wwPDB EM Validation Summary Report (i)

Apr 15, 2026 – 06:18 PM JST

PDB ID	:	9LET / pdb_00009let
EMDB ID	:	EMD-63033
Title	:	Cryo-EM structure of human ZAC in zinc Binding State
Authors	:	Qu, Q.; Zhou, Z.
Deposited on	:	2025-01-07
Resolution	:	2.62 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 (i) 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 (i)) were used in the production of this report:

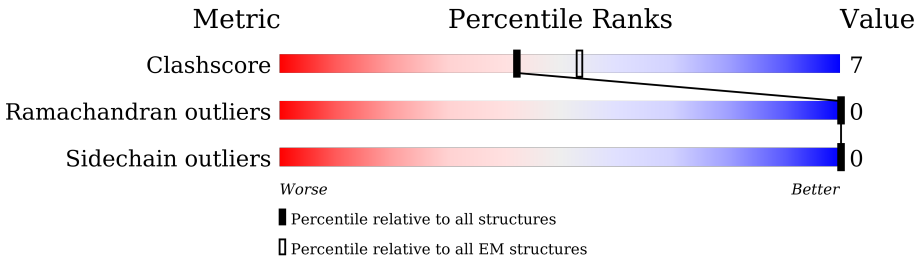
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

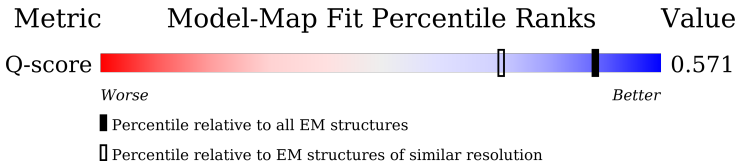
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.62 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8810 (2.12 - 3.12)

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	705	36% 8% 56%
1	B	705	34% 10% 56%
1	C	705	36% 9% 56%
1	D	705	34% 10% 56%

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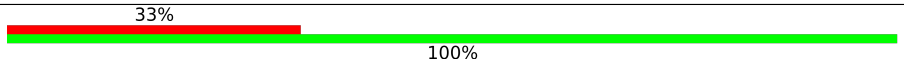
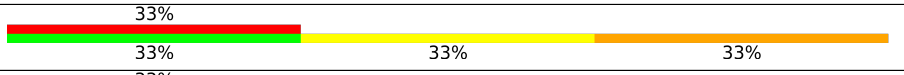
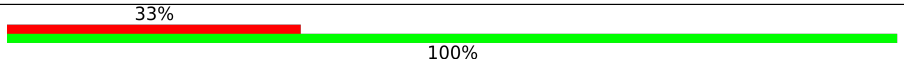
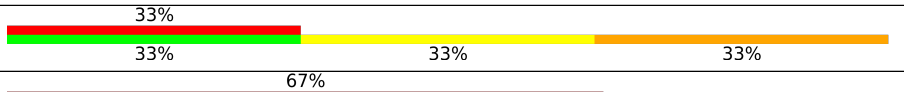
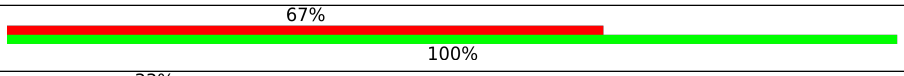
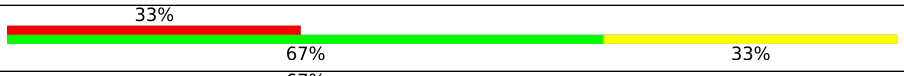
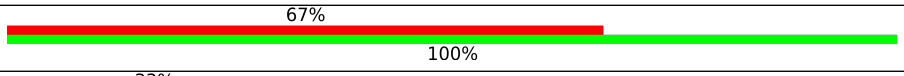
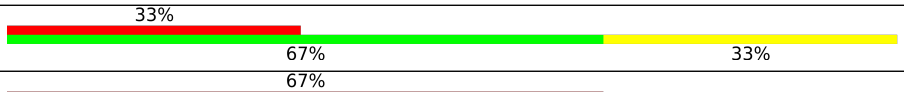
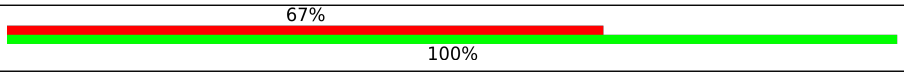
Mol	Chain	Length	Quality of chain
1	E	705	
2	F	3	
2	G	3	
2	H	3	
2	I	3	
2	J	3	
2	K	3	
2	L	3	
2	M	3	
2	N	3	
2	O	3	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 12745 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 Ligand-gated cation channel ZACN,Genome polyprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	311	Total	C	N	O	S	0	0
			2470	1613	410	436	11		
1	B	311	Total	C	N	O	S	0	0
			2470	1613	410	436	11		
1	E	311	Total	C	N	O	S	0	0
			2470	1613	410	436	11		
1	D	311	Total	C	N	O	S	0	0
			2470	1613	410	436	11		
1	C	311	Total	C	N	O	S	0	0
			2470	1613	410	436	11		

There are 280 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	152	THR	ALA	engineered mutation	UNP Q401N2
A	413	SER	-	linker	UNP Q401N2
A	414	ASP	-	linker	UNP Q401N2
A	415	LEU	-	linker	UNP Q401N2
A	416	GLU	-	linker	UNP Q401N2
A	417	VAL	-	linker	UNP Q401N2
A	418	LEU	-	linker	UNP Q401N2
A	419	PHE	-	linker	UNP Q401N2
A	420	GLN	-	linker	UNP Q401N2
A	421	GLY	-	linker	UNP Q401N2
A	422	PRO	-	linker	UNP Q401N2
A	423	GLU	-	linker	UNP Q401N2
A	424	PHE	-	linker	UNP Q401N2
A	425	TRP	-	linker	UNP Q401N2
A	426	SER	-	linker	UNP Q401N2
A	427	HIS	-	linker	UNP Q401N2
A	428	PRO	-	linker	UNP Q401N2
A	429	GLN	-	linker	UNP Q401N2
A	430	PHE	-	linker	UNP Q401N2
A	431	GLU	-	linker	UNP Q401N2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	432	LYS	-	linker	UNP Q401N2
A	433	GLY	-	linker	UNP Q401N2
A	434	GLY	-	linker	UNP Q401N2
A	435	GLY	-	linker	UNP Q401N2
A	436	SER	-	linker	UNP Q401N2
A	437	GLY	-	linker	UNP Q401N2
A	438	GLY	-	linker	UNP Q401N2
A	439	GLY	-	linker	UNP Q401N2
A	440	SER	-	linker	UNP Q401N2
A	441	GLY	-	linker	UNP Q401N2
A	442	GLY	-	linker	UNP Q401N2
A	443	SER	-	linker	UNP Q401N2
A	444	ALA	-	linker	UNP Q401N2
A	445	TRP	-	linker	UNP Q401N2
A	446	SER	-	linker	UNP Q401N2
A	447	HIS	-	linker	UNP Q401N2
A	448	PRO	-	linker	UNP Q401N2
A	449	GLN	-	linker	UNP Q401N2
A	450	PHE	-	linker	UNP Q401N2
A	451	GLU	-	linker	UNP Q401N2
A	452	LYS	-	linker	UNP Q401N2
A	453	GLU	-	linker	UNP Q401N2
A	454	PHE	-	linker	UNP Q401N2
A	455	ASP	-	linker	UNP Q401N2
A	456	ILE	-	linker	UNP Q401N2
A	457	ASP	-	linker	UNP Q401N2
A	458	TYR	-	linker	UNP Q401N2
A	459	LYS	-	linker	UNP Q401N2
A	460	ASP	-	linker	UNP Q401N2
A	461	ASP	-	linker	UNP Q401N2
A	462	ASP	-	linker	UNP Q401N2
A	463	ASP	-	linker	UNP Q401N2
A	464	LYS	-	linker	UNP Q401N2
A	465	SER	-	linker	UNP Q401N2
A	466	ARG	-	linker	UNP Q401N2
A	467	MET	-	linker	UNP Q401N2
B	152	THR	ALA	engineered mutation	UNP Q401N2
B	413	SER	-	linker	UNP Q401N2
B	414	ASP	-	linker	UNP Q401N2
B	415	LEU	-	linker	UNP Q401N2
B	416	GLU	-	linker	UNP Q401N2
B	417	VAL	-	linker	UNP Q401N2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	418	LEU	-	linker	UNP Q401N2
B	419	PHE	-	linker	UNP Q401N2
B	420	GLN	-	linker	UNP Q401N2
B	421	GLY	-	linker	UNP Q401N2
B	422	PRO	-	linker	UNP Q401N2
B	423	GLU	-	linker	UNP Q401N2
B	424	PHE	-	linker	UNP Q401N2
B	425	TRP	-	linker	UNP Q401N2
B	426	SER	-	linker	UNP Q401N2
B	427	HIS	-	linker	UNP Q401N2
B	428	PRO	-	linker	UNP Q401N2
B	429	GLN	-	linker	UNP Q401N2
B	430	PHE	-	linker	UNP Q401N2
B	431	GLU	-	linker	UNP Q401N2
B	432	LYS	-	linker	UNP Q401N2
B	433	GLY	-	linker	UNP Q401N2
B	434	GLY	-	linker	UNP Q401N2
B	435	GLY	-	linker	UNP Q401N2
B	436	SER	-	linker	UNP Q401N2
B	437	GLY	-	linker	UNP Q401N2
B	438	GLY	-	linker	UNP Q401N2
B	439	GLY	-	linker	UNP Q401N2
B	440	SER	-	linker	UNP Q401N2
B	441	GLY	-	linker	UNP Q401N2
B	442	GLY	-	linker	UNP Q401N2
B	443	SER	-	linker	UNP Q401N2
B	444	ALA	-	linker	UNP Q401N2
B	445	TRP	-	linker	UNP Q401N2
B	446	SER	-	linker	UNP Q401N2
B	447	HIS	-	linker	UNP Q401N2
B	448	PRO	-	linker	UNP Q401N2
B	449	GLN	-	linker	UNP Q401N2
B	450	PHE	-	linker	UNP Q401N2
B	451	GLU	-	linker	UNP Q401N2
B	452	LYS	-	linker	UNP Q401N2
B	453	GLU	-	linker	UNP Q401N2
B	454	PHE	-	linker	UNP Q401N2
B	455	ASP	-	linker	UNP Q401N2
B	456	ILE	-	linker	UNP Q401N2
B	457	ASP	-	linker	UNP Q401N2
B	458	TYR	-	linker	UNP Q401N2
B	459	LYS	-	linker	UNP Q401N2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	460	ASP	-	linker	UNP Q401N2
B	461	ASP	-	linker	UNP Q401N2
B	462	ASP	-	linker	UNP Q401N2
B	463	ASP	-	linker	UNP Q401N2
B	464	LYS	-	linker	UNP Q401N2
B	465	SER	-	linker	UNP Q401N2
B	466	ARG	-	linker	UNP Q401N2
B	467	MET	-	linker	UNP Q401N2
E	152	THR	ALA	engineered mutation	UNP Q401N2
E	413	SER	-	linker	UNP Q401N2
E	414	ASP	-	linker	UNP Q401N2
E	415	LEU	-	linker	UNP Q401N2
E	416	GLU	-	linker	UNP Q401N2
E	417	VAL	-	linker	UNP Q401N2
E	418	LEU	-	linker	UNP Q401N2
E	419	PHE	-	linker	UNP Q401N2
E	420	GLN	-	linker	UNP Q401N2
E	421	GLY	-	linker	UNP Q401N2
E	422	PRO	-	linker	UNP Q401N2
E	423	GLU	-	linker	UNP Q401N2
E	424	PHE	-	linker	UNP Q401N2
E	425	TRP	-	linker	UNP Q401N2
E	426	SER	-	linker	UNP Q401N2
E	427	HIS	-	linker	UNP Q401N2
E	428	PRO	-	linker	UNP Q401N2
E	429	GLN	-	linker	UNP Q401N2
E	430	PHE	-	linker	UNP Q401N2
E	431	GLU	-	linker	UNP Q401N2
E	432	LYS	-	linker	UNP Q401N2
E	433	GLY	-	linker	UNP Q401N2
E	434	GLY	-	linker	UNP Q401N2
E	435	GLY	-	linker	UNP Q401N2
E	436	SER	-	linker	UNP Q401N2
E	437	GLY	-	linker	UNP Q401N2
E	438	GLY	-	linker	UNP Q401N2
E	439	GLY	-	linker	UNP Q401N2
E	440	SER	-	linker	UNP Q401N2
E	441	GLY	-	linker	UNP Q401N2
E	442	GLY	-	linker	UNP Q401N2
E	443	SER	-	linker	UNP Q401N2
E	444	ALA	-	linker	UNP Q401N2
E	445	TRP	-	linker	UNP Q401N2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	446	SER	-	linker	UNP Q401N2
E	447	HIS	-	linker	UNP Q401N2
E	448	PRO	-	linker	UNP Q401N2
E	449	GLN	-	linker	UNP Q401N2
E	450	PHE	-	linker	UNP Q401N2
E	451	GLU	-	linker	UNP Q401N2
E	452	LYS	-	linker	UNP Q401N2
E	453	GLU	-	linker	UNP Q401N2
E	454	PHE	-	linker	UNP Q401N2
E	455	ASP	-	linker	UNP Q401N2
E	456	ILE	-	linker	UNP Q401N2
E	457	ASP	-	linker	UNP Q401N2
E	458	TYR	-	linker	UNP Q401N2
E	459	LYS	-	linker	UNP Q401N2
E	460	ASP	-	linker	UNP Q401N2
E	461	ASP	-	linker	UNP Q401N2
E	462	ASP	-	linker	UNP Q401N2
E	463	ASP	-	linker	UNP Q401N2
E	464	LYS	-	linker	UNP Q401N2
E	465	SER	-	linker	UNP Q401N2
E	466	ARG	-	linker	UNP Q401N2
E	467	MET	-	linker	UNP Q401N2
D	152	THR	ALA	engineered mutation	UNP Q401N2
D	413	SER	-	linker	UNP Q401N2
D	414	ASP	-	linker	UNP Q401N2
D	415	LEU	-	linker	UNP Q401N2
D	416	GLU	-	linker	UNP Q401N2
D	417	VAL	-	linker	UNP Q401N2
D	418	LEU	-	linker	UNP Q401N2
D	419	PHE	-	linker	UNP Q401N2
D	420	GLN	-	linker	UNP Q401N2
D	421	GLY	-	linker	UNP Q401N2
D	422	PRO	-	linker	UNP Q401N2
D	423	GLU	-	linker	UNP Q401N2
D	424	PHE	-	linker	UNP Q401N2
D	425	TRP	-	linker	UNP Q401N2
D	426	SER	-	linker	UNP Q401N2
D	427	HIS	-	linker	UNP Q401N2
D	428	PRO	-	linker	UNP Q401N2
D	429	GLN	-	linker	UNP Q401N2
D	430	PHE	-	linker	UNP Q401N2
D	431	GLU	-	linker	UNP Q401N2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	432	LYS	-	linker	UNP Q401N2
D	433	GLY	-	linker	UNP Q401N2
D	434	GLY	-	linker	UNP Q401N2
D	435	GLY	-	linker	UNP Q401N2
D	436	SER	-	linker	UNP Q401N2
D	437	GLY	-	linker	UNP Q401N2
D	438	GLY	-	linker	UNP Q401N2
D	439	GLY	-	linker	UNP Q401N2
D	440	SER	-	linker	UNP Q401N2
D	441	GLY	-	linker	UNP Q401N2
D	442	GLY	-	linker	UNP Q401N2
D	443	SER	-	linker	UNP Q401N2
D	444	ALA	-	linker	UNP Q401N2
D	445	TRP	-	linker	UNP Q401N2
D	446	SER	-	linker	UNP Q401N2
D	447	HIS	-	linker	UNP Q401N2
D	448	PRO	-	linker	UNP Q401N2
D	449	GLN	-	linker	UNP Q401N2
D	450	PHE	-	linker	UNP Q401N2
D	451	GLU	-	linker	UNP Q401N2
D	452	LYS	-	linker	UNP Q401N2
D	453	GLU	-	linker	UNP Q401N2
D	454	PHE	-	linker	UNP Q401N2
D	455	ASP	-	linker	UNP Q401N2
D	456	ILE	-	linker	UNP Q401N2
D	457	ASP	-	linker	UNP Q401N2
D	458	TYR	-	linker	UNP Q401N2
D	459	LYS	-	linker	UNP Q401N2
D	460	ASP	-	linker	UNP Q401N2
D	461	ASP	-	linker	UNP Q401N2
D	462	ASP	-	linker	UNP Q401N2
D	463	ASP	-	linker	UNP Q401N2
D	464	LYS	-	linker	UNP Q401N2
D	465	SER	-	linker	UNP Q401N2
D	466	ARG	-	linker	UNP Q401N2
D	467	MET	-	linker	UNP Q401N2
C	152	THR	ALA	engineered mutation	UNP Q401N2
C	413	SER	-	linker	UNP Q401N2
C	414	ASP	-	linker	UNP Q401N2
C	415	LEU	-	linker	UNP Q401N2
C	416	GLU	-	linker	UNP Q401N2
C	417	VAL	-	linker	UNP Q401N2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	418	LEU	-	linker	UNP Q401N2
C	419	PHE	-	linker	UNP Q401N2
C	420	GLN	-	linker	UNP Q401N2
C	421	GLY	-	linker	UNP Q401N2
C	422	PRO	-	linker	UNP Q401N2
C	423	GLU	-	linker	UNP Q401N2
C	424	PHE	-	linker	UNP Q401N2
C	425	TRP	-	linker	UNP Q401N2
C	426	SER	-	linker	UNP Q401N2
C	427	HIS	-	linker	UNP Q401N2
C	428	PRO	-	linker	UNP Q401N2
C	429	GLN	-	linker	UNP Q401N2
C	430	PHE	-	linker	UNP Q401N2
C	431	GLU	-	linker	UNP Q401N2
C	432	LYS	-	linker	UNP Q401N2
C	433	GLY	-	linker	UNP Q401N2
C	434	GLY	-	linker	UNP Q401N2
C	435	GLY	-	linker	UNP Q401N2
C	436	SER	-	linker	UNP Q401N2
C	437	GLY	-	linker	UNP Q401N2
C	438	GLY	-	linker	UNP Q401N2
C	439	GLY	-	linker	UNP Q401N2
C	440	SER	-	linker	UNP Q401N2
C	441	GLY	-	linker	UNP Q401N2
C	442	GLY	-	linker	UNP Q401N2
C	443	SER	-	linker	UNP Q401N2
C	444	ALA	-	linker	UNP Q401N2
C	445	TRP	-	linker	UNP Q401N2
C	446	SER	-	linker	UNP Q401N2
C	447	HIS	-	linker	UNP Q401N2
C	448	PRO	-	linker	UNP Q401N2
C	449	GLN	-	linker	UNP Q401N2
C	450	PHE	-	linker	UNP Q401N2
C	451	GLU	-	linker	UNP Q401N2
C	452	LYS	-	linker	UNP Q401N2
C	453	GLU	-	linker	UNP Q401N2
C	454	PHE	-	linker	UNP Q401N2
C	455	ASP	-	linker	UNP Q401N2
C	456	ILE	-	linker	UNP Q401N2
C	457	ASP	-	linker	UNP Q401N2
C	458	TYR	-	linker	UNP Q401N2
C	459	LYS	-	linker	UNP Q401N2

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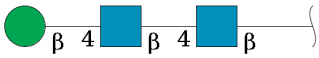
Chain	Residue	Modelled	Actual	Comment	Reference
C	460	ASP	-	linker	UNP Q401N2
C	461	ASP	-	linker	UNP Q401N2
C	462	ASP	-	linker	UNP Q401N2
C	463	ASP	-	linker	UNP Q401N2
C	464	LYS	-	linker	UNP Q401N2
C	465	SER	-	linker	UNP Q401N2
C	466	ARG	-	linker	UNP Q401N2
C	467	MET	-	linker	UNP Q401N2

- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
2	F	3	Total	C	N	O	0	0
			39	22	2	15		
2	G	3	Total	C	N	O	0	0
			39	22	2	15		
2	H	3	Total	C	N	O	0	0
			39	22	2	15		
2	I	3	Total	C	N	O	0	0
			39	22	2	15		
2	J	3	Total	C	N	O	0	0
			39	22	2	15		
2	K	3	Total	C	N	O	0	0
			39	22	2	15		
2	L	3	Total	C	N	O	0	0
			39	22	2	15		
2	M	3	Total	C	N	O	0	0
			39	22	2	15		
2	N	3	Total	C	N	O	0	0
			39	22	2	15		
2	O	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
3	A	2	Total Zn 2 2	0
3	B	1	Total Zn 1 1	0
3	D	1	Total Zn 1 1	0
3	C	1	Total Zn 1 1	0

3 Residue-property plots (i)

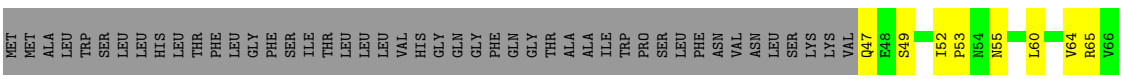
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

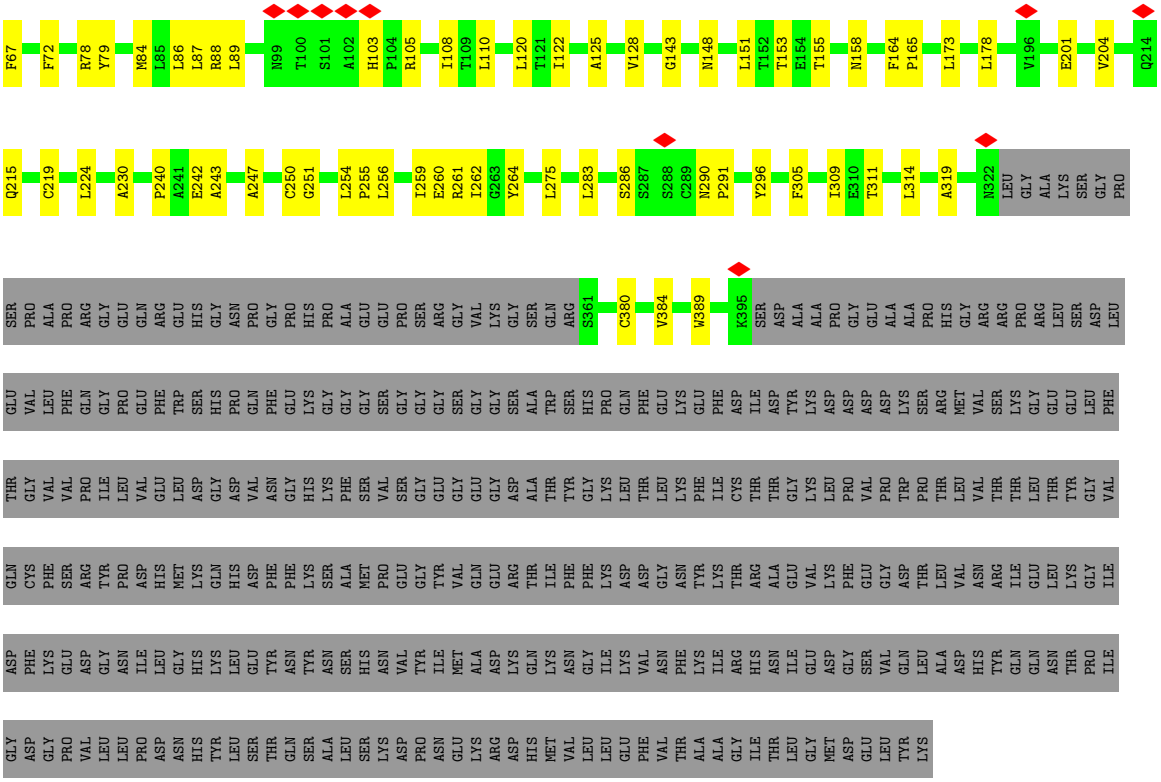
• Molecule 1: Ligand-gated cation channel ZACN,Genome polyprotein

Chain A:

• Molecule 1: Ligand-gated cation channel ZACN,Genome polyprotein

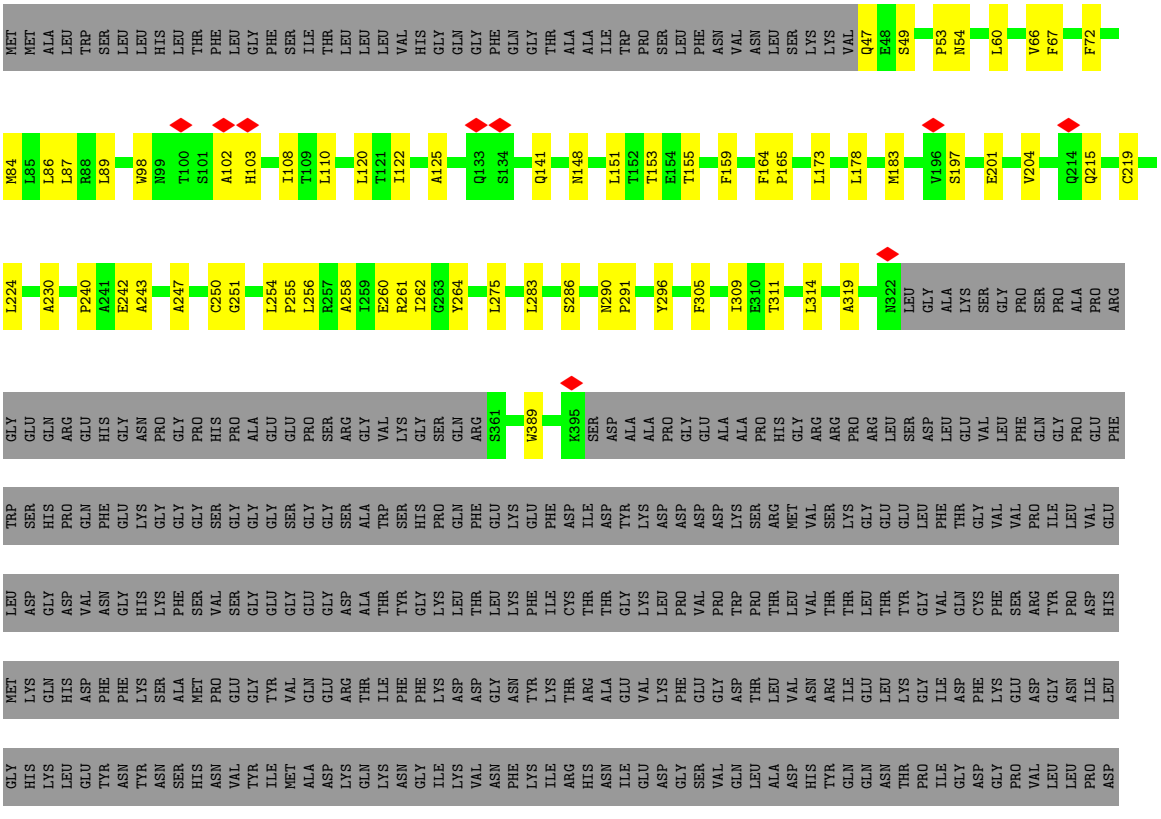
Chain B:





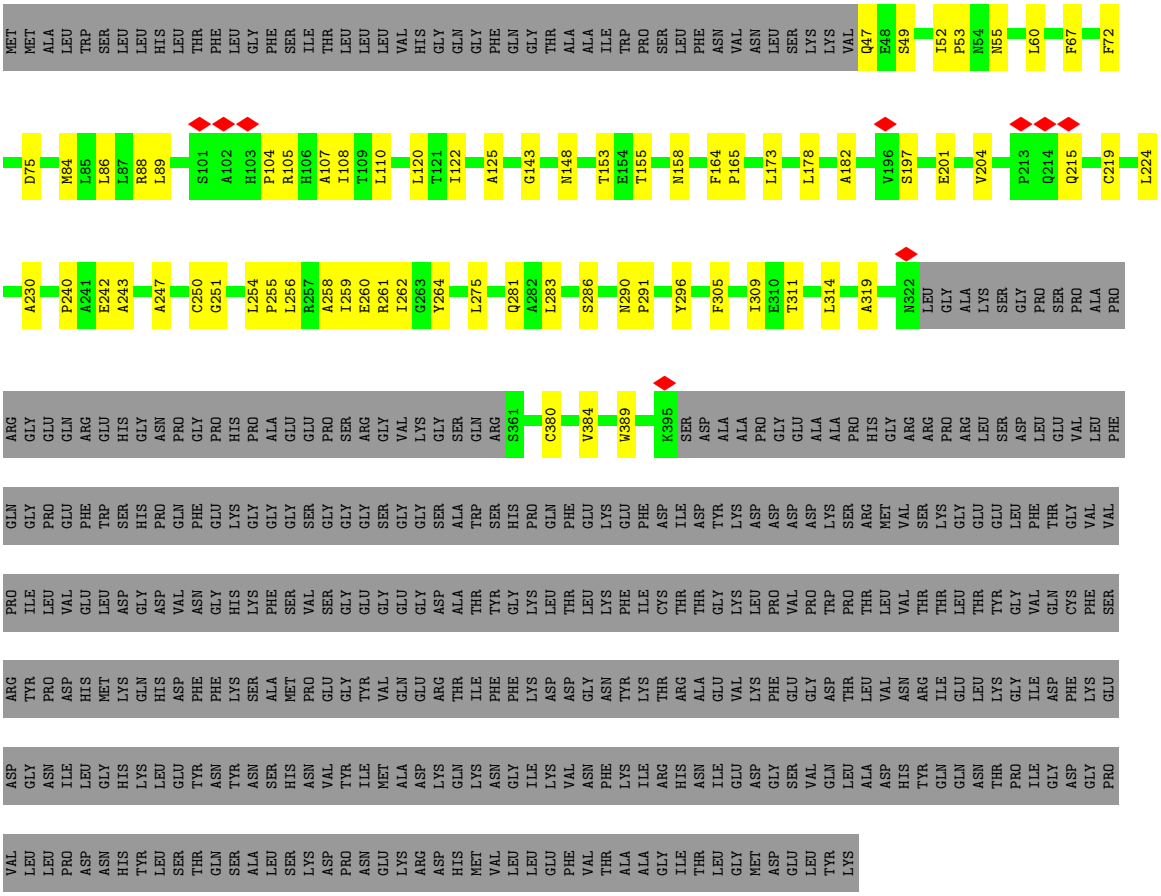
• Molecule 1: Ligand-gated cation channel ZACN,Genome polyprotein

Chain E:



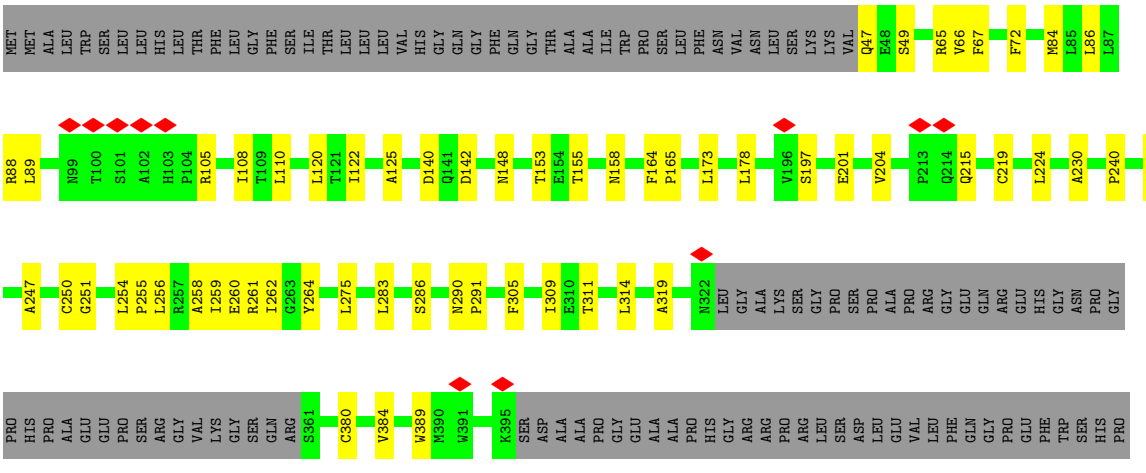
• Molecule 1: Ligand-gated cation channel ZACN,Genome polyprotein

Chain D:



• Molecule 1: Ligand-gated cation channel ZACN,Genome polyprotein

Chain C:



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

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

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

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

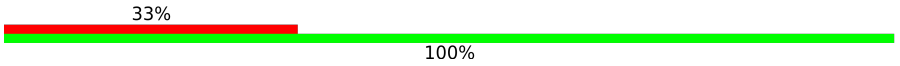
SER THR GLN SER ALA LEU SER LYS ASP PRO ASN GLU LYS ARG ASP HIS MET VAL LEU LEU GLU PHE VAL THR ALA ALA GLY ILE THR LEU GLY MET ASP GLU LEU TYR LYS

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:

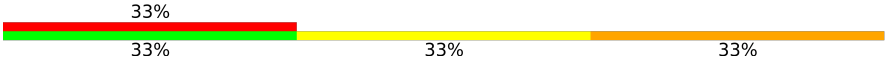
• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:



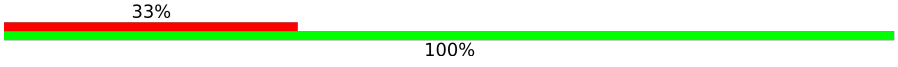
• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:



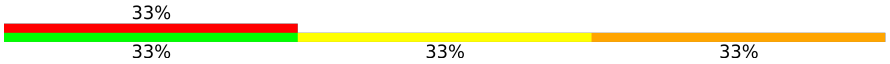
• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:



• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:



• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	164569	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.685	Depositor
Minimum map value	-1.867	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.069	Depositor
Recommended contour level	0.22	Depositor
Map size (Å)	279.6, 279.6, 279.6	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93200004, 0.93200004, 0.93200004	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, NAG, BMA

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	0.56	2/2530 (0.1%)	0.58	2/3464 (0.1%)
1	B	0.43	2/2530 (0.1%)	0.52	2/3464 (0.1%)
1	C	0.39	2/2530 (0.1%)	0.44	0/3464
1	D	0.51	3/2530 (0.1%)	0.53	4/3464 (0.1%)
1	E	0.36	1/2530 (0.0%)	0.51	3/3464 (0.1%)
All	All	0.46	10/12650 (0.1%)	0.52	11/17320 (0.1%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	65	ARG	C-O	-5.80	1.17	1.24
1	B	65	ARG	C-O	-5.68	1.17	1.24
1	C	66	VAL	C-O	-5.63	1.17	1.24
1	D	107	ALA	CA-C	-5.39	1.45	1.52
1	A	64	VAL	C-O	-5.39	1.18	1.24

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	55	ASN	N-CA-C	-6.75	103.12	112.30
1	A	197	SER	N-CA-C	6.51	119.43	108.23
1	D	55	ASN	N-CA-C	-5.76	103.50	110.88
1	E	159	PHE	N-CA-C	5.68	117.94	109.59
1	D	52	ILE	N-CA-C	5.58	115.05	108.96

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	A	2470	0	2513	38	0
1	B	2470	0	2513	46	0
1	C	2470	0	2513	43	0
1	D	2470	0	2513	44	0
1	E	2470	0	2513	42	0
2	F	39	0	34	0	0
2	G	39	0	34	0	0
2	H	39	0	34	1	0
2	I	39	0	34	0	0
2	J	39	0	34	1	0
2	K	39	0	34	0	0
2	L	39	0	34	0	0
2	M	39	0	34	0	0
2	N	39	0	34	0	0
2	O	39	0	34	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
All	All	12745	0	12905	172	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 7.

The worst 5 of 172 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:C:201:GLU:HG3	1:C:230:ALA:HB2	1.62	0.82
1:D:201:GLU:HG3	1:D:230:ALA:HB2	1.62	0.81
1:E:201:GLU:HG3	1:E:230:ALA:HB2	1.62	0.80
1:B:201:GLU:HG3	1:B:230:ALA:HB2	1.62	0.80
1:B:215:GLN:NE2	1:B:219:CYS:SG	2.57	0.77

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	A	307/705 (44%)	296 (96%)	11 (4%)	0	100	100
1	B	307/705 (44%)	298 (97%)	9 (3%)	0	100	100
1	C	307/705 (44%)	298 (97%)	9 (3%)	0	100	100
1	D	307/705 (44%)	299 (97%)	8 (3%)	0	100	100
1	E	307/705 (44%)	299 (97%)	8 (3%)	0	100	100
All	All	1535/3525 (44%)	1490 (97%)	45 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	A	277/610 (45%)	277 (100%)	0	100	100
1	B	277/610 (45%)	277 (100%)	0	100	100
1	C	277/610 (45%)	277 (100%)	0	100	100
1	D	277/610 (45%)	277 (100%)	0	100	100
1	E	277/610 (45%)	277 (100%)	0	100	100
All	All	1385/3050 (45%)	1385 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	47	GLN
1	C	73	ASN
1	C	148	ASN
1	B	221	GLN
1	B	215	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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)

30 monosaccharides 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	$\#\|Z\| > 2$
2	NAG	F	1	2,1	14,14,15	0.57	0	17,19,21	1.20	1 (5%)
2	NAG	F	2	2	14,14,15	0.29	0	17,19,21	0.65	0
2	BMA	F	3	2	11,11,12	0.23	0	15,15,17	0.46	0
2	NAG	G	1	2,1	14,14,15	0.33	0	17,19,21	0.53	0
2	NAG	G	2	2	14,14,15	0.30	0	17,19,21	0.52	0
2	BMA	G	3	2	11,11,12	0.23	0	15,15,17	0.55	0
2	NAG	H	1	2,1	14,14,15	0.56	0	17,19,21	0.98	1 (5%)
2	NAG	H	2	2	14,14,15	0.30	0	17,19,21	0.63	0
2	BMA	H	3	2	11,11,12	0.23	0	15,15,17	0.47	0
2	NAG	I	1	2,1	14,14,15	0.32	0	17,19,21	0.51	0
2	NAG	I	2	2	14,14,15	0.30	0	17,19,21	0.56	0
2	BMA	I	3	2	11,11,12	0.24	0	15,15,17	0.53	0
2	NAG	J	1	2,1	14,14,15	0.54	0	17,19,21	1.10	1 (5%)
2	NAG	J	2	2	14,14,15	0.30	0	17,19,21	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	BMA	J	3	2	11,11,12	0.24	0	15,15,17	0.49	0
2	NAG	K	1	2,1	14,14,15	0.33	0	17,19,21	0.58	0
2	NAG	K	2	2	14,14,15	0.31	0	17,19,21	0.53	0
2	BMA	K	3	2	11,11,12	0.25	0	15,15,17	0.51	0
2	NAG	L	1	2,1	14,14,15	0.55	0	17,19,21	1.01	1 (5%)
2	NAG	L	2	2	14,14,15	0.29	0	17,19,21	0.67	0
2	BMA	L	3	2	11,11,12	0.25	0	15,15,17	0.57	0
2	NAG	M	1	2,1	14,14,15	0.35	0	17,19,21	0.59	0
2	NAG	M	2	2	14,14,15	0.29	0	17,19,21	0.53	0
2	BMA	M	3	2	11,11,12	0.23	0	15,15,17	0.56	0
2	NAG	N	1	2,1	14,14,15	0.54	0	17,19,21	1.26	1 (5%)
2	NAG	N	2	2	14,14,15	0.29	0	17,19,21	0.72	0
2	BMA	N	3	2	11,11,12	0.23	0	15,15,17	0.51	0
2	NAG	O	1	2,1	14,14,15	0.36	0	17,19,21	0.65	0
2	NAG	O	2	2	14,14,15	0.30	0	17,19,21	0.54	0
2	BMA	O	3	2	11,11,12	0.23	0	15,15,17	0.55	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
2	NAG	F	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	BMA	F	3	2	-	1/2/19/22	0/1/1/1
2	NAG	G	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	BMA	G	3	2	-	0/2/19/22	0/1/1/1
2	NAG	H	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1
2	BMA	H	3	2	-	1/2/19/22	0/1/1/1
2	NAG	I	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	I	2	2	-	1/6/23/26	0/1/1/1
2	BMA	I	3	2	-	0/2/19/22	0/1/1/1
2	NAG	J	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	J	2	2	-	2/6/23/26	0/1/1/1
2	BMA	J	3	2	-	0/2/19/22	0/1/1/1
2	NAG	K	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	K	2	2	-	0/6/23/26	0/1/1/1
2	BMA	K	3	2	-	0/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	L	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	L	2	2	-	0/6/23/26	0/1/1/1
2	BMA	L	3	2	-	1/2/19/22	1/1/1/1
2	NAG	M	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	M	2	2	-	0/6/23/26	0/1/1/1
2	BMA	M	3	2	-	0/2/19/22	0/1/1/1
2	NAG	N	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	N	2	2	-	2/6/23/26	0/1/1/1
2	BMA	N	3	2	-	0/2/19/22	0/1/1/1
2	NAG	O	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	O	2	2	-	0/6/23/26	0/1/1/1
2	BMA	O	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	N	1	NAG	C3-C4-C5	-4.19	102.77	110.24
2	F	1	NAG	C3-C4-C5	-3.62	103.78	110.24
2	L	1	NAG	C3-C4-C5	-3.20	104.53	110.24
2	J	1	NAG	C1-O5-C5	2.83	116.02	112.19
2	H	1	NAG	C3-C4-C5	-2.30	106.14	110.24

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	1	NAG	C8-C7-N2-C2
2	G	1	NAG	O7-C7-N2-C2
2	I	1	NAG	C8-C7-N2-C2
2	I	1	NAG	O7-C7-N2-C2
2	K	1	NAG	C8-C7-N2-C2

All (1) ring outliers are listed below:

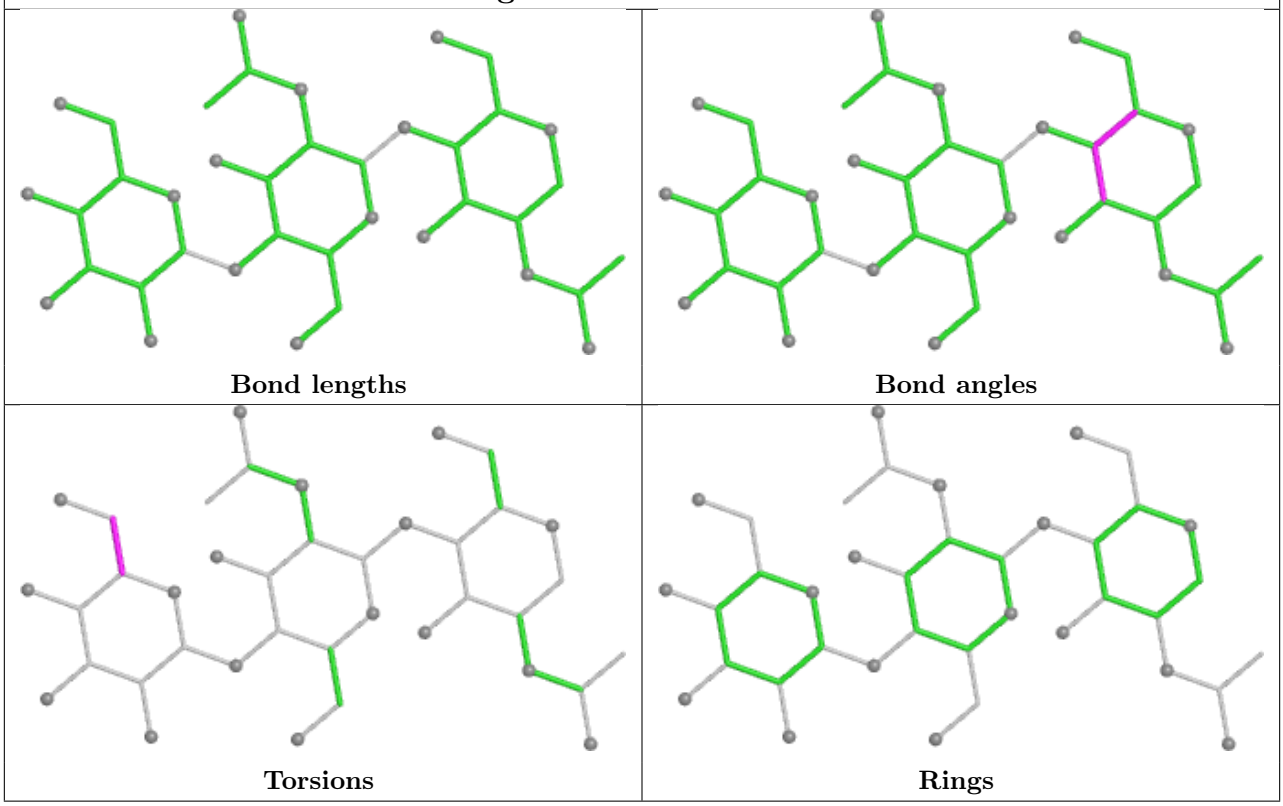
Mol	Chain	Res	Type	Atoms
2	L	3	BMA	C1-C2-C3-C4-C5-O5

4 monomers are involved in 2 short contacts:

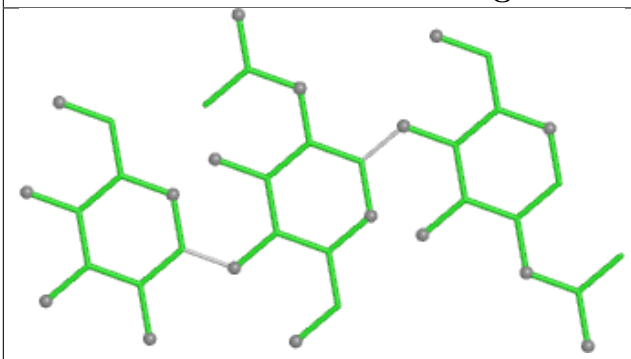
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	1	NAG	1	0
2	J	1	NAG	1	0
2	H	2	NAG	1	0
2	J	2	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

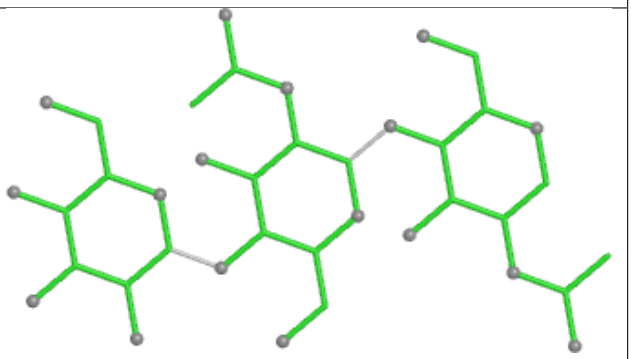
Oligosaccharide Chain F



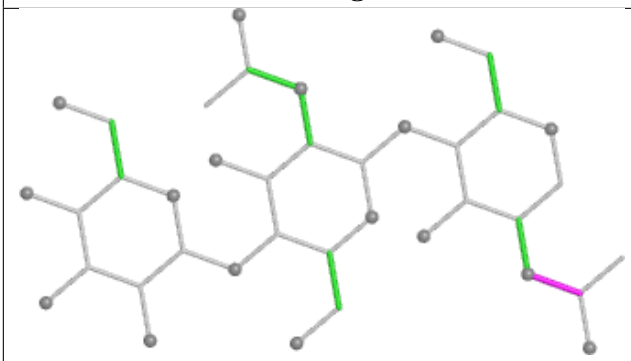
Oligosaccharide Chain G



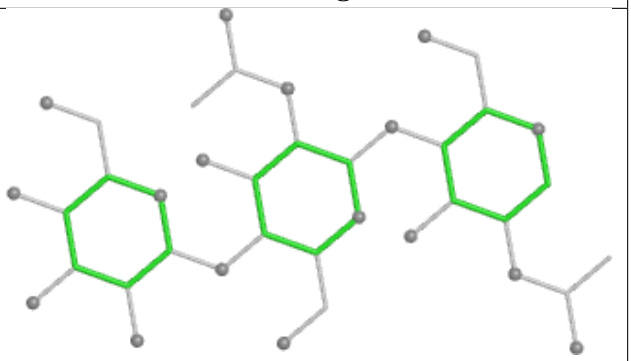
Bond lengths



Bond angles

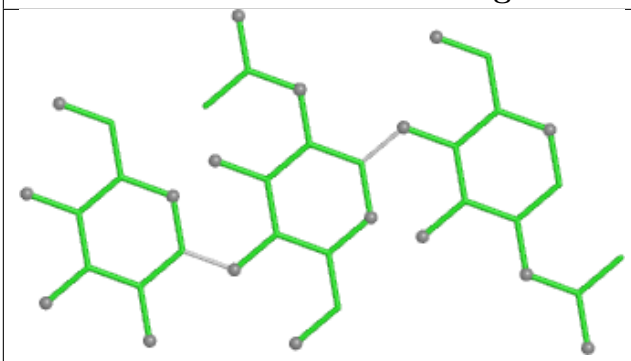


Torsions

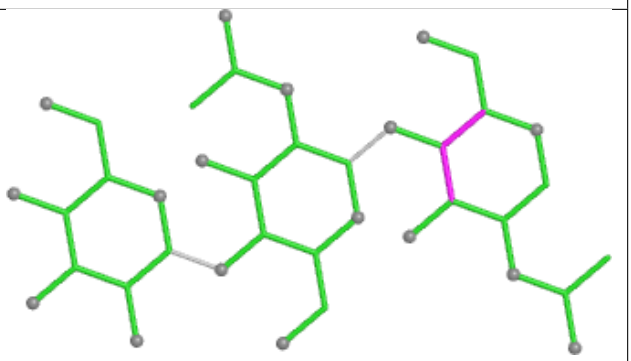


Rings

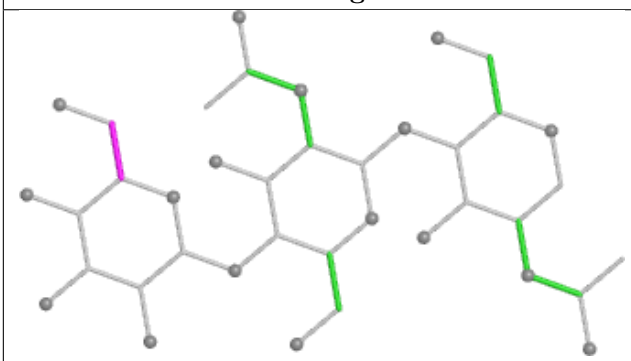
Oligosaccharide Chain H



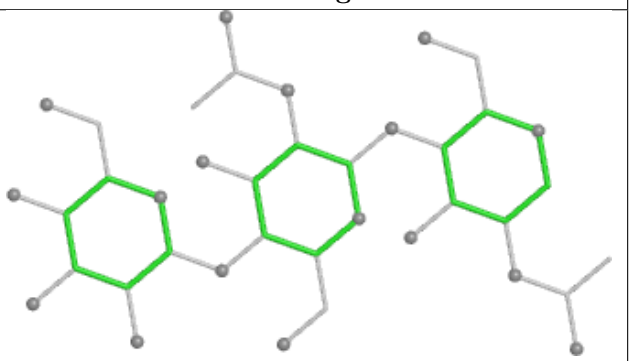
Bond lengths



Bond angles

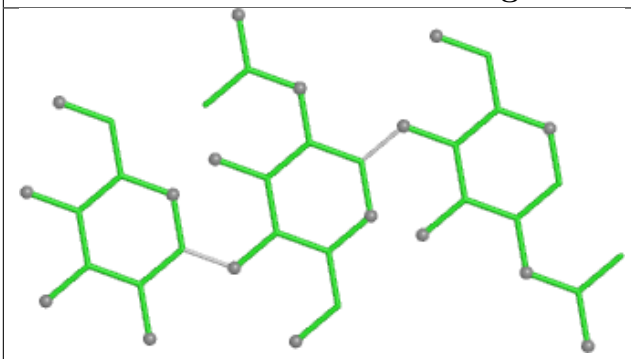


Torsions

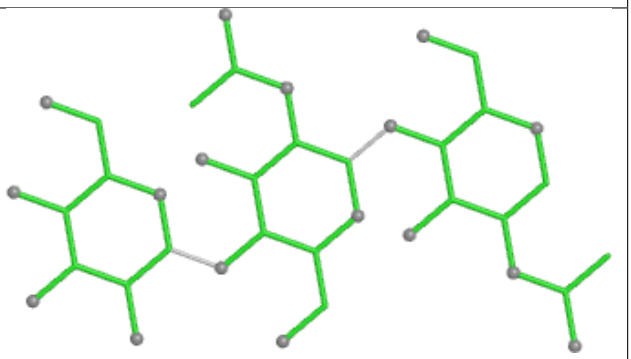


Rings

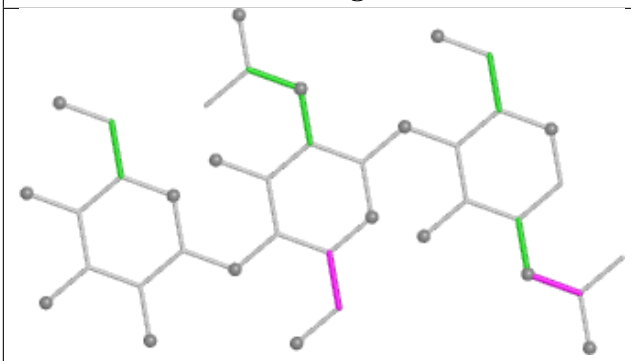
Oligosaccharide Chain I



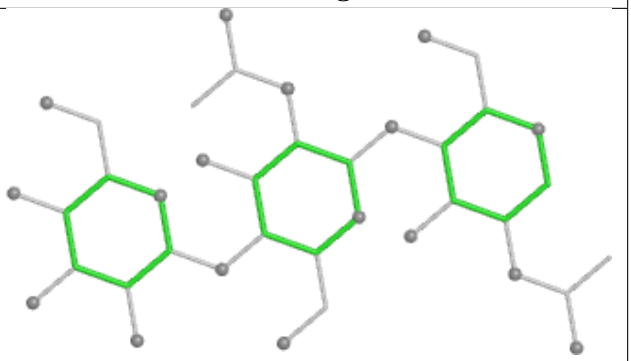
Bond lengths



Bond angles

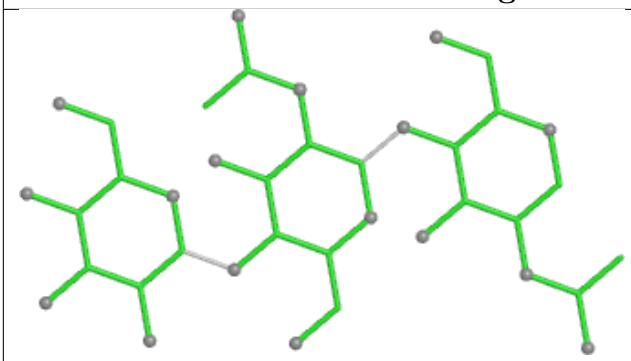


Torsions

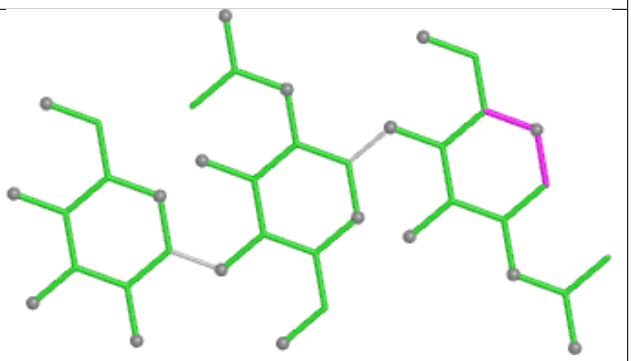


Rings

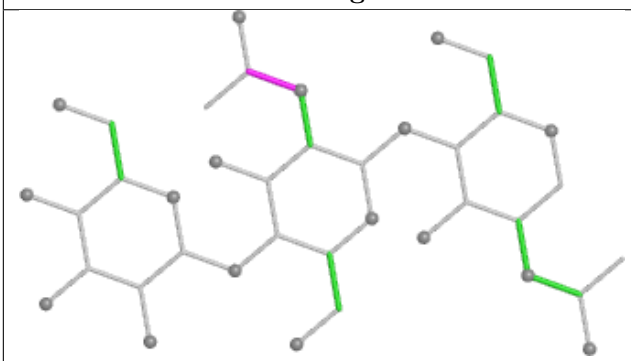
Oligosaccharide Chain J



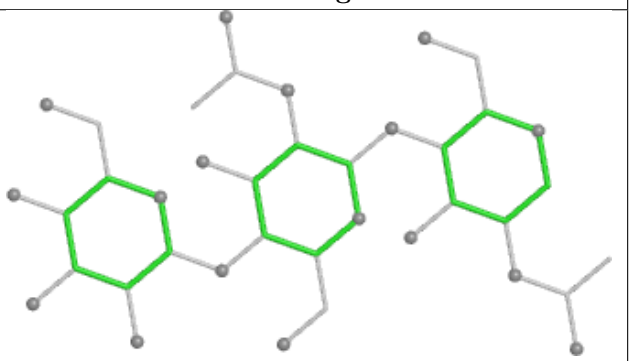
Bond lengths



Bond angles

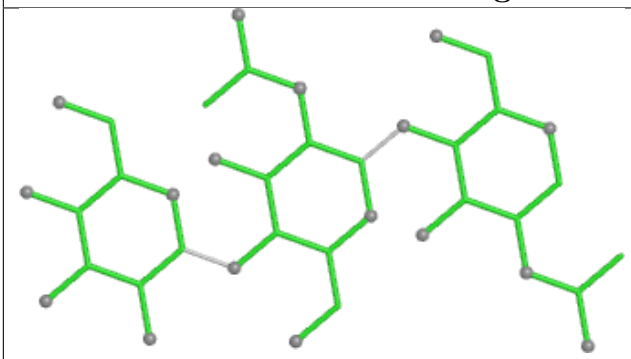


Torsions

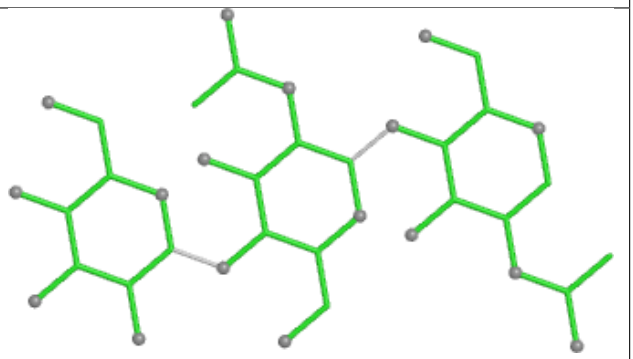


Rings

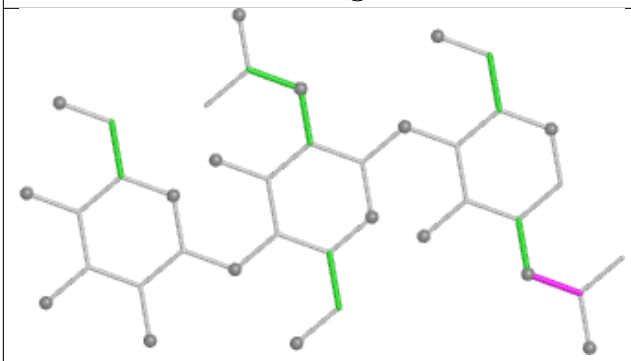
Oligosaccharide Chain K



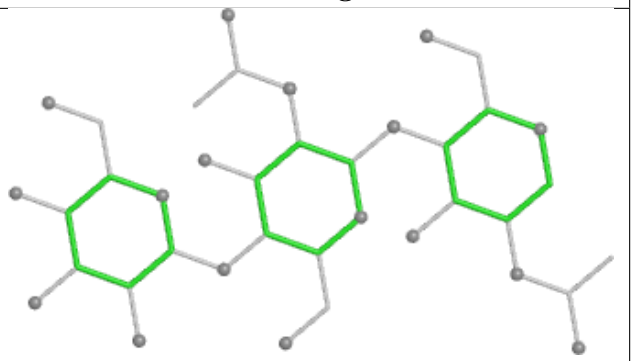
Bond lengths



Bond angles

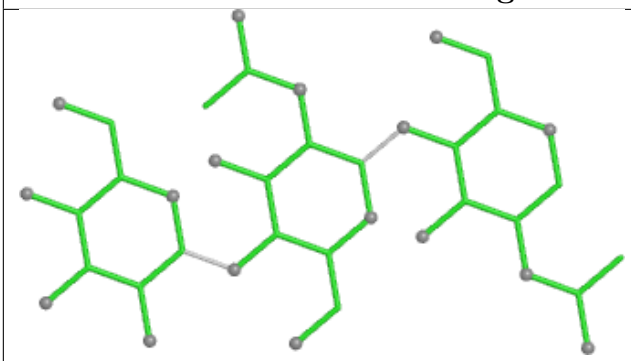


Torsions

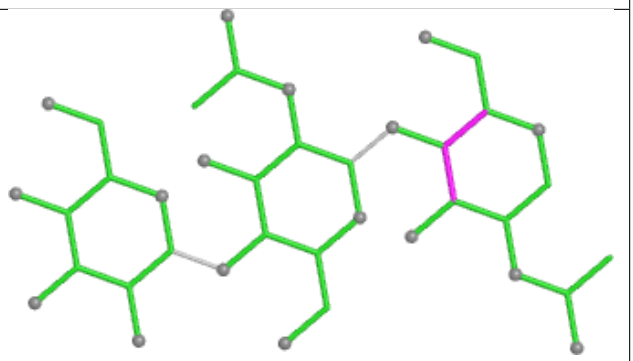


Rings

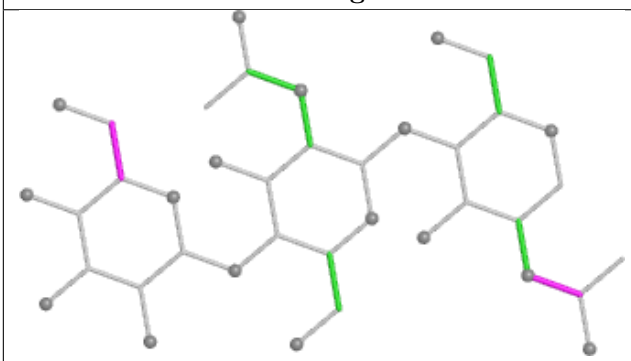
Oligosaccharide Chain L



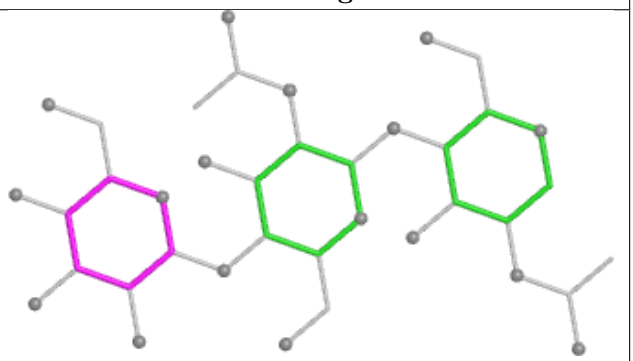
Bond lengths



Bond angles

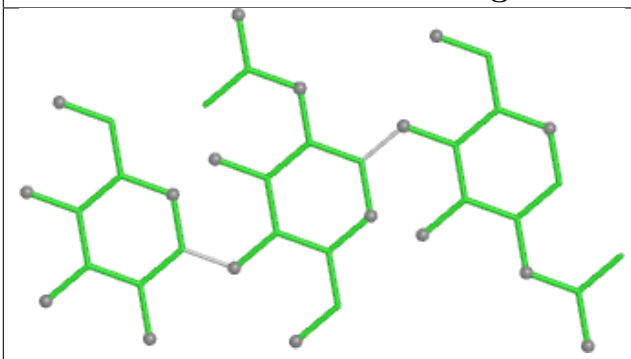


Torsions

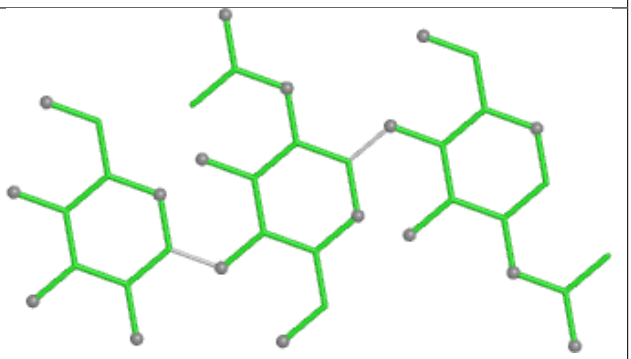


Rings

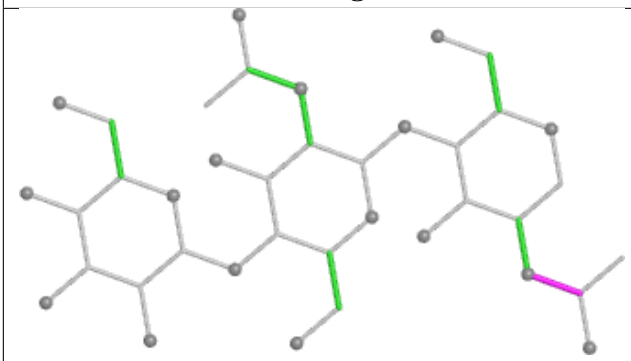
Oligosaccharide Chain M



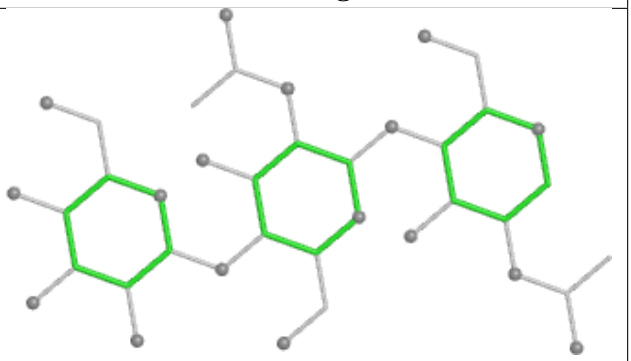
Bond lengths



Bond angles

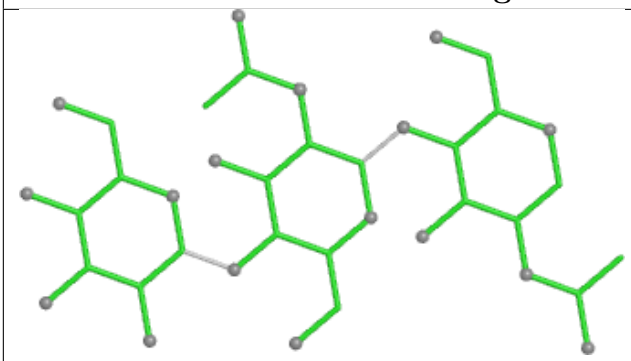


Torsions

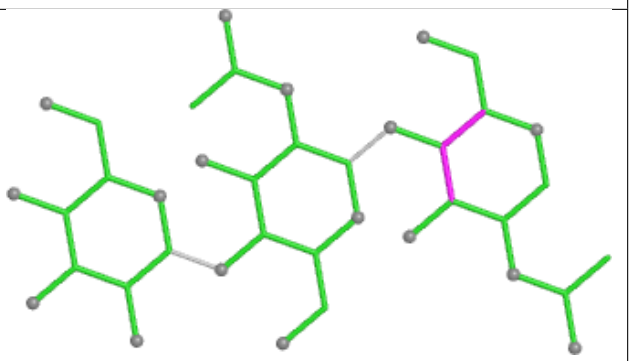


Rings

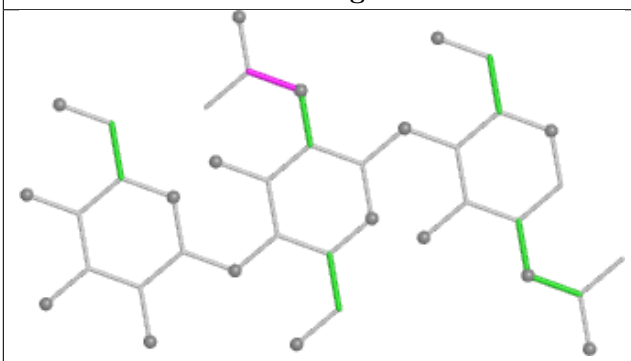
Oligosaccharide Chain N



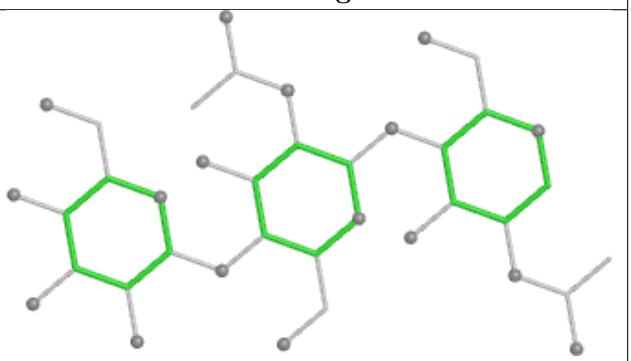
Bond lengths



Bond angles

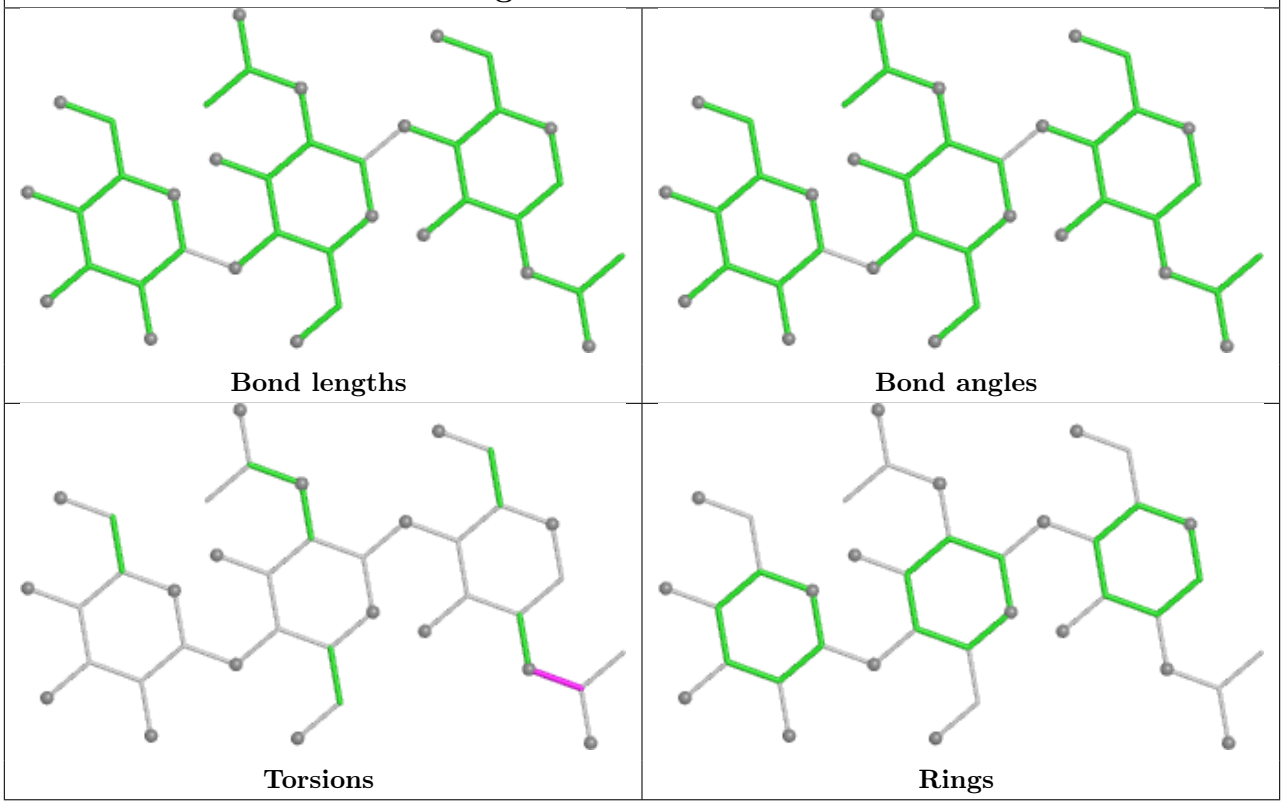


Torsions



Rings

Oligosaccharide Chain O



5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

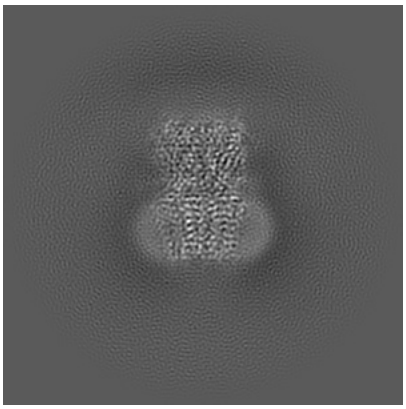
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-63033. These allow visual inspection of the internal detail of the map and identification of artifacts.

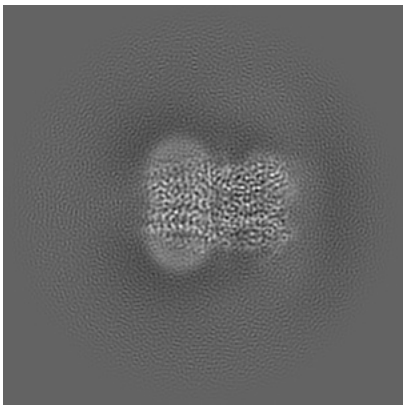
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

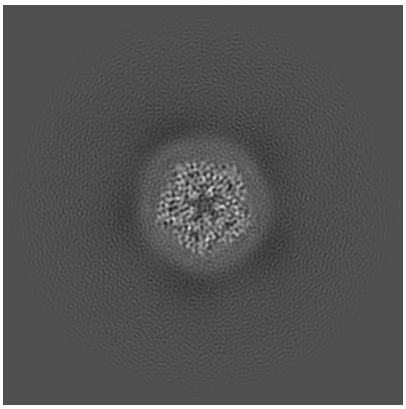
6.1.1 Primary map



X

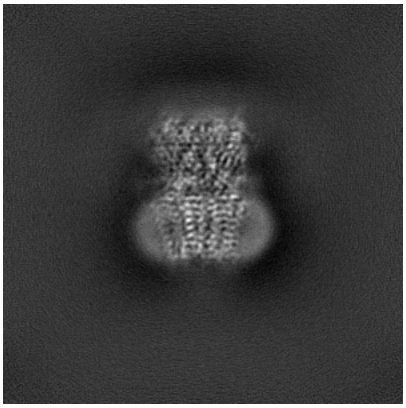


Y

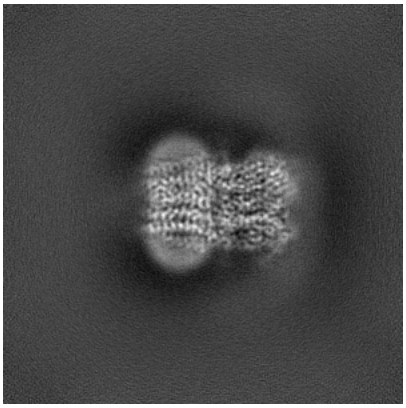


Z

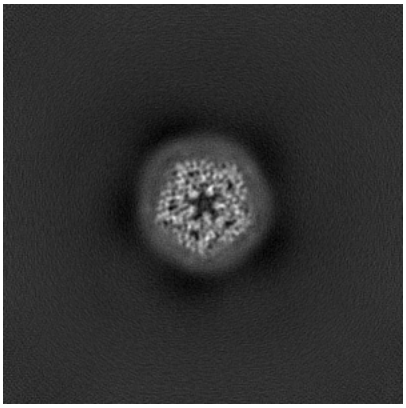
6.1.2 Raw map



X



Y

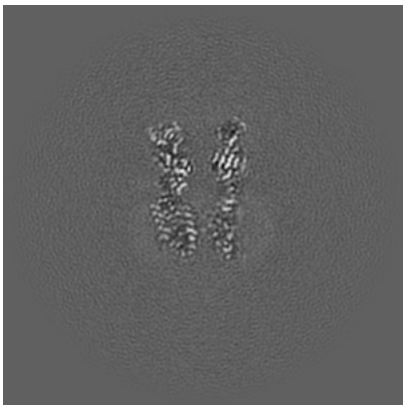


Z

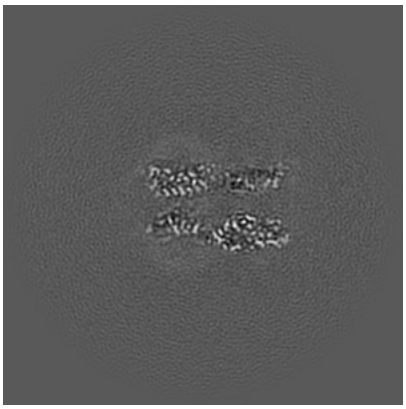
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

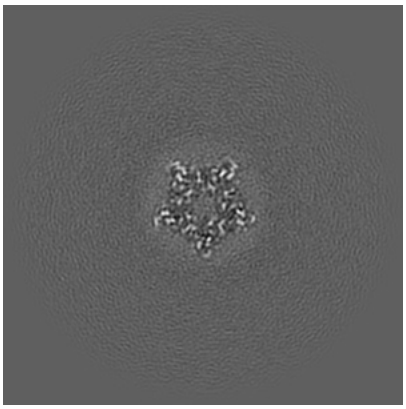
6.2.1 Primary map



X Index: 150

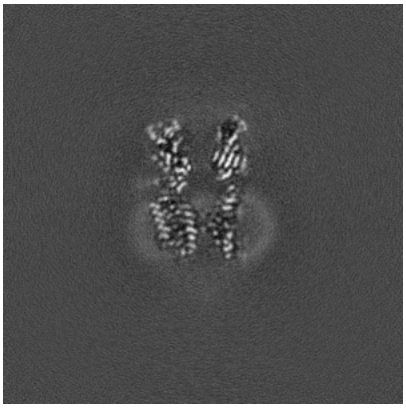


Y Index: 150

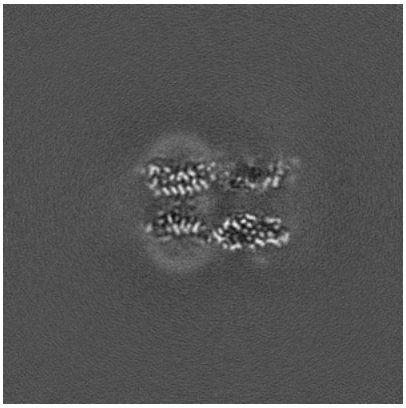


Z Index: 150

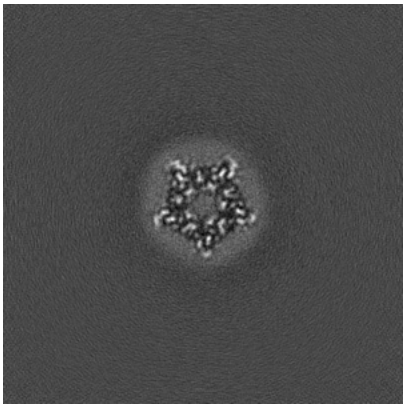
6.2.2 Raw map



X Index: 150



Y Index: 150

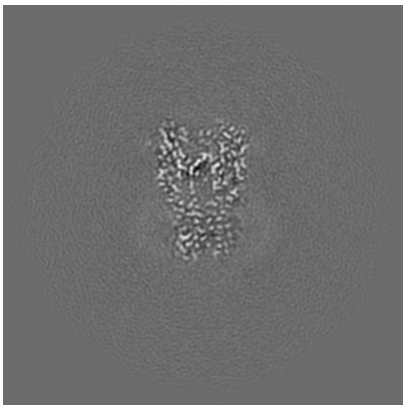


Z Index: 150

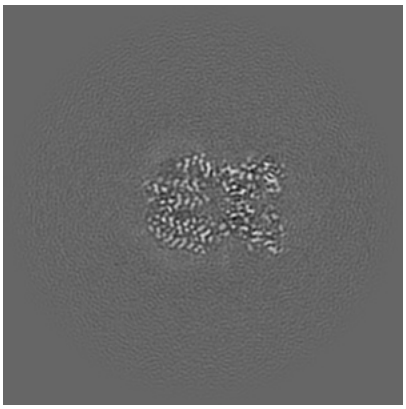
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

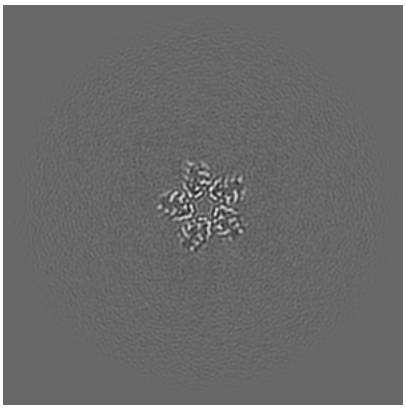
6.3.1 Primary map



X Index: 139

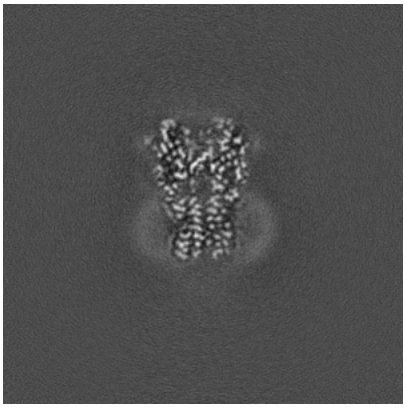


Y Index: 138

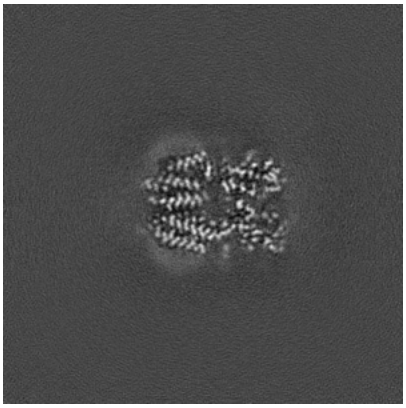


Z Index: 178

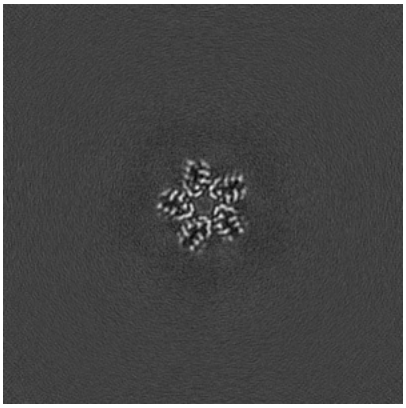
6.3.2 Raw map



X Index: 140



Y Index: 139

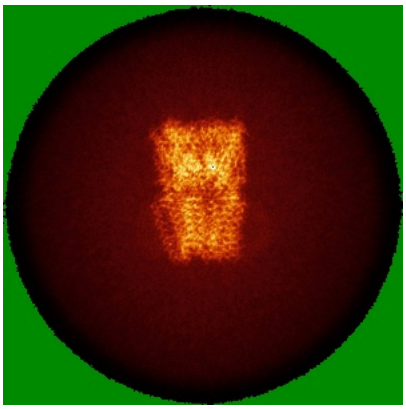


Z Index: 178

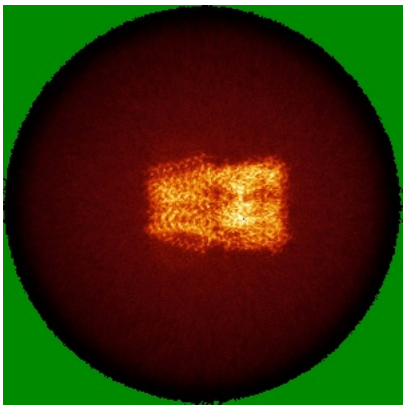
The images above show the largest variance slices of the map in three orthogonal directions.

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

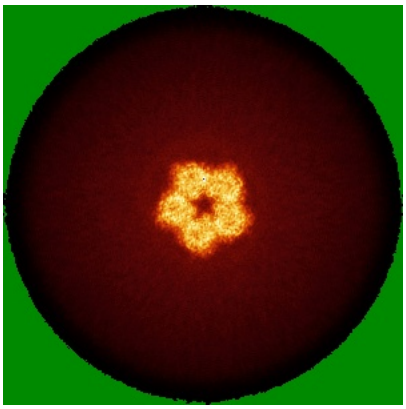
6.4.1 Primary map



X

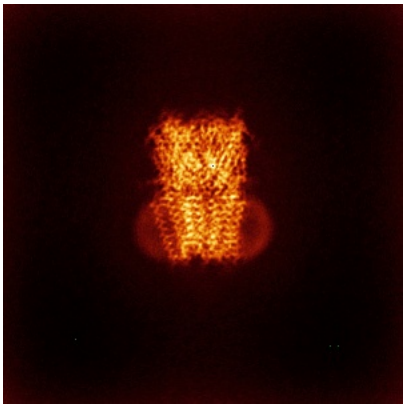


Y

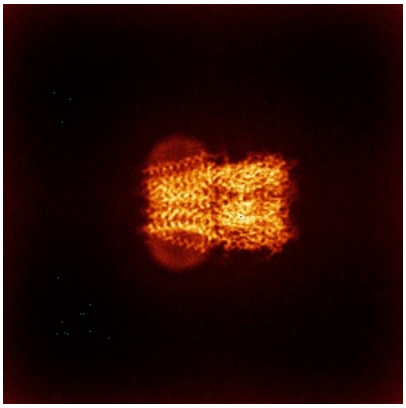


Z

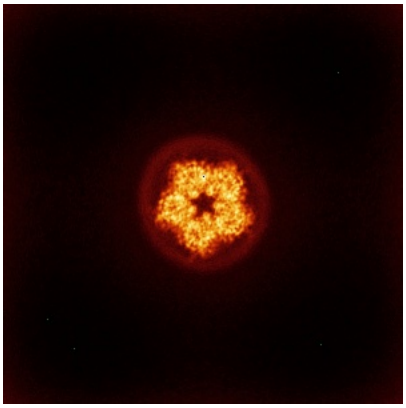
6.4.2 Raw map



X



Y

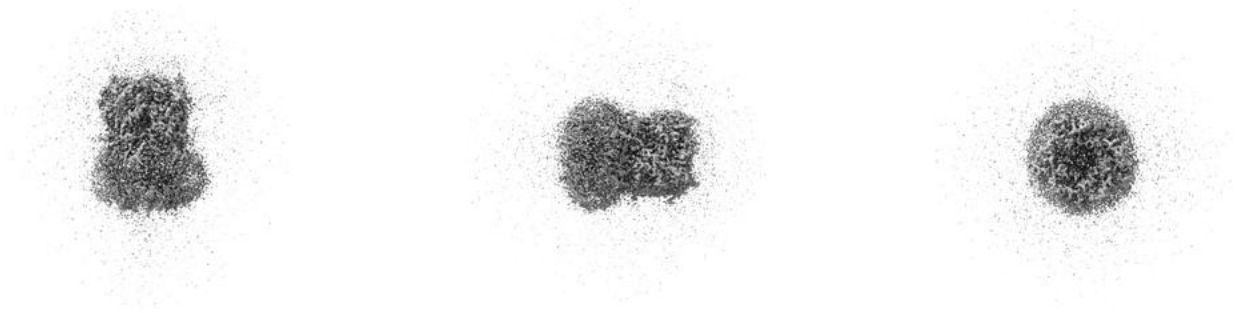


Z

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 0.22. 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.

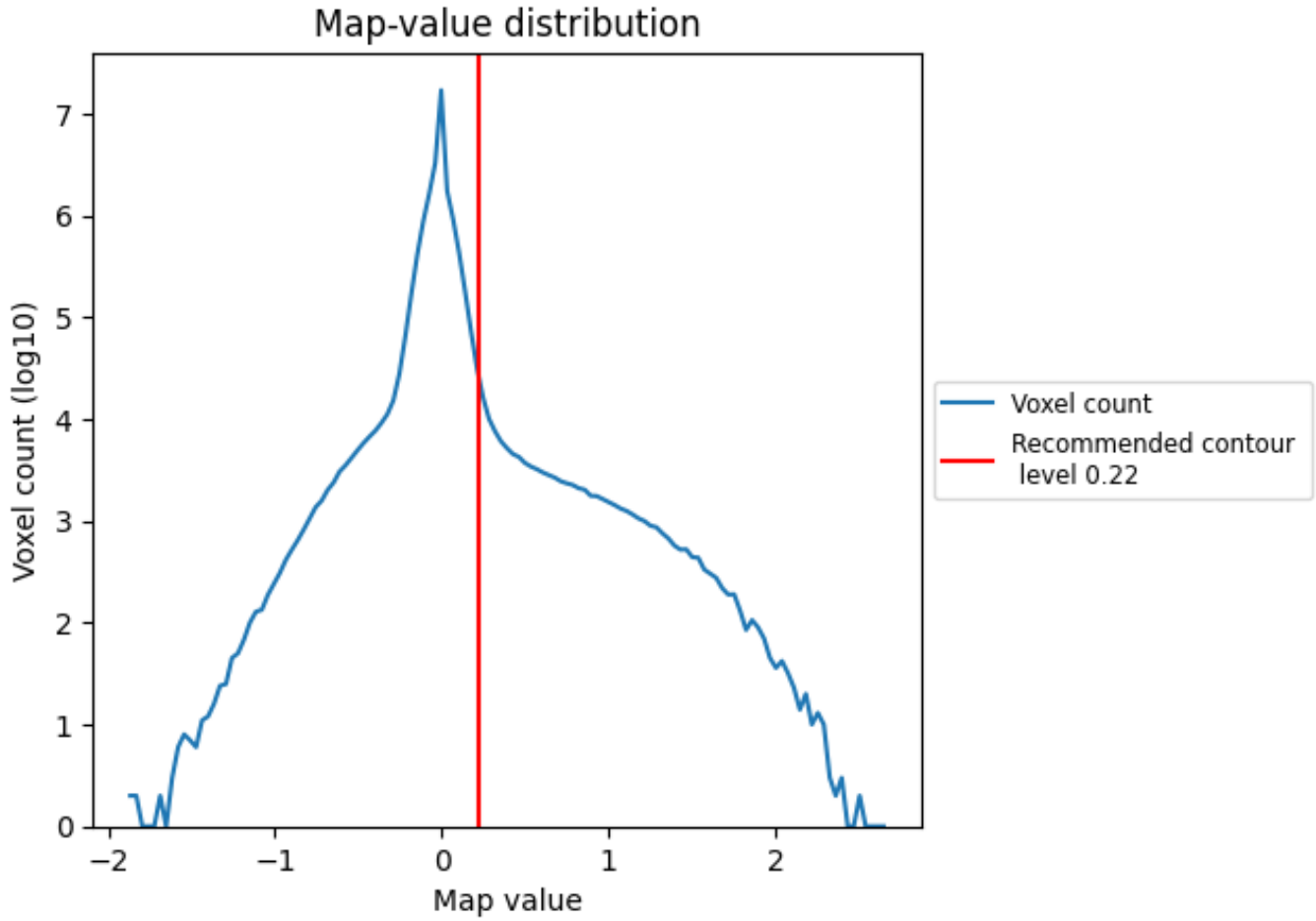
6.6 Mask visualisation (i)

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

7 Map analysis

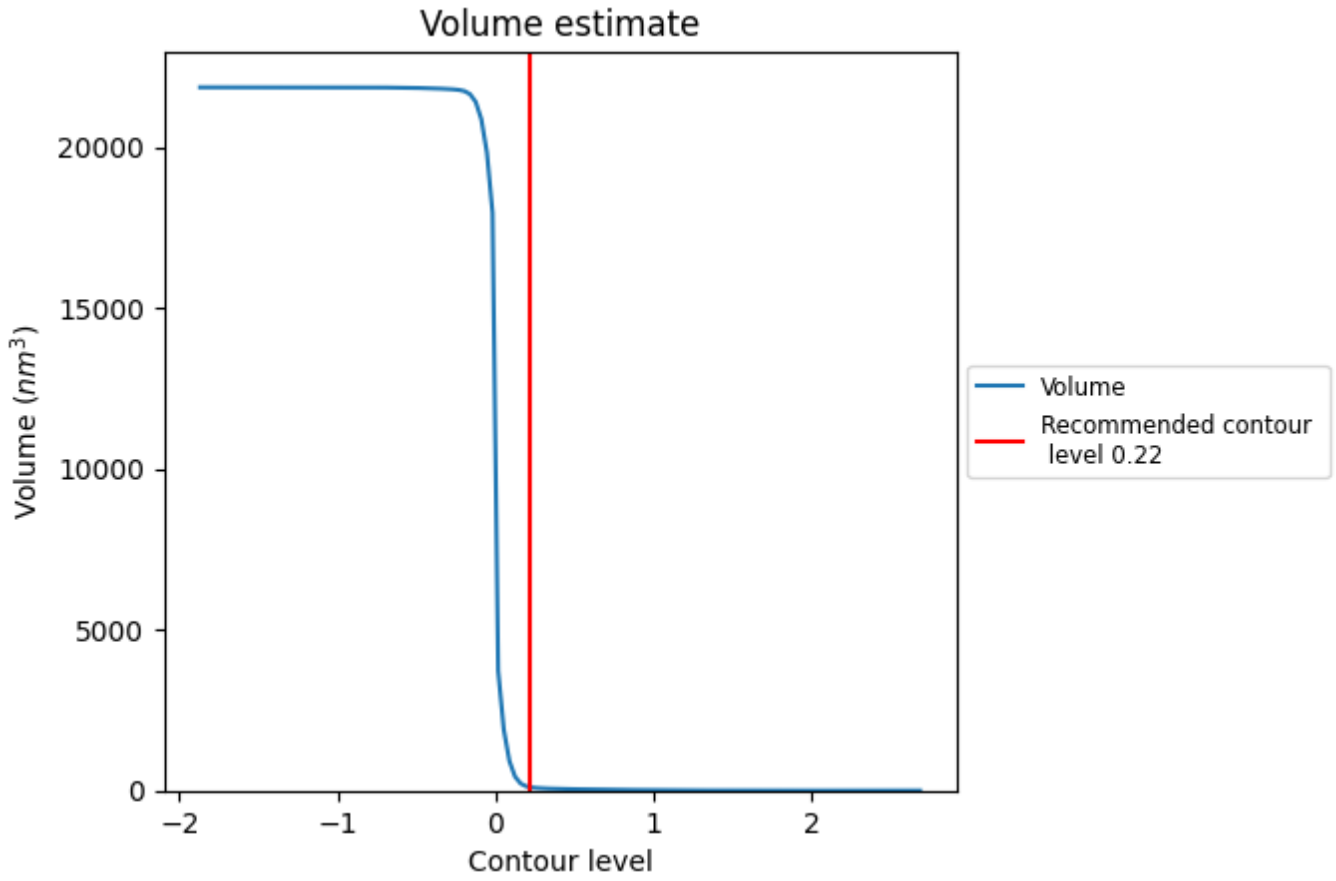
This section contains the results of statistical analysis of the map.

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.

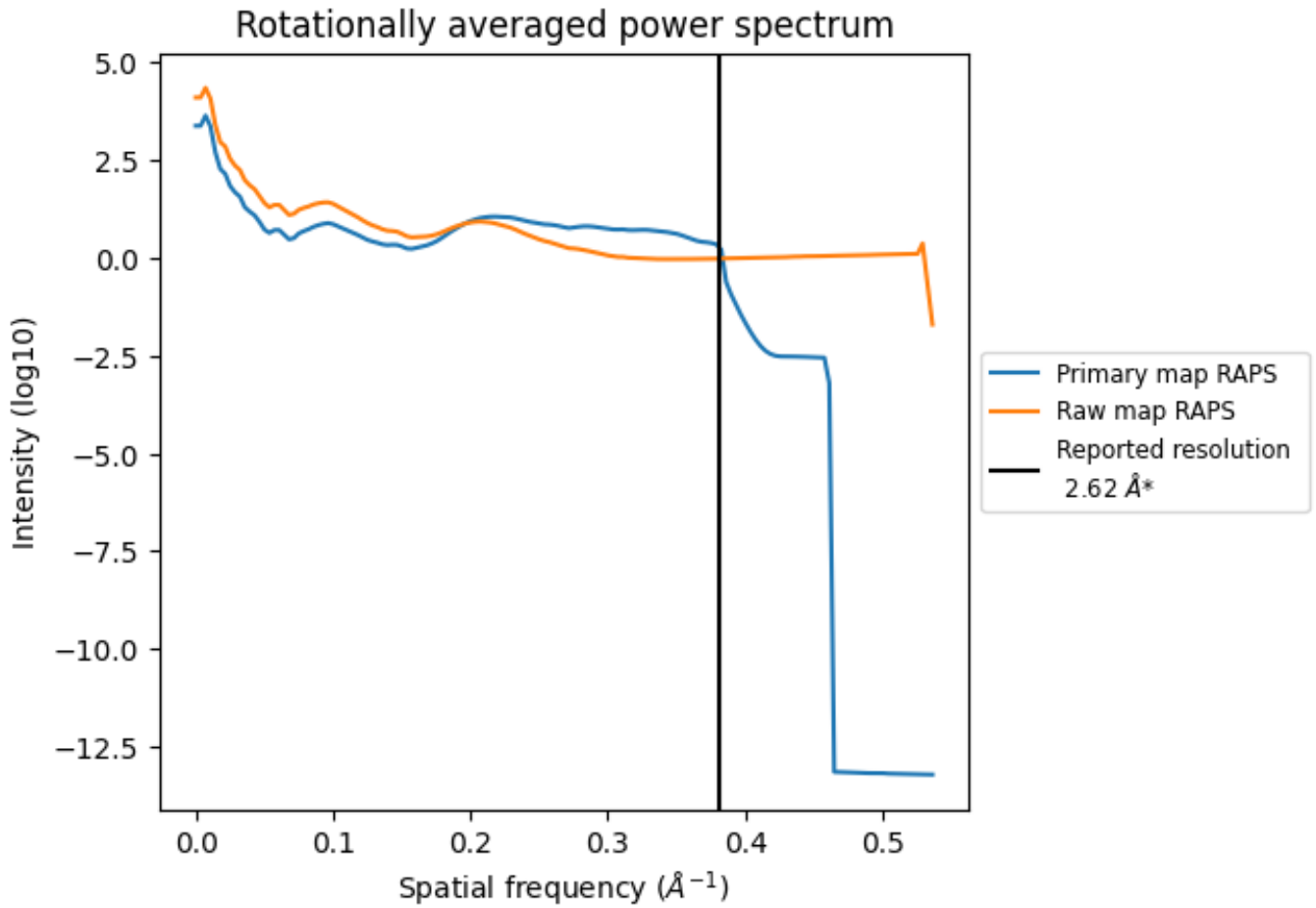
7.2 Volume estimate



The volume at the recommended contour level is 106 nm^3; this corresponds to an approximate mass of 96 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)

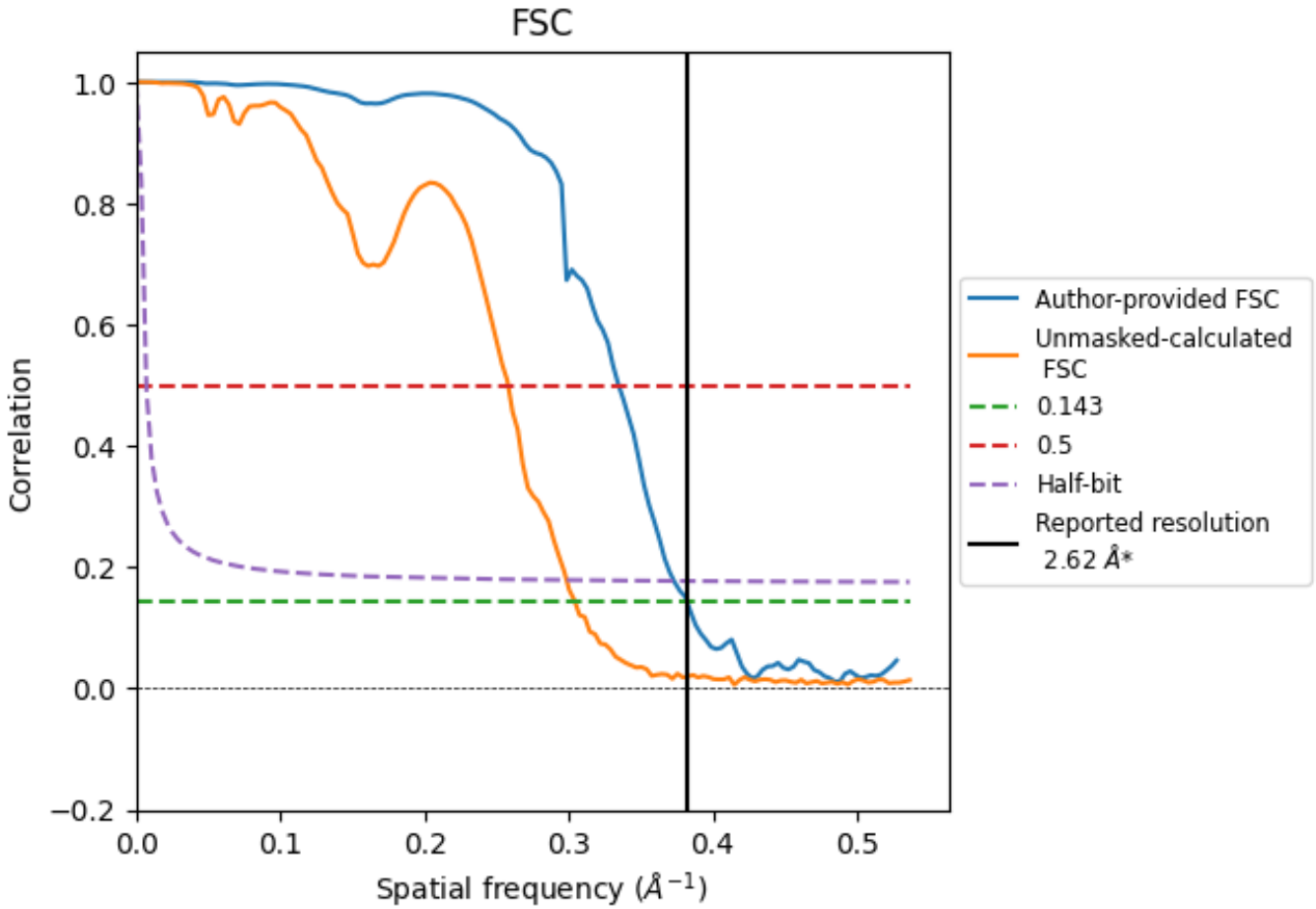


*Reported resolution corresponds to spatial frequency of 0.382 $Å^{-1}$

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 0.382 Å^{-1}

8.2 Resolution estimates (i)

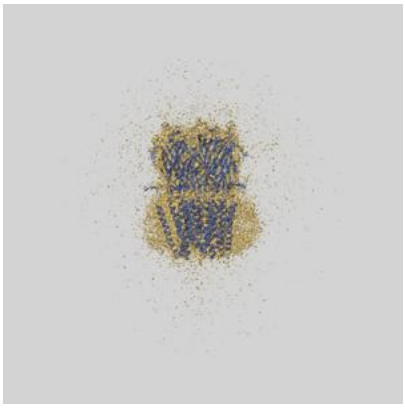
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.62	-	-
Author-provided FSC curve	2.62	2.99	2.68
Unmasked-calculated*	3.29	3.88	3.35

*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 3.29 differs from the reported value 2.62 by more than 10 %

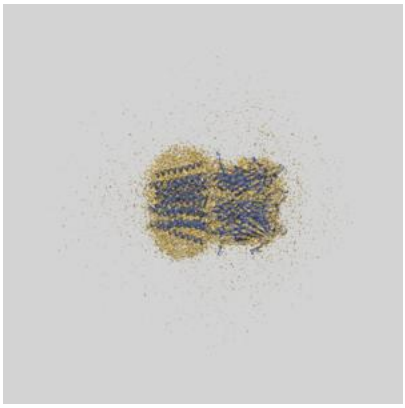
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-63033 and PDB model 9LET. Per-residue inclusion information can be found in section 3 on page 13.

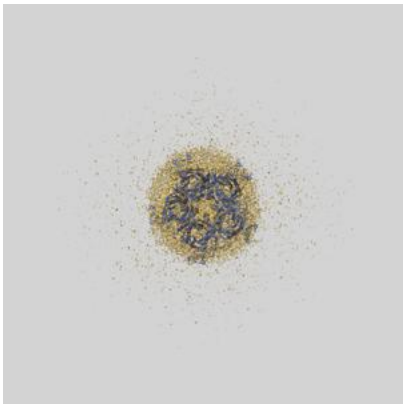
9.1 Map-model overlay



X



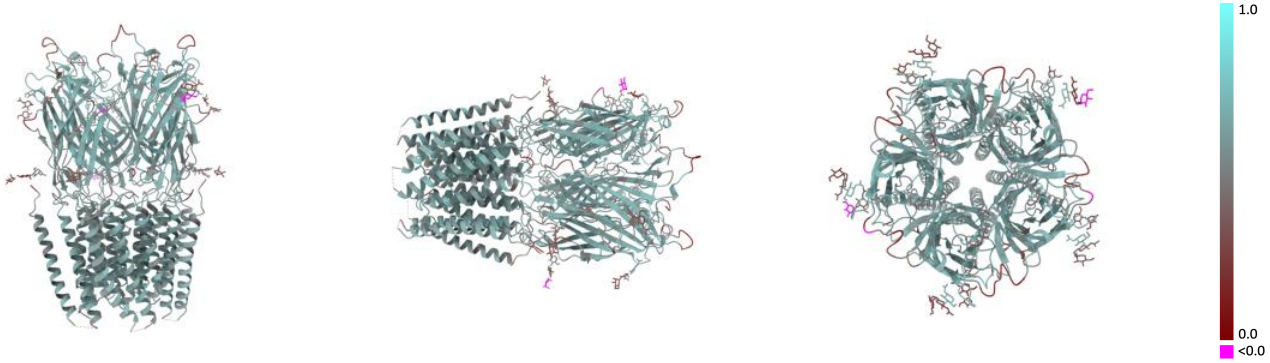
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.22 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.

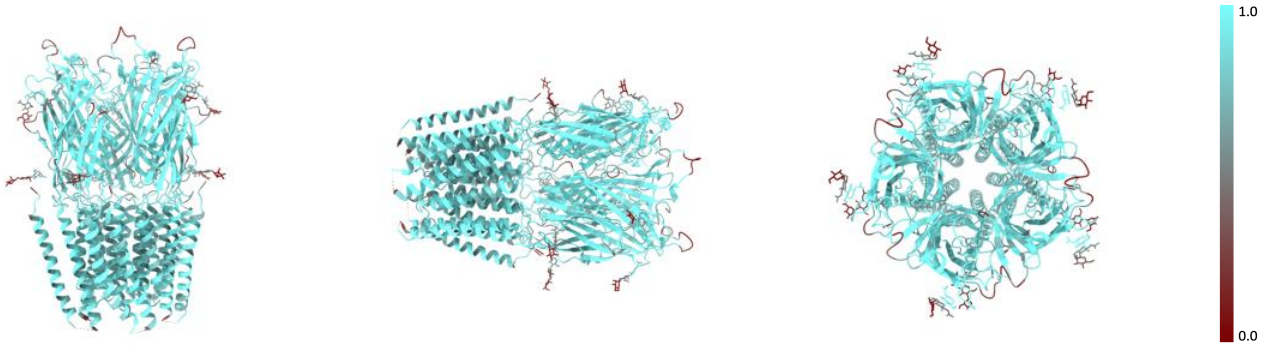
9.2 Q-score mapped to coordinate model (i)



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.

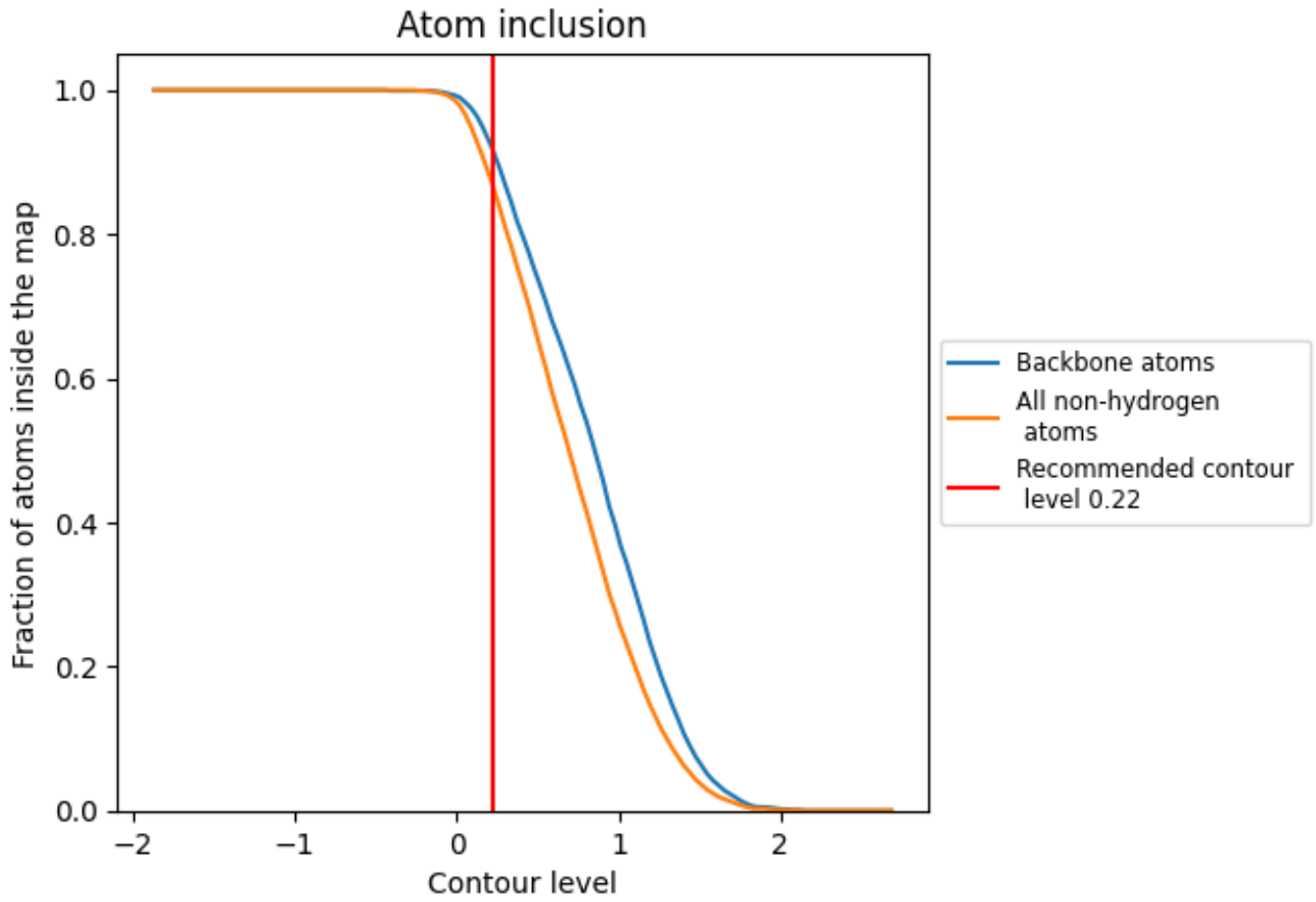
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.22).

9.4 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 87% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8700	0.5710
A	0.8840	0.5820
B	0.8840	0.5750
C	0.8820	0.5740
D	0.8860	0.5760
E	0.8810	0.5780
F	0.4870	0.2910
G	0.4100	0.4440
H	0.4870	0.3750
I	0.4620	0.3790
J	0.6670	0.4780
K	0.3850	0.3710
L	0.5130	0.4080
M	0.3330	0.2510
N	0.4870	0.4280
O	0.3850	0.3090