



Full wwPDB EM Validation Report ⓘ

Apr 16, 2024 – 06:46 am BST

PDB ID : 7PWO
EMDB ID : EMD-13683
Title : Cryo-EM structure of Giardia lamblia ribosome at 2.75 Å resolution
Authors : Hiregange, D.G.; Rivalta, A.; Bose, T.; Breiner-Goldstein, E.; Samiya, S.; Cimicata, G.; Kulakova, L.; Zimmerman, E.; Bashan, A.; Herzberg, O.; Yonath, A.
Deposited on : 2021-10-07
Resolution : 2.75 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

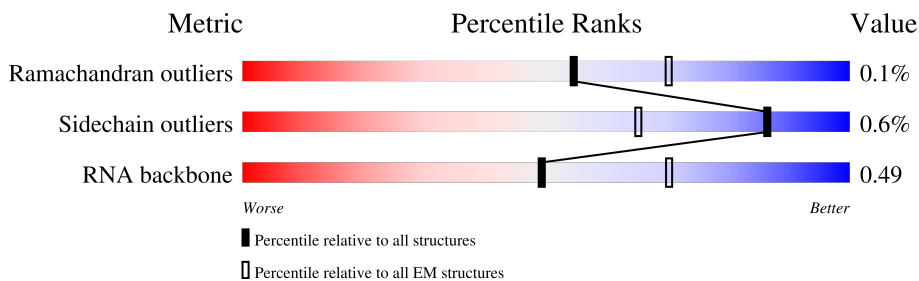
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.75 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.








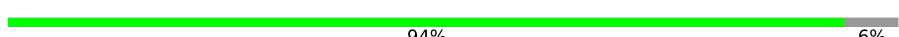




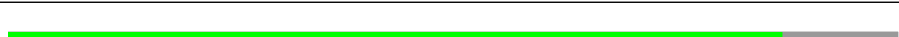


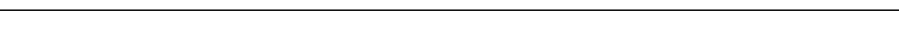
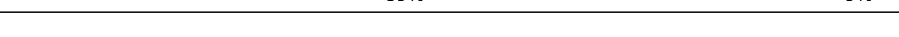
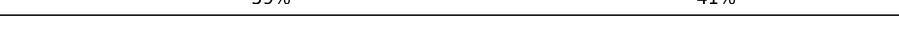



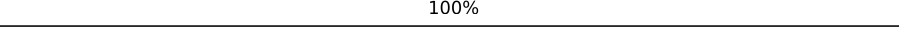
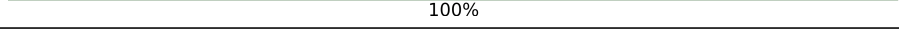
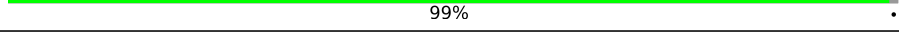



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	T1	139	
2	N1	154	
3	J1	189	
4	D1	217	
5	X1	143	
6	S1	154	
7	Q1	158	
8	C1	242	
9	B1	248	

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Mol	Chain	Length	Quality of chain
10	b1	124	 63% 36%
11	a1	109	 89% 11%
12	V1	89	 92% 8%
13	R1	137	 72% 28%
14	K1	134	 62% 38%
15	I1	174	 94% 6%
16	e1	69	 54% 46%
17	H1	190	 85% 15%
18	n1	41	 59% 41%
19	c1	64	 84% 14%
20	O1	145	 87% 13%
21	W1	130	 99%
22	E1	268	 96%
23	L1	199	 89% 9%
24	U1	126	 59% 41%
25	1	2707	 69% 20% 10%
26	3	120	 80% 17%
27	42	139	 71% 27%
28	A2	251	 100%
29	B2	379	 100%
30	C2	316	 99%
31	D2	297	 89% 10%
32	F2	235	 91% 9%
33	G2	225	 80% 19%
34	H2	185	 99%


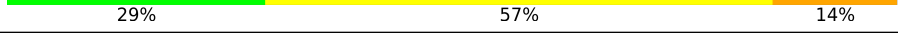

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Mol	Chain	Length	Quality of chain
35	I2	210	95% 5%
36	J2	173	94% 5%
37	L2	234	81% 19%
38	M2	131	97% ..
39	N2	204	100%
40	O2	197	99% .
41	P2	164	94% 6%
42	Q2	179	99% .
43	R2	196	88% . 10%
44	S2	173	99% .
45	T2	159	96% ..
46	U2	171	58% 42%
47	V2	142	97% ..
48	X2	141	82% 18%
49	Y2	135	99% .
50	Z2	135	96% .
51	a2	149	99% .
52	b2	62	90% 10%
53	c2	109	92% 8%
54	d2	106	89% 11%
55	e2	136	93% 7%
56	f2	123	99% .
57	g2	120	82% 18%
58	h2	124	97% .
59	i2	90	94% 6%

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Mol	Chain	Length	Quality of chain
60	j2	89	 98%
61	k2	77	 86% 14%
62	l2	51	 96%
63	m2	127	 39% 60%
64	o2	106	 89% 11%
65	p2	94	 94%
66	w2	14	 29% 57% 14%
67	W2	102	 64% 36%
68	E	3	 33% 67%
69	d1	137	 34% 65%
70	F1	190	 78% 6% 15%
71	Y1	132	 67% 31%
72	G1	248	 73% 24%
73	2	1452	 64% 25% 7%
74	A1	245	 79% 21%

2 Entry composition [i](#)

There are 76 unique types of molecules in this entry. The entry contains 163704 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	T1	108	795	503	148	142	2	0	0

- Molecule 2 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	N1	152	1192	759	227	201	5	0	0

- Molecule 3 is a protein called Ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	J1	166	1322	827	257	232	6	0	0

- Molecule 4 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D1	182	1402	890	254	244	14	0	0

- Molecule 5 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	X1	142	1104	697	219	184	4	0	0

- Molecule 6 is a protein called Ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	S1	133	1055	651	210	188	6	0	0

- Molecule 7 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	Q1	125	960	603	190	164	3	0	0

- Molecule 8 is a protein called Ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	C1	212	1641	1043	298	296	4	0	0

- Molecule 9 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	B1	218	1758	1113	323	309	13	0	0

- Molecule 10 is a protein called Ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	b1	79	614	389	105	114	6	0	0

- Molecule 11 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	a1	97	785	484	162	131	8	0	0

- Molecule 12 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	V1	82	605	377	112	110	6	0	0

- Molecule 13 is a protein called Ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	R1	99	767	476	141	147	3	0	0

- Molecule 14 is a protein called Ribosomal protein S10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K1	83	Total	C	N	O	S	0	0
			689	446	116	123	4		

- Molecule 15 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I1	163	Total	C	N	O	S	0	0
			1282	804	246	229	3		

- Molecule 16 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	e1	37	Total	C	N	O	S	0	0
			291	185	59	46	1		

- Molecule 17 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H1	162	Total	C	N	O	S	0	0
			1195	773	210	207	5		

- Molecule 18 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	n1	24	Total	C	N	O	S	0	0
			217	134	55	25	3		

- Molecule 19 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	c1	55	Total	C	N	O	S	0	0
			439	269	89	80	1		

- Molecule 20 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O1	126	Total	C	N	O	S	0	0
			935	572	189	170	4		

- Molecule 21 is a protein called Ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	W1	129	1031	659	192	177	3	0	0

- Molecule 22 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	E1	258	2062	1320	378	352	12	0	0

- Molecule 23 is a protein called SSU ribosomal protein S17P.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	L1	181	1487	936	296	248	7	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L1	12	SER	GLY	conflict	UNP V6TVJ7

- Molecule 24 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	U1	74	609	394	111	102	2	0	0

- Molecule 25 is a RNA chain called rRNA 28S.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
25	1	2448	52571	23373	9743	17007	2448	0	0

- Molecule 26 is a RNA chain called rRNA 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
26	3	117	2501	1116	458	810	117	0	0

- Molecule 27 is a RNA chain called rRNA 5.8S.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
27	42	138	2958	1315	553	952	138	0	0

- Molecule 28 is a protein called Ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	A2	250	1873	1157	383	320	13	0	0

- Molecule 29 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	B2	378	2987	1886	566	514	21	0	0

- Molecule 30 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	C2	314	2446	1539	474	424	9	0	0

- Molecule 31 is a protein called Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	D2	266	2115	1341	391	375	8	0	0

- Molecule 32 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	F2	214	1730	1100	315	310	5	0	0

- Molecule 33 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	G2	182	1446	921	264	255	6	0	0

- Molecule 34 is a protein called Ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	H2	184	1442	912	263	257	10	0	0

- Molecule 35 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	I2	200	1621	1019	321	273	8	0	0

- Molecule 36 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	J2	164	1305	821	246	233	5	0	0

- Molecule 37 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	L2	189	1512	942	309	255	6	0	0

- Molecule 38 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	M2	128	990	626	178	181	5	0	0

- Molecule 39 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	N2	204	1712	1083	358	265	6	0	0

- Molecule 40 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	O2	195	1587	997	310	267	13	0	0

- Molecule 41 is a protein called Ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	P2	154	1235	781	239	211	4	0	0

- Molecule 42 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	Q2	178	1402	871	279	243	9	0	0

- Molecule 43 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	R2	177	1463	902	313	243	5	0	0

- Molecule 44 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	S2	173	1418	895	274	240	9	0	0

- Molecule 45 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	T2	153	1226	766	252	201	7	0	0

- Molecule 46 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	U2	100	820	524	141	153	2	0	0

- Molecule 47 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	V2	139	1063	668	207	183	5	0	0

- Molecule 48 is a protein called Ribosomal protein L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	X2	116	936	601	169	163	3	0	0

- Molecule 49 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	Y2	133	1076	665	219	184	8	0	0

- Molecule 50 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	Z2	129	980	623	179	173	5	0	0

- Molecule 51 is a protein called Ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	a2	148	1201	759	240	199	3	0	0

- Molecule 52 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	b2	56	463	280	104	77	2	0	0

- Molecule 53 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	c2	100	750	470	132	144	4	0	0

- Molecule 54 is a protein called Ribosomal protein L31B.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
54	d2	94	752	482	149	121	0	0

- Molecule 55 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	e2	126	1039	661	207	165	6	0	0

- Molecule 56 is a protein called Ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	f2	123	974	619	180	171	4	0	0

- Molecule 57 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	g2	99	798	493	167	134	4	0	0

- Molecule 58 is a protein called Ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	h2	120	960	610	185	160	5	0	0

- Molecule 59 is a protein called Ribosomal protein L36-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	i2	85	691	438	138	111	4	0	0

- Molecule 60 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	j2	87	692	423	146	116	7	0	0

- Molecule 61 is a protein called Ribosomal L38e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	k2	66	504	320	86	94	4	0	0

- Molecule 62 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	l2	50	Total	C	N	O	0	0
			434	278	91	65		

- Molecule 63 is a protein called Ubiquitin/Ribosomal protein L40e.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	m2	51	Total	C	N	O	S	0	0
			421	257	88	69	7		

- Molecule 64 is a protein called Ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	o2	94	Total	C	N	O	S	0	0
			762	474	157	126	5		

- Molecule 65 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	p2	91	Total	C	N	O	S	0	0
			708	436	144	122	6		

- Molecule 66 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	w2	14	Total	C	N	O	P	0	0
			299	133	56	96	14		

- Molecule 67 is a protein called Ribosomal protein L24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	W2	65	Total	C	N	O	S	0	0
			540	343	110	85	2		

- Molecule 68 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	E	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

- Molecule 69 is a protein called Ribosomal protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	d1	48	Total	C	N	O	S	0	0
			392	250	72	65	5		

- Molecule 70 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	F1	161	Total	C	N	O	S	0	0
			1246	771	240	227	8		

- Molecule 71 is a protein called Ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Y1	91	Total	C	N	O	S	0	0
			713	454	126	127	6		

- Molecule 72 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	G1	189	Total	C	N	O	S	0	0
			1453	914	280	249	10		

- Molecule 73 is a RNA chain called rRNA 18S.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	2	1355	Total	C	N	O	P	0	0
			29096	12946	5388	9407	1355		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
74	A1	194	Total	C	N	O	S	0	0
			1546	998	269	271	8		

- Molecule 75 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
75	N1	3	Total	K	0
			3	3	
75	X1	1	Total	K	0
			1	1	
75	S1	2	Total	K	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
75	b1	2	Total 2	K 2	0
75	a1	1	Total 1	K 1	0
75	I1	2	Total 2	K 2	0
75	O1	5	Total 5	K 5	0
75	W1	1	Total 1	K 1	0
75	E1	4	Total 4	K 4	0
75	L1	4	Total 4	K 4	0
75	U1	1	Total 1	K 1	0
75	1	181	Total 181	K 181	0
75	3	1	Total 1	K 1	0
75	42	2	Total 2	K 2	0
75	A2	4	Total 4	K 4	0
75	B2	3	Total 3	K 3	0
75	C2	4	Total 4	K 4	0
75	I2	1	Total 1	K 1	0
75	L2	1	Total 1	K 1	0
75	N2	2	Total 2	K 2	0
75	V2	1	Total 1	K 1	0
75	a2	2	Total 2	K 2	0
75	e2	1	Total 1	K 1	0
75	j2	1	Total 1	K 1	0

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Mol	Chain	Residues	Atoms		AltConf
75	o2	1	Total 1	K 1	0
75	G1	1	Total 1	K 1	0
75	2	222	Total 222	K 222	0
75	A1	1	Total 1	K 1	0


- Molecule 76 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

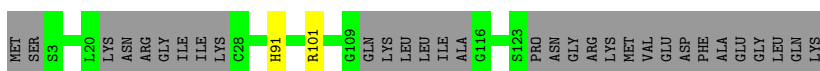
Mol	Chain	Residues	Atoms		AltConf
76	N1	1	Total 1	Mg 1	0
76	E1	1	Total 1	Mg 1	0
76	L1	1	Total 1	Mg 1	0
76	1	71	Total 71	Mg 71	0
76	42	1	Total 1	Mg 1	0
76	C2	1	Total 1	Mg 1	0
76	F2	1	Total 1	Mg 1	0
76	P2	1	Total 1	Mg 1	0
76	V2	1	Total 1	Mg 1	0
76	b2	1	Total 1	Mg 1	0
76	o2	1	Total 1	Mg 1	0
76	G1	1	Total 1	Mg 1	0
76	2	19	Total 19	Mg 19	0

3 Residue-property plots [i](#)

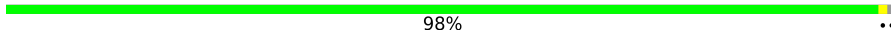
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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: Ribosomal protein S19e

Chain T1:  76% 22%




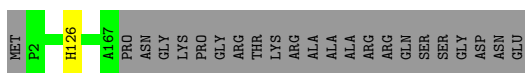
- Molecule 2: Ribosomal protein S13

Chain N1:  98%




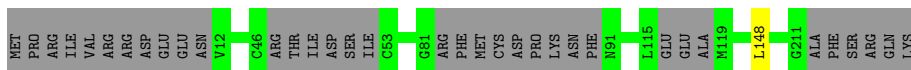
- Molecule 3: Ribosomal protein S9

Chain J1:  87% 12%



- Molecule 4: Ribosomal protein S3

Chain D1:  83% 16%




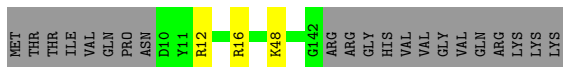
- Molecule 5: Ribosomal protein S23

Chain X1:  99%

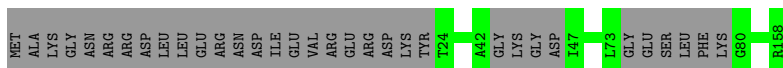
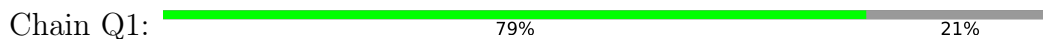


- Molecule 6: Ribosomal protein S18

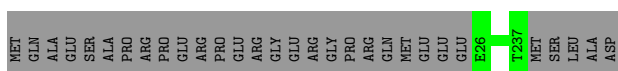
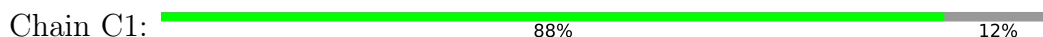
Chain S1:  84% 14%



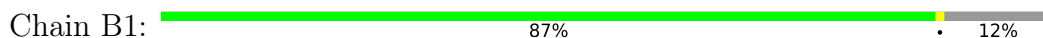
- Molecule 7: Ribosomal protein S16



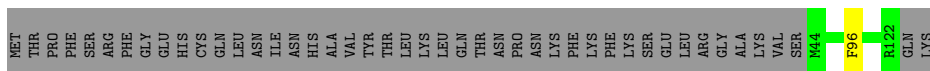
- Molecule 8: Ribosomal protein S2



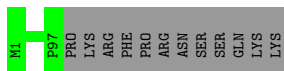
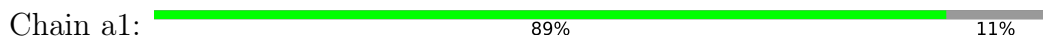
- Molecule 9: 40S ribosomal protein S3a



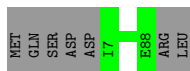
- Molecule 10: Ribosomal protein S27



- Molecule 11: 40S ribosomal protein S26



- Molecule 12: 40S ribosomal protein S21



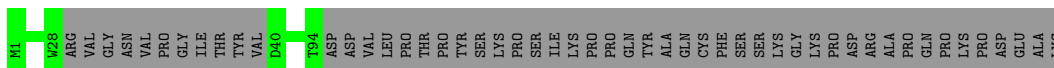
- Molecule 13: Ribosomal protein S17





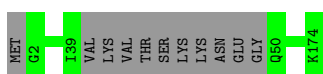
- Molecule 14: Ribosomal protein S10B

Chain K1: 62% 38%



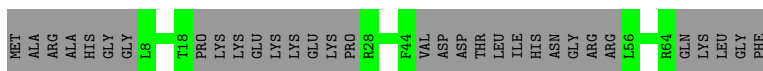
- Molecule 15: 40S ribosomal protein S8

Chain I1: 94% 6%



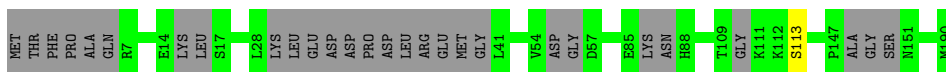
- Molecule 16: 40S ribosomal protein S30

Chain e1: 54% 46%



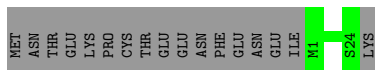
- Molecule 17: 40S ribosomal protein S7

Chain H1: 85% 15%



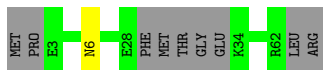
- Molecule 18: Ribosomal protein eL41

Chain n1: 59% 41%



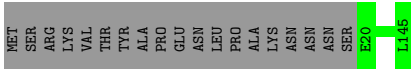
- Molecule 19: Ribosomal protein S28

Chain c1: 84% 14%



- Molecule 20: Ribosomal protein S14

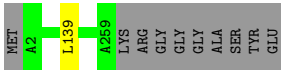
Chain O1: 87% 13%



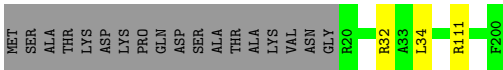
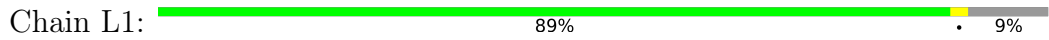
- Molecule 21: Ribosomal protein S15A



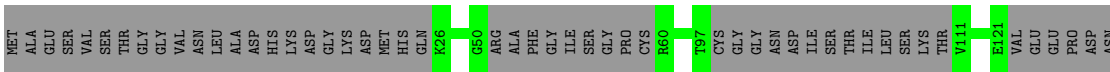
- Molecule 22: 40S ribosomal protein S4



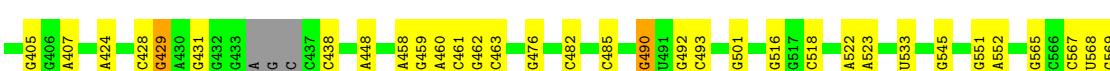
- Molecule 23: SSU ribosomal protein S17P



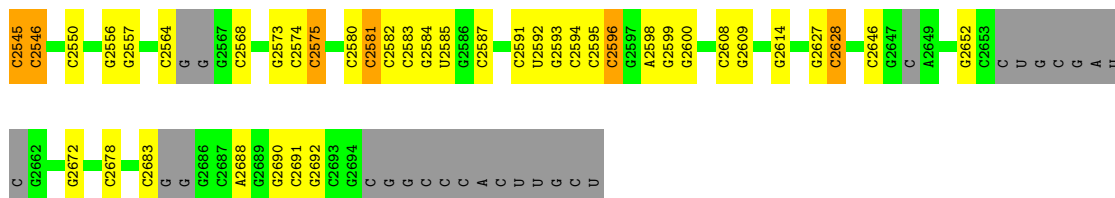
- Molecule 24: Ribosomal protein S20



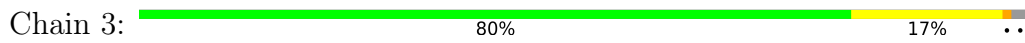
- Molecule 25: rRNA 28S



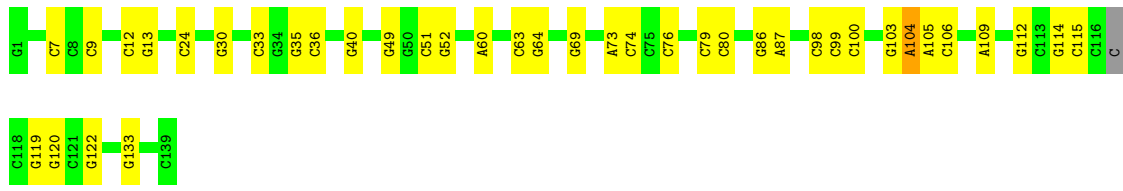
G570	G	C886	A	C1050	G1241	C1388	A1539	A1731	G1856	G2029	G2163	U2282	G2411
G573	G	C889	G	C1061	G1244	G1405	A1540	G1732	G1857	G2030	G2175	C2289	C2415
A574	G	C896	G	G1066	C1244	G1411	G1542	G1733	G1858	G2037	G2176	C2292	G2418
G575	G	C896	A	G1066	G1245	G1412	C1543	G1736	A1859	U2040	A1860	C2293	G2418
G576	G	C896	G	G1066	G1245	G1412	C1543	G1737	G1861	G2041	G1862	A2294	G2422
C577	C	C896	U	G1072	G1247	A1413	G1544	G1738	C1862	G2042	G1863	U2295	A2423
G685	C	G900	U	G1074	C1248	C	G1545	A1739	G1863	G2049	C2196	G2296	G2429
C589	C	G906	G	G1080	C1252	C1416	G1565	U1741	G1864	C2050	G2200	C2297	G2433
U590	C	G907	U	C1253	C1254	G1417	G1566	A1742	C1865	G2059	G2201	G2299	G2433
C595	C	G908	A	G1106	C1254	G1418	G1566	C	G1866	A2060	C2202	G2300	G2434
G611	C	G911	A	G1107	G1255	A1439	G1579	U	C1871	G	G2208	C2301	G2443
A612	C	G912	A	G1108	A1259	C1452	G	A1746	C1872	C2074	C2209	U2304	A
G623	C	G915	C	G1118	C1261	C	C	G1759	G1880	G2075	G2210	U2305	G2445
G624	C	G915	C	G1121	G1285	C	C	G1760	G1881	C2078	G2211	C2309	G2466
A630	C	C	C	C1124	G1285	G	C	G1765	G1882	A2079	G2212	C2310	G2467
A631	C	C	C	G1137	A1277	C1458	G1587	A1766	C1884	U2088	G2213	C2321	C2468
G632	C	C	C	G1138	C1280	G1472	G1588	A1768	A1888	G2091	G2215	A2331	G2494
A633	C	C	C	C	C1280	A1473	G1589	U1769	G1890	C2092	U2217	A2333	G
A637	C	C	C	G1140	G1281	C1477	G1589	G1775	A1891	C	G2218	U2345	A2496
U638	C	C	C	C1149	C1292	A1477	A1600	C1791	C1894	G2096	G2222	C2499	G2499
C639	C	C	C	G1151	C	A1478	A1601	G1792	U1895	A2037	A2223	C2504	C2504
G640	C	C	C	C1151	C	G	C1602	U	U1897	G	A2224	C2505	C2505
A641	C	C	C	G1158	G1288	C1480	C1606	G1794	U1898	G	U2228	C2506	C2506
G653	C	C	C	G1159	G1288	G1482	G1609	U1797	U1903	A	U2229	C2507	C2507
G656	C	C	C	A1160	C1307	A1484	G1610	A1800	G1904	C	A2230	C2508	C2508
G657	C	C	C	C991	C	A1484	G1619	U1801	G1905	C	C2231	C2509	C2509
U658	C	C	C	U1162	C	U1486	A1619	G1802	A1906	C	C2232	C2513	G2514
U659	C	C	C	G1163	C	G1487	C1620	G1802	C1907	C	A2233	C2515	G2515
G660	C	C	C	A1164	G1310	C1488	U1628	A1808	U1908	C	G2234	A2367	G2519
G675	C	C	C	G1166	C1314	G1489	U1646	C1809	G1922	C	G2235	G2368	G2519
C676	C	C	C	G1167	C1322	G1490	G1647	G1812	G1923	C	G2236	G2372	G2522
G680	C	C	C	U1178	C1326	G1501	U1663	G1813	G1924	G	A2241	U2376	G2524
G801	C	C	C	C1179	C1326	U1502	U1675	U1814	G1931	C	G2242	C2380	C2525
G802	C	C	C	G1186	G1330	G1508	A1675	U1815	G1932	C	U2251	U2386	U2526
G803	C	C	C	G1203	G1331	C1509	C1684	C1816	C	G	A2138	U2386	G2527
G804	C	C	C	U1204	C1337	G1510	C1694	C1816	C	G	G2129	C2391	C2528
G805	C	C	C	U1205	C1349	G1515	A1691	U1822	G	C	C2139	A	C2529
G806	C	C	C	G1208	G1358	G1516	C	U1823	C	C	C2149	C2391	C2530
G807	C	C	C	C1030	G1358	G1520	G1693	C1824	G	C	C2150	A	C2531
A808	C	C	C	G1031	G1358	G1520	A1694	C1831	G	C	C2011	G2393	C2532
G813	C	C	C	A1230	G1381	G1529	C1694	G1832	C	C	G2152	G2394	U2533
G826	C	C	C	G1231	C1381	G1529	C1696	C1833	C	C	G2154	U2401	A2536
G840	C	C	C	U1232	G1382	A1532	U1712	C1849	A	C	C2155	C2404	A2538
G853	C	C	C	C1045	G1383	G1537	A1719	A1850	G	C	G2156	C2406	C2543
A868	C	C	C	G1046	C1384	C1538	A1719	G1852	G	C	G2157	C2406	A2544
C869	C	C	C	G1047	C1384	C1538	A1719	C1852	G	C	C2158	C2406	A2544



• Molecule 26: rRNA 5S



• Molecule 27: rRNA 5.8S



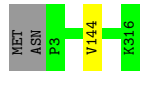
• Molecule 28: Ribosomal protein L2



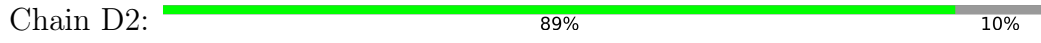
• Molecule 29: Ribosomal protein L3

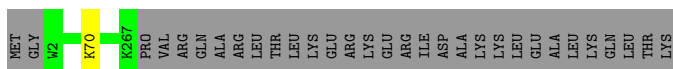


• Molecule 30: Ribosomal protein L4

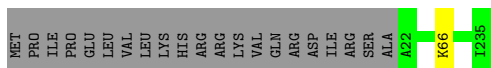


• Molecule 31: Ribosomal protein L5

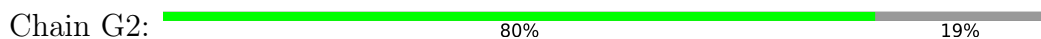




- Molecule 32: Ribosomal protein L7



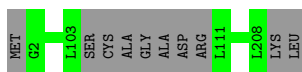
- Molecule 33: 60S ribosomal protein L7a



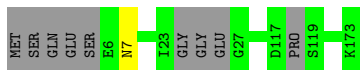
- Molecule 34: Ribosomal protein L6



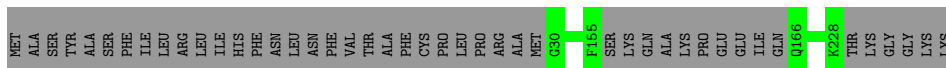
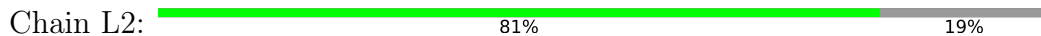
- Molecule 35: Ribosomal protein L10



- Molecule 36: Ribosomal protein L11

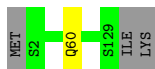


- Molecule 37: 60S ribosomal protein L13



- Molecule 38: Ribosomal protein L14





- Molecule 39: Ribosomal protein L15

Chain N2: 100%



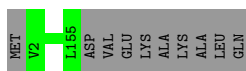
- Molecule 40: Ribosomal protein L13a

Chain O2: 99%



- Molecule 41: Ribosomal protein L17

Chain P2: 94% 6%



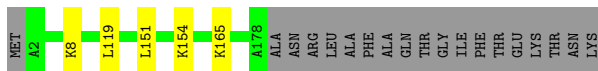
- Molecule 42: Ribosomal protein L18

Chain Q2: 99%



- Molecule 43: Ribosomal protein L19

Chain R2: 88% 10%



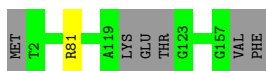
- Molecule 44: 60S ribosomal protein L18a

Chain S2: 99%

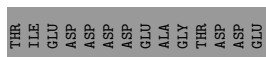
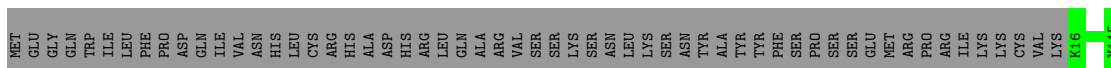


- Molecule 45: Ribosomal protein L21

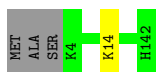
Chain T2: 96%



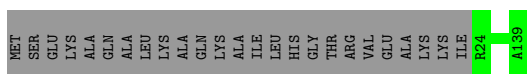
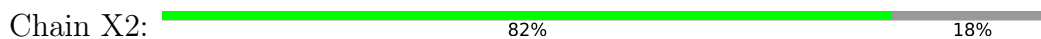
- Molecule 46: Ribosomal protein eL22



- Molecule 47: Ribosomal protein L23



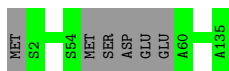
- Molecule 48: Ribosomal protein L23A



- Molecule 49: Ribosomal protein L26



- Molecule 50: 60S ribosomal protein L27



- Molecule 51: Ribosomal protein L27a



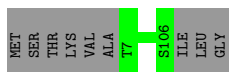
- Molecule 52: 60S ribosomal protein L29

Chain b2:  90% 10%




- Molecule 53: Ribosomal protein L30

Chain c2:  92% 8%



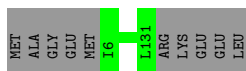
- Molecule 54: Ribosomal protein L31B

Chain d2:  89% 11%



- Molecule 55: Ribosomal protein L32

Chain e2:  93% 7%




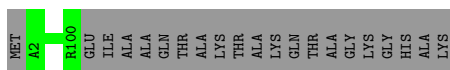
- Molecule 56: Ribosomal protein L35a

Chain f2:  99%



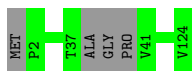
- Molecule 57: Ribosomal protein L34

Chain g2:  82% 18%

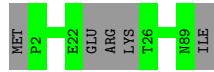


- Molecule 58: Ribosomal protein L35

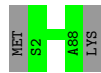
Chain h2:  97%



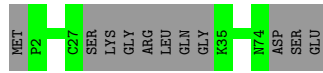
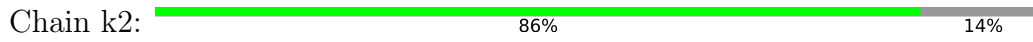
- Molecule 59: Ribosomal protein L36-1



● Molecule 60: Ribosomal protein L37



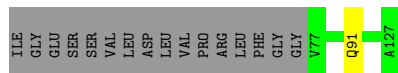
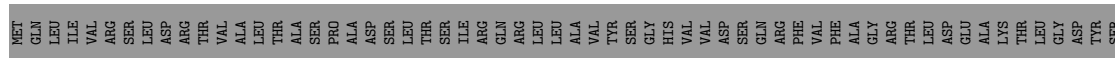
● Molecule 61: Ribosomal L38e



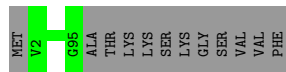
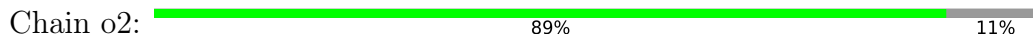
● Molecule 62: Ribosomal protein L39



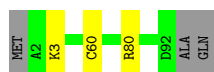
● Molecule 63: Ubiquitin/Ribosomal protein L40e



● Molecule 64: Ribosomal protein L44



● Molecule 65: Ribosomal protein L37a



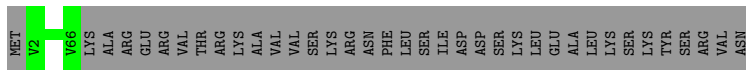
- Molecule 66: E-site tRNA

Chain w2:  29% 57% 14%



- Molecule 67: Ribosomal protein L24A

Chain W2:  64% 36%



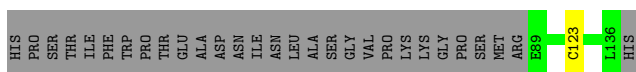
- Molecule 68: P-site tRNA

Chain E:  33% 67%




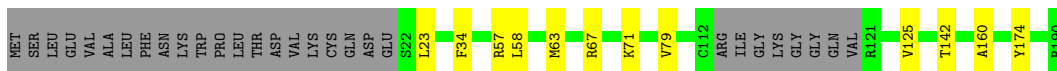
- Molecule 69: Ribosomal protein S29A

Chain d1:  34% 65%



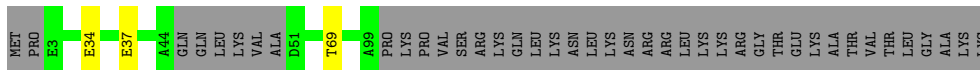
- Molecule 70: Ribosomal protein S5

Chain F1:  78% 6% 15%




- Molecule 71: Ribosomal protein S24

Chain Y1:  67% 31%



- Molecule 72: 40S ribosomal protein S6

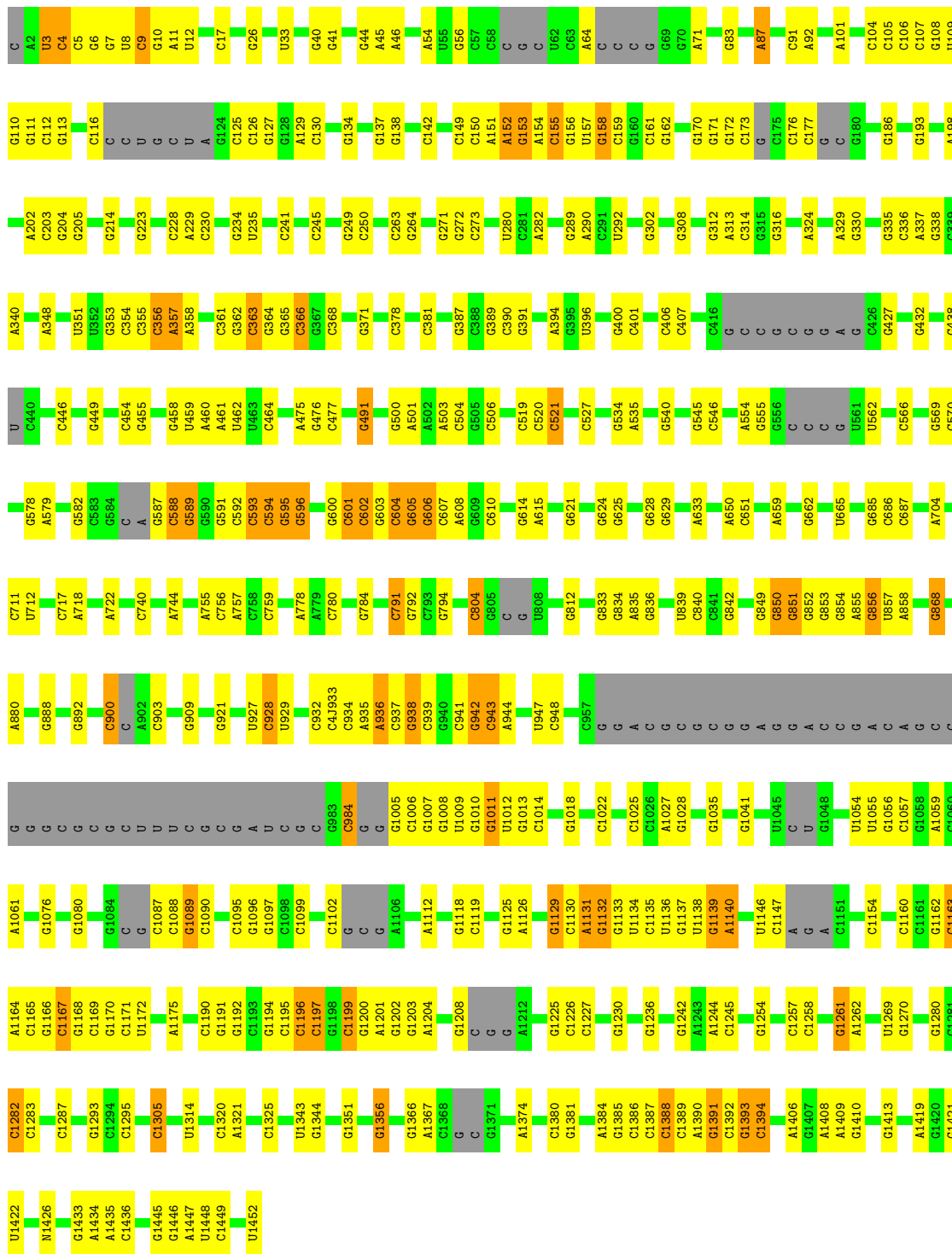
Chain G1:  73% 24%




LEU
LYS
ASN
GLY
GLU
LYS
LYS
L186
K187
P189
K231
GLY
LYS
GLN
HIS
ASN
ILE
ARG
ILE
TYR
G44
A45
PRO
ALA
LYS
THR
VAL
GLU

● Molecule 73: rRNA 18S

Chain 2: 64% 25% 7%



● Molecule 74: 40S ribosomal protein SA

Chain A1:  79% 21%

MET	SER	THR	GLU	LYS	THR	SER	GLN	ALA	SER	LYS	GLU	TYR	GLN	LEU	LYS	E17	R38	L210	PRO	GLU	GLU	ILE	PRO	ASP	GLU	GLU	GLU	SER	GLU	ASP	PHE	TYR	ASP	ASP	ASP	GLU	GLU	GLU	ASP	GLU	PHE	SER	ALA	GLY	ASN	GLY	ASN	LEU	PHE	ASP	GLU	TYR
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	91058	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	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: M7A, 4AC, 7MG, OMU, C4J, OMC, MG, K, OMG, 5MC, MA6, A2M, 4OC

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	T1	0.33	0/812	0.56	0/1098
2	N1	0.35	0/1215	0.59	1/1634 (0.1%)
3	J1	0.34	0/1340	0.63	0/1796
4	D1	0.37	0/1422	0.60	1/1909 (0.1%)
5	X1	0.34	0/1119	0.63	0/1498
6	S1	0.33	0/1070	0.68	0/1435
7	Q1	0.35	0/968	0.64	0/1295
8	C1	0.36	0/1674	0.59	0/2259
9	B1	0.36	0/1793	0.61	1/2419 (0.0%)
10	b1	0.38	0/628	0.78	1/852 (0.1%)
11	a1	0.34	0/797	0.54	0/1072
12	V1	0.41	0/613	0.61	0/823
13	R1	0.38	0/773	0.61	0/1037
14	K1	0.34	0/707	0.64	0/957
15	I1	0.33	0/1302	0.59	0/1746
16	e1	0.31	0/294	0.53	0/392
17	H1	0.34	0/1211	0.55	0/1640
18	n1	0.36	0/219	0.64	0/280
19	c1	0.47	0/439	0.63	0/585
20	O1	0.34	0/947	0.59	0/1273
21	W1	0.37	0/1048	0.59	0/1412
22	E1	0.33	0/2108	0.60	1/2845 (0.0%)
23	L1	0.35	0/1520	0.63	1/2037 (0.0%)
24	U1	0.35	0/619	0.64	0/833
25	1	0.78	0/58145	1.10	239/90686 (0.3%)
26	3	0.61	0/2797	1.00	7/4359 (0.2%)
27	42	0.75	0/3277	1.03	4/5109 (0.1%)
28	A2	0.39	0/1906	0.63	0/2561
29	B2	0.38	0/3058	0.59	0/4129
30	C2	0.40	0/2498	0.61	0/3388
31	D2	0.35	0/2157	0.56	0/2899
32	F2	0.39	0/1760	0.59	0/2374

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	G2	0.37	0/1472	0.59	0/1989
34	H2	0.37	0/1469	0.61	1/1985 (0.1%)
35	I2	0.36	0/1657	0.61	0/2219
36	J2	0.35	0/1325	0.59	0/1776
37	L2	0.38	0/1533	0.59	0/2052
38	M2	0.36	0/1002	0.59	0/1349
39	N2	0.40	0/1755	0.62	0/2353
40	O2	0.41	0/1618	0.58	0/2169
41	P2	0.40	0/1261	0.63	0/1688
42	Q2	0.34	0/1425	0.59	0/1907
43	R2	0.60	0/1478	0.64	0/1954
44	S2	0.38	0/1452	0.57	0/1955
45	T2	0.37	0/1251	0.59	1/1682 (0.1%)
46	U2	0.41	0/836	0.59	0/1124
47	V2	0.35	0/1083	0.58	0/1458
48	X2	0.35	0/956	0.60	0/1293
49	Y2	0.36	0/1091	0.61	0/1454
50	Z2	0.37	0/997	0.54	0/1352
51	a2	0.40	0/1231	0.60	0/1647
52	b2	0.34	0/471	0.56	0/624
53	c2	0.33	0/758	0.64	0/1025
54	d2	0.36	0/764	0.62	0/1026
55	e2	0.39	0/1063	0.56	0/1418
56	f2	0.37	0/994	0.61	1/1338 (0.1%)
57	g2	0.34	0/813	0.54	0/1092
58	h2	0.36	0/971	0.61	0/1295
59	i2	0.36	0/700	0.55	0/927
60	j2	0.38	0/708	0.59	0/941
61	k2	0.33	0/507	0.57	0/679
62	l2	0.34	0/445	0.64	0/594
63	m2	0.34	0/426	0.56	0/568
64	o2	0.40	0/773	0.62	0/1023
65	p2	0.39	0/717	0.71	1/956 (0.1%)
66	w2	0.93	1/332 (0.3%)	1.40	7/511 (1.4%)
67	W2	0.37	0/551	0.58	0/738
68	E	0.43	0/68	1.11	1/103 (1.0%)
69	d1	0.45	0/400	0.60	0/532
70	F1	0.65	0/1264	0.63	0/1697
71	Y1	0.45	0/724	0.67	0/971
72	G1	0.42	0/1466	0.67	0/1956
73	2	0.62	0/32117	1.10	172/50066 (0.3%)
74	A1	0.31	0/1580	0.50	0/2149
All	All	0.60	1/173740 (0.0%)	0.93	440/254267 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	w2	1	A	OP3-P	-10.48	1.48	1.61

All (440) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	2	155	C	P-O3'-C3'	-10.72	106.83	119.70
73	2	595	G	P-O3'-C3'	-10.62	106.96	119.70
73	2	138	G	P-O3'-C3'	-10.38	107.24	119.70
73	2	606	G	P-O3'-C3'	-10.24	107.41	119.70
10	b1	96	PHE	C-N-CA	10.16	147.09	121.70
26	3	52	G	P-O3'-C3'	-10.05	107.64	119.70
73	2	937	C	P-O3'-C3'	-9.90	107.82	119.70
73	2	1007	G	P-O3'-C3'	-9.88	107.85	119.70
25	1	2376	U	P-O3'-C3'	-9.80	107.94	119.70
73	2	366	C	P-O3'-C3'	-9.71	108.05	119.70
73	2	156	G	P-O3'-C3'	-9.70	108.07	119.70
73	2	1132	G	P-O3'-C3'	-9.64	108.13	119.70
25	1	2156	G	P-O3'-C3'	-9.56	108.22	119.70
73	2	9	C	P-O3'-C3'	-9.53	108.27	119.70
73	2	111	G	P-O3'-C3'	-9.51	108.29	119.70
73	2	1135	C	P-O3'-C3'	-9.41	108.41	119.70
73	2	1133	G	P-O3'-C3'	-9.38	108.44	119.70
73	2	943	C	P-O3'-C3'	-9.35	108.48	119.70
73	2	109	U	P-O3'-C3'	-9.28	108.56	119.70
73	2	1011	OMG	P-O3'-C3'	-9.27	108.58	119.70
25	1	1547	U	P-O3'-C3'	-9.25	108.60	119.70
73	2	127	G	P-O3'-C3'	-9.21	108.64	119.70
25	1	1326	C	P-O3'-C3'	-9.20	108.67	119.70
73	2	594	C	P-O3'-C3'	-9.19	108.67	119.70
73	2	1137	G	P-O3'-C3'	-9.17	108.70	119.70
73	2	939	C	P-O3'-C3'	-9.15	108.72	119.70
73	2	1168	G	P-O3'-C3'	-9.12	108.76	119.70
73	2	1392	C	P-O3'-C3'	-9.01	108.88	119.70
25	1	1849	C	C6-N1-C2	-9.00	116.70	120.30
25	1	386	OMG	P-O3'-C3'	-8.88	109.05	119.70
25	1	1833	C	P-O3'-C3'	-8.88	109.05	119.70
25	1	2537	A	P-O3'-C3'	-8.74	109.21	119.70
73	2	11	A	P-O3'-C3'	-8.74	109.21	119.70
73	2	4	C	P-O3'-C3'	-8.72	109.23	119.70
25	1	889	C	C2-N1-C1'	-8.72	109.21	118.80
73	2	363	C	P-O3'-C3'	-8.72	109.24	119.70
73	2	1172	U	P-O3'-C3'	-8.62	109.35	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	1	1487	C	P-O3'-C3'	-8.59	109.40	119.70
73	2	6	G	P-O3'-C3'	-8.56	109.43	119.70
73	2	521	C	C2-N1-C1'	8.56	128.22	118.80
25	1	355	G	O4'-C1'-N9	8.54	115.03	108.20
73	2	159	C	P-O3'-C3'	-8.53	109.46	119.70
25	1	2154	C	P-O3'-C3'	-8.51	109.48	119.70
73	2	361	C	P-O3'-C3'	-8.51	109.49	119.70
73	2	1138	U	P-O3'-C3'	-8.49	109.50	119.70
73	2	5	C	P-O3'-C3'	-8.49	109.51	119.70
73	2	1008	G	P-O3'-C3'	-8.44	109.57	119.70
73	2	12	U	P-O3'-C3'	-8.43	109.59	119.70
73	2	1140	A	P-O3'-C3'	-8.43	109.59	119.70
73	2	1131	A	P-O3'-C3'	-8.42	109.60	119.70
25	1	2531	C	P-O3'-C3'	-8.41	109.61	119.70
66	w2	69	C	P-O3'-C3'	-8.32	109.71	119.70
73	2	110	G	P-O3'-C3'	-8.32	109.71	119.70
73	2	521	C	N1-C2-O2	8.30	123.88	118.90
73	2	1134	U	P-O3'-C3'	-8.29	109.75	119.70
25	1	2296	G	P-O3'-C3'	-8.29	109.76	119.70
73	2	1169	C	P-O3'-C3'	-8.29	109.76	119.70
73	2	944	A	P-O3'-C3'	-8.28	109.76	119.70
73	2	1166	G	P-O3'-C3'	-8.27	109.77	119.70
73	2	604	C	P-O3'-C3'	-8.27	109.78	119.70
73	2	1130	C	P-O3'-C3'	-8.26	109.79	119.70
73	2	1386	C	P-O3'-C3'	-8.24	109.81	119.70
25	1	1814	A	P-O3'-C3'	-8.24	109.81	119.70
26	3	51	A	P-O3'-C3'	-8.19	109.87	119.70
73	2	1005	G	P-O3'-C3'	-8.17	109.90	119.70
25	1	2298	C	P-O3'-C3'	-8.16	109.90	119.70
73	2	1196	C	P-O3'-C3'	-8.16	109.91	119.70
73	2	900	C	N1-C2-O2	8.14	123.79	118.90
73	2	1167	C	P-O3'-C3'	-8.14	109.93	119.70
73	2	104	OMC	P-O3'-C3'	-8.11	109.97	119.70
25	1	2152	U	P-O3'-C3'	-8.10	109.98	119.70
25	1	1501	C	P-O3'-C3'	-8.06	110.02	119.70
66	w2	70	G	P-O3'-C3'	-8.06	110.03	119.70
73	2	106	C	P-O3'-C3'	-8.05	110.04	119.70
73	2	1388	C	P-O3'-C3'	-8.01	110.09	119.70
25	1	32	G	P-O3'-C3'	-7.99	110.12	119.70
25	1	552	A	P-O3'-C3'	-7.97	110.13	119.70
73	2	900	C	N3-C2-O2	-7.97	116.32	121.90
25	1	2211	C	P-O3'-C3'	-7.97	110.14	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	2	602	C	P-O3'-C3'	-7.97	110.14	119.70
66	w2	68	C	P-O3'-C3'	-7.93	110.18	119.70
73	2	900	C	C2-N1-C1'	7.93	127.52	118.80
73	2	10	G	P-O3'-C3'	-7.92	110.20	119.70
73	2	942	G	P-O3'-C3'	-7.88	110.24	119.70
73	2	7	G	P-O3'-C3'	-7.88	110.25	119.70
25	1	1866	G	P-O3'-C3'	-7.87	110.25	119.70
25	1	2232	C	P-O3'-C3'	-7.86	110.27	119.70
73	2	1006	C	P-O3'-C3'	-7.85	110.28	119.70
73	2	107	C	P-O3'-C3'	-7.85	110.28	119.70
25	1	2527	G	P-O3'-C3'	-7.83	110.30	119.70
73	2	854	G	P-O3'-C3'	-7.83	110.30	119.70
73	2	158	G	P-O3'-C3'	-7.82	110.32	119.70
25	1	1520	OMG	P-O3'-C3'	-7.80	110.34	119.70
25	1	2213	G	P-O3'-C3'	-7.79	110.35	119.70
25	1	1383	C	P-O3'-C3'	-7.79	110.36	119.70
25	1	568	U	P-O3'-C3'	-7.79	110.36	119.70
73	2	1197	C	P-O3'-C3'	-7.78	110.36	119.70
73	2	1170	G	P-O3'-C3'	-7.78	110.37	119.70
73	2	1136	U	P-O3'-C3'	-7.77	110.38	119.70
73	2	362	G	P-O3'-C3'	-7.74	110.41	119.70
25	1	569	G	P-O3'-C3'	-7.74	110.42	119.70
73	2	1164	A	P-O3'-C3'	-7.71	110.44	119.70
25	1	1832	G	P-O3'-C3'	-7.70	110.46	119.70
73	2	1387	C	P-O3'-C3'	-7.69	110.47	119.70
25	1	1813	G	P-O3'-C3'	-7.68	110.48	119.70
73	2	108	G	P-O3'-C3'	-7.68	110.48	119.70
73	2	150	C	P-O3'-C3'	-7.68	110.48	119.70
66	w2	72	C	P-O3'-C3'	-7.67	110.50	119.70
25	1	1858	G	P-O3'-C3'	-7.65	110.52	119.70
73	2	3	U	P-O3'-C3'	-7.64	110.53	119.70
66	w2	71	C	P-O3'-C3'	-7.63	110.54	119.70
25	1	1490	G	P-O3'-C3'	-7.62	110.56	119.70
25	1	1161	C	P-O3'-C3'	-7.61	110.56	119.70
73	2	1385	G	P-O3'-C3'	-7.59	110.59	119.70
73	2	151	A	P-O3'-C3'	-7.55	110.64	119.70
25	1	889	C	C6-N1-C1'	7.55	129.86	120.80
25	1	656	G	P-O3'-C3'	-7.52	110.68	119.70
73	2	948	C	P-O3'-C3'	-7.51	110.69	119.70
73	2	157	U	P-O3'-C3'	-7.51	110.69	119.70
73	2	900	C	C6-N1-C2	-7.48	117.31	120.30
25	1	2040	U	N3-C2-O2	-7.47	116.97	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	2	1391	G	P-O3'-C3'	-7.44	110.78	119.70
25	1	1483	G	P-O3'-C3'	-7.43	110.78	119.70
73	2	152	A	P-O3'-C3'	-7.42	110.79	119.70
25	1	2529	C	P-O3'-C3'	-7.42	110.80	119.70
73	2	1165	C	P-O3'-C3'	-7.41	110.81	119.70
25	1	2265	C	C6-N1-C2	-7.41	117.34	120.30
73	2	126	C	P-O3'-C3'	-7.34	110.89	119.70
25	1	2059	C	C2-N1-C1'	7.34	126.88	118.80
73	2	371	OMG	P-O3'-C3'	-7.34	110.89	119.70
25	1	2526	U	P-O3'-C3'	-7.32	110.92	119.70
25	1	1384	C	P-O3'-C3'	-7.30	110.94	119.70
73	2	591	G	P-O3'-C3'	-7.29	110.95	119.70
73	2	853	G	P-O3'-C3'	-7.29	110.95	119.70
73	2	588	C	P-O3'-C3'	-7.24	111.01	119.70
73	2	1013	G	P-O3'-C3'	-7.19	111.07	119.70
73	2	938	G	P-O3'-C3'	-7.17	111.09	119.70
25	1	1491	G	P-O3'-C3'	-7.16	111.11	119.70
25	1	2157	G	P-O3'-C3'	-7.15	111.12	119.70
25	1	2214	A	P-O3'-C3'	-7.15	111.12	119.70
25	1	2151	G	P-O3'-C3'	-7.12	111.15	119.70
73	2	852	G	P-O3'-C3'	-7.12	111.16	119.70
25	1	2235	A	P-O3'-C3'	-7.11	111.17	119.70
25	1	1484	A	P-O3'-C3'	-7.08	111.20	119.70
25	1	405	G	P-O3'-C3'	-7.07	111.22	119.70
73	2	929	U	P-O3'-C3'	-7.07	111.22	119.70
25	1	2386	U	P-O3'-C3'	-7.07	111.22	119.70
25	1	1824	OMC	P-O3'-C3'	-6.99	111.31	119.70
73	2	521	C	C6-N1-C1'	-6.99	112.41	120.80
25	1	2406	C	P-O3'-C3'	-6.98	111.32	119.70
73	2	1087	C	C2-N1-C1'	6.98	126.47	118.80
73	2	105	C	P-O3'-C3'	-6.97	111.33	119.70
73	2	462	U	C2-N1-C1'	6.95	126.04	117.70
25	1	1849	C	N3-C2-O2	-6.94	117.04	121.90
73	2	1163	C	P-O3'-C3'	-6.92	111.39	119.70
25	1	2212	G	P-O3'-C3'	-6.91	111.41	119.70
25	1	1812	G	P-O3'-C3'	-6.91	111.41	119.70
25	1	2059	C	N1-C2-O2	6.90	123.04	118.90
26	3	50	A	P-O3'-C3'	-6.89	111.43	119.70
73	2	1394	C	P-O3'-C3'	-6.89	111.43	119.70
73	2	596	G	P-O3'-C3'	-6.87	111.45	119.70
66	w2	73	A	P-O3'-C3'	-6.87	111.46	119.70
73	2	153	G	P-O3'-C3'	-6.86	111.46	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	1	1486	U	P-O3'-C3'	-6.85	111.47	119.70
25	1	300	C	N3-C2-O2	-6.84	117.11	121.90
25	1	1815	U	P-O3'-C3'	-6.84	111.49	119.70
25	1	2524	G	P-O3'-C3'	-6.83	111.50	119.70
73	2	849	G	P-O3'-C3'	-6.83	111.51	119.70
73	2	401	C	P-O3'-C3'	-6.83	111.51	119.70
73	2	1012	U	P-O3'-C3'	-6.81	111.53	119.70
73	2	1393	G	P-O3'-C3'	-6.81	111.53	119.70
25	1	1382	G	P-O3'-C3'	-6.80	111.54	119.70
25	1	2230	A	P-O3'-C3'	-6.80	111.54	119.70
25	1	2575	C	C2-N1-C1'	6.79	126.27	118.80
25	1	2155	C	P-O3'-C3'	-6.79	111.56	119.70
73	2	355	C	P-O3'-C3'	-6.79	111.56	119.70
25	1	2265	C	N1-C2-O2	6.79	122.97	118.90
25	1	2228	U	P-O3'-C3'	-6.76	111.59	119.70
73	2	356	C	P-O3'-C3'	-6.76	111.59	119.70
25	1	1904	U	P-O3'-C3'	-6.75	111.60	119.70
25	1	2265	C	N3-C2-O2	-6.74	117.18	121.90
73	2	358	A	P-O3'-C3'	-6.70	111.66	119.70
73	2	850	G	P-O3'-C3'	-6.70	111.66	119.70
25	1	300	C	N1-C2-O2	6.69	122.92	118.90
73	2	462	U	N1-C2-O2	6.69	127.48	122.80
25	1	2210	G	P-O3'-C3'	-6.67	111.70	119.70
73	2	858	A	P-O3'-C3'	-6.67	111.70	119.70
25	1	300	C	C6-N1-C2	-6.65	117.64	120.30
73	2	857	U	P-O3'-C3'	-6.65	111.72	119.70
25	1	2301	C	P-O3'-C3'	-6.64	111.73	119.70
73	2	1139	G	P-O3'-C3'	-6.64	111.73	119.70
25	1	1485	C	P-O3'-C3'	-6.63	111.74	119.70
25	1	2153	G	P-O3'-C3'	-6.62	111.75	119.70
25	1	1546	C	P-O3'-C3'	-6.61	111.77	119.70
25	1	300	C	C2-N1-C1'	6.61	126.07	118.80
25	1	1529	G	P-O3'-C3'	-6.61	111.77	119.70
25	1	1849	C	N3-C4-C5	-6.57	119.27	121.90
73	2	1258	C	C2-N1-C1'	6.57	126.03	118.80
25	1	2234	C	P-O3'-C3'	-6.55	111.84	119.70
25	1	2522	G	P-O3'-C3'	-6.52	111.87	119.70
25	1	2018	C	N3-C2-O2	-6.50	117.35	121.90
25	1	2299	G	P-O3'-C3'	-6.46	111.95	119.70
25	1	2149	C	P-O3'-C3'	-6.45	111.96	119.70
25	1	2300	G	P-O3'-C3'	-6.44	111.98	119.70
25	1	2304	U	P-O3'-C3'	-6.40	112.02	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	2	1171	C	P-O3'-C3'	-6.39	112.04	119.70
25	1	2209	C	P-O3'-C3'	-6.38	112.05	119.70
25	1	2233	A	P-O3'-C3'	-6.37	112.05	119.70
25	1	1808	A	P-O3'-C3'	-6.37	112.05	119.70
25	1	37	U	P-O3'-C3'	-6.37	112.06	119.70
25	1	2268	C	N3-C2-O2	-6.37	117.44	121.90
25	1	2040	U	N1-C2-N3	6.34	118.70	114.90
25	1	1620	C	C6-N1-C2	-6.33	117.77	120.30
25	1	2295	U	N3-C2-O2	-6.33	117.77	122.20
27	42	104	A	O5'-P-OP1	-6.33	100.00	105.70
25	1	567	C	P-O3'-C3'	-6.32	112.11	119.70
73	2	928	C	P-O3'-C3'	-6.32	112.12	119.70
25	1	1544	G	P-O3'-C3'	-6.32	112.12	119.70
25	1	1162	U	P-O3'-C3'	-6.31	112.13	119.70
25	1	112	C	C2-N1-C1'	6.30	125.73	118.80
25	1	178	G	N3-C4-N9	6.30	129.78	126.00
25	1	1482	G	P-O3'-C3'	-6.30	112.14	119.70
73	2	851	G	P-O3'-C3'	-6.29	112.15	119.70
25	1	1809	C	P-O3'-C3'	-6.29	112.15	119.70
73	2	624	G	N3-C4-N9	6.26	129.75	126.00
73	2	1095	C	P-O3'-C3'	-6.26	112.19	119.70
27	42	98	C	C2-N1-C1'	6.25	125.68	118.80
25	1	1816	C	P-O3'-C3'	-6.24	112.21	119.70
73	2	589	G	P-O3'-C3'	-6.24	112.21	119.70
25	1	2158	C	P-O3'-C3'	-6.24	112.22	119.70
73	2	1258	C	N1-C2-O2	6.24	122.64	118.90
25	1	1849	C	C4-C5-C6	6.23	120.51	117.40
26	3	28	C	P-O3'-C3'	-6.22	112.23	119.70
25	1	1489	G	P-O3'-C3'	-6.22	112.23	119.70
25	1	1539	A	P-O3'-C3'	-6.22	112.24	119.70
73	2	947	U	P-O3'-C3'	-6.21	112.25	119.70
2	N1	135	LEU	CA-CB-CG	6.20	129.56	115.30
73	2	462	U	N3-C2-O2	-6.20	117.86	122.20
73	2	610	C	N3-C4-C5	6.19	124.38	121.90
25	1	2150	C	P-O3'-C3'	-6.18	112.28	119.70
25	1	1861	C	P-O3'-C3'	-6.16	112.31	119.70
25	1	2546	C	C2-N1-C1'	6.14	125.56	118.80
25	1	1252	C	O4'-C1'-N1	6.14	113.11	108.20
25	1	570	G	P-O3'-C3'	-6.13	112.35	119.70
25	1	1163	G	P-O3'-C3'	-6.12	112.36	119.70
25	1	2354	U	P-O3'-C3'	6.11	127.03	119.70
73	2	1201	A	P-O3'-C3'	-6.11	112.37	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	2	491	G	C4-N9-C1'	6.10	134.43	126.50
25	1	1871	C	C6-N1-C2	-6.09	117.86	120.30
73	2	1202	G	P-O3'-C3'	-6.08	112.40	119.70
25	1	388	C	P-O3'-C3'	-6.05	112.44	119.70
25	1	1903	U	P-O3'-C3'	-6.01	112.48	119.70
25	1	1179	C	C2-N1-C1'	6.01	125.41	118.80
25	1	429	G	N7-C8-N9	6.01	116.10	113.10
25	1	1905	G	P-O3'-C3'	-6.00	112.50	119.70
73	2	407	C	C2-N1-C1'	6.00	125.40	118.80
25	1	2265	C	C2-N1-C1'	5.98	125.38	118.80
25	1	1602	C	C6-N1-C2	-5.96	117.92	120.30
25	1	2231	C	P-O3'-C3'	-5.94	112.57	119.70
66	w2	75	C	N3-C2-O2	-5.94	117.74	121.90
73	2	624	G	N3-C4-C5	-5.94	125.63	128.60
25	1	2533	U	P-O3'-C3'	-5.94	112.57	119.70
73	2	686	C	C2-N1-C1'	5.94	125.33	118.80
25	1	1871	C	C2-N1-C1'	5.93	125.33	118.80
73	2	1089	G	O4'-C1'-N9	5.93	112.94	108.20
25	1	399	G	N3-C4-C5	-5.93	125.64	128.60
73	2	601	C	P-O3'-C3'	-5.92	112.60	119.70
73	2	354	C	P-O3'-C3'	-5.91	112.60	119.70
73	2	357	A	P-O3'-C3'	-5.91	112.61	119.70
25	1	2018	C	N1-C2-O2	5.91	122.44	118.90
25	1	551	G	P-O3'-C3'	-5.90	112.62	119.70
25	1	2422	C	O4'-C1'-N1	5.90	112.92	108.20
25	1	1541	G	P-O3'-C3'	-5.90	112.62	119.70
25	1	35	C	P-O3'-C3'	-5.89	112.63	119.70
25	1	41	C	P-O3'-C3'	-5.88	112.64	119.70
73	2	368	C	P-O3'-C3'	-5.88	112.65	119.70
25	1	34	A	P-O3'-C3'	-5.87	112.66	119.70
73	2	592	C	P-O3'-C3'	-5.85	112.68	119.70
25	1	2018	C	C6-N1-C2	-5.84	117.96	120.30
25	1	36	U	P-O3'-C3'	-5.84	112.69	119.70
73	2	1199	C	C6-N1-C2	-5.84	117.96	120.30
25	1	1277	A	O4'-C1'-N9	5.82	112.86	108.20
73	2	607	C	P-O3'-C3'	-5.82	112.72	119.70
25	1	638	U	C2-N1-C1'	5.81	124.67	117.70
25	1	2217	U	P-O3'-C3'	-5.80	112.73	119.70
73	2	587	G	P-O3'-C3'	-5.80	112.74	119.70
25	1	589	C	P-O3'-C3'	5.80	126.66	119.70
25	1	2546	C	N1-C2-O2	5.79	122.37	118.90
73	2	1087	C	C6-N1-C1'	-5.79	113.86	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	1	2543	C	C5-C6-N1	5.78	123.89	121.00
26	3	94	U	N3-C2-O2	-5.78	118.16	122.20
73	2	610	C	N1-C2-O2	5.78	122.37	118.90
73	2	621	G	N3-C4-C5	-5.78	125.71	128.60
73	2	235	U	C2-N1-C1'	5.76	124.62	117.70
25	1	156	G	O4'-C1'-N9	5.75	112.80	108.20
73	2	491	G	C8-N9-C1'	-5.73	119.55	127.00
73	2	935	A	P-O3'-C3'	-5.73	112.83	119.70
25	1	2499	G	N3-C4-N9	5.71	129.43	126.00
25	1	2499	G	N3-C4-C5	-5.69	125.75	128.60
73	2	535	A	O4'-C1'-N9	5.69	112.75	108.20
25	1	2268	C	C6-N1-C2	-5.68	118.03	120.30
25	1	2215	G	P-O3'-C3'	-5.67	112.90	119.70
73	2	1282	C	N1-C2-O2	5.67	122.30	118.90
25	1	575	G	P-O3'-C3'	-5.66	112.90	119.70
65	p2	60	CYS	CA-CB-SG	5.66	124.19	114.00
73	2	1195	C	P-O3'-C3'	-5.66	112.91	119.70
25	1	1261	C	N1-C2-O2	5.64	122.28	118.90
25	1	611	G	N3-C4-N9	5.63	129.38	126.00
27	42	99	C	C2-N1-C1'	5.63	124.99	118.80
25	1	1542	C	P-O3'-C3'	-5.63	112.94	119.70
73	2	593	C	P-O3'-C3'	-5.62	112.95	119.70
73	2	804	C	C6-N1-C2	-5.62	118.05	120.30
23	L1	34	LEU	CA-CB-CG	5.62	128.22	115.30
25	1	1850	A	P-O3'-C3'	-5.62	112.96	119.70
25	1	1863	G	P-O3'-C3'	-5.60	112.98	119.70
73	2	855	A	P-O3'-C3'	-5.58	113.00	119.70
25	1	1760	G	O4'-C1'-N9	5.57	112.66	108.20
73	2	755	A	O4'-C1'-N9	5.57	112.65	108.20
25	1	1865	C	P-O3'-C3'	-5.57	113.02	119.70
25	1	802	C	N1-C2-O2	5.55	122.23	118.90
25	1	2258	C	N1-C2-O2	5.55	122.23	118.90
73	2	280	U	N3-C2-O2	-5.54	118.32	122.20
25	1	1208	C	C6-N1-C2	-5.53	118.09	120.30
73	2	1282	C	C2-N1-C1'	5.52	124.87	118.80
25	1	112	C	C6-N1-C2	-5.52	118.09	120.30
25	1	545	G	O4'-C1'-N9	5.51	112.61	108.20
73	2	112	C	P-O3'-C3'	-5.50	113.09	119.70
73	2	856	G	P-O3'-C3'	-5.50	113.10	119.70
73	2	1356	G	N3-C4-N9	5.49	129.29	126.00
73	2	791	C	C6-N1-C2	-5.49	118.10	120.30
25	1	1864	G	P-O3'-C3'	-5.48	113.12	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	2	149	C	P-O3'-C3'	-5.48	113.12	119.70
25	1	2305	U	P-O3'-C3'	-5.48	113.13	119.70
25	1	2258	C	N3-C2-O2	-5.47	118.07	121.90
25	1	396	A2M	P-O3'-C3'	-5.47	113.14	119.70
25	1	178	G	N3-C4-C5	-5.46	125.87	128.60
25	1	33	A	P-O3'-C3'	-5.46	113.15	119.70
25	1	611	G	N3-C4-C5	-5.45	125.88	128.60
73	2	113	G	P-O3'-C3'	-5.45	113.16	119.70
25	1	658	U	P-O3'-C3'	-5.45	113.16	119.70
25	1	1160	A	P-O3'-C3'	-5.45	113.16	119.70
25	1	886	C	C6-N1-C2	-5.42	118.13	120.30
25	1	2208	G	P-O3'-C3'	-5.42	113.19	119.70
73	2	1258	C	N3-C2-O2	-5.42	118.11	121.90
73	2	1421	G	N3-C4-C5	5.42	131.31	128.60
22	E1	139	LEU	CA-CB-CG	5.42	127.76	115.30
25	1	1792	G	O4'-C1'-N9	5.42	112.53	108.20
73	2	1097	G	P-O3'-C3'	-5.41	113.20	119.70
25	1	2040	U	C4-C5-C6	5.40	122.94	119.70
25	1	2545	C	C6-N1-C2	-5.40	118.14	120.30
73	2	717	C	C2-N1-C1'	5.39	124.73	118.80
25	1	2528	C	P-O3'-C3'	-5.39	113.23	119.70
25	1	889	C	N1-C2-O2	-5.39	115.67	118.90
25	1	2059	C	C6-N1-C1'	-5.38	114.34	120.80
25	1	429	G	C5-N7-C8	-5.38	101.61	104.30
25	1	2129	G	C4-N9-C1'	5.38	133.50	126.50
25	1	2538	A	P-O3'-C3'	-5.38	113.24	119.70
25	1	2268	C	C2-N1-C1'	5.38	124.72	118.80
73	2	1154	C	C6-N1-C2	-5.37	118.15	120.30
25	1	1856	G	N3-C4-N9	5.37	129.22	126.00
25	1	2596	C	N1-C2-O2	5.37	122.12	118.90
25	1	1502	U	P-O3'-C3'	-5.36	113.27	119.70
25	1	989	G	N3-C4-N9	5.36	129.22	126.00
73	2	521	C	N3-C2-O2	-5.35	118.15	121.90
25	1	1894	C	C6-N1-C2	-5.35	118.16	120.30
25	1	2297	U	P-O3'-C3'	-5.34	113.29	119.70
25	1	2513	G	N3-C4-C5	-5.33	125.94	128.60
25	1	2268	C	N1-C2-O2	5.32	122.09	118.90
68	E	74	C	C6-N1-C2	-5.31	118.17	120.30
25	1	490	G	C6-C5-N7	-5.30	127.22	130.40
56	f2	9	PHE	C-N-CA	5.30	134.94	121.70
25	1	518	C	C6-N1-C2	-5.29	118.18	120.30
73	2	936	A	P-O3'-C3'	-5.29	113.35	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	1	1882	OMG	P-O3'-C3'	-5.29	113.35	119.70
27	42	98	C	N3-C2-O2	-5.29	118.20	121.90
25	1	1538	C	P-O3'-C3'	-5.28	113.37	119.70
25	1	2258	C	C2-N1-C1'	5.27	124.60	118.80
73	2	381	C	N3-C2-O2	-5.27	118.21	121.90
25	1	2289	C	C6-N1-C2	-5.27	118.19	120.30
25	1	376	C	C6-N1-C2	-5.27	118.19	120.30
26	3	77	U	N3-C2-O2	-5.26	118.52	122.20
25	1	1381	C	P-O3'-C3'	-5.25	113.40	119.70
25	1	576	G	P-O3'-C3'	-5.25	113.41	119.70
25	1	165	G	N3-C4-C5	5.24	131.22	128.60
73	2	83	G	P-O3'-C3'	-5.23	113.42	119.70
25	1	545	G	C4-N9-C1'	5.23	133.30	126.50
25	1	632	G	P-O3'-C3'	5.23	125.97	119.70
25	1	1849	C	N1-C2-N3	5.23	122.86	119.20
25	1	1261	C	N3-C2-O2	-5.22	118.24	121.90
25	1	186	A	O4'-C1'-N9	5.22	112.38	108.20
73	2	605	G	P-O3'-C3'	-5.22	113.43	119.70
25	1	2575	C	C6-N1-C2	-5.22	118.21	120.30
25	1	387	U	P-O3'-C3'	-5.21	113.44	119.70
25	1	2543	C	C6-N1-C2	-5.21	118.21	120.30
73	2	1199	C	N3-C2-O2	-5.21	118.25	121.90
25	1	2523	C	P-O3'-C3'	-5.21	113.44	119.70
25	1	1006	G	O4'-C1'-N9	5.21	112.37	108.20
25	1	2575	C	O4'-C1'-N1	5.20	112.36	108.20
25	1	1871	C	N3-C2-O2	-5.20	118.26	121.90
26	3	94	U	C2-N1-C1'	5.20	123.94	117.70
25	1	1178	U	N3-C2-O2	-5.19	118.57	122.20
25	1	724	C	C6-N1-C2	-5.19	118.22	120.30
25	1	2019	C	C6-N1-C2	-5.18	118.23	120.30
25	1	1924	G	N3-C4-N9	5.18	129.11	126.00
73	2	984	C	C6-N1-C2	-5.17	118.23	120.30
25	1	1330	G	N3-C4-N9	5.17	129.10	126.00
25	1	1545	G	P-O3'-C3'	-5.17	113.50	119.70
25	1	989	G	C6-C5-N7	-5.17	127.30	130.40
73	2	364	G	P-O3'-C3'	-5.16	113.51	119.70
73	2	1305	C	C6-N1-C2	-5.16	118.24	120.30
25	1	2581	C	C2-N1-C1'	5.16	124.47	118.80
25	1	126	U	N3-C2-O2	-5.15	118.59	122.20
45	T2	81	ARG	CA-CB-CG	5.15	124.73	113.40
25	1	2596	C	C2-N1-C1'	5.14	124.46	118.80
25	1	185	C	C6-N1-C2	-5.14	118.24	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	1	376	C	C2-N1-C1'	5.13	124.44	118.80
25	1	802	C	N3-C2-O2	-5.13	118.31	121.90
25	1	1831	C	P-O3'-C3'	-5.13	113.55	119.70
25	1	2550	C	N3-C2-O2	-5.13	118.31	121.90
25	1	2418	G	N3-C4-C5	-5.12	126.04	128.60
25	1	1488	C	P-O3'-C3'	-5.12	113.56	119.70
25	1	2628	C	N1-C2-O2	5.11	121.97	118.90
4	D1	148	LEU	CA-CB-CG	-5.10	103.58	115.30
25	1	1280	C	C2-N1-C1'	5.10	124.41	118.80
25	1	2367	A	P-O3'-C3'	-5.09	113.59	119.70
73	2	280	U	C2-N1-C1'	5.08	123.79	117.70
25	1	2596	C	C6-N1-C2	-5.06	118.28	120.30
25	1	763	C	C5-C6-N1	5.05	123.53	121.00
73	2	1129	G	N3-C4-C5	-5.05	126.07	128.60
9	B1	31	ILE	C-N-CA	5.05	134.33	121.70
25	1	1532	A	P-O3'-C3'	-5.05	113.64	119.70
25	1	438	C	C6-N1-C2	-5.03	118.29	120.30
25	1	178	G	C4-N9-C1'	5.02	133.03	126.50
25	1	574	A	P-O3'-C3'	-5.01	113.69	119.70
25	1	638	U	N1-C2-O2	5.01	126.31	122.80
25	1	2415	C	C2-N1-C1'	5.01	124.31	118.80
34	H2	159	GLU	CA-CB-CG	5.01	124.42	113.40
73	2	1199	C	N1-C2-O2	5.01	121.91	118.90
25	1	2628	C	C2-N1-C1'	5.01	124.31	118.80
25	1	1537	G	C8-N9-C4	-5.00	104.40	106.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T1	102/139 (73%)	97 (95%)	5 (5%)	0	100	100
2	N1	150/154 (97%)	142 (95%)	8 (5%)	0	100	100
3	J1	164/189 (87%)	153 (93%)	11 (7%)	0	100	100
4	D1	174/217 (80%)	163 (94%)	11 (6%)	0	100	100
5	X1	140/143 (98%)	130 (93%)	10 (7%)	0	100	100
6	S1	131/154 (85%)	113 (86%)	18 (14%)	0	100	100
7	Q1	119/158 (75%)	108 (91%)	11 (9%)	0	100	100
8	C1	210/242 (87%)	195 (93%)	15 (7%)	0	100	100
9	B1	216/248 (87%)	207 (96%)	9 (4%)	0	100	100
10	b1	77/124 (62%)	71 (92%)	6 (8%)	0	100	100
11	a1	95/109 (87%)	90 (95%)	5 (5%)	0	100	100
12	V1	80/89 (90%)	72 (90%)	8 (10%)	0	100	100
13	R1	93/137 (68%)	87 (94%)	6 (6%)	0	100	100
14	K1	79/134 (59%)	70 (89%)	9 (11%)	0	100	100
15	I1	159/174 (91%)	147 (92%)	12 (8%)	0	100	100
16	e1	31/69 (45%)	29 (94%)	2 (6%)	0	100	100
17	H1	148/190 (78%)	133 (90%)	15 (10%)	0	100	100
18	n1	22/41 (54%)	22 (100%)	0	0	100	100
19	c1	51/64 (80%)	47 (92%)	4 (8%)	0	100	100
20	O1	124/145 (86%)	121 (98%)	3 (2%)	0	100	100
21	W1	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
22	E1	256/268 (96%)	234 (91%)	22 (9%)	0	100	100
23	L1	179/199 (90%)	169 (94%)	10 (6%)	0	100	100
24	U1	68/126 (54%)	63 (93%)	5 (7%)	0	100	100
28	A2	248/251 (99%)	237 (96%)	11 (4%)	0	100	100
29	B2	376/379 (99%)	357 (95%)	19 (5%)	0	100	100
30	C2	312/316 (99%)	295 (95%)	17 (5%)	0	100	100
31	D2	264/297 (89%)	247 (94%)	17 (6%)	0	100	100
32	F2	212/235 (90%)	209 (99%)	3 (1%)	0	100	100
33	G2	178/225 (79%)	173 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	H2	182/185 (98%)	172 (94%)	10 (6%)	0	100	100
35	I2	196/210 (93%)	187 (95%)	9 (5%)	0	100	100
36	J2	158/173 (91%)	144 (91%)	14 (9%)	0	100	100
37	L2	185/234 (79%)	183 (99%)	2 (1%)	0	100	100
38	M2	126/131 (96%)	115 (91%)	11 (9%)	0	100	100
39	N2	202/204 (99%)	192 (95%)	10 (5%)	0	100	100
40	O2	193/197 (98%)	186 (96%)	7 (4%)	0	100	100
41	P2	152/164 (93%)	143 (94%)	9 (6%)	0	100	100
42	Q2	176/179 (98%)	169 (96%)	7 (4%)	0	100	100
43	R2	175/196 (89%)	166 (95%)	9 (5%)	0	100	100
44	S2	171/173 (99%)	165 (96%)	6 (4%)	0	100	100
45	T2	149/159 (94%)	145 (97%)	4 (3%)	0	100	100
46	U2	98/171 (57%)	90 (92%)	8 (8%)	0	100	100
47	V2	137/142 (96%)	133 (97%)	4 (3%)	0	100	100
48	X2	114/141 (81%)	109 (96%)	5 (4%)	0	100	100
49	Y2	131/135 (97%)	126 (96%)	5 (4%)	0	100	100
50	Z2	125/135 (93%)	115 (92%)	10 (8%)	0	100	100
51	a2	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
52	b2	54/62 (87%)	54 (100%)	0	0	100	100
53	c2	98/109 (90%)	97 (99%)	1 (1%)	0	100	100
54	d2	90/106 (85%)	81 (90%)	9 (10%)	0	100	100
55	e2	124/136 (91%)	119 (96%)	5 (4%)	0	100	100
56	f2	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
57	g2	97/120 (81%)	94 (97%)	3 (3%)	0	100	100
58	h2	116/124 (94%)	114 (98%)	2 (2%)	0	100	100
59	i2	81/90 (90%)	76 (94%)	5 (6%)	0	100	100
60	j2	85/89 (96%)	83 (98%)	2 (2%)	0	100	100
61	k2	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
62	l2	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
63	m2	49/127 (39%)	46 (94%)	3 (6%)	0	100	100
64	o2	92/106 (87%)	90 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	p2	89/94 (95%)	85 (96%)	4 (4%)	0	100	100
67	W2	63/102 (62%)	59 (94%)	4 (6%)	0	100	100
69	d1	46/137 (34%)	40 (87%)	6 (13%)	0	100	100
70	F1	157/190 (83%)	127 (81%)	27 (17%)	3 (2%)	8	14
71	Y1	87/132 (66%)	76 (87%)	10 (12%)	1 (1%)	14	25
72	G1	177/248 (71%)	134 (76%)	37 (21%)	6 (3%)	3	5
74	A1	192/245 (78%)	185 (96%)	7 (4%)	0	100	100
All	All	9329/10892 (86%)	8754 (94%)	565 (6%)	10 (0%)	54	75

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
72	G1	103	ILE
72	G1	114	ALA
72	G1	106	CYS
70	F1	34	PHE
72	G1	65	GLN
72	G1	110	PRO
70	F1	71	LYS
70	F1	160	ALA
71	Y1	34	GLU
72	G1	77	GLN

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	
1	T1	78/115 (68%)	76 (97%)	2 (3%)	46	66
2	N1	123/130 (95%)	123 (100%)	0	100	100
3	J1	141/164 (86%)	140 (99%)	1 (1%)	84	89
4	D1	142/182 (78%)	142 (100%)	0	100	100
5	X1	113/114 (99%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	S1	112/131 (86%)	109 (97%)	3 (3%)	44	65
7	Q1	101/130 (78%)	101 (100%)	0	100	100
8	C1	176/201 (88%)	176 (100%)	0	100	100
9	B1	196/220 (89%)	195 (100%)	1 (0%)	88	92
10	b1	70/112 (62%)	70 (100%)	0	100	100
11	a1	90/103 (87%)	90 (100%)	0	100	100
12	V1	62/72 (86%)	62 (100%)	0	100	100
13	R1	81/123 (66%)	80 (99%)	1 (1%)	71	82
14	K1	73/119 (61%)	73 (100%)	0	100	100
15	I1	138/148 (93%)	138 (100%)	0	100	100
16	e1	30/58 (52%)	30 (100%)	0	100	100
17	H1	116/170 (68%)	115 (99%)	1 (1%)	78	87
18	n1	21/38 (55%)	21 (100%)	0	100	100
19	c1	49/57 (86%)	48 (98%)	1 (2%)	55	72
20	O1	91/113 (80%)	91 (100%)	0	100	100
21	W1	114/115 (99%)	114 (100%)	0	100	100
22	E1	225/232 (97%)	225 (100%)	0	100	100
23	L1	155/173 (90%)	153 (99%)	2 (1%)	69	81
24	U1	68/110 (62%)	68 (100%)	0	100	100
28	A2	189/192 (98%)	189 (100%)	0	100	100
29	B2	312/313 (100%)	312 (100%)	0	100	100
30	C2	261/263 (99%)	260 (100%)	1 (0%)	91	93
31	D2	210/242 (87%)	209 (100%)	1 (0%)	88	92
32	F2	184/204 (90%)	183 (100%)	1 (0%)	88	92
33	G2	159/198 (80%)	158 (99%)	1 (1%)	86	90
34	H2	160/164 (98%)	160 (100%)	0	100	100
35	I2	166/177 (94%)	166 (100%)	0	100	100
36	J2	137/149 (92%)	136 (99%)	1 (1%)	84	89
37	L2	159/197 (81%)	159 (100%)	0	100	100
38	M2	103/111 (93%)	102 (99%)	1 (1%)	76	85
39	N2	174/175 (99%)	173 (99%)	1 (1%)	86	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	O2	164/165 (99%)	164 (100%)	0	100	100
41	P2	130/139 (94%)	130 (100%)	0	100	100
42	Q2	154/155 (99%)	154 (100%)	0	100	100
43	R2	149/167 (89%)	144 (97%)	5 (3%)	37	58
44	S2	147/154 (96%)	146 (99%)	1 (1%)	84	89
45	T2	126/133 (95%)	126 (100%)	0	100	100
46	U2	87/153 (57%)	87 (100%)	0	100	100
47	V2	112/114 (98%)	111 (99%)	1 (1%)	78	87
48	X2	104/123 (85%)	104 (100%)	0	100	100
49	Y2	114/115 (99%)	114 (100%)	0	100	100
50	Z2	101/119 (85%)	101 (100%)	0	100	100
51	a2	126/127 (99%)	126 (100%)	0	100	100
52	b2	51/57 (90%)	51 (100%)	0	100	100
53	c2	84/92 (91%)	84 (100%)	0	100	100
54	d2	78/92 (85%)	78 (100%)	0	100	100
55	e2	112/120 (93%)	112 (100%)	0	100	100
56	f2	102/103 (99%)	102 (100%)	0	100	100
57	g2	87/100 (87%)	87 (100%)	0	100	100
58	h2	102/107 (95%)	102 (100%)	0	100	100
59	i2	72/78 (92%)	72 (100%)	0	100	100
60	j2	70/74 (95%)	70 (100%)	0	100	100
61	k2	56/68 (82%)	56 (100%)	0	100	100
62	l2	46/48 (96%)	45 (98%)	1 (2%)	52	70
63	m2	46/110 (42%)	45 (98%)	1 (2%)	52	70
64	o2	81/93 (87%)	81 (100%)	0	100	100
65	p2	71/73 (97%)	69 (97%)	2 (3%)	43	63
67	W2	58/92 (63%)	58 (100%)	0	100	100
69	d1	41/116 (35%)	40 (98%)	1 (2%)	49	68
70	F1	132/157 (84%)	123 (93%)	9 (7%)	16	28
71	Y1	77/113 (68%)	75 (97%)	2 (3%)	46	66
72	G1	153/213 (72%)	152 (99%)	1 (1%)	84	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
74	A1	168/217 (77%)	167 (99%)	1 (1%)	86	90
All	All	7980/9302 (86%)	7936 (99%)	44 (1%)	86	90

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	T1	91	HIS
1	T1	101	ARG
3	J1	126	HIS
6	S1	12	ARG
6	S1	16	ARG
6	S1	48	LYS
9	B1	99	ASN
13	R1	28	ASP
17	H1	113	SER
19	c1	6	ASN
23	L1	32	ARG
23	L1	111	ARG
30	C2	144	VAL
31	D2	70	LYS
32	F2	66	LYS
33	G2	90	ARG
36	J2	7	ASN
38	M2	60	GLN
39	N2	96	ARG
43	R2	8	LYS
43	R2	119	LEU
43	R2	151	LEU
43	R2	154	LYS
43	R2	165	LYS
44	S2	167	ARG
47	V2	14	LYS
62	l2	46	ARG
63	m2	91	GLN
65	p2	3	LYS
65	p2	80	ARG
69	d1	123	CYS
70	F1	23	LEU
70	F1	57	ARG
70	F1	58	LEU
70	F1	63	MET
70	F1	67	ARG

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Mol	Chain	Res	Type
70	F1	79	VAL
70	F1	125	VAL
70	F1	142	THR
70	F1	174	TYR
71	Y1	37	GLU
71	Y1	69	THR
72	G1	7	CYS
74	A1	38	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
3	J1	112	GLN
4	D1	168	HIS
7	Q1	101	GLN
8	C1	194	GLN
9	B1	81	ASN
9	B1	108	HIS
9	B1	232	HIS
13	R1	77	GLN
21	W1	18	GLN
21	W1	59	ASN
22	E1	69	ASN
29	B2	71	GLN
29	B2	162	HIS
29	B2	354	GLN
30	C2	210	ASN
30	C2	274	GLN
33	G2	62	ASN
35	I2	51	HIS
42	Q2	87	ASN
45	T2	75	GLN
45	T2	105	HIS
51	a2	86	GLN
70	F1	37	HIS
70	F1	68	ASN
70	F1	189	ASN
71	Y1	14	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	1	2419/2707 (89%)	410 (16%)	24 (0%)
26	3	116/120 (96%)	16 (13%)	2 (1%)
27	42	136/139 (97%)	35 (25%)	2 (1%)
66	w2	12/14 (85%)	4 (33%)	0
68	E	2/3 (66%)	1 (50%)	0
73	2	1329/1452 (91%)	304 (22%)	17 (1%)
All	All	4014/4435 (90%)	770 (19%)	45 (1%)

All (770) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	1	5	G
25	1	21	G
25	1	39	A
25	1	42	A
25	1	48	G
25	1	56	C
25	1	58	G
25	1	59	A
25	1	64	A
25	1	65	A
25	1	71	C
25	1	73	G
25	1	84	U
25	1	89	G
25	1	90	C
25	1	106	A
25	1	107	G
25	1	108	C
25	1	110	C
25	1	117	A
25	1	120	G
25	1	122	G
25	1	127	G
25	1	128	U
25	1	156	G
25	1	157	G
25	1	165	G
25	1	166	G
25	1	171	C
25	1	176	G
25	1	180	G
25	1	184	G

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Mol	Chain	Res	Type
25	1	185	C
25	1	186	A
25	1	187	A
25	1	188	G
25	1	192	C
25	1	198	G
25	1	201	G
25	1	219	C
25	1	222	G
25	1	239	U
25	1	248	A
25	1	250	G
25	1	280	G
25	1	288	A
25	1	301	C
25	1	313	OMG
25	1	321	U
25	1	326	A
25	1	327	G
25	1	341	C
25	1	347	A
25	1	348	A
25	1	349	A
25	1	350	G
25	1	351	A
25	1	375	C
25	1	376	C
25	1	377	G
25	1	378	C
25	1	383	C
25	1	396	A2M
25	1	400	A
25	1	407	A
25	1	424	A
25	1	428	C
25	1	429	G
25	1	431	G
25	1	448	A
25	1	458	A
25	1	459	G
25	1	460	A
25	1	461	C

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Mol	Chain	Res	Type
25	1	462	G
25	1	463	C
25	1	476	G
25	1	482	C
25	1	485	C
25	1	490	G
25	1	493	C
25	1	501	G
25	1	516	G
25	1	522	A
25	1	533	U
25	1	565	G
25	1	573	G
25	1	574	A
25	1	577	C
25	1	585	G
25	1	590	U
25	1	595	C
25	1	611	G
25	1	612	A
25	1	623	G
25	1	630	A
25	1	632	G
25	1	633	A
25	1	637	A
25	1	639	C
25	1	640	G
25	1	641	A
25	1	653	G
25	1	660	G
25	1	675	C
25	1	676	C
25	1	690	G
25	1	705	C
25	1	722	G
25	1	759	A
25	1	761	C
25	1	776	C
25	1	790	G
25	1	791	C
25	1	793	U
25	1	798	G

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Mol	Chain	Res	Type
25	1	800	G
25	1	801	G
25	1	803	G
25	1	804	G
25	1	806	C
25	1	807	G
25	1	808	A
25	1	813	G
25	1	826	G
25	1	840	G
25	1	853	G
25	1	868	A
25	1	869	C
25	1	889	C
25	1	906	G
25	1	907	C
25	1	908	G
25	1	911	G
25	1	912	G
25	1	915	G
25	1	989	G
25	1	990	G
25	1	992	C
25	1	1004	U
25	1	1006	G
25	1	1008	G
25	1	1012	G
25	1	1014	C
25	1	1015	G
25	1	1016	G
25	1	1017	A
25	1	1018	G
25	1	1029	G
25	1	1030	C
25	1	1031	G
25	1	1042	G
25	1	1045	C
25	1	1046	G
25	1	1047	C
25	1	1050	C
25	1	1061	C
25	1	1066	G

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Mol	Chain	Res	Type
25	1	1072	C
25	1	1074	G
25	1	1080	G
25	1	1106	C
25	1	1108	G
25	1	1118	G
25	1	1121	OMG
25	1	1124	C
25	1	1137	G
25	1	1149	C
25	1	1158	G
25	1	1164	A
25	1	1166	G
25	1	1167	G
25	1	1186	G
25	1	1203	G
25	1	1205	U
25	1	1230	A
25	1	1232	A
25	1	1236	G
25	1	1238	A
25	1	1241	G
25	1	1244	C
25	1	1246	U
25	1	1247	G
25	1	1248	C
25	1	1252	C
25	1	1253	C
25	1	1254	C
25	1	1256	U
25	1	1259	A
25	1	1261	C
25	1	1265	G
25	1	1277	A
25	1	1291	G
25	1	1292	G
25	1	1314	C
25	1	1322	C
25	1	1331	G
25	1	1337	C
25	1	1349	C
25	1	1358	G

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Mol	Chain	Res	Type
25	1	1380	A
25	1	1381	C
25	1	1382	G
25	1	1388	C
25	1	1405	G
25	1	1411	G
25	1	1418	G
25	1	1439	A
25	1	1452	C
25	1	1472	G
25	1	1473	A
25	1	1481	A
25	1	1487	C
25	1	1488	C
25	1	1502	U
25	1	1508	G
25	1	1509	C
25	1	1510	G
25	1	1515	C
25	1	1516	G
25	1	1537	G
25	1	1538	C
25	1	1565	G
25	1	1566	G
25	1	1588	G
25	1	1589	G
25	1	1599	G
25	1	1600	A
25	1	1606	C
25	1	1609	G
25	1	1610	G
25	1	1619	A
25	1	1628	U
25	1	1646	A
25	1	1647	G
25	1	1663	U
25	1	1675	A
25	1	1694	A
25	1	1696	C
25	1	1712	U
25	1	1719	A
25	1	1731	A

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Mol	Chain	Res	Type
25	1	1733	G
25	1	1736	G
25	1	1737	G
25	1	1739	A
25	1	1740	G
25	1	1742	A
25	1	1759	G
25	1	1760	G
25	1	1766	A
25	1	1767	A
25	1	1768	A2M
25	1	1769	U
25	1	1775	OMG
25	1	1791	C
25	1	1797	U
25	1	1800	A
25	1	1801	U
25	1	1802	G
25	1	1812	G
25	1	1821	U
25	1	1823	U
25	1	1852	C
25	1	1860	A
25	1	1861	C
25	1	1862	G
25	1	1872	C
25	1	1880	G
25	1	1884	C
25	1	1888	A
25	1	1889	A
25	1	1890	G
25	1	1891	A
25	1	1898	U
25	1	1905	G
25	1	1906	A
25	1	1908	OMU
25	1	1922	G
25	1	1931	G
25	1	1992	C
25	1	1999	C
25	1	2004	G
25	1	2007	C

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Mol	Chain	Res	Type
25	1	2011	C
25	1	2012	G
25	1	2016	A
25	1	2019	C
25	1	2029	G
25	1	2030	G
25	1	2037	G
25	1	2049	G
25	1	2050	C
25	1	2060	A
25	1	2075	U
25	1	2078	C
25	1	2079	A
25	1	2088	U
25	1	2091	G
25	1	2092	C
25	1	2096	G
25	1	2097	A
25	1	2098	C
25	1	2112	G
25	1	2113	G
25	1	2114	A
25	1	2117	A
25	1	2127	A
25	1	2137	G
25	1	2139	C
25	1	2151	G
25	1	2163	G
25	1	2175	G
25	1	2176	G
25	1	2185	A
25	1	2196	C
25	1	2200	G
25	1	2202	C
25	1	2213	G
25	1	2218	G
25	1	2222	G
25	1	2223	A
25	1	2224	A
25	1	2233	A
25	1	2236	G
25	1	2239	A

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Mol	Chain	Res	Type
25	1	2241	A
25	1	2243	C
25	1	2251	U
25	1	2264	C
25	1	2267	G
25	1	2269	A
25	1	2275	G
25	1	2282	U
25	1	2293	G
25	1	2294	A
25	1	2297	U
25	1	2309	A
25	1	2310	C
25	1	2321	C
25	1	2333	A
25	1	2345	U
25	1	2350	C
25	1	2355	C
25	1	2356	A
25	1	2357	A
25	1	2359	G
25	1	2363	C
25	1	2368	G
25	1	2372	G
25	1	2394	G
25	1	2401	U
25	1	2404	C
25	1	2411	G
25	1	2423	A
25	1	2429	C
25	1	2433	G
25	1	2434	G
25	1	2466	C
25	1	2468	C
25	1	2494	G
25	1	2504	C
25	1	2506	C
25	1	2508	G
25	1	2509	G
25	1	2514	G
25	1	2515	G
25	1	2519	C

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Mol	Chain	Res	Type
25	1	2528	C
25	1	2530	G
25	1	2531	C
25	1	2537	A
25	1	2545	C
25	1	2546	C
25	1	2556	G
25	1	2557	G
25	1	2564	C
25	1	2568	C
25	1	2573	G
25	1	2574	C
25	1	2575	C
25	1	2580	C
25	1	2581	C
25	1	2582	C
25	1	2583	C
25	1	2584	G
25	1	2585	U
25	1	2587	C
25	1	2591	C
25	1	2592	U
25	1	2593	G
25	1	2594	C
25	1	2596	C
25	1	2598	A
25	1	2599	G
25	1	2600	G
25	1	2608	C
25	1	2609	G
25	1	2614	G
25	1	2627	G
25	1	2628	C
25	1	2646	C
25	1	2652	G
25	1	2672	G
25	1	2678	C
25	1	2683	C
25	1	2688	A
25	1	2690	G
25	1	2691	C
25	1	2692	G

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Mol	Chain	Res	Type
26	3	13	C
26	3	19	G
26	3	23	A
26	3	37	G
26	3	38	U
26	3	39	U
26	3	54	G
26	3	65	A
26	3	73	C
26	3	77	U
26	3	101	A
26	3	107	G
26	3	108	G
26	3	111	G
26	3	115	A
26	3	117	C
27	42	7	C
27	42	9	C
27	42	12	C
27	42	13	G
27	42	24	C
27	42	30	G
27	42	33	C
27	42	35	G
27	42	36	C
27	42	40	G
27	42	49	G
27	42	51	C
27	42	52	G
27	42	60	A
27	42	63	C
27	42	64	G
27	42	69	G
27	42	73	A
27	42	74	C
27	42	76	C
27	42	79	C
27	42	80	C
27	42	86	G
27	42	87	A
27	42	100	C
27	42	104	A

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Mol	Chain	Res	Type
27	42	105	A
27	42	106	C
27	42	109	A
27	42	112	G
27	42	114	G
27	42	115	C
27	42	119	G
27	42	120	G
27	42	122	G
66	w2	2	G
66	w2	69	C
66	w2	70	G
66	w2	76	A
68	E	76	A
73	2	3	U
73	2	4	C
73	2	9	C
73	2	17	C
73	2	26	G
73	2	33	U
73	2	40	G
73	2	41	G
73	2	44	G
73	2	45	A
73	2	46	A
73	2	54	A
73	2	56	G
73	2	64	A
73	2	71	A
73	2	87	A2M
73	2	91	C
73	2	92	A
73	2	101	A
73	2	116	C
73	2	125	C
73	2	129	A
73	2	130	C
73	2	134	G
73	2	137	G
73	2	142	C
73	2	152	A
73	2	153	G

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Mol	Chain	Res	Type
73	2	154	A
73	2	155	C
73	2	158	G
73	2	161	C
73	2	162	G
73	2	170	G
73	2	171	G
73	2	172	G
73	2	173	C
73	2	176	C
73	2	177	C
73	2	186	G
73	2	193	G
73	2	198	A
73	2	202	A
73	2	203	C
73	2	204	G
73	2	205	G
73	2	214	G
73	2	223	G
73	2	228	C
73	2	229	A
73	2	230	C
73	2	234	G
73	2	241	C
73	2	245	C
73	2	249	G
73	2	250	C
73	2	263	C
73	2	264	G
73	2	271	G
73	2	272	G
73	2	273	C
73	2	282	A
73	2	289	G
73	2	290	A
73	2	292	U
73	2	302	G
73	2	308	G
73	2	312	G
73	2	313	A
73	2	314	C

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Mol	Chain	Res	Type
73	2	316	G
73	2	324	A
73	2	329	A
73	2	330	G
73	2	335	G
73	2	336	C
73	2	337	A
73	2	338	G
73	2	340	A
73	2	351	U
73	2	353	G
73	2	356	C
73	2	357	A
73	2	363	C
73	2	365	G
73	2	366	C
73	2	378	C
73	2	387	G
73	2	389	G
73	2	390	C
73	2	391	G
73	2	394	A
73	2	396	U
73	2	400	G
73	2	406	C
73	2	427	G
73	2	432	G
73	2	438	G
73	2	446	C
73	2	449	G
73	2	454	C
73	2	455	G
73	2	458	G
73	2	459	U
73	2	460	A
73	2	461	A
73	2	464	C
73	2	475	A
73	2	476	G
73	2	477	C
73	2	491	G
73	2	500	G

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Mol	Chain	Res	Type
73	2	501	A
73	2	503	A
73	2	504	C
73	2	506	C
73	2	519	C
73	2	520	C
73	2	521	C
73	2	527	C
73	2	534	G
73	2	540	G
73	2	545	G
73	2	546	C
73	2	554	A
73	2	555	G
73	2	562	U
73	2	566	C
73	2	569	G
73	2	570	C
73	2	578	G
73	2	579	A
73	2	582	G
73	2	588	C
73	2	589	G
73	2	594	C
73	2	595	G
73	2	600	G
73	2	601	C
73	2	602	C
73	2	603	G
73	2	604	C
73	2	605	G
73	2	606	G
73	2	608	A
73	2	614	G
73	2	615	A
73	2	625	G
73	2	628	G
73	2	629	G
73	2	633	A
73	2	650	A
73	2	651	C
73	2	659	A

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Mol	Chain	Res	Type
73	2	662	G
73	2	665	U
73	2	685	G
73	2	687	C
73	2	704	A
73	2	711	C
73	2	712	U
73	2	718	A
73	2	722	A
73	2	740	C
73	2	744	A
73	2	756	C
73	2	757	A
73	2	759	C
73	2	778	A
73	2	780	C
73	2	784	G
73	2	791	C
73	2	792	G
73	2	794	G
73	2	804	C
73	2	812	G
73	2	833	G
73	2	834	G
73	2	836	G
73	2	839	U
73	2	840	C
73	2	842	G
73	2	850	G
73	2	851	G
73	2	856	G
73	2	868	OMG
73	2	880	A
73	2	888	G
73	2	892	G
73	2	900	C
73	2	903	C
73	2	909	G
73	2	921	G
73	2	927	U
73	2	928	C
73	2	932	C

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Mol	Chain	Res	Type
73	2	934	C
73	2	936	A
73	2	938	G
73	2	942	G
73	2	943	C
73	2	984	C
73	2	1009	U
73	2	1010	G
73	2	1011	OMG
73	2	1014	C
73	2	1018	G
73	2	1022	C
73	2	1025	C
73	2	1027	A
73	2	1028	G
73	2	1041	G
73	2	1054	U
73	2	1055	U
73	2	1056	G
73	2	1057	C
73	2	1059	A
73	2	1061	A
73	2	1076	G
73	2	1080	G
73	2	1088	C
73	2	1089	G
73	2	1090	C
73	2	1096	G
73	2	1099	C
73	2	1102	C
73	2	1112	A
73	2	1119	C
73	2	1125	G
73	2	1126	A
73	2	1129	G
73	2	1131	A
73	2	1132	G
73	2	1139	G
73	2	1140	A
73	2	1146	U
73	2	1147	C
73	2	1160	C

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Mol	Chain	Res	Type
73	2	1162	G
73	2	1163	C
73	2	1167	C
73	2	1175	A
73	2	1190	C
73	2	1191	G
73	2	1192	G
73	2	1194	G
73	2	1196	C
73	2	1197	C
73	2	1200	G
73	2	1203	G
73	2	1204	A
73	2	1208	G
73	2	1225	G
73	2	1226	C
73	2	1227	C
73	2	1230	G
73	2	1236	G
73	2	1242	G
73	2	1244	A
73	2	1245	C
73	2	1254	G
73	2	1257	C
73	2	1261	7MG
73	2	1262	A
73	2	1269	U
73	2	1270	G
73	2	1280	G
73	2	1282	C
73	2	1283	C
73	2	1287	C
73	2	1293	G
73	2	1295	C
73	2	1305	C
73	2	1320	C
73	2	1321	A
73	2	1343	U
73	2	1344	G
73	2	1351	G
73	2	1356	G
73	2	1366	G

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Mol	Chain	Res	Type
73	2	1367	A
73	2	1374	A
73	2	1381	G
73	2	1384	A
73	2	1388	C
73	2	1389	C
73	2	1391	G
73	2	1393	G
73	2	1394	C
73	2	1406	A
73	2	1408	A
73	2	1409	A
73	2	1410	G
73	2	1413	G
73	2	1419	A
73	2	1422	U
73	2	1433	G
73	2	1436	C
73	2	1445	G
73	2	1446	G
73	2	1447	A
73	2	1448	U
73	2	1449	C
73	2	1452	U

All (45) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	1	218	G
25	1	325	A
25	1	348	A
25	1	492	G
25	1	573	G
25	1	576	G
25	1	589	C
25	1	632	G
25	1	675	C
25	1	790	G
25	1	807	G
25	1	1204	OMG
25	1	1247	G
25	1	1381	C

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Mol	Chain	Res	Type
25	1	1477	C
25	1	1487	C
25	1	1587	G
25	1	1860	A
25	1	1871	C
25	1	1905	G
25	1	2354	U
25	1	2530	G
25	1	2536	A
25	1	2595	C
26	3	38	U
26	3	107	G
27	42	103	G
27	42	114	G
73	2	8	U
73	2	204	G
73	2	329	A
73	2	365	G
73	2	589	G
73	2	593	C
73	2	596	G
73	2	600	G
73	2	603	G
73	2	835	A
73	2	850	G
73	2	941	C
73	2	1009	U
73	2	1118	G
73	2	1199	C
73	2	1203	G
73	2	1380	C

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

40 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
73	OMC	2	104	73	19,22,23	0.85	0	26,31,34	0.99	1 (3%)
25	OMG	1	1520	25	18,26,27	1.02	1 (5%)	19,38,41	1.20	3 (15%)
25	OMG	1	1882	25,75	18,26,27	1.02	1 (5%)	19,38,41	1.37	3 (15%)
73	MA6	2	1435	73	18,26,27	1.02	1 (5%)	19,38,41	3.68	2 (10%)
73	7MG	2	1261	73	22,26,27	3.75	10 (45%)	29,39,42	2.09	9 (31%)
25	OMG	1	1204	25	18,26,27	2.34	7 (38%)	19,38,41	1.86	7 (36%)
25	OMG	1	1775	25	18,26,27	2.30	8 (44%)	19,38,41	1.46	3 (15%)
25	OMG	1	2074	25	18,26,27	2.30	7 (38%)	19,38,41	1.41	3 (15%)
25	A2M	1	1768	25	18,25,26	3.64	8 (44%)	18,36,39	3.47	6 (33%)
25	OMU	1	1897	25,75	19,22,23	2.90	7 (36%)	26,31,34	1.77	4 (15%)
25	OMC	1	2380	25	19,22,23	2.82	8 (42%)	26,31,34	0.89	1 (3%)
73	A2M	2	87	73,75	18,25,26	3.66	7 (38%)	18,36,39	3.28	4 (22%)
73	OMU	2	1314	73	19,22,23	2.90	8 (42%)	26,31,34	1.74	5 (19%)
27	OMG	42	133	27,25	18,26,27	2.34	8 (44%)	19,38,41	1.36	4 (21%)
25	A2M	1	396	25,75	18,25,26	0.95	1 (5%)	18,36,39	1.27	2 (11%)
73	M7A	2	1390	73	20,25,26	0.42	0	28,37,40	0.69	1 (3%)
25	A2M	1	393	25	18,25,26	3.56	8 (44%)	18,36,39	3.24	4 (22%)
25	OMC	1	1824	25	19,22,23	0.79	0	26,31,34	1.19	1 (3%)
73	A2M	2	348	76,73	18,25,26	3.62	8 (44%)	18,36,39	3.39	3 (16%)
25	OMG	1	313	25	18,26,27	2.33	8 (44%)	19,38,41	1.51	3 (15%)
25	OMG	1	2237	25,75	18,26,27	1.05	1 (5%)	19,38,41	1.06	2 (10%)
73	OMG	2	371	73	18,26,27	1.08	1 (5%)	19,38,41	1.35	3 (15%)
25	OMU	1	1896	25,75	19,22,23	2.89	8 (42%)	26,31,34	1.75	5 (19%)
25	OMU	1	49	25,75	19,22,23	2.94	7 (36%)	26,31,34	1.71	6 (23%)
25	A2M	1	523	25	18,25,26	3.54	8 (44%)	18,36,39	3.47	4 (22%)
25	OMG	1	624	25,75	18,26,27	2.33	7 (38%)	19,38,41	1.70	5 (26%)
73	4AC	2	1426	73,75	21,24,25	4.44	16 (76%)	29,34,37	1.37	3 (10%)
73	MA6	2	1434	73	18,26,27	1.04	1 (5%)	19,38,41	3.44	2 (10%)
25	OMC	1	1684	25,75	19,22,23	2.75	7 (36%)	26,31,34	0.97	1 (3%)
73	OMG	2	1035	73,75	18,26,27	2.44	8 (44%)	19,38,41	1.64	4 (21%)
25	OMU	1	1908	25	19,22,23	4.24	15 (78%)	26,31,34	1.92	7 (26%)
73	OMG	2	868	73	18,26,27	2.35	8 (44%)	19,38,41	1.40	2 (10%)
25	5MC	1	1765	25	18,22,23	3.26	7 (38%)	26,32,35	1.10	3 (11%)
25	OMG	1	1121	25	18,26,27	1.04	1 (5%)	19,38,41	1.45	3 (15%)
25	5MC	1	2292	25,75	18,22,23	3.36	7 (38%)	26,32,35	1.29	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
73	OMG	2	1011	73	18,26,27	1.00	1 (5%)	19,38,41	1.18	3 (15%)
73	C4J	2	933	73	24,29,30	3.35	9 (37%)	29,42,45	1.35	4 (13%)
25	OMG	1	386	25	18,26,27	0.98	1 (5%)	19,38,41	1.12	3 (15%)
25	OMG	1	2042	25,68	18,26,27	2.33	8 (44%)	19,38,41	1.41	3 (15%)
73	4OC	2	1325	73	20,23,24	3.04	8 (40%)	26,32,35	0.96	1 (3%)

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
73	OMC	2	104	73	-	1/9/27/28	0/2/2/2
25	OMG	1	1520	25	-	1/5/27/28	0/3/3/3
25	OMG	1	1882	25,75	-	0/5/27/28	0/3/3/3
73	MA6	2	1435	73	-	3/7/29/30	0/3/3/3
73	7MG	2	1261	73	-	0/7/37/38	0/3/3/3
25	OMG	1	1204	25	-	0/5/27/28	0/3/3/3
25	OMG	1	1775	25	-	2/5/27/28	0/3/3/3
25	OMG	1	2074	25	-	1/5/27/28	0/3/3/3
25	A2M	1	1768	25	-	2/5/27/28	0/3/3/3
25	OMU	1	1897	25,75	-	0/9/27/28	0/2/2/2
25	OMC	1	2380	25	-	0/9/27/28	0/2/2/2
73	A2M	2	87	73,75	-	3/5/27/28	0/3/3/3
73	OMU	2	1314	73	-	0/9/27/28	0/2/2/2
27	OMG	42	133	27,25	-	0/5/27/28	0/3/3/3
25	A2M	1	396	25,75	-	1/5/27/28	0/3/3/3
73	M7A	2	1390	73	-	2/7/37/38	0/3/3/3
25	A2M	1	393	25	-	0/5/27/28	0/3/3/3
25	OMC	1	1824	25	-	1/9/27/28	0/2/2/2
73	A2M	2	348	76,73	-	0/5/27/28	0/3/3/3
25	OMG	1	313	25	-	2/5/27/28	0/3/3/3
25	OMG	1	2237	25,75	-	0/5/27/28	0/3/3/3
73	OMG	2	371	73	-	1/5/27/28	0/3/3/3
25	OMU	1	1896	25,75	-	0/9/27/28	0/2/2/2
25	OMU	1	49	25,75	-	1/9/27/28	0/2/2/2
25	A2M	1	523	25	-	1/5/27/28	0/3/3/3
25	OMG	1	624	25,75	-	1/5/27/28	0/3/3/3
73	4AC	2	1426	73,75	-	2/11/29/30	0/2/2/2
73	MA6	2	1434	73	-	0/7/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	OMC	1	1684	25,75	-	4/9/27/28	0/2/2/2
73	OMG	2	1035	73,75	-	1/5/27/28	0/3/3/3
25	OMU	1	1908	25	-	2/9/27/28	0/2/2/2
73	OMG	2	868	73	-	3/5/27/28	0/3/3/3
25	5MC	1	1765	25	-	0/7/25/26	0/2/2/2
25	OMG	1	1121	25	-	2/5/27/28	0/3/3/3
25	5MC	1	2292	25,75	-	4/7/25/26	0/2/2/2
73	OMG	2	1011	73	-	1/5/27/28	0/3/3/3
73	C4J	2	933	73	-	6/16/34/35	0/2/2/2
25	OMG	1	386	25	-	0/5/27/28	0/3/3/3
25	OMG	1	2042	25,68	-	0/5/27/28	0/3/3/3
73	4OC	2	1325	73	-	0/9/29/30	0/2/2/2

All (235) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
73	2	933	C4J	C6-C5	12.11	1.52	1.34
25	1	1908	OMU	C3'-C2'	-10.39	1.29	1.52
25	1	2292	5MC	C6-C5	8.97	1.49	1.34
25	1	523	A2M	C3'-C4'	-8.76	1.30	1.53
73	2	87	A2M	C3'-C4'	-8.73	1.30	1.53
73	2	1426	4AC	O4'-C1'	8.71	1.62	1.42
25	1	393	A2M	C3'-C4'	-8.68	1.30	1.53
73	2	1261	7MG	C8-N9	8.64	1.50	1.46
25	1	1765	5MC	C6-C5	8.56	1.48	1.34
73	2	348	A2M	C3'-C4'	-8.42	1.31	1.53
25	1	1768	A2M	C3'-C4'	-8.40	1.31	1.53
73	2	87	A2M	O4'-C4'	8.05	1.63	1.45
25	1	1768	A2M	O4'-C1'	-7.76	1.30	1.41
73	2	1261	7MG	C5-N7	7.71	1.44	1.35
73	2	348	A2M	O4'-C4'	7.66	1.62	1.45
73	2	348	A2M	O4'-C1'	-7.55	1.30	1.41
25	1	393	A2M	O4'-C4'	7.49	1.61	1.45
25	1	1768	A2M	O4'-C4'	7.36	1.61	1.45
25	1	523	A2M	O4'-C1'	-7.36	1.30	1.41
73	2	87	A2M	O4'-C1'	-7.13	1.31	1.41
25	1	523	A2M	O4'-C4'	7.10	1.60	1.45
25	1	393	A2M	O4'-C1'	-7.10	1.31	1.41
25	1	1896	OMU	C2-N1	7.05	1.49	1.38
25	1	1897	OMU	C2-N1	6.93	1.49	1.38
73	2	1426	4AC	C4-N3	6.90	1.44	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
73	2	1426	4AC	C2'-C1'	-6.79	1.31	1.53
25	1	49	OMU	C2-N1	6.75	1.49	1.38
73	2	1426	4AC	C6-C5	6.74	1.50	1.35
73	2	1325	4OC	C4-N3	6.69	1.44	1.32
73	2	1314	OMU	C2-N1	6.60	1.49	1.38
73	2	1314	OMU	C2-N3	6.49	1.49	1.38
25	1	1908	OMU	C2-N1	6.32	1.48	1.38
25	1	49	OMU	C2-N3	6.32	1.49	1.38
73	2	933	C4J	C2-N3	6.26	1.49	1.38
25	1	1896	OMU	C2-N3	6.14	1.48	1.38
73	2	1261	7MG	C2-N3	5.99	1.47	1.33
73	2	1325	4OC	C6-C5	5.97	1.48	1.35
25	1	2380	OMC	C6-C5	5.97	1.48	1.35
25	1	1897	OMU	C2-N3	5.96	1.48	1.38
73	2	1261	7MG	C4-N9	5.90	1.44	1.37
25	1	1908	OMU	C2-N3	5.71	1.48	1.38
73	2	1325	4OC	C2-N3	5.65	1.47	1.36
25	1	2380	OMC	C2-N3	5.60	1.47	1.36
73	2	1261	7MG	C4-N3	5.59	1.47	1.34
25	1	1684	OMC	C2-N3	5.59	1.47	1.36
25	1	1684	OMC	C6-C5	5.59	1.48	1.35
25	1	49	OMU	C6-C5	5.51	1.47	1.35
25	1	2292	5MC	C4-N3	5.39	1.43	1.34
25	1	1765	5MC	C4-N3	5.39	1.43	1.34
25	1	2042	OMG	C2-N3	5.35	1.46	1.33
25	1	1765	5MC	C2-N3	5.31	1.47	1.36
73	2	1035	OMG	C2-N3	5.30	1.46	1.33
27	42	133	OMG	C2-N3	5.29	1.46	1.33
73	2	1426	4AC	C2-N1	5.28	1.51	1.40
73	2	1314	OMU	C6-C5	5.28	1.47	1.35
25	1	624	OMG	C2-N3	5.27	1.46	1.33
25	1	1908	OMU	C6-C5	5.26	1.47	1.35
25	1	1896	OMU	C6-C5	5.23	1.47	1.35
25	1	1897	OMU	C6-C5	5.22	1.47	1.35
25	1	2292	5MC	C2-N3	5.18	1.46	1.36
25	1	1775	OMG	C2-N3	5.09	1.45	1.33
73	2	868	OMG	C2-N3	5.02	1.45	1.33
73	2	1261	7MG	C2-N2	4.98	1.46	1.34
73	2	1426	4AC	C2-N3	4.94	1.46	1.36
25	1	1204	OMG	C2-N3	4.88	1.45	1.33
73	2	1426	4AC	O4'-C4'	-4.86	1.34	1.45
25	1	313	OMG	C2-N3	4.83	1.44	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
73	2	1426	4AC	C7-N4	4.76	1.46	1.37
73	2	1325	4OC	C4-N4	4.69	1.45	1.35
25	1	2074	OMG	C2-N3	4.68	1.44	1.33
25	1	1908	OMU	O4'-C1'	-4.68	1.30	1.42
25	1	1908	OMU	O4'-C4'	4.67	1.55	1.45
25	1	1684	OMC	C4-N3	4.65	1.43	1.34
25	1	2042	OMG	C4-N3	4.62	1.48	1.37
25	1	2074	OMG	C4-N3	4.61	1.48	1.37
25	1	2380	OMC	C4-N4	4.58	1.44	1.33
25	1	624	OMG	C4-N3	4.48	1.48	1.37
25	1	2292	5MC	C6-N1	4.47	1.45	1.38
27	42	133	OMG	C4-N3	4.47	1.48	1.37
73	2	1035	OMG	C4-N3	4.41	1.48	1.37
25	1	313	OMG	C4-N3	4.40	1.48	1.37
73	2	1426	4AC	C4-N4	4.38	1.46	1.39
25	1	1775	OMG	C4-N3	4.31	1.47	1.37
25	1	2380	OMC	C4-N3	4.29	1.43	1.34
25	1	1684	OMC	C4-N4	4.24	1.43	1.33
73	2	868	OMG	C4-N3	4.20	1.47	1.37
25	1	2380	OMC	C2-N1	4.18	1.49	1.40
25	1	1204	OMG	C4-N3	4.16	1.47	1.37
25	1	1765	5MC	C6-N1	4.09	1.45	1.38
73	2	868	OMG	C2-N2	4.09	1.43	1.34
25	1	2292	5MC	C2-N1	4.06	1.48	1.40
25	1	1908	OMU	O4-C4	-4.03	1.16	1.24
73	2	1261	7MG	C2-N1	3.95	1.47	1.37
73	2	1325	4OC	C2-N1	3.94	1.48	1.40
25	1	1684	OMC	C2-N1	3.94	1.48	1.40
73	2	1426	4AC	C5-C4	3.94	1.49	1.40
73	2	1035	OMG	C2-N2	3.87	1.43	1.34
73	2	933	C4J	C6-N1	3.86	1.46	1.36
73	2	1314	OMU	C4-N3	3.85	1.45	1.38
25	1	1765	5MC	C4-N4	3.80	1.44	1.34
25	1	1768	A2M	O3'-C3'	3.78	1.51	1.43
25	1	1204	OMG	C2-N2	3.75	1.43	1.34
73	2	933	C4J	C2-N1	3.75	1.50	1.39
25	1	1775	OMG	C2-N2	3.74	1.43	1.34
25	1	2042	OMG	C2-N2	3.73	1.43	1.34
27	42	133	OMG	C2-N2	3.72	1.43	1.34
25	1	1908	OMU	C2'-C1'	3.71	1.62	1.53
73	2	1426	4AC	O3'-C3'	-3.69	1.34	1.43
25	1	2292	5MC	C4-N4	3.69	1.43	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	1	1765	5MC	C2-N1	3.69	1.48	1.40
25	1	1897	OMU	C4-N3	3.67	1.45	1.38
73	2	933	C4J	C1'-C5	-3.67	1.41	1.50
25	1	1765	5MC	O2-C2	-3.66	1.16	1.23
25	1	2292	5MC	O2-C2	-3.64	1.17	1.23
73	2	1035	OMG	C6-N1	3.64	1.43	1.37
25	1	49	OMU	O4-C4	-3.61	1.17	1.24
25	1	1896	OMU	O4-C4	-3.58	1.17	1.24
25	1	1897	OMU	O4-C4	-3.54	1.17	1.24
25	1	1908	OMU	C5'-C4'	-3.53	1.40	1.51
25	1	624	OMG	C2-N2	3.51	1.42	1.34
25	1	1684	OMC	O2-C2	-3.48	1.17	1.23
73	2	1325	4OC	C5-C4	3.48	1.48	1.40
73	2	1261	7MG	C5-C6	3.47	1.52	1.43
73	2	1426	4AC	CM7-C7	3.45	1.57	1.50
25	1	49	OMU	C4-N3	3.43	1.44	1.38
25	1	313	OMG	C2-N2	3.41	1.42	1.34
25	1	2074	OMG	C2-N2	3.38	1.42	1.34
73	2	1325	4OC	O2-C2	-3.36	1.17	1.23
25	1	313	OMG	O6-C6	-3.31	1.16	1.23
73	2	933	C4J	C4-N3	3.28	1.46	1.40
25	1	1204	OMG	C6-N1	3.27	1.42	1.37
73	2	1314	OMU	O4-C4	-3.25	1.18	1.24
25	1	1908	OMU	O2-C2	-3.23	1.17	1.23
27	42	133	OMG	C6-N1	3.22	1.42	1.37
73	2	868	OMG	O6-C6	-3.21	1.16	1.23
25	1	49	OMU	O2-C2	-3.21	1.17	1.23
25	1	1897	OMU	O2-C2	-3.21	1.17	1.23
25	1	1896	OMU	C4-N3	3.18	1.44	1.38
73	2	348	A2M	O3'-C3'	3.17	1.50	1.43
25	1	2380	OMC	O2-C2	-3.14	1.17	1.23
25	1	2074	OMG	C6-N1	3.14	1.42	1.37
25	1	2380	OMC	C6-N1	3.12	1.45	1.38
73	2	1325	4OC	C6-N1	3.11	1.45	1.38
73	2	1426	4AC	O5'-C5'	-3.11	1.37	1.44
73	2	933	C4J	O4-C4	-3.10	1.16	1.23
25	1	2074	OMG	O6-C6	-3.09	1.17	1.23
25	1	1908	OMU	C4-N3	3.09	1.44	1.38
25	1	1204	OMG	C5-C4	-3.08	1.35	1.43
73	2	868	OMG	C6-N1	3.06	1.42	1.37
25	1	2237	OMG	C6-N1	-3.06	1.33	1.37
73	2	1035	OMG	C5-C4	-3.03	1.35	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
73	2	348	A2M	C6-N6	3.03	1.45	1.34
25	1	1684	OMC	C6-N1	3.02	1.45	1.38
25	1	1768	A2M	C5-C4	-3.02	1.33	1.40
73	2	1261	7MG	C6-N1	3.00	1.44	1.38
25	1	523	A2M	C6-N6	2.99	1.45	1.34
25	1	313	OMG	C5-C4	-2.99	1.35	1.43
73	2	87	A2M	C6-N6	2.99	1.45	1.34
25	1	313	OMG	C6-N1	2.96	1.42	1.37
25	1	1775	OMG	O6-C6	-2.94	1.17	1.23
25	1	624	OMG	C6-N1	2.93	1.42	1.37
73	2	87	A2M	O3'-C3'	2.88	1.49	1.43
73	2	1426	4AC	O2'-C2'	2.88	1.49	1.43
73	2	1035	OMG	O6-C6	-2.88	1.17	1.23
25	1	624	OMG	C5-C4	-2.87	1.35	1.43
25	1	1204	OMG	O6-C6	-2.87	1.17	1.23
25	1	393	A2M	C5-C4	-2.86	1.33	1.40
25	1	1882	OMG	C6-N1	-2.86	1.33	1.37
25	1	2042	OMG	O6-C6	-2.86	1.17	1.23
73	2	1434	MA6	C5-C4	-2.85	1.33	1.40
25	1	2074	OMG	C5-C4	-2.85	1.35	1.43
25	1	523	A2M	O3'-C3'	2.85	1.49	1.43
73	2	933	C4J	O4'-C1'	-2.84	1.39	1.43
25	1	624	OMG	C5-C6	2.84	1.53	1.47
25	1	1775	OMG	C5-C4	-2.82	1.35	1.43
25	1	1896	OMU	O2-C2	-2.82	1.17	1.23
73	2	1426	4AC	O7-C7	-2.82	1.16	1.23
25	1	313	OMG	C5-C6	2.81	1.53	1.47
25	1	1204	OMG	C5-C6	2.80	1.53	1.47
73	2	87	A2M	C5-C4	-2.78	1.33	1.40
73	2	1435	MA6	C5-C4	-2.78	1.33	1.40
25	1	2074	OMG	C5-C6	2.77	1.53	1.47
25	1	393	A2M	O2'-C2'	-2.76	1.35	1.42
25	1	386	OMG	C6-N1	-2.75	1.33	1.37
25	1	1768	A2M	C6-N6	2.73	1.44	1.34
25	1	1520	OMG	C6-N1	-2.72	1.33	1.37
25	1	1908	OMU	C6-N1	2.72	1.44	1.38
73	2	1314	OMU	O2-C2	-2.72	1.18	1.23
73	2	1314	OMU	C6-N1	2.69	1.44	1.38
25	1	624	OMG	O6-C6	-2.69	1.17	1.23
25	1	2042	OMG	C5-C6	2.69	1.52	1.47
25	1	49	OMU	C6-N1	2.69	1.44	1.38
25	1	1121	OMG	C6-N1	-2.68	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
73	2	348	A2M	O2'-C2'	-2.68	1.35	1.42
25	1	1896	OMU	C6-N1	2.68	1.44	1.38
73	2	348	A2M	C5-C4	-2.67	1.33	1.40
25	1	393	A2M	C6-N6	2.66	1.43	1.34
27	42	133	OMG	O6-C6	-2.66	1.17	1.23
73	2	371	OMG	C6-N1	-2.65	1.33	1.37
73	2	868	OMG	C2-N1	2.65	1.44	1.37
25	1	1908	OMU	O5'-C5'	-2.65	1.38	1.44
73	2	1261	7MG	O6-C6	-2.62	1.18	1.23
25	1	1908	OMU	O3'-C3'	2.62	1.49	1.43
73	2	87	A2M	O2'-C2'	-2.61	1.35	1.42
27	42	133	OMG	C5-C4	-2.61	1.36	1.43
25	1	2042	OMG	C6-N1	2.61	1.41	1.37
73	2	1011	OMG	C6-N1	-2.59	1.34	1.37
25	1	1768	A2M	O2'-C2'	-2.57	1.36	1.42
25	1	523	A2M	O2'-C2'	-2.56	1.36	1.42
25	1	523	A2M	C5-C4	-2.55	1.34	1.40
25	1	2042	OMG	C5-C4	-2.53	1.36	1.43
25	1	1897	OMU	C6-N1	2.53	1.44	1.38
25	1	1775	OMG	C6-N1	2.51	1.41	1.37
73	2	1426	4AC	C6-N1	2.51	1.44	1.38
27	42	133	OMG	C5-C6	2.50	1.52	1.47
73	2	1035	OMG	C5-C6	2.48	1.52	1.47
25	1	393	A2M	O3'-C3'	2.47	1.48	1.43
25	1	396	A2M	C5-C4	2.41	1.47	1.40
73	2	868	OMG	C5-C4	-2.40	1.37	1.43
25	1	1775	OMG	C5-C6	2.38	1.52	1.47
73	2	933	C4J	O2-C2	-2.34	1.18	1.22
73	2	1035	OMG	C2-N1	2.33	1.43	1.37
25	1	2380	OMC	C5-C4	2.31	1.48	1.42
25	1	1775	OMG	C2-N1	2.31	1.43	1.37
25	1	313	OMG	C2-N1	2.29	1.43	1.37
73	2	868	OMG	C5-C6	2.24	1.52	1.47
27	42	133	OMG	C2-N1	2.20	1.43	1.37
25	1	1908	OMU	C5-C4	2.18	1.48	1.43
25	1	523	A2M	O5'-C5'	-2.13	1.39	1.44
25	1	1896	OMU	C5-C4	2.12	1.48	1.43
73	2	1314	OMU	C5-C4	2.10	1.48	1.43
25	1	1768	A2M	O5'-C5'	-2.06	1.39	1.44
73	2	348	A2M	C2-N3	2.05	1.35	1.32
25	1	2042	OMG	C2-N1	2.01	1.42	1.37
25	1	393	A2M	O5'-C5'	-2.01	1.39	1.44

All (136) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	2	1435	MA6	N1-C6-N6	-14.68	101.61	117.06
73	2	1434	MA6	N1-C6-N6	-13.78	102.55	117.06
25	1	523	A2M	C5-C6-N6	10.88	136.88	120.35
73	2	348	A2M	C5-C6-N6	10.56	136.40	120.35
73	2	87	A2M	C5-C6-N6	10.32	136.03	120.35
25	1	1768	A2M	C5-C6-N6	10.24	135.91	120.35
25	1	393	A2M	C5-C6-N6	9.77	135.21	120.35
25	1	1768	A2M	N6-C6-N1	-7.28	103.47	118.57
73	2	348	A2M	N6-C6-N1	-7.27	103.49	118.57
25	1	523	A2M	N6-C6-N1	-7.26	103.50	118.57
25	1	393	A2M	N6-C6-N1	-6.89	104.27	118.57
73	2	87	A2M	N6-C6-N1	-6.75	104.57	118.57
25	1	1768	A2M	N3-C2-N1	-5.69	119.79	128.68
25	1	523	A2M	N3-C2-N1	-5.51	120.07	128.68
73	2	1435	MA6	N3-C2-N1	-5.48	120.12	128.68
73	2	1314	OMU	C4-N3-C2	-5.44	119.40	126.58
25	1	1897	OMU	C4-N3-C2	-5.38	119.49	126.58
25	1	393	A2M	N3-C2-N1	-5.37	120.28	128.68
73	2	348	A2M	N3-C2-N1	-5.35	120.31	128.68
73	2	1434	MA6	N3-C2-N1	-5.23	120.50	128.68
73	2	1261	7MG	C5-C6-N1	5.20	120.16	110.99
73	2	87	A2M	N3-C2-N1	-5.11	120.69	128.68
25	1	1896	OMU	C4-N3-C2	-5.02	119.95	126.58
25	1	49	OMU	C4-N3-C2	-4.83	120.21	126.58
25	1	1908	OMU	C4-N3-C2	-4.70	120.38	126.58
73	2	1261	7MG	C2-N3-C4	4.64	120.56	112.30
25	1	49	OMU	N3-C2-N1	4.39	120.72	114.89
73	2	1261	7MG	C5-C4-N3	-4.27	119.99	128.13
25	1	1824	OMC	C2'-C1'-N1	-4.20	106.06	114.22
25	1	1908	OMU	N3-C2-N1	4.02	120.23	114.89
25	1	1896	OMU	N3-C2-N1	3.86	120.02	114.89
73	2	933	C4J	C4-N3-C2	-3.84	120.61	125.46
25	1	1897	OMU	N3-C2-N1	3.77	119.90	114.89
73	2	1314	OMU	C5-C4-N3	3.76	120.47	114.84
25	1	1897	OMU	C5-C4-N3	3.73	120.42	114.84
25	1	1896	OMU	C5-C4-N3	3.65	120.30	114.84
73	2	1035	OMG	C5-C6-N1	3.63	120.36	113.95
73	2	1314	OMU	N3-C2-N1	3.56	119.62	114.89
25	1	2292	5MC	C5-C6-N1	-3.55	119.68	123.34
25	1	1204	OMG	C5-C6-N1	3.49	120.11	113.95
25	1	1775	OMG	C5-C6-N1	3.38	119.92	113.95
25	1	313	OMG	C5-C6-N1	3.29	119.77	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	1	2042	OMG	C5-C6-N1	3.24	119.68	113.95
73	2	1035	OMG	C2-N1-C6	-3.24	119.13	125.10
73	2	868	OMG	C5-C6-N1	3.21	119.62	113.95
25	1	1897	OMU	O4-C4-C5	-3.18	119.57	125.16
25	1	2074	OMG	C5-C6-N1	3.17	119.55	113.95
25	1	624	OMG	C5-C6-N1	3.17	119.55	113.95
25	1	393	A2M	C1'-N9-C4	3.17	132.21	126.64
73	2	1314	OMU	O4-C4-C5	-3.15	119.63	125.16
25	1	396	A2M	N3-C2-N1	-3.12	123.80	128.68
25	1	1908	OMU	C5-C4-N3	3.09	119.47	114.84
25	1	1775	OMG	C2-N1-C6	-3.05	119.48	125.10
27	42	133	OMG	C5-C6-N1	3.04	119.32	113.95
73	2	1261	7MG	C4-C5-N7	3.02	109.72	105.53
25	1	1121	OMG	O2'-C2'-C1'	3.01	115.06	109.09
73	2	371	OMG	O2'-C2'-C1'	-3.01	103.13	109.09
73	2	1426	4AC	C5'-C4'-C3'	-3.01	103.92	115.18
73	2	87	A2M	C1'-N9-C4	2.99	131.90	126.64
25	1	624	OMG	C8-N7-C5	2.98	108.68	102.99
25	1	313	OMG	C8-N7-C5	2.98	108.67	102.99
25	1	1204	OMG	C8-N7-C5	2.94	108.60	102.99
25	1	1204	OMG	C2-N1-C6	-2.94	119.69	125.10
73	2	1261	7MG	N9-C4-N3	2.93	129.85	125.47
73	2	1261	7MG	C5-C4-N9	2.93	110.15	106.35
25	1	1882	OMG	C8-N7-C5	2.90	108.51	102.99
73	2	1035	OMG	C8-N7-C5	2.89	108.50	102.99
25	1	2042	OMG	C2-N1-C6	-2.87	119.81	125.10
73	2	1261	7MG	C2-N1-C6	-2.86	119.88	125.10
25	1	624	OMG	C2-N1-C6	-2.86	119.84	125.10
25	1	1765	5MC	C5-C6-N1	-2.85	120.41	123.34
25	1	49	OMU	C5-C4-N3	2.83	119.07	114.84
73	2	104	OMC	C2'-C1'-N1	-2.82	108.76	114.22
25	1	2074	OMG	C8-N7-C5	2.80	108.32	102.99
73	2	1261	7MG	O6-C6-C5	-2.76	120.76	127.54
25	1	1896	OMU	O4-C4-C5	-2.76	120.31	125.16
25	1	1204	OMG	O3'-C3'-C4'	2.75	119.00	111.05
25	1	624	OMG	O2'-C2'-C1'	2.74	114.53	109.09
25	1	396	A2M	C4-C5-N7	-2.71	106.57	109.40
25	1	1775	OMG	C8-N7-C5	2.71	108.15	102.99
25	1	2074	OMG	C2-N1-C6	-2.71	120.11	125.10
25	1	1908	OMU	O4'-C4'-C3'	-2.71	99.76	105.11
25	1	313	OMG	C2-N1-C6	-2.70	120.12	125.10
25	1	2042	OMG	C8-N7-C5	2.68	108.09	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	1	1204	OMG	O3'-C3'-C2'	2.67	118.75	111.17
25	1	386	OMG	C5-C6-N1	2.63	118.59	113.95
27	42	133	OMG	C2-N1-C6	-2.59	120.32	125.10
73	2	1426	4AC	O2-C2-N3	-2.58	118.14	122.33
25	1	1882	OMG	C5-C6-N1	2.56	118.48	113.95
73	2	1325	4OC	C6-C5-C4	2.55	120.08	116.96
25	1	1121	OMG	C8-N7-C5	2.52	107.78	102.99
25	1	1908	OMU	O4'-C4'-C5'	2.52	117.65	109.37
73	2	1011	OMG	C5-C6-N1	2.50	118.37	113.95
27	42	133	OMG	C8-N7-C5	2.50	107.75	102.99
25	1	1520	OMG	C5-C6-N1	2.48	118.34	113.95
25	1	1765	5MC	CM5-C5-C6	-2.48	119.53	122.85
73	2	868	OMG	C2-N1-C6	-2.48	120.53	125.10
25	1	2237	OMG	C8-N7-C5	2.42	107.60	102.99
25	1	1121	OMG	C5-C6-N1	2.41	118.21	113.95
25	1	49	OMU	O4-C4-C5	-2.41	120.93	125.16
25	1	1896	OMU	C1'-N1-C2	2.40	121.91	117.57
25	1	386	OMG	C8-N7-C5	2.39	107.54	102.99
25	1	1765	5MC	O2-C2-N3	-2.39	118.45	122.33
73	2	371	OMG	C5-C6-N1	2.39	118.16	113.95
73	2	1426	4AC	C5-C4-N3	-2.38	118.76	122.59
25	1	1520	OMG	C8-N7-C5	2.37	107.50	102.99
25	1	2237	OMG	C5-C6-N1	2.36	118.12	113.95
73	2	933	C4J	O35-C34-C32	2.35	121.38	113.38
25	1	2292	5MC	C1'-N1-C6	2.33	125.00	121.12
25	1	1768	A2M	O2'-C2'-C1'	2.31	113.68	109.09
73	2	1035	OMG	O6-C6-C5	-2.31	119.86	124.37
73	2	1011	OMG	C8-N7-C5	2.31	107.39	102.99
25	1	1908	OMU	O4'-C1'-N1	2.30	113.61	108.36
25	1	1768	A2M	O3'-C3'-C4'	2.29	117.67	111.05
25	1	2292	5MC	O2-C2-N3	-2.29	118.61	122.33
25	1	49	OMU	C6-N1-C2	-2.28	118.07	120.99
73	2	371	OMG	C8-N7-C5	2.27	107.31	102.99
73	2	1261	7MG	N9-C8-N7	2.24	106.59	103.38
73	2	933	C4J	C5-C4-N3	2.22	120.29	116.17
25	1	1882	OMG	C5'-C4'-C3'	-2.21	106.91	115.18
25	1	624	OMG	CM2-O2'-C2'	2.20	120.30	114.52
25	1	1768	A2M	O3'-C3'-C2'	2.20	117.41	111.17
25	1	1908	OMU	C5'-C4'-C3'	-2.17	107.03	115.18
25	1	2380	OMC	O2-C2-N3	-2.13	118.86	122.33
73	2	1314	OMU	O2-C2-N1	-2.12	119.97	122.79
27	42	133	OMG	O6-C6-C5	-2.10	120.27	124.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	2	933	C4J	N3-C2-N1	2.10	119.72	116.76
25	1	1520	OMG	O6-C6-C5	-2.08	120.31	124.37
25	1	1684	OMC	O2-C2-N3	-2.07	118.97	122.33
25	1	1204	OMG	C3'-C2'-C1'	-2.07	99.00	102.89
25	1	49	OMU	O2-C2-N1	-2.07	120.04	122.79
25	1	386	OMG	O6-C6-C5	-2.05	120.36	124.37
25	1	523	A2M	O2'-C2'-C1'	2.05	113.16	109.09
25	1	1204	OMG	N2-C2-N1	2.02	121.02	116.71
73	2	1390	M7A	C5-C4-N9	2.01	109.26	106.44
73	2	1011	OMG	O6-C6-C5	-2.01	120.46	124.37

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	1	49	OMU	C1'-C2'-O2'-CM2
25	1	313	OMG	O4'-C4'-C5'-O5'
25	1	396	A2M	C1'-C2'-O2'-CM'
25	1	523	A2M	C1'-C2'-O2'-CM'
25	1	624	OMG	C1'-C2'-O2'-CM2
25	1	1121	OMG	C1'-C2'-O2'-CM2
25	1	1520	OMG	C1'-C2'-O2'-CM2
25	1	1775	OMG	O4'-C4'-C5'-O5'
25	1	1824	OMC	C1'-C2'-O2'-CM2
25	1	1908	OMU	C3'-C4'-C5'-O5'
25	1	1908	OMU	O4'-C4'-C5'-O5'
73	2	87	A2M	C1'-C2'-O2'-CM'
73	2	104	OMC	C1'-C2'-O2'-CM2
73	2	371	OMG	C3'-C2'-O2'-CM2
73	2	868	OMG	C1'-C2'-O2'-CM2
73	2	933	C4J	C3'-C4'-C5'-O5'
73	2	933	C4J	C4'-C5'-O5'-P
73	2	1011	OMG	C1'-C2'-O2'-CM2
73	2	1435	MA6	O4'-C4'-C5'-O5'
25	1	313	OMG	C3'-C4'-C5'-O5'
25	1	1775	OMG	C3'-C4'-C5'-O5'
73	2	87	A2M	O4'-C4'-C5'-O5'
73	2	1435	MA6	C3'-C4'-C5'-O5'
25	1	1684	OMC	C2'-C1'-N1-C6
25	1	1768	A2M	C3'-C4'-C5'-O5'
73	2	87	A2M	C3'-C4'-C5'-O5'
73	2	933	C4J	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
25	1	1684	OMC	C2'-C1'-N1-C2
73	2	868	OMG	C3'-C4'-C5'-O5'
73	2	1426	4AC	C3'-C4'-C5'-O5'
25	1	1768	A2M	O4'-C4'-C5'-O5'
73	2	868	OMG	O4'-C4'-C5'-O5'
73	2	933	C4J	C3-C31-C32-N33
73	2	1426	4AC	O4'-C4'-C5'-O5'
25	1	1684	OMC	O4'-C1'-N1-C6
25	1	1684	OMC	O4'-C1'-N1-C2
73	2	933	C4J	C31-C32-C34-O35
73	2	933	C4J	C31-C32-C34-O36
25	1	2292	5MC	C2'-C1'-N1-C6
25	1	2292	5MC	O4'-C1'-N1-C6
25	1	2074	OMG	C3'-C2'-O2'-CM2
73	2	1390	M7A	C4'-C5'-O5'-P
73	2	1435	MA6	C4'-C5'-O5'-P
25	1	1121	OMG	C4'-C5'-O5'-P
25	1	2292	5MC	O4'-C4'-C5'-O5'
25	1	2292	5MC	O4'-C1'-N1-C2
73	2	1035	OMG	C1'-C2'-O2'-CM2
73	2	1390	M7A	C2'-C1'-N9-C8

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 556 ligands modelled in this entry, 556 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
66	w2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	w2	5:G	O3'	68:C	P	17.08

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13683. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis

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

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.