



Full wwPDB EM Validation Report ⓘ

Jun 18, 2026 – 12:14 pm BST

PDB ID : 6HRM / pdb_00006hrm
EMDB ID : EMD-0261
Title : E. coli 70S d2d8 stapled ribosome
Authors : Schmied, W.H.; Tnimov, Z.; Uttamapinant, C.; Rae, C.D.; Fried, S.D.; Chin, J.W.
Deposited on : 2018-09-27
Resolution : 2.96 Å(reported)
Based on initial model : 5MDZ

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

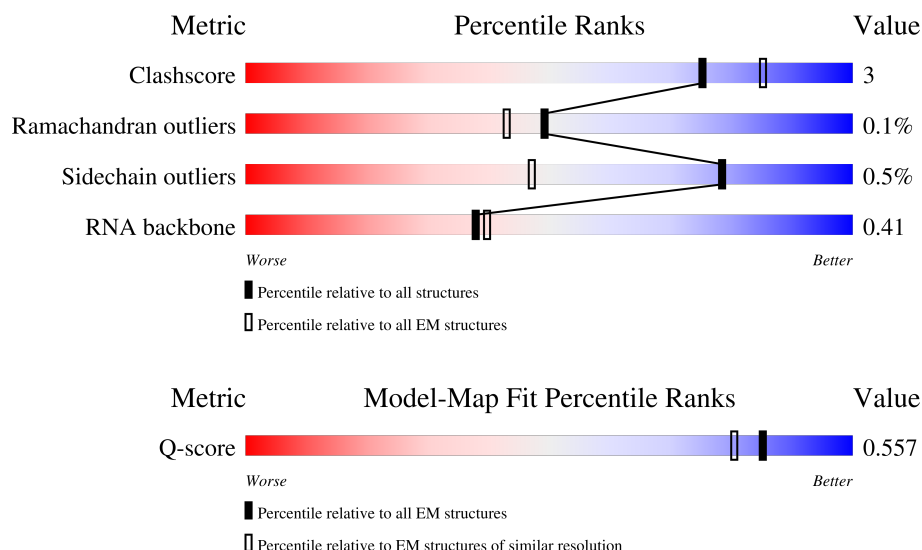
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.96 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13155 (2.46 - 3.46)

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

Mol	Chain	Length	Quality of chain
1	1	4458	15% 71% 25% .
2	3	120	8% 71% 27% .
3	B	271	. 87% 13%

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Mol	Chain	Length	Quality of chain
4	C	209	
5	D	201	
6	E	177	
7	F	175	
8	G	149	
9	H	130	
10	I	135	
11	J	142	
12	K	123	
13	L	144	
14	M	136	
15	N	119	
16	O	116	
17	P	114	
18	Q	117	
19	R	103	
20	S	110	
21	T	94	
22	U	103	
23	V	94	
24	W	76	
25	X	77	
26	Y	62	
27	Z	58	
28	a	66	

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Mol	Chain	Length	Quality of chain
29	b	56	
30	c	52	
31	d	46	
32	e	64	
33	f	38	
34	g	225	
35	h	208	
36	i	205	
37	j	156	
38	k	104	
39	l	151	
40	m	129	
41	n	127	
42	o	99	
43	p	117	
44	q	123	
45	r	116	
46	s	100	
47	t	88	
48	u	82	
49	v	80	
50	w	66	
51	x	83	
52	y	86	
53	z	70	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	4OC	1	1402	X	-	-	-
1	1MG	1	2251	X	-	-	-
1	PSU	1	2252	X	-	-	-
1	5MU	1	2253	X	-	-	-
1	PSU	1	2461	X	-	-	-
1	6MZ	1	3124	X	-	-	-
1	PSU	1	3417	X	-	-	-
1	3TD	1	3421	X	-	-	-
1	PSU	1	3423	X	-	-	-
1	5MU	1	3445	X	-	-	-
1	6MZ	1	3536	X	-	-	-
1	G7M	1	3575	X	-	-	-
1	OMG	1	3757	X	-	-	-
1	PSU	1	3963	X	-	-	-
1	OMC	1	4004	X	-	-	-
1	2MA	1	4009	X	-	-	-
1	PSU	1	4010	X	-	-	-
1	OMU	1	4058	X	-	-	-
1	PSU	1	4086	X	-	-	-
1	PSU	1	4111	X	-	-	-
1	PSU	1	516	X	-	-	-
1	7MG	1	527	X	-	-	-

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 145179 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called stapled 16S-23S rRNA,stapled 16S-23S rRNA,stapled 16S-23S rRNA,stapled 16S-23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	4450	Total	C	N	O	P	0	0
			95544	42634	17562	30898	4450		

There are 153 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1450	G	-	linker	GB 1370526422
1	1451	G	-	linker	GB 1370526422
1	1452	U	-	linker	GB 1370526422
1	1453	C	-	linker	GB 1370526422
1	1454	A	-	linker	GB 1370526422
1	1455	A	-	linker	GB 1370526422
1	1456	C	-	linker	GB 1370526422
1	1457	A	-	linker	GB 1370526422
1	1458	G	-	linker	GB 1370526422
1	1459	C	-	linker	GB 1370526422
1	1460	C	-	linker	GB 1370526422
1	1461	G	-	linker	GB 1370526422
1	1462	U	-	linker	GB 1370526422
1	1463	U	-	linker	GB 1370526422
1	1464	U	-	linker	GB 1370526422
1	1465	G	-	linker	GB 1370526422
1	1466	A	-	linker	GB 1370526422
1	1467	G	-	linker	GB 1370526422
1	1468	C	-	linker	GB 1370526422
1	1469	U	-	linker	GB 1370526422
1	1470	A	-	linker	GB 1370526422
1	1471	A	-	linker	GB 1370526422
1	1472	C	-	linker	GB 1370526422
1	1473	C	-	linker	GB 1370526422
1	1474	G	-	linker	GB 1370526422
1	1475	G	-	linker	GB 1370526422
1	1476	U	-	linker	GB 1370526422

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Chain	Residue	Modelled	Actual	Comment	Reference
1	1477	A	-	linker	GB 1370526422
1	1478	C	-	linker	GB 1370526422
1	1479	U	-	linker	GB 1370526422
1	1480	A	-	linker	GB 1370526422
1	1481	A	-	linker	GB 1370526422
1	1482	U	-	linker	GB 1370526422
1	1483	G	-	linker	GB 1370526422
1	1484	A	-	linker	GB 1370526422
1	1485	A	-	linker	GB 1370526422
1	1486	C	-	linker	GB 1370526422
1	1487	C	-	linker	GB 1370526422
1	1488	G	-	linker	GB 1370526422
1	1489	U	-	linker	GB 1370526422
1	1490	G	-	linker	GB 1370526422
1	1491	A	-	linker	GB 1370526422
1	1492	G	-	linker	GB 1370526422
1	1493	G	-	linker	GB 1370526422
1	1494	C	-	linker	GB 1370526422
1	1495	U	-	linker	GB 1370526422
1	1496	U	-	linker	GB 1370526422
1	1497	A	-	linker	GB 1370526422
1	1498	A	-	linker	GB 1370526422
1	1499	C	-	linker	GB 1370526422
1	1500	C	-	linker	GB 1370526422
1	1504	A	U	conflict	GB 1063812051
1	4358	A	-	expression tag	GB 1063812051
1	4359	C	-	expression tag	GB 1063812051
1	4360	G	-	expression tag	GB 1063812051
1	4361	G	-	expression tag	GB 1063812051
1	4362	A	-	expression tag	GB 1063812051
1	4363	C	-	expression tag	GB 1063812051
1	4364	A	-	expression tag	GB 1063812051
1	4365	U	-	expression tag	GB 1063812051
1	4366	G	-	expression tag	GB 1063812051
1	4367	G	-	expression tag	GB 1063812051
1	4368	U	-	expression tag	GB 1063812051
1	4369	U	-	expression tag	GB 1063812051
1	4370	G	-	expression tag	GB 1063812051
1	4371	G	-	expression tag	GB 1063812051
1	4372	A	-	expression tag	GB 1063812051
1	4373	G	-	expression tag	GB 1063812051
1	4374	G	-	expression tag	GB 1063812051

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Chain	Residue	Modelled	Actual	Comment	Reference
1	4375	G	-	expression tag	GB 1063812051
1	4376	C	-	expression tag	GB 1063812051
1	4377	G	-	expression tag	GB 1063812051
1	4378	C	-	expression tag	GB 1063812051
1	4379	U	-	expression tag	GB 1063812051
1	4380	U	-	expression tag	GB 1063812051
1	4381	A	-	expression tag	GB 1063812051
1	4382	C	-	expression tag	GB 1063812051
1	4383	C	-	expression tag	GB 1063812051
1	4384	A	-	expression tag	GB 1063812051
1	4385	C	-	expression tag	GB 1063812051
1	4386	U	-	expression tag	GB 1063812051
1	4387	U	-	expression tag	GB 1063812051
1	4388	U	-	expression tag	GB 1063812051
1	4389	G	-	expression tag	GB 1063812051
1	4390	U	-	expression tag	GB 1063812051
1	4391	G	-	expression tag	GB 1063812051
1	4392	A	-	expression tag	GB 1063812051
1	4393	U	-	expression tag	GB 1063812051
1	4394	U	-	expression tag	GB 1063812051
1	4395	C	-	expression tag	GB 1063812051
1	4396	A	-	expression tag	GB 1063812051
1	4397	U	-	expression tag	GB 1063812051
1	4398	G	-	expression tag	GB 1063812051
1	4399	A	-	expression tag	GB 1063812051
1	4400	C	-	expression tag	GB 1063812051
1	4401	U	-	expression tag	GB 1063812051
1	4402	G	-	expression tag	GB 1063812051
1	4403	G	-	expression tag	GB 1063812051
1	4404	G	-	expression tag	GB 1063812051
1	4405	G	-	expression tag	GB 1063812051
1	4406	U	-	expression tag	GB 1063812051
1	4407	G	-	expression tag	GB 1063812051
1	4408	A	-	expression tag	GB 1063812051
1	4409	A	-	expression tag	GB 1063812051
1	4410	G	-	expression tag	GB 1063812051
1	4411	U	-	expression tag	GB 1063812051
1	4412	C	-	expression tag	GB 1063812051
1	4413	G	-	expression tag	GB 1063812051
1	4414	UR3	-	expression tag	GB 1063812051
1	4415	A	-	expression tag	GB 1063812051
1	4416	A	-	expression tag	GB 1063812051

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Chain	Residue	Modelled	Actual	Comment	Reference
1	4417	C	-	expression tag	GB 1063812051
1	4418	A	-	expression tag	GB 1063812051
1	4419	A	-	expression tag	GB 1063812051
1	4420	G	-	expression tag	GB 1063812051
1	4421	G	-	expression tag	GB 1063812051
1	4422	U	-	expression tag	GB 1063812051
1	4423	A	-	expression tag	GB 1063812051
1	4424	A	-	expression tag	GB 1063812051
1	4425	C	-	expression tag	GB 1063812051
1	4426	C	-	expression tag	GB 1063812051
1	4427	G	-	expression tag	GB 1063812051
1	4428	U	-	expression tag	GB 1063812051
1	4429	A	-	expression tag	GB 1063812051
1	4430	G	-	expression tag	GB 1063812051
1	4431	G	-	expression tag	GB 1063812051
1	4432	2MG	-	expression tag	GB 1063812051
1	4433	G	-	expression tag	GB 1063812051
1	4434	MA6	-	expression tag	GB 1063812051
1	4435	MA6	-	expression tag	GB 1063812051
1	4436	C	-	expression tag	GB 1063812051
1	4437	C	-	expression tag	GB 1063812051
1	4438	U	-	expression tag	GB 1063812051
1	4439	G	-	expression tag	GB 1063812051
1	4440	C	-	expression tag	GB 1063812051
1	4441	G	-	expression tag	GB 1063812051
1	4442	G	-	expression tag	GB 1063812051
1	4443	U	-	expression tag	GB 1063812051
1	4444	U	-	expression tag	GB 1063812051
1	4445	G	-	expression tag	GB 1063812051
1	4446	G	-	expression tag	GB 1063812051
1	4447	A	-	expression tag	GB 1063812051
1	4448	U	-	expression tag	GB 1063812051
1	4449	C	-	expression tag	GB 1063812051
1	4450	A	-	expression tag	GB 1063812051
1	4451	C	-	expression tag	GB 1063812051
1	4452	C	-	expression tag	GB 1063812051
1	4453	U	-	expression tag	GB 1063812051
1	4454	C	-	expression tag	GB 1063812051
1	4455	C	-	expression tag	GB 1063812051
1	4456	U	-	expression tag	GB 1063812051
1	4457	U	-	expression tag	GB 1063812051
1	4458	A	-	expression tag	GB 1063812051

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	130	Total	C	N	O	S	0	0
			980	620	174	182	4		

- Molecule 10 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	135	Total	C	N	O	S	0	0
			984	622	171	185	6		

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 23 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	1	422	Total	Mg	0
			422	422	
54	3	8	Total	Mg	0
			8	8	
54	N	1	Total	Mg	0
			1	1	
54	P	1	Total	Mg	0
			1	1	
54	Q	1	Total	Mg	0
			1	1	
54	U	1	Total	Mg	0
			1	1	
54	b	1	Total	Mg	0
			1	1	
54	i	1	Total	Mg	0
			1	1	

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	a	1	Total	Zn	0
			1	1	
55	f	1	Total	Zn	0
			1	1	

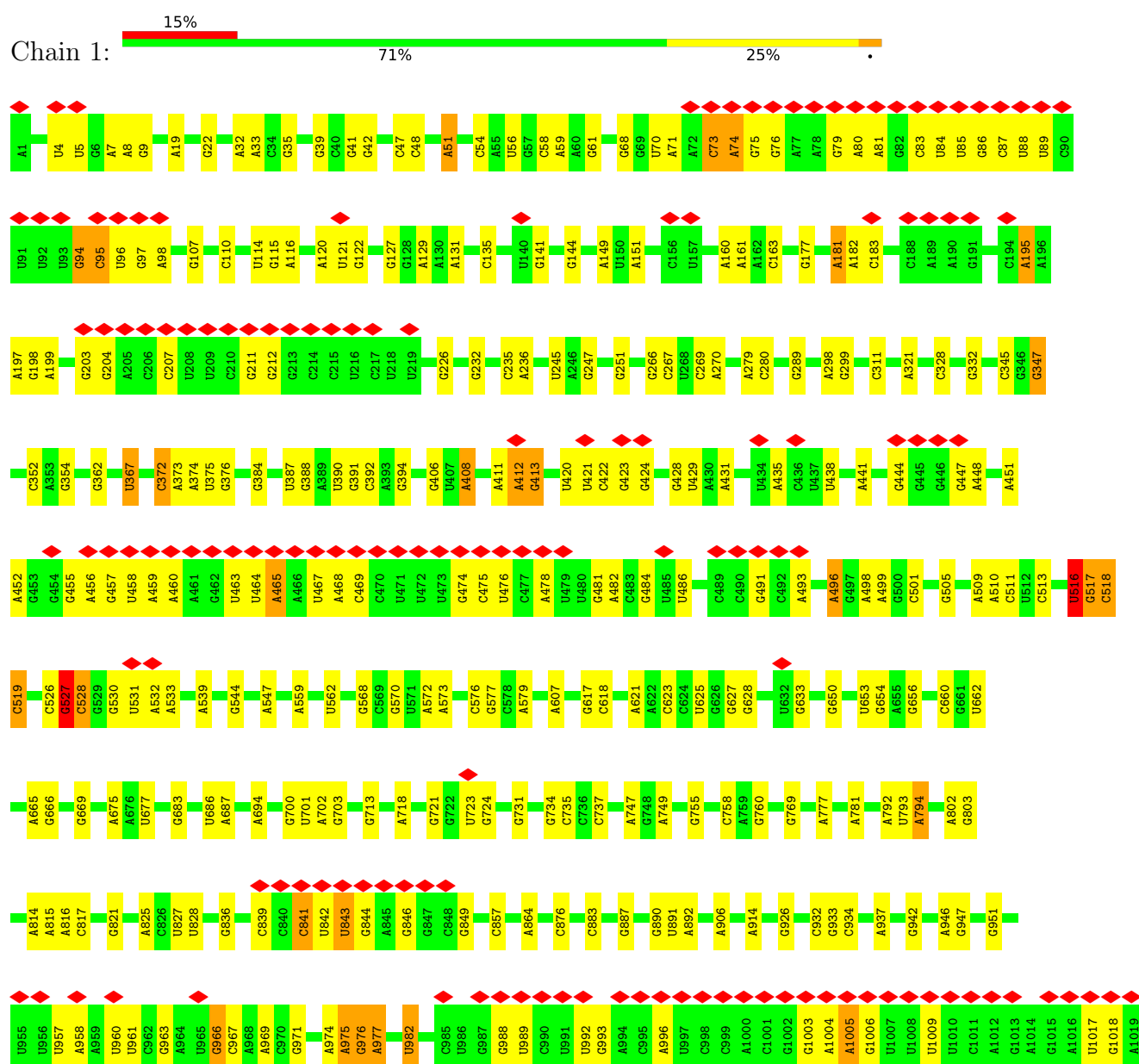
- Molecule 56 is water.

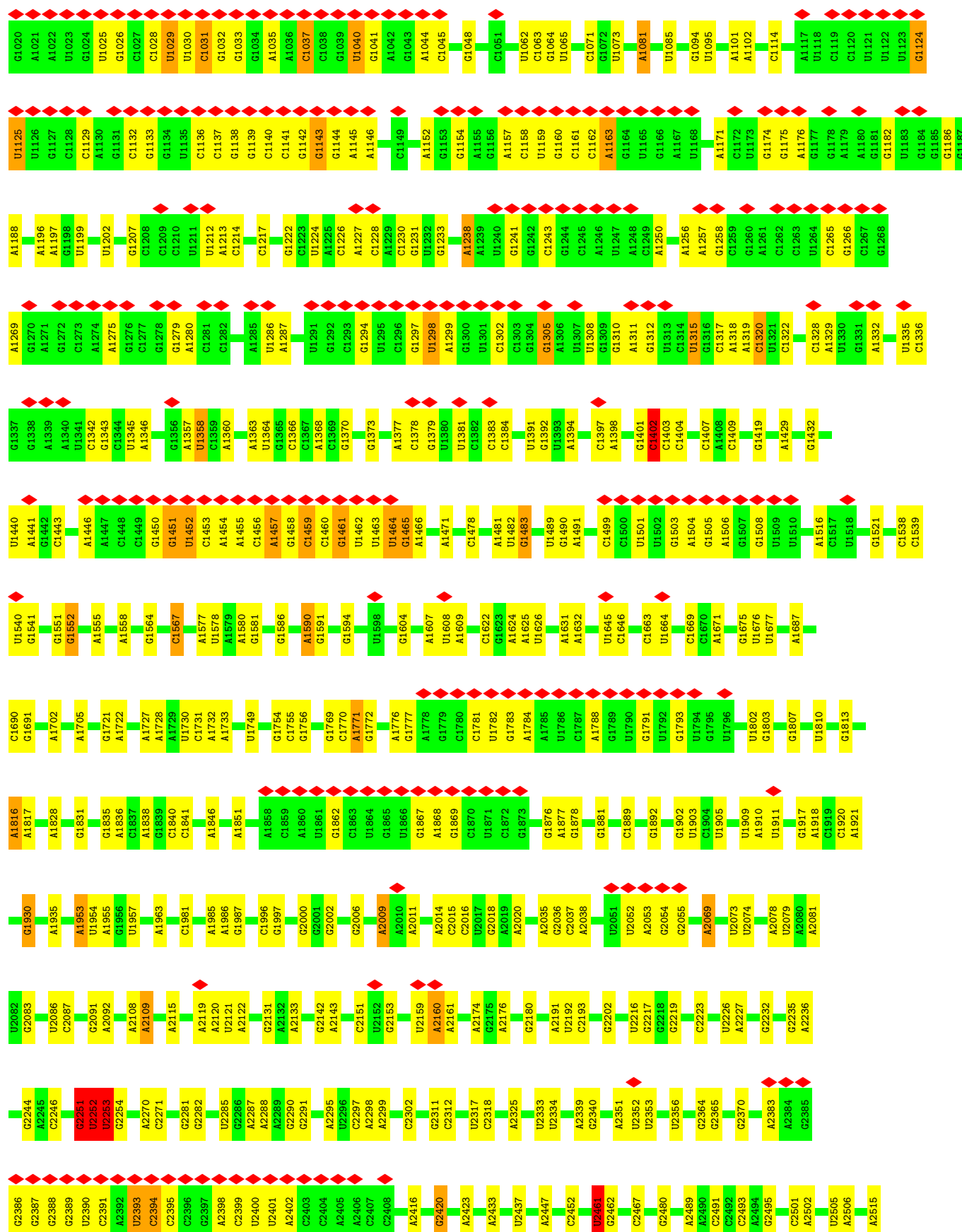
Mol	Chain	Residues	Atoms		AltConf
56	B	2	Total	O	0
			2	2	

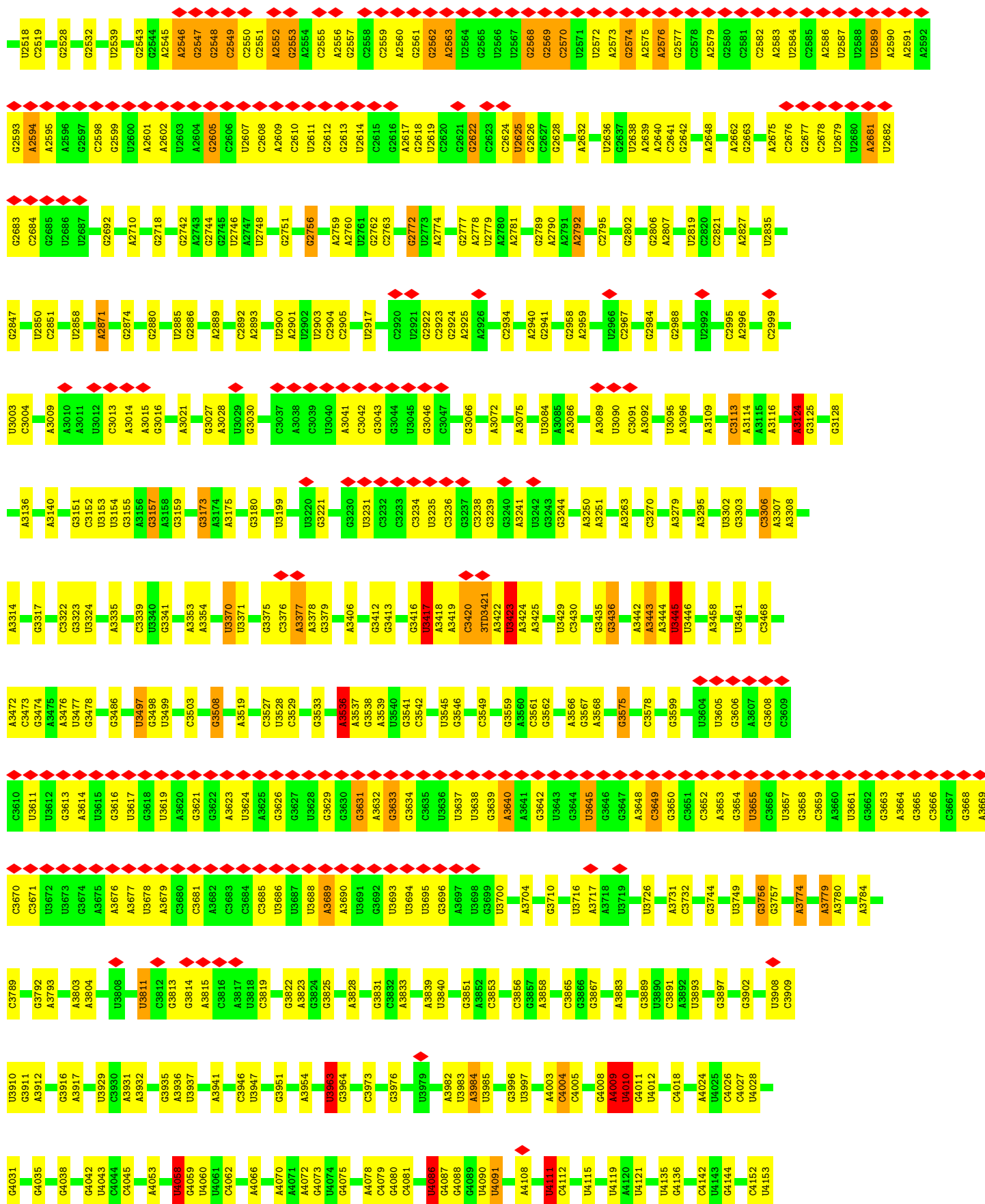
3 Residue-property plots [i](#)

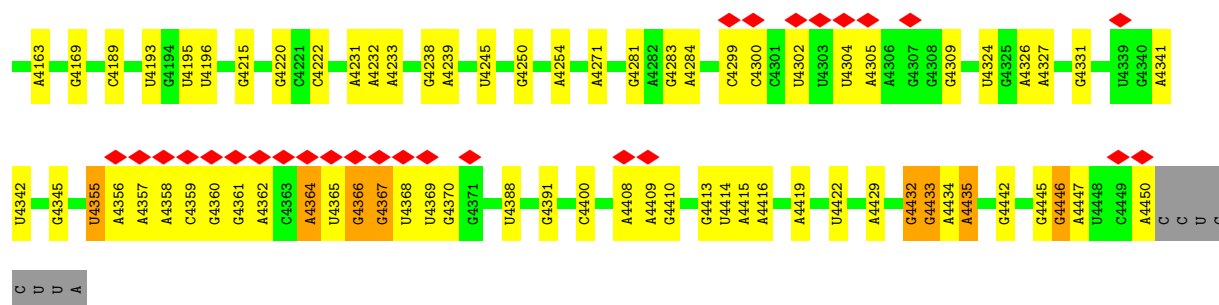
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: stapled 16S-23S rRNA, stapled 16S-23S rRNA, stapled 16S-23S rRNA, stapled 16S-23S rRNA

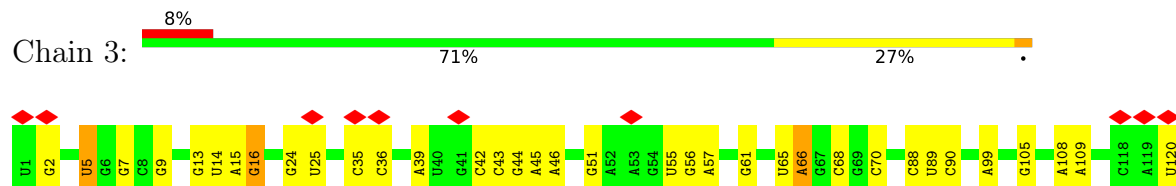




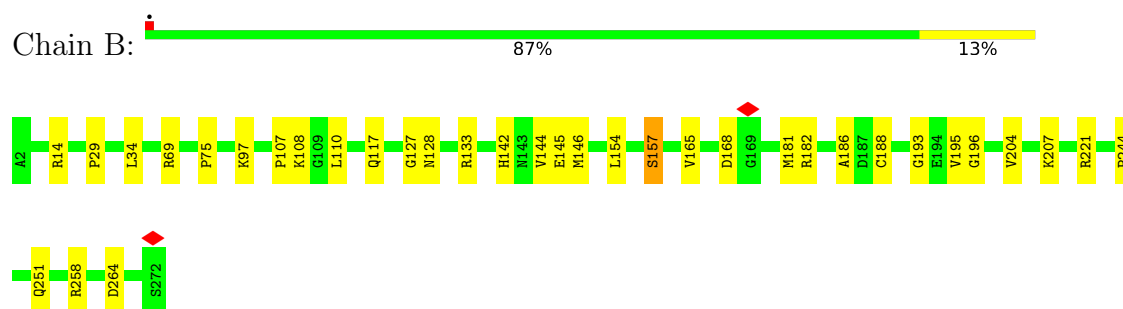




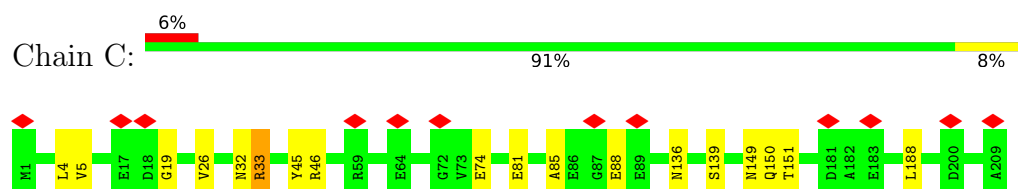
• Molecule 2: 5S ribosomal RNA



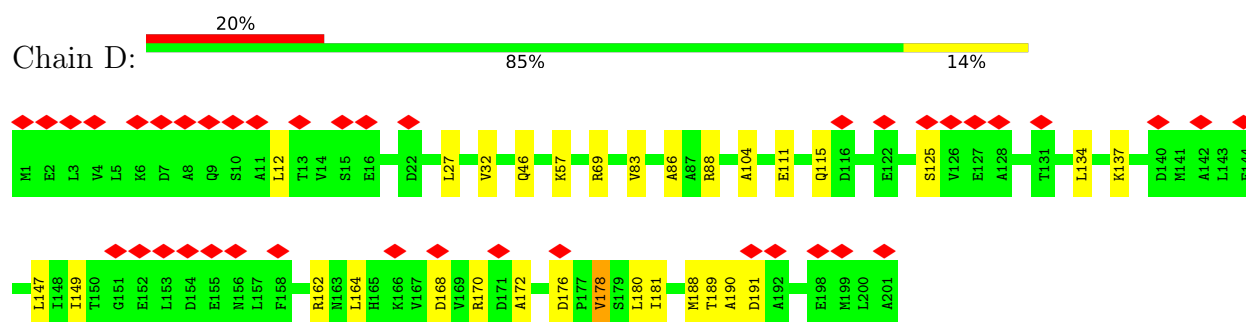
• Molecule 3: 50S ribosomal protein L2



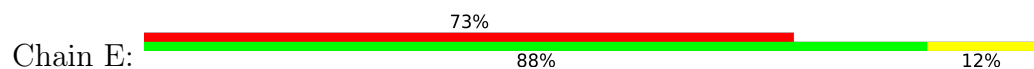
• Molecule 4: 50S ribosomal protein L3

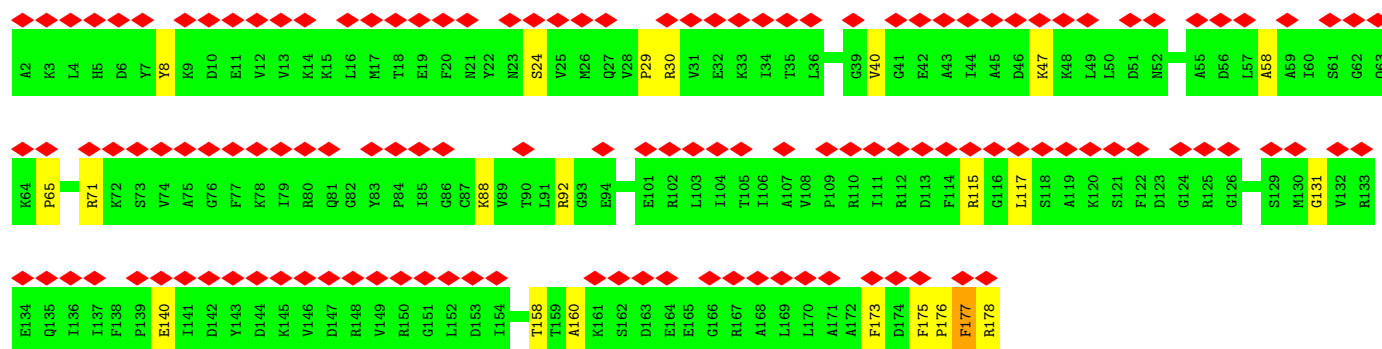


• Molecule 5: 50S ribosomal protein L4



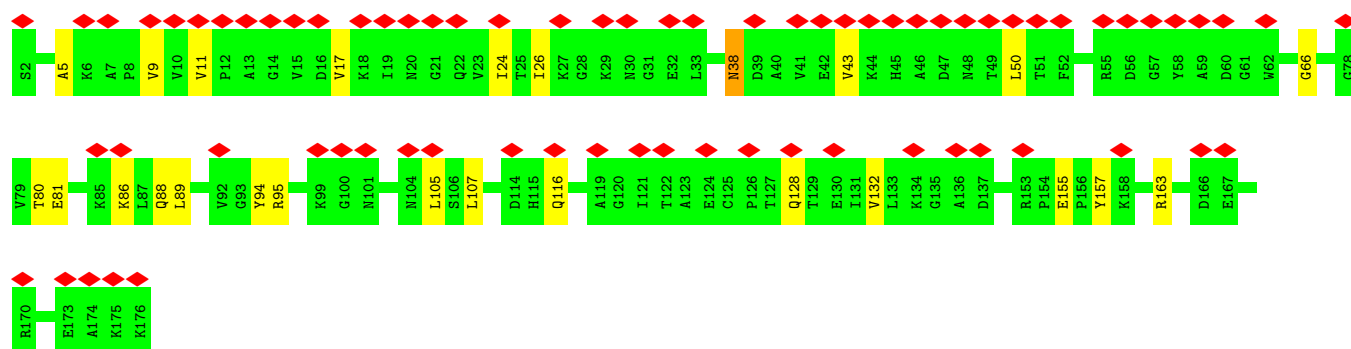
• Molecule 6: 50S ribosomal protein L5





• Molecule 7: 50S ribosomal protein L6

Chain F: 41% 86% 14% .



• Molecule 8: 50S ribosomal protein L9

Chain G: 87% 91% 9%



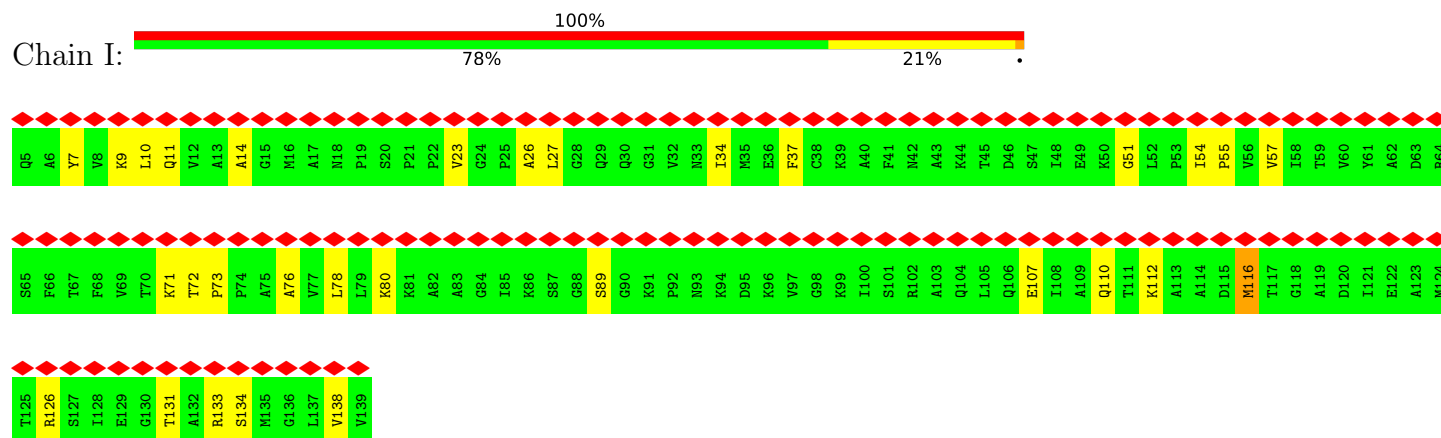
• Molecule 9: 50S ribosomal protein L10

Chain H: 100% 68% 32%

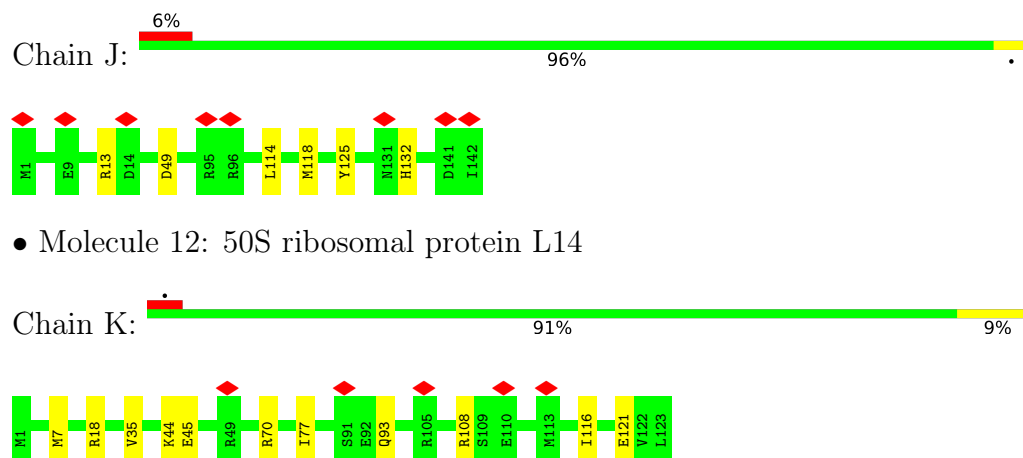




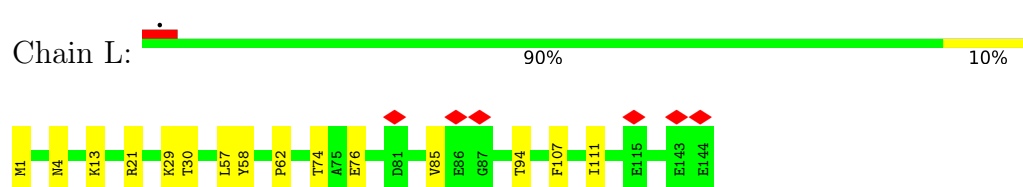
- Molecule 10: 50S ribosomal protein L11



- Molecule 11: 50S ribosomal protein L13



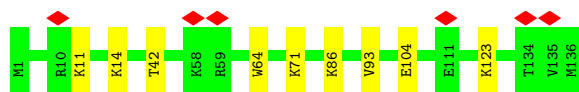
- Molecule 12: 50S ribosomal protein L14



- Molecule 13: 50S ribosomal protein L15



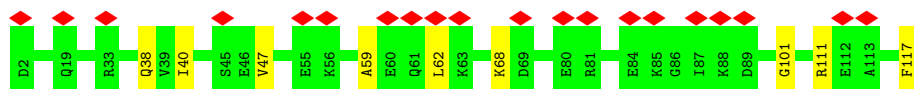
- Molecule 14: 50S ribosomal protein L16



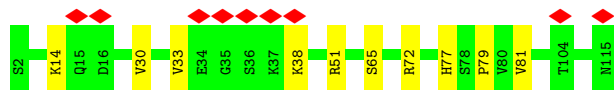
- Molecule 15: 50S ribosomal protein L17



- Molecule 16: 50S ribosomal protein L18



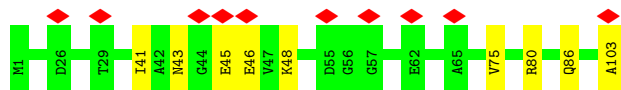
- Molecule 17: 50S ribosomal protein L19



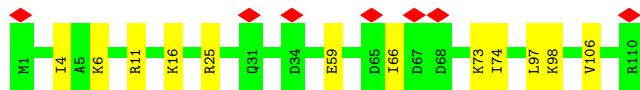
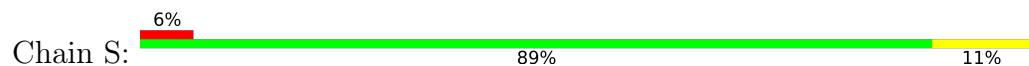
- Molecule 18: 50S ribosomal protein L20



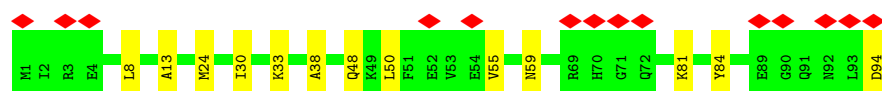
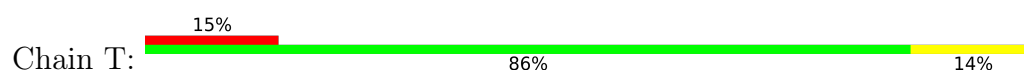
- Molecule 19: 50S ribosomal protein L21



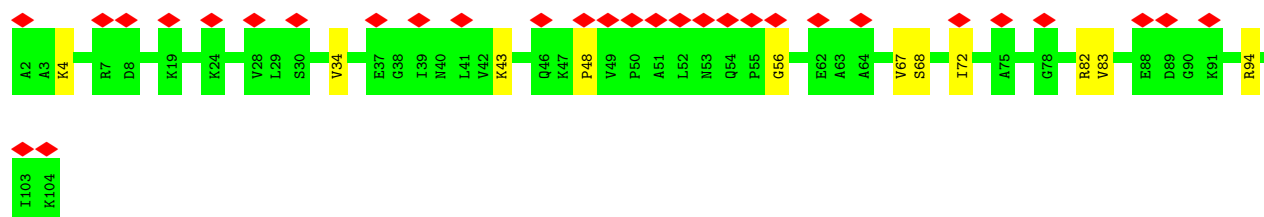
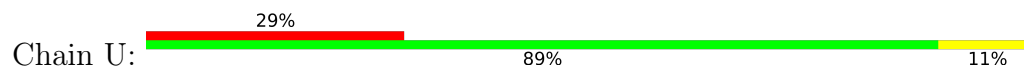
- Molecule 20: 50S ribosomal protein L22



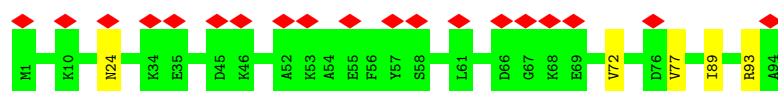
- Molecule 21: 50S ribosomal protein L23



- Molecule 22: 50S ribosomal protein L24



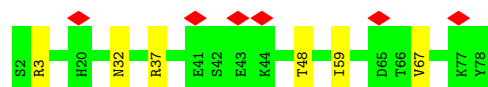
- Molecule 23: 50S ribosomal protein L25



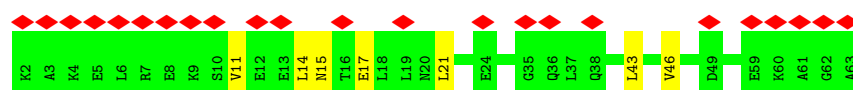
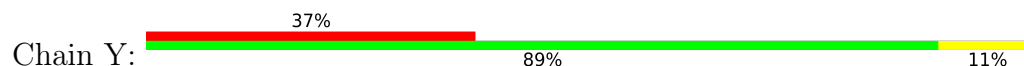
- Molecule 24: 50S ribosomal protein L27



- Molecule 25: 50S ribosomal protein L28



- Molecule 26: 50S ribosomal protein L29

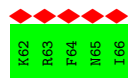
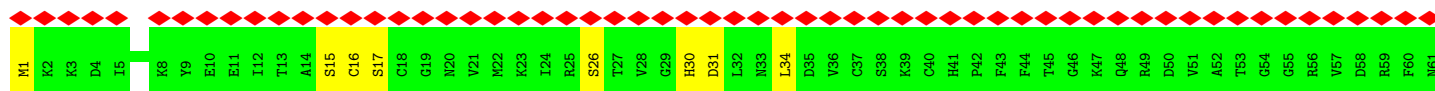
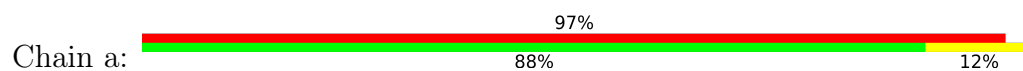


- Molecule 27: 50S ribosomal protein L30

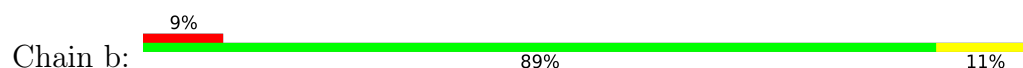




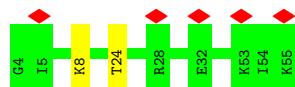
- Molecule 28: 50S ribosomal protein L31



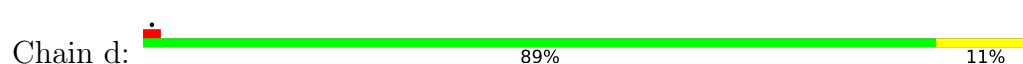
- Molecule 29: 50S ribosomal protein L32



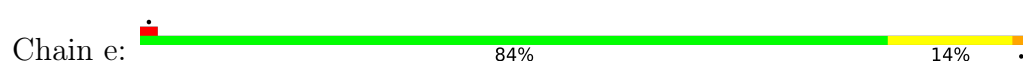
- Molecule 30: 50S ribosomal protein L33



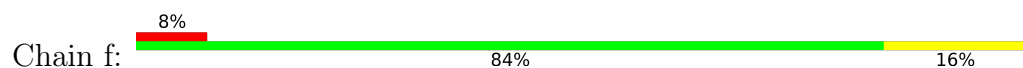
- Molecule 31: 50S ribosomal protein L34

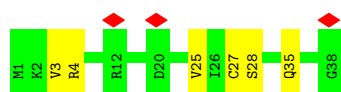


- Molecule 32: 50S ribosomal protein L35

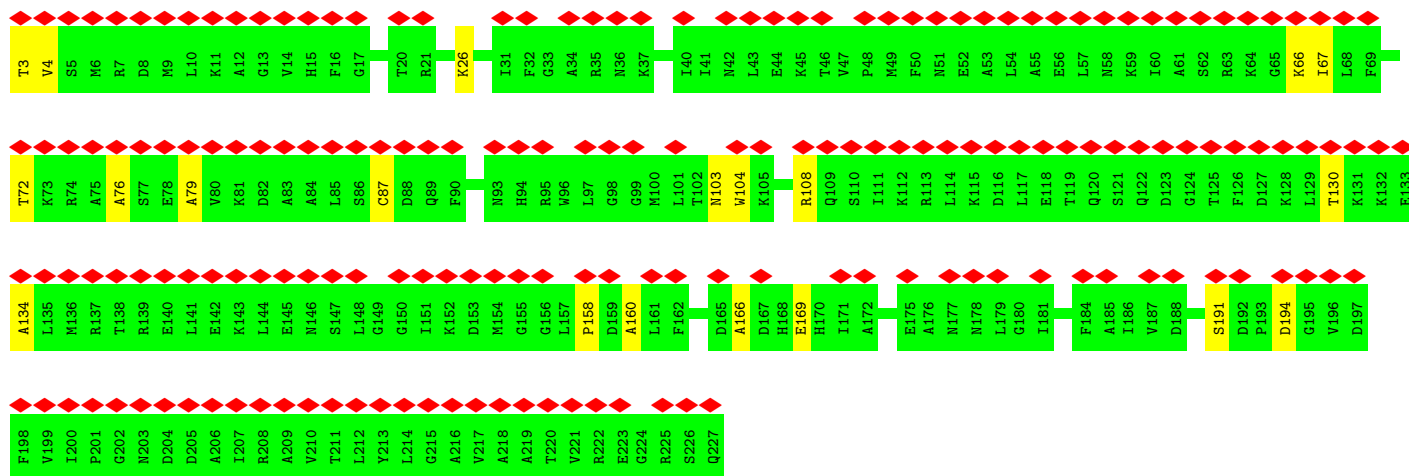
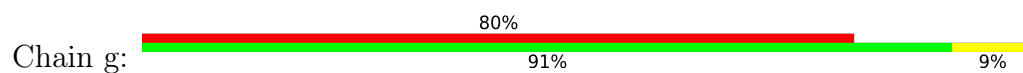


- Molecule 33: 50S ribosomal protein L36

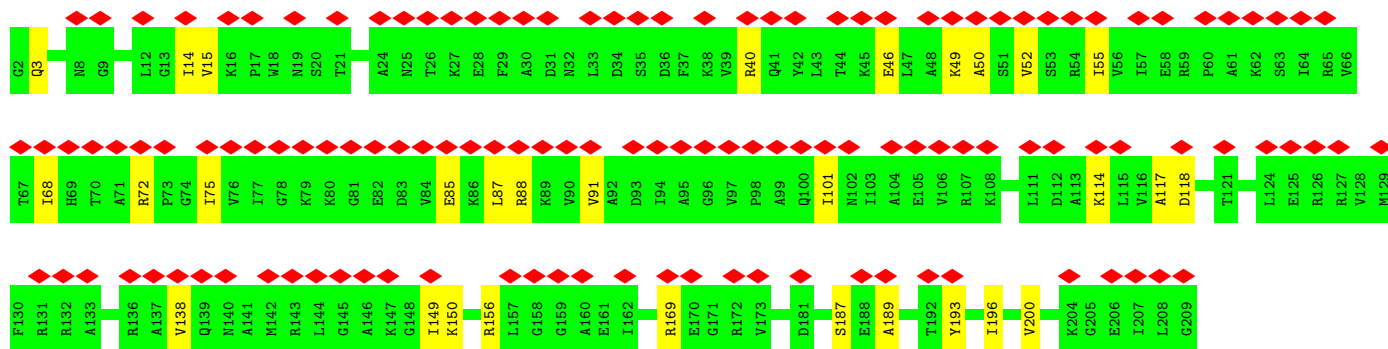
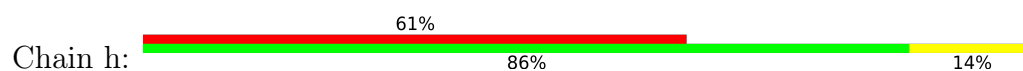




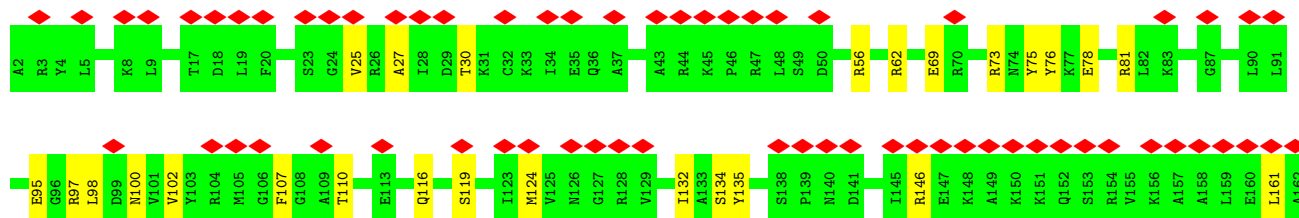
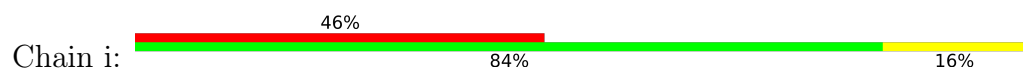
• Molecule 34: 30S ribosomal protein S2

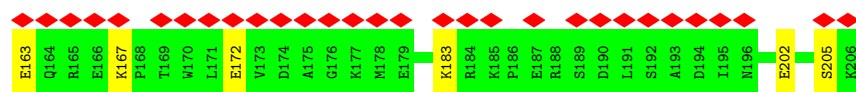


• Molecule 35: 30S ribosomal protein S3

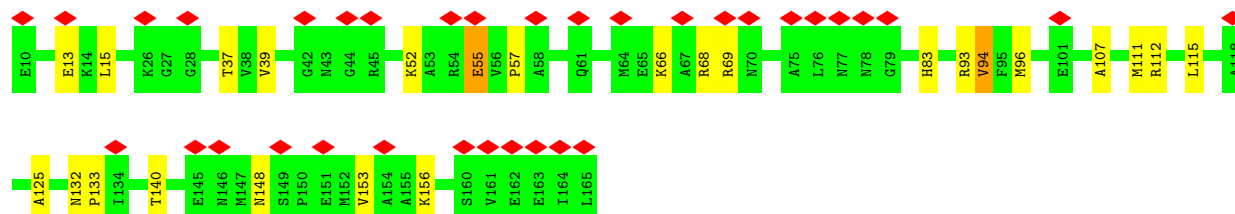
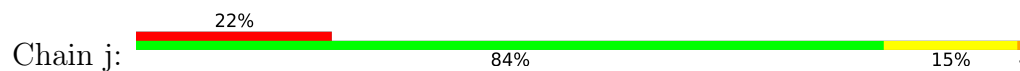


• Molecule 36: 30S ribosomal protein S4

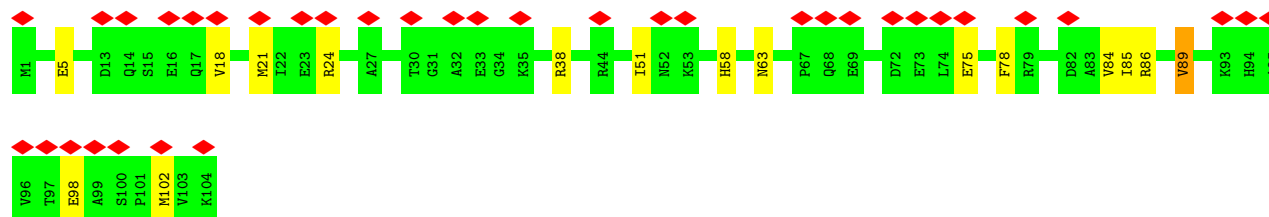
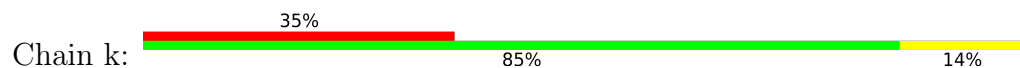




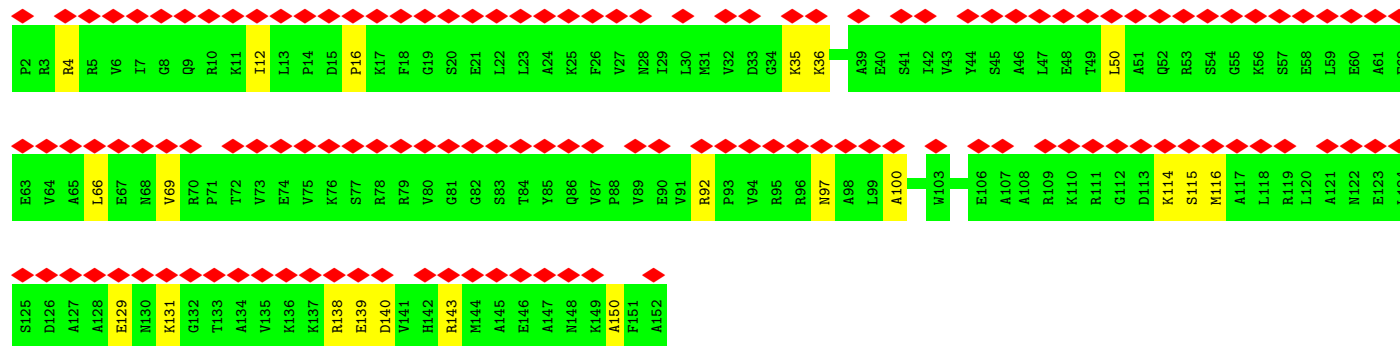
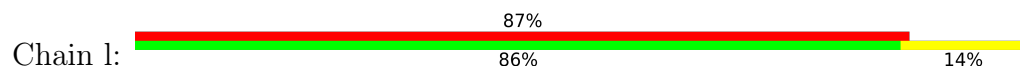
- Molecule 37: 30S ribosomal protein S5



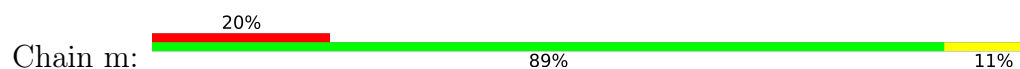
- Molecule 38: 30S ribosomal protein S6

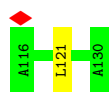


- Molecule 39: 30S ribosomal protein S7

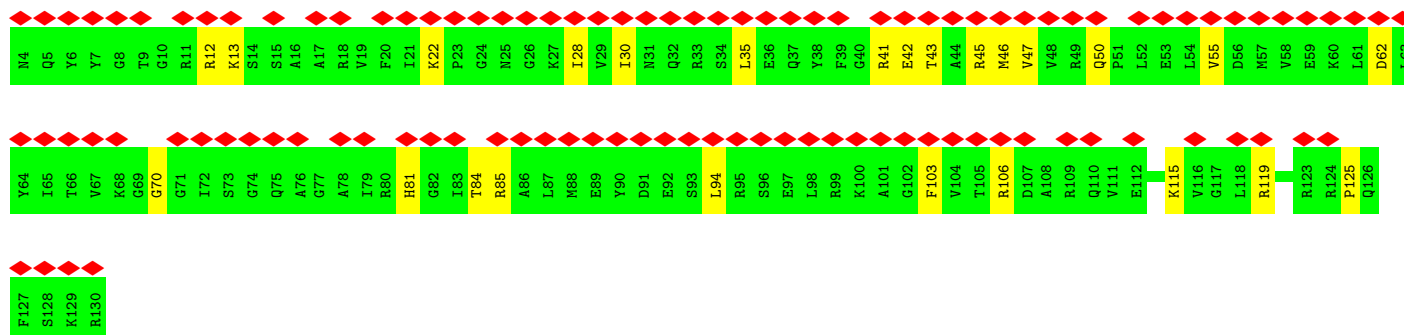
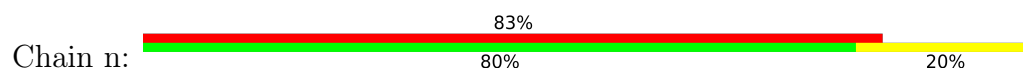


- Molecule 40: 30S ribosomal protein S8

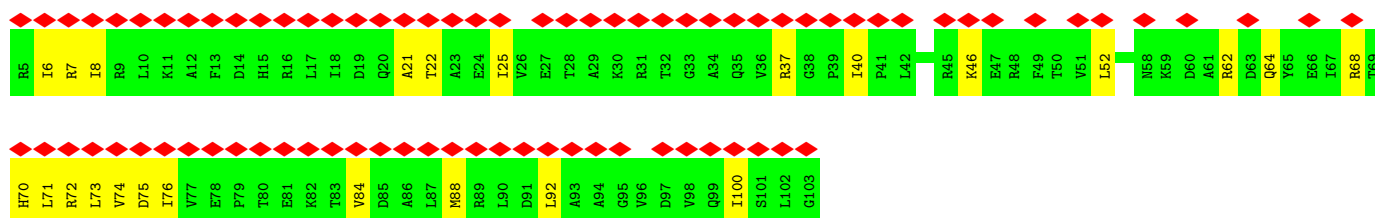
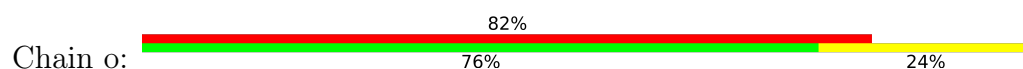




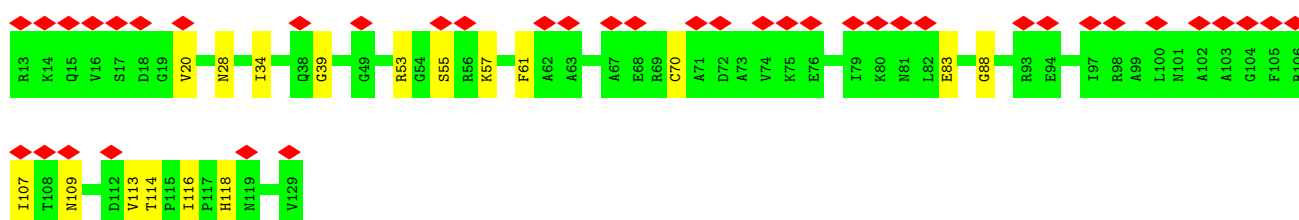
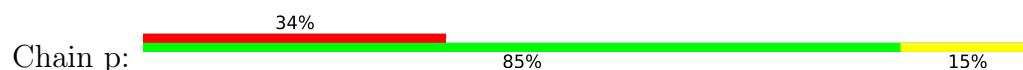
- Molecule 41: 30S ribosomal protein S9



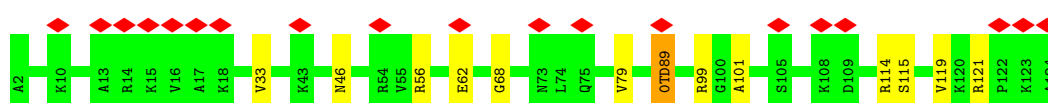
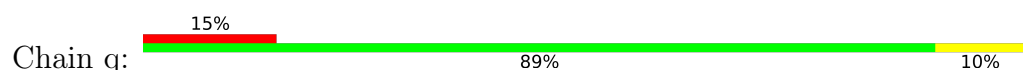
- Molecule 42: 30S ribosomal protein S10



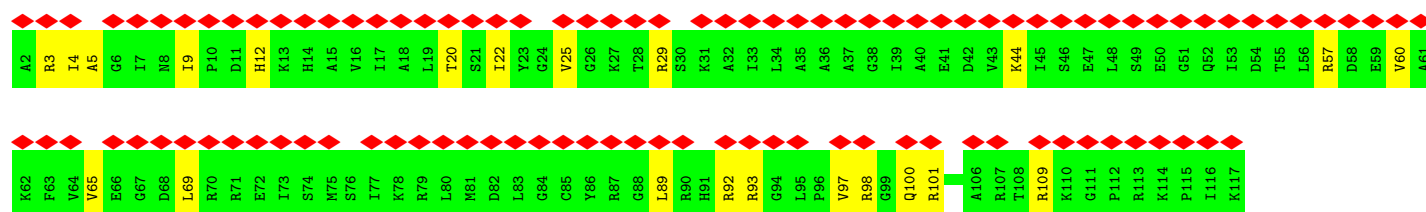
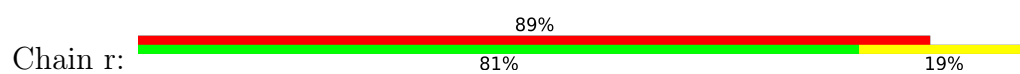
- Molecule 43: 30S ribosomal protein S11



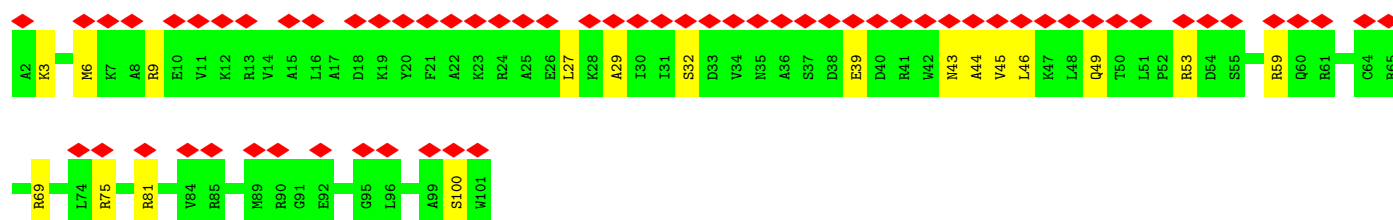
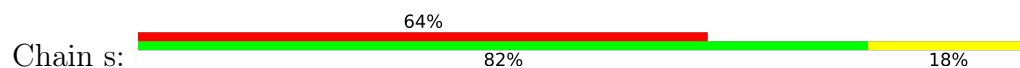
- Molecule 44: 30S ribosomal protein S12



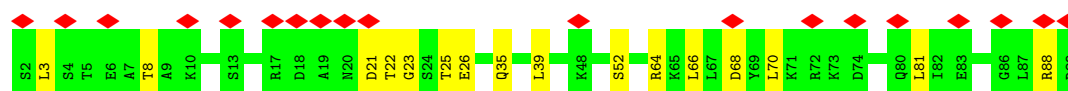
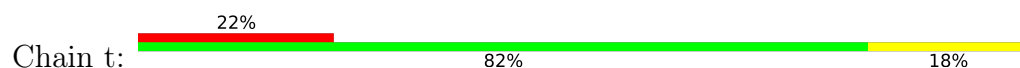
- Molecule 45: 30S ribosomal protein S13



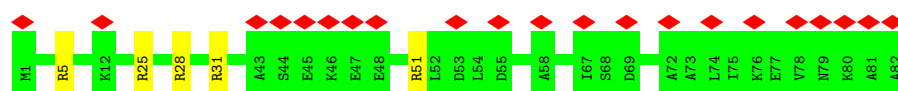
• Molecule 46: 30S ribosomal protein S14



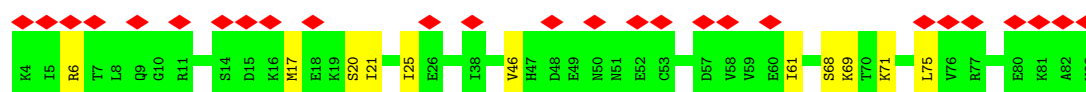
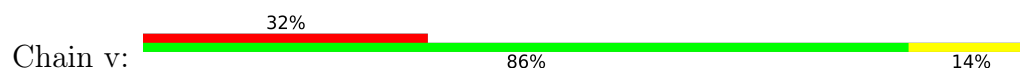
• Molecule 47: 30S ribosomal protein S15



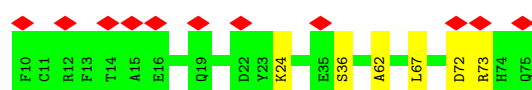
• Molecule 48: 30S ribosomal protein S16



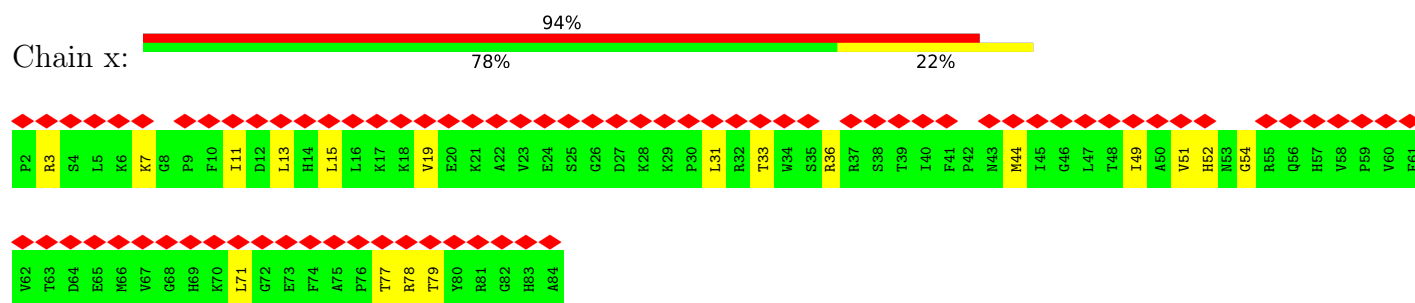
• Molecule 49: 30S ribosomal protein S17



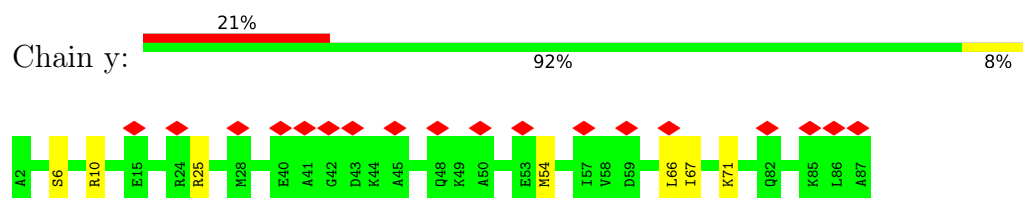
• Molecule 50: 30S ribosomal protein S18



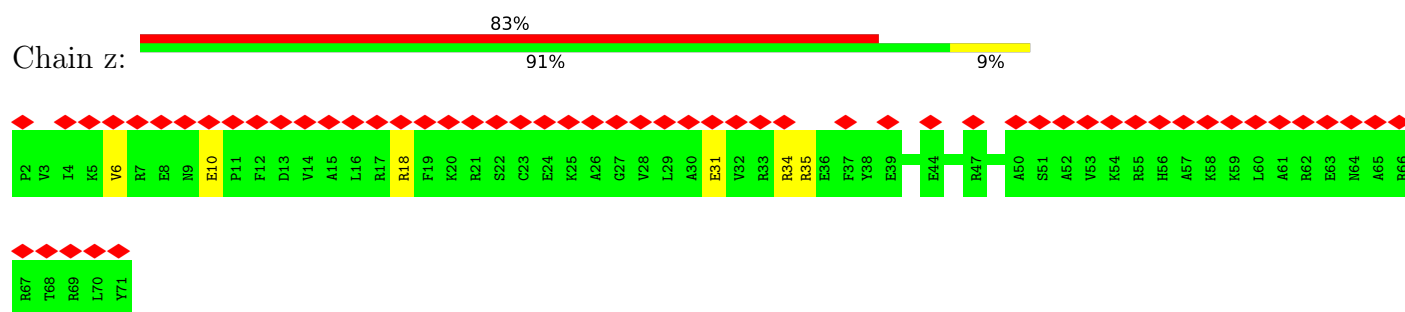
• Molecule 51: 30S ribosomal protein S19



• Molecule 52: 30S ribosomal protein S20



• Molecule 53: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94371	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 ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.875	Depositor
Minimum map value	-0.602	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	392.19998, 392.19998, 392.19998	wwPDB
Map dimensions	370, 370, 370	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MA6, G7M, 2MA, UR3, MG, OMG, 5MU, OMU, 7MG, 3TD, 4OC, 5MC, 0TD, 1MG, OMC, 6MZ, 2MG, ZN, PSU

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	1	0.44	2/106185 (0.0%)	0.45	3/165633 (0.0%)
2	3	0.35	0/2872	0.40	0/4478
3	B	0.49	0/2122	0.68	0/2852
4	C	0.47	0/1586	0.67	0/2134
5	D	0.41	0/1571	0.63	0/2113
6	E	0.29	0/1435	0.66	2/1926 (0.1%)
7	F	0.29	0/1333	0.60	2/1805 (0.1%)
8	G	0.25	0/1122	0.58	0/1515
9	H	0.32	0/993	0.79	2/1340 (0.1%)
10	I	0.30	0/998	0.71	0/1348
11	J	0.44	0/1152	0.58	0/1551
12	K	0.46	0/955	0.68	0/1279
13	L	0.43	0/1062	0.63	0/1413
14	M	0.42	0/1093	0.60	0/1460
15	N	0.48	0/964	0.68	0/1289
16	O	0.33	0/902	0.63	0/1209
17	P	0.42	0/929	0.61	0/1242
18	Q	0.49	0/960	0.73	1/1278 (0.1%)
19	R	0.42	0/829	0.65	0/1107
20	S	0.46	0/864	0.61	0/1156
21	T	0.36	0/752	0.62	0/1005
22	U	0.34	0/796	0.67	0/1062
23	V	0.37	0/766	0.58	0/1025
24	W	0.43	0/589	0.59	0/779
25	X	0.43	0/635	0.61	0/848
26	Y	0.32	0/502	0.56	0/667
27	Z	0.39	0/452	0.61	0/605
28	a	0.25	0/531	0.61	0/709
29	b	0.46	0/450	0.74	0/599
30	c	0.39	0/433	0.65	0/576
31	d	0.54	0/380	0.78	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.48	0/513	0.78	0/676
33	f	0.45	0/303	0.65	0/397
34	g	0.29	0/1791	0.66	2/2413 (0.1%)
35	h	0.28	0/1663	0.60	1/2241 (0.0%)
36	i	0.30	0/1665	0.58	0/2227
37	j	0.39	0/1165	0.74	2/1568 (0.1%)
38	k	0.33	0/867	0.64	0/1171
39	l	0.27	0/1195	0.71	2/1602 (0.1%)
40	m	0.36	0/989	0.61	0/1326
41	n	0.29	0/1034	0.69	0/1375
42	o	0.29	0/800	0.65	0/1082
43	p	0.33	0/893	0.57	0/1205
44	q	0.38	0/960	0.68	2/1286 (0.2%)
45	r	0.28	0/909	0.69	0/1215
46	s	0.28	0/817	0.52	0/1088
47	t	0.38	0/722	0.60	0/964
48	u	0.32	0/659	0.62	0/884
49	v	0.32	0/658	0.67	0/881
50	w	0.35	0/553	0.59	0/743
51	x	0.25	0/680	0.56	0/915
52	y	0.33	0/675	0.54	0/895
53	z	0.27	0/597	0.57	0/792
All	All	0.42	2/156321 (0.0%)	0.51	19/233447 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	39	0
3	B	0	2
10	I	0	1
12	K	0	1
32	e	0	1
38	k	0	1
All	All	39	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2393	U	C1'-N1	6.77	1.58	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	4058	OMU	O3'-P	5.32	1.61	1.56

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	l	12	ILE	CA-C-N	8.44	132.90	120.83
39	l	12	ILE	C-N-CA	8.44	132.90	120.83
7	F	116	GLN	CA-C-N	7.44	130.77	120.65
7	F	116	GLN	C-N-CA	7.44	130.77	120.65
1	1	4058	OMU	P-O3'-C3'	6.64	127.67	119.70
37	j	55	GLU	CA-C-N	6.24	125.33	120.33
37	j	55	GLU	C-N-CA	6.24	125.33	120.33
9	H	54	VAL	N-CA-C	-6.09	106.80	112.83
44	q	101	ALA	CA-C-N	5.50	132.04	121.54
44	q	101	ALA	C-N-CA	5.50	132.04	121.54
1	1	2018	G	O4'-C1'-N9	5.45	116.37	108.20
9	H	81	LEU	CA-CB-CG	5.38	135.15	116.30
34	g	87	CYS	CA-C-N	5.21	131.49	121.54
34	g	87	CYS	C-N-CA	5.21	131.49	121.54
6	E	173	PHE	CA-C-N	5.20	131.47	121.54
6	E	173	PHE	C-N-CA	5.20	131.47	121.54
1	1	1461	G	P-O3'-C3'	5.19	127.98	120.20
18	Q	92	ARG	CA-CB-CG	5.19	124.47	114.10
35	h	75	ILE	N-CA-C	-5.04	107.52	113.42

All (39) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	516	PSU	C4',C3'
1	1	527	7MG	C3'
1	1	1402	4OC	C1',C3'
1	1	2251	1MG	C2',C1'
1	1	2252	PSU	C4',C3'
1	1	2253	5MU	C4',C2'
1	1	2461	PSU	C4',C3'
1	1	3124	6MZ	C2',C3'
1	1	3417	PSU	C4',C3'
1	1	3421	3TD	C3'
1	1	3423	PSU	C4',C3'
1	1	3445	5MU	C4',C2'
1	1	3536	6MZ	C2',C3'
1	1	3575	G7M	C2'

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Mol	Chain	Res	Type	Atom
1	1	3757	OMG	C2'
1	1	3963	PSU	C4',C3'
1	1	4004	OMC	C4'
1	1	4009	2MA	C2',C3'
1	1	4010	PSU	C4',C3'
1	1	4058	OMU	C2',C3'
1	1	4086	PSU	C4',C3'
1	1	4111	PSU	C4',C3'

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	157	SER	Peptide
3	B	195	VAL	Peptide
10	I	116	MET	Peptide
12	K	93	GLN	Peptide
32	e	31	HIS	Peptide
38	k	102	MET	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	95544	0	48102	281	0
2	3	2569	0	1301	9	0
3	B	2083	0	2154	20	0
4	C	1565	0	1616	12	0
5	D	1552	0	1619	19	0
6	E	1411	0	1444	13	0
7	F	1313	0	1358	12	0
8	G	1111	0	1148	7	0
9	H	980	0	1013	26	0
10	I	984	0	1035	19	0
11	J	1129	0	1162	3	0
12	K	946	0	1023	7	0
13	L	1053	0	1129	12	0
14	M	1074	0	1157	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	N	951	0	994	5	0
16	O	892	0	923	6	0
17	P	917	0	962	7	0
18	Q	947	0	1019	7	0
19	R	816	0	839	6	0
20	S	857	0	922	8	0
21	T	746	0	811	8	0
22	U	788	0	844	8	0
23	V	753	0	780	2	0
24	W	582	0	599	3	0
25	X	625	0	652	4	0
26	Y	501	0	531	4	0
27	Z	448	0	488	2	0
28	a	522	0	521	5	0
29	b	444	0	458	4	0
30	c	426	0	464	2	0
31	d	377	0	418	2	0
32	e	504	0	572	9	0
33	f	302	0	340	4	0
34	g	1760	0	1787	10	0
35	h	1636	0	1710	16	0
36	i	1643	0	1707	18	0
37	j	1152	0	1196	17	0
38	k	848	0	846	9	0
39	l	1181	0	1238	15	0
40	m	979	0	1031	9	0
41	n	1022	0	1070	17	0
42	o	790	0	831	16	0
43	p	877	0	887	13	0
44	q	957	0	1017	9	0
45	r	900	0	965	16	0
46	s	805	0	844	16	0
47	t	714	0	734	8	0
48	u	649	0	666	5	0
49	v	649	0	691	7	0
50	w	544	0	560	4	0
51	x	663	0	688	14	0
52	y	669	0	719	4	0
53	z	589	0	629	5	0
54	1	422	0	0	0	0
54	3	8	0	0	0	0
54	N	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	P	1	0	0	0	0
54	Q	1	0	0	0	0
54	U	1	0	0	0	0
54	b	1	0	0	0	0
54	i	1	0	0	0	0
55	a	1	0	0	0	0
55	f	1	0	0	0	0
56	B	2	0	0	0	0
All	All	145179	0	98214	637	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (637) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:p:88:GLY:H	43:p:114:THR:HG22	1.54	0.71
4:C:33:ARG:HH22	4:C:74:GLU:HB3	1.56	0.70
45:r:4:ILE:HB	45:r:9:ILE:HD12	1.76	0.68
20:S:11:ARG:HH12	20:S:98:LYS:HG2	1.59	0.68
1:1:4302:U:H3	1:1:4305:A:H61	1.40	0.68
36:i:132:ILE:HG22	36:i:134:SER:H	1.60	0.67
27:Z:31:ARG:HD2	27:Z:34:HIS:HB2	1.77	0.66
1:1:2561:G:O6	1:1:2610:C:N4	2.29	0.65
1:1:75:G:H2'	1:1:76:G:H8	1.62	0.65
1:1:4045:C:H5'	33:f:3:VAL:HG11	1.79	0.64
45:r:25:VAL:HG12	45:r:29:ARG:HD2	1.80	0.64
4:C:5:VAL:H	4:C:32:ASN:HD21	1.46	0.64
16:O:40:ILE:HG12	16:O:47:VAL:HG12	1.79	0.64
41:n:84:THR:HG21	41:n:103:PHE:HB3	1.78	0.64
22:U:34:VAL:HG13	22:U:67:VAL:HG22	1.80	0.63
1:1:73:C:N3	1:1:74:A:N6	2.46	0.63
1:1:617:G:H1	1:1:623:C:H42	1.45	0.63
1:1:2091:G:N7	18:Q:6:ARG:NH1	2.47	0.63
9:H:73:LYS:HE3	9:H:117:LEU:HD11	1.79	0.63
42:o:37:ARG:HB3	42:o:75:ASP:HB3	1.80	0.63
1:1:2078:A:OP2	19:R:80:ARG:NH2	2.30	0.62
17:P:14:LYS:HE2	17:P:77:HIS:HA	1.82	0.62
1:1:3113:C:N4	1:1:3128:G:OP2	2.31	0.62
2:3:43:C:O2	6:E:92:ARG:NH2	2.32	0.62
1:1:1243:C:H42	1:1:1294:G:H1	1.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:951:G:OP2	45:r:101:ARG:NH2	2.33	0.62
20:S:4:ILE:HG12	20:S:106:VAL:HG22	1.80	0.62
35:h:46:GLU:HG2	35:h:87:LEU:HD21	1.80	0.62
10:I:11:GLN:NE2	10:I:54:ILE:O	2.32	0.61
1:1:1305:G:H21	1:1:1332:A:H2	1.48	0.61
1:1:3231:U:H3	1:1:3241:A:H61	1.48	0.61
9:H:23:LEU:HD12	9:H:118:ILE:HD13	1.82	0.61
5:D:149:ILE:HD11	5:D:188:MET:HE3	1.82	0.61
1:1:441:A:H61	1:1:493:A:H61	1.48	0.61
1:1:107:G:N7	52:y:10:ARG:NH2	2.48	0.61
1:1:937:A:N6	1:1:1345:U:O4	2.31	0.61
1:1:1409:C:O2'	1:1:3420:C:N4	2.34	0.61
35:h:40:ARG:NH1	35:h:55:ILE:O	2.34	0.60
9:H:53:ARG:HB3	9:H:55:VAL:HG22	1.81	0.60
37:j:83:HIS:NE2	37:j:148:ASN:OD1	2.33	0.60
47:t:25:THR:HG23	47:t:66:LEU:HD12	1.82	0.60
1:1:2562:G:N2	1:1:2609:A:OP2	2.34	0.60
35:h:49:LYS:O	35:h:72:ARG:NH1	2.34	0.60
45:r:3:ARG:O	45:r:57:ARG:NH2	2.34	0.60
7:F:88:GLN:HE21	7:F:163:ARG:HD2	1.67	0.60
39:l:66:LEU:HD21	39:l:97:ASN:HD21	1.67	0.60
7:F:24:ILE:HD11	7:F:43:VAL:HG11	1.84	0.60
10:I:76:ALA:HB1	10:I:80:LYS:HE3	1.84	0.60
16:O:111:ARG:NH2	16:O:117:PHE:OXT	2.35	0.60
36:i:124:MET:HG3	36:i:146:ARG:HB3	1.84	0.60
1:1:1328:C:O2'	45:r:29:ARG:NH1	2.34	0.59
1:1:1373:G:H5''	39:l:36:LYS:HE3	1.84	0.59
6:E:115:ARG:HE	6:E:178:ARG:HH12	1.48	0.59
1:1:890:G:O2'	1:1:906:A:N6	2.36	0.59
6:E:140:GLU:OE2	28:a:26:SER:OG	2.20	0.59
13:L:58:TYR:O	32:e:13:ARG:NH2	2.36	0.59
35:h:189:ALA:HB3	35:h:196:ILE:HB	1.84	0.59
36:i:62:ARG:NH1	36:i:69:GLU:OE1	2.36	0.59
35:h:14:ILE:HG22	35:h:15:VAL:HG13	1.85	0.59
1:1:501:C:OP1	44:q:114:ARG:NH2	2.36	0.59
1:1:1776:A:H5'	1:1:1777:G:H5''	1.83	0.59
1:1:3645:U:O2	1:1:3658:G:N1	2.36	0.59
10:I:73:PRO:HG2	10:I:78:LEU:HD12	1.84	0.58
9:H:94:ARG:HG2	9:H:129:LEU:HB3	1.83	0.58
21:T:38:ALA:O	21:T:81:LYS:NZ	2.36	0.58
1:1:3199:U:O2	3:B:14:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:n:46:MET:HE3	41:n:50:GLN:HE21	1.68	0.58
42:o:8:ILE:HG12	42:o:100:ILE:HG22	1.86	0.58
5:D:189:THR:HG22	5:D:191:ASP:H	1.68	0.58
1:1:1222:G:H5''	51:x:78:ARG:HD2	1.86	0.58
31:d:24:THR:HG23	31:d:27:GLY:H	1.69	0.58
36:i:172:GLU:HB2	36:i:183:LYS:HD2	1.86	0.58
1:1:203:G:O2'	1:1:465:A:N1	2.37	0.57
4:C:46:ARG:NH1	4:C:85:ALA:O	2.35	0.57
9:H:29:ASP:OD2	9:H:56:ARG:NH2	2.37	0.57
1:1:1663:C:H42	1:1:1675:G:H1	1.52	0.57
42:o:52:LEU:HB2	46:s:81:ARG:HD2	1.87	0.57
1:1:61:G:N7	52:y:6:SER:OG	2.38	0.57
1:1:2586:A:N6	1:1:2594:A:OP2	2.37	0.57
1:1:1846:A:O2'	5:D:162:ARG:NH1	2.38	0.57
9:H:63:ALA:O	9:H:67:THR:OG1	2.23	0.57
49:v:61:ILE:HA	49:v:75:LEU:HA	1.87	0.57
22:U:48:PRO:HG3	22:U:56:GLY:HA3	1.87	0.56
36:i:75:TYR:OH	36:i:97:ARG:NH1	2.38	0.56
1:1:2000:G:H4'	20:S:6:LYS:HB2	1.87	0.56
1:1:3295:A:OP2	3:B:221:ARG:NH1	2.38	0.56
7:F:89:LEU:HD23	7:F:94:TYR:HB3	1.85	0.56
38:k:75:GLU:HG2	38:k:89:VAL:HG11	1.87	0.56
1:1:1315:U:HO2'	1:1:1360:A:HO2'	1.54	0.56
46:s:3:LYS:HB2	46:s:6:MET:HG2	1.86	0.56
49:v:68:SER:HB3	49:v:71:LYS:HB3	1.88	0.56
1:1:2073:U:OP2	13:L:29:LYS:NZ	2.39	0.56
9:H:103:ASN:HA	9:H:107:GLU:HB3	1.86	0.56
37:j:13:GLU:OE2	37:j:68:ARG:NH1	2.39	0.56
1:1:1807:G:OP2	22:U:82:ARG:NH1	2.39	0.56
17:P:30:VAL:HG12	17:P:81:VAL:HG12	1.87	0.56
39:l:140:ASP:OD1	39:l:143:ARG:NH1	2.38	0.56
40:m:43:GLU:HG2	40:m:101:ILE:HG12	1.87	0.56
1:1:677:U:H3	1:1:713:G:H22	1.54	0.56
41:n:12:ARG:O	41:n:106:ARG:NH2	2.39	0.56
1:1:3375:G:N2	1:1:3377:A:O2'	2.39	0.55
4:C:19:GLY:HA2	17:P:79:PRO:HG2	1.89	0.55
5:D:168:ASP:OD2	5:D:170:ARG:NE	2.38	0.55
44:q:114:ARG:HG2	44:q:119:VAL:HB	1.89	0.55
5:D:149:ILE:HG12	5:D:188:MET:HG2	1.87	0.55
43:p:83:GLU:OE1	43:p:109:ASN:ND2	2.40	0.55
47:t:35:GLN:HE21	47:t:39:LEU:HD13	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:29:PRO:HG2	3:B:34:LEU:HD11	1.88	0.55
1:1:517:G:N2	1:1:530:G:OP1	2.39	0.55
10:I:23:VAL:HG11	10:I:27:LEU:HG	1.87	0.55
10:I:107:GLU:HA	10:I:110:GLN:HE21	1.72	0.55
5:D:32:VAL:HG13	5:D:178:VAL:HG23	1.88	0.55
36:i:95:GLU:HA	36:i:100:ASN:HD22	1.72	0.55
1:1:3973:C:O2	14:M:123:LYS:NZ	2.40	0.55
3:B:108:LYS:HA	3:B:196:GLY:HA2	1.89	0.55
4:C:136:ASN:HD21	4:C:139:SER:HB2	1.71	0.55
3:B:107:PRO:HD2	3:B:110:LEU:HD22	1.89	0.55
1:1:444:G:N2	1:1:491:G:N3	2.55	0.55
1:1:1457:A:O2'	1:1:1459:C:N4	2.40	0.55
3:B:165:VAL:HG21	3:B:181:MET:HE1	1.88	0.55
22:U:4:LYS:O	22:U:94:ARG:NH2	2.39	0.55
1:1:1073:U:O2	34:g:103:ASN:ND2	2.40	0.54
1:1:3306:C:OP2	3:B:182:ARG:NH1	2.40	0.54
1:1:2599:G:O2'	1:1:2605:G:N2	2.40	0.54
1:1:4364:A:OP2	1:1:4366:G:N2	2.40	0.54
7:F:86:LYS:HG2	7:F:132:VAL:HG22	1.87	0.54
14:M:42:THR:HG22	14:M:93:VAL:HG12	1.89	0.54
37:j:83:HIS:HE2	37:j:148:ASN:H	1.56	0.54
1:1:2871:A:OP1	25:X:3:ARG:NH2	2.35	0.54
21:T:13:ALA:HB3	21:T:33:LYS:HD2	1.90	0.54
14:M:64:TRP:HB2	14:M:104:GLU:HB2	1.89	0.54
1:1:2552:A:O2'	9:H:62:ARG:NH2	2.41	0.54
10:I:133:ARG:HG3	10:I:138:VAL:HA	1.89	0.54
24:W:37:ILE:HG22	24:W:38:VAL:HG23	1.90	0.54
37:j:55:GLU:HG3	37:j:57:PRO:HD2	1.90	0.54
1:1:841:C:H2'	1:1:843:U:H5'	1.89	0.54
1:1:2160:A:H61	32:e:19:LYS:HE2	1.73	0.54
20:S:73:LYS:HB2	20:S:106:VAL:HB	1.90	0.54
1:1:2608:C:H2'	1:1:2609:A:H8	1.73	0.54
1:1:4090:U:H2'	1:1:4091:U:H2'	1.88	0.54
43:p:113:VAL:HG12	50:w:73:ARG:HD2	1.89	0.54
1:1:988:G:N2	1:1:1217:C:O2	2.38	0.54
1:1:1029:U:N3	1:1:1031:C:O2	2.40	0.54
1:1:2006:G:N1	1:1:2009:A:OP2	2.37	0.54
46:s:46:LEU:HB3	51:x:13:LEU:HD13	1.90	0.54
1:1:2789:G:N2	1:1:2792:A:OP2	2.37	0.53
41:n:47:VAL:HA	41:n:50:GLN:HG3	1.89	0.53
21:T:48:GLN:HE21	21:T:55:VAL:H	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:4028:U:O2'	1:1:4153:U:OP1	2.24	0.53
1:1:1159:U:O4'	1:1:1182:G:N2	2.42	0.53
1:1:3804:A:OP1	6:E:71:ARG:NH2	2.39	0.53
26:Y:21:LEU:HD12	26:Y:46:VAL:HG13	1.91	0.53
1:1:4366:G:H1'	1:1:4367:G:H2'	1.89	0.53
10:I:7:TYR:HB2	10:I:57:VAL:HG13	1.90	0.53
42:o:40:ILE:HD12	42:o:73:LEU:HD12	1.90	0.53
46:s:39:GLU:O	46:s:43:ASN:ND2	2.42	0.53
1:1:1955:A:O2'	18:Q:3:ARG:NH2	2.42	0.53
18:Q:76:TYR:OH	18:Q:92:ARG:NH1	2.41	0.53
44:q:46:ASN:ND2	44:q:89:OTD:SB	2.74	0.53
50:w:62:ALA:HB1	50:w:67:LEU:HB2	1.91	0.53
1:1:127:G:O2'	49:v:6:ARG:NH1	2.41	0.53
1:1:1368:A:OP1	42:o:64:GLN:NE2	2.42	0.53
1:1:1233:G:OP1	41:n:119:ARG:NH1	2.42	0.53
5:D:181:ILE:HG12	13:L:1:MET:HE3	1.91	0.53
1:1:2074:U:H1'	1:1:3536:6MZ:H9C1	1.91	0.52
3:B:258:ARG:NH1	3:B:264:ASP:OD1	2.42	0.52
1:1:1320:C:N3	51:x:36:ARG:NH1	2.56	0.52
1:1:1483:G:O6	29:b:40:ARG:NH2	2.41	0.52
1:1:2570:C:N4	1:1:2576:A:OP2	2.41	0.52
1:1:2940:A:H2'	1:1:2941:G:C8	2.45	0.52
10:I:72:THR:H	10:I:116:MET:HE3	1.74	0.52
36:i:76:TYR:OH	36:i:205:SER:OG	2.27	0.52
45:r:89:LEU:HD23	45:r:92:ARG:HE	1.74	0.52
1:1:1241:G:OP1	39:l:35:LYS:NZ	2.43	0.52
1:1:3822:G:H2'	1:1:3823:A:H8	1.75	0.52
1:1:1005:A:H3'	1:1:1006:G:H8	1.75	0.52
1:1:1186:G:O3'	41:n:115:LYS:NZ	2.41	0.52
1:1:2591:A:O2'	1:1:2610:C:O2	2.28	0.52
51:x:19:VAL:HG11	51:x:44:MET:HG2	1.92	0.52
1:1:35:G:N3	44:q:115:SER:OG	2.43	0.52
5:D:111:GLU:OE2	5:D:115:GLN:NE2	2.43	0.52
49:v:17:MET:HG3	49:v:20:SER:HB2	1.90	0.52
1:1:51:A:N7	1:1:114:U:O2'	2.37	0.52
41:n:81:HIS:HE1	41:n:85:ARG:HH21	1.56	0.52
1:1:683:G:N2	43:p:39:GLY:O	2.42	0.52
7:F:9:VAL:HB	7:F:50:LEU:HB2	1.91	0.52
1:1:2772:G:OP1	29:b:16:ARG:NE	2.40	0.52
1:1:3443:A:N7	1:1:3445:5MU:O2'	2.43	0.52
3:B:142:HIS:ND1	3:B:193:GLY:O	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:r:5:ALA:HB2	45:r:60:VAL:HG11	1.92	0.51
46:s:49:GLN:NE2	51:x:11:ILE:O	2.35	0.51
1:1:2180:G:H1'	5:D:69:ARG:HD3	1.93	0.51
8:G:3:VAL:HG23	8:G:38:PRO:HA	1.92	0.51
1:1:3157:G:H5'	15:N:39:PRO:HG2	1.92	0.51
1:1:2217:G:H1	1:1:2226:U:H3	1.57	0.51
9:H:68:PRO:HA	9:H:72:LEU:HG	1.93	0.51
35:h:50:ALA:HA	35:h:72:ARG:HH11	1.75	0.51
1:1:662:U:O2'	1:1:836:G:OP1	2.28	0.51
1:1:2751:G:OP1	13:L:13:LYS:NZ	2.44	0.51
1:1:3370:U:OP1	1:1:3916:G:O2'	2.26	0.51
1:1:311:C:OP1	48:u:31:ARG:NH1	2.42	0.51
1:1:58:C:O2'	1:1:388:G:N7	2.39	0.51
46:s:29:ALA:HA	46:s:32:SER:HB2	1.91	0.51
1:1:2589:U:O2'	1:1:2591:A:OP2	2.29	0.51
14:M:11:LYS:HD3	14:M:86:LYS:HD3	1.93	0.51
21:T:59:ASN:HB2	21:T:84:TYR:HB2	1.93	0.51
44:q:56:ARG:NE	44:q:62:GLU:OE1	2.38	0.51
3:B:244:PRO:O	3:B:251:GLN:NE2	2.44	0.51
35:h:114:LYS:NZ	35:h:118:ASP:OD2	2.44	0.51
39:l:16:PRO:HB3	41:n:46:MET:HB2	1.93	0.51
51:x:19:VAL:HG21	51:x:44:MET:HE3	1.93	0.50
1:1:1876:G:O2'	1:1:1930:G:OP1	2.27	0.50
1:1:2568:G:N2	10:I:134:SER:O	2.44	0.50
4:C:26:VAL:HG22	4:C:188:LEU:HD22	1.94	0.50
1:1:1727:A:N1	1:1:1771:A:O2'	2.44	0.50
4:C:46:ARG:NH2	4:C:88:GLU:O	2.42	0.50
5:D:83:VAL:HB	5:D:86:ALA:HB2	1.93	0.50
19:R:41:ILE:HD13	19:R:103:ALA:HA	1.93	0.50
30:c:8:LYS:HA	30:c:24:THR:HA	1.93	0.50
1:1:2553:G:H3'	9:H:59:LEU:HD21	1.93	0.50
36:i:98:LEU:HB2	36:i:135:TYR:HB3	1.93	0.50
12:K:7:MET:HE1	12:K:44:LYS:HG3	1.94	0.50
37:j:111:MET:HE2	37:j:125:ALA:HB1	1.93	0.50
1:1:1048:G:H5''	46:s:3:LYS:HG2	1.93	0.50
38:k:51:ILE:HD12	38:k:85:ILE:HG21	1.93	0.50
49:v:21:ILE:HG13	49:v:46:VAL:HB	1.92	0.50
1:1:8:A:N6	36:i:202:GLU:O	2.41	0.50
1:1:1551:G:H5''	1:1:1552:G:H5'	1.94	0.50
9:H:33:VAL:HG12	9:H:35:VAL:H	1.77	0.50
38:k:21:MET:HG2	38:k:24:ARG:HH21	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:976:G:OP2	1:1:1358:U:O2'	2.29	0.50
1:1:3640:A:O2'	1:1:3665:G:N3	2.45	0.49
2:3:5:U:OP1	2:3:61:G:O2'	2.28	0.49
9:H:117:LEU:HB2	9:H:120:ALA:HA	1.94	0.49
28:a:15:SER:O	28:a:34:LEU:N	2.45	0.49
30:c:8:LYS:HB3	30:c:24:THR:HG22	1.94	0.49
34:g:26:LYS:NZ	34:g:194:ASP:OD2	2.38	0.49
37:j:96:MET:HE1	37:j:115:LEU:HD21	1.94	0.49
1:1:374:A:OP1	1:1:452:A:N6	2.45	0.49
1:1:1266:G:N2	1:1:1269:A:OP2	2.37	0.49
3:B:133:ARG:HB3	3:B:186:ALA:HB1	1.94	0.49
51:x:51:VAL:HG21	51:x:71:LEU:HB3	1.93	0.49
2:3:7:G:O2'	16:O:38:GLN:NE2	2.46	0.49
1:1:1986:A:O2'	22:U:43:LYS:O	2.30	0.49
41:n:42:GLU:OE2	41:n:45:ARG:NH1	2.46	0.49
1:1:1217:C:OP2	46:s:9:ARG:NH2	2.43	0.49
1:1:3649:C:H3'	1:1:3650:G:H8	1.77	0.49
41:n:28:ILE:HG21	41:n:35:LEU:HD13	1.93	0.49
42:o:6:ILE:HB	42:o:76:ILE:HB	1.95	0.49
1:1:957:U:H4'	51:x:79:THR:HG23	1.93	0.49
1:1:1464:U:H3'	1:1:1465:G:H4'	1.93	0.49
44:q:68:GLY:O	44:q:99:ARG:NH1	2.45	0.49
1:1:408:A:OP1	36:i:110:THR:OG1	2.31	0.49
9:H:94:ARG:HA	9:H:129:LEU:HD22	1.94	0.49
25:X:37:ARG:HG2	25:X:48:THR:HG22	1.94	0.49
32:e:9:GLY:O	32:e:13:ARG:NH2	2.45	0.49
1:1:373:A:N1	1:1:391:G:O2'	2.39	0.49
1:1:501:C:OP2	44:q:121:ARG:NH1	2.45	0.49
3:B:117:GLN:O	3:B:128:ASN:ND2	2.46	0.49
10:I:34:ILE:HA	10:I:37:PHE:HD2	1.77	0.49
44:q:33:VAL:HG22	44:q:79:VAL:HG22	1.94	0.49
1:1:1538:C:N4	1:1:1953:A:OP2	2.46	0.49
16:O:68:LYS:HE2	16:O:101:GLY:HA2	1.95	0.49
22:U:4:LYS:HD3	22:U:83:VAL:HB	1.95	0.49
26:Y:14:LEU:HA	26:Y:17:GLU:HB3	1.95	0.49
1:1:518:C:H4'	1:1:519:C:H5''	1.94	0.48
1:1:1003:G:N2	1:1:1037:C:O2	2.36	0.48
1:1:59:A:H5''	1:1:387:U:H5''	1.95	0.48
1:1:937:A:O2'	1:1:1378:C:N4	2.46	0.48
1:1:2020:A:N3	1:1:2087:C:O2'	2.44	0.48
1:1:544:G:OP1	36:i:56:ARG:NH2	2.35	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1451:G:H4'	1:1:1452:U:H5''	1.95	0.48
1:1:3436:G:O2'	1:1:3474:G:O6	2.29	0.48
39:l:115:SER:OG	39:l:116:MET:N	2.46	0.48
1:1:932:C:OP1	39:l:4:ARG:NE	2.46	0.48
1:1:1298:U:H3	39:l:114:LYS:HG2	1.78	0.48
1:1:4189:C:O2	12:K:70:ARG:NH2	2.47	0.48
1:1:444:G:H22	1:1:491:G:H1'	1.77	0.48
1:1:1458:G:N2	1:1:4367:G:O6	2.46	0.48
34:g:66:LYS:HB2	34:g:158:PRO:HA	1.96	0.48
19:R:41:ILE:HB	19:R:48:LYS:HD3	1.96	0.48
1:1:1297:G:N2	39:l:114:LYS:O	2.46	0.48
1:1:1769:G:O2'	1:1:1935:A:N3	2.46	0.48
1:1:2083:G:O2'	1:1:2760:A:OP1	2.31	0.48
5:D:134:LEU:HD23	5:D:164:LEU:HD12	1.95	0.48
11:J:125:TYR:OH	11:J:132:HIS:NE2	2.42	0.48
1:1:2548:G:H21	1:1:2619:U:H3	1.61	0.48
1:1:2569:G:H21	10:I:89:SER:HB3	1.78	0.48
5:D:27:LEU:HG	5:D:104:ALA:HB2	1.96	0.48
20:S:25:ARG:NH1	20:S:74:ILE:O	2.46	0.48
24:W:18:ALA:O	24:W:20:ARG:NH1	2.47	0.48
34:g:67:ILE:HG23	34:g:160:ALA:HB3	1.96	0.48
1:1:975:A:N1	1:1:1366:C:O2'	2.42	0.48
1:1:2570:C:N4	1:1:2575:A:O2'	2.47	0.48
12:K:121:GLU:OE1	17:P:65:SER:OG	2.32	0.48
33:f:25:VAL:HB	33:f:35:GLN:HB2	1.96	0.48
1:1:3865:C:O2'	32:e:54:ASP:OD2	2.27	0.47
6:E:8:TYR:OH	6:E:29:PRO:O	2.30	0.47
9:H:122:GLN:HG2	9:H:124:ASP:H	1.79	0.47
40:m:64:LYS:HG2	40:m:71:VAL:HG21	1.95	0.47
1:1:816:A:OP1	1:1:4442:G:O2'	2.27	0.47
2:3:39:A:O2'	2:3:46:A:N1	2.46	0.47
19:R:43:ASN:HB3	19:R:46:GLU:HB3	1.95	0.47
23:V:72:VAL:HG12	23:V:93:ARG:HA	1.96	0.47
42:o:71:LEU:O	42:o:72:ARG:NH1	2.39	0.47
6:E:30:ARG:O	6:E:158:THR:OG1	2.26	0.47
13:L:76:GLU:HB2	13:L:111:ILE:HD13	1.96	0.47
45:r:20:THR:HA	45:r:25:VAL:HG23	1.97	0.47
1:1:4432:2MG:N2	1:1:4435:MA6:OP2	2.42	0.47
9:H:26:VAL:HG21	9:H:114:GLU:HG2	1.95	0.47
1:1:367:U:O4'	1:1:394:G:N2	2.48	0.47
1:1:1590:A:N1	1:1:1604:G:O2'	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2681:A:H4'	1:1:2682:U:H5'	1.97	0.47
1:1:3151:G:H5''	1:1:3152:C:H5'	1.97	0.47
5:D:149:ILE:HD12	5:D:172:ALA:HA	1.96	0.47
7:F:5:ALA:HB2	7:F:66:GLY:HA2	1.96	0.47
38:k:38:ARG:NH1	38:k:98:GLU:O	2.45	0.47
42:o:22:THR:HA	42:o:25:ILE:HG22	1.96	0.47
51:x:31:LEU:HB2	51:x:49:ILE:HG22	1.97	0.47
1:1:2394:C:OP2	45:r:93:ARG:NH2	2.48	0.47
1:1:3689:A:H2'	1:1:3690:A:C8	2.50	0.47
7:F:17:VAL:HG22	7:F:26:ILE:HG12	1.97	0.47
21:T:24:MET:HE2	21:T:30:ILE:HG22	1.96	0.47
1:1:2900:U:H4'	1:1:3109:A:H4'	1.96	0.47
9:H:31:ARG:HH21	9:H:108:VAL:HG21	1.79	0.47
13:L:29:LYS:HG3	13:L:30:THR:HG23	1.97	0.47
21:T:8:LEU:HD23	21:T:50:LEU:HD21	1.97	0.47
1:1:3159:G:H3'	15:N:2:ARG:HG3	1.97	0.47
13:L:57:LEU:HD22	32:e:54:ASP:HB3	1.96	0.47
1:1:1567:C:H5''	26:Y:43:LEU:HD12	1.96	0.46
1:1:3631:G:N3	1:1:3679:A:N6	2.62	0.46
41:n:119:ARG:HG3	41:n:125:PRO:HG3	1.98	0.46
1:1:1063:C:H3'	1:1:1064:G:H2'	1.98	0.46
43:p:20:VAL:HG13	43:p:83:GLU:HG3	1.97	0.46
1:1:1813:G:N1	1:1:1816:A:OP2	2.44	0.46
1:1:2219:G:OP2	47:t:88:ARG:NH2	2.48	0.46
42:o:21:ALA:HB1	42:o:92:LEU:HD23	1.96	0.46
1:1:1297:G:O2'	39:l:114:LYS:NZ	2.33	0.46
1:1:1981:C:O2	1:1:1985:A:N6	2.45	0.46
1:1:2423:A:H5''	1:1:3774:A:H61	1.79	0.46
1:1:2545:A:N6	1:1:2546:A:N1	2.63	0.46
1:1:2555:C:H2'	1:1:2556:A:H8	1.80	0.46
1:1:3458:A:N3	1:1:4066:A:O2'	2.45	0.46
9:H:18:VAL:HA	9:H:86:MET:HE2	1.97	0.46
1:1:1073:U:H3	1:1:1102:A:H61	1.63	0.46
1:1:1749:U:OP2	32:e:8:ARG:NH1	2.49	0.46
1:1:2393:U:O2'	1:1:2395:C:OP2	2.32	0.46
45:r:97:VAL:HG23	45:r:109:ARG:HH22	1.81	0.46
1:1:1152:A:OP1	42:o:70:HIS:ND1	2.49	0.46
3:B:144:VAL:HB	3:B:154:LEU:HB2	1.97	0.46
6:E:117:LEU:N	6:E:177:PHE:O	2.46	0.46
16:O:59:ALA:HA	16:O:62:LEU:HD12	1.98	0.46
1:1:694:A:OP1	43:p:55:SER:OG	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:946:A:H2'	1:1:947:G:C8	2.51	0.46
1:1:3985:U:OP1	1:1:4043:U:O2'	2.32	0.46
9:H:34:THR:HB	9:H:38:MET:HE3	1.98	0.46
1:1:974:A:OP1	46:s:69:ARG:NH1	2.49	0.46
37:j:153:VAL:HG21	40:m:99:LEU:HD22	1.97	0.46
49:v:25:ILE:HD11	49:v:61:ILE:HD11	1.98	0.46
1:1:526:C:H2'	1:1:527:7MG:H4'	1.98	0.45
1:1:2317:U:H2'	13:L:21:ARG:HA	1.97	0.45
47:t:64:ARG:NH1	47:t:68:ASP:OD1	2.49	0.45
1:1:413:G:O2'	1:1:428:G:N2	2.49	0.45
1:1:1124:G:N2	1:1:1125:U:O4	2.36	0.45
1:1:2069:A:N3	18:Q:37:GLN:NE2	2.63	0.45
1:1:4081:C:H5'	4:C:149:ASN:HB2	1.98	0.45
37:j:111:MET:HG3	37:j:140:THR:HG21	1.99	0.45
46:s:49:GLN:OE1	51:x:13:LEU:N	2.46	0.45
46:s:53:ARG:HD3	46:s:59:ARG:HH12	1.81	0.45
7:F:80:THR:HG23	7:F:81:GLU:HG3	1.98	0.45
45:r:12:HIS:HA	45:r:44:LYS:HD3	1.98	0.45
1:1:459:A:H2'	1:1:460:A:C8	2.50	0.45
1:1:1040:U:H2'	1:1:1041:G:H8	1.81	0.45
1:1:1062:U:O4	35:h:3:GLN:NE2	2.40	0.45
34:g:3:THR:OG1	34:g:4:VAL:N	2.48	0.45
42:o:84:VAL:O	42:o:88:MET:N	2.50	0.45
4:C:4:LEU:HG	4:C:32:ASN:HD22	1.80	0.45
41:n:12:ARG:HG3	41:n:13:LYS:H	1.80	0.45
42:o:52:LEU:HD23	42:o:62:ARG:HG2	1.97	0.45
1:1:1329:A:H5'	45:r:29:ARG:HH11	1.80	0.45
1:1:3811:U:H5''	6:E:131:GLY:HA3	1.98	0.45
5:D:46:GLN:O	5:D:88:ARG:NH2	2.50	0.45
7:F:155:GLU:HG2	7:F:157:TYR:H	1.81	0.45
1:1:41:G:H2'	1:1:42:G:C8	2.52	0.45
1:1:2548:G:N2	1:1:2549:C:H42	2.14	0.45
5:D:125:SER:O	5:D:137:LYS:NZ	2.49	0.45
45:r:98:ARG:HB2	45:r:100:GLN:HE22	1.81	0.45
1:1:4:U:H2'	1:1:5:U:H2'	1.99	0.45
1:1:769:G:H4'	1:1:4429:A:H4'	1.98	0.45
5:D:176:ASP:OD1	5:D:176:ASP:N	2.50	0.45
10:I:71:LYS:HE2	10:I:116:MET:HE1	1.97	0.45
50:w:36:SER:HA	50:w:72:ASP:HB3	1.98	0.45
1:1:666:G:N2	47:t:52:SER:OG	2.50	0.45
3:B:69:ARG:NH2	3:B:127:GLY:O	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:e:32:ILE:H	32:e:32:ILE:HG13	1.59	0.45
43:p:28:ASN:O	43:p:57:LYS:NZ	2.42	0.45
1:1:1238:A:H5'	1:1:1336:C:H41	1.81	0.45
1:1:1360:A:OP2	46:s:75:ARG:NH2	2.50	0.45
1:1:3911:G:O2'	1:1:3917:A:N6	2.50	0.45
8:G:113:SER:O	8:G:116:ARG:NH1	2.46	0.45
34:g:76:ALA:HB1	34:g:79:ALA:HB3	1.99	0.45
1:1:627:G:OP1	48:u:51:ARG:NH1	2.48	0.44
1:1:4142:C:O2'	4:C:45:TYR:OH	2.34	0.44
1:1:4189:C:OP1	17:P:51:ARG:NH2	2.50	0.44
8:G:26:ALA:HA	8:G:30:LEU:HB2	1.99	0.44
32:e:52:LYS:HB3	32:e:52:LYS:HE3	1.84	0.44
1:1:390:U:H2'	1:1:391:G:H8	1.82	0.44
1:1:438:U:H3	1:1:496:A:H62	1.64	0.44
1:1:1342:C:H2'	1:1:1343:G:C8	2.53	0.44
28:a:16:CYS:SG	28:a:17:SER:N	2.90	0.44
34:g:104:TRP:HE1	34:g:108:ARG:HH21	1.63	0.44
34:g:166:ALA:HB3	34:g:191:SER:HB3	1.97	0.44
41:n:22:LYS:O	41:n:62:ASP:N	2.44	0.44
1:1:235:C:H2'	1:1:236:A:C8	2.52	0.44
1:1:372:C:N4	1:1:388:G:OP2	2.42	0.44
1:1:2543:G:N2	1:1:2625:U:O2	2.49	0.44
1:1:4144:G:O2'	1:1:4281:G:N2	2.46	0.44
1:1:4446:G:H2'	1:1:4447:A:C8	2.53	0.44
1:1:110:C:O2'	48:u:25:ARG:O	2.32	0.44
1:1:1081:A:OP2	37:j:52:LYS:NZ	2.39	0.44
1:1:1143:G:H2'	1:1:1144:G:C8	2.52	0.44
2:3:66:A:OP2	2:3:108:A:N6	2.46	0.44
49:v:68:SER:OG	49:v:69:LYS:N	2.50	0.44
1:1:1063:C:OP2	1:1:1064:G:O2'	2.32	0.44
1:1:2587:U:H5'	10:I:126:ARG:HE	1.83	0.44
1:1:4038:G:O2'	1:1:4163:A:N1	2.49	0.44
2:3:43:C:H5''	28:a:1:MET:HG2	1.99	0.44
7:F:95:ARG:HB2	7:F:128:GLN:HB3	1.99	0.44
36:i:25:VAL:HG22	36:i:161:LEU:HD21	1.98	0.44
1:1:269:C:H2'	1:1:270:A:C8	2.53	0.44
1:1:891:U:H2'	1:1:892:A:H8	1.82	0.44
1:1:958:A:N6	51:x:77:THR:O	2.51	0.44
1:1:2545:A:H61	1:1:2622:G:H1	1.66	0.44
1:1:2847:G:H1'	21:T:59:ASN:HB3	2.00	0.44
1:1:3657:U:H2'	1:1:3658:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:23:VAL:HG13	10:I:26:ALA:HB3	2.00	0.44
43:p:116:ILE:HD12	53:z:31:GLU:HG2	2.00	0.44
1:1:375:U:O2	48:u:28:ARG:NH2	2.45	0.44
1:1:412:A:H62	1:1:431:A:H61	1.65	0.44
1:1:2302:C:OP1	5:D:57:LYS:NZ	2.47	0.44
1:1:2772:G:N7	20:S:16:LYS:HE3	2.33	0.44
9:H:103:ASN:HD21	9:H:109:LYS:HA	1.81	0.44
36:i:78:GLU:OE2	36:i:81:ARG:NH1	2.38	0.44
39:l:69:VAL:HG23	39:l:100:ALA:HB1	1.99	0.44
52:y:25:ARG:HG3	52:y:66:LEU:HD11	1.99	0.44
1:1:2551:C:O2	9:H:61:ARG:NH2	2.51	0.44
1:1:3324:U:H5''	3:B:157:SER:HB2	2.00	0.44
8:G:94:ILE:HG23	8:G:98:ASP:HB3	1.98	0.44
34:g:72:THR:OG1	34:g:169:GLU:OE2	2.27	0.44
36:i:69:GLU:O	36:i:73:ARG:N	2.45	0.44
52:y:67:ILE:HB	52:y:71:LYS:HD3	2.00	0.44
1:1:3893:U:OP1	24:W:55:ARG:NH2	2.40	0.44
11:J:13:ARG:NH1	11:J:49:ASP:O	2.49	0.44
18:Q:104:VAL:HG11	19:R:45:GLU:HG3	1.99	0.44
36:i:27:ALA:O	36:i:30:THR:OG1	2.33	0.44
45:r:9:ILE:HD11	45:r:22:ILE:HG13	2.00	0.43
51:x:3:ARG:HE	51:x:7:LYS:HD3	1.82	0.43
1:1:181:A:N6	1:1:195:A:OP2	2.52	0.43
1:1:669:G:H1	1:1:737:C:H42	1.66	0.43
1:1:802:A:H3'	1:1:803:G:H8	1.83	0.43
1:1:1404:C:O2	1:1:4435:MA6:O2'	2.31	0.43
10:I:112:LYS:HB3	10:I:116:MET:HG3	2.00	0.43
41:n:55:VAL:HG11	41:n:94:LEU:HD13	2.00	0.43
1:1:3883:A:O2'	16:O:117:PHE:O	2.35	0.43
5:D:12:LEU:HD13	5:D:190:ALA:HB1	1.98	0.43
6:E:158:THR:HG23	6:E:160:ALA:H	1.82	0.43
13:L:62:PRO:HB2	32:e:30:ARG:HH11	1.82	0.43
18:Q:50:ARG:O	18:Q:54:LYS:NZ	2.48	0.43
35:h:156:ARG:HD3	35:h:193:TYR:HB3	2.01	0.43
37:j:94:VAL:HG11	37:j:140:THR:HG22	2.00	0.43
41:n:41:ARG:HE	41:n:43:THR:HB	1.83	0.43
46:s:45:VAL:HG13	46:s:46:LEU:HD22	2.00	0.43
6:E:58:ALA:HB2	6:E:65:PRO:HD3	2.01	0.43
9:H:30:SER:HB2	9:H:110:ALA:HB2	1.99	0.43
36:i:116:GLN:HA	36:i:119:SER:HB3	1.99	0.43
40:m:5:ASP:OD1	40:m:77:ARG:NH1	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:x:52:HIS:CD2	51:x:54:GLY:H	2.36	0.43
12:K:108:ARG:HB3	12:K:116:ILE:HG21	2.01	0.43
35:h:85:GLU:OE2	35:h:88:ARG:NH1	2.44	0.43
40:m:112:THR:HG23	40:m:115:ALA:H	1.84	0.43
10:I:76:ALA:O	10:I:80:LYS:N	2.52	0.43
12:K:77:ILE:HG12	17:P:72:ARG:HG3	2.01	0.43
21:T:94:ASP:OD1	21:T:94:ASP:N	2.50	0.43
35:h:138:VAL:HA	35:h:149:ILE:HG21	2.00	0.43
37:j:156:LYS:HG2	40:m:71:VAL:HG13	2.01	0.43
1:1:2563:A:N6	1:1:2587:U:O4	2.46	0.43
1:1:3559:G:H5'	4:C:150:GLN:H	1.83	0.43
1:1:3648:A:H61	1:1:3655:U:H3	1.65	0.43
10:I:131:THR:O	10:I:134:SER:OG	2.32	0.43
1:1:161:A:N1	1:1:347:G:O2'	2.46	0.43
1:1:1690:C:H2'	1:1:1691:G:C8	2.54	0.43
1:1:2547:G:H5''	1:1:2548:G:C8	2.54	0.43
1:1:2748:U:O2	13:L:4:ASN:ND2	2.50	0.43
1:1:3756:G:N3	1:1:3756:G:H5'	2.34	0.43
3:B:145:GLU:HB2	3:B:188:CYS:HB3	2.00	0.43
10:I:14:ALA:HB3	10:I:51:GLY:H	1.82	0.43
29:b:38:HIS:ND1	29:b:39:LEU:O	2.52	0.43
34:g:130:THR:O	34:g:134:ALA:N	2.52	0.43
1:1:1802:U:H2'	1:1:1803:G:C8	2.54	0.43
1:1:2356:U:H5''	27:Z:19:LYS:HG3	2.01	0.43
41:n:30:ILE:HD12	41:n:35:LEU:HA	2.01	0.43
51:x:15:LEU:HD13	51:x:33:THR:HG21	2.00	0.43
1:1:420:U:O2'	1:1:423:G:O6	2.28	0.42
1:1:1250:A:H4'	41:n:70:GLY:H	1.84	0.42
1:1:1402:4OC:O2	1:1:4416:A:N1	2.52	0.42
1:1:1466:A:C2	1:1:4355:U:H4'	2.53	0.42
1:1:3779:A:H2'	1:1:3780:A:C8	2.54	0.42
22:U:72:ILE:HD12	22:U:83:VAL:HG21	2.01	0.42
1:1:2109:A:N1	1:1:2131:G:O2'	2.46	0.42
8:G:14:SER:OG	8:G:15:LEU:N	2.51	0.42
23:V:77:VAL:HG23	23:V:89:ILE:HG12	2.00	0.42
36:i:163:GLU:HA	36:i:167:LYS:HE2	2.02	0.42
1:1:825:A:O2'	40:m:9:ASP:OD2	2.36	0.42
1:1:1622:C:O2'	1:1:1632:A:N3	2.51	0.42
1:1:2386:G:H2'	1:1:2387:G:H8	1.84	0.42
1:1:3545:U:H2'	1:1:3546:G:C8	2.54	0.42
12:K:18:ARG:HB3	12:K:45:GLU:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:l:129:GLU:OE1	39:l:131:LYS:NZ	2.37	0.42
42:o:8:ILE:HD13	42:o:25:ILE:HD11	2.01	0.42
43:p:53:ARG:HH21	43:p:57:LYS:HE2	1.84	0.42
47:t:26:GLU:HG3	47:t:81:LEU:HD13	2.00	0.42
1:1:1920:C:H2'	1:1:1921:A:C8	2.54	0.42
1:1:2802:G:OP1	1:1:4215:G:O2'	2.25	0.42
1:1:3519:A:OP1	20:S:97:LEU:N	2.48	0.42
1:1:3984:A:O2'	1:1:4042:G:N2	2.50	0.42
1:1:1841:C:O2	22:U:68:SER:OG	2.36	0.42
1:1:3250:A:H3'	1:1:3251:A:H8	1.85	0.42
37:j:13:GLU:HG2	37:j:39:VAL:HG12	2.02	0.42
1:1:792:A:O2'	1:1:794:A:N7	2.50	0.42
2:3:15:A:H3'	2:3:16:G:H8	1.84	0.42
9:H:67:THR:HG21	9:H:75:ALA:N	2.35	0.42
19:R:75:VAL:HG22	19:R:86:GLN:HE22	1.85	0.42
26:Y:11:VAL:O	26:Y:15:ASN:ND2	2.52	0.42
53:z:10:GLU:OE2	53:z:18:ARG:NH1	2.53	0.42
1:1:94:G:H1'	1:1:95:C:H5	1.85	0.42
1:1:2924:G:O2'	1:1:3086:A:N6	2.53	0.42
35:h:91:VAL:HG21	35:h:101:ILE:HD11	2.02	0.42
1:1:528:C:N4	44:q:46:ASN:OD1	2.42	0.42
1:1:2892:C:H2'	1:1:2893:A:C8	2.55	0.42
35:h:150:LYS:HD3	35:h:169:ARG:HE	1.85	0.42
43:p:34:ILE:HG12	43:p:70:CYS:SG	2.60	0.42
1:1:1499:C:H42	1:1:1508:G:H1	1.67	0.42
1:1:1903:U:H5''	25:X:32:ASN:HB2	2.02	0.42
1:1:2756:G:H5''	18:Q:6:ARG:HD3	2.01	0.42
1:1:4027:C:O2'	1:1:4070:A:N3	2.49	0.42
2:3:14:U:OP2	2:3:70:C:O2'	2.33	0.42
3:B:75:PRO:HG2	3:B:97:LYS:HG3	2.00	0.42
35:h:117:ALA:HB1	35:h:187:SER:HB2	2.02	0.42
1:1:3425:A:O2'	1:1:4433:G:N3	2.51	0.42
42:o:46:LYS:HG2	42:o:68:ARG:HG2	2.02	0.42
45:r:98:ARG:HB2	45:r:100:GLN:NE2	2.35	0.42
1:1:79:G:H2'	1:1:80:A:H8	1.83	0.41
1:1:376:G:H4'	48:u:5:ARG:HD2	2.02	0.41
1:1:1230:C:H2'	1:1:1231:G:H8	1.85	0.41
1:1:2193:C:H5''	31:d:2:LYS:HE2	2.02	0.41
11:J:114:LEU:HG	11:J:118:MET:HE3	2.01	0.41
17:P:33:VAL:HG22	17:P:38:LYS:HG2	2.01	0.41
1:1:982:U:H5''	46:s:6:MET:HE2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1114:C:O2'	46:s:100:SER:O	2.32	0.41
1:1:3173:G:O2'	1:1:3497:U:O4	2.33	0.41
28:a:30:HIS:ND1	28:a:31:ASP:O	2.53	0.41
43:p:107:ILE:HG23	53:z:6:VAL:HG21	2.02	0.41
1:1:2574:G:O2'	1:1:2576:A:N6	2.53	0.41
3:B:146:MET:HE3	3:B:154:LEU:HD21	2.01	0.41
4:C:45:TYR:OH	4:C:81:GLU:OE2	2.34	0.41
6:E:175:PHE:HA	6:E:176:PRO:HD3	1.89	0.41
35:h:52:VAL:HG23	35:h:68:ILE:HG23	2.02	0.41
1:1:977:A:N6	1:1:1224:U:O5'	2.53	0.41
1:1:3633:G:H2'	1:1:3634:G:C8	2.56	0.41
2:3:55:U:HO2'	6:E:24:SER:HG	1.66	0.41
9:H:121:SER:OG	9:H:122:GLN:N	2.53	0.41
14:M:14:LYS:O	14:M:71:LYS:NZ	2.39	0.41
42:o:8:ILE:HB	42:o:74:VAL:HB	2.01	0.41
1:1:198:G:H2'	1:1:199:A:C8	2.55	0.41
1:1:618:C:N4	1:1:621:A:OP2	2.53	0.41
1:1:932:C:H2'	1:1:933:G:C8	2.55	0.41
1:1:2226:U:H2'	1:1:2227:A:C8	2.56	0.41
9:H:121:SER:HG	9:H:122:GLN:H	1.69	0.41
10:I:9:LYS:HG2	10:I:55:PRO:HB2	2.01	0.41
36:i:102:VAL:HG13	36:i:107:PHE:HB2	2.01	0.41
38:k:18:VAL:HG21	38:k:58:HIS:CD2	2.56	0.41
40:m:53:GLY:HA3	40:m:57:PRO:HA	2.02	0.41
1:1:3508:G:H5'	15:N:13:ASN:HA	2.03	0.41
37:j:107:ALA:O	37:j:112:ARG:NH2	2.49	0.41
42:o:7:ARG:NH1	42:o:75:ASP:OD2	2.54	0.41
47:t:21:ASP:O	47:t:23:GLY:N	2.53	0.41
1:1:2493:C:O2'	1:1:2506:A:N3	2.50	0.41
7:F:38:ASN:HD22	7:F:38:ASN:HA	1.67	0.41
37:j:66:LYS:HA	37:j:69:ARG:HE	1.86	0.41
53:z:31:GLU:OE2	53:z:35:ARG:NE	2.40	0.41
1:1:3302:U:H2'	1:1:3303:G:C8	2.55	0.41
13:L:85:VAL:HB	13:L:94:THR:HG22	2.01	0.41
38:k:5:GLU:OE2	50:w:24:LYS:NZ	2.42	0.41
45:r:65:VAL:O	45:r:69:LEU:N	2.54	0.41
1:1:675:A:H1'	43:p:118:HIS:CD2	2.56	0.41
1:1:2339:A:H2'	1:1:2340:G:C8	2.56	0.41
1:1:2370:G:O2'	1:1:2420:G:O6	2.38	0.41
1:1:2559:C:H42	1:1:2612:G:H1	1.69	0.41
1:1:2582:C:H2'	1:1:2583:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3983:U:O2	33:f:4:ARG:NH2	2.54	0.41
1:1:4345:G:N2	15:N:91:ALA:O	2.48	0.41
15:N:28:LEU:HD23	15:N:48:VAL:HG11	2.03	0.41
20:S:59:GLU:HB2	20:S:66:ILE:HD11	2.02	0.41
46:s:27:LEU:HD22	46:s:44:ALA:HA	2.02	0.41
53:z:31:GLU:OE2	53:z:34:ARG:NH2	2.53	0.41
1:1:1062:U:H2'	1:1:1063:C:C6	2.56	0.41
1:1:1162:C:H2'	1:1:1163:A:C8	2.56	0.41
12:K:7:MET:HB3	12:K:18:ARG:HD2	2.02	0.41
25:X:59:ILE:HG12	25:X:67:VAL:HG21	2.02	0.41
47:t:3:LEU:HD23	47:t:8:THR:HG22	2.03	0.41
1:1:3819:C:H5''	6:E:88:LYS:HD2	2.03	0.40
3:B:168:ASP:OD1	3:B:168:ASP:N	2.55	0.40
9:H:122:GLN:HE22	9:H:126:LEU:HD21	1.85	0.40
35:h:156:ARG:NH1	35:h:193:TYR:HB3	2.35	0.40
37:j:132:ASN:HD22	37:j:133:PRO:HD2	1.86	0.40
1:1:2235:G:C6	3:B:207:LYS:HB2	2.56	0.40
1:1:2598:C:H3'	1:1:2599:G:H8	1.86	0.40
5:D:147:LEU:HD23	5:D:180:LEU:HD23	2.03	0.40
9:H:24:SER:OG	9:H:86:MET:SD	2.71	0.40
13:L:74:THR:HG22	13:L:107:PHE:HB2	2.03	0.40
33:f:27:CYS:SG	33:f:28:SER:N	2.94	0.40
1:1:3302:U:H2'	1:1:3303:G:H8	1.87	0.40
37:j:96:MET:HE2	37:j:96:MET:HB3	1.91	0.40
38:k:38:ARG:HG2	38:k:63:ASN:HB2	2.04	0.40
1:1:1377:A:OP1	39:l:92:ARG:NH1	2.55	0.40
8:G:30:LEU:HB3	8:G:36:ALA:HB3	2.04	0.40
39:l:138:ARG:NE	39:l:139:GLU:OE2	2.53	0.40
39:l:150:ALA:HA	43:p:61:PHE:HB3	2.04	0.40
1:1:687:A:O2'	1:1:701:U:O4	2.23	0.40
1:1:1391:U:H2'	1:1:1392:G:C8	2.55	0.40
7:F:105:LEU:HD13	7:F:107:LEU:HD11	2.04	0.40
8:G:78:VAL:HB	8:G:144:VAL:HG22	2.03	0.40
29:b:30:VAL:HG22	29:b:37:LYS:HG2	2.04	0.40
37:j:15:LEU:HA	37:j:37:THR:HA	2.04	0.40
38:k:51:ILE:HG21	38:k:86:ARG:HE	1.86	0.40
38:k:78:PHE:HD1	38:k:84:VAL:HG11	1.85	0.40
40:m:77:ARG:HA	40:m:77:ARG:HD2	1.94	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	269/271 (99%)	259 (96%)	10 (4%)	0	100	100
4	C	207/209 (99%)	199 (96%)	8 (4%)	0	100	100
5	D	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
6	E	175/177 (99%)	159 (91%)	15 (9%)	1 (1%)	21	45
7	F	173/175 (99%)	163 (94%)	10 (6%)	0	100	100
8	G	147/149 (99%)	134 (91%)	13 (9%)	0	100	100
9	H	128/130 (98%)	105 (82%)	23 (18%)	0	100	100
10	I	133/135 (98%)	120 (90%)	13 (10%)	0	100	100
11	J	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
12	K	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
13	L	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
14	M	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
15	N	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
16	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
17	P	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
18	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
19	R	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
20	S	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
21	T	92/94 (98%)	92 (100%)	0	0	100	100
22	U	101/103 (98%)	91 (90%)	10 (10%)	0	100	100
23	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
24	W	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
25	X	75/77 (97%)	75 (100%)	0	0	100	100
26	Y	60/62 (97%)	60 (100%)	0	0	100	100
27	Z	56/58 (97%)	52 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	a	64/66 (97%)	58 (91%)	6 (9%)	0	100	100
29	b	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
30	c	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
31	d	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
32	e	62/64 (97%)	56 (90%)	5 (8%)	1 (2%)	7	21
33	f	36/38 (95%)	36 (100%)	0	0	100	100
34	g	223/225 (99%)	212 (95%)	11 (5%)	0	100	100
35	h	206/208 (99%)	190 (92%)	16 (8%)	0	100	100
36	i	203/205 (99%)	200 (98%)	3 (2%)	0	100	100
37	j	154/156 (99%)	136 (88%)	18 (12%)	0	100	100
38	k	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
39	l	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
40	m	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
41	n	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
42	o	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
43	p	115/117 (98%)	104 (90%)	11 (10%)	0	100	100
44	q	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
45	r	114/116 (98%)	103 (90%)	11 (10%)	0	100	100
46	s	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
47	t	86/88 (98%)	82 (95%)	3 (4%)	1 (1%)	10	28
48	u	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
49	v	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
50	w	64/66 (97%)	61 (95%)	3 (5%)	0	100	100
51	x	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
52	y	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
53	z	68/70 (97%)	65 (96%)	3 (4%)	0	100	100
All	All	5869/5972 (98%)	5563 (95%)	303 (5%)	3 (0%)	49	72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	e	32	ILE
6	E	177	PHE

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Mol	Chain	Res	Type
47	t	22	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	B	216/216 (100%)	215 (100%)	1 (0%)	81	90
4	C	164/164 (100%)	162 (99%)	2 (1%)	63	79
5	D	165/165 (100%)	164 (99%)	1 (1%)	78	89
6	E	148/148 (100%)	146 (99%)	2 (1%)	59	77
7	F	136/136 (100%)	134 (98%)	2 (2%)	57	76
8	G	114/114 (100%)	113 (99%)	1 (1%)	70	83
9	H	99/99 (100%)	99 (100%)	0	100	100
10	I	104/104 (100%)	103 (99%)	1 (1%)	68	82
11	J	116/116 (100%)	116 (100%)	0	100	100
12	K	104/104 (100%)	103 (99%)	1 (1%)	68	82
13	L	103/103 (100%)	103 (100%)	0	100	100
14	M	109/109 (100%)	109 (100%)	0	100	100
15	N	99/99 (100%)	99 (100%)	0	100	100
16	O	86/86 (100%)	86 (100%)	0	100	100
17	P	99/99 (100%)	99 (100%)	0	100	100
18	Q	89/89 (100%)	89 (100%)	0	100	100
19	R	84/84 (100%)	84 (100%)	0	100	100
20	S	93/93 (100%)	93 (100%)	0	100	100
21	T	81/81 (100%)	81 (100%)	0	100	100
22	U	84/84 (100%)	84 (100%)	0	100	100
23	V	78/78 (100%)	77 (99%)	1 (1%)	61	78
24	W	58/58 (100%)	58 (100%)	0	100	100
25	X	67/67 (100%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	Y	54/54 (100%)	54 (100%)	0	100	100
27	Z	48/48 (100%)	48 (100%)	0	100	100
28	a	59/59 (100%)	59 (100%)	0	100	100
29	b	47/47 (100%)	47 (100%)	0	100	100
30	c	47/47 (100%)	47 (100%)	0	100	100
31	d	38/38 (100%)	36 (95%)	2 (5%)	20	45
32	e	51/51 (100%)	50 (98%)	1 (2%)	48	71
33	f	34/34 (100%)	34 (100%)	0	100	100
34	g	187/187 (100%)	187 (100%)	0	100	100
35	h	171/171 (100%)	170 (99%)	1 (1%)	78	89
36	i	172/172 (100%)	172 (100%)	0	100	100
37	j	119/119 (100%)	117 (98%)	2 (2%)	53	73
38	k	91/91 (100%)	90 (99%)	1 (1%)	65	80
39	l	124/124 (100%)	123 (99%)	1 (1%)	73	85
40	m	104/104 (100%)	102 (98%)	2 (2%)	50	71
41	n	105/105 (100%)	105 (100%)	0	100	100
42	o	86/86 (100%)	86 (100%)	0	100	100
43	p	90/90 (100%)	90 (100%)	0	100	100
44	q	102/102 (100%)	102 (100%)	0	100	100
45	r	94/94 (100%)	94 (100%)	0	100	100
46	s	83/83 (100%)	83 (100%)	0	100	100
47	t	76/76 (100%)	75 (99%)	1 (1%)	61	78
48	u	65/65 (100%)	65 (100%)	0	100	100
49	v	74/74 (100%)	74 (100%)	0	100	100
50	w	57/57 (100%)	57 (100%)	0	100	100
51	x	72/72 (100%)	72 (100%)	0	100	100
52	y	65/65 (100%)	64 (98%)	1 (2%)	57	76
53	z	60/60 (100%)	60 (100%)	0	100	100
All	All	4871/4871 (100%)	4847 (100%)	24 (0%)	78	90

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	204	VAL
4	C	33	ARG
4	C	151	THR
5	D	178	VAL
6	E	40	VAL
6	E	47	LYS
7	F	11	VAL
7	F	38	ASN
8	G	41	LYS
10	I	10	LEU
12	K	35	VAL
23	V	24	ASN
31	d	42	LEU
31	d	44	VAL
32	e	55	LEU
35	h	200	VAL
37	j	93	ARG
37	j	94	VAL
38	k	89	VAL
39	l	50	LEU
40	m	83	LEU
40	m	121	LEU
47	t	70	LEU
52	y	54	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	86	ASN
3	B	90	ASN
3	B	134	ASN
3	B	251	GLN
3	B	260	ASN
4	C	32	ASN
4	C	136	ASN
4	C	150	GLN
5	D	163	ASN
7	F	22	GLN
7	F	88	GLN
8	G	128	HIS
10	I	110	GLN
11	J	76	HIS
12	K	29	HIS

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Mol	Chain	Res	Type
13	L	104	GLN
14	M	60	GLN
15	N	31	HIS
15	N	62	ASN
16	O	19	GLN
16	O	29	HIS
16	O	38	GLN
16	O	100	HIS
17	P	56	HIS
19	R	12	HIS
19	R	86	GLN
20	S	15	GLN
20	S	61	ASN
21	T	48	GLN
23	V	24	ASN
23	V	87	GLN
24	W	76	ASN
25	X	34	HIS
27	Z	20	HIS
27	Z	34	HIS
28	a	20	ASN
30	c	19	HIS
34	g	39	HIS
34	g	94	HIS
35	h	41	GLN
37	j	89	HIS
37	j	132	ASN
38	k	55	HIS
38	k	63	ASN
39	l	28	ASN
39	l	97	ASN
39	l	130	ASN
40	m	4	GLN
40	m	18	GLN
41	n	81	HIS
44	q	5	ASN
45	r	8	ASN
45	r	100	GLN
47	t	20	ASN
47	t	40	GLN
47	t	50	HIS
48	u	29	ASN

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Mol	Chain	Res	Type
50	w	52	GLN
51	x	57	HIS
52	y	3	ASN
52	y	20	HIS
52	y	70	ASN
52	y	82	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	4444/4458 (99%)	960 (21%)	24 (0%)
2	3	119/120 (99%)	25 (21%)	0
All	All	4563/4578 (99%)	985 (21%)	24 (0%)

All (985) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	7	A
1	1	9	G
1	1	19	A
1	1	22	G
1	1	32	A
1	1	33	A
1	1	39	G
1	1	47	C
1	1	48	C
1	1	51	A
1	1	54	C
1	1	56	U
1	1	68	G
1	1	70	U
1	1	71	A
1	1	73	C
1	1	74	A
1	1	81	A
1	1	83	C
1	1	84	U
1	1	85	U
1	1	86	G
1	1	87	C
1	1	88	U

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Mol	Chain	Res	Type
1	1	89	U
1	1	94	G
1	1	95	C
1	1	96	U
1	1	97	G
1	1	98	A
1	1	115	G
1	1	116	A
1	1	120	A
1	1	121	U
1	1	122	G
1	1	129	A
1	1	131	A
1	1	135	C
1	1	141	G
1	1	144	G
1	1	149	A
1	1	151	A
1	1	160	A
1	1	163	C
1	1	177	G
1	1	181	A
1	1	182	A
1	1	183	C
1	1	195	A
1	1	197	A
1	1	204	G
1	1	207	C
1	1	211	G
1	1	212	G
1	1	226	G
1	1	232	G
1	1	245	U
1	1	247	G
1	1	251	G
1	1	266	G
1	1	267	C
1	1	279	A
1	1	280	C
1	1	289	G
1	1	298	A
1	1	299	G

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Mol	Chain	Res	Type
1	1	321	A
1	1	328	C
1	1	332	G
1	1	345	C
1	1	347	G
1	1	352	C
1	1	354	G
1	1	362	G
1	1	367	U
1	1	372	C
1	1	384	G
1	1	392	C
1	1	406	G
1	1	408	A
1	1	411	A
1	1	412	A
1	1	413	G
1	1	421	U
1	1	422	C
1	1	424	G
1	1	429	U
1	1	435	A
1	1	447	G
1	1	448	A
1	1	451	A
1	1	455	G
1	1	456	A
1	1	457	G
1	1	458	U
1	1	463	U
1	1	464	U
1	1	465	A
1	1	467	U
1	1	468	A
1	1	469	C
1	1	474	G
1	1	475	C
1	1	476	U
1	1	478	A
1	1	481	G
1	1	482	A
1	1	484	G

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Mol	Chain	Res	Type
1	1	486	U
1	1	496	A
1	1	498	A
1	1	499	A
1	1	505	G
1	1	509	A
1	1	510	A
1	1	511	C
1	1	513	C
1	1	516	PSU
1	1	517	G
1	1	518	C
1	1	519	C
1	1	527	7MG
1	1	528	C
1	1	531	U
1	1	532	A
1	1	533	A
1	1	539	A
1	1	547	A
1	1	559	A
1	1	562	U
1	1	568	G
1	1	570	G
1	1	572	A
1	1	573	A
1	1	576	C
1	1	577	G
1	1	579	A
1	1	607	A
1	1	625	U
1	1	628	G
1	1	633	G
1	1	650	G
1	1	653	U
1	1	654	G
1	1	656	G
1	1	660	C
1	1	665	A
1	1	686	U
1	1	700	G
1	1	702	A

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Mol	Chain	Res	Type
1	1	703	G
1	1	718	A
1	1	721	G
1	1	723	U
1	1	724	G
1	1	731	G
1	1	734	G
1	1	735	C
1	1	747	A
1	1	749	A
1	1	755	G
1	1	758	C
1	1	760	G
1	1	777	A
1	1	781	A
1	1	793	U
1	1	794	A
1	1	814	A
1	1	815	A
1	1	817	C
1	1	821	G
1	1	827	U
1	1	828	U
1	1	839	C
1	1	841	C
1	1	842	U
1	1	843	U
1	1	844	G
1	1	846	G
1	1	849	G
1	1	857	C
1	1	864	A
1	1	876	C
1	1	883	C
1	1	887	G
1	1	914	A
1	1	926	G
1	1	934	C
1	1	942	G
1	1	960	U
1	1	961	U
1	1	963	G

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Mol	Chain	Res	Type
1	1	966	2MG
1	1	969	A
1	1	971	G
1	1	975	A
1	1	976	G
1	1	977	A
1	1	982	U
1	1	989	U
1	1	992	U
1	1	993	G
1	1	996	A
1	1	1004	A
1	1	1005	A
1	1	1009	U
1	1	1017	U
1	1	1018	G
1	1	1025	U
1	1	1026	G
1	1	1028	C
1	1	1029	U
1	1	1030	U
1	1	1031	C
1	1	1032	G
1	1	1033	G
1	1	1035	A
1	1	1037	C
1	1	1040	U
1	1	1044	A
1	1	1045	C
1	1	1065	U
1	1	1071	C
1	1	1081	A
1	1	1085	U
1	1	1094	G
1	1	1095	U
1	1	1101	A
1	1	1124	G
1	1	1125	U
1	1	1129	C
1	1	1132	C
1	1	1133	G
1	1	1136	C

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Mol	Chain	Res	Type
1	1	1137	C
1	1	1138	G
1	1	1139	G
1	1	1140	C
1	1	1141	C
1	1	1142	G
1	1	1143	G
1	1	1145	A
1	1	1146	A
1	1	1154	G
1	1	1157	A
1	1	1158	C
1	1	1160	G
1	1	1161	C
1	1	1163	A
1	1	1171	A
1	1	1174	G
1	1	1175	G
1	1	1176	A
1	1	1188	A
1	1	1196	A
1	1	1197	A
1	1	1199	U
1	1	1202	U
1	1	1212	U
1	1	1213	A
1	1	1214	C
1	1	1226	C
1	1	1227	A
1	1	1228	C
1	1	1238	A
1	1	1256	A
1	1	1257	A
1	1	1258	G
1	1	1265	C
1	1	1275	A
1	1	1279	G
1	1	1280	A
1	1	1286	U
1	1	1287	A
1	1	1298	U
1	1	1299	A

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Mol	Chain	Res	Type
1	1	1302	C
1	1	1305	G
1	1	1308	U
1	1	1310	G
1	1	1311	A
1	1	1312	G
1	1	1315	U
1	1	1317	C
1	1	1318	A
1	1	1319	A
1	1	1320	C
1	1	1322	C
1	1	1335	U
1	1	1346	A
1	1	1357	A
1	1	1358	U
1	1	1363	A
1	1	1364	U
1	1	1370	G
1	1	1379	G
1	1	1381	U
1	1	1383	C
1	1	1384	C
1	1	1394	A
1	1	1397	C
1	1	1398	A
1	1	1401	G
1	1	1402	4OC
1	1	1403	C
1	1	1419	G
1	1	1429	A
1	1	1432	G
1	1	1440	U
1	1	1441	A
1	1	1443	C
1	1	1446	A
1	1	1450	G
1	1	1451	G
1	1	1452	U
1	1	1453	C
1	1	1454	A
1	1	1455	A

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Mol	Chain	Res	Type
1	1	1456	C
1	1	1457	A
1	1	1459	C
1	1	1460	C
1	1	1461	G
1	1	1462	U
1	1	1463	U
1	1	1464	U
1	1	1465	G
1	1	1471	A
1	1	1478	C
1	1	1481	A
1	1	1482	U
1	1	1483	G
1	1	1489	U
1	1	1490	G
1	1	1491	A
1	1	1501	U
1	1	1503	G
1	1	1504	A
1	1	1505	G
1	1	1506	A
1	1	1516	A
1	1	1521	G
1	1	1539	C
1	1	1540	U
1	1	1541	G
1	1	1552	G
1	1	1555	A
1	1	1558	A
1	1	1564	G
1	1	1567	C
1	1	1577	A
1	1	1578	U
1	1	1580	A
1	1	1581	G
1	1	1586	G
1	1	1590	A
1	1	1591	G
1	1	1594	G
1	1	1607	A
1	1	1608	U

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Mol	Chain	Res	Type
1	1	1609	A
1	1	1624	A
1	1	1625	A
1	1	1626	U
1	1	1631	A
1	1	1645	U
1	1	1646	C
1	1	1664	U
1	1	1669	C
1	1	1671	A
1	1	1676	U
1	1	1677	U
1	1	1687	A
1	1	1702	A
1	1	1705	A
1	1	1721	G
1	1	1722	A
1	1	1728	A
1	1	1730	U
1	1	1731	C
1	1	1732	A
1	1	1733	A
1	1	1754	G
1	1	1755	C
1	1	1756	G
1	1	1770	C
1	1	1771	A
1	1	1772	G
1	1	1781	C
1	1	1782	U
1	1	1783	G
1	1	1784	A
1	1	1788	A
1	1	1791	G
1	1	1793	G
1	1	1810	U
1	1	1816	A
1	1	1817	A
1	1	1828	A
1	1	1831	G
1	1	1835	G
1	1	1836	A

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Mol	Chain	Res	Type
1	1	1838	A
1	1	1840	C
1	1	1851	A
1	1	1862	G
1	1	1867	G
1	1	1868	A
1	1	1869	G
1	1	1877	A
1	1	1878	G
1	1	1881	G
1	1	1889	C
1	1	1892	G
1	1	1902	G
1	1	1905	U
1	1	1909	U
1	1	1910	A
1	1	1911	U
1	1	1917	G
1	1	1918	A
1	1	1930	G
1	1	1953	A
1	1	1954	U
1	1	1957	U
1	1	1963	A
1	1	1987	G
1	1	1996	C
1	1	1997	G
1	1	2002	G
1	1	2009	A
1	1	2011	A
1	1	2014	A
1	1	2015	C
1	1	2016	C
1	1	2035	A
1	1	2036	G
1	1	2037	C
1	1	2038	A
1	1	2052	U
1	1	2053	A
1	1	2054	G
1	1	2055	G
1	1	2069	A

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Mol	Chain	Res	Type
1	1	2079	U
1	1	2081	A
1	1	2086	U
1	1	2092	A
1	1	2108	A
1	1	2109	A
1	1	2115	A
1	1	2119	A
1	1	2120	A
1	1	2121	U
1	1	2122	A
1	1	2133	A
1	1	2142	G
1	1	2143	A
1	1	2151	C
1	1	2153	G
1	1	2159	U
1	1	2160	A
1	1	2161	A
1	1	2174	A
1	1	2176	A
1	1	2191	A
1	1	2192	U
1	1	2202	G
1	1	2216	U
1	1	2223	C
1	1	2232	G
1	1	2236	A
1	1	2244	G
1	1	2246	C
1	1	2251	1MG
1	1	2252	PSU
1	1	2253	5MU
1	1	2254	G
1	1	2270	A
1	1	2271	C
1	1	2281	G
1	1	2282	G
1	1	2285	U
1	1	2287	A
1	1	2288	A
1	1	2290	G

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Mol	Chain	Res	Type
1	1	2291	G
1	1	2295	A
1	1	2297	C
1	1	2298	A
1	1	2299	A
1	1	2311	G
1	1	2312	C
1	1	2318	C
1	1	2325	A
1	1	2333	U
1	1	2334	U
1	1	2351	A
1	1	2352	U
1	1	2353	U
1	1	2364	G
1	1	2365	G
1	1	2383	A
1	1	2388	G
1	1	2389	G
1	1	2390	U
1	1	2391	C
1	1	2394	C
1	1	2398	A
1	1	2399	C
1	1	2401	U
1	1	2402	A
1	1	2416	A
1	1	2420	G
1	1	2433	A
1	1	2437	U
1	1	2447	A
1	1	2452	C
1	1	2461	PSU
1	1	2462	G
1	1	2467	C
1	1	2480	G
1	1	2489	A
1	1	2491	C
1	1	2495	G
1	1	2501	C
1	1	2502	A
1	1	2505	U

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Mol	Chain	Res	Type
1	1	2515	A
1	1	2518	U
1	1	2519	C
1	1	2528	G
1	1	2532	G
1	1	2539	U
1	1	2546	A
1	1	2547	G
1	1	2548	G
1	1	2549	C
1	1	2550	C
1	1	2552	A
1	1	2553	G
1	1	2557	G
1	1	2560	A
1	1	2562	G
1	1	2563	A
1	1	2568	G
1	1	2569	G
1	1	2570	C
1	1	2572	U
1	1	2573	A
1	1	2574	G
1	1	2576	A
1	1	2577	G
1	1	2579	A
1	1	2584	U
1	1	2589	U
1	1	2590	A
1	1	2593	G
1	1	2594	A
1	1	2595	A
1	1	2601	A
1	1	2602	A
1	1	2605	G
1	1	2607	U
1	1	2611	U
1	1	2613	G
1	1	2614	U
1	1	2617	A
1	1	2618	G
1	1	2622	G

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Mol	Chain	Res	Type
1	1	2624	C
1	1	2625	U
1	1	2626	G
1	1	2628	G
1	1	2632	A
1	1	2636	U
1	1	2638	U
1	1	2639	A
1	1	2640	A
1	1	2641	C
1	1	2642	G
1	1	2648	A
1	1	2662	A
1	1	2663	G
1	1	2675	A
1	1	2676	C
1	1	2677	G
1	1	2678	C
1	1	2679	U
1	1	2681	A
1	1	2683	G
1	1	2684	C
1	1	2692	G
1	1	2710	A
1	1	2718	G
1	1	2742	G
1	1	2744	G
1	1	2746	U
1	1	2756	G
1	1	2759	A
1	1	2762	G
1	1	2763	C
1	1	2772	G
1	1	2774	A
1	1	2777	G
1	1	2778	A
1	1	2779	U
1	1	2781	A
1	1	2790	A
1	1	2792	A
1	1	2795	C
1	1	2806	G

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Mol	Chain	Res	Type
1	1	2807	A
1	1	2819	U
1	1	2821	C
1	1	2827	A
1	1	2835	U
1	1	2850	U
1	1	2851	C
1	1	2858	U
1	1	2871	A
1	1	2874	G
1	1	2880	G
1	1	2885	U
1	1	2886	G
1	1	2889	A
1	1	2901	A
1	1	2903	U
1	1	2904	C
1	1	2905	C
1	1	2917	U
1	1	2922	G
1	1	2923	C
1	1	2925	A
1	1	2934	C
1	1	2958	G
1	1	2959	A
1	1	2967	C
1	1	2984	G
1	1	2988	G
1	1	2995	C
1	1	2996	A
1	1	2999	C
1	1	3003	U
1	1	3004	C
1	1	3009	A
1	1	3013	C
1	1	3014	A
1	1	3015	A
1	1	3016	G
1	1	3021	A
1	1	3027	G
1	1	3028	A
1	1	3030	G

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Mol	Chain	Res	Type
1	1	3041	A
1	1	3042	C
1	1	3043	G
1	1	3046	G
1	1	3066	G
1	1	3072	A
1	1	3075	A
1	1	3084	U
1	1	3089	A
1	1	3090	U
1	1	3091	C
1	1	3092	A
1	1	3095	U
1	1	3096	A
1	1	3113	C
1	1	3114	A
1	1	3116	A
1	1	3124	6MZ
1	1	3125	G
1	1	3136	A
1	1	3140	A
1	1	3153	U
1	1	3154	U
1	1	3155	G
1	1	3157	G
1	1	3173	G
1	1	3175	A
1	1	3180	G
1	1	3221	G
1	1	3234	C
1	1	3235	U
1	1	3236	C
1	1	3238	C
1	1	3239	G
1	1	3244	G
1	1	3263	A
1	1	3270	C
1	1	3279	A
1	1	3306	C
1	1	3307	A
1	1	3308	A
1	1	3314	A

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Mol	Chain	Res	Type
1	1	3317	G
1	1	3322	C
1	1	3323	G
1	1	3335	A
1	1	3339	C
1	1	3353	A
1	1	3354	A
1	1	3370	U
1	1	3371	U
1	1	3376	C
1	1	3377	A
1	1	3378	A
1	1	3379	G
1	1	3406	A
1	1	3412	G
1	1	3413	G
1	1	3416	G
1	1	3417	PSU
1	1	3418	A
1	1	3419	A
1	1	3420	C
1	1	3421	3TD
1	1	3422	A
1	1	3423	PSU
1	1	3424	A
1	1	3429	U
1	1	3430	C
1	1	3435	G
1	1	3436	G
1	1	3442	A
1	1	3443	A
1	1	3444	A
1	1	3445	5MU
1	1	3446	U
1	1	3461	U
1	1	3472	A
1	1	3473	C
1	1	3476	A
1	1	3477	U
1	1	3478	G
1	1	3486	G
1	1	3497	U

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Mol	Chain	Res	Type
1	1	3498	G
1	1	3499	U
1	1	3503	C
1	1	3508	G
1	1	3527	C
1	1	3528	U
1	1	3529	C
1	1	3533	G
1	1	3536	6MZ
1	1	3537	A
1	1	3538	G
1	1	3539	A
1	1	3541	G
1	1	3542	C
1	1	3549	C
1	1	3561	C
1	1	3562	G
1	1	3566	A
1	1	3567	G
1	1	3568	A
1	1	3575	G7M
1	1	3578	C
1	1	3599	G
1	1	3605	U
1	1	3606	G
1	1	3608	G
1	1	3611	U
1	1	3613	G
1	1	3614	A
1	1	3616	G
1	1	3617	U
1	1	3619	U
1	1	3621	G
1	1	3623	A
1	1	3624	U
1	1	3626	G
1	1	3629	G
1	1	3631	G
1	1	3632	A
1	1	3633	G
1	1	3637	U
1	1	3638	U

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Mol	Chain	Res	Type
1	1	3639	G
1	1	3640	A
1	1	3642	G
1	1	3645	U
1	1	3649	C
1	1	3652	C
1	1	3653	A
1	1	3654	G
1	1	3655	U
1	1	3659	C
1	1	3661	U
1	1	3663	G
1	1	3664	A
1	1	3666	C
1	1	3668	G
1	1	3669	A
1	1	3670	C
1	1	3671	C
1	1	3676	A
1	1	3677	A
1	1	3678	U
1	1	3681	C
1	1	3685	C
1	1	3686	U
1	1	3688	U
1	1	3689	A
1	1	3693	U
1	1	3694	U
1	1	3695	U
1	1	3696	G
1	1	3700	U
1	1	3704	A
1	1	3710	G
1	1	3716	U
1	1	3717	A
1	1	3726	U
1	1	3731	A
1	1	3732	C
1	1	3744	G
1	1	3749	U
1	1	3756	G
1	1	3774	A

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Mol	Chain	Res	Type
1	1	3779	A
1	1	3784	A
1	1	3789	C
1	1	3792	G
1	1	3793	A
1	1	3803	A
1	1	3811	U
1	1	3813	G
1	1	3815	A
1	1	3825	G
1	1	3828	A
1	1	3831	G
1	1	3833	A
1	1	3839	A
1	1	3840	U
1	1	3851	G
1	1	3853	C
1	1	3856	C
1	1	3858	A
1	1	3867	G
1	1	3889	G
1	1	3891	C
1	1	3897	G
1	1	3902	G
1	1	3908	U
1	1	3909	C
1	1	3910	U
1	1	3912	A
1	1	3929	U
1	1	3931	A
1	1	3932	A
1	1	3935	G
1	1	3936	A
1	1	3937	U
1	1	3941	A
1	1	3946	C
1	1	3947	U
1	1	3954	A
1	1	3963	PSU
1	1	3964	G
1	1	3976	G
1	1	3982	A

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Mol	Chain	Res	Type
1	1	3984	A
1	1	3996	G
1	1	3997	U
1	1	4003	A
1	1	4004	OMC
1	1	4005	C
1	1	4008	G
1	1	4009	2MA
1	1	4010	PSU
1	1	4011	G
1	1	4012	U
1	1	4018	C
1	1	4024	A
1	1	4026	C
1	1	4031	G
1	1	4035	G
1	1	4053	A
1	1	4058	OMU
1	1	4059	G
1	1	4060	U
1	1	4062	C
1	1	4072	A
1	1	4073	G
1	1	4075	G
1	1	4078	A
1	1	4079	C
1	1	4080	G
1	1	4086	PSU
1	1	4087	G
1	1	4088	G
1	1	4091	U
1	1	4108	A
1	1	4111	PSU
1	1	4112	C
1	1	4115	U
1	1	4119	U
1	1	4121	U
1	1	4135	U
1	1	4136	G
1	1	4152	C
1	1	4169	G
1	1	4193	U

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Mol	Chain	Res	Type
1	1	4195	U
1	1	4196	U
1	1	4220	G
1	1	4222	C
1	1	4231	A
1	1	4232	A
1	1	4233	A
1	1	4238	G
1	1	4239	A
1	1	4245	U
1	1	4250	G
1	1	4254	A
1	1	4271	A
1	1	4283	G
1	1	4284	A
1	1	4299	C
1	1	4300	C
1	1	4304	U
1	1	4309	G
1	1	4324	U
1	1	4326	A
1	1	4327	A
1	1	4331	G
1	1	4341	A
1	1	4342	U
1	1	4355	U
1	1	4356	A
1	1	4357	A
1	1	4358	A
1	1	4359	C
1	1	4360	G
1	1	4361	G
1	1	4362	A
1	1	4364	A
1	1	4365	U
1	1	4366	G
1	1	4367	G
1	1	4368	U
1	1	4369	U
1	1	4370	G
1	1	4388	U
1	1	4391	G

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Mol	Chain	Res	Type
1	1	4400	C
1	1	4408	A
1	1	4409	A
1	1	4410	G
1	1	4413	G
1	1	4415	A
1	1	4419	A
1	1	4422	U
1	1	4433	G
1	1	4445	G
1	1	4446	G
1	1	4450	A
2	3	2	G
2	3	5	U
2	3	9	G
2	3	13	G
2	3	16	G
2	3	24	G
2	3	25	U
2	3	35	C
2	3	36	C
2	3	42	C
2	3	44	G
2	3	45	A
2	3	51	G
2	3	56	G
2	3	57	A
2	3	65	U
2	3	66	A
2	3	68	C
2	3	88	C
2	3	89	U
2	3	90	C
2	3	99	A
2	3	105	G
2	3	109	A
2	3	120	U

All (24) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	496	A

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Mol	Chain	Res	Type
1	1	516	PSU
1	1	527	7MG
1	1	1145	A
1	1	1461	G
1	1	1910	A
1	1	2192	U
1	1	2253	5MU
1	1	2290	G
1	1	2400	U
1	1	2461	PSU
1	1	2885	U
1	1	3417	PSU
1	1	3423	PSU
1	1	3445	5MU
1	1	3652	C
1	1	3668	G
1	1	3814	G
1	1	3931	A
1	1	3963	PSU
1	1	4004	OMC
1	1	4010	PSU
1	1	4086	PSU
1	1	4111	PSU

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

34 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	$\# Z > 2$
1	MA6	1	4434	1	23,26,27	1.37	3 (13%)	34,38,41	2.21	10 (29%)
1	PSU	1	4010	1	18,21,22	2.35	5 (27%)	22,30,33	2.37	5 (22%)
1	UR3	1	4414	1	19,22,23	2.82	6 (31%)	26,32,35	1.45	3 (11%)
1	2MG	1	966	1	23,26,27	2.63	6 (26%)	32,38,41	2.42	8 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	G7M	1	3575	1	23,26,27	2.76	6 (26%)	35,39,42	1.99	7 (20%)
1	1MG	1	2251	1	22,26,27	2.58	6 (27%)	33,39,42	2.88	16 (48%)
1	5MC	1	3468	1	18,22,23	2.14	3 (16%)	26,32,35	1.41	4 (15%)
1	2MA	1	4009	1,54	22,25,26	1.59	3 (13%)	33,37,40	2.36	11 (33%)
1	4OC	1	1402	1	20,23,24	2.44	5 (25%)	26,32,35	2.32	9 (34%)
1	5MU	1	3445	1	19,22,23	2.52	7 (36%)	28,32,35	3.54	9 (32%)
1	PSU	1	3417	1	18,21,22	1.97	5 (27%)	22,30,33	2.12	4 (18%)
1	2MG	1	3951	1	23,26,27	2.65	6 (26%)	32,38,41	2.28	9 (28%)
1	5MC	1	1407	1	18,22,23	2.05	3 (16%)	26,32,35	1.38	3 (11%)
1	PSU	1	3423	1	18,21,22	2.11	5 (27%)	22,30,33	2.07	5 (22%)
1	5MU	1	2253	1	19,22,23	2.32	7 (36%)	28,32,35	4.01	13 (46%)
1	2MG	1	4432	1	23,26,27	2.62	6 (26%)	32,38,41	2.47	11 (34%)
1	OMC	1	4004	1,54	19,22,23	1.77	6 (31%)	26,31,34	2.10	9 (34%)
1	3TD	1	3421	1	18,22,23	2.84	8 (44%)	22,32,35	1.72	2 (9%)
1	PSU	1	2461	1	18,21,22	2.25	5 (27%)	22,30,33	2.22	5 (22%)
1	OMG	1	3757	1	23,26,27	2.64	7 (30%)	33,38,41	2.35	10 (30%)
1	6MZ	1	3536	1	22,25,26	2.91	4 (18%)	30,36,39	3.18	19 (63%)
1	PSU	1	4111	1	18,21,22	2.18	5 (27%)	22,30,33	2.09	4 (18%)
1	PSU	1	516	1	18,21,22	2.10	6 (33%)	22,30,33	2.20	5 (22%)
1	OMU	1	4058	1	19,22,23	2.76	7 (36%)	26,31,34	2.38	12 (46%)
1	PSU	1	4086	1	18,21,22	2.17	5 (27%)	22,30,33	2.14	7 (31%)
1	MA6	1	4435	1	23,26,27	1.27	3 (13%)	34,38,41	2.27	9 (26%)
1	5MC	1	967	1,54	18,22,23	2.01	3 (16%)	26,32,35	1.44	4 (15%)
1	PSU	1	2252	1,54	18,21,22	2.25	6 (33%)	22,30,33	2.30	5 (22%)
1	2MG	1	3341	1	23,26,27	2.56	6 (26%)	32,38,41	2.45	9 (28%)
44	0TD	q	89	44	7,9,10	1.40	0	6,11,13	2.82	3 (50%)
1	PSU	1	3963	1	18,21,22	2.29	5 (27%)	22,30,33	2.29	5 (22%)
1	2MG	1	1207	1	23,26,27	2.58	6 (26%)	32,38,41	2.37	10 (31%)
1	7MG	1	527	1	22,26,27	6.31	6 (27%)	29,39,42	2.43	10 (34%)
1	6MZ	1	3124	1	22,25,26	2.82	4 (18%)	30,36,39	2.43	12 (40%)

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
1	MA6	1	4434	1	-	1/11/29/30	0/3/3/3
1	PSU	1	4010	1	2/2/5/5	3/7/25/26	0/2/2/2
1	UR3	1	4414	1	-	0/7/25/26	0/2/2/2
1	2MG	1	966	1	-	4/9/27/28	0/3/3/3
1	G7M	1	3575	1	1/1/5/5	2/7/25/26	0/3/3/3
1	1MG	1	2251	1	2/2/5/5	2/7/25/26	0/3/3/3
1	5MC	1	3468	1	-	0/7/25/26	0/2/2/2
1	2MA	1	4009	1,54	2/2/5/5	4/7/25/26	0/3/3/3
1	4OC	1	1402	1	2/2/5/6	4/9/29/30	0/2/2/2
1	5MU	1	3445	1	2/2/5/5	1/7/25/26	0/2/2/2
1	PSU	1	3417	1	2/2/5/5	3/7/25/26	0/2/2/2
1	2MG	1	3951	1	-	0/9/27/28	0/3/3/3
1	PSU	1	3423	1	2/2/5/5	3/7/25/26	0/2/2/2
1	5MC	1	1407	1	-	0/7/25/26	0/2/2/2
1	5MU	1	2253	1	2/2/5/5	5/7/25/26	0/2/2/2
1	2MG	1	4432	1	-	0/9/27/28	0/3/3/3
1	OMC	1	4004	1,54	1/1/5/5	4/9/27/28	0/2/2/2
1	3TD	1	3421	1	1/1/5/5	4/7/25/26	0/2/2/2
1	PSU	1	2461	1	2/2/5/5	3/7/25/26	0/2/2/2
1	OMG	1	3757	1	1/1/5/5	2/9/27/28	0/3/3/3
1	6MZ	1	3536	1	2/2/5/6	2/9/27/28	0/3/3/3
1	PSU	1	4111	1	2/2/5/5	3/7/25/26	0/2/2/2
1	PSU	1	516	1	2/2/5/5	5/7/25/26	0/2/2/2
1	OMU	1	4058	1	2/2/5/5	3/9/27/28	0/2/2/2
1	PSU	1	4086	1	2/2/5/5	3/7/25/26	0/2/2/2
1	MA6	1	4435	1	-	3/11/29/30	0/3/3/3
1	5MC	1	967	1,54	-	0/7/25/26	0/2/2/2
1	PSU	1	2252	1,54	2/2/5/5	3/7/25/26	0/2/2/2
1	2MG	1	3341	1	-	0/9/27/28	0/3/3/3
44	0TD	q	89	44	-	1/7/12/14	-
1	PSU	1	3963	1	2/2/5/5	3/7/25/26	0/2/2/2
1	2MG	1	1207	1	-	0/9/27/28	0/3/3/3
1	7MG	1	527	1	1/1/7/7	3/7/37/38	0/3/3/3
1	6MZ	1	3124	1	2/2/5/6	7/9/27/28	0/3/3/3

All (174) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	527	7MG	C8-N9	-27.11	1.30	1.46
1	1	3124	6MZ	C6-N6	11.86	1.47	1.34
1	1	3536	6MZ	C6-N6	11.66	1.46	1.34
1	1	3575	G7M	O6-C6	10.22	1.43	1.23
1	1	966	2MG	O6-C6	9.34	1.41	1.23
1	1	3757	OMG	O6-C6	9.17	1.41	1.23
1	1	1207	2MG	O6-C6	9.15	1.41	1.23
1	1	4432	2MG	O6-C6	8.88	1.40	1.23
1	1	3951	2MG	O6-C6	8.72	1.40	1.23
1	1	3341	2MG	O6-C6	8.70	1.40	1.23
1	1	1402	4OC	O2-C2	8.64	1.39	1.23
1	1	4414	UR3	O4-C4	8.37	1.41	1.23
1	1	3421	3TD	O4-C4	8.00	1.40	1.23
1	1	527	7MG	O6-C6	7.78	1.38	1.23
1	1	4058	OMU	O4-C4	7.62	1.39	1.24
1	1	2251	1MG	O6-C6	7.50	1.38	1.23
1	1	527	7MG	C2-N2	6.38	1.49	1.34
1	1	967	5MC	C4-N4	6.36	1.50	1.34
1	1	3468	5MC	C4-N4	6.31	1.50	1.34
1	1	1407	5MC	C4-N4	6.18	1.50	1.34
1	1	3445	5MU	C2-N1	-6.05	1.28	1.38
1	1	966	2MG	C2-N2	5.95	1.46	1.33
1	1	4432	2MG	C2-N2	5.66	1.46	1.33
1	1	1207	2MG	C2-N2	5.65	1.46	1.33
1	1	3951	2MG	C2-N2	5.63	1.45	1.33
1	1	2251	1MG	C2-N2	5.49	1.44	1.34
1	1	3341	2MG	C2-N2	5.26	1.45	1.33
1	1	3468	5MC	C2-N1	-5.11	1.28	1.40
1	1	4010	PSU	C4-N3	-5.09	1.29	1.38
1	1	516	PSU	C4-N3	-5.09	1.29	1.38
1	1	3963	PSU	C4-N3	-5.08	1.29	1.38
1	1	4086	PSU	C4-N3	-5.05	1.29	1.38
1	1	2252	PSU	C4-N3	-5.04	1.29	1.38
1	1	2461	PSU	C4-N3	-5.01	1.29	1.38
1	1	3423	PSU	C4-N3	-4.94	1.29	1.38
1	1	4111	PSU	C4-N3	-4.91	1.29	1.38
1	1	3963	PSU	C2-N1	-4.84	1.30	1.36
1	1	3421	3TD	C2-N1	-4.69	1.31	1.37
1	1	2253	5MU	C2-N1	-4.65	1.31	1.38
1	1	4010	PSU	C2-N1	-4.64	1.30	1.36
1	1	1407	5MC	C2-N1	-4.61	1.30	1.40
1	1	2251	1MG	C6-N1	-4.59	1.30	1.40
1	1	3575	G7M	C2-N2	4.57	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	3445	5MU	C2-N3	-4.54	1.29	1.38
1	1	3417	PSU	C4-N3	-4.53	1.30	1.38
1	1	4010	PSU	C6-C5	4.47	1.40	1.35
1	1	967	5MC	C2-N1	-4.43	1.30	1.40
1	1	4009	2MA	C6-N6	4.41	1.45	1.34
1	1	3575	G7M	C6-N1	-4.39	1.30	1.38
1	1	3757	OMG	C2-N2	4.37	1.44	1.34
1	1	2252	PSU	C6-C5	4.35	1.40	1.35
1	1	2461	PSU	C2-N1	-4.30	1.30	1.36
1	1	4086	PSU	C2-N1	-4.28	1.30	1.36
1	1	4058	OMU	C2-N3	-4.27	1.30	1.38
1	1	4414	UR3	C4-N3	-4.26	1.31	1.40
1	1	4414	UR3	C2-N1	-4.26	1.32	1.38
1	1	4111	PSU	C2-N1	-4.25	1.31	1.36
1	1	4058	OMU	C4-N3	-4.22	1.31	1.38
1	1	2253	5MU	C2-N3	-4.21	1.30	1.38
1	1	3963	PSU	C6-N1	-4.19	1.29	1.36
1	1	2252	PSU	C2-N1	-4.15	1.31	1.36
1	1	4004	OMC	C4-N4	4.13	1.43	1.33
1	1	1402	4OC	C4-N4	4.11	1.44	1.35
1	1	3757	OMG	C6-N1	-4.10	1.31	1.38
1	1	3951	2MG	C6-N1	-4.09	1.31	1.38
1	1	4058	OMU	C2-N1	-4.07	1.31	1.38
1	1	516	PSU	C6-C5	4.04	1.40	1.35
1	1	3423	PSU	C6-C5	4.02	1.40	1.35
1	1	527	7MG	C4-N9	-4.01	1.33	1.37
1	1	2461	PSU	C6-C5	3.99	1.40	1.35
1	1	4432	2MG	C6-N1	-3.94	1.31	1.38
1	1	3421	3TD	C4-N3	-3.92	1.32	1.40
1	1	4010	PSU	C6-N1	-3.92	1.29	1.36
1	1	3341	2MG	C6-N1	-3.91	1.31	1.38
1	1	4086	PSU	C6-N1	-3.91	1.29	1.36
1	1	3536	6MZ	C8-N9	-3.85	1.30	1.37
1	1	3423	PSU	C2-N1	-3.83	1.31	1.36
1	1	4111	PSU	C6-N1	-3.81	1.29	1.36
1	1	2461	PSU	C6-N1	-3.81	1.29	1.36
1	1	4009	2MA	C8-N9	-3.79	1.30	1.37
1	1	4434	MA6	C8-N9	-3.71	1.30	1.37
1	1	3575	G7M	C5-N7	-3.70	1.34	1.39
1	1	4111	PSU	C6-C5	3.68	1.39	1.35
1	1	3124	6MZ	C8-N9	-3.68	1.30	1.37
1	1	3417	PSU	C2-N1	-3.65	1.31	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2253	5MU	O2-C2	-3.64	1.16	1.23
1	1	3963	PSU	C6-C5	3.61	1.39	1.35
1	1	3417	PSU	C6-C5	3.61	1.39	1.35
1	1	3417	PSU	C6-N1	-3.54	1.30	1.36
1	1	4414	UR3	C2-N3	-3.53	1.32	1.39
1	1	3445	5MU	C6-C5	3.53	1.40	1.34
1	1	4058	OMU	O2-C2	-3.52	1.16	1.23
1	1	2252	PSU	C6-N1	-3.51	1.30	1.36
1	1	4414	UR3	O2-C2	-3.49	1.16	1.22
1	1	3445	5MU	C6-N1	-3.46	1.32	1.38
1	1	3423	PSU	C6-N1	-3.43	1.30	1.36
1	1	3341	2MG	C2-N1	-3.41	1.31	1.36
1	1	2253	5MU	C6-C5	3.37	1.40	1.34
1	1	3445	5MU	O2-C2	-3.33	1.17	1.23
1	1	4435	MA6	C8-N9	-3.31	1.31	1.37
1	1	3445	5MU	O4-C4	-3.30	1.17	1.23
1	1	3757	OMG	C8-N9	-3.30	1.30	1.37
1	1	2253	5MU	C4-N3	-3.30	1.32	1.38
1	1	1207	2MG	C6-N1	-3.30	1.32	1.38
1	1	4086	PSU	C6-C5	3.29	1.39	1.35
1	1	4004	OMC	C5-C4	-3.28	1.35	1.42
1	1	3445	5MU	C4-N3	-3.27	1.32	1.38
1	1	4434	MA6	C6-N6	3.24	1.46	1.36
1	1	3951	2MG	C2-N1	-3.22	1.31	1.36
1	1	2253	5MU	C6-N1	-3.22	1.32	1.38
1	1	2251	1MG	C5-N7	-3.21	1.32	1.39
1	1	3536	6MZ	C5-N7	-3.20	1.33	1.39
1	1	516	PSU	C6-N1	-3.20	1.30	1.36
1	1	527	7MG	C6-N1	-3.19	1.32	1.38
1	1	966	2MG	C6-N1	-3.17	1.32	1.38
1	1	4435	MA6	C6-N6	3.16	1.46	1.36
1	1	516	PSU	C2-N1	-3.11	1.32	1.36
1	1	2253	5MU	O4-C4	-3.10	1.17	1.23
1	1	3757	OMG	C5-N7	-3.06	1.33	1.39
1	1	2461	PSU	C2-N3	-3.02	1.32	1.37
1	1	3421	3TD	C2-N3	-3.01	1.31	1.38
1	1	3421	3TD	C6-C5	2.98	1.38	1.35
1	1	516	PSU	C2-N3	-2.98	1.32	1.37
1	1	2251	1MG	C8-N9	-2.96	1.30	1.37
1	1	3951	2MG	C8-N9	-2.96	1.30	1.37
1	1	1402	4OC	C2-N1	-2.91	1.33	1.40
1	1	2252	PSU	C2-N3	-2.90	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	4086	PSU	C2-N3	-2.90	1.32	1.37
1	1	4004	OMC	O2-C2	-2.89	1.18	1.23
1	1	3951	2MG	C5-N7	-2.88	1.33	1.39
1	1	4432	2MG	C2-N1	-2.88	1.32	1.36
1	1	4432	2MG	C8-N9	-2.87	1.31	1.37
1	1	4009	2MA	C5-N7	-2.86	1.33	1.39
1	1	3421	3TD	O2-C2	-2.86	1.17	1.23
1	1	3757	OMG	C2-N1	-2.85	1.30	1.37
1	1	4111	PSU	C2-N3	-2.83	1.32	1.37
1	1	3341	2MG	C8-N9	-2.80	1.31	1.37
1	1	4010	PSU	C2-N3	-2.78	1.32	1.37
1	1	4414	UR3	C6-N1	-2.76	1.31	1.38
1	1	527	7MG	C2-N1	-2.75	1.30	1.37
1	1	1207	2MG	C2-N1	-2.75	1.32	1.36
1	1	4434	MA6	C5-N7	-2.70	1.33	1.39
1	1	4058	OMU	C5-C4	-2.70	1.37	1.43
1	1	3124	6MZ	C5-N7	-2.69	1.33	1.39
1	1	4432	2MG	C5-N7	-2.66	1.33	1.39
1	1	1407	5MC	C2-N3	-2.65	1.31	1.36
1	1	2251	1MG	C5-C6	-2.63	1.38	1.45
1	1	966	2MG	C5-N7	-2.61	1.34	1.39
1	1	4004	OMC	C2-N1	-2.60	1.34	1.40
1	1	3757	OMG	O2'-CM2	-2.59	1.33	1.42
1	1	966	2MG	C8-N9	-2.57	1.31	1.37
1	1	3341	2MG	C5-N7	-2.54	1.34	1.39
1	1	3421	3TD	C6-N1	-2.54	1.32	1.36
1	1	1207	2MG	C8-N9	-2.51	1.32	1.37
1	1	3423	PSU	C2-N3	-2.50	1.33	1.37
1	1	3963	PSU	C2-N3	-2.49	1.33	1.37
1	1	3468	5MC	C2-N3	-2.47	1.31	1.36
1	1	3421	3TD	O4'-C1'	-2.44	1.40	1.43
1	1	3575	G7M	C2-N1	-2.43	1.31	1.37
1	1	4058	OMU	C6-N1	-2.38	1.32	1.38
1	1	966	2MG	C2-N1	-2.38	1.32	1.36
1	1	1402	4OC	C2-N3	-2.37	1.31	1.36
1	1	1207	2MG	C5-N7	-2.37	1.34	1.39
1	1	4435	MA6	C5-N7	-2.36	1.34	1.39
1	1	3417	PSU	C2-N3	-2.34	1.33	1.37
1	1	4004	OMC	C2-N3	-2.27	1.31	1.36
1	1	1402	4OC	C6-N1	-2.26	1.32	1.38
1	1	967	5MC	C2-N3	-2.25	1.31	1.36
1	1	3536	6MZ	C6-N1	-2.25	1.31	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	3124	6MZ	C6-N1	-2.22	1.31	1.35
1	1	516	PSU	O4'-C1'	-2.20	1.40	1.43
1	1	3575	G7M	C8-N7	-2.07	1.29	1.33
1	1	2252	PSU	O4'-C1'	-2.05	1.41	1.43
1	1	4004	OMC	C4-N3	-2.05	1.30	1.34

All (267) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2253	5MU	N3-C2-N1	9.66	127.72	114.89
1	1	2253	5MU	C5M-C5-C4	9.47	129.19	118.77
1	1	3445	5MU	C5M-C5-C4	8.86	128.52	118.77
1	1	3536	6MZ	C9-N6-C6	-8.64	115.43	122.87
1	1	3445	5MU	N3-C2-N1	8.41	126.06	114.89
1	1	4432	2MG	C2-N3-C4	8.16	122.15	112.04
1	1	3341	2MG	C2-N3-C4	8.12	122.11	112.04
1	1	966	2MG	C2-N3-C4	7.96	121.91	112.04
1	1	1207	2MG	C2-N3-C4	7.72	121.61	112.04
1	1	3951	2MG	C2-N3-C4	7.59	121.45	112.04
1	1	3445	5MU	C4-N3-C2	-7.58	117.54	127.35
1	1	4009	2MA	C5-C4-N3	-7.41	118.86	127.19
1	1	3757	OMG	C5-C4-N3	-7.33	116.57	128.46
1	1	2253	5MU	C5M-C5-C6	-7.31	113.09	122.85
1	1	2253	5MU	C4-N3-C2	-7.26	117.95	127.35
1	1	3341	2MG	C5-C4-N3	-6.79	117.44	128.46
1	1	2252	PSU	N1-C2-N3	6.78	122.81	115.13
1	1	966	2MG	C5-C4-N3	-6.71	117.57	128.46
1	1	4432	2MG	C5-C4-N3	-6.52	117.88	128.46
1	1	1207	2MG	C5-C4-N3	-6.38	118.11	128.46
1	1	3445	5MU	C5M-C5-C6	-6.35	114.37	122.85
1	1	4010	PSU	C6-C5-C4	-6.34	113.77	118.20
1	1	2251	1MG	O4'-C1'-N9	6.31	122.78	108.36
1	1	516	PSU	N1-C2-N3	6.31	122.28	115.13
1	1	3963	PSU	N1-C2-N3	6.28	122.24	115.13
1	1	2253	5MU	C1'-N1-C2	6.22	128.82	117.57
1	1	3423	PSU	N1-C2-N3	6.20	122.15	115.13
1	1	3421	3TD	N1-C2-N3	6.17	121.01	116.14
1	1	527	7MG	N9-C4-N3	6.06	134.53	125.47
1	1	2251	1MG	C5-C4-N3	-6.03	118.68	128.46
1	1	2461	PSU	N1-C2-N3	5.96	121.89	115.13
1	1	4086	PSU	N1-C2-N3	5.93	121.85	115.13
1	1	4004	OMC	O2-C2-N3	-5.91	112.71	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	3445	5MU	C5-C4-N3	5.88	120.33	115.31
1	1	3951	2MG	C5-C4-N3	-5.84	118.99	128.46
1	1	3417	PSU	N1-C2-N3	5.78	121.68	115.13
1	1	4435	MA6	C5-C4-N3	-5.68	119.34	126.75
1	1	4434	MA6	C5-C4-N3	-5.66	119.36	126.75
1	1	3575	G7M	C2-N3-C4	5.62	122.32	112.30
1	1	3757	OMG	C2-N3-C4	5.61	122.29	112.30
1	1	4010	PSU	N1-C2-N3	5.55	121.42	115.13
1	1	3124	6MZ	C5-C4-N3	-5.46	119.63	126.75
1	1	4009	2MA	N3-C4-N9	5.40	134.49	126.99
1	1	4111	PSU	N1-C2-N3	5.39	121.24	115.13
44	q	89	0TD	OD2-CG-CB	5.38	124.77	113.15
1	1	4414	UR3	C4-N3-C2	-5.30	119.57	124.56
1	1	1402	4OC	C1'-N1-C2	5.30	130.24	118.42
1	1	4435	MA6	N1-C2-N3	-5.27	120.37	128.60
1	1	2253	5MU	O2-C2-N3	-5.25	111.72	121.50
1	1	527	7MG	C5-C6-N1	5.25	120.24	110.99
1	1	3445	5MU	C5-C6-N1	-5.19	117.99	123.34
1	1	3963	PSU	O2-C2-N1	-5.16	117.11	122.79
1	1	1402	4OC	O2-C2-N3	-5.12	113.99	122.33
1	1	3536	6MZ	N1-C2-N3	-5.07	120.67	128.60
1	1	3124	6MZ	N1-C2-N3	-4.99	120.79	128.60
1	1	3536	6MZ	O3'-C3'-C4'	4.94	125.33	111.05
1	1	4058	OMU	N3-C2-N1	4.89	121.38	114.89
1	1	966	2MG	N9-C4-N3	4.88	135.74	125.94
1	1	3468	5MC	C5-C6-N1	-4.84	118.35	123.34
1	1	4434	MA6	N1-C2-N3	-4.84	121.03	128.60
1	1	527	7MG	C2-N3-C4	4.83	120.90	112.30
1	1	1207	2MG	N9-C4-N3	4.82	135.62	125.94
1	1	2251	1MG	N9-C4-N3	4.82	135.61	125.94
1	1	3757	OMG	N9-C4-N3	4.78	135.54	125.94
1	1	2461	PSU	C6-C5-C4	-4.75	114.88	118.20
1	1	3536	6MZ	C6-C5-N7	4.74	137.52	132.39
1	1	3575	G7M	C5-C4-N3	-4.73	119.07	128.15
1	1	1402	4OC	C1'-N1-C6	-4.69	110.62	120.84
1	1	4434	MA6	C2-N1-C6	4.68	122.80	111.75
1	1	4435	MA6	C2-N1-C6	4.64	122.72	111.75
1	1	3341	2MG	N9-C4-N3	4.62	135.22	125.94
1	1	2251	1MG	C2'-C1'-N9	4.60	126.25	113.22
1	1	2253	5MU	C1'-N1-C6	-4.58	113.50	121.12
1	1	3536	6MZ	C5-C4-N3	-4.56	120.80	126.75
1	1	4111	PSU	C6-C5-C4	-4.49	115.06	118.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	527	7MG	C5-C4-N3	-4.46	119.62	128.13
1	1	2251	1MG	C1'-N9-C8	-4.42	114.11	126.70
1	1	2253	5MU	C5-C4-N3	4.38	119.05	115.31
1	1	3417	PSU	O2-C2-N1	-4.35	118.00	122.79
1	1	3575	G7M	C5-C6-N1	4.35	120.86	111.79
1	1	4435	MA6	C2-N3-C4	4.34	121.99	111.75
1	1	516	PSU	C4-N3-C2	-4.32	120.12	126.34
1	1	4058	OMU	C4-N3-C2	-4.29	120.92	126.58
1	1	4010	PSU	O2-C2-N1	-4.28	118.07	122.79
1	1	967	5MC	C5-C6-N1	-4.26	118.95	123.34
1	1	3341	2MG	C2-N1-C6	-4.26	119.58	124.48
1	1	2251	1MG	O3'-C3'-C4'	4.23	123.29	111.05
1	1	3951	2MG	N9-C4-N3	4.22	134.42	125.94
1	1	4058	OMU	C1'-N1-C2	4.20	125.18	117.57
1	1	4058	OMU	O3'-C3'-C4'	4.20	123.18	111.05
1	1	3124	6MZ	N3-C4-N9	4.18	133.97	127.08
1	1	3417	PSU	C4-N3-C2	-4.17	120.33	126.34
1	1	4432	2MG	N9-C4-N3	4.17	134.32	125.94
1	1	2251	1MG	O2'-C2'-C3'	4.17	125.30	111.82
1	1	4434	MA6	C4-C5-N7	-4.13	105.58	110.62
1	1	3536	6MZ	C5-N7-C8	4.11	109.35	103.51
1	1	2253	5MU	C6-N1-C2	-4.09	117.16	121.30
1	1	3536	6MZ	C4-C5-N7	-4.06	105.67	110.62
1	1	4435	MA6	C4-C5-N7	-4.03	105.71	110.62
1	1	4434	MA6	C2-N3-C4	4.01	121.22	111.75
1	1	4009	2MA	C5-N7-C8	4.01	109.20	103.51
1	1	2252	PSU	C4-N3-C2	-4.00	120.58	126.34
1	1	4009	2MA	N9-C8-N7	-3.99	108.46	113.91
1	1	4432	2MG	C2-N1-C6	-3.98	119.90	124.48
1	1	3575	G7M	C6-C5-N7	3.96	137.04	132.25
1	1	3124	6MZ	C5-N7-C8	3.92	109.07	103.51
1	1	1407	5MC	O2-C2-N3	-3.90	115.99	122.33
1	1	3124	6MZ	C2-N3-C4	3.88	120.91	111.75
1	1	3757	OMG	CM2-O2'-C2'	-3.85	104.42	114.52
1	1	2252	PSU	O2-C2-N1	-3.81	118.59	122.79
1	1	966	2MG	C2-N1-C6	-3.80	120.11	124.48
1	1	3536	6MZ	N9-C8-N7	-3.80	108.72	113.91
1	1	527	7MG	N9-C8-N7	3.79	108.81	103.38
1	1	3536	6MZ	C2-N3-C4	3.78	120.69	111.75
1	1	3423	PSU	O2-C2-N1	-3.78	118.63	122.79
1	1	4058	OMU	C5-C4-N3	3.78	120.49	114.84
1	1	3963	PSU	C4-N3-C2	-3.77	120.91	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	4435	MA6	C5-N7-C8	3.72	108.80	103.51
1	1	4086	PSU	C4-N3-C2	-3.72	120.98	126.34
1	1	4004	OMC	C6-N1-C2	-3.70	114.07	120.49
1	1	2251	1MG	O2'-C2'-C1'	3.68	122.32	110.02
1	1	4004	OMC	O2-C2-N1	3.66	126.44	118.89
1	1	3124	6MZ	N9-C8-N7	-3.61	108.97	113.91
1	1	3445	5MU	O2-C2-N3	-3.61	114.78	121.50
1	1	3575	G7M	N9-C4-N3	3.61	133.18	125.94
1	1	4434	MA6	C5-N7-C8	3.59	108.61	103.51
1	1	1402	4OC	C2'-C1'-N1	3.59	121.19	114.22
1	1	4111	PSU	C4-N3-C2	-3.58	121.18	126.34
1	1	967	5MC	O2-C2-N3	-3.58	116.51	122.33
1	1	3445	5MU	O4-C4-N3	-3.57	113.28	120.12
1	1	516	PSU	C6-C5-C4	-3.56	115.71	118.20
1	1	3536	6MZ	C2'-C1'-N9	3.55	122.30	113.30
1	1	2461	PSU	O2-C2-N1	-3.50	118.93	122.79
1	1	4086	PSU	O2-C2-N1	-3.48	118.96	122.79
1	1	4111	PSU	O2-C2-N1	-3.48	118.96	122.79
1	1	1407	5MC	C5-C6-N1	-3.47	119.77	123.34
1	1	4435	MA6	N3-C4-N9	3.44	132.74	127.08
1	1	1207	2MG	C2-N1-C6	-3.42	120.55	124.48
1	1	3951	2MG	C2-N1-C6	-3.40	120.56	124.48
1	1	2253	5MU	O4-C4-N3	-3.40	113.60	120.12
1	1	4058	OMU	O2-C2-N3	-3.37	115.22	121.50
1	1	2461	PSU	C4-N3-C2	-3.36	121.50	126.34
1	1	4434	MA6	N3-C4-N9	3.35	132.60	127.08
1	1	3423	PSU	C4-N3-C2	-3.34	121.53	126.34
1	1	2251	1MG	C5'-C4'-C3'	3.32	127.61	115.18
1	1	4009	2MA	C4-C5-N7	-3.31	106.59	110.62
1	1	3124	6MZ	C1'-N9-C8	-3.29	119.70	127.14
1	1	3124	6MZ	C4-C5-N7	-3.26	106.65	110.62
1	1	527	7MG	C6-C5-N7	3.26	137.03	131.91
1	1	4010	PSU	C4-N3-C2	-3.21	121.71	126.34
1	1	2251	1MG	C2-N3-C4	3.18	119.14	111.98
1	1	2251	1MG	O3'-C3'-C2'	3.17	122.09	111.82
1	1	1402	4OC	O2-C2-N1	3.15	125.40	118.89
1	1	2253	5MU	C5-C6-N1	-3.08	120.17	123.34
1	1	2252	PSU	C6-N1-C2	-3.07	119.55	122.68
1	1	4009	2MA	C4-N9-C8	3.06	109.05	105.73
1	1	2461	PSU	C6-N1-C2	-3.04	119.57	122.68
1	1	3757	OMG	C2-N1-C6	-3.04	119.55	125.10
1	1	3423	PSU	C6-N1-C2	-3.02	119.59	122.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	4009	2MA	N3-C2-N1	-3.02	120.17	125.72
1	1	4058	OMU	C1'-N1-C6	-2.97	114.36	120.84
1	1	2252	PSU	C6-C5-C4	-2.97	116.12	118.20
1	1	2251	1MG	C1'-N9-C4	2.97	135.33	126.50
1	1	3963	PSU	C6-C5-C4	-2.97	116.12	118.20
44	q	89	0TD	OD1-CG-CB	-2.95	116.25	122.44
1	1	3417	PSU	C6-C5-C4	-2.94	116.14	118.20
1	1	3536	6MZ	C3'-C2'-C1'	-2.94	95.84	101.43
1	1	4004	OMC	C5-C6-N1	2.94	126.73	121.81
1	1	516	PSU	O4-C4-N3	-2.92	114.52	120.12
1	1	3536	6MZ	C4-N9-C1'	-2.92	119.65	126.59
1	1	3124	6MZ	C4-N9-C8	2.90	108.88	105.73
1	1	527	7MG	C6-C5-C4	-2.89	116.65	122.62
1	1	4432	2MG	C5-C6-N1	2.84	120.41	113.19
1	1	3124	6MZ	C6-C5-N7	2.83	135.45	132.39
1	1	2251	1MG	O4'-C4'-C5'	2.81	118.63	109.37
1	1	3468	5MC	O2-C2-N3	-2.81	117.76	122.33
1	1	4086	PSU	C6-C5-C4	-2.79	116.25	118.20
1	1	3341	2MG	C5-C6-N1	2.77	120.22	113.19
1	1	3963	PSU	C6-N1-C2	-2.77	119.85	122.68
1	1	4058	OMU	O4-C4-C5	-2.76	120.30	125.16
1	1	4432	2MG	C6-C5-N7	2.75	135.37	130.25
1	1	3445	5MU	O2-C2-N1	-2.73	119.16	122.79
1	1	3951	2MG	C5-C6-N1	2.72	120.09	113.19
1	1	4435	MA6	N9-C8-N7	-2.70	110.22	113.91
1	1	4010	PSU	C6-N1-C2	-2.69	119.94	122.68
1	1	3536	6MZ	O4'-C1'-N9	2.68	113.33	108.06
1	1	3757	OMG	C5-C6-N1	2.67	119.98	113.19
1	1	1207	2MG	C5-C6-N1	2.67	119.97	113.19
1	1	1402	4OC	CM4-N4-C4	-2.67	117.23	122.45
1	1	1402	4OC	O4'-C1'-N1	2.67	114.46	108.36
1	1	3468	5MC	C5-C4-N3	-2.67	118.80	121.67
1	1	3421	3TD	C4-N3-C2	-2.66	121.72	124.61
1	1	966	2MG	C5-C6-N1	2.65	119.91	113.19
1	1	516	PSU	O2-C2-N3	-2.64	116.84	121.82
1	1	4432	2MG	C4-C5-N7	-2.63	106.56	110.72
1	1	3575	G7M	O6-C6-C5	-2.60	122.18	128.06
1	1	3124	6MZ	C2'-C1'-N9	2.58	119.84	113.30
1	1	966	2MG	O6-C6-C5	-2.57	119.78	126.60
1	1	2251	1MG	C8-N7-C5	2.55	108.86	104.24
1	1	3468	5MC	N1-C2-N3	2.55	123.44	118.81
1	1	3536	6MZ	O3'-C3'-C2'	2.53	120.01	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	4004	OMC	C1'-N1-C2	2.53	124.06	118.42
1	1	4086	PSU	O3'-C3'-C4'	2.52	118.32	111.05
1	1	3575	G7M	C2-N1-C6	-2.50	120.53	125.10
1	1	2251	1MG	N9-C8-N7	-2.46	108.75	113.39
1	1	527	7MG	O4'-C1'-N9	-2.43	105.98	109.30
1	1	3757	OMG	C1'-N9-C4	2.43	133.73	126.50
1	1	3951	2MG	C6-C5-N7	2.43	134.77	130.25
1	1	3341	2MG	CM2-N2-C2	-2.42	118.52	123.86
1	1	3951	2MG	O6-C6-C5	-2.40	120.24	126.60
1	1	1207	2MG	CM2-N2-C2	-2.39	118.59	123.86
1	1	3951	2MG	N9-C8-N7	-2.37	108.93	113.39
1	1	3757	OMG	C4-C5-N7	-2.37	106.97	110.72
1	1	4004	OMC	C4-N3-C2	2.36	124.06	120.25
1	1	3536	6MZ	N3-C4-N9	2.34	130.93	127.08
1	1	4434	MA6	N9-C8-N7	-2.34	110.72	113.91
1	1	3341	2MG	O6-C6-C5	-2.32	120.45	126.60
1	1	4004	OMC	O3'-C3'-C2'	2.31	117.72	111.17
1	1	4058	OMU	O3'-C3'-C2'	2.31	117.72	111.17
1	1	527	7MG	O6-C6-C5	-2.31	121.88	127.54
1	1	527	7MG	C2-N1-C6	-2.30	120.91	125.10
1	1	4414	UR3	C5-C6-N1	-2.30	117.96	121.81
1	1	1402	4OC	C3'-C2'-C1'	-2.29	98.58	102.89
1	1	2253	5MU	C2'-C1'-N1	2.28	119.68	113.22
44	q	89	0TD	OD2-CG-OD1	-2.28	118.92	124.09
1	1	3341	2MG	C6-C5-N7	2.27	134.47	130.25
1	1	1407	5MC	C5-C4-N3	-2.27	119.23	121.67
1	1	3341	2MG	C4-C5-N7	-2.26	107.14	110.72
1	1	4009	2MA	C2-N3-C4	2.26	122.54	116.99
1	1	2251	1MG	C4-C5-N7	-2.24	107.17	110.72
1	1	3423	PSU	C6-C5-C4	-2.23	116.64	118.20
1	1	1207	2MG	O6-C6-C5	-2.23	120.67	126.60
1	1	4432	2MG	CM2-N2-C2	-2.23	118.94	123.86
1	1	4432	2MG	C8-N7-C5	2.20	108.22	104.24
1	1	4086	PSU	O3'-C3'-C2'	2.20	118.93	111.82
1	1	4414	UR3	C3U-N3-C2	2.19	121.14	117.31
1	1	1402	4OC	C5-C4-N3	-2.17	119.11	122.59
1	1	4009	2MA	C6-C5-N7	2.13	135.99	132.02
1	1	4058	OMU	C5'-C4'-C3'	2.12	123.14	115.18
1	1	967	5MC	C1'-N1-C6	-2.12	117.60	121.12
1	1	3536	6MZ	C5-C4-N9	2.11	108.24	105.78
1	1	2253	5MU	O4-C4-C5	2.11	127.35	124.90
1	1	1207	2MG	N9-C8-N7	-2.11	109.42	113.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1207	2MG	C6-C5-N7	2.10	134.15	130.25
1	1	966	2MG	C4-C5-N7	-2.10	107.40	110.72
1	1	4009	2MA	C2'-C1'-N9	2.09	118.60	113.30
1	1	966	2MG	C8-N7-C5	2.09	108.02	104.24
1	1	3536	6MZ	C2-N1-C6	2.09	122.26	115.25
1	1	3757	OMG	C1'-N9-C8	-2.09	120.75	126.70
1	1	4009	2MA	CM2-C2-N3	2.08	120.41	117.15
1	1	3757	OMG	C6-C5-N7	2.08	134.12	130.25
1	1	4058	OMU	CM2-O2'-C2'	-2.08	109.06	114.52
1	1	3536	6MZ	C1'-N9-C8	2.08	131.83	127.14
1	1	3124	6MZ	C2-N1-C6	2.08	122.22	115.25
1	1	4432	2MG	N9-C8-N7	-2.07	109.50	113.39
1	1	967	5MC	C5-C4-N3	-2.06	119.45	121.67
1	1	4435	MA6	C6-C5-N7	2.06	136.74	133.28
1	1	4004	OMC	C6-C5-C4	-2.06	114.19	117.50
1	1	4086	PSU	C6-N1-C2	-2.06	120.58	122.68
1	1	4432	2MG	O6-C6-C5	-2.04	121.18	126.60
1	1	1207	2MG	C8-N7-C5	2.04	107.93	104.24
1	1	4434	MA6	C4-C5-C6	2.03	118.16	115.88
1	1	4434	MA6	C9-N6-C6	2.02	125.65	120.40
1	1	4058	OMU	C6-C5-C4	-2.02	116.76	119.52
1	1	3536	6MZ	C4-N9-C8	2.01	107.91	105.73
1	1	4004	OMC	O3'-C3'-C4'	2.00	116.84	111.05
1	1	3951	2MG	C8-N7-C5	2.00	107.86	104.24

All (39) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	516	PSU	C4'
1	1	516	PSU	C3'
1	1	527	7MG	C3'
1	1	1402	4OC	C1'
1	1	1402	4OC	C3'
1	1	2251	1MG	C2'
1	1	2251	1MG	C1'
1	1	2252	PSU	C4'
1	1	2252	PSU	C3'
1	1	2253	5MU	C4'
1	1	2253	5MU	C2'
1	1	2461	PSU	C4'
1	1	2461	PSU	C3'
1	1	3124	6MZ	C2'

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Mol	Chain	Res	Type	Atom
1	1	3124	6MZ	C3'
1	1	3417	PSU	C4'
1	1	3417	PSU	C3'
1	1	3421	3TD	C3'
1	1	3423	PSU	C4'
1	1	3423	PSU	C3'
1	1	3445	5MU	C4'
1	1	3445	5MU	C2'
1	1	3536	6MZ	C2'
1	1	3536	6MZ	C3'
1	1	3575	G7M	C2'
1	1	3757	OMG	C2'
1	1	3963	PSU	C4'
1	1	3963	PSU	C3'
1	1	4004	OMC	C4'
1	1	4009	2MA	C2'
1	1	4009	2MA	C3'
1	1	4010	PSU	C4'
1	1	4010	PSU	C3'
1	1	4058	OMU	C2'
1	1	4058	OMU	C3'
1	1	4086	PSU	C4'
1	1	4086	PSU	C3'
1	1	4111	PSU	C4'
1	1	4111	PSU	C3'

All (81) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	516	PSU	O4'-C1'-C5-C4
1	1	516	PSU	O4'-C1'-C5-C6
1	1	516	PSU	C3'-C4'-C5'-O5'
1	1	516	PSU	O4'-C4'-C5'-O5'
1	1	527	7MG	C3'-C4'-C5'-O5'
1	1	966	2MG	O4'-C4'-C5'-O5'
1	1	966	2MG	C3'-C4'-C5'-O5'
1	1	966	2MG	N1-C2-N2-CM2
1	1	966	2MG	N3-C2-N2-CM2
1	1	1402	4OC	O4'-C4'-C5'-O5'
1	1	2253	5MU	C3'-C4'-C5'-O5'
1	1	2253	5MU	O4'-C4'-C5'-O5'
1	1	3124	6MZ	N1-C6-N6-C9

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Mol	Chain	Res	Type	Atoms
1	1	3124	6MZ	O4'-C4'-C5'-O5'
1	1	3124	6MZ	C3'-C4'-C5'-O5'
1	1	3417	PSU	C3'-C4'-C5'-O5'
1	1	3421	3TD	O4'-C1'-C5-C4
1	1	3421	3TD	O4'-C1'-C5-C6
1	1	3421	3TD	C3'-C4'-C5'-O5'
1	1	3421	3TD	O4'-C4'-C5'-O5'
1	1	3423	PSU	C3'-C4'-C5'-O5'
1	1	3536	6MZ	O4'-C4'-C5'-O5'
1	1	3536	6MZ	C3'-C4'-C5'-O5'
1	1	3963	PSU	C3'-C4'-C5'-O5'
1	1	4004	OMC	C3'-C4'-C5'-O5'
1	1	4004	OMC	C4'-C5'-O5'-P
1	1	4009	2MA	O4'-C4'-C5'-O5'
1	1	4009	2MA	C3'-C4'-C5'-O5'
1	1	4058	OMU	O4'-C4'-C5'-O5'
1	1	4086	PSU	C3'-C4'-C5'-O5'
1	1	4111	PSU	C3'-C4'-C5'-O5'
1	1	4111	PSU	O4'-C4'-C5'-O5'
44	q	89	0TD	CG-CB-SB-CSB
1	1	1402	4OC	C2'-C1'-N1-C2
1	1	2461	PSU	C4'-C5'-O5'-P
1	1	1402	4OC	C3'-C4'-C5'-O5'
1	1	4058	OMU	C3'-C4'-C5'-O5'
1	1	1402	4OC	C2'-C1'-N1-C6
1	1	527	7MG	O4'-C4'-C5'-O5'
1	1	3417	PSU	O4'-C4'-C5'-O5'
1	1	3963	PSU	O4'-C4'-C5'-O5'
1	1	4010	PSU	O4'-C4'-C5'-O5'
1	1	4086	PSU	O4'-C4'-C5'-O5'
1	1	4435	MA6	O4'-C4'-C5'-O5'
1	1	4010	PSU	C3'-C4'-C5'-O5'
1	1	3417	PSU	C4'-C5'-O5'-P
1	1	3423	PSU	C4'-C5'-O5'-P
1	1	3445	5MU	C4'-C5'-O5'-P
1	1	3423	PSU	O4'-C4'-C5'-O5'
1	1	4004	OMC	O4'-C4'-C5'-O5'
1	1	527	7MG	C4'-C5'-O5'-P
1	1	3963	PSU	C4'-C5'-O5'-P
1	1	4111	PSU	C4'-C5'-O5'-P
1	1	4435	MA6	C3'-C4'-C5'-O5'
1	1	516	PSU	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
1	1	2253	5MU	C4'-C5'-O5'-P
1	1	3124	6MZ	C5-C6-N6-C9
1	1	4009	2MA	O4'-C1'-N9-C4
1	1	2251	1MG	C4'-C5'-O5'-P
1	1	4058	OMU	C4'-C5'-O5'-P
1	1	3124	6MZ	C2'-C1'-N9-C8
1	1	2461	PSU	C3'-C4'-C5'-O5'
1	1	3124	6MZ	C4'-C5'-O5'-P
1	1	3757	OMG	O4'-C4'-C5'-O5'
1	1	4010	PSU	C4'-C5'-O5'-P
1	1	4086	PSU	C4'-C5'-O5'-P
1	1	3575	G7M	C4'-C5'-O5'-P
1	1	2252	PSU	O4'-C1'-C5-C4
1	1	2253	5MU	C2'-C1'-N1-C6
1	1	4009	2MA	O4'-C1'-N9-C8
1	1	2461	PSU	O4'-C4'-C5'-O5'
1	1	4434	MA6	O4'-C4'-C5'-O5'
1	1	3124	6MZ	C2'-C1'-N9-C4
1	1	4435	MA6	C5-C6-N6-C10
1	1	2252	PSU	O4'-C1'-C5-C6
1	1	2252	PSU	C3'-C4'-C5'-O5'
1	1	3575	G7M	O4'-C4'-C5'-O5'
1	1	3757	OMG	C3'-C4'-C5'-O5'
1	1	2253	5MU	C2'-C1'-N1-C2
1	1	4004	OMC	C2'-C1'-N1-C2
1	1	2251	1MG	C2'-C1'-N9-C4

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	1402	4OC	1	0
1	1	3445	5MU	1	0
1	1	4432	2MG	1	0
1	1	3536	6MZ	1	0
1	1	4435	MA6	2	0
44	q	89	0TD	1	0
1	1	527	7MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 438 ligands modelled in this entry, 438 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	1501:U	O3'	1502:U	P	3.88
1	1	1276:G	O3'	1277:C	P	3.82
1	1	3820:A	O3'	3821:G	P	3.74
1	1	1383:C	O3'	1384:C	P	3.50
1	1	147:G	O3'	148:G	P	3.31

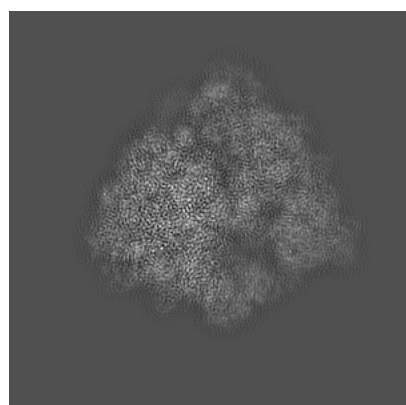
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0261. These allow visual inspection of the internal detail of the map and identification of artifacts.

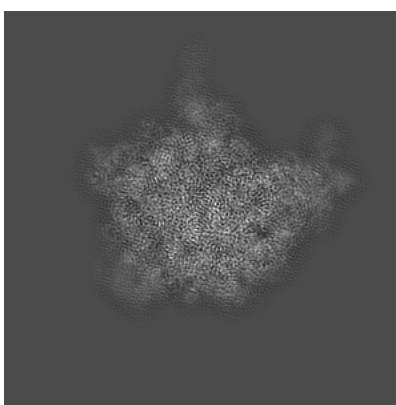
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

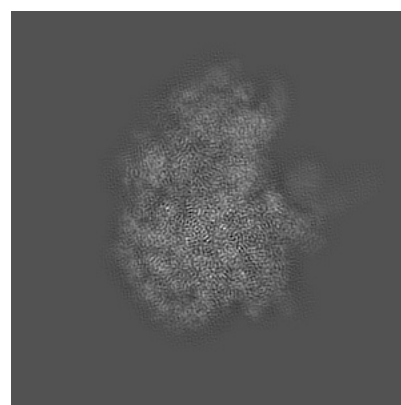
6.1.1 Primary map



X



Y

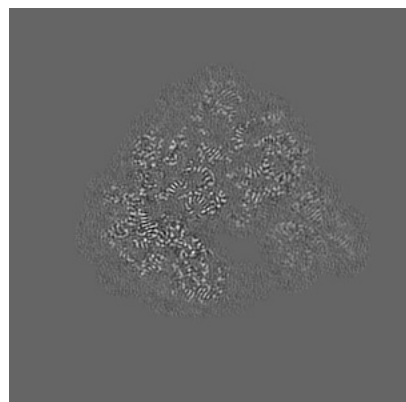


Z

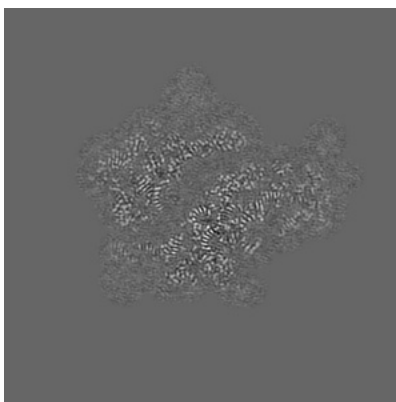
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

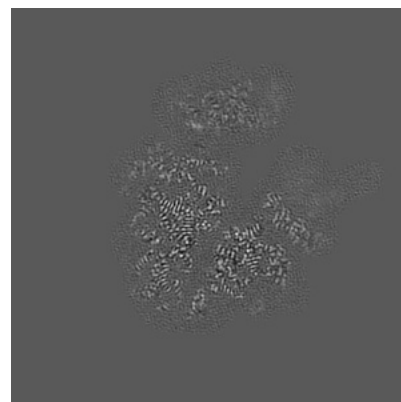
6.2.1 Primary map



X Index: 185



Y Index: 185

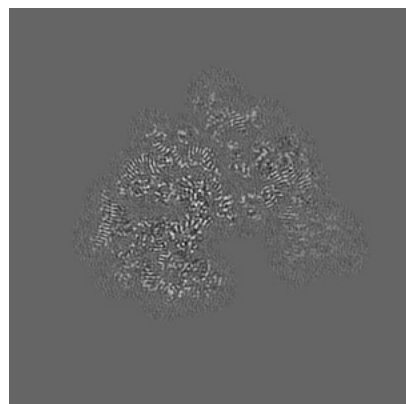


Z Index: 185

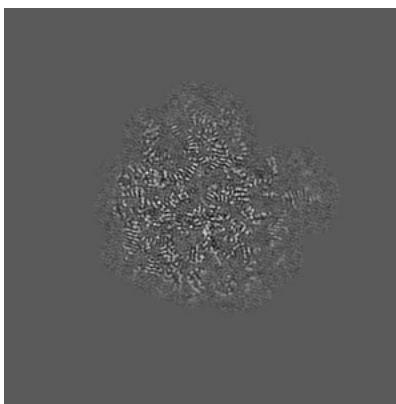
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

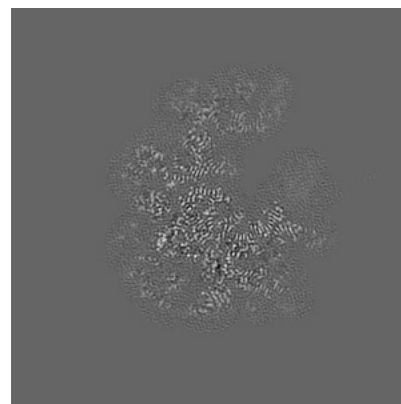
6.3.1 Primary map



X Index: 175



Y Index: 168

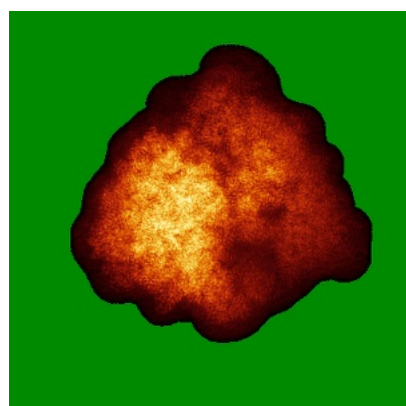


Z Index: 194

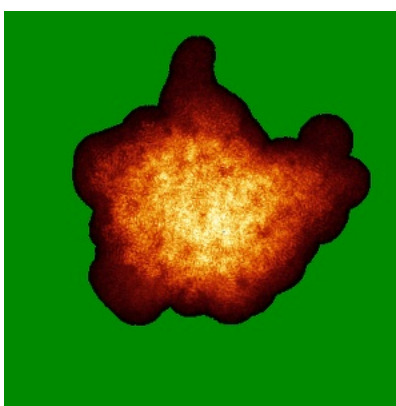
The images above show the largest variance slices of the map in three orthogonal directions.

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

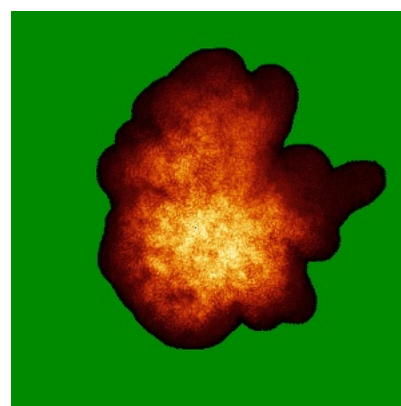
6.4.1 Primary map



X



Y

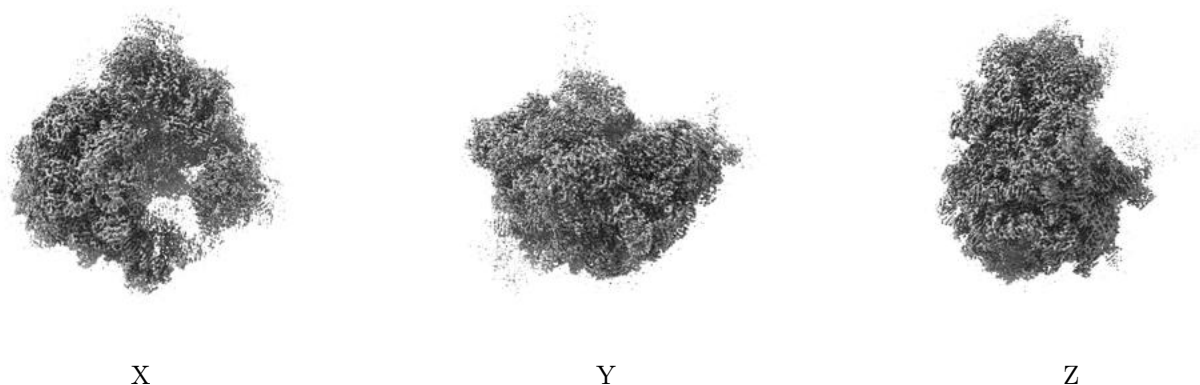


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

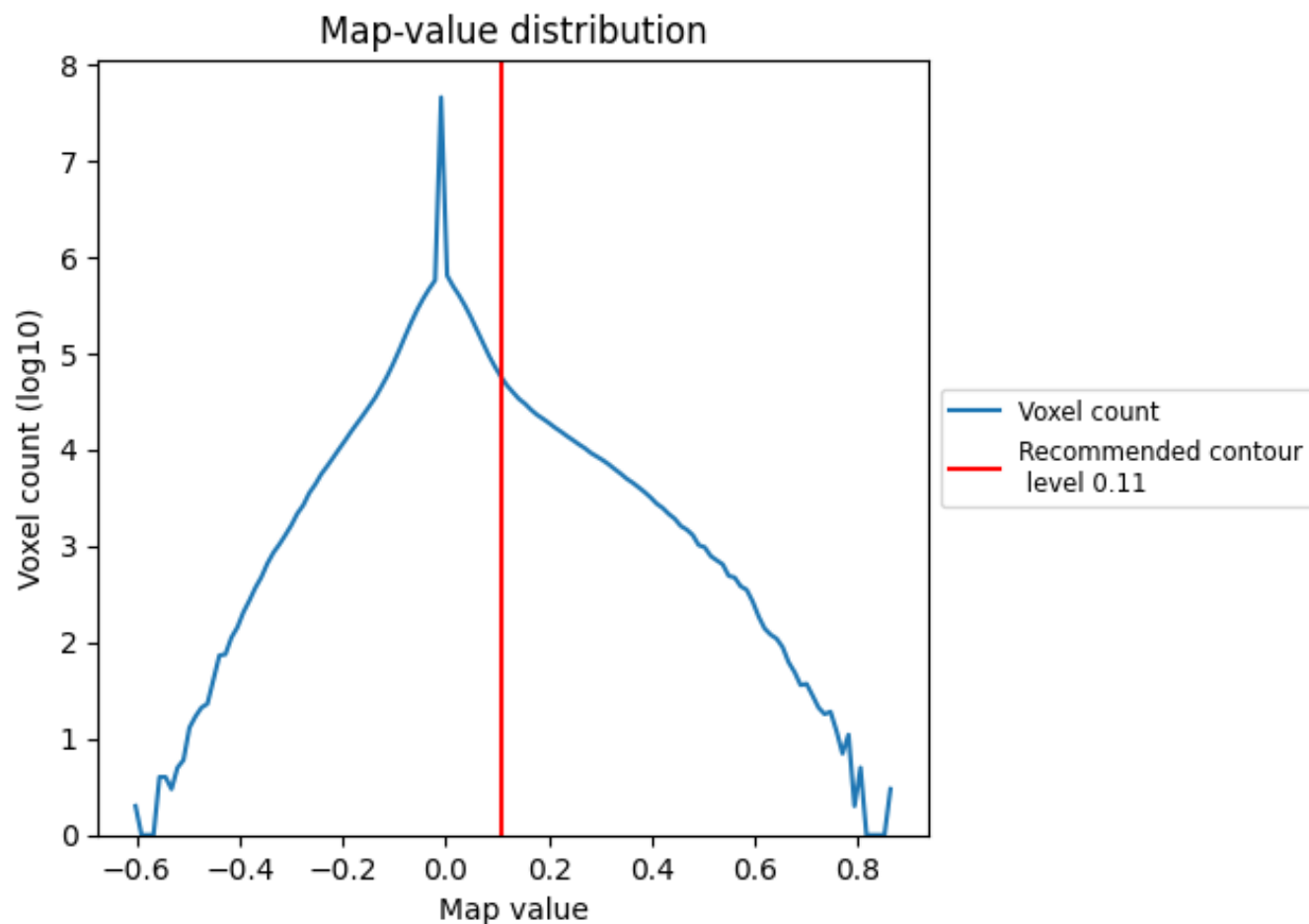
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

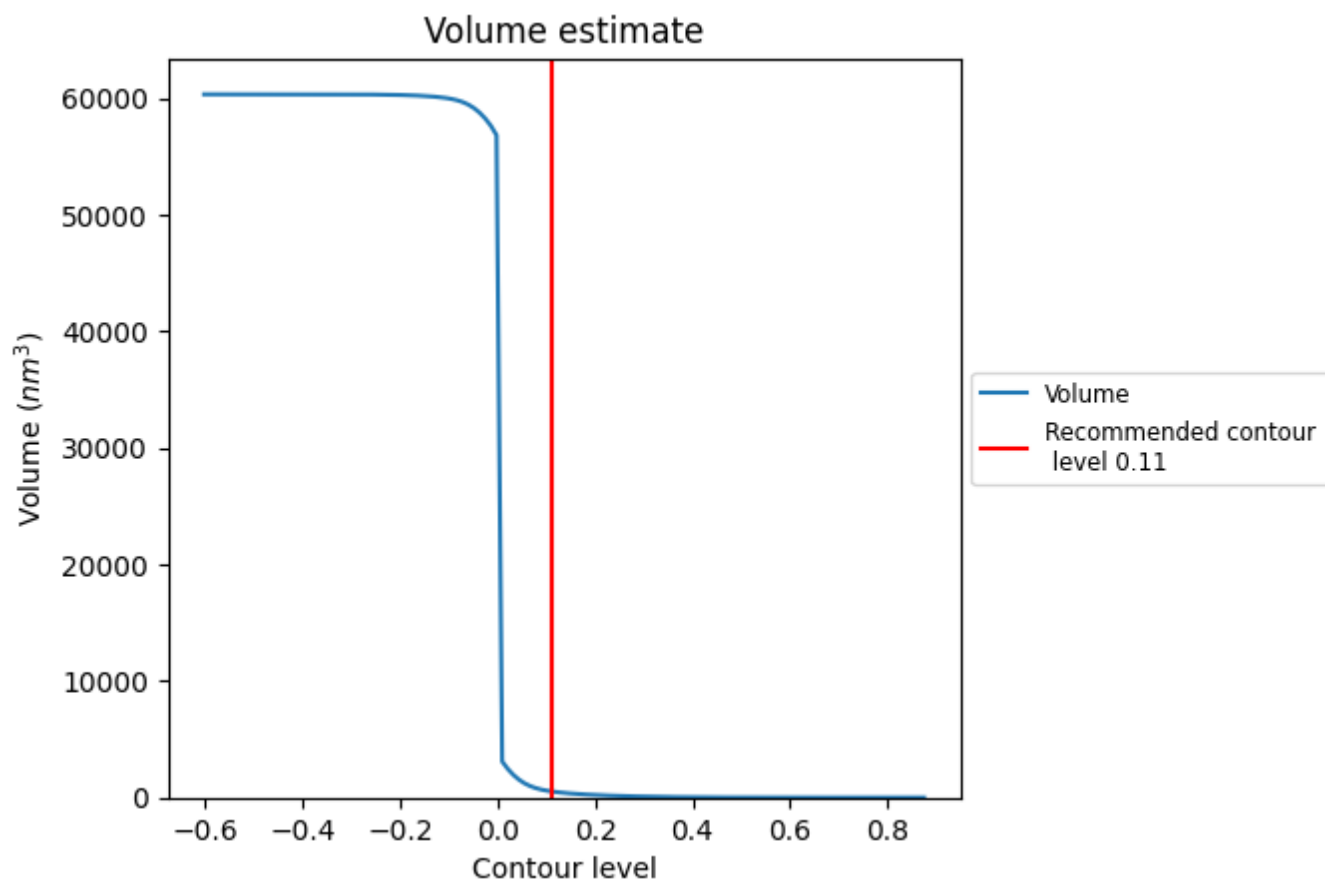
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

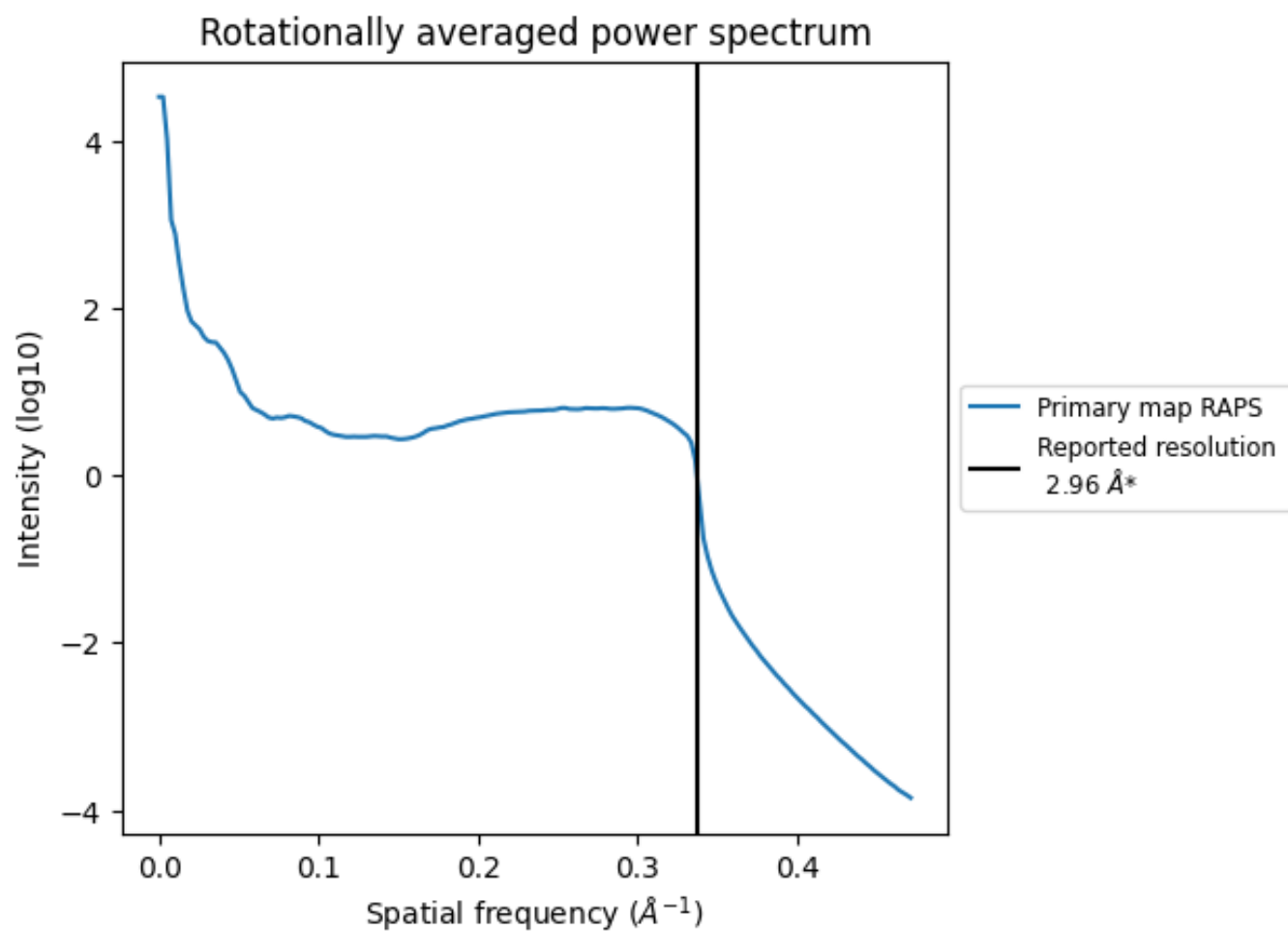
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 532 nm³; this corresponds to an approximate mass of 480 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

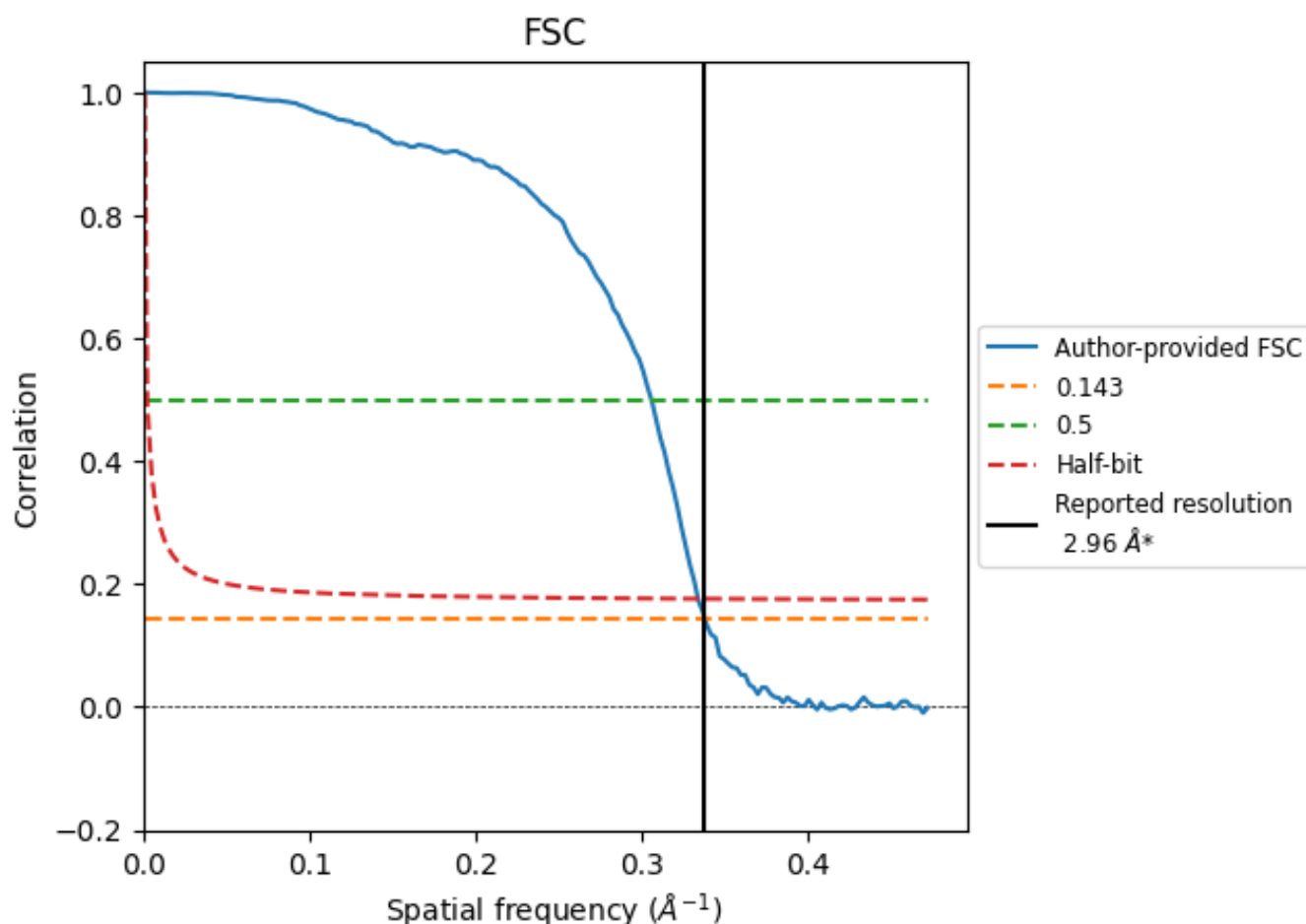


*Reported resolution corresponds to spatial frequency of 0.338 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.338 Å⁻¹

8.2 Resolution estimates [i](#)

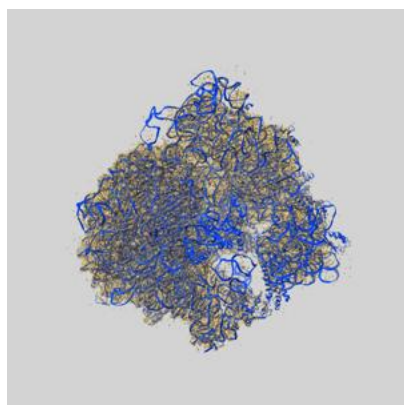
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.96	-	-
Author-provided FSC curve	2.96	3.27	3.00
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

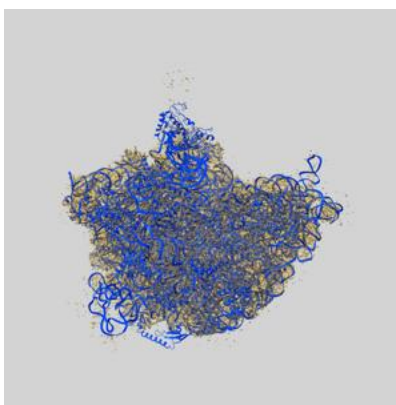
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0261 and PDB model 6HRM. Per-residue inclusion information can be found in section [3](#) on page [19](#).

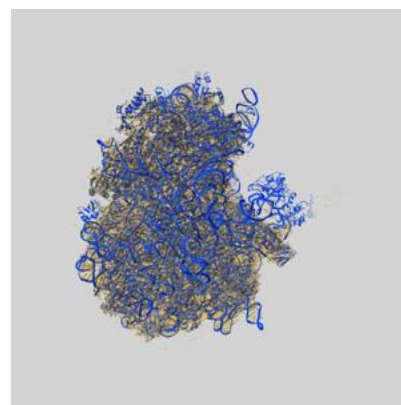
9.1 Map-model overlay [i](#)



X



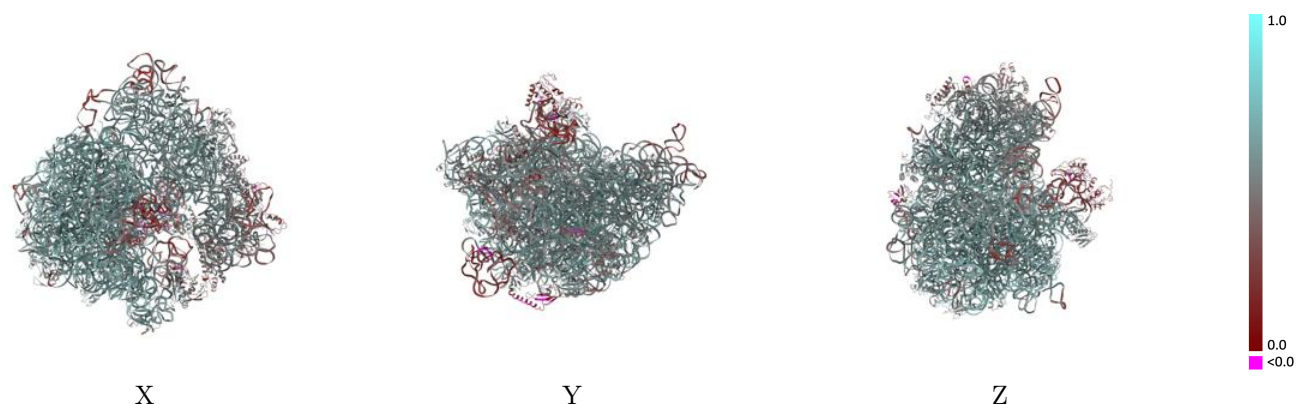
Y



Z

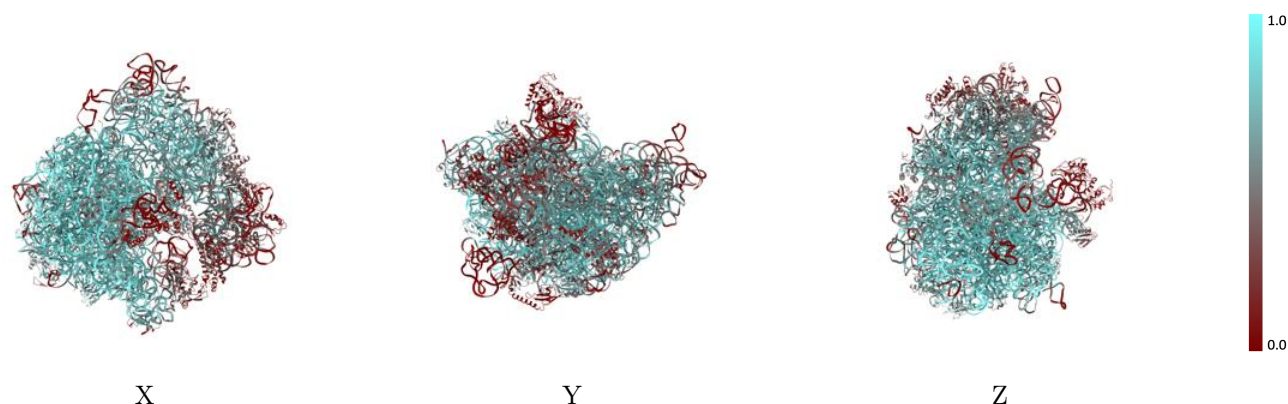
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



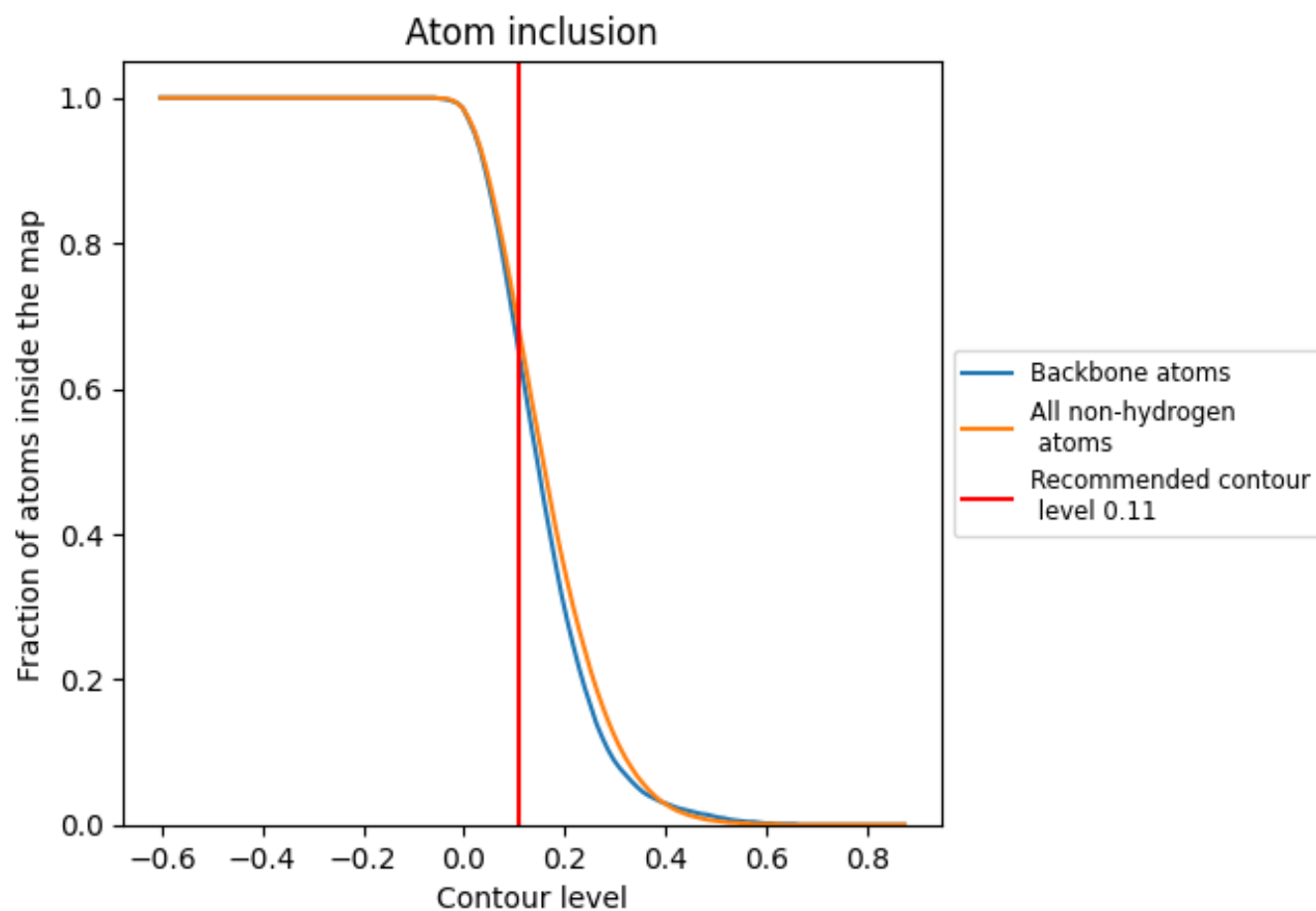
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6800	 0.5570
1	 0.7540	 0.5750
3	 0.7280	 0.5840
B	 0.8470	 0.6190
C	 0.7980	 0.6040
D	 0.6460	 0.5600
E	 0.2810	 0.4640
F	 0.4600	 0.5240
G	 0.1190	 0.2870
H	 0.0070	 0.2210
I	 0.0030	 0.2590
J	 0.7960	 0.6100
K	 0.7950	 0.6010
L	 0.7540	 0.5920
M	 0.7700	 0.5990
N	 0.8370	 0.6130
O	 0.6140	 0.5590
P	 0.7450	 0.5980
Q	 0.8240	 0.6160
R	 0.7240	 0.5830
S	 0.7670	 0.6060
T	 0.6750	 0.5670
U	 0.5510	 0.5240
V	 0.6480	 0.5690
W	 0.7970	 0.6160
X	 0.7640	 0.6030
Y	 0.4970	 0.5300
Z	 0.7480	 0.5870
a	 0.1230	 0.3660
b	 0.7580	 0.6050
c	 0.6910	 0.5810
d	 0.8620	 0.6100
e	 0.8350	 0.6260
f	 0.7820	 0.5930
g	 0.2600	 0.4290



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Chain	Atom inclusion	Q-score
h	 0.3520	 0.4760
i	 0.4220	 0.4960
j	 0.5740	 0.5210
k	 0.5080	 0.5170
l	 0.1840	 0.4350
m	 0.6050	 0.5470
n	 0.1950	 0.4340
o	 0.2340	 0.3990
p	 0.5250	 0.5310
q	 0.6450	 0.5530
r	 0.1840	 0.4320
s	 0.3330	 0.4810
t	 0.6320	 0.5630
u	 0.5330	 0.5260
v	 0.5130	 0.5240
w	 0.6180	 0.5470
x	 0.1510	 0.4140
y	 0.5810	 0.5540
z	 0.2330	 0.4530