



Full wwPDB EM Validation Report ⓘ

Jun 27, 2026 – 02:00 PM EDT

PDB ID : 9P7G / pdb_00009p7g
EMDB ID : EMD-71341
Title : In situ HHT and CHX treated A-P-Z state 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2025-06-20
Resolution : 3.54 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

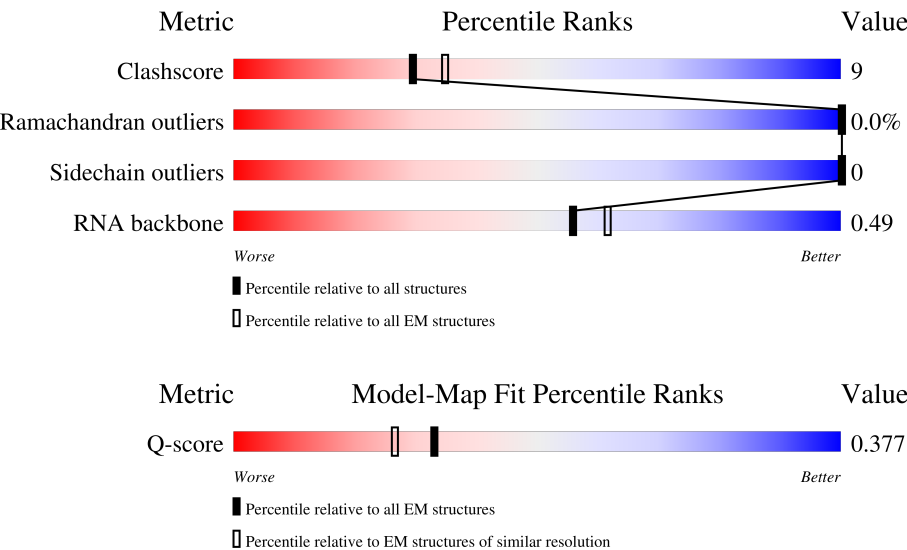
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.54 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.



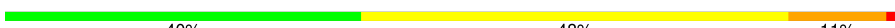
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12891 (3.04 - 4.04)

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	Zt	75	36%52%12%
2	SA	221	75%25%
3	SB	214	72%28%

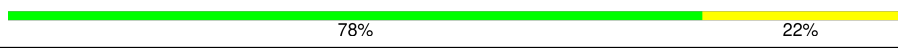
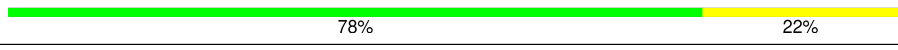
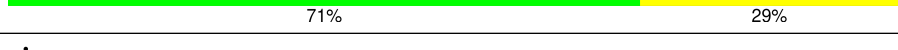
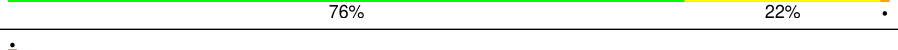
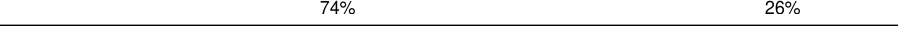
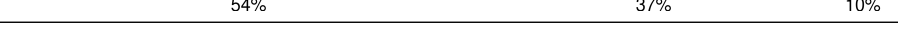
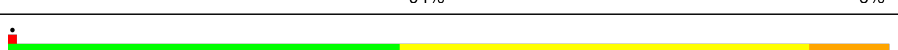
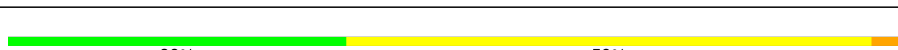
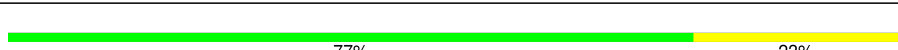
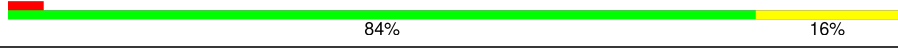
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Mol	Chain	Length	Quality of chain
4	SC	222	
5	SE	262	
6	SG	237	
7	SH	189	
8	SI	206	
9	SJ	185	
10	SL	153	
11	SN	150	
12	SO	140	
13	SV	83	
14	SW	129	
15	SX	141	
16	SY	131	
17	Sa	102	
18	Sb	83	
19	Se	58	
20	S2	1740	
21	LR	187	
22	LW	124	
23	SR	135	
24	SD	227	
25	SF	189	
26	SK	98	
27	SM	122	
28	SP	121	

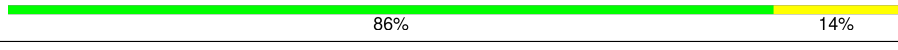
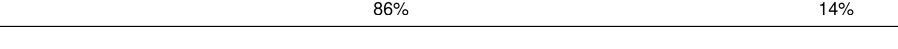
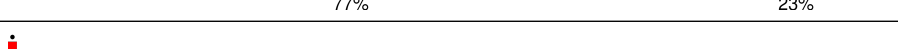
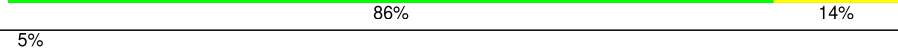
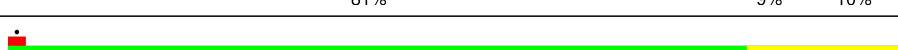
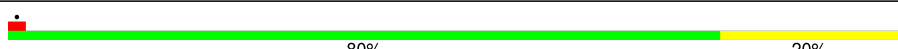
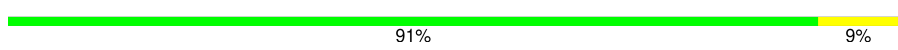
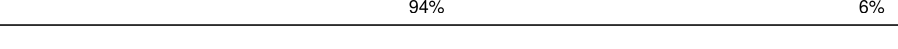
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Mol	Chain	Length	Quality of chain
29	SQ	144	
30	SS	145	
31	ST	143	
32	SU	104	
33	SZ	75	
34	Sc	64	
35	Sd	55	
36	Sf	67	
37	Sg	313	
38	At	71	
39	Pt	74	
40	CI	31	
41	L5	3655	
42	L7	120	
43	L8	156	
44	LA	248	
45	LB	402	
46	LC	368	
47	LD	293	
48	LE	250	
49	LF	225	
50	LG	241	
51	LH	190	
52	LI	213	
53	LJ	176	

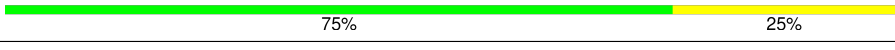
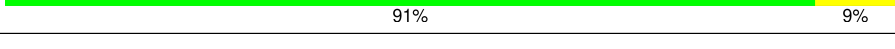
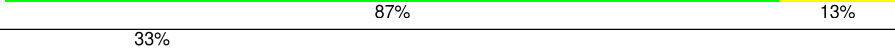
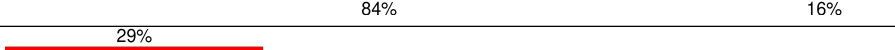
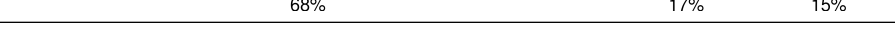
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Mol	Chain	Length	Quality of chain
54	LL	210	
55	LM	139	
56	LN	203	
57	LO	201	
58	LP	153	
59	LQ	187	
60	LS	175	
61	LT	159	
62	LU	101	
63	LV	131	
64	LX	120	
65	LY	134	
66	LZ	135	
67	La	147	
68	Lb	121	
69	Lc	98	
70	Ld	107	
71	Le	128	
72	Lf	109	
73	Lg	114	
74	Lh	122	
75	Li	102	
76	Lj	86	
77	Lk	69	
78	Ll	50	

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Mol	Chain	Length	Quality of chain
79	Lm	52	
80	Ln	24	
81	Lo	105	
82	Lp	91	
83	Lr	125	
84	Ls	196	
85	Lt	157	

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 221543 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

- Molecule 2 is a protein called 40S ribosomal protein SA.

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

- Molecule 3 is a protein called 40S ribosomal protein S3a.

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

- Molecule 4 is a protein called 40S ribosomal protein S2.

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

- Molecule 5 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 6 is a protein called 40S ribosomal protein S6.

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

- Molecule 7 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 8 is a protein called 40S ribosomal protein S8.

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

- Molecule 9 is a protein called 40S ribosomal protein S9.

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

- Molecule 10 is a protein called 40S ribosomal protein S11.

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

- Molecule 11 is a protein called 40S ribosomal protein S13.

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

- Molecule 12 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 13 is a protein called Small ribosomal subunit protein eS21.

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

- Molecule 14 is a protein called 40S ribosomal protein S15a.

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

- Molecule 15 is a protein called 40S ribosomal protein S23.

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

- Molecule 16 is a protein called 40S ribosomal protein S24.

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

- Molecule 17 is a protein called 40S ribosomal protein S26.

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

- Molecule 18 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 19 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 20 is a RNA chain called 18S rRNA [Homo sapiens].

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

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

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

- Molecule 22 is a protein called Ribosomal protein L24.

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

- Molecule 23 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 24 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 25 is a protein called 40S ribosomal protein S5.

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

- Molecule 26 is a protein called 40S ribosomal protein S10.

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

- Molecule 27 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 28 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 29 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 30 is a protein called 40S ribosomal protein S18.

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

- Molecule 31 is a protein called 40S ribosomal protein S19.

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

- Molecule 32 is a protein called 40S ribosomal protein S20.

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

- Molecule 33 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 34 is a protein called 40S ribosomal protein S28.

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

- Molecule 35 is a protein called 40S ribosomal protein S29.

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

- Molecule 36 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 37 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 38 is a RNA chain called A site tRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
38	At	71	Total	C	N	O	P	0	0
			1514	677	275	492	70		

- Molecule 39 is a RNA chain called P site tRNA [Homo sapiens].

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

- Molecule 40 is a protein called Transcription factor BTF3.

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

- Molecule 41 is a RNA chain called 28S rRNA [Homo sapiens].

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

- Molecule 42 is a RNA chain called 5S rRNA [Homo sapiens].

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

- Molecule 43 is a RNA chain called 5.8S rRNA [Homo sapiens].

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

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

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

- Molecule 45 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 46 is a protein called 60S ribosomal protein L4.

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

- Molecule 47 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 48 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 49 is a protein called 60S ribosomal protein L7.

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

- Molecule 50 is a protein called 60S ribosomal protein L7a.

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

- Molecule 51 is a protein called 60S ribosomal protein L9.

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

- Molecule 52 is a protein called Ribosomal protein uL16-like.

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

- Molecule 53 is a protein called 60S ribosomal protein L11.

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

- Molecule 54 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 55 is a protein called 60S ribosomal protein L14.

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

- Molecule 56 is a protein called 60S ribosomal protein L15.

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

- Molecule 57 is a protein called 60S ribosomal protein L13a.

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

- Molecule 58 is a protein called 60S ribosomal protein L17.

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

- Molecule 59 is a protein called 60S ribosomal protein L18.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L21.

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

- Molecule 62 is a protein called Heparin-binding protein HBp15.

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

- Molecule 63 is a protein called 60S ribosomal protein L23.

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

- Molecule 64 is a protein called 60S ribosomal protein L23a.

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

- Molecule 65 is a protein called 60S ribosomal protein L26.

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

- Molecule 66 is a protein called 60S ribosomal protein L27.

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

- Molecule 67 is a protein called 60S ribosomal protein L27a.

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

- Molecule 68 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 69 is a protein called 60S ribosomal protein L30.

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

- Molecule 70 is a protein called 60S ribosomal protein L31.

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

- Molecule 71 is a protein called 60S ribosomal protein L32.

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

- Molecule 72 is a protein called 60S ribosomal protein L35a.

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

- Molecule 73 is a protein called 60S ribosomal protein L34.

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

- Molecule 74 is a protein called 60S ribosomal protein L35.

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

- Molecule 75 is a protein called 60S ribosomal protein L36.

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

- Molecule 76 is a protein called 60S ribosomal protein L37.

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

- Molecule 77 is a protein called 60S ribosomal protein L38.

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

- Molecule 78 is a protein called 60S ribosomal protein L39.

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

- Molecule 79 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 80 is a protein called 60S ribosomal protein L41.

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

- Molecule 81 is a protein called 60S ribosomal protein L36a.

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

- Molecule 82 is a protein called 60S ribosomal protein L37a.

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

- Molecule 83 is a protein called 60S ribosomal protein L28.

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

- Molecule 84 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 85 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
86	SG	1	Total	Mg	0
			1	1	
86	S2	27	Total	Mg	0
			27	27	
86	SS	1	Total	Mg	0
			1	1	
86	L5	177	Total	Mg	0
			177	177	
86	L7	3	Total	Mg	0
			3	3	
86	L8	4	Total	Mg	0
			4	4	
86	LA	1	Total	Mg	0
			1	1	
86	LB	2	Total	Mg	0
			2	2	
86	LV	1	Total	Mg	0
			1	1	
86	Le	2	Total	Mg	0
			2	2	

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

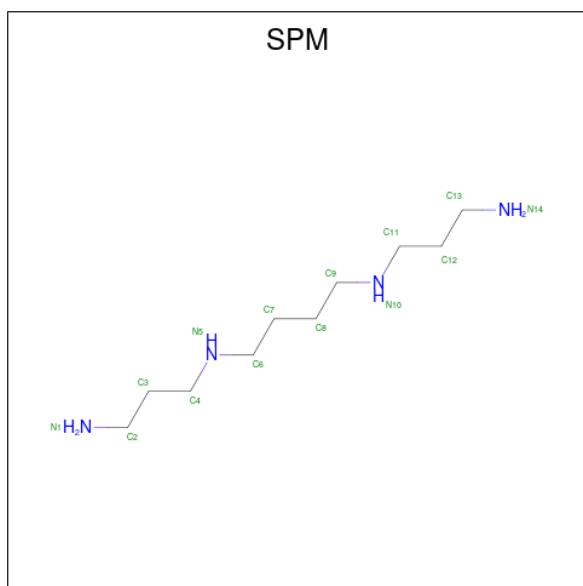
Mol	Chain	Residues	Atoms		AltConf
87	Sa	1	Total	Zn	0
			1	1	
87	Lg	1	Total	Zn	0
			1	1	

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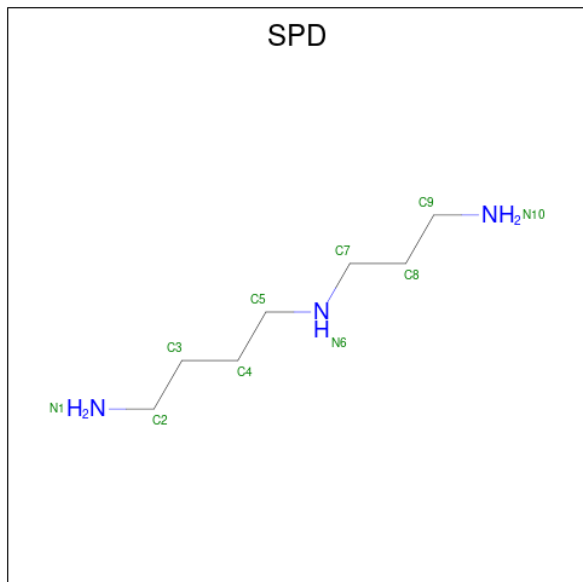
Mol	Chain	Residues	Atoms		AltConf
87	Lj	1	Total	Zn	0
			1	1	
87	Lm	1	Total	Zn	0
			1	1	
87	Lo	1	Total	Zn	0
			1	1	
87	Lp	1	Total	Zn	0
			1	1	

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



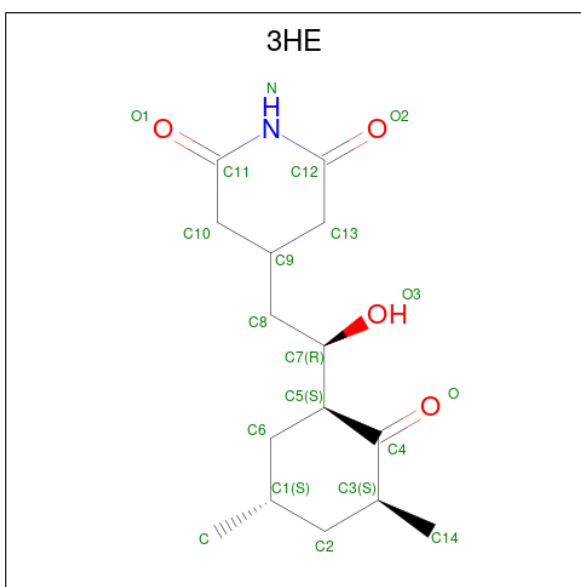
Mol	Chain	Residues	Atoms			AltConf
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	
88	L5	1	Total	C	N	0
			14	10	4	

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



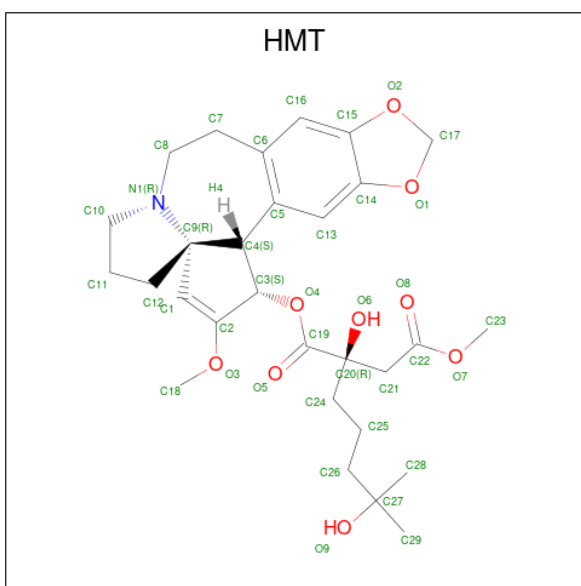
Mol	Chain	Residues	Atoms			AltConf
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L5	1	Total	C	N	0
			10	7	3	
89	L8	1	Total	C	N	0
			10	7	3	

- Molecule 90 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: $C_{15}H_{23}NO_4$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 91 is (3beta)-O 3 -[(2R)-2,6-dihydroxy-2-(2-methoxy-2-oxoethyl)-6-methylheptanoyl]cephalotaxine (CCD ID: HMT) (formula: $C_{29}H_{39}NO_9$) (labeled as "Ligand of Interest" by depositor).

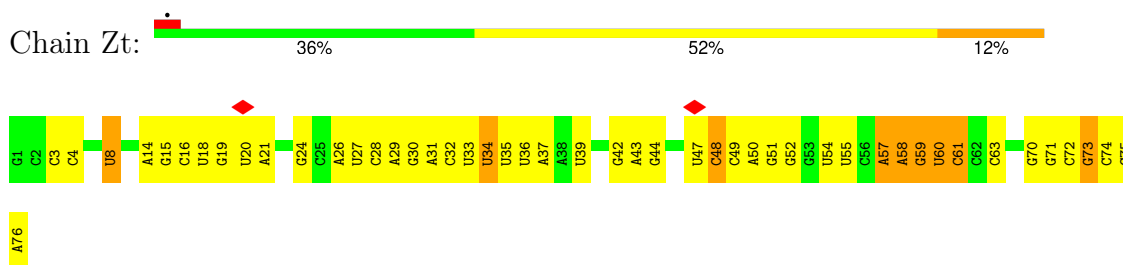


Mol	Chain	Residues	Atoms				AltConf
91	L5	1	Total	C	N	O	0
			39	29	1	9	

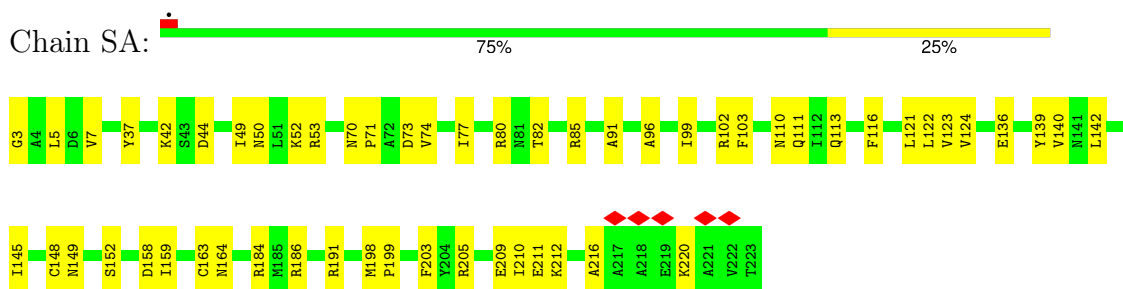
3 Residue-property plots

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: Z site tRNA [Homo sapiens]



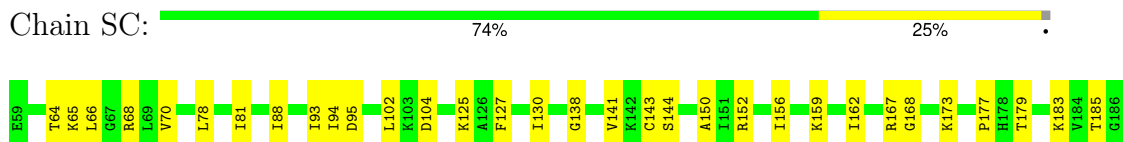
- Molecule 2: 40S ribosomal protein SA



- Molecule 3: 40S ribosomal protein S3a



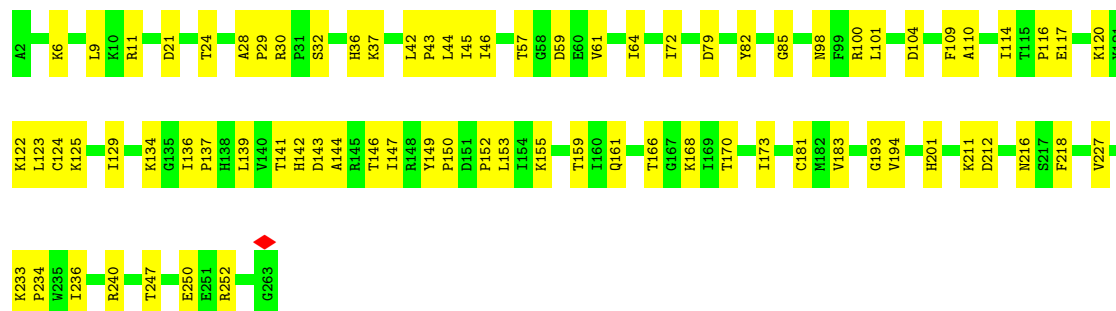
- Molecule 4: 40S ribosomal protein S2





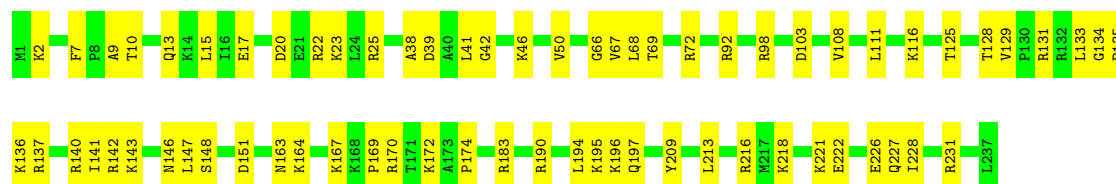
- Molecule 5: Small ribosomal subunit protein eS4, X isoform

Chain SE: 71% 29%



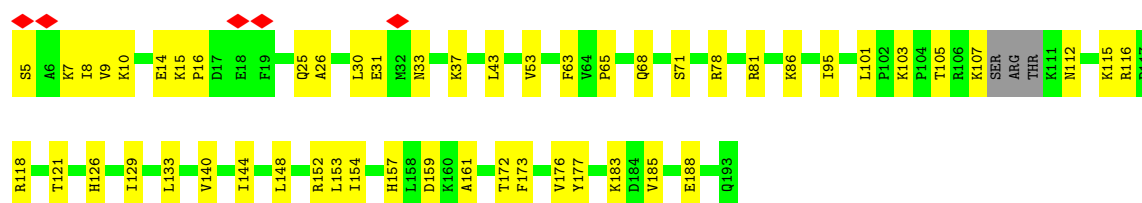
- Molecule 6: 40S ribosomal protein S6

Chain SG: 71% 29%



- Molecule 7: Small ribosomal subunit protein eS7

Chain SH: 71% 28%



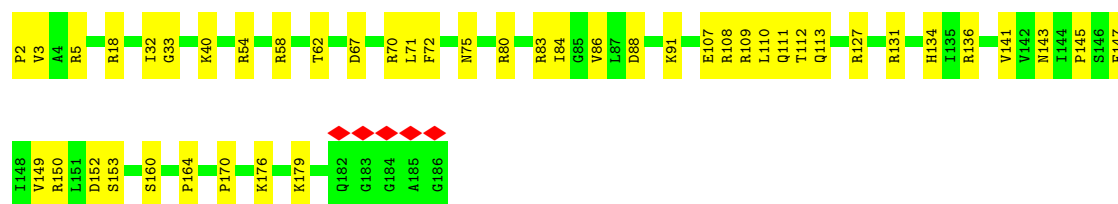
- Molecule 8: 40S ribosomal protein S8

Chain SI: 78% 22%



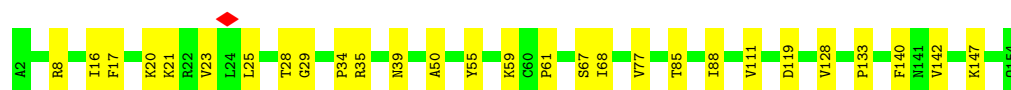
- Molecule 9: 40S ribosomal protein S9

Chain SJ:  76% 24%



- Molecule 10: 40S ribosomal protein S11

Chain SL:  82% 18%



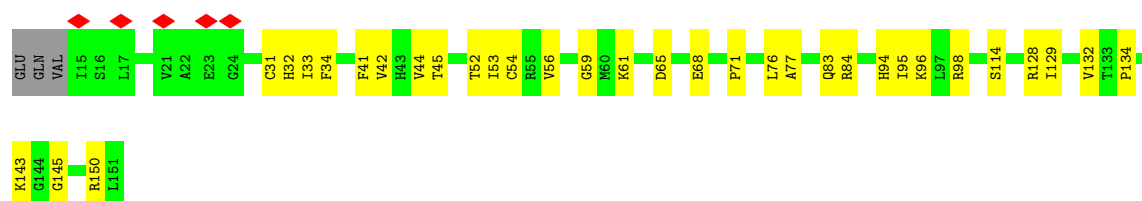
- Molecule 11: 40S ribosomal protein S13

Chain SN:  78% 22%



- Molecule 12: Small ribosomal subunit protein uS11

Chain SO:  74% 24%



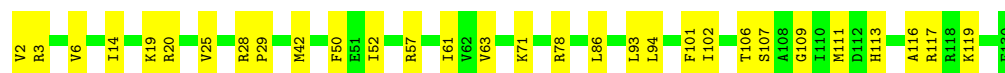
- Molecule 13: Small ribosomal subunit protein eS21

Chain SV:  82% 18%



- Molecule 14: 40S ribosomal protein S15a

Chain SW:  77% 23%



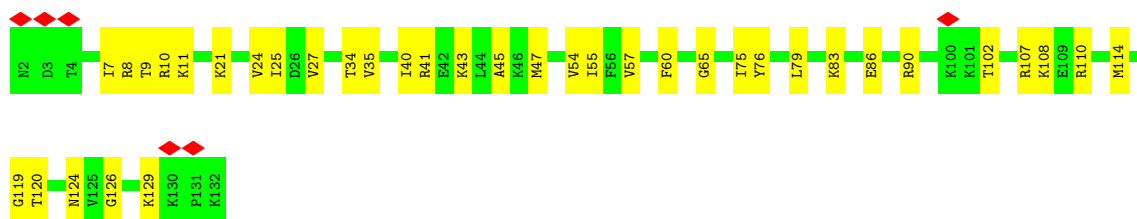
- Molecule 15: 40S ribosomal protein S23

Chain SX:  84% 16%



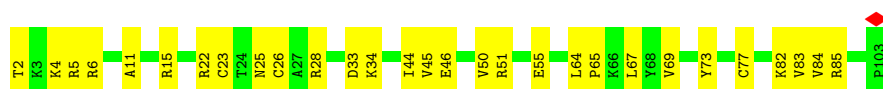
- Molecule 16: 40S ribosomal protein S24

Chain SY:  5% 72% 28%



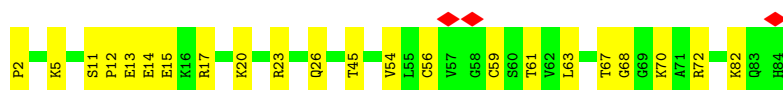
- Molecule 17: 40S ribosomal protein S26

Chain Sa:  72% 28%



- Molecule 18: Small ribosomal subunit protein eS27

Chain Sb:  73% 27%

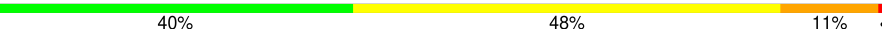


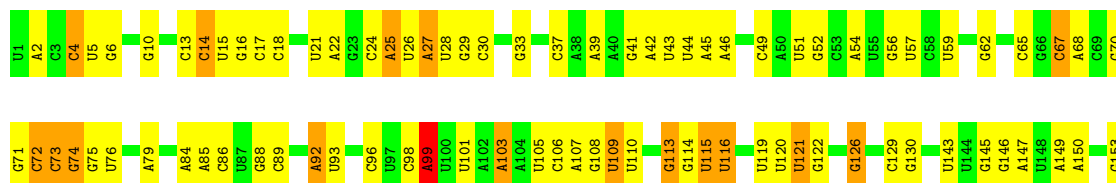
- Molecule 19: Small ribosomal subunit protein eS30

Chain Se:  74% 26%

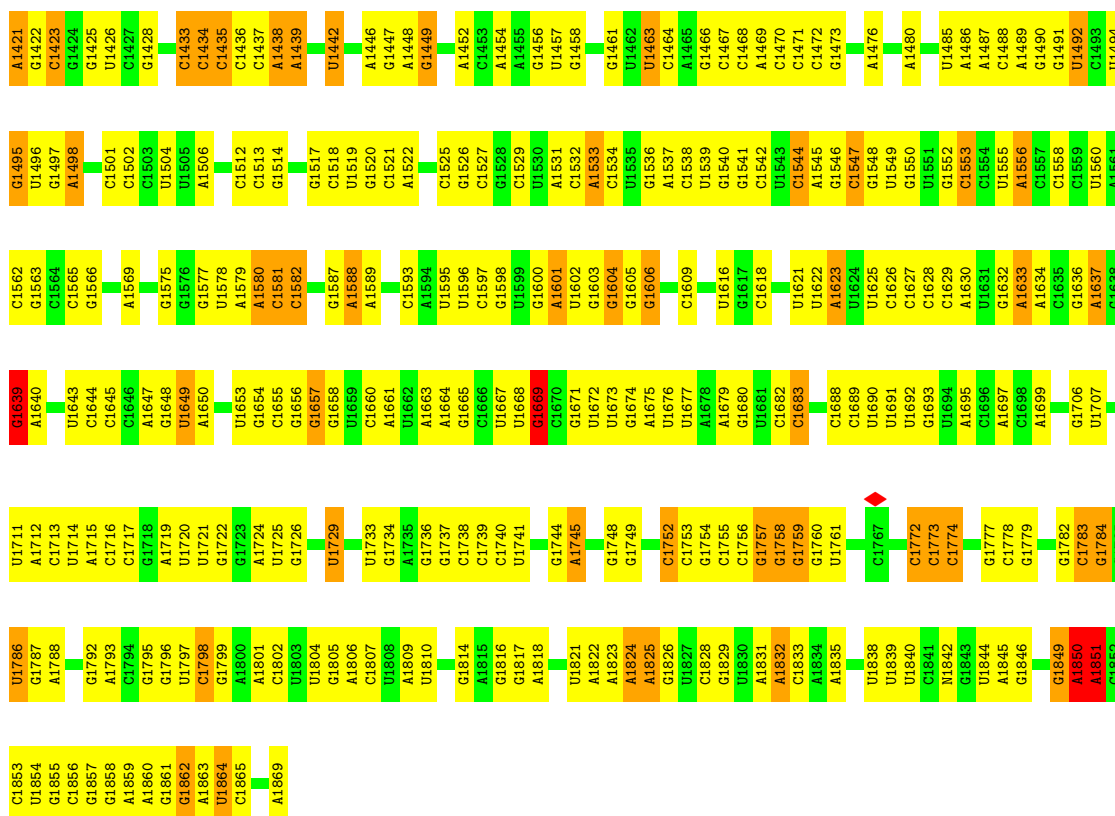


- Molecule 20: 18S rRNA [Homo sapiens]

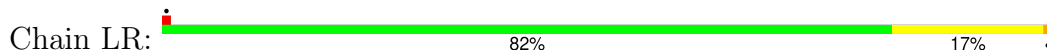
Chain S2:  40% 48% 11%



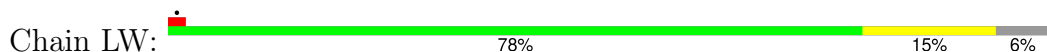




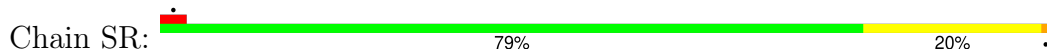
- Molecule 21: 60S ribosomal protein L19



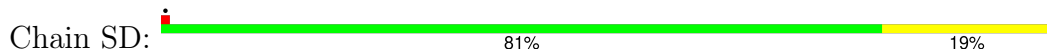
- Molecule 22: Ribosomal protein L24

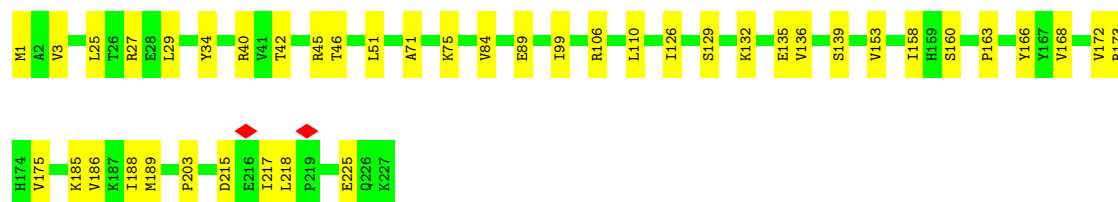


- Molecule 23: Small ribosomal subunit protein eS17



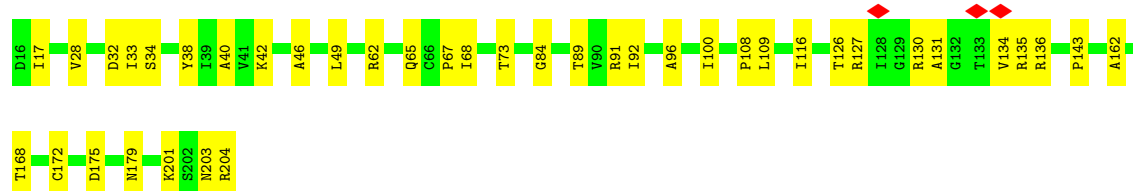
- Molecule 24: Small ribosomal subunit protein uS3





- Molecule 25: 40S ribosomal protein S5

Chain SF: 79% 21%



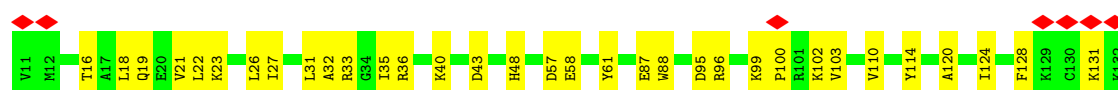
- Molecule 26: 40S ribosomal protein S10

Chain SK: 83% 17%



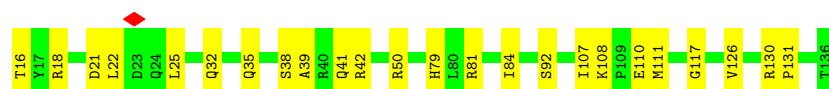
- Molecule 27: Small ribosomal subunit protein eS12

Chain SM: 6% 73% 27%



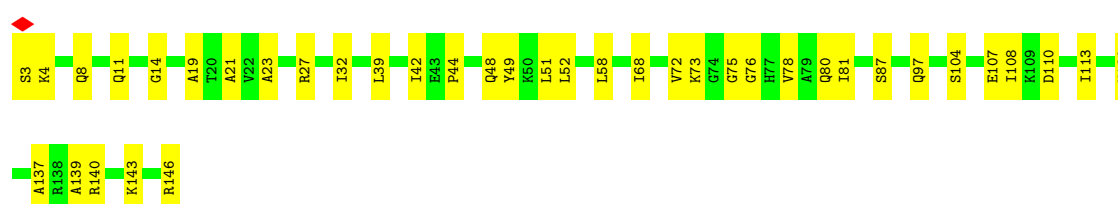
- Molecule 28: Small ribosomal subunit protein uS19

Chain SP: 80% 20%

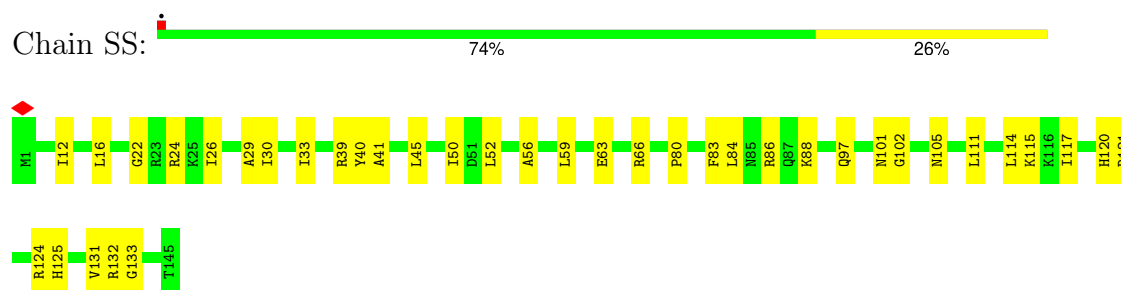


- Molecule 29: Small ribosomal subunit protein uS9

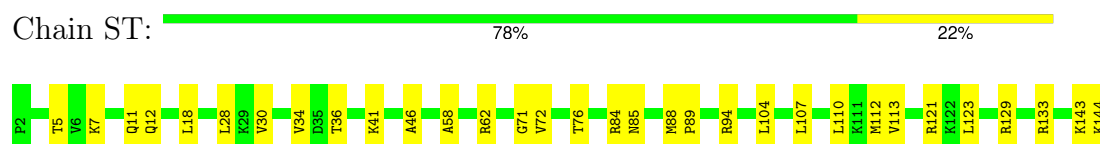
Chain SQ: 73% 27%



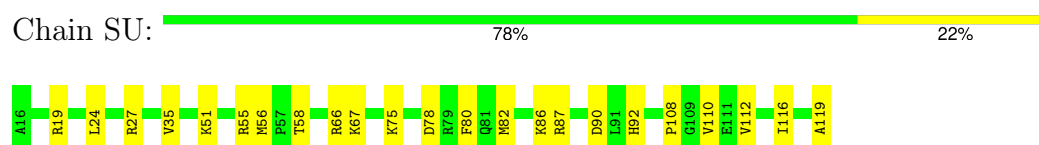
- Molecule 30: 40S ribosomal protein S18



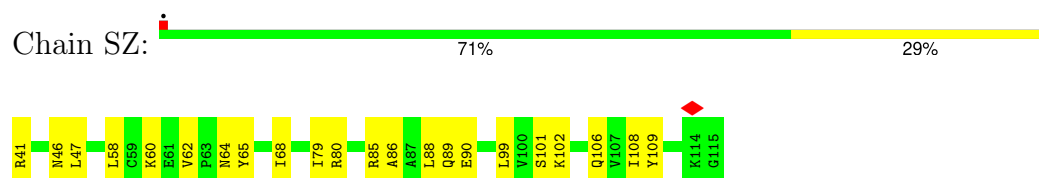
- Molecule 31: 40S ribosomal protein S19



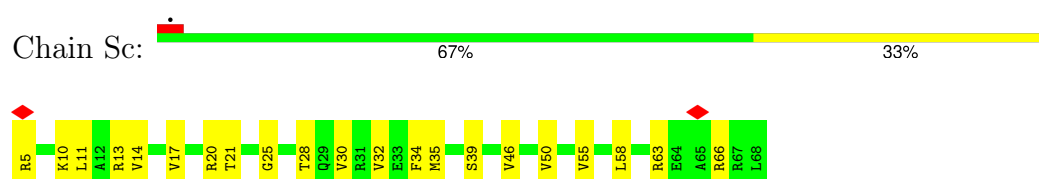
- Molecule 32: 40S ribosomal protein S20



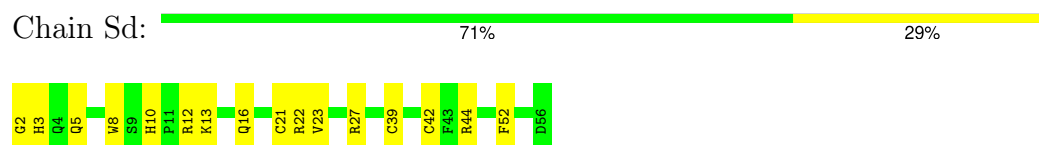
- Molecule 33: Small ribosomal subunit protein eS25



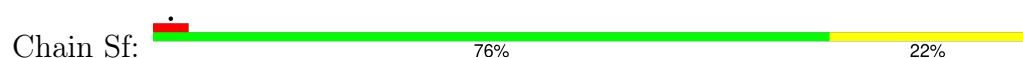
- Molecule 34: 40S ribosomal protein S28



- Molecule 35: 40S ribosomal protein S29



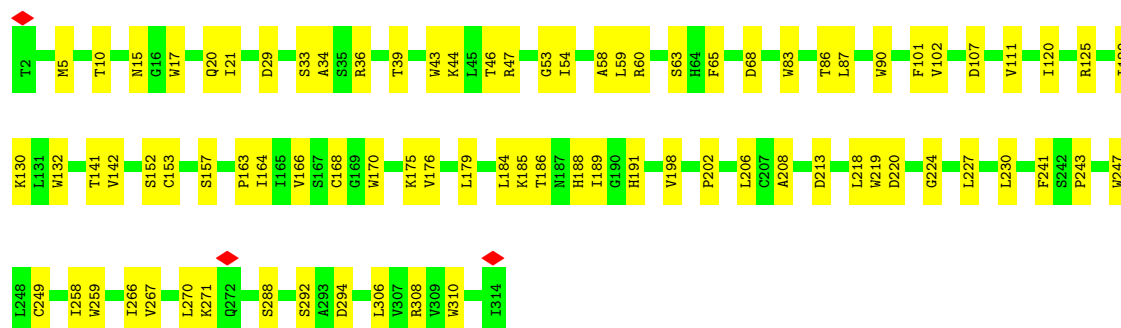
- Molecule 36: Ubiquitin-40S ribosomal protein S27a





- Molecule 37: Receptor of activated protein C kinase 1

Chain Sg: 74% 26%



- Molecule 38: A site tRNA [Homo sapiens]

Chain At: 54% 37% 10%



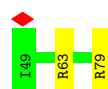
- Molecule 39: P site tRNA [Homo sapiens]

Chain Pt: 43% 47% 9%



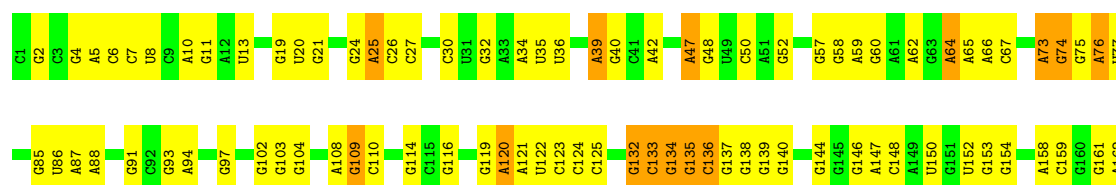
- Molecule 40: Transcription factor BTF3

Chain CI: 94% 6%



- Molecule 41: 28S rRNA [Homo sapiens]

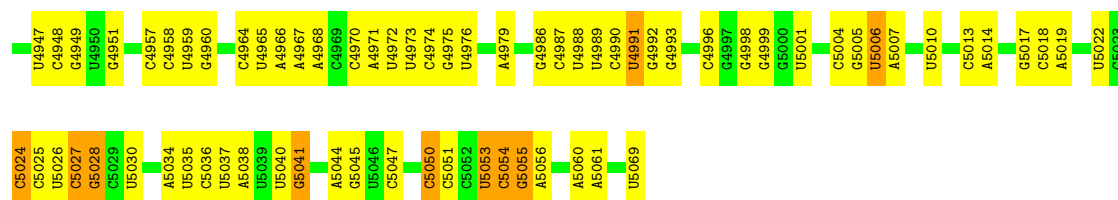
Chain L5: 44% 46% 9%



G1670	U1582	G1502	C1409	A1337	C1272	C1180	C972	G908	C691	C503	U424	C249	A163
U1571	A1583	A1503	U1410	G1338	G1273	C1181		A909	A692	G504	U425		G164
C1674	G1584	G1504	C1412	C1339	C1411	C1182	C977	G910	C696	G505	A426	C255	A165
C1675		C1505	C1413	U1341	G1276	C1183	U950	U911	C697	C506	A427	G256	G169
C1676	G1587	G1506	C1414	A1342	C1277	G1189	C981	G912					
U1677	U1591	C1507	G1415	A1343	C1278		U982	U913	C698	A509	G431	C260	
G1680	U1594	A1508	G1416	C1344	A1279	C1193	C983	U914	C699	U510	A432	G261	C172
U1683	G1595	C1509	C1417	A1345	G1280	G1194	C984	A915	G700	C173	U433	G262	
A1684	U1596	G1510		C1346	G1281	G1195	C985	C916	G701	C174	G263	C264	C175
G1685	G1597	U1511	A1420	U1347	G1282	G1196	C986	A917	U702	C175	C264	C176	C176
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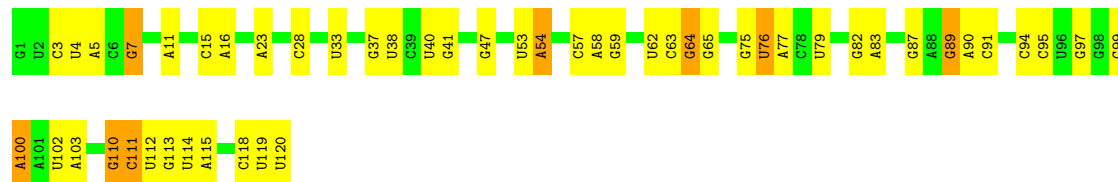
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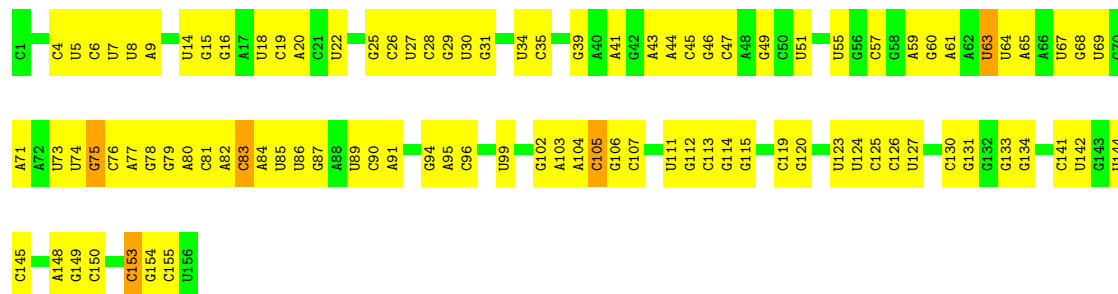
• Molecule 42: 5S rRNA [Homo sapiens]

Chain L7: 58% 35% 7%



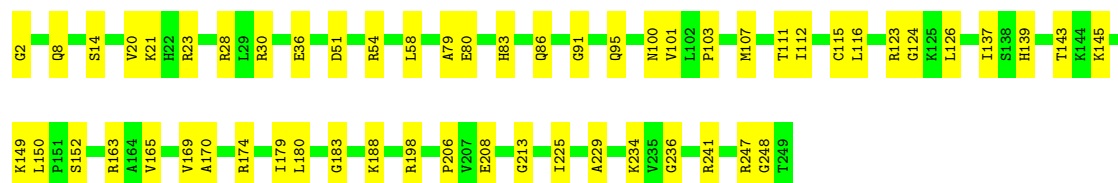
• Molecule 43: 5.8S rRNA [Homo sapiens]

Chain L8: 38% 59% 3%



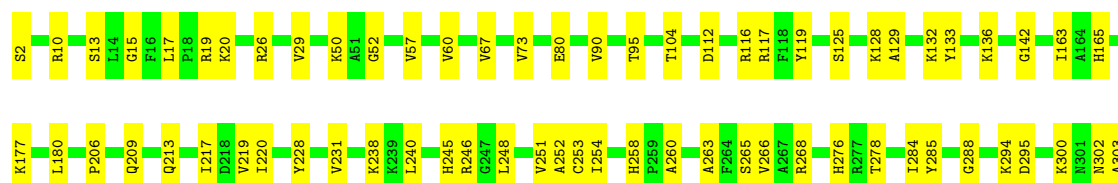
• Molecule 44: 60S ribosomal protein L8

Chain LA: 77% 23% 0%



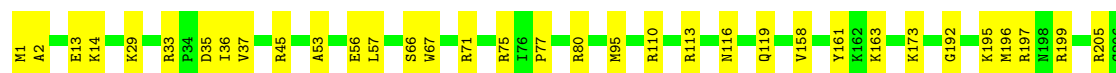
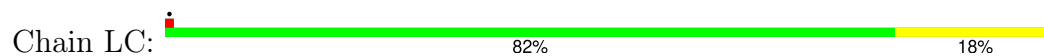
• Molecule 45: Large ribosomal subunit protein uL3

Chain LB: 80% 20% 0%

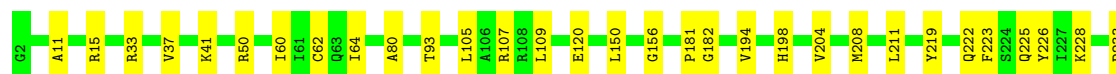
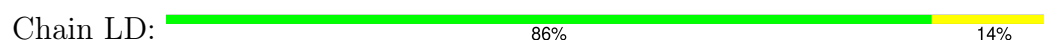




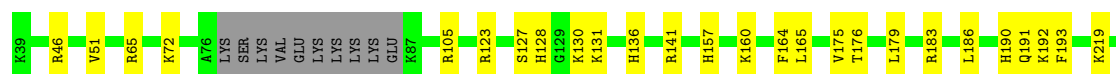
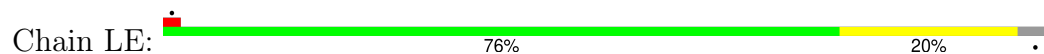
- Molecule 46: 60S ribosomal protein L4



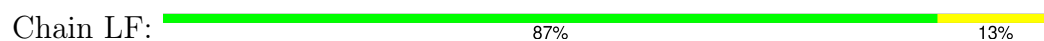
- Molecule 47: Large ribosomal subunit protein uL18



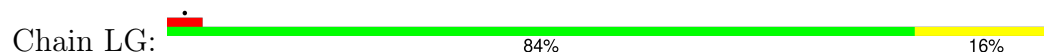
- Molecule 48: Large ribosomal subunit protein eL6

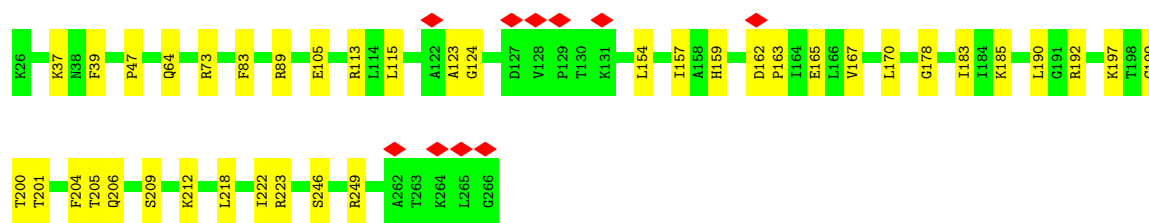


- Molecule 49: 60S ribosomal protein L7



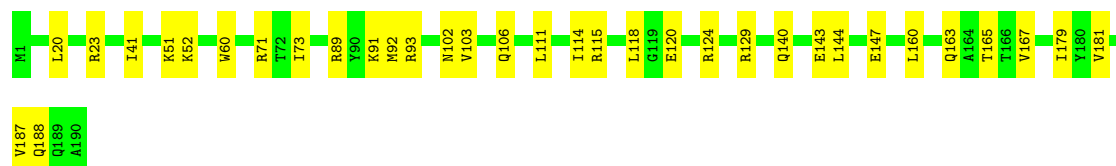
- Molecule 50: 60S ribosomal protein L7a





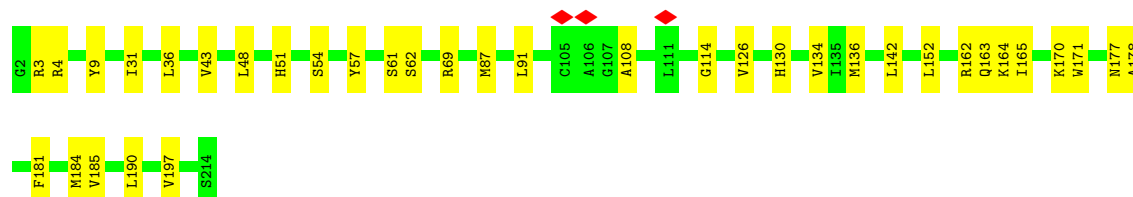
- Molecule 51: 60S ribosomal protein L9

Chain LH: 82% 18%



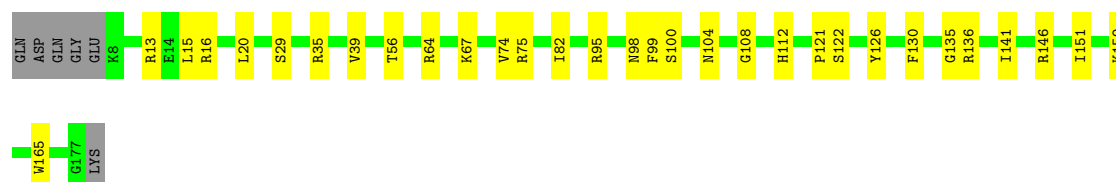
- Molecule 52: Ribosomal protein uL16-like

Chain LI: 83% 17%



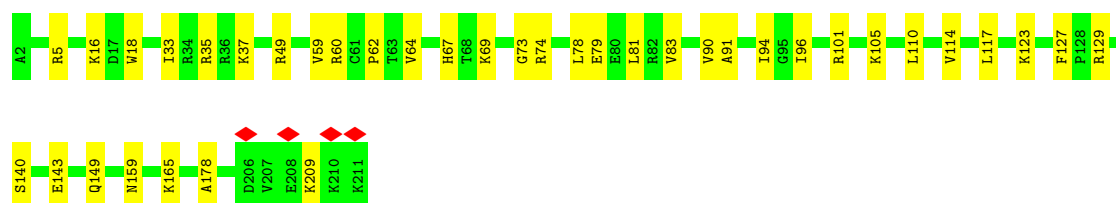
- Molecule 53: 60S ribosomal protein L11

Chain LJ: 79% 18%



- Molecule 54: Large ribosomal subunit protein eL13

Chain LL: 82% 18%



- Molecule 55: 60S ribosomal protein L14

Chain LM:  86% 14%



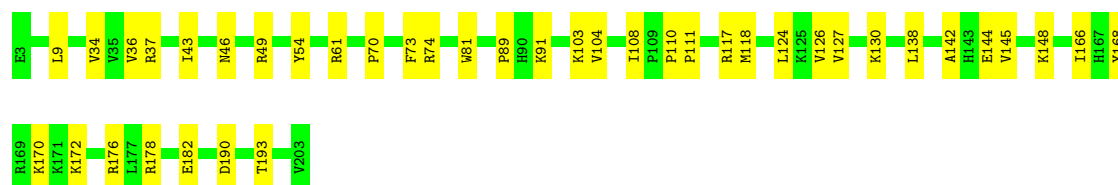
- Molecule 56: 60S ribosomal protein L15

Chain LN:  86% 14%



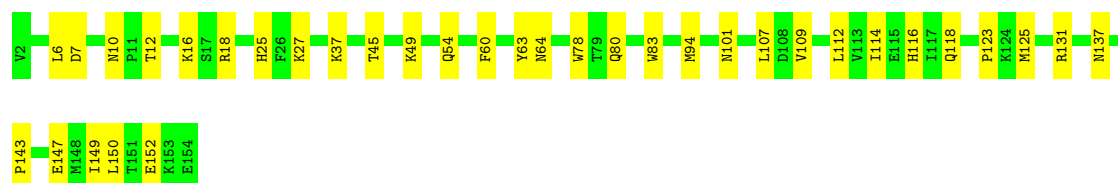
- Molecule 57: 60S ribosomal protein L13a

Chain LO:  80% 20%



- Molecule 58: 60S ribosomal protein L17

Chain LP:  77% 23%



- Molecule 59: 60S ribosomal protein L18

Chain LQ:  89% 11%



- Molecule 60: 60S ribosomal protein L18a

Chain LS:  87% 13%

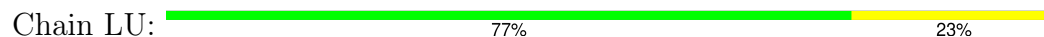


- Molecule 61: 60S ribosomal protein L21

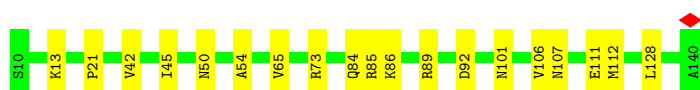
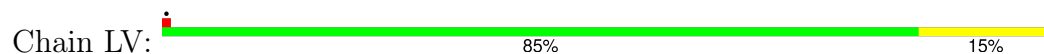
Chain LT:  89% 11%



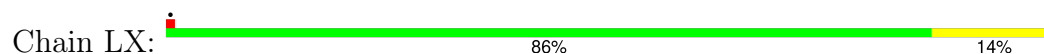
- Molecule 62: Heparin-binding protein HBp15



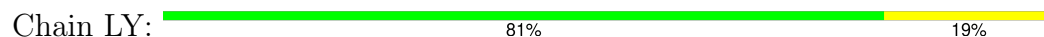
- Molecule 63: 60S ribosomal protein L23



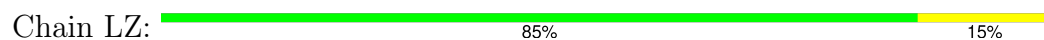
- Molecule 64: 60S ribosomal protein L23a



- Molecule 65: 60S ribosomal protein L26



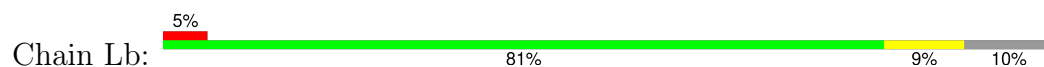
- Molecule 66: 60S ribosomal protein L27

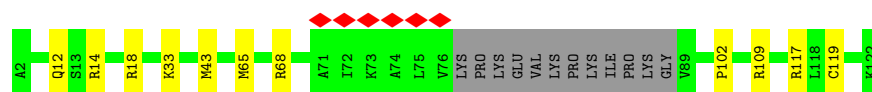


- Molecule 67: 60S ribosomal protein L27a

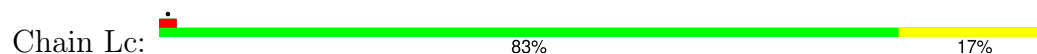


- Molecule 68: Large ribosomal subunit protein eL29

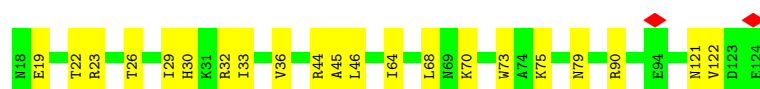
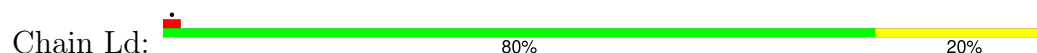




- Molecule 69: 60S ribosomal protein L30



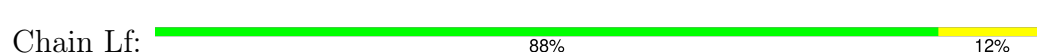
- Molecule 70: 60S ribosomal protein L31



- Molecule 71: 60S ribosomal protein L32



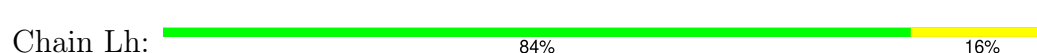
- Molecule 72: 60S ribosomal protein L35a



- Molecule 73: 60S ribosomal protein L34



- Molecule 74: 60S ribosomal protein L35



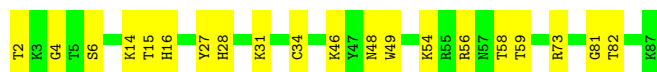
- Molecule 75: 60S ribosomal protein L36





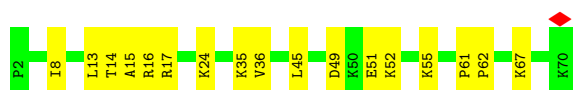
- Molecule 76: 60S ribosomal protein L37

Chain Lj: 77% 23%



- Molecule 77: 60S ribosomal protein L38

Chain Lk: 75% 25%



- Molecule 78: 60S ribosomal protein L39

Chain Ll: 82% 18%



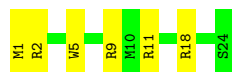
- Molecule 79: Large ribosomal subunit protein eL40

Chain Lm: 85% 15%



- Molecule 80: 60S ribosomal protein L41

Chain Ln: 75% 25%



- Molecule 81: 60S ribosomal protein L36a

Chain Lo: 86% 14%



- Molecule 82: 60S ribosomal protein L37a

Chain Lp: 91% 9%



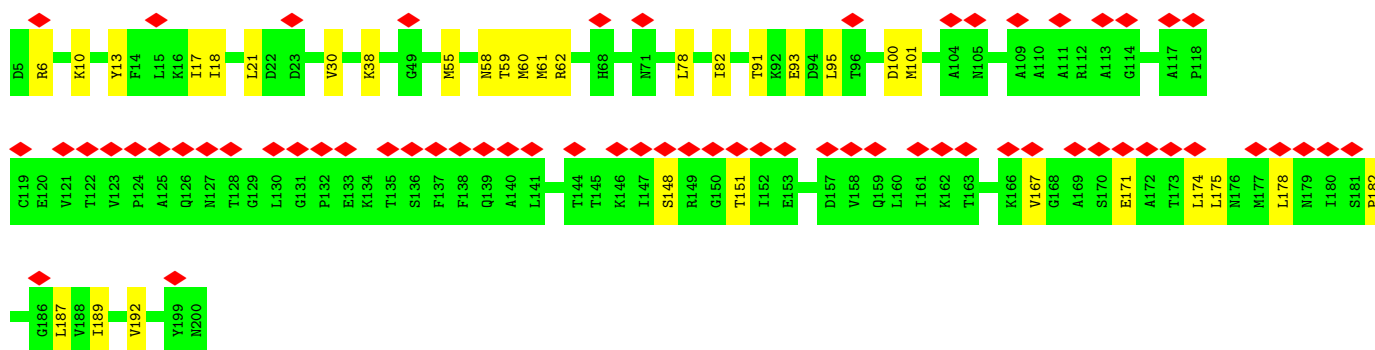
- Molecule 83: 60S ribosomal protein L28

Chain Lr: 87% 13%



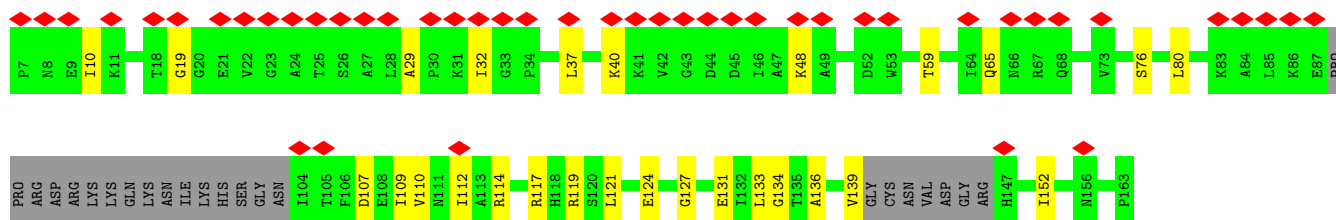
- Molecule 84: 60S acidic ribosomal protein P0

Chain Ls: 33% 84% 16%



- Molecule 85: Large ribosomal subunit protein uL11

Chain Lt: 29% 68% 17% 15%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15150	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.584	Depositor
Minimum map value	-0.226	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.0764	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: 1MA, SPD, SPM, MG, OMU, ZN, HMT, 3HE, UY1, B8N, OMG, 4AC, 6MZ, MA6, UR3, PSU, 5MC, G7M, OMC, 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	Zt	0.13	0/1779	0.29	0/2771
2	SA	0.21	0/1778	0.43	0/2416
3	SB	0.14	0/1765	0.33	0/2362
4	SC	0.17	0/1744	0.37	0/2357
5	SE	0.15	0/2118	0.35	0/2849
6	SG	0.15	0/1946	0.34	0/2590
7	SH	0.16	0/1519	0.40	0/2033
8	SI	0.17	0/1715	0.37	0/2287
9	SJ	0.15	0/1550	0.35	0/2069
10	SL	0.14	0/1268	0.31	0/1696
11	SN	0.14	0/1232	0.28	0/1656
12	SO	0.17	0/1037	0.36	0/1391
13	SV	0.14	0/643	0.32	0/860
14	SW	0.18	0/1051	0.34	0/1406
15	SX	0.18	0/1116	0.36	0/1490
16	SY	0.18	0/1083	0.41	0/1438
17	Sa	0.17	0/836	0.34	0/1121
18	Sb	0.16	0/665	0.41	0/891
19	Se	0.14	0/465	0.38	0/612
20	S2	0.19	0/39756	0.28	2/61939 (0.0%)
21	LR	0.23	0/1582	0.42	0/2091
22	LW	0.15	0/959	0.29	0/1270
23	SR	0.23	0/1105	0.49	0/1484
24	SD	0.15	0/1793	0.34	0/2414
25	SF	0.15	0/1516	0.33	0/2037
26	SK	0.16	0/851	0.39	0/1147
27	SM	0.13	0/950	0.35	0/1275
28	SP	0.14	0/1003	0.35	0/1342
29	SQ	0.17	0/1160	0.37	0/1553
30	SS	0.17	0/1216	0.35	0/1628
31	ST	0.14	0/1131	0.31	0/1515

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	SU	0.15	0/831	0.36	0/1115
33	SZ	0.17	0/604	0.44	0/810
34	Sc	0.13	0/508	0.30	0/680
35	Sd	0.15	0/470	0.31	0/623
36	Sf	0.20	0/560	0.56	1/745 (0.1%)
37	Sg	0.15	0/2493	0.37	0/3394
38	At	0.12	0/1692	0.22	0/2634
39	Pt	0.13	0/1761	0.24	0/2741
40	CI	0.13	0/247	0.31	0/323
41	L5	0.20	0/85098	0.28	0/132762
42	L7	0.18	0/2861	0.24	0/4459
43	L8	0.19	0/3631	0.29	0/5657
44	LA	0.19	0/1936	0.35	0/2596
45	LB	0.18	0/3306	0.33	0/4424
46	LC	0.18	0/2981	0.32	0/4002
47	LD	0.16	0/2428	0.30	0/3252
48	LE	0.17	0/1973	0.39	0/2645
49	LF	0.19	0/1905	0.32	0/2539
50	LG	0.17	0/1960	0.36	0/2637
51	LH	0.17	0/1537	0.33	0/2066
52	LI	0.17	0/1751	0.30	0/2340
53	LJ	0.16	0/1385	0.35	0/1852
54	LL	0.17	0/1732	0.30	0/2315
55	LM	0.19	0/1161	0.34	0/1554
56	LN	0.19	0/1746	0.32	0/2338
57	LO	0.18	0/1682	0.32	0/2250
58	LP	0.18	0/1268	0.32	0/1701
59	LQ	0.18	0/1537	0.29	0/2052
60	LS	0.18	0/1493	0.30	0/2003
61	LT	0.17	0/1326	0.30	0/1770
62	LU	0.17	0/839	0.43	0/1126
63	LV	0.18	0/993	0.32	0/1332
64	LX	0.15	0/1002	0.28	0/1345
65	LY	0.16	0/1132	0.30	0/1504
66	LZ	0.16	0/1130	0.33	0/1507
67	La	0.17	0/1191	0.28	0/1591
68	Lb	0.16	0/889	0.35	0/1175
69	Lc	0.17	0/774	0.35	0/1038
70	Ld	0.18	0/903	0.34	0/1216
71	Le	0.17	0/1071	0.29	0/1429
72	Lf	0.18	0/895	0.33	0/1198
73	Lg	0.17	0/916	0.30	0/1220
74	Lh	0.15	0/1023	0.30	0/1351

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Li	0.16	0/843	0.29	0/1115
76	Lj	0.18	0/720	0.32	0/952
77	Lk	0.16	0/575	0.34	0/761
78	Ll	0.17	0/454	0.26	0/599
79	Lm	0.17	0/435	0.36	0/575
80	Ln	0.14	0/231	0.25	0/294
81	Lo	0.18	0/876	0.32	0/1156
82	Lp	0.17	0/718	0.33	0/953
83	Lr	0.17	0/1017	0.29	0/1364
84	Ls	0.12	0/1519	0.34	0/2052
85	Lt	0.17	0/1009	0.52	0/1363
All	All	0.18	0/233350	0.31	3/342485 (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
23	SR	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	S2	1669	G	OP1-P-O3'	-9.12	80.64	108.00
20	S2	1669	G	OP2-P-O3'	-7.84	84.47	108.00
36	Sf	141	CYS	CA-CB-SG	5.81	127.76	114.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	SR	78	ARG	Sidechain

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	Zt	1593	0	809	25	0
2	SA	1741	0	1744	41	0
3	SB	1738	0	1809	44	0
4	SC	1707	0	1791	34	0
5	SE	2076	0	2177	56	0
6	SG	1923	0	2089	56	0
7	SH	1497	0	1590	35	0
8	SI	1686	0	1772	39	0
9	SJ	1525	0	1640	31	0
10	SL	1247	0	1323	20	0
11	SN	1208	0	1294	23	0
12	SO	1024	0	1050	23	0
13	SV	636	0	637	12	0
14	SW	1034	0	1080	25	0
15	SX	1098	0	1167	16	0
16	SY	1065	0	1142	30	0
17	Sa	821	0	870	20	0
18	Sb	651	0	670	15	0
19	Se	459	0	503	12	0
20	S2	36952	0	18678	736	0
21	LR	1566	0	1729	26	0
22	LW	945	0	1003	14	0
23	SR	1090	0	1149	20	0
24	SD	1765	0	1865	29	0
25	SF	1495	0	1549	28	0
26	SK	827	0	854	10	0
27	SM	940	0	965	21	0
28	SP	985	0	1031	17	0
29	SQ	1142	0	1213	29	0
30	SS	1198	0	1261	30	0
31	ST	1112	0	1146	25	0
32	SU	821	0	883	16	0
33	SZ	598	0	656	17	0
34	Sc	506	0	536	16	0
35	Sd	459	0	449	14	0
36	Sf	548	0	551	16	0
37	Sg	2436	0	2391	50	0
38	At	1514	0	770	21	0
39	Pt	1576	0	803	30	0
40	CI	247	0	283	2	0
41	L5	78444	0	39718	1374	0
42	L7	2561	0	1295	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	L8	3315	0	1685	71	0
44	LA	1898	0	1993	44	0
45	LB	3238	0	3376	61	0
46	LC	2927	0	3104	49	0
47	LD	2382	0	2410	29	0
48	LE	1935	0	2096	43	0
49	LF	1870	0	1996	26	0
50	LG	1927	0	2074	28	0
51	LH	1518	0	1601	26	0
52	LI	1711	0	1749	25	0
53	LJ	1362	0	1399	18	0
54	LL	1701	0	1818	30	0
55	LM	1138	0	1204	15	0
56	LN	1701	0	1749	22	0
57	LO	1650	0	1794	27	0
58	LP	1242	0	1269	23	0
59	LQ	1513	0	1628	17	0
60	LS	1453	0	1490	14	0
61	LT	1298	0	1366	17	0
62	LU	825	0	850	14	0
63	LV	979	0	1039	12	0
64	LX	985	0	1066	13	0
65	LY	1115	0	1205	22	0
66	LZ	1107	0	1182	15	0
67	La	1162	0	1213	14	0
68	Lb	876	0	948	11	0
69	Lc	764	0	804	12	0
70	Ld	888	0	930	14	0
71	Le	1053	0	1147	8	0
72	Lf	876	0	912	10	0
73	Lg	906	0	998	6	0
74	Lh	1015	0	1148	16	0
75	Li	832	0	917	6	0
76	Lj	705	0	737	17	0
77	Lk	569	0	637	9	0
78	Ll	444	0	483	8	0
79	Lm	429	0	465	5	0
80	Ln	230	0	276	5	0
81	Lo	862	0	929	12	0
82	Lp	708	0	756	7	0
83	Lr	1002	0	1068	12	0
84	Ls	1496	0	1540	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	Lt	998	0	1032	21	0
86	L5	177	0	0	1	0
86	L7	3	0	0	0	0
86	L8	4	0	0	0	0
86	LA	1	0	0	0	0
86	LB	2	0	0	0	0
86	LV	1	0	0	0	0
86	Le	2	0	0	0	0
86	S2	27	0	0	0	0
86	SG	1	0	0	0	0
86	SS	1	0	0	0	0
87	Lg	1	0	0	0	0
87	Lj	1	0	0	0	0
87	Lm	1	0	0	0	0
87	Lo	1	0	0	0	0
87	Lp	1	0	0	0	0
87	Sa	1	0	0	0	0
88	L5	98	0	182	11	0
89	L5	90	0	171	8	0
89	L8	10	0	19	0	0
90	L5	20	0	23	1	0
91	L5	39	0	39	0	0
All	All	221543	0	164452	3423	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (3423) 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)
41:L5:2845:A:H61	41:L5:3843:C:H42	1.07	1.00
38:At:15:G:N2	38:At:48:C:H42	1.60	0.99
41:L5:1095:A:H2	41:L5:1200:G:H1	1.06	0.98
38:At:15:G:H22	38:At:48:C:N4	1.62	0.97
39:Pt:50:U:H3	39:Pt:64:G:H1	1.00	0.97
38:At:15:G:H22	38:At:48:C:H42	1.01	0.96
41:L5:2845:A:H61	41:L5:3843:C:N4	1.69	0.90
41:L5:1177:U:H3	41:L5:1183:C:H42	1.18	0.89
20:S2:1351:G:H1	20:S2:1360:U:H3	1.21	0.89
41:L5:505:G:H1	41:L5:653:U:H3	1.21	0.88
41:L5:3930:U:H3	41:L5:4180:G:H1	1.16	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1095:A:C2	41:L5:1200:G:N1	2.41	0.88
41:L5:4421:C:N4	41:L5:4475:G:H22	1.72	0.87
41:L5:4421:C:H42	41:L5:4475:G:N2	1.72	0.87
41:L5:4421:C:H42	41:L5:4475:G:H22	1.23	0.86
14:SW:2:VAL:N	20:S2:1091:C:HO2'	1.74	0.85
20:S2:1324:G:H1	20:S2:1504:U:H3	1.24	0.85
7:SH:144:ILE:HD11	7:SH:152:ARG:HB3	1.57	0.85
41:L5:3946:G:H1	41:L5:4067:U:H3	1.24	0.83
20:S2:1033:G:H1	20:S2:1080:A:HO2'	1.27	0.82
20:S2:1656:G:H1	20:S2:1668:U:H3	0.85	0.82
41:L5:2845:A:N6	41:L5:3843:C:H42	1.76	0.81
20:S2:1657:G:H1	20:S2:1667:U:H3	1.29	0.80
41:L5:1870:C:H2'	41:L5:1871:A2M:H8	1.63	0.79
41:L5:2520:C:O2	41:L5:2640:G:N2	2.16	0.79
6:SG:183:ARG:HH12	20:S2:316:G:H5''	1.48	0.78
41:L5:3899:OMG:HN1	41:L5:4562:C:H42	1.31	0.77
41:L5:1095:A:H2	41:L5:1200:G:N1	1.78	0.77
2:SA:70:ASN:HB3	2:SA:73:ASP:HB2	1.65	0.77
41:L5:518:G:H1	41:L5:643:C:H2'	1.50	0.77
41:L5:2749:C:H2'	41:L5:2750:G:H8	1.47	0.77
7:SH:105:THR:HG23	7:SH:107:LYS:H	1.50	0.76
20:S2:1752:C:N3	20:S2:1779:G:N1	2.33	0.76
30:SS:22:GLY:HA2	30:SS:56:ALA:HB3	1.68	0.76
41:L5:2557:G:H1	41:L5:2570:U:H3	1.33	0.76
41:L5:280:G:H5''	56:LN:14:LYS:HE2	1.67	0.76
41:L5:2554:U:O2	41:L5:2764:A:N7	2.20	0.75
24:SD:168:VAL:HA	24:SD:188:ILE:O	1.87	0.74
33:SZ:58:LEU:HD12	33:SZ:62:VAL:HG21	1.69	0.74
25:SF:204:ARG:HG2	34:Sc:63:ARG:HH21	1.52	0.74
41:L5:1629:G:H1	44:LA:208:GLU:HG2	1.53	0.74
5:SE:240:ARG:HH12	20:S2:844:U:H5'	1.53	0.73
41:L5:3697:U:H5''	41:L5:3698:G:H5'	1.70	0.73
37:Sg:247:TRP:HB3	37:Sg:258:ILE:HD11	1.70	0.73
20:S2:1043:G:N2	20:S2:1073:U:O4	2.22	0.73
2:SA:77:ILE:HD11	2:SA:124:VAL:HG22	1.71	0.73
41:L5:4910:G:H4'	45:LB:95:THR:HG22	1.70	0.73
8:SI:64:ASN:ND2	20:S2:302:A:N3	2.37	0.73
20:S2:1752:C:C4	20:S2:1779:G:N2	2.57	0.72
21:LR:169:ALA:HA	21:LR:172:ARG:HE	1.53	0.72
35:Sd:21:CYS:SG	35:Sd:39:CYS:N	2.62	0.72
18:Sb:11:SER:OG	18:Sb:14:GLU:OE1	2.08	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1974:U:H4'	41:L5:1975:G:H3'	1.72	0.72
20:S2:639:C:H2'	20:S2:640:A:H8	1.53	0.71
20:S2:851:C:H5''	20:S2:852:G:H5'	1.72	0.71
41:L5:2362:U:H2'	41:L5:2363:A2M:H8	1.72	0.71
2:SA:77:ILE:HG22	2:SA:99:ILE:HB	1.72	0.71
6:SG:66:GLY:HA2	20:S2:1745:A:H1'	1.71	0.71
41:L5:2400:G:H21	73:Lg:6:THR:HG22	1.55	0.71
8:SI:87:ASN:HB3	8:SI:90:LEU:HD23	1.73	0.70
41:L5:1670:G:OP1	68:Lb:12:GLN:NE2	2.23	0.70
41:L5:416:U:H4'	41:L5:2330:G:H4'	1.73	0.70
41:L5:4457:PSU:OP1	63:LV:50:ASN:ND2	2.24	0.70
14:SW:111:MET:HE1	14:SW:119:LYS:HD2	1.74	0.70
41:L5:1996:C:N3	41:L5:2000:G:N1	2.39	0.70
41:L5:1996:C:N4	41:L5:2000:G:N2	2.40	0.70
41:L5:4101:C:N3	41:L5:4107:G:N2	2.40	0.69
20:S2:508:A:H3'	20:S2:509:OMG:H8	1.57	0.69
20:S2:690:G:H3'	20:S2:691:G:H21	1.56	0.69
41:L5:188:G:N2	41:L5:190:G:O6	2.24	0.69
41:L5:1195:G:H2'	41:L5:1196:G:C8	2.27	0.69
20:S2:693:A:N6	20:S2:737:G:N7	2.39	0.69
41:L5:4440:G:H5'	52:LI:108:ALA:HB2	1.73	0.69
41:L5:418:A:H4'	41:L5:2311:C:H5'	1.75	0.69
41:L5:1095:A:N1	41:L5:1200:G:O6	2.26	0.69
41:L5:1976:G:O6	41:L5:1990:A:N1	2.26	0.69
2:SA:163:CYS:SG	2:SA:164:ASN:N	2.61	0.69
20:S2:1435:C:H42	32:SU:92:HIS:HB3	1.56	0.69
41:L5:2517:A:H5'	73:Lg:62:LYS:HD3	1.74	0.69
41:L5:3610:A:H2'	41:L5:3611:A:H8	1.58	0.68
20:S2:928:G:H2'	20:S2:929:G:C8	2.28	0.68
5:SE:45:ILE:HG13	5:SE:61:VAL:HG11	1.75	0.68
18:Sb:56:CYS:HB2	18:Sb:59:CYS:H	1.58	0.68
41:L5:1951:G:H1	41:L5:2032:U:H3	1.41	0.68
16:SY:55:ILE:HG23	16:SY:75:ILE:HG22	1.76	0.68
38:At:18:G:O6	38:At:55:U:O2	2.12	0.68
41:L5:3937:C:H1'	56:LN:125:SER:HB3	1.75	0.68
1:Zt:58:A:O2'	1:Zt:61:C:N4	2.27	0.68
19:Se:58:ASN:ND2	20:S2:606:G:N3	2.41	0.68
12:SO:34:PHE:HB3	12:SO:41:PHE:HB2	1.75	0.68
57:LO:126:VAL:HG13	57:LO:127:VAL:HG13	1.75	0.68
41:L5:5024:C:H41	41:L5:5028:G:H21	1.42	0.68
42:L7:47:G:H21	47:LD:222:GLN:HE22	1.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SB:109:LYS:HG3	3:SB:113:MET:HE2	1.74	0.67
12:SO:33:ILE:HG22	12:SO:42:VAL:HA	1.76	0.67
20:S2:1266:C:N3	20:S2:1517:G:N2	2.42	0.67
41:L5:1802:A:N3	61:LT:130:ARG:NH2	2.41	0.67
42:L7:77:A:H62	42:L7:99:G:H21	1.41	0.67
20:S2:113:G:N1	20:S2:292:A:N7	2.43	0.67
41:L5:4884:G:N7	48:LE:272:ARG:NH2	2.41	0.67
42:L7:28:C:H1'	42:L7:54:A:H61	1.59	0.67
20:S2:924:G:H1	20:S2:1018:U:H3	1.41	0.67
41:L5:2486:G:O6	41:L5:2493:G:O6	2.13	0.67
44:LA:20:VAL:HA	44:LA:23:ARG:HG3	1.76	0.67
28:SP:108:LYS:HG3	28:SP:110:GLU:H	1.60	0.67
41:L5:121:A:H62	41:L5:152:U:H3	1.43	0.67
20:S2:191:A:N6	20:S2:208:G:O2'	2.29	0.66
27:SM:36:ARG:NH2	36:Sf:129:GLY:O	2.28	0.66
66:LZ:113:GLU:OE2	66:LZ:117:LYS:NZ	2.28	0.66
84:Ls:10:LYS:HA	84:Ls:60:MET:HE1	1.77	0.66
20:S2:993:G:OP1	20:S2:1131:G:N2	2.29	0.66
45:LB:90:VAL:HG23	45:LB:163:ILE:HD11	1.77	0.66
6:SG:2:LYS:HB2	6:SG:108:VAL:HG12	1.76	0.66
20:S2:1816:G:HO2'	41:L5:3807:A:HO2'	1.42	0.66
34:Sc:17:VAL:HA	34:Sc:30:VAL:HG12	1.76	0.66
41:L5:1996:C:C4	41:L5:2000:G:N2	2.63	0.66
4:SC:102:LEU:HD23	4:SC:130:ILE:HD12	1.75	0.66
41:L5:4615:C:H5''	45:LB:357:ARG:HD2	1.77	0.66
54:LL:64:VAL:HA	54:LL:67:HIS:HD2	1.59	0.66
5:SE:159:THR:HB	5:SE:173:ILE:HB	1.78	0.66
20:S2:304:C:H5''	20:S2:305:U:H5'	1.78	0.66
41:L5:2297:G:H4'	46:LC:242:PRO:HB2	1.76	0.66
41:L5:4926:C:H5''	41:L5:4927:G:H21	1.61	0.66
29:SQ:19:ALA:HB2	29:SQ:75:GLY:HA3	1.78	0.66
15:SX:67:ARG:HG3	15:SX:115:ILE:HG12	1.77	0.66
20:S2:1658:G:OP2	20:S2:1660:C:N4	2.29	0.66
41:L5:404:U:O3'	65:LY:87:ARG:NH2	2.29	0.66
41:L5:1541:C:H1'	41:L5:2448:G:H21	1.61	0.66
2:SA:52:LYS:HB2	23:SR:109:LEU:HD13	1.79	0.65
20:S2:1010:G:H2'	20:S2:1011:A:H8	1.59	0.65
20:S2:1244:PSU:H2'	20:S2:1245:G:H8	1.62	0.65
31:ST:129:ARG:HD2	31:ST:133:ARG:HH21	1.61	0.65
41:L5:25:A:H61	41:L5:58:G:H1	1.42	0.65
1:Zt:54:U:C2	1:Zt:58:A:N7	2.64	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:602:G:N2	20:S2:620:G:N7	2.44	0.65
41:L5:2335:C:H2'	41:L5:2336:G:H8	1.59	0.65
41:L5:4587:G:OP1	57:LO:61:ARG:NH1	2.28	0.65
48:LE:223:ARG:HH22	48:LE:238:GLU:HG3	1.61	0.65
6:SG:42:GLY:O	6:SG:46:LYS:NZ	2.29	0.65
41:L5:1969:G:H21	41:L5:1999:A:H1'	1.61	0.65
45:LB:165:HIS:HB3	45:LB:180:LEU:HD23	1.79	0.65
29:SQ:32:ILE:HG12	29:SQ:68:ILE:HD12	1.79	0.65
41:L5:665:C:H4'	41:L5:666:G:H5'	1.78	0.65
41:L5:1587:G:OP2	89:L5:5280:SPD:N1	2.29	0.65
25:SF:127:ARG:HG3	25:SF:136:ARG:HB3	1.77	0.65
1:Zt:54:U:N3	1:Zt:58:A:C8	2.65	0.65
41:L5:2701:U:H3	41:L5:2715:G:H1	1.42	0.65
15:SX:107:ARG:HG3	15:SX:110:HIS:HB3	1.79	0.65
41:L5:148:C:OP2	50:LG:197:LYS:NZ	2.29	0.65
41:L5:4091:G:N7	41:L5:4114:C:N4	2.45	0.65
41:L5:511:C:H5'	54:LL:165:LYS:HG3	1.77	0.64
1:Zt:54:U:O2	1:Zt:58:A:C5	2.50	0.64
37:Sg:87:LEU:HB2	37:Sg:101:PHE:HB2	1.78	0.64
41:L5:3870:C:H2'	41:L5:3871:A:H8	1.62	0.64
20:S2:220:U:O4	20:S2:302:A:N6	2.30	0.64
20:S2:1752:C:N4	20:S2:1779:G:N2	2.46	0.64
38:At:15:G:N1	38:At:48:C:N3	2.38	0.64
9:SJ:18:ARG:HH21	20:S2:4:C:H1'	1.61	0.64
20:S2:98:C:OP2	20:S2:426:A:O2'	2.15	0.64
20:S2:1854:U:H2'	20:S2:1855:G:H8	1.63	0.64
41:L5:989:U:O2	41:L5:1064:G:O6	2.16	0.64
41:L5:1437:C:H1'	41:L5:2098:G:H3'	1.79	0.64
58:LP:10:ASN:ND2	58:LP:12:THR:OG1	2.31	0.64
7:SH:43:LEU:HD11	7:SH:71:SER:HB2	1.80	0.64
20:S2:1271:C:O2	35:Sd:2:GLY:N	2.30	0.64
6:SG:136:LYS:HB2	20:S2:65:C:H41	1.62	0.64
41:L5:2624:G:OP2	62:LU:97:ARG:NH2	2.31	0.64
41:L5:4272:G:N2	41:L5:4272:G:OP2	2.31	0.64
53:LJ:100:SER:OG	53:LJ:104:ASN:OD1	2.16	0.64
2:SA:42:LYS:HG3	2:SA:44:ASP:H	1.63	0.64
20:S2:1556:A:N6	35:Sd:12:ARG:O	2.30	0.64
20:S2:1737:G:H1	20:S2:1797:U:H3	1.44	0.64
41:L5:248:C:O2	65:LY:121:ARG:NH2	2.30	0.64
83:Lr:26:SER:OG	83:Lr:28:GLU:OE1	2.16	0.64
20:S2:57:U:O2'	20:S2:499:G:N3	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L7:7:G:OP1	47:LD:33:ARG:NH1	2.30	0.64
3:SB:123:ALA:HB1	3:SB:169:MET:HG3	1.80	0.64
11:SN:66:VAL:HG23	11:SN:67:THR:HG23	1.80	0.64
41:L5:655:C:OP1	46:LC:268:ARG:NH1	2.31	0.64
41:L5:1743:A:N1	41:L5:1789:C:O2'	2.30	0.64
81:Lo:34:TYR:O	81:Lo:39:ARG:NH1	2.28	0.64
2:SA:148:CYS:SG	2:SA:163:CYS:N	2.70	0.64
4:SC:193:VAL:HG11	4:SC:240:THR:HG22	1.80	0.64
41:L5:24:G:N7	76:Lj:46:LYS:NZ	2.46	0.64
41:L5:262:G:H2'	41:L5:263:G:H8	1.63	0.64
41:L5:1974:U:H3	41:L5:1993:C:H42	1.45	0.64
41:L5:3633:C:OP1	88:L5:5288:SPM:N10	2.30	0.64
46:LC:33:ARG:HD3	46:LC:36:ILE:HD12	1.80	0.64
41:L5:2780:C:H2'	41:L5:2781:G:H8	1.62	0.63
41:L5:3944:G:H1	41:L5:4069:U:H3	0.74	0.63
8:SI:75:LYS:HD2	20:S2:303:C:H5'	1.80	0.63
20:S2:567:C:O2'	20:S2:583:A:N6	2.31	0.63
41:L5:2601:A:N6	41:L5:2744:A:OP2	2.26	0.63
41:L5:3873:G:H2'	41:L5:3874:G:C8	2.32	0.63
41:L5:4210:U:H3	41:L5:4222:G:H1	1.46	0.63
25:SF:62:ARG:O	25:SF:65:GLN:NE2	2.31	0.63
23:SR:70:SER:HB3	23:SR:73:LEU:HB2	1.80	0.63
43:L8:19:C:H2'	43:L8:20:A:H8	1.62	0.63
12:SO:95:ILE:HB	12:SO:129:ILE:HG22	1.80	0.63
41:L5:88:A:N7	59:LQ:173:LYS:NZ	2.47	0.63
41:L5:1100:U:H1'	41:L5:1167:C:H41	1.64	0.63
5:SE:144:ALA:HB3	20:S2:121:OMU:HM23	1.79	0.63
20:S2:165:G:OP2	20:S2:165:G:N2	2.31	0.63
20:S2:864:A:H2'	20:S2:865:A:H8	1.63	0.63
29:SQ:72:VAL:HG11	29:SQ:80:GLN:HG3	1.79	0.63
41:L5:4238:G:H2'	41:L5:4239:A:H8	1.64	0.63
50:LG:154:LEU:HB3	50:LG:204:PHE:HB2	1.79	0.63
20:S2:26:U:H2'	20:S2:27:A2M:H8	1.80	0.63
20:S2:146:G:H2'	20:S2:147:A:H8	1.63	0.63
37:Sg:46:THR:H	37:Sg:53:GLY:HA2	1.62	0.63
1:Zt:55:U:N3	1:Zt:58:A:OP2	2.26	0.63
15:SX:28:LYS:HD2	15:SX:32:LEU:HD22	1.81	0.63
20:S2:557:U:H2'	20:S2:558:G:C8	2.34	0.63
20:S2:609:U:H2'	20:S2:610:G:H8	1.63	0.63
24:SD:40:ARG:HG2	32:SU:108:PRO:HG3	1.81	0.63
41:L5:907:C:H2'	41:L5:908:G:H8	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1914:C:H4'	57:LO:89:PRO:HD3	1.81	0.63
41:L5:2745:A:H2'	41:L5:2746:A:H8	1.63	0.63
9:SJ:86:VAL:HG12	9:SJ:108:ARG:HG3	1.80	0.63
41:L5:4630:G:H2'	41:L5:4631:G:H8	1.64	0.63
6:SG:39:ASP:O	6:SG:46:LYS:NZ	2.31	0.62
30:SS:12:ILE:HD11	53:LJ:121:PRO:HD3	1.80	0.62
20:S2:1261:C:O2	35:Sd:10:HIS:NE2	2.29	0.62
51:LH:106:GLN:HB2	51:LH:111:LEU:HB3	1.80	0.62
20:S2:919:A:O2'	20:S2:1020:A:N1	2.27	0.62
41:L5:1461:C:H2'	41:L5:1462:A:H8	1.64	0.62
41:L5:4174:U:H2'	41:L5:4175:G:H8	1.65	0.62
41:L5:4581:G:OP2	45:LB:26:ARG:NH2	2.32	0.62
81:Lo:63:THR:O	81:Lo:87:ARG:NH1	2.32	0.62
20:S2:291:G:H2'	20:S2:292:A:C8	2.35	0.62
41:L5:758:G:H4'	51:LH:51:LYS:HD3	1.82	0.62
41:L5:2088:A:OP2	59:LQ:37:ARG:NH2	2.32	0.62
49:LF:105:VAL:HG13	49:LF:136:VAL:HG12	1.80	0.62
20:S2:690:G:OP2	20:S2:690:G:N2	2.32	0.62
20:S2:1461:G:H3'	20:S2:1463:U:H3	1.65	0.62
41:L5:163:A:H2'	41:L5:164:G:H8	1.65	0.62
41:L5:654:C:H4'	46:LC:269:LYS:HD3	1.79	0.62
41:L5:4929:C:OP1	55:LM:117:LYS:NZ	2.27	0.62
6:SG:22:ARG:HA	6:SG:25:ARG:HE	1.64	0.62
7:SH:7:LYS:NZ	7:SH:15:LYS:O	2.24	0.62
20:S2:1337:4AC:H2'	20:S2:1338:G:H8	1.64	0.62
25:SF:175:ASP:O	25:SF:179:ASN:ND2	2.33	0.62
32:SU:35:VAL:HG11	32:SU:110:VAL:HG21	1.82	0.62
41:L5:2092:G:O2'	41:L5:2262:G:N2	2.32	0.62
41:L5:2749:C:H2'	41:L5:2750:G:C8	2.33	0.62
41:L5:2869:U:O2'	41:L5:2881:A:N7	2.32	0.62
51:LH:187:VAL:HG12	51:LH:188:GLN:HG3	1.82	0.62
41:L5:2884:G:H2'	41:L5:2885:A:H8	1.65	0.62
1:Zt:28:C:H2'	1:Zt:29:A:H8	1.65	0.62
37:Sg:163:PRO:HB2	37:Sg:179:LEU:HD12	1.82	0.62
41:L5:20:U:H3'	41:L5:21:G:H8	1.65	0.62
41:L5:2702:C:OP1	62:LU:101:ARG:NH2	2.33	0.62
41:L5:3722:G:H2'	41:L5:3723:A:H8	1.65	0.62
21:LR:21:LYS:HE3	21:LR:55:VAL:HA	1.82	0.61
41:L5:2093:A:N3	41:L5:2094:G:N1	2.48	0.61
43:L8:75:OMG:OP2	65:LY:74:TYR:OH	2.18	0.61
19:Se:26:LYS:NZ	20:S2:525:A:OP2	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:532:C:H2'	20:S2:533:A:H8	1.65	0.61
41:L5:308:G:N2	41:L5:308:G:OP2	2.30	0.61
41:L5:4090:G:H2'	41:L5:4091:G:C8	2.34	0.61
46:LC:1:MET:HE3	46:LC:29:LYS:HE2	1.82	0.61
17:Sa:23:CYS:HB3	17:Sa:28:ARG:H	1.64	0.61
26:SK:55:ARG:NH1	26:SK:78:TYR:OH	2.33	0.61
41:L5:1194:G:H2'	41:L5:1195:G:C8	2.35	0.61
47:LD:41:LYS:NZ	61:LT:32:ARG:O	2.33	0.61
11:SN:15:ALA:HB2	18:Sb:20:LYS:HD3	1.83	0.61
20:S2:1598:G:O2'	33:SZ:80:ARG:O	2.18	0.61
45:LB:117:ARG:HA	45:LB:177:LYS:HD2	1.81	0.61
21:LR:43:LYS:HD2	41:L5:2709:C:H5'	1.83	0.61
30:SS:111:LEU:HG	30:SS:115:LYS:HE3	1.82	0.61
41:L5:181:C:H2'	41:L5:182:G:C8	2.34	0.61
41:L5:4541:G:N2	41:L5:4544:A:OP2	2.34	0.61
20:S2:1562:C:H2'	20:S2:1563:G:H8	1.65	0.61
29:SQ:42:ILE:HG23	29:SQ:44:PRO:HD2	1.83	0.61
41:L5:1855:G:O6	41:L5:1880:G:N2	2.34	0.61
41:L5:4518:A:OP2	45:LB:258:HIS:ND1	2.32	0.61
41:L5:4736:C:H2'	41:L5:4737:G:H8	1.64	0.61
67:La:89:ASN:O	67:La:93:ASN:HB2	2.01	0.61
20:S2:1277:C:H2'	20:S2:1278:A:H8	1.64	0.61
41:L5:3944:G:O6	41:L5:4069:U:O4	2.18	0.61
41:L5:4153:C:H2'	41:L5:4154:G:H8	1.65	0.61
41:L5:5022:U:O2'	41:L5:5024:C:OP2	2.18	0.61
20:S2:388:U:H2'	20:S2:389:A:H8	1.65	0.61
28:SP:130:ARG:HD3	28:SP:131:PRO:HD2	1.83	0.61
41:L5:1927:U:OP1	41:L5:1949:U:O2'	2.15	0.61
41:L5:4496:A:H61	41:L5:4504:C:H42	1.49	0.61
42:L7:23:A:N3	42:L7:118:C:O2'	2.31	0.61
48:LE:225:PRO:HG2	48:LE:226:ARG:HH11	1.63	0.61
27:SM:31:LEU:HB3	27:SM:33:ARG:HG3	1.82	0.61
41:L5:62:A:N3	41:L5:77:U:O2'	2.31	0.61
41:L5:977:C:OP1	46:LC:333:LYS:NZ	2.33	0.61
55:LM:100:ARG:HA	55:LM:103:LYS:HG2	1.83	0.61
70:Ld:22:THR:HG23	70:Ld:122:VAL:HG13	1.82	0.61
7:SH:65:PRO:HG2	7:SH:68:GLN:HB2	1.83	0.60
20:S2:436:OMG:OP2	20:S2:471:G:O2'	2.19	0.60
30:SS:80:PRO:HG2	31:ST:36:THR:HG21	1.82	0.60
41:L5:1390:G:N2	41:L5:1393:G:OP2	2.31	0.60
41:L5:1669:A:N3	41:L5:1852:U:O2'	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:4523:A2M:H5''	41:L5:4524:G:H5'	1.82	0.60
16:SY:11:LYS:HB2	16:SY:24:VAL:HG12	1.84	0.60
20:S2:1259:A:N6	20:S2:1519:U:O5'	2.33	0.60
25:SF:131:ALA:HA	25:SF:136:ARG:HB2	1.82	0.60
26:SK:3:MET:HE1	26:SK:48:ALA:HB2	1.83	0.60
41:L5:330:G:N7	89:L5:5281:SPD:N1	2.49	0.60
41:L5:4088:C:H2'	41:L5:4089:G:H8	1.66	0.60
6:SG:135:PRO:HG2	6:SG:141:ILE:HG22	1.83	0.60
10:SL:133:PRO:HG2	20:S2:383:G:H21	1.64	0.60
20:S2:1218:C:H1'	20:S2:1683:C:H42	1.64	0.60
41:L5:94:A:H5''	67:La:34:ASN:HB2	1.82	0.60
41:L5:1906:U:H2'	41:L5:1907:A:H8	1.66	0.60
41:L5:4580:U:OP1	45:LB:26:ARG:NH1	2.33	0.60
42:L7:87:G:N2	42:L7:90:A:OP2	2.33	0.60
17:Sa:11:ALA:O	17:Sa:15:ARG:NH2	2.34	0.60
20:S2:1228:A:H2'	20:S2:1229:G:H8	1.66	0.60
41:L5:1177:U:H3	41:L5:1183:C:N4	1.95	0.60
41:L5:1505:C:H2'	41:L5:1506:G:H8	1.64	0.60
41:L5:4097:G:O6	41:L5:4098:A:N6	2.34	0.60
41:L5:4740:G:O6	41:L5:4959:U:O2	2.20	0.60
41:L5:4935:C:H2'	41:L5:4936:G:C8	2.36	0.60
56:LN:120:TRP:HE1	56:LN:123:GLU:HB3	1.66	0.60
62:LU:96:LEU:HB3	62:LU:100:LEU:HD12	1.83	0.60
20:S2:106:C:H2'	20:S2:107:A:H8	1.66	0.60
39:Pt:50:U:O2	39:Pt:64:G:N2	2.27	0.60
41:L5:1850:A:N3	41:L5:2283:G:O2'	2.34	0.60
41:L5:4301:U:OP2	41:L5:4303:C:N4	2.35	0.60
44:LA:107:MET:HB3	44:LA:111:THR:HG21	1.83	0.60
49:LF:29:LYS:HZ2	49:LF:32:ARG:HH12	1.49	0.60
16:SY:119:GLY:O	20:S2:84:A:O2'	2.19	0.60
17:Sa:4:LYS:NZ	20:S2:1864:U:OP2	2.35	0.60
25:SF:134:VAL:HG12	25:SF:135:ARG:HG2	1.83	0.60
36:Sf:126:CYS:HB2	36:Sf:144:CYS:SG	2.41	0.60
41:L5:4304:A:OP2	41:L5:4305:G:N2	2.34	0.60
42:L7:75:G:N2	42:L7:100:A:OP2	2.33	0.60
8:SI:133:GLU:HA	8:SI:136:ILE:HG12	1.84	0.60
20:S2:115:U:H2'	20:S2:116:OMU:H6	1.83	0.60
41:L5:500:G:H1'	41:L5:504:G:H2'	1.84	0.60
41:L5:4587:G:N2	45:LB:15:GLY:O	2.33	0.60
7:SH:144:ILE:HD13	7:SH:154:ILE:HG13	1.84	0.60
20:S2:649:PSU:H2'	20:S2:650:A:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1228:A:H2'	20:S2:1229:G:C8	2.37	0.60
20:S2:1729:U:H3	20:S2:1805:G:H1	1.50	0.60
41:L5:109:G:OP2	54:LL:74:ARG:NH2	2.34	0.60
41:L5:966:A:OP2	41:L5:2092:G:N2	2.34	0.60
41:L5:3717:A:H2'	41:L5:3718:A2M:H8	1.84	0.60
12:SO:129:ILE:HD11	17:Sa:65:PRO:HD2	1.84	0.60
14:SW:28:ARG:NH2	20:S2:1094:C:OP1	2.35	0.60
20:S2:1536:G:H2'	20:S2:1537:A:H8	1.67	0.60
27:SM:26:LEU:HA	27:SM:31:LEU:HD21	1.84	0.60
31:ST:76:THR:HG23	31:ST:94:ARG:HD3	1.83	0.60
37:Sg:206:LEU:HD11	37:Sg:227:LEU:HD12	1.84	0.60
41:L5:1514:U:H2'	41:L5:1515:A:C8	2.37	0.60
77:Lk:14:THR:HA	77:Lk:17:ARG:HD3	1.84	0.60
29:SQ:97:GLN:HE21	37:Sg:58:ALA:HB3	1.66	0.59
37:Sg:176:VAL:HG23	37:Sg:185:LYS:HB2	1.84	0.59
37:Sg:191:HIS:ND1	37:Sg:213:ASP:OD2	2.35	0.59
37:Sg:208:ALA:HB2	37:Sg:218:LEU:HD13	1.84	0.59
41:L5:2:G:OP2	64:LX:39:LYS:NZ	2.35	0.59
41:L5:2318:G:N2	41:L5:2321:G:OP2	2.33	0.59
41:L5:4299:PSU:OP1	68:Lb:33:LYS:NZ	2.34	0.59
41:L5:4992:G:H2'	41:L5:4993:G:C8	2.37	0.59
37:Sg:39:THR:OG1	37:Sg:60:ARG:NH1	2.36	0.59
41:L5:1986:U:O4	41:L5:2013:A:N6	2.35	0.59
41:L5:4371:G:OP1	81:Lo:64:LYS:NZ	2.33	0.59
43:L8:14:U:H5''	58:LP:123:PRO:HG3	1.84	0.59
50:LG:178:GLY:O	50:LG:223:ARG:NH2	2.34	0.59
20:S2:323:C:N4	20:S2:328:U:O4	2.35	0.59
20:S2:587:A:H5'	20:S2:592:C:H41	1.67	0.59
30:SS:114:LEU:HD13	30:SS:117:ILE:HD11	1.83	0.59
41:L5:436:C:H2'	41:L5:437:G:H8	1.68	0.59
5:SE:79:ASP:HB3	5:SE:82:TYR:HB2	1.82	0.59
20:S2:830:A:OP2	20:S2:846:G:N2	2.29	0.59
41:L5:679:C:H2'	41:L5:680:G:H8	1.66	0.59
41:L5:1207:C:H2'	41:L5:1208:G:H8	1.67	0.59
53:LJ:29:SER:OG	53:LJ:67:LYS:O	2.17	0.59
20:S2:388:U:H2'	20:S2:389:A:C8	2.37	0.59
43:L8:155:C:OP2	50:LG:89:ARG:NH1	2.36	0.59
48:LE:72:LYS:HD3	68:Lb:119:CYS:HB3	1.85	0.59
6:SG:148:SER:OG	6:SG:151:ASP:OD2	2.21	0.59
15:SX:68:LYS:NZ	20:S2:616:A:OP1	2.34	0.59
44:LA:107:MET:O	44:LA:139:HIS:NE2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:85:G:O2'	41:L5:97:G:O6	2.21	0.59
65:LY:55:VAL:HG12	65:LY:106:ILE:HA	1.84	0.59
68:Lb:102:PRO:O	68:Lb:109:ARG:NH2	2.36	0.59
16:SY:21:LYS:HD2	16:SY:75:ILE:HD11	1.84	0.59
20:S2:1096:G:H1	20:S2:1136:U:H3	1.51	0.59
21:LR:74:ARG:NE	41:L5:2891:U:OP2	2.35	0.59
41:L5:453:G:OP1	48:LE:228:GLN:NE2	2.35	0.59
41:L5:2407:G:N2	41:L5:2407:G:OP2	2.36	0.59
50:LG:105:GLU:OE2	50:LG:113:ARG:NH2	2.24	0.59
52:LI:61:SER:HA	52:LI:126:VAL:HG12	1.85	0.59
83:Lr:59:GLY:O	83:Lr:121:GLN:NE2	2.32	0.59
7:SH:101:LEU:O	7:SH:116:ARG:NH1	2.35	0.59
7:SH:154:ILE:HB	7:SH:185:VAL:HG22	1.84	0.59
20:S2:1396:A:N7	20:S2:1449:G:O6	2.35	0.59
35:Sd:22:ARG:HG3	35:Sd:23:VAL:HG23	1.84	0.59
41:L5:1516:G:O2'	54:LL:18:TRP:NE1	2.36	0.59
41:L5:2458:C:H1'	41:L5:3671:G:H21	1.67	0.59
46:LC:67:TRP:HB3	46:LC:71:ARG:HD3	1.84	0.59
54:LL:140:SER:HA	54:LL:143:GLU:HG2	1.84	0.59
12:SO:52:THR:HG21	20:S2:952:G:H21	1.67	0.58
20:S2:1286:G:N2	20:S2:1312:G:O2'	2.34	0.58
41:L5:231:U:O2	65:LY:103:LYS:NZ	2.34	0.58
41:L5:1333:A:H2'	41:L5:1334:A:H8	1.68	0.58
41:L5:2505:C:N4	41:L5:4085:A:OP2	2.35	0.58
52:LI:36:LEU:HD11	52:LI:69:ARG:HD2	1.85	0.58
7:SH:10:LYS:NZ	7:SH:14:GLU:O	2.35	0.58
20:S2:1337:4AC:H2'	20:S2:1338:G:C8	2.38	0.58
41:L5:1095:A:N1	41:L5:1200:G:C6	2.71	0.58
41:L5:1762:C:OP2	41:L5:1764:G:N2	2.35	0.58
41:L5:3680:U:OP1	44:LA:54:ARG:NH2	2.35	0.58
41:L5:3855:C:H2'	41:L5:3856:A:H8	1.68	0.58
41:L5:4594:U:H2'	41:L5:4595:G:H8	1.67	0.58
41:L5:4699:U:H1'	41:L5:4700:A:H5''	1.84	0.58
5:SE:6:LYS:NZ	20:S2:431:G:OP1	2.36	0.58
6:SG:131:ARG:HB2	22:LW:82:ILE:HG22	1.85	0.58
10:SL:35:ARG:NH2	10:SL:55:TYR:O	2.36	0.58
20:S2:201:C:H3'	20:S2:202:G:H21	1.68	0.58
20:S2:1720:U:HO2'	41:L5:3796:U:HO2'	1.48	0.58
41:L5:2351:OMC:HM22	46:LC:95:MET:HG3	1.85	0.58
1:Zt:34:U:H5'	33:SZ:65:TYR:HB3	1.85	0.58
20:S2:910:G:OP1	21:LR:176:ARG:NH2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1130:G:N2	20:S2:1130:G:OP2	2.36	0.58
41:L5:3824:A:H3'	41:L5:3825:A2M:H8	1.85	0.58
20:S2:110:U:H3	20:S2:351:G:H1	1.48	0.58
41:L5:66:A:N6	41:L5:282:C:O2'	2.34	0.58
41:L5:3641:U:OP2	41:L5:3646:A:N6	2.35	0.58
41:L5:4391:G:OP1	46:LC:75:ARG:NH1	2.31	0.58
41:L5:4472:G:O2'	79:Lm:100:TYR:O	2.21	0.58
48:LE:141:ARG:NH1	48:LE:191:GLN:O	2.36	0.58
41:L5:2458:C:O2'	41:L5:3671:G:N3	2.34	0.58
41:L5:4185:G:OP1	44:LA:2:GLY:N	2.37	0.58
41:L5:4717:A:H4'	45:LB:20:LYS:HD3	1.84	0.58
61:LT:75:VAL:HG22	61:LT:88:ARG:HG2	1.85	0.58
5:SE:247:THR:N	5:SE:250:GLU:OE2	2.35	0.58
18:Sb:17:ARG:NH1	20:S2:1128:C:OP1	2.36	0.58
41:L5:36:U:OP1	41:L5:1651:G:N2	2.36	0.58
41:L5:1889:U:O4	41:L5:1939:A:N6	2.36	0.58
41:L5:4251:A:H5''	53:LJ:108:GLY:HA3	1.86	0.58
41:L5:4405:G:H1	41:L5:4439:U:H3	1.52	0.58
76:Lj:27:TYR:HA	76:Lj:34:CYS:HA	1.86	0.58
20:S2:634:A:H2'	20:S2:635:G:H8	1.68	0.58
30:SS:121:ARG:HG3	30:SS:131:VAL:HB	1.86	0.58
41:L5:5040:U:OP2	45:LB:396:ARG:NH2	2.36	0.58
51:LH:120:GLU:OE2	51:LH:124:ARG:NH2	2.36	0.58
62:LU:65:ARG:HG2	62:LU:67:LYS:H	1.69	0.58
20:S2:1472:C:O3'	37:Sg:15:ASN:ND2	2.36	0.58
41:L5:305:A:OP2	56:LN:15:GLN:NE2	2.36	0.58
43:L8:67:U:H2'	43:L8:68:G:H8	1.69	0.58
9:SJ:134:HIS:NE2	20:S2:561:A:O2'	2.28	0.58
11:SN:119:GLU:O	11:SN:123:HIS:ND1	2.37	0.58
20:S2:588:G:OP2	20:S2:588:G:N2	2.30	0.58
22:LW:44:ARG:HD3	41:L5:3615:G:H1'	1.85	0.58
41:L5:1346:C:H2'	41:L5:1347:G:H8	1.67	0.58
41:L5:2411:C:H2'	41:L5:2412:A:H8	1.69	0.58
48:LE:227:HIS:HE1	48:LE:230:GLY:HA2	1.69	0.58
10:SL:20:LYS:NZ	20:S2:223:C:OP1	2.34	0.57
20:S2:807:G:H2'	20:S2:808:A:H8	1.68	0.57
20:S2:1588:A:H2'	20:S2:1589:A:C8	2.38	0.57
27:SM:128:PHE:HD1	27:SM:131:LYS:HZ3	1.52	0.57
31:ST:107:LEU:HD23	31:ST:113:VAL:HG21	1.85	0.57
37:Sg:17:TRP:HB2	37:Sg:36:ARG:HD2	1.84	0.57
41:L5:268:G:H2'	41:L5:269:G:H8	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1332:C:H2'	41:L5:1333:A:H8	1.69	0.57
41:L5:1982:G:H21	41:L5:2009:A:H1'	1.68	0.57
41:L5:2274:C:H2'	41:L5:2275:G:H8	1.68	0.57
3:SB:122:GLU:HG2	3:SB:140:VAL:HG12	1.85	0.57
6:SG:142:ARG:HA	6:SG:147:LEU:HD23	1.86	0.57
6:SG:164:LYS:H	6:SG:167:LYS:HE3	1.69	0.57
9:SJ:71:LEU:O	9:SJ:75:ASN:ND2	2.37	0.57
18:Sb:67:THR:OG1	18:Sb:70:LYS:O	2.21	0.57
41:L5:2108:G:H2'	41:L5:2109:G:C8	2.39	0.57
41:L5:4126:C:H5''	41:L5:4127:A:H5''	1.86	0.57
41:L5:4153:C:H2'	41:L5:4154:G:C8	2.39	0.57
41:L5:4260:U:H2'	41:L5:4261:C:H6	1.69	0.57
41:L5:4694:G:O2'	51:LH:71:ARG:NH2	2.31	0.57
47:LD:223:PHE:HB3	47:LD:226:TYR:HB2	1.86	0.57
77:Lk:13:LEU:HA	77:Lk:16:ARG:HG2	1.85	0.57
11:SN:2:GLY:N	20:S2:1092:G:OP1	2.36	0.57
20:S2:70:G:H21	20:S2:79:A:H62	1.50	0.57
30:SS:84:LEU:HB3	30:SS:97:GLN:HB2	1.85	0.57
41:L5:2870:A:OP2	41:L5:2879:A:N6	2.34	0.57
41:L5:4091:G:C6	41:L5:4092:G:O6	2.57	0.57
43:L8:148:A:H2'	43:L8:149:G:C8	2.40	0.57
4:SC:191:VAL:HG11	4:SC:236:PHE:HA	1.86	0.57
8:SI:124:LYS:NZ	41:L5:5024:C:O5'	2.37	0.57
20:S2:1410:C:H2'	20:S2:1411:G:H8	1.70	0.57
20:S2:1536:G:H2'	20:S2:1537:A:C8	2.40	0.57
29:SQ:130:LYS:HA	29:SQ:137:ALA:HA	1.86	0.57
32:SU:51:LYS:HB2	32:SU:90:ASP:HB2	1.87	0.57
35:Sd:39:CYS:HB2	35:Sd:42:CYS:HB2	1.85	0.57
41:L5:970:G:OP1	48:LE:123:ARG:NH1	2.36	0.57
41:L5:1972:G:H2'	41:L5:1973:G:C8	2.40	0.57
41:L5:4239:A:H2'	41:L5:4240:G:C8	2.39	0.57
3:SB:117:TRP:HB3	3:SB:153:THR:HG22	1.87	0.57
4:SC:207:ALA:O	4:SC:211:LYS:HB2	2.03	0.57
6:SG:129:VAL:O	22:LW:80:ARG:NH2	2.38	0.57
15:SX:102:VAL:HG12	15:SX:122:VAL:HA	1.86	0.57
20:S2:1030:A:H2'	20:S2:1031:A2M:H8	1.86	0.57
43:L8:47:C:H1'	43:L8:61:A:H2'	1.85	0.57
20:S2:874:G:H2'	20:S2:875:A:H8	1.68	0.57
22:LW:61:LYS:NZ	41:L5:5038:A:OP1	2.33	0.57
41:L5:1962:A:H5''	41:L5:2024:G:H22	1.68	0.57
41:L5:1975:G:N2	41:L5:1984:A:N7	2.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:2021:G:OP1	84:Ls:58:ASN:N	2.37	0.57
51:LH:103:VAL:HG11	51:LH:144:LEU:HD21	1.86	0.57
9:SJ:67:ASP:HB3	9:SJ:70:ARG:HB3	1.86	0.57
20:S2:1525:C:H2'	20:S2:1526:G:H8	1.69	0.57
41:L5:88:A:OP1	59:LQ:172:ARG:NH2	2.37	0.57
41:L5:1195:G:H2'	41:L5:1196:G:H8	1.69	0.57
41:L5:1511:U:H2'	41:L5:1512:G:H8	1.69	0.57
41:L5:4389:C:H2'	41:L5:4390:A:H8	1.69	0.57
41:L5:4431:PSU:OP2	52:LI:3:ARG:NH2	2.35	0.57
41:L5:4563:U:H2'	41:L5:4564:A:H8	1.70	0.57
56:LN:5:LYS:HG3	75:Li:40:VAL:HG11	1.86	0.57
5:SE:11:ARG:NH1	5:SE:21:ASP:O	2.38	0.57
20:S2:1179:G:N2	20:S2:1182:A:OP2	2.32	0.57
37:Sg:10:THR:HG22	37:Sg:308:ARG:HG2	1.86	0.57
41:L5:3689:G:O2'	41:L5:3818:UY1:OP2	2.22	0.57
41:L5:4210:U:O2	41:L5:4222:G:N2	2.28	0.57
25:SF:130:ARG:O	25:SF:136:ARG:NH1	2.37	0.57
41:L5:4966:A:H5''	45:LB:128:LYS:HG3	1.87	0.57
20:S2:28:U:H2'	20:S2:29:G:H8	1.69	0.57
37:Sg:44:LYS:N	37:Sg:54:ILE:O	2.37	0.57
41:L5:1346:C:H2'	41:L5:1347:G:C8	2.40	0.57
41:L5:2693:G:OP2	41:L5:2694:G:O2'	2.23	0.57
41:L5:2764:A:H2'	41:L5:2765:A:H8	1.70	0.57
41:L5:4239:A:H2'	41:L5:4240:G:H8	1.70	0.57
43:L8:22:U:OP1	65:LY:11:ARG:NE	2.38	0.57
47:LD:194:VAL:O	47:LD:198:HIS:ND1	2.32	0.57
54:LL:49:ARG:O	54:LL:149:GLN:NE2	2.37	0.57
20:S2:981:A:H2'	20:S2:982:G:C8	2.40	0.56
20:S2:1512:C:H5''	35:Sd:8:TRP:HZ3	1.70	0.56
41:L5:691:C:H2'	41:L5:692:A:H8	1.69	0.56
46:LC:230:LEU:HD21	46:LC:236:ASN:H	1.70	0.56
20:S2:1606:G:H1	20:S2:1632:G:HO2'	1.53	0.56
41:L5:1077:C:OP1	41:L5:1215:C:O2'	2.23	0.56
41:L5:3653:A:H4'	44:LA:179:ILE:HB	1.87	0.56
41:L5:3880:G:H2'	41:L5:3881:G:C8	2.40	0.56
41:L5:4517:A:OP2	45:LB:2:SER:N	2.37	0.56
41:L5:4612:C:C2	51:LH:120:GLU:HB2	2.40	0.56
63:LV:84:GLN:NE2	63:LV:86:LYS:O	2.37	0.56
83:Lr:38:PHE:O	83:Lr:45:HIS:NE2	2.32	0.56
14:SW:78:ARG:NH1	20:S2:863:PSU:O2'	2.38	0.56
18:Sb:54:VAL:HG23	18:Sb:63:LEU:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:SM:96:ARG:NH2	27:SM:100:PRO:O	2.38	0.56
29:SQ:139:ALA:O	29:SQ:140:ARG:NH1	2.38	0.56
41:L5:153:G:H2'	41:L5:154:G:H8	1.69	0.56
41:L5:469:C:N3	48:LE:105:ARG:NH2	2.40	0.56
41:L5:3896:C:O2	45:LB:268:ARG:NH2	2.38	0.56
41:L5:4076:G:OP1	50:LG:73:ARG:NE	2.39	0.56
41:L5:4220:6MZ:H2'	41:L5:4222:G:H5''	1.88	0.56
41:L5:4764:A:N6	51:LH:60:TRP:O	2.35	0.56
43:L8:76:C:H2'	43:L8:77:A:C8	2.39	0.56
44:LA:206:PRO:HG3	44:LA:213:GLY:HA3	1.87	0.56
85:Lt:10:ILE:HG12	85:Lt:65:GLN:HG2	1.86	0.56
4:SC:194:ARG:NH1	20:S2:1156:U:O4	2.39	0.56
15:SX:46:HIS:HB3	15:SX:101:LEU:HD11	1.88	0.56
20:S2:74:G:H21	20:S2:75:G:H1	1.52	0.56
20:S2:1513:C:H2'	20:S2:1514:G:H8	1.70	0.56
21:LR:168:GLU:HA	21:LR:171:LYS:HG2	1.86	0.56
33:SZ:68:ILE:HG23	33:SZ:109:TYR:HB2	1.87	0.56
36:Sf:119:ARG:HB2	36:Sf:132:MET:HB2	1.87	0.56
41:L5:2520:C:H2'	41:L5:2521:G:H8	1.70	0.56
41:L5:4220:6MZ:H8	41:L5:4220:6MZ:OP2	2.05	0.56
47:LD:238:GLU:HG3	47:LD:242:LYS:HE2	1.87	0.56
58:LP:16:LYS:HG2	58:LP:149:ILE:HG12	1.88	0.56
4:SC:173:LYS:HD3	13:SV:3:ASN:HA	1.88	0.56
20:S2:1069:U:H5''	44:LA:248:GLY:HA2	1.87	0.56
20:S2:1373:C:H5'	23:SR:6:THR:HA	1.88	0.56
39:Pt:18:G:H21	39:Pt:58:A:H5'	1.71	0.56
41:L5:75:G:O2'	54:LL:101:ARG:NH1	2.36	0.56
41:L5:1354:A:N6	41:L5:1503:A:O4'	2.38	0.56
41:L5:1834:U:N3	61:LT:126:VAL:O	2.35	0.56
41:L5:2754:G:O2'	66:LZ:51:ARG:NH1	2.38	0.56
44:LA:101:VAL:HG22	44:LA:165:VAL:HG22	1.87	0.56
37:Sg:220:ASP:HB3	37:Sg:224:GLY:H	1.71	0.56
12:SO:150:ARG:NH2	20:S2:1854:U:OP1	2.34	0.56
20:S2:969:U:O2	20:S2:971:G:N1	2.38	0.56
37:Sg:120:ILE:HB	37:Sg:132:TRP:HB2	1.88	0.56
41:L5:1541:C:H5''	44:LA:21:LYS:HG2	1.88	0.56
41:L5:2448:G:OP2	41:L5:2510:G:N1	2.26	0.56
41:L5:2492:C:H2'	41:L5:2493:G:H8	1.70	0.56
41:L5:4421:C:N4	41:L5:4475:G:N2	2.41	0.56
43:L8:94:G:H21	76:Lj:82:THR:HB	1.70	0.56
1:Zt:18:U:O2'	1:Zt:57:A:N1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:SW:106:THR:OG1	14:SW:109:GLY:O	2.22	0.56
29:SQ:3:SER:OG	29:SQ:4:LYS:N	2.38	0.56
41:L5:1982:G:N2	41:L5:2009:A:O2'	2.39	0.56
45:LB:213:GLN:NE2	45:LB:285:TYR:O	2.31	0.56
58:LP:109:VAL:HA	58:LP:112:LEU:HD13	1.88	0.56
28:SP:18:ARG:NH1	30:SS:88:LYS:O	2.38	0.56
32:SU:56:MET:HG3	32:SU:86:LYS:HD2	1.86	0.56
41:L5:1865:G:N2	41:L5:1868:A:OP2	2.34	0.56
41:L5:2770:C:H2'	41:L5:2771:G:H8	1.71	0.56
41:L5:4353:PSU:H5'	41:L5:4354:U:H5'	1.86	0.56
2:SA:209:GLU:C	2:SA:211:GLU:H	2.14	0.56
28:SP:92:SER:HB2	28:SP:107:ILE:HD13	1.87	0.56
41:L5:728:U:OP1	49:LF:76:ARG:NH2	2.33	0.56
64:LX:64:SER:HB2	74:Lh:69:LEU:HD13	1.86	0.56
72:Lf:40:GLU:O	72:Lf:109:ARG:NH2	2.39	0.56
79:Lm:110:CYS:HB3	79:Lm:115:CYS:SG	2.46	0.56
4:SC:196:ILE:HB	4:SC:223:TYR:HB2	1.87	0.55
20:S2:329:G:H2'	20:S2:330:G:C8	2.41	0.55
41:L5:490:C:N4	41:L5:491:G:O6	2.39	0.55
41:L5:1584:G:O6	89:L5:5282:SPD:N1	2.39	0.55
41:L5:2274:C:H2'	41:L5:2275:G:C8	2.41	0.55
41:L5:3823:G:N2	41:L5:3823:G:OP2	2.39	0.55
42:L7:40:U:O2	53:LJ:75:ARG:NE	2.29	0.55
43:L8:102:G:OP2	43:L8:104:A:O2'	2.23	0.55
48:LE:190:HIS:HB3	48:LE:193:PHE:HD1	1.70	0.55
51:LH:140:GLN:HB2	51:LH:143:GLU:HG3	1.87	0.55
66:LZ:103:ASP:HB3	66:LZ:106:LEU:HB2	1.88	0.55
2:SA:123:VAL:HA	2:SA:145:ILE:O	2.05	0.55
8:SI:125:LYS:HB2	8:SI:128:LYS:HZ1	1.70	0.55
20:S2:149:A:H3'	20:S2:150:A:H8	1.71	0.55
20:S2:1144:A:H2'	20:S2:1145:A:C8	2.41	0.55
20:S2:1233:G:N3	20:S2:1252:C:O2'	2.34	0.55
23:SR:94:GLU:O	23:SR:116:ASN:ND2	2.39	0.55
41:L5:1326:A2M:OP2	41:L5:4445:U:O2'	2.25	0.55
20:S2:1297:U:O2'	20:S2:1299:A:N7	2.39	0.55
37:Sg:68:ASP:HB3	37:Sg:111:VAL:HG12	1.88	0.55
41:L5:1876:U:H2'	41:L5:1877:G:H8	1.71	0.55
41:L5:4637:OMG:OP1	70:Ld:30:HIS:NE2	2.39	0.55
48:LE:222:LEU:HB3	48:LE:237:LYS:HE2	1.88	0.55
20:S2:531:A:H3'	20:S2:532:C:H5''	1.87	0.55
20:S2:629:A:O2'	20:S2:631:U:OP1	2.25	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1217:A:H2'	20:S2:1218:C:C6	2.41	0.55
20:S2:1221:G:H2'	20:S2:1222:G:H8	1.71	0.55
41:L5:1457:G:O2'	59:LQ:75:ARG:NH2	2.39	0.55
41:L5:3688:U:OP2	44:LA:198:ARG:NH2	2.38	0.55
41:L5:3932:U:H2'	41:L5:3933:G:H8	1.70	0.55
41:L5:4670:C:O2'	41:L5:4672:A:OP2	2.23	0.55
3:SB:65:ARG:H	3:SB:88:THR:HG22	1.71	0.55
4:SC:104:ASP:HA	4:SC:130:ILE:HG22	1.88	0.55
16:SY:57:VAL:HB	16:SY:60:PHE:HE1	1.71	0.55
20:S2:1271:C:OP1	36:Sf:92:LYS:NZ	2.39	0.55
20:S2:1360:U:O2'	20:S2:1379:A:OP2	2.22	0.55
41:L5:136:C:N4	74:Lh:77:LYS:O	2.40	0.55
41:L5:2848:G:O2'	41:L5:3838:U:O4	2.24	0.55
43:L8:153:C:H2'	43:L8:154:G:H8	1.71	0.55
46:LC:2:ALA:HA	46:LC:29:LYS:HD2	1.88	0.55
51:LH:102:ASN:HB2	51:LH:115:ARG:HB2	1.88	0.55
64:LX:115:LYS:HE3	64:LX:116:LEU:HD23	1.87	0.55
10:SL:59:LYS:NZ	20:S2:374:G:OP1	2.38	0.55
12:SO:83:GLN:OE1	34:Sc:5:ARG:NH1	2.39	0.55
20:S2:1010:G:H2'	20:S2:1011:A:C8	2.41	0.55
20:S2:1673:U:O2'	25:SF:84:GLY:O	2.23	0.55
41:L5:1741:G:O2'	41:L5:1781:PSU:OP2	2.20	0.55
41:L5:1802:A:H5''	41:L5:1803:G:H5'	1.88	0.55
41:L5:2739:C:O2	44:LA:188:LYS:NZ	2.36	0.55
41:L5:3717:A:OP2	41:L5:3735:G:N2	2.35	0.55
48:LE:131:LYS:O	48:LE:136:HIS:NE2	2.38	0.55
51:LH:51:LYS:HG3	51:LH:52:LYS:HG2	1.89	0.55
41:L5:2295:C:H2'	41:L5:2296:G:H8	1.72	0.55
85:Lt:109:ILE:HA	85:Lt:112:ILE:HG12	1.89	0.55
4:SC:168:GLY:N	4:SC:179:THR:O	2.34	0.55
17:Sa:5:ARG:HH21	20:S2:1864:U:H3'	1.72	0.55
20:S2:1616:U:O2'	20:S2:1661:A:N3	2.34	0.55
24:SD:158:ILE:HG23	24:SD:189:MET:HE1	1.87	0.55
27:SM:16:THR:HA	27:SM:19:GLN:HB3	1.88	0.55
39:Pt:50:U:O4	39:Pt:64:G:O6	2.24	0.55
40:CI:79:ARG:HH12	41:L5:2708:U:H4'	1.72	0.55
41:L5:730:G:N3	49:LF:73:ARG:NH1	2.54	0.55
41:L5:1730:U:H1'	61:LT:101:SER:HB3	1.88	0.55
41:L5:3848:U:H2'	41:L5:3849:A:H8	1.71	0.55
41:L5:5005:G:N2	41:L5:5041:G:O2'	2.39	0.55
5:SE:45:ILE:HA	5:SE:61:VAL:HG21	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:SI:163:GLU:O	8:SI:167:GLN:HG2	2.07	0.55
12:SO:145:GLY:O	17:Sa:22:ARG:NH2	2.40	0.55
20:S2:1438:A:H2'	20:S2:1439:A:C8	2.42	0.55
20:S2:1829:G:H1'	20:S2:1850:MA6:H2	1.88	0.55
21:LR:38:ARG:NH2	41:L5:2527:A:OP1	2.35	0.55
37:Sg:292:SER:OG	37:Sg:294:ASP:OD1	2.24	0.55
41:L5:260:C:N4	41:L5:261:G:O6	2.40	0.55
41:L5:2279:A:O2'	71:Le:48:ARG:NH2	2.40	0.55
41:L5:3653:A:N1	41:L5:3692:A:H4'	2.21	0.55
41:L5:4389:C:H2'	41:L5:4390:A:C8	2.42	0.55
51:LH:114:ILE:HB	51:LH:124:ARG:HB2	1.88	0.55
57:LO:54:TYR:OH	57:LO:73:PHE:O	2.25	0.55
3:SB:224:GLU:HB3	3:SB:227:LYS:HE3	1.88	0.55
3:SB:228:LEU:HD12	3:SB:231:LEU:HD11	1.89	0.55
6:SG:218:LYS:HA	6:SG:221:LYS:HE3	1.89	0.55
11:SN:47:PRO:HD2	11:SN:86:GLU:HG3	1.89	0.55
11:SN:75:LEU:HB3	11:SN:81:ALA:HB2	1.89	0.55
20:S2:1221:G:H2'	20:S2:1222:G:C8	2.42	0.55
28:SP:32:GLN:HA	28:SP:35:GLN:HG2	1.88	0.55
41:L5:947:C:OP1	46:LC:336:ARG:NH1	2.40	0.55
41:L5:4363:A:H5''	81:Lo:36:GLN:HG2	1.88	0.55
48:LE:127:SER:HB3	48:LE:130:LYS:HD3	1.89	0.55
41:L5:1461:C:H2'	41:L5:1462:A:C8	2.42	0.54
41:L5:1976:G:N2	85:Lt:139:VAL:O	2.40	0.54
41:L5:2059:C:H2'	41:L5:2060:G:H8	1.72	0.54
41:L5:4274:A:H2'	41:L5:4275:G:H8	1.71	0.54
6:SG:133:LEU:O	20:S2:168:C:O2'	2.25	0.54
20:S2:1679:A:H5''	34:Sc:20:ARG:HH22	1.71	0.54
41:L5:4991:U:H2'	41:L5:4992:G:H8	1.72	0.54
41:L5:5037:U:H2'	41:L5:5038:A:C8	2.43	0.54
52:LI:43:VAL:HG11	52:LI:197:VAL:HG13	1.89	0.54
54:LL:127:PHE:HB2	74:Lh:118:LYS:HB3	1.89	0.54
3:SB:120:MET:HE2	3:SB:142:PHE:HE1	1.73	0.54
3:SB:134:LEU:HB3	3:SB:218:LEU:HB2	1.88	0.54
5:SE:9:LEU:HB2	5:SE:30:ARG:HD3	1.89	0.54
20:S2:640:A:H2'	20:S2:641:A:C8	2.42	0.54
20:S2:1446:A:H5''	32:SU:58:THR:HG23	1.89	0.54
41:L5:959:G:O2'	41:L5:2263:A:N6	2.38	0.54
41:L5:2363:A2M:H2'	41:L5:2364:OMG:O4'	2.08	0.54
41:L5:3726:A:O2'	41:L5:3727:A:O5'	2.22	0.54
41:L5:4077:A:N1	41:L5:4171:C:N4	2.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:4573:G:N2	41:L5:4722:G:OP2	2.41	0.54
53:LJ:112:HIS:ND1	53:LJ:126:TYR:O	2.38	0.54
2:SA:71:PRO:HB3	2:SA:186:ARG:HH12	1.72	0.54
20:S2:671:A:H4'	20:S2:672:A:H5''	1.88	0.54
20:S2:1560:U:O2	20:S2:1575:G:O6	2.25	0.54
32:SU:80:PHE:HB3	35:Sd:52:PHE:HB3	1.89	0.54
37:Sg:202:PRO:HG2	37:Sg:243:PRO:HA	1.88	0.54
41:L5:102:G:H2'	41:L5:103:G:H8	1.72	0.54
41:L5:279:A:OP1	56:LN:50:ARG:NH1	2.41	0.54
41:L5:425:U:H2'	41:L5:426:A:H8	1.72	0.54
41:L5:1628:C:OP1	44:LA:14:SER:OG	2.24	0.54
41:L5:1876:U:H2'	41:L5:1877:G:C8	2.43	0.54
43:L8:79:G:H2'	43:L8:80:A:N3	2.23	0.54
45:LB:219:VAL:HG11	45:LB:337:VAL:HG13	1.88	0.54
10:SL:85:THR:HG21	20:S2:373:G:H4'	1.89	0.54
10:SL:119:ASP:O	10:SL:147:LYS:NZ	2.39	0.54
37:Sg:166:VAL:HG12	37:Sg:176:VAL:HG12	1.89	0.54
41:L5:1591:U:OP2	41:L5:2856:C:O2'	2.25	0.54
41:L5:2634:C:H2'	41:L5:2635:U:H6	1.73	0.54
41:L5:3607:U:H2'	41:L5:3608:A:H8	1.73	0.54
41:L5:3732:A:H2'	41:L5:3733:A:H8	1.73	0.54
41:L5:3844:PSU:H2'	41:L5:3845:A:H8	1.72	0.54
2:SA:102:ARG:HH12	20:S2:1377:U:H3'	1.73	0.54
4:SC:70:VAL:HG11	4:SC:93:ILE:HG12	1.90	0.54
15:SX:51:VAL:HA	15:SX:72:VAL:HG22	1.89	0.54
20:S2:652:U:H2'	20:S2:653:A:C8	2.42	0.54
30:SS:63:GLU:HG2	30:SS:66:ARG:HH21	1.73	0.54
41:L5:2558:C:H2'	41:L5:2559:G:H8	1.71	0.54
41:L5:2758:G:O2'	41:L5:2765:A:N3	2.35	0.54
88:L5:5290:SPM:H112	57:LO:91:LYS:HD3	1.90	0.54
49:LF:127:LYS:HB2	61:LT:133:ALA:HB3	1.89	0.54
50:LG:205:THR:HG22	50:LG:206:GLN:H	1.72	0.54
3:SB:216:LYS:NZ	20:S2:943:U:OP1	2.41	0.54
6:SG:227:GLN:HB3	6:SG:231:ARG:HH21	1.71	0.54
8:SI:184:ARG:HD2	20:S2:219:U:H1'	1.89	0.54
20:S2:807:G:H2'	20:S2:808:A:C8	2.43	0.54
20:S2:1093:A:H2'	20:S2:1094:C:C6	2.42	0.54
20:S2:1182:A:OP1	80:Ln:18:ARG:NH1	2.40	0.54
20:S2:1851:MA6:OP1	80:Ln:9:ARG:NH2	2.36	0.54
24:SD:99:ILE:HG23	24:SD:173:ARG:HH21	1.71	0.54
27:SM:48:HIS:HB3	27:SM:114:TYR:CZ	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:ST:85:ASN:HB3	31:ST:88:MET:HB2	1.89	0.54
41:L5:120:A:N1	41:L5:148:C:O2'	2.36	0.54
41:L5:909:A:H2'	41:L5:910:G:H8	1.72	0.54
41:L5:1732:C:H5''	61:LT:43:LYS:HE2	1.88	0.54
41:L5:3664:G:H2'	41:L5:3665:G:H8	1.72	0.54
41:L5:3918:G:H1	41:L5:4383:U:H3	1.54	0.54
41:L5:4601:U:H2'	41:L5:4602:A:H8	1.71	0.54
69:Lc:60:ILE:HD13	69:Lc:93:THR:HG21	1.88	0.54
7:SH:63:PHE:HA	7:SH:95:ILE:O	2.07	0.54
41:L5:146:G:H2'	41:L5:147:A:H8	1.72	0.54
41:L5:513:U:N3	41:L5:516:C:OP2	2.32	0.54
41:L5:1495:G:H4'	59:LQ:187:LYS:HE3	1.90	0.54
41:L5:2032:U:H2'	41:L5:2033:A:C8	2.42	0.54
41:L5:2327:G:H2'	41:L5:2328:G:H8	1.73	0.54
41:L5:3928:A:OP1	56:LN:90:ASN:ND2	2.41	0.54
48:LE:164:PHE:HA	48:LE:175:VAL:HG12	1.89	0.54
53:LJ:15:LEU:HD12	53:LJ:165:TRP:HB2	1.88	0.54
3:SB:124:HIS:HA	3:SB:137:LEU:O	2.07	0.54
16:SY:41:ARG:HG3	16:SY:55:ILE:HB	1.90	0.54
20:S2:797:C:O2'	20:S2:799:OMU:OP1	2.25	0.54
20:S2:1748:G:H1	20:S2:1786:U:H3	1.54	0.54
24:SD:135:GLU:HB2	24:SD:153:VAL:HG23	1.88	0.54
41:L5:4991:U:H2'	41:L5:4992:G:C8	2.43	0.54
57:LO:81:TRP:HB2	57:LO:104:VAL:HG21	1.90	0.54
85:Lt:59:THR:HA	85:Lt:80:LEU:HD11	1.88	0.54
8:SI:3:ILE:O	8:SI:30:GLY:N	2.41	0.54
20:S2:430:C:H2'	20:S2:431:G:H8	1.73	0.54
20:S2:528:A:H2'	20:S2:529:A:C8	2.43	0.54
20:S2:1166:G:H1	20:S2:1193:U:H3	1.55	0.54
20:S2:1420:G:O2'	20:S2:1421:A:N3	2.41	0.54
27:SM:58:GLU:OE1	27:SM:61:TYR:N	2.40	0.54
35:Sd:3:HIS:CE1	35:Sd:5:GLN:HB2	2.42	0.54
41:L5:183:C:H1'	41:L5:184:U:H5	1.72	0.54
41:L5:444:G:H2'	41:L5:445:U:H6	1.73	0.54
41:L5:1548:G:O2'	41:L5:2812:A:N3	2.38	0.54
41:L5:1556:C:O2'	41:L5:2669:C:OP1	2.24	0.54
71:Le:65:LYS:O	71:Le:75:ARG:NH2	2.36	0.54
1:Zt:43:A:H2'	1:Zt:44:G:C8	2.43	0.53
2:SA:209:GLU:HA	2:SA:212:LYS:HG2	1.89	0.53
6:SG:10:THR:HA	6:SG:128:THR:HG23	1.88	0.53
10:SL:39:ASN:O	20:S2:292:A:O2'	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LR:100:ARG:NE	41:L5:2667:C:OP1	2.37	0.53
23:SR:78:ARG:O	23:SR:79:GLU:C	2.50	0.53
38:At:9:A:H1'	38:At:45:G:H2'	1.89	0.53
41:L5:2714:G:H2'	41:L5:2715:G:H8	1.72	0.53
41:L5:2835:A:O2'	45:LB:228:TYR:O	2.24	0.53
41:L5:4441:A:H5''	52:LI:114:GLY:HA2	1.88	0.53
41:L5:4575:G:H2'	41:L5:4576:PSU:H6	1.73	0.53
41:L5:4967:A:OP1	45:LB:125:SER:OG	2.23	0.53
7:SH:157:HIS:ND1	7:SH:188:GLU:OE2	2.41	0.53
20:S2:517:OMC:HM22	20:S2:518:G:H5'	1.90	0.53
20:S2:1174:PSU:H2'	20:S2:1175:G:H8	1.74	0.53
20:S2:1314:U:O2'	26:SK:8:ARG:NH2	2.42	0.53
20:S2:1720:U:O2'	41:L5:3796:U:O2'	2.21	0.53
41:L5:194:C:O2	65:LY:121:ARG:NH2	2.41	0.53
41:L5:1700:G:OP2	41:L5:1700:G:N2	2.35	0.53
41:L5:4503:A:H2'	41:L5:4504:C:C6	2.43	0.53
6:SG:67:VAL:HG12	6:SG:69:THR:HG22	1.90	0.53
37:Sg:157:SER:HB3	37:Sg:164:ILE:HG22	1.89	0.53
41:L5:512:U:H3	41:L5:647:G:H1	1.54	0.53
41:L5:1824:G:H2'	41:L5:1825:A:C8	2.44	0.53
41:L5:2663:G:N2	41:L5:2676:A:O2'	2.40	0.53
41:L5:4149:C:OP1	66:LZ:59:LYS:N	2.39	0.53
41:L5:4322:G:N2	41:L5:4325:A:OP2	2.36	0.53
65:LY:33:PRO:HG2	65:LY:105:VAL:HG12	1.90	0.53
6:SG:2:LYS:HD3	6:SG:15:LEU:HD21	1.89	0.53
8:SI:47:ARG:HH22	20:S2:446:G:P	2.31	0.53
20:S2:432:G:H2'	20:S2:433:A:C8	2.44	0.53
20:S2:603:C:N4	20:S2:620:G:O6	2.41	0.53
20:S2:1422:G:H4'	20:S2:1423:C:H3'	1.90	0.53
27:SM:32:ALA:HB3	27:SM:110:VAL:HB	1.89	0.53
28:SP:22:LEU:HA	28:SP:25:LEU:HB2	1.88	0.53
41:L5:173:C:H5''	54:LL:129:ARG:HH12	1.71	0.53
41:L5:492:U:H2'	41:L5:493:G:C8	2.43	0.53
41:L5:1478:C:H2'	41:L5:1479:G:H8	1.73	0.53
41:L5:1480:C:O2'	41:L5:1482:G:OP2	2.26	0.53
41:L5:1645:C:H2'	41:L5:1646:A:C8	2.43	0.53
41:L5:3893:C:H2'	41:L5:3894:A:H8	1.72	0.53
41:L5:5047:C:O2'	41:L5:5050:C:OP2	2.23	0.53
43:L8:41:A:HO2'	76:Lj:59:THR:HG1	1.57	0.53
57:LO:168:TYR:CE2	57:LO:172:LYS:HD2	2.43	0.53
3:SB:114:VAL:O	20:S2:1869:A:N6	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:SH:30:LEU:HB3	7:SH:37:LYS:HZ2	1.72	0.53
11:SN:110:ASP:OD2	20:S2:934:G:N2	2.38	0.53
20:S2:588:G:H4'	20:S2:589:G:H5'	1.91	0.53
20:S2:1103:C:H2'	20:S2:1104:G:C8	2.44	0.53
20:S2:1547:C:O2	20:S2:1669:G:N2	2.36	0.53
20:S2:1759:G:N2	20:S2:1760:G:O6	2.41	0.53
34:Sc:21:THR:OG1	34:Sc:66:ARG:NH2	2.38	0.53
45:LB:17:LEU:O	45:LB:19:ARG:N	2.41	0.53
60:LS:83:ARG:HG3	60:LS:125:GLN:HB3	1.91	0.53
3:SB:88:THR:HA	3:SB:98:THR:HA	1.89	0.53
20:S2:1804:U:H2'	20:S2:1805:G:H8	1.73	0.53
25:SF:17:ILE:HG21	25:SF:46:ALA:HB1	1.91	0.53
25:SF:49:LEU:HD22	29:SQ:49:TYR:HB2	1.91	0.53
41:L5:10:A:H2'	41:L5:11:G:C8	2.44	0.53
41:L5:172:C:H4'	41:L5:173:C:H5'	1.89	0.53
41:L5:208:A:N3	41:L5:232:G:O2'	2.42	0.53
41:L5:267:G:OP1	74:Lh:109:ARG:NH2	2.40	0.53
41:L5:375:G:N7	76:Lj:56:ARG:NH2	2.55	0.53
41:L5:1094:G:O6	41:L5:1201:U:O2	2.27	0.53
41:L5:1097:C:H2'	41:L5:1098:G:C8	2.44	0.53
41:L5:1197:C:H2'	41:L5:1198:G:C8	2.44	0.53
41:L5:3944:G:N2	41:L5:4069:U:O2	2.27	0.53
41:L5:4683:U:OP2	41:L5:4706:G:N1	2.32	0.53
42:L7:15:C:H2'	42:L7:16:A:H8	1.74	0.53
6:SG:13:GLN:HE21	20:S2:153:G:H21	1.55	0.53
25:SF:68:ILE:HD11	25:SF:116:ILE:HG13	1.90	0.53
37:Sg:21:ILE:N	37:Sg:288:SER:OG	2.41	0.53
41:L5:66:A:O2'	41:L5:326:C:O2	2.23	0.53
41:L5:1415:G:H2'	41:L5:1416:G:H8	1.73	0.53
41:L5:1458:C:H5''	59:LQ:69:LYS:HD2	1.91	0.53
41:L5:1942:A:H2'	41:L5:1943:A:C8	2.44	0.53
42:L7:28:C:O2'	42:L7:54:A:N1	2.41	0.53
3:SB:136:ARG:HB2	3:SB:216:LYS:HG3	1.91	0.53
6:SG:92:ARG:O	20:S2:453:C:O2'	2.21	0.53
19:Se:32:ALA:HB2	20:S2:525:A:H5''	1.91	0.53
20:S2:1293:A:N3	36:Sf:138:ARG:NH2	2.56	0.53
21:LR:134:ASN:H	21:LR:137:ILE:HD11	1.74	0.53
24:SD:172:VAL:HG22	24:SD:185:LYS:HG2	1.91	0.53
39:Pt:9:A:O2'	39:Pt:10:G:N7	2.32	0.53
41:L5:4537:C:H2'	41:L5:4538:G:H8	1.74	0.53
44:LA:95:GLN:O	44:LA:100:ASN:ND2	2.35	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:Lk:8:ILE:HD13	77:Lk:45:LEU:HD21	1.90	0.53
77:Lk:49:ASP:HB3	77:Lk:52:LYS:HB2	1.90	0.53
5:SE:6:LYS:O	5:SE:30:ARG:NH2	2.41	0.53
7:SH:140:VAL:HG12	11:SN:19:ARG:HD3	1.90	0.53
20:S2:573:U:O2	20:S2:576:A2M:H8	2.08	0.53
24:SD:163:PRO:HA	24:SD:166:TYR:CZ	2.44	0.53
41:L5:1787:A:O3'	88:L5:5255:SPM:N14	2.42	0.53
41:L5:2640:G:H2'	41:L5:2641:A:C8	2.44	0.53
41:L5:2699:C:H2'	41:L5:2700:G:H8	1.74	0.53
46:LC:14:LYS:HA	46:LC:173:LYS:HD3	1.89	0.53
58:LP:18:ARG:NH2	58:LP:147:GLU:OE1	2.41	0.53
1:Zt:28:C:H2'	1:Zt:29:A:C8	2.44	0.53
20:S2:656:G:H21	20:S2:663:C:H5''	1.74	0.53
20:S2:1113:A:N6	20:S2:1121:G:O6	2.42	0.53
20:S2:1826:G:HO2'	41:L5:3759:A:HO2'	1.57	0.53
41:L5:1332:C:H2'	41:L5:1333:A:C8	2.44	0.53
41:L5:1845:U:H2'	41:L5:1846:G:H8	1.74	0.53
41:L5:4106:G:H3'	41:L5:4107:G:H8	1.73	0.53
3:SB:63:LYS:NZ	3:SB:90:ASP:OD1	2.30	0.52
3:SB:128:LYS:HE3	3:SB:134:LEU:HD13	1.91	0.52
3:SB:171:ILE:HD11	3:SB:197:ILE:HG12	1.89	0.52
7:SH:53:VAL:HG11	7:SH:172:THR:HA	1.90	0.52
16:SY:79:LEU:O	16:SY:83:LYS:HG3	2.09	0.52
20:S2:934:G:O6	20:S2:1008:A:N1	2.42	0.52
24:SD:75:LYS:HZ1	26:SK:18:GLU:HG3	1.74	0.52
41:L5:399:G:N2	58:LP:101:ASN:OD1	2.39	0.52
41:L5:935:A:N7	55:LM:46:ARG:NH2	2.56	0.52
41:L5:1333:A:H2'	41:L5:1334:A:C8	2.44	0.52
41:L5:2458:C:H5''	56:LN:67:ARG:HD2	1.91	0.52
41:L5:4188:U:H2'	41:L5:4189:U:C6	2.43	0.52
41:L5:4274:A:H2'	41:L5:4275:G:C8	2.44	0.52
41:L5:4458:C:H2'	41:L5:4459:U:C6	2.44	0.52
42:L7:63:C:H5'	42:L7:64:G:H5''	1.91	0.52
43:L8:60:G:O6	74:Lh:62:ASN:ND2	2.28	0.52
4:SC:78:LEU:HD12	4:SC:81:ILE:HD12	1.91	0.52
16:SY:86:GLU:OE2	16:SY:90:ARG:NH1	2.41	0.52
20:S2:454:U:H2'	20:S2:455:A:H8	1.75	0.52
20:S2:1231:C:H42	20:S2:1527:C:H42	1.56	0.52
20:S2:1386:A:OP2	24:SD:160:SER:OG	2.24	0.52
20:S2:1533:A:H62	20:S2:1602:U:H3	1.56	0.52
29:SQ:78:VAL:HA	29:SQ:81:ILE:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Sg:10:THR:HB	37:Sg:306:LEU:HD21	1.91	0.52
41:L5:2846:G:H2'	41:L5:2847:G:H8	1.73	0.52
43:L8:28:C:H2'	43:L8:29:G:H8	1.73	0.52
1:Zt:61:C:O5'	41:L5:4056:A:O2'	2.24	0.52
5:SE:57:THR:OG1	5:SE:59:ASP:OD1	2.26	0.52
9:SJ:109:ARG:NH2	9:SJ:111:GLN:OE1	2.42	0.52
12:SO:59:GLY:HA2	12:SO:68:GLU:HG2	1.91	0.52
20:S2:1407:U:O2'	29:SQ:11:GLN:OE1	2.25	0.52
20:S2:1546:G:H1	20:S2:1655:C:H1'	1.75	0.52
20:S2:1562:C:H2'	20:S2:1563:G:C8	2.43	0.52
29:SQ:21:ALA:O	29:SQ:87:SER:OG	2.27	0.52
32:SU:27:ARG:HD3	32:SU:82:MET:HE3	1.90	0.52
41:L5:422:C:H2'	41:L5:423:G:H8	1.74	0.52
41:L5:1514:U:H2'	41:L5:1515:A:H8	1.74	0.52
41:L5:1751:A:H2'	41:L5:1752:G:H8	1.73	0.52
41:L5:4260:U:H2'	41:L5:4261:C:C6	2.44	0.52
41:L5:4761:G:OP2	57:LO:37:ARG:NH2	2.41	0.52
49:LF:236:ARG:HD3	49:LF:239:GLN:HB2	1.91	0.52
84:Ls:100:ASP:OD1	84:Ls:101:MET:N	2.42	0.52
9:SJ:145:PRO:HD2	20:S2:522:A:H5''	1.91	0.52
17:Sa:51:ARG:O	17:Sa:55:GLU:HG2	2.10	0.52
39:Pt:52:G:H2'	39:Pt:53:G:H8	1.74	0.52
41:L5:163:A:H2'	41:L5:164:G:C8	2.45	0.52
41:L5:1854:G:N2	41:L5:4394:A:O4'	2.42	0.52
41:L5:5051:C:H4'	45:LB:324:GLY:HA2	1.91	0.52
44:LA:229:ALA:HB3	44:LA:234:LYS:HB3	1.92	0.52
45:LB:57:VAL:HG22	45:LB:73:VAL:HG12	1.91	0.52
3:SB:84:PHE:HB3	3:SB:86:LEU:HD23	1.91	0.52
6:SG:195:LYS:NZ	20:S2:126:G:OP2	2.42	0.52
11:SN:103:GLU:HA	11:SN:106:ARG:HH11	1.75	0.52
20:S2:888:U:H4'	20:S2:889:U:H5'	1.92	0.52
20:S2:1344:A:N1	20:S2:1385:G:O2'	2.40	0.52
20:S2:1468:C:H2'	20:S2:1469:A:H8	1.74	0.52
33:SZ:99:LEU:HD21	33:SZ:102:LYS:HB2	1.91	0.52
41:L5:2017:A:O2'	41:L5:2018:C:O5'	2.25	0.52
41:L5:2348:G:OP1	41:L5:2351:OMC:N4	2.43	0.52
41:L5:2444:U:HO2'	43:L8:112:G:HO2'	1.55	0.52
41:L5:2606:G:O2'	41:L5:2667:C:N3	2.42	0.52
41:L5:3917:A:H2'	41:L5:3918:G:H8	1.75	0.52
41:L5:4321:U:H2'	41:L5:4322:G:C8	2.44	0.52
41:L5:4890:G:H2'	41:L5:4891:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:LC:116:ASN:HB2	46:LC:119:GLN:HG3	1.91	0.52
47:LD:62:CYS:HB3	47:LD:105:LEU:HD22	1.92	0.52
70:Ld:23:ARG:HG2	70:Ld:121:ASN:HA	1.92	0.52
77:Lk:15:ALA:HA	77:Lk:36:VAL:HG21	1.91	0.52
84:Ls:175:LEU:HD21	84:Ls:182:PRO:HB3	1.91	0.52
3:SB:127:VAL:HG21	3:SB:176:VAL:HB	1.92	0.52
10:SL:128:VAL:HG12	10:SL:142:VAL:HA	1.92	0.52
14:SW:101:PHE:HA	14:SW:113:HIS:HE1	1.75	0.52
20:S2:991:G:C6	20:S2:1134:G:H4'	2.45	0.52
38:At:15:G:O6	38:At:48:C:O2	2.28	0.52
41:L5:1645:C:H2'	41:L5:1646:A:H8	1.75	0.52
41:L5:2295:C:O2'	46:LC:45:ARG:NH2	2.43	0.52
41:L5:2483:G:O6	41:L5:2495:U:O2	2.28	0.52
41:L5:3816:A:OP1	41:L5:3818:UY1:N1	2.43	0.52
2:SA:122:LEU:HB2	2:SA:142:LEU:HD21	1.92	0.52
8:SI:31:ARG:HE	20:S2:380:G:H5''	1.75	0.52
16:SY:7:ILE:HG13	16:SY:43:LYS:HG2	1.91	0.52
18:Sb:72:ARG:HH22	20:S2:1119:A:H2'	1.74	0.52
20:S2:1545:A:H2'	20:S2:1546:G:C8	2.45	0.52
25:SF:135:ARG:O	25:SF:203:ASN:ND2	2.43	0.52
41:L5:10:A:H2'	41:L5:11:G:H8	1.74	0.52
41:L5:1241:C:H1'	68:Lb:119:CYS:HA	1.92	0.52
41:L5:1646:A:O2'	76:Lj:49:TRP:O	2.26	0.52
41:L5:2386:U:H2'	41:L5:2387:G:H8	1.74	0.52
41:L5:2573:A:O3'	66:LZ:115:LYS:NZ	2.41	0.52
8:SI:7:ASN:O	8:SI:18:ARG:NH1	2.42	0.52
8:SI:89:GLU:HA	8:SI:92:ARG:HD3	1.91	0.52
16:SY:7:ILE:HG23	16:SY:27:VAL:HG12	1.92	0.52
20:S2:359:U:H3	20:S2:403:G:H1	1.58	0.52
20:S2:1103:C:H2'	20:S2:1104:G:H8	1.75	0.52
20:S2:1542:C:H4'	31:ST:11:GLN:HB2	1.90	0.52
25:SF:40:ALA:HB3	25:SF:67:PRO:HA	1.92	0.52
41:L5:1996:C:H4'	85:Lt:124:GLU:HG3	1.91	0.52
41:L5:4657:U:O2'	41:L5:4659:G:OP2	2.27	0.52
54:LL:69:LYS:HG3	54:LL:159:ASN:HD21	1.74	0.52
79:Lm:99:CYS:HB2	79:Lm:114:LYS:HE3	1.91	0.52
17:Sa:34:LYS:NZ	20:S2:1862:G:O6	2.42	0.52
20:S2:17:C:H2'	20:S2:18:C:H6	1.75	0.52
20:S2:432:G:H2'	20:S2:433:A:H8	1.75	0.52
20:S2:804:U:H3	20:S2:859:G:H1	1.57	0.52
20:S2:907:G:H2'	20:S2:908:A:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:SD:106:ARG:HG2	24:SD:175:VAL:HG22	1.90	0.52
24:SD:218:LEU:HD11	37:Sg:189:ILE:HB	1.91	0.52
41:L5:300:A:H2'	41:L5:301:G:H8	1.73	0.52
41:L5:676:C:H2'	41:L5:677:G:H8	1.75	0.52
41:L5:1878:G:H2'	41:L5:1879:C:C6	2.44	0.52
41:L5:2055:G:O5'	57:LO:130:LYS:NZ	2.39	0.52
4:SC:68:ARG:HG2	4:SC:277:HIS:HB2	1.92	0.52
4:SC:138:GLY:HA3	4:SC:162:ILE:HD13	1.90	0.52
5:SE:37:LYS:NZ	20:S2:346:C:OP2	2.42	0.52
5:SE:152:PRO:HG3	6:SG:213:LEU:HD13	1.90	0.52
20:S2:895:G:H2'	20:S2:896:U:H4'	1.91	0.52
20:S2:1628:C:H2'	20:S2:1629:C:C6	2.45	0.52
37:Sg:152:SER:OG	37:Sg:168:CYS:SG	2.64	0.52
41:L5:248:C:H2'	41:L5:249:C:H6	1.74	0.52
41:L5:1446:C:H2'	41:L5:1447:C:C6	2.45	0.52
41:L5:2483:G:O6	41:L5:2495:U:C2	2.63	0.52
41:L5:2609:G:H1	41:L5:2730:U:H3	1.58	0.52
4:SC:207:ALA:HB2	20:S2:4:C:H4'	1.91	0.51
41:L5:1326:A2M:H2'	41:L5:1327:C:C6	2.45	0.51
41:L5:1350:C:H2'	41:L5:1351:G:H8	1.75	0.51
41:L5:2395:A:HO2'	41:L5:2806:A:HO2'	1.51	0.51
41:L5:4736:C:H2'	41:L5:4737:G:C8	2.44	0.51
41:L5:5037:U:H2'	41:L5:5038:A:H8	1.75	0.51
18:Sb:59:CYS:SG	18:Sb:61:THR:OG1	2.69	0.51
20:S2:5:U:H2'	20:S2:6:G:H8	1.76	0.51
20:S2:1203:G:H2'	20:S2:1204:A:C8	2.44	0.51
20:S2:1277:C:H2'	20:S2:1278:A:C8	2.44	0.51
23:SR:58:MET:HA	23:SR:61:ILE:HG22	1.93	0.51
25:SF:28:VAL:HG11	25:SF:109:LEU:HB2	1.91	0.51
41:L5:2296:G:O2'	46:LC:242:PRO:O	2.22	0.51
41:L5:3667:C:H4'	44:LA:8:GLN:HA	1.92	0.51
41:L5:3707:U:H3	41:L5:3743:G:H1	1.57	0.51
41:L5:3727:A:H2'	41:L5:3728:A:C8	2.46	0.51
41:L5:3867:A2M:H2'	41:L5:3868:G:O4'	2.10	0.51
41:L5:3916:G:H2'	41:L5:3917:A:H8	1.75	0.51
41:L5:4492:U:H5''	41:L5:4493:PSU:H5''	1.93	0.51
54:LL:59:VAL:HG21	54:LL:73:GLY:HA3	1.91	0.51
54:LL:60:ARG:NH1	54:LL:67:HIS:O	2.42	0.51
2:SA:136:GLU:HA	2:SA:139:TYR:HD2	1.74	0.51
8:SI:73:THR:N	20:S2:301:A:O2'	2.43	0.51
20:S2:72:C:OP1	20:S2:73:C:N4	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LR:134:ASN:OD1	21:LR:135:LYS:N	2.43	0.51
25:SF:32:ASP:OD2	25:SF:34:SER:OG	2.28	0.51
29:SQ:72:VAL:HB	29:SQ:80:GLN:HE21	1.75	0.51
41:L5:4227:OMU:HM21	41:L5:4336:A:H1'	1.92	0.51
42:L7:112:U:H2'	42:L7:113:G:H8	1.75	0.51
59:LQ:151:HIS:ND1	59:LQ:164:LYS:O	2.41	0.51
20:S2:1673:U:H5''	29:SQ:78:VAL:HG12	1.91	0.51
41:L5:2019:C:H2'	41:L5:2020:U:C6	2.45	0.51
41:L5:2361:G:O2'	41:L5:3859:G:O6	2.27	0.51
41:L5:2599:G:N2	41:L5:2747:U:O4	2.43	0.51
41:L5:4761:G:H2'	41:L5:4762:A:C8	2.45	0.51
46:LC:205:ARG:HG3	46:LC:242:PRO:HB3	1.91	0.51
69:Lc:48:LEU:HD11	69:Lc:60:ILE:HG21	1.91	0.51
2:SA:80:ARG:NE	2:SA:82:THR:OG1	2.43	0.51
7:SH:26:ALA:HB1	7:SH:86:LYS:HD3	1.92	0.51
20:S2:509:OMG:H2'	20:S2:510:G:H8	1.75	0.51
41:L5:499:G:N2	41:L5:504:G:O6	2.44	0.51
41:L5:1933:G:H2'	41:L5:1934:A:C8	2.45	0.51
41:L5:2647:A:H3'	41:L5:2648:G:H8	1.75	0.51
41:L5:3726:A:H2'	41:L5:3727:A:C8	2.46	0.51
41:L5:4592:C:H2'	41:L5:4593:C:C6	2.46	0.51
41:L5:4704:C:H2'	41:L5:4705:A:H8	1.76	0.51
41:L5:4759:C:H2'	41:L5:4760:G:C8	2.46	0.51
44:LA:103:PRO:HA	44:LA:163:ARG:HA	1.91	0.51
47:LD:107:ARG:HH12	47:LD:120:GLU:HA	1.74	0.51
55:LM:15:VAL:HG22	55:LM:50:MET:HE1	1.92	0.51
65:LY:56:GLN:HB3	65:LY:67:ILE:HD13	1.91	0.51
4:SC:210:PRO:HB3	4:SC:240:THR:HG21	1.93	0.51
20:S2:1468:C:H2'	20:S2:1469:A:C8	2.46	0.51
20:S2:1777:G:H2'	20:S2:1778:C:H6	1.75	0.51
41:L5:951:G:H2'	41:L5:952:G:H8	1.75	0.51
41:L5:2580:U:OP1	66:LZ:36:ARG:NH1	2.42	0.51
41:L5:2777:G:H5''	41:L5:2778:G:H5'	1.92	0.51
41:L5:4373:G:N7	81:Lo:61:LYS:NZ	2.54	0.51
42:L7:94:C:H2'	42:L7:95:C:H6	1.76	0.51
1:Zt:48:C:H2'	1:Zt:59:G:H1'	1.93	0.51
4:SC:94:ILE:HD11	4:SC:159:LYS:HG2	1.92	0.51
6:SG:137:ARG:HB3	6:SG:140:ARG:HG3	1.93	0.51
20:S2:71:G:H2'	20:S2:72:C:H4'	1.93	0.51
20:S2:1540:G:H2'	20:S2:1541:G:H8	1.76	0.51
20:S2:1588:A:H2'	20:S2:1589:A:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:659:G:H2'	41:L5:660:A:H8	1.74	0.51
41:L5:1086:C:H2'	41:L5:1087:A:H8	1.75	0.51
41:L5:2419:C:H2'	41:L5:2420:A:H8	1.75	0.51
41:L5:4459:U:H2'	41:L5:4460:U:C6	2.45	0.51
41:L5:4761:G:H2'	41:L5:4762:A:H8	1.76	0.51
57:LO:124:LEU:HB3	57:LO:126:VAL:HG12	1.93	0.51
60:LS:173:ASN:ND2	60:LS:175:PHE:O	2.44	0.51
69:Lc:52:CYS:HB3	69:Lc:57:LYS:HE2	1.92	0.51
6:SG:133:LEU:HD12	20:S2:65:C:C4	2.46	0.51
20:S2:980:A:H2'	20:S2:981:A:C8	2.46	0.51
20:S2:1545:A:H4'	29:SQ:75:GLY:H	1.76	0.51
20:S2:1850:MA6:H8	20:S2:1850:MA6:O5'	2.10	0.51
27:SM:99:LYS:HE3	27:SM:102:LYS:H	1.75	0.51
41:L5:32:G:H21	41:L5:50:C:H5	1.57	0.51
41:L5:733:A:N6	41:L5:933:G:O6	2.43	0.51
41:L5:1795:A:N3	42:L7:79:U:O2'	2.44	0.51
41:L5:2611:A:H5'	41:L5:2688:G:H4'	1.93	0.51
43:L8:60:G:OP1	64:LX:68:ARG:NH2	2.38	0.51
85:Lt:76:SER:HB2	85:Lt:117:ARG:HB3	1.92	0.51
4:SC:167:ARG:HB3	4:SC:177:PRO:HB2	1.93	0.51
20:S2:639:C:H2'	20:S2:640:A:C8	2.42	0.51
20:S2:1828:C:H2'	20:S2:1829:G:C8	2.46	0.51
41:L5:419:A:N3	41:L5:1332:C:O2'	2.42	0.51
41:L5:1273:G:N7	68:Lb:117:ARG:NH1	2.59	0.51
41:L5:1677:PSU:H4'	41:L5:1680:G:C2	2.46	0.51
45:LB:302:ASN:HB3	45:LB:314:ILE:H	1.75	0.51
65:LY:82:ILE:HD12	65:LY:85:VAL:HG21	1.93	0.51
84:Ls:95:LEU:HD11	84:Ls:192:VAL:HG11	1.93	0.51
20:S2:29:G:H2'	20:S2:30:C:H6	1.76	0.51
41:L5:1258:G:H2'	41:L5:1259:G:C8	2.45	0.51
41:L5:4362:A:H2'	41:L5:4363:A:H8	1.75	0.51
85:Lt:29:ALA:HA	85:Lt:32:ILE:HG22	1.93	0.51
6:SG:174:PRO:HB3	20:S2:65:C:C6	2.46	0.50
8:SI:49:ARG:HE	20:S2:446:G:H5''	1.76	0.50
10:SL:35:ARG:NH1	10:SL:50:ALA:O	2.44	0.50
20:S2:533:A:H61	20:S2:550:C:H42	1.57	0.50
20:S2:553:U:O4	20:S2:554:A:N6	2.42	0.50
20:S2:952:G:H2'	20:S2:953:C:C6	2.45	0.50
20:S2:1004:PSU:H2'	20:S2:1005:G:H8	1.75	0.50
20:S2:1605:G:N2	20:S2:1633:A:OP2	2.43	0.50
24:SD:215:ASP:HB2	24:SD:217:ILE:HG12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Sc:20:ARG:HD3	34:Sc:28:THR:HG22	1.93	0.50
39:Pt:29:C:H2'	39:Pt:30:G:H8	1.75	0.50
41:L5:745:G:H2'	41:L5:746:A:C8	2.46	0.50
41:L5:2018:C:H2'	41:L5:2019:C:C6	2.46	0.50
41:L5:2361:G:N2	41:L5:3860:A:OP2	2.43	0.50
41:L5:4992:G:H2'	41:L5:4993:G:H8	1.75	0.50
4:SC:64:THR:HG22	4:SC:66:LEU:H	1.77	0.50
9:SJ:131:ARG:NH1	9:SJ:143:ASN:O	2.42	0.50
20:S2:454:U:H2'	20:S2:455:A:C8	2.46	0.50
20:S2:1048:G:N1	20:S2:1069:U:OP2	2.40	0.50
20:S2:1692:U:H2'	20:S2:1693:G:C8	2.47	0.50
30:SS:101:ASN:O	30:SS:105:ASN:ND2	2.44	0.50
31:ST:104:LEU:HD22	31:ST:121:ARG:HD2	1.92	0.50
39:Pt:6:C:H2'	39:Pt:7:G:C8	2.46	0.50
41:L5:278:G:OP2	75:Li:30:ARG:NH2	2.43	0.50
41:L5:1505:C:H2'	41:L5:1506:G:C8	2.46	0.50
41:L5:3683:C:O2'	44:LA:174:ARG:NH2	2.45	0.50
5:SE:134:LYS:N	20:S2:298:G:OP1	2.39	0.50
20:S2:1093:A:H2'	20:S2:1094:C:H6	1.77	0.50
41:L5:180:C:H2'	41:L5:181:C:C6	2.46	0.50
41:L5:907:C:H2'	41:L5:908:G:C8	2.45	0.50
41:L5:1089:G:H2'	41:L5:1090:G:H8	1.76	0.50
41:L5:1315:C:H2'	41:L5:1316:OMG:H8	1.75	0.50
41:L5:1751:A:H2'	41:L5:1752:G:C8	2.46	0.50
43:L8:15:G:O2'	43:L8:16:G:O4'	2.18	0.50
57:LO:34:VAL:HG22	57:LO:103:LYS:HB2	1.94	0.50
79:Lm:79:GLU:OE2	79:Lm:81:SER:OG	2.25	0.50
2:SA:184:ARG:HE	2:SA:191:ARG:HA	1.76	0.50
15:SX:52:LEU:N	15:SX:71:ARG:O	2.39	0.50
20:S2:367:U:H4'	20:S2:371:A:C8	2.45	0.50
20:S2:864:A:H2'	20:S2:865:A:C8	2.44	0.50
20:S2:1101:U:H2'	20:S2:1102:G:H8	1.77	0.50
20:S2:1217:A:H2'	20:S2:1218:C:H6	1.76	0.50
41:L5:1070:G:OP2	48:LE:65:ARG:NH1	2.44	0.50
41:L5:1472:C:N4	41:L5:1493:G:O6	2.43	0.50
41:L5:3861:A:H2'	41:L5:3862:A:H8	1.76	0.50
41:L5:4392:OMG:H2'	41:L5:4447:5MC:HM51	1.94	0.50
1:Zt:8:U:H1'	1:Zt:48:C:H1'	1.92	0.50
18:Sb:68:GLY:HA2	20:S2:928:G:H21	1.75	0.50
20:S2:24:C:O2'	20:S2:25:A:O5'	2.29	0.50
20:S2:1447:G:H2'	20:S2:1448:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:SS:39:ARG:HH11	31:ST:46:ALA:HB2	1.76	0.50
41:L5:261:G:H2'	41:L5:262:G:C8	2.47	0.50
41:L5:326:C:OP2	75:Li:28:ARG:NH2	2.40	0.50
41:L5:382:G:N1	41:L5:385:A:OP2	2.43	0.50
41:L5:1994:C:H2'	41:L5:1995:G:C8	2.46	0.50
41:L5:2275:G:H2'	41:L5:2276:A:C8	2.46	0.50
41:L5:3893:C:H2'	41:L5:3894:A:C8	2.47	0.50
41:L5:4151:G:H2'	41:L5:4152:G:H8	1.76	0.50
49:LF:227:PHE:N	49:LF:233:ALA:O	2.43	0.50
63:LV:13:LYS:HD3	63:LV:128:LEU:HD22	1.92	0.50
72:Lf:58:VAL:HG12	72:Lf:64:PRO:HG3	1.93	0.50
5:SE:29:PRO:HA	20:S2:496:C:H5'	1.94	0.50
7:SH:10:LYS:NZ	7:SH:16:PRO:O	2.43	0.50
7:SH:78:ARG:HH11	7:SH:81:ARG:HH11	1.59	0.50
20:S2:1581:C:H5'	20:S2:1582:C:H5	1.77	0.50
20:S2:1593:C:O2	31:ST:12:GLN:NE2	2.38	0.50
20:S2:1797:U:H2'	20:S2:1798:C:C6	2.47	0.50
22:LW:87:LEU:HD12	22:LW:90:ILE:HD11	1.94	0.50
37:Sg:188:HIS:HD1	37:Sg:219:TRP:CG	2.29	0.50
41:L5:1238:A:O3'	49:LF:48:LYS:NZ	2.44	0.50
41:L5:1348:U:H2'	41:L5:1349:G:H8	1.77	0.50
41:L5:1662:C:H2'	41:L5:1663:C:C6	2.46	0.50
41:L5:2654:C:H2'	41:L5:2655:C:C6	2.46	0.50
41:L5:2754:G:OP2	66:LZ:133:LYS:NZ	2.45	0.50
41:L5:3938:G:N2	41:L5:4171:C:OP2	2.42	0.50
41:L5:4221:C:OP1	88:L5:5260:SPM:N14	2.45	0.50
41:L5:4584:A:OP2	57:LO:148:LYS:NZ	2.34	0.50
42:L7:110:G:H2'	42:L7:111:C:C6	2.46	0.50
45:LB:303:ALA:HB3	45:LB:312:LYS:HG3	1.93	0.50
66:LZ:119:GLU:O	66:LZ:123:LYS:HG2	2.12	0.50
9:SJ:88:ASP:HB3	9:SJ:91:LYS:HB2	1.94	0.50
20:S2:908:A:H5''	21:LR:172:ARG:HH12	1.76	0.50
20:S2:1415:C:H2'	20:S2:1416:C:H6	1.77	0.50
24:SD:225:GLU:O	37:Sg:186:THR:OG1	2.29	0.50
31:ST:18:LEU:HD22	31:ST:58:ALA:HA	1.94	0.50
39:Pt:56:C:C4	81:Lo:104:ILE:HG21	2.47	0.50
41:L5:2495:U:H2'	41:L5:2496:G:C8	2.47	0.50
41:L5:2830:G:H2'	41:L5:2831:G:H8	1.77	0.50
41:L5:4898:G:O6	41:L5:4923:C:N4	2.45	0.50
70:Ld:19:GLU:HA	70:Ld:90:ARG:HH11	1.77	0.50
20:S2:146:G:H2'	20:S2:147:A:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:496:C:H2'	20:S2:497:C:H6	1.77	0.50
20:S2:1409:A:H2'	20:S2:1410:C:C6	2.46	0.50
20:S2:1795:G:H2'	20:S2:1796:G:H8	1.77	0.50
24:SD:126:ILE:O	24:SD:129:SER:OG	2.30	0.50
26:SK:63:ALA:HB2	26:SK:68:TYR:CE2	2.46	0.50
41:L5:1791:U:OP2	88:L5:5255:SPM:N5	2.40	0.50
43:L8:76:C:H2'	43:L8:77:A:H8	1.75	0.50
46:LC:13:GLU:OE1	46:LC:161:TYR:OH	2.26	0.50
12:SO:96:LYS:HD3	12:SO:132:VAL:HG11	1.94	0.50
17:Sa:44:ILE:HG23	17:Sa:45:VAL:HG13	1.93	0.50
20:S2:979:C:H2'	20:S2:980:A:H8	1.76	0.50
32:SU:24:LEU:HD22	32:SU:112:VAL:HG12	1.93	0.50
39:Pt:6:C:H2'	39:Pt:7:G:H8	1.77	0.50
41:L5:52:G:OP1	76:Lj:48:ASN:N	2.38	0.50
41:L5:337:U:OP1	54:LL:35:ARG:NH2	2.44	0.50
41:L5:440:U:H2'	41:L5:441:G:H8	1.77	0.50
41:L5:1995:G:H2'	41:L5:1996:C:C6	2.47	0.50
41:L5:3911:C:H2'	41:L5:3912:U:H6	1.77	0.50
69:Lc:46:VAL:HB	69:Lc:71:VAL:HG22	1.94	0.50
74:Lh:80:PRO:HD2	74:Lh:83:LEU:HD12	1.94	0.50
2:SA:158:ASP:HB2	2:SA:159:ILE:HD12	1.93	0.49
6:SG:133:LEU:HB2	20:S2:65:C:C2	2.46	0.49
7:SH:30:LEU:HG	7:SH:33:ASN:HD22	1.77	0.49
20:S2:1420:G:H21	20:S2:1421:A:H1'	1.76	0.49
26:SK:80:ARG:HH11	26:SK:87:PRO:HA	1.77	0.49
29:SQ:8:GLN:OE1	29:SQ:27:ARG:NH1	2.45	0.49
38:At:40:C:H2'	38:At:41:G:H8	1.75	0.49
41:L5:310:G:H2'	41:L5:311:G:H8	1.77	0.49
41:L5:701:G:H2'	41:L5:702:U:C6	2.46	0.49
41:L5:1269:G:O2'	41:L5:1270:A:O4'	2.27	0.49
41:L5:2759:G:H5'	41:L5:2765:A:H1'	1.94	0.49
51:LH:92:MET:HG2	51:LH:181:VAL:HG22	1.94	0.49
52:LI:162:ARG:HH21	52:LI:164:LYS:HE3	1.77	0.49
53:LJ:35:ARG:O	53:LJ:39:VAL:HG23	2.12	0.49
85:Lt:117:ARG:HE	85:Lt:119:ARG:H	1.59	0.49
8:SI:116:HIS:CE1	8:SI:152:ARG:HH21	2.30	0.49
20:S2:1018:U:H2'	20:S2:1019:C:H6	1.77	0.49
20:S2:1279:C:H2'	20:S2:1280:G:H8	1.77	0.49
22:LW:9:SER:HA	22:LW:52:THR:HG23	1.94	0.49
42:L7:77:A:H62	42:L7:99:G:N2	2.09	0.49
66:LZ:46:ILE:HA	66:LZ:70:SER:HA	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:Ls:13:TYR:OH	84:Ls:61:MET:SD	2.67	0.49
6:SG:164:LYS:HB2	6:SG:167:LYS:HG2	1.94	0.49
20:S2:28:U:H2'	20:S2:29:G:C8	2.47	0.49
20:S2:429:C:H2'	20:S2:430:C:H6	1.76	0.49
20:S2:1452:A:H5''	23:SR:48:ASN:HD22	1.77	0.49
20:S2:1655:C:H2'	20:S2:1656:G:H8	1.77	0.49
20:S2:1711:U:H2'	20:S2:1712:A:H8	1.77	0.49
37:Sg:5:MET:HB2	37:Sg:270:LEU:HD21	1.95	0.49
37:Sg:107:ASP:HB2	37:Sg:125:ARG:HD2	1.93	0.49
37:Sg:153:CYS:SG	37:Sg:198:VAL:HG12	2.52	0.49
41:L5:173:C:OP1	54:LL:129:ARG:NH1	2.45	0.49
41:L5:691:C:H2'	41:L5:692:A:C8	2.46	0.49
41:L5:1758:G:H2'	41:L5:1759:G:C8	2.48	0.49
41:L5:3898:G:H5'	45:LB:254:ILE:HG13	1.94	0.49
41:L5:4158:C:H2'	41:L5:4159:C:C6	2.47	0.49
41:L5:4238:G:H2'	41:L5:4239:A:C8	2.44	0.49
20:S2:857:U:H2'	20:S2:858:A:C8	2.47	0.49
41:L5:133:C:H2'	41:L5:134:G:H4'	1.94	0.49
41:L5:223:G:N3	46:LC:223:ASN:ND2	2.52	0.49
41:L5:238:C:OP2	65:LY:45:ARG:NH2	2.46	0.49
41:L5:2843:U:O2'	41:L5:4632:U:OP1	2.30	0.49
41:L5:3610:A:H2'	41:L5:3611:A:C8	2.44	0.49
41:L5:3700:C:O2'	41:L5:3774:A:N3	2.37	0.49
41:L5:4195:G:N2	41:L5:4221:C:O2'	2.45	0.49
41:L5:4414:A:P	41:L5:4422:A:H61	2.36	0.49
41:L5:5055:G:H2'	41:L5:5056:A:C8	2.47	0.49
14:SW:14:ILE:HA	14:SW:25:VAL:HG21	1.95	0.49
14:SW:20:ARG:NH2	20:S2:1096:G:OP1	2.41	0.49
20:S2:88:G:H21	20:S2:500:A:H5'	1.78	0.49
20:S2:575:A:C2	20:S2:576:A2M:H1'	2.48	0.49
20:S2:1540:G:H2'	20:S2:1541:G:C8	2.47	0.49
20:S2:1713:C:H2'	20:S2:1714:U:C6	2.48	0.49
41:L5:1800:U:H2'	41:L5:1801:A:H8	1.77	0.49
41:L5:1890:G:N2	41:L5:1890:G:OP2	2.43	0.49
41:L5:2254:G:H4'	41:L5:2255:C:C5	2.47	0.49
41:L5:3819:G:H2'	41:L5:3820:G:H8	1.78	0.49
41:L5:4098:A:H2'	41:L5:4099:G:H4'	1.95	0.49
41:L5:4414:A:O2'	41:L5:4427:G:N2	2.40	0.49
41:L5:4872:G:OP2	55:LM:94:LYS:NZ	2.43	0.49
45:LB:90:VAL:HG22	45:LB:104:THR:HG23	1.93	0.49
46:LC:340:ILE:HD13	48:LE:51:VAL:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:LD:225:GLN:HA	47:LD:228:LYS:HD3	1.95	0.49
49:LF:237:GLU:OE1	60:LS:38:VAL:HG22	2.13	0.49
51:LH:129:ARG:HH21	51:LH:160:LEU:HD11	1.77	0.49
55:LM:24:LEU:HD11	55:LM:86:TRP:CG	2.48	0.49
70:Ld:64:ILE:HG23	70:Ld:68:LEU:HD23	1.93	0.49
83:Lr:16:PHE:HB3	83:Lr:27:THR:H	1.76	0.49
85:Lt:117:ARG:HG3	85:Lt:119:ARG:HB2	1.94	0.49
1:Zt:31:A:H2'	1:Zt:32:C:H6	1.78	0.49
2:SA:148:CYS:CB	2:SA:163:CYS:H	2.24	0.49
20:S2:29:G:H2'	20:S2:30:C:C6	2.48	0.49
20:S2:145:G:H2'	20:S2:146:G:H8	1.78	0.49
20:S2:1373:C:H5''	23:SR:7:LYS:HG3	1.94	0.49
29:SQ:110:ASP:HA	29:SQ:113:ILE:HG22	1.95	0.49
37:Sg:130:LYS:HG2	37:Sg:141:THR:HG22	1.93	0.49
41:L5:2652:G:H22	82:Lp:59:SER:HA	1.77	0.49
41:L5:2906:G:N2	41:L5:3585:G:O6	2.43	0.49
41:L5:3684:G:H2'	41:L5:3685:C:C6	2.48	0.49
41:L5:4088:C:H2'	41:L5:4089:G:C8	2.45	0.49
41:L5:4192:A:H2'	41:L5:4193:C:H6	1.77	0.49
3:SB:103:MET:HB3	3:SB:215:VAL:HG12	1.95	0.49
4:SC:202:THR:HA	9:SJ:54:ARG:HH21	1.77	0.49
20:S2:564:A:H2'	20:S2:565:G:O4'	2.13	0.49
20:S2:948:C:H2'	20:S2:949:G:H8	1.78	0.49
28:SP:16:THR:HG22	28:SP:21:ASP:HB3	1.95	0.49
41:L5:318:A:H2'	41:L5:319:A:H8	1.76	0.49
41:L5:518:G:N1	41:L5:643:C:H2'	2.25	0.49
41:L5:908:G:H2'	41:L5:909:A:H8	1.77	0.49
41:L5:1508:A:H5''	46:LC:113:ARG:HD2	1.94	0.49
41:L5:1727:U:OP1	49:LF:131:ASN:ND2	2.40	0.49
41:L5:2382:A:H2	41:L5:2830:G:H4'	1.78	0.49
41:L5:2554:U:O2'	41:L5:2574:G:N2	2.46	0.49
41:L5:2740:U:O2'	41:L5:2742:G:N2	2.46	0.49
41:L5:4680:G:H2'	41:L5:4681:A:C8	2.48	0.49
41:L5:4710:C:H2'	41:L5:4711:C:C6	2.48	0.49
41:L5:4922:C:H2'	41:L5:4923:C:H6	1.77	0.49
48:LE:264:ILE:HD11	48:LE:267:LEU:HD22	1.95	0.49
50:LG:190:LEU:HB3	50:LG:199:CYS:HB3	1.94	0.49
53:LJ:13:ARG:O	53:LJ:136:ARG:NH1	2.39	0.49
53:LJ:16:ARG:O	53:LJ:135:GLY:N	2.45	0.49
64:LX:129:ARG:NH2	64:LX:131:ASP:OD2	2.45	0.49
76:Lj:2:THR:HG22	76:Lj:4:GLY:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:300:U:H2'	20:S2:301:A:C8	2.48	0.49
20:S2:1563:G:H5''	31:ST:121:ARG:HH21	1.78	0.49
20:S2:1757:G:C8	20:S2:1758:G:H1'	2.47	0.49
41:L5:267:G:H2'	41:L5:268:G:H8	1.78	0.49
41:L5:2407:G:O6	78:L1:2:SER:OG	2.27	0.49
41:L5:2778:G:N2	43:L8:113:C:OP2	2.45	0.49
41:L5:4340:U:N3	90:L5:5291:3HE:O1	2.31	0.49
41:L5:4525:C:H4'	45:LB:245:HIS:H	1.77	0.49
41:L5:4578:G:H2'	41:L5:4579:PSU:H6	1.75	0.49
47:LD:41:LYS:NZ	61:LT:30:TYR:O	2.38	0.49
47:LD:64:ILE:HD13	47:LD:109:LEU:HD22	1.93	0.49
50:LG:159:HIS:ND1	50:LG:185:LYS:HA	2.27	0.49
58:LP:125:MET:HE2	58:LP:143:PRO:HG3	1.95	0.49
67:La:36:GLY:HA3	67:La:40:HIS:CE1	2.48	0.49
69:Lc:22:MET:O	69:Lc:23:LYS:HG3	2.13	0.49
69:Lc:52:CYS:HB3	69:Lc:57:LYS:HG3	1.94	0.49
73:Lg:84:ALA:O	73:Lg:88:ARG:HG3	2.13	0.49
5:SE:61:VAL:HA	5:SE:64:ILE:HG22	1.95	0.49
7:SH:148:LEU:HA	14:SW:42:MET:HE2	1.94	0.49
20:S2:1606:G:OP1	31:ST:84:ARG:NH2	2.36	0.49
20:S2:1657:G:H2'	20:S2:1658:G:H8	1.78	0.49
24:SD:29:LEU:HB3	24:SD:34:TYR:HB2	1.93	0.49
41:L5:690:C:H2'	41:L5:691:C:H6	1.78	0.49
41:L5:1278:C:H2'	41:L5:1279:A:O4'	2.13	0.49
41:L5:2386:U:H2'	41:L5:2387:G:C8	2.48	0.49
2:SA:49:ILE:HD13	2:SA:163:CYS:HA	1.95	0.49
6:SG:172:LYS:HD3	20:S2:65:C:H4'	1.94	0.49
8:SI:114:GLU:HB3	8:SI:136:ILE:HD12	1.95	0.49
20:S2:666:U:H2'	20:S2:667:U:C6	2.48	0.49
20:S2:1470:C:H2'	20:S2:1471:C:H6	1.77	0.49
20:S2:1845:A:H2'	20:S2:1846:G:H8	1.78	0.49
21:LR:39:GLN:NE2	41:L5:2710:C:O5'	2.46	0.49
22:LW:96:GLN:HB3	22:LW:100:VAL:HB	1.95	0.49
24:SD:46:THR:O	24:SD:84:VAL:HA	2.12	0.49
36:Sf:133:ALA:O	36:Sf:139:HIS:ND1	2.45	0.49
41:L5:350:C:OP2	46:LC:199:ARG:NH2	2.43	0.49
41:L5:406:C:O2'	41:L5:407:A:OP1	2.30	0.49
41:L5:679:C:H2'	41:L5:680:G:C8	2.47	0.49
41:L5:1504:G:H2'	41:L5:1505:C:C6	2.48	0.49
41:L5:1837:A:OP2	61:LT:108:ARG:NH1	2.45	0.49
41:L5:2295:C:H2'	41:L5:2296:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:2588:C:OP1	41:L5:2768:C:O2'	2.22	0.49
42:L7:57:C:H2'	42:L7:58:A:H8	1.78	0.49
48:LE:281:ILE:HD12	48:LE:286:LEU:HD11	1.94	0.49
50:LG:167:VAL:HG12	50:LG:170:LEU:HD12	1.95	0.49
57:LO:36:VAL:HG21	57:LO:117:ARG:HD3	1.95	0.49
20:S2:652:U:H2'	20:S2:653:A:H8	1.78	0.48
41:L5:325:U:H2'	41:L5:326:C:C6	2.47	0.48
41:L5:1284:G:H21	48:LE:130:LYS:HG3	1.78	0.48
41:L5:1733:G:N3	41:L5:4214:A:H2'	2.28	0.48
41:L5:1994:C:H2'	41:L5:1995:G:N7	2.28	0.48
41:L5:2079:G:H2'	41:L5:2080:U:C6	2.48	0.48
41:L5:3736:A:H2'	41:L5:3737:A:C8	2.48	0.48
41:L5:4630:G:H2'	41:L5:4631:G:C8	2.46	0.48
43:L8:153:C:H2'	43:L8:154:G:C8	2.47	0.48
47:LD:41:LYS:HD2	61:LT:93:ILE:HG21	1.94	0.48
64:LX:88:LYS:O	64:LX:92:ASP:HB2	2.12	0.48
74:Lh:72:PHE:O	74:Lh:76:LYS:NZ	2.41	0.48
1:Zt:73:G:H2'	1:Zt:74:C:C6	2.49	0.48
5:SE:212:ASP:OD1	5:SE:216:ASN:N	2.46	0.48
16:SY:34:THR:O	20:S2:570:C:O2'	2.30	0.48
20:S2:27:A2M:H2'	20:S2:28:U:O4'	2.13	0.48
20:S2:683:OMG:N1	20:S2:1022:U:OP2	2.35	0.48
20:S2:1405:A:H2'	20:S2:1406:G:O4'	2.12	0.48
20:S2:1656:G:O6	20:S2:1668:U:O4	2.31	0.48
20:S2:1817:G:H2'	20:S2:1818:A:C8	2.48	0.48
41:L5:1350:C:H2'	41:L5:1351:G:C8	2.47	0.48
41:L5:2098:G:H2'	41:L5:2099:G:C8	2.48	0.48
41:L5:3916:G:H2'	41:L5:3917:A:C8	2.48	0.48
41:L5:4648:A:H2'	41:L5:4649:G:H8	1.78	0.48
42:L7:82:G:H2'	42:L7:83:A:C8	2.48	0.48
43:L8:90:C:H1'	65:LY:24:HIS:HB3	1.95	0.48
4:SC:183:LYS:HA	4:SC:195:LEU:O	2.13	0.48
9:SJ:134:HIS:HE2	20:S2:561:A:HO2'	1.55	0.48
14:SW:57:ARG:HD2	20:S2:919:A:H5'	1.96	0.48
20:S2:17:C:H2'	20:S2:18:C:C6	2.48	0.48
20:S2:54:A:H3'	20:S2:451:G:H22	1.78	0.48
20:S2:549:C:H2'	20:S2:550:C:C6	2.48	0.48
20:S2:1208:A:H2'	20:S2:1209:A:H8	1.77	0.48
20:S2:1589:A:N3	20:S2:1653:U:O2'	2.42	0.48
41:L5:19:G:H2'	41:L5:20:U:C6	2.48	0.48
41:L5:62:A:OP1	56:LN:172:ARG:NH1	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:270:U:H2'	41:L5:271:C:C6	2.48	0.48
41:L5:3599:A:H2'	41:L5:3600:G:C8	2.48	0.48
41:L5:3687:A:O2'	44:LA:236:GLY:N	2.46	0.48
43:L8:90:C:H2'	43:L8:91:A:C8	2.49	0.48
78:L1:41:ARG:HA	78:L1:41:ARG:HD2	1.64	0.48
2:SA:216:ALA:O	2:SA:220:LYS:HG2	2.13	0.48
3:SB:131:ASP:HB3	3:SB:133:TYR:HD1	1.78	0.48
6:SG:15:LEU:HD22	20:S2:155:G:H4'	1.96	0.48
9:SJ:58:ARG:O	9:SJ:62:THR:HG23	2.13	0.48
9:SJ:136:ARG:HD3	9:SJ:160:SER:HA	1.95	0.48
16:SY:54:VAL:HG22	16:SY:76:TYR:HB2	1.96	0.48
18:Sb:26:GLN:NE2	20:S2:921:G:OP2	2.46	0.48
20:S2:1213:C:H2'	20:S2:1214:A:H8	1.79	0.48
20:S2:1410:C:H2'	20:S2:1411:G:C8	2.48	0.48
27:SM:35:ILE:HD11	27:SM:61:TYR:CZ	2.47	0.48
27:SM:95:ASP:HB3	27:SM:99:LYS:HB3	1.96	0.48
41:L5:730:G:C4	49:LF:73:ARG:HD3	2.48	0.48
41:L5:1800:U:H2'	41:L5:1801:A:C8	2.47	0.48
41:L5:2539:C:H2'	41:L5:2540:C:C6	2.48	0.48
41:L5:2558:C:H2'	41:L5:2559:G:C8	2.48	0.48
41:L5:2789:A:H1'	78:L1:45:ARG:HH22	1.78	0.48
41:L5:4704:C:H2'	41:L5:4705:A:C8	2.49	0.48
43:L8:27:U:H2'	43:L8:28:C:H6	1.78	0.48
44:LA:79:ALA:HA	44:LA:169:VAL:HA	1.95	0.48
5:SE:139:LEU:HD22	5:SE:147:ILE:HD11	1.95	0.48
20:S2:1598:G:O6	33:SZ:85:ARG:NE	2.46	0.48
24:SD:132:LYS:HB2	24:SD:189:MET:HG2	1.95	0.48
25:SF:131:ALA:HA	25:SF:136:ARG:HD3	1.95	0.48
41:L5:64:A:H1'	41:L5:76:A:H1'	1.96	0.48
41:L5:405:U:O2'	41:L5:407:A:N7	2.43	0.48
41:L5:444:G:H2'	41:L5:445:U:C6	2.47	0.48
41:L5:714:G:H2'	41:L5:715:G:H8	1.78	0.48
41:L5:1662:C:H2'	41:L5:1663:C:H6	1.78	0.48
41:L5:3918:G:OP2	88:L5:5264:SPM:N14	2.47	0.48
41:L5:4064:C:N4	41:L5:4065:G:O6	2.46	0.48
41:L5:4622:A:H2'	41:L5:4623:OMG:H8	1.79	0.48
48:LE:261:ILE:HG23	48:LE:267:LEU:HD23	1.96	0.48
50:LG:200:THR:HG22	50:LG:201:THR:HG23	1.95	0.48
62:LU:26:THR:HG1	62:LU:68:SER:HG	1.60	0.48
4:SC:185:THR:HG1	20:S2:1154:U:HO2'	1.51	0.48
6:SG:72:ARG:NH1	20:S2:467:G:O5'	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:SI:181:GLN:HE21	20:S2:379:C:P	2.37	0.48
14:SW:94:LEU:HD21	14:SW:102:ILE:HG13	1.96	0.48
20:S2:610:G:H2'	20:S2:611:G:H8	1.78	0.48
20:S2:1419:C:H2'	20:S2:1420:G:C8	2.48	0.48
20:S2:1845:A:H2'	20:S2:1846:G:C8	2.48	0.48
23:SR:42:PRO:HG3	24:SD:203:PRO:HG2	1.96	0.48
25:SF:33:ILE:HD11	34:Sc:35:MET:HE1	1.96	0.48
41:L5:318:A:H2'	41:L5:319:A:C8	2.49	0.48
41:L5:689:U:H2'	41:L5:690:C:H6	1.78	0.48
41:L5:3830:A2M:HM'3	41:L5:3830:A2M:H1'	1.56	0.48
41:L5:3927:U:H2'	41:L5:3928:A:H8	1.79	0.48
41:L5:3927:U:H2'	41:L5:3928:A:C8	2.49	0.48
41:L5:4600:G:H4'	41:L5:4601:U:O5'	2.14	0.48
41:L5:5006:U:H4'	41:L5:5007:A:H5'	1.95	0.48
43:L8:19:C:H2'	43:L8:20:A:C8	2.47	0.48
45:LB:112:ASP:O	45:LB:116:ARG:HG3	2.13	0.48
45:LB:217:ILE:HD12	45:LB:347:LEU:HB3	1.96	0.48
50:LG:209:SER:HA	50:LG:212:LYS:HG3	1.94	0.48
57:LO:142:ALA:HA	57:LO:145:VAL:HG12	1.94	0.48
84:Ls:59:THR:HA	84:Ls:62:ARG:HE	1.78	0.48
20:S2:15:U:H2'	20:S2:16:G:O4'	2.14	0.48
20:S2:106:C:OP1	20:S2:431:G:O2'	2.26	0.48
20:S2:1298:G:N9	28:SP:79:HIS:HD2	2.12	0.48
20:S2:1655:C:H2'	20:S2:1656:G:C8	2.48	0.48
20:S2:1804:U:H2'	20:S2:1805:G:C8	2.49	0.48
25:SF:201:LYS:HG3	25:SF:204:ARG:HE	1.79	0.48
35:Sd:16:GLN:O	35:Sd:27:ARG:NH1	2.46	0.48
41:L5:67:C:OP2	41:L5:312:G:N2	2.46	0.48
41:L5:93:G:H2'	41:L5:94:A:C8	2.48	0.48
41:L5:966:A:H5''	41:L5:2092:G:H22	1.77	0.48
41:L5:1669:A:H4'	41:L5:1685:G:H21	1.78	0.48
41:L5:4113:U:H4'	41:L5:4115:G:C6	2.49	0.48
52:LI:57:TYR:HD1	52:LI:130:HIS:HA	1.78	0.48
77:Lk:24:LYS:HA	77:Lk:67:LYS:O	2.14	0.48
4:SC:81:ILE:HG21	4:SC:88:ILE:HD11	1.96	0.48
5:SE:194:VAL:N	5:SE:211:LYS:O	2.46	0.48
6:SG:50:VAL:HG21	6:SG:111:LEU:HB3	1.96	0.48
14:SW:107:SER:HB2	20:S2:860:G:H21	1.79	0.48
20:S2:85:A:H2'	20:S2:86:C:H6	1.78	0.48
20:S2:940:U:H3	20:S2:1002:U:H3	1.62	0.48
20:S2:1058:A:OP1	39:Pt:38:C:O2'	2.24	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1844:U:OP1	80:Ln:11:ARG:NH2	2.47	0.48
29:SQ:14:GLY:N	29:SQ:21:ALA:O	2.46	0.48
41:L5:749:G:N2	41:L5:912:G:O2'	2.46	0.48
41:L5:1846:G:H2'	41:L5:1847:C:C6	2.49	0.48
41:L5:1973:G:H3'	41:L5:1974:U:H2'	1.96	0.48
41:L5:2269:C:O2'	83:Lr:11:ARG:NH2	2.47	0.48
41:L5:2884:G:H2'	41:L5:2885:A:C8	2.48	0.48
45:LB:50:LYS:NZ	45:LB:337:VAL:O	2.44	0.48
49:LF:92:VAL:O	49:LF:120:GLY:HA2	2.13	0.48
56:LN:146:PRO:HB2	74:Lh:104:THR:HG23	1.96	0.48
5:SE:44:LEU:HD11	5:SE:72:ILE:HD11	1.95	0.48
8:SI:141:ARG:NH1	20:S2:190:G:O3'	2.47	0.48
17:Sa:25:ASN:HB2	17:Sa:73:TYR:HE1	1.79	0.48
20:S2:1777:G:H2'	20:S2:1778:C:C6	2.48	0.48
41:L5:369:G:N2	41:L5:372:A:OP2	2.46	0.48
41:L5:717:U:H2'	41:L5:718:C:C6	2.49	0.48
41:L5:1847:C:H2'	41:L5:1848:C:C6	2.48	0.48
41:L5:2475:G:N1	64:LX:51:THR:O	2.34	0.48
41:L5:3661:G:H4'	41:L5:3662:A:H5'	1.95	0.48
41:L5:3932:U:H2'	41:L5:3933:G:C8	2.49	0.48
41:L5:4080:C:H2'	41:L5:4081:G:H8	1.78	0.48
41:L5:4448:G:H5''	41:L5:4449:A:H5'	1.96	0.48
41:L5:4619:U:H2'	41:L5:4620:OMU:H6	1.95	0.48
45:LB:10:ARG:HH12	45:LB:265:SER:HB2	1.79	0.48
45:LB:240:LEU:HB2	45:LB:248:LEU:HA	1.95	0.48
46:LC:315:LYS:HD2	49:LF:168:ALA:HB1	1.95	0.48
69:Lc:28:VAL:HG11	69:Lc:37:MET:HG3	1.96	0.48
1:Zt:54:U:O2	1:Zt:58:A:N7	2.47	0.48
3:SB:224:GLU:HG3	3:SB:227:LYS:H	1.79	0.48
8:SI:64:ASN:HA	8:SI:75:LYS:HA	1.96	0.48
10:SL:8:ARG:NH2	20:S2:390:C:O2'	2.47	0.48
10:SL:77:VAL:HA	10:SL:88:ILE:HG22	1.94	0.48
20:S2:1390:U:H2'	20:S2:1391:OMC:H6	1.79	0.48
20:S2:1668:U:H2'	20:S2:1669:G:C8	2.49	0.48
28:SP:39:ALA:HA	28:SP:42:ARG:HD3	1.96	0.48
41:L5:26:C:O2'	41:L5:338:A:N3	2.43	0.48
41:L5:651:C:H2'	41:L5:652:G:H8	1.79	0.48
41:L5:3607:U:H2'	41:L5:3608:A:C8	2.49	0.48
48:LE:176:THR:HB	48:LE:186:LEU:HA	1.96	0.48
20:S2:43:U:OP2	20:S2:485:A:N6	2.37	0.47
20:S2:159:A2M:H1'	20:S2:159:A2M:HM'3	1.56	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:907:G:H2'	20:S2:908:A:H8	1.77	0.47
20:S2:979:C:H2'	20:S2:980:A:C8	2.49	0.47
20:S2:1334:G:OP1	24:SD:139:SER:OG	2.31	0.47
20:S2:1858:G:H2'	20:S2:1859:A:H8	1.79	0.47
34:Sc:13:ARG:NH2	34:Sc:35:MET:SD	2.87	0.47
39:Pt:43:A:H2'	39:Pt:44:A:C8	2.48	0.47
41:L5:86:U:H2'	41:L5:87:A:C8	2.49	0.47
41:L5:676:C:H2'	41:L5:677:G:C8	2.48	0.47
41:L5:1415:G:H2'	41:L5:1416:G:C8	2.49	0.47
41:L5:4108:G:H2'	41:L5:4109:G:H8	1.79	0.47
41:L5:4716:C:OP1	45:LB:276:HIS:ND1	2.42	0.47
15:SX:91:LEU:HD21	19:Se:6:LEU:HD23	1.96	0.47
17:Sa:6:ARG:NH1	20:S2:1147:C:OP1	2.33	0.47
20:S2:323:C:H2'	20:S2:327:G:H1	1.79	0.47
20:S2:601:OMG:HM22	20:S2:601:OMG:H1'	1.66	0.47
20:S2:1657:G:H2'	20:S2:1658:G:C8	2.49	0.47
25:SF:34:SER:HA	34:Sc:55:VAL:HG13	1.96	0.47
41:L5:677:G:H2'	41:L5:678:C:H6	1.79	0.47
41:L5:1336:G:H2'	41:L5:2346:C:H42	1.79	0.47
41:L5:1497:A:OP1	59:LQ:180:ARG:NH1	2.47	0.47
41:L5:2380:G:N1	41:L5:2425:U:OP1	2.44	0.47
41:L5:2775:C:H2'	41:L5:2776:G:C8	2.49	0.47
41:L5:3948:C:H2'	41:L5:3949:A:C5	2.50	0.47
41:L5:4146:G:H2'	41:L5:4147:G:C8	2.49	0.47
41:L5:4233:A:C8	41:L5:4235:G:C8	3.02	0.47
41:L5:4286:C:N4	41:L5:4287:G:O6	2.47	0.47
41:L5:4967:A:H2'	41:L5:4968:A:C8	2.49	0.47
57:LO:61:ARG:HA	57:LO:70:PRO:HD2	1.96	0.47
70:Ld:36:VAL:HG21	70:Ld:44:ARG:HG2	1.96	0.47
6:SG:7:PHE:CD2	6:SG:10:THR:HG22	2.49	0.47
16:SY:35:VAL:HG13	16:SY:40:ILE:HD11	1.95	0.47
20:S2:1609:C:H4'	30:SS:125:HIS:HE1	1.79	0.47
39:Pt:23:C:H2'	39:Pt:24:A:C8	2.50	0.47
41:L5:2730:U:H2'	41:L5:2731:C:C6	2.49	0.47
41:L5:2876:OMG:HM22	41:L5:2877:G:H5'	1.95	0.47
41:L5:5055:G:H2'	41:L5:5056:A:H8	1.79	0.47
43:L8:26:C:O2'	46:LC:53:ALA:O	2.29	0.47
47:LD:182:GLY:HA2	47:LD:194:VAL:HG23	1.95	0.47
47:LD:204:VAL:O	47:LD:208:MET:HG3	2.15	0.47
5:SE:124:CYS:HB3	5:SE:141:THR:OG1	2.14	0.47
11:SN:70:LYS:NZ	20:S2:1020:A:OP2	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Sa:45:VAL:HG22	17:Sa:64:LEU:HD21	1.96	0.47
19:Se:22:GLN:O	19:Se:24:LYS:NZ	2.39	0.47
20:S2:5:U:H2'	20:S2:6:G:C8	2.49	0.47
41:L5:2610:G:H2'	41:L5:2611:A:C8	2.49	0.47
41:L5:2745:A:H2'	41:L5:2746:A:C8	2.47	0.47
41:L5:3911:C:H2'	41:L5:3912:U:C6	2.49	0.47
41:L5:4638:U:H3'	41:L5:4639:G:H21	1.80	0.47
41:L5:4743:G:H2'	41:L5:4744:A:C8	2.49	0.47
41:L5:4765:G:OP1	51:LH:23:ARG:NE	2.47	0.47
41:L5:4996:C:OP1	70:Ld:32:ARG:NH1	2.36	0.47
43:L8:71:A:N6	43:L8:83:C:O4'	2.47	0.47
44:LA:83:HIS:CE1	44:LA:86:GLN:HB2	2.49	0.47
48:LE:179:LEU:HD12	48:LE:183:ARG:HA	1.96	0.47
57:LO:178:ARG:O	57:LO:182:GLU:HG3	2.15	0.47
84:Ls:30:VAL:HG21	84:Ls:187:LEU:HG	1.97	0.47
4:SC:227:ARG:NH2	20:S2:663:C:O2'	2.47	0.47
11:SN:12:SER:OG	20:S2:1015:U:O4	2.31	0.47
20:S2:107:A:H2'	20:S2:108:G:C8	2.50	0.47
20:S2:406:PSU:H2'	20:S2:408:A:H8	1.79	0.47
20:S2:603:C:H1'	20:S2:604:A:N7	2.30	0.47
20:S2:614:C:H2'	20:S2:626:G:C8	2.49	0.47
20:S2:1859:A:H2'	20:S2:1860:A:C8	2.50	0.47
31:ST:143:LYS:HG3	31:ST:144:LYS:HE3	1.95	0.47
32:SU:116:ILE:HG13	32:SU:119:ALA:H	1.80	0.47
37:Sg:175:LYS:HB3	37:Sg:184:LEU:HD11	1.95	0.47
38:At:14:A:N1	38:At:21:A:O2'	2.39	0.47
41:L5:746:A:H2'	41:L5:747:A:C8	2.49	0.47
41:L5:2284:G:OP1	67:La:7:LYS:NZ	2.44	0.47
41:L5:2609:G:H2'	41:L5:2610:G:H8	1.80	0.47
41:L5:3785:A2M:H2	41:L5:4551:U:O2	2.14	0.47
41:L5:3919:C:H2'	41:L5:3920:PSU:H6	1.79	0.47
43:L8:30:U:H2'	43:L8:31:G:C8	2.49	0.47
43:L8:105:C:H4'	43:L8:106:G:H5''	1.96	0.47
45:LB:220:ILE:HG23	45:LB:278:THR:HG22	1.97	0.47
49:LF:96:ARG:HD3	49:LF:139:TYR:HA	1.97	0.47
70:Ld:46:LEU:HD11	70:Ld:73:TRP:HE1	1.79	0.47
5:SE:117:GLU:HA	5:SE:120:LYS:HG3	1.95	0.47
5:SE:201:HIS:CD2	20:S2:857:U:H4'	2.48	0.47
8:SI:145:ILE:HD13	20:S2:190:G:H5'	1.96	0.47
12:SO:143:LYS:HB2	20:S2:1047:C:H5''	1.95	0.47
20:S2:945:U:H2'	20:S2:946:U:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1383:A2M:HM'3	20:S2:1383:A2M:H1'	1.55	0.47
30:SS:125:HIS:CD2	30:SS:131:VAL:HG11	2.50	0.47
38:At:68:G:H2'	38:At:69:A:H8	1.79	0.47
41:L5:248:C:H2'	41:L5:249:C:C6	2.50	0.47
41:L5:1070:G:O2'	41:L5:1071:C:O5'	2.28	0.47
41:L5:1352:C:O2'	41:L5:1356:U:OP1	2.32	0.47
41:L5:3870:C:H2'	41:L5:3871:A:C8	2.46	0.47
41:L5:4622:A:H2'	41:L5:4623:OMG:C8	2.49	0.47
41:L5:4681:A:O2'	57:LO:144:GLU:OE1	2.32	0.47
52:LI:170:LYS:HA	52:LI:177:ASN:HA	1.96	0.47
56:LN:146:PRO:HG3	74:Lh:102:LEU:HD12	1.97	0.47
63:LV:106:VAL:HG12	63:LV:112:MET:HA	1.96	0.47
85:Lt:37:LEU:HA	85:Lt:40:LYS:HE3	1.96	0.47
5:SE:36:HIS:CG	5:SE:85:GLY:HA3	2.50	0.47
9:SJ:5:ARG:NH1	20:S2:39:A:OP1	2.48	0.47
13:SV:30:ALA:O	13:SV:60:ARG:HD3	2.15	0.47
19:Se:36:MET:HE3	19:Se:40:ARG:HH12	1.79	0.47
20:S2:414:A:H2'	20:S2:415:A:H8	1.78	0.47
20:S2:560:A:N6	20:S2:588:G:O6	2.48	0.47
20:S2:562:U:H2'	20:S2:563:G:C8	2.50	0.47
20:S2:1215:C:O2'	20:S2:1645:C:OP2	2.26	0.47
20:S2:1288:OMU:HN3	20:S2:1311:C:H42	1.63	0.47
20:S2:1434:C:O2'	20:S2:1435:C:OP1	2.29	0.47
20:S2:1498:A:P	24:SD:27:ARG:HH22	2.37	0.47
20:S2:1713:C:H2'	20:S2:1714:U:H6	1.79	0.47
20:S2:1783:C:H4'	20:S2:1784:G:H8	1.78	0.47
21:LR:62:ARG:NH1	41:L5:4645:C:OP2	2.45	0.47
25:SF:38:TYR:HE2	25:SF:143:PRO:HG2	1.78	0.47
25:SF:100:ILE:HD11	25:SF:108:PRO:HB3	1.97	0.47
37:Sg:249:CYS:HB3	37:Sg:258:ILE:HD13	1.97	0.47
41:L5:505:G:N2	41:L5:653:U:O2	2.33	0.47
41:L5:734:G:H22	41:L5:929:A:H2	1.61	0.47
41:L5:909:A:H2'	41:L5:910:G:C8	2.49	0.47
41:L5:1270:A:H8	41:L5:2106:G:H21	1.63	0.47
41:L5:1323:A2M:H2'	41:L5:1324:A:O4'	2.15	0.47
41:L5:1503:A:H4'	41:L5:1504:G:H5'	1.97	0.47
41:L5:1735:U:OP2	88:L5:5255:SPM:N10	2.48	0.47
41:L5:1767:A:N6	41:L5:1769:G:O2'	2.48	0.47
41:L5:2017:A:O2'	41:L5:2018:C:H6	1.98	0.47
41:L5:2458:C:O2	41:L5:3671:G:N2	2.48	0.47
41:L5:2699:C:H2'	41:L5:2700:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:3699:C:O2'	41:L5:3775:A:O2'	2.31	0.47
41:L5:4192:A:H2'	41:L5:4193:C:C6	2.49	0.47
42:L7:62:U:O2'	42:L7:64:G:O4'	2.32	0.47
45:LB:300:LYS:O	45:LB:304:SER:HB3	2.15	0.47
50:LG:246:SER:HA	50:LG:249:ARG:HE	1.80	0.47
56:LN:193:ARG:O	56:LN:197:THR:OG1	2.22	0.47
63:LV:21:PRO:HA	63:LV:54:ALA:HA	1.95	0.47
65:LY:85:VAL:HG12	65:LY:97:VAL:HB	1.97	0.47
3:SB:105:LEU:HD13	3:SB:113:MET:HE1	1.96	0.47
20:S2:5:U:O2'	20:S2:602:G:H4'	2.15	0.47
20:S2:835:C:H5'	20:S2:836:G:H5'	1.97	0.47
20:S2:1577:G:O2'	20:S2:1579:A:N3	2.44	0.47
20:S2:1618:C:H4'	28:SP:50:ARG:HH21	1.80	0.47
36:Sf:103:LEU:HB2	36:Sf:105:TYR:CE2	2.50	0.47
38:At:7:G:O2'	38:At:49:C:O5'	2.29	0.47
41:L5:1100:U:O2	41:L5:1167:C:N4	2.48	0.47
41:L5:1959:U:H5''	41:L5:1961:G:H1'	1.96	0.47
41:L5:2554:U:C2	41:L5:2764:A:N7	2.82	0.47
41:L5:2830:G:H2'	41:L5:2831:G:C8	2.50	0.47
41:L5:3700:C:H2'	41:L5:3746:A:H61	1.80	0.47
41:L5:4642:U:H2'	41:L5:4643:G:H8	1.80	0.47
43:L8:28:C:H2'	43:L8:29:G:C8	2.50	0.47
43:L8:67:U:H2'	43:L8:68:G:C8	2.48	0.47
45:LB:206:PRO:HG2	45:LB:209:GLN:HG3	1.96	0.47
3:SB:87:ILE:H	3:SB:101:HIS:HB2	1.79	0.47
5:SE:129:ILE:HD13	5:SE:139:LEU:HD12	1.96	0.47
20:S2:929:G:H2'	20:S2:930:C:O4'	2.15	0.47
20:S2:1033:G:N1	20:S2:1080:A:O2'	2.27	0.47
20:S2:1096:G:H2'	20:S2:1097:G:C8	2.50	0.47
20:S2:1822:A:H2'	20:S2:1823:A:C8	2.50	0.47
21:LR:102:LEU:O	21:LR:105:LEU:N	2.48	0.47
28:SP:38:SER:OG	28:SP:41:GLN:OE1	2.31	0.47
30:SS:45:LEU:HD13	30:SS:50:ILE:HD11	1.97	0.47
37:Sg:258:ILE:HG23	37:Sg:267:VAL:HB	1.97	0.47
38:At:49:C:H2'	38:At:50:U:C6	2.50	0.47
41:L5:1392:A:H2'	41:L5:1393:G:C8	2.49	0.47
41:L5:1509:C:H2'	41:L5:1510:G:C8	2.49	0.47
41:L5:1732:C:H2'	41:L5:1733:G:C8	2.50	0.47
41:L5:2520:C:H2'	41:L5:2521:G:C8	2.49	0.47
41:L5:3661:G:C4	44:LA:150:LEU:HD13	2.50	0.47
41:L5:3675:G:H2'	41:L5:3676:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:4584:A:H2'	41:L5:4585:U:O4'	2.15	0.47
84:Ls:91:THR:OG1	84:Ls:93:GLU:OE1	2.32	0.47
12:SO:44:VAL:HG13	12:SO:53:ILE:HB	1.96	0.47
41:L5:950:G:H2'	41:L5:951:G:H8	1.79	0.47
41:L5:1444:G:H22	41:L5:2104:G:N2	2.13	0.47
41:L5:1509:C:H2'	41:L5:1510:G:H8	1.80	0.47
41:L5:1820:C:H2'	41:L5:1822:U:H5'	1.96	0.47
41:L5:2669:C:H2'	41:L5:2670:C:O4'	2.15	0.47
41:L5:4069:U:H2'	41:L5:4070:U:H6	1.80	0.47
41:L5:4443:C:O2	41:L5:4444:C:N4	2.43	0.47
41:L5:4730:C:H2'	41:L5:4731:G:C8	2.50	0.47
41:L5:5044:A:H2'	41:L5:5045:G:H8	1.80	0.47
43:L8:57:C:O2	43:L8:61:A:O2'	2.27	0.47
43:L8:144:U:H2'	43:L8:145:C:C6	2.50	0.47
51:LH:92:MET:HE2	51:LH:179:ILE:HG22	1.97	0.47
3:SB:68:GLU:OE1	12:SO:96:LYS:NZ	2.44	0.46
9:SJ:152:ASP:OD1	9:SJ:153:SER:N	2.48	0.46
10:SL:67:SER:OG	20:S2:114:G:OP2	2.32	0.46
16:SY:110:ARG:NH1	16:SY:114:MET:SD	2.88	0.46
20:S2:601:OMG:H2'	20:S2:602:G:C8	2.50	0.46
20:S2:906:U:H2'	20:S2:907:G:C8	2.49	0.46
20:S2:1004:PSU:H2'	20:S2:1005:G:C8	2.50	0.46
41:L5:2516:G:O2'	73:Lg:62:LYS:NZ	2.48	0.46
45:LB:258:HIS:HA	45:LB:260:ALA:H	1.81	0.46
46:LC:298:ILE:HD13	59:LQ:131:PRO:HB3	1.97	0.46
46:LC:322:LEU:O	46:LC:326:LEU:HG	2.15	0.46
59:LQ:79:THR:HB	59:LQ:136:THR:HG22	1.96	0.46
71:Le:105:SER:HA	71:Le:108:ARG:HG2	1.96	0.46
3:SB:70:SER:OG	3:SB:71:LEU:N	2.49	0.46
15:SX:64:SER:OG	20:S2:1824:A:N6	2.48	0.46
17:Sa:2:THR:HG22	20:S2:1199:A:H5''	1.97	0.46
20:S2:329:G:H2'	20:S2:330:G:H8	1.79	0.46
29:SQ:104:SER:HA	29:SQ:107:GLU:HG3	1.98	0.46
33:SZ:86:ALA:O	33:SZ:89:GLN:HG2	2.15	0.46
36:Sf:141:CYS:H	36:Sf:145:CYS:HB2	1.79	0.46
38:At:43:A:H2'	38:At:44:A:C8	2.50	0.46
41:L5:703:G:N2	41:L5:704:C:O2	2.48	0.46
41:L5:1084:C:H2'	41:L5:1085:C:C6	2.49	0.46
41:L5:1308:C:H2'	41:L5:1309:C:C6	2.50	0.46
41:L5:3813:A:N3	41:L5:4538:G:O2'	2.36	0.46
41:L5:4159:C:H2'	41:L5:4160:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:4209:G:O6	41:L5:4224:A:N6	2.49	0.46
47:LD:211:LEU:HB3	47:LD:219:TYR:HB2	1.96	0.46
52:LI:181:PHE:O	52:LI:185:VAL:HG23	2.15	0.46
59:LQ:133:GLY:O	59:LQ:136:THR:OG1	2.27	0.46
65:LY:67:ILE:O	65:LY:84:ARG:NH2	2.48	0.46
85:Lt:114:ARG:HE	85:Lt:117:ARG:HD2	1.80	0.46
14:SW:71:LYS:NZ	20:S2:1156:U:OP1	2.42	0.46
16:SY:79:LEU:HG	16:SY:83:LYS:HE2	1.96	0.46
20:S2:1051:G:H2'	20:S2:1052:A:H8	1.80	0.46
20:S2:1550:G:H3'	20:S2:1579:A:H61	1.80	0.46
20:S2:1623:A:C8	30:SS:132:ARG:HB3	2.51	0.46
24:SD:1:MET:HG2	24:SD:3:VAL:H	1.80	0.46
24:SD:51:LEU:HD13	24:SD:89:GLU:HB2	1.98	0.46
37:Sg:20:GLN:HB3	37:Sg:34:ALA:HB3	1.97	0.46
41:L5:262:G:H2'	41:L5:263:G:C8	2.47	0.46
41:L5:415:G:O6	43:L8:20:A:N6	2.48	0.46
41:L5:432:U:H1'	88:L5:5290:SPM:H82	1.97	0.46
41:L5:711:A:H2'	41:L5:712:C:C6	2.50	0.46
41:L5:1594:C:HO2'	41:L5:1597:G:HO2'	1.62	0.46
41:L5:1601:A:OP2	41:L5:3643:A:N6	2.48	0.46
41:L5:3666:C:OP1	44:LA:234:LYS:NZ	2.48	0.46
41:L5:3867:A2M:HM'3	41:L5:3867:A2M:H1'	1.46	0.46
41:L5:4069:U:H2'	41:L5:4070:U:C6	2.51	0.46
41:L5:4177:C:H2'	41:L5:4178:A:H8	1.80	0.46
41:L5:4773:C:H2'	41:L5:4774:C:C6	2.50	0.46
41:L5:4935:C:H2'	41:L5:4936:G:H8	1.80	0.46
50:LG:157:ILE:HA	50:LG:201:THR:HG22	1.97	0.46
52:LI:31:ILE:HG22	52:LI:62:SER:HB2	1.97	0.46
54:LL:79:GLU:O	54:LL:83:VAL:HG22	2.15	0.46
74:Lh:88:THR:HB	74:Lh:91:MET:HB2	1.96	0.46
5:SE:125:LYS:O	5:SE:142:HIS:N	2.47	0.46
8:SI:12:ARG:HH12	20:S2:103:A:H5'	1.81	0.46
13:SV:17:CYS:HB2	13:SV:56:CYS:HB3	1.96	0.46
16:SY:8:ARG:HD3	20:S2:837:A:H62	1.80	0.46
16:SY:119:GLY:HA2	20:S2:85:A:H5'	1.96	0.46
20:S2:199:C:O2'	20:S2:201:C:OP2	2.28	0.46
20:S2:675:U:H2'	20:S2:676:C:H6	1.80	0.46
33:SZ:60:LYS:O	33:SZ:64:ASN:ND2	2.48	0.46
39:Pt:51:C:H2'	39:Pt:52:G:H8	1.80	0.46
41:L5:323:C:H2'	41:L5:324:A:H8	1.80	0.46
41:L5:689:U:H2'	41:L5:690:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1199:G:H2'	41:L5:1200:G:H8	1.80	0.46
41:L5:1399:G:H2'	41:L5:1400:G:H8	1.80	0.46
41:L5:1705:G:OP1	41:L5:1705:G:N2	2.27	0.46
43:L8:119:C:H2'	43:L8:120:G:C8	2.51	0.46
66:LZ:11:VAL:HG12	66:LZ:82:PRO:HA	1.97	0.46
13:SV:22:ARG:NH2	14:SW:19:LYS:O	2.49	0.46
20:S2:325:C:N3	20:S2:326:C:O2'	2.48	0.46
20:S2:928:G:H2'	20:S2:929:G:H8	1.80	0.46
20:S2:1622:U:OP1	30:SS:120:HIS:ND1	2.48	0.46
41:L5:678:C:H2'	41:L5:679:C:H6	1.80	0.46
41:L5:3658:C:H2'	41:L5:3659:G:H8	1.80	0.46
41:L5:3660:C:OP1	44:LA:241:ARG:NH2	2.39	0.46
41:L5:3690:U:H2'	41:L5:3691:G:O4'	2.16	0.46
41:L5:4208:U:N3	41:L5:4209:G:N7	2.64	0.46
41:L5:4653:C:H2'	41:L5:4654:C:C6	2.51	0.46
48:LE:165:LEU:HD11	48:LE:176:THR:HG22	1.97	0.46
50:LG:218:LEU:O	50:LG:222:ILE:HG12	2.15	0.46
20:S2:291:G:O2'	20:S2:292:A:O4'	2.29	0.46
20:S2:495:U:H2'	20:S2:496:C:O4'	2.14	0.46
20:S2:1816:G:O2'	41:L5:3807:A:O2'	2.19	0.46
20:S2:1856:C:H2'	20:S2:1857:G:H8	1.79	0.46
21:LR:105:LEU:HD23	21:LR:138:LEU:HD23	1.98	0.46
21:LR:136:ARG:O	21:LR:139:MET:HB2	2.16	0.46
31:ST:5:THR:HG22	31:ST:7:LYS:H	1.81	0.46
41:L5:1100:U:H3	41:L5:1194:G:H1	1.64	0.46
41:L5:1626:G:OP2	56:LN:77:LYS:NZ	2.49	0.46
41:L5:2580:U:P	66:LZ:36:ARG:HH12	2.38	0.46
41:L5:2634:C:H2'	41:L5:2635:U:C6	2.51	0.46
41:L5:4708:A:N3	41:L5:4709:U:H5'	2.31	0.46
41:L5:4732:G:N2	41:L5:4734:A:N7	2.63	0.46
44:LA:143:THR:HG23	44:LA:145:LYS:HG2	1.97	0.46
46:LC:192:GLY:O	46:LC:195:LYS:NZ	2.49	0.46
49:LF:182:TYR:HB3	49:LF:200:ARG:HG3	1.98	0.46
60:LS:51:LEU:HD21	61:LT:153:PRO:HA	1.97	0.46
84:Ls:30:VAL:HA	84:Ls:189:ILE:HA	1.97	0.46
85:Lt:114:ARG:HG3	85:Lt:133:LEU:HD22	1.97	0.46
8:SI:99:ASN:HB2	20:S2:377:G:O5'	2.15	0.46
20:S2:602:G:H1	20:S2:621:C:H42	1.64	0.46
20:S2:1199:A:H2'	20:S2:1200:A:C8	2.51	0.46
25:SF:162:ALA:HB2	25:SF:172:CYS:SG	2.56	0.46
39:Pt:1:G:H2'	39:Pt:2:U:H6	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1655:C:OP2	67:La:26:ARG:NH1	2.48	0.46
41:L5:1877:G:H2'	41:L5:1878:G:C8	2.50	0.46
41:L5:1967:A:N6	41:L5:2021:G:O6	2.49	0.46
41:L5:2375:A:H2'	41:L5:2376:A:H8	1.80	0.46
41:L5:2663:G:H2'	41:L5:2664:G:H8	1.81	0.46
41:L5:2898:G:H2'	41:L5:2899:C:C6	2.50	0.46
41:L5:3722:G:H2'	41:L5:3723:A:C8	2.49	0.46
41:L5:4281:A:H2'	41:L5:4282:A:H8	1.81	0.46
41:L5:4678:G:N2	41:L5:4713:G:H1'	2.30	0.46
41:L5:4775:C:H41	41:L5:4859:C:N4	2.14	0.46
41:L5:4948:C:OP2	41:L5:4949:G:O2'	2.26	0.46
52:LI:184:MET:HE2	52:LI:190:LEU:HG	1.98	0.46
53:LJ:56:THR:OG1	53:LJ:64:ARG:N	2.49	0.46
69:Lc:46:VAL:O	69:Lc:71:VAL:HA	2.15	0.46
84:Ls:174:LEU:O	84:Ls:178:LEU:HB2	2.15	0.46
3:SB:136:ARG:HG3	3:SB:218:LEU:HD21	1.98	0.46
8:SI:8:TRP:HA	8:SI:18:ARG:HD2	1.96	0.46
20:S2:1821:U:O4	20:S2:1822:A:N6	2.49	0.46
36:Sf:103:LEU:HD12	36:Sf:105:TYR:CZ	2.51	0.46
38:At:40:C:H2'	38:At:41:G:C8	2.50	0.46
39:Pt:22:U:H2'	39:Pt:23:C:H6	1.80	0.46
41:L5:34:A:H2'	41:L5:35:U:H6	1.81	0.46
41:L5:86:U:H2'	41:L5:87:A:H8	1.81	0.46
41:L5:161:G:H2'	41:L5:162:A:H8	1.80	0.46
41:L5:730:G:OP2	49:LF:76:ARG:NE	2.42	0.46
41:L5:2266:C:O2	83:Lr:39:ARG:NH2	2.49	0.46
41:L5:2362:U:H2'	41:L5:2363:A2M:C8	2.43	0.46
41:L5:2683:C:H2'	41:L5:2684:C:H6	1.81	0.46
41:L5:4336:A:H5''	41:L5:4337:C:H5'	1.98	0.46
41:L5:4482:U:H2'	41:L5:4483:C:H6	1.81	0.46
41:L5:4906:C:H2'	41:L5:4907:G:H8	1.81	0.46
54:LL:105:LYS:HE2	54:LL:105:LYS:HB3	1.77	0.46
56:LN:75:VAL:HG11	56:LN:80:THR:HG22	1.98	0.46
65:LY:4:ASN:HB3	65:LY:7:VAL:HG12	1.97	0.46
67:La:71:PRO:HG2	67:La:108:TYR:HA	1.98	0.46
4:SC:144:SER:HB3	4:SC:150:ALA:HB2	1.98	0.46
9:SJ:141:VAL:HG11	16:SY:65:GLY:HA3	1.98	0.46
20:S2:92:A:H61	20:S2:444:G:H1'	1.81	0.46
20:S2:737:G:H8	20:S2:738:C:H4'	1.80	0.46
20:S2:874:G:H2'	20:S2:875:A:C8	2.50	0.46
20:S2:887:U:O2	20:S2:900:C:N4	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1464:C:H4'	23:SR:60:ARG:NH1	2.31	0.46
33:SZ:102:LYS:HA	33:SZ:102:LYS:HD3	1.82	0.46
37:Sg:59:LEU:HD23	37:Sg:90:TRP:CD2	2.51	0.46
41:L5:347:A:H2'	41:L5:348:G:C8	2.51	0.46
41:L5:400:A2M:HM'3	41:L5:400:A2M:H1'	1.50	0.46
41:L5:424:U:H2'	41:L5:425:U:C6	2.51	0.46
41:L5:718:C:OP1	49:LF:217:ARG:NH1	2.49	0.46
41:L5:1281:G:C6	48:LE:128:HIS:HB2	2.51	0.46
41:L5:1504:G:OP1	59:LQ:147:GLU:N	2.49	0.46
41:L5:1687:U:H2'	41:L5:1688:G:C8	2.50	0.46
41:L5:1989:G:H2'	41:L5:1990:A:C8	2.50	0.46
41:L5:2078:C:H2'	41:L5:2079:G:C8	2.51	0.46
41:L5:3868:G:N2	41:L5:3900:G:O2'	2.49	0.46
41:L5:4344:U:H3	41:L5:4368:G:H1	1.63	0.46
41:L5:4637:OMG:HM23	41:L5:4637:OMG:H1'	1.66	0.46
41:L5:4750:G:H2'	41:L5:4751:G:H8	1.81	0.46
41:L5:4890:G:H2'	41:L5:4891:G:C8	2.51	0.46
43:L8:15:G:H2'	43:L8:16:G:C4	2.51	0.46
48:LE:277:LEU:HB2	72:Lf:4:ARG:HB3	1.98	0.46
58:LP:27:LYS:HD3	58:LP:63:TYR:HB3	1.98	0.46
74:Lh:89:ARG:O	74:Lh:93:ARG:HG2	2.16	0.46
83:Lr:28:GLU:HG2	83:Lr:31:ASN:HB2	1.98	0.46
3:SB:71:LEU:HD13	3:SB:84:PHE:HE2	1.81	0.46
4:SC:251:LEU:HD13	13:SV:23:ILE:HG12	1.98	0.46
20:S2:287:U:H2'	20:S2:288:G:C8	2.51	0.46
20:S2:1143:A:O3'	20:S2:1355:C:N4	2.48	0.46
33:SZ:86:ALA:O	33:SZ:90:GLU:HG2	2.16	0.46
37:Sg:33:SER:OG	37:Sg:43:TRP:NE1	2.39	0.46
41:L5:137:G:H2'	41:L5:138:G:H8	1.80	0.46
41:L5:729:G:H5''	49:LF:76:ARG:HD2	1.97	0.46
41:L5:1519:C:H2'	41:L5:1520:C:H6	1.81	0.46
41:L5:1519:C:H2'	41:L5:1520:C:C6	2.51	0.46
41:L5:2743:A:H2'	41:L5:2744:A:C8	2.51	0.46
41:L5:3602:C:H2'	41:L5:3603:G:C8	2.51	0.46
41:L5:4434:C:H2'	41:L5:4435:U:C6	2.51	0.46
41:L5:4594:U:H2'	41:L5:4595:G:C8	2.48	0.46
41:L5:4662:C:O2'	41:L5:5004:C:OP1	2.33	0.46
43:L8:95:A:OP1	76:Lj:81:GLY:N	2.47	0.46
54:LL:90:VAL:O	54:LL:94:ILE:HG12	2.15	0.46
65:LY:19:PHE:O	65:LY:26:ARG:NH2	2.49	0.46
17:Sa:82:LYS:HB3	17:Sa:85:ARG:HH12	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:156:G:H2'	20:S2:157:U:C6	2.50	0.45
20:S2:1399:C:H2'	20:S2:1400:U:C6	2.51	0.45
20:S2:1806:A:H2'	20:S2:1807:C:C6	2.51	0.45
24:SD:106:ARG:HH11	24:SD:110:LEU:HD12	1.81	0.45
30:SS:26:ILE:O	30:SS:30:ILE:HG12	2.16	0.45
41:L5:239:C:H2'	41:L5:240:G:C8	2.51	0.45
41:L5:1194:G:H2'	41:L5:1195:G:H8	1.80	0.45
41:L5:2387:G:H2'	41:L5:2388:A:H8	1.80	0.45
41:L5:3650:C:H2'	41:L5:3651:A:H8	1.80	0.45
41:L5:3653:A:C2	41:L5:3692:A:H4'	2.51	0.45
41:L5:3707:U:H2'	41:L5:3708:C:C6	2.51	0.45
41:L5:4524:G:C2	45:LB:252:ALA:HB1	2.50	0.45
58:LP:60:PHE:O	58:LP:78:TRP:NE1	2.48	0.45
62:LU:45:GLU:HA	62:LU:54:GLY:HA2	1.98	0.45
3:SB:24:PRO:O	3:SB:28:LYS:HG2	2.15	0.45
5:SE:141:THR:HG23	5:SE:143:ASP:N	2.31	0.45
7:SH:115:LYS:HD2	20:S2:868:G:C2	2.52	0.45
18:Sb:45:THR:HG23	18:Sb:82:LYS:HE3	1.98	0.45
20:S2:1542:C:OP1	31:ST:62:ARG:NH2	2.39	0.45
23:SR:99:ASP:HB3	23:SR:102:THR:HG23	1.98	0.45
29:SQ:58:LEU:HD13	29:SQ:108:ILE:HD11	1.97	0.45
36:Sf:132:MET:HE3	36:Sf:145:CYS:HB3	1.98	0.45
37:Sg:29:ASP:HA	37:Sg:47:ARG:HH21	1.81	0.45
39:Pt:52:G:H2'	39:Pt:53:G:C8	2.50	0.45
41:L5:1084:C:H2'	41:L5:1085:C:H6	1.82	0.45
41:L5:1685:G:H2'	41:L5:1686:C:H6	1.81	0.45
41:L5:1824:G:H2'	41:L5:1825:A:H8	1.79	0.45
41:L5:2049:G:H2'	41:L5:2050:G:C8	2.51	0.45
41:L5:2319:C:N3	71:Le:58:ILE:HD12	2.31	0.45
41:L5:2407:G:H2'	78:Ll:13:LEU:HD22	1.96	0.45
41:L5:2730:U:H2'	41:L5:2731:C:H6	1.81	0.45
41:L5:3736:A:H2'	41:L5:3737:A:H8	1.81	0.45
41:L5:4967:A:H2'	41:L5:4968:A:H8	1.80	0.45
43:L8:119:C:H2'	43:L8:120:G:H8	1.82	0.45
70:Ld:33:ILE:HD11	70:Ld:45:ALA:HA	1.96	0.45
76:Lj:14:LYS:NZ	78:Ll:51:LEU:OXT	2.49	0.45
2:SA:110:ASN:HB3	2:SA:113:GLN:HE22	1.82	0.45
3:SB:155:TYR:OH	20:S2:989:C:OP2	2.22	0.45
9:SJ:32:ILE:HD11	9:SJ:40:LYS:HG2	1.98	0.45
14:SW:50:PHE:HB2	14:SW:63:VAL:HG22	1.98	0.45
14:SW:52:ILE:HG12	14:SW:61:ILE:HG12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:SY:10:ARG:HA	20:S2:839:C:H41	1.82	0.45
20:S2:70:G:N2	20:S2:79:A:H62	2.15	0.45
20:S2:1298:G:C4	28:SP:79:HIS:HD2	2.34	0.45
22:LW:107:GLN:HA	22:LW:110:ARG:HG3	1.98	0.45
41:L5:436:C:H2'	41:L5:437:G:C8	2.50	0.45
41:L5:1604:G:H2'	41:L5:1605:G:C8	2.51	0.45
41:L5:2072:C:OP1	59:LQ:2:GLY:N	2.49	0.45
41:L5:2578:G:H2'	41:L5:2579:G:C8	2.51	0.45
41:L5:4711:C:H2'	41:L5:4712:C:C6	2.52	0.45
41:L5:4716:C:H2'	41:L5:4717:A:H8	1.81	0.45
41:L5:4878:C:H2'	41:L5:4879:C:C6	2.52	0.45
43:L8:22:U:OP2	46:LC:196:MET:HG2	2.17	0.45
43:L8:43:A:H2'	43:L8:44:A:H8	1.81	0.45
43:L8:141:C:H2'	43:L8:142:U:C6	2.51	0.45
44:LA:54:ARG:HH11	44:LA:58:LEU:HD21	1.82	0.45
52:LI:36:LEU:HD21	52:LI:69:ARG:HH11	1.80	0.45
52:LI:54:SER:HA	52:LI:163:GLN:HG3	1.98	0.45
58:LP:94:MET:HE3	58:LP:94:MET:HB2	1.85	0.45
67:La:99:PRO:HG2	67:La:122:VAL:HG23	1.98	0.45
7:SH:118:ARG:HD3	7:SH:121:THR:HG21	1.99	0.45
20:S2:145:G:H2'	20:S2:146:G:C8	2.50	0.45
20:S2:1039:C:H2'	20:S2:1040:G:H8	1.80	0.45
20:S2:1129:G:H2'	20:S2:1130:G:N3	2.31	0.45
20:S2:1398:G:H1'	37:Sg:63:SER:HB2	1.98	0.45
34:Sc:20:ARG:HB3	34:Sc:25:GLY:HA2	1.97	0.45
41:L5:25:A:N6	41:L5:58:G:H1	2.11	0.45
41:L5:426:A:H2'	41:L5:427:A:H8	1.81	0.45
41:L5:491:G:H2'	41:L5:492:U:C6	2.51	0.45
41:L5:1468:C:H2'	41:L5:1469:C:H6	1.81	0.45
41:L5:1779:U:H2'	41:L5:1780:A:C8	2.50	0.45
41:L5:2109:G:H2'	41:L5:2110:C:C6	2.52	0.45
41:L5:2413:U:H2'	41:L5:2414:G:C8	2.52	0.45
41:L5:2518:G:HO2'	41:L5:2538:U:HO2'	1.58	0.45
41:L5:2610:G:H2'	41:L5:2611:A:H8	1.81	0.45
41:L5:4870:G:H2'	55:LM:91:TRP:CZ2	2.52	0.45
89:L5:5281:SPD:H51	89:L5:5281:SPD:H82	1.80	0.45
47:LD:288:LEU:O	47:LD:292:GLU:HG2	2.16	0.45
53:LJ:74:VAL:HG11	53:LJ:82:ILE:HD12	1.99	0.45
84:Ls:18:ILE:HD12	84:Ls:21:LEU:HD21	1.97	0.45
1:Zt:26:A:N1	1:Zt:44:G:O6	2.49	0.45
20:S2:198:U:H2'	20:S2:199:C:H2'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1031:A2M:HM'3	20:S2:1031:A2M:H1'	1.59	0.45
20:S2:1294:G:O6	20:S2:1295:A:N6	2.50	0.45
31:ST:30:VAL:HG13	31:ST:34:VAL:HG11	1.98	0.45
37:Sg:270:LEU:HD13	37:Sg:310:TRP:CD2	2.50	0.45
41:L5:678:C:H2'	41:L5:679:C:C6	2.52	0.45
41:L5:716:C:OP1	46:LC:317:ASN:HB2	2.16	0.45
41:L5:1341:U:H2'	41:L5:1342:A:H8	1.81	0.45
41:L5:1369:C:OP2	41:L5:1370:G:O2'	2.27	0.45
41:L5:1387:A:O2'	41:L5:1396:G:N2	2.44	0.45
41:L5:2389:A:H5'	70:Ld:70:LYS:HD3	1.97	0.45
41:L5:4080:C:H2'	41:L5:4081:G:C8	2.52	0.45
45:LB:80:GLU:OE1	45:LB:323:TYR:OH	2.30	0.45
55:LM:25:VAL:HB	55:LM:38:VAL:HG22	1.98	0.45
1:Zt:73:G:H2'	1:Zt:74:C:H6	1.82	0.45
11:SN:29:THR:OG1	11:SN:31:ASP:OD1	2.19	0.45
14:SW:102:ILE:H	14:SW:113:HIS:CE1	2.34	0.45
20:S2:307:G:P	20:S2:307:G:H8	2.39	0.45
41:L5:7:C:H2'	41:L5:8:U:C6	2.52	0.45
41:L5:1298:C:H2'	41:L5:1299:G:C8	2.51	0.45
41:L5:1962:A:H5''	41:L5:2024:G:N2	2.32	0.45
41:L5:2382:A:H2'	41:L5:2383:C:C6	2.52	0.45
41:L5:2437:C:H5'	64:LX:127:LEU:HB3	1.99	0.45
41:L5:3688:U:H2'	41:L5:3689:G:C8	2.52	0.45
41:L5:4986:G:H2'	41:L5:4987:C:C6	2.52	0.45
47:LD:156:GLY:HA2	47:LD:181:PRO:HG3	1.99	0.45
49:LF:88:LYS:HA	49:LF:125:LEU:HB2	1.98	0.45
52:LI:136:MET:HE3	52:LI:136:MET:HB2	1.83	0.45
2:SA:3:GLY:N	13:SV:78:ILE:O	2.49	0.45
2:SA:110:ASN:ND2	20:S2:1350:U:O2	2.44	0.45
2:SA:140:VAL:HG13	2:SA:142:LEU:HB2	1.99	0.45
4:SC:253:PRO:HA	4:SC:256:TRP:CE2	2.51	0.45
5:SE:166:THR:HB	5:SE:168:LYS:HG2	1.98	0.45
9:SJ:127:ARG:NE	20:S2:523:A:OP1	2.48	0.45
14:SW:6:VAL:HG13	14:SW:29:PRO:HG2	1.99	0.45
20:S2:467:G:H2'	20:S2:468:A2M:H8	1.98	0.45
20:S2:1198:G:H2'	20:S2:1199:A:H8	1.81	0.45
41:L5:162:A:H2'	41:L5:163:A:H8	1.80	0.45
41:L5:368:C:H2'	41:L5:369:G:C8	2.52	0.45
41:L5:1316:OMG:HM23	41:L5:1316:OMG:H1'	1.67	0.45
41:L5:4076:G:H5'	50:LG:73:ARG:HG3	1.98	0.45
41:L5:4622:A:H4'	45:LB:13:SER:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:LC:361:LEU:HG	46:LC:364:LYS:HZ3	1.82	0.45
51:LH:41:ILE:HG21	51:LH:73:ILE:HD11	1.99	0.45
69:Lc:17:ARG:HD2	69:Lc:103:ASP:HB2	1.99	0.45
71:Le:117:GLN:O	83:Lr:119:ARG:NH1	2.49	0.45
1:Zt:31:A:H2'	1:Zt:32:C:C6	2.52	0.45
4:SC:127:PHE:HD1	4:SC:141:VAL:HG22	1.82	0.45
5:SE:104:ASP:HB3	5:SE:110:ALA:HB2	1.99	0.45
6:SG:20:ASP:HB3	6:SG:23:LYS:HG3	1.98	0.45
20:S2:1650:A:H5''	29:SQ:139:ALA:HB2	1.98	0.45
23:SR:60:ARG:HG2	23:SR:66:VAL:HG22	1.98	0.45
27:SM:120:ALA:O	27:SM:124:ILE:HG12	2.17	0.45
36:Sf:133:ALA:N	36:Sf:140:TYR:O	2.47	0.45
37:Sg:86:THR:HG22	37:Sg:102:VAL:HG12	1.98	0.45
38:At:9:A:O2'	38:At:10:G:N7	2.50	0.45
41:L5:297:U:C2	41:L5:298:G:C8	3.05	0.45
41:L5:307:A:N3	41:L5:310:G:O2'	2.49	0.45
41:L5:418:A:H2'	41:L5:419:A:C8	2.52	0.45
41:L5:1098:G:H2'	41:L5:1099:C:C6	2.52	0.45
41:L5:1304:C:H2'	41:L5:1305:C:H6	1.82	0.45
41:L5:1327:C:H2'	41:L5:1328:G:C8	2.51	0.45
41:L5:1450:C:H2'	41:L5:1451:G:O4'	2.17	0.45
41:L5:2638:G:N1	41:L5:2718:U:H2'	2.32	0.45
41:L5:4101:C:H42	41:L5:4107:G:H1	1.65	0.45
41:L5:4473:A:P	79:Lm:102:ARG:HH21	2.40	0.45
44:LA:51:ASP:HB3	44:LA:54:ARG:HB3	1.98	0.45
44:LA:145:LYS:HD3	44:LA:145:LYS:HA	1.74	0.45
45:LB:116:ARG:HD3	45:LB:177:LYS:HA	1.98	0.45
48:LE:227:HIS:CE1	48:LE:230:GLY:HA2	2.51	0.45
51:LH:165:THR:HG21	51:LH:179:ILE:HG13	1.99	0.45
15:SX:129:SER:HB2	20:S2:29:G:H4'	1.99	0.45
20:S2:99:A2M:HM'3	20:S2:99:A2M:H1'	1.71	0.45
20:S2:1249:C:O3'	29:SQ:143:LYS:NZ	2.47	0.45
20:S2:1793:A:O3'	22:LW:47:ARG:NH2	2.50	0.45
41:L5:178:C:N4	41:L5:179:G:O6	2.50	0.45
41:L5:310:G:H2'	41:L5:311:G:C8	2.52	0.45
41:L5:432:U:H1'	88:L5:5290:SPM:H61	1.99	0.45
41:L5:1705:G:H2'	41:L5:1706:A:C8	2.52	0.45
41:L5:1759:G:H1	41:L5:1773:U:H3	1.63	0.45
41:L5:2059:C:H2'	41:L5:2060:G:C8	2.51	0.45
41:L5:2309:G:O6	41:L5:2330:G:N2	2.49	0.45
41:L5:3796:U:H2'	41:L5:3797:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:4591:U:OP1	89:L5:5286:SPD:N1	2.45	0.45
41:L5:4957:C:H2'	41:L5:4958:C:C6	2.52	0.45
52:LI:4:ARG:NH1	52:LI:9:TYR:OH	2.40	0.45
57:LO:37:ARG:HD2	57:LO:108:ILE:HD11	1.99	0.45
4:SC:65:LYS:HD2	4:SC:273:LEU:HD13	1.98	0.45
12:SO:56:VAL:HG13	12:SO:77:ALA:HB1	1.99	0.45
18:Sb:12:PRO:HA	18:Sb:15:GLU:HB2	1.99	0.45
20:S2:655:A:H4'	20:S2:656:G:H3'	1.98	0.45
20:S2:1392:U:H2'	20:S2:1393:G:H8	1.80	0.45
20:S2:1556:A:C8	35:Sd:13:LYS:HG3	2.52	0.45
27:SM:18:LEU:HA	27:SM:21:VAL:HB	1.99	0.45
32:SU:55:ARG:HG3	32:SU:87:ARG:CZ	2.47	0.45
41:L5:57:G:H5''	56:LN:154:PRO:HB2	1.99	0.45
41:L5:956:A:H1'	41:L5:2076:G:H5''	1.98	0.45
41:L5:1091:C:H2'	41:L5:1092:G:H8	1.82	0.45
41:L5:1759:G:N2	41:L5:1773:U:O2	2.49	0.45
41:L5:2382:A:N1	41:L5:2830:G:O2'	2.41	0.45
41:L5:3605:C:H2'	41:L5:3606:U:C6	2.52	0.45
41:L5:4108:G:H2'	41:L5:4109:G:C8	2.52	0.45
41:L5:4492:U:O2'	41:L5:4512:U:O2	2.30	0.45
41:L5:4537:C:H2'	41:L5:4538:G:C8	2.51	0.45
43:L8:8:U:H2'	43:L8:9:A:C8	2.52	0.45
53:LJ:95:ARG:H	53:LJ:98:ASN:HD22	1.64	0.45
56:LN:51:LEU:HD13	56:LN:117:ASN:HB3	1.98	0.45
78:Ll:33:ASN:ND2	78:Ll:35:ILE:O	2.50	0.45
5:SE:98:ASN:HD22	5:SE:116:PRO:HA	1.81	0.44
5:SE:136:ILE:HD12	5:SE:149:TYR:HE1	1.82	0.44
8:SI:151:GLU:O	8:SI:154:LYS:HG2	2.17	0.44
14:SW:2:VAL:N	20:S2:1091:C:O2'	2.45	0.44
20:S2:534:G:H2'	20:S2:535:G:H8	1.83	0.44
20:S2:551:U:H2'	20:S2:552:G:C8	2.52	0.44
20:S2:1340:U:OP2	20:S2:1341:C:O2'	2.28	0.44
20:S2:1456:G:H2'	20:S2:1457:U:C6	2.52	0.44
20:S2:1623:A:C5	30:SS:132:ARG:HD3	2.52	0.44
39:Pt:49:C:H2'	39:Pt:50:U:H6	1.82	0.44
41:L5:949:G:H2'	41:L5:950:G:H8	1.82	0.44
41:L5:1404:G:O6	41:L5:1413:C:N4	2.50	0.44
41:L5:1534:A2M:H8	76:Lj:15:THR:OG1	2.16	0.44
41:L5:2318:G:H21	41:L5:2320:G:H8	1.65	0.44
41:L5:2419:C:H2'	41:L5:2420:A:C8	2.52	0.44
41:L5:2765:A:H2'	41:L5:2766:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:2833:A:OP1	70:Ld:44:ARG:NH1	2.49	0.44
41:L5:3718:A2M:H2'	41:L5:3719:A:O4'	2.17	0.44
41:L5:4139:G:H21	41:L5:4140:C:H5	1.65	0.44
41:L5:4892:A:C6	41:L5:4893:A:C6	3.05	0.44
41:L5:4938:A:P	48:LE:183:ARG:HH21	2.40	0.44
57:LO:9:LEU:HD23	57:LO:118:MET:HB2	1.99	0.44
20:S2:649:PSU:H2'	20:S2:650:A:C8	2.49	0.44
20:S2:1545:A:H4'	29:SQ:75:GLY:N	2.31	0.44
22:LW:2:LYS:HZ3	63:LV:92:ASP:HB2	1.82	0.44
24:SD:42:THR:OG1	24:SD:45:ARG:O	2.26	0.44
28:SP:108:LYS:HG2	28:SP:111:MET:SD	2.58	0.44
41:L5:1197:C:H2'	41:L5:1198:G:H8	1.81	0.44
41:L5:1307:A:H2'	41:L5:1308:C:C6	2.52	0.44
41:L5:1962:A:OP2	41:L5:2024:G:N1	2.41	0.44
41:L5:2029:A:H2'	41:L5:2030:A:H8	1.81	0.44
41:L5:3672:G:OP2	41:L5:3672:G:N2	2.30	0.44
41:L5:4723:A:H2'	41:L5:4724:A:C8	2.52	0.44
53:LJ:99:PHE:HB2	53:LJ:159:LYS:HE3	1.99	0.44
54:LL:123:LYS:HA	74:Lh:122:LYS:NZ	2.32	0.44
60:LS:70:LYS:HD3	60:LS:70:LYS:HA	1.73	0.44
70:Ld:75:LYS:HB2	70:Ld:79:ASN:O	2.18	0.44
3:SB:136:ARG:NH2	20:S2:941:C:OP1	2.50	0.44
10:SL:61:PRO:HB3	10:SL:68:ILE:HD11	1.98	0.44
20:S2:441:C:H2'	20:S2:442:C:C6	2.52	0.44
20:S2:644:OMG:HM23	20:S2:644:OMG:H1'	1.67	0.44
20:S2:902:G:O2'	20:S2:903:A:O4'	2.36	0.44
20:S2:962:A:N1	20:S2:1055:A:O2'	2.50	0.44
20:S2:1787:G:H2'	20:S2:1788:A:C8	2.53	0.44
37:Sg:65:PHE:HB2	37:Sg:83:TRP:CG	2.52	0.44
41:L5:138:G:H2'	41:L5:139:G:H8	1.83	0.44
41:L5:268:G:H2'	41:L5:269:G:C8	2.49	0.44
41:L5:325:U:H3'	75:Li:28:ARG:HH21	1.83	0.44
41:L5:441:G:H2'	41:L5:442:G:H8	1.81	0.44
41:L5:460:C:H2'	41:L5:461:G:C8	2.52	0.44
41:L5:2422:OMC:N3	41:L5:2829:U:H1'	2.32	0.44
41:L5:2622:G:H2'	41:L5:2623:A:H8	1.82	0.44
41:L5:2640:G:H2'	41:L5:2641:A:H8	1.83	0.44
41:L5:3861:A:H2'	41:L5:3862:A:C8	2.52	0.44
41:L5:4067:U:H2'	41:L5:4068:U:C6	2.52	0.44
44:LA:225:ILE:HG12	44:LA:234:LYS:HA	2.00	0.44
49:LF:221:LYS:HA	49:LF:221:LYS:HD3	1.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:LN:28:TRP:O	56:LN:32:GLN:HG2	2.17	0.44
62:LU:23:LEU:HD13	62:LU:110:TYR:HB2	1.99	0.44
64:LX:124:VAL:HG22	64:LX:138:VAL:HG13	1.98	0.44
64:LX:129:ARG:HD2	64:LX:135:LYS:HE2	1.99	0.44
66:LZ:88:ASP:OD1	66:LZ:121:ARG:NH1	2.51	0.44
3:SB:198:GLU:O	3:SB:202:GLN:HG2	2.17	0.44
7:SH:8:ILE:HG13	7:SH:9:VAL:HG23	1.98	0.44
7:SH:126:HIS:HA	7:SH:129:ILE:HG12	1.98	0.44
14:SW:3:ARG:HD3	14:SW:6:VAL:HG22	1.99	0.44
20:S2:526:A:H2'	20:S2:527:C:C6	2.52	0.44
20:S2:1433:C:O2	32:SU:19:ARG:NH2	2.51	0.44
20:S2:1627:C:H5''	31:ST:41:LYS:HD2	1.99	0.44
20:S2:1711:U:H2'	20:S2:1712:A:C8	2.53	0.44
41:L5:299:C:H2'	41:L5:300:A:H8	1.83	0.44
41:L5:398:A2M:HM'3	41:L5:398:A2M:H1'	1.64	0.44
41:L5:433:A:C2	41:L5:3867:A2M:H4'	2.51	0.44
41:L5:671:G:H2'	41:L5:672:C:C6	2.52	0.44
41:L5:700:G:N1	41:L5:701:G:C6	2.85	0.44
41:L5:946:C:H2'	41:L5:947:C:C6	2.52	0.44
41:L5:1577:G:O2'	41:L5:1612:G:H4'	2.17	0.44
41:L5:1830:G:H2'	41:L5:1831:G:C8	2.52	0.44
41:L5:1973:G:H21	85:Lt:136:ALA:HB2	1.83	0.44
41:L5:2028:C:H2'	41:L5:2029:A:H8	1.82	0.44
41:L5:2381:A:H1'	41:L5:2383:C:P	2.57	0.44
41:L5:2518:G:O2'	41:L5:2538:U:O2'	2.32	0.44
43:L8:49:G:O6	43:L8:77:A:N6	2.50	0.44
45:LB:217:ILE:HD13	45:LB:284:ILE:HD11	1.99	0.44
46:LC:212:ASN:HD22	46:LC:255:SER:HB3	1.82	0.44
60:LS:45:TRP:HA	60:LS:48:VAL:HG22	1.98	0.44
67:La:8:THR:HG23	67:La:17:HIS:CE1	2.53	0.44
83:Lr:39:ARG:HG3	83:Lr:103:ARG:HH22	1.82	0.44
5:SE:181:CYS:HA	5:SE:227:VAL:HA	1.98	0.44
9:SJ:84:ILE:HA	9:SJ:150:ARG:HA	1.99	0.44
16:SY:126:GLY:HA2	16:SY:129:LYS:HG2	2.00	0.44
20:S2:1204:A:H2'	20:S2:1205:C:C6	2.52	0.44
20:S2:1425:G:H2'	20:S2:1426:U:H6	1.83	0.44
20:S2:1639:G7M:H8	20:S2:1639:G7M:H2'	1.26	0.44
41:L5:750:U:H1'	41:L5:917:A:C8	2.53	0.44
41:L5:1304:C:H2'	41:L5:1305:C:C6	2.53	0.44
41:L5:1503:A:H62	59:LQ:87:THR:HG21	1.81	0.44
41:L5:1671:U:H1'	68:Lb:12:GLN:NE2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1857:C:H2'	41:L5:1858:A:C8	2.52	0.44
41:L5:3930:U:O2	41:L5:4180:G:N2	2.42	0.44
41:L5:5004:C:H2'	41:L5:5005:G:O4'	2.18	0.44
41:L5:5018:C:H2'	41:L5:5019:A:H8	1.83	0.44
43:L8:27:U:H2'	43:L8:28:C:C6	2.53	0.44
47:LD:11:ALA:O	47:LD:15:ARG:HG3	2.17	0.44
56:LN:64:ILE:HG13	56:LN:106:ALA:HB2	2.00	0.44
6:SG:228:ILE:HD13	6:SG:231:ARG:HD2	2.00	0.44
9:SJ:2:PRO:O	20:S2:509:OMG:H5''	2.18	0.44
10:SL:28:THR:HA	10:SL:29:GLY:HA2	1.66	0.44
16:SY:45:ALA:HB2	16:SY:55:ILE:HG13	2.00	0.44
16:SY:107:ARG:NH2	20:S2:492:C:OP2	2.49	0.44
20:S2:14:C:H2'	20:S2:15:U:C6	2.52	0.44
20:S2:396:U:O2'	20:S2:401:A:O2'	2.30	0.44
20:S2:996:A:H2'	20:S2:997:A:C8	2.53	0.44
20:S2:1415:C:H2'	20:S2:1416:C:C6	2.53	0.44
20:S2:1643:U:H2'	20:S2:1644:C:C6	2.53	0.44
20:S2:1757:G:H8	20:S2:1758:G:H1'	1.82	0.44
41:L5:481:G:H2'	41:L5:482:G:C8	2.53	0.44
41:L5:1091:C:H2'	41:L5:1092:G:C8	2.53	0.44
41:L5:1207:C:H2'	41:L5:1208:G:C8	2.49	0.44
41:L5:1270:A:O2'	41:L5:1439:C:O2	2.28	0.44
41:L5:1317:U:H2'	41:L5:1318:C:C6	2.53	0.44
41:L5:3600:G:H2'	41:L5:3601:C:C6	2.53	0.44
41:L5:4056:A:O2'	41:L5:4057:C:OP1	2.36	0.44
41:L5:4996:C:H4'	70:Ld:26:THR:HG23	1.99	0.44
43:L8:7:U:H2'	43:L8:8:U:C6	2.53	0.44
43:L8:75:OMG:H2'	43:L8:76:C:C6	2.53	0.44
43:L8:94:G:OP1	76:Lj:73:ARG:HG2	2.18	0.44
43:L8:149:G:H21	50:LG:64:GLN:HE22	1.66	0.44
54:LL:91:ALA:HB1	54:LL:96:ILE:HB	1.99	0.44
69:Lc:26:LYS:N	69:Lc:98:ASP:OD1	2.43	0.44
84:Ls:148:SER:O	84:Ls:151:THR:OG1	2.35	0.44
4:SC:125:LYS:HG3	4:SC:143:CYS:HB2	1.99	0.44
5:SE:233:LYS:HD2	5:SE:234:PRO:HD2	1.99	0.44
6:SG:116:LYS:HE3	6:SG:125:THR:HG21	1.99	0.44
6:SG:170:ARG:HE	20:S2:67:C:N4	2.16	0.44
20:S2:1198:G:H2'	20:S2:1199:A:C8	2.52	0.44
20:S2:1597:C:H4'	20:S2:1603:G:C6	2.52	0.44
21:LR:36:ASN:OD1	21:LR:40:GLN:NE2	2.51	0.44
41:L5:425:U:H2'	41:L5:426:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:505:G:H2'	41:L5:506:C:C6	2.53	0.44
41:L5:746:A:H2	41:L5:918:G:H22	1.66	0.44
41:L5:1472:C:H2'	41:L5:1473:U:H6	1.82	0.44
41:L5:2579:G:OP2	66:LZ:107:LYS:NZ	2.51	0.44
41:L5:2658:G:O2'	41:L5:2675:G:N2	2.47	0.44
41:L5:3794:C:H2'	41:L5:3795:A:H8	1.82	0.44
41:L5:3873:G:H2'	41:L5:3874:G:H8	1.79	0.44
41:L5:4728:U:OP1	45:LB:132:LYS:NZ	2.51	0.44
43:L8:45:C:H2'	43:L8:46:G:H8	1.83	0.44
46:LC:207:PRO:HB3	46:LC:249:PHE:CD2	2.52	0.44
46:LC:316:LYS:HB2	46:LC:324:ILE:HG13	1.99	0.44
63:LV:42:VAL:HB	63:LV:45:ILE:HG13	2.00	0.44
68:Lb:65:MET:HE3	68:Lb:65:MET:HB2	1.82	0.44
7:SH:159:ASP:C	7:SH:161:ALA:H	2.26	0.44
8:SI:8:TRP:CE3	8:SI:20:PRO:HB3	2.53	0.44
10:SL:21:LYS:HE3	10:SL:23:VAL:HG11	1.98	0.44
16:SY:120:THR:O	16:SY:124:ASN:HB2	2.18	0.44
17:Sa:11:ALA:HB3	17:Sa:33:ASP:HB2	2.00	0.44
17:Sa:51:ARG:HH22	34:Sc:39:SER:HB2	1.81	0.44
20:S2:27:A2M:HM'3	20:S2:27:A2M:H1'	1.49	0.44
20:S2:430:C:H2'	20:S2:431:G:C8	2.52	0.44
20:S2:534:G:H2'	20:S2:535:G:C8	2.53	0.44
20:S2:634:A:H2'	20:S2:635:G:C8	2.51	0.44
20:S2:694:G:H2'	20:S2:695:C:C6	2.53	0.44
20:S2:929:G:N2	20:S2:1104:G:H4'	2.33	0.44
20:S2:1740:C:H2'	20:S2:1741:U:C6	2.53	0.44
20:S2:1795:G:H2'	20:S2:1796:G:C8	2.53	0.44
21:LR:83:GLY:N	41:L5:2812:A:OP1	2.41	0.44
21:LR:135:LYS:HB2	41:L5:2897:G:OP1	2.18	0.44
25:SF:126:THR:HA	25:SF:135:ARG:HD2	2.00	0.44
31:ST:113:VAL:HG22	31:ST:123:LEU:HD23	2.00	0.44
32:SU:66:ARG:HH12	32:SU:75:LYS:HD3	1.83	0.44
34:Sc:11:LEU:HB2	34:Sc:35:MET:HE2	2.00	0.44
37:Sg:271:LYS:HA	37:Sg:271:LYS:HD2	1.80	0.44
38:At:43:A:H2'	38:At:44:A:H8	1.83	0.44
41:L5:281:U:H2'	41:L5:282:C:H6	1.83	0.44
41:L5:396:A:OP2	41:L5:396:A:H8	2.01	0.44
41:L5:500:G:OP1	41:L5:504:G:N1	2.51	0.44
41:L5:937:U:OP1	55:LM:46:ARG:NE	2.51	0.44
41:L5:957:G:C2	41:L5:1283:G:H2'	2.53	0.44
41:L5:1085:C:H2'	41:L5:1086:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1341:U:H2'	41:L5:1342:A:C8	2.53	0.44
41:L5:1877:G:H2'	41:L5:1878:G:H8	1.81	0.44
41:L5:2049:G:H2'	41:L5:2050:G:H8	1.82	0.44
41:L5:2784:C:H2'	41:L5:2785:C:C6	2.53	0.44
41:L5:4246:G:H2'	41:L5:4247:G:H8	1.83	0.44
41:L5:4369:A:H2'	41:L5:4370:OMG:C8	2.53	0.44
41:L5:4530:UR3:H2'	41:L5:4531:U:H2'	1.98	0.44
44:LA:36:GLU:HG3	44:LA:91:GLY:HA2	1.98	0.44
63:LV:65:VAL:HG23	63:LV:73:ARG:HA	2.00	0.44
6:SG:163:ASN:OD1	6:SG:169:PRO:HB3	2.17	0.44
12:SO:32:HIS:CD2	12:SO:96:LYS:HD2	2.52	0.44
12:SO:98:ARG:HG3	12:SO:134:PRO:HD3	2.00	0.44
20:S2:354:OMU:HM23	20:S2:354:OMU:H1'	1.67	0.44
20:S2:433:A:H2'	20:S2:434:G:C8	2.53	0.44
20:S2:527:C:H2'	20:S2:528:A:C8	2.53	0.44
20:S2:1365:G:H2'	20:S2:1366:G:H8	1.83	0.44
20:S2:1392:U:H2'	20:S2:1393:G:C8	2.52	0.44
20:S2:1407:U:H2'	20:S2:1408:U:C6	2.53	0.44
20:S2:1839:U:H2'	20:S2:1840:U:C6	2.53	0.44
30:SS:102:GLY:HA2	30:SS:105:ASN:HD21	1.82	0.44
41:L5:287:U:H2'	41:L5:288:G:C8	2.53	0.44
41:L5:1377:G:H4'	41:L5:1378:C:H3'	2.00	0.44
41:L5:1893:C:O2'	41:L5:1937:C:O2	2.33	0.44
41:L5:2309:G:O2'	43:L8:18:U:O2	2.35	0.44
41:L5:2376:A:H2'	41:L5:2377:C:C6	2.53	0.44
41:L5:2626:U:C6	62:LU:92:LYS:HG2	2.52	0.44
41:L5:2857:A:H2'	41:L5:2858:A:O4'	2.18	0.44
41:L5:4218:U:OP2	61:LT:9:ARG:NH2	2.51	0.44
41:L5:4291:G:H5'	41:L5:4293:PSU:C6	2.53	0.44
41:L5:4488:A:OP1	88:L5:5285:SPM:N14	2.42	0.44
41:L5:4503:A:H2'	41:L5:4504:C:H6	1.82	0.44
41:L5:4637:OMG:H2'	41:L5:4638:U:C6	2.53	0.44
68:Lb:43:MET:HE2	68:Lb:43:MET:HB3	1.85	0.44
2:SA:123:VAL:HG22	2:SA:145:ILE:HB	2.00	0.43
3:SB:144:LYS:HB2	3:SB:208:HIS:ND1	2.33	0.43
5:SE:122:LYS:HE2	5:SE:124:CYS:SG	2.58	0.43
10:SL:16:ILE:HG23	10:SL:34:PRO:HG2	2.00	0.43
20:S2:403:G:H2'	20:S2:404:G:H8	1.83	0.43
20:S2:695:C:H42	20:S2:737:G:H1'	1.83	0.43
20:S2:1143:A:O2'	20:S2:1355:C:N4	2.50	0.43
20:S2:1289:U:H4'	26:SK:2:LEU:HD21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1491:G:H2'	20:S2:1492:U:C6	2.53	0.43
20:S2:1667:U:H2'	20:S2:1668:U:C6	2.53	0.43
20:S2:1716:C:H2'	20:S2:1717:C:H6	1.83	0.43
28:SP:41:GLN:HG3	28:SP:84:ILE:HG21	2.00	0.43
41:L5:460:C:H2'	41:L5:461:G:H8	1.83	0.43
41:L5:713:C:H2'	41:L5:714:G:H8	1.82	0.43
41:L5:1086:C:H2'	41:L5:1087:A:C8	2.52	0.43
41:L5:1479:G:H2'	41:L5:1480:C:C6	2.53	0.43
41:L5:1578:U:H2'	41:L5:1579:C:H6	1.82	0.43
41:L5:2540:C:H2'	41:L5:2541:G:C8	2.53	0.43
41:L5:2588:C:H4'	41:L5:2589:C:H5''	2.00	0.43
41:L5:3872:A:H2'	41:L5:3873:G:H8	1.83	0.43
41:L5:4522:G:O2'	41:L5:4525:C:OP2	2.29	0.43
41:L5:4524:G:H2'	41:L5:4525:C:C6	2.53	0.43
41:L5:4688:C:H2'	41:L5:4689:PSU:C6	2.53	0.43
41:L5:4913:G:H4'	41:L5:4914:C:O5'	2.18	0.43
42:L7:4:U:H2'	42:L7:5:A:H8	1.83	0.43
43:L8:5:U:H2'	43:L8:6:C:H6	1.83	0.43
46:LC:269:LYS:HA	46:LC:269:LYS:HD2	1.83	0.43
59:LQ:25:LEU:HD12	59:LQ:28:LEU:HD11	2.00	0.43
6:SG:23:LYS:HD3	6:SG:41:LEU:HA	2.00	0.43
13:SV:56:CYS:O	13:SV:60:ARG:HG2	2.18	0.43
20:S2:71:G:N2	20:S2:73:C:OP1	2.51	0.43
20:S2:186:C:H2'	20:S2:187:G:C8	2.52	0.43
20:S2:462:OMC:HM23	20:S2:462:OMC:H1'	1.74	0.43
20:S2:925:G:H1	20:S2:1017:U:H3	1.66	0.43
20:S2:1565:C:H2'	20:S2:1566:G:C8	2.54	0.43
20:S2:1773:C:H2'	20:S2:1774:C:H5''	1.99	0.43
20:S2:1778:C:H2'	20:S2:1779:G:O4'	2.17	0.43
30:SS:26:ILE:HD13	30:SS:56:ALA:HA	2.00	0.43
38:At:23:C:H2'	38:At:24:A:C8	2.53	0.43
41:L5:123:C:H2'	41:L5:124:C:H6	1.83	0.43
41:L5:271:C:H2'	41:L5:272:U:C6	2.53	0.43
41:L5:751:G:H2'	41:L5:752:G:O4'	2.17	0.43
41:L5:1472:C:H2'	41:L5:1473:U:C6	2.53	0.43
41:L5:2019:C:OP1	84:Ls:6:ARG:NH1	2.50	0.43
41:L5:2038:U:H2'	41:L5:2039:G:O4'	2.18	0.43
41:L5:2333:G:H5''	46:LC:195:LYS:HE3	2.00	0.43
41:L5:3917:A:H2'	41:L5:3918:G:C8	2.52	0.43
41:L5:4586:G:O6	41:L5:4717:A:N6	2.52	0.43
41:L5:4947:U:H2'	41:L5:4948:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L7:114:U:H2'	42:L7:115:A:C8	2.53	0.43
43:L8:6:C:H2'	43:L8:7:U:H6	1.84	0.43
45:LB:393:LYS:HG3	45:LB:396:ARG:HH21	1.82	0.43
55:LM:104:MET:HG2	55:LM:109:ARG:HG3	2.00	0.43
72:Lf:7:SER:HB2	72:Lf:103:VAL:HB	2.00	0.43
85:Lt:134:GLY:HA3	85:Lt:152:ILE:HD11	2.00	0.43
3:SB:85:LYS:HB2	3:SB:101:HIS:HB3	1.98	0.43
5:SE:32:SER:OG	5:SE:79:ASP:OD2	2.32	0.43
9:SJ:3:VAL:HB	9:SJ:5:ARG:HD3	1.99	0.43
16:SY:9:THR:HG22	20:S2:837:A:H61	1.83	0.43
20:S2:16:G:H2'	20:S2:17:C:C6	2.53	0.43
20:S2:96:C:O2	20:S2:473:A:O2'	2.29	0.43
20:S2:880:G:H3'	20:S2:881:G:H8	1.83	0.43
20:S2:1425:G:H2'	20:S2:1426:U:C6	2.54	0.43
40:CI:63:ARG:HD2	40:CI:63:ARG:HA	1.87	0.43
41:L5:455:C:O2'	41:L5:456:C:H5'	2.18	0.43
41:L5:467:U:C4	41:L5:468:U:H1'	2.54	0.43
41:L5:710:G:H2'	41:L5:711:A:H8	1.82	0.43
41:L5:980:U:OP2	48:LE:46:ARG:NH2	2.51	0.43
41:L5:1320:U:O2'	41:L5:1891:A:N1	2.45	0.43
41:L5:2029:A:H2'	41:L5:2030:A:C8	2.53	0.43
41:L5:2422:OMC:N4	41:L5:2828:U:O2'	2.35	0.43
41:L5:2824:OMC:HM23	41:L5:2824:OMC:H1'	1.68	0.43
41:L5:4585:U:OP1	57:LO:74:ARG:N	2.46	0.43
41:L5:4974:C:N4	41:L5:4975:G:O6	2.50	0.43
41:L5:5018:C:H2'	41:L5:5019:A:C8	2.54	0.43
42:L7:58:A:H2'	42:L7:59:G:H8	1.83	0.43
43:L8:6:C:H2'	43:L8:7:U:C6	2.53	0.43
47:LD:265:ARG:HD3	47:LD:269:PRO:HG3	2.00	0.43
50:LG:165:GLU:OE2	56:LN:26:ARG:NH1	2.50	0.43
2:SA:91:ALA:HA	2:SA:96:ALA:HB3	1.99	0.43
3:SB:124:HIS:HE1	20:S2:1003:U:H1'	1.82	0.43
3:SB:204:ILE:O	20:S2:1121:G:O2'	2.35	0.43
5:SE:43:PRO:HB2	5:SE:45:ILE:HG22	2.01	0.43
6:SG:98:ARG:NH2	6:SG:103:ASP:OD1	2.51	0.43
20:S2:509:OMG:H2'	20:S2:510:G:C8	2.52	0.43
20:S2:696:G:O2'	20:S2:735:C:O4'	2.32	0.43
20:S2:1553:C:H41	35:Sd:22:ARG:HH22	1.66	0.43
41:L5:6:C:H2'	41:L5:7:C:H6	1.82	0.43
41:L5:74:G:H1'	54:LL:62:PRO:HG3	2.00	0.43
41:L5:1334:A:H2'	41:L5:1335:G:H8	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1613:A:H5''	44:LA:183:GLY:CA	2.49	0.43
41:L5:2320:G:O2'	41:L5:2321:G:O4'	2.30	0.43
41:L5:3604:A:H2'	41:L5:3605:C:C6	2.53	0.43
41:L5:4311:A:H2'	41:L5:4312:PSU:H6	1.83	0.43
41:L5:4466:C:H2'	41:L5:4467:A:H8	1.84	0.43
41:L5:4561:C:H2'	41:L5:4562:C:C6	2.54	0.43
41:L5:5053:U:H5'	41:L5:5054:C:C4	2.54	0.43
43:L8:130:C:H2'	43:L8:131:G:C8	2.53	0.43
45:LB:397:ILE:HA	45:LB:400:GLU:HB2	2.01	0.43
60:LS:147:ASP:HB3	60:LS:150:ILE:HB	1.99	0.43
64:LX:127:LEU:HD11	64:LX:135:LYS:HE3	2.00	0.43
77:Lk:61:PRO:HA	77:Lk:62:PRO:HD3	1.92	0.43
11:SN:55:ARG:HD3	20:S2:1017:U:H5'	2.00	0.43
17:Sa:26:CYS:HB3	17:Sa:77:CYS:SG	2.58	0.43
20:S2:456:C:H2'	20:S2:457:C:C6	2.53	0.43
20:S2:527:C:O2	20:S2:559:G:N2	2.52	0.43
20:S2:1146:C:O2'	20:S2:1150:A:N1	2.45	0.43
20:S2:1351:G:N2	20:S2:1360:U:O2	2.44	0.43
20:S2:1403:C:OP2	20:S2:1405:A:N6	2.44	0.43
20:S2:1532:C:H3'	20:S2:1637:A:H62	1.82	0.43
20:S2:1706:G:O2'	20:S2:1850:MA6:O2'	2.19	0.43
20:S2:1787:G:H2'	20:S2:1788:A:H8	1.82	0.43
27:SM:40:LYS:HA	36:Sf:129:GLY:HA3	2.00	0.43
29:SQ:23:ALA:HB2	29:SQ:87:SER:HB3	2.01	0.43
29:SQ:39:LEU:HD11	29:SQ:51:LEU:HB3	2.00	0.43
41:L5:701:G:H2'	41:L5:702:U:H6	1.83	0.43
41:L5:702:U:H2'	41:L5:703:G:O4'	2.18	0.43
41:L5:1193:C:H2'	41:L5:1194:G:H5'	1.99	0.43
41:L5:1617:G:H1'	41:L5:2513:A:H61	1.83	0.43
41:L5:2575:U:H5''	41:L5:2576:G:H5'	2.01	0.43
41:L5:2614:C:O2'	41:L5:2808:G:OP1	2.34	0.43
41:L5:2811:G:N1	41:L5:2814:C:OP2	2.49	0.43
41:L5:3633:C:H2'	41:L5:3634:G:C8	2.53	0.43
41:L5:3684:G:H2'	41:L5:3685:C:H6	1.84	0.43
41:L5:4178:A:H2'	41:L5:4179:G:C8	2.53	0.43
41:L5:4740:G:C6	41:L5:4959:U:O2	2.71	0.43
41:L5:4770:U:H2'	41:L5:4771:C:C6	2.53	0.43
88:L5:5261:SPM:H62	88:L5:5261:SPM:H31	1.81	0.43
46:LC:245:HIS:ND1	83:Lr:13:CYS:SG	2.91	0.43
48:LE:225:PRO:O	48:LE:226:ARG:HD3	2.19	0.43
53:LJ:141:ILE:HD11	53:LJ:151:ILE:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SE:153:LEU:HD12	6:SG:216:ARG:HH11	1.83	0.43
8:SI:99:ASN:ND2	20:S2:376:A:O3'	2.52	0.43
11:SN:99:ARG:HE	11:SN:115:LEU:HD21	1.83	0.43
20:S2:1053:C:H2'	20:S2:1054:G:H8	1.83	0.43
20:S2:1824:A:H2'	20:S2:1825:A:C4	2.53	0.43
20:S2:1856:C:H2'	20:S2:1857:G:C8	2.54	0.43
21:LR:148:ASP:OD1	21:LR:149:LYS:N	2.52	0.43
24:SD:136:VAL:HG12	24:SD:186:VAL:HG22	2.01	0.43
27:SM:43:ASP:OD1	36:Sf:129:GLY:HA2	2.19	0.43
38:At:29:C:H2'	38:At:30:G:H8	1.84	0.43
41:L5:102:G:O2'	41:L5:1381:U:O2'	2.19	0.43
41:L5:150:U:H3	50:LG:163:PRO:HD2	1.82	0.43
41:L5:370:U:HO2'	76:Lj:16:HIS:HD1	1.67	0.43
41:L5:1339:U:H2'	41:L5:1340:OMC:C6	2.54	0.43
41:L5:2046:G:O2'	41:L5:2047:A:N7	2.49	0.43
41:L5:2406:G:N7	78:Li:2:SER:N	2.66	0.43
41:L5:2695:A:H1'	41:L5:2697:A:N7	2.33	0.43
41:L5:4343:U:O2'	81:Lo:31:ASP:OD1	2.35	0.43
41:L5:4507:A:H2'	41:L5:4508:C:C6	2.53	0.43
41:L5:4998:G:H2'	41:L5:4999:G:C8	2.54	0.43
41:L5:4998:G:H2'	41:L5:4999:G:H8	1.83	0.43
42:L7:114:U:H2'	42:L7:115:A:H8	1.82	0.43
45:LB:73:VAL:HG23	63:LV:89:ARG:HH21	1.83	0.43
48:LE:223:ARG:NH2	48:LE:234:ASP:O	2.51	0.43
63:LV:85:ARG:N	63:LV:101:ASN:OD1	2.51	0.43
5:SE:193:GLY:HA2	5:SE:212:ASP:HA	2.00	0.43
6:SG:137:ARG:NE	20:S2:171:A:OP1	2.49	0.43
10:SL:17:PHE:CG	20:S2:222:U:H5''	2.53	0.43
11:SN:88:LEU:HD13	11:SN:125:LEU:HD23	2.01	0.43
20:S2:1116:C:H2'	20:S2:1117:C:C6	2.53	0.43
20:S2:1597:C:H4'	20:S2:1603:G:O6	2.19	0.43
20:S2:1673:U:H2'	20:S2:1674:G:O4'	2.19	0.43
24:SD:71:ALA:O	24:SD:75:LYS:HG3	2.18	0.43
25:SF:42:LYS:HD3	25:SF:42:LYS:HA	1.73	0.43
37:Sg:230:LEU:HD21	37:Sg:259:TRP:CZ2	2.54	0.43
41:L5:351:C:OP2	46:LC:197:ARG:NH1	2.40	0.43
41:L5:677:G:H2'	41:L5:678:C:C6	2.54	0.43
41:L5:735:G:H2'	41:L5:736:C:C6	2.53	0.43
41:L5:918:G:H5'	55:LM:72:TYR:CZ	2.53	0.43
41:L5:1069:G:OP1	48:LE:65:ARG:NH2	2.51	0.43
41:L5:1097:C:H2'	41:L5:1098:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1196:G:H2'	41:L5:1197:C:C6	2.54	0.43
41:L5:1283:G:N1	41:L5:2076:G:OP1	2.41	0.43
41:L5:1511:U:H2'	41:L5:1512:G:C8	2.51	0.43
41:L5:1880:G:H5''	86:L5:5126:MG:MG	1.44	0.43
41:L5:2382:A:C2	41:L5:2830:G:H4'	2.54	0.43
41:L5:2732:G:H2'	41:L5:2733:C:C6	2.53	0.43
41:L5:3606:U:H2'	41:L5:3607:U:C6	2.54	0.43
41:L5:3848:U:H2'	41:L5:3849:A:C8	2.53	0.43
41:L5:4156:G:H3'	41:L5:4157:A:H8	1.83	0.43
41:L5:4263:C:H2'	41:L5:4264:G:O4'	2.18	0.43
43:L8:90:C:H2'	43:L8:91:A:H8	1.82	0.43
48:LE:183:ARG:HA	48:LE:183:ARG:HD2	1.80	0.43
51:LH:118:LEU:HD11	51:LH:167:VAL:HG22	2.00	0.43
55:LM:81:ASP:N	55:LM:81:ASP:OD1	2.51	0.43
60:LS:82:LEU:HA	60:LS:127:MET:HG2	2.00	0.43
84:Ls:167:VAL:HG13	84:Ls:171:GLU:HG2	2.00	0.43
1:Zt:29:A:H2'	1:Zt:30:G:H8	1.83	0.43
3:SB:142:PHE:CD2	3:SB:209:ASP:HB3	2.54	0.43
4:SC:94:ILE:HG13	4:SC:95:ASP:N	2.33	0.43
8:SI:117:TYR:HB3	8:SI:119:LEU:HD13	1.99	0.43
19:Se:31:ARG:HH22	20:S2:525:A:H4'	1.84	0.43
19:Se:34:ARG:HD3	19:Se:37:GLN:NE2	2.34	0.43
20:S2:24:C:O2'	20:S2:25:A:H8	2.01	0.43
20:S2:391:C:H2'	20:S2:392:A:H8	1.83	0.43
20:S2:443:U:H2'	20:S2:444:G:O4'	2.19	0.43
20:S2:1849:G:N7	20:S2:1850:MA6:H103	2.33	0.43
20:S2:1853:C:H2'	20:S2:1854:U:C6	2.53	0.43
21:LR:173:ARG:HG2	21:LR:176:ARG:NH2	2.34	0.43
30:SS:24:ARG:HG3	30:SS:29:ALA:HB2	2.00	0.43
41:L5:440:U:H2'	41:L5:441:G:C8	2.54	0.43
41:L5:461:G:H2'	41:L5:462:G:C8	2.53	0.43
41:L5:1089:G:H2'	41:L5:1090:G:C8	2.53	0.43
41:L5:1621:A:H2'	41:L5:1622:U:C6	2.53	0.43
41:L5:1646:A:H2'	41:L5:1647:U:C6	2.54	0.43
41:L5:1683:PSU:H2'	41:L5:1684:A:C8	2.54	0.43
41:L5:1704:C:O3'	49:LF:46:ARG:NH1	2.51	0.43
41:L5:1741:G:O6	42:L7:103:A:O2'	2.25	0.43
41:L5:1879:C:H2'	41:L5:1880:G:O4'	2.18	0.43
41:L5:1985:G:N2	41:L5:2004:U:O4	2.43	0.43
41:L5:2107:C:H2'	41:L5:2108:G:H8	1.84	0.43
41:L5:2308:A:OP1	71:Le:101:HIS:NE2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:3883:U:H2'	41:L5:3884:PSU:C6	2.54	0.43
41:L5:4466:C:H2'	41:L5:4467:A:C8	2.54	0.43
41:L5:4476:C:O2'	41:L5:4478:G:OP2	2.29	0.43
41:L5:4621:C:H2'	41:L5:4622:A:H8	1.84	0.43
47:LD:37:VAL:HG12	47:LD:50:ARG:HD3	2.00	0.43
58:LP:45:THR:HG22	58:LP:49:LYS:HE2	2.01	0.43
60:LS:85:ASP:HB2	60:LS:123:SER:HB3	2.00	0.43
70:Ld:29:ILE:O	70:Ld:33:ILE:HG12	2.18	0.43
74:Lh:3:LYS:HB3	74:Lh:3:LYS:HE2	1.81	0.43
2:SA:50:ASN:ND2	2:SA:53:ARG:HG3	2.33	0.43
2:SA:205:ARG:CZ	2:SA:210:ILE:HG13	2.48	0.43
3:SB:217:MET:HE3	3:SB:217:MET:HB2	1.88	0.43
5:SE:123:LEU:HB2	5:SE:236:ILE:HD11	2.00	0.43
6:SG:146:ASN:HB2	22:LW:101:ARG:HH22	1.83	0.43
7:SH:173:PHE:HA	7:SH:176:VAL:HG12	2.01	0.43
11:SN:4:MET:HG2	11:SN:5:HIS:CD2	2.53	0.43
20:S2:115:U:H2'	20:S2:116:OMU:C6	2.46	0.43
20:S2:173:A:H2'	20:S2:174:OMC:O4'	2.19	0.43
20:S2:373:G:O6	20:S2:392:A:N6	2.52	0.43
20:S2:595:U:H2'	20:S2:596:U:C6	2.54	0.43
20:S2:900:C:H5'	20:S2:901:G:N7	2.34	0.43
20:S2:931:C:H2'	20:S2:932:G:C8	2.53	0.43
20:S2:977:C:H2'	20:S2:978:G:O4'	2.18	0.43
20:S2:1373:C:H2'	20:S2:1374:C:C6	2.54	0.43
20:S2:1529:C:H4'	31:ST:89:PRO:HG3	2.00	0.43
20:S2:1623:A:O5'	30:SS:133:GLY:HA3	2.19	0.43
20:S2:1690:U:H2'	20:S2:1691:U:C6	2.54	0.43
20:S2:1842:4AC:O5'	20:S2:1842:4AC:H6	2.19	0.43
31:ST:72:VAL:HG22	31:ST:104:LEU:HD12	2.00	0.43
41:L5:358:C:H2'	41:L5:359:A:C8	2.54	0.43
41:L5:405:U:P	65:LY:87:ARG:HH22	2.42	0.43
41:L5:423:G:H2'	41:L5:424:U:C6	2.54	0.43
41:L5:470:A:H61	41:L5:684:G:H1'	1.84	0.43
41:L5:502:C:H3'	41:L5:503:C:H3'	2.01	0.43
41:L5:1759:G:O6	41:L5:1760:G:N2	2.52	0.43
41:L5:2644:G:H2'	41:L5:2645:G:H8	1.84	0.43
41:L5:2648:G:H2'	41:L5:2649:G:C8	2.53	0.43
41:L5:2898:G:H2'	41:L5:2899:C:H6	1.84	0.43
41:L5:4070:U:H2'	41:L5:4071:U:H6	1.84	0.43
41:L5:4208:U:OP2	61:LT:4:THR:OG1	2.31	0.43
41:L5:4236:G:H2'	41:L5:4237:C:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:4499:OMG:C2	41:L5:4529:G:H1'	2.54	0.43
41:L5:5024:C:H41	41:L5:5028:G:N2	2.14	0.43
42:L7:15:C:H2'	42:L7:16:A:C8	2.52	0.43
43:L8:63:U:O2'	74:Lh:52:LYS:NZ	2.42	0.43
44:LA:137:ILE:HD11	44:LA:149:LYS:HB2	2.01	0.43
53:LJ:20:LEU:HD21	53:LJ:130:PHE:CD2	2.53	0.43
54:LL:110:LEU:O	54:LL:114:VAL:HG13	2.19	0.43
82:Lp:55:TRP:CE2	82:Lp:71:TYR:HA	2.53	0.43
1:Zt:49:C:H2'	1:Zt:50:A:H8	1.84	0.43
6:SG:2:LYS:HG2	6:SG:17:GLU:HG3	2.00	0.43
8:SI:148:LYS:O	8:SI:151:GLU:HG3	2.18	0.43
18:Sb:13:GLU:HG2	18:Sb:14:GLU:H	1.84	0.43
20:S2:796:G:N2	20:S2:798:G:O6	2.52	0.43
20:S2:835:C:H4'	20:S2:836:G:H8	1.84	0.43
20:S2:1373:C:O2'	23:SR:10:LYS:NZ	2.39	0.43
20:S2:1595:U:H2'	20:S2:1596:U:C6	2.53	0.43
20:S2:1801:A:H2'	20:S2:1802:C:C6	2.54	0.43
20:S2:1805:G:H2'	20:S2:1806:A:H8	1.84	0.43
31:ST:110:LEU:HD23	31:ST:112:MET:HE3	2.01	0.43
33:SZ:47:LEU:HB2	33:SZ:79:ILE:HG22	2.01	0.43
39:Pt:1:G:H2'	39:Pt:2:U:C6	2.53	0.43
41:L5:6:C:H2'	41:L5:7:C:C6	2.54	0.43
41:L5:135:G:N7	74:Lh:97:LYS:HG2	2.34	0.43
41:L5:651:C:H2'	41:L5:652:G:C8	2.53	0.43
41:L5:667:A:H5''	41:L5:668:C:H5''	2.01	0.43
41:L5:930:G:H2'	41:L5:931:C:C6	2.54	0.43
41:L5:1569:U:H2'	41:L5:1570:G:C8	2.53	0.43
41:L5:1700:G:H5'	41:L5:1702:C:OP2	2.19	0.43
41:L5:1738:A:H2'	41:L5:1739:G:H8	1.83	0.43
41:L5:1777:C:H2'	41:L5:1778:C:C6	2.54	0.43
41:L5:1976:G:P	41:L5:1984:A:H4'	2.59	0.43
41:L5:2500:U:H2'	41:L5:2501:C:C6	2.53	0.43
41:L5:2626:U:O4	62:LU:97:ARG:NH1	2.52	0.43
41:L5:2763:U:H4'	41:L5:2764:A:H5''	2.01	0.43
41:L5:3825:A2M:H2'	41:L5:3826:C:C6	2.54	0.43
41:L5:3938:G:O6	41:L5:4173:G:N1	2.51	0.43
41:L5:4318:C:H4'	81:Lo:17:LYS:HA	2.00	0.43
41:L5:4410:G:C6	41:L5:4433:G:C6	3.06	0.43
57:LO:166:ILE:HG22	57:LO:170:LYS:HE2	2.01	0.43
58:LP:107:LEU:HB2	58:LP:152:GLU:OE2	2.19	0.43
2:SA:111:GLN:HA	2:SA:116:PHE:CG	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:SG:194:LEU:HA	6:SG:197:GLN:NE2	2.34	0.42
12:SO:54:CYS:HB3	12:SO:84:ARG:HG2	2.00	0.42
20:S2:85:A:H2'	20:S2:86:C:C6	2.54	0.42
20:S2:692:G:N7	20:S2:693:A:N6	2.67	0.42
20:S2:1330:G:N7	20:S2:1492:U:H3'	2.34	0.42
20:S2:1452:A:OP2	23:SR:32:LYS:NZ	2.52	0.42
20:S2:1501:C:H2'	20:S2:1502:C:H6	1.84	0.42
20:S2:1600:G:P	33:SZ:41:ARG:HH12	2.41	0.42
20:S2:1647:A:N1	20:S2:1675:A:H5''	2.33	0.42
21:LR:3:MET:HG3	41:L5:2385:U:H4'	2.00	0.42
22:LW:104:GLN:O	22:LW:107:GLN:HG3	2.19	0.42
27:SM:22:LEU:HD13	27:SM:88:TRP:HB3	2.00	0.42
37:Sg:152:SER:HB3	37:Sg:170:TRP:HE1	1.84	0.42
41:L5:946:C:H2'	41:L5:947:C:H6	1.84	0.42
41:L5:1199:G:H2'	41:L5:1200:G:C8	2.54	0.42
41:L5:1683:PSU:H2'	41:L5:1684:A:H8	1.83	0.42
41:L5:1811:G:H2'	41:L5:1812:C:H6	1.83	0.42
41:L5:2351:OMC:HM23	41:L5:2351:OMC:H1'	1.74	0.42
41:L5:2609:G:H2'	41:L5:2610:G:C8	2.55	0.42
41:L5:3744:OMG:HM23	41:L5:3744:OMG:H1'	1.71	0.42
43:L8:133:G:H2'	43:L8:134:G:H8	1.83	0.42
44:LA:30:ARG:NH1	44:LA:36:GLU:OE1	2.48	0.42
47:LD:150:LEU:HD12	53:LJ:146:ARG:HG3	2.00	0.42
52:LI:51:HIS:HB3	52:LI:134:VAL:HG13	2.01	0.42
58:LP:116:HIS:CD2	58:LP:149:ILE:HD12	2.54	0.42
69:Lc:33:GLN:O	69:Lc:37:MET:HG2	2.19	0.42
71:Le:88:LEU:HD12	71:Le:97:ALA:HB2	2.00	0.42
1:Zt:60:U:H2'	41:L5:4056:A:C4	2.54	0.42
2:SA:209:GLU:C	2:SA:211:GLU:N	2.72	0.42
6:SG:134:GLY:O	20:S2:65:C:N4	2.31	0.42
8:SI:12:ARG:NH1	20:S2:103:A:H5'	2.34	0.42
8:SI:98:LYS:HB3	20:S2:377:G:H5'	2.01	0.42
9:SJ:164:PRO:HB3	9:SJ:170:PRO:HA	2.01	0.42
15:SX:71:ARG:HA	15:SX:71:ARG:HD2	1.88	0.42
20:S2:21:U:H2'	20:S2:22:A:C8	2.54	0.42
20:S2:323:C:H5'	20:S2:324:C:OP1	2.19	0.42
20:S2:680:G:H2'	20:S2:681:PSU:H6	1.83	0.42
20:S2:1336:C:H2'	20:S2:1337:4AC:H6	2.01	0.42
20:S2:1417:C:O2	20:S2:1421:A:N6	2.52	0.42
20:S2:1487:A:H2'	20:S2:1488:C:C6	2.54	0.42
20:S2:1828:C:H2'	20:S2:1829:G:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:SR:35:CYS:HA	23:SR:38:ILE:HG12	2.01	0.42
41:L5:426:A:H2'	41:L5:427:A:C8	2.54	0.42
41:L5:989:U:O2	41:L5:1064:G:C6	2.72	0.42
41:L5:1305:C:OP1	89:L5:5284:SPD:N1	2.52	0.42
41:L5:1458:C:C2	41:L5:1459:A:C8	3.07	0.42
41:L5:1674:C:H1'	67:La:43:ILE:HD11	2.02	0.42
41:L5:2353:U:H2'	41:L5:2354:G:H8	1.85	0.42
41:L5:2485:U:H3	41:L5:2491:C:H41	1.67	0.42
41:L5:2728:U:H2'	41:L5:2729:C:C6	2.54	0.42
41:L5:3923:A:H2'	41:L5:3924:C:C6	2.54	0.42
41:L5:4091:G:H2'	41:L5:4092:G:C8	2.54	0.42
41:L5:4162:C:H6	50:LG:73:ARG:HH22	1.67	0.42
41:L5:4344:U:HO2'	81:Lo:29:GLY:H	1.62	0.42
46:LC:33:ARG:HG2	46:LC:35:ASP:OD1	2.19	0.42
57:LO:46:ASN:OD1	57:LO:49:ARG:N	2.41	0.42
72:Lf:78:HIS:N	72:Lf:83:MET:O	2.52	0.42
73:Lg:5:LEU:HD21	73:Lg:30:ILE:HB	2.01	0.42
2:SA:74:VAL:HG23	2:SA:121:LEU:HB3	2.00	0.42
2:SA:99:ILE:HG21	2:SA:103:PHE:HD1	1.85	0.42
7:SH:118:ARG:HD3	7:SH:118:ARG:HA	1.88	0.42
13:SV:38:GLU:OE2	13:SV:49:GLN:HG2	2.19	0.42
16:SY:9:THR:HG22	20:S2:837:A:N6	2.35	0.42
20:S2:314:U:H2'	20:S2:315:C:C6	2.55	0.42
20:S2:1259:A:H1'	20:S2:1264:C:H42	1.84	0.42
20:S2:1498:A:OP2	24:SD:27:ARG:NH2	2.52	0.42
20:S2:1556:A:C5	35:Sd:13:LYS:HA	2.55	0.42
28:SP:81:ARG:HB2	28:SP:117:GLY:HA3	2.01	0.42
29:SQ:48:GLN:O	29:SQ:52:LEU:HG	2.19	0.42
41:L5:35:U:H4'	41:L5:1525:A:C2	2.55	0.42
41:L5:153:G:H2'	41:L5:154:G:C8	2.51	0.42
41:L5:442:G:OP1	72:Lf:68:ARG:NH1	2.47	0.42
41:L5:492:U:H2'	41:L5:493:G:H8	1.81	0.42
41:L5:699:C:H2'	41:L5:700:G:H8	1.85	0.42
41:L5:920:C:H2'	41:L5:921:C:C6	2.54	0.42
41:L5:986:C:H2'	41:L5:987:C:H6	1.85	0.42
41:L5:1403:G:N2	41:L5:1415:G:C4	2.87	0.42
41:L5:1846:G:H2'	41:L5:1847:C:H6	1.84	0.42
41:L5:2751:G:H2'	41:L5:2752:G:H8	1.85	0.42
41:L5:3856:A:H5''	58:LP:83:TRP:O	2.20	0.42
41:L5:4066:U:H2'	41:L5:4067:U:H6	1.84	0.42
41:L5:4303:C:O2'	41:L5:4306:OMU:H5	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:4324:A:H2'	41:L5:4325:A:C8	2.54	0.42
41:L5:4593:C:H2'	41:L5:4594:U:H6	1.84	0.42
42:L7:3:C:H2'	42:L7:4:U:C6	2.54	0.42
44:LA:28:ARG:HB3	44:LA:123:ARG:HD3	2.00	0.42
45:LB:294:LYS:HG3	45:LB:295:ASP:H	1.85	0.42
48:LE:243:THR:HG22	48:LE:245:GLN:H	1.84	0.42
54:LL:78:LEU:HA	54:LL:81:LEU:HD12	2.00	0.42
85:Lt:19:GLY:HA2	85:Lt:48:LYS:HZ2	1.84	0.42
85:Lt:107:ASP:HA	85:Lt:110:VAL:HG12	2.01	0.42
1:Zt:51:G:H2'	1:Zt:52:G:H8	1.84	0.42
1:Zt:75:C:H2'	1:Zt:76:A:C8	2.54	0.42
2:SA:145:ILE:HG13	2:SA:159:ILE:HB	2.00	0.42
2:SA:198:MET:HE1	23:SR:86:PRO:HG2	2.00	0.42
3:SB:142:PHE:HD2	3:SB:209:ASP:HB3	1.85	0.42
5:SE:141:THR:HG23	5:SE:143:ASP:H	1.84	0.42
8:SI:81:VAL:HA	8:SI:102:VAL:HG12	2.00	0.42
9:SJ:33:GLY:HA3	19:Se:38:TYR:CD1	2.55	0.42
20:S2:675:U:H2'	20:S2:676:C:C6	2.55	0.42
20:S2:1421:A:H3'	20:S2:1422:G:H8	1.84	0.42
20:S2:1470:C:H2'	20:S2:1471:C:C6	2.53	0.42
20:S2:1531:A:O2'	20:S2:1604:G:N2	2.46	0.42
39:Pt:53:G:H2'	39:Pt:54:U:C6	2.54	0.42
41:L5:951:G:H5'	72:Lf:109:ARG:HD3	2.02	0.42
41:L5:1079:C:H2'	41:L5:1080:C:H6	1.84	0.42
41:L5:2540:C:H2'	41:L5:2541:G:H8	1.83	0.42
41:L5:2696:A:H62	77:Lk:35:LYS:NZ	2.17	0.42
41:L5:4196:OMG:HM23	41:L5:4196:OMG:H1'	1.90	0.42
43:L8:78:G:H2'	43:L8:79:G:C4	2.53	0.42
45:LB:17:LEU:HD23	45:LB:17:LEU:HA	1.88	0.42
49:LF:241:ASN:O	49:LF:245:ARG:HG2	2.19	0.42
52:LI:152:LEU:HB3	52:LI:165:ILE:HD12	2.01	0.42
57:LO:43:ILE:HD11	57:LO:138:LEU:HD13	2.01	0.42
62:LU:63:ILE:HD13	62:LU:72:VAL:HG22	2.02	0.42
81:Lo:26:TYR:HB3	81:Lo:67:VAL:HB	2.02	0.42
3:SB:114:VAL:HG11	20:S2:987:A:H2'	2.02	0.42
5:SE:42:LEU:HD12	5:SE:101:LEU:HD11	2.01	0.42
8:SI:181:GLN:NE2	20:S2:380:G:OP2	2.51	0.42
9:SJ:80:ARG:O	9:SJ:84:ILE:HG12	2.20	0.42
9:SJ:110:LEU:HD22	9:SJ:147:PHE:HD2	1.84	0.42
20:S2:404:G:H2'	20:S2:405:G:H8	1.85	0.42
20:S2:1192:U:H2'	20:S2:1193:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1404:U:H3	20:S2:1580:A:P	2.43	0.42
20:S2:1433:C:H42	32:SU:92:HIS:HD2	1.67	0.42
20:S2:1457:U:H2'	20:S2:1458:G:C8	2.54	0.42
20:S2:1473:G:N1	20:S2:1476:A:OP2	2.50	0.42
20:S2:1601:A:O4'	20:S2:1636:G:N2	2.53	0.42
21:LR:69:ALA:HB1	21:LR:74:ARG:HB2	2.01	0.42
25:SF:73:THR:O	25:SF:89:THR:HG21	2.18	0.42
25:SF:168:THR:OG1	33:SZ:106:GLN:OE1	2.20	0.42
41:L5:1085:C:H2'	41:L5:1086:C:H6	1.85	0.42
41:L5:1368:A:H2'	41:L5:1369:C:O4'	2.20	0.42
41:L5:2286:G:H2'	41:L5:2287:G:C8	2.54	0.42
41:L5:2460:A:OP2	89:L5:5289:SPD:N10	2.52	0.42
41:L5:3589:G:N2	41:L5:3590:G:O6	2.53	0.42
41:L5:3659:G:OP1	44:LA:241:ARG:NH1	2.52	0.42
41:L5:4262:C:H2'	41:L5:4263:C:H6	1.83	0.42
41:L5:4305:G:N7	61:LT:87:LYS:NZ	2.54	0.42
41:L5:4540:C:H2'	41:L5:4541:G:C8	2.54	0.42
41:L5:4592:C:H2'	41:L5:4593:C:H6	1.83	0.42
52:LI:171:TRP:HB2	52:LI:178:ALA:HA	2.01	0.42
60:LS:118:ARG:O	60:LS:120:ARG:NH1	2.52	0.42
61:LT:30:TYR:HA	61:LT:93:ILE:HD12	2.00	0.42
62:LU:60:VAL:HG13	62:LU:61:VAL:HG23	2.01	0.42
63:LV:107:ASN:OD1	63:LV:111:GLU:N	2.52	0.42
65:LY:24:HIS:CE1	65:LY:25:ILE:HG23	2.55	0.42
76:Lj:54:LYS:O	76:Lj:58:THR:HB	2.18	0.42
80:Ln:2:ARG:HB3	80:Ln:5:TRP:CD1	2.55	0.42
84:Ls:38:LYS:HD3	84:Ls:38:LYS:HA	1.83	0.42
5:SE:146:THR:HG21	20:S2:122:G:H21	1.83	0.42
5:SE:252:ARG:HH21	9:SJ:72:PHE:HD1	1.67	0.42
11:SN:91:LEU:HB3	11:SN:122:ILE:HG12	2.01	0.42
16:SY:25:ILE:HD11	16:SY:60:PHE:HZ	1.84	0.42
20:S2:735:C:H3'	20:S2:736:C:O4'	2.19	0.42
20:S2:941:C:H2'	20:S2:942:G:H8	1.84	0.42
20:S2:1047:C:H2'	20:S2:1048:G:O4'	2.20	0.42
20:S2:1544:C:O2'	29:SQ:76:GLY:O	2.30	0.42
30:SS:16:LEU:HD12	30:SS:33:ILE:HG21	2.00	0.42
38:At:51:C:H2'	38:At:52:G:H8	1.83	0.42
41:L5:162:A:H2'	41:L5:163:A:C8	2.55	0.42
41:L5:299:C:H2'	41:L5:300:A:C8	2.54	0.42
41:L5:1309:C:H2'	41:L5:1310:C:C6	2.54	0.42
41:L5:1340:OMC:H1'	41:L5:1340:OMC:HM23	1.74	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1455:G:H2'	41:L5:1456:C:C6	2.55	0.42
41:L5:1538:U:H2'	41:L5:1539:G:H8	1.85	0.42
41:L5:1887:G:H21	41:L5:1938:C:N4	2.17	0.42
41:L5:1933:G:H8	41:L5:1933:G:O5'	2.01	0.42
41:L5:2317:C:H2'	41:L5:2318:G:C8	2.55	0.42
41:L5:4536:OMC:HM22	41:L5:4537:C:O4'	2.20	0.42
41:L5:4578:G:H2'	41:L5:4579:PSU:C6	2.53	0.42
41:L5:4928:C:H2'	41:L5:4929:C:C6	2.55	0.42
61:LT:14:MET:HG2	61:LT:58:HIS:ND1	2.35	0.42
66:LZ:42:LEU:HD21	66:LZ:96:VAL:HG12	2.00	0.42
2:SA:198:MET:HG2	2:SA:199:PRO:HD2	2.02	0.42
6:SG:222:GLU:O	6:SG:226:GLU:HG2	2.20	0.42
8:SI:130:THR:HA	8:SI:133:GLU:HG3	2.02	0.42
12:SO:71:PRO:HB3	12:SO:114:SER:HB3	2.02	0.42
20:S2:406:PSU:H2'	20:S2:408:A:C8	2.54	0.42
20:S2:673:G:H2'	20:S2:674:C:C6	2.54	0.42
20:S2:818:A:H2'	20:S2:819:G:C8	2.55	0.42
20:S2:867:OMG:HM23	20:S2:867:OMG:H1'	1.85	0.42
20:S2:996:A:H2'	20:S2:997:A:H8	1.84	0.42
20:S2:1719:A:N6	20:S2:1814:G:O2'	2.52	0.42
25:SF:96:ALA:O	25:SF:100:ILE:HG23	2.19	0.42
41:L5:1613:A:H5''	44:LA:183:GLY:HA2	2.02	0.42
41:L5:2079:G:H2'	41:L5:2080:U:H6	1.84	0.42
41:L5:2277:C:H2'	41:L5:2278:G:C8	2.55	0.42
41:L5:2486:G:N7	41:L5:2493:G:N1	2.58	0.42
41:L5:2497:C:H2'	41:L5:2498:C:H6	1.85	0.42
41:L5:4173:G:H2'	41:L5:4174:U:C6	2.55	0.42
41:L5:4277:G:O2'	41:L5:4282:A:N6	2.52	0.42
41:L5:4505:C:H2'	41:L5:4506:C:C6	2.55	0.42
47:LD:208:MET:HE2	47:LD:233:PRO:HG3	2.01	0.42
48:LE:192:LYS:HG2	72:Lf:107:PRO:HA	2.02	0.42
54:LL:178:ALA:N	67:La:134:GLU:OE2	2.44	0.42
2:SA:5:LEU:HB3	2:SA:7:VAL:HG12	2.01	0.42
2:SA:209:GLU:HG3	2:SA:212:LYS:HE3	2.01	0.42
11:SN:112:LYS:O	11:SN:116:ILE:HG13	2.20	0.42
15:SX:9:THR:HG22	20:S2:681:PSU:H4'	2.01	0.42
20:S2:197:U:H2'	20:S2:203:G:N2	2.35	0.42
20:S2:373:G:H2'	20:S2:374:G:H8	1.84	0.42
20:S2:468:A2M:H2'	20:S2:469:A:O4'	2.20	0.42
20:S2:677:G:H21	20:S2:1028:A:H62	1.66	0.42
20:S2:1101:U:H2'	20:S2:1102:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1238:U:H1'	28:SP:126:VAL:HG23	2.02	0.42
20:S2:1533:A:H2	20:S2:1536:G:N3	2.17	0.42
20:S2:1626:C:H2'	20:S2:1627:C:H6	1.85	0.42
27:SM:23:LYS:O	27:SM:27:ILE:HG12	2.20	0.42
30:SS:86:ARG:HD3	30:SS:86:ARG:HA	1.91	0.42
41:L5:39:A:OP1	89:L5:5258:SPD:N1	2.37	0.42
41:L5:307:A:H2'	41:L5:308:G:C4	2.55	0.42
41:L5:714:G:H2'	41:L5:715:G:C8	2.55	0.42
41:L5:1251:C:H2'	41:L5:1252:C:C6	2.55	0.42
41:L5:2283:G:H2'	41:L5:2284:G:H8	1.85	0.42
41:L5:3661:G:N7	44:LA:152:SER:OG	2.51	0.42
41:L5:3951:G:O2'	41:L5:4062:A:N1	2.41	0.42
41:L5:4679:G:H2'	41:L5:4680:G:H8	1.85	0.42
44:LA:180:LEU:HD21	82:Lp:22:LEU:HB3	2.01	0.42
45:LB:29:VAL:HA	45:LB:220:ILE:HD13	2.02	0.42
45:LB:119:TYR:OH	45:LB:129:ALA:N	2.51	0.42
50:LG:115:LEU:HD23	50:LG:115:LEU:HA	1.87	0.42
65:LY:28:LYS:HE3	65:LY:28:LYS:HB3	1.94	0.42
2:SA:148:CYS:HB3	2:SA:163:CYS:H	1.85	0.42
4:SC:203:GLY:O	4:SC:221:ASP:HA	2.19	0.42
5:SE:9:LEU:HB3	5:SE:28:ALA:HB3	2.01	0.42
5:SE:11:ARG:NH1	5:SE:24:THR:OG1	2.51	0.42
8:SI:44:HIS:ND1	20:S2:1740:C:OP1	2.52	0.42
13:SV:11:LEU:HD23	13:SV:11:LEU:H	1.85	0.42
20:S2:464:A:H5'	20:S2:465:A:C8	2.55	0.42
20:S2:674:C:H2'	20:S2:675:U:C6	2.55	0.42
20:S2:1373:C:H2'	20:S2:1374:C:H6	1.85	0.42
20:S2:1738:C:H2'	20:S2:1739:C:H6	1.85	0.42
41:L5:139:G:H2'	41:L5:140:G:H8	1.84	0.42
41:L5:374:G:OP2	76:Lj:56:ARG:NH1	2.53	0.42
41:L5:396:A:H2'	41:L5:397:G:C8	2.54	0.42
41:L5:422:C:H2'	41:L5:423:G:C8	2.54	0.42
41:L5:1081:C:C2'	41:L5:1082:C:H5'	2.50	0.42
41:L5:2325:C:O2'	71:Le:124:ASN:ND2	2.53	0.42
41:L5:3709:U:H2'	41:L5:3710:G:O4'	2.20	0.42
41:L5:3798:U:O2'	41:L5:3800:A:N7	2.51	0.42
41:L5:4174:U:H2'	41:L5:4175:G:C8	2.49	0.42
41:L5:4194:U:N3	41:L5:4198:G:OP2	2.53	0.42
41:L5:4520:G:N2	45:LB:253:CYS:SG	2.93	0.42
41:L5:4970:C:C2	41:L5:4971:A:C8	3.08	0.42
46:LC:221:PHE:HB2	46:LC:229:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:LP:37:LYS:HB3	58:LP:37:LYS:HE2	1.86	0.42
65:LY:54:GLU:HB2	65:LY:67:ILE:HG22	2.02	0.42
2:SA:149:ASN:HB3	2:SA:152:SER:HB3	2.02	0.42
4:SC:271:ASP:O	4:SC:275:LYS:HG3	2.20	0.42
8:SI:129:LEU:HD12	8:SI:129:LEU:HA	1.88	0.42
14:SW:86:LEU:HB3	14:SW:117:ARG:NH2	2.35	0.42
20:S2:550:C:H2'	20:S2:551:U:C6	2.55	0.42
20:S2:1143:A:H2'	20:S2:1144:A:C8	2.55	0.42
20:S2:1393:G:H2'	20:S2:1394:G:C8	2.55	0.42
41:L5:73:A:O2'	54:LL:62:PRO:HA	2.20	0.42
41:L5:683:C:H2'	41:L5:684:G:O4'	2.19	0.42
41:L5:1314:C:C2	41:L5:1315:C:C5	3.07	0.42
41:L5:1366:G:N2	54:LL:33:ILE:HD13	2.34	0.42
41:L5:1884:C:H2'	41:L5:1885:G:H8	1.84	0.42
41:L5:2364:OMG:H1'	41:L5:2364:OMG:HM23	1.64	0.42
41:L5:2446:C:H2'	41:L5:2447:U:C6	2.54	0.42
41:L5:2582:A:N3	41:L5:2654:C:H1'	2.34	0.42
41:L5:2654:C:H2'	41:L5:2655:C:H6	1.84	0.42
41:L5:2662:G:H2'	41:L5:2663:G:C8	2.55	0.42
41:L5:2674:A:N6	82:Lp:42:CYS:HA	2.35	0.42
41:L5:2748:C:H2'	41:L5:2749:C:C6	2.55	0.42
41:L5:3825:A2M:H1'	41:L5:3825:A2M:HM'3	1.49	0.42
41:L5:4071:U:H2'	41:L5:4072:C:H6	1.84	0.42
41:L5:4431:PSU:P	52:LI:3:ARG:HH22	2.42	0.42
45:LB:238:LYS:HE2	45:LB:238:LYS:HB2	1.75	0.42
46:LC:56:GLU:HG2	46:LC:57:LEU:HG	2.01	0.42
65:LY:22:PRO:HD2	65:LY:25:ILE:HD11	2.01	0.42
77:Lk:51:GLU:O	77:Lk:55:LYS:HG2	2.20	0.42
5:SE:137:PRO:HG2	5:SE:150:PRO:HD2	2.02	0.41
16:SY:43:LYS:NZ	16:SY:47:MET:HB2	2.35	0.41
20:S2:10:G:O4'	20:S2:1697:A:O2'	2.38	0.41
20:S2:627:OMU:H2'	20:S2:627:OMU:H6	1.82	0.41
20:S2:1467:C:H5''	23:SR:1:MET:HA	2.02	0.41
20:S2:1545:A:H2	20:S2:1671:G:H1'	1.85	0.41
20:S2:1706:G:H5'	80:Ln:1:MET:HG3	2.01	0.41
20:S2:1736:G:H2'	20:S2:1737:G:H8	1.85	0.41
20:S2:1758:G:O6	20:S2:1772:C:N4	2.53	0.41
23:SR:114:LEU:HB2	23:SR:117:LEU:HG	2.01	0.41
26:SK:5:LYS:O	26:SK:9:ILE:HG12	2.20	0.41
34:Sc:10:LYS:HD2	34:Sc:34:PHE:CE2	2.55	0.41
39:Pt:23:C:H2'	39:Pt:24:A:H8	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:323:C:H2'	41:L5:324:A:C8	2.55	0.41
41:L5:1449:C:H2'	41:L5:1450:C:H6	1.85	0.41
41:L5:1578:U:H2'	41:L5:1579:C:C6	2.54	0.41
41:L5:1998:A:N7	84:Ls:55:MET:HB3	2.35	0.41
41:L5:2735:G:H2'	41:L5:2736:G:H8	1.85	0.41
41:L5:2890:C:H2'	41:L5:2891:U:C6	2.55	0.41
41:L5:3664:G:H2'	41:L5:3665:G:C8	2.52	0.41
41:L5:3859:G:OP2	58:LP:25:HIS:NE2	2.52	0.41
41:L5:3878:C:OP1	41:L5:4400:G:O2'	2.31	0.41
41:L5:4593:C:H2'	41:L5:4594:U:C6	2.55	0.41
43:L8:4:C:H2'	43:L8:5:U:H6	1.85	0.41
43:L8:89:U:H2'	43:L8:90:C:C6	2.55	0.41
46:LC:334:THR:HA	46:LC:337:ARG:HG2	2.01	0.41
50:LG:83:PHE:HA	50:LG:183:ILE:HD13	2.02	0.41
52:LI:36:LEU:HD21	52:LI:69:ARG:NH1	2.35	0.41
58:LP:118:GLN:HB3	58:LP:147:GLU:HG2	2.00	0.41
83:Lr:28:GLU:OE2	83:Lr:31:ASN:ND2	2.53	0.41
3:SB:222:LYS:HD2	3:SB:222:LYS:HA	1.75	0.41
6:SG:143:LYS:HA	6:SG:143:LYS:HD3	1.78	0.41
7:SH:133:LEU:HD11	7:SH:176:VAL:HG13	2.01	0.41
12:SO:65:ASP:HB3	20:S2:963:A:OP1	2.19	0.41
13:SV:27:LYS:HA	13:SV:27:LYS:HD3	1.77	0.41
20:S2:498:C:H2'	20:S2:499:G:C8	2.56	0.41
20:S2:943:U:C2	20:S2:944:A:C8	3.08	0.41
20:S2:1286:G:H21	20:S2:1313:A:H62	1.68	0.41
20:S2:1541:G:H2'	20:S2:1542:C:C6	2.55	0.41
39:Pt:8:U:O2'	39:Pt:21:A:N1	2.42	0.41
41:L5:40:G:N2	41:L5:4380:A:H62	2.17	0.41
41:L5:229:G:OP1	65:LY:11:ARG:NH1	2.40	0.41
41:L5:959:G:C8	48:LE:123:ARG:HG2	2.55	0.41
41:L5:982:U:H2'	41:L5:983:C:C6	2.55	0.41
41:L5:983:C:H2'	41:L5:984:C:H6	1.85	0.41
41:L5:1092:G:H2'	41:L5:1093:C:C6	2.55	0.41
41:L5:1211:G:H2'	41:L5:1212:G:H8	1.83	0.41
41:L5:1351:G:H2'	41:L5:1352:C:C6	2.55	0.41
41:L5:1366:G:O6	54:LL:37:LYS:NZ	2.36	0.41
41:L5:1820:C:O2'	41:L5:1821:G:N7	2.52	0.41
41:L5:1830:G:H4'	68:Lb:68:ARG:NH1	2.34	0.41
41:L5:1972:G:C6	41:L5:1973:G:O6	2.73	0.41
41:L5:2386:U:C2	41:L5:2387:G:C8	3.08	0.41
41:L5:3670:C:N4	41:L5:3671:G:O6	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:3874:G:H2'	41:L5:3875:G:C8	2.55	0.41
41:L5:4240:G:H2'	41:L5:4241:C:C6	2.55	0.41
41:L5:4517:A:H5''	41:L5:4518:A:H5''	2.01	0.41
41:L5:4638:U:H3	41:L5:4661:G:H1	1.68	0.41
41:L5:4884:G:O6	48:LE:272:ARG:NH1	2.50	0.41
45:LB:60:VAL:HG11	45:LB:67:VAL:HG23	2.01	0.41
49:LF:36:LYS:HD3	49:LF:36:LYS:HA	1.89	0.41
51:LH:20:LEU:HD23	51:LH:20:LEU:HA	1.92	0.41
55:LM:30:VAL:HG21	60:LS:152:PHE:HZ	1.84	0.41
56:LN:164:LEU:O	56:LN:169:ARG:NH2	2.54	0.41
76:Lj:28:HIS:CE1	76:Lj:31:LYS:HD3	2.56	0.41
85:Lt:127:GLY:O	85:Lt:131:GLU:HG2	2.20	0.41
5:SE:149:TYR:HB3	6:SG:209:TYR:HB2	2.01	0.41
6:SG:196:LYS:HD3	20:S2:126:G:O6	2.20	0.41
17:Sa:67:LEU:HG	17:Sa:69:VAL:HG23	2.02	0.41
20:S2:121:OMU:HM22	20:S2:122:G:H5'	2.02	0.41
20:S2:935:G:H2'	20:S2:936:G:H8	1.85	0.41
20:S2:1336:C:O3'	35:Sd:44:ARG:NH2	2.53	0.41
20:S2:1380:C:H2'	20:S2:1381:G:C8	2.55	0.41
20:S2:1466:G:H4'	23:SR:4:VAL:HG22	2.02	0.41
20:S2:1706:G:H2'	20:S2:1707:U:H6	1.86	0.41
20:S2:1748:G:O6	22:LW:73:ARG:NH2	2.53	0.41
24:SD:215:ASP:OD1	24:SD:215:ASP:N	2.52	0.41
32:SU:67:LYS:HG2	32:SU:78:ASP:HB2	2.01	0.41
34:Sc:14:VAL:HA	34:Sc:32:VAL:HG12	2.02	0.41
41:L5:179:G:H2'	41:L5:180:C:C6	2.56	0.41
41:L5:229:G:H2'	41:L5:230:G:H8	1.85	0.41
41:L5:1908:A:H2'	41:L5:1909:G:O4'	2.20	0.41
41:L5:2759:G:O2'	41:L5:2760:G:O4'	2.28	0.41
41:L5:2787:A2M:HM'2	41:L5:2787:A2M:H1'	1.59	0.41
41:L5:3910:C:H2'	41:L5:3911:C:H6	1.84	0.41
41:L5:4320:G:H2'	41:L5:4321:U:C6	2.55	0.41
41:L5:4685:U:H2'	41:L5:4686:G:C8	2.55	0.41
41:L5:4769:G:H5''	57:LO:176:ARG:HD3	2.03	0.41
43:L8:45:C:H2'	43:L8:46:G:C8	2.56	0.41
46:LC:37:VAL:HG11	46:LC:246:VAL:HG13	2.03	0.41
46:LC:366:ASP:HB3	46:LC:368:LYS:HE2	2.02	0.41
48:LE:284:HIS:CE1	48:LE:285:LYS:HG2	2.55	0.41
55:LM:14:TYR:OH	55:LM:22:GLY:HA2	2.21	0.41
62:LU:24:ASP:HB3	62:LU:111:GLU:HG2	2.02	0.41
5:SE:139:LEU:HB2	5:SE:150:PRO:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:SW:93:LEU:HD23	14:SW:93:LEU:HA	1.87	0.41
20:S2:201:C:H3'	20:S2:202:G:N2	2.33	0.41
20:S2:202:G:N2	20:S2:202:G:OP2	2.51	0.41
20:S2:404:G:H2'	20:S2:405:G:C8	2.55	0.41
20:S2:1037:G:H4'	20:S2:1845:A:H4'	2.03	0.41
20:S2:1298:G:H8	20:S2:1298:G:OP1	2.03	0.41
22:LW:97:LYS:O	22:LW:99:GLU:N	2.51	0.41
27:SM:31:LEU:HG	27:SM:33:ARG:NH1	2.36	0.41
33:SZ:101:SER:HB3	33:SZ:108:ILE:HD12	2.03	0.41
36:Sf:140:TYR:HB2	36:Sf:147:THR:HG22	2.02	0.41
37:Sg:206:LEU:HD12	37:Sg:218:LEU:HB3	2.01	0.41
41:L5:749:G:C6	41:L5:912:G:C8	3.08	0.41
41:L5:937:U:H2'	41:L5:938:C:C6	2.55	0.41
41:L5:1382:G:C2	41:L5:1383:G:N7	2.89	0.41
41:L5:1666:C:H2'	41:L5:1667:G:O4'	2.21	0.41
41:L5:1669:A:C2	41:L5:1852:U:H4'	2.55	0.41
41:L5:2017:A:HO2'	41:L5:2018:C:C5'	2.33	0.41
41:L5:2275:G:H2'	41:L5:2276:A:H8	1.83	0.41
41:L5:2538:U:H2'	41:L5:2539:C:H6	1.86	0.41
41:L5:2617:G:H2'	41:L5:2618:G:O4'	2.19	0.41
41:L5:3867:A2M:H2'	41:L5:3868:G:C8	2.54	0.41
41:L5:3910:C:H2'	41:L5:3911:C:C6	2.55	0.41
41:L5:3936:A:N6	41:L5:4175:G:O6	2.53	0.41
41:L5:4156:G:H5''	41:L5:4157:A:H2'	2.01	0.41
42:L7:75:G:H1'	42:L7:76:U:H5	1.85	0.41
46:LC:66:SER:HA	46:LC:77:PRO:HA	2.02	0.41
48:LE:252:ALA:O	48:LE:255:SER:OG	2.37	0.41
58:LP:6:LEU:HD22	58:LP:116:HIS:ND1	2.35	0.41
58:LP:114:ILE:HG12	58:LP:150:LEU:HD22	2.03	0.41
60:LS:16:CYS:SG	60:LS:54:MET:HG2	2.60	0.41
68:Lb:14:ARG:O	68:Lb:18:ARG:HG3	2.19	0.41
84:Ls:17:ILE:HG13	84:Ls:21:LEU:HD23	2.01	0.41
4:SC:187:ARG:HA	4:SC:187:ARG:HD2	1.84	0.41
14:SW:28:ARG:HG2	14:SW:29:PRO:HD3	2.02	0.41
15:SX:86:PRO:HG3	15:SX:121:LYS:HD2	2.03	0.41
16:SY:108:LYS:NZ	20:S2:506:G:OP1	2.45	0.41
17:Sa:46:GLU:O	17:Sa:50:VAL:HG23	2.20	0.41
20:S2:186:C:H2'	20:S2:187:G:H8	1.85	0.41
20:S2:604:A:H1'	20:S2:639:C:O2'	2.21	0.41
20:S2:944:A:H2'	20:S2:945:U:H6	1.84	0.41
20:S2:1518:C:OP1	20:S2:1519:U:H2'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1538:C:H2'	20:S2:1539:U:C6	2.55	0.41
20:S2:1806:A:H2'	20:S2:1807:C:H6	1.86	0.41
21:LR:110:ARG:HE	21:LR:110:ARG:HB3	1.71	0.41
41:L5:443:G:H5''	72:Lf:54:LYS:HB3	2.01	0.41
41:L5:1837:A:OP2	61:LT:130:ARG:NE	2.54	0.41
41:L5:1874:A:H2'	41:L5:1875:C:C6	2.55	0.41
41:L5:2648:G:H2'	41:L5:2649:G:H8	1.84	0.41
41:L5:2683:C:H2'	41:L5:2684:C:C6	2.56	0.41
41:L5:3921:U:H1'	41:L5:4543:G:H21	1.85	0.41
41:L5:4070:U:H2'	41:L5:4071:U:C6	2.54	0.41
41:L5:4081:G:H2'	41:L5:4082:G:C8	2.55	0.41
41:L5:4577:U:H2'	41:L5:4578:G:C8	2.54	0.41
46:LC:158:VAL:HG12	46:LC:217:ILE:HD12	2.02	0.41
47:LD:60:ILE:H	47:LD:80:ALA:HB3	1.86	0.41
52:LI:91:LEU:HD23	52:LI:91:LEU:HA	1.94	0.41
2:SA:85:ARG:HD3	2:SA:203:PHE:O	2.21	0.41
7:SH:7:LYS:HE2	7:SH:10:LYS:HB3	2.02	0.41
11:SN:63:VAL:O	11:SN:67:THR:OG1	2.36	0.41
12:SO:31:CYS:HA	12:SO:44:VAL:HA	2.02	0.41
12:SO:61:LYS:NZ	12:SO:76:LEU:HB3	2.35	0.41
18:Sb:2:PRO:HB2	18:Sb:5:LYS:HG2	2.02	0.41
20:S2:293:C:O2'	20:S2:295:C:H5'	2.20	0.41
20:S2:455:A:H2'	20:S2:456:C:C6	2.56	0.41
20:S2:533:A:H61	20:S2:550:C:N4	2.19	0.41
20:S2:678:U:C2	20:S2:679:A:C8	3.09	0.41
20:S2:737:G:C8	20:S2:738:C:H4'	2.55	0.41
20:S2:825:A:H2'	20:S2:826:A:C8	2.56	0.41
20:S2:963:A:H2'	20:S2:964:A:C8	2.55	0.41
20:S2:1031:A2M:H2'	20:S2:1032:C:C6	2.55	0.41
20:S2:1266:C:C4	20:S2:1517:G:N2	2.88	0.41
20:S2:1406:G:H2'	20:S2:1407:U:C6	2.55	0.41
20:S2:1495:G:H2'	20:S2:1496:U:C6	2.55	0.41
20:S2:1738:C:H2'	20:S2:1739:C:C6	2.56	0.41
33:SZ:88:LEU:HA	33:SZ:88:LEU:HD23	1.82	0.41
33:SZ:101:SER:OG	33:SZ:108:ILE:N	2.52	0.41
34:Sc:46:VAL:HG21	34:Sc:50:VAL:HG21	2.03	0.41
37:Sg:164:ILE:HD11	37:Sg:176:VAL:HB	2.02	0.41
39:Pt:19:G:H4'	39:Pt:20(A):U:H5''	2.03	0.41
41:L5:161:G:H2'	41:L5:162:A:C8	2.55	0.41
41:L5:500:G:N3	41:L5:504:G:O2'	2.47	0.41
41:L5:680:G:H2'	41:L5:681:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:725:G:H2'	41:L5:726:G:H8	1.85	0.41
41:L5:1414:C:H2'	41:L5:1415:G:H8	1.86	0.41
41:L5:1596:U:O2	41:L5:3861:A:O2'	2.33	0.41
41:L5:2080:U:H2'	41:L5:2081:C:C6	2.55	0.41
41:L5:2293:U:H2'	41:L5:2294:G:C8	2.56	0.41
41:L5:2384:U:H2'	41:L5:2385:U:H6	1.86	0.41
41:L5:2434:G:H2'	41:L5:2435:G:C8	2.55	0.41
41:L5:2533:C:H2'	41:L5:2534:C:H6	1.86	0.41
41:L5:2874:U:H1'	82:Lp:20:ALA:HB2	2.02	0.41
41:L5:4979:A:OP1	45:LB:228:TYR:HB2	2.21	0.41
42:L7:47:G:H21	47:LD:222:GLN:NE2	2.15	0.41
42:L7:120:U:H5'	47:LD:261:VAL:HG23	2.03	0.41
43:L8:64:U:C2	43:L8:65:A:C8	3.09	0.41
43:L8:77:A:H2'	43:L8:78:G:C8	2.56	0.41
44:LA:116:LEU:HB3	44:LA:126:LEU:HB2	2.03	0.41
57:LO:190:ASP:HA	57:LO:193:THR:HB	2.02	0.41
60:LS:76:LYS:NZ	60:LS:100:LEU:O	2.49	0.41
3:SB:56:LYS:HB3	3:SB:56:LYS:HE3	1.78	0.41
5:SE:28:ALA:O	20:S2:496:C:H4'	2.21	0.41
5:SE:42:LEU:HG	5:SE:109:PHE:HD2	1.85	0.41
11:SN:124:ARG:NH2	20:S2:1024:A:OP2	2.44	0.41
20:S2:569:A:H2'	20:S2:570:C:O4'	2.21	0.41
20:S2:1079:C:H4'	20:S2:1182:A:H61	1.86	0.41
20:S2:1365:G:H2'	20:S2:1366:G:C8	2.55	0.41
20:S2:1671:G:H2'	20:S2:1672:U:C6	2.56	0.41
20:S2:1792:G:H2'	20:S2:1793:A:H8	1.86	0.41
20:S2:1832:6MZ:H9C2	20:S2:1833:C:H41	1.85	0.41
39:Pt:3:C:H2'	39:Pt:4:U:C6	2.56	0.41
39:Pt:22:U:H2'	39:Pt:23:C:C6	2.56	0.41
41:L5:398:A2M:H8	41:L5:398:A2M:O5'	2.21	0.41
41:L5:1079:C:H2'	41:L5:1080:C:C6	2.55	0.41
41:L5:1096:C:H2'	41:L5:1097:C:C6	2.56	0.41
41:L5:1510:G:H2'	41:L5:1511:U:C6	2.55	0.41
41:L5:1688:G:H2'	41:L5:1689:G:C8	2.55	0.41
41:L5:1798:G:H2'	41:L5:1799:G:H8	1.86	0.41
41:L5:1864:G:O6	41:L5:1871:A2M:N6	2.53	0.41
41:L5:2088:A:OP1	59:LQ:38:ARG:NH1	2.53	0.41
41:L5:3783:A:N7	41:L5:3792:OMG:C8	2.89	0.41
41:L5:4252:C:OP2	41:L5:4253:A:O2'	2.34	0.41
41:L5:4277:G:H2'	41:L5:4278:C:C6	2.56	0.41
41:L5:4505:C:H2'	41:L5:4506:C:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:4551:U:H2'	41:L5:4552:PSU:C6	2.55	0.41
41:L5:4590:A2M:HM'3	41:L5:4590:A2M:H1'	1.56	0.41
41:L5:4620:OMU:H1'	41:L5:4620:OMU:HM23	1.78	0.41
41:L5:4679:G:H2'	41:L5:4680:G:C8	2.55	0.41
41:L5:5053:U:H5'	41:L5:5054:C:C5	2.56	0.41
42:L7:76:U:H2'	42:L7:77:A:H8	1.85	0.41
46:LC:110:ARG:HB2	56:LN:204:ARG:HH21	1.85	0.41
52:LI:48:LEU:HD12	52:LI:142:LEU:HD12	2.02	0.41
52:LI:87:MET:HE3	52:LI:87:MET:HB2	1.84	0.41
54:LL:117:LEU:HD23	54:LL:117:LEU:HA	1.88	0.41
75:LI:99:LYS:HG3	75:LI:103:LYS:NZ	2.35	0.41
76:Lj:2:THR:HB	76:Lj:6:SER:HB2	2.01	0.41
83:Lr:2:SER:OG	83:Lr:3:ALA:N	2.53	0.41
4:SC:152:ARG:O	4:SC:156:ILE:HG12	2.20	0.41
5:SE:161:GLN:HG3	5:SE:170:THR:HB	2.03	0.41
8:SI:42:ARG:NH1	20:S2:1741:U:OP1	2.51	0.41
15:SX:68:LYS:HE2	19:Se:9:ALA:HB2	2.02	0.41
20:S2:935:G:H2'	20:S2:936:G:C8	2.56	0.41
20:S2:1259:A:H1'	20:S2:1264:C:N4	2.34	0.41
20:S2:1798:C:H2'	20:S2:1799:G:O4'	2.21	0.41
20:S2:1849:G:H2'	20:S2:1850:MA6:C8	2.50	0.41
41:L5:47:A:H5''	54:LL:16:LYS:HG2	2.03	0.41
41:L5:303:C:OP2	56:LN:68:ARG:NH2	2.39	0.41
41:L5:306:A:H2'	41:L5:307:A:C8	2.55	0.41
41:L5:513:U:H3'	41:L5:514:U:H4'	2.01	0.41
41:L5:1198:G:H2'	41:L5:1199:G:C8	2.56	0.41
41:L5:1323:A2M:HM'3	41:L5:1323:A2M:H1'	1.44	0.41
41:L5:1545:G:H2'	41:L5:1546:C:C6	2.55	0.41
41:L5:1997:U:H2'	41:L5:1999:A:OP2	2.21	0.41
41:L5:4342:C:O3'	81:Lo:37:GLY:HA3	2.20	0.41
41:L5:4940:C:C2	48:LE:219:LYS:HA	2.55	0.41
45:LB:288:GLY:HA3	45:LB:330:PHE:CE1	2.55	0.41
48:LE:157:HIS:HA	48:LE:160:LYS:HE3	2.02	0.41
50:LG:123:ALA:HA	50:LG:124:GLY:HA2	1.84	0.41
62:LU:49:VAL:HB	62:LU:57:GLY:HA3	2.02	0.41
78:Ll:23:ILE:HG23	78:Ll:38:ASN:HB2	2.02	0.41
85:Lt:114:ARG:HH21	85:Lt:117:ARG:NH1	2.19	0.41
5:SE:100:ARG:HB2	5:SE:114:ILE:HD13	2.03	0.41
7:SH:112:ASN:ND2	20:S2:875:A:O3'	2.52	0.41
7:SH:144:ILE:HD12	7:SH:153:LEU:O	2.21	0.41
9:SJ:107:GLU:O	9:SJ:112:THR:OG1	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:SJ:131:ARG:HD2	9:SJ:131:ARG:HA	1.77	0.41
10:SL:8:ARG:HH21	20:S2:390:C:H4'	1.86	0.41
14:SW:111:MET:HE3	14:SW:116:ALA:HA	2.02	0.41
20:S2:51:U:H2'	20:S2:52:G:C8	2.56	0.41
20:S2:89:C:O2'	20:S2:499:G:H5''	2.20	0.41
20:S2:107:A:H2'	20:S2:108:G:H8	1.86	0.41
20:S2:109:PSU:H2'	20:S2:110:U:C6	2.56	0.41
20:S2:448:A:H4'	20:S2:449:A:H5''	2.03	0.41
20:S2:574:A:H2'	20:S2:575:A:C8	2.56	0.41
20:S2:605:A:N3	20:S2:639:C:H1'	2.35	0.41
20:S2:1096:G:H2'	20:S2:1097:G:H8	1.86	0.41
20:S2:1203:G:H2'	20:S2:1204:A:H8	1.83	0.41
20:S2:1205:C:H2'	20:S2:1206:G:C8	2.56	0.41
20:S2:1205:C:H2'	20:S2:1206:G:H8	1.85	0.41
20:S2:1272:OMC:OP1	36:Sf:94:LYS:NZ	2.50	0.41
20:S2:1548:G:H2'	20:S2:1549:U:C6	2.55	0.41
20:S2:1606:G:N2	20:S2:1632:G:HO2'	2.19	0.41
20:S2:1618:C:H4'	28:SP:50:ARG:HE	1.86	0.41
20:S2:1650:A:H1'	20:S2:1675:A:N6	2.36	0.41
20:S2:1688:C:H2'	20:S2:1689:C:H6	1.86	0.41
20:S2:1724:A:H2'	20:S2:1725:U:H6	1.86	0.41
20:S2:1733:U:H2'	20:S2:1734:G:O4'	2.21	0.41
20:S2:1805:G:H2'	20:S2:1806:A:C8	2.55	0.41
21:LR:72:LYS:O	21:LR:74:ARG:NH1	2.54	0.41
30:SS:41:ALA:O	30:SS:45:LEU:HG	2.20	0.41
30:SS:52:LEU:HD23	30:SS:52:LEU:HA	1.86	0.41
30:SS:59:LEU:HD12	30:SS:63:GLU:HB3	2.02	0.41
30:SS:63:GLU:HG2	30:SS:66:ARG:NH2	2.36	0.41
31:ST:28:LEU:HD12	31:ST:28:LEU:HA	1.86	0.41
34:Sc:58:LEU:HD23	34:Sc:58:LEU:HA	1.91	0.41
38:At:36:C:C2	38:At:37:A:C8	3.09	0.41
39:Pt:3:C:H2'	39:Pt:4:U:H6	1.86	0.41
39:Pt:51:C:H2'	39:Pt:52:G:C8	2.56	0.41
41:L5:13:U:O4	43:L8:115:G:N2	2.43	0.41
41:L5:20:U:H3'	41:L5:21:G:C8	2.51	0.41
41:L5:114:G:N2	41:L5:158:A:H61	2.19	0.41
41:L5:132:G:N3	41:L5:133:C:O2'	2.53	0.41
41:L5:286:U:H2'	41:L5:287:U:C6	2.55	0.41
41:L5:381:U:H2'	41:L5:382:G:O4'	2.21	0.41
41:L5:663:G:H2'	41:L5:664:G:C8	2.55	0.41
41:L5:728:U:H5''	49:LF:76:ARG:NH1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1178:G:OP1	41:L5:1178:G:N2	2.50	0.41
41:L5:1471:U:H2'	41:L5:1472:C:C6	2.56	0.41
41:L5:1478:C:H2'	41:L5:1479:G:C8	2.53	0.41
41:L5:1685:G:H2'	41:L5:1686:C:C6	2.55	0.41
41:L5:1738:A:H2'	41:L5:1739:G:C8	2.56	0.41
41:L5:1870:C:H2'	41:L5:1871:A2M:C8	2.44	0.41
41:L5:1973:G:N2	85:Lt:136:ALA:HB2	2.36	0.41
41:L5:1976:G:C6	41:L5:1990:A:N1	2.89	0.41
41:L5:2272:C:H2'	41:L5:2273:G:H8	1.86	0.41
41:L5:2411:C:H2'	41:L5:2412:A:C8	2.54	0.41
41:L5:2474:G:H2'	41:L5:2502:G:N2	2.36	0.41
41:L5:2644:G:H2'	41:L5:2645:G:C8	2.56	0.41
41:L5:2691:U:H2'	41:L5:2692:U:C6	2.56	0.41
41:L5:2728:U:H2'	41:L5:2729:C:H6	1.85	0.41
41:L5:3825:A2M:H2'	41:L5:3826:C:O4'	2.21	0.41
41:L5:3925:OMU:HM23	41:L5:3925:OMU:H1'	1.80	0.41
41:L5:4288:C:H2'	41:L5:4289:U:O4'	2.21	0.41
41:L5:4508:C:N3	41:L5:4512:U:H5	2.19	0.41
41:L5:4860:G:H2'	41:L5:4861:G:C8	2.56	0.41
41:L5:5035:U:H2'	41:L5:5036:C:H6	1.85	0.41
43:L8:73:U:H2'	43:L8:74:U:O4'	2.21	0.41
43:L8:96:C:H5''	74:Lh:66:LYS:HG2	2.03	0.41
46:LC:163:LYS:HE3	46:LC:163:LYS:HB3	1.85	0.41
50:LG:162:ASP:HB3	50:LG:163:PRO:HD3	2.02	0.41
51:LH:51:LYS:HG3	51:LH:52:LYS:N	2.36	0.41
58:LP:131:ARG:HG3	58:LP:137:ASN:OD1	2.20	0.41
81:Lo:35:ALA:O	81:Lo:39:ARG:HG3	2.21	0.41
1:Zt:34:U:H2'	1:Zt:35:U:C6	2.56	0.41
3:SB:36:PRO:HB2	3:SB:38:MET:HE3	2.03	0.41
6:SG:68:LEU:HD23	6:SG:68:LEU:HA	1.93	0.41
6:SG:194:LEU:HD13	6:SG:197:GLN:HE21	1.86	0.41
7:SH:5:SER:OG	7:SH:25:GLN:OE1	2.32	0.41
8:SI:168:GLN:O	41:L5:5027:C:N4	2.53	0.41
11:SN:75:LEU:HD23	11:SN:75:LEU:HA	1.95	0.41
11:SN:99:ARG:NH2	11:SN:143:SER:OG	2.54	0.41
12:SO:45:THR:HG22	12:SO:52:THR:HG22	2.03	0.41
14:SW:86:LEU:HD21	14:SW:113:HIS:HB2	2.03	0.41
16:SY:102:THR:O	16:SY:107:ARG:NH1	2.54	0.41
19:Se:24:LYS:HB2	19:Se:24:LYS:HE2	1.73	0.41
19:Se:39:ASN:HA	19:Se:43:VAL:HG22	2.03	0.41
20:S2:941:C:H2'	20:S2:942:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S2:1279:C:H2'	20:S2:1280:G:C8	2.55	0.41
20:S2:1401:A:H2'	20:S2:1402:A:C8	2.56	0.41
20:S2:1724:A:H2'	20:S2:1725:U:C6	2.55	0.41
25:SF:91:ARG:HG3	25:SF:92:ILE:N	2.36	0.41
37:Sg:259:TRP:HE1	37:Sg:266:ILE:HG12	1.86	0.41
41:L5:124:C:H2'	41:L5:125:C:H6	1.86	0.41
41:L5:137:G:H2'	41:L5:138:G:C8	2.56	0.41
41:L5:690:C:H2'	41:L5:691:C:C6	2.55	0.41
41:L5:1080:C:N3	41:L5:1220:G:N1	2.69	0.41
41:L5:1209:U:O2'	41:L5:1211:G:H8	2.04	0.41
41:L5:1727:U:H2'	41:L5:1728:U:C6	2.56	0.41
41:L5:1995:G:N2	85:Lt:121:LEU:O	2.50	0.41
41:L5:2765:A:H2'	41:L5:2766:A:H8	1.86	0.41
41:L5:2844:A:O2'	41:L5:4631:G:H4'	2.21	0.41
41:L5:4076:G:OP2	41:L5:4163:U:N3	2.45	0.41
41:L5:4273:A:H2'	41:L5:4274:A:C8	2.56	0.41
41:L5:4377:G:O6	67:La:42:ARG:NH1	2.52	0.41
41:L5:4435:U:H2'	41:L5:4436:U:C2	2.56	0.41
41:L5:4558:U:OP2	45:LB:246:ARG:NH2	2.54	0.41
41:L5:4957:C:H2'	41:L5:4958:C:H6	1.86	0.41
41:L5:4964:C:H2'	41:L5:4965:U:C6	2.56	0.41
44:LA:115:CYS:SG	44:LA:124:GLY:HA3	2.61	0.41
45:LB:136:LYS:HB2	45:LB:142:GLY:HA3	2.03	0.41
46:LC:321:ASN:HB3	46:LC:324:ILE:HB	2.03	0.41
57:LO:110:PRO:N	57:LO:111:PRO:HD2	2.36	0.41
63:LV:128:LEU:HD12	63:LV:128:LEU:HA	1.85	0.41
3:SB:126:ASP:OD1	3:SB:136:ARG:HG2	2.21	0.40
5:SE:43:PRO:HG2	5:SE:46:ILE:HG12	2.02	0.40
6:SG:68:LEU:HD21	20:S2:1745:A:H4'	2.02	0.40
7:SH:31:GLU:HA	7:SH:37:LYS:HG3	2.03	0.40
7:SH:103:LYS:NZ	20:S2:862:A:OP2	2.37	0.40
9:SJ:176:LYS:HA	9:SJ:179:LYS:HG2	2.03	0.40
10:SL:111:VAL:HG12	10:SL:140:PHE:HB2	2.03	0.40
16:SY:65:GLY:H	20:S2:581:U:P	2.44	0.40
20:S2:693:A:C2	20:S2:739:C:H4'	2.56	0.40
20:S2:1062:A:H2'	20:S2:1063:C:C6	2.55	0.40
20:S2:1201:U:H2'	20:S2:1202:U:C6	2.56	0.40
27:SM:87:GLU:HG3	27:SM:103:VAL:HG11	2.02	0.40
32:SU:24:LEU:HD13	32:SU:35:VAL:HG13	2.03	0.40
37:Sg:129:ILE:HB	37:Sg:142:VAL:HB	2.02	0.40
41:L5:315:G:C8	67:La:62:HIS:HB2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:957:G:N2	41:L5:1283:G:OP2	2.54	0.40
41:L5:1664:U:H2'	41:L5:1665:C:H6	1.86	0.40
41:L5:1700:G:H5''	41:L5:1704:C:H42	1.85	0.40
41:L5:2333:G:OP1	43:L8:20:A:O2'	2.38	0.40
41:L5:3706:C:H2'	41:L5:3707:U:C6	2.56	0.40
41:L5:3718:A2M:HM'3	41:L5:3718:A2M:H1'	1.71	0.40
42:L7:89:G:OP2	42:L7:89:G:H8	2.04	0.40
44:LA:112:ILE:HD11	82:Lp:79:VAL:HG13	2.03	0.40
45:LB:133:TYR:O	45:LB:136:LYS:HG2	2.22	0.40
45:LB:263:ALA:HB3	45:LB:266:VAL:HG23	2.03	0.40
51:LH:89:ARG:NH2	51:LH:147:GLU:OE2	2.51	0.40
58:LP:54:GLN:HA	58:LP:83:TRP:CD1	2.56	0.40
64:LX:73:HIS:ND1	64:LX:115:LYS:HE2	2.36	0.40
5:SE:183:VAL:HG21	5:SE:218:PHE:HE2	1.86	0.40
6:SG:190:ARG:HH12	20:S2:333:G:H3'	1.87	0.40
7:SH:118:ARG:NH1	20:S2:686:PSU:O4	2.42	0.40
8:SI:19:LYS:HD3	20:S2:101:U:H5''	2.03	0.40
9:SJ:113:GLN:HG3	9:SJ:149:VAL:HG21	2.03	0.40
20:S2:429:C:H2'	20:S2:430:C:C6	2.55	0.40
20:S2:480:G:H2'	20:S2:481:C:C6	2.57	0.40
20:S2:511:U:H2'	20:S2:512:A:C8	2.55	0.40
20:S2:600:G:H2'	20:S2:601:OMG:H8	1.86	0.40
20:S2:654:A:OP2	20:S2:655:A:O2'	2.28	0.40
20:S2:845:G:H2'	20:S2:846:G:C8	2.56	0.40
20:S2:1025:U:H2'	20:S2:1026:C:O4'	2.22	0.40
20:S2:1115:U:O2'	20:S2:1117:C:OP2	2.37	0.40
20:S2:1288:OMU:HM23	20:S2:1288:OMU:H1'	1.85	0.40
20:S2:1485:U:H2'	20:S2:1486:A:O4'	2.21	0.40
20:S2:1542:C:H5''	31:ST:62:ARG:CZ	2.52	0.40
20:S2:1625:U:H2'	20:S2:1626:C:C6	2.56	0.40
20:S2:1676:U:H2'	20:S2:1677:U:O4'	2.21	0.40
20:S2:1748:G:H2'	20:S2:1749:G:C8	2.57	0.40
20:S2:1752:C:N3	20:S2:1779:G:C2	2.88	0.40
26:SK:41:PRO:HG2	26:SK:44:HIS:CG	2.57	0.40
29:SQ:73:LYS:HA	29:SQ:73:LYS:HD2	1.83	0.40
31:ST:11:GLN:HB3	31:ST:62:ARG:HD2	2.03	0.40
41:L5:5:A:H1'	50:LG:192:ARG:HH21	1.86	0.40
41:L5:27:C:O3'	41:L5:60:G:N2	2.54	0.40
41:L5:227:A:H2'	41:L5:228:C:O4'	2.21	0.40
41:L5:1176:C:H4'	47:LD:279:ARG:HD2	2.03	0.40
41:L5:1299:G:H2'	41:L5:1300:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:1372:A:C4	41:L5:1373:A:C8	3.09	0.40
41:L5:1507:C:H2'	41:L5:1508:A:H8	1.86	0.40
41:L5:1553:A:H2'	41:L5:1554:A:C8	2.56	0.40
41:L5:1978:C:H2'	41:L5:1979:A:H8	1.86	0.40
41:L5:2353:U:H2'	41:L5:2354:G:C8	2.56	0.40
41:L5:2365:OMC:HM23	41:L5:2365:OMC:H1'	1.75	0.40
41:L5:3619:G:H22	41:L5:3624:A:H1'	1.86	0.40
41:L5:4261:C:H2'	41:L5:4262:C:H6	1.86	0.40
41:L5:4342:C:H2'	41:L5:4343:U:H6	1.87	0.40
42:L7:119:U:C2	47:LD:261:VAL:HG21	2.56	0.40
43:L8:78:G:H2'	43:L8:79:G:C5	2.57	0.40
51:LH:89:ARG:HD3	51:LH:91:LYS:HZ3	1.87	0.40
52:LI:48:LEU:HB2	52:LI:142:LEU:HA	2.02	0.40
55:LM:97:ALA:HA	55:LM:100:ARG:HG2	2.03	0.40
64:LX:81:LEU:HG	64:LX:83:THR:HG23	2.03	0.40
66:LZ:106:LEU:HD23	66:LZ:106:LEU:HA	1.89	0.40
69:Lc:18:LEU:O	69:Lc:22:MET:HG2	2.21	0.40
84:Ls:78:LEU:O	84:Ls:82:ILE:HG12	2.22	0.40
6:SG:38:ALA:HB1	6:SG:41:LEU:HD13	2.03	0.40
12:SO:94:HIS:CE1	12:SO:128:ARG:H	2.38	0.40
17:Sa:83:VAL:HG13	17:Sa:84:VAL:HG13	2.03	0.40
20:S2:857:U:H2'	20:S2:858:A:H8	1.87	0.40
20:S2:1104:G:H2'	20:S2:1105:G:H8	1.86	0.40
20:S2:1269:G:H2'	20:S2:1270:G:C8	2.56	0.40
20:S2:1512:C:H2'	20:S2:1513:C:C6	2.56	0.40
20:S2:1783:C:H4'	20:S2:1784:G:C8	2.56	0.40
21:LR:84:THR:HG22	21:LR:86:ASN:H	1.86	0.40
24:SD:25:LEU:HD23	24:SD:25:LEU:HA	1.92	0.40
29:SQ:146:ARG:NH2	39:Pt:35:A:OP2	2.55	0.40
30:SS:124:ARG:HB2	30:SS:131:VAL:HG12	2.03	0.40
33:SZ:46:ASN:HB3	33:SZ:79:ILE:C	2.46	0.40
41:L5:139:G:H2'	41:L5:140:G:C8	2.55	0.40
41:L5:203:U:H2'	41:L5:204:U:C6	2.56	0.40
41:L5:730:G:C2	49:LF:73:ARG:HD3	2.56	0.40
41:L5:1290:G:H2'	41:L5:1291:G:H8	1.85	0.40
41:L5:1340:OMC:H2'	41:L5:1341:U:H6	1.87	0.40
41:L5:1932:A:N7	57:LO:49:ARG:NH2	2.69	0.40
41:L5:1995:G:O5'	41:L5:1995:G:H8	2.04	0.40
41:L5:2044:U:H3	41:L5:3871:A:H5''	1.87	0.40
41:L5:2273:G:H2'	41:L5:2274:C:C6	2.57	0.40
41:L5:2739:C:OP2	82:Lp:49:ARG:NH2	2.41	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:2820:C:H2'	41:L5:2821:U:H6	1.86	0.40
41:L5:3825:A2M:H2'	41:L5:3826:C:H6	1.86	0.40
41:L5:4082:G:H2'	41:L5:4083:U:C6	2.57	0.40
41:L5:4253:A:H5'	41:L5:4254:G:C8	2.57	0.40
41:L5:4262:C:H2'	41:L5:4263:C:C6	2.56	0.40
41:L5:4348:A:C6	41:L5:4350:C:C4	3.10	0.40
41:L5:4758:U:H6	41:L5:4758:U:H2'	1.69	0.40
41:L5:4921:C:H2'	41:L5:4922:C:C6	2.57	0.40
41:L5:4936:G:C5	48:LE:183:ARG:HD3	2.56	0.40
42:L7:38:U:N3	42:L7:41:G:OP2	2.54	0.40
44:LA:247:ARG:HD3	44:LA:247:ARG:HA	1.96	0.40
45:LB:128:LYS:HA	45:LB:128:LYS:HD2	1.82	0.40
47:LD:60:ILE:HG13	47:LD:93:THR:HA	2.04	0.40
47:LD:262:LYS:HE3	47:LD:264:LYS:HB2	2.02	0.40
49:LF:115:ARG:HH11	59:LQ:5:ILE:HG22	1.86	0.40
58:LP:64:ASN:O	58:LP:80:GLN:NE2	2.55	0.40
67:La:79:TRP:CE3	67:La:87:ARG:HG3	2.56	0.40
72:Lf:45:LYS:HA	72:Lf:107:PRO:HD2	2.03	0.40
2:SA:37:TYR:HE1	13:SV:83:PHE:HZ	1.69	0.40
6:SG:7:PHE:CE2	6:SG:9:ALA:HB3	2.56	0.40
15:SX:59:ALA:HB1	15:SX:114:ASP:HB2	2.03	0.40
20:S2:119:U:H2'	20:S2:120:U:H6	1.86	0.40
20:S2:520:A:O2'	20:S2:825:A:N3	2.51	0.40
20:S2:648:A:H2'	20:S2:649:PSU:C6	2.56	0.40
20:S2:920:A:O2'	20:S2:922:A:O5'	2.40	0.40
20:S2:1275:G:H22	20:S2:1506:A:P	2.45	0.40
20:S2:1644:C:H2'	20:S2:1645:C:C6	2.56	0.40
23:SR:105:MET:HE2	23:SR:105:MET:HB3	1.86	0.40
26:SK:14:LEU:HD23	26:SK:21:MET:HE1	2.04	0.40
36:Sf:94:LYS:HA	36:Sf:94:LYS:HD2	1.96	0.40
41:L5:659:G:H2'	41:L5:660:A:C8	2.54	0.40
41:L5:1248:C:H2'	41:L5:1249:C:H6	1.87	0.40
41:L5:1645:C:OP1	46:LC:80:ARG:NH2	2.39	0.40
41:L5:1845:U:H2'	41:L5:1846:G:C8	2.56	0.40
41:L5:1850:A:P	54:LL:5:ARG:HH12	2.44	0.40
41:L5:2344:U:O4	67:La:3:SER:OG	2.40	0.40
41:L5:2861:OMC:HM23	41:L5:2861:OMC:H1'	1.80	0.40
41:L5:3621:A:C8	41:L5:4642:U:H1'	2.56	0.40
41:L5:4458:C:H2'	41:L5:4459:U:H6	1.86	0.40
41:L5:4524:G:H2'	41:L5:4525:C:H6	1.86	0.40
41:L5:4642:U:H2'	41:L5:4643:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:4653:C:H2'	41:L5:4654:C:H6	1.85	0.40
41:L5:4937:C:C2	48:LE:239:LYS:HE2	2.56	0.40
42:L7:64:G:H2'	42:L7:65:G:C8	2.57	0.40
43:L8:130:C:H2'	43:L8:131:G:H8	1.86	0.40
43:L8:148:A:H2'	43:L8:149:G:H8	1.83	0.40
44:LA:80:GLU:HB2	44:LA:170:ALA:HA	2.02	0.40
45:LB:231:VAL:HG21	45:LB:251:VAL:HG23	2.04	0.40
48:LE:128:HIS:O	48:LE:128:HIS:ND1	2.54	0.40
50:LG:39:PHE:CE1	50:LG:47:PRO:HD3	2.57	0.40
53:LJ:35:ARG:HD2	53:LJ:122:SER:O	2.22	0.40
58:LP:7:ASP:OD1	58:LP:7:ASP:N	2.53	0.40
75:Li:94:LEU:HA	75:Li:94:LEU:HD23	1.85	0.40
85:Lt:110:VAL:O	85:Lt:114:ARG:HG2	2.21	0.40
5:SE:155:LYS:HA	5:SE:155:LYS:HD3	1.93	0.40
7:SH:177:TYR:HE2	7:SH:183:LYS:HG3	1.87	0.40
9:SJ:80:ARG:HA	9:SJ:83:ARG:HB2	2.03	0.40
10:SL:23:VAL:HG23	10:SL:25:LEU:HG	2.04	0.40
11:SN:11:LEU:HD12	11:SN:11:LEU:HA	1.90	0.40
13:SV:15:ARG:HH21	13:SV:24:ILE:HG21	1.85	0.40
18:Sb:20:LYS:HA	18:Sb:23:ARG:HE	1.86	0.40
20:S2:944:A:H2'	20:S2:945:U:C6	2.57	0.40
20:S2:1285:G:N2	27:SM:57:ASP:OD1	2.54	0.40
20:S2:1562:C:H5''	31:ST:71:GLY:HA3	2.02	0.40
20:S2:1649:U:H2'	20:S2:1650:A:H8	1.87	0.40
30:SS:40:TYR:HA	30:SS:83:PHE:HE2	1.87	0.40
37:Sg:202:PRO:HD3	37:Sg:241:PHE:HB3	2.03	0.40
38:At:50:U:H3	38:At:64:G:H1	1.68	0.40
39:Pt:4:U:H2'	39:Pt:5:C:C6	2.56	0.40
39:Pt:27:U:H2'	39:Pt:28:U:H6	1.86	0.40
41:L5:124:C:H2'	41:L5:125:C:C6	2.57	0.40
41:L5:179:G:H2'	41:L5:180:C:H6	1.87	0.40
41:L5:189:G:H2'	41:L5:190:G:H8	1.86	0.40
41:L5:197:A:N6	41:L5:242:U:H3	2.19	0.40
41:L5:274:C:O2'	41:L5:275:C:H5'	2.21	0.40
41:L5:1399:G:H2'	41:L5:1400:G:C8	2.56	0.40
41:L5:1867:A:H2'	41:L5:1868:A:C8	2.57	0.40
41:L5:2643:G:H1	41:L5:2691:U:H3	1.70	0.40
41:L5:2716:C:H2'	41:L5:2717:G:C8	2.56	0.40
41:L5:2769:U:C2	73:Lg:69:LYS:HB2	2.55	0.40
41:L5:3721:U:H2'	41:L5:3722:G:C8	2.56	0.40
41:L5:3753:G:H2'	41:L5:3754:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L5:4071:U:H2'	41:L5:4072:C:C6	2.56	0.40
41:L5:4686:G:N3	51:LH:163:GLN:NE2	2.50	0.40
45:LB:52:GLY:HA2	45:LB:341:LYS:HE3	2.04	0.40
50:LG:37:LYS:HE2	50:LG:37:LYS:HB3	1.88	0.40
50:LG:73:ARG:HD3	50:LG:73:ARG:HA	1.85	0.40
51:LH:60:TRP:CD2	60:LS:153:PRO:HD2	2.56	0.40
51:LH:93:ARG:HD2	51:LH:143:GLU:HG2	2.04	0.40
54:LL:209:LYS:H	54:LL:209:LYS:HG2	1.74	0.40
62:LU:28:PRO:HB2	62:LU:34:MET:HG3	2.02	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	
2	SA	219/221 (99%)	205 (94%)	14 (6%)	0	100	100
3	SB	212/214 (99%)	201 (95%)	11 (5%)	0	100	100
4	SC	218/222 (98%)	205 (94%)	13 (6%)	0	100	100
5	SE	260/262 (99%)	245 (94%)	15 (6%)	0	100	100
6	SG	235/237 (99%)	220 (94%)	15 (6%)	0	100	100
7	SH	182/189 (96%)	168 (92%)	14 (8%)	0	100	100
8	SI	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
9	SJ	183/185 (99%)	173 (94%)	10 (6%)	0	100	100
10	SL	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
11	SN	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
12	SO	135/140 (96%)	126 (93%)	9 (7%)	0	100	100
13	SV	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
14	SW	127/129 (98%)	121 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	SX	139/141 (99%)	132 (95%)	7 (5%)	0	100	100
16	SY	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
17	Sa	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
18	Sb	81/83 (98%)	73 (90%)	8 (10%)	0	100	100
19	Se	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
21	LR	185/187 (99%)	179 (97%)	5 (3%)	1 (0%)	24	58
22	LW	112/124 (90%)	110 (98%)	2 (2%)	0	100	100
23	SR	133/135 (98%)	124 (93%)	8 (6%)	1 (1%)	16	50
24	SD	225/227 (99%)	218 (97%)	7 (3%)	0	100	100
25	SF	187/189 (99%)	178 (95%)	9 (5%)	0	100	100
26	SK	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
27	SM	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
28	SP	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
29	SQ	142/144 (99%)	130 (92%)	12 (8%)	0	100	100
30	SS	143/145 (99%)	137 (96%)	6 (4%)	0	100	100
31	ST	141/143 (99%)	139 (99%)	2 (1%)	0	100	100
32	SU	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
33	SZ	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
34	Sc	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
35	Sd	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
36	Sf	65/67 (97%)	56 (86%)	9 (14%)	0	100	100
37	Sg	311/313 (99%)	290 (93%)	21 (7%)	0	100	100
40	CI	29/31 (94%)	29 (100%)	0	0	100	100
44	LA	246/248 (99%)	236 (96%)	10 (4%)	0	100	100
45	LB	400/402 (100%)	384 (96%)	16 (4%)	0	100	100
46	LC	366/368 (100%)	353 (96%)	13 (4%)	0	100	100
47	LD	291/293 (99%)	283 (97%)	8 (3%)	0	100	100
48	LE	236/250 (94%)	215 (91%)	21 (9%)	0	100	100
49	LF	223/225 (99%)	218 (98%)	5 (2%)	0	100	100
50	LG	239/241 (99%)	226 (95%)	13 (5%)	0	100	100
51	LH	188/190 (99%)	183 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	LI	211/213 (99%)	203 (96%)	8 (4%)	0	100	100
53	LJ	168/176 (96%)	166 (99%)	2 (1%)	0	100	100
54	LL	208/210 (99%)	200 (96%)	8 (4%)	0	100	100
55	LM	137/139 (99%)	132 (96%)	5 (4%)	0	100	100
56	LN	201/203 (99%)	195 (97%)	6 (3%)	0	100	100
57	LO	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
58	LP	151/153 (99%)	143 (95%)	8 (5%)	0	100	100
59	LQ	185/187 (99%)	181 (98%)	4 (2%)	0	100	100
60	LS	173/175 (99%)	166 (96%)	7 (4%)	0	100	100
61	LT	157/159 (99%)	152 (97%)	5 (3%)	0	100	100
62	LU	99/101 (98%)	94 (95%)	5 (5%)	0	100	100
63	LV	129/131 (98%)	126 (98%)	3 (2%)	0	100	100
64	LX	118/120 (98%)	116 (98%)	2 (2%)	0	100	100
65	LY	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
66	LZ	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
67	La	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
68	Lb	105/121 (87%)	99 (94%)	6 (6%)	0	100	100
69	Lc	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
70	Ld	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
71	Le	126/128 (98%)	125 (99%)	1 (1%)	0	100	100
72	Lf	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
73	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
74	Lh	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
75	Li	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
76	Lj	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
77	Lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
78	Ll	48/50 (96%)	48 (100%)	0	0	100	100
79	Lm	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
80	Ln	22/24 (92%)	22 (100%)	0	0	100	100
81	Lo	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
82	Lp	89/91 (98%)	85 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
83	Lr	123/125 (98%)	119 (97%)	4 (3%)	0	100	100
84	Ls	194/196 (99%)	186 (96%)	8 (4%)	0	100	100
85	Lt	128/157 (82%)	106 (83%)	22 (17%)	0	100	100
All	All	11672/11907 (98%)	11152 (96%)	518 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	LR	134	ASN
23	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	
2	SA	183/183 (100%)	183 (100%)	0	100	100
3	SB	195/195 (100%)	195 (100%)	0	100	100
4	SC	186/188 (99%)	186 (100%)	0	100	100
5	SE	224/224 (100%)	224 (100%)	0	100	100
6	SG	207/207 (100%)	207 (100%)	0	100	100
7	SH	166/169 (98%)	166 (100%)	0	100	100
8	SI	178/178 (100%)	178 (100%)	0	100	100
9	SJ	161/161 (100%)	161 (100%)	0	100	100
10	SL	137/137 (100%)	137 (100%)	0	100	100
11	SN	130/130 (100%)	130 (100%)	0	100	100
12	SO	107/110 (97%)	107 (100%)	0	100	100
13	SV	67/67 (100%)	67 (100%)	0	100	100
14	SW	112/112 (100%)	112 (100%)	0	100	100
15	SX	113/113 (100%)	113 (100%)	0	100	100
16	SY	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	Sa	89/89 (100%)	89 (100%)	0	100	100
18	Sb	75/75 (100%)	75 (100%)	0	100	100
19	Se	47/47 (100%)	47 (100%)	0	100	100
21	LR	166/166 (100%)	166 (100%)	0	100	100
22	LW	95/103 (92%)	95 (100%)	0	100	100
23	SR	122/122 (100%)	122 (100%)	0	100	100
24	SD	190/190 (100%)	190 (100%)	0	100	100
25	SF	159/159 (100%)	159 (100%)	0	100	100
26	SK	89/89 (100%)	89 (100%)	0	100	100
27	SM	102/104 (98%)	102 (100%)	0	100	100
28	SP	107/107 (100%)	107 (100%)	0	100	100
29	SQ	119/119 (100%)	119 (100%)	0	100	100
30	SS	126/126 (100%)	126 (100%)	0	100	100
31	ST	113/113 (100%)	113 (100%)	0	100	100
32	SU	94/94 (100%)	94 (100%)	0	100	100
33	SZ	66/66 (100%)	66 (100%)	0	100	100
34	Sc	57/57 (100%)	57 (100%)	0	100	100
35	Sd	48/48 (100%)	48 (100%)	0	100	100
36	Sf	60/60 (100%)	60 (100%)	0	100	100
37	Sg	272/272 (100%)	272 (100%)	0	100	100
40	CI	25/25 (100%)	25 (100%)	0	100	100
44	LA	190/190 (100%)	190 (100%)	0	100	100
45	LB	348/348 (100%)	348 (100%)	0	100	100
46	LC	306/306 (100%)	306 (100%)	0	100	100
47	LD	246/247 (100%)	246 (100%)	0	100	100
48	LE	212/222 (96%)	212 (100%)	0	100	100
49	LF	194/194 (100%)	194 (100%)	0	100	100
50	LG	203/205 (99%)	203 (100%)	0	100	100
51	LH	169/169 (100%)	169 (100%)	0	100	100
52	LI	180/180 (100%)	180 (100%)	0	100	100
53	LJ	143/148 (97%)	143 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	LL	176/176 (100%)	176 (100%)	0	100	100
55	LM	118/118 (100%)	118 (100%)	0	100	100
56	LN	171/171 (100%)	171 (100%)	0	100	100
57	LO	173/173 (100%)	173 (100%)	0	100	100
58	LP	134/134 (100%)	134 (100%)	0	100	100
59	LQ	164/164 (100%)	164 (100%)	0	100	100
60	LS	156/156 (100%)	156 (100%)	0	100	100
61	LT	139/139 (100%)	139 (100%)	0	100	100
62	LU	91/91 (100%)	91 (100%)	0	100	100
63	LV	101/101 (100%)	101 (100%)	0	100	100
64	LX	108/108 (100%)	108 (100%)	0	100	100
65	LY	124/124 (100%)	124 (100%)	0	100	100
66	LZ	117/117 (100%)	117 (100%)	0	100	100
67	La	120/120 (100%)	120 (100%)	0	100	100
68	Lb	88/101 (87%)	88 (100%)	0	100	100
69	Lc	83/83 (100%)	83 (100%)	0	100	100
70	Ld	98/98 (100%)	98 (100%)	0	100	100
71	Le	114/114 (100%)	114 (100%)	0	100	100
72	Lf	88/88 (100%)	88 (100%)	0	100	100
73	Lg	98/98 (100%)	98 (100%)	0	100	100
74	Lh	109/109 (100%)	109 (100%)	0	100	100
75	Li	86/86 (100%)	86 (100%)	0	100	100
76	Lj	73/73 (100%)	73 (100%)	0	100	100
77	Lk	64/64 (100%)	64 (100%)	0	100	100
78	Ll	47/47 (100%)	47 (100%)	0	100	100
79	Lm	48/48 (100%)	48 (100%)	0	100	100
80	Ln	23/23 (100%)	23 (100%)	0	100	100
81	Lo	93/93 (100%)	93 (100%)	0	100	100
82	Lp	74/74 (100%)	74 (100%)	0	100	100
83	Lr	109/109 (100%)	109 (100%)	0	100	100
84	Ls	162/164 (99%)	162 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
85	Lt	107/130 (82%)	107 (100%)	0	100	100
All	All	10147/10221 (99%)	10147 (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 (92) such sidechains are listed below:

Mol	Chain	Res	Type
2	SA	50	ASN
3	SB	75	GLN
3	SB	158	HIS
3	SB	202	GLN
4	SC	115	GLN
4	SC	136	HIS
5	SE	197	ASN
6	SG	197	GLN
7	SH	12	ASN
7	SH	162	GLN
8	SI	99	ASN
9	SJ	75	ASN
10	SL	13	GLN
10	SL	19	ASN
13	SV	29	HIS
13	SV	35	ASN
14	SW	98	GLN
18	Sb	9	HIS
22	LW	104	GLN
24	SD	101	GLN
25	SF	137	GLN
26	SK	44	HIS
27	SM	73	GLN
28	SP	46	ASN
28	SP	79	HIS
29	SQ	48	GLN
29	SQ	97	GLN
30	SS	72	GLN
30	SS	105	ASN
31	ST	85	ASN
33	SZ	64	ASN
33	SZ	112	ASN
35	Sd	37	ASN

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Mol	Chain	Res	Type
37	Sg	20	GLN
37	Sg	76	GLN
37	Sg	196	ASN
37	Sg	226	HIS
44	LA	97	ASN
44	LA	132	ASN
44	LA	194	ASN
45	LB	121	ASN
45	LB	301	ASN
46	LC	21	ASN
46	LC	41	HIS
46	LC	187	GLN
46	LC	203	GLN
46	LC	329	ASN
46	LC	347	HIS
46	LC	362	GLN
47	LD	138	GLN
47	LD	225	GLN
47	LD	250	ASN
48	LE	266	GLN
49	LF	58	HIS
49	LF	205	ASN
50	LG	64	GLN
50	LG	90	GLN
50	LG	94	GLN
50	LG	225	ASN
51	LH	98	HIS
51	LH	138	GLN
51	LH	156	ASN
52	LI	73	ASN
53	LJ	97	ASN
53	LJ	155	HIS
54	LL	15	HIS
56	LN	15	GLN
56	LN	32	GLN
57	LO	96	GLN
59	LQ	162	HIS
61	LT	69	GLN
65	LY	14	ASN
65	LY	56	GLN
65	LY	72	GLN
67	La	34	ASN

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Mol	Chain	Res	Type
67	La	62	HIS
68	Lb	6	ASN
68	Lb	12	GLN
68	Lb	60	ASN
70	Ld	79	ASN
71	Le	57	ASN
72	Lf	21	GLN
72	Lf	99	HIS
73	Lg	3	GLN
74	Lh	96	ASN
75	Li	26	HIS
76	Lj	66	HIS
78	Ll	4	HIS
83	Lr	36	ASN
84	Ls	190	GLN
84	Ls	195	ASN
85	Lt	66	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Zt	74/75 (98%)	29 (39%)	0
20	S2	1715/1740 (98%)	415 (24%)	4 (0%)
38	At	69/71 (97%)	13 (18%)	0
39	Pt	72/74 (97%)	15 (20%)	0
41	L5	3644/3655 (99%)	798 (21%)	17 (0%)
42	L7	119/120 (99%)	15 (12%)	0
43	L8	155/156 (99%)	28 (18%)	0
All	All	5848/5891 (99%)	1313 (22%)	21 (0%)

All (1313) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Zt	3	C
1	Zt	4	C
1	Zt	8	U
1	Zt	14	A
1	Zt	15	G
1	Zt	16	C
1	Zt	19	G
1	Zt	20	U

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Mol	Chain	Res	Type
1	Zt	21	A
1	Zt	24	G
1	Zt	27	U
1	Zt	33	U
1	Zt	34	U
1	Zt	36	U
1	Zt	37	A
1	Zt	39	U
1	Zt	42	G
1	Zt	47	U
1	Zt	48	C
1	Zt	57	A
1	Zt	58	A
1	Zt	59	G
1	Zt	60	U
1	Zt	61	C
1	Zt	63	C
1	Zt	70	G
1	Zt	71	G
1	Zt	72	C
1	Zt	73	G
20	S2	2	A
20	S2	4	C
20	S2	13	C
20	S2	14	C
20	S2	25	A
20	S2	33	G
20	S2	37	C
20	S2	41	G
20	S2	42	A
20	S2	44	U
20	S2	45	A
20	S2	46	A
20	S2	49	C
20	S2	56	G
20	S2	59	U
20	S2	62	G
20	S2	67	C
20	S2	68	A
20	S2	72	C
20	S2	73	C
20	S2	74	G

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Mol	Chain	Res	Type
20	S2	76	U
20	S2	92	A
20	S2	99	A2M
20	S2	103	A
20	S2	113	G
20	S2	115	U
20	S2	126	G
20	S2	129	C
20	S2	130	G
20	S2	143	U
20	S2	158	A
20	S2	160	U
20	S2	161	U
20	S2	162	C
20	S2	170	A
20	S2	171	A
20	S2	175	A
20	S2	179	C
20	S2	184	G
20	S2	186	C
20	S2	190	G
20	S2	196	C
20	S2	197	U
20	S2	198	U
20	S2	200	G
20	S2	203	G
20	S2	204	G
20	S2	207	G
20	S2	208	G
20	S2	211	G
20	S2	213	G
20	S2	214	U
20	S2	220	U
20	S2	288	G
20	S2	291	G
20	S2	292	A
20	S2	295	C
20	S2	302	A
20	S2	303	C
20	S2	305	U
20	S2	306	C
20	S2	307	G

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Mol	Chain	Res	Type
20	S2	308	G
20	S2	309	G
20	S2	312	G
20	S2	318	A
20	S2	319	C
20	S2	323	C
20	S2	324	C
20	S2	325	C
20	S2	326	C
20	S2	328	U
20	S2	329	G
20	S2	332	G
20	S2	339	A
20	S2	340	C
20	S2	347	G
20	S2	351	G
20	S2	360	A
20	S2	361	U
20	S2	362	C
20	S2	364	A
20	S2	368	U
20	S2	369	C
20	S2	370	G
20	S2	383	G
20	S2	385	G
20	S2	386	C
20	S2	397	G
20	S2	407	G
20	S2	408	A
20	S2	409	C
20	S2	426	A
20	S2	428	OMU
20	S2	436	OMG
20	S2	448	A
20	S2	449	A
20	S2	450	C
20	S2	452	G
20	S2	464	A
20	S2	465	A
20	S2	471	G
20	S2	472	C
20	S2	473	A

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Mol	Chain	Res	Type
20	S2	474	G
20	S2	476	A
20	S2	482	G
20	S2	483	C
20	S2	487	U
20	S2	488	U
20	S2	492	C
20	S2	493	A
20	S2	500	A
20	S2	502	C
20	S2	532	C
20	S2	536	A
20	S2	537	C
20	S2	540	U
20	S2	542	U
20	S2	544	G
20	S2	546	G
20	S2	547	G
20	S2	551	U
20	S2	554	A
20	S2	557	U
20	S2	558	G
20	S2	559	G
20	S2	563	G
20	S2	564	A
20	S2	566	U
20	S2	576	A2M
20	S2	583	A
20	S2	587	A
20	S2	589	G
20	S2	590	A
20	S2	591	U
20	S2	593	C
20	S2	602	G
20	S2	604	A
20	S2	607	U
20	S2	611	G
20	S2	614	C
20	S2	617	G
20	S2	621	C
20	S2	627	OMU
20	S2	628	A

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Mol	Chain	Res	Type
20	S2	631	U
20	S2	638	C
20	S2	643	A
20	S2	644	OMG
20	S2	655	A
20	S2	660	C
20	S2	668	A2M
20	S2	669	A
20	S2	671	A
20	S2	672	A
20	S2	673	G
20	S2	683	OMG
20	S2	688	U
20	S2	689	U
20	S2	692	G
20	S2	693	A
20	S2	696	G
20	S2	697	G
20	S2	732	U
20	S2	733	C
20	S2	734	C
20	S2	736	C
20	S2	738	C
20	S2	749	U
20	S2	751	G
20	S2	752	G
20	S2	753	C
20	S2	787	G
20	S2	788	G
20	S2	790	C
20	S2	791	C
20	S2	792	C
20	S2	797	C
20	S2	798	G
20	S2	799	OMU
20	S2	801	PSU
20	S2	810	A
20	S2	821	G
20	S2	822	U
20	S2	823	U
20	S2	824	C
20	S2	827	A

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Mol	Chain	Res	Type
20	S2	830	A
20	S2	834	C
20	S2	835	C
20	S2	836	G
20	S2	837	A
20	S2	838	G
20	S2	839	C
20	S2	841	G
20	S2	842	C
20	S2	844	U
20	S2	847	A
20	S2	859	G
20	S2	861	A
20	S2	863	PSU
20	S2	864	A
20	S2	867	OMG
20	S2	870	A
20	S2	874	G
20	S2	877	C
20	S2	878	G
20	S2	886	A
20	S2	888	U
20	S2	889	U
20	S2	890	U
20	S2	891	G
20	S2	894	G
20	S2	896	U
20	S2	897	U
20	S2	898	U
20	S2	899	U
20	S2	900	C
20	S2	901	G
20	S2	903	A
20	S2	905	C
20	S2	913	A
20	S2	914	U
20	S2	919	A
20	S2	920	A
20	S2	933	G
20	S2	934	G
20	S2	970	G
20	S2	971	G

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Mol	Chain	Res	Type
20	S2	972	A
20	S2	978	G
20	S2	990	A
20	S2	992	A
20	S2	999	G
20	S2	1001	A
20	S2	1002	U
20	S2	1008	A
20	S2	1017	U
20	S2	1023	A
20	S2	1027	A
20	S2	1044	G
20	S2	1045	PSU
20	S2	1061	U
20	S2	1062	A
20	S2	1067	C
20	S2	1083	A
20	S2	1085	C
20	S2	1108	G
20	S2	1109	C
20	S2	1113	A
20	S2	1116	C
20	S2	1118	C
20	S2	1119	A
20	S2	1121	G
20	S2	1123	C
20	S2	1133	A
20	S2	1138	C
20	S2	1139	C
20	S2	1153	C
20	S2	1154	U
20	S2	1170	A
20	S2	1195	A
20	S2	1200	A
20	S2	1207	G
20	S2	1208	A
20	S2	1215	C
20	S2	1216	C
20	S2	1217	A
20	S2	1220	A
20	S2	1224	G
20	S2	1242	U

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Mol	Chain	Res	Type
20	S2	1243	U
20	S2	1248	B8N
20	S2	1251	A
20	S2	1253	A
20	S2	1256	G
20	S2	1257	G
20	S2	1264	C
20	S2	1271	C
20	S2	1272	OMC
20	S2	1274	G
20	S2	1275	G
20	S2	1282	A
20	S2	1283	C
20	S2	1286	G
20	S2	1288	OMU
20	S2	1294	G
20	S2	1295	A
20	S2	1298	G
20	S2	1301	A
20	S2	1302	G
20	S2	1303	C
20	S2	1308	U
20	S2	1333	U
20	S2	1342	U
20	S2	1354	G
20	S2	1357	A
20	S2	1371	U
20	S2	1376	A
20	S2	1378	A
20	S2	1382	A
20	S2	1401	A
20	S2	1402	A
20	S2	1404	U
20	S2	1406	G
20	S2	1408	U
20	S2	1413	G
20	S2	1414	A
20	S2	1418	C
20	S2	1419	C
20	S2	1421	A
20	S2	1423	C
20	S2	1428	G

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Mol	Chain	Res	Type
20	S2	1433	C
20	S2	1435	C
20	S2	1436	C
20	S2	1437	C
20	S2	1438	A
20	S2	1439	A
20	S2	1442	OMU
20	S2	1449	G
20	S2	1454	A
20	S2	1463	U
20	S2	1480	A
20	S2	1489	A
20	S2	1490	OMG
20	S2	1492	U
20	S2	1494	U
20	S2	1495	G
20	S2	1497	G
20	S2	1498	A
20	S2	1520	G
20	S2	1521	C
20	S2	1522	A
20	S2	1533	A
20	S2	1534	C
20	S2	1544	C
20	S2	1547	C
20	S2	1552	G
20	S2	1553	C
20	S2	1555	U
20	S2	1556	A
20	S2	1558	C
20	S2	1569	A
20	S2	1578	U
20	S2	1580	A
20	S2	1581	C
20	S2	1582	C
20	S2	1587	G
20	S2	1588	A
20	S2	1601	A
20	S2	1604	G
20	S2	1606	G
20	S2	1621	U
20	S2	1623	A

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Mol	Chain	Res	Type
20	S2	1630	A
20	S2	1633	A
20	S2	1634	A
20	S2	1637	A
20	S2	1639	G7M
20	S2	1640	A
20	S2	1648	G
20	S2	1649	U
20	S2	1654	G
20	S2	1657	G
20	S2	1663	A
20	S2	1664	A
20	S2	1665	G
20	S2	1669	G
20	S2	1680	G
20	S2	1682	C
20	S2	1683	C
20	S2	1695	A
20	S2	1699	A
20	S2	1715	A
20	S2	1721	U
20	S2	1722	G
20	S2	1726	G
20	S2	1729	U
20	S2	1744	G
20	S2	1745	A
20	S2	1752	C
20	S2	1753	C
20	S2	1754	G
20	S2	1755	C
20	S2	1756	C
20	S2	1757	G
20	S2	1758	G
20	S2	1759	G
20	S2	1761	U
20	S2	1772	C
20	S2	1773	C
20	S2	1774	C
20	S2	1782	G
20	S2	1783	C
20	S2	1784	G
20	S2	1786	U

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Mol	Chain	Res	Type
20	S2	1798	C
20	S2	1809	A
20	S2	1810	U
20	S2	1824	A
20	S2	1825	A
20	S2	1831	A
20	S2	1835	A
20	S2	1838	U
20	S2	1849	G
20	S2	1850	MA6
20	S2	1851	MA6
20	S2	1861	G
20	S2	1862	G
20	S2	1863	A
20	S2	1864	U
20	S2	1865	C
38	At	9	A
38	At	10	G
38	At	13	U
38	At	21	A
38	At	22	U
38	At	36	C
38	At	47	U
38	At	48	C
38	At	49	C
38	At	58	A
38	At	64	G
38	At	67	G
38	At	70	A
39	Pt	8	U
39	Pt	9	A
39	Pt	13	U
39	Pt	19	G
39	Pt	20(A)	U
39	Pt	21	A
39	Pt	46	G
39	Pt	47	U
39	Pt	48	C
39	Pt	49	C
39	Pt	58	A
39	Pt	67	G
39	Pt	70	A

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Mol	Chain	Res	Type
39	Pt	74	C
39	Pt	75	C
41	L5	4	G
41	L5	25	A
41	L5	30	C
41	L5	39	A
41	L5	42	A
41	L5	47	A
41	L5	48	G
41	L5	59	A
41	L5	64	A
41	L5	65	A
41	L5	73	A
41	L5	74	G
41	L5	76	A
41	L5	91	G
41	L5	104	G
41	L5	108	A
41	L5	109	G
41	L5	110	C
41	L5	116	G
41	L5	119	G
41	L5	120	A
41	L5	122	U
41	L5	132	G
41	L5	133	C
41	L5	134	G
41	L5	135	G
41	L5	136	C
41	L5	144	G
41	L5	159	C
41	L5	164	G
41	L5	165	A
41	L5	169	G
41	L5	172	C
41	L5	175	C
41	L5	176	G
41	L5	182	G
41	L5	183	C
41	L5	184	U
41	L5	185	C
41	L5	186	G

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Mol	Chain	Res	Type
41	L5	188	G
41	L5	197	A
41	L5	200	U
41	L5	204	U
41	L5	209	U
41	L5	216	C
41	L5	217	C
41	L5	218	A
41	L5	234	G
41	L5	255	C
41	L5	256	G
41	L5	261	G
41	L5	265	C
41	L5	266	C
41	L5	267	G
41	L5	275	C
41	L5	278	G
41	L5	280	G
41	L5	281	U
41	L5	296	A
41	L5	297	U
41	L5	306	A
41	L5	310	G
41	L5	315	G
41	L5	316	U
41	L5	340	C
41	L5	357	U
41	L5	373	G
41	L5	385	A
41	L5	387	G
41	L5	388	A
41	L5	396	A
41	L5	407	A
41	L5	409	G
41	L5	410	A
41	L5	411	G
41	L5	412	G
41	L5	413	G
41	L5	431	G
41	L5	432	U
41	L5	440	U
41	L5	446	C

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Mol	Chain	Res	Type
41	L5	449	C
41	L5	452	A
41	L5	453	G
41	L5	456	C
41	L5	457	G
41	L5	464	G
41	L5	467	U
41	L5	478	G
41	L5	485	C
41	L5	486	C
41	L5	489	C
41	L5	497	G
41	L5	498	C
41	L5	499	G
41	L5	500	G
41	L5	502	C
41	L5	503	C
41	L5	504	G
41	L5	505	G
41	L5	509	A
41	L5	510	U
41	L5	512	U
41	L5	513	U
41	L5	514	U
41	L5	516	C
41	L5	517	C
41	L5	518	G
41	L5	643	C
41	L5	645	G
41	L5	646	G
41	L5	654	C
41	L5	655	C
41	L5	656	C
41	L5	657	C
41	L5	659	G
41	L5	666	G
41	L5	667	A
41	L5	668	C
41	L5	669	C
41	L5	672	C
41	L5	673	C
41	L5	685	C

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Mol	Chain	Res	Type
41	L5	686	A
41	L5	687	U
41	L5	696	C
41	L5	697	G
41	L5	704	C
41	L5	708	G
41	L5	719	C
41	L5	731	G
41	L5	738	C
41	L5	739	G
41	L5	742	G
41	L5	750	U
41	L5	759	G
41	L5	904	C
41	L5	905	C
41	L5	910	G
41	L5	912	G
41	L5	913	U
41	L5	914	U
41	L5	915	A
41	L5	916	C
41	L5	917	A
41	L5	923	C
41	L5	924	C
41	L5	926	G
41	L5	927	G
41	L5	932	A
41	L5	933	G
41	L5	935	A
41	L5	936	C
41	L5	937	U
41	L5	941	C
41	L5	943	A
41	L5	944	A
41	L5	945	U
41	L5	956	A
41	L5	959	G
41	L5	960	A
41	L5	961	G
41	L5	962	C
41	L5	965	G
41	L5	966	A

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Mol	Chain	Res	Type
41	L5	967	C
41	L5	969	C
41	L5	970	G
41	L5	972	C
41	L5	982	U
41	L5	985	C
41	L5	989	U
41	L5	1070	G
41	L5	1071	C
41	L5	1072	C
41	L5	1075	G
41	L5	1082	C
41	L5	1083	U
41	L5	1095	A
41	L5	1168	G
41	L5	1171	G
41	L5	1172	C
41	L5	1173	G
41	L5	1174	G
41	L5	1179	U
41	L5	1180	C
41	L5	1181	C
41	L5	1182	C
41	L5	1183	C
41	L5	1189	G
41	L5	1193	C
41	L5	1194	G
41	L5	1202	C
41	L5	1203	G
41	L5	1210	C
41	L5	1211	G
41	L5	1214	C
41	L5	1215	C
41	L5	1218	G
41	L5	1219	G
41	L5	1222	A
41	L5	1246	G
41	L5	1253	G
41	L5	1254	A
41	L5	1257	A
41	L5	1258	G
41	L5	1262	G

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Mol	Chain	Res	Type
41	L5	1266	G
41	L5	1269	G
41	L5	1271	G
41	L5	1272	C
41	L5	1273	G
41	L5	1274	A
41	L5	1275	G
41	L5	1277	G
41	L5	1280	C
41	L5	1284	G
41	L5	1285	U
41	L5	1287	G
41	L5	1293	G
41	L5	1294	A
41	L5	1295	C
41	L5	1296	G
41	L5	1301	C
41	L5	1302	U
41	L5	1314	C
41	L5	1326	A2M
41	L5	1337	A
41	L5	1344	C
41	L5	1354	A
41	L5	1359	G
41	L5	1365	C
41	L5	1366	G
41	L5	1367	C
41	L5	1379	C
41	L5	1387	A
41	L5	1394	G
41	L5	1404	G
41	L5	1405	C
41	L5	1407	C
41	L5	1409	C
41	L5	1410	U
41	L5	1412	G
41	L5	1415	G
41	L5	1417	C
41	L5	1420	A
41	L5	1425	G
41	L5	1437	C
41	L5	1438	U

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Mol	Chain	Res	Type
41	L5	1439	C
41	L5	1442	C
41	L5	1443	A
41	L5	1444	G
41	L5	1445	U
41	L5	1446	C
41	L5	1457	G
41	L5	1465	G
41	L5	1482	G
41	L5	1483	C
41	L5	1497	A
41	L5	1498	G
41	L5	1502	G
41	L5	1516	G
41	L5	1517	G
41	L5	1523	A
41	L5	1524	A2M
41	L5	1534	A2M
41	L5	1537	A
41	L5	1543	G
41	L5	1547	A
41	L5	1562	G
41	L5	1564	A
41	L5	1566	C
41	L5	1574	G
41	L5	1578	U
41	L5	1591	U
41	L5	1596	U
41	L5	1597	G
41	L5	1612	G
41	L5	1614	C
41	L5	1624	G
41	L5	1625	OMG
41	L5	1631	A
41	L5	1633	G
41	L5	1634	A
41	L5	1641	G
41	L5	1654	G
41	L5	1661	C
41	L5	1676	C
41	L5	1677	PSU
41	L5	1691	G

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Mol	Chain	Res	Type
41	L5	1697	G
41	L5	1698	C
41	L5	1699	A
41	L5	1700	G
41	L5	1701	A
41	L5	1702	C
41	L5	1705	G
41	L5	1717	C
41	L5	1718	C
41	L5	1719	A
41	L5	1731	C
41	L5	1741	G
41	L5	1742	A
41	L5	1750	G
41	L5	1753	G
41	L5	1757	U
41	L5	1758	G
41	L5	1761	G
41	L5	1762	C
41	L5	1763	C
41	L5	1765	A
41	L5	1766	A
41	L5	1768	C
41	L5	1769	G
41	L5	1770	A
41	L5	1775	A
41	L5	1787	A
41	L5	1803	G
41	L5	1804	A
41	L5	1806	G
41	L5	1810	G
41	L5	1820	C
41	L5	1821	G
41	L5	1822	U
41	L5	1833	G
41	L5	1836	G
41	L5	1837	A
41	L5	1842	G
41	L5	1855	G
41	L5	1869	G
41	L5	1881	C
41	L5	1888	A

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Mol	Chain	Res	Type
41	L5	1897	A
41	L5	1899	G
41	L5	1917	A
41	L5	1918	U
41	L5	1919	G
41	L5	1920	C
41	L5	1921	C
41	L5	1922	G
41	L5	1925	G
41	L5	1931	C
41	L5	1932	A
41	L5	1938	C
41	L5	1940	G
41	L5	1948	G
41	L5	1961	G
41	L5	1962	A
41	L5	1971	C
41	L5	1972	G
41	L5	1974	U
41	L5	1975	G
41	L5	1978	C
41	L5	1980	U
41	L5	1982	G
41	L5	1983	A
41	L5	1984	A
41	L5	1985	G
41	L5	1986	U
41	L5	1987	C
41	L5	1989	G
41	L5	1990	A
41	L5	1991	A
41	L5	1993	C
41	L5	1995	G
41	L5	1997	U
41	L5	1999	A
41	L5	2001	G
41	L5	2002	A
41	L5	2003	G
41	L5	2011	C
41	L5	2014	C
41	L5	2017	A
41	L5	2018	C

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Mol	Chain	Res	Type
41	L5	2024	G
41	L5	2026	A
41	L5	2034	G
41	L5	2046	G
41	L5	2048	U
41	L5	2052	G
41	L5	2055	G
41	L5	2056	G
41	L5	2069	A
41	L5	2084	C
41	L5	2085	G
41	L5	2092	G
41	L5	2093	A
41	L5	2095	A
41	L5	2096	G
41	L5	2097	U
41	L5	2098	G
41	L5	2101	C
41	L5	2102	G
41	L5	2103	G
41	L5	2105	A
41	L5	2107	C
41	L5	2108	G
41	L5	2110	C
41	L5	2112	G
41	L5	2250	C
41	L5	2252	G
41	L5	2253	A
41	L5	2254	G
41	L5	2256	C
41	L5	2258	C
41	L5	2289	C
41	L5	2300	A
41	L5	2301	G
41	L5	2306	G
41	L5	2313	A
41	L5	2316	G
41	L5	2322	G
41	L5	2331	G
41	L5	2333	G
41	L5	2348	G
41	L5	2351	OMC

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Mol	Chain	Res	Type
41	L5	2360	A
41	L5	2364	OMG
41	L5	2395	A
41	L5	2397	G
41	L5	2402	G
41	L5	2410	C
41	L5	2411	C
41	L5	2416	G
41	L5	2417	A
41	L5	2422	OMC
41	L5	2425	U
41	L5	2453	A
41	L5	2464	C
41	L5	2465	C
41	L5	2471	G
41	L5	2474	G
41	L5	2475	G
41	L5	2478	C
41	L5	2483	G
41	L5	2484	A
41	L5	2485	U
41	L5	2486	G
41	L5	2487	G
41	L5	2488	C
41	L5	2489	C
41	L5	2490	U
41	L5	2491	C
41	L5	2494	U
41	L5	2504	C
41	L5	2505	C
41	L5	2506	G
41	L5	2507	A
41	L5	2513	A
41	L5	2519	U
41	L5	2529	A
41	L5	2537	A
41	L5	2544	G
41	L5	2545	U
41	L5	2546	G
41	L5	2547	G
41	L5	2554	U
41	L5	2555	G

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Mol	Chain	Res	Type
41	L5	2559	G
41	L5	2560	C
41	L5	2565	A
41	L5	2573	A
41	L5	2583	C
41	L5	2586	G
41	L5	2587	A
41	L5	2589	C
41	L5	2607	C
41	L5	2627	C
41	L5	2653	C
41	L5	2662	G
41	L5	2670	C
41	L5	2675	G
41	L5	2676	A
41	L5	2687	U
41	L5	2694	G
41	L5	2695	A
41	L5	2696	A
41	L5	2701	U
41	L5	2706	G
41	L5	2707	U
41	L5	2708	U
41	L5	2710	C
41	L5	2711	G
41	L5	2712	G
41	L5	2719	C
41	L5	2721	G
41	L5	2724	G
41	L5	2726	G
41	L5	2739	C
41	L5	2742	G
41	L5	2743	A
41	L5	2754	G
41	L5	2761	U
41	L5	2763	U
41	L5	2769	U
41	L5	2770	C
41	L5	2787	A2M
41	L5	2788	U
41	L5	2790	U
41	L5	2794	C

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Mol	Chain	Res	Type
41	L5	2799	G
41	L5	2806	A
41	L5	2814	C
41	L5	2826	U
41	L5	2827	G
41	L5	2830	G
41	L5	2833	A
41	L5	2835	A
41	L5	2855	G
41	L5	2867	C
41	L5	2869	U
41	L5	2877	G
41	L5	2895	A
41	L5	2899	C
41	L5	2900	U
41	L5	2902	G
41	L5	2903	G
41	L5	2904	U
41	L5	2905	C
41	L5	2906	G
41	L5	2907	G
41	L5	2908	U
41	L5	3585	G
41	L5	3588	C
41	L5	3590	G
41	L5	3591	C
41	L5	3594	C
41	L5	3595	U
41	L5	3596	A
41	L5	3597	G
41	L5	3605	C
41	L5	3626	G
41	L5	3630	A
41	L5	3635	A
41	L5	3644	U
41	L5	3646	A
41	L5	3662	A
41	L5	3664	G
41	L5	3670	C
41	L5	3673	C
41	L5	3674	G
41	L5	3691	G

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Mol	Chain	Res	Type
41	L5	3692	A
41	L5	3698	G
41	L5	3701	OMC
41	L5	3710	G
41	L5	3711	A
41	L5	3713	U
41	L5	3726	A
41	L5	3727	A
41	L5	3740	G
41	L5	3748	A
41	L5	3753	G
41	L5	3760	A
41	L5	3770	U
41	L5	3771	C
41	L5	3774	A
41	L5	3776	G
41	L5	3777	G
41	L5	3785	A2M
41	L5	3786	U
41	L5	3789	C
41	L5	3792	OMG
41	L5	3811	G
41	L5	3812	C
41	L5	3817	A
41	L5	3819	G
41	L5	3824	A
41	L5	3838	U
41	L5	3839	G
41	L5	3840	U
41	L5	3867	A2M
41	L5	3876	A
41	L5	3877	A
41	L5	3878	C
41	L5	3879	G
41	L5	3890	A
41	L5	3892	U
41	L5	3897	G
41	L5	3898	G
41	L5	3901	A
41	L5	3905	A
41	L5	3906	A
41	L5	3907	G

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Mol	Chain	Res	Type
41	L5	3908	A
41	L5	3915	U
41	L5	3938	G
41	L5	3943	A
41	L5	3944	G
41	L5	3946	G
41	L5	3947	A
41	L5	3948	C
41	L5	3949	A
41	L5	3950	U
41	L5	3952	A
41	L5	4057	C
41	L5	4059	C
41	L5	4062	A
41	L5	4064	C
41	L5	4068	U
41	L5	4069	U
41	L5	4076	G
41	L5	4094	G
41	L5	4095	G
41	L5	4097	G
41	L5	4099	G
41	L5	4101	C
41	L5	4104	G
41	L5	4105	A
41	L5	4106	G
41	L5	4107	G
41	L5	4108	G
41	L5	4111	U
41	L5	4114	C
41	L5	4115	G
41	L5	4116	C
41	L5	4117	U
41	L5	4120	U
41	L5	4122	G
41	L5	4127	A
41	L5	4128	A
41	L5	4133	C
41	L5	4141	G
41	L5	4142	C
41	L5	4143	G
41	L5	4144	C

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Mol	Chain	Res	Type
41	L5	4146	G
41	L5	4157	A
41	L5	4162	C
41	L5	4163	U
41	L5	4170	A
41	L5	4183	G
41	L5	4184	G
41	L5	4191	G
41	L5	4203	A
41	L5	4212	A
41	L5	4220	6MZ
41	L5	4229	U
41	L5	4232	U
41	L5	4233	A
41	L5	4234	A
41	L5	4241	C
41	L5	4243	C
41	L5	4249	G
41	L5	4251	A
41	L5	4254	G
41	L5	4257	A
41	L5	4258	C
41	L5	4265	U
41	L5	4268	A
41	L5	4273	A
41	L5	4281	A
41	L5	4290	U
41	L5	4291	G
41	L5	4295	U
41	L5	4304	A
41	L5	4305	G
41	L5	4306	OMU
41	L5	4314	C
41	L5	4319	C
41	L5	4329	G
41	L5	4330	G
41	L5	4332	C
41	L5	4349	C
41	L5	4350	C
41	L5	4354	U
41	L5	4373	G
41	L5	4376	A

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Mol	Chain	Res	Type
41	L5	4377	G
41	L5	4378	A
41	L5	4379	A
41	L5	4387	C
41	L5	4391	G
41	L5	4393	G
41	L5	4394	A
41	L5	4421	C
41	L5	4422	A
41	L5	4436	U
41	L5	4437	U
41	L5	4444	C
41	L5	4447	5MC
41	L5	4448	G
41	L5	4449	A
41	L5	4464	A
41	L5	4466	C
41	L5	4500	PSU
41	L5	4512	U
41	L5	4513	A
41	L5	4518	A
41	L5	4519	C
41	L5	4524	G
41	L5	4527	G
41	L5	4529	G
41	L5	4545	G
41	L5	4548	A
41	L5	4549	G
41	L5	4560	C
41	L5	4567	G
41	L5	4570	G
41	L5	4575	G
41	L5	4581	G
41	L5	4584	A
41	L5	4589	A
41	L5	4590	A2M
41	L5	4599	A
41	L5	4601	U
41	L5	4618	OMG
41	L5	4627	U
41	L5	4635	A
41	L5	4636	PSU

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Mol	Chain	Res	Type
41	L5	4637	OMG
41	L5	4652	G
41	L5	4656	A
41	L5	4670	C
41	L5	4671	C
41	L5	4672	A
41	L5	4693	C
41	L5	4695	C
41	L5	4700	A
41	L5	4707	A
41	L5	4708	A
41	L5	4709	U
41	L5	4719	G
41	L5	4728	U
41	L5	4733	C
41	L5	4734	A
41	L5	4735	G
41	L5	4740	G
41	L5	4741	C
41	L5	4742	G
41	L5	4745	G
41	L5	4750	G
41	L5	4754	G
41	L5	4757	C
41	L5	4759	C
41	L5	4761	G
41	L5	4765	G
41	L5	4771	C
41	L5	4772	C
41	L5	4775	C
41	L5	4859	C
41	L5	4862	G
41	L5	4863	G
41	L5	4867	G
41	L5	4870	G
41	L5	4871	C
41	L5	4875	G
41	L5	4881	U
41	L5	4882	U
41	L5	4883	C
41	L5	4887	C
41	L5	4889	G

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Mol	Chain	Res	Type
41	L5	4892	A
41	L5	4893	A
41	L5	4895	C
41	L5	4896	G
41	L5	4898	G
41	L5	4900	C
41	L5	4901	G
41	L5	4910	G
41	L5	4912	G
41	L5	4914	C
41	L5	4925	U
41	L5	4927	G
41	L5	4928	C
41	L5	4934	A
41	L5	4940	C
41	L5	4941	G
41	L5	4943	A
41	L5	4944	C
41	L5	4951	G
41	L5	4960	G
41	L5	4976	U
41	L5	4988	U
41	L5	4989	U
41	L5	4990	C
41	L5	4991	U
41	L5	5006	U
41	L5	5013	C
41	L5	5014	A
41	L5	5017	G
41	L5	5024	C
41	L5	5025	C
41	L5	5026	U
41	L5	5027	C
41	L5	5028	G
41	L5	5030	U
41	L5	5034	A
41	L5	5041	G
41	L5	5050	C
41	L5	5053	U
41	L5	5054	C
41	L5	5055	G
41	L5	5060	A

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Mol	Chain	Res	Type
41	L5	5061	A
41	L5	5069	U
42	L7	7	G
42	L7	11	A
42	L7	33	U
42	L7	37	G
42	L7	53	U
42	L7	54	A
42	L7	64	G
42	L7	76	U
42	L7	89	G
42	L7	91	C
42	L7	97	G
42	L7	100	A
42	L7	102	U
42	L7	110	G
42	L7	111	C
43	L8	25	G
43	L8	34	U
43	L8	35	C
43	L8	39	G
43	L8	51	U
43	L8	59	A
43	L8	63	U
43	L8	75	OMG
43	L8	81	C
43	L8	82	A
43	L8	83	C
43	L8	84	A
43	L8	85	U
43	L8	86	U
43	L8	87	G
43	L8	99	U
43	L8	103	A
43	L8	105	C
43	L8	107	C
43	L8	111	U
43	L8	114	G
43	L8	123	U
43	L8	124	U
43	L8	125	C
43	L8	126	C

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Mol	Chain	Res	Type
43	L8	127	U
43	L8	150	C
43	L8	153	C

All (21) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	S2	291	G
20	S2	563	G
20	S2	688	U
20	S2	1434	C
41	L5	406	C
41	L5	914	U
41	L5	1082	C
41	L5	1366	G
41	L5	1633	G
41	L5	1977	C
41	L5	2252	G
41	L5	2416	G
41	L5	2675	G
41	L5	2760	G
41	L5	3673	C
41	L5	3788	C
41	L5	4056	A
41	L5	4447	5MC
41	L5	4600	G
41	L5	4699	U
41	L5	4913	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
41	PSU	L5	3920	41,86	18,21,22	1.06	1 (5%)	21,30,33	1.96	5 (23%)
41	A2M	L5	4523	41,86	22,25,26	1.26	2 (9%)	30,36,39	1.56	8 (26%)
20	OMC	S2	462	20	19,22,23	0.52	0	25,31,34	0.65	0
20	6MZ	S2	1832	20,86	22,25,26	4.03	11 (50%)	29,36,39	2.31	11 (37%)
20	A2M	S2	468	20	22,25,26	1.25	1 (4%)	30,36,39	1.59	7 (23%)
20	OMU	S2	1288	20	19,22,23	3.43	7 (36%)	25,31,34	1.80	5 (20%)
41	PSU	L5	4457	41	18,21,22	1.08	1 (5%)	21,30,33	1.91	5 (23%)
41	PSU	L5	4636	41	18,21,22	1.08	1 (5%)	21,30,33	2.03	6 (28%)
41	PSU	L5	3639	41	18,21,22	1.10	2 (11%)	21,30,33	2.02	6 (28%)
20	PSU	S2	1244	20	18,21,22	1.10	1 (5%)	21,30,33	1.95	4 (19%)
41	PSU	L5	4521	41,86	18,21,22	1.06	2 (11%)	21,30,33	1.97	5 (23%)
41	PSU	L5	1792	41	18,21,22	1.03	1 (5%)	21,30,33	1.91	4 (19%)
41	OMU	L5	3925	41	19,22,23	3.31	7 (36%)	25,31,34	1.88	5 (20%)
20	PSU	S2	109	20	18,21,22	1.11	1 (5%)	21,30,33	1.97	5 (23%)
41	OMG	L5	1522	41	23,26,27	0.48	0	32,38,41	0.54	0
41	PSU	L5	1860	41	18,21,22	1.12	2 (11%)	21,30,33	1.97	4 (19%)
20	OMU	S2	799	20	19,22,23	3.40	7 (36%)	25,31,34	1.80	5 (20%)
41	OMU	L5	4306	41	19,22,23	3.30	7 (36%)	25,31,34	1.76	4 (16%)
41	A2M	L5	398	41	22,25,26	1.20	1 (4%)	30,36,39	1.62	8 (26%)
20	OMU	S2	1442	20	19,22,23	3.37	7 (36%)	25,31,34	1.78	4 (16%)
20	A2M	S2	484	20	22,25,26	1.20	1 (4%)	30,36,39	1.49	7 (23%)
41	PSU	L5	4500	41	18,21,22	1.10	1 (5%)	21,30,33	2.01	5 (23%)
20	OMC	S2	174	20	19,22,23	0.54	0	25,31,34	0.57	0
20	B8N	S2	1248	20	25,29,30	3.25	7 (28%)	28,42,45	2.07	8 (28%)
20	OMG	S2	867	20	23,26,27	0.48	0	32,38,41	0.45	0
41	OMG	L5	2424	41	23,26,27	0.49	0	32,38,41	0.51	0
41	OMG	L5	4392	41	23,26,27	0.53	0	32,38,41	0.47	0
41	PSU	L5	4471	41	18,21,22	1.09	1 (5%)	21,30,33	1.98	4 (19%)
41	PSU	L5	4361	41	18,21,22	1.07	1 (5%)	21,30,33	1.94	5 (23%)
43	PSU	L8	69	43	18,21,22	1.08	1 (5%)	21,30,33	1.92	5 (23%)
41	A2M	L5	1534	41,86	22,25,26	1.16	1 (4%)	30,36,39	1.69	8 (26%)
41	PSU	L5	4552	41	18,21,22	1.04	1 (5%)	21,30,33	1.96	4 (19%)
41	PSU	L5	1862	41	18,21,22	1.08	1 (5%)	21,30,33	1.95	4 (19%)
41	PSU	L5	3695	41	18,21,22	1.07	1 (5%)	21,30,33	1.99	6 (28%)
20	OMG	S2	1328	20	23,26,27	0.46	0	32,38,41	0.43	0
20	PSU	S2	681	20	18,21,22	1.04	1 (5%)	21,30,33	1.95	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
41	A2M	L5	1326	41,86	22,25,26	1.19	2 (9%)	30,36,39	1.55	9 (30%)
41	PSU	L5	1744	41,86	18,21,22	1.08	2 (11%)	21,30,33	2.02	6 (28%)
41	OMC	L5	2861	41	19,22,23	0.57	0	25,31,34	0.94	2 (8%)
41	PSU	L5	4403	41	18,21,22	1.11	3 (16%)	21,30,33	2.05	6 (28%)
41	OMC	L5	4536	41	19,22,23	0.58	0	25,31,34	0.76	0
41	OMC	L5	2804	41	19,22,23	0.56	0	25,31,34	0.65	0
41	PSU	L5	4431	41	18,21,22	1.08	1 (5%)	21,30,33	1.94	4 (19%)
41	PSU	L5	3844	41	18,21,22	1.09	1 (5%)	21,30,33	1.96	4 (19%)
20	PSU	S2	814	20	18,21,22	1.12	1 (5%)	21,30,33	1.90	4 (19%)
41	OMG	L5	3899	41	23,26,27	0.52	0	32,38,41	0.54	0
41	OMU	L5	2837	41	19,22,23	3.32	7 (36%)	25,31,34	1.87	4 (16%)
41	PSU	L5	4532	41	18,21,22	1.08	1 (5%)	21,30,33	1.88	4 (19%)
20	PSU	S2	1046	20	18,21,22	1.09	1 (5%)	21,30,33	1.86	4 (19%)
20	4AC	S2	1842	20	21,24,25	0.37	0	28,34,37	0.45	0
41	OMC	L5	2824	41	19,22,23	0.53	0	25,31,34	0.63	0
20	MA6	S2	1850	20	23,26,27	2.63	8 (34%)	33,38,41	3.50	14 (42%)
41	OMG	L5	2364	41,86	23,26,27	0.52	0	32,38,41	0.54	0
41	OMC	L5	3701	41	19,22,23	0.54	0	25,31,34	0.74	0
41	PSU	L5	4493	41	18,21,22	1.08	1 (5%)	21,30,33	1.96	5 (23%)
41	1MA	L5	1322	41,86	21,25,26	0.49	0	30,37,40	0.76	1 (3%)
41	PSU	L5	4353	41	18,21,22	1.07	1 (5%)	21,30,33	1.99	6 (28%)
41	PSU	L5	4579	41	18,21,22	1.05	1 (5%)	21,30,33	1.94	4 (19%)
41	OMC	L5	1340	41	19,22,23	0.57	0	25,31,34	0.64	0
20	PSU	S2	866	20	18,21,22	1.11	1 (5%)	21,30,33	2.01	5 (23%)
41	A2M	L5	4590	41	22,25,26	1.16	1 (4%)	30,36,39	1.54	8 (26%)
20	A2M	S2	166	20	22,25,26	1.24	1 (4%)	30,36,39	1.60	7 (23%)
20	OMC	S2	1272	20	19,22,23	0.55	0	25,31,34	0.76	1 (4%)
41	OMG	L5	3744	41	23,26,27	0.48	0	32,38,41	0.43	0
20	OMU	S2	354	20	19,22,23	3.35	7 (36%)	25,31,34	1.83	5 (20%)
20	OMU	S2	627	20	19,22,23	3.32	7 (36%)	25,31,34	1.84	5 (20%)
41	5MC	L5	3782	41,86	19,22,23	0.56	0	26,32,35	0.82	1 (3%)
41	OMC	L5	4456	41	19,22,23	0.62	0	25,31,34	0.82	1 (4%)
41	PSU	L5	4576	41	18,21,22	1.08	1 (5%)	21,30,33	1.86	5 (23%)
41	OMG	L5	3627	41	23,26,27	0.48	0	32,38,41	0.51	0
41	UY1	L5	3818	41	19,22,23	4.91	9 (47%)	21,31,34	2.03	5 (23%)
41	OMU	L5	4498	41	19,22,23	3.33	7 (36%)	25,31,34	1.84	5 (20%)
41	A2M	L5	400	41	22,25,26	1.25	2 (9%)	30,36,39	1.55	9 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
41	PSU	L5	5001	41	18,21,22	1.07	1 (5%)	21,30,33	1.96	4 (19%)
20	OMU	S2	1326	20	19,22,23	3.32	7 (36%)	25,31,34	1.83	5 (20%)
41	A2M	L5	3785	41,86	22,25,26	1.18	1 (4%)	30,36,39	1.74	9 (30%)
41	OMC	L5	3808	41	19,22,23	0.56	0	25,31,34	0.98	2 (8%)
41	PSU	L5	1536	41	18,21,22	1.09	2 (11%)	21,30,33	2.02	5 (23%)
20	PSU	S2	1081	20	18,21,22	1.07	1 (5%)	21,30,33	2.02	5 (23%)
41	OMC	L5	2365	41,86	19,22,23	0.56	0	25,31,34	0.58	0
20	PSU	S2	651	20	18,21,22	1.10	1 (5%)	21,30,33	1.97	5 (23%)
41	OMU	L5	4620	41	19,22,23	3.27	7 (36%)	25,31,34	1.81	5 (20%)
20	G7M	S2	1639	20	23,26,27	2.67	9 (39%)	34,39,42	2.42	11 (32%)
41	OMC	L5	3887	41	19,22,23	0.58	0	25,31,34	0.73	0
41	OMC	L5	3841	41	19,22,23	0.56	0	25,31,34	0.63	0
41	A2M	L5	1871	41,86	22,25,26	1.20	1 (4%)	30,36,39	1.56	8 (26%)
41	OMG	L5	4623	41	23,26,27	0.50	0	32,38,41	0.47	0
41	OMG	L5	4228	41	23,26,27	0.51	0	32,38,41	0.60	0
41	OMG	L5	3792	41	23,26,27	0.49	0	32,38,41	0.48	0
20	PSU	S2	406	20	18,21,22	1.06	1 (5%)	21,30,33	1.97	4 (19%)
41	OMG	L5	4618	41	23,26,27	0.53	0	32,38,41	0.47	0
41	A2M	L5	1524	41	22,25,26	1.24	2 (9%)	30,36,39	1.52	8 (26%)
41	PSU	L5	1677	41	18,21,22	1.08	1 (5%)	21,30,33	2.07	6 (28%)
41	UR3	L5	4530	41	19,22,23	2.74	7 (36%)	26,32,35	1.60	2 (7%)
41	PSU	L5	4972	41	18,21,22	1.04	1 (5%)	21,30,33	1.90	4 (19%)
20	PSU	S2	1174	20	18,21,22	1.08	1 (5%)	21,30,33	1.94	4 (19%)
20	OMU	S2	116	20	19,22,23	3.32	7 (36%)	25,31,34	1.69	4 (16%)
20	OMG	S2	601	20	23,26,27	0.55	0	32,38,41	0.61	0
20	OMU	S2	121	20	19,22,23	3.34	7 (36%)	25,31,34	1.86	5 (20%)
20	A2M	S2	1031	20	22,25,26	1.20	1 (4%)	30,36,39	1.56	8 (26%)
41	A2M	L5	2815	41	22,25,26	1.15	1 (4%)	30,36,39	1.44	5 (16%)
41	OMG	L5	4196	41,39	23,26,27	0.49	0	32,38,41	0.47	0
20	OMC	S2	1391	20	19,22,23	0.56	0	25,31,34	0.78	1 (4%)
41	PSU	L5	4689	41	18,21,22	1.05	1 (5%)	21,30,33	2.00	4 (19%)
41	A2M	L5	3718	41	22,25,26	1.20	1 (4%)	30,36,39	1.54	7 (23%)
41	PSU	L5	2839	41	18,21,22	1.08	1 (5%)	21,30,33	1.98	5 (23%)
20	OMU	S2	428	20	19,22,23	3.36	7 (36%)	25,31,34	1.83	5 (20%)
20	OMC	S2	517	20	19,22,23	0.57	0	25,31,34	0.79	1 (4%)
20	PSU	S2	801	20	18,21,22	1.12	1 (5%)	21,30,33	1.87	4 (19%)
41	OMC	L5	2422	41,86	19,22,23	0.62	0	25,31,34	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
20	A2M	S2	159	20	22,25,26	1.19	1 (4%)	30,36,39	1.51	8 (26%)
41	A2M	L5	2363	41,86	22,25,26	1.19	1 (4%)	30,36,39	1.55	8 (26%)
41	PSU	L5	4293	41	18,21,22	1.10	2 (11%)	21,30,33	2.00	5 (23%)
20	PSU	S2	1232	20	18,21,22	1.09	1 (5%)	21,30,33	1.96	4 (19%)
20	A2M	S2	576	20	22,25,26	1.20	1 (4%)	30,36,39	1.55	6 (20%)
41	PSU	L5	1781	41	18,21,22	1.05	1 (5%)	21,30,33	1.90	4 (19%)
41	A2M	L5	2787	41	22,25,26	1.17	1 (4%)	30,36,39	1.51	7 (23%)
41	OMC	L5	3869	41	19,22,23	0.53	0	25,31,34	0.68	0
41	PSU	L5	4673	41	18,21,22	1.09	2 (11%)	21,30,33	2.03	5 (23%)
41	OMG	L5	4499	41	23,26,27	0.48	0	32,38,41	0.52	0
41	PSU	L5	3637	41	18,21,22	1.06	1 (5%)	21,30,33	1.95	4 (19%)
41	PSU	L5	1782	41	18,21,22	1.11	1 (5%)	21,30,33	1.93	4 (19%)
20	OMG	S2	509	20	23,26,27	0.49	0	32,38,41	0.47	0
41	PSU	L5	3822	41	18,21,22	1.12	2 (11%)	21,30,33	2.09	6 (28%)
41	A2M	L5	4571	41	22,25,26	1.21	1 (4%)	30,36,39	1.52	7 (23%)
20	PSU	S2	686	20	18,21,22	1.09	1 (5%)	21,30,33	1.97	5 (23%)
20	4AC	S2	1337	20	21,24,25	0.39	0	28,34,37	0.71	1 (3%)
41	OMC	L5	2351	41,86	19,22,23	0.56	0	25,31,34	0.78	1 (4%)
41	6MZ	L5	4220	41	22,25,26	2.96	5 (22%)	29,36,39	2.37	10 (34%)
41	OMG	L5	4637	41	23,26,27	0.49	0	32,38,41	0.48	0
20	PSU	S2	649	20	18,21,22	1.15	1 (5%)	21,30,33	1.90	4 (19%)
20	PSU	S2	863	20	18,21,22	1.06	1 (5%)	21,30,33	1.94	4 (19%)
41	PSU	L5	3884	41	18,21,22	1.05	1 (5%)	21,30,33	2.01	5 (23%)
20	A2M	S2	668	20,86	22,25,26	1.34	2 (9%)	30,36,39	1.58	7 (23%)
41	PSU	L5	2632	41	18,21,22	1.13	1 (5%)	21,30,33	2.02	5 (23%)
41	A2M	L5	3867	41	22,25,26	1.22	2 (9%)	30,36,39	1.57	9 (30%)
41	PSU	L5	4628	41	18,21,22	1.13	2 (11%)	21,30,33	2.02	5 (23%)
20	PSU	S2	1056	20	18,21,22	1.09	1 (5%)	21,30,33	1.94	4 (19%)
41	OMG	L5	4370	41	23,26,27	0.48	0	32,38,41	0.45	0
41	PSU	L5	4973	41	18,21,22	1.09	1 (5%)	21,30,33	2.00	5 (23%)
43	PSU	L8	55	43	18,21,22	1.10	1 (5%)	21,30,33	1.97	5 (23%)
41	PSU	L5	4296	41	18,21,22	1.11	1 (5%)	21,30,33	1.97	4 (19%)
20	OMU	S2	172	20	19,22,23	3.34	7 (36%)	25,31,34	1.81	5 (20%)
20	A2M	S2	1383	20	22,25,26	1.19	1 (4%)	30,36,39	1.63	9 (30%)
20	OMC	S2	1703	20	19,22,23	0.53	0	25,31,34	0.67	0
20	MA6	S2	1851	20	23,26,27	1.27	2 (8%)	33,38,41	3.35	12 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
41	5MC	L5	4447	41	19,22,23	0.72	0	26,32,35	0.64	0
41	PSU	L5	3851	41	18,21,22	1.11	1 (5%)	21,30,33	1.95	5 (23%)
41	OMG	L5	4494	41	23,26,27	0.51	0	32,38,41	0.47	0
41	PSU	L5	5010	41	18,21,22	1.12	1 (5%)	21,30,33	1.95	4 (19%)
20	PSU	S2	1004	20	18,21,22	1.08	1 (5%)	21,30,33	1.86	4 (19%)
41	PSU	L5	3853	41,86	18,21,22	1.12	1 (5%)	21,30,33	2.06	6 (28%)
41	OMG	L5	2876	41	23,26,27	0.51	0	32,38,41	0.49	0
20	A2M	S2	99	20,86	22,25,26	1.19	1 (4%)	30,36,39	1.53	8 (26%)
20	PSU	S2	1045	20	18,21,22	1.10	1 (5%)	21,30,33	1.94	5 (23%)
20	PSU	S2	93	20	18,21,22	1.09	1 (5%)	21,30,33	1.82	4 (19%)
41	PSU	L5	4312	41	18,21,22	1.08	1 (5%)	21,30,33	1.90	4 (19%)
20	PSU	S2	1177	20	18,21,22	1.06	1 (5%)	21,30,33	1.88	4 (19%)
41	A2M	L5	2401	41	22,25,26	1.19	1 (4%)	30,36,39	1.55	8 (26%)
41	OMG	L5	1316	41	23,26,27	0.50	0	32,38,41	0.51	0
41	PSU	L5	1683	41	18,21,22	1.10	2 (11%)	21,30,33	1.97	4 (19%)
41	A2M	L5	3830	41	22,25,26	1.21	1 (4%)	30,36,39	1.54	7 (23%)
20	OMG	S2	683	20	23,26,27	0.49	0	32,38,41	0.45	0
41	OMG	L5	1625	41	23,26,27	0.51	0	32,38,41	0.45	0
43	OMG	L8	75	43	23,26,27	0.47	0	32,38,41	0.48	0
20	OMG	S2	436	20	23,26,27	0.50	0	32,38,41	0.48	0
41	PSU	L5	4442	41	18,21,22	1.10	3 (16%)	21,30,33	2.07	6 (28%)
20	OMG	S2	1490	20	23,26,27	0.51	0	32,38,41	0.48	0
41	A2M	L5	1323	41	22,25,26	1.23	2 (9%)	30,36,39	1.59	9 (30%)
41	PSU	L5	1582	41	18,21,22	1.10	1 (5%)	21,30,33	1.93	4 (19%)
20	OMG	S2	644	20	23,26,27	0.46	0	32,38,41	0.47	0
20	PSU	S2	966	20,86	18,21,22	1.09	1 (5%)	21,30,33	1.90	5 (23%)
20	PSU	S2	105	20	18,21,22	1.09	1 (5%)	21,30,33	1.91	4 (19%)
20	A2M	S2	27	20	22,25,26	1.22	1 (4%)	30,36,39	1.53	7 (23%)
41	OMU	L5	4227	41	19,22,23	3.30	7 (36%)	25,31,34	1.86	5 (20%)
41	PSU	L5	4299	41	18,21,22	1.05	1 (5%)	21,30,33	1.92	4 (19%)
41	A2M	L5	3825	41	22,25,26	1.19	1 (4%)	30,36,39	1.55	9 (30%)
20	PSU	S2	1367	20	18,21,22	1.10	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
41	PSU	L5	3920	41,86	-	0/7/25/26	0/2/2/2
41	A2M	L5	4523	41,86	-	0/9/27/28	0/3/3/3
20	OMC	S2	462	20	-	1/9/27/28	0/2/2/2
20	6MZ	S2	1832	20,86	-	2/9/27/28	0/3/3/3
20	A2M	S2	468	20	-	0/9/27/28	0/3/3/3
20	OMU	S2	1288	20	-	2/9/27/28	0/2/2/2
41	PSU	L5	4457	41	-	0/7/25/26	0/2/2/2
41	PSU	L5	4636	41	-	2/7/25/26	0/2/2/2
41	PSU	L5	3639	41	-	0/7/25/26	0/2/2/2
20	PSU	S2	1244	20	-	0/7/25/26	0/2/2/2
41	PSU	L5	4521	41,86	-	0/7/25/26	0/2/2/2
41	PSU	L5	1792	41	-	0/7/25/26	0/2/2/2
41	OMU	L5	3925	41	-	0/9/27/28	0/2/2/2
20	PSU	S2	109	20	-	0/7/25/26	0/2/2/2
41	OMG	L5	1522	41	-	0/9/27/28	0/3/3/3
41	PSU	L5	1860	41	-	0/7/25/26	0/2/2/2
20	OMU	S2	799	20	-	2/9/27/28	0/2/2/2
41	OMU	L5	4306	41	-	0/9/27/28	0/2/2/2
41	A2M	L5	398	41	-	2/9/27/28	0/3/3/3
20	OMU	S2	1442	20	-	3/9/27/28	0/2/2/2
20	A2M	S2	484	20	-	0/9/27/28	0/3/3/3
41	PSU	L5	4500	41	-	3/7/25/26	0/2/2/2
20	OMC	S2	174	20	-	0/9/27/28	0/2/2/2
20	B8N	S2	1248	20	-	6/16/34/35	0/2/2/2
20	OMG	S2	867	20	-	1/9/27/28	0/3/3/3
41	OMG	L5	2424	41	-	0/9/27/28	0/3/3/3
41	OMG	L5	4392	41	-	0/9/27/28	0/3/3/3
41	PSU	L5	4471	41	-	0/7/25/26	0/2/2/2
41	PSU	L5	4361	41	-	0/7/25/26	0/2/2/2
43	PSU	L8	69	43	-	0/7/25/26	0/2/2/2
41	A2M	L5	1534	41,86	-	1/9/27/28	0/3/3/3
41	PSU	L5	4552	41	-	0/7/25/26	0/2/2/2
41	PSU	L5	1862	41	-	0/7/25/26	0/2/2/2
41	PSU	L5	3695	41	-	0/7/25/26	0/2/2/2
20	OMG	S2	1328	20	-	1/9/27/28	0/3/3/3
20	PSU	S2	681	20	-	0/7/25/26	0/2/2/2
41	A2M	L5	1326	41,86	-	3/9/27/28	0/3/3/3
41	PSU	L5	1744	41,86	-	0/7/25/26	0/2/2/2
41	OMC	L5	2861	41	-	1/9/27/28	0/2/2/2
41	PSU	L5	4403	41	-	0/7/25/26	0/2/2/2
41	OMC	L5	4536	41	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
41	OMC	L5	2804	41	-	0/9/27/28	0/2/2/2
41	PSU	L5	4431	41	-	0/7/25/26	0/2/2/2
41	PSU	L5	3844	41	-	1/7/25/26	0/2/2/2
20	PSU	S2	814	20	-	0/7/25/26	0/2/2/2
41	OMG	L5	3899	41	-	2/9/27/28	0/3/3/3
41	OMU	L5	2837	41	-	0/9/27/28	0/2/2/2
41	PSU	L5	4532	41	-	0/7/25/26	0/2/2/2
20	PSU	S2	1046	20	-	0/7/25/26	0/2/2/2
20	4AC	S2	1842	20	-	0/11/29/30	0/2/2/2
41	OMC	L5	2824	41	-	1/9/27/28	0/2/2/2
20	MA6	S2	1850	20	-	1/11/29/30	0/3/3/3
41	OMG	L5	2364	41,86	-	3/9/27/28	0/3/3/3
41	OMC	L5	3701	41	-	4/9/27/28	0/2/2/2
41	PSU	L5	4493	41	-	0/7/25/26	0/2/2/2
41	1MA	L5	1322	41,86	-	0/7/25/26	0/3/3/3
41	PSU	L5	4353	41	-	0/7/25/26	0/2/2/2
41	PSU	L5	4579	41	-	0/7/25/26	0/2/2/2
41	OMC	L5	1340	41	-	1/9/27/28	0/2/2/2
20	PSU	S2	866	20	-	0/7/25/26	0/2/2/2
41	A2M	L5	4590	41	-	4/9/27/28	0/3/3/3
20	A2M	S2	166	20	-	0/9/27/28	0/3/3/3
20	OMC	S2	1272	20	-	2/9/27/28	0/2/2/2
41	OMG	L5	3744	41	-	1/9/27/28	0/3/3/3
20	OMU	S2	354	20	-	1/9/27/28	0/2/2/2
20	OMU	S2	627	20	-	6/9/27/28	0/2/2/2
41	5MC	L5	3782	41,86	-	0/7/25/26	0/2/2/2
41	OMC	L5	4456	41	-	0/9/27/28	0/2/2/2
41	PSU	L5	4576	41	-	0/7/25/26	0/2/2/2
41	OMG	L5	3627	41	-	1/9/27/28	0/3/3/3
41	UY1	L5	3818	41	-	1/9/27/28	0/2/2/2
41	OMU	L5	4498	41	-	0/9/27/28	0/2/2/2
41	A2M	L5	400	41	-	1/9/27/28	0/3/3/3
41	PSU	L5	5001	41	-	0/7/25/26	0/2/2/2
20	OMU	S2	1326	20	-	0/9/27/28	0/2/2/2
41	A2M	L5	3785	41,86	-	2/9/27/28	0/3/3/3
41	OMC	L5	3808	41	-	0/9/27/28	0/2/2/2
41	PSU	L5	1536	41	-	2/7/25/26	0/2/2/2
20	PSU	S2	1081	20	-	1/7/25/26	0/2/2/2
41	OMC	L5	2365	41,86	-	1/9/27/28	0/2/2/2
20	PSU	S2	651	20	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
41	OMU	L5	4620	41	-	1/9/27/28	0/2/2/2
20	G7M	S2	1639	20	-	4/7/25/26	0/3/3/3
41	OMC	L5	3887	41	-	1/9/27/28	0/2/2/2
41	OMC	L5	3841	41	-	0/9/27/28	0/2/2/2
41	A2M	L5	1871	41,86	-	0/9/27/28	0/3/3/3
41	OMG	L5	4623	41	-	0/9/27/28	0/3/3/3
41	OMG	L5	4228	41	-	2/9/27/28	0/3/3/3
41	OMG	L5	3792	41	-	3/9/27/28	0/3/3/3
20	PSU	S2	406	20	-	0/7/25/26	0/2/2/2
41	OMG	L5	4618	41	-	2/9/27/28	0/3/3/3
41	A2M	L5	1524	41	-	3/9/27/28	0/3/3/3
41	PSU	L5	1677	41	-	1/7/25/26	0/2/2/2
41	UR3	L5	4530	41	-	0/7/25/26	0/2/2/2
41	PSU	L5	4972	41	-	0/7/25/26	0/2/2/2
20	PSU	S2	1174	20	-	0/7/25/26	0/2/2/2
20	OMU	S2	116	20	-	1/9/27/28	0/2/2/2
20	OMG	S2	601	20	-	1/9/27/28	0/3/3/3
20	OMU	S2	121	20	-	0/9/27/28	0/2/2/2
20	A2M	S2	1031	20	-	1/9/27/28	0/3/3/3
41	A2M	L5	2815	41	-	0/9/27/28	0/3/3/3
41	OMG	L5	4196	41,39	-	0/9/27/28	0/3/3/3
20	OMC	S2	1391	20	-	0/9/27/28	0/2/2/2
41	PSU	L5	4689	41	-	0/7/25/26	0/2/2/2
41	A2M	L5	3718	41	-	0/9/27/28	0/3/3/3
41	PSU	L5	2839	41	-	0/7/25/26	0/2/2/2
20	OMU	S2	428	20	-	6/9/27/28	0/2/2/2
20	OMC	S2	517	20	-	1/9/27/28	0/2/2/2
20	PSU	S2	801	20	-	2/7/25/26	0/2/2/2
41	OMC	L5	2422	41,86	-	3/9/27/28	0/2/2/2
20	A2M	S2	159	20	-	1/9/27/28	0/3/3/3
41	A2M	L5	2363	41,86	-	1/9/27/28	0/3/3/3
41	PSU	L5	4293	41	-	0/7/25/26	0/2/2/2
20	PSU	S2	1232	20	-	0/7/25/26	0/2/2/2
20	A2M	S2	576	20	-	4/9/27/28	0/3/3/3
41	PSU	L5	1781	41	-	1/7/25/26	0/2/2/2
41	A2M	L5	2787	41	-	5/9/27/28	0/3/3/3
41	OMC	L5	3869	41	-	0/9/27/28	0/2/2/2
41	PSU	L5	4673	41	-	0/7/25/26	0/2/2/2
41	OMG	L5	4499	41	-	0/9/27/28	0/3/3/3
41	PSU	L5	3637	41	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
41	PSU	L5	1782	41	-	0/7/25/26	0/2/2/2
20	OMG	S2	509	20	-	0/9/27/28	0/3/3/3
41	PSU	L5	3822	41	-	3/7/25/26	0/2/2/2
41	A2M	L5	4571	41	-	0/9/27/28	0/3/3/3
20	PSU	S2	686	20	-	0/7/25/26	0/2/2/2
20	4AC	S2	1337	20	-	1/11/29/30	0/2/2/2
41	OMC	L5	2351	41,86	-	1/9/27/28	0/2/2/2
41	6MZ	L5	4220	41	-	5/9/27/28	0/3/3/3
41	OMG	L5	4637	41	-	3/9/27/28	0/3/3/3
20	PSU	S2	649	20	-	2/7/25/26	0/2/2/2
20	PSU	S2	863	20	-	2/7/25/26	0/2/2/2
41	PSU	L5	3884	41	-	0/7/25/26	0/2/2/2
20	A2M	S2	668	20,86	-	4/9/27/28	0/3/3/3
41	PSU	L5	2632	41	-	0/7/25/26	0/2/2/2
41	A2M	L5	3867	41	-	3/9/27/28	0/3/3/3
41	PSU	L5	4628	41	-	1/7/25/26	0/2/2/2
20	PSU	S2	1056	20	-	0/7/25/26	0/2/2/2
41	OMG	L5	4370	41	-	0/9/27/28	0/3/3/3
41	PSU	L5	4973	41	-	0/7/25/26	0/2/2/2
43	PSU	L8	55	43	-	0/7/25/26	0/2/2/2
41	PSU	L5	4296	41	-	0/7/25/26	0/2/2/2
20	OMU	S2	172	20	-	0/9/27/28	0/2/2/2
20	A2M	S2	1383	20	-	1/9/27/28	0/3/3/3
20	OMC	S2	1703	20	-	1/9/27/28	0/2/2/2
20	MA6	S2	1851	20	-	3/11/29/30	0/3/3/3
41	5MC	L5	4447	41	-	4/7/25/26	0/2/2/2
41	PSU	L5	3851	41	-	1/7/25/26	0/2/2/2
41	OMG	L5	4494	41	-	0/9/27/28	0/3/3/3
41	PSU	L5	5010	41	-	2/7/25/26	0/2/2/2
20	PSU	S2	1004	20	-	0/7/25/26	0/2/2/2
41	PSU	L5	3853	41,86	-	0/7/25/26	0/2/2/2
41	OMG	L5	2876	41	-	1/9/27/28	0/3/3/3
20	A2M	S2	99	20,86	-	2/9/27/28	0/3/3/3
20	PSU	S2	1045	20	-	2/7/25/26	0/2/2/2
20	PSU	S2	93	20	-	0/7/25/26	0/2/2/2
41	PSU	L5	4312	41	-	0/7/25/26	0/2/2/2
20	PSU	S2	1177	20	-	0/7/25/26	0/2/2/2
41	A2M	L5	2401	41	-	1/9/27/28	0/3/3/3
41	OMG	L5	1316	41	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
41	PSU	L5	1683	41	-	0/7/25/26	0/2/2/2
41	A2M	L5	3830	41	-	1/9/27/28	0/3/3/3
20	OMG	S2	683	20	-	2/9/27/28	0/3/3/3
41	OMG	L5	1625	41	-	3/9/27/28	0/3/3/3
43	OMG	L8	75	43	-	2/9/27/28	0/3/3/3
20	OMG	S2	436	20	-	0/9/27/28	0/3/3/3
41	PSU	L5	4442	41	-	1/7/25/26	0/2/2/2
20	OMG	S2	1490	20	-	1/9/27/28	0/3/3/3
41	A2M	L5	1323	41	-	3/9/27/28	0/3/3/3
41	PSU	L5	1582	41	-	0/7/25/26	0/2/2/2
20	OMG	S2	644	20	-	4/9/27/28	0/3/3/3
20	PSU	S2	966	20,86	-	0/7/25/26	0/2/2/2
20	PSU	S2	105	20	-	0/7/25/26	0/2/2/2
20	A2M	S2	27	20	-	1/9/27/28	0/3/3/3
41	OMU	L5	4227	41	-	0/9/27/28	0/2/2/2
41	PSU	L5	4299	41	-	0/7/25/26	0/2/2/2
41	A2M	L5	3825	41	-	1/9/27/28	0/3/3/3
20	PSU	S2	1367	20	-	0/7/25/26	0/2/2/2

All (292) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	L5	3818	UY1	C6-C5	12.71	1.49	1.35
20	S2	1832	6MZ	C6-N6	12.63	1.48	1.34
41	L5	4220	6MZ	C6-N6	12.12	1.48	1.34
41	L5	3818	UY1	C2-N1	11.85	1.52	1.36
20	S2	1288	OMU	C2-N1	8.80	1.52	1.38
20	S2	799	OMU	C2-N1	8.61	1.51	1.38
20	S2	1832	6MZ	C3'-C2'	-8.52	1.30	1.53
20	S2	1442	OMU	C2-N1	8.32	1.51	1.38
20	S2	428	OMU	C2-N1	8.26	1.51	1.38
20	S2	172	OMU	C2-N1	8.17	1.51	1.38
20	S2	121	OMU	C2-N1	8.17	1.51	1.38
20	S2	354	OMU	C2-N1	8.17	1.51	1.38
41	L5	2837	OMU	C2-N1	8.11	1.51	1.38
20	S2	116	OMU	C2-N1	8.09	1.51	1.38
41	L5	4306	OMU	C2-N1	8.09	1.51	1.38
41	L5	4498	OMU	C2-N1	8.07	1.51	1.38
41	L5	3925	OMU	C2-N1	8.06	1.51	1.38
20	S2	627	OMU	C2-N1	8.05	1.51	1.38
20	S2	1326	OMU	C2-N1	7.99	1.51	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	L5	4227	OMU	C2-N1	7.97	1.50	1.38
41	L5	4620	OMU	C2-N1	7.96	1.50	1.38
41	L5	3818	UY1	C2-N3	7.85	1.50	1.37
20	S2	1248	B8N	C6-N1	7.82	1.55	1.36
20	S2	1248	B8N	C4-N3	-7.79	1.26	1.40
20	S2	1850	MA6	C3'-C2'	-7.74	1.32	1.53
20	S2	1248	B8N	C4-C5	6.98	1.63	1.47
20	S2	116	OMU	C2-N3	6.91	1.50	1.38
20	S2	1326	OMU	C2-N3	6.90	1.50	1.38
20	S2	428	OMU	C2-N3	6.89	1.50	1.38
20	S2	1442	OMU	C2-N3	6.89	1.50	1.38
20	S2	354	OMU	C2-N3	6.88	1.49	1.38
20	S2	799	OMU	C2-N3	6.88	1.49	1.38
41	L5	4498	OMU	C2-N3	6.86	1.49	1.38
20	S2	121	OMU	C2-N3	6.86	1.49	1.38
20	S2	627	OMU	C2-N3	6.86	1.49	1.38
20	S2	172	OMU	C2-N3	6.84	1.49	1.38
41	L5	3925	OMU	C2-N3	6.82	1.49	1.38
41	L5	2837	OMU	C2-N3	6.79	1.49	1.38
20	S2	1288	OMU	C2-N3	6.77	1.49	1.38
41	L5	4227	OMU	C2-N3	6.76	1.49	1.38
41	L5	4306	OMU	C2-N3	6.74	1.49	1.38
41	L5	4620	OMU	C2-N3	6.67	1.49	1.38
20	S2	1639	G7M	C4-N3	6.59	1.49	1.34
41	L5	4530	UR3	C2-N1	6.46	1.47	1.38
41	L5	4530	UR3	C6-C5	6.19	1.49	1.35
20	S2	1288	OMU	C6-C5	5.95	1.48	1.35
20	S2	1248	B8N	C2-N1	5.92	1.56	1.39
20	S2	354	OMU	C6-C5	5.89	1.48	1.35
41	L5	4530	UR3	C2-N3	5.85	1.50	1.39
20	S2	116	OMU	C6-C5	5.84	1.48	1.35
20	S2	172	OMU	C6-C5	5.84	1.48	1.35
41	L5	2837	OMU	C6-C5	5.84	1.48	1.35
20	S2	1326	OMU	C6-C5	5.83	1.48	1.35
20	S2	1442	OMU	C6-C5	5.83	1.48	1.35
20	S2	428	OMU	C6-C5	5.82	1.48	1.35
20	S2	799	OMU	C6-C5	5.81	1.48	1.35
41	L5	4227	OMU	C6-C5	5.81	1.48	1.35
41	L5	4498	OMU	C6-C5	5.80	1.48	1.35
41	L5	3925	OMU	C6-C5	5.79	1.48	1.35
20	S2	121	OMU	C6-C5	5.78	1.48	1.35
20	S2	627	OMU	C6-C5	5.77	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	L5	4306	OMU	C6-C5	5.76	1.48	1.35
41	L5	4620	OMU	C6-C5	5.68	1.48	1.35
41	L5	4620	OMU	O4-C4	-5.52	1.13	1.24
41	L5	4306	OMU	O4-C4	-5.51	1.13	1.24
41	L5	2837	OMU	O4-C4	-5.51	1.13	1.24
41	L5	4227	OMU	O4-C4	-5.50	1.13	1.24
20	S2	121	OMU	O4-C4	-5.50	1.13	1.24
20	S2	354	OMU	O4-C4	-5.49	1.13	1.24
41	L5	3925	OMU	O4-C4	-5.48	1.13	1.24
41	L5	4498	OMU	O4-C4	-5.47	1.13	1.24
20	S2	1639	G7M	C2-N3	5.46	1.46	1.33
41	L5	3818	UY1	C6-N1	5.46	1.45	1.36
20	S2	1442	OMU	O4-C4	-5.46	1.13	1.24
20	S2	172	OMU	O4-C4	-5.45	1.13	1.24
20	S2	799	OMU	O4-C4	-5.44	1.13	1.24
20	S2	1288	OMU	O4-C4	-5.44	1.13	1.24
20	S2	627	OMU	O4-C4	-5.43	1.13	1.24
20	S2	428	OMU	O4-C4	-5.43	1.13	1.24
20	S2	1326	OMU	O4-C4	-5.41	1.14	1.24
20	S2	116	OMU	O4-C4	-5.37	1.14	1.24
20	S2	1248	B8N	C6-C5	5.26	1.42	1.35
20	S2	1639	G7M	C2-N2	4.97	1.45	1.34
20	S2	1832	6MZ	O4'-C4'	4.74	1.55	1.45
20	S2	1832	6MZ	O4'-C1'	-4.73	1.31	1.42
20	S2	1639	G7M	C5-N7	-4.63	1.33	1.39
41	L5	3818	UY1	C4-N3	4.53	1.47	1.38
20	S2	1832	6MZ	C5'-C4'	-4.49	1.38	1.51
20	S2	627	OMU	C4-N3	4.40	1.46	1.38
20	S2	172	OMU	C4-N3	4.36	1.46	1.38
20	S2	428	OMU	C4-N3	4.35	1.46	1.38
20	S2	799	OMU	C4-N3	4.34	1.46	1.38
20	S2	1326	OMU	C4-N3	4.33	1.46	1.38
20	S2	1442	OMU	C4-N3	4.32	1.46	1.38
41	L5	4498	OMU	C4-N3	4.32	1.46	1.38
20	S2	121	OMU	C4-N3	4.31	1.46	1.38
20	S2	354	OMU	C4-N3	4.27	1.45	1.38
41	L5	4227	OMU	C4-N3	4.22	1.45	1.38
20	S2	116	OMU	C4-N3	4.21	1.45	1.38
20	S2	1288	OMU	C4-N3	4.21	1.45	1.38
20	S2	1850	MA6	O4'-C4'	4.20	1.54	1.45
41	L5	2837	OMU	C4-N3	4.18	1.45	1.38
41	L5	3925	OMU	C4-N3	4.17	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	L5	4620	OMU	C4-N3	4.16	1.45	1.38
20	S2	1850	MA6	C5'-C4'	-4.14	1.39	1.51
41	L5	4306	OMU	C4-N3	4.13	1.45	1.38
20	S2	1639	G7M	C5-C6	3.84	1.54	1.43
20	S2	801	PSU	C6-C5	3.74	1.39	1.35
20	S2	649	PSU	C6-C5	3.73	1.39	1.35
41	L5	2632	PSU	C6-C5	3.65	1.39	1.35
41	L5	3818	UY1	O4-C4	-3.64	1.16	1.23
41	L5	5010	PSU	C6-C5	3.63	1.39	1.35
20	S2	1850	MA6	O4'-C1'	-3.62	1.33	1.42
20	S2	1367	PSU	C6-C5	3.58	1.39	1.35
41	L5	4296	PSU	C6-C5	3.58	1.39	1.35
20	S2	93	PSU	C6-C5	3.58	1.39	1.35
20	S2	814	PSU	C6-C5	3.58	1.39	1.35
20	S2	1244	PSU	C6-C5	3.56	1.39	1.35
41	L5	1782	PSU	C6-C5	3.56	1.39	1.35
20	S2	1248	B8N	C1'-C5	3.55	1.58	1.50
43	L8	55	PSU	C6-C5	3.55	1.39	1.35
41	L5	1860	PSU	C6-C5	3.55	1.39	1.35
20	S2	866	PSU	C6-C5	3.55	1.39	1.35
20	S2	651	PSU	C6-C5	3.55	1.39	1.35
20	S2	668	A2M	O5'-C5'	-3.55	1.33	1.44
20	S2	1232	PSU	C6-C5	3.53	1.39	1.35
20	S2	1045	PSU	C6-C5	3.52	1.39	1.35
41	L5	4532	PSU	C6-C5	3.52	1.39	1.35
20	S2	966	PSU	C6-C5	3.48	1.39	1.35
43	L8	69	PSU	C6-C5	3.47	1.39	1.35
41	L5	4500	PSU	C6-C5	3.47	1.39	1.35
20	S2	109	PSU	C6-C5	3.47	1.39	1.35
41	L5	4628	PSU	C6-C5	3.47	1.39	1.35
41	L5	1582	PSU	C6-C5	3.46	1.39	1.35
20	S2	1046	PSU	C6-C5	3.46	1.39	1.35
20	S2	99	A2M	O5'-C5'	-3.46	1.34	1.44
41	L5	1862	PSU	C6-C5	3.45	1.39	1.35
41	L5	3853	PSU	C6-C5	3.45	1.39	1.35
20	S2	105	PSU	C6-C5	3.44	1.39	1.35
20	S2	1004	PSU	C6-C5	3.44	1.39	1.35
41	L5	4431	PSU	C6-C5	3.44	1.39	1.35
41	L5	3844	PSU	C6-C5	3.43	1.39	1.35
41	L5	3851	PSU	C6-C5	3.43	1.39	1.35
41	L5	1683	PSU	C6-C5	3.43	1.39	1.35
41	L5	4493	PSU	C6-C5	3.42	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	L5	3637	PSU	C6-C5	3.42	1.39	1.35
41	L5	1323	A2M	O5'-C5'	-3.42	1.34	1.44
20	S2	1056	PSU	C6-C5	3.41	1.39	1.35
41	L5	4312	PSU	C6-C5	3.41	1.39	1.35
20	S2	468	A2M	O5'-C5'	-3.41	1.34	1.44
20	S2	686	PSU	C6-C5	3.40	1.39	1.35
41	L5	3822	PSU	C6-C5	3.40	1.39	1.35
20	S2	576	A2M	O5'-C5'	-3.40	1.34	1.44
41	L5	3825	A2M	O5'-C5'	-3.40	1.34	1.44
20	S2	1177	PSU	C6-C5	3.40	1.39	1.35
41	L5	1781	PSU	C6-C5	3.39	1.39	1.35
41	L5	3718	A2M	O5'-C5'	-3.39	1.34	1.44
41	L5	4293	PSU	C6-C5	3.39	1.39	1.35
41	L5	400	A2M	O5'-C5'	-3.38	1.34	1.44
41	L5	4361	PSU	C6-C5	3.37	1.39	1.35
20	S2	1081	PSU	C6-C5	3.36	1.39	1.35
41	L5	3695	PSU	C6-C5	3.36	1.39	1.35
41	L5	4576	PSU	C6-C5	3.36	1.39	1.35
41	L5	1871	A2M	O5'-C5'	-3.36	1.34	1.44
41	L5	4457	PSU	C6-C5	3.36	1.39	1.35
20	S2	1383	A2M	O5'-C5'	-3.36	1.34	1.44
20	S2	166	A2M	O5'-C5'	-3.35	1.34	1.44
41	L5	4471	PSU	C6-C5	3.35	1.39	1.35
20	S2	1031	A2M	O5'-C5'	-3.35	1.34	1.44
41	L5	2401	A2M	O5'-C5'	-3.35	1.34	1.44
41	L5	1326	A2M	O5'-C5'	-3.34	1.34	1.44
41	L5	2839	PSU	C6-C5	3.33	1.39	1.35
41	L5	3785	A2M	O5'-C5'	-3.33	1.34	1.44
41	L5	1792	PSU	C6-C5	3.33	1.39	1.35
41	L5	3830	A2M	O5'-C5'	-3.33	1.34	1.44
41	L5	4973	PSU	C6-C5	3.32	1.39	1.35
20	S2	484	A2M	O5'-C5'	-3.32	1.34	1.44
41	L5	4636	PSU	C6-C5	3.32	1.39	1.35
41	L5	1534	A2M	O5'-C5'	-3.31	1.34	1.44
41	L5	4442	PSU	C6-C5	3.30	1.38	1.35
41	L5	4972	PSU	C6-C5	3.30	1.38	1.35
41	L5	1744	PSU	C6-C5	3.30	1.38	1.35
41	L5	4673	PSU	C6-C5	3.30	1.38	1.35
41	L5	1677	PSU	C6-C5	3.29	1.38	1.35
41	L5	398	A2M	O5'-C5'	-3.29	1.34	1.44
41	L5	3639	PSU	C6-C5	3.29	1.38	1.35
41	L5	5001	PSU	C6-C5	3.28	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	L5	1536	PSU	C6-C5	3.28	1.38	1.35
41	L5	4299	PSU	C6-C5	3.28	1.38	1.35
41	L5	4571	A2M	O5'-C5'	-3.28	1.34	1.44
20	S2	406	PSU	C6-C5	3.28	1.38	1.35
20	S2	1174	PSU	C6-C5	3.28	1.38	1.35
20	S2	863	PSU	C6-C5	3.27	1.38	1.35
41	L5	4353	PSU	C6-C5	3.26	1.38	1.35
41	L5	2787	A2M	O5'-C5'	-3.26	1.34	1.44
41	L5	4220	6MZ	C5-N7	-3.26	1.33	1.39
41	L5	3920	PSU	C6-C5	3.26	1.38	1.35
41	L5	4403	PSU	C6-C5	3.25	1.38	1.35
41	L5	4523	A2M	O5'-C5'	-3.25	1.34	1.44
41	L5	1524	A2M	O5'-C5'	-3.25	1.34	1.44
41	L5	2815	A2M	O5'-C5'	-3.25	1.34	1.44
20	S2	27	A2M	O5'-C5'	-3.25	1.34	1.44
41	L5	2363	A2M	O5'-C5'	-3.24	1.34	1.44
41	L5	3818	UY1	O2-C2	-3.24	1.16	1.23
41	L5	4220	6MZ	C5-C4	-3.24	1.33	1.39
20	S2	159	A2M	O5'-C5'	-3.23	1.34	1.44
41	L5	4579	PSU	C6-C5	3.22	1.38	1.35
41	L5	3818	UY1	C1'-C5	3.22	1.57	1.50
41	L5	4521	PSU	C6-C5	3.22	1.38	1.35
41	L5	4552	PSU	C6-C5	3.21	1.38	1.35
41	L5	3867	A2M	O5'-C5'	-3.19	1.34	1.44
41	L5	4590	A2M	O5'-C5'	-3.18	1.34	1.44
20	S2	1832	6MZ	C5-N7	-3.18	1.33	1.39
20	S2	1850	MA6	C6-N6	3.13	1.45	1.36
20	S2	1832	6MZ	C5-C4	-3.12	1.33	1.39
41	L5	4689	PSU	C6-C5	3.12	1.38	1.35
41	L5	3884	PSU	C6-C5	3.11	1.38	1.35
20	S2	1832	6MZ	C2'-C1'	3.09	1.63	1.53
20	S2	681	PSU	C6-C5	3.07	1.38	1.35
20	S2	1639	G7M	C2-N1	2.94	1.44	1.37
20	S2	1832	6MZ	C8-N9	-2.93	1.32	1.37
41	L5	4220	6MZ	C8-N9	-2.92	1.32	1.37
20	S2	1851	MA6	C6-N6	2.91	1.44	1.36
20	S2	1326	OMU	C5-C4	2.89	1.50	1.43
20	S2	1288	OMU	C5-C4	2.88	1.49	1.43
20	S2	172	OMU	C5-C4	2.84	1.49	1.43
20	S2	1850	MA6	O3'-C3'	2.84	1.50	1.43
20	S2	1442	OMU	C5-C4	2.83	1.49	1.43
20	S2	354	OMU	C5-C4	2.83	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	S2	428	OMU	C5-C4	2.80	1.49	1.43
20	S2	627	OMU	C5-C4	2.78	1.49	1.43
20	S2	799	OMU	C5-C4	2.78	1.49	1.43
20	S2	1288	OMU	C6-N1	2.76	1.44	1.38
20	S2	116	OMU	C5-C4	2.74	1.49	1.43
41	L5	4498	OMU	C5-C4	2.74	1.49	1.43
41	L5	4227	OMU	C5-C4	2.74	1.49	1.43
20	S2	121	OMU	C5-C4	2.73	1.49	1.43
41	L5	3925	OMU	C5-C4	2.72	1.49	1.43
20	S2	799	OMU	C6-N1	2.72	1.44	1.38
41	L5	2837	OMU	C5-C4	2.69	1.49	1.43
41	L5	4620	OMU	C5-C4	2.67	1.49	1.43
20	S2	1442	OMU	C6-N1	2.66	1.44	1.38
41	L5	4306	OMU	C5-C4	2.64	1.49	1.43
41	L5	4498	OMU	C6-N1	2.61	1.44	1.38
41	L5	2837	OMU	C6-N1	2.61	1.44	1.38
20	S2	121	OMU	C6-N1	2.61	1.44	1.38
20	S2	354	OMU	C6-N1	2.60	1.44	1.38
20	S2	1326	OMU	C6-N1	2.59	1.44	1.38
20	S2	428	OMU	C6-N1	2.58	1.44	1.38
20	S2	627	OMU	C6-N1	2.58	1.44	1.38
20	S2	172	OMU	C6-N1	2.58	1.44	1.38
20	S2	668	A2M	O4'-C4'	-2.57	1.39	1.45
41	L5	4530	UR3	O2-C2	-2.57	1.17	1.22
41	L5	4227	OMU	C6-N1	2.57	1.44	1.38
41	L5	3925	OMU	C6-N1	2.56	1.44	1.38
20	S2	1832	6MZ	O3'-C3'	2.55	1.49	1.43
20	S2	116	OMU	C6-N1	2.55	1.44	1.38
41	L5	4530	UR3	C6-N1	2.53	1.44	1.38
20	S2	1639	G7M	C6-N1	2.53	1.43	1.38
20	S2	1639	G7M	O6-C6	-2.52	1.18	1.23
41	L5	4306	OMU	C6-N1	2.50	1.44	1.38
41	L5	4620	OMU	C6-N1	2.48	1.44	1.38
20	S2	1850	MA6	C2'-C1'	2.41	1.61	1.53
20	S2	1851	MA6	C5-C4	-2.36	1.34	1.39
41	L5	4530	UR3	C3U-N3	2.31	1.51	1.47
41	L5	4530	UR3	C5-C4	2.29	1.49	1.43
41	L5	1323	A2M	O4'-C4'	-2.25	1.40	1.45
41	L5	4220	6MZ	C6-N1	-2.20	1.31	1.35
20	S2	1832	6MZ	C6-N1	-2.18	1.31	1.35
41	L5	4673	PSU	C4-C5	-2.18	1.38	1.44
20	S2	1850	MA6	C5-C4	-2.18	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	L5	3867	A2M	O4'-C4'	-2.15	1.40	1.45
20	S2	1639	G7M	C4-N9	-2.14	1.32	1.38
41	L5	4403	PSU	O4'-C1'	-2.14	1.40	1.43
41	L5	1524	A2M	O4'-C4'	-2.13	1.40	1.45
41	L5	3822	PSU	O4'-C1'	-2.09	1.41	1.43
41	L5	4628	PSU	C4-C5	-2.07	1.38	1.44
20	S2	1248	B8N	O4'-C1'	-2.05	1.41	1.43
41	L5	4442	PSU	C4-C5	-2.05	1.38	1.44
41	L5	4293	PSU	C4-C5	-2.04	1.38	1.44
41	L5	1536	PSU	C4-C5	-2.03	1.38	1.44
41	L5	3818	UY1	C4-C5	2.03	1.50	1.44
41	L5	1744	PSU	C4-C5	-2.02	1.38	1.44
41	L5	4521	PSU	C4-C5	-2.02	1.38	1.44
41	L5	400	A2M	O4'-C4'	-2.02	1.40	1.45
41	L5	1326	A2M	O4'-C4'	-2.02	1.40	1.45
41	L5	1860	PSU	C4-C5	-2.02	1.38	1.44
41	L5	4523	A2M	O3'-C3'	-2.01	1.38	1.43
41	L5	1683	PSU	C4-C5	-2.01	1.38	1.44
41	L5	4442	PSU	O4'-C1'	-2.01	1.41	1.43
41	L5	4403	PSU	C4-C5	-2.00	1.38	1.44
41	L5	3639	PSU	C4-C5	-2.00	1.38	1.44

All (721) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	S2	1851	MA6	N1-C6-N6	-12.03	102.20	116.86
20	S2	1850	MA6	N1-C6-N6	-12.02	102.22	116.86
20	S2	1850	MA6	C5-C6-N6	8.12	138.19	125.33
20	S2	1851	MA6	C5-C6-N6	7.70	137.52	125.33
20	S2	1639	G7M	C1'-N9-C4	6.51	145.71	126.49
20	S2	1639	G7M	C1'-N9-C8	-6.44	104.98	126.74
41	L5	4227	OMU	C4-N3-C2	-5.86	119.33	126.61
41	L5	3925	OMU	C4-N3-C2	-5.81	119.39	126.61
20	S2	1326	OMU	C4-N3-C2	-5.79	119.43	126.61
20	S2	627	OMU	C4-N3-C2	-5.74	119.49	126.61
41	L5	4530	UR3	C4-N3-C2	-5.73	119.97	124.58
20	S2	121	OMU	C4-N3-C2	-5.69	119.55	126.61
20	S2	1832	6MZ	N1-C2-N3	-5.69	119.97	128.58
41	L5	4620	OMU	C4-N3-C2	-5.68	119.56	126.61
20	S2	428	OMU	C4-N3-C2	-5.67	119.57	126.61
20	S2	354	OMU	C4-N3-C2	-5.66	119.58	126.61
41	L5	4498	OMU	C4-N3-C2	-5.66	119.58	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	S2	172	OMU	C4-N3-C2	-5.62	119.64	126.61
41	L5	2837	OMU	C4-N3-C2	-5.62	119.64	126.61
41	L5	4220	6MZ	N1-C2-N3	-5.60	120.11	128.58
20	S2	1442	OMU	C4-N3-C2	-5.51	119.77	126.61
20	S2	1851	MA6	N1-C2-N3	-5.49	120.27	128.58
20	S2	799	OMU	C4-N3-C2	-5.45	119.85	126.61
20	S2	1248	B8N	C5-C4-N3	5.43	126.01	116.15
41	L5	4306	OMU	C4-N3-C2	-5.43	119.88	126.61
20	S2	1850	MA6	N1-C2-N3	-5.39	120.42	128.58
20	S2	1288	OMU	C4-N3-C2	-5.30	120.03	126.61
41	L5	4636	PSU	C4-N3-C2	-5.27	119.11	126.37
41	L5	1677	PSU	C4-N3-C2	-5.23	119.17	126.37
20	S2	1851	MA6	N9-C8-N7	-5.17	106.60	113.94
20	S2	1081	PSU	C4-N3-C2	-5.16	119.26	126.37
41	L5	3639	PSU	C4-N3-C2	-5.14	119.30	126.37
41	L5	3822	PSU	C4-N3-C2	-5.13	119.31	126.37
41	L5	3884	PSU	C4-N3-C2	-5.13	119.31	126.37
20	S2	863	PSU	C4-N3-C2	-5.12	119.32	126.37
41	L5	2632	PSU	N1-C2-N3	5.12	120.57	115.17
41	L5	4293	PSU	C4-N3-C2	-5.11	119.33	126.37
41	L5	3853	PSU	C4-N3-C2	-5.10	119.34	126.37
41	L5	4353	PSU	C4-N3-C2	-5.10	119.34	126.37
20	S2	1850	MA6	N9-C8-N7	-5.10	106.70	113.94
20	S2	1248	B8N	C4-N3-C2	-5.10	119.35	125.62
20	S2	1174	PSU	C4-N3-C2	-5.10	119.35	126.37
41	L5	4628	PSU	C4-N3-C2	-5.10	119.35	126.37
41	L5	4673	PSU	C4-N3-C2	-5.08	119.37	126.37
41	L5	3637	PSU	N1-C2-N3	5.07	120.52	115.17
41	L5	1536	PSU	N1-C2-N3	5.06	120.50	115.17
20	S2	1081	PSU	N1-C2-N3	5.06	120.50	115.17
41	L5	3853	PSU	N1-C2-N3	5.05	120.50	115.17
20	S2	116	OMU	C4-N3-C2	-5.05	120.34	126.61
41	L5	4689	PSU	C4-N3-C2	-5.04	119.43	126.37
41	L5	3822	PSU	N1-C2-N3	5.04	120.48	115.17
41	L5	4471	PSU	C4-N3-C2	-5.04	119.43	126.37
41	L5	4973	PSU	C4-N3-C2	-5.04	119.43	126.37
20	S2	406	PSU	C4-N3-C2	-5.03	119.44	126.37
20	S2	866	PSU	C4-N3-C2	-5.03	119.44	126.37
41	L5	4521	PSU	C4-N3-C2	-5.02	119.45	126.37
41	L5	1744	PSU	C4-N3-C2	-5.02	119.45	126.37
20	S2	686	PSU	C4-N3-C2	-5.02	119.46	126.37
41	L5	4493	PSU	C4-N3-C2	-5.01	119.47	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	1677	PSU	N1-C2-N3	5.01	120.45	115.17
41	L5	5001	PSU	C4-N3-C2	-5.01	119.47	126.37
41	L5	3695	PSU	N1-C2-N3	5.01	120.45	115.17
41	L5	4500	PSU	N1-C2-N3	5.00	120.45	115.17
41	L5	4689	PSU	N1-C2-N3	5.00	120.45	115.17
41	L5	1536	PSU	C4-N3-C2	-5.00	119.48	126.37
41	L5	3695	PSU	C4-N3-C2	-5.00	119.49	126.37
20	S2	681	PSU	C4-N3-C2	-5.00	119.49	126.37
20	S2	651	PSU	C4-N3-C2	-5.00	119.49	126.37
41	L5	3639	PSU	N1-C2-N3	4.99	120.43	115.17
41	L5	2632	PSU	C4-N3-C2	-4.99	119.50	126.37
41	L5	3818	UY1	C4-N3-C2	-4.98	119.50	126.37
41	L5	4296	PSU	C4-N3-C2	-4.98	119.51	126.37
41	L5	3844	PSU	C4-N3-C2	-4.98	119.51	126.37
41	L5	4673	PSU	N1-C2-N3	4.98	120.42	115.17
41	L5	1860	PSU	C4-N3-C2	-4.97	119.52	126.37
41	L5	3851	PSU	C4-N3-C2	-4.97	119.53	126.37
41	L5	4500	PSU	C4-N3-C2	-4.97	119.53	126.37
41	L5	2839	PSU	C4-N3-C2	-4.97	119.53	126.37
41	L5	3884	PSU	N1-C2-N3	4.96	120.40	115.17
43	L8	55	PSU	C4-N3-C2	-4.96	119.54	126.37
41	L5	1744	PSU	N1-C2-N3	4.96	120.40	115.17
41	L5	1683	PSU	C4-N3-C2	-4.96	119.54	126.37
41	L5	3844	PSU	N1-C2-N3	4.95	120.39	115.17
20	S2	109	PSU	C4-N3-C2	-4.95	119.55	126.37
20	S2	649	PSU	C4-N3-C2	-4.95	119.55	126.37
41	L5	4403	PSU	C4-N3-C2	-4.95	119.55	126.37
41	L5	3920	PSU	N1-C2-N3	4.95	120.39	115.17
20	S2	1045	PSU	C4-N3-C2	-4.95	119.56	126.37
41	L5	4628	PSU	N1-C2-N3	4.94	120.38	115.17
20	S2	866	PSU	N1-C2-N3	4.94	120.38	115.17
41	L5	5010	PSU	C4-N3-C2	-4.94	119.57	126.37
41	L5	4972	PSU	C4-N3-C2	-4.94	119.57	126.37
20	S2	1244	PSU	C4-N3-C2	-4.94	119.57	126.37
41	L5	4442	PSU	N1-C2-N3	4.94	120.37	115.17
20	S2	1232	PSU	C4-N3-C2	-4.93	119.58	126.37
41	L5	3637	PSU	C4-N3-C2	-4.93	119.58	126.37
20	S2	1232	PSU	N1-C2-N3	4.93	120.37	115.17
41	L5	3920	PSU	C4-N3-C2	-4.93	119.58	126.37
20	S2	651	PSU	N1-C2-N3	4.93	120.37	115.17
20	S2	406	PSU	N1-C2-N3	4.93	120.36	115.17
41	L5	2839	PSU	N1-C2-N3	4.93	120.36	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	L8	55	PSU	N1-C2-N3	4.92	120.36	115.17
41	L5	4299	PSU	C4-N3-C2	-4.92	119.59	126.37
41	L5	1862	PSU	N1-C2-N3	4.92	120.36	115.17
20	S2	814	PSU	C4-N3-C2	-4.92	119.60	126.37
41	L5	4296	PSU	N1-C2-N3	4.92	120.36	115.17
41	L5	4471	PSU	N1-C2-N3	4.92	120.36	115.17
41	L5	4973	PSU	N1-C2-N3	4.92	120.36	115.17
41	L5	4636	PSU	N1-C2-N3	4.92	120.35	115.17
41	L5	4579	PSU	C4-N3-C2	-4.91	119.60	126.37
41	L5	4361	PSU	N1-C2-N3	4.91	120.35	115.17
20	S2	1367	PSU	C4-N3-C2	-4.91	119.61	126.37
41	L5	5010	PSU	N1-C2-N3	4.91	120.34	115.17
41	L5	4431	PSU	C4-N3-C2	-4.91	119.61	126.37
41	L5	4552	PSU	C4-N3-C2	-4.90	119.62	126.37
41	L5	1792	PSU	N1-C2-N3	4.90	120.34	115.17
20	S2	966	PSU	C4-N3-C2	-4.90	119.62	126.37
20	S2	1367	PSU	N1-C2-N3	4.90	120.33	115.17
41	L5	4442	PSU	C4-N3-C2	-4.90	119.63	126.37
41	L5	4493	PSU	N1-C2-N3	4.89	120.33	115.17
41	L5	1781	PSU	N1-C2-N3	4.89	120.33	115.17
41	L5	4353	PSU	N1-C2-N3	4.89	120.33	115.17
20	S2	1056	PSU	N1-C2-N3	4.89	120.33	115.17
41	L5	5001	PSU	N1-C2-N3	4.89	120.33	115.17
41	L5	4579	PSU	N1-C2-N3	4.89	120.32	115.17
20	S2	109	PSU	N1-C2-N3	4.87	120.31	115.17
41	L5	1860	PSU	N1-C2-N3	4.87	120.31	115.17
43	L8	69	PSU	N1-C2-N3	4.87	120.31	115.17
41	L5	4403	PSU	N1-C2-N3	4.87	120.31	115.17
41	L5	4293	PSU	N1-C2-N3	4.87	120.30	115.17
20	S2	1244	PSU	N1-C2-N3	4.87	120.30	115.17
41	L5	1792	PSU	C4-N3-C2	-4.87	119.67	126.37
20	S2	1177	PSU	C4-N3-C2	-4.86	119.67	126.37
41	L5	1582	PSU	C4-N3-C2	-4.86	119.67	126.37
20	S2	105	PSU	N1-C2-N3	4.86	120.30	115.17
20	S2	686	PSU	N1-C2-N3	4.86	120.30	115.17
41	L5	1782	PSU	N1-C2-N3	4.86	120.29	115.17
41	L5	4431	PSU	N1-C2-N3	4.86	120.29	115.17
41	L5	4552	PSU	N1-C2-N3	4.86	120.29	115.17
20	S2	1045	PSU	N1-C2-N3	4.85	120.28	115.17
20	S2	681	PSU	N1-C2-N3	4.85	120.28	115.17
41	L5	1683	PSU	N1-C2-N3	4.85	120.28	115.17
20	S2	1056	PSU	C4-N3-C2	-4.85	119.69	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	1862	PSU	C4-N3-C2	-4.85	119.69	126.37
41	L5	1782	PSU	C4-N3-C2	-4.85	119.70	126.37
41	L5	1781	PSU	C4-N3-C2	-4.83	119.72	126.37
41	L5	4299	PSU	N1-C2-N3	4.82	120.25	115.17
20	S2	863	PSU	N1-C2-N3	4.81	120.24	115.17
20	S2	801	PSU	N1-C2-N3	4.81	120.24	115.17
41	L5	4457	PSU	N1-C2-N3	4.81	120.24	115.17
41	L5	4521	PSU	N1-C2-N3	4.81	120.24	115.17
43	L8	69	PSU	C4-N3-C2	-4.81	119.75	126.37
41	L5	4312	PSU	C4-N3-C2	-4.80	119.76	126.37
41	L5	4361	PSU	C4-N3-C2	-4.79	119.77	126.37
20	S2	1174	PSU	N1-C2-N3	4.79	120.22	115.17
41	L5	4457	PSU	C4-N3-C2	-4.78	119.78	126.37
41	L5	4532	PSU	N1-C2-N3	4.78	120.21	115.17
41	L5	4532	PSU	C4-N3-C2	-4.77	119.80	126.37
20	S2	1832	6MZ	N9-C8-N7	-4.76	107.18	113.94
41	L5	4312	PSU	N1-C2-N3	4.75	120.17	115.17
20	S2	105	PSU	C4-N3-C2	-4.74	119.83	126.37
20	S2	1004	PSU	C4-N3-C2	-4.74	119.84	126.37
41	L5	1582	PSU	N1-C2-N3	4.74	120.17	115.17
41	L5	4972	PSU	N1-C2-N3	4.73	120.16	115.17
41	L5	3851	PSU	N1-C2-N3	4.73	120.16	115.17
20	S2	1177	PSU	N1-C2-N3	4.72	120.15	115.17
41	L5	4220	6MZ	C9-N6-C6	-4.72	118.47	122.85
20	S2	966	PSU	N1-C2-N3	4.72	120.14	115.17
41	L5	4220	6MZ	N9-C8-N7	-4.69	107.29	113.94
20	S2	1046	PSU	N1-C2-N3	4.68	120.10	115.17
20	S2	814	PSU	N1-C2-N3	4.67	120.09	115.17
20	S2	93	PSU	C4-N3-C2	-4.67	119.94	126.37
20	S2	93	PSU	N1-C2-N3	4.66	120.09	115.17
20	S2	1850	MA6	C5-C4-N3	-4.66	120.30	126.72
41	L5	4220	6MZ	C5-C4-N3	-4.65	120.31	126.72
20	S2	1046	PSU	C4-N3-C2	-4.64	119.98	126.37
20	S2	649	PSU	N1-C2-N3	4.64	120.06	115.17
20	S2	1004	PSU	N1-C2-N3	4.63	120.06	115.17
41	L5	4576	PSU	N1-C2-N3	4.63	120.05	115.17
20	S2	1851	MA6	C5-C4-N3	-4.62	120.36	126.72
20	S2	801	PSU	C4-N3-C2	-4.62	120.01	126.37
41	L5	4576	PSU	C4-N3-C2	-4.56	120.09	126.37
20	S2	1639	G7M	C2-N3-C4	4.48	120.02	112.30
20	S2	1832	6MZ	C5-C4-N3	-4.48	120.55	126.72
41	L5	3818	UY1	N1-C2-N3	4.41	119.82	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	3925	OMU	N3-C2-N1	4.21	120.37	114.89
20	S2	1850	MA6	C3'-C2'-C1'	4.13	109.28	101.46
41	L5	2837	OMU	N3-C2-N1	4.06	120.18	114.89
20	S2	121	OMU	N3-C2-N1	4.04	120.15	114.89
20	S2	1639	G7M	C5-C6-N1	4.03	120.18	111.84
20	S2	1288	OMU	N3-C2-N1	4.01	120.12	114.89
20	S2	354	OMU	N3-C2-N1	4.01	120.11	114.89
41	L5	4227	OMU	N3-C2-N1	4.00	120.10	114.89
20	S2	1851	MA6	C4-N9-C8	3.99	109.92	105.74
41	L5	398	A2M	C3'-C2'-C1'	-3.98	95.19	102.81
41	L5	4498	OMU	N3-C2-N1	3.95	120.03	114.89
41	L5	1534	A2M	C3'-C2'-C1'	-3.94	95.26	102.81
20	S2	1850	MA6	C4-C5-C6	3.94	119.98	115.91
20	S2	1326	OMU	N3-C2-N1	3.90	119.96	114.89
20	S2	1383	A2M	C3'-C2'-C1'	-3.88	95.38	102.81
20	S2	1639	G7M	C5-C4-N3	-3.86	120.85	128.15
41	L5	2363	A2M	C2'-C1'-N9	3.85	120.09	113.75
20	S2	172	OMU	N3-C2-N1	3.84	119.89	114.89
20	S2	1850	MA6	C4-N9-C8	3.80	109.73	105.74
41	L5	4620	OMU	C5-C4-N3	3.79	120.11	114.80
41	L5	4306	OMU	N3-C2-N1	3.79	119.83	114.89
20	S2	627	OMU	C5-C4-N3	3.79	120.11	114.80
20	S2	428	OMU	N3-C2-N1	3.76	119.78	114.89
41	L5	4227	OMU	C5-C4-N3	3.74	120.04	114.80
20	S2	627	OMU	N3-C2-N1	3.73	119.75	114.89
41	L5	4530	UR3	C5-C4-N3	3.73	119.95	115.04
20	S2	1442	OMU	N3-C2-N1	3.72	119.74	114.89
41	L5	4620	OMU	N3-C2-N1	3.72	119.73	114.89
20	S2	799	OMU	C5-C4-N3	3.70	119.98	114.80
20	S2	116	OMU	N3-C2-N1	3.69	119.70	114.89
20	S2	428	OMU	C5-C4-N3	3.68	119.96	114.80
20	S2	1851	MA6	C4-C5-C6	3.64	119.67	115.91
20	S2	1442	OMU	C5-C4-N3	3.64	119.89	114.80
20	S2	799	OMU	N3-C2-N1	3.64	119.63	114.89
41	L5	3925	OMU	C5-C4-N3	3.61	119.85	114.80
20	S2	1326	OMU	C5-C4-N3	3.60	119.85	114.80
20	S2	121	OMU	C5-C4-N3	3.60	119.84	114.80
41	L5	2837	OMU	C5-C4-N3	3.59	119.82	114.80
20	S2	576	A2M	C3'-C2'-C1'	-3.57	95.96	102.81
41	L5	4498	OMU	C5-C4-N3	3.55	119.78	114.80
20	S2	1851	MA6	N3-C4-N9	3.55	133.20	127.17
20	S2	354	OMU	C5-C4-N3	3.54	119.76	114.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	S2	576	A2M	O3'-C3'-C2'	3.52	121.05	111.19
20	S2	172	OMU	C5-C4-N3	3.51	119.72	114.80
41	L5	398	A2M	O3'-C3'-C2'	3.51	121.00	111.19
20	S2	1248	B8N	N3-C2-N1	3.48	120.97	116.72
20	S2	1850	MA6	C2-N1-C6	3.48	120.32	111.83
41	L5	3785	A2M	C3'-C2'-C1'	-3.46	96.19	102.81
20	S2	1639	G7M	O6-C6-C5	-3.42	120.38	128.01
41	L5	4306	OMU	C5-C4-N3	3.40	119.57	114.80
41	L5	3818	UY1	C6-C5-C4	3.39	120.46	118.17
20	S2	1288	OMU	C5-C4-N3	3.37	119.51	114.80
20	S2	1850	MA6	N3-C4-N9	3.36	132.89	127.17
20	S2	1248	B8N	C1'-C5-C4	3.36	122.70	117.61
41	L5	4220	6MZ	C2-N3-C4	3.34	119.98	111.83
41	L5	3718	A2M	C3'-C2'-C1'	-3.32	96.44	102.81
20	S2	1851	MA6	C2-N1-C6	3.31	119.92	111.83
20	S2	1832	6MZ	C2-N3-C4	3.31	119.91	111.83
20	S2	116	OMU	C5-C4-N3	3.30	119.42	114.80
41	L5	3785	A2M	C4'-O4'-C1'	-3.29	102.20	109.47
20	S2	1383	A2M	O3'-C3'-C2'	3.25	120.29	111.19
41	L5	4442	PSU	O2-C2-N1	-3.23	119.46	122.79
41	L5	4220	6MZ	C4-N9-C8	3.22	109.12	105.74
41	L5	4220	6MZ	N3-C4-N9	3.22	132.65	127.17
41	L5	3718	A2M	O3'-C3'-C2'	3.22	120.19	111.19
20	S2	99	A2M	O3'-C3'-C2'	3.20	120.15	111.19
41	L5	1536	PSU	O2-C2-N1	-3.20	119.49	122.79
20	S2	99	A2M	C3'-C2'-C1'	-3.20	96.69	102.81
41	L5	1871	A2M	C3'-C2'-C1'	-3.19	96.70	102.81
20	S2	1832	6MZ	C4-N9-C8	3.19	109.09	105.74
41	L5	3867	A2M	C2'-C1'-N9	3.17	118.97	113.75
41	L5	4628	PSU	O2-C2-N1	-3.16	119.53	122.79
41	L5	1683	PSU	O2-C2-N1	-3.14	119.55	122.79
41	L5	1323	A2M	C2'-C1'-N9	3.14	118.92	113.75
41	L5	2401	A2M	O3'-C3'-C2'	3.14	119.98	111.19
20	S2	1851	MA6	C2-N3-C4	3.14	119.50	111.83
20	S2	484	A2M	O3'-C3'-C2'	3.14	119.98	111.19
20	S2	27	A2M	O3'-C3'-C2'	3.14	119.97	111.19
20	S2	1639	G7M	CN7-N7-C5	3.14	130.71	126.80
20	S2	1850	MA6	C5-N7-C8	3.13	108.38	103.45
20	S2	468	A2M	C3'-C2'-C1'	-3.13	96.81	102.81
41	L5	1524	A2M	O3'-C3'-C2'	3.13	119.94	111.19
41	L5	4523	A2M	C3'-C2'-C1'	-3.12	96.84	102.81
41	L5	4523	A2M	C4-N9-C1'	-3.11	119.36	126.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	4552	PSU	O2-C2-N1	-3.11	119.58	122.79
20	S2	166	A2M	O3'-C3'-C2'	3.11	119.89	111.19
41	L5	4689	PSU	O2-C2-N1	-3.10	119.59	122.79
41	L5	3808	OMC	C1'-N1-C2	3.10	125.28	118.44
20	S2	468	A2M	C4-N9-C1'	-3.10	119.39	126.63
20	S2	1850	MA6	C2-N3-C4	3.09	119.37	111.83
20	S2	1832	6MZ	C5-N7-C8	3.08	108.30	103.45
20	S2	428	OMU	O4-C4-C5	-3.08	119.85	125.16
20	S2	627	OMU	O4-C4-C5	-3.08	119.86	125.16
41	L5	3785	A2M	C4-N9-C1'	-3.07	119.45	126.63
41	L5	4500	PSU	O2-C2-N1	-3.07	119.62	122.79
41	L5	3825	A2M	O3'-C3'-C2'	3.07	119.77	111.19
41	L5	1862	PSU	O2-C2-N1	-3.05	119.64	122.79
41	L5	1744	PSU	O2-C2-N1	-3.05	119.64	122.79
20	S2	799	OMU	O4-C4-C5	-3.05	119.91	125.16
41	L5	2787	A2M	O4'-C1'-C2'	3.04	111.82	106.59
41	L5	5010	PSU	O2-C2-N1	-3.03	119.66	122.79
41	L5	4590	A2M	C3'-C2'-C1'	-3.03	97.01	102.81
20	S2	166	A2M	C4-N9-C1'	-3.03	119.56	126.63
20	S2	668	A2M	C4-N9-C1'	-3.02	119.56	126.63
41	L5	3884	PSU	O2-C2-N1	-3.02	119.67	122.79
41	L5	3830	A2M	C3'-C2'-C1'	-3.02	97.03	102.81
41	L5	4498	OMU	O4-C4-C5	-3.01	119.97	125.16
41	L5	4673	PSU	O2-C2-N1	-3.01	119.69	122.79
20	S2	1851	MA6	C5-N7-C8	3.01	108.18	103.45
20	S2	1056	PSU	O2-C2-N1	-3.01	119.69	122.79
41	L5	4521	PSU	O2-C2-N1	-3.00	119.69	122.79
20	S2	649	PSU	O2-C2-N1	-3.00	119.69	122.79
41	L5	1534	A2M	C4-N9-C1'	-3.00	119.62	126.63
41	L5	2632	PSU	O2-C2-N1	-3.00	119.70	122.79
41	L5	1871	A2M	C4-N9-C1'	-3.00	119.63	126.63
41	L5	3822	PSU	O2-C2-N1	-2.99	119.70	122.79
20	S2	1031	A2M	O3'-C3'-C2'	2.99	119.56	111.19
41	L5	3818	UY1	C6-N1-C2	-2.99	119.92	122.69
41	L5	4361	PSU	O2-C2-N1	-2.99	119.71	122.79
41	L5	4973	PSU	O2-C2-N1	-2.99	119.71	122.79
20	S2	121	OMU	O4-C4-C5	-2.99	120.01	125.16
20	S2	1639	G7M	C2-N1-C6	-2.98	119.70	125.11
41	L5	2837	OMU	O4-C4-C5	-2.98	120.02	125.16
20	S2	1031	A2M	C3'-C2'-C1'	-2.98	97.10	102.81
20	S2	468	A2M	O3'-C3'-C2'	2.97	119.50	111.19
20	S2	1232	PSU	O2-C2-N1	-2.97	119.73	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	2401	A2M	C4-N9-C1'	-2.97	119.69	126.63
41	L5	4620	OMU	O4-C4-C5	-2.96	120.05	125.16
41	L5	3830	A2M	O3'-C3'-C2'	2.96	119.46	111.19
20	S2	1174	PSU	O2-C2-N1	-2.95	119.74	122.79
20	S2	1031	A2M	C4-N9-C1'	-2.95	119.73	126.63
20	S2	1442	OMU	O4-C4-C5	-2.95	120.08	125.16
41	L5	3867	A2M	C4-N9-C1'	-2.95	119.74	126.63
20	S2	1244	PSU	O2-C2-N1	-2.95	119.75	122.79
20	S2	1383	A2M	C4-N9-C1'	-2.95	119.74	126.63
20	S2	1832	6MZ	N3-C4-N9	2.95	132.18	127.17
41	L5	1582	PSU	O2-C2-N1	-2.95	119.75	122.79
41	L5	2401	A2M	C3'-C2'-C1'	-2.94	97.18	102.81
41	L5	1860	PSU	O2-C2-N1	-2.93	119.77	122.79
43	L8	69	PSU	O2-C2-N1	-2.93	119.77	122.79
41	L5	4471	PSU	O2-C2-N1	-2.92	119.77	122.79
20	S2	406	PSU	O2-C2-N1	-2.92	119.78	122.79
41	L5	4227	OMU	O4-C4-C5	-2.92	120.13	125.16
20	S2	354	OMU	O4-C4-C5	-2.91	120.14	125.16
20	S2	801	PSU	O2-C2-N1	-2.91	119.78	122.79
41	L5	4299	PSU	O2-C2-N1	-2.91	119.78	122.79
41	L5	4220	6MZ	C4-C5-C6	2.91	119.20	116.78
41	L5	3925	OMU	O4-C4-C5	-2.91	120.14	125.16
41	L5	4590	A2M	O3'-C3'-C2'	2.90	119.31	111.19
41	L5	3853	PSU	O2-C2-N1	-2.90	119.80	122.79
41	L5	4403	PSU	O2-C2-N1	-2.89	119.81	122.79
20	S2	27	A2M	C3'-C2'-C1'	-2.89	97.28	102.81
20	S2	866	PSU	O2-C2-N1	-2.89	119.81	122.79
20	S2	105	PSU	O2-C2-N1	-2.88	119.81	122.79
41	L5	400	A2M	O3'-C3'-C2'	2.88	119.25	111.19
20	S2	863	PSU	O2-C2-N1	-2.88	119.82	122.79
41	L5	1534	A2M	C1'-N9-C8	2.88	133.48	127.09
20	S2	1081	PSU	O2-C2-N1	-2.88	119.82	122.79
20	S2	166	A2M	C3'-C2'-C1'	-2.88	97.30	102.81
41	L5	1677	PSU	O2-C2-N1	-2.87	119.83	122.79
41	L5	4576	PSU	O2-C2-N1	-2.87	119.83	122.79
20	S2	172	OMU	O4-C4-C5	-2.87	120.22	125.16
41	L5	2839	PSU	O2-C2-N1	-2.87	119.83	122.79
41	L5	4353	PSU	O2-C2-N1	-2.86	119.83	122.79
41	L5	3920	PSU	O2-C2-N1	-2.86	119.84	122.79
41	L5	1781	PSU	O2-C2-N1	-2.86	119.84	122.79
20	S2	1639	G7M	N9-C4-N3	2.86	131.67	125.95
20	S2	1832	6MZ	C4-C5-C6	2.85	119.15	116.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	5001	PSU	O2-C2-N1	-2.85	119.85	122.79
41	L5	4312	PSU	O2-C2-N1	-2.85	119.85	122.79
20	S2	668	A2M	O4'-C1'-C2'	2.85	111.49	106.59
41	L5	4220	6MZ	C5-N7-C8	2.84	107.92	103.45
41	L5	1782	PSU	O2-C2-N1	-2.84	119.86	122.79
41	L5	4590	A2M	C4-N9-C1'	-2.84	120.00	126.63
20	S2	468	A2M	C1'-N9-C8	2.84	133.39	127.09
41	L5	2861	OMC	C1'-N1-C2	2.83	124.69	118.44
41	L5	4579	PSU	O2-C2-N1	-2.83	119.87	122.79
41	L5	3830	A2M	C4-N9-C1'	-2.83	120.01	126.63
20	S2	109	PSU	O2-C2-N1	-2.83	119.87	122.79
20	S2	1367	PSU	O2-C2-N1	-2.83	119.87	122.79
41	L5	398	A2M	C4-N9-C1'	-2.83	120.02	126.63
20	S2	27	A2M	C4-N9-C1'	-2.83	120.02	126.63
41	L5	1323	A2M	C4-N9-C1'	-2.82	120.03	126.63
41	L5	4571	A2M	O3'-C3'-C2'	2.82	119.09	111.19
41	L5	1871	A2M	C1'-N9-C8	2.82	133.36	127.09
20	S2	1326	OMU	O4-C4-C5	-2.82	120.30	125.16
20	S2	651	PSU	O2-C2-N1	-2.82	119.88	122.79
41	L5	3785	A2M	C1'-N9-C8	2.82	133.34	127.09
41	L5	4972	PSU	O2-C2-N1	-2.82	119.89	122.79
41	L5	4296	PSU	O2-C2-N1	-2.81	119.89	122.79
20	S2	686	PSU	O2-C2-N1	-2.81	119.89	122.79
20	S2	1177	PSU	O2-C2-N1	-2.81	119.89	122.79
41	L5	3844	PSU	O2-C2-N1	-2.81	119.89	122.79
43	L8	55	PSU	O2-C2-N1	-2.80	119.90	122.79
41	L5	3785	A2M	O3'-C3'-C2'	2.80	119.02	111.19
20	S2	1046	PSU	O2-C2-N1	-2.80	119.90	122.79
20	S2	681	PSU	O2-C2-N1	-2.80	119.91	122.79
41	L5	2787	A2M	O3'-C3'-C2'	2.79	119.00	111.19
41	L5	3637	PSU	O2-C2-N1	-2.79	119.91	122.79
41	L5	4571	A2M	C3'-C2'-C1'	-2.79	97.47	102.81
41	L5	3639	PSU	O2-C2-N1	-2.79	119.92	122.79
41	L5	1326	A2M	O3'-C3'-C2'	2.78	118.98	111.19
41	L5	1871	A2M	O3'-C3'-C2'	2.78	118.98	111.19
20	S2	159	A2M	O3'-C3'-C2'	2.78	118.97	111.19
41	L5	4523	A2M	C1'-N9-C8	2.78	133.26	127.09
41	L5	4306	OMU	O4-C4-C5	-2.78	120.38	125.16
41	L5	1792	PSU	O2-C2-N1	-2.77	119.93	122.79
20	S2	166	A2M	C1'-N9-C8	2.77	133.25	127.09
41	L5	4532	PSU	O2-C2-N1	-2.77	119.93	122.79
20	S2	668	A2M	O3'-C3'-C2'	2.77	118.94	111.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	S2	159	A2M	C3'-C2'-C1'	-2.77	97.51	102.81
41	L5	4571	A2M	C4-N9-C1'	-2.76	120.17	126.63
41	L5	2401	A2M	C1'-N9-C8	2.76	133.23	127.09
41	L5	3867	A2M	C1'-N9-C8	2.76	133.22	127.09
41	L5	4293	PSU	O2-C2-N1	-2.76	119.94	122.79
20	S2	668	A2M	C1'-N9-C8	2.76	133.22	127.09
20	S2	159	A2M	C4-N9-C1'	-2.75	120.19	126.63
41	L5	4431	PSU	O2-C2-N1	-2.75	119.95	122.79
41	L5	3825	A2M	C3'-C2'-C1'	-2.74	97.56	102.81
41	L5	1326	A2M	C4-N9-C1'	-2.74	120.23	126.63
20	S2	1248	B8N	O4-C4-N3	-2.74	115.54	119.99
41	L5	3851	PSU	O2-C2-N1	-2.73	119.97	122.79
41	L5	1323	A2M	O4'-C1'-C2'	2.73	111.29	106.59
41	L5	3718	A2M	C4-N9-C1'	-2.73	120.25	126.63
41	L5	1534	A2M	O3'-C3'-C2'	2.73	118.82	111.19
20	S2	116	OMU	O4-C4-C5	-2.73	120.46	125.16
20	S2	814	PSU	O2-C2-N1	-2.73	119.98	122.79
20	S2	1383	A2M	C1'-N9-C8	2.72	133.14	127.09
20	S2	99	A2M	C4-N9-C1'	-2.72	120.28	126.63
20	S2	801	PSU	C6-N1-C2	-2.72	120.17	122.69
41	L5	4576	PSU	C6-N1-C2	-2.72	120.17	122.69
41	L5	1524	A2M	O4'-C1'-C2'	2.72	111.26	106.59
41	L5	2787	A2M	C4-N9-C1'	-2.71	120.30	126.63
41	L5	4457	PSU	O2-C2-N1	-2.71	120.00	122.79
20	S2	1031	A2M	C1'-N9-C8	2.70	133.09	127.09
20	S2	1045	PSU	O2-C2-N1	-2.70	120.00	122.79
41	L5	4442	PSU	C6-N1-C2	-2.70	120.19	122.69
41	L5	4636	PSU	O2-C2-N1	-2.69	120.01	122.79
41	L5	1677	PSU	C6-C5-C4	2.69	119.99	118.17
41	L5	4493	PSU	O2-C2-N1	-2.68	120.02	122.79
41	L5	1534	A2M	C2'-C1'-N9	2.68	118.17	113.75
41	L5	3853	PSU	C6-C5-C4	2.68	119.98	118.17
20	S2	27	A2M	C1'-N9-C8	2.68	133.04	127.09
41	L5	3825	A2M	C4-N9-C1'	-2.68	120.36	126.63
41	L5	1536	PSU	C6-N1-C2	-2.67	120.21	122.69
41	L5	4403	PSU	O4'-C1'-C2'	2.67	108.85	105.15
20	S2	1046	PSU	C6-N1-C2	-2.67	120.21	122.69
41	L5	1323	A2M	C1'-N9-C8	2.66	133.00	127.09
41	L5	4689	PSU	C6-N1-C2	-2.66	120.22	122.69
20	S2	1004	PSU	O2-C2-N1	-2.66	120.05	122.79
41	L5	2815	A2M	O3'-C3'-C2'	2.64	118.58	111.19
41	L5	3818	UY1	O2-C2-N1	-2.63	120.08	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	3695	PSU	O2-C2-N1	-2.63	120.08	122.79
20	S2	93	PSU	O2-C2-N1	-2.62	120.09	122.79
20	S2	484	A2M	C4-N9-C1'	-2.62	120.52	126.63
20	S2	99	A2M	C1'-N9-C8	2.61	132.88	127.09
41	L5	4590	A2M	C1'-N9-C8	2.61	132.88	127.09
41	L5	3718	A2M	C1'-N9-C8	2.60	132.87	127.09
20	S2	576	A2M	C4-N9-C1'	-2.60	120.55	126.63
20	S2	1288	OMU	O4-C4-C5	-2.59	120.69	125.16
41	L5	398	A2M	C1'-N9-C8	2.59	132.84	127.09
20	S2	484	A2M	C3'-C2'-C1'	-2.59	97.85	102.81
41	L5	4571	A2M	C1'-N9-C8	2.59	132.83	127.09
41	L5	4220	6MZ	C5-C6-N1	2.58	120.92	118.15
41	L5	4552	PSU	C6-N1-C2	-2.58	120.30	122.69
20	S2	406	PSU	C6-N1-C2	-2.58	120.30	122.69
41	L5	4500	PSU	C6-N1-C2	-2.58	120.30	122.69
41	L5	3830	A2M	C1'-N9-C8	2.57	132.81	127.09
20	S2	1850	MA6	C1'-N9-C8	-2.57	121.39	127.09
43	L8	69	PSU	C6-N1-C2	-2.57	120.31	122.69
20	S2	484	A2M	C1'-N9-C8	2.57	132.79	127.09
20	S2	159	A2M	C1'-N9-C8	2.57	132.79	127.09
41	L5	2839	PSU	C6-N1-C2	-2.56	120.31	122.69
20	S2	966	PSU	O2-C2-N1	-2.56	120.15	122.79
41	L5	400	A2M	C4-N9-C1'	-2.56	120.65	126.63
20	S2	1056	PSU	C6-N1-C2	-2.56	120.32	122.69
41	L5	2632	PSU	C6-N1-C2	-2.55	120.32	122.69
41	L5	1683	PSU	C6-N1-C2	-2.55	120.32	122.69
41	L5	1323	A2M	O3'-C3'-C2'	2.55	118.33	111.19
20	S2	105	PSU	C6-N1-C2	-2.55	120.32	122.69
41	L5	4442	PSU	O4'-C1'-C2'	2.55	108.68	105.15
20	S2	1639	G7M	CN7-N7-C8	-2.54	120.94	124.79
41	L5	5010	PSU	C6-N1-C2	-2.54	120.33	122.69
20	S2	1337	4AC	N4-C4-N3	2.54	117.99	113.87
41	L5	1326	A2M	O4'-C1'-C2'	2.53	110.94	106.59
41	L5	3825	A2M	C1'-N9-C8	2.53	132.71	127.09
41	L5	4457	PSU	C6-N1-C2	-2.53	120.35	122.69
41	L5	4523	A2M	O3'-C3'-C2'	2.52	118.25	111.19
20	S2	1248	B8N	C31-N3-C2	2.52	121.36	117.64
41	L5	4579	PSU	C6-N1-C2	-2.52	120.35	122.69
41	L5	1782	PSU	C6-N1-C2	-2.52	120.35	122.69
41	L5	4312	PSU	C6-N1-C2	-2.52	120.35	122.69
41	L5	2787	A2M	C1'-N9-C8	2.52	132.69	127.09
20	S2	1232	PSU	C6-N1-C2	-2.51	120.36	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	1326	A2M	C1'-N9-C8	2.51	132.67	127.09
41	L5	3920	PSU	C6-N1-C2	-2.51	120.36	122.69
41	L5	4673	PSU	C6-N1-C2	-2.51	120.36	122.69
41	L5	3844	PSU	C6-N1-C2	-2.51	120.36	122.69
41	L5	3822	PSU	O4'-C1'-C2'	2.50	108.61	105.15
20	S2	109	PSU	C6-N1-C2	-2.50	120.37	122.69
41	L5	4361	PSU	C6-N1-C2	-2.49	120.38	122.69
41	L5	1862	PSU	C6-N1-C2	-2.49	120.38	122.69
41	L5	4471	PSU	C6-N1-C2	-2.49	120.38	122.69
41	L5	4227	OMU	O2-C2-N1	-2.49	119.56	122.80
41	L5	2787	A2M	O4'-C4'-C3'	2.49	110.09	105.15
41	L5	3637	PSU	C6-N1-C2	-2.48	120.39	122.69
20	S2	681	PSU	C6-N1-C2	-2.48	120.39	122.69
41	L5	4403	PSU	C6-N1-C2	-2.48	120.39	122.69
20	S2	576	A2M	C1'-N9-C8	2.48	132.60	127.09
20	S2	1177	PSU	C6-N1-C2	-2.47	120.40	122.69
41	L5	1744	PSU	C6-N1-C2	-2.46	120.40	122.69
41	L5	2815	A2M	C2'-C1'-N9	2.46	117.81	113.75
41	L5	1524	A2M	C4-N9-C1'	-2.45	120.90	126.63
20	S2	1326	OMU	O2-C2-N1	-2.45	119.61	122.80
20	S2	1851	MA6	C1'-N9-C8	-2.44	121.67	127.09
41	L5	4431	PSU	C6-N1-C2	-2.44	120.43	122.69
20	S2	1288	OMU	C1'-N1-C2	2.43	121.96	117.59
41	L5	4628	PSU	C6-N1-C2	-2.43	120.44	122.69
41	L5	1781	PSU	C6-N1-C2	-2.43	120.44	122.69
41	L5	4296	PSU	C6-N1-C2	-2.43	120.44	122.69
41	L5	3808	OMC	C1'-N1-C6	-2.43	115.59	120.78
41	L5	4532	PSU	C6-N1-C2	-2.43	120.44	122.69
41	L5	3695	PSU	C6-N1-C2	-2.42	120.45	122.69
41	L5	1860	PSU	C6-N1-C2	-2.42	120.45	122.69
41	L5	400	A2M	C1'-N9-C8	2.42	132.46	127.09
20	S2	1004	PSU	C6-N1-C2	-2.41	120.45	122.69
41	L5	2363	A2M	O4'-C1'-C2'	2.41	110.74	106.59
20	S2	866	PSU	C6-N1-C2	-2.41	120.46	122.69
41	L5	3884	PSU	C6-N1-C2	-2.41	120.46	122.69
20	S2	866	PSU	C6-C5-C4	2.40	119.80	118.17
20	S2	651	PSU	C6-N1-C2	-2.40	120.46	122.69
41	L5	3853	PSU	C6-N1-C2	-2.40	120.46	122.69
41	L5	400	A2M	O4'-C1'-C2'	2.40	110.72	106.59
41	L5	4403	PSU	C6-C5-C4	2.40	119.79	118.17
41	L5	4973	PSU	C6-C5-C4	2.40	119.79	118.17
20	S2	166	A2M	O4'-C1'-C2'	2.40	110.72	106.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	4500	PSU	C6-C5-C4	2.39	119.79	118.17
20	S2	1248	B8N	O4-C4-C5	-2.39	118.45	122.58
41	L5	1744	PSU	C6-C5-C4	2.39	119.78	118.17
41	L5	4523	A2M	O4'-C1'-C2'	2.38	110.69	106.59
20	S2	1244	PSU	C6-N1-C2	-2.38	120.48	122.69
41	L5	3822	PSU	C6-N1-C2	-2.38	120.49	122.69
41	L5	5001	PSU	C6-N1-C2	-2.38	120.49	122.69
20	S2	1367	PSU	C6-N1-C2	-2.37	120.49	122.69
41	L5	1524	A2M	C1'-N9-C8	2.37	132.35	127.09
41	L5	2815	A2M	O4'-C4'-C3'	2.36	109.83	105.15
43	L8	55	PSU	C6-N1-C2	-2.35	120.51	122.69
41	L5	4636	PSU	C6-C5-C4	2.35	119.76	118.17
41	L5	1582	PSU	C6-N1-C2	-2.35	120.51	122.69
41	L5	4293	PSU	C6-C5-C4	2.34	119.76	118.17
20	S2	649	PSU	C6-N1-C2	-2.34	120.52	122.69
41	L5	4299	PSU	C6-N1-C2	-2.34	120.52	122.69
41	L5	4973	PSU	C6-N1-C2	-2.34	120.52	122.69
20	S2	166	A2M	C6-C5-C4	-2.34	113.99	117.18
41	L5	400	A2M	C2'-C1'-N9	2.34	117.60	113.75
41	L5	2632	PSU	C6-C5-C4	2.33	119.75	118.17
41	L5	3822	PSU	C6-C5-C4	2.33	119.75	118.17
41	L5	3639	PSU	C6-N1-C2	-2.32	120.54	122.69
41	L5	4493	PSU	C6-N1-C2	-2.32	120.54	122.69
20	S2	468	A2M	C6-C5-C4	-2.31	114.02	117.18
41	L5	400	A2M	C3'-C2'-C1'	-2.31	98.38	102.81
41	L5	2363	A2M	O3'-C3'-C2'	2.31	117.66	111.19
41	L5	3925	OMU	O2-C2-N1	-2.31	119.79	122.80
41	L5	3782	5MC	C1'-N1-C6	-2.31	117.35	121.15
20	S2	686	PSU	C6-C5-C4	2.30	119.73	118.17
41	L5	1326	A2M	C3'-C2'-C1'	-2.30	98.41	102.81
41	L5	3867	A2M	O4'-C1'-C2'	2.29	110.53	106.59
20	S2	468	A2M	O4'-C1'-C2'	2.28	110.52	106.59
20	S2	863	PSU	C6-N1-C2	-2.28	120.57	122.69
41	L5	4442	PSU	C6-C5-C4	2.28	119.71	118.17
41	L5	1792	PSU	C6-N1-C2	-2.28	120.58	122.69
41	L5	3851	PSU	O4'-C1'-C2'	2.28	108.30	105.15
41	L5	1322	1MA	N1-C6-N6	2.27	125.42	119.71
41	L5	4456	OMC	C1'-N1-C2	2.27	123.44	118.44
20	S2	1045	PSU	C6-N1-C2	-2.27	120.59	122.69
20	S2	686	PSU	C6-N1-C2	-2.26	120.59	122.69
20	S2	1081	PSU	C6-N1-C2	-2.26	120.59	122.69
20	S2	1031	A2M	O4'-C1'-C2'	2.26	110.47	106.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	1534	A2M	C4'-O4'-C1'	-2.25	104.51	109.47
41	L5	3867	A2M	O3'-C3'-C2'	2.24	117.47	111.19
41	L5	4523	A2M	C6-C5-C4	-2.24	114.11	117.18
20	S2	159	A2M	O4'-C1'-C2'	2.24	110.45	106.59
20	S2	93	PSU	C6-N1-C2	-2.24	120.62	122.69
41	L5	4353	PSU	C6-N1-C2	-2.23	120.62	122.69
41	L5	1871	A2M	C6-C5-C4	-2.23	114.13	117.18
20	S2	1639	G7M	N9-C8-N7	-2.23	107.07	112.48
20	S2	1248	B8N	O4'-C1'-C2'	2.23	108.23	105.15
41	L5	2363	A2M	C3'-C2'-C1'	-2.22	98.55	102.81
20	S2	1081	PSU	C6-C5-C4	2.22	119.67	118.17
41	L5	1326	A2M	C2'-C1'-N9	2.22	117.41	113.75
20	S2	1045	PSU	C6-C5-C4	2.22	119.67	118.17
41	L5	3851	PSU	C6-N1-C2	-2.22	120.63	122.69
20	S2	1367	PSU	C6-C5-C4	2.22	119.67	118.17
41	L5	3695	PSU	C6-C5-C4	2.21	119.67	118.17
20	S2	966	PSU	C6-N1-C2	-2.21	120.64	122.69
41	L5	4498	OMU	O2-C2-N1	-2.21	119.92	122.80
20	S2	1850	MA6	C2'-C3'-C4'	2.21	106.88	102.61
41	L5	2861	OMC	C1'-N1-C6	-2.20	116.07	120.78
41	L5	4521	PSU	C6-N1-C2	-2.20	120.65	122.69
20	S2	668	A2M	C6-C5-C4	-2.20	114.17	117.18
41	L5	3639	PSU	C6-C5-C4	2.20	119.66	118.17
41	L5	4293	PSU	C6-N1-C2	-2.20	120.65	122.69
20	S2	354	OMU	O2-C2-N1	-2.20	119.94	122.80
41	L5	1323	A2M	C6-C5-C4	-2.19	114.19	117.18
41	L5	1871	A2M	O4'-C1'-C2'	2.19	110.36	106.59
41	L5	4576	PSU	O4'-C1'-C2'	2.19	108.18	105.15
20	S2	1031	A2M	C6-C5-C4	-2.19	114.19	117.18
41	L5	1534	A2M	C6-C5-C4	-2.18	114.20	117.18
41	L5	3867	A2M	C6-C5-C4	-2.18	114.20	117.18
41	L5	3785	A2M	C6-C5-C4	-2.18	114.20	117.18
41	L5	2351	OMC	C1'-N1-C2	2.18	123.25	118.44
41	L5	1323	A2M	C3'-C2'-C1'	-2.17	98.65	102.81
20	S2	1174	PSU	C6-N1-C2	-2.17	120.68	122.69
20	S2	1383	A2M	C4'-O4'-C1'	-2.17	104.67	109.47
41	L5	3867	A2M	C3'-C2'-C1'	-2.17	98.66	102.81
20	S2	814	PSU	C6-N1-C2	-2.17	120.68	122.69
41	L5	2363	A2M	C2-N1-C6	-2.17	115.17	118.73
41	L5	2401	A2M	C6-C5-C4	-2.16	114.22	117.18
41	L5	2815	A2M	C2-N1-C6	-2.16	115.19	118.73
41	L5	3785	A2M	C2-N1-C6	-2.15	115.20	118.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	2815	A2M	C5-C6-N1	2.15	122.97	117.51
41	L5	4590	A2M	C6-C5-C4	-2.15	114.25	117.18
41	L5	3825	A2M	O4'-C1'-C2'	2.14	110.28	106.59
20	S2	627	OMU	O2-C2-N1	-2.14	120.01	122.80
20	S2	1383	A2M	C6-C5-C4	-2.14	114.25	117.18
41	L5	4571	A2M	C6-C5-C4	-2.14	114.25	117.18
41	L5	3785	A2M	C5-C6-N1	2.14	122.94	117.51
41	L5	4590	A2M	O4'-C1'-C2'	2.14	110.27	106.59
41	L5	400	A2M	O3'-C3'-C4'	-2.14	104.95	111.08
20	S2	109	PSU	C6-C5-C4	2.14	119.61	118.17
41	L5	3695	PSU	O4'-C1'-C2'	2.13	108.10	105.15
20	S2	1272	OMC	C1'-N1-C2	2.13	123.14	118.44
41	L5	3825	A2M	C2'-C1'-N9	2.13	117.25	113.75
41	L5	2401	A2M	O4'-C1'-C2'	2.13	110.25	106.59
43	L8	55	PSU	C6-C5-C4	2.12	119.61	118.17
41	L5	400	A2M	C6-C5-C4	-2.12	114.28	117.18
41	L5	3825	A2M	C6-C5-C4	-2.12	114.28	117.18
41	L5	3830	A2M	C6-C5-C4	-2.12	114.28	117.18
41	L5	4972	PSU	C6-N1-C2	-2.12	120.72	122.69
41	L5	2363	A2M	C1'-N9-C8	2.12	131.79	127.09
41	L5	2839	PSU	C6-C5-C4	2.12	119.60	118.17
41	L5	1871	A2M	C5-C6-N1	2.12	122.88	117.51
41	L5	1677	PSU	C6-N1-C2	-2.11	120.73	122.69
41	L5	1326	A2M	C2-N1-C6	-2.11	115.26	118.73
20	S2	1832	6MZ	C5-C6-N1	2.11	120.42	118.15
41	L5	1536	PSU	C6-C5-C4	2.11	119.60	118.17
41	L5	2363	A2M	C5-C6-N1	2.11	122.86	117.51
20	S2	1832	6MZ	C4-C5-N7	-2.11	108.17	110.58
20	S2	166	A2M	C5-C6-N1	2.11	122.86	117.51
41	L5	4353	PSU	C6-C5-C4	2.11	119.59	118.17
41	L5	2363	A2M	C4-N9-C1'	-2.10	121.71	126.63
41	L5	4457	PSU	O4'-C1'-C2'	2.10	108.06	105.15
20	S2	517	OMC	C1'-N1-C2	2.10	123.08	118.44
41	L5	4673	PSU	C6-C5-C4	2.10	119.59	118.17
20	S2	121	OMU	O2-C2-N1	-2.10	120.06	122.80
41	L5	3830	A2M	O4'-C1'-C2'	2.09	110.18	106.59
20	S2	576	A2M	C6-C5-C4	-2.09	114.33	117.18
41	L5	4493	PSU	C6-C5-C4	2.08	119.58	118.17
41	L5	1524	A2M	C5-C6-N1	2.08	122.80	117.51
20	S2	27	A2M	O4'-C1'-C2'	2.08	110.17	106.59
41	L5	4590	A2M	C5-C6-N1	2.08	122.80	117.51
20	S2	468	A2M	C5-C6-N1	2.08	122.78	117.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	S2	1031	A2M	C5-C6-N1	2.08	122.78	117.51
20	S2	27	A2M	C6-C5-C4	-2.07	114.34	117.18
41	L5	2401	A2M	C2-N1-C6	-2.07	115.32	118.73
41	L5	4571	A2M	C5-C6-N1	2.07	122.78	117.51
20	S2	99	A2M	C5-C6-N1	2.07	122.78	117.51
20	S2	99	A2M	C6-C5-C4	-2.07	114.35	117.18
41	L5	400	A2M	C5-C6-N1	2.07	122.77	117.51
41	L5	2401	A2M	C5-C6-N1	2.07	122.77	117.51
41	L5	3830	A2M	C5-C6-N1	2.07	122.77	117.51
20	S2	799	OMU	C1'-N1-C2	2.07	121.31	117.59
41	L5	3718	A2M	C6-C5-C4	-2.07	114.35	117.18
20	S2	484	A2M	C2-N1-C6	-2.07	115.33	118.73
41	L5	3853	PSU	O4'-C1'-C2'	2.07	108.01	105.15
20	S2	1383	A2M	O4'-C1'-C2'	2.07	110.15	106.59
20	S2	1383	A2M	C5-C6-N1	2.07	122.76	117.51
41	L5	1326	A2M	C5-C6-N1	2.06	122.75	117.51
20	S2	966	PSU	O4'-C1'-C2'	2.06	108.00	105.15
20	S2	484	A2M	C5-C6-N1	2.06	122.74	117.51
41	L5	4361	PSU	C6-C5-C4	2.06	119.56	118.17
20	S2	1383	A2M	C2-N1-C6	-2.06	115.35	118.73
41	L5	1677	PSU	O4'-C1'-C2'	2.06	108.00	105.15
41	L5	1323	A2M	C5-C6-N1	2.06	122.73	117.51
41	L5	3867	A2M	C2-N1-C6	-2.06	115.35	118.73
41	L5	1524	A2M	C4'-O4'-C1'	-2.06	104.93	109.47
20	S2	159	A2M	C2-N1-C6	-2.05	115.36	118.73
41	L5	1524	A2M	C2-N1-C6	-2.05	115.36	118.73
20	S2	172	OMU	O2-C2-N1	-2.05	120.12	122.80
41	L5	2787	A2M	C6-C5-C4	-2.05	114.37	117.18
41	L5	398	A2M	C2-N1-C6	-2.05	115.36	118.73
41	L5	3639	PSU	O4'-C1'-C2'	2.05	107.99	105.15
41	L5	1871	A2M	C2-N1-C6	-2.05	115.36	118.73
20	S2	668	A2M	C5-C6-N1	2.05	122.72	117.51
20	S2	159	A2M	C6-C5-C4	-2.05	114.38	117.18
41	L5	4636	PSU	O4'-C1'-C2'	2.05	107.99	105.15
20	S2	1031	A2M	C2-N1-C6	-2.05	115.36	118.73
41	L5	1326	A2M	C6-C5-C4	-2.05	114.38	117.18
41	L5	3884	PSU	C6-C5-C4	2.05	119.56	118.17
20	S2	651	PSU	C6-C5-C4	2.05	119.55	118.17
41	L5	398	A2M	C6-C5-C4	-2.04	114.39	117.18
20	S2	159	A2M	C5-C6-N1	2.04	122.69	117.51
41	L5	3718	A2M	C2-N1-C6	-2.04	115.38	118.73
41	L5	3718	A2M	C5-C6-N1	2.04	122.68	117.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L5	3825	A2M	C5-C6-N1	2.04	122.68	117.51
20	S2	99	A2M	C2-N1-C6	-2.03	115.39	118.73
41	L5	1534	A2M	C5-C6-N1	2.03	122.67	117.51
41	L5	4523	A2M	C5-C6-N1	2.03	122.67	117.51
41	L5	4571	A2M	C2-N1-C6	-2.03	115.39	118.73
20	S2	27	A2M	C5-C6-N1	2.03	122.66	117.51
20	S2	428	OMU	O2-C2-N1	-2.03	120.16	122.80
41	L5	398	A2M	C4'-O4'-C1'	-2.02	105.00	109.47
41	L5	4523	A2M	C2-N1-C6	-2.02	115.41	118.73
20	S2	99	A2M	O4'-C1'-C2'	2.02	110.07	106.59
20	S2	668	A2M	C2-N1-C6	-2.02	115.41	118.73
41	L5	3825	A2M	C2-N1-C6	-2.02	115.41	118.73
41	L5	4590	A2M	C2-N1-C6	-2.02	115.41	118.73
41	L5	4636	PSU	C6-N1-C2	-2.02	120.82	122.69
20	S2	1391	OMC	C1'-N1-C2	2.02	122.89	118.44
41	L5	4353	PSU	O4'-C1'-C2'	2.01	107.94	105.15
41	L5	1524	A2M	C6-C5-C4	-2.01	114.43	117.18
43	L8	69	PSU	O4'-C1'-C2'	2.01	107.94	105.15
41	L5	3920	PSU	O4'-C1'-C2'	2.01	107.94	105.15
41	L5	4628	PSU	O4'-C1'-C2'	2.01	107.94	105.15
41	L5	2787	A2M	C2-N1-C6	-2.01	115.43	118.73
41	L5	3867	A2M	C5-C6-N1	2.01	122.61	117.51
20	S2	681	PSU	O4'-C1'-C2'	2.01	107.93	105.15
20	S2	576	A2M	C5-C6-N1	2.01	122.61	117.51
41	L5	3785	A2M	C2'-C1'-N9	2.01	117.06	113.75
20	S2	1832	6MZ	C9-N6-C6	-2.01	120.99	122.85
20	S2	484	A2M	C6-C5-C4	-2.01	114.44	117.18
41	L5	1744	PSU	O4'-C1'-C2'	2.01	107.93	105.15
41	L5	4620	OMU	O2-C2-N1	-2.01	120.18	122.80
41	L5	398	A2M	C5-C6-N1	2.00	122.60	117.51
41	L5	4521	PSU	C6-C5-C4	2.00	119.53	118.17
41	L5	1323	A2M	C2-N1-C6	-2.00	115.44	118.73

There are no chirality outliers.

All (173) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
43	L8	75	OMG	C1'-C2'-O2'-CM2
20	S2	27	A2M	C1'-C2'-O2'-CM'
20	S2	159	A2M	C1'-C2'-O2'-CM'
20	S2	354	OMU	C1'-C2'-O2'-CM2
20	S2	462	OMC	C1'-C2'-O2'-CM2

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Mol	Chain	Res	Type	Atoms
20	S2	601	OMG	C1'-C2'-O2'-CM2
20	S2	627	OMU	C2'-C1'-N1-C2
20	S2	627	OMU	C2'-C1'-N1-C6
20	S2	627	OMU	O4'-C4'-C5'-O5'
20	S2	644	OMG	O4'-C4'-C5'-O5'
20	S2	644	OMG	C1'-C2'-O2'-CM2
20	S2	649	PSU	C2'-C1'-C5-C4
20	S2	683	OMG	C3'-C4'-C5'-O5'
20	S2	801	PSU	C3'-C4'-C5'-O5'
20	S2	801	PSU	O4'-C4'-C5'-O5'
20	S2	1031	A2M	C1'-C2'-O2'-CM'
20	S2	1045	PSU	O4'-C4'-C5'-O5'
20	S2	1248	B8N	O4'-C4'-C5'-O5'
20	S2	1272	OMC	C3'-C4'-C5'-O5'
20	S2	1272	OMC	O4'-C4'-C5'-O5'
20	S2	1288	OMU	O4'-C4'-C5'-O5'
20	S2	1337	4AC	N3-C4-N4-C7
20	S2	1383	A2M	C1'-C2'-O2'-CM'
20	S2	1442	OMU	O4'-C4'-C5'-O5'
20	S2	1639	G7M	O4'-C4'-C5'-O5'
20	S2	1832	6MZ	C5-C6-N6-C9
20	S2	1832	6MZ	N1-C6-N6-C9
20	S2	1851	MA6	C5-C6-N6-C10
41	L5	398	A2M	C1'-C2'-O2'-CM'
41	L5	400	A2M	C1'-C2'-O2'-CM'
41	L5	1316	OMG	C1'-C2'-O2'-CM2
41	L5	1323	A2M	C1'-C2'-O2'-CM'
41	L5	1326	A2M	O4'-C4'-C5'-O5'
41	L5	1326	A2M	C1'-C2'-O2'-CM'
41	L5	1340	OMC	C1'-C2'-O2'-CM2
41	L5	1524	A2M	C1'-C2'-O2'-CM'
41	L5	1625	OMG	O4'-C4'-C5'-O5'
41	L5	1625	OMG	C3'-C4'-C5'-O5'
41	L5	1677	PSU	C2'-C1'-C5-C4
41	L5	2351	OMC	C1'-C2'-O2'-CM2
41	L5	2363	A2M	C1'-C2'-O2'-CM'
41	L5	2364	OMG	O4'-C4'-C5'-O5'
41	L5	2364	OMG	C1'-C2'-O2'-CM2
41	L5	2365	OMC	C1'-C2'-O2'-CM2
41	L5	2422	OMC	C1'-C2'-O2'-CM2
41	L5	2787	A2M	C1'-C2'-O2'-CM'
41	L5	2787	A2M	C2'-C1'-N9-C8

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Mol	Chain	Res	Type	Atoms
41	L5	2824	OMC	C1'-C2'-O2'-CM2
41	L5	3701	OMC	O4'-C4'-C5'-O5'
41	L5	3744	OMG	C1'-C2'-O2'-CM2
41	L5	3792	OMG	O4'-C4'-C5'-O5'
41	L5	3825	A2M	C1'-C2'-O2'-CM'
41	L5	3830	A2M	C1'-C2'-O2'-CM'
41	L5	3867	A2M	C1'-C2'-O2'-CM'
41	L5	4220	6MZ	C5-C6-N6-C9
41	L5	4220	6MZ	N1-C6-N6-C9
41	L5	4220	6MZ	O4'-C4'-C5'-O5'
41	L5	4447	5MC	C2'-C1'-N1-C2
41	L5	4447	5MC	C2'-C1'-N1-C6
41	L5	4500	PSU	O4'-C4'-C5'-O5'
41	L5	4590	A2M	C3'-C4'-C5'-O5'
41	L5	4590	A2M	C1'-C2'-O2'-CM'
41	L5	4618	OMG	C3'-C4'-C5'-O5'
41	L5	4637	OMG	C1'-C2'-O2'-CM2
20	S2	627	OMU	C3'-C4'-C5'-O5'
20	S2	683	OMG	O4'-C4'-C5'-O5'
20	S2	863	PSU	C3'-C4'-C5'-O5'
20	S2	863	PSU	O4'-C4'-C5'-O5'
20	S2	1288	OMU	C3'-C4'-C5'-O5'
20	S2	1639	G7M	C3'-C4'-C5'-O5'
41	L5	1326	A2M	C3'-C4'-C5'-O5'
41	L5	2787	A2M	C3'-C4'-C5'-O5'
41	L5	3701	OMC	C3'-C4'-C5'-O5'
41	L5	3867	A2M	C3'-C4'-C5'-O5'
41	L5	3899	OMG	O4'-C4'-C5'-O5'
41	L5	4500	PSU	C3'-C4'-C5'-O5'
20	S2	99	A2M	O4'-C4'-C5'-O5'
20	S2	1045	PSU	C3'-C4'-C5'-O5'
20	S2	1442	OMU	C3'-C4'-C5'-O5'
41	L5	1524	A2M	O4'-C4'-C5'-O5'
41	L5	1524	A2M	C3'-C4'-C5'-O5'
41	L5	1536	PSU	C3'-C4'-C5'-O5'
41	L5	1536	PSU	O4'-C4'-C5'-O5'
41	L5	2422	OMC	C3'-C4'-C5'-O5'
41	L5	2422	OMC	O4'-C4'-C5'-O5'
41	L5	3899	OMG	C3'-C4'-C5'-O5'
41	L5	4590	A2M	O4'-C4'-C5'-O5'
41	L5	4618	OMG	O4'-C4'-C5'-O5'
41	L5	4637	OMG	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
41	L5	4637	OMG	C3'-C4'-C5'-O5'
41	L5	2787	A2M	C2'-C1'-N9-C4
20	S2	1851	MA6	N1-C6-N6-C10
20	S2	428	OMU	C2'-C1'-N1-C6
20	S2	1248	B8N	C3'-C4'-C5'-O5'
41	L5	2364	OMG	C3'-C4'-C5'-O5'
41	L5	4220	6MZ	C3'-C4'-C5'-O5'
20	S2	644	OMG	C3'-C4'-C5'-O5'
20	S2	799	OMU	C3'-C4'-C5'-O5'
41	L5	3792	OMG	C3'-C4'-C5'-O5'
41	L5	3822	PSU	C3'-C4'-C5'-O5'
20	S2	428	OMU	O4'-C4'-C5'-O5'
20	S2	799	OMU	O4'-C4'-C5'-O5'
41	L5	2787	A2M	O4'-C4'-C5'-O5'
41	L5	3822	PSU	O4'-C4'-C5'-O5'
41	L5	3867	A2M	O4'-C4'-C5'-O5'
20	S2	1850	MA6	C5-C6-N6-C9
20	S2	1851	MA6	C5-C6-N6-C9
20	S2	428	OMU	C3'-C4'-C5'-O5'
20	S2	668	A2M	O4'-C4'-C5'-O5'
41	L5	1323	A2M	O4'-C4'-C5'-O5'
20	S2	1248	B8N	N34-C33-C34-O36
20	S2	99	A2M	C3'-C4'-C5'-O5'
41	L5	3701	OMC	O4'-C1'-N1-C6
41	L5	4590	A2M	C4'-C5'-O5'-P
20	S2	668	A2M	C3'-C4'-C5'-O5'
41	L5	3701	OMC	O4'-C1'-N1-C2
20	S2	576	A2M	C1'-C2'-O2'-CM'
20	S2	1328	OMG	C1'-C2'-O2'-CM2
20	S2	1442	OMU	C1'-C2'-O2'-CM2
41	L5	4620	OMU	C1'-C2'-O2'-CM2
20	S2	576	A2M	C3'-C4'-C5'-O5'
41	L5	3818	UY1	C4'-C5'-O5'-P
20	S2	428	OMU	C2'-C1'-N1-C2
41	L5	2876	OMG	C3'-C2'-O2'-CM2
20	S2	1703	OMC	O4'-C4'-C5'-O5'
20	S2	428	OMU	O4'-C1'-N1-C6
20	S2	576	A2M	O4'-C4'-C5'-O5'
20	S2	428	OMU	O4'-C1'-N1-C2
20	S2	867	OMG	C4'-C5'-O5'-P
20	S2	576	A2M	C4'-C5'-O5'-P
20	S2	644	OMG	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
20	S2	649	PSU	O4'-C1'-C5-C4
20	S2	1248	B8N	O4'-C1'-C5-C4
41	L5	3822	PSU	O4'-C1'-C5-C4
41	L5	4442	PSU	O4'-C1'-C5-C4
41	L5	4628	PSU	O4'-C1'-C5-C4
41	L5	4636	PSU	O4'-C1'-C5-C4
41	L5	5010	PSU	O4'-C1'-C5-C4
41	L5	1323	A2M	C3'-C4'-C5'-O5'
43	L8	75	OMG	C4'-C5'-O5'-P
41	L5	1625	OMG	C4'-C5'-O5'-P
20	S2	627	OMU	O4'-C1'-N1-C6
41	L5	3785	A2M	C2'-C1'-N9-C8
41	L5	4500	PSU	C4'-C5'-O5'-P
41	L5	4447	5MC	O4'-C1'-N1-C6
20	S2	1639	G7M	C2'-C1'-N9-C4
41	L5	3844	PSU	C4'-C5'-O5'-P
20	S2	668	A2M	O4'-C1'-N9-C8
41	L5	3785	A2M	O4'-C1'-N9-C8
20	S2	1490	OMG	C4'-C5'-O5'-P
41	L5	3792	OMG	C4'-C5'-O5'-P
20	S2	116	OMU	C1'-C2'-O2'-CM2
41	L5	3627	OMG	C1'-C2'-O2'-CM2
41	L5	4228	OMG	O4'-C4'-C5'-O5'
20	S2	1248	B8N	O4'-C1'-C5-C6
41	L5	4636	PSU	O4'-C1'-C5-C6
41	L5	5010	PSU	O4'-C1'-C5-C6
41	L5	2401	A2M	C3'-C2'-O2'-CM'
20	S2	1248	B8N	C4'-C5'-O5'-P
41	L5	1534	A2M	O4'-C4'-C5'-O5'
20	S2	1639	G7M	C2'-C1'-N9-C8
41	L5	398	A2M	O4'-C4'-C5'-O5'
41	L5	1781	PSU	C3'-C4'-C5'-O5'
41	L5	4228	OMG	C3'-C4'-C5'-O5'
41	L5	3887	OMC	C4'-C5'-O5'-P
20	S2	668	A2M	C2'-C1'-N9-C8
20	S2	517	OMC	C3'-C2'-O2'-CM2
20	S2	1081	PSU	C4'-C5'-O5'-P
41	L5	4447	5MC	O4'-C1'-N1-C2
41	L5	4220	6MZ	C4'-C5'-O5'-P
41	L5	2861	OMC	C2'-C1'-N1-C2
20	S2	627	OMU	O4'-C1'-N1-C2
41	L5	3851	PSU	C3'-C4'-C5'-O5'

There are no ring outliers.

99 monomers are involved in 155 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
41	L5	3920	PSU	1	0
41	L5	4523	A2M	1	0
20	S2	462	OMC	1	0
20	S2	1832	6MZ	1	0
20	S2	468	A2M	2	0
20	S2	1288	OMU	2	0
41	L5	4457	PSU	1	0
20	S2	1244	PSU	1	0
41	L5	3925	OMU	1	0
20	S2	109	PSU	1	0
20	S2	799	OMU	1	0
41	L5	4306	OMU	1	0
41	L5	398	A2M	2	0
20	S2	174	OMC	1	0
20	S2	867	OMG	1	0
41	L5	4392	OMG	1	0
41	L5	1534	A2M	1	0
41	L5	4552	PSU	1	0
20	S2	681	PSU	2	0
41	L5	1326	A2M	2	0
41	L5	2861	OMC	1	0
41	L5	4536	OMC	1	0
41	L5	4431	PSU	2	0
41	L5	3844	PSU	1	0
41	L5	3899	OMG	1	0
20	S2	1842	4AC	1	0
41	L5	2824	OMC	1	0
20	S2	1850	MA6	5	0
41	L5	2364	OMG	2	0
41	L5	4493	PSU	1	0
41	L5	4353	PSU	1	0
41	L5	4579	PSU	2	0
41	L5	1340	OMC	3	0
41	L5	4590	A2M	1	0
20	S2	1272	OMC	1	0
41	L5	3744	OMG	1	0
20	S2	354	OMU	1	0
20	S2	627	OMU	1	0
41	L5	4576	PSU	1	0
41	L5	3818	UY1	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
41	L5	400	A2M	1	0
41	L5	3785	A2M	1	0
41	L5	2365	OMC	1	0
41	L5	4620	OMU	2	0
20	S2	1639	G7M	1	0
41	L5	1871	A2M	3	0
41	L5	4623	OMG	2	0
41	L5	3792	OMG	1	0
20	S2	406	PSU	2	0
41	L5	1677	PSU	1	0
41	L5	4530	UR3	1	0
20	S2	1174	PSU	1	0
20	S2	116	OMU	2	0
20	S2	601	OMG	3	0
20	S2	121	OMU	2	0
20	S2	1031	A2M	3	0
41	L5	4196	OMG	1	0
20	S2	1391	OMC	1	0
41	L5	4689	PSU	1	0
41	L5	3718	A2M	3	0
20	S2	517	OMC	1	0
41	L5	2422	OMC	2	0
20	S2	159	A2M	1	0
41	L5	2363	A2M	3	0
41	L5	4293	PSU	1	0
20	S2	576	A2M	2	0
41	L5	1781	PSU	1	0
41	L5	2787	A2M	1	0
41	L5	4499	OMG	1	0
20	S2	509	OMG	4	0
20	S2	686	PSU	1	0
20	S2	1337	4AC	3	0
41	L5	2351	OMC	3	0
41	L5	4220	6MZ	2	0
41	L5	4637	OMG	3	0
20	S2	649	PSU	3	0
20	S2	863	PSU	1	0
41	L5	3884	PSU	1	0
41	L5	3867	A2M	4	0
41	L5	4370	OMG	1	0
20	S2	1383	A2M	1	0
20	S2	1851	MA6	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
41	L5	4447	5MC	1	0
20	S2	1004	PSU	2	0
41	L5	2876	OMG	1	0
20	S2	99	A2M	1	0
41	L5	4312	PSU	1	0
41	L5	1316	OMG	2	0
41	L5	1683	PSU	2	0
41	L5	3830	A2M	1	0
20	S2	683	OMG	1	0
43	L8	75	OMG	2	0
20	S2	436	OMG	1	0
41	L5	1323	A2M	2	0
20	S2	644	OMG	1	0
20	S2	27	A2M	3	0
41	L5	4227	OMU	1	0
41	L5	4299	PSU	1	0
41	L5	3825	A2M	5	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 244 ligands modelled in this entry, 225 are monoatomic - leaving 19 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
89	SPD	L5	5281	-	9,9,9	0.33	0	8,8,8	0.91	0
88	SPM	L5	5260	-	13,13,13	0.36	0	12,12,12	1.02	0
89	SPD	L5	5280	-	9,9,9	0.32	0	8,8,8	0.91	0
90	3HE	L5	5291	41	21,21,21	0.53	0	23,30,30	1.16	3 (13%)
89	SPD	L5	5287	-	9,9,9	0.32	0	8,8,8	0.87	0
91	HMT	L5	5292	-	41,43,43	0.72	1 (2%)	43,66,66	0.69	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
89	SPD	L5	5258	-	9,9,9	0.31	0	8,8,8	1.00	0
89	SPD	L5	5286	-	9,9,9	0.32	0	8,8,8	0.89	0
88	SPM	L5	5285	-	13,13,13	0.35	0	12,12,12	0.91	0
88	SPM	L5	5261	-	13,13,13	0.35	0	12,12,12	0.99	0
88	SPM	L5	5255	-	13,13,13	0.35	0	12,12,12	0.98	0
89	SPD	L8	201	-	9,9,9	0.33	0	8,8,8	0.86	0
89	SPD	L5	5283	-	9,9,9	0.33	0	8,8,8	0.79	0
89	SPD	L5	5282	-	9,9,9	0.34	0	8,8,8	0.88	0
88	SPM	L5	5288	-	13,13,13	0.34	0	12,12,12	0.85	0
88	SPM	L5	5290	-	13,13,13	0.35	0	12,12,12	0.91	0
89	SPD	L5	5289	-	9,9,9	0.33	0	8,8,8	0.89	0
88	SPM	L5	5264	-	13,13,13	0.34	0	12,12,12	0.95	0
89	SPD	L5	5284	-	9,9,9	0.32	0	8,8,8	0.86	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
89	SPD	L5	5281	-	-	1/7/7/7	-
88	SPM	L5	5260	-	-	1/11/11/11	-
89	SPD	L5	5280	-	-	2/7/7/7	-
90	3HE	L5	5291	41	-	4/8/36/36	0/2/2/2
89	SPD	L5	5287	-	-	3/7/7/7	-
91	HMT	L5	5292	-	-	7/27/74/74	0/5/5/5
89	SPD	L5	5258	-	-	1/7/7/7	-
89	SPD	L5	5286	-	-	0/7/7/7	-
88	SPM	L5	5285	-	-	3/11/11/11	-
88	SPM	L5	5261	-	-	0/11/11/11	-
88	SPM	L5	5255	-	-	1/11/11/11	-
89	SPD	L8	201	-	-	2/7/7/7	-
89	SPD	L5	5283	-	-	1/7/7/7	-
89	SPD	L5	5282	-	-	0/7/7/7	-
88	SPM	L5	5288	-	-	4/11/11/11	-
88	SPM	L5	5290	-	-	2/11/11/11	-
89	SPD	L5	5289	-	-	0/7/7/7	-
88	SPM	L5	5264	-	-	2/11/11/11	-
89	SPD	L5	5284	-	-	0/7/7/7	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
91	L5	5292	HMT	C20-C19	-3.01	1.50	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	L5	5292	HMT	O6-C20-C24	-2.65	104.64	108.88
90	L5	5291	3HE	C2-C3-C4	2.58	114.80	109.66
90	L5	5291	3HE	C6-C5-C4	2.53	112.47	108.29
90	L5	5291	3HE	O3-C7-C8	2.09	113.33	109.15

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
90	L5	5291	3HE	C4-C5-C7-C8
90	L5	5291	3HE	C6-C5-C7-C8
88	L5	5288	SPM	N10-C11-C12-C13
88	L5	5288	SPM	C2-C3-C4-N5
88	L5	5260	SPM	C2-C3-C4-N5
89	L5	5287	SPD	N6-C7-C8-C9
90	L5	5291	3HE	C4-C5-C7-O3
89	L5	5281	SPD	C3-C4-C5-N6
89	L5	5287	SPD	C3-C4-C5-N6
88	L5	5285	SPM	C6-C7-C8-C9
91	L5	5292	HMT	C24-C20-C21-C22
89	L5	5280	SPD	N6-C7-C8-C9
91	L5	5292	HMT	O5-C19-C20-C24
88	L5	5264	SPM	C11-C12-C13-N14
88	L5	5285	SPM	N1-C2-C3-C4
88	L5	5290	SPM	C11-C12-C13-N14
91	L5	5292	HMT	O4-C19-C20-C24
89	L5	5280	SPD	N1-C2-C3-C4
88	L5	5288	SPM	C6-C7-C8-C9
88	L5	5264	SPM	C6-C7-C8-C9
89	L5	5258	SPD	N6-C7-C8-C9
91	L5	5292	HMT	C20-C24-C25-C26
91	L5	5292	HMT	O5-C19-C20-O6
89	L8	201	SPD	C4-C5-N6-C7
88	L5	5285	SPM	N10-C11-C12-C13
88	L5	5255	SPM	C6-C7-C8-C9
89	L8	201	SPD	C2-C3-C4-C5
89	L5	5287	SPD	C4-C5-N6-C7

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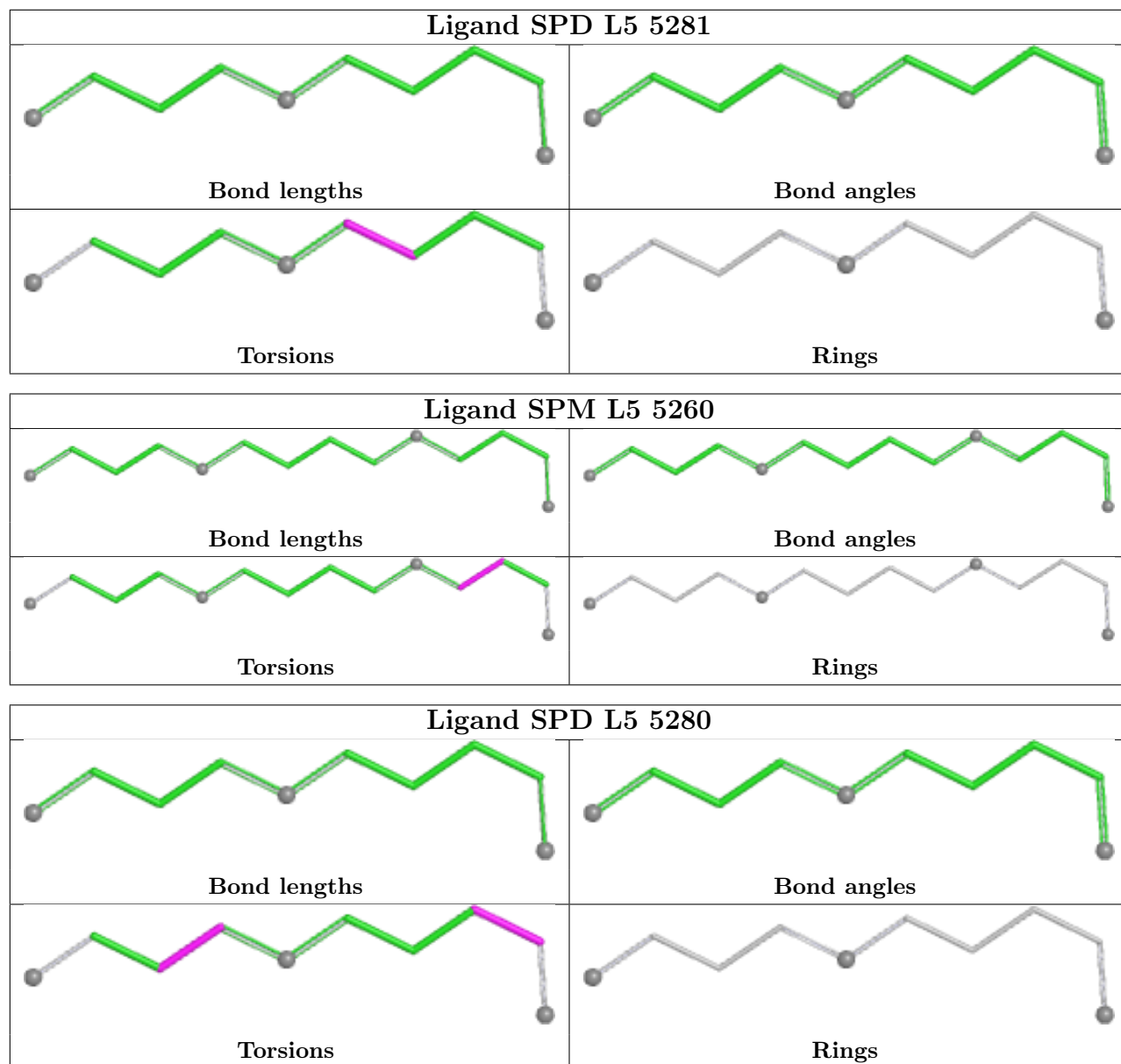
Mol	Chain	Res	Type	Atoms
90	L5	5291	3HE	C6-C5-C7-O3
88	L5	5288	SPM	C3-C4-N5-C6
88	L5	5290	SPM	N1-C2-C3-C4
89	L5	5283	SPD	C7-C8-C9-N10
91	L5	5292	HMT	C19-C20-C21-C22
91	L5	5292	HMT	O6-C20-C21-C22

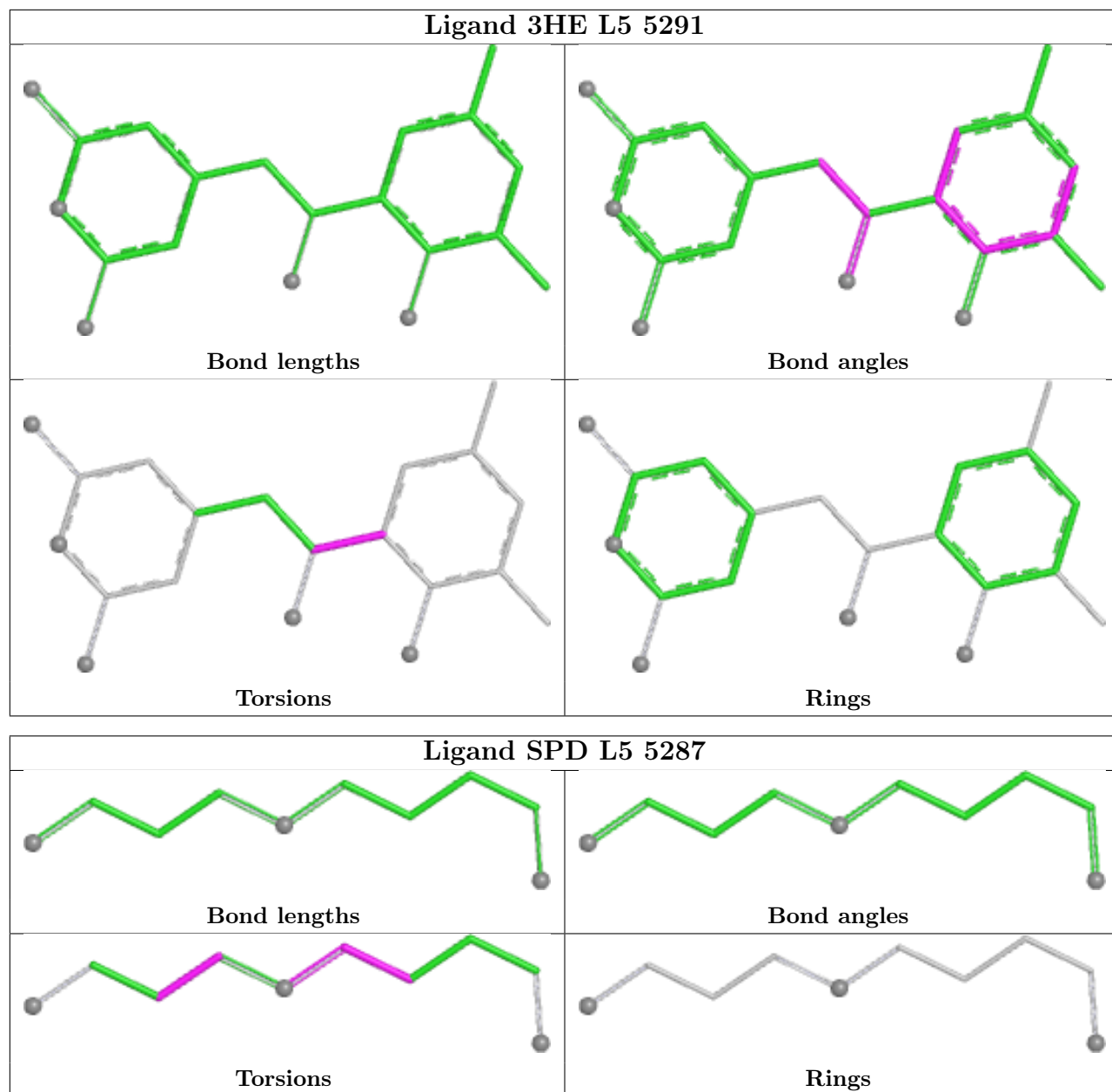
There are no ring outliers.

15 monomers are involved in 20 short contacts:

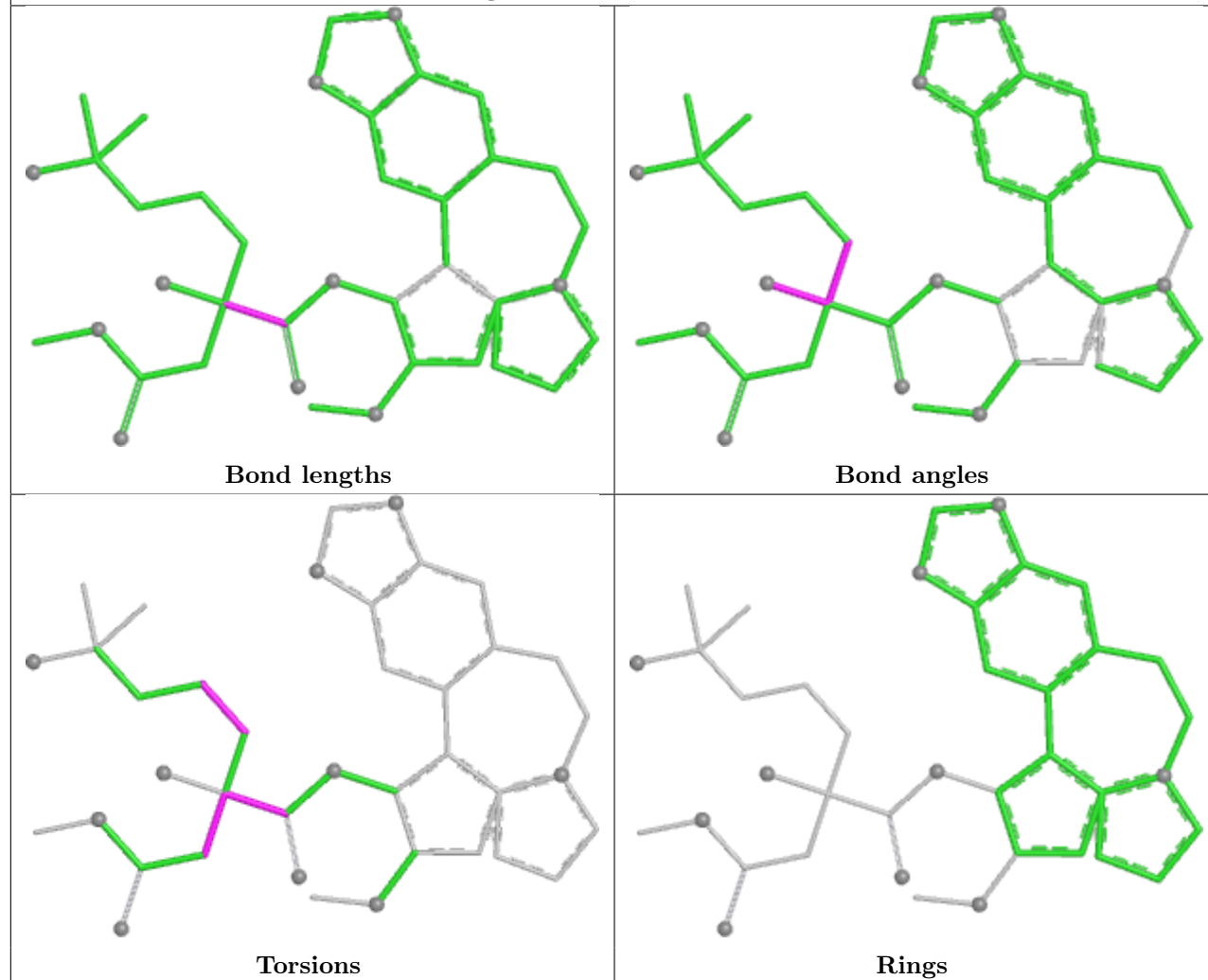
Mol	Chain	Res	Type	Clashes	Symm-Clashes
89	L5	5281	SPD	2	0
88	L5	5260	SPM	1	0
89	L5	5280	SPD	1	0
90	L5	5291	3HE	1	0
89	L5	5258	SPD	1	0
89	L5	5286	SPD	1	0
88	L5	5285	SPM	1	0
88	L5	5261	SPM	1	0
88	L5	5255	SPM	3	0
89	L5	5282	SPD	1	0
88	L5	5288	SPM	1	0
88	L5	5290	SPM	3	0
89	L5	5289	SPD	1	0
88	L5	5264	SPM	1	0
89	L5	5284	SPD	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.

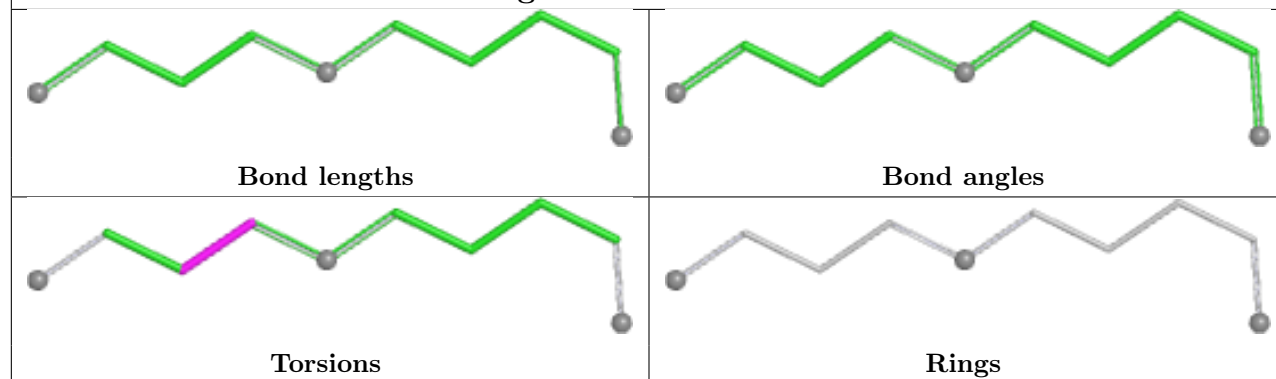


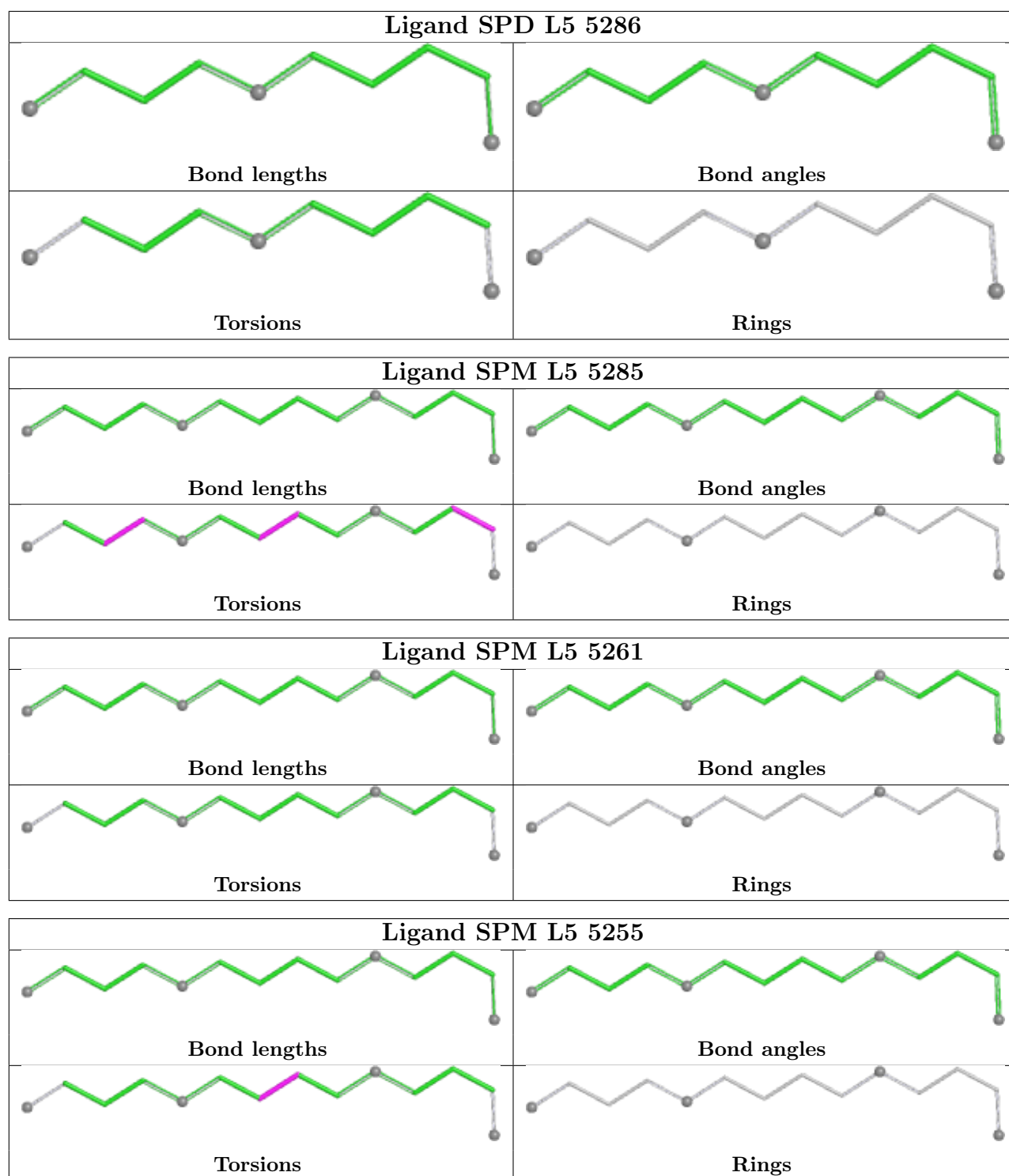


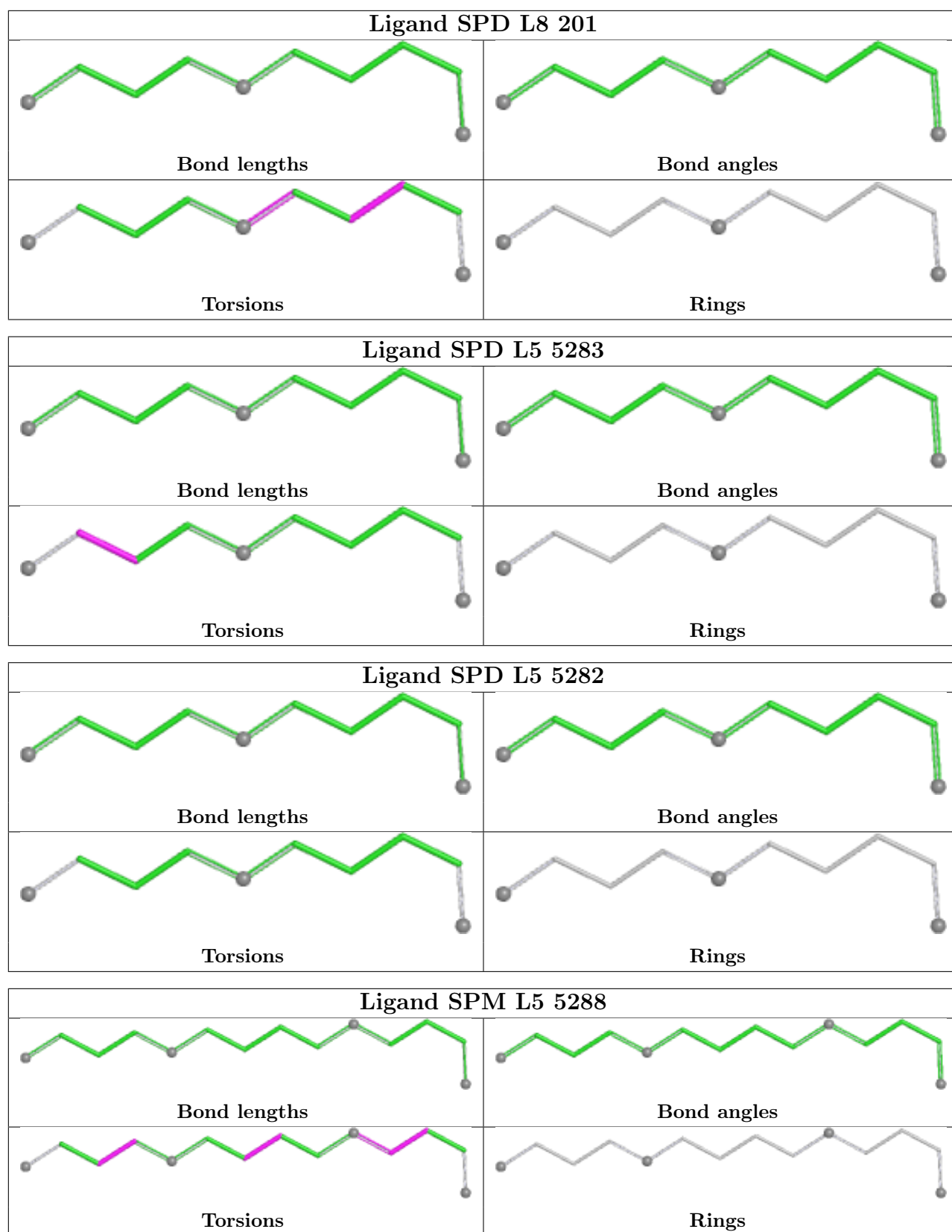
Ligand HMT L5 5292

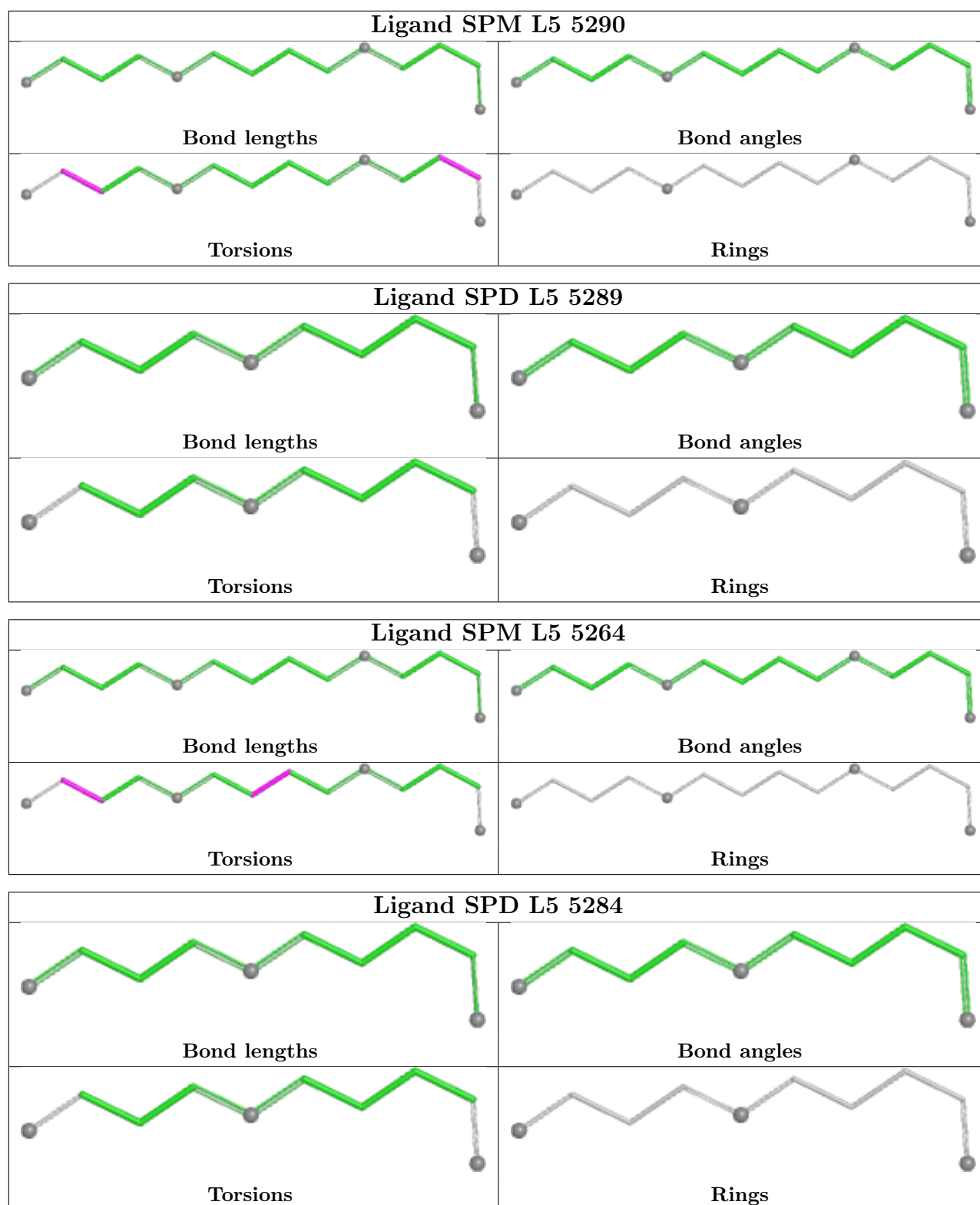


Ligand SPD L5 5258









5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
41	L5	10
20	S2	4
38	At	1
39	Pt	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	753:C	O3'	785:C	P	26.54
1	L5	1706:A	O3'	1716:G	P	20.99
1	L5	2910:G	O3'	3584:C	P	20.73
1	L5	760:G	O3'	903:C	P	17.20
1	L5	519:C	O3'	642:G	P	15.30
1	L5	2112:G	O3'	2249:C	P	14.26
1	L5	3954:A	O3'	4056:A	P	14.22
1	S2	698:G	O3'	730:C	P	14.01
1	S2	739:C	O3'	746:C	P	13.60
1	L5	4776:G	O3'	4858:C	P	13.38
1	L5	1222:A	O3'	1234:G	P	11.91
1	At	15:G	O3'	18:G	P	11.38
1	L5	990:C	O3'	1064:G	P	11.05
1	Pt	15:G	O3'	18:G	P	9.16
1	S2	225:G	O3'	287:U	P	7.75
1	L5	1100:U	O3'	1167:C	P	5.81

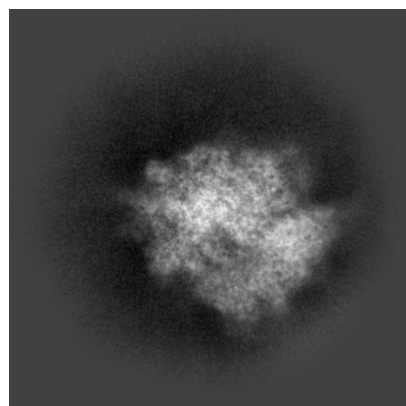
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71341. These allow visual inspection of the internal detail of the map and identification of artifacts.

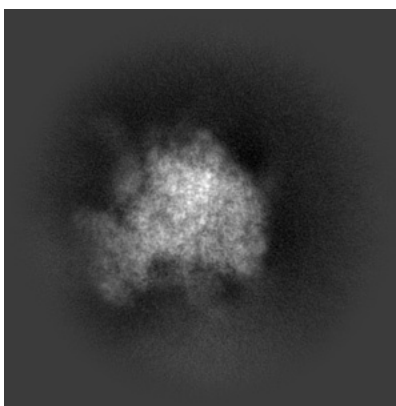
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

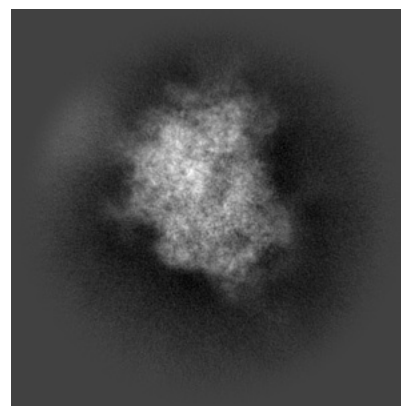
6.1.1 Primary map



X

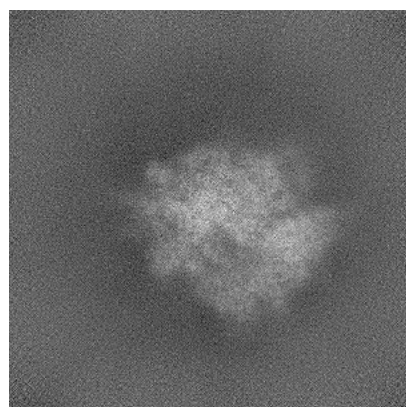


Y

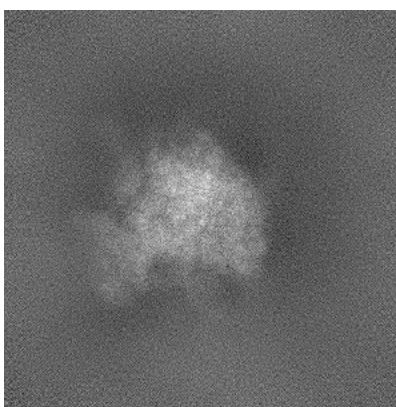


Z

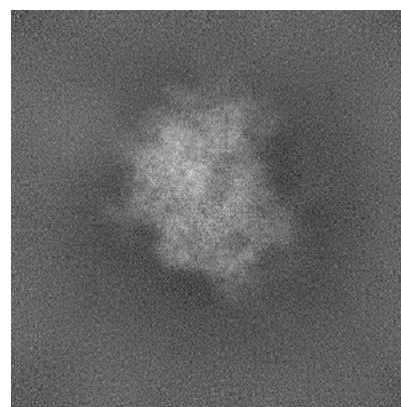
6.1.2 Raw map



X



Y

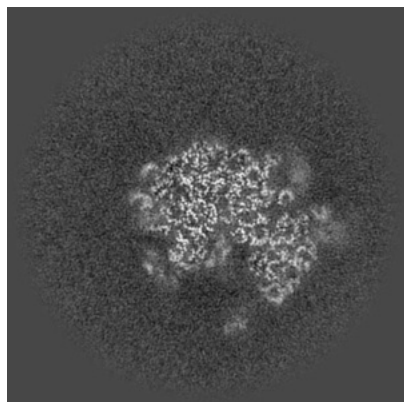


Z

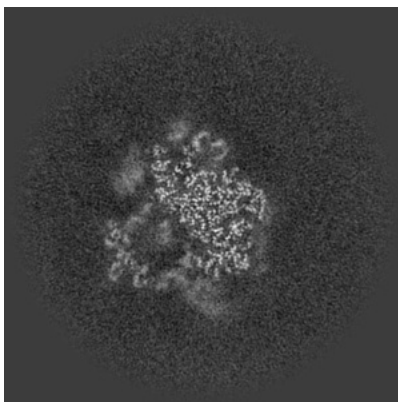
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

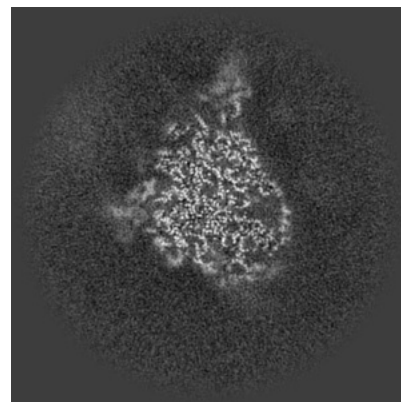
6.2.1 Primary map



X Index: 256

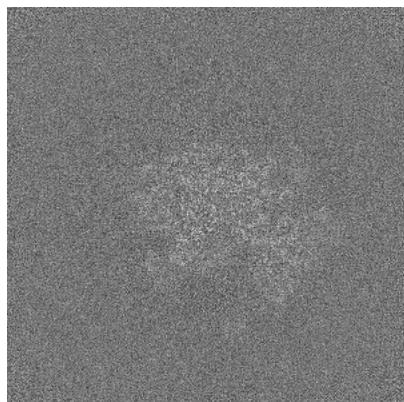


Y Index: 256

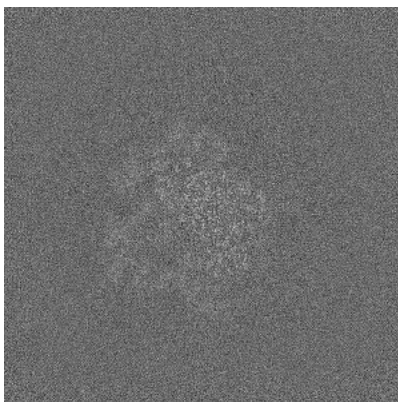


Z Index: 256

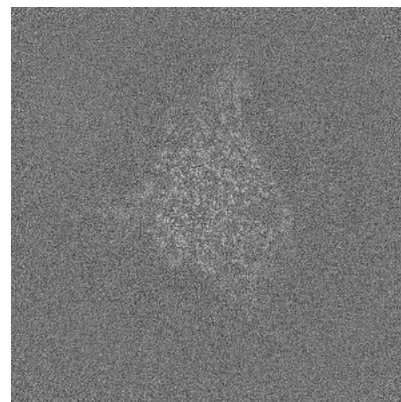
6.2.2 Raw map



X Index: 256



Y Index: 256

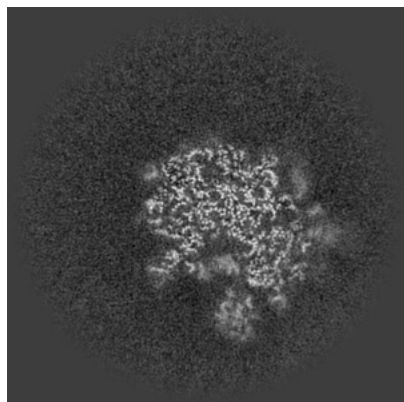


Z Index: 256

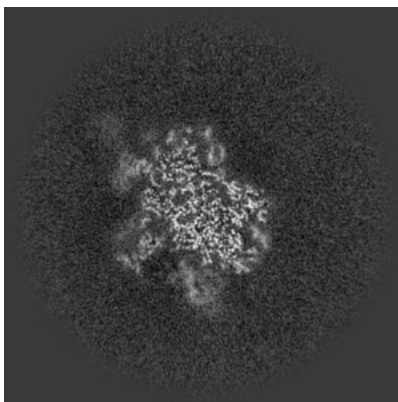
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

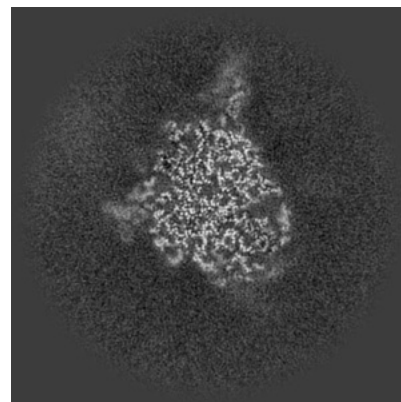
6.3.1 Primary map



X Index: 243

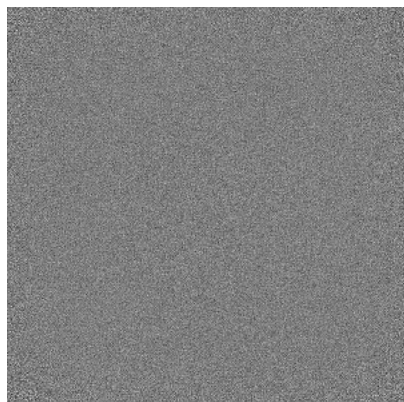


Y Index: 243

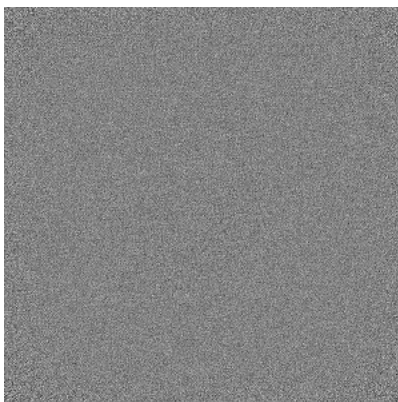


Z Index: 258

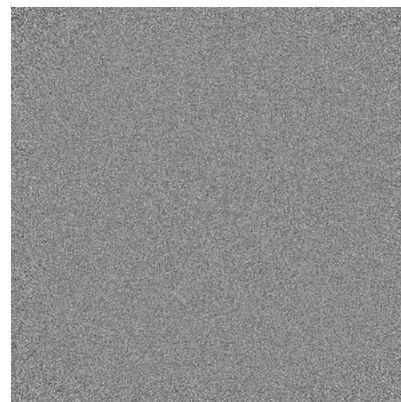
6.3.2 Raw map



X Index: 0



Y Index: 0

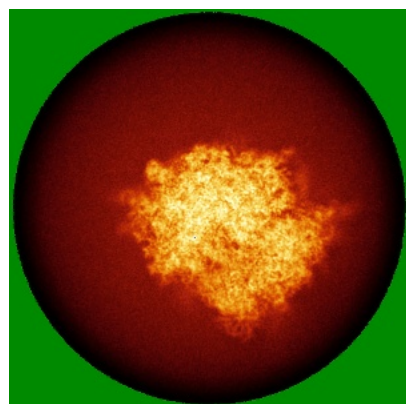


Z Index: 0

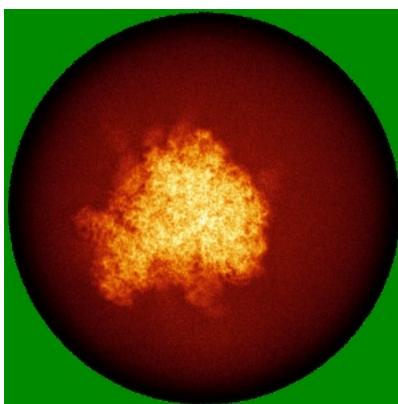
The images above show the largest variance slices of the map in three orthogonal directions.

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

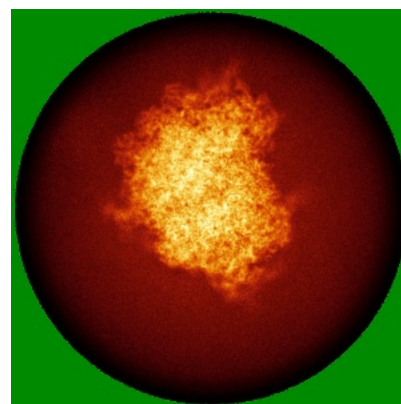
6.4.1 Primary map



X

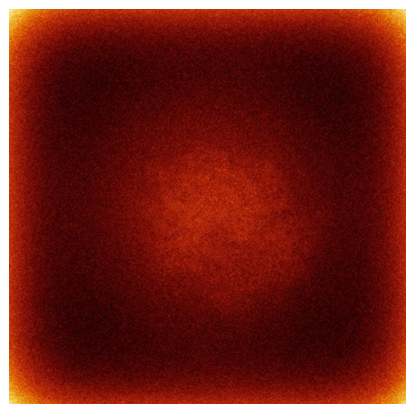


Y

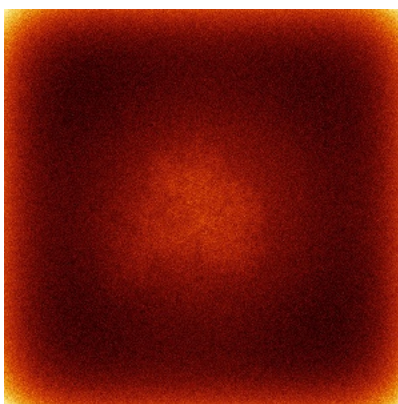


Z

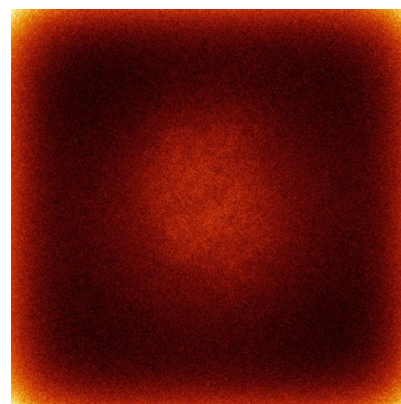
6.4.2 Raw map



X



Y

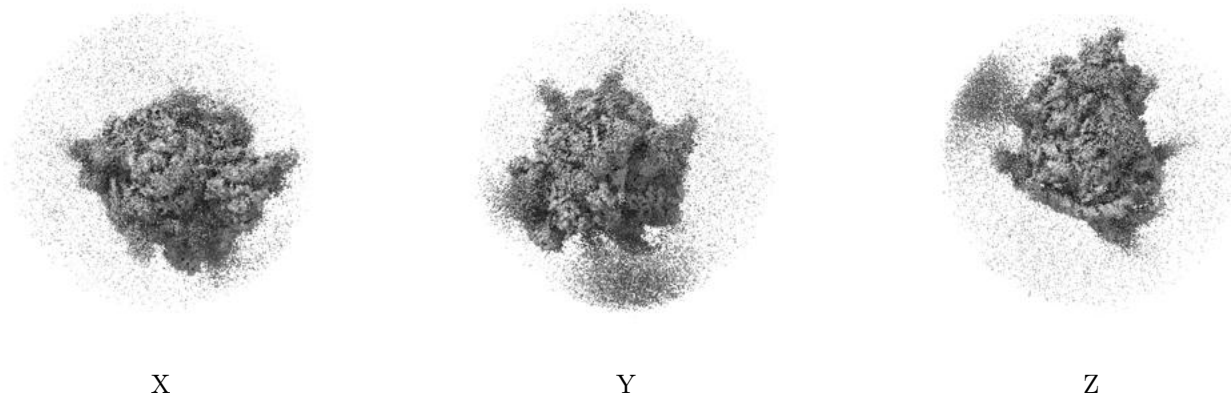


Z

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

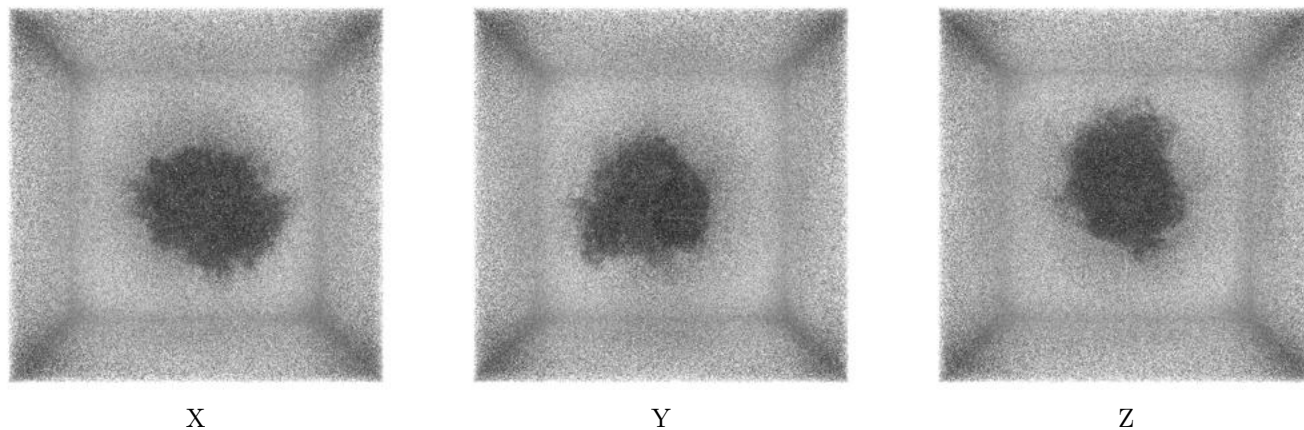
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0764. 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.

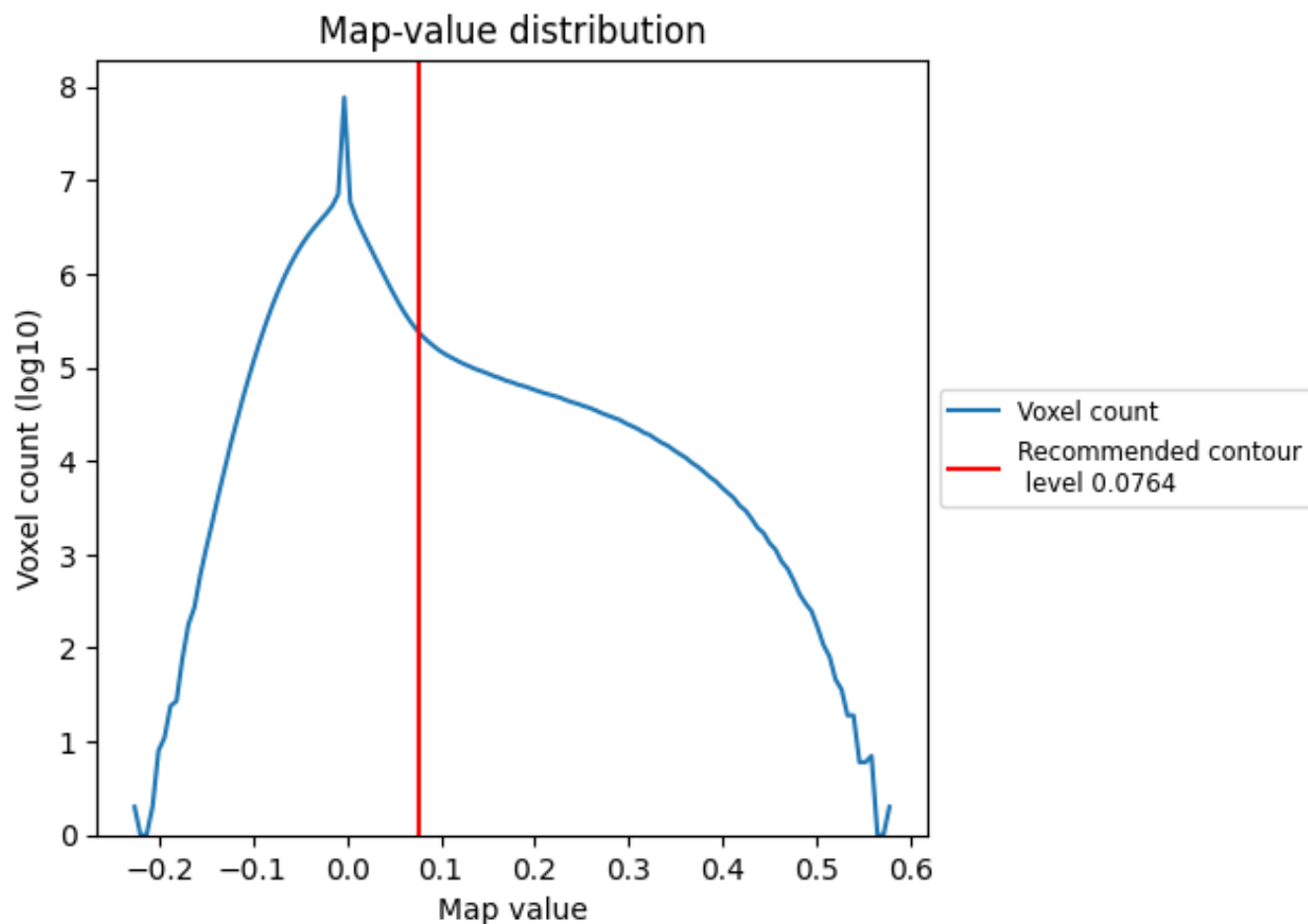
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

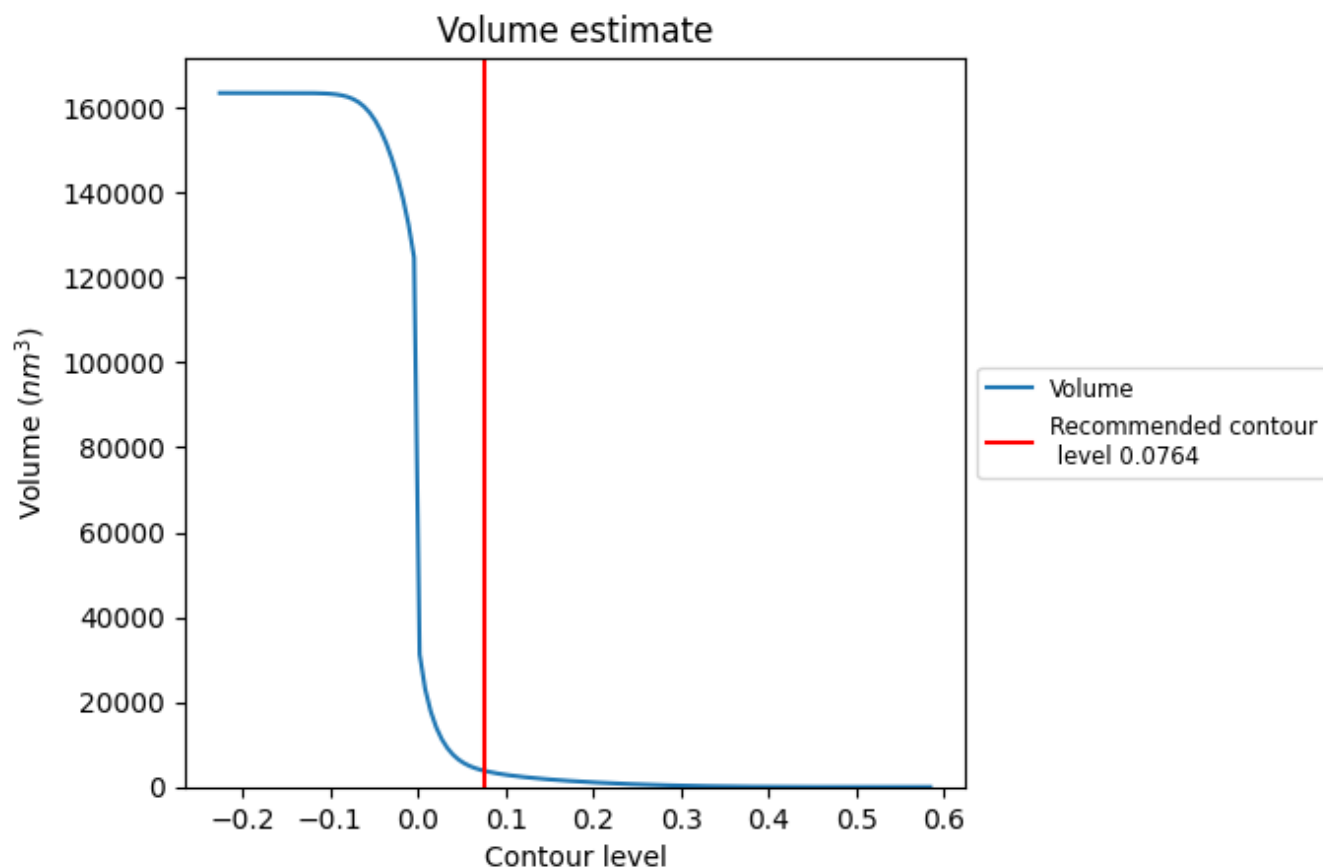
This section contains the results of statistical analysis of the map.

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.

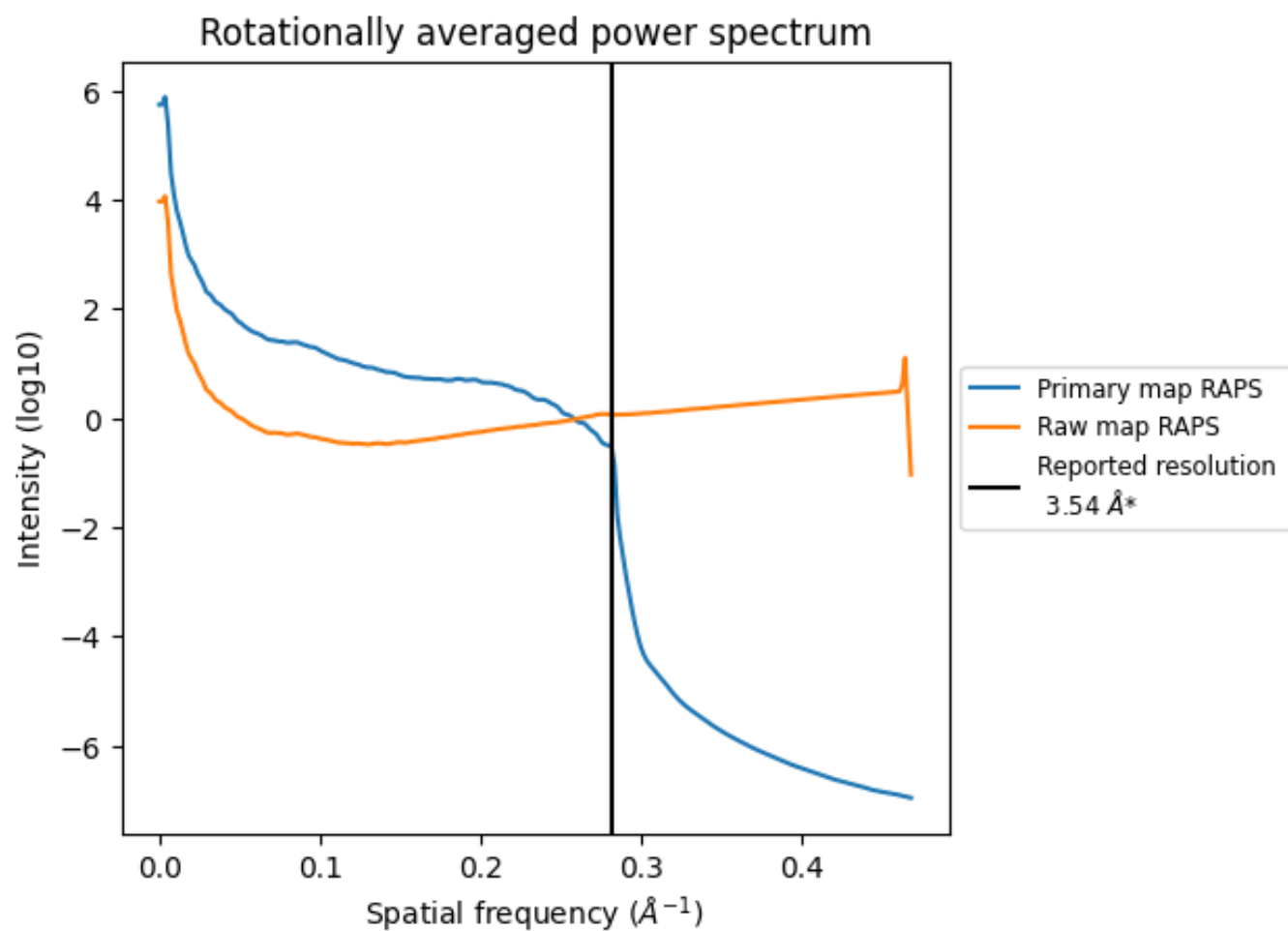
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3770 nm³; this corresponds to an approximate mass of 3406 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 ⓘ

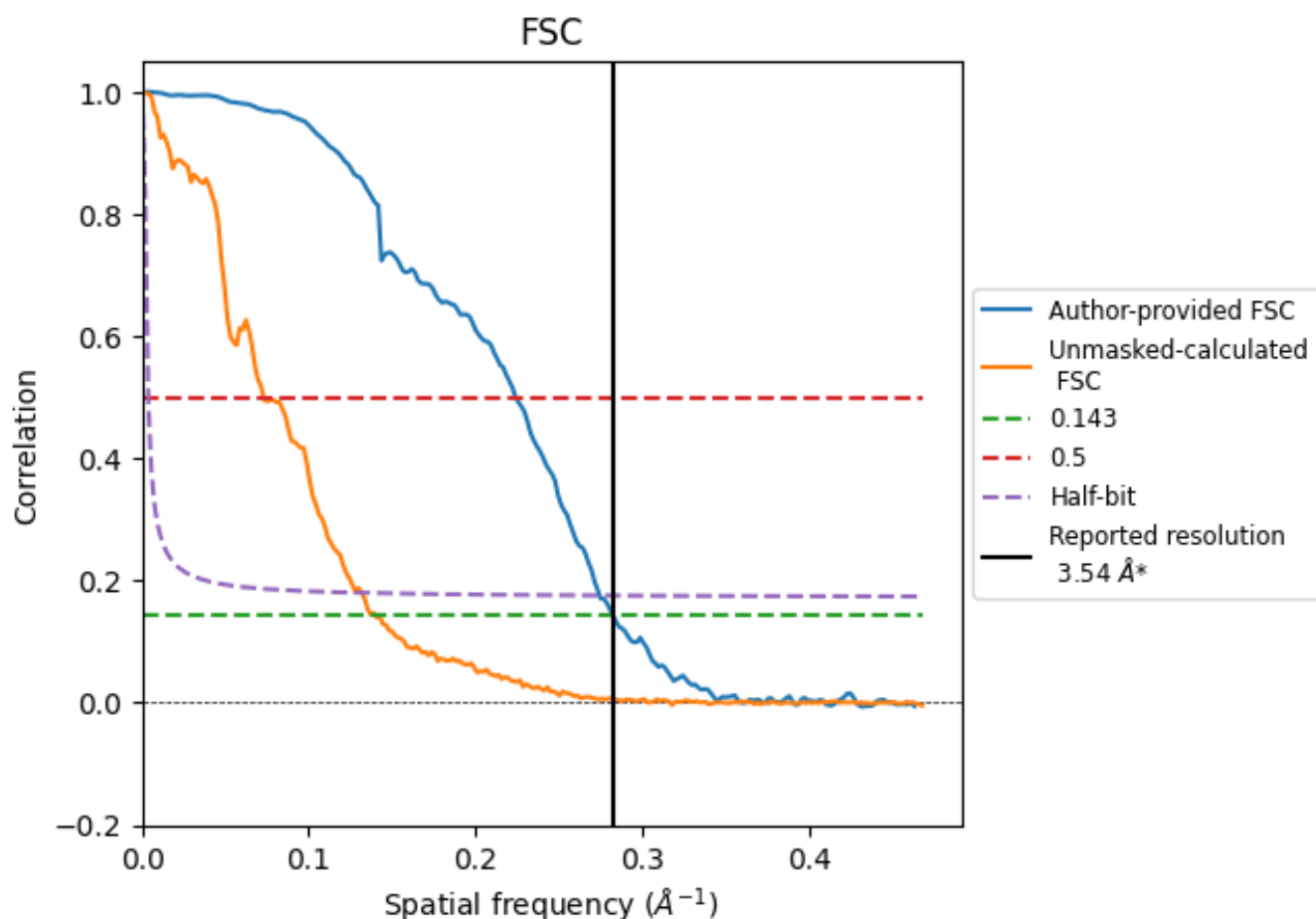


*Reported resolution corresponds to spatial frequency of 0.282 $\text{\AA}^{-1}$

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 0.282 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

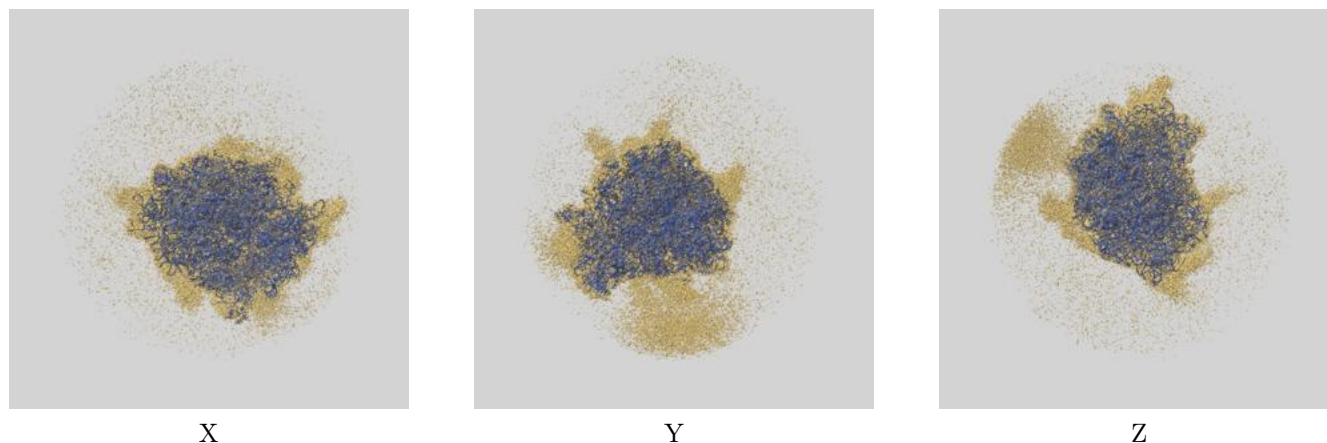
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	3.54	4.46	3.64
Unmasked-calculated*	7.15	13.74	7.59

*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 7.15 differs from the reported value 3.54 by more than 10 %

9 Map-model fit [i](#)

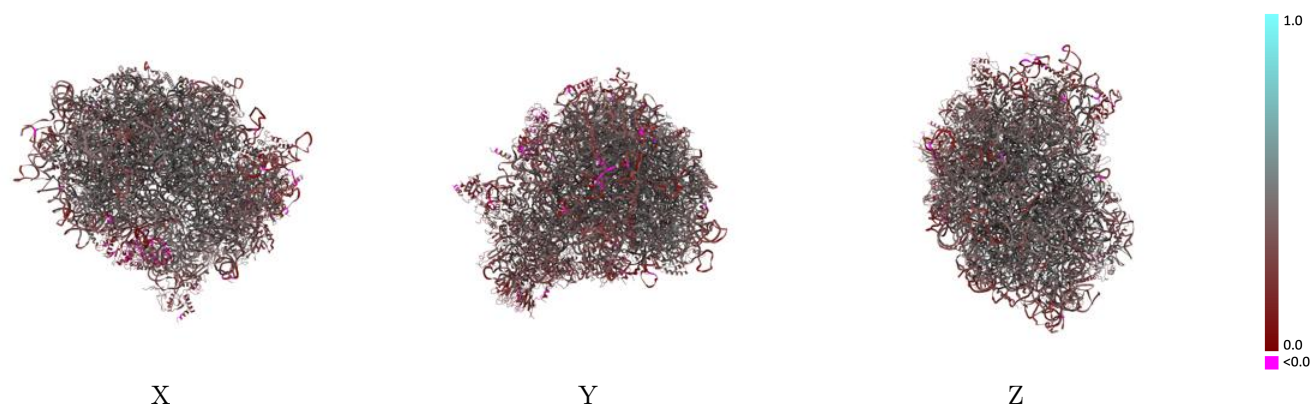
This section contains information regarding the fit between EMDB map EMD-71341 and PDB model 9P7G. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



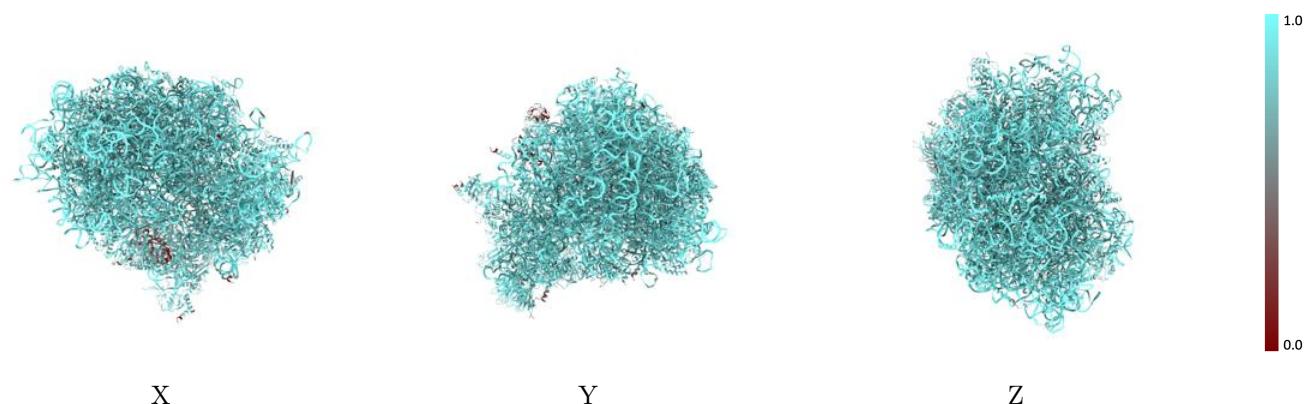
The images above show the 3D surface view of the map at the recommended contour level 0.0764 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



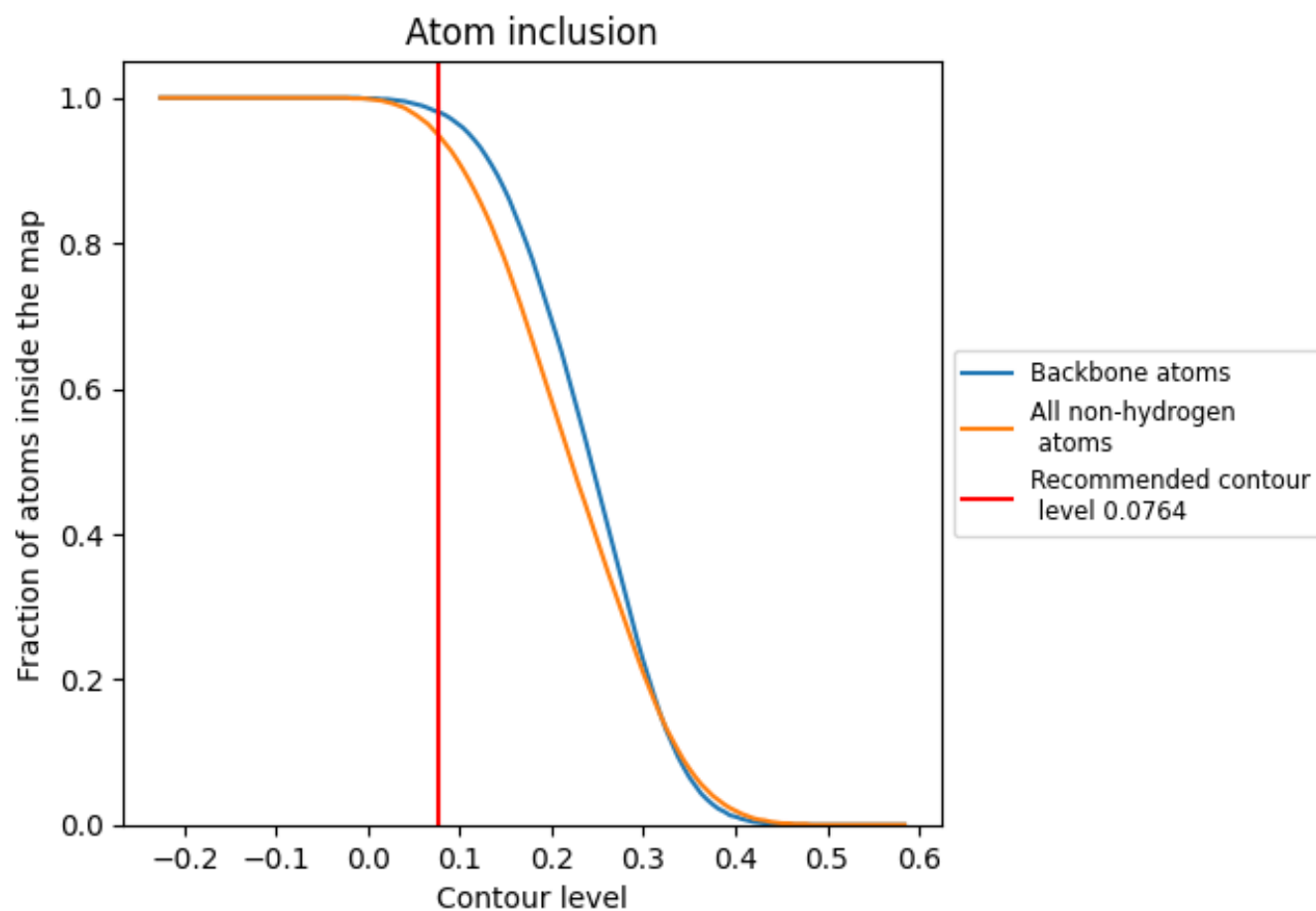
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0764).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% 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 (0.0764) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9490	 0.3770
At	 0.9650	 0.2730
CI	 0.7450	 0.3290
L5	 0.9860	 0.3890
L7	 0.9980	 0.4100
L8	 0.9910	 0.3980
LA	 0.9440	 0.4470
LB	 0.9260	 0.4360
LC	 0.9220	 0.4320
LD	 0.9300	 0.3840
LE	 0.9060	 0.3760
LF	 0.9290	 0.4230
LG	 0.8820	 0.3770
LH	 0.9120	 0.4210
LI	 0.9210	 0.4230
LJ	 0.8940	 0.3560
LL	 0.9080	 0.4010
LM	 0.9320	 0.3940
LN	 0.9570	 0.4460
LO	 0.9290	 0.4240
LP	 0.9200	 0.4410
LQ	 0.9410	 0.4430
LR	 0.9210	 0.3870
LS	 0.9490	 0.4470
LT	 0.9380	 0.4440
LU	 0.9090	 0.3610
LV	 0.9290	 0.4450
LW	 0.8850	 0.3290
LX	 0.9290	 0.4200
LY	 0.9220	 0.4150
LZ	 0.9370	 0.4050
La	 0.9560	 0.4490
Lb	 0.9040	 0.3650
Lc	 0.8890	 0.3830
Ld	 0.9190	 0.4150



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Chain	Atom inclusion	Q-score
Le	 0.9270	 0.4470
Lf	 0.9490	 0.4550
Lg	 0.9370	 0.4260
Lh	 0.9150	 0.4000
Li	 0.9290	 0.4080
Lj	 0.9540	 0.4430
Lk	 0.9070	 0.3840
Ll	 0.9480	 0.4330
Lm	 0.9420	 0.4470
Ln	 0.9520	 0.4040
Lo	 0.9290	 0.4260
Lp	 0.9090	 0.4150
Lr	 0.9330	 0.4420
Ls	 0.6020	 0.1540
Lt	 0.5490	 0.1260
Pt	 0.9750	 0.3220
S2	 0.9900	 0.3690
SA	 0.8810	 0.3280
SB	 0.8720	 0.3290
SC	 0.9280	 0.3850
SD	 0.8830	 0.3380
SE	 0.9210	 0.3720
SF	 0.8560	 0.3140
SG	 0.8880	 0.3140
SH	 0.8340	 0.2880
SI	 0.9180	 0.3620
SJ	 0.8930	 0.3560
SK	 0.8970	 0.2990
SL	 0.9130	 0.3930
SM	 0.7880	 0.2010
SN	 0.8980	 0.3660
SO	 0.8740	 0.3420
SP	 0.9030	 0.3330
SQ	 0.9010	 0.3290
SR	 0.8550	 0.3040
SS	 0.8680	 0.3200
ST	 0.8990	 0.3190
SU	 0.8810	 0.3130
SV	 0.9200	 0.3490
SW	 0.9380	 0.3920
SX	 0.9200	 0.4180
SY	 0.8650	 0.3100

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Chain	Atom inclusion	Q-score
SZ	 0.8320	 0.2800
Sa	 0.9150	 0.3790
Sb	 0.8750	 0.3430
Sc	 0.8760	 0.3410
Sd	 0.9520	 0.3730
Se	 0.8780	 0.3550
Sf	 0.8610	 0.2290
Sg	 0.8770	 0.2550
Zt	 0.8560	 0.1530