O	63:Sd:50:ILE:HD12	2.14	0.47
68:SC:110:MET:HG2	68:SC:125:LYS:HB3	1.97	0.47
70:SG:162:LEU:HG	70:SG:167:LYS:HE3	1.95	0.47
77:SV:17:CYS:HB2	77:SV:56:CYS:HB3	1.97	0.47
81:Sa:34:LYS:NZ	84:S2:1862:G:N7	2.62	0.47
84:S2:520:A:O2'	84:S2:825:A:N3	2.40	0.47
84:S2:528:A:H2'	84:S2:529:A:C8	2.49	0.47
84:S2:747:U:C2	84:S2:796:G:N1	2.83	0.47
84:S2:1221:G:O2'	84:S2:1676:U:O2	2.31	0.47
84:S2:1286:G:N2	84:S2:1312:G:O2'	2.48	0.47
84:S2:1337:4AC:H2'	84:S2:1338:G:H8	1.79	0.47
84:S2:1736:G:H2'	84:S2:1737:G:H8	1.80	0.47
4:L5:318:A:H2'	4:L5:319:A:C8	2.50	0.47
4:L5:2111:G:N2	4:L5:2251:G:O2'	2.48	0.47
4:L5:2492:C:H2'	4:L5:2493:G:C8	2.49	0.47
13:LG:162:ASP:HB3	13:LG:163:PRO:HD3	1.96	0.47
15:LI:54:SER:HB3	15:LI:135:ILE:HD11	1.96	0.47
24:LS:99:ASP:OD1	24:LS:100:LEU:N	2.45	0.47
51:SD:32:ASP:OD2	51:SD:65:ARG:NH1	2.48	0.47
72:SI:4:SER:OG	72:SI:6:ASP:OD2	2.26	0.47
84:S2:102:A:H4'	84:S2:104:A:C8	2.50	0.47
84:S2:1533:A:H2	84:S2:1536:G:N3	2.13	0.47
84:S2:1643:U:H2'	84:S2:1644:C:C6	2.49	0.47
86:CF:10:ILE:HG12	86:CF:111:CYS:HB3	1.95	0.47
4:L5:1188:C:H2'	4:L5:1189:G:H8	1.80	0.47
4:L5:4088:C:H2'	4:L5:4089:G:C8	2.50	0.47
14:LH:115:ARG:HD3	14:LH:123:ILE:HD12	1.96	0.47
18:LM:96:GLU:O	18:LM:100:ARG:HG2	2.15	0.47
18:LM:130:LEU:HB3	20:LO:177:LEU:HD11	1.96	0.47
26:LU:39:PHE:HD1	26:LU:90:TYR:CD2	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:Lr:47:LYS:O	48:Lr:103:ARG:HD2	2.15	0.47
49:Ls:114:GLY:HA2	49:Ls:166:LYS:HD2	1.97	0.47
59:ST:42:HIS:NE2	59:ST:43:LYS:HE3	2.30	0.47
64:Sf:124:ASP:OD1	64:Sf:124:ASP:N	2.44	0.47
68:SC:104:ASP:OD1	68:SC:105:GLU:N	2.48	0.47
79:SX:90:CYS:HA	79:SX:93:PHE:HD2	1.79	0.47
84:S2:159:A2M:HM'3	84:S2:159:A2M:H1'	1.59	0.47
4:L5:455:C:O2'	4:L5:456:C:H5'	2.14	0.47
4:L5:1414:C:H2'	4:L5:1415:G:C8	2.47	0.47
4:L5:1695:U:O2'	4:L5:1719:A:N3	2.39	0.47
4:L5:1942:A:N3	4:L5:4432:C:O2'	2.44	0.47
4:L5:2112:G:H5''	4:L5:2251:G:H1	1.79	0.47
4:L5:4095:G:H2'	4:L5:4096:C:C6	2.50	0.47
4:L5:4954:G:H2'	4:L5:4955:A:C8	2.49	0.47
6:L8:67:U:H2'	6:L8:68:G:H8	1.80	0.47
7:LA:114:CYS:N	7:LA:165:VAL:O	2.47	0.47
7:LA:116:LEU:HB3	7:LA:126:LEU:HB2	1.96	0.47
48:Lr:119:ARG:HA	48:Lr:122:LYS:HE3	1.95	0.47
53:SK:7:ASN:HB2	53:SK:40:VAL:HG22	1.97	0.47
67:SB:23:ASP:N	67:SB:23:ASP:OD1	2.48	0.47
68:SC:70:VAL:HG21	68:SC:93:ILE:HG23	1.97	0.47
70:SG:85:ARG:O	70:SG:87:ARG:NH1	2.48	0.47
73:SJ:59:GLU:O	73:SJ:62:THR:OG1	2.30	0.47
84:S2:51:U:H2'	84:S2:52:G:C8	2.50	0.47
84:S2:329:G:H2'	84:S2:330:G:H8	1.80	0.47
84:S2:468:A2M:HM'3	84:S2:468:A2M:H1'	1.67	0.47
84:S2:1189:A:H2'	84:S2:1190:A:H8	1.80	0.47
84:S2:1189:A:H2'	84:S2:1190:A:C8	2.50	0.47
84:S2:1550:G:O2'	84:S2:1558:C:O2	2.24	0.47
4:L5:1340:OMC:HM23	4:L5:1340:OMC:H1'	1.74	0.46
4:L5:1408:G:O2'	4:L5:1411:C:N4	2.48	0.46
4:L5:2033:A:OP1	15:LI:162:ARG:NH2	2.46	0.46
60:SU:56:MET:HB2	60:SU:86:LYS:HG3	1.96	0.46
63:Sd:14:PHE:HB2	84:S2:1661:A:H8	1.81	0.46
65:Sg:212:LYS:HA	65:Sg:235:ILE:HG13	1.96	0.46
66:SA:102:ARG:NH1	84:S2:1378:A:OP2	2.46	0.46
73:SJ:145:PRO:HD2	84:S2:522:A:H5''	1.97	0.46
84:S2:962:A:N1	84:S2:1055:A:O2'	2.47	0.46
4:L5:1298:C:H2'	4:L5:1299:G:C8	2.51	0.46
4:L5:1324:A:O2'	4:L5:1326:A2M:OP1	2.26	0.46
4:L5:2299:G:O6	9:LC:188:ARG:NH2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:3796:U:O2'	84:S2:1720:U:O2'	2.26	0.46
4:L5:3867:A2M:HM'3	4:L5:3867:A2M:H1'	1.64	0.46
4:L5:3950:U:H3	4:L5:4063:U:H3	1.62	0.46
11:LE:223:ARG:HB3	11:LE:224:LYS:HB2	1.97	0.46
11:LE:261:ILE:HG23	11:LE:267:LEU:HD23	1.96	0.46
53:SK:32:HIS:CD2	53:SK:45:VAL:HG11	2.50	0.46
56:SQ:139:ALA:HB2	84:S2:1650:A:H5''	1.96	0.46
59:ST:114:GLU:OE1	59:ST:114:GLU:N	2.47	0.46
64:Sf:105:TYR:HE1	64:Sf:131:PHE:HD2	1.63	0.46
65:Sg:82:SER:OG	65:Sg:83:TRP:N	2.47	0.46
72:SI:98:LYS:HG3	72:SI:178:ARG:HG2	1.98	0.46
84:S2:51:U:H2'	84:S2:52:G:H8	1.80	0.46
84:S2:325:C:N3	84:S2:326:C:O2'	2.46	0.46
86:CF:356:GLY:H	86:CF:372:PHE:HB2	1.80	0.46
2:Pt:29:C:H2'	2:Pt:30:G:H8	1.80	0.46
3:Et:12:U:H2'	3:Et:13:C:C6	2.51	0.46
4:L5:106:A:H2'	4:L5:107:G:O4'	2.15	0.46
4:L5:162:A:H2'	4:L5:163:A:C8	2.51	0.46
4:L5:965:G:N2	4:L5:2092:G:H1'	2.30	0.46
4:L5:1308:C:OP1	20:LO:93:LYS:NZ	2.46	0.46
4:L5:1725:U:H2'	4:L5:1726:U:H6	1.81	0.46
4:L5:2382:A:N1	4:L5:2829:U:O2'	2.45	0.46
4:L5:2848:G:O2'	4:L5:3838:U:O4	2.23	0.46
4:L5:2910:G:N2	4:L5:3585:G:O2'	2.48	0.46
4:L5:4492:U:O2'	4:L5:4512:U:O2	2.27	0.46
12:LF:57:TYR:OH	12:LF:189:ASP:OD1	2.31	0.46
12:LF:182:TYR:HB3	12:LF:200:ARG:HG3	1.97	0.46
22:LQ:154:LYS:NZ	22:LQ:159:PRO:O	2.47	0.46
34:Lc:47:ILE:HD12	34:Lc:94:LEU:HD11	1.97	0.46
34:Lc:48:LEU:HD13	34:Lc:57:LYS:HG3	1.97	0.46
51:SD:223:ILE:HD11	65:Sg:189:ILE:HD12	1.97	0.46
67:SB:186:ASN:HA	67:SB:189:ILE:HD12	1.98	0.46
83:Se:11:LYS:O	83:Se:15:GLN:HG3	2.16	0.46
84:S2:420:G:O2'	84:S2:660:C:N3	2.45	0.46
84:S2:674:C:H2'	84:S2:675:U:C6	2.50	0.46
84:S2:1231:C:O2'	84:S2:1253:A:N6	2.49	0.46
4:L5:170:C:H42	4:L5:266:C:N4	2.13	0.46
4:L5:1398:A:N1	4:L5:1419:G:O2'	2.47	0.46
4:L5:2580:U:O2'	31:LZ:79:HIS:ND1	2.43	0.46
4:L5:3664:G:H2'	4:L5:3665:G:C8	2.50	0.46
4:L5:3932:U:H2'	4:L5:3933:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4476:C:O2'	4:L5:4478:G:OP2	2.26	0.46
4:L5:4775:C:H41	4:L5:4859:C:N4	2.13	0.46
50:Lt:28:LEU:HD23	50:Lt:28:LEU:H	1.80	0.46
56:Sg:98:LYS:O	65:Sg:57:ARG:NH1	2.37	0.46
65:Sg:120:ILE:HB	65:Sg:132:TRP:HB2	1.97	0.46
66:SA:74:VAL:HG23	66:SA:121:LEU:HB3	1.96	0.46
70:SG:2:LYS:HB3	70:SG:15:LEU:HD11	1.97	0.46
84:S2:66:G:H2'	84:S2:67:C:H4'	1.97	0.46
85:AT:2:U:H2'	85:AT:3:C:C6	2.50	0.46
86:CF:178:ILE:CG1	86:CF:183:TYR:HB2	2.45	0.46
86:CF:381:ARG:HH22	86:CF:397:GLY:HA2	1.80	0.46
4:L5:2611:A:H2'	4:L5:2612:G:C8	2.50	0.46
4:L5:2696:A:H62	42:Lk:35:LYS:NZ	2.13	0.46
4:L5:3861:A:H2'	4:L5:3862:A:C8	2.50	0.46
4:L5:4441:A:H5''	15:LI:114:GLY:HA2	1.97	0.46
6:L8:96:C:H5''	39:Lh:66:LYS:HG2	1.98	0.46
7:LA:131:GLY:H	7:LA:169:VAL:HG13	1.80	0.46
7:LA:206:PRO:HG3	7:LA:213:GLY:HA3	1.97	0.46
12:LF:37:PHE:HZ	33:Lb:113:ALA:HB1	1.81	0.46
13:LG:143:VAL:HG22	13:LG:203:ALA:HB2	1.97	0.46
32:La:72:THR:HG22	32:La:110:LYS:HB3	1.97	0.46
59:ST:6:VAL:HG12	59:ST:135:ALA:HB2	1.98	0.46
65:Sg:10:THR:HG22	65:Sg:308:ARG:HG2	1.97	0.46
66:SA:184:ARG:HG2	66:SA:189:ILE:HB	1.97	0.46
71:SH:33:ASN:ND2	71:SH:36:LEU:HB3	2.30	0.46
3:Et:7:A:O2'	3:Et:49:C:O4'	2.30	0.46
4:L5:327:U:HO2'	40:Li:30:ARG:HH11	1.59	0.46
4:L5:4775:C:H41	4:L5:4859:C:H42	1.64	0.46
7:LA:142:GLU:O	7:LA:143:THR:OG1	2.31	0.46
8:LB:50:LYS:NZ	8:LB:337:VAL:O	2.46	0.46
11:LE:161:ARG:O	11:LE:182:ASN:ND2	2.48	0.46
12:LF:162:ILE:HD12	12:LF:167:ILE:HB	1.98	0.46
16:LJ:56:THR:OG1	16:LJ:64:ARG:N	2.45	0.46
72:SI:44:HIS:ND1	84:S2:1740:C:OP1	2.37	0.46
4:L5:1194:G:H2'	4:L5:1195:G:C8	2.51	0.46
4:L5:1696:C:H5'	4:L5:1719:A:H1'	1.98	0.46
4:L5:1811:G:H21	33:Lb:57:MET:HE2	1.81	0.46
20:LO:166:ILE:HG12	20:LO:169:ARG:HH21	1.81	0.46
49:Ls:91:THR:HG21	49:Ls:98:ILE:HG13	1.98	0.46
69:SE:134:LYS:N	84:S2:298:G:OP1	2.45	0.46
71:SH:30:LEU:HG	71:SH:33:ASN:HD22	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:S2:693:A:H2'	84:S2:694:G:C8	2.51	0.46
84:S2:1755:C:H2'	84:S2:1756:C:C6	2.51	0.46
4:L5:3932:U:H2'	4:L5:3933:G:H8	1.81	0.46
4:L5:4093:G:H3'	4:L5:4094:G:H8	1.81	0.46
4:L5:4389:C:H2'	4:L5:4390:A:C8	2.51	0.46
11:LE:222:LEU:HB2	11:LE:237:LYS:HD2	1.97	0.46
12:LF:46:ARG:HH21	33:Lb:102:PRO:HG3	1.81	0.46
14:LH:4:ILE:HG12	14:LH:61:TRP:CH2	2.51	0.46
23:LR:175:GLU:O	23:LR:178:GLN:HG3	2.16	0.46
27:LV:42:VAL:HB	27:LV:45:ILE:HG13	1.98	0.46
38:Lg:82:MET:HE3	38:Lg:82:MET:HB2	1.88	0.46
51:SD:77:PHE:HB2	51:SD:79:PHE:CE1	2.50	0.46
52:SF:127:ARG:HG2	52:SF:136:ARG:HB2	1.98	0.46
65:Sg:289:LEU:HD11	65:Sg:298:LEU:HD21	1.98	0.46
67:SB:214:LYS:NZ	84:S2:943:U:OP1	2.39	0.46
84:S2:5:U:H2'	84:S2:6:G:C8	2.51	0.46
84:S2:1215:C:O2'	84:S2:1645:C:OP2	2.33	0.46
84:S2:1775:U:H2'	84:S2:1776:G:C2	2.51	0.46
3:Et:8:U:H5'	3:Et:49:C:H5''	1.98	0.46
3:Et:51:G:H2'	3:Et:52:G:C8	2.51	0.46
4:L5:1494:U:H2'	4:L5:1495:G:H8	1.80	0.46
4:L5:2724:G:O2'	4:L5:2726:G:OP2	2.31	0.46
4:L5:4504:C:H2'	4:L5:4505:C:C6	2.51	0.46
4:L5:4543:G:H2'	4:L5:4544:A:C8	2.51	0.46
10:LD:181:PRO:HD2	10:LD:195:HIS:CD2	2.51	0.46
11:LE:99:ASP:OD1	11:LE:99:ASP:N	2.49	0.46
13:LG:83:PHE:HA	13:LG:183:ILE:HD13	1.98	0.46
22:LQ:3:VAL:HG13	22:LQ:5:ILE:HG12	1.98	0.46
35:Ld:57:MET:HG2	35:Ld:88:LEU:HD23	1.98	0.46
61:SZ:91:LEU:HG	61:SZ:96:LEU:HD21	1.98	0.46
65:Sg:21:ILE:HG21	65:Sg:299:PHE:HB2	1.97	0.46
68:SC:185:THR:OG1	84:S2:1155:U:OP1	2.24	0.46
69:SE:59:ASP:O	69:SE:63:LYS:HG3	2.16	0.46
78:SW:62:VAL:HG11	82:Sb:8:LEU:HG	1.97	0.46
84:S2:1337:4AC:H2'	84:S2:1338:G:C8	2.50	0.46
86:CF:8:ILE:HD12	86:CF:10:ILE:HG13	1.97	0.46
4:L5:162:A:H2'	4:L5:163:A:H8	1.80	0.46
4:L5:1194:G:H2'	4:L5:1195:G:H8	1.81	0.46
4:L5:1669:A:H4'	4:L5:1685:G:N2	2.30	0.46
4:L5:4302:U:H4'	25:LT:5:LYS:HD3	1.98	0.46
4:L5:4524:G:C2	8:LB:252:ALA:HB1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LJ:15:LEU:HD12	16:LJ:165:TRP:HB2	1.98	0.46
54:SM:87:GLU:HG3	54:SM:103:VAL:HG11	1.98	0.46
58:SS:121:ARG:HG3	58:SS:131:VAL:HB	1.98	0.46
70:SG:49:VAL:HB	70:SG:115:LYS:HG2	1.97	0.46
71:SH:142:LYS:HB3	78:SW:54:ASP:HB3	1.98	0.46
73:SJ:64:ASP:OD1	73:SJ:65:GLU:N	2.49	0.46
79:SX:60:LYS:H	79:SX:114:ASP:HB2	1.81	0.46
83:Se:31:ARG:NH2	84:S2:525:A:O3'	2.48	0.46
84:S2:327:G:H5''	84:S2:328:U:C2	2.50	0.46
84:S2:563:G:O2'	84:S2:564:A:OP1	2.32	0.46
84:S2:1201:U:H2'	84:S2:1202:U:C6	2.51	0.46
3:Et:26:A:N6	3:Et:44:G:N1	2.35	0.45
4:L5:1327:C:H2'	4:L5:1328:G:C8	2.52	0.45
4:L5:4401:G:H2'	4:L5:4402:C:H6	1.80	0.45
4:L5:4419:U:H1'	85:AT:57:C:H42	1.81	0.45
8:LB:302:ASN:HB2	8:LB:313:SER:HA	1.98	0.45
9:LC:183:VAL:HA	9:LC:204:ARG:HB3	1.98	0.45
9:LC:334:THR:HG22	9:LC:337:ARG:HH21	1.80	0.45
10:LD:108:ARG:CZ	10:LD:253:TYR:HB2	2.46	0.45
15:LI:101:LYS:NZ	15:LI:102:MET:O	2.47	0.45
58:SS:60:THR:OG1	58:SS:62:ASP:OD1	2.26	0.45
72:SI:141:ARG:NH2	84:S2:192:C:OP2	2.49	0.45
75:SN:5:HIS:HB3	75:SN:117:LEU:HD13	1.98	0.45
84:S2:115:U:H2'	84:S2:116:OMU:C6	2.46	0.45
84:S2:1850:MA6:H8	84:S2:1850:MA6:O5'	2.16	0.45
85:AT:5:C:H2'	85:AT:6:C:C6	2.51	0.45
4:L5:715:G:OP1	9:LC:321:ASN:ND2	2.46	0.45
4:L5:1733:G:N3	4:L5:4214:A:H2'	2.30	0.45
4:L5:4571:A2M:H2'	4:L5:4572:U:C6	2.50	0.45
12:LF:222:LYS:N	12:LF:232:ASP:OD1	2.48	0.45
13:LG:187:LYS:HB2	13:LG:198:THR:HG23	1.98	0.45
36:Le:76:LYS:HD2	36:Le:98:GLU:CD	2.42	0.45
52:SF:103:LEU:HD11	61:SZ:67:LEU:HD22	1.98	0.45
56:SQ:102:GLU:HA	56:SQ:105:LYS:HB3	1.98	0.45
57:SR:29:HIS:HA	57:SR:32:LYS:HG2	1.98	0.45
62:Sc:10:LYS:HE2	62:Sc:34:PHE:HD2	1.82	0.45
72:SI:126:GLY:O	72:SI:128:LYS:NZ	2.48	0.45
79:SX:63:ASN:OD1	84:S2:624:C:N4	2.41	0.45
83:Se:8:ARG:HG2	83:Se:11:LYS:HD3	1.98	0.45
4:L5:1751:A:H2'	4:L5:1752:G:C8	2.52	0.45
4:L5:2521:G:H4'	38:Lg:26:PRO:HD2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2846:G:O2'	27:LV:19:GLY:O	2.27	0.45
4:L5:4934:A:H2'	4:L5:4935:C:C6	2.51	0.45
10:LD:152:ARG:HG3	10:LD:154:THR:HG23	1.99	0.45
56:SQ:37:ARG:NH2	84:S2:1543:U:OP1	2.40	0.45
70:SG:67:VAL:HG12	70:SG:69:THR:HG22	1.99	0.45
70:SG:191:ARG:HH22	84:S2:312:G:H2'	1.81	0.45
77:SV:74:LYS:HZ1	77:SV:83:PHE:HB3	1.82	0.45
82:Sb:68:GLY:O	84:S2:928:G:N2	2.45	0.45
86:CF:55:LYS:HE3	86:CF:56:TYR:CE2	2.52	0.45
4:L5:197:A:N1	4:L5:225:G:O2'	2.47	0.45
4:L5:381:U:H4'	4:L5:415:G:H5'	1.98	0.45
4:L5:4219:A:H2'	4:L5:4220:6MZ:H8	1.98	0.45
4:L5:4345:C:H2'	4:L5:4346:U:H6	1.81	0.45
88:L5:5290:SPM:H31	88:L5:5290:SPM:H62	1.80	0.45
8:LB:92:TYR:HB3	8:LB:99:LEU:HD22	1.98	0.45
8:LB:258:HIS:HA	8:LB:260:ALA:H	1.80	0.45
14:LH:93:ARG:HG2	14:LH:182:SER:HB3	1.97	0.45
28:LW:7:SER:HB2	28:LW:13:ILE:HD11	1.98	0.45
57:SR:52:GLY:O	57:SR:55:THR:OG1	2.34	0.45
80:SY:76:TYR:OH	80:SY:86:GLU:OE1	2.20	0.45
84:S2:29:G:H2'	84:S2:30:C:C6	2.52	0.45
84:S2:830:A:OP2	84:S2:846:G:N2	2.49	0.45
84:S2:929:G:H2'	84:S2:930:C:O4'	2.17	0.45
84:S2:1084:A:OP1	84:S2:1858:G:O2'	2.28	0.45
84:S2:1139:C:H5	84:S2:1149:A:H62	1.65	0.45
84:S2:1221:G:H2'	84:S2:1222:G:C8	2.52	0.45
84:S2:1232:PSU:H2'	84:S2:1233:G:C8	2.52	0.45
84:S2:1420:G:O2'	84:S2:1421:A:N3	2.49	0.45
86:CF:241:PRO:HB2	86:CF:244:LYS:HG3	1.99	0.45
4:L5:659:G:H2'	4:L5:660:A:C8	2.51	0.45
4:L5:662:C:H2'	4:L5:663:G:H8	1.82	0.45
4:L5:1683:PSU:H2'	4:L5:1684:A:C8	2.51	0.45
4:L5:2676:A:OP2	4:L5:2676:A:H8	2.00	0.45
4:L5:3611:A:C2	4:L5:5016:A:H8	2.34	0.45
4:L5:4315:A:OP1	25:LT:69:GLN:NE2	2.47	0.45
4:L5:4456:OMC:HM21	8:LB:241:PRO:HD3	1.98	0.45
30:LY:10:ASP:HB3	30:LY:13:LYS:HB2	1.99	0.45
31:LZ:123:LYS:O	31:LZ:124:THR:OG1	2.25	0.45
55:SP:34:MET:HB3	55:SP:42:ARG:HG3	1.97	0.45
58:SS:63:GLU:O	58:SS:67:VAL:HG23	2.17	0.45
65:Sg:62:HIS:NE2	65:Sg:80:SER:OG	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SH:37:LYS:HA	71:SH:40:LEU:HB3	1.98	0.45
84:S2:1240:A:N3	84:S2:1267:C:O2'	2.41	0.45
84:S2:1259:A:N6	84:S2:1519:U:O5'	2.50	0.45
84:S2:1667:U:H2'	84:S2:1668:U:C6	2.51	0.45
84:S2:1801:A:H2'	84:S2:1802:C:H6	1.81	0.45
85:AT:59:A:O2'	85:AT:61:A:OP2	2.34	0.45
4:L5:252:C:H2'	4:L5:253:G:H8	1.82	0.45
4:L5:3861:A:H2'	4:L5:3862:A:H8	1.82	0.45
4:L5:3893:C:O2'	4:L5:4979:A:N1	2.49	0.45
4:L5:4260:U:H2'	4:L5:4261:C:H6	1.82	0.45
4:L5:4536:OMC:HM22	4:L5:4537:C:O4'	2.17	0.45
13:LG:81:ASN:O	13:LG:84:THR:OG1	2.31	0.45
20:LO:61:ARG:HA	20:LO:70:PRO:HD2	1.99	0.45
21:LP:5:SER:OG	21:LP:118:GLN:NE2	2.50	0.45
22:LQ:32:TYR:HD2	22:LQ:51:LEU:HD11	1.80	0.45
35:Ld:114:PHE:HA	35:Ld:117:LEU:HD12	1.99	0.45
39:Lh:89:ARG:O	39:Lh:93:ARG:HG2	2.17	0.45
52:SF:187:SER:OG	52:SF:190:ILE:HG12	2.16	0.45
55:SP:81:ARG:NH1	55:SP:120:SER:OG	2.49	0.45
65:Sg:191:HIS:ND1	65:Sg:195:LEU:HD21	2.31	0.45
66:SA:206:ASP:HB3	66:SA:209:GLU:OE1	2.17	0.45
67:SB:136:ARG:HB3	67:SB:216:LYS:HG3	1.97	0.45
74:SL:132:ARG:HD3	84:S2:114:G:H5'	1.98	0.45
82:Sb:42:LYS:HZ1	82:Sb:58:GLY:H	1.65	0.45
84:S2:1255:G:OP1	84:S2:1256:G:O2'	2.24	0.45
4:L5:423:G:H5'	21:LP:26:PHE:HZ	1.82	0.45
4:L5:1346:C:H2'	4:L5:1347:G:H8	1.81	0.45
4:L5:2079:G:H2'	4:L5:2080:U:C6	2.52	0.45
4:L5:3760:A:C5	84:S2:1826:G:H4'	2.52	0.45
4:L5:4524:G:N3	8:LB:252:ALA:HB1	2.31	0.45
9:LC:150:LEU:O	9:LC:152:LEU:N	2.50	0.45
13:LG:73:ARG:HD3	13:LG:73:ARG:HA	1.81	0.45
18:LM:24:LEU:HB2	18:LM:43:THR:HG21	1.99	0.45
28:LW:19:ARG:NH2	28:LW:37:GLU:OE2	2.50	0.45
58:SS:37:GLY:N	84:S2:1630:A:H5'	2.32	0.45
66:SA:42:LYS:HD3	66:SA:46:ILE:HB	1.98	0.45
69:SE:10:LYS:NZ	84:S2:95:G:OP1	2.33	0.45
71:SH:145:ARG:HE	78:SW:51:GLU:HB2	1.82	0.45
72:SI:56:ARG:HA	72:SI:180:GLY:HA2	1.98	0.45
86:CF:10:ILE:HD12	86:CF:87:VAL:HG21	1.98	0.45
4:L5:150:U:OP2	13:LG:200:THR:OG1	2.27	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2474:G:H2'	4:L5:2502:G:N2	2.31	0.45
4:L5:2878:G:OP2	4:L5:2879:A:O2'	2.29	0.45
4:L5:3595:U:H5''	4:L5:3597:G:OP2	2.17	0.45
4:L5:3856:A:H5''	21:LP:83:TRP:O	2.17	0.45
4:L5:4088:C:H2'	4:L5:4089:G:H8	1.82	0.45
5:L7:120:U:H5''	10:LD:262:LYS:HG2	1.97	0.45
6:L8:66:A:H2'	6:L8:67:U:C6	2.51	0.45
14:LH:24:THR:HA	14:LH:37:ASP:HA	1.99	0.45
14:LH:187:VAL:HG12	14:LH:188:GLN:HG3	1.99	0.45
21:LP:52:THR:HG23	21:LP:85:LYS:HG3	1.99	0.45
31:LZ:11:VAL:HG12	31:LZ:82:PRO:HA	1.99	0.45
55:SP:22:LEU:HA	55:SP:25:LEU:HB2	1.99	0.45
58:SS:62:ASP:OD1	58:SS:62:ASP:N	2.49	0.45
67:SB:145:LYS:HB2	67:SB:145:LYS:HE3	1.72	0.45
70:SG:147:LEU:HD12	70:SG:151:ASP:HB2	1.99	0.45
84:S2:629:A:O2'	84:S2:631:U:OP1	2.34	0.45
84:S2:639:C:H2'	84:S2:640:A:C8	2.52	0.45
84:S2:1217:A:H2'	84:S2:1218:C:C6	2.50	0.45
2:Pt:10:G:N2	2:Pt:26:G:H1'	2.32	0.45
4:L5:1647:U:OP1	89:L5:5288:SPD:H51	2.17	0.45
4:L5:3726:A:H2'	4:L5:3727:A:C8	2.51	0.45
4:L5:4238:G:H2'	4:L5:4239:A:H8	1.82	0.45
4:L5:4587:G:OP1	20:LO:61:ARG:NH1	2.46	0.45
16:LJ:83:LEU:HD22	16:LJ:132:VAL:HG11	1.99	0.45
72:SI:45:THR:OG1	84:S2:308:G:OP1	2.27	0.45
74:SL:127:THR:HB	74:SL:144:LYS:HB3	1.99	0.45
84:S2:186:C:H2'	84:S2:187:G:H8	1.82	0.45
84:S2:494:C:N4	84:S2:509:OMG:HN22	2.15	0.45
84:S2:1243:U:OP2	84:S2:1518:C:O2'	2.24	0.45
3:Et:6:G:H2'	3:Et:7:A:C8	2.52	0.45
4:L5:66:A:O2'	4:L5:326:C:O2	2.35	0.45
4:L5:137:G:H2'	4:L5:138:G:C8	2.50	0.45
4:L5:1912:G:N2	20:LO:87:MET:HE2	2.32	0.45
4:L5:2870:A:H2'	4:L5:2871:A:C8	2.52	0.45
4:L5:3841:OMC:HM23	4:L5:3841:OMC:H1'	1.73	0.45
4:L5:4419:U:H1'	85:AT:57:C:N4	2.32	0.45
6:L8:5:U:H2'	6:L8:6:C:C6	2.52	0.45
8:LB:206:PRO:HG2	8:LB:209:GLN:HG3	1.98	0.45
15:LI:52:MET:HE3	15:LI:163:GLN:HG2	1.99	0.45
39:Lh:107:GLN:O	39:Lh:111:GLU:HG3	2.17	0.45
53:SK:42:ASN:HA	53:SK:45:VAL:HG12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SR:99:ASP:OD2	66:SA:42:LYS:NZ	2.31	0.45
58:SS:38:ARG:HD2	59:ST:45:LEU:HD11	1.99	0.45
59:ST:39:LEU:HD21	59:ST:52:TRP:CZ3	2.52	0.45
70:SG:7:PHE:CE2	70:SG:9:ALA:HB3	2.52	0.45
81:Sa:12:LYS:HG3	81:Sa:15:ARG:HB2	1.99	0.45
84:S2:349:A:H2'	84:S2:350:C:C6	2.51	0.45
84:S2:563:G:HO2'	84:S2:564:A:P	2.39	0.45
4:L5:424:U:H2'	4:L5:425:U:C6	2.52	0.44
4:L5:684:G:H5''	11:LE:100:LYS:HE3	1.99	0.44
4:L5:1818:G:O2'	4:L5:1820:C:OP2	2.26	0.44
4:L5:2072:C:OP1	22:LQ:2:GLY:N	2.50	0.44
4:L5:2306:G:H1'	4:L5:2332:A:N6	2.32	0.44
4:L5:5004:C:H2'	4:L5:5005:G:O4'	2.15	0.44
8:LB:17:LEU:HD23	8:LB:17:LEU:HA	1.79	0.44
11:LE:198:SER:OG	11:LE:288:PHE:O	2.25	0.44
19:LN:75:VAL:HG21	19:LN:80:THR:HG22	1.99	0.44
27:LV:107:ASN:ND2	27:LV:111:GLU:OE2	2.44	0.44
50:Lt:114:ARG:NH2	50:Lt:162:CYS:SG	2.90	0.44
65:Sg:268:ASP:OD1	65:Sg:269:GLU:N	2.50	0.44
79:SX:105:PHE:CE2	79:SX:112:VAL:HB	2.52	0.44
84:S2:348:A:H2'	84:S2:349:A:C8	2.51	0.44
84:S2:441:C:H2'	84:S2:442:C:C6	2.52	0.44
84:S2:454:U:H2'	84:S2:455:A:C8	2.52	0.44
84:S2:1681:U:H2'	84:S2:1682:C:C6	2.51	0.44
86:CF:248:LEU:HD23	86:CF:267:VAL:HA	1.99	0.44
4:L5:85:G:O2'	4:L5:97:G:O6	2.29	0.44
4:L5:138:G:H2'	4:L5:139:G:C8	2.52	0.44
4:L5:1282:G:OP2	11:LE:128:HIS:NE2	2.50	0.44
4:L5:1824:G:H5''	25:LT:35:LYS:HE2	1.99	0.44
4:L5:1960:A:C4	49:Ls:14:PHE:HE2	2.35	0.44
4:L5:3654:G:O2'	4:L5:3693:U:OP1	2.26	0.44
4:L5:4897:G:H2'	4:L5:4898:G:H8	1.81	0.44
13:LG:175:ARG:HG2	13:LG:230:TYR:CD2	2.52	0.44
17:LL:126:LEU:N	17:LL:138:ASP:OD2	2.27	0.44
51:SD:55:THR:HA	51:SD:58:VAL:HG12	1.99	0.44
53:SK:32:HIS:HD2	53:SK:45:VAL:HG11	1.82	0.44
64:Sf:107:LYS:NZ	64:Sf:108:VAL:O	2.51	0.44
70:SG:87:ARG:HD3	70:SG:87:ARG:HA	1.70	0.44
71:SH:18:GLU:OE1	71:SH:18:GLU:N	2.50	0.44
80:SY:9:THR:HG22	84:S2:837:A:N6	2.32	0.44
4:L5:454:U:H2'	4:L5:455:C:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:965:G:H21	4:L5:2092:G:H1'	1.82	0.44
4:L5:1881:C:H5'	4:L5:2281:U:H1'	1.98	0.44
4:L5:1895:G:OP1	12:LF:96:ARG:NH2	2.47	0.44
4:L5:4238:G:H2'	4:L5:4239:A:C8	2.52	0.44
4:L5:4419:U:OP1	4:L5:4475:G:N2	2.48	0.44
17:LL:140:SER:HA	17:LL:143:GLU:HG2	1.99	0.44
50:Lt:151:ILE:O	50:Lt:155:ILE:HB	2.18	0.44
61:SZ:86:ALA:HA	61:SZ:89:GLN:HE21	1.81	0.44
66:SA:18:PHE:CD1	66:SA:23:THR:HG21	2.51	0.44
69:SE:18:TRP:HH2	69:SE:31:PRO:HD3	1.81	0.44
69:SE:72:ILE:HD12	69:SE:77:ARG:HB2	1.99	0.44
80:SY:77:ASP:OD1	80:SY:77:ASP:N	2.47	0.44
4:L5:1998:A:N6	49:Ls:40:MET:SD	2.90	0.44
4:L5:2434:G:H5''	29:LX:83:THR:CG2	2.48	0.44
4:L5:2876:OMG:HM22	4:L5:2877:G:H5'	1.99	0.44
4:L5:4084:G:O6	7:LA:72:ARG:NH2	2.49	0.44
4:L5:4508:C:N3	4:L5:4512:U:H5	2.15	0.44
4:L5:4594:U:H2'	4:L5:4595:G:C8	2.48	0.44
4:L5:4611:A:H2'	4:L5:4612:C:H6	1.83	0.44
7:LA:80:GLU:HB2	7:LA:170:ALA:HA	1.98	0.44
8:LB:113:GLU:OE2	8:LB:169:ARG:NH1	2.50	0.44
35:Ld:44:ARG:HA	35:Ld:47:LYS:HE3	1.99	0.44
56:SQ:97:GLN:HB2	56:SQ:105:LYS:HG3	1.98	0.44
59:ST:39:LEU:HA	59:ST:39:LEU:HD23	1.74	0.44
66:SA:6:ASP:OD1	66:SA:6:ASP:N	2.50	0.44
69:SE:152:PRO:HG2	70:SG:216:ARG:HG3	1.99	0.44
75:SN:83:ASP:OD1	75:SN:84:LEU:N	2.50	0.44
76:SO:149:ARG:NH2	84:S2:961:G:OP1	2.50	0.44
77:SV:18:SER:HB3	77:SV:72:LEU:HD21	2.00	0.44
84:S2:99:A2M:H8	84:S2:99:A2M:O5'	2.18	0.44
84:S2:1560:U:O2	84:S2:1575:G:O6	2.35	0.44
3:Et:43:A:H2'	3:Et:44:G:H8	1.82	0.44
4:L5:979:C:OP2	11:LE:66:LYS:HD3	2.17	0.44
4:L5:4364:G:H2'	4:L5:4365:C:H6	1.83	0.44
6:L8:26:C:O2'	9:LC:53:ALA:O	2.34	0.44
22:LQ:86:ILE:HD11	22:LQ:100:VAL:HG11	1.98	0.44
40:Li:35:LYS:HE3	40:Li:35:LYS:HB3	1.82	0.44
55:SP:37:TYR:HB3	55:SP:41:GLN:HB2	1.99	0.44
57:SR:24:LEU:HD23	57:SR:34:VAL:HG21	2.00	0.44
69:SE:100:ARG:NH2	69:SE:118:GLU:OE2	2.50	0.44
84:S2:932:G:O2'	84:S2:934:G:OP2	2.27	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:S2:1010:G:H2'	84:S2:1011:A:H8	1.82	0.44
84:S2:1037:G:H4'	84:S2:1845:A:H4'	1.98	0.44
86:CF:256:ILE:HB	86:CF:259:ILE:HG22	2.00	0.44
86:CF:353:ILE:CG2	86:CF:394:LEU:HB2	2.47	0.44
4:L5:473:C:H2'	4:L5:474:C:C6	2.52	0.44
4:L5:4742:G:OP1	4:L5:4900:C:N4	2.36	0.44
5:L7:110:G:H2'	5:L7:111:C:C6	2.53	0.44
7:LA:28:ARG:HD2	7:LA:123:ARG:HG3	1.99	0.44
34:Lc:38:ILE:HG21	34:Lc:63:TYR:HB3	1.98	0.44
65:Sg:59:LEU:HD23	65:Sg:90:TRP:CD2	2.53	0.44
68:SC:121:ARG:HH12	68:SC:123:ARG:HE	1.65	0.44
72:SI:86:SER:OG	84:S2:376:A:N3	2.44	0.44
73:SJ:5:ARG:HB3	84:S2:38:A:H5''	2.00	0.44
85:AT:30:C:O2'	85:AT:42:G:N2	2.49	0.44
4:L5:1084:C:H2'	4:L5:1085:C:H6	1.83	0.44
4:L5:1359:G:H4'	19:LN:203:TYR:HB2	2.00	0.44
4:L5:2399:G:O2'	4:L5:2822:G:O2'	2.34	0.44
11:LE:183:ARG:HA	11:LE:183:ARG:HD2	1.80	0.44
17:LL:111:GLN:HA	17:LL:114:VAL:HG22	2.00	0.44
29:LX:122:ALA:N	29:LX:139:ARG:O	2.44	0.44
56:SQ:90:LYS:HA	56:SQ:93:VAL:HG22	1.99	0.44
59:ST:96:SER:HB3	59:ST:99:VAL:HB	1.99	0.44
63:Sd:8:TRP:HZ3	84:S2:1512:C:H5''	1.83	0.44
79:SX:107:ARG:HG2	79:SX:112:VAL:HG22	2.00	0.44
83:Se:12:VAL:HG23	84:S2:616:A:H1'	1.98	0.44
84:S2:495:U:H2'	84:S2:496:C:O4'	2.18	0.44
84:S2:1563:G:H2'	84:S2:1564:C:H6	1.82	0.44
4:L5:132:G:H2'	4:L5:133:C:H4'	1.99	0.44
4:L5:173:C:H2'	4:L5:174:C:C6	2.53	0.44
4:L5:1613:A:H5''	7:LA:183:GLY:CA	2.48	0.44
4:L5:2694:G:OP2	42:Lk:35:LYS:NZ	2.46	0.44
4:L5:5057:C:H2'	4:L5:5058:A:C8	2.53	0.44
29:LX:127:LEU:HD11	29:LX:135:LYS:HE3	2.00	0.44
35:Ld:54:MET:HE3	35:Ld:60:PRO:HA	1.99	0.44
51:SD:27:ARG:NH1	84:S2:1498:A:OP2	2.42	0.44
65:Sg:183:LYS:HA	65:Sg:183:LYS:HD2	1.83	0.44
67:SB:29:ASP:OD1	67:SB:29:ASP:N	2.51	0.44
72:SI:150:ASP:HA	72:SI:153:LYS:CG	2.48	0.44
81:Sa:59:PHE:HB2	81:Sa:62:TYR:HB2	2.00	0.44
82:Sb:42:LYS:HE3	82:Sb:57:VAL:HG22	2.00	0.44
84:S2:525:A:H2'	84:S2:526:A:C8	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:S2:573:U:O2	84:S2:576:A2M:H8	2.17	0.44
84:S2:1628:C:H2'	84:S2:1629:C:C6	2.52	0.44
84:S2:1683:C:H2'	84:S2:1684:C:H6	1.83	0.44
84:S2:1777:G:H2'	84:S2:1778:C:C6	2.53	0.44
85:AT:38:A:C2	85:AT:39:C:C2	3.05	0.44
86:CF:155:MET:HE3	86:CF:192:PRO:CB	2.48	0.44
4:L5:494:U:H2'	4:L5:495:C:C6	2.53	0.44
4:L5:696:C:H42	11:LE:221:LYS:HG3	1.82	0.44
4:L5:716:C:OP1	9:LC:317:ASN:HB2	2.18	0.44
4:L5:1537:A:H2'	4:L5:1538:U:C6	2.53	0.44
4:L5:1677:PSU:H4'	4:L5:1680:G:C2	2.53	0.44
4:L5:2364:OMG:HM23	4:L5:2364:OMG:H1'	1.84	0.44
4:L5:2667:C:O4'	23:LR:96:MET:HG2	2.17	0.44
4:L5:2765:A:H2'	4:L5:2766:A:C8	2.52	0.44
4:L5:2809:G:H5''	23:LR:63:CYS:SG	2.58	0.44
4:L5:3813:A:N3	4:L5:4538:G:O2'	2.45	0.44
4:L5:4327:C:OP1	25:LT:70:HIS:NE2	2.50	0.44
14:LH:128:MET:SD	14:LH:157:SER:HB3	2.58	0.44
18:LM:104:MET:HG3	18:LM:108:ASP:HB2	2.00	0.44
34:Lc:47:ILE:HB	34:Lc:94:LEU:HG	2.00	0.44
34:Lc:82:GLY:HA2	34:Lc:91:VAL:HG12	2.00	0.44
49:Ls:18:ILE:HD12	49:Ls:21:LEU:HD11	1.99	0.44
57:SR:35:CYS:HA	57:SR:38:ILE:HG12	1.99	0.44
58:SS:13:LEU:HD22	58:SS:20:ILE:HD11	1.99	0.44
59:ST:101:ARG:NH2	84:S2:1566:G:N7	2.65	0.44
60:SU:87:ARG:HH22	84:S2:1447:G:P	2.41	0.44
66:SA:220:LYS:HA	66:SA:220:LYS:HD3	1.84	0.44
86:CF:360:VAL:HG13	86:CF:427:ARG:HB2	2.00	0.44
4:L5:1563:A:N6	84:S2:1028:A:N1	2.65	0.43
4:L5:2303:C:H5''	36:Le:104:SER:HB3	2.00	0.43
4:L5:2570:U:H2'	4:L5:2571:C:C6	2.53	0.43
4:L5:2607:C:O5'	23:LR:96:MET:HE1	2.18	0.43
4:L5:2808:G:O3'	23:LR:60:ARG:NH1	2.51	0.43
10:LD:33:ARG:O	10:LD:37:VAL:HG22	2.18	0.43
12:LF:46:ARG:NH2	33:Lb:102:PRO:HG3	2.33	0.43
12:LF:182:TYR:CZ	12:LF:203:GLU:HG2	2.53	0.43
18:LM:115:ALA:HB1	20:LO:192:TYR:HB3	2.00	0.43
28:LW:119:LYS:O	28:LW:123:LYS:HB2	2.18	0.43
53:SK:37:ASP:OD1	53:SK:37:ASP:N	2.47	0.43
58:SS:102:GLY:HA2	58:SS:105:ASN:HD21	1.83	0.43
69:SE:101:LEU:HD12	69:SE:101:LEU:HA	1.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:S2:293:C:O2'	84:S2:294:U:H3'	2.18	0.43
84:S2:835:C:H4'	84:S2:836:G:C8	2.53	0.43
86:CF:350:PRO:HG2	86:CF:429:MET:HE1	1.99	0.43
1:CI:66:GLY:HA3	35:Ld:70:LYS:NZ	2.33	0.43
3:Et:41:U:O3'	52:SF:198:ARG:NE	2.51	0.43
4:L5:1538:U:H2'	4:L5:1539:G:H8	1.83	0.43
4:L5:3606:U:H2'	4:L5:3607:U:C6	2.53	0.43
4:L5:4111:U:H2'	4:L5:4112:C:H5	1.83	0.43
4:L5:4364:G:H2'	4:L5:4365:C:C6	2.53	0.43
12:LF:147:LEU:O	12:LF:151:ASN:ND2	2.43	0.43
64:Sf:139:HIS:O	64:Sf:147:THR:HA	2.17	0.43
69:SE:80:ILE:HG23	69:SE:81:THR:HG23	2.00	0.43
74:SL:23:VAL:HG23	74:SL:25:LEU:HG	2.00	0.43
76:SO:101:GLY:HA3	76:SO:134:PRO:HD2	2.00	0.43
85:AT:8:U:HO2'	85:AT:21:U:H3	1.64	0.43
4:L5:268:G:H2'	4:L5:269:G:C8	2.51	0.43
4:L5:1662:C:H2'	4:L5:1663:C:H6	1.84	0.43
4:L5:2696:A:OP1	42:Lk:26:LYS:NZ	2.41	0.43
4:L5:2845:A:H61	4:L5:3843:C:N4	2.16	0.43
4:L5:2864:A:H2'	4:L5:2865:U:C6	2.52	0.43
4:L5:3599:A:H2'	4:L5:3600:G:C8	2.52	0.43
4:L5:3873:G:H2'	4:L5:3874:G:C8	2.54	0.43
4:L5:3911:C:H2'	4:L5:3912:U:C6	2.52	0.43
4:L5:3928:A:H2'	4:L5:3929:G:O4'	2.17	0.43
4:L5:4076:G:H5'	13:LG:73:ARG:HG3	1.99	0.43
4:L5:4126:C:OP1	13:LG:37:LYS:NZ	2.52	0.43
4:L5:4291:G:H5'	4:L5:4293:PSU:C6	2.53	0.43
4:L5:4743:G:H2'	4:L5:4744:A:C8	2.53	0.43
4:L5:4927:G:H5''	4:L5:4928:C:H5	1.82	0.43
5:L7:55:A:H4'	16:LJ:155:HIS:HB2	1.99	0.43
5:L7:119:U:C2	10:LD:261:VAL:HG11	2.53	0.43
14:LH:8:GLN:HG2	14:LH:74:CYS:SG	2.58	0.43
16:LJ:17:ILE:HD12	16:LJ:80:GLU:HG2	2.00	0.43
18:LM:118:MET:HG2	20:LO:192:TYR:CZ	2.53	0.43
36:Le:85:LEU:HD21	36:Le:115:ALA:HB2	2.00	0.43
54:SM:91:LEU:HD23	54:SM:91:LEU:HA	1.80	0.43
56:SQ:98:LYS:HE3	56:SQ:99:TYR:CZ	2.54	0.43
65:Sg:10:THR:HB	65:Sg:306:LEU:HD21	2.00	0.43
66:SA:42:LYS:HD2	66:SA:48:ILE:HD11	2.00	0.43
66:SA:145:ILE:HG12	66:SA:159:ILE:HB	1.99	0.43
69:SE:122:LYS:HE2	69:SE:124:CYS:SG	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:SG:174:PRO:HB3	84:S2:65:C:C6	2.54	0.43
84:S2:601:OMG:HM23	84:S2:601:OMG:H1'	1.71	0.43
85:AT:4:U:H2'	85:AT:5:C:H6	1.82	0.43
86:CF:418:TYR:CD2	86:CF:421:LEU:HD12	2.53	0.43
3:Et:2:C:H2'	3:Et:3:C:C6	2.52	0.43
3:Et:76:A:H62	4:L5:4371:G:H5'	1.83	0.43
4:L5:1081:C:C2'	4:L5:1082:C:H5'	2.49	0.43
4:L5:1826:G:H4'	33:Lb:43:MET:HE3	2.00	0.43
4:L5:2017:A:HO2'	4:L5:2018:C:P	2.42	0.43
4:L5:2664:G:H4'	4:L5:2677:G:H4'	1.99	0.43
4:L5:3690:U:H2'	4:L5:3691:G:O4'	2.19	0.43
4:L5:4156:G:H5''	4:L5:4157:A:H2'	2.00	0.43
4:L5:4590:A2M:HM'3	4:L5:4590:A2M:H1'	1.78	0.43
17:LL:55:ILE:O	17:LL:97:SER:OG	2.33	0.43
29:LX:121:VAL:HA	29:LX:140:LEU:HA	2.00	0.43
38:Lg:69:LYS:HG3	38:Lg:73:HIS:CD2	2.53	0.43
46:Lo:74:GLU:HB3	46:Lo:77:CYS:HB3	2.01	0.43
49:Ls:29:ILE:HD11	49:Ls:191:GLN:HG2	1.99	0.43
61:SZ:86:ALA:O	61:SZ:90:GLU:HG2	2.18	0.43
65:Sg:135:LEU:HD23	65:Sg:135:LEU:HA	1.88	0.43
66:SA:184:ARG:NE	66:SA:191:ARG:HD3	2.33	0.43
71:SH:18:GLU:C	71:SH:20:GLU:H	2.26	0.43
71:SH:177:TYR:O	71:SH:181:THR:HB	2.19	0.43
84:S2:136:C:H5''	84:S2:137:U:H5''	2.00	0.43
84:S2:152:U:H2'	84:S2:153:G:C8	2.53	0.43
84:S2:867:OMG:H1'	84:S2:867:OMG:HM23	1.74	0.43
84:S2:1533:A:C8	84:S2:1604:G:H1'	2.53	0.43
4:L5:691:C:H2'	4:L5:692:A:H8	1.83	0.43
4:L5:1195:G:H2'	4:L5:1196:G:C8	2.54	0.43
4:L5:2347:A:C4	36:Le:31:ILE:HD11	2.54	0.43
6:L8:36:G:C5	39:Lh:89:ARG:HD3	2.53	0.43
7:LA:22:HIS:O	7:LA:24:LYS:NZ	2.48	0.43
8:LB:29:VAL:HA	8:LB:220:ILE:HD13	2.00	0.43
11:LE:194:VAL:O	37:Lf:108:SER:OG	2.29	0.43
37:Lf:45:LYS:HA	37:Lf:107:PRO:HD2	2.00	0.43
45:Ln:17:ARG:NH1	84:S2:1173:A:OP1	2.52	0.43
70:SG:170:ARG:NH1	84:S2:72:C:O2	2.52	0.43
77:SV:74:LYS:NZ	77:SV:83:PHE:HB3	2.33	0.43
85:AT:18:G:H4'	85:AT:61:A:C6	2.53	0.43
4:L5:1977:C:O2'	4:L5:1978:C:OP1	2.36	0.43
4:L5:2421:G:OP2	4:L5:2828:U:H1'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2671:C:H2'	4:L5:2672:C:C6	2.54	0.43
4:L5:2730:U:H2'	4:L5:2731:C:C6	2.53	0.43
4:L5:4458:C:H2'	4:L5:4459:U:C6	2.54	0.43
4:L5:4507:A:HO2'	27:LV:41:SER:HG	1.66	0.43
7:LA:115:CYS:SG	7:LA:124:GLY:HA3	2.59	0.43
20:LO:88:LEU:HD12	20:LO:99:LEU:HD13	2.01	0.43
28:LW:97:LYS:O	28:LW:99:GLU:N	2.50	0.43
50:Lt:81:ILE:HD13	50:Lt:113:ALA:HB1	2.01	0.43
53:SK:31:LYS:HZ3	53:SK:39:ASN:N	2.16	0.43
72:SI:149:TYR:O	72:SI:153:LYS:HG2	2.19	0.43
80:SY:9:THR:HG22	84:S2:837:A:H61	1.84	0.43
84:S2:27:A2M:HM'3	84:S2:27:A2M:H1'	1.62	0.43
84:S2:1047:C:H2'	84:S2:1048:G:O4'	2.19	0.43
84:S2:1101:U:H2'	84:S2:1102:G:C8	2.54	0.43
4:L5:92:C:OP2	4:L5:4341:C:O2'	2.28	0.43
4:L5:408:A:O2'	4:L5:411:G:OP2	2.25	0.43
4:L5:498:C:C2	4:L5:499:G:H1'	2.54	0.43
4:L5:1466:G:OP2	33:Lb:44:ARG:NH2	2.51	0.43
4:L5:4685:U:H2'	4:L5:4686:G:C8	2.53	0.43
8:LB:46:PHE:CZ	8:LB:84:MET:HG2	2.53	0.43
10:LD:203:ASN:OD1	10:LD:203:ASN:N	2.51	0.43
12:LF:214:SER:OG	12:LF:215:SER:N	2.51	0.43
19:LN:159:ARG:HB3	19:LN:164:LEU:HB2	1.99	0.43
30:LY:72:GLN:HE21	30:LY:74:TYR:HD1	1.67	0.43
33:Lb:43:MET:HE2	33:Lb:47:LYS:NZ	2.33	0.43
45:Ln:2:ARG:NE	84:S2:1842:4AC:OP2	2.42	0.43
62:Sc:10:LYS:HE2	62:Sc:34:PHE:CD2	2.54	0.43
67:SB:147:ASN:OD1	67:SB:148:ASN:N	2.51	0.43
68:SC:64:THR:HG22	68:SC:66:LEU:H	1.83	0.43
70:SG:136:LYS:HB2	84:S2:65:C:H41	1.84	0.43
72:SI:139:LYS:HE2	72:SI:139:LYS:HB2	1.70	0.43
76:SO:63:LYS:HD3	76:SO:63:LYS:HA	1.86	0.43
84:S2:1347:U:H2'	84:S2:1348:G:N3	2.33	0.43
84:S2:1653:U:H2'	84:S2:1654:G:C8	2.53	0.43
84:S2:1839:U:H2'	84:S2:1840:U:C6	2.54	0.43
4:L5:457:G:H2'	4:L5:458:C:C6	2.54	0.43
4:L5:1645:C:H2'	4:L5:1646:A:C8	2.54	0.43
4:L5:3610:A:H2'	4:L5:3611:A:C8	2.54	0.43
4:L5:4742:G:H2'	4:L5:4743:G:C8	2.54	0.43
4:L5:4913:G:H4'	4:L5:4914:C:O5'	2.18	0.43
6:L8:39:G:H1'	6:L8:103:A:N6	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L8:90:C:H1'	30:LY:24:HIS:HB3	2.00	0.43
9:LC:221:PHE:O	9:LC:222:ARG:HG2	2.19	0.43
18:LM:37:LEU:HD22	24:LS:75:VAL:HG23	2.00	0.43
28:LW:52:THR:O	28:LW:56:ARG:HG2	2.18	0.43
30:LY:23:SER:HA	30:LY:26:ARG:HB2	2.00	0.43
35:Ld:33:ILE:HD11	35:Ld:45:ALA:HA	1.99	0.43
39:Lh:95:LEU:HD22	39:Lh:99:GLU:HG3	1.99	0.43
43:Ll:12:PHE:CE2	43:Ll:51:LEU:HD22	2.54	0.43
50:Lt:150:ASP:OD1	50:Lt:151:ILE:N	2.51	0.43
57:SR:111:PHE:HE1	66:SA:12:GLU:HG3	1.84	0.43
60:SU:19:ARG:HB3	60:SU:92:HIS:CD2	2.54	0.43
66:SA:177:MET:SD	66:SA:180:ARG:NH2	2.92	0.43
68:SC:74:LYS:HA	68:SC:74:LYS:HD3	1.88	0.43
71:SH:58:LYS:HA	71:SH:58:LYS:HD2	1.82	0.43
84:S2:116:OMU:HN3	84:S2:347:G:H1	1.66	0.43
84:S2:194:C:H2'	84:S2:195:C:H6	1.84	0.43
84:S2:609:U:H2'	84:S2:610:G:H8	1.82	0.43
85:AT:60:A:H3'	85:AT:61:A:H8	1.83	0.43
4:L5:400:A2M:H1'	4:L5:400:A2M:HM'3	1.63	0.43
4:L5:490:C:H2'	4:L5:491:G:H8	1.82	0.43
4:L5:730:G:OP2	12:LF:76:ARG:NE	2.47	0.43
4:L5:1404:G:N7	4:L5:1408:G:N1	2.66	0.43
4:L5:1847:C:H2'	4:L5:1848:C:C6	2.54	0.43
4:L5:2465:C:H2'	4:L5:2466:G:O4'	2.19	0.43
4:L5:3785:A2M:H2	4:L5:4551:U:O2	2.18	0.43
4:L5:4187:G:OP1	88:L5:5266:SPM:H111	2.19	0.43
8:LB:393:LYS:HG3	8:LB:396:ARG:HH21	1.83	0.43
10:LD:211:LEU:HB3	10:LD:219:TYR:HB2	2.01	0.43
11:LE:203:ILE:O	11:LE:206:VAL:HG22	2.19	0.43
19:LN:200:LEU:HD22	19:LN:204:ARG:NH1	2.33	0.43
23:LR:182:GLU:HA	23:LR:185:ILE:HD13	2.01	0.43
46:Lo:78:ARG:O	46:Lo:80:LYS:NZ	2.52	0.43
61:SZ:48:VAL:HG23	61:SZ:80:ARG:HD2	2.00	0.43
65:Sg:17:TRP:HB2	65:Sg:36:ARG:HD3	2.00	0.43
72:SI:64:ASN:OD1	72:SI:73:THR:HG22	2.18	0.43
84:S2:1279:C:H2'	84:S2:1280:G:H8	1.84	0.43
84:S2:1754:G:N7	84:S2:1779:G:N2	2.66	0.43
84:S2:1759:G:N2	84:S2:1760:G:O6	2.50	0.43
85:AT:10:G:H2'	85:AT:11:U:H6	1.83	0.43
86:CF:244:LYS:H	86:CF:244:LYS:HG2	1.63	0.43
3:Et:15:G:N1	3:Et:59:G:N7	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:108:A:N1	4:L5:333:U:O2'	2.49	0.43
4:L5:262:G:H2'	4:L5:263:G:C8	2.53	0.43
4:L5:1392:A:H2'	4:L5:1393:G:C8	2.54	0.43
4:L5:1751:A:H2'	4:L5:1752:G:H8	1.84	0.43
4:L5:2415:U:H2'	4:L5:2416:G:C8	2.54	0.43
4:L5:3722:G:H2'	4:L5:3723:A:H8	1.83	0.43
88:L5:5262:SPM:HN0	88:L5:5262:SPM:H131	1.54	0.43
5:L7:63:C:H5'	5:L7:64:G:H5''	2.01	0.43
41:Lj:67:LEU:HD23	41:Lj:67:LEU:HA	1.87	0.43
59:ST:104:LEU:HD22	59:ST:121:ARG:HD2	2.01	0.43
60:SU:38:ASP:OD1	60:SU:39:LEU:N	2.51	0.43
63:Sd:56:ASP:OXT	84:S2:1480:A:O2'	2.31	0.43
68:SC:167:ARG:HB3	68:SC:177:PRO:HB2	2.00	0.43
68:SC:214:LEU:HD22	68:SC:244:ILE:HD11	2.01	0.43
76:SO:113:GLN:OE1	81:Sa:46:GLU:N	2.52	0.43
80:SY:68:LYS:HE2	80:SY:68:LYS:HB3	1.76	0.43
84:S2:1102:G:H2'	84:S2:1103:C:C6	2.54	0.43
84:S2:1278:A:H2'	84:S2:1279:C:C6	2.54	0.43
84:S2:1540:G:H2'	84:S2:1541:G:H8	1.84	0.43
84:S2:1797:U:H2'	84:S2:1798:C:C6	2.54	0.43
84:S2:1845:A:H2'	84:S2:1846:G:H8	1.82	0.43
86:CF:281:ALA:HB2	86:CF:334:PRO:HB2	2.00	0.43
4:L5:264:C:H2'	4:L5:265:C:C4	2.54	0.42
4:L5:1084:C:H2'	4:L5:1085:C:C6	2.53	0.42
4:L5:2864:A:H2'	4:L5:2865:U:H6	1.84	0.42
4:L5:3782:5MC:OP1	45:Ln:23:ARG:NH2	2.52	0.42
4:L5:3867:A2M:H2'	4:L5:3868:G:O4'	2.18	0.42
4:L5:4392:OMG:H2'	4:L5:4447:5MC:HM51	2.01	0.42
4:L5:4589:A:N1	4:L5:4621:C:O2'	2.40	0.42
5:L7:111:C:H2'	5:L7:112:U:O4'	2.19	0.42
6:L8:67:U:H2'	6:L8:68:G:C8	2.54	0.42
7:LA:20:VAL:HA	7:LA:23:ARG:HG3	1.99	0.42
15:LI:73:ASN:HB2	15:LI:87:MET:HE1	2.00	0.42
29:LX:82:THR:HG21	39:Lh:37:THR:HG22	2.01	0.42
55:SP:120:SER:OG	55:SP:120:SER:O	2.35	0.42
65:Sg:270:LEU:HD13	65:Sg:310:TRP:CE3	2.54	0.42
65:Sg:283:PRO:O	65:Sg:285:GLN:NE2	2.52	0.42
66:SA:147:LEU:HD13	66:SA:161:ILE:HB	2.01	0.42
78:SW:28:ARG:HB3	78:SW:29:PRO:HD3	2.00	0.42
79:SX:88:ASP:HA	84:S2:617:G:H4'	2.01	0.42
85:AT:51:U:H3	85:AT:65:G:H1	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:252:C:H2'	4:L5:253:G:C8	2.54	0.42
4:L5:922:C:H2'	4:L5:923:C:O4'	2.19	0.42
4:L5:1625:OMG:HM23	19:LN:81:TYR:HE2	1.84	0.42
4:L5:2638:G:H22	4:L5:2719:C:P	2.41	0.42
4:L5:3718:A2M:H2'	4:L5:3719:A:O4'	2.19	0.42
4:L5:4322:G:N2	4:L5:4325:A:OP2	2.43	0.42
4:L5:4887:C:N4	4:L5:4932:U:H3	2.16	0.42
89:L5:5282:SPD:H82	89:L5:5282:SPD:H51	1.78	0.42
5:L7:4:U:H2'	5:L7:5:A:H8	1.84	0.42
25:LT:28:ALA:O	25:LT:32:ARG:HG2	2.19	0.42
41:Lj:85:LYS:HB3	41:Lj:85:LYS:HE3	1.71	0.42
51:SD:215:ASP:OD1	51:SD:216:GLU:N	2.46	0.42
52:SF:79:HIS:O	52:SF:81:ARG:N	2.48	0.42
52:SF:167:LYS:HA	61:SZ:71:ALA:HB1	2.01	0.42
56:SQ:110:ASP:OD1	56:SQ:110:ASP:N	2.49	0.42
67:SB:83:LYS:HD3	67:SB:106:THR:HG22	2.01	0.42
76:SO:147:ARG:HH22	84:S2:1854:U:P	2.42	0.42
84:S2:166:A2M:HM'3	84:S2:166:A2M:H1'	1.66	0.42
84:S2:186:C:H2'	84:S2:187:G:C8	2.54	0.42
84:S2:194:C:H2'	84:S2:195:C:C6	2.53	0.42
84:S2:693:A:H2'	84:S2:694:G:N7	2.33	0.42
84:S2:1217:A:H2'	84:S2:1218:C:H6	1.84	0.42
84:S2:1259:A:H1'	84:S2:1264:C:N4	2.34	0.42
84:S2:1719:A:N6	84:S2:1814:G:O2'	2.52	0.42
1:CI:72:ARG:NH2	23:LR:25:ASP:OD2	2.47	0.42
3:Et:35:U:H2'	3:Et:36:U:C6	2.54	0.42
4:L5:908:G:H2'	4:L5:909:A:H8	1.83	0.42
4:L5:1175:A:H2	4:L5:1185:G:H1	1.66	0.42
4:L5:1178:G:H2'	10:LD:286:SER:HB3	2.00	0.42
4:L5:1278:C:H2'	4:L5:1279:A:O4'	2.19	0.42
4:L5:1510:G:H2'	4:L5:1511:U:C6	2.55	0.42
4:L5:1981:G:N1	4:L5:1982:G:O6	2.52	0.42
4:L5:2335:C:H2'	4:L5:2336:G:H8	1.85	0.42
4:L5:2448:G:H2'	4:L5:2449:A:C8	2.55	0.42
4:L5:4524:G:OP1	4:L5:4559:A:N6	2.47	0.42
4:L5:4987:C:P	8:LB:116:ARG:HH22	2.41	0.42
20:LO:142:ALA:HA	20:LO:145:VAL:HG12	2.00	0.42
22:LQ:110:ARG:HG3	22:LQ:120:ILE:HD12	2.00	0.42
36:Le:35:TRP:CZ2	36:Le:56:PRO:HD2	2.54	0.42
53:SK:91:PRO:HB2	53:SK:94:LEU:HD23	2.01	0.42
67:SB:214:LYS:HE2	67:SB:216:LYS:HE3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SE:186:GLY:HA3	84:S2:809:A:OP1	2.20	0.42
84:S2:659:G:O2'	84:S2:662:G:O2'	2.29	0.42
84:S2:1112:U:O2	84:S2:1121:G:O6	2.38	0.42
84:S2:1401:A:H2'	84:S2:1402:A:C8	2.53	0.42
84:S2:1563:G:H2'	84:S2:1564:C:C6	2.55	0.42
86:CF:237:PRO:HA	86:CF:238:PRO:HD3	1.92	0.42
86:CF:347:LEU:C	86:CF:396:SER:HG	2.27	0.42
4:L5:1352:C:O2'	4:L5:1356:U:OP1	2.32	0.42
4:L5:1979:A:H1'	4:L5:1988:G:N2	2.34	0.42
4:L5:3656:A:H2'	4:L5:3657:U:H6	1.83	0.42
4:L5:3937:C:O2'	19:LN:124:ASP:OD1	2.37	0.42
4:L5:5006:U:H4'	4:L5:5007:A:H5'	2.01	0.42
6:L8:102:G:H5''	41:Lj:39:TYR:HE1	1.83	0.42
10:LD:37:VAL:HG12	10:LD:50:ARG:HD3	2.01	0.42
16:LJ:35:ARG:O	16:LJ:39:VAL:HG23	2.20	0.42
20:LO:28:LEU:HD23	20:LO:28:LEU:HA	1.94	0.42
23:LR:176:ARG:NH1	23:LR:177:LEU:HG	2.35	0.42
25:LT:39:ILE:HG13	25:LT:102:ARG:HE	1.85	0.42
58:SS:78:LYS:HD3	58:SS:78:LYS:HA	1.75	0.42
68:SC:202:THR:HG23	73:SJ:54:ARG:HH22	1.84	0.42
73:SJ:28:GLU:OE2	73:SJ:44:TRP:NE1	2.41	0.42
78:SW:5:ASN:HB3	78:SW:8:ALA:HB3	2.00	0.42
84:S2:517:OMC:H2'	84:S2:518:G:O4'	2.19	0.42
84:S2:888:U:O2'	84:S2:898:U:N3	2.49	0.42
84:S2:1279:C:H2'	84:S2:1280:G:C8	2.54	0.42
84:S2:1733:U:H2'	84:S2:1734:G:O4'	2.20	0.42
84:S2:1779:G:H2'	84:S2:1780:G:C8	2.53	0.42
85:AT:22:A:H2'	85:AT:23:U:C6	2.53	0.42
4:L5:37:U:H2'	4:L5:38:A:O4'	2.19	0.42
4:L5:491:G:H2'	4:L5:492:U:C6	2.55	0.42
4:L5:1410:U:H3	33:Lb:52:LYS:NZ	2.17	0.42
4:L5:1631:A:C8	7:LA:199:VAL:HG21	2.55	0.42
4:L5:1806:G:H2'	4:L5:1807:C:H6	1.83	0.42
4:L5:2017:A:HO2'	4:L5:2018:C:C5'	2.31	0.42
4:L5:2517:A:N3	4:L5:2539:C:O2'	2.49	0.42
7:LA:145:LYS:HA	7:LA:145:LYS:HD3	1.84	0.42
43:Ll:28:ARG:HA	43:Ll:33:ASN:ND2	2.32	0.42
51:SD:163:PRO:O	51:SD:167:TYR:HB2	2.20	0.42
53:SK:64:TRP:CD2	63:Sd:23:VAL:HG22	2.54	0.42
59:ST:72:VAL:O	59:ST:76:THR:HG23	2.19	0.42
66:SA:104:THR:O	66:SA:107:THR:OG1	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SA:215:GLN:O	66:SA:219:GLU:HG2	2.19	0.42
70:SG:227:GLN:HB3	70:SG:231:ARG:HH21	1.83	0.42
71:SH:118:ARG:HD3	71:SH:118:ARG:HA	1.90	0.42
76:SO:96:LYS:HD3	76:SO:132:VAL:HG11	2.02	0.42
79:SX:9:THR:HG22	84:S2:681:PSU:H4'	2.02	0.42
79:SX:28:LYS:O	79:SX:32:LEU:HB2	2.19	0.42
84:S2:1597:C:H4'	84:S2:1603:G:O6	2.19	0.42
85:AT:18:G:H4'	85:AT:61:A:N1	2.34	0.42
85:AT:53:G:C2	85:AT:64:G:C2	3.07	0.42
4:L5:1308:C:H2'	4:L5:1309:C:C6	2.55	0.42
4:L5:2543:A:H2	4:L5:2773:G:H22	1.67	0.42
4:L5:2844:A:O2'	4:L5:4631:G:H4'	2.20	0.42
4:L5:3822:PSU:OP1	88:L5:5289:SPM:N5	2.31	0.42
4:L5:4389:C:H2'	4:L5:4390:A:H8	1.85	0.42
4:L5:4637:OMG:HM23	4:L5:4637:OMG:H1'	1.77	0.42
6:L8:144:U:H2'	6:L8:145:C:C6	2.54	0.42
8:LB:337:VAL:HG11	8:LB:345:LEU:HD13	2.02	0.42
10:LD:53:VAL:HG11	10:LD:159:VAL:HA	2.01	0.42
11:LE:227:HIS:HE1	11:LE:230:GLY:HA2	1.83	0.42
12:LF:236:ARG:HD3	12:LF:239:GLN:HB2	2.02	0.42
22:LQ:69:LYS:HA	22:LQ:69:LYS:HD3	1.89	0.42
31:LZ:41:ALA:HB2	31:LZ:77:TYR:HE1	1.84	0.42
36:Le:99:ILE:HD13	36:Le:108:ARG:HB2	2.02	0.42
46:Lo:4:VAL:HG23	46:Lo:93:LEU:HD23	2.02	0.42
49:Ls:78:LEU:O	49:Ls:82:ILE:HG12	2.19	0.42
52:SF:112:LEU:HD13	52:SF:177:LEU:HD21	2.02	0.42
62:Sc:44:ARG:NH2	62:Sc:63:ARG:HH11	2.18	0.42
72:SI:141:ARG:HA	72:SI:141:ARG:CZ	2.50	0.42
77:SV:11:LEU:HD23	77:SV:11:LEU:H	1.84	0.42
79:SX:34:THR:HG21	84:S2:1189:A:H4'	2.01	0.42
84:S2:382:C:H2'	84:S2:383:G:C8	2.55	0.42
4:L5:72:C:H5	17:LL:67:HIS:HD1	1.66	0.42
4:L5:1613:A:H5''	7:LA:183:GLY:HA2	2.02	0.42
4:L5:2326:G:H5''	36:Le:127:ALA:HB1	2.00	0.42
4:L5:4113:U:H4'	4:L5:4115:G:C5	2.55	0.42
4:L5:4578:G:H2'	4:L5:4579:PSU:C6	2.55	0.42
4:L5:4638:U:H2'	4:L5:4639:G:N3	2.35	0.42
4:L5:4940:C:H5'	4:L5:4941:G:H5''	2.01	0.42
9:LC:279:LEU:HD23	9:LC:279:LEU:HA	1.88	0.42
15:LI:14:ASN:O	15:LI:128:ARG:NH2	2.24	0.42
15:LI:51:HIS:CD2	15:LI:168:SER:HB3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LP:76:TRP:CD1	21:LP:76:TRP:H	2.37	0.42
24:LS:69:GLU:HG3	24:LS:71:SER:H	1.84	0.42
24:LS:93:MET:HE1	24:LS:117:HIS:CE1	2.54	0.42
28:LW:47:ARG:HE	28:LW:54:LEU:HD22	1.85	0.42
30:LY:50:ARG:HB3	30:LY:53:ASP:OD2	2.19	0.42
40:Li:76:ARG:HD3	40:Li:76:ARG:HA	1.80	0.42
50:Lt:119:ARG:NH2	50:Lt:123:ARG:HH12	2.18	0.42
60:SU:19:ARG:HH11	60:SU:92:HIS:HB3	1.85	0.42
71:SH:63:PHE:HB3	71:SH:97:GLN:HG3	2.01	0.42
84:S2:24:C:HO2'	84:S2:25:A:H8	1.66	0.42
84:S2:496:C:H2'	84:S2:497:C:H6	1.85	0.42
3:Et:2:C:H2'	3:Et:3:C:H6	1.85	0.42
4:L5:1172:C:O2'	4:L5:1173:G:H8	2.02	0.42
4:L5:1177:U:O2'	10:LD:286:SER:OG	2.28	0.42
4:L5:1703:C:O2'	4:L5:1704:C:O5'	2.38	0.42
4:L5:2521:G:H5'	4:L5:2640:G:H1'	2.02	0.42
4:L5:2823:G:N7	23:LR:20:LYS:HD3	2.35	0.42
4:L5:3684:G:H2'	4:L5:3685:C:C6	2.55	0.42
13:LG:176:LYS:HD3	40:Li:43:MET:HE1	2.02	0.42
23:LR:82:LYS:HA	23:LR:82:LYS:HD2	1.87	0.42
33:Lb:65:MET:HG3	33:Lb:68:ARG:HH12	1.85	0.42
52:SF:123:GLU:OE1	62:Sc:63:ARG:NH2	2.53	0.42
53:SK:47:LYS:HZ2	84:S2:1274:G:H4'	1.84	0.42
54:SM:20:GLU:HG2	54:SM:119:GLN:HB2	2.00	0.42
57:SR:7:LYS:NZ	84:S2:1373:C:OP1	2.41	0.42
58:SS:92:ASP:OD1	58:SS:92:ASP:N	2.51	0.42
60:SU:61:LEU:HB2	60:SU:82:MET:HB3	2.02	0.42
69:SE:27:PHE:O	84:S2:495:U:O2'	2.37	0.42
69:SE:139:LEU:HD22	69:SE:147:ILE:HD11	2.01	0.42
70:SG:31:ARG:NH1	84:S2:1745:A:O3'	2.52	0.42
72:SI:161:LEU:HD23	72:SI:195:LEU:HG	2.01	0.42
84:S2:1139:C:H2'	84:S2:1140:G:O4'	2.19	0.42
84:S2:1328:OMG:H1'	84:S2:1328:OMG:HM23	1.80	0.42
84:S2:1533:A:H62	84:S2:1602:U:H3	1.67	0.42
1:CI:63:ARG:HD2	1:CI:63:ARG:HA	1.85	0.42
3:Et:43:A:H2'	3:Et:44:G:C8	2.55	0.42
4:L5:89:C:OP1	32:La:59:LYS:NZ	2.42	0.42
4:L5:120:A:H2'	4:L5:149:A:H61	1.85	0.42
4:L5:959:G:C8	11:LE:123:ARG:HG2	2.55	0.42
4:L5:982:U:H2'	4:L5:983:C:C6	2.55	0.42
4:L5:4192:A:H2'	4:L5:4193:C:H6	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4239:A:H2'	4:L5:4240:G:H8	1.85	0.42
4:L5:4305:G:C6	25:LT:80:VAL:HG21	2.55	0.42
5:L7:4:U:H2'	5:L7:5:A:C8	2.55	0.42
6:L8:58:G:O6	41:Lj:63:ARG:NH1	2.53	0.42
7:LA:7:GLY:HA2	7:LA:10:LYS:HG3	2.02	0.42
24:LS:15:ARG:HD2	24:LS:25:PRO:HG2	2.00	0.42
25:LT:4:THR:OG1	25:LT:9:ARG:HD3	2.20	0.42
30:LY:22:PRO:HD2	30:LY:25:ILE:HD11	2.01	0.42
51:SD:213:PRO:HB3	57:SR:20:TYR:CE1	2.55	0.42
54:SM:17:ALA:O	54:SM:20:GLU:HG3	2.18	0.42
55:SP:56:LEU:HG	55:SP:60:LEU:HD13	2.02	0.42
60:SU:104:ILE:HB	60:SU:106:ILE:HG12	2.01	0.42
67:SB:120:MET:HE1	84:S2:987:A:C6	2.55	0.42
67:SB:141:GLY:HA3	67:SB:207:LEU:HD23	2.02	0.42
68:SC:64:THR:HG22	68:SC:66:LEU:N	2.35	0.42
69:SE:160:ILE:HD12	69:SE:162:ILE:HD11	2.00	0.42
71:SH:43:LEU:HB3	71:SH:72:PHE:CE1	2.55	0.42
81:Sa:13:LYS:HA	81:Sa:13:LYS:HD3	1.71	0.42
84:S2:64:A:N6	84:S2:83:A:OP2	2.53	0.42
84:S2:352:U:H2'	84:S2:353:C:C6	2.55	0.42
84:S2:692:G:N7	84:S2:693:A:N6	2.67	0.42
84:S2:804:U:H2'	84:S2:805:U:C6	2.55	0.42
84:S2:808:A:H2	84:S2:855:G:H22	1.68	0.42
84:S2:1232:PSU:H2'	84:S2:1233:G:H8	1.85	0.42
84:S2:1393:G:H2'	84:S2:1394:G:C8	2.55	0.42
84:S2:1670:C:H2'	84:S2:1671:G:C8	2.55	0.42
84:S2:1705:C:H2'	84:S2:1706:G:C8	2.55	0.42
2:Pt:9:A:O2'	2:Pt:10:G:N7	2.37	0.42
4:L5:223:G:H4'	4:L5:225:G:C8	2.54	0.42
4:L5:270:U:H2'	4:L5:271:C:C6	2.55	0.42
4:L5:1345:A:H2'	4:L5:1346:C:C6	2.54	0.42
4:L5:1444:G:H22	4:L5:2104:G:N2	2.18	0.42
4:L5:4991:U:H2'	4:L5:4992:G:C8	2.55	0.42
11:LE:157:HIS:HA	11:LE:160:LYS:HE3	2.01	0.42
14:LH:43:VAL:HG21	14:LH:73:ILE:HD13	2.02	0.42
24:LS:83:ARG:HG3	24:LS:125:GLN:HB2	2.01	0.42
50:Lt:79:ALA:HA	50:Lt:82:ILE:HG22	2.01	0.42
52:SF:59:LYS:HB3	52:SF:62:ARG:HG3	2.02	0.42
54:SM:31:LEU:HG	54:SM:33:ARG:HG3	2.01	0.42
61:SZ:102:LYS:HA	61:SZ:102:LYS:HD3	1.80	0.42
75:SN:29:THR:O	75:SN:33:VAL:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:CF:218:ARG:HD3	86:CF:236:LEU:HD11	2.02	0.42
86:CF:353:ILE:HG22	86:CF:394:LEU:HB2	2.02	0.42
4:L5:10:A:H2'	4:L5:11:G:H8	1.83	0.41
4:L5:153:G:H2'	4:L5:154:G:H8	1.84	0.41
4:L5:1405:C:N3	4:L5:1413:C:N4	2.68	0.41
4:L5:2558:C:H2'	4:L5:2559:G:H8	1.84	0.41
4:L5:4102:C:H1'	4:L5:4108:G:H1	1.85	0.41
4:L5:4723:A:H2'	4:L5:4724:A:C8	2.55	0.41
6:L8:92:U:H2'	6:L8:93:C:O4'	2.20	0.41
9:LC:33:ARG:HG2	9:LC:36:ILE:HD12	2.02	0.41
9:LC:318:PRO:O	9:LC:319:LEU:HB2	2.20	0.41
12:LF:228:VAL:HG12	24:LS:38:VAL:HG12	2.02	0.41
16:LJ:20:LEU:HD21	16:LJ:130:PHE:CD2	2.55	0.41
16:LJ:113:ILE:HD11	58:SS:14:ARG:HD3	2.01	0.41
23:LR:105:LEU:HD23	23:LR:138:LEU:HD23	2.01	0.41
30:LY:50:ARG:NH1	30:LY:51:LYS:HB3	2.34	0.41
47:Lp:23:ARG:HA	47:Lp:26:VAL:HG12	2.03	0.41
50:Lt:147:HIS:HA	50:Lt:148:PRO:HD3	1.83	0.41
52:SF:193:LYS:O	52:SF:197:GLU:HG2	2.20	0.41
58:SS:61:GLU:HA	58:SS:64:VAL:HG12	2.02	0.41
59:ST:71:GLY:O	59:ST:75:MET:HG2	2.19	0.41
65:Sg:101:PHE:CD2	65:Sg:136:GLY:HA2	2.55	0.41
65:Sg:227:LEU:HD23	65:Sg:228:TYR:HB2	2.02	0.41
66:SA:180:ARG:HH11	66:SA:184:ARG:HH11	1.68	0.41
67:SB:71:LEU:HD22	67:SB:82:ARG:HD2	2.02	0.41
69:SE:212:ASP:OD1	69:SE:216:ASN:N	2.52	0.41
71:SH:25:GLN:O	71:SH:28:LEU:HG	2.19	0.41
72:SI:141:ARG:NE	84:S2:191:A:OP1	2.53	0.41
74:SL:48:LYS:HD3	74:SL:52:GLU:OE2	2.20	0.41
76:SO:140:THR:HB	84:S2:1046:PSU:H1'	2.01	0.41
84:S2:43:U:OP2	84:S2:485:A:N6	2.45	0.41
84:S2:71:G:H2'	84:S2:72:C:H4'	2.01	0.41
4:L5:279:A:OP2	19:LN:8:GLN:NE2	2.42	0.41
4:L5:1346:C:H2'	4:L5:1347:G:C8	2.54	0.41
4:L5:1631:A:C2	7:LA:204:MET:HG2	2.54	0.41
4:L5:1973:G:O2'	50:Lt:117:ARG:NH2	2.48	0.41
4:L5:4578:G:H2'	4:L5:4579:PSU:H6	1.86	0.41
8:LB:154:LYS:HE2	8:LB:154:LYS:HB2	1.72	0.41
29:LX:80:PRO:HA	29:LX:98:PHE:HA	2.00	0.41
50:Lt:12:VAL:HG11	50:Lt:65:GLN:N	2.35	0.41
64:Sf:123:SER:HG	64:Sf:144:CYS:HB3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:Sg:54:ILE:HD12	65:Sg:55:PRO:HD2	2.02	0.41
79:SX:22:TRP:HE3	79:SX:28:LYS:HD2	1.84	0.41
84:S2:433:A:H2'	84:S2:434:G:C8	2.56	0.41
84:S2:562:U:H2'	84:S2:563:G:C8	2.55	0.41
84:S2:1713:C:H2'	84:S2:1714:U:C6	2.55	0.41
86:CF:78:TRP:CD1	86:CF:79:LYS:N	2.88	0.41
86:CF:96:ARG:HH22	86:CF:431:GLN:HG2	1.84	0.41
4:L5:1086:C:H2'	4:L5:1087:A:H8	1.85	0.41
4:L5:1317:U:H2'	4:L5:1318:C:C6	2.54	0.41
4:L5:1693:U:H2'	4:L5:1694:C:O4'	2.20	0.41
4:L5:2424:OMG:H1'	4:L5:2424:OMG:HM23	1.80	0.41
4:L5:2656:U:H5''	31:LZ:38:TYR:HB3	2.02	0.41
4:L5:2803:U:H2'	4:L5:2804:OMC:H6	1.85	0.41
4:L5:3607:U:H2'	4:L5:3608:A:C8	2.55	0.41
4:L5:4617:G:OP1	8:LB:62:ARG:NH1	2.41	0.41
4:L5:4653:C:H2'	4:L5:4654:C:C6	2.55	0.41
4:L5:4680:G:H2'	4:L5:4681:A:C8	2.55	0.41
5:L7:7:G:H5''	10:LD:22:ARG:HD3	2.02	0.41
5:L7:35:U:O2	5:L7:45:U:O2'	2.35	0.41
7:LA:131:GLY:N	7:LA:169:VAL:HG13	2.34	0.41
13:LG:30:PRO:HG2	31:LZ:124:THR:HA	2.02	0.41
13:LG:207:VAL:O	13:LG:212:LYS:NZ	2.54	0.41
18:LM:86:TRP:O	18:LM:89:THR:OG1	2.34	0.41
31:LZ:95:VAL:HG12	31:LZ:110:ALA:HA	2.02	0.41
34:Lc:18:LEU:O	34:Lc:22:MET:HG2	2.20	0.41
49:Ls:57:LYS:O	49:Ls:61:MET:HG2	2.20	0.41
64:Sf:108:VAL:HB	64:Sf:113:LYS:H	1.85	0.41
66:SA:5:LEU:HD11	77:SV:41:LYS:HD2	2.01	0.41
70:SG:136:LYS:O	70:SG:176:ILE:HG13	2.19	0.41
73:SJ:81:LEU:HD23	73:SJ:81:LEU:HA	1.92	0.41
73:SJ:176:LYS:HA	73:SJ:179:LYS:HG2	2.01	0.41
77:SV:40:ASP:OD1	77:SV:44:GLY:N	2.53	0.41
84:S2:484:A2M:H8	84:S2:484:A2M:O5'	2.19	0.41
84:S2:1199:A:H2'	84:S2:1200:A:C8	2.55	0.41
84:S2:1348:G:OP2	84:S2:1348:G:N2	2.50	0.41
4:L5:1497:A:N6	22:LQ:175:GLU:O	2.53	0.41
4:L5:2073:C:OP1	12:LF:212:LYS:HE3	2.20	0.41
4:L5:2368:A:N6	4:L5:2827:G:O2'	2.52	0.41
4:L5:2743:A:H2'	4:L5:2744:A:C8	2.55	0.41
4:L5:4069:U:H2'	4:L5:4070:U:C6	2.55	0.41
4:L5:4227:OMU:HM23	4:L5:4227:OMU:H1'	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4619:U:H2'	4:L5:4620:OMU:H6	2.01	0.41
4:L5:4670:C:O2'	4:L5:4672:A:OP2	2.29	0.41
6:L8:148:A:H2'	6:L8:149:G:C8	2.55	0.41
7:LA:75:LEU:HD12	7:LA:75:LEU:HA	1.89	0.41
23:LR:99:MET:HE2	23:LR:99:MET:HA	2.02	0.41
52:SF:182:LYS:HE3	52:SF:182:LYS:HB2	1.88	0.41
55:SP:86:LEU:H	55:SP:89:MET:CE	2.33	0.41
55:SP:93:MET:HE1	55:SP:106:GLU:OE1	2.19	0.41
66:SA:122:LEU:HD22	66:SA:137:ALA:HB2	2.01	0.41
68:SC:256:TRP:CE2	78:SW:68:ARG:HD3	2.55	0.41
69:SE:89:VAL:HG11	69:SE:119:ALA:HB1	2.01	0.41
69:SE:242:LYS:HD3	69:SE:242:LYS:HA	1.76	0.41
80:SY:42:GLU:O	80:SY:46:LYS:HG3	2.20	0.41
84:S2:834:C:H42	84:S2:839:C:H42	1.68	0.41
84:S2:1025:U:H2'	84:S2:1026:C:O4'	2.20	0.41
84:S2:1417:C:O2	84:S2:1422:G:C6	2.74	0.41
4:L5:126:C:H2'	4:L5:127:G:H8	1.84	0.41
4:L5:462:G:H2'	4:L5:463:A:C8	2.55	0.41
4:L5:1419:G:H5''	22:LQ:71:LYS:NZ	2.36	0.41
4:L5:1972:G:H2'	4:L5:1973:G:C8	2.55	0.41
4:L5:5002:U:H2'	4:L5:5003:U:C6	2.55	0.41
21:LP:32:THR:HG23	21:LP:58:VAL:HG11	2.01	0.41
57:SR:60:ARG:HA	57:SR:63:ARG:HG2	2.02	0.41
59:ST:62:ARG:CZ	84:S2:1542:C:H5''	2.50	0.41
62:Sc:44:ARG:HH22	62:Sc:63:ARG:HH11	1.69	0.41
74:SL:82:MET:HE3	74:SL:82:MET:HB2	1.94	0.41
78:SW:106:THR:OG1	78:SW:111:MET:HE2	2.20	0.41
84:S2:595:U:H2'	84:S2:596:U:C6	2.56	0.41
84:S2:880:G:H3'	84:S2:881:G:H8	1.85	0.41
85:AT:25:A:H2'	85:AT:26:C:O4'	2.21	0.41
85:AT:36:A:C6	85:AT:37:C:C5	3.08	0.41
3:Et:51:G:H2'	3:Et:52:G:H8	1.84	0.41
4:L5:398:A2M:HM'3	4:L5:398:A2M:H1'	1.79	0.41
4:L5:513:U:H3'	4:L5:514:U:H4'	2.02	0.41
4:L5:956:A:H1'	4:L5:2076:G:H5''	2.02	0.41
4:L5:1558:A:H2'	4:L5:1559:G:C8	2.55	0.41
4:L5:2749:C:H2'	4:L5:2750:G:C8	2.56	0.41
4:L5:3689:G:O2'	4:L5:3818:UY1:OP2	2.34	0.41
4:L5:4196:OMG:HM23	4:L5:4196:OMG:H1'	1.70	0.41
4:L5:4749:C:H2'	4:L5:4750:G:O4'	2.20	0.41
5:L7:7:G:OP1	10:LD:33:ARG:NH1	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LA:13:GLY:O	7:LA:17:ARG:HG3	2.20	0.41
21:LP:94:MET:HE1	21:LP:146:ILE:HB	2.03	0.41
30:LY:47:MET:HE3	30:LY:48:PRO:HD2	2.01	0.41
31:LZ:135:ARG:HD2	31:LZ:135:ARG:HA	1.85	0.41
36:Le:89:LEU:HD13	36:Le:118:LEU:HD22	2.02	0.41
39:Lh:52:LYS:HA	39:Lh:52:LYS:HD3	1.80	0.41
57:SR:6:THR:HA	84:S2:1373:C:H5'	2.02	0.41
60:SU:70:CYS:HG	84:S2:1491:G:HO2'	1.53	0.41
64:Sf:117:LEU:HD12	64:Sf:118:ARG:HD3	2.01	0.41
65:Sg:207:CYS:SG	65:Sg:219:TRP:HB2	2.61	0.41
65:Sg:251:ALA:HA	65:Sg:256:ILE:HD13	2.03	0.41
72:SI:5:ARG:NE	84:S2:379:C:O2	2.53	0.41
72:SI:23:LYS:NZ	84:S2:435:A:OP1	2.54	0.41
83:Se:56:ASN:ND2	84:S2:606:G:O4'	2.49	0.41
84:S2:943:U:C2	84:S2:944:A:C8	3.09	0.41
84:S2:1351:G:O2'	84:S2:1378:A:N1	2.53	0.41
86:CF:111:CYS:SG	86:CF:112:ALA:N	2.94	0.41
4:L5:260:C:H2'	4:L5:261:G:C8	2.55	0.41
4:L5:302:C:H2'	4:L5:303:C:C6	2.55	0.41
4:L5:330:G:N7	89:L5:5282:SPD:N1	2.68	0.41
4:L5:1504:G:H2'	4:L5:1505:C:C6	2.56	0.41
4:L5:2264:C:H2'	4:L5:2265:G:O4'	2.20	0.41
4:L5:2376:A:H2'	4:L5:2377:C:C6	2.55	0.41
4:L5:2622:G:O6	26:LU:81:ARG:NH2	2.53	0.41
4:L5:2632:PSU:H2'	4:L5:2633:U:C6	2.55	0.41
4:L5:4184:G:H5'	7:LA:233:ARG:HB2	2.03	0.41
4:L5:4232:U:H5'	46:Lo:3:ASN:HB3	2.03	0.41
4:L5:4739:C:H2'	4:L5:4740:G:H5'	2.03	0.41
4:L5:5047:C:O2'	4:L5:5050:C:OP2	2.29	0.41
9:LC:158:VAL:HG12	9:LC:217:ILE:HD12	2.02	0.41
16:LJ:40:LEU:HD23	16:LJ:40:LEU:HA	1.91	0.41
17:LL:18:TRP:CD1	17:LL:18:TRP:H	2.38	0.41
22:LQ:43:PHE:CD2	22:LQ:133:GLY:HA3	2.56	0.41
60:SU:32:LEU:CD1	60:SU:85:HIS:HB2	2.51	0.41
66:SA:11:LYS:O	66:SA:15:VAL:HG23	2.20	0.41
70:SG:14:LYS:HE2	70:SG:16:ILE:HD11	2.03	0.41
70:SG:133:LEU:HB2	84:S2:65:C:C2	2.56	0.41
70:SG:191:ARG:NH1	84:S2:312:G:H2'	2.34	0.41
72:SI:26:LYS:HE3	84:S2:444:G:O6	2.20	0.41
80:SY:93:ARG:HH21	84:S2:575:A:P	2.43	0.41
84:S2:116:OMU:H1'	84:S2:116:OMU:HM23	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:S2:120:U:H2'	84:S2:121:OMU:H6	2.02	0.41
84:S2:291:G:HO2'	84:S2:292:A:P	2.43	0.41
84:S2:463:C:O2'	84:S2:466:G:O6	2.36	0.41
4:L5:7:C:H2'	4:L5:8:U:C6	2.56	0.41
4:L5:423:G:H2'	4:L5:424:U:C6	2.56	0.41
4:L5:499:G:H2'	4:L5:499:G:N3	2.36	0.41
4:L5:2464:C:HO2'	4:L5:2465:C:H6	1.64	0.41
4:L5:2610:G:H2'	4:L5:2611:A:C8	2.56	0.41
4:L5:3893:C:H2'	4:L5:3894:A:C8	2.56	0.41
4:L5:4391:G:OP1	9:LC:75:ARG:NH1	2.35	0.41
8:LB:71:GLU:HB2	28:LW:2:LYS:HD3	2.01	0.41
15:LI:51:HIS:ND1	15:LI:137:SER:OG	2.48	0.41
17:LL:194:ILE:HD12	17:LL:194:ILE:HA	1.89	0.41
23:LR:35:ALA:HA	23:LR:40:GLN:OE1	2.20	0.41
27:LV:111:GLU:H	27:LV:111:GLU:CD	2.29	0.41
36:Le:19:LYS:HE3	36:Le:19:LYS:HB3	1.90	0.41
50:Lt:114:ARG:NH1	50:Lt:126:SER:O	2.44	0.41
52:SF:60:ARG:HE	84:S2:1679:A:P	2.43	0.41
55:SP:47:ARG:NE	84:S2:1619:A:OP1	2.40	0.41
57:SR:109:LEU:HG	57:SR:111:PHE:HD2	1.86	0.41
60:SU:52:GLY:HA3	84:S2:1401:A:H4'	2.02	0.41
65:Sg:314:ILE:HD12	65:Sg:314:ILE:HA	1.91	0.41
66:SA:80:ARG:HH21	66:SA:126:ASP:HB2	1.86	0.41
67:SB:44:ILE:HG23	67:SB:69:VAL:HG11	2.02	0.41
67:SB:114:VAL:O	84:S2:1869:A:N6	2.53	0.41
69:SE:128:LYS:HG2	69:SE:140:VAL:HB	2.03	0.41
81:Sa:39:PHE:CE2	81:Sa:41:ILE:HD11	2.55	0.41
84:S2:815:U:C2	84:S2:816:A:C8	3.09	0.41
84:S2:1406:G:H2'	84:S2:1407:U:C6	2.56	0.41
86:CF:241:PRO:HB2	86:CF:244:LYS:CG	2.50	0.41
3:Et:32:C:H2'	3:Et:33:U:C2	2.56	0.41
4:L5:302:C:H2'	4:L5:303:C:H6	1.86	0.41
4:L5:1186:U:H2'	4:L5:1187:G:N3	2.36	0.41
4:L5:1494:U:H2'	4:L5:1495:G:C8	2.56	0.41
4:L5:1974:U:H4'	4:L5:1975:G:H3'	2.03	0.41
4:L5:2412:A:H2'	4:L5:2413:U:C6	2.56	0.41
4:L5:3687:A:O2'	7:LA:236:GLY:N	2.52	0.41
4:L5:3865:A:H61	4:L5:3881:G:H1	1.67	0.41
4:L5:3871:A:H2'	4:L5:3872:A:C8	2.56	0.41
4:L5:4070:U:H2'	4:L5:4071:U:C6	2.56	0.41
4:L5:4232:U:H5''	46:Lo:3:ASN:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4688:C:H2'	4:L5:4689:PSU:C6	2.56	0.41
4:L5:4708:A:N3	4:L5:4709:U:H5'	2.36	0.41
7:LA:112:ILE:HD11	47:Lp:79:VAL:HG22	2.03	0.41
8:LB:122:TRP:CE2	8:LB:127:LYS:HE3	2.56	0.41
13:LG:178:GLY:O	13:LG:223:ARG:NH2	2.54	0.41
14:LH:27:VAL:HG12	14:LH:84:VAL:HG21	2.02	0.41
14:LH:95:VAL:HG12	44:Lm:82:LEU:HD13	2.03	0.41
20:LO:145:VAL:O	20:LO:145:VAL:HG22	2.21	0.41
21:LP:95:LEU:HD23	21:LP:95:LEU:HA	1.96	0.41
25:LT:44:GLY:HA2	25:LT:95:HIS:HB3	2.03	0.41
27:LV:87:SER:HA	27:LV:97:TYR:HB3	2.03	0.41
29:LX:64:SER:HB2	39:Lh:69:LEU:HD13	2.02	0.41
30:LY:13:LYS:O	30:LY:17:ARG:HD3	2.21	0.41
34:Lc:20:LEU:O	34:Lc:24:SER:HB3	2.21	0.41
37:Lf:25:THR:HB	37:Lf:87:LYS:HD3	2.02	0.41
38:Lg:41:ALA:O	38:Lg:52:ARG:HD3	2.21	0.41
48:Lr:47:LYS:HB2	48:Lr:102:TYR:CZ	2.55	0.41
55:SP:92:SER:HB2	55:SP:107:ILE:HD13	2.03	0.41
59:ST:113:VAL:HG22	59:ST:123:LEU:HD23	2.02	0.41
61:SZ:68:ILE:HB	61:SZ:109:TYR:HB2	2.03	0.41
63:Sd:13:LYS:HG3	84:S2:1556:A:C8	2.56	0.41
66:SA:172:GLY:HA3	66:SA:203:PHE:HD1	1.85	0.41
68:SC:212:LYS:HE2	68:SC:212:LYS:HB3	1.87	0.41
68:SC:271:ASP:OD1	68:SC:272:HIS:N	2.52	0.41
69:SE:252:ARG:O	69:SE:256:LEU:HG	2.21	0.41
70:SG:174:PRO:HG3	84:S2:65:C:C2	2.55	0.41
71:SH:91:HIS:ND1	71:SH:169:LYS:HG2	2.35	0.41
72:SI:114:GLU:HG3	72:SI:119:LEU:O	2.21	0.41
75:SN:37:ILE:HG23	75:SN:50:ILE:HG21	2.03	0.41
76:SO:131:ASP:OD1	76:SO:133:THR:OG1	2.33	0.41
77:SV:27:LYS:HD3	77:SV:27:LYS:HA	1.86	0.41
78:SW:57:ARG:HG2	84:S2:920:A:H4'	2.02	0.41
83:Se:8:ARG:NH1	84:S2:615:C:O3'	2.54	0.41
84:S2:28:U:H2'	84:S2:29:G:C8	2.54	0.41
84:S2:67:C:N4	84:S2:70:G:N7	2.68	0.41
84:S2:436:OMG:HM23	84:S2:436:OMG:H1'	1.94	0.41
84:S2:576:A2M:H1'	84:S2:576:A2M:HM'3	1.81	0.41
84:S2:747:U:O2	84:S2:796:G:C2	2.74	0.41
84:S2:1374:C:H2'	84:S2:1375:G:O4'	2.21	0.41
84:S2:1540:G:H2'	84:S2:1541:G:C8	2.56	0.41
85:AT:59:A:O2'	85:AT:62:C:N4	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Pt:3:C:H42	2:Pt:70:A:N6	2.19	0.41
4:L5:99:A:H2'	4:L5:100:C:O2	2.20	0.41
4:L5:267:G:H2'	4:L5:268:G:C8	2.54	0.41
4:L5:286:U:H2'	4:L5:287:U:C6	2.56	0.41
4:L5:293:G:OP1	88:L5:5263:SPM:N1	2.37	0.41
4:L5:512:U:OP2	17:LL:165:LYS:NZ	2.40	0.41
4:L5:1382:G:OP1	17:LL:66:TYR:OH	2.35	0.41
4:L5:2404:A:H1'	41:Lj:12:ARG:HH21	1.84	0.41
4:L5:2422:OMC:HM23	4:L5:2422:OMC:H1'	1.90	0.41
4:L5:4174:U:H2'	4:L5:4175:G:H8	1.86	0.41
4:L5:4291:G:H4'	4:L5:4292:A:H5''	2.03	0.41
4:L5:5015:G:H2'	4:L5:5016:A:C2	2.56	0.41
7:LA:130:SER:HB2	7:LA:171:GLY:HA3	2.03	0.41
7:LA:171:GLY:O	47:Lp:68:ALA:HB2	2.21	0.41
10:LD:289:ARG:O	10:LD:292:GLU:HG3	2.21	0.41
11:LE:282:TYR:HE1	37:Lf:31:GLU:HG2	1.86	0.41
22:LQ:32:TYR:HD1	22:LQ:32:TYR:HA	1.71	0.41
22:LQ:59:PRO:HG3	22:LQ:143:ARG:HA	2.02	0.41
36:Le:100:ALA:HB3	36:Le:103:VAL:HG23	2.04	0.41
38:Lg:60:ARG:HD2	38:Lg:60:ARG:HA	1.83	0.41
50:Lt:22:VAL:HA	50:Lt:48:LYS:HG2	2.02	0.41
57:SR:7:LYS:HG3	84:S2:1373:C:OP1	2.20	0.41
61:SZ:56:ASP:OD1	61:SZ:57:LYS:N	2.54	0.41
65:Sg:37:ASP:OD1	65:Sg:39:THR:OG1	2.32	0.41
65:Sg:101:PHE:CE2	65:Sg:136:GLY:HA2	2.55	0.41
66:SA:57:LYS:HA	66:SA:57:LYS:HD2	1.79	0.41
67:SB:67:PHE:CE2	76:SO:48:SER:HB3	2.56	0.41
71:SH:76:GLN:O	71:SH:80:VAL:HG23	2.21	0.41
84:S2:945:U:H2'	84:S2:946:U:C6	2.56	0.41
84:S2:1088:U:H4'	84:S2:1089:G:OP2	2.21	0.41
84:S2:1360:U:O2'	84:S2:1379:A:OP2	2.33	0.41
2:Pt:72:C:H3'	2:Pt:73:A:H8	1.86	0.40
4:L5:135:G:N3	4:L5:135:G:H2'	2.36	0.40
4:L5:705:G:H2'	4:L5:706:C:C6	2.56	0.40
4:L5:1081:C:O2'	4:L5:1082:C:H5'	2.20	0.40
4:L5:1403:G:N2	4:L5:1415:G:C4	2.89	0.40
4:L5:1431:C:H2'	4:L5:1432:G:O4'	2.21	0.40
4:L5:1741:G:O6	5:L7:103:A:O2'	2.26	0.40
4:L5:2409:U:H5	4:L5:2783:A:N1	2.19	0.40
4:L5:2630:U:OP1	26:LU:48:LYS:NZ	2.40	0.40
4:L5:2739:C:OP2	47:Lp:33:GLN:NE2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:3896:C:H1'	8:LB:268:ARG:NH2	2.36	0.40
4:L5:4236:G:H4'	4:L5:4328:G:O2'	2.21	0.40
4:L5:4258:C:H2'	4:L5:4259:C:C6	2.56	0.40
4:L5:4906:C:H2'	4:L5:4907:G:H8	1.86	0.40
8:LB:161:ARG:HG2	8:LB:184:GLN:HA	2.03	0.40
10:LD:209:ARG:O	10:LD:213:GLU:HG2	2.21	0.40
16:LJ:119:TYR:CG	58:SS:12:ILE:HG12	2.56	0.40
23:LR:185:ILE:H	23:LR:185:ILE:HD12	1.86	0.40
54:SM:95:ASP:HB3	54:SM:99:LYS:HB3	2.03	0.40
63:Sd:34:TYR:OH	84:S2:1549:U:OP1	2.34	0.40
65:Sg:230:LEU:HD11	65:Sg:259:TRP:CG	2.56	0.40
67:SB:103:MET:HG2	67:SB:188:LEU:HD13	2.03	0.40
84:S2:165:G:H2'	84:S2:166:A2M:H8	2.03	0.40
84:S2:693:A:H2	84:S2:739:C:H4'	1.85	0.40
86:CF:408:LYS:HA	86:CF:409:PRO:HD3	1.91	0.40
2:Pt:18:G:H4'	2:Pt:60:A:C2	2.56	0.40
3:Et:28:C:H2'	3:Et:29:A:C8	2.55	0.40
4:L5:262:G:H2'	4:L5:263:G:H8	1.85	0.40
4:L5:919:C:H2'	4:L5:920:C:C6	2.56	0.40
4:L5:1558:A:H2'	4:L5:1559:G:H8	1.87	0.40
4:L5:2720:C:H2'	4:L5:2721:G:O4'	2.22	0.40
4:L5:4169:G:H4'	4:L5:4171:C:C2	2.56	0.40
4:L5:4318:C:H4'	46:Lo:17:LYS:HA	2.03	0.40
4:L5:4344:U:H2'	4:L5:4345:C:C6	2.57	0.40
4:L5:4770:U:H2'	4:L5:4771:C:C6	2.57	0.40
4:L5:4927:G:H5''	4:L5:4928:C:C5	2.56	0.40
5:L7:26:C:O2'	16:LJ:147:ARG:NH1	2.52	0.40
6:L8:8:U:H2'	6:L8:9:A:C8	2.57	0.40
7:LA:60:LYS:HB2	7:LA:60:LYS:HE3	1.87	0.40
7:LA:132:ASN:O	7:LA:169:VAL:HG12	2.22	0.40
8:LB:117:ARG:HA	8:LB:177:LYS:HD2	2.02	0.40
30:LY:126:ARG:HG2	30:LY:130:LYS:HE2	2.03	0.40
53:SK:80:ARG:HH22	53:SK:90:VAL:HG12	1.87	0.40
70:SG:195:LYS:HD3	84:S2:126:G:H5'	2.04	0.40
71:SH:58:LYS:HB2	71:SH:90:LYS:HG2	2.03	0.40
72:SI:42:ARG:HH21	72:SI:59:ARG:NH1	2.19	0.40
75:SN:20:ARG:HH21	78:SW:56:HIS:HB3	1.86	0.40
78:SW:57:ARG:NH2	82:Sb:26:GLN:HB2	2.37	0.40
81:Sa:36:ILE:HD11	81:Sa:75:VAL:HG12	2.02	0.40
81:Sa:98:PRO:HA	81:Sa:99:PRO:HD3	1.92	0.40
84:S2:527:C:H2'	84:S2:528:A:C8	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:S2:874:G:H2'	84:S2:875:A:C8	2.52	0.40
2:Pt:56:C:O4'	16:LJ:64:ARG:NE	2.47	0.40
2:Pt:62:C:H2'	2:Pt:63:G:H8	1.86	0.40
3:Et:75:C:O2'	46:Lo:54:PRO:O	2.30	0.40
4:L5:19:G:P	39:Lh:93:ARG:HE	2.44	0.40
4:L5:1174:G:H1	4:L5:1186:U:H3	1.69	0.40
4:L5:1339:U:OP1	32:La:8:THR:OG1	2.35	0.40
4:L5:1356:U:H2'	4:L5:1357:C:C6	2.57	0.40
4:L5:1588:U:H2'	4:L5:1589:C:C6	2.57	0.40
4:L5:2019:C:H2'	4:L5:2020:U:C6	2.56	0.40
4:L5:2461:G:H2'	4:L5:2462:C:C6	2.56	0.40
4:L5:3707:U:H2'	4:L5:3708:C:H6	1.86	0.40
4:L5:3848:U:H2'	4:L5:3849:A:C8	2.57	0.40
6:L8:47:C:H1'	6:L8:61:A:H2'	2.02	0.40
9:LC:289:LEU:HD21	22:LQ:31:LEU:HB2	2.02	0.40
10:LD:260:GLU:O	10:LD:260:GLU:CD	2.64	0.40
12:LF:148:LYS:O	12:LF:152:GLU:HG2	2.22	0.40
13:LG:160:ASP:OD1	13:LG:160:ASP:N	2.54	0.40
28:LW:102:LYS:HA	28:LW:105:ARG:HG2	2.03	0.40
30:LY:74:TYR:HE2	30:LY:77:LYS:HG3	1.86	0.40
39:Lh:19:LYS:NZ	39:Lh:23:ASP:OD1	2.54	0.40
46:Lo:11:PHE:O	46:Lo:81:ARG:NH2	2.54	0.40
58:SS:62:ASP:O	58:SS:65:GLU:HG3	2.22	0.40
65:Sg:205:SER:HA	65:Sg:221:LEU:HB2	2.02	0.40
66:SA:219:GLU:HA	66:SA:222:VAL:HG12	2.03	0.40
67:SB:40:ASN:OD1	67:SB:41:ILE:HD12	2.22	0.40
73:SJ:142:VAL:HG12	73:SJ:144:ILE:H	1.85	0.40
78:SW:125:ILE:HA	78:SW:125:ILE:HD12	1.84	0.40
82:Sb:33:MET:HE3	82:Sb:48:SER:HA	2.04	0.40
82:Sb:81:ARG:HA	82:Sb:81:ARG:HD2	1.96	0.40
84:S2:1223:A:H2'	84:S2:1224:G:O4'	2.21	0.40
85:AT:15:G:N2	85:AT:49:C:C2	2.89	0.40
86:CF:8:ILE:O	86:CF:8:ILE:HG13	2.18	0.40
4:L5:65:A:N6	4:L5:75:G:H1'	2.36	0.40
4:L5:161:G:H2'	4:L5:162:A:H8	1.85	0.40
4:L5:223:G:N7	9:LC:165:LYS:HE3	2.37	0.40
4:L5:468:U:C5	4:L5:469:C:H5	2.40	0.40
4:L5:495:C:H2'	4:L5:496:G:C8	2.56	0.40
4:L5:654:C:O3'	9:LC:268:ARG:NH1	2.53	0.40
4:L5:1172:C:H42	4:L5:1188:C:H42	1.70	0.40
4:L5:1834:U:N3	25:LT:126:VAL:O	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2683:C:H2'	4:L5:2684:C:C6	2.57	0.40
4:L5:4069:U:H2'	4:L5:4070:U:H6	1.86	0.40
18:LM:37:LEU:HD12	18:LM:37:LEU:HA	1.83	0.40
31:LZ:47:ASP:N	31:LZ:69:LYS:O	2.52	0.40
65:Sg:125:ARG:HD3	65:Sg:150:TRP:CE2	2.57	0.40
68:SC:117:ARG:NE	84:S2:1204:A:OP1	2.45	0.40
71:SH:36:LEU:HD12	71:SH:39:GLN:NE2	2.37	0.40
72:SI:81:VAL:HG22	72:SI:102:VAL:HG12	2.03	0.40
84:S2:15:U:H2'	84:S2:16:G:O4'	2.21	0.40
84:S2:835:C:H4'	84:S2:836:G:H8	1.86	0.40
86:CF:323:GLY:CA	86:CF:366:ALA:HB2	2.51	0.40
3:Et:65:G:O2'	3:Et:66:U:H5'	2.21	0.40
4:L5:288:G:H2'	4:L5:289:C:C6	2.57	0.40
4:L5:1253:G:H2'	4:L5:1256:G:H5'	2.04	0.40
4:L5:1281:G:C6	11:LE:128:HIS:HB2	2.56	0.40
4:L5:1401:C:H2'	4:L5:1402:C:C6	2.57	0.40
4:L5:1806:G:H2'	4:L5:1807:C:C6	2.56	0.40
4:L5:1857:C:H2'	4:L5:1858:A:H8	1.86	0.40
4:L5:1907:A:H2'	4:L5:1908:A:C8	2.57	0.40
4:L5:2060:G:N2	24:LS:115:ALA:HB2	2.37	0.40
4:L5:3693:U:O3'	47:Lp:21:SER:OG	2.37	0.40
4:L5:3736:A:H2'	4:L5:3737:A:H8	1.84	0.40
4:L5:4710:C:H2'	4:L5:4711:C:C6	2.57	0.40
4:L5:4859:C:H2'	4:L5:4860:G:C8	2.57	0.40
4:L5:4965:U:H4'	4:L5:4966:A:H5'	2.03	0.40
10:LD:86:TYR:CE1	10:LD:247:ILE:HG13	2.56	0.40
15:LI:66:GLU:OE2	15:LI:69:ARG:NH2	2.31	0.40
15:LI:207:ASP:HA	15:LI:210:ARG:HG2	2.04	0.40
18:LM:38:VAL:O	18:LM:47:ARG:HA	2.19	0.40
25:LT:50:LYS:HB3	25:LT:50:LYS:HE2	1.80	0.40
51:SD:222:PRO:HB3	65:Sg:190:GLY:HA3	2.04	0.40
52:SF:73:THR:O	52:SF:89:THR:HG21	2.21	0.40
56:SQ:34:VAL:HG22	56:SQ:70:VAL:HB	2.03	0.40
63:Sd:3:HIS:CE1	63:Sd:5:GLN:HB2	2.57	0.40
67:SB:89:GLU:OE2	67:SB:99:ASN:HB3	2.21	0.40
70:SG:133:LEU:HB2	84:S2:65:C:N3	2.36	0.40
73:SJ:124:HIS:HD2	83:Se:31:ARG:HE	1.69	0.40
78:SW:77:PRO:HG2	78:SW:79:PHE:CE2	2.57	0.40
80:SY:86:GLU:CD	80:SY:87:PRO:HD2	2.46	0.40
80:SY:129:LYS:HA	80:SY:129:LYS:HD3	1.84	0.40
81:Sa:11:ALA:HB3	81:Sa:33:ASP:HB2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:S2:1227:G:C2	84:S2:1228:A:C8	3.09	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CI	29/31 (94%)	29 (100%)	0	0	100	100
7	LA	246/248 (99%)	227 (92%)	19 (8%)	0	100	100
8	LB	400/402 (100%)	385 (96%)	15 (4%)	0	100	100
9	LC	366/368 (100%)	352 (96%)	14 (4%)	0	100	100
10	LD	291/293 (99%)	283 (97%)	8 (3%)	0	100	100
11	LE	236/250 (94%)	223 (94%)	13 (6%)	0	100	100
12	LF	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
13	LG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
14	LH	188/190 (99%)	183 (97%)	5 (3%)	0	100	100
15	LI	211/213 (99%)	204 (97%)	7 (3%)	0	100	100
16	LJ	168/176 (96%)	164 (98%)	4 (2%)	0	100	100
17	LL	208/210 (99%)	201 (97%)	7 (3%)	0	100	100
18	LM	137/139 (99%)	132 (96%)	5 (4%)	0	100	100
19	LN	201/203 (99%)	198 (98%)	3 (2%)	0	100	100
20	LO	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
21	LP	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
22	LQ	185/187 (99%)	182 (98%)	3 (2%)	0	100	100
23	LR	185/187 (99%)	181 (98%)	4 (2%)	0	100	100
24	LS	173/175 (99%)	164 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	LT	157/159 (99%)	154 (98%)	3 (2%)	0	100	100
26	LU	99/101 (98%)	94 (95%)	5 (5%)	0	100	100
27	LV	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
28	LW	112/124 (90%)	108 (96%)	4 (4%)	0	100	100
29	LX	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
30	LY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
31	LZ	133/135 (98%)	125 (94%)	8 (6%)	0	100	100
32	La	145/147 (99%)	139 (96%)	6 (4%)	0	100	100
33	Lb	105/121 (87%)	99 (94%)	6 (6%)	0	100	100
34	Lc	96/98 (98%)	92 (96%)	4 (4%)	0	100	100
35	Ld	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
36	Le	126/128 (98%)	125 (99%)	1 (1%)	0	100	100
37	Lf	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
38	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
39	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
40	Li	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
41	Lj	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
42	Lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
43	Ll	48/50 (96%)	48 (100%)	0	0	100	100
44	Lm	50/52 (96%)	50 (100%)	0	0	100	100
45	Ln	22/24 (92%)	22 (100%)	0	0	100	100
46	Lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
47	Lp	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
48	Lr	123/125 (98%)	120 (98%)	3 (2%)	0	100	100
49	Ls	194/196 (99%)	181 (93%)	13 (7%)	0	100	100
50	Lt	128/157 (82%)	110 (86%)	18 (14%)	0	100	100
51	SD	225/227 (99%)	219 (97%)	6 (3%)	0	100	100
52	SF	187/189 (99%)	174 (93%)	13 (7%)	0	100	100
53	SK	96/98 (98%)	87 (91%)	9 (9%)	0	100	100
54	SM	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
55	SP	119/121 (98%)	116 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	SQ	142/144 (99%)	130 (92%)	12 (8%)	0	100	100
57	SR	133/135 (98%)	125 (94%)	7 (5%)	1 (1%)	16	44
58	SS	143/145 (99%)	134 (94%)	9 (6%)	0	100	100
59	ST	141/143 (99%)	137 (97%)	4 (3%)	0	100	100
60	SU	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
61	SZ	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
62	Sc	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
63	Sd	53/55 (96%)	53 (100%)	0	0	100	100
64	Sf	65/67 (97%)	56 (86%)	9 (14%)	0	100	100
65	Sg	311/313 (99%)	292 (94%)	19 (6%)	0	100	100
66	SA	219/221 (99%)	206 (94%)	13 (6%)	0	100	100
67	SB	212/214 (99%)	203 (96%)	9 (4%)	0	100	100
68	SC	218/222 (98%)	202 (93%)	16 (7%)	0	100	100
69	SE	260/262 (99%)	247 (95%)	13 (5%)	0	100	100
70	SG	235/237 (99%)	222 (94%)	13 (6%)	0	100	100
71	SH	182/189 (96%)	171 (94%)	11 (6%)	0	100	100
72	SI	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
73	SJ	183/185 (99%)	175 (96%)	8 (4%)	0	100	100
74	SL	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
75	SN	148/150 (99%)	146 (99%)	2 (1%)	0	100	100
76	SO	135/140 (96%)	127 (94%)	8 (6%)	0	100	100
77	SV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
78	SW	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
79	SX	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
80	SY	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
81	Sa	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
82	Sb	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
83	Se	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
86	CF	438/441 (99%)	429 (98%)	9 (2%)	0	100	100
All	All	12110/12348 (98%)	11594 (96%)	515 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
57	SR	129	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CI	25/25 (100%)	25 (100%)	0	100	100
7	LA	190/190 (100%)	190 (100%)	0	100	100
8	LB	348/348 (100%)	348 (100%)	0	100	100
9	LC	306/306 (100%)	306 (100%)	0	100	100
10	LD	246/247 (100%)	246 (100%)	0	100	100
11	LE	212/222 (96%)	212 (100%)	0	100	100
12	LF	194/194 (100%)	194 (100%)	0	100	100
13	LG	203/205 (99%)	203 (100%)	0	100	100
14	LH	169/169 (100%)	169 (100%)	0	100	100
15	LI	180/180 (100%)	180 (100%)	0	100	100
16	LJ	143/148 (97%)	143 (100%)	0	100	100
17	LL	176/176 (100%)	176 (100%)	0	100	100
18	LM	118/118 (100%)	118 (100%)	0	100	100
19	LN	171/171 (100%)	171 (100%)	0	100	100
20	LO	173/173 (100%)	173 (100%)	0	100	100
21	LP	134/134 (100%)	134 (100%)	0	100	100
22	LQ	164/164 (100%)	164 (100%)	0	100	100
23	LR	166/166 (100%)	166 (100%)	0	100	100
24	LS	156/156 (100%)	156 (100%)	0	100	100
25	LT	139/139 (100%)	139 (100%)	0	100	100
26	LU	91/91 (100%)	91 (100%)	0	100	100
27	LV	101/101 (100%)	101 (100%)	0	100	100
28	LW	95/103 (92%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	LX	108/108 (100%)	108 (100%)	0	100	100
30	LY	124/124 (100%)	124 (100%)	0	100	100
31	LZ	117/117 (100%)	117 (100%)	0	100	100
32	La	120/120 (100%)	120 (100%)	0	100	100
33	Lb	88/101 (87%)	88 (100%)	0	100	100
34	Lc	83/83 (100%)	83 (100%)	0	100	100
35	Ld	98/98 (100%)	98 (100%)	0	100	100
36	Le	114/114 (100%)	114 (100%)	0	100	100
37	Lf	88/88 (100%)	88 (100%)	0	100	100
38	Lg	98/98 (100%)	98 (100%)	0	100	100
39	Lh	109/109 (100%)	109 (100%)	0	100	100
40	Li	86/86 (100%)	86 (100%)	0	100	100
41	Lj	73/73 (100%)	73 (100%)	0	100	100
42	Lk	64/64 (100%)	64 (100%)	0	100	100
43	Ll	47/47 (100%)	47 (100%)	0	100	100
44	Lm	48/48 (100%)	48 (100%)	0	100	100
45	Ln	23/23 (100%)	23 (100%)	0	100	100
46	Lo	93/93 (100%)	93 (100%)	0	100	100
47	Lp	74/74 (100%)	74 (100%)	0	100	100
48	Lr	109/109 (100%)	109 (100%)	0	100	100
49	Ls	162/164 (99%)	162 (100%)	0	100	100
50	Lt	107/130 (82%)	107 (100%)	0	100	100
51	SD	190/190 (100%)	190 (100%)	0	100	100
52	SF	159/159 (100%)	159 (100%)	0	100	100
53	SK	89/89 (100%)	89 (100%)	0	100	100
54	SM	102/104 (98%)	102 (100%)	0	100	100
55	SP	107/107 (100%)	107 (100%)	0	100	100
56	SQ	119/119 (100%)	119 (100%)	0	100	100
57	SR	122/122 (100%)	122 (100%)	0	100	100
58	SS	126/126 (100%)	126 (100%)	0	100	100
59	ST	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
60	SU	94/94 (100%)	94 (100%)	0	100	100
61	SZ	66/66 (100%)	66 (100%)	0	100	100
62	Sc	57/57 (100%)	57 (100%)	0	100	100
63	Sd	48/48 (100%)	48 (100%)	0	100	100
64	Sf	60/60 (100%)	60 (100%)	0	100	100
65	Sg	272/272 (100%)	272 (100%)	0	100	100
66	SA	183/183 (100%)	183 (100%)	0	100	100
67	SB	195/195 (100%)	195 (100%)	0	100	100
68	SC	186/188 (99%)	186 (100%)	0	100	100
69	SE	224/224 (100%)	224 (100%)	0	100	100
70	SG	207/207 (100%)	207 (100%)	0	100	100
71	SH	166/169 (98%)	166 (100%)	0	100	100
72	SI	178/178 (100%)	178 (100%)	0	100	100
73	SJ	161/161 (100%)	161 (100%)	0	100	100
74	SL	137/137 (100%)	137 (100%)	0	100	100
75	SN	130/130 (100%)	130 (100%)	0	100	100
76	SO	107/110 (97%)	107 (100%)	0	100	100
77	SV	67/67 (100%)	67 (100%)	0	100	100
78	SW	112/112 (100%)	112 (100%)	0	100	100
79	SX	113/113 (100%)	113 (100%)	0	100	100
80	SY	113/113 (100%)	113 (100%)	0	100	100
81	Sa	89/89 (100%)	89 (100%)	0	100	100
82	Sb	75/75 (100%)	75 (100%)	0	100	100
83	Se	47/47 (100%)	47 (100%)	0	100	100
86	CF	365/366 (100%)	365 (100%)	0	100	100
All	All	10512/10587 (99%)	10512 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (81) such sidechains are listed below:

Mol	Chain	Res	Type
7	LA	97	ASN

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Mol	Chain	Res	Type
8	LB	68	ASN
8	LB	145	GLN
8	LB	184	GLN
8	LB	203	GLN
8	LB	301	ASN
9	LC	329	ASN
9	LC	347	HIS
12	LF	239	GLN
13	LG	112	GLN
14	LH	98	HIS
14	LH	138	GLN
15	LI	59	GLN
17	LL	19	GLN
17	LL	149	GLN
18	LM	34	ASN
19	LN	117	ASN
20	LO	42	ASN
20	LO	50	ASN
20	LO	199	HIS
21	LP	97	ASN
21	LP	118	GLN
21	LP	137	ASN
24	LS	23	HIS
24	LS	37	HIS
24	LS	108	GLN
25	LT	144	ASN
26	LU	94	ASN
27	LV	77	HIS
28	LW	79	GLN
28	LW	104	GLN
30	LY	61	HIS
32	La	34	ASN
32	La	67	GLN
32	La	120	GLN
33	Lb	60	ASN
36	Le	52	GLN
40	Li	15	HIS
41	Lj	66	HIS
43	Ll	33	ASN
44	Lm	117	HIS
47	Lp	33	GLN
48	Lr	4	HIS

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Mol	Chain	Res	Type
48	Lr	21	ASN
50	Lt	65	GLN
50	Lt	149	HIS
52	SF	29	GLN
53	SK	28	HIS
53	SK	32	HIS
54	SM	19	GLN
56	SQ	48	GLN
60	SU	81	GLN
60	SU	92	HIS
61	SZ	89	GLN
63	Sd	5	GLN
64	Sf	93	HIS
65	Sg	285	GLN
66	SA	9	GLN
66	SA	84	GLN
66	SA	132	GLN
67	SB	76	ASN
67	SB	95	ASN
67	SB	158	HIS
68	SC	267	GLN
69	SE	188	ASN
70	SG	227	GLN
71	SH	76	GLN
71	SH	114	GLN
71	SH	162	GLN
72	SI	35	ASN
72	SI	52	ASN
74	SL	19	ASN
74	SL	65	ASN
75	SN	105	ASN
77	SV	35	ASN
79	SX	16	HIS
79	SX	31	HIS
81	Sa	72	HIS
86	CF	15	HIS
86	CF	197	ASN
86	CF	348	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	Pt	72/74 (97%)	14 (19%)	0
3	Et	73/75 (97%)	24 (32%)	0
4	L5	3643/3655 (99%)	710 (19%)	15 (0%)
5	L7	119/120 (99%)	9 (7%)	0
6	L8	155/156 (99%)	23 (14%)	0
84	S2	1714/1740 (98%)	360 (21%)	4 (0%)
85	AT	74/76 (97%)	43 (58%)	1 (1%)
All	All	5850/5896 (99%)	1183 (20%)	20 (0%)

All (1183) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	Pt	9	A
2	Pt	13	U
2	Pt	19	G
2	Pt	21	A
2	Pt	46	G
2	Pt	47	U
2	Pt	48	C
2	Pt	49	C
2	Pt	58	A
2	Pt	66	C
2	Pt	67	G
2	Pt	70	A
2	Pt	74	C
2	Pt	76	A
3	Et	9	A
3	Et	10	G
3	Et	11	C
3	Et	19	G
3	Et	20	U
3	Et	21	A
3	Et	31	A
3	Et	33	U
3	Et	36	U
3	Et	40	C
3	Et	42	G
3	Et	46	G
3	Et	47	U
3	Et	48	C
3	Et	49	C
3	Et	55	U
3	Et	58	A

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Mol	Chain	Res	Type
3	Et	60	U
3	Et	63	C
3	Et	65	G
3	Et	66	U
3	Et	70	G
3	Et	73	G
3	Et	76	A
4	L5	2	G
4	L5	25	A
4	L5	30	C
4	L5	39	A
4	L5	42	A
4	L5	48	G
4	L5	56	A
4	L5	59	A
4	L5	64	A
4	L5	65	A
4	L5	73	A
4	L5	91	G
4	L5	104	G
4	L5	108	A
4	L5	109	G
4	L5	110	C
4	L5	119	G
4	L5	120	A
4	L5	127	G
4	L5	132	G
4	L5	133	C
4	L5	134	G
4	L5	135	G
4	L5	136	C
4	L5	159	C
4	L5	165	A
4	L5	172	C
4	L5	181	C
4	L5	182	G
4	L5	183	C
4	L5	184	U
4	L5	185	C
4	L5	187	U
4	L5	188	G
4	L5	189	G

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Mol	Chain	Res	Type
4	L5	200	U
4	L5	209	U
4	L5	210	C
4	L5	216	C
4	L5	218	A
4	L5	220	C
4	L5	234	G
4	L5	237	G
4	L5	255	C
4	L5	256	G
4	L5	261	G
4	L5	263	G
4	L5	264	C
4	L5	265	C
4	L5	266	C
4	L5	267	G
4	L5	280	G
4	L5	297	U
4	L5	306	A
4	L5	315	G
4	L5	316	U
4	L5	340	C
4	L5	373	G
4	L5	385	A
4	L5	387	G
4	L5	388	A
4	L5	396	A
4	L5	407	A
4	L5	409	G
4	L5	410	A
4	L5	411	G
4	L5	412	G
4	L5	432	U
4	L5	449	C
4	L5	452	A
4	L5	453	G
4	L5	454	U
4	L5	456	C
4	L5	457	G
4	L5	467	U
4	L5	484	U
4	L5	485	C

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Mol	Chain	Res	Type
4	L5	486	C
4	L5	489	C
4	L5	494	U
4	L5	497	G
4	L5	498	C
4	L5	499	G
4	L5	500	G
4	L5	502	C
4	L5	503	C
4	L5	504	G
4	L5	509	A
4	L5	510	U
4	L5	512	U
4	L5	513	U
4	L5	514	U
4	L5	518	G
4	L5	643	C
4	L5	646	G
4	L5	654	C
4	L5	655	C
4	L5	656	C
4	L5	657	C
4	L5	659	G
4	L5	666	G
4	L5	667	A
4	L5	668	C
4	L5	669	C
4	L5	672	C
4	L5	673	C
4	L5	685	C
4	L5	686	A
4	L5	687	U
4	L5	696	C
4	L5	704	C
4	L5	708	G
4	L5	730	G
4	L5	731	G
4	L5	738	C
4	L5	739	G
4	L5	742	G
4	L5	746	A
4	L5	759	G

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Mol	Chain	Res	Type
4	L5	904	C
4	L5	905	C
4	L5	910	G
4	L5	913	U
4	L5	914	U
4	L5	915	A
4	L5	917	A
4	L5	923	C
4	L5	924	C
4	L5	932	A
4	L5	933	G
4	L5	936	C
4	L5	943	A
4	L5	944	A
4	L5	945	U
4	L5	946	C
4	L5	956	A
4	L5	959	G
4	L5	960	A
4	L5	961	G
4	L5	962	C
4	L5	965	G
4	L5	966	A
4	L5	967	C
4	L5	969	C
4	L5	970	G
4	L5	977	C
4	L5	982	U
4	L5	985	C
4	L5	1070	G
4	L5	1071	C
4	L5	1072	C
4	L5	1075	G
4	L5	1082	C
4	L5	1083	U
4	L5	1168	G
4	L5	1171	G
4	L5	1172	C
4	L5	1173	G
4	L5	1179	U
4	L5	1180	C
4	L5	1181	C

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Mol	Chain	Res	Type
4	L5	1182	C
4	L5	1183	C
4	L5	1187	G
4	L5	1202	C
4	L5	1203	G
4	L5	1210	C
4	L5	1211	G
4	L5	1214	C
4	L5	1215	C
4	L5	1219	G
4	L5	1222	A
4	L5	1246	G
4	L5	1253	G
4	L5	1254	A
4	L5	1257	A
4	L5	1258	G
4	L5	1262	G
4	L5	1266	G
4	L5	1267	C
4	L5	1269	G
4	L5	1271	G
4	L5	1272	C
4	L5	1273	G
4	L5	1275	G
4	L5	1280	C
4	L5	1284	G
4	L5	1285	U
4	L5	1287	G
4	L5	1293	G
4	L5	1294	A
4	L5	1295	C
4	L5	1296	G
4	L5	1301	C
4	L5	1302	U
4	L5	1326	A2M
4	L5	1337	A
4	L5	1354	A
4	L5	1359	G
4	L5	1365	C
4	L5	1366	G
4	L5	1367	C
4	L5	1379	C

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Mol	Chain	Res	Type
4	L5	1387	A
4	L5	1394	G
4	L5	1397	A
4	L5	1398	A
4	L5	1403	G
4	L5	1404	G
4	L5	1407	C
4	L5	1409	C
4	L5	1410	U
4	L5	1411	C
4	L5	1417	C
4	L5	1420	A
4	L5	1425	G
4	L5	1437	C
4	L5	1439	C
4	L5	1442	C
4	L5	1443	A
4	L5	1444	G
4	L5	1446	C
4	L5	1447	C
4	L5	1482	G
4	L5	1483	C
4	L5	1497	A
4	L5	1498	G
4	L5	1502	G
4	L5	1517	G
4	L5	1524	A2M
4	L5	1534	A2M
4	L5	1537	A
4	L5	1547	A
4	L5	1564	A
4	L5	1566	C
4	L5	1578	U
4	L5	1591	U
4	L5	1596	U
4	L5	1621	A
4	L5	1624	G
4	L5	1625	OMG
4	L5	1631	A
4	L5	1633	G
4	L5	1634	A
4	L5	1638	A

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Mol	Chain	Res	Type
4	L5	1640	C
4	L5	1641	G
4	L5	1642	A
4	L5	1654	G
4	L5	1661	C
4	L5	1676	C
4	L5	1677	PSU
4	L5	1678	C
4	L5	1694	C
4	L5	1697	G
4	L5	1699	A
4	L5	1700	G
4	L5	1701	A
4	L5	1702	C
4	L5	1704	C
4	L5	1705	G
4	L5	1717	C
4	L5	1718	C
4	L5	1719	A
4	L5	1721	G
4	L5	1726	U
4	L5	1731	C
4	L5	1734	G
4	L5	1742	A
4	L5	1750	G
4	L5	1755	C
4	L5	1757	U
4	L5	1758	G
4	L5	1760	G
4	L5	1761	G
4	L5	1762	C
4	L5	1763	C
4	L5	1764	G
4	L5	1765	A
4	L5	1766	A
4	L5	1767	A
4	L5	1768	C
4	L5	1770	A
4	L5	1787	A
4	L5	1804	A
4	L5	1806	G
4	L5	1810	G

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Mol	Chain	Res	Type
4	L5	1815	G
4	L5	1821	G
4	L5	1822	U
4	L5	1834	U
4	L5	1836	G
4	L5	1837	A
4	L5	1842	G
4	L5	1855	G
4	L5	1869	G
4	L5	1882	U
4	L5	1897	A
4	L5	1917	A
4	L5	1918	U
4	L5	1919	G
4	L5	1920	C
4	L5	1921	C
4	L5	1922	G
4	L5	1925	G
4	L5	1930	U
4	L5	1931	C
4	L5	1932	A
4	L5	1940	G
4	L5	1948	G
4	L5	1951	G
4	L5	1961	G
4	L5	1962	A
4	L5	1974	U
4	L5	1975	G
4	L5	1978	C
4	L5	1980	U
4	L5	1981	G
4	L5	1982	G
4	L5	1983	A
4	L5	1984	A
4	L5	1985	G
4	L5	1986	U
4	L5	1991	A
4	L5	1993	C
4	L5	1997	U
4	L5	1998	A
4	L5	1999	A
4	L5	2001	G

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Mol	Chain	Res	Type
4	L5	2002	A
4	L5	2003	G
4	L5	2004	U
4	L5	2011	C
4	L5	2017	A
4	L5	2018	C
4	L5	2024	G
4	L5	2026	A
4	L5	2046	G
4	L5	2048	U
4	L5	2055	G
4	L5	2056	G
4	L5	2069	A
4	L5	2084	C
4	L5	2085	G
4	L5	2092	G
4	L5	2093	A
4	L5	2095	A
4	L5	2097	U
4	L5	2098	G
4	L5	2101	C
4	L5	2102	G
4	L5	2107	C
4	L5	2110	C
4	L5	2111	G
4	L5	2112	G
4	L5	2250	C
4	L5	2252	G
4	L5	2256	C
4	L5	2261	G
4	L5	2289	C
4	L5	2300	A
4	L5	2301	G
4	L5	2313	A
4	L5	2333	G
4	L5	2348	G
4	L5	2351	OMC
4	L5	2360	A
4	L5	2364	OMG
4	L5	2383	C
4	L5	2395	A
4	L5	2397	G

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Mol	Chain	Res	Type
4	L5	2417	A
4	L5	2425	U
4	L5	2450	G
4	L5	2453	A
4	L5	2464	C
4	L5	2465	C
4	L5	2469	C
4	L5	2471	G
4	L5	2474	G
4	L5	2475	G
4	L5	2478	C
4	L5	2479	G
4	L5	2483	G
4	L5	2484	A
4	L5	2485	U
4	L5	2487	G
4	L5	2488	C
4	L5	2489	C
4	L5	2490	U
4	L5	2494	U
4	L5	2504	C
4	L5	2505	C
4	L5	2506	G
4	L5	2507	A
4	L5	2513	A
4	L5	2519	U
4	L5	2520	C
4	L5	2529	A
4	L5	2537	A
4	L5	2544	G
4	L5	2546	G
4	L5	2547	G
4	L5	2554	U
4	L5	2555	G
4	L5	2556	G
4	L5	2560	C
4	L5	2565	A
4	L5	2567	G
4	L5	2573	A
4	L5	2583	C
4	L5	2587	A
4	L5	2589	C

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Mol	Chain	Res	Type
4	L5	2602	G
4	L5	2627	C
4	L5	2653	C
4	L5	2662	G
4	L5	2669	C
4	L5	2675	G
4	L5	2676	A
4	L5	2687	U
4	L5	2694	G
4	L5	2695	A
4	L5	2696	A
4	L5	2706	G
4	L5	2707	U
4	L5	2708	U
4	L5	2710	C
4	L5	2711	G
4	L5	2712	G
4	L5	2721	G
4	L5	2724	G
4	L5	2726	G
4	L5	2739	C
4	L5	2742	G
4	L5	2743	A
4	L5	2746	A
4	L5	2761	U
4	L5	2763	U
4	L5	2769	U
4	L5	2770	C
4	L5	2788	U
4	L5	2790	U
4	L5	2806	A
4	L5	2814	C
4	L5	2826	U
4	L5	2827	G
4	L5	2829	U
4	L5	2838	G
4	L5	2855	G
4	L5	2867	C
4	L5	2877	G
4	L5	2892	C
4	L5	2894	A
4	L5	2899	C

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Mol	Chain	Res	Type
4	L5	2900	U
4	L5	2902	G
4	L5	2903	G
4	L5	2904	U
4	L5	2905	C
4	L5	2907	G
4	L5	2908	U
4	L5	3590	G
4	L5	3591	C
4	L5	3592	G
4	L5	3594	C
4	L5	3595	U
4	L5	3596	A
4	L5	3597	G
4	L5	3604	A
4	L5	3605	C
4	L5	3616	U
4	L5	3617	G
4	L5	3626	G
4	L5	3630	A
4	L5	3635	A
4	L5	3644	U
4	L5	3646	A
4	L5	3648	A
4	L5	3662	A
4	L5	3664	G
4	L5	3670	C
4	L5	3673	C
4	L5	3674	G
4	L5	3691	G
4	L5	3701	OMC
4	L5	3710	G
4	L5	3711	A
4	L5	3713	U
4	L5	3726	A
4	L5	3727	A
4	L5	3748	A
4	L5	3753	G
4	L5	3760	A
4	L5	3770	U
4	L5	3774	A
4	L5	3775	A

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Mol	Chain	Res	Type
4	L5	3776	G
4	L5	3777	G
4	L5	3785	A2M
4	L5	3786	U
4	L5	3792	OMG
4	L5	3811	G
4	L5	3812	C
4	L5	3814	U
4	L5	3817	A
4	L5	3819	G
4	L5	3824	A
4	L5	3838	U
4	L5	3839	G
4	L5	3840	U
4	L5	3867	A2M
4	L5	3877	A
4	L5	3878	C
4	L5	3879	G
4	L5	3885	G
4	L5	3892	U
4	L5	3897	G
4	L5	3901	A
4	L5	3906	A
4	L5	3907	G
4	L5	3908	A
4	L5	3915	U
4	L5	3923	A
4	L5	3938	G
4	L5	3939	G
4	L5	3942	A
4	L5	3947	A
4	L5	3949	A
4	L5	3950	U
4	L5	3953	G
4	L5	4057	C
4	L5	4058	U
4	L5	4059	C
4	L5	4061	G
4	L5	4062	A
4	L5	4064	C
4	L5	4065	G
4	L5	4068	U

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Mol	Chain	Res	Type
4	L5	4076	G
4	L5	4084	G
4	L5	4095	G
4	L5	4097	G
4	L5	4098	A
4	L5	4099	G
4	L5	4101	C
4	L5	4104	G
4	L5	4108	G
4	L5	4111	U
4	L5	4112	C
4	L5	4114	C
4	L5	4115	G
4	L5	4116	C
4	L5	4122	G
4	L5	4127	A
4	L5	4133	C
4	L5	4140	C
4	L5	4141	G
4	L5	4142	C
4	L5	4143	G
4	L5	4144	C
4	L5	4146	G
4	L5	4149	C
4	L5	4162	C
4	L5	4163	U
4	L5	4170	A
4	L5	4183	G
4	L5	4184	G
4	L5	4191	G
4	L5	4203	A
4	L5	4219	A
4	L5	4220	6MZ
4	L5	4222	G
4	L5	4225	G
4	L5	4229	U
4	L5	4233	A
4	L5	4251	A
4	L5	4254	G
4	L5	4257	A
4	L5	4258	C
4	L5	4265	U

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Mol	Chain	Res	Type
4	L5	4268	A
4	L5	4273	A
4	L5	4281	A
4	L5	4291	G
4	L5	4295	U
4	L5	4304	A
4	L5	4305	G
4	L5	4306	OMU
4	L5	4314	C
4	L5	4319	C
4	L5	4329	G
4	L5	4330	G
4	L5	4332	C
4	L5	4349	C
4	L5	4350	C
4	L5	4354	U
4	L5	4373	G
4	L5	4376	A
4	L5	4377	G
4	L5	4378	A
4	L5	4379	A
4	L5	4387	C
4	L5	4391	G
4	L5	4394	A
4	L5	4421	C
4	L5	4422	A
4	L5	4438	U
4	L5	4448	G
4	L5	4449	A
4	L5	4464	A
4	L5	4466	C
4	L5	4475	G
4	L5	4488	A
4	L5	4500	PSU
4	L5	4512	U
4	L5	4513	A
4	L5	4515	G
4	L5	4519	C
4	L5	4524	G
4	L5	4525	C
4	L5	4545	G
4	L5	4548	A

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Mol	Chain	Res	Type
4	L5	4557	U
4	L5	4560	C
4	L5	4567	G
4	L5	4575	G
4	L5	4584	A
4	L5	4589	A
4	L5	4590	A2M
4	L5	4600	G
4	L5	4601	U
4	L5	4617	G
4	L5	4636	PSU
4	L5	4637	OMG
4	L5	4652	G
4	L5	4656	A
4	L5	4670	C
4	L5	4672	A
4	L5	4679	G
4	L5	4687	A
4	L5	4694	G
4	L5	4695	C
4	L5	4700	A
4	L5	4708	A
4	L5	4709	U
4	L5	4719	G
4	L5	4733	C
4	L5	4734	A
4	L5	4740	G
4	L5	4741	C
4	L5	4742	G
4	L5	4745	G
4	L5	4754	G
4	L5	4757	C
4	L5	4759	C
4	L5	4761	G
4	L5	4765	G
4	L5	4771	C
4	L5	4772	C
4	L5	4775	C
4	L5	4859	C
4	L5	4870	G
4	L5	4871	C
4	L5	4875	G

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Mol	Chain	Res	Type
4	L5	4882	U
4	L5	4883	C
4	L5	4889	G
4	L5	4895	C
4	L5	4896	G
4	L5	4897	G
4	L5	4899	G
4	L5	4900	C
4	L5	4901	G
4	L5	4910	G
4	L5	4912	G
4	L5	4914	C
4	L5	4922	C
4	L5	4925	U
4	L5	4926	C
4	L5	4927	G
4	L5	4928	C
4	L5	4934	A
4	L5	4940	C
4	L5	4941	G
4	L5	4943	A
4	L5	4951	G
4	L5	4955	A
4	L5	4960	G
4	L5	4976	U
4	L5	4985	U
4	L5	4988	U
4	L5	4989	U
4	L5	4991	U
4	L5	4995	U
4	L5	5013	C
4	L5	5014	A
4	L5	5017	G
4	L5	5022	U
4	L5	5023	C
4	L5	5024	C
4	L5	5028	G
4	L5	5030	U
4	L5	5034	A
4	L5	5041	G
4	L5	5050	C
4	L5	5054	C

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Mol	Chain	Res	Type
4	L5	5055	G
4	L5	5061	A
4	L5	5069	U
5	L7	33	U
5	L7	38	U
5	L7	53	U
5	L7	54	A
5	L7	64	G
5	L7	97	G
5	L7	100	A
5	L7	110	G
5	L7	120	U
6	L8	23	C
6	L8	25	G
6	L8	34	U
6	L8	35	C
6	L8	59	A
6	L8	62	A
6	L8	63	U
6	L8	80	A
6	L8	82	A
6	L8	84	A
6	L8	85	U
6	L8	87	G
6	L8	94	G
6	L8	103	A
6	L8	105	C
6	L8	111	U
6	L8	114	G
6	L8	123	U
6	L8	124	U
6	L8	125	C
6	L8	126	C
6	L8	127	U
6	L8	153	C
84	S2	13	C
84	S2	14	C
84	S2	17	C
84	S2	25	A
84	S2	33	G
84	S2	41	G
84	S2	44	U

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Mol	Chain	Res	Type
84	S2	45	A
84	S2	46	A
84	S2	56	G
84	S2	58	C
84	S2	59	U
84	S2	65	C
84	S2	67	C
84	S2	68	A
84	S2	72	C
84	S2	73	C
84	S2	74	G
84	S2	76	U
84	S2	99	A2M
84	S2	103	A
84	S2	113	G
84	S2	114	G
84	S2	115	U
84	S2	126	G
84	S2	130	G
84	S2	142	C
84	S2	143	U
84	S2	149	A
84	S2	158	A
84	S2	160	U
84	S2	162	C
84	S2	170	A
84	S2	175	A
84	S2	179	C
84	S2	190	G
84	S2	191	A
84	S2	196	C
84	S2	197	U
84	S2	198	U
84	S2	200	G
84	S2	203	G
84	S2	204	G
84	S2	207	G
84	S2	208	G
84	S2	214	U
84	S2	291	G
84	S2	292	A
84	S2	295	C

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Mol	Chain	Res	Type
84	S2	302	A
84	S2	306	C
84	S2	307	G
84	S2	308	G
84	S2	309	G
84	S2	311	C
84	S2	312	G
84	S2	313	A
84	S2	318	A
84	S2	319	C
84	S2	323	C
84	S2	324	C
84	S2	325	C
84	S2	326	C
84	S2	328	U
84	S2	329	G
84	S2	332	G
84	S2	339	A
84	S2	340	C
84	S2	347	G
84	S2	360	A
84	S2	362	C
84	S2	364	A
84	S2	368	U
84	S2	370	G
84	S2	385	G
84	S2	386	C
84	S2	398	A
84	S2	407	G
84	S2	408	A
84	S2	409	C
84	S2	436	OMG
84	S2	438	G
84	S2	448	A
84	S2	449	A
84	S2	450	C
84	S2	452	G
84	S2	464	A
84	S2	465	A
84	S2	471	G
84	S2	472	C
84	S2	473	A

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Mol	Chain	Res	Type
84	S2	474	G
84	S2	476	A
84	S2	482	G
84	S2	487	U
84	S2	488	U
84	S2	492	C
84	S2	493	A
84	S2	502	C
84	S2	516	A
84	S2	517	OMC
84	S2	531	A
84	S2	532	C
84	S2	536	A
84	S2	537	C
84	S2	540	U
84	S2	542	U
84	S2	544	G
84	S2	546	G
84	S2	547	G
84	S2	557	U
84	S2	558	G
84	S2	559	G
84	S2	563	G
84	S2	564	A
84	S2	576	A2M
84	S2	583	A
84	S2	587	A
84	S2	589	G
84	S2	590	A
84	S2	591	U
84	S2	593	C
84	S2	604	A
84	S2	614	C
84	S2	617	G
84	S2	623	G
84	S2	628	A
84	S2	631	U
84	S2	643	A
84	S2	644	OMG
84	S2	655	A
84	S2	660	C
84	S2	664	A

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Mol	Chain	Res	Type
84	S2	668	A2M
84	S2	669	A
84	S2	671	A
84	S2	672	A
84	S2	673	G
84	S2	683	OMG
84	S2	688	U
84	S2	689	U
84	S2	692	G
84	S2	696	G
84	S2	697	G
84	S2	698	G
84	S2	731	G
84	S2	732	U
84	S2	733	C
84	S2	736	C
84	S2	737	G
84	S2	738	C
84	S2	749	U
84	S2	751	G
84	S2	752	G
84	S2	753	C
84	S2	788	G
84	S2	791	C
84	S2	792	C
84	S2	798	G
84	S2	799	OMU
84	S2	801	PSU
84	S2	821	G
84	S2	822	U
84	S2	823	U
84	S2	824	C
84	S2	830	A
84	S2	834	C
84	S2	835	C
84	S2	836	G
84	S2	837	A
84	S2	838	G
84	S2	839	C
84	S2	842	C
84	S2	844	U
84	S2	847	A

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Mol	Chain	Res	Type
84	S2	867	OMG
84	S2	870	A
84	S2	874	G
84	S2	877	C
84	S2	878	G
84	S2	880	G
84	S2	888	U
84	S2	889	U
84	S2	891	G
84	S2	893	U
84	S2	894	G
84	S2	896	U
84	S2	897	U
84	S2	898	U
84	S2	899	U
84	S2	900	C
84	S2	901	G
84	S2	903	A
84	S2	913	A
84	S2	920	A
84	S2	930	C
84	S2	933	G
84	S2	934	G
84	S2	943	U
84	S2	963	A
84	S2	970	G
84	S2	971	G
84	S2	972	A
84	S2	985	G
84	S2	990	A
84	S2	992	A
84	S2	999	G
84	S2	1001	A
84	S2	1008	A
84	S2	1017	U
84	S2	1023	A
84	S2	1027	A
84	S2	1060	A
84	S2	1061	U
84	S2	1062	A
84	S2	1080	A
84	S2	1083	A

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Mol	Chain	Res	Type
84	S2	1085	C
84	S2	1109	C
84	S2	1113	A
84	S2	1114	U
84	S2	1116	C
84	S2	1121	G
84	S2	1123	C
84	S2	1133	A
84	S2	1138	C
84	S2	1148	A
84	S2	1150	A
84	S2	1153	C
84	S2	1154	U
84	S2	1195	A
84	S2	1207	G
84	S2	1208	A
84	S2	1215	C
84	S2	1216	C
84	S2	1217	A
84	S2	1224	G
84	S2	1227	G
84	S2	1242	U
84	S2	1243	U
84	S2	1248	B8N
84	S2	1251	A
84	S2	1253	A
84	S2	1256	G
84	S2	1257	G
84	S2	1259	A
84	S2	1271	C
84	S2	1272	OMC
84	S2	1274	G
84	S2	1275	G
84	S2	1283	C
84	S2	1286	G
84	S2	1288	OMU
84	S2	1294	G
84	S2	1295	A
84	S2	1301	A
84	S2	1302	G
84	S2	1303	C
84	S2	1304	U

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Mol	Chain	Res	Type
84	S2	1308	U
84	S2	1342	U
84	S2	1357	A
84	S2	1358	U
84	S2	1371	U
84	S2	1372	U
84	S2	1376	A
84	S2	1378	A
84	S2	1382	A
84	S2	1402	A
84	S2	1413	G
84	S2	1418	C
84	S2	1419	C
84	S2	1420	G
84	S2	1421	A
84	S2	1422	G
84	S2	1423	C
84	S2	1433	C
84	S2	1435	C
84	S2	1437	C
84	S2	1438	A
84	S2	1439	A
84	S2	1442	OMU
84	S2	1449	G
84	S2	1454	A
84	S2	1463	U
84	S2	1478	U
84	S2	1487	A
84	S2	1489	A
84	S2	1490	OMG
84	S2	1492	U
84	S2	1494	U
84	S2	1495	G
84	S2	1497	G
84	S2	1498	A
84	S2	1521	C
84	S2	1531	A
84	S2	1533	A
84	S2	1544	C
84	S2	1546	G
84	S2	1552	G
84	S2	1556	A

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Mol	Chain	Res	Type
84	S2	1558	C
84	S2	1574	C
84	S2	1575	G
84	S2	1578	U
84	S2	1580	A
84	S2	1581	C
84	S2	1587	G
84	S2	1588	A
84	S2	1600	G
84	S2	1604	G
84	S2	1606	G
84	S2	1621	U
84	S2	1623	A
84	S2	1631	U
84	S2	1633	A
84	S2	1634	A
84	S2	1637	A
84	S2	1648	G
84	S2	1654	G
84	S2	1663	A
84	S2	1665	G
84	S2	1683	C
84	S2	1686	G
84	S2	1695	A
84	S2	1698	C
84	S2	1699	A
84	S2	1715	A
84	S2	1721	U
84	S2	1722	G
84	S2	1744	G
84	S2	1745	A
84	S2	1752	C
84	S2	1753	C
84	S2	1754	G
84	S2	1755	C
84	S2	1757	G
84	S2	1759	G
84	S2	1761	U
84	S2	1772	C
84	S2	1773	C
84	S2	1774	C
84	S2	1777	G

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Mol	Chain	Res	Type
84	S2	1782	G
84	S2	1783	C
84	S2	1784	G
84	S2	1786	U
84	S2	1798	C
84	S2	1810	U
84	S2	1825	A
84	S2	1826	G
84	S2	1831	A
84	S2	1835	A
84	S2	1838	U
84	S2	1849	G
84	S2	1851	MA6
84	S2	1861	G
84	S2	1862	G
84	S2	1863	A
84	S2	1865	C
85	AT	3	C
85	AT	4	U
85	AT	8	U
85	AT	9	A
85	AT	10	G
85	AT	12	G
85	AT	13	U
85	AT	14	A
85	AT	16	C
85	AT	19	G
85	AT	20	U
85	AT	21	U
85	AT	22	A
85	AT	26	C
85	AT	27	G
85	AT	31	G
85	AT	32	C
85	AT	33	C
85	AT	34	U
85	AT	37	C
85	AT	40	G
85	AT	41	C
85	AT	43	A
85	AT	45	A
85	AT	46	G

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Mol	Chain	Res	Type
85	AT	47	G
85	AT	49	C
85	AT	50	C
85	AT	51	U
85	AT	53	G
85	AT	58	G
85	AT	59	A
85	AT	60	A
85	AT	62	C
85	AT	64	G
85	AT	65	G
85	AT	68	G
85	AT	69	G
85	AT	70	A
85	AT	72	A
85	AT	73	C
85	AT	76	C
85	AT	77	A

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	L5	406	C
4	L5	493	G
4	L5	914	U
4	L5	1082	C
4	L5	1590	C
4	L5	1633	G
4	L5	1703	C
4	L5	1977	C
4	L5	2416	G
4	L5	2675	G
4	L5	2760	G
4	L5	3673	C
4	L5	4600	G
4	L5	4699	U
4	L5	4913	G
84	S2	291	G
84	S2	563	G
84	S2	688	U
84	S2	1477	U
85	AT	7	G

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

179 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	A2M	L5	1323	4	22,25,26	1.28	2 (9%)	30,36,39	1.61	6 (20%)
84	PSU	S2	406	84	18,21,22	1.10	1 (5%)	21,30,33	1.92	5 (23%)
84	OMG	S2	867	84	23,26,27	0.51	0	32,38,41	0.48	0
84	OMU	S2	121	84	19,22,23	3.37	7 (36%)	25,31,34	1.81	5 (20%)
4	OMG	L5	3627	4	23,26,27	0.52	0	32,38,41	0.63	0
86	SEP	CF	163	86	8,9,10	1.60	1 (12%)	7,12,14	1.41	1 (14%)
4	A2M	L5	398	4	22,25,26	1.22	1 (4%)	30,36,39	1.64	5 (16%)
4	OMC	L5	2824	4	19,22,23	0.56	0	25,31,34	0.62	0
4	PSU	L5	4579	4	18,21,22	1.06	1 (5%)	21,30,33	1.89	4 (19%)
4	PSU	L5	4493	4	18,21,22	1.10	1 (5%)	21,30,33	1.88	5 (23%)
4	A2M	L5	4590	4	22,25,26	1.23	1 (4%)	30,36,39	1.57	7 (23%)
4	OMC	L5	2365	4,87	19,22,23	0.55	0	25,31,34	0.60	0
84	OMC	S2	174	84	19,22,23	0.50	0	25,31,34	0.65	0
4	OMC	L5	1340	4	19,22,23	0.59	0	25,31,34	0.81	0
4	PSU	L5	4972	4	18,21,22	1.05	1 (5%)	21,30,33	1.92	5 (23%)
84	B8N	S2	1248	84	25,29,30	3.26	6 (24%)	28,42,45	1.95	7 (25%)
4	PSU	L5	1781	4	18,21,22	1.06	1 (5%)	21,30,33	1.80	4 (19%)
4	OMG	L5	3792	4	23,26,27	0.50	0	32,38,41	0.50	0
84	MA6	S2	1851	84	23,26,27	1.28	2 (8%)	33,38,41	3.41	12 (36%)
4	PSU	L5	4353	4	18,21,22	1.06	1 (5%)	21,30,33	2.05	6 (28%)
84	PSU	S2	1232	84	18,21,22	1.12	1 (5%)	21,30,33	1.91	4 (19%)
84	PSU	S2	105	84	18,21,22	1.09	1 (5%)	21,30,33	1.84	4 (19%)
84	G7M	S2	1639	84,2	23,26,27	2.64	9 (39%)	34,39,42	2.53	11 (32%)
4	PSU	L5	3637	4	18,21,22	1.07	1 (5%)	21,30,33	1.89	4 (19%)
4	PSU	L5	5001	4	18,21,22	1.10	1 (5%)	21,30,33	1.86	4 (19%)
84	A2M	S2	27	84	22,25,26	1.28	1 (4%)	30,36,39	1.59	6 (20%)
4	A2M	L5	1326	4	22,25,26	1.27	2 (9%)	30,36,39	1.52	7 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	OMC	L5	3869	4	19,22,23	0.58	0	25,31,34	0.72	0
4	PSU	L5	4296	4	18,21,22	1.09	1 (5%)	21,30,33	1.92	4 (19%)
4	A2M	L5	1534	4,87	22,25,26	1.25	2 (9%)	30,36,39	1.47	8 (26%)
84	OMU	S2	428	84	19,22,23	3.35	7 (36%)	25,31,34	1.80	5 (20%)
4	PSU	L5	4442	4	18,21,22	1.08	1 (5%)	21,30,33	2.00	6 (28%)
4	OMG	L5	4618	4	23,26,27	0.53	0	32,38,41	0.53	0
4	PSU	L5	3853	4,87	18,21,22	1.12	1 (5%)	21,30,33	1.85	4 (19%)
4	OMG	L5	4494	4	23,26,27	0.53	0	32,38,41	0.52	0
84	PSU	S2	1046	84	18,21,22	1.13	1 (5%)	21,30,33	1.87	4 (19%)
4	A2M	L5	2815	4	22,25,26	1.24	2 (9%)	30,36,39	1.55	6 (20%)
4	A2M	L5	3830	4	22,25,26	1.24	1 (4%)	30,36,39	1.57	6 (20%)
6	OMG	L8	75	6	23,26,27	0.50	0	32,38,41	0.48	0
4	OMG	L5	1522	4	23,26,27	0.54	0	32,38,41	0.66	0
4	OMG	L5	4637	4	23,26,27	0.49	0	32,38,41	0.52	0
84	OMU	S2	1442	84	19,22,23	3.37	7 (36%)	25,31,34	1.78	5 (20%)
84	PSU	S2	1045	84	18,21,22	1.08	1 (5%)	21,30,33	1.94	5 (23%)
4	OMG	L5	1625	4	23,26,27	0.49	0	32,38,41	0.51	0
84	PSU	S2	686	84	18,21,22	1.07	1 (5%)	21,30,33	1.95	5 (23%)
4	OMU	L5	4306	4	19,22,23	3.28	7 (36%)	25,31,34	1.85	4 (16%)
4	A2M	L5	2363	4,87	22,25,26	1.20	2 (9%)	30,36,39	1.57	8 (26%)
4	PSU	L5	4431	4	18,21,22	1.07	1 (5%)	21,30,33	1.92	4 (19%)
4	PSU	L5	1536	4	18,21,22	1.05	1 (5%)	21,30,33	1.94	4 (19%)
84	PSU	S2	801	84	18,21,22	1.09	1 (5%)	21,30,33	1.85	4 (19%)
4	OMG	L5	4228	4	23,26,27	0.51	0	32,38,41	0.65	0
4	OMG	L5	2876	4	23,26,27	0.51	0	32,38,41	0.57	0
4	A2M	L5	400	4	22,25,26	1.26	1 (4%)	30,36,39	1.59	8 (26%)
4	OMU	L5	4498	4	19,22,23	3.27	7 (36%)	25,31,34	1.84	5 (20%)
84	A2M	S2	484	84	22,25,26	1.25	1 (4%)	30,36,39	1.50	6 (20%)
84	PSU	S2	651	84	18,21,22	1.12	1 (5%)	21,30,33	1.95	5 (23%)
84	4AC	S2	1842	84	21,24,25	0.39	0	28,34,37	0.48	0
4	OMU	L5	2837	4	19,22,23	3.34	7 (36%)	25,31,34	1.89	5 (20%)
4	PSU	L5	4689	4	18,21,22	1.11	1 (5%)	21,30,33	2.04	4 (19%)
4	PSU	L5	2839	4	18,21,22	1.12	1 (5%)	21,30,33	1.96	5 (23%)
84	OMC	S2	462	84	19,22,23	0.51	0	25,31,34	0.70	0
4	OMG	L5	4392	4	23,26,27	0.51	0	32,38,41	0.52	0
84	6MZ	S2	1832	84,87	26,26,26	2.88	5 (19%)	36,39,39	2.01	9 (25%)
4	PSU	L5	4471	4	18,21,22	1.07	1 (5%)	21,30,33	1.82	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	A2M	L5	2787	4	22,25,26	1.17	1 (4%)	30,36,39	1.53	7 (23%)
4	OMC	L5	2804	4	19,22,23	0.56	0	25,31,34	0.71	0
4	OMC	L5	4456	4	19,22,23	0.63	0	25,31,34	0.79	1 (4%)
4	A2M	L5	2401	4	22,25,26	1.24	1 (4%)	30,36,39	1.66	6 (20%)
84	A2M	S2	576	84	22,25,26	1.24	1 (4%)	30,36,39	1.53	5 (16%)
4	PSU	L5	4299	4	18,21,22	1.07	1 (5%)	21,30,33	1.88	4 (19%)
84	OMC	S2	1391	84	19,22,23	0.50	0	25,31,34	0.68	0
4	PSU	L5	4636	4	18,21,22	1.13	1 (5%)	21,30,33	2.02	6 (28%)
84	A2M	S2	1031	84	22,25,26	1.22	1 (4%)	30,36,39	1.60	6 (20%)
84	PSU	S2	1244	84	18,21,22	1.10	1 (5%)	21,30,33	1.91	5 (23%)
4	PSU	L5	4500	4	18,21,22	1.13	1 (5%)	21,30,33	1.99	5 (23%)
84	PSU	S2	1056	84	18,21,22	1.10	1 (5%)	21,30,33	1.99	5 (23%)
4	OMG	L5	1316	4	23,26,27	0.56	0	32,38,41	0.56	0
84	OMC	S2	1272	84	19,22,23	0.51	0	25,31,34	0.85	1 (4%)
84	PSU	S2	1177	84	18,21,22	1.11	1 (5%)	21,30,33	1.94	5 (23%)
4	OMG	L5	2364	4,87	23,26,27	0.52	0	32,38,41	0.47	0
4	PSU	L5	4293	4	18,21,22	1.10	2 (11%)	21,30,33	1.92	4 (19%)
4	A2M	L5	3825	4	22,25,26	1.23	1 (4%)	30,36,39	1.58	6 (20%)
4	UR3	L5	4530	4	19,22,23	2.74	7 (36%)	26,32,35	1.56	2 (7%)
6	PSU	L8	55	6	18,21,22	1.06	1 (5%)	21,30,33	1.93	5 (23%)
4	PSU	L5	4312	4	18,21,22	1.09	1 (5%)	21,30,33	1.91	4 (19%)
4	OMU	L5	4227	4	19,22,23	3.36	7 (36%)	25,31,34	1.87	5 (20%)
4	OMG	L5	4370	4	23,26,27	0.51	0	32,38,41	0.54	0
4	OMC	L5	2422	4,87	19,22,23	0.60	0	25,31,34	0.71	0
4	PSU	L5	1860	4	18,21,22	1.10	1 (5%)	21,30,33	2.01	5 (23%)
4	PSU	L5	1782	4	18,21,22	1.06	1 (5%)	21,30,33	1.89	4 (19%)
4	PSU	L5	3695	4	18,21,22	1.09	1 (5%)	21,30,33	1.87	4 (19%)
4	PSU	L5	4973	4	18,21,22	1.07	1 (5%)	21,30,33	1.91	5 (23%)
4	1MA	L5	1322	4,87	21,25,26	0.59	0	30,37,40	0.80	1 (3%)
6	PSU	L8	69	6	18,21,22	1.12	1 (5%)	21,30,33	1.95	6 (28%)
4	5MC	L5	4447	4	19,22,23	0.79	0	26,32,35	0.67	0
84	OMG	S2	509	84	23,26,27	0.49	0	32,38,41	0.50	0
4	PSU	L5	4628	4	18,21,22	1.03	1 (5%)	21,30,33	1.89	5 (23%)
4	OMG	L5	4623	4	23,26,27	0.53	0	32,38,41	0.59	0
84	PSU	S2	1081	84	18,21,22	1.07	1 (5%)	21,30,33	1.91	5 (23%)
84	PSU	S2	1367	84	18,21,22	1.13	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
4	PSU	L5	1744	4,87	18,21,22	1.09	1 (5%)	21,30,33	1.89	4 (19%)
4	A2M	L5	1871	4,87	22,25,26	1.53	3 (13%)	30,36,39	1.93	9 (30%)
4	PSU	L5	3844	4	18,21,22	1.13	1 (5%)	21,30,33	1.79	4 (19%)
4	A2M	L5	3718	4	22,25,26	1.14	1 (4%)	30,36,39	1.54	7 (23%)
4	PSU	L5	3884	4	18,21,22	1.10	2 (11%)	21,30,33	1.89	4 (19%)
84	PSU	S2	109	84	18,21,22	1.13	1 (5%)	21,30,33	1.92	5 (23%)
4	A2M	L5	1524	4	22,25,26	1.28	2 (9%)	30,36,39	1.53	6 (20%)
84	OMU	S2	354	84	19,22,23	3.33	7 (36%)	25,31,34	1.83	5 (20%)
4	PSU	L5	4552	4	18,21,22	1.10	1 (5%)	21,30,33	2.00	5 (23%)
4	PSU	L5	4457	4	18,21,22	1.10	1 (5%)	21,30,33	1.94	5 (23%)
84	OMU	S2	1326	84	19,22,23	3.34	7 (36%)	25,31,34	1.85	5 (20%)
4	6MZ	L5	4220	4	22,25,26	4.30	11 (50%)	29,36,39	2.60	13 (44%)
4	PSU	L5	4521	4,87	18,21,22	1.13	2 (11%)	21,30,33	2.01	6 (28%)
4	PSU	L5	3851	4	18,21,22	1.08	1 (5%)	21,30,33	1.89	5 (23%)
84	A2M	S2	166	84	22,25,26	1.28	1 (4%)	30,36,39	1.62	6 (20%)
84	OMG	S2	644	84	23,26,27	0.46	0	32,38,41	0.51	0
4	OMC	L5	3887	4	19,22,23	0.56	0	25,31,34	0.67	0
84	A2M	S2	1383	84	22,25,26	1.21	1 (4%)	30,36,39	1.65	7 (23%)
4	UY1	L5	3818	4	19,22,23	4.89	10 (52%)	21,31,34	1.95	5 (23%)
4	PSU	L5	2632	4	18,21,22	1.13	1 (5%)	21,30,33	1.96	5 (23%)
4	OMG	L5	3899	4	23,26,27	0.57	0	32,38,41	0.55	0
4	PSU	L5	4673	4,87	18,21,22	1.07	1 (5%)	21,30,33	1.88	4 (19%)
4	PSU	L5	4361	4	18,21,22	1.09	1 (5%)	21,30,33	1.85	4 (19%)
84	A2M	S2	668	84,87	22,25,26	1.35	2 (9%)	30,36,39	1.64	7 (23%)
4	A2M	L5	4571	4	22,25,26	1.33	2 (9%)	30,36,39	1.59	8 (26%)
84	OMU	S2	172	84	19,22,23	3.36	7 (36%)	25,31,34	1.84	5 (20%)
84	OMU	S2	799	84	19,22,23	3.39	7 (36%)	25,31,34	1.80	5 (20%)
84	A2M	S2	99	84,87	22,25,26	1.25	1 (4%)	30,36,39	1.57	5 (16%)
4	PSU	L5	3639	4	18,21,22	1.12	1 (5%)	21,30,33	1.96	5 (23%)
4	5MC	L5	3782	4,87	19,22,23	0.62	0	26,32,35	0.78	1 (3%)
84	OMU	S2	116	84	19,22,23	3.33	7 (36%)	25,31,34	1.73	4 (16%)
84	A2M	S2	468	84	22,25,26	1.27	1 (4%)	30,36,39	1.57	6 (20%)
84	OMG	S2	683	84	23,26,27	0.51	0	32,38,41	0.49	0
4	OMU	L5	3925	4	19,22,23	3.26	7 (36%)	25,31,34	1.87	5 (20%)
4	PSU	L5	3822	4	18,21,22	1.10	1 (5%)	21,30,33	1.96	6 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
84	PSU	S2	814	84	18,21,22	1.09	1 (5%)	21,30,33	1.84	4 (19%)
84	OMG	S2	1328	84	23,26,27	0.46	0	32,38,41	0.45	0
4	PSU	L5	1677	4	18,21,22	1.07	2 (11%)	21,30,33	1.84	3 (14%)
4	A2M	L5	3785	4,87	22,25,26	1.16	1 (4%)	30,36,39	1.63	10 (33%)
84	PSU	S2	1004	84	18,21,22	1.12	1 (5%)	21,30,33	1.98	5 (23%)
84	4AC	S2	1337	84	21,24,25	0.39	0	28,34,37	0.80	2 (7%)
84	OMU	S2	627	84	19,22,23	3.37	7 (36%)	25,31,34	1.81	5 (20%)
84	PSU	S2	966	84,87	18,21,22	1.07	1 (5%)	21,30,33	1.85	4 (19%)
4	PSU	L5	4403	4	18,21,22	1.06	1 (5%)	21,30,33	2.00	6 (28%)
4	OMU	L5	4620	4	19,22,23	3.25	7 (36%)	25,31,34	1.70	4 (16%)
4	PSU	L5	5010	4	18,21,22	1.10	1 (5%)	21,30,33	1.90	4 (19%)
4	OMC	L5	3808	4,87	19,22,23	0.63	0	25,31,34	0.76	1 (4%)
84	PSU	S2	681	84	18,21,22	1.07	1 (5%)	21,30,33	1.83	4 (19%)
4	OMG	L5	3744	4	23,26,27	0.51	0	32,38,41	0.48	0
84	MA6	S2	1850	84	23,26,27	1.28	2 (8%)	33,38,41	3.35	12 (36%)
4	A2M	L5	4523	4,87	22,25,26	1.30	1 (4%)	30,36,39	1.60	6 (20%)
4	PSU	L5	1792	4	18,21,22	1.06	1 (5%)	21,30,33	1.85	4 (19%)
4	PSU	L5	4576	4	18,21,22	1.09	1 (5%)	21,30,33	1.90	4 (19%)
4	OMC	L5	4536	4	19,22,23	0.61	0	25,31,34	0.75	0
4	OMG	L5	4499	4	23,26,27	0.50	0	32,38,41	0.49	0
84	OMC	S2	1703	84	19,22,23	0.55	0	25,31,34	0.61	0
4	OMC	L5	3701	4	19,22,23	0.65	0	25,31,34	1.74	4 (16%)
84	OMG	S2	601	84	23,26,27	0.49	0	32,38,41	0.43	0
4	OMG	L5	4196	2,4	23,26,27	0.53	0	32,38,41	0.46	0
84	OMC	S2	517	84	19,22,23	0.49	0	25,31,34	0.65	0
84	PSU	S2	866	84	18,21,22	1.09	1 (5%)	21,30,33	2.06	6 (28%)
4	PSU	L5	1683	4	18,21,22	1.09	1 (5%)	21,30,33	1.95	5 (23%)
84	PSU	S2	863	84	18,21,22	1.12	1 (5%)	21,30,33	1.87	4 (19%)
84	PSU	S2	649	84	18,21,22	1.11	1 (5%)	21,30,33	1.96	4 (19%)
84	PSU	S2	1174	84	18,21,22	1.10	1 (5%)	21,30,33	1.86	4 (19%)
84	OMU	S2	1288	84	19,22,23	3.43	7 (36%)	25,31,34	1.76	5 (20%)
4	A2M	L5	3867	4	22,25,26	1.28	2 (9%)	30,36,39	1.52	8 (26%)
4	PSU	L5	4532	4	18,21,22	1.12	1 (5%)	21,30,33	1.87	4 (19%)
84	PSU	S2	93	84	18,21,22	1.06	1 (5%)	21,30,33	1.80	4 (19%)
84	A2M	S2	159	84	22,25,26	1.20	1 (4%)	30,36,39	1.51	6 (20%)
4	OMC	L5	3841	4	19,22,23	0.57	0	25,31,34	0.68	0
4	OMG	L5	2424	4	23,26,27	0.53	0	32,38,41	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
84	OMG	S2	1490	84	23,26,27	0.53	0	32,38,41	0.53	0
4	PSU	L5	1582	4	18,21,22	1.08	1 (5%)	21,30,33	1.76	4 (19%)
4	OMC	L5	2861	4	19,22,23	0.57	0	25,31,34	0.79	1 (4%)
4	OMC	L5	2351	4,87	19,22,23	0.60	0	25,31,34	0.94	2 (8%)
4	PSU	L5	1862	4	18,21,22	1.08	1 (5%)	21,30,33	1.89	4 (19%)
84	OMG	S2	436	84	23,26,27	0.48	0	32,38,41	0.55	0
4	PSU	L5	3920	4,87	18,21,22	1.07	1 (5%)	21,30,33	1.96	5 (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
4	A2M	L5	1323	4	-	2/9/27/28	0/3/3/3
84	PSU	S2	406	84	-	0/7/25/26	0/2/2/2
84	OMG	S2	867	84	-	3/9/27/28	0/3/3/3
84	OMU	S2	121	84	-	0/9/27/28	0/2/2/2
4	OMG	L5	3627	4	-	0/9/27/28	0/3/3/3
86	SEP	CF	163	86	-	6/6/8/10	-
4	A2M	L5	398	4	-	1/9/27/28	0/3/3/3
4	OMC	L5	2824	4	-	0/9/27/28	0/2/2/2
4	PSU	L5	4579	4	-	0/7/25/26	0/2/2/2
4	PSU	L5	4493	4	-	0/7/25/26	0/2/2/2
4	A2M	L5	4590	4	-	3/9/27/28	0/3/3/3
4	OMC	L5	2365	4,87	-	0/9/27/28	0/2/2/2
84	OMC	S2	174	84	-	0/9/27/28	0/2/2/2
4	OMC	L5	1340	4	-	1/9/27/28	0/2/2/2
4	PSU	L5	4972	4	-	0/7/25/26	0/2/2/2
84	B8N	S2	1248	84	-	4/16/34/35	0/2/2/2
4	PSU	L5	1781	4	-	1/7/25/26	0/2/2/2
4	OMG	L5	3792	4	-	2/9/27/28	0/3/3/3
84	MA6	S2	1851	84	-	1/11/29/30	0/3/3/3
4	PSU	L5	4353	4	-	0/7/25/26	0/2/2/2
84	PSU	S2	1232	84	-	0/7/25/26	0/2/2/2
84	PSU	S2	105	84	-	0/7/25/26	0/2/2/2
84	G7M	S2	1639	84,2	-	2/7/25/26	0/3/3/3
4	PSU	L5	3637	4	-	0/7/25/26	0/2/2/2
4	PSU	L5	5001	4	-	0/7/25/26	0/2/2/2
84	A2M	S2	27	84	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A2M	L5	1326	4	-	4/9/27/28	0/3/3/3
4	OMC	L5	3869	4	-	2/9/27/28	0/2/2/2
4	PSU	L5	4296	4	-	0/7/25/26	0/2/2/2
4	A2M	L5	1534	4,87	-	1/9/27/28	0/3/3/3
84	OMU	S2	428	84	-	6/9/27/28	0/2/2/2
4	PSU	L5	4442	4	-	0/7/25/26	0/2/2/2
4	OMG	L5	4618	4	-	2/9/27/28	0/3/3/3
4	PSU	L5	3853	4,87	-	0/7/25/26	0/2/2/2
4	OMG	L5	4494	4	-	0/9/27/28	0/3/3/3
84	PSU	S2	1046	84	-	0/7/25/26	0/2/2/2
4	A2M	L5	2815	4	-	2/9/27/28	0/3/3/3
4	A2M	L5	3830	4	-	0/9/27/28	0/3/3/3
6	OMG	L8	75	6	-	1/9/27/28	0/3/3/3
4	OMG	L5	1522	4	-	0/9/27/28	0/3/3/3
4	OMG	L5	4637	4	-	3/9/27/28	0/3/3/3
84	OMU	S2	1442	84	-	2/9/27/28	0/2/2/2
84	PSU	S2	1045	84	-	2/7/25/26	0/2/2/2
4	OMG	L5	1625	4	-	2/9/27/28	0/3/3/3
84	PSU	S2	686	84	-	0/7/25/26	0/2/2/2
4	OMU	L5	4306	4	-	0/9/27/28	0/2/2/2
4	A2M	L5	2363	4,87	-	0/9/27/28	0/3/3/3
4	PSU	L5	4431	4	-	0/7/25/26	0/2/2/2
4	PSU	L5	1536	4	-	2/7/25/26	0/2/2/2
84	PSU	S2	801	84	-	2/7/25/26	0/2/2/2
4	OMG	L5	4228	4	-	0/9/27/28	0/3/3/3
4	OMG	L5	2876	4	-	2/9/27/28	0/3/3/3
4	A2M	L5	400	4	-	1/9/27/28	0/3/3/3
4	OMU	L5	4498	4	-	0/9/27/28	0/2/2/2
84	A2M	S2	484	84	-	0/9/27/28	0/3/3/3
84	PSU	S2	651	84	-	0/7/25/26	0/2/2/2
84	4AC	S2	1842	84	-	0/11/29/30	0/2/2/2
4	OMU	L5	2837	4	-	0/9/27/28	0/2/2/2
4	PSU	L5	4689	4	-	0/7/25/26	0/2/2/2
4	PSU	L5	2839	4	-	0/7/25/26	0/2/2/2
84	OMC	S2	462	84	-	0/9/27/28	0/2/2/2
4	OMG	L5	4392	4	-	0/9/27/28	0/3/3/3
84	6MZ	S2	1832	84,87	-	3/12/28/28	0/3/3/3
4	PSU	L5	4471	4	-	0/7/25/26	0/2/2/2
4	A2M	L5	2787	4	-	5/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	OMC	L5	2804	4	-	0/9/27/28	0/2/2/2
4	OMC	L5	4456	4	-	0/9/27/28	0/2/2/2
4	A2M	L5	2401	4	-	0/9/27/28	0/3/3/3
84	A2M	S2	576	84	-	3/9/27/28	0/3/3/3
4	PSU	L5	4299	4	-	0/7/25/26	0/2/2/2
84	OMC	S2	1391	84	-	0/9/27/28	0/2/2/2
4	PSU	L5	4636	4	-	0/7/25/26	0/2/2/2
84	A2M	S2	1031	84	-	0/9/27/28	0/3/3/3
84	PSU	S2	1244	84	-	0/7/25/26	0/2/2/2
4	PSU	L5	4500	4	-	3/7/25/26	0/2/2/2
84	PSU	S2	1056	84	-	0/7/25/26	0/2/2/2
4	OMG	L5	1316	4	-	0/9/27/28	0/3/3/3
84	OMC	S2	1272	84	-	2/9/27/28	0/2/2/2
84	PSU	S2	1177	84	-	0/7/25/26	0/2/2/2
4	OMG	L5	2364	4,87	-	2/9/27/28	0/3/3/3
4	PSU	L5	4293	4	-	0/7/25/26	0/2/2/2
4	A2M	L5	3825	4	-	0/9/27/28	0/3/3/3
4	UR3	L5	4530	4	-	0/7/25/26	0/2/2/2
6	PSU	L8	55	6	-	0/7/25/26	0/2/2/2
4	PSU	L5	4312	4	-	0/7/25/26	0/2/2/2
4	OMU	L5	4227	4	-	0/9/27/28	0/2/2/2
4	OMG	L5	4370	4	-	0/9/27/28	0/3/3/3
4	OMC	L5	2422	4,87	-	2/9/27/28	0/2/2/2
4	PSU	L5	1860	4	-	0/7/25/26	0/2/2/2
4	PSU	L5	1782	4	-	0/7/25/26	0/2/2/2
4	PSU	L5	3695	4	-	0/7/25/26	0/2/2/2
4	PSU	L5	4973	4	-	0/7/25/26	0/2/2/2
4	1MA	L5	1322	4,87	-	1/7/25/26	0/3/3/3
6	PSU	L8	69	6	-	0/7/25/26	0/2/2/2
4	5MC	L5	4447	4	-	4/7/25/26	0/2/2/2
84	OMG	S2	509	84	-	0/9/27/28	0/3/3/3
4	PSU	L5	4628	4	-	0/7/25/26	0/2/2/2
4	OMG	L5	4623	4	-	0/9/27/28	0/3/3/3
84	PSU	S2	1081	84	-	0/7/25/26	0/2/2/2
84	PSU	S2	1367	84	-	0/7/25/26	0/2/2/2
4	PSU	L5	1744	4,87	-	0/7/25/26	0/2/2/2
4	A2M	L5	1871	4,87	-	0/9/27/28	0/3/3/3
4	PSU	L5	3844	4	-	1/7/25/26	0/2/2/2
4	A2M	L5	3718	4	-	0/9/27/28	0/3/3/3
4	PSU	L5	3884	4	-	0/7/25/26	0/2/2/2
84	PSU	S2	109	84	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A2M	L5	1524	4	-	2/9/27/28	0/3/3/3
84	OMU	S2	354	84	-	0/9/27/28	0/2/2/2
4	PSU	L5	4552	4	-	0/7/25/26	0/2/2/2
4	PSU	L5	4457	4	-	0/7/25/26	0/2/2/2
84	OMU	S2	1326	84	-	0/9/27/28	0/2/2/2
4	6MZ	L5	4220	4	-	2/9/27/28	0/3/3/3
4	PSU	L5	4521	4,87	-	0/7/25/26	0/2/2/2
4	PSU	L5	3851	4	-	1/7/25/26	0/2/2/2
84	A2M	S2	166	84	-	1/9/27/28	0/3/3/3
84	OMG	S2	644	84	-	3/9/27/28	0/3/3/3
4	OMC	L5	3887	4	-	1/9/27/28	0/2/2/2
84	A2M	S2	1383	84	-	3/9/27/28	0/3/3/3
4	UY1	L5	3818	4	-	2/9/27/28	0/2/2/2
4	PSU	L5	2632	4	-	0/7/25/26	0/2/2/2
4	OMG	L5	3899	4	-	2/9/27/28	0/3/3/3
4	PSU	L5	4673	4,87	-	0/7/25/26	0/2/2/2
4	PSU	L5	4361	4	-	0/7/25/26	0/2/2/2
84	A2M	S2	668	84,87	-	2/9/27/28	0/3/3/3
4	A2M	L5	4571	4	-	0/9/27/28	0/3/3/3
84	OMU	S2	172	84	-	0/9/27/28	0/2/2/2
84	OMU	S2	799	84	-	2/9/27/28	0/2/2/2
84	A2M	S2	99	84,87	-	2/9/27/28	0/3/3/3
4	PSU	L5	3639	4	-	0/7/25/26	0/2/2/2
4	5MC	L5	3782	4,87	-	1/7/25/26	0/2/2/2
84	OMU	S2	116	84	-	0/9/27/28	0/2/2/2
84	A2M	S2	468	84	-	1/9/27/28	0/3/3/3
84	OMG	S2	683	84	-	2/9/27/28	0/3/3/3
4	OMU	L5	3925	4	-	0/9/27/28	0/2/2/2
4	PSU	L5	3822	4	-	0/7/25/26	0/2/2/2
84	PSU	S2	814	84	-	0/7/25/26	0/2/2/2
84	OMG	S2	1328	84	-	0/9/27/28	0/3/3/3
4	PSU	L5	1677	4	-	3/7/25/26	0/2/2/2
4	A2M	L5	3785	4,87	-	1/9/27/28	0/3/3/3
84	PSU	S2	1004	84	-	0/7/25/26	0/2/2/2
84	4AC	S2	1337	84	-	1/11/29/30	0/2/2/2
84	OMU	S2	627	84	-	1/9/27/28	0/2/2/2
84	PSU	S2	966	84,87	-	0/7/25/26	0/2/2/2
4	PSU	L5	4403	4	-	0/7/25/26	0/2/2/2
4	OMU	L5	4620	4	-	0/9/27/28	0/2/2/2
4	PSU	L5	5010	4	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	OMC	L5	3808	4,87	-	0/9/27/28	0/2/2/2
84	PSU	S2	681	84	-	0/7/25/26	0/2/2/2
4	OMG	L5	3744	4	-	0/9/27/28	0/3/3/3
84	MA6	S2	1850	84	-	0/11/29/30	0/3/3/3
4	A2M	L5	4523	4,87	-	0/9/27/28	0/3/3/3
4	PSU	L5	1792	4	-	0/7/25/26	0/2/2/2
4	PSU	L5	4576	4	-	0/7/25/26	0/2/2/2
4	OMC	L5	4536	4	-	0/9/27/28	0/2/2/2
4	OMG	L5	4499	4	-	0/9/27/28	0/3/3/3
84	OMC	S2	1703	84	-	1/9/27/28	0/2/2/2
4	OMC	L5	3701	4	-	6/9/27/28	0/2/2/2
84	OMG	S2	601	84	-	1/9/27/28	0/3/3/3
4	OMG	L5	4196	2,4	-	1/9/27/28	0/3/3/3
84	OMC	S2	517	84	-	2/9/27/28	0/2/2/2
84	PSU	S2	866	84	-	0/7/25/26	0/2/2/2
4	PSU	L5	1683	4	-	0/7/25/26	0/2/2/2
84	PSU	S2	863	84	-	0/7/25/26	0/2/2/2
84	PSU	S2	649	84	-	0/7/25/26	0/2/2/2
84	PSU	S2	1174	84	-	0/7/25/26	0/2/2/2
84	OMU	S2	1288	84	-	2/9/27/28	0/2/2/2
4	A2M	L5	3867	4	-	2/9/27/28	0/3/3/3
4	PSU	L5	4532	4	-	0/7/25/26	0/2/2/2
84	PSU	S2	93	84	-	0/7/25/26	0/2/2/2
84	A2M	S2	159	84	-	1/9/27/28	0/3/3/3
4	OMC	L5	3841	4	-	1/9/27/28	0/2/2/2
4	OMG	L5	2424	4	-	0/9/27/28	0/3/3/3
84	OMG	S2	1490	84	-	1/9/27/28	0/3/3/3
4	PSU	L5	1582	4	-	0/7/25/26	0/2/2/2
4	OMC	L5	2861	4	-	0/9/27/28	0/2/2/2
4	OMC	L5	2351	4,87	-	3/9/27/28	0/2/2/2
4	PSU	L5	1862	4	-	0/7/25/26	0/2/2/2
84	OMG	S2	436	84	-	2/9/27/28	0/3/3/3
4	PSU	L5	3920	4,87	-	0/7/25/26	0/2/2/2

All (281) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	S2	1832	6MZ	C6-N6	13.00	1.49	1.34
4	L5	3818	UY1	C6-C5	12.72	1.49	1.35
4	L5	4220	6MZ	C6-N6	12.52	1.48	1.34
4	L5	3818	UY1	C2-N1	11.82	1.52	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L5	4220	6MZ	C3'-C2'	-8.80	1.29	1.53
84	S2	1288	OMU	C2-N1	8.67	1.52	1.38
84	S2	799	OMU	C2-N1	8.55	1.51	1.38
4	L5	4227	OMU	C2-N1	8.33	1.51	1.38
84	S2	121	OMU	C2-N1	8.30	1.51	1.38
84	S2	172	OMU	C2-N1	8.26	1.51	1.38
84	S2	1442	OMU	C2-N1	8.25	1.51	1.38
84	S2	1326	OMU	C2-N1	8.19	1.51	1.38
84	S2	627	OMU	C2-N1	8.19	1.51	1.38
4	L5	2837	OMU	C2-N1	8.17	1.51	1.38
4	L5	4306	OMU	C2-N1	8.15	1.51	1.38
84	S2	116	OMU	C2-N1	8.14	1.51	1.38
84	S2	428	OMU	C2-N1	8.11	1.51	1.38
84	S2	354	OMU	C2-N1	8.08	1.51	1.38
84	S2	1248	B8N	C4-N3	-7.97	1.26	1.40
4	L5	3925	OMU	C2-N1	7.95	1.50	1.38
4	L5	4620	OMU	C2-N1	7.87	1.50	1.38
84	S2	1248	B8N	C6-N1	7.83	1.55	1.36
4	L5	4498	OMU	C2-N1	7.79	1.50	1.38
4	L5	3818	UY1	C2-N3	7.61	1.50	1.37
84	S2	116	OMU	C2-N3	6.97	1.50	1.38
84	S2	172	OMU	C2-N3	6.95	1.50	1.38
84	S2	1288	OMU	C2-N3	6.94	1.50	1.38
84	S2	121	OMU	C2-N3	6.94	1.50	1.38
84	S2	627	OMU	C2-N3	6.92	1.50	1.38
84	S2	1442	OMU	C2-N3	6.91	1.50	1.38
84	S2	428	OMU	C2-N3	6.90	1.50	1.38
84	S2	1248	B8N	C4-C5	6.86	1.63	1.47
4	L5	4227	OMU	C2-N3	6.84	1.49	1.38
4	L5	2837	OMU	C2-N3	6.82	1.49	1.38
84	S2	799	OMU	C2-N3	6.82	1.49	1.38
84	S2	354	OMU	C2-N3	6.78	1.49	1.38
84	S2	1326	OMU	C2-N3	6.74	1.49	1.38
4	L5	4498	OMU	C2-N3	6.70	1.49	1.38
4	L5	3925	OMU	C2-N3	6.65	1.49	1.38
4	L5	4620	OMU	C2-N3	6.62	1.49	1.38
4	L5	4306	OMU	C2-N3	6.58	1.49	1.38
84	S2	1639	G7M	C4-N3	6.57	1.49	1.34
4	L5	4530	UR3	C2-N1	6.45	1.47	1.38
4	L5	4530	UR3	C6-C5	6.29	1.49	1.35
84	S2	1288	OMU	C6-C5	5.92	1.48	1.35
84	S2	121	OMU	C6-C5	5.89	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	S2	1248	B8N	C2-N1	5.88	1.56	1.39
84	S2	428	OMU	C6-C5	5.86	1.48	1.35
84	S2	172	OMU	C6-C5	5.85	1.48	1.35
84	S2	627	OMU	C6-C5	5.84	1.48	1.35
84	S2	1326	OMU	C6-C5	5.84	1.48	1.35
4	L5	2837	OMU	C6-C5	5.84	1.48	1.35
84	S2	799	OMU	C6-C5	5.83	1.48	1.35
84	S2	1442	OMU	C6-C5	5.83	1.48	1.35
84	S2	354	OMU	C6-C5	5.83	1.48	1.35
4	L5	4498	OMU	C6-C5	5.80	1.48	1.35
4	L5	4530	UR3	C2-N3	5.78	1.50	1.39
4	L5	4227	OMU	C6-C5	5.77	1.48	1.35
84	S2	116	OMU	C6-C5	5.72	1.48	1.35
4	L5	4620	OMU	C6-C5	5.70	1.48	1.35
4	L5	4306	OMU	C6-C5	5.68	1.48	1.35
4	L5	3925	OMU	C6-C5	5.66	1.48	1.35
4	L5	4620	OMU	O4-C4	-5.58	1.13	1.24
4	L5	4220	6MZ	O4'-C4'	5.56	1.57	1.45
4	L5	3925	OMU	O4-C4	-5.53	1.13	1.24
4	L5	4227	OMU	O4-C4	-5.53	1.13	1.24
4	L5	2837	OMU	O4-C4	-5.51	1.13	1.24
4	L5	4306	OMU	O4-C4	-5.50	1.13	1.24
84	S2	799	OMU	O4-C4	-5.50	1.13	1.24
84	S2	354	OMU	O4-C4	-5.49	1.13	1.24
4	L5	4498	OMU	O4-C4	-5.48	1.13	1.24
84	S2	1326	OMU	O4-C4	-5.48	1.13	1.24
84	S2	116	OMU	O4-C4	-5.47	1.13	1.24
84	S2	1442	OMU	O4-C4	-5.45	1.13	1.24
4	L5	3818	UY1	C6-N1	5.45	1.45	1.36
84	S2	428	OMU	O4-C4	-5.44	1.13	1.24
84	S2	121	OMU	O4-C4	-5.42	1.13	1.24
84	S2	627	OMU	O4-C4	-5.41	1.14	1.24
4	L5	4220	6MZ	C5'-C4'	-5.41	1.35	1.51
84	S2	172	OMU	O4-C4	-5.40	1.14	1.24
84	S2	1639	G7M	C2-N3	5.40	1.46	1.33
84	S2	1288	OMU	O4-C4	-5.37	1.14	1.24
84	S2	1248	B8N	C6-C5	5.36	1.42	1.35
84	S2	1639	G7M	C2-N2	4.91	1.45	1.34
4	L5	4220	6MZ	O4'-C1'	-4.71	1.31	1.42
84	S2	1639	G7M	C5-N7	-4.68	1.33	1.39
84	S2	627	OMU	C4-N3	4.51	1.46	1.38
84	S2	1442	OMU	C4-N3	4.44	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L5	3818	UY1	C4-N3	4.43	1.47	1.38
84	S2	428	OMU	C4-N3	4.41	1.46	1.38
84	S2	1288	OMU	C4-N3	4.36	1.46	1.38
84	S2	172	OMU	C4-N3	4.35	1.46	1.38
84	S2	116	OMU	C4-N3	4.34	1.46	1.38
84	S2	121	OMU	C4-N3	4.33	1.46	1.38
84	S2	1326	OMU	C4-N3	4.33	1.46	1.38
84	S2	354	OMU	C4-N3	4.26	1.45	1.38
4	L5	2837	OMU	C4-N3	4.25	1.45	1.38
84	S2	799	OMU	C4-N3	4.24	1.45	1.38
4	L5	4227	OMU	C4-N3	4.23	1.45	1.38
4	L5	4498	OMU	C4-N3	4.20	1.45	1.38
4	L5	4220	6MZ	C6-N1	-4.04	1.28	1.35
4	L5	4306	OMU	C4-N3	4.03	1.45	1.38
4	L5	4620	OMU	C4-N3	4.01	1.45	1.38
4	L5	3925	OMU	C4-N3	3.98	1.45	1.38
4	L5	4220	6MZ	C5-C4	-3.91	1.32	1.39
4	L5	4220	6MZ	C5-N7	-3.87	1.32	1.39
4	L5	4220	6MZ	C8-N9	-3.85	1.31	1.37
84	S2	1639	G7M	C5-C6	3.84	1.54	1.43
84	S2	1367	PSU	C6-C5	3.71	1.39	1.35
84	S2	1004	PSU	C6-C5	3.69	1.39	1.35
84	S2	863	PSU	C6-C5	3.69	1.39	1.35
84	S2	1232	PSU	C6-C5	3.68	1.39	1.35
84	S2	1244	PSU	C6-C5	3.66	1.39	1.35
4	L5	2632	PSU	C6-C5	3.66	1.39	1.35
84	S2	651	PSU	C6-C5	3.65	1.39	1.35
84	S2	1248	B8N	C1'-C5	3.64	1.58	1.50
4	L5	4532	PSU	C6-C5	3.63	1.39	1.35
4	L5	2401	A2M	O5'-C5'	-3.62	1.33	1.44
4	L5	3844	PSU	C6-C5	3.62	1.39	1.35
84	S2	1046	PSU	C6-C5	3.62	1.39	1.35
4	L5	3818	UY1	O4-C4	-3.61	1.16	1.23
84	S2	801	PSU	C6-C5	3.61	1.39	1.35
4	L5	4636	PSU	C6-C5	3.60	1.39	1.35
84	S2	814	PSU	C6-C5	3.59	1.39	1.35
4	L5	1862	PSU	C6-C5	3.57	1.39	1.35
84	S2	649	PSU	C6-C5	3.57	1.39	1.35
84	S2	109	PSU	C6-C5	3.57	1.39	1.35
4	L5	3853	PSU	C6-C5	3.56	1.39	1.35
4	L5	1860	PSU	C6-C5	3.56	1.39	1.35
84	S2	406	PSU	C6-C5	3.56	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	S2	1177	PSU	C6-C5	3.55	1.39	1.35
4	L5	3639	PSU	C6-C5	3.54	1.39	1.35
84	S2	1045	PSU	C6-C5	3.53	1.39	1.35
84	S2	1174	PSU	C6-C5	3.52	1.39	1.35
4	L5	5001	PSU	C6-C5	3.52	1.39	1.35
4	L5	5010	PSU	C6-C5	3.52	1.39	1.35
4	L5	4552	PSU	C6-C5	3.51	1.39	1.35
84	S2	105	PSU	C6-C5	3.51	1.39	1.35
4	L5	4500	PSU	C6-C5	3.50	1.39	1.35
4	L5	4296	PSU	C6-C5	3.50	1.39	1.35
4	L5	4361	PSU	C6-C5	3.49	1.39	1.35
4	L5	4493	PSU	C6-C5	3.49	1.39	1.35
4	L5	3785	A2M	O5'-C5'	-3.49	1.34	1.44
84	S2	1081	PSU	C6-C5	3.48	1.39	1.35
84	S2	966	PSU	C6-C5	3.48	1.39	1.35
4	L5	1744	PSU	C6-C5	3.48	1.39	1.35
4	L5	4312	PSU	C6-C5	3.48	1.39	1.35
84	S2	668	A2M	O5'-C5'	-3.48	1.34	1.44
4	L5	2839	PSU	C6-C5	3.47	1.39	1.35
4	L5	2787	A2M	O5'-C5'	-3.47	1.34	1.44
84	S2	1056	PSU	C6-C5	3.47	1.39	1.35
4	L5	3830	A2M	O5'-C5'	-3.46	1.34	1.44
84	S2	99	A2M	O5'-C5'	-3.46	1.34	1.44
86	CF	163	SEP	P-O1P	3.46	1.61	1.50
4	L5	1582	PSU	C6-C5	3.46	1.39	1.35
4	L5	4521	PSU	C6-C5	3.46	1.39	1.35
4	L5	3825	A2M	O5'-C5'	-3.45	1.34	1.44
84	S2	866	PSU	C6-C5	3.44	1.39	1.35
4	L5	3695	PSU	C6-C5	3.44	1.39	1.35
84	S2	686	PSU	C6-C5	3.44	1.39	1.35
4	L5	1323	A2M	O5'-C5'	-3.44	1.34	1.44
4	L5	4431	PSU	C6-C5	3.44	1.39	1.35
4	L5	400	A2M	O5'-C5'	-3.43	1.34	1.44
84	S2	1031	A2M	O5'-C5'	-3.43	1.34	1.44
4	L5	1683	PSU	C6-C5	3.43	1.39	1.35
4	L5	4293	PSU	C6-C5	3.43	1.39	1.35
84	S2	93	PSU	C6-C5	3.42	1.39	1.35
4	L5	4576	PSU	C6-C5	3.42	1.39	1.35
4	L5	4689	PSU	C6-C5	3.42	1.39	1.35
4	L5	4299	PSU	C6-C5	3.42	1.39	1.35
4	L5	3718	A2M	O5'-C5'	-3.41	1.34	1.44
4	L5	3884	PSU	C6-C5	3.41	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L5	1781	PSU	C6-C5	3.41	1.39	1.35
4	L5	1326	A2M	O5'-C5'	-3.41	1.34	1.44
4	L5	3851	PSU	C6-C5	3.41	1.39	1.35
4	L5	1792	PSU	C6-C5	3.41	1.39	1.35
4	L5	2815	A2M	O5'-C5'	-3.40	1.34	1.44
4	L5	1524	A2M	O5'-C5'	-3.40	1.34	1.44
6	L8	69	PSU	C6-C5	3.40	1.39	1.35
84	S2	27	A2M	O5'-C5'	-3.40	1.34	1.44
4	L5	3822	PSU	C6-C5	3.39	1.39	1.35
84	S2	576	A2M	O5'-C5'	-3.39	1.34	1.44
84	S2	1383	A2M	O5'-C5'	-3.39	1.34	1.44
4	L5	1782	PSU	C6-C5	3.38	1.39	1.35
6	L8	55	PSU	C6-C5	3.36	1.39	1.35
4	L5	4471	PSU	C6-C5	3.36	1.39	1.35
4	L5	4457	PSU	C6-C5	3.36	1.39	1.35
84	S2	468	A2M	O5'-C5'	-3.35	1.34	1.44
4	L5	4673	PSU	C6-C5	3.35	1.39	1.35
4	L5	3637	PSU	C6-C5	3.35	1.39	1.35
4	L5	4571	A2M	O5'-C5'	-3.34	1.34	1.44
84	S2	681	PSU	C6-C5	3.34	1.39	1.35
4	L5	4523	A2M	O5'-C5'	-3.33	1.34	1.44
4	L5	4972	PSU	C6-C5	3.32	1.39	1.35
4	L5	3867	A2M	O5'-C5'	-3.32	1.34	1.44
4	L5	4973	PSU	C6-C5	3.30	1.38	1.35
4	L5	3920	PSU	C6-C5	3.30	1.38	1.35
4	L5	4590	A2M	O5'-C5'	-3.30	1.34	1.44
4	L5	2363	A2M	O5'-C5'	-3.30	1.34	1.44
4	L5	4579	PSU	C6-C5	3.29	1.38	1.35
84	S2	166	A2M	O5'-C5'	-3.29	1.34	1.44
84	S2	484	A2M	O5'-C5'	-3.28	1.34	1.44
4	L5	3818	UY1	C1'-C5	3.28	1.57	1.50
4	L5	1871	A2M	O4'-C4'	-3.27	1.37	1.45
4	L5	4442	PSU	C6-C5	3.27	1.38	1.35
4	L5	4220	6MZ	O3'-C3'	3.26	1.51	1.43
4	L5	398	A2M	O5'-C5'	-3.23	1.34	1.44
4	L5	1536	PSU	C6-C5	3.19	1.38	1.35
4	L5	4403	PSU	C6-C5	3.18	1.38	1.35
4	L5	3818	UY1	O2-C2	-3.18	1.16	1.23
4	L5	4353	PSU	C6-C5	3.17	1.38	1.35
84	S2	1851	MA6	C6-N6	3.16	1.45	1.36
84	S2	1832	6MZ	C5-N7	-3.16	1.33	1.39
84	S2	1850	MA6	C6-N6	3.15	1.45	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L5	4628	PSU	C6-C5	3.13	1.38	1.35
84	S2	159	A2M	O5'-C5'	-3.13	1.35	1.44
4	L5	1534	A2M	O5'-C5'	-3.12	1.35	1.44
4	L5	1871	A2M	O5'-C5'	-3.04	1.35	1.44
4	L5	1677	PSU	C6-C5	3.00	1.38	1.35
84	S2	1832	6MZ	C5-C4	-2.99	1.33	1.39
84	S2	1288	OMU	C5-C4	2.88	1.50	1.43
84	S2	1326	OMU	C5-C4	2.87	1.49	1.43
84	S2	627	OMU	C5-C4	2.87	1.49	1.43
84	S2	172	OMU	C5-C4	2.87	1.49	1.43
84	S2	1832	6MZ	C8-N9	-2.86	1.32	1.37
84	S2	668	A2M	O4'-C4'	-2.86	1.38	1.45
84	S2	428	OMU	C5-C4	2.85	1.49	1.43
4	L5	4227	OMU	C5-C4	2.84	1.49	1.43
84	S2	354	OMU	C5-C4	2.83	1.49	1.43
84	S2	1442	OMU	C5-C4	2.82	1.49	1.43
84	S2	799	OMU	C5-C4	2.82	1.49	1.43
84	S2	1639	G7M	C2-N1	2.80	1.44	1.37
84	S2	121	OMU	C5-C4	2.77	1.49	1.43
4	L5	4220	6MZ	C2'-C1'	2.74	1.62	1.53
84	S2	1288	OMU	C6-N1	2.72	1.44	1.38
4	L5	3925	OMU	C5-C4	2.71	1.49	1.43
4	L5	4498	OMU	C5-C4	2.71	1.49	1.43
84	S2	799	OMU	C6-N1	2.69	1.44	1.38
84	S2	354	OMU	C6-N1	2.69	1.44	1.38
4	L5	2837	OMU	C5-C4	2.69	1.49	1.43
84	S2	627	OMU	C6-N1	2.66	1.44	1.38
84	S2	1442	OMU	C6-N1	2.66	1.44	1.38
4	L5	4306	OMU	C5-C4	2.65	1.49	1.43
4	L5	2837	OMU	C6-N1	2.64	1.44	1.38
84	S2	116	OMU	C5-C4	2.64	1.49	1.43
84	S2	121	OMU	C6-N1	2.63	1.44	1.38
84	S2	428	OMU	C6-N1	2.63	1.44	1.38
4	L5	4498	OMU	C6-N1	2.62	1.44	1.38
84	S2	1326	OMU	C6-N1	2.60	1.44	1.38
4	L5	4227	OMU	C6-N1	2.59	1.44	1.38
84	S2	172	OMU	C6-N1	2.58	1.44	1.38
4	L5	4306	OMU	C6-N1	2.58	1.44	1.38
4	L5	4530	UR3	C6-N1	2.56	1.44	1.38
4	L5	4620	OMU	C5-C4	2.56	1.49	1.43
4	L5	4620	OMU	C6-N1	2.55	1.44	1.38
84	S2	1851	MA6	C5-C4	-2.54	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L5	4530	UR3	O2-C2	-2.53	1.17	1.22
4	L5	1323	A2M	O4'-C4'	-2.52	1.39	1.45
84	S2	116	OMU	C6-N1	2.51	1.44	1.38
84	S2	1850	MA6	C5-C4	-2.51	1.34	1.39
4	L5	3925	OMU	C6-N1	2.49	1.44	1.38
4	L5	1534	A2M	O4'-C4'	-2.49	1.39	1.45
84	S2	1639	G7M	O6-C6	-2.47	1.18	1.23
4	L5	1524	A2M	O4'-C4'	-2.47	1.39	1.45
84	S2	1639	G7M	C6-N1	2.42	1.43	1.38
4	L5	4571	A2M	O4'-C4'	-2.36	1.39	1.45
4	L5	1326	A2M	O4'-C4'	-2.35	1.39	1.45
4	L5	3867	A2M	O4'-C4'	-2.33	1.39	1.45
4	L5	1871	A2M	C4-N3	2.28	1.38	1.34
4	L5	4530	UR3	C5-C4	2.26	1.49	1.43
4	L5	2363	A2M	O4'-C4'	-2.26	1.40	1.45
4	L5	3818	UY1	O4'-C1'	-2.26	1.40	1.43
84	S2	1832	6MZ	C6-N1	-2.20	1.31	1.35
4	L5	4530	UR3	C3U-N3	2.19	1.50	1.47
84	S2	1639	G7M	C4-N9	-2.13	1.32	1.38
4	L5	2815	A2M	O4'-C4'	-2.12	1.40	1.45
4	L5	3884	PSU	C4-C5	-2.08	1.38	1.44
4	L5	3818	UY1	C4-C5	2.06	1.50	1.44
4	L5	4293	PSU	C4-C5	-2.05	1.38	1.44
4	L5	4521	PSU	C4-C5	-2.03	1.38	1.44
4	L5	1677	PSU	C4-C5	-2.02	1.38	1.44

All (685) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	S2	1851	MA6	N1-C6-N6	-12.04	102.18	116.86
84	S2	1850	MA6	N1-C6-N6	-11.82	102.46	116.86
84	S2	1851	MA6	C5-C6-N6	8.02	138.02	125.33
84	S2	1850	MA6	C5-C6-N6	7.97	137.94	125.33
84	S2	1639	G7M	C1'-N9-C4	7.31	148.08	126.49
84	S2	1639	G7M	C1'-N9-C8	-7.18	102.49	126.74
4	L5	4220	6MZ	C9-N6-C6	-6.08	117.22	122.85
84	S2	1851	MA6	N1-C2-N3	-5.90	119.65	128.58
84	S2	1832	6MZ	N1-C2-N3	-5.88	119.68	128.58
4	L5	4227	OMU	C4-N3-C2	-5.88	119.32	126.61
4	L5	3925	OMU	C4-N3-C2	-5.86	119.34	126.61
84	S2	1326	OMU	C4-N3-C2	-5.78	119.43	126.61
4	L5	2837	OMU	C4-N3-C2	-5.72	119.51	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	4498	OMU	C4-N3-C2	-5.69	119.55	126.61
4	L5	4306	OMU	C4-N3-C2	-5.69	119.55	126.61
84	S2	627	OMU	C4-N3-C2	-5.67	119.57	126.61
84	S2	172	OMU	C4-N3-C2	-5.67	119.58	126.61
84	S2	1851	MA6	N9-C8-N7	-5.63	105.95	113.94
84	S2	428	OMU	C4-N3-C2	-5.62	119.64	126.61
84	S2	354	OMU	C4-N3-C2	-5.56	119.71	126.61
84	S2	799	OMU	C4-N3-C2	-5.53	119.74	126.61
4	L5	4530	UR3	C4-N3-C2	-5.51	120.14	124.58
84	S2	1850	MA6	N1-C2-N3	-5.51	120.25	128.58
84	S2	121	OMU	C4-N3-C2	-5.50	119.79	126.61
84	S2	1850	MA6	N9-C8-N7	-5.48	106.16	113.94
84	S2	1442	OMU	C4-N3-C2	-5.47	119.82	126.61
4	L5	3701	OMC	C1'-N1-C2	5.36	130.28	118.44
84	S2	1288	OMU	C4-N3-C2	-5.31	120.02	126.61
4	L5	4689	PSU	N1-C2-N3	5.29	120.75	115.17
84	S2	1248	B8N	C5-C4-N3	5.20	125.60	116.15
84	S2	116	OMU	C4-N3-C2	-5.18	120.18	126.61
4	L5	4353	PSU	N1-C2-N3	5.14	120.58	115.17
4	L5	4353	PSU	C4-N3-C2	-5.13	119.31	126.37
4	L5	4552	PSU	N1-C2-N3	5.09	120.53	115.17
4	L5	1860	PSU	N1-C2-N3	5.08	120.53	115.17
84	S2	866	PSU	N1-C2-N3	5.08	120.53	115.17
4	L5	1677	PSU	C4-N3-C2	-5.06	119.40	126.37
84	S2	1004	PSU	N1-C2-N3	5.05	120.49	115.17
4	L5	4636	PSU	N1-C2-N3	5.03	120.47	115.17
84	S2	1056	PSU	N1-C2-N3	5.02	120.47	115.17
84	S2	651	PSU	N1-C2-N3	5.01	120.45	115.17
4	L5	4403	PSU	N1-C2-N3	4.98	120.42	115.17
4	L5	3920	PSU	N1-C2-N3	4.98	120.42	115.17
4	L5	4442	PSU	C4-N3-C2	-4.97	119.52	126.37
4	L5	2632	PSU	N1-C2-N3	4.97	120.41	115.17
4	L5	4442	PSU	N1-C2-N3	4.97	120.41	115.17
4	L5	4620	OMU	C4-N3-C2	-4.97	120.45	126.61
4	L5	3637	PSU	N1-C2-N3	4.97	120.41	115.17
4	L5	4457	PSU	N1-C2-N3	4.95	120.39	115.17
4	L5	1536	PSU	N1-C2-N3	4.94	120.38	115.17
4	L5	4636	PSU	C4-N3-C2	-4.94	119.56	126.37
4	L5	4500	PSU	N1-C2-N3	4.94	120.38	115.17
4	L5	4521	PSU	C4-N3-C2	-4.94	119.57	126.37
84	S2	649	PSU	C4-N3-C2	-4.93	119.58	126.37
4	L5	3639	PSU	N1-C2-N3	4.93	120.37	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	4220	6MZ	N1-C2-N3	-4.92	121.13	128.58
4	L5	4296	PSU	C4-N3-C2	-4.92	119.59	126.37
84	S2	649	PSU	N1-C2-N3	4.91	120.35	115.17
4	L5	4521	PSU	N1-C2-N3	4.91	120.35	115.17
4	L5	4689	PSU	C4-N3-C2	-4.91	119.61	126.37
4	L5	4403	PSU	C4-N3-C2	-4.91	119.61	126.37
84	S2	1045	PSU	N1-C2-N3	4.91	120.34	115.17
84	S2	686	PSU	C4-N3-C2	-4.90	119.62	126.37
4	L5	1860	PSU	C4-N3-C2	-4.90	119.62	126.37
4	L5	1683	PSU	N1-C2-N3	4.90	120.33	115.17
84	S2	866	PSU	C4-N3-C2	-4.90	119.63	126.37
4	L5	3822	PSU	N1-C2-N3	4.90	120.33	115.17
4	L5	4552	PSU	C4-N3-C2	-4.89	119.64	126.37
4	L5	4220	6MZ	N9-C8-N7	-4.88	107.01	113.94
4	L5	4972	PSU	N1-C2-N3	4.88	120.31	115.17
4	L5	4431	PSU	N1-C2-N3	4.87	120.31	115.17
84	S2	1081	PSU	N1-C2-N3	4.87	120.30	115.17
4	L5	4973	PSU	C4-N3-C2	-4.87	119.67	126.37
4	L5	2839	PSU	N1-C2-N3	4.86	120.30	115.17
84	S2	1177	PSU	N1-C2-N3	4.86	120.29	115.17
4	L5	4293	PSU	N1-C2-N3	4.85	120.29	115.17
84	S2	1232	PSU	C4-N3-C2	-4.85	119.69	126.37
84	S2	686	PSU	N1-C2-N3	4.84	120.27	115.17
84	S2	1045	PSU	C4-N3-C2	-4.84	119.70	126.37
4	L5	4312	PSU	N1-C2-N3	4.83	120.27	115.17
84	S2	1081	PSU	C4-N3-C2	-4.83	119.72	126.37
4	L5	1862	PSU	N1-C2-N3	4.83	120.26	115.17
6	L8	55	PSU	N1-C2-N3	4.82	120.26	115.17
84	S2	1367	PSU	C4-N3-C2	-4.82	119.73	126.37
84	S2	1056	PSU	C4-N3-C2	-4.81	119.74	126.37
4	L5	3851	PSU	N1-C2-N3	4.81	120.24	115.17
84	S2	1244	PSU	N1-C2-N3	4.81	120.24	115.17
4	L5	5010	PSU	C4-N3-C2	-4.81	119.75	126.37
84	S2	1177	PSU	C4-N3-C2	-4.81	119.75	126.37
4	L5	4628	PSU	N1-C2-N3	4.80	120.23	115.17
4	L5	4431	PSU	C4-N3-C2	-4.80	119.76	126.37
84	S2	1367	PSU	N1-C2-N3	4.79	120.22	115.17
4	L5	4296	PSU	N1-C2-N3	4.79	120.22	115.17
84	S2	406	PSU	N1-C2-N3	4.79	120.22	115.17
84	S2	406	PSU	C4-N3-C2	-4.77	119.80	126.37
4	L5	5010	PSU	N1-C2-N3	4.77	120.20	115.17
4	L5	4361	PSU	N1-C2-N3	4.77	120.20	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	4299	PSU	N1-C2-N3	4.77	120.20	115.17
4	L5	4532	PSU	N1-C2-N3	4.77	120.20	115.17
6	L8	69	PSU	C4-N3-C2	-4.76	119.81	126.37
84	S2	1046	PSU	N1-C2-N3	4.76	120.19	115.17
84	S2	1232	PSU	N1-C2-N3	4.76	120.19	115.17
84	S2	1004	PSU	C4-N3-C2	-4.76	119.81	126.37
84	S2	863	PSU	N1-C2-N3	4.76	120.19	115.17
84	S2	651	PSU	C4-N3-C2	-4.76	119.81	126.37
6	L8	69	PSU	N1-C2-N3	4.76	120.19	115.17
4	L5	3920	PSU	C4-N3-C2	-4.76	119.82	126.37
84	S2	109	PSU	C4-N3-C2	-4.76	119.82	126.37
4	L5	4299	PSU	C4-N3-C2	-4.76	119.82	126.37
4	L5	4312	PSU	C4-N3-C2	-4.75	119.83	126.37
4	L5	1782	PSU	N1-C2-N3	4.75	120.17	115.17
4	L5	4579	PSU	C4-N3-C2	-4.75	119.83	126.37
84	S2	1244	PSU	C4-N3-C2	-4.74	119.83	126.37
84	S2	801	PSU	N1-C2-N3	4.74	120.17	115.17
4	L5	4576	PSU	N1-C2-N3	4.74	120.17	115.17
4	L5	4579	PSU	N1-C2-N3	4.74	120.17	115.17
4	L5	1862	PSU	C4-N3-C2	-4.74	119.84	126.37
6	L8	55	PSU	C4-N3-C2	-4.73	119.85	126.37
4	L5	4500	PSU	C4-N3-C2	-4.73	119.85	126.37
4	L5	1782	PSU	C4-N3-C2	-4.73	119.85	126.37
4	L5	1683	PSU	C4-N3-C2	-4.73	119.86	126.37
4	L5	5001	PSU	N1-C2-N3	4.73	120.16	115.17
4	L5	4972	PSU	C4-N3-C2	-4.73	119.86	126.37
4	L5	4576	PSU	C4-N3-C2	-4.72	119.86	126.37
4	L5	4457	PSU	C4-N3-C2	-4.72	119.86	126.37
4	L5	3853	PSU	N1-C2-N3	4.72	120.15	115.17
4	L5	3884	PSU	C4-N3-C2	-4.72	119.87	126.37
4	L5	4673	PSU	N1-C2-N3	4.72	120.15	115.17
4	L5	3818	UY1	C4-N3-C2	-4.72	119.88	126.37
84	S2	1832	6MZ	N9-C8-N7	-4.71	107.25	113.94
84	S2	966	PSU	N1-C2-N3	4.71	120.14	115.17
4	L5	4973	PSU	N1-C2-N3	4.71	120.14	115.17
84	S2	105	PSU	N1-C2-N3	4.71	120.13	115.17
4	L5	1792	PSU	N1-C2-N3	4.71	120.13	115.17
4	L5	4493	PSU	N1-C2-N3	4.70	120.13	115.17
84	S2	109	PSU	N1-C2-N3	4.70	120.13	115.17
4	L5	4293	PSU	C4-N3-C2	-4.70	119.90	126.37
84	S2	1174	PSU	C4-N3-C2	-4.70	119.90	126.37
4	L5	1744	PSU	C4-N3-C2	-4.69	119.91	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	4532	PSU	C4-N3-C2	-4.69	119.91	126.37
4	L5	5001	PSU	C4-N3-C2	-4.69	119.91	126.37
4	L5	1792	PSU	C4-N3-C2	-4.69	119.91	126.37
4	L5	2632	PSU	C4-N3-C2	-4.69	119.92	126.37
4	L5	2839	PSU	C4-N3-C2	-4.69	119.92	126.37
4	L5	3884	PSU	N1-C2-N3	4.68	120.11	115.17
4	L5	3695	PSU	N1-C2-N3	4.68	120.10	115.17
4	L5	1744	PSU	N1-C2-N3	4.67	120.10	115.17
4	L5	4471	PSU	N1-C2-N3	4.67	120.10	115.17
4	L5	3637	PSU	C4-N3-C2	-4.66	119.95	126.37
4	L5	4493	PSU	C4-N3-C2	-4.66	119.95	126.37
84	S2	681	PSU	C4-N3-C2	-4.66	119.95	126.37
4	L5	3639	PSU	C4-N3-C2	-4.66	119.96	126.37
4	L5	3851	PSU	C4-N3-C2	-4.65	119.97	126.37
4	L5	4361	PSU	C4-N3-C2	-4.65	119.97	126.37
4	L5	4628	PSU	C4-N3-C2	-4.64	119.97	126.37
4	L5	1536	PSU	C4-N3-C2	-4.64	119.97	126.37
84	S2	814	PSU	C4-N3-C2	-4.64	119.98	126.37
4	L5	3822	PSU	C4-N3-C2	-4.64	119.98	126.37
84	S2	863	PSU	C4-N3-C2	-4.64	119.98	126.37
4	L5	1781	PSU	N1-C2-N3	4.63	120.05	115.17
84	S2	1174	PSU	N1-C2-N3	4.63	120.05	115.17
84	S2	966	PSU	C4-N3-C2	-4.61	120.02	126.37
84	S2	93	PSU	C4-N3-C2	-4.61	120.02	126.37
84	S2	814	PSU	N1-C2-N3	4.59	120.00	115.17
84	S2	681	PSU	N1-C2-N3	4.58	120.00	115.17
84	S2	1046	PSU	C4-N3-C2	-4.58	120.06	126.37
4	L5	1582	PSU	N1-C2-N3	4.58	120.00	115.17
4	L5	3695	PSU	C4-N3-C2	-4.57	120.07	126.37
4	L5	1677	PSU	N1-C2-N3	4.56	119.98	115.17
84	S2	105	PSU	C4-N3-C2	-4.55	120.10	126.37
4	L5	3844	PSU	N1-C2-N3	4.54	119.95	115.17
84	S2	93	PSU	N1-C2-N3	4.53	119.95	115.17
84	S2	801	PSU	C4-N3-C2	-4.52	120.15	126.37
4	L5	4471	PSU	C4-N3-C2	-4.49	120.18	126.37
84	S2	1851	MA6	C4-N9-C8	4.49	110.45	105.74
4	L5	4673	PSU	C4-N3-C2	-4.49	120.19	126.37
4	L5	3853	PSU	C4-N3-C2	-4.48	120.19	126.37
84	S2	1639	G7M	C2-N3-C4	4.48	120.01	112.30
84	S2	1248	B8N	C4-N3-C2	-4.45	120.14	125.62
84	S2	1832	6MZ	C5-C4-N3	-4.44	120.60	126.72
4	L5	1781	PSU	C4-N3-C2	-4.44	120.26	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	S2	1383	A2M	C3'-C2'-C1'	-4.40	94.39	102.81
4	L5	1871	A2M	C3'-C2'-C1'	-4.38	94.41	102.81
4	L5	3844	PSU	C4-N3-C2	-4.37	120.35	126.37
84	S2	1850	MA6	C5-C4-N3	-4.37	120.70	126.72
4	L5	1582	PSU	C4-N3-C2	-4.32	120.42	126.37
84	S2	1851	MA6	C5-C4-N3	-4.30	120.79	126.72
84	S2	1850	MA6	C4-N9-C8	4.26	110.21	105.74
4	L5	3818	UY1	N1-C2-N3	4.24	119.64	115.17
4	L5	3701	OMC	C1'-N1-C6	-4.21	111.78	120.78
4	L5	4523	A2M	C3'-C2'-C1'	-4.11	94.94	102.81
4	L5	3830	A2M	C3'-C2'-C1'	-4.07	95.02	102.81
4	L5	4498	OMU	N3-C2-N1	4.05	120.17	114.89
4	L5	3925	OMU	N3-C2-N1	4.01	120.11	114.89
84	S2	354	OMU	N3-C2-N1	3.99	120.08	114.89
84	S2	121	OMU	N3-C2-N1	3.98	120.07	114.89
84	S2	1639	G7M	C5-C4-N3	-3.98	120.64	128.15
4	L5	4220	6MZ	C5-C4-N3	-3.97	121.25	126.72
84	S2	1639	G7M	C5-C6-N1	3.96	120.02	111.84
4	L5	4306	OMU	N3-C2-N1	3.94	120.02	114.89
4	L5	398	A2M	C3'-C2'-C1'	-3.92	95.31	102.81
4	L5	2837	OMU	N3-C2-N1	3.88	119.94	114.89
84	S2	1326	OMU	N3-C2-N1	3.88	119.94	114.89
4	L5	4227	OMU	N3-C2-N1	3.86	119.92	114.89
4	L5	4227	OMU	C5-C4-N3	3.86	120.21	114.80
84	S2	172	OMU	N3-C2-N1	3.84	119.89	114.89
4	L5	4220	6MZ	C5'-C4'-C3'	-3.79	101.55	115.21
84	S2	799	OMU	N3-C2-N1	3.76	119.79	114.89
4	L5	4530	UR3	C5-C4-N3	3.75	119.97	115.04
84	S2	627	OMU	C5-C4-N3	3.74	120.03	114.80
4	L5	4306	OMU	C5-C4-N3	3.73	120.03	114.80
84	S2	1288	OMU	N3-C2-N1	3.73	119.75	114.89
4	L5	3925	OMU	C5-C4-N3	3.73	120.02	114.80
84	S2	799	OMU	C5-C4-N3	3.72	120.02	114.80
84	S2	428	OMU	N3-C2-N1	3.72	119.74	114.89
4	L5	2837	OMU	C5-C4-N3	3.70	119.99	114.80
84	S2	1442	OMU	N3-C2-N1	3.69	119.70	114.89
4	L5	2401	A2M	O3'-C3'-C2'	3.69	121.51	111.19
84	S2	1326	OMU	C5-C4-N3	3.68	119.95	114.80
4	L5	4620	OMU	N3-C2-N1	3.67	119.67	114.89
4	L5	398	A2M	O3'-C3'-C2'	3.67	121.45	111.19
4	L5	4220	6MZ	C4-N9-C8	3.66	109.58	105.74
84	S2	627	OMU	N3-C2-N1	3.65	119.65	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	S2	1851	MA6	C2-N1-C6	3.65	120.74	111.83
4	L5	4590	A2M	C3'-C2'-C1'	-3.64	95.83	102.81
84	S2	116	OMU	N3-C2-N1	3.63	119.62	114.89
84	S2	1248	B8N	C1'-C5-C4	3.63	123.12	117.61
84	S2	428	OMU	C5-C4-N3	3.61	119.86	114.80
84	S2	1031	A2M	C3'-C2'-C1'	-3.60	95.92	102.81
84	S2	1850	MA6	C4-C5-C6	3.60	119.63	115.91
4	L5	4498	OMU	C5-C4-N3	3.60	119.84	114.80
84	S2	99	A2M	C3'-C2'-C1'	-3.57	95.97	102.81
84	S2	1442	OMU	C5-C4-N3	3.57	119.80	114.80
84	S2	172	OMU	C5-C4-N3	3.56	119.78	114.80
84	S2	27	A2M	C3'-C2'-C1'	-3.54	96.03	102.81
84	S2	354	OMU	C5-C4-N3	3.53	119.74	114.80
84	S2	1850	MA6	C2-N1-C6	3.52	120.43	111.83
4	L5	2787	A2M	O3'-C3'-C2'	3.49	120.95	111.19
84	S2	121	OMU	C5-C4-N3	3.48	119.67	114.80
84	S2	1288	OMU	C5-C4-N3	3.47	119.66	114.80
84	S2	468	A2M	C3'-C2'-C1'	-3.45	96.20	102.81
4	L5	3718	A2M	C3'-C2'-C1'	-3.45	96.21	102.81
84	S2	576	A2M	O3'-C3'-C2'	3.41	120.72	111.19
4	L5	4220	6MZ	C4-C5-C6	3.40	119.61	116.78
4	L5	1323	A2M	C2'-C1'-N9	3.39	119.33	113.75
84	S2	1248	B8N	N3-C2-N1	3.38	120.84	116.72
84	S2	116	OMU	C5-C4-N3	3.37	119.52	114.80
4	L5	3825	A2M	C3'-C2'-C1'	-3.37	96.35	102.81
84	S2	1832	6MZ	C2-N3-C4	3.36	120.05	111.83
84	S2	1383	A2M	O3'-C3'-C2'	3.36	120.59	111.19
4	L5	2401	A2M	C3'-C2'-C1'	-3.35	96.38	102.81
84	S2	166	A2M	C3'-C2'-C1'	-3.34	96.41	102.81
4	L5	4620	OMU	C5-C4-N3	3.33	119.46	114.80
4	L5	1871	A2M	C4-C5-N7	3.30	114.36	110.58
4	L5	1871	A2M	C1'-N9-C8	3.29	134.39	127.09
84	S2	1639	G7M	O6-C6-C5	-3.28	120.68	128.01
84	S2	166	A2M	O3'-C3'-C2'	3.28	120.37	111.19
84	S2	1851	MA6	C2-N3-C4	3.28	119.83	111.83
4	L5	3818	UY1	C6-C5-C4	3.26	120.37	118.17
4	L5	1534	A2M	C3'-C2'-C1'	-3.26	96.57	102.81
84	S2	1850	MA6	C5-N7-C8	3.26	108.57	103.45
84	S2	1851	MA6	C5-N7-C8	3.25	108.56	103.45
84	S2	576	A2M	C3'-C2'-C1'	-3.24	96.60	102.81
84	S2	1832	6MZ	C5-N7-C8	3.24	108.53	103.45
84	S2	668	A2M	C4-N9-C1'	-3.23	119.07	126.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	1536	PSU	O2-C2-N1	-3.22	119.47	122.79
4	L5	2401	A2M	C4-N9-C1'	-3.22	119.10	126.63
4	L5	1871	A2M	CM'-O2'-C2'	-3.21	106.23	114.47
4	L5	4220	6MZ	N3-C4-N9	3.20	132.62	127.17
4	L5	1524	A2M	O3'-C3'-C2'	3.19	120.12	111.19
4	L5	3718	A2M	O3'-C3'-C2'	3.19	120.12	111.19
84	S2	99	A2M	O3'-C3'-C2'	3.18	120.09	111.19
84	S2	1851	MA6	C4-C5-C6	3.18	119.19	115.91
84	S2	159	A2M	O3'-C3'-C2'	3.18	120.08	111.19
84	S2	1850	MA6	N3-C4-N9	3.18	132.57	127.17
84	S2	1851	MA6	N3-C4-N9	3.16	132.54	127.17
4	L5	400	A2M	O3'-C3'-C2'	3.16	120.02	111.19
4	L5	3825	A2M	O3'-C3'-C2'	3.15	119.99	111.19
4	L5	3830	A2M	O3'-C3'-C2'	3.15	119.99	111.19
4	L5	1323	A2M	O3'-C3'-C2'	3.14	119.98	111.19
4	L5	400	A2M	C3'-C2'-C1'	-3.14	96.80	102.81
84	S2	866	PSU	C6-C5-C4	3.14	120.29	118.17
4	L5	3785	A2M	C4'-O4'-C1'	-3.13	102.56	109.47
84	S2	468	A2M	O3'-C3'-C2'	3.12	119.92	111.19
84	S2	1031	A2M	O3'-C3'-C2'	3.12	119.92	111.19
4	L5	2815	A2M	C2'-C1'-N9	3.12	118.88	113.75
4	L5	1683	PSU	O2-C2-N1	-3.10	119.59	122.79
4	L5	2837	OMU	O4-C4-C5	-3.10	119.82	125.16
84	S2	1850	MA6	C2-N3-C4	3.10	119.39	111.83
84	S2	1442	OMU	O4-C4-C5	-3.10	119.82	125.16
6	L8	55	PSU	O2-C2-N1	-3.09	119.60	122.79
4	L5	4689	PSU	C6-N1-C2	-3.09	119.83	122.69
84	S2	1639	G7M	CN7-N7-C5	3.09	130.65	126.80
84	S2	1639	G7M	N9-C4-N3	3.06	132.07	125.95
4	L5	4571	A2M	O3'-C3'-C2'	3.05	119.73	111.19
84	S2	116	OMU	O4-C4-C5	-3.04	119.92	125.16
4	L5	4220	6MZ	C4'-O4'-C1'	-3.03	102.77	109.47
84	S2	1004	PSU	O2-C2-N1	-3.03	119.67	122.79
84	S2	627	OMU	O4-C4-C5	-3.03	119.94	125.16
4	L5	4227	OMU	O4-C4-C5	-3.02	119.95	125.16
4	L5	1860	PSU	O2-C2-N1	-3.02	119.67	122.79
84	S2	668	A2M	O3'-C3'-C2'	3.01	119.61	111.19
4	L5	2363	A2M	C3'-C2'-C1'	-3.00	97.06	102.81
4	L5	3825	A2M	C4-N9-C1'	-3.00	119.62	126.63
4	L5	4306	OMU	O4-C4-C5	-3.00	119.99	125.16
84	S2	1056	PSU	O2-C2-N1	-3.00	119.70	122.79
84	S2	1832	6MZ	C4-N9-C8	2.99	108.88	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	S2	1031	A2M	C4-N9-C1'	-2.98	119.65	126.63
84	S2	468	A2M	C4-N9-C1'	-2.98	119.66	126.63
84	S2	166	A2M	C4-N9-C1'	-2.98	119.66	126.63
4	L5	3867	A2M	C2'-C1'-N9	2.97	118.64	113.75
4	L5	1871	A2M	O3'-C3'-C2'	2.96	119.46	111.19
4	L5	4628	PSU	O2-C2-N1	-2.96	119.74	122.79
4	L5	2401	A2M	C1'-N9-C8	2.96	133.65	127.09
84	S2	27	A2M	C4-N9-C1'	-2.95	119.73	126.63
4	L5	3818	UY1	C6-N1-C2	-2.95	119.95	122.69
84	S2	1639	G7M	C2-N1-C6	-2.95	119.77	125.11
84	S2	668	A2M	C1'-N9-C8	2.94	133.62	127.09
4	L5	3822	PSU	O2-C2-N1	-2.94	119.75	122.79
4	L5	4673	PSU	O2-C2-N1	-2.94	119.76	122.79
4	L5	4403	PSU	O2-C2-N1	-2.94	119.76	122.79
4	L5	4571	A2M	C3'-C2'-C1'	-2.93	97.19	102.81
84	S2	686	PSU	O2-C2-N1	-2.92	119.77	122.79
84	S2	1326	OMU	O4-C4-C5	-2.92	120.12	125.16
84	S2	99	A2M	C4-N9-C1'	-2.92	119.80	126.63
84	S2	1337	4AC	N4-C4-N3	2.92	118.60	113.87
4	L5	2839	PSU	O2-C2-N1	-2.92	119.78	122.79
86	CF	163	SEP	OG-CB-CA	2.92	110.98	108.14
84	S2	801	PSU	O2-C2-N1	-2.92	119.78	122.79
4	L5	4636	PSU	O2-C2-N1	-2.91	119.78	122.79
4	L5	398	A2M	C4-N9-C1'	-2.91	119.83	126.63
4	L5	3925	OMU	O4-C4-C5	-2.91	120.15	125.16
84	S2	172	OMU	O4-C4-C5	-2.91	120.15	125.16
4	L5	4523	A2M	O3'-C3'-C2'	2.91	119.33	111.19
4	L5	4500	PSU	O2-C2-N1	-2.91	119.79	122.79
4	L5	4590	A2M	C4-N9-C1'	-2.90	119.84	126.63
4	L5	4689	PSU	O2-C2-N1	-2.90	119.80	122.79
4	L5	3639	PSU	O2-C2-N1	-2.89	119.81	122.79
4	L5	3785	A2M	O3'-C3'-C2'	2.89	119.28	111.19
4	L5	2363	A2M	O3'-C3'-C2'	2.89	119.28	111.19
4	L5	4293	PSU	C6-N1-C2	-2.89	120.01	122.69
4	L5	4431	PSU	O2-C2-N1	-2.89	119.81	122.79
4	L5	4523	A2M	C4-N9-C1'	-2.89	119.88	126.63
84	S2	799	OMU	O4-C4-C5	-2.88	120.19	125.16
4	L5	4552	PSU	O2-C2-N1	-2.88	119.82	122.79
4	L5	1326	A2M	O3'-C3'-C2'	2.87	119.23	111.19
84	S2	27	A2M	O3'-C3'-C2'	2.87	119.23	111.19
4	L5	4576	PSU	O2-C2-N1	-2.87	119.83	122.79
84	S2	428	OMU	O4-C4-C5	-2.87	120.21	125.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	4498	OMU	O4-C4-C5	-2.87	120.21	125.16
84	S2	1244	PSU	O2-C2-N1	-2.87	119.83	122.79
4	L5	2632	PSU	O2-C2-N1	-2.86	119.83	122.79
84	S2	1383	A2M	C4-N9-C1'	-2.86	119.95	126.63
84	S2	866	PSU	O2-C2-N1	-2.85	119.84	122.79
84	S2	1232	PSU	O2-C2-N1	-2.85	119.85	122.79
4	L5	4353	PSU	O2-C2-N1	-2.85	119.85	122.79
84	S2	121	OMU	O4-C4-C5	-2.85	120.25	125.16
84	S2	484	A2M	O3'-C3'-C2'	2.84	119.14	111.19
4	L5	4500	PSU	C6-N1-C2	-2.84	120.06	122.69
6	L8	69	PSU	O2-C2-N1	-2.83	119.86	122.79
84	S2	814	PSU	O2-C2-N1	-2.83	119.87	122.79
4	L5	4442	PSU	O2-C2-N1	-2.83	119.87	122.79
84	S2	1004	PSU	C6-N1-C2	-2.82	120.07	122.69
84	S2	668	A2M	O4'-C1'-C2'	2.82	111.45	106.59
84	S2	1832	6MZ	N3-C4-N9	2.82	131.97	127.17
84	S2	1045	PSU	O2-C2-N1	-2.82	119.88	122.79
4	L5	3851	PSU	O2-C2-N1	-2.81	119.89	122.79
4	L5	4571	A2M	C4-N9-C1'	-2.81	120.06	126.63
84	S2	354	OMU	O4-C4-C5	-2.81	120.31	125.16
4	L5	2839	PSU	C6-N1-C2	-2.81	120.08	122.69
84	S2	159	A2M	C4-N9-C1'	-2.81	120.07	126.63
84	S2	484	A2M	C4-N9-C1'	-2.81	120.07	126.63
4	L5	1744	PSU	O2-C2-N1	-2.80	119.90	122.79
4	L5	3639	PSU	C6-N1-C2	-2.80	120.09	122.69
84	S2	109	PSU	O2-C2-N1	-2.80	119.90	122.79
4	L5	2787	A2M	O4'-C1'-C2'	2.80	111.41	106.59
84	S2	1177	PSU	O2-C2-N1	-2.80	119.90	122.79
4	L5	3844	PSU	O2-C2-N1	-2.80	119.91	122.79
84	S2	1288	OMU	O4-C4-C5	-2.79	120.36	125.16
84	S2	1832	6MZ	C4-C5-C6	2.78	119.09	116.78
4	L5	1536	PSU	C6-N1-C2	-2.78	120.11	122.69
4	L5	2363	A2M	C2'-C1'-N9	2.77	118.31	113.75
4	L5	4457	PSU	C6-N1-C2	-2.77	120.12	122.69
84	S2	649	PSU	O2-C2-N1	-2.77	119.94	122.79
4	L5	4521	PSU	O2-C2-N1	-2.76	119.94	122.79
4	L5	3830	A2M	C4-N9-C1'	-2.76	120.17	126.63
4	L5	3822	PSU	C6-N1-C2	-2.76	120.13	122.69
4	L5	4590	A2M	O3'-C3'-C2'	2.76	118.92	111.19
4	L5	4972	PSU	O2-C2-N1	-2.76	119.94	122.79
4	L5	4620	OMU	O4-C4-C5	-2.76	120.41	125.16
4	L5	4673	PSU	C6-N1-C2	-2.76	120.13	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	1323	A2M	C3'-C2'-C1'	-2.76	97.53	102.81
4	L5	1524	A2M	C4'-O4'-C1'	-2.75	103.39	109.47
84	S2	651	PSU	O2-C2-N1	-2.75	119.95	122.79
4	L5	3867	A2M	C4-N9-C1'	-2.75	120.21	126.63
84	S2	159	A2M	C1'-N9-C8	2.74	133.18	127.09
4	L5	3920	PSU	O2-C2-N1	-2.74	119.96	122.79
4	L5	4579	PSU	O2-C2-N1	-2.73	119.97	122.79
4	L5	1871	A2M	C4'-O4'-C1'	-2.73	103.43	109.47
4	L5	4521	PSU	C6-C5-C4	2.73	120.02	118.17
84	S2	93	PSU	O2-C2-N1	-2.73	119.97	122.79
4	L5	4220	6MZ	C5-N7-C8	2.73	107.74	103.45
4	L5	1862	PSU	O2-C2-N1	-2.73	119.98	122.79
4	L5	5010	PSU	O2-C2-N1	-2.72	119.98	122.79
84	S2	1367	PSU	O2-C2-N1	-2.72	119.98	122.79
4	L5	1326	A2M	C4-N9-C1'	-2.72	120.28	126.63
4	L5	3853	PSU	C6-N1-C2	-2.72	120.17	122.69
84	S2	1031	A2M	C1'-N9-C8	2.71	133.12	127.09
4	L5	1323	A2M	O4'-C1'-C2'	2.71	111.26	106.59
4	L5	2632	PSU	C6-N1-C2	-2.71	120.17	122.69
4	L5	3825	A2M	C1'-N9-C8	2.71	133.11	127.09
4	L5	4299	PSU	O2-C2-N1	-2.71	120.00	122.79
84	S2	1248	B8N	O4-C4-N3	-2.71	115.60	119.99
84	S2	99	A2M	C1'-N9-C8	2.71	133.10	127.09
84	S2	166	A2M	C1'-N9-C8	2.70	133.10	127.09
84	S2	801	PSU	C6-N1-C2	-2.70	120.18	122.69
84	S2	576	A2M	C4-N9-C1'	-2.70	120.31	126.63
4	L5	3884	PSU	O2-C2-N1	-2.70	120.00	122.79
4	L5	2815	A2M	O3'-C3'-C2'	2.70	118.74	111.19
4	L5	4296	PSU	O2-C2-N1	-2.70	120.00	122.79
4	L5	2351	OMC	C1'-N1-C2	2.70	124.40	118.44
4	L5	1326	A2M	C3'-C2'-C1'	-2.70	97.64	102.81
4	L5	1683	PSU	C6-N1-C2	-2.69	120.19	122.69
84	S2	406	PSU	O2-C2-N1	-2.69	120.01	122.79
4	L5	4293	PSU	O2-C2-N1	-2.69	120.02	122.79
4	L5	3853	PSU	O2-C2-N1	-2.69	120.02	122.79
4	L5	3844	PSU	C6-N1-C2	-2.69	120.20	122.69
84	S2	1056	PSU	C6-N1-C2	-2.69	120.20	122.69
4	L5	398	A2M	C1'-N9-C8	2.68	133.05	127.09
84	S2	651	PSU	C6-N1-C2	-2.68	120.20	122.69
4	L5	3701	OMC	O2-C2-N1	2.68	124.15	118.90
4	L5	3785	A2M	C3'-C2'-C1'	-2.68	97.68	102.81
84	S2	468	A2M	C1'-N9-C8	2.67	133.03	127.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	1860	PSU	C6-N1-C2	-2.67	120.21	122.69
84	S2	27	A2M	C1'-N9-C8	2.67	133.03	127.09
84	S2	1174	PSU	O2-C2-N1	-2.67	120.03	122.79
4	L5	1782	PSU	O2-C2-N1	-2.67	120.04	122.79
84	S2	1081	PSU	O2-C2-N1	-2.67	120.04	122.79
4	L5	4590	A2M	C1'-N9-C8	2.66	133.00	127.09
4	L5	3695	PSU	C6-N1-C2	-2.66	120.22	122.69
4	L5	3785	A2M	C4-N9-C1'	-2.66	120.42	126.63
4	L5	4312	PSU	O2-C2-N1	-2.66	120.05	122.79
4	L5	3701	OMC	O2-C2-N3	-2.65	118.15	122.33
4	L5	1781	PSU	C6-N1-C2	-2.65	120.23	122.69
4	L5	2363	A2M	C4-N9-C1'	-2.65	120.43	126.63
4	L5	4552	PSU	C6-N1-C2	-2.65	120.23	122.69
84	S2	1046	PSU	C6-N1-C2	-2.65	120.23	122.69
4	L5	4493	PSU	O2-C2-N1	-2.65	120.06	122.79
4	L5	4457	PSU	O2-C2-N1	-2.65	120.06	122.79
4	L5	1792	PSU	O2-C2-N1	-2.64	120.06	122.79
4	L5	1781	PSU	O2-C2-N1	-2.64	120.06	122.79
84	S2	484	A2M	C1'-N9-C8	2.64	132.96	127.09
4	L5	3920	PSU	C6-N1-C2	-2.64	120.24	122.69
4	L5	4636	PSU	C6-N1-C2	-2.63	120.25	122.69
4	L5	3718	A2M	C1'-N9-C8	2.63	132.93	127.09
4	L5	5001	PSU	O2-C2-N1	-2.63	120.08	122.79
4	L5	4312	PSU	C6-N1-C2	-2.63	120.25	122.69
4	L5	1582	PSU	C6-N1-C2	-2.62	120.26	122.69
84	S2	863	PSU	C6-N1-C2	-2.62	120.26	122.69
4	L5	4471	PSU	O2-C2-N1	-2.62	120.09	122.79
4	L5	4471	PSU	C6-N1-C2	-2.62	120.26	122.69
4	L5	3718	A2M	C4-N9-C1'	-2.61	120.53	126.63
4	L5	2815	A2M	C3'-C2'-C1'	-2.61	97.81	102.81
84	S2	681	PSU	O2-C2-N1	-2.60	120.10	122.79
4	L5	4500	PSU	C6-C5-C4	2.60	119.93	118.17
84	S2	966	PSU	O2-C2-N1	-2.60	120.11	122.79
84	S2	159	A2M	C3'-C2'-C1'	-2.59	97.84	102.81
84	S2	1046	PSU	O2-C2-N1	-2.59	120.12	122.79
4	L5	3867	A2M	C1'-N9-C8	2.59	132.84	127.09
4	L5	1582	PSU	O2-C2-N1	-2.59	120.12	122.79
4	L5	400	A2M	C4-N9-C1'	-2.58	120.59	126.63
4	L5	3637	PSU	C6-N1-C2	-2.58	120.30	122.69
4	L5	3830	A2M	C1'-N9-C8	2.58	132.81	127.09
84	S2	105	PSU	C6-N1-C2	-2.58	120.30	122.69
84	S2	1383	A2M	C1'-N9-C8	2.57	132.80	127.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	1871	A2M	O4'-C1'-C2'	2.57	111.02	106.59
4	L5	3695	PSU	O2-C2-N1	-2.57	120.14	122.79
4	L5	4523	A2M	C1'-N9-C8	2.56	132.78	127.09
4	L5	4973	PSU	O2-C2-N1	-2.56	120.15	122.79
4	L5	1871	A2M	C4-N9-C1'	-2.56	120.64	126.63
4	L5	4628	PSU	C6-N1-C2	-2.56	120.32	122.69
4	L5	2787	A2M	C4-N9-C1'	-2.56	120.65	126.63
84	S2	863	PSU	O2-C2-N1	-2.56	120.15	122.79
4	L5	1524	A2M	O4'-C1'-C2'	2.56	110.99	106.59
4	L5	4361	PSU	C6-N1-C2	-2.52	120.35	122.69
6	L8	69	PSU	C6-N1-C2	-2.52	120.35	122.69
4	L5	4576	PSU	C6-N1-C2	-2.52	120.35	122.69
84	S2	1177	PSU	C6-N1-C2	-2.52	120.35	122.69
4	L5	2815	A2M	C4-N9-C1'	-2.51	120.75	126.63
4	L5	4579	PSU	C6-N1-C2	-2.51	120.36	122.69
4	L5	1862	PSU	C6-N1-C2	-2.51	120.36	122.69
4	L5	4571	A2M	C1'-N9-C8	2.51	132.66	127.09
4	L5	3884	PSU	C6-N1-C2	-2.51	120.36	122.69
4	L5	4532	PSU	O2-C2-N1	-2.50	120.21	122.79
4	L5	4403	PSU	C6-N1-C2	-2.50	120.37	122.69
4	L5	4972	PSU	C6-N1-C2	-2.50	120.37	122.69
84	S2	866	PSU	C6-N1-C2	-2.50	120.37	122.69
4	L5	1326	A2M	C1'-N9-C8	2.50	132.65	127.09
4	L5	4353	PSU	C6-C5-C4	2.50	119.86	118.17
6	L8	55	PSU	C6-N1-C2	-2.50	120.37	122.69
84	S2	681	PSU	C6-N1-C2	-2.50	120.37	122.69
84	S2	576	A2M	C1'-N9-C8	2.49	132.63	127.09
4	L5	2632	PSU	C6-C5-C4	2.49	119.85	118.17
84	S2	1639	G7M	CN7-N7-C8	-2.49	121.02	124.79
4	L5	1744	PSU	C6-N1-C2	-2.48	120.39	122.69
4	L5	400	A2M	C2'-C1'-N9	2.48	117.83	113.75
4	L5	2363	A2M	O4'-C1'-C2'	2.48	110.85	106.59
4	L5	2363	A2M	C1'-N9-C8	2.48	132.59	127.09
4	L5	5001	PSU	C6-N1-C2	-2.47	120.39	122.69
84	S2	966	PSU	C6-N1-C2	-2.47	120.40	122.69
84	S2	668	A2M	C2'-C1'-N9	2.47	117.81	113.75
4	L5	4431	PSU	C6-N1-C2	-2.46	120.41	122.69
4	L5	5010	PSU	C6-N1-C2	-2.46	120.41	122.69
84	S2	649	PSU	C6-N1-C2	-2.46	120.41	122.69
4	L5	400	A2M	C1'-N9-C8	2.45	132.53	127.09
4	L5	1524	A2M	C4-N9-C1'	-2.44	120.92	126.63
84	S2	109	PSU	C6-N1-C2	-2.44	120.43	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	4532	PSU	C6-N1-C2	-2.44	120.43	122.69
4	L5	3851	PSU	C6-N1-C2	-2.43	120.43	122.69
84	S2	484	A2M	O4'-C1'-C2'	2.43	110.77	106.59
4	L5	4498	OMU	O2-C2-N1	-2.43	119.64	122.80
4	L5	1782	PSU	C6-N1-C2	-2.42	120.45	122.69
4	L5	3818	UY1	O2-C2-N1	-2.42	120.30	122.79
4	L5	4442	PSU	C6-C5-C4	2.41	119.80	118.17
4	L5	4353	PSU	C6-N1-C2	-2.41	120.46	122.69
84	S2	1244	PSU	C6-N1-C2	-2.41	120.46	122.69
4	L5	1534	A2M	O3'-C3'-C4'	-2.40	104.18	111.08
84	S2	1367	PSU	C6-N1-C2	-2.40	120.46	122.69
4	L5	1323	A2M	C4-N9-C1'	-2.40	121.02	126.63
84	S2	814	PSU	C6-N1-C2	-2.40	120.46	122.69
4	L5	4493	PSU	C6-N1-C2	-2.39	120.47	122.69
84	S2	406	PSU	C6-N1-C2	-2.39	120.48	122.69
84	S2	1174	PSU	C6-N1-C2	-2.39	120.48	122.69
84	S2	1045	PSU	C6-N1-C2	-2.38	120.48	122.69
4	L5	4299	PSU	C6-N1-C2	-2.38	120.48	122.69
84	S2	1232	PSU	C6-N1-C2	-2.37	120.49	122.69
84	S2	166	A2M	O4'-C1'-C2'	2.37	110.66	106.59
4	L5	4220	6MZ	C2-N3-C4	2.36	117.60	111.83
84	S2	105	PSU	O2-C2-N1	-2.36	120.36	122.79
4	L5	2861	OMC	C1'-N1-C2	2.36	123.65	118.44
4	L5	3785	A2M	C1'-N9-C8	2.36	132.32	127.09
4	L5	1677	PSU	O2-C2-N1	-2.35	120.37	122.79
84	S2	1248	B8N	O4'-C1'-C2'	2.35	108.40	105.15
84	S2	93	PSU	C6-N1-C2	-2.35	120.51	122.69
4	L5	2815	A2M	C1'-N9-C8	2.34	132.29	127.09
4	L5	3822	PSU	O4'-C1'-C2'	2.34	108.39	105.15
4	L5	2787	A2M	C1'-N9-C8	2.34	132.29	127.09
84	S2	1832	6MZ	C4-C5-N7	-2.34	107.91	110.58
4	L5	2815	A2M	O4'-C1'-C2'	2.34	110.61	106.59
84	S2	1081	PSU	C6-N1-C2	-2.33	120.53	122.69
4	L5	1792	PSU	C6-N1-C2	-2.33	120.53	122.69
84	S2	1272	OMC	C1'-N1-C2	2.33	123.58	118.44
4	L5	4521	PSU	C6-N1-C2	-2.32	120.53	122.69
4	L5	3785	A2M	C2-N1-C6	-2.32	114.92	118.73
4	L5	2401	A2M	C6-C5-C4	-2.32	114.01	117.18
4	L5	2839	PSU	C6-C5-C4	2.32	119.74	118.17
4	L5	1326	A2M	O4'-C1'-C2'	2.31	110.57	106.59
4	L5	4442	PSU	C6-N1-C2	-2.31	120.55	122.69
4	L5	1322	1MA	N1-C6-N6	2.30	125.50	119.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L5	4571	A2M	O4'-C1'-C2'	2.30	110.54	106.59
84	S2	406	PSU	C6-C5-C4	2.30	119.72	118.17
4	L5	1524	A2M	C1'-N9-C8	2.29	132.18	127.09
84	S2	686	PSU	C6-N1-C2	-2.29	120.56	122.69
4	L5	4973	PSU	C6-N1-C2	-2.29	120.57	122.69
4	L5	3867	A2M	O3'-C3'-C2'	2.28	117.57	111.19
4	L5	4590	A2M	C6-C5-C4	-2.28	114.07	117.18
4	L5	4361	PSU	O2-C2-N1	-2.27	120.44	122.79
84	S2	27	A2M	C6-C5-C4	-2.27	114.07	117.18
84	S2	166	A2M	C6-C5-C4	-2.27	114.08	117.18
84	S2	109	PSU	C6-C5-C4	2.26	119.70	118.17
4	L5	1534	A2M	C4-N9-C1'	-2.26	121.34	126.63
4	L5	3925	OMU	O2-C2-N1	-2.26	119.86	122.80
6	L8	69	PSU	O4'-C1'-C2'	2.26	108.27	105.15
4	L5	3920	PSU	C6-C5-C4	2.26	119.70	118.17
4	L5	4571	A2M	C2'-C1'-N9	2.25	117.46	113.75
84	S2	1288	OMU	C1'-N1-C2	2.25	121.64	117.59
4	L5	4403	PSU	C6-C5-C4	2.25	119.69	118.17
84	S2	1639	G7M	N9-C8-N7	-2.25	107.02	112.48
4	L5	1534	A2M	O4'-C1'-C2'	2.25	110.45	106.59
4	L5	3808	OMC	C1'-N1-C2	2.24	123.40	118.44
4	L5	1326	A2M	C2'-C1'-N9	2.24	117.44	113.75
84	S2	1056	PSU	C6-C5-C4	2.24	119.69	118.17
84	S2	354	OMU	O2-C2-N1	-2.24	119.88	122.80
84	S2	1383	A2M	C4'-O4'-C1'	-2.24	104.52	109.47
84	S2	1850	MA6	C1'-N9-C8	-2.24	122.13	127.09
84	S2	484	A2M	O4'-C4'-C3'	2.24	109.59	105.15
84	S2	1337	4AC	C5-C4-N4	-2.23	119.18	122.94
84	S2	27	A2M	O4'-C1'-C2'	2.23	110.43	106.59
4	L5	4523	A2M	C4'-O4'-C1'	-2.23	104.55	109.47
4	L5	3639	PSU	C6-C5-C4	2.23	119.68	118.17
84	S2	1851	MA6	C1'-N9-C8	-2.22	122.17	127.09
4	L5	1323	A2M	C1'-N9-C8	2.22	132.01	127.09
4	L5	3867	A2M	C3'-C2'-C1'	-2.21	98.58	102.81
4	L5	3867	A2M	O4'-C1'-C2'	2.21	110.39	106.59
4	L5	4442	PSU	O4'-C1'-C2'	2.20	108.20	105.15
84	S2	668	A2M	C6-C5-C4	-2.20	114.17	117.18
84	S2	172	OMU	O2-C2-N1	-2.20	119.93	122.80
84	S2	428	OMU	O2-C2-N1	-2.20	119.94	122.80
4	L5	3825	A2M	C6-C5-C4	-2.20	114.18	117.18
4	L5	4552	PSU	C6-C5-C4	2.19	119.66	118.17
84	S2	686	PSU	C6-C5-C4	2.19	119.66	118.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	S2	468	A2M	C6-C5-C4	-2.19	114.19	117.18
4	L5	4403	PSU	O4'-C1'-C2'	2.19	108.18	105.15
4	L5	1871	A2M	C5-C6-N1	2.19	123.06	117.51
4	L5	3867	A2M	C6-C5-C4	-2.19	114.19	117.18
84	S2	1248	B8N	O4-C4-C5	-2.18	118.80	122.58
4	L5	4296	PSU	C6-N1-C2	-2.18	120.67	122.69
4	L5	3785	A2M	C5-C6-N1	2.18	123.04	117.51
4	L5	4636	PSU	O4'-C1'-C2'	2.18	108.16	105.15
4	L5	1860	PSU	C6-C5-C4	2.18	119.64	118.17
84	S2	1031	A2M	C6-C5-C4	-2.18	114.21	117.18
4	L5	398	A2M	C6-C5-C4	-2.17	114.22	117.18
4	L5	4972	PSU	C6-C5-C4	2.17	119.64	118.17
4	L5	400	A2M	O4'-C1'-C2'	2.17	110.32	106.59
84	S2	576	A2M	C6-C5-C4	-2.16	114.23	117.18
4	L5	4220	6MZ	C3'-C2'-C1'	2.16	105.55	101.46
84	S2	484	A2M	C6-C5-C4	-2.15	114.24	117.18
84	S2	1081	PSU	O4'-C1'-C2'	2.15	108.13	105.15
84	S2	1383	A2M	C6-C5-C4	-2.15	114.25	117.18
6	L8	69	PSU	C6-C5-C4	2.14	119.62	118.17
4	L5	4523	A2M	C6-C5-C4	-2.14	114.25	117.18
84	S2	99	A2M	C6-C5-C4	-2.14	114.25	117.18
84	S2	1004	PSU	C6-C5-C4	2.13	119.61	118.17
84	S2	468	A2M	O4'-C1'-C2'	2.13	110.26	106.59
4	L5	1534	A2M	C1'-N9-C8	2.13	131.82	127.09
4	L5	4571	A2M	C6-C5-C4	-2.13	114.27	117.18
4	L5	2837	OMU	O2-C2-N1	-2.13	120.03	122.80
84	S2	159	A2M	C6-C5-C4	-2.12	114.28	117.18
84	S2	799	OMU	C1'-N1-C2	2.12	121.41	117.59
4	L5	2787	A2M	O4'-C4'-C3'	2.12	109.36	105.15
84	S2	651	PSU	C6-C5-C4	2.12	119.61	118.17
4	L5	3785	A2M	O4'-C1'-N9	2.12	112.16	108.09
4	L5	3830	A2M	C6-C5-C4	-2.12	114.29	117.18
4	L5	4220	6MZ	C5-C6-N1	2.12	120.42	118.15
4	L5	3822	PSU	C6-C5-C4	2.11	119.60	118.17
4	L5	1326	A2M	C6-C5-C4	-2.11	114.29	117.18
4	L5	4571	A2M	O3'-C3'-C4'	-2.11	105.03	111.08
4	L5	400	A2M	C6-C5-C4	-2.10	114.31	117.18
4	L5	3785	A2M	O4'-C4'-C3'	2.10	109.32	105.15
4	L5	4636	PSU	C6-C5-C4	2.10	119.59	118.17
4	L5	3867	A2M	C2-N1-C6	-2.09	115.29	118.73
84	S2	159	A2M	O4'-C1'-C2'	2.09	110.19	106.59
84	S2	121	OMU	O2-C2-N1	-2.09	120.08	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	S2	627	OMU	O2-C2-N1	-2.09	120.08	122.80
84	S2	1442	OMU	O2-C2-N1	-2.09	120.08	122.80
4	L5	2401	A2M	O4'-C1'-C2'	2.09	110.18	106.59
6	L8	55	PSU	C6-C5-C4	2.09	119.58	118.17
4	L5	3718	A2M	C6-C5-C4	-2.08	114.33	117.18
84	S2	866	PSU	O4'-C1'-C2'	2.08	108.03	105.15
4	L5	3782	5MC	C1'-N1-C6	-2.08	117.73	121.15
4	L5	3718	A2M	C2-N1-C6	-2.08	115.32	118.73
84	S2	1244	PSU	C6-C5-C4	2.07	119.57	118.17
84	S2	1326	OMU	O2-C2-N1	-2.07	120.10	122.80
84	S2	1177	PSU	C6-C5-C4	2.07	119.57	118.17
84	S2	1045	PSU	C6-C5-C4	2.07	119.57	118.17
4	L5	2351	OMC	C1'-N1-C6	-2.07	116.36	120.78
4	L5	1534	A2M	C6-C5-C4	-2.06	114.37	117.18
4	L5	4457	PSU	O4'-C1'-C2'	2.06	108.00	105.15
4	L5	3825	A2M	O4'-C1'-C2'	2.05	110.12	106.59
4	L5	4227	OMU	O2-C2-N1	-2.05	120.13	122.80
84	S2	668	A2M	O3'-C3'-C4'	-2.05	105.20	111.08
4	L5	4973	PSU	C6-C5-C4	2.05	119.56	118.17
4	L5	1534	A2M	C2-N1-C6	-2.05	115.37	118.73
4	L5	1683	PSU	C6-C5-C4	2.04	119.55	118.17
4	L5	3637	PSU	C6-C5-C4	2.04	119.55	118.17
4	L5	2787	A2M	C2-N1-C6	-2.03	115.39	118.73
4	L5	1534	A2M	C5-C6-N1	2.03	122.68	117.51
4	L5	3851	PSU	C6-C5-C4	2.03	119.54	118.17
4	L5	4493	PSU	C6-C5-C4	2.03	119.54	118.17
4	L5	4521	PSU	O4'-C1'-C2'	2.03	107.96	105.15
4	L5	4590	A2M	O4'-C1'-C2'	2.03	110.08	106.59
4	L5	4353	PSU	O4'-C1'-C2'	2.03	107.95	105.15
84	S2	1383	A2M	C5-C6-N1	2.02	122.65	117.51
4	L5	2787	A2M	C6-C5-C4	-2.02	114.42	117.18
4	L5	3785	A2M	C6-C5-C4	-2.02	114.42	117.18
4	L5	3830	A2M	C4'-O4'-C1'	-2.01	105.02	109.47
4	L5	400	A2M	C2-N1-C6	-2.01	115.42	118.73
4	L5	2363	A2M	C2-N1-C6	-2.01	115.42	118.73
4	L5	1524	A2M	C6-C5-C4	-2.01	114.44	117.18
4	L5	4456	OMC	C1'-N1-C2	2.01	122.88	118.44
4	L5	2363	A2M	C5-C6-N1	2.01	122.61	117.51
84	S2	1031	A2M	O4'-C1'-C2'	2.01	110.04	106.59
4	L5	4628	PSU	O4'-C1'-C2'	2.00	107.92	105.15
4	L5	3718	A2M	C5-C6-N1	2.00	122.60	117.51
4	L5	4590	A2M	C4'-O4'-C1'	-2.00	105.05	109.47

There are no chirality outliers.

All (143) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L8	75	OMG	C1'-C2'-O2'-CM2
86	CF	163	SEP	C-CA-CB-OG
86	CF	163	SEP	CA-CB-OG-P
86	CF	163	SEP	CB-OG-P-O1P
86	CF	163	SEP	CB-OG-P-O2P
86	CF	163	SEP	CB-OG-P-O3P
4	L5	1326	A2M	O4'-C4'-C5'-O5'
4	L5	1326	A2M	C1'-C2'-O2'-CM'
4	L5	1340	OMC	C1'-C2'-O2'-CM2
4	L5	1625	OMG	O4'-C4'-C5'-O5'
4	L5	2351	OMC	C1'-C2'-O2'-CM2
4	L5	2787	A2M	C1'-C2'-O2'-CM'
4	L5	3701	OMC	O4'-C4'-C5'-O5'
4	L5	3792	OMG	O4'-C4'-C5'-O5'
4	L5	3841	OMC	C1'-C2'-O2'-CM2
4	L5	4196	OMG	C1'-C2'-O2'-CM2
4	L5	4220	6MZ	O4'-C4'-C5'-O5'
4	L5	4590	A2M	O4'-C4'-C5'-O5'
4	L5	4637	OMG	O4'-C4'-C5'-O5'
84	S2	27	A2M	C1'-C2'-O2'-CM'
84	S2	159	A2M	C1'-C2'-O2'-CM'
84	S2	601	OMG	C1'-C2'-O2'-CM2
84	S2	644	OMG	O4'-C4'-C5'-O5'
84	S2	1248	B8N	O4'-C4'-C5'-O5'
84	S2	1272	OMC	O4'-C4'-C5'-O5'
84	S2	1288	OMU	O4'-C4'-C5'-O5'
84	S2	1337	4AC	N3-C4-N4-C7
84	S2	1383	A2M	C1'-C2'-O2'-CM'
84	S2	1442	OMU	O4'-C4'-C5'-O5'
84	S2	1832	6MZ	C5-C6-N6-C9
84	S2	1832	6MZ	N1-C6-N6-C9
4	L5	3701	OMC	C2'-C1'-N1-C2
4	L5	2364	OMG	O4'-C4'-C5'-O5'
4	L5	3701	OMC	C3'-C4'-C5'-O5'
4	L5	4500	PSU	C3'-C4'-C5'-O5'
4	L5	4500	PSU	O4'-C4'-C5'-O5'
4	L5	4590	A2M	C3'-C4'-C5'-O5'
84	S2	436	OMG	O4'-C4'-C5'-O5'
84	S2	576	A2M	O4'-C4'-C5'-O5'
84	S2	576	A2M	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
84	S2	683	OMG	C3'-C4'-C5'-O5'
84	S2	799	OMU	C3'-C4'-C5'-O5'
84	S2	799	OMU	O4'-C4'-C5'-O5'
84	S2	801	PSU	C3'-C4'-C5'-O5'
84	S2	867	OMG	C3'-C4'-C5'-O5'
84	S2	1272	OMC	C3'-C4'-C5'-O5'
84	S2	1288	OMU	C3'-C4'-C5'-O5'
4	L5	1323	A2M	O4'-C4'-C5'-O5'
4	L5	1536	PSU	C3'-C4'-C5'-O5'
4	L5	1536	PSU	O4'-C4'-C5'-O5'
4	L5	1625	OMG	C3'-C4'-C5'-O5'
4	L5	2815	A2M	O4'-C4'-C5'-O5'
4	L5	3792	OMG	C3'-C4'-C5'-O5'
4	L5	3867	A2M	C3'-C4'-C5'-O5'
84	S2	99	A2M	O4'-C4'-C5'-O5'
84	S2	683	OMG	O4'-C4'-C5'-O5'
84	S2	1442	OMU	C3'-C4'-C5'-O5'
4	L5	3701	OMC	C2'-C1'-N1-C6
4	L5	1326	A2M	C3'-C4'-C5'-O5'
4	L5	4220	6MZ	C3'-C4'-C5'-O5'
84	S2	644	OMG	C3'-C4'-C5'-O5'
4	L5	4447	5MC	C2'-C1'-N1-C6
4	L5	1677	PSU	C3'-C4'-C5'-O5'
4	L5	1677	PSU	O4'-C4'-C5'-O5'
4	L5	2364	OMG	C3'-C4'-C5'-O5'
4	L5	2876	OMG	C3'-C4'-C5'-O5'
4	L5	3899	OMG	C3'-C4'-C5'-O5'
4	L5	4637	OMG	C3'-C4'-C5'-O5'
84	S2	517	OMC	C3'-C4'-C5'-O5'
84	S2	668	A2M	O4'-C4'-C5'-O5'
84	S2	668	A2M	C3'-C4'-C5'-O5'
84	S2	1248	B8N	C3'-C4'-C5'-O5'
84	S2	428	OMU	C2'-C1'-N1-C6
4	L5	2787	A2M	C3'-C4'-C5'-O5'
4	L5	2815	A2M	C3'-C4'-C5'-O5'
84	S2	436	OMG	C3'-C4'-C5'-O5'
84	S2	517	OMC	O4'-C4'-C5'-O5'
84	S2	801	PSU	O4'-C4'-C5'-O5'
84	S2	867	OMG	O4'-C4'-C5'-O5'
4	L5	1524	A2M	O4'-C4'-C5'-O5'
4	L5	3899	OMG	O4'-C4'-C5'-O5'
4	L5	2787	A2M	C2'-C1'-N9-C8

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Mol	Chain	Res	Type	Atoms
4	L5	1524	A2M	C3'-C4'-C5'-O5'
4	L5	2876	OMG	O4'-C4'-C5'-O5'
4	L5	4618	OMG	C3'-C4'-C5'-O5'
4	L5	1323	A2M	C3'-C4'-C5'-O5'
4	L5	3867	A2M	O4'-C4'-C5'-O5'
84	S2	99	A2M	C3'-C4'-C5'-O5'
4	L5	4590	A2M	C4'-C5'-O5'-P
4	L5	2422	OMC	O4'-C4'-C5'-O5'
84	S2	428	OMU	O4'-C4'-C5'-O5'
84	S2	1045	PSU	O4'-C4'-C5'-O5'
84	S2	1248	B8N	N34-C33-C34-O36
4	L5	400	A2M	C1'-C2'-O2'-CM'
84	S2	166	A2M	C1'-C2'-O2'-CM'
84	S2	468	A2M	C1'-C2'-O2'-CM'
4	L5	2422	OMC	C3'-C4'-C5'-O5'
84	S2	1248	B8N	C31-C32-C33-C34
4	L5	3851	PSU	C3'-C4'-C5'-O5'
84	S2	1045	PSU	C3'-C4'-C5'-O5'
84	S2	1639	G7M	C3'-C4'-C5'-O5'
4	L5	4447	5MC	C2'-C1'-N1-C2
4	L5	4447	5MC	O4'-C1'-N1-C6
84	S2	428	OMU	O4'-C1'-N1-C6
84	S2	1383	A2M	O4'-C4'-C5'-O5'
4	L5	4447	5MC	O4'-C1'-N1-C2
4	L5	3701	OMC	O4'-C1'-N1-C6
86	CF	163	SEP	N-CA-CB-OG
4	L5	1534	A2M	C4'-C5'-O5'-P
4	L5	3818	UY1	C4'-C5'-O5'-P
4	L5	4500	PSU	C4'-C5'-O5'-P
4	L5	3818	UY1	O4'-C1'-C5'-C4
4	L5	2787	A2M	C2'-C1'-N9-C4
4	L5	1781	PSU	C3'-C4'-C5'-O5'
84	S2	428	OMU	C3'-C4'-C5'-O5'
84	S2	1383	A2M	C3'-C4'-C5'-O5'
84	S2	428	OMU	C2'-C1'-N1-C2
4	L5	3887	OMC	C4'-C5'-O5'-P
84	S2	576	A2M	C4'-C5'-O5'-P
84	S2	627	OMU	O4'-C4'-C5'-O5'
4	L5	3869	OMC	C3'-C2'-O2'-CM2
84	S2	1490	OMG	C4'-C5'-O5'-P
4	L5	3782	5MC	O4'-C4'-C5'-O5'
4	L5	4618	OMG	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
84	S2	1703	OMC	O4'-C4'-C5'-O5'
84	S2	644	OMG	C4'-C5'-O5'-P
84	S2	1851	MA6	C4'-C5'-O5'-P
84	S2	428	OMU	O4'-C1'-N1-C2
4	L5	3869	OMC	C1'-C2'-O2'-CM2
4	L5	4637	OMG	C1'-C2'-O2'-CM2
84	S2	867	OMG	C1'-C2'-O2'-CM2
4	L5	3844	PSU	C4'-C5'-O5'-P
4	L5	398	A2M	O4'-C4'-C5'-O5'
4	L5	1677	PSU	O4'-C1'-C5-C6
4	L5	3785	A2M	C3'-C2'-O2'-CM'
4	L5	3701	OMC	O4'-C1'-N1-C2
84	S2	1832	6MZ	O4'-C4'-C5'-O5'
4	L5	1322	1MA	C2'-C1'-N9-C8
4	L5	2787	A2M	O4'-C1'-N9-C8
4	L5	2351	OMC	O4'-C4'-C5'-O5'
84	S2	1639	G7M	O4'-C4'-C5'-O5'
4	L5	1326	A2M	C4'-C5'-O5'-P
4	L5	2351	OMC	C2'-C1'-N1-C2

There are no ring outliers.

68 monomers are involved in 96 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	S2	867	OMG	1	0
84	S2	121	OMU	2	0
4	L5	398	A2M	1	0
4	L5	4579	PSU	2	0
4	L5	4590	A2M	1	0
4	L5	1340	OMC	2	0
84	S2	1232	PSU	2	0
84	S2	1639	G7M	1	0
84	S2	27	A2M	1	0
4	L5	1326	A2M	3	0
4	L5	4618	OMG	1	0
84	S2	1046	PSU	1	0
6	L8	75	OMG	2	0
4	L5	4637	OMG	1	0
4	L5	1625	OMG	1	0
4	L5	2363	A2M	1	0
4	L5	4431	PSU	1	0
4	L5	2876	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L5	400	A2M	1	0
84	S2	484	A2M	1	0
84	S2	1842	4AC	1	0
4	L5	4689	PSU	1	0
4	L5	4392	OMG	1	0
4	L5	2804	OMC	1	0
4	L5	4456	OMC	1	0
84	S2	576	A2M	2	0
4	L5	4636	PSU	1	0
4	L5	2364	OMG	1	0
4	L5	4293	PSU	1	0
4	L5	4227	OMU	1	0
4	L5	2422	OMC	1	0
4	L5	4447	5MC	1	0
84	S2	509	OMG	2	0
4	L5	1871	A2M	1	0
4	L5	3718	A2M	3	0
4	L5	3884	PSU	1	0
4	L5	4457	PSU	1	0
4	L5	4220	6MZ	5	0
84	S2	166	A2M	3	0
84	S2	1383	A2M	1	0
4	L5	3818	UY1	1	0
4	L5	2632	PSU	1	0
4	L5	4571	A2M	2	0
84	S2	99	A2M	1	0
4	L5	3782	5MC	1	0
84	S2	116	OMU	3	0
84	S2	468	A2M	1	0
4	L5	3822	PSU	1	0
84	S2	1328	OMG	1	0
4	L5	1677	PSU	1	0
4	L5	3785	A2M	1	0
84	S2	1337	4AC	3	0
4	L5	4620	OMU	2	0
84	S2	681	PSU	1	0
84	S2	1850	MA6	2	0
4	L5	4536	OMC	1	0
4	L5	3701	OMC	1	0
84	S2	601	OMG	1	0
4	L5	4196	OMG	1	0
84	S2	517	OMC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L5	1683	PSU	2	0
84	S2	1288	OMU	1	0
4	L5	3867	A2M	3	0
84	S2	159	A2M	2	0
4	L5	3841	OMC	1	0
4	L5	2424	OMG	1	0
4	L5	2351	OMC	1	0
84	S2	436	OMG	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 242 ligands modelled in this entry, 225 are monoatomic - leaving 17 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
88	SPM	L5	5263	-	13,13,13	0.35	0	12,12,12	1.01	0
89	SPD	L5	5283	-	9,9,9	0.31	0	8,8,8	0.92	0
89	SPD	L5	5285	-	9,9,9	0.31	0	8,8,8	0.84	0
89	SPD	L8	202	-	9,9,9	0.32	0	8,8,8	0.89	0
88	SPM	L5	5290	-	13,13,13	0.36	0	12,12,12	0.89	0
89	SPD	LN	301	-	9,9,9	0.34	0	8,8,8	0.86	0
89	SPD	L5	5287	-	9,9,9	0.32	0	8,8,8	0.85	0
89	SPD	L5	5260	-	9,9,9	0.32	0	8,8,8	0.95	0
89	SPD	L5	5282	-	9,9,9	0.32	0	8,8,8	0.79	0
88	SPM	L5	5262	-	13,13,13	0.43	0	12,12,12	0.91	0
89	SPD	L5	5284	-	9,9,9	0.33	0	8,8,8	0.81	0
88	SPM	L5	5289	-	13,13,13	0.36	0	12,12,12	0.89	0
89	SPD	L5	5288	-	9,9,9	0.32	0	8,8,8	0.80	0
88	SPM	L5	5286	87	13,13,13	0.37	0	12,12,12	1.01	0
88	SPM	L5	5258	-	13,13,13	0.35	0	12,12,12	1.00	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	SPM	L5	5266	-	13,13,13	0.37	0	12,12,12	1.11	0
89	SPD	L5	5281	-	9,9,9	0.34	0	8,8,8	0.85	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
88	SPM	L5	5263	-	-	4/11/11/11	-
89	SPD	L5	5283	-	-	4/7/7/7	-
89	SPD	L5	5285	-	-	1/7/7/7	-
89	SPD	L8	202	-	-	3/7/7/7	-
88	SPM	L5	5290	-	-	3/11/11/11	-
89	SPD	LN	301	-	-	1/7/7/7	-
89	SPD	L5	5287	-	-	1/7/7/7	-
89	SPD	L5	5260	-	-	0/7/7/7	-
89	SPD	L5	5282	-	-	1/7/7/7	-
88	SPM	L5	5262	-	-	10/11/11/11	-
89	SPD	L5	5284	-	-	0/7/7/7	-
88	SPM	L5	5289	-	-	3/11/11/11	-
89	SPD	L5	5288	-	-	3/7/7/7	-
88	SPM	L5	5286	87	-	4/11/11/11	-
88	SPM	L5	5258	-	-	2/11/11/11	-
88	SPM	L5	5266	-	-	5/11/11/11	-
89	SPD	L5	5281	-	-	1/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	L5	5283	SPD	C3-C4-C5-N6
88	L5	5262	SPM	C7-C8-C9-N10
88	L5	5289	SPM	C7-C8-C9-N10
89	L8	202	SPD	C3-C4-C5-N6
88	L5	5262	SPM	N5-C6-C7-C8

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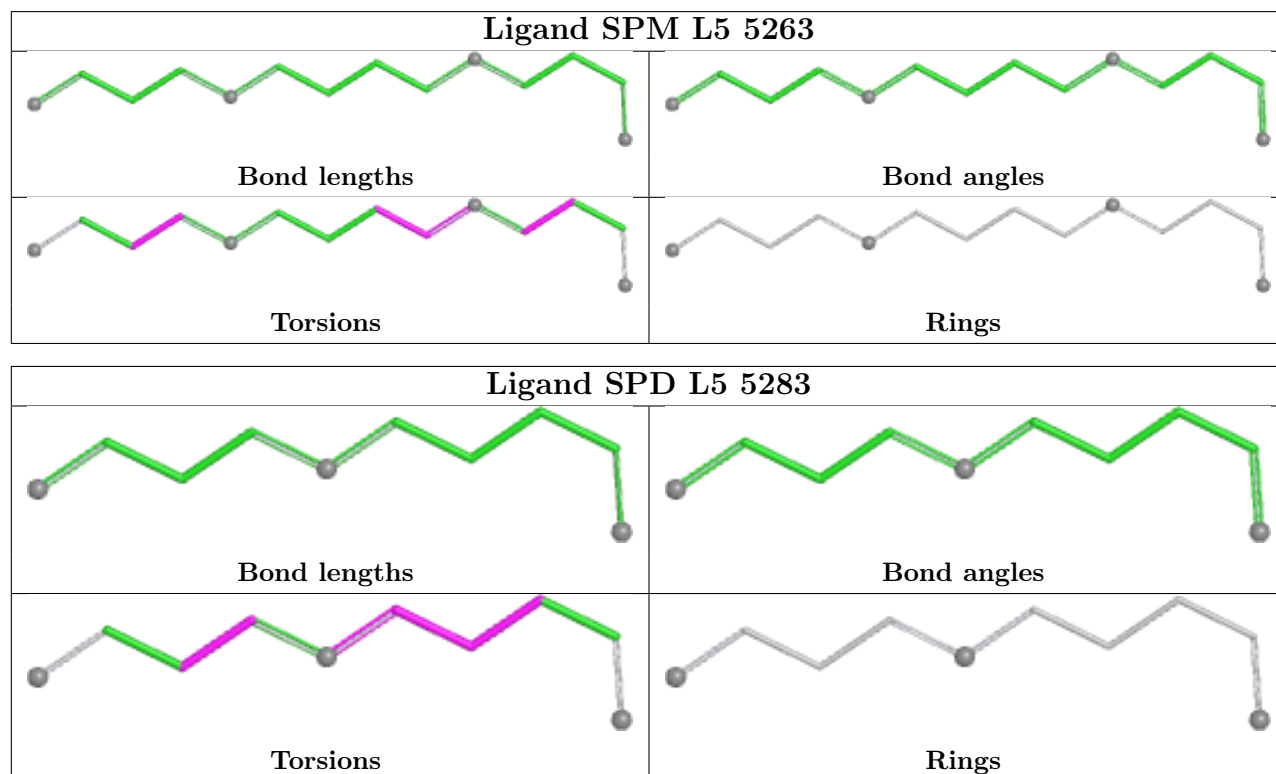
Mol	Chain	Res	Type	Atoms
89	L5	5283	SPD	N6-C7-C8-C9
89	L5	5282	SPD	C3-C4-C5-N6
88	L5	5262	SPM	C2-C3-C4-N5
88	L5	5266	SPM	N10-C11-C12-C13
88	L5	5258	SPM	C3-C4-N5-C6
88	L5	5262	SPM	C3-C4-N5-C6
88	L5	5286	SPM	C12-C11-N10-C9
88	L5	5262	SPM	N10-C11-C12-C13
88	L5	5289	SPM	N10-C11-C12-C13
88	L5	5290	SPM	C8-C9-N10-C11
89	L5	5283	SPD	C4-C5-N6-C7
89	L5	5283	SPD	C2-C3-C4-C5
88	L5	5266	SPM	C7-C8-C9-N10
88	L5	5286	SPM	C7-C6-N5-C4
88	L5	5266	SPM	C2-C3-C4-N5
88	L5	5263	SPM	C7-C6-N5-C4
88	L5	5258	SPM	C6-C7-C8-C9
88	L5	5262	SPM	C6-C7-C8-C9
88	L5	5266	SPM	C6-C7-C8-C9
88	L5	5263	SPM	N5-C6-C7-C8
88	L5	5290	SPM	C6-C7-C8-C9
88	L5	5286	SPM	C8-C9-N10-C11
88	L5	5290	SPM	C7-C6-N5-C4
89	L5	5288	SPD	C4-C5-N6-C7
88	L5	5262	SPM	N1-C2-C3-C4
88	L5	5262	SPM	C11-C12-C13-N14
88	L5	5286	SPM	N1-C2-C3-C4
89	L5	5287	SPD	C2-C3-C4-C5
88	L5	5262	SPM	C7-C6-N5-C4
89	LN	301	SPD	C4-C5-N6-C7
89	L5	5281	SPD	C2-C3-C4-C5
89	L5	5288	SPD	C8-C7-N6-C5
89	L5	5288	SPD	N1-C2-C3-C4
88	L5	5263	SPM	N10-C11-C12-C13
89	L8	202	SPD	N6-C7-C8-C9
88	L5	5263	SPM	C2-C3-C4-N5
88	L5	5266	SPM	N5-C6-C7-C8
88	L5	5289	SPM	N5-C6-C7-C8
89	L8	202	SPD	C8-C7-N6-C5
89	L5	5285	SPD	C8-C7-N6-C5
88	L5	5262	SPM	C8-C9-N10-C11

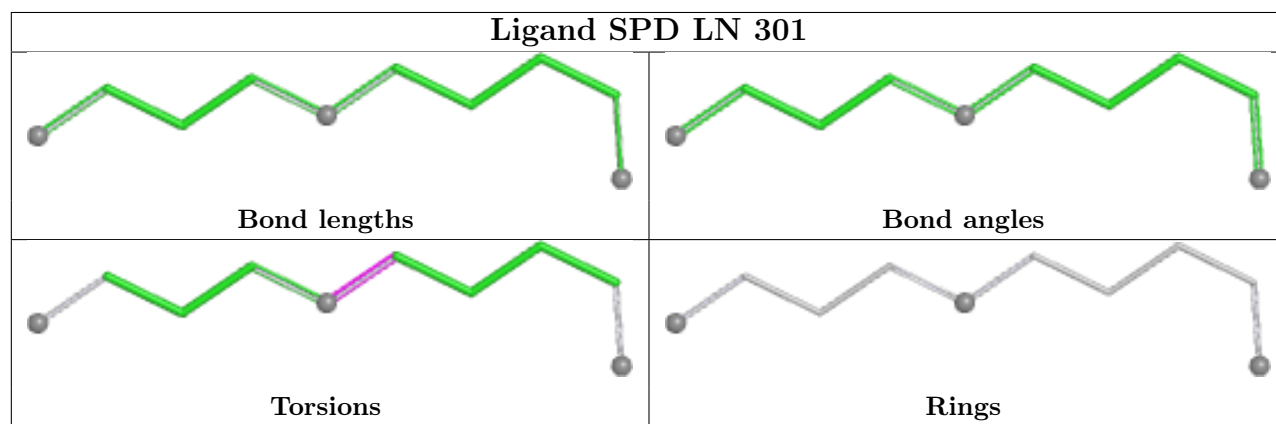
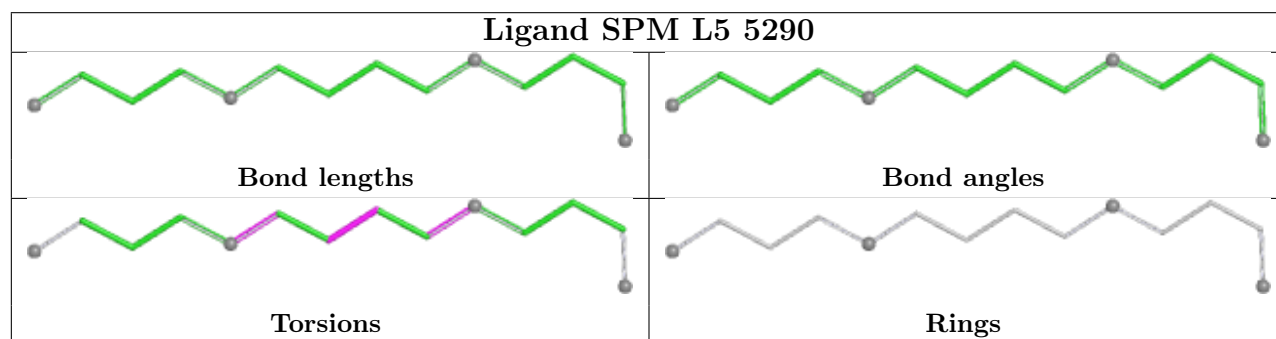
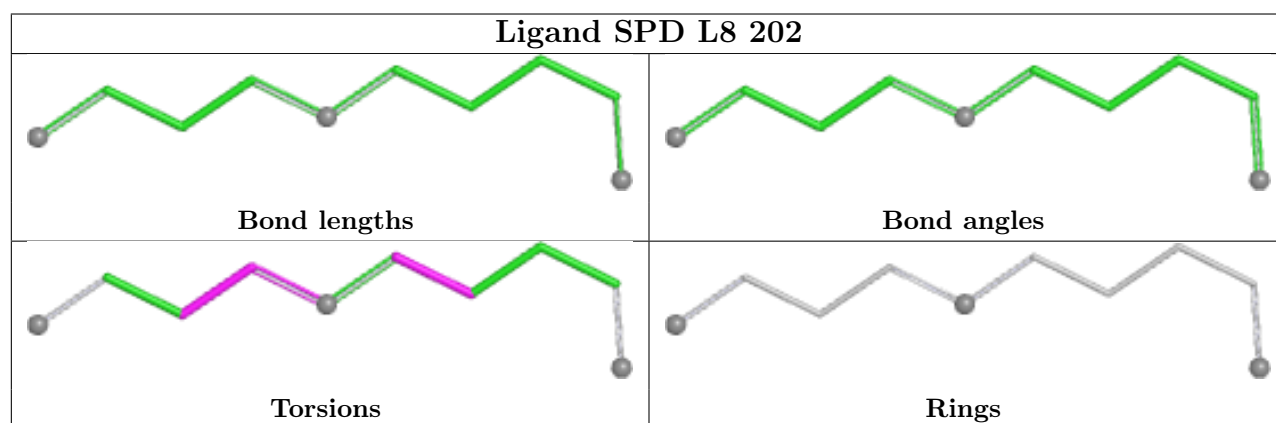
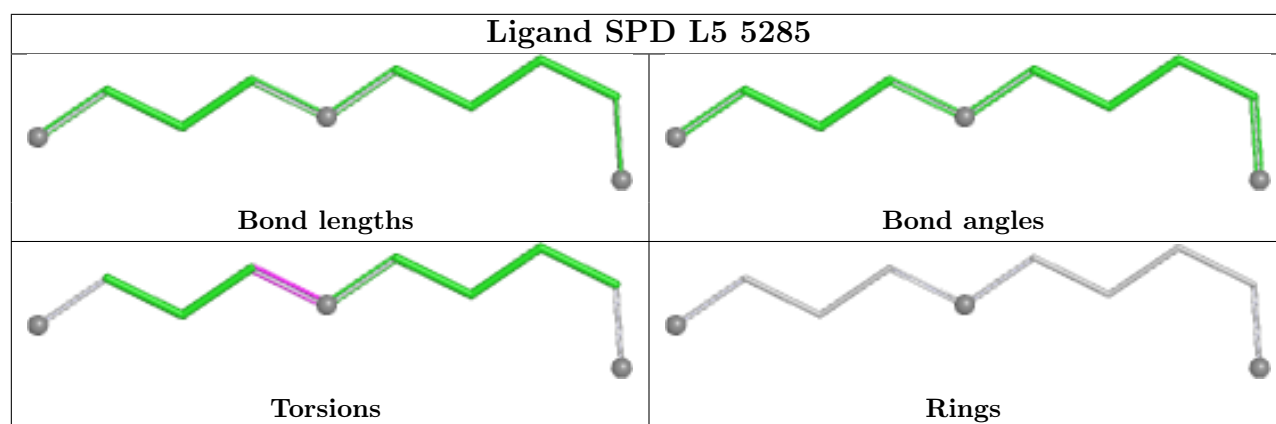
There are no ring outliers.

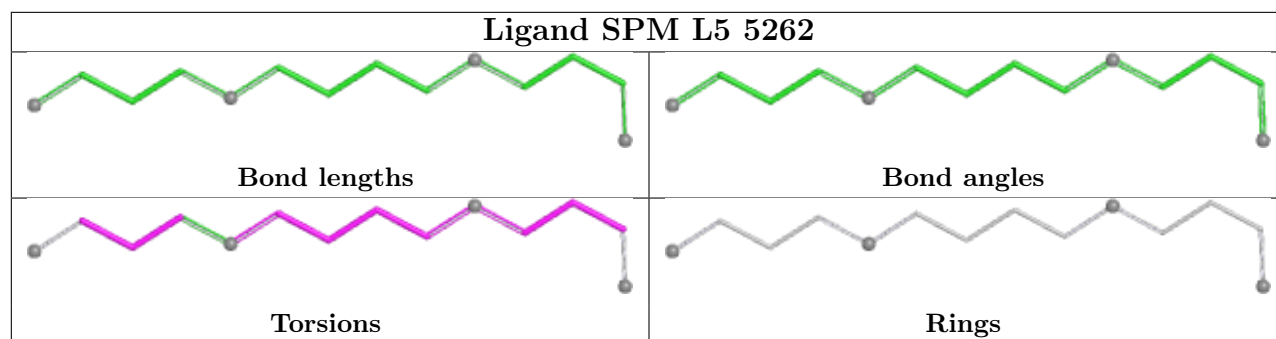
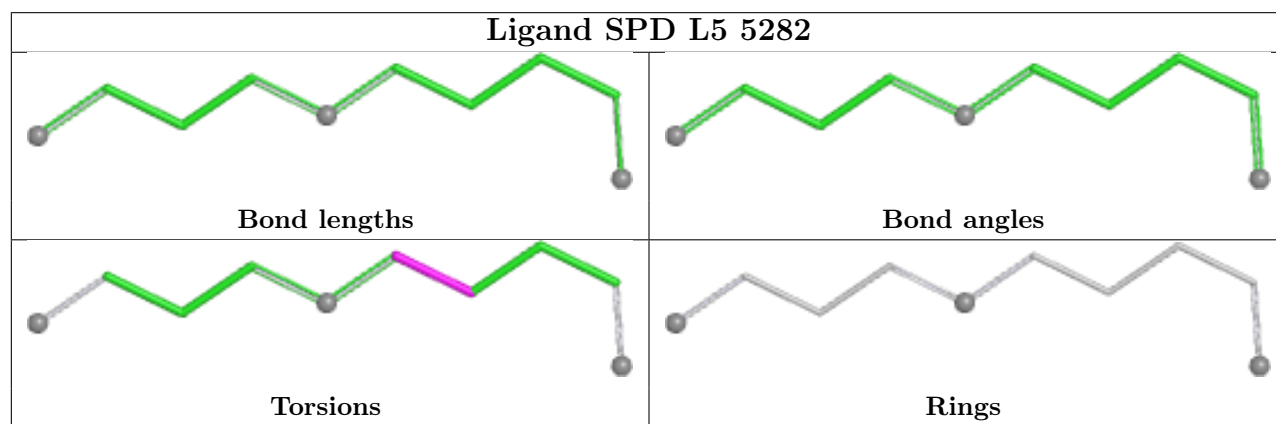
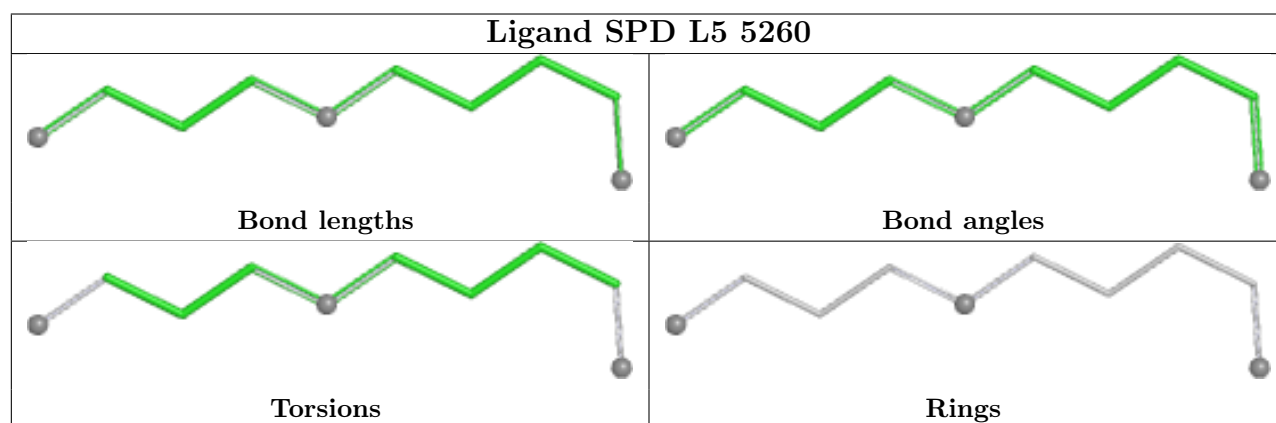
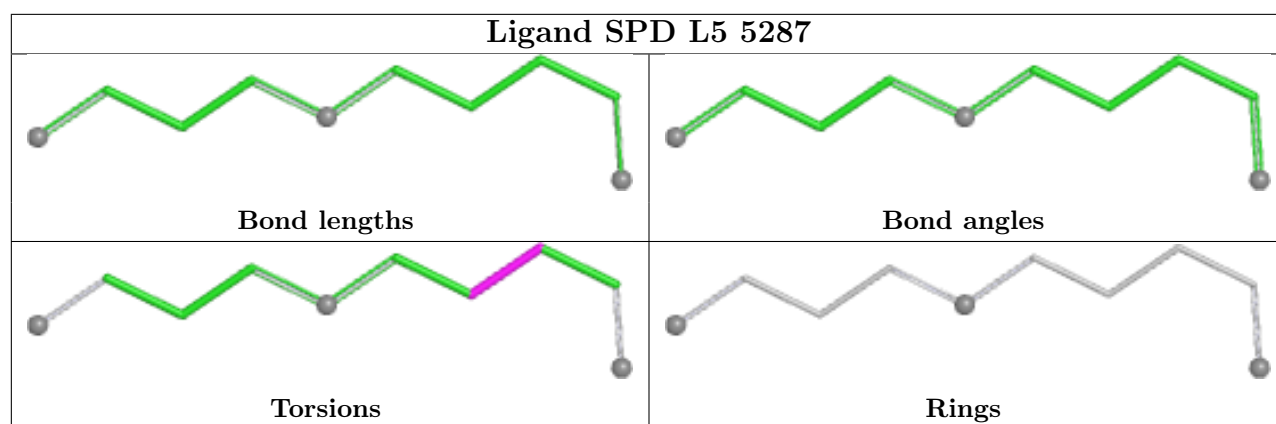
9 monomers are involved in 11 short contacts:

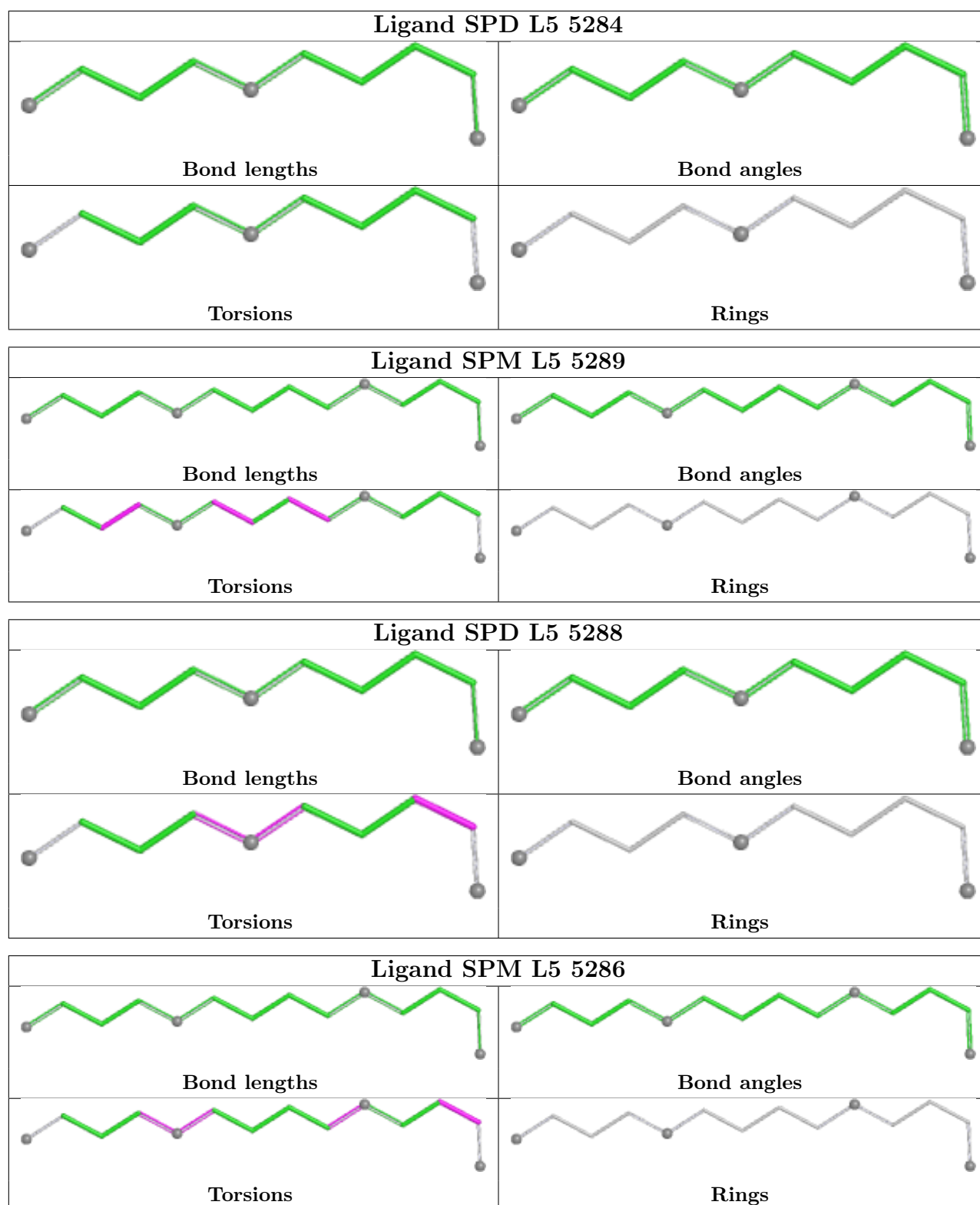
Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	L5	5263	SPM	1	0
88	L5	5290	SPM	2	0
89	LN	301	SPD	1	0
89	L5	5260	SPD	1	0
89	L5	5282	SPD	2	0
88	L5	5262	SPM	1	0
88	L5	5289	SPM	1	0
89	L5	5288	SPD	1	0
88	L5	5266	SPM	1	0

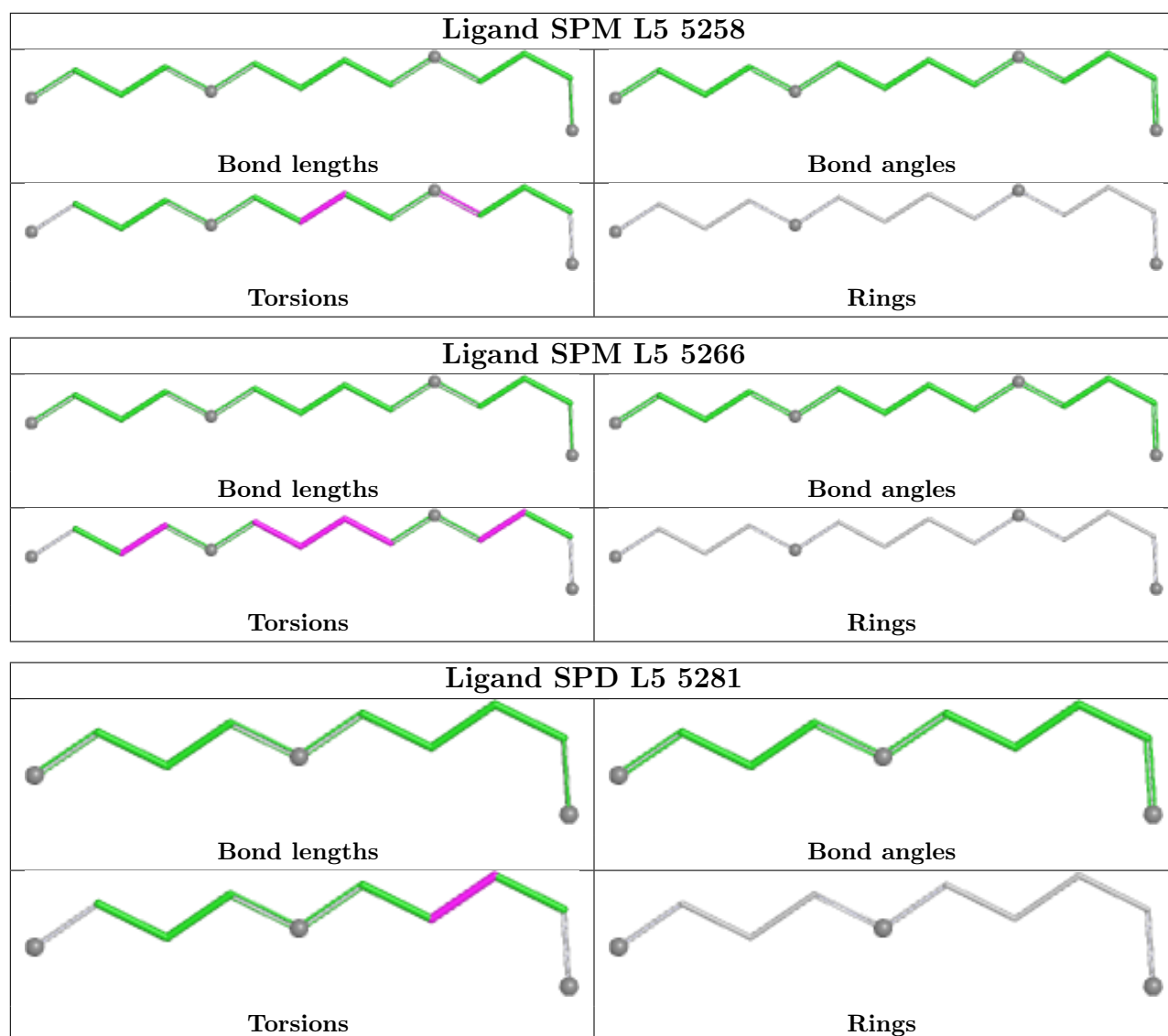
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	L5	10
84	S2	5
2	Pt	1
3	Et	1
85	AT	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	753:C	O3'	785:C	P	29.37
1	L5	1706:A	O3'	1716:G	P	21.25
1	L5	2910:G	O3'	3584:C	P	21.20
1	L5	760:G	O3'	903:C	P	16.82
1	L5	519:C	O3'	642:G	P	15.80
1	L5	2112:G	O3'	2249:C	P	15.22
1	L5	4776:G	O3'	4858:C	P	15.05
1	S2	698:G	O3'	730:C	P	14.63
1	L5	3954:A	O3'	4056:A	P	13.42
1	S2	739:C	O3'	746:C	P	12.44
1	L5	990:C	O3'	1064:G	P	12.34
1	L5	1222:A	O3'	1234:G	P	10.82
1	Pt	15:G	O3'	18:G	P	9.99
1	S2	225:G	O3'	287:U	P	7.52
1	L5	1100:U	O3'	1167:C	P	7.02
1	Et	16:C	O3'	18:U	P	6.26
1	AT	16:C	O3'	18:G	P	5.32
1	S2	1831:A	O3'	1832:6MZ	P	4.27

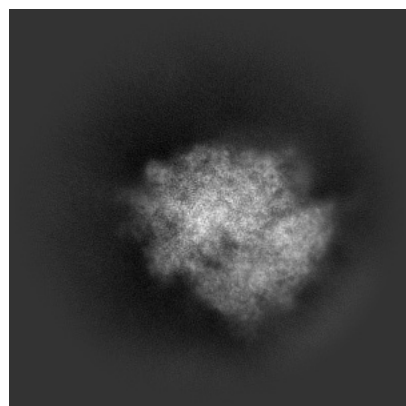
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71345. These allow visual inspection of the internal detail of the map and identification of artifacts.

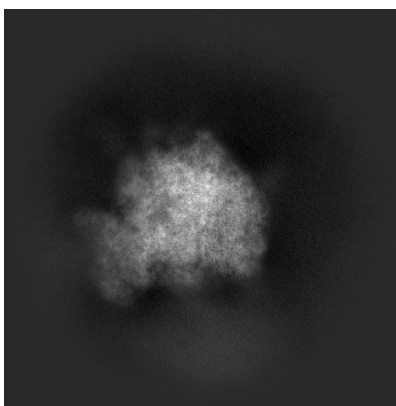
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

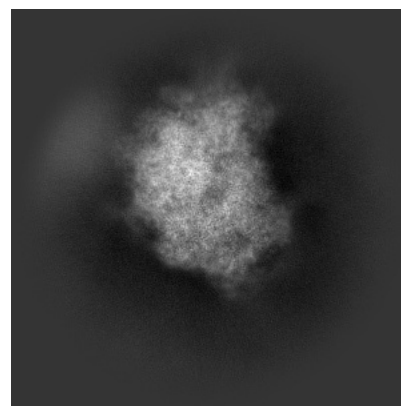
6.1.1 Primary map



X

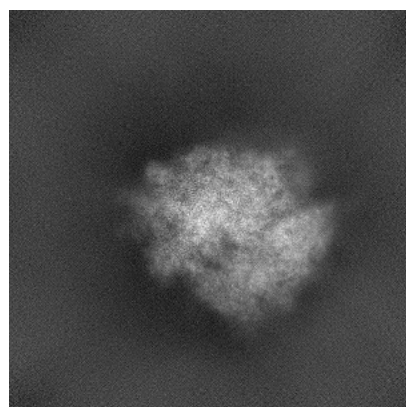


Y

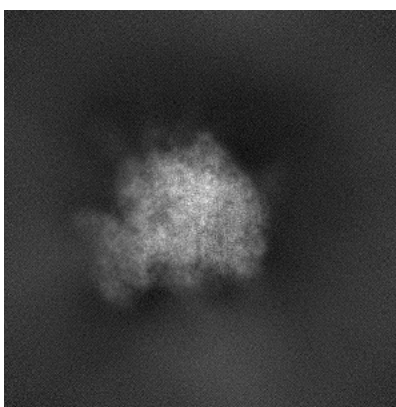


Z

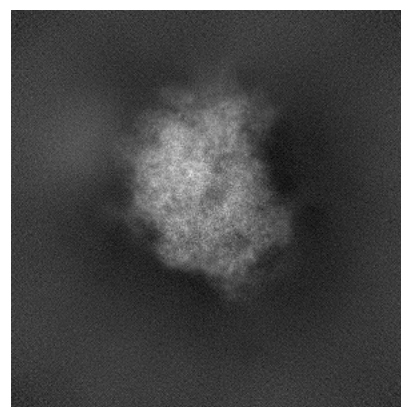
6.1.2 Raw map



X



Y

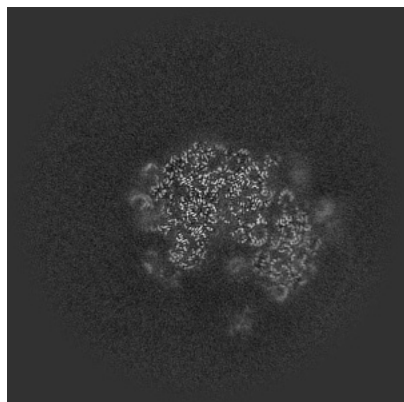


Z

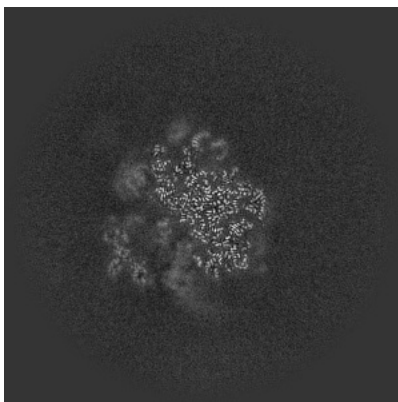
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

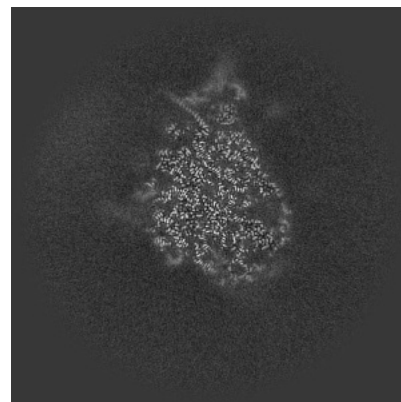
6.2.1 Primary map



X Index: 256

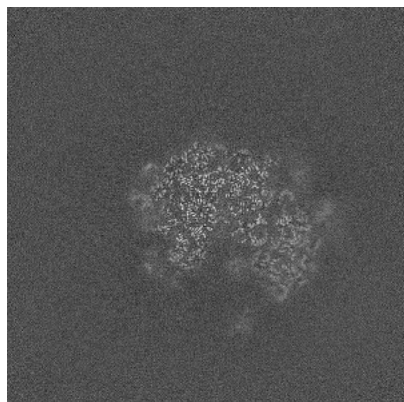


Y Index: 256

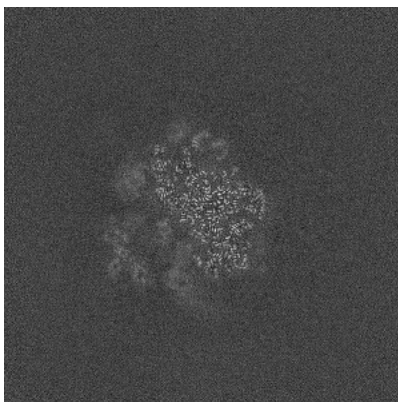


Z Index: 256

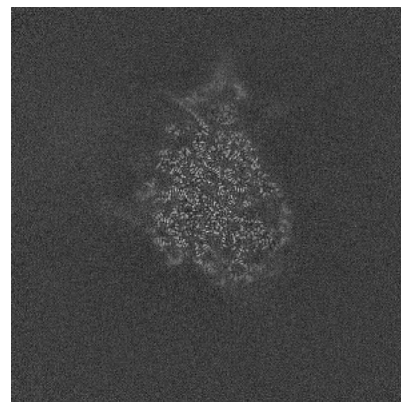
6.2.2 Raw map



X Index: 256



Y Index: 256

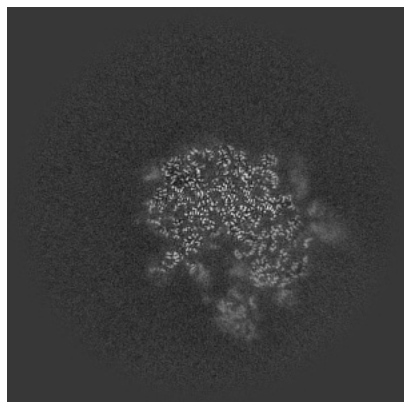


Z Index: 256

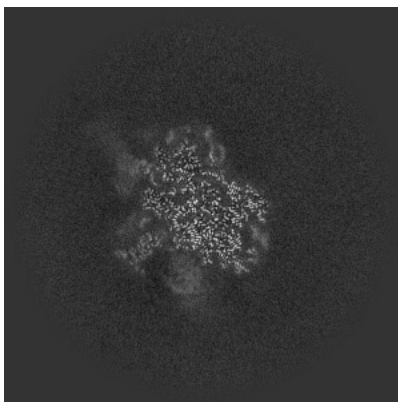
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

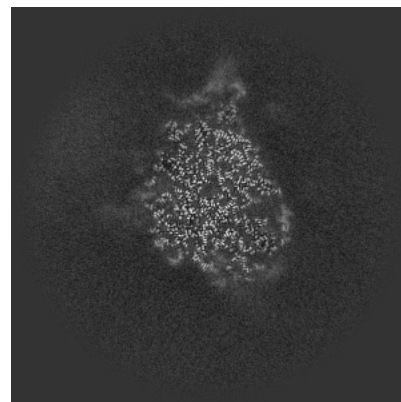
6.3.1 Primary map



X Index: 242

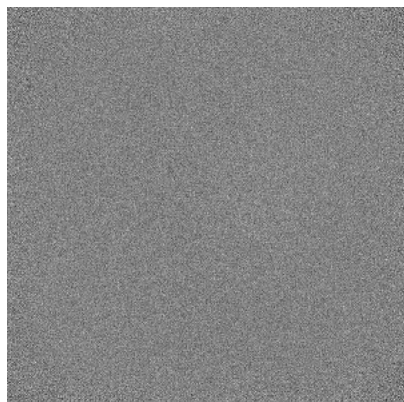


Y Index: 243

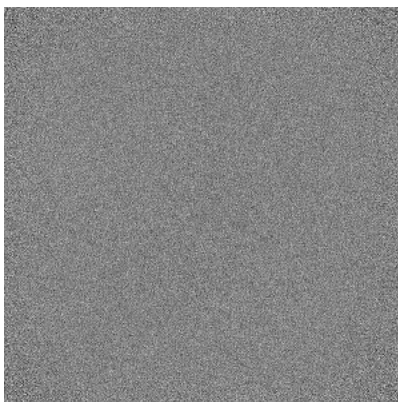


Z Index: 258

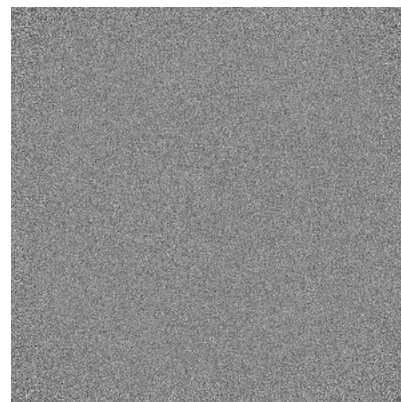
6.3.2 Raw map



X Index: 0



Y Index: 0

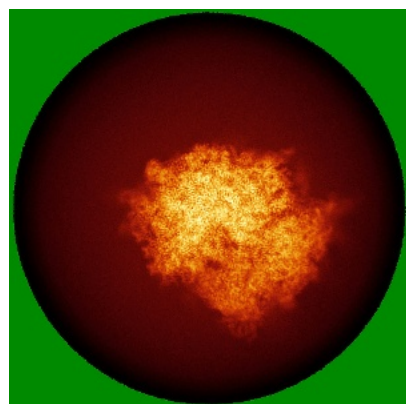


Z Index: 0

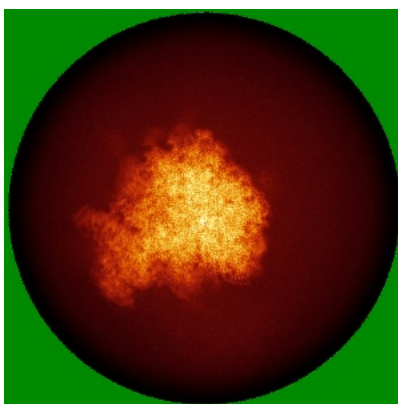
The images above show the largest variance slices of the map in three orthogonal directions.

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

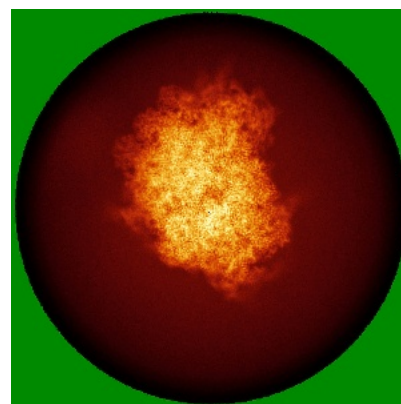
6.4.1 Primary map



X

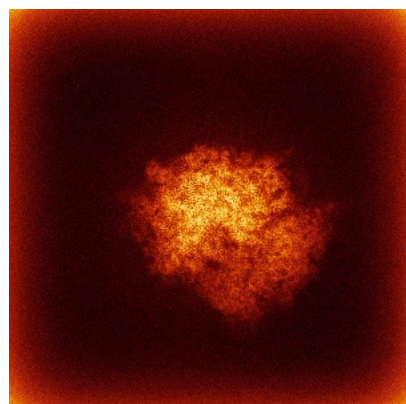


Y

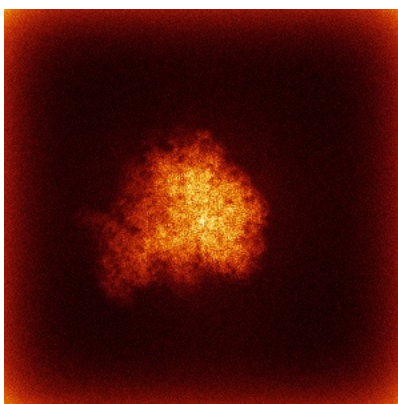


Z

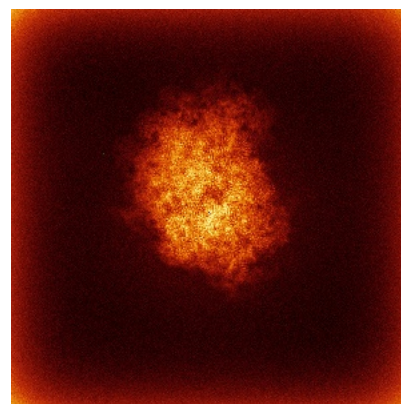
6.4.2 Raw map



X



Y

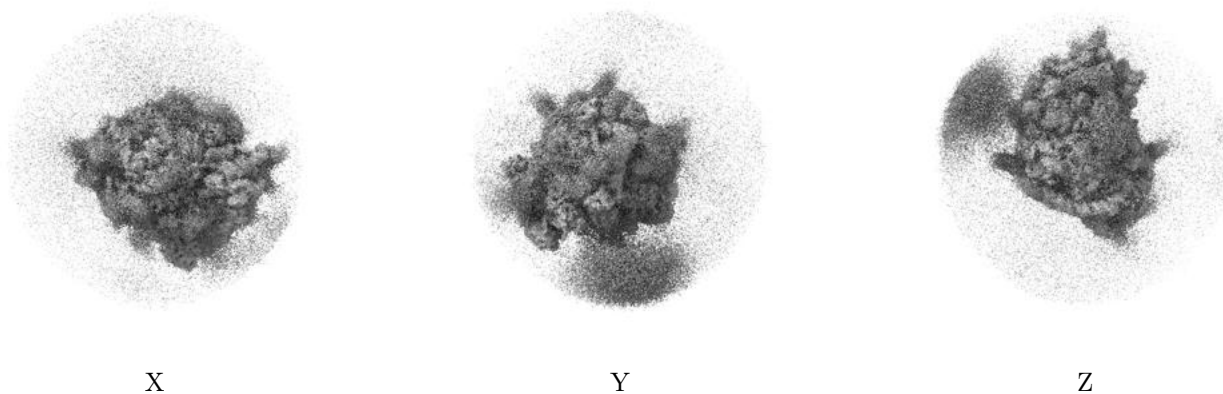


Z

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

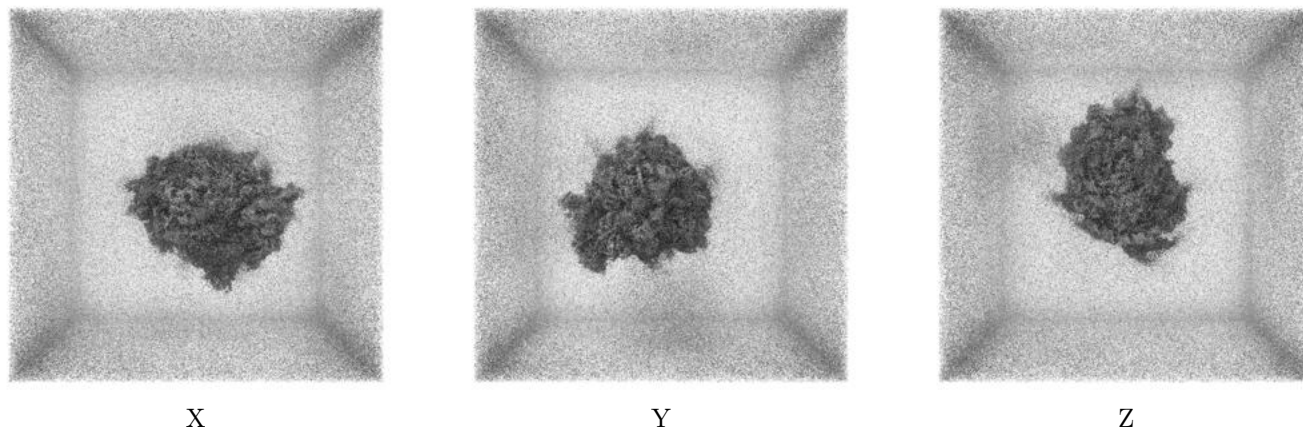
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0226. 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.

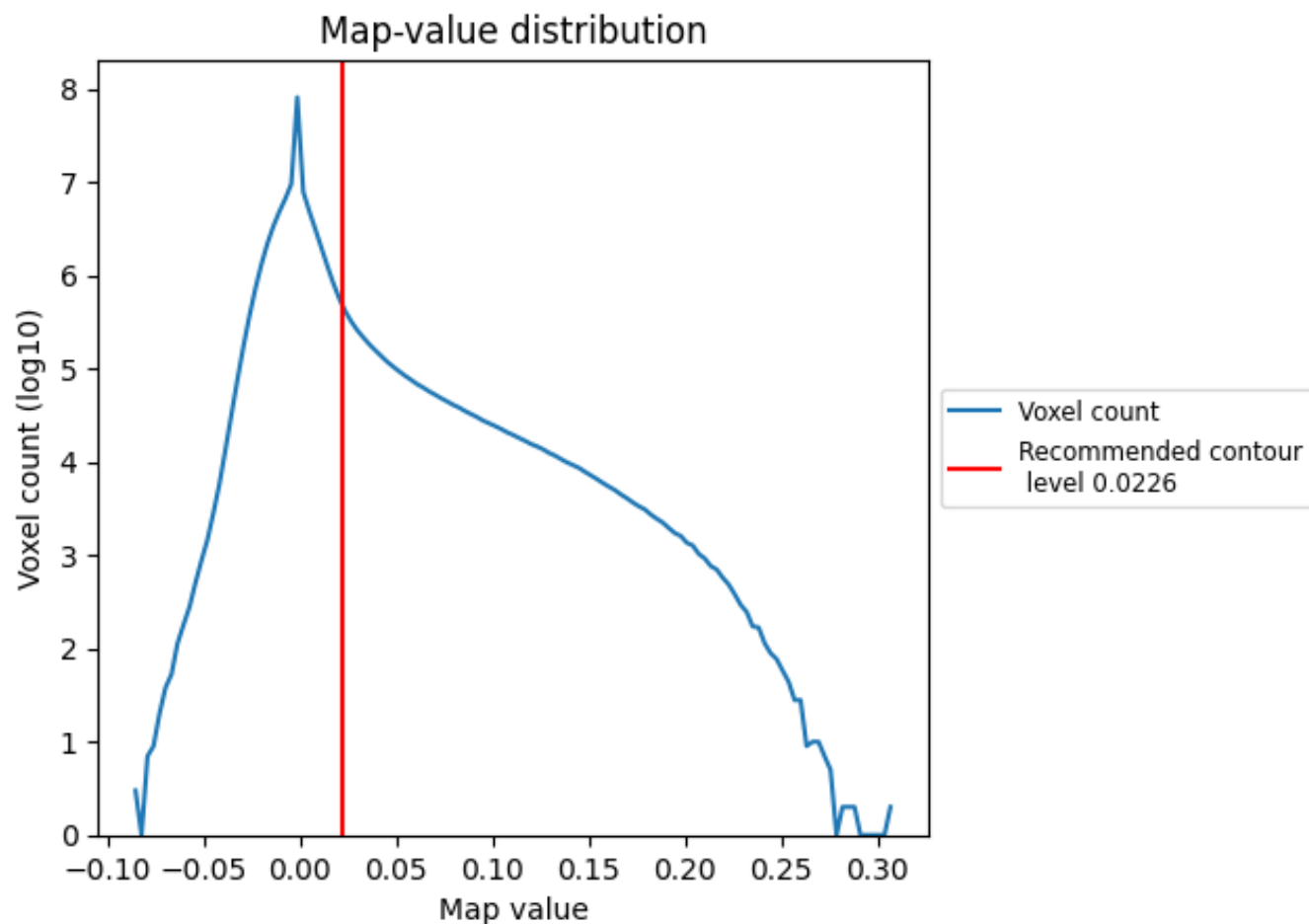
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

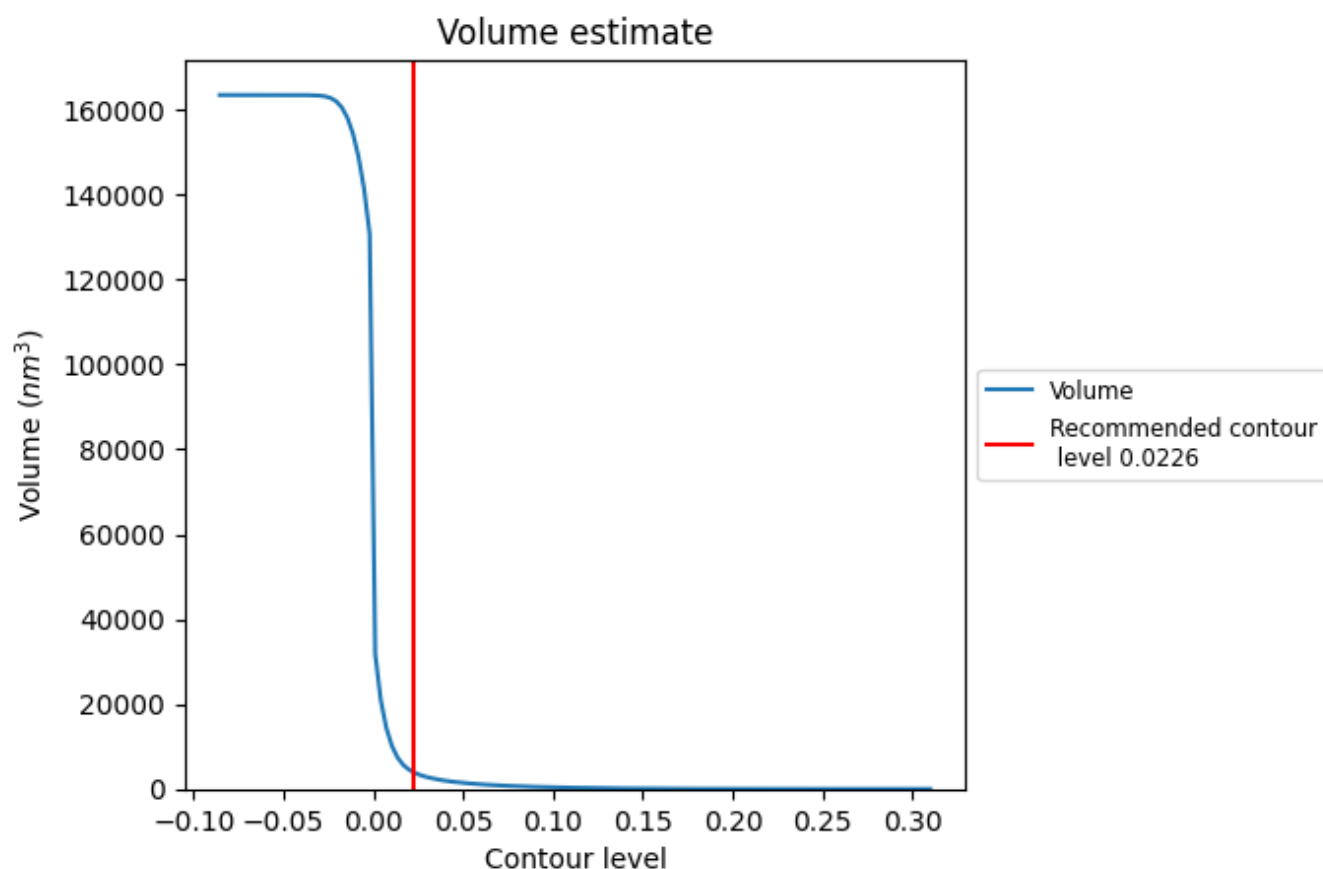
This section contains the results of statistical analysis of the map.

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.

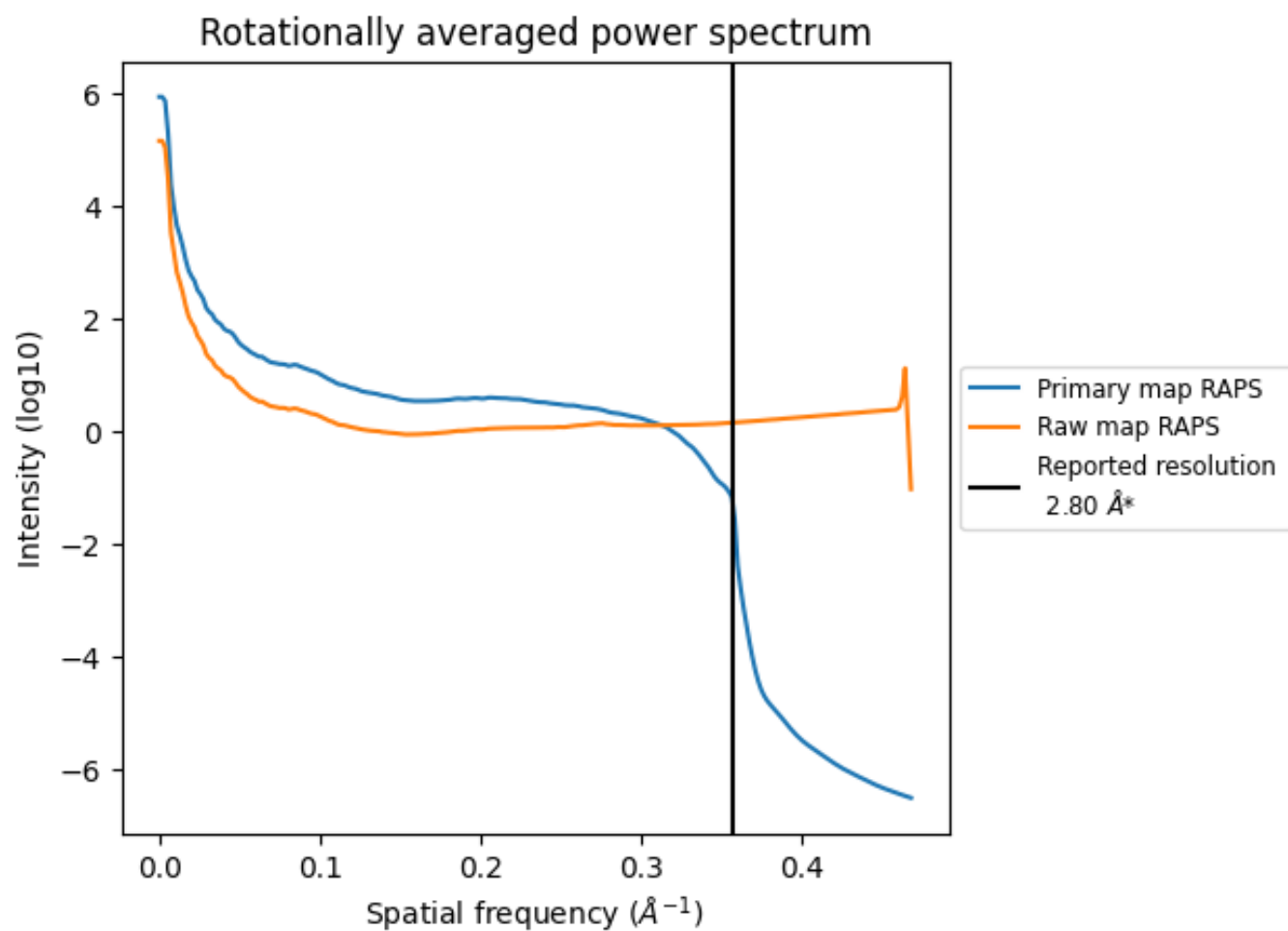
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3897 nm^3 ; this corresponds to an approximate mass of 3520 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 ⓘ

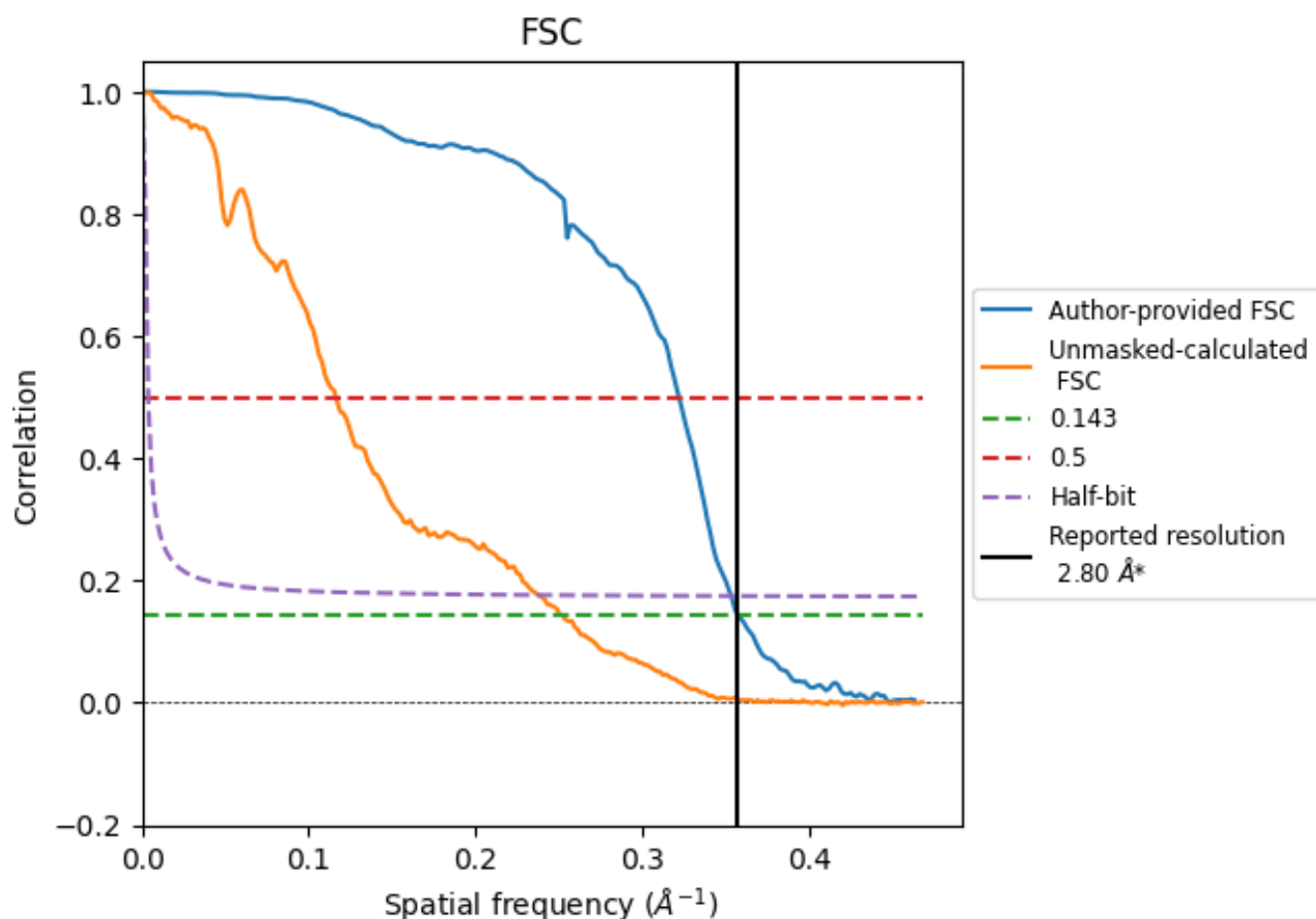


*Reported resolution corresponds to spatial frequency of 0.357 $\text{\AA}^{-1}$

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 0.357 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

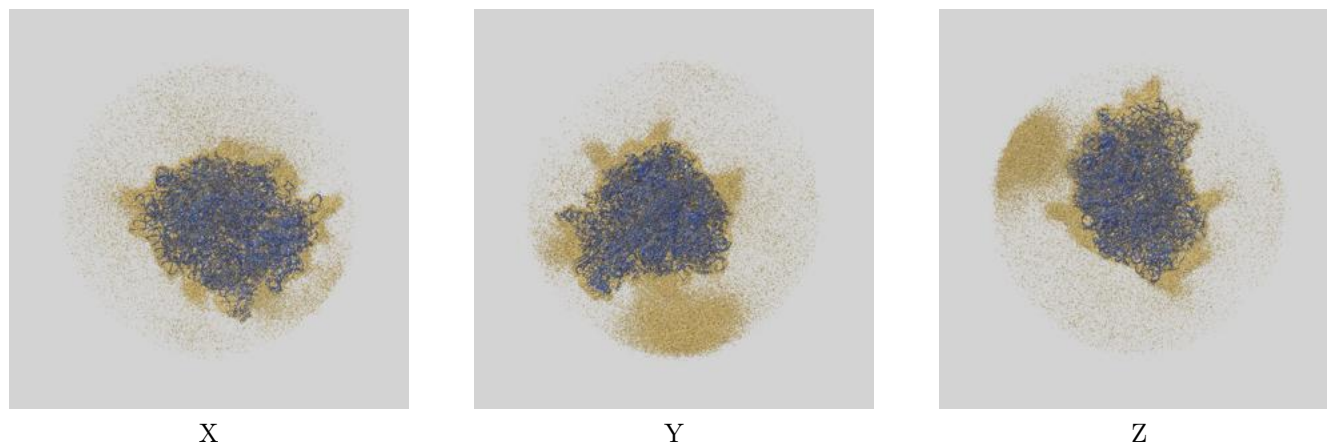
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.80	3.10	2.83
Unmasked-calculated*	3.97	8.60	4.20

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.97 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

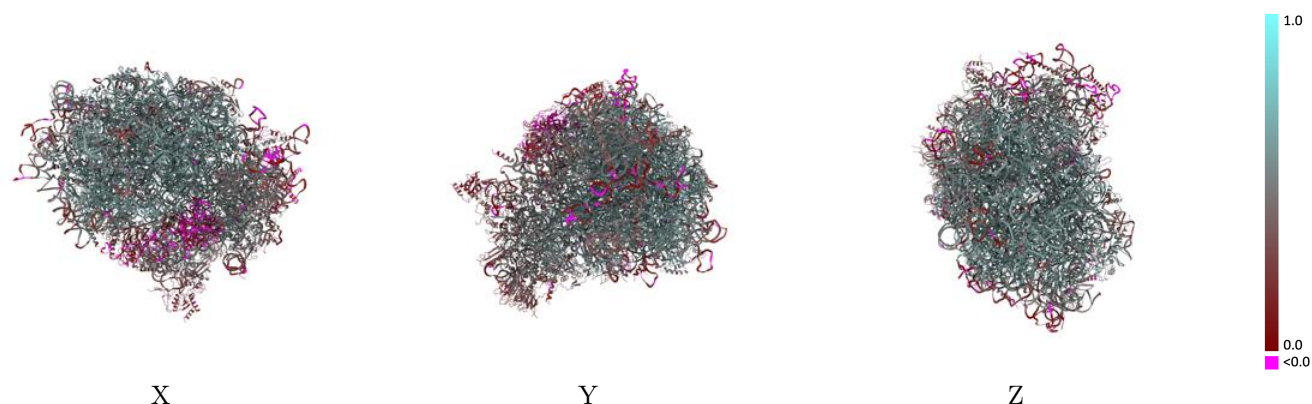
This section contains information regarding the fit between EMDB map EMD-71345 and PDB model 9P7K. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



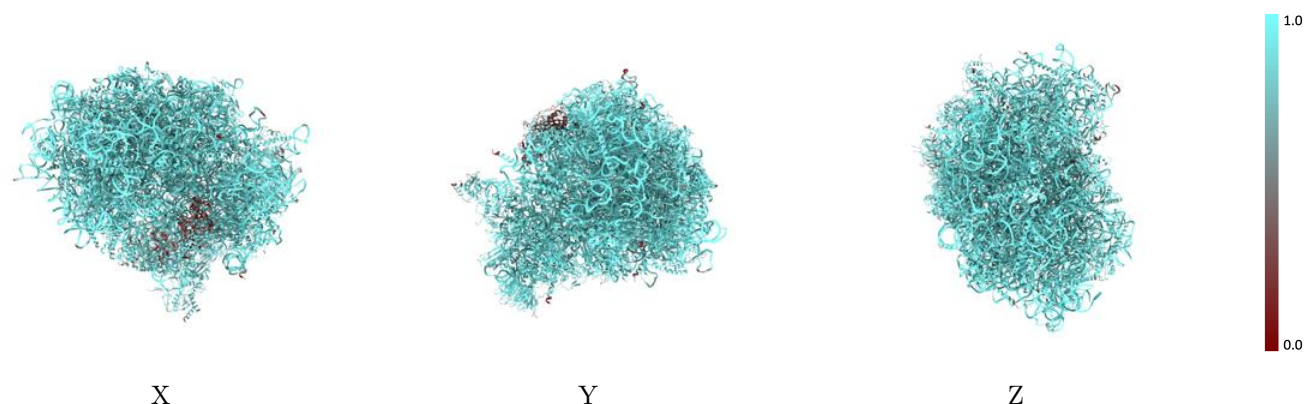
The images above show the 3D surface view of the map at the recommended contour level 0.0226 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



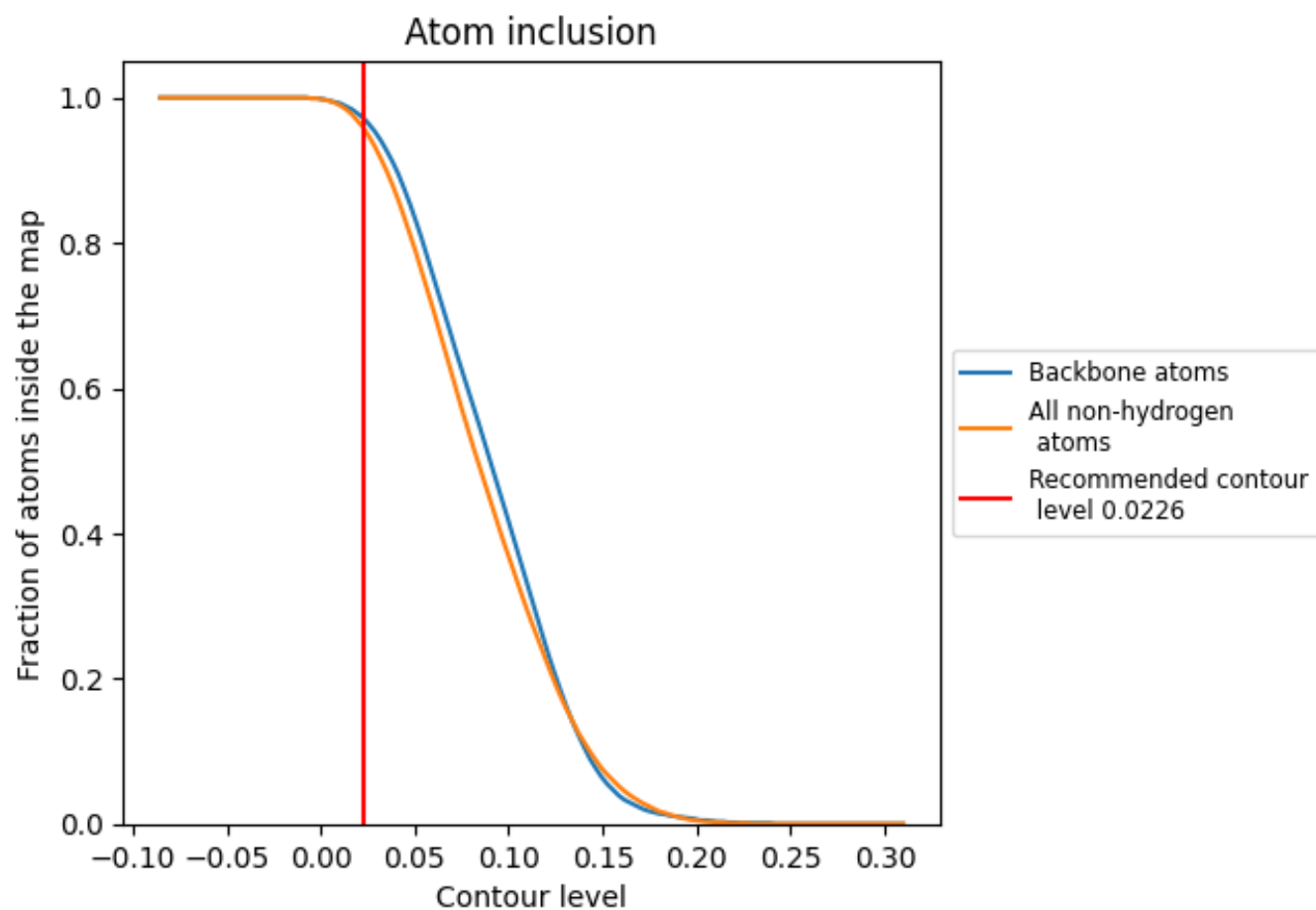
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0226).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0226) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9590	 0.4840
AT	 0.9050	 0.1160
CF	 0.4740	 0.0290
CI	 0.8410	 0.4160
Et	 0.8260	 0.1710
L5	 0.9870	 0.5240
L7	 0.9980	 0.5760
L8	 0.9900	 0.5520
LA	 0.9900	 0.5910
LB	 0.9650	 0.5630
LC	 0.9680	 0.5630
LD	 0.9580	 0.5180
LE	 0.9410	 0.4910
LF	 0.9860	 0.5640
LG	 0.9270	 0.4940
LH	 0.9740	 0.5500
LI	 0.9750	 0.5560
LJ	 0.9460	 0.4940
LL	 0.9390	 0.5330
LM	 0.9680	 0.5400
LN	 0.9960	 0.6030
LO	 0.9760	 0.5650
LP	 0.9740	 0.5750
LQ	 0.9870	 0.5880
LR	 0.9410	 0.5150
LS	 0.9840	 0.5870
LT	 0.9640	 0.5490
LU	 0.9440	 0.4710
LV	 0.9840	 0.5740
LW	 0.9030	 0.3760
LX	 0.9600	 0.5400
LY	 0.9660	 0.5510
LZ	 0.9790	 0.5420
La	 0.9850	 0.5920
Lb	 0.9290	 0.4810



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Chain	Atom inclusion	Q-score
Lc	 0.9630	 0.5310
Ld	 0.9670	 0.5510
Le	 0.9840	 0.5840
Lf	 0.9860	 0.5960
Lg	 0.9710	 0.5600
Lh	 0.9560	 0.5410
Li	 0.9740	 0.5430
Lj	 0.9910	 0.5940
Lk	 0.9350	 0.4850
Ll	 0.9840	 0.5780
Lm	 0.9660	 0.5620
Ln	 0.9860	 0.5650
Lo	 0.9800	 0.5570
Lp	 0.9740	 0.5650
Lr	 0.9810	 0.5710
Ls	 0.6300	 0.0970
Lt	 0.6060	 0.0910
Pt	 0.9890	 0.4560
S2	 0.9890	 0.4660
SA	 0.9320	 0.4530
SB	 0.9430	 0.4860
SC	 0.9660	 0.4950
SD	 0.9330	 0.3800
SE	 0.9640	 0.4460
SF	 0.9280	 0.4120
SG	 0.9180	 0.3450
SH	 0.8970	 0.3830
SI	 0.9400	 0.4680
SJ	 0.9340	 0.4340
SK	 0.9240	 0.3370
SL	 0.9380	 0.4940
SM	 0.7570	 0.1730
SN	 0.9690	 0.5230
SO	 0.9550	 0.5040
SP	 0.8970	 0.3650
SQ	 0.9250	 0.4080
SR	 0.8990	 0.3950
SS	 0.8980	 0.3940
ST	 0.9320	 0.3910
SU	 0.9060	 0.3500
SV	 0.9550	 0.4620
SW	 0.9760	 0.5180

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Chain	Atom inclusion	Q-score
SX	 0.9660	 0.5000
SY	 0.9080	 0.3660
SZ	 0.8680	 0.3750
Sa	 0.9580	 0.5070
Sb	 0.9370	 0.4610
Sc	 0.8890	 0.3780
Sd	 0.9730	 0.4520
Se	 0.9080	 0.3570
Sf	 0.8220	 0.1880
Sg	 0.8990	 0.3100