Full wwPDB EM Validation Report ⓘ

Mar 12, 2025 – 01:22 PM EDT

PDB ID	:	8G7P
EMDB ID	:	EMD-29819
Title	:	Structure of the Escherichia coli 70S ribosome in complex with EF-Tu and Ile-tRNAIle(LAU) bound to the cognate AUA codon (Structure I)
Authors	:	Rybak, M.Y.; Gagnon, M.G.
Deposited on	:	2023-02-16
Resolution	:	2.90 Å(reported)
Based on initial models	:	5UYM, 7K00

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

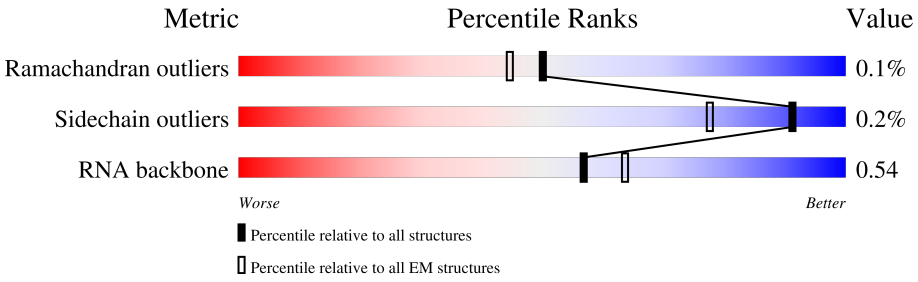
EMDB validation analysis	:	0.0.1.dev117
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	a	1542	85% 13%
2	b	241	93% 7%
3	c	233	88% 12%
4	d	206	99%
5	e	167	93% 7%
6	f	131	79% 21%
7	g	156	97%
8	h	130	99%

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Mol	Chain	Length	Quality of chain
9	i	130	97%
10	j	103	93% 5%
11	k	129	90% 9%
12	l	124	97%
13	m	118	97%
14	n	101	99%
15	o	89	99%
16	p	82	99%
17	q	84	94% 6%
18	r	75	72% 28%
19	s	92	90% 10%
20	t	87	99%
21	u	71	99%
22	w	76	71% 18% 11%
22	y	76	61% 32% 8%
23	x	77	84% 14%
24	v	27	44% 52%
25	z	392	99%
26	A	2904	85% 15%
27	B	120	83% 13%
28	C	273	99%
29	D	209	100%
30	E	201	100%
31	F	179	98%
32	G	177	99%

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Mol	Chain	Length	Quality of chain
33	H	149	28% 72%
34	J	142	47% 99%
35	L	142	100%
36	M	123	100%
37	N	144	100%
38	O	136	99%
39	P	127	93% 7%
40	Q	117	99%
41	R	115	99%
42	S	118	99%
43	T	103	100%
44	U	110	100%
45	V	100	92% 7%
46	W	104	98%
47	X	94	100%
48	Y	85	88% 11%
49	Z	78	99%
50	1	63	97%
51	2	59	98%
52	3	70	86% 14%
53	4	57	96%
54	5	55	93% 7%
55	6	46	98%
56	7	65	97%
57	8	38	100%

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 151823 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 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	a	1529	32825	14647	6024	10625	1529	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	b	224	1754	1110	315	321	8	0	0

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

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

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

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

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

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

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	152	Total	C	N	O	S	0	0
			1191	741	230	216	4		

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	119	IAS	ASN	modified residue	UNP A0A0H3PWX2

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	121	Total	C	N	O	S	0	0
			942	582	193	162	5		

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	r	54	Total	C	N	O	0	0
			446	283	85	78		

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

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

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

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

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

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

- Molecule 22 is a RNA chain called Isoleucine tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	w	76	Total	C	N	O	P	S	0	0
			1647	740	292	538	76	1		
22	y	76	Total	C	N	O	P	S	0	0
			1644	740	292	536	75	1		

- Molecule 23 is a RNA chain called P-site initiator tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	x	76	Total	C	N	O	P	S	0	0
			1625	725	294	529	76	1		

- Molecule 24 is a RNA chain called M-I mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	v	13	Total	C	N	O	P	0	0
			284	128	59	84	13		

- Molecule 25 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	z	392	Total	C	N	O	S	0	0
			3029	1915	521	580	13		

- Molecule 26 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	2899	Total	C	N	O	P	0	0
			62252	27778	11456	20119	2899		

- Molecule 27 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B	120	Total	C	N	O	P	0	0
			2572	1145	470	837	120		

- Molecule 28 is a protein called 50S ribosomal protein L2.

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

- Molecule 29 is a protein called 50S ribosomal protein L3.

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

- Molecule 30 is a protein called 50S ribosomal protein L4.

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

- Molecule 31 is a protein called 50S ribosomal protein L5.

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

- Molecule 32 is a protein called 50S ribosomal protein L6.

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

- Molecule 33 is a protein called 50S ribosomal protein L9.

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

- Molecule 34 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	J	141	Total	C	N	O	0	0
			693	411	141	141		

- Molecule 35 is a protein called 50S ribosomal protein L13.

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

- Molecule 36 is a protein called 50S ribosomal protein L14.

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

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	N	144	Total	C	N	O	S	0	0
			1052	653	207	190	2		

- Molecule 38 is a protein called 50S ribosomal protein L16.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	82	MS6	MET	modified residue	UNP E6BI61

- Molecule 39 is a protein called 50S ribosomal protein L17.

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

- Molecule 40 is a protein called 50S ribosomal protein L18.

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

- Molecule 41 is a protein called 50S ribosomal protein L19.

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

- Molecule 42 is a protein called 50S ribosomal protein L20.

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

- Molecule 43 is a protein called Ribosomal protein L21.

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

- Molecule 44 is a protein called 50S ribosomal protein L22.

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

- Molecule 45 is a protein called 50S ribosomal protein L23.

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

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	W	102	Total 779	C 492	N 146	O 141	0	0

- Molecule 47 is a protein called 50S ribosomal protein L25.

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

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Y	76	Total	C	N	O	S	0	0
			580	359	117	103	1		

- Molecule 49 is a protein called 50S ribosomal protein L28.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 51 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	60	Total	C	N	O	S	0	0
			476	296	89	85	6		

- Molecule 53 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	4	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 54 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	5	51	Total 417	C 269	N 76	O 72	0	0

- Molecule 55 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	6	46	Total 373	C 225	N 89	O 57	S 2	0	0

- Molecule 56 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	7	64	Total 504	C 323	N 105	O 74	S 2	0	0

- Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	8	38	Total 302	C 185	N 65	O 48	S 4	0	0

- Molecule 58 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	a	182	Total 182	Mg 182	0
58	j	2	Total 2	Mg 2	0
58	n	2	Total 2	Mg 2	0
58	p	1	Total 1	Mg 1	0
58	w	1	Total 1	Mg 1	0
58	x	2	Total 2	Mg 2	0
58	v	3	Total 3	Mg 3	0
58	z	2	Total 2	Mg 2	0
58	A	640	Total 640	Mg 640	0

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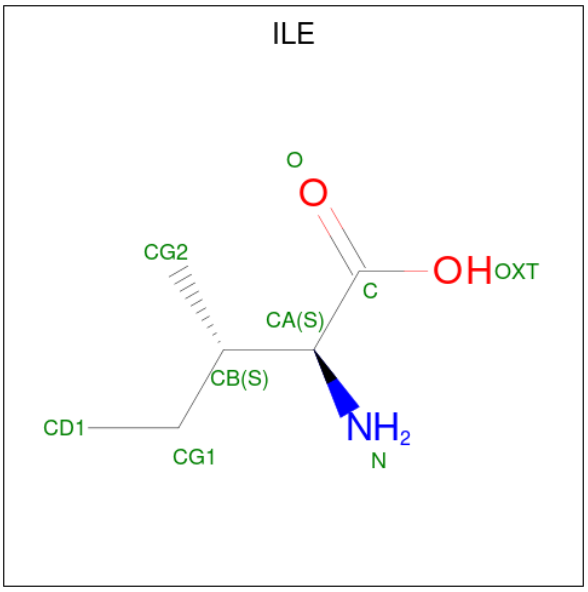
Mol	Chain	Residues	Atoms	AltConf
58	B	9	Total Mg 9 9	0
58	D	1	Total Mg 1 1	0
58	E	2	Total Mg 2 2	0
58	G	1	Total Mg 1 1	0
58	L	3	Total Mg 3 3	0
58	N	5	Total Mg 5 5	0
58	R	2	Total Mg 2 2	0
58	U	1	Total Mg 1 1	0
58	V	2	Total Mg 2 2	0
58	W	1	Total Mg 1 1	0
58	Z	1	Total Mg 1 1	0
58	2	2	Total Mg 2 2	0
58	4	3	Total Mg 3 3	0
58	6	6	Total Mg 6 6	0
58	8	2	Total Mg 2 2	0

- Molecule 59 is POTASSIUM ION (three-letter code: K) (formula: K).

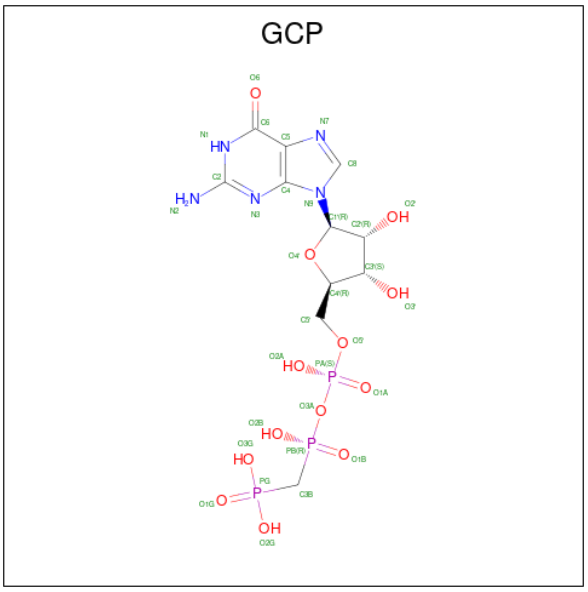
Mol	Chain	Residues	Atoms	AltConf
59	a	1	Total K 1 1	0
59	l	1	Total K 1 1	0

- Molecule 60 is ISOLEUCINE (three-letter code: ILE) (formula: $C_6H_{13}NO_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
60	w	1	Total	C	N	O	0
			8	6	1	1	
60	y	1	Total	C	N	O	0
			8	6	1	1	

- Molecule 61 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
61	z	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 62 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
62	3	1	Total Zn 1 1	0
62	8	1	Total Zn 1 1	0

- Molecule 63 is water.

Mol	Chain	Residues	Atoms	AltConf
63	a	131	Total O 131 131	0
63	i	2	Total O 2 2	0
63	l	1	Total O 1 1	0
63	m	1	Total O 1 1	0
63	n	3	Total O 3 3	0
63	p	4	Total O 4 4	0
63	t	1	Total O 1 1	0
63	v	1	Total O 1 1	0
63	A	517	Total O 517 517	0
63	B	8	Total O 8 8	0
63	C	3	Total O 3 3	0
63	D	2	Total O 2 2	0
63	E	1	Total O 1 1	0
63	L	2	Total O 2 2	0
63	N	4	Total O 4 4	0
63	P	5	Total O 5 5	0
63	S	5	Total O 5 5	0

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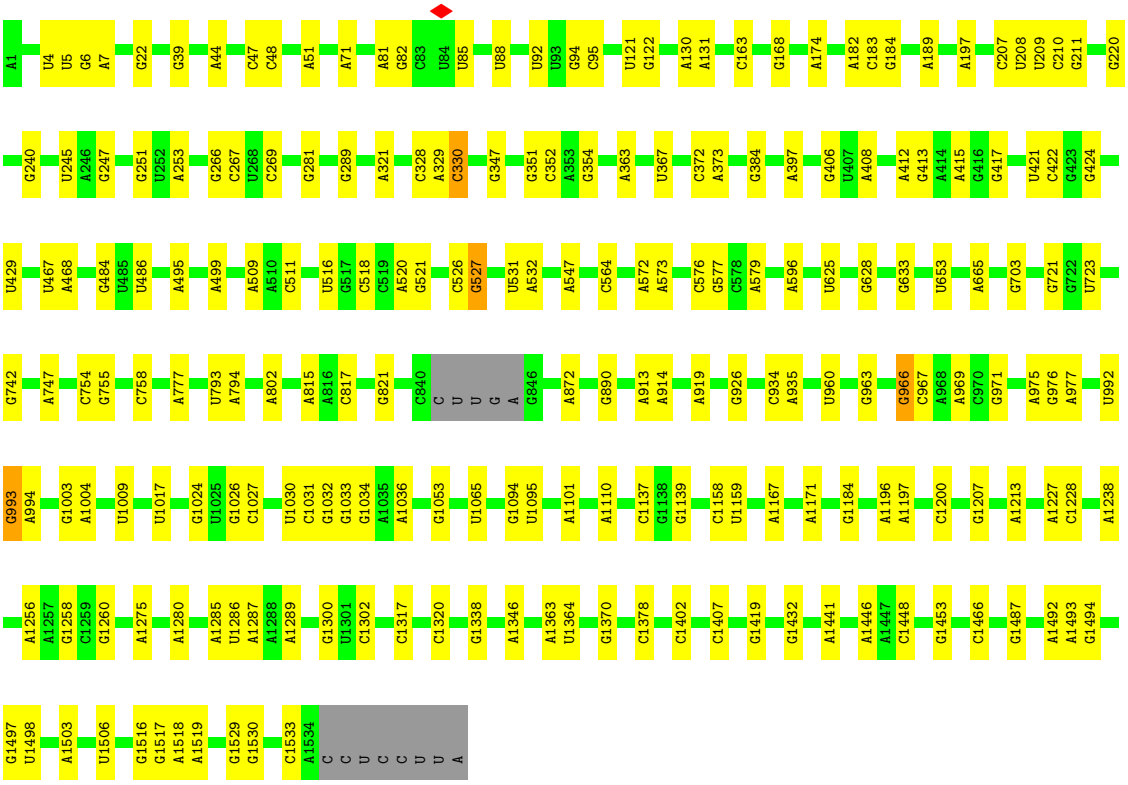
Mol	Chain	Residues	Atoms	AltConf
63	T	3	Total O 3 3	0
63	U	2	Total O 2 2	0
63	V	2	Total O 2 2	0
63	W	4	Total O 4 4	0
63	Y	3	Total O 3 3	0
63	2	1	Total O 1 1	0
63	4	5	Total O 5 5	0
63	6	3	Total O 3 3	0
63	7	1	Total O 1 1	0
63	8	1	Total O 1 1	0

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.

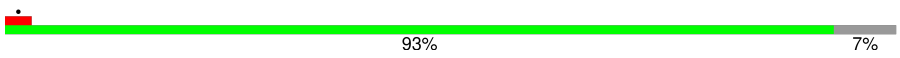
• Molecule 1: 16S Ribosomal RNA

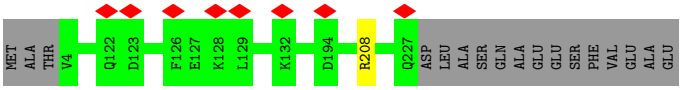
Chain a:



• Molecule 2: 30S ribosomal protein S2

Chain b:



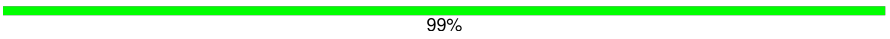


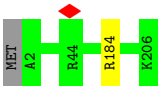
• Molecule 3: 30S ribosomal protein S3

Chain c:

• Molecule 4: 30S ribosomal protein S4

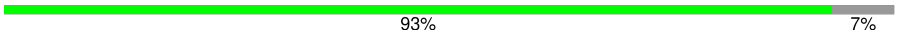
Chain d:





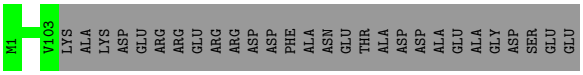
• Molecule 5: 30S ribosomal protein S5

Chain e:



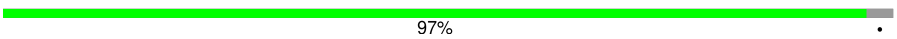
• Molecule 6: 30S ribosomal protein S6

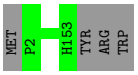
Chain f:



• Molecule 7: 30S ribosomal protein S7

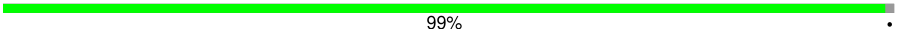
Chain g:





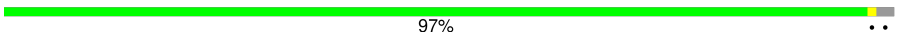
• Molecule 8: 30S ribosomal protein S8

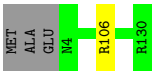
Chain h:



• Molecule 9: 30S ribosomal protein S9

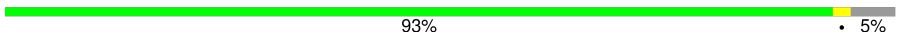
Chain i:





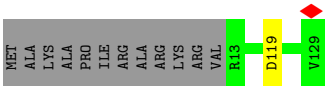
• Molecule 10: 30S ribosomal protein S10

Chain j:



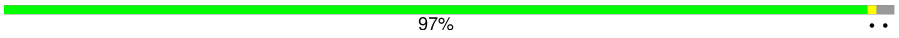
• Molecule 11: 30S ribosomal protein S11

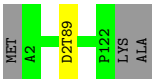
Chain k:



• Molecule 12: 30S ribosomal protein S12

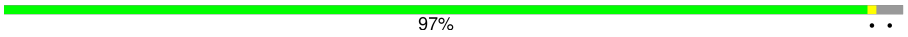
Chain l:





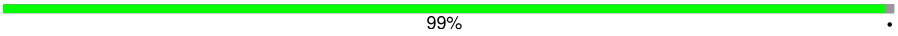
• Molecule 13: 30S ribosomal protein S13

Chain m:



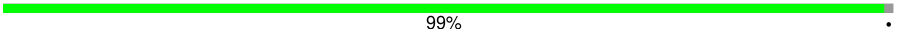
• Molecule 14: 30S ribosomal protein S14

Chain n:



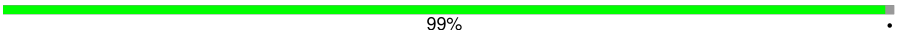
• Molecule 15: 30S ribosomal protein S15

Chain o:



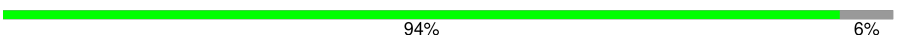
• Molecule 16: 30S ribosomal protein S16

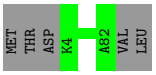
Chain p:



• Molecule 17: 30S ribosomal protein S17

Chain q:



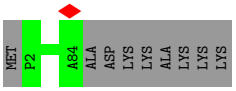


• Molecule 18: 30S ribosomal protein S18

Chain r:

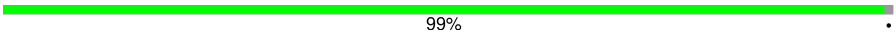
• Molecule 19: 30S ribosomal protein S19

Chain s:



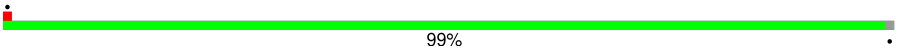
• Molecule 20: 30S ribosomal protein S20

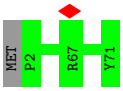
Chain t:



• Molecule 21: 30S ribosomal protein S21

Chain u:



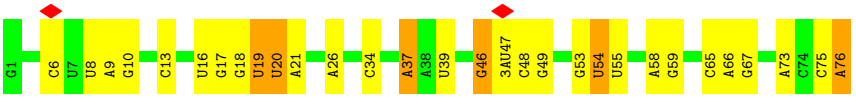


• Molecule 22: Isoleucine tRNA

Chain w:

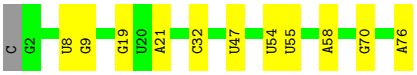
• Molecule 22: Isoleucine tRNA

Chain y:



• Molecule 23: P-site initiator tRNA

Chain x:

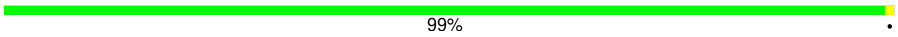


• Molecule 24: M-I mRNA

Chain v:

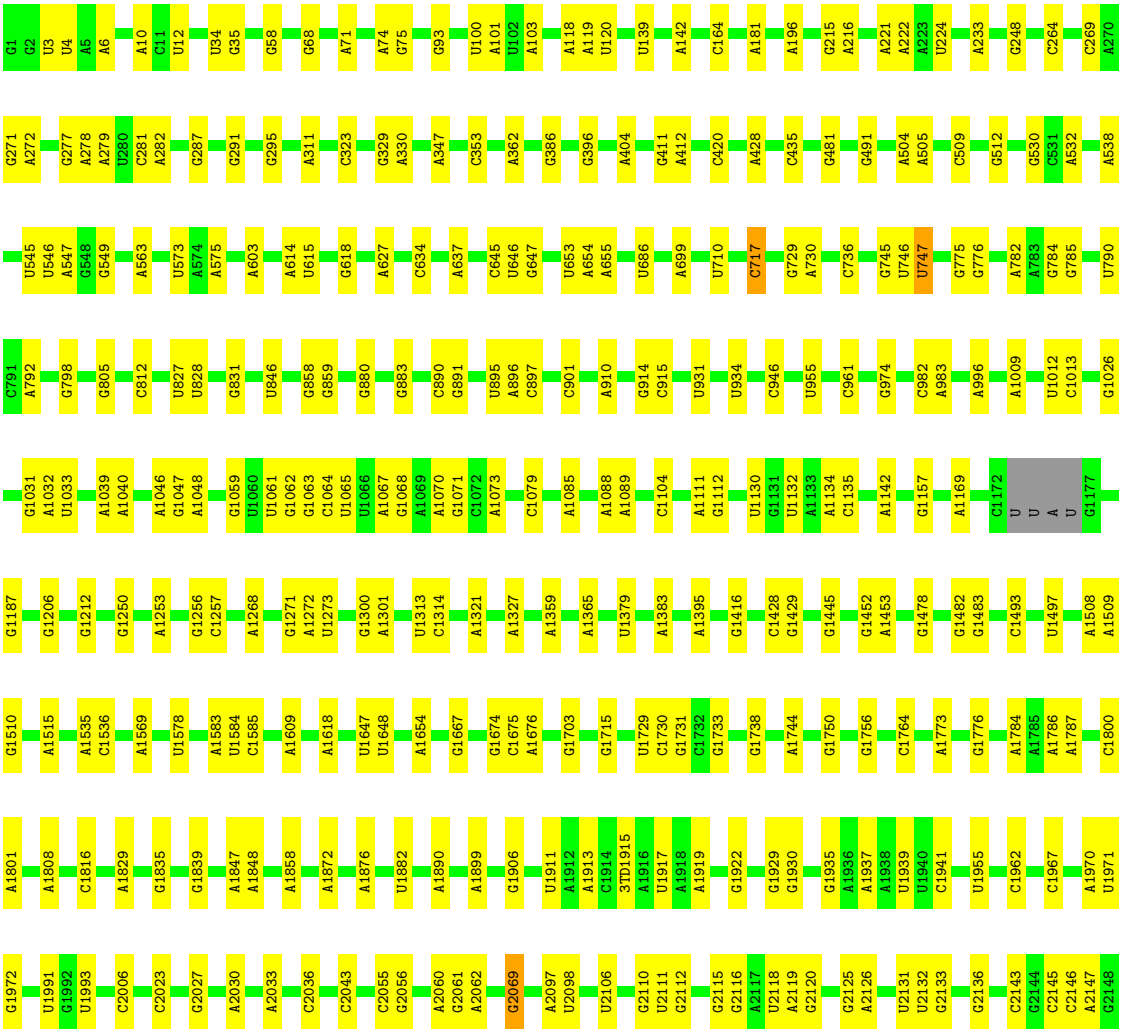
• Molecule 25: Elongation factor Tu

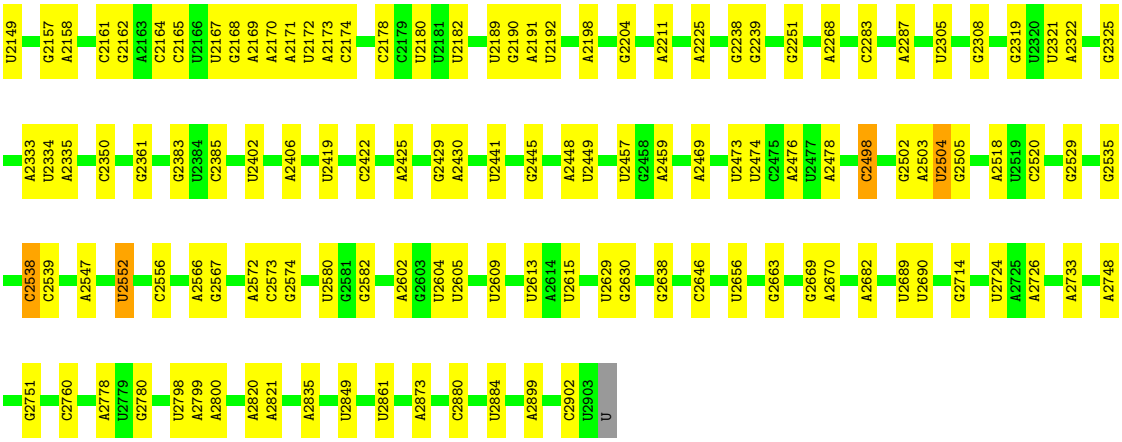
Chain z:



• Molecule 26: 23S Ribosomal RNA

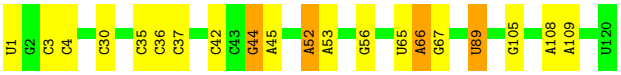
Chain A:





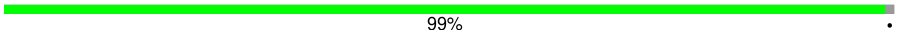
• Molecule 27: 5S Ribosomal RNA

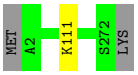
Chain B:



• Molecule 28: 50S ribosomal protein L2

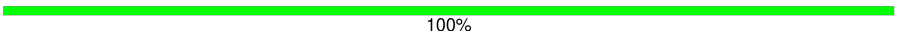
Chain C:





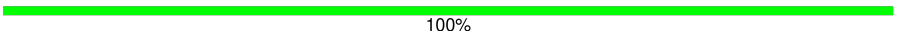
• Molecule 29: 50S ribosomal protein L3

Chain D:



• Molecule 30: 50S ribosomal protein L4

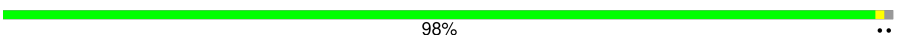
Chain E:



There are no outlier residues recorded for this chain.

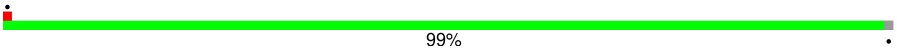
• Molecule 31: 50S ribosomal protein L5

Chain F:



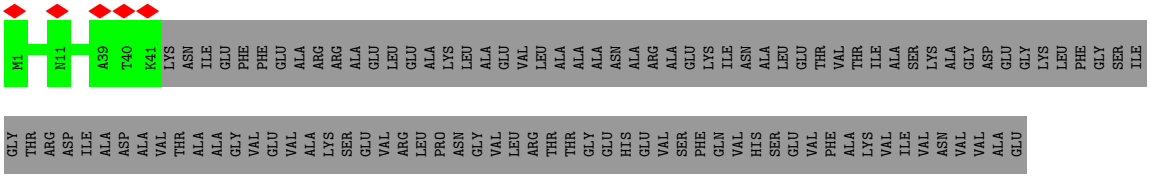
• Molecule 32: 50S ribosomal protein L6

Chain G:



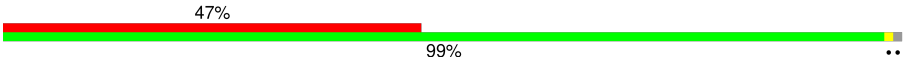
• Molecule 33: 50S ribosomal protein L9

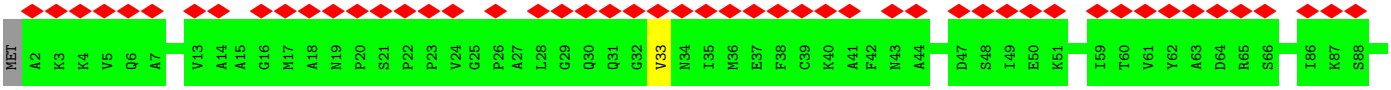
Chain H:

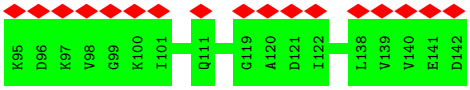


• Molecule 34: 50S ribosomal protein L11

Chain J:

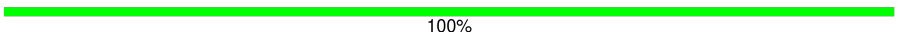






• Molecule 35: 50S ribosomal protein L13

Chain L:



There are no outlier residues recorded for this chain.

• Molecule 36: 50S ribosomal protein L14

Chain M:

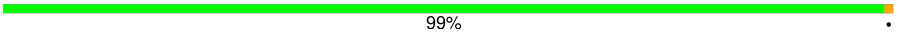
There are no outlier residues recorded for this chain.

• Molecule 37: 50S ribosomal protein L15

Chain N:

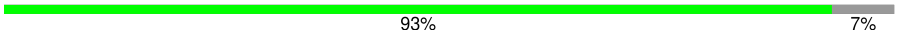
• Molecule 38: 50S ribosomal protein L16

Chain O:



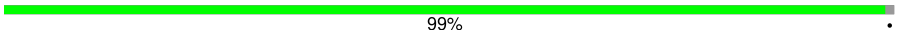
• Molecule 39: 50S ribosomal protein L17

Chain P:



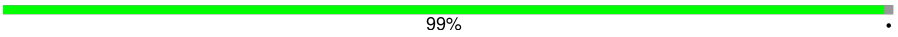
• Molecule 40: 50S ribosomal protein L18

Chain Q:



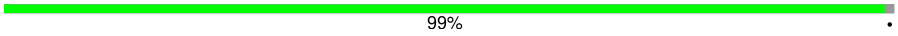
• Molecule 41: 50S ribosomal protein L19

Chain R:



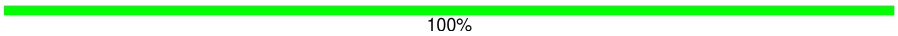
• Molecule 42: 50S ribosomal protein L20

Chain S:



• Molecule 43: Ribosomal protein L21

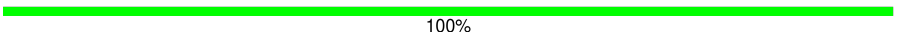
Chain T:



There are no outlier residues recorded for this chain.

• Molecule 44: 50S ribosomal protein L22

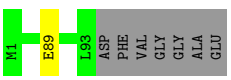
Chain U:



There are no outlier residues recorded for this chain.

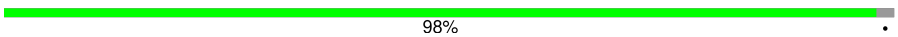
• Molecule 45: 50S ribosomal protein L23

Chain V:

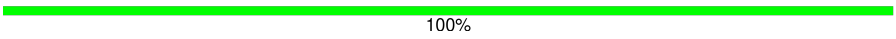


• Molecule 46: 50S ribosomal protein L24

Chain W:



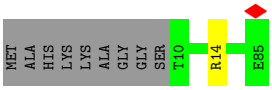
• Molecule 47: 50S ribosomal protein L25

Chain X: 

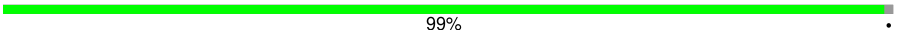
There are no outlier residues recorded for this chain.

• Molecule 48: 50S ribosomal protein L27

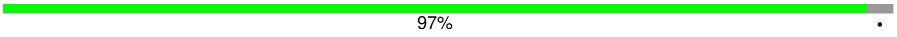
Chain Y: 



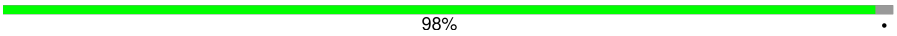
• Molecule 49: 50S ribosomal protein L28

Chain Z: 

• Molecule 50: 50S ribosomal protein L29

Chain 1: 

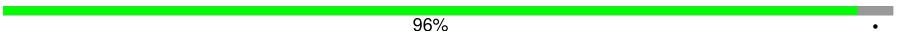
• Molecule 51: 50S ribosomal protein L30

Chain 2: 

• Molecule 52: 50S ribosomal protein L31

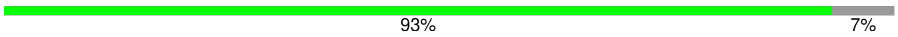
Chain 3: 

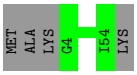
• Molecule 53: 50S ribosomal protein L32

Chain 4: 

• Molecule 54: 50S ribosomal protein L33

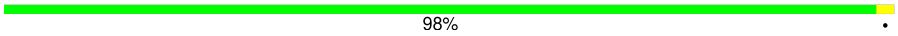
Chain 5:





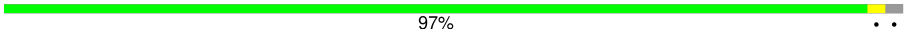
• Molecule 55: 50S ribosomal protein L34

Chain 6:



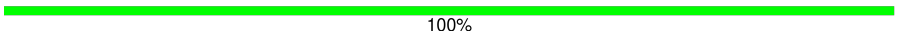
• Molecule 56: 50S ribosomal protein L35

Chain 7:



• Molecule 57: 50S ribosomal protein L36

Chain 8:



There are no outlier residues recorded for this chain.

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	135882	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.944	Depositor
Minimum map value	-0.636	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.097	Depositor
Recommended contour level	0.19	Depositor
Map size (Å)	440.32, 440.32, 440.32	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MA6, K, 2MA, 5MC, 2MG, 6MZ, MG, T6A, OMC, 4OC, MS6, GCP, 1MG, PSU, H2U, MEQ, OMU, OMG, 5MU, 4D4, D2T, ZN, M3X, G7M, 3TD, 4SU, IAS, UR3, 3AU

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	0.35	0/36475	0.85	8/56895 (0.0%)
2	b	0.27	0/1785	0.54	0/2404
3	c	0.25	0/1651	0.54	0/2225
4	d	0.27	0/1665	0.58	0/2227
5	e	0.26	0/1165	0.54	0/1568
6	f	0.27	0/858	0.58	0/1160
7	g	0.25	0/1206	0.55	0/1617
8	h	0.27	0/989	0.58	0/1326
9	i	0.26	0/1034	0.62	0/1375
10	j	0.27	0/796	0.64	1/1077 (0.1%)
11	k	0.26	0/884	0.58	0/1191
12	l	0.27	0/945	0.61	0/1268
13	m	0.26	0/900	0.61	0/1204
14	n	0.26	0/817	0.58	0/1088
15	o	0.29	0/722	0.58	0/964
16	p	0.26	0/653	0.57	0/877
17	q	0.26	0/650	0.57	0/871
18	r	0.28	0/453	0.58	0/609
19	s	0.25	0/680	0.52	0/915
20	t	0.27	0/676	0.49	0/895
21	u	0.27	0/597	0.59	0/792
22	w	0.63	3/1552 (0.2%)	1.09	9/2412 (0.4%)
22	y	0.62	3/1549 (0.2%)	1.20	11/2408 (0.5%)
23	x	0.31	0/1725	0.86	0/2689
24	v	0.31	0/320	0.79	0/497
25	z	0.29	0/3085	0.57	1/4173 (0.0%)
26	A	0.40	0/69147	0.88	11/107869 (0.0%)
27	B	0.40	1/2876 (0.0%)	0.91	7/4483 (0.2%)
28	C	0.28	0/2121	0.61	0/2852
29	D	0.28	0/1576	0.55	0/2119
30	E	0.25	0/1571	0.53	0/2113

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
31	F	0.26	0/1434	0.54	0/1926
32	G	0.26	0/1343	0.54	0/1816
33	H	0.25	0/306	0.54	0/413
34	J	0.24	0/692	0.43	0/960
35	L	0.26	0/1152	0.53	0/1551
36	M	0.26	0/955	0.59	0/1279
37	N	0.26	0/1061	0.58	0/1412
38	O	0.26	0/1073	0.57	0/1433
39	P	0.26	0/958	0.59	0/1281
40	Q	0.26	0/902	0.56	0/1209
41	R	0.27	0/929	0.54	0/1242
42	S	0.27	0/960	0.54	0/1278
43	T	0.28	0/829	0.57	0/1107
44	U	0.24	0/864	0.53	0/1156
45	V	0.25	0/744	0.54	0/994
46	W	0.28	0/787	0.56	0/1051
47	X	0.26	0/766	0.51	0/1025
48	Y	0.27	0/587	0.58	0/776
49	Z	0.25	0/635	0.59	0/848
50	1	0.23	0/496	0.52	0/660
51	2	0.26	0/453	0.56	0/605
52	3	0.29	0/484	0.55	0/645
53	4	0.27	0/440	0.61	0/588
54	5	0.24	0/424	0.54	0/565
55	6	0.25	0/376	0.67	0/494
56	7	0.25	0/513	0.56	0/676
57	8	0.26	0/303	0.61	0/397
All	All	0.36	7/161589 (0.0%)	0.81	48/241550 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
38	O	0	1
56	7	0	1
All	All	0	2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	w	76	A	C6-N6	18.06	1.48	1.33
22	y	76	A	C6-N6	17.65	1.48	1.33
27	B	1	U	OP3-P	-10.66	1.48	1.61
22	y	76	A	N7-C5	-7.41	1.34	1.39
22	w	76	A	N7-C5	-7.34	1.34	1.39
22	y	76	A	N9-C8	-6.67	1.32	1.37
22	w	76	A	N9-C8	-6.54	1.32	1.37

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	y	76	A	C2-N3-C4	20.77	120.98	110.60
22	w	76	A	C2-N3-C4	20.62	120.91	110.60
22	y	76	A	N1-C2-N3	-16.20	121.20	129.30
22	w	76	A	N1-C2-N3	-16.11	121.25	129.30
22	w	76	A	N3-C4-C5	-11.12	119.01	126.80
22	y	76	A	N3-C4-C5	-11.08	119.05	126.80
22	y	76	A	C5-N7-C8	8.56	108.18	103.90
22	y	76	A	N7-C8-N9	-8.28	109.66	113.80
22	w	76	A	N3-C4-N9	8.22	133.97	127.40
22	y	76	A	N3-C4-N9	7.90	133.72	127.40
22	w	76	A	C5-N7-C8	7.78	107.79	103.90
22	w	76	A	N7-C8-N9	-7.70	109.95	113.80
22	w	75	C	OP1-P-O3'	7.58	121.87	105.20
22	y	76	A	C4-C5-N7	-7.48	106.96	110.70
22	y	6	C	C6-N1-C1'	7.42	129.70	120.80
26	A	1313	U	C2-N1-C1'	7.41	126.59	117.70
22	y	75	C	OP1-P-O3'	7.14	120.91	105.20
1	a	754	C	C2-N1-C1'	6.97	126.47	118.80
22	y	6	C	C2-N1-C1'	-6.78	111.35	118.80
22	w	76	A	C4-C5-N7	-6.77	107.32	110.70
26	A	790	U	C2-N1-C1'	6.75	125.80	117.70
26	A	2321	U	C2-N1-C1'	6.65	125.68	117.70
26	A	1314	C	C2-N1-C1'	6.09	125.50	118.80
10	j	88	MET	CA-CB-CG	6.04	123.58	113.30
26	A	512	G	O4'-C1'-N9	6.01	113.01	108.20
27	B	89	U	C2-N1-C1'	5.77	124.62	117.70
1	a	993	G	C4-N9-C1'	5.75	133.97	126.50
26	A	323	C	C2-N1-C1'	5.72	125.09	118.80
26	A	1157	G	N3-C4-N9	5.71	129.42	126.00
1	a	1466	C	N3-C2-O2	-5.62	117.96	121.90
1	a	330	C	C2-N1-C1'	5.58	124.94	118.80
26	A	2538	C	P-O3'-C3'	5.51	126.31	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
27	B	52	A	P-O3'-C3'	5.44	126.23	119.70
27	B	89	U	N1-C2-O2	5.43	126.60	122.80
25	z	358	MET	N-CA-CB	5.42	120.36	110.60
22	y	76	A	C8-N9-C4	5.40	107.96	105.80
27	B	89	U	N3-C2-O2	-5.39	118.43	122.20
26	A	717	C	C2-N1-C1'	5.35	124.69	118.80
22	w	76	A	C8-N9-C4	5.33	107.93	105.80
1	a	993	G	N3-C4-N9	5.29	129.18	126.00
1	a	872	A	O4'-C1'-N9	5.26	112.41	108.20
27	B	44	G	C8-N9-C1'	5.22	133.79	127.00
27	B	44	G	C4-N9-C1'	-5.17	119.78	126.50
1	a	330	C	N1-C2-O2	5.14	121.99	118.90
27	B	66	A	P-O3'-C3'	5.13	125.86	119.70
1	a	754	C	C6-N1-C1'	-5.06	114.73	120.80
26	A	729	G	O4'-C1'-N9	5.06	112.25	108.20
26	A	1313	U	N3-C2-O2	-5.01	118.69	122.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
56	7	30	ARG	Peptide
38	O	81	4D4	Mainchain

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	222/241 (92%)	206 (93%)	16 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	c	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
4	d	203/206 (98%)	199 (98%)	4 (2%)	0	100	100
5	e	154/167 (92%)	148 (96%)	6 (4%)	0	100	100
6	f	101/131 (77%)	96 (95%)	5 (5%)	0	100	100
7	g	150/156 (96%)	140 (93%)	10 (7%)	0	100	100
8	h	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
9	i	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
10	j	96/103 (93%)	91 (95%)	4 (4%)	1 (1%)	13	40
11	k	113/129 (88%)	104 (92%)	9 (8%)	0	100	100
12	l	118/124 (95%)	114 (97%)	4 (3%)	0	100	100
13	m	113/118 (96%)	106 (94%)	7 (6%)	0	100	100
14	n	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
15	o	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	p	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
17	q	77/84 (92%)	75 (97%)	2 (3%)	0	100	100
18	r	52/75 (69%)	51 (98%)	1 (2%)	0	100	100
19	s	81/92 (88%)	77 (95%)	4 (5%)	0	100	100
20	t	84/87 (97%)	81 (96%)	3 (4%)	0	100	100
21	u	68/71 (96%)	65 (96%)	3 (4%)	0	100	100
25	z	390/392 (100%)	361 (93%)	27 (7%)	2 (0%)	25	56
28	C	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
29	D	206/209 (99%)	196 (95%)	9 (4%)	1 (0%)	25	56
30	E	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
31	F	175/179 (98%)	170 (97%)	5 (3%)	0	100	100
32	G	174/177 (98%)	169 (97%)	5 (3%)	0	100	100
33	H	39/149 (26%)	33 (85%)	6 (15%)	0	100	100
34	J	139/142 (98%)	125 (90%)	13 (9%)	1 (1%)	19	49
35	L	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
36	M	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
37	N	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
38	O	132/136 (97%)	129 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	P	116/127 (91%)	114 (98%)	2 (2%)	0	100	100
40	Q	114/117 (97%)	112 (98%)	2 (2%)	0	100	100
41	R	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
42	S	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
43	T	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
44	U	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
45	V	91/100 (91%)	83 (91%)	7 (8%)	1 (1%)	12	37
46	W	100/104 (96%)	94 (94%)	6 (6%)	0	100	100
47	X	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
48	Y	74/85 (87%)	71 (96%)	3 (4%)	0	100	100
49	Z	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
50	1	59/63 (94%)	55 (93%)	4 (7%)	0	100	100
51	2	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
52	3	56/70 (80%)	52 (93%)	4 (7%)	0	100	100
53	4	53/57 (93%)	52 (98%)	1 (2%)	0	100	100
54	5	49/55 (89%)	44 (90%)	5 (10%)	0	100	100
55	6	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
56	7	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
57	8	36/38 (95%)	36 (100%)	0	0	100	100
All	All	5990/6420 (93%)	5721 (96%)	263 (4%)	6 (0%)	50	77

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	z	314	ASP
10	j	57	VAL
29	D	149	ASN
45	V	89	GLU
34	J	33	VAL
25	z	347	VAL

5.3.2 Protein sidechains (i)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	b	186/199 (94%)	185 (100%)	1 (0%)	86 96
3	c	170/190 (90%)	170 (100%)	0	100 100
4	d	172/173 (99%)	171 (99%)	1 (1%)	84 95
5	e	119/126 (94%)	119 (100%)	0	100 100
6	f	90/112 (80%)	90 (100%)	0	100 100
7	g	125/129 (97%)	125 (100%)	0	100 100
8	h	104/105 (99%)	104 (100%)	0	100 100
9	i	105/107 (98%)	104 (99%)	1 (1%)	73 91
10	j	86/90 (96%)	86 (100%)	0	100 100
11	k	89/98 (91%)	89 (100%)	0	100 100
12	l	101/103 (98%)	101 (100%)	0	100 100
13	m	93/96 (97%)	92 (99%)	1 (1%)	70 90
14	n	83/84 (99%)	83 (100%)	0	100 100
15	o	76/77 (99%)	76 (100%)	0	100 100
16	p	65/65 (100%)	65 (100%)	0	100 100
17	q	73/78 (94%)	73 (100%)	0	100 100
18	r	47/65 (72%)	47 (100%)	0	100 100
19	s	72/79 (91%)	72 (100%)	0	100 100
20	t	65/66 (98%)	65 (100%)	0	100 100
21	u	60/61 (98%)	60 (100%)	0	100 100
25	z	324/325 (100%)	324 (100%)	0	100 100
28	C	216/218 (99%)	215 (100%)	1 (0%)	86 96
29	D	163/163 (100%)	163 (100%)	0	100 100
30	E	165/165 (100%)	165 (100%)	0	100 100
31	F	148/150 (99%)	147 (99%)	1 (1%)	81 94
32	G	137/138 (99%)	137 (100%)	0	100 100
33	H	32/114 (28%)	32 (100%)	0	100 100
35	L	116/116 (100%)	116 (100%)	0	100 100
36	M	104/104 (100%)	104 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
37	N	103/103 (100%)	103 (100%)	0	100 100
38	O	107/107 (100%)	107 (100%)	0	100 100
39	P	98/103 (95%)	98 (100%)	0	100 100
40	Q	86/87 (99%)	86 (100%)	0	100 100
41	R	99/100 (99%)	99 (100%)	0	100 100
42	S	89/90 (99%)	89 (100%)	0	100 100
43	T	84/84 (100%)	84 (100%)	0	100 100
44	U	93/93 (100%)	93 (100%)	0	100 100
45	V	80/84 (95%)	80 (100%)	0	100 100
46	W	83/85 (98%)	83 (100%)	0	100 100
47	X	78/78 (100%)	78 (100%)	0	100 100
48	Y	57/63 (90%)	56 (98%)	1 (2%)	54 82
49	Z	67/68 (98%)	67 (100%)	0	100 100
50	1	54/55 (98%)	54 (100%)	0	100 100
51	2	48/49 (98%)	48 (100%)	0	100 100
52	3	54/62 (87%)	54 (100%)	0	100 100
53	4	46/48 (96%)	46 (100%)	0	100 100
54	5	46/49 (94%)	46 (100%)	0	100 100
55	6	37/38 (97%)	36 (97%)	1 (3%)	40 73
56	7	51/52 (98%)	51 (100%)	0	100 100
57	8	34/34 (100%)	34 (100%)	0	100 100
All	All	4880/5128 (95%)	4872 (100%)	8 (0%)	91 98

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	b	208	ARG
4	d	184	ARG
9	i	106	ARG
13	m	57	ARG
28	C	111	LYS
31	F	133	ARG
48	Y	14	ARG
55	6	25	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
2	b	177	ASN
3	c	176	HIS
5	e	70	ASN
6	f	11	HIS
6	f	17	GLN
7	g	9	GLN
7	g	148	ASN
11	k	15	GLN
11	k	109	ASN
13	m	52	GLN
14	n	49	GLN
14	n	66	GLN
15	o	40	GLN
15	o	80	GLN
16	p	9	HIS
17	q	9	GLN
20	t	21	ASN
20	t	48	GLN
25	z	48	GLN
25	z	159	GLN
25	z	319	HIS
28	C	53	HIS
28	C	128	ASN
28	C	260	ASN
29	D	32	ASN
29	D	49	GLN
29	D	130	GLN
30	E	41	GLN
31	F	63	GLN
32	G	64	GLN
32	G	88	GLN
32	G	111	HIS
35	L	136	GLN
38	O	60	GLN
39	P	18	GLN
41	R	12	GLN
41	R	75	GLN
43	T	86	GLN
44	U	61	ASN
45	V	48	GLN
47	X	75	GLN

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Mol	Chain	Res	Type
50	1	39	GLN
50	1	45	GLN
56	7	31	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1524/1542 (98%)	199 (13%)	0
22	w	73/76 (96%)	17 (23%)	0
22	y	73/76 (96%)	22 (30%)	0
23	x	75/77 (97%)	7 (9%)	0
24	v	12/27 (44%)	1 (8%)	0
26	A	2893/2904 (99%)	397 (13%)	14 (0%)
27	B	119/120 (99%)	17 (14%)	3 (2%)
All	All	4769/4822 (98%)	660 (13%)	17 (0%)

All (660) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	4	U
1	a	5	U
1	a	6	G
1	a	7	A
1	a	22	G
1	a	39	G
1	a	44	A
1	a	47	C
1	a	48	C
1	a	51	A
1	a	71	A
1	a	81	A
1	a	82	G
1	a	85	U
1	a	88	U
1	a	92	U
1	a	94	G
1	a	95	C
1	a	121	U
1	a	122	G
1	a	130	A
1	a	131	A

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Mol	Chain	Res	Type
1	a	163	C
1	a	168	G
1	a	174	A
1	a	182	A
1	a	183	C
1	a	184	G
1	a	189	A
1	a	197	A
1	a	207	C
1	a	208	U
1	a	209	U
1	a	210	C
1	a	211	G
1	a	220	G
1	a	240	G
1	a	245	U
1	a	247	G
1	a	251	G
1	a	253	A
1	a	266	G
1	a	267	C
1	a	269	C
1	a	281	G
1	a	289	G
1	a	321	A
1	a	328	C
1	a	329	A
1	a	330	C
1	a	347	G
1	a	351	G
1	a	352	C
1	a	354	G
1	a	363	A
1	a	367	U
1	a	372	C
1	a	373	A
1	a	384	G
1	a	397	A
1	a	406	G
1	a	408	A
1	a	412	A
1	a	413	G

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Mol	Chain	Res	Type
1	a	415	A
1	a	417	G
1	a	421	U
1	a	422	C
1	a	424	G
1	a	429	U
1	a	467	U
1	a	468	A
1	a	484	G
1	a	486	U
1	a	495	A
1	a	499	A
1	a	509	A
1	a	511	C
1	a	518	C
1	a	520	A
1	a	521	G
1	a	526	C
1	a	527	G7M
1	a	531	U
1	a	532	A
1	a	547	A
1	a	564	C
1	a	572	A
1	a	573	A
1	a	576	C
1	a	577	G
1	a	579	A
1	a	596	A
1	a	625	U
1	a	628	G
1	a	633	G
1	a	653	U
1	a	665	A
1	a	703	G
1	a	721	G
1	a	723	U
1	a	742	G
1	a	747	A
1	a	755	G
1	a	758	C
1	a	777	A

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Mol	Chain	Res	Type
1	a	793	U
1	a	794	A
1	a	802	A
1	a	815	A
1	a	817	C
1	a	821	G
1	a	890	G
1	a	913	A
1	a	914	A
1	a	919	A
1	a	926	G
1	a	934	C
1	a	935	A
1	a	960	U
1	a	963	G
1	a	966	2MG
1	a	969	A
1	a	971	G
1	a	975	A
1	a	976	G
1	a	977	A
1	a	992	U
1	a	993	G
1	a	994	A
1	a	1003	G
1	a	1004	A
1	a	1009	U
1	a	1017	U
1	a	1024	G
1	a	1026	G
1	a	1027	C
1	a	1030	U
1	a	1031	C
1	a	1032	G
1	a	1033	G
1	a	1034	G
1	a	1036	A
1	a	1053	G
1	a	1065	U
1	a	1094	G
1	a	1095	U
1	a	1101	A

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Mol	Chain	Res	Type
1	a	1110	A
1	a	1137	C
1	a	1139	G
1	a	1158	C
1	a	1159	U
1	a	1167	A
1	a	1171	A
1	a	1184	G
1	a	1196	A
1	a	1197	A
1	a	1200	C
1	a	1213	A
1	a	1227	A
1	a	1228	C
1	a	1238	A
1	a	1256	A
1	a	1258	G
1	a	1260	G
1	a	1275	A
1	a	1280	A
1	a	1285	A
1	a	1286	U
1	a	1287	A
1	a	1289	A
1	a	1300	G
1	a	1302	C
1	a	1317	C
1	a	1320	C
1	a	1338	G
1	a	1346	A
1	a	1363	A
1	a	1364	U
1	a	1370	G
1	a	1378	C
1	a	1419	G
1	a	1432	G
1	a	1441	A
1	a	1446	A
1	a	1448	C
1	a	1453	G
1	a	1487	G
1	a	1492	A

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Mol	Chain	Res	Type
1	a	1493	A
1	a	1494	G
1	a	1497	G
1	a	1503	A
1	a	1506	U
1	a	1517	G
1	a	1529	G
1	a	1530	G
1	a	1533	C
22	w	8	4SU
22	w	9	A
22	w	16	U
22	w	17	OMG
22	w	18	G
22	w	19	H2U
22	w	20	H2U
22	w	21	A
22	w	22	G
22	w	39	PSU
22	w	44	U
22	w	46	G7M
22	w	48	C
22	w	55	PSU
22	w	56	C
22	w	58	A
22	w	76	A
23	x	9	G
23	x	19	G
23	x	21	A
23	x	47	U
23	x	58	A
23	x	70	G
23	x	76	A
22	y	9	A
22	y	10	G
22	y	13	C
22	y	16	U
22	y	18	G
22	y	19	H2U
22	y	20	H2U
22	y	21	A
22	y	26	A

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Mol	Chain	Res	Type
22	y	37	T6A
22	y	46	G7M
22	y	48	C
22	y	49	G
22	y	53	G
22	y	54	5MU
22	y	58	A
22	y	59	G
22	y	65	C
22	y	66	A
22	y	67	G
22	y	73	A
22	y	76	A
24	v	23	A
26	A	4	U
26	A	6	A
26	A	10	A
26	A	12	U
26	A	34	U
26	A	35	G
26	A	58	G
26	A	68	G
26	A	71	A
26	A	74	A
26	A	75	G
26	A	93	G
26	A	100	U
26	A	101	A
26	A	103	A
26	A	118	A
26	A	119	A
26	A	120	U
26	A	139	U
26	A	142	A
26	A	164	C
26	A	181	A
26	A	196	A
26	A	215	G
26	A	216	A
26	A	221	A
26	A	222	A
26	A	224	U

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Mol	Chain	Res	Type
26	A	233	A
26	A	248	G
26	A	264	C
26	A	269	C
26	A	271	G
26	A	272	A
26	A	278	A
26	A	279	A
26	A	281	C
26	A	282	A
26	A	287	G
26	A	291	G
26	A	295	G
26	A	311	A
26	A	329	G
26	A	330	A
26	A	347	A
26	A	353	C
26	A	362	A
26	A	386	G
26	A	396	G
26	A	404	A
26	A	411	G
26	A	412	A
26	A	420	C
26	A	428	A
26	A	435	C
26	A	481	G
26	A	491	G
26	A	504	A
26	A	505	A
26	A	509	C
26	A	530	G
26	A	532	A
26	A	538	A
26	A	545	U
26	A	546	U
26	A	547	A
26	A	549	G
26	A	563	A
26	A	573	U
26	A	575	A

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Mol	Chain	Res	Type
26	A	603	A
26	A	614	A
26	A	615	U
26	A	618	G
26	A	627	A
26	A	634	C
26	A	637	A
26	A	645	C
26	A	646	U
26	A	647	G
26	A	653	U
26	A	654	A
26	A	655	A
26	A	686	U
26	A	699	A
26	A	710	U
26	A	717	C
26	A	730	A
26	A	736	C
26	A	747	5MU
26	A	775	G
26	A	776	G
26	A	782	A
26	A	784	G
26	A	785	G
26	A	792	A
26	A	798	G
26	A	805	G
26	A	812	C
26	A	827	U
26	A	828	U
26	A	831	G
26	A	846	U
26	A	858	G
26	A	859	G
26	A	880	G
26	A	883	G
26	A	890	C
26	A	891	G
26	A	895	U
26	A	896	A
26	A	897	C

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Mol	Chain	Res	Type
26	A	901	C
26	A	910	A
26	A	914	G
26	A	915	C
26	A	931	U
26	A	934	U
26	A	946	C
26	A	961	C
26	A	974	G
26	A	982	C
26	A	983	A
26	A	996	A
26	A	1009	A
26	A	1012	U
26	A	1013	C
26	A	1026	G
26	A	1032	A
26	A	1033	U
26	A	1039	A
26	A	1040	A
26	A	1046	A
26	A	1047	G
26	A	1048	A
26	A	1059	G
26	A	1061	U
26	A	1062	G
26	A	1063	G
26	A	1064	C
26	A	1065	U
26	A	1067	A
26	A	1068	G
26	A	1070	A
26	A	1071	G
26	A	1073	A
26	A	1079	C
26	A	1085	A
26	A	1088	A
26	A	1089	A
26	A	1104	C
26	A	1111	A
26	A	1112	G
26	A	1130	U

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Mol	Chain	Res	Type
26	A	1132	U
26	A	1134	A
26	A	1135	C
26	A	1142	A
26	A	1169	A
26	A	1187	G
26	A	1206	G
26	A	1212	G
26	A	1250	G
26	A	1253	A
26	A	1256	G
26	A	1257	C
26	A	1268	A
26	A	1271	G
26	A	1272	A
26	A	1273	U
26	A	1300	G
26	A	1301	A
26	A	1321	A
26	A	1327	A
26	A	1359	A
26	A	1365	A
26	A	1379	U
26	A	1383	A
26	A	1395	A
26	A	1416	G
26	A	1428	C
26	A	1429	G
26	A	1445	G
26	A	1452	G
26	A	1453	A
26	A	1478	G
26	A	1482	G
26	A	1483	G
26	A	1493	C
26	A	1497	U
26	A	1508	A
26	A	1509	A
26	A	1510	G
26	A	1515	A
26	A	1535	A
26	A	1536	C

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Mol	Chain	Res	Type
26	A	1569	A
26	A	1578	U
26	A	1583	A
26	A	1584	U
26	A	1585	C
26	A	1609	A
26	A	1647	U
26	A	1648	U
26	A	1654	A
26	A	1667	G
26	A	1674	G
26	A	1675	C
26	A	1676	A
26	A	1703	G
26	A	1715	G
26	A	1729	U
26	A	1730	C
26	A	1731	G
26	A	1733	G
26	A	1738	G
26	A	1744	A
26	A	1750	G
26	A	1756	G
26	A	1764	C
26	A	1773	A
26	A	1776	G
26	A	1784	A
26	A	1786	A
26	A	1787	A
26	A	1800	C
26	A	1801	A
26	A	1808	A
26	A	1816	C
26	A	1829	A
26	A	1839	G
26	A	1847	A
26	A	1848	A
26	A	1858	A
26	A	1872	A
26	A	1876	A
26	A	1882	U
26	A	1890	A

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Mol	Chain	Res	Type
26	A	1899	A
26	A	1906	G
26	A	1913	A
26	A	1919	A
26	A	1922	G
26	A	1929	G
26	A	1930	G
26	A	1935	G
26	A	1937	A
26	A	1941	C
26	A	1955	U
26	A	1967	C
26	A	1970	A
26	A	1971	U
26	A	1972	G
26	A	1991	U
26	A	1993	U
26	A	2006	C
26	A	2023	C
26	A	2027	G
26	A	2033	A
26	A	2036	C
26	A	2043	C
26	A	2055	C
26	A	2056	G
26	A	2060	A
26	A	2061	G
26	A	2062	A
26	A	2069	G7M
26	A	2098	U
26	A	2106	U
26	A	2110	G
26	A	2111	U
26	A	2112	G
26	A	2115	G
26	A	2116	G
26	A	2118	U
26	A	2119	A
26	A	2120	G
26	A	2125	G
26	A	2126	A
26	A	2131	U

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Mol	Chain	Res	Type
26	A	2132	U
26	A	2133	G
26	A	2136	G
26	A	2143	C
26	A	2145	C
26	A	2146	C
26	A	2147	A
26	A	2149	U
26	A	2157	G
26	A	2158	A
26	A	2161	C
26	A	2162	G
26	A	2164	C
26	A	2165	C
26	A	2167	U
26	A	2168	G
26	A	2169	A
26	A	2170	A
26	A	2171	A
26	A	2172	U
26	A	2173	A
26	A	2174	C
26	A	2178	C
26	A	2180	U
26	A	2182	U
26	A	2189	U
26	A	2190	G
26	A	2192	U
26	A	2198	A
26	A	2204	G
26	A	2211	A
26	A	2225	A
26	A	2238	G
26	A	2239	G
26	A	2268	A
26	A	2283	C
26	A	2287	A
26	A	2305	U
26	A	2308	G
26	A	2319	G
26	A	2322	A
26	A	2325	G

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Mol	Chain	Res	Type
26	A	2333	A
26	A	2334	U
26	A	2335	A
26	A	2350	C
26	A	2361	G
26	A	2383	G
26	A	2385	C
26	A	2402	U
26	A	2406	A
26	A	2419	U
26	A	2422	C
26	A	2425	A
26	A	2429	G
26	A	2430	A
26	A	2441	U
26	A	2448	A
26	A	2459	A
26	A	2469	A
26	A	2474	U
26	A	2476	A
26	A	2478	A
26	A	2498	OMC
26	A	2502	G
26	A	2504	PSU
26	A	2505	G
26	A	2518	A
26	A	2520	C
26	A	2529	G
26	A	2535	G
26	A	2539	C
26	A	2547	A
26	A	2552	OMU
26	A	2556	C
26	A	2566	A
26	A	2567	G
26	A	2572	A
26	A	2573	C
26	A	2574	G
26	A	2582	G
26	A	2602	A
26	A	2609	U
26	A	2613	U

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Mol	Chain	Res	Type
26	A	2615	U
26	A	2629	U
26	A	2630	G
26	A	2638	G
26	A	2646	C
26	A	2656	U
26	A	2663	G
26	A	2669	G
26	A	2670	A
26	A	2682	A
26	A	2689	U
26	A	2690	U
26	A	2714	G
26	A	2724	U
26	A	2726	A
26	A	2733	A
26	A	2748	A
26	A	2751	G
26	A	2760	C
26	A	2778	A
26	A	2780	G
26	A	2798	U
26	A	2800	A
26	A	2820	A
26	A	2821	A
26	A	2835	A
26	A	2849	U
26	A	2861	U
26	A	2873	A
26	A	2880	C
26	A	2884	U
26	A	2899	A
26	A	2902	C
27	B	4	C
27	B	30	C
27	B	35	C
27	B	36	C
27	B	37	C
27	B	42	C
27	B	44	G
27	B	45	A
27	B	53	A

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Mol	Chain	Res	Type
27	B	56	G
27	B	65	U
27	B	66	A
27	B	67	G
27	B	89	U
27	B	105	G
27	B	108	A
27	B	109	A

All (17) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	A	3	U
26	A	271	G
26	A	277	G
26	A	784	G
26	A	1026	G
26	A	1031	G
26	A	1111	A
26	A	1730	C
26	A	2097	A
26	A	2189	U
26	A	2191	A
26	A	2473	U
26	A	2538	C
26	A	2799	A
27	B	3	C
27	B	52	A
27	B	66	A

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

65 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	$\#\|Z\|>2$
22	H2U	y	20	22	18,21,22	1.05	2 (11%)	19,30,33	0.75	1 (5%)
22	PSU	w	39	22	18,21,22	1.40	2 (11%)	21,30,33	2.04	3 (14%)
26	PSU	A	2605	26	18,21,22	1.39	3 (16%)	21,30,33	2.13	4 (19%)
23	PSU	x	55	23	18,21,22	1.37	2 (11%)	21,30,33	2.06	3 (14%)
22	OMG	y	17	22	19,26,27	0.90	1 (5%)	21,38,41	1.17	2 (9%)
22	OMG	w	17	22	19,26,27	0.93	1 (5%)	21,38,41	1.09	2 (9%)
22	T6A	w	37	22	26,34,35	0.96	1 (3%)	28,49,52	1.83	5 (17%)
26	OMC	A	2498	58,26	19,22,23	0.81	0	25,31,34	1.02	1 (4%)
1	5MC	a	967	1	19,22,23	1.57	3 (15%)	26,32,35	1.13	3 (11%)
22	M3X	w	34	24,22	24,30,31	2.19	4 (16%)	24,41,44	1.02	1 (4%)
1	PSU	a	516	58,1	18,21,22	1.37	3 (16%)	21,30,33	2.05	5 (23%)
1	G7M	a	527	1	20,26,27	1.18	2 (10%)	16,39,42	0.59	0
26	1MG	A	745	26	19,26,27	0.84	1 (5%)	18,39,42	1.20	2 (11%)
26	H2U	A	2449	26	18,21,22	1.12	3 (16%)	19,30,33	0.86	0
22	PSU	w	55	22	18,21,22	1.37	2 (11%)	21,30,33	2.09	4 (19%)
23	5MU	x	54	23	19,22,23	1.40	6 (31%)	27,32,35	2.14	6 (22%)
26	OMG	A	2251	26,23	19,26,27	0.93	1 (5%)	21,38,41	1.05	2 (9%)
22	4SU	w	8	22	18,21,22	1.94	5 (27%)	25,30,33	2.20	5 (20%)
22	G7M	y	46	22	20,26,27	1.20	2 (10%)	16,39,42	0.65	0
22	T6A	y	37	22	26,34,35	0.98	0	28,49,52	1.83	6 (21%)
22	G7M	w	46	22	20,26,27	1.22	2 (10%)	16,39,42	0.56	0
1	UR3	a	1498	1	19,22,23	0.94	0	26,32,35	1.76	2 (7%)
22	4SU	y	8	22	18,21,22	1.90	5 (27%)	25,30,33	2.30	5 (20%)
26	OMU	A	2552	26	19,22,23	1.27	3 (15%)	25,31,34	1.85	5 (20%)
1	MA6	a	1519	1	19,26,27	1.01	1 (5%)	18,38,41	2.35	7 (38%)
23	4SU	x	8	23	18,21,22	1.83	4 (22%)	25,30,33	2.25	4 (16%)
22	M3X	y	34	22	24,30,31	2.26	4 (16%)	24,41,44	1.10	2 (8%)
26	5MU	A	747	26	19,22,23	1.41	6 (31%)	27,32,35	2.04	6 (22%)
26	PSU	A	2504	26	18,21,22	1.39	2 (11%)	21,30,33	2.07	4 (19%)
22	3AU	w	47	22	24,28,29	2.70	9 (37%)	30,40,43	1.38	3 (10%)
26	PSU	A	1917	26	18,21,22	1.42	4 (22%)	21,30,33	2.04	3 (14%)
26	PSU	A	2580	26	18,21,22	1.39	4 (22%)	21,30,33	2.07	5 (23%)
1	2MG	a	1516	1	18,26,27	0.89	1 (5%)	16,38,41	1.37	3 (18%)
38	4D4	O	81	38	9,11,12	2.67	3 (33%)	7,13,15	0.86	0
26	PSU	A	2604	26	18,21,22	1.40	3 (16%)	21,30,33	2.10	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
26	2MG	A	1835	26	18,26,27	0.91	1 (5%)	16,38,41	1.24	2 (12%)
26	PSU	A	2457	26	18,21,22	1.40	3 (16%)	21,30,33	2.07	4 (19%)
22	3AU	y	47	22	24,28,29	2.72	9 (37%)	30,40,43	1.34	3 (10%)
26	2MG	A	2445	58,26	18,26,27	0.94	1 (5%)	16,38,41	1.27	2 (12%)
26	6MZ	A	1618	26	17,25,26	0.93	1 (5%)	15,36,39	2.12	4 (26%)
26	G7M	A	2069	26	20,26,27	1.20	2 (10%)	16,39,42	0.59	0
1	4OC	a	1402	58,1	20,23,24	0.75	0	25,32,35	1.03	2 (8%)
22	5MU	w	54	22	19,22,23	1.38	6 (31%)	27,32,35	2.21	6 (22%)
22	5MU	y	54	22	19,22,23	1.37	5 (26%)	27,32,35	2.05	6 (22%)
26	PSU	A	955	26	18,21,22	1.42	3 (16%)	21,30,33	2.05	4 (19%)
26	5MU	A	1939	58,26	19,22,23	1.43	5 (26%)	27,32,35	2.19	6 (22%)
22	PSU	y	39	22	18,21,22	1.41	3 (16%)	21,30,33	1.98	3 (14%)
26	6MZ	A	2030	26	17,25,26	0.88	1 (5%)	15,36,39	2.44	4 (26%)
22	PSU	y	55	22	18,21,22	1.36	2 (11%)	21,30,33	2.00	3 (14%)
1	2MG	a	966	1	18,26,27	0.91	1 (5%)	16,38,41	1.18	2 (12%)
11	IAS	k	119	11	6,7,8	0.98	0	3,8,10	1.46	1 (33%)
22	H2U	w	19	22	18,21,22	1.00	2 (11%)	19,30,33	0.81	1 (5%)
26	5MC	A	1962	26	19,22,23	1.59	3 (15%)	26,32,35	1.14	3 (11%)
1	2MG	a	1207	1	18,26,27	0.90	1 (5%)	16,38,41	1.29	3 (18%)
22	H2U	w	20	22	18,21,22	0.99	2 (11%)	19,30,33	0.85	1 (5%)
26	2MA	A	2503	58,26	18,25,26	0.69	0	20,37,40	2.02	4 (20%)
29	MEQ	D	150	29	8,9,10	0.51	0	5,10,12	0.17	0
1	5MC	a	1407	1	19,22,23	1.53	3 (15%)	26,32,35	1.20	3 (11%)
26	PSU	A	1911	26	18,21,22	1.40	3 (16%)	21,30,33	2.10	5 (23%)
26	PSU	A	746	58,26	18,21,22	1.43	2 (11%)	21,30,33	2.10	3 (14%)
26	3TD	A	1915	26	19,22,23	4.19	7 (36%)	23,32,35	1.72	2 (8%)
23	5MC	x	32	23	19,22,23	1.46	3 (15%)	26,32,35	1.34	3 (11%)
22	H2U	y	19	22	18,21,22	1.01	2 (11%)	19,30,33	0.80	0
1	MA6	a	1518	1	19,26,27	0.99	1 (5%)	18,38,41	2.24	7 (38%)
12	D2T	l	89	12	8,9,10	1.42	1 (12%)	6,11,13	2.59	3 (50%)

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
22	H2U	y	20	22	-	5/7/38/39	0/2/2/2
22	PSU	w	39	22	-	0/7/25/26	0/2/2/2
26	PSU	A	2605	26	-	0/7/25/26	0/2/2/2
23	PSU	x	55	23	-	0/7/25/26	0/2/2/2
22	OMG	y	17	22	-	0/5/27/28	0/3/3/3
22	OMG	w	17	22	-	3/5/27/28	0/3/3/3
22	T6A	w	37	22	-	0/19/41/42	0/3/3/3
26	OMC	A	2498	58,26	-	4/9/27/28	0/2/2/2
1	5MC	a	967	1	-	0/7/25/26	0/2/2/2
22	M3X	w	34	24,22	-	8/17/37/38	0/2/2/2
1	PSU	a	516	58,1	-	0/7/25/26	0/2/2/2
1	G7M	a	527	1	-	2/3/25/26	0/3/3/3
26	1MG	A	745	26	-	0/3/25/26	0/3/3/3
26	H2U	A	2449	26	-	0/7/38/39	0/2/2/2
22	PSU	w	55	22	-	2/7/25/26	0/2/2/2
23	5MU	x	54	23	-	0/7/25/26	0/2/2/2
26	OMG	A	2251	26,23	-	0/5/27/28	0/3/3/3
22	4SU	w	8	22	-	0/7/25/26	0/2/2/2
22	G7M	y	46	22	-	2/3/25/26	0/3/3/3
22	T6A	y	37	22	-	12/19/41/42	0/3/3/3
22	G7M	w	46	22	-	3/3/25/26	0/3/3/3
1	UR3	a	1498	1	-	0/7/25/26	0/2/2/2
22	4SU	y	8	22	-	1/7/25/26	0/2/2/2
26	OMU	A	2552	26	-	2/9/27/28	0/2/2/2
1	MA6	a	1519	1	-	3/7/29/30	0/3/3/3
23	4SU	x	8	23	-	0/7/25/26	0/2/2/2
22	M3X	y	34	22	-	4/17/37/38	0/2/2/2
26	5MU	A	747	26	-	0/7/25/26	0/2/2/2
26	PSU	A	2504	26	-	2/7/25/26	0/2/2/2
22	3AU	w	47	22	-	7/16/34/35	0/2/2/2
26	PSU	A	1917	26	-	2/7/25/26	0/2/2/2
26	PSU	A	2580	26	-	0/7/25/26	0/2/2/2
1	2MG	a	1516	1	-	0/5/27/28	0/3/3/3
38	4D4	O	81	38	-	3/11/12/14	-
26	PSU	A	2604	26	-	0/7/25/26	0/2/2/2
26	2MG	A	1835	26	-	0/5/27/28	0/3/3/3
26	PSU	A	2457	26	-	0/7/25/26	0/2/2/2
22	3AU	y	47	22	-	6/16/34/35	0/2/2/2
26	2MG	A	2445	58,26	-	0/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	6MZ	A	1618	26	-	0/5/27/28	0/3/3/3
26	G7M	A	2069	26	-	0/3/25/26	0/3/3/3
1	4OC	a	1402	58,1	-	2/9/29/30	0/2/2/2
22	5MU	w	54	22	-	0/7/25/26	0/2/2/2
22	5MU	y	54	22	-	4/7/25/26	0/2/2/2
26	PSU	A	955	26	-	0/7/25/26	0/2/2/2
26	5MU	A	1939	58,26	-	0/7/25/26	0/2/2/2
22	PSU	y	39	22	-	1/7/25/26	0/2/2/2
26	6MZ	A	2030	26	-	2/5/27/28	0/3/3/3
22	PSU	y	55	22	-	3/7/25/26	0/2/2/2
1	2MG	a	966	1	-	1/5/27/28	0/3/3/3
11	IAS	k	119	11	-	0/7/7/8	-
22	H2U	w	19	22	-	6/7/38/39	0/2/2/2
26	5MC	A	1962	26	-	0/7/25/26	0/2/2/2
1	2MG	a	1207	1	-	1/5/27/28	0/3/3/3
22	H2U	w	20	22	-	5/7/38/39	0/2/2/2
26	2MA	A	2503	58,26	-	2/3/25/26	0/3/3/3
29	MEQ	D	150	29	-	2/8/9/11	-
1	5MC	a	1407	1	-	0/7/25/26	0/2/2/2
26	PSU	A	1911	26	-	0/7/25/26	0/2/2/2
26	PSU	A	746	58,26	-	2/7/25/26	0/2/2/2
26	3TD	A	1915	26	-	0/7/25/26	0/2/2/2
23	5MC	x	32	23	-	0/7/25/26	0/2/2/2
22	H2U	y	19	22	-	4/7/38/39	0/2/2/2
1	MA6	a	1518	1	-	1/7/29/30	0/3/3/3
12	D2T	l	89	12	-	5/7/12/14	-

All (168) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	A	1915	3TD	C6-C5	12.45	1.49	1.35
26	A	1915	3TD	C2-N1	9.68	1.49	1.37
22	y	34	M3X	C2-N2	8.96	1.48	1.34
22	w	34	M3X	C2-N2	8.63	1.47	1.34
22	w	47	3AU	C2-N1	6.33	1.47	1.38
22	y	47	3AU	C2-N3	6.33	1.49	1.38
22	w	47	3AU	C2-N3	6.31	1.49	1.38
38	O	81	4D4	CZ-NE	6.22	1.45	1.33
22	y	47	3AU	C2-N1	6.21	1.47	1.38
22	y	47	3AU	C6-C5	6.04	1.49	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	w	47	3AU	C6-C5	5.96	1.48	1.35
26	A	1915	3TD	C6-N1	5.82	1.45	1.36
26	A	1962	5MC	C5-C4	5.68	1.48	1.44
1	a	967	5MC	C5-C4	5.62	1.48	1.44
1	a	1407	5MC	C5-C4	5.51	1.48	1.44
22	w	8	4SU	C4-S4	-5.11	1.59	1.68
22	y	8	4SU	C4-S4	-5.02	1.59	1.68
23	x	8	4SU	C4-S4	-5.01	1.59	1.68
23	x	32	5MC	C5-C4	4.97	1.47	1.44
26	A	1915	3TD	C2-N3	4.92	1.48	1.38
22	y	34	M3X	C4-N4	-3.75	1.24	1.35
22	w	34	M3X	C4-N4	-3.74	1.24	1.35
38	O	81	4D4	CZ-NH2	3.73	1.45	1.32
22	w	8	4SU	C4-N3	-3.67	1.33	1.37
22	y	47	3AU	O2-C2	-3.62	1.15	1.22
22	y	47	3AU	C6-N1	3.59	1.46	1.38
22	w	46	G7M	C5-C4	3.56	1.46	1.39
22	w	47	3AU	C6-N1	3.54	1.46	1.38
1	a	527	G7M	C5-C4	3.52	1.46	1.39
22	w	47	3AU	O2-C2	-3.50	1.16	1.22
22	y	8	4SU	C4-N3	-3.47	1.34	1.37
22	y	46	G7M	C5-C4	3.44	1.46	1.39
22	y	47	3AU	C4-N3	3.44	1.46	1.40
26	A	2069	G7M	C5-C4	3.41	1.45	1.39
26	A	2504	PSU	C6-C5	3.40	1.39	1.35
22	y	55	PSU	C6-C5	3.35	1.39	1.35
22	w	47	3AU	C4-N3	3.35	1.46	1.40
23	x	8	4SU	C4-N3	-3.33	1.34	1.37
23	x	55	PSU	C6-C5	3.31	1.39	1.35
22	w	55	PSU	C6-C5	3.31	1.39	1.35
22	y	39	PSU	C6-C5	3.30	1.38	1.35
26	A	1917	PSU	C6-C5	3.24	1.38	1.35
22	w	39	PSU	C6-C5	3.21	1.38	1.35
26	A	2604	PSU	C6-C5	3.20	1.38	1.35
26	A	955	PSU	C6-C5	3.10	1.38	1.35
26	A	1911	PSU	C6-C5	3.09	1.38	1.35
26	A	746	PSU	C6-C5	3.08	1.38	1.35
22	y	34	M3X	C6-N1	-3.05	1.32	1.36
22	w	8	4SU	C5-C4	-3.05	1.38	1.42
1	a	516	PSU	C6-C5	3.02	1.38	1.35
22	w	34	M3X	C6-N1	-3.00	1.32	1.36
26	A	2605	PSU	C6-C5	3.00	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	A	2552	OMU	C4-N3	-2.97	1.33	1.38
26	A	2605	PSU	C4-N3	-2.97	1.33	1.38
26	A	2449	H2U	C2-N3	-2.96	1.32	1.38
26	A	2457	PSU	C6-C5	2.96	1.38	1.35
26	A	1939	5MU	C4-N3	-2.95	1.33	1.38
22	y	54	5MU	C6-C5	2.91	1.39	1.34
26	A	1911	PSU	C4-N3	-2.91	1.33	1.38
26	A	955	PSU	C4-N3	-2.91	1.33	1.38
26	A	2604	PSU	C4-N3	-2.91	1.33	1.38
26	A	747	5MU	C4-N3	-2.89	1.33	1.38
26	A	2251	OMG	C6-N1	-2.89	1.33	1.37
26	A	2580	PSU	C6-C5	2.87	1.38	1.35
26	A	746	PSU	C4-N3	-2.82	1.33	1.38
22	y	20	H2U	C2-N3	-2.82	1.33	1.38
22	y	8	4SU	C5-C4	-2.80	1.39	1.42
26	A	2457	PSU	C4-N3	-2.78	1.33	1.38
26	A	1939	5MU	C6-C5	2.78	1.39	1.34
26	A	1915	3TD	C4-N3	2.76	1.46	1.40
12	l	89	D2T	CB-CA	-2.75	1.53	1.54
26	A	2445	2MG	C6-N1	-2.75	1.33	1.37
23	x	54	5MU	C4-N3	-2.74	1.33	1.38
26	A	2504	PSU	C4-N3	-2.74	1.33	1.38
26	A	1917	PSU	C4-N3	-2.72	1.33	1.38
22	y	39	PSU	C4-N3	-2.72	1.33	1.38
1	a	516	PSU	C4-N3	-2.71	1.33	1.38
22	w	20	H2U	C2-N3	-2.70	1.33	1.38
26	A	2069	G7M	C6-N1	-2.70	1.33	1.37
26	A	1962	5MC	C6-C5	2.69	1.39	1.34
22	w	39	PSU	C4-N3	-2.69	1.33	1.38
26	A	1835	2MG	C6-N1	-2.69	1.33	1.37
22	w	55	PSU	C4-N3	-2.68	1.33	1.38
23	x	8	4SU	C5-C4	-2.68	1.39	1.42
23	x	55	PSU	C4-N3	-2.67	1.33	1.38
26	A	2580	PSU	C4-N3	-2.66	1.33	1.38
22	y	55	PSU	C4-N3	-2.66	1.33	1.38
26	A	2449	H2U	C4-N3	-2.65	1.33	1.37
22	y	19	H2U	C2-N3	-2.65	1.33	1.38
26	A	747	5MU	C6-C5	2.65	1.38	1.34
22	w	54	5MU	C4-N3	-2.64	1.33	1.38
22	w	19	H2U	C2-N3	-2.64	1.33	1.38
22	w	54	5MU	C6-C5	2.63	1.38	1.34
1	a	966	2MG	C6-N1	-2.63	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	y	54	5MU	C4-N3	-2.62	1.33	1.38
22	y	8	4SU	C2-N1	2.59	1.42	1.38
1	a	1207	2MG	C6-N1	-2.59	1.33	1.37
1	a	967	5MC	C6-C5	2.59	1.38	1.34
26	A	2552	OMU	C2-N3	-2.57	1.33	1.38
1	a	1519	MA6	C6-C5	2.55	1.48	1.44
26	A	1915	3TD	O2-C2	-2.53	1.18	1.23
23	x	32	5MC	C6-N1	-2.52	1.33	1.38
23	x	54	5MU	C6-C5	2.51	1.38	1.34
1	a	527	G7M	C6-N1	-2.50	1.34	1.37
23	x	32	5MC	C6-C5	2.50	1.38	1.34
22	y	20	H2U	C4-N3	-2.49	1.33	1.37
22	w	17	OMG	C6-N1	-2.49	1.34	1.37
22	w	20	H2U	C4-N3	-2.47	1.33	1.37
26	A	1939	5MU	C2-N3	-2.47	1.33	1.38
22	y	19	H2U	C4-N3	-2.46	1.33	1.37
26	A	2030	6MZ	C6-C5	2.44	1.48	1.44
22	w	19	H2U	C4-N3	-2.43	1.33	1.37
22	w	47	3AU	O4-C4	-2.42	1.18	1.23
1	a	967	5MC	C6-N1	-2.41	1.33	1.38
22	y	47	3AU	O4-C4	-2.41	1.18	1.23
1	a	1516	2MG	C6-N1	-2.41	1.34	1.37
38	O	81	4D4	CZ-NH1	-2.40	1.25	1.34
26	A	1939	5MU	C6-N1	-2.40	1.33	1.38
22	w	46	G7M	C6-N1	-2.39	1.34	1.37
26	A	747	5MU	C6-N1	-2.39	1.33	1.38
22	w	8	4SU	C2-N3	-2.38	1.33	1.38
22	y	54	5MU	C4-C5	2.37	1.48	1.44
1	a	1407	5MC	C6-C5	2.37	1.38	1.34
22	y	47	3AU	O30-C13	2.36	1.29	1.22
23	x	54	5MU	C6-N1	-2.35	1.34	1.38
22	w	54	5MU	C6-N1	-2.35	1.34	1.38
1	a	1407	5MC	C6-N1	-2.35	1.34	1.38
26	A	1962	5MC	C6-N1	-2.35	1.34	1.38
26	A	1618	6MZ	C6-C5	2.35	1.48	1.44
22	w	54	5MU	C4-C5	2.33	1.48	1.44
1	a	1518	MA6	C6-C5	2.32	1.48	1.44
22	w	47	3AU	O30-C13	2.31	1.28	1.22
22	y	46	G7M	C6-N1	-2.30	1.34	1.37
26	A	2580	PSU	O4'-C1'	-2.29	1.40	1.43
23	x	54	5MU	C4-C5	2.29	1.48	1.44
26	A	747	5MU	C2-N3	-2.28	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	A	1915	3TD	O4-C4	-2.23	1.18	1.23
23	x	8	4SU	C2-N3	-2.23	1.34	1.38
23	x	54	5MU	C2-N1	2.21	1.41	1.38
22	w	37	T6A	C6-C5	2.20	1.48	1.44
22	y	17	OMG	C6-N1	-2.20	1.34	1.37
26	A	2552	OMU	C5-C4	-2.19	1.38	1.43
26	A	955	PSU	C2-N3	-2.19	1.33	1.37
22	y	8	4SU	C2-N3	-2.18	1.34	1.38
23	x	54	5MU	C2-N3	-2.18	1.34	1.38
26	A	2605	PSU	C2-N3	-2.17	1.33	1.37
22	w	8	4SU	C2-N1	2.17	1.41	1.38
22	w	47	3AU	C11-C10	2.16	1.59	1.52
26	A	745	1MG	C2-N1	2.16	1.41	1.37
26	A	2604	PSU	C2-N3	-2.16	1.33	1.37
26	A	747	5MU	C4-C5	2.15	1.48	1.44
26	A	1939	5MU	C4-C5	2.14	1.48	1.44
1	a	516	PSU	C2-N3	-2.13	1.34	1.37
26	A	2457	PSU	C2-N3	-2.13	1.34	1.37
22	y	47	3AU	C11-C10	2.12	1.59	1.52
26	A	1911	PSU	C2-N3	-2.09	1.34	1.37
22	y	54	5MU	C6-N1	-2.07	1.34	1.38
22	y	54	5MU	C2-N3	-2.06	1.34	1.38
22	y	39	PSU	C2-N3	-2.06	1.34	1.37
22	y	34	M3X	O-C	-2.04	1.24	1.30
26	A	1917	PSU	C2-N1	-2.03	1.34	1.36
26	A	747	5MU	C2-N1	2.03	1.41	1.38
22	w	54	5MU	C2-N3	-2.02	1.34	1.38
26	A	2449	H2U	C2-N1	-2.02	1.32	1.35
26	A	2580	PSU	C2-N3	-2.01	1.34	1.37
26	A	1917	PSU	C2-N3	-2.00	1.34	1.37
22	w	34	M3X	O-C	-2.00	1.24	1.30
22	w	54	5MU	C2-N1	2.00	1.41	1.38

All (198) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	A	2503	2MA	C2-N3-C4	7.08	121.17	115.46
1	a	1498	UR3	C4-N3-C2	-7.03	118.92	124.58
23	x	8	4SU	C4-N3-C2	-6.93	120.68	127.31
22	y	8	4SU	C4-N3-C2	-6.71	120.88	127.31
26	A	746	PSU	N1-C2-N3	6.62	122.15	115.17
26	A	2030	6MZ	C2-N1-C6	6.61	121.73	116.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	A	2604	PSU	N1-C2-N3	6.55	122.08	115.17
26	A	2605	PSU	N1-C2-N3	6.51	122.03	115.17
26	A	1911	PSU	N1-C2-N3	6.51	122.03	115.17
22	w	55	PSU	N1-C2-N3	6.47	122.00	115.17
22	w	39	PSU	N1-C2-N3	6.42	121.94	115.17
26	A	2457	PSU	N1-C2-N3	6.40	121.92	115.17
26	A	2504	PSU	N1-C2-N3	6.40	121.92	115.17
23	x	55	PSU	N1-C2-N3	6.40	121.92	115.17
26	A	955	PSU	N1-C2-N3	6.40	121.92	115.17
26	A	1917	PSU	N1-C2-N3	6.37	121.88	115.17
22	w	8	4SU	C4-N3-C2	-6.23	121.34	127.31
22	y	39	PSU	N1-C2-N3	6.22	121.72	115.17
22	y	55	PSU	N1-C2-N3	6.19	121.70	115.17
1	a	516	PSU	N1-C2-N3	6.17	121.67	115.17
22	w	37	T6A	C2-N1-C6	6.16	121.38	116.60
26	A	2580	PSU	N1-C2-N3	6.11	121.61	115.17
26	A	1618	6MZ	C2-N1-C6	6.08	121.32	116.60
22	y	37	T6A	C2-N1-C6	5.75	121.06	116.60
22	w	8	4SU	C5-C4-N3	5.75	120.09	114.75
22	y	8	4SU	C5-C4-N3	5.68	120.04	114.75
26	A	1939	5MU	N3-C2-N1	5.57	122.14	114.89
23	x	8	4SU	C5-C4-N3	5.53	119.90	114.75
22	w	54	5MU	C4-N3-C2	-5.48	120.15	127.34
26	A	1939	5MU	C4-N3-C2	-5.41	120.25	127.34
22	w	54	5MU	N3-C2-N1	5.34	121.84	114.89
23	x	54	5MU	C4-N3-C2	-5.21	120.50	127.34
22	y	54	5MU	N3-C2-N1	5.13	121.57	114.89
26	A	1915	3TD	N1-C2-N3	5.13	119.86	116.13
1	a	1519	MA6	C2-N1-C6	5.12	121.86	116.84
26	A	747	5MU	N3-C2-N1	5.09	121.51	114.89
23	x	54	5MU	N3-C2-N1	5.08	121.51	114.89
26	A	2552	OMU	C4-N3-C2	-5.00	120.41	126.61
1	a	1518	MA6	C2-N1-C6	4.91	121.65	116.84
22	y	54	5MU	C4-N3-C2	-4.85	120.99	127.34
26	A	747	5MU	C4-N3-C2	-4.83	121.00	127.34
22	w	54	5MU	C5-C4-N3	4.54	119.27	115.32
26	A	2552	OMU	N3-C2-N1	4.50	120.75	114.89
26	A	2605	PSU	C4-N3-C2	-4.49	120.19	126.37
23	x	54	5MU	C5-C4-N3	4.45	119.19	115.32
22	y	37	T6A	N6-C6-N1	4.39	123.65	118.71
23	x	8	4SU	N3-C2-N1	4.34	120.54	114.89
26	A	1911	PSU	C4-N3-C2	-4.33	120.40	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	A	746	PSU	C4-N3-C2	-4.33	120.41	126.37
26	A	2604	PSU	C4-N3-C2	-4.32	120.42	126.37
26	A	1915	3TD	C4-N3-C2	-4.28	120.08	124.61
26	A	1939	5MU	C5-C4-N3	4.28	119.04	115.32
1	a	516	PSU	C4-N3-C2	-4.27	120.49	126.37
26	A	2504	PSU	C4-N3-C2	-4.26	120.50	126.37
12	l	89	D2T	CB1-SB-CB	4.23	109.97	102.36
22	y	8	4SU	N3-C2-N1	4.22	120.39	114.89
26	A	955	PSU	C4-N3-C2	-4.19	120.59	126.37
22	w	55	PSU	C4-N3-C2	-4.19	120.60	126.37
26	A	2457	PSU	C4-N3-C2	-4.19	120.60	126.37
26	A	2580	PSU	C4-N3-C2	-4.19	120.60	126.37
26	A	1939	5MU	C5-C6-N1	-4.17	118.78	123.31
23	x	55	PSU	C4-N3-C2	-4.12	120.70	126.37
26	A	2030	6MZ	C9-N6-C6	-4.10	119.04	122.85
1	a	1518	MA6	N1-C6-N6	4.09	121.56	116.83
22	y	47	3AU	C4-N3-C2	-4.09	119.86	124.66
26	A	746	PSU	O2-C2-N1	-4.08	118.58	122.79
22	w	54	5MU	O4-C4-C5	-4.00	120.34	124.92
23	x	54	5MU	O4-C4-C5	-3.99	120.35	124.92
26	A	747	5MU	C5-C4-N3	3.98	118.78	115.32
22	w	47	3AU	C4-N3-C2	-3.97	119.99	124.66
26	A	1917	PSU	O2-C2-N1	-3.97	118.70	122.79
22	w	39	PSU	C4-N3-C2	-3.97	120.91	126.37
26	A	1917	PSU	C4-N3-C2	-3.96	120.91	126.37
22	y	39	PSU	C4-N3-C2	-3.94	120.95	126.37
22	w	37	T6A	N6-C10-N11	3.93	119.18	113.77
22	w	8	4SU	C5-C4-S4	-3.92	119.83	124.31
22	y	55	PSU	C4-N3-C2	-3.90	121.00	126.37
22	y	54	5MU	C5-C4-N3	3.89	118.70	115.32
22	y	8	4SU	C5-C4-S4	-3.88	119.88	124.31
26	A	2552	OMU	C5-C4-N3	3.86	120.21	114.80
23	x	55	PSU	O2-C2-N1	-3.86	118.81	122.79
22	w	39	PSU	O2-C2-N1	-3.85	118.82	122.79
23	x	8	4SU	C5-C4-S4	-3.83	119.94	124.31
22	w	55	PSU	O2-C2-N1	-3.82	118.85	122.79
22	w	8	4SU	N3-C2-N1	3.79	119.82	114.89
22	y	37	T6A	N6-C10-N11	3.78	118.97	113.77
26	A	1939	5MU	O4-C4-C5	-3.77	120.60	124.92
1	a	1519	MA6	C9-N6-C6	-3.72	109.13	119.40
22	y	55	PSU	O2-C2-N1	-3.72	118.95	122.79
26	A	2580	PSU	O2-C2-N1	-3.72	118.96	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	y	54	5MU	O2-C2-N1	-3.70	117.97	122.80
26	A	2457	PSU	O2-C2-N1	-3.70	118.97	122.79
1	a	1519	MA6	C10-N6-C6	-3.70	109.21	119.40
26	A	747	5MU	O4-C4-C5	-3.66	120.73	124.92
1	a	1519	MA6	N3-C2-N1	-3.66	123.71	128.67
12	l	89	D2T	OD2-CG-CB	3.63	121.00	113.15
26	A	1911	PSU	O2-C2-N1	-3.62	119.06	122.79
26	A	2030	6MZ	N3-C2-N1	-3.61	123.77	128.67
22	y	54	5MU	O4-C4-C5	-3.58	120.82	124.92
1	a	1518	MA6	N3-C2-N1	-3.57	123.83	128.67
1	a	1518	MA6	C10-N6-C6	-3.56	109.59	119.40
22	w	54	5MU	C5-C6-N1	-3.55	119.46	123.31
23	x	54	5MU	C5-C6-N1	-3.53	119.48	123.31
26	A	2504	PSU	O2-C2-N1	-3.51	119.16	122.79
26	A	2605	PSU	O2-C2-N1	-3.51	119.17	122.79
23	x	32	5MC	C5-C6-N1	-3.48	119.53	123.31
22	y	54	5MU	C5-C6-N1	-3.48	119.54	123.31
26	A	955	PSU	O2-C2-N1	-3.46	119.22	122.79
26	A	1618	6MZ	N3-C2-N1	-3.45	123.99	128.67
1	a	516	PSU	O2-C2-N1	-3.44	119.24	122.79
26	A	2604	PSU	O2-C2-N1	-3.44	119.24	122.79
26	A	1962	5MC	C5-C6-N1	-3.44	119.58	123.31
22	w	37	T6A	N3-C2-N1	-3.38	124.09	128.67
22	y	39	PSU	O2-C2-N1	-3.37	119.31	122.79
1	a	1498	UR3	C5-C4-N3	3.37	119.48	115.04
1	a	1518	MA6	C9-N6-C6	-3.34	110.18	119.40
26	A	747	5MU	C5-C6-N1	-3.33	119.69	123.31
1	a	1407	5MC	C5-C6-N1	-3.22	119.81	123.31
23	x	32	5MC	C5-C4-N3	-3.21	118.46	121.75
22	y	8	4SU	C1'-N1-C2	3.16	123.26	117.59
26	A	2030	6MZ	C4-C5-N7	-3.13	106.03	109.34
22	w	47	3AU	C5-C4-N3	3.12	119.96	115.64
1	a	1519	MA6	C4-C5-N7	-3.10	106.06	109.34
22	y	47	3AU	C5-C4-N3	3.10	119.92	115.64
1	a	967	5MC	C5-C6-N1	-3.09	119.96	123.31
22	y	37	T6A	N3-C2-N1	-3.07	124.50	128.67
22	w	37	T6A	N6-C6-N1	3.06	122.15	118.71
1	a	1516	2MG	C8-N7-C5	3.04	107.72	102.55
1	a	1519	MA6	N1-C6-N6	3.00	120.30	116.83
22	w	54	5MU	O2-C2-N1	-3.00	118.89	122.80
22	w	17	OMG	C8-N7-C5	2.91	107.50	102.55
26	A	745	1MG	C8-N7-C5	2.90	107.49	102.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	a	967	5MC	C5-C4-N3	-2.89	118.79	121.75
1	a	1519	MA6	C10-N6-C9	-2.87	106.96	116.18
26	A	1939	5MU	O2-C2-N1	-2.87	119.06	122.80
23	x	32	5MC	O2-C2-N3	-2.86	117.81	122.33
22	y	17	OMG	C8-N7-C5	2.86	107.43	102.55
26	A	2552	OMU	O4-C4-C5	-2.85	120.25	125.16
1	a	966	2MG	C8-N7-C5	2.84	107.39	102.55
22	w	47	3AU	C6-N1-C2	-2.83	119.48	121.80
22	w	8	4SU	C1'-N1-C2	2.83	122.67	117.59
26	A	2498	OMC	O2-C2-N3	-2.83	117.87	122.33
26	A	2445	2MG	C8-N7-C5	2.82	107.35	102.55
26	A	1618	6MZ	C4-C5-N7	-2.82	106.36	109.34
22	w	34	M3X	C5-C4-N3	-2.81	118.45	121.83
1	a	1207	2MG	C8-N7-C5	2.80	107.31	102.55
26	A	1962	5MC	C5-C4-N3	-2.80	118.89	121.75
26	A	2251	OMG	C8-N7-C5	2.78	107.29	102.55
26	A	1618	6MZ	C9-N6-C6	-2.78	120.27	122.85
1	a	1407	5MC	C5-C4-N3	-2.76	118.92	121.75
26	A	1835	2MG	C8-N7-C5	2.76	107.25	102.55
26	A	745	1MG	C5-C6-N1	2.69	117.85	113.96
26	A	2503	2MA	C2-N1-C6	2.69	122.23	118.10
22	w	37	T6A	C4-C5-N7	-2.64	106.55	109.34
1	a	1518	MA6	C4-C5-N7	-2.61	106.57	109.34
26	A	2503	2MA	C4-C5-N7	-2.59	106.60	109.34
1	a	1402	4OC	C6-C5-C4	2.55	120.07	117.00
26	A	2580	PSU	O4'-C1'-C2'	2.49	108.60	105.15
22	y	34	M3X	C5-C4-N3	-2.47	118.86	121.83
11	k	119	IAS	OD1-CG-CB	-2.43	118.29	125.38
23	x	54	5MU	O2-C2-N1	-2.42	119.64	122.80
26	A	2552	OMU	O2-C2-N1	-2.40	119.67	122.80
1	a	1407	5MC	O2-C2-N3	-2.39	118.56	122.33
26	A	2605	PSU	C5-C6-N1	-2.38	118.83	122.14
22	y	34	M3X	N4-C4-N3	2.38	120.42	116.59
22	y	47	3AU	C6-N1-C2	-2.37	119.86	121.80
1	a	1516	2MG	N1-C2-N2	2.32	118.93	116.56
26	A	1911	PSU	C5-C6-N1	-2.30	118.95	122.14
26	A	2445	2MG	C5-C6-N1	2.29	118.44	114.07
26	A	2604	PSU	C5-C6-N1	-2.28	118.98	122.14
26	A	2251	OMG	C5-C6-N1	2.26	118.39	114.07
1	a	1516	2MG	C5-C6-N1	2.25	118.36	114.07
1	a	516	PSU	O4'-C1'-C2'	2.24	108.25	105.15
22	w	19	H2U	C5-C6-N1	-2.23	104.76	111.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	a	1402	4OC	O2-C2-N3	-2.22	118.82	122.33
26	A	1835	2MG	C5-C6-N1	2.22	118.31	114.07
1	a	1207	2MG	C5-C6-N1	2.20	118.26	114.07
22	w	55	PSU	C5-C6-N1	-2.18	119.11	122.14
22	w	17	OMG	C5-C6-N1	2.18	118.22	114.07
1	a	966	2MG	C5-C6-N1	2.17	118.21	114.07
22	y	37	T6A	O10-C10-N6	-2.16	119.81	123.64
22	y	17	OMG	C5-C6-N1	2.14	118.16	114.07
26	A	2504	PSU	C5-C6-N1	-2.13	119.18	122.14
12	l	89	D2T	OD2-CG-OD1	-2.12	119.28	124.08
22	y	37	T6A	C4-C5-N7	-2.12	107.10	109.34
1	a	1518	MA6	C10-N6-C9	-2.11	109.42	116.18
26	A	955	PSU	C5-C6-N1	-2.10	119.22	122.14
26	A	1911	PSU	O4'-C1'-C2'	2.10	108.06	105.15
26	A	2503	2MA	C5-C6-N1	-2.10	118.36	120.84
1	a	967	5MC	O2-C2-N3	-2.09	119.04	122.33
26	A	2457	PSU	O4'-C1'-C2'	2.08	108.03	105.15
26	A	747	5MU	O2-C2-N1	-2.06	120.12	122.80
26	A	1962	5MC	O2-C2-N3	-2.05	119.10	122.33
1	a	1207	2MG	N1-C2-N2	2.04	118.65	116.56
22	w	20	H2U	C5-C6-N1	-2.04	105.36	111.52
1	a	516	PSU	C5-C6-N1	-2.04	119.31	122.14
22	y	20	H2U	C5-C6-N1	-2.03	105.39	111.52
26	A	2580	PSU	C5-C6-N1	-2.02	119.34	122.14

There are no chirality outliers.

All (112) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	a	527	G7M	O4'-C4'-C5'-O5'
1	a	527	G7M	C3'-C4'-C5'-O5'
1	a	1207	2MG	N3-C2-N2-CM2
1	a	1402	4OC	O4'-C4'-C5'-O5'
1	a	1519	MA6	C5-C6-N6-C9
12	l	89	D2T	CG-CB-SB-CB1
12	l	89	D2T	CA-CB-CG-OD1
12	l	89	D2T	CA-CB-CG-OD2
22	w	17	OMG	O4'-C4'-C5'-O5'
22	w	19	H2U	O4'-C1'-N1-C2
22	w	19	H2U	O4'-C1'-N1-C6
22	w	20	H2U	O4'-C1'-N1-C2
22	w	20	H2U	O4'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
22	w	34	M3X	N1-C2-N2-CE
22	w	34	M3X	N3-C2-N2-CE
22	w	34	M3X	CG-CB-CZ-N
22	w	34	M3X	CG-CB-CZ-C
22	y	34	M3X	C2'-C1'-N1-C6
22	y	37	T6A	N6-C10-N11-C12
22	y	37	T6A	C13-C12-C14-C15
22	w	46	G7M	O4'-C4'-C5'-O5'
22	w	47	3AU	C10-C11-C12-C13
22	w	47	3AU	C10-C11-C12-N40
22	w	47	3AU	N40-C12-C13-O30
22	y	47	3AU	C10-C11-C12-C13
22	y	47	3AU	C10-C11-C12-N40
22	y	54	5MU	C2'-C1'-N1-C2
22	y	54	5MU	C2'-C1'-N1-C6
22	w	55	PSU	O4'-C4'-C5'-O5'
22	y	55	PSU	O4'-C1'-C5-C4
22	y	55	PSU	C2'-C1'-C5-C6
22	y	55	PSU	O4'-C1'-C5-C6
22	w	34	M3X	CE-CD-CG-CB
22	y	37	T6A	O10-C10-N11-C12
22	w	17	OMG	C3'-C4'-C5'-O5'
22	y	20	H2U	O4'-C4'-C5'-O5'
22	y	20	H2U	C3'-C4'-C5'-O5'
22	y	47	3AU	O4'-C4'-C5'-O5'
22	w	55	PSU	C3'-C4'-C5'-O5'
26	A	2498	OMC	O4'-C4'-C5'-O5'
26	A	2552	OMU	O4'-C4'-C5'-O5'
22	y	47	3AU	N40-C12-C13-O31
22	w	19	H2U	O4'-C4'-C5'-O5'
22	y	19	H2U	O4'-C4'-C5'-O5'
22	y	19	H2U	C3'-C4'-C5'-O5'
22	w	47	3AU	O4'-C4'-C5'-O5'
26	A	2504	PSU	O4'-C4'-C5'-O5'
22	w	47	3AU	N40-C12-C13-O31
1	a	1519	MA6	N1-C6-N6-C9
29	D	150	MEQ	NE2-CD-CG-CB
22	w	19	H2U	C2'-C1'-N1-C6
22	w	20	H2U	C2'-C1'-N1-C6
1	a	1402	4OC	C3'-C4'-C5'-O5'
22	w	46	G7M	C3'-C4'-C5'-O5'
22	w	47	3AU	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
29	D	150	MEQ	OE1-CD-CG-CB
22	w	17	OMG	C4'-C5'-O5'-P
22	y	37	T6A	N11-C12-C14-O14
22	y	37	T6A	C14-C12-C13-ODB
26	A	1917	PSU	C3'-C4'-C5'-O5'
26	A	2498	OMC	C3'-C4'-C5'-O5'
22	y	37	T6A	N11-C12-C13-ODA
22	y	47	3AU	C3'-C4'-C5'-O5'
26	A	1917	PSU	O4'-C4'-C5'-O5'
26	A	2552	OMU	C3'-C4'-C5'-O5'
22	y	46	G7M	C3'-C4'-C5'-O5'
26	A	2030	6MZ	O4'-C4'-C5'-O5'
22	y	20	H2U	C4'-C5'-O5'-P
22	w	47	3AU	C4'-C5'-O5'-P
22	y	37	T6A	C13-C12-C14-O14
22	w	20	H2U	C2'-C1'-N1-C2
22	y	37	T6A	C14-C12-C13-ODA
22	w	34	M3X	CZ-CB-CG-CD
22	y	37	T6A	N11-C12-C13-ODB
22	w	19	H2U	C2'-C1'-N1-C2
22	y	19	H2U	C4'-C5'-O5'-P
26	A	2498	OMC	C3'-C2'-O2'-CM2
22	y	34	M3X	N1-C2-N2-CE
22	y	20	H2U	C2'-C1'-N1-C2
22	y	46	G7M	C4'-C5'-O5'-P
26	A	2030	6MZ	C3'-C4'-C5'-O5'
22	w	19	H2U	C3'-C4'-C5'-O5'
26	A	2504	PSU	C3'-C4'-C5'-O5'
22	y	20	H2U	C2'-C1'-N1-C6
22	y	54	5MU	O4'-C1'-N1-C6
22	y	37	T6A	N11-C12-C14-C15
38	O	81	4D4	CG-CD-NE-CZ
22	w	34	M3X	C3'-C4'-C5'-O5'
12	l	89	D2T	CA-CB-SB-CB1
12	l	89	D2T	SB-CB-CG-OD2
38	O	81	4D4	OB-CB-CG-CD
22	y	54	5MU	O4'-C1'-N1-C2
26	A	746	PSU	O4'-C1'-C5-C6
26	A	2503	2MA	C4'-C5'-O5'-P
1	a	1519	MA6	O4'-C4'-C5'-O5'
22	y	34	M3X	CG-CB-CZ-C
1	a	966	2MG	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
26	A	2503	2MA	O4'-C4'-C5'-O5'
22	w	46	G7M	C4'-C5'-O5'-P
22	y	37	T6A	O10-C10-N6-C6
26	A	746	PSU	C2'-C1'-C5-C6
38	O	81	4D4	O-C-CA-CB
22	y	34	M3X	N3-C2-N2-CE
22	y	37	T6A	N11-C10-N6-C6
22	w	34	M3X	O4'-C4'-C5'-O5'
22	y	8	4SU	C2'-C1'-N1-C2
22	y	19	H2U	C2'-C1'-N1-C6
22	w	20	H2U	C4'-C5'-O5'-P
1	a	1518	MA6	N1-C6-N6-C9
26	A	2498	OMC	C2'-C1'-N1-C2
22	y	47	3AU	N40-C12-C13-O30
22	y	39	PSU	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 883 ligands modelled in this entry, 880 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	$\#\|Z\| > 2$
61	GCP	z	401	58	27,34,34	1.40	4 (14%)	35,54,54	1.87	8 (22%)
60	ILE	w	102	22	6,7,8	0.61	0	4,8,10	1.07	0
60	ILE	y	101	22	6,7,8	0.52	0	4,8,10	1.08	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
61	GCP	z	401	58	-	2/15/38/38	0/3/3/3
60	ILE	w	102	22	-	4/7/8/10	-
60	ILE	y	101	22	-	2/7/8/10	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	z	401	GCP	C5-C6	3.99	1.48	1.41
61	z	401	GCP	PG-O3G	2.82	1.61	1.55
61	z	401	GCP	PG-O2G	2.66	1.60	1.55
61	z	401	GCP	PB-O3A	2.04	1.60	1.58

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
61	z	401	GCP	C2-N3-C4	5.11	120.99	115.48
61	z	401	GCP	C2-N1-C6	4.49	122.21	115.96
61	z	401	GCP	C5-C6-N1	-3.97	118.11	123.42
61	z	401	GCP	N3-C2-N1	-3.37	122.92	127.21
61	z	401	GCP	PB-O3A-PA	-2.80	123.25	132.37
61	z	401	GCP	O4'-C1'-N9	2.72	112.35	108.75
61	z	401	GCP	C4-C5-C6	-2.67	117.16	121.23
61	z	401	GCP	C4-C5-N7	-2.66	106.52	109.34

There are no chirality outliers.

All (8) torsion outliers are listed below:

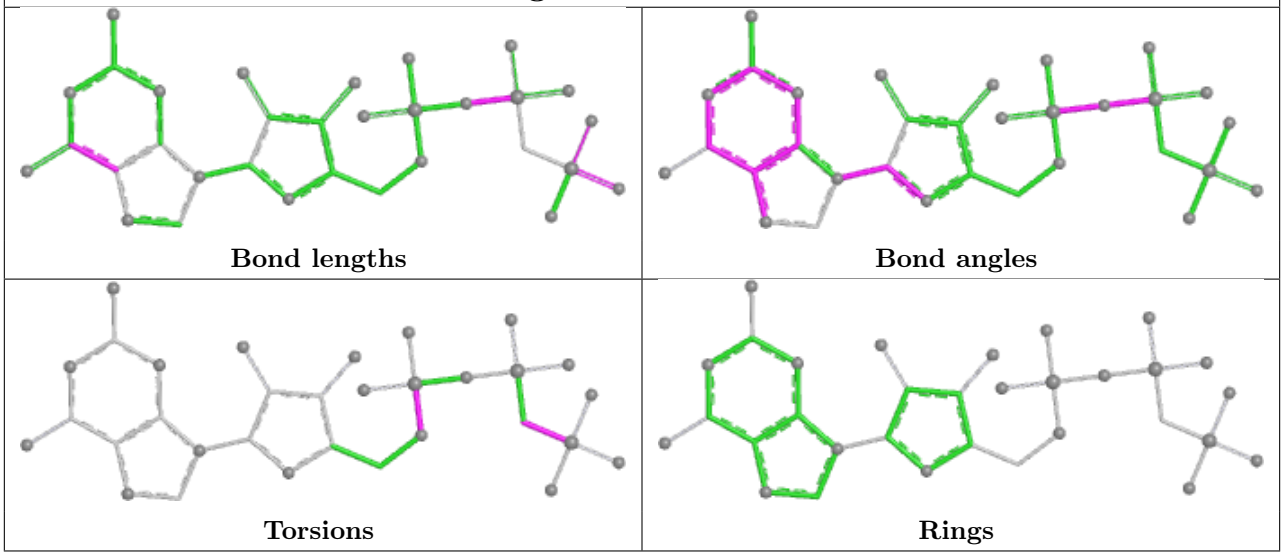
Mol	Chain	Res	Type	Atoms
60	w	102	ILE	O-C-CA-CB
60	w	102	ILE	C-CA-CB-CG1
60	w	102	ILE	C-CA-CB-CG2
60	y	101	ILE	C-CA-CB-CG2
61	z	401	GCP	C5'-O5'-PA-O2A
60	y	101	ILE	C-CA-CB-CG1
60	w	102	ILE	N-CA-CB-CG2
61	z	401	GCP	PB-C3B-PG-O1G

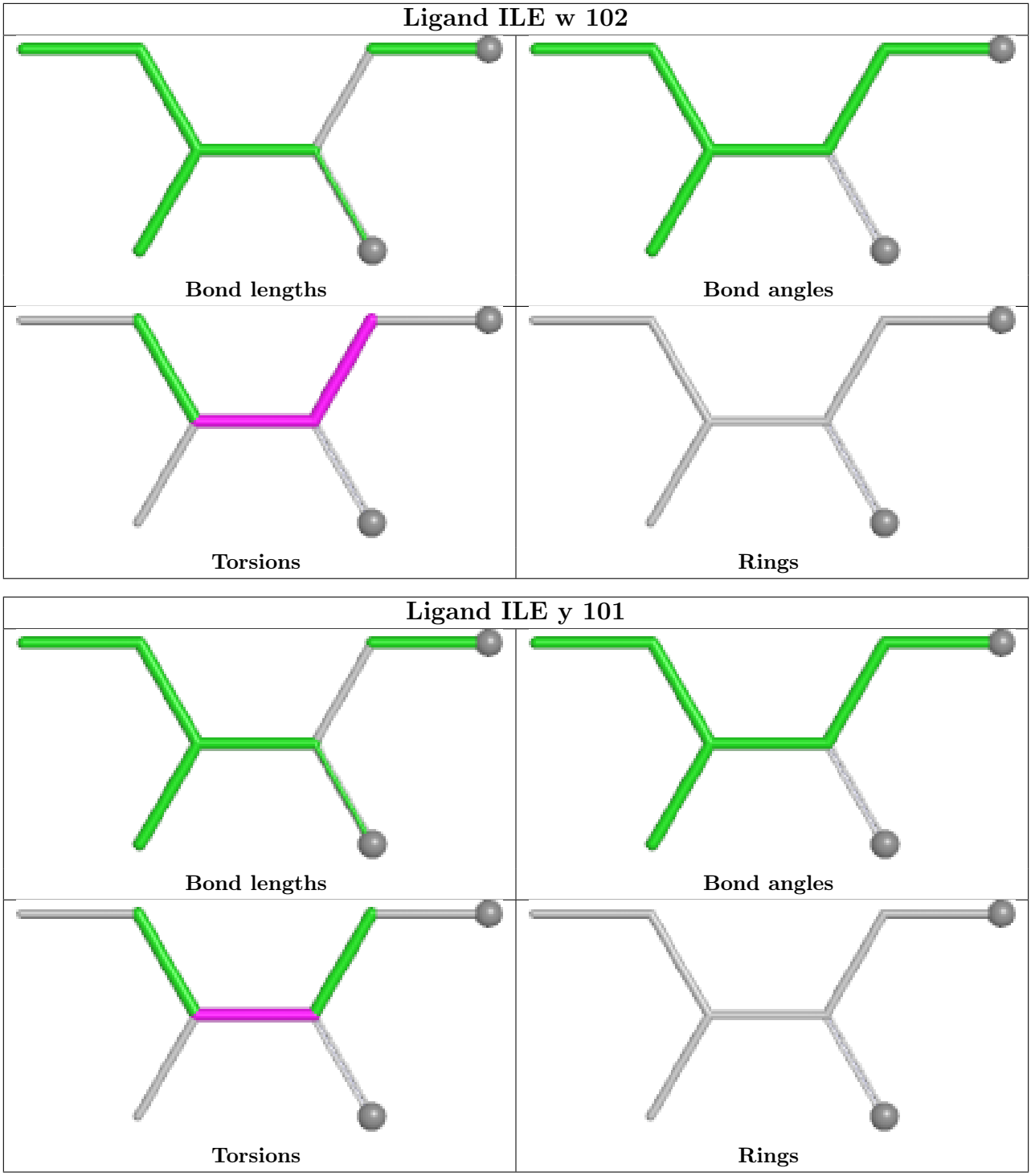
There are no ring outliers.

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 then 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.

Ligand GCP z 401





5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

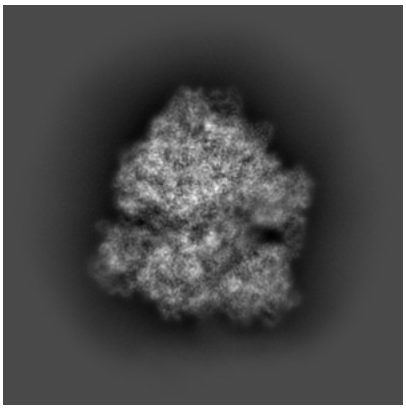
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-29819. These allow visual inspection of the internal detail of the map and identification of artifacts.

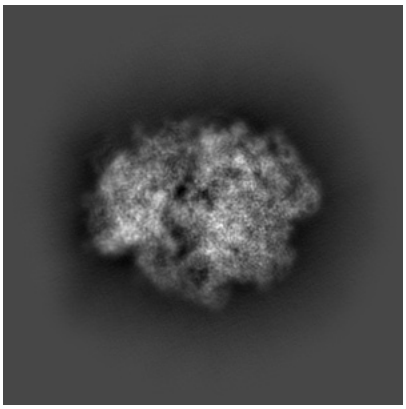
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

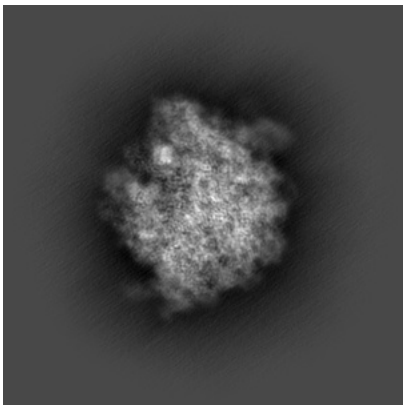
6.1.1 Primary map



X

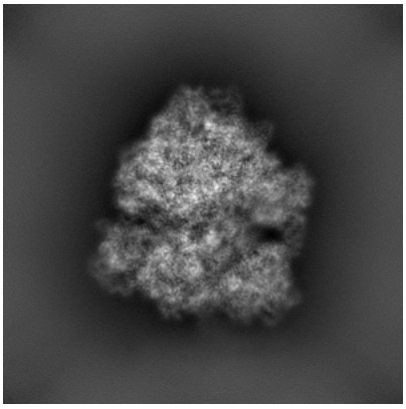


Y

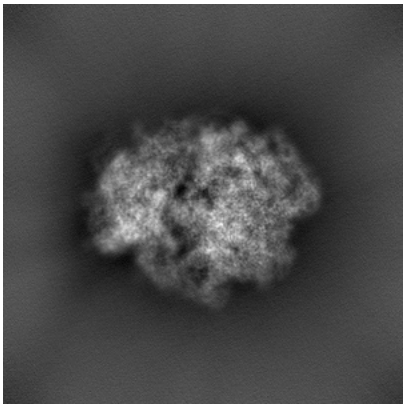


Z

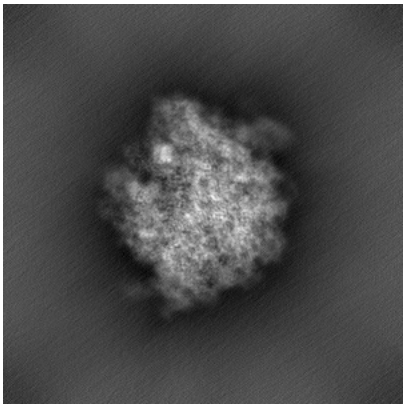
6.1.2 Raw map



X



Y

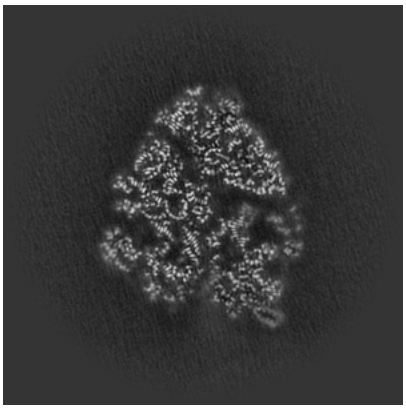


Z

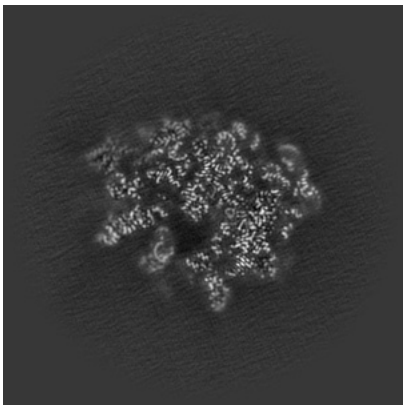
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

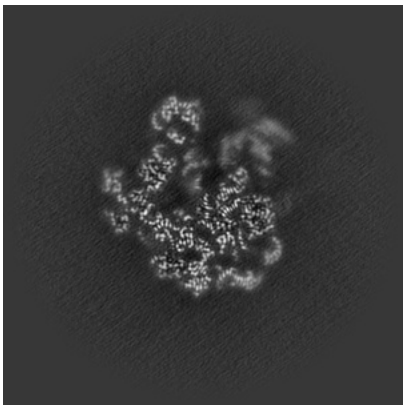
6.2.1 Primary map



X Index: 256

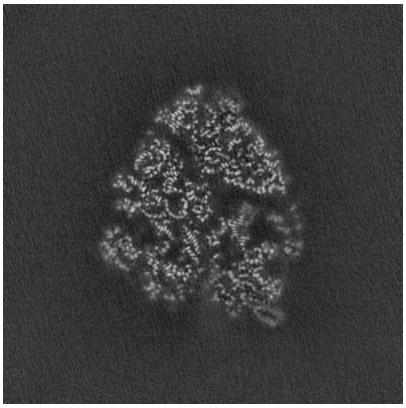


Y Index: 256

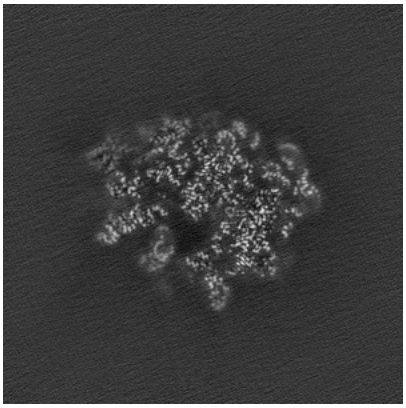


Z Index: 256

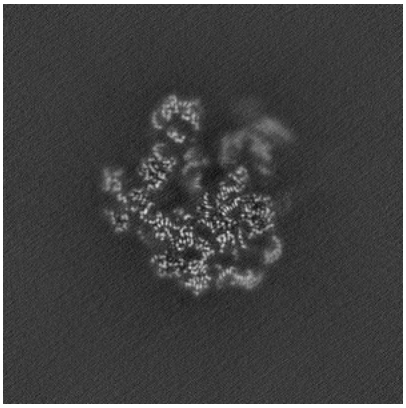
6.2.2 Raw map



X Index: 256



Y Index: 256

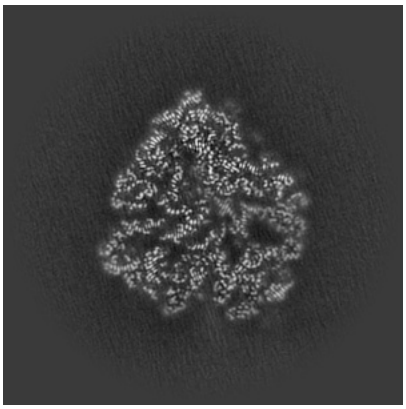


Z Index: 256

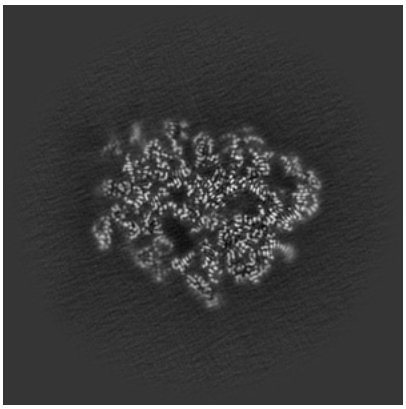
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

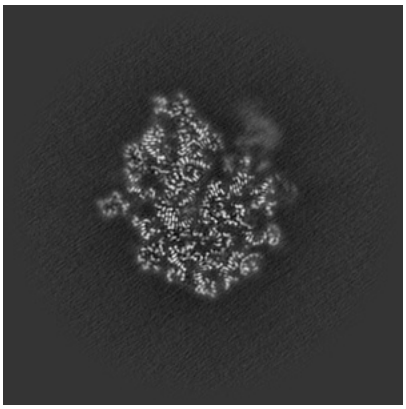
6.3.1 Primary map



X Index: 247

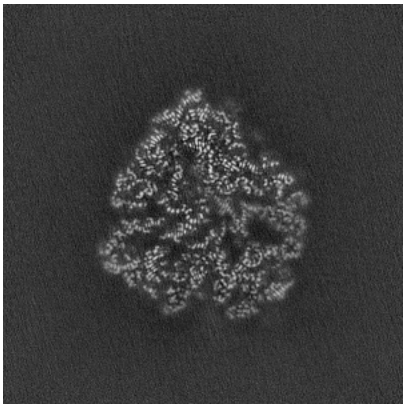


Y Index: 239

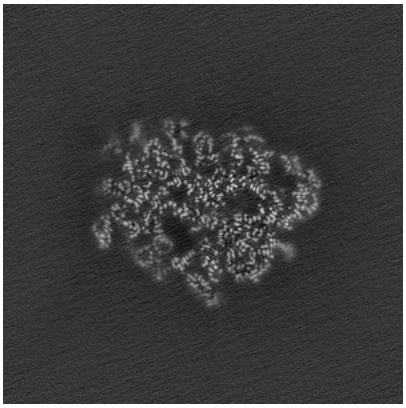


Z Index: 279

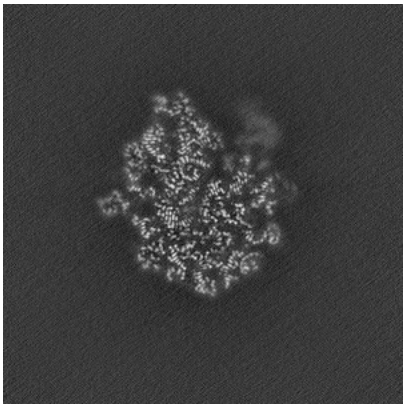
6.3.2 Raw map



X Index: 247



Y Index: 239

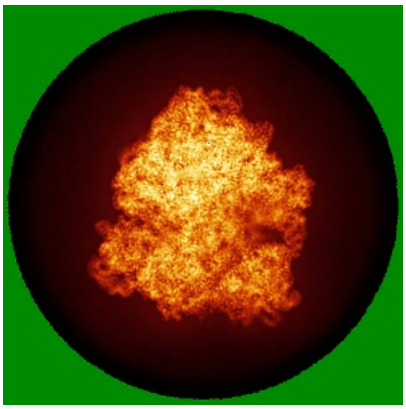


Z Index: 279

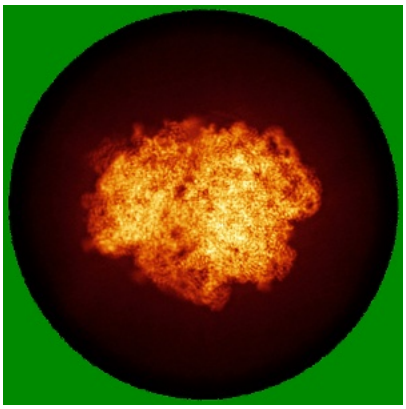
The images above show the largest variance slices of the map in three orthogonal directions.

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

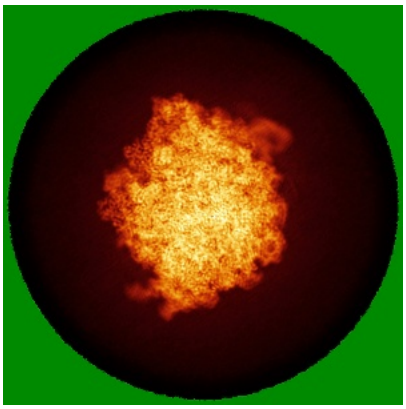
6.4.1 Primary map



X

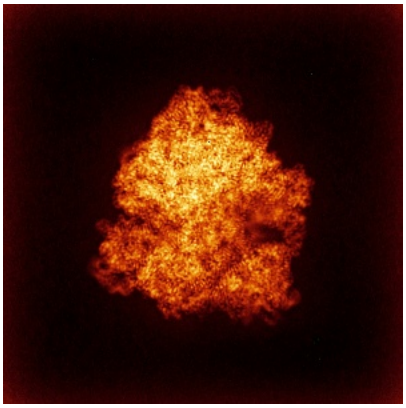


Y

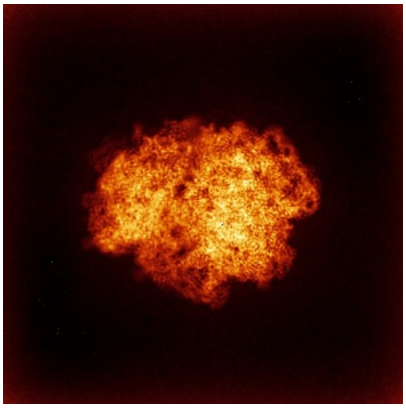


Z

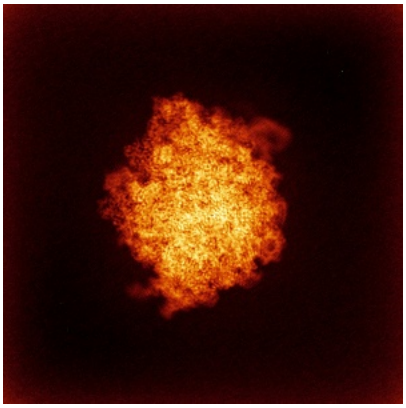
6.4.2 Raw map



X



Y



Z

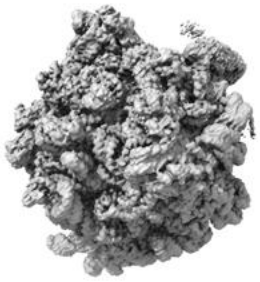
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X

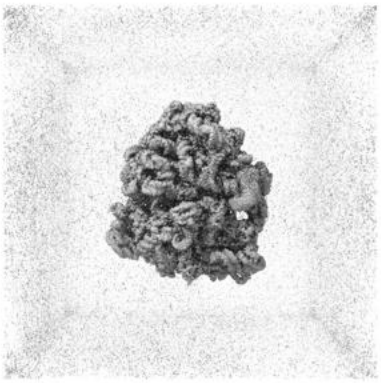
Y



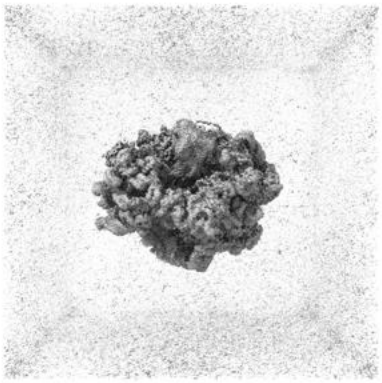
Z

The images above show the 3D surface view of the map at the recommended contour level 0.19. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y

Z

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

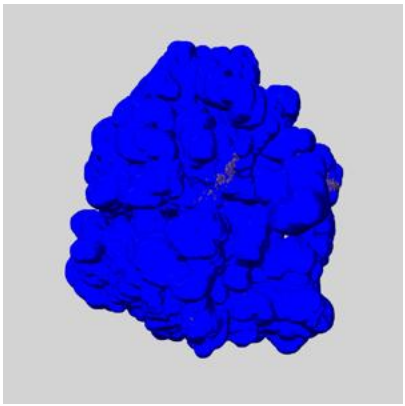
6.6 Mask visualisation

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

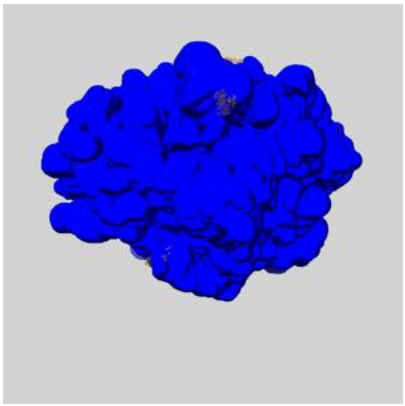
A mask typically either:

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

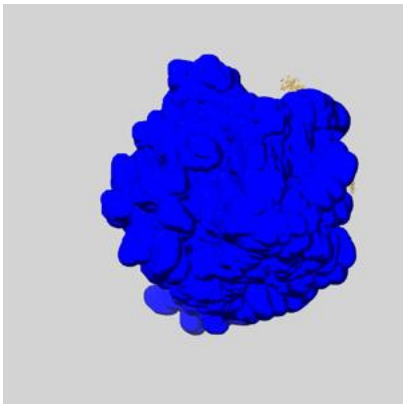
6.6.1 emd_29819_msk_1.map



X



Y

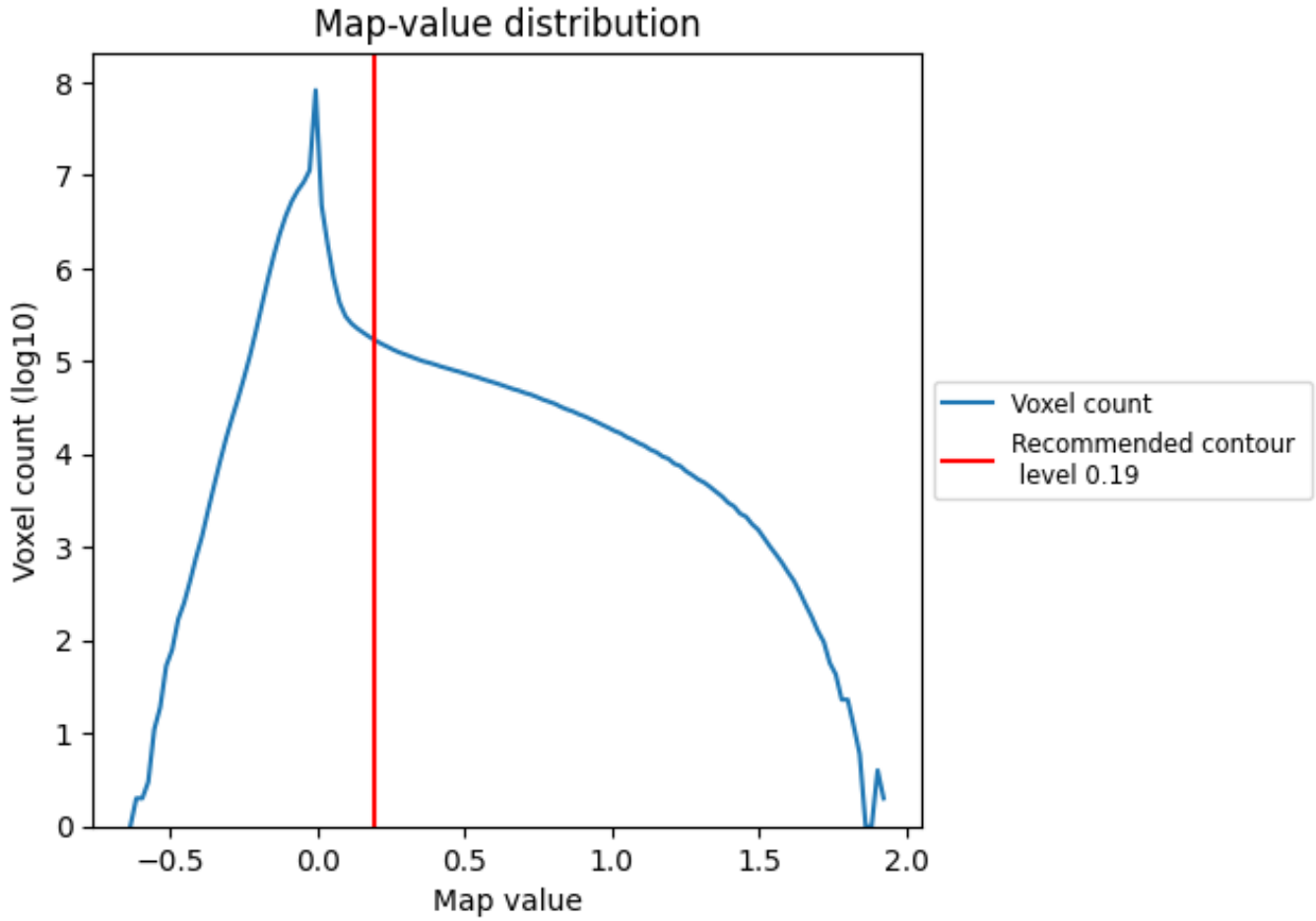


Z

7 Map analysis

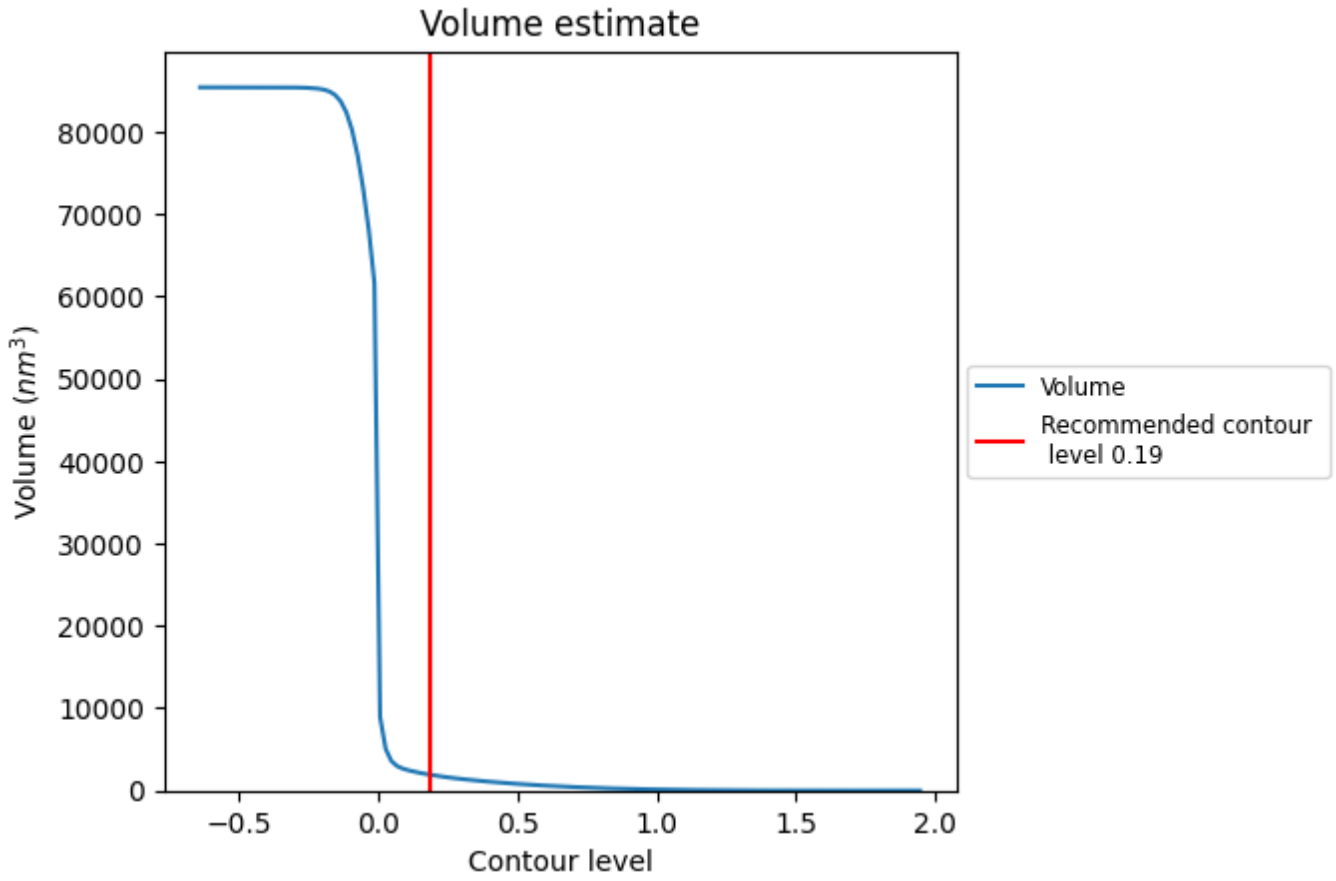
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

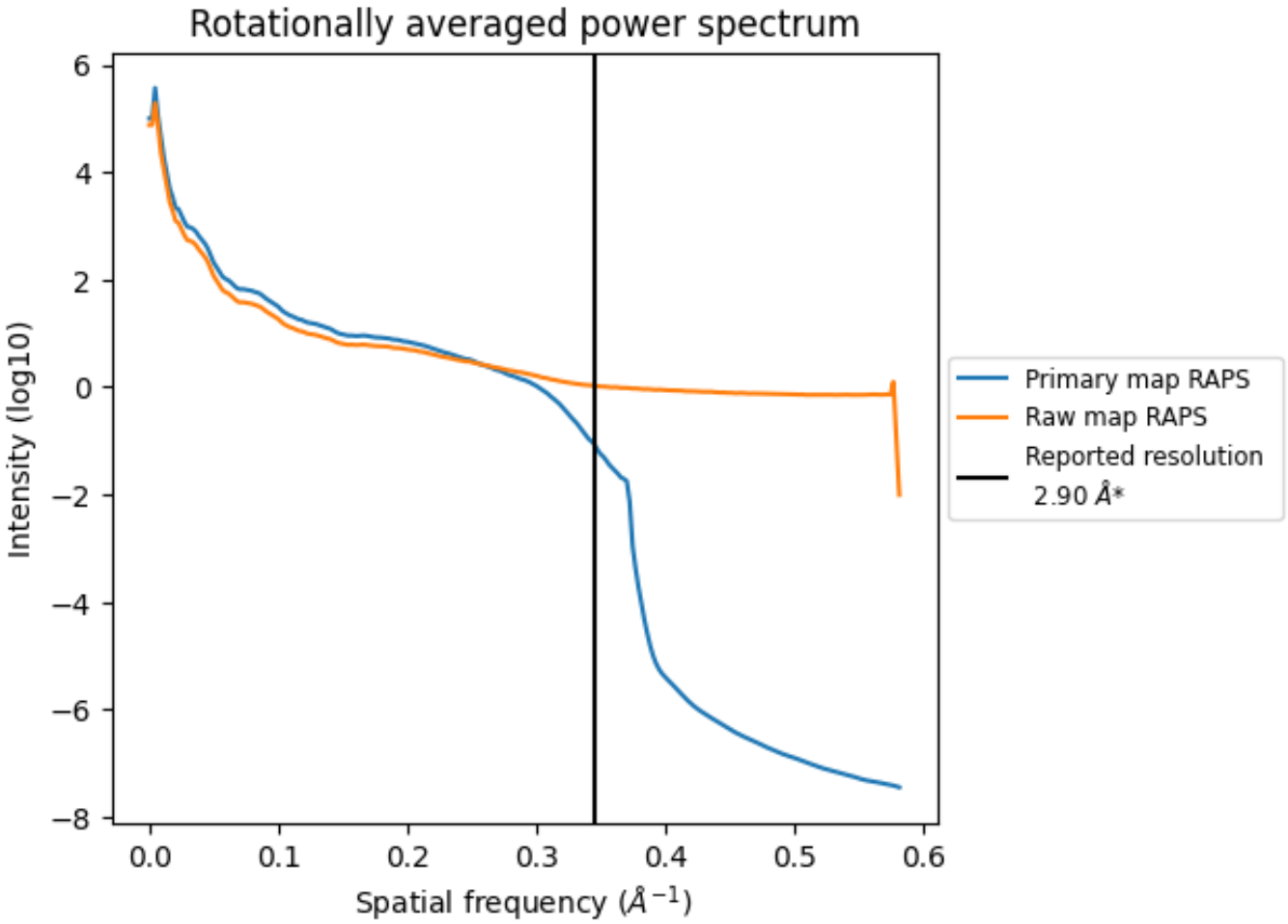
7.2 Volume estimate



The volume at the recommended contour level is 1908 nm^3; this corresponds to an approximate mass of 1723 kDa.

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

7.3 Rotationally averaged power spectrum (i)

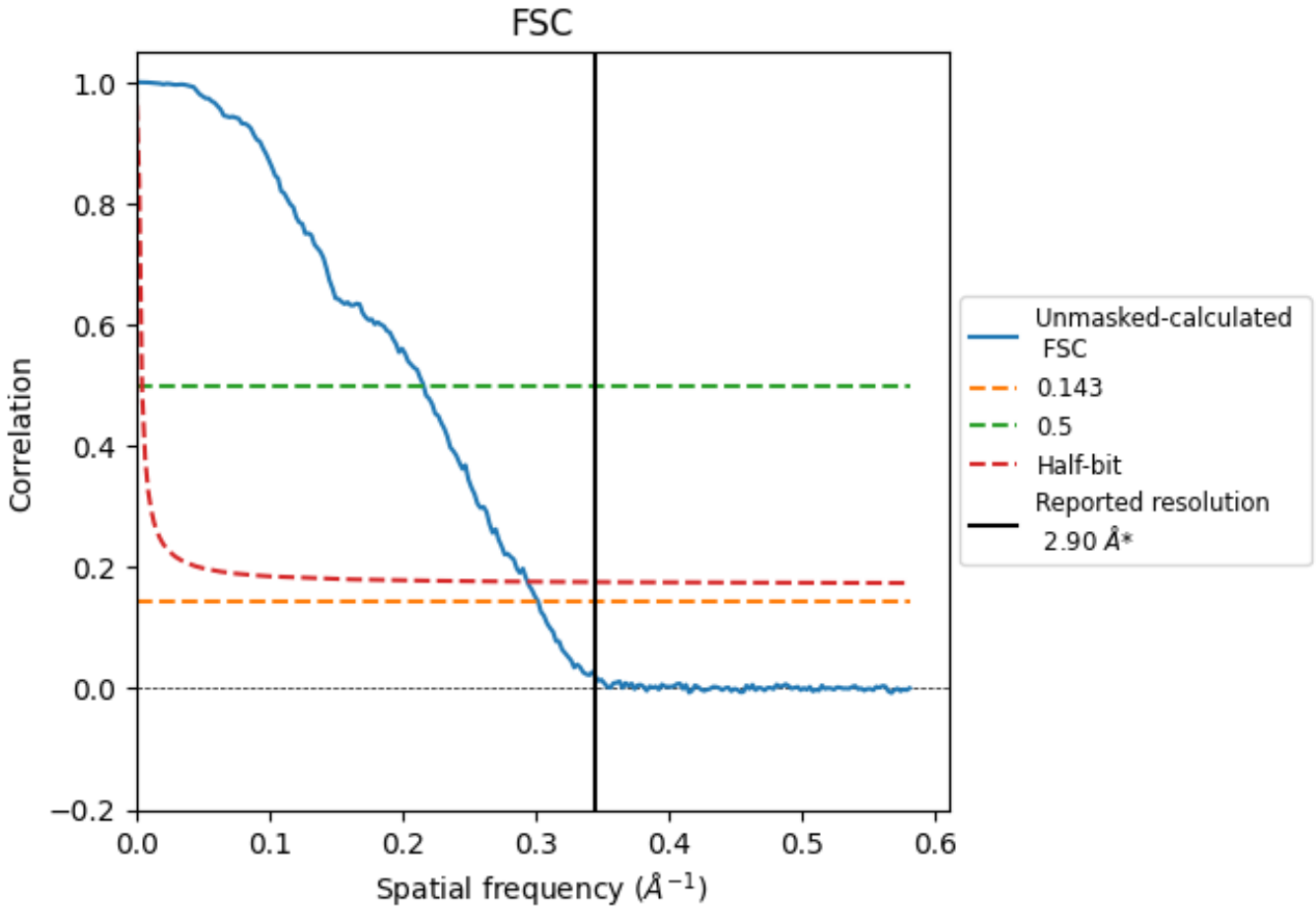


*Reported resolution corresponds to spatial frequency of 0.345 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.345 Å^{-1}

8.2 Resolution estimates (i)

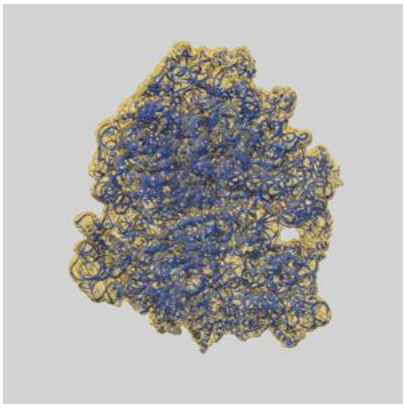
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.31	4.63	3.40

*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 3.31 differs from the reported value 2.9 by more than 10 %

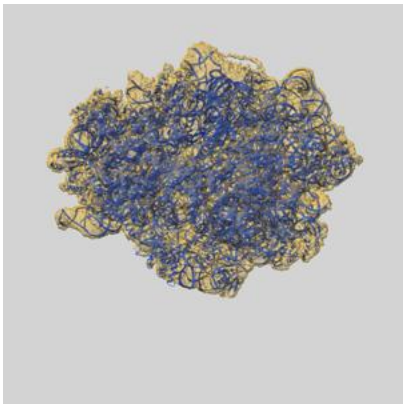
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-29819 and PDB model 8G7P. Per-residue inclusion information can be found in section 3 on page 18.

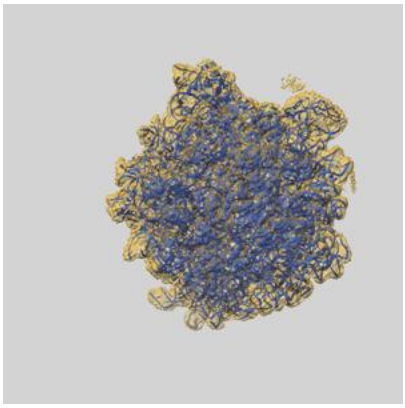
9.1 Map-model overlay



X



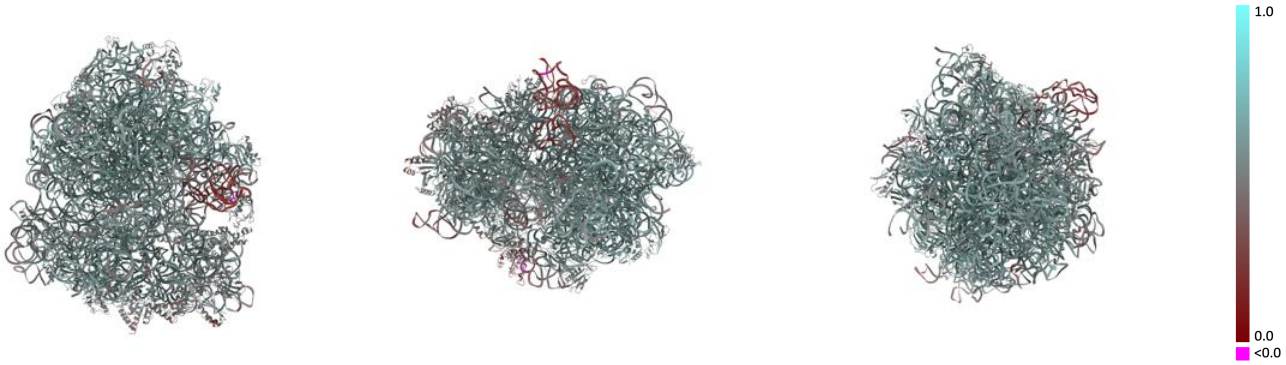
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.19 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

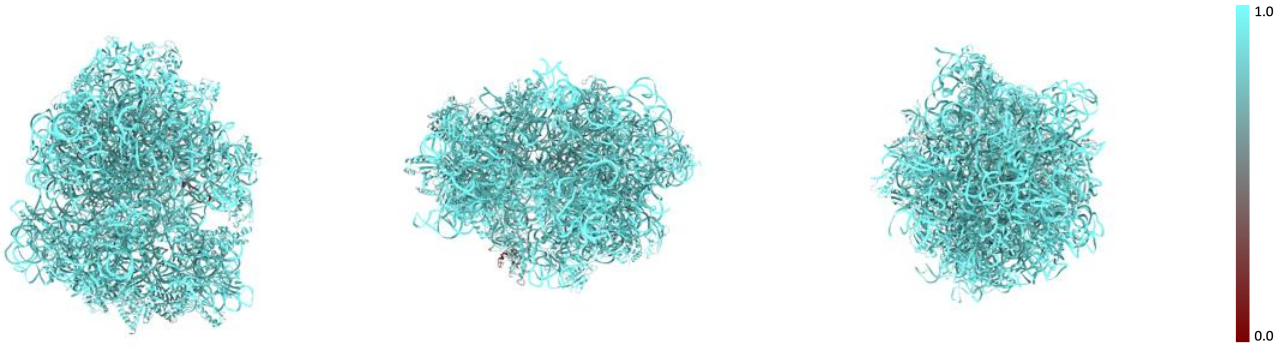
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

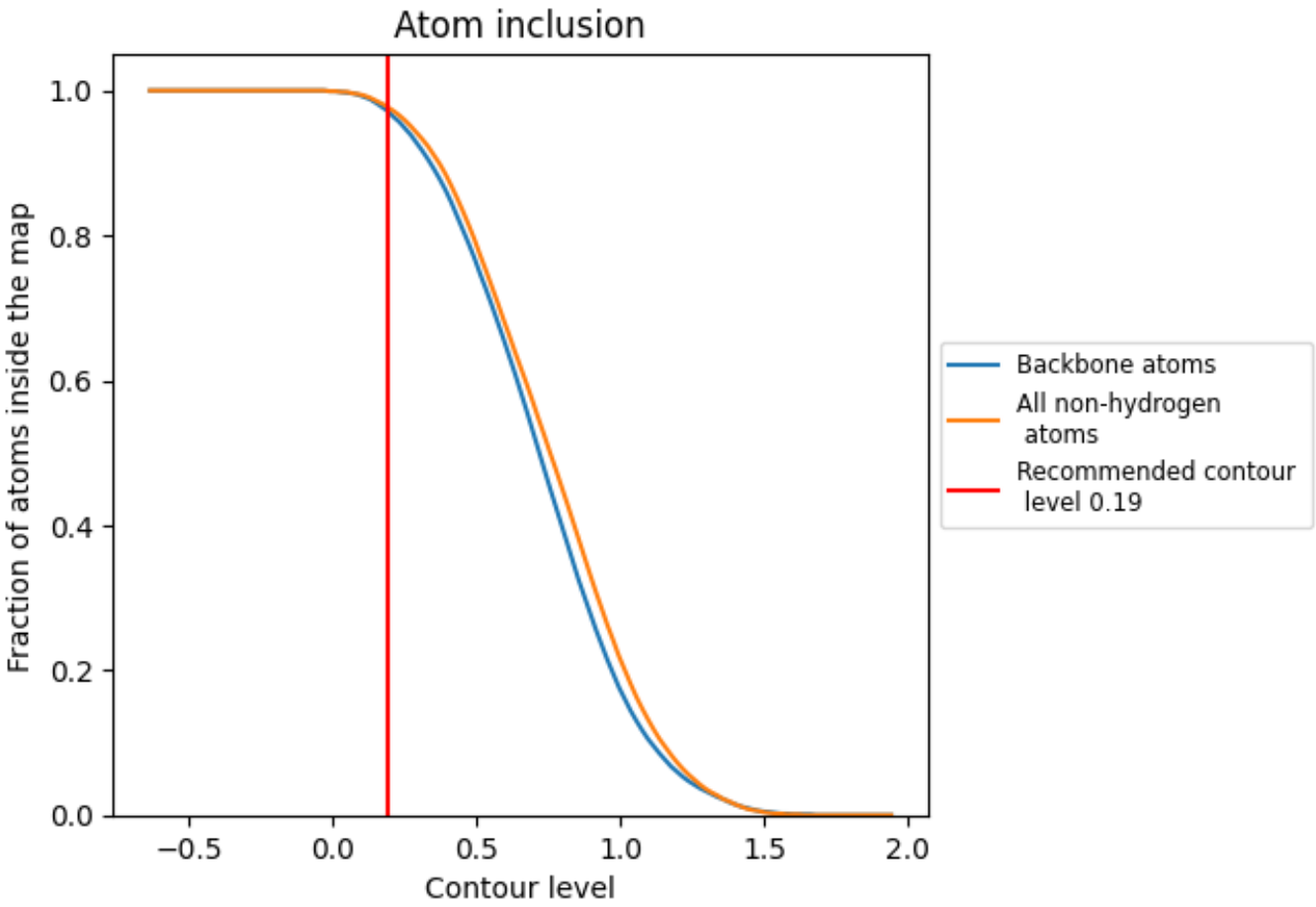
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.19).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 98% 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 (0.19) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9780	0.5570
1	0.9730	0.5220
2	0.9660	0.5790
3	0.9700	0.4940
4	0.9810	0.5910
5	0.9340	0.5690
6	0.9610	0.6060
7	0.9760	0.6100
8	0.9700	0.5850
A	0.9940	0.5710
B	0.9970	0.5520
C	0.9680	0.5970
D	0.9770	0.5890
E	0.9570	0.5580
F	0.9650	0.5200
G	0.9570	0.5260
H	0.6570	0.4750
J	0.4910	0.2940
L	0.9750	0.5890
M	0.9560	0.5850
N	0.9710	0.5840
O	0.9700	0.5840
P	0.9920	0.5990
Q	0.9830	0.5450
R	0.9580	0.5820
S	0.9910	0.5990
T	0.9720	0.5750
U	0.9630	0.5890
V	0.9570	0.5580
W	0.9750	0.5460
X	0.9620	0.5560
Y	0.9680	0.5920
Z	0.9680	0.5850
a	0.9960	0.5560
b	0.8150	0.4700

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Chain	Atom inclusion	Q-score
c	0.9430	0.5380
d	0.9550	0.5390
e	0.9600	0.5570
f	0.9220	0.5030
g	0.9320	0.5050
h	0.9640	0.5570
i	0.9680	0.5230
j	0.9070	0.4900
k	0.9560	0.5420
l	0.9640	0.5930
m	0.9620	0.5300
n	0.9650	0.5430
o	0.9550	0.5270
p	0.9710	0.5590
q	0.9680	0.5580
r	0.9390	0.5490
s	0.9550	0.5310
t	0.9620	0.5250
u	0.8610	0.4830
v	0.9860	0.5760
w	0.9740	0.5290
x	0.9870	0.5430
y	0.8870	0.3640
z	0.9550	0.5340