



## Full wwPDB EM Validation Report ⓘ

Nov 5, 2022 – 10:22 PM EDT

PDB ID : 5WFK  
EMDB ID : EMD-8828  
Title : 70S ribosome-EF-Tu H84A complex with GTP and near-cognate tRNA (Complex C3)  
Authors : Fislage, M.; Frank, J.  
Deposited on : 2017-07-12  
Resolution : 3.40 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:

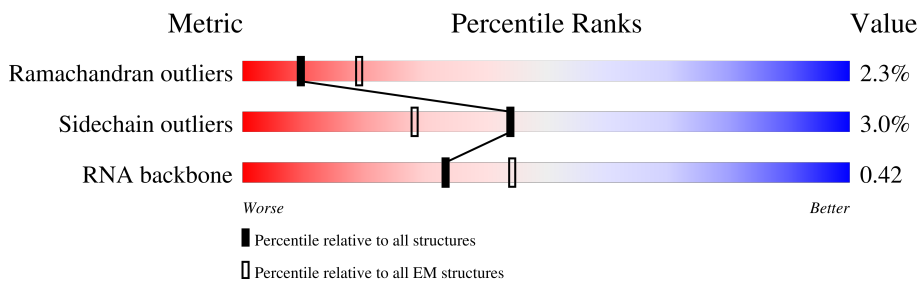
EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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	2903	
2	B	120	
3	C	271	
4	D	208	
5	E	200	
6	F	177	
7	G	174	
8	H	149	


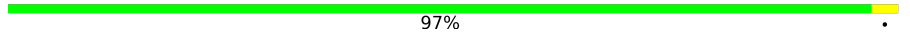
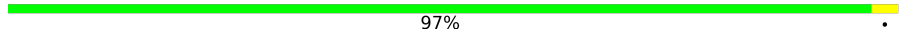
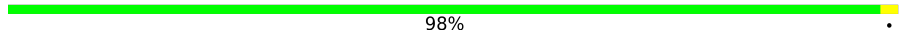
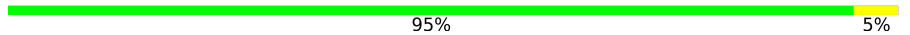

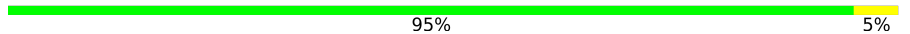
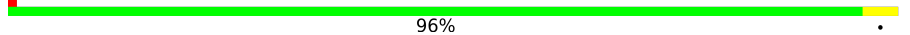







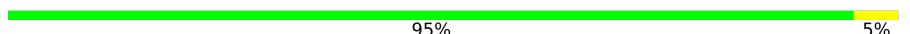
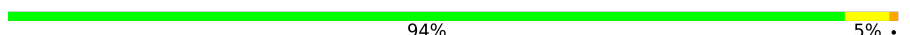

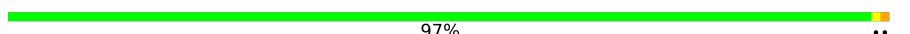
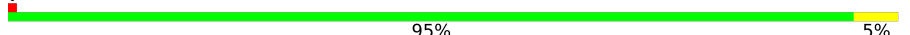





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Mol	Chain	Length	Quality of chain
9	I	141	 19% 91% 9%
10	J	141	 98%
11	K	122	 93% 7%
12	L	143	 93% 6%
13	M	136	 98%
14	N	119	 97%
15	O	116	 97%
16	P	114	 99%
17	Q	115	 98%
18	R	102	 95% 5%
19	S	109	 98%
20	T	92	 97%
21	U	102	 96%
22	V	92	 97%
23	W	75	 93% 7%
24	X	77	 100%
25	Y	60	 98%
26	Z	56	 98%
27	0	55	 96%
28	1	51	 96%
29	2	45	 93% 7%
30	3	64	 95% 5%
31	4	38	 100%
32	5	131	 72% 92% 8%
33	6	66	 95% 5%

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Mol	Chain	Length	Quality of chain
34	a	1540	 70% 30%
35	b	218	 97%
36	c	206	 97%
37	d	205	 98%
38	e	157	 95% 5%
39	f	100	 92% 8%
40	g	151	 95% 5%
41	h	129	 96%
42	i	127	 92% 7%
43	j	98	 88% 12%
44	k	116	 94% 5%
45	l	121	 93% 6%
46	m	115	 96%
47	n	101	 92% 8%
48	o	88	 92% 8%
49	p	82	 95% 5%
50	q	80	 94% 5%
51	r	65	 88% 12%
52	s	79	 97%
53	t	85	 95% 5%
54	u	65	 78% 20%
55	v	77	 74% 23%
55	w	77	 52% 43% 5%
56	x	12	 42% 58%
57	y	76	 22% 42% 49% 9%

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Mol	Chain	Length	Quality of chain
58	z	393	 <p>A horizontal bar chart showing the quality of chain. The bar is divided into two segments: a red segment on the left labeled '42%' and a green segment on the right labeled '97%'. The green segment extends almost to the end of the bar, with a small yellow segment at the very end.</p>

## 2 Entry composition [i](#)

There are 64 unique types of molecules in this entry. The entry contains 154325 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	2900	62277	27788	11459	20130	2900	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	120	2572	1145	471	836	120	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	120	A	-	expression tag	GB 1324665466

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	208	1557	974	287	293	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	200	1544	969	282	289	4	0	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	174	Total	C	N	O	S	0	0
			1304	820	239	243	2		

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

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

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	141	Total	C	N	O	S	0	0
			1120	708	211	197	4		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	143	Total	C	N	O	S	0	0
			1043	649	206	186	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

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

- Molecule 14 is a protein called 50S ribosomal protein L17.

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

- Molecule 15 is a protein called 50S ribosomal protein L18.

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

- Molecule 16 is a protein called 50S ribosomal protein L19.

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

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	Q	115	933	595	190	148	0	0

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	R	102	810	513	152	143	2	0	0

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	S	109	845	526	162	154	3	0	0

- Molecule 20 is a protein called 50S ribosomal protein L23.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	T	92	730	461	138	130	1	0	0

- Molecule 21 is a protein called 50S ribosomal protein L24.

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

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	V	92	739	471	135	131	2	0	0

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	W	75	572	355	116	100	1	0	0

- Molecule 24 is a protein called 50S ribosomal protein L28.

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

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Y	60	494	305	96	91	2	0	0

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Z	56	434	273	85	74	2	0	0

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	0	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	51	Total	C	N	O	S	0	0
			417	269	76	72			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	45	Total	C	N	O	S	0	0
			367	222	88	55	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 33 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 34 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
34	a	1540	33095	14768	6067	10718	1542	2	0

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	b	218	1704	1081	305	311	7	0	0

- Molecule 36 is a protein called 30S ribosomal protein S3.

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

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	e	157	1164	724	221	213	6	1	0

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	f	100	817	515	148	148	6	0	0

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

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

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	k	116	869	535	173	158	3	0	0

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	l	121	940	581	193	162	4	0	0

- Molecule 46 is a protein called 30S ribosomal protein S13.

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

- Molecule 47 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	n	101	810	502	165	140	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP P0AG59

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	q	80	648	411	121	113	3	0	0

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	r	65	535	339	100	95	1	0	0

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	s	79	637	408	120	107	2	0	0

- Molecule 53 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	t	85	665	411	137	114	3	0	0

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 55 is a RNA chain called tRNA-fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace	
55	v	77	Total	C	N	O	P	S	0	0
			1644	733	297	536	77	1		
55	w	77	Total	C	N	O	P	S	0	0
			1644	733	297	536	77	1		

- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	12	Total	C	N	O	P	0	0
			252	113	43	84	12		

- Molecule 57 is a RNA chain called Phe-tRNA-Phe.

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

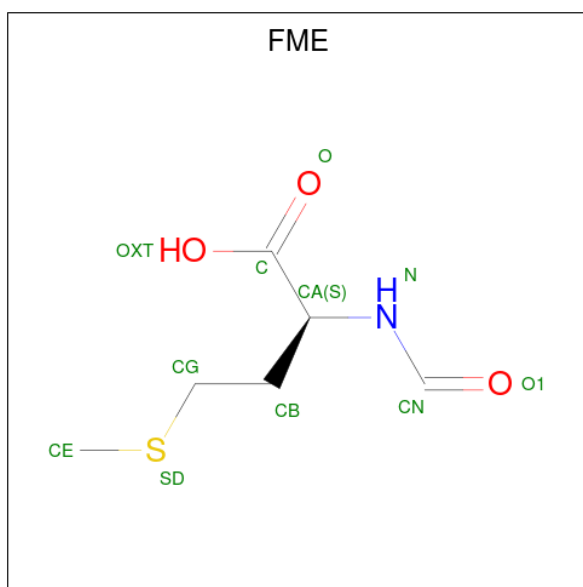
- Molecule 58 is a protein called Elongation factor Tu 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	z	393	Total	C	N	O	S	0	0
			3031	1915	522	581	13		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	47	ASN	ASP	conflict	UNP P0CE48
z	84	ALA	HIS	engineered mutation	UNP P0CE48

- Molecule 59 is N-FORMYLMETHIONINE (three-letter code: FME) (formula: C<sub>6</sub>H<sub>11</sub>NO<sub>3</sub>S).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
59	A	1	10	6	1	2	1	0

- Molecule 60 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
60	A	965	965	965	0
60	B	27	27	27	0
60	C	2	2	2	0
60	D	3	3	3	0
60	E	3	3	3	0
60	H	1	1	1	0
60	L	3	3	3	0
60	N	1	1	1	0
60	Q	1	1	1	0
60	S	1	1	1	0
60	U	1	1	1	0

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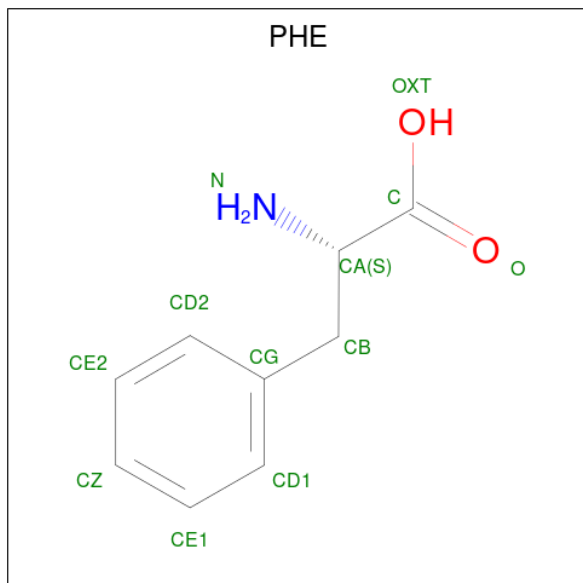
Mol	Chain	Residues	Atoms		AltConf
60	X	1	Total 1	Mg 1	0
60	Y	1	Total 1	Mg 1	0
60	Z	1	Total 1	Mg 1	0
60	0	1	Total 1	Mg 1	0
60	2	1	Total 1	Mg 1	0
60	4	1	Total 1	Mg 1	0
60	a	375	Total 375	Mg 375	0
60	c	1	Total 1	Mg 1	0
60	d	1	Total 1	Mg 1	0
60	e	1	Total 1	Mg 1	0
60	f	1	Total 1	Mg 1	0
60	g	1	Total 1	Mg 1	0
60	i	2	Total 2	Mg 2	0
60	k	1	Total 1	Mg 1	0
60	l	1	Total 1	Mg 1	0
60	m	1	Total 1	Mg 1	0
60	q	1	Total 1	Mg 1	0
60	v	9	Total 9	Mg 9	0
60	w	3	Total 3	Mg 3	0
60	x	1	Total 1	Mg 1	0

- Molecule 61 is POTASSIUM ION (three-letter code: K) (formula: K).



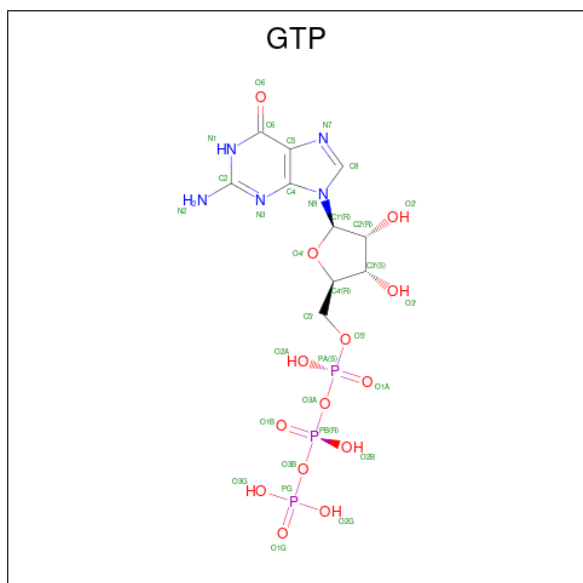
Mol	Chain	Residues	Atoms	AltConf
61	A	1	Total K 1 1	0

- Molecule 62 is PHENYLALANINE (three-letter code: PHE) (formula: C<sub>9</sub>H<sub>11</sub>NO<sub>2</sub>).



Mol	Chain	Residues	Atoms	AltConf
62	z	1	Total C N O 11 9 1 1	0

- Molecule 63 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
63	z	1	32	10	5	14	3	0

- Molecule 64 is water.

Mol	Chain	Residues	Atoms		AltConf
64	A	293	Total 293	O 293	0
64	B	8	Total 8	O 8	0
64	C	3	Total 3	O 3	0
64	D	3	Total 3	O 3	0
64	L	1	Total 1	O 1	0
64	N	1	Total 1	O 1	0
64	O	1	Total 1	O 1	0
64	Q	1	Total 1	O 1	0
64	V	1	Total 1	O 1	0
64	W	1	Total 1	O 1	0
64	0	1	Total 1	O 1	0
64	2	1	Total 1	O 1	0
64	3	1	Total 1	O 1	0
64	a	93	Total 93	O 93	0
64	l	1	Total 1	O 1	0
64	m	1	Total 1	O 1	0
64	o	1	Total 1	O 1	0
64	s	3	Total 3	O 3	0
64	t	1	Total 1	O 1	0

*Continued on next page...*

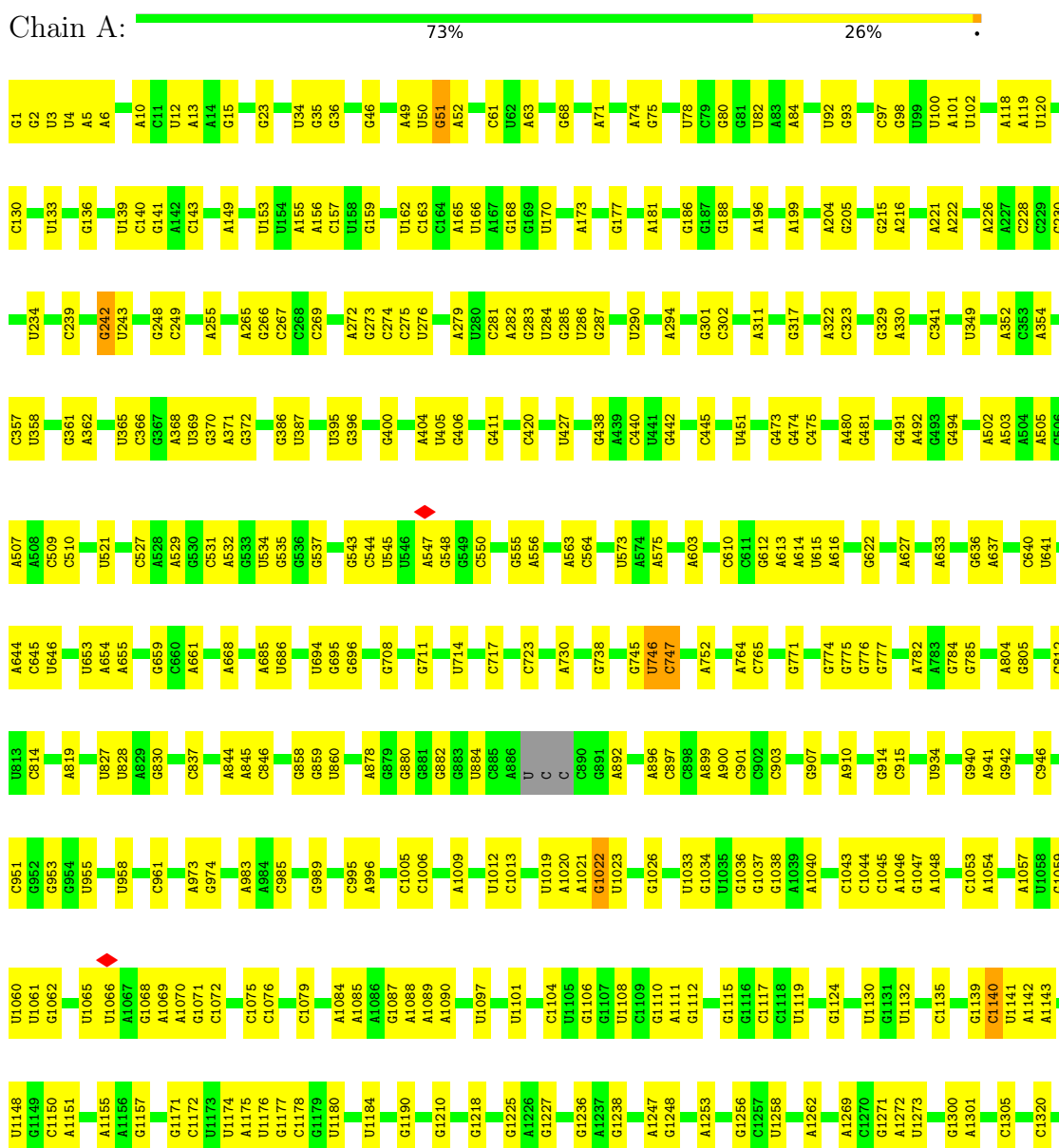
*Continued from previous page...*

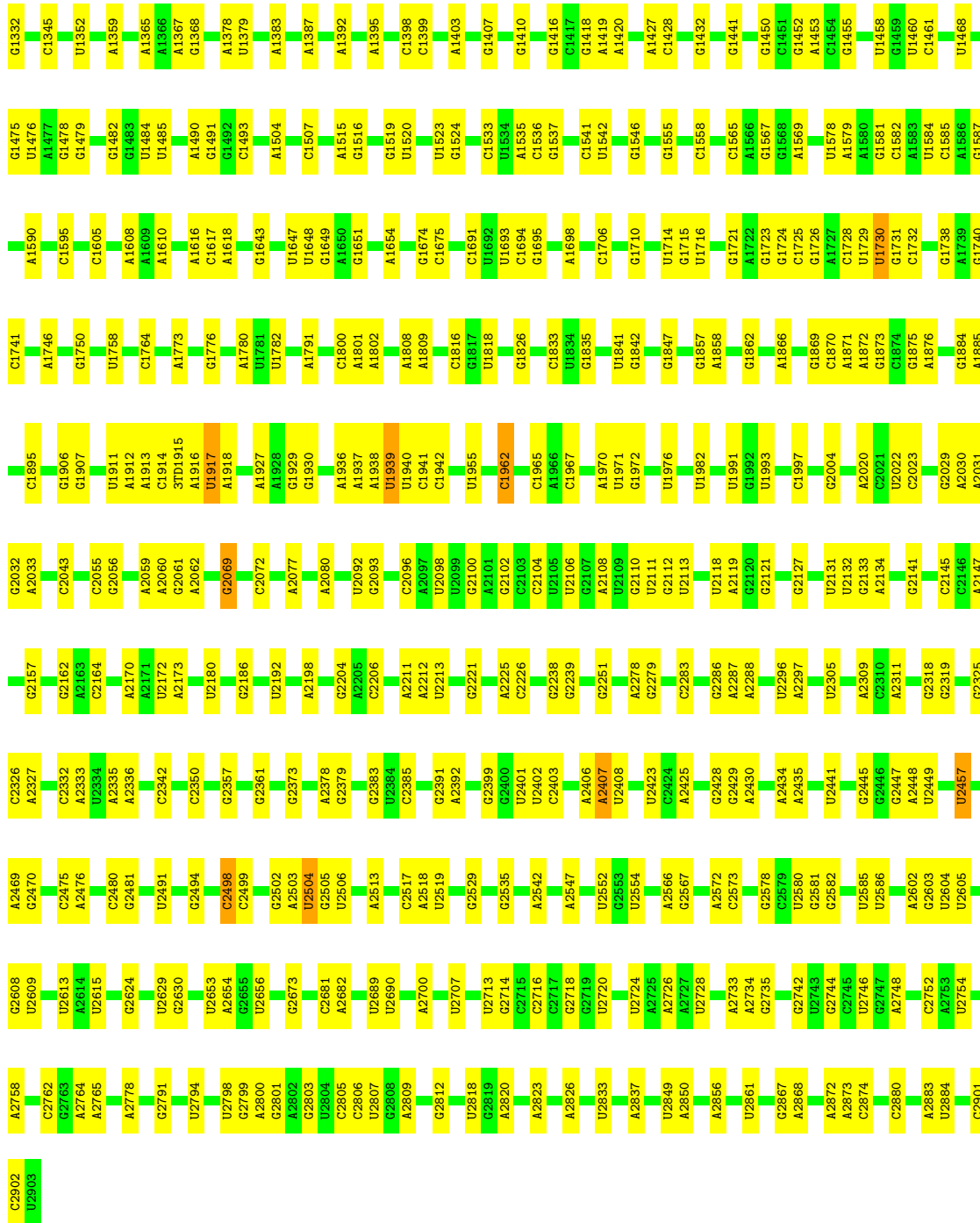
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
64	u	1	Total 1	O 1	0
64	v	1	Total 1	O 1	0
64	w	1	Total 1	O 1	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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: 23S rRNA





- Molecule 2: 5S rRNA



- Molecule 3: 50S ribosomal protein L2

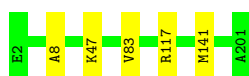




- Molecule 4: 50S ribosomal protein L3



- Molecule 5: 50S ribosomal protein L4



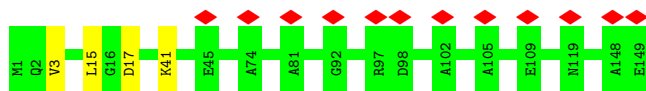
- Molecule 6: 50S ribosomal protein L5



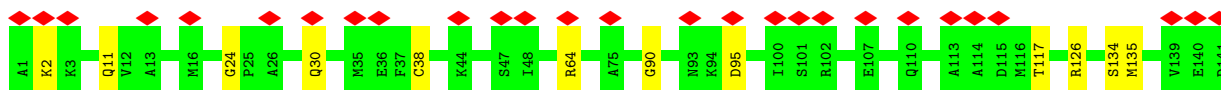
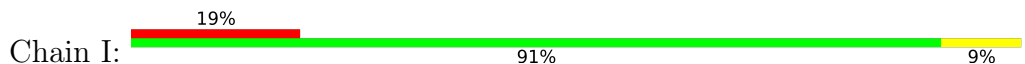
- Molecule 7: 50S ribosomal protein L6



- Molecule 8: 50S ribosomal protein L9



- Molecule 9: 50S ribosomal protein L11



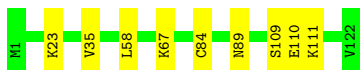
- Molecule 10: 50S ribosomal protein L13





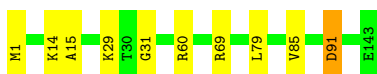
- Molecule 11: 50S ribosomal protein L14

Chain K: 93% 7%



- Molecule 12: 50S ribosomal protein L15

Chain L: 93% 6%



- Molecule 13: 50S ribosomal protein L16

Chain M: 98%



- Molecule 14: 50S ribosomal protein L17

Chain N: 97%



- Molecule 15: 50S ribosomal protein L18

Chain O: 97%



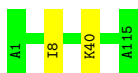
- Molecule 16: 50S ribosomal protein L19

Chain P: 99%



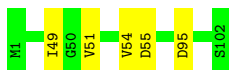
- Molecule 17: 50S ribosomal protein L20

Chain Q: 98%



- Molecule 18: 50S ribosomal protein L21

Chain R: 95% 5%



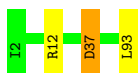
- Molecule 19: 50S ribosomal protein L22

Chain S: 98% .



- Molecule 20: 50S ribosomal protein L23

Chain T: 97% ..



- Molecule 21: 50S ribosomal protein L24

Chain U: 96% .



- Molecule 22: 50S ribosomal protein L25

Chain V: 97% .



- Molecule 23: 50S ribosomal protein L27

Chain W: 93% 7%



- Molecule 24: 50S ribosomal protein L28

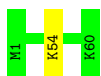
Chain X: 100%

There are no outlier residues recorded for this chain.



- Molecule 25: 50S ribosomal protein L29

Chain Y:  98%



- Molecule 26: 50S ribosomal protein L30

Chain Z:  98%



- Molecule 27: 50S ribosomal protein L32

Chain 0:  96%



- Molecule 28: 50S ribosomal protein L33

Chain 1:  96%



- Molecule 29: 50S ribosomal protein L34

Chain 2:  93% 7%



- Molecule 30: 50S ribosomal protein L35

Chain 3:  95% 5%

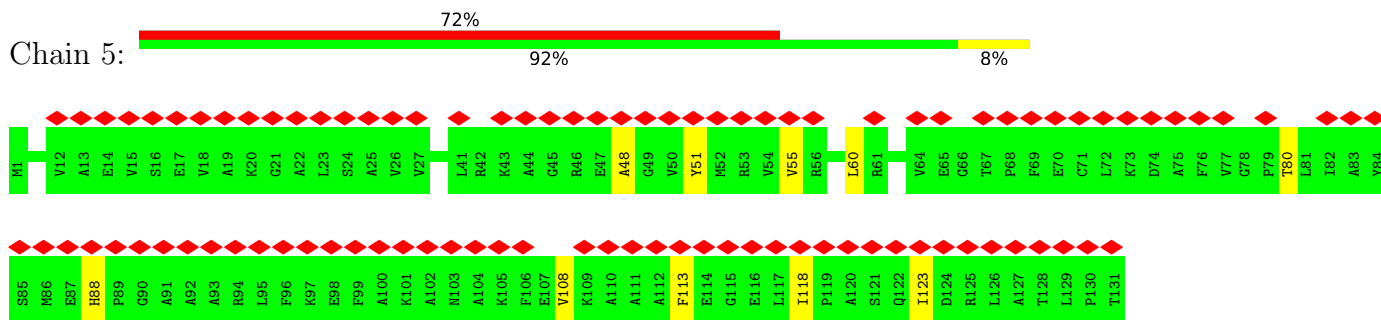


- Molecule 31: 50S ribosomal protein L36

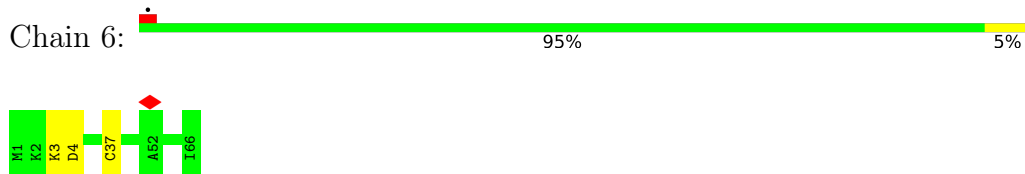
Chain 4:  100%

There are no outlier residues recorded for this chain.

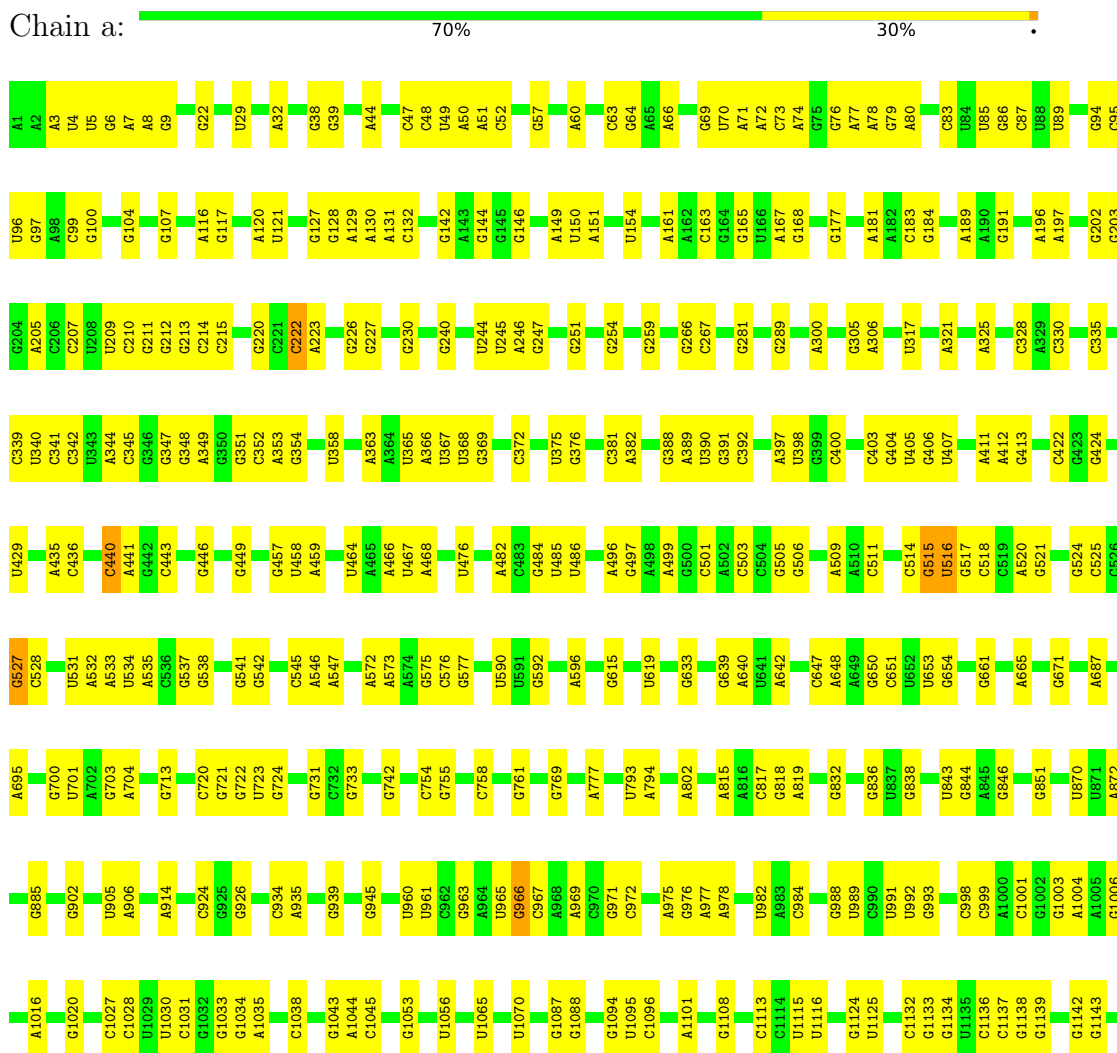
- Molecule 32: 50S ribosomal protein L10

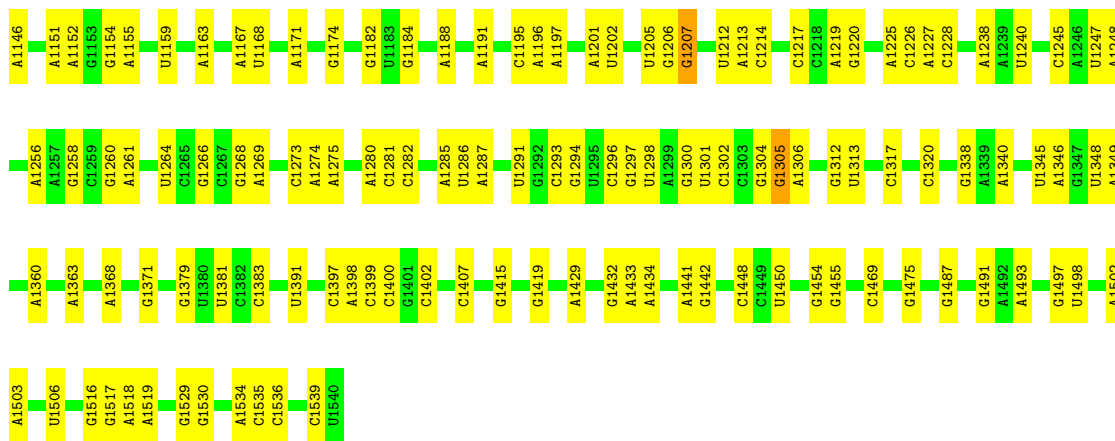


• Molecule 33: 50S ribosomal protein L31



• Molecule 34: 16S rRNA





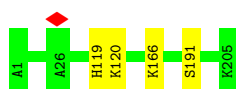
- Molecule 35: 30S ribosomal protein S2



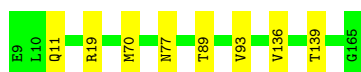
- Molecule 36: 30S ribosomal protein S3



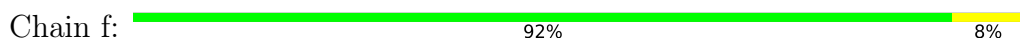
- Molecule 37: 30S ribosomal protein S4



- Molecule 38: 30S ribosomal protein S5



- Molecule 39: 30S ribosomal protein S6



- Molecule 40: 30S ribosomal protein S7

Chain g:  95% 5%

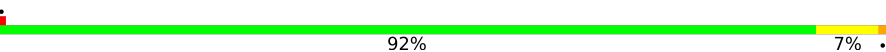


- Molecule 41: 30S ribosomal protein S8

Chain h:  96% .




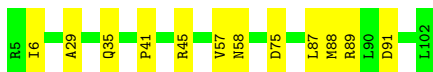
- Molecule 42: 30S ribosomal protein S9

Chain i:  92% 7% .



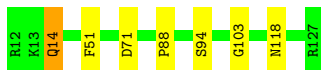
- Molecule 43: 30S ribosomal protein S10

Chain j:  88% 12%



- Molecule 44: 30S ribosomal protein S11

Chain k:  94% 5% .



- Molecule 45: 30S ribosomal protein S12

Chain l:  93% 6% .



- Molecule 46: 30S ribosomal protein S13

Chain m:  96% .



- Molecule 47: 30S ribosomal protein S14

Chain n:  92% 8%



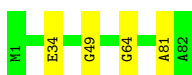
- Molecule 48: 30S ribosomal protein S15

Chain o:  92% 8%



- Molecule 49: 30S ribosomal protein S16

Chain p:  95% 5%




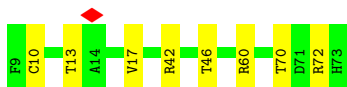
- Molecule 50: 30S ribosomal protein S17

Chain q:  94% 5%



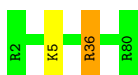
- Molecule 51: 30S ribosomal protein S18

Chain r:  88% 12%



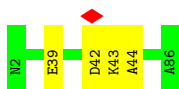
- Molecule 52: 30S ribosomal protein S19

Chain s:  97% ..

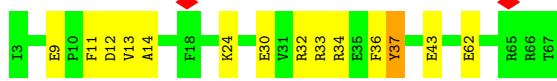
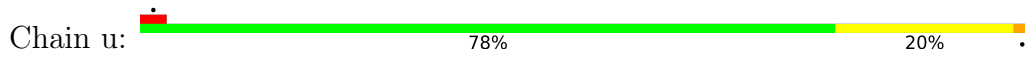


- Molecule 53: 30S ribosomal protein S20

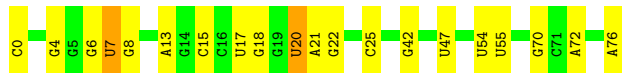
Chain t:  95% 5%



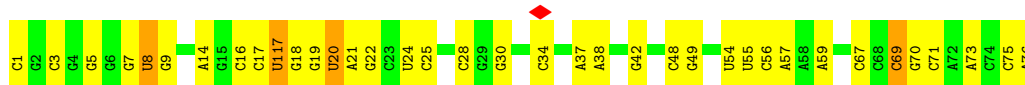
- Molecule 54: 30S ribosomal protein S21



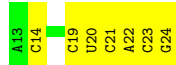
• Molecule 55: tRNA-fMet



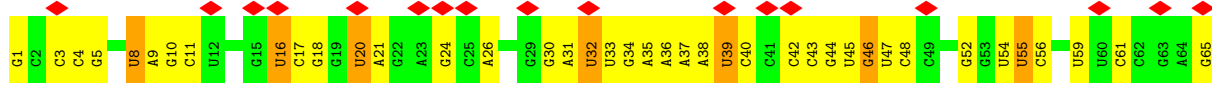
• Molecule 55: tRNA-fMet



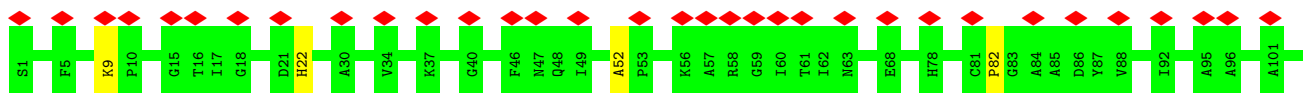
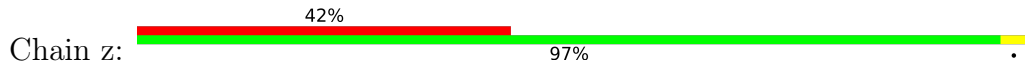
• Molecule 56: mRNA

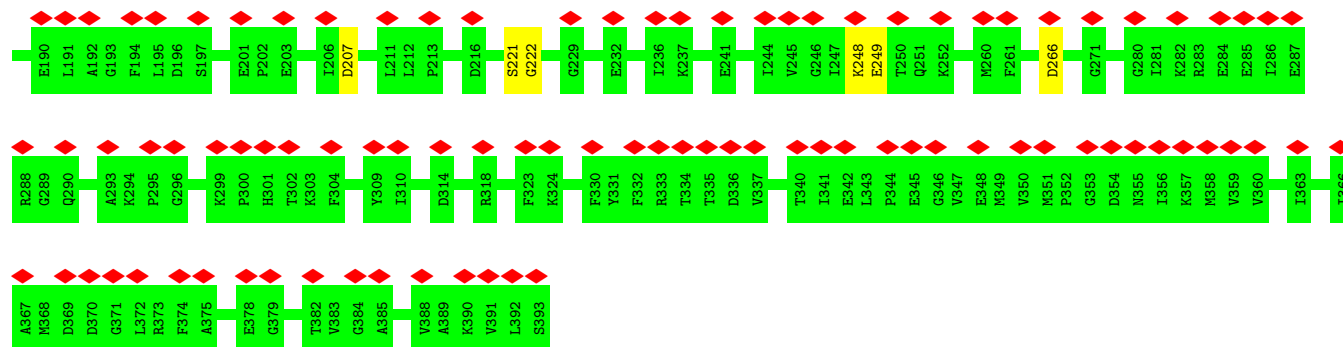


• Molecule 57: Phe-tRNA-Phe



• Molecule 58: Elongation factor Tu 2





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	17523	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	67	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	51020	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.178	Depositor
Minimum map value	-0.106	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.00651	Depositor
Map size (Å)	390.04, 390.04, 390.04	wwPDB
Map dimensions	398, 398, 398	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.98, 0.98, 0.98	Depositor



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UR3, 3TD, OMC, GTP, OMG, 6MZ, 7MG, FME, 4SU, MIA, PSU, 2MA, 1MG, 5MC, OMU, K, MA6, H2U, 2MG, 5MU, MG, 4OC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.21	1/69174 (0.0%)	0.68	6/107907 (0.0%)
2	B	0.27	1/2876 (0.0%)	0.67	1/4483 (0.0%)
3	C	0.35	0/2121	0.65	0/2852
4	D	0.36	0/1578	0.61	0/2124
5	E	0.35	0/1563	0.59	0/2103
6	F	0.38	0/1434	0.61	0/1926
7	G	0.35	0/1324	0.54	0/1794
8	H	0.37	0/1122	0.50	0/1515
9	I	0.41	0/1046	0.59	0/1410
10	J	0.35	0/1143	0.58	0/1540
11	K	0.35	0/947	0.63	0/1268
12	L	0.37	0/1052	0.66	0/1401
13	M	0.36	0/1093	0.61	0/1460
14	N	0.40	0/964	0.70	0/1289
15	O	0.37	0/902	0.60	0/1209
16	P	0.35	0/929	0.62	0/1242
17	Q	0.38	0/946	0.65	0/1260
18	R	0.36	0/823	0.62	0/1100
19	S	0.34	0/852	0.65	0/1142
20	T	0.36	0/736	0.63	0/984
21	U	0.35	0/787	0.58	0/1051
22	V	0.35	0/752	0.58	1/1008 (0.1%)
23	W	0.36	0/579	0.63	0/767
24	X	0.37	0/635	0.63	0/848
25	Y	0.38	0/495	0.60	0/658
26	Z	0.37	0/438	0.60	0/586
27	0	0.34	0/440	0.63	0/588
28	1	0.34	0/424	0.55	0/565
29	2	0.42	0/370	0.78	0/487
30	3	0.34	0/513	0.59	0/676
31	4	0.33	0/303	0.63	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	5	0.42	0/1001	0.60	0/1350
33	6	0.39	0/531	0.55	0/709
34	a	0.22	0/36776	0.70	7/57365 (0.0%)
35	b	0.37	0/1735	0.52	0/2338
36	c	0.36	0/1651	0.57	0/2225
37	d	0.37	0/1665	0.60	0/2227
38	e	0.36	0/1180	0.60	0/1587
39	f	0.38	0/835	0.60	0/1128
40	g	0.37	0/1195	0.60	0/1602
41	h	0.35	0/989	0.60	0/1326
42	i	0.38	0/1034	0.65	0/1375
43	j	0.36	0/796	0.66	0/1077
44	k	0.36	0/885	0.61	0/1195
45	l	0.37	0/954	0.68	0/1282
46	m	0.37	0/900	0.64	0/1204
47	n	0.38	0/822	0.64	0/1095
48	o	0.36	0/722	0.59	0/964
49	p	0.37	0/659	0.62	0/884
50	q	0.37	0/657	0.62	0/881
51	r	0.39	0/544	0.58	0/731
52	s	0.38	0/652	0.60	0/877
53	t	0.37	0/671	0.60	0/888
54	u	0.45	0/550	0.83	0/728
55	v	0.32	1/1747 (0.1%)	0.68	0/2721
55	w	0.98	2/1747 (0.1%)	0.85	4/2721 (0.1%)
56	x	0.21	0/280	0.64	0/433
57	y	0.32	1/1607 (0.1%)	0.65	0/2501
58	z	0.36	0/3086	0.56	0/4175
All	All	0.29	6/164232 (0.0%)	0.67	19/245229 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	w	117	U	O3'-P	-38.77	1.14	1.61
55	v	0	C	OP3-P	-10.19	1.49	1.61
55	w	1	C	OP3-P	-10.19	1.49	1.61
1	A	1	G	OP3-P	-10.16	1.49	1.61
57	y	1	G	OP3-P	-10.16	1.49	1.61
2	B	1	U	OP3-P	-10.09	1.49	1.61

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	w	117	U	P-O3'-C3'	23.71	148.16	119.70
55	w	117	U	OP2-P-O3'	-9.57	84.14	105.20
55	w	117	U	O3'-P-O5'	8.49	120.13	104.00
34	a	515	G	C2'-C3'-O3'	7.46	125.90	109.50
1	A	2407	A	C2'-C3'-O3'	7.18	125.31	109.50
1	A	51	G	C2'-C3'-O3'	6.27	123.73	113.70
34	a	63	C	C2'-C3'-O3'	6.07	123.42	113.70
34	a	1305	G	C2'-C3'-O3'	6.04	123.36	113.70
1	A	242	G	C2'-C3'-O3'	5.98	123.27	113.70
1	A	1022	G	C2'-C3'-O3'	5.50	122.49	113.70
34	a	440	C	C2'-C3'-O3'	5.45	122.43	113.70
1	A	1140	C	C2'-C3'-O3'	5.42	122.38	113.70
34	a	515	G	N9-C1'-C2'	5.40	121.02	114.00
34	a	214	C	C2'-C3'-O3'	5.29	122.17	113.70
2	B	66	A	C4'-C3'-O3'	5.23	123.46	113.00
22	V	18	ARG	NE-CZ-NH1	5.23	122.91	120.30
1	A	1730	U	C2'-C3'-O3'	5.19	122.01	113.70
34	a	222	C	N1-C1'-C2'	5.11	120.64	114.00
55	w	69	C	C2'-C3'-O3'	5.06	121.80	113.70

There are no chirality outliers.

There are no planarity outliers.

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

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

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	269/271 (99%)	240 (89%)	26 (10%)	3 (1%)	14	44
4	D	206/208 (99%)	187 (91%)	16 (8%)	3 (2%)	10	36

*Continued on next page...*

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	198/200 (99%)	181 (91%)	15 (8%)	2 (1%)	15	46
6	F	175/177 (99%)	157 (90%)	18 (10%)	0	100	100
7	G	172/174 (99%)	158 (92%)	14 (8%)	0	100	100
8	H	147/149 (99%)	127 (86%)	17 (12%)	3 (2%)	7	30
9	I	139/141 (99%)	109 (78%)	26 (19%)	4 (3%)	4	24
10	J	139/141 (99%)	132 (95%)	7 (5%)	0	100	100
11	K	120/122 (98%)	105 (88%)	12 (10%)	3 (2%)	5	26
12	L	141/143 (99%)	116 (82%)	20 (14%)	5 (4%)	3	21
13	M	134/136 (98%)	126 (94%)	6 (4%)	2 (2%)	10	36
14	N	117/119 (98%)	104 (89%)	11 (9%)	2 (2%)	9	34
15	O	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
16	P	112/114 (98%)	98 (88%)	14 (12%)	0	100	100
17	Q	113/115 (98%)	112 (99%)	1 (1%)	0	100	100
18	R	100/102 (98%)	80 (80%)	16 (16%)	4 (4%)	3	18
19	S	107/109 (98%)	96 (90%)	10 (9%)	1 (1%)	17	49
20	T	90/92 (98%)	81 (90%)	8 (9%)	1 (1%)	14	44
21	U	100/102 (98%)	86 (86%)	11 (11%)	3 (3%)	4	23
22	V	90/92 (98%)	83 (92%)	6 (7%)	1 (1%)	14	44
23	W	73/75 (97%)	66 (90%)	6 (8%)	1 (1%)	11	37
24	X	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
25	Y	58/60 (97%)	54 (93%)	4 (7%)	0	100	100
26	Z	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
27	0	53/55 (96%)	49 (92%)	3 (6%)	1 (2%)	8	31
28	1	49/51 (96%)	42 (86%)	6 (12%)	1 (2%)	7	30
29	2	43/45 (96%)	42 (98%)	1 (2%)	0	100	100
30	3	62/64 (97%)	57 (92%)	5 (8%)	0	100	100
31	4	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
32	5	129/131 (98%)	98 (76%)	21 (16%)	10 (8%)	1	6
33	6	64/66 (97%)	55 (86%)	8 (12%)	1 (2%)	9	34
35	b	216/218 (99%)	187 (87%)	23 (11%)	6 (3%)	5	24
36	c	204/206 (99%)	187 (92%)	12 (6%)	5 (2%)	5	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	d	203/205 (99%)	181 (89%)	20 (10%)	2 (1%)	15	46
38	e	156/157 (99%)	133 (85%)	20 (13%)	3 (2%)	8	31
39	f	98/100 (98%)	85 (87%)	9 (9%)	4 (4%)	3	18
40	g	149/151 (99%)	132 (89%)	13 (9%)	4 (3%)	5	26
41	h	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
42	i	125/127 (98%)	94 (75%)	26 (21%)	5 (4%)	3	18
43	j	96/98 (98%)	73 (76%)	15 (16%)	8 (8%)	1	5
44	k	114/116 (98%)	100 (88%)	9 (8%)	5 (4%)	2	16
45	l	119/121 (98%)	96 (81%)	15 (13%)	8 (7%)	1	8
46	m	113/115 (98%)	102 (90%)	9 (8%)	2 (2%)	8	32
47	n	99/101 (98%)	85 (86%)	9 (9%)	5 (5%)	2	14
48	o	86/88 (98%)	79 (92%)	2 (2%)	5 (6%)	1	11
49	p	80/82 (98%)	69 (86%)	8 (10%)	3 (4%)	3	19
50	q	78/80 (98%)	68 (87%)	9 (12%)	1 (1%)	12	39
51	r	63/65 (97%)	52 (82%)	7 (11%)	4 (6%)	1	9
52	s	77/79 (98%)	67 (87%)	9 (12%)	1 (1%)	12	39
53	t	83/85 (98%)	75 (90%)	6 (7%)	2 (2%)	6	28
54	u	63/65 (97%)	40 (64%)	14 (22%)	9 (14%)	0	1
58	z	391/393 (100%)	349 (89%)	32 (8%)	10 (3%)	5	26
All	All	6219/6322 (98%)	5471 (88%)	605 (10%)	143 (2%)	9	28

All (143) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	K	89	ASN
11	K	111	LYS
12	L	31	GLY
18	R	51	VAL
21	U	6	ARG
32	5	60	LEU
32	5	123	ILE
36	c	96	VAL
40	g	64	ALA
42	i	46	VAL
42	i	90	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
43	j	57	VAL
43	j	89	ARG
44	k	88	PRO
44	k	94	SER
48	o	45	HIS
48	o	47	LYS
53	t	39	GLU
54	u	13	VAL
54	u	14	ALA
54	u	37	TYR
4	D	58	ASN
5	E	8	ALA
5	E	83	VAL
9	I	24	GLY
18	R	49	ILE
18	R	54	VAL
18	R	55	ASP
20	T	37	ASP
36	c	156	LEU
38	e	77	ASN
40	g	20	GLU
40	g	129	ASN
42	i	57	VAL
42	i	108	ARG
43	j	29	ALA
44	k	51	PHE
45	l	42	LYS
45	l	75	GLU
45	l	88	ASP
46	m	7	ASN
47	n	2	LYS
47	n	22	LYS
47	n	38	ASP
47	n	55	SER
47	n	90	ARG
49	p	81	ALA
51	r	10	CYS
51	r	17	VAL
54	u	9	GLU
54	u	36	PHE
3	C	13	ARG
4	D	31	ALA

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	D	154	LYS
9	I	38	CYS
9	I	64	ARG
12	L	15	ALA
14	N	59	SER
22	V	58	SER
27	0	2	VAL
32	5	88	HIS
33	6	4	ASP
35	b	73	ARG
37	d	191	SER
40	g	19	SER
42	i	124	PRO
43	j	35	GLN
43	j	41	PRO
44	k	14	GLN
44	k	103	GLY
45	l	35	ARG
49	p	64	GLY
50	q	17	GLU
51	r	46	THR
52	s	36	ARG
54	u	24	LYS
54	u	30	GLU
58	z	249	GLU
8	H	15	LEU
8	H	41	LYS
12	L	29	LYS
12	L	91	ASP
13	M	69	PRO
14	N	117	ASP
21	U	97	SER
32	5	48	ALA
32	5	55	VAL
32	5	80	THR
32	5	118	ILE
35	b	192	PRO
36	c	147	GLY
37	d	166	LYS
38	e	89	THR
39	f	33	GLU
39	f	63	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
43	j	58	ASN
45	l	43	LYS
45	l	77	SER
46	m	102	LYS
48	o	13	GLU
51	r	70	THR
54	u	11	PHE
54	u	12	ASP
58	z	180	GLY
58	z	221	SER
58	z	222	GLY
8	H	3	VAL
11	K	35	VAL
13	M	6	ARG
19	S	65	ASP
23	W	72	ASN
32	5	51	TYR
32	5	113	PHE
35	b	11	ALA
35	b	86	CYS
36	c	95	GLY
38	e	93	VAL
39	f	92	THR
43	j	75	ASP
45	l	46	SER
48	o	2	LEU
48	o	48	ASP
49	p	49	GLY
53	t	44	ALA
58	z	9	LYS
58	z	207	ASP
3	C	120	ASP
3	C	121	ALA
32	5	108	VAL
35	b	63	LYS
35	b	151	LYS
39	f	99	ALA
43	j	6	ILE
45	l	33	CYS
58	z	126	GLY
58	z	248	LYS
36	c	144	GLY

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Mol	Chain	Res	Type
58	z	52	ALA
12	L	85	VAL
21	U	38	ILE
28	1	4	ILE
58	z	82	PRO
9	I	90	GLY

### 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	
3	C	216/216 (100%)	207 (96%)	9 (4%)	30	59
4	D	163/163 (100%)	153 (94%)	10 (6%)	18	48
5	E	164/164 (100%)	161 (98%)	3 (2%)	59	79
6	F	148/148 (100%)	143 (97%)	5 (3%)	37	65
7	G	135/135 (100%)	133 (98%)	2 (2%)	65	82
8	H	114/114 (100%)	113 (99%)	1 (1%)	78	90
9	I	109/109 (100%)	101 (93%)	8 (7%)	14	43
10	J	115/115 (100%)	112 (97%)	3 (3%)	46	72
11	K	103/103 (100%)	97 (94%)	6 (6%)	20	50
12	L	102/102 (100%)	96 (94%)	6 (6%)	19	49
13	M	109/109 (100%)	108 (99%)	1 (1%)	78	90
14	N	99/99 (100%)	96 (97%)	3 (3%)	41	68
15	O	86/86 (100%)	83 (96%)	3 (4%)	36	65
16	P	99/99 (100%)	98 (99%)	1 (1%)	76	88
17	Q	88/88 (100%)	86 (98%)	2 (2%)	50	74
18	R	84/84 (100%)	83 (99%)	1 (1%)	71	85
19	S	92/92 (100%)	91 (99%)	1 (1%)	73	86
20	T	79/79 (100%)	76 (96%)	3 (4%)	33	61
21	U	83/83 (100%)	82 (99%)	1 (1%)	71	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	V	77/77 (100%)	76 (99%)	1 (1%)	69	84
23	W	57/57 (100%)	53 (93%)	4 (7%)	15	44
24	X	67/67 (100%)	67 (100%)	0	100	100
25	Y	55/55 (100%)	54 (98%)	1 (2%)	59	79
26	Z	47/47 (100%)	46 (98%)	1 (2%)	53	76
27	0	46/46 (100%)	45 (98%)	1 (2%)	52	75
28	1	46/46 (100%)	45 (98%)	1 (2%)	52	75
29	2	37/37 (100%)	34 (92%)	3 (8%)	11	38
30	3	51/51 (100%)	48 (94%)	3 (6%)	19	49
31	4	34/34 (100%)	34 (100%)	0	100	100
32	5	100/100 (100%)	100 (100%)	0	100	100
33	6	59/59 (100%)	57 (97%)	2 (3%)	37	65
35	b	180/180 (100%)	179 (99%)	1 (1%)	86	94
36	c	170/170 (100%)	169 (99%)	1 (1%)	86	94
37	d	172/172 (100%)	170 (99%)	2 (1%)	71	85
38	e	120/119 (101%)	115 (96%)	5 (4%)	30	59
39	f	87/87 (100%)	83 (95%)	4 (5%)	27	57
40	g	124/124 (100%)	121 (98%)	3 (2%)	49	74
41	h	104/104 (100%)	99 (95%)	5 (5%)	25	56
42	i	105/105 (100%)	99 (94%)	6 (6%)	20	50
43	j	86/86 (100%)	82 (95%)	4 (5%)	26	57
44	k	89/89 (100%)	86 (97%)	3 (3%)	37	65
45	l	102/102 (100%)	99 (97%)	3 (3%)	42	69
46	m	93/93 (100%)	90 (97%)	3 (3%)	39	67
47	n	83/83 (100%)	80 (96%)	3 (4%)	35	63
48	o	76/76 (100%)	74 (97%)	2 (3%)	46	72
49	p	65/65 (100%)	64 (98%)	1 (2%)	65	82
50	q	74/74 (100%)	69 (93%)	5 (7%)	16	45
51	r	56/56 (100%)	52 (93%)	4 (7%)	14	44
52	s	70/70 (100%)	68 (97%)	2 (3%)	42	69
53	t	65/65 (100%)	63 (97%)	2 (3%)	40	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	u	55/55 (100%)	49 (89%)	6 (11%)	6	23
58	z	325/325 (100%)	323 (99%)	2 (1%)	86	94
All	All	5165/5164 (100%)	5012 (97%)	153 (3%)	44	68

All (153) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	12	ARG
3	C	35	LYS
3	C	38	LYS
3	C	42	ARG
3	C	69	ASN
3	C	85	ASN
3	C	212	TRP
3	C	241	LYS
3	C	269	ARG
4	D	12	THR
4	D	39	ASP
4	D	59	ARG
4	D	77	ARG
4	D	99	GLU
4	D	118	PHE
4	D	148	GLN
4	D	150	GLN
4	D	151	THR
4	D	200	ASP
5	E	47	LYS
5	E	117	ARG
5	E	141	MET
6	F	70	ARG
6	F	87	LYS
6	F	91	ARG
6	F	112	ASP
6	F	132	ARG
7	G	63	GLN
7	G	121	THR
8	H	17	ASP
9	I	2	LYS
9	I	11	GLN
9	I	30	GLN
9	I	95	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	I	117	THR
9	I	126	ARG
9	I	134	SER
9	I	135	MET
10	J	3	THR
10	J	61	LYS
10	J	80	HIS
11	K	23	LYS
11	K	58	LEU
11	K	67	LYS
11	K	84	CYS
11	K	109	SER
11	K	110	GLU
12	L	1	MET
12	L	14	LYS
12	L	60	ARG
12	L	69	ARG
12	L	79	LEU
12	L	91	ASP
13	M	110	GLU
14	N	35	LYS
14	N	69	ARG
14	N	117	ASP
15	O	13	ARG
15	O	62	LEU
15	O	104	GLN
16	P	38	ARG
17	Q	8	ILE
17	Q	40	LYS
18	R	95	ASP
19	S	57	ASN
20	T	12	ARG
20	T	37	ASP
20	T	93	LEU
21	U	65	GLN
22	V	42	LEU
23	W	8	ASN
23	W	15	LYS
23	W	21	ARG
23	W	68	LYS
25	Y	54	LYS
26	Z	44	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
27	0	53	VAL
28	1	31	GLU
29	2	22	MET
29	2	41	ARG
29	2	43	THR
30	3	51	LYS
30	3	53	ASP
30	3	61	LEU
33	6	3	LYS
33	6	37	CYS
35	b	21	TYR
36	c	182	ASP
37	d	119	HIS
37	d	120	LYS
38	e	11	GLN
38	e	19	ARG
38	e	70	MET
38	e	136	VAL
38	e	139	THR
39	f	38	ARG
39	f	39	LEU
39	f	44	ARG
39	f	91	ARG
40	g	2	ARG
40	g	11	ILE
40	g	78	ARG
41	h	54	THR
41	h	79	ARG
41	h	106	SER
41	h	110	MET
41	h	120	LEU
42	i	10	ARG
42	i	41	GLU
42	i	42	THR
42	i	44	ARG
42	i	108	ARG
42	i	129	ARG
43	j	45	ARG
43	j	87	LEU
43	j	88	MET
43	j	91	ASP
44	k	14	GLN

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Mol	Chain	Res	Type
44	k	71	ASP
44	k	118	ASN
45	l	23	LEU
45	l	77	SER
45	l	88	ASP
46	m	15	VAL
46	m	47	LEU
46	m	89	ARG
47	n	10	VAL
47	n	40	ASP
47	n	69	ARG
48	o	46	LYS
48	o	88	ARG
49	p	34	GLU
50	q	3	LYS
50	q	4	ILE
50	q	17	GLU
50	q	63	CYS
50	q	66	LEU
51	r	13	THR
51	r	42	ARG
51	r	60	ARG
51	r	72	ARG
52	s	5	LYS
52	s	36	ARG
53	t	42	ASP
53	t	43	LYS
54	u	32	ARG
54	u	33	ARG
54	u	34	ARG
54	u	37	TYR
54	u	43	GLU
54	u	62	GLU
58	z	22	HIS
58	z	266	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	231	HIS
4	D	67	HIS
5	E	41	GLN

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Mol	Chain	Res	Type
5	E	62	GLN
37	d	119	HIS
38	e	121	ASN
45	l	72	ASN
48	o	19	ASN
48	o	45	HIS
53	t	69	ASN
58	z	135	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2893/2903 (99%)	724 (25%)	73 (2%)
2	B	119/120 (99%)	27 (22%)	4 (3%)
34	a	1534/1540 (99%)	460 (29%)	0
55	v	76/77 (98%)	17 (22%)	0
55	w	76/77 (98%)	34 (44%)	0
56	x	11/12 (91%)	7 (63%)	0
57	y	74/76 (97%)	41 (55%)	0
All	All	4783/4805 (99%)	1310 (27%)	77 (1%)

All (1310) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	G
1	A	3	U
1	A	4	U
1	A	5	A
1	A	6	A
1	A	10	A
1	A	12	U
1	A	13	A
1	A	15	G
1	A	23	G
1	A	34	U
1	A	35	G
1	A	36	G
1	A	46	G
1	A	49	A
1	A	50	U
1	A	51	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	52	A
1	A	61	C
1	A	63	A
1	A	68	G
1	A	71	A
1	A	74	A
1	A	75	G
1	A	78	U
1	A	80	G
1	A	82	U
1	A	84	A
1	A	92	U
1	A	93	G
1	A	97	C
1	A	98	G
1	A	100	U
1	A	101	A
1	A	102	U
1	A	118	A
1	A	119	A
1	A	120	U
1	A	130	C
1	A	133	U
1	A	136	G
1	A	139	U
1	A	140	C
1	A	141	G
1	A	143	C
1	A	149	A
1	A	153	U
1	A	155	A
1	A	156	A
1	A	157	C
1	A	159	G
1	A	162	U
1	A	163	C
1	A	165	A
1	A	166	U
1	A	168	G
1	A	170	U
1	A	173	A
1	A	181	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	186	G
1	A	188	G
1	A	196	A
1	A	205	G
1	A	215	G
1	A	216	A
1	A	221	A
1	A	222	A
1	A	226	A
1	A	228	C
1	A	230	G
1	A	234	U
1	A	239	C
1	A	242	G
1	A	243	U
1	A	248	G
1	A	249	C
1	A	255	A
1	A	265	A
1	A	266	G
1	A	267	C
1	A	269	C
1	A	272	A
1	A	273	G
1	A	274	C
1	A	275	C
1	A	276	U
1	A	279	A
1	A	281	C
1	A	282	A
1	A	283	G
1	A	284	U
1	A	285	G
1	A	286	U
1	A	287	G
1	A	290	U
1	A	294	A
1	A	301	G
1	A	302	C
1	A	311	A
1	A	317	G
1	A	322	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	323	C
1	A	329	G
1	A	330	A
1	A	349	U
1	A	352	A
1	A	354	A
1	A	357	C
1	A	358	U
1	A	361	G
1	A	362	A
1	A	365	U
1	A	366	C
1	A	368	A
1	A	369	U
1	A	370	G
1	A	371	A
1	A	372	G
1	A	386	G
1	A	387	U
1	A	395	U
1	A	396	G
1	A	400	G
1	A	404	A
1	A	405	U
1	A	406	G
1	A	411	G
1	A	420	C
1	A	427	U
1	A	438	G
1	A	442	G
1	A	445	C
1	A	451	U
1	A	473	G
1	A	475	C
1	A	480	A
1	A	481	G
1	A	491	G
1	A	492	A
1	A	494	G
1	A	503	A
1	A	505	A
1	A	507	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	509	C
1	A	510	C
1	A	521	U
1	A	527	C
1	A	529	A
1	A	531	C
1	A	532	A
1	A	535	G
1	A	543	G
1	A	544	C
1	A	545	U
1	A	547	A
1	A	548	G
1	A	550	C
1	A	555	G
1	A	556	A
1	A	563	A
1	A	564	C
1	A	573	U
1	A	575	A
1	A	603	A
1	A	610	C
1	A	612	G
1	A	613	A
1	A	614	A
1	A	615	U
1	A	616	A
1	A	622	G
1	A	627	A
1	A	633	A
1	A	636	G
1	A	637	A
1	A	640	C
1	A	644	A
1	A	645	C
1	A	646	U
1	A	653	U
1	A	654	A
1	A	655	A
1	A	659	G
1	A	661	A
1	A	668	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	685	A
1	A	686	U
1	A	694	U
1	A	695	G
1	A	696	G
1	A	708	G
1	A	711	G
1	A	714	U
1	A	717	C
1	A	723	C
1	A	730	A
1	A	738	G
1	A	747	5MC
1	A	752	A
1	A	764	A
1	A	765	C
1	A	771	G
1	A	775	G
1	A	776	G
1	A	777	G
1	A	782	A
1	A	784	G
1	A	785	G
1	A	804	A
1	A	805	G
1	A	812	C
1	A	814	C
1	A	819	A
1	A	827	U
1	A	828	U
1	A	830	G
1	A	837	C
1	A	844	A
1	A	845	A
1	A	846	C
1	A	858	G
1	A	860	U
1	A	878	A
1	A	880	G
1	A	882	G
1	A	892	A
1	A	896	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	897	C
1	A	899	A
1	A	900	A
1	A	901	C
1	A	903	C
1	A	907	G
1	A	910	A
1	A	914	G
1	A	915	C
1	A	934	U
1	A	940	G
1	A	941	A
1	A	942	G
1	A	946	C
1	A	951	C
1	A	953	G
1	A	958	U
1	A	961	C
1	A	973	A
1	A	974	G
1	A	983	A
1	A	985	C
1	A	989	G
1	A	995	C
1	A	996	A
1	A	1005	C
1	A	1006	C
1	A	1009	A
1	A	1012	U
1	A	1013	C
1	A	1019	U
1	A	1020	A
1	A	1021	A
1	A	1022	G
1	A	1023	U
1	A	1026	G
1	A	1033	U
1	A	1034	G
1	A	1036	G
1	A	1037	G
1	A	1038	G
1	A	1040	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1043	C
1	A	1044	C
1	A	1045	C
1	A	1046	A
1	A	1047	G
1	A	1048	A
1	A	1053	C
1	A	1054	A
1	A	1057	A
1	A	1059	G
1	A	1060	U
1	A	1061	U
1	A	1062	G
1	A	1065	U
1	A	1066	U
1	A	1068	G
1	A	1069	A
1	A	1070	A
1	A	1071	G
1	A	1072	C
1	A	1075	C
1	A	1076	C
1	A	1079	C
1	A	1084	A
1	A	1085	A
1	A	1087	G
1	A	1088	A
1	A	1089	A
1	A	1090	A
1	A	1097	U
1	A	1101	U
1	A	1104	C
1	A	1106	G
1	A	1108	U
1	A	1110	G
1	A	1111	A
1	A	1112	G
1	A	1115	G
1	A	1117	C
1	A	1119	U
1	A	1130	U
1	A	1132	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1135	C
1	A	1139	G
1	A	1141	U
1	A	1142	A
1	A	1143	A
1	A	1148	U
1	A	1150	C
1	A	1151	A
1	A	1155	A
1	A	1157	G
1	A	1171	G
1	A	1172	C
1	A	1174	U
1	A	1175	A
1	A	1176	U
1	A	1177	G
1	A	1178	C
1	A	1180	U
1	A	1184	U
1	A	1210	G
1	A	1218	G
1	A	1225	G
1	A	1227	G
1	A	1236	G
1	A	1238	G
1	A	1247	A
1	A	1248	G
1	A	1253	A
1	A	1256	G
1	A	1258	U
1	A	1262	A
1	A	1269	A
1	A	1271	G
1	A	1272	A
1	A	1273	U
1	A	1300	G
1	A	1301	A
1	A	1305	C
1	A	1320	C
1	A	1332	G
1	A	1345	C
1	A	1352	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1359	A
1	A	1365	A
1	A	1367	A
1	A	1368	G
1	A	1378	A
1	A	1379	U
1	A	1383	A
1	A	1387	A
1	A	1392	A
1	A	1395	A
1	A	1398	C
1	A	1403	A
1	A	1407	G
1	A	1410	G
1	A	1416	G
1	A	1418	G
1	A	1419	A
1	A	1420	A
1	A	1427	A
1	A	1428	C
1	A	1441	G
1	A	1450	G
1	A	1452	G
1	A	1453	A
1	A	1455	G
1	A	1458	U
1	A	1460	U
1	A	1461	C
1	A	1468	U
1	A	1475	G
1	A	1476	U
1	A	1478	G
1	A	1479	G
1	A	1482	G
1	A	1484	U
1	A	1485	U
1	A	1490	A
1	A	1491	G
1	A	1493	C
1	A	1504	A
1	A	1507	C
1	A	1515	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1516	G
1	A	1519	G
1	A	1520	U
1	A	1523	U
1	A	1524	G
1	A	1533	C
1	A	1535	A
1	A	1536	C
1	A	1537	G
1	A	1541	C
1	A	1542	U
1	A	1546	G
1	A	1555	G
1	A	1565	C
1	A	1567	G
1	A	1569	A
1	A	1578	U
1	A	1579	A
1	A	1581	G
1	A	1582	C
1	A	1584	U
1	A	1585	C
1	A	1587	G
1	A	1590	A
1	A	1595	C
1	A	1605	C
1	A	1608	A
1	A	1610	A
1	A	1616	A
1	A	1617	C
1	A	1643	G
1	A	1647	U
1	A	1648	U
1	A	1649	G
1	A	1651	G
1	A	1654	A
1	A	1674	G
1	A	1675	C
1	A	1691	C
1	A	1693	U
1	A	1694	C
1	A	1695	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1698	A
1	A	1706	C
1	A	1710	G
1	A	1714	U
1	A	1715	G
1	A	1716	U
1	A	1721	G
1	A	1723	G
1	A	1724	G
1	A	1725	C
1	A	1726	G
1	A	1728	C
1	A	1729	U
1	A	1730	U
1	A	1731	G
1	A	1732	C
1	A	1738	G
1	A	1740	G
1	A	1741	C
1	A	1746	A
1	A	1750	G
1	A	1758	U
1	A	1764	C
1	A	1773	A
1	A	1776	G
1	A	1780	A
1	A	1782	U
1	A	1791	A
1	A	1800	C
1	A	1801	A
1	A	1802	A
1	A	1808	A
1	A	1809	A
1	A	1816	C
1	A	1826	G
1	A	1833	C
1	A	1841	U
1	A	1842	G
1	A	1847	G
1	A	1858	A
1	A	1862	G
1	A	1866	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1869	G
1	A	1870	C
1	A	1871	A
1	A	1872	A
1	A	1873	G
1	A	1875	G
1	A	1876	A
1	A	1884	G
1	A	1885	A
1	A	1895	C
1	A	1906	G
1	A	1907	G
1	A	1912	A
1	A	1913	A
1	A	1914	C
1	A	1916	A
1	A	1917	PSU
1	A	1927	A
1	A	1929	G
1	A	1930	G
1	A	1936	A
1	A	1937	A
1	A	1938	A
1	A	1939	5MU
1	A	1940	U
1	A	1941	C
1	A	1942	C
1	A	1955	U
1	A	1962	5MC
1	A	1965	C
1	A	1967	C
1	A	1970	A
1	A	1971	U
1	A	1972	G
1	A	1982	U
1	A	1991	U
1	A	1993	U
1	A	1997	C
1	A	2004	G
1	A	2020	A
1	A	2022	U
1	A	2023	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2029	G
1	A	2031	A
1	A	2032	G
1	A	2033	A
1	A	2043	C
1	A	2055	C
1	A	2056	G
1	A	2059	A
1	A	2060	A
1	A	2061	G
1	A	2062	A
1	A	2069	7MG
1	A	2072	C
1	A	2077	A
1	A	2080	A
1	A	2092	U
1	A	2093	G
1	A	2096	C
1	A	2098	U
1	A	2100	G
1	A	2102	G
1	A	2104	C
1	A	2106	U
1	A	2108	A
1	A	2110	G
1	A	2111	U
1	A	2112	G
1	A	2113	U
1	A	2118	U
1	A	2119	A
1	A	2121	G
1	A	2127	G
1	A	2131	U
1	A	2132	U
1	A	2133	G
1	A	2134	A
1	A	2141	G
1	A	2145	C
1	A	2147	A
1	A	2157	G
1	A	2162	G
1	A	2164	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2170	A
1	A	2172	U
1	A	2173	A
1	A	2180	U
1	A	2186	G
1	A	2192	U
1	A	2198	A
1	A	2204	G
1	A	2206	C
1	A	2211	A
1	A	2212	A
1	A	2213	U
1	A	2221	G
1	A	2225	A
1	A	2226	C
1	A	2238	G
1	A	2239	G
1	A	2278	A
1	A	2279	G
1	A	2283	C
1	A	2286	G
1	A	2287	A
1	A	2288	A
1	A	2297	A
1	A	2305	U
1	A	2309	A
1	A	2311	A
1	A	2318	G
1	A	2319	G
1	A	2325	G
1	A	2326	C
1	A	2327	A
1	A	2332	C
1	A	2333	A
1	A	2335	A
1	A	2336	A
1	A	2342	C
1	A	2350	C
1	A	2357	G
1	A	2361	G
1	A	2373	G
1	A	2378	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2379	G
1	A	2383	G
1	A	2385	C
1	A	2392	A
1	A	2399	G
1	A	2402	U
1	A	2403	C
1	A	2406	A
1	A	2408	U
1	A	2423	U
1	A	2425	A
1	A	2428	G
1	A	2429	G
1	A	2430	A
1	A	2434	A
1	A	2435	A
1	A	2441	U
1	A	2447	G
1	A	2448	A
1	A	2457	PSU
1	A	2469	A
1	A	2470	G
1	A	2475	C
1	A	2476	A
1	A	2480	C
1	A	2481	G
1	A	2491	U
1	A	2494	G
1	A	2498	OMC
1	A	2499	C
1	A	2502	G
1	A	2504	PSU
1	A	2505	G
1	A	2506	U
1	A	2513	A
1	A	2518	A
1	A	2519	U
1	A	2529	G
1	A	2535	G
1	A	2542	A
1	A	2547	A
1	A	2554	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2566	A
1	A	2567	G
1	A	2572	A
1	A	2573	C
1	A	2578	G
1	A	2582	G
1	A	2585	U
1	A	2586	U
1	A	2602	A
1	A	2603	G
1	A	2608	G
1	A	2609	U
1	A	2613	U
1	A	2615	U
1	A	2624	G
1	A	2629	U
1	A	2630	G
1	A	2653	U
1	A	2654	A
1	A	2656	U
1	A	2673	G
1	A	2682	A
1	A	2689	U
1	A	2690	U
1	A	2700	A
1	A	2707	U
1	A	2713	U
1	A	2714	G
1	A	2716	C
1	A	2718	G
1	A	2720	U
1	A	2724	U
1	A	2726	A
1	A	2728	U
1	A	2733	A
1	A	2734	A
1	A	2735	G
1	A	2742	G
1	A	2744	G
1	A	2746	U
1	A	2748	A
1	A	2752	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2754	U
1	A	2758	A
1	A	2762	C
1	A	2764	A
1	A	2765	A
1	A	2778	A
1	A	2791	G
1	A	2794	U
1	A	2798	U
1	A	2799	G
1	A	2800	A
1	A	2801	G
1	A	2803	G
1	A	2805	C
1	A	2806	C
1	A	2807	U
1	A	2809	A
1	A	2812	G
1	A	2818	U
1	A	2820	A
1	A	2823	A
1	A	2826	A
1	A	2837	A
1	A	2850	A
1	A	2856	A
1	A	2861	U
1	A	2867	G
1	A	2868	A
1	A	2872	A
1	A	2874	C
1	A	2880	C
1	A	2883	A
1	A	2884	U
1	A	2901	C
1	A	2902	C
2	B	4	C
2	B	12	C
2	B	13	G
2	B	21	G
2	B	26	C
2	B	28	C
2	B	30	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	B	31	C
2	B	33	G
2	B	35	C
2	B	36	C
2	B	42	C
2	B	44	G
2	B	65	U
2	B	66	A
2	B	67	G
2	B	84	G
2	B	89	U
2	B	90	C
2	B	105	G
2	B	108	A
2	B	109	A
2	B	111	U
2	B	113	C
2	B	114	C
2	B	117	G
2	B	118	C
34	a	3	A
34	a	4	U
34	a	5	U
34	a	6	G
34	a	7	A
34	a	8	A
34	a	9	G
34	a	22	G
34	a	29	U
34	a	32	A
34	a	38	G
34	a	39	G
34	a	44	A
34	a	47	C
34	a	48	C
34	a	49	U
34	a	50	A
34	a	51	A
34	a	52	C
34	a	57	G
34	a	60	A
34	a	64	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	66	A
34	a	69	G
34	a	70	U
34	a	71	A
34	a	72	A
34	a	73	C
34	a	74	A
34	a	76	G
34	a	77	A
34	a	78	A
34	a	79	G
34	a	80	A
34	a	83	C
34	a	85	U
34	a	86	G
34	a	87	C
34	a	89	U
34	a	94	G
34	a	95	C
34	a	96	U
34	a	97	G
34	a	99	C
34	a	100	G
34	a	104	G
34	a	107	G
34	a	116	A
34	a	117	G
34	a	120	A
34	a	121	U
34	a	127	G
34	a	128	G
34	a	129	A
34	a	130	A
34	a	131	A
34	a	132	C
34	a	142	G
34	a	144	G
34	a	146	G
34	a	149	A
34	a	150	U
34	a	151	A
34	a	154	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	161	A
34	a	163	C
34	a	165	G
34	a	167	A
34	a	168	G
34	a	177	G
34	a	181	A
34	a	183	C
34	a	184	G
34	a	189	A
34	a	191	G
34	a	196	A
34	a	197	A
34	a	202	G
34	a	203	G
34	a	205	A
34	a	207	C
34	a	209	U
34	a	210	C
34	a	211	G
34	a	212	G
34	a	213	G
34	a	215	C
34	a	220	G
34	a	222	C
34	a	223	A
34	a	226	G
34	a	227	G
34	a	230	G
34	a	240	G
34	a	244	U
34	a	245	U
34	a	246	A
34	a	247	G
34	a	251	G
34	a	254	G
34	a	259	G
34	a	266	G
34	a	267	C
34	a	281	G
34	a	289	G
34	a	300	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	305	G
34	a	306	A
34	a	317	U
34	a	321	A
34	a	325	A
34	a	328	C
34	a	330	C
34	a	335	C
34	a	339	C
34	a	340	U
34	a	341	C
34	a	342	C
34	a	344	A
34	a	345	C
34	a	347	G
34	a	348	G
34	a	349	A
34	a	351	G
34	a	352	C
34	a	353	A
34	a	354	G
34	a	358	U
34	a	363	A
34	a	365	U
34	a	366	A
34	a	367	U
34	a	368	U
34	a	369	G
34	a	372	C
34	a	375	U
34	a	376	G
34	a	381	C
34	a	382	A
34	a	388	G
34	a	389	A
34	a	390	U
34	a	391	G
34	a	392	C
34	a	397	A
34	a	398	U
34	a	400	C
34	a	403	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	404	G
34	a	405	U
34	a	406	G
34	a	407	U
34	a	411	A
34	a	412	A
34	a	413	G
34	a	422	C
34	a	424	G
34	a	429	U
34	a	435	A
34	a	436	C
34	a	440	C
34	a	441	A
34	a	443	C
34	a	446	G
34	a	449	G
34	a	457	G
34	a	458	U
34	a	459	A
34	a	464	U
34	a	466	A
34	a	467	U
34	a	468	A
34	a	476	U
34	a	482	A
34	a	484	G
34	a	485	U
34	a	486	U
34	a	496	A
34	a	497	G
34	a	499	A
34	a	501	C
34	a	503	C
34	a	505	G
34	a	506	G
34	a	509	A
34	a	511	C
34	a	514	C
34	a	515	G
34	a	516	PSU
34	a	517	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	518	C
34	a	520	A
34	a	521	G
34	a	524	G
34	a	525	C
34	a	527	7MG
34	a	528	C
34	a	531	U
34	a	532	A
34	a	533	A
34	a	534	U
34	a	535	A
34	a	537	G
34	a	538	G
34	a	541	G
34	a	542	G
34	a	545	C
34	a	546	A
34	a	547	A
34	a	572	A
34	a	573	A
34	a	575	G
34	a	576	C
34	a	577	G
34	a	590	U
34	a	592	G
34	a	596	A
34	a	615	G
34	a	619	U
34	a	633	G
34	a	639	G
34	a	640	A
34	a	642	A
34	a	647	C
34	a	648	A
34	a	650	G
34	a	651	C
34	a	653	U
34	a	654	G
34	a	661	G
34	a	665	A
34	a	671	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	687	A
34	a	695	A
34	a	700	G
34	a	701	U
34	a	703	G
34	a	704	A
34	a	713	G
34	a	720	C
34	a	721	G
34	a	722	G
34	a	723	U
34	a	724	G
34	a	731	G
34	a	733	G
34	a	742	G
34	a	754	C
34	a	755	G
34	a	758	C
34	a	761	G
34	a	769	G
34	a	777	A
34	a	793	U
34	a	794	A
34	a	802	A
34	a	815	A
34	a	817	C
34	a	818	G
34	a	819	A
34	a	832	G
34	a	836	G
34	a	838	G
34	a	843	U
34	a	844	G
34	a	846	G
34	a	851	G
34	a	870	U
34	a	872	A
34	a	885	G
34	a	902	G
34	a	905	U
34	a	906	A
34	a	914	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	924	C
34	a	926	G
34	a	934	C
34	a	935	A
34	a	939	G
34	a	945	G
34	a	960	U
34	a	961	U
34	a	963	G
34	a	965	U
34	a	966	2MG
34	a	969	A
34	a	971	G
34	a	972	C
34	a	975	A
34	a	976	G
34	a	977	A
34	a	978	A
34	a	982	U
34	a	984	C
34	a	988	G
34	a	989	U
34	a	991	U
34	a	992	U
34	a	993	G
34	a	998	C
34	a	999	C
34	a	1001	C
34	a	1003	G
34	a	1004	A
34	a	1006	G
34	a	1016	A
34	a	1020	G
34	a	1027	C
34	a	1028	C
34	a	1030	U
34	a	1031	C
34	a	1033	G
34	a	1034	G
34	a	1035	A
34	a	1038	C
34	a	1043	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	1044	A
34	a	1045	C
34	a	1053	G
34	a	1056	U
34	a	1065	U
34	a	1070	U
34	a	1087	G
34	a	1088	G
34	a	1094	G
34	a	1095	U
34	a	1096	C
34	a	1101	A
34	a	1108	G
34	a	1113	C
34	a	1115	U
34	a	1116	U
34	a	1124	G
34	a	1125	U
34	a	1132	C
34	a	1133	G
34	a	1134	G
34	a	1136	C
34	a	1137	C
34	a	1138	G
34	a	1139	G
34	a	1142	G
34	a	1143	G
34	a	1146	A
34	a	1151	A
34	a	1152	A
34	a	1154	G
34	a	1155	A
34	a	1159	U
34	a	1163	A
34	a	1167	A
34	a	1168	U
34	a	1171	A
34	a	1174	G
34	a	1182	G
34	a	1184	G
34	a	1188	A
34	a	1191	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	1195	C
34	a	1196	A
34	a	1197	A
34	a	1201	A
34	a	1202	U
34	a	1205	U
34	a	1206	G
34	a	1207	2MG
34	a	1212	U
34	a	1213	A
34	a	1214	C
34	a	1217	C
34	a	1219	A
34	a	1220	G
34	a	1225	A
34	a	1226	C
34	a	1227	A
34	a	1228	C
34	a	1238	A
34	a	1240	U
34	a	1245	C
34	a	1247	U
34	a	1248	A
34	a	1256	A
34	a	1258	G
34	a	1260	G
34	a	1261	A
34	a	1264	U
34	a	1266	G
34	a	1268	G
34	a	1269	A
34	a	1273	C
34	a	1274	A
34	a	1275	A
34	a	1280	A
34	a	1281	C
34	a	1282	C
34	a	1285	A
34	a	1286	U
34	a	1287	A
34	a	1291	U
34	a	1293	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	1294	G
34	a	1296	C
34	a	1297	G
34	a	1298	U
34	a	1300	G
34	a	1301	U
34	a	1302	C
34	a	1304	G
34	a	1305	G
34	a	1306	A
34	a	1312	G
34	a	1313	U
34	a	1317	C
34	a	1320	C
34	a	1338	G
34	a	1340	A
34	a	1345	U
34	a	1346	A
34	a	1348	U
34	a	1349	A
34	a	1360	A
34	a	1363	A
34	a	1368	A
34	a	1371	G
34	a	1379	G
34	a	1381	U
34	a	1383	C
34	a	1391	U
34	a	1397	C
34	a	1398	A
34	a	1399	C
34	a	1400	C
34	a	1415	G
34	a	1419	G
34	a	1429	A
34	a	1432	G
34	a	1433	A
34	a	1434	A
34	a	1441	A
34	a	1442	G
34	a	1448	C
34	a	1450	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	1454	G
34	a	1455	G
34	a	1469	C
34	a	1475	G
34	a	1487	G
34	a	1491	G
34	a	1493	A
34	a	1497	G
34	a	1502	A
34	a	1503	A
34	a	1506	U
34	a	1517	G
34	a	1529	G
34	a	1530	G
34	a	1534	A
34	a	1535	C
34	a	1536	C
34	a	1539	C
55	v	4	G
55	v	6	G
55	v	7	4SU
55	v	8	G
55	v	13	A
55	v	15	C
55	v	17	U
55	v	18	G
55	v	20	H2U
55	v	21	A
55	v	22	G
55	v	25	C
55	v	42	G
55	v	47	U
55	v	70	G
55	v	72	A
55	v	76	A
55	w	3	C
55	w	5	G
55	w	7	G
55	w	8	4SU
55	w	9	G
55	w	14	A
55	w	16	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
55	w	17	C
55	w	117	U
55	w	18	G
55	w	19	G
55	w	20	H2U
55	w	21	A
55	w	22	G
55	w	24	U
55	w	25	C
55	w	28	C
55	w	30	G
55	w	34	C
55	w	37	A
55	w	38	A
55	w	42	G
55	w	48	C
55	w	49	G
55	w	56	C
55	w	57	A
55	w	59	A
55	w	67	C
55	w	69	C
55	w	70	G
55	w	71	C
55	w	73	A
55	w	75	C
55	w	76	A
56	x	14	C
56	x	19	C
56	x	20	U
56	x	21	C
56	x	22	A
56	x	23	C
56	x	24	G
57	y	3	C
57	y	4	C
57	y	5	G
57	y	8	4SU
57	y	9	A
57	y	10	G
57	y	11	C
57	y	16	H2U

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Mol	Chain	Res	Type
57	y	17	C
57	y	18	G
57	y	20	H2U
57	y	21	A
57	y	24	G
57	y	26	A
57	y	30	G
57	y	31	A
57	y	32	PSU
57	y	33	U
57	y	34	G
57	y	35	A
57	y	36	A
57	y	38	A
57	y	39	PSU
57	y	40	C
57	y	42	C
57	y	43	C
57	y	44	G
57	y	45	U
57	y	46	7MG
57	y	47	U
57	y	48	C
57	y	52	G
57	y	55	PSU
57	y	56	C
57	y	59	U
57	y	61	C
57	y	65	G
57	y	68	C
57	y	69	G
57	y	73	A
57	y	76	A

All (77) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	12	U
1	A	51	G
1	A	162	U
1	A	177	G
1	A	199	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	204	A
1	A	242	G
1	A	265	A
1	A	301	G
1	A	341	C
1	A	440	C
1	A	474	G
1	A	502	A
1	A	534	U
1	A	537	G
1	A	555	G
1	A	613	A
1	A	641	U
1	A	653	U
1	A	746	PSU
1	A	752	A
1	A	764	A
1	A	774	G
1	A	775	G
1	A	784	G
1	A	827	U
1	A	859	G
1	A	884	U
1	A	1020	A
1	A	1022	G
1	A	1033	U
1	A	1046	A
1	A	1070	A
1	A	1089	A
1	A	1111	A
1	A	1124	G
1	A	1140	C
1	A	1190	G
1	A	1378	A
1	A	1399	C
1	A	1432	G
1	A	1475	G
1	A	1523	U
1	A	1555	G
1	A	1558	C
1	A	1567	G
1	A	1608	A

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Mol	Chain	Res	Type
1	A	1647	U
1	A	1706	C
1	A	1730	U
1	A	1818	U
1	A	1857	G
1	A	1918	A
1	A	1939	5MU
1	A	1940	U
1	A	1976	U
1	A	2238	G
1	A	2296	U
1	A	2319	G
1	A	2326	C
1	A	2333	A
1	A	2391	G
1	A	2401	U
1	A	2402	U
1	A	2407	A
1	A	2517	C
1	A	2566	A
1	A	2581	G
1	A	2681	C
1	A	2798	U
1	A	2833	U
1	A	2849	U
1	A	2873	A
2	B	34	A
2	B	56	G
2	B	66	A
2	B	108	A

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

52 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
55	5MU	w	54	55	19,22,23	1.48	4 (21%)	28,32,35	2.03	10 (35%)
55	PSU	w	55	55	18,21,22	1.30	2 (11%)	22,30,33	1.94	5 (22%)
1	5MC	A	747	1	18,22,23	0.96	1 (5%)	26,32,35	1.46	3 (11%)
55	H2U	v	20	55	18,21,22	0.82	1 (5%)	21,30,33	1.67	4 (19%)
1	2MA	A	2503	1,60	17,25,26	1.14	1 (5%)	17,37,40	1.20	3 (17%)
57	7MG	y	46	57	22,26,27	1.42	2 (9%)	29,39,42	2.36	7 (24%)
34	2MG	a	1516	34	18,26,27	0.98	1 (5%)	16,38,41	1.16	2 (12%)
1	OMC	A	2498	1,60	19,22,23	0.87	0	26,31,34	1.22	3 (11%)
1	1MG	A	745	1	18,26,27	1.06	0	19,39,42	1.44	3 (15%)
1	PSU	A	1917	1	18,21,22	1.39	2 (11%)	22,30,33	1.93	5 (22%)
1	OMU	A	2552	1,60	19,22,23	1.27	3 (15%)	26,31,34	1.93	8 (30%)
1	PSU	A	746	1,60	18,21,22	1.39	2 (11%)	22,30,33	1.91	5 (22%)
1	PSU	A	955	1	18,21,22	1.36	2 (11%)	22,30,33	1.92	4 (18%)
1	PSU	A	2605	1	18,21,22	1.38	2 (11%)	22,30,33	1.89	4 (18%)
57	PSU	y	55	57	18,21,22	1.33	2 (11%)	22,30,33	1.90	4 (18%)
1	PSU	A	2457	1	18,21,22	1.41	2 (11%)	22,30,33	1.93	5 (22%)
1	PSU	A	2504	1	18,21,22	1.37	2 (11%)	22,30,33	1.86	4 (18%)
1	3TD	A	1915	1	18,22,23	7.30	12 (66%)	22,32,35	1.77	3 (13%)
1	PSU	A	2604	1	18,21,22	1.40	2 (11%)	22,30,33	1.87	5 (22%)
57	H2U	y	16	57	18,21,22	0.81	1 (5%)	21,30,33	1.50	4 (19%)
55	4SU	v	7	55	18,21,22	1.69	4 (22%)	26,30,33	2.25	6 (23%)
34	MA6	a	1519	34	19,26,27	1.23	3 (15%)	18,38,41	1.73	4 (22%)
1	5MC	A	1962	1	18,22,23	1.05	1 (5%)	26,32,35	1.39	3 (11%)
1	7MG	A	2069	1,60	22,26,27	1.48	3 (13%)	29,39,42	2.42	12 (41%)
55	PSU	v	55	55	18,21,22	1.34	2 (11%)	22,30,33	1.86	4 (18%)
1	H2U	A	2449	1	18,21,22	0.92	2 (11%)	21,30,33	1.56	4 (19%)
34	5MC	a	967	34	18,22,23	1.03	1 (5%)	26,32,35	1.44	3 (11%)
55	4SU	w	8	55	18,21,22	1.73	5 (27%)	26,30,33	2.15	5 (19%)
34	7MG	a	527	34	22,26,27	1.41	2 (9%)	29,39,42	2.48	8 (27%)
57	5MU	y	54	57	19,22,23	1.45	4 (21%)	28,32,35	2.03	8 (28%)
1	6MZ	A	1618	1	18,25,26	1.01	1 (5%)	16,36,39	2.29	5 (31%)
1	PSU	A	1911	1	18,21,22	1.40	2 (11%)	22,30,33	2.03	5 (22%)
1	6MZ	A	2030	1	18,25,26	1.02	1 (5%)	16,36,39	2.28	5 (31%)
57	MIA	y	37	57	24,31,32	2.27	4 (16%)	26,44,47	2.68	10 (38%)
55	5MU	v	54	55	19,22,23	1.48	4 (21%)	28,32,35	1.93	8 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	5MU	A	1939	1	19,22,23	1.49	4 (21%)	28,32,35	2.05	8 (28%)
34	UR3	a	1498	34	19,22,23	1.15	2 (10%)	26,32,35	1.69	4 (15%)
1	PSU	A	2580	1	18,21,22	1.44	2 (11%)	22,30,33	1.94	5 (22%)
57	PSU	y	32	57	18,21,22	1.30	2 (11%)	22,30,33	2.12	4 (18%)
1	OMG	A	2251	55,1	18,26,27	1.05	2 (11%)	19,38,41	1.07	2 (10%)
1	2MG	A	1835	1	18,26,27	1.02	2 (11%)	16,38,41	1.21	2 (12%)
34	2MG	a	1207	34	18,26,27	0.91	0	16,38,41	1.31	4 (25%)
34	PSU	a	516	34	18,21,22	1.32	3 (16%)	22,30,33	1.97	5 (22%)
1	2MG	A	2445	1	18,26,27	0.95	0	16,38,41	1.16	2 (12%)
34	5MC	a	1407	34	18,22,23	1.04	1 (5%)	26,32,35	1.57	4 (15%)
34	MA6	a	1518	34	19,26,27	1.24	2 (10%)	18,38,41	1.76	4 (22%)
34	4OC	a	1402	34	20,23,24	0.84	1 (5%)	26,32,35	1.27	4 (15%)
57	4SU	y	8	57	18,21,22	1.73	5 (27%)	26,30,33	2.29	7 (26%)
57	H2U	y	20	57	18,21,22	0.85	1 (5%)	21,30,33	1.57	4 (19%)
55	H2U	w	20	55	18,21,22	0.81	0	21,30,33	1.70	3 (14%)
34	2MG	a	966	34	18,26,27	0.99	1 (5%)	16,38,41	1.39	3 (18%)
57	PSU	y	39	57	18,21,22	1.31	2 (11%)	22,30,33	2.13	4 (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
55	5MU	w	54	55	-	0/7/25/26	0/2/2/2
55	PSU	w	55	55	-	1/7/25/26	0/2/2/2
1	5MC	A	747	1	-	0/7/25/26	0/2/2/2
55	H2U	v	20	55	-	0/7/38/39	0/2/2/2
1	2MA	A	2503	1,60	-	2/3/25/26	0/3/3/3
57	7MG	y	46	57	-	4/7/37/38	0/3/3/3
34	2MG	a	1516	34	-	0/5/27/28	0/3/3/3
1	OMC	A	2498	1,60	-	0/9/27/28	0/2/2/2
1	1MG	A	745	1	-	0/3/25/26	0/3/3/3
1	PSU	A	1917	1	-	2/7/25/26	0/2/2/2
1	OMU	A	2552	1,60	-	2/9/27/28	0/2/2/2
1	PSU	A	746	1,60	-	1/7/25/26	0/2/2/2
1	PSU	A	955	1	-	0/7/25/26	0/2/2/2
1	PSU	A	2605	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	PSU	y	55	57	-	2/7/25/26	0/2/2/2
1	PSU	A	2457	1	-	2/7/25/26	0/2/2/2
1	PSU	A	2504	1	-	2/7/25/26	0/2/2/2
1	3TD	A	1915	1	-	4/7/25/26	0/2/2/2
1	PSU	A	2604	1	-	0/7/25/26	0/2/2/2
57	H2U	y	16	57	-	2/7/38/39	0/2/2/2
55	4SU	v	7	55	-	2/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	3/7/29/30	0/3/3/3
1	5MC	A	1962	1	-	2/7/25/26	0/2/2/2
1	7MG	A	2069	1,60	-	2/7/37/38	0/3/3/3
55	PSU	v	55	55	-	2/7/25/26	0/2/2/2
1	H2U	A	2449	1	-	0/7/38/39	0/2/2/2
34	5MC	a	967	34	-	0/7/25/26	0/2/2/2
55	4SU	w	8	55	-	6/7/25/26	0/2/2/2
34	7MG	a	527	34	-	2/7/37/38	0/3/3/3
57	5MU	y	54	57	-	0/7/25/26	0/2/2/2
1	6MZ	A	1618	1	-	3/5/27/28	0/3/3/3
1	PSU	A	1911	1	-	0/7/25/26	0/2/2/2
1	6MZ	A	2030	1	-	3/5/27/28	0/3/3/3
57	MIA	y	37	57	-	7/11/33/34	0/3/3/3
55	5MU	v	54	55	-	0/7/25/26	0/2/2/2
1	5MU	A	1939	1	-	2/7/25/26	0/2/2/2
34	UR3	a	1498	34	-	2/7/25/26	0/2/2/2
1	PSU	A	2580	1	-	0/7/25/26	0/2/2/2
57	PSU	y	32	57	-	0/7/25/26	0/2/2/2
1	OMG	A	2251	55,1	-	0/5/27/28	0/3/3/3
1	2MG	A	1835	1	-	0/5/27/28	0/3/3/3
34	2MG	a	1207	34	-	2/5/27/28	0/3/3/3
34	PSU	a	516	34	-	3/7/25/26	0/2/2/2
1	2MG	A	2445	1	-	2/5/27/28	0/3/3/3
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
34	MA6	a	1518	34	-	2/7/29/30	0/3/3/3
34	4OC	a	1402	34	-	2/9/29/30	0/2/2/2
57	4SU	y	8	57	-	2/7/25/26	0/2/2/2
57	H2U	y	20	57	-	2/7/38/39	0/2/2/2
55	H2U	w	20	55	-	2/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	2MG	a	966	34	-	3/5/27/28	0/3/3/3
57	PSU	y	39	57	-	2/7/25/26	0/2/2/2

All (113) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1915	3TD	O4'-C1'	16.51	1.66	1.43
1	A	1915	3TD	C2'-C1'	-16.25	1.32	1.53
1	A	1915	3TD	C6-C5	14.56	1.52	1.35
1	A	1915	3TD	C2-N1	8.16	1.47	1.37
57	y	37	MIA	C13-C14	7.14	1.52	1.32
57	y	37	MIA	C2-S10	-6.82	1.69	1.75
1	A	1915	3TD	O4'-C4'	-6.10	1.31	1.45
1	A	1915	3TD	C2-N3	5.52	1.50	1.38
1	A	1915	3TD	C6-N1	5.21	1.44	1.36
55	v	7	4SU	C4-S4	-4.44	1.60	1.68
55	w	8	4SU	C4-S4	-4.42	1.60	1.68
57	y	8	4SU	C4-S4	-4.41	1.60	1.68
1	A	2580	PSU	C6-C5	4.31	1.40	1.35
1	A	1911	PSU	C6-C5	4.23	1.40	1.35
1	A	746	PSU	C6-C5	4.16	1.40	1.35
1	A	2604	PSU	C6-C5	4.13	1.40	1.35
1	A	2605	PSU	C6-C5	4.10	1.40	1.35
1	A	2457	PSU	C6-C5	4.10	1.40	1.35
1	A	2069	7MG	C4-N9	-4.10	1.33	1.37
1	A	1917	PSU	C6-C5	4.10	1.40	1.35
1	A	955	PSU	C6-C5	4.05	1.40	1.35
1	A	2504	PSU	C6-C5	4.04	1.40	1.35
55	v	55	PSU	C6-C5	3.92	1.39	1.35
34	a	516	PSU	C6-C5	3.88	1.39	1.35
57	y	55	PSU	C6-C5	3.88	1.39	1.35
55	w	55	PSU	C6-C5	3.88	1.39	1.35
1	A	1915	3TD	C10-N3	-3.48	1.40	1.47
34	a	1407	5MC	C6-C5	3.33	1.40	1.34
1	A	1939	5MU	C6-C5	3.30	1.40	1.34
57	y	46	7MG	C4-N9	-3.29	1.33	1.37
57	y	39	PSU	C6-C5	3.23	1.39	1.35
55	v	54	5MU	C6-C5	3.22	1.39	1.34
1	A	1962	5MC	C6-C5	3.21	1.39	1.34
57	y	32	PSU	C6-C5	3.17	1.39	1.35
34	a	527	7MG	C5-C4	3.15	1.48	1.38
57	y	46	7MG	C5-C4	3.15	1.48	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	967	5MC	C6-C5	3.13	1.39	1.34
34	a	527	7MG	C4-N9	-3.09	1.34	1.37
55	w	54	5MU	C6-C5	3.05	1.39	1.34
1	A	1915	3TD	O2'-C2'	3.04	1.50	1.43
57	y	54	5MU	C2-N1	3.03	1.43	1.38
55	w	8	4SU	C2-N1	3.01	1.43	1.38
55	w	54	5MU	C2-N1	3.01	1.43	1.38
1	A	1915	3TD	O3'-C3'	-2.96	1.36	1.43
1	A	2069	7MG	C5-C4	2.94	1.47	1.38
57	y	8	4SU	C2-N1	2.93	1.43	1.38
1	A	747	5MC	C6-C5	2.92	1.39	1.34
57	y	54	5MU	C6-C5	2.91	1.39	1.34
1	A	2552	OMU	C2-N1	2.89	1.43	1.38
34	a	1518	MA6	C5-C4	2.87	1.48	1.40
57	y	8	4SU	C4-N3	-2.86	1.34	1.37
55	w	8	4SU	C4-N3	-2.83	1.34	1.37
34	a	1519	MA6	C5-C4	2.79	1.48	1.40
55	w	54	5MU	C4-C5	2.76	1.49	1.44
55	v	54	5MU	C2-N1	2.75	1.42	1.38
1	A	1939	5MU	C4-C5	2.74	1.49	1.44
1	A	1939	5MU	C2-N1	2.72	1.42	1.38
34	a	1498	UR3	C2-N1	2.72	1.42	1.38
55	v	7	4SU	C2-N1	2.71	1.42	1.38
57	y	32	PSU	C4-N3	-2.63	1.34	1.38
55	v	54	5MU	C4-C5	2.61	1.49	1.44
57	y	39	PSU	C4-N3	-2.60	1.34	1.38
57	y	54	5MU	C4-C5	2.58	1.49	1.44
55	v	7	4SU	C4-N3	-2.54	1.34	1.37
1	A	1915	3TD	O2-C2	-2.53	1.18	1.23
1	A	2030	6MZ	C5-C4	2.52	1.47	1.40
57	y	37	MIA	C5-C4	2.50	1.47	1.40
55	v	54	5MU	C4-N3	-2.48	1.34	1.38
1	A	2457	PSU	C4-N3	-2.48	1.34	1.38
1	A	1618	6MZ	C5-C4	2.47	1.47	1.40
1	A	2503	2MA	C2-N3	2.46	1.36	1.31
1	A	2580	PSU	C4-N3	-2.46	1.34	1.38
1	A	1939	5MU	C4-N3	-2.43	1.34	1.38
1	A	2604	PSU	C4-N3	-2.42	1.34	1.38
1	A	2552	OMU	C4-N3	-2.41	1.34	1.38
1	A	2504	PSU	C4-N3	-2.37	1.34	1.38
1	A	1917	PSU	C4-N3	-2.37	1.34	1.38
1	A	2605	PSU	C4-N3	-2.35	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	y	8	4SU	C5-C4	-2.34	1.39	1.42
57	y	55	PSU	C4-N3	-2.33	1.34	1.38
55	v	7	4SU	C5-C4	-2.33	1.39	1.42
57	y	54	5MU	C4-N3	-2.31	1.34	1.38
55	w	8	4SU	C5-C4	-2.31	1.39	1.42
34	a	1518	MA6	C6-N1	2.29	1.36	1.33
34	a	966	2MG	O4'-C1'	2.29	1.44	1.41
34	a	516	PSU	C4-N3	-2.28	1.34	1.38
1	A	2449	H2U	C2-N3	-2.27	1.33	1.38
1	A	746	PSU	C4-N3	-2.26	1.34	1.38
1	A	2449	H2U	C4-N3	-2.26	1.33	1.37
55	w	54	5MU	C4-N3	-2.25	1.34	1.38
1	A	2069	7MG	C8-N9	2.23	1.47	1.46
1	A	1835	2MG	C6-N1	-2.23	1.34	1.37
1	A	1835	2MG	O4'-C1'	2.22	1.44	1.41
1	A	955	PSU	C4-N3	-2.22	1.34	1.38
55	w	55	PSU	C4-N3	-2.21	1.34	1.38
55	v	55	PSU	C4-N3	-2.19	1.34	1.38
34	a	1519	MA6	O4'-C1'	2.17	1.44	1.41
1	A	1915	3TD	C3'-C4'	2.16	1.58	1.53
34	a	1519	MA6	C6-N1	2.15	1.36	1.33
1	A	2251	OMG	C6-N1	-2.14	1.34	1.37
1	A	1911	PSU	C4-N3	-2.13	1.34	1.38
34	a	1498	UR3	C6-C5	2.13	1.40	1.35
57	y	20	H2U	C2-N3	-2.10	1.34	1.38
1	A	2552	OMU	C6-C5	2.09	1.39	1.35
1	A	2251	OMG	O4'-C1'	2.08	1.44	1.41
34	a	1402	4OC	C6-C5	2.06	1.39	1.35
55	w	8	4SU	C6-C5	2.06	1.39	1.35
57	y	16	H2U	C2-N3	-2.04	1.34	1.38
57	y	8	4SU	C6-C5	2.04	1.39	1.35
57	y	37	MIA	C6-N1	2.04	1.35	1.32
55	v	20	H2U	C2-N3	-2.03	1.34	1.38
34	a	516	PSU	C4-C5	2.00	1.49	1.44
34	a	1516	2MG	O4'-C1'	2.00	1.43	1.41

All (250) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	y	37	MIA	C12-C13-C14	-8.31	110.97	127.14
34	a	527	7MG	N9-C4-N3	8.29	137.88	125.47
57	y	46	7MG	N9-C4-N3	7.95	137.35	125.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2069	7MG	N9-C4-N3	7.13	136.13	125.47
57	y	8	4SU	C4-N3-C2	-6.37	121.15	127.34
55	v	7	4SU	C4-N3-C2	-6.35	121.17	127.34
55	w	8	4SU	C4-N3-C2	-6.13	121.38	127.34
1	A	1618	6MZ	C2-N1-C6	6.01	121.74	116.59
57	y	39	PSU	N1-C2-N3	5.98	121.91	115.13
1	A	2030	6MZ	C2-N1-C6	5.95	121.69	116.59
57	y	32	PSU	N1-C2-N3	5.94	121.86	115.13
34	a	1498	UR3	C4-N3-C2	-5.92	118.99	124.56
57	y	55	PSU	N1-C2-N3	5.91	121.82	115.13
55	w	55	PSU	N1-C2-N3	5.83	121.74	115.13
1	A	2457	PSU	N1-C2-N3	5.81	121.71	115.13
1	A	1911	PSU	N1-C2-N3	5.81	121.71	115.13
1	A	746	PSU	N1-C2-N3	5.79	121.69	115.13
1	A	2504	PSU	N1-C2-N3	5.79	121.69	115.13
34	a	516	PSU	N1-C2-N3	5.75	121.64	115.13
1	A	1917	PSU	N1-C2-N3	5.73	121.62	115.13
55	v	55	PSU	N1-C2-N3	5.70	121.59	115.13
1	A	2605	PSU	N1-C2-N3	5.70	121.58	115.13
1	A	2604	PSU	N1-C2-N3	5.66	121.54	115.13
1	A	2580	PSU	N1-C2-N3	5.59	121.46	115.13
1	A	955	PSU	N1-C2-N3	5.59	121.46	115.13
55	v	7	4SU	C5-C4-N3	5.44	119.74	114.69
57	y	8	4SU	C5-C4-N3	5.33	119.63	114.69
55	w	8	4SU	C5-C4-N3	5.33	119.63	114.69
34	a	527	7MG	C5-C4-N3	-5.18	118.26	128.13
55	v	20	H2U	O4'-C1'-N1	5.15	116.32	109.30
1	A	1915	3TD	N1-C2-N3	5.06	120.13	116.14
1	A	1939	5MU	N3-C2-N1	5.02	121.56	114.89
57	y	46	7MG	C5-C4-N3	-5.01	118.58	128.13
55	v	54	5MU	N3-C2-N1	4.89	121.38	114.89
1	A	2069	7MG	C5-C4-N3	-4.82	118.94	128.13
57	y	8	4SU	N3-C2-N1	4.80	121.26	114.89
1	A	2552	OMU	N3-C2-N1	4.78	121.24	114.89
55	w	54	5MU	N3-C2-N1	4.78	121.24	114.89
1	A	2069	7MG	C2-N3-C4	4.72	120.71	112.30
1	A	1939	5MU	C4-N3-C2	-4.71	121.25	127.35
57	y	54	5MU	N3-C2-N1	4.65	121.06	114.89
1	A	2069	7MG	N9-C8-N7	-4.60	96.80	103.38
55	w	20	H2U	O4'-C1'-N1	4.50	115.43	109.30
57	y	54	5MU	C4-N3-C2	-4.50	121.53	127.35
57	y	46	7MG	C2-N3-C4	4.49	120.29	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	w	54	5MU	C4-N3-C2	-4.49	121.55	127.35
34	a	527	7MG	C2-N3-C4	4.47	120.26	112.30
57	y	46	7MG	N9-C8-N7	-4.44	97.02	103.38
55	w	8	4SU	N3-C2-N1	4.43	120.78	114.89
34	a	527	7MG	N9-C8-N7	-4.35	97.16	103.38
55	v	7	4SU	N3-C2-N1	4.35	120.66	114.89
57	y	54	5MU	C5-C4-N3	4.26	118.95	115.31
57	y	37	MIA	C2-N3-C4	4.25	121.18	115.32
55	v	54	5MU	C4-N3-C2	-4.24	121.86	127.35
1	A	2552	OMU	C4-N3-C2	-4.24	120.99	126.58
34	a	1519	MA6	C4-C5-N7	-4.22	105.00	109.40
1	A	1939	5MU	C5-C4-N3	4.22	118.91	115.31
1	A	747	5MC	CM5-C5-C6	-4.16	117.29	122.85
55	v	7	4SU	C5-C4-S4	-4.13	119.15	124.47
55	w	54	5MU	C5-C4-N3	4.12	118.83	115.31
57	y	37	MIA	C16-C14-C13	-4.04	110.97	122.65
57	y	37	MIA	C15-C14-C13	-4.03	110.99	122.65
1	A	1911	PSU	O2-C2-N1	-4.02	118.36	122.79
1	A	1915	3TD	C4-N3-C2	-4.02	120.25	124.61
57	y	39	PSU	C4-N3-C2	-3.97	120.62	126.34
55	w	20	H2U	C4-N3-C2	-3.96	122.51	125.79
57	y	32	PSU	C4-N3-C2	-3.92	120.69	126.34
57	y	32	PSU	C3'-C2'-C1'	3.89	106.17	101.64
57	y	39	PSU	C3'-C2'-C1'	3.88	106.16	101.64
55	v	54	5MU	C5-C4-N3	3.88	118.62	115.31
34	a	1518	MA6	C4-C5-N7	-3.85	105.39	109.40
1	A	2605	PSU	C4-N3-C2	-3.83	120.82	126.34
34	a	967	5MC	CM5-C5-C6	-3.82	117.75	122.85
1	A	955	PSU	C4-N3-C2	-3.81	120.85	126.34
57	y	55	PSU	C4-N3-C2	-3.79	120.87	126.34
34	a	516	PSU	C4-N3-C2	-3.79	120.88	126.34
1	A	1911	PSU	C4-N3-C2	-3.77	120.91	126.34
34	a	1518	MA6	N3-C2-N1	-3.75	122.82	128.68
1	A	2504	PSU	C4-N3-C2	-3.73	120.96	126.34
55	w	55	PSU	C4-N3-C2	-3.73	120.97	126.34
34	a	1407	5MC	C5-C4-N3	-3.73	117.65	121.67
1	A	746	PSU	C4-N3-C2	-3.70	121.01	126.34
1	A	2604	PSU	C4-N3-C2	-3.62	121.13	126.34
1	A	2457	PSU	C4-N3-C2	-3.61	121.14	126.34
57	y	54	5MU	O4-C4-C5	-3.57	120.76	124.90
55	v	55	PSU	C4-N3-C2	-3.56	121.21	126.34
1	A	1917	PSU	C4-N3-C2	-3.56	121.21	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	y	8	4SU	C5-C4-S4	-3.55	119.89	124.47
34	a	1519	MA6	N3-C2-N1	-3.54	123.15	128.68
34	a	1407	5MC	CM5-C5-C6	-3.51	118.16	122.85
1	A	1962	5MC	CM5-C5-C6	-3.51	118.17	122.85
57	y	37	MIA	C5-C6-N1	-3.49	117.91	120.81
55	v	20	H2U	C4-N3-C2	-3.48	122.91	125.79
57	y	20	H2U	C4-N3-C2	-3.47	122.92	125.79
57	y	37	MIA	C3'-C2'-C1'	3.45	106.18	100.98
1	A	1618	6MZ	C3'-C2'-C1'	3.43	106.15	100.98
1	A	2030	6MZ	C3'-C2'-C1'	3.43	106.14	100.98
55	w	8	4SU	C5-C4-S4	-3.41	120.07	124.47
57	y	16	H2U	C4-N3-C2	-3.41	122.97	125.79
1	A	2580	PSU	C4-N3-C2	-3.39	121.45	126.34
57	y	32	PSU	O2-C2-N1	-3.38	119.06	122.79
57	y	39	PSU	O2-C2-N1	-3.38	119.07	122.79
1	A	2449	H2U	N3-C2-N1	3.38	120.22	116.65
1	A	955	PSU	O2-C2-N1	-3.37	119.08	122.79
57	y	55	PSU	O2-C2-N1	-3.36	119.09	122.79
1	A	746	PSU	O2-C2-N1	-3.36	119.09	122.79
57	y	20	H2U	O4'-C1'-N1	3.35	113.86	109.30
34	a	516	PSU	O2-C2-N1	-3.34	119.12	122.79
1	A	2030	6MZ	C9-N6-C6	-3.33	120.01	122.87
1	A	955	PSU	C6-C5-C4	-3.32	115.88	118.20
55	w	55	PSU	O2-C2-N1	-3.32	119.14	122.79
1	A	1917	PSU	O2-C2-N1	-3.31	119.14	122.79
1	A	747	5MC	C5-C4-N3	-3.31	118.11	121.67
34	a	967	5MC	C5-C4-N3	-3.30	118.11	121.67
1	A	2449	H2U	O4'-C1'-N1	3.30	113.80	109.30
1	A	1618	6MZ	C9-N6-C6	-3.30	120.03	122.87
55	v	55	PSU	O2-C2-N1	-3.29	119.16	122.79
34	a	1498	UR3	C1'-N1-C2	3.28	122.53	116.99
1	A	2580	PSU	C6-C5-C4	-3.28	115.91	118.20
1	A	2504	PSU	O2-C2-N1	-3.25	119.21	122.79
55	w	54	5MU	C5M-C5-C4	3.24	122.33	118.77
1	A	2552	OMU	C1'-N1-C2	3.24	123.44	117.57
1	A	1962	5MC	C5-C4-N3	-3.22	118.20	121.67
1	A	2457	PSU	O2-C2-N1	-3.21	119.26	122.79
1	A	2552	OMU	C5-C4-N3	3.19	119.62	114.84
1	A	1618	6MZ	N3-C2-N1	-3.18	123.71	128.68
1	A	2030	6MZ	N3-C2-N1	-3.17	123.73	128.68
1	A	2604	PSU	O2-C2-N1	-3.17	119.31	122.79
57	y	54	5MU	C5M-C5-C4	3.15	122.24	118.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2605	PSU	O2-C2-N1	-3.14	119.33	122.79
1	A	1962	5MC	O2-C2-N3	-3.08	117.32	122.33
55	w	54	5MU	O4-C4-C5	-3.07	121.35	124.90
1	A	1911	PSU	C6-C5-C4	-3.06	116.06	118.20
34	a	1407	5MC	O2-C2-N3	-3.06	117.36	122.33
1	A	1939	5MU	O4-C4-C5	-3.03	121.39	124.90
1	A	1917	PSU	C3'-C2'-C1'	3.01	105.15	101.64
55	w	55	PSU	C3'-C2'-C1'	3.01	105.14	101.64
34	a	1518	MA6	C3'-C2'-C1'	3.00	105.49	100.98
57	y	37	MIA	C11-S10-C2	-3.00	100.03	102.27
1	A	2069	7MG	C5-C6-N1	2.99	116.25	110.99
1	A	2498	OMC	O2-C2-N3	-2.97	117.50	122.33
1	A	2449	H2U	C5-C4-N3	2.95	119.97	116.65
34	a	527	7MG	C5-C6-N1	2.94	116.18	110.99
57	y	8	4SU	C6-N1-C2	-2.92	117.26	120.99
1	A	2580	PSU	C3'-C2'-C1'	2.91	105.02	101.64
1	A	745	1MG	O6-C6-C5	-2.91	119.05	124.19
57	y	46	7MG	C5-C6-N1	2.89	116.08	110.99
1	A	1939	5MU	O4'-C1'-N1	2.88	114.96	108.36
1	A	1939	5MU	C5-C6-N1	-2.88	120.38	123.34
34	a	966	2MG	C3'-C2'-C1'	2.87	105.29	100.98
1	A	2552	OMU	O4-C4-C5	-2.86	120.13	125.16
1	A	2605	PSU	C6-C5-C4	-2.81	116.23	118.20
55	v	54	5MU	O4-C4-C5	-2.81	121.64	124.90
55	v	54	5MU	C5M-C5-C4	2.79	121.84	118.77
1	A	2449	H2U	C4-N3-C2	-2.76	123.50	125.79
34	a	1519	MA6	C10-N6-C6	-2.74	111.23	119.51
34	a	967	5MC	O2-C2-N3	-2.74	117.88	122.33
1	A	2030	6MZ	C4-C5-N7	-2.73	106.55	109.40
57	y	37	MIA	C4-C5-N7	-2.70	106.58	109.40
34	a	966	2MG	C5-C6-N1	2.69	118.71	113.95
1	A	745	1MG	C5-C6-N1	2.69	117.95	113.90
34	a	1407	5MC	O4'-C1'-N1	2.69	114.50	108.36
57	y	37	MIA	C2-N1-C6	2.68	121.98	117.19
1	A	2580	PSU	O2-C2-N1	-2.67	119.85	122.79
1	A	1618	6MZ	C4-C5-N7	-2.66	106.63	109.40
1	A	2552	OMU	C6-N1-C2	-2.66	117.59	120.99
34	a	1402	4OC	C6-C5-C4	2.66	120.21	116.96
57	y	20	H2U	C5-C4-N3	2.65	119.63	116.65
34	a	1498	UR3	C3U-N3-C2	2.65	121.95	117.31
1	A	1835	2MG	C5-C6-N1	2.64	118.61	113.95
1	A	2457	PSU	C3'-C2'-C1'	2.64	104.71	101.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	w	20	H2U	C5-C6-N1	-2.64	102.93	111.61
1	A	2445	2MG	C5-C6-N1	2.63	118.59	113.95
34	a	1518	MA6	C9-N6-C6	-2.63	111.55	119.51
34	a	1207	2MG	C5-C6-N1	2.62	118.58	113.95
1	A	745	1MG	C8-N7-C5	2.59	107.93	102.99
1	A	2498	OMC	O4'-C1'-N1	2.59	114.27	108.36
1	A	2457	PSU	C6-C5-C4	-2.56	116.41	118.20
1	A	2503	2MA	C8-N7-C5	2.55	107.85	102.99
57	y	16	H2U	C5-C4-N3	2.54	119.50	116.65
1	A	1939	5MU	C5M-C5-C4	2.54	121.56	118.77
55	w	8	4SU	C6-N1-C2	-2.53	117.76	120.99
1	A	2069	7MG	O4'-C1'-N9	2.53	112.74	109.30
1	A	746	PSU	C6-C5-C4	-2.52	116.44	118.20
34	a	527	7MG	O4'-C1'-N9	2.51	112.72	109.30
34	a	1516	2MG	C8-N7-C5	2.51	107.77	102.99
1	A	2503	2MA	C5-C6-N1	2.51	118.35	114.02
1	A	1917	PSU	C6-C5-C4	-2.50	116.45	118.20
1	A	2445	2MG	C8-N7-C5	2.49	107.73	102.99
34	a	966	2MG	C8-N7-C5	2.49	107.73	102.99
34	a	1498	UR3	C6-N1-C2	-2.48	119.57	121.79
1	A	2604	PSU	C6-C5-C4	-2.47	116.47	118.20
1	A	747	5MC	C5-C6-N1	-2.47	120.80	123.34
55	v	20	H2U	C5-C4-N3	2.46	119.41	116.65
55	v	55	PSU	C6-C5-C4	-2.46	116.48	118.20
34	a	1516	2MG	C5-C6-N1	2.46	118.29	113.95
34	a	1519	MA6	C10-N6-C9	-2.45	108.24	116.12
34	a	1207	2MG	O6-C6-C5	-2.45	119.60	124.37
34	a	516	PSU	C6-C5-C4	-2.43	116.50	118.20
57	y	16	H2U	O4'-C1'-N1	2.43	112.61	109.30
1	A	2504	PSU	C6-C5-C4	-2.43	116.50	118.20
1	A	2552	OMU	O2-C2-N3	-2.42	117.00	121.50
34	a	1402	4OC	O2-C2-N3	-2.41	118.41	122.33
1	A	1911	PSU	C3'-C2'-C1'	2.41	104.44	101.64
34	a	516	PSU	C3'-C2'-C1'	2.40	104.43	101.64
55	v	54	5MU	O4'-C1'-N1	2.39	113.84	108.36
34	a	1402	4OC	C5-C4-N3	-2.39	118.74	122.59
1	A	2251	OMG	C5-C6-N1	2.39	118.17	113.95
1	A	1915	3TD	C3'-C2'-C1'	2.38	104.41	101.64
1	A	2069	7MG	N2-C2-N1	2.35	121.72	116.71
34	a	1207	2MG	C8-N7-C5	2.35	107.46	102.99
55	w	54	5MU	C5M-C5-C6	-2.34	119.72	122.85
34	a	527	7MG	CM7-N7-C5	2.34	132.45	126.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	y	37	MIA	N3-C2-N1	-2.33	122.70	126.98
34	a	1402	4OC	O4'-C1'-N1	2.32	113.67	108.36
1	A	2069	7MG	N2-C2-N3	-2.32	115.22	119.73
1	A	1835	2MG	C8-N7-C5	2.31	107.39	102.99
57	y	8	4SU	O2-C2-N3	-2.30	117.21	121.50
55	w	54	5MU	C3'-C2'-C1'	2.28	105.77	101.43
1	A	2503	2MA	C3'-C2'-C1'	2.25	104.36	100.98
57	y	46	7MG	CM7-N7-C5	2.24	132.18	126.40
55	w	54	5MU	C5-C6-N1	-2.24	121.04	123.34
57	y	16	H2U	C3'-C2'-C1'	2.24	105.68	101.43
57	y	55	PSU	C3'-C2'-C1'	2.23	104.23	101.64
1	A	2069	7MG	O6-C6-C5	-2.23	122.08	127.54
57	y	20	H2U	C3'-C2'-C1'	2.22	105.65	101.43
1	A	2251	OMG	C8-N7-C5	2.22	107.22	102.99
55	v	7	4SU	C6-N1-C2	-2.20	118.18	120.99
55	w	54	5MU	O4'-C1'-N1	2.19	113.37	108.36
1	A	746	PSU	C3'-C2'-C1'	2.19	104.19	101.64
1	A	2498	OMC	C2'-C1'-N1	-2.19	109.98	114.22
55	v	54	5MU	C5-C6-N1	-2.18	121.09	123.34
34	a	527	7MG	O6-C6-C5	-2.17	122.22	127.54
1	A	2604	PSU	C3'-C2'-C1'	2.16	104.15	101.64
55	v	54	5MU	C6-N1-C2	-2.15	119.12	121.30
55	v	7	4SU	O4'-C1'-N1	2.15	113.28	108.36
57	y	54	5MU	C1'-N1-C2	2.15	121.46	117.57
57	y	8	4SU	C1'-N1-C2	2.15	121.45	117.57
57	y	54	5MU	C5M-C5-C6	-2.12	120.02	122.85
34	a	1207	2MG	C3'-C2'-C1'	2.09	104.13	100.98
1	A	1939	5MU	O2-C2-N1	-2.09	120.01	122.79
1	A	2552	OMU	O4'-C1'-N1	2.08	113.12	108.36
1	A	2069	7MG	C6-C5-N7	2.07	135.17	131.91
55	w	54	5MU	O2-C2-N3	-2.07	117.65	121.50
57	y	54	5MU	C6-N1-C2	-2.07	119.20	121.30
57	y	46	7MG	O6-C6-C5	-2.06	122.49	127.54
1	A	2069	7MG	C6-C5-C4	-2.06	118.38	122.62
55	v	20	H2U	C5-C6-N1	-2.04	104.89	111.61
55	w	55	PSU	C6-C5-C4	-2.03	116.78	118.20
1	A	2069	7MG	CM7-N7-C5	2.02	131.61	126.40

There are no chirality outliers.

All (82) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	a	1402	4OC	O4'-C4'-C5'-O5'
34	a	1518	MA6	C5-C6-N6-C9
34	a	1519	MA6	C5-C6-N6-C10
55	v	55	PSU	O4'-C1'-C5-C4
55	v	55	PSU	O4'-C1'-C5-C6
55	w	8	4SU	C3'-C4'-C5'-O5'
55	w	8	4SU	O4'-C4'-C5'-O5'
1	A	1618	6MZ	C5-C6-N6-C9
1	A	1618	6MZ	N1-C6-N6-C9
1	A	1915	3TD	O4'-C1'-C5-C4
1	A	1915	3TD	O4'-C1'-C5-C6
1	A	1915	3TD	C3'-C4'-C5'-O5'
1	A	1915	3TD	O4'-C4'-C5'-O5'
1	A	1917	PSU	O4'-C4'-C5'-O5'
1	A	1962	5MC	O4'-C4'-C5'-O5'
1	A	1962	5MC	C3'-C4'-C5'-O5'
1	A	2030	6MZ	C4'-C5'-O5'-P
1	A	2030	6MZ	C3'-C4'-C5'-O5'
1	A	2069	7MG	C3'-C4'-C5'-O5'
1	A	2445	2MG	O4'-C4'-C5'-O5'
1	A	2445	2MG	C3'-C4'-C5'-O5'
1	A	2503	2MA	O4'-C4'-C5'-O5'
1	A	2552	OMU	O4'-C1'-N1-C2
1	A	2552	OMU	O4'-C1'-N1-C6
57	y	20	H2U	O4'-C1'-N1-C2
57	y	20	H2U	O4'-C1'-N1-C6
57	y	37	MIA	C5-C6-N6-C12
57	y	37	MIA	N1-C6-N6-C12
57	y	37	MIA	N6-C12-C13-C14
57	y	37	MIA	C12-C13-C14-C15
57	y	37	MIA	C12-C13-C14-C16
57	y	39	PSU	C3'-C4'-C5'-O5'
34	a	1498	UR3	O4'-C1'-N1-C2
34	a	966	2MG	C4'-C5'-O5'-P
34	a	966	2MG	O4'-C4'-C5'-O5'
34	a	966	2MG	C3'-C4'-C5'-O5'
34	a	1402	4OC	C3'-C4'-C5'-O5'
1	A	1917	PSU	C3'-C4'-C5'-O5'
1	A	2457	PSU	C3'-C4'-C5'-O5'
1	A	2457	PSU	O4'-C4'-C5'-O5'
57	y	46	7MG	O4'-C4'-C5'-O5'
57	y	55	PSU	C3'-C4'-C5'-O5'
55	v	7	4SU	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
1	A	2030	6MZ	O4'-C4'-C5'-O5'
1	A	2503	2MA	C3'-C4'-C5'-O5'
1	A	2504	PSU	O4'-C4'-C5'-O5'
57	y	39	PSU	O4'-C4'-C5'-O5'
57	y	46	7MG	C3'-C4'-C5'-O5'
34	a	1518	MA6	N1-C6-N6-C9
34	a	1519	MA6	N1-C6-N6-C10
55	w	8	4SU	C2'-C1'-N1-C6
34	a	1207	2MG	C3'-C4'-C5'-O5'
1	A	2504	PSU	C3'-C4'-C5'-O5'
34	a	1498	UR3	O4'-C1'-N1-C6
55	v	7	4SU	C3'-C4'-C5'-O5'
57	y	16	H2U	O4'-C4'-C5'-O5'
57	y	16	H2U	C3'-C4'-C5'-O5'
57	y	55	PSU	O4'-C4'-C5'-O5'
1	A	2069	7MG	O4'-C4'-C5'-O5'
57	y	46	7MG	C2'-C1'-N9-C8
34	a	1207	2MG	O4'-C4'-C5'-O5'
55	w	8	4SU	O4'-C1'-N1-C6
55	w	8	4SU	C2'-C1'-N1-C2
1	A	1618	6MZ	C4'-C5'-O5'-P
57	y	37	MIA	C3'-C4'-C5'-O5'
55	w	8	4SU	O4'-C1'-N1-C2
34	a	516	PSU	O4'-C4'-C5'-O5'
1	A	1939	5MU	O4'-C4'-C5'-O5'
57	y	37	MIA	O4'-C4'-C5'-O5'
34	a	527	7MG	C4'-C5'-O5'-P
34	a	516	PSU	C3'-C4'-C5'-O5'
34	a	1519	MA6	C4'-C5'-O5'-P
34	a	527	7MG	C3'-C4'-C5'-O5'
55	w	20	H2U	C2'-C1'-N1-C6
57	y	46	7MG	O4'-C1'-N9-C8
1	A	1939	5MU	C3'-C4'-C5'-O5'
57	y	8	4SU	C2'-C1'-N1-C2
34	a	516	PSU	O4'-C1'-C5-C6
55	w	55	PSU	O4'-C1'-C5-C6
1	A	746	PSU	O4'-C1'-C5-C6
55	w	20	H2U	C2'-C1'-N1-C2
57	y	8	4SU	O4'-C4'-C5'-O5'

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 1417 ligands modelled in this entry, 1414 are monoatomic - leaving 3 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
62	PHE	z	401	-	10,11,12	0.46	0	10,13,15	0.25	0
63	GTP	z	402	-	26,34,34	0.91	0	32,54,54	1.44	5 (15%)
59	FME	A	3001	-	8,9,10	0.50	0	7,9,11	0.97	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
62	PHE	z	401	-	-	0/5/6/8	0/1/1/1
63	GTP	z	402	-	-	2/18/38/38	0/3/3/3
59	FME	A	3001	-	-	1/7/9/11	-

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
63	z	402	GTP	PB-O3B-PG	-3.20	121.86	132.83
63	z	402	GTP	C3'-C2'-C1'	3.12	105.68	100.98
63	z	402	GTP	PA-O3A-PB	-3.09	122.23	132.83
63	z	402	GTP	C5-C6-N1	2.50	118.37	113.95
63	z	402	GTP	C8-N7-C5	2.45	107.65	102.99

There are no chirality outliers.



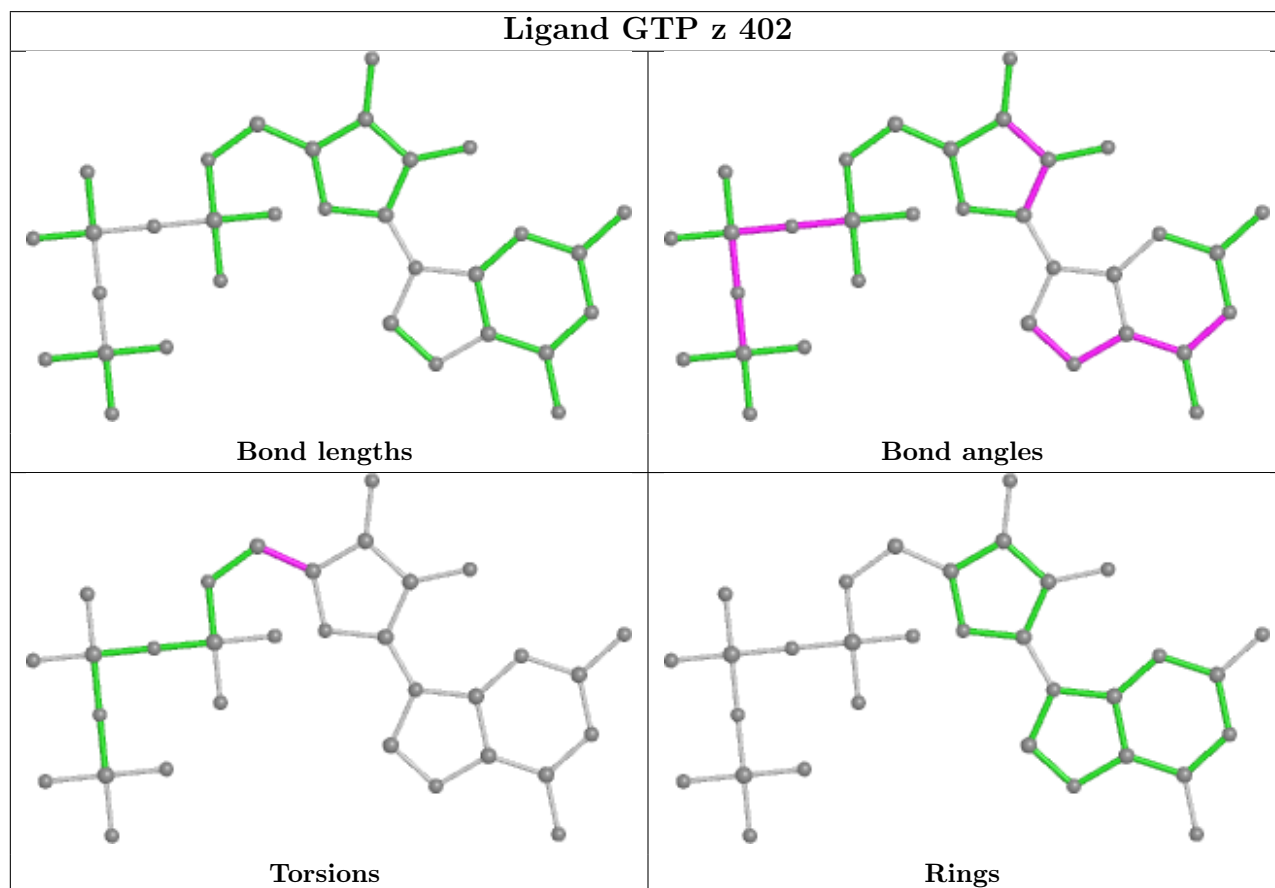
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	A	3001	FME	O-C-CA-CB
63	z	402	GTP	C3'-C4'-C5'-O5'
63	z	402	GTP	O4'-C4'-C5'-O5'

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
55	w	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	w	117:U	O3'	18:G	P	1.14

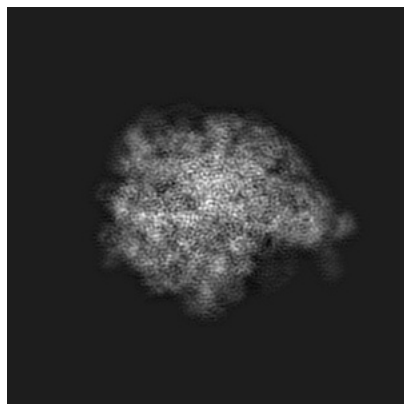
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8828. These allow visual inspection of the internal detail of the map and identification of artifacts.

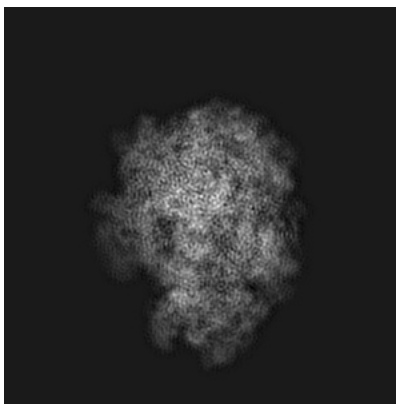
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

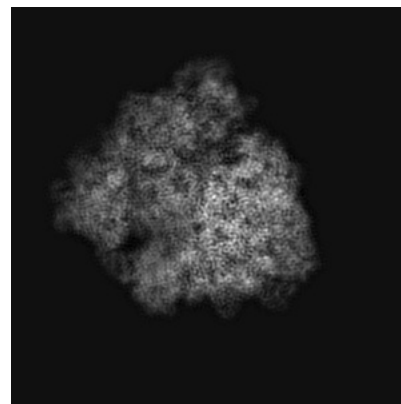
#### 6.1.1 Primary map



X

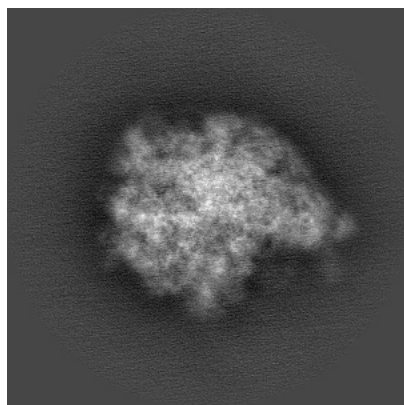


Y

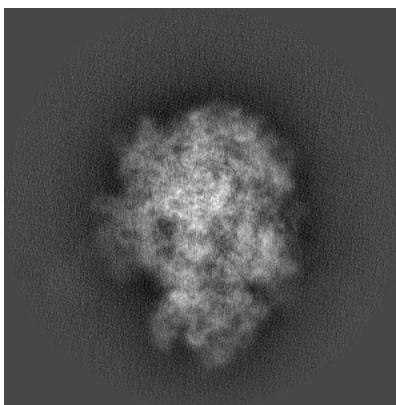


Z

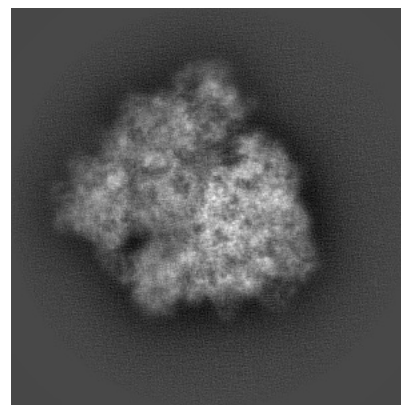
#### 6.1.2 Raw map



X



Y

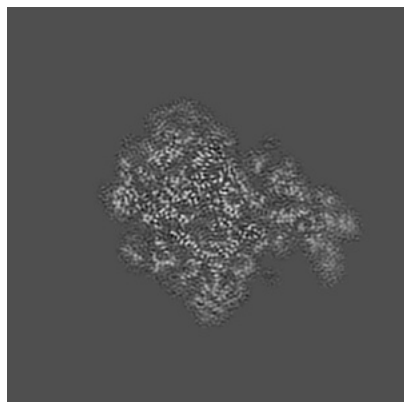


Z

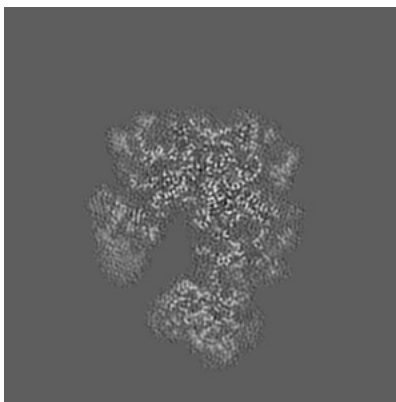
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

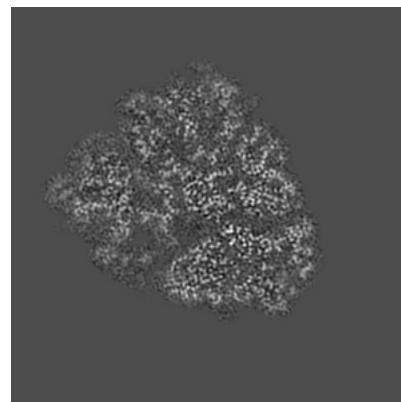
### 6.2.1 Primary map



X Index: 199

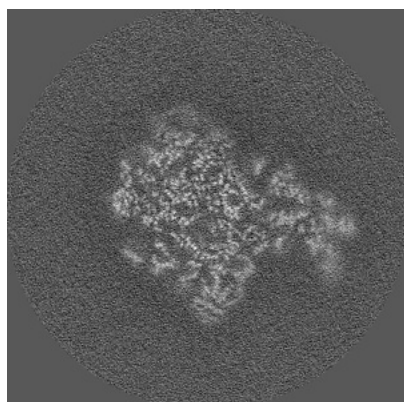


Y Index: 199

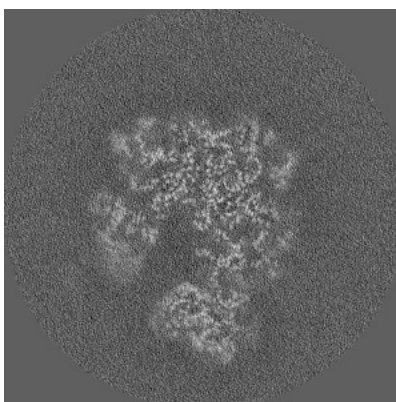


Z Index: 199

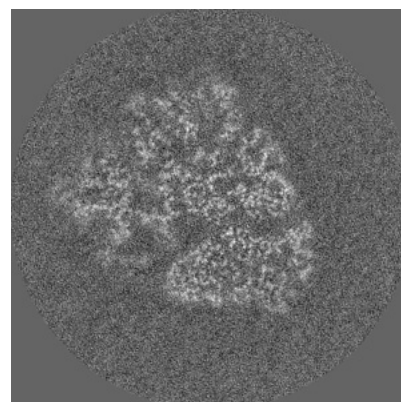
### 6.2.2 Raw map



X Index: 199



Y Index: 199

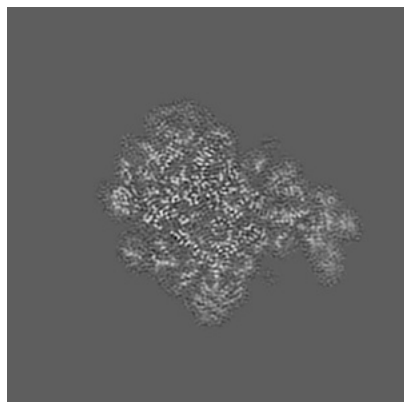


Z Index: 199

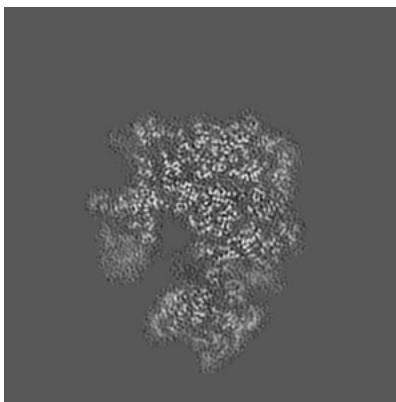
The images above show central slices of the map in three orthogonal directions.

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

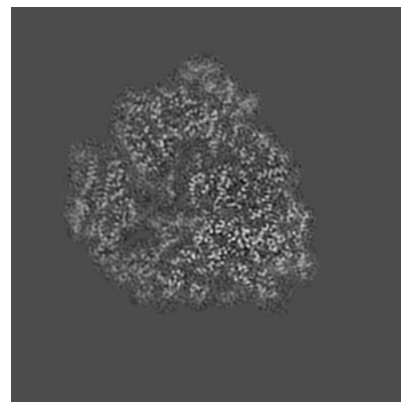
### 6.3.1 Primary map



X Index: 200

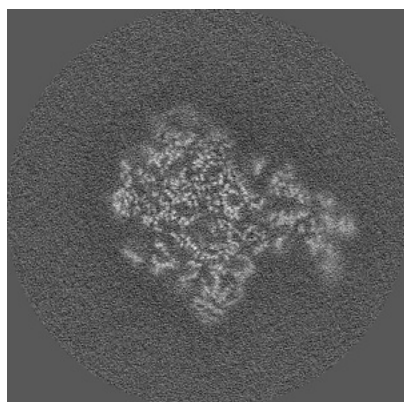


Y Index: 207

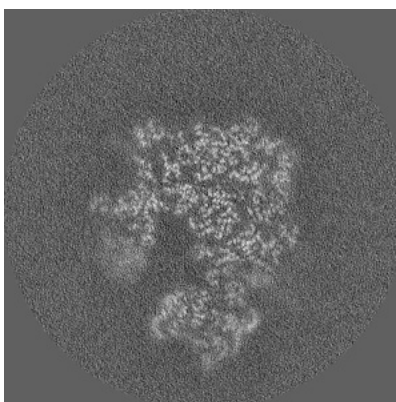


Z Index: 189

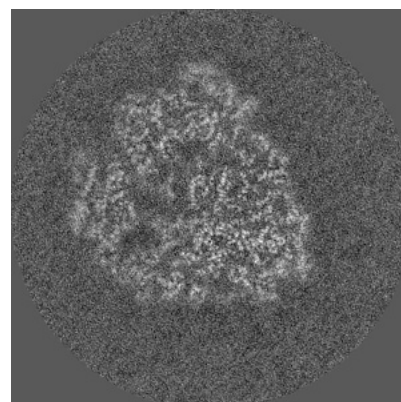
### 6.3.2 Raw map



X Index: 199



Y Index: 207

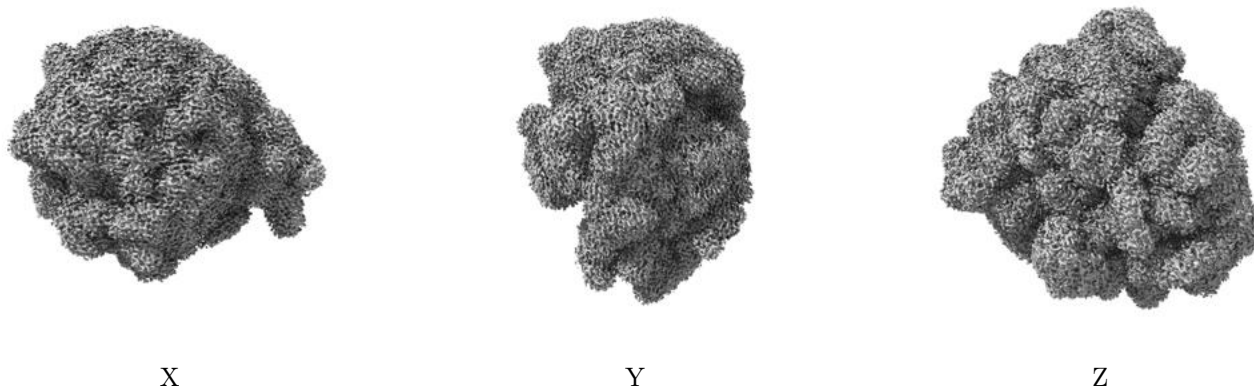


Z Index: 189

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

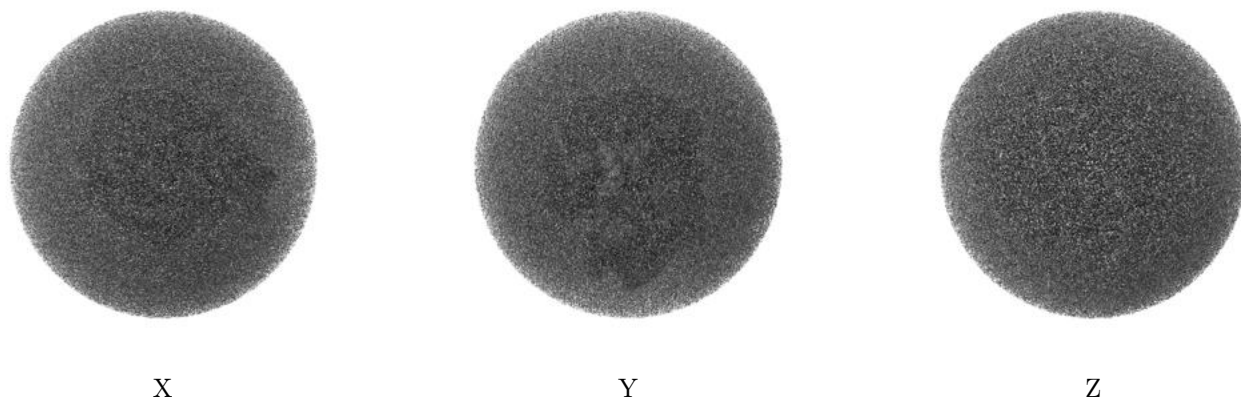
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00651. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 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.



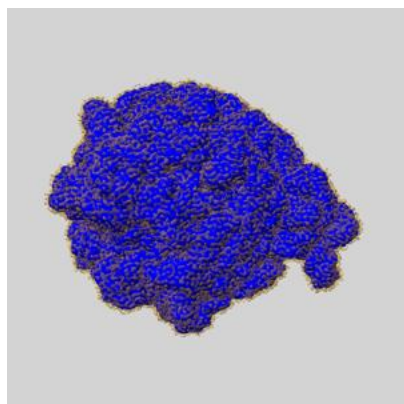
## 6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

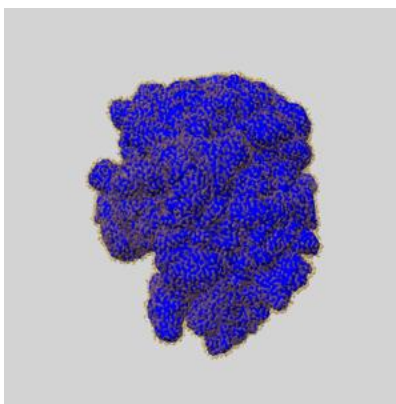
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

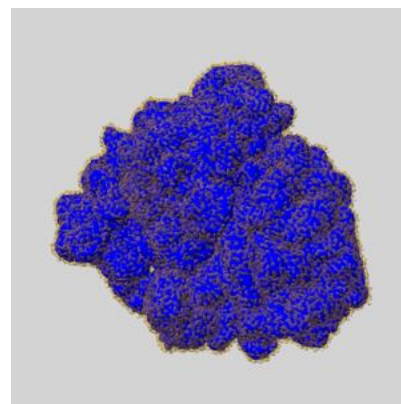
### 6.5.1 emd\_8828\_msk\_1.map [i](#)



X



Y

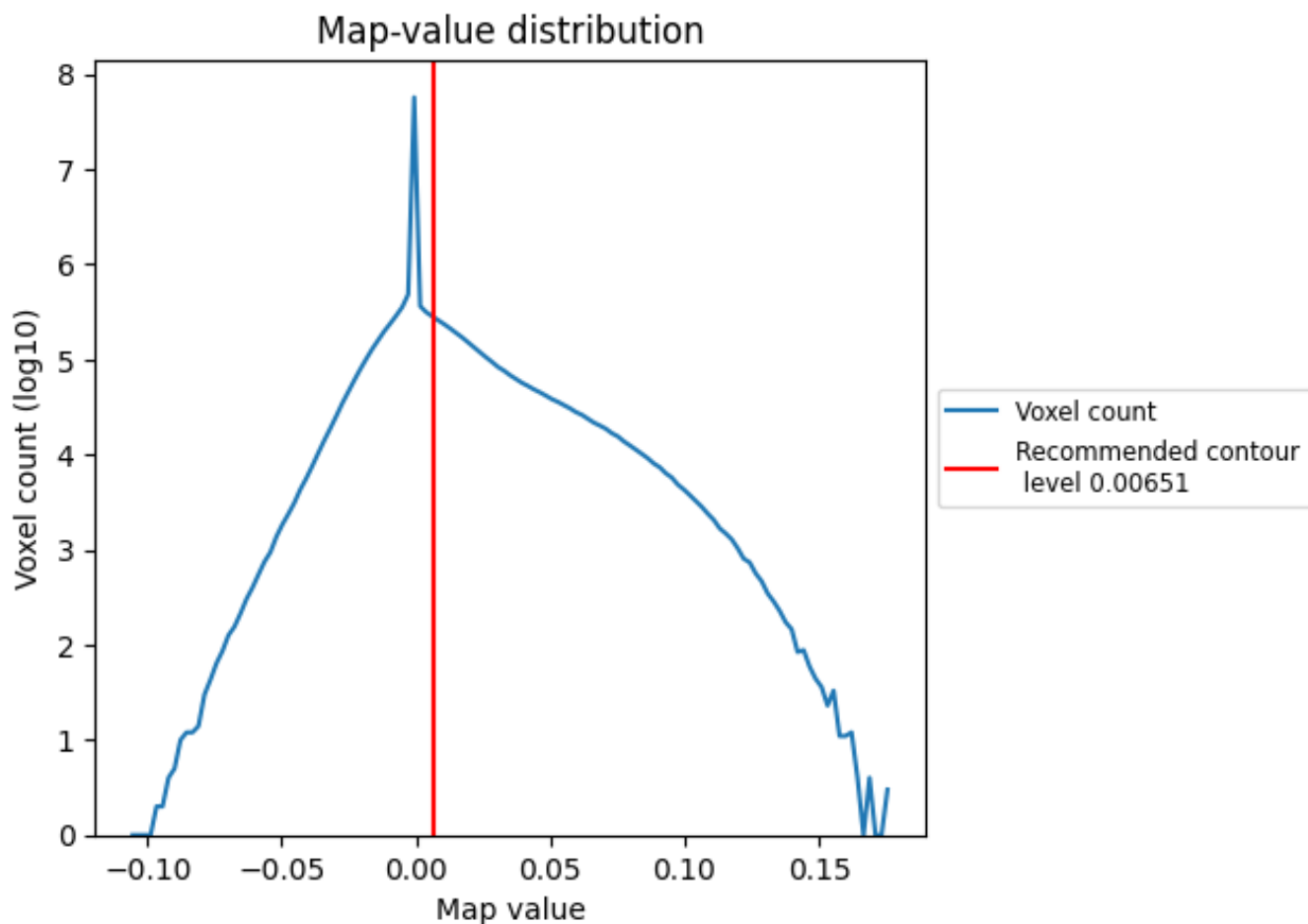


Z

## 7 Map analysis [i](#)

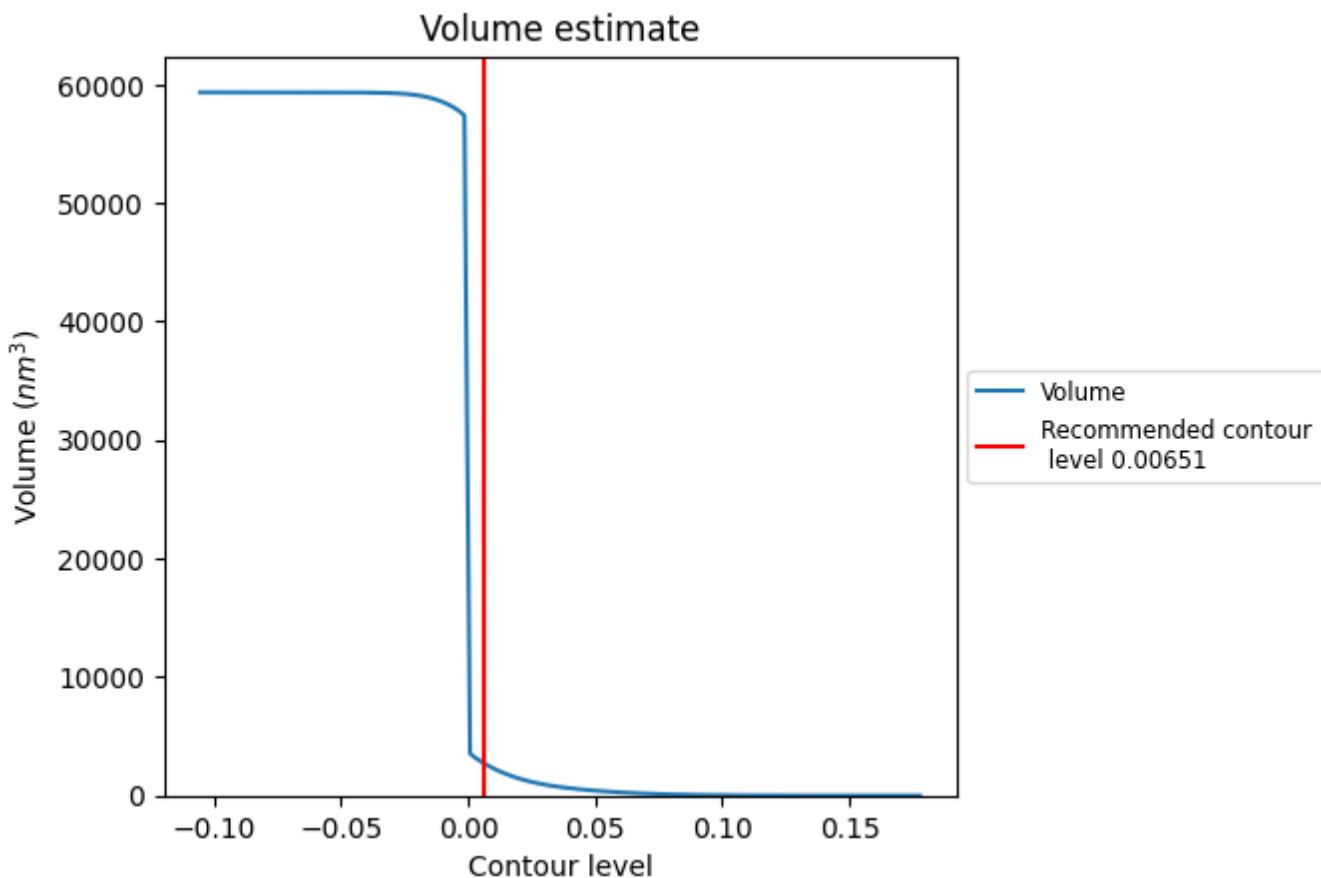
This section contains the results of statistical analysis of the map.

### 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](#)

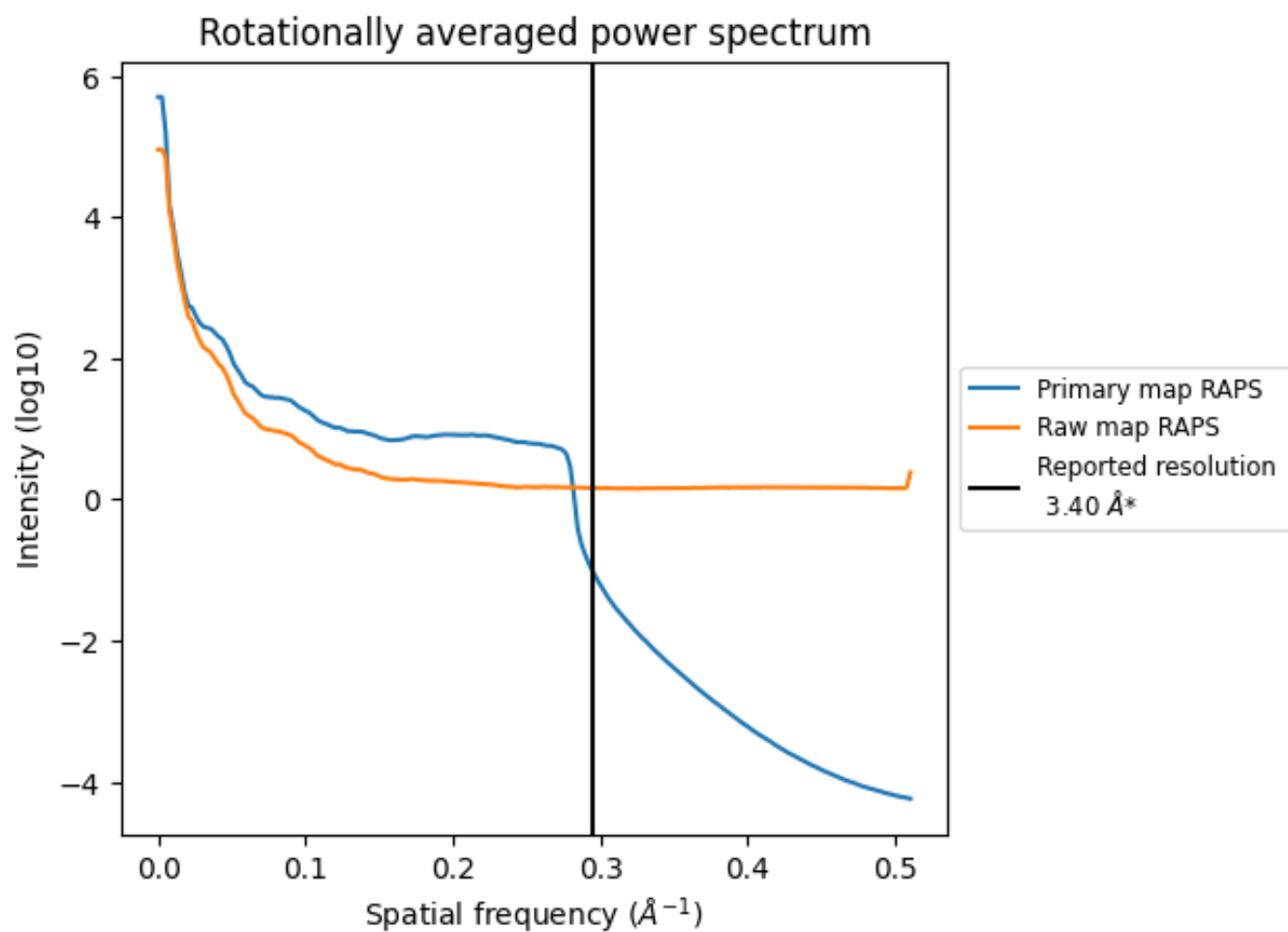


The volume at the recommended contour level is 2690 nm<sup>3</sup>; this corresponds to an approximate mass of 2430 kDa.

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

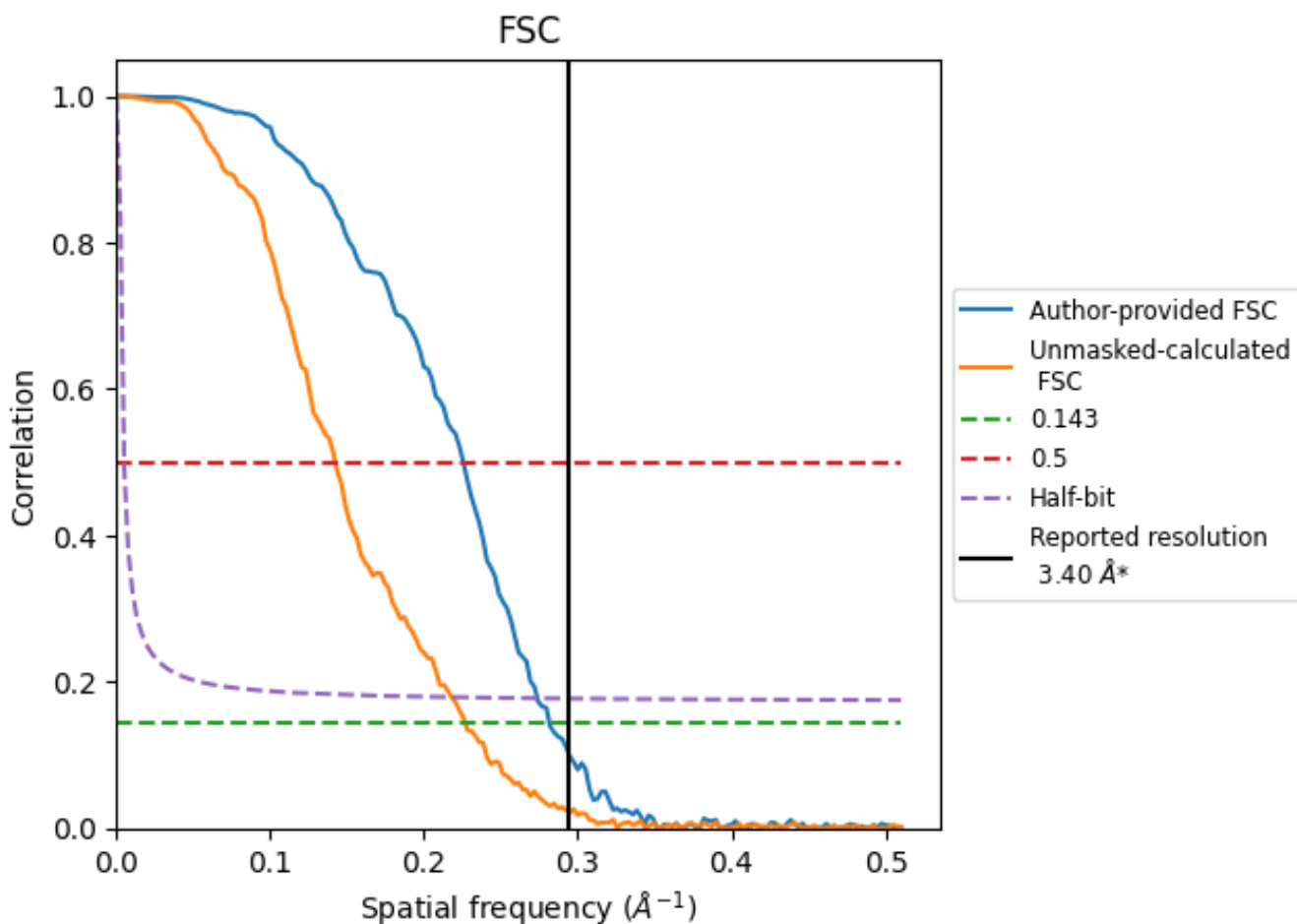


\*Reported resolution corresponds to spatial frequency of 0.294 Å<sup>-1</sup>

## 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 0.294 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

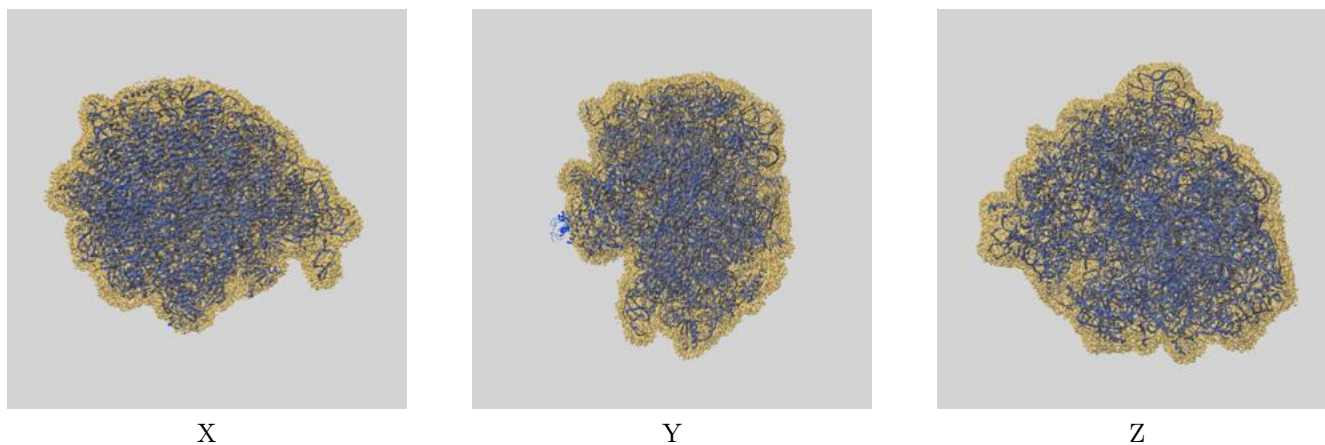
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.55	4.43	3.65
Unmasked-calculated*	4.41	7.03	4.59

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.41 differs from the reported value 3.4 by more than 10 %

## 9 Map-model fit [i](#)

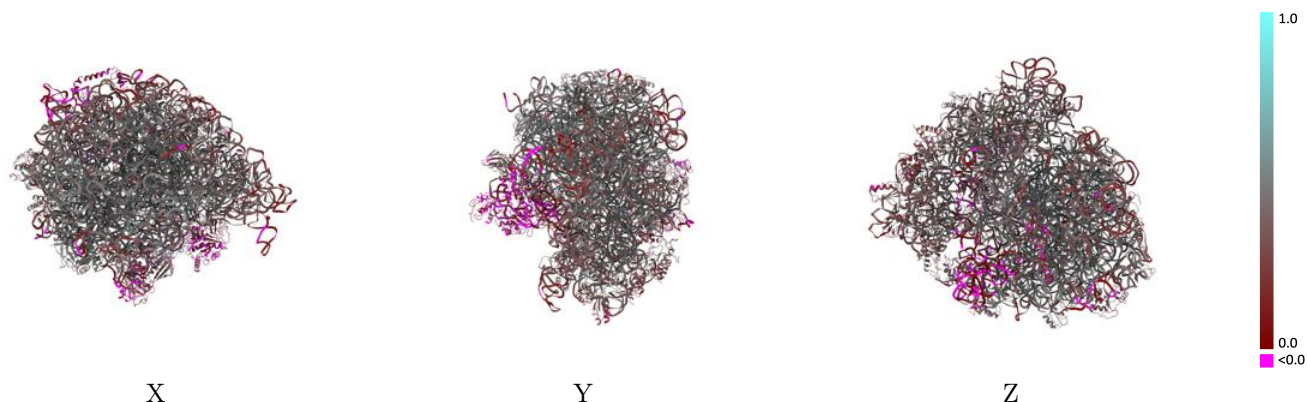
This section contains information regarding the fit between EMDB map EMD-8828 and PDB model 5WFK. Per-residue inclusion information can be found in section 3 on page 20.

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



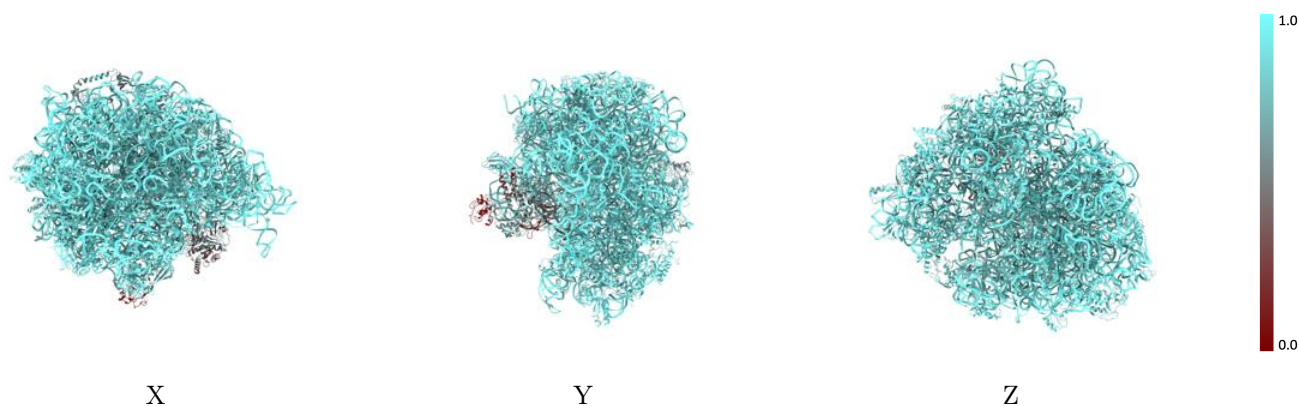
The images above show the 3D surface view of the map at the recommended contour level 0.00651 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



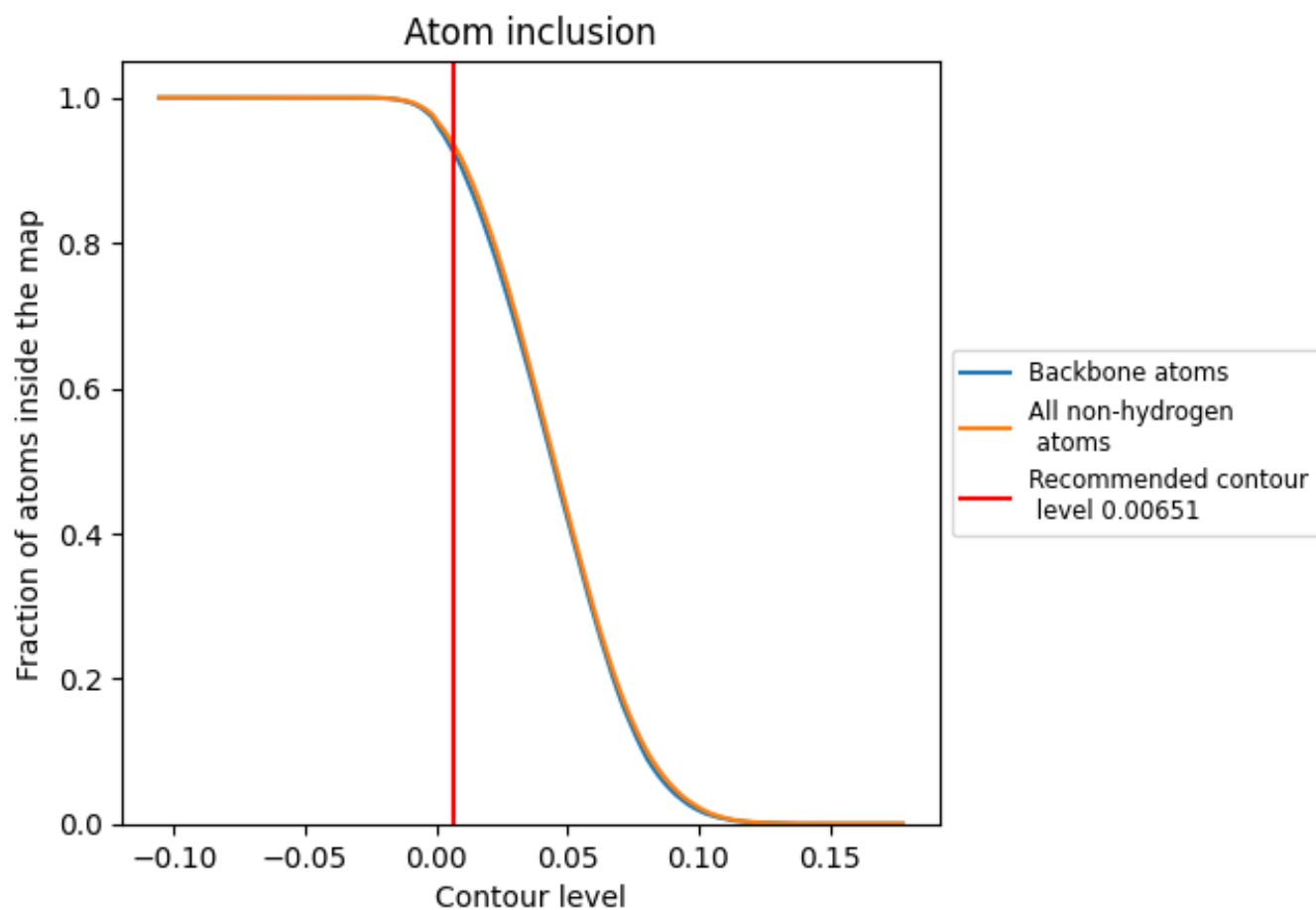
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00651).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% 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 (0.00651) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9359	 0.3850
0	 0.9570	 0.4610
1	 0.9487	 0.4460
2	 0.9422	 0.4900
3	 0.9552	 0.5060
4	 0.9420	 0.4720
5	 0.2242	 0.0090
6	 0.8748	 0.2840
A	 0.9746	 0.4110
B	 0.9823	 0.3850
C	 0.9430	 0.4790
D	 0.9511	 0.4630
E	 0.9360	 0.4350
F	 0.9184	 0.3570
G	 0.9186	 0.3330
H	 0.6955	 0.1660
I	 0.6223	 0.0280
J	 0.9358	 0.4550
K	 0.9113	 0.4420
L	 0.9518	 0.4600
M	 0.9539	 0.4540
N	 0.9540	 0.4660
O	 0.9560	 0.4010
P	 0.9493	 0.4570
Q	 0.9654	 0.4790
R	 0.9456	 0.4430
S	 0.9468	 0.4680
T	 0.9216	 0.4040
U	 0.9479	 0.4070
V	 0.9351	 0.4100
W	 0.9532	 0.4760
X	 0.9385	 0.4610
Y	 0.9400	 0.3860
Z	 0.9645	 0.4830
a	 0.9788	 0.3950



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Chain	Atom inclusion	Q-score
b	 0.8979	 0.3220
c	 0.9120	 0.3800
d	 0.9214	 0.3730
e	 0.9286	 0.4330
f	 0.9097	 0.3760
g	 0.9144	 0.3330
h	 0.9167	 0.4230
i	 0.9011	 0.3380
j	 0.9028	 0.3210
k	 0.9468	 0.4200
l	 0.9162	 0.4290
m	 0.9221	 0.3680
n	 0.9178	 0.3640
o	 0.9362	 0.4000
p	 0.9362	 0.4140
q	 0.9368	 0.3840
r	 0.9027	 0.3720
s	 0.9452	 0.3970
t	 0.9138	 0.3650
u	 0.8182	 0.2530
v	 0.9552	 0.3780
w	 0.7960	 0.0760
x	 0.9328	 0.3390
y	 0.5282	 0.0470
z	 0.4551	 0.0680