



## Full wwPDB EM Validation Report ⓘ

Feb 5, 2024 – 05:32 PM JST

PDB ID : 8IFC  
EMDB ID : EMD-35412  
Title : Arbekacin-bound E.coli 70S ribosome in the PURE system  
Authors : Tomono, J.; Asano, K.; Chiashi, T.; Tanaka, Y.; Yokoyama, T.  
Deposited on : 2023-02-17  
Resolution : 2.90 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

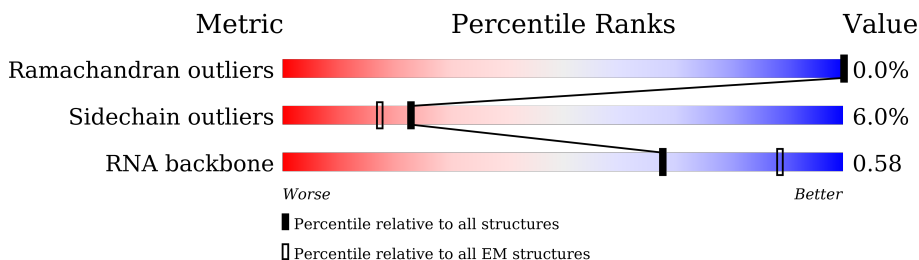
EMDB validation analysis : 0.0.1.dev70  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	A	1542	
2	B	241	
3	C	233	
4	D	206	
5	E	167	
6	F	135	
7	G	179	
8	H	130	

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Mol	Chain	Length	Quality of chain
9	I	130	34% 92% 5%
10	J	103	50% 90% 5% 5%
11	K	129	21% 87% 9%
12	L	124	17% 92% 7%
13	M	118	37% 94% ..
14	N	101	23% 97% ..
15	O	89	20% 92% 7%
16	P	82	34% 95% ..
17	Q	84	25% 88% 6% 6%
18	R	75	24% 81% 7% 12%
19	S	92	29% 87% 9%
20	T	87	44% 94% 5%
21	U	71	62% 90% 8%
22	a	2904	6% 82% 12% 5%
23	b	120	6% 89% 10%
24	c	273	. 97% ..
25	d	209	6% 96% .
26	e	201	13% 98% .
27	f	179	44% 91% 8%
28	g	177	42% 89% 10%
29	h	149	13% 25% 72%
30	i	142	. 98% .
31	j	123	. 96% .
32	k	144	. 99% .
33	l	136	. 98% ..

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Mol	Chain	Length	Quality of chain
34	m	127	88% 5% 7%
35	n	117	97% ..
36	o	115	93% 6% .
37	p	118	97% ..
38	q	103	96% .
39	r	110	96% .
40	s	100	90% . 7%
41	t	104	96% ..
42	u	94	97% .
43	v	85	86% 6% 8%
44	w	78	95% ..
45	x	63	94% 5% .
46	y	59	95% ..
47	z	57	98% .
48	0	55	87% 5% 7%
49	1	46	93% 7%
50	2	65	95% ..
51	3	38	89% 11%
52	4	70	79% 7% 14%
53	5	76	70% 28% .
54	6	77	75% 23% .
55	7	10	100%

## 2 Entry composition [i](#)

There are 60 unique types of molecules in this entry. The entry contains 143000 atoms, of which 440 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1519	32612	14552	5986	10555	1519	0	0

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	224	1753	1109	315	321	8	0	0

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	206	1624	1028	305	288	3	0	0

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

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

- Molecule 6 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	103	839	530	151	151	7	0	0

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	153	1203	750	231	218	4	0	0

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	98	786	493	150	142	1	0	0

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	117	877	540	173	161	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	modified residue	UNP P0A7R9

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

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

- Molecule 22 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	2753	Total	C	N	O	P	0	0
			59130	26384	10897	19096	2753		

- Molecule 23 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 26 is a protein called 50S ribosomal protein L4.

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

- Molecule 27 is a protein called 50S ribosomal protein L5.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	f	177	1410	899	249	256	6	0	0

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	g	176	1323	832	243	246	2	0	0

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	h	41	303	194	54	54	1	0	0

- Molecule 30 is a protein called 50S ribosomal protein L13.

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

- Molecule 31 is a protein called 50S ribosomal protein L14.

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

- Molecule 32 is a protein called 50S ribosomal protein L15.

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

- Molecule 33 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	l	136	1075	686	205	177	7	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
l	82	MS6	MET	modified residue	UNP P0ADY7

- Molecule 34 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	m	118	945	585	194	161	5	0	0

- Molecule 35 is a protein called 50S ribosomal protein L18.

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

- Molecule 36 is a protein called 50S ribosomal protein L19.

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

- Molecule 37 is a protein called 50S ribosomal protein L20.

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

- Molecule 38 is a protein called 50S ribosomal protein L21.

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

- Molecule 39 is a protein called 50S ribosomal protein L22.

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

- Molecule 40 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	s	93	738	466	139	131	2	0	0

- Molecule 41 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	t	102	779	492	146	141		0	0

- Molecule 42 is a protein called 50S ribosomal protein L25.

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

- Molecule 43 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	v	78	586	362	116	107	1	0	0

- Molecule 44 is a protein called 50S ribosomal protein L28.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

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

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	y	58	449	281	87	79	2	0	0

- Molecule 47 is a protein called 50S ribosomal protein L32.

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

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 53 is a RNA chain called A-site tRNA-Phe.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	5	76	Total	C	N	O	P	S	0	0
			1632	731	290	533	76	2		

- Molecule 54 is a RNA chain called P-site tRNA<sup>f</sup>-Met.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	N	O	P			S
54	6	77	1645	734	297	536	77	1	0	0

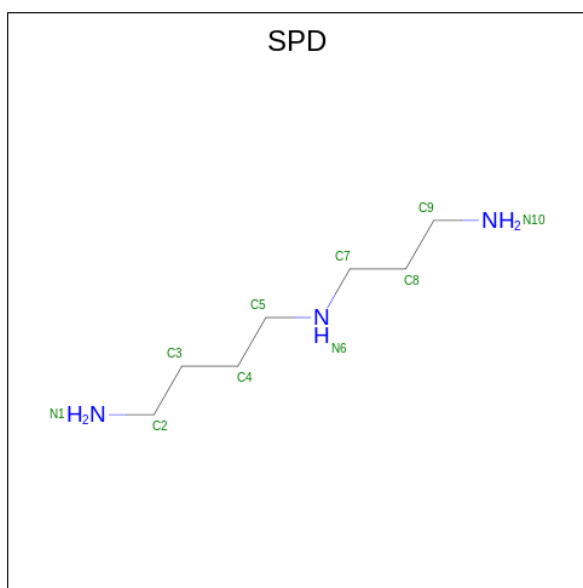
- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	N	O	P			S
55	7	10	209	95	37	68	9		0	0

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	A	188	Total	Mg	0
			188	188	
56	C	3	Total	Mg	0
			3	3	
56	E	2	Total	Mg	0
			2	2	
56	G	1	Total	Mg	0
			1	1	
56	K	1	Total	Mg	0
			1	1	
56	M	9	Total	Mg	0
			9	9	
56	S	2	Total	Mg	0
			2	2	
56	a	233	Total	Mg	0
			233	233	
56	b	11	Total	Mg	0
			11	11	
56	c	1	Total	Mg	0
			1	1	
56	d	2	Total	Mg	0
			2	2	
56	l	1	Total	Mg	0
			1	1	
56	z	2	Total	Mg	0
			2	2	
56	4	2	Total	Mg	0
			2	2	
56	6	1	Total	Mg	0
			1	1	
56	7	1	Total	Mg	0
			1	1	

- Molecule 57 is SPERMIDINE (three-letter code: SPD) (formula: C<sub>7</sub>H<sub>19</sub>N<sub>3</sub>).



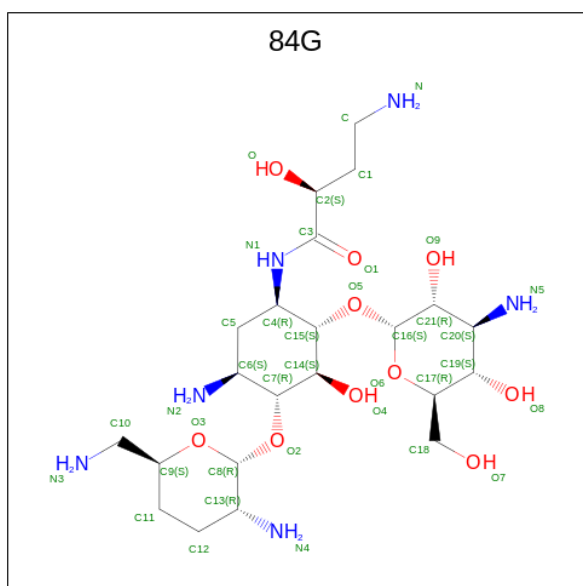
Mol	Chain	Residues	Atoms			AltConf
57	A	1	Total	C	N	0
			10	7	3	
57	A	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	

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Mol	Chain	Residues	Atoms			AltConf
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	

- Molecule 58 is Arbekacin (three-letter code: 84G) (formula:  $C_{22}H_{44}N_6O_{10}$ ) (labeled as "Ligand of Interest" by depositor).



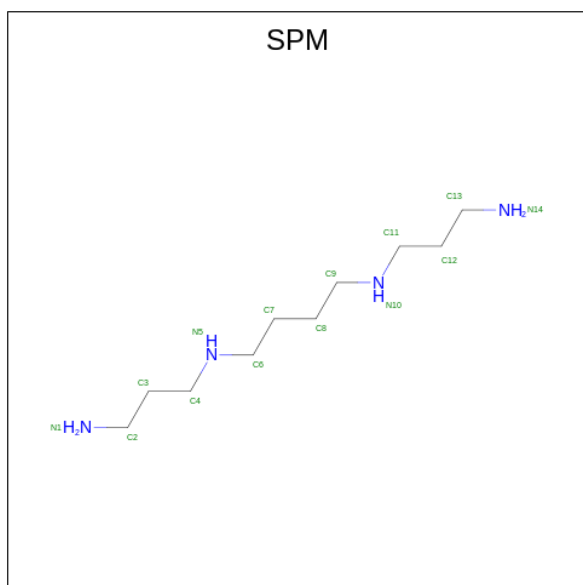
Mol	Chain	Residues	Atoms					AltConf
58	A	1	Total	C	H	N	O	0
			82	22	44	6	10	
58	A	1	Total	C	H	N	O	0
			82	22	44	6	10	
58	A	1	Total	C	H	N	O	0
			82	22	44	6	10	
58	a	1	Total	C	H	N	O	0
			82	22	44	6	10	
58	a	1	Total	C	H	N	O	0
			82	22	44	6	10	
58	a	1	Total	C	H	N	O	0
			82	22	44	6	10	
58	a	1	Total	C	H	N	O	0
			82	22	44	6	10	

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Mol	Chain	Residues	Atoms				AltConf	
58	a	1	Total	C	H	N	O	0
			82	22	44	6	10	
58	a	1	Total	C	H	N	O	0
			82	22	44	6	10	

- Molecule 59 is SPERMINE (three-letter code: SPM) (formula: C<sub>10</sub>H<sub>26</sub>N<sub>4</sub>).



Mol	Chain	Residues	Atoms			AltConf
59	a	1	Total	C	N	0
			14	10	4	

- Molecule 60 is ZINC ION (three-letter code: ZN) (formula: Zn).

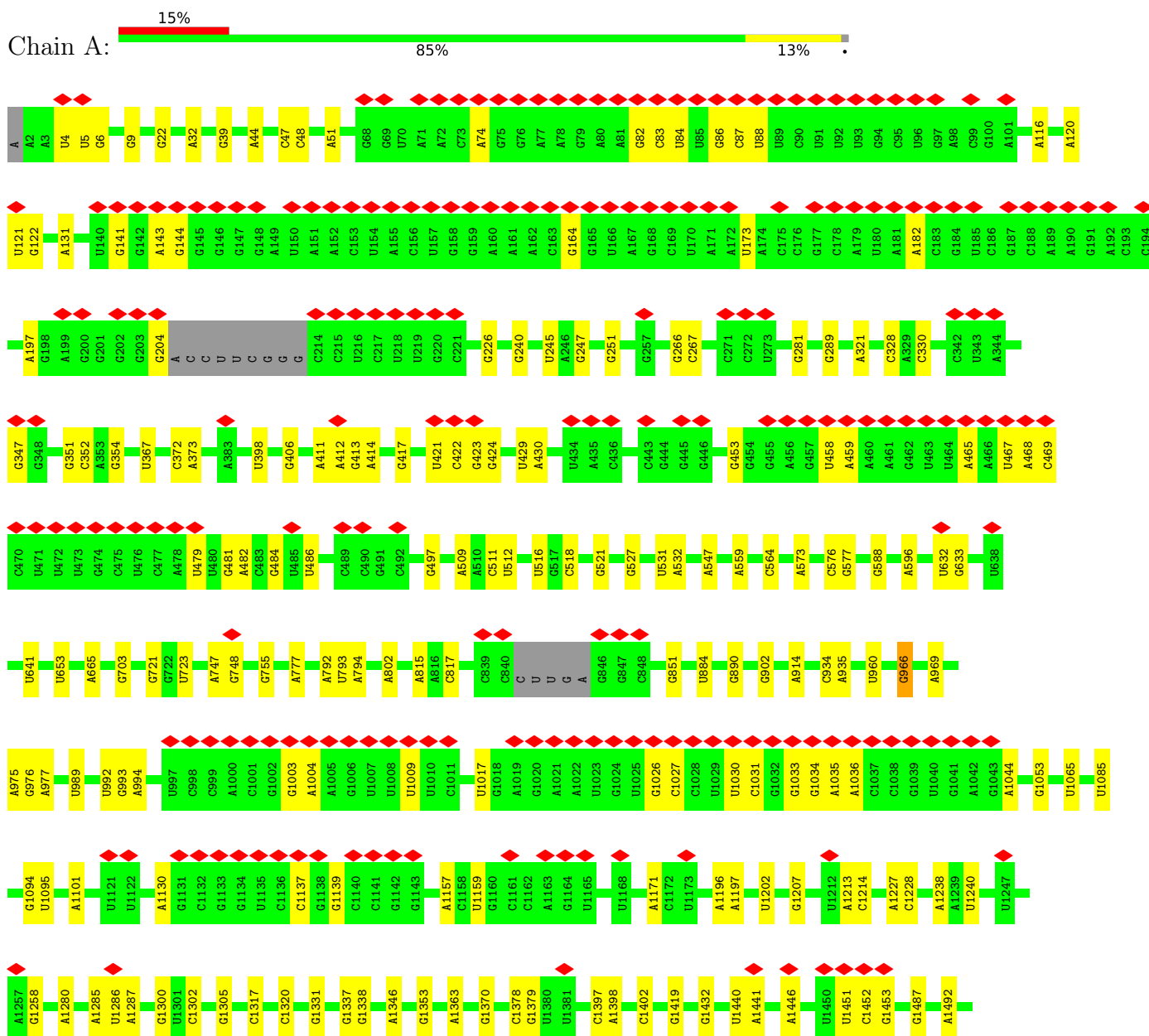
Mol	Chain	Residues	Atoms		AltConf
60	3	1	Total	Zn	0
			1	1	

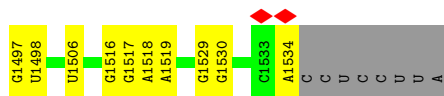


### 3 Residue-property plots

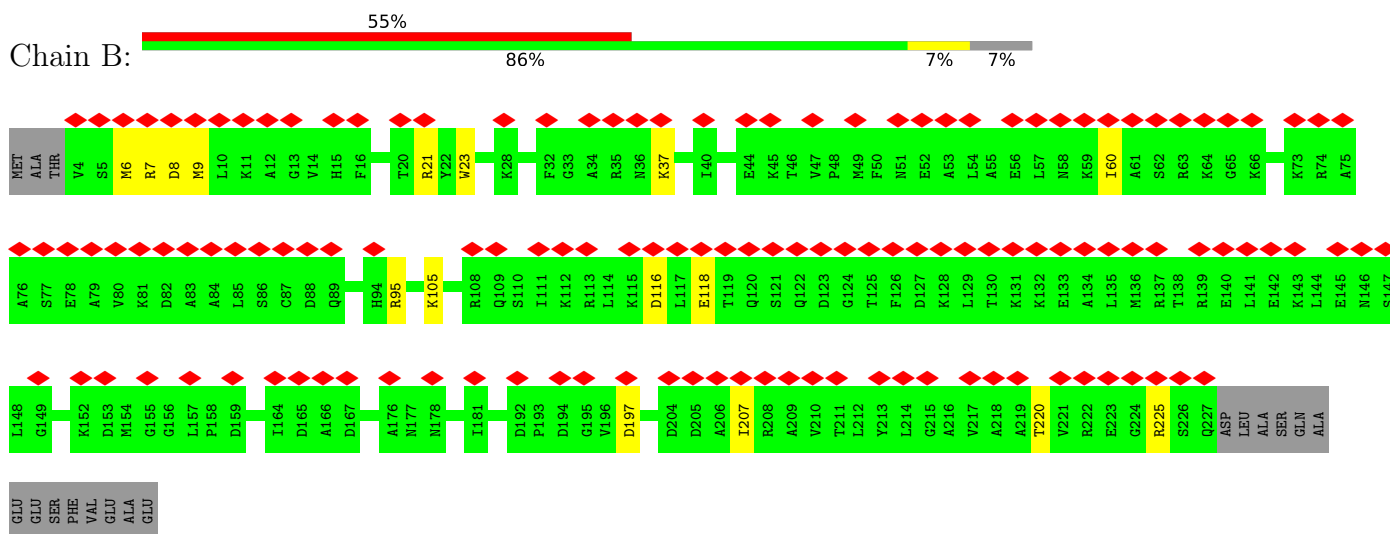
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 16S ribosomal RNA

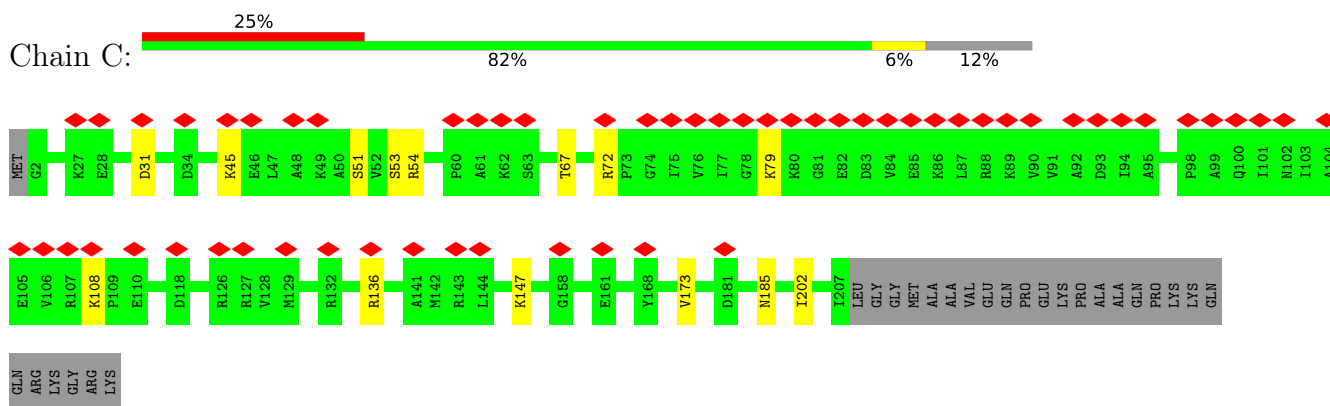




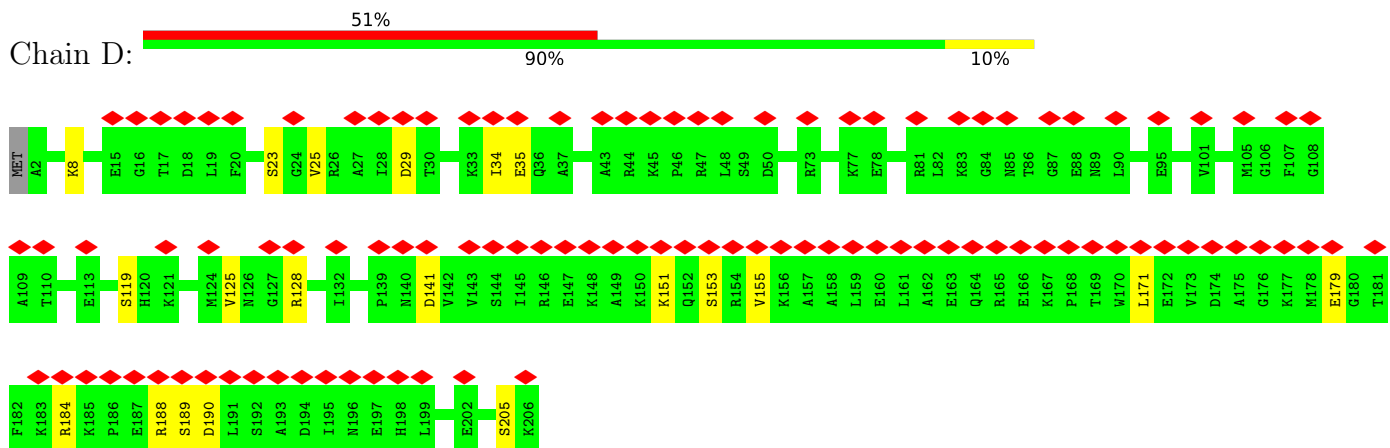
- Molecule 2: 30S ribosomal protein S2



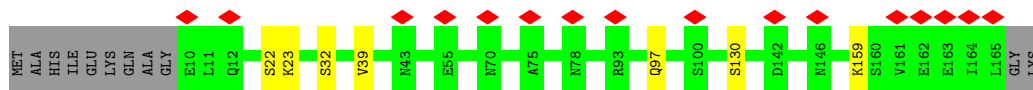
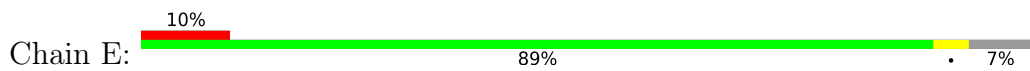
- Molecule 3: 30S ribosomal protein S3



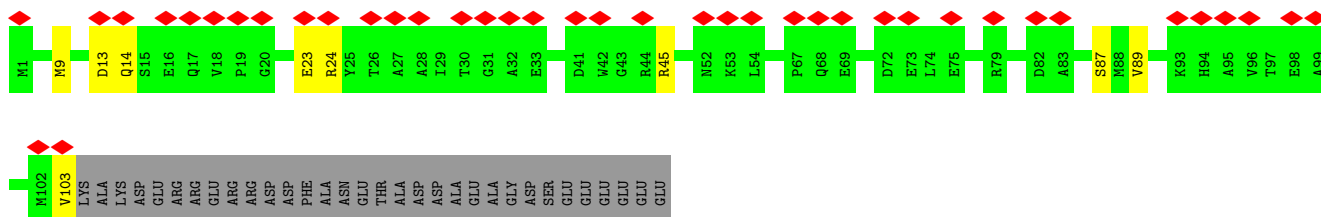
- Molecule 4: 30S ribosomal protein S4



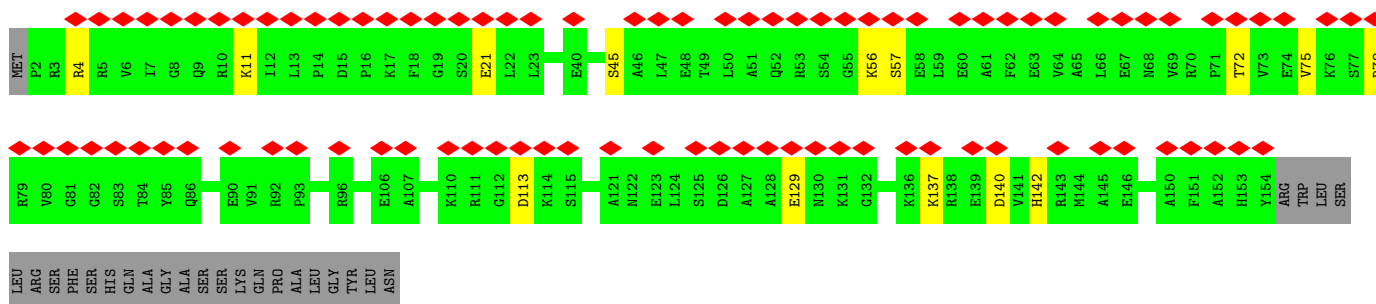
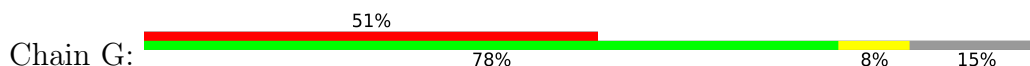
- Molecule 5: 30S ribosomal protein S5



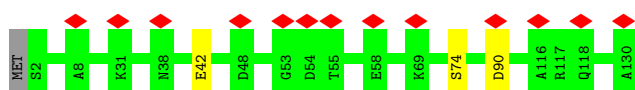
• Molecule 6: 30S ribosomal protein S6, fully modified isoform



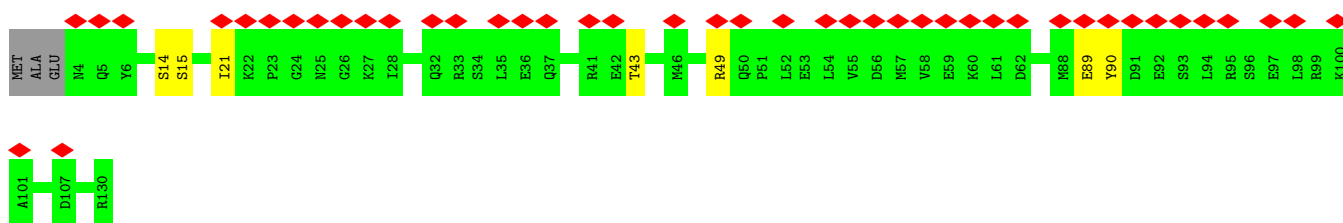
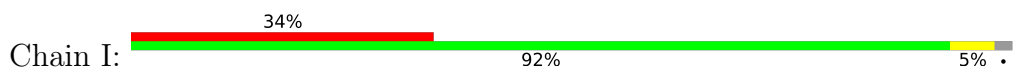
• Molecule 7: 30S ribosomal protein S7



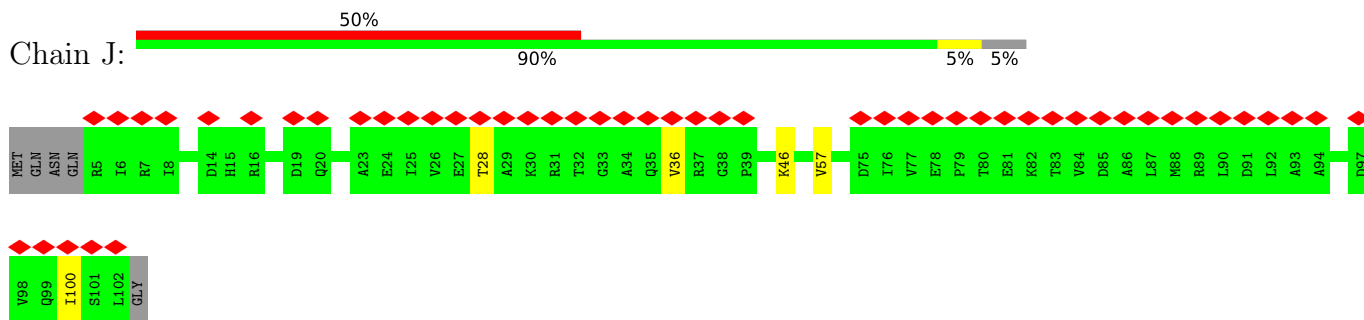
• Molecule 8: 30S ribosomal protein S8



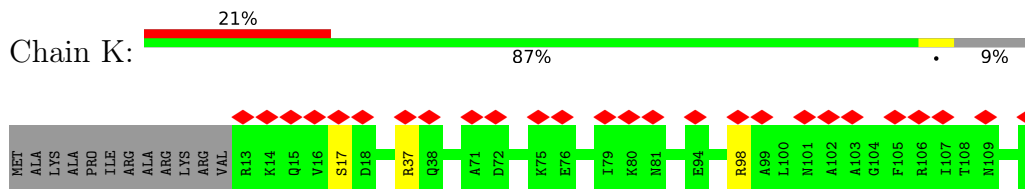
• Molecule 9: 30S ribosomal protein S9



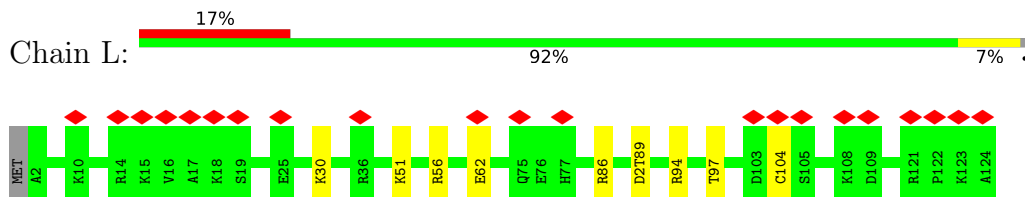
• Molecule 10: 30S ribosomal protein S10



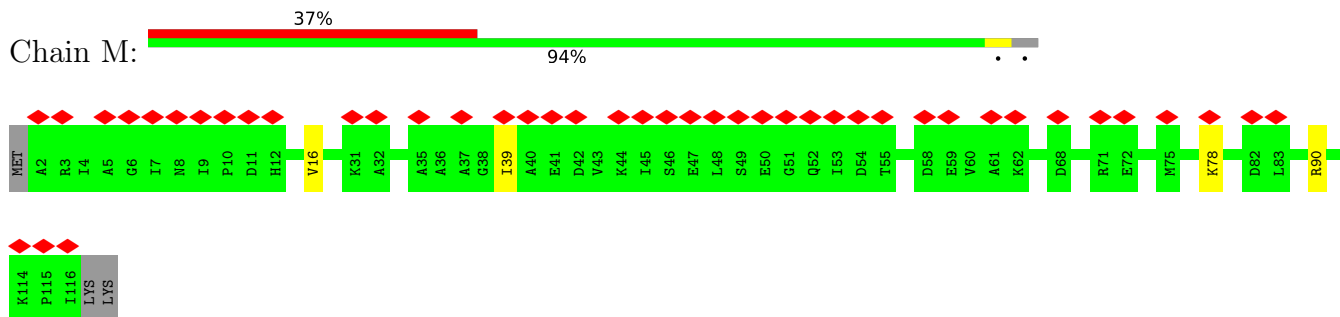
• Molecule 11: 30S ribosomal protein S11



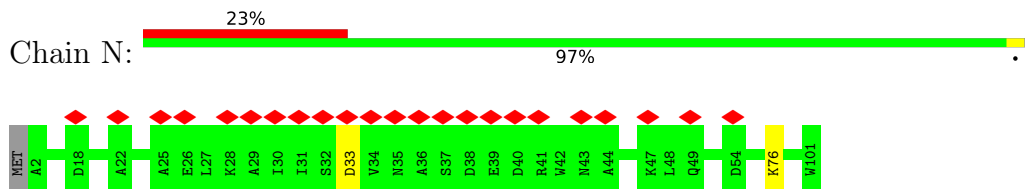
• Molecule 12: 30S ribosomal protein S12



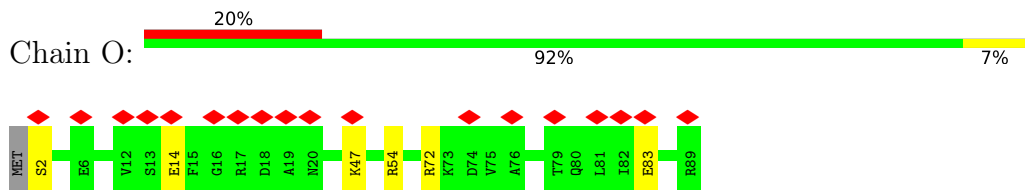
• Molecule 13: 30S ribosomal protein S13



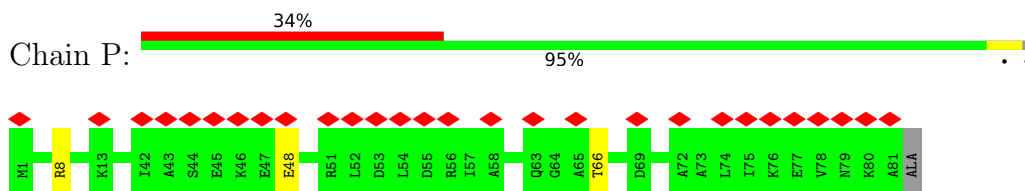
• Molecule 14: 30S ribosomal protein S14



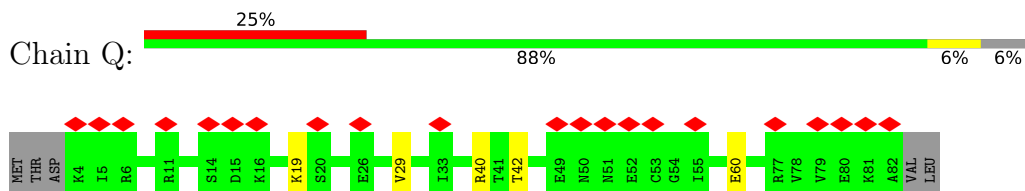
• Molecule 15: 30S ribosomal protein S15



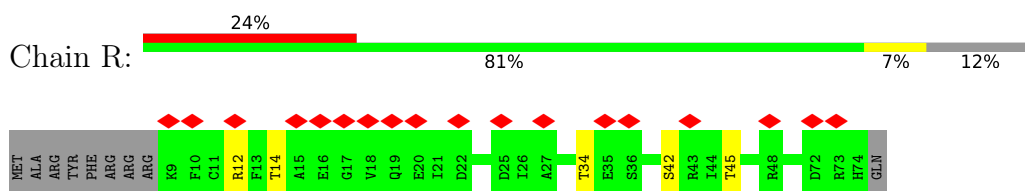
- Molecule 16: 30S ribosomal protein S16



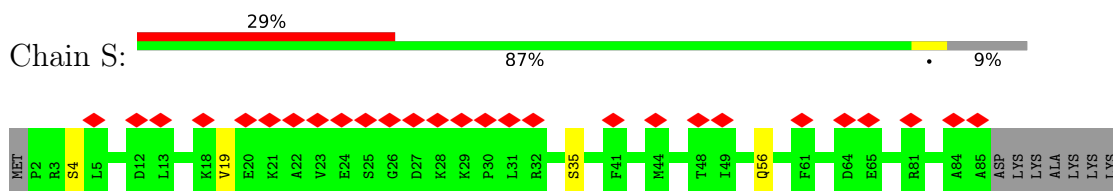
- Molecule 17: 30S ribosomal protein S17



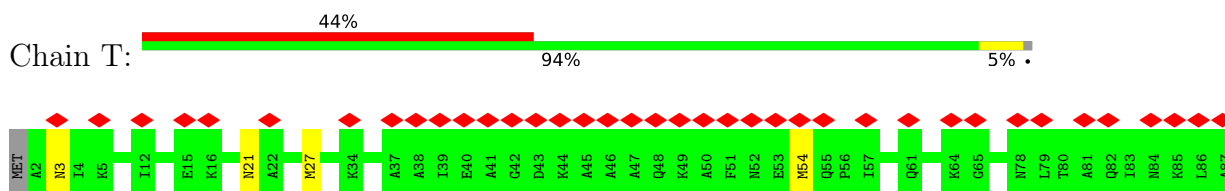
- Molecule 18: 30S ribosomal protein S18



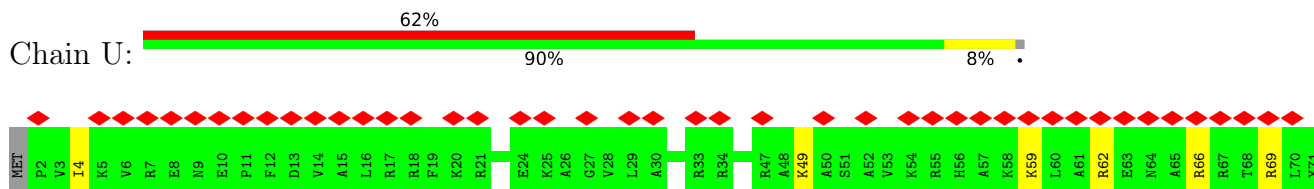
- Molecule 19: 30S ribosomal protein S19



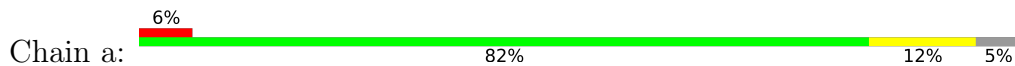
- Molecule 20: 30S ribosomal protein S20



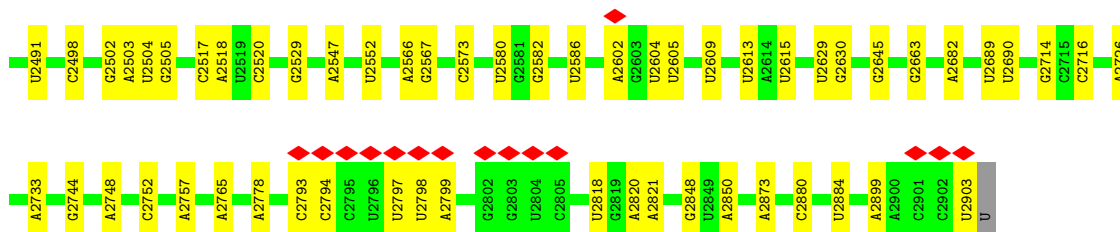
- Molecule 21: 30S ribosomal protein S21



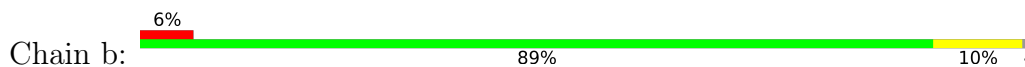
- Molecule 22: 23S ribosomal RNA



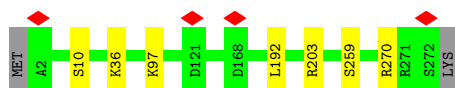




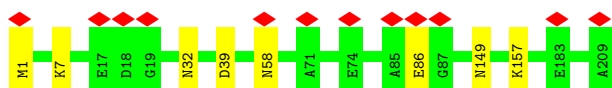
• Molecule 23: 5S ribosomal RNA



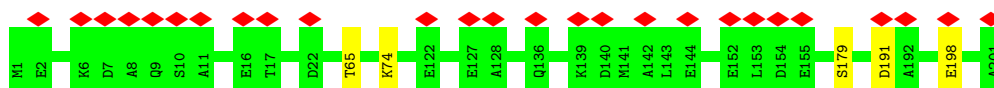
• Molecule 24: 50S ribosomal protein L2



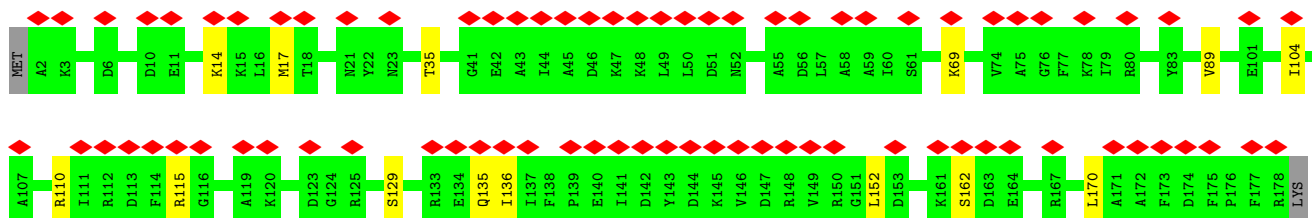
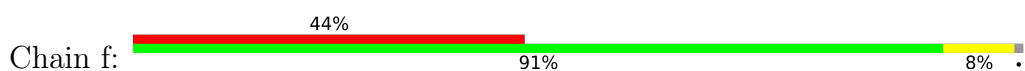
• Molecule 25: 50S ribosomal protein L3



• Molecule 26: 50S ribosomal protein L4



• Molecule 27: 50S ribosomal protein L5

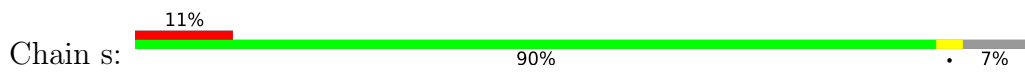


• Molecule 28: 50S ribosomal protein L6

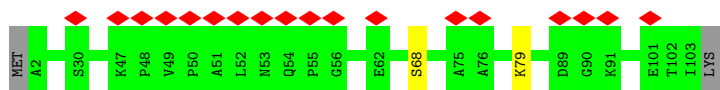
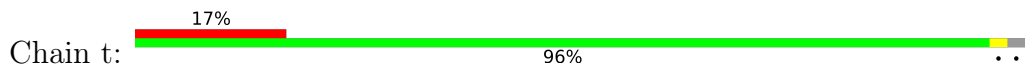




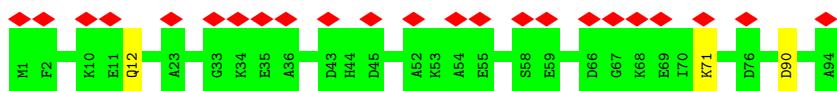




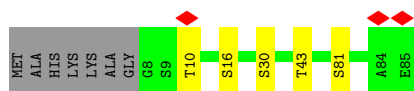
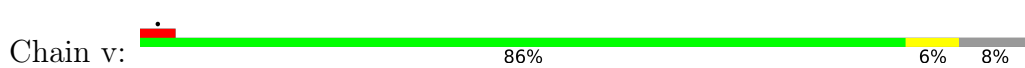
• Molecule 41: 50S ribosomal protein L24



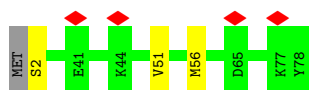
• Molecule 42: 50S ribosomal protein L25



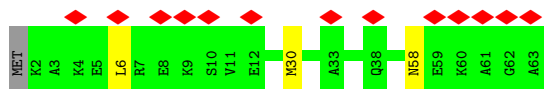
• Molecule 43: 50S ribosomal protein L27



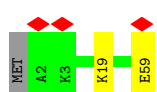
• Molecule 44: 50S ribosomal protein L28



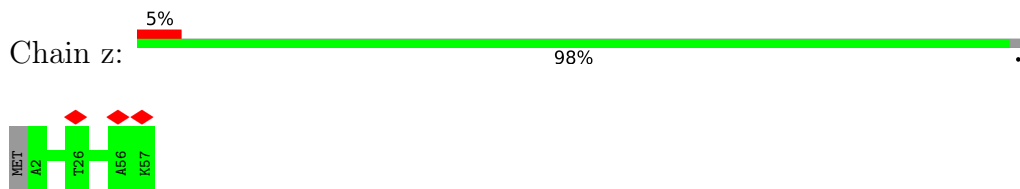
• Molecule 45: 50S ribosomal protein L29



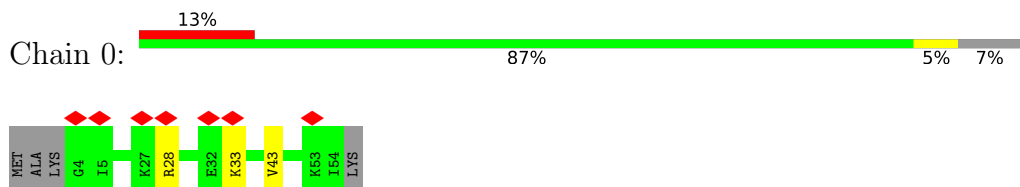
• Molecule 46: 50S ribosomal protein L30



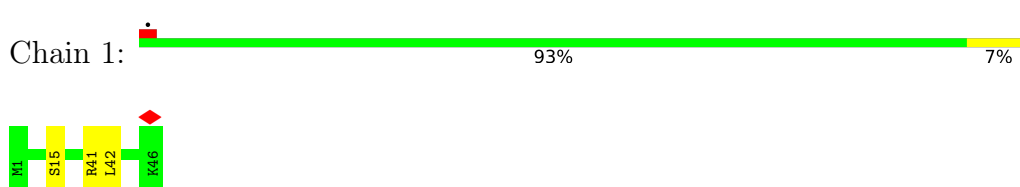
- Molecule 47: 50S ribosomal protein L32



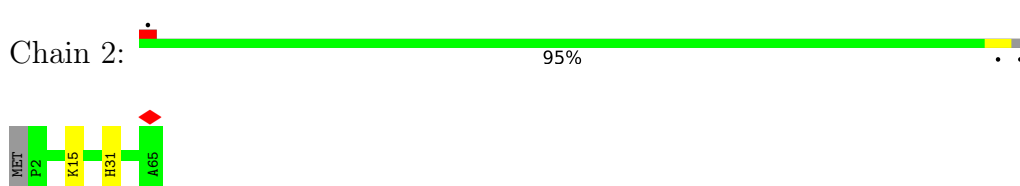
- Molecule 48: 50S ribosomal protein L33



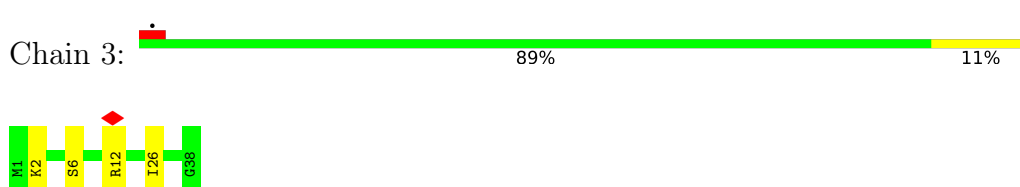
- Molecule 49: 50S ribosomal protein L34



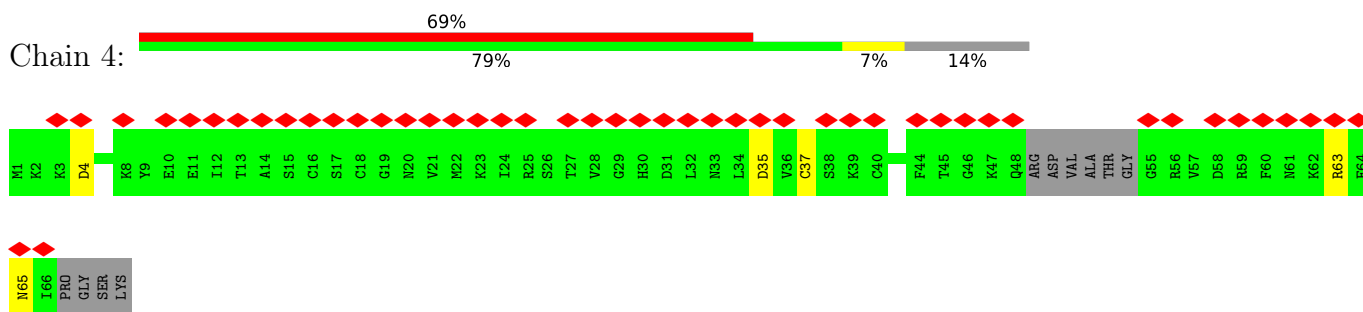
- Molecule 50: 50S ribosomal protein L35



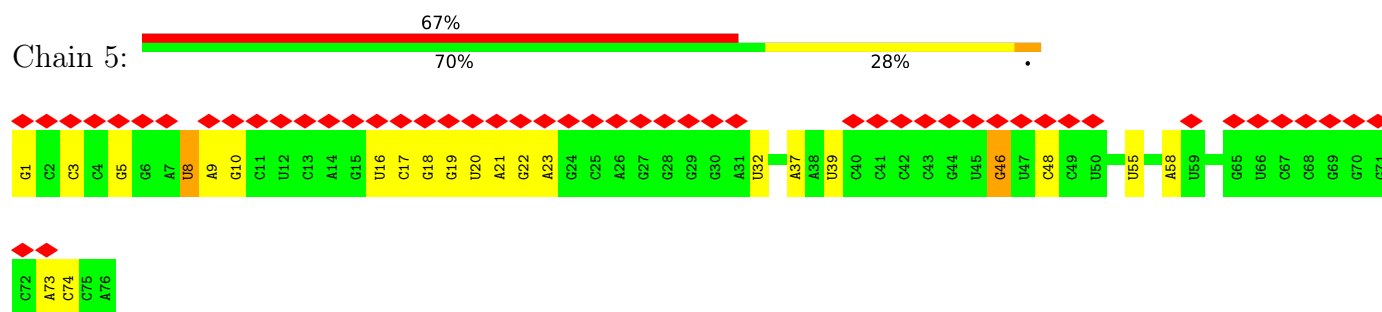
- Molecule 51: 50S ribosomal protein L36



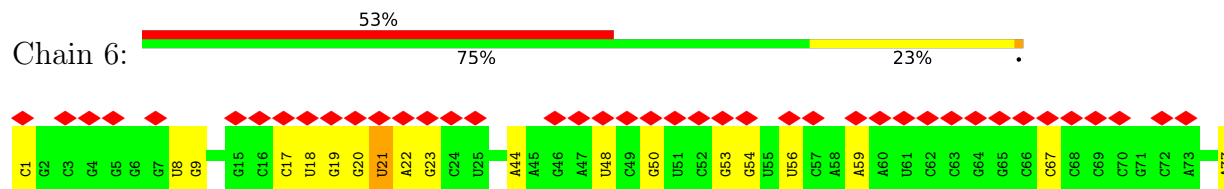
- Molecule 52: 50S ribosomal protein L31



- Molecule 53: A-site tRNA-Phe



- Molecule 54: P-site tRNA<sup>f</sup>-Met



- Molecule 55: mRNA



There are no outlier residues recorded for this chain.

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	125897	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	60000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.239	Depositor
Minimum map value	-0.129	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	403.456, 403.456, 403.456	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.788, 0.788, 0.788	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 4OC, OMC, MS6, 2MA, 3TD, 6MZ, MEQ, D2T, 5MC, MA6, MG, 1MG, OMG, H2U, 5MU, OMU, UR3, 84G, ZN, PSU, MIA, 2MG, G7M, IAS, 4D4, SPM, 4SU, SPD

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	A	0.57	0/36236	0.76	0/56520
2	B	0.28	0/1784	0.49	0/2403
3	C	0.30	0/1651	0.52	0/2225
4	D	0.28	0/1665	0.51	0/2227
5	E	0.33	0/1165	0.52	0/1568
6	F	0.30	0/858	0.52	0/1160
7	G	0.27	0/1219	0.52	0/1635
8	H	0.32	0/989	0.51	0/1326
9	I	0.30	0/1034	0.57	0/1375
10	J	0.29	0/796	0.56	0/1077
11	K	0.27	0/884	0.56	0/1191
12	L	0.28	0/960	0.59	0/1286
13	M	0.28	0/900	0.55	0/1204
14	N	0.29	0/817	0.54	0/1088
15	O	0.29	0/722	0.54	0/964
16	P	0.28	0/653	0.57	0/877
17	Q	0.31	0/650	0.53	0/871
18	R	0.32	0/553	0.55	0/742
19	S	0.29	0/685	0.51	0/922
20	T	0.28	0/676	0.49	0/895
21	U	0.30	0/597	0.56	0/792
22	a	0.76	0/65651	0.79	6/102413 (0.0%)
23	b	0.59	0/2850	0.75	0/4444
24	c	0.38	0/2121	0.58	0/2852
25	d	0.37	0/1576	0.55	0/2119
26	e	0.34	0/1571	0.52	0/2113
27	f	0.30	0/1434	0.51	0/1926
28	g	0.29	0/1343	0.52	0/1816
29	h	1.40	2/306 (0.7%)	0.82	3/413 (0.7%)
30	i	0.39	0/1152	0.53	0/1551
31	j	0.34	0/955	0.58	0/1279

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	k	0.36	0/1062	0.58	0/1413
33	l	0.36	0/1073	0.55	0/1433
34	m	0.38	0/958	0.59	0/1281
35	n	0.32	0/902	0.54	0/1209
36	o	0.36	0/929	0.55	0/1242
37	p	0.42	0/960	0.55	0/1278
38	q	0.37	0/829	0.57	0/1107
39	r	0.34	0/864	0.55	0/1156
40	s	0.33	0/744	0.53	0/994
41	t	0.33	0/787	0.53	0/1051
42	u	0.34	0/766	0.51	0/1025
43	v	0.36	0/593	0.54	0/785
44	w	0.35	0/635	0.58	0/848
45	x	0.28	0/502	0.50	0/667
46	y	0.31	0/453	0.55	0/605
47	z	0.37	0/450	0.59	0/599
48	0	0.36	0/424	0.51	0/565
49	1	0.37	0/380	0.66	0/498
50	2	0.33	0/513	0.55	0/676
51	3	0.36	0/303	0.58	0/397
52	4	0.27	0/488	0.48	0/649
53	5	0.45	1/1651 (0.1%)	0.75	0/2569
54	6	0.47	1/1725 (0.1%)	0.77	0/2687
55	7	0.51	0/233	0.78	0/361
All	All	0.61	4/152677 (0.0%)	0.72	9/228369 (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
33	l	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	h	38	PRO	N-CD	22.82	1.79	1.47
53	5	1	G	OP3-P	-10.59	1.48	1.61
54	6	1	C	OP3-P	-10.56	1.48	1.61
29	h	37	VAL	C-N	6.31	1.46	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	h	38	PRO	N-CD-CG	-9.04	89.64	103.20
22	a	512	G	O4'-C1'-N9	8.35	114.88	108.20
22	a	704	G	O4'-C1'-N9	5.96	112.97	108.20
29	h	37	VAL	C-N-CD	5.81	140.61	128.40
22	a	748	G	O4'-C1'-N9	5.54	112.63	108.20
29	h	38	PRO	N-CA-CB	-5.50	96.55	102.60
22	a	481	G	O4'-C1'-N9	5.36	112.49	108.20
22	a	2848	G	O4'-C1'-N9	5.15	112.32	108.20
22	a	1313	U	C2-N1-C1'	5.04	123.75	117.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	l	81	4D4	Mainchain

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	222/241 (92%)	211 (95%)	11 (5%)	0	100	100
3	C	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
4	D	203/206 (98%)	197 (97%)	6 (3%)	0	100	100
5	E	154/167 (92%)	151 (98%)	3 (2%)	0	100	100
6	F	101/135 (75%)	96 (95%)	5 (5%)	0	100	100
7	G	151/179 (84%)	141 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
9	I	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
10	J	96/103 (93%)	91 (95%)	5 (5%)	0	100	100
11	K	113/129 (88%)	106 (94%)	7 (6%)	0	100	100
12	L	120/124 (97%)	114 (95%)	6 (5%)	0	100	100
13	M	113/118 (96%)	105 (93%)	8 (7%)	0	100	100
14	N	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
15	O	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
16	P	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
17	Q	77/84 (92%)	73 (95%)	4 (5%)	0	100	100
18	R	64/75 (85%)	58 (91%)	6 (9%)	0	100	100
19	S	82/92 (89%)	78 (95%)	4 (5%)	0	100	100
20	T	84/87 (97%)	81 (96%)	3 (4%)	0	100	100
21	U	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
24	c	269/273 (98%)	262 (97%)	7 (3%)	0	100	100
25	d	206/209 (99%)	200 (97%)	5 (2%)	1 (0%)	29	61
26	e	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
27	f	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
28	g	174/177 (98%)	159 (91%)	15 (9%)	0	100	100
29	h	39/149 (26%)	33 (85%)	6 (15%)	0	100	100
30	i	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
31	j	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
32	k	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
33	l	132/136 (97%)	128 (97%)	4 (3%)	0	100	100
34	m	116/127 (91%)	110 (95%)	6 (5%)	0	100	100
35	n	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
36	o	112/115 (97%)	106 (95%)	6 (5%)	0	100	100
37	p	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
38	q	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
39	r	108/110 (98%)	108 (100%)	0	0	100	100
40	s	91/100 (91%)	88 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	t	100/104 (96%)	92 (92%)	8 (8%)	0	100	100
42	u	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
43	v	76/85 (89%)	73 (96%)	3 (4%)	0	100	100
44	w	75/78 (96%)	75 (100%)	0	0	100	100
45	x	60/63 (95%)	56 (93%)	4 (7%)	0	100	100
46	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
47	z	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
48	0	49/55 (89%)	46 (94%)	3 (6%)	0	100	100
49	1	44/46 (96%)	44 (100%)	0	0	100	100
50	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
51	3	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
52	4	56/70 (80%)	49 (88%)	7 (12%)	0	100	100
All	All	5481/5913 (93%)	5240 (96%)	240 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	d	149	ASN

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	186/199 (94%)	170 (91%)	16 (9%)	10	30
3	C	170/190 (90%)	156 (92%)	14 (8%)	11	32
4	D	172/173 (99%)	152 (88%)	20 (12%)	5	16
5	E	119/126 (94%)	112 (94%)	7 (6%)	19	49
6	F	90/116 (78%)	81 (90%)	9 (10%)	7	23
7	G	126/147 (86%)	112 (89%)	14 (11%)	6	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	104/105 (99%)	101 (97%)	3 (3%)	42	76
9	I	105/107 (98%)	98 (93%)	7 (7%)	16	43
10	J	86/90 (96%)	81 (94%)	5 (6%)	20	50
11	K	89/98 (91%)	85 (96%)	4 (4%)	27	61
12	L	102/103 (99%)	94 (92%)	8 (8%)	12	34
13	M	93/96 (97%)	89 (96%)	4 (4%)	29	62
14	N	83/84 (99%)	81 (98%)	2 (2%)	49	79
15	O	76/77 (99%)	70 (92%)	6 (8%)	12	34
16	P	65/65 (100%)	62 (95%)	3 (5%)	27	60
17	Q	73/78 (94%)	68 (93%)	5 (7%)	16	42
18	R	57/65 (88%)	52 (91%)	5 (9%)	10	30
19	S	72/79 (91%)	68 (94%)	4 (6%)	21	52
20	T	65/66 (98%)	61 (94%)	4 (6%)	18	47
21	U	60/61 (98%)	54 (90%)	6 (10%)	7	23
24	c	216/218 (99%)	209 (97%)	7 (3%)	39	73
25	d	163/163 (100%)	156 (96%)	7 (4%)	29	62
26	e	165/165 (100%)	160 (97%)	5 (3%)	41	75
27	f	148/150 (99%)	134 (90%)	14 (10%)	8	26
28	g	137/138 (99%)	119 (87%)	18 (13%)	4	12
29	h	32/114 (28%)	30 (94%)	2 (6%)	18	46
30	i	116/116 (100%)	113 (97%)	3 (3%)	46	77
31	j	104/104 (100%)	99 (95%)	5 (5%)	25	58
32	k	103/103 (100%)	102 (99%)	1 (1%)	76	92
33	l	107/107 (100%)	105 (98%)	2 (2%)	57	84
34	m	98/103 (95%)	92 (94%)	6 (6%)	18	48
35	n	86/87 (99%)	83 (96%)	3 (4%)	36	70
36	o	99/100 (99%)	92 (93%)	7 (7%)	14	40
37	p	89/90 (99%)	87 (98%)	2 (2%)	52	81
38	q	84/84 (100%)	80 (95%)	4 (5%)	25	58
39	r	93/93 (100%)	89 (96%)	4 (4%)	29	62
40	s	80/84 (95%)	77 (96%)	3 (4%)	33	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	t	83/85 (98%)	81 (98%)	2 (2%)	49	79
42	u	78/78 (100%)	75 (96%)	3 (4%)	33	67
43	v	58/63 (92%)	53 (91%)	5 (9%)	10	30
44	w	67/68 (98%)	64 (96%)	3 (4%)	27	61
45	x	54/55 (98%)	51 (94%)	3 (6%)	21	52
46	y	48/49 (98%)	46 (96%)	2 (4%)	30	63
47	z	47/48 (98%)	47 (100%)	0	100	100
48	0	46/49 (94%)	43 (94%)	3 (6%)	17	45
49	1	38/38 (100%)	35 (92%)	3 (8%)	12	34
50	2	51/52 (98%)	49 (96%)	2 (4%)	32	66
51	3	34/34 (100%)	30 (88%)	4 (12%)	5	16
52	4	55/62 (89%)	50 (91%)	5 (9%)	9	28
All	All	4572/4825 (95%)	4298 (94%)	274 (6%)	23	49

All (274) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	6	MET
2	B	7	ARG
2	B	8	ASP
2	B	9	MET
2	B	21	ARG
2	B	23	TRP
2	B	37	LYS
2	B	60	ILE
2	B	95	ARG
2	B	105	LYS
2	B	116	ASP
2	B	118	GLU
2	B	197	ASP
2	B	207	ILE
2	B	220	THR
2	B	225	ARG
3	C	31	ASP
3	C	45	LYS
3	C	51	SER
3	C	53	SER
3	C	54	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	C	67	THR
3	C	72	ARG
3	C	79	LYS
3	C	108	LYS
3	C	136	ARG
3	C	147	LYS
3	C	173	VAL
3	C	185	ASN
3	C	202	ILE
4	D	8	LYS
4	D	23	SER
4	D	25	VAL
4	D	29	ASP
4	D	34	ILE
4	D	35	GLU
4	D	119	SER
4	D	125	VAL
4	D	128	ARG
4	D	141	ASP
4	D	151	LYS
4	D	153	SER
4	D	155	VAL
4	D	171	LEU
4	D	179	GLU
4	D	184	ARG
4	D	188	ARG
4	D	189	SER
4	D	190	ASP
4	D	205	SER
5	E	22	SER
5	E	23	LYS
5	E	32	SER
5	E	39	VAL
5	E	97	GLN
5	E	130	SER
5	E	159	LYS
6	F	9	MET
6	F	13	ASP
6	F	14	GLN
6	F	23	GLU
6	F	24	ARG
6	F	45	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
6	F	87	SER
6	F	89	VAL
6	F	103	VAL
7	G	4	ARG
7	G	11	LYS
7	G	21	GLU
7	G	45	SER
7	G	56	LYS
7	G	57	SER
7	G	72	THR
7	G	75	VAL
7	G	78	ARG
7	G	113	ASP
7	G	129	GLU
7	G	137	LYS
7	G	140	ASP
7	G	142	HIS
8	H	42	GLU
8	H	74	SER
8	H	90	ASP
9	I	14	SER
9	I	15	SER
9	I	21	ILE
9	I	43	THR
9	I	49	ARG
9	I	89	GLU
9	I	90	TYR
10	J	28	THR
10	J	36	VAL
10	J	46	LYS
10	J	57	VAL
10	J	100	ILE
11	K	17	SER
11	K	37	ARG
11	K	98	ARG
11	K	122	ARG
12	L	30	LYS
12	L	51	LYS
12	L	56	ARG
12	L	62	GLU
12	L	86	ARG
12	L	94	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
12	L	97	THR
12	L	104	CYS
13	M	16	VAL
13	M	39	ILE
13	M	78	LYS
13	M	90	ARG
14	N	33	ASP
14	N	76	LYS
15	O	2	SER
15	O	14	GLU
15	O	47	LYS
15	O	54	ARG
15	O	72	ARG
15	O	83	GLU
16	P	8	ARG
16	P	48	GLU
16	P	66	THR
17	Q	19	LYS
17	Q	29	VAL
17	Q	40	ARG
17	Q	42	THR
17	Q	60	GLU
18	R	12	ARG
18	R	14	THR
18	R	34	THR
18	R	42	SER
18	R	45	THR
19	S	4	SER
19	S	19	VAL
19	S	35	SER
19	S	56	GLN
20	T	3	ASN
20	T	21	ASN
20	T	27	MET
20	T	54	MET
21	U	4	ILE
21	U	49	LYS
21	U	59	LYS
21	U	62	ARG
21	U	66	ARG
21	U	69	ARG
24	c	10	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
24	c	36	LYS
24	c	97	LYS
24	c	192	LEU
24	c	203	ARG
24	c	259	SER
24	c	270	ARG
25	d	1	MET
25	d	7	LYS
25	d	32	ASN
25	d	39	ASP
25	d	58	ASN
25	d	86	GLU
25	d	157	LYS
26	e	65	THR
26	e	74	LYS
26	e	179	SER
26	e	191	ASP
26	e	198	GLU
27	f	14	LYS
27	f	17	MET
27	f	35	THR
27	f	69	LYS
27	f	89	VAL
27	f	104	ILE
27	f	110	ARG
27	f	115	ARG
27	f	129	SER
27	f	135	GLN
27	f	136	ILE
27	f	152	LEU
27	f	162	SER
27	f	170	LEU
28	g	9	VAL
28	g	10	VAL
28	g	18	LYS
28	g	25	THR
28	g	36	THR
28	g	39	ASP
28	g	43	VAL
28	g	45	HIS
28	g	60	ASP
28	g	74	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
28	g	75	MET
28	g	110	SER
28	g	116	GLN
28	g	128	GLN
28	g	129	THR
28	g	134	LYS
28	g	166	ASP
28	g	176	LYS
29	h	12	LEU
29	h	17	ASP
30	i	10	THR
30	i	96	ARG
30	i	136	GLN
31	j	58	LEU
31	j	76	VAL
31	j	80	ASP
31	j	114	LYS
31	j	123	LEU
32	k	40	SER
33	l	6	ARG
33	l	25	ASP
34	m	6	SER
34	m	14	SER
34	m	15	SER
34	m	30	ARG
34	m	72	ASP
34	m	98	LEU
35	n	13	ARG
35	n	25	ARG
35	n	54	VAL
36	o	7	GLN
36	o	19	SER
36	o	32	VAL
36	o	37	LYS
36	o	39	ARG
36	o	53	ARG
36	o	103	ARG
37	p	51	ARG
37	p	87	SER
38	q	6	GLN
38	q	13	ARG
38	q	51	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
38	q	62	GLU
39	r	7	HIS
39	r	22	ASP
39	r	73	LYS
39	r	83	LYS
40	s	26	LYS
40	s	49	LYS
40	s	64	LYS
41	t	68	SER
41	t	79	LYS
42	u	12	GLN
42	u	71	LYS
42	u	90	ASP
43	v	10	THR
43	v	16	SER
43	v	30	SER
43	v	43	THR
43	v	81	SER
44	w	2	SER
44	w	51	VAL
44	w	56	MET
45	x	6	LEU
45	x	30	MET
45	x	58	ASN
46	y	19	LYS
46	y	59	GLU
48	0	28	ARG
48	0	33	LYS
48	0	43	VAL
49	1	15	SER
49	1	41	ARG
49	1	42	LEU
50	2	15	LYS
50	2	31	HIS
51	3	2	LYS
51	3	6	SER
51	3	12	ARG
51	3	26	ILE
52	4	4	ASP
52	4	35	ASP
52	4	37	CYS
52	4	63	ARG

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Mol	Chain	Res	Type
52	4	65	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
6	F	11	HIS
9	I	25	ASN
12	L	112	GLN
18	R	74	HIS
24	c	260	ASN
31	j	29	HIS
32	k	4	ASN
52	4	33	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1513/1542 (98%)	190 (12%)	9 (0%)
22	a	2745/2904 (94%)	346 (12%)	0
23	b	118/120 (98%)	12 (10%)	0
53	5	74/76 (97%)	18 (24%)	2 (2%)
54	6	76/77 (98%)	16 (21%)	1 (1%)
55	7	9/10 (90%)	0	0
All	All	4535/4729 (95%)	582 (12%)	12 (0%)

All (582) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	5	U
1	A	6	G
1	A	9	G
1	A	22	G
1	A	32	A
1	A	39	G
1	A	44	A
1	A	47	C
1	A	48	C
1	A	51	A
1	A	74	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	82	G
1	A	83	C
1	A	84	U
1	A	86	G
1	A	87	C
1	A	88	U
1	A	116	A
1	A	121	U
1	A	122	G
1	A	131	A
1	A	141	G
1	A	143	A
1	A	144	G
1	A	164	G
1	A	173	U
1	A	182	A
1	A	197	A
1	A	204	G
1	A	226	G
1	A	240	G
1	A	245	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	281	G
1	A	289	G
1	A	321	A
1	A	328	C
1	A	330	C
1	A	347	G
1	A	351	G
1	A	352	C
1	A	354	G
1	A	367	U
1	A	372	C
1	A	373	A
1	A	398	U
1	A	406	G
1	A	411	A
1	A	412	A
1	A	413	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	414	A
1	A	417	G
1	A	421	U
1	A	422	C
1	A	423	G
1	A	424	G
1	A	429	U
1	A	430	A
1	A	453	G
1	A	458	U
1	A	459	A
1	A	465	A
1	A	467	U
1	A	468	A
1	A	469	C
1	A	479	U
1	A	481	G
1	A	482	A
1	A	484	G
1	A	486	U
1	A	497	G
1	A	509	A
1	A	511	C
1	A	512	U
1	A	518	C
1	A	521	G
1	A	531	U
1	A	532	A
1	A	547	A
1	A	559	A
1	A	564	C
1	A	573	A
1	A	576	C
1	A	577	G
1	A	588	G
1	A	596	A
1	A	632	U
1	A	633	G
1	A	641	U
1	A	653	U
1	A	665	A
1	A	703	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	721	G
1	A	723	U
1	A	747	A
1	A	748	G
1	A	755	G
1	A	777	A
1	A	792	A
1	A	793	U
1	A	794	A
1	A	802	A
1	A	815	A
1	A	817	C
1	A	851	G
1	A	884	U
1	A	890	G
1	A	902	G
1	A	914	A
1	A	934	C
1	A	935	A
1	A	960	U
1	A	966	2MG
1	A	969	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	989	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1003	G
1	A	1004	A
1	A	1009	U
1	A	1017	U
1	A	1027	C
1	A	1030	U
1	A	1031	C
1	A	1033	G
1	A	1034	G
1	A	1036	A
1	A	1044	A
1	A	1053	G
1	A	1065	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1085	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1130	A
1	A	1137	C
1	A	1139	G
1	A	1157	A
1	A	1159	U
1	A	1171	A
1	A	1196	A
1	A	1197	A
1	A	1202	U
1	A	1213	A
1	A	1214	C
1	A	1227	A
1	A	1228	C
1	A	1238	A
1	A	1258	G
1	A	1280	A
1	A	1285	A
1	A	1286	U
1	A	1287	A
1	A	1300	G
1	A	1302	C
1	A	1305	G
1	A	1317	C
1	A	1320	C
1	A	1331	G
1	A	1338	G
1	A	1346	A
1	A	1353	G
1	A	1363	A
1	A	1370	G
1	A	1378	C
1	A	1379	G
1	A	1398	A
1	A	1419	G
1	A	1432	G
1	A	1441	A
1	A	1446	A
1	A	1451	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1452	C
1	A	1453	G
1	A	1487	G
1	A	1492	A
1	A	1497	G
1	A	1506	U
1	A	1517	G
1	A	1529	G
1	A	1530	G
1	A	1534	A
22	a	10	A
22	a	15	G
22	a	27	G
22	a	34	U
22	a	42	A
22	a	58	G
22	a	61	C
22	a	71	A
22	a	72	U
22	a	74	A
22	a	75	G
22	a	101	A
22	a	102	U
22	a	118	A
22	a	119	A
22	a	120	U
22	a	125	A
22	a	139	U
22	a	142	A
22	a	163	C
22	a	181	A
22	a	196	A
22	a	199	A
22	a	215	G
22	a	216	A
22	a	221	A
22	a	222	A
22	a	224	U
22	a	233	A
22	a	248	G
22	a	265	A
22	a	267	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
22	a	272	A
22	a	277	G
22	a	278	A
22	a	279	A
22	a	285	G
22	a	287	G
22	a	294	A
22	a	311	A
22	a	329	G
22	a	330	A
22	a	356	G
22	a	362	A
22	a	385	C
22	a	386	G
22	a	396	G
22	a	405	U
22	a	411	G
22	a	412	A
22	a	429	A
22	a	436	C
22	a	481	G
22	a	491	G
22	a	501	A
22	a	504	A
22	a	505	A
22	a	508	A
22	a	509	C
22	a	530	G
22	a	531	C
22	a	532	A
22	a	544	C
22	a	546	U
22	a	547	A
22	a	548	G
22	a	563	A
22	a	568	U
22	a	573	U
22	a	575	A
22	a	577	G
22	a	603	A
22	a	614	A
22	a	615	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
22	a	627	A
22	a	637	A
22	a	645	C
22	a	646	U
22	a	647	G
22	a	653	U
22	a	654	A
22	a	655	A
22	a	685	A
22	a	686	U
22	a	704	G
22	a	717	C
22	a	730	A
22	a	747	5MU
22	a	764	A
22	a	775	G
22	a	776	G
22	a	782	A
22	a	784	G
22	a	785	G
22	a	787	C
22	a	789	A
22	a	805	G
22	a	812	C
22	a	827	U
22	a	828	U
22	a	846	U
22	a	847	U
22	a	859	G
22	a	881	G
22	a	883	G
22	a	884	U
22	a	885	C
22	a	890	C
22	a	891	G
22	a	895	U
22	a	896	A
22	a	910	A
22	a	914	G
22	a	915	C
22	a	927	A
22	a	931	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
22	a	934	U
22	a	945	A
22	a	946	C
22	a	961	C
22	a	974	G
22	a	983	A
22	a	984	A
22	a	990	A
22	a	996	A
22	a	1012	U
22	a	1013	C
22	a	1033	U
22	a	1040	A
22	a	1045	C
22	a	1046	A
22	a	1047	G
22	a	1048	A
22	a	1108	U
22	a	1110	G
22	a	1111	A
22	a	1112	G
22	a	1116	G
22	a	1132	U
22	a	1133	A
22	a	1135	C
22	a	1136	G
22	a	1141	U
22	a	1142	A
22	a	1168	G
22	a	1172	C
22	a	1206	G
22	a	1236	G
22	a	1241	A
22	a	1250	G
22	a	1253	A
22	a	1256	G
22	a	1271	G
22	a	1272	A
22	a	1273	U
22	a	1275	A
22	a	1287	A
22	a	1289	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
22	a	1300	G
22	a	1301	A
22	a	1352	U
22	a	1365	A
22	a	1379	U
22	a	1383	A
22	a	1395	A
22	a	1413	A
22	a	1416	G
22	a	1417	C
22	a	1420	A
22	a	1428	C
22	a	1452	G
22	a	1482	G
22	a	1483	G
22	a	1493	C
22	a	1494	A
22	a	1495	A
22	a	1497	U
22	a	1508	A
22	a	1509	A
22	a	1510	G
22	a	1515	A
22	a	1524	G
22	a	1535	A
22	a	1536	C
22	a	1537	G
22	a	1542	U
22	a	1554	U
22	a	1566	A
22	a	1569	A
22	a	1578	U
22	a	1583	A
22	a	1585	C
22	a	1586	A
22	a	1607	C
22	a	1608	A
22	a	1634	A
22	a	1647	U
22	a	1648	U
22	a	1649	G
22	a	1653	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
22	a	1674	G
22	a	1675	C
22	a	1715	G
22	a	1729	U
22	a	1730	C
22	a	1738	G
22	a	1739	A
22	a	1758	U
22	a	1759	A
22	a	1764	C
22	a	1773	A
22	a	1776	G
22	a	1782	U
22	a	1784	A
22	a	1786	A
22	a	1800	C
22	a	1801	A
22	a	1807	G
22	a	1808	A
22	a	1816	C
22	a	1829	A
22	a	1847	A
22	a	1858	A
22	a	1871	A
22	a	1872	A
22	a	1873	G
22	a	1882	U
22	a	1884	G
22	a	1906	G
22	a	1929	G
22	a	1930	G
22	a	1937	A
22	a	1938	A
22	a	1941	C
22	a	1955	U
22	a	1962	5MC
22	a	1964	G
22	a	1965	C
22	a	1967	C
22	a	1970	A
22	a	1971	U
22	a	1972	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
22	a	1991	U
22	a	1993	U
22	a	2021	C
22	a	2023	C
22	a	2033	A
22	a	2035	G
22	a	2036	C
22	a	2043	C
22	a	2055	C
22	a	2056	G
22	a	2060	A
22	a	2061	G
22	a	2062	A
22	a	2069	G7M
22	a	2093	G
22	a	2198	A
22	a	2204	G
22	a	2211	A
22	a	2225	A
22	a	2238	G
22	a	2239	G
22	a	2267	A
22	a	2268	A
22	a	2269	G
22	a	2273	A
22	a	2279	G
22	a	2283	C
22	a	2287	A
22	a	2305	U
22	a	2307	G
22	a	2308	G
22	a	2322	A
22	a	2325	G
22	a	2333	A
22	a	2335	A
22	a	2347	C
22	a	2350	C
22	a	2361	G
22	a	2377	A
22	a	2383	G
22	a	2385	C
22	a	2402	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
22	a	2406	A
22	a	2424	C
22	a	2425	A
22	a	2428	G
22	a	2429	G
22	a	2430	A
22	a	2435	A
22	a	2441	U
22	a	2445	2MG
22	a	2448	A
22	a	2449	H2U
22	a	2474	U
22	a	2476	A
22	a	2491	U
22	a	2498	OMC
22	a	2502	G
22	a	2505	G
22	a	2517	C
22	a	2518	A
22	a	2520	C
22	a	2529	G
22	a	2547	A
22	a	2566	A
22	a	2567	G
22	a	2573	C
22	a	2582	G
22	a	2586	U
22	a	2602	A
22	a	2609	U
22	a	2613	U
22	a	2615	U
22	a	2629	U
22	a	2630	G
22	a	2645	G
22	a	2663	G
22	a	2682	A
22	a	2689	U
22	a	2690	U
22	a	2714	G
22	a	2716	C
22	a	2726	A
22	a	2733	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
22	a	2744	G
22	a	2748	A
22	a	2752	C
22	a	2757	A
22	a	2765	A
22	a	2778	A
22	a	2793	C
22	a	2794	C
22	a	2797	U
22	a	2798	U
22	a	2799	A
22	a	2818	U
22	a	2820	A
22	a	2821	A
22	a	2850	A
22	a	2873	A
22	a	2880	C
22	a	2884	U
22	a	2899	A
22	a	2903	U
23	b	13	G
23	b	16	G
23	b	24	G
23	b	35	C
23	b	42	C
23	b	45	A
23	b	56	G
23	b	67	G
23	b	89	U
23	b	90	C
23	b	99	A
23	b	109	A
53	5	3	C
53	5	5	G
53	5	8	4SU
53	5	9	A
53	5	10	G
53	5	16	U
53	5	17	C
53	5	18	G
53	5	19	G
53	5	20	U

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Mol	Chain	Res	Type
53	5	21	A
53	5	22	G
53	5	23	A
53	5	46	G7M
53	5	48	C
53	5	58	A
53	5	73	A
53	5	74	C
54	6	9	G
54	6	17	C
54	6	18	U
54	6	19	G
54	6	20	G
54	6	21	H2U
54	6	22	A
54	6	23	G
54	6	44	A
54	6	48	U
54	6	50	G
54	6	53	G
54	6	54	G
54	6	59	A
54	6	67	C
54	6	77	A

All (12) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	120	A
1	A	429	U
1	A	467	U
1	A	1026	G
1	A	1035	A
1	A	1240	U
1	A	1337	G
1	A	1397	C
1	A	1440	U
53	5	8	4SU
53	5	21	A
54	6	21	H2U

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

51 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	A	1519	1	19,26,27	1.09	1 (5%)	18,38,41	5.40	3 (16%)
54	H2U	6	21	54	18,21,22	0.58	0	21,30,33	1.28	2 (9%)
53	PSU	5	32	53	18,21,22	1.05	1 (5%)	22,30,33	1.87	6 (27%)
22	PSU	a	2504	22	18,21,22	1.10	1 (5%)	22,30,33	1.69	3 (13%)
22	PSU	a	2604	22	18,21,22	1.04	1 (5%)	22,30,33	1.97	5 (22%)
22	1MG	a	745	22	18,26,27	2.53	5 (27%)	19,39,42	1.39	3 (15%)
22	PSU	a	1911	22	18,21,22	1.08	1 (5%)	22,30,33	1.81	4 (18%)
11	IAS	K	119	11,21	6,7,8	1.39	1 (16%)	6,8,10	1.38	0
22	PSU	a	746	22,56	18,21,22	1.05	2 (11%)	22,30,33	1.73	4 (18%)
1	2MG	A	1516	1	18,26,27	1.25	3 (16%)	16,38,41	0.89	1 (6%)
1	2MG	A	1207	1	18,26,27	1.18	3 (16%)	16,38,41	0.93	1 (6%)
54	5MU	6	55	54	19,22,23	0.46	0	28,32,35	0.57	0
22	PSU	a	2605	22	18,21,22	1.07	2 (11%)	22,30,33	1.82	3 (13%)
1	5MC	A	967	1	18,22,23	0.63	0	26,32,35	0.62	0
53	G7M	5	46	53	20,26,27	2.76	7 (35%)	17,39,42	1.06	1 (5%)
22	PSU	a	1917	22	18,21,22	1.00	1 (5%)	22,30,33	1.83	5 (22%)
1	2MG	A	966	1	18,26,27	1.20	2 (11%)	16,38,41	0.97	1 (6%)
54	OMC	6	33	54	19,22,23	0.64	0	26,31,34	0.61	0
1	G7M	A	527	1	20,26,27	2.67	7 (35%)	17,39,42	1.10	1 (5%)
22	5MU	a	747	22	19,22,23	0.61	0	28,32,35	0.63	0
22	G7M	a	2069	22	20,26,27	2.57	7 (35%)	17,39,42	1.12	2 (11%)
22	OMU	a	2552	22	19,22,23	2.71	6 (31%)	26,31,34	1.76	4 (15%)
54	4SU	6	8	54	18,21,22	3.59	7 (38%)	26,30,33	2.25	5 (19%)
1	5MC	A	1407	1	18,22,23	0.74	0	26,32,35	0.60	0
22	5MC	a	1962	22	18,22,23	0.69	0	26,32,35	0.63	0
53	PSU	5	39	53	18,21,22	1.01	1 (5%)	22,30,33	1.82	4 (18%)
12	D2T	L	89	12	7,9,10	1.39	1 (14%)	6,11,13	2.38	3 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
25	MEQ	d	150	25	8,9,10	0.93	0	5,10,12	0.61	0
1	MA6	A	1518	1	19,26,27	1.15	1 (5%)	18,38,41	5.10	3 (16%)
1	UR3	A	1498	1	19,22,23	2.64	7 (36%)	26,32,35	1.33	2 (7%)
1	PSU	A	516	56,1	18,21,22	1.00	1 (5%)	22,30,33	1.86	4 (18%)
22	2MA	a	2503	22,56	17,25,26	2.25	4 (23%)	17,37,40	1.36	3 (17%)
53	MIA	5	37	53	24,31,32	3.06	3 (12%)	26,44,47	4.24	8 (30%)
22	OMG	a	2251	22,56,54	18,26,27	1.30	3 (16%)	19,38,41	0.82	1 (5%)
53	5MU	5	54	53	19,22,23	0.49	0	28,32,35	0.57	0
33	4D4	l	81	33	9,11,12	1.95	3 (33%)	8,13,15	1.81	3 (37%)
54	PSU	6	56	54	18,21,22	1.07	1 (5%)	22,30,33	1.71	4 (18%)
1	4OC	A	1402	1	20,23,24	2.98	8 (40%)	26,32,35	0.90	1 (3%)
22	PSU	a	955	22	18,21,22	1.02	1 (5%)	22,30,33	2.02	5 (22%)
22	6MZ	a	1618	22	18,25,26	1.95	2 (11%)	16,36,39	2.03	3 (18%)
22	3TD	a	1915	22	19,22,23	3.96	7 (36%)	21,32,35	1.79	3 (14%)
22	H2U	a	2449	22	18,21,22	0.55	0	21,30,33	1.01	2 (9%)
53	4SU	5	8	53	18,21,22	3.59	7 (38%)	26,30,33	2.22	5 (19%)
22	2MG	a	2445	22	18,26,27	1.30	3 (16%)	16,38,41	0.87	1 (6%)
22	PSU	a	2580	22	18,21,22	1.10	2 (11%)	22,30,33	2.08	6 (27%)
22	PSU	a	2457	22	18,21,22	1.05	1 (5%)	22,30,33	1.85	4 (18%)
22	OMC	a	2498	22,56	19,22,23	0.68	0	26,31,34	0.74	0
22	2MG	a	1835	22	18,26,27	1.24	3 (16%)	16,38,41	0.88	1 (6%)
53	PSU	5	55	53	18,21,22	1.08	1 (5%)	22,30,33	1.87	5 (22%)
22	5MU	a	1939	22	19,22,23	0.66	0	28,32,35	0.50	0
22	6MZ	a	2030	22	18,25,26	1.96	2 (11%)	16,36,39	2.21	3 (18%)

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	A	1519	1	-	0/7/29/30	0/3/3/3
54	H2U	6	21	54	-	3/7/38/39	0/2/2/2
53	PSU	5	32	53	-	0/7/25/26	0/2/2/2
22	PSU	a	2504	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2604	22	-	0/7/25/26	0/2/2/2
22	1MG	a	745	22	-	0/3/25/26	0/3/3/3
22	PSU	a	1911	22	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	IAS	K	119	11,21	-	1/7/7/8	-
22	PSU	a	746	22,56	-	1/7/25/26	0/2/2/2
1	2MG	A	1516	1	-	0/5/27/28	0/3/3/3
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
54	5MU	6	55	54	-	2/7/25/26	0/2/2/2
22	PSU	a	2605	22	-	0/7/25/26	0/2/2/2
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
53	G7M	5	46	53	-	2/3/25/26	0/3/3/3
22	PSU	a	1917	22	-	0/7/25/26	0/2/2/2
1	2MG	A	966	1	-	2/5/27/28	0/3/3/3
54	OMC	6	33	54	-	0/9/27/28	0/2/2/2
1	G7M	A	527	1	-	2/3/25/26	0/3/3/3
22	5MU	a	747	22	-	1/7/25/26	0/2/2/2
22	G7M	a	2069	22	-	1/3/25/26	0/3/3/3
22	OMU	a	2552	22	-	0/9/27/28	0/2/2/2
54	4SU	6	8	54	-	0/7/25/26	0/2/2/2
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
22	5MC	a	1962	22	-	0/7/25/26	0/2/2/2
53	PSU	5	39	53	-	0/7/25/26	0/2/2/2
12	D2T	L	89	12	-	1/7/12/14	-
25	MEQ	d	150	25	-	4/8/9/11	-
1	MA6	A	1518	1	-	0/7/29/30	0/3/3/3
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
1	PSU	A	516	56,1	-	0/7/25/26	0/2/2/2
22	2MA	a	2503	22,56	-	2/3/25/26	0/3/3/3
53	MIA	5	37	53	-	3/11/33/34	0/3/3/3
22	OMG	a	2251	22,56,54	-	2/5/27/28	0/3/3/3
53	5MU	5	54	53	-	0/7/25/26	0/2/2/2
33	4D4	l	81	33	-	1/11/12/14	-
54	PSU	6	56	54	-	2/7/25/26	0/2/2/2
1	4OC	A	1402	1	-	2/9/29/30	0/2/2/2
22	PSU	a	955	22	-	0/7/25/26	0/2/2/2
22	6MZ	a	1618	22	-	0/5/27/28	0/3/3/3
22	3TD	a	1915	22	-	0/7/25/26	0/2/2/2
22	H2U	a	2449	22	-	1/7/38/39	0/2/2/2
53	4SU	5	8	53	-	0/7/25/26	0/2/2/2
22	2MG	a	2445	22	-	2/5/27/28	0/3/3/3
22	PSU	a	2580	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2457	22	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	OMC	a	2498	22,56	-	2/9/27/28	0/2/2/2
22	2MG	a	1835	22	-	0/5/27/28	0/3/3/3
53	PSU	5	55	53	-	1/7/25/26	0/2/2/2
22	5MU	a	1939	22	-	0/7/25/26	0/2/2/2
22	6MZ	a	2030	22	-	2/5/27/28	0/3/3/3

All (120) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	1915	3TD	C6-C5	12.11	1.49	1.35
53	5	37	MIA	C2-S10	10.64	1.84	1.75
53	5	37	MIA	C6-N6	9.36	1.51	1.34
22	a	1915	3TD	C2-N1	8.72	1.48	1.37
22	a	2030	6MZ	C6-N6	7.12	1.46	1.35
22	a	1618	6MZ	C6-N6	7.11	1.46	1.35
54	6	8	4SU	C2-N3	6.99	1.50	1.38
53	5	8	4SU	C2-N3	6.94	1.50	1.38
1	A	1498	UR3	C2-N1	6.82	1.48	1.38
54	6	8	4SU	C2-N1	6.78	1.49	1.38
53	5	8	4SU	C2-N1	6.72	1.49	1.38
22	a	2503	2MA	C2-N3	6.71	1.45	1.31
54	6	8	4SU	C4-N3	6.71	1.44	1.37
53	5	8	4SU	C4-N3	6.67	1.44	1.37
53	5	46	G7M	C2-N2	6.58	1.49	1.34
1	A	1402	4OC	C4-N3	6.54	1.44	1.32
22	a	2552	OMU	C2-N1	6.43	1.48	1.38
1	A	527	G7M	C2-N2	6.28	1.49	1.34
22	a	2069	G7M	C2-N2	6.25	1.49	1.34
1	A	1402	4OC	C6-C5	6.06	1.49	1.35
22	a	2552	OMU	C2-N3	5.94	1.48	1.38
22	a	745	1MG	C2-N2	5.94	1.44	1.34
22	a	745	1MG	C2-N3	5.92	1.45	1.34
1	A	1498	UR3	C6-C5	5.91	1.48	1.35
22	a	1915	3TD	C6-N1	5.87	1.46	1.36
53	5	46	G7M	C2-N3	5.70	1.47	1.33
1	A	1402	4OC	C2-N3	5.68	1.47	1.36
53	5	8	4SU	C5-C4	5.62	1.49	1.42
54	6	8	4SU	C5-C4	5.58	1.49	1.42
53	5	8	4SU	C6-C5	5.51	1.47	1.35
54	6	8	4SU	C6-C5	5.45	1.47	1.35
22	a	2552	OMU	C6-C5	5.43	1.47	1.35
1	A	527	G7M	C2-N3	5.39	1.46	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	2069	G7M	C2-N3	5.16	1.45	1.33
53	5	46	G7M	C4-N3	5.04	1.49	1.37
1	A	527	G7M	C4-N3	4.91	1.49	1.37
22	a	2069	G7M	C4-N3	4.61	1.48	1.37
22	a	745	1MG	C4-N3	4.58	1.48	1.37
33	l	81	4D4	CZ-NE	4.53	1.42	1.33
22	a	2503	2MA	C4-N3	4.45	1.48	1.37
1	A	1498	UR3	C2-N3	4.45	1.47	1.39
54	6	8	4SU	C4-S4	-4.38	1.60	1.68
53	5	8	4SU	C4-S4	-4.31	1.60	1.68
1	A	1402	4OC	C4-N4	4.30	1.44	1.35
53	5	46	G7M	C6-N1	4.23	1.44	1.37
22	a	1915	3TD	C2-N3	4.18	1.47	1.38
1	A	527	G7M	C6-N1	4.11	1.44	1.37
1	A	1402	4OC	C2-N1	3.75	1.48	1.40
1	A	1402	4OC	C5-C4	3.71	1.48	1.40
22	a	2069	G7M	C6-N1	3.65	1.43	1.37
54	6	56	PSU	C6-C5	3.40	1.39	1.35
22	a	2504	PSU	C6-C5	3.38	1.39	1.35
53	5	55	PSU	C6-C5	3.34	1.39	1.35
53	5	46	G7M	C5-C6	3.30	1.53	1.45
22	a	2445	2MG	C8-N7	-3.26	1.29	1.35
22	a	1835	2MG	C8-N7	-3.22	1.29	1.35
22	a	1911	PSU	C6-C5	3.17	1.39	1.35
22	a	2251	OMG	C8-N7	-3.16	1.29	1.35
1	A	1518	MA6	C5-C4	-3.09	1.32	1.40
1	A	966	2MG	C8-N7	-3.09	1.29	1.35
1	A	527	G7M	C5-C6	3.08	1.53	1.45
1	A	1402	4OC	O2-C2	-3.07	1.18	1.23
1	A	1516	2MG	C8-N7	-3.06	1.29	1.35
1	A	1519	MA6	C5-C4	-3.05	1.32	1.40
53	5	32	PSU	C6-C5	3.04	1.38	1.35
22	a	2552	OMU	O4-C4	-3.03	1.18	1.24
22	a	745	1MG	C5-C4	-3.03	1.35	1.43
1	A	1207	2MG	C8-N7	-3.01	1.29	1.35
53	5	46	G7M	C2-N1	2.97	1.45	1.37
53	5	37	MIA	C5-C4	-2.97	1.33	1.40
22	a	2552	OMU	O2-C2	-2.96	1.17	1.23
53	5	39	PSU	C6-C5	2.96	1.38	1.35
22	a	2605	PSU	C6-C5	2.95	1.38	1.35
22	a	2503	2MA	C2-N1	2.94	1.45	1.36
22	a	2069	G7M	C5-C6	2.94	1.53	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1402	4OC	C6-N1	2.91	1.45	1.38
22	a	2604	PSU	C6-C5	2.91	1.38	1.35
22	a	2552	OMU	C4-N3	2.88	1.43	1.38
1	A	527	G7M	C2-N1	2.88	1.44	1.37
22	a	2030	6MZ	C5-C4	-2.84	1.33	1.40
1	A	1498	UR3	C6-N1	2.84	1.44	1.38
22	a	2457	PSU	C6-C5	2.83	1.38	1.35
22	a	2251	OMG	C5-C6	-2.82	1.41	1.47
22	a	1917	PSU	C6-C5	2.81	1.38	1.35
22	a	1618	6MZ	C5-C4	-2.81	1.33	1.40
1	A	516	PSU	C6-C5	2.77	1.38	1.35
22	a	955	PSU	C6-C5	2.76	1.38	1.35
53	5	8	4SU	C6-N1	2.75	1.44	1.38
22	a	746	PSU	C6-C5	2.75	1.38	1.35
54	6	8	4SU	C6-N1	2.73	1.44	1.38
22	a	2580	PSU	C6-C5	2.67	1.38	1.35
22	a	2445	2MG	C5-C6	-2.65	1.42	1.47
1	A	1516	2MG	C5-C6	-2.64	1.42	1.47
11	K	119	IAS	O-C	2.60	1.30	1.22
22	a	2069	G7M	O6-C6	-2.59	1.18	1.23
1	A	966	2MG	C5-C6	-2.56	1.42	1.47
22	a	1835	2MG	C5-C6	-2.56	1.42	1.47
22	a	2503	2MA	C5-C4	-2.55	1.36	1.43
22	a	2069	G7M	C2-N1	2.54	1.44	1.37
22	a	1915	3TD	C4-N3	2.54	1.45	1.40
33	l	81	4D4	O-C	2.49	1.29	1.19
1	A	1498	UR3	O2-C2	-2.47	1.18	1.22
1	A	1498	UR3	O4-C4	-2.46	1.18	1.23
1	A	527	G7M	O6-C6	-2.36	1.18	1.23
1	A	1207	2MG	C5-C6	-2.34	1.42	1.47
22	a	1915	3TD	O4-C4	-2.33	1.18	1.23
22	a	2445	2MG	C5-C4	-2.30	1.37	1.43
33	l	81	4D4	CZ-NH1	2.26	1.44	1.34
1	A	1516	2MG	C5-C4	-2.25	1.37	1.43
53	5	46	G7M	O6-C6	-2.23	1.18	1.23
22	a	2580	PSU	O4'-C1'	-2.20	1.40	1.43
22	a	745	1MG	O6-C6	-2.17	1.18	1.22
22	a	1835	2MG	C5-C4	-2.17	1.37	1.43
22	a	1915	3TD	O2-C2	-2.15	1.19	1.23
22	a	2251	OMG	C5-C4	-2.13	1.37	1.43
1	A	1498	UR3	C5-C4	2.08	1.49	1.43
1	A	1207	2MG	C5-C4	-2.04	1.37	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	L	89	D2T	CB1-SB	-2.02	1.75	1.79
22	a	2605	PSU	C4-C5	-2.01	1.38	1.44
22	a	746	PSU	C4-C5	-2.00	1.38	1.44

All (128) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1519	MA6	N1-C6-N6	-19.64	96.39	117.06
1	A	1518	MA6	N1-C6-N6	-18.46	97.63	117.06
53	5	37	MIA	C1'-N9-C4	15.29	153.51	126.64
53	5	37	MIA	C11-S10-C2	10.18	109.87	102.27
1	A	1519	MA6	C1'-N9-C4	-10.10	108.89	126.64
1	A	1518	MA6	C1'-N9-C4	-9.60	109.77	126.64
54	6	8	4SU	C4-N3-C2	-7.84	119.73	127.34
53	5	8	4SU	C4-N3-C2	-7.72	119.84	127.34
53	5	37	MIA	S10-C2-N3	7.24	141.23	116.10
1	A	1519	MA6	N3-C2-N1	-5.68	119.81	128.68
54	6	8	4SU	C5-C4-N3	5.60	119.88	114.69
22	a	2030	6MZ	N3-C2-N1	-5.58	119.96	128.68
22	a	2552	OMU	C4-N3-C2	-5.52	119.29	126.58
53	5	8	4SU	C5-C4-N3	5.46	119.75	114.69
1	A	1518	MA6	N3-C2-N1	-5.45	120.16	128.68
22	a	1618	6MZ	N3-C2-N1	-5.43	120.19	128.68
22	a	1915	3TD	N1-C2-N3	5.37	120.38	116.14
22	a	2580	PSU	N1-C2-N3	5.37	121.21	115.13
22	a	955	PSU	N1-C2-N3	5.19	121.01	115.13
22	a	955	PSU	C4-N3-C2	-5.07	119.04	126.34
22	a	2604	PSU	N1-C2-N3	5.05	120.85	115.13
53	5	37	MIA	S10-C2-N1	-5.04	98.57	116.01
22	a	2580	PSU	C4-N3-C2	-4.97	119.19	126.34
1	A	1498	UR3	C4-N3-C2	-4.88	119.96	124.56
22	a	2604	PSU	C4-N3-C2	-4.85	119.35	126.34
1	A	516	PSU	C4-N3-C2	-4.82	119.39	126.34
22	a	2457	PSU	N1-C2-N3	4.82	120.59	115.13
53	5	55	PSU	N1-C2-N3	4.77	120.54	115.13
53	5	55	PSU	C4-N3-C2	-4.77	119.47	126.34
53	5	32	PSU	C4-N3-C2	-4.76	119.48	126.34
53	5	39	PSU	C4-N3-C2	-4.75	119.50	126.34
53	5	32	PSU	N1-C2-N3	4.73	120.49	115.13
22	a	2457	PSU	C4-N3-C2	-4.71	119.55	126.34
22	a	2605	PSU	C4-N3-C2	-4.71	119.55	126.34
22	a	1911	PSU	C4-N3-C2	-4.69	119.58	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	2605	PSU	N1-C2-N3	4.68	120.43	115.13
22	a	1917	PSU	C4-N3-C2	-4.65	119.64	126.34
22	a	1917	PSU	N1-C2-N3	4.64	120.38	115.13
22	a	746	PSU	C4-N3-C2	-4.60	119.70	126.34
22	a	1911	PSU	N1-C2-N3	4.59	120.33	115.13
53	5	39	PSU	N1-C2-N3	4.53	120.27	115.13
54	6	56	PSU	C4-N3-C2	-4.52	119.83	126.34
1	A	516	PSU	N1-C2-N3	4.51	120.24	115.13
22	a	746	PSU	N1-C2-N3	4.45	120.17	115.13
22	a	2504	PSU	N1-C2-N3	4.41	120.13	115.13
22	a	2030	6MZ	C9-N6-C6	-4.31	119.16	122.87
22	a	1915	3TD	C4-N3-C2	-4.30	119.95	124.61
54	6	56	PSU	N1-C2-N3	4.30	120.00	115.13
22	a	2030	6MZ	C2-N1-C6	4.29	120.27	116.59
22	a	2504	PSU	C4-N3-C2	-4.20	120.29	126.34
22	a	745	1MG	C5-C6-N1	4.16	120.16	113.90
12	L	89	D2T	OD2-CG-CB	4.14	122.10	113.15
22	a	1618	6MZ	C9-N6-C6	-3.90	119.51	122.87
22	a	2552	OMU	C5-C4-N3	3.85	120.59	114.84
22	a	1618	6MZ	C2-N1-C6	3.82	119.87	116.59
53	5	8	4SU	N3-C2-N1	3.79	119.93	114.89
22	a	2552	OMU	N3-C2-N1	3.70	119.80	114.89
53	5	37	MIA	N3-C2-N1	-3.69	120.20	126.98
54	6	8	4SU	N3-C2-N1	3.64	119.72	114.89
54	6	8	4SU	C5-C4-S4	-3.62	119.81	124.47
22	a	2503	2MA	C5-C6-N1	3.59	120.22	114.02
54	6	21	H2U	C5-C4-N3	-3.35	112.89	116.65
53	5	8	4SU	C5-C4-S4	-3.32	120.19	124.47
53	5	37	MIA	C2-N3-C4	3.19	119.73	115.32
22	a	2580	PSU	O2-C2-N1	-3.17	119.30	122.79
33	l	81	4D4	NE-CZ-NH2	3.16	126.25	120.70
22	a	955	PSU	O2-C2-N1	-3.11	119.37	122.79
1	A	527	G7M	C2-N1-C6	-3.07	119.44	125.10
1	A	516	PSU	O2-C2-N1	-3.05	119.43	122.79
53	5	46	G7M	C2-N1-C6	-3.02	119.53	125.10
22	a	2552	OMU	O4-C4-C5	-3.00	119.89	125.16
22	a	2069	G7M	C2-N1-C6	-2.92	119.72	125.10
22	a	2580	PSU	C6-C5-C4	2.82	120.17	118.20
22	a	2504	PSU	C6-N1-C2	-2.77	119.85	122.68
53	5	39	PSU	O2-C2-N1	-2.77	119.74	122.79
22	a	746	PSU	O2-C2-N1	-2.76	119.75	122.79
22	a	2449	H2U	C5-C4-N3	-2.75	113.56	116.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	2604	PSU	O2-C2-N1	-2.73	119.79	122.79
22	a	2503	2MA	C8-N7-C5	2.72	108.17	102.99
22	a	955	PSU	C6-C5-C4	2.68	120.07	118.20
53	5	37	MIA	C12-C13-C14	-2.66	121.96	127.14
22	a	2604	PSU	C6-C5-C4	2.65	120.05	118.20
22	a	1917	PSU	O2-C2-N1	-2.65	119.88	122.79
12	L	89	D2T	OD1-CG-CB	-2.62	116.95	122.44
22	a	2580	PSU	C6-N1-C2	-2.61	120.01	122.68
53	5	32	PSU	O2-C2-N1	-2.61	119.92	122.79
22	a	2457	PSU	O2-C2-N1	-2.61	119.92	122.79
53	5	55	PSU	O2-C2-N1	-2.57	119.96	122.79
22	a	745	1MG	C8-N7-C5	2.55	107.86	102.99
53	5	37	MIA	C16-C14-C15	2.52	120.16	114.60
33	l	81	4D4	O-C-CA	-2.51	118.20	124.78
54	6	21	H2U	O2-C2-N1	2.47	126.21	123.11
1	A	1207	2MG	O6-C6-C5	2.47	129.19	124.37
22	a	2457	PSU	C6-N1-C2	-2.42	120.21	122.68
22	a	2580	PSU	O4'-C1'-C2'	2.36	108.47	105.14
22	a	955	PSU	C6-N1-C2	-2.35	120.28	122.68
1	A	516	PSU	O4'-C1'-C2'	2.35	108.45	105.14
53	5	32	PSU	C6-C5-C4	2.35	119.84	118.20
22	a	1917	PSU	C6-N1-C2	-2.32	120.32	122.68
54	6	56	PSU	O2-C2-N1	-2.31	120.25	122.79
22	a	2604	PSU	C6-N1-C2	-2.29	120.34	122.68
1	A	1402	4OC	C6-C5-C4	2.29	119.76	116.96
53	5	55	PSU	C6-N1-C2	-2.28	120.36	122.68
22	a	2605	PSU	C6-N1-C2	-2.27	120.36	122.68
22	a	1835	2MG	O6-C6-C5	2.26	128.78	124.37
22	a	746	PSU	C6-N1-C2	-2.25	120.38	122.68
22	a	1911	PSU	C6-N1-C2	-2.25	120.38	122.68
22	a	2251	OMG	O6-C6-C5	2.25	128.77	124.37
1	A	966	2MG	O6-C6-C5	2.24	128.74	124.37
53	5	32	PSU	C6-N1-C2	-2.22	120.42	122.68
22	a	745	1MG	O6-C6-C5	-2.21	120.27	124.19
1	A	1516	2MG	O6-C6-C5	2.20	128.67	124.37
22	a	1911	PSU	O2-C2-N1	-2.20	120.37	122.79
54	6	8	4SU	O2-C2-N1	-2.18	119.89	122.79
22	a	2445	2MG	O6-C6-C5	2.17	128.62	124.37
53	5	55	PSU	C6-C5-C4	2.17	119.72	118.20
53	5	39	PSU	C6-N1-C2	-2.16	120.48	122.68
53	5	8	4SU	O2-C2-N1	-2.16	119.92	122.79
12	L	89	D2T	CB-CA-N	2.13	113.63	109.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	1915	3TD	C6-C5-C4	2.13	119.69	118.22
22	a	2449	H2U	C4-N3-C2	2.11	127.55	125.79
53	5	32	PSU	O4'-C1'-C2'	2.09	108.10	105.14
22	a	1917	PSU	C6-C5-C4	2.09	119.66	118.20
33	l	81	4D4	NH1-CZ-NE	-2.06	114.43	119.19
22	a	2069	G7M	N1-C2-N3	-2.04	119.50	123.32
54	6	56	PSU	C6-N1-C2	-2.04	120.59	122.68
22	a	2503	2MA	N1-C2-N3	-2.04	119.67	123.06
1	A	1498	UR3	C6-N1-C2	-2.01	119.99	121.79

There are no chirality outliers.

All (40) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	L	89	D2T	CG-CB-SB-CB1
25	d	150	MEQ	N-CA-CB-CG
53	5	37	MIA	N1-C2-S10-C11
53	5	37	MIA	N3-C2-S10-C11
54	6	56	PSU	O4'-C1'-C5-C4
54	6	56	PSU	O4'-C1'-C5-C6
22	a	2251	OMG	C1'-C2'-O2'-CM2
22	a	2445	2MG	O4'-C4'-C5'-O5'
22	a	2445	2MG	C3'-C4'-C5'-O5'
22	a	2030	6MZ	O4'-C4'-C5'-O5'
22	a	2030	6MZ	C3'-C4'-C5'-O5'
22	a	2498	OMC	O4'-C4'-C5'-O5'
25	d	150	MEQ	OE1-CD-CG-CB
25	d	150	MEQ	NE2-CD-CG-CB
54	6	21	H2U	C2'-C1'-N1-C2
53	5	46	G7M	C4'-C5'-O5'-P
1	A	966	2MG	C3'-C4'-C5'-O5'
54	6	21	H2U	C2'-C1'-N1-C6
25	d	150	MEQ	C-CA-CB-CG
53	5	46	G7M	C3'-C4'-C5'-O5'
1	A	1402	4OC	O4'-C4'-C5'-O5'
1	A	966	2MG	O4'-C4'-C5'-O5'
22	a	2503	2MA	C4'-C5'-O5'-P
53	5	37	MIA	C13-C12-N6-C6
54	6	21	H2U	C4'-C5'-O5'-P
22	a	2498	OMC	C3'-C4'-C5'-O5'
54	6	55	5MU	C3'-C4'-C5'-O5'
53	5	55	PSU	O4'-C1'-C5-C4

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Mol	Chain	Res	Type	Atoms
33	l	81	4D4	CG-CD-NE-CZ
1	A	527	G7M	C3'-C4'-C5'-O5'
54	6	55	5MU	O4'-C4'-C5'-O5'
22	a	747	5MU	C3'-C4'-C5'-O5'
22	a	2449	H2U	O4'-C4'-C5'-O5'
22	a	746	PSU	O4'-C1'-C5-C6
22	a	2069	G7M	O4'-C4'-C5'-O5'
22	a	2503	2MA	O4'-C4'-C5'-O5'
11	K	119	IAS	CA-CB-CG-OD1
1	A	1402	4OC	C3'-C4'-C5'-O5'
1	A	527	G7M	C4'-C5'-O5'-P
22	a	2251	OMG	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 488 ligands modelled in this entry, 461 are monoatomic - leaving 27 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
57	SPD	A	1667	1	9,9,9	0.33	0	8,8,8	0.72	0
57	SPD	a	6200	-	9,9,9	0.34	0	8,8,8	0.82	0
57	SPD	a	6201	-	9,9,9	0.32	0	8,8,8	0.88	0
57	SPD	a	6203	-	9,9,9	0.34	0	8,8,8	0.76	0
59	SPM	a	6204	-	13,13,13	0.34	0	12,12,12	0.73	0
58	84G	A	1791	-	39,40,40	1.91	9 (23%)	47,57,57	1.24	5 (10%)
57	SPD	a	6195	-	9,9,9	0.33	0	8,8,8	0.86	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
58	84G	a	6253	-	39,40,40	1.86	8 (20%)	47,57,57	1.12	3 (6%)
58	84G	A	1793	-	39,40,40	1.86	9 (23%)	47,57,57	1.01	3 (6%)
57	SPD	a	6197	-	9,9,9	0.32	0	8,8,8	0.95	0
58	84G	a	6251	-	39,40,40	1.92	7 (17%)	47,57,57	1.15	5 (10%)
57	SPD	a	6196	-	9,9,9	0.33	0	8,8,8	0.81	0
57	SPD	a	6191	-	9,9,9	0.33	0	8,8,8	0.79	0
58	84G	a	6250	-	39,40,40	1.86	9 (23%)	47,57,57	1.07	4 (8%)
57	SPD	a	6199	-	9,9,9	0.30	0	8,8,8	0.73	0
58	84G	a	6249	-	39,40,40	1.86	6 (15%)	47,57,57	1.22	4 (8%)
57	SPD	a	6190	-	9,9,9	0.33	0	8,8,8	0.78	0
57	SPD	a	6202	-	9,9,9	0.34	0	8,8,8	0.90	0
58	84G	a	6254	-	39,40,40	1.80	6 (15%)	47,57,57	1.13	3 (6%)
58	84G	a	6252	-	39,40,40	1.88	7 (17%)	47,57,57	1.17	4 (8%)
57	SPD	a	6193	-	9,9,9	0.32	0	8,8,8	0.83	0
58	84G	A	1792	-	39,40,40	1.88	8 (20%)	47,57,57	1.26	6 (12%)
58	84G	a	6255	-	39,40,40	1.84	6 (15%)	47,57,57	1.26	5 (10%)
57	SPD	a	6192	-	9,9,9	0.33	0	8,8,8	0.99	0
57	SPD	A	1668	1	9,9,9	0.32	0	8,8,8	0.90	0
57	SPD	a	6198	-	9,9,9	0.33	0	8,8,8	0.87	0
57	SPD	a	6194	-	9,9,9	0.30	0	8,8,8	0.88	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	SPD	A	1667	1	-	3/7/7/7	-
57	SPD	a	6200	-	-	3/7/7/7	-
57	SPD	a	6201	-	-	1/7/7/7	-
57	SPD	a	6203	-	-	1/7/7/7	-
59	SPM	a	6204	-	-	3/11/11/11	-
58	84G	A	1791	-	-	3/23/76/76	0/3/3/3
57	SPD	a	6195	-	-	6/7/7/7	-
58	84G	a	6253	-	-	4/23/76/76	0/3/3/3
58	84G	A	1793	-	-	3/23/76/76	0/3/3/3
57	SPD	a	6197	-	-	3/7/7/7	-
58	84G	a	6251	-	-	5/23/76/76	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	SPD	a	6196	-	-	3/7/7/7	-
57	SPD	a	6191	-	-	5/7/7/7	-
58	84G	a	6250	-	-	8/23/76/76	0/3/3/3
57	SPD	a	6199	-	-	3/7/7/7	-
58	84G	a	6249	-	-	3/23/76/76	0/3/3/3
57	SPD	a	6190	-	-	3/7/7/7	-
57	SPD	a	6202	-	-	1/7/7/7	-
58	84G	a	6254	-	-	4/23/76/76	0/3/3/3
58	84G	a	6252	-	-	11/23/76/76	0/3/3/3
57	SPD	a	6193	-	-	1/7/7/7	-
58	84G	A	1792	-	-	4/23/76/76	0/3/3/3
58	84G	a	6255	-	-	4/23/76/76	0/3/3/3
57	SPD	a	6192	-	-	3/7/7/7	-
57	SPD	A	1668	1	-	3/7/7/7	-
57	SPD	a	6198	-	-	2/7/7/7	-
57	SPD	a	6194	-	-	3/7/7/7	-

All (75) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	a	6250	84G	C3-N1	6.56	1.48	1.34
58	a	6253	84G	C3-N1	6.49	1.48	1.34
58	a	6249	84G	C3-N1	6.48	1.48	1.34
58	A	1793	84G	C3-N1	6.45	1.48	1.34
58	a	6252	84G	C3-N1	6.39	1.48	1.34
58	a	6254	84G	C3-N1	6.32	1.48	1.34
58	A	1791	84G	C3-N1	6.31	1.47	1.34
58	a	6255	84G	C3-N1	6.25	1.47	1.34
58	a	6251	84G	C3-N1	6.16	1.47	1.34
58	a	6251	84G	C19-C20	-6.11	1.45	1.53
58	A	1792	84G	C3-N1	6.03	1.47	1.34
58	A	1791	84G	C19-C20	-5.51	1.46	1.53
58	A	1792	84G	C19-C20	-5.36	1.46	1.53
58	a	6252	84G	C19-C20	-5.27	1.46	1.53
58	A	1793	84G	C19-C20	-5.22	1.47	1.53
58	a	6253	84G	C19-C20	-5.14	1.47	1.53
58	a	6249	84G	C19-C20	-5.09	1.47	1.53
58	a	6250	84G	C19-C20	-5.08	1.47	1.53
58	a	6255	84G	C19-C20	-4.92	1.47	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	a	6254	84G	C19-C20	-4.86	1.47	1.53
58	A	1792	84G	C21-C20	-4.15	1.48	1.53
58	a	6251	84G	C21-C20	-3.98	1.48	1.53
58	A	1791	84G	C21-C20	-3.85	1.48	1.53
58	a	6252	84G	C21-C20	-3.68	1.48	1.53
58	A	1793	84G	C21-C20	-3.67	1.48	1.53
58	a	6249	84G	C21-C20	-3.49	1.49	1.53
58	a	6253	84G	C21-C20	-3.28	1.49	1.53
58	a	6250	84G	C21-C20	-3.28	1.49	1.53
58	a	6255	84G	C21-C20	-3.27	1.49	1.53
58	a	6254	84G	C21-C20	-3.24	1.49	1.53
58	A	1792	84G	C20-N5	3.23	1.52	1.47
58	a	6255	84G	C20-N5	3.14	1.52	1.47
58	a	6254	84G	C20-N5	3.11	1.52	1.47
58	a	6250	84G	C20-N5	3.10	1.52	1.47
58	a	6252	84G	C20-N5	3.08	1.52	1.47
58	a	6253	84G	C20-N5	3.06	1.51	1.47
58	A	1793	84G	C20-N5	3.06	1.51	1.47
58	a	6251	84G	C20-N5	3.05	1.51	1.47
58	a	6249	84G	C20-N5	2.94	1.51	1.47
58	A	1791	84G	C20-N5	2.90	1.51	1.47
58	a	6250	84G	O3-C8	2.81	1.49	1.41
58	a	6255	84G	O3-C8	2.70	1.48	1.41
58	a	6253	84G	O3-C8	2.66	1.48	1.41
58	a	6249	84G	O3-C8	2.65	1.48	1.41
58	A	1791	84G	O3-C8	2.60	1.48	1.41
58	A	1792	84G	O3-C8	2.56	1.48	1.41
58	a	6252	84G	O3-C8	2.48	1.48	1.41
58	A	1793	84G	O3-C8	2.47	1.48	1.41
58	a	6254	84G	O3-C8	2.47	1.48	1.41
58	a	6251	84G	O3-C8	2.44	1.48	1.41
58	A	1792	84G	O1-C3	-2.36	1.18	1.23
58	a	6255	84G	O1-C3	-2.35	1.18	1.23
58	A	1791	84G	O1-C3	-2.34	1.18	1.23
58	a	6253	84G	O1-C3	-2.30	1.18	1.23
58	a	6251	84G	O1-C3	-2.27	1.18	1.23
58	a	6250	84G	O1-C3	-2.26	1.18	1.23
58	a	6252	84G	C2-C3	2.18	1.55	1.52
58	A	1793	84G	O1-C3	-2.18	1.19	1.23
58	a	6252	84G	O1-C3	-2.16	1.19	1.23
58	a	6251	84G	O6-C17	2.15	1.49	1.44
58	a	6253	84G	C11-C12	-2.13	1.47	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	A	1791	84G	C11-C12	-2.10	1.47	1.52
58	A	1791	84G	O6-C17	2.10	1.49	1.44
58	a	6254	84G	O1-C3	-2.09	1.19	1.23
58	A	1792	84G	C11-C12	-2.08	1.47	1.52
58	A	1793	84G	C11-C12	-2.07	1.47	1.52
58	A	1792	84G	O6-C17	2.06	1.49	1.44
58	a	6250	84G	C11-C12	-2.05	1.47	1.52
58	A	1791	84G	O-C2	-2.05	1.38	1.42
58	a	6249	84G	O1-C3	-2.05	1.19	1.23
58	A	1793	84G	O6-C16	2.04	1.47	1.41
58	A	1793	84G	O6-C17	2.02	1.49	1.44
58	a	6253	84G	O6-C17	2.01	1.49	1.44
58	a	6250	84G	O-C2	-2.01	1.38	1.42
58	a	6250	84G	O6-C16	2.00	1.47	1.41

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	A	1792	84G	O3-C9-C11	3.87	114.02	109.86
58	A	1791	84G	O3-C9-C11	3.73	113.87	109.86
58	a	6255	84G	O3-C9-C11	3.56	113.69	109.86
58	a	6249	84G	O3-C9-C11	3.33	113.44	109.86
58	A	1791	84G	C5-C4-N1	-3.27	105.80	110.86
58	a	6254	84G	O3-C9-C11	3.05	113.14	109.86
58	a	6253	84G	C8-O2-C7	-2.95	110.66	117.96
58	a	6252	84G	C5-C4-N1	-2.82	106.50	110.86
58	A	1792	84G	C5-C4-N1	-2.79	106.54	110.86
58	a	6249	84G	C7-C14-C15	2.77	114.71	108.96
58	a	6254	84G	C8-O2-C7	-2.76	111.13	117.96
58	a	6251	84G	C5-C4-N1	-2.67	106.73	110.86
58	a	6251	84G	C19-C20-N5	-2.63	105.66	111.05
58	a	6252	84G	C7-C14-C15	2.59	114.33	108.96
58	A	1793	84G	C16-C21-C20	2.58	113.86	110.40
58	A	1791	84G	C7-C14-C15	2.57	114.28	108.96
58	A	1792	84G	C16-O5-C15	-2.49	111.81	117.96
58	a	6250	84G	C16-O5-C15	-2.47	111.84	117.96
58	A	1791	84G	C11-C9-C10	-2.47	108.11	112.83
58	A	1792	84G	C8-O2-C7	-2.46	111.88	117.96
58	a	6252	84G	O6-C17-C19	2.46	114.16	109.69
58	a	6249	84G	C16-O5-C15	-2.41	111.99	117.96
58	a	6249	84G	C11-C9-C10	-2.34	108.36	112.83
58	a	6253	84G	O3-C9-C11	2.32	112.35	109.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	A	1792	84G	C11-C9-C10	-2.30	108.44	112.83
58	a	6252	84G	O3-C9-C11	2.29	112.32	109.86
58	a	6251	84G	C16-O5-C15	-2.24	112.41	117.96
58	a	6255	84G	C16-O5-C15	-2.23	112.44	117.96
58	a	6250	84G	C8-O2-C7	-2.19	112.55	117.96
58	a	6255	84G	C16-C21-C20	2.17	113.32	110.40
58	A	1793	84G	C8-O2-C7	-2.17	112.60	117.96
58	a	6250	84G	O3-C8-C13	2.13	115.00	110.25
58	A	1791	84G	O2-C7-C6	-2.11	104.15	109.18
58	A	1792	84G	O6-C17-C19	2.10	113.51	109.69
58	a	6254	84G	C11-C9-C10	-2.08	108.86	112.83
58	a	6250	84G	C16-C21-C20	2.07	113.18	110.40
58	a	6251	84G	C8-O2-C7	-2.06	112.86	117.96
58	a	6251	84G	C21-C20-N5	-2.05	106.86	111.05
58	a	6255	84G	C5-C4-N1	-2.04	107.71	110.86
58	a	6255	84G	C8-O2-C7	-2.04	112.92	117.96
58	A	1793	84G	C16-O5-C15	-2.03	112.95	117.96
58	a	6253	84G	C11-C9-C10	-2.01	108.99	112.83

There are no chirality outliers.

All (96) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	a	6198	SPD	C8-C7-N6-C5
58	A	1793	84G	N3-C10-C9-O3
58	A	1793	84G	N3-C10-C9-C11
58	a	6250	84G	C-C1-C2-C3
58	a	6250	84G	N3-C10-C9-O3
58	a	6250	84G	N3-C10-C9-C11
58	a	6251	84G	N3-C10-C9-O3
58	a	6251	84G	N3-C10-C9-C11
58	a	6252	84G	C-C1-C2-O
58	a	6252	84G	C1-C2-C3-O1
58	a	6252	84G	C1-C2-C3-N1
58	a	6252	84G	O-C2-C3-N1
58	a	6252	84G	N3-C10-C9-O3
58	a	6252	84G	N3-C10-C9-C11
58	a	6253	84G	N3-C10-C9-O3
58	a	6253	84G	N3-C10-C9-C11
58	a	6254	84G	C-C1-C2-O
58	a	6255	84G	C-C1-C2-O
58	a	6255	84G	N3-C10-C9-O3

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Mol	Chain	Res	Type	Atoms
58	a	6255	84G	N3-C10-C9-C11
57	a	6195	SPD	C2-C3-C4-C5
58	a	6254	84G	C19-C17-C18-O7
58	a	6249	84G	C19-C17-C18-O7
57	A	1668	SPD	C3-C4-C5-N6
58	A	1792	84G	O6-C17-C18-O7
57	a	6195	SPD	C3-C4-C5-N6
57	a	6192	SPD	N6-C7-C8-C9
58	a	6249	84G	O6-C17-C18-O7
58	a	6254	84G	O6-C17-C18-O7
57	a	6200	SPD	C3-C4-C5-N6
58	A	1791	84G	O6-C17-C18-O7
57	a	6191	SPD	C3-C4-C5-N6
58	A	1791	84G	C19-C17-C18-O7
57	a	6194	SPD	C3-C4-C5-N6
57	a	6195	SPD	N6-C7-C8-C9
57	a	6196	SPD	N6-C7-C8-C9
58	a	6251	84G	O6-C17-C18-O7
57	a	6191	SPD	N6-C7-C8-C9
58	a	6251	84G	C19-C17-C18-O7
58	A	1792	84G	C19-C17-C18-O7
57	a	6196	SPD	C3-C4-C5-N6
58	a	6250	84G	C19-C17-C18-O7
58	a	6254	84G	O6-C16-O5-C15
57	a	6193	SPD	C3-C4-C5-N6
58	a	6252	84G	C19-C17-C18-O7
57	A	1667	SPD	C2-C3-C4-C5
58	a	6250	84G	O6-C17-C18-O7
58	a	6253	84G	C19-C17-C18-O7
58	a	6252	84G	O-C2-C3-O1
57	a	6197	SPD	C3-C4-C5-N6
57	a	6190	SPD	C7-C8-C9-N10
59	a	6204	SPM	C11-C12-C13-N14
58	a	6252	84G	O6-C17-C18-O7
57	a	6197	SPD	C2-C3-C4-C5
57	a	6198	SPD	C2-C3-C4-C5
57	a	6199	SPD	C2-C3-C4-C5
58	a	6250	84G	C-C1-C2-O
57	A	1667	SPD	C3-C4-C5-N6
57	a	6190	SPD	N6-C7-C8-C9
58	a	6253	84G	O6-C17-C18-O7
57	a	6199	SPD	C3-C4-C5-N6

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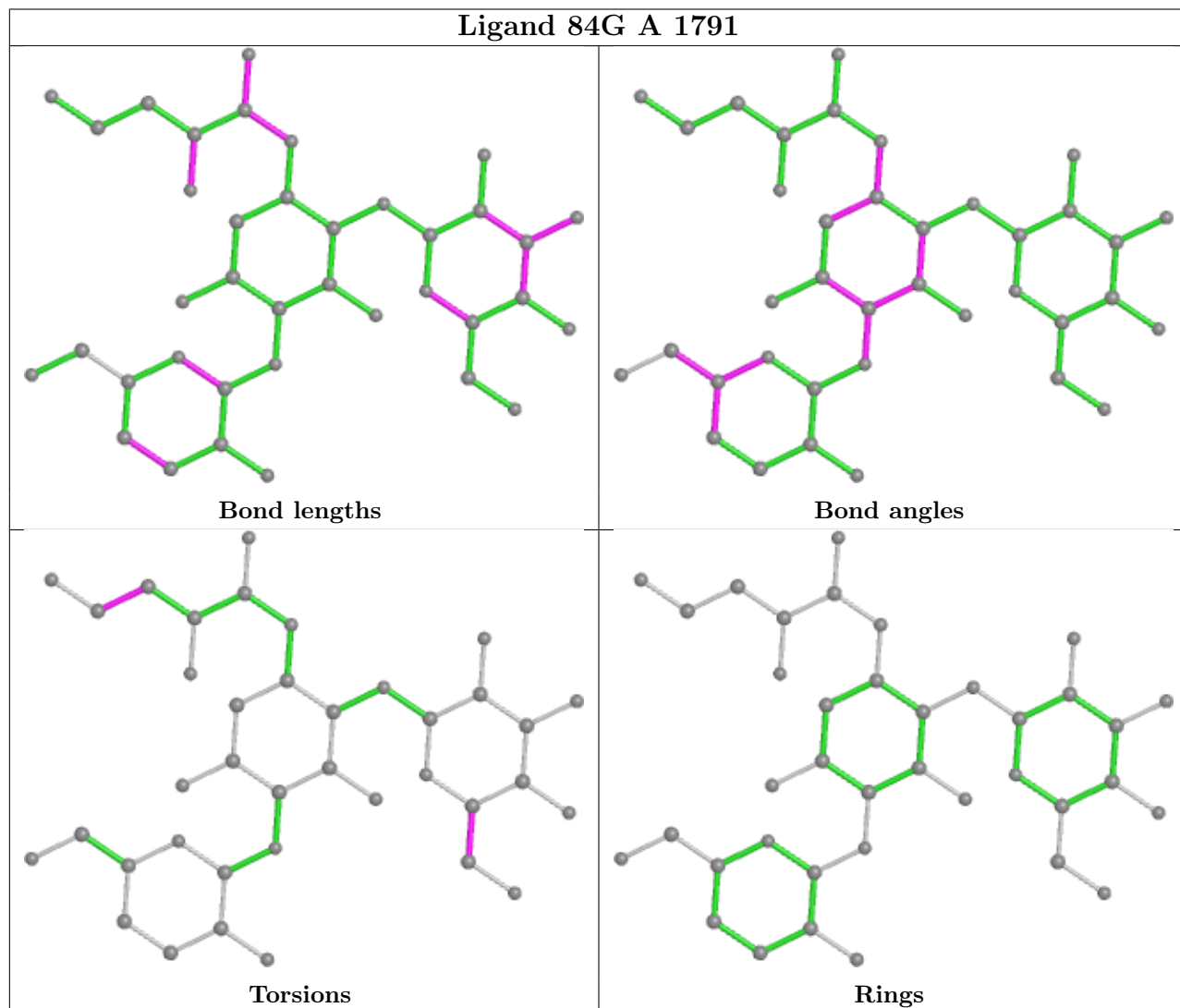
Mol	Chain	Res	Type	Atoms
59	a	6204	SPM	C7-C8-C9-N10
57	a	6200	SPD	C8-C7-N6-C5
57	a	6195	SPD	C7-C8-C9-N10
57	a	6202	SPD	C4-C5-N6-C7
58	A	1791	84G	N-C-C1-C2
58	a	6249	84G	N-C-C1-C2
58	a	6251	84G	N-C-C1-C2
57	a	6194	SPD	C4-C5-N6-C7
57	a	6191	SPD	C2-C3-C4-C5
57	a	6201	SPD	N6-C7-C8-C9
57	A	1668	SPD	C8-C7-N6-C5
57	a	6195	SPD	C4-C5-N6-C7
57	a	6197	SPD	C8-C7-N6-C5
57	a	6191	SPD	N1-C2-C3-C4
57	a	6203	SPD	N1-C2-C3-C4
57	a	6191	SPD	C4-C5-N6-C7
58	A	1793	84G	O3-C8-O2-C7
57	a	6199	SPD	N6-C7-C8-C9
58	a	6252	84G	O6-C16-O5-C15
59	a	6204	SPM	C3-C4-N5-C6
57	a	6194	SPD	C8-C7-N6-C5
58	a	6252	84G	C21-C16-O5-C15
57	a	6192	SPD	C8-C7-N6-C5
58	a	6250	84G	C14-C7-O2-C8
57	A	1667	SPD	C4-C5-N6-C7
57	A	1668	SPD	C4-C5-N6-C7
57	a	6192	SPD	N1-C2-C3-C4
57	a	6196	SPD	N1-C2-C3-C4
58	A	1792	84G	N-C-C1-C2
58	A	1792	84G	O-C2-C3-N1
58	a	6255	84G	C14-C7-O2-C8
57	a	6200	SPD	C4-C5-N6-C7
57	a	6190	SPD	C8-C7-N6-C5
57	a	6195	SPD	C8-C7-N6-C5
58	a	6250	84G	O6-C16-O5-C15

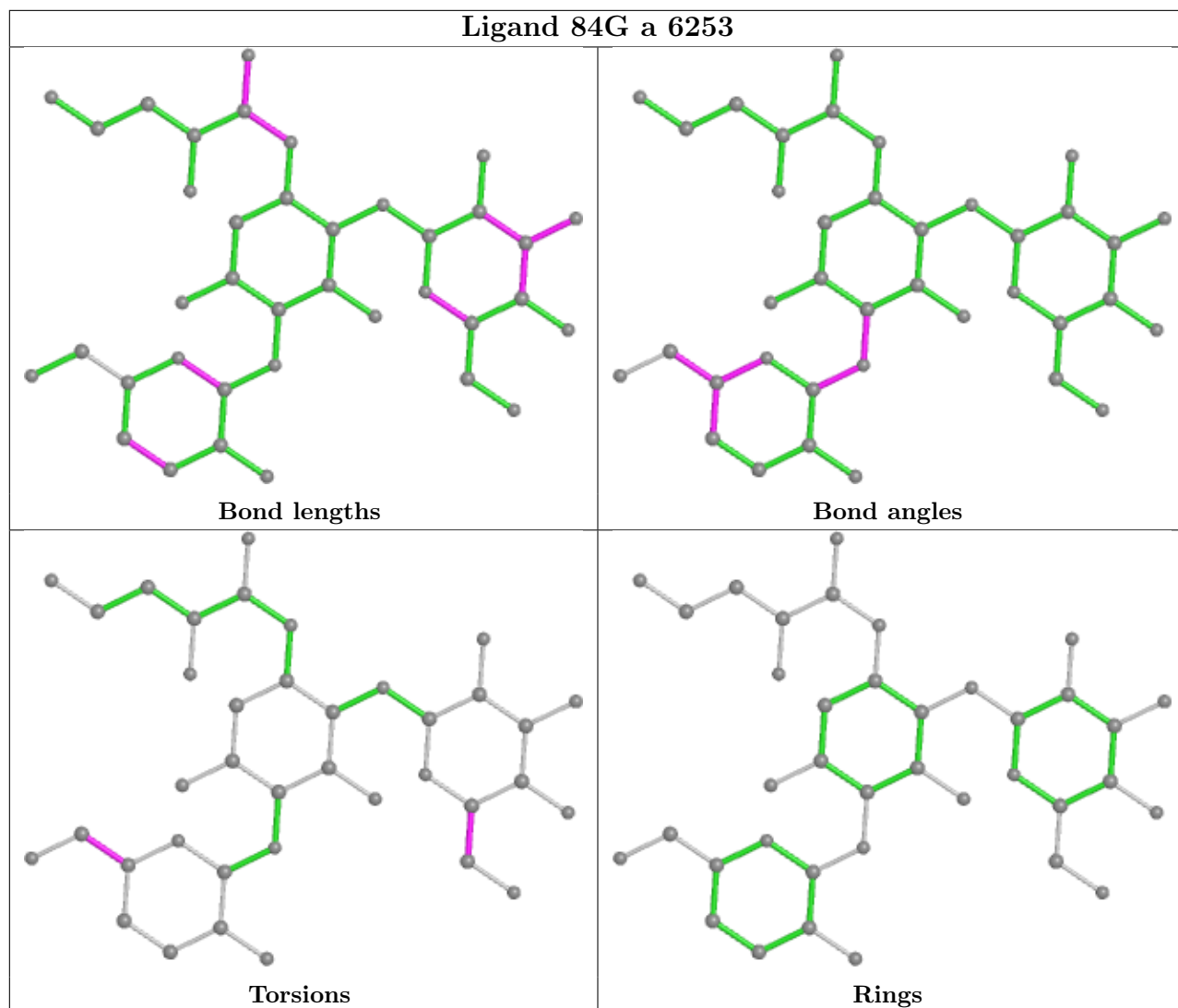
There are no ring outliers.

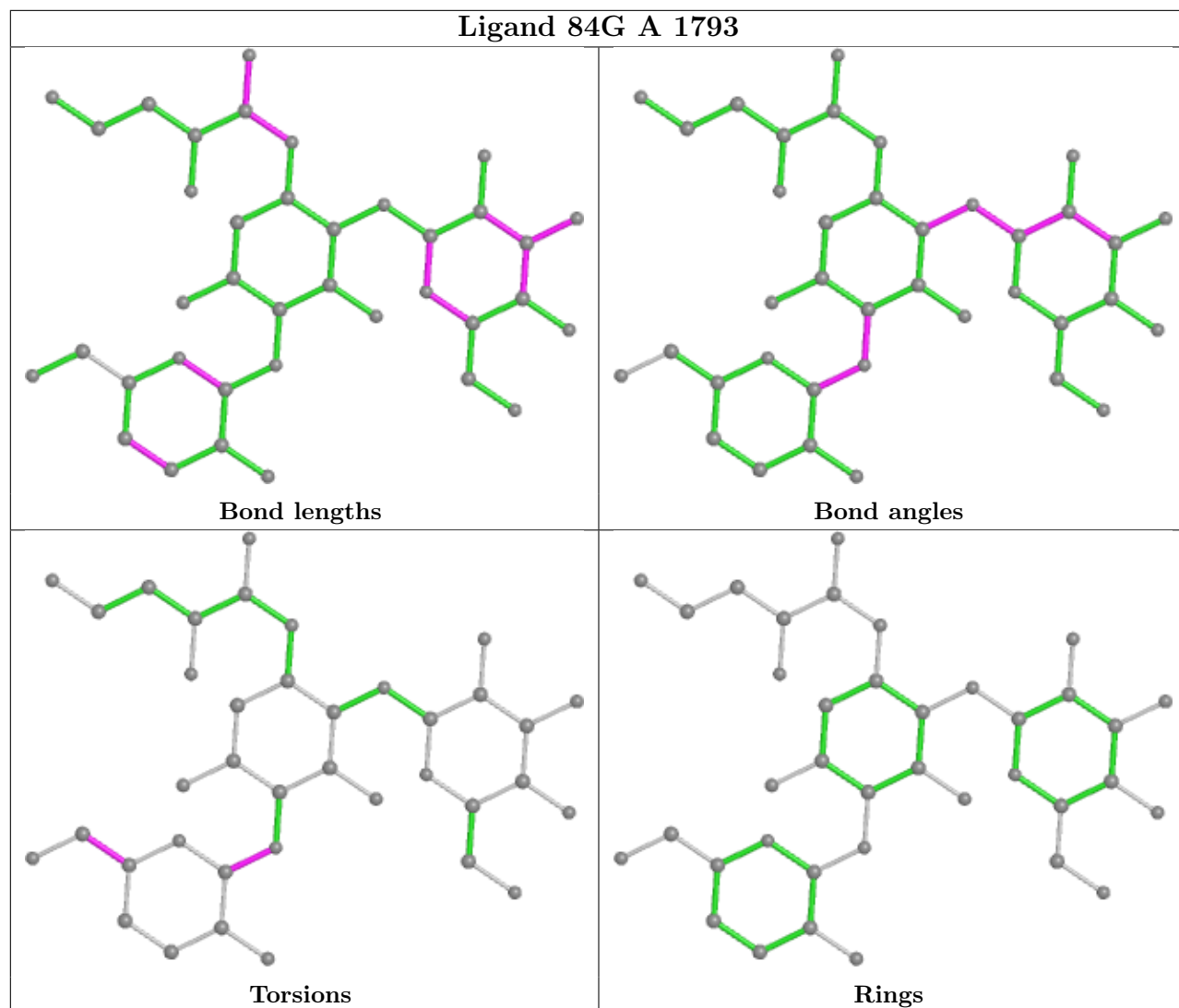
No monomer is involved in short contacts.

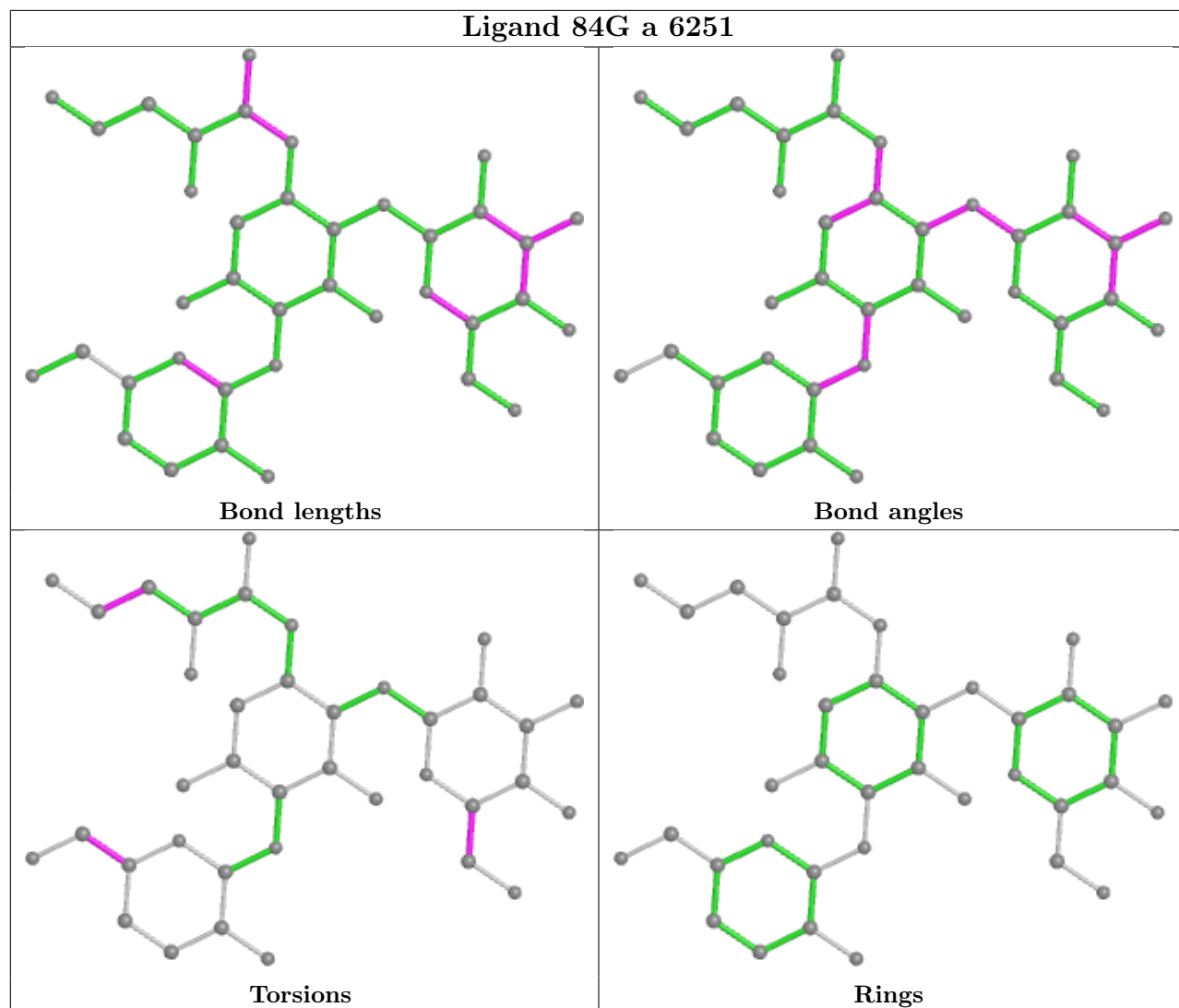
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

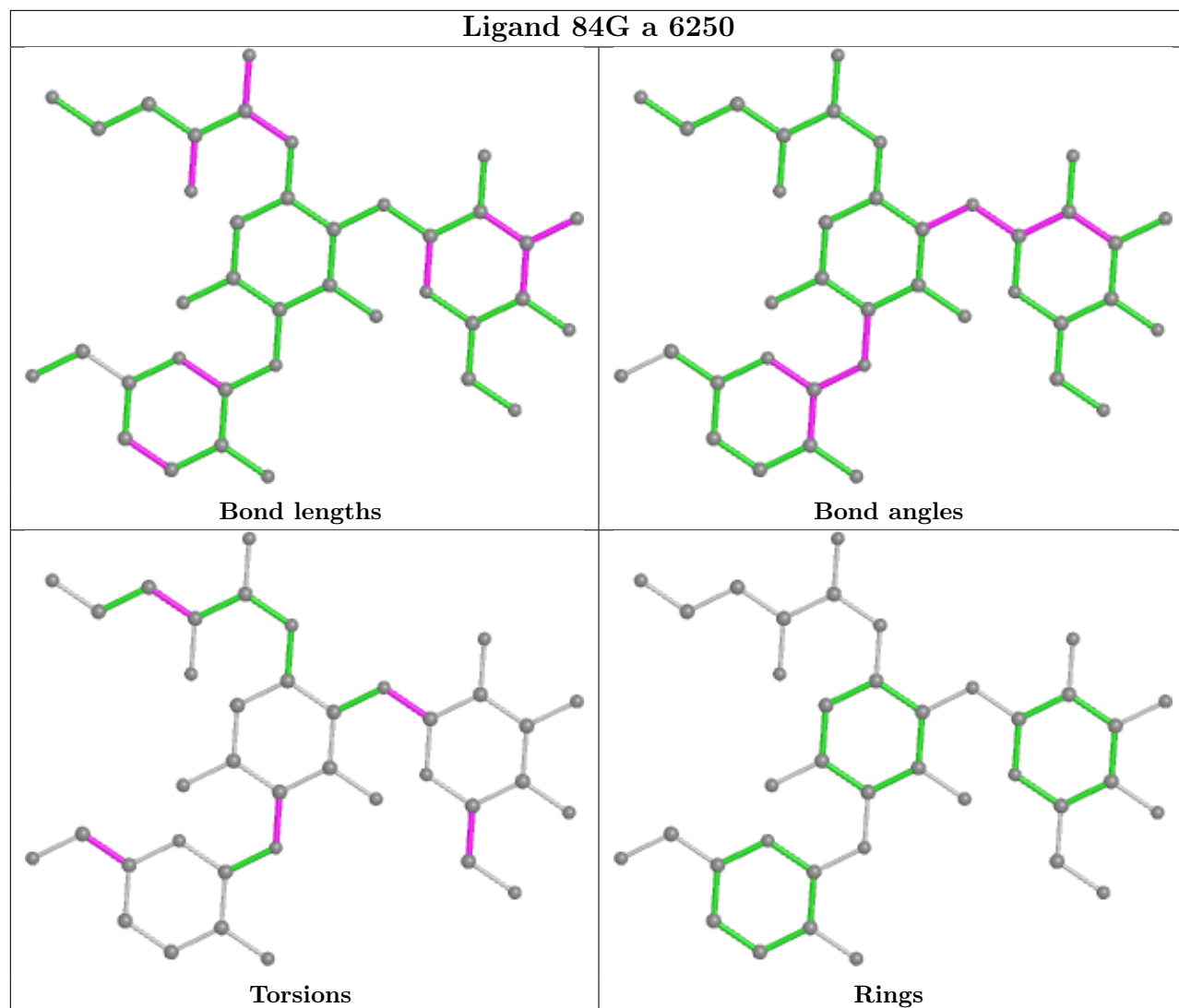
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



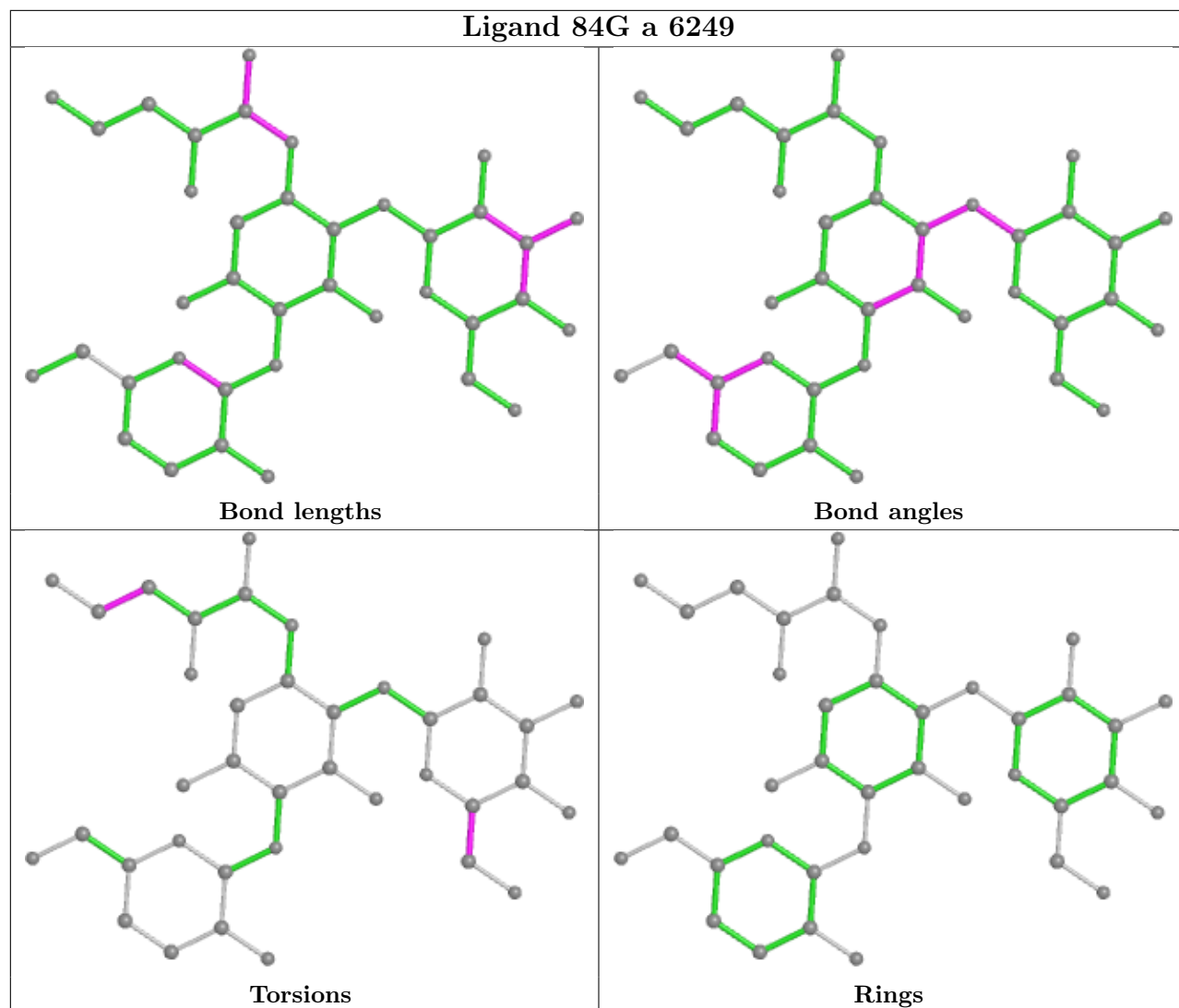


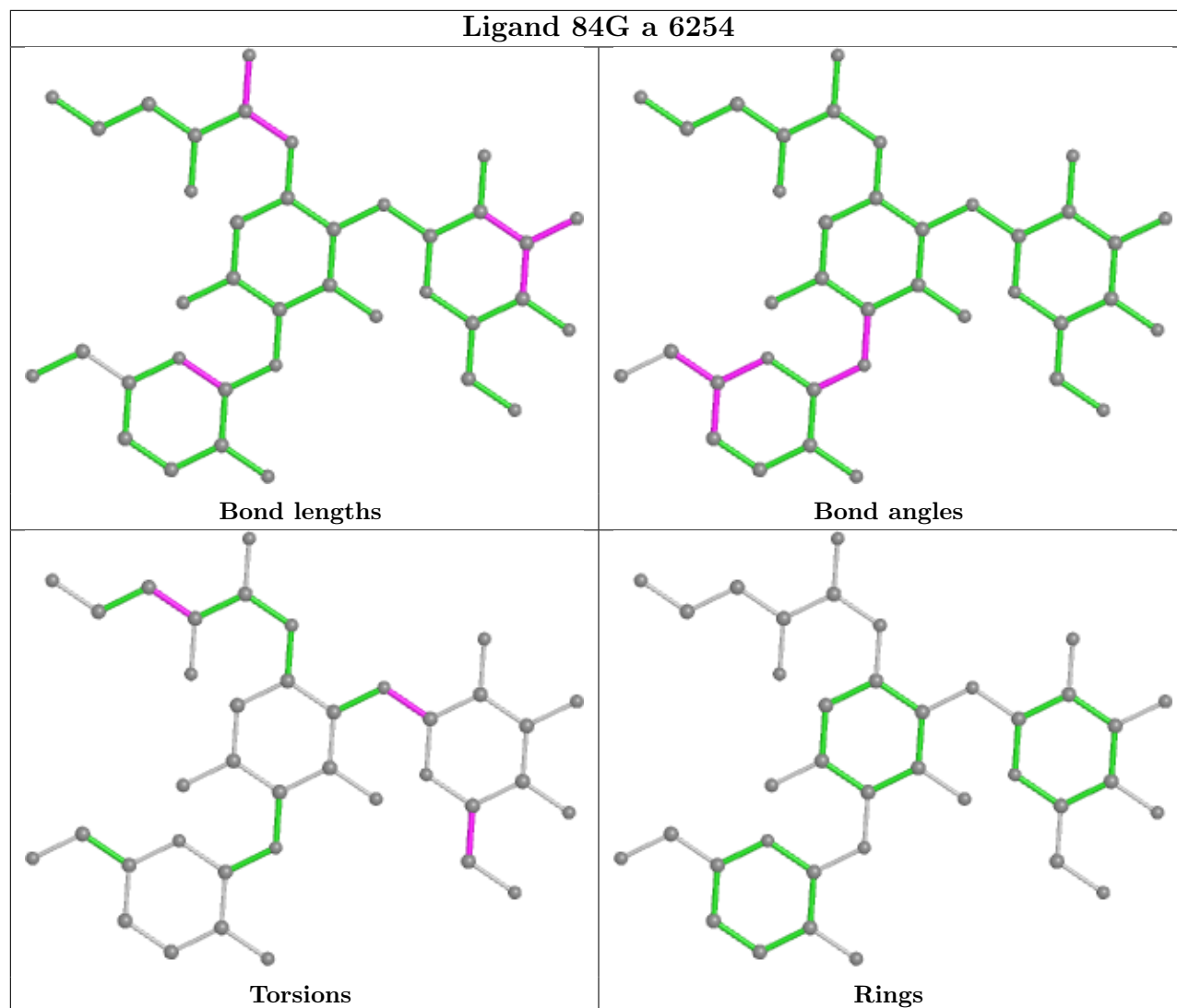


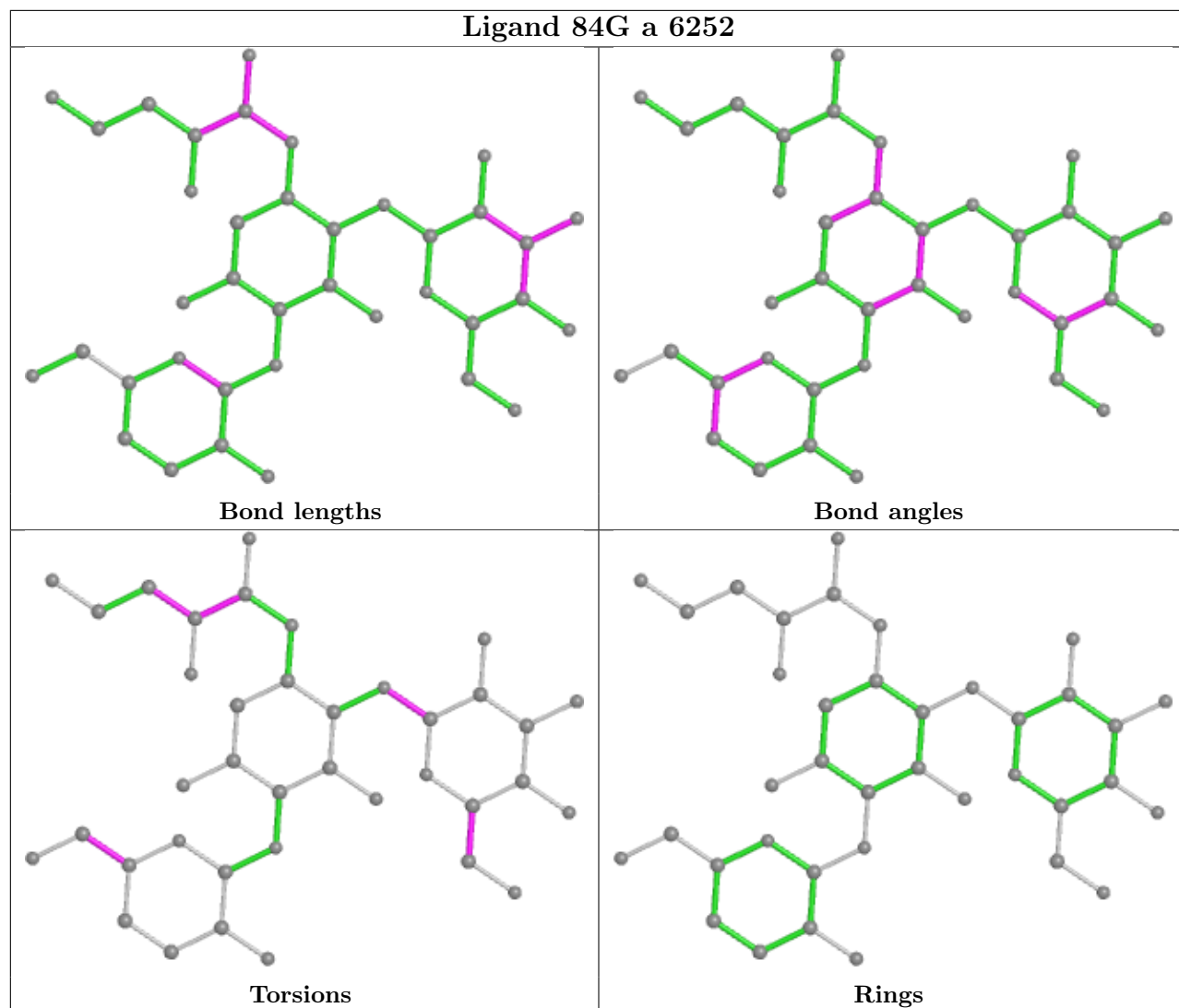


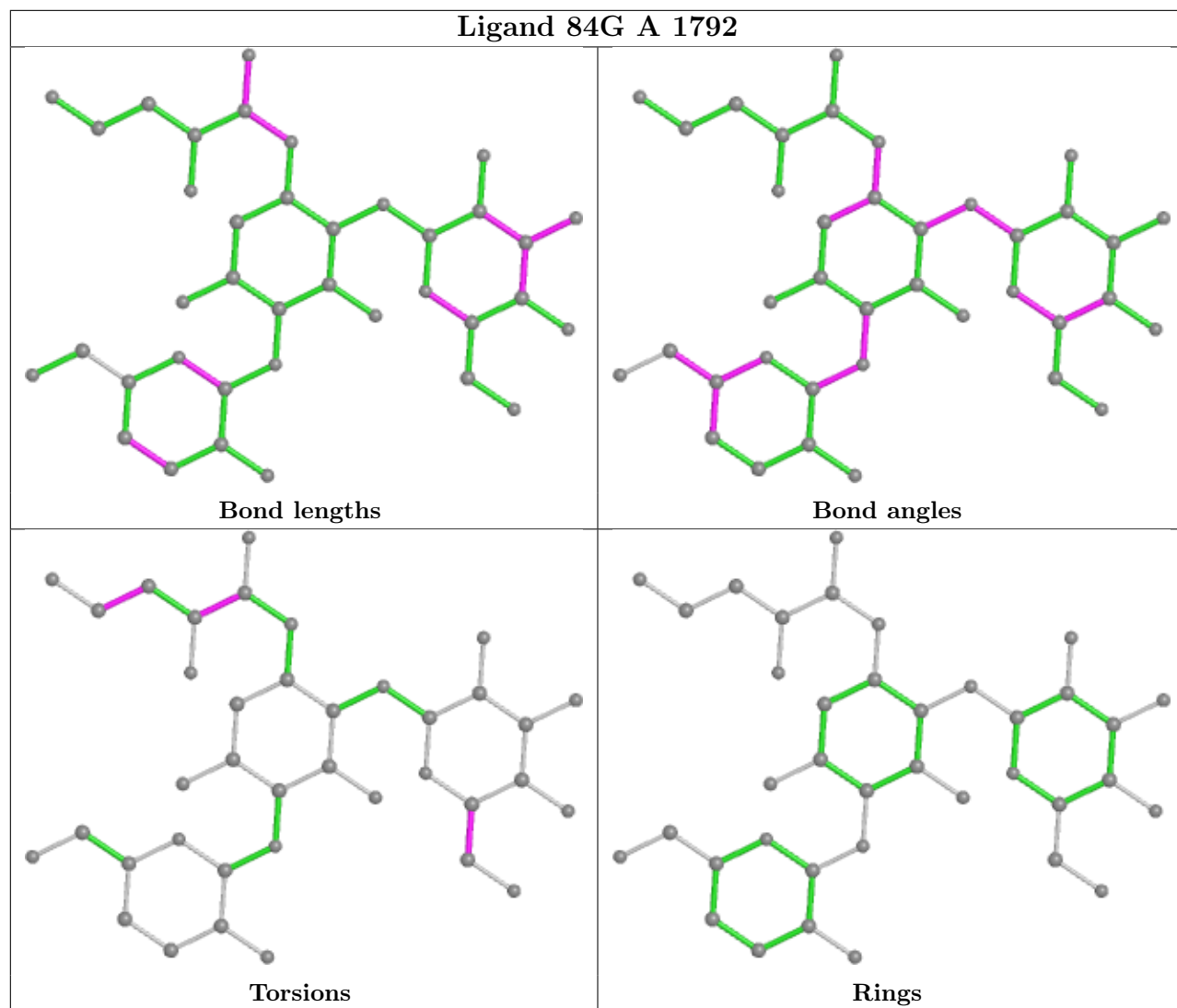


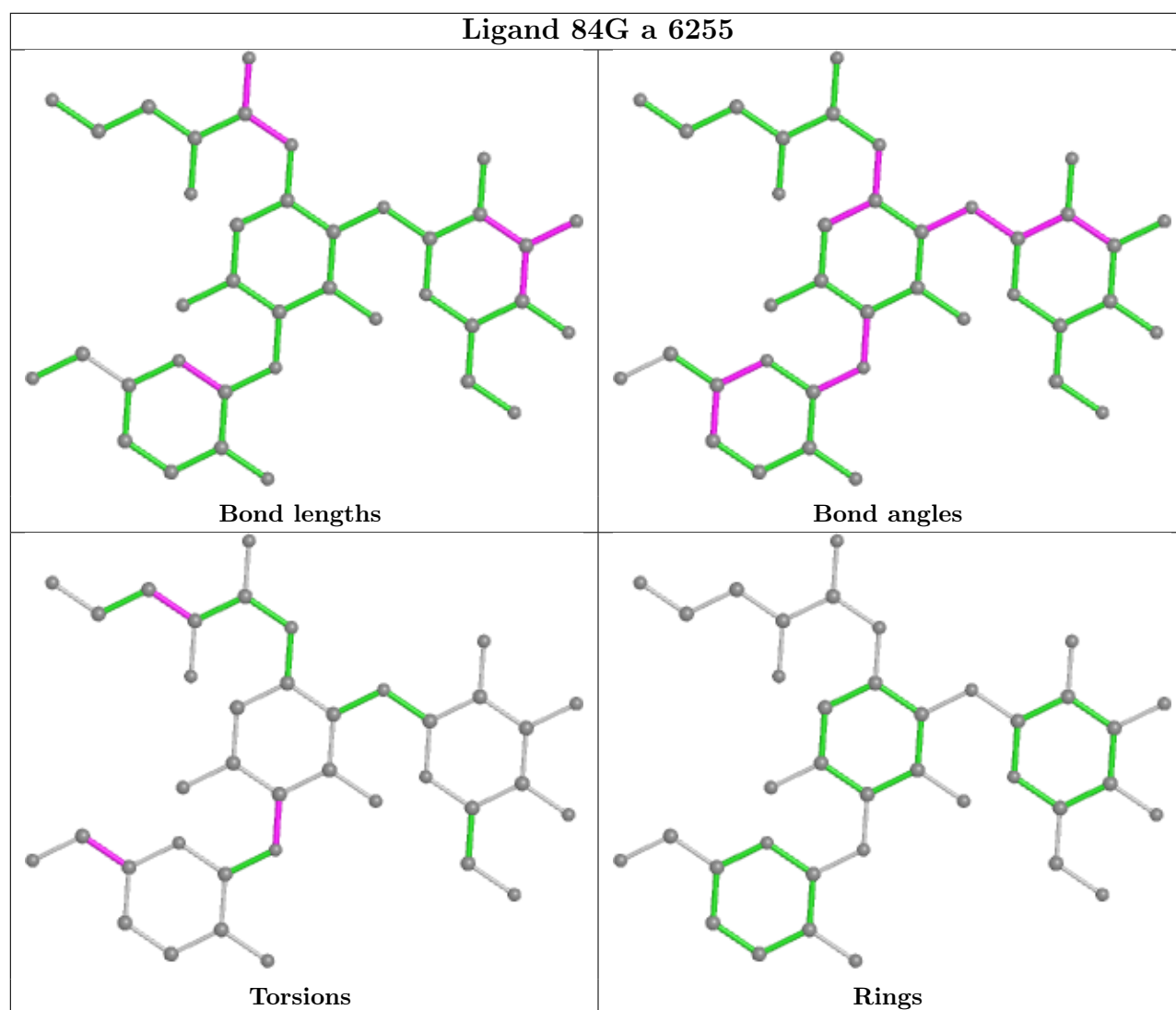












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

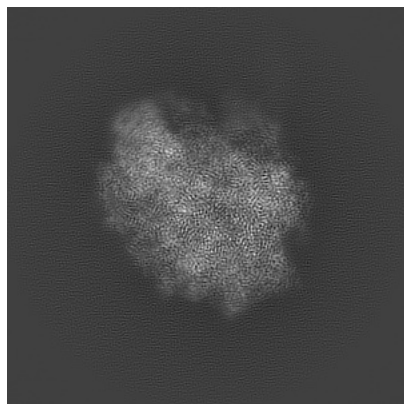
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35412. These allow visual inspection of the internal detail of the map and identification of artifacts.

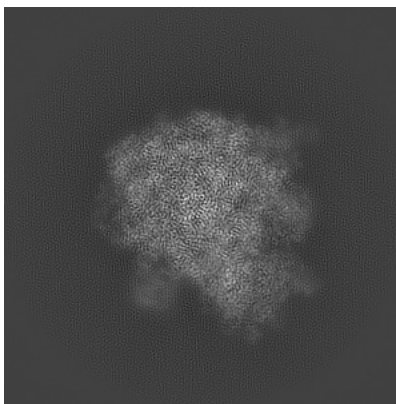
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

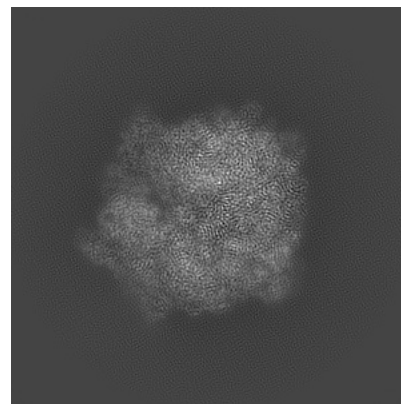
#### 6.1.1 Primary map



X

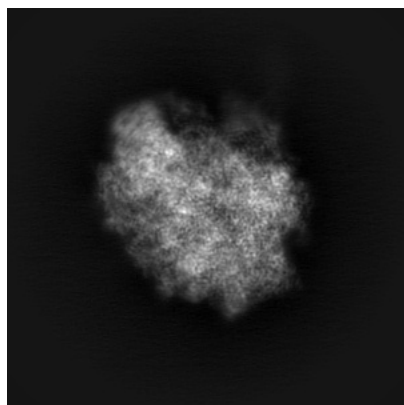


Y

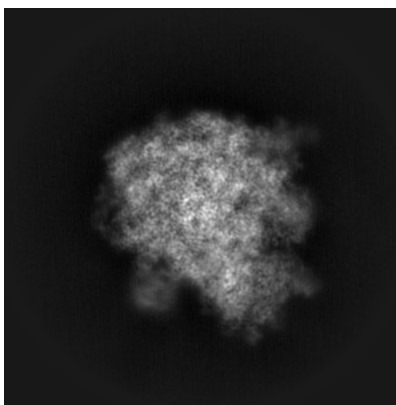


Z

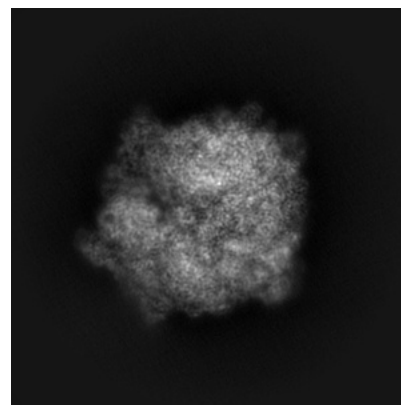
#### 6.1.2 Raw map



X



Y

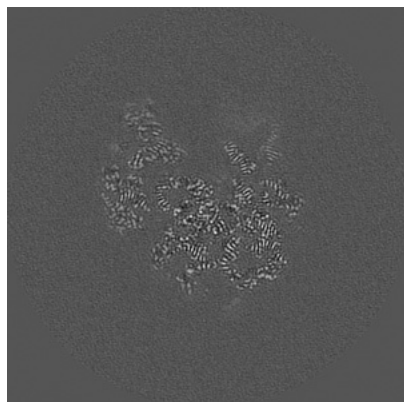


Z

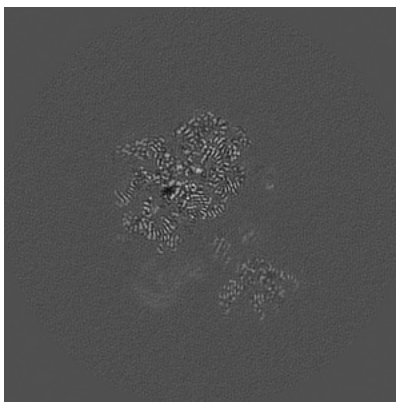
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

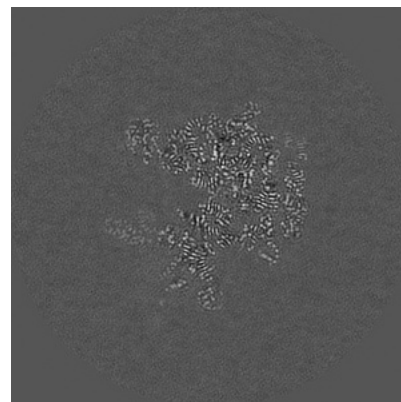
### 6.2.1 Primary map



X Index: 256

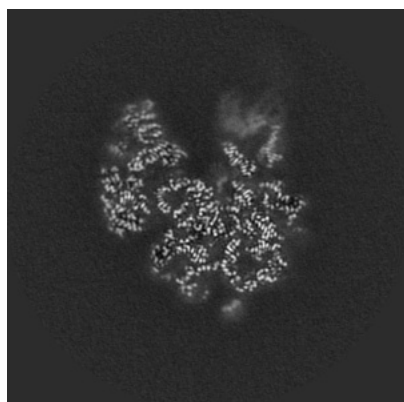


Y Index: 256

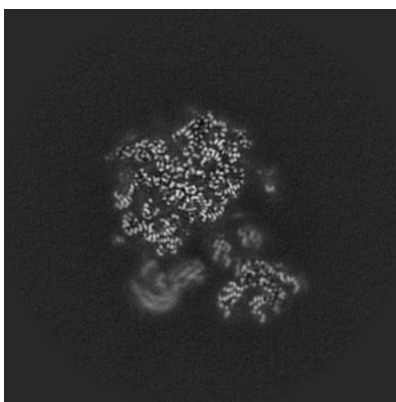


Z Index: 256

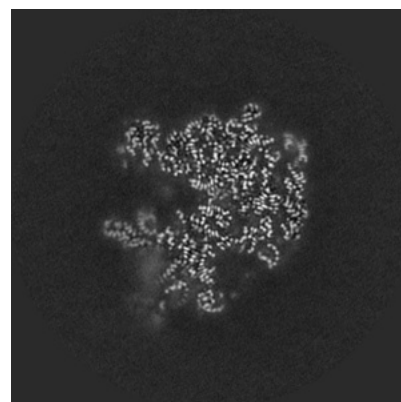
### 6.2.2 Raw map



X Index: 256



Y Index: 256

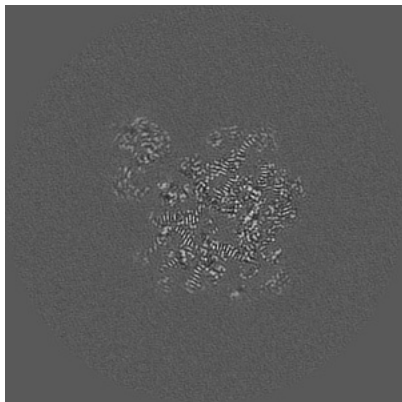


Z Index: 256

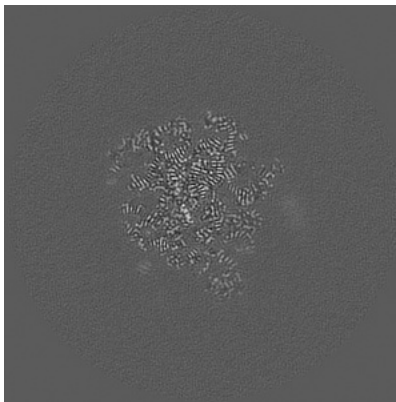
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

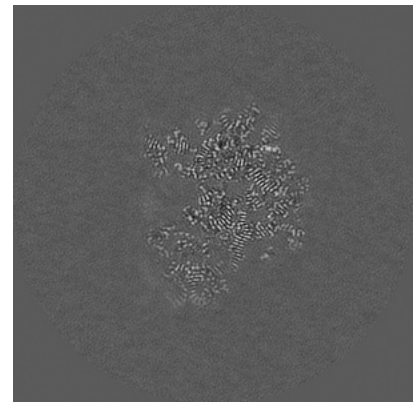
### 6.3.1 Primary map



X Index: 293

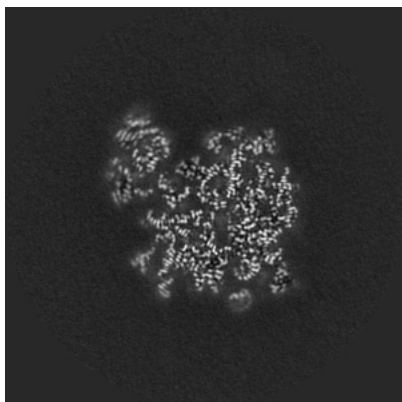


Y Index: 313

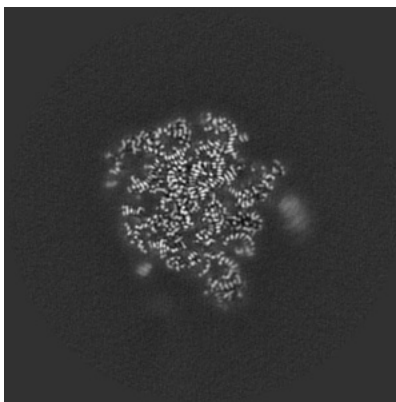


Z Index: 238

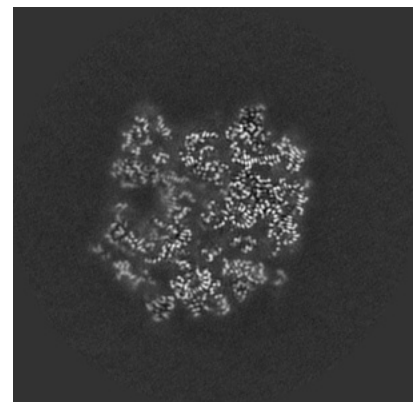
### 6.3.2 Raw map



X Index: 288



Y Index: 313



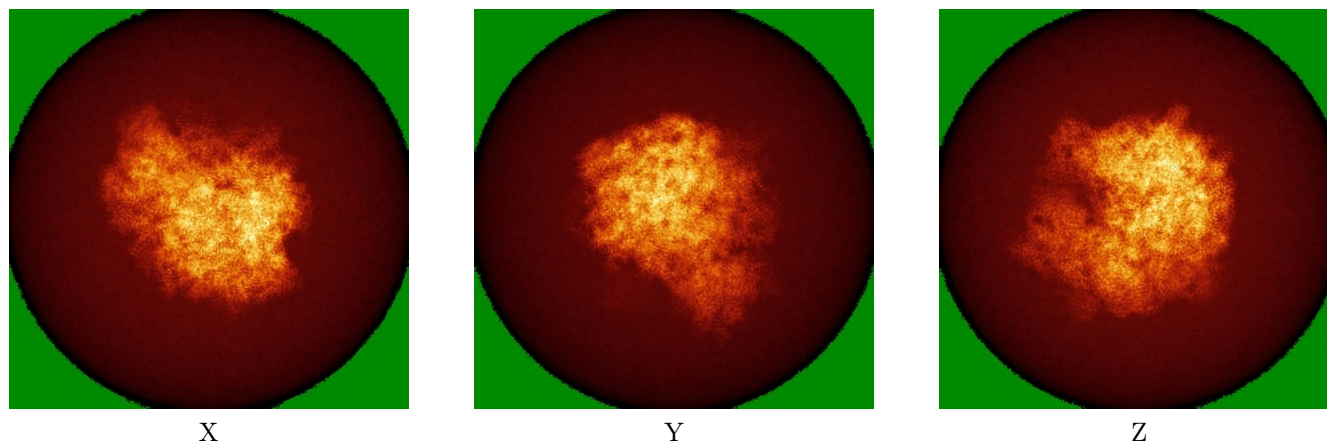
Z Index: 275

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

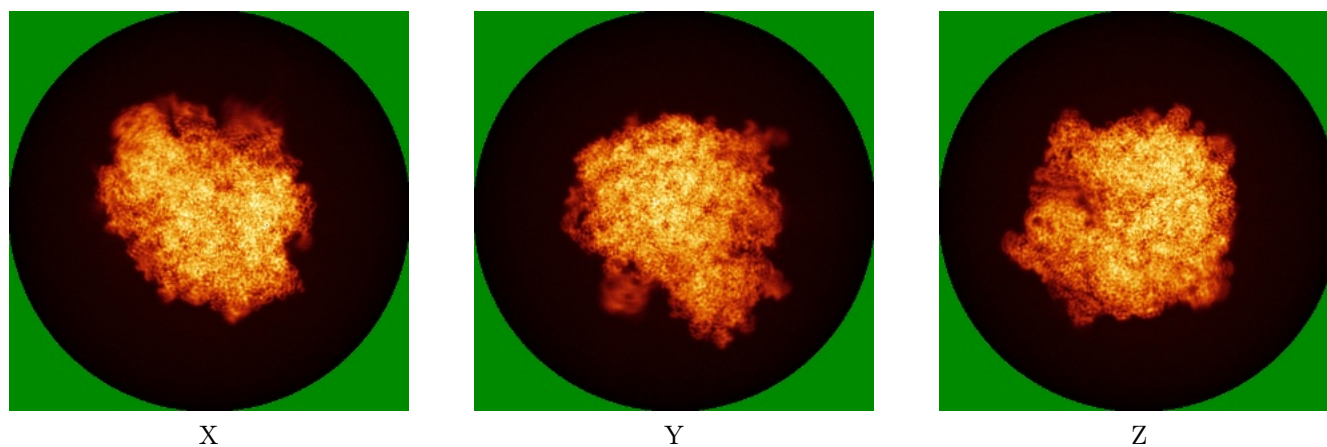


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

### 6.4.1 Primary map



### 6.4.2 Raw map



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 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

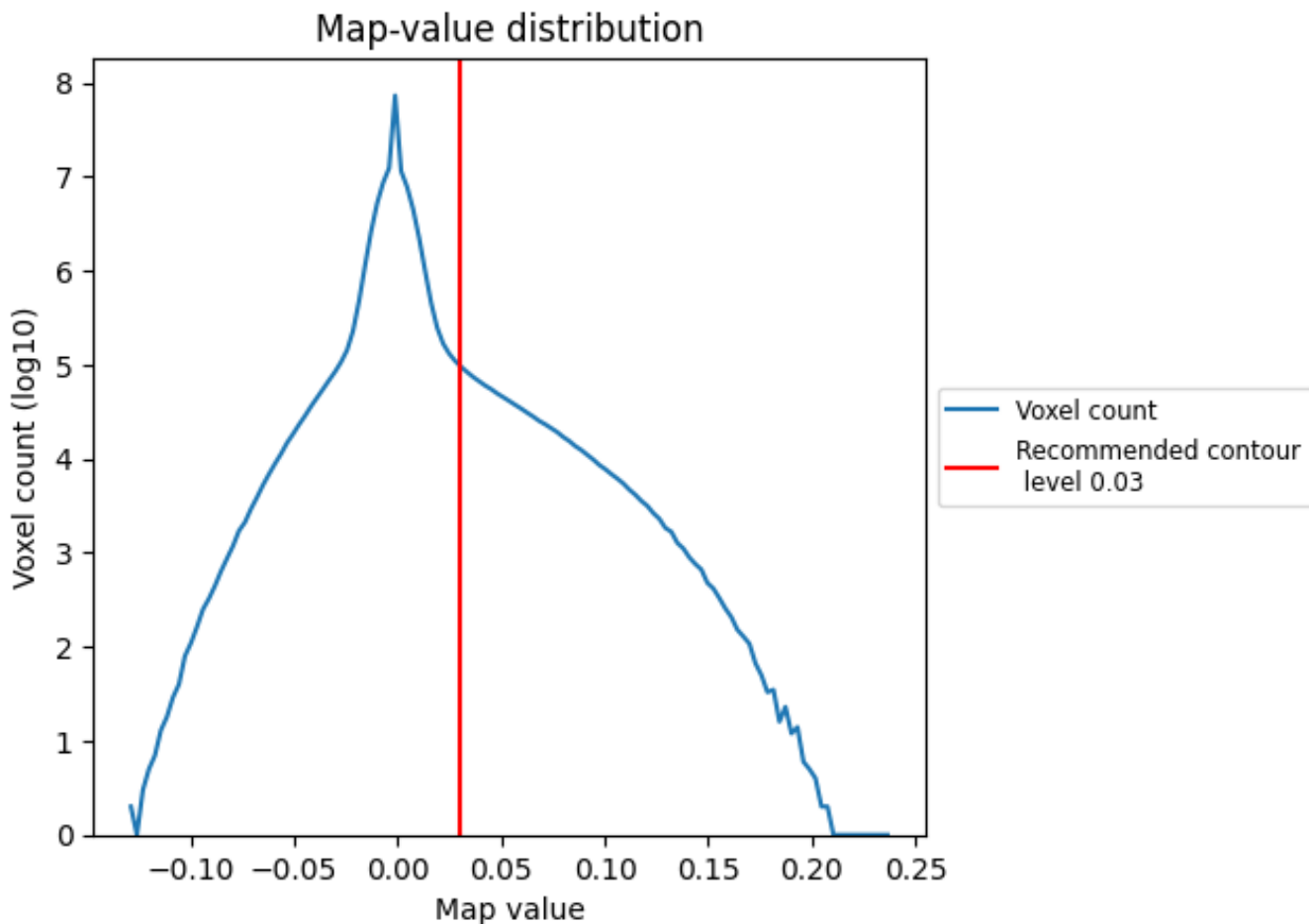
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

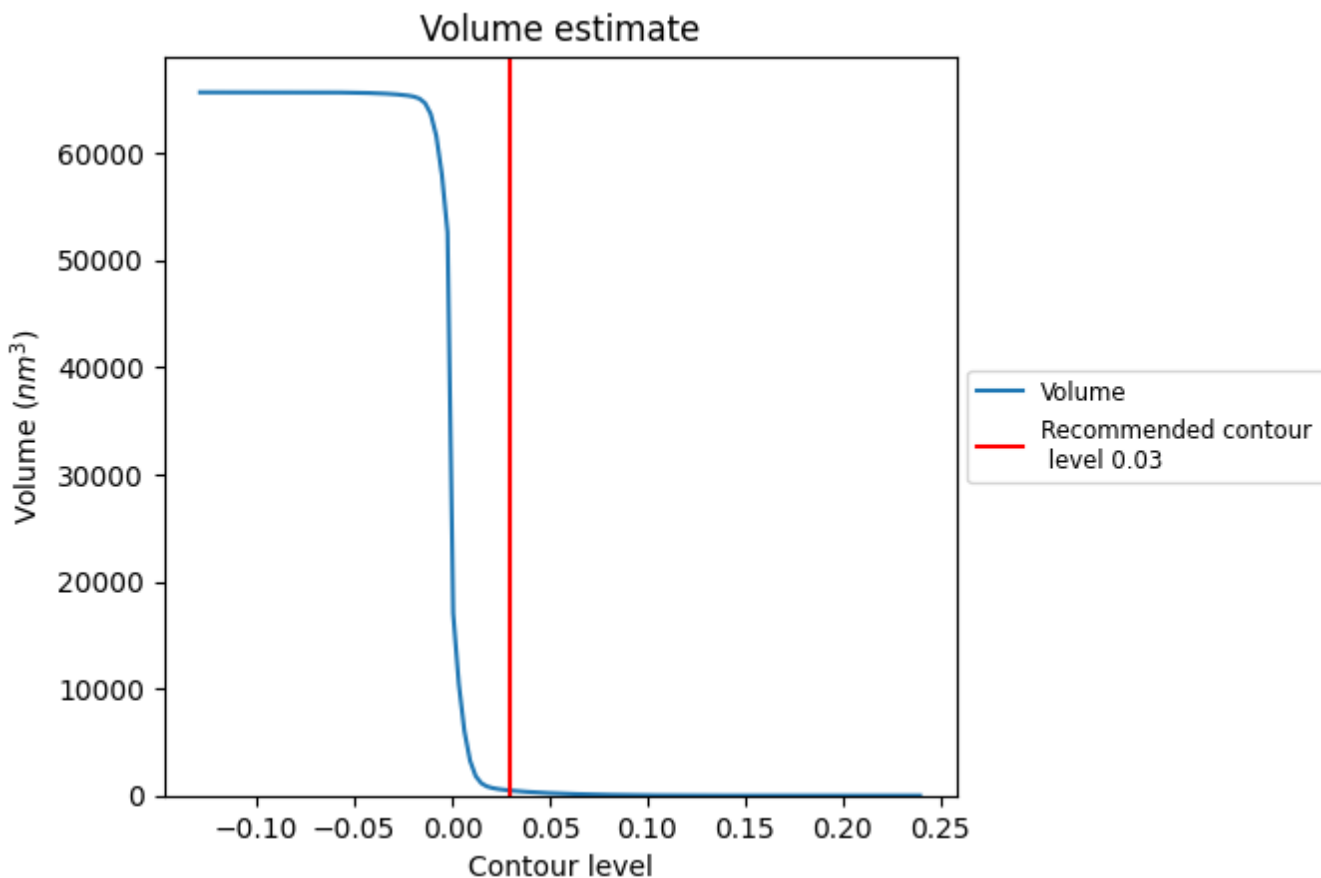
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

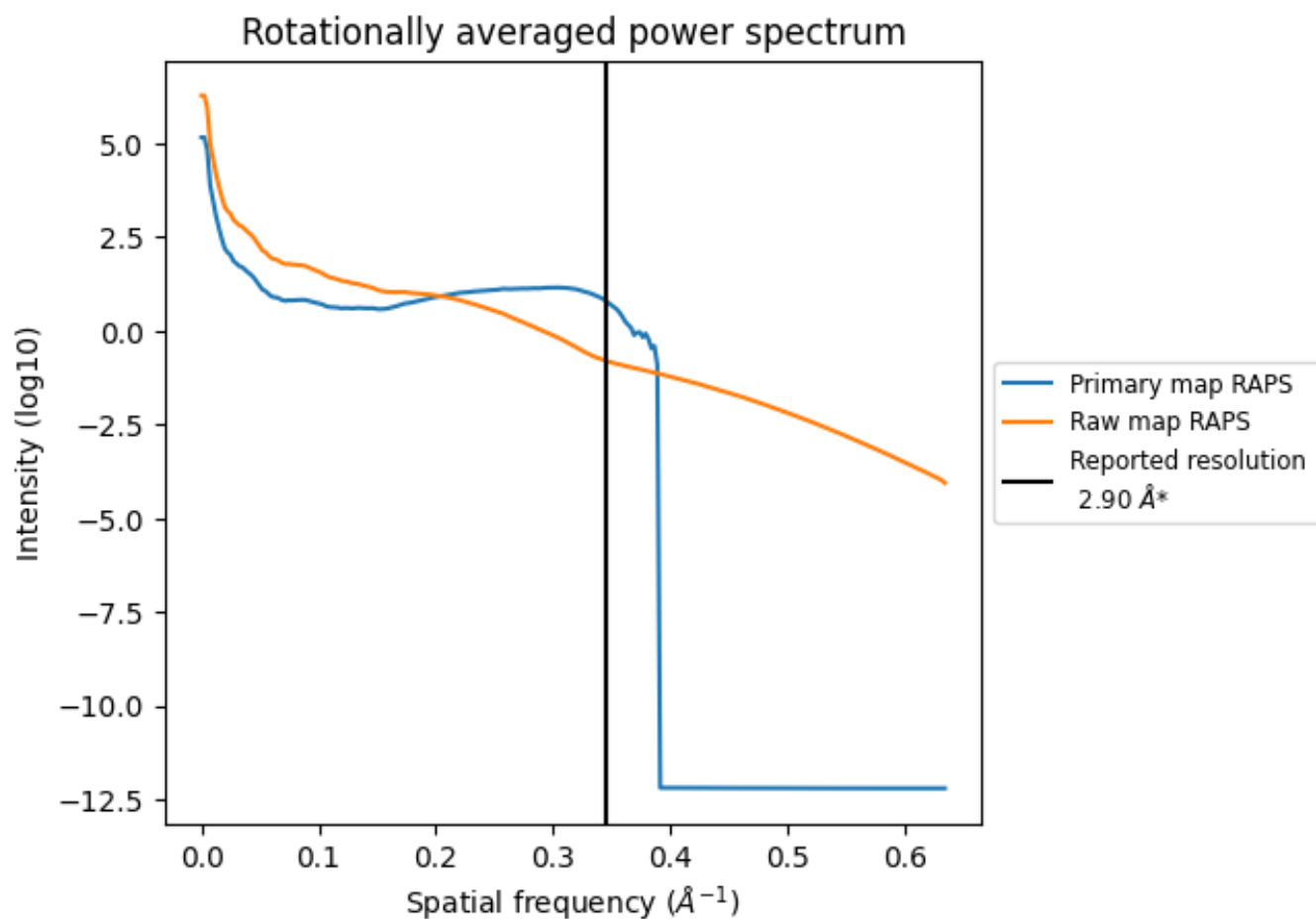
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 470 nm<sup>3</sup>; this corresponds to an approximate mass of 425 kDa.

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

### 7.3 Rotationally averaged power spectrum i

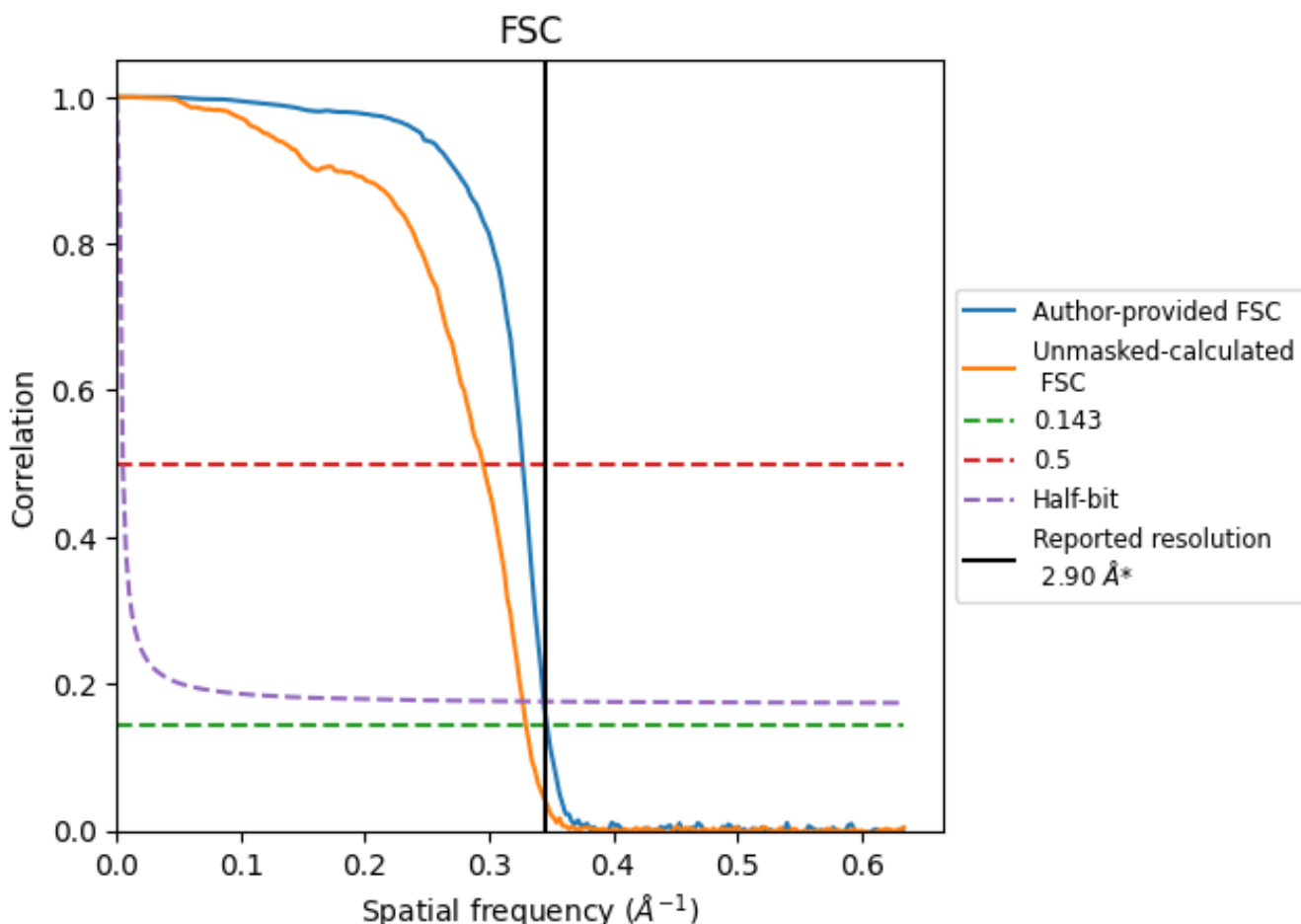


\*Reported resolution corresponds to spatial frequency of  $0.345 \text{ \AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

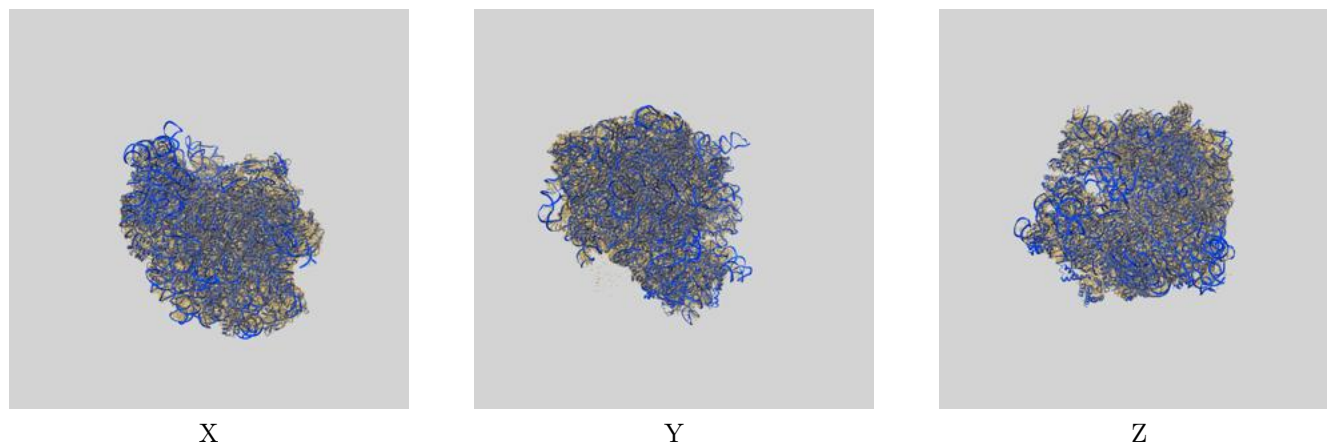
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.88	3.06	2.91
Unmasked-calculated*	3.03	3.39	3.06

\*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-35412 and PDB model 8IFC. Per-residue inclusion information can be found in section 3 on page 17.

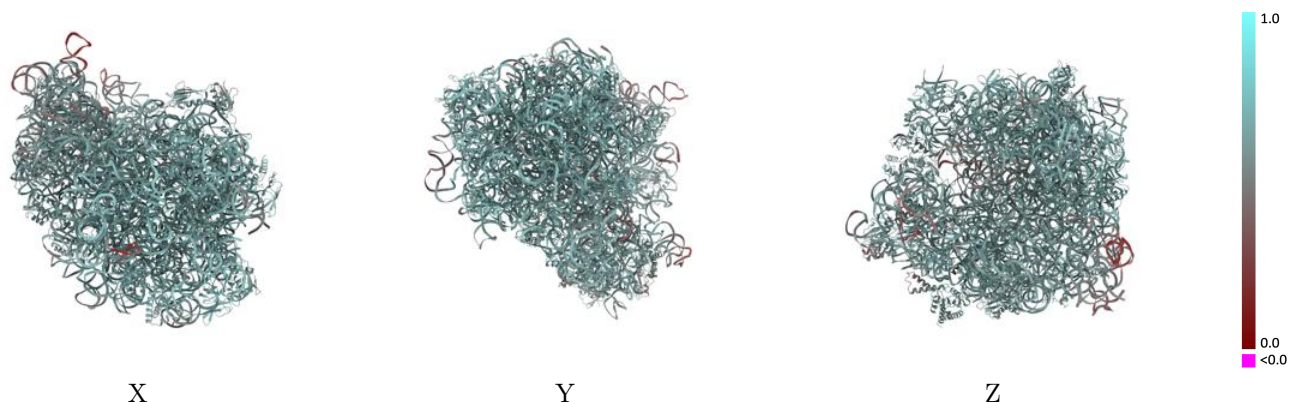
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.03 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.

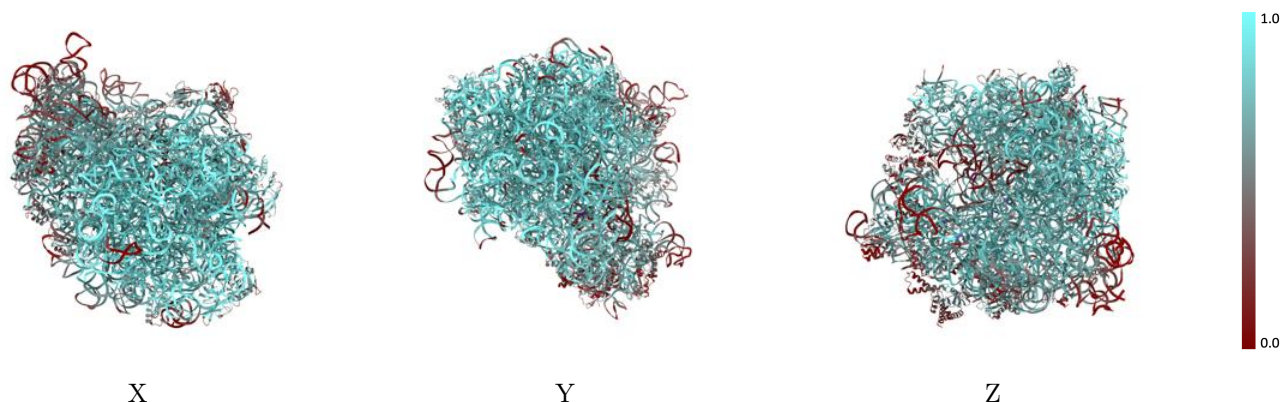


## 9.2 Q-score mapped to coordinate model [i](#)



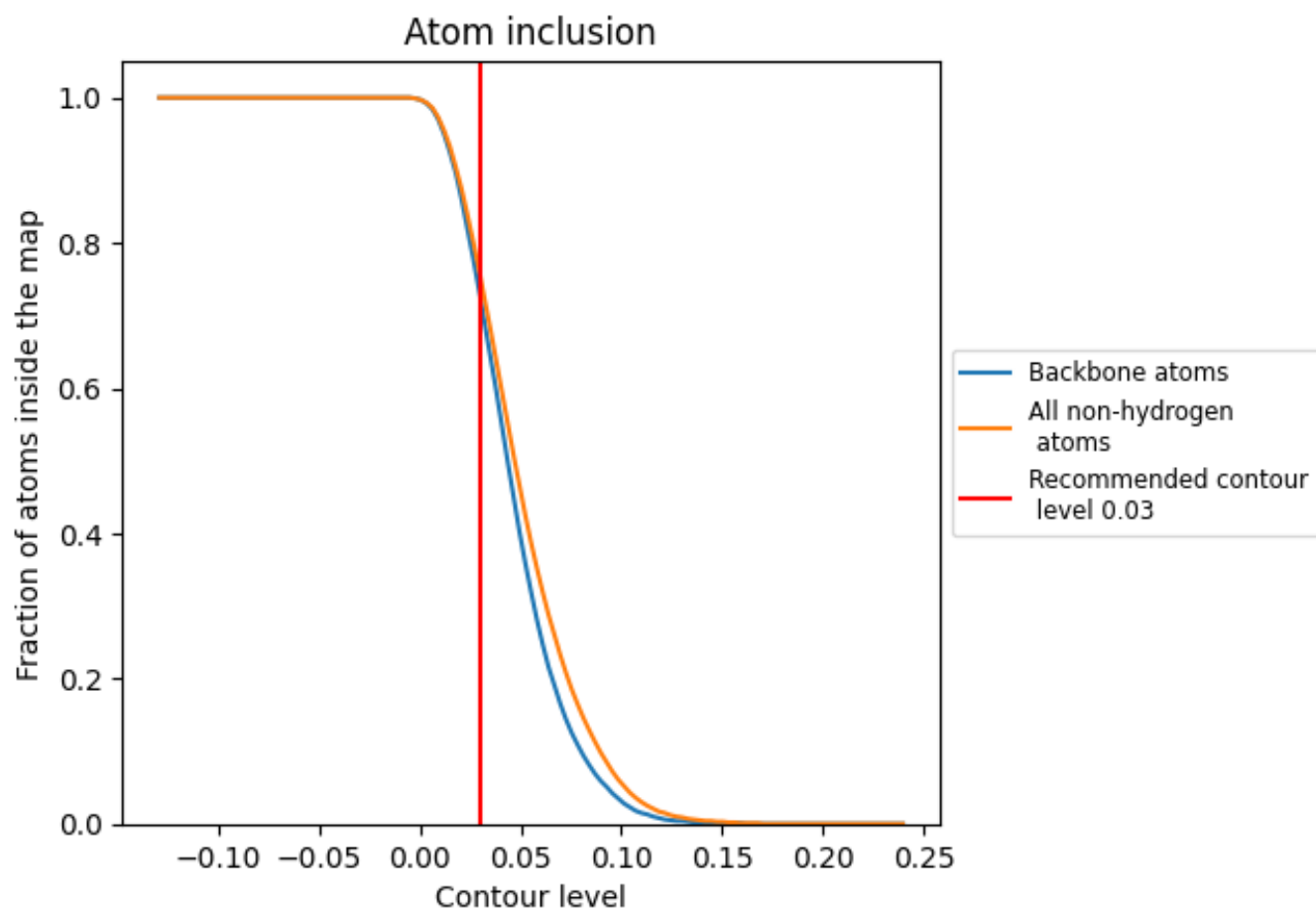
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 76% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7550	 0.6200
0	 0.7160	 0.6410
1	 0.8930	 0.6600
2	 0.8900	 0.6640
3	 0.8260	 0.6570
4	 0.2620	 0.5450
5	 0.3380	 0.5220
6	 0.4090	 0.5360
7	 0.7620	 0.6160
A	 0.7190	 0.5990
B	 0.3700	 0.5720
C	 0.5790	 0.6140
D	 0.4030	 0.5900
E	 0.7030	 0.6370
F	 0.4940	 0.6020
G	 0.3440	 0.5500
H	 0.6930	 0.6270
I	 0.5100	 0.5960
J	 0.4000	 0.5570
K	 0.6030	 0.5960
L	 0.6210	 0.5980
M	 0.5060	 0.6010
N	 0.6060	 0.6010
O	 0.6130	 0.6220
P	 0.5200	 0.5850
Q	 0.5630	 0.6040
R	 0.5870	 0.6060
S	 0.5260	 0.5930
T	 0.4670	 0.5800
U	 0.3470	 0.5320
a	 0.8760	 0.6380
b	 0.7920	 0.6190
c	 0.8680	 0.6620
d	 0.8350	 0.6550
e	 0.7280	 0.6350



*Continued on next page...*

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Chain	Atom inclusion	Q-score
f	 0.4780	 0.6000
g	 0.4500	 0.5800
h	 0.4200	 0.5690
i	 0.8260	 0.6550
j	 0.8210	 0.6540
k	 0.7860	 0.6450
l	 0.8050	 0.6520
m	 0.8890	 0.6570
n	 0.6900	 0.6230
o	 0.7570	 0.6480
p	 0.8680	 0.6570
q	 0.7670	 0.6440
r	 0.8170	 0.6460
s	 0.7380	 0.6380
t	 0.6570	 0.6210
u	 0.6370	 0.6290
v	 0.8360	 0.6590
w	 0.8050	 0.6460
x	 0.6240	 0.6090
y	 0.7830	 0.6380
z	 0.8000	 0.6480