Full wwPDB EM Validation Report (i)

Sep 20, 2026 – 11:23 am BST

PDB ID	:	9TT7 / pdb_00009tt7
EMDB ID	:	EMD-56227
Title	:	80S ribosome of WT EBV infected human B-cells
Authors	:	Fedorenko, A.; Bashan, A.; Yonath, A.
Deposited on	:	2026-01-06
Resolution	:	2.20 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 (i) 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 (1)) were used in the production of this report:

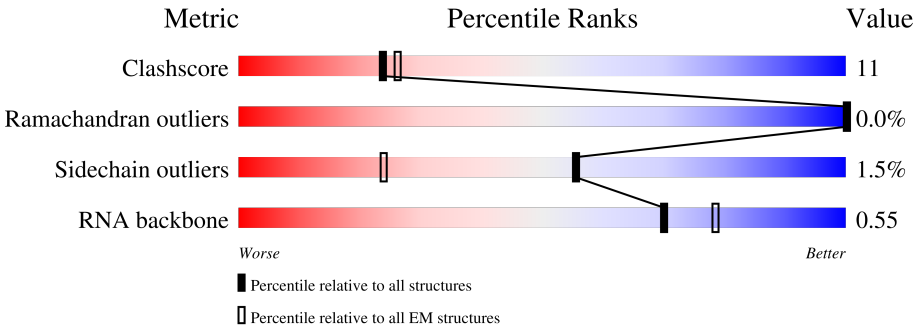
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

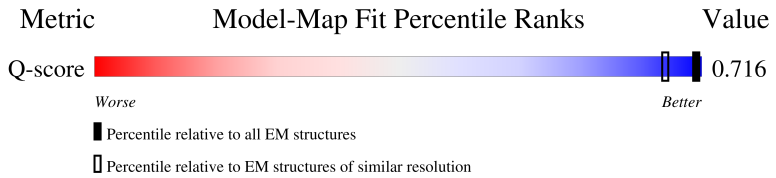
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.20 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	3184 (1.71 - 2.70)

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 <=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	L5	5054	30% 27% • 39%
2	L7	121	64% 28% 6% •
3	L8	156	44% 43% 6% 7%

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Mol	Chain	Length	Quality of chain
4	LC	427	67% 15% 18%
5	LD	297	74% 22% •
6	LE	288	54% 18% • 27%
7	LF	248	71% 17% 12%
8	LG	266	65% 14% 21%
9	LJ	178	17% 7% 76%
10	LM	215	45% 16% 39%
11	LN	204	85% 15%
12	LO	203	79% 18% •
13	LP	184	65% 17% 17%
14	LQ	188	84% 15% •
15	LT	160	82% 11% 8%
16	LU	128	48% 26% 26%
17	LX	156	66% 9% 25%
18	LY	145	70% 17% • 12%
19	LZ	136	74% 25% ••
20	La	148	91% 7% •
21	Lb	159	45% 8% 47%
22	Lc	115	62% 16% 23%
23	Ld	125	59% 18% 22%
24	Le	135	80% 13% 7%
25	Lf	110	89% 8% •
26	Lg	117	75% 11% 14%
27	Lh	123	84% 15% •
28	Li	105	65% 25% 10%

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Mol	Chain	Length	Quality of chain
29	Lj	97	78% 10% 11%
30	Lk	70	71% 20% 9%
31	Ll	51	73% 24% •
32	Lm	128	34% • 62%
33	Lo	106	73% 15% 12%
34	Lp	92	75% 20% 5%
35	Lr	137	75% 12% 13%
36	LA	257	83% 12% 5%
37	LB	403	80% 17% •
38	LH	192	71% 22% • 6%
39	LI	214	72% 18% 9%
40	LL	211	79% 11% 10%
41	LS	176	77% 19% • •
42	S2	1869	35% 37% 8% 20%
43	SA	295	50% 19% 31%
44	SB	264	53% 23% • 24%
45	SC	293	60% 12% 28%
46	SD	243	59% 26% 15%
47	SE	263	76% 21% •
48	SF	204	66% 22% 13%
49	SG	249	56% 18% 26%
50	SH	194	58% 16% • 25%
51	SI	208	69% 12% 19%
52	SJ	194	77% 15% 8%
53	SK	165	42% 13% • 44%

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Mol	Chain	Length	Quality of chain
54	SL	158	69% 15% 16%
55	SN	151	73% 21% 6%
56	SO	151	63% 19% • 18%
57	SP	145	71% 8% 21%
58	SQ	146	64% 30% • •
59	SR	135	61% 24% • 13%
60	SS	152	64% 27% 9%
61	ST	145	77% 20% • •
62	SU	119	53% 16% • 30%
63	SV	83	65% 35%
64	SW	130	75% 24% •
65	SX	143	78% 20% •
66	SY	133	56% 32% • 12%
67	SZ	125	45% 11% 44%
68	Sa	115	65% 19% • 15%
69	Sb	84	51% 21% 27%
70	Sc	69	70% 7% 23%
71	Sd	56	64% 16% 20%
72	Se	98	38% 7% • 54%
73	Sg	310	60% 29% • 10%
74	Ln	25	60% 40%
75	LR	196	68% 10% 21%
76	S6	14	7% 57% 29% 7%
77	LV	140	80% 13% 7%
78	LW	157	32% 7% 61%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
42	OMU	S2	1804	-	-	X	-

2 Entry composition (i)

There are 83 unique types of molecules in this entry. The entry contains 185896 atoms, of which 13 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 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	L5	3066	65849	29368	12063	21352	3066	0	0

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	L7	119	2538	1132	455	833	118	0	0

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	L8	145	3094	1381	553	1015	145	0	0

- Molecule 4 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	LC	352	2761	1743	549	455	14	0	0

- Molecule 5 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LD	285	2281	1443	411	414	13	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	LE	210	1675	1082	314	276	3	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	LF	218	1770	1134	337	291	8	0	0

- Molecule 8 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	LG	209	1527	979	285	259	4	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	LJ	43	321	203	67	48	3	0	0

- Molecule 10 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LM	132	1074	687	207	173	7	0	0

- Molecule 11 is a protein called 60S ribosomal protein L15.

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

- Molecule 12 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LO	198	1575	1015	305	250	5	0	0

- Molecule 13 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LP	152	1211	759	238	205	9	0	0

- Molecule 14 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	LQ	187	1473	919	303	246	5	0	0

- Molecule 15 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	LT	148	1168	743	232	188	5	0	0

- Molecule 16 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	LU	95	619	399	111	108	1	0	0

- Molecule 17 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	LX	117	902	581	166	154	1	0	0

- Molecule 18 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	LY	128	998	632	200	163	3	0	0

- Molecule 19 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	LZ	135	1041	673	192	173	3	0	0

- Molecule 20 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	La	145	1116	708	229	176	3	0	0

- Molecule 21 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	Lb	84	610	380	127	102	1	0	0

- Molecule 22 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Lc	89	648	411	113	118	6	0	0

- Molecule 23 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Ld	97	769	491	151	126	1	0	0

- Molecule 24 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Le	126	988	625	201	157	5	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Lf	107	830	529	164	134	3	0	0

- Molecule 26 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Lg	101	765	477	156	126	6	0	0

- Molecule 27 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Lh	121	930	586	188	155	1	0	0

- Molecule 28 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	Li	94	692	437	139	112	4	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	Lj	86	687	422	152	108	5	0	0

- Molecule 30 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Lk	64	446	284	83	78	1	0	0

- Molecule 31 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
31	Ll	49	400	256	83	61	0	0

- Molecule 32 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	Lm	48	361	221	75	59	6	0	0

- Molecule 33 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Lo	93	723	454	145	118	6	0	0

- Molecule 34 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Lp	87	641	404	120	110	7	0	0

- Molecule 35 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Lr	119	933	578	192	159	4	1	0

- Molecule 36 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	LA	245	1794	1124	362	302	6	0	0

- Molecule 37 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	LB	391	2950	1883	558	497	12	0	0

- Molecule 38 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	LH	180	1312	834	242	230	6	0	0

- Molecule 39 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	LI	195	1472	937	277	247	11	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	49	CYS	GLY	conflict	UNP Q96L21

- Molecule 40 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	LL	190	1422	895	293	230	4	0	0

- Molecule 41 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	LS	170	1376	879	262	225	10	0	0

- Molecule 42 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
42	S2	1503	32177	14387	13	5797	10478	1502	0	0

- Molecule 43 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	SA	205	1568	1004	278	278	8	0	0

- Molecule 44 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	SB	201	1525	975	275	262	13	0	0

- Molecule 45 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	SC	212	1545	1006	264	266	9	0	0

- Molecule 46 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	SD	206	1364	881	240	238	5	0	0

- Molecule 47 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	SE	257	1940	1244	361	327	8	0	0

- Molecule 48 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	SF	178	1319	835	248	229	7	0	0

- Molecule 49 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	SG	185	1307	826	259	217	5	0	0

- Molecule 50 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
50	SH	146	1022	659	191	172	0	0

- Molecule 51 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	SI	169	1284	811	247	223	3	0	0

- Molecule 52 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	SJ	178	1321	849	267	203	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	SK	92	652	428	117	102	5	0	0

- Molecule 54 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	SL	132	1010	641	190	173	6	0	0

- Molecule 55 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	SN	142	1077	694	201	181	1	0	0

- Molecule 56 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	SO	124	892	548	177	162	5	0	0

- Molecule 57 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	SP	114	835	539	155	135	6	0	0

- Molecule 58 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	SQ	140	1065	681	200	181	3	0	0

- Molecule 59 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	SR	117	833	530	156	143	4	0	0

- Molecule 60 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	SS	139	1057	676	210	170	1	0	0

- Molecule 61 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	ST	142	1055	662	205	186	2	0	0

- Molecule 62 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	SU	83	609	380	118	107	4	0	0

- Molecule 63 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	SV	83	622	385	114	118	5	0	0

- Molecule 64 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	SW	129	1020	651	189	174	6	0	0

- Molecule 65 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	SX	139	1060	669	211	177	3	0	0

- Molecule 66 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	SY	117	934	592	184	153	5	0	0

- Molecule 67 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	SZ	70	518	333	92	92	1	0	0

- Molecule 68 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	Sa	98	740	465	150	120	5	0	0

- Molecule 69 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Sb	61	463	294	88	79	2	0	0

- Molecule 70 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	Sc	53	370	228	76	65	1	0	0

- Molecule 71 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	Sd	45	356	220	74	57	5	0	0

- Molecule 72 is a protein called FAU ubiquitin like and ribosomal protein S30 fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	Se	45	341	208	78	54	1	0	0

- Molecule 73 is a protein called RS8_HUMAN Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	Sg	278	2055	1312	360	374	9	0	0

- Molecule 74 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	Ln	25	199	121	51	26	1	0	0

- Molecule 75 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	LR	154	1200	751	256	184	9	0	0

- Molecule 76 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
76	S6	13	281	125	55	88	13	0	0

- Molecule 77 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	LV	130	943	595	177	166	5	1	0

- Molecule 78 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	LW	61	477	304	91	80	2	0	0

- Molecule 79 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
79	L5	142	142	142	0
79	L7	2	2	2	0
79	L8	3	3	3	0
79	LN	1	1	1	0
79	LP	1	1	1	0
79	LI	1	1	1	0
79	S2	25	25	25	0
79	LV	1	1	1	0

- Molecule 80 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
			Total	K	
80	L5	24	24	24	0
80	L7	1	1	1	0

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Mol	Chain	Residues	Atoms	AltConf
80	Lf	1	Total K 1 1	0
80	Lo	1	Total K 1 1	0
80	LA	2	Total K 2 2	0
80	LH	1	Total K 1 1	0
80	LI	1	Total K 1 1	0
80	S2	3	Total K 3 3	0
80	SF	1	Total K 1 1	0
80	SL	1	Total K 1 1	0
80	SO	1	Total K 1 1	0

- Molecule 81 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	AltConf
81	L5	12	Total Na 12 12	0
81	S2	1	Total Na 1 1	0

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
82	Sd	1	1	1	0

- Molecule 83 is water.

Mol	Chain	Residues	Atoms		AltConf
			Total	O	
83	L5	2093	2093	2093	0
			Total	O	
83	L7	51	51	51	0
			Total	O	
83	L8	135	135	135	0
			Total	O	
83	LC	85	85	85	0
			Total	O	
83	LD	15	15	15	0
			Total	O	
83	LE	10	10	10	0
			Total	O	
83	LF	42	42	42	0
			Total	O	
83	LG	10	10	10	0
			Total	O	
83	LM	2	2	2	0
			Total	O	
83	LN	69	69	69	0
			Total	O	
83	LO	34	34	34	0
			Total	O	
83	LP	33	33	33	0
			Total	O	
83	LQ	59	59	59	0
			Total	O	
83	LT	26	26	26	0
			Total	O	
83	LX	7	7	7	0
			Total	O	
83	LY	14	14	14	0
			Total	O	
83	LZ	4	4	4	0
			Total	O	
83	La	43	43	43	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	O	
83	Lb	13	13	13	0
			Total	O	
83	Lc	2	2	2	0
			Total	O	
83	Ld	9	9	9	0
			Total	O	
83	Le	41	41	41	0
			Total	O	
83	Lf	20	20	20	0
			Total	O	
83	Lg	22	22	22	0
			Total	O	
83	Lh	5	5	5	0
			Total	O	
83	Li	7	7	7	0
			Total	O	
83	Lj	21	21	21	0
			Total	O	
83	Lk	1	1	1	0
			Total	O	
83	Ll	8	8	8	0
			Total	O	
83	Lm	2	2	2	0
			Total	O	
83	Lo	11	11	11	0
			Total	O	
83	Lp	12	12	12	0
			Total	O	
83	Lr	19	19	19	0
			Total	O	
83	LA	75	75	75	0
			Total	O	
83	LB	70	70	70	0
			Total	O	
83	LH	7	7	7	0
			Total	O	
83	LI	6	6	6	0
			Total	O	
83	LL	32	32	32	0
			Total	O	
83	LS	5	5	5	0

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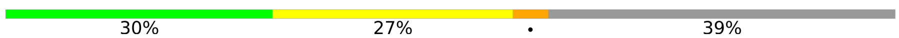
Mol	Chain	Residues	Atoms		AltConf
			Total	O	
83	S2	29	29	29	0
			Total	O	
83	SS	2	2	2	0
			Total	O	
83	Sa	2	2	2	0
			Total	O	
83	Sb	1	1	1	0
			Total	O	
83	LR	8	8	8	0
			Total	O	
83	S6	2	2	2	0
			Total	O	
83	LV	18	18	18	0
			Total	O	
83	LW	2	2	2	0

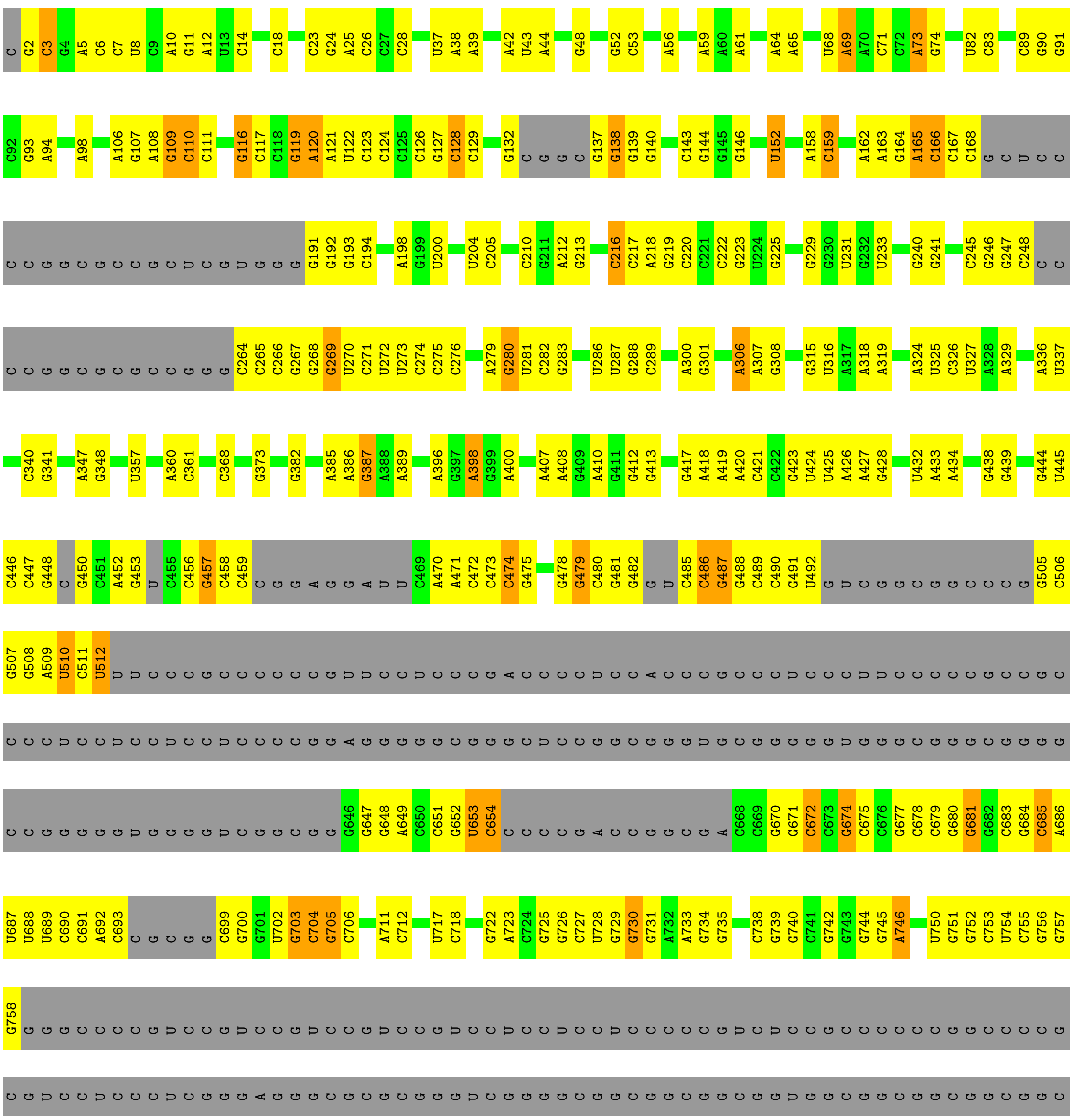
3 Residue-property plots

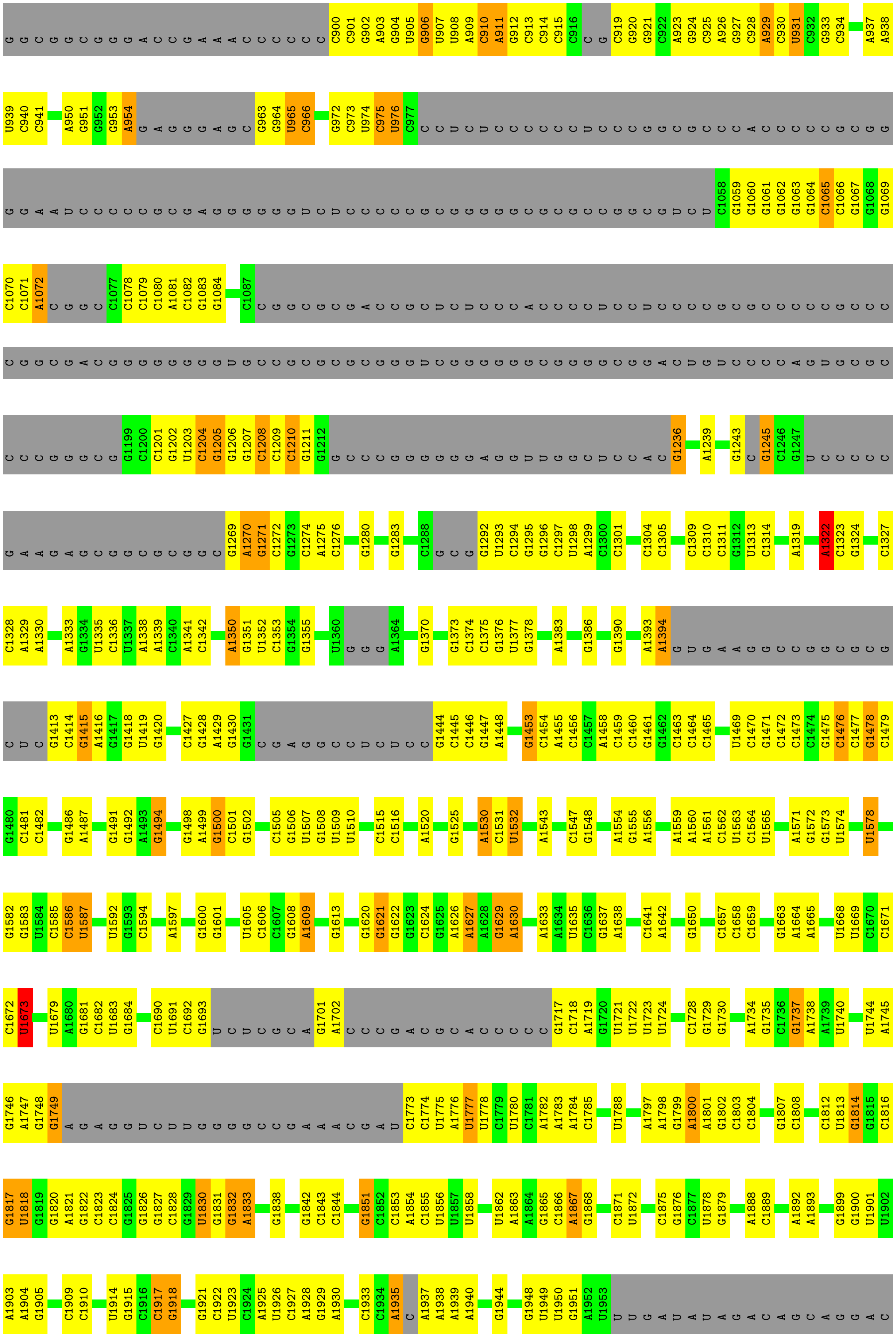
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 28S rRNA

Chain L5:



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G A A G A G C G G C G C G G C G1269 A1270 G1271 C1272 G1273 C1274 A1275 C1276 G1280 G1283 C1288 G C G G1292 U1293 C1294 G1295 G1296 C1297 U1298 A1299 C1300 C1301 C1304 C1305 C1309 C1310 C1311 G1312 U1313 C1314 A1319 A1322 C1323 G1324 C1327
C1328 A1329 A1330 A1333 G1334 U1335 C1336 U1337 A1338 A1339 C1340 A1341 C1342 A1350 G1351 U1352 C1353 G1354 G1355 U1360 G G G A1364 G1370 G1373 C1374 C1375 G1376 U1377 G1378 A1383 G1386 G1390 A1393 A1394 G U G A A G G C C G G C G C G
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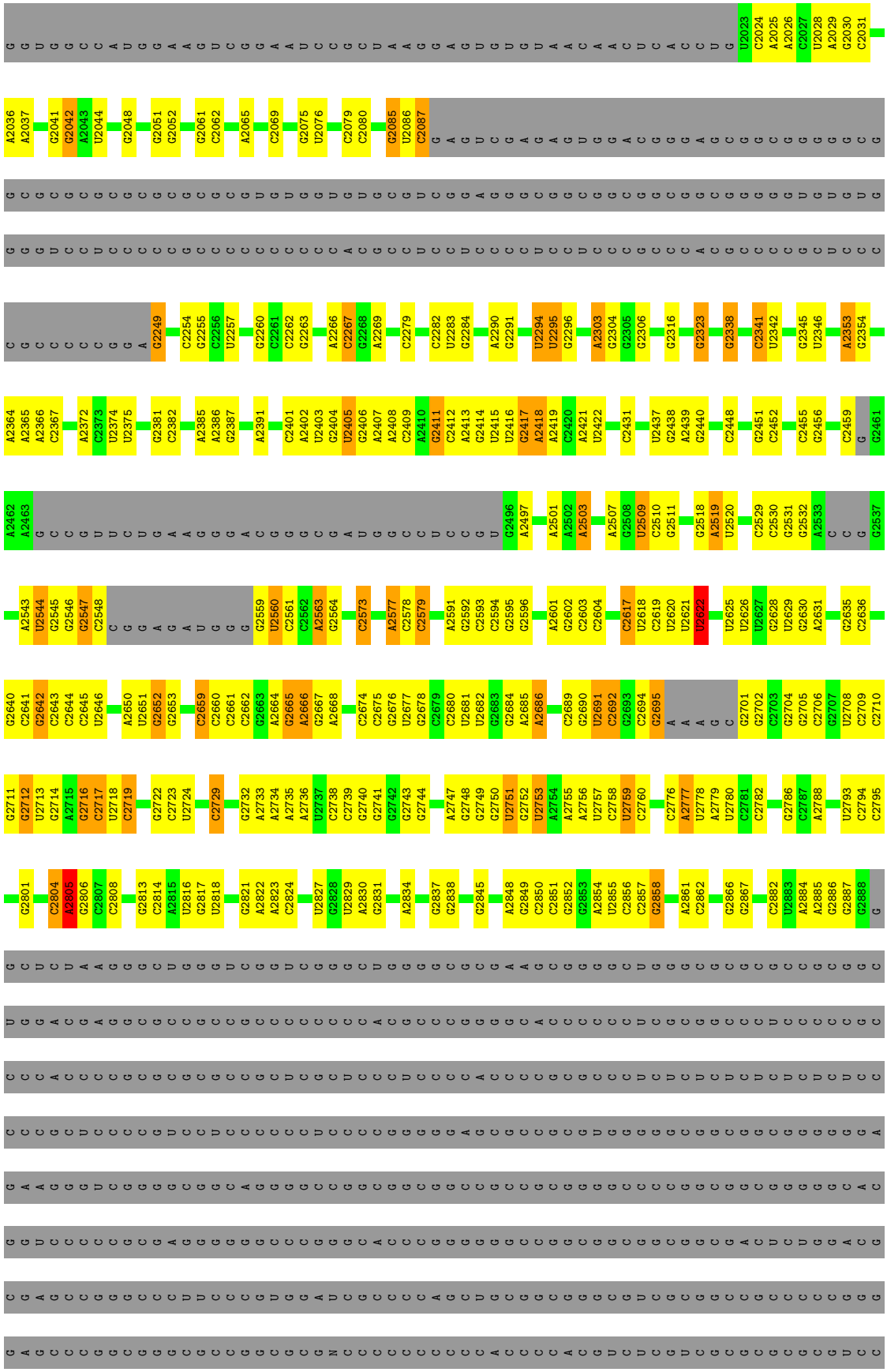
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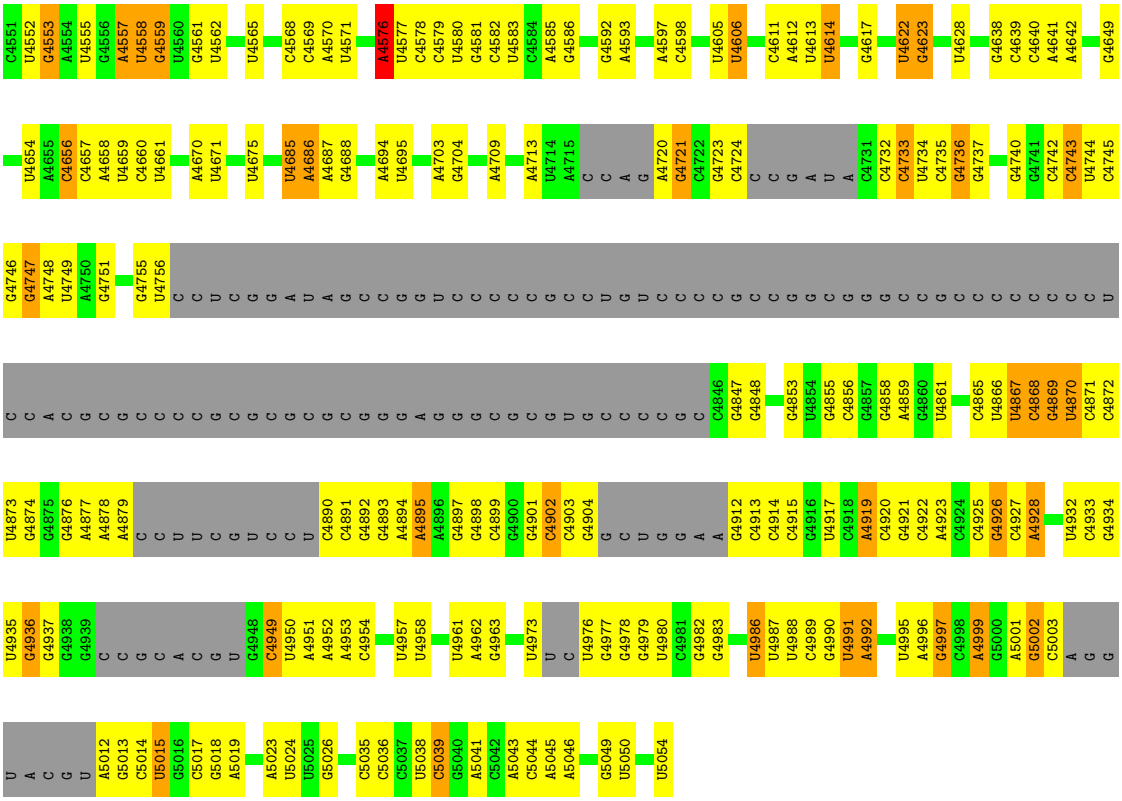
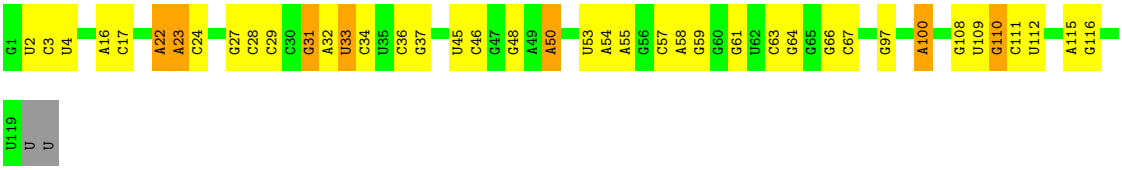


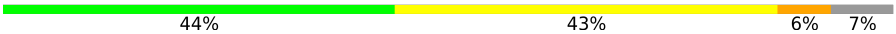
- Molecule 2: 5S rRNA

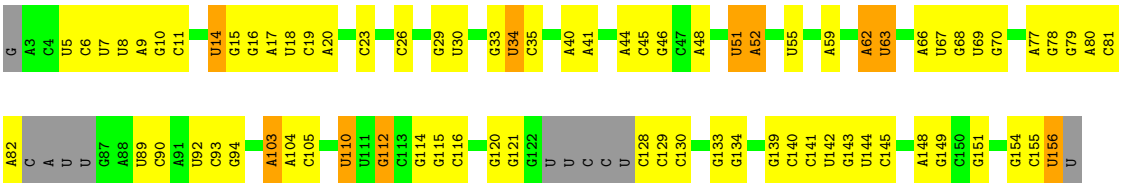
Chain L7:



- Molecule 3: 5.8S rRNA

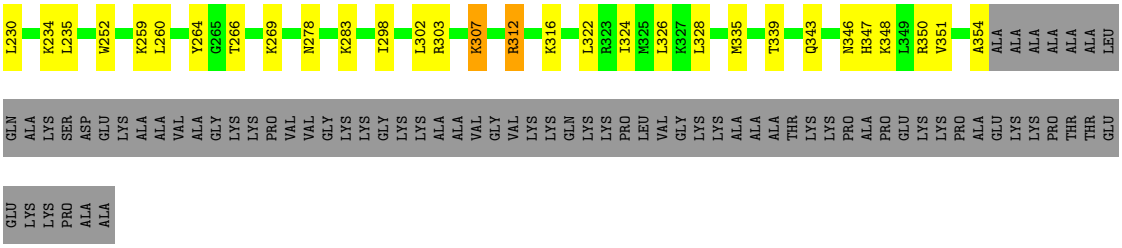
Chain L8:





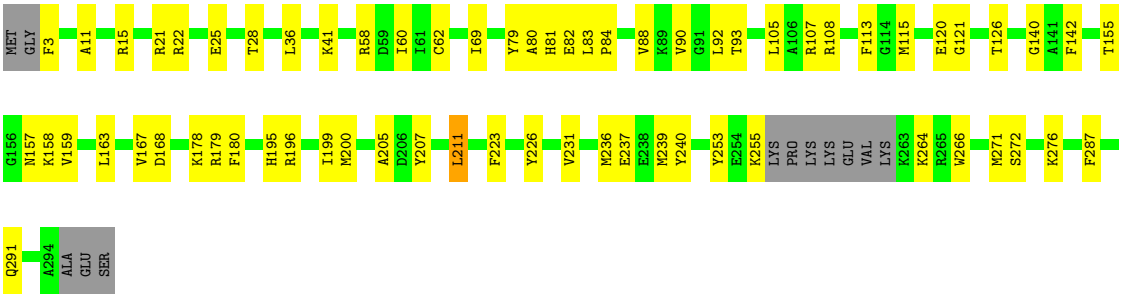
- Molecule 4: 60S ribosomal protein L4

Chain LC:



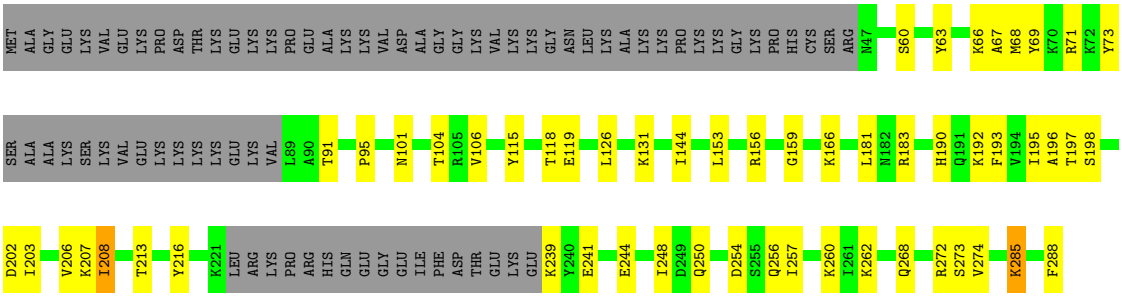
• Molecule 5: 60S ribosomal protein L5

Chain LD:



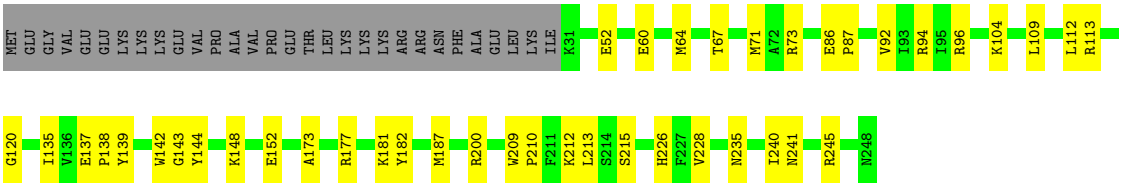
• Molecule 6: Large ribosomal subunit protein eL6

Chain LE:



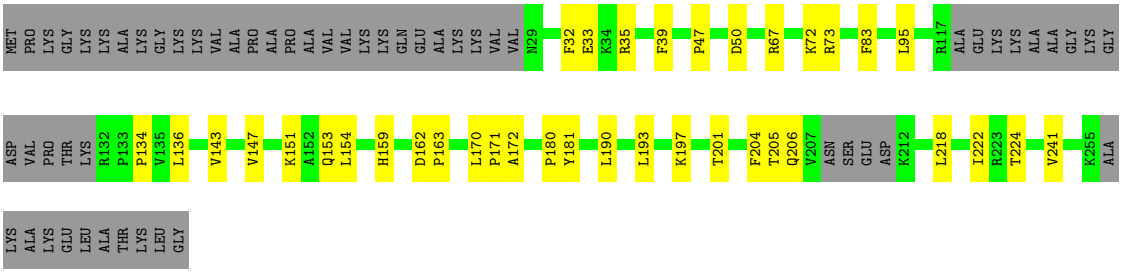
• Molecule 7: Large ribosomal subunit protein uL30

Chain LF:



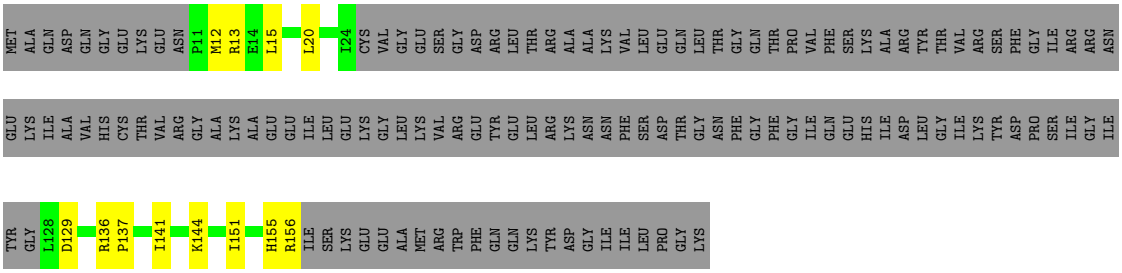
• Molecule 8: 60S ribosomal protein L7a

Chain LG:



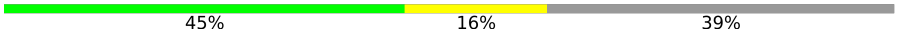
- Molecule 9: Large ribosomal subunit protein uL5

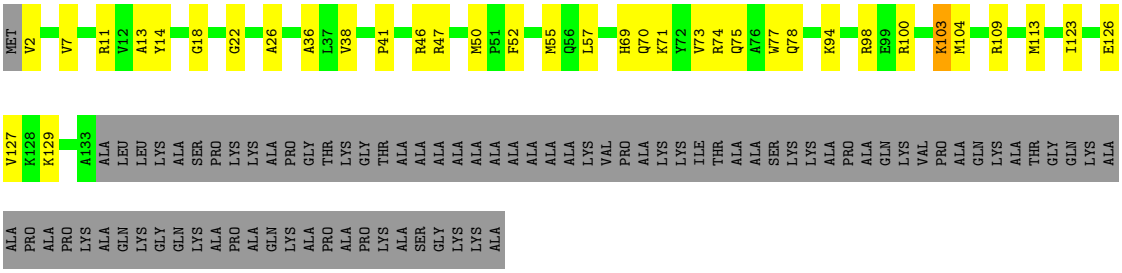
Chain LJ:



- Molecule 10: 60S ribosomal protein L14

Chain LM:



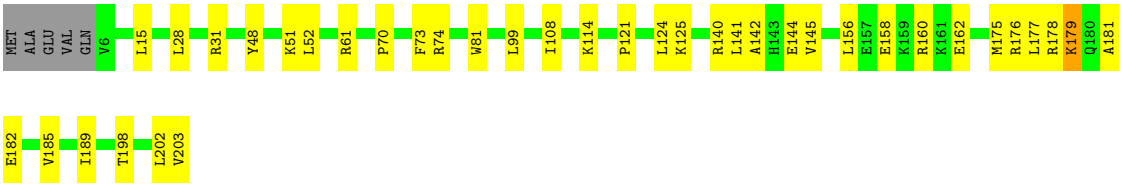


- Molecule 11: 60S ribosomal protein L15

Chain LN:

- Molecule 12: 60S ribosomal protein L13a

Chain LO:



- Molecule 13: 60S ribosomal protein L17

Chain LP: 65% 17% 17%

MET V2 R3 L6 T12 K13 K16 T29 R30 E31 T32 A33 I41 T45 K46 Y47 L48 K49 D50 V51 Q54 W83 E89 M94 L95 K105 G106 L107 I114 I117 M125 Y139 M140 P143 I146 E147 M148 I149 E152 K153 GLU GLN

ILE VAL PRO LYS PRO GLU GLU GLU VAL ALA GLN LYS LYS LYS ILE SER GLN LYS LYS LEU LYS LYS GLN LYS LEU MET ALA ARG GLU

- Molecule 14: 60S ribosomal protein L18

Chain LQ: 84% 15% •

MET G2 K9 R14 D22 R26 F34 R38 R50 M53 S64 R65 M66 K69 M70 K71 L72 R75 T79 A80 I86 V92 K99 V100 R143 K144 E147 R150 V167 R172 A177 R178 R184 M188

- Molecule 15: 60S ribosomal protein L21

Chain LT: 82% 11% 8%

MET T2 R17 I39 T47 V91 R92 I93 S99 F105 R108 V109 K116 LYS GLU ALA LYS GLU LYS GLY THR TRP VAL Q127 L128 K129 R130 R136 F140 V141 R142 L150 P153 M159 ALA

- Molecule 16: 60S ribosomal protein L22

Chain LU: 48% 26% 26%

MET ALA PRO VAL LYS LYS LEU VAL VAL LYS GLY GLY LYS LYS LYS LYS GLN VAL L19 K20 F21 T22 L23 D24 C25 T26 H27 P28 I33 M34 ASP ALA A37 N38 F39 L43 I47 K48 K52 A53 L56 G59 V60 S68 T71 V72 T73 S74 E75 V76 P77

K80 L83 K84 Y85 L86 T87 K88 L91 L100 E108 S109 Y110 E111 L112 F115 GLN ILE ASN GLN ASP GLU GLU GLU GLU GLU GLU ASP GLU ASP

- Molecule 17: 60S ribosomal protein L23a

Chain LX: 66% 9% 25%

MET ALA PRO LYS ALA LYS LYS GLU ALA PRO ALA PRO PRO LYS ALA GLU ALA LYS ALA LYS ALA LEU LYS ALA LYS LYS ALA VAL LEU LYS GLY VAL HIS SER HIS LYS LYS LYS K39 I40 R53 K89 T95 D101 V102 K103 K110 K114 Y117 D118 I119 L127

V138 V149 I153 G154 I155 ILE

- Molecule 18: 60S ribosomal protein L26

Chain LY: 70% 17% • 12%

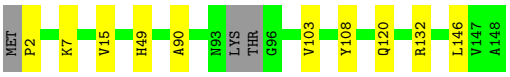
M1 R11 R27 L38 Y42 N43 Q56 V57 V58 I67 G68 K69 V70 V71 Y74 R75 K76 K77 I80 Y81 I82 E83 N91 G92 T93 T94 V95 K103 T107 K116 E120 R126 Q127 V128 GLY LYS GLU LYS GLY LYS TYR LYS GLU GLU THR ILE

• Molecule 19: 60S ribosomal protein L27

Chain LZ:

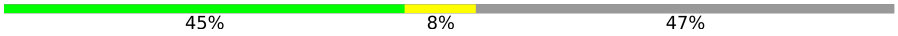
• Molecule 20: Large ribosomal subunit protein uL15

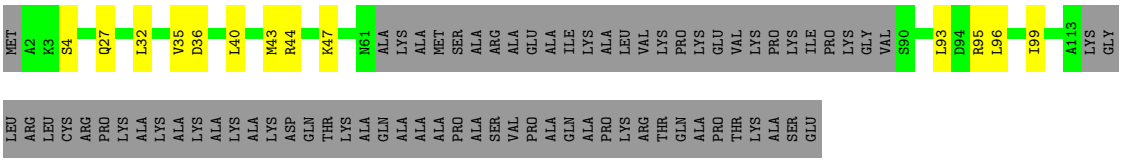
Chain La:



• Molecule 21: 60S ribosomal protein L29

Chain Lb:



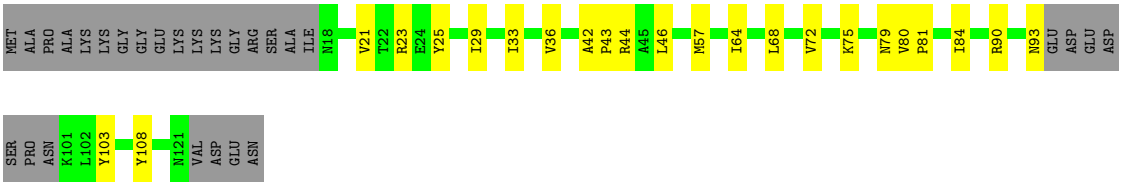


• Molecule 22: 60S ribosomal protein L30

Chain Lc:

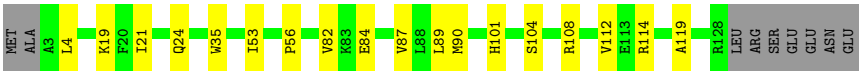
• Molecule 23: 60S ribosomal protein L31

Chain Ld:



• Molecule 24: 60S ribosomal protein L32

Chain Le:

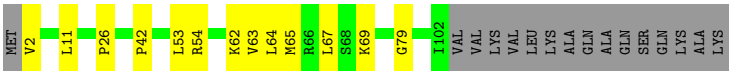


• Molecule 25: Large ribosomal subunit protein eL33

Chain Lf:

• Molecule 26: 60S ribosomal protein L34

Chain Lg:



• Molecule 27: 60S ribosomal protein L35

Chain Lh:

• Molecule 28: 60S ribosomal protein L36

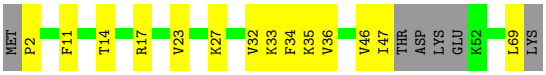
Chain Li:

• Molecule 29: Large ribosomal subunit protein eL37

Chain Lj:

• Molecule 30: 60S ribosomal protein L38

Chain Lk:



• Molecule 31: 60S ribosomal protein L39

Chain Ll: 73% 24% •

MET S2 T6 I9 K10 R11 F12 L13 K16 Q17 I23 T31 H43 W44 R45 L49 G50 LEU

• Molecule 32: Ubiquitin-60S ribosomal protein L40

Chain Lm: 34% • 62%

MET GLN ILE PHE VAL LYS THR LEU THR GLY LYS THR ILE THR LEU GLU VAL GLU PRO SER ASP THR ILE GLU ASN VAL LYS ALA LYS ILE GLN ASP LYS GLU GLY ILE PRO PRO ASP GLN GLN ARG LEU ILE PHE ALA GLY LYS GLN LEU GLU ASP GLY ARG THR LEU SER ASP TYR ASN

ILE GLN LYS GLU SER THR LEU HIS LEU VAL LEU ARG LEU ARG GLY GLY ILE ILE E79 L82 C91 H104 A107 K125 K126 VAL LYS

• Molecule 33: 60S ribosomal protein L36a

Chain Lo: 73% 15% 12%

MET V2 K6 K14 V23 A35 Q36 G37 K38 R39 I66 V67 L68 R69 L70 M82 L83 A84 R87 C88 G94 GLY ASP LYS LYS ARG LYS GLY GLN VAL ILE GLN PHE

• Molecule 34: 60S ribosomal protein L37a

Chain Lp: 75% 20% 5%

MET A2 V8 V11 Y18 R23 K24 M25 V26 I29 E30 T38 T45 V64 W69 T78 V79 R80 S81 A82 I83 R84 R85 E88 LEU LYS ASP GLN

• Molecule 35: 60S ribosomal protein L28

Chain Lr: 75% 12% 13%

MET S2 S14 L17 S26 K33 S37 Y40 K47 A54 ALA ASP G57 V60 I64 K65 R66 R67 T75 S76 Y77 V78 R79 Y102 I117 K122 PRO VAL MET VAL LYS ARG LYS ARG THR ARG PRO THR LYS SER SER

• Molecule 36: 60S ribosomal protein L8

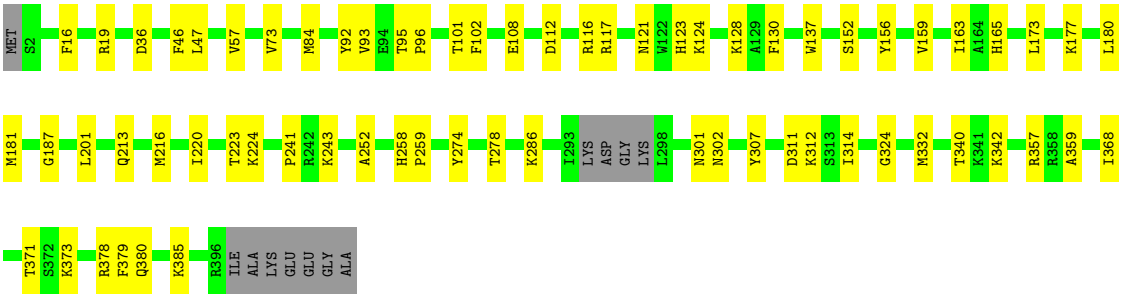
Chain LA: 83% 12% 5%

MET G2 R9 V20 K21 H22 R23 K24 R28 L29 R30 I49 P52 E74 H83 Q86 V101 L102 E117 G124 A129 N132 T135 V136 I137 P141 K149 V165 I175 L180 G183 M204 N205 P206 K221 R233

A240 R241 R242 L246 ARG GLY THR LYS THR VAL GLN GLU LYS GLU ASN

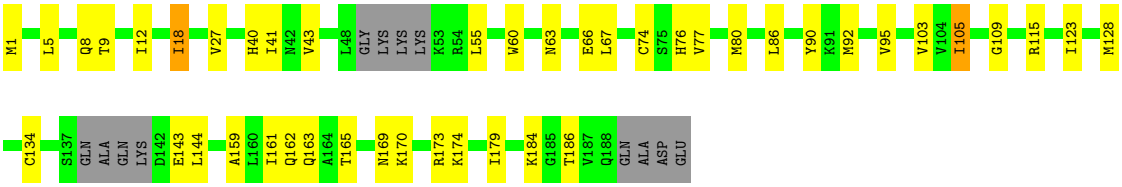
• Molecule 37: Large ribosomal subunit protein uL3

Chain LB: 80% 17% •



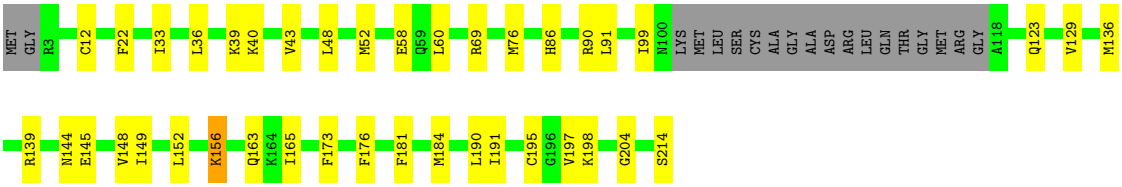
- Molecule 38: 60S ribosomal protein L9

Chain LH:



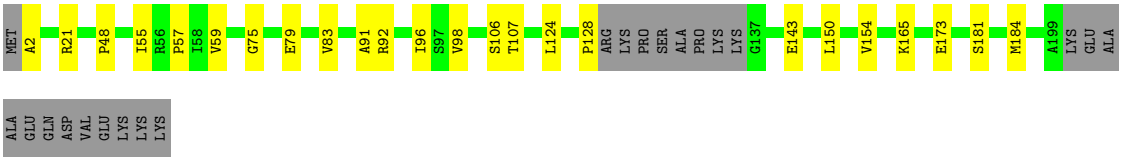
- Molecule 39: 60S ribosomal protein L10-like

Chain LI:



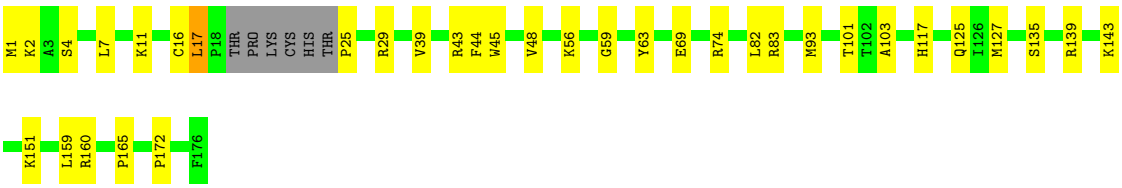
- Molecule 40: Large ribosomal subunit protein eL13

Chain LL:



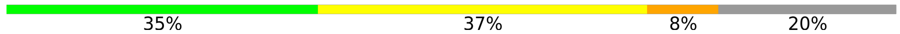
- Molecule 41: 60S ribosomal protein L18a

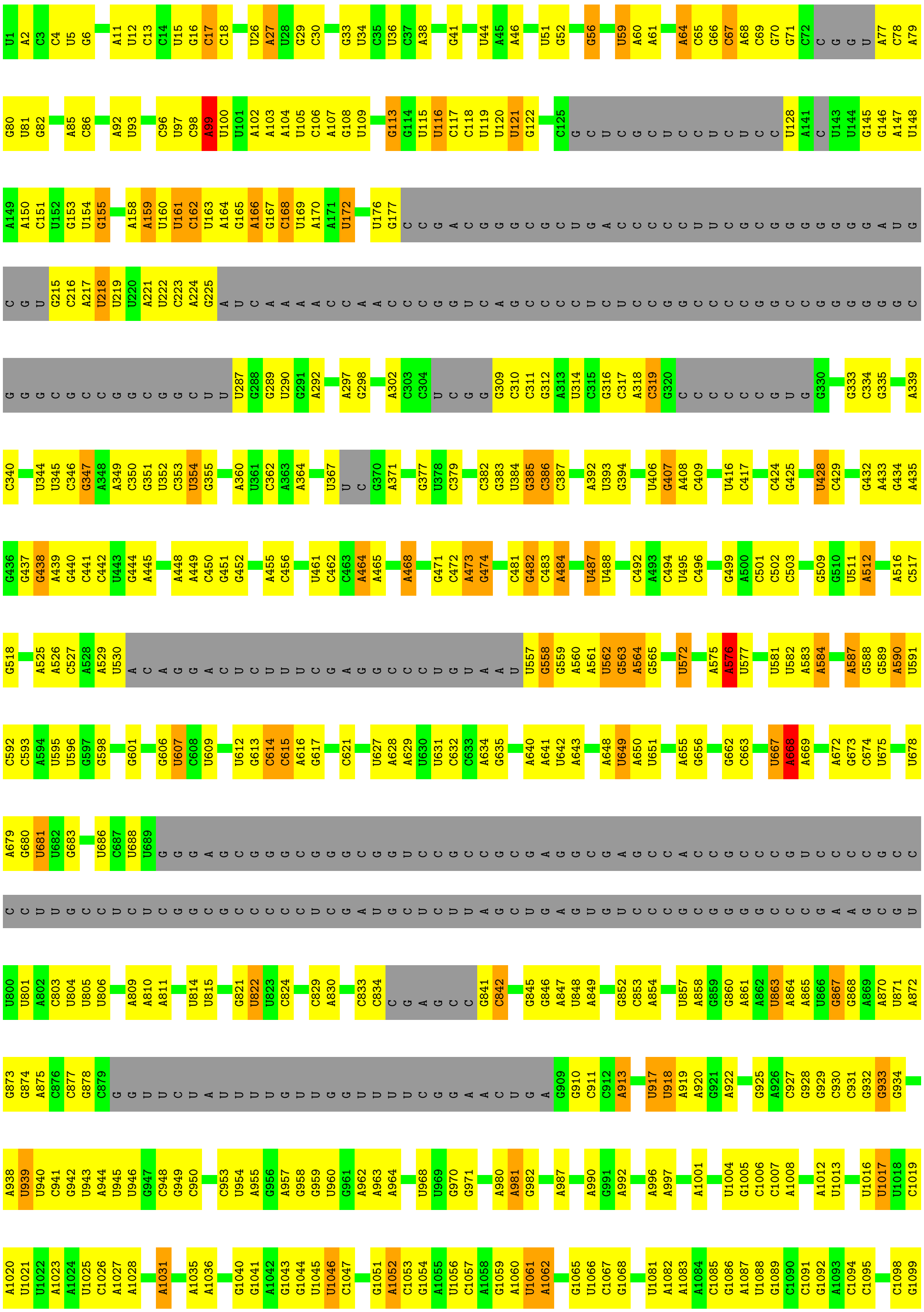
Chain LS:

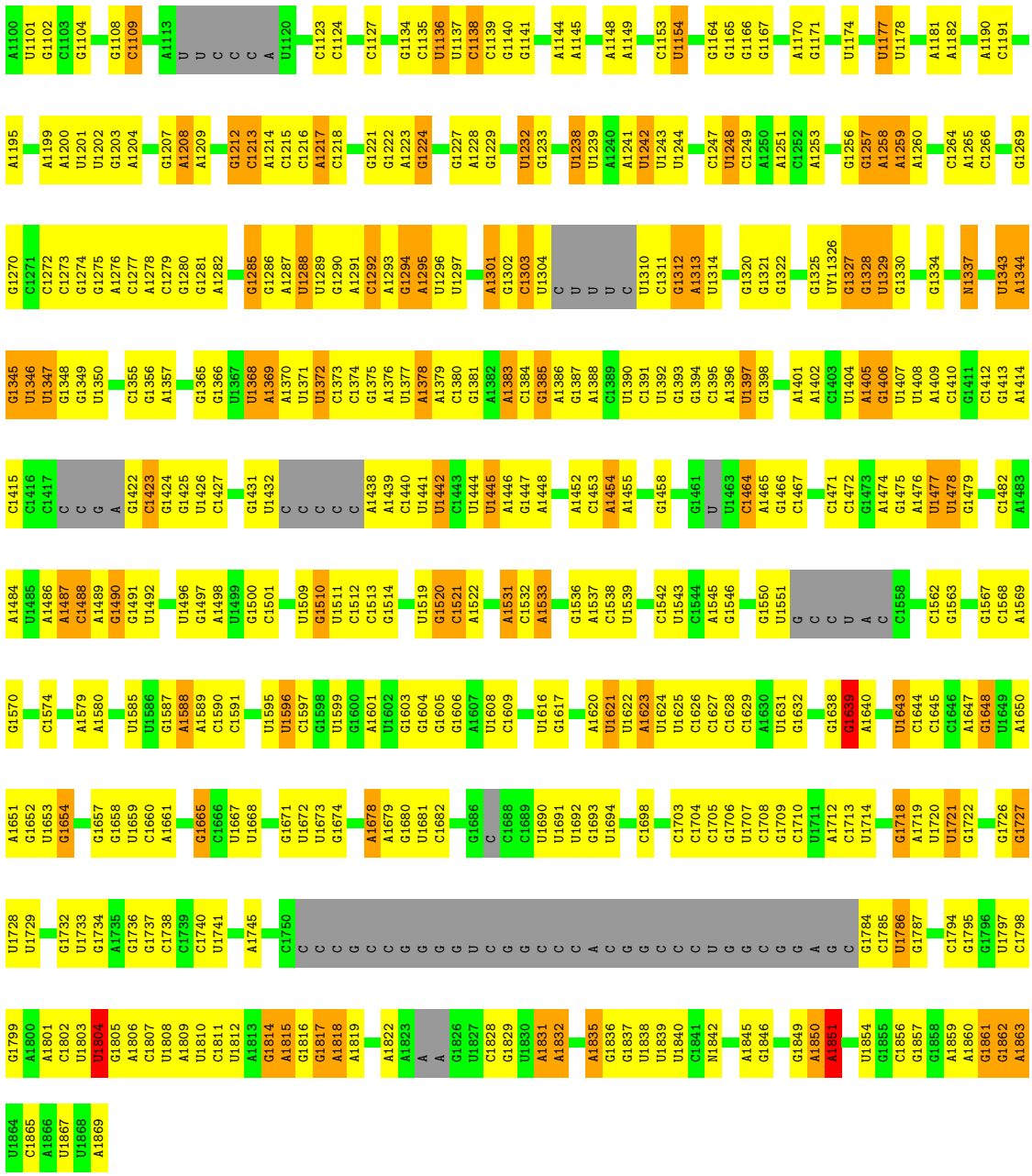


- Molecule 42: 18S rRNA

Chain S2:

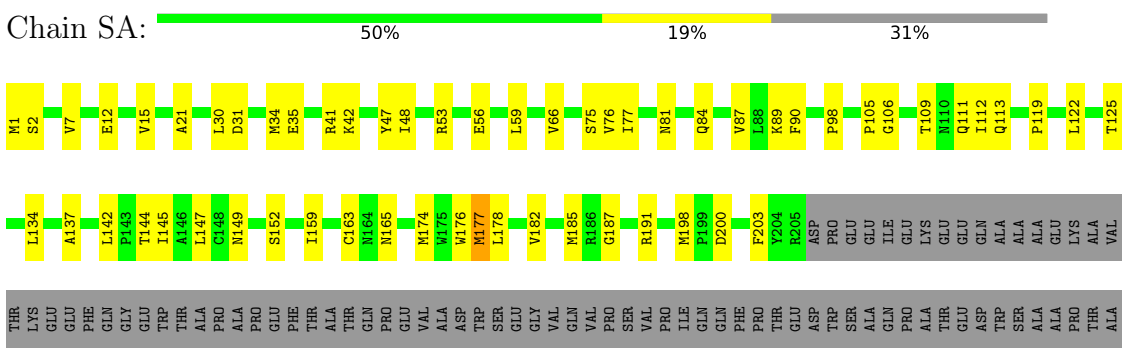






- Molecule 43: 40S ribosomal protein SA

Chain SA:



GLN ALA THR GLU TRP VAL GLY ALA THR THR ASP TRP SER

- Molecule 44: 40S ribosomal protein S3a

Chain SB: 53% 23% • 24%

MET ALA VAL GLY LYS ASN LYS ARG LEU THR LYS GLY GLY LYS LYS GLY ALA LYS LYS LYS VAL V22 F25 K28 P36 A37 M38 I41 L48 V49 T50 ARG THR GLN GLY THR LYS ILE A58 S59 L62 R65 E68 L71 A72 D73 V79 A80 F81 R82

K83 M103 D104 M110 C111 S112 M113 V114 K115 M120 I121 E122 A123 H124 V125 D126 V127 K128 T129 T130 Y133 L134 L135 R136 L137 F138 K144 K145 Q149 I150 R151 Q159 Q163 I164 R165 M168 M169 M172 E175 N179 D180 L181 V185 N186 K187 P190

I197 H208 F211 V212 R213 K214 L218 K219 K220 P221 M229 GLU LEU HIS GLY GLU GLY SER SER SER GLY LYS ALA THR GLY ASP GLU THR GLY ALA LYS VAL GLU ARG ALA ASP GLY TYR GLU PRO PRO VAL GLN GLU SER VAL

- Molecule 45: 40S ribosomal protein S2

Chain SC: 60% 12% 28%

MET ALA ASP ASP ALA GLY ALA ALA GLY GLY PRO GLY GLY PRO GLY GLY PRO GLY MET GLY ASN ARG GLY GLY PHE ARG GLY GLY PHE GLY SER GLY ILE ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ALA ARG GLY GLY LYS ALA GLU ASP K58 V63

L69 I75 E79 F84 I88 K89 E90 S101 L102 P111 R123 F124 K125 I130 G131 D132 C143 L160 S161 I162 V163 R166 R167 G168 Y169 K173 V184 R187 L195 S206 T224 R227 D242 K246 T247 S264 P265

F269 THR ASP HIS LEU VAL LYS THR HIS THR ARG VAL SER VAL GLN ARG THR GLN ALA PRO ALA VAL ALA THR THR

- Molecule 46: 40S ribosomal protein S3

Chain SD: 59% 26% 15%

MET ALA VAL Q4 I5 S6 K7 K8 R9 V12 I16 L25 D32 V41 THR PRO THR ARG T46 E47 I48 I49 I50 R54 T55 V58 L59 G60 G63 R64 R65 I66 R67 E68 L69 T70 A71 V72 K75 L86 Y87 A88 G95 Q101 L105 L109

L110 V115 I126 M127 E128 S129 G133 C134 V138 S139 G140 K141 L142 R143 G144 M150 D154 G155 L156 G161 D162 P163 V164 N165 Y166 Y167 V168 V172 V175 L182 G183 I184 K185 G196 G199 V208 S209 I210 P213 LYS ASP GLU ILE LEU PRO THR

THR PRO ILE SER GLU GLN LYS GLY GLY LYS PRO GLU PRO PRO PRO ALA MET PRO GLN PRO VAL PRO THR ALA

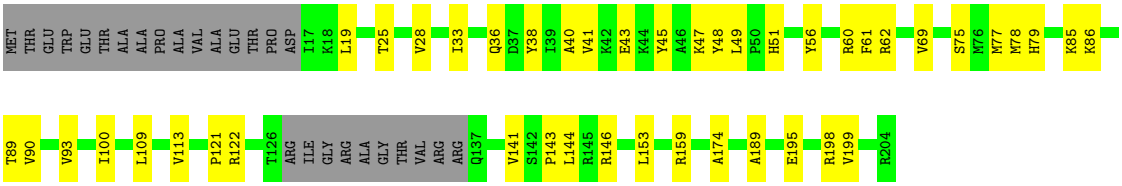
- Molecule 47: Small ribosomal subunit protein eS4, X isoform

Chain SE: 76% 21% •

MET A2 R3 G4 K10 R11 V12 W18 M19 L20 D21 P29 R30 P31 S32 T33 L38 R39 E40 L44 I45 I46 R49 A55 E60 V61 M66 I70 K71 V76 L101 I102 Y103 D104 T105 A110 V131 G135 I136 P137 H138 L139 Y149 P150

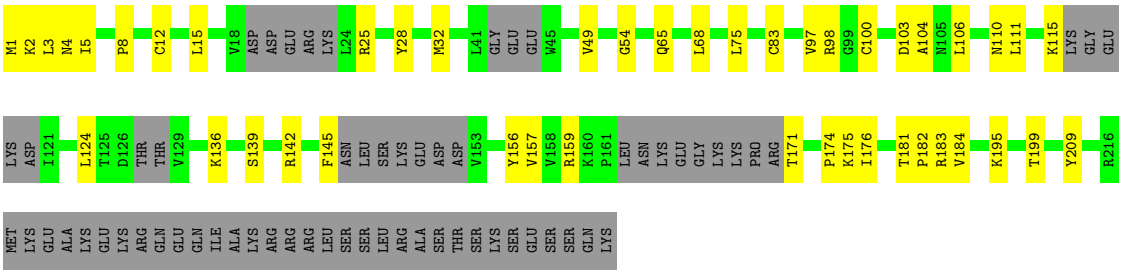
• Molecule 48: 40S ribosomal protein S5

Chain SF:



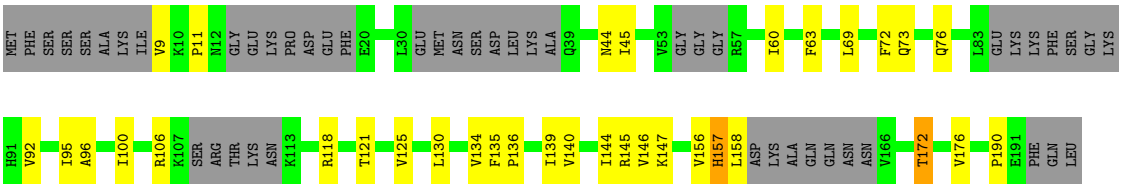
• Molecule 49: 40S ribosomal protein S6

Chain SG:



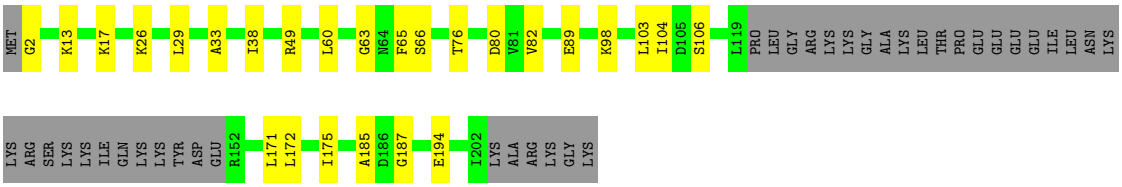
• Molecule 50: 40S ribosomal protein S7

Chain SH:



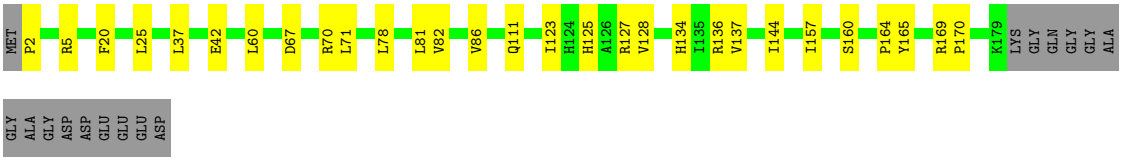
• Molecule 51: 40S ribosomal protein S8

Chain SI:



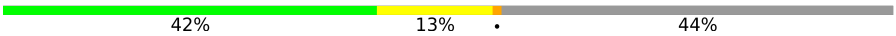
• Molecule 52: 40S ribosomal protein S9

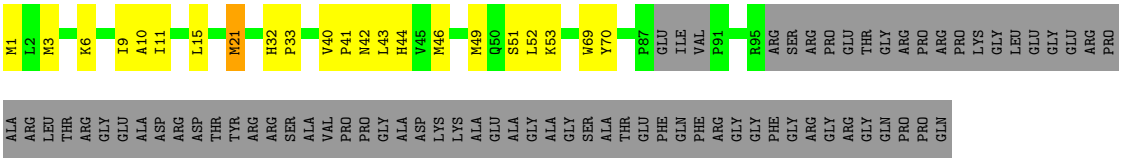
Chain SJ:



• Molecule 53: 40S ribosomal protein S10

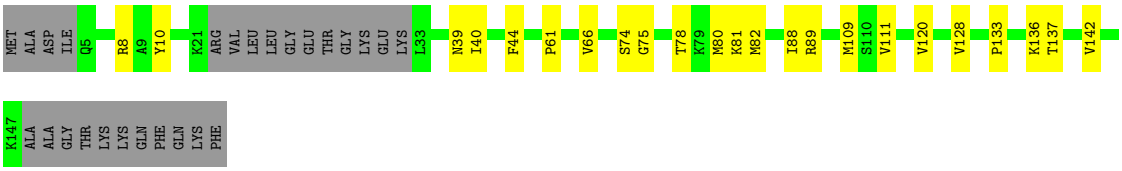
Chain SK:





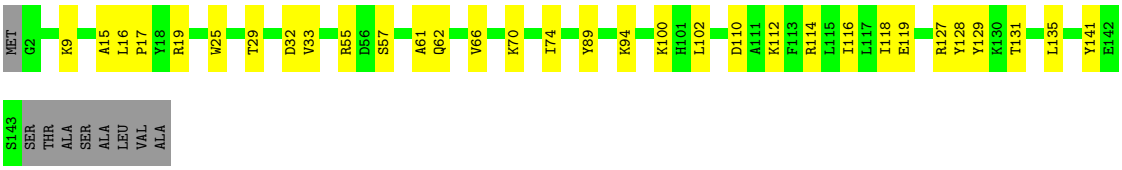
• Molecule 54: Small ribosomal subunit protein uS17

Chain SL:



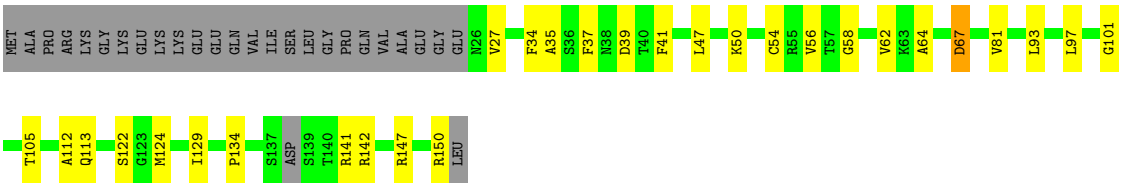
• Molecule 55: 40S ribosomal protein S13

Chain SN:



• Molecule 56: 40S ribosomal protein S14

Chain SO:



• Molecule 57: 40S ribosomal protein S15

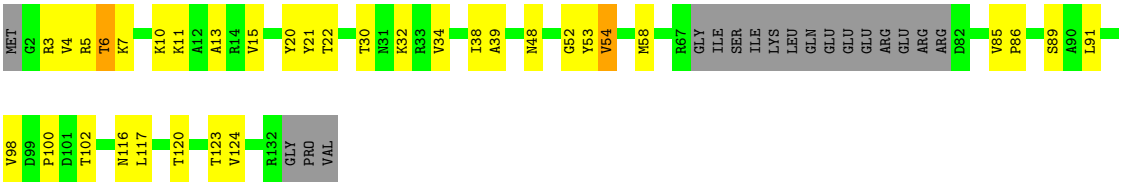
Chain SP:

- Molecule 58: 40S ribosomal protein S16

Chain SQ:

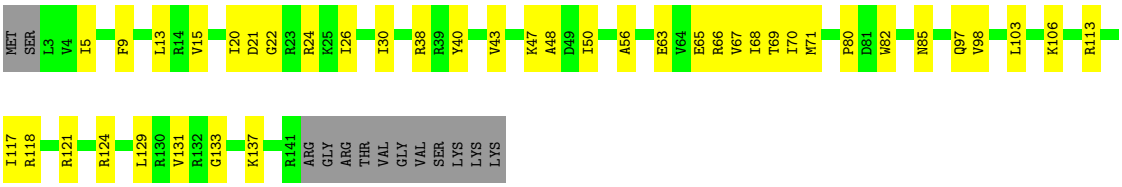
- Molecule 59: 40S ribosomal protein S17

Chain SR:



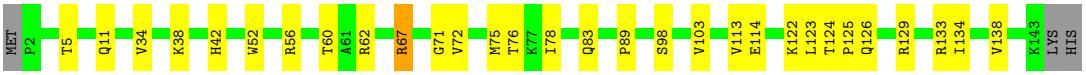
- Molecule 60: 40S ribosomal protein S18

Chain SS:



- Molecule 61: Small ribosomal subunit protein eS19

Chain ST:



- Molecule 62: 40S ribosomal protein S20

Chain SU:

- Molecule 63: 40S ribosomal protein S21

Chain SV: 65% 35%

M1 Q2 F8 V9 Y12 V13 P14 R15 K16 I23 K27 A30 S31 I32 A37 E38 V39 T43 G44 R45 F46 T52 C56 G57 A58 I59 R60 R61 M62 L70 K74 I78 V79 S80 F83

- Molecule 64: 40S ribosomal protein S15a

Chain SW: 75% 24% •

MET V2 R3 M4 K12 S13 I14 N15 E18 L26 I27 R28 P29 C30 S31 V35 M42 E49 F50 E51 I52 D55 H56 R57 A58 G59 K60 I61 L65 K71 V74 D80 L86 T105 M111 E115 K124 F130

- Molecule 65: 40S ribosomal protein S23

Chain SX: 78% 20% •

MET G2 L36 F41 A47 K48 G49 K54 K60 I66 V72 K76 N77 P86 N87 L91 E95 D98 E99 V100 L101 V102 F105 G106 R107 K108 G109 H110 I115 P116 G117 V118 V125 L130 R140 PRO ARG SER

- Molecule 66: 40S ribosomal protein S24

Chain SY: 56% 32% • 12%

MET ASN ASP T4 V5 T6 I7 F12 M13 T14 N15 L18 Q19 R20 K21 Q22 I25 D26 V27 L28 H29 P30 A33 A45 K46 M47 T50 I55 F56 V57 F60 G66 T69 T70 G71 F72 G73 M74 T75 Y76 L79 A82 K83 E86 P87 K88 H89

R90 R93 L96 Y97 GLU LYS LYS LYS THR S103 R104 K105 Q106 R107 K108 E109 R110 K111 N112 K115 V125 GLY ALA GLY LYS LYS PRO LYS GLU

- Molecule 67: Small ribosomal subunit protein eS25

Chain SZ: 45% 11% 44%

MET PRO PRO LYS ASP ASP LYS LYS LYS LYS ASP ALA GLY LYS SER ALA LYS LYS ASP LYS ASP PRO VAL ASN LYS SER GLY GLY LYS ALA LYS LYS LYS LYS TRP SER LYS GLY LYS VAL ARG ASP K43 N46 L58 V62 Y65 I68 T69 P70 V73 R76

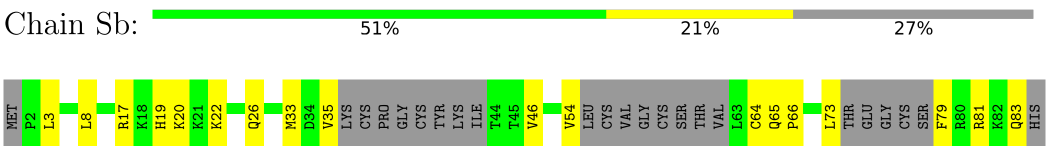
R80 L88 Q89 E90 K94 V107 I108 Y109 N112 THR LYS GLY GLY ASP ALA PRO ALA ALA GLY GLU ASP ALA

- Molecule 68: 40S ribosomal protein S26

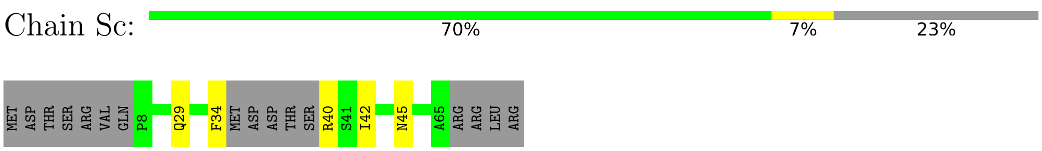
Chain Sa: 65% 19% • 15%

MET T2 K3 A11 K12 I21 R22 D33 V40 I41 I44 V45 E46 A47 V50 L64 P65 K66 L67 Y68 V69 H72 I79 S88 R92 P98 P99 ARG PHE ARG PRO ALA GLY ALA ALA PRO ARG PRO PRO PRO LYS PRO MET

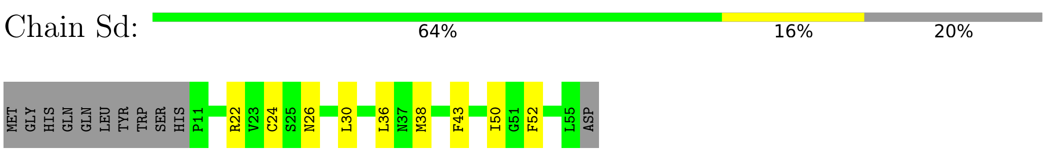
- Molecule 69: 40S ribosomal protein S27



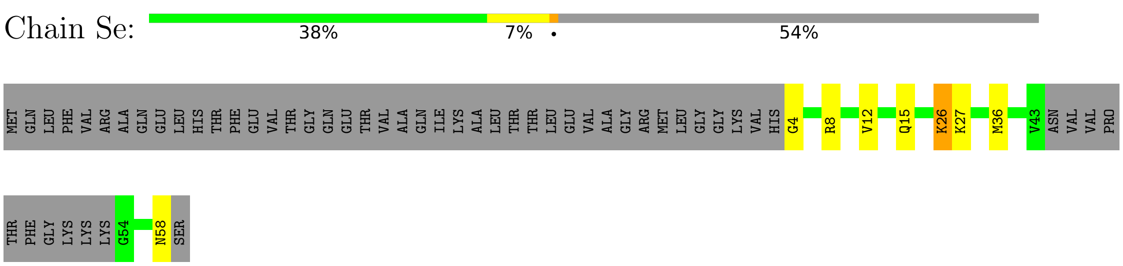
- Molecule 70: 40S ribosomal protein S28



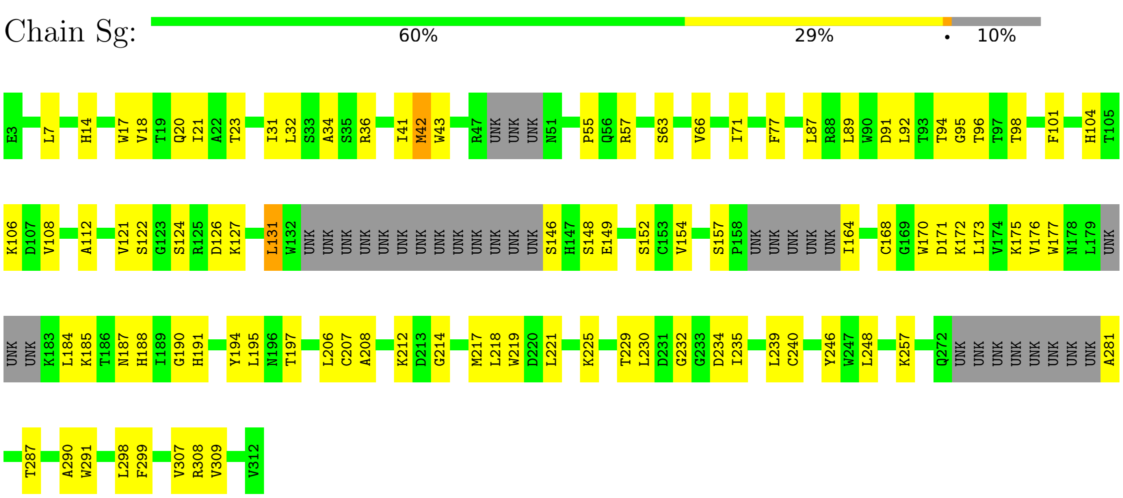
- Molecule 71: 40S ribosomal protein S29



- Molecule 72: FAU ubiquitin like and ribosomal protein S30 fusion



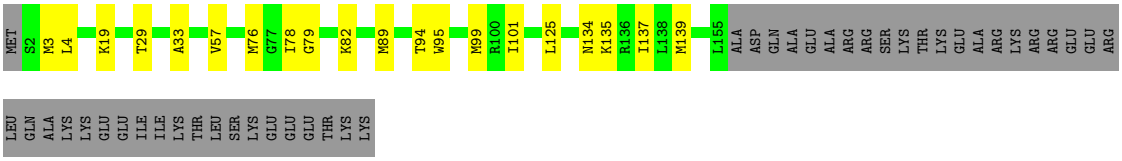
- Molecule 73: RS8_HUMAN Small ribosomal subunit protein eS8



- Molecule 74: 60S ribosomal protein L41

• Molecule 75: 60S ribosomal protein L19

Chain LR:

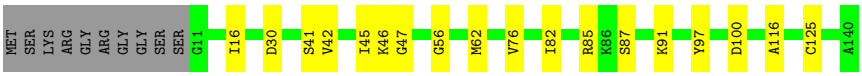


• Molecule 76: E-site tRNA

Chain S6:

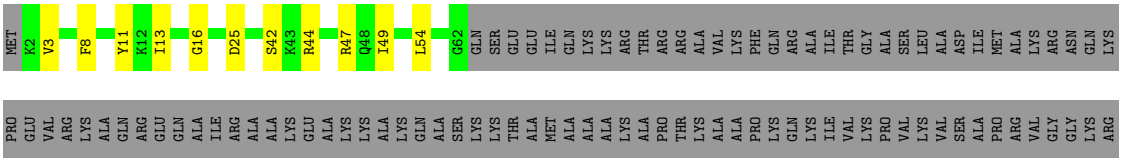
• Molecule 77: 60S ribosomal protein L23

Chain LV:



• Molecule 78: 60S ribosomal protein L24

Chain LW:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	178121	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	37.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.190	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	395.52, 395.52, 395.52	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.824, 0.824, 0.824	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 4AC, OMC, 6MZ, PSU, OMG, A2M, MA6, 1MA, 5MC, K, UR3, NA, UY1, ZN, V5N, HIC, G7M, NMM, MG, OMU

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	L5	0.17	2/70852 (0.0%)	0.31	0/110442
2	L7	0.13	0/2836	0.27	0/4421
3	L8	0.16	0/3361	0.28	0/5233
4	LC	0.12	0/2815	0.30	0/3790
5	LD	0.12	0/2325	0.27	0/3124
6	LE	0.11	0/1707	0.26	0/2293
7	LF	0.13	0/1804	0.31	0/2415
8	LG	0.12	0/1557	0.29	0/2128
9	LJ	0.12	0/325	0.32	0/430
10	LM	0.14	0/1096	0.30	0/1470
11	LN	0.13	0/1746	0.32	0/2338
12	LO	0.14	0/1607	0.31	0/2162
13	LP	0.12	0/1237	0.33	0/1663
14	LQ	0.13	0/1497	0.31	0/2008
15	LT	0.11	0/1193	0.28	0/1599
16	LU	0.12	0/627	0.37	1/856 (0.1%)
17	LX	0.10	0/919	0.28	0/1247
18	LY	0.11	0/1015	0.28	0/1364
19	LZ	0.11	0/1064	0.23	0/1434
20	La	0.14	0/1131	0.29	0/1513
21	Lb	0.12	0/622	0.28	0/838
22	Lc	0.12	0/658	0.29	0/893
23	Ld	0.13	0/782	0.31	0/1059
24	Le	0.12	0/1006	0.28	0/1354
25	Lf	0.12	0/849	0.29	0/1143
26	Lg	0.13	0/775	0.30	0/1040
27	Lh	0.11	0/938	0.26	0/1255
28	Li	0.11	0/702	0.27	0/943
29	Lj	0.13	0/702	0.31	0/932
30	Lk	0.14	0/451	0.31	0/611
31	Ll	0.13	0/410	0.29	0/548

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	Lm	0.11	0/367	0.28	0/492
33	Lo	0.12	0/735	0.29	0/978
34	Lp	0.13	0/651	0.31	0/873
35	Lr	0.12	0/946	0.30	0/1273
36	LA	0.13	0/1831	0.34	0/2474
37	LB	0.12	0/3003	0.31	0/4056
38	LH	0.12	0/1329	0.28	0/1806
39	LI	0.11	0/1510	0.29	0/2041
40	LL	0.11	0/1449	0.29	0/1963
41	LS	0.13	0/1413	0.29	0/1901
42	S2	0.17	2/34033 (0.0%)	0.28	0/52999
43	SA	0.10	0/1603	0.26	0/2186
44	SB	0.10	0/1550	0.28	0/2090
45	SC	0.12	0/1580	0.30	0/2152
46	SD	0.09	0/1385	0.26	0/1893
47	SE	0.10	0/1982	0.27	0/2688
48	SF	0.10	0/1339	0.29	1/1813 (0.1%)
49	SG	0.10	0/1322	0.26	0/1787
50	SH	0.11	0/1034	0.26	0/1403
51	SI	0.11	0/1309	0.29	0/1768
52	SJ	0.10	0/1346	0.25	0/1826
53	SK	0.10	0/672	0.27	0/919
54	SL	0.11	0/1029	0.29	0/1390
55	SN	0.13	0/1101	0.29	0/1497
56	SO	0.24	0/903	0.39	0/1215
57	SP	0.08	0/851	0.23	0/1151
58	SQ	0.11	0/1082	0.29	0/1455
59	SR	0.11	0/846	0.28	0/1150
60	SS	0.09	0/1075	0.25	0/1455
61	ST	0.08	0/1061	0.22	0/1431
62	SU	0.09	0/615	0.27	0/832
63	SV	0.10	0/629	0.29	0/844
64	SW	0.12	0/1037	0.28	0/1390
65	SX	0.10	0/1077	0.26	0/1442
66	SY	0.10	0/950	0.26	0/1267
67	SZ	0.09	0/524	0.24	0/715
68	Sa	0.10	0/753	0.24	0/1016
69	Sb	0.10	0/470	0.26	0/629
70	Sc	0.09	0/371	0.22	0/500
71	Sd	0.09	0/362	0.22	0/480
72	Se	0.09	0/343	0.34	0/451
73	Sg	0.10	0/2105	0.29	0/2874
74	Ln	0.15	0/200	0.31	0/261

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
75	LR	0.12	0/1216	0.26	0/1623
76	S6	0.13	0/313	0.30	0/484
77	LV	0.11	0/957	0.30	0/1293
78	LW	0.11	0/490	0.26	0/662
All	All	0.15	4/191358 (0.0%)	0.30	2/281434 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
56	SO	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S2	576	A2M	O3'-P	5.22	1.61	1.56
1	L5	1322	A2M	O3'-P	5.13	1.61	1.56
42	S2	484	A2M	O3'-P	5.04	1.61	1.56
1	L5	3771	A2M	O3'-P	5.04	1.61	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
48	SF	43	GLU	CB-CA-C	-5.28	110.05	117.23
16	LU	33	ILE	N-CA-C	-5.09	108.33	113.47

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
56	SO	141	ARG	Sidechain
56	SO	142	ARG	Sidechain

5.2 Too-close contacts (i)

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	65849	0	33336	1217	0
2	L7	2538	0	1286	33	0
3	L8	3094	0	1572	62	0
4	LC	2761	0	2891	48	0
5	LD	2281	0	2251	57	0
6	LE	1675	0	1807	51	0
7	LF	1770	0	1831	29	0
8	LG	1527	0	1467	28	0
9	LJ	321	0	323	10	0
10	LM	1074	0	1110	30	0
11	LN	1701	0	1749	27	0
12	LO	1575	0	1658	32	0
13	LP	1211	0	1229	23	0
14	LQ	1473	0	1543	23	0
15	LT	1168	0	1205	15	0
16	LU	619	0	522	37	0
17	LX	902	0	926	11	0
18	LY	998	0	1022	21	0
19	LZ	1041	0	1043	23	0
20	La	1116	0	1130	7	0
21	Lb	610	0	558	14	0
22	Lc	648	0	623	14	0
23	Ld	769	0	787	18	0
24	Le	988	0	1020	13	0
25	Lf	830	0	842	7	0
26	Lg	765	0	793	11	0
27	Lh	930	0	972	14	0
28	Li	692	0	679	25	0
29	Lj	687	0	695	10	0
30	Lk	446	0	406	12	0
31	Ll	400	0	404	17	0
32	Lm	361	0	347	5	0
33	Lo	723	0	741	11	0
34	Lp	641	0	650	20	0
35	Lr	933	0	955	10	0
36	LA	1794	0	1784	30	0
37	LB	2950	0	2880	51	0
38	LH	1312	0	1268	32	0
39	LI	1472	0	1380	42	0
40	LL	1422	0	1402	18	0
41	LS	1376	0	1375	27	0
42	S2	32164	13	16296	721	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	SA	1568	0	1562	47	0
44	SB	1525	0	1498	47	0
45	SC	1545	0	1540	28	0
46	SD	1364	0	1248	46	0
47	SE	1940	0	1951	41	0
48	SF	1319	0	1295	37	0
49	SG	1307	0	1250	43	0
50	SH	1022	0	951	36	0
51	SI	1284	0	1232	22	0
52	SJ	1321	0	1287	19	0
53	SK	652	0	574	18	0
54	SL	1010	0	977	19	0
55	SN	1077	0	1070	25	0
56	SO	892	0	888	19	0
57	SP	835	0	802	6	0
58	SQ	1065	0	1095	40	0
59	SR	833	0	793	30	0
60	SS	1057	0	1059	26	0
61	ST	1055	0	1034	24	0
62	SU	609	0	604	17	0
63	SV	622	0	609	28	0
64	SW	1020	0	1054	28	0
65	SX	1060	0	1106	22	0
66	SY	934	0	970	33	0
67	SZ	518	0	522	11	0
68	Sa	740	0	764	22	0
69	Sb	463	0	466	14	0
70	Sc	370	0	364	5	0
71	Sd	356	0	344	6	0
72	Se	341	0	360	9	0
73	Sg	2055	0	1923	63	0
74	Ln	199	0	203	15	0
75	LR	1200	0	1253	17	0
76	S6	281	0	145	17	0
77	LV	943	0	957	16	0
78	LW	477	0	440	10	0
79	L5	142	0	0	0	0
79	L7	2	0	0	0	0
79	L8	3	0	0	0	0
79	LI	1	0	0	0	0
79	LN	1	0	0	0	0
79	LP	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	LV	1	0	0	0	0
79	S2	25	0	0	0	0
80	L5	24	0	0	0	0
80	L7	1	0	0	0	0
80	LA	2	0	0	0	0
80	LH	1	0	0	0	0
80	LI	1	0	0	0	0
80	Lf	1	0	0	0	0
80	Lo	1	0	0	0	0
80	S2	3	0	0	0	0
80	SF	1	0	0	0	0
80	SL	1	0	0	0	0
80	SO	1	0	0	0	0
81	L5	12	0	0	0	0
81	S2	1	0	0	0	0
82	Lg	1	0	0	0	0
82	Lj	1	0	0	0	0
82	Lm	1	0	0	0	0
82	Lo	1	0	0	0	0
82	Lp	1	0	0	0	0
82	Sa	1	0	0	0	0
82	Sd	1	0	0	0	0
83	L5	2093	0	0	13	0
83	L7	51	0	0	0	0
83	L8	135	0	0	1	0
83	LA	75	0	0	0	0
83	LB	70	0	0	0	0
83	LC	85	0	0	0	0
83	LD	15	0	0	0	0
83	LE	10	0	0	0	0
83	LF	42	0	0	0	0
83	LG	10	0	0	1	0
83	LH	7	0	0	0	0
83	LI	6	0	0	0	0
83	LL	32	0	0	0	0
83	LM	2	0	0	0	0
83	LN	69	0	0	3	0
83	LO	34	0	0	0	0
83	LP	33	0	0	0	0
83	LQ	59	0	0	1	0
83	LR	8	0	0	0	0
83	LS	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	LT	26	0	0	0	0
83	LV	18	0	0	1	0
83	LW	2	0	0	0	0
83	LX	7	0	0	0	0
83	LY	14	0	0	0	0
83	LZ	4	0	0	1	0
83	La	43	0	0	2	0
83	Lb	13	0	0	0	0
83	Lc	2	0	0	0	0
83	Ld	9	0	0	0	0
83	Le	41	0	0	2	0
83	Lf	20	0	0	0	0
83	Lg	22	0	0	0	0
83	Lh	5	0	0	0	0
83	Li	7	0	0	0	0
83	Lj	21	0	0	0	0
83	Lk	1	0	0	0	0
83	Ll	8	0	0	2	0
83	Lm	2	0	0	0	0
83	Lo	11	0	0	0	0
83	Lp	12	0	0	0	0
83	Lr	19	0	0	1	0
83	S2	29	0	0	0	0
83	S6	2	0	0	0	0
83	SS	2	0	0	0	0
83	Sa	2	0	0	0	0
83	Sb	1	0	0	0	0
All	All	185883	13	130948	3415	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 11.

All (3415) 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)
76:S6:74:A:H2'	76:S6:75:C:H5"	1.39	1.02
42:S2:1816:G:H2'	42:S2:1817:G:H5"	1.38	1.01
73:Sg:212:LYS:HA	73:Sg:235:ILE:HG23	1.42	0.97
6:LE:68:MET:HA	6:LE:68:MET:HE3	1.46	0.97
42:S2:1816:G:C2'	42:S2:1817:G:H5"	1.97	0.95
42:S2:512:A2M:H4'	42:S2:576:A2M:H2	1.49	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:70:G:H21	42:S2:79:A:H62	0.98	0.95
7:LF:86:GLU:OE2	15:LT:136:ARG:HB3	1.66	0.95
42:S2:1384:C:O2'	42:S2:1484:A:H1'	1.68	0.94
68:Sa:40:VAL:HB	68:Sa:69:VAL:HG23	1.50	0.93
69:Sb:33:MET:HE1	69:Sb:73:LEU:HD21	1.50	0.92
76:S6:70:C:H2'	76:S6:71:G:H8	1.33	0.91
67:SZ:58:LEU:HD12	67:SZ:62:VAL:HG21	1.50	0.91
42:S2:70:G:N2	42:S2:79:A:H62	1.69	0.91
73:Sg:17:TRP:HB2	73:Sg:36:ARG:HG3	1.51	0.90
1:L5:1816:C:H2'	1:L5:1818:U:H5'	1.55	0.89
51:SI:106:SER:HB3	51:SI:171:LEU:HD13	1.55	0.88
76:S6:4:G:H22	76:S6:71:G:H1	1.16	0.88
1:L5:2507:A:H5'	26:Lg:62:LYS:HD3	1.54	0.88
30:Lk:23:VAL:HG22	30:Lk:36:VAL:HG22	1.56	0.88
39:LI:36:LEU:HD11	39:LI:69:ARG:HD2	1.54	0.88
1:L5:450:G:H22	1:L5:1293:U:H3	1.21	0.87
42:S2:1718:G:H2'	42:S2:1814:G:H22	1.39	0.87
1:L5:3590:A:H2'	1:L5:3591:C:O4'	1.75	0.86
1:L5:3704:A2M:H2	1:L5:3920:G:O4'	1.75	0.86
49:SG:157:VAL:HG21	49:SG:176:ILE:HD11	1.55	0.86
16:LU:28:PRO:HG3	16:LU:100:LEU:HD11	1.58	0.86
1:L5:389:A:H1'	18:LY:91:ASN:HA	1.57	0.86
2:L7:28:C:H2'	2:L7:29:C:H5'	1.58	0.86
42:S2:1051:G:H2'	42:S2:1052:A:H5'	1.57	0.86
1:L5:4576:A2M:HM'2	1:L5:4577:U:H5'	1.58	0.85
44:SB:25:PHE:HA	44:SB:28:LYS:HG3	1.57	0.85
58:SQ:94:ALA:HA	58:SQ:97:GLN:HE21	1.39	0.85
76:S6:74:A:C2'	76:S6:75:C:H5"	2.06	0.85
42:S2:928:G:H1	42:S2:1013:U:H3	1.24	0.85
42:S2:1345:G:O2'	42:S2:1346:U:H5'	1.76	0.85
78:LW:47:ARG:HE	78:LW:54:LEU:HD22	1.42	0.84
1:L5:1063:G:O2'	1:L5:1064:G:H5'	1.76	0.84
43:SA:198:MET:HE2	59:SR:89:SER:HB2	1.59	0.84
42:S2:1051:G:C2'	42:S2:1052:A:H5'	2.08	0.84
3:L8:45:C:H4'	31:Ll:11:ARG:CD	2.07	0.84
42:S2:1164:G:O2'	42:S2:1165:G:H5'	1.78	0.84
1:L5:2621:U:H4'	1:L5:2622:PSU:OP2	1.78	0.84
43:SA:137:ALA:HB1	43:SA:142:LEU:HB3	1.60	0.84
60:SS:15:VAL:HG13	60:SS:68:ILE:HD11	1.60	0.83
8:LG:50:ASP:HB2	17:LX:40:ILE:HG13	1.61	0.83
42:S2:170:A:H4'	49:SG:136:LYS:HD3	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3589:G:C2'	1:L5:3590:A:H5"	2.09	0.83
1:L5:2341:OMC:HM22	1:L5:2342:U:H5'	1.60	0.83
42:S2:1385:G:H2'	42:S2:1386:A:H5'	1.61	0.83
44:SB:159:GLN:O	44:SB:163:GLN:HG3	1.79	0.83
42:S2:874:G:H2'	42:S2:875:A:H8	1.44	0.82
1:L5:3703:A:H2'	1:L5:3704:A2M:C8	2.09	0.82
1:L5:3686:C:P	42:S2:1052:A:H5"	2.20	0.82
49:SG:25:ARG:HA	49:SG:28:TYR:CD2	2.14	0.82
1:L5:1475:G:H2'	1:L5:1476:C:C6	2.14	0.82
1:L5:4244:C:O2'	1:L5:4245:C:H5'	1.78	0.82
42:S2:1374:C:H5'	42:S2:1465:A:H1'	1.60	0.82
38:LH:18:ILE:HD13	38:LH:27:VAL:HG22	1.60	0.82
39:LI:52:MET:HE3	39:LI:136:MET:HE3	1.62	0.82
76:S6:70:C:H2'	76:S6:71:G:C8	2.14	0.82
35:Lr:67:ARG:HB3	35:Lr:67:ARG:HH11	1.44	0.81
42:S2:116:OMU:HN3	42:S2:347:G:H1	1.24	0.81
1:L5:2560:U:H2'	1:L5:2561:C:C6	2.15	0.81
39:LI:48:LEU:HD11	39:LI:145:GLU:HG3	1.59	0.81
1:L5:974:U:H2'	1:L5:975:C:C6	2.15	0.81
14:LQ:50:ARG:HA	14:LQ:53:MET:HG3	1.63	0.81
1:L5:4903:C:H2'	1:L5:4904:G:H8	1.44	0.81
4:LC:169:LEU:O	4:LC:173:LYS:HG2	1.81	0.81
22:Lc:21:VAL:HG11	22:Lc:96:ILE:HD12	1.63	0.81
35:Lr:67:ARG:HB3	35:Lr:67:ARG:NH1	1.95	0.81
45:SC:69:LEU:HD13	45:SC:269:PHE:HD2	1.46	0.81
1:L5:3703:A:H2'	1:L5:3704:A2M:H8	1.61	0.81
42:S2:70:G:H21	42:S2:79:A:N6	1.78	0.81
63:SV:16:LYS:HG2	63:SV:23:ILE:HD13	1.63	0.81
55:SN:127:ARG:O	55:SN:131:THR:HG23	1.80	0.80
1:L5:108:A:H4'	1:L5:109:G:OP1	1.82	0.80
1:L5:2621:U:H3'	1:L5:2622:PSU:H5"	1.61	0.80
10:LM:71:LYS:O	10:LM:75:GLN:HG3	1.80	0.80
65:SX:60:LYS:HG3	65:SX:116:PRO:HD3	1.61	0.80
16:LU:48:LYS:HG3	16:LU:53:ALA:HB2	1.62	0.80
42:S2:1228:A:H2'	42:S2:1229:G:C8	2.16	0.80
1:L5:4557:A2M:H2'	1:L5:4558:U:H6	1.47	0.79
49:SG:181:THR:HG22	49:SG:183:ARG:H	1.47	0.79
1:L5:1270:A:O2'	1:L5:1271:G:H5'	1.81	0.79
10:LM:126:GLU:HG3	12:LO:181:ALA:HB1	1.64	0.79
1:L5:162:A:H2'	1:L5:163:A:H8	1.47	0.79
42:S2:1395:C:O2'	42:S2:1396:A:H5'	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:S6:3:C:H2'	76:S6:4:G:C8	2.18	0.79
49:SG:3:LEU:HB3	49:SG:5:ILE:HD11	1.65	0.79
1:L5:2804:C:H5'	1:L5:2805:A2M:OP2	1.83	0.79
27:Lh:112:ARG:HG2	27:Lh:112:ARG:HH11	1.48	0.79
1:L5:2405:OMU:O2'	1:L5:2406:G:H5'	1.82	0.79
1:L5:2601:A:H5'	1:L5:2678:G:H4'	1.65	0.79
1:L5:4865:C:H2'	1:L5:4866:U:O4'	1.83	0.79
1:L5:512:U:O2	1:L5:647:G:O6	2.01	0.78
59:SR:7:LYS:O	59:SR:11:LYS:HG2	1.83	0.78
42:S2:1521:C:H5'	57:SP:126:VAL:HB	1.64	0.78
1:L5:4611:C:O2'	1:L5:4612:A:H5'	1.83	0.78
42:S2:1678:A2M:O2'	42:S2:1679:A:H5'	1.83	0.78
7:LF:182:TYR:HB3	7:LF:200:ARG:HG3	1.66	0.78
1:L5:4732:C:O2'	1:L5:4733:C:H5'	1.84	0.78
1:L5:4878:A:O2'	1:L5:4879:A:H5'	1.84	0.78
1:L5:4577:U:H2'	1:L5:4578:C:C6	2.19	0.77
59:SR:98:VAL:HG13	59:SR:102:THR:HB	1.65	0.77
1:L5:162:A:H2'	1:L5:163:A:C8	2.18	0.77
42:S2:1213:C:H5'	42:S2:1370:A:OP1	1.84	0.77
42:S2:1445:PSU:O2'	42:S2:1446:A:H5'	1.85	0.77
1:L5:745:G:H2'	1:L5:746:A:H1'	1.65	0.77
38:LH:63:ASN:OD1	38:LH:66:GLU:HG3	1.84	0.77
48:SF:33:ILE:HA	48:SF:36:GLN:HG3	1.64	0.77
1:L5:1803:C:O2'	1:L5:1804:C:H5'	1.85	0.77
1:L5:3707:U:C2'	1:L5:3708:G:H5'	2.14	0.77
1:L5:4557:A2M:H2'	1:L5:4558:U:C6	2.18	0.77
6:LE:95:PRO:HA	6:LE:104:THR:HG22	1.66	0.77
42:S2:1088:U:H4'	42:S2:1089:G:OP2	1.83	0.77
1:L5:903:A:H2'	1:L5:904:G:H8	1.49	0.77
14:LQ:66:MET:O	14:LQ:70:MET:HG2	1.85	0.77
45:SC:187:ARG:HB3	45:SC:187:ARG:HH11	1.48	0.77
34:Lp:81:SER:HB3	42:S2:938:A:H4'	1.67	0.77
49:SG:195:LYS:O	49:SG:199:THR:HG23	1.85	0.77
1:L5:2711:G:C2'	1:L5:2712:G:H5'	2.15	0.77
56:SO:101:GLY:HA3	56:SO:134:PRO:HD2	1.65	0.77
49:SG:25:ARG:HA	49:SG:28:TYR:HD2	1.50	0.76
1:L5:745:G:H2'	1:L5:746:A:C1'	2.15	0.76
1:L5:1202:G:O2'	1:L5:1203:U:H5'	1.85	0.76
5:LD:60:ILE:HD11	5:LD:93:THR:HA	1.67	0.76
10:LM:104:MET:HE2	10:LM:109:ARG:HG2	1.67	0.76
1:L5:4246:U:H2'	1:L5:4247:C:H6	1.51	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:680:G:C2'	1:L5:681:G:H5'	2.16	0.76
1:L5:1066:C:H2'	1:L5:1067:G:C8	2.20	0.76
1:L5:3695:U:H2'	42:S2:970:G:H21	1.50	0.76
1:L5:4448:C:O2'	1:L5:4449:U:H5'	1.85	0.76
42:S2:1476:A:H4'	42:S2:1477:U:H5"	1.65	0.76
75:LR:135:LYS:O	75:LR:139:MET:HG3	1.86	0.76
16:LU:87:THR:O	16:LU:91:LEU:HD23	1.85	0.76
1:L5:1475:G:O2'	1:L5:1476:C:H5'	1.85	0.76
1:L5:74:G:H5'	40:LL:59:VAL:HB	1.68	0.76
16:LU:39:PHE:HZ	16:LU:87:THR:HG22	1.51	0.76
1:L5:1814:G:H2'	1:L5:1816:C:OP2	1.86	0.76
16:LU:60:VAL:O	16:LU:74:SER:HA	1.86	0.76
61:ST:124:THR:HG23	61:ST:125:PRO:HD2	1.68	0.76
1:L5:1658:C:H2'	1:L5:1659:C:C6	2.22	0.75
16:LU:83:LEU:O	16:LU:87:THR:HG23	1.86	0.75
42:S2:925:G:H1	42:S2:1017:U:H3	1.32	0.75
1:L5:974:U:O2'	1:L5:975:C:H5'	1.86	0.75
42:S2:1214:A:O4'	42:S2:1343:U:H5'	1.87	0.75
42:S2:1588:A:H2'	42:S2:1589:A:C8	2.21	0.75
1:L5:270:U:H2'	1:L5:271:C:C6	2.22	0.75
1:L5:4364:A:O2'	1:L5:4365:A:H2'	1.86	0.75
42:S2:1521:C:N4	60:SS:137:LYS:HG3	2.02	0.75
42:S2:829:C:OP1	47:SE:21:ASP:HB2	1.87	0.75
19:LZ:87:VAL:CG1	19:LZ:89:ILE:HG13	2.17	0.75
42:S2:942:G:H2'	42:S2:943:U:C6	2.22	0.75
42:S2:1144:A:H5'	42:S2:1355:C:H41	1.51	0.75
48:SF:49:LEU:HD11	58:SQ:49:TYR:HB2	1.68	0.75
1:L5:3590:A:H2'	1:L5:3591:C:C4'	2.17	0.74
1:L5:4902:C:H2'	1:L5:4903:C:C6	2.22	0.74
38:LH:76:HIS:O	38:LH:80:MET:HG3	1.86	0.74
5:LD:22:ARG:HB3	5:LD:28:THR:HG22	1.66	0.74
1:L5:4260:A:H2'	1:L5:4261:G:C8	2.22	0.74
42:S2:1536:G:H2'	42:S2:1537:A:C8	2.22	0.74
1:L5:1063:G:C2'	1:L5:1064:G:H5'	2.17	0.74
42:S2:1536:G:H2'	42:S2:1537:A:H8	1.53	0.74
1:L5:1773:C:H2'	1:L5:1774:C:C6	2.22	0.74
67:SZ:68:ILE:HB	67:SZ:109:TYR:HB2	1.68	0.74
1:L5:4490:C:H2'	1:L5:4491:C:C6	2.22	0.74
53:SK:49:MET:HE2	53:SK:49:MET:HA	1.67	0.74
1:L5:1817:G:H3'	1:L5:1817:G:N3	2.01	0.74
76:S6:4:G:N2	76:S6:71:G:H1	1.85	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Lj:31:LYS:HB3	29:Lj:33:THR:HG22	1.68	0.74
44:SB:165:ARG:HG2	44:SB:169:MET:HE3	1.69	0.74
44:SB:130:THR:HG23	44:SB:179:ASN:O	1.87	0.74
1:L5:903:A:H2'	1:L5:904:G:C8	2.22	0.73
42:S2:155:G:H4'	49:SG:15:LEU:HD12	1.69	0.73
1:L5:711:A:H2'	1:L5:712:C:C6	2.23	0.73
1:L5:1414:C:C2'	1:L5:1415:G:H5'	2.17	0.73
1:L5:2689:C:O2'	1:L5:2690:G:H5'	1.87	0.73
61:ST:124:THR:HG22	61:ST:126:GLN:H	1.51	0.73
1:L5:1335:U:H2'	1:L5:1336:OMC:C6	2.23	0.73
42:S2:164:A:O2'	42:S2:165:G:H5'	1.88	0.73
42:S2:1718:G:H2'	42:S2:1814:G:N2	2.01	0.73
49:SG:181:THR:O	49:SG:184:VAL:HG22	1.88	0.73
76:S6:3:C:H2'	76:S6:4:G:H8	1.53	0.73
1:L5:25:A:H2'	1:L5:26:C:H6	1.53	0.73
1:L5:1817:G:H21	1:L5:1818:U:H5"	1.53	0.73
42:S2:1217:A:H2'	42:S2:1218:C:C6	2.23	0.73
1:L5:2752:G:H3'	1:L5:2753:U:H5"	1.71	0.73
42:S2:981:A:H2'	42:S2:982:G:C8	2.24	0.73
49:SG:5:ILE:CD1	49:SG:111:LEU:HD12	2.18	0.73
1:L5:2628:G:O2'	1:L5:2629:U:H5'	1.89	0.73
53:SK:41:PRO:HG2	53:SK:44:HIS:CG	2.23	0.73
3:L8:45:C:H4'	31:Ll:11:ARG:HD2	1.70	0.73
11:LN:121:VAL:HG11	11:LN:131:GLU:HG3	1.70	0.73
1:L5:4903:C:H2'	1:L5:4904:G:C8	2.23	0.73
39:LI:76:MET:HE1	39:LI:148:VAL:HG22	1.69	0.73
50:SH:130:LEU:HD21	50:SH:156:VAL:HG21	1.69	0.73
56:SO:58:GLY:O	56:SO:62:VAL:HG22	1.87	0.73
1:L5:699:C:H2'	1:L5:700:G:C8	2.24	0.73
1:L5:1071:C:H3'	1:L5:1072:A:H5"	1.71	0.73
1:L5:2866:OMG:HM22	1:L5:2867:G:O5'	1.87	0.73
1:L5:4060:C:O2'	1:L5:4061:U:H5'	1.88	0.72
42:S2:1803:U:H2'	42:S2:1804:OMU:H6	1.70	0.72
73:Sg:7:LEU:HD11	73:Sg:308:ARG:HG2	1.71	0.72
1:L5:4523:C:H2'	1:L5:4524:G:C8	2.24	0.72
42:S2:1585:U:O4	61:ST:67:NMM:HG2	1.88	0.72
42:S2:1713:C:O2'	42:S2:1714:U:H5'	1.89	0.72
1:L5:3707:U:H2'	1:L5:3708:G:H5'	1.71	0.72
44:SB:82:ARG:HD3	44:SB:103:MET:HE2	1.69	0.72
1:L5:4246:U:H2'	1:L5:4247:C:C6	2.24	0.72
36:LA:137:ILE:HG12	42:S2:981:A:OP1	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:1621:U:OP1	42:S2:1621:U:H2'	1.89	0.72
1:L5:685:C:OP1	6:LE:101:ASN:HB2	1.89	0.72
1:L5:3700:G:N2	76:S6:72:C:H4'	2.03	0.72
62:SU:56:MET:HE3	62:SU:88:LEU:HD22	1.70	0.72
1:L5:3896:C:H2'	1:L5:3897:C:C6	2.24	0.72
1:L5:447:C:O2'	1:L5:448:G:H5'	1.90	0.72
1:L5:4605:U:H2'	1:L5:4606:OMU:H6	1.72	0.72
48:SF:78:MET:HB2	48:SF:159:ARG:CZ	2.19	0.72
42:S2:1597:C:H4'	42:S2:1603:G:C6	2.25	0.72
66:SY:13:MET:HE3	66:SY:22:GLN:HE21	1.54	0.72
1:L5:4952:A:H2'	1:L5:4953:A:H8	1.55	0.71
1:L5:1629:G:H5'	1:L5:1630:A:OP1	1.88	0.71
18:LY:38:LEU:HD22	18:LY:42:TYR:HE2	1.55	0.71
37:LB:108:GLU:HG3	37:LB:137:TRP:CB	2.20	0.71
1:L5:473:C:C2'	1:L5:474:C:H5'	2.21	0.71
1:L5:3686:C:OP2	42:S2:1052:A:H5"	1.89	0.71
1:L5:3695:U:H2'	42:S2:970:G:N2	2.05	0.71
3:L8:79:G:O2'	3:L8:80:A:H5'	1.90	0.71
58:SQ:116:ASP:OD1	58:SQ:118:THR:HG22	1.90	0.71
1:L5:4720:A:O2'	1:L5:4721:G:H5"	1.91	0.71
42:S2:1804:OMU:HM22	42:S2:1805:G:H5'	1.71	0.71
54:SL:8:ARG:HG2	54:SL:8:ARG:HH11	1.54	0.71
4:LC:14:LYS:HE2	4:LC:14:LYS:HA	1.73	0.71
16:LU:60:VAL:HG13	16:LU:76:VAL:HG22	1.73	0.71
42:S2:557:U:O2'	42:S2:558:G:H5'	1.91	0.71
42:S2:640:A:H2'	42:S2:641:A:C8	2.26	0.71
1:L5:4921:G:C5	6:LE:183:ARG:HD3	2.25	0.71
42:S2:107:A:H2'	42:S2:108:G:C8	2.26	0.71
42:S2:318:A:H5'	42:S2:319:C:OP2	1.91	0.71
1:L5:674:G:H2'	1:L5:675:C:C6	2.25	0.71
1:L5:1773:C:H2'	1:L5:1774:C:H6	1.54	0.71
52:SJ:111:GLN:NE2	52:SJ:127:ARG:HB2	2.06	0.71
76:S6:72:C:H2'	76:S6:73:A:C8	2.25	0.71
1:L5:671:G:C2'	1:L5:672:C:H5'	2.21	0.71
39:LI:176:PHE:CD1	39:LI:184:MET:HE1	2.25	0.71
42:S2:1519:U:O2'	42:S2:1520:G:H5'	1.91	0.71
66:SY:27:VAL:HB	66:SY:69:THR:HG23	1.73	0.71
49:SG:181:THR:HG23	49:SG:182:PRO:HD2	1.73	0.70
60:SS:98:VAL:HG23	60:SS:103:LEU:HD13	1.73	0.70
1:L5:1701:G:H2'	1:L5:1702:A:O4'	1.90	0.70
1:L5:4685:U:H1'	1:L5:4686:A:H5"	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3700:G:H21	76:S6:72:C:H4'	1.54	0.70
42:S2:1628:C:H2'	42:S2:1629:C:C6	2.27	0.70
42:S2:1801:A:H2'	42:S2:1802:C:C6	2.26	0.70
1:L5:4755:G:H5"	12:LO:176:ARG:HD3	1.74	0.70
42:S2:29:G:H2'	42:S2:30:C:C6	2.25	0.70
43:SA:145:ILE:HG12	43:SA:159:ILE:HB	1.73	0.70
1:L5:4895:A:H4'	37:LB:95:THR:HG22	1.74	0.70
42:S2:1228:A:H2'	42:S2:1229:G:H8	1.54	0.70
3:L8:45:C:H4'	31:Ll:11:ARG:HD3	1.74	0.70
48:SF:77:MET:HG2	48:SF:89:THR:HG21	1.74	0.70
50:SH:69:LEU:HD22	50:SH:96:ALA:HB2	1.74	0.70
19:LZ:26:VAL:HG22	19:LZ:91:LEU:HD23	1.73	0.70
44:SB:144:LYS:HE2	44:SB:208:HIS:HB3	1.74	0.70
1:L5:2830:A:O2'	1:L5:2831:G:H5'	1.92	0.70
48:SF:109:LEU:O	48:SF:113:VAL:HG23	1.91	0.70
1:L5:3924:G:OP2	11:LN:24:ARG:HD2	1.92	0.70
1:L5:4118:C:H2'	1:L5:4119:C:O4'	1.91	0.70
42:S2:392:A:O2'	42:S2:393:U:H5'	1.92	0.70
8:LG:134:PRO:HB3	8:LG:206:GLN:O	1.92	0.69
42:S2:1667:U:H2'	42:S2:1668:U:C6	2.26	0.69
60:SS:13:LEU:HB2	60:SS:20:ILE:HB	1.74	0.69
39:LI:36:LEU:HD21	39:LI:69:ARG:NH1	2.07	0.69
42:S2:1533:A:C8	42:S2:1604:G:H1'	2.26	0.69
76:S6:71:G:H2'	76:S6:72:C:H5'	1.74	0.69
1:L5:937:A:N3	4:LC:335:MET:HE1	2.08	0.69
1:L5:1296:G:H2'	1:L5:1297:C:C6	2.27	0.69
1:L5:2887:G:OP1	75:LR:135:LYS:HG3	1.93	0.69
1:L5:4078:G:O2'	1:L5:4100:G:H5'	1.92	0.69
12:LO:178:ARG:O	12:LO:182:GLU:HG3	1.91	0.69
1:L5:1889:C:H1'	1:L5:1933:C:O2	1.92	0.69
1:L5:4510:G:OP2	1:L5:4510:G:H4'	1.91	0.69
42:S2:29:G:H2'	42:S2:30:C:H6	1.57	0.69
42:S2:81:U:H2'	42:S2:82:G:O4'	1.91	0.69
42:S2:1365:G:H2'	42:S2:1366:G:C8	2.27	0.69
43:SA:77:ILE:HD12	43:SA:122:LEU:HD11	1.73	0.69
1:L5:473:C:H2'	1:L5:474:C:H5'	1.74	0.69
1:L5:3718:A:H2'	1:L5:3719:A:C8	2.28	0.69
42:S2:1288:OMU:HM22	42:S2:1289:U:O4'	1.92	0.69
42:S2:1407:U:H2'	42:S2:1408:U:C6	2.27	0.69
1:L5:4876:G:H2'	1:L5:4877:A:H5'	1.75	0.69
42:S2:455:A:H2'	42:S2:456:C:C6	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:S6:2:G:H22	76:S6:73:A:H2	1.39	0.69
1:L5:267:G:H2'	1:L5:268:G:H8	1.56	0.69
1:L5:1064:G:O2'	1:L5:1065:C:H5'	1.92	0.69
42:S2:1203:G:H2'	42:S2:1204:A:C8	2.28	0.69
58:SQ:12:VAL:HG21	58:SQ:91:ALA:HA	1.75	0.69
73:Sg:87:LEU:HD21	73:Sg:122:SER:HB3	1.75	0.69
1:L5:4117:G:O2'	1:L5:4118:C:H5'	1.93	0.69
1:L5:4732:C:C2'	1:L5:4733:C:H5'	2.23	0.69
36:LA:135:THR:HG22	36:LA:149:LYS:HB3	1.74	0.69
51:SI:194:GLU:HG3	54:SL:10:TYR:CD2	2.28	0.69
1:L5:1547:C:C2'	1:L5:1548:G:H5'	2.23	0.69
7:LF:137:GLU:HB3	7:LF:138:PRO:HD3	1.73	0.69
42:S2:1801:A:H2'	42:S2:1802:C:H6	1.58	0.69
7:LF:60:GLU:O	7:LF:64:MET:HG3	1.92	0.68
28:Li:7:MET:HE1	40:LL:181:SER:HB3	1.74	0.68
42:S2:215:G:H2'	42:S2:216:C:H6	1.58	0.68
42:S2:223:C:H2'	42:S2:224:A:C8	2.27	0.68
42:S2:1595:U:H2'	42:S2:1596:PSU:C6	2.28	0.68
53:SK:49:MET:HE1	53:SK:52:LEU:HD12	1.75	0.68
1:L5:4260:A:H2'	1:L5:4261:G:H8	1.56	0.68
1:L5:4867:U:H5"	1:L5:4868:C:OP1	1.92	0.68
49:SG:1:MET:HE2	49:SG:106:LEU:O	1.92	0.68
1:L5:119:G:H3'	1:L5:120:A:C5'	2.23	0.68
1:L5:931:U:OP1	10:LM:46:ARG:HD3	1.94	0.68
16:LU:25:CYS:SG	16:LU:112:LEU:HD13	2.33	0.68
42:S2:160:U:O2'	42:S2:161:U:H3'	1.93	0.68
1:L5:325:U:H2'	1:L5:326:C:C6	2.28	0.68
1:L5:691:C:H2'	1:L5:692:A:C8	2.28	0.68
14:LQ:178:ARG:HA	14:LQ:184:ARG:O	1.93	0.68
73:Sg:87:LEU:HB2	73:Sg:101:PHE:HB2	1.75	0.68
1:L5:216:C:H5'	1:L5:219:G:O3'	1.93	0.68
1:L5:974:U:H2'	1:L5:975:C:H6	1.58	0.68
19:LZ:112:ARG:O	19:LZ:116:VAL:HG22	1.93	0.68
42:S2:38:A:OP1	52:SJ:5:ARG:HG2	1.94	0.68
42:S2:860:G:H2'	42:S2:861:A:O4'	1.93	0.68
42:S2:512:A2M:H4'	42:S2:576:A2M:C2	2.22	0.68
48:SF:49:LEU:CD1	58:SQ:49:TYR:HB2	2.24	0.68
55:SN:25:TRP:HZ3	69:Sb:83:GLN:HB2	1.57	0.68
14:LQ:79:THR:OG1	14:LQ:99:LYS:HD3	1.94	0.68
42:S2:996:A:H2'	42:S2:997:A:C8	2.28	0.68
42:S2:1378:A:H4'	42:S2:1379:A:O5'	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1826:G:O2'	1:L5:1827:G:H5'	1.94	0.68
42:S2:587:A:H5'	42:S2:592:C:H41	1.59	0.68
42:S2:1031:A2M:HM'3	55:SN:116:ILE:HD12	1.76	0.68
1:L5:2621:U:C3'	1:L5:2622:PSU:H5"	2.23	0.68
6:LE:192:LYS:HD2	25:Lf:107:PRO:HB3	1.76	0.68
43:SA:1:MET:CB	63:SV:79:VAL:HA	2.24	0.68
1:L5:2559:G:C2'	1:L5:2560:U:H5'	2.23	0.67
42:S2:354:OMU:HM22	42:S2:355:G:H5'	1.76	0.67
44:SB:134:LEU:HG	44:SB:218:LEU:HD12	1.76	0.67
44:SB:186:ASN:O	44:SB:190:PRO:HD2	1.93	0.67
49:SG:2:LYS:HB3	49:SG:15:LEU:HD21	1.74	0.67
55:SN:15:ALA:HB2	69:Sb:20:LYS:HE3	1.75	0.67
1:L5:689:U:H2'	1:L5:690:C:C6	2.29	0.67
1:L5:2024:C:O2'	1:L5:2025:A:H5'	1.93	0.67
1:L5:4237:A:H5"	9:LJ:129:ASP:CB	2.24	0.67
13:LP:45:THR:O	13:LP:49:LYS:HG3	1.94	0.67
42:S2:1374:C:H2'	42:S2:1375:G:O4'	1.94	0.67
1:L5:1204:C:H3'	1:L5:1205:G:H5'	1.75	0.67
5:LD:92:LEU:O	5:LD:93:THR:HB	1.94	0.67
38:LH:92:MET:HE2	38:LH:179:ILE:HG22	1.77	0.67
44:SB:36:PRO:HB2	44:SB:38:MET:SD	2.33	0.67
6:LE:66:LYS:HB3	6:LE:71:ARG:NH2	2.10	0.67
11:LN:138:PHE:HA	11:LN:143:ARG:HD2	1.77	0.67
13:LP:13:LYS:HD2	13:LP:152:GLU:OE1	1.95	0.67
1:L5:4973:U:H2'	1:L5:5046:A:H62	1.59	0.67
42:S2:12:U:H2'	42:S2:13:C:C6	2.28	0.67
1:L5:1328:C:H2'	1:L5:1329:A:H8	1.60	0.67
1:L5:3896:C:H2'	1:L5:3897:C:H6	1.58	0.67
1:L5:4445:U:H2'	1:L5:4446:U:C6	2.30	0.67
4:LC:76:ILE:HG13	4:LC:77:PRO:HD2	1.74	0.67
38:LH:105:ILE:CG2	38:LH:109:GLY:HA2	2.25	0.67
42:S2:1265:A:H5'	42:S2:1266:C:OP2	1.94	0.67
66:SY:103:SER:O	66:SY:107:ARG:HG3	1.95	0.67
1:L5:1243:G:H5"	1:L5:1245:G:OP1	1.94	0.67
1:L5:3685:C:OP1	42:S2:1051:G:H4'	1.95	0.67
10:LM:126:GLU:HG3	12:LO:181:ALA:CB	2.24	0.67
12:LO:181:ALA:O	12:LO:185:VAL:HG22	1.95	0.67
50:SH:146:VAL:O	64:SW:49:GLU:HG2	1.94	0.67
1:L5:1917:C:O2'	1:L5:1918:G:H4'	1.94	0.67
1:L5:1939:A:C2'	1:L5:1940:A:H5'	2.24	0.67
46:SD:25:LEU:HD13	46:SD:50:ILE:HG12	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:LW:8:PHE:HZ	78:LW:49:ILE:HG13	1.59	0.67
31:Ll:23:ILE:HD12	31:Ll:23:ILE:O	1.95	0.67
56:SO:113:GLN:HE22	68:Sa:45:VAL:HA	1.60	0.67
75:LR:101:ILE:CG2	75:LR:135:LYS:HD2	2.25	0.67
42:S2:215:G:H2'	42:S2:216:C:C6	2.30	0.67
42:S2:1277:C:H2'	42:S2:1278:A:H8	1.60	0.67
56:SO:34:PHE:HB3	56:SO:41:PHE:HB2	1.77	0.67
1:L5:3859:G:H2'	1:L5:3860:G:C8	2.30	0.66
5:LD:90:VAL:HG11	5:LD:231:VAL:HG21	1.77	0.66
12:LO:203:VAL:OXT	12:LO:203:VAL:HG13	1.93	0.66
19:LZ:47:ASP:HB3	19:LZ:69:LYS:HG2	1.77	0.66
42:S2:1217:A:H2'	42:S2:1218:C:H6	1.59	0.66
56:SO:35:ALA:CB	56:SO:112:ALA:HB2	2.25	0.66
1:L5:418:A:C2	3:L8:17:A:H1'	2.30	0.66
1:L5:4067:G:O2'	1:L5:4068:G:H5'	1.96	0.66
42:S2:118:C:H1'	42:S2:445:A:C5	2.29	0.66
1:L5:1586:C:H5"	1:L5:1587:U:O5'	1.95	0.66
1:L5:2711:G:H2'	1:L5:2712:G:H5'	1.76	0.66
1:L5:4379:G:O4'	1:L5:4433:5MC:HM53	1.96	0.66
42:S2:128:U:H5'	42:S2:215:G:H5'	1.77	0.66
42:S2:155:G:H4'	49:SG:15:LEU:CD1	2.25	0.66
42:S2:1154:U:O4	45:SC:227:ARG:HD2	1.95	0.66
42:S2:1272:C:O2'	42:S2:1273:C:H5'	1.94	0.66
1:L5:165:A:O2'	1:L5:166:C:H5'	1.95	0.66
1:L5:4735:C:H2'	1:L5:4736:G:O4'	1.94	0.66
9:LJ:151:ILE:HD11	9:LJ:156:ARG:HG2	1.77	0.66
42:S2:1136:PSU:O2'	42:S2:1137:U:H5'	1.96	0.66
60:SS:15:VAL:HG13	60:SS:68:ILE:CD1	2.25	0.66
1:L5:4224:G:H2'	1:L5:4225:A:H8	1.60	0.66
1:L5:4687:A:H2'	1:L5:4688:G:H5'	1.77	0.66
1:L5:4901:G:C2'	1:L5:4902:C:H5'	2.25	0.66
7:LF:52:GLU:HG3	21:Lb:96:LEU:CD1	2.24	0.66
12:LO:15:LEU:HD21	12:LO:125:LYS:HG3	1.77	0.66
38:LH:18:ILE:CD1	38:LH:27:VAL:HG22	2.24	0.66
1:L5:1562:C:O2'	1:L5:1563:U:H5'	1.94	0.66
1:L5:4976:U:O2'	1:L5:4977:G:H5'	1.94	0.66
10:LM:100:ARG:HA	10:LM:103:LYS:HE3	1.78	0.66
42:S2:455:A:H2'	42:S2:456:C:H6	1.61	0.66
1:L5:3853:A2M:O2'	1:L5:3854:G:H5'	1.95	0.66
42:S2:1269:G:C2'	42:S2:1270:G:H5'	2.26	0.66
42:S2:1385:G:C2'	42:S2:1386:A:H5'	2.24	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:SB:179:ASN:ND2	44:SB:187:LYS:HE2	2.11	0.66
1:L5:126:C:H2'	1:L5:127:G:H8	1.60	0.66
42:S2:1221:G:H2'	42:S2:1222:G:H8	1.61	0.66
42:S2:1344:A:H4'	42:S2:1345:G:H5'	1.78	0.66
45:SC:242:ASP:O	45:SC:246:LYS:HG2	1.96	0.66
73:Sg:57:ARG:HD3	73:Sg:95:GLY:HA3	1.78	0.66
1:L5:1851:G:OP1	21:Lb:4:SER:HB2	1.95	0.65
42:S2:145:G:H2'	42:S2:146:G:C8	2.32	0.65
42:S2:1690:U:H2'	42:S2:1691:U:C6	2.31	0.65
42:S2:562:U:H2'	42:S2:563:G:C8	2.32	0.65
49:SG:5:ILE:HD12	49:SG:111:LEU:HD12	1.78	0.65
64:SW:14:ILE:HD11	64:SW:27:ILE:HD11	1.78	0.65
76:S6:72:C:H2'	76:S6:73:A:H8	1.61	0.65
42:S2:949:G:H2'	42:S2:950:C:C6	2.31	0.65
1:L5:2405:OMU:HM22	1:L5:2406:G:O4'	1.96	0.65
19:LZ:9:LYS:HB3	19:LZ:25:ILE:HD12	1.78	0.65
42:S2:928:G:H2'	42:S2:929:G:C8	2.31	0.65
48:SF:25:THR:HG22	48:SF:109:LEU:HD13	1.77	0.65
1:L5:1429:A:H2'	1:L5:1430:G:O4'	1.97	0.65
6:LE:213:THR:H	6:LE:216:TYR:HB3	1.61	0.65
61:ST:42:HIS:CB	61:ST:83:GLN:HB2	2.27	0.65
73:Sg:112:ALA:HB3	73:Sg:121:VAL:HG12	1.77	0.65
27:Lh:91:MET:O	27:Lh:94:ARG:HG2	1.96	0.65
46:SD:16:ILE:HD13	71:Sd:50:ILE:HG12	1.78	0.65
63:SV:37:ALA:HB1	63:SV:46:PHE:CD1	2.32	0.65
16:LU:48:LYS:HG2	16:LU:53:ALA:N	2.12	0.65
51:SI:106:SER:CB	51:SI:171:LEU:HD13	2.25	0.65
66:SY:83:LYS:NZ	66:SY:96:LEU:HD13	2.12	0.65
1:L5:385:A:N3	1:L5:387:G:H5"	2.12	0.65
10:LM:74:ARG:O	10:LM:78:GLN:HG3	1.96	0.65
39:LI:184:MET:HE2	39:LI:190:LEU:HG	1.78	0.65
42:S2:501:C:O2	42:S2:501:C:H2'	1.97	0.65
42:S2:1139:C:H2'	42:S2:1140:G:O4'	1.97	0.65
42:S2:1409:A:H2'	42:S2:1410:C:C6	2.32	0.65
1:L5:1069:G:H2'	1:L5:1070:C:C6	2.32	0.65
1:L5:4109:C:O2'	1:L5:4110:G:H5'	1.97	0.65
2:L7:108:G:O2'	2:L7:109:U:H5'	1.97	0.65
3:L8:89:U:H2'	3:L8:90:C:C6	2.31	0.65
1:L5:23:C:H2'	1:L5:24:G:O4'	1.94	0.65
1:L5:4523:C:H2'	1:L5:4524:G:H8	1.60	0.65
16:LU:43:LEU:HD22	16:LU:47:ILE:HD11	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:92:U:H2'	3:L8:93:C:O4'	1.96	0.64
83:L8:425:HOH:O	29:Lj:63:ARG:HD2	1.97	0.64
38:LH:86:LEU:HB3	38:LH:186:THR:OG1	1.97	0.64
42:S2:1279:C:H2'	42:S2:1280:G:H8	1.62	0.64
9:LJ:141:ILE:HA	9:LJ:144:LYS:HD3	1.79	0.64
10:LM:38:VAL:HG21	10:LM:50:MET:HE3	1.79	0.64
42:S2:344:U:H2'	42:S2:345:U:C6	2.31	0.64
42:S2:1440:C:O2'	42:S2:1441:U:H5'	1.96	0.64
42:S2:1797:U:H2'	42:S2:1798:C:C6	2.33	0.64
44:SB:179:ASN:HD21	44:SB:187:LYS:HE2	1.62	0.64
61:ST:60:THR:HG23	61:ST:75:MET:HE2	1.77	0.64
68:Sa:47:ALA:HA	68:Sa:50:VAL:HG23	1.80	0.64
1:L5:116:G:H2'	1:L5:117:C:C6	2.31	0.64
1:L5:126:C:H2'	1:L5:127:G:C8	2.32	0.64
1:L5:2857:C:C2'	1:L5:2858:G:H5'	2.28	0.64
1:L5:3601:G:H1'	78:LW:44:ARG:HD3	1.79	0.64
73:Sg:94:THR:OG1	73:Sg:96:THR:HG22	1.98	0.64
1:L5:4490:C:H2'	1:L5:4491:C:H6	1.62	0.64
1:L5:4952:A:H2'	1:L5:4953:A:C8	2.31	0.64
42:S2:1052:A:H2'	42:S2:1053:C:O4'	1.98	0.64
1:L5:4224:G:H2'	1:L5:4225:A:C8	2.32	0.64
42:S2:495:U:H2'	42:S2:496:C:O4'	1.98	0.64
1:L5:2630:G:H2'	1:L5:2631:A:C8	2.32	0.64
1:L5:2743:G:O2'	1:L5:2744:G:H5'	1.97	0.64
12:LO:158:GLU:O	12:LO:162:GLU:HG2	1.98	0.64
42:S2:867:OMG:O2'	42:S2:868:G:H5'	1.98	0.64
42:S2:877:C:H2'	42:S2:878:G:C8	2.32	0.64
42:S2:1238:PSU:O4	42:S2:1242:U:H5	1.80	0.64
42:S2:1344:A:H4'	42:S2:1345:G:OP1	1.97	0.64
43:SA:81:ASN:HA	43:SA:84:GLN:HG3	1.78	0.64
21:Lb:32:LEU:HD11	21:Lb:43:MET:HE1	1.79	0.64
42:S2:367:U:H4'	42:S2:371:A:C8	2.32	0.64
42:S2:945:U:H2'	42:S2:946:U:C6	2.33	0.64
42:S2:1344:A:C4'	42:S2:1345:G:H5'	2.28	0.64
1:L5:4901:G:O2'	1:L5:4902:C:H5'	1.97	0.64
1:L5:4977:G:H2'	1:L5:4978:G:N3	2.12	0.64
16:LU:76:VAL:HB	16:LU:77:PRO:HD2	1.80	0.64
44:SB:181:LEU:O	44:SB:185:VAL:HG23	1.98	0.64
46:SD:70:THR:HA	46:SD:86:LEU:HD13	1.78	0.64
75:LR:95:TRP:CH2	75:LR:99:MET:HE3	2.33	0.64
77:LV:85[B]:ARG:HE	77:LV:100:ASP:HA	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1658:C:H2'	1:L5:1659:C:H6	1.61	0.64
1:L5:3866:G:H2'	1:L5:3867:G:C8	2.33	0.64
4:LC:212:ASN:OD1	4:LC:259:LYS:HE3	1.98	0.64
42:S2:656:G:H5'	42:S2:662:G:N2	2.13	0.64
42:S2:674:C:H2'	42:S2:675:U:C6	2.32	0.64
42:S2:1712:A:H2'	42:S2:1713:C:C6	2.33	0.64
46:SD:5:ILE:HD11	46:SD:9:ARG:NH2	2.13	0.64
76:S6:5:G:H2'	76:S6:6:G:C8	2.33	0.64
3:L8:144:U:H2'	3:L8:145:C:C6	2.33	0.64
21:Lb:32:LEU:CD1	21:Lb:43:MET:HE1	2.28	0.64
42:S2:346:C:H2'	42:S2:347:G:O4'	1.98	0.64
42:S2:913:A:OP1	42:S2:913:A:H2'	1.98	0.64
42:S2:1264:C:H4'	42:S2:1265:A:O4'	1.98	0.64
1:L5:727:C:O2'	1:L5:728:U:H5'	1.96	0.63
1:L5:1900:G:C2'	1:L5:1901:U:H5'	2.28	0.63
5:LD:108:ARG:CZ	5:LD:253:TYR:HB2	2.28	0.63
45:SC:101:SER:HB3	45:SC:132:ASP:HB2	1.79	0.63
65:SX:66:ILE:HD12	72:Se:4:GLY:HA3	1.77	0.63
73:Sg:299:PHE:HD1	73:Sg:309:VAL:HG22	1.63	0.63
1:L5:1206:G:O2'	1:L5:1207:G:H5'	1.98	0.63
42:S2:167:G:OP1	49:SG:8:PRO:HB3	1.99	0.63
60:SS:85:ASN:HB2	60:SS:97:GLN:CD	2.23	0.63
1:L5:3757:C:H2'	1:L5:3758:U:H5'	1.80	0.63
42:S2:987:A:N1	44:SB:120:MET:HE1	2.14	0.63
63:SV:58:ALA:O	63:SV:62:MET:HG2	1.98	0.63
1:L5:1060:G:O2'	1:L5:1061:G:H5'	1.99	0.63
1:L5:2294:U:H5"	1:L5:2296:G:O4'	1.99	0.63
1:L5:2751:U:H4'	1:L5:2752:G:O4'	1.98	0.63
5:LD:115:MET:HE1	5:LD:140:GLY:O	1.99	0.63
44:SB:175:GLU:OE1	44:SB:175:GLU:HA	1.99	0.63
46:SD:172:VAL:HG22	46:SD:185:LYS:HD3	1.80	0.63
4:LC:208:CYS:SG	4:LC:230:LEU:HD12	2.39	0.63
42:S2:1388:A:H61	46:SD:161:GLY:HA3	1.64	0.63
42:S2:1653:U:H2'	42:S2:1654:G:C8	2.33	0.63
1:L5:4403:C:H2'	1:L5:4408:G:O4'	1.99	0.63
1:L5:444:G:O2'	1:L5:445:U:H5'	1.99	0.63
1:L5:680:G:H2'	1:L5:681:G:H5'	1.81	0.63
1:L5:1817:G:H21	1:L5:1818:U:C5'	2.11	0.63
83:L5:6761:HOH:O	4:LC:69:THR:HG21	1.98	0.63
42:S2:678:U:H2'	42:S2:679:A:C8	2.34	0.63
1:L5:1071:C:C3'	1:L5:1072:A:H5"	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1692:C:H2'	1:L5:1693:G:O4'	1.99	0.63
1:L5:1780:U:H4'	39:LI:90:ARG:O	1.98	0.63
1:L5:4894:A:H2'	37:LB:156:TYR:CE1	2.34	0.63
8:LG:143:VAL:O	8:LG:147:VAL:HG23	1.99	0.63
42:S2:1816:G:C3'	42:S2:1817:G:H5"	2.27	0.63
53:SK:6:LYS:O	53:SK:9:ILE:HG13	1.98	0.63
1:L5:127:G:H2'	1:L5:128:C:H6	1.64	0.63
1:L5:5043:A:O2'	1:L5:5044:C:H5'	1.99	0.63
3:L8:66:A:H2'	3:L8:67:U:C6	2.34	0.63
24:Le:104:SER:O	24:Le:108:ARG:HG3	1.97	0.63
42:S2:392:A:C2'	42:S2:393:U:H5'	2.28	0.63
42:S2:1446:A:O2'	42:S2:1447:OMG:H5"	1.99	0.63
42:S2:1533:A:H2	42:S2:1536:G:N3	1.96	0.63
51:SI:80:ASP:OD1	51:SI:103:LEU:HB2	1.98	0.63
1:L5:3589:G:H2'	1:L5:3590:A:H5"	1.79	0.62
42:S2:66:G:H5"	42:S2:67:C:OP2	1.99	0.62
69:Sb:19:HIS:HB3	69:Sb:22:LYS:HG3	1.80	0.62
1:L5:1245:G:C8	21:Lb:95:ARG:HG3	2.34	0.62
1:L5:2254:C:H2'	1:L5:2255:G:O4'	1.98	0.62
2:L7:22:A:H2'	2:L7:23:A:C8	2.35	0.62
4:LC:298:ILE:O	4:LC:302:LEU:HG	1.99	0.62
43:SA:137:ALA:CB	43:SA:142:LEU:HB3	2.28	0.62
1:L5:4877:A:H2'	1:L5:4878:A:O4'	1.99	0.62
2:L7:48:G:H5'	5:LD:226:TYR:HE1	1.64	0.62
16:LU:48:LYS:CG	16:LU:53:ALA:HB2	2.29	0.62
1:L5:4949:C:O2'	1:L5:4950:U:H5'	1.99	0.62
3:L8:62:A:H4'	3:L8:63:U:O5'	1.98	0.62
55:SN:94:LYS:HG2	55:SN:118:ILE:HD13	1.82	0.62
1:L5:1478:G:H5'	1:L5:1479:C:C5	2.35	0.62
1:L5:1499:A:H4'	1:L5:1500:G:H5'	1.80	0.62
1:L5:2592:G:H2'	1:L5:2593:C:H6	1.64	0.62
1:L5:3890:G:H5"	1:L5:3891:A:OP2	2.00	0.62
42:S2:1845:A:H2'	42:S2:1846:G:C8	2.35	0.62
66:SY:105:LYS:O	66:SY:109:GLU:HG3	1.99	0.62
67:SZ:58:LEU:HD12	67:SZ:62:VAL:CG2	2.25	0.62
1:L5:1624:C:OP2	36:LA:9:ARG:HD2	1.98	0.62
1:L5:4871:C:O2'	1:L5:4872:C:H5'	1.99	0.62
83:L5:5694:HOH:O	7:LF:212:LYS:HD2	1.97	0.62
3:L8:33:G:H5"	3:L8:34:U:OP1	1.99	0.62
1:L5:25:A:H2'	1:L5:26:C:C6	2.35	0.62
1:L5:1304:C:H2'	1:L5:1305:C:C6	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:1784:G:O2'	42:S2:1785:C:H5'	1.99	0.62
52:SJ:136:ARG:HD3	52:SJ:160:SER:HA	1.81	0.62
58:SQ:125:ARG:O	58:SQ:126:ARG:HD3	1.98	0.62
1:L5:507:G:O2'	1:L5:508:G:H5'	2.00	0.62
1:L5:976:U:C5	6:LE:71:ARG:HD3	2.34	0.62
1:L5:4723:G:O2'	1:L5:4724:C:H5'	2.00	0.62
17:LX:149:VAL:O	17:LX:153:ILE:HG13	1.99	0.62
35:Lr:66:ARG:HD2	35:Lr:75:THR:O	2.00	0.62
42:S2:377:G:H5'	51:SI:98:LYS:HB3	1.82	0.62
42:S2:1223:A:H2'	42:S2:1224:G:O4'	2.00	0.62
60:SS:65:GLU:O	60:SS:69:THR:HG22	1.99	0.62
61:ST:71:GLY:O	61:ST:75:MET:HG2	2.00	0.62
1:L5:4101:G:O2'	1:L5:4102:C:H5'	1.98	0.62
36:LA:135:THR:CG2	36:LA:149:LYS:HB3	2.29	0.62
42:S2:1288:OMU:HN3	42:S2:1311:C:H42	1.48	0.62
59:SR:21:TYR:CD1	59:SR:58:MET:HE1	2.35	0.62
1:L5:1573:G:O2'	1:L5:1608:G:H4'	2.00	0.62
3:L8:155:C:H2'	3:L8:156:U:H5"	1.81	0.62
42:S2:953:C:H2'	42:S2:954:U:O4'	1.99	0.62
42:S2:1794:C:H2'	42:S2:1795:G:C8	2.35	0.62
45:SC:187:ARG:HB3	45:SC:187:ARG:NH1	2.15	0.62
53:SK:49:MET:CE	53:SK:52:LEU:HD12	2.30	0.62
73:Sg:299:PHE:CD1	73:Sg:309:VAL:HG22	2.35	0.62
1:L5:1414:C:H2'	1:L5:1415:G:H5'	1.81	0.61
10:LM:104:MET:CE	10:LM:109:ARG:HG2	2.30	0.61
30:Lk:46:VAL:O	30:Lk:47:ILE:HD13	1.98	0.61
38:LH:159:ALA:O	38:LH:163:GLN:HG3	2.00	0.61
42:S2:1690:U:H2'	42:S2:1691:U:H6	1.65	0.61
65:SX:86:PRO:O	65:SX:87:ASN:HB2	1.98	0.61
1:L5:2338:G:H5"	1:L5:2341:OMC:C5	2.35	0.61
1:L5:4847:G:H2'	1:L5:4848:G:C8	2.35	0.61
6:LE:268:GLN:O	6:LE:272:ARG:HG3	2.00	0.61
37:LB:108:GLU:HG3	37:LB:137:TRP:HB2	1.82	0.61
58:SQ:62:ARG:HD3	58:SQ:108:ILE:HD11	1.82	0.61
59:SR:54:VAL:O	59:SR:58:MET:HG2	1.99	0.61
1:L5:1681:G:H2'	1:L5:1682:C:H6	1.64	0.61
16:LU:26:THR:HA	16:LU:68:SER:CB	2.30	0.61
42:S2:1491:G:H2'	42:S2:1492:U:C6	2.35	0.61
50:SH:100:ILE:HG12	50:SH:125:VAL:HG21	1.81	0.61
1:L5:106:A:H2'	1:L5:107:G:O4'	2.01	0.61
1:L5:1747:A:O2'	1:L5:1748:G:H5'	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2701:G:H3'	1:L5:2702:G:C5'	2.30	0.61
1:L5:3589:G:O2'	1:L5:3590:A:H5"	2.00	0.61
1:L5:3638:A:H2'	1:L5:3639:A:C8	2.36	0.61
39:LI:36:LEU:HD21	39:LI:69:ARG:HH11	1.65	0.61
42:S2:1804:OMU:HM22	42:S2:1805:G:C5'	2.30	0.61
46:SD:109:LEU:HD12	46:SD:184:ILE:HD11	1.82	0.61
51:SI:49:ARG:HH11	51:SI:49:ARG:HG3	1.64	0.61
56:SO:113:GLN:NE2	68:Sa:45:VAL:HA	2.14	0.61
67:SZ:65:TYR:HB2	67:SZ:68:ILE:HG12	1.83	0.61
1:L5:280:G:H5"	11:LN:14:LYS:HE2	1.82	0.61
1:L5:4912:G:H5"	1:L5:4913:C:H5	1.64	0.61
5:LD:93:THR:O	5:LD:158:LYS:HE3	2.00	0.61
16:LU:23:LEU:CD2	16:LU:87:THR:HG21	2.29	0.61
42:S2:1091:C:HO2'	64:SW:2:VAL:N	1.98	0.61
42:S2:1414:A:H2'	42:S2:1415:C:C6	2.36	0.61
42:S2:1726:G:H1	42:S2:1808:U:H3	1.48	0.61
76:S6:71:G:C2'	76:S6:72:C:H5'	2.31	0.61
1:L5:3642:A:H2'	1:L5:3643:U:H6	1.66	0.61
27:Lh:119:TYR:HB2	40:LL:124:LEU:HD11	1.82	0.61
42:S2:1214:A:C4'	42:S2:1343:U:H5'	2.31	0.61
42:S2:1221:G:H2'	42:S2:1222:G:C8	2.36	0.61
1:L5:438:G:O2'	1:L5:439:G:H5'	2.00	0.61
1:L5:1748:G:H2'	1:L5:1749:G:H8	1.65	0.61
1:L5:4895:A:H4'	37:LB:95:THR:CG2	2.30	0.61
6:LE:95:PRO:CA	6:LE:104:THR:HG22	2.29	0.61
42:S2:97:U:O2'	42:S2:98:C:H5'	2.00	0.61
49:SG:49:VAL:HB	49:SG:115:LYS:CB	2.31	0.61
1:L5:965:U:H4'	1:L5:966:C:C6	2.36	0.61
1:L5:1564:C:H2'	1:L5:1565:U:H6	1.65	0.61
1:L5:1717:G:H2'	1:L5:1718:C:C6	2.36	0.61
1:L5:2686:A:C2	30:Lk:69:LEU:HD21	2.36	0.61
1:L5:4348:A:O2'	1:L5:4349:A:H5'	2.01	0.61
5:LD:287:PHE:CZ	39:LI:214:SER:HB3	2.35	0.61
42:S2:581:U:O2'	42:S2:582:U:H5'	1.99	0.61
49:SG:68:LEU:HD23	49:SG:100:CYS:SG	2.41	0.61
53:SK:15:LEU:HD22	53:SK:49:MET:HE1	1.82	0.61
60:SS:21:ASP:HB3	60:SS:24:ARG:HG3	1.83	0.61
62:SU:111:GLU:HA	62:SU:111:GLU:OE2	2.00	0.61
66:SY:7:ILE:HG22	66:SY:47:MET:HE1	1.83	0.61
1:L5:752:G:C2'	1:L5:753:C:H5'	2.31	0.61
1:L5:3649:A:N3	1:L5:3649:A:H2'	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3757:C:C2'	1:L5:3758:U:H5'	2.31	0.61
1:L5:4866:U:N3	10:LM:113:MET:HG3	2.16	0.61
83:L5:7069:HOH:O	34:Lp:25:MET:HE1	1.99	0.61
37:LB:57:VAL:HG22	37:LB:73:VAL:HG22	1.81	0.61
42:S2:1657:G:O2'	42:S2:1658:G:H5'	2.00	0.61
1:L5:450:G:N2	1:L5:1293:U:H3	1.93	0.61
1:L5:1341:A:H2'	1:L5:1342:C:C6	2.36	0.61
2:L7:36:C:O2'	2:L7:37:G:H5'	2.01	0.61
22:Lc:80:GLU:HG2	55:SN:100:LYS:NZ	2.16	0.61
42:S2:218:PSU:O2'	42:S2:219:U:H5'	2.01	0.61
42:S2:1740:C:H2'	42:S2:1741:U:C6	2.36	0.61
1:L5:18:C:H4'	11:LN:138:PHE:CD2	2.36	0.60
1:L5:1204:C:H3'	1:L5:1205:G:C5'	2.31	0.60
1:L5:2573:C:OP1	26:Lg:54:ARG:HB2	2.01	0.60
1:L5:2717:C:H2'	1:L5:2718:U:C6	2.36	0.60
1:L5:4868:C:C2'	1:L5:4869:G:H5'	2.29	0.60
43:SA:187:GLY:CA	63:SV:45:ARG:HE	2.13	0.60
46:SD:142:LEU:HD13	46:SD:150:MET:HG3	1.84	0.60
50:SH:11:PRO:CD	50:SH:44:ASN:HD22	2.13	0.60
68:Sa:47:ALA:HA	68:Sa:50:VAL:CG2	2.30	0.60
78:LW:3:VAL:HG13	78:LW:13:ILE:O	2.00	0.60
1:L5:1802:G:H2'	1:L5:1803:C:C6	2.36	0.60
1:L5:2640:G:O2'	1:L5:2641:C:H5'	2.01	0.60
1:L5:2757:U:O2'	1:L5:2758:C:H5'	2.01	0.60
45:SC:125:LYS:HG2	45:SC:143:CYS:HB2	1.83	0.60
1:L5:674:G:H2'	1:L5:675:C:H6	1.66	0.60
1:L5:1078:C:H2'	1:L5:1079:C:O4'	2.01	0.60
1:L5:2578:C:H5"	1:L5:2579:C:H5"	1.84	0.60
1:L5:1939:A:H2'	1:L5:1940:A:H5'	1.81	0.60
1:L5:2406:G:C2	1:L5:2415:U:H5"	2.37	0.60
1:L5:2592:G:H2'	1:L5:2593:C:C6	2.36	0.60
1:L5:4951:A:H5"	37:LB:128:LYS:HG3	1.82	0.60
12:LO:51:LYS:HA	12:LO:141:LEU:HD21	1.83	0.60
42:S2:1638:G:H5"	42:S2:1639:G7M:OP1	2.02	0.60
1:L5:1748:G:H2'	1:L5:1749:G:C8	2.36	0.60
1:L5:265:C:H2'	1:L5:266:C:O4'	2.01	0.60
1:L5:424:U:H2'	1:L5:425:U:C6	2.36	0.60
1:L5:1328:C:H2'	1:L5:1329:A:C8	2.36	0.60
1:L5:3712:A:H2'	1:L5:3713:A:C8	2.36	0.60
3:L8:144:U:H2'	3:L8:145:C:H6	1.66	0.60
13:LP:94:MET:HE1	13:LP:146:ILE:HB	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:614:C:H5"	42:S2:615:C:C6	2.36	0.60
42:S2:1808:U:H2'	42:S2:1809:A:H8	1.65	0.60
56:SO:93:LEU:HG	56:SO:124:MET:HE2	1.83	0.60
1:L5:1746:G:OP1	39:LI:39:LYS:HE3	2.01	0.60
1:L5:5017:C:C2'	1:L5:5018:G:H5'	2.31	0.60
42:S2:439:A:O2'	42:S2:440:G:H5'	2.00	0.60
42:S2:1804:OMU:HM22	42:S2:1805:G:C4'	2.31	0.60
50:SH:157:HIS:HB3	50:SH:190:PRO:HG3	1.84	0.60
70:Sc:34:PHE:CD2	70:Sc:40:ARG:HD3	2.37	0.60
1:L5:164:G:H2'	1:L5:165:A:C8	2.37	0.60
1:L5:3718:A:H2'	1:L5:3719:A:H8	1.66	0.60
3:L8:94:G:N3	29:Lj:82:THR:HG23	2.17	0.60
41:LS:139:ARG:O	41:LS:143:LYS:HG3	2.01	0.60
42:S2:449:A:H4'	47:SE:3:ARG:HD3	1.84	0.60
42:S2:678:U:H2'	42:S2:679:A:H8	1.66	0.60
42:S2:1296:U:H2'	42:S2:1297:U:O4'	2.02	0.60
42:S2:1413:G:O2'	42:S2:1414:A:H5'	2.01	0.60
42:S2:1426:U:O2'	42:S2:1427:C:H5'	2.02	0.60
1:L5:1582:G:O2'	1:L5:1583:G:H5'	2.02	0.60
1:L5:2665:G:O6	22:Lc:30:GLY:HA3	2.02	0.60
1:L5:3866:G:O2'	1:L5:3867:G:H5'	2.02	0.60
31:Ll:16:LYS:HG3	31:Ll:49:LEU:HD22	1.84	0.60
42:S2:1817:G:H2'	42:S2:1818:A:O4'	2.02	0.60
1:L5:2323:G:N7	4:LC:189:MET:HE3	2.17	0.60
1:L5:3772:U:O2	1:L5:3800:U:H4'	2.01	0.60
1:L5:3851:A:H2'	1:L5:3852:C:H6	1.66	0.60
5:LD:163:LEU:HD23	5:LD:163:LEU:C	2.27	0.60
5:LD:200:MET:HA	5:LD:200:MET:HE3	1.84	0.60
33:Lo:23:VAL:HG22	33:Lo:70:LEU:CD2	2.31	0.60
42:S2:222:U:O2'	42:S2:223:C:H5'	2.01	0.60
42:S2:224:A:H2'	42:S2:225:G:C8	2.37	0.60
42:S2:949:G:H2'	42:S2:950:C:H6	1.67	0.60
42:S2:1349:G:H2'	42:S2:1350:U:C6	2.37	0.60
1:L5:654:C:O2'	4:LC:269:LYS:HD2	2.02	0.59
1:L5:1664:A:C2'	1:L5:1665:A:H5'	2.32	0.59
1:L5:4510:G:C2	37:LB:252:ALA:HB1	2.37	0.59
9:LJ:12:MET:HE3	9:LJ:137:PRO:HB2	1.84	0.59
34:Lp:82:ALA:HA	42:S2:938:A:O3'	2.02	0.59
39:LI:181:PHE:CE1	39:LI:197:VAL:HG11	2.37	0.59
42:S2:167:G:H2'	42:S2:168:C:H5"	1.84	0.59
42:S2:1431:G:O2'	42:S2:1432:U:H5'	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:SE:200:ARG:HA	47:SE:206:ASP:OD1	2.02	0.59
50:SH:140:VAL:HG12	55:SN:19:ARG:HD3	1.84	0.59
1:L5:905:U:H2'	1:L5:906:G:O4'	2.02	0.59
1:L5:929:A:H2'	10:LM:46:ARG:HD2	1.84	0.59
1:L5:4592:G:H2'	1:L5:4593:A:C8	2.37	0.59
1:L5:4748:A:O2'	1:L5:4749:U:H5'	2.02	0.59
6:LE:206:VAL:HG13	6:LE:256:GLN:HB2	1.83	0.59
42:S2:1337:4AC:CM7	42:S2:1337:4AC:H5	2.32	0.59
42:S2:1374:C:H5'	42:S2:1465:A:C1'	2.32	0.59
1:L5:2691:U:H2'	1:L5:2692:C:C6	2.38	0.59
1:L5:4687:A:C2'	1:L5:4688:G:H5'	2.32	0.59
36:LA:117:GLU:HG2	36:LA:124:GLY:H	1.65	0.59
36:LA:149:LYS:HD3	42:S2:981:A:H5'	1.83	0.59
42:S2:1181:A:H2'	42:S2:1182:A:C8	2.36	0.59
1:L5:269:G:O2'	1:L5:270:U:H5'	2.02	0.59
1:L5:2559:G:O2'	1:L5:2560:U:H5'	2.03	0.59
2:L7:54:A:H1'	9:LJ:13:ARG:HG3	1.83	0.59
5:LD:287:PHE:HZ	39:LI:214:SER:HB3	1.66	0.59
20:La:90:ALA:HB3	20:La:120:GLN:NE2	2.18	0.59
42:S2:575:A:H2'	42:S2:576:A2M:O4'	2.03	0.59
51:SI:98:LYS:O	51:SI:175:ILE:HB	2.02	0.59
68:Sa:46:GLU:O	68:Sa:50:VAL:HG23	2.00	0.59
1:L5:1827:G:H2'	1:L5:1828:C:C6	2.37	0.59
42:S2:1374:C:C5'	42:S2:1465:A:H1'	2.31	0.59
1:L5:2756:A:H2'	1:L5:2757:U:H5'	1.85	0.59
5:LD:205:ALA:HB2	5:LD:236:MET:HG3	1.83	0.59
6:LE:67:ALA:HA	6:LE:69:TYR:CE1	2.37	0.59
6:LE:159:GLY:C	6:LE:274:VAL:HG23	2.27	0.59
23:Ld:46:LEU:HD22	23:Ld:72:VAL:HG11	1.83	0.59
36:LA:24:LYS:HG3	36:LA:49:ILE:HD12	1.83	0.59
42:S2:85:A:H2'	42:S2:86:C:H6	1.68	0.59
42:S2:1384:C:H2'	42:S2:1385:G:H5'	1.83	0.59
66:SY:83:LYS:HZ3	66:SY:96:LEU:HD13	1.67	0.59
1:L5:4921:G:C6	6:LE:183:ARG:HD3	2.38	0.59
39:LI:86:HIS:HB3	39:LI:139:ARG:HG2	1.85	0.59
42:S2:650:A:OP2	65:SX:108:LYS:HD2	2.03	0.59
42:S2:1545:A:H2'	42:S2:1546:G:C8	2.37	0.59
1:L5:93:G:H2'	1:L5:94:A:C8	2.38	0.59
1:L5:4367:A:H5"	83:L5:5881:HOH:O	2.02	0.59
16:LU:23:LEU:HD22	16:LU:87:THR:HG21	1.84	0.59
38:LH:161:ILE:O	38:LH:165:THR:HG23	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:SA:41:ARG:HD2	43:SA:47:TYR:CZ	2.37	0.59
46:SD:59:LEU:HD11	46:SD:88:ALA:HB3	1.85	0.59
66:SY:25:ILE:HD11	66:SY:73:GLY:HA3	1.83	0.59
75:LR:134:ASN:OD1	75:LR:137:ILE:HG12	2.03	0.59
1:L5:2529:C:H2'	1:L5:2530:C:C6	2.37	0.59
1:L5:3592:U:H2'	1:L5:3593:U:C6	2.37	0.59
1:L5:4218:U:H4'	1:L5:4219:A:O4'	2.03	0.59
1:L5:4638:G:H2'	1:L5:4639:C:C6	2.38	0.59
42:S2:344:U:H2'	42:S2:345:U:H6	1.67	0.59
52:SJ:67:ASP:O	52:SJ:71:LEU:HG	2.03	0.59
1:L5:751:G:H2'	1:L5:752:G:C8	2.37	0.59
1:L5:1842:G:H2'	1:L5:1843:C:C6	2.37	0.59
1:L5:4868:C:H2'	1:L5:4869:G:H5'	1.83	0.59
3:L8:128:C:H2'	3:L8:129:C:C6	2.38	0.59
42:S2:496:C:OP1	47:SE:29:PRO:HD3	2.02	0.59
42:S2:1477:U:H2'	42:S2:1478:U:H5'	1.85	0.59
42:S2:1533:A:N3	42:S2:1533:A:H2'	2.18	0.59
1:L5:2708:U:C5'	1:L5:2709:C:H5'	2.33	0.58
1:L5:3598:C:O2'	1:L5:3599:U:H5'	2.03	0.58
1:L5:4115:G:H5'	8:LG:33:GLU:O	2.03	0.58
1:L5:5046:A:H5'	37:LB:123:HIS:NE2	2.17	0.58
11:LN:163:GLY:O	11:LN:169:ARG:HG3	2.03	0.58
42:S2:1201:U:H2'	42:S2:1202:U:C6	2.37	0.58
42:S2:1445:PSU:C2'	42:S2:1446:A:H5'	2.33	0.58
68:Sa:88:SER:O	68:Sa:92:ARG:HG3	2.03	0.58
42:S2:176:U:H2'	42:S2:177:G:C8	2.38	0.58
63:SV:14:PRO:HG2	63:SV:23:ILE:HD12	1.84	0.58
75:LR:4:LEU:HD21	75:LR:33:ALA:HB2	1.85	0.58
1:L5:1564:C:H2'	1:L5:1565:U:C6	2.37	0.58
1:L5:4399:C:C2'	1:L5:4400:A:H5'	2.32	0.58
1:L5:4861:U:OP2	41:LS:165:PRO:HG3	2.03	0.58
42:S2:874:G:H2'	42:S2:875:A:C8	2.31	0.58
42:S2:1454:A:H5"	59:SR:3:ARG:HD2	1.85	0.58
73:Sg:157:SER:HB3	73:Sg:164:ILE:CD1	2.33	0.58
1:L5:2404:G:O2'	1:L5:2405:OMU:H5"	2.03	0.58
1:L5:3627:U:C6	1:L5:3631:U:C4	2.92	0.58
11:LN:72:LYS:HB2	83:LN:405:HOH:O	2.03	0.58
13:LP:125:MET:HE3	13:LP:143:PRO:HG3	1.84	0.58
41:LS:1:MET:HG3	41:LS:39:VAL:HG11	1.84	0.58
42:S2:1568:C:H2'	42:S2:1569:A:C8	2.39	0.58
46:SD:133:GLY:HA3	46:SD:156:LEU:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SW:31:SER:O	64:SW:35:VAL:HG23	2.04	0.58
65:SX:60:LYS:HD3	65:SX:116:PRO:HB3	1.85	0.58
1:L5:3598:C:C2'	1:L5:3599:U:H5'	2.34	0.58
1:L5:4580:U:H2'	1:L5:4581:G:H8	1.68	0.58
9:LJ:12:MET:O	9:LJ:137:PRO:HD2	2.03	0.58
42:S2:385:G:H3'	54:SL:136:LYS:HB2	1.85	0.58
44:SB:120:MET:HE2	44:SB:122:GLU:OE1	2.03	0.58
1:L5:2617:C:O2	1:L5:2617:C:H2'	2.02	0.58
1:L5:4474:A:H4'	1:L5:4475:G:C8	2.39	0.58
22:Lc:37:MET:SD	22:Lc:97:ILE:HD11	2.43	0.58
42:S2:1409:A:H2'	42:S2:1410:C:H6	1.66	0.58
65:SX:41:PHE:CZ	65:SX:102:VAL:HG23	2.39	0.58
73:Sg:18:VAL:HG11	73:Sg:307:VAL:HG22	1.86	0.58
1:L5:1476:C:HO2'	1:L5:1478:G:P	2.27	0.58
1:L5:2813:G:O2'	1:L5:2814:OMC:H5"	2.03	0.58
34:Lp:26:VAL:O	34:Lp:30:GLU:HG2	2.03	0.58
42:S2:606:G:H1'	72:Se:58:ASN:OD1	2.03	0.58
42:S2:1452:A:H5"	59:SR:48:ASN:ND2	2.18	0.58
42:S2:1648:G:H5"	58:SQ:125:ARG:HG2	1.84	0.58
1:L5:3715:U:O2'	1:L5:3716:U:H5'	2.03	0.58
1:L5:4605:U:H2'	1:L5:4606:OMU:C6	2.33	0.58
5:LD:287:PHE:O	5:LD:291:GLN:HG2	2.04	0.58
42:S2:1016:U:O2	55:SN:61:ALA:HB1	2.03	0.58
56:SO:35:ALA:HB2	56:SO:112:ALA:HB2	1.86	0.58
78:LW:8:PHE:CZ	78:LW:49:ILE:HG13	2.38	0.58
1:L5:648:G:H2'	1:L5:649:A:C8	2.39	0.58
1:L5:1842:G:H2'	1:L5:1843:C:H6	1.68	0.58
1:L5:2025:A:O2'	1:L5:2026:A:H5'	2.04	0.58
1:L5:3613:OMG:HM22	1:L5:3614:G:O4'	2.04	0.58
8:LG:50:ASP:CB	17:LX:40:ILE:HG13	2.33	0.58
28:Li:2:ALA:O	28:Li:3:LEU:HD12	2.04	0.58
42:S2:918:PSU:H2'	42:S2:919:A:O4'	2.04	0.58
42:S2:1384:C:C2'	42:S2:1385:G:H5'	2.34	0.58
73:Sg:290:ALA:O	73:Sg:298:LEU:HD12	2.03	0.58
1:L5:474:C:H2'	1:L5:475:G:O4'	2.03	0.58
1:L5:928:C:H5"	1:L5:929:A:O5'	2.04	0.58
1:L5:2619:C:H2'	1:L5:2620:U:O2	2.04	0.58
1:L5:4114:A:H1'	8:LG:35:ARG:HG3	1.85	0.58
1:L5:4174:U:H2'	1:L5:4175:U:C6	2.39	0.58
5:LD:79:TYR:O	5:LD:82:GLU:HG2	2.03	0.58
42:S2:529:A:H2'	42:S2:530:U:O4'	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:1279:C:H2'	42:S2:1280:G:C8	2.38	0.58
42:S2:1828:C:H2'	42:S2:1829:G:O4'	2.04	0.58
64:SW:18:GLU:HG2	64:SW:65:LEU:HD13	1.86	0.58
1:L5:1681:G:H2'	1:L5:1682:C:C6	2.38	0.57
28:Li:50:PHE:CD2	28:Li:58:MET:HE1	2.39	0.57
31:Ll:16:LYS:HG3	31:Ll:49:LEU:CD2	2.33	0.57
42:S2:662:G:H4'	42:S2:663:C:OP1	2.02	0.57
43:SA:76:VAL:HG23	43:SA:98:PRO:HA	1.85	0.57
61:ST:129:ARG:HD3	61:ST:133:ARG:NH2	2.19	0.57
1:L5:127:G:H2'	1:L5:128:C:C6	2.38	0.57
1:L5:512:U:O2	1:L5:647:G:C6	2.57	0.57
1:L5:751:G:H2'	1:L5:752:G:H8	1.69	0.57
1:L5:2642:G:OP2	1:L5:2642:G:H4'	2.04	0.57
1:L5:4890:C:O2'	1:L5:4891:C:H5'	2.04	0.57
8:LG:151:LYS:O	8:LG:205:THR:HG22	2.03	0.57
17:LX:110:LYS:O	17:LX:114:LYS:HG3	2.03	0.57
42:S2:1603:G:H4'	60:SS:38:ARG:NH2	2.19	0.57
1:L5:4866:U:C2	10:LM:113:MET:HG3	2.39	0.57
41:LS:2:LYS:HG2	41:LS:4:SER:OG	2.03	0.57
42:S2:167:G:C3'	42:S2:168:C:H5"	2.34	0.57
63:SV:2:GLN:HB2	63:SV:8:PHE:CE1	2.40	0.57
1:L5:1547:C:H2'	1:L5:1548:G:H5'	1.85	0.57
1:L5:2681:U:H2'	1:L5:2682:U:H6	1.69	0.57
18:LY:69:LYS:O	18:LY:83:GLU:HG3	2.05	0.57
42:S2:1447:OMG:O2'	42:S2:1448:A:H5'	2.04	0.57
43:SA:111:GLN:OE1	45:SC:89:LYS:HD3	2.04	0.57
61:ST:42:HIS:HB3	61:ST:83:GLN:HB2	1.86	0.57
65:SX:95:GLU:HB3	65:SX:98:ASP:OD1	2.05	0.57
1:L5:3781:A:O2'	1:L5:3782:U:H5'	2.03	0.57
2:L7:58:A:H2'	2:L7:59:G:C8	2.40	0.57
2:L7:111:C:H2'	2:L7:112:U:O4'	2.04	0.57
40:LL:91:ALA:HB1	40:LL:96:ILE:HB	1.86	0.57
42:S2:845:G:H2'	42:S2:846:G:O4'	2.04	0.57
42:S2:1327:G:C2'	42:S2:1328:OMG:H5'	2.34	0.57
42:S2:1393:G:O2'	42:S2:1394:G:H5'	2.04	0.57
46:SD:55:THR:O	46:SD:59:LEU:HD12	2.03	0.57
1:L5:1917:C:N4	10:LM:18:GLY:HA2	2.19	0.57
1:L5:3851:A:H2'	1:L5:3852:C:C6	2.38	0.57
1:L5:4999:A:H3'	1:L5:4999:A:OP1	2.05	0.57
28:Li:73:ILE:O	28:Li:77:VAL:HG22	2.04	0.57
37:LB:220:ILE:HG12	37:LB:278:THR:HG23	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:689:U:H2'	1:L5:690:C:H6	1.69	0.57
1:L5:745:G:H2'	1:L5:746:A:O4'	2.04	0.57
1:L5:1722:U:H5'	7:LF:135:ILE:HD11	1.87	0.57
1:L5:2402:A:H2'	1:L5:2403:U:C6	2.39	0.57
1:L5:4870:U:O2'	1:L5:4871:C:H5'	2.03	0.57
9:LJ:15:LEU:HD23	9:LJ:136:ARG:HG2	1.86	0.57
42:S2:803:C:H4'	64:SW:80:ASP:OD2	2.04	0.57
42:S2:980:A:H2'	42:S2:981:A:C8	2.40	0.57
61:ST:124:THR:HG22	61:ST:126:GLN:N	2.20	0.57
1:L5:1508:G:O2'	1:L5:1509:U:H5'	2.05	0.57
1:L5:2601:A:H2'	1:L5:2602:G:C8	2.40	0.57
1:L5:2823:A:C2'	1:L5:2824:C:H5'	2.35	0.57
1:L5:4228:U:H4'	1:L5:4229:C:OP1	2.05	0.57
66:SY:6:THR:HG22	66:SY:28:LEU:HD23	1.86	0.57
1:L5:4496:A:C8	77:LV:46:LYS:HE2	2.40	0.57
1:L5:4928:A:H8	1:L5:4928:A:OP2	1.87	0.57
42:S2:1476:A:H4'	42:S2:1477:U:C5'	2.33	0.57
1:L5:279:A:C4	11:LN:12:ARG:HG2	2.40	0.57
2:L7:16:A:H2'	2:L7:17:C:C6	2.40	0.57
3:L8:19:C:H2'	3:L8:20:A:C8	2.39	0.57
4:LC:339:THR:O	4:LC:343:GLN:HG3	2.05	0.57
5:LD:223:PHE:HD1	5:LD:226:TYR:CD1	2.22	0.57
19:LZ:119:GLU:O	19:LZ:123:LYS:HG2	2.04	0.57
37:LB:92:TYR:HB2	37:LB:159:VAL:HB	1.86	0.57
42:S2:1092:G:OP2	55:SN:9:LYS:HE3	2.04	0.57
42:S2:1453:C:O2'	59:SR:52:GLY:HA3	2.05	0.57
44:SB:62:LEU:O	44:SB:65:ARG:HG3	2.05	0.57
1:L5:276:C:H2'	28:Li:29:ARG:NH1	2.19	0.56
10:LM:13:ALA:HB3	10:LM:55:MET:HE2	1.86	0.56
13:LP:31:GLU:HA	13:LP:31:GLU:OE1	2.05	0.56
42:S2:499:G:H2'	42:S2:501:C:H5	1.70	0.56
42:S2:1365:G:H2'	42:S2:1366:G:H8	1.67	0.56
42:S2:1478:U:O2'	42:S2:1479:G:H5'	2.05	0.56
71:Sd:22:ARG:HD2	71:Sd:36:LEU:O	2.04	0.56
1:L5:2402:A:H2'	1:L5:2403:U:H6	1.70	0.56
73:Sg:175:LYS:HG2	73:Sg:187:ASN:OD1	2.05	0.56
1:L5:901:C:H2'	1:L5:902:G:C8	2.40	0.56
1:L5:1664:A:H2'	1:L5:1665:A:H5'	1.87	0.56
1:L5:1737:G:N3	1:L5:1777:PSU:H5"	2.20	0.56
1:L5:1782:A:H2'	1:L5:1785:C:C5	2.40	0.56
1:L5:1814:G:H1'	1:L5:1818:U:C2	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2303:A:O2'	1:L5:2304:G:H5'	2.04	0.56
3:L8:115:G:H2'	3:L8:116:C:C6	2.41	0.56
8:LG:73:ARG:HD3	8:LG:241:VAL:O	2.06	0.56
39:LI:36:LEU:HD11	39:LI:69:ARG:CD	2.30	0.56
42:S2:120:U:H1'	47:SE:33:THR:O	2.06	0.56
42:S2:1606:G:N2	42:S2:1632:G:H1'	2.19	0.56
46:SD:63:GLY:O	46:SD:66:ILE:HG22	2.05	0.56
47:SE:160:ILE:HD12	47:SE:162:ILE:HD11	1.86	0.56
50:SH:11:PRO:HG2	50:SH:44:ASN:HD22	1.71	0.56
73:Sg:112:ALA:HB3	73:Sg:121:VAL:CG1	2.34	0.56
1:L5:168:C:H2'	1:L5:191:G:H8	1.70	0.56
1:L5:1938:A:H2'	1:L5:1939:A:C8	2.41	0.56
1:L5:2681:U:H2'	1:L5:2682:U:C6	2.40	0.56
1:L5:4154:G:H2'	1:L5:4155:G:H5'	1.87	0.56
1:L5:4914:C:O2'	1:L5:4915:C:H5'	2.04	0.56
1:L5:5043:A:H5'	23:Ld:23:ARG:NH1	2.21	0.56
25:Lf:47:CYS:SG	25:Lf:74:VAL:HG23	2.46	0.56
42:S2:158:A:H2'	42:S2:159:A2M:O4'	2.05	0.56
42:S2:1368:U:OP2	42:S2:1467:C:H4'	2.05	0.56
48:SF:78:MET:O	48:SF:79:HIS:HB2	2.05	0.56
50:SH:172:THR:O	50:SH:176:VAL:HG23	2.05	0.56
1:L5:1464:C:H2'	1:L5:1465:C:C6	2.41	0.56
1:L5:2854:A:H5'	75:LR:82:LYS:O	2.05	0.56
1:L5:2857:C:H2'	1:L5:2858:G:H5'	1.87	0.56
1:L5:3676:U:O2'	1:L5:3677:G:H5'	2.05	0.56
5:LD:60:ILE:CD1	5:LD:93:THR:HA	2.35	0.56
16:LU:80:LYS:HG2	16:LU:110:TYR:CE2	2.41	0.56
26:Lg:42:PRO:HB2	26:Lg:53:LEU:HD12	1.88	0.56
37:LB:378:ARG:HD3	78:LW:11:TYR:CD2	2.40	0.56
42:S2:107:A:H2'	42:S2:108:G:H8	1.70	0.56
42:S2:464:A:H4'	42:S2:465:A:OP2	2.06	0.56
58:SQ:51:LEU:O	58:SQ:54:PRO:HD2	2.05	0.56
58:SQ:86:GLN:HE22	58:SQ:122:ALA:HB2	1.71	0.56
58:SQ:129:SER:O	58:SQ:131:LYS:HE3	2.05	0.56
1:L5:137:G:H2'	1:L5:138:G:C8	2.41	0.56
1:L5:4638:G:H2'	1:L5:4639:C:H6	1.70	0.56
5:LD:62:CYS:HB3	5:LD:105:LEU:HD22	1.88	0.56
27:Lh:88:THR:O	27:Lh:92:ARG:HG3	2.05	0.56
47:SE:184:THR:C	47:SE:189:LEU:HD13	2.30	0.56
1:L5:1202:G:H2'	1:L5:1203:U:O2	2.05	0.56
12:LO:48:TYR:CE2	12:LO:52:LEU:HD11	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LY:56:GLN:HG2	18:LY:67:ILE:HG12	1.88	0.56
23:Ld:68:LEU:HD13	23:Ld:108:TYR:HB2	1.87	0.56
42:S2:576:A2M:HM'2	42:S2:577:U:H5'	1.87	0.56
42:S2:1474:A:H2'	42:S2:1475:G:O4'	2.05	0.56
44:SB:112:SER:O	44:SB:115:LYS:HE3	2.06	0.56
73:Sg:32:LEU:HD22	73:Sg:71:ILE:HG12	1.88	0.56
1:L5:505:G:H1	1:L5:653:U:H3	1.53	0.56
1:L5:1081:A:N1	1:L5:1203:U:H5	2.03	0.56
1:L5:3740:G:H2'	1:L5:3741:G:O4'	2.06	0.56
1:L5:3916:U:H2'	1:L5:3917:C:C6	2.40	0.56
42:S2:1007:C:H2'	42:S2:1008:A:C8	2.41	0.56
1:L5:1295:G:O2'	1:L5:1296:G:H5'	2.05	0.56
42:S2:1589:A:H2'	42:S2:1590:C:C6	2.40	0.56
44:SB:68:GLU:OE2	44:SB:83:LYS:HE3	2.06	0.56
44:SB:168:MET:O	44:SB:172:MET:HG3	2.05	0.56
63:SV:32:ILE:HG12	63:SV:60:ARG:HD2	1.86	0.56
1:L5:165:A:H2'	1:L5:166:C:C6	2.40	0.56
1:L5:4685:U:C1'	1:L5:4686:A:H5"	2.36	0.56
2:L7:28:C:C2'	2:L7:29:C:H5'	2.34	0.56
5:LD:88:VAL:HG13	5:LD:239:MET:HE3	1.88	0.56
42:S2:287:U:O2	47:SE:131:VAL:HG21	2.05	0.56
42:S2:940:U:H2'	42:S2:941:C:C6	2.41	0.56
42:S2:1712:A:H2'	42:S2:1713:C:H6	1.70	0.56
46:SD:60:GLY:H	46:SD:65:ARG:HB3	1.71	0.56
48:SF:56:TYR:O	48:SF:62:ARG:HB3	2.06	0.56
1:L5:165:A:H2'	1:L5:166:C:H6	1.70	0.55
1:L5:4170:G:H5'	36:LA:233:ARG:HB2	1.87	0.55
3:L8:66:A:H2'	3:L8:67:U:H6	1.70	0.55
40:LL:128:PRO:HD3	40:LL:143:GLU:OE2	2.06	0.55
42:S2:563:G:HO2'	42:S2:564:A:H8	1.53	0.55
42:S2:1370:A:N3	42:S2:1372:U:H5'	2.21	0.55
43:SA:187:GLY:HA2	63:SV:45:ARG:HE	1.70	0.55
48:SF:51:HIS:O	58:SQ:50:LYS:HE2	2.07	0.55
50:SH:60:ILE:HB	50:SH:92:VAL:HG22	1.89	0.55
73:Sg:291:TRP:CE2	73:Sg:298:LEU:HD13	2.41	0.55
1:L5:965:U:H4'	1:L5:966:C:H6	1.71	0.55
1:L5:4361:C:H5"	1:L5:4362:A:OP1	2.06	0.55
4:LC:350:ARG:HG2	4:LC:350:ARG:HH11	1.71	0.55
42:S2:1628:C:H2'	42:S2:1629:C:H6	1.69	0.55
47:SE:139:LEU:HD23	47:SE:150:PRO:HB3	1.88	0.55
49:SG:12:CYS:CB	49:SG:124:LEU:HA	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SL:109:MET:HG2	54:SL:111:VAL:HG13	1.88	0.55
58:SQ:12:VAL:CG2	58:SQ:91:ALA:HA	2.35	0.55
62:SU:90:ASP:O	62:SU:91:LEU:HD23	2.06	0.55
1:L5:674:G:O2'	1:L5:675:C:H5'	2.05	0.55
1:L5:1069:G:H2'	1:L5:1070:C:H6	1.71	0.55
1:L5:4496:A:N7	77:LV:46:LYS:HE2	2.21	0.55
1:L5:4878:A:C2'	1:L5:4879:A:H5'	2.36	0.55
83:L5:6954:HOH:O	36:LA:206:PRO:HD2	2.05	0.55
8:LG:153:GLN:O	8:LG:180:PRO:HD2	2.06	0.55
37:LB:216:MET:HE2	37:LB:359:ALA:HA	1.89	0.55
42:S2:85:A:H2'	42:S2:86:C:C6	2.40	0.55
42:S2:1303:C:H2'	42:S2:1304:U:O4'	2.05	0.55
42:S2:1621:U:OP2	42:S2:1621:U:H6	1.88	0.55
42:S2:1839:U:H2'	42:S2:1840:U:C6	2.41	0.55
64:SW:55:ASP:OD1	64:SW:57:ARG:HB2	2.07	0.55
1:L5:137:G:H2'	1:L5:138:G:H8	1.71	0.55
1:L5:1464:C:H2'	1:L5:1465:C:H6	1.72	0.55
1:L5:1613:G:H1'	1:L5:2503:A:N6	2.21	0.55
1:L5:1831:G:OP1	1:L5:1831:G:H3'	2.07	0.55
1:L5:2694:C:H2'	1:L5:2695:G:C1'	2.36	0.55
1:L5:2734:A:H2'	1:L5:2735:A:C8	2.41	0.55
1:L5:4936:G:H2'	1:L5:4937:G:H8	1.72	0.55
42:S2:12:U:H2'	42:S2:13:C:H6	1.70	0.55
42:S2:805:U:O2'	42:S2:806:U:H5'	2.06	0.55
42:S2:1786:U:H2'	42:S2:1787:G:H8	1.71	0.55
45:SC:69:LEU:HD13	45:SC:269:PHE:CD2	2.35	0.55
46:SD:138:VAL:HG12	46:SD:142:LEU:HD21	1.87	0.55
1:L5:1506:G:H2'	1:L5:1507:U:C6	2.42	0.55
1:L5:1668:U:H2'	1:L5:1669:U:C6	2.42	0.55
2:L7:31:G:O2'	2:L7:32:A:H5'	2.07	0.55
4:LC:76:ILE:HG13	4:LC:77:PRO:CD	2.36	0.55
4:LC:94:ASN:HA	4:LC:100:ARG:O	2.07	0.55
10:LM:36:ALA:HB2	10:LM:52:PHE:CE1	2.41	0.55
42:S2:614:C:H5"	42:S2:615:C:C5	2.41	0.55
42:S2:1681:U:H2'	42:S2:1682:C:C6	2.42	0.55
56:SO:150:ARG:HG3	56:SO:150:ARG:HH11	1.70	0.55
58:SQ:34:VAL:HG22	58:SQ:70:VAL:HB	1.88	0.55
1:L5:424:U:H2'	1:L5:425:U:H6	1.72	0.55
1:L5:753:C:H2'	1:L5:754:U:C6	2.42	0.55
1:L5:1394:A:H4'	1:L5:1413:G:OP1	2.07	0.55
1:L5:2674:C:O2'	1:L5:2675:C:H5'	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4362:A:H5"	1:L5:4363:G:O5'	2.07	0.55
39:LI:181:PHE:HE1	39:LI:197:VAL:HG11	1.71	0.55
42:S2:316:G:O2'	42:S2:317:C:H5'	2.07	0.55
47:SE:139:LEU:C	47:SE:139:LEU:HD12	2.31	0.55
1:L5:4872:C:H2'	1:L5:4873:U:O4'	2.07	0.55
42:S2:1520:G:O2'	42:S2:1521:C:OP1	2.25	0.55
44:SB:110:MET:HA	44:SB:110:MET:HE3	1.89	0.55
44:SB:218:LEU:O	44:SB:219:LYS:HD3	2.06	0.55
47:SE:182:MET:HE3	47:SE:192:ILE:HD11	1.88	0.55
61:ST:11:GLN:OE1	61:ST:62:ARG:HD2	2.06	0.55
1:L5:2365:A:O2'	1:L5:2366:A:H5'	2.06	0.55
1:L5:2882:C:H5'	1:L5:5003:C:H4'	1.88	0.55
5:LD:21:ARG:O	5:LD:25:GLU:HG3	2.06	0.55
34:Lp:8:VAL:O	34:Lp:11:VAL:HG22	2.07	0.55
41:LS:16:CYS:SG	41:LS:25:PRO:HB3	2.47	0.55
59:SR:98:VAL:CG1	59:SR:102:THR:HB	2.36	0.55
1:L5:954:A:H2'	1:L5:964:G:N7	2.22	0.55
1:L5:1374:C:H5"	1:L5:1376:G:OP2	2.07	0.55
1:L5:1377:U:H2'	1:L5:1378:G:H5'	1.88	0.55
1:L5:4988:U:H2'	1:L5:4989:C:C6	2.41	0.55
11:LN:197:THR:HG23	40:LL:21:ARG:O	2.07	0.55
12:LO:121:PRO:HA	12:LO:124:LEU:HD12	1.89	0.55
27:Lh:123:ALA:HA	40:LL:150:LEU:CD1	2.37	0.55
58:SQ:9:SER:HB2	58:SQ:24:HIS:HE1	1.71	0.55
73:Sg:124:SER:HB3	73:Sg:126:ASP:OD1	2.07	0.55
73:Sg:146:SER:HA	73:Sg:177:TRP:HH2	1.72	0.55
1:L5:1827:G:H2'	1:L5:1828:C:H6	1.72	0.55
1:L5:2625:U:O2'	1:L5:2626:U:H5'	2.06	0.55
5:LD:200:MET:HB3	5:LD:237:GLU:HG3	1.89	0.55
13:LP:54:GLN:HA	13:LP:83:TRP:CD1	2.42	0.55
30:Lk:23:VAL:CG2	30:Lk:36:VAL:HG22	2.34	0.55
42:S2:499:G:H2'	42:S2:501:C:C5	2.42	0.55
42:S2:593:C:H4'	72:Se:26:LYS:HE2	1.88	0.55
1:L5:3759:U:H2'	1:L5:3761:A:OP2	2.07	0.54
1:L5:4348:A:C2'	1:L5:4349:A:H5'	2.37	0.54
1:L5:4558:U:H2'	1:L5:4559:G:C8	2.42	0.54
1:L5:4736:G:H4'	1:L5:4736:G:OP1	2.06	0.54
5:LD:107:ARG:HH12	5:LD:120:GLU:HA	1.70	0.54
19:LZ:26:VAL:CG2	19:LZ:91:LEU:HD23	2.36	0.54
28:Li:16:LYS:N	28:Li:16:LYS:HD2	2.22	0.54
36:LA:30:ARG:HA	36:LA:74:GLU:OE2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:1139:C:H5	42:S2:1149:A:H62	1.54	0.54
42:S2:1798:C:O2'	51:SI:2:GLY:HA2	2.07	0.54
43:SA:12:GLU:O	43:SA:15:VAL:HG12	2.07	0.54
55:SN:25:TRP:CZ3	69:Sb:83:GLN:HB2	2.41	0.54
56:SO:64:ALA:HB3	56:SO:67:ASP:OD1	2.07	0.54
1:L5:326:C:O2'	1:L5:327:U:H5'	2.06	0.54
3:L8:141:C:H2'	3:L8:142:U:C6	2.41	0.54
29:Lj:39:TYR:CD1	29:Lj:40:PRO:HA	2.41	0.54
38:LH:105:ILE:HG21	38:LH:109:GLY:HA2	1.88	0.54
42:S2:526:A:O2'	42:S2:527:C:H5'	2.08	0.54
1:L5:3634:A:H1'	1:L5:3771:A2M:N6	2.22	0.54
1:L5:3722:A:H2'	1:L5:3723:A:C8	2.43	0.54
1:L5:4333:G:O2'	1:L5:4334:A:H5'	2.08	0.54
43:SA:77:ILE:CD1	43:SA:122:LEU:HD11	2.37	0.54
1:L5:1627:A:C2	36:LA:204:MET:HG2	2.42	0.54
1:L5:2421:A:O2'	1:L5:2422:U:H5'	2.08	0.54
1:L5:3854:G:H22	1:L5:3886:G:H1'	1.72	0.54
1:L5:4109:C:C2'	1:L5:4110:G:H5'	2.38	0.54
15:LT:39:ILE:HG22	15:LT:99:SER:HB3	1.88	0.54
39:LI:52:MET:CE	39:LI:136:MET:HE3	2.35	0.54
42:S2:416:U:H2'	42:S2:417:C:O4'	2.07	0.54
42:S2:1288:OMU:O2'	42:S2:1289:U:H5'	2.08	0.54
42:S2:1587:G:O6	61:ST:67:NMM:HD3	2.08	0.54
42:S2:1845:A:H2'	42:S2:1846:G:H8	1.72	0.54
1:L5:2547:G:H2'	1:L5:2548:C:C6	2.43	0.54
1:L5:4178:A:H2'	1:L5:4179:C:H6	1.73	0.54
1:L5:4585:A:H4'	1:L5:4586:G:OP1	2.08	0.54
42:S2:1164:G:C2'	42:S2:1165:G:H5'	2.37	0.54
61:ST:42:HIS:HB2	61:ST:83:GLN:HB2	1.90	0.54
61:ST:114:GLU:HG2	61:ST:124:THR:OG1	2.07	0.54
1:L5:486:C:H2'	1:L5:487:G:O4'	2.07	0.54
1:L5:2852:G:H4'	1:L5:3611:G:N7	2.23	0.54
1:L5:4074:C:H2'	1:L5:4075:G:H8	1.73	0.54
3:L8:78:G:H2'	3:L8:79:G:O4'	2.08	0.54
6:LE:202:ASP:O	6:LE:260:LYS:HD3	2.08	0.54
20:La:146:LEU:HD12	28:Li:7:MET:HE2	1.90	0.54
38:LH:5:LEU:HD22	38:LH:60:TRP:CH2	2.43	0.54
42:S2:1815:A:H2'	42:S2:1816:G:O4'	2.08	0.54
50:SH:63:PHE:HA	50:SH:95:ILE:O	2.08	0.54
50:SH:145:ARG:HB2	64:SW:51:GLU:OE1	2.07	0.54
58:SQ:98:LYS:HG3	58:SQ:98:LYS:O	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:Ln:13:LEU:HD12	74:Ln:13:LEU:O	2.08	0.54
1:L5:248:C:O2'	1:L5:264:C:H5'	2.08	0.54
1:L5:752:G:O2'	1:L5:753:C:H5'	2.07	0.54
1:L5:755:C:H2'	1:L5:756:G:H8	1.72	0.54
1:L5:1201:C:H2'	1:L5:1202:G:H8	1.73	0.54
1:L5:4568:C:O2'	1:L5:4569:C:H5'	2.07	0.54
6:LE:203:ILE:O	6:LE:203:ILE:HG13	2.06	0.54
23:Ld:21:VAL:HG23	23:Ld:57:MET:HE1	1.90	0.54
41:LS:83:ARG:HG3	41:LS:125:GLN:HB2	1.90	0.54
1:L5:726:G:O2'	1:L5:727:C:H5'	2.08	0.54
1:L5:2529:C:H2'	1:L5:2530:C:H6	1.73	0.54
1:L5:2694:C:H2'	1:L5:2695:G:O4'	2.07	0.54
83:L5:5307:HOH:O	31:Ll:17:GLN:HG3	2.06	0.54
42:S2:92:A:O2'	47:SE:4:GLY:HA3	2.08	0.54
46:SD:162:ASP:N	46:SD:163:PRO:HD2	2.23	0.54
54:SL:80:MET:HE1	54:SL:120:VAL:O	2.07	0.54
73:Sg:23:THR:HG22	73:Sg:31:ILE:HG22	1.89	0.54
74:Ln:12:ARG:HG3	74:Ln:15:ARG:NH2	2.22	0.54
1:L5:679:C:H2'	1:L5:680:G:C8	2.43	0.54
2:L7:33:U:O2'	2:L7:34:C:H5'	2.08	0.54
2:L7:58:A:H2'	2:L7:59:G:H8	1.73	0.54
7:LF:209:TRP:CD1	7:LF:210:PRO:HD2	2.43	0.54
12:LO:141:LEU:O	12:LO:145:VAL:HG22	2.07	0.54
12:LO:202:LEU:O	12:LO:203:VAL:HG12	2.08	0.54
16:LU:28:PRO:HG3	16:LU:100:LEU:CD1	2.35	0.54
42:S2:60:A:O2'	42:S2:61:A:H5'	2.07	0.54
42:S2:354:OMU:HM22	42:S2:355:G:O4'	2.07	0.54
42:S2:595:U:H2'	42:S2:596:U:C6	2.42	0.54
43:SA:42:LYS:HD2	43:SA:48:ILE:HD11	1.90	0.54
2:L7:23:A:H2'	2:L7:24:C:C6	2.43	0.54
24:Le:21:ILE:HD11	24:Le:53:ILE:HD11	1.89	0.54
24:Le:82:VAL:HG13	24:Le:114:ARG:HG2	1.89	0.54
39:LI:190:LEU:O	39:LI:191:ILE:HD13	2.08	0.54
42:S2:428:OMU:O3'	52:SJ:2:PRO:HD2	2.07	0.54
42:S2:612:U:O2'	42:S2:613:G:H5'	2.08	0.54
52:SJ:134:HIS:CE1	52:SJ:164:PRO:HD2	2.43	0.54
54:SL:128:VAL:HG12	54:SL:142:VAL:HA	1.89	0.54
62:SU:40:ILE:HD12	62:SU:50:VAL:HG21	1.88	0.54
65:SX:60:LYS:CG	65:SX:116:PRO:HD3	2.36	0.54
1:L5:905:U:H3'	1:L5:906:G:C8	2.43	0.53
1:L5:2086:U:H4'	1:L5:2087:C:H3'	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2621:U:H3'	1:L5:2622:PSU:C5'	2.35	0.53
1:L5:4709:A:N3	37:LB:101:THR:HG21	2.22	0.53
16:LU:47:ILE:HG13	16:LU:86:LEU:CD1	2.39	0.53
36:LA:22:HIS:O	36:LA:52:PRO:HG2	2.08	0.53
42:S2:1138:C:O2'	63:SV:61:ARG:HD2	2.08	0.53
1:L5:267:G:H2'	1:L5:268:G:C8	2.42	0.53
1:L5:270:U:H2'	1:L5:271:C:H6	1.70	0.53
1:L5:2709:C:O2'	1:L5:2710:C:H5'	2.08	0.53
1:L5:3897:C:H2'	1:L5:3898:U:H6	1.73	0.53
38:LH:169:ASN:O	38:LH:170:LYS:HG2	2.08	0.53
42:S2:160:U:H3'	42:S2:161:U:H5"	1.90	0.53
42:S2:841:G:O2'	42:S2:842:C:H6	1.92	0.53
49:SG:28:TYR:HE1	49:SG:104:ALA:HA	1.73	0.53
1:L5:1609:A:H5'	36:LA:183:GLY:HA2	1.89	0.53
1:L5:1862:U:H2'	1:L5:1863:A:O4'	2.09	0.53
1:L5:3876:A:C2'	1:L5:3877:A:H5'	2.38	0.53
11:LN:160:GLU:HA	83:LN:445:HOH:O	2.08	0.53
12:LO:48:TYR:HE2	12:LO:52:LEU:HD11	1.74	0.53
42:S2:80:G:O2'	42:S2:81:U:H5'	2.08	0.53
42:S2:1303:C:H2'	42:S2:1304:U:O2	2.08	0.53
42:S2:1328:OMG:HM22	42:S2:1329:U:O4'	2.08	0.53
49:SG:32:MET:HE3	49:SG:65:GLN:HB2	1.89	0.53
57:SP:85:ILE:HD13	57:SP:111:MET:HB3	1.90	0.53
1:L5:750:U:H1'	1:L5:911:A:C8	2.43	0.53
1:L5:3695:U:H3	1:L5:3727:C:H42	1.56	0.53
1:L5:4075:G:O2'	1:L5:4076:G:H5'	2.07	0.53
1:L5:4934:G:H4'	1:L5:4935:U:H2'	1.90	0.53
16:LU:39:PHE:O	16:LU:39:PHE:HD1	1.92	0.53
16:LU:76:VAL:HB	16:LU:77:PRO:CD	2.39	0.53
34:Lp:81:SER:CB	42:S2:938:A:H4'	2.37	0.53
41:LS:159:LEU:HD12	41:LS:160:ARG:H	1.72	0.53
42:S2:96:C:H2'	42:S2:97:U:C6	2.44	0.53
42:S2:484:A2M:H8	42:S2:484:A2M:O5'	2.09	0.53
42:S2:572:PSU:H5"	66:SY:60:PHE:O	2.07	0.53
42:S2:1414:A:H2'	42:S2:1415:C:H6	1.72	0.53
60:SS:48:ALA:HB2	60:SS:70:ILE:HD12	1.90	0.53
1:L5:2805:A2M:H2'	1:L5:2806:G:C8	2.44	0.53
1:L5:3909:A:H2'	1:L5:3910:C:C6	2.44	0.53
1:L5:4213:OMU:HM22	1:L5:4214:OMG:O4'	2.09	0.53
1:L5:4524:G:H2'	1:L5:4525:U:C6	2.43	0.53
1:L5:4950:U:H4'	1:L5:4951:A:H5'	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LE:197:THR:HB	6:LE:288:PHE:OXT	2.08	0.53
7:LF:87:PRO:HG2	7:LF:144:TYR:CZ	2.43	0.53
8:LG:154:LEU:HD23	8:LG:204:PHE:HD2	1.74	0.53
16:LU:60:VAL:HG13	16:LU:76:VAL:CG2	2.36	0.53
42:S2:65:C:C5	49:SG:174:PRO:HB3	2.43	0.53
42:S2:1301:A:H3'	42:S2:1301:A:N3	2.24	0.53
42:S2:1850:MA6:H103	42:S2:1851:MA6:H102	1.90	0.53
73:Sg:207:CYS:HB2	73:Sg:221:LEU:HD11	1.90	0.53
1:L5:2085:G:O2'	4:LC:307:LYS:HE3	2.09	0.53
1:L5:4917:U:OP1	6:LE:262:LYS:HD3	2.09	0.53
42:S2:607:U:O4	46:SD:143:ARG:HA	2.09	0.53
45:SC:166:ARG:HB3	45:SC:247:THR:HB	1.89	0.53
46:SD:8:LYS:O	46:SD:12:VAL:HG23	2.09	0.53
54:SL:78:THR:HG21	54:SL:89:ARG:HB2	1.90	0.53
1:L5:1728:C:O2'	1:L5:1729:G:H5'	2.08	0.53
1:L5:4580:U:H2'	1:L5:4581:G:C8	2.44	0.53
41:LS:17:LEU:HD22	41:LS:59:GLY:HA2	1.90	0.53
42:S2:1124:C:P	44:SB:151:ARG:HD2	2.48	0.53
42:S2:1531:A:H2'	42:S2:1532:C:C6	2.44	0.53
60:SS:113:ARG:O	60:SS:117:ILE:HG12	2.08	0.53
1:L5:2708:U:H5"	1:L5:2709:C:H5'	1.91	0.53
1:L5:2756:A:C2'	1:L5:2757:U:H5'	2.38	0.53
1:L5:3639:A:C2	1:L5:3678:A:O4'	2.62	0.53
1:L5:4919:A:H2'	1:L5:4920:C:O4'	2.08	0.53
8:LG:154:LEU:HD23	8:LG:204:PHE:CD2	2.43	0.53
11:LN:10:LEU:HD12	11:LN:10:LEU:O	2.08	0.53
22:Lc:28:VAL:CG2	22:Lc:95:ALA:HB3	2.38	0.53
42:S2:1407:U:H2'	42:S2:1408:U:H6	1.70	0.53
42:S2:1589:A:H2'	42:S2:1590:C:H6	1.73	0.53
42:S2:1816:G:H2'	42:S2:1817:G:C5'	2.26	0.53
43:SA:1:MET:HA	43:SA:59:LEU:HB3	1.90	0.53
50:SH:69:LEU:HD13	50:SH:96:ALA:HB2	1.89	0.53
60:SS:40:TYR:O	60:SS:43:VAL:HG12	2.08	0.53
1:L5:168:C:H2'	1:L5:191:G:C8	2.44	0.53
1:L5:274:C:O2'	1:L5:275:C:H5'	2.09	0.53
1:L5:725:G:O2'	1:L5:726:G:H5'	2.09	0.53
1:L5:2564:G:H1	1:L5:2752:G:H1	1.57	0.53
1:L5:3686:C:OP1	42:S2:1052:A:H5"	2.08	0.53
19:LZ:74:VAL:HG23	19:LZ:101:PHE:CE2	2.44	0.53
22:Lc:34:THR:O	22:Lc:38:ILE:HG13	2.08	0.53
27:Lh:112:ARG:HG2	27:Lh:112:ARG:NH1	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:1490:OMG:H3'	42:S2:1490:OMG:OP2	2.09	0.53
43:SA:134:LEU:CD2	43:SA:144:THR:HG21	2.39	0.53
57:SP:77:LYS:HD2	57:SP:102:PHE:CG	2.44	0.53
66:SY:12:PHE:HZ	66:SY:21:LYS:HD3	1.72	0.53
1:L5:678:C:H2'	1:L5:679:C:H6	1.73	0.53
1:L5:924:G:H2'	1:L5:925:C:C6	2.44	0.53
1:L5:4996:A:O2'	1:L5:4997:G:H5'	2.08	0.53
22:Lc:80:GLU:HG2	55:SN:100:LYS:HZ1	1.73	0.53
42:S2:945:U:H2'	42:S2:946:U:H6	1.74	0.53
42:S2:1031:A2M:HM'3	55:SN:116:ILE:CD1	2.38	0.53
42:S2:1311:C:O2'	42:S2:1312:G:H5'	2.09	0.53
42:S2:1620:A:H1'	42:S2:1624:U:OP2	2.09	0.53
44:SB:104:ASP:OD1	44:SB:214:LYS:HG3	2.08	0.53
45:SC:63:VAL:HG22	45:SC:90:GLU:OE2	2.08	0.53
60:SS:22:GLY:HA2	60:SS:56:ALA:HB3	1.90	0.53
68:Sa:44:ILE:HG22	68:Sa:65:PRO:O	2.09	0.53
1:L5:2295:U:H4'	1:L5:2296:G:OP2	2.08	0.52
1:L5:2510:C:H2'	1:L5:2511:G:C8	2.44	0.52
1:L5:3700:G:H21	76:S6:72:C:C4'	2.20	0.52
1:L5:4065:C:O2'	1:L5:4066:C:H5'	2.09	0.52
38:LH:8:GLN:HG2	38:LH:74:CYS:SG	2.49	0.52
46:SD:127:MET:HE3	46:SD:134:CYS:SG	2.49	0.52
49:SG:3:LEU:CB	49:SG:5:ILE:HD11	2.37	0.52
63:SV:16:LYS:CG	63:SV:23:ILE:HD13	2.36	0.52
1:L5:247:G:O2'	1:L5:248:C:H5'	2.09	0.52
1:L5:2635:G:O2'	1:L5:2636:C:H5'	2.09	0.52
1:L5:2823:A:H2'	1:L5:2824:C:H5'	1.91	0.52
1:L5:4703:A:C2'	1:L5:4704:G:H5'	2.39	0.52
3:L8:148:A:H2'	3:L8:149:G:C8	2.44	0.52
4:LC:60:HIS:HA	4:LC:92:PHE:HE1	1.73	0.52
6:LE:239:LYS:HG2	6:LE:241:GLU:OE2	2.08	0.52
16:LU:27:HIS:HB2	16:LU:28:PRO:HD3	1.90	0.52
37:LB:258:HIS:HA	37:LB:259:PRO:C	2.33	0.52
42:S2:51:U:H2'	42:S2:52:G:C8	2.44	0.52
42:S2:150:A:N3	42:S2:150:A:H2'	2.25	0.52
42:S2:564:A:H2'	42:S2:565:G:H5'	1.92	0.52
42:S2:1232:PSU:H2'	42:S2:1233:G:C8	2.44	0.52
42:S2:1327:G:H2'	42:S2:1328:OMG:H5'	1.91	0.52
42:S2:1329:U:H5"	42:S2:1330:G:OP2	2.09	0.52
59:SR:21:TYR:CE1	59:SR:58:MET:HE1	2.44	0.52
60:SS:124:ARG:NH2	60:SS:129:LEU:HB3	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4387:G:H2'	1:L5:4388:C:H6	1.74	0.52
1:L5:4894:A:H2'	37:LB:156:TYR:CD1	2.44	0.52
42:S2:59:U:H2'	42:S2:61:A:OP2	2.09	0.52
42:S2:153:G:O2'	42:S2:154:U:H5'	2.09	0.52
42:S2:166:A2M:HM'2	42:S2:167:G:H5'	1.90	0.52
42:S2:958:G:H2'	42:S2:959:G:C8	2.45	0.52
42:S2:1376:A:H2'	42:S2:1377:U:O4'	2.09	0.52
43:SA:30:LEU:HD11	43:SA:35:GLU:HA	1.92	0.52
47:SE:173:ILE:HD11	47:SE:235:TRP:CE3	2.44	0.52
51:SI:13:LYS:HG3	54:SL:137:THR:HG21	1.91	0.52
55:SN:110:ASP:O	55:SN:114:ARG:HG2	2.09	0.52
58:SQ:97:GLN:HB2	58:SQ:105:LYS:HD3	1.90	0.52
1:L5:1826:G:C2'	1:L5:1827:G:H5'	2.40	0.52
1:L5:2254:C:O2'	1:L5:2255:G:H5'	2.08	0.52
1:L5:4445:U:H2'	1:L5:4446:U:H6	1.71	0.52
1:L5:4512:U:O2'	1:L5:4513:G:H5'	2.10	0.52
1:L5:4902:C:H2'	1:L5:4903:C:H6	1.74	0.52
30:Lk:33:LYS:HG2	30:Lk:46:VAL:HG22	1.91	0.52
34:Lp:38:THR:HA	34:Lp:45:THR:HA	1.91	0.52
38:LH:105:ILE:HG23	38:LH:109:GLY:HA2	1.90	0.52
42:S2:441:C:H2'	42:S2:442:C:C6	2.45	0.52
42:S2:1736:G:H2'	42:S2:1737:G:C8	2.44	0.52
42:S2:1831:A:O2'	42:S2:1832:6MZ:H5'1	2.08	0.52
47:SE:131:VAL:CG1	47:SE:135:GLY:HA2	2.39	0.52
49:SG:98:ARG:HH11	49:SG:98:ARG:HG3	1.75	0.52
50:SH:139:ILE:HG12	50:SH:156:VAL:CG1	2.39	0.52
1:L5:1803:C:C2'	1:L5:1804:C:H5'	2.39	0.52
1:L5:3681:PSU:H5'	42:S2:1181:A:H4'	1.92	0.52
25:Lf:106:TYR:HA	25:Lf:107:PRO:C	2.34	0.52
42:S2:1406:G:H2'	42:S2:1407:U:C6	2.45	0.52
42:S2:1458:G:P	73:Sg:281:ALA:HB2	2.50	0.52
42:S2:1471:C:O2'	42:S2:1472:C:H5'	2.10	0.52
48:SF:78:MET:HB2	48:SF:159:ARG:NH2	2.23	0.52
63:SV:30:ALA:O	63:SV:60:ARG:HD3	2.10	0.52
65:SX:47:ALA:O	65:SX:101:LEU:HD12	2.10	0.52
1:L5:478:G:O2'	1:L5:479:G:H5'	2.10	0.52
1:L5:1444:G:H2'	1:L5:1445:C:C6	2.44	0.52
1:L5:2283:U:H2'	1:L5:2284:G:C8	2.45	0.52
1:L5:4979:G:H2'	1:L5:4980:U:C6	2.44	0.52
5:LD:155:THR:HG23	5:LD:180:PHE:O	2.10	0.52
10:LM:123:ILE:O	10:LM:127:VAL:HG23	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LP:16:LYS:HG2	13:LP:149:ILE:HG12	1.90	0.52
22:Lc:19:GLN:OE1	55:SN:89:TYR:CE1	2.62	0.52
42:S2:59:U:H5"	42:S2:503:C:N4	2.23	0.52
42:S2:1301:A:H2'	42:S2:1303:C:O2	2.10	0.52
42:S2:1604:G:H2'	42:S2:1605:G:H5'	1.91	0.52
51:SI:103:LEU:HD23	51:SI:172:LEU:HD23	1.91	0.52
1:L5:972:G:H2'	1:L5:973:C:C6	2.44	0.52
1:L5:4311:A:H1'	5:LD:36:LEU:HD12	1.92	0.52
1:L5:4872:C:H2'	1:L5:4873:U:C6	2.45	0.52
5:LD:22:ARG:HB3	5:LD:28:THR:CG2	2.38	0.52
7:LF:52:GLU:HG3	21:Lb:96:LEU:HD11	1.90	0.52
38:LH:55:LEU:HD23	38:LH:77:VAL:HG11	1.91	0.52
39:LI:144:ASN:O	39:LI:148:VAL:HG23	2.10	0.52
42:S2:354:OMU:HM22	42:S2:355:G:C4'	2.40	0.52
42:S2:1867:U:C5	68:Sa:98:PRO:HG2	2.44	0.52
1:L5:445:U:H2'	1:L5:446:C:C6	2.45	0.52
1:L5:1446:C:O2'	1:L5:1447:G:H5'	2.10	0.52
1:L5:4953:A:H2'	1:L5:4954:C:H6	1.73	0.52
3:L8:154:G:H2'	3:L8:155:C:C6	2.45	0.52
30:Lk:23:VAL:HG22	30:Lk:36:VAL:CG2	2.34	0.52
42:S2:502:C:O4'	47:SE:66:MET:HG3	2.09	0.52
42:S2:938:A:C2'	42:S2:939:U:H5'	2.40	0.52
42:S2:1293:A:H2'	42:S2:1294:G:C8	2.45	0.52
43:SA:76:VAL:HG11	43:SA:90:PHE:CD1	2.44	0.52
43:SA:134:LEU:HD22	43:SA:144:THR:HG21	1.91	0.52
56:SO:50:LYS:O	56:SO:50:LYS:HG3	2.08	0.52
58:SQ:62:ARG:HD3	58:SQ:108:ILE:CD1	2.40	0.52
60:SS:63:GLU:O	60:SS:67:VAL:HG23	2.10	0.52
1:L5:43:U:H2'	1:L5:44:A:H5'	1.91	0.52
1:L5:1866:C:H2'	1:L5:1867:A2M:H8	1.91	0.52
1:L5:2666:A:P	1:L5:2666:A:H8	2.32	0.52
1:L5:3706:G:H1	1:L5:3719:A:H61	1.57	0.52
1:L5:3847:A:H2'	1:L5:3848:A:C8	2.45	0.52
1:L5:4548:C:H2'	1:L5:4549:U:C6	2.45	0.52
36:LA:20:VAL:HA	36:LA:23:ARG:HG3	1.91	0.52
38:LH:63:ASN:O	38:LH:67:LEU:HG	2.10	0.52
42:S2:167:G:C2'	42:S2:168:C:H5"	2.40	0.52
42:S2:616:A:H1'	72:Se:12:VAL:HG23	1.92	0.52
42:S2:1067:C:H2'	42:S2:1068:G:O4'	2.10	0.52
65:SX:107:ARG:HB3	65:SX:110:HIS:HB3	1.91	0.52
1:L5:1833:A:H4'	15:LT:130:ARG:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4892:G:O2'	1:L5:4893:G:H5'	2.10	0.52
9:LJ:20:LEU:O	9:LJ:20:LEU:HD23	2.09	0.52
42:S2:564:A:C2'	42:S2:565:G:H5'	2.40	0.52
42:S2:1356:G:H2'	42:S2:1357:A:C8	2.45	0.52
47:SE:31:PRO:HG2	47:SE:38:LEU:HG	1.92	0.52
66:SY:60:PHE:CD1	66:SY:71:GLY:HA3	2.44	0.52
1:L5:677:G:H2'	1:L5:678:C:H6	1.75	0.51
1:L5:2411:G:OP2	1:L5:2818:U:H1'	2.10	0.51
1:L5:3857:A:H2'	1:L5:3858:A:C8	2.45	0.51
1:L5:4510:G:N3	37:LB:252:ALA:HB1	2.25	0.51
1:L5:4979:G:H2'	1:L5:4980:U:H6	1.76	0.51
42:S2:957:A:O2'	42:S2:958:G:H5'	2.10	0.51
42:S2:1404:U:C4	62:SU:88:LEU:HD21	2.45	0.51
44:SB:124:HIS:HA	44:SB:137:LEU:O	2.10	0.51
50:SH:73:GLN:HB3	50:SH:135:PHE:CZ	2.46	0.51
73:Sg:232:GLY:O	73:Sg:257:LYS:HE2	2.10	0.51
1:L5:272:U:H2'	1:L5:273:U:C6	2.45	0.51
1:L5:347:A:H2'	1:L5:348:G:C8	2.45	0.51
1:L5:2509:U:H1'	1:L5:2510:C:C6	2.44	0.51
1:L5:3903:A:H2'	1:L5:3904:G:H8	1.75	0.51
1:L5:4174:U:H2'	1:L5:4175:U:H6	1.75	0.51
1:L5:4325:A:H2'	1:L5:4326:U:H6	1.74	0.51
1:L5:4355:A:H4'	33:Lo:67:VAL:CG2	2.40	0.51
1:L5:4593:A:O5'	1:L5:4593:A:H8	1.93	0.51
17:LX:101:ASP:OD1	17:LX:103:LYS:HB2	2.09	0.51
34:Lp:29:ILE:HG23	34:Lp:69:TRP:HB3	1.93	0.51
39:LI:139:ARG:HB3	39:LI:173:PHE:CE1	2.45	0.51
39:LI:184:MET:HE2	39:LI:190:LEU:CG	2.38	0.51
42:S2:1144:A:H2'	42:S2:1145:A:C8	2.45	0.51
58:SQ:9:SER:HB2	58:SQ:24:HIS:CE1	2.44	0.51
66:SY:20:ARG:HD2	66:SY:74:MET:CG	2.40	0.51
1:L5:116:G:H2'	1:L5:117:C:H6	1.75	0.51
1:L5:706:C:O2'	1:L5:1295:G:H5'	2.10	0.51
1:L5:1609:A:H5'	36:LA:183:GLY:CA	2.41	0.51
1:L5:4922:C:O2'	1:L5:4923:A:H2'	2.10	0.51
41:LS:159:LEU:HD22	41:LS:172:PRO:HB3	1.91	0.51
42:S2:121:OMU:HM22	42:S2:122:G:O4'	2.11	0.51
42:S2:927:C:O2'	42:S2:928:G:H5'	2.10	0.51
42:S2:1453:C:H3'	42:S2:1453:C:O2	2.10	0.51
45:SC:167:ARG:O	63:SV:1:MET:HE3	2.11	0.51
46:SD:32:ASP:OD1	46:SD:58:VAL:HG22	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:SF:60:ARG:HD3	48:SF:61:PHE:CE2	2.44	0.51
53:SK:15:LEU:HD13	53:SK:21:MET:HE2	1.92	0.51
11:LN:31:ARG:HD3	11:LN:124:ASP:OD2	2.09	0.51
18:LY:43:ASN:O	18:LY:126:ARG:HD3	2.09	0.51
38:LH:12:ILE:HD13	38:LH:18:ILE:HG13	1.92	0.51
42:S2:1213:C:H1'	42:S2:1343:U:O3'	2.10	0.51
42:S2:1285:G:OP1	42:S2:1285:G:H2'	2.11	0.51
42:S2:1500:G:H2'	42:S2:1501:C:C6	2.46	0.51
55:SN:16:LEU:HD12	55:SN:17:PRO:HD2	1.91	0.51
66:SY:88:LYS:HG3	66:SY:97:TYR:CZ	2.45	0.51
1:L5:1746:G:H5'	39:LI:40:LYS:HG3	1.93	0.51
1:L5:1797:A:O2'	1:L5:1798:A:H5'	2.11	0.51
1:L5:2249:G:OP1	1:L5:2249:G:H3'	2.10	0.51
1:L5:2630:G:H2'	1:L5:2631:A:H8	1.75	0.51
1:L5:2741:G:H5'	26:Lg:79:GLY:O	2.11	0.51
2:L7:110:G:H2'	2:L7:111:C:C6	2.46	0.51
4:LC:14:LYS:HE2	4:LC:14:LYS:CA	2.40	0.51
11:LN:44:ARG:HB3	83:LN:443:HOH:O	2.09	0.51
22:Lc:57:LYS:O	22:Lc:61:GLU:HG3	2.10	0.51
42:S2:1101:U:H2'	42:S2:1102:G:C8	2.44	0.51
42:S2:1177:PSU:H2'	42:S2:1178:U:C6	2.46	0.51
42:S2:1269:G:O2'	42:S2:1270:G:H5'	2.10	0.51
42:S2:1673:U:H2'	42:S2:1674:G:O4'	2.10	0.51
42:S2:1706:G:H5"	74:Ln:1:MET:HE2	1.91	0.51
43:SA:56:GLU:HG3	63:SV:83:PHE:HD1	1.74	0.51
1:L5:212:A:O2'	1:L5:213:G:H5'	2.10	0.51
1:L5:507:G:C2'	1:L5:508:G:H5'	2.40	0.51
1:L5:1594:C:H1'	1:L5:2788:A:C8	2.46	0.51
1:L5:3876:A:H2'	1:L5:3877:A:H5'	1.91	0.51
1:L5:3897:C:H2'	1:L5:3898:U:C6	2.45	0.51
1:L5:4466:A:O2'	1:L5:4467:U:H5'	2.11	0.51
1:L5:4470:A:O2'	1:L5:4471:C:H5'	2.11	0.51
3:L8:79:G:C2'	3:L8:80:A:H5'	2.41	0.51
6:LE:156:ARG:HG2	6:LE:156:ARG:HH11	1.75	0.51
39:LI:152:LEU:HD12	39:LI:165:ILE:HG23	1.93	0.51
42:S2:216:C:H2'	42:S2:217:A:H5'	1.91	0.51
42:S2:354:OMU:HM22	42:S2:355:G:C5'	2.40	0.51
42:S2:1016:U:H5'	55:SN:15:ALA:O	2.11	0.51
42:S2:1086:G:O2'	42:S2:1087:A:H5'	2.11	0.51
56:SO:129:ILE:HD12	68:Sa:64:LEU:CD1	2.41	0.51
63:SV:2:GLN:O	63:SV:2:GLN:HG2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SV:70:LEU:HD21	63:SV:83:PHE:CE2	2.44	0.51
77:LV:47:GLY:HA3	83:LV:308:HOH:O	2.10	0.51
1:L5:678:C:H2'	1:L5:679:C:C6	2.46	0.51
1:L5:2716:G:H2'	1:L5:2717:C:C6	2.45	0.51
3:L8:133:G:O2'	3:L8:134:G:H5'	2.11	0.51
5:LD:223:PHE:HB3	5:LD:226:TYR:HB2	1.92	0.51
44:SB:48:LEU:HD23	44:SB:48:LEU:H	1.75	0.51
50:SH:45:ILE:O	50:SH:45:ILE:HG13	2.10	0.51
1:L5:705:G:H2'	1:L5:706:C:C6	2.46	0.51
1:L5:1236:G:H8	1:L5:1236:G:OP2	1.94	0.51
1:L5:2413:A:O2'	1:L5:2414:OMG:H5'	2.10	0.51
1:L5:4685:U:H4'	1:L5:4686:A:OP1	2.10	0.51
6:LE:68:MET:HE3	6:LE:71:ARG:HB3	1.93	0.51
38:LH:143:GLU:C	38:LH:144:LEU:HD22	2.36	0.51
42:S2:333:G:O2'	42:S2:334:C:H5'	2.11	0.51
42:S2:461:U:O2	42:S2:468:A2M:H2	2.10	0.51
42:S2:1208:A:H4'	42:S2:1835:A:N7	2.25	0.51
64:SW:2:VAL:CG2	64:SW:4:MET:HE2	2.40	0.51
65:SX:54:LYS:HB3	65:SX:91:LEU:HD11	1.91	0.51
77:LV:62:MET:HE3	77:LV:76:VAL:HG12	1.93	0.51
1:L5:268:G:O2'	1:L5:269:G:H5'	2.11	0.51
1:L5:1921:G:O2'	1:L5:1922:C:H5'	2.11	0.51
1:L5:2619:C:O2'	1:L5:2620:U:H5'	2.11	0.51
1:L5:3906:PSU:H2'	1:L5:3907:U:C6	2.46	0.51
1:L5:4330:U:H2'	1:L5:4331:C:C6	2.46	0.51
3:L8:5:U:O2'	3:L8:6:C:H5'	2.11	0.51
42:S2:438:G:N3	42:S2:438:G:H5"	2.26	0.51
47:SE:160:ILE:CD1	47:SE:162:ILE:HD11	2.41	0.51
48:SF:48:TYR:CZ	58:SQ:56:LEU:HD13	2.46	0.51
49:SG:4:ASN:HB3	49:SG:110:ASN:OD1	2.11	0.51
50:SH:11:PRO:CG	50:SH:44:ASN:HD22	2.24	0.51
52:SJ:78:LEU:O	52:SJ:82:VAL:HG23	2.09	0.51
53:SK:49:MET:HG3	53:SK:69:TRP:CE3	2.46	0.51
63:SV:56:CYS:SG	63:SV:59:ILE:HG12	2.51	0.51
1:L5:699:C:H2'	1:L5:700:G:H8	1.72	0.51
1:L5:950:A:H8	1:L5:951:G:C8	2.29	0.51
1:L5:1776:A:O2'	39:LI:198:LYS:HE3	2.11	0.51
1:L5:1925:A:H5'	1:L5:1926:U:OP1	2.10	0.51
1:L5:2882:C:OP1	1:L5:5003:C:H1'	2.11	0.51
1:L5:3756:U:H2'	1:L5:3757:C:H6	1.75	0.51
1:L5:5038:U:H3'	1:L5:5039:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LE:68:MET:HA	6:LE:68:MET:CE	2.30	0.51
38:LH:128:MET:HE2	38:LH:128:MET:HA	1.93	0.51
38:LH:128:MET:SD	38:LH:134:CYS:HB2	2.51	0.51
40:LL:79:GLU:O	40:LL:83:VAL:HG23	2.11	0.51
42:S2:946:U:H4'	42:S2:1046:PSU:OP1	2.12	0.51
42:S2:1706:G:C5'	74:Ln:1:MET:HE2	2.40	0.51
42:S2:1706:G:H5'	74:Ln:1:MET:HB2	1.93	0.51
1:L5:306:A:O2'	1:L5:307:A:H5'	2.11	0.50
1:L5:1061:G:H2'	1:L5:1062:G:O4'	2.11	0.50
1:L5:1800:A:H4'	1:L5:1801:A:O5'	2.11	0.50
1:L5:2414:OMG:H8	1:L5:2414:OMG:O5'	1.94	0.50
1:L5:2518:G:H2'	1:L5:2519:A:O4'	2.11	0.50
2:L7:115:A:O2'	2:L7:116:G:H5'	2.10	0.50
7:LF:226:HIS:ND1	7:LF:228:VAL:HG22	2.26	0.50
7:LF:241:ASN:O	7:LF:245:ARG:HG2	2.11	0.50
42:S2:386:C:H2'	42:S2:387:C:C6	2.46	0.50
42:S2:1377:U:O2	42:S2:1379:A:H5'	2.11	0.50
42:S2:1454:A:C8	59:SR:3:ARG:HG3	2.47	0.50
65:SX:115:ILE:HG22	65:SX:118:VAL:HB	1.92	0.50
66:SY:88:LYS:HG3	66:SY:97:TYR:CE1	2.46	0.50
1:L5:1671:C:C4	1:L5:1673:PSU:H1'	2.46	0.50
1:L5:1878:U:C4	1:L5:2269:A:C2	2.99	0.50
1:L5:4058:C:H2'	1:L5:4059:A:O4'	2.11	0.50
42:S2:641:A:H2'	42:S2:642:U:O4'	2.11	0.50
42:S2:833:C:O2'	42:S2:834:C:H5'	2.10	0.50
42:S2:1060:A:H1'	42:S2:1062:A:N7	2.27	0.50
42:S2:1213:C:H5'	42:S2:1370:A:P	2.50	0.50
42:S2:1310:U:H2'	42:S2:1311:C:H6	1.76	0.50
42:S2:1707:U:H5'	74:Ln:9:ARG:NH2	2.27	0.50
1:L5:137:G:H2'	1:L5:138:G:O4'	2.11	0.50
6:LE:159:GLY:O	6:LE:274:VAL:HG23	2.12	0.50
37:LB:117:ARG:CZ	37:LB:177:LYS:HD3	2.41	0.50
42:S2:1446:A:H1'	62:SU:55:ARG:HD2	1.93	0.50
67:SZ:70:PRO:HD3	67:SZ:107:VAL:HG13	1.93	0.50
1:L5:18:C:H4'	11:LN:138:PHE:CE2	2.46	0.50
1:L5:755:C:H2'	1:L5:756:G:C8	2.46	0.50
1:L5:1683:U:O2'	1:L5:1684:G:H5'	2.12	0.50
1:L5:2547:G:H2'	1:L5:2548:C:H6	1.75	0.50
1:L5:2708:U:O5'	1:L5:2709:C:H5'	2.12	0.50
1:L5:2739:C:H4'	26:Lg:64:LEU:HB3	1.92	0.50
1:L5:4074:C:H2'	1:L5:4075:G:C8	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4570:A:H2'	1:L5:4571:U:O4'	2.12	0.50
10:LM:14:TYR:CE1	10:LM:22:GLY:HA2	2.47	0.50
27:Lh:89:ARG:O	27:Lh:93:ARG:HG2	2.11	0.50
32:Lm:104:HIS:CE1	32:Lm:107:ALA:HB2	2.47	0.50
42:S2:939:U:O2'	42:S2:940:U:H5'	2.11	0.50
42:S2:1170:A:H4'	42:S2:1171:G:OP1	2.12	0.50
42:S2:1239:U:H2'	42:S2:1241:A:OP2	2.10	0.50
42:S2:1533:A:C2	42:S2:1536:G:N3	2.78	0.50
50:SH:147:LYS:HA	64:SW:49:GLU:HG2	1.93	0.50
1:L5:448:G:HO2'	1:L5:450:G:H8	1.58	0.50
1:L5:4460:A:H2'	1:L5:4462:C:O5'	2.11	0.50
1:L5:4571:U:OP1	12:LO:73:PHE:HA	2.12	0.50
35:Lr:77:TYR:HB2	35:Lr:79[B]:ARG:HH12	1.77	0.50
36:LA:175:ILE:C	36:LA:175:ILE:HD12	2.36	0.50
42:S2:216:C:C2'	42:S2:217:A:H5'	2.41	0.50
42:S2:581:U:H4'	66:SY:66:GLY:HA2	1.93	0.50
42:S2:1227:G:C2	42:S2:1228:A:C8	2.99	0.50
42:S2:1705:C:H2'	42:S2:1706:G:C8	2.46	0.50
42:S2:1718:G:H5'	74:Ln:21:ARG:HA	1.93	0.50
52:SJ:134:HIS:HE1	52:SJ:164:PRO:HD2	1.76	0.50
59:SR:13:ALA:CB	59:SR:53:TYR:HD2	2.24	0.50
75:LR:101:ILE:HG23	75:LR:135:LYS:HD2	1.94	0.50
1:L5:446:C:H1'	1:L5:2304:G:H4'	1.93	0.50
1:L5:457:G:C5'	6:LE:115:TYR:HB3	2.42	0.50
1:L5:677:G:H2'	1:L5:678:C:C6	2.46	0.50
1:L5:2738:C:H4'	26:Lg:65:MET:HE2	1.93	0.50
4:LC:190:ARG:O	4:LC:195:LYS:HD3	2.12	0.50
5:LD:93:THR:O	5:LD:93:THR:CG2	2.59	0.50
7:LF:87:PRO:HG2	7:LF:144:TYR:CE2	2.46	0.50
42:S2:963:A:H2'	42:S2:964:A:C8	2.46	0.50
42:S2:1144:A:H5'	42:S2:1355:C:N4	2.22	0.50
42:S2:1616:U:H2'	42:S2:1617:G:O4'	2.11	0.50
42:S2:1850:MA6:H103	42:S2:1851:MA6:C10	2.42	0.50
44:SB:110:MET:SD	44:SB:213:ARG:HG3	2.51	0.50
45:SC:163:VAL:HG12	63:SV:27:LYS:HE3	1.93	0.50
1:L5:717:U:H2'	1:L5:718:C:C6	2.46	0.50
1:L5:2777:A2M:C3'	1:L5:2777:A2M:H8	2.39	0.50
1:L5:3847:A:H2'	1:L5:3848:A:H8	1.77	0.50
14:LQ:64:SER:HB3	14:LQ:92:VAL:HG23	1.94	0.50
42:S2:162:C:H2'	42:S2:163:U:O4'	2.12	0.50
42:S2:1190:A:H2'	42:S2:1191:C:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:1737:G:H2'	42:S2:1738:C:H6	1.77	0.50
55:SN:70:LYS:O	55:SN:74:ILE:HG13	2.12	0.50
1:L5:1059:G:H2'	1:L5:1060:G:C8	2.47	0.50
1:L5:1600:G:H2'	1:L5:1601:G:C8	2.47	0.50
1:L5:1900:G:O2'	1:L5:1901:U:H5'	2.12	0.50
1:L5:2510:C:H2'	1:L5:2511:G:H8	1.77	0.50
1:L5:2793:U:H2'	1:L5:2794:OMC:H6	1.77	0.50
12:LO:108:ILE:HD12	12:LO:160:ARG:CZ	2.41	0.50
39:LI:145:GLU:O	39:LI:149:ILE:HD12	2.12	0.50
42:S2:77:A:O2'	42:S2:78:C:H5'	2.10	0.50
42:S2:1380:C:H2'	42:S2:1381:G:O4'	2.12	0.50
44:SB:113:MET:HE1	44:SB:211:PHE:CD2	2.47	0.50
46:SD:95:GLY:HA3	46:SD:129:SER:OG	2.11	0.50
46:SD:172:VAL:CG2	46:SD:185:LYS:HD3	2.41	0.50
49:SG:181:THR:HG22	49:SG:183:ARG:N	2.23	0.50
58:SQ:58:LEU:HD11	58:SQ:108:ILE:HG23	1.93	0.50
59:SR:13:ALA:HB3	59:SR:53:TYR:HD2	1.76	0.50
66:SY:79:LEU:HG	66:SY:83:LYS:HE2	1.94	0.50
73:Sg:42:MET:HE2	73:Sg:92:LEU:HD22	1.94	0.50
1:L5:3707:U:O2'	1:L5:3708:G:H5'	2.11	0.50
1:L5:3756:U:H2'	1:L5:3757:C:C6	2.46	0.50
1:L5:4328:C:O3'	33:Lo:37:GLY:HA3	2.12	0.50
7:LF:143:GLY:HA3	7:LF:240:ILE:HB	1.94	0.50
39:LI:99:ILE:HG22	39:LI:123:GLN:HB2	1.94	0.50
42:S2:1568:C:P	61:ST:98:SER:HB2	2.51	0.50
42:S2:1623:A:O5'	60:SS:133:GLY:HA3	2.12	0.50
1:L5:1461:G:H5'	21:Lb:44:ARG:NH1	2.27	0.49
1:L5:2448:C:H4'	1:L5:3658:G:O4'	2.12	0.49
1:L5:2503:A:OP1	26:Lg:11:LEU:HD13	2.12	0.49
1:L5:2735:A:H2'	1:L5:2736:A:C8	2.47	0.49
8:LG:39:PHE:CD1	8:LG:47:PRO:HD3	2.47	0.49
20:La:103:VAL:HG23	20:La:108:TYR:O	2.11	0.49
23:Ld:46:LEU:CD2	23:Ld:72:VAL:HG11	2.41	0.49
31:Ll:23:ILE:HG13	83:Ll:106:HOH:O	2.12	0.49
42:S2:948:C:H2'	42:S2:949:G:H8	1.76	0.49
1:L5:1478:G:H5'	1:L5:1479:C:H5	1.76	0.49
1:L5:1494:G:OP1	14:LQ:150:ARG:HD3	2.12	0.49
1:L5:3694:C:O2'	1:L5:3695:U:H5'	2.11	0.49
1:L5:4865:C:H2'	1:L5:4866:U:C4'	2.42	0.49
2:L7:33:U:O2	5:LD:207:TYR:HB2	2.12	0.49
4:LC:13:GLU:HG3	4:LC:14:LYS:HE3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Le:90:MET:HE2	83:Lr:217:HOH:O	2.12	0.49
42:S2:297:A:H4'	47:SE:131:VAL:HG12	1.94	0.49
42:S2:481:C:H2'	42:S2:482:G:O4'	2.12	0.49
42:S2:1061:U:O4	42:S2:1850:MA6:H91	2.12	0.49
49:SG:28:TYR:CE1	49:SG:104:ALA:HA	2.47	0.49
54:SL:61:PRO:HA	54:SL:66:VAL:CG2	2.42	0.49
70:Sc:40:ARG:HH12	70:Sc:42:ILE:HG23	1.77	0.49
1:L5:488:G:C2	1:L5:489:C:H1'	2.48	0.49
1:L5:1571:A:O2'	1:L5:1572:G:H5'	2.12	0.49
1:L5:1663:G:H5'	1:L5:1684:G:OP1	2.12	0.49
1:L5:2353:A2M:H2'	1:L5:2354:OMG:O4'	2.12	0.49
1:L5:2518:G:H3'	1:L5:2518:G:N3	2.27	0.49
1:L5:2705:G:H2'	1:L5:2706:C:C6	2.48	0.49
1:L5:2884:A:H2'	1:L5:2885:A:C8	2.47	0.49
3:L8:18:U:H2'	3:L8:19:C:C6	2.47	0.49
5:LD:90:VAL:HG22	5:LD:226:TYR:CZ	2.48	0.49
33:Lo:14:LYS:HB2	33:Lo:14:LYS:NZ	2.25	0.49
41:LS:45:TRP:CD1	41:LS:56:LYS:HD3	2.48	0.49
42:S2:65:C:C6	49:SG:174:PRO:HB3	2.48	0.49
42:S2:1422:G:H3'	42:S2:1424:G:OP2	2.12	0.49
42:S2:1425:G:H2'	42:S2:1426:U:C6	2.47	0.49
49:SG:75:LEU:HD12	49:SG:97:VAL:HG21	1.92	0.49
58:SQ:31:LEU:HB3	58:SQ:67:ASP:OD1	2.12	0.49
67:SZ:46:ASN:HB3	67:SZ:80:ARG:HG2	1.94	0.49
69:Sb:54:VAL:HB	69:Sb:64:CYS:SG	2.52	0.49
1:L5:124:C:OP1	11:LN:144:ARG:HD2	2.13	0.49
1:L5:1202:G:C2'	1:L5:1203:U:H5'	2.42	0.49
1:L5:1486:G:H2'	1:L5:1487:A:H8	1.77	0.49
1:L5:1938:A:H2'	1:L5:1939:A:H8	1.77	0.49
1:L5:2849:G:H2'	1:L5:2850:C:H6	1.77	0.49
1:L5:4444:C:H2'	1:L5:4445:U:C6	2.48	0.49
1:L5:4557:A2M:HM'2	1:L5:4558:U:O4'	2.11	0.49
1:L5:4703:A:O2'	1:L5:4704:G:H5'	2.13	0.49
1:L5:4973:U:C2'	1:L5:5046:A:H62	2.25	0.49
28:Li:26:HIS:O	28:Li:29:ARG:HG2	2.12	0.49
28:Li:63:VAL:O	28:Li:63:VAL:HG12	2.13	0.49
42:S2:145:G:H2'	42:S2:146:G:H8	1.73	0.49
42:S2:310:C:O2'	42:S2:311:C:H5'	2.11	0.49
42:S2:1850:MA6:H92	42:S2:1851:MA6:H93	1.94	0.49
50:SH:11:PRO:HD2	50:SH:44:ASN:HD22	1.77	0.49
54:SL:109:MET:HG2	54:SL:111:VAL:CG1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:347:A:O2'	1:L5:348:G:H5'	2.12	0.49
1:L5:2665:G:H1'	1:L5:2666:A:OP2	2.13	0.49
1:L5:3600:G:O2'	1:L5:3601:G:OP1	2.27	0.49
1:L5:4557:A2M:H8	1:L5:4557:A2M:O5'	2.12	0.49
1:L5:4986:PSU:H2'	1:L5:4987:U:O4'	2.13	0.49
14:LQ:34:PHE:CE1	14:LQ:38:ARG:HG3	2.47	0.49
16:LU:48:LYS:HG2	16:LU:52:LYS:C	2.37	0.49
16:LU:59:GLY:O	16:LU:60:VAL:HB	2.12	0.49
35:Lr:14:SER:HB3	35:Lr:17:LEU:HG	1.93	0.49
41:LS:69:GLU:HG2	41:LS:101:THR:HG22	1.95	0.49
42:S2:483:C:H2'	42:S2:484:A2M:O4'	2.13	0.49
42:S2:501:C:O2	42:S2:501:C:C2'	2.59	0.49
47:SE:103:TYR:CD2	47:SE:189:LEU:HD11	2.48	0.49
48:SF:40:ALA:HB1	48:SF:45:TYR:CG	2.46	0.49
63:SV:43:THR:OG1	63:SV:45:ARG:HB2	2.12	0.49
1:L5:123:C:H2'	1:L5:124:C:C6	2.48	0.49
1:L5:433:A:H2'	1:L5:434:A:O4'	2.11	0.49
1:L5:4512:U:C2'	1:L5:4513:G:H5'	2.42	0.49
7:LF:52:GLU:HG3	21:Lb:96:LEU:HD12	1.93	0.49
14:LQ:22:ASP:O	14:LQ:26:ARG:HG3	2.12	0.49
19:LZ:87:VAL:HG13	19:LZ:89:ILE:HG13	1.95	0.49
42:S2:6:G:H21	42:S2:621:OMC:CM2	2.26	0.49
42:S2:803:C:H2'	42:S2:804:U:C6	2.48	0.49
42:S2:848:U:H2'	42:S2:849:A:H8	1.76	0.49
42:S2:1861:G:H5"	68:Sa:3:LYS:HA	1.95	0.49
47:SE:55:ALA:HB1	47:SE:60:GLU:HB2	1.95	0.49
60:SS:98:VAL:CG2	60:SS:103:LEU:HD13	2.41	0.49
1:L5:82:U:O2'	1:L5:83:C:H5'	2.12	0.49
1:L5:282:C:H2'	1:L5:283:G:O4'	2.13	0.49
1:L5:3708:G:H2'	1:L5:3709:A:H8	1.77	0.49
1:L5:4106:U:O2	1:L5:4106:U:H2'	2.12	0.49
1:L5:4639:C:H2'	1:L5:4640:C:C6	2.48	0.49
17:LX:127:LEU:C	17:LX:127:LEU:HD12	2.37	0.49
24:Le:21:ILE:HD11	24:Le:53:ILE:CD1	2.43	0.49
34:Lp:23:ARG:O	34:Lp:26:VAL:HG12	2.13	0.49
37:LB:46:PHE:CZ	37:LB:84:MET:HG3	2.48	0.49
48:SF:38:TYR:CD2	48:SF:143:PRO:HB2	2.48	0.49
50:SH:147:LYS:HA	64:SW:49:GLU:CG	2.43	0.49
1:L5:123:C:H2'	1:L5:124:C:H6	1.78	0.49
1:L5:152:U:H4'	11:LN:56:LYS:HD3	1.94	0.49
1:L5:423:G:O2'	1:L5:424:U:H5'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1418:G:O2'	1:L5:1419:U:H5'	2.12	0.49
1:L5:1587:U:OP1	37:LB:243:LYS:HG2	2.13	0.49
1:L5:2323:G:N7	4:LC:189:MET:CE	2.75	0.49
28:Li:36:HIS:O	28:Li:40:VAL:HG23	2.13	0.49
41:LS:2:LYS:HE2	41:LS:4:SER:OG	2.13	0.49
42:S2:1809:A:H2'	42:S2:1810:U:C6	2.47	0.49
1:L5:1079:C:H2'	1:L5:1080:C:H6	1.78	0.49
1:L5:2854:A:H2'	1:L5:2855:U:C6	2.48	0.49
1:L5:3693:U:H2'	1:L5:3694:C:C6	2.47	0.49
3:L8:10:G:H2'	3:L8:11:C:O4'	2.13	0.49
5:LD:83:LEU:N	5:LD:84:PRO:CD	2.76	0.49
13:LP:47:TYR:O	13:LP:51:VAL:HG23	2.12	0.49
18:LY:67:ILE:HD13	18:LY:107:THR:HG21	1.94	0.49
24:Le:35:TRP:CZ2	24:Le:56:PRO:HD2	2.48	0.49
34:Lp:64:VAL:HG22	36:LA:83:HIS:HB3	1.94	0.49
34:Lp:81:SER:HB3	42:S2:938:A:C4'	2.39	0.49
42:S2:309:G:O2'	42:S2:310:C:H5'	2.12	0.49
51:SI:49:ARG:HG3	51:SI:49:ARG:NH1	2.23	0.49
56:SO:97:LEU:HD23	68:Sa:44:ILE:HD11	1.93	0.49
59:SR:100:PRO:HD3	59:SR:120:THR:O	2.12	0.49
77:LV:41:SER:OG	77:LV:62:MET:HB2	2.13	0.49
1:L5:193:G:O2'	1:L5:194:C:H5'	2.13	0.49
1:L5:702:U:H2'	1:L5:703:G:O4'	2.12	0.49
1:L5:1879:G:O6	1:L5:1892:A:H2	1.96	0.49
1:L5:2885:A:H2'	1:L5:2886:G:C8	2.47	0.49
1:L5:3592:U:H2'	1:L5:3593:U:H6	1.77	0.49
1:L5:4953:A:H2'	1:L5:4954:C:C6	2.47	0.49
37:LB:379:PHE:CD2	37:LB:385:LYS:HG3	2.48	0.49
46:SD:164:VAL:HG23	46:SD:168:VAL:HG21	1.94	0.49
47:SE:139:LEU:HD21	47:SE:169:ILE:HD11	1.94	0.49
50:SH:135:PHE:HB3	50:SH:136:PRO:HD3	1.95	0.49
60:SS:124:ARG:HH21	60:SS:129:LEU:HB3	1.78	0.49
66:SY:27:VAL:HB	66:SY:69:THR:CG2	2.42	0.49
1:L5:368:C:O4'	4:LC:83:GLY:HA3	2.12	0.48
1:L5:1948:G:O2'	1:L5:1949:U:H5'	2.13	0.48
1:L5:2069:C:H5'	7:LF:213:LEU:O	2.12	0.48
1:L5:4488:C:H2'	1:L5:4489:A:H5'	1.95	0.48
16:LU:21:PHE:HD1	16:LU:108:GLU:HA	1.79	0.48
16:LU:84:LYS:HB2	16:LU:110:TYR:CZ	2.48	0.48
28:Li:81:ILE:HG13	28:Li:82:ARG:N	2.28	0.48
42:S2:824:C:H1'	52:SJ:144:ILE:HG21	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:863:PSU:O4	64:SW:124:LYS:HE3	2.12	0.48
42:S2:1248:U:O3'	42:S2:1249:C:P	2.71	0.48
42:S2:1587:G:C5	61:ST:78:ILE:HD11	2.48	0.48
42:S2:1859:A:O2'	42:S2:1860:A:H5'	2.13	0.48
43:SA:1:MET:N	63:SV:78:ILE:HG22	2.28	0.48
63:SV:1:MET:HB3	63:SV:9:VAL:CG2	2.43	0.48
67:SZ:90:GLU:OE2	67:SZ:94:LYS:HD3	2.13	0.48
74:Ln:6:ARG:O	74:Ln:6:ARG:HD2	2.13	0.48
1:L5:444:G:H2'	1:L5:445:U:O2	2.13	0.48
1:L5:734:G:C2	1:L5:735:G:C8	3.01	0.48
1:L5:1350:A:H4'	1:L5:1351:G:O5'	2.13	0.48
1:L5:1486:G:H2'	1:L5:1487:A:C8	2.48	0.48
1:L5:1547:C:O2'	1:L5:1548:G:H5'	2.13	0.48
1:L5:1853:C:H2'	1:L5:1854:A:H8	1.78	0.48
1:L5:2617:C:C2	1:L5:2618:U:C5	3.01	0.48
1:L5:3669:C:H4'	1:L5:3670:G:OP2	2.14	0.48
1:L5:3898:U:O2'	1:L5:3899:G:H5'	2.13	0.48
3:L8:141:C:H2'	3:L8:142:U:H6	1.78	0.48
8:LG:190:LEU:O	8:LG:193:LEU:HB2	2.13	0.48
12:LO:175:MET:HE1	12:LO:179:LYS:HD3	1.94	0.48
22:Lc:28:VAL:HG22	22:Lc:95:ALA:HB3	1.95	0.48
43:SA:187:GLY:HA3	63:SV:45:ARG:HE	1.78	0.48
48:SF:198:ARG:HG3	48:SF:199:VAL:N	2.27	0.48
64:SW:30:CYS:HB2	64:SW:61:ILE:HG13	1.93	0.48
1:L5:458:C:H2'	1:L5:459:C:H6	1.78	0.48
1:L5:2401:C:H2'	1:L5:2402:A:C8	2.48	0.48
1:L5:4742:C:H5"	1:L5:4743:C:OP1	2.14	0.48
4:LC:348:LYS:O	4:LC:351:VAL:HG22	2.13	0.48
5:LD:58:ARG:HH11	5:LD:58:ARG:HG3	1.77	0.48
5:LD:90:VAL:HG21	5:LD:226:TYR:CG	2.48	0.48
24:Le:89:LEU:HD12	83:Le:207:HOH:O	2.12	0.48
37:LB:121:ASN:OD1	37:LB:124:LYS:HG3	2.13	0.48
42:S2:106:C:OP1	42:S2:432:G:H5'	2.13	0.48
42:S2:147:A:C2'	42:S2:148:U:H5'	2.43	0.48
42:S2:616:A:N3	72:Se:12:VAL:HG21	2.28	0.48
46:SD:9:ARG:HH11	46:SD:9:ARG:HG3	1.78	0.48
46:SD:68:GLU:O	46:SD:72:VAL:HG22	2.13	0.48
46:SD:69:LEU:HA	46:SD:72:VAL:HG22	1.93	0.48
73:Sg:188:HIS:HB3	73:Sg:219:TRP:CH2	2.49	0.48
1:L5:458:C:H2'	1:L5:459:C:C6	2.49	0.48
1:L5:2531:G:C2'	1:L5:2532:G:H5'	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LD:264:LYS:HG2	5:LD:266:TRP:NE1	2.29	0.48
10:LM:126:GLU:CG	12:LO:181:ALA:HB1	2.40	0.48
42:S2:64:A:H2'	42:S2:64:A:N3	2.28	0.48
42:S2:1288:OMU:CM2	42:S2:1289:U:H5'	2.43	0.48
48:SF:38:TYR:CD1	48:SF:144:LEU:HD13	2.49	0.48
54:SL:8:ARG:HH11	54:SL:8:ARG:CG	2.23	0.48
55:SN:57:SER:HB3	69:Sb:54:VAL:HG22	1.94	0.48
58:SQ:130:LYS:HG2	58:SQ:131:LYS:N	2.28	0.48
73:Sg:127:LYS:HG2	73:Sg:149:GLU:C	2.38	0.48
1:L5:1338:A:O2'	1:L5:1339:A:H5'	2.13	0.48
1:L5:4450:A:H2'	1:L5:4450:A:N3	2.28	0.48
5:LD:179:ARG:HA	5:LD:179:ARG:HD3	1.60	0.48
42:S2:511:U:H2'	42:S2:512:A2M:O4'	2.13	0.48
42:S2:1017:U:H5'	55:SN:55:ARG:HD3	1.95	0.48
42:S2:1390:U:H2'	42:S2:1391:OMC:C6	2.48	0.48
42:S2:1464:C:O2'	42:S2:1465:A:H5'	2.13	0.48
43:SA:106:GLY:HA2	43:SA:109:THR:OG1	2.12	0.48
44:SB:136:ARG:HG2	44:SB:138:PHE:CE2	2.48	0.48
60:SS:43:VAL:O	60:SS:47:LYS:HG2	2.13	0.48
1:L5:900:C:H2'	1:L5:901:C:H6	1.78	0.48
1:L5:2030:G:H2'	1:L5:2031:C:C6	2.48	0.48
1:L5:2455:C:H2'	1:L5:2456:G:O4'	2.12	0.48
1:L5:3686:C:OP1	42:S2:1052:A:C5'	2.62	0.48
1:L5:4225:A:H2'	1:L5:4226:G:C8	2.49	0.48
1:L5:4421:U:O2'	1:L5:4422:U:H5'	2.12	0.48
1:L5:4443:PSU:H1'	37:LB:252:ALA:HB3	1.96	0.48
1:L5:4656:C:O3'	1:L5:4657:C:H3'	2.14	0.48
1:L5:4962:A:O2'	1:L5:4963:G:H5'	2.13	0.48
11:LN:28:TRP:O	11:LN:32:GLN:HG2	2.13	0.48
18:LY:76:LYS:HE3	31:Ll:31:THR:HB	1.96	0.48
37:LB:302:ASN:HB2	37:LB:314:ILE:H	1.78	0.48
39:LI:190:LEU:HD13	39:LI:197:VAL:HG21	1.94	0.48
40:LL:57:PRO:HG3	40:LL:75:GLY:C	2.38	0.48
42:S2:1140:G:O2'	42:S2:1141:G:H5'	2.13	0.48
42:S2:1355:C:C2'	42:S2:1356:G:H5'	2.43	0.48
42:S2:1693:G:O2'	42:S2:1694:U:H5'	2.14	0.48
42:S2:1720:U:H3'	42:S2:1721:U:C5'	2.44	0.48
47:SE:149:TYR:HB3	49:SG:209:TYR:CD1	2.49	0.48
72:Se:26:LYS:HG2	72:Se:27:LYS:N	2.27	0.48
73:Sg:229:THR:C	73:Sg:230:LEU:HD23	2.38	0.48
1:L5:360:A:H4'	1:L5:361:C:OP2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1459:C:O2'	1:L5:1460:C:H5'	2.13	0.48
1:L5:1900:G:H2'	1:L5:1901:U:H5'	1.94	0.48
1:L5:2661:C:H2'	1:L5:2662:C:C6	2.48	0.48
1:L5:2664:A:H4'	1:L5:2665:G:OP2	2.13	0.48
1:L5:2855:U:O2'	1:L5:2856:C:H5'	2.13	0.48
1:L5:4060:C:C2'	1:L5:4061:U:H5'	2.44	0.48
1:L5:4479:U:H5	1:L5:4498:U:HO2'	1.60	0.48
10:LM:94:LYS:O	10:LM:98:ARG:HG3	2.14	0.48
23:Ld:68:LEU:HD11	23:Ld:84:ILE:CD1	2.43	0.48
37:LB:224:LYS:HG2	37:LB:340:THR:HG22	1.96	0.48
42:S2:77:A:H1'	49:SG:176:ILE:HD12	1.95	0.48
42:S2:172:OMU:H6	42:S2:314:U:O2'	2.13	0.48
42:S2:1272:C:H2'	42:S2:1273:C:C6	2.49	0.48
48:SF:77:MET:HG2	48:SF:89:THR:CG2	2.42	0.48
65:SX:48:LYS:HD3	65:SX:99:GLU:OE2	2.13	0.48
1:L5:1909:C:O2'	1:L5:1910:C:H5'	2.13	0.48
1:L5:1937:A:C2	1:L5:4420:C:H5'	2.49	0.48
1:L5:2386:A:C8	1:L5:2804:C:H2'	2.49	0.48
1:L5:2691:U:H2'	1:L5:2692:C:H6	1.79	0.48
1:L5:3628:A:C4	29:Lj:3:LYS:HB3	2.49	0.48
6:LE:166:LYS:HD3	6:LE:208:ILE:HG21	1.95	0.48
12:LO:203:VAL:OXT	12:LO:203:VAL:CG1	2.61	0.48
14:LQ:64:SER:HB3	14:LQ:92:VAL:CG2	2.44	0.48
42:S2:15:U:H2'	42:S2:16:G:O4'	2.14	0.48
42:S2:1325:G:H1'	42:S2:1510:G:H5"	1.95	0.48
42:S2:1404:U:C5	62:SU:88:LEU:HD21	2.48	0.48
42:S2:1438:A:H2'	42:S2:1439:A:C8	2.48	0.48
42:S2:1631:U:C2'	42:S2:1632:G:H5'	2.44	0.48
43:SA:31:ASP:HB3	43:SA:34:MET:HB2	1.95	0.48
1:L5:336:A:H5"	1:L5:337:U:OP2	2.14	0.48
1:L5:1351:G:H2'	1:L5:1352:U:C6	2.48	0.48
1:L5:1691:U:H2'	1:L5:1692:C:C6	2.49	0.48
1:L5:4891:C:H2'	1:L5:4892:G:C8	2.48	0.48
2:L7:50:A:H8	2:L7:50:A:O5'	1.97	0.48
3:L8:110:U:N3	3:L8:112:G:H1'	2.29	0.48
8:LG:95:LEU:HD11	8:LG:204:PHE:HE2	1.79	0.48
42:S2:1027:A:H5'	42:S2:1028:A:OP2	2.14	0.48
44:SB:79:VAL:HB	44:SB:81:PHE:CE2	2.48	0.48
47:SE:44:LEU:HD11	47:SE:70:ILE:HG21	1.95	0.48
52:SJ:81:LEU:HD22	52:SJ:86:VAL:HG21	1.95	0.48
53:SK:32:HIS:CG	53:SK:33:PRO:HD2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SV:1:MET:HB3	63:SV:9:VAL:HG23	1.95	0.48
73:Sg:208:ALA:HB2	73:Sg:218:LEU:HD13	1.96	0.48
73:Sg:219:TRP:HB3	73:Sg:225:LYS:O	2.13	0.48
1:L5:671:G:H2'	1:L5:672:C:H5'	1.94	0.48
1:L5:1723:U:H2'	1:L5:1724:U:C6	2.49	0.48
1:L5:2622:PSU:OP2	1:L5:2622:PSU:H6	1.97	0.48
1:L5:4204:U:H5"	1:L5:4205:A:OP1	2.14	0.48
1:L5:4613:U:H4'	37:LB:373:LYS:HD2	1.95	0.48
4:LC:186:SER:O	4:LC:188:ARG:HD3	2.14	0.48
18:LY:38:LEU:HD22	18:LY:42:TYR:CE2	2.43	0.48
22:Lc:87:LYS:HD2	22:Lc:89:TYR:OH	2.14	0.48
43:SA:1:MET:H3	63:SV:78:ILE:HG22	1.78	0.48
49:SG:157:VAL:CG2	49:SG:176:ILE:HD11	2.35	0.48
62:SU:32:LEU:CD2	62:SU:85:HIS:HB2	2.44	0.48
1:L5:12:A:H4'	17:LX:53:ARG:HG2	1.95	0.47
1:L5:106:A:O2'	1:L5:107:G:H5'	2.14	0.47
1:L5:481:G:O2'	1:L5:482:G:H5'	2.14	0.47
1:L5:752:G:H2'	1:L5:753:C:H5'	1.96	0.47
1:L5:2041:G:O2'	1:L5:2042:G:H5"	2.13	0.47
1:L5:2808:C:OP1	1:L5:4641:A:H4'	2.14	0.47
1:L5:3916:U:H2'	1:L5:3917:C:H6	1.79	0.47
1:L5:4548:C:H2'	1:L5:4549:U:H6	1.79	0.47
1:L5:4868:C:OP2	6:LE:274:VAL:HG12	2.13	0.47
17:LX:114:LYS:HE2	17:LX:114:LYS:HB3	1.56	0.47
42:S2:56:G:OP2	66:SY:115:LYS:HE2	2.13	0.47
42:S2:1313:A:H2'	42:S2:1313:A:OP2	2.14	0.47
48:SF:121:PRO:O	48:SF:146:ARG:HG2	2.13	0.47
64:SW:14:ILE:CD1	64:SW:27:ILE:HD11	2.43	0.47
1:L5:438:G:C2'	1:L5:439:G:H5'	2.45	0.47
1:L5:485:C:C2'	1:L5:486:C:OP1	2.62	0.47
1:L5:1560:A:H2'	1:L5:1561:A:O4'	2.15	0.47
1:L5:1586:C:H4'	1:L5:1587:U:OP2	2.14	0.47
1:L5:1813:U:H2'	1:L5:1814:G:O4'	2.14	0.47
1:L5:2283:U:H2'	1:L5:2284:G:H8	1.77	0.47
1:L5:2854:A:H2'	1:L5:2855:U:H6	1.79	0.47
15:LT:150:LEU:HB2	41:LS:29:ARG:NH2	2.28	0.47
17:LX:117:TYR:O	17:LX:119:ILE:HG23	2.13	0.47
18:LY:116:LYS:O	18:LY:120:GLU:HG3	2.13	0.47
39:LI:76:MET:CE	39:LI:148:VAL:HG22	2.41	0.47
42:S2:852:G:N3	42:S2:852:G:H2'	2.28	0.47
42:S2:1247:C:O3'	42:S2:1248:U:P	2.72	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SI:29:LEU:C	51:SI:29:LEU:HD12	2.39	0.47
69:Sb:33:MET:CE	69:Sb:73:LEU:HD21	2.34	0.47
1:L5:1555:G:O2'	1:L5:1556:A:H5'	2.15	0.47
1:L5:4461:G:OP2	1:L5:4462:C:H5"	2.15	0.47
3:L8:70:G:H5"	18:LY:27:ARG:CZ	2.44	0.47
10:LM:41:PRO:HG3	10:LM:73:VAL:HG12	1.96	0.47
19:LZ:16:GLY:HA3	83:LZ:201:HOH:O	2.13	0.47
35:Lr:47:LYS:HD3	35:Lr:102:TYR:CE2	2.50	0.47
42:S2:1061:U:C4	42:S2:1850:MA6:H91	2.49	0.47
44:SB:41:ILE:HD12	44:SB:41:ILE:H	1.79	0.47
1:L5:929:A:N6	10:LM:70:GLN:HE22	2.13	0.47
1:L5:1427:C:H2'	1:L5:1428:G:C5'	2.45	0.47
1:L5:2448:C:H5"	11:LN:67:ARG:HD2	1.96	0.47
1:L5:2747:A:O2'	1:L5:2748:G:H5'	2.14	0.47
3:L8:120:G:O2'	3:L8:121:G:H5'	2.13	0.47
7:LF:112:LEU:O	7:LF:113:ARG:HB2	2.14	0.47
11:LN:178:HIS:HA	11:LN:181:HIS:NE2	2.29	0.47
21:Lb:32:LEU:HD13	21:Lb:40:LEU:HD11	1.96	0.47
37:LB:16:PHE:HB2	37:LB:19:ARG:HH21	1.79	0.47
38:LH:41:ILE:HG22	38:LH:43:VAL:HG13	1.96	0.47
42:S2:1708:C:H2'	42:S2:1709:G:H8	1.79	0.47
50:SH:130:LEU:HD21	50:SH:156:VAL:CG2	2.39	0.47
67:SZ:65:TYR:OH	67:SZ:76:ARG:HG2	2.15	0.47
74:Ln:12:ARG:HG3	74:Ln:15:ARG:HH22	1.78	0.47
1:L5:2:G:H2'	1:L5:3:C:C6	2.49	0.47
1:L5:671:G:O2'	1:L5:672:C:H5'	2.14	0.47
1:L5:1949:U:O2'	1:L5:1950:U:H5'	2.14	0.47
1:L5:2755:A:H2'	1:L5:2756:A:C8	2.49	0.47
1:L5:3922:A:O2'	1:L5:3923:C:H5'	2.13	0.47
1:L5:4660:C:H2'	1:L5:4661:U:C6	2.50	0.47
1:L5:4989:C:H2'	1:L5:4990:G:O4'	2.14	0.47
2:L7:61:G:H5"	5:LD:271:MET:SD	2.55	0.47
7:LF:142:TRP:CE2	7:LF:235:ASN:HB2	2.49	0.47
7:LF:142:TRP:CZ2	7:LF:235:ASN:HB2	2.50	0.47
12:LO:140:ARG:O	12:LO:144:GLU:HG3	2.15	0.47
16:LU:39:PHE:CZ	16:LU:87:THR:HG22	2.41	0.47
33:Lo:14:LYS:HB2	33:Lo:14:LYS:HZ1	1.79	0.47
41:LS:82:LEU:C	41:LS:82:LEU:HD12	2.40	0.47
42:S2:77:A:H2	49:SG:175:LYS:HG3	1.79	0.47
42:S2:581:U:C2'	42:S2:582:U:H5'	2.44	0.47
42:S2:1127:C:H4'	69:Sb:17:ARG:HE	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:1591:C:H5”	48:SF:85:LYS:HE2	1.97	0.47
43:SA:75:SER:HB2	43:SA:119:PRO:HB3	1.96	0.47
47:SE:45:ILE:HA	47:SE:61:VAL:HG11	1.96	0.47
49:SG:139:SER:HA	49:SG:142:ARG:NH2	2.30	0.47
1:L5:1323:C:H2’	1:L5:1324:G:C8	2.49	0.47
1:L5:2266:A:H2’	1:L5:2267:C:O4’	2.14	0.47
1:L5:2682:U:O2	30:Lk:2:PRO:HB2	2.15	0.47
1:L5:4424:U:H2’	1:L5:4425:U:O4’	2.15	0.47
1:L5:4858:G:H4’	1:L5:4859:A:OP2	2.15	0.47
83:L5:5695:HOH:O	75:LR:78:ILE:HG23	2.14	0.47
42:S2:51:U:H2’	42:S2:52:G:H8	1.79	0.47
42:S2:218:PSU:H2’	42:S2:219:U:C6	2.50	0.47
42:S2:221:A:O2’	42:S2:222:U:H5’	2.14	0.47
42:S2:1019:C:O2’	42:S2:1020:A:H5’	2.14	0.47
42:S2:1422:G:H3’	42:S2:1423:C:H3’	1.97	0.47
42:S2:1803:U:H4’	42:S2:1804:OMU:OP1	2.14	0.47
69:Sb:65:GLN:OE1	69:Sb:66:PRO:HD2	2.14	0.47
77:LV:62:MET:HE3	77:LV:76:VAL:CG1	2.44	0.47
1:L5:929:A:H61	10:LM:70:GLN:HE22	1.62	0.47
1:L5:974:U:C2’	1:L5:975:C:H5’	2.43	0.47
1:L5:1078:C:O2’	1:L5:1079:C:H5’	2.14	0.47
1:L5:1723:U:O2’	1:L5:1724:U:H5’	2.13	0.47
1:L5:2341:OMC:O2	1:L5:2341:OMC:H2’	2.15	0.47
1:L5:2414:OMG:H2’	1:L5:2416:U:C5	2.50	0.47
1:L5:2451:G:H2’	1:L5:2452:C:C6	2.49	0.47
1:L5:2594:C:O2’	1:L5:2595:G:H5’	2.15	0.47
1:L5:2701:G:H3’	1:L5:2702:G:H5’	1.96	0.47
1:L5:3835:A:O2’	1:L5:3836:C:H5’	2.15	0.47
1:L5:3925:G:N3	1:L5:3925:G:H2’	2.30	0.47
1:L5:4579:C:H2’	1:L5:4580:U:H6	1.80	0.47
3:L8:139:G:H2’	3:L8:140:C:O4’	2.15	0.47
7:LF:173:ALA:O	7:LF:177:ARG:HG3	2.15	0.47
13:LP:41:ILE:CD1	13:LP:95:LEU:HD22	2.44	0.47
15:LT:108:ARG:HD2	15:LT:130:ARG:HD3	1.96	0.47
19:LZ:33:THR:HG22	19:LZ:34:SER:H	1.80	0.47
21:Lb:35:VAL:HG12	21:Lb:36:ASP:N	2.29	0.47
23:Ld:29:ILE:O	23:Ld:33:ILE:HG12	2.14	0.47
25:Lf:24:HIS:O	25:Lf:87:LYS:HE2	2.14	0.47
27:Lh:6:ALA:O	27:Lh:10:ARG:HG2	2.14	0.47
34:Lp:85:ARG:CB	42:S2:939:U:H4’	2.45	0.47
36:LA:135:THR:HG21	36:LA:149:LYS:HE2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:LH:103:VAL:HG11	38:LH:144:LEU:HD11	1.97	0.47
41:LS:17:LEU:HD22	41:LS:59:GLY:CA	2.45	0.47
42:S2:1046:PSU:H2'	42:S2:1047:C:O4'	2.15	0.47
42:S2:1520:G:N3	42:S2:1520:G:H2'	2.29	0.47
42:S2:1550:G:H3'	42:S2:1579:A:H61	1.80	0.47
42:S2:1665:G:O5'	61:ST:89:PRO:HG2	2.15	0.47
43:SA:42:LYS:CD	43:SA:48:ILE:HD11	2.44	0.47
45:SC:184:VAL:CG2	45:SC:195:LEU:HB2	2.44	0.47
45:SC:206:SER:HB2	45:SC:224:THR:HG21	1.97	0.47
46:SD:196:GLY:HA2	46:SD:199:GLY:O	2.14	0.47
47:SE:196:THR:HG22	47:SE:197:ASN:OD1	2.15	0.47
51:SI:89:GLU:OE1	51:SI:89:GLU:HA	2.14	0.47
59:SR:22:THR:O	73:Sg:212:LYS:HE3	2.15	0.47
1:L5:1210:C:H2'	1:L5:1211:G:O4'	2.15	0.47
1:L5:1322:A2M:H2'	1:L5:1323:C:C6	2.49	0.47
1:L5:1478:G:H22	40:LL:184:MET:HE1	1.80	0.47
1:L5:1561:A:H2'	1:L5:1562:C:C5'	2.45	0.47
1:L5:2416:U:HO2'	1:L5:2417:G:H8	1.62	0.47
1:L5:2667:G:H2'	1:L5:2668:A:H5'	1.96	0.47
1:L5:4137:G:O2'	1:L5:4138:G:H5'	2.15	0.47
1:L5:4474:A:H4'	1:L5:4475:G:H8	1.77	0.47
1:L5:4891:C:H2'	1:L5:4892:G:H8	1.79	0.47
1:L5:5017:C:O2'	1:L5:5018:G:H5'	2.15	0.47
16:LU:47:ILE:HG13	16:LU:86:LEU:HD12	1.97	0.47
19:LZ:92:ASP:HB3	19:LZ:95:VAL:HG22	1.96	0.47
31:Ll:9:ILE:HG13	83:Ll:105:HOH:O	2.14	0.47
41:LS:7:LEU:O	41:LS:103:ALA:HB1	2.14	0.47
42:S2:170:A:C4'	49:SG:136:LYS:HD3	2.40	0.47
42:S2:1223:A:OP1	48:SF:79:HIS:HA	2.15	0.47
42:S2:1542:C:O2'	42:S2:1543:U:H5'	2.14	0.47
42:S2:1737:G:H2'	42:S2:1738:C:C6	2.50	0.47
42:S2:1808:U:H2'	42:S2:1809:A:C8	2.47	0.47
70:Sc:40:ARG:HG2	70:Sc:40:ARG:HH11	1.79	0.47
73:Sg:104:HIS:CD2	73:Sg:108:VAL:HG22	2.50	0.47
73:Sg:214:GLY:HA2	73:Sg:234:ASP:O	2.15	0.47
1:L5:730:G:C5	7:LF:73:ARG:HD3	2.50	0.47
1:L5:755:C:O2'	1:L5:756:G:H5'	2.15	0.47
1:L5:1066:C:H1'	6:LE:69:TYR:CE2	2.50	0.47
1:L5:1531:C:H2'	1:L5:1532:PSU:O4'	2.15	0.47
1:L5:3702:C:O2'	1:L5:3703:A:H5'	2.14	0.47
83:L5:6807:HOH:O	37:LB:116:ARG:HD3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Ld:68:LEU:CD1	23:Ld:84:ILE:HD11	2.44	0.47
42:S2:297:A:C2'	42:S2:298:G:H5'	2.45	0.47
42:S2:1166:G:O2'	42:S2:1167:G:H5'	2.14	0.47
64:SW:29:PRO:HB2	64:SW:58:ALA:HB1	1.96	0.47
64:SW:56:HIS:O	64:SW:57:ARG:HG3	2.15	0.47
73:Sg:188:HIS:HB3	73:Sg:219:TRP:CZ3	2.50	0.47
1:L5:652:G:H2'	1:L5:653:U:C6	2.50	0.47
1:L5:1274:C:H2'	1:L5:1275:A:O4'	2.15	0.47
1:L5:2603:C:H4'	26:Lg:2:VAL:HG21	1.96	0.47
1:L5:4171:G:O2'	1:L5:4172:A:H5'	2.15	0.47
2:L7:116:G:P	5:LD:255:LYS:HE2	2.55	0.47
3:L8:52:A:C5	31:Ll:23:ILE:HG22	2.49	0.47
15:LT:153:PRO:O	41:LS:127:MET:HG2	2.15	0.47
19:LZ:29:ILE:HD13	19:LZ:40:HIS:CD2	2.50	0.47
23:Ld:23:ARG:HB3	23:Ld:25:TYR:CE1	2.50	0.47
42:S2:1803:U:H2'	42:S2:1804:OMU:C6	2.42	0.47
58:SQ:12:VAL:HG11	58:SQ:90:LYS:HB3	1.97	0.47
61:ST:72:VAL:O	61:ST:76:THR:HG23	2.15	0.47
73:Sg:171:ASP:O	73:Sg:173:LEU:HG	2.15	0.47
73:Sg:240:CYS:O	73:Sg:248:LEU:HD12	2.15	0.47
1:L5:1239:A:OP2	6:LE:60:SER:HB2	2.15	0.46
1:L5:1690:C:H2'	1:L5:1691:U:O2	2.15	0.46
1:L5:2282:C:H2'	1:L5:2283:U:C6	2.50	0.46
1:L5:2413:A:H2'	1:L5:2414:OMG:C8	2.50	0.46
1:L5:3676:U:H2'	1:L5:3677:G:O4'	2.15	0.46
1:L5:3757:C:H2'	1:L5:3758:U:C5'	2.45	0.46
1:L5:4744:U:C4	12:LO:114:LYS:HE3	2.50	0.46
42:S2:424:C:O2'	42:S2:425:G:H5'	2.15	0.46
42:S2:1203:G:H2'	42:S2:1204:A:H8	1.78	0.46
42:S2:1303:C:O2	42:S2:1303:C:H5'	2.15	0.46
42:S2:1384:C:HO2'	42:S2:1484:A:H1'	1.73	0.46
44:SB:123:ALA:HB2	44:SB:165:ARG:HG3	1.97	0.46
73:Sg:157:SER:HB3	73:Sg:164:ILE:HD12	1.96	0.46
1:L5:756:G:H2'	1:L5:757:G:O4'	2.15	0.46
1:L5:1271:G:H2'	1:L5:1272:C:O4'	2.15	0.46
1:L5:2028:U:O2'	1:L5:2029:A:H5'	2.15	0.46
1:L5:2563:A:O2'	19:LZ:115:LYS:HE2	2.16	0.46
1:L5:2601:A:H5'	1:L5:2678:G:C4'	2.41	0.46
1:L5:4229:C:N4	1:L5:4252:G:H21	2.12	0.46
1:L5:4484:OMU:O5'	1:L5:4484:OMU:H6	2.14	0.46
5:LD:41:LYS:HE3	15:LT:93:ILE:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LZ:10:VAL:HG11	19:LZ:129:TRP:HZ3	1.80	0.46
21:Lb:95:ARG:HD2	21:Lb:99:ILE:HD11	1.97	0.46
35:Lr:64:ILE:HG23	35:Lr:102:TYR:CZ	2.50	0.46
37:LB:101:THR:HG23	37:LB:101:THR:O	2.15	0.46
37:LB:173:LEU:HD22	37:LB:342:LYS:CD	2.45	0.46
37:LB:173:LEU:HD22	37:LB:342:LYS:HD2	1.97	0.46
41:LS:82:LEU:C	41:LS:127:MET:HE2	2.41	0.46
42:S2:352:U:H2'	42:S2:353:C:C6	2.50	0.46
42:S2:648:A:H2'	42:S2:649:PSU:C6	2.50	0.46
42:S2:1148:A:H4'	42:S2:1149:A:O4'	2.14	0.46
42:S2:1707:U:H5'	74:Ln:9:ARG:HH22	1.80	0.46
44:SB:110:MET:HE3	44:SB:110:MET:CA	2.43	0.46
45:SC:169:TYR:CD1	45:SC:173:LYS:HG2	2.49	0.46
67:SZ:73:VAL:HG21	67:SZ:88:LEU:HD21	1.97	0.46
1:L5:900:C:H2'	1:L5:901:C:C6	2.50	0.46
1:L5:2644:C:H2'	1:L5:2645:C:H6	1.81	0.46
1:L5:2701:G:H3'	1:L5:2702:G:H5"	1.97	0.46
1:L5:4164:A:H2'	1:L5:4165:G:C8	2.50	0.46
1:L5:4592:G:O2'	1:L5:4593:A:H5'	2.16	0.46
42:S2:1144:A:H2	42:S2:1199:A:H4'	1.80	0.46
42:S2:1311:C:H2'	42:S2:1312:G:O4'	2.16	0.46
53:SK:53:LYS:HE2	53:SK:53:LYS:HB3	1.71	0.46
1:L5:1269:G:H2'	1:L5:1269:G:N3	2.31	0.46
1:L5:1784:A:H2'	39:LI:22:PHE:CZ	2.50	0.46
1:L5:2794:OMC:C2	1:L5:2795:C:C5	3.04	0.46
1:L5:4748:A:H2'	1:L5:4749:U:O4'	2.15	0.46
8:LG:162:ASP:HA	8:LG:163:PRO:C	2.41	0.46
13:LP:12:THR:O	13:LP:107:LEU:HD21	2.15	0.46
20:La:132:ARG:HH11	20:La:132:ARG:HG3	1.80	0.46
23:Ld:80:VAL:HG13	23:Ld:81:PRO:HD2	1.97	0.46
29:Lj:39:TYR:CG	29:Lj:40:PRO:HA	2.50	0.46
42:S2:407:G:N1	65:SX:36:LEU:HD11	2.30	0.46
42:S2:444:G:O6	51:SI:26:LYS:HE2	2.15	0.46
42:S2:804:U:H2'	42:S2:805:U:C6	2.50	0.46
42:S2:1291:A:O2'	42:S2:1292:C:H5'	2.16	0.46
42:S2:1538:C:H2'	42:S2:1539:U:C6	2.50	0.46
42:S2:1713:C:C2'	42:S2:1714:U:H5'	2.46	0.46
65:SX:76:LYS:HG3	65:SX:77:ASN:N	2.30	0.46
66:SY:57:VAL:HB	66:SY:60:PHE:CE2	2.51	0.46
66:SY:111:LYS:HE3	66:SY:112:ASN:OD1	2.15	0.46
1:L5:52:G:H4'	1:L5:1525:G:H4'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:680:G:O2'	1:L5:681:G:H5'	2.16	0.46
1:L5:1831:G:P	1:L5:1831:G:H2'	2.56	0.46
1:L5:2595:G:H2'	1:L5:2596:G:H8	1.80	0.46
1:L5:2830:A:C2'	1:L5:2831:G:H5'	2.46	0.46
4:LC:350:ARG:HG2	4:LC:350:ARG:NH1	2.30	0.46
24:Le:108:ARG:O	24:Le:112:VAL:HG23	2.16	0.46
42:S2:461:U:H2'	42:S2:462:OMC:H6	1.80	0.46
42:S2:1520:G:HO2'	42:S2:1521:C:P	2.38	0.46
44:SB:145:LYS:HG3	44:SB:149:GLN:CD	2.41	0.46
46:SD:6:SER:OG	46:SD:9:ARG:HG3	2.15	0.46
46:SD:69:LEU:HA	46:SD:72:VAL:CG2	2.46	0.46
55:SN:62:GLN:O	55:SN:66:VAL:HG23	2.15	0.46
56:SO:150:ARG:HG3	56:SO:150:ARG:NH1	2.31	0.46
73:Sg:77:PHE:HB3	73:Sg:89:LEU:HD11	1.97	0.46
1:L5:204:U:H2'	1:L5:205:C:H6	1.81	0.46
1:L5:306:A:OP1	28:Li:53:TYR:HE1	1.98	0.46
1:L5:914:C:H2'	1:L5:915:C:H6	1.80	0.46
1:L5:1428:G:HO2'	1:L5:1429:A:H8	1.59	0.46
1:L5:2509:U:C2	1:L5:2510:C:C5	3.03	0.46
1:L5:2650:A:H4'	1:L5:2651:U:OP1	2.16	0.46
1:L5:3831:A:O3'	1:L5:4654:U:H4'	2.15	0.46
1:L5:4890:C:H2'	1:L5:4891:C:O4'	2.15	0.46
6:LE:250:GLN:HE21	6:LE:254:ASP:CG	2.24	0.46
11:LN:65:ARG:HB2	11:LN:129:PHE:CE1	2.50	0.46
42:S2:1269:G:H2'	42:S2:1270:G:H5'	1.98	0.46
42:S2:1378:A:C4	43:SA:105:PRO:HB2	2.51	0.46
42:S2:1621:U:H6	42:S2:1621:U:P	2.39	0.46
48:SF:195:GLU:O	48:SF:199:VAL:HG23	2.16	0.46
1:L5:5:A:H2'	1:L5:6:C:O4'	2.16	0.46
1:L5:389:A:C1'	18:LY:91:ASN:HA	2.37	0.46
1:L5:4270:C:O2'	1:L5:4271:U:H5'	2.15	0.46
3:L8:140:C:H2'	3:L8:141:C:C6	2.50	0.46
11:LN:47:LYS:HD2	11:LN:50:ARG:HH11	1.81	0.46
24:Le:24:GLN:HA	83:Le:202:HOH:O	2.14	0.46
42:S2:1486:A:H2'	42:S2:1487:A:O4'	2.16	0.46
42:S2:1856:C:H2'	42:S2:1857:G:C8	2.51	0.46
48:SF:86:LYS:O	48:SF:90:VAL:HG23	2.15	0.46
52:SJ:60:LEU:HD22	52:SJ:70:ARG:HA	1.98	0.46
62:SU:40:ILE:HD11	62:SU:89:ILE:HG12	1.97	0.46
73:Sg:23:THR:HG22	73:Sg:31:ILE:CG2	2.45	0.46
1:L5:7:C:H2'	1:L5:8:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:10:A:H2'	1:L5:11:G:C8	2.51	0.46
1:L5:166:C:O2'	1:L5:167:C:H5'	2.15	0.46
1:L5:268:G:H2'	1:L5:269:G:H8	1.81	0.46
1:L5:325:U:H2'	1:L5:326:C:H6	1.76	0.46
1:L5:913:C:H2'	1:L5:914:C:H6	1.79	0.46
1:L5:1505:C:O3'	20:La:2:PRO:HD2	2.16	0.46
1:L5:2759:U:C2	26:Lg:69:LYS:HB2	2.51	0.46
1:L5:3784:U:H2'	1:L5:3786:A:OP2	2.15	0.46
1:L5:4467:U:H2'	1:L5:4468:U:C6	2.51	0.46
1:L5:5012:A:O2'	1:L5:5013:G:H5'	2.16	0.46
36:LA:233:ARG:O	36:LA:233:ARG:HG3	2.15	0.46
42:S2:102:A:H4'	42:S2:104:A:C8	2.51	0.46
42:S2:595:U:O2'	42:S2:596:U:H5'	2.15	0.46
42:S2:1511:U:H2'	42:S2:1512:C:C6	2.50	0.46
1:L5:703:G:N3	1:L5:703:G:H5"	2.31	0.46
1:L5:1807:G:H2'	1:L5:1808:C:H6	1.80	0.46
1:L5:3656:C:O2'	1:L5:3657:G:H5'	2.16	0.46
1:L5:4148:C:C5	8:LG:72:LYS:HE3	2.51	0.46
42:S2:349:A:H2'	42:S2:350:C:C6	2.50	0.46
42:S2:803:C:H2'	42:S2:804:U:H6	1.81	0.46
42:S2:958:G:OP2	56:SO:39:ASP:HB2	2.16	0.46
42:S2:1478:U:H2'	42:S2:1479:G:C8	2.51	0.46
43:SA:149:ASN:HB2	43:SA:165:ASN:OD1	2.15	0.46
45:SC:84:PHE:CZ	45:SC:264:SER:HA	2.51	0.46
50:SH:11:PRO:HG2	50:SH:44:ASN:ND2	2.30	0.46
68:Sa:44:ILE:HG21	68:Sa:65:PRO:HG2	1.97	0.46
74:Ln:14:LYS:HE3	74:Ln:14:LYS:HB3	1.62	0.46
1:L5:704:C:O2	1:L5:704:C:H2'	2.16	0.46
1:L5:2834:A:O2'	1:L5:4617:G:H4'	2.16	0.46
4:LC:252:TRP:CZ3	4:LC:260:LEU:HD11	2.51	0.46
7:LF:67:THR:O	7:LF:71:MET:HG2	2.16	0.46
13:LP:29:THR:HG21	13:LP:146:ILE:HD11	1.98	0.46
41:LS:11:LYS:HD3	41:LS:63:TYR:CE2	2.51	0.46
42:S2:484:A2M:HM'3	42:S2:484:A2M:H1'	1.69	0.46
42:S2:612:U:C2'	42:S2:613:G:H5'	2.46	0.46
42:S2:917:U:O4'	50:SH:118:ARG:HG2	2.16	0.46
42:S2:1040:G:O2'	42:S2:1041:G:H5'	2.16	0.46
42:S2:1413:G:H2'	42:S2:1414:A:H8	1.81	0.46
45:SC:111:PRO:HA	45:SC:123:ARG:O	2.15	0.46
46:SD:71:ALA:O	46:SD:75:LYS:HG3	2.15	0.46
67:SZ:88:LEU:HD13	67:SZ:109:TYR:CD2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Sc:29:GLN:HG3	70:Sc:45:ASN:OD1	2.15	0.46
1:L5:479:G:H2'	1:L5:480:C:C6	2.51	0.45
1:L5:923:A:H2'	1:L5:924:G:O4'	2.16	0.45
1:L5:964:G:C2	6:LE:126:LEU:HD21	2.51	0.45
1:L5:1201:C:H2'	1:L5:1202:G:C8	2.51	0.45
1:L5:1871:C:H2'	1:L5:1872:U:C6	2.51	0.45
1:L5:2729:C:H5"	34:Lp:69:TRP:CH2	2.51	0.45
1:L5:2782:C:O2	29:Lj:9:GLY:HA2	2.15	0.45
1:L5:4576:A2M:CM'	1:L5:4577:U:H5'	2.37	0.45
1:L5:4597:A:H2'	1:L5:4598:C:H6	1.81	0.45
1:L5:5001:A:H5"	1:L5:5002:G:OP2	2.16	0.45
6:LE:153:LEU:HD11	6:LE:195:ILE:HG13	1.97	0.45
14:LQ:80:ALA:HB3	14:LQ:100:VAL:HG12	1.98	0.45
42:S2:1466:G:C5'	59:SR:4:VAL:HG22	2.45	0.45
43:SA:200:ASP:HA	43:SA:203:PHE:CD2	2.51	0.45
48:SF:77:MET:CG	48:SF:89:THR:HG21	2.45	0.45
59:SR:10:LYS:HD3	59:SR:53:TYR:CZ	2.50	0.45
59:SR:20:TYR:CD2	59:SR:38:ILE:HD13	2.51	0.45
73:Sg:234:ASP:OD1	73:Sg:235:ILE:HD12	2.16	0.45
1:L5:965:U:H5"	1:L5:966:C:OP1	2.16	0.45
1:L5:1081:A:H2'	1:L5:1082:C:H6	1.81	0.45
1:L5:1296:G:H2'	1:L5:1297:C:H6	1.74	0.45
1:L5:1775:U:H2'	1:L5:1776:A:C8	2.50	0.45
1:L5:2689:C:C2'	1:L5:2690:G:H5'	2.46	0.45
3:L8:155:C:C2'	3:L8:156:U:H5"	2.44	0.45
5:LD:287:PHE:HZ	39:LI:214:SER:CB	2.29	0.45
15:LT:17:ARG:HD3	15:LT:47:THR:OG1	2.17	0.45
16:LU:56:LEU:O	16:LU:60:VAL:HB	2.16	0.45
27:Lh:52:LYS:HD3	27:Lh:52:LYS:HA	1.72	0.45
42:S2:292:A:H4'	54:SL:39:ASN:O	2.15	0.45
42:S2:857:U:H2'	42:S2:858:A:C8	2.51	0.45
46:SD:47:GLU:HG2	46:SD:49:ILE:HD11	1.97	0.45
49:SG:1:MET:CE	49:SG:106:LEU:HB2	2.46	0.45
50:SH:146:VAL:HG12	64:SW:42:MET:HE1	1.98	0.45
1:L5:685:C:O5'	1:L5:685:C:H6	1.98	0.45
1:L5:901:C:H2'	1:L5:902:G:H8	1.78	0.45
1:L5:2547:G:H1	1:L5:2560:U:H3	1.65	0.45
11:LN:121:VAL:CG1	11:LN:131:GLU:HG3	2.43	0.45
19:LZ:9:LYS:HD2	19:LZ:83:THR:O	2.15	0.45
33:Lo:35:ALA:O	33:Lo:39:ARG:HG3	2.16	0.45
39:LI:48:LEU:O	39:LI:139:ARG:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:113:G:N2	42:S2:292:A:H2'	2.31	0.45
42:S2:1031:A2M:HM'3	42:S2:1031:A2M:H1'	1.73	0.45
42:S2:1589:A:H2'	42:S2:1590:C:O4'	2.15	0.45
45:SC:79:GLU:HG3	63:SV:12:TYR:HB3	1.98	0.45
48:SF:19:LEU:HD21	48:SF:69:VAL:HG11	1.97	0.45
50:SH:144:ILE:HB	64:SW:52:ILE:HB	1.98	0.45
1:L5:4932:U:O2'	1:L5:4933:C:H5'	2.16	0.45
5:LD:157:ASN:OD1	5:LD:159:VAL:HG22	2.15	0.45
8:LG:67:ARG:HD2	83:LG:305:HOH:O	2.15	0.45
25:Lf:78:HIS:HB2	25:Lf:85:ARG:HG3	1.97	0.45
27:Lh:5:LYS:O	27:Lh:9:LEU:HG	2.16	0.45
29:Lj:25:LYS:HE2	31:Ll:50:GLY:O	2.16	0.45
42:S2:461:U:H2'	42:S2:462:OMC:C6	2.51	0.45
42:S2:803:C:H4'	64:SW:80:ASP:CG	2.42	0.45
42:S2:1057:C:H2'	42:S2:1059:G:OP2	2.16	0.45
42:S2:1282:A:H2	42:S2:1287:A:H1'	1.82	0.45
43:SA:53:ARG:HB3	63:SV:83:PHE:CZ	2.51	0.45
45:SC:102:LEU:HD13	45:SC:130:ILE:CD1	2.47	0.45
50:SH:72:PHE:O	50:SH:76:GLN:HB2	2.16	0.45
54:SL:40:ILE:HD11	54:SL:44:PHE:HB2	1.99	0.45
73:Sg:197:THR:HG21	73:Sg:239:LEU:N	2.31	0.45
1:L5:725:G:H5'	4:LC:346:ASN:ND2	2.31	0.45
1:L5:1561:A:H2'	1:L5:1562:C:H5'	1.98	0.45
1:L5:1718:C:O2'	1:L5:1719:A:H5'	2.16	0.45
1:L5:2036:A:H4'	1:L5:2037:A:O5'	2.16	0.45
1:L5:2345:G:O2'	1:L5:2346:U:H5'	2.16	0.45
1:L5:3806:G:C2'	1:L5:3807:A:H5'	2.47	0.45
2:L7:45:U:H2'	2:L7:46:C:O4'	2.16	0.45
3:L8:115:G:H2'	3:L8:116:C:H6	1.79	0.45
6:LE:68:MET:HE3	6:LE:68:MET:CA	2.31	0.45
6:LE:285:LYS:HB3	6:LE:285:LYS:HE2	1.60	0.45
10:LM:38:VAL:O	10:LM:47:ARG:HA	2.17	0.45
12:LO:125:LYS:HE3	12:LO:125:LYS:HB3	1.74	0.45
19:LZ:41:ALA:HB2	19:LZ:77:TYR:HE1	1.81	0.45
23:Ld:42:ALA:HB3	23:Ld:43:PRO:HD3	1.99	0.45
31:Ll:16:LYS:HD3	31:Ll:16:LYS:HA	1.60	0.45
32:Lm:82:LEU:HD22	38:LH:95:VAL:HG22	1.98	0.45
33:Lo:69:ARG:HG3	33:Lo:82:MET:HE1	1.98	0.45
39:LI:156:LYS:HG2	39:LI:163:GLN:HB2	1.99	0.45
42:S2:1098:C:H2'	42:S2:1099:G:C8	2.51	0.45
44:SB:71:LEU:O	44:SB:71:LEU:HD13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SU:67:LYS:HE2	62:SU:78:ASP:OD1	2.17	0.45
74:Ln:11:ARG:O	74:Ln:14:LYS:HE3	2.17	0.45
77:LV:87:SER:HA	77:LV:97:TYR:HB3	1.98	0.45
1:L5:222:C:O2'	1:L5:223:G:H5'	2.17	0.45
1:L5:300:A:H2'	1:L5:301:G:H8	1.80	0.45
1:L5:2531:G:O2'	1:L5:2532:G:H5'	2.16	0.45
1:L5:2644:C:H2'	1:L5:2645:C:C6	2.52	0.45
1:L5:2821:G:C2'	1:L5:2822:A:H5'	2.47	0.45
1:L5:3834:U:H2'	1:L5:3835:A:C8	2.51	0.45
1:L5:4275:U:H2'	1:L5:4276:U:C6	2.51	0.45
1:L5:4466:A:H2'	1:L5:4467:U:O4'	2.17	0.45
1:L5:5014:C:H2'	1:L5:5015:U:O4'	2.17	0.45
5:LD:207:TYR:CE1	5:LD:211:LEU:HG	2.52	0.45
23:Ld:93:ASN:HB2	23:Ld:103:TYR:HD2	1.82	0.45
42:S2:1643:PSU:O2'	42:S2:1644:C:H5'	2.16	0.45
42:S2:1671:G:H2'	42:S2:1672:U:C6	2.51	0.45
42:S2:1804:OMU:HM22	42:S2:1805:G:O4'	2.17	0.45
51:SI:103:LEU:CD2	51:SI:172:LEU:HD23	2.46	0.45
56:SO:56:VAL:HB	56:SO:81:VAL:HG23	1.98	0.45
60:SS:66:ARG:HA	60:SS:69:THR:CG2	2.46	0.45
69:Sb:46:VAL:HG22	69:Sb:54:VAL:HG11	1.98	0.45
73:Sg:176:VAL:O	73:Sg:184:LEU:HD12	2.17	0.45
77:LV:42:VAL:HB	77:LV:45:ILE:HG13	1.98	0.45
1:L5:307:A:O2'	1:L5:308:G:H5'	2.16	0.45
1:L5:2821:G:O2'	1:L5:2822:A:H5'	2.16	0.45
1:L5:4639:C:H2'	1:L5:4640:C:H6	1.79	0.45
1:L5:4991:U:H4'	1:L5:4992:A:H5'	1.98	0.45
4:LC:60:HIS:HA	4:LC:92:PHE:CE1	2.51	0.45
5:LD:264:LYS:HG2	5:LD:266:TRP:CE2	2.51	0.45
8:LG:83:PHE:O	8:LG:159:HIS:HB2	2.16	0.45
14:LQ:167:VAL:HG22	83:LQ:211:HOH:O	2.15	0.45
17:LX:89:LYS:HA	17:LX:89:LYS:HD2	1.79	0.45
27:Lh:112:ARG:NH1	27:Lh:112:ARG:CG	2.79	0.45
42:S2:1311:C:H2'	42:S2:1312:G:C8	2.51	0.45
42:S2:1466:G:H2'	42:S2:1467:C:C6	2.52	0.45
42:S2:1850:MA6:H8	42:S2:1850:MA6:O5'	2.17	0.45
42:S2:1869:A:N1	44:SB:112:SER:HA	2.32	0.45
46:SD:163:PRO:HA	46:SD:166:TYR:CZ	2.52	0.45
54:SL:75:GLY:HA3	54:SL:88:ILE:HD12	1.97	0.45
55:SN:119:GLU:HG2	55:SN:141:TYR:HE2	1.81	0.45
64:SW:15:ASN:ND2	64:SW:71:LYS:HD2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SX:107:ARG:C	65:SX:108:LYS:HG2	2.42	0.45
66:SY:20:ARG:HD2	66:SY:74:MET:HG3	1.99	0.45
68:Sa:21:ILE:HD13	68:Sa:72:HIS:HB2	1.99	0.45
1:L5:512:U:C2	1:L5:647:G:O6	2.69	0.45
1:L5:1310:C:C2	1:L5:1311:C:C5	3.04	0.45
1:L5:2075:G:H2'	1:L5:2076:U:C6	2.51	0.45
1:L5:2364:A:H5'	23:Ld:64:ILE:O	2.17	0.45
1:L5:4196:U:O2'	1:L5:4197:C:H5'	2.17	0.45
7:LF:86:GLU:OE2	15:LT:136:ARG:NH1	2.50	0.45
14:LQ:177:ALA:O	14:LQ:178:ARG:C	2.59	0.45
38:LH:90:TYR:CE2	38:LH:184:LYS:HD3	2.51	0.45
42:S2:379:C:H5'	51:SI:33:ALA:HA	1.99	0.45
42:S2:560:A:C2'	42:S2:561:A:H5'	2.47	0.45
47:SE:20:LEU:HD21	47:SE:46:ILE:HD12	1.99	0.45
51:SI:17:LYS:HE3	51:SI:17:LYS:HB2	1.86	0.45
58:SQ:76:GLY:O	58:SQ:80:GLN:HG3	2.16	0.45
72:Se:12:VAL:HA	72:Se:15:GLN:HG2	1.99	0.45
74:Ln:5:TRP:HA	74:Ln:5:TRP:CE3	2.52	0.45
74:Ln:5:TRP:HA	74:Ln:5:TRP:HE3	1.82	0.45
1:L5:68:U:H2'	1:L5:69:A:O4'	2.16	0.45
1:L5:1621:OMG:H4'	1:L5:1622:G:O5'	2.17	0.45
1:L5:3590:A:H3'	1:L5:3590:A:N3	2.32	0.45
1:L5:3929:A:HO2'	44:SB:58:ALA:N	2.15	0.45
4:LC:303:ARG:HG2	14:LQ:38:ARG:O	2.17	0.45
34:Lp:38:THR:HG23	34:Lp:38:THR:O	2.17	0.45
42:S2:1259:A:H1'	42:S2:1264:C:N4	2.31	0.45
43:SA:7:VAL:HG22	43:SA:191:ARG:CD	2.47	0.45
52:SJ:125:HIS:O	52:SJ:128:VAL:HG22	2.17	0.45
59:SR:85:VAL:CG2	59:SR:86:PRO:HD2	2.47	0.45
59:SR:116:ASN:O	59:SR:117:LEU:HD23	2.17	0.45
60:SS:80:PRO:HB2	60:SS:82:TRP:CD1	2.52	0.45
1:L5:139:G:O2'	1:L5:140:G:H5'	2.16	0.45
1:L5:152:U:H5'	11:LN:56:LYS:HG2	1.99	0.45
1:L5:1582:G:H2'	1:L5:1583:G:C8	2.51	0.45
1:L5:2338:G:H5"	1:L5:2341:OMC:H5	1.80	0.45
1:L5:2814:OMC:HM23	1:L5:2814:OMC:H1'	1.54	0.45
1:L5:2837:G:C2'	1:L5:2838:G:H5'	2.47	0.45
1:L5:4744:U:O4	12:LO:114:LYS:HE3	2.18	0.45
18:LY:56:GLN:CG	18:LY:67:ILE:HG12	2.47	0.45
39:LI:43:VAL:HG21	39:LI:197:VAL:HG13	1.99	0.45
42:S2:4:C:O2	42:S2:4:C:H2'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:120:U:H2'	42:S2:121:OMU:H6	1.99	0.45
42:S2:929:G:H2'	42:S2:930:C:O4'	2.17	0.45
42:S2:1025:U:H2'	42:S2:1026:C:O4'	2.17	0.45
45:SC:161:SER:O	45:SC:163:VAL:HG13	2.16	0.45
47:SE:49:ARG:HE	47:SE:49:ARG:HB3	1.66	0.45
50:SH:69:LEU:CD2	50:SH:96:ALA:HB2	2.45	0.45
59:SR:5:ARG:HB2	59:SR:10:LYS:CE	2.48	0.45
66:SY:45:ALA:HB1	66:SY:50:THR:O	2.16	0.45
73:Sg:194:TYR:CZ	73:Sg:212:LYS:HB2	2.52	0.45
1:L5:165:A:C2'	1:L5:166:C:H5'	2.47	0.44
1:L5:318:A:H2'	1:L5:319:A:C8	2.52	0.44
1:L5:722:G:H2'	1:L5:723:A:O4'	2.16	0.44
1:L5:752:G:H5"	1:L5:910:C:N4	2.32	0.44
1:L5:933:G:H2'	1:L5:934:C:C6	2.52	0.44
1:L5:1723:U:H2'	1:L5:1724:U:H6	1.82	0.44
1:L5:2366:A:O2'	1:L5:2367:C:H5'	2.16	0.44
1:L5:2591:A:H2'	1:L5:2591:A:N3	2.31	0.44
1:L5:3614:G:O2'	1:L5:3615:A:H5'	2.17	0.44
1:L5:3642:A:H2'	1:L5:3643:U:C6	2.48	0.44
1:L5:4733:C:H2'	1:L5:4734:U:O4'	2.16	0.44
2:L7:63:C:H3'	39:LI:204:GLY:O	2.17	0.44
5:LD:79:TYR:HB3	5:LD:81:HIS:CD2	2.53	0.44
5:LD:108:ARG:NH2	5:LD:253:TYR:HB2	2.32	0.44
37:LB:213:GLN:OE1	37:LB:286:LYS:HA	2.17	0.44
39:LI:48:LEU:HD11	39:LI:145:GLU:CG	2.39	0.44
42:S2:27:A2M:HM'3	42:S2:27:A2M:H1'	1.75	0.44
42:S2:918:PSU:O2'	42:S2:919:A:H5'	2.17	0.44
42:S2:1260:A:C2	42:S2:1620:A:C4	3.06	0.44
42:S2:1444:U:H2'	42:S2:1445:PSU:H6	1.82	0.44
42:S2:1829:G:H1'	42:S2:1850:MA6:H2	1.98	0.44
45:SC:88:ILE:O	45:SC:160:LEU:HD22	2.17	0.44
46:SD:185:LYS:HB2	46:SD:185:LYS:HE2	1.61	0.44
77:LV:82:ILE:HG22	77:LV:125:CYS:SG	2.57	0.44
1:L5:2405:OMU:C2'	1:L5:2406:G:H5'	2.46	0.44
1:L5:3914:A:H2'	1:L5:3915:G:O4'	2.18	0.44
1:L5:4159:G:H2'	1:L5:4160:U:C6	2.52	0.44
1:L5:4493:A:H2'	1:L5:4494:C:C6	2.52	0.44
6:LE:68:MET:CE	6:LE:71:ARG:HB3	2.48	0.44
22:Lc:94:LEU:HD12	22:Lc:94:LEU:C	2.42	0.44
42:S2:6:G:H21	42:S2:621:OMC:HM21	1.82	0.44
42:S2:158:A:H2'	42:S2:159:A2M:H8	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:1631:U:H2'	42:S2:1632:G:H5'	1.99	0.44
45:SC:123:ARG:HB3	45:SC:143:CYS:SG	2.57	0.44
51:SI:76:THR:HG21	51:SI:104:ILE:CD1	2.47	0.44
1:L5:478:G:H2'	1:L5:479:G:C8	2.53	0.44
1:L5:1313:U:H2'	1:L5:1314:C:C6	2.53	0.44
1:L5:2667:G:C2'	1:L5:2668:A:H5'	2.47	0.44
1:L5:3650:G:H2'	1:L5:3651:G:H8	1.83	0.44
1:L5:3670:G:H2'	1:L5:3671:C:C6	2.52	0.44
1:L5:3704:A2M:H8	1:L5:3704:A2M:O5'	2.16	0.44
1:L5:4579:C:O2'	1:L5:4580:U:H5'	2.17	0.44
3:L8:19:C:H2'	3:L8:20:A:H8	1.81	0.44
4:LC:328:LEU:HD13	7:LF:187:MET:CE	2.48	0.44
37:LB:112:ASP:O	37:LB:116:ARG:HG3	2.16	0.44
42:S2:44:U:O2	42:S2:482:G:H1'	2.17	0.44
42:S2:116:OMU:O5'	42:S2:116:OMU:H6	2.17	0.44
42:S2:434:G:O2'	42:S2:435:A:H5'	2.17	0.44
42:S2:864:A:O3'	42:S2:865:A:P	2.76	0.44
42:S2:1391:OMC:O2'	42:S2:1392:U:H5'	2.16	0.44
47:SE:105:THR:HG23	47:SE:243:GLY:HA2	1.99	0.44
1:L5:385:A:H4'	1:L5:386:A:OP1	2.17	0.44
1:L5:937:A:C4	4:LC:335:MET:HE1	2.52	0.44
1:L5:1515:C:O2'	1:L5:1516:C:H5'	2.16	0.44
1:L5:1633:A:OP1	1:L5:1635:U:H5	1.99	0.44
1:L5:2752:G:C3'	1:L5:2753:U:H5"	2.44	0.44
1:L5:3622:C:O2	1:L5:3622:C:H2'	2.16	0.44
1:L5:4338:U:O2'	1:L5:4339:PSU:H5"	2.17	0.44
1:L5:4623:OMG:H1'	1:L5:4623:OMG:HM23	1.55	0.44
37:LB:165:HIS:HB3	37:LB:180:LEU:HD12	1.99	0.44
42:S2:1644:C:H2'	42:S2:1645:C:O4'	2.17	0.44
42:S2:1653:U:H3	42:S2:1671:G:H1	1.65	0.44
50:SH:158:LEU:O	50:SH:190:PRO:HD2	2.17	0.44
62:SU:68:THR:HG23	62:SU:70:CYS:O	2.18	0.44
1:L5:223:G:H4'	1:L5:225:G:N7	2.33	0.44
1:L5:445:U:O4	1:L5:1297:C:N3	2.51	0.44
1:L5:4178:A:O2'	1:L5:4179:C:H5'	2.18	0.44
1:L5:4736:G:H2'	1:L5:4737:G:C8	2.52	0.44
1:L5:5017:C:H2'	1:L5:5018:G:H5'	2.00	0.44
1:L5:5049:G:O2'	1:L5:5050:U:H5'	2.18	0.44
8:LG:172:ALA:HB3	28:Li:43:MET:HE1	1.98	0.44
13:LP:46:LYS:HE2	13:LP:46:LYS:HB2	1.70	0.44
23:Ld:68:LEU:CD1	23:Ld:108:TYR:HB2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:433:A:H2'	42:S2:434:G:C8	2.53	0.44
43:SA:163:CYS:SG	43:SA:174:MET:HG3	2.58	0.44
60:SS:121:ARG:HG3	60:SS:131:VAL:HB	1.98	0.44
73:Sg:191:HIS:CE1	73:Sg:195:LEU:HD21	2.53	0.44
1:L5:152:U:H5'	11:LN:56:LYS:CG	2.48	0.44
1:L5:1083:G:O2'	1:L5:1084:G:H5'	2.16	0.44
1:L5:1373:G:H2'	1:L5:1373:G:N3	2.33	0.44
1:L5:1458:A:O4'	21:Lb:27:GLN:NE2	2.43	0.44
1:L5:1605:U:H2'	1:L5:1606:C:O4'	2.18	0.44
1:L5:2438:G:H2'	1:L5:2439:A:C8	2.53	0.44
1:L5:3638:A:H2'	1:L5:3639:A:C5	2.53	0.44
1:L5:4154:G:C2'	1:L5:4155:G:H5'	2.47	0.44
1:L5:4399:C:O2'	1:L5:4400:A:H5'	2.18	0.44
5:LD:80:ALA:O	5:LD:83:LEU:HG	2.18	0.44
12:LO:202:LEU:HA	12:LO:202:LEU:HD23	1.73	0.44
15:LT:39:ILE:HG22	15:LT:99:SER:CB	2.48	0.44
15:LT:105:PHE:O	15:LT:109:VAL:HG23	2.17	0.44
33:Lo:83:LEU:HD12	33:Lo:84:ALA:N	2.33	0.44
41:LS:44:PHE:O	41:LS:48:VAL:HG23	2.17	0.44
42:S2:563:G:O2'	42:S2:564:A:H8	2.01	0.44
42:S2:1280:G:N2	42:S2:1281:G:H1'	2.33	0.44
42:S2:1728:U:H2'	42:S2:1729:U:O4'	2.17	0.44
43:SA:2:SER:HA	43:SA:59:LEU:CD2	2.48	0.44
46:SD:115:VAL:HG13	46:SD:150:MET:HE1	1.99	0.44
50:SH:139:ILE:HG12	50:SH:156:VAL:HG13	1.99	0.44
60:SS:26:ILE:O	60:SS:30:ILE:HG12	2.17	0.44
1:L5:14:C:OP1	1:L5:14:C:H3'	2.18	0.44
1:L5:28:C:H4'	1:L5:61:A:H4'	2.00	0.44
1:L5:419:A:N6	3:L8:15:G:H1'	2.33	0.44
1:L5:750:U:H1'	1:L5:911:A:C5	2.53	0.44
1:L5:1377:U:C2'	1:L5:1378:G:H5'	2.47	0.44
1:L5:1419:U:O2'	1:L5:1420:G:H5'	2.16	0.44
1:L5:1798:A:H4'	15:LT:105:PHE:CD1	2.53	0.44
1:L5:1903:A:H2'	1:L5:1904:A:C8	2.53	0.44
1:L5:3637:A:O2'	1:L5:3638:A:H5'	2.18	0.44
1:L5:4442:OMC:HM21	37:LB:241:PRO:HD3	2.00	0.44
2:L7:31:G:C2'	2:L7:32:A:H5'	2.48	0.44
3:L8:40:A:H2'	3:L8:41:A:C8	2.53	0.44
4:LC:351:VAL:O	4:LC:354:ALA:HB3	2.17	0.44
5:LD:11:ALA:O	5:LD:15:ARG:HG2	2.18	0.44
7:LF:148:LYS:HG2	7:LF:152:GLU:OE1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LG:153:GLN:HG3	8:LG:205:THR:O	2.17	0.44
12:LO:81:TRP:CZ2	12:LO:99:LEU:HD21	2.52	0.44
20:La:49:HIS:HE1	83:La:215:HOH:O	2.01	0.44
30:Lk:11:PHE:CZ	30:Lk:34:PHE:HB3	2.53	0.44
42:S2:511:U:H2'	42:S2:512:A2M:H8	2.00	0.44
42:S2:1587:G:C6	61:ST:78:ILE:HD11	2.52	0.44
43:SA:178:LEU:O	43:SA:182:VAL:HG23	2.18	0.44
50:SH:130:LEU:HG	50:SH:139:ILE:HD11	1.99	0.44
61:ST:34:VAL:HG23	61:ST:52:TRP:CZ2	2.53	0.44
64:SW:111:MET:SD	64:SW:115:GLU:HG2	2.57	0.44
1:L5:1294:C:H2'	1:L5:1295:G:H8	1.82	0.44
1:L5:2419:A:H5"	31:Ll:43:HIS:NE2	2.33	0.44
1:L5:2625:U:H2'	1:L5:2626:U:C6	2.53	0.44
1:L5:3730:OMG:HM23	1:L5:3730:OMG:H1'	1.64	0.44
1:L5:4065:C:C2'	1:L5:4066:C:H5'	2.48	0.44
1:L5:4169:G:H2'	1:L5:4169:G:N3	2.32	0.44
4:LC:322:LEU:O	4:LC:326:LEU:HG	2.18	0.44
13:LP:114:ILE:O	13:LP:114:ILE:HG22	2.18	0.44
26:Lg:63:VAL:O	26:Lg:67:LEU:HG	2.18	0.44
42:S2:150:A:H5"	42:S2:151:C:OP2	2.18	0.44
42:S2:582:U:C2	42:S2:583:A:C8	3.06	0.44
42:S2:674:C:H2'	42:S2:675:U:H6	1.83	0.44
42:S2:1490:OMG:HM22	62:SU:72:GLU:OE2	2.18	0.44
46:SD:105:LEU:HG	46:SD:184:ILE:HD13	1.99	0.44
46:SD:163:PRO:O	46:SD:167:TYR:HB2	2.17	0.44
50:SH:100:ILE:CG1	50:SH:125:VAL:HG21	2.48	0.44
59:SR:85:VAL:HG22	59:SR:86:PRO:HD2	1.99	0.44
73:Sg:34:ALA:HB1	73:Sg:66:VAL:CG1	2.47	0.44
73:Sg:190:GLY:O	73:Sg:217:MET:HE1	2.18	0.44
1:L5:281:U:HO2'	1:L5:329:A:H1'	1.83	0.44
1:L5:281:U:O2'	1:L5:329:A:H1'	2.17	0.44
1:L5:505:G:O6	1:L5:653:U:O4	2.36	0.44
1:L5:929:A:H61	10:LM:70:GLN:NE2	2.16	0.44
1:L5:976:U:OP1	6:LE:73:TYR:HE2	2.01	0.44
1:L5:1463:C:C2	1:L5:1464:C:C5	3.06	0.44
1:L5:3882:C:O2	1:L5:4550:A:N1	2.51	0.44
1:L5:3897:C:C2	1:L5:3898:U:C5	3.06	0.44
1:L5:4330:U:H2'	1:L5:4331:C:H6	1.82	0.44
1:L5:4733:C:H2'	1:L5:4734:U:H6	1.83	0.44
5:LD:195:HIS:O	5:LD:199:ILE:HG13	2.17	0.44
6:LE:181:LEU:CD2	6:LE:268:GLN:HE21	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Li:2:ALA:C	28:Li:3:LEU:HD12	2.43	0.44
42:S2:1295:A:N1	42:S2:1304:U:H5	2.15	0.44
42:S2:1401:A:H2'	42:S2:1402:A:C8	2.53	0.44
42:S2:1720:U:O5'	42:S2:1720:U:H6	1.99	0.44
42:S2:1850:MA6:C9	42:S2:1851:MA6:H93	2.48	0.44
51:SI:65:PHE:HA	51:SI:187:GLY:O	2.18	0.44
58:SQ:112:LEU:O	58:SQ:115:TYR:O	2.36	0.44
73:Sg:194:TYR:CE2	73:Sg:212:LYS:HD2	2.52	0.44
1:L5:286:U:H2'	1:L5:287:U:C6	2.53	0.43
1:L5:474:C:H2'	1:L5:475:G:C8	2.53	0.43
1:L5:928:C:H3'	1:L5:928:C:H6	1.83	0.43
1:L5:973:C:O2'	1:L5:974:U:H5'	2.18	0.43
1:L5:1585:C:H2'	1:L5:1586:C:C6	2.53	0.43
1:L5:1867:A2M:O2'	1:L5:1868:G:H5'	2.18	0.43
1:L5:3607:A:C8	1:L5:4628:U:H1'	2.53	0.43
1:L5:3806:G:O2'	1:L5:3807:A:H5'	2.18	0.43
8:LG:170:LEU:HB3	8:LG:171:PRO:HD3	1.99	0.43
18:LY:71:VAL:HG22	18:LY:81:TYR:O	2.19	0.43
19:LZ:105:ALA:HA	19:LZ:108:ARG:HH11	1.83	0.43
35:Lr:60:VAL:HG12	35:Lr:117:ILE:HG21	2.00	0.43
37:LB:224:LYS:HG2	37:LB:340:THR:CG2	2.48	0.43
42:S2:339:A:H2'	42:S2:340:C:H6	1.83	0.43
42:S2:960:U:H2'	42:S2:962:A:OP2	2.18	0.43
42:S2:1337:4AC:H5	42:S2:1337:4AC:HM72	2.00	0.43
42:S2:1446:A:O2'	42:S2:1447:OMG:H8	2.01	0.43
42:S2:1591:C:C5'	48:SF:85:LYS:HE2	2.48	0.43
43:SA:66:VAL:HG21	43:SA:185:MET:HB3	2.00	0.43
43:SA:125:THR:O	43:SA:147:LEU:HB2	2.18	0.43
46:SD:127:MET:HE1	46:SD:133:GLY:CA	2.48	0.43
48:SF:28:VAL:HG11	48:SF:41:VAL:HG21	2.00	0.43
52:SJ:20:PHE:HA	52:SJ:25:LEU:HD11	2.00	0.43
61:ST:56:ARG:HG3	61:ST:103:VAL:HG21	2.00	0.43
71:Sd:38:MET:SD	71:Sd:43:PHE:HA	2.57	0.43
73:Sg:20:GLN:HG3	73:Sg:21:ILE:N	2.32	0.43
1:L5:2511:G:H5'	1:L5:2630:G:H1'	2.00	0.43
1:L5:2595:G:H2'	1:L5:2596:G:C8	2.53	0.43
1:L5:4119:C:O2	1:L5:4119:C:H2'	2.16	0.43
6:LE:181:LEU:HD21	6:LE:268:GLN:HE21	1.83	0.43
6:LE:190:HIS:HB3	6:LE:193:PHE:HD2	1.83	0.43
33:Lo:23:VAL:HG22	33:Lo:70:LEU:HD22	1.98	0.43
42:S2:69:C:H2'	42:S2:70:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:167:G:H3'	42:S2:168:C:H5"	2.00	0.43
42:S2:943:U:C2	42:S2:944:A:C8	3.06	0.43
42:S2:1098:C:O2'	42:S2:1099:G:H5'	2.18	0.43
42:S2:1337:4AC:O2'	62:SU:68:THR:HB	2.18	0.43
44:SB:48:LEU:HD23	44:SB:48:LEU:N	2.34	0.43
58:SQ:44:PRO:HD3	58:SQ:77:HIS:HB3	2.00	0.43
62:SU:59:LYS:HB2	62:SU:84:ILE:HB	2.01	0.43
74:Ln:14:LYS:NZ	74:Ln:15:ARG:HG3	2.33	0.43
1:L5:428:G:H1'	1:L5:1301:C:O2'	2.18	0.43
1:L5:2686:A:C4	30:Lk:69:LEU:CD2	3.02	0.43
1:L5:2752:G:H8	1:L5:2753:U:H5"	1.84	0.43
1:L5:3794:OMC:O2'	1:L5:3795:G:H5'	2.17	0.43
1:L5:4329:U:H2'	1:L5:4330:U:C6	2.53	0.43
1:L5:4444:C:H2'	1:L5:4445:U:H6	1.83	0.43
1:L5:4497:A:H2'	1:L5:4498:U:O4'	2.17	0.43
2:L7:2:U:H2'	2:L7:3:C:H6	1.83	0.43
2:L7:27:G:H2'	2:L7:28:C:C6	2.53	0.43
3:L8:129:C:O2'	3:L8:130:C:H5'	2.18	0.43
16:LU:48:LYS:HA	16:LU:53:ALA:HA	1.99	0.43
42:S2:168:C:O2'	42:S2:169:U:H5'	2.19	0.43
42:S2:439:A:C2'	42:S2:440:G:H5'	2.48	0.43
42:S2:561:A:H4'	52:SJ:165:TYR:OH	2.18	0.43
42:S2:1512:C:O2'	42:S2:1513:C:H5'	2.19	0.43
42:S2:1720:U:H3'	42:S2:1721:U:H5'	2.00	0.43
42:S2:1803:U:O2'	42:S2:1804:OMU:P	2.76	0.43
47:SE:139:LEU:HD23	47:SE:150:PRO:CB	2.47	0.43
48:SF:78:MET:HE3	48:SF:78:MET:HB3	1.77	0.43
58:SQ:58:LEU:HB2	58:SQ:63:PHE:HE1	1.83	0.43
64:SW:105:THR:HG23	64:SW:105:THR:O	2.17	0.43
1:L5:192:G:H2'	1:L5:192:G:N3	2.33	0.43
1:L5:1206:G:C2'	1:L5:1207:G:H5'	2.49	0.43
1:L5:1444:G:H2'	1:L5:1445:C:H6	1.81	0.43
1:L5:1721:U:H5"	7:LF:104:LYS:HG2	1.99	0.43
1:L5:2381:G:H2'	1:L5:2382:C:C6	2.52	0.43
1:L5:2543:A:H4'	1:L5:2544:U:O5'	2.18	0.43
1:L5:3710:A2M:HM'3	1:L5:3710:A2M:H1'	1.65	0.43
3:L8:33:G:H4'	3:L8:34:U:C5	2.53	0.43
3:L8:103:A:H3'	3:L8:104:A:H5"	2.01	0.43
19:LZ:23:ALA:HA	19:LZ:45:GLY:HA2	2.00	0.43
28:Li:50:PHE:CZ	28:Li:93:VAL:HG21	2.54	0.43
28:Li:63:VAL:O	28:Li:63:VAL:CG1	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lp:26:VAL:HG21	36:LA:180:LEU:HD11	2.01	0.43
36:LA:135:THR:CG2	36:LA:149:LYS:HE2	2.49	0.43
42:S2:496:C:P	47:SE:29:PRO:HD3	2.58	0.43
42:S2:1257:G:H4'	42:S2:1258:A:C5'	2.48	0.43
42:S2:1337:4AC:H5	42:S2:1337:4AC:HM73	2.01	0.43
42:S2:1369:A:H2'	42:S2:1370:A:O4'	2.19	0.43
42:S2:1395:C:H1'	42:S2:1474:A:C4	2.53	0.43
42:S2:1406:G:H2'	42:S2:1407:U:H6	1.81	0.43
42:S2:1862:G:H4'	42:S2:1863:A:OP1	2.19	0.43
59:SR:38:ILE:HG13	59:SR:39:ALA:N	2.34	0.43
68:Sa:22:ARG:HA	68:Sa:22:ARG:HD2	1.86	0.43
73:Sg:184:LEU:HD12	73:Sg:185:LYS:H	1.83	0.43
1:L5:2374:U:H2'	1:L5:2375:U:C6	2.53	0.43
1:L5:2601:A:C5'	1:L5:2678:G:H4'	2.43	0.43
1:L5:3644:C:H4'	36:LA:240:ALA:CB	2.49	0.43
1:L5:3827:OMC:HM22	1:L5:3828:C:O4'	2.19	0.43
1:L5:4336:C:C2	1:L5:4337:U:C5	3.06	0.43
1:L5:4488:C:C2'	1:L5:4489:A:H5'	2.49	0.43
5:LD:22:ARG:CB	5:LD:28:THR:HG22	2.42	0.43
5:LD:93:THR:O	5:LD:93:THR:HG22	2.17	0.43
19:LZ:36:ARG:HG2	19:LZ:38:TYR:CZ	2.54	0.43
23:Ld:36:VAL:HG21	23:Ld:44:ARG:HG2	2.00	0.43
35:Lr:33:LYS:HD2	35:Lr:40:TYR:CZ	2.53	0.43
42:S2:116:OMU:HM22	42:S2:117:C:O4'	2.19	0.43
42:S2:964:A:H1'	42:S2:1054:G:O2'	2.18	0.43
42:S2:1533:A:N7	42:S2:1604:G:H1'	2.32	0.43
42:S2:1811:C:H2'	42:S2:1812:U:C6	2.54	0.43
42:S2:1816:G:C3'	42:S2:1817:G:C5'	2.96	0.43
49:SG:136:LYS:O	49:SG:136:LYS:HG2	2.18	0.43
49:SG:145:PHE:HE2	49:SG:156:TYR:O	2.00	0.43
52:SJ:137:VAL:HG22	52:SJ:157:ILE:HG12	2.01	0.43
60:SS:5:ILE:HD11	60:SS:9:PHE:CD2	2.53	0.43
60:SS:117:ILE:O	60:SS:118:ARG:HB2	2.19	0.43
68:Sa:40:VAL:HB	68:Sa:69:VAL:CG2	2.35	0.43
1:L5:6:C:H5"	8:LG:197:LYS:HG2	2.00	0.43
1:L5:1690:C:O2'	1:L5:1691:U:H5'	2.19	0.43
1:L5:1799:G:N7	1:L5:1832:G:H2'	2.34	0.43
1:L5:1935:A:H2'	1:L5:1935:A:N3	2.34	0.43
1:L5:4536:G:C2'	1:L5:4537:U:H5'	2.48	0.43
2:L7:3:C:H2'	2:L7:4:U:C6	2.54	0.43
3:L8:14:OMU:HM23	3:L8:14:OMU:H1'	1.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:29:G:O2'	3:L8:30:U:H5'	2.19	0.43
3:L8:81:C:H2'	3:L8:82:A:H2'	2.01	0.43
4:LC:234:LYS:HE2	4:LC:234:LYS:HB2	1.74	0.43
8:LG:32:PHE:CE2	19:LZ:55:ALA:HA	2.53	0.43
8:LG:172:ALA:CB	28:Li:43:MET:HE1	2.48	0.43
12:LO:185:VAL:O	12:LO:189:ILE:HG23	2.19	0.43
34:Lp:79:VAL:O	34:Lp:83:ILE:HG12	2.19	0.43
39:LI:58:GLU:O	39:LI:129:VAL:HG12	2.18	0.43
42:S2:384:U:H5'	54:SL:133:PRO:O	2.19	0.43
42:S2:656:G:N2	42:S2:663:C:H5"	2.34	0.43
42:S2:853:C:C2	42:S2:854:A:C8	3.06	0.43
42:S2:932:G:H2'	42:S2:934:G:OP1	2.18	0.43
44:SB:38:MET:HE2	44:SB:185:VAL:HG11	2.01	0.43
44:SB:113:MET:HE1	44:SB:211:PHE:CE2	2.53	0.43
44:SB:125:VAL:HG13	44:SB:169:MET:HG2	2.00	0.43
45:SC:75:ILE:CD1	45:SC:265:PRO:HB3	2.49	0.43
45:SC:102:LEU:HD13	45:SC:130:ILE:HD11	2.00	0.43
45:SC:206:SER:CB	45:SC:224:THR:HG21	2.49	0.43
53:SK:49:MET:HG3	53:SK:69:TRP:CZ3	2.53	0.43
59:SR:11:LYS:O	59:SR:15:VAL:HG23	2.18	0.43
64:SW:26:LEU:HD11	64:SW:60:LYS:HB3	2.00	0.43
75:LR:19:LYS:HB2	75:LR:19:LYS:HE2	1.68	0.43
75:LR:82:LYS:HA	75:LR:82:LYS:HD2	1.84	0.43
1:L5:480:C:OP2	35:Lr:67:ARG:HD3	2.18	0.43
1:L5:508:G:H2'	1:L5:510:U:OP2	2.18	0.43
1:L5:750:U:H1'	1:L5:911:A:N7	2.34	0.43
1:L5:2723:C:O2'	1:L5:2724:U:H5'	2.19	0.43
1:L5:3632:A:H4'	1:L5:3633:A:C5'	2.49	0.43
1:L5:5023:A:H2'	1:L5:5024:U:O4'	2.19	0.43
3:L8:6:C:H2'	3:L8:7:U:C6	2.54	0.43
14:LQ:69:LYS:O	14:LQ:75:ARG:HD2	2.19	0.43
14:LQ:70:MET:SD	14:LQ:80:ALA:HB2	2.59	0.43
36:LA:101:VAL:C	36:LA:102:LEU:HD12	2.44	0.43
41:LS:43:ARG:HA	41:LS:43:ARG:HD2	1.74	0.43
42:S2:1303:C:O2	42:S2:1303:C:O4'	2.37	0.43
42:S2:1487:A:C2'	42:S2:1488:C:H5'	2.49	0.43
42:S2:1736:G:H2'	42:S2:1737:G:H8	1.83	0.43
42:S2:1817:G:H2'	42:S2:1818:A:C8	2.54	0.43
54:SL:8:ARG:CG	54:SL:8:ARG:NH1	2.82	0.43
64:SW:30:CYS:SG	64:SW:31:SER:N	2.92	0.43
1:L5:110:C:O2'	1:L5:111:C:H5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1079:C:H2'	1:L5:1080:C:C6	2.54	0.43
1:L5:1554:A:OP1	75:LR:125:LEU:HD13	2.19	0.43
1:L5:2628:G:H8	26:Lg:26:PRO:O	2.02	0.43
1:L5:4412:C:H2'	1:L5:4413:G:O4'	2.18	0.43
1:L5:4557:A2M:H2'	1:L5:4558:U:C5	2.52	0.43
5:LD:272:SER:O	5:LD:276:LYS:HG3	2.19	0.43
6:LE:131:LYS:HB2	6:LE:131:LYS:HE2	1.80	0.43
13:LP:140:MET:HE3	13:LP:140:MET:HB3	1.90	0.43
28:Li:2:ALA:N	40:LL:173:GLU:HA	2.34	0.43
28:Li:86:LYS:O	28:Li:90:LEU:HG	2.19	0.43
30:Lk:27:LYS:CB	30:Lk:32:VAL:HG22	2.49	0.43
36:LA:149:LYS:HB3	36:LA:149:LYS:HE2	1.70	0.43
40:LL:55:ILE:HD12	40:LL:154:VAL:HG12	2.01	0.43
42:S2:69:C:H3'	42:S2:70:G:H8	1.82	0.43
42:S2:163:U:O3'	49:SG:83:CYS:HA	2.19	0.43
42:S2:424:C:C2'	42:S2:425:G:H5'	2.49	0.43
42:S2:487:U:O2	42:S2:512:A2M:H2	2.19	0.43
42:S2:667:PSU:O5'	42:S2:667:PSU:O4	2.37	0.43
42:S2:1043:G:O2'	42:S2:1044:G:H5'	2.19	0.43
42:S2:1232:PSU:H2'	42:S2:1233:G:H8	1.82	0.43
42:S2:1257:G:H4'	42:S2:1258:A:O5'	2.18	0.43
44:SB:168:MET:HG2	44:SB:197:ILE:HG21	2.01	0.43
51:SI:80:ASP:OD1	51:SI:80:ASP:N	2.52	0.43
73:Sg:14:HIS:CE1	73:Sg:41:ILE:HG13	2.54	0.43
73:Sg:43:TRP:CZ3	73:Sg:55:PRO:HG3	2.53	0.43
1:L5:240:G:H2'	1:L5:241:G:O4'	2.18	0.43
1:L5:308:G:H1'	28:Li:31:GLY:O	2.19	0.43
1:L5:324:A:O2'	1:L5:325:U:H5'	2.18	0.43
1:L5:1718:C:H2'	1:L5:1719:A:C8	2.54	0.43
1:L5:2437:U:O2'	1:L5:2438:G:H5'	2.19	0.43
1:L5:2665:G:C6	22:Lc:30:GLY:HA3	2.54	0.43
1:L5:4670:A:H2'	1:L5:4671:U:O4'	2.19	0.43
13:LP:3:ARG:HB3	13:LP:3:ARG:NH1	2.34	0.43
16:LU:25:CYS:C	16:LU:28:PRO:HD2	2.44	0.43
18:LY:58:VAL:HG22	18:LY:103:LYS:O	2.19	0.43
18:LY:71:VAL:CG1	18:LY:83:GLU:HG2	2.49	0.43
21:Lb:43:MET:HE3	21:Lb:47:LYS:NZ	2.34	0.43
24:Le:19:LYS:HE3	24:Le:19:LYS:HB3	1.82	0.43
34:Lp:85:ARG:CB	42:S2:939:U:C5'	2.97	0.43
39:LI:60:LEU:HD12	39:LI:91:LEU:CD1	2.49	0.43
41:LS:93:MET:HE1	41:LS:117:HIS:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:1608:U:H2'	42:S2:1609:C:O4'	2.19	0.43
43:SA:112:ILE:C	43:SA:112:ILE:HD12	2.44	0.43
44:SB:133:TYR:CE2	44:SB:221:PRO:HD2	2.54	0.43
47:SE:101:LEU:HD23	47:SE:101:LEU:HA	1.85	0.43
49:SG:181:THR:HG23	49:SG:182:PRO:CD	2.47	0.43
58:SQ:82:TYR:HA	58:SQ:85:ARG:CD	2.49	0.43
59:SR:5:ARG:HB2	59:SR:10:LYS:HE2	2.01	0.43
59:SR:6:THR:CG2	59:SR:7:LYS:N	2.81	0.43
1:L5:10:A:H2'	1:L5:11:G:H8	1.84	0.43
1:L5:1904:A:C2'	1:L5:1905:G:H5'	2.49	0.43
1:L5:2459:C:O2	1:L5:2459:C:C2'	2.67	0.43
1:L5:2686:A:H62	30:Lk:35:LYS:NZ	2.17	0.43
83:L5:6056:HOH:O	2:L7:100:A:H1'	2.18	0.43
2:L7:115:A:C2'	2:L7:116:G:H5'	2.49	0.43
8:LG:193:LEU:HD23	8:LG:193:LEU:HA	1.91	0.43
13:LP:117:ILE:HD12	13:LP:148:MET:HE2	1.99	0.43
16:LU:48:LYS:HA	16:LU:52:LYS:O	2.19	0.43
42:S2:17:C:H2'	42:S2:18:C:C6	2.54	0.43
42:S2:80:G:C2'	42:S2:81:U:H5'	2.49	0.43
42:S2:394:G:H5'	54:SL:81:LYS:CB	2.48	0.43
42:S2:517:OMC:H2'	42:S2:518:G:O4'	2.19	0.43
42:S2:560:A:H2'	42:S2:561:A:H5'	2.01	0.43
42:S2:1314:U:H3'	42:S2:1314:U:O2	2.19	0.43
42:S2:1807:C:H2'	42:S2:1808:U:C6	2.54	0.43
47:SE:18:TRP:HH2	47:SE:31:PRO:HD3	1.84	0.43
51:SI:63:GLY:HA3	51:SI:185:ALA:O	2.18	0.43
62:SU:87:ARG:O	62:SU:88:LEU:HD12	2.19	0.43
67:SZ:70:PRO:CD	67:SZ:107:VAL:HG13	2.49	0.43
68:Sa:11:ALA:O	68:Sa:33:ASP:HB2	2.19	0.43
1:L5:398:A2M:O5'	1:L5:398:A2M:H8	2.19	0.42
1:L5:457:G:H5'	6:LE:115:TYR:HB3	2.01	0.42
1:L5:685:C:H5'	6:LE:101:ASN:OD1	2.19	0.42
1:L5:1460:C:H5'	83:L5:5359:HOH:O	2.19	0.42
1:L5:1641:C:H2'	1:L5:1642:A:C8	2.54	0.42
1:L5:3845:G:H4'	13:LP:139:TYR:CE1	2.54	0.42
1:L5:4306:G:H2'	1:L5:4307:U:C6	2.54	0.42
1:L5:4670:A:C2'	1:L5:4671:U:H5'	2.49	0.42
4:LC:13:GLU:HA	4:LC:170:LEU:CD1	2.49	0.42
7:LF:96:ARG:HB2	7:LF:139:TYR:CD2	2.54	0.42
12:LO:61:ARG:HA	12:LO:70:PRO:HD2	2.01	0.42
12:LO:74:ARG:O	12:LO:142:ALA:HB1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LU:21:PHE:CD1	16:LU:108:GLU:HA	2.53	0.42
18:LY:103:LYS:HA	18:LY:103:LYS:HD3	1.86	0.42
36:LA:83:HIS:CE1	36:LA:86:GLN:HB2	2.54	0.42
41:LS:159:LEU:HD12	41:LS:160:ARG:N	2.33	0.42
42:S2:1397:U:O4	58:SQ:12:VAL:HA	2.19	0.42
42:S2:1477:U:C2'	42:S2:1478:U:H5'	2.48	0.42
42:S2:1490:OMG:HM23	42:S2:1490:OMG:H1'	1.54	0.42
47:SE:104:ASP:HB3	47:SE:110:ALA:HB2	2.01	0.42
48:SF:86:LYS:HA	48:SF:89:THR:OG1	2.19	0.42
53:SK:1:MET:HE1	53:SK:43:LEU:CD2	2.49	0.42
1:L5:482:G:C2	1:L5:485:C:C4	3.07	0.42
1:L5:679:C:H2'	1:L5:680:G:H8	1.83	0.42
1:L5:726:G:H2'	1:L5:727:C:C6	2.54	0.42
1:L5:972:G:H2'	1:L5:973:C:H6	1.84	0.42
1:L5:1081:A:H2'	1:L5:1082:C:C6	2.54	0.42
1:L5:1294:C:H2'	1:L5:1295:G:C8	2.53	0.42
1:L5:1807:G:H2'	1:L5:1808:C:C6	2.54	0.42
1:L5:1854:A:C2	1:L5:1855:C:C5	3.07	0.42
1:L5:2401:C:H2'	1:L5:2402:A:H8	1.84	0.42
1:L5:2510:C:O2	1:L5:2630:G:N2	2.52	0.42
1:L5:3590:A:H2'	1:L5:3591:C:C5'	2.49	0.42
1:L5:3622:C:C4'	1:L5:3811:A2M:H2	2.49	0.42
1:L5:4746:G:H2'	1:L5:4747:G:O4'	2.19	0.42
13:LP:3:ARG:HB3	13:LP:3:ARG:HH11	1.84	0.42
13:LP:33:ALA:HB1	13:LP:117:ILE:HG12	2.01	0.42
14:LQ:66:MET:HE1	14:LQ:86:ILE:HD13	2.01	0.42
38:LH:115:ARG:NH2	38:LH:123:ILE:HD13	2.34	0.42
42:S2:481:C:H2'	42:S2:482:G:C1'	2.49	0.42
42:S2:582:U:H1'	66:SY:33:ALA:HB2	2.02	0.42
42:S2:1021:U:H5"	55:SN:128:TYR:CE1	2.54	0.42
42:S2:1278:A:H2'	42:S2:1279:C:C6	2.54	0.42
42:S2:1344:A:O4'	42:S2:1345:G:H5'	2.20	0.42
42:S2:1453:C:C5	42:S2:1455:A:H1'	2.53	0.42
42:S2:1511:U:H2'	42:S2:1512:C:H6	1.84	0.42
47:SE:10:LYS:HD3	47:SE:10:LYS:HA	1.87	0.42
68:Sa:67:LEU:HD12	68:Sa:67:LEU:HA	1.85	0.42
1:L5:89:C:C2'	1:L5:90:G:H5'	2.49	0.42
1:L5:158:A:H5"	1:L5:159:C:H2'	2.00	0.42
1:L5:382:G:H4'	1:L5:407:A:N1	2.34	0.42
1:L5:445:U:O2	1:L5:445:U:O5'	2.37	0.42
1:L5:1728:C:C2'	1:L5:1729:G:H5'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2694:C:H5"	1:L5:2695:G:OP2	2.19	0.42
1:L5:3716:U:H2'	1:L5:3717:C:C6	2.55	0.42
1:L5:4390:U:H5	83:L5:7358:HOH:O	2.01	0.42
3:L8:51:U:O2'	3:L8:52:A:C8	2.72	0.42
5:LD:60:ILE:CG1	5:LD:93:THR:HA	2.49	0.42
6:LE:207:LYS:O	6:LE:207:LYS:CG	2.67	0.42
6:LE:207:LYS:O	6:LE:207:LYS:HG3	2.18	0.42
12:LO:185:VAL:O	12:LO:189:ILE:HG12	2.19	0.42
28:Li:18:THR:HG23	40:LL:107:THR:OG1	2.19	0.42
34:Lp:78:THR:HA	42:S2:938:A:OP1	2.18	0.42
41:LS:1:MET:HG3	41:LS:39:VAL:CG1	2.50	0.42
42:S2:349:A:H2'	42:S2:350:C:O4'	2.19	0.42
42:S2:468:A2M:HM'3	42:S2:468:A2M:H1'	1.75	0.42
42:S2:668:A2M:HM'3	42:S2:668:A2M:H1'	1.87	0.42
42:S2:1035:A:H2'	42:S2:1036:A:O4'	2.19	0.42
42:S2:1295:A:H2'	42:S2:1295:A:N3	2.34	0.42
43:SA:7:VAL:HG22	43:SA:191:ARG:HD2	2.02	0.42
46:SD:68:GLU:OE1	53:SK:70:TYR:HB3	2.18	0.42
66:SY:6:THR:CG2	66:SY:28:LEU:HD23	2.47	0.42
66:SY:57:VAL:HB	66:SY:60:PHE:HE2	1.84	0.42
77:LV:85[A]:ARG:HG2	77:LV:85[A]:ARG:HH11	1.83	0.42
1:L5:398:A2M:H1'	1:L5:398:A2M:HM'3	1.68	0.42
1:L5:426:A:H2'	1:L5:427:A:C8	2.54	0.42
1:L5:704:C:H2'	1:L5:706:C:OP2	2.19	0.42
1:L5:1823:C:O2'	1:L5:1824:C:H5'	2.20	0.42
1:L5:3605:G:H4'	75:LR:79:GLY:O	2.19	0.42
1:L5:4140:G:O2'	1:L5:4141:C:H5'	2.19	0.42
1:L5:4198:A:H4'	1:L5:4199:A:N3	2.34	0.42
1:L5:4926:G:O2'	1:L5:4927:C:H5'	2.18	0.42
2:L7:55:A:H4'	9:LJ:155:HIS:HB2	2.00	0.42
3:L8:110:U:C2	3:L8:112:G:H1'	2.53	0.42
10:LM:113:MET:HE2	10:LM:113:MET:HB3	1.87	0.42
42:S2:874:G:N3	42:S2:875:A:C8	2.87	0.42
42:S2:917:U:H2'	42:S2:918:PSU:C6	2.54	0.42
42:S2:1065:G:O2'	42:S2:1066:U:H5'	2.20	0.42
42:S2:1144:A:C2	42:S2:1199:A:H4'	2.54	0.42
42:S2:1212:G:N1	42:S2:1213:C:C4	2.88	0.42
42:S2:1397:U:O4'	42:S2:1442:OMU:H5"	2.19	0.42
42:S2:1513:C:H2'	42:S2:1514:G:H8	1.84	0.42
43:SA:198:MET:HG2	43:SA:200:ASP:HB2	2.02	0.42
45:SC:101:SER:CB	45:SC:132:ASP:HB2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:SE:137:PRO:HB2	47:SE:150:PRO:HD2	2.02	0.42
53:SK:9:ILE:HD12	53:SK:10:ALA:N	2.34	0.42
58:SQ:58:LEU:CD1	58:SQ:108:ILE:HG23	2.49	0.42
69:Sb:35:VAL:HG22	69:Sb:79:PHE:CB	2.49	0.42
73:Sg:106:LYS:HG3	73:Sg:126:ASP:HB3	2.01	0.42
1:L5:193:G:C2'	1:L5:194:C:H5'	2.49	0.42
1:L5:288:G:H2'	1:L5:289:C:C6	2.54	0.42
1:L5:447:C:C2'	1:L5:448:G:H5'	2.49	0.42
1:L5:1456:C:H5"	14:LQ:144:LYS:HG3	2.01	0.42
1:L5:1734:A:O2'	1:L5:1735:G:H5'	2.19	0.42
1:L5:2294:U:H4'	1:L5:2295:U:OP2	2.19	0.42
1:L5:2577:A:H3'	1:L5:2578:C:C6	2.54	0.42
1:L5:2680:C:H2'	1:L5:2681:U:O4'	2.19	0.42
1:L5:3788:U:O2	1:L5:4483:U:O2	2.38	0.42
1:L5:4439:C:O5'	1:L5:4439:C:H6	2.03	0.42
1:L5:4537:U:H2'	1:L5:4538:PSU:C6	2.55	0.42
1:L5:4614:PSU:H4'	78:LW:16:GLY:O	2.18	0.42
1:L5:4869:G:H2'	1:L5:4870:U:C6	2.54	0.42
5:LD:113:PHE:HE2	5:LD:142:PHE:CE1	2.37	0.42
11:LN:10:LEU:HD13	28:Li:48:CYS:SG	2.60	0.42
16:LU:47:ILE:O	16:LU:53:ALA:HA	2.19	0.42
42:S2:289:G:O2'	42:S2:290:U:H5'	2.20	0.42
42:S2:668:A2M:H2'	42:S2:668:A2M:H8	1.66	0.42
42:S2:878:G:H8	42:S2:878:G:O5'	2.02	0.42
42:S2:1405:A:H2'	42:S2:1406:G:O4'	2.20	0.42
42:S2:1732:G:H2'	42:S2:1733:U:O4'	2.20	0.42
42:S2:1798:C:H2'	42:S2:1799:G:O4'	2.19	0.42
64:SW:12:LYS:HA	64:SW:12:LYS:HD3	1.74	0.42
65:SX:41:PHE:HZ	65:SX:102:VAL:HG23	1.85	0.42
69:Sb:81:ARG:HE	69:Sb:81:ARG:HB3	1.63	0.42
72:Se:36:MET:HE2	72:Se:36:MET:HB3	1.95	0.42
77:LV:16:ILE:HD11	77:LV:56:GLY:HA3	2.02	0.42
1:L5:457:G:H5"	6:LE:115:TYR:HB3	2.01	0.42
1:L5:683:C:H2'	1:L5:684:G:O4'	2.20	0.42
1:L5:1083:G:H5'	15:LT:140:PHE:CE1	2.54	0.42
1:L5:1386:G:H1'	83:L5:6894:HOH:O	2.18	0.42
1:L5:1929:G:H2'	1:L5:1930:A:C8	2.55	0.42
1:L5:2645:C:O2'	1:L5:2646:U:H5'	2.19	0.42
1:L5:2851:OMC:H2'	1:L5:2852:G:O4'	2.19	0.42
1:L5:4075:G:C2'	1:L5:4076:G:H5'	2.50	0.42
1:L5:4179:C:C2'	1:L5:4180:U:H5'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4215:U:O2	1:L5:4215:U:H2'	2.19	0.42
2:L7:28:C:H2'	2:L7:28:C:O2	2.19	0.42
3:L8:155:C:H2'	3:L8:156:U:C5'	2.49	0.42
5:LD:239:MET:HE2	5:LD:240:TYR:CE1	2.54	0.42
40:LL:92:ARG:NH2	40:LL:98:VAL:HB	2.35	0.42
42:S2:1227:G:H2'	42:S2:1227:G:N3	2.35	0.42
42:S2:1438:A:H2'	42:S2:1439:A:H8	1.84	0.42
43:SA:112:ILE:HD12	43:SA:113:GLN:N	2.34	0.42
46:SD:140:GLY:HA3	46:SD:182:LEU:HD23	2.01	0.42
47:SE:161:GLN:HG2	47:SE:170:THR:OG1	2.19	0.42
49:SG:32:MET:SD	49:SG:54:GLY:HA2	2.59	0.42
58:SQ:82:TYR:HA	58:SQ:85:ARG:HD3	2.00	0.42
68:Sa:47:ALA:CA	68:Sa:50:VAL:HG23	2.47	0.42
73:Sg:230:LEU:HD23	73:Sg:230:LEU:N	2.34	0.42
1:L5:433:A:C2	1:L5:3853:A2M:H4'	2.55	0.42
1:L5:488:G:N2	1:L5:489:C:H1'	2.34	0.42
1:L5:648:G:H2'	1:L5:649:A:H8	1.81	0.42
1:L5:1875:C:C2'	1:L5:1876:G:H5'	2.50	0.42
1:L5:1899:G:OP1	25:Lf:87:LYS:HE3	2.20	0.42
1:L5:2345:G:C2'	1:L5:2346:U:H5'	2.50	0.42
1:L5:2779:A:H1'	31:Ll:45:ARG:HH22	1.83	0.42
1:L5:2805:A2M:H1'	1:L5:2805:A2M:HM'3	1.78	0.42
1:L5:3842:A:H5"	13:LP:83:TRP:O	2.20	0.42
1:L5:3920:G:H2'	1:L5:3921:C:C6	2.55	0.42
1:L5:4399:C:H2'	1:L5:4400:A:H5'	2.00	0.42
1:L5:4448:C:C2'	1:L5:4449:U:H5'	2.50	0.42
32:Lm:82:LEU:HD13	38:LH:95:VAL:HG22	2.02	0.42
36:LA:129:ALA:HB3	36:LA:132:ASN:OD1	2.20	0.42
42:S2:382:C:H2'	42:S2:383:G:H8	1.85	0.42
42:S2:473:A:H2'	42:S2:474:G:OP2	2.20	0.42
42:S2:509:OMG:OP1	52:SJ:2:PRO:HB3	2.19	0.42
42:S2:583:A:C2	42:S2:584:A:C5	3.07	0.42
42:S2:1374:C:O3'	42:S2:1464:C:O2	2.37	0.42
42:S2:1709:G:C2	42:S2:1710:C:C5	3.07	0.42
58:SQ:82:TYR:O	58:SQ:85:ARG:HG2	2.19	0.42
64:SW:86:LEU:HD12	64:SW:86:LEU:HA	1.80	0.42
65:SX:125:VAL:HG23	65:SX:130:LEU:HD13	2.00	0.42
66:SY:28:LEU:HD22	66:SY:28:LEU:N	2.34	0.42
1:L5:106:A:C2'	1:L5:107:G:H5'	2.50	0.42
1:L5:425:U:H4'	13:LP:6:LEU:HD11	2.01	0.42
1:L5:471:A:H2'	1:L5:472:C:H6	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:478:G:H2'	1:L5:479:G:H8	1.84	0.42
1:L5:651:C:O2'	1:L5:652:G:H5'	2.20	0.42
1:L5:705:G:H2'	1:L5:706:C:H6	1.84	0.42
1:L5:1071:C:OP1	1:L5:1209:C:H4'	2.19	0.42
1:L5:1270:A:H1'	1:L5:1271:G:H5"	2.01	0.42
1:L5:1818:U:H3'	1:L5:1818:U:OP2	2.20	0.42
1:L5:2418:A:H2'	1:L5:2418:A:N3	2.35	0.42
1:L5:3693:U:H2'	1:L5:3694:C:H6	1.85	0.42
1:L5:4155:G:H4'	1:L5:4157:C:C2	2.54	0.42
1:L5:4524:G:H2'	1:L5:4525:U:H6	1.85	0.42
3:L8:67:U:H2'	3:L8:68:G:H8	1.84	0.42
5:LD:196:ARG:O	5:LD:200:MET:HG2	2.20	0.42
6:LE:244:GLU:O	6:LE:248:ILE:HD12	2.19	0.42
10:LM:26:ALA:HB2	10:LM:77:TRP:HZ3	1.84	0.42
23:Ld:75:LYS:HB2	23:Ld:79:ASN:O	2.20	0.42
27:Lh:118:LYS:NZ	40:LL:48:PRO:HD3	2.35	0.42
28:Li:50:PHE:CG	28:Li:58:MET:HE1	2.55	0.42
37:LB:332:MET:HE1	37:LB:368:ILE:HD13	2.01	0.42
38:LH:8:GLN:HG3	38:LH:9:THR:H	1.85	0.42
42:S2:99:A2M:HM'3	42:S2:99:A2M:H1'	1.74	0.42
42:S2:601:OMG:HM23	42:S2:601:OMG:H1'	1.84	0.42
42:S2:680:G:H2'	42:S2:681:PSU:C6	2.55	0.42
42:S2:1108:G:C2'	42:S2:1109:C:H5"	2.50	0.42
42:S2:1222:G:H5"	48:SF:78:MET:HE1	2.01	0.42
42:S2:1398:G:H1'	73:Sg:63:SER:HB3	2.02	0.42
42:S2:1622:U:OP2	42:S2:1623:A:H1'	2.19	0.42
42:S2:1639:G7M:H2'	42:S2:1640:A:C8	2.55	0.42
43:SA:89:LYS:HA	43:SA:89:LYS:HD3	1.76	0.42
46:SD:161:GLY:O	46:SD:164:VAL:HG12	2.19	0.42
50:SH:121:THR:O	50:SH:125:VAL:HG23	2.20	0.42
59:SR:34:VAL:O	59:SR:38:ILE:HG12	2.20	0.42
65:SX:49:GLY:HA3	65:SX:72:VAL:CG1	2.50	0.42
73:Sg:172:LYS:HB3	73:Sg:191:HIS:O	2.19	0.42
1:L5:73:A:OP1	40:LL:106:SER:HB3	2.20	0.42
1:L5:357:U:OP1	3:L8:26:C:H4'	2.20	0.42
1:L5:417:G:N3	3:L8:16:G:C2	2.87	0.42
1:L5:690:C:O2'	1:L5:691:C:H5'	2.20	0.42
1:L5:1500:G:H2'	1:L5:1501:C:C6	2.55	0.42
1:L5:1547:C:H2'	1:L5:1548:G:C5'	2.49	0.42
1:L5:1744:U:O2'	1:L5:1745:A:H5'	2.19	0.42
1:L5:2861:A:H2'	1:L5:2862:C:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3700:G:H2'	1:L5:3701:PSU:O4'	2.20	0.42
1:L5:4488:C:H2'	1:L5:4489:A:C5'	2.50	0.42
3:L8:155:C:C3'	3:L8:156:U:H5"	2.50	0.42
10:LM:7:VAL:O	41:LS:151:LYS:HA	2.19	0.42
19:LZ:87:VAL:HG12	19:LZ:89:ILE:HG13	2.00	0.42
41:LS:44:PHE:CZ	41:LS:48:VAL:HG21	2.54	0.42
42:S2:26:U:H2'	42:S2:27:A2M:O4'	2.20	0.42
42:S2:848:U:H2'	42:S2:849:A:C8	2.54	0.42
42:S2:980:A:O2'	42:S2:981:A:O5'	2.32	0.42
42:S2:1208:A:H2'	42:S2:1209:A:C8	2.55	0.42
42:S2:1703:OMC:HM22	42:S2:1704:C:H5'	2.01	0.42
61:ST:124:THR:HG23	61:ST:125:PRO:CD	2.44	0.42
62:SU:90:ASP:C	62:SU:91:LEU:HD23	2.45	0.42
64:SW:2:VAL:HG23	64:SW:4:MET:HE2	2.01	0.42
78:LW:42:SER:OG	78:LW:44:ARG:HG3	2.20	0.42
1:L5:219:G:N2	1:L5:220:C:H41	2.18	0.42
1:L5:940:C:O2'	1:L5:941:C:H5'	2.19	0.42
1:L5:1821:A:H2'	1:L5:1822:G:C8	2.55	0.42
1:L5:2659:C:H2'	1:L5:2660:C:O4'	2.19	0.42
3:L8:78:G:O2'	27:Lh:42:SER:HA	2.20	0.42
3:L8:142:U:H2'	3:L8:143:G:O4'	2.20	0.42
5:LD:60:ILE:HD11	5:LD:93:THR:CA	2.43	0.42
5:LD:121:GLY:HA3	5:LD:168:ASP:O	2.20	0.42
10:LM:11:ARG:HG2	10:LM:57:LEU:HD22	2.01	0.42
11:LN:104:GLU:HA	11:LN:160:GLU:HG3	2.02	0.42
37:LB:223:THR:O	37:LB:274:TYR:HA	2.20	0.42
42:S2:1005:G:H2'	42:S2:1006:C:H6	1.85	0.42
42:S2:1012:A:H2'	42:S2:1013:U:O4'	2.20	0.42
42:S2:1212:G:H2'	42:S2:1212:G:N3	2.34	0.42
42:S2:1368:U:H3'	42:S2:1370:A:OP2	2.20	0.42
42:S2:1496:U:H4'	71:Sd:24:CYS:HB2	2.01	0.42
48:SF:100:ILE:HG13	48:SF:174:ALA:HB1	2.02	0.42
56:SO:37:PHE:CE1	56:SO:105:THR:HG21	2.55	0.42
64:SW:14:ILE:HD11	64:SW:27:ILE:CD1	2.48	0.42
66:SY:90:ARG:HA	66:SY:93:ARG:HD2	2.02	0.42
73:Sg:175:LYS:HD2	73:Sg:177:TRP:CZ2	2.55	0.42
1:L5:1469:U:H2'	1:L5:1470:C:C6	2.55	0.41
1:L5:1472:C:O2'	1:L5:1473:C:H5'	2.19	0.41
1:L5:3592:U:H5"	75:LR:76:MET:CE	2.50	0.41
1:L5:4146:C:H2'	1:L5:4147:G:C8	2.55	0.41
6:LE:118:THR:C	6:LE:119:GLU:HG3	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:LB:301:ASN:HA	37:LB:312:LYS:O	2.20	0.41
42:S2:931:C:H5'	42:S2:1104:G:OP1	2.20	0.41
42:S2:1213:C:O2'	42:S2:1214:A:H5'	2.19	0.41
42:S2:1466:G:H2'	42:S2:1467:C:H6	1.84	0.41
42:S2:1726:G:H2'	42:S2:1727:G:C8	2.54	0.41
43:SA:1:MET:O	43:SA:59:LEU:HD23	2.19	0.41
48:SF:153:LEU:HB3	48:SF:189:ALA:CB	2.50	0.41
68:Sa:41:ILE:HG23	68:Sa:68:TYR:CD2	2.55	0.41
73:Sg:152:SER:HB2	73:Sg:168:CYS:SG	2.60	0.41
73:Sg:170:TRP:CG	73:Sg:194:TYR:HB2	2.55	0.41
1:L5:268:G:H2'	1:L5:269:G:C8	2.55	0.41
1:L5:1578:PSU:O4	1:L5:1578:PSU:O4'	2.38	0.41
1:L5:1939:A:H2'	1:L5:1940:A:O4'	2.20	0.41
1:L5:2408:A:C5	1:L5:2409:C:C5	3.07	0.41
1:L5:2546:G:H2'	1:L5:2547:G:C8	2.55	0.41
1:L5:3840:C:O2'	1:L5:3841:C:H5'	2.21	0.41
1:L5:4331:C:H2'	1:L5:4332:U:C6	2.55	0.41
1:L5:4552:U:H2'	1:L5:4553:G:O4'	2.21	0.41
1:L5:4982:G:O2'	1:L5:4983:G:H5'	2.20	0.41
4:LC:157:LYS:HE2	4:LC:157:LYS:HB2	1.76	0.41
4:LC:266:THR:O	4:LC:278:ASN:OD1	2.38	0.41
9:LJ:15:LEU:HD23	9:LJ:15:LEU:HA	1.89	0.41
14:LQ:9:LYS:HB3	14:LQ:9:LYS:HE3	1.95	0.41
37:LB:93:VAL:HG12	37:LB:156:TYR:O	2.19	0.41
37:LB:201:LEU:HD23	37:LB:201:LEU:HA	1.94	0.41
37:LB:371:THR:HG23	37:LB:380:GLN:NE2	2.35	0.41
39:LI:33:ILE:HB	39:LI:69:ARG:NH1	2.35	0.41
42:S2:678:U:H2'	42:S2:679:A:O4'	2.20	0.41
42:S2:680:G:H2'	42:S2:681:PSU:H6	1.85	0.41
42:S2:809:A:H2'	42:S2:810:A:O4'	2.20	0.41
42:S2:1276:A:O2'	53:SK:51:SER:HA	2.20	0.41
50:SH:69:LEU:HD22	50:SH:96:ALA:CB	2.47	0.41
52:SJ:111:GLN:HG2	52:SJ:123:ILE:CD1	2.49	0.41
1:L5:25:A:C4	1:L5:26:C:C6	3.08	0.41
1:L5:1429:A:H3'	1:L5:1430:G:H8	1.85	0.41
1:L5:1478:G:H5'	1:L5:1479:C:C6	2.55	0.41
1:L5:1867:A2M:H1'	1:L5:4181:G:O6	2.20	0.41
1:L5:2716:G:H2'	1:L5:2717:C:H6	1.84	0.41
1:L5:3757:C:H3'	1:L5:3758:U:O2	2.20	0.41
25:Lf:22:ARG:N	25:Lf:22:ARG:HD3	2.35	0.41
37:LB:47:LEU:HG	37:LB:181:MET:SD	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:147:A:O2'	42:S2:148:U:H5'	2.20	0.41
42:S2:634:A:H2'	42:S2:635:G:C8	2.56	0.41
42:S2:674:C:O2	42:S2:1031:A2M:N1	2.53	0.41
42:S2:1320:G:H2'	42:S2:1321:G:O4'	2.19	0.41
42:S2:1425:G:H21	61:ST:5:THR:HG21	1.86	0.41
42:S2:1426:U:C2'	42:S2:1427:C:H5'	2.50	0.41
42:S2:1604:G:C2'	42:S2:1605:G:H5'	2.50	0.41
52:SJ:169:ARG:HB2	52:SJ:170:PRO:HD2	2.02	0.41
58:SQ:16:LYS:O	58:SQ:17:LYS:HB2	2.20	0.41
71:Sd:26:ASN:O	71:Sd:30:LEU:HD21	2.20	0.41
75:LR:95:TRP:CZ2	75:LR:99:MET:HE3	2.55	0.41
1:L5:37:U:H2'	1:L5:38:A:O4'	2.21	0.41
1:L5:420:A:C8	1:L5:421:C:C5	3.08	0.41
1:L5:1329:A:H2'	1:L5:1330:A:C8	2.55	0.41
1:L5:3879:C:H2'	1:L5:3880:A:C8	2.56	0.41
1:L5:4229:C:O2	1:L5:4229:C:H2'	2.20	0.41
2:L7:66:G:H2'	2:L7:67:C:H6	1.84	0.41
3:L8:93:C:O2'	3:L8:94:G:H8	2.03	0.41
4:LC:174:LEU:O	4:LC:175:LYS:HB2	2.20	0.41
4:LC:235:LEU:HD12	4:LC:264:TYR:OH	2.20	0.41
4:LC:347:HIS:O	4:LC:351:VAL:HG13	2.19	0.41
6:LE:63:TYR:CZ	6:LE:68:MET:HB2	2.55	0.41
7:LF:92:VAL:O	7:LF:120:GLY:HA2	2.20	0.41
10:LM:13:ALA:CB	10:LM:55:MET:HE2	2.50	0.41
29:Lj:67:LEU:HA	29:Lj:67:LEU:HD23	1.85	0.41
36:LA:141:PRO:CG	44:SB:219:LYS:HZ3	2.34	0.41
42:S2:1372:U:H2'	42:S2:1373:C:O4'	2.20	0.41
42:S2:1482:C:O2	42:S2:1482:C:O4'	2.38	0.41
42:S2:1652:G:C2'	42:S2:1653:U:H5'	2.51	0.41
48:SF:33:ILE:CA	48:SF:36:GLN:HG3	2.43	0.41
52:SJ:37:LEU:HB3	52:SJ:42:GLU:OE1	2.20	0.41
56:SO:47:LEU:HD23	56:SO:47:LEU:HA	1.90	0.41
63:SV:39:VAL:HA	63:SV:45:ARG:O	2.20	0.41
66:SY:76:TYR:CE2	66:SY:86:GLU:HG2	2.55	0.41
1:L5:229:G:H5"	18:LY:11:ARG:HG3	2.02	0.41
1:L5:269:G:H2'	1:L5:270:U:C6	2.55	0.41
1:L5:654:C:OP2	1:L5:654:C:H6	2.04	0.41
1:L5:1427:C:H2'	1:L5:1428:G:H5'	2.03	0.41
1:L5:2061:G:H2'	1:L5:2062:C:O4'	2.20	0.41
1:L5:2316:G:OP2	24:Le:101:HIS:HB2	2.20	0.41
1:L5:2431:C:H5'	83:L5:5339:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2620:U:O2'	1:L5:2622:PSU:H4'	2.20	0.41
1:L5:3869:U:H2'	1:L5:3870:PSU:C6	2.56	0.41
1:L5:4493:A:O2'	77:LV:41:SER:CB	2.68	0.41
3:L8:45:C:H2'	3:L8:46:G:H8	1.86	0.41
4:LC:29:LYS:HA	4:LC:29:LYS:HD2	1.75	0.41
13:LP:89:GLU:HA	13:LP:89:GLU:OE1	2.20	0.41
24:Le:4:LEU:HD13	24:Le:119:ALA:O	2.20	0.41
30:Lk:14:THR:O	30:Lk:17:ARG:HB2	2.21	0.41
34:Lp:85:ARG:CB	42:S2:939:U:C4'	2.99	0.41
37:LB:102:PHE:HE2	37:LB:152:SER:OG	2.03	0.41
42:S2:1265:A:H2	42:S2:1266:C:C6	2.38	0.41
42:S2:1334:G:O3'	46:SD:183:GLY:HA3	2.21	0.41
42:S2:1386:A:H2'	42:S2:1387:G:O4'	2.20	0.41
42:S2:1395:C:H1'	42:S2:1474:A:C5	2.56	0.41
44:SB:127:VAL:HG22	44:SB:128:LYS:N	2.36	0.41
57:SP:17:TYR:HB3	57:SP:25:LEU:HD11	2.03	0.41
66:SY:15:ASN:ND2	66:SY:18:LEU:HD12	2.35	0.41
66:SY:82:ALA:O	66:SY:86:GLU:HB2	2.21	0.41
77:LV:30:ASP:HA	77:LV:116:ALA:O	2.19	0.41
1:L5:138:G:H5"	27:Lh:98:HIS:CD2	2.55	0.41
1:L5:198:A:OP2	18:LY:126:ARG:NH2	2.52	0.41
1:L5:1327:C:H2'	1:L5:1328:C:C6	2.55	0.41
1:L5:1747:A:H2'	1:L5:1748:G:H8	1.84	0.41
1:L5:1904:A:H2'	1:L5:1905:G:H5'	2.02	0.41
1:L5:2079:C:OP2	14:LQ:14:ARG:NH2	2.53	0.41
1:L5:2414:OMG:H1'	1:L5:2414:OMG:HM23	1.59	0.41
1:L5:2722:G:H2'	1:L5:2723:C:C6	2.56	0.41
1:L5:3823:C:H2'	1:L5:3824:U:O4'	2.21	0.41
1:L5:3909:A:H2'	1:L5:3910:C:H6	1.84	0.41
1:L5:3918:U:H2'	1:L5:3919:G:C8	2.55	0.41
1:L5:4858:G:N7	12:LO:179:LYS:HE3	2.36	0.41
2:L7:3:C:H2'	2:L7:4:U:H6	1.85	0.41
15:LT:91:VAL:HG12	15:LT:92:ARG:O	2.21	0.41
16:LU:84:LYS:HG2	16:LU:88:LYS:HE2	2.02	0.41
17:LX:95:THR:HG23	17:LX:138:VAL:C	2.46	0.41
31:Ll:6:THR:OG1	31:Ll:9:ILE:HG12	2.21	0.41
38:LH:92:MET:HE2	38:LH:92:MET:HB3	1.96	0.41
42:S2:121:OMU:H6	42:S2:121:OMU:O5'	2.21	0.41
42:S2:1447:OMG:HM23	42:S2:1447:OMG:H1'	1.54	0.41
45:SC:125:LYS:HE3	45:SC:125:LYS:HB3	1.91	0.41
58:SQ:58:LEU:CD1	58:SQ:92:LEU:HD23	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SS:50:ILE:HD13	60:SS:50:ILE:HA	1.89	0.41
66:SY:50:THR:CG2	66:SY:55:ILE:HD11	2.51	0.41
68:Sa:12:LYS:HB2	68:Sa:33:ASP:OD2	2.20	0.41
75:LR:89:MET:HE3	75:LR:94:THR:OG1	2.21	0.41
1:L5:511:C:OP1	40:LL:165:LYS:HA	2.21	0.41
1:L5:1081:A:N1	1:L5:1203:U:C5	2.86	0.41
1:L5:1635:U:OP1	29:Lj:3:LYS:HE3	2.21	0.41
1:L5:3758:U:O2	1:L5:3758:U:O4'	2.38	0.41
1:L5:3834:U:H2'	1:L5:3835:A:H8	1.85	0.41
1:L5:3903:A:H2'	1:L5:3904:G:C8	2.54	0.41
1:L5:4870:U:C2'	1:L5:4871:C:H5'	2.51	0.41
1:L5:4878:A:H5'	10:LM:129:LYS:NZ	2.36	0.41
8:LG:197:LYS:HE2	8:LG:197:LYS:HB2	1.72	0.41
83:La:213:HOH:O	40:LL:2:ALA:HB2	2.21	0.41
23:Ld:57:MET:SD	23:Ld:90:ARG:HB2	2.61	0.41
37:LB:307:TYR:CD1	37:LB:307:TYR:N	2.88	0.41
39:LI:86:HIS:HB3	39:LI:139:ARG:CG	2.50	0.41
39:LI:99:ILE:HG21	39:LI:123:GLN:HG3	2.03	0.41
42:S2:861:A:C6	50:SH:106:ARG:HD2	2.55	0.41
42:S2:1081:U:O2	42:S2:1081:U:H2'	2.19	0.41
42:S2:1123:C:C4	42:S2:1124:C:C5	3.09	0.41
42:S2:1348:G:C8	42:S2:1349:G:C8	3.09	0.41
42:S2:1402:A:N1	42:S2:1405:A:C2	2.89	0.41
55:SN:129:TYR:HB3	55:SN:135:LEU:HG	2.02	0.41
62:SU:80:PHE:HB3	71:Sd:52:PHE:HB3	2.03	0.41
73:Sg:127:LYS:HG2	73:Sg:149:GLU:O	2.21	0.41
1:L5:165:A:H2'	1:L5:166:C:O4'	2.20	0.41
1:L5:231:U:O2'	18:LY:103:LYS:HE2	2.20	0.41
1:L5:745:G:H5"	1:L5:746:A:OP2	2.20	0.41
1:L5:1370:G:OP1	4:LC:120:LYS:HD2	2.21	0.41
1:L5:1597:A:C8	1:L5:3629:A:C8	3.08	0.41
1:L5:2257:U:H6	1:L5:2260:G:H4'	1.86	0.41
1:L5:2381:G:H2'	1:L5:2382:C:H6	1.86	0.41
1:L5:2718:U:H2'	1:L5:2719:C:C6	2.55	0.41
1:L5:3593:U:H2'	1:L5:3594:A:C8	2.56	0.41
1:L5:4105:C:O2	1:L5:4105:C:H2'	2.20	0.41
1:L5:4222:G:H4'	1:L5:4314:G:O2'	2.20	0.41
1:L5:4355:A:H4'	33:Lo:67:VAL:HG21	2.03	0.41
1:L5:4582:C:O2'	1:L5:4583:U:H5'	2.20	0.41
4:LC:316:LYS:HB2	4:LC:324:ILE:HG13	2.02	0.41
18:LY:74:TYR:CD1	18:LY:77:LYS:HG3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:LB:301:ASN:HB2	37:LB:311:ASP:HA	2.03	0.41
42:S2:634:A:H2'	42:S2:635:G:H8	1.86	0.41
42:S2:1391:OMC:HM23	42:S2:1391:OMC:H1'	1.87	0.41
42:S2:1395:C:C2'	42:S2:1396:A:H5'	2.51	0.41
42:S2:1587:G:C6	61:ST:67:NMM:HD3	2.56	0.41
43:SA:21:ALA:HB2	59:SR:91:LEU:HD13	2.03	0.41
47:SE:156:VAL:O	47:SE:157:ASN:HB2	2.20	0.41
48:SF:89:THR:O	48:SF:93:VAL:HG23	2.21	0.41
54:SL:40:ILE:HD11	54:SL:44:PHE:CB	2.51	0.41
66:SY:28:LEU:C	66:SY:30:PRO:HD3	2.46	0.41
78:LW:3:VAL:HG13	78:LW:13:ILE:C	2.45	0.41
1:L5:1922:C:O2'	1:L5:1923:U:H5'	2.21	0.41
1:L5:2262:C:O2'	1:L5:2263:G:H5'	2.21	0.41
1:L5:2740:G:H2'	1:L5:2741:G:O4'	2.21	0.41
1:L5:2776:C:H5"	1:L5:2777:A2M:O5'	2.21	0.41
1:L5:2801:G:H1'	1:L5:2805:A2M:H62	1.86	0.41
1:L5:3794:OMC:HM23	1:L5:3794:OMC:H1'	1.88	0.41
1:L5:3906:PSU:H2'	1:L5:3907:U:H6	1.86	0.41
1:L5:4245:C:C2	1:L5:4246:U:C5	3.09	0.41
1:L5:4289:C:O2'	1:L5:4290:A:H2'	2.20	0.41
1:L5:4460:A:H5"	32:Lm:125:LYS:HG3	2.03	0.41
1:L5:4493:A:H2'	1:L5:4494:C:H6	1.86	0.41
1:L5:4534:A:H5'	1:L5:4535:G:C5'	2.50	0.41
1:L5:4649:G:O2'	1:L5:4988:U:H4'	2.21	0.41
1:L5:4868:C:O5'	6:LE:273:SER:HA	2.21	0.41
1:L5:4991:U:H4'	1:L5:4992:A:C5'	2.51	0.41
3:L8:8:U:H2'	3:L8:9:A:C8	2.56	0.41
4:LC:150:LEU:HA	4:LC:151:PRO:C	2.45	0.41
4:LC:252:TRP:CH2	4:LC:260:LEU:HD11	2.55	0.41
5:LD:178:LYS:HE3	5:LD:179:ARG:NH2	2.36	0.41
6:LE:206:VAL:HG21	6:LE:257:ILE:HD13	2.02	0.41
8:LG:181:TYR:O	8:LG:222:ILE:HG23	2.21	0.41
13:LP:30:ARG:C	13:LP:30:ARG:HD3	2.46	0.41
16:LU:84:LYS:HG2	16:LU:88:LYS:CE	2.51	0.41
16:LU:100:LEU:HD12	16:LU:112:LEU:HB3	2.02	0.41
20:La:7:LYS:HB3	20:La:7:LYS:HE3	1.68	0.41
22:Lc:35:LEU:HD23	22:Lc:35:LEU:HA	1.96	0.41
28:Li:43:MET:HE3	28:Li:43:MET:HB3	1.87	0.41
31:Ll:9:ILE:O	31:Ll:13:LEU:HG	2.21	0.41
32:Lm:91:CYS:SG	38:LH:173:ARG:HG2	2.61	0.41
36:LA:242:ARG:HG3	36:LA:242:ARG:HH11	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:LH:40:HIS:ND1	38:LH:41:ILE:HG13	2.36	0.41
39:LI:152:LEU:CD1	39:LI:165:ILE:HG23	2.51	0.41
42:S2:5:U:H2'	42:S2:6:G:H8	1.85	0.41
42:S2:159:A2M:H2	42:S2:468:A2M:O4'	2.21	0.41
42:S2:160:U:C3'	42:S2:161:U:H5"	2.50	0.41
42:S2:176:U:H2'	42:S2:177:G:H8	1.83	0.41
42:S2:588:G:O4'	42:S2:590:A2M:H4'	2.20	0.41
42:S2:1199:A:H2'	42:S2:1200:A:C8	2.56	0.41
42:S2:1277:C:H2'	42:S2:1278:A:C8	2.47	0.41
42:S2:1562:C:H2'	42:S2:1563:G:H8	1.85	0.41
42:S2:1733:U:H2'	42:S2:1734:G:O4'	2.20	0.41
42:S2:1836:G:H4'	42:S2:1837:G:C4	2.56	0.41
42:S2:1854:U:P	56:SO:147:ARG:HH22	2.43	0.41
44:SB:220:LYS:HB3	44:SB:220:LYS:HE2	1.83	0.41
46:SD:25:LEU:CD1	46:SD:50:ILE:HG12	2.49	0.41
46:SD:54:ARG:O	46:SD:58:VAL:HG23	2.21	0.41
46:SD:110:LEU:HD13	46:SD:175:VAL:CG1	2.51	0.41
47:SE:181:CYS:SG	47:SE:210:VAL:HG21	2.61	0.41
47:SE:192:ILE:HD13	47:SE:238:LEU:CD1	2.50	0.41
48:SF:122:ARG:O	48:SF:141:VAL:HG23	2.21	0.41
51:SI:38:ILE:HA	51:SI:60:LEU:O	2.21	0.41
53:SK:11:ILE:HD11	53:SK:40:VAL:CG1	2.51	0.41
55:SN:33:VAL:HG21	55:SN:66:VAL:HG11	2.01	0.41
57:SP:34:MET:HE2	57:SP:45:LEU:HB3	2.02	0.41
59:SR:6:THR:HG23	59:SR:7:LYS:N	2.35	0.41
61:ST:134:ILE:O	61:ST:138:VAL:HG23	2.21	0.41
63:SV:74:LYS:HB2	63:SV:74:LYS:HE3	1.77	0.41
70:Sc:34:PHE:HE2	70:Sc:42:ILE:HG12	1.86	0.41
73:Sg:206:LEU:HD11	73:Sg:246:TYR:OH	2.20	0.41
1:L5:121:A:H5"	1:L5:122:U:OP2	2.21	0.41
1:L5:757:G:N3	1:L5:757:G:H2'	2.36	0.41
1:L5:1352:U:H2'	1:L5:1353:C:C6	2.56	0.41
1:L5:1455:A:O2'	14:LQ:143:ARG:HG3	2.21	0.41
1:L5:1491:G:C2'	1:L5:1492:G:H5'	2.51	0.41
1:L5:1843:C:H2'	1:L5:1844:C:C6	2.55	0.41
1:L5:3638:A:H2'	1:L5:3639:A:N7	2.36	0.41
1:L5:3694:C:C2'	1:L5:3695:U:H5'	2.51	0.41
1:L5:4463:A:C4	1:L5:4464:G:C8	3.09	0.41
1:L5:4489:A:H2'	1:L5:4490:C:O4'	2.21	0.41
1:L5:4713:A:H5'	37:LB:130:PHE:H	1.85	0.41
1:L5:5036:C:O3'	37:LB:324:GLY:HA2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LC:69:THR:HG22	4:LC:75:ARG:HD3	2.03	0.41
14:LQ:69:LYS:HD3	14:LQ:69:LYS:HA	1.71	0.41
37:LB:36:ASP:O	37:LB:187:GLY:HA2	2.21	0.41
38:LH:1:MET:HE3	38:LH:1:MET:HB2	1.83	0.41
38:LH:162:GLN:HG3	38:LH:179:ILE:O	2.21	0.41
42:S2:11:A:C2'	42:S2:12:U:H5'	2.50	0.41
42:S2:106:C:H2'	42:S2:107:A:H8	1.85	0.41
42:S2:910:G:H2'	42:S2:911:C:O4'	2.21	0.41
42:S2:1139:C:O2	42:S2:1139:C:O5'	2.39	0.41
46:SD:208:VAL:HG12	46:SD:210:ILE:HD12	2.03	0.41
48:SF:51:HIS:O	58:SQ:50:LYS:CE	2.68	0.41
65:SX:49:GLY:HA3	65:SX:72:VAL:HG12	2.02	0.41
69:Sb:8:LEU:HA	69:Sb:8:LEU:HD12	1.79	0.41
75:LR:135:LYS:HE2	75:LR:135:LYS:HB3	1.63	0.41
1:L5:1817:G:N3	1:L5:1817:G:C3'	2.78	0.40
1:L5:1820:G:H2'	1:L5:1821:A:C8	2.56	0.40
1:L5:1830:U:O2	15:LT:128:LEU:HD12	2.21	0.40
1:L5:2294:U:C4'	1:L5:2295:U:OP2	2.68	0.40
1:L5:2421:A:H2'	1:L5:2422:U:C6	2.56	0.40
1:L5:2665:G:C1'	1:L5:2666:A:OP2	2.69	0.40
1:L5:4056:U:H6	1:L5:4056:U:P	2.44	0.40
1:L5:4310:A:O2'	1:L5:4311:A:H5'	2.21	0.40
1:L5:4316:G:O2'	1:L5:4317:G:H5'	2.21	0.40
1:L5:4670:A:H2'	1:L5:4671:U:H5'	2.03	0.40
3:L8:44:A:O2'	3:L8:45:C:H5'	2.21	0.40
3:L8:77:A:H2'	3:L8:78:G:O4'	2.21	0.40
41:LS:74:ARG:HG2	41:LS:74:ARG:NH1	2.36	0.40
42:S2:120:U:H2'	42:S2:121:OMU:C6	2.52	0.40
42:S2:1626:C:H2'	42:S2:1627:C:H6	1.87	0.40
42:S2:1658:G:H2'	42:S2:1659:U:O4'	2.21	0.40
44:SB:83:LYS:HE2	44:SB:83:LYS:HB2	1.84	0.40
49:SG:159:ARG:HH11	49:SG:171:THR:HG22	1.86	0.40
53:SK:42:ASN:O	53:SK:46:MET:HG3	2.21	0.40
57:SP:72:LYS:HA	57:SP:73:PRO:HD3	1.93	0.40
65:SX:130:LEU:HD12	65:SX:130:LEU:HA	1.95	0.40
77:LV:91:LYS:HA	77:LV:91:LYS:HD3	1.92	0.40
1:L5:245:C:H5"	1:L5:246:G:O5'	2.21	0.40
1:L5:1293:U:C2	1:L5:1294:C:C6	3.10	0.40
1:L5:2559:G:H2'	1:L5:2560:U:H5'	2.02	0.40
1:L5:3601:G:H1'	78:LW:44:ARG:CD	2.48	0.40
1:L5:3621:A:N6	34:Lp:18:TYR:HA	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4331:C:H2'	1:L5:4332:U:H6	1.86	0.40
1:L5:4377:G:O2'	1:L5:4378:OMG:H5'	2.21	0.40
1:L5:4744:U:O2	1:L5:4744:U:O4'	2.39	0.40
1:L5:4936:G:H2'	1:L5:4937:G:C8	2.53	0.40
3:L8:77:A:H2'	3:L8:78:G:C8	2.56	0.40
7:LF:94:ARG:CZ	7:LF:109:LEU:HD13	2.51	0.40
11:LN:200:LEU:HD23	11:LN:200:LEU:HA	1.91	0.40
12:LO:28:LEU:HD23	12:LO:28:LEU:HA	1.92	0.40
12:LO:156:LEU:CD1	37:LB:96:PRO:HD3	2.51	0.40
39:LI:152:LEU:HD12	39:LI:165:ILE:CG2	2.51	0.40
42:S2:351:G:C2	42:S2:352:U:C6	3.09	0.40
42:S2:1019:C:H2'	42:S2:1020:A:O4'	2.22	0.40
42:S2:1094:C:O2'	42:S2:1095:C:H5'	2.21	0.40
42:S2:1238:PSU:C2'	42:S2:1239:U:H5'	2.52	0.40
42:S2:1650:A:H2'	42:S2:1651:A:O4'	2.21	0.40
43:SA:7:VAL:HG22	43:SA:7:VAL:O	2.21	0.40
53:SK:49:MET:HA	53:SK:49:MET:CE	2.45	0.40
58:SQ:47:LEU:O	58:SQ:50:LYS:HB2	2.21	0.40
59:SR:30:THR:O	59:SR:34:VAL:HG23	2.22	0.40
73:Sg:121:VAL:HG23	73:Sg:131:LEU:HD22	2.03	0.40
1:L5:53:C:O3'	1:L5:2452:C:H1'	2.21	0.40
1:L5:1080:C:O2'	1:L5:1081:A:H5'	2.21	0.40
1:L5:1501:C:O2'	1:L5:1502:G:H5'	2.22	0.40
1:L5:1555:G:C2'	1:L5:1556:A:H5'	2.51	0.40
1:L5:1626:A:H2	1:L5:3624:G:N3	2.18	0.40
1:L5:2560:U:H2'	1:L5:2561:C:C5	2.55	0.40
1:L5:2848:A:H2'	1:L5:2849:G:O4'	2.21	0.40
1:L5:4446:U:H2'	1:L5:4447:C:C6	2.56	0.40
4:LC:78:ARG:HA	4:LC:89:GLN:O	2.21	0.40
18:LY:80:ILE:HD11	18:LY:82:ILE:HD11	2.04	0.40
23:Ld:68:LEU:HD11	23:Ld:84:ILE:HD11	2.03	0.40
37:LB:163:ILE:CG2	37:LB:180:LEU:HD21	2.52	0.40
42:S2:494:C:N4	42:S2:509:OMG:HN22	2.18	0.40
42:S2:1134:G:H2'	42:S2:1135:C:H6	1.86	0.40
42:S2:1212:G:C2	42:S2:1213:C:C5	3.09	0.40
42:S2:1567:G:H21	42:S2:1628:C:H4'	1.86	0.40
42:S2:1863:A:H1'	68:Sa:79:ILE:HD13	2.03	0.40
44:SB:41:ILE:HD13	44:SB:73:ASP:O	2.21	0.40
46:SD:101:GLN:HG3	46:SD:126:ILE:HG12	2.04	0.40
50:SH:134:VAL:O	50:SH:135:PHE:C	2.64	0.40
54:SL:82:MET:HE3	54:SL:82:MET:HB2	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SQ:53:GLU:O	58:SQ:57:LEU:HG	2.22	0.40
58:SQ:89:SER:HB3	58:SQ:112:LEU:HD13	2.03	0.40
65:SX:36:LEU:HD22	65:SX:36:LEU:HA	1.92	0.40
73:Sg:91:ASP:HB2	73:Sg:98:THR:HG21	2.03	0.40
73:Sg:121:VAL:HG13	73:Sg:154:VAL:HG13	2.03	0.40
77:LV:100:ASP:OD1	77:LV:100:ASP:C	2.63	0.40
1:L5:920:G:H2'	1:L5:921:G:H8	1.87	0.40
1:L5:925:C:O5'	1:L5:925:C:H6	2.04	0.40
1:L5:1208:C:O5'	1:L5:1208:C:H6	2.05	0.40
1:L5:1453:G:O2'	1:L5:1454:C:H5'	2.21	0.40
1:L5:1471:G:N2	1:L5:1486:G:C5	2.90	0.40
1:L5:2603:C:O2'	1:L5:2604:C:H5'	2.21	0.40
1:L5:2652:G:H2'	1:L5:2653:G:O4'	2.22	0.40
1:L5:3621:A:H2'	1:L5:3622:C:H5'	2.03	0.40
4:LC:101:MET:HE2	4:LC:102:PHE:O	2.22	0.40
4:LC:312:ARG:HG3	4:LC:312:ARG:HH11	1.87	0.40
5:LD:90:VAL:HG21	5:LD:226:TYR:CD2	2.56	0.40
14:LQ:147:GLU:O	14:LQ:147:GLU:HG3	2.19	0.40
19:LZ:105:ALA:HA	19:LZ:108:ARG:NH1	2.35	0.40
24:Le:84:GLU:O	24:Le:87:VAL:HG22	2.22	0.40
28:Li:51:ALA:HB1	28:Li:52:PRO:HD2	2.03	0.40
42:S2:853:C:C2'	42:S2:854:A:H5'	2.52	0.40
42:S2:933:G:H1'	42:S2:1001:A:O4'	2.21	0.40
42:S2:1383:A2M:H2'	42:S2:1384:C:H6	1.85	0.40
43:SA:176:TRP:CE3	43:SA:177:MET:HG2	2.57	0.40
72:Se:8:ARG:HE	72:Se:8:ARG:HB2	1.77	0.40
73:Sg:121:VAL:HG23	73:Sg:131:LEU:CD2	2.52	0.40
1:L5:1458:A:C4'	21:Lb:27:GLN:HE21	2.35	0.40
1:L5:3735:C:H4'	36:LA:221:LYS:O	2.22	0.40
1:L5:3829:C:H4'	1:L5:3830:PSU:OP1	2.20	0.40
2:L7:57:C:H2'	2:L7:58:A:H8	1.86	0.40
3:L8:18:U:H2'	3:L8:19:C:H6	1.86	0.40
6:LE:91:THR:HB	6:LE:106:VAL:HG12	2.03	0.40
6:LE:144:ILE:HG12	6:LE:196:ALA:HB2	2.03	0.40
8:LG:218:LEU:O	8:LG:222:ILE:HD13	2.21	0.40
14:LQ:72:LEU:O	14:LQ:75:ARG:HG3	2.22	0.40
33:Lo:66:ILE:HG13	33:Lo:88:CYS:SG	2.62	0.40
36:LA:101:VAL:HG22	36:LA:165:VAL:HG22	2.04	0.40
42:S2:96:C:H2'	42:S2:97:U:H6	1.87	0.40
42:S2:429:C:H4'	47:SE:12:VAL:CG1	2.52	0.40
42:S2:607:U:H3	46:SD:144:GLY:N	2.19	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S2:1177:PSU:H2'	42:S2:1178:U:H6	1.85	0.40
47:SE:71:LYS:HD3	47:SE:76:VAL:HG23	2.02	0.40
48:SF:47:LYS:HA	48:SF:47:LYS:HD3	1.98	0.40
49:SG:28:TYR:HE1	49:SG:103:ASP:C	2.30	0.40
55:SN:102:LEU:HD11	55:SN:112:LYS:HA	2.03	0.40
58:SQ:58:LEU:HD23	58:SQ:58:LEU:HA	1.91	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LC	350/427 (82%)	345 (99%)	5 (1%)	0	100	100
5	LD	281/297 (95%)	276 (98%)	5 (2%)	0	100	100
6	LE	204/288 (71%)	199 (98%)	5 (2%)	0	100	100
7	LF	216/248 (87%)	209 (97%)	7 (3%)	0	100	100
8	LG	203/266 (76%)	197 (97%)	6 (3%)	0	100	100
9	LJ	39/178 (22%)	39 (100%)	0	0	100	100
10	LM	130/215 (60%)	127 (98%)	3 (2%)	0	100	100
11	LN	201/204 (98%)	198 (98%)	3 (2%)	0	100	100
12	LO	196/203 (97%)	195 (100%)	1 (0%)	0	100	100
13	LP	150/184 (82%)	148 (99%)	2 (1%)	0	100	100
14	LQ	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
15	LT	144/160 (90%)	142 (99%)	2 (1%)	0	100	100
16	LU	91/128 (71%)	83 (91%)	8 (9%)	0	100	100
17	LX	115/156 (74%)	113 (98%)	2 (2%)	0	100	100
18	LY	126/145 (87%)	122 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	LZ	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
20	La	140/148 (95%)	132 (94%)	7 (5%)	1 (1%)	18	19
21	Lb	80/159 (50%)	79 (99%)	1 (1%)	0	100	100
22	Lc	87/115 (76%)	83 (95%)	4 (5%)	0	100	100
23	Ld	93/125 (74%)	92 (99%)	1 (1%)	0	100	100
24	Le	124/135 (92%)	122 (98%)	2 (2%)	0	100	100
25	Lf	105/110 (96%)	105 (100%)	0	0	100	100
26	Lg	99/117 (85%)	96 (97%)	3 (3%)	0	100	100
27	Lh	119/123 (97%)	118 (99%)	1 (1%)	0	100	100
28	Li	90/105 (86%)	88 (98%)	2 (2%)	0	100	100
29	Lj	84/97 (87%)	84 (100%)	0	0	100	100
30	Lk	60/70 (86%)	56 (93%)	4 (7%)	0	100	100
31	Ll	47/51 (92%)	46 (98%)	1 (2%)	0	100	100
32	Lm	46/128 (36%)	46 (100%)	0	0	100	100
33	Lo	91/106 (86%)	87 (96%)	4 (4%)	0	100	100
34	Lp	85/92 (92%)	80 (94%)	5 (6%)	0	100	100
35	Lr	116/137 (85%)	116 (100%)	0	0	100	100
36	LA	243/257 (95%)	228 (94%)	15 (6%)	0	100	100
37	LB	386/403 (96%)	372 (96%)	14 (4%)	0	100	100
38	LH	174/192 (91%)	173 (99%)	1 (1%)	0	100	100
39	LI	191/214 (89%)	186 (97%)	5 (3%)	0	100	100
40	LL	186/211 (88%)	181 (97%)	5 (3%)	0	100	100
41	LS	166/176 (94%)	164 (99%)	2 (1%)	0	100	100
43	SA	203/295 (69%)	198 (98%)	5 (2%)	0	100	100
44	SB	197/264 (75%)	192 (98%)	5 (2%)	0	100	100
45	SC	210/293 (72%)	202 (96%)	8 (4%)	0	100	100
46	SD	202/243 (83%)	198 (98%)	4 (2%)	0	100	100
47	SE	255/263 (97%)	250 (98%)	5 (2%)	0	100	100
48	SF	174/204 (85%)	168 (97%)	6 (3%)	0	100	100
49	SG	171/249 (69%)	168 (98%)	3 (2%)	0	100	100
50	SH	132/194 (68%)	129 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	SI	165/208 (79%)	158 (96%)	7 (4%)	0	100	100
52	SJ	176/194 (91%)	171 (97%)	5 (3%)	0	100	100
53	SK	88/165 (53%)	84 (96%)	4 (4%)	0	100	100
54	SL	128/158 (81%)	124 (97%)	4 (3%)	0	100	100
55	SN	140/151 (93%)	132 (94%)	8 (6%)	0	100	100
56	SO	120/151 (80%)	117 (98%)	3 (2%)	0	100	100
57	SP	110/145 (76%)	110 (100%)	0	0	100	100
58	SQ	138/146 (94%)	132 (96%)	6 (4%)	0	100	100
59	SR	113/135 (84%)	109 (96%)	4 (4%)	0	100	100
60	SS	137/152 (90%)	134 (98%)	3 (2%)	0	100	100
61	ST	139/145 (96%)	136 (98%)	3 (2%)	0	100	100
62	SU	79/119 (66%)	77 (98%)	2 (2%)	0	100	100
63	SV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
64	SW	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
65	SX	137/143 (96%)	135 (98%)	2 (2%)	0	100	100
66	SY	113/133 (85%)	113 (100%)	0	0	100	100
67	SZ	68/125 (54%)	67 (98%)	1 (2%)	0	100	100
68	Sa	96/115 (84%)	93 (97%)	3 (3%)	0	100	100
69	Sb	53/84 (63%)	52 (98%)	1 (2%)	0	100	100
70	Sc	49/69 (71%)	49 (100%)	0	0	100	100
71	Sd	43/56 (77%)	42 (98%)	1 (2%)	0	100	100
72	Se	41/98 (42%)	40 (98%)	1 (2%)	0	100	100
73	Sg	266/310 (86%)	253 (95%)	13 (5%)	0	100	100
74	Ln	23/25 (92%)	23 (100%)	0	0	100	100
75	LR	152/196 (78%)	150 (99%)	2 (1%)	0	100	100
77	LV	129/140 (92%)	128 (99%)	1 (1%)	0	100	100
78	LW	59/157 (38%)	57 (97%)	2 (3%)	0	100	100
All	All	10090/12432 (81%)	9836 (98%)	253 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	La	15	VAL

5.3.2 Protein sidechains (i)

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	
4	LC	285/348 (82%)	280 (98%)	5 (2%)	51	68
5	LD	230/250 (92%)	225 (98%)	5 (2%)	45	61
6	LE	182/252 (72%)	179 (98%)	3 (2%)	55	71
7	LF	178/215 (83%)	176 (99%)	2 (1%)	65	79
8	LG	140/223 (63%)	137 (98%)	3 (2%)	47	63
9	LJ	29/149 (20%)	29 (100%)	0	100	100
10	LM	109/161 (68%)	106 (97%)	3 (3%)	38	52
11	LN	171/172 (99%)	170 (99%)	1 (1%)	78	89
12	LO	158/174 (91%)	154 (98%)	4 (2%)	42	56
13	LP	127/163 (78%)	126 (99%)	1 (1%)	73	85
14	LQ	155/165 (94%)	154 (99%)	1 (1%)	78	89
15	LT	120/140 (86%)	119 (99%)	1 (1%)	73	85
16	LU	44/115 (38%)	42 (96%)	2 (4%)	24	33
17	LX	91/133 (68%)	91 (100%)	0	100	100
18	LY	102/135 (76%)	98 (96%)	4 (4%)	28	39
19	LZ	101/118 (86%)	99 (98%)	2 (2%)	48	64
20	La	109/120 (91%)	109 (100%)	0	100	100
21	Lb	51/126 (40%)	50 (98%)	1 (2%)	48	64
22	Lc	62/97 (64%)	61 (98%)	1 (2%)	55	71
23	Ld	78/110 (71%)	78 (100%)	0	100	100
24	Le	101/121 (84%)	101 (100%)	0	100	100
25	Lf	79/89 (89%)	79 (100%)	0	100	100
26	Lg	77/100 (77%)	77 (100%)	0	100	100
27	Lh	89/110 (81%)	88 (99%)	1 (1%)	65	79
28	Li	62/89 (70%)	61 (98%)	1 (2%)	55	71
29	Lj	68/80 (85%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Lk	37/65 (57%)	37 (100%)	0	100	100
31	Ll	39/48 (81%)	39 (100%)	0	100	100
32	Lm	36/116 (31%)	36 (100%)	0	100	100
33	Lo	73/94 (78%)	70 (96%)	3 (4%)	27	37
34	Lp	63/75 (84%)	63 (100%)	0	100	100
35	Lr	97/121 (80%)	95 (98%)	2 (2%)	47	63
36	LA	167/199 (84%)	166 (99%)	1 (1%)	78	89
37	LB	284/348 (82%)	283 (100%)	1 (0%)	84	92
38	LH	127/171 (74%)	124 (98%)	3 (2%)	43	58
39	LI	139/182 (76%)	136 (98%)	3 (2%)	45	61
40	LL	129/177 (73%)	129 (100%)	0	100	100
41	LS	143/157 (91%)	141 (99%)	2 (1%)	59	75
43	SA	159/243 (65%)	156 (98%)	3 (2%)	50	66
44	SB	153/231 (66%)	150 (98%)	3 (2%)	48	64
45	SC	152/225 (68%)	152 (100%)	0	100	100
46	SD	109/202 (54%)	107 (98%)	2 (2%)	51	68
47	SE	194/225 (86%)	190 (98%)	4 (2%)	47	63
48	SF	125/170 (74%)	124 (99%)	1 (1%)	73	85
49	SG	113/218 (52%)	113 (100%)	0	100	100
50	SH	89/174 (51%)	86 (97%)	3 (3%)	32	44
51	SI	120/180 (67%)	118 (98%)	2 (2%)	53	69
52	SJ	115/168 (68%)	115 (100%)	0	100	100
53	SK	51/136 (38%)	49 (96%)	2 (4%)	28	39
54	SL	101/142 (71%)	100 (99%)	1 (1%)	68	81
55	SN	104/131 (79%)	102 (98%)	2 (2%)	50	66
56	SO	87/119 (73%)	83 (95%)	4 (5%)	24	32
57	SP	76/130 (58%)	76 (100%)	0	100	100
58	SQ	103/121 (85%)	101 (98%)	2 (2%)	50	66
59	SR	76/122 (62%)	71 (93%)	5 (7%)	15	18
60	SS	98/132 (74%)	96 (98%)	2 (2%)	48	64
61	ST	97/114 (85%)	93 (96%)	4 (4%)	27	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	SU	61/107 (57%)	60 (98%)	1 (2%)	55	71
63	SV	63/67 (94%)	61 (97%)	2 (3%)	34	47
64	SW	109/113 (96%)	108 (99%)	1 (1%)	70	84
65	SX	106/115 (92%)	105 (99%)	1 (1%)	70	84
66	SY	95/115 (83%)	93 (98%)	2 (2%)	47	63
67	SZ	52/103 (50%)	52 (100%)	0	100	100
68	Sa	76/98 (78%)	75 (99%)	1 (1%)	61	76
69	Sb	49/76 (64%)	47 (96%)	2 (4%)	27	37
70	Sc	35/62 (56%)	35 (100%)	0	100	100
71	Sd	36/49 (74%)	36 (100%)	0	100	100
72	Se	31/79 (39%)	30 (97%)	1 (3%)	34	47
73	Sg	206/239 (86%)	202 (98%)	4 (2%)	50	66
74	Ln	15/24 (62%)	15 (100%)	0	100	100
75	LR	116/175 (66%)	113 (97%)	3 (3%)	40	55
77	LV	91/107 (85%)	91 (100%)	0	100	100
78	LW	45/126 (36%)	44 (98%)	1 (2%)	45	61
All	All	7640/10546 (72%)	7525 (98%)	115 (2%)	55	73

All (115) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LC	62	THR
4	LC	80	ARG
4	LC	283	LYS
4	LC	307	LYS
4	LC	312	ARG
5	LD	3	PHE
5	LD	69	ILE
5	LD	126	THR
5	LD	167	VAL
5	LD	211	LEU
6	LE	198	SER
6	LE	208	ILE
6	LE	285	LYS
7	LF	181	LYS
7	LF	215	SER

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Mol	Chain	Res	Type
8	LG	136	LEU
8	LG	201	THR
8	LG	224	THR
10	LM	2	VAL
10	LM	69	HIS
10	LM	103	LYS
11	LN	13	LYS
12	LO	31	ARG
12	LO	177	LEU
12	LO	179	LYS
12	LO	198	THR
13	LP	105	LYS
14	LQ	172	ARG
15	LT	142	ARG
16	LU	71	THR
16	LU	73	THR
18	LY	67	ILE
18	LY	93	THR
18	LY	94	THR
18	LY	95	VAL
19	LZ	43	VAL
19	LZ	91	LEU
21	Lb	93	LEU
22	Lc	16	SER
27	Lh	36	VAL
28	Li	84	LYS
33	Lo	2	VAL
33	Lo	6	LYS
33	Lo	87	ARG
35	Lr	26	SER
35	Lr	37	SER
36	LA	28	ARG
37	LB	357	ARG
38	LH	18	ILE
38	LH	105	ILE
38	LH	174	LYS
39	LI	12	CYS
39	LI	156	LYS
39	LI	195	CYS
41	LS	17	LEU
41	LS	135	SER
43	SA	87	VAL

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Mol	Chain	Res	Type
43	SA	152	SER
43	SA	177	MET
44	SB	59	SER
44	SB	113	MET
44	SB	151	ARG
46	SD	154	ASP
46	SD	185	LYS
47	SE	40	GLU
47	SE	139	LEU
47	SE	237	SER
47	SE	246	LEU
48	SF	75	SER
50	SH	9	VAL
50	SH	157	HIS
50	SH	172	THR
51	SI	66	SER
51	SI	82	VAL
53	SK	3	MET
53	SK	21	MET
54	SL	74	SER
55	SN	29	THR
55	SN	32	ASP
56	SO	27	VAL
56	SO	54	CYS
56	SO	67	ASP
56	SO	122	SER
58	SQ	53	GLU
58	SQ	118	THR
59	SR	6	THR
59	SR	32	LYS
59	SR	54	VAL
59	SR	123	THR
59	SR	124	VAL
60	SS	71	MET
60	SS	106	LYS
61	ST	38	LYS
61	ST	113	VAL
61	ST	122	LYS
61	ST	123	LEU
62	SU	88	LEU
63	SV	52	THR
63	SV	80	SER

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Mol	Chain	Res	Type
64	SW	74	VAL
65	SX	105	PHE
66	SY	4	THR
66	SY	69	THR
68	Sa	69	VAL
69	Sb	3	LEU
69	Sb	26	GLN
72	Se	26	LYS
73	Sg	42	MET
73	Sg	131	LEU
73	Sg	148	SER
73	Sg	287	THR
75	LR	3	MET
75	LR	29	THR
75	LR	57	VAL
78	LW	25	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (67) such sidechains are listed below:

Mol	Chain	Res	Type
4	LC	43	ASN
4	LC	187	GLN
4	LC	329	ASN
4	LC	346	ASN
5	LD	275	GLN
6	LE	191	GLN
6	LE	245	GLN
8	LG	153	GLN
8	LG	240	ASN
10	LM	20	HIS
10	LM	34	ASN
10	LM	78	GLN
12	LO	180	GLN
13	LP	21	ASN
13	LP	75	GLN
14	LQ	77	ASN
15	LT	54	HIS
15	LT	131	GLN
16	LU	55	ASN
18	LY	18	HIS
18	LY	43	ASN
18	LY	96	HIS

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Mol	Chain	Res	Type
21	Lb	19	ASN
21	Lb	101	HIS
22	Lc	73	HIS
23	Ld	69	ASN
24	Le	92	ASN
25	Lf	56	ASN
27	Lh	20	GLN
28	Li	15	HIS
28	Li	20	ASN
29	Lj	57	ASN
29	Lj	66	HIS
35	Lr	4	HIS
35	Lr	21	ASN
36	LA	100	ASN
39	LI	59	GLN
39	LI	73	ASN
39	LI	166	HIS
40	LL	19	GLN
40	LL	104	ASN
41	LS	173	ASN
43	SA	169	HIS
44	SB	101	HIS
46	SD	159	HIS
48	SF	83	ASN
48	SF	149	GLN
49	SG	187	HIS
52	SJ	156	HIS
54	SL	19	ASN
54	SL	39	ASN
56	SO	113	GLN
58	SQ	77	HIS
58	SQ	86	GLN
58	SQ	97	GLN
60	SS	19	ASN
60	SS	72	GLN
65	SX	16	HIS
65	SX	73	GLN
65	SX	92	ASN
65	SX	127	ASN
66	SY	29	HIS
67	SZ	45	ASN
69	Sb	83	GLN

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Mol	Chain	Res	Type
73	Sg	56	GLN
73	Sg	117	ASN
75	LR	40	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3014/5054 (59%)	438 (14%)	9 (0%)
2	L7	118/121 (97%)	10 (8%)	0
3	L8	142/156 (91%)	16 (11%)	0
42	S2	1480/1869 (79%)	221 (14%)	2 (0%)
76	S6	11/14 (78%)	5 (45%)	0
All	All	4765/7214 (66%)	690 (14%)	11 (0%)

All (690) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	3	C
1	L5	39	A
1	L5	42	A
1	L5	48	G
1	L5	56	A
1	L5	59	A
1	L5	64	A
1	L5	65	A
1	L5	69	A
1	L5	71	C
1	L5	73	A
1	L5	91	G
1	L5	98	A
1	L5	109	G
1	L5	110	C
1	L5	116	G
1	L5	119	G
1	L5	120	A
1	L5	128	C
1	L5	129	C
1	L5	132	G
1	L5	138	G
1	L5	143	C
1	L5	144	G

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Mol	Chain	Res	Type
1	L5	146	G
1	L5	152	U
1	L5	159	C
1	L5	165	A
1	L5	166	C
1	L5	200	U
1	L5	210	C
1	L5	216	C
1	L5	217	C
1	L5	218	A
1	L5	233	U
1	L5	269	G
1	L5	280	G
1	L5	306	A
1	L5	315	G
1	L5	316	U
1	L5	340	C
1	L5	341	G
1	L5	373	G
1	L5	387	G
1	L5	396	A
1	L5	408	A
1	L5	410	A
1	L5	412	G
1	L5	413	G
1	L5	432	U
1	L5	452	A
1	L5	453	G
1	L5	456	C
1	L5	457	G
1	L5	470	A
1	L5	474	C
1	L5	479	G
1	L5	486	C
1	L5	487	G
1	L5	490	C
1	L5	491	G
1	L5	492	U
1	L5	506	C
1	L5	509	A
1	L5	510	U
1	L5	512	U

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Mol	Chain	Res	Type
1	L5	653	U
1	L5	654	C
1	L5	670	G
1	L5	672	C
1	L5	674	G
1	L5	681	G
1	L5	685	C
1	L5	686	A
1	L5	687	U
1	L5	688	U
1	L5	693	C
1	L5	703	G
1	L5	704	C
1	L5	705	G
1	L5	729	G
1	L5	730	G
1	L5	731	G
1	L5	733	A
1	L5	738	C
1	L5	739	G
1	L5	740	G
1	L5	742	G
1	L5	744	G
1	L5	746	A
1	L5	758	G
1	L5	906	G
1	L5	907	U
1	L5	908	U
1	L5	909	A
1	L5	910	C
1	L5	911	A
1	L5	912	G
1	L5	919	C
1	L5	926	A
1	L5	927	G
1	L5	929	A
1	L5	930	C
1	L5	931	U
1	L5	938	A
1	L5	939	U
1	L5	953	G
1	L5	954	A

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Mol	Chain	Res	Type
1	L5	963	G
1	L5	965	U
1	L5	966	C
1	L5	975	C
1	L5	976	U
1	L5	1065	C
1	L5	1072	A
1	L5	1204	C
1	L5	1205	G
1	L5	1208	C
1	L5	1210	C
1	L5	1236	G
1	L5	1245	G
1	L5	1270	A
1	L5	1271	G
1	L5	1276	C
1	L5	1280	G
1	L5	1283	G
1	L5	1292	G
1	L5	1298	U
1	L5	1299	A
1	L5	1309	C
1	L5	1322	A2M
1	L5	1333	A
1	L5	1350	A
1	L5	1355	G
1	L5	1375	C
1	L5	1383	A
1	L5	1390	G
1	L5	1393	A
1	L5	1394	A
1	L5	1415	G
1	L5	1416	A
1	L5	1448	A
1	L5	1453	G
1	L5	1476	C
1	L5	1477	C
1	L5	1478	G
1	L5	1481	C
1	L5	1482	C
1	L5	1494	G
1	L5	1498	G

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Mol	Chain	Res	Type
1	L5	1500	G
1	L5	1510	U
1	L5	1530	A2M
1	L5	1543	A
1	L5	1559	A
1	L5	1574	U
1	L5	1587	U
1	L5	1592	U
1	L5	1609	A
1	L5	1620	G
1	L5	1621	OMG
1	L5	1627	A
1	L5	1629	G
1	L5	1630	A
1	L5	1637	G
1	L5	1638	A
1	L5	1650	G
1	L5	1657	C
1	L5	1672	C
1	L5	1673	PSU
1	L5	1730	G
1	L5	1737	G
1	L5	1738	A
1	L5	1749	G
1	L5	1783	A
1	L5	1800	A
1	L5	1812	C
1	L5	1814	G
1	L5	1817	G
1	L5	1818	U
1	L5	1830	U
1	L5	1832	G
1	L5	1833	A
1	L5	1838	G
1	L5	1851	G
1	L5	1865	G
1	L5	1888	A
1	L5	1893	A
1	L5	1914	U
1	L5	1915	G
1	L5	1917	C
1	L5	1918	G

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Mol	Chain	Res	Type
1	L5	1927	C
1	L5	1928	A
1	L5	1935	A
1	L5	1944	G
1	L5	1951	G
1	L5	2042	G
1	L5	2044	U
1	L5	2048	G
1	L5	2051	G
1	L5	2052	G
1	L5	2065	A
1	L5	2080	C
1	L5	2085	G
1	L5	2087	C
1	L5	2249	G
1	L5	2267	C
1	L5	2279	C
1	L5	2290	A
1	L5	2291	G
1	L5	2295	U
1	L5	2303	A
1	L5	2306	G
1	L5	2323	G
1	L5	2338	G
1	L5	2341	OMC
1	L5	2372	A
1	L5	2385	A
1	L5	2387	G
1	L5	2407	A
1	L5	2411	G
1	L5	2412	OMC
1	L5	2417	G
1	L5	2418	A
1	L5	2440	G
1	L5	2497	A
1	L5	2501	A
1	L5	2503	A
1	L5	2509	U
1	L5	2519	A
1	L5	2520	U
1	L5	2544	U
1	L5	2545	G

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Mol	Chain	Res	Type
1	L5	2547	G
1	L5	2560	U
1	L5	2563	A
1	L5	2573	C
1	L5	2577	A
1	L5	2579	C
1	L5	2617	C
1	L5	2622	PSU
1	L5	2642	G
1	L5	2643	C
1	L5	2652	G
1	L5	2659	C
1	L5	2666	A
1	L5	2676	G
1	L5	2677	U
1	L5	2684	G
1	L5	2685	A
1	L5	2686	A
1	L5	2691	U
1	L5	2692	C
1	L5	2695	G
1	L5	2704	G
1	L5	2712	G
1	L5	2713	U
1	L5	2714	G
1	L5	2716	G
1	L5	2717	C
1	L5	2719	C
1	L5	2729	C
1	L5	2732	G
1	L5	2733	A
1	L5	2749	G
1	L5	2750	G
1	L5	2751	U
1	L5	2753	U
1	L5	2759	U
1	L5	2760	C
1	L5	2778	U
1	L5	2780	U
1	L5	2786	G
1	L5	2804	C
1	L5	2805	A2M

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Mol	Chain	Res	Type
1	L5	2816	U
1	L5	2817	G
1	L5	2845	G
1	L5	2858	G
1	L5	3590	A
1	L5	3591	C
1	L5	3592	U
1	L5	3601	G
1	L5	3604	C
1	L5	3612	G
1	L5	3621	A
1	L5	3630	U
1	L5	3648	A
1	L5	3650	G
1	L5	3659	C
1	L5	3690	U
1	L5	3708	G
1	L5	3709	A
1	L5	3710	A2M
1	L5	3734	A
1	L5	3739	G
1	L5	3742	A
1	L5	3762	G
1	L5	3763	G
1	L5	3771	A2M
1	L5	3772	U
1	L5	3788	U
1	L5	3797	G
1	L5	3800	U
1	L5	3803	A
1	L5	3805	G
1	L5	3809	G
1	L5	3824	U
1	L5	3826	U
1	L5	3830	PSU
1	L5	3863	A
1	L5	3864	C
1	L5	3865	G
1	L5	3883	G
1	L5	3884	G
1	L5	3887	A
1	L5	3892	A

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Mol	Chain	Res	Type
1	L5	3893	G
1	L5	3894	A
1	L5	3901	U
1	L5	3925	G
1	L5	3930	G
1	L5	4062	G
1	L5	4066	C
1	L5	4102	C
1	L5	4104	U
1	L5	4105	C
1	L5	4108	G
1	L5	4110	G
1	L5	4113	A
1	L5	4121	G
1	L5	4134	C
1	L5	4137	G
1	L5	4148	C
1	L5	4149	U
1	L5	4156	A
1	L5	4163	C
1	L5	4169	G
1	L5	4170	G
1	L5	4177	G
1	L5	4189	A
1	L5	4208	G
1	L5	4215	U
1	L5	4219	A
1	L5	4235	G
1	L5	4237	A
1	L5	4245	C
1	L5	4246	U
1	L5	4252	G
1	L5	4254	A
1	L5	4259	A
1	L5	4267	A
1	L5	4277	G
1	L5	4281	U
1	L5	4291	G
1	L5	4315	G
1	L5	4316	G
1	L5	4318	C
1	L5	4359	G

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Mol	Chain	Res	Type
1	L5	4362	A
1	L5	4363	G
1	L5	4364	A
1	L5	4366	A
1	L5	4373	C
1	L5	4380	A
1	L5	4401	A
1	L5	4423	U
1	L5	4430	C
1	L5	4434	G
1	L5	4435	A
1	L5	4450	A
1	L5	4461	G
1	L5	4463	A
1	L5	4486	PSU
1	L5	4498	U
1	L5	4499	A
1	L5	4505	C
1	L5	4510	G
1	L5	4531	G
1	L5	4534	A
1	L5	4535	G
1	L5	4546	C
1	L5	4553	G
1	L5	4558	U
1	L5	4559	G
1	L5	4561	G
1	L5	4576	A2M
1	L5	4622	PSU
1	L5	4623	OMG
1	L5	4642	A
1	L5	4656	C
1	L5	4658	A
1	L5	4686	A
1	L5	4694	A
1	L5	4695	U
1	L5	4721	G
1	L5	4733	C
1	L5	4736	G
1	L5	4740	G
1	L5	4743	C
1	L5	4745	C

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Mol	Chain	Res	Type
1	L5	4747	G
1	L5	4751	G
1	L5	4756	U
1	L5	4853	G
1	L5	4855	G
1	L5	4856	C
1	L5	4867	U
1	L5	4868	C
1	L5	4869	G
1	L5	4870	U
1	L5	4874	G
1	L5	4895	A
1	L5	4897	G
1	L5	4898	G
1	L5	4899	C
1	L5	4902	C
1	L5	4919	A
1	L5	4925	C
1	L5	4926	G
1	L5	4928	A
1	L5	4936	G
1	L5	4949	C
1	L5	4961	U
1	L5	4991	U
1	L5	4992	A
1	L5	4997	G
1	L5	4999	A
1	L5	5002	G
1	L5	5015	U
1	L5	5019	A
1	L5	5026	G
1	L5	5035	C
1	L5	5039	C
1	L5	5041	A
1	L5	5045	A
1	L5	5054	U
2	L7	22	A
2	L7	23	A
2	L7	31	G
2	L7	33	U
2	L7	50	A
2	L7	53	U

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Mol	Chain	Res	Type
2	L7	64	G
2	L7	97	G
2	L7	100	A
2	L7	110	G
3	L8	23	C
3	L8	34	U
3	L8	35	C
3	L8	48	A
3	L8	51	U
3	L8	52	A
3	L8	59	A
3	L8	62	A
3	L8	63	U
3	L8	103	A
3	L8	105	C
3	L8	110	U
3	L8	112	G
3	L8	114	G
3	L8	151	G
3	L8	156	U
42	S2	2	A
42	S2	17	C
42	S2	33	G
42	S2	41	G
42	S2	46	A
42	S2	56	G
42	S2	59	U
42	S2	64	A
42	S2	67	C
42	S2	68	A
42	S2	71	G
42	S2	99	A2M
42	S2	103	A
42	S2	113	G
42	S2	115	U
42	S2	155	G
42	S2	161	U
42	S2	162	C
42	S2	168	C
42	S2	302	A
42	S2	312	G
42	S2	319	C

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Mol	Chain	Res	Type
42	S2	335	G
42	S2	347	G
42	S2	360	A
42	S2	362	C
42	S2	364	A
42	S2	385	G
42	S2	386	C
42	S2	407	G
42	S2	408	A
42	S2	409	C
42	S2	437	G
42	S2	438	G
42	S2	448	A
42	S2	450	C
42	S2	451	G
42	S2	452	G
42	S2	464	A
42	S2	471	G
42	S2	472	C
42	S2	473	A
42	S2	474	G
42	S2	482	G
42	S2	487	U
42	S2	488	U
42	S2	492	C
42	S2	516	A
42	S2	525	A
42	S2	558	G
42	S2	559	G
42	S2	562	U
42	S2	563	G
42	S2	564	A
42	S2	576	A2M
42	S2	584	A
42	S2	587	A
42	S2	589	G
42	S2	591	U
42	S2	598	G
42	S2	607	U
42	S2	614	C
42	S2	615	C
42	S2	617	G

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Mol	Chain	Res	Type
42	S2	627	U
42	S2	628	A
42	S2	629	A
42	S2	631	U
42	S2	632	C
42	S2	643	A
42	S2	655	A
42	S2	668	A2M
42	S2	669	A
42	S2	672	A
42	S2	673	G
42	S2	683	OMG
42	S2	688	U
42	S2	811	A
42	S2	821	G
42	S2	822	PSU
42	S2	830	A
42	S2	842	C
42	S2	847	A
42	S2	867	OMG
42	S2	870	A
42	S2	871	U
42	S2	872	A
42	S2	873	G
42	S2	913	A
42	S2	917	U
42	S2	920	A
42	S2	922	A
42	S2	933	G
42	S2	939	U
42	S2	955	A
42	S2	968	U
42	S2	971	G
42	S2	981	A
42	S2	990	A
42	S2	992	A
42	S2	1017	U
42	S2	1023	A
42	S2	1052	A
42	S2	1061	U
42	S2	1062	A
42	S2	1082	A

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Mol	Chain	Res	Type
42	S2	1083	A
42	S2	1085	C
42	S2	1109	C
42	S2	1138	C
42	S2	1153	C
42	S2	1154	U
42	S2	1195	A
42	S2	1207	G
42	S2	1208	A
42	S2	1212	G
42	S2	1213	C
42	S2	1215	C
42	S2	1216	C
42	S2	1217	A
42	S2	1224	G
42	S2	1242	U
42	S2	1243	U
42	S2	1248	U
42	S2	1251	A
42	S2	1253	A
42	S2	1256	G
42	S2	1257	G
42	S2	1258	A
42	S2	1259	A
42	S2	1274	G
42	S2	1275	G
42	S2	1285	G
42	S2	1286	G
42	S2	1290	G
42	S2	1292	C
42	S2	1294	G
42	S2	1295	A
42	S2	1301	A
42	S2	1302	G
42	S2	1303	C
42	S2	1312	G
42	S2	1313	A
42	S2	1322	G
42	S2	1327	G
42	S2	1328	OMG
42	S2	1329	U
42	S2	1343	U

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Mol	Chain	Res	Type
42	S2	1345	G
42	S2	1346	U
42	S2	1347	PSU
42	S2	1368	U
42	S2	1369	A
42	S2	1371	U
42	S2	1372	U
42	S2	1378	A
42	S2	1385	G
42	S2	1397	U
42	S2	1405	A
42	S2	1406	G
42	S2	1412	C
42	S2	1423	C
42	S2	1454	A
42	S2	1464	C
42	S2	1477	U
42	S2	1478	U
42	S2	1487	A
42	S2	1488	C
42	S2	1489	A
42	S2	1490	OMG
42	S2	1497	G
42	S2	1498	A
42	S2	1509	U
42	S2	1510	G
42	S2	1520	G
42	S2	1521	C
42	S2	1522	A
42	S2	1531	A
42	S2	1533	A
42	S2	1551	U
42	S2	1570	G
42	S2	1574	C
42	S2	1580	A
42	S2	1588	A
42	S2	1599	U
42	S2	1601	A
42	S2	1621	U
42	S2	1623	A
42	S2	1639	G7M
42	S2	1647	A

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Mol	Chain	Res	Type
42	S2	1648	G
42	S2	1654	G
42	S2	1660	C
42	S2	1661	A
42	S2	1665	G
42	S2	1680	G
42	S2	1698	C
42	S2	1718	G
42	S2	1719	A
42	S2	1721	U
42	S2	1722	G
42	S2	1727	G
42	S2	1745	A
42	S2	1786	U
42	S2	1804	OMU
42	S2	1806	A
42	S2	1814	G
42	S2	1815	A
42	S2	1817	G
42	S2	1818	A
42	S2	1819	A
42	S2	1822	A
42	S2	1831	A
42	S2	1835	A
42	S2	1838	U
42	S2	1849	G
42	S2	1851	MA6
42	S2	1861	G
42	S2	1862	G
42	S2	1863	A
42	S2	1865	C
76	S6	6	G
76	S6	72	C
76	S6	73	A
76	S6	74	A
76	S6	77	A

All (11) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	908	U
1	L5	1586	C

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Mol	Chain	Res	Type
1	L5	1629	G
1	L5	2294	U
1	L5	2665	G
1	L5	3600	G
1	L5	3862	A
1	L5	4364	A
1	L5	4685	U
42	S2	1344	A
42	S2	1520	G

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

205 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	$\#\|Z\| > 2$
42	OMG	S2	1447	42	23,26,27	0.48	0	33,38,41	0.48	0
1	5MC	L5	3768	1,81	18,22,23	0.62	0	26,32,35	0.52	0
42	OMU	S2	1288	42	19,22,23	3.30	8 (42%)	26,31,34	1.67	4 (15%)
1	PSU	L5	4428	1	18,21,22	1.09	1 (5%)	22,30,33	1.84	6 (27%)
42	PSU	S2	1136	42	18,21,22	1.11	1 (5%)	22,30,33	1.78	4 (18%)
1	A2M	L5	1322	1	22,25,26	4.13	12 (54%)	31,36,39	3.24	12 (38%)
42	MA6	S2	1851	42	23,26,27	1.52	3 (13%)	34,38,41	3.72	12 (35%)
1	PSU	L5	1777	1	18,21,22	1.08	1 (5%)	22,30,33	1.77	5 (22%)
42	OMU	S2	121	42	19,22,23	3.21	8 (42%)	26,31,34	1.62	5 (19%)
1	OMG	L5	2866	1	23,26,27	0.53	0	33,38,41	0.50	0
1	OMC	L5	2851	1	19,22,23	0.27	0	26,31,34	0.35	0
1	OMC	L5	3794	1	19,22,23	0.32	0	26,31,34	0.37	0
1	PSU	L5	3830	1	18,21,22	1.05	1 (5%)	22,30,33	1.79	4 (18%)
37	HIC	LB	245	37	10,11,12	0.47	0	8,14,16	0.69	0
3	PSU	L8	69	3	18,21,22	1.10	1 (5%)	22,30,33	1.76	5 (22%)
1	PSU	L5	3906	79,1	18,21,22	1.12	1 (5%)	22,30,33	1.61	3 (13%)
42	OMC	S2	1391	42	19,22,23	0.28	0	26,31,34	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	PSU	L5	4507	79,1,80	18,21,22	1.13	1 (5%)	22,30,33	1.71	4 (18%)
42	PSU	S2	109	42	18,21,22	1.09	1 (5%)	22,30,33	1.77	4 (18%)
42	PSU	S2	822	42	18,21,22	1.09	1 (5%)	22,30,33	1.74	5 (22%)
42	OMG	S2	1328	42	23,26,27	0.50	0	33,38,41	0.47	0
42	PSU	S2	681	42	18,21,22	1.08	1 (5%)	22,30,33	1.71	5 (22%)
42	OMG	S2	867	42	23,26,27	0.48	0	33,38,41	0.49	0
1	OMU	L5	4292	1	19,22,23	3.24	8 (42%)	26,31,34	1.63	5 (19%)
1	A2M	L5	2391	1	22,25,26	4.08	12 (54%)	31,36,39	3.26	13 (41%)
42	A2M	S2	166	42	22,25,26	4.16	12 (54%)	31,36,39	3.46	14 (45%)
42	PSU	S2	801	42	18,21,22	1.10	1 (5%)	22,30,33	1.77	5 (22%)
1	PSU	L5	4565	1	18,21,22	1.06	1 (5%)	22,30,33	1.75	5 (22%)
42	PSU	S2	863	42	18,21,22	1.07	1 (5%)	22,30,33	1.77	4 (18%)
1	OMG	L5	3730	1	23,26,27	0.51	0	33,38,41	0.53	0
42	PSU	S2	667	42	18,21,22	1.09	1 (5%)	22,30,33	1.68	3 (13%)
1	A2M	L5	1319	1	22,25,26	4.10	12 (54%)	31,36,39	3.23	11 (35%)
1	A2M	L5	1520	1	22,25,26	4.11	12 (54%)	31,36,39	3.37	10 (32%)
1	OMG	L5	3885	1	23,26,27	0.53	0	33,38,41	0.60	0
1	PSU	L5	4347	1	18,21,22	1.08	1 (5%)	22,30,33	1.75	4 (18%)
1	PSU	L5	4659	1	18,21,22	1.08	1 (5%)	22,30,33	1.70	4 (18%)
1	OMC	L5	4522	1	19,22,23	0.29	0	26,31,34	0.51	0
1	A2M	L5	3816	1	22,25,26	4.12	12 (54%)	31,36,39	3.30	12 (38%)
42	A2M	S2	1678	42	22,25,26	4.12	12 (54%)	31,36,39	3.44	14 (45%)
1	PSU	L5	4995	1	18,21,22	1.08	1 (5%)	22,30,33	1.75	4 (18%)
42	OMC	S2	174	42	19,22,23	0.28	0	26,31,34	0.49	0
42	PSU	S2	1056	42	18,21,22	1.10	1 (5%)	22,30,33	1.72	4 (18%)
42	OMG	S2	509	42	23,26,27	0.50	0	33,38,41	0.54	0
42	A2M	S2	1383	42	22,25,26	4.16	12 (54%)	31,36,39	3.43	14 (45%)
1	OMC	L5	2355	1	19,22,23	0.29	0	26,31,34	0.44	0
1	PSU	L5	3808	1	18,21,22	1.10	1 (5%)	22,30,33	1.77	4 (18%)
1	A2M	L5	1530	79,1	22,25,26	4.12	12 (54%)	31,36,39	3.25	12 (38%)
20	V5N	La	39	20	9,11,12	0.72	0	9,14,16	1.09	0
42	A2M	S2	512	42	22,25,26	4.14	12 (54%)	31,36,39	3.40	13 (41%)
42	PSU	S2	1692	42	18,21,22	1.05	1 (5%)	22,30,33	1.74	4 (18%)
42	PSU	S2	1244	42	18,21,22	1.06	1 (5%)	22,30,33	1.77	5 (22%)
1	A2M	L5	3771	1	22,25,26	4.09	11 (50%)	31,36,39	3.32	14 (45%)
42	OMU	S2	172	42	19,22,23	3.23	8 (42%)	26,31,34	1.70	5 (19%)
1	OMC	L5	3855	1	19,22,23	0.30	0	26,31,34	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
42	4AC	S2	1337	42	21,24,25	3.45	9 (42%)	29,34,37	1.34	4 (13%)
1	A2M	L5	3853	1	22,25,26	4.13	12 (54%)	31,36,39	3.33	11 (35%)
1	PSU	L5	4622	1	18,21,22	1.06	1 (5%)	22,30,33	1.85	5 (22%)
42	A2M	S2	576	42	22,25,26	4.14	12 (54%)	31,36,39	3.32	12 (38%)
1	OMU	L5	4213	1	19,22,23	3.27	8 (42%)	26,31,34	1.74	5 (19%)
1	PSU	L5	4538	1	18,21,22	1.06	1 (5%)	22,30,33	1.78	4 (18%)
42	A2M	S2	590	42	22,25,26	4.13	11 (50%)	31,36,39	3.51	13 (41%)
1	PSU	L5	4285	1	18,21,22	1.06	1 (5%)	22,30,33	1.76	4 (18%)
42	G7M	S2	1639	42	23,26,27	2.87	10 (43%)	35,39,42	2.15	10 (28%)
42	PSU	S2	1004	42	18,21,22	1.10	1 (5%)	22,30,33	1.68	4 (18%)
42	PSU	S2	1347	42	18,21,22	1.06	1 (5%)	22,30,33	1.78	5 (22%)
1	PSU	L5	3701	1	18,21,22	1.04	1 (5%)	22,30,33	1.75	5 (22%)
42	PSU	S2	649	42	18,21,22	1.09	1 (5%)	22,30,33	1.74	4 (18%)
1	A2M	L5	4509	79,1	22,25,26	4.10	12 (54%)	31,36,39	3.33	13 (41%)
1	PSU	L5	4614	1	18,21,22	1.12	1 (5%)	22,30,33	1.76	4 (18%)
42	PSU	S2	609	42	18,21,22	1.07	1 (5%)	22,30,33	1.74	4 (18%)
1	PSU	L5	1778	1	18,21,22	1.08	1 (5%)	22,30,33	1.70	4 (18%)
1	A2M	L5	2777	1	22,25,26	4.10	12 (54%)	31,36,39	3.07	11 (35%)
1	PSU	L5	3870	1	18,21,22	1.13	1 (5%)	22,30,33	1.70	4 (18%)
42	PSU	S2	572	42	18,21,22	1.07	1 (5%)	22,30,33	1.73	5 (22%)
1	A2M	L5	4557	1	22,25,26	4.12	12 (54%)	31,36,39	3.39	12 (38%)
42	PSU	S2	1177	42	18,21,22	1.06	1 (5%)	22,30,33	1.74	3 (13%)
1	PSU	L5	3623	1	18,21,22	1.04	1 (5%)	22,30,33	1.72	4 (18%)
42	OMU	S2	116	42	19,22,23	3.23	8 (42%)	26,31,34	1.73	5 (19%)
1	A2M	L5	400	1	22,25,26	4.14	12 (54%)	31,36,39	3.32	12 (38%)
1	PSU	L5	1856	1	18,21,22	1.06	1 (5%)	22,30,33	1.77	5 (22%)
1	5MC	L5	4433	1	18,22,23	0.68	0	26,32,35	0.66	0
1	PSU	L5	4675	1	18,21,22	1.09	1 (5%)	22,30,33	1.78	5 (22%)
42	PSU	S2	105	42	18,21,22	1.08	1 (5%)	22,30,33	1.77	4 (18%)
1	A2M	L5	1867	79,1	22,25,26	4.12	12 (54%)	31,36,39	3.24	13 (41%)
42	PSU	S2	1596	42	18,21,22	1.09	1 (5%)	22,30,33	1.73	5 (22%)
1	A2M	L5	398	1	22,25,26	4.08	11 (50%)	31,36,39	3.33	11 (35%)
1	PSU	L5	4389	1	18,21,22	1.11	1 (5%)	22,30,33	1.67	5 (22%)
42	PSU	S2	218	42	18,21,22	1.05	1 (5%)	22,30,33	1.73	4 (18%)
1	PSU	L5	4339	1	18,21,22	1.04	1 (5%)	22,30,33	1.76	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	PSU	L5	4518	1	18,21,22	1.06	1 (5%)	22,30,33	1.74	4 (18%)
42	OMC	S2	621	42	19,22,23	0.29	0	26,31,34	0.38	0
1	PSU	L5	1740	1	18,21,22	1.02	1 (5%)	22,30,33	1.76	4 (18%)
42	OMG	S2	601	42	23,26,27	0.50	0	33,38,41	0.45	0
1	UR3	L5	4516	1	19,22,23	2.87	7 (36%)	26,32,35	1.28	2 (7%)
3	PSU	L8	55	3	18,21,22	1.06	1 (5%)	22,30,33	1.72	4 (18%)
1	PSU	L5	4957	1	18,21,22	1.11	1 (5%)	22,30,33	1.78	4 (18%)
42	PSU	S2	1238	42	18,21,22	1.11	1 (5%)	22,30,33	1.84	5 (22%)
1	PSU	L5	1673	1	18,21,22	1.11	2 (11%)	22,30,33	1.82	6 (27%)
42	PSU	S2	119	42	18,21,22	1.09	1 (5%)	22,30,33	1.76	4 (18%)
42	A2M	S2	668	79,42	22,25,26	4.11	12 (54%)	31,36,39	3.22	13 (41%)
1	OMG	L5	4356	1	23,26,27	0.49	0	33,38,41	0.50	0
1	PSU	L5	4555	1	18,21,22	1.11	1 (5%)	22,30,33	1.73	4 (18%)
1	PSU	L5	4298	1	18,21,22	1.04	1 (5%)	22,30,33	1.69	3 (13%)
1	OMC	L5	2814	1	19,22,23	0.29	0	26,31,34	0.37	0
1	PSU	L5	1788	1,80	18,21,22	1.05	1 (5%)	22,30,33	1.70	3 (13%)
1	PSU	L5	4517	1	18,21,22	1.03	1 (5%)	22,30,33	1.83	5 (22%)
1	PSU	L5	4409	1	18,21,22	1.05	1 (5%)	22,30,33	1.79	5 (22%)
42	PSU	S2	34	42	18,21,22	1.07	1 (5%)	22,30,33	1.78	5 (22%)
42	OMC	S2	462	42	19,22,23	0.29	0	26,31,34	0.48	0
42	PSU	S2	651	42	18,21,22	1.07	1 (5%)	22,30,33	1.80	5 (22%)
1	PSU	L5	1578	1	18,21,22	1.07	1 (5%)	22,30,33	1.63	4 (18%)
42	PSU	S2	406	42	18,21,22	1.09	1 (5%)	22,30,33	1.76	4 (18%)
1	OMG	L5	2354	1	23,26,27	0.49	0	33,38,41	0.53	0
42	A2M	S2	99	42	22,25,26	4.11	12 (54%)	31,36,39	3.37	13 (41%)
42	PSU	S2	1045	42	18,21,22	1.06	1 (5%)	22,30,33	1.78	3 (13%)
42	A2M	S2	468	42	22,25,26	4.13	12 (54%)	31,36,39	3.39	13 (41%)
1	PSU	L5	2829	1	18,21,22	1.11	1 (5%)	22,30,33	1.69	4 (18%)
1	OMG	L5	3613	1	23,26,27	0.51	0	33,38,41	0.70	0
1	OMG	L5	1312	1	23,26,27	0.55	0	33,38,41	0.64	0
42	OMU	S2	1804	42	19,22,23	3.26	8 (42%)	26,31,34	1.64	4 (15%)
61	NMM	ST	67	61	9,11,12	0.59	0	6,12,14	2.80	2 (33%)
1	UY1	L5	3804	79,1,80	19,22,23	0.45	0	22,31,34	0.55	0
42	PSU	S2	918	42	18,21,22	1.12	1 (5%)	22,30,33	1.83	6 (27%)
1	6MZ	L5	4206	1	22,25,26	2.54	4 (18%)	30,36,39	2.46	10 (33%)
42	A2M	S2	159	42	22,25,26	4.14	12 (54%)	31,36,39	3.40	12 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
42	OMU	S2	354	42	19,22,23	3.25	8 (42%)	26,31,34	1.72	5 (19%)
1	PSU	L5	4986	1	18,21,22	1.09	1 (5%)	22,30,33	1.77	4 (18%)
1	OMU	L5	4606	1	19,22,23	3.22	8 (42%)	26,31,34	1.57	5 (19%)
1	A2M	L5	3704	1	22,25,26	4.14	11 (50%)	31,36,39	3.29	12 (38%)
42	MA6	S2	1850	42	23,26,27	1.52	4 (17%)	34,38,41	3.61	11 (32%)
1	PSU	L5	3681	1	18,21,22	1.05	1 (5%)	22,30,33	1.73	4 (18%)
1	A2M	L5	2805	1	22,25,26	4.11	12 (54%)	31,36,39	3.28	12 (38%)
42	OMG	S2	644	42	23,26,27	0.50	0	33,38,41	0.48	0
1	PSU	L5	1532	1	18,21,22	1.09	1 (5%)	22,30,33	1.67	4 (18%)
42	PSU	S2	36	42	18,21,22	1.09	1 (5%)	22,30,33	1.73	4 (18%)
1	A2M	L5	4576	1	22,25,26	4.14	11 (50%)	31,36,39	3.28	13 (41%)
1	OMG	L5	1518	1	23,26,27	0.52	0	33,38,41	0.62	0
42	A2M	S2	27	42	22,25,26	4.13	12 (54%)	31,36,39	3.31	13 (41%)
42	OMC	S2	517	42	19,22,23	0.28	0	26,31,34	0.46	0
1	OMC	L5	2341	1	19,22,23	0.28	0	26,31,34	0.38	0
42	PSU	S2	100	42	18,21,22	1.07	1 (5%)	22,30,33	1.76	3 (13%)
42	PSU	S2	1232	42	18,21,22	1.07	1 (5%)	22,30,33	1.80	5 (22%)
42	OMU	S2	1442	79,42	19,22,23	3.28	8 (42%)	26,31,34	1.68	4 (15%)
1	OMU	L5	3911	1	19,22,23	3.22	8 (42%)	26,31,34	1.61	5 (19%)
1	OMU	L5	4484	1	19,22,23	3.21	8 (42%)	26,31,34	1.67	5 (19%)
1	PSU	L5	4457	1	18,21,22	1.13	1 (5%)	22,30,33	1.74	5 (22%)
1	PSU	L5	4486	1	18,21,22	1.08	1 (5%)	22,30,33	1.81	5 (22%)
1	OMG	L5	4609	1	23,26,27	0.52	0	33,38,41	0.62	0
3	OMU	L8	14	3,1	19,22,23	3.24	8 (42%)	26,31,34	1.70	5 (19%)
1	OMG	L5	4182	79,1	23,26,27	0.51	0	33,38,41	0.48	0
42	PSU	S2	814	42	18,21,22	1.04	1 (5%)	22,30,33	1.77	4 (18%)
1	PSU	L5	3837	1	18,21,22	1.08	1 (5%)	22,30,33	1.77	4 (18%)
1	1MA	L5	1318	79,1	21,25,26	0.47	0	31,37,40	0.75	0
1	OMG	L5	4604	1	23,26,27	0.52	0	33,38,41	0.55	0
1	OMG	L5	4623	1	23,26,27	0.50	0	33,38,41	0.51	0
1	OMC	L5	3687	1,80	19,22,23	0.25	0	26,31,34	0.47	0
42	PSU	S2	1046	42	18,21,22	1.10	1 (5%)	22,30,33	1.74	4 (18%)
1	OMG	L5	4485	1	23,26,27	0.49	0	33,38,41	0.57	0
42	OMU	S2	428	42	19,22,23	3.27	8 (42%)	26,31,34	1.68	5 (19%)
1	OMU	L5	2405	1	19,22,23	3.22	8 (42%)	26,31,34	1.57	5 (19%)
42	6MZ	S2	1832	79,42,80	22,25,26	2.55	4 (18%)	30,36,39	2.45	10 (33%)
1	PSU	L5	4562	1	18,21,22	1.07	1 (5%)	22,30,33	1.73	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	PSU	L5	4417	1	18,21,22	1.09	1 (5%)	22,30,33	1.77	4 (18%)
1	OMG	L5	4378	1	23,26,27	0.49	0	33,38,41	0.48	0
3	OMG	L8	75	3	23,26,27	0.49	0	33,38,41	0.52	0
42	OMG	S2	436	42	23,26,27	0.50	0	33,38,41	0.52	0
1	OMC	L5	4442	1	19,22,23	0.27	0	26,31,34	0.39	0
1	PSU	L5	1679	1	18,21,22	1.04	1 (5%)	22,30,33	1.72	3 (13%)
1	OMG	L5	2414	1	23,26,27	0.49	0	33,38,41	0.47	0
1	OMC	L5	3827	1	19,22,23	0.28	0	26,31,34	0.42	0
1	PSU	L5	3839	79,1	18,21,22	1.09	1 (5%)	22,30,33	1.75	4 (18%)
42	UY1	S2	1326	42	19,22,23	0.33	0	22,31,34	0.87	2 (9%)
1	OMC	L5	1336	1	19,22,23	0.29	0	26,31,34	0.44	0
42	PSU	S2	686	42	18,21,22	1.07	1 (5%)	22,30,33	1.75	4 (18%)
1	A2M	L5	3811	1	22,25,26	4.13	12 (54%)	31,36,39	3.29	12 (38%)
1	OMG	L5	4480	1	23,26,27	0.50	0	33,38,41	0.49	0
1	OMG	L5	1621	1,80	23,26,27	0.53	0	33,38,41	0.47	0
1	OMC	L5	2412	79,1	19,22,23	0.30	0	26,31,34	0.40	0
1	OMC	L5	2794	1	19,22,23	0.30	0	26,31,34	0.36	0
42	PSU	S2	93	42	18,21,22	1.09	1 (5%)	22,30,33	1.76	3 (13%)
42	PSU	S2	1625	42	18,21,22	1.10	1 (5%)	22,30,33	1.73	4 (18%)
42	A2M	S2	484	42	22,25,26	4.11	11 (50%)	31,36,39	3.31	11 (35%)
42	A2M	S2	1031	42	22,25,26	4.13	12 (54%)	31,36,39	3.33	13 (41%)
42	4AC	S2	1842	42	21,24,25	3.37	10 (47%)	29,34,37	0.91	2 (6%)
1	A2M	L5	2353	79,1	22,25,26	4.13	12 (54%)	31,36,39	3.21	12 (38%)
1	PSU	L5	3625	1	18,21,22	1.06	1 (5%)	22,30,33	1.63	5 (22%)
42	OMG	S2	1490	42	23,26,27	0.51	0	33,38,41	0.50	0
1	PSU	L5	2622	1	18,21,22	1.08	1 (5%)	22,30,33	1.74	5 (22%)
1	PSU	L5	4282	1	18,21,22	1.04	1 (5%)	22,30,33	1.68	4 (18%)
1	PSU	L5	4279	1	18,21,22	1.09	1 (5%)	22,30,33	1.69	4 (18%)
1	OMU	L5	2827	1	19,22,23	3.24	8 (42%)	26,31,34	1.68	5 (19%)
1	PSU	L5	1858	1	18,21,22	1.06	1 (5%)	22,30,33	1.85	4 (18%)
1	OMC	L5	1877	79,1	19,22,23	0.25	0	26,31,34	0.62	0
1	A2M	L5	3710	1	22,25,26	4.14	11 (50%)	31,36,39	3.37	12 (38%)
1	OMG	L5	4214	1	23,26,27	0.49	0	33,38,41	0.65	0
42	PSU	S2	1643	42	18,21,22	1.08	1 (5%)	22,30,33	1.71	4 (18%)
1	OMC	L5	3873	1	19,22,23	0.29	0	26,31,34	0.52	0
42	PSU	S2	1445	42	18,21,22	1.07	1 (5%)	22,30,33	1.74	5 (22%)
42	PSU	S2	1174	42	18,21,22	1.08	1 (5%)	22,30,33	1.75	4 (18%)
1	OMG	L5	3778	1	23,26,27	0.50	0	33,38,41	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	PSU	L5	4443	1	18,21,22	1.12	1 (5%)	22,30,33	1.68	5 (22%)
42	OMG	S2	683	42	23,26,27	0.49	0	33,38,41	0.58	0
1	PSU	L5	4958	1	18,21,22	1.08	1 (5%)	22,30,33	1.76	6 (27%)
42	PSU	S2	815	42	18,21,22	1.06	1 (5%)	22,30,33	1.76	3 (13%)
42	OMC	S2	1703	42	19,22,23	0.27	0	26,31,34	0.46	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
42	OMG	S2	1447	42	-	3/9/27/28	0/3/3/3
1	5MC	L5	3768	1,81	-	0/7/25/26	0/2/2/2
42	OMU	S2	1288	42	-	1/9/27/28	0/2/2/2
1	PSU	L5	4428	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	1136	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	1322	1	-	1/9/27/28	0/3/3/3
42	MA6	S2	1851	42	-	3/11/29/30	0/3/3/3
1	PSU	L5	1777	1	-	0/7/25/26	0/2/2/2
42	OMU	S2	121	42	-	0/9/27/28	0/2/2/2
1	OMG	L5	2866	1	-	0/9/27/28	0/3/3/3
1	OMC	L5	2851	1	-	0/9/27/28	0/2/2/2
1	OMC	L5	3794	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	3830	1	-	3/7/25/26	0/2/2/2
37	HIC	LB	245	37	-	1/5/6/8	0/1/1/1
3	PSU	L8	69	3	-	0/7/25/26	0/2/2/2
1	PSU	L5	3906	79,1	-	0/7/25/26	0/2/2/2
42	OMC	S2	1391	42	-	0/9/27/28	0/2/2/2
1	PSU	L5	4507	79,1,80	-	1/7/25/26	0/2/2/2
42	PSU	S2	109	42	-	0/7/25/26	0/2/2/2
42	PSU	S2	822	42	-	0/7/25/26	0/2/2/2
42	OMG	S2	1328	42	-	2/9/27/28	0/3/3/3
42	PSU	S2	681	42	-	0/7/25/26	0/2/2/2
42	OMG	S2	867	42	-	4/9/27/28	0/3/3/3
1	OMU	L5	4292	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	2391	1	-	0/9/27/28	0/3/3/3
42	A2M	S2	166	42	-	2/9/27/28	0/3/3/3
42	PSU	S2	801	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	4565	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	863	42	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	L5	3730	1	-	1/9/27/28	0/3/3/3
42	PSU	S2	667	42	-	2/7/25/26	0/2/2/2
1	A2M	L5	1319	1	-	1/9/27/28	0/3/3/3
1	A2M	L5	1520	1	-	1/9/27/28	0/3/3/3
1	OMG	L5	3885	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4347	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4659	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	4522	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	3816	1	-	1/9/27/28	0/3/3/3
42	A2M	S2	1678	42	-	2/9/27/28	0/3/3/3
1	PSU	L5	4995	1	-	0/7/25/26	0/2/2/2
42	OMC	S2	174	42	-	0/9/27/28	0/2/2/2
42	PSU	S2	1056	42	-	0/7/25/26	0/2/2/2
42	OMG	S2	509	42	-	0/9/27/28	0/3/3/3
42	A2M	S2	1383	42	-	2/9/27/28	0/3/3/3
1	OMC	L5	2355	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	3808	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	1530	79,1	-	2/9/27/28	0/3/3/3
20	V5N	La	39	20	-	0/9/10/12	0/1/1/1
42	A2M	S2	512	42	-	3/9/27/28	0/3/3/3
42	PSU	S2	1692	42	-	0/7/25/26	0/2/2/2
42	PSU	S2	1244	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	3771	1	-	1/9/27/28	0/3/3/3
42	OMU	S2	172	42	-	0/9/27/28	0/2/2/2
1	OMC	L5	3855	1	-	0/9/27/28	0/2/2/2
42	4AC	S2	1337	42	-	2/11/29/30	0/2/2/2
1	A2M	L5	3853	1	-	4/9/27/28	0/3/3/3
1	PSU	L5	4622	1	-	3/7/25/26	0/2/2/2
42	A2M	S2	576	42	-	2/9/27/28	0/3/3/3
1	OMU	L5	4213	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	4538	1	-	0/7/25/26	0/2/2/2
42	A2M	S2	590	42	-	5/9/27/28	0/3/3/3
1	PSU	L5	4285	1	-	0/7/25/26	0/2/2/2
42	G7M	S2	1639	42	-	2/7/25/26	0/3/3/3
42	PSU	S2	1004	42	-	0/7/25/26	0/2/2/2
42	PSU	S2	1347	42	-	2/7/25/26	0/2/2/2
1	PSU	L5	3701	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	649	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	4509	79,1	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	L5	4614	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	609	42	-	1/7/25/26	0/2/2/2
1	PSU	L5	1778	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	2777	1	-	3/9/27/28	0/3/3/3
1	PSU	L5	3870	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	572	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	4557	1	-	0/9/27/28	0/3/3/3
42	PSU	S2	1177	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	3623	1	-	0/7/25/26	0/2/2/2
42	OMU	S2	116	42	-	0/9/27/28	0/2/2/2
1	A2M	L5	400	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	1856	1	-	0/7/25/26	0/2/2/2
1	5MC	L5	4433	1	-	3/7/25/26	0/2/2/2
1	PSU	L5	4675	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	105	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	1867	79,1	-	1/9/27/28	0/3/3/3
42	PSU	S2	1596	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	398	1	-	2/9/27/28	0/3/3/3
1	PSU	L5	4389	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	218	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	4339	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4518	1	-	0/7/25/26	0/2/2/2
42	OMC	S2	621	42	-	0/9/27/28	0/2/2/2
1	PSU	L5	1740	1	-	0/7/25/26	0/2/2/2
42	OMG	S2	601	42	-	0/9/27/28	0/3/3/3
1	UR3	L5	4516	1	-	0/7/25/26	0/2/2/2
3	PSU	L8	55	3	-	0/7/25/26	0/2/2/2
1	PSU	L5	4957	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	1238	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	1673	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	119	42	-	0/7/25/26	0/2/2/2
42	A2M	S2	668	79,42	-	4/9/27/28	0/3/3/3
1	OMG	L5	4356	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4555	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4298	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	2814	1	-	1/9/27/28	0/2/2/2
1	PSU	L5	1788	1,80	-	0/7/25/26	0/2/2/2
1	PSU	L5	4517	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4409	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	34	42	-	0/7/25/26	0/2/2/2
42	OMC	S2	462	42	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
42	PSU	S2	651	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	1578	1	-	2/7/25/26	0/2/2/2
42	PSU	S2	406	42	-	0/7/25/26	0/2/2/2
1	OMG	L5	2354	1	-	0/9/27/28	0/3/3/3
42	A2M	S2	99	42	-	3/9/27/28	0/3/3/3
42	PSU	S2	1045	42	-	0/7/25/26	0/2/2/2
42	A2M	S2	468	42	-	1/9/27/28	0/3/3/3
1	PSU	L5	2829	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	3613	1	-	0/9/27/28	0/3/3/3
1	OMG	L5	1312	1	-	0/9/27/28	0/3/3/3
42	OMU	S2	1804	42	-	1/9/27/28	0/2/2/2
61	NMM	ST	67	61	-	3/9/11/13	-
1	UY1	L5	3804	79,1,80	-	1/9/27/28	0/2/2/2
42	PSU	S2	918	42	-	1/7/25/26	0/2/2/2
1	6MZ	L5	4206	1	-	0/9/27/28	0/3/3/3
42	A2M	S2	159	42	-	3/9/27/28	0/3/3/3
42	OMU	S2	354	42	-	0/9/27/28	0/2/2/2
1	PSU	L5	4986	1	-	0/7/25/26	0/2/2/2
1	OMU	L5	4606	1	-	0/9/27/28	0/2/2/2
1	A2M	L5	3704	1	-	1/9/27/28	0/3/3/3
42	MA6	S2	1850	42	-	0/11/29/30	0/3/3/3
1	PSU	L5	3681	1	-	0/7/25/26	0/2/2/2
1	A2M	L5	2805	1	-	4/9/27/28	0/3/3/3
42	OMG	S2	644	42	-	2/9/27/28	0/3/3/3
1	PSU	L5	1532	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	36	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	4576	1	-	1/9/27/28	0/3/3/3
1	OMG	L5	1518	1	-	0/9/27/28	0/3/3/3
42	A2M	S2	27	42	-	1/9/27/28	0/3/3/3
42	OMC	S2	517	42	-	0/9/27/28	0/2/2/2
1	OMC	L5	2341	1	-	3/9/27/28	0/2/2/2
42	PSU	S2	100	42	-	2/7/25/26	0/2/2/2
42	PSU	S2	1232	42	-	0/7/25/26	0/2/2/2
42	OMU	S2	1442	79,42	-	0/9/27/28	0/2/2/2
1	OMU	L5	3911	1	-	1/9/27/28	0/2/2/2
1	OMU	L5	4484	1	-	1/9/27/28	0/2/2/2
1	PSU	L5	4457	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4486	1	-	3/7/25/26	0/2/2/2
1	OMG	L5	4609	1	-	0/9/27/28	0/3/3/3
3	OMU	L8	14	3,1	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	L5	4182	79,1	-	3/9/27/28	0/3/3/3
42	PSU	S2	814	42	-	0/7/25/26	0/2/2/2
1	PSU	L5	3837	1	-	0/7/25/26	0/2/2/2
1	1MA	L5	1318	79,1	-	2/7/25/26	0/3/3/3
1	OMG	L5	4604	1	-	0/9/27/28	0/3/3/3
1	OMG	L5	4623	1	-	1/9/27/28	0/3/3/3
1	OMC	L5	3687	1,80	-	4/9/27/28	0/2/2/2
42	PSU	S2	1046	42	-	0/7/25/26	0/2/2/2
1	OMG	L5	4485	1	-	0/9/27/28	0/3/3/3
42	OMU	S2	428	42	-	4/9/27/28	0/2/2/2
1	OMU	L5	2405	1	-	0/9/27/28	0/2/2/2
42	6MZ	S2	1832	79,42,80	-	0/9/27/28	0/3/3/3
1	PSU	L5	4562	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4417	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	4378	1	-	0/9/27/28	0/3/3/3
3	OMG	L8	75	3	-	0/9/27/28	0/3/3/3
42	OMG	S2	436	42	-	0/9/27/28	0/3/3/3
1	OMC	L5	4442	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	1679	1	-	0/7/25/26	0/2/2/2
1	OMG	L5	2414	1	-	1/9/27/28	0/3/3/3
1	OMC	L5	3827	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	3839	79,1	-	0/7/25/26	0/2/2/2
42	UY1	S2	1326	42	-	3/9/27/28	0/2/2/2
1	OMC	L5	1336	1	-	0/9/27/28	0/2/2/2
42	PSU	S2	686	42	-	0/7/25/26	0/2/2/2
1	A2M	L5	3811	1	-	1/9/27/28	0/3/3/3
1	OMG	L5	4480	1	-	0/9/27/28	0/3/3/3
1	OMG	L5	1621	1,80	-	1/9/27/28	0/3/3/3
1	OMC	L5	2412	79,1	-	1/9/27/28	0/2/2/2
1	OMC	L5	2794	1	-	0/9/27/28	0/2/2/2
42	PSU	S2	93	42	-	0/7/25/26	0/2/2/2
42	PSU	S2	1625	42	-	0/7/25/26	0/2/2/2
42	A2M	S2	484	42	-	1/9/27/28	0/3/3/3
42	A2M	S2	1031	42	-	1/9/27/28	0/3/3/3
42	4AC	S2	1842	42	-	0/11/29/30	0/2/2/2
1	A2M	L5	2353	79,1	-	0/9/27/28	0/3/3/3
1	PSU	L5	3625	1	-	0/7/25/26	0/2/2/2
42	OMG	S2	1490	42	-	3/9/27/28	0/3/3/3
1	PSU	L5	2622	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4282	1	-	0/7/25/26	0/2/2/2
1	PSU	L5	4279	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	L5	2827	1	-	0/9/27/28	0/2/2/2
1	PSU	L5	1858	1	-	0/7/25/26	0/2/2/2
1	OMC	L5	1877	79,1	-	0/9/27/28	0/2/2/2
1	A2M	L5	3710	1	-	3/9/27/28	0/3/3/3
1	OMG	L5	4214	1	-	0/9/27/28	0/3/3/3
42	PSU	S2	1643	42	-	0/7/25/26	0/2/2/2
1	OMC	L5	3873	1	-	1/9/27/28	0/2/2/2
42	PSU	S2	1445	42	-	0/7/25/26	0/2/2/2
42	PSU	S2	1174	42	-	0/7/25/26	0/2/2/2
1	OMG	L5	3778	1	-	0/9/27/28	0/3/3/3
1	PSU	L5	4443	1	-	0/7/25/26	0/2/2/2
42	OMG	S2	683	42	-	2/9/27/28	0/3/3/3
1	PSU	L5	4958	1	-	0/7/25/26	0/2/2/2
42	PSU	S2	815	42	-	0/7/25/26	0/2/2/2
42	OMC	S2	1703	42	-	0/9/27/28	0/2/2/2

All (659) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S2	166	A2M	C3'-C2'	-13.29	1.23	1.52
1	L5	3710	A2M	C3'-C2'	-13.22	1.23	1.52
1	L5	4576	A2M	C3'-C2'	-13.21	1.23	1.52
1	L5	3853	A2M	C3'-C2'	-13.21	1.23	1.52
42	S2	27	A2M	C3'-C2'	-13.20	1.23	1.52
42	S2	1383	A2M	C3'-C2'	-13.19	1.23	1.52
42	S2	159	A2M	C3'-C2'	-13.18	1.23	1.52
42	S2	512	A2M	C3'-C2'	-13.18	1.23	1.52
1	L5	2353	A2M	C3'-C2'	-13.17	1.23	1.52
1	L5	400	A2M	C3'-C2'	-13.17	1.23	1.52
42	S2	590	A2M	C3'-C2'	-13.16	1.23	1.52
42	S2	1031	A2M	C3'-C2'	-13.16	1.23	1.52
42	S2	468	A2M	C3'-C2'	-13.14	1.23	1.52
1	L5	1322	A2M	C3'-C2'	-13.14	1.23	1.52
1	L5	3811	A2M	C3'-C2'	-13.14	1.23	1.52
42	S2	576	A2M	C3'-C2'	-13.12	1.23	1.52
1	L5	3704	A2M	C3'-C2'	-13.12	1.23	1.52
1	L5	1530	A2M	C3'-C2'	-13.10	1.23	1.52
42	S2	1678	A2M	C3'-C2'	-13.09	1.23	1.52
42	S2	99	A2M	C3'-C2'	-13.07	1.23	1.52
1	L5	3816	A2M	C3'-C2'	-13.06	1.23	1.52
1	L5	2777	A2M	C3'-C2'	-13.06	1.23	1.52
1	L5	1867	A2M	C3'-C2'	-13.05	1.23	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	4557	A2M	C3'-C2'	-13.05	1.23	1.52
1	L5	1319	A2M	C3'-C2'	-13.02	1.23	1.52
1	L5	2805	A2M	C3'-C2'	-13.00	1.24	1.52
1	L5	398	A2M	C3'-C2'	-12.98	1.24	1.52
1	L5	2391	A2M	C3'-C2'	-12.96	1.24	1.52
1	L5	4509	A2M	C3'-C2'	-12.95	1.24	1.52
1	L5	3771	A2M	C3'-C2'	-12.95	1.24	1.52
1	L5	1520	A2M	C3'-C2'	-12.93	1.24	1.52
42	S2	484	A2M	C3'-C2'	-12.93	1.24	1.52
42	S2	668	A2M	C3'-C2'	-12.68	1.24	1.52
42	S2	1832	6MZ	C6-N6	10.65	1.45	1.34
1	L5	4206	6MZ	C6-N6	10.50	1.45	1.34
42	S2	1288	OMU	C2-N1	7.83	1.51	1.38
1	L5	4516	UR3	C2-N1	7.76	1.49	1.38
42	S2	1442	OMU	C2-N1	7.75	1.50	1.38
42	S2	1804	OMU	C2-N1	7.74	1.50	1.38
1	L5	4213	OMU	C2-N1	7.66	1.50	1.38
42	S2	428	OMU	C2-N1	7.63	1.50	1.38
42	S2	354	OMU	C2-N1	7.62	1.50	1.38
1	L5	2827	OMU	C2-N1	7.59	1.50	1.38
42	S2	172	OMU	C2-N1	7.57	1.50	1.38
1	L5	4292	OMU	C2-N1	7.56	1.50	1.38
42	S2	1288	OMU	C2-N3	7.54	1.51	1.38
1	L5	3911	OMU	C2-N1	7.52	1.50	1.38
42	S2	116	OMU	C2-N3	7.51	1.51	1.38
3	L8	14	OMU	C2-N1	7.49	1.50	1.38
42	S2	1442	OMU	C2-N3	7.48	1.51	1.38
3	L8	14	OMU	C2-N3	7.45	1.51	1.38
42	S2	428	OMU	C2-N3	7.43	1.51	1.38
42	S2	1804	OMU	C2-N3	7.43	1.51	1.38
1	L5	4213	OMU	C2-N3	7.40	1.51	1.38
42	S2	121	OMU	C2-N1	7.40	1.50	1.38
1	L5	2405	OMU	C2-N1	7.39	1.50	1.38
1	L5	2405	OMU	C2-N3	7.37	1.51	1.38
1	L5	4606	OMU	C2-N1	7.37	1.50	1.38
42	S2	354	OMU	C2-N3	7.36	1.51	1.38
42	S2	172	OMU	C2-N3	7.35	1.51	1.38
42	S2	121	OMU	C2-N3	7.34	1.51	1.38
1	L5	4484	OMU	C2-N1	7.34	1.50	1.38
1	L5	2827	OMU	C2-N3	7.31	1.51	1.38
42	S2	116	OMU	C2-N1	7.31	1.50	1.38
1	L5	4292	OMU	C2-N3	7.30	1.51	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	4484	OMU	C2-N3	7.30	1.51	1.38
1	L5	4606	OMU	C2-N3	7.29	1.51	1.38
1	L5	3911	OMU	C2-N3	7.24	1.50	1.38
42	S2	1337	4AC	C4-N3	7.03	1.45	1.32
42	S2	1842	4AC	C4-N3	7.02	1.45	1.32
42	S2	668	A2M	O4'-C4'	-6.89	1.29	1.45
42	S2	1678	A2M	O4'-C4'	-6.75	1.29	1.45
1	L5	2777	A2M	O4'-C4'	-6.70	1.30	1.45
1	L5	1520	A2M	O4'-C4'	-6.67	1.30	1.45
1	L5	400	A2M	O4'-C4'	-6.67	1.30	1.45
1	L5	1530	A2M	O4'-C4'	-6.67	1.30	1.45
1	L5	2805	A2M	O4'-C4'	-6.66	1.30	1.45
1	L5	3853	A2M	O4'-C4'	-6.66	1.30	1.45
42	S2	1337	4AC	C6-C5	6.61	1.50	1.35
1	L5	4557	A2M	O4'-C4'	-6.59	1.30	1.45
1	L5	1319	A2M	O4'-C4'	-6.57	1.30	1.45
42	S2	484	A2M	O4'-C4'	-6.57	1.30	1.45
42	S2	159	A2M	O4'-C4'	-6.56	1.30	1.45
1	L5	3710	A2M	O4'-C4'	-6.55	1.30	1.45
1	L5	2353	A2M	O4'-C4'	-6.54	1.30	1.45
1	L5	1322	A2M	O4'-C4'	-6.54	1.30	1.45
42	S2	166	A2M	O4'-C4'	-6.53	1.30	1.45
42	S2	1842	4AC	C6-C5	6.52	1.50	1.35
1	L5	1867	A2M	O4'-C4'	-6.51	1.30	1.45
1	L5	3704	A2M	O4'-C4'	-6.50	1.30	1.45
42	S2	468	A2M	O4'-C4'	-6.50	1.30	1.45
1	L5	3811	A2M	O4'-C4'	-6.47	1.30	1.45
42	S2	1639	G7M	C4-N3	6.47	1.49	1.34
42	S2	1031	A2M	O4'-C4'	-6.45	1.30	1.45
42	S2	1639	G7M	C5-N7	-6.45	1.31	1.39
42	S2	590	A2M	O4'-C4'	-6.44	1.30	1.45
42	S2	27	A2M	O4'-C4'	-6.44	1.30	1.45
1	L5	2391	A2M	O4'-C4'	-6.44	1.30	1.45
42	S2	428	OMU	C6-C5	6.43	1.50	1.35
42	S2	1383	A2M	O4'-C4'	-6.43	1.30	1.45
42	S2	576	A2M	O4'-C4'	-6.42	1.30	1.45
1	L5	2405	OMU	C6-C5	6.42	1.50	1.35
42	S2	512	A2M	O4'-C4'	-6.41	1.30	1.45
1	L5	3816	A2M	O4'-C4'	-6.41	1.30	1.45
1	L5	4576	A2M	O4'-C4'	-6.41	1.30	1.45
1	L5	398	A2M	O4'-C4'	-6.39	1.30	1.45
1	L5	4509	A2M	O4'-C4'	-6.39	1.30	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	4606	OMU	C6-C5	6.38	1.49	1.35
1	L5	4213	OMU	C6-C5	6.37	1.49	1.35
42	S2	99	A2M	O4'-C4'	-6.37	1.30	1.45
1	L5	3771	A2M	O4'-C4'	-6.37	1.30	1.45
1	L5	4516	UR3	C6-C5	6.37	1.49	1.35
42	S2	1288	OMU	C6-C5	6.36	1.49	1.35
1	L5	2827	OMU	C6-C5	6.36	1.49	1.35
1	L5	3911	OMU	C6-C5	6.32	1.49	1.35
42	S2	121	OMU	C6-C5	6.32	1.49	1.35
42	S2	1442	OMU	C6-C5	6.32	1.49	1.35
42	S2	116	OMU	C6-C5	6.30	1.49	1.35
42	S2	172	OMU	C6-C5	6.29	1.49	1.35
1	L5	4484	OMU	C6-C5	6.29	1.49	1.35
42	S2	1804	OMU	C6-C5	6.28	1.49	1.35
42	S2	354	OMU	C6-C5	6.26	1.49	1.35
1	L5	4292	OMU	C6-C5	6.22	1.49	1.35
3	L8	14	OMU	C6-C5	6.15	1.49	1.35
42	S2	1337	4AC	C2-N3	6.14	1.48	1.36
42	S2	1842	4AC	C2-N3	6.06	1.48	1.36
1	L5	3771	A2M	C3'-C4'	6.01	1.68	1.53
42	S2	668	A2M	C3'-C4'	5.71	1.67	1.53
42	S2	1031	A2M	C3'-C4'	5.68	1.67	1.53
1	L5	1322	A2M	C3'-C4'	5.67	1.67	1.53
1	L5	3816	A2M	C3'-C4'	5.66	1.67	1.53
1	L5	4509	A2M	C3'-C4'	5.65	1.67	1.53
1	L5	2353	A2M	C3'-C4'	5.64	1.67	1.53
42	S2	484	A2M	C3'-C4'	5.64	1.67	1.53
42	S2	1383	A2M	C3'-C4'	5.64	1.67	1.53
1	L5	4576	A2M	C3'-C4'	5.63	1.67	1.53
1	L5	3704	A2M	C3'-C4'	5.60	1.67	1.53
42	S2	576	A2M	C3'-C4'	5.60	1.67	1.53
1	L5	4557	A2M	C3'-C4'	5.59	1.67	1.53
1	L5	1530	A2M	C3'-C4'	5.58	1.67	1.53
1	L5	1319	A2M	C3'-C4'	5.57	1.67	1.53
42	S2	1678	A2M	C3'-C4'	5.56	1.67	1.53
42	S2	512	A2M	C3'-C4'	5.54	1.67	1.53
1	L5	3811	A2M	C3'-C4'	5.53	1.67	1.53
1	L5	1867	A2M	C3'-C4'	5.52	1.67	1.53
1	L5	3710	A2M	C3'-C4'	5.52	1.67	1.53
42	S2	27	A2M	C3'-C4'	5.51	1.67	1.53
1	L5	1520	A2M	C3'-C4'	5.50	1.67	1.53
42	S2	99	A2M	C3'-C4'	5.49	1.67	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	400	A2M	C3'-C4'	5.48	1.67	1.53
1	L5	398	A2M	C3'-C4'	5.47	1.67	1.53
42	S2	468	A2M	C3'-C4'	5.45	1.66	1.53
42	S2	590	A2M	C3'-C4'	5.44	1.66	1.53
1	L5	3853	A2M	C3'-C4'	5.42	1.66	1.53
1	L5	2391	A2M	C3'-C4'	5.42	1.66	1.53
1	L5	2805	A2M	C3'-C4'	5.38	1.66	1.53
42	S2	166	A2M	C3'-C4'	5.36	1.66	1.53
42	S2	159	A2M	C3'-C4'	5.35	1.66	1.53
42	S2	1337	4AC	C7-N4	5.35	1.47	1.37
42	S2	1639	G7M	C2-N3	5.29	1.45	1.33
1	L5	2777	A2M	C3'-C4'	5.29	1.66	1.53
42	S2	1337	4AC	C4-N4	5.21	1.47	1.39
42	S2	1842	4AC	C7-N4	4.95	1.46	1.37
1	L5	1520	A2M	C1'-N9	-4.85	1.32	1.46
42	S2	1031	A2M	C1'-N9	-4.83	1.32	1.46
42	S2	512	A2M	C1'-N9	-4.82	1.32	1.46
42	S2	1383	A2M	C1'-N9	-4.82	1.32	1.46
42	S2	590	A2M	C1'-N9	-4.81	1.32	1.46
42	S2	159	A2M	C1'-N9	-4.77	1.32	1.46
1	L5	1867	A2M	C1'-N9	-4.77	1.32	1.46
1	L5	4576	A2M	C1'-N9	-4.75	1.32	1.46
42	S2	1842	4AC	C4-N4	4.73	1.46	1.39
42	S2	576	A2M	C1'-N9	-4.70	1.33	1.46
42	S2	668	A2M	C1'-N9	-4.70	1.33	1.46
1	L5	3710	A2M	C1'-N9	-4.70	1.33	1.46
42	S2	1850	MA6	C6-N6	4.69	1.50	1.36
42	S2	468	A2M	C1'-N9	-4.69	1.33	1.46
1	L5	3816	A2M	C1'-N9	-4.68	1.33	1.46
42	S2	166	A2M	C1'-N9	-4.68	1.33	1.46
42	S2	1851	MA6	C6-N6	4.66	1.50	1.36
1	L5	3853	A2M	C1'-N9	-4.66	1.33	1.46
42	S2	27	A2M	C1'-N9	-4.65	1.33	1.46
42	S2	1678	A2M	C1'-N9	-4.65	1.33	1.46
42	S2	99	A2M	C1'-N9	-4.64	1.33	1.46
1	L5	4516	UR3	C2-N3	4.63	1.48	1.39
1	L5	2391	A2M	C1'-N9	-4.63	1.33	1.46
1	L5	400	A2M	C1'-N9	-4.61	1.33	1.46
1	L5	2805	A2M	C1'-N9	-4.60	1.33	1.46
1	L5	3704	A2M	C1'-N9	-4.59	1.33	1.46
1	L5	4509	A2M	C1'-N9	-4.59	1.33	1.46
1	L5	1322	A2M	C1'-N9	-4.59	1.33	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	3811	A2M	C1'-N9	-4.58	1.33	1.46
1	L5	2353	A2M	C1'-N9	-4.57	1.33	1.46
1	L5	1530	A2M	C1'-N9	-4.57	1.33	1.46
1	L5	1319	A2M	C1'-N9	-4.57	1.33	1.46
1	L5	3771	A2M	C1'-N9	-4.55	1.33	1.46
1	L5	4557	A2M	C1'-N9	-4.52	1.33	1.46
1	L5	398	A2M	C1'-N9	-4.51	1.33	1.46
42	S2	1337	4AC	C5-C4	4.48	1.50	1.40
42	S2	484	A2M	C1'-N9	-4.45	1.33	1.46
42	S2	1639	G7M	C2-N2	4.44	1.44	1.34
42	S2	1288	OMU	C4-N3	4.44	1.46	1.38
42	S2	1804	OMU	C4-N3	4.40	1.46	1.38
42	S2	116	OMU	C4-N3	4.39	1.46	1.38
42	S2	1442	OMU	C4-N3	4.36	1.46	1.38
1	L5	2777	A2M	C1'-N9	-4.33	1.34	1.46
42	S2	354	OMU	C4-N3	4.31	1.46	1.38
1	L5	4484	OMU	C4-N3	4.31	1.46	1.38
3	L8	14	OMU	C4-N3	4.31	1.46	1.38
42	S2	1842	4AC	C5-C4	4.30	1.50	1.40
1	L5	4213	OMU	C4-N3	4.30	1.46	1.38
42	S2	172	OMU	C4-N3	4.30	1.46	1.38
42	S2	428	OMU	C4-N3	4.30	1.46	1.38
42	S2	121	OMU	C4-N3	4.27	1.46	1.38
1	L5	4292	OMU	C4-N3	4.24	1.46	1.38
1	L5	2405	OMU	C4-N3	4.22	1.46	1.38
1	L5	2827	OMU	C4-N3	4.19	1.46	1.38
1	L5	4606	OMU	C4-N3	4.15	1.46	1.38
1	L5	3911	OMU	C4-N3	4.15	1.46	1.38
42	S2	166	A2M	O4'-C1'	4.14	1.51	1.42
42	S2	1842	4AC	C2-N1	4.12	1.48	1.40
42	S2	1383	A2M	C5-C4	-4.12	1.31	1.39
1	L5	4509	A2M	O4'-C1'	4.11	1.51	1.42
42	S2	512	A2M	C5-C4	-4.11	1.31	1.39
42	S2	166	A2M	C6-N6	4.10	1.44	1.34
42	S2	468	A2M	C6-N6	4.09	1.44	1.34
42	S2	668	A2M	C5-C4	-4.09	1.31	1.39
1	L5	4576	A2M	O4'-C1'	4.09	1.51	1.42
1	L5	2353	A2M	C6-N6	4.09	1.44	1.34
1	L5	4509	A2M	C5-C4	-4.08	1.31	1.39
1	L5	3704	A2M	C6-N6	4.08	1.44	1.34
1	L5	3710	A2M	O4'-C1'	4.07	1.51	1.42
1	L5	3771	A2M	C5-C4	-4.07	1.31	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	1322	A2M	C6-N6	4.07	1.44	1.34
42	S2	590	A2M	O4'-C1'	4.06	1.51	1.42
42	S2	576	A2M	C6-N6	4.06	1.44	1.34
1	L5	3710	A2M	C5-C4	-4.06	1.31	1.39
42	S2	1031	A2M	C5-C4	-4.06	1.31	1.39
42	S2	99	A2M	C6-N6	4.05	1.44	1.34
1	L5	3816	A2M	O4'-C1'	4.05	1.51	1.42
1	L5	2777	A2M	C5-C4	-4.05	1.31	1.39
42	S2	484	A2M	C6-N6	4.05	1.44	1.34
1	L5	3811	A2M	O4'-C1'	4.05	1.51	1.42
42	S2	159	A2M	O4'-C1'	4.04	1.51	1.42
42	S2	1678	A2M	C6-N6	4.04	1.44	1.34
1	L5	400	A2M	O4'-C1'	4.04	1.51	1.42
42	S2	1383	A2M	C6-N6	4.04	1.44	1.34
1	L5	400	A2M	C6-N6	4.04	1.44	1.34
42	S2	27	A2M	C6-N6	4.03	1.44	1.34
1	L5	4557	A2M	C6-N6	4.03	1.44	1.34
1	L5	1867	A2M	C5-C4	-4.03	1.31	1.39
42	S2	1678	A2M	C5-C4	-4.03	1.31	1.39
1	L5	398	A2M	O4'-C1'	4.03	1.51	1.42
1	L5	4576	A2M	C5-C4	-4.02	1.31	1.39
42	S2	576	A2M	C5-C4	-4.02	1.31	1.39
1	L5	1867	A2M	C6-N6	4.02	1.44	1.34
1	L5	3816	A2M	C5-C4	-4.02	1.31	1.39
42	S2	1337	4AC	C2-N1	4.01	1.48	1.40
42	S2	27	A2M	C5-C4	-4.01	1.31	1.39
1	L5	3704	A2M	O4'-C1'	4.01	1.51	1.42
42	S2	99	A2M	O4'-C1'	4.01	1.51	1.42
42	S2	99	A2M	C5-C4	-4.01	1.31	1.39
1	L5	398	A2M	C6-N6	4.01	1.44	1.34
1	L5	3710	A2M	C6-N6	4.01	1.44	1.34
42	S2	668	A2M	C6-N6	4.01	1.44	1.34
1	L5	2777	A2M	C6-N6	4.00	1.44	1.34
42	S2	1678	A2M	O4'-C1'	4.00	1.51	1.42
1	L5	3853	A2M	C5-C4	-4.00	1.31	1.39
1	L5	1530	A2M	C6-N6	4.00	1.44	1.34
1	L5	3811	A2M	C6-N6	4.00	1.44	1.34
1	L5	1319	A2M	C6-N6	3.99	1.44	1.34
1	L5	3853	A2M	C6-N6	3.99	1.44	1.34
42	S2	512	A2M	C6-N6	3.99	1.44	1.34
42	S2	159	A2M	C6-N6	3.99	1.44	1.34
1	L5	400	A2M	C5-C4	-3.99	1.31	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S2	590	A2M	C5-C4	-3.99	1.31	1.39
42	S2	512	A2M	O4'-C1'	3.98	1.51	1.42
42	S2	166	A2M	C5-C4	-3.98	1.31	1.39
1	L5	2391	A2M	C6-N6	3.98	1.44	1.34
1	L5	2805	A2M	C6-N6	3.98	1.44	1.34
42	S2	468	A2M	C5-C4	-3.98	1.31	1.39
42	S2	590	A2M	C6-N6	3.97	1.44	1.34
42	S2	1383	A2M	O4'-C1'	3.97	1.51	1.42
1	L5	1530	A2M	C5-C4	-3.97	1.31	1.39
1	L5	1867	A2M	O4'-C1'	3.97	1.51	1.42
42	S2	468	A2M	O4'-C1'	3.96	1.51	1.42
1	L5	1520	A2M	C6-N6	3.96	1.44	1.34
42	S2	484	A2M	C5-C4	-3.96	1.31	1.39
1	L5	4557	A2M	O4'-C1'	3.95	1.51	1.42
42	S2	27	A2M	O4'-C1'	3.95	1.51	1.42
1	L5	2805	A2M	O4'-C1'	3.95	1.51	1.42
1	L5	2391	A2M	C5-C4	-3.95	1.31	1.39
1	L5	4576	A2M	C6-N6	3.94	1.44	1.34
42	S2	1031	A2M	C6-N6	3.94	1.44	1.34
1	L5	3704	A2M	C5-C4	-3.94	1.31	1.39
42	S2	159	A2M	C5-C4	-3.94	1.31	1.39
1	L5	4509	A2M	C6-N6	3.93	1.44	1.34
1	L5	398	A2M	C5-C4	-3.93	1.31	1.39
1	L5	3811	A2M	C5-C4	-3.93	1.31	1.39
1	L5	2805	A2M	C5-C4	-3.93	1.31	1.39
1	L5	3816	A2M	C6-N6	3.92	1.44	1.34
1	L5	1319	A2M	C5-C4	-3.92	1.31	1.39
42	S2	576	A2M	O4'-C1'	3.90	1.51	1.42
1	L5	3771	A2M	C6-N6	3.89	1.43	1.34
1	L5	1322	A2M	C5-C4	-3.89	1.31	1.39
1	L5	2391	A2M	O4'-C1'	3.89	1.51	1.42
1	L5	3853	A2M	O4'-C1'	3.88	1.51	1.42
1	L5	4557	A2M	C5-C4	-3.88	1.31	1.39
1	L5	1319	A2M	O4'-C1'	3.88	1.51	1.42
42	S2	1031	A2M	O4'-C1'	3.87	1.51	1.42
1	L5	1530	A2M	O4'-C1'	3.86	1.51	1.42
1	L5	2353	A2M	O4'-C1'	3.84	1.51	1.42
1	L5	2353	A2M	C5-C4	-3.84	1.31	1.39
1	L5	2805	A2M	O2'-C2'	3.84	1.52	1.42
1	L5	1520	A2M	C5-C4	-3.84	1.31	1.39
1	L5	2777	A2M	O4'-C1'	3.82	1.51	1.42
1	L5	1322	A2M	O2'-C2'	3.81	1.52	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S2	668	A2M	O2'-C2'	3.81	1.52	1.42
1	L5	3811	A2M	O2'-C2'	3.80	1.52	1.42
1	L5	3710	A2M	O2'-C2'	3.79	1.52	1.42
1	L5	2777	A2M	O2'-C2'	3.79	1.52	1.42
1	L5	1322	A2M	O4'-C1'	3.79	1.51	1.42
1	L5	4576	A2M	O2'-C2'	3.79	1.52	1.42
42	S2	484	A2M	O4'-C1'	3.78	1.51	1.42
1	L5	4509	A2M	O2'-C2'	3.78	1.52	1.42
1	L5	1520	A2M	O2'-C2'	3.77	1.52	1.42
42	S2	1383	A2M	O2'-C2'	3.77	1.52	1.42
1	L5	1520	A2M	O4'-C1'	3.77	1.50	1.42
42	S2	590	A2M	O2'-C2'	3.76	1.52	1.42
42	S2	27	A2M	O2'-C2'	3.76	1.52	1.42
42	S2	99	A2M	O2'-C2'	3.76	1.52	1.42
42	S2	512	A2M	O2'-C2'	3.76	1.52	1.42
1	L5	3816	A2M	O2'-C2'	3.75	1.52	1.42
42	S2	576	A2M	O2'-C2'	3.74	1.52	1.42
42	S2	159	A2M	O2'-C2'	3.74	1.52	1.42
1	L5	4443	PSU	C6-C5	3.74	1.39	1.35
1	L5	2353	A2M	O2'-C2'	3.73	1.52	1.42
42	S2	468	A2M	O2'-C2'	3.72	1.52	1.42
1	L5	3906	PSU	C6-C5	3.71	1.39	1.35
1	L5	1867	A2M	O2'-C2'	3.71	1.52	1.42
1	L5	3853	A2M	O2'-C2'	3.71	1.52	1.42
42	S2	668	A2M	O4'-C1'	3.71	1.50	1.42
1	L5	1530	A2M	O2'-C2'	3.71	1.52	1.42
1	L5	4557	A2M	O2'-C2'	3.71	1.52	1.42
42	S2	484	A2M	O2'-C2'	3.70	1.52	1.42
42	S2	1031	A2M	O2'-C2'	3.69	1.52	1.42
1	L5	3704	A2M	O2'-C2'	3.69	1.52	1.42
1	L5	400	A2M	O2'-C2'	3.68	1.52	1.42
42	S2	166	A2M	O2'-C2'	3.68	1.52	1.42
1	L5	3870	PSU	C6-C5	3.67	1.39	1.35
42	S2	1639	G7M	C5-C6	3.67	1.53	1.43
1	L5	4507	PSU	C6-C5	3.66	1.39	1.35
1	L5	2391	A2M	O2'-C2'	3.65	1.52	1.42
1	L5	4389	PSU	C6-C5	3.65	1.39	1.35
1	L5	398	A2M	O2'-C2'	3.64	1.52	1.42
1	L5	4457	PSU	C6-C5	3.63	1.39	1.35
1	L5	1319	A2M	O2'-C2'	3.63	1.51	1.42
42	S2	406	PSU	C6-C5	3.58	1.39	1.35
42	S2	1004	PSU	C6-C5	3.56	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S2	1046	PSU	C6-C5	3.56	1.39	1.35
1	L5	1778	PSU	C6-C5	3.56	1.39	1.35
1	L5	4614	PSU	C6-C5	3.55	1.39	1.35
42	S2	1678	A2M	O2'-C2'	3.55	1.51	1.42
1	L5	4957	PSU	C6-C5	3.55	1.39	1.35
42	S2	119	PSU	C6-C5	3.55	1.39	1.35
42	S2	801	PSU	C6-C5	3.54	1.39	1.35
1	L5	4986	PSU	C6-C5	3.54	1.39	1.35
42	S2	1056	PSU	C6-C5	3.54	1.39	1.35
1	L5	4995	PSU	C6-C5	3.54	1.39	1.35
42	S2	1136	PSU	C6-C5	3.53	1.39	1.35
1	L5	2829	PSU	C6-C5	3.52	1.39	1.35
3	L8	69	PSU	C6-C5	3.52	1.39	1.35
42	S2	93	PSU	C6-C5	3.52	1.39	1.35
1	L5	4347	PSU	C6-C5	3.51	1.39	1.35
42	S2	1625	PSU	C6-C5	3.51	1.39	1.35
42	S2	109	PSU	C6-C5	3.51	1.39	1.35
1	L5	3771	A2M	O2'-C2'	3.50	1.51	1.42
42	S2	1174	PSU	C6-C5	3.50	1.39	1.35
1	L5	4428	PSU	C6-C5	3.50	1.39	1.35
1	L5	4555	PSU	C6-C5	3.50	1.39	1.35
42	S2	1643	PSU	C6-C5	3.49	1.39	1.35
1	L5	4279	PSU	C6-C5	3.48	1.39	1.35
1	L5	4659	PSU	C6-C5	3.48	1.39	1.35
42	S2	1639	G7M	C2-N1	3.48	1.46	1.37
1	L5	4518	PSU	C6-C5	3.48	1.39	1.35
1	L5	2777	A2M	C2'-C1'	3.48	1.62	1.53
42	S2	1596	PSU	C6-C5	3.47	1.39	1.35
42	S2	484	A2M	C2'-C1'	3.47	1.62	1.53
42	S2	667	PSU	C6-C5	3.47	1.39	1.35
1	L5	4675	PSU	C6-C5	3.47	1.39	1.35
1	L5	3808	PSU	C6-C5	3.47	1.39	1.35
42	S2	822	PSU	C6-C5	3.47	1.39	1.35
42	S2	918	PSU	C6-C5	3.46	1.39	1.35
1	L5	3837	PSU	C6-C5	3.46	1.39	1.35
42	S2	649	PSU	C6-C5	3.46	1.39	1.35
42	S2	686	PSU	C6-C5	3.46	1.39	1.35
42	S2	1045	PSU	C6-C5	3.45	1.39	1.35
1	L5	3771	A2M	O4'-C1'	3.45	1.50	1.42
42	S2	34	PSU	C6-C5	3.45	1.39	1.35
1	L5	4486	PSU	C6-C5	3.44	1.39	1.35
1	L5	4958	PSU	C6-C5	3.44	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	3839	PSU	C6-C5	3.44	1.39	1.35
1	L5	4417	PSU	C6-C5	3.44	1.39	1.35
42	S2	1232	PSU	C6-C5	3.43	1.39	1.35
1	L5	1532	PSU	C6-C5	3.43	1.39	1.35
1	L5	4562	PSU	C6-C5	3.43	1.39	1.35
42	S2	105	PSU	C6-C5	3.43	1.39	1.35
42	S2	1177	PSU	C6-C5	3.43	1.39	1.35
42	S2	1244	PSU	C6-C5	3.43	1.39	1.35
42	S2	1238	PSU	C6-C5	3.42	1.39	1.35
42	S2	863	PSU	C6-C5	3.42	1.39	1.35
1	L5	4565	PSU	C6-C5	3.42	1.39	1.35
42	S2	36	PSU	C6-C5	3.41	1.39	1.35
42	S2	100	PSU	C6-C5	3.41	1.39	1.35
42	S2	651	PSU	C6-C5	3.41	1.39	1.35
1	L5	4339	PSU	C6-C5	3.41	1.39	1.35
1	L5	2622	PSU	C6-C5	3.40	1.39	1.35
42	S2	1445	PSU	C6-C5	3.40	1.39	1.35
42	S2	681	PSU	C6-C5	3.40	1.39	1.35
1	L5	3830	PSU	C6-C5	3.40	1.39	1.35
42	S2	218	PSU	C6-C5	3.40	1.39	1.35
1	L5	4538	PSU	C6-C5	3.40	1.39	1.35
42	S2	1692	PSU	C6-C5	3.39	1.39	1.35
1	L5	4285	PSU	C6-C5	3.39	1.39	1.35
1	L5	1777	PSU	C6-C5	3.39	1.39	1.35
1	L5	3625	PSU	C6-C5	3.39	1.39	1.35
3	L8	55	PSU	C6-C5	3.38	1.39	1.35
42	S2	609	PSU	C6-C5	3.38	1.39	1.35
42	S2	1383	A2M	C2'-C1'	3.38	1.61	1.53
42	S2	1842	4AC	C6-N1	3.37	1.46	1.38
42	S2	1347	PSU	C6-C5	3.37	1.39	1.35
1	L5	1520	A2M	C2'-C1'	3.36	1.61	1.53
42	S2	815	PSU	C6-C5	3.36	1.39	1.35
1	L5	1578	PSU	C6-C5	3.36	1.39	1.35
1	L5	3623	PSU	C6-C5	3.35	1.39	1.35
1	L5	3681	PSU	C6-C5	3.35	1.39	1.35
1	L5	4298	PSU	C6-C5	3.34	1.39	1.35
42	S2	572	PSU	C6-C5	3.34	1.39	1.35
42	S2	668	A2M	C2'-C1'	3.33	1.61	1.53
1	L5	1856	PSU	C6-C5	3.32	1.39	1.35
1	L5	1858	PSU	C6-C5	3.32	1.39	1.35
1	L5	4409	PSU	C6-C5	3.31	1.39	1.35
42	S2	1337	4AC	C6-N1	3.31	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	3701	PSU	C6-C5	3.31	1.39	1.35
1	L5	1679	PSU	C6-C5	3.30	1.39	1.35
1	L5	4282	PSU	C6-C5	3.30	1.39	1.35
1	L5	4517	PSU	C6-C5	3.30	1.39	1.35
1	L5	4622	PSU	C6-C5	3.29	1.39	1.35
1	L5	1788	PSU	C6-C5	3.29	1.39	1.35
1	L5	398	A2M	C2'-C1'	3.28	1.61	1.53
1	L5	3811	A2M	C2'-C1'	3.27	1.61	1.53
1	L5	2391	A2M	C2'-C1'	3.26	1.61	1.53
42	S2	814	PSU	C6-C5	3.26	1.39	1.35
1	L5	3704	A2M	C8-N9	-3.25	1.31	1.37
42	S2	590	A2M	C8-N9	-3.24	1.31	1.37
42	S2	99	A2M	C2'-C1'	3.24	1.61	1.53
1	L5	1673	PSU	C6-C5	3.23	1.39	1.35
1	L5	4557	A2M	C8-N9	-3.22	1.31	1.37
42	S2	576	A2M	C2'-C1'	3.22	1.61	1.53
1	L5	1740	PSU	C6-C5	3.21	1.39	1.35
1	L5	400	A2M	C8-N9	-3.21	1.31	1.37
42	S2	590	A2M	C2'-C1'	3.21	1.61	1.53
42	S2	166	A2M	C2'-C1'	3.20	1.61	1.53
42	S2	468	A2M	C2'-C1'	3.20	1.61	1.53
1	L5	3771	A2M	C8-N9	-3.20	1.31	1.37
1	L5	4557	A2M	C2'-C1'	3.18	1.61	1.53
42	S2	166	A2M	C8-N9	-3.18	1.31	1.37
42	S2	1678	A2M	C8-N9	-3.18	1.31	1.37
42	S2	1639	G7M	O6-C6	-3.18	1.17	1.23
1	L5	1322	A2M	C2'-C1'	3.18	1.61	1.53
42	S2	159	A2M	C2'-C1'	3.18	1.61	1.53
42	S2	668	A2M	C8-N9	-3.17	1.31	1.37
1	L5	4516	UR3	O2-C2	-3.17	1.16	1.22
1	L5	2805	A2M	C2'-C1'	3.17	1.61	1.53
1	L5	4509	A2M	C2'-C1'	3.16	1.61	1.53
42	S2	576	A2M	C8-N9	-3.16	1.31	1.37
1	L5	1520	A2M	C8-N9	-3.16	1.31	1.37
42	S2	484	A2M	C8-N9	-3.15	1.31	1.37
1	L5	3853	A2M	C8-N9	-3.14	1.31	1.37
1	L5	1530	A2M	C2'-C1'	3.14	1.61	1.53
42	S2	512	A2M	C2'-C1'	3.14	1.61	1.53
42	S2	27	A2M	C2'-C1'	3.14	1.61	1.53
42	S2	1383	A2M	C8-N9	-3.14	1.31	1.37
1	L5	3704	A2M	C2'-C1'	3.13	1.61	1.53
1	L5	2353	A2M	C2'-C1'	3.12	1.61	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S2	512	A2M	C8-N9	-3.12	1.31	1.37
1	L5	3816	A2M	C2'-C1'	3.12	1.61	1.53
1	L5	3771	A2M	C2'-C1'	3.12	1.61	1.53
42	S2	99	A2M	C8-N9	-3.11	1.31	1.37
1	L5	400	A2M	C2'-C1'	3.10	1.61	1.53
42	S2	468	A2M	C8-N9	-3.10	1.32	1.37
1	L5	3710	A2M	C8-N9	-3.10	1.32	1.37
1	L5	4576	A2M	C8-N9	-3.09	1.32	1.37
1	L5	2405	OMU	C6-N1	3.09	1.45	1.38
1	L5	2353	A2M	C8-N9	-3.08	1.32	1.37
1	L5	2805	A2M	C8-N9	-3.08	1.32	1.37
1	L5	4509	A2M	C8-N9	-3.08	1.32	1.37
42	S2	159	A2M	C8-N9	-3.07	1.32	1.37
1	L5	1319	A2M	C8-N9	-3.07	1.32	1.37
1	L5	3816	A2M	C8-N9	-3.07	1.32	1.37
1	L5	2391	A2M	C8-N9	-3.06	1.32	1.37
1	L5	3811	A2M	C8-N9	-3.06	1.32	1.37
1	L5	3710	A2M	C2'-C1'	3.06	1.60	1.53
1	L5	398	A2M	C8-N9	-3.06	1.32	1.37
42	S2	27	A2M	C8-N9	-3.06	1.32	1.37
1	L5	1867	A2M	C2'-C1'	3.05	1.60	1.53
42	S2	1031	A2M	C2'-C1'	3.05	1.60	1.53
1	L5	1322	A2M	C8-N9	-3.05	1.32	1.37
42	S2	1288	OMU	C6-N1	3.03	1.45	1.38
1	L5	4576	A2M	C2'-C1'	3.02	1.60	1.53
42	S2	428	OMU	C6-N1	3.02	1.45	1.38
42	S2	1031	A2M	C8-N9	-3.01	1.32	1.37
1	L5	4484	OMU	C6-N1	3.00	1.45	1.38
1	L5	4606	OMU	C6-N1	3.00	1.45	1.38
42	S2	484	A2M	O3'-C3'	3.00	1.50	1.43
1	L5	3853	A2M	C2'-C1'	3.00	1.60	1.53
1	L5	1319	A2M	C2'-C1'	2.99	1.60	1.53
1	L5	4292	OMU	C6-N1	2.99	1.45	1.38
42	S2	116	OMU	C6-N1	2.98	1.45	1.38
1	L5	3911	OMU	C6-N1	2.98	1.45	1.38
1	L5	4213	OMU	C6-N1	2.98	1.45	1.38
1	L5	1867	A2M	C8-N9	-2.97	1.32	1.37
42	S2	1804	OMU	C6-N1	2.97	1.45	1.38
42	S2	1442	OMU	C6-N1	2.96	1.45	1.38
42	S2	354	OMU	C6-N1	2.94	1.45	1.38
3	L8	14	OMU	C6-N1	2.94	1.45	1.38
42	S2	121	OMU	C6-N1	2.94	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	2777	A2M	C8-N9	-2.94	1.32	1.37
1	L5	1530	A2M	C8-N9	-2.93	1.32	1.37
42	S2	1842	4AC	O2-C2	-2.92	1.18	1.23
42	S2	172	OMU	C6-N1	2.89	1.45	1.38
1	L5	3771	A2M	O3'-C3'	2.87	1.49	1.43
1	L5	2827	OMU	C6-N1	2.84	1.44	1.38
42	S2	576	A2M	O3'-C3'	2.84	1.49	1.43
1	L5	4292	OMU	O4-C4	-2.83	1.19	1.24
42	S2	1678	A2M	C2'-C1'	2.82	1.60	1.53
1	L5	3704	A2M	O3'-C3'	2.81	1.49	1.43
1	L5	1319	A2M	O3'-C3'	2.80	1.49	1.43
1	L5	1530	A2M	O3'-C3'	2.80	1.49	1.43
42	S2	668	A2M	O3'-C3'	2.79	1.49	1.43
42	S2	1337	4AC	O2-C2	-2.78	1.18	1.23
1	L5	398	A2M	O3'-C3'	2.76	1.49	1.43
1	L5	1520	A2M	O3'-C3'	2.76	1.49	1.43
1	L5	4557	A2M	O3'-C3'	2.76	1.49	1.43
42	S2	428	OMU	C5-C4	2.75	1.49	1.43
42	S2	116	OMU	C5-C4	2.74	1.49	1.43
1	L5	4206	6MZ	C5-C4	-2.74	1.33	1.39
1	L5	1322	A2M	O3'-C3'	2.74	1.49	1.43
1	L5	2827	OMU	O4-C4	-2.74	1.19	1.24
1	L5	4206	6MZ	C5-N7	-2.74	1.33	1.39
1	L5	3911	OMU	O4-C4	-2.73	1.19	1.24
1	L5	2391	A2M	O3'-C3'	2.73	1.49	1.43
42	S2	27	A2M	O3'-C3'	2.72	1.49	1.43
1	L5	4484	OMU	C5-C4	2.72	1.49	1.43
42	S2	354	OMU	C5-C4	2.72	1.49	1.43
42	S2	1442	OMU	C5-C4	2.72	1.49	1.43
42	S2	121	OMU	C5-C4	2.72	1.49	1.43
1	L5	4213	OMU	C5-C4	2.71	1.49	1.43
42	S2	1288	OMU	C5-C4	2.71	1.49	1.43
3	L8	14	OMU	C5-C4	2.71	1.49	1.43
1	L5	4516	UR3	O4-C4	-2.70	1.17	1.23
3	L8	14	OMU	O4-C4	-2.70	1.19	1.24
1	L5	4606	OMU	O4-C4	-2.70	1.19	1.24
1	L5	3911	OMU	C5-C4	2.69	1.49	1.43
42	S2	172	OMU	C5-C4	2.69	1.49	1.43
1	L5	2353	A2M	O3'-C3'	2.69	1.49	1.43
1	L5	4606	OMU	C5-C4	2.68	1.49	1.43
42	S2	1031	A2M	O3'-C3'	2.68	1.49	1.43
1	L5	2827	OMU	C5-C4	2.68	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S2	1851	MA6	C5-C4	-2.68	1.34	1.39
42	S2	1850	MA6	C5-C4	-2.67	1.34	1.39
1	L5	4292	OMU	C5-C4	2.67	1.49	1.43
42	S2	354	OMU	O4-C4	-2.65	1.19	1.24
42	S2	1804	OMU	C5-C4	2.65	1.49	1.43
42	S2	1383	A2M	O3'-C3'	2.65	1.49	1.43
42	S2	99	A2M	O3'-C3'	2.64	1.49	1.43
42	S2	166	A2M	O3'-C3'	2.64	1.49	1.43
1	L5	1867	A2M	O3'-C3'	2.63	1.49	1.43
1	L5	3811	A2M	O3'-C3'	2.62	1.49	1.43
42	S2	1832	6MZ	C5-N7	-2.62	1.34	1.39
1	L5	3816	A2M	O3'-C3'	2.62	1.49	1.43
42	S2	512	A2M	O3'-C3'	2.60	1.49	1.43
42	S2	1832	6MZ	C5-C4	-2.60	1.34	1.39
42	S2	590	A2M	O3'-C3'	2.60	1.49	1.43
1	L5	2777	A2M	O3'-C3'	2.58	1.49	1.43
42	S2	159	A2M	O3'-C3'	2.58	1.49	1.43
1	L5	3710	A2M	O3'-C3'	2.57	1.49	1.43
42	S2	1678	A2M	O3'-C3'	2.57	1.49	1.43
1	L5	2805	A2M	O3'-C3'	2.56	1.49	1.43
1	L5	4484	OMU	O4-C4	-2.56	1.19	1.24
42	S2	1639	G7M	CN7-N7	-2.56	1.42	1.46
42	S2	468	A2M	O3'-C3'	2.55	1.49	1.43
42	S2	1804	OMU	O4-C4	-2.55	1.19	1.24
42	S2	116	OMU	O4-C4	-2.54	1.19	1.24
42	S2	1442	OMU	O4-C4	-2.54	1.19	1.24
42	S2	428	OMU	O4-C4	-2.53	1.19	1.24
1	L5	4509	A2M	O3'-C3'	2.53	1.48	1.43
42	S2	121	OMU	O4-C4	-2.53	1.19	1.24
1	L5	4213	OMU	O4-C4	-2.52	1.19	1.24
1	L5	2405	OMU	C5-C4	2.51	1.49	1.43
1	L5	400	A2M	O3'-C3'	2.51	1.48	1.43
42	S2	172	OMU	O4-C4	-2.51	1.19	1.24
1	L5	4576	A2M	O3'-C3'	2.50	1.48	1.43
1	L5	3853	A2M	O3'-C3'	2.47	1.48	1.43
42	S2	1639	G7M	C6-N1	2.46	1.43	1.38
1	L5	2405	OMU	O4-C4	-2.45	1.19	1.24
42	S2	1288	OMU	O4-C4	-2.41	1.19	1.24
1	L5	4516	UR3	C6-N1	2.39	1.43	1.38
3	L8	14	OMU	O2-C2	-2.33	1.18	1.23
1	L5	3911	OMU	O2-C2	-2.32	1.18	1.23
42	S2	1850	MA6	C5-N7	-2.30	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	4292	OMU	O2-C2	-2.29	1.18	1.23
42	S2	159	A2M	O5'-C5'	-2.28	1.39	1.44
42	S2	1639	G7M	C4-N9	-2.27	1.32	1.38
1	L5	4516	UR3	C5-C4	2.26	1.49	1.43
1	L5	2405	OMU	O2-C2	-2.26	1.18	1.23
1	L5	4484	OMU	O2-C2	-2.26	1.18	1.23
1	L5	3853	A2M	O5'-C5'	-2.25	1.39	1.44
1	L5	2827	OMU	O2-C2	-2.25	1.18	1.23
42	S2	116	OMU	O2-C2	-2.25	1.18	1.23
1	L5	4606	OMU	O2-C2	-2.24	1.19	1.23
1	L5	4213	OMU	O2-C2	-2.22	1.19	1.23
1	L5	2777	A2M	O5'-C5'	-2.21	1.39	1.44
42	S2	428	OMU	O2-C2	-2.21	1.19	1.23
1	L5	3811	A2M	O5'-C5'	-2.21	1.39	1.44
42	S2	1851	MA6	C5-N7	-2.20	1.34	1.39
42	S2	166	A2M	O5'-C5'	-2.20	1.39	1.44
1	L5	1673	PSU	O4'-C1'	-2.20	1.40	1.43
1	L5	4206	6MZ	C8-N9	-2.19	1.33	1.37
42	S2	1442	OMU	O2-C2	-2.18	1.19	1.23
42	S2	354	OMU	O2-C2	-2.17	1.19	1.23
42	S2	172	OMU	O2-C2	-2.17	1.19	1.23
42	S2	121	OMU	O2-C2	-2.17	1.19	1.23
42	S2	1832	6MZ	C8-N9	-2.16	1.33	1.37
1	L5	1867	A2M	O5'-C5'	-2.16	1.39	1.44
1	L5	2391	A2M	O5'-C5'	-2.15	1.39	1.44
42	S2	1288	OMU	O2-C2	-2.15	1.19	1.23
42	S2	468	A2M	O5'-C5'	-2.12	1.39	1.44
1	L5	2353	A2M	O5'-C5'	-2.11	1.39	1.44
1	L5	2805	A2M	O5'-C5'	-2.10	1.39	1.44
42	S2	668	A2M	O5'-C5'	-2.08	1.39	1.44
1	L5	400	A2M	O5'-C5'	-2.07	1.39	1.44
1	L5	4509	A2M	O5'-C5'	-2.07	1.39	1.44
1	L5	1319	A2M	O5'-C5'	-2.07	1.39	1.44
1	L5	1530	A2M	O5'-C5'	-2.07	1.39	1.44
42	S2	1678	A2M	O5'-C5'	-2.06	1.39	1.44
42	S2	1804	OMU	O2-C2	-2.06	1.19	1.23
1	L5	1520	A2M	O5'-C5'	-2.06	1.39	1.44
42	S2	27	A2M	O5'-C5'	-2.05	1.39	1.44
42	S2	1850	MA6	C8-N9	-2.04	1.33	1.37
42	S2	1842	4AC	O7-C7	-2.04	1.18	1.23
1	L5	1322	A2M	O5'-C5'	-2.04	1.39	1.44
1	L5	3816	A2M	O5'-C5'	-2.04	1.39	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S2	512	A2M	O5'-C5'	-2.03	1.39	1.44
1	L5	4557	A2M	O5'-C5'	-2.02	1.39	1.44
42	S2	1031	A2M	O5'-C5'	-2.02	1.39	1.44
42	S2	1383	A2M	O5'-C5'	-2.01	1.39	1.44
42	S2	576	A2M	O5'-C5'	-2.01	1.39	1.44
42	S2	99	A2M	O5'-C5'	-2.01	1.39	1.44

All (935) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	S2	1851	MA6	N1-C6-N6	-15.45	100.19	117.08
42	S2	1850	MA6	N1-C6-N6	-14.94	100.75	117.08
1	L5	1520	A2M	C1'-N9-C8	-10.78	102.79	127.14
42	S2	590	A2M	C1'-N9-C8	-10.76	102.83	127.14
1	L5	4557	A2M	C1'-N9-C8	-10.59	103.21	127.14
42	S2	1678	A2M	C1'-N9-C8	-10.53	103.35	127.14
42	S2	166	A2M	C1'-N9-C8	-10.51	103.41	127.14
42	S2	159	A2M	C1'-N9-C8	-10.41	103.63	127.14
42	S2	468	A2M	C1'-N9-C8	-10.28	103.93	127.14
1	L5	400	A2M	C1'-N9-C8	-10.26	103.96	127.14
1	L5	3853	A2M	C1'-N9-C8	-10.26	103.98	127.14
1	L5	3710	A2M	C1'-N9-C8	-10.21	104.08	127.14
42	S2	99	A2M	C1'-N9-C8	-10.20	104.10	127.14
42	S2	1383	A2M	C1'-N9-C8	-10.19	104.13	127.14
1	L5	398	A2M	C1'-N9-C8	-10.17	104.18	127.14
1	L5	3704	A2M	C1'-N9-C8	-10.14	104.23	127.14
42	S2	576	A2M	C1'-N9-C8	-10.12	104.28	127.14
42	S2	484	A2M	C1'-N9-C8	-10.02	104.52	127.14
42	S2	512	A2M	C1'-N9-C8	-10.01	104.53	127.14
1	L5	1322	A2M	C1'-N9-C8	-9.96	104.66	127.14
1	L5	2805	A2M	C1'-N9-C8	-9.93	104.70	127.14
1	L5	3811	A2M	C1'-N9-C8	-9.91	104.77	127.14
1	L5	3816	A2M	C1'-N9-C8	-9.86	104.87	127.14
42	S2	1031	A2M	C1'-N9-C8	-9.82	104.96	127.14
42	S2	27	A2M	C1'-N9-C8	-9.78	105.06	127.14
1	L5	2391	A2M	C1'-N9-C8	-9.78	105.06	127.14
1	L5	1319	A2M	C1'-N9-C8	-9.77	105.08	127.14
1	L5	2353	A2M	C1'-N9-C8	-9.65	105.35	127.14
1	L5	4509	A2M	C1'-N9-C8	-9.60	105.45	127.14
1	L5	4576	A2M	C1'-N9-C8	-9.39	105.94	127.14
42	S2	668	A2M	C1'-N9-C8	-9.37	105.98	127.14
1	L5	1530	A2M	C1'-N9-C8	-9.29	106.15	127.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	1867	A2M	C1'-N9-C8	-9.20	106.36	127.14
1	L5	3771	A2M	C1'-N9-C8	-9.05	106.69	127.14
42	S2	1851	MA6	C5-C6-N6	8.27	139.70	125.30
1	L5	2777	A2M	C1'-N9-C8	-8.23	108.55	127.14
1	L5	4557	A2M	C4-N9-C1'	8.23	146.21	126.59
1	L5	1520	A2M	C4-N9-C1'	8.17	146.07	126.59
42	S2	590	A2M	C4-N9-C1'	8.17	146.06	126.59
42	S2	166	A2M	C4-N9-C1'	8.06	145.79	126.59
42	S2	1850	MA6	C5-C6-N6	8.06	139.33	125.30
42	S2	159	A2M	C4-N9-C1'	7.92	145.46	126.59
42	S2	1678	A2M	C4-N9-C1'	7.90	145.43	126.59
1	L5	398	A2M	C4-N9-C1'	7.88	145.38	126.59
1	L5	3704	A2M	C4-N9-C1'	7.87	145.35	126.59
1	L5	400	A2M	C4-N9-C1'	7.86	145.31	126.59
42	S2	99	A2M	C4-N9-C1'	7.78	145.14	126.59
1	L5	3853	A2M	C4-N9-C1'	7.77	145.11	126.59
42	S2	468	A2M	C4-N9-C1'	7.76	145.09	126.59
42	S2	484	A2M	C4-N9-C1'	7.72	145.00	126.59
1	L5	3710	A2M	C4-N9-C1'	7.71	144.97	126.59
1	L5	1322	A2M	C4-N9-C1'	7.68	144.90	126.59
42	S2	576	A2M	C4-N9-C1'	7.67	144.86	126.59
42	S2	1383	A2M	C4-N9-C1'	7.64	144.79	126.59
1	L5	2805	A2M	C4-N9-C1'	7.59	144.69	126.59
1	L5	3811	A2M	C4-N9-C1'	7.53	144.53	126.59
1	L5	3816	A2M	C4-N9-C1'	7.52	144.52	126.59
42	S2	512	A2M	C4-N9-C1'	7.42	144.28	126.59
1	L5	1319	A2M	C4-N9-C1'	7.42	144.27	126.59
42	S2	27	A2M	C4-N9-C1'	7.36	144.13	126.59
1	L5	2391	A2M	C4-N9-C1'	7.36	144.12	126.59
1	L5	2353	A2M	C4-N9-C1'	7.30	143.98	126.59
42	S2	1031	A2M	C4-N9-C1'	7.27	143.91	126.59
1	L5	4509	A2M	C4-N9-C1'	7.19	143.72	126.59
1	L5	1530	A2M	C4-N9-C1'	6.87	142.97	126.59
42	S2	668	A2M	C4-N9-C1'	6.84	142.88	126.59
1	L5	4576	A2M	C4-N9-C1'	6.83	142.87	126.59
1	L5	1867	A2M	C4-N9-C1'	6.80	142.80	126.59
1	L5	3771	A2M	C4-N9-C1'	6.59	142.28	126.59
42	S2	668	A2M	N9-C8-N7	-6.21	105.42	113.91
42	S2	1031	A2M	N9-C8-N7	-6.20	105.43	113.91
1	L5	3771	A2M	N9-C8-N7	-6.18	105.46	113.91
1	L5	4576	A2M	N9-C8-N7	-6.14	105.52	113.91
42	S2	512	A2M	N9-C8-N7	-6.11	105.56	113.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	3710	A2M	N9-C8-N7	-6.11	105.56	113.91
1	L5	1867	A2M	N9-C8-N7	-6.10	105.57	113.91
1	L5	1530	A2M	N9-C8-N7	-6.10	105.57	113.91
1	L5	2777	A2M	C4-N9-C1'	6.10	141.13	126.59
42	S2	1678	A2M	N9-C8-N7	-6.04	105.65	113.91
42	S2	590	A2M	N9-C8-N7	-6.04	105.65	113.91
1	L5	4509	A2M	N9-C8-N7	-6.04	105.66	113.91
1	L5	1867	A2M	N3-C2-N1	-6.00	119.22	128.60
42	S2	1383	A2M	N9-C8-N7	-6.00	105.71	113.91
42	S2	27	A2M	N9-C8-N7	-5.99	105.73	113.91
42	S2	576	A2M	N9-C8-N7	-5.98	105.74	113.91
1	L5	3853	A2M	N9-C8-N7	-5.97	105.75	113.91
42	S2	468	A2M	N9-C8-N7	-5.96	105.76	113.91
1	L5	2391	A2M	N9-C8-N7	-5.95	105.78	113.91
1	L5	3811	A2M	N9-C8-N7	-5.94	105.79	113.91
1	L5	2777	A2M	N3-C2-N1	-5.92	119.34	128.60
42	S2	1031	A2M	N3-C2-N1	-5.92	119.34	128.60
1	L5	1520	A2M	N9-C8-N7	-5.92	105.82	113.91
1	L5	4576	A2M	N3-C2-N1	-5.92	119.34	128.60
42	S2	166	A2M	N9-C8-N7	-5.92	105.82	113.91
42	S2	159	A2M	N9-C8-N7	-5.87	105.89	113.91
1	L5	1319	A2M	N9-C8-N7	-5.85	105.91	113.91
1	L5	1530	A2M	N3-C2-N1	-5.85	119.45	128.60
1	L5	400	A2M	N9-C8-N7	-5.85	105.92	113.91
1	L5	2805	A2M	N3-C2-N1	-5.84	119.47	128.60
42	S2	99	A2M	N9-C8-N7	-5.83	105.94	113.91
42	S2	512	A2M	N3-C2-N1	-5.83	119.49	128.60
1	L5	2805	A2M	N9-C8-N7	-5.83	105.94	113.91
1	L5	2353	A2M	N9-C8-N7	-5.82	105.95	113.91
42	S2	668	A2M	N3-C2-N1	-5.80	119.54	128.60
1	L5	400	A2M	N3-C2-N1	-5.79	119.54	128.60
1	L5	398	A2M	N9-C8-N7	-5.79	106.00	113.91
1	L5	1322	A2M	N3-C2-N1	-5.78	119.55	128.60
42	S2	484	A2M	N9-C8-N7	-5.76	106.04	113.91
42	S2	1851	MA6	N1-C2-N3	-5.75	119.61	128.60
1	L5	3816	A2M	N9-C8-N7	-5.75	106.05	113.91
42	S2	27	A2M	N3-C2-N1	-5.74	119.62	128.60
1	L5	2777	A2M	N9-C8-N7	-5.74	106.06	113.91
61	ST	67	NMM	NE-CZ-NH2	-5.74	114.22	119.48
1	L5	3771	A2M	N3-C2-N1	-5.73	119.63	128.60
1	L5	2353	A2M	N3-C2-N1	-5.70	119.69	128.60
1	L5	3811	A2M	N3-C2-N1	-5.70	119.69	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	2391	A2M	N3-C2-N1	-5.69	119.71	128.60
42	S2	1383	A2M	N3-C2-N1	-5.68	119.72	128.60
1	L5	3853	A2M	N3-C2-N1	-5.67	119.73	128.60
1	L5	1322	A2M	N9-C8-N7	-5.67	106.16	113.91
1	L5	4557	A2M	N9-C8-N7	-5.67	106.17	113.91
1	L5	3710	A2M	N3-C2-N1	-5.64	119.78	128.60
42	S2	484	A2M	N3-C2-N1	-5.62	119.81	128.60
42	S2	166	A2M	N3-C2-N1	-5.62	119.81	128.60
42	S2	1678	A2M	N3-C2-N1	-5.62	119.81	128.60
1	L5	3704	A2M	N9-C8-N7	-5.61	106.24	113.91
42	S2	590	A2M	N3-C2-N1	-5.59	119.85	128.60
42	S2	99	A2M	N3-C2-N1	-5.59	119.86	128.60
1	L5	398	A2M	N3-C2-N1	-5.58	119.87	128.60
1	L5	1319	A2M	N3-C2-N1	-5.57	119.89	128.60
1	L5	4509	A2M	N3-C2-N1	-5.57	119.89	128.60
1	L5	4206	6MZ	N1-C2-N3	-5.56	119.90	128.60
42	S2	468	A2M	N3-C2-N1	-5.51	119.98	128.60
42	S2	1832	6MZ	C5-C4-N3	-5.50	119.58	126.75
42	S2	159	A2M	N3-C2-N1	-5.50	120.00	128.60
42	S2	1850	MA6	N1-C2-N3	-5.49	120.01	128.60
1	L5	4206	6MZ	C5-C4-N3	-5.48	119.61	126.75
1	L5	4557	A2M	N3-C2-N1	-5.47	120.05	128.60
42	S2	1832	6MZ	N1-C2-N3	-5.46	120.06	128.60
1	L5	3816	A2M	N3-C2-N1	-5.46	120.07	128.60
1	L5	1520	A2M	N3-C2-N1	-5.43	120.11	128.60
42	S2	576	A2M	N3-C2-N1	-5.41	120.14	128.60
1	L5	4213	OMU	C4-N3-C2	-5.38	119.48	126.58
42	S2	116	OMU	C4-N3-C2	-5.35	119.52	126.58
42	S2	428	OMU	C4-N3-C2	-5.24	119.66	126.58
42	S2	1850	MA6	C5-C4-N3	-5.24	119.92	126.75
42	S2	1639	G7M	CN7-N7-C5	5.23	133.27	126.77
42	S2	1442	OMU	C4-N3-C2	-5.21	119.70	126.58
42	S2	172	OMU	C4-N3-C2	-5.17	119.76	126.58
3	L8	14	OMU	C4-N3-C2	-5.15	119.78	126.58
42	S2	1851	MA6	C5-C4-N3	-5.14	120.05	126.75
1	L5	4484	OMU	C4-N3-C2	-5.13	119.81	126.58
42	S2	354	OMU	C4-N3-C2	-5.13	119.82	126.58
42	S2	1288	OMU	C4-N3-C2	-5.05	119.92	126.58
1	L5	4576	A2M	C4-N9-C8	5.03	111.18	105.73
1	L5	3704	A2M	N3-C2-N1	-5.03	120.74	128.60
1	L5	2827	OMU	C4-N3-C2	-4.99	120.00	126.58
42	S2	1678	A2M	C4-N9-C8	4.99	111.14	105.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	1520	A2M	C4-N9-C8	4.98	111.13	105.73
42	S2	512	A2M	C4-N9-C8	4.95	111.09	105.73
1	L5	4292	OMU	C4-N3-C2	-4.94	120.06	126.58
42	S2	1031	A2M	C4-N9-C8	4.94	111.08	105.73
1	L5	4622	PSU	C4-N3-C2	-4.94	119.22	126.34
1	L5	4557	A2M	C5-C4-N3	-4.92	120.33	126.75
42	S2	590	A2M	C4-N9-C8	4.92	111.06	105.73
42	S2	121	OMU	C4-N3-C2	-4.91	120.11	126.58
42	S2	1804	OMU	C4-N3-C2	-4.90	120.12	126.58
42	S2	668	A2M	C4-N9-C8	4.88	111.02	105.73
1	L5	3911	OMU	C4-N3-C2	-4.87	120.15	126.58
1	L5	3771	A2M	C4-N9-C8	4.87	111.00	105.73
42	S2	166	A2M	C5-C4-N3	-4.85	120.42	126.75
1	L5	3710	A2M	C4-N9-C8	4.81	110.95	105.73
42	S2	468	A2M	C4-N9-C8	4.80	110.92	105.73
42	S2	1238	PSU	C4-N3-C2	-4.79	119.44	126.34
1	L5	3704	A2M	C5-C4-N3	-4.79	120.50	126.75
1	L5	398	A2M	C5-C4-N3	-4.79	120.50	126.75
1	L5	3853	A2M	C4-N9-C8	4.78	110.91	105.73
42	S2	1383	A2M	C4-N9-C8	4.78	110.91	105.73
42	S2	667	PSU	C4-N3-C2	-4.78	119.45	126.34
42	S2	484	A2M	C5-C4-N3	-4.73	120.58	126.75
42	S2	159	A2M	C4-N9-C8	4.73	110.85	105.73
1	L5	1858	PSU	C4-N3-C2	-4.71	119.55	126.34
1	L5	4517	PSU	C4-N3-C2	-4.71	119.56	126.34
1	L5	4517	PSU	N1-C2-N3	4.71	120.46	115.13
1	L5	4538	PSU	C4-N3-C2	-4.70	119.57	126.34
1	L5	2405	OMU	C4-N3-C2	-4.69	120.39	126.58
1	L5	1867	A2M	C4-N9-C8	4.69	110.81	105.73
42	S2	576	A2M	C4-N9-C8	4.69	110.81	105.73
1	L5	2391	A2M	C4-N9-C8	4.69	110.81	105.73
1	L5	3830	PSU	C4-N3-C2	-4.69	119.59	126.34
42	S2	1851	MA6	N9-C8-N7	-4.67	107.52	113.91
42	S2	1045	PSU	C4-N3-C2	-4.67	119.61	126.34
1	L5	4428	PSU	C4-N3-C2	-4.66	119.62	126.34
42	S2	27	A2M	C4-N9-C8	4.66	110.78	105.73
42	S2	166	A2M	C4-N9-C8	4.65	110.77	105.73
1	L5	1530	A2M	C4-N9-C8	4.65	110.76	105.73
42	S2	99	A2M	C5-C4-N3	-4.65	120.69	126.75
1	L5	4516	UR3	C4-N3-C2	-4.64	120.20	124.56
42	S2	651	PSU	C4-N3-C2	-4.64	119.66	126.34
42	S2	590	A2M	C5-C4-N3	-4.63	120.71	126.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	S2	100	PSU	C4-N3-C2	-4.63	119.66	126.34
42	S2	93	PSU	C4-N3-C2	-4.63	119.67	126.34
42	S2	468	A2M	C5-C4-N3	-4.63	120.72	126.75
42	S2	1678	A2M	C5-C4-N3	-4.63	120.72	126.75
42	S2	815	PSU	C4-N3-C2	-4.61	119.69	126.34
1	L5	400	A2M	C4-N9-C8	4.61	110.73	105.73
1	L5	1673	PSU	C4-N3-C2	-4.61	119.70	126.34
1	L5	4509	A2M	C4-N9-C8	4.61	110.72	105.73
1	L5	3811	A2M	C5-C4-N3	-4.61	120.74	126.75
42	S2	34	PSU	C4-N3-C2	-4.60	119.70	126.34
42	S2	105	PSU	C4-N3-C2	-4.59	119.72	126.34
42	S2	512	A2M	C2'-C1'-N9	-4.59	105.81	113.53
1	L5	4486	PSU	C4-N3-C2	-4.58	119.74	126.34
1	L5	4957	PSU	C4-N3-C2	-4.58	119.74	126.34
1	L5	3811	A2M	C4-N9-C8	4.58	110.69	105.73
42	S2	99	A2M	C4-N9-C8	4.57	110.68	105.73
42	S2	1232	PSU	C4-N3-C2	-4.57	119.75	126.34
1	L5	4206	6MZ	C4-C5-C6	4.57	120.35	116.81
42	S2	1347	PSU	C4-N3-C2	-4.57	119.75	126.34
1	L5	1322	A2M	C5-C4-N3	-4.56	120.80	126.75
1	L5	2353	A2M	C4-N9-C8	4.56	110.67	105.73
42	S2	814	PSU	C4-N3-C2	-4.56	119.77	126.34
1	L5	1777	PSU	C4-N3-C2	-4.56	119.77	126.34
1	L5	3808	PSU	C4-N3-C2	-4.56	119.77	126.34
42	S2	159	A2M	C5-C4-N3	-4.56	120.81	126.75
1	L5	3837	PSU	N1-C2-N3	4.56	120.29	115.13
1	L5	4417	PSU	C4-N3-C2	-4.55	119.78	126.34
42	S2	109	PSU	C4-N3-C2	-4.55	119.79	126.34
1	L5	4606	OMU	C4-N3-C2	-4.54	120.59	126.58
1	L5	4986	PSU	C4-N3-C2	-4.54	119.79	126.34
1	L5	3839	PSU	N1-C2-N3	4.54	120.28	115.13
1	L5	4614	PSU	C4-N3-C2	-4.54	119.80	126.34
1	L5	4507	PSU	C4-N3-C2	-4.54	119.80	126.34
42	S2	1136	PSU	C4-N3-C2	-4.54	119.80	126.34
1	L5	4428	PSU	N1-C2-N3	4.54	120.27	115.13
1	L5	3830	PSU	N1-C2-N3	4.54	120.27	115.13
1	L5	3853	A2M	C5-C4-N3	-4.54	120.83	126.75
1	L5	1319	A2M	C4-N9-C8	4.54	110.64	105.73
42	S2	218	PSU	C4-N3-C2	-4.53	119.81	126.34
42	S2	1383	A2M	C2'-C1'-N9	-4.53	105.89	113.53
1	L5	1679	PSU	C4-N3-C2	-4.53	119.82	126.34
42	S2	406	PSU	C4-N3-C2	-4.53	119.82	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	3681	PSU	C4-N3-C2	-4.52	119.82	126.34
42	S2	1046	PSU	C4-N3-C2	-4.52	119.82	126.34
42	S2	863	PSU	C4-N3-C2	-4.52	119.82	126.34
1	L5	1788	PSU	C4-N3-C2	-4.52	119.83	126.34
1	L5	3710	A2M	C5-C4-N3	-4.52	120.85	126.75
42	S2	686	PSU	C4-N3-C2	-4.51	119.84	126.34
1	L5	1858	PSU	N1-C2-N3	4.51	120.24	115.13
42	S2	1244	PSU	C4-N3-C2	-4.51	119.84	126.34
1	L5	2805	A2M	C4-N9-C8	4.51	110.61	105.73
1	L5	4538	PSU	N1-C2-N3	4.50	120.23	115.13
42	S2	1232	PSU	N1-C2-N3	4.50	120.23	115.13
1	L5	3816	A2M	C5-C4-N3	-4.50	120.88	126.75
42	S2	1177	PSU	C4-N3-C2	-4.50	119.86	126.34
42	S2	119	PSU	C4-N3-C2	-4.50	119.86	126.34
1	L5	4409	PSU	C4-N3-C2	-4.50	119.86	126.34
42	S2	651	PSU	N1-C2-N3	4.50	120.22	115.13
42	S2	801	PSU	N1-C2-N3	4.50	120.22	115.13
1	L5	4347	PSU	C4-N3-C2	-4.49	119.86	126.34
42	S2	1692	PSU	C4-N3-C2	-4.49	119.86	126.34
1	L5	4675	PSU	C4-N3-C2	-4.49	119.87	126.34
42	S2	576	A2M	C5-C4-N3	-4.49	120.89	126.75
1	L5	3837	PSU	C4-N3-C2	-4.49	119.87	126.34
1	L5	4995	PSU	C4-N3-C2	-4.49	119.87	126.34
42	S2	863	PSU	N1-C2-N3	4.49	120.21	115.13
42	S2	27	A2M	C5-C4-N3	-4.48	120.90	126.75
1	L5	4279	PSU	C4-N3-C2	-4.48	119.88	126.34
1	L5	4509	A2M	C5-C4-N3	-4.48	120.91	126.75
1	L5	4557	A2M	C4-N9-C8	4.48	110.58	105.73
1	L5	4409	PSU	N1-C2-N3	4.48	120.20	115.13
1	L5	4986	PSU	N1-C2-N3	4.47	120.20	115.13
42	S2	609	PSU	C4-N3-C2	-4.47	119.89	126.34
42	S2	649	PSU	C4-N3-C2	-4.47	119.89	126.34
42	S2	1174	PSU	C4-N3-C2	-4.47	119.89	126.34
1	L5	4518	PSU	C4-N3-C2	-4.47	119.90	126.34
42	S2	814	PSU	N1-C2-N3	4.47	120.19	115.13
1	L5	3808	PSU	N1-C2-N3	4.47	120.19	115.13
1	L5	4339	PSU	C4-N3-C2	-4.47	119.91	126.34
1	L5	4457	PSU	C4-N3-C2	-4.47	119.91	126.34
1	L5	4957	PSU	N1-C2-N3	4.46	120.19	115.13
1	L5	400	A2M	C5-C4-N3	-4.46	120.93	126.75
1	L5	3623	PSU	C4-N3-C2	-4.46	119.91	126.34
1	L5	4958	PSU	C4-N3-C2	-4.46	119.91	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	1856	PSU	N1-C2-N3	4.46	120.19	115.13
1	L5	4675	PSU	N1-C2-N3	4.46	120.18	115.13
3	L8	69	PSU	C4-N3-C2	-4.46	119.91	126.34
1	L5	4443	PSU	C4-N3-C2	-4.45	119.92	126.34
1	L5	4339	PSU	N1-C2-N3	4.45	120.18	115.13
1	L5	4614	PSU	N1-C2-N3	4.45	120.18	115.13
1	L5	4417	PSU	N1-C2-N3	4.45	120.17	115.13
1	L5	4565	PSU	N1-C2-N3	4.45	120.17	115.13
1	L5	4486	PSU	N1-C2-N3	4.45	120.17	115.13
42	S2	1174	PSU	N1-C2-N3	4.45	120.17	115.13
42	S2	119	PSU	N1-C2-N3	4.45	120.17	115.13
42	S2	801	PSU	C4-N3-C2	-4.45	119.93	126.34
42	S2	406	PSU	N1-C2-N3	4.44	120.17	115.13
3	L8	55	PSU	C4-N3-C2	-4.44	119.94	126.34
1	L5	1740	PSU	C4-N3-C2	-4.44	119.94	126.34
42	S2	1244	PSU	N1-C2-N3	4.44	120.16	115.13
1	L5	4298	PSU	C4-N3-C2	-4.44	119.94	126.34
1	L5	1777	PSU	N1-C2-N3	4.44	120.16	115.13
42	S2	686	PSU	N1-C2-N3	4.44	120.16	115.13
42	S2	572	PSU	C4-N3-C2	-4.44	119.94	126.34
1	L5	1673	PSU	N1-C2-N3	4.43	120.15	115.13
42	S2	1136	PSU	N1-C2-N3	4.43	120.15	115.13
1	L5	1520	A2M	C5-C4-N3	-4.43	120.97	126.75
1	L5	4995	PSU	N1-C2-N3	4.43	120.15	115.13
1	L5	2777	A2M	C5-C4-N3	-4.43	120.97	126.75
1	L5	4622	PSU	N1-C2-N3	4.43	120.15	115.13
42	S2	34	PSU	N1-C2-N3	4.43	120.15	115.13
1	L5	3701	PSU	C4-N3-C2	-4.43	119.96	126.34
1	L5	4285	PSU	N1-C2-N3	4.43	120.14	115.13
42	S2	105	PSU	N1-C2-N3	4.42	120.14	115.13
1	L5	1740	PSU	N1-C2-N3	4.42	120.14	115.13
1	L5	4562	PSU	N1-C2-N3	4.42	120.14	115.13
3	L8	69	PSU	N1-C2-N3	4.42	120.14	115.13
42	S2	1045	PSU	N1-C2-N3	4.42	120.14	115.13
42	S2	918	PSU	N1-C2-N3	4.42	120.14	115.13
42	S2	109	PSU	N1-C2-N3	4.42	120.14	115.13
1	L5	3816	A2M	C4-N9-C8	4.42	110.52	105.73
42	S2	1056	PSU	C4-N3-C2	-4.42	119.97	126.34
42	S2	1850	MA6	N9-C8-N7	-4.42	107.87	113.91
42	S2	1383	A2M	C5-C4-N3	-4.41	120.99	126.75
42	S2	1832	6MZ	C4-C5-C6	4.40	120.22	116.81
1	L5	4285	PSU	C4-N3-C2	-4.40	119.99	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	1319	A2M	C5-C4-N3	-4.40	121.01	126.75
42	S2	918	PSU	C4-N3-C2	-4.40	120.00	126.34
1	L5	4555	PSU	N1-C2-N3	4.40	120.11	115.13
42	S2	1445	PSU	C4-N3-C2	-4.39	120.01	126.34
1	L5	2391	A2M	C5-C4-N3	-4.39	121.02	126.75
42	S2	822	PSU	N1-C2-N3	4.39	120.11	115.13
42	S2	93	PSU	N1-C2-N3	4.39	120.10	115.13
42	S2	1643	PSU	C4-N3-C2	-4.39	120.02	126.34
1	L5	3701	PSU	N1-C2-N3	4.39	120.10	115.13
42	S2	1692	PSU	N1-C2-N3	4.38	120.10	115.13
42	S2	512	A2M	C5-C4-N3	-4.38	121.03	126.75
1	L5	1532	PSU	C4-N3-C2	-4.37	120.04	126.34
42	S2	484	A2M	C4-N9-C8	4.37	110.47	105.73
1	L5	2805	A2M	C5-C4-N3	-4.37	121.05	126.75
42	S2	815	PSU	N1-C2-N3	4.37	120.08	115.13
42	S2	822	PSU	C4-N3-C2	-4.37	120.04	126.34
1	L5	4518	PSU	N1-C2-N3	4.37	120.08	115.13
1	L5	4282	PSU	C4-N3-C2	-4.37	120.05	126.34
42	S2	1238	PSU	N1-C2-N3	4.36	120.07	115.13
1	L5	3870	PSU	N1-C2-N3	4.36	120.07	115.13
1	L5	1778	PSU	C4-N3-C2	-4.36	120.06	126.34
1	L5	4347	PSU	N1-C2-N3	4.36	120.07	115.13
42	S2	1347	PSU	N1-C2-N3	4.36	120.07	115.13
42	S2	1337	4AC	CM7-C7-N4	4.36	122.83	115.29
1	L5	3870	PSU	C4-N3-C2	-4.35	120.06	126.34
1	L5	1322	A2M	C4-N9-C8	4.35	110.45	105.73
42	S2	609	PSU	N1-C2-N3	4.35	120.06	115.13
42	S2	36	PSU	C4-N3-C2	-4.35	120.07	126.34
1	L5	4659	PSU	C4-N3-C2	-4.35	120.07	126.34
42	S2	1596	PSU	C4-N3-C2	-4.35	120.07	126.34
42	S2	1177	PSU	N1-C2-N3	4.35	120.06	115.13
42	S2	1596	PSU	N1-C2-N3	4.34	120.05	115.13
1	L5	1578	PSU	C4-N3-C2	-4.34	120.08	126.34
1	L5	1856	PSU	C4-N3-C2	-4.34	120.08	126.34
42	S2	1625	PSU	C4-N3-C2	-4.34	120.08	126.34
42	S2	1639	G7M	C2-N3-C4	4.34	120.04	112.30
1	L5	4457	PSU	N1-C2-N3	4.34	120.05	115.13
1	L5	2622	PSU	N1-C2-N3	4.34	120.05	115.13
42	S2	1046	PSU	N1-C2-N3	4.34	120.05	115.13
1	L5	3623	PSU	N1-C2-N3	4.34	120.05	115.13
42	S2	1625	PSU	N1-C2-N3	4.34	120.05	115.13
1	L5	4565	PSU	C4-N3-C2	-4.34	120.09	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	3681	PSU	N1-C2-N3	4.34	120.04	115.13
1	L5	1778	PSU	N1-C2-N3	4.33	120.04	115.13
1	L5	398	A2M	C4-N9-C8	4.33	110.42	105.73
1	L5	4958	PSU	N1-C2-N3	4.33	120.04	115.13
42	S2	649	PSU	N1-C2-N3	4.33	120.04	115.13
1	L5	3839	PSU	C4-N3-C2	-4.32	120.11	126.34
1	L5	4562	PSU	C4-N3-C2	-4.31	120.12	126.34
1	L5	4659	PSU	N1-C2-N3	4.30	120.01	115.13
42	S2	572	PSU	N1-C2-N3	4.30	120.01	115.13
1	L5	4555	PSU	C4-N3-C2	-4.30	120.14	126.34
1	L5	3704	A2M	C4-N9-C8	4.30	110.39	105.73
42	S2	1445	PSU	N1-C2-N3	4.29	120.00	115.13
1	L5	2777	A2M	C2'-C1'-N9	4.29	120.76	113.53
42	S2	681	PSU	N1-C2-N3	4.29	119.99	115.13
42	S2	100	PSU	N1-C2-N3	4.29	119.98	115.13
42	S2	36	PSU	N1-C2-N3	4.28	119.98	115.13
42	S2	218	PSU	N1-C2-N3	4.28	119.98	115.13
1	L5	2353	A2M	C5-C4-N3	-4.28	121.17	126.75
42	S2	681	PSU	C4-N3-C2	-4.27	120.19	126.34
42	S2	1004	PSU	C4-N3-C2	-4.26	120.20	126.34
1	L5	4507	PSU	N1-C2-N3	4.26	119.95	115.13
42	S2	1643	PSU	N1-C2-N3	4.25	119.95	115.13
1	L5	1530	A2M	C5-C4-N3	-4.25	121.20	126.75
1	L5	3771	A2M	C5-C4-N3	-4.25	121.20	126.75
42	S2	1056	PSU	N1-C2-N3	4.25	119.95	115.13
1	L5	2622	PSU	C4-N3-C2	-4.25	120.22	126.34
3	L8	55	PSU	N1-C2-N3	4.24	119.94	115.13
1	L5	4206	6MZ	N9-C8-N7	-4.24	108.12	113.91
1	L5	2829	PSU	C4-N3-C2	-4.24	120.23	126.34
1	L5	4279	PSU	N1-C2-N3	4.23	119.93	115.13
1	L5	1679	PSU	N1-C2-N3	4.23	119.93	115.13
1	L5	3625	PSU	C4-N3-C2	-4.23	120.25	126.34
1	L5	3771	A2M	C4'-O4'-C1'	-4.22	100.17	109.47
1	L5	4389	PSU	N1-C2-N3	4.21	119.90	115.13
1	L5	3771	A2M	O4'-C1'-N9	4.20	116.34	108.06
42	S2	1004	PSU	N1-C2-N3	4.20	119.89	115.13
1	L5	4443	PSU	N1-C2-N3	4.20	119.89	115.13
42	S2	1639	G7M	C1'-N9-C4	-4.19	114.05	126.50
1	L5	1578	PSU	N1-C2-N3	4.19	119.88	115.13
42	S2	668	A2M	C5-C4-N3	-4.19	121.28	126.75
1	L5	4282	PSU	N1-C2-N3	4.19	119.88	115.13
1	L5	2829	PSU	N1-C2-N3	4.19	119.88	115.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	4298	PSU	N1-C2-N3	4.19	119.88	115.13
1	L5	3906	PSU	C4-N3-C2	-4.19	120.31	126.34
1	L5	1788	PSU	N1-C2-N3	4.16	119.84	115.13
42	S2	1031	A2M	C5-C4-N3	-4.16	121.33	126.75
1	L5	1532	PSU	N1-C2-N3	4.16	119.84	115.13
42	S2	1832	6MZ	N9-C8-N7	-4.14	108.25	113.91
1	L5	4389	PSU	C4-N3-C2	-4.14	120.38	126.34
1	L5	4509	A2M	O4'-C1'-N9	4.12	116.17	108.06
1	L5	2777	A2M	C4-N9-C8	4.09	110.17	105.73
42	S2	667	PSU	N1-C2-N3	4.09	119.77	115.13
42	S2	1639	G7M	C5-C4-N3	-4.07	120.35	128.15
1	L5	4213	OMU	N3-C2-N1	4.04	120.25	114.89
1	L5	3625	PSU	N1-C2-N3	4.03	119.70	115.13
1	L5	1867	A2M	C5-C4-N3	-3.98	121.55	126.75
1	L5	3816	A2M	C2'-C1'-N9	-3.95	106.88	113.53
1	L5	3906	PSU	N1-C2-N3	3.93	119.59	115.13
42	S2	1832	6MZ	C4-N9-C1'	-3.91	117.29	126.59
1	L5	4206	6MZ	C4-N9-C1'	-3.90	117.29	126.59
1	L5	4576	A2M	C5-C4-N3	-3.90	121.66	126.75
42	S2	1031	A2M	C5-N7-C8	3.87	109.01	103.51
1	L5	3771	A2M	C5-N7-C8	3.87	109.01	103.51
1	L5	4509	A2M	C5-N7-C8	3.86	109.00	103.51
42	S2	1639	G7M	CN7-N7-C8	-3.86	118.88	124.84
42	S2	668	A2M	C5-N7-C8	3.86	108.99	103.51
42	S2	1639	G7M	C5-C6-N1	3.86	119.84	111.79
1	L5	3710	A2M	C5-N7-C8	3.84	108.97	103.51
1	L5	3811	A2M	C5-N7-C8	3.84	108.97	103.51
1	L5	1530	A2M	C5-N7-C8	3.84	108.96	103.51
1	L5	4576	A2M	O4'-C1'-N9	3.82	115.59	108.06
42	S2	172	OMU	N3-C2-N1	3.82	119.96	114.89
1	L5	398	A2M	C5-N7-C8	3.81	108.93	103.51
42	S2	1850	MA6	C4-C5-C6	3.79	120.13	115.88
42	S2	166	A2M	C5-N7-C8	3.79	108.89	103.51
42	S2	576	A2M	C5-N7-C8	3.79	108.89	103.51
42	S2	27	A2M	C5-N7-C8	3.79	108.89	103.51
42	S2	590	A2M	C5-N7-C8	3.78	108.88	103.51
42	S2	116	OMU	N3-C2-N1	3.78	119.91	114.89
1	L5	1867	A2M	C5-N7-C8	3.77	108.87	103.51
1	L5	1319	A2M	C5-N7-C8	3.75	108.84	103.51
1	L5	2827	OMU	N3-C2-N1	3.75	119.87	114.89
1	L5	2405	OMU	N3-C2-N1	3.74	119.86	114.89
42	S2	428	OMU	N3-C2-N1	3.74	119.86	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	S2	1442	OMU	N3-C2-N1	3.74	119.86	114.89
3	L8	14	OMU	N3-C2-N1	3.74	119.85	114.89
1	L5	2777	A2M	C5-N7-C8	3.73	108.82	103.51
42	S2	512	A2M	C5-N7-C8	3.73	108.81	103.51
42	S2	1383	A2M	C5-N7-C8	3.73	108.81	103.51
42	S2	1678	A2M	C5-N7-C8	3.73	108.80	103.51
42	S2	484	A2M	C5-N7-C8	3.71	108.79	103.51
1	L5	3853	A2M	C5-N7-C8	3.71	108.78	103.51
1	L5	2805	A2M	C5-N7-C8	3.71	108.78	103.51
1	L5	400	A2M	C5-N7-C8	3.70	108.77	103.51
1	L5	4557	A2M	N3-C4-N9	3.70	133.19	127.08
42	S2	468	A2M	C5-N7-C8	3.70	108.77	103.51
1	L5	2391	A2M	C5-N7-C8	3.70	108.77	103.51
1	L5	4557	A2M	C5-N7-C8	3.69	108.75	103.51
42	S2	99	A2M	C5-N7-C8	3.68	108.73	103.51
42	S2	159	A2M	C2'-C1'-N9	-3.67	107.34	113.53
42	S2	354	OMU	N3-C2-N1	3.67	119.77	114.89
42	S2	166	A2M	N3-C4-N9	3.66	133.12	127.08
42	S2	1288	OMU	N3-C2-N1	3.66	119.75	114.89
42	S2	159	A2M	C5-N7-C8	3.64	108.68	103.51
1	L5	4576	A2M	C2'-C1'-N9	-3.63	107.42	113.53
1	L5	4484	OMU	N3-C2-N1	3.63	119.71	114.89
42	S2	1851	MA6	C2-N3-C4	3.63	120.32	111.75
1	L5	3816	A2M	C5-N7-C8	3.63	108.66	103.51
1	L5	4206	6MZ	N3-C4-N9	3.62	133.06	127.08
42	S2	1832	6MZ	C2-N3-C4	3.62	120.29	111.75
1	L5	4576	A2M	C5-N7-C8	3.61	108.64	103.51
42	S2	1678	A2M	N3-C4-N9	3.61	133.02	127.08
1	L5	2353	A2M	C5-N7-C8	3.60	108.63	103.51
1	L5	1867	A2M	O4'-C1'-N9	3.60	115.16	108.06
1	L5	4206	6MZ	C2-N3-C4	3.58	120.22	111.75
1	L5	1520	A2M	C5-N7-C8	3.58	108.60	103.51
1	L5	1322	A2M	C5-N7-C8	3.58	108.60	103.51
42	S2	590	A2M	C2'-C1'-N9	-3.57	107.52	113.53
42	S2	1851	MA6	C2-N1-C6	3.57	120.19	111.75
1	L5	3704	A2M	C5-N7-C8	3.56	108.56	103.51
1	L5	2777	A2M	C2-N3-C4	3.55	120.14	111.75
42	S2	1639	G7M	O6-C6-C5	-3.55	120.05	128.06
42	S2	590	A2M	N3-C4-N9	3.55	132.93	127.08
42	S2	166	A2M	C2-N3-C4	3.53	120.09	111.75
42	S2	484	A2M	C2-N3-C4	3.52	120.07	111.75
42	S2	1850	MA6	C2-N1-C6	3.52	120.06	111.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	3811	A2M	C2-N3-C4	3.51	120.04	111.75
42	S2	468	A2M	N3-C4-N9	3.50	132.85	127.08
1	L5	398	A2M	C2-N3-C4	3.50	120.02	111.75
1	L5	1867	A2M	C2'-C1'-N9	-3.49	107.66	113.53
42	S2	27	A2M	C2-N3-C4	3.48	119.98	111.75
1	L5	4606	OMU	N3-C2-N1	3.48	119.51	114.89
42	S2	121	OMU	N3-C2-N1	3.48	119.51	114.89
42	S2	159	A2M	N3-C4-N9	3.48	132.82	127.08
42	S2	1850	MA6	C2-N3-C4	3.48	119.97	111.75
1	L5	3911	OMU	N3-C2-N1	3.48	119.50	114.89
1	L5	4557	A2M	C2-N3-C4	3.47	119.94	111.75
1	L5	1322	A2M	C2-N3-C4	3.47	119.94	111.75
42	S2	1804	OMU	N3-C2-N1	3.46	119.48	114.89
1	L5	1530	A2M	C2-N3-C4	3.46	119.92	111.75
1	L5	4509	A2M	C2-N3-C4	3.46	119.92	111.75
1	L5	3771	A2M	C2-N3-C4	3.46	119.91	111.75
1	L5	2805	A2M	C2-N3-C4	3.46	119.91	111.75
42	S2	1678	A2M	C2-N3-C4	3.46	119.91	111.75
1	L5	1520	A2M	N3-C4-N9	3.45	132.77	127.08
42	S2	590	A2M	C2-N3-C4	3.44	119.89	111.75
1	L5	2391	A2M	C2-N3-C4	3.44	119.89	111.75
42	S2	512	A2M	C2-N3-C4	3.44	119.88	111.75
42	S2	99	A2M	C2-N3-C4	3.44	119.87	111.75
42	S2	1851	MA6	C4-C5-C6	3.44	119.73	115.88
1	L5	3853	A2M	C2-N3-C4	3.43	119.86	111.75
1	L5	2353	A2M	C2-N3-C4	3.43	119.86	111.75
1	L5	1319	A2M	C2-N3-C4	3.43	119.86	111.75
1	L5	3710	A2M	C2-N3-C4	3.43	119.84	111.75
42	S2	668	A2M	C2-N3-C4	3.42	119.84	111.75
42	S2	116	OMU	C5-C4-N3	3.42	119.96	114.84
42	S2	1832	6MZ	C1'-N9-C8	3.42	134.86	127.14
1	L5	3853	A2M	N3-C4-N9	3.41	132.70	127.08
42	S2	99	A2M	N3-C4-N9	3.41	132.69	127.08
42	S2	428	OMU	C5-C4-N3	3.40	119.93	114.84
1	L5	400	A2M	C2-N3-C4	3.40	119.79	111.75
42	S2	1031	A2M	C2'-C1'-N9	-3.40	107.81	113.53
42	S2	1383	A2M	C2-N3-C4	3.39	119.77	111.75
1	L5	398	A2M	N3-C4-N9	3.39	132.66	127.08
42	S2	468	A2M	C2-N3-C4	3.38	119.75	111.75
42	S2	1850	MA6	N3-C4-N9	3.38	132.65	127.08
1	L5	4484	OMU	C5-C4-N3	3.38	119.89	114.84
1	L5	1867	A2M	C2-N3-C4	3.37	119.72	111.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	S2	1031	A2M	C2-N3-C4	3.37	119.72	111.75
1	L5	3710	A2M	N3-C4-N9	3.37	132.64	127.08
1	L5	4292	OMU	C5-C4-N3	3.37	119.88	114.84
42	S2	159	A2M	C2-N3-C4	3.36	119.70	111.75
1	L5	1530	A2M	C2'-C1'-N9	3.36	119.19	113.53
42	S2	1442	OMU	C5-C4-N3	3.36	119.86	114.84
42	S2	1832	6MZ	C5-N7-C8	3.35	108.28	103.51
1	L5	4292	OMU	N3-C2-N1	3.35	119.33	114.89
1	L5	4576	A2M	C2-N3-C4	3.33	119.62	111.75
1	L5	3704	A2M	N3-C4-N9	3.33	132.57	127.08
42	S2	1832	6MZ	N3-C4-N9	3.33	132.56	127.08
1	L5	3816	A2M	C2-N3-C4	3.33	119.61	111.75
42	S2	512	A2M	N3-C4-N9	3.32	132.55	127.08
42	S2	576	A2M	C2-N3-C4	3.32	119.58	111.75
42	S2	484	A2M	N3-C4-N9	3.31	132.54	127.08
42	S2	1383	A2M	N3-C4-N9	3.31	132.53	127.08
3	L8	14	OMU	C5-C4-N3	3.30	119.78	114.84
42	S2	354	OMU	C5-C4-N3	3.30	119.78	114.84
1	L5	4213	OMU	C5-C4-N3	3.29	119.76	114.84
1	L5	1520	A2M	C2-N3-C4	3.28	119.51	111.75
1	L5	3911	OMU	C5-C4-N3	3.28	119.75	114.84
42	S2	121	OMU	C5-C4-N3	3.28	119.75	114.84
42	S2	1288	OMU	C5-C4-N3	3.27	119.73	114.84
42	S2	1804	OMU	C5-C4-N3	3.27	119.73	114.84
1	L5	400	A2M	N3-C4-N9	3.27	132.47	127.08
1	L5	3811	A2M	N3-C4-N9	3.26	132.46	127.08
42	S2	172	OMU	C5-C4-N3	3.26	119.71	114.84
1	L5	4206	6MZ	C1'-N9-C8	3.26	134.49	127.14
42	S2	1639	G7M	C1'-N9-C8	3.24	137.68	126.74
1	L5	4509	A2M	C2'-C1'-N9	-3.24	108.07	113.53
42	S2	99	A2M	C2'-C1'-N9	-3.24	108.07	113.53
1	L5	3816	A2M	N3-C4-N9	3.24	132.42	127.08
42	S2	27	A2M	O4'-C1'-N9	3.24	114.44	108.06
42	S2	1851	MA6	C5-N7-C8	3.22	108.09	103.51
1	L5	3704	A2M	C2-N3-C4	3.21	119.34	111.75
1	L5	1322	A2M	N3-C4-N9	3.20	132.35	127.08
42	S2	576	A2M	N3-C4-N9	3.20	132.35	127.08
42	S2	27	A2M	N3-C4-N9	3.19	132.34	127.08
42	S2	1851	MA6	N3-C4-N9	3.17	132.31	127.08
1	L5	2827	OMU	C5-C4-N3	3.14	119.54	114.84
1	L5	1319	A2M	O4'-C1'-N9	3.13	114.24	108.06
1	L5	4206	6MZ	C5-N7-C8	3.13	107.96	103.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	2391	A2M	N3-C4-N9	3.12	132.22	127.08
1	L5	4509	A2M	N3-C4-N9	3.11	132.21	127.08
1	L5	1319	A2M	N3-C4-N9	3.10	132.19	127.08
42	S2	27	A2M	C2'-C1'-N9	-3.07	108.36	113.53
3	L8	14	OMU	O4-C4-C5	-3.07	119.76	125.16
61	ST	67	NMM	NE-CZ-NH1	3.04	125.96	120.26
42	S2	1850	MA6	C5-N7-C8	3.04	107.83	103.51
1	L5	2805	A2M	N3-C4-N9	3.04	132.09	127.08
42	S2	1031	A2M	O4'-C1'-N9	3.03	114.03	108.06
42	S2	576	A2M	C2'-C1'-N9	-3.02	108.45	113.53
42	S2	1031	A2M	N3-C4-N9	3.01	132.05	127.08
42	S2	166	A2M	C2'-C1'-N9	-3.00	108.47	113.53
1	L5	3816	A2M	O4'-C1'-N9	2.98	113.94	108.06
1	L5	4606	OMU	C5-C4-N3	2.97	119.29	114.84
42	S2	116	OMU	O4-C4-C5	-2.97	119.94	125.16
42	S2	1804	OMU	O4-C4-C5	-2.96	119.96	125.16
1	L5	2405	OMU	C5-C4-N3	2.96	119.26	114.84
42	S2	99	A2M	O4'-C1'-N9	2.95	113.87	108.06
1	L5	2353	A2M	O4'-C1'-N9	2.95	113.86	108.06
42	S2	1639	G7M	N9-C4-N3	2.94	131.84	125.94
42	S2	1383	A2M	O4'-C1'-N9	2.94	113.85	108.06
42	S2	1288	OMU	O4-C4-C5	-2.93	120.02	125.16
1	L5	2353	A2M	N3-C4-N9	2.92	131.89	127.08
42	S2	468	A2M	C2'-C1'-N9	-2.91	108.64	113.53
1	L5	4409	PSU	O2-C2-N1	-2.90	119.60	122.79
42	S2	668	A2M	N3-C4-N9	2.90	131.85	127.08
1	L5	3771	A2M	N3-C4-N9	2.88	131.82	127.08
42	S2	1639	G7M	C2-N1-C6	-2.88	119.86	125.10
42	S2	428	OMU	O4-C4-C5	-2.86	120.13	125.16
1	L5	3701	PSU	O2-C2-N1	-2.86	119.64	122.79
1	L5	4517	PSU	O2-C2-N1	-2.86	119.64	122.79
42	S2	1442	OMU	O4-C4-C5	-2.86	120.13	125.16
1	L5	1530	A2M	N3-C4-N9	2.85	131.78	127.08
1	L5	4576	A2M	C4'-O4'-C1'	-2.85	103.18	109.47
1	L5	3771	A2M	O4'-C1'-C2'	-2.84	101.58	106.57
42	S2	172	OMU	O4-C4-C5	-2.83	120.18	125.16
1	L5	4428	PSU	O2-C2-N1	-2.83	119.68	122.79
1	L5	4484	OMU	O4-C4-C5	-2.81	120.22	125.16
1	L5	3710	A2M	C4'-O4'-C1'	-2.81	103.27	109.47
42	S2	512	A2M	O4'-C1'-N9	2.81	113.59	108.06
42	S2	468	A2M	O4'-C1'-N9	2.80	113.58	108.06
1	L5	2777	A2M	N3-C4-N9	2.80	131.69	127.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	S2	590	A2M	C4'-O4'-C1'	-2.78	103.33	109.47
42	S2	863	PSU	O2-C2-N1	-2.76	119.75	122.79
1	L5	4576	A2M	N3-C4-N9	2.76	131.63	127.08
42	S2	121	OMU	O4-C4-C5	-2.76	120.31	125.16
1	L5	3704	A2M	C2'-C1'-N9	-2.76	108.89	113.53
42	S2	354	OMU	O4-C4-C5	-2.75	120.33	125.16
1	L5	4292	OMU	O4-C4-C5	-2.75	120.33	125.16
42	S2	918	PSU	O2-C2-N1	-2.74	119.77	122.79
1	L5	3710	A2M	O4'-C1'-N9	2.74	113.46	108.06
1	L5	1788	PSU	O2-C2-N1	-2.73	119.79	122.79
1	L5	2391	A2M	O4'-C1'-N9	2.72	113.42	108.06
42	S2	1445	PSU	O2-C2-N1	-2.71	119.80	122.79
1	L5	4562	PSU	O2-C2-N1	-2.71	119.80	122.79
42	S2	116	OMU	O2-C2-N1	-2.71	119.18	122.79
1	L5	1740	PSU	O2-C2-N1	-2.71	119.81	122.79
1	L5	4213	OMU	O4-C4-C5	-2.69	120.42	125.16
1	L5	2827	OMU	O4-C4-C5	-2.69	120.42	125.16
1	L5	3837	PSU	O2-C2-N1	-2.67	119.85	122.79
1	L5	3811	A2M	O4'-C1'-N9	2.66	113.30	108.06
42	S2	1045	PSU	O2-C2-N1	-2.66	119.87	122.79
1	L5	398	A2M	O4'-C1'-N9	2.65	113.29	108.06
1	L5	2622	PSU	C6-N1-C2	-2.65	119.97	122.68
42	S2	1337	4AC	C6-C5-C4	2.65	120.20	116.96
1	L5	1867	A2M	N3-C4-N9	2.65	131.44	127.08
1	L5	4339	PSU	O2-C2-N1	-2.64	119.88	122.79
42	S2	651	PSU	O2-C2-N1	-2.64	119.89	122.79
1	L5	3704	A2M	O4'-C1'-N9	2.64	113.26	108.06
1	L5	4285	PSU	O2-C2-N1	-2.63	119.89	122.79
42	S2	1851	MA6	C4-N9-C8	2.62	108.57	105.73
42	S2	814	PSU	O2-C2-N1	-2.62	119.90	122.79
42	S2	484	A2M	O4'-C1'-N9	2.62	113.22	108.06
1	L5	4347	PSU	O2-C2-N1	-2.62	119.91	122.79
42	S2	822	PSU	O2-C2-N1	-2.62	119.91	122.79
1	L5	3839	PSU	C6-N1-C2	-2.62	120.01	122.68
1	L5	1777	PSU	O2-C2-N1	-2.62	119.91	122.79
42	S2	218	PSU	O2-C2-N1	-2.61	119.92	122.79
42	S2	1692	PSU	O2-C2-N1	-2.61	119.92	122.79
42	S2	406	PSU	O2-C2-N1	-2.61	119.92	122.79
42	S2	468	A2M	C4'-O4'-C1'	-2.61	103.72	109.47
1	L5	1858	PSU	O2-C2-N1	-2.60	119.93	122.79
1	L5	3808	PSU	O2-C2-N1	-2.60	119.93	122.79
1	L5	2622	PSU	O2-C2-N1	-2.60	119.93	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	4518	PSU	O2-C2-N1	-2.59	119.93	122.79
3	L8	69	PSU	O2-C2-N1	-2.59	119.94	122.79
42	S2	1232	PSU	O2-C2-N1	-2.58	119.94	122.79
42	S2	1046	PSU	O2-C2-N1	-2.58	119.95	122.79
1	L5	1856	PSU	O2-C2-N1	-2.58	119.95	122.79
42	S2	1136	PSU	O2-C2-N1	-2.57	119.96	122.79
1	L5	4486	PSU	O2-C2-N1	-2.57	119.96	122.79
42	S2	590	A2M	O4'-C1'-N9	2.56	113.11	108.06
1	L5	4282	PSU	O2-C2-N1	-2.56	119.97	122.79
42	S2	1244	PSU	O2-C2-N1	-2.55	119.98	122.79
42	S2	686	PSU	O2-C2-N1	-2.55	119.98	122.79
1	L5	1858	PSU	C6-C5-C4	2.55	119.98	118.20
42	S2	105	PSU	O2-C2-N1	-2.54	119.99	122.79
42	S2	1678	A2M	C4'-O4'-C1'	-2.54	103.87	109.47
42	S2	609	PSU	O2-C2-N1	-2.54	120.00	122.79
1	L5	4614	PSU	O2-C2-N1	-2.53	120.00	122.79
42	S2	1625	PSU	O2-C2-N1	-2.53	120.00	122.79
1	L5	400	A2M	C4'-O4'-C1'	-2.53	103.89	109.47
42	S2	119	PSU	O2-C2-N1	-2.52	120.01	122.79
1	L5	3771	A2M	C4-C5-N7	-2.52	107.55	110.62
42	S2	36	PSU	O2-C2-N1	-2.52	120.02	122.79
1	L5	4606	OMU	O4-C4-C5	-2.52	120.73	125.16
42	S2	668	A2M	C4'-O4'-C1'	-2.52	103.92	109.47
42	S2	1174	PSU	O2-C2-N1	-2.52	120.02	122.79
1	L5	1679	PSU	O2-C2-N1	-2.51	120.02	122.79
42	S2	649	PSU	O2-C2-N1	-2.51	120.02	122.79
42	S2	1238	PSU	O2-C2-N1	-2.51	120.03	122.79
1	L5	4555	PSU	C6-N1-C2	-2.51	120.12	122.68
1	L5	2405	OMU	O4-C4-C5	-2.51	120.75	125.16
42	S2	801	PSU	O2-C2-N1	-2.50	120.04	122.79
42	S2	918	PSU	O4'-C1'-C2'	2.50	108.67	105.14
1	L5	2391	A2M	C2'-C1'-N9	-2.49	109.34	113.53
1	L5	2777	A2M	C4-C5-N7	-2.48	107.59	110.62
1	L5	4517	PSU	C6-C5-C4	2.48	119.93	118.20
1	L5	4555	PSU	O2-C2-N1	-2.48	120.06	122.79
42	S2	815	PSU	O2-C2-N1	-2.48	120.06	122.79
42	S2	1177	PSU	O2-C2-N1	-2.48	120.06	122.79
42	S2	109	PSU	O2-C2-N1	-2.48	120.06	122.79
1	L5	4958	PSU	O2-C2-N1	-2.48	120.06	122.79
1	L5	4986	PSU	O2-C2-N1	-2.48	120.06	122.79
1	L5	3681	PSU	O2-C2-N1	-2.47	120.07	122.79
1	L5	4457	PSU	O2-C2-N1	-2.47	120.07	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	S2	572	PSU	O2-C2-N1	-2.47	120.07	122.79
1	L5	1867	A2M	C4'-O4'-C1'	-2.46	104.05	109.47
42	S2	681	PSU	O2-C2-N1	-2.46	120.08	122.79
1	L5	4389	PSU	O2-C2-N1	-2.46	120.09	122.79
42	S2	668	A2M	C2'-C1'-N9	2.46	117.67	113.53
42	S2	1850	MA6	C4-N9-C8	2.45	108.39	105.73
1	L5	4562	PSU	C6-N1-C2	-2.45	120.18	122.68
1	L5	4389	PSU	C6-N1-C2	-2.45	120.18	122.68
3	L8	55	PSU	O2-C2-N1	-2.45	120.10	122.79
42	S2	576	A2M	O4'-C1'-N9	2.44	112.88	108.06
42	S2	1643	PSU	O2-C2-N1	-2.44	120.11	122.79
1	L5	3911	OMU	O4-C4-C5	-2.44	120.88	125.16
42	S2	1596	PSU	O2-C2-N1	-2.43	120.12	122.79
42	S2	34	PSU	O2-C2-N1	-2.43	120.12	122.79
42	S2	166	A2M	O4'-C1'-N9	2.42	112.84	108.06
1	L5	1530	A2M	C4-C5-N7	-2.42	107.68	110.62
1	L5	4659	PSU	O2-C2-N1	-2.41	120.13	122.79
1	L5	1778	PSU	O2-C2-N1	-2.41	120.14	122.79
1	L5	1856	PSU	C6-N1-C2	-2.41	120.22	122.68
1	L5	4417	PSU	O2-C2-N1	-2.41	120.14	122.79
1	L5	4538	PSU	O2-C2-N1	-2.40	120.14	122.79
42	S2	100	PSU	O2-C2-N1	-2.40	120.15	122.79
42	S2	1347	PSU	O2-C2-N1	-2.40	120.15	122.79
42	S2	668	A2M	C4-C5-N7	-2.40	107.70	110.62
42	S2	166	A2M	C4'-O4'-C1'	-2.39	104.19	109.47
42	S2	668	A2M	C2'-C3'-C4'	2.39	107.18	101.99
1	L5	3839	PSU	O2-C2-N1	-2.39	120.16	122.79
42	S2	1383	A2M	C4'-O4'-C1'	-2.38	104.21	109.47
1	L5	4509	A2M	C4'-O4'-C1'	-2.38	104.22	109.47
1	L5	4565	PSU	C6-N1-C2	-2.38	120.25	122.68
42	S2	1326	UY1	O3'-C3'-C2'	2.38	117.92	111.17
42	S2	918	PSU	C6-N1-C2	-2.38	120.25	122.68
1	L5	4509	A2M	C4-C5-N7	-2.37	107.73	110.62
1	L5	4517	PSU	C6-N1-C2	-2.37	120.26	122.68
42	S2	1625	PSU	C6-N1-C2	-2.37	120.26	122.68
1	L5	4675	PSU	C6-C5-C4	2.37	119.85	118.20
1	L5	4565	PSU	O2-C2-N1	-2.36	120.19	122.79
1	L5	1867	A2M	C4-C5-N7	-2.36	107.74	110.62
1	L5	2827	OMU	O2-C2-N1	-2.36	119.65	122.79
1	L5	4486	PSU	C6-C5-C4	2.36	119.85	118.20
1	L5	4622	PSU	C6-C5-C4	2.35	119.84	118.20
1	L5	3811	A2M	C4-C5-N7	-2.35	107.76	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	4995	PSU	O2-C2-N1	-2.35	120.21	122.79
42	S2	1832	6MZ	C4-C5-N7	-2.34	107.76	110.62
42	S2	1326	UY1	O3'-C3'-C4'	2.34	117.83	111.05
42	S2	822	PSU	C6-N1-C2	-2.34	120.29	122.68
1	L5	3837	PSU	C6-N1-C2	-2.34	120.29	122.68
1	L5	4484	OMU	O2-C2-N1	-2.33	119.69	122.79
1	L5	3853	A2M	C4'-O4'-C1'	-2.33	104.33	109.47
42	S2	1056	PSU	O2-C2-N1	-2.33	120.22	122.79
1	L5	3625	PSU	O2-C2-N1	-2.33	120.23	122.79
1	L5	1740	PSU	C6-N1-C2	-2.33	120.30	122.68
1	L5	4614	PSU	C6-N1-C2	-2.33	120.30	122.68
1	L5	1578	PSU	O2-C2-N1	-2.33	120.23	122.79
1	L5	3830	PSU	O2-C2-N1	-2.33	120.23	122.79
1	L5	1532	PSU	O2-C2-N1	-2.33	120.23	122.79
1	L5	2805	A2M	O4'-C1'-N9	2.32	112.64	108.06
3	L8	14	OMU	O2-C2-N1	-2.32	119.70	122.79
1	L5	4957	PSU	C6-N1-C2	-2.32	120.31	122.68
42	S2	801	PSU	C6-N1-C2	-2.32	120.31	122.68
42	S2	576	A2M	C4-C5-N7	-2.32	107.79	110.62
1	L5	2805	A2M	C4-C5-N7	-2.32	107.79	110.62
1	L5	2353	A2M	C4'-O4'-C1'	-2.32	104.36	109.47
1	L5	4443	PSU	O2-C2-N1	-2.31	120.24	122.79
1	L5	4622	PSU	O2-C2-N1	-2.31	120.24	122.79
1	L5	1319	A2M	C4-C5-N7	-2.31	107.80	110.62
1	L5	3701	PSU	C6-N1-C2	-2.31	120.32	122.68
1	L5	2829	PSU	C6-N1-C2	-2.31	120.33	122.68
42	S2	572	PSU	C6-N1-C2	-2.31	120.33	122.68
1	L5	4213	OMU	O2-C2-N1	-2.31	119.72	122.79
42	S2	484	A2M	C4-C5-N7	-2.30	107.81	110.62
1	L5	2353	A2M	C4-C5-N7	-2.30	107.82	110.62
1	L5	4957	PSU	O2-C2-N1	-2.30	120.26	122.79
1	L5	398	A2M	C4-C5-N7	-2.30	107.82	110.62
1	L5	2805	A2M	C4'-O4'-C1'	-2.30	104.41	109.47
1	L5	4206	6MZ	C4-N9-C8	2.29	108.21	105.73
3	L8	69	PSU	C6-N1-C2	-2.29	120.34	122.68
42	S2	863	PSU	C6-N1-C2	-2.29	120.34	122.68
42	S2	36	PSU	C6-N1-C2	-2.29	120.34	122.68
42	S2	1596	PSU	C6-N1-C2	-2.29	120.34	122.68
1	L5	2391	A2M	C4'-O4'-C1'	-2.28	104.43	109.47
1	L5	1673	PSU	O2-C2-N1	-2.28	120.28	122.79
1	L5	4409	PSU	C6-N1-C2	-2.28	120.36	122.68
42	S2	27	A2M	C4-C5-N7	-2.27	107.85	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	S2	1031	A2M	C4-C5-N7	-2.27	107.85	110.62
3	L8	69	PSU	O4'-C1'-C2'	2.27	108.35	105.14
42	S2	93	PSU	O2-C2-N1	-2.27	120.29	122.79
1	L5	4285	PSU	C6-N1-C2	-2.27	120.37	122.68
1	L5	4409	PSU	C6-C5-C4	2.26	119.78	118.20
1	L5	1322	A2M	O4'-C1'-N9	2.26	112.51	108.06
1	L5	4298	PSU	O2-C2-N1	-2.25	120.31	122.79
1	L5	3704	A2M	C4-C5-N7	-2.25	107.88	110.62
1	L5	2391	A2M	C4-C5-N7	-2.25	107.88	110.62
1	L5	4417	PSU	C6-N1-C2	-2.25	120.39	122.68
42	S2	119	PSU	C6-N1-C2	-2.24	120.39	122.68
42	S2	681	PSU	C6-N1-C2	-2.24	120.39	122.68
1	L5	4986	PSU	C6-N1-C2	-2.24	120.39	122.68
1	L5	3870	PSU	C6-N1-C2	-2.24	120.40	122.68
1	L5	4279	PSU	O2-C2-N1	-2.24	120.33	122.79
42	S2	1136	PSU	C6-N1-C2	-2.23	120.40	122.68
1	L5	4516	UR3	C6-N1-C2	-2.23	119.79	121.79
1	L5	2829	PSU	O2-C2-N1	-2.23	120.33	122.79
42	S2	428	OMU	O2-C2-N1	-2.23	119.82	122.79
42	S2	814	PSU	C6-N1-C2	-2.23	120.40	122.68
42	S2	512	A2M	C4'-O4'-C1'	-2.23	104.55	109.47
42	S2	1174	PSU	C6-N1-C2	-2.23	120.40	122.68
42	S2	1337	4AC	O7-C7-N4	-2.22	118.21	121.82
42	S2	822	PSU	O4'-C1'-C2'	2.22	108.28	105.14
42	S2	686	PSU	C6-N1-C2	-2.22	120.41	122.68
1	L5	3906	PSU	O2-C2-N1	-2.22	120.35	122.79
1	L5	1856	PSU	C6-C5-C4	2.22	119.75	118.20
42	S2	172	OMU	O2-C2-N1	-2.22	119.84	122.79
42	S2	1445	PSU	C6-N1-C2	-2.21	120.42	122.68
42	S2	1238	PSU	C6-C5-C4	2.21	119.74	118.20
1	L5	4995	PSU	C6-N1-C2	-2.21	120.42	122.68
1	L5	4507	PSU	O2-C2-N1	-2.21	120.36	122.79
1	L5	1673	PSU	O4'-C1'-C2'	2.20	108.25	105.14
42	S2	1232	PSU	C6-C5-C4	2.20	119.74	118.20
42	S2	1692	PSU	C6-N1-C2	-2.20	120.43	122.68
42	S2	159	A2M	O4'-C1'-N9	2.20	112.39	108.06
1	L5	1322	A2M	C4-C5-N7	-2.19	107.94	110.62
1	L5	4339	PSU	C6-N1-C2	-2.19	120.44	122.68
1	L5	3623	PSU	O2-C2-N1	-2.19	120.38	122.79
1	L5	4518	PSU	C6-C5-C4	2.19	119.73	118.20
1	L5	4576	A2M	C4-C5-N7	-2.19	107.95	110.62
1	L5	3808	PSU	C6-N1-C2	-2.18	120.45	122.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	4428	PSU	C6-C5-C4	2.18	119.72	118.20
42	S2	1232	PSU	C6-N1-C2	-2.17	120.46	122.68
1	L5	1778	PSU	C6-N1-C2	-2.17	120.46	122.68
1	L5	400	A2M	C4-C5-N7	-2.17	107.98	110.62
1	L5	1777	PSU	C6-N1-C2	-2.17	120.47	122.68
42	S2	34	PSU	C6-C5-C4	2.17	119.71	118.20
42	S2	1678	A2M	C2'-C1'-N9	2.16	117.17	113.53
42	S2	1643	PSU	C6-N1-C2	-2.16	120.47	122.68
42	S2	1004	PSU	O2-C2-N1	-2.16	120.41	122.79
1	L5	4675	PSU	C6-N1-C2	-2.16	120.48	122.68
42	S2	609	PSU	C6-N1-C2	-2.16	120.48	122.68
1	L5	4675	PSU	O2-C2-N1	-2.15	120.43	122.79
42	S2	1004	PSU	C6-N1-C2	-2.15	120.49	122.68
1	L5	2405	OMU	O2-C2-N1	-2.15	119.93	122.79
1	L5	3811	A2M	C4'-O4'-C1'	-2.14	104.74	109.47
42	S2	27	A2M	C4'-O4'-C1'	-2.14	104.75	109.47
1	L5	400	A2M	O4'-C1'-N9	2.14	112.28	108.06
1	L5	3710	A2M	C4-C5-N7	-2.14	108.01	110.62
1	L5	4557	A2M	C4-C5-N7	-2.14	108.01	110.62
42	S2	1842	4AC	N4-C4-N3	2.14	117.44	113.85
42	S2	649	PSU	C6-N1-C2	-2.14	120.50	122.68
1	L5	1673	PSU	C6-N1-C2	-2.14	120.50	122.68
42	S2	99	A2M	C4-C5-N7	-2.13	108.02	110.62
42	S2	1337	4AC	C5-C4-N3	-2.13	119.17	122.59
1	L5	4958	PSU	C6-N1-C2	-2.13	120.51	122.68
42	S2	354	OMU	C2'-C1'-N1	-2.12	110.10	114.22
1	L5	2622	PSU	O4'-C1'-C2'	2.12	108.14	105.14
1	L5	3830	PSU	C6-N1-C2	-2.12	120.51	122.68
1	L5	4659	PSU	C6-N1-C2	-2.12	120.52	122.68
42	S2	590	A2M	C4-C5-N7	-2.12	108.04	110.62
42	S2	1244	PSU	C6-N1-C2	-2.12	120.52	122.68
1	L5	4292	OMU	C2'-C1'-N1	-2.12	110.11	114.22
1	L5	4428	PSU	O4'-C1'-C2'	2.12	108.13	105.14
1	L5	3771	A2M	C2'-C3'-C4'	2.11	106.58	101.99
42	S2	651	PSU	C6-C5-C4	2.11	119.67	118.20
1	L5	4958	PSU	C6-C5-C4	2.11	119.67	118.20
42	S2	1238	PSU	O4-C4-C5	-2.11	118.53	124.05
42	S2	166	A2M	C4-C5-N7	-2.11	108.05	110.62
42	S2	651	PSU	C6-N1-C2	-2.10	120.53	122.68
1	L5	4457	PSU	C6-N1-C2	-2.10	120.53	122.68
42	S2	1056	PSU	C6-N1-C2	-2.10	120.53	122.68
1	L5	4538	PSU	C6-N1-C2	-2.10	120.53	122.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	3816	A2M	C4-C5-N7	-2.10	108.06	110.62
42	S2	1445	PSU	O4'-C1'-C2'	2.10	108.10	105.14
3	L8	55	PSU	C6-N1-C2	-2.10	120.54	122.68
42	S2	121	OMU	O2-C2-N1	-2.10	120.00	122.79
42	S2	918	PSU	C6-C5-C4	2.10	119.66	118.20
42	S2	105	PSU	C6-N1-C2	-2.09	120.55	122.68
1	L5	4428	PSU	C6-N1-C2	-2.09	120.55	122.68
42	S2	1678	A2M	C2'-C3'-C4'	2.08	106.52	101.99
1	L5	3625	PSU	C6-N1-C2	-2.08	120.55	122.68
42	S2	1383	A2M	C4-C5-N7	-2.08	108.08	110.62
42	S2	406	PSU	C6-N1-C2	-2.08	120.56	122.68
1	L5	3853	A2M	C4-C5-N7	-2.08	108.09	110.62
1	L5	3870	PSU	O2-C2-N1	-2.08	120.50	122.79
42	S2	109	PSU	C6-N1-C2	-2.07	120.56	122.68
1	L5	1777	PSU	C6-C5-C4	2.07	119.64	118.20
1	L5	4282	PSU	C6-N1-C2	-2.07	120.57	122.68
1	L5	4622	PSU	O4'-C1'-C2'	2.07	108.06	105.14
42	S2	468	A2M	C4-C5-N7	-2.07	108.10	110.62
42	S2	512	A2M	C4-C5-N7	-2.07	108.10	110.62
1	L5	1532	PSU	C6-N1-C2	-2.06	120.57	122.68
42	S2	1347	PSU	C6-N1-C2	-2.06	120.57	122.68
1	L5	3681	PSU	C6-N1-C2	-2.06	120.57	122.68
1	L5	4557	A2M	C5-C6-N6	-2.06	118.94	123.43
1	L5	1322	A2M	C4'-O4'-C1'	-2.06	104.92	109.47
42	S2	1596	PSU	C6-C5-C4	2.06	119.64	118.20
1	L5	3625	PSU	O4'-C1'-C2'	2.05	108.04	105.14
42	S2	801	PSU	C6-C5-C4	2.05	119.63	118.20
42	S2	1244	PSU	C6-C5-C4	2.05	119.63	118.20
42	S2	1842	4AC	C6-C5-C4	2.05	119.47	116.96
42	S2	572	PSU	O4'-C1'-C2'	2.05	108.03	105.14
1	L5	4486	PSU	C6-N1-C2	-2.05	120.59	122.68
42	S2	99	A2M	C4'-O4'-C1'	-2.05	104.96	109.47
1	L5	4557	A2M	O4'-C1'-N9	2.05	112.09	108.06
1	L5	4443	PSU	O4'-C1'-C2'	2.04	108.03	105.14
1	L5	1520	A2M	C4'-O4'-C1'	-2.04	104.97	109.47
1	L5	4443	PSU	C6-N1-C2	-2.04	120.60	122.68
1	L5	4457	PSU	C6-C5-C4	2.04	119.62	118.20
1	L5	4347	PSU	C6-C5-C4	2.04	119.62	118.20
42	S2	1046	PSU	C6-N1-C2	-2.04	120.60	122.68
42	S2	1678	A2M	C5-C6-N6	-2.04	119.00	123.43
1	L5	4565	PSU	C6-C5-C4	2.03	119.62	118.20
1	L5	1578	PSU	C6-N1-C2	-2.03	120.61	122.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	S2	1678	A2M	C4-C5-N7	-2.03	108.15	110.62
1	L5	4606	OMU	O2-C2-N1	-2.03	120.09	122.79
42	S2	159	A2M	C5-C6-N6	-2.03	119.02	123.43
42	S2	681	PSU	C6-C5-C4	2.03	119.61	118.20
42	S2	1347	PSU	C6-C5-C4	2.03	119.61	118.20
1	L5	3623	PSU	C6-N1-C2	-2.02	120.61	122.68
42	S2	166	A2M	C5-C6-N6	-2.02	119.03	123.43
42	S2	218	PSU	C6-N1-C2	-2.02	120.61	122.68
1	L5	4389	PSU	O4'-C1'-C2'	2.02	107.99	105.14
1	L5	4279	PSU	C6-N1-C2	-2.02	120.62	122.68
1	L5	4958	PSU	O4'-C1'-C2'	2.02	107.99	105.14
1	L5	1673	PSU	C6-C5-C4	2.02	119.61	118.20
42	S2	667	PSU	O2-C2-N1	-2.02	120.57	122.79
1	L5	1530	A2M	C3'-C2'-C1'	-2.01	99.10	102.89
42	S2	34	PSU	C6-N1-C2	-2.01	120.62	122.68
42	S2	1851	MA6	C4-C5-N7	-2.01	108.17	110.62
1	L5	4507	PSU	O4'-C1'-C2'	2.01	107.98	105.14
42	S2	1383	A2M	C5-C6-N6	-2.01	119.06	123.43
1	L5	3701	PSU	O4'-C1'-C2'	2.01	107.97	105.14
42	S2	1031	A2M	C4'-O4'-C1'	-2.01	105.05	109.47
1	L5	3911	OMU	O2-C2-N1	-2.00	120.12	122.79

There are no chirality outliers.

All (140) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L8	14	OMU	C1'-C2'-O2'-CM2
37	LB	245	HIC	O-C-CA-CB
61	ST	67	NMM	O-C-CA-CB
1	L5	398	A2M	C1'-C2'-O2'-CM'
1	L5	1578	PSU	O4'-C1'-C5-C4
1	L5	1578	PSU	O4'-C1'-C5-C6
1	L5	1867	A2M	C1'-C2'-O2'-CM'
1	L5	2414	OMG	C1'-C2'-O2'-CM2
1	L5	2805	A2M	O4'-C4'-C5'-O5'
1	L5	2805	A2M	C3'-C4'-C5'-O5'
1	L5	2805	A2M	C1'-C2'-O2'-CM'
1	L5	2814	OMC	C1'-C2'-O2'-CM2
1	L5	3687	OMC	C2'-C1'-N1-C6
1	L5	3704	A2M	C1'-C2'-O2'-CM'
1	L5	3710	A2M	C1'-C2'-O2'-CM'
1	L5	3730	OMG	C1'-C2'-O2'-CM2

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Mol	Chain	Res	Type	Atoms
1	L5	3811	A2M	C1'-C2'-O2'-CM'
1	L5	3816	A2M	C1'-C2'-O2'-CM'
1	L5	3853	A2M	C1'-C2'-O2'-CM'
1	L5	4182	OMG	C1'-C2'-O2'-CM2
1	L5	4509	A2M	C1'-C2'-O2'-CM'
1	L5	4576	A2M	C4'-C5'-O5'-P
1	L5	4622	PSU	C3'-C4'-C5'-O5'
1	L5	4623	OMG	C1'-C2'-O2'-CM2
42	S2	27	A2M	C1'-C2'-O2'-CM'
42	S2	99	A2M	C1'-C2'-O2'-CM'
42	S2	468	A2M	C1'-C2'-O2'-CM'
42	S2	484	A2M	C1'-C2'-O2'-CM'
42	S2	512	A2M	C1'-C2'-O2'-CM'
42	S2	576	A2M	O4'-C4'-C5'-O5'
42	S2	576	A2M	C3'-C4'-C5'-O5'
42	S2	667	PSU	O4'-C1'-C5-C4
42	S2	667	PSU	O4'-C1'-C5-C6
42	S2	668	A2M	C1'-C2'-O2'-CM'
42	S2	683	OMG	O4'-C4'-C5'-O5'
42	S2	867	OMG	C1'-C2'-O2'-CM2
42	S2	1031	A2M	C1'-C2'-O2'-CM'
42	S2	1326	UY1	C2'-C1'-C5-C4
42	S2	1383	A2M	C1'-C2'-O2'-CM'
42	S2	1447	OMG	C3'-C4'-C5'-O5'
42	S2	1447	OMG	C1'-C2'-O2'-CM2
42	S2	1490	OMG	C1'-C2'-O2'-CM2
42	S2	1678	A2M	C1'-C2'-O2'-CM'
42	S2	1851	MA6	O4'-C4'-C5'-O5'
1	L5	4486	PSU	C3'-C4'-C5'-O5'
1	L5	4486	PSU	O4'-C4'-C5'-O5'
42	S2	159	A2M	C3'-C4'-C5'-O5'
42	S2	668	A2M	O4'-C4'-C5'-O5'
42	S2	683	OMG	C3'-C4'-C5'-O5'
42	S2	867	OMG	C3'-C4'-C5'-O5'
42	S2	1328	OMG	O4'-C4'-C5'-O5'
42	S2	1490	OMG	O4'-C4'-C5'-O5'
42	S2	1851	MA6	C3'-C4'-C5'-O5'
1	L5	3687	OMC	C2'-C1'-N1-C2
1	L5	3710	A2M	O4'-C4'-C5'-O5'
1	L5	3710	A2M	C3'-C4'-C5'-O5'
1	L5	4622	PSU	O4'-C4'-C5'-O5'
42	S2	99	A2M	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
42	S2	668	A2M	C3'-C4'-C5'-O5'
42	S2	867	OMG	O4'-C4'-C5'-O5'
42	S2	1328	OMG	C3'-C4'-C5'-O5'
1	L5	2777	A2M	C2'-C1'-N9-C4
1	L5	1621	OMG	C3'-C2'-O2'-CM2
42	S2	166	A2M	C3'-C4'-C5'-O5'
1	L5	3830	PSU	O4'-C4'-C5'-O5'
1	L5	4182	OMG	O4'-C4'-C5'-O5'
42	S2	159	A2M	O4'-C4'-C5'-O5'
42	S2	512	A2M	O4'-C4'-C5'-O5'
42	S2	1447	OMG	O4'-C4'-C5'-O5'
1	L5	2777	A2M	C2'-C1'-N9-C8
1	L5	3853	A2M	C3'-C4'-C5'-O5'
42	S2	1639	G7M	O4'-C4'-C5'-O5'
42	S2	428	OMU	C2'-C1'-N1-C6
1	L5	4182	OMG	C3'-C4'-C5'-O5'
42	S2	100	PSU	O4'-C4'-C5'-O5'
42	S2	1337	4AC	O7-C7-N4-C4
42	S2	1337	4AC	CM7-C7-N4-C4
1	L5	3911	OMU	C1'-C2'-O2'-CM2
1	L5	1530	A2M	C4'-C5'-O5'-P
1	L5	3804	UY1	C4'-C5'-O5'-P
1	L5	4486	PSU	C4'-C5'-O5'-P
42	S2	1639	G7M	C3'-C4'-C5'-O5'
42	S2	1678	A2M	C3'-C2'-O2'-CM'
42	S2	1804	OMU	C3'-C2'-O2'-CM2
1	L5	3687	OMC	O4'-C1'-N1-C6
42	S2	1490	OMG	C4'-C5'-O5'-P
1	L5	1318	1MA	C2'-C1'-N9-C8
1	L5	1322	A2M	C4'-C5'-O5'-P
1	L5	3687	OMC	O4'-C1'-N1-C2
1	L5	398	A2M	O4'-C4'-C5'-O5'
1	L5	2805	A2M	C4'-C5'-O5'-P
1	L5	4433	5MC	O4'-C1'-N1-C6
42	S2	428	OMU	O4'-C1'-N1-C6
42	S2	644	OMG	C4'-C5'-O5'-P
1	L5	3771	A2M	O4'-C4'-C5'-O5'
1	L5	3830	PSU	C3'-C4'-C5'-O5'
1	L5	4433	5MC	C2'-C1'-N1-C6
1	L5	1318	1MA	C2'-C1'-N9-C4
1	L5	1530	A2M	O4'-C4'-C5'-O5'
1	L5	2341	OMC	C2'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
61	ST	67	NMM	CA-CB-CG-CD
1	L5	4507	PSU	O4'-C1'-C5-C4
42	S2	1326	UY1	O4'-C1'-C5-C4
42	S2	1347	PSU	O4'-C1'-C5-C4
42	S2	159	A2M	C3'-C2'-O2'-CM'
1	L5	3853	A2M	O4'-C4'-C5'-O5'
1	L5	4433	5MC	O4'-C1'-N1-C2
42	S2	428	OMU	O4'-C1'-N1-C2
1	L5	3830	PSU	C4'-C5'-O5'-P
42	S2	166	A2M	O4'-C4'-C5'-O5'
42	S2	609	PSU	O4'-C4'-C5'-O5'
42	S2	590	A2M	O4'-C1'-N9-C8
42	S2	99	A2M	C3'-C4'-C5'-O5'
42	S2	590	A2M	C3'-C4'-C5'-O5'
42	S2	918	PSU	O4'-C4'-C5'-O5'
42	S2	590	A2M	C2'-C1'-N9-C4
1	L5	4484	OMU	C3'-C2'-O2'-CM2
42	S2	867	OMG	C3'-C2'-O2'-CM2
42	S2	1383	A2M	C3'-C2'-O2'-CM'
1	L5	2341	OMC	C2'-C1'-N1-C2
42	S2	1288	OMU	C2'-C1'-N1-C2
1	L5	2777	A2M	O4'-C1'-N9-C8
1	L5	1319	A2M	O4'-C4'-C5'-O5'
42	S2	100	PSU	C3'-C4'-C5'-O5'
1	L5	4622	PSU	O4'-C1'-C5-C6
42	S2	1326	UY1	O4'-C1'-C5-C6
42	S2	1347	PSU	O4'-C1'-C5-C6
42	S2	428	OMU	C2'-C1'-N1-C2
1	L5	2341	OMC	O4'-C4'-C5'-O5'
1	L5	2412	OMC	O4'-C4'-C5'-O5'
42	S2	512	A2M	C3'-C4'-C5'-O5'
42	S2	590	A2M	C2'-C1'-N9-C8
42	S2	668	A2M	C2'-C1'-N9-C8
61	ST	67	NMM	CG-CD-NE-CZ
42	S2	1851	MA6	C4'-C5'-O5'-P
1	L5	1520	A2M	C3'-C2'-O2'-CM'
1	L5	3853	A2M	C3'-C2'-O2'-CM'
42	S2	590	A2M	C3'-C2'-O2'-CM'
1	L5	3873	OMC	C4'-C5'-O5'-P
42	S2	644	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

104 monomers are involved in 205 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
42	S2	1447	OMG	4	0
42	S2	1288	OMU	4	0
42	S2	1136	PSU	1	0
1	L5	1322	A2M	1	0
42	S2	1851	MA6	4	0
1	L5	1777	PSU	1	0
42	S2	121	OMU	4	0
1	L5	2866	OMG	1	0
1	L5	2851	OMC	1	0
1	L5	3794	OMC	2	0
1	L5	3830	PSU	1	0
1	L5	3906	PSU	2	0
42	S2	1391	OMC	3	0
42	S2	1328	OMG	3	0
42	S2	681	PSU	2	0
42	S2	867	OMG	1	0
42	S2	166	A2M	1	0
42	S2	863	PSU	1	0
1	L5	3730	OMG	1	0
42	S2	667	PSU	1	0
42	S2	1678	A2M	1	0
42	S2	509	OMG	2	0
42	S2	1383	A2M	1	0
42	S2	512	A2M	5	0
1	L5	3771	A2M	1	0
42	S2	172	OMU	1	0
42	S2	1337	4AC	4	0
1	L5	3853	A2M	2	0
42	S2	576	A2M	4	0
1	L5	4213	OMU	1	0
1	L5	4538	PSU	1	0
42	S2	590	A2M	1	0
42	S2	1639	G7M	2	0
1	L5	3701	PSU	1	0
42	S2	649	PSU	1	0
1	L5	4614	PSU	1	0
1	L5	2777	A2M	2	0
1	L5	3870	PSU	1	0
42	S2	572	PSU	1	0
1	L5	4557	A2M	5	0
42	S2	1177	PSU	2	0
42	S2	116	OMU	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L5	4433	5MC	1	0
1	L5	1867	A2M	3	0
42	S2	1596	PSU	1	0
1	L5	398	A2M	2	0
42	S2	218	PSU	2	0
1	L5	4339	PSU	1	0
42	S2	621	OMC	2	0
42	S2	601	OMG	1	0
42	S2	1238	PSU	2	0
1	L5	1673	PSU	1	0
42	S2	668	A2M	2	0
1	L5	2814	OMC	2	0
42	S2	462	OMC	2	0
1	L5	1578	PSU	1	0
1	L5	2354	OMG	1	0
42	S2	99	A2M	1	0
42	S2	468	A2M	3	0
1	L5	3613	OMG	1	0
42	S2	1804	OMU	8	0
61	ST	67	NMM	3	0
42	S2	918	PSU	3	0
42	S2	159	A2M	3	0
42	S2	354	OMU	4	0
1	L5	4986	PSU	1	0
1	L5	4606	OMU	2	0
1	L5	3704	A2M	4	0
42	S2	1850	MA6	8	0
1	L5	3681	PSU	1	0
1	L5	2805	A2M	4	0
1	L5	1532	PSU	1	0
1	L5	4576	A2M	2	0
42	S2	27	A2M	2	0
42	S2	517	OMC	1	0
1	L5	2341	OMC	4	0
42	S2	1232	PSU	2	0
42	S2	1442	OMU	1	0
1	L5	4484	OMU	1	0
3	L8	14	OMU	1	0
1	L5	4623	OMG	1	0
42	S2	1046	PSU	2	0
42	S2	428	OMU	1	0
1	L5	2405	OMU	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
42	S2	1832	6MZ	1	0
1	L5	4378	OMG	1	0
1	L5	4442	OMC	1	0
1	L5	2414	OMG	5	0
1	L5	3827	OMC	1	0
1	L5	1336	OMC	1	0
1	L5	3811	A2M	1	0
1	L5	1621	OMG	1	0
1	L5	2794	OMC	2	0
42	S2	484	A2M	3	0
42	S2	1031	A2M	4	0
1	L5	2353	A2M	1	0
42	S2	1490	OMG	3	0
1	L5	2622	PSU	6	0
1	L5	3710	A2M	1	0
1	L5	4214	OMG	1	0
42	S2	1643	PSU	1	0
42	S2	1445	PSU	3	0
1	L5	4443	PSU	1	0
42	S2	1703	OMC	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 233 ligands modelled in this entry, 233 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	L5	17
42	S2	4
76	S6	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L5	191:G	O3'	192:G	P	55.88
1	L5	266:C	O3'	267:G	P	46.82
1	L5	4731:C	O3'	4732:C	P	27.22
1	L5	1211:G	O3'	1212:G	P	24.08
1	S2	128:U	O3'	141:A	P	20.46
1	L5	1058:C	O3'	1059:G	P	19.91
1	L5	1077:C	O3'	1078:C	P	19.41
1	L5	4846:C	O3'	4847:G	P	17.91
1	L5	4132:G	O3'	4133:G	P	17.32
1	L5	2249:G	O3'	2250:C	P	17.30
1	L5	5013:G	O3'	5014:C	P	17.15
1	L5	1413:G	O3'	1414:C	P	16.42
1	S6	6:G	O3'	70:C	P	15.92
1	L5	963:G	O3'	964:G	P	11.98
1	L5	4100:G	O3'	4101:G	P	11.97
1	L5	1292:G	O3'	1293:U	P	11.56
1	L5	4408:G	O3'	4409:PSU	P	11.48
1	L5	1241:G	O3'	1242:C	P	10.99
1	L5	919:C	O3'	920:G	P	9.86
1	S2	864:A	O3'	865:A	P	2.76
1	S2	1247:C	O3'	1248:U	P	2.72
1	S2	1248:U	O3'	1249:C	P	2.71

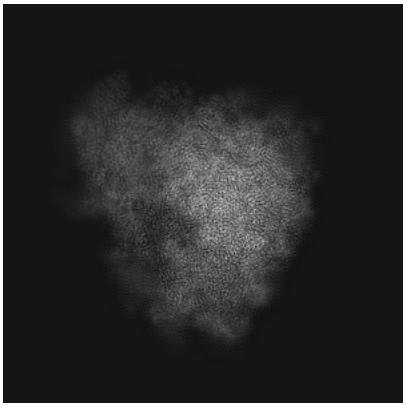
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-56227. These allow visual inspection of the internal detail of the map and identification of artifacts.

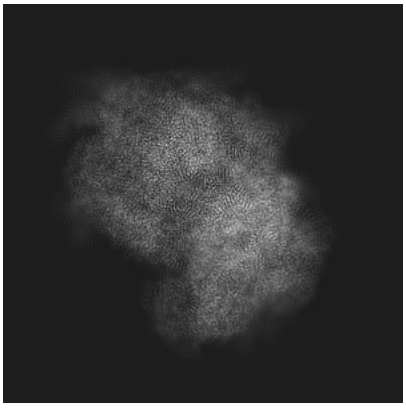
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

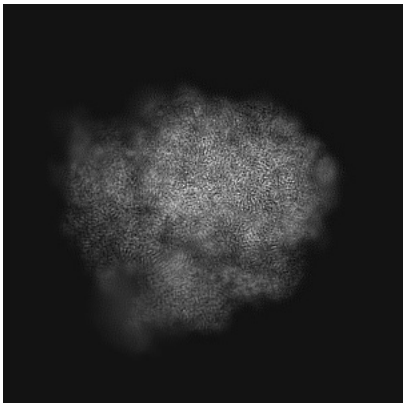
6.1.1 Primary map



X



Y

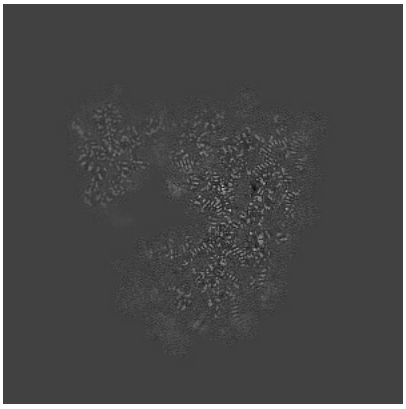


Z

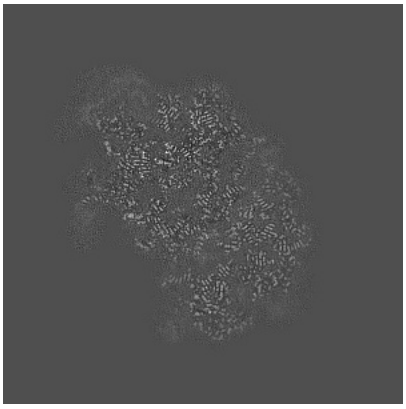
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

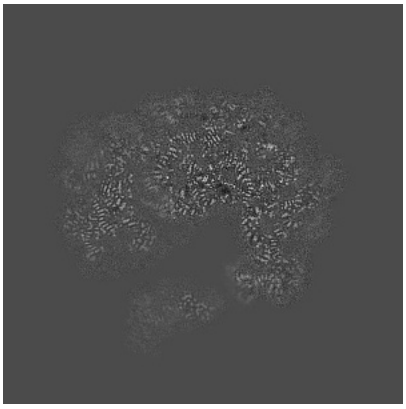
6.2.1 Primary map



X Index: 240



Y Index: 240

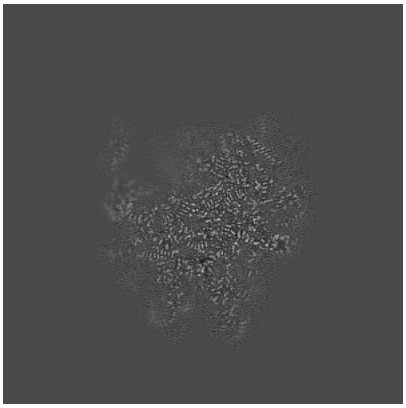


Z Index: 240

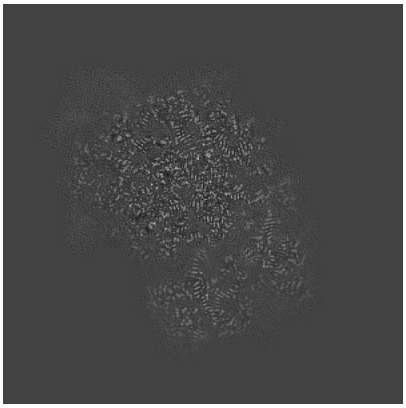
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 292



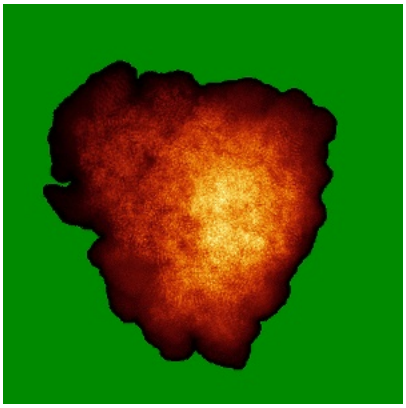
Y Index: 261

Z Index: 246

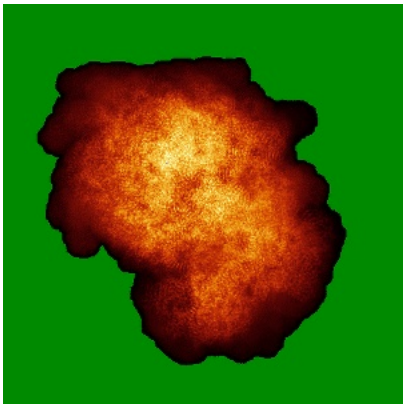
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

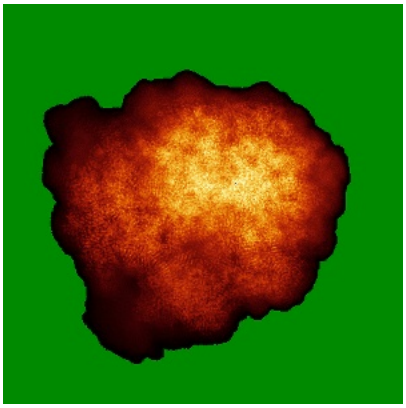
6.4.1 Primary map



X



Y

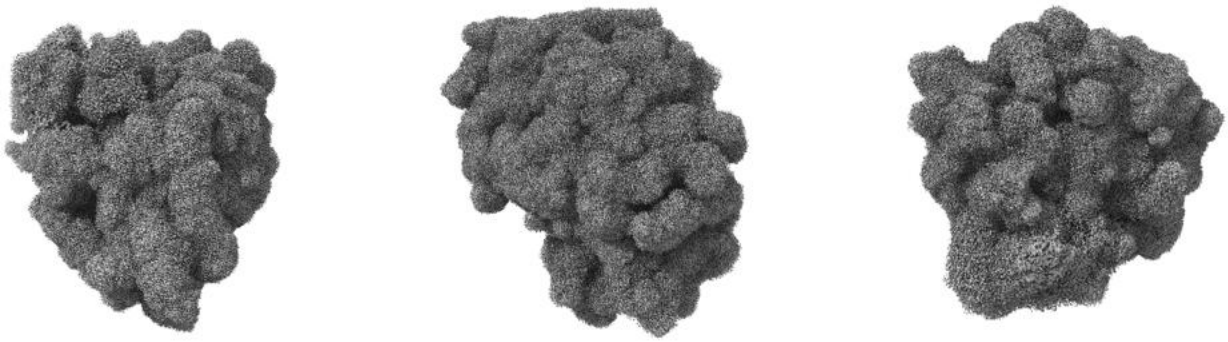


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

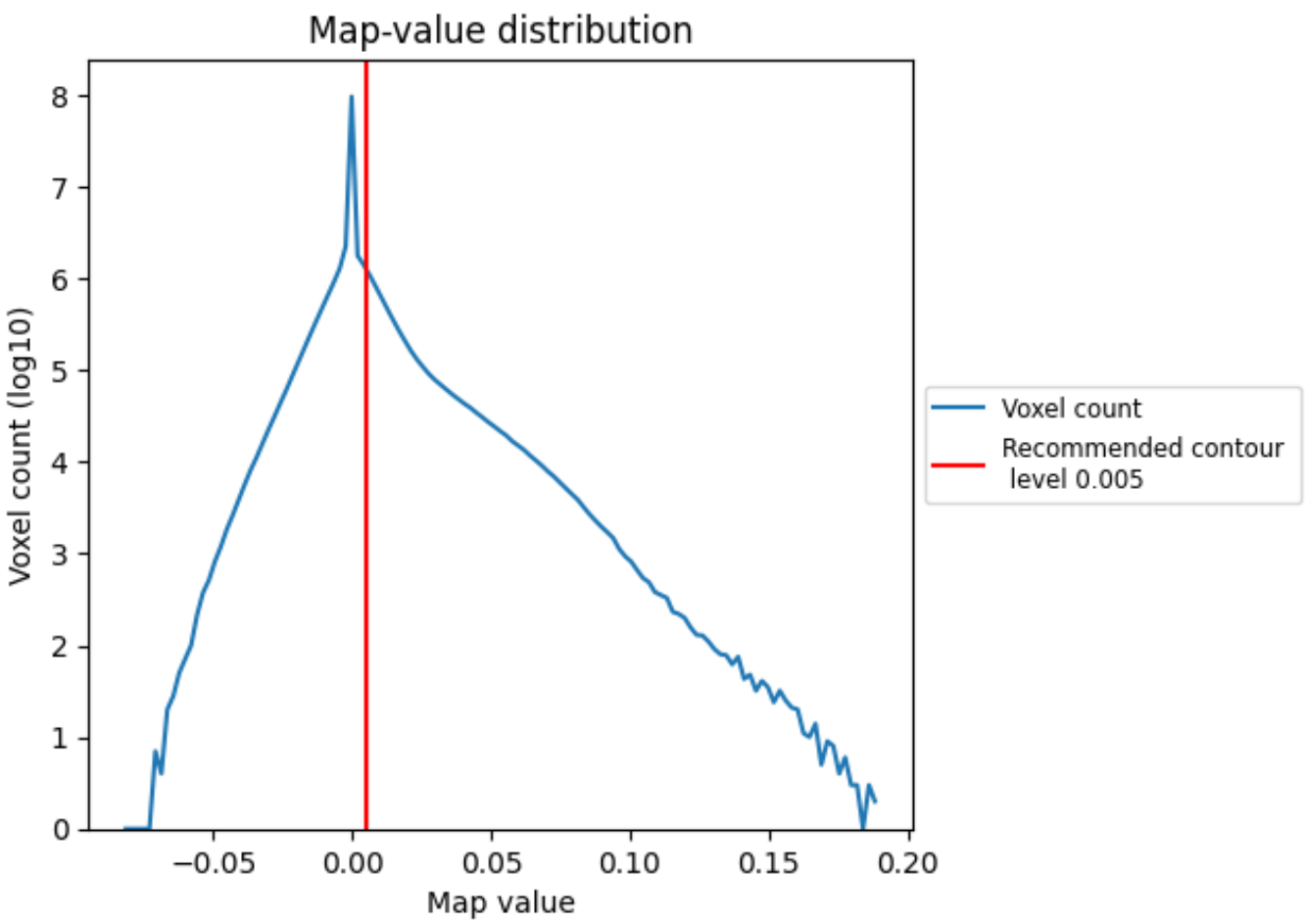
6.6 Mask visualisation (i)

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

7 Map analysis (i)

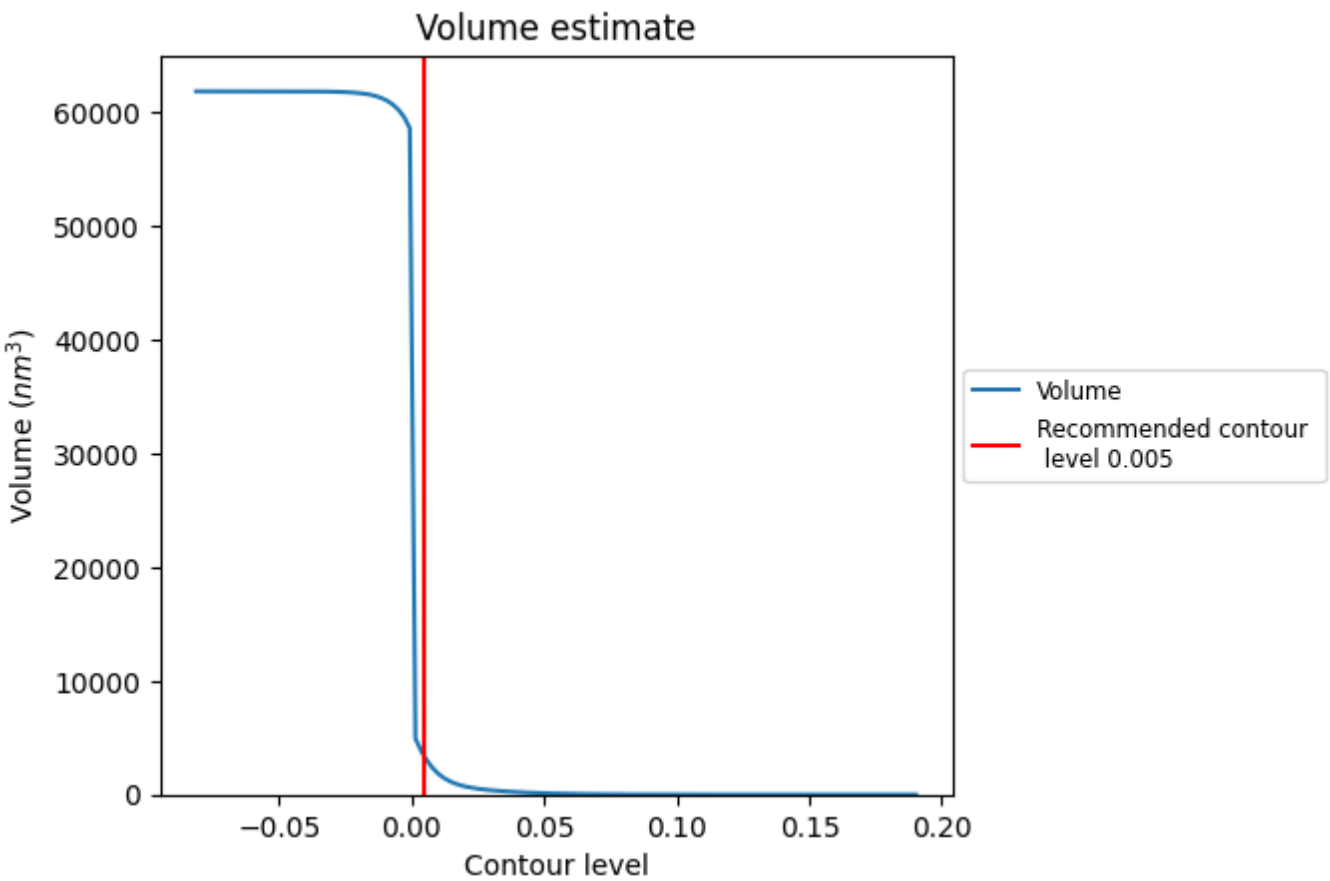
This section contains the results of statistical analysis of the map.

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.

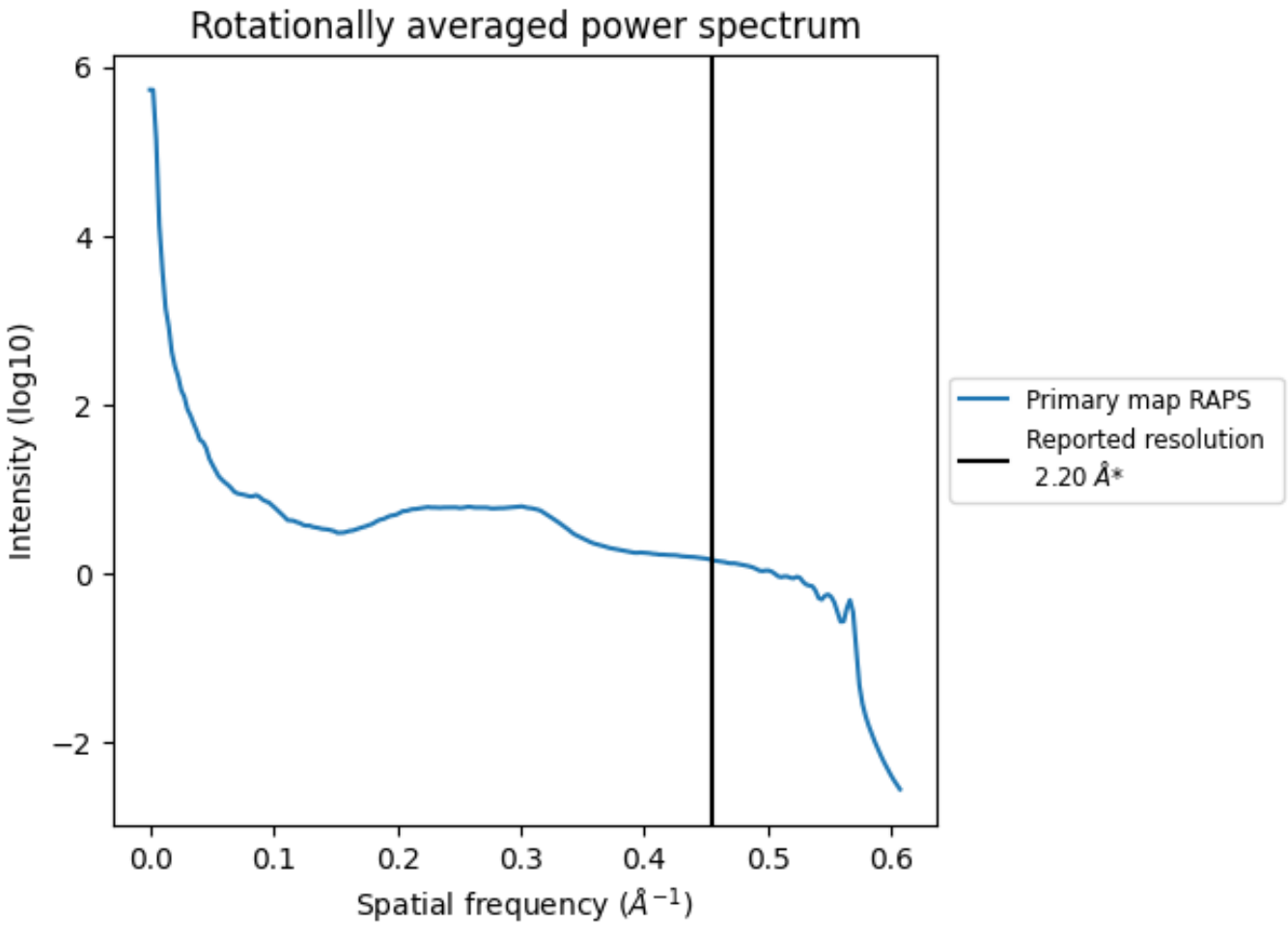
7.2 Volume estimate (i)



The volume at the recommended contour level is 3283 nm^3; this corresponds to an approximate mass of 2965 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 (i)



*Reported resolution corresponds to spatial frequency of 0.455 Å^{-1}

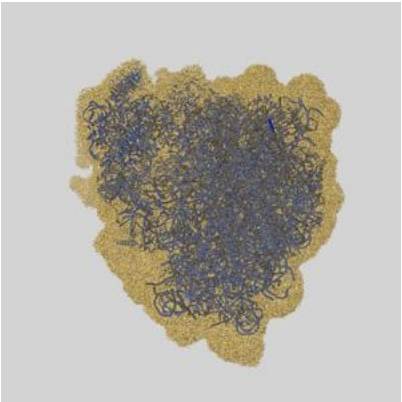
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

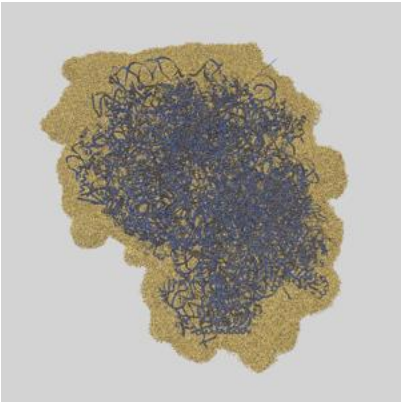
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-56227 and PDB model 9TT7. Per-residue inclusion information can be found in section 3 on page 23.

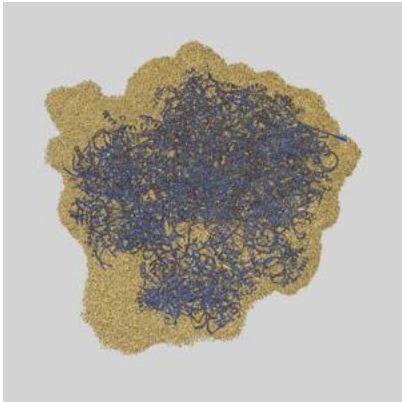
9.1 Map-model overlay (i)



X



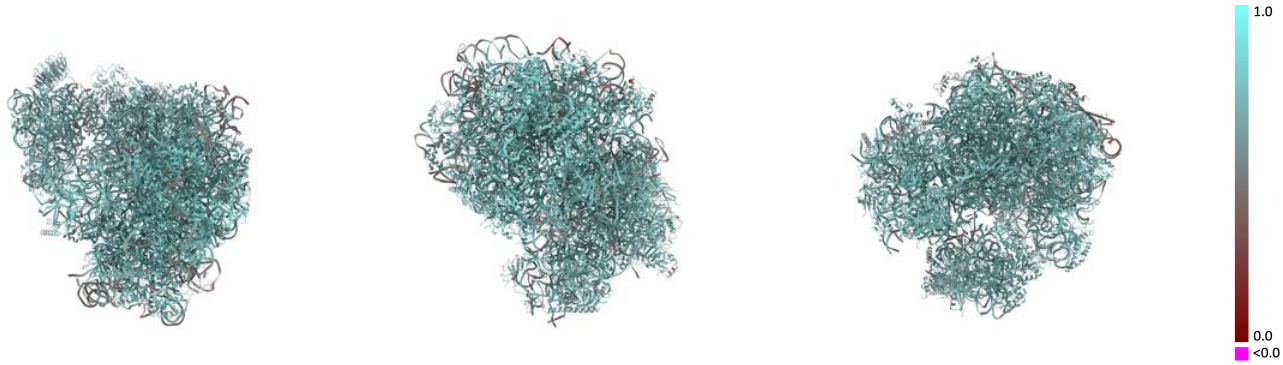
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.005 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.

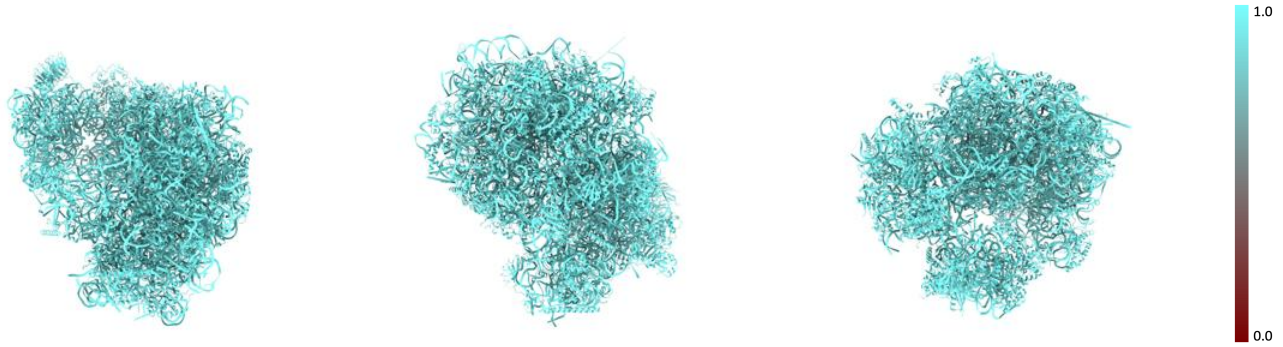
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

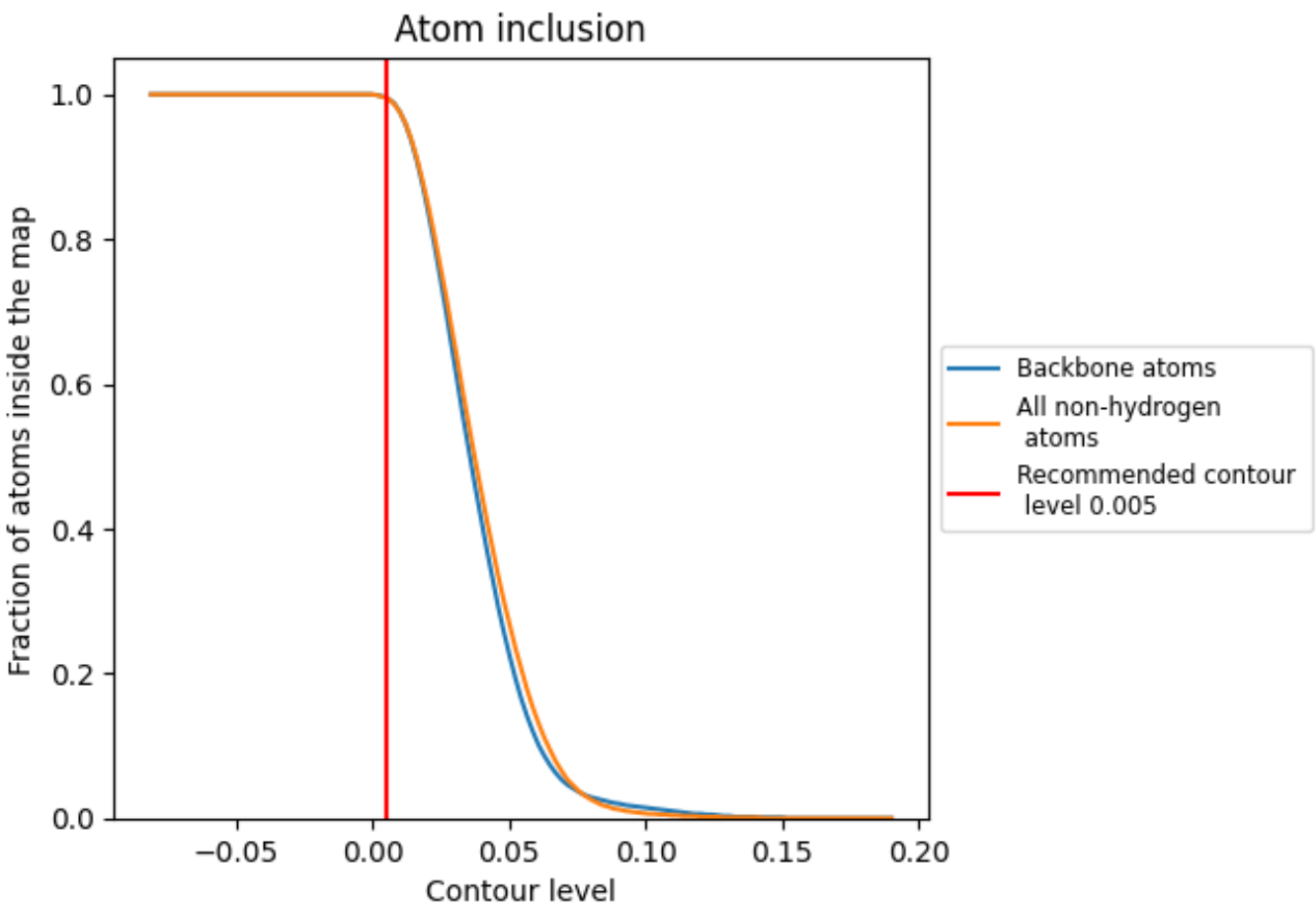
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.005).

9.4 Atom inclusion (i)



At the recommended contour level, 100% of all backbone atoms, 100% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9950	0.7160
L5	0.9930	0.7150
L7	1.0000	0.7200
L8	0.9980	0.7290
LA	0.9990	0.7850
LB	0.9990	0.7750
LC	1.0000	0.7740
LD	0.9950	0.7000
LE	0.9930	0.7030
LF	0.9980	0.7770
LG	0.9950	0.7120
LH	0.9990	0.7210
LI	0.9970	0.7260
LJ	0.9940	0.6700
LL	0.9980	0.7500
LM	1.0000	0.7330
LN	0.9990	0.7850
LO	0.9990	0.7730
LP	1.0000	0.7830
LQ	1.0000	0.7860
LR	1.0000	0.7440
LS	1.0000	0.7700
LT	0.9990	0.7650
LU	0.9760	0.5630
LV	1.0000	0.7760
LW	1.0000	0.7460
LX	0.9990	0.7480
LY	1.0000	0.7570
LZ	0.9990	0.7070
La	0.9990	0.7810
Lb	1.0000	0.7230
Lc	0.9970	0.7130
Ld	1.0000	0.7640
Le	1.0000	0.7870
Lf	1.0000	0.7930

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Chain	Atom inclusion	Q-score
Lg	1.0000	0.7700
Lh	1.0000	0.7340
Li	0.9970	0.7160
Lj	1.0000	0.7840
Lk	0.9980	0.6800
Ll	0.9970	0.7710
Lm	1.0000	0.7190
Ln	1.0000	0.6720
Lo	0.9990	0.7630
Lp	1.0000	0.7720
Lr	1.0000	0.7710
S2	0.9950	0.6830
S6	0.9890	0.5840
SA	0.9970	0.7110
SB	0.9960	0.7000
SC	0.9980	0.7270
SD	0.9940	0.6650
SE	1.0000	0.7180
SF	0.9950	0.6950
SG	0.9950	0.6610
SH	0.9960	0.6580
SI	0.9980	0.7200
SJ	1.0000	0.7250
SK	0.9940	0.6380
SL	0.9990	0.7430
SN	0.9960	0.7160
SO	0.9990	0.7050
SP	0.9980	0.7040
SQ	0.9970	0.6990
SR	0.9900	0.6330
SS	0.9980	0.6980
ST	0.9980	0.7020
SU	0.9900	0.6740
SV	0.9950	0.6980
SW	1.0000	0.7480
SX	0.9970	0.7410
SY	0.9980	0.6970
SZ	0.9980	0.6690
Sa	1.0000	0.7210
Sb	0.9960	0.7050
Sc	0.9970	0.6610
Sd	1.0000	0.7110

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Chain	Atom inclusion	Q-score
Se	0.9910	0.7070
Sg	0.9910	0.6400