



wwPDB EM Validation Summary Report ⓘ

Apr 23, 2024 – 05:35 am BST

PDB ID : 7ABG
EMDB ID : EMD-11695
Title : Human pre-Bact-1 spliceosome
Authors : Townsend, C.; Kastner, B.; Leelaram, M.N.; Bertram, K.; Stark, H.;
Luehrmann, R.
Deposited on : 2020-09-07
Resolution : 7.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

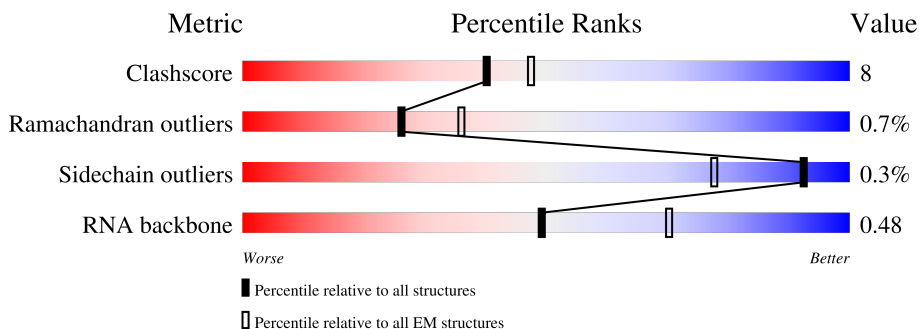
EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

1 Overall quality at a glance i

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

The reported resolution of this entry is 7.80 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.




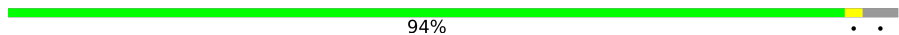
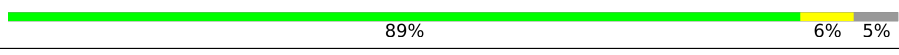


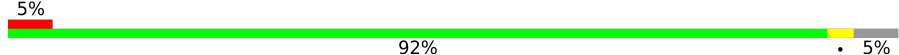






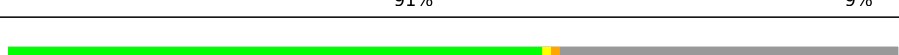

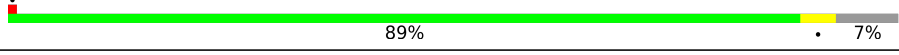

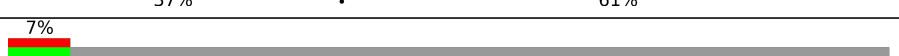
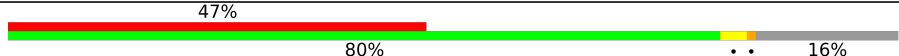


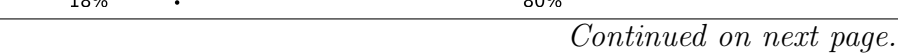


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	A5	790	
2	A2	103	
3	z	125	
4	F	464	
5	D	357	
6	W	255	
7	B	225	

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Mol	Chain	Length	Quality of chain
8	s	2136	
9	Q	144	
10	A1	156	
11	5	116	
12	L	802	
13	R	229	
14	V	95	
15	9	102	
16	C	139	
17	H	91	
18	J	80	
19	2	188	
20	A3	96	
21	K	439	
22	y	110	
23	G	514	
24	Z	230	
25	A	2335	
26	I	312	
27	P	420	
28	p	793	
29	4	501	
30	A4	1098	
31	u	1304	
32	T	895	


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Mol	Chain	Length	Quality of chain
33	E	1217	91% 6%
34	w	424	18% 82%
35	x	86	91% 8%
36	v	536	22% 78%
37	0	396	37% 62%
38	N	199	26% 72%
39	r	972	87% 13%
40	Y	904	9% 89%
41	6	106	42% 27% 26%
42	A6	248	27% 70%
43	a	118	66% 34%
43	h	118	9% 81%
44	b	86	19% 85%
44	i	86	19% 84%
45	f	240	27% 73%
45	m	240	8% 34%
46	e	126	62% 38%
46	l	126	51% 66%
47	d	76	91% 9%
47	k	76	83% 96%
48	c	92	85% 15%
48	j	92	66% 88%
49	g	119	78% 22%
49	n	119	67% 33%
50	q	73	100%

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Mol	Chain	Length	Quality of chain
51	X	641	 6% 94%

2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 73818 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Nuclear cap-binding protein subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A5	732	3723	2259	732	732	0	0

- Molecule 2 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	A2	79	393	235	79	79	0	0

- Molecule 3 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	z	108	544	328	108	108	0	0

- Molecule 4 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	F	49	242	144	49	49	0	0

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	D	302	1506	902	302	302	0	0

- Molecule 6 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	W	162	816	492	162	162	0	0

- Molecule 7 is a protein called U2 small nuclear ribonucleoprotein B''.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	B	169	851	513	169	169	0	0

- Molecule 8 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	s	1722	8688	5244	1722	1722	0	0

- Molecule 9 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	Q	138	695	419	138	138	0	0

- Molecule 10 is a protein called Nuclear cap-binding protein subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	A1	148	724	428	148	148	0	0

- Molecule 11 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	5	114	2397	1074	399	810	114	0	0

- Molecule 12 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	L	103	517	311	103	103	0	0

- Molecule 13 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	R	9	45	27	9	9	0	0

- Molecule 14 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	V	90	Total	C	N	O	0	0
			453	273	90	90		

- Molecule 15 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	9	73	Total	C	N	O	0	0
			369	223	73	73		

- Molecule 16 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	C	80	Total	C	N	O	0	0
			404	244	80	80		

- Molecule 17 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	H	76	Total	C	N	O	0	0
			380	228	76	76		

- Molecule 18 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	J	69	Total	C	N	O	0	0
			342	204	69	69		

- Molecule 19 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	2	145	Total	C	N	O	P	0	0
			3077	1374	533	1025	145		

- Molecule 20 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	A3	62	Total	C	N	O	0	0
			304	180	62	62		

- Molecule 21 is a protein called Microfibrillar-associated protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	K	123	Total	C	N	O	0	0
			614	368	123	123		

- Molecule 22 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	y	100	Total	C	N	O	0	0
			498	298	100	100		

- Molecule 23 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	G	320	Total	C	N	O	0	0
			1604	964	320	320		

- Molecule 24 is a RNA chain called MINX M3 pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	47	Total	C	N	O	P	0	0
			998	447	177	327	47		

- Molecule 25 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	A	2174	Total	C	N	O	0	0
			11024	6676	2174	2174		

- Molecule 26 is a protein called Pre-mRNA-splicing factor 38A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	I	176	Total	C	N	O	0	0
			883	531	176	176		

- Molecule 27 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	P	162	Total	C	N	O	0	0
			825	501	162	162		

- Molecule 28 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	p	60	Total	C	N	O	0	0
			301	181	60	60		

- Molecule 29 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	4	421	Total	C	N	O	0	0
			2110	1268	421	421		

- Molecule 30 is a protein called Transcription elongation regulator 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	A4	405	Total	C	N	O	0	0
			2034	1224	405	405		

- Molecule 31 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	u	836	Total	C	N	O	0	0
			4207	2535	836	836		

- Molecule 32 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	T	183	Total	C	N	O	0	0
			942	576	183	183		

- Molecule 33 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	E	1177	Total	C	N	O	0	0
			5926	3572	1177	1177		

- Molecule 34 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	w	78	Total	C	N	O	0	0
			391	235	78	78		

- Molecule 35 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
35	x	79	397	239	79	79	0	0

- Molecule 36 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
36	v	119	605	367	119	119	0	0

- Molecule 37 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	0	150	761	461	150	150	0	0

- Molecule 38 is a protein called Zinc finger matrin-type protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
38	N	56	277	165	56	56	0	0

- Molecule 39 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
39	r	844	4265	2577	844	844	0	0

- Molecule 40 is a protein called Serine/arginine repetitive matrix protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	Y	95	478	288	95	95	0	0

- Molecule 41 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
41	6	78	1672	747	309	538	78	0	0

- Molecule 42 is a protein called Serine/arginine-rich splicing factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	A6	74	368	220	74	74	0	0

- Molecule 43 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
43	h	95	482	292	95	95	0	0
43	a	78	393	237	78	78	0	0

- Molecule 44 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
44	i	72	359	215	72	72	0	0
44	b	73	364	218	73	73	0	0

- Molecule 45 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
45	m	82	413	249	82	82	0	0
45	f	64	319	191	64	64	0	0

- Molecule 46 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
46	l	83	415	249	83	83	0	0
46	e	78	390	234	78	78	0	0

- Molecule 47 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
47	k	73	364	218	73	73	0	0
47	d	69	344	206	69	69	0	0

- Molecule 48 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	j	81	Total	C	N	O	0	0
			403	241	81	81		
48	c	78	Total	C	N	O	0	0
			388	232	78	78		

- Molecule 49 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	n	80	Total	C	N	O	0	0
			402	242	80	80		
49	g	93	Total	C	N	O	0	0
			469	283	93	93		

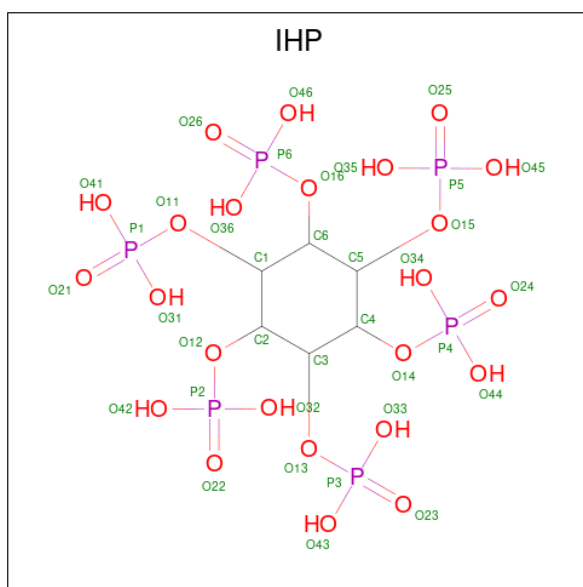
- Molecule 50 is a protein called Ubiquitin-like protein 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	q	73	Total	C	N	O	0	0
			360	214	73	73		

- Molecule 51 is a protein called WW domain-binding protein 11.

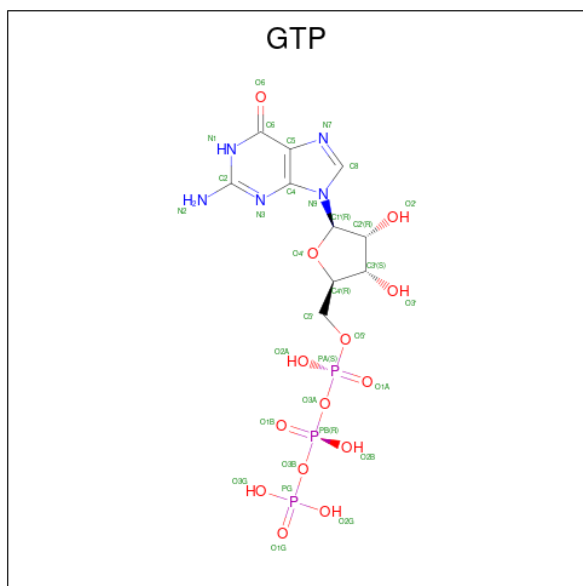
Mol	Chain	Residues	Atoms				AltConf	Trace
51	X	36	Total	C	N	O	0	0
			182	110	36	36		

- Molecule 52 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).



Mol	Chain	Residues	Atoms				AltConf
52	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 53 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

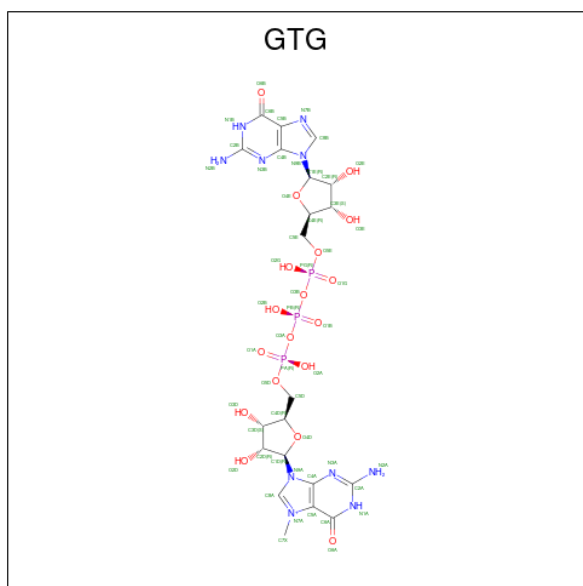


Mol	Chain	Residues	Atoms					AltConf
53	r	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 54 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	r	1	Total	Mg	0
			1	1	

- Molecule 55 is 7-METHYL-GUANOSINE-5'-TRIPHOSPHATE-5'-GUANOSINE (three-letter code: GTG) (formula: C₂₁H₃₀N₁₀O₁₈P₃).

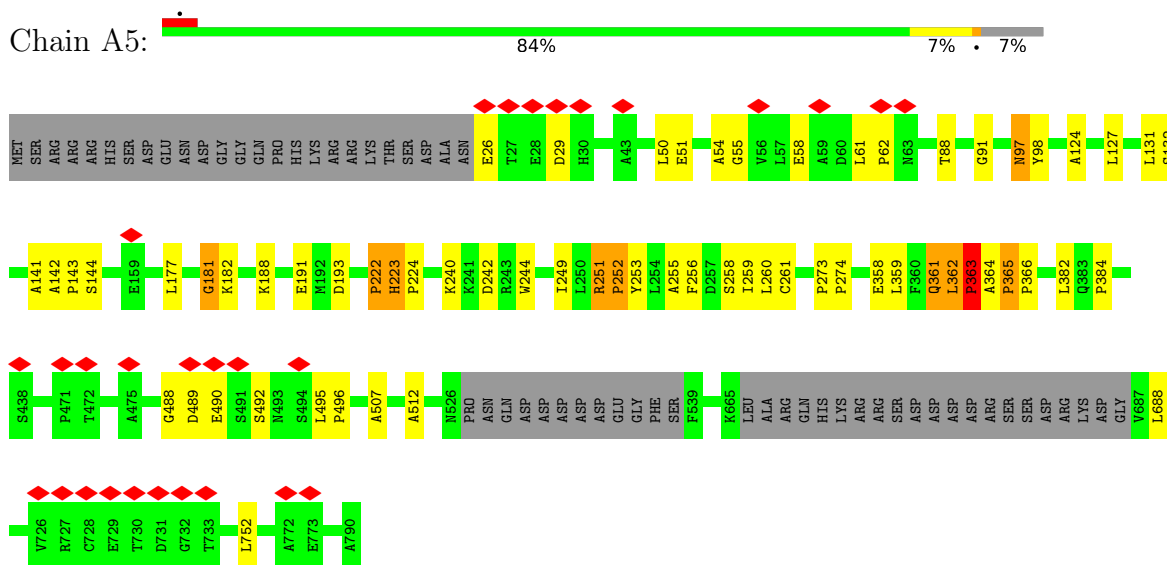


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
55	A6	1	52	21	10	18	3	0

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: Nuclear cap-binding protein subunit 1



PHE
GLU
GLU
LEU
ALA
LYS
LYS
HIS
GLU
ASP
SER
SER
ALA
ILE
PRO
ARG
ARG
GLU
CYS
LEU
LYS
GLU
ASP
VAL
GLN
ARG
GLN
GLN
GLN
GLU
ARG
GLU
LYS
GLU
LEU
GLN
HIS
ARG
TYR
ALA
ASP
LEU
LEU
GLU
LYS
LYS
THR
LEU
LYS
SER
LYS
PHE

- Molecule 13: Spliceosome-associated protein CWC15 homolog

Chain R:  96%

MET
THR
THR
LYS
ASP
ALA
LYS
ARG
PRO
THR
PHE
GLU
PRO
ALA
ARG
GLY
GLY
ASN
ASP
GLY
LYS
ARG
GLY
GLU
THR
ARG
GLY
GLU
ASP
HIS
LEU
THR
SER
GLN
LEU
SER
SER
LYS
SER
TYR
GLN
VAL
SER
SER
LYS
PRO
ARG
ASP
LEU
GLU
GLN
SER
SER
HIS
THR
LYS
ILE
ALA
LYS
TYR
LEU
ASP
ALA
GLN
THR
THR
GLN
ASP
LEU
THR
ALA
PRO
ASP
PHE
ARG
GLU
PHE
ARG
GLU

ARG
GLU
LEU
GLU
ASP
GLU
ARG
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ALA
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LEU
ALA
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SER
LYS
SER
SER
GLN
VAL
SER
SER
LYS
LYS
ALA
GLU
GLU
GLU
GLU
GLU
ARG
ILE
SER
ARG
MET
GLU
ASN
ASN
LYS
LEU
SER
GLY
ASN
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LEU
LEU
LEU
ASN
LEU
THR
THR
GLY
PRO
SER
GLN
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GLU
ALA

ASN
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ASP
VAL
PHE
ASN
CYS
ALA
LYS
GLY
VAL
ASP
GLN
LYS
LYS
ASP
LYS
LYS
LYS
PHE
VAL
SER
VAL
ASN
THR
THR
SER
SER
E218
K228
LYS

- Molecule 14: U6 snRNA-associated Sm-like protein LSm2

Chain V:  5% 92% 5%

M1
K13
P52
L55
D75
D78
T79
Q80
L81
A90
LEU
GLN
GLN
LYS
GLN

- Molecule 15: U6 snRNA-associated Sm-like protein LSm3

Chain 9:  5% 68% 28%

MET
ALA
ASP
ASP
VAL
GLN
GLN
GLN
THR
THR
ASN
VAL
E16
N35
A45
Y46
N51
D56
I64
GLU
ILE
ASP
GLU
GLU
THR
TYR
GLU
GLU
ILE
Y75
P83
P98
LEU
ARG
VAL
GLY

- Molecule 16: U6 snRNA-associated Sm-like protein LSm4

Chain C:  54% 42%

M1
M12
H13
P14
N39
C59
F72
K90
VAL
VAL
ALA
LYS
GLY
ARG
GLY
ARG
GLY
GLY
LEU
GLN
GLN
GLN
LYS
GLN
GLN
LYS
LYS
ARG
GLY
GLY
MET
GLY
GLY
ALA
GLY
ARG
VAL
PHE
GLY
GLY
GLY
ARG
GLY
GLY
ILE
PRO
GLY
THR
GLY
ARG
GLY
GLN

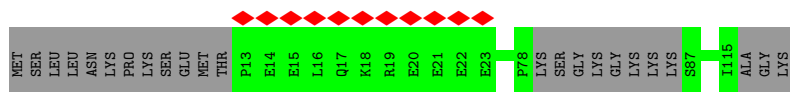
PRO
GLU
LYS
LYS
PRO
GLY
ARG
GLN
ALA
GLY
LYS
GLN

- Molecule 17: U6 snRNA-associated Sm-like protein LSm5

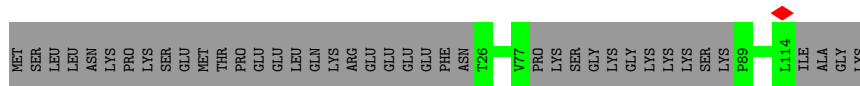
Chain H:  11% 70% 13% 16%

MET
ALA
ASN
THR
THR
ASN
PRO
S10
Q11
L12
L13
P14
L15
E16
K20
I26
I36
V37
D53
W54
T55
T60
P61
I66
T67
K68
I69
D70
G85
GLY
GLU
GLU
PRO
GLU
VAL

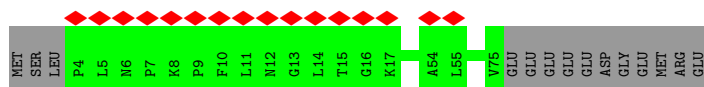
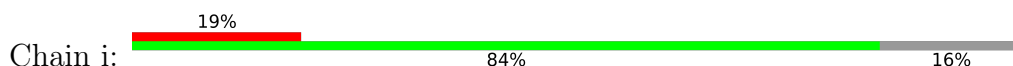
- Molecule 18: U6 snRNA-associated Sm-like protein LSm6



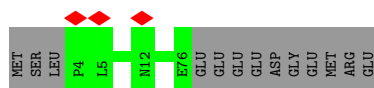
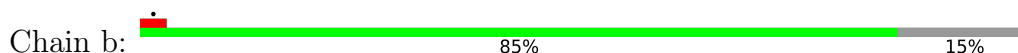
• Molecule 43: Small nuclear ribonucleoprotein Sm D2



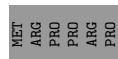
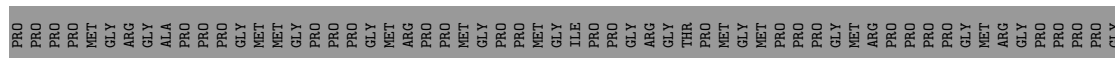
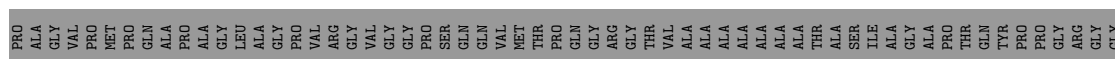
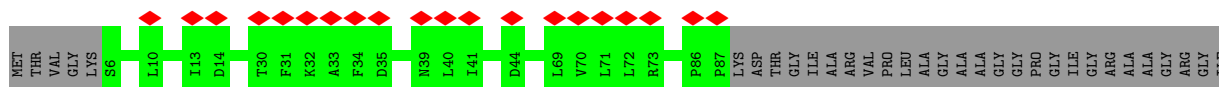
• Molecule 44: Small nuclear ribonucleoprotein F



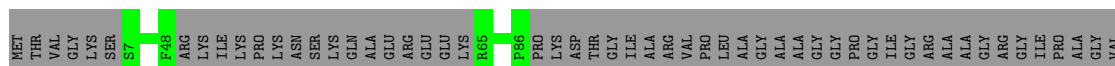
• Molecule 44: Small nuclear ribonucleoprotein F



• Molecule 45: Small nuclear ribonucleoprotein-associated proteins B and B'



• Molecule 45: Small nuclear ribonucleoprotein-associated proteins B and B'



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84539	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.055	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0095	Depositor
Map size (Å)	445.44, 445.44, 445.44	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	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: MG, IHP, GTG, GTP

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	A5	0.45	4/3759 (0.1%)	0.66	3/5280 (0.1%)
2	A2	0.56	0/395	0.96	1/549 (0.2%)
3	z	0.31	0/548	0.50	0/766
4	F	0.36	0/241	0.51	0/334
5	D	0.87	0/1515	0.93	0/2113
6	W	0.27	0/821	0.53	0/1149
7	B	0.67	0/857	0.82	1/1196 (0.1%)
8	s	0.24	0/8766	0.46	2/12286 (0.0%)
9	Q	0.24	0/700	0.43	0/979
10	A1	0.35	0/723	0.76	0/1001
11	5	0.27	0/2672	0.81	3/4154 (0.1%)
12	L	0.24	0/519	0.47	0/725
13	R	0.21	0/44	0.32	0/60
14	V	0.45	0/455	0.84	0/636
15	9	0.47	0/371	0.99	1/517 (0.2%)
16	C	0.45	0/407	0.89	0/569
17	H	0.51	0/382	0.96	0/532
18	J	0.59	0/343	0.94	0/475
19	2	0.46	6/3430 (0.2%)	1.09	31/5329 (0.6%)
20	A3	0.52	0/302	0.91	1/416 (0.2%)
21	K	0.23	0/615	0.41	0/858
22	y	0.24	0/501	0.49	0/697
23	G	0.28	0/1616	0.54	1/2258 (0.0%)
24	Z	0.55	4/1114 (0.4%)	0.84	0/1730
25	A	0.27	1/11142 (0.0%)	0.46	0/15633
26	I	0.25	0/888	0.45	0/1241
27	P	0.47	1/835 (0.1%)	0.72	0/1170
28	p	0.54	0/301	0.99	0/420
29	4	0.52	0/2119	0.97	1/2960 (0.0%)
30	A4	0.33	0/2037	0.49	1/2850 (0.0%)
31	u	0.31	0/4241	0.50	0/5935
32	T	0.58	3/957 (0.3%)	0.64	2/1341 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	E	0.26	0/5980	0.48	0/8363
34	w	0.63	0/394	0.68	0/549
35	x	0.46	0/399	0.46	0/557
36	v	0.28	0/607	0.44	0/847
37	0	0.24	0/770	0.48	0/1079
38	N	0.28	0/276	0.39	0/383
39	r	0.25	0/4313	0.47	0/6044
40	Y	0.30	0/481	0.44	0/672
41	6	0.25	0/1870	0.80	1/2909 (0.0%)
42	A6	0.19	0/369	0.34	0/513
43	a	0.23	0/394	0.45	0/548
43	h	0.33	0/485	0.54	0/677
44	b	0.24	0/367	0.46	0/509
44	i	0.36	0/362	0.55	0/502
45	f	0.23	0/319	0.45	0/442
45	m	0.36	0/416	0.55	0/581
46	e	0.24	0/392	0.48	0/546
46	l	0.39	0/417	0.60	0/581
47	d	0.24	0/346	0.48	0/481
47	k	0.39	0/366	0.60	0/509
48	c	0.23	0/388	0.47	0/540
48	j	0.36	0/403	0.55	0/561
49	g	0.23	0/471	0.44	0/657
49	n	0.34	0/404	0.55	0/564
50	q	0.25	0/359	0.53	0/498
51	X	0.22	0/182	0.32	0/254
All	All	0.36	19/75146 (0.0%)	0.63	49/106525 (0.0%)

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A5	252	PRO	N-CA	13.43	1.70	1.47
1	A5	365	PRO	C-N	8.55	1.50	1.34
32	T	605	LYS	C-N	8.45	1.50	1.34
1	A5	223	HIS	C-N	8.43	1.50	1.34
27	P	188	ASP	C-N	8.41	1.50	1.34

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	4	472	GLN	C-N-CD	-16.15	85.08	120.60
1	A5	252	PRO	CA-N-CD	-9.81	97.77	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	A4	845	GLU	CA-C-O	-9.14	100.90	120.10
1	A5	222	PRO	CA-N-CD	-8.79	99.19	111.50
23	G	382	PRO	CA-N-CD	-8.79	99.20	111.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A5	3723	0	1806	60	0
2	A2	393	0	183	4	0
3	z	544	0	264	0	0
4	F	242	0	118	11	0
5	D	1506	0	737	30	0
6	W	816	0	386	2	0
7	B	851	0	423	7	0
8	s	8688	0	4220	0	0
9	Q	695	0	327	2	0
10	A1	724	0	335	13	0
11	5	2397	0	1216	54	0
12	L	517	0	257	3	0
13	R	45	0	17	0	0
14	V	453	0	212	1	0
15	9	369	0	174	1	0
16	C	404	0	189	2	0
17	H	380	0	172	6	0
18	J	342	0	164	10	0
19	2	3077	0	1559	86	0
20	A3	304	0	137	7	0
21	K	614	0	284	7	0
22	y	498	0	241	0	0
23	G	1604	0	795	22	0
24	Z	998	0	504	44	0
25	A	11024	0	5384	54	0
26	I	883	0	414	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	P	825	0	409	21	0
28	p	301	0	134	0	0
29	4	2110	0	987	35	0
30	A4	2034	0	912	27	0
31	u	4207	0	2103	0	0
32	T	942	0	490	13	0
33	E	5926	0	2964	63	0
34	w	391	0	197	0	0
35	x	397	0	191	0	0
36	v	605	0	311	0	0
37	0	761	0	376	6	0
38	N	277	0	114	3	0
39	r	4265	0	2120	0	0
40	Y	478	0	226	15	0
41	6	1672	0	846	34	0
42	A6	368	0	175	23	0
43	a	393	0	176	0	0
43	h	482	0	220	0	0
44	b	364	0	181	0	0
44	i	359	0	179	0	0
45	f	319	0	144	0	0
45	m	413	0	193	0	0
46	e	390	0	188	0	0
46	l	415	0	198	0	0
47	d	344	0	168	0	0
47	k	364	0	176	0	0
48	c	388	0	167	0	0
48	j	403	0	173	0	0
49	g	469	0	214	0	0
49	n	402	0	184	0	0
50	q	360	0	159	0	0
51	X	182	0	85	0	0
52	A	36	0	6	0	0
53	r	32	0	12	0	0
54	r	1	0	0	0	0
55	A6	52	0	26	11	0
All	All	73818	0	35922	516	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 516 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:258:SER:CB	30:A4:766:MET:HA	1.27	1.64
1:A5:258:SER:CB	30:A4:766:MET:CA	1.77	1.63
25:A:1772:PHE:CB	25:A:2246:ASN:CB	1.79	1.60
30:A4:731:ASP:CB	30:A4:759:ARG:CA	1.77	1.59
30:A4:731:ASP:CB	30:A4:759:ARG:CB	1.75	1.58

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A5	726/790 (92%)	655 (90%)	61 (8%)	10 (1%)	11	46
2	A2	77/103 (75%)	71 (92%)	3 (4%)	3 (4%)	3	23
3	z	106/125 (85%)	92 (87%)	12 (11%)	2 (2%)	8	38
4	F	47/464 (10%)	46 (98%)	0	1 (2%)	7	36
5	D	300/357 (84%)	276 (92%)	17 (6%)	7 (2%)	6	34
6	W	160/255 (63%)	147 (92%)	13 (8%)	0	100	100
7	B	165/225 (73%)	158 (96%)	4 (2%)	3 (2%)	8	40
8	s	1720/2136 (80%)	1660 (96%)	58 (3%)	2 (0%)	51	86
9	Q	136/144 (94%)	114 (84%)	22 (16%)	0	100	100
10	A1	146/156 (94%)	137 (94%)	7 (5%)	2 (1%)	11	46
12	L	101/802 (13%)	97 (96%)	4 (4%)	0	100	100
13	R	7/229 (3%)	7 (100%)	0	0	100	100
14	V	88/95 (93%)	79 (90%)	7 (8%)	2 (2%)	6	34
15	9	69/102 (68%)	66 (96%)	2 (3%)	1 (1%)	11	46
16	C	78/139 (56%)	73 (94%)	4 (5%)	1 (1%)	12	48
17	H	74/91 (81%)	64 (86%)	8 (11%)	2 (3%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	J	67/80 (84%)	57 (85%)	9 (13%)	1 (2%)	10	46
20	A3	58/96 (60%)	53 (91%)	4 (7%)	1 (2%)	9	42
21	K	121/439 (28%)	98 (81%)	23 (19%)	0	100	100
22	y	98/110 (89%)	96 (98%)	2 (2%)	0	100	100
23	G	318/514 (62%)	292 (92%)	22 (7%)	4 (1%)	12	48
25	A	2164/2335 (93%)	1904 (88%)	239 (11%)	21 (1%)	15	55
26	I	174/312 (56%)	152 (87%)	22 (13%)	0	100	100
27	P	158/420 (38%)	128 (81%)	30 (19%)	0	100	100
28	p	58/793 (7%)	53 (91%)	3 (5%)	2 (3%)	3	26
29	4	415/501 (83%)	369 (89%)	35 (8%)	11 (3%)	5	31
30	A4	399/1098 (36%)	387 (97%)	10 (2%)	2 (0%)	29	69
31	u	832/1304 (64%)	728 (88%)	98 (12%)	6 (1%)	22	63
32	T	175/895 (20%)	159 (91%)	15 (9%)	1 (1%)	25	66
33	E	1165/1217 (96%)	1143 (98%)	19 (2%)	3 (0%)	41	77
34	w	76/424 (18%)	69 (91%)	6 (8%)	1 (1%)	12	48
35	x	77/86 (90%)	68 (88%)	8 (10%)	1 (1%)	12	48
36	v	111/536 (21%)	98 (88%)	13 (12%)	0	100	100
37	0	148/396 (37%)	146 (99%)	2 (1%)	0	100	100
38	N	54/199 (27%)	53 (98%)	1 (2%)	0	100	100
39	r	842/972 (87%)	781 (93%)	61 (7%)	0	100	100
40	Y	93/904 (10%)	90 (97%)	2 (2%)	1 (1%)	14	52
42	A6	72/248 (29%)	61 (85%)	10 (14%)	1 (1%)	11	46
43	a	74/118 (63%)	71 (96%)	3 (4%)	0	100	100
43	h	91/118 (77%)	86 (94%)	5 (6%)	0	100	100
44	b	71/86 (83%)	70 (99%)	1 (1%)	0	100	100
44	i	70/86 (81%)	69 (99%)	1 (1%)	0	100	100
45	f	60/240 (25%)	57 (95%)	3 (5%)	0	100	100
45	m	80/240 (33%)	74 (92%)	6 (8%)	0	100	100
46	e	76/126 (60%)	73 (96%)	3 (4%)	0	100	100
46	l	81/126 (64%)	76 (94%)	5 (6%)	0	100	100
47	d	67/76 (88%)	63 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	k	71/76 (93%)	69 (97%)	2 (3%)	0	100	100
48	c	76/92 (83%)	70 (92%)	6 (8%)	0	100	100
48	j	79/92 (86%)	77 (98%)	2 (2%)	0	100	100
49	g	89/119 (75%)	83 (93%)	6 (7%)	0	100	100
49	n	78/119 (66%)	75 (96%)	3 (4%)	0	100	100
50	q	71/73 (97%)	65 (92%)	6 (8%)	0	100	100
51	X	34/641 (5%)	34 (100%)	0	0	100	100
All	All	12843/22520 (57%)	11839 (92%)	912 (7%)	92 (1%)	26	63

5 of 92 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A5	188	LYS
1	A5	222	PRO
1	A5	361	GLN
1	A5	362	LEU
3	z	99	GLN

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A5	39/724 (5%)	39 (100%)	0	100	100
2	A2	3/91 (3%)	3 (100%)	0	100	100
3	z	5/109 (5%)	5 (100%)	0	100	100
5	D	10/300 (3%)	10 (100%)	0	100	100
6	W	6/218 (3%)	6 (100%)	0	100	100
7	B	8/195 (4%)	8 (100%)	0	100	100
8	s	79/1908 (4%)	79 (100%)	0	100	100
9	Q	6/130 (5%)	6 (100%)	0	100	100
12	L	3/709 (0%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	V	3/88 (3%)	3 (100%)	0	100	100
15	9	4/94 (4%)	4 (100%)	0	100	100
16	C	4/111 (4%)	4 (100%)	0	100	100
17	H	3/80 (4%)	3 (100%)	0	100	100
18	J	2/70 (3%)	2 (100%)	0	100	100
21	K	2/395 (0%)	2 (100%)	0	100	100
22	y	4/95 (4%)	4 (100%)	0	100	100
23	G	13/441 (3%)	13 (100%)	0	100	100
25	A	123/2108 (6%)	123 (100%)	0	100	100
26	I	6/293 (2%)	6 (100%)	0	100	100
27	P	12/361 (3%)	12 (100%)	0	100	100
28	p	1/709 (0%)	1 (100%)	0	100	100
29	4	12/446 (3%)	11 (92%)	1 (8%)	11	34
30	A4	6/956 (1%)	6 (100%)	0	100	100
31	u	36/1104 (3%)	36 (100%)	0	100	100
32	T	19/776 (2%)	19 (100%)	0	100	100
33	E	60/1051 (6%)	59 (98%)	1 (2%)	60	78
34	w	4/336 (1%)	4 (100%)	0	100	100
35	x	3/77 (4%)	3 (100%)	0	100	100
36	v	6/459 (1%)	6 (100%)	0	100	100
37	0	10/349 (3%)	10 (100%)	0	100	100
39	r	49/866 (6%)	49 (100%)	0	100	100
40	Y	4/831 (0%)	4 (100%)	0	100	100
42	A6	2/203 (1%)	2 (100%)	0	100	100
43	a	3/110 (3%)	3 (100%)	0	100	100
43	h	5/110 (4%)	5 (100%)	0	100	100
44	b	4/74 (5%)	4 (100%)	0	100	100
44	i	4/74 (5%)	4 (100%)	0	100	100
45	f	2/177 (1%)	2 (100%)	0	100	100
45	m	4/177 (2%)	4 (100%)	0	100	100
46	e	3/101 (3%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	l	3/101 (3%)	3 (100%)	0	100	100
47	d	3/66 (4%)	3 (100%)	0	100	100
47	k	3/66 (4%)	3 (100%)	0	100	100
48	c	1/84 (1%)	1 (100%)	0	100	100
48	j	1/84 (1%)	1 (100%)	0	100	100
49	g	4/101 (4%)	4 (100%)	0	100	100
49	n	3/101 (3%)	3 (100%)	0	100	100
51	X	1/554 (0%)	1 (100%)	0	100	100
All	All	591/18663 (3%)	589 (100%)	2 (0%)	92	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	4	78	PRO
33	E	406	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	5	113/116 (97%)	40 (35%)	2 (1%)
19	2	139/188 (73%)	29 (20%)	1 (0%)
24	Z	45/230 (19%)	12 (26%)	0
41	6	75/106 (70%)	24 (32%)	0
All	All	372/640 (58%)	105 (28%)	3 (0%)

5 of 105 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	5	8	G
11	5	9	G
11	5	10	U
11	5	15	C
11	5	19	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	5	26	A
11	5	78	U
19	2	60	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is 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
55	GTG	A6	301	-	46,57,57	2.65	16 (34%)	47,90,90	3.18	14 (29%)
53	GTP	r	1500	54	26,34,34	1.09	1 (3%)	32,54,54	1.85	7 (21%)
52	IHP	A	3001	-	36,36,36	1.52	6 (16%)	54,60,60	0.71	1 (1%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	GTG	A6	301	-	-	11/24/64/64	0/6/6/6
53	GTP	r	1500	54	-	6/18/38/38	0/3/3/3
52	IHP	A	3001	-	-	7/30/54/54	0/1/1/1

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	A6	301	GTG	O4E-C1E	10.58	1.55	1.41
55	A6	301	GTG	O4E-C4E	5.88	1.58	1.45
55	A6	301	GTG	C8B-N7B	-5.01	1.26	1.35
55	A6	301	GTG	C2E-C1E	-4.44	1.47	1.53
55	A6	301	GTG	C5E-C4E	-4.19	1.38	1.51

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	A6	301	GTG	C5E-C4E-C3E	-10.27	76.70	115.18
55	A6	301	GTG	C2E-C3E-C4E	7.25	116.72	102.64
55	A6	301	GTG	O5E-C5E-C4E	7.24	133.90	108.99
55	A6	301	GTG	PG-O5E-C5E	6.50	159.81	121.68
55	A6	301	GTG	O4E-C4E-C3E	-5.95	93.35	105.11

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

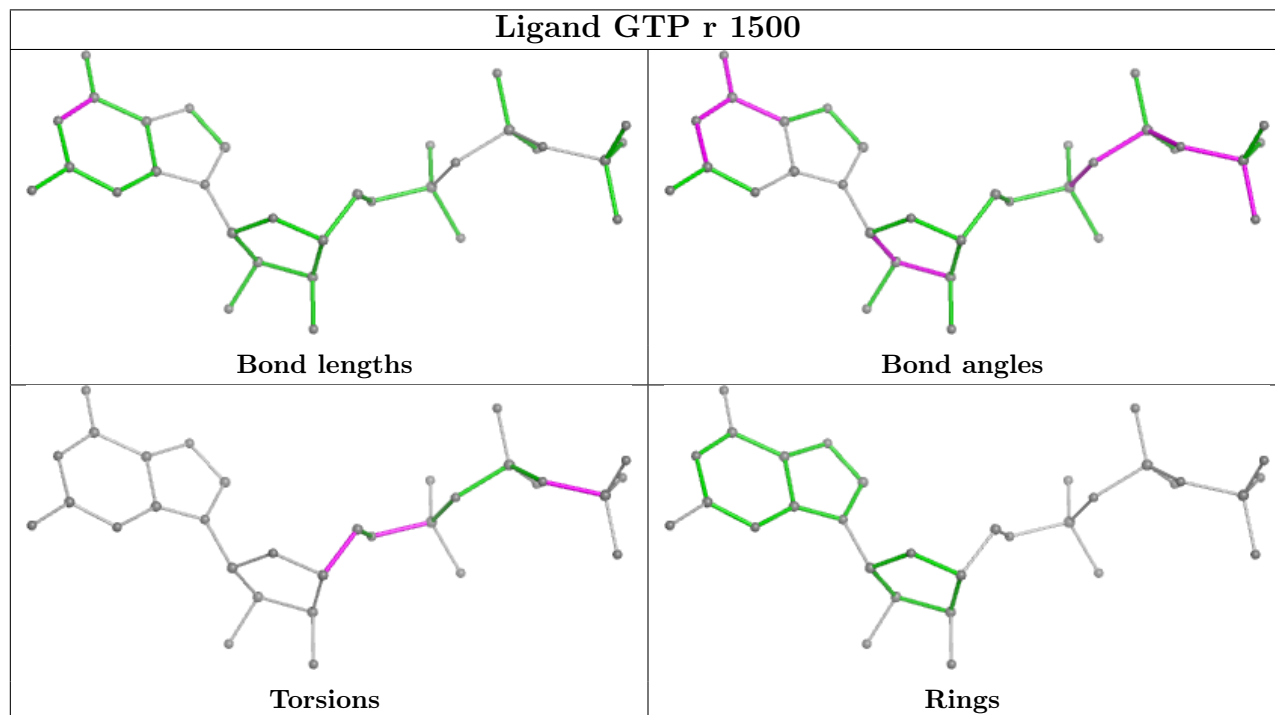
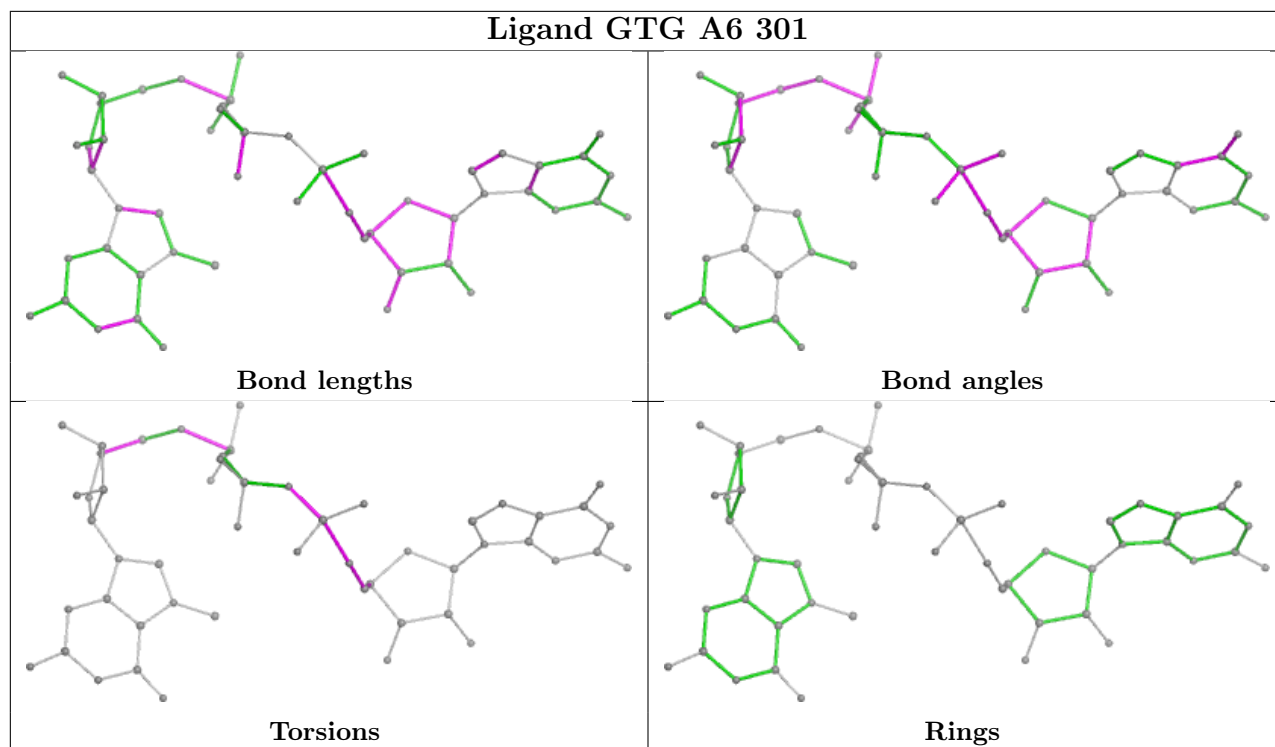
Mol	Chain	Res	Type	Atoms
52	A	3001	IHP	C1-C2-O12-P2
52	A	3001	IHP	C4-O14-P4-O24
53	r	1500	GTP	C5'-O5'-PA-O3A
53	r	1500	GTP	C5'-O5'-PA-O1A
53	r	1500	GTP	C5'-O5'-PA-O2A

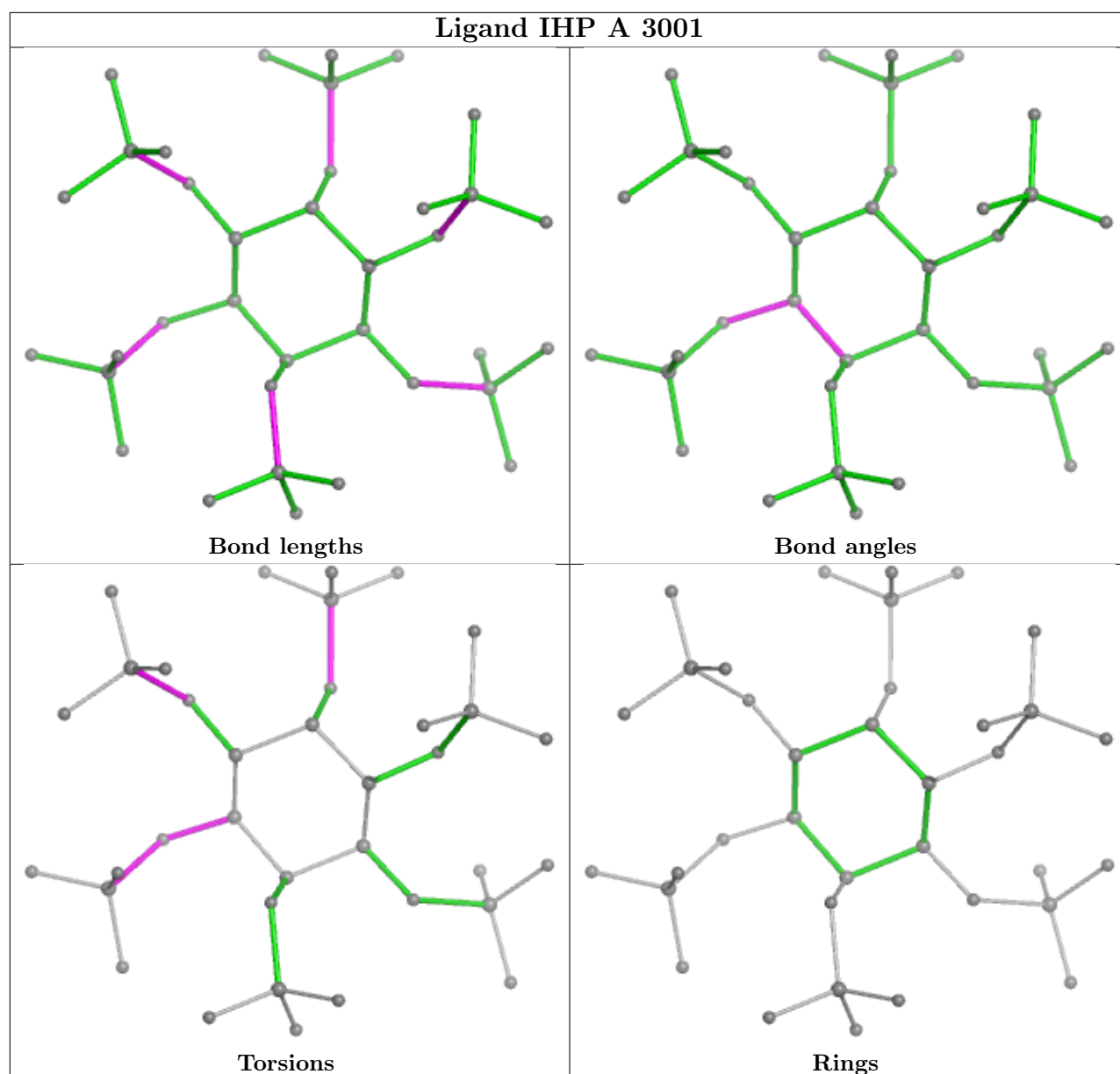
There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	A6	301	GTG	11	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

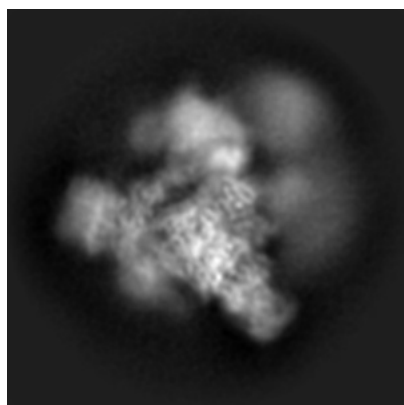
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11695. These allow visual inspection of the internal detail of the map and identification of artifacts.

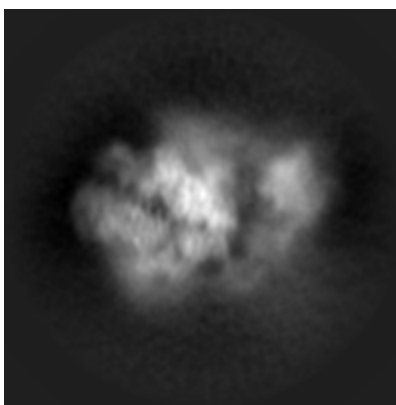
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

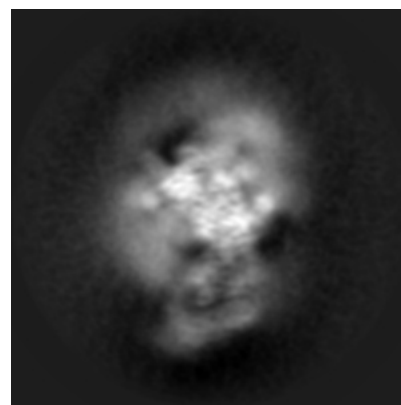
6.1.1 Primary map



X



Y

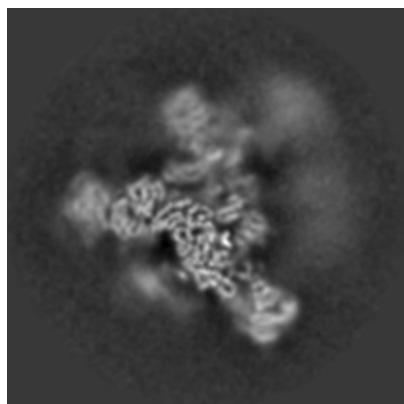


Z

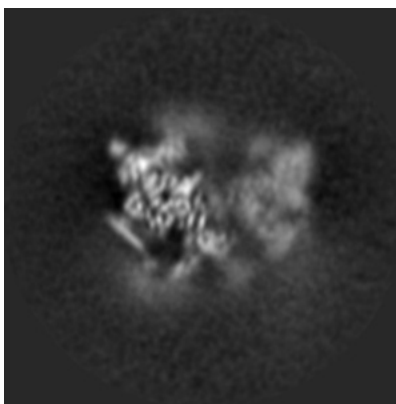
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

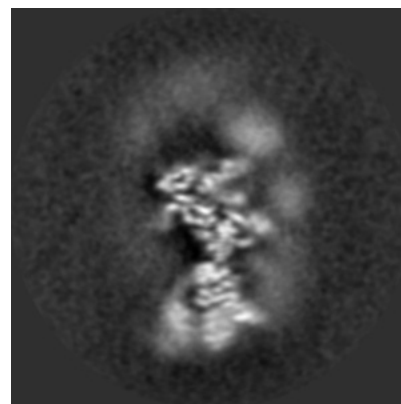
6.2.1 Primary map



X Index: 192



Y Index: 192

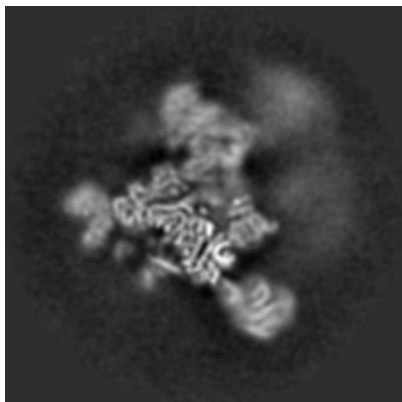


Z Index: 192

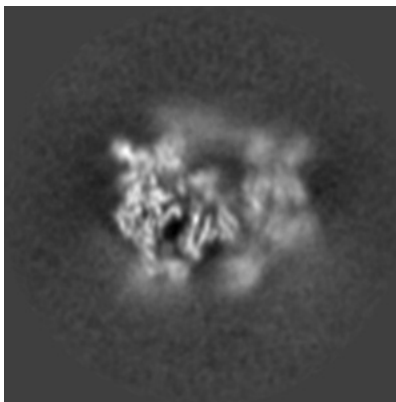
The images above show central slices of the map in three orthogonal directions.

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

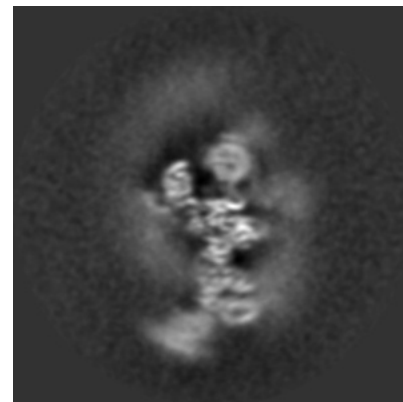
6.3.1 Primary map



X Index: 202



Y Index: 201

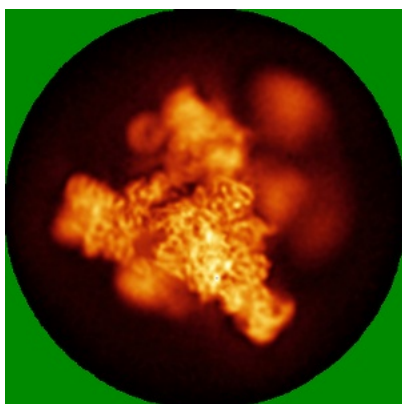


Z Index: 175

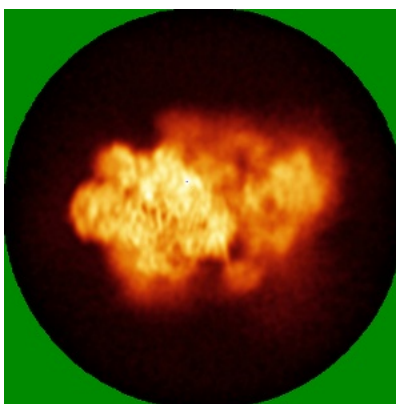
The images above show the largest variance slices of the map in three orthogonal directions.

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

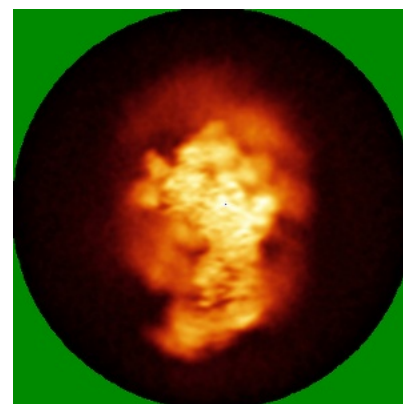
6.4.1 Primary map



X



Y

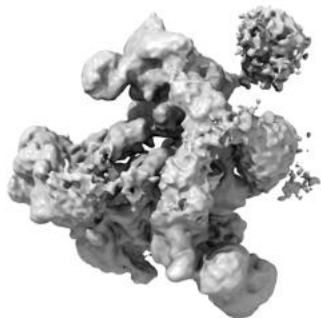


Z

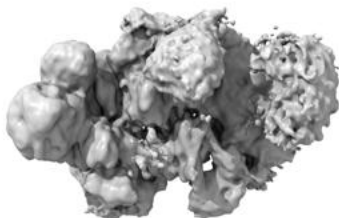
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

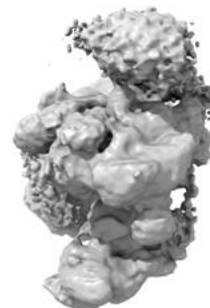
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0095. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

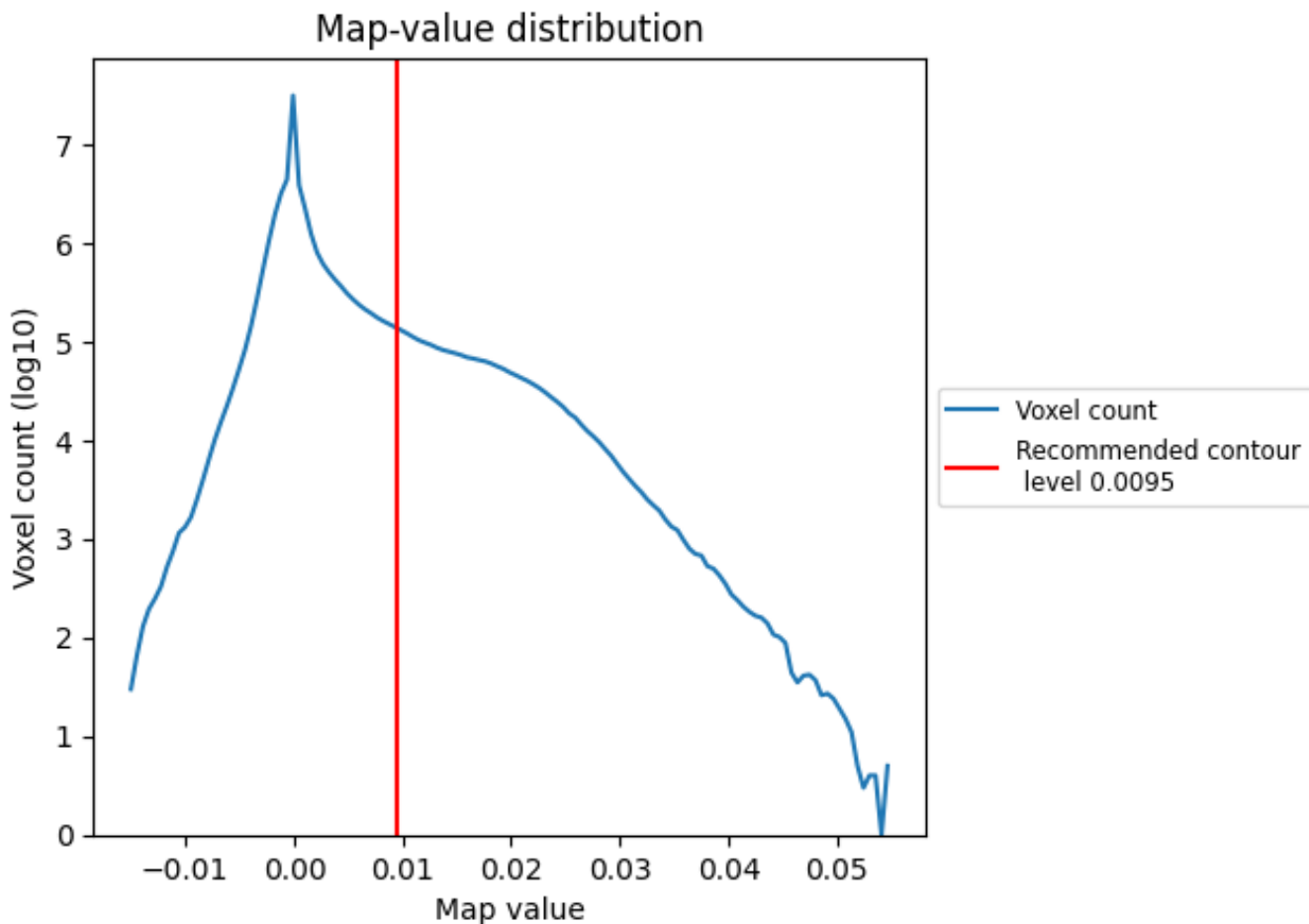
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

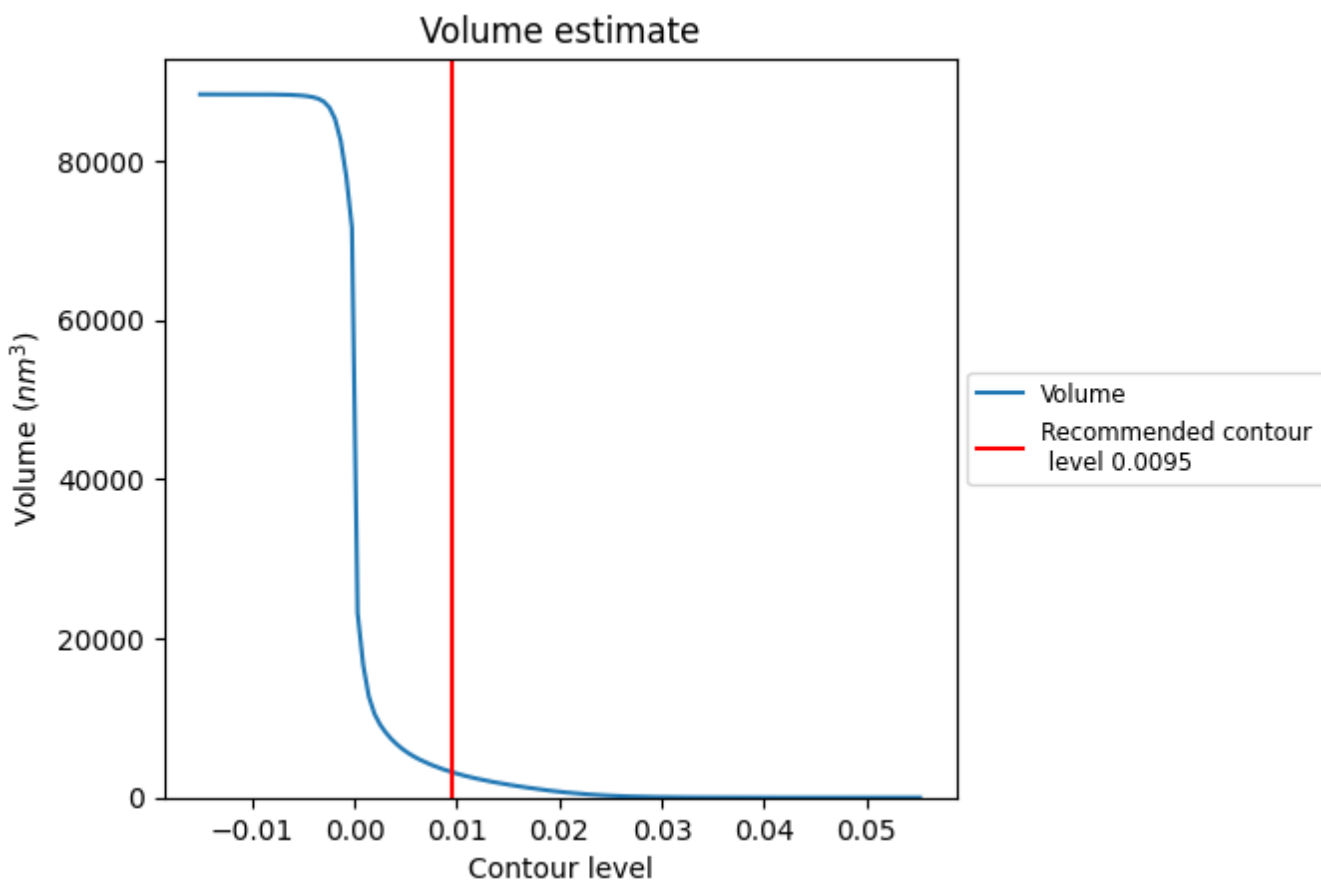
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

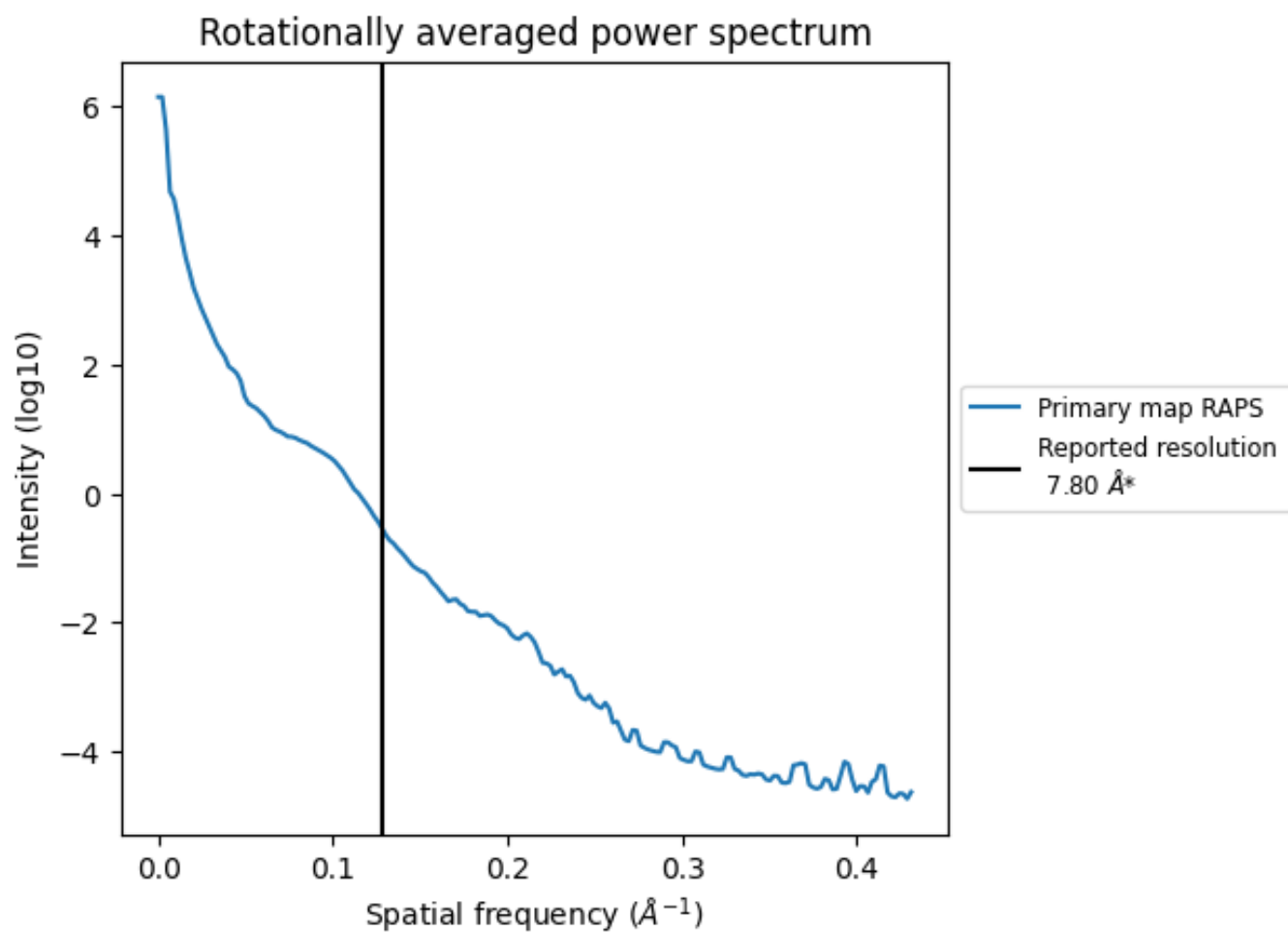
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3218 nm^3 ; this corresponds to an approximate mass of 2907 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 0.128 Å⁻¹

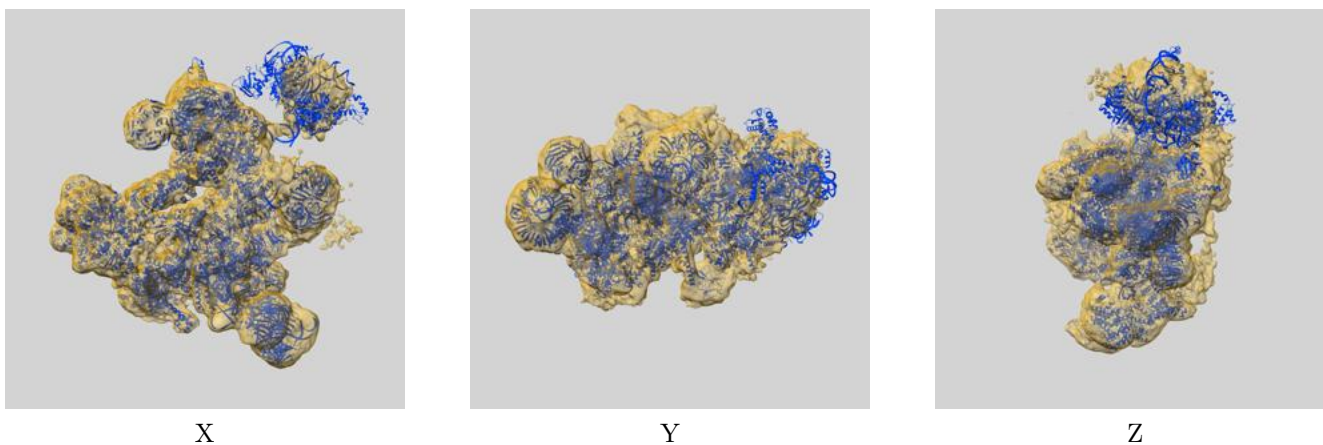
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

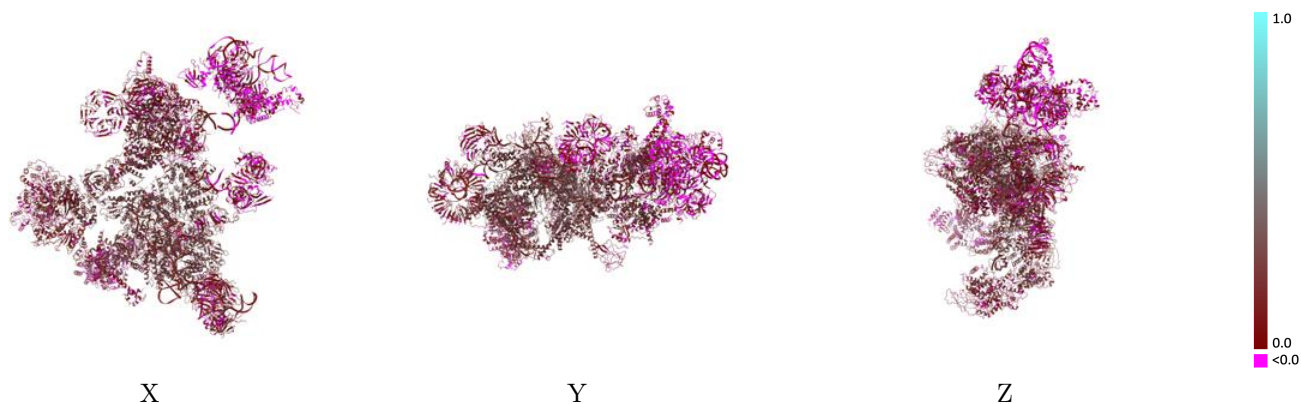
This section contains information regarding the fit between EMDB map EMD-11695 and PDB model 7ABG. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



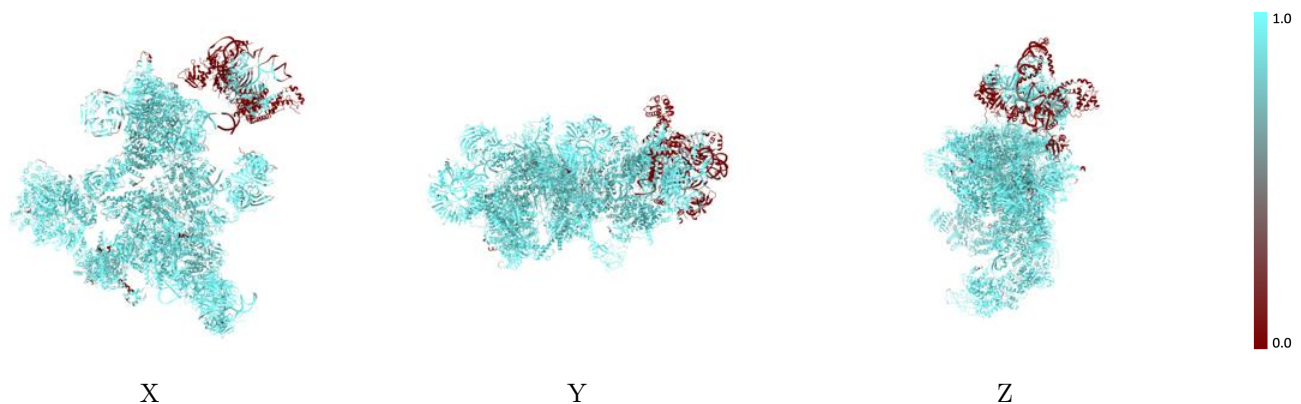
The images above show the 3D surface view of the map at the recommended contour level 0.0095 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



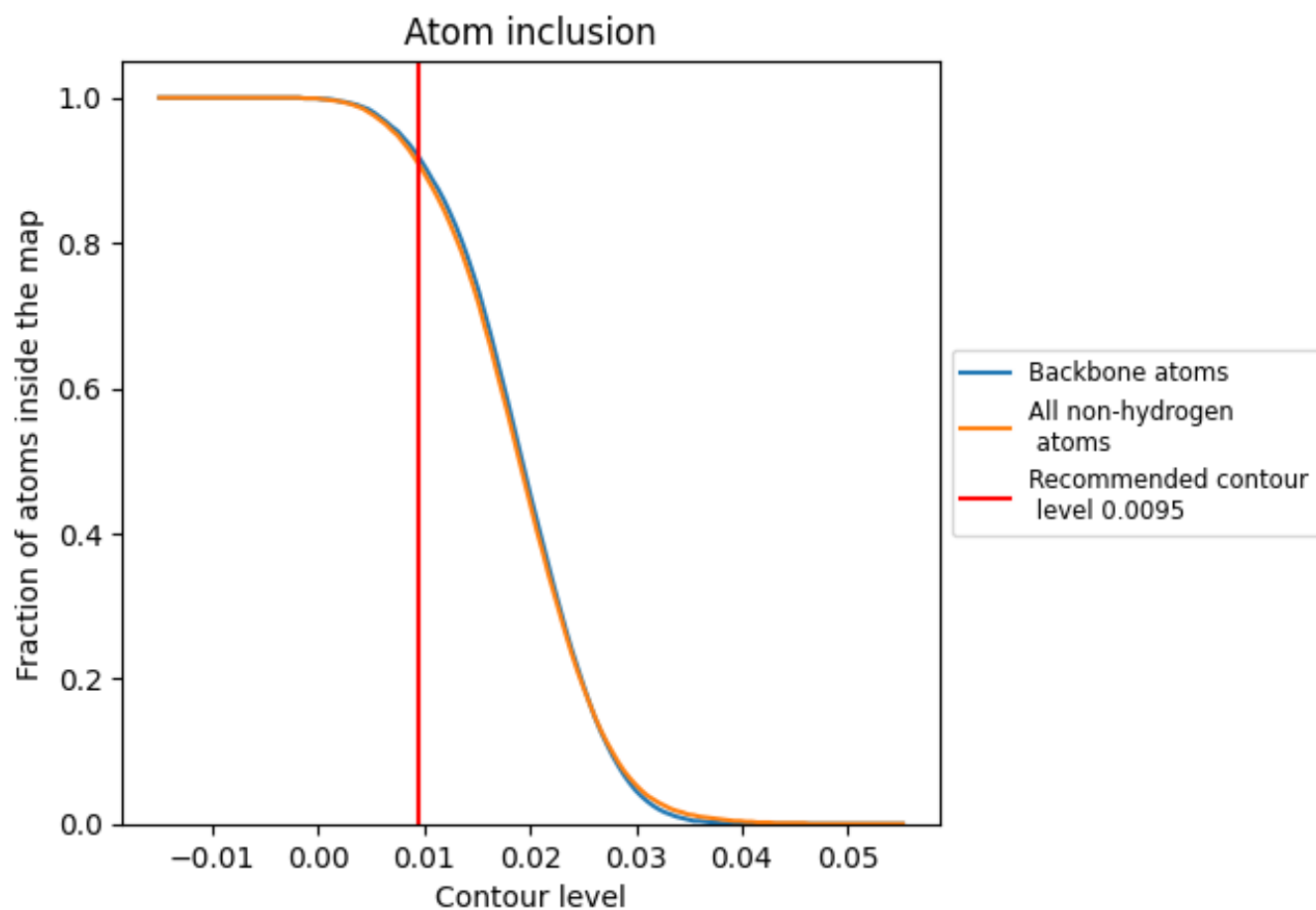
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0095).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 91% 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 (0.0095) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9080	 0.1470
0	 0.9720	 0.0750
2	 0.5410	 0.0490
4	 0.4400	 0.0250
5	 0.9880	 0.1780
6	 0.9690	 0.1550
9	 0.9050	 0.0210
A	 0.9870	 0.2520
A1	 0.9970	 0.0610
A2	 0.9620	 0.0650
A3	 1.0000	 0.0740
A4	 0.9420	 0.1610
A5	 0.9620	 0.0740
A6	 1.0000	 0.0640
B	 0.0010	 -0.0040
C	 0.9880	 0.0570
D	 0.9960	 0.0960
E	 0.9520	 0.1080
F	 0.8800	 0.0670
G	 0.9980	 0.1600
H	 0.8580	 0.0370
I	 0.9970	 0.2580
J	 0.9880	 0.0780
K	 0.9940	 0.2720
L	 0.9480	 0.1760
N	 1.0000	 0.2480
P	 0.9960	 0.1760
Q	 0.9990	 0.2290
R	 0.9560	 0.2570
T	 0.9930	 0.1120
V	 0.9450	 0.0510
W	 0.4860	 0.0180
X	 1.0000	 0.2510
Y	 0.9330	 0.1320
Z	 1.0000	 0.1940



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Chain	Atom inclusion	Q-score
a	 0.9900	 0.1530
b	 0.9560	 0.1180
c	 0.9510	 0.1160
d	 0.9940	 0.1820
e	 0.9970	 0.1990
f	 1.0000	 0.1560
g	 0.9700	 0.1360
h	 0.8750	 -0.0140
i	 0.7600	 0.0090
j	 0.2360	 0.0320
k	 0.1320	 0.0160
l	 0.2020	 0.0100
m	 0.7360	 0.0420
n	 0.9730	 0.0000
p	 0.0200	 0.0700
q	 1.0000	 0.2990
r	 0.9980	 0.2390
s	 0.9870	 0.1560
u	 0.9850	 0.1630
v	 0.9350	 0.2120
w	 0.9850	 0.0730
x	 1.0000	 0.1200
y	 0.9940	 0.1280
z	 0.9040	 0.1010