wwPDB EM Validation Summary Report

Oct 26, 2026 – 02:46 PM EDT

PDB ID	:	9OCN / pdb_00009ocn
EMDB ID	:	EMD-70319
Title	:	PC68_L31_570 Fab in complex with HIV-1 Env BG505 SOSIP.664 and RM20A3 Fab
Authors	:	Ozorowski, G.; Torres, J.L.; Ward, A.B.
Deposited on	:	2025-04-24
Resolution	:	3.00 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:

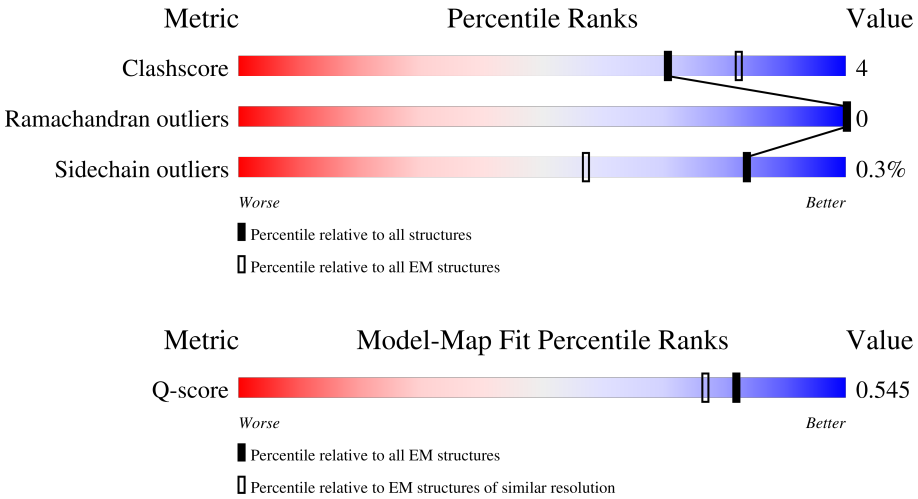
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	516	78% 8% 14%
1	C	516	78% 8% 14%
1	D	516	77% 8% 14%
2	B	153	67% 12% 21%

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Mol	Chain	Length	Quality of chain
2	E	153	67% 12% 21%
2	F	153	67% 12% 21%
3	G	127	86% 13%
3	H	127	86% 13%
3	I	127	86% 13%
4	J	104	8% 95%
4	K	104	9% 95%
4	L	104	8% 95%
5	M	125	90% 9%
5	O	125	90% 9%
5	P	125	90% 9%
6	N	110	93% 6%
6	Q	110	94% 5%
6	R	110	93% 6%
7	S	2	100%
7	U	2	50% 50%
7	V	2	100%
7	W	2	50% 100%
7	Y	2	100%
7	a	2	50% 50%
7	b	2	100%
7	c	2	100%
7	e	2	100%
7	g	2	50% 50%
7	h	2	100%

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Mol	Chain	Length	Quality of chain
7	i	2	50% 100%
8	T	4	50% 50%
8	Z	4	50% 50%
8	f	4	50% 50%
9	X	3	33% 33% 67%
9	d	3	67% 33% 67%
9	j	3	33% 33% 67%

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 24999 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 HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	442	Total	C	N	O	S	0	0
			3485	2189	616	652	28		
1	C	442	Total	C	N	O	S	0	0
			3485	2189	616	652	28		
1	D	442	Total	C	N	O	S	0	0
			3485	2189	616	652	28		

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	MET	-	expression tag	UNP Q2N0S6
A	-3	ASP	-	expression tag	UNP Q2N0S6
A	-2	ALA	-	expression tag	UNP Q2N0S6
A	-1	MET	-	expression tag	UNP Q2N0S6
A	0	LYS	-	expression tag	UNP Q2N0S6
A	1	ARG	-	expression tag	UNP Q2N0S6
A	2	GLY	-	expression tag	UNP Q2N0S6
A	3	LEU	-	expression tag	UNP Q2N0S6
A	4	CYS	-	expression tag	UNP Q2N0S6
A	5	CYS	-	expression tag	UNP Q2N0S6
A	6	VAL	-	expression tag	UNP Q2N0S6
A	7	LEU	-	expression tag	UNP Q2N0S6
A	8	LEU	-	expression tag	UNP Q2N0S6
A	9	LEU	-	expression tag	UNP Q2N0S6
A	10	CYS	-	expression tag	UNP Q2N0S6
A	11	GLY	-	expression tag	UNP Q2N0S6
A	12	ALA	-	expression tag	UNP Q2N0S6
A	13	VAL	-	expression tag	UNP Q2N0S6
A	14	PHE	-	expression tag	UNP Q2N0S6
A	15	VAL	-	expression tag	UNP Q2N0S6
A	16	SER	-	expression tag	UNP Q2N0S6
A	17	PRO	-	expression tag	UNP Q2N0S6
A	18	SER	-	expression tag	UNP Q2N0S6
A	19	GLN	-	expression tag	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	20	GLU	-	expression tag	UNP Q2N0S6
A	21	ILE	-	expression tag	UNP Q2N0S6
A	22	HIS	-	expression tag	UNP Q2N0S6
A	23	ALA	-	expression tag	UNP Q2N0S6
A	24	ARG	-	expression tag	UNP Q2N0S6
A	25	PHE	-	expression tag	UNP Q2N0S6
A	26	ARG	-	expression tag	UNP Q2N0S6
A	27	ARG	-	expression tag	UNP Q2N0S6
A	28	GLY	-	expression tag	UNP Q2N0S6
A	29	ALA	-	expression tag	UNP Q2N0S6
A	30	ARG	-	expression tag	UNP Q2N0S6
A	332	ASN	THR	engineered mutation	UNP Q2N0S6
A	501	CYS	ALA	engineered mutation	UNP Q2N0S6
A	509	ARG	-	expression tag	UNP Q2N0S6
A	510	ARG	-	expression tag	UNP Q2N0S6
A	511	ARG	-	expression tag	UNP Q2N0S6
A	512	ARG	-	expression tag	UNP Q2N0S6
A	513	ARG	-	expression tag	UNP Q2N0S6
C	-4	MET	-	expression tag	UNP Q2N0S6
C	-3	ASP	-	expression tag	UNP Q2N0S6
C	-2	ALA	-	expression tag	UNP Q2N0S6
C	-1	MET	-	expression tag	UNP Q2N0S6
C	0	LYS	-	expression tag	UNP Q2N0S6
C	1	ARG	-	expression tag	UNP Q2N0S6
C	2	GLY	-	expression tag	UNP Q2N0S6
C	3	LEU	-	expression tag	UNP Q2N0S6
C	4	CYS	-	expression tag	UNP Q2N0S6
C	5	CYS	-	expression tag	UNP Q2N0S6
C	6	VAL	-	expression tag	UNP Q2N0S6
C	7	LEU	-	expression tag	UNP Q2N0S6
C	8	LEU	-	expression tag	UNP Q2N0S6
C	9	LEU	-	expression tag	UNP Q2N0S6
C	10	CYS	-	expression tag	UNP Q2N0S6
C	11	GLY	-	expression tag	UNP Q2N0S6
C	12	ALA	-	expression tag	UNP Q2N0S6
C	13	VAL	-	expression tag	UNP Q2N0S6
C	14	PHE	-	expression tag	UNP Q2N0S6
C	15	VAL	-	expression tag	UNP Q2N0S6
C	16	SER	-	expression tag	UNP Q2N0S6
C	17	PRO	-	expression tag	UNP Q2N0S6
C	18	SER	-	expression tag	UNP Q2N0S6
C	19	GLN	-	expression tag	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	20	GLU	-	expression tag	UNP Q2N0S6
C	21	ILE	-	expression tag	UNP Q2N0S6
C	22	HIS	-	expression tag	UNP Q2N0S6
C	23	ALA	-	expression tag	UNP Q2N0S6
C	24	ARG	-	expression tag	UNP Q2N0S6
C	25	PHE	-	expression tag	UNP Q2N0S6
C	26	ARG	-	expression tag	UNP Q2N0S6
C	27	ARG	-	expression tag	UNP Q2N0S6
C	28	GLY	-	expression tag	UNP Q2N0S6
C	29	ALA	-	expression tag	UNP Q2N0S6
C	30	ARG	-	expression tag	UNP Q2N0S6
C	332	ASN	THR	engineered mutation	UNP Q2N0S6
C	501	CYS	ALA	engineered mutation	UNP Q2N0S6
C	509	ARG	-	expression tag	UNP Q2N0S6
C	510	ARG	-	expression tag	UNP Q2N0S6
C	511	ARG	-	expression tag	UNP Q2N0S6
C	512	ARG	-	expression tag	UNP Q2N0S6
C	513	ARG	-	expression tag	UNP Q2N0S6
D	-4	MET	-	expression tag	UNP Q2N0S6
D	-3	ASP	-	expression tag	UNP Q2N0S6
D	-2	ALA	-	expression tag	UNP Q2N0S6
D	-1	MET	-	expression tag	UNP Q2N0S6
D	0	LYS	-	expression tag	UNP Q2N0S6
D	1	ARG	-	expression tag	UNP Q2N0S6
D	2	GLY	-	expression tag	UNP Q2N0S6
D	3	LEU	-	expression tag	UNP Q2N0S6
D	4	CYS	-	expression tag	UNP Q2N0S6
D	5	CYS	-	expression tag	UNP Q2N0S6
D	6	VAL	-	expression tag	UNP Q2N0S6
D	7	LEU	-	expression tag	UNP Q2N0S6
D	8	LEU	-	expression tag	UNP Q2N0S6
D	9	LEU	-	expression tag	UNP Q2N0S6
D	10	CYS	-	expression tag	UNP Q2N0S6
D	11	GLY	-	expression tag	UNP Q2N0S6
D	12	ALA	-	expression tag	UNP Q2N0S6
D	13	VAL	-	expression tag	UNP Q2N0S6
D	14	PHE	-	expression tag	UNP Q2N0S6
D	15	VAL	-	expression tag	UNP Q2N0S6
D	16	SER	-	expression tag	UNP Q2N0S6
D	17	PRO	-	expression tag	UNP Q2N0S6
D	18	SER	-	expression tag	UNP Q2N0S6
D	19	GLN	-	expression tag	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	20	GLU	-	expression tag	UNP Q2N0S6
D	21	ILE	-	expression tag	UNP Q2N0S6
D	22	HIS	-	expression tag	UNP Q2N0S6
D	23	ALA	-	expression tag	UNP Q2N0S6
D	24	ARG	-	expression tag	UNP Q2N0S6
D	25	PHE	-	expression tag	UNP Q2N0S6
D	26	ARG	-	expression tag	UNP Q2N0S6
D	27	ARG	-	expression tag	UNP Q2N0S6
D	28	GLY	-	expression tag	UNP Q2N0S6
D	29	ALA	-	expression tag	UNP Q2N0S6
D	30	ARG	-	expression tag	UNP Q2N0S6
D	332	ASN	THR	engineered mutation	UNP Q2N0S6
D	501	CYS	ALA	engineered mutation	UNP Q2N0S6
D	509	ARG	-	expression tag	UNP Q2N0S6
D	510	ARG	-	expression tag	UNP Q2N0S6
D	511	ARG	-	expression tag	UNP Q2N0S6
D	512	ARG	-	expression tag	UNP Q2N0S6
D	513	ARG	-	expression tag	UNP Q2N0S6

- Molecule 2 is a protein called Transmembrane protein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	121	Total	C	N	O	S	0	0
			964	607	167	184	6		
2	E	121	Total	C	N	O	S	0	0
			964	607	167	184	6		
2	F	121	Total	C	N	O	S	0	0
			964	607	167	184	6		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	engineered mutation	UNP Q2N0S5
B	605	CYS	THR	engineered mutation	UNP Q2N0S5
E	559	PRO	ILE	engineered mutation	UNP Q2N0S5
E	605	CYS	THR	engineered mutation	UNP Q2N0S5
F	559	PRO	ILE	engineered mutation	UNP Q2N0S5
F	605	CYS	THR	engineered mutation	UNP Q2N0S5

- Molecule 3 is a protein called PC68_L31_570 heavy chain Fv.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	125	Total	C	N	O	S	0	0
			988	629	174	181	4		
3	G	125	Total	C	N	O	S	0	0
			988	629	174	181	4		
3	I	125	Total	C	N	O	S	0	0
			988	629	174	181	4		

- Molecule 4 is a protein called PC68_L31_570 light chain Fv.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	103	Total	C	N	O	S	0	0
			753	463	140	147	3		
4	J	103	Total	C	N	O	S	0	0
			753	463	140	147	3		
4	K	103	Total	C	N	O	S	0	0
			753	463	140	147	3		

- Molecule 5 is a protein called RM20A3 heavy chain Fv.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	123	Total	C	N	O	S	0	0
			937	592	160	180	5		
5	O	123	Total	C	N	O	S	0	0
			937	592	160	180	5		
5	P	123	Total	C	N	O	S	0	0
			937	592	160	180	5		

- Molecule 6 is a protein called RM20A3 light chain Fv.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	109	Total	C	N	O	S	0	0
			809	502	136	168	3		
6	Q	109	Total	C	N	O	S	0	0
			809	502	136	168	3		
6	R	109	Total	C	N	O	S	0	0
			809	502	136	168	3		

- Molecule 7 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



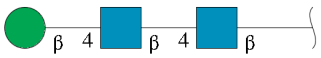
Mol	Chain	Residues	Atoms				AltConf	Trace
7	S	2	Total	C	N	O	0	0
			28	16	2	10		
7	U	2	Total	C	N	O	0	0
			28	16	2	10		
7	V	2	Total	C	N	O	0	0
			28	16	2	10		
7	W	2	Total	C	N	O	0	0
			28	16	2	10		
7	Y	2	Total	C	N	O	0	0
			28	16	2	10		
7	a	2	Total	C	N	O	0	0
			28	16	2	10		
7	b	2	Total	C	N	O	0	0
			28	16	2	10		
7	c	2	Total	C	N	O	0	0
			28	16	2	10		
7	e	2	Total	C	N	O	0	0
			28	16	2	10		
7	g	2	Total	C	N	O	0	0
			28	16	2	10		
7	h	2	Total	C	N	O	0	0
			28	16	2	10		
7	i	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



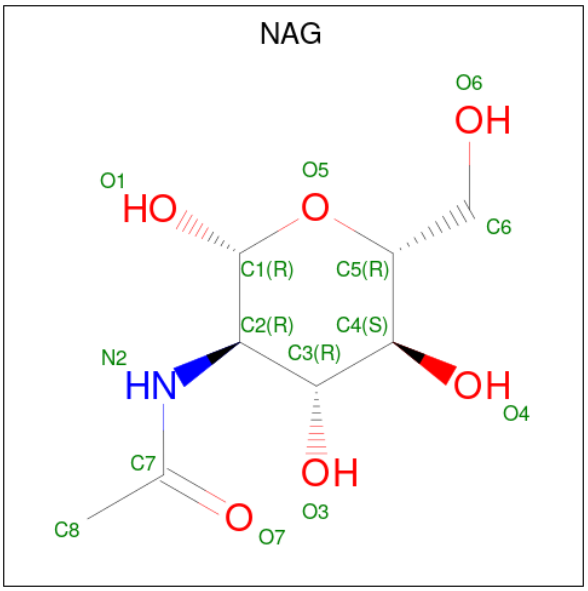
Mol	Chain	Residues	Atoms				AltConf	Trace
8	T	4	Total	C	N	O	0	0
			50	28	2	20		
8	Z	4	Total	C	N	O	0	0
			50	28	2	20		
8	f	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 9 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
9	X	3	Total C N O 39 22 2 15	0	0
9	d	3	Total C N O 39 22 2 15	0	0
9	j	3	Total C N O 39 22 2 15	0	0

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	AltConf
10	A	1	Total C N O 14 8 1 5	0
10	A	1	Total C N O 14 8 1 5	0
10	A	1	Total C N O 14 8 1 5	0
10	A	1	Total C N O 14 8 1 5	0
10	A	1	Total C N O 14 8 1 5	0
10	A	1	Total C N O 14 8 1 5	0

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Mol	Chain	Residues	Atoms				AltConf
10	A	1	Total	C	N	O	0
			14	8	1	5	
10	A	1	Total	C	N	O	0
			14	8	1	5	
10	A	1	Total	C	N	O	0
			14	8	1	5	
10	A	1	Total	C	N	O	0
			14	8	1	5	
10	A	1	Total	C	N	O	0
			14	8	1	5	
10	B	1	Total	C	N	O	0
			14	8	1	5	
10	B	1	Total	C	N	O	0
			14	8	1	5	
10	B	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	C	1	Total	C	N	O	0
			14	8	1	5	
10	E	1	Total	C	N	O	0
			14	8	1	5	
10	E	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
10	E	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	D	1	Total	C	N	O	0
			14	8	1	5	
10	F	1	Total	C	N	O	0
			14	8	1	5	
10	F	1	Total	C	N	O	0
			14	8	1	5	
10	F	1	Total	C	N	O	0
			14	8	1	5	

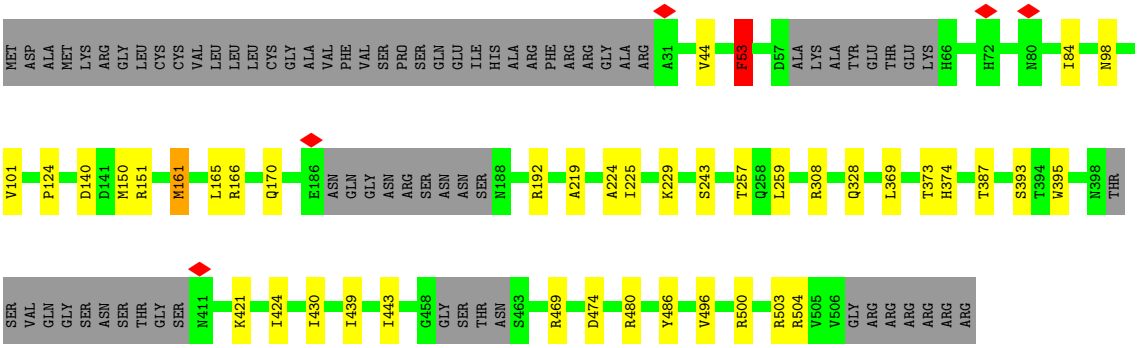
3 Residue-property plots (i)

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: HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp120

Chain A:

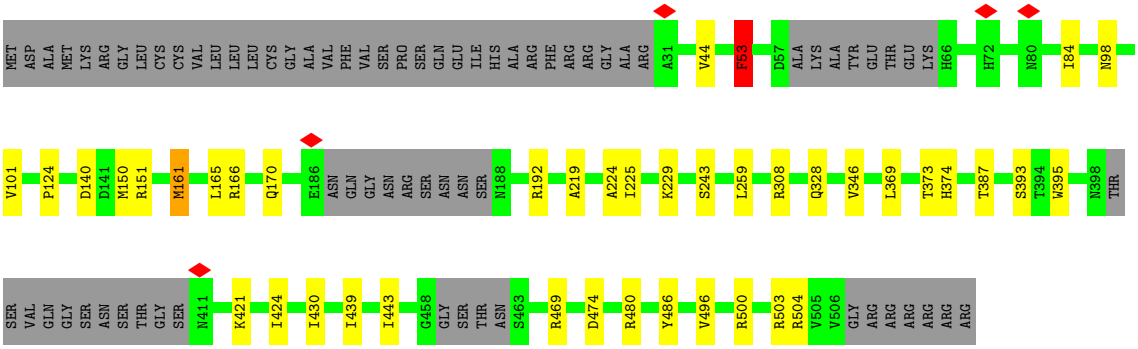




• Molecule 1: HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp120

Chain C:



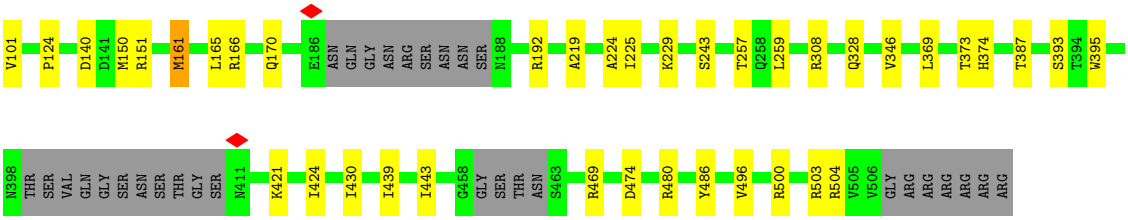


• Molecule 1: HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp120

Chain D:



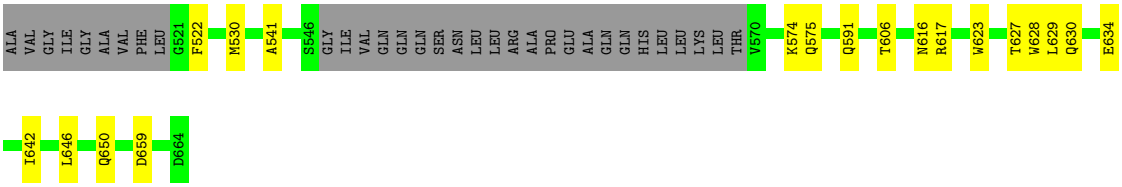




• Molecule 2: Transmembrane protein gp41

Chain B:

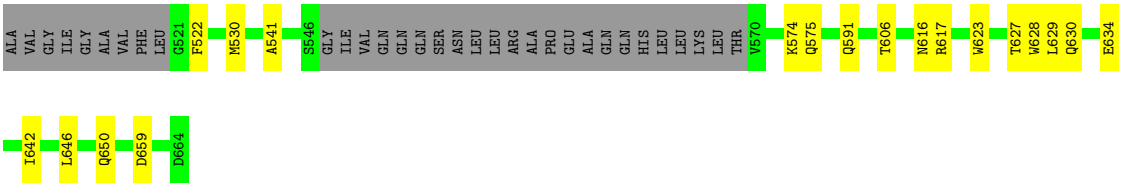




• Molecule 2: Transmembrane protein gp41

Chain E:

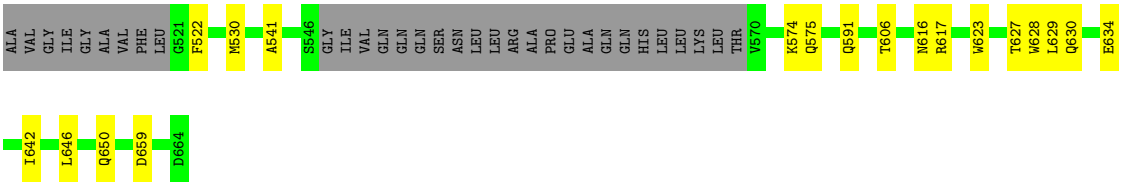




• Molecule 2: Transmembrane protein gp41

Chain F:

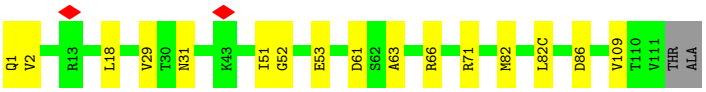




• Molecule 3: PC68_L31_570 heavy chain Fv

Chain H:

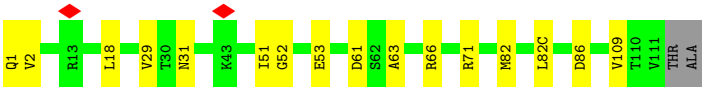




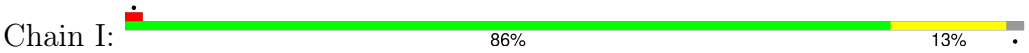
• Molecule 3: PC68_L31_570 heavy chain Fv

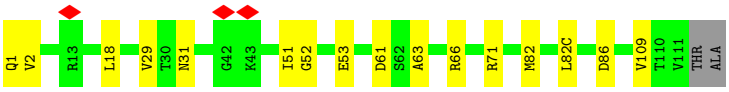
Chain G:



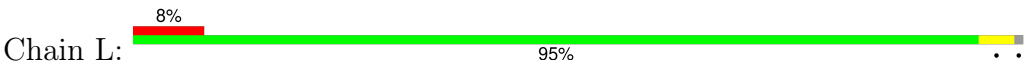


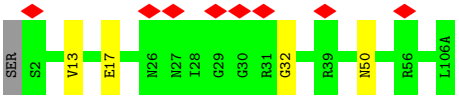
• Molecule 3: PC68_L31_570 heavy chain Fv



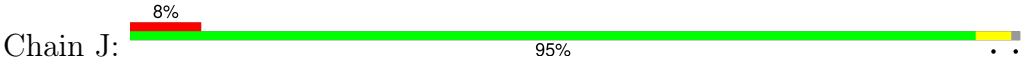


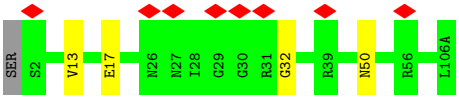
• Molecule 4: PC68_L31_570 light chain Fv



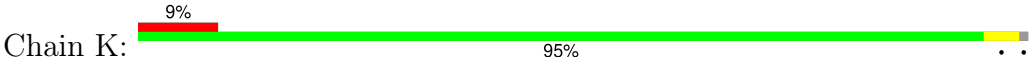


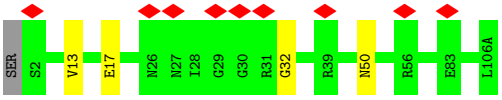
• Molecule 4: PC68_L31_570 light chain Fv



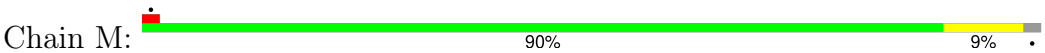


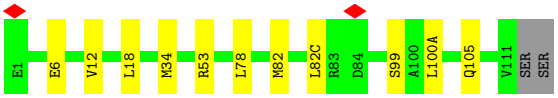
• Molecule 4: PC68_L31_570 light chain Fv



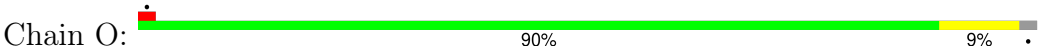


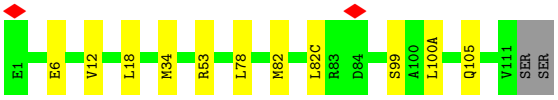
• Molecule 5: RM20A3 heavy chain Fv





• Molecule 5: RM20A3 heavy chain Fv

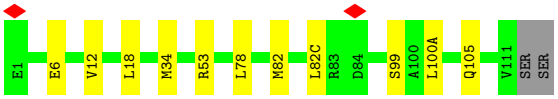




• Molecule 5: RM20A3 heavy chain Fv

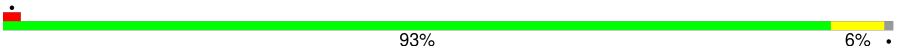
Chain P:

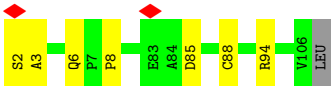




• Molecule 6: RM20A3 light chain Fv

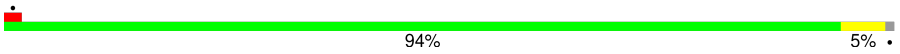
Chain N:

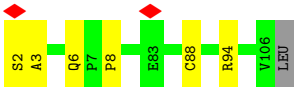




• Molecule 6: RM20A3 light chain Fv

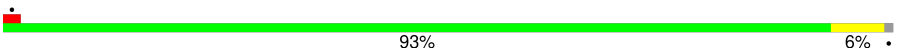
Chain Q:

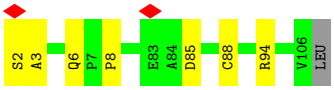




• Molecule 6: RM20A3 light chain Fv

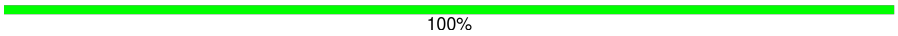
Chain R:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

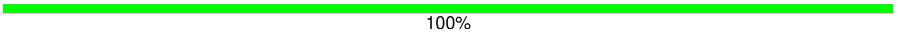
Chain U:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

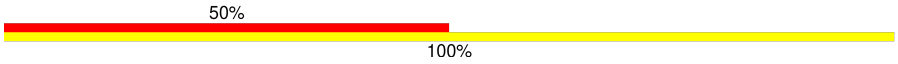
Chain V:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

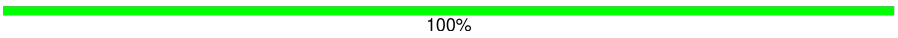
Chain a:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

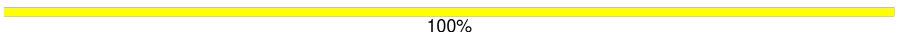
Chain b:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

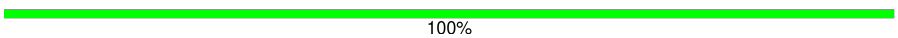
Chain c:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain e:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain g:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

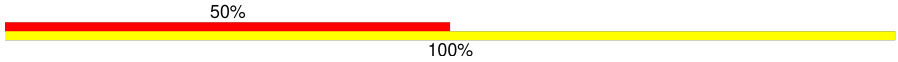
Chain h:





• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain i:





• Molecule 8: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:





• Molecule 8: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:





• Molecule 8: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain f:





• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X:





• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d:





• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain j:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	71955	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	43	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.414	Depositor
Minimum map value	-0.880	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	417.6, 417.6, 417.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.044, 1.044, 1.044	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, 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	0.38	0/3556	0.83	5/4827 (0.1%)
1	C	0.38	0/3556	0.83	5/4827 (0.1%)
1	D	0.38	0/3556	0.83	5/4827 (0.1%)
2	B	0.41	0/981	0.78	1/1330 (0.1%)
2	E	0.42	0/981	0.78	1/1330 (0.1%)
2	F	0.41	0/981	0.78	1/1330 (0.1%)
3	G	0.37	0/1018	0.81	0/1379
3	H	0.37	0/1018	0.81	0/1379
3	I	0.37	0/1018	0.81	0/1379
4	J	0.37	0/769	0.78	0/1050
4	K	0.37	0/769	0.78	0/1050
4	L	0.36	0/769	0.78	0/1050
5	M	0.33	0/957	0.79	0/1292
5	O	0.33	0/957	0.79	0/1292
5	P	0.33	0/957	0.79	0/1292
6	N	1.14	1/828 (0.1%)	0.93	1/1126 (0.1%)
6	Q	1.14	1/828 (0.1%)	0.93	1/1126 (0.1%)
6	R	1.14	1/828 (0.1%)	0.93	1/1126 (0.1%)
All	All	0.51	3/24327 (0.0%)	0.83	21/33012 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	N	8	PRO	N-CD	-30.35	1.05	1.47
6	Q	8	PRO	N-CD	-30.35	1.05	1.47
6	R	8	PRO	N-CD	-30.32	1.05	1.47

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	53	PHE	CA-CB-CG	9.01	122.81	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	53	PHE	CA-CB-CG	8.99	122.79	113.80
1	A	53	PHE	CA-CB-CG	8.98	122.78	113.80
6	Q	8	PRO	N-CD-CG	7.07	113.81	103.20
6	R	8	PRO	N-CD-CG	7.06	113.79	103.20

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	3485	0	3418	37	0
1	C	3485	0	3418	37	0
1	D	3485	0	3418	38	0
2	B	964	0	936	19	0
2	E	964	0	936	19	0
2	F	964	0	936	19	0
3	G	988	0	932	11	0
3	H	988	0	932	11	0
3	I	988	0	932	11	0
4	J	753	0	729	2	0
4	K	753	0	729	2	0
4	L	753	0	729	2	0
5	M	937	0	910	7	0
5	O	937	0	910	7	0
5	P	937	0	910	7	0
6	N	809	0	761	6	0
6	Q	809	0	761	5	0
6	R	809	0	761	6	0
7	S	28	0	25	0	0
7	U	28	0	25	0	0
7	V	28	0	25	0	0
7	W	28	0	25	0	0
7	Y	28	0	25	0	0
7	a	28	0	25	0	0
7	b	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	c	28	0	25	0	0
7	e	28	0	25	0	0
7	g	28	0	25	0	0
7	h	28	0	25	0	0
7	i	28	0	25	0	0
8	T	50	0	43	0	0
8	Z	50	0	43	0	0
8	f	50	0	43	0	0
9	X	39	0	34	0	0
9	d	39	0	34	0	0
9	j	39	0	34	0	0
10	A	154	0	143	0	0
10	B	42	0	39	0	0
10	C	154	0	143	0	0
10	D	154	0	143	0	0
10	E	42	0	39	0	0
10	F	42	0	39	0	0
All	All	24999	0	24135	174	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 4.

The worst 5 of 174 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:A:504:ARG:HH12	6:N:94:ARG:HH12	1.31	0.79
1:D:504:ARG:HH12	6:R:94:ARG:HH12	1.31	0.78
1:C:504:ARG:HH12	6:Q:94:ARG:HH12	1.31	0.78
1:C:53:PHE:HB2	2:E:575:GLN:HE22	1.54	0.73
1:A:53:PHE:HB2	2:B:575:GLN:HE22	1.54	0.72

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	432/516 (84%)	420 (97%)	12 (3%)	0	100	100
1	C	432/516 (84%)	420 (97%)	12 (3%)	0	100	100
1	D	432/516 (84%)	420 (97%)	12 (3%)	0	100	100
2	B	117/153 (76%)	117 (100%)	0	0	100	100
2	E	117/153 (76%)	117 (100%)	0	0	100	100
2	F	117/153 (76%)	117 (100%)	0	0	100	100
3	G	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
3	H	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
3	I	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
4	J	101/104 (97%)	101 (100%)	0	0	100	100
4	K	101/104 (97%)	101 (100%)	0	0	100	100
4	L	101/104 (97%)	101 (100%)	0	0	100	100
5	M	121/125 (97%)	119 (98%)	2 (2%)	0	100	100
5	O	121/125 (97%)	119 (98%)	2 (2%)	0	100	100
5	P	121/125 (97%)	119 (98%)	2 (2%)	0	100	100
6	N	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
6	Q	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
6	R	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
All	All	3003/3405 (88%)	2940 (98%)	63 (2%)	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	396/456 (87%)	394 (100%)	2 (0%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	396/456 (87%)	394 (100%)	2 (0%)	81 89
1	D	396/456 (87%)	394 (100%)	2 (0%)	81 89
2	B	104/129 (81%)	104 (100%)	0	100 100
2	E	104/129 (81%)	104 (100%)	0	100 100
2	F	104/129 (81%)	104 (100%)	0	100 100
3	G	102/103 (99%)	101 (99%)	1 (1%)	68 84
3	H	102/103 (99%)	101 (99%)	1 (1%)	68 84
3	I	102/103 (99%)	101 (99%)	1 (1%)	68 84
4	J	80/81 (99%)	80 (100%)	0	100 100
4	K	80/81 (99%)	80 (100%)	0	100 100
4	L	80/81 (99%)	80 (100%)	0	100 100
5	M	100/102 (98%)	100 (100%)	0	100 100
5	O	100/102 (98%)	100 (100%)	0	100 100
5	P	100/102 (98%)	100 (100%)	0	100 100
6	N	89/90 (99%)	89 (100%)	0	100 100
6	Q	89/90 (99%)	89 (100%)	0	100 100
6	R	89/90 (99%)	89 (100%)	0	100 100
All	All	2613/2883 (91%)	2604 (100%)	9 (0%)	84 91

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	387	THR
3	I	2	VAL
1	C	53	PHE
1	C	387	THR
3	G	2	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	32	HIS
3	I	58	HIS
6	R	37	GLN
1	C	258	GLN

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Mol	Chain	Res	Type
1	C	170	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)

45 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	$\#\|Z\| > 2$
7	NAG	S	1	1,7	14,14,15	0.43	0	17,19,21	0.63	0
7	NAG	S	2	7	14,14,15	0.30	0	17,19,21	0.60	0
8	NAG	T	1	1,8	14,14,15	0.38	0	17,19,21	0.68	0
8	NAG	T	2	8	14,14,15	0.43	0	17,19,21	0.75	0
8	BMA	T	3	8	11,11,12	1.07	1 (9%)	15,15,17	0.84	1 (6%)
8	MAN	T	4	8	11,11,12	1.09	2 (18%)	15,15,17	1.09	2 (13%)
7	NAG	U	1	1,7	14,14,15	0.34	0	17,19,21	0.81	1 (5%)
7	NAG	U	2	7	14,14,15	0.61	0	17,19,21	0.54	0
7	NAG	V	1	1,7	14,14,15	0.33	0	17,19,21	0.76	0
7	NAG	V	2	7	14,14,15	0.28	0	17,19,21	0.67	0
7	NAG	W	1	1,7	14,14,15	0.56	0	17,19,21	1.20	2 (11%)
7	NAG	W	2	7	14,14,15	0.87	1 (7%)	17,19,21	1.10	2 (11%)
9	NAG	X	1	1,9	14,14,15	0.36	0	17,19,21	0.63	0
9	NAG	X	2	9	14,14,15	0.41	0	17,19,21	0.80	1 (5%)
9	BMA	X	3	9	11,11,12	1.10	1 (9%)	15,15,17	0.95	2 (13%)
7	NAG	Y	1	1,7	14,14,15	0.43	0	17,19,21	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	NAG	Y	2	7	14,14,15	0.30	0	17,19,21	0.60	0
8	NAG	Z	1	1,8	14,14,15	0.38	0	17,19,21	0.68	0
8	NAG	Z	2	8	14,14,15	0.43	0	17,19,21	0.75	0
8	BMA	Z	3	8	11,11,12	1.07	1 (9%)	15,15,17	0.84	1 (6%)
8	MAN	Z	4	8	11,11,12	1.09	2 (18%)	15,15,17	1.08	2 (13%)
7	NAG	a	1	1,7	14,14,15	0.34	0	17,19,21	0.81	1 (5%)
7	NAG	a	2	7	14,14,15	0.61	0	17,19,21	0.54	0
7	NAG	b	1	1,7	14,14,15	0.34	0	17,19,21	0.76	0
7	NAG	b	2	7	14,14,15	0.29	0	17,19,21	0.67	0
7	NAG	c	1	1,7	14,14,15	0.56	0	17,19,21	1.20	2 (11%)
7	NAG	c	2	7	14,14,15	0.87	1 (7%)	17,19,21	1.10	2 (11%)
9	NAG	d	1	1,9	14,14,15	0.36	0	17,19,21	0.63	0
9	NAG	d	2	9	14,14,15	0.41	0	17,19,21	0.79	1 (5%)
9	BMA	d	3	9	11,11,12	1.10	1 (9%)	15,15,17	0.95	2 (13%)
7	NAG	e	1	1,7	14,14,15	0.44	0	17,19,21	0.63	0
7	NAG	e	2	7	14,14,15	0.30	0	17,19,21	0.60	0
8	NAG	f	1	1,8	14,14,15	0.38	0	17,19,21	0.67	0
8	NAG	f	2	8	14,14,15	0.43	0	17,19,21	0.75	0
8	BMA	f	3	8	11,11,12	1.07	1 (9%)	15,15,17	0.84	1 (6%)
8	MAN	f	4	8	11,11,12	1.09	2 (18%)	15,15,17	1.09	2 (13%)
7	NAG	g	1	1,7	14,14,15	0.34	0	17,19,21	0.81	1 (5%)
7	NAG	g	2	7	14,14,15	0.62	0	17,19,21	0.54	0
7	NAG	h	1	1,7	14,14,15	0.33	0	17,19,21	0.76	0
7	NAG	h	2	7	14,14,15	0.28	0	17,19,21	0.67	0
7	NAG	i	1	1,7	14,14,15	0.57	0	17,19,21	1.20	2 (11%)
7	NAG	i	2	7	14,14,15	0.88	1 (7%)	17,19,21	1.10	2 (11%)
9	NAG	j	1	1,9	14,14,15	0.36	0	17,19,21	0.64	0
9	NAG	j	2	9	14,14,15	0.41	0	17,19,21	0.79	1 (5%)
9	BMA	j	3	9	11,11,12	1.10	1 (9%)	15,15,17	0.95	2 (13%)

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
7	NAG	S	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	S	2	7	-	0/6/23/26	0/1/1/1
8	NAG	T	1	1,8	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	T	2	8	-	0/6/23/26	0/1/1/1
8	BMA	T	3	8	-	1/2/19/22	0/1/1/1
8	MAN	T	4	8	-	0/2/19/22	0/1/1/1
7	NAG	U	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	U	2	7	-	0/6/23/26	0/1/1/1
7	NAG	V	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	V	2	7	-	0/6/23/26	0/1/1/1
7	NAG	W	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	W	2	7	-	2/6/23/26	0/1/1/1
9	NAG	X	1	1,9	-	0/6/23/26	0/1/1/1
9	NAG	X	2	9	-	0/6/23/26	0/1/1/1
9	BMA	X	3	9	-	0/2/19/22	0/1/1/1
7	NAG	Y	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	Y	2	7	-	0/6/23/26	0/1/1/1
8	NAG	Z	1	1,8	-	0/6/23/26	0/1/1/1
8	NAG	Z	2	8	-	0/6/23/26	0/1/1/1
8	BMA	Z	3	8	-	1/2/19/22	0/1/1/1
8	MAN	Z	4	8	-	0/2/19/22	0/1/1/1
7	NAG	a	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	a	2	7	-	0/6/23/26	0/1/1/1
7	NAG	b	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	b	2	7	-	0/6/23/26	0/1/1/1
7	NAG	c	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	c	2	7	-	2/6/23/26	0/1/1/1
9	NAG	d	1	1,9	-	0/6/23/26	0/1/1/1
9	NAG	d	2	9	-	0/6/23/26	0/1/1/1
9	BMA	d	3	9	-	0/2/19/22	0/1/1/1
7	NAG	e	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	e	2	7	-	0/6/23/26	0/1/1/1
8	NAG	f	1	1,8	-	0/6/23/26	0/1/1/1
8	NAG	f	2	8	-	0/6/23/26	0/1/1/1
8	BMA	f	3	8	-	1/2/19/22	0/1/1/1
8	MAN	f	4	8	-	0/2/19/22	0/1/1/1
7	NAG	g	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	g	2	7	-	0/6/23/26	0/1/1/1
7	NAG	h	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	h	2	7	-	0/6/23/26	0/1/1/1
7	NAG	i	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	i	2	7	-	2/6/23/26	0/1/1/1
9	NAG	j	1	1,9	-	0/6/23/26	0/1/1/1
9	NAG	j	2	9	-	0/6/23/26	0/1/1/1
9	BMA	j	3	9	-	0/2/19/22	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	j	3	BMA	O5-C5	3.03	1.49	1.43
9	d	3	BMA	O5-C5	3.03	1.49	1.43
9	X	3	BMA	O5-C5	3.02	1.49	1.43
7	i	2	NAG	O5-C1	2.65	1.48	1.43
7	c	2	NAG	O5-C1	2.64	1.48	1.43

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	i	2	NAG	C2-N2-C7	3.34	127.38	122.90
7	c	2	NAG	C2-N2-C7	3.34	127.38	122.90
7	W	2	NAG	C2-N2-C7	3.34	127.38	122.90
7	i	1	NAG	C1-O5-C5	3.25	116.54	112.19
7	W	1	NAG	C1-O5-C5	3.24	116.52	112.19

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

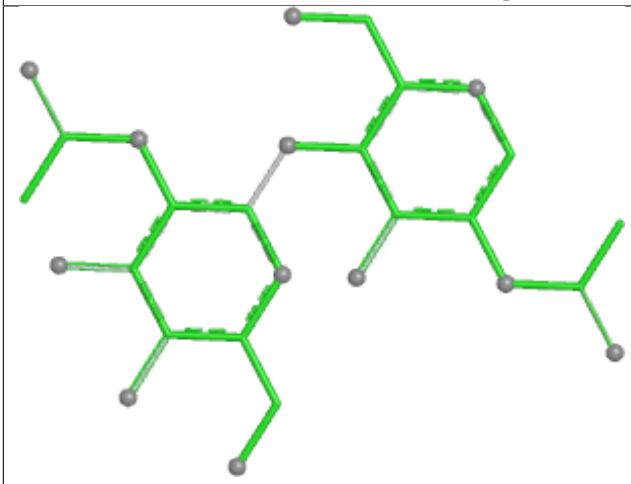
Mol	Chain	Res	Type	Atoms
8	T	3	BMA	O5-C5-C6-O6
8	Z	3	BMA	O5-C5-C6-O6
8	f	3	BMA	O5-C5-C6-O6
7	W	2	NAG	C1-C2-N2-C7
7	c	2	NAG	C1-C2-N2-C7

There are no ring outliers.

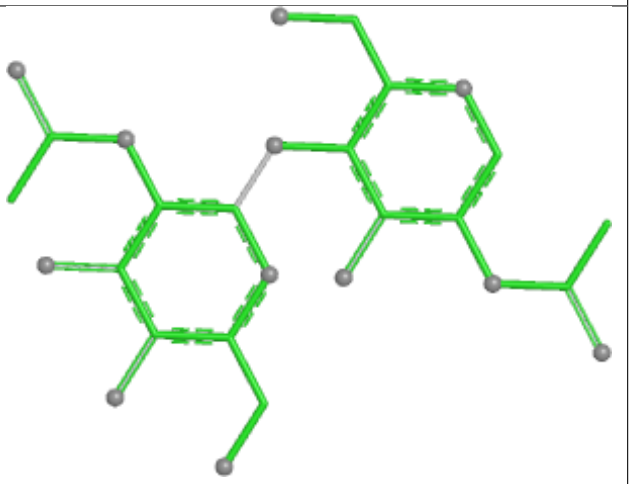
No monomer is involved in short contacts.

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

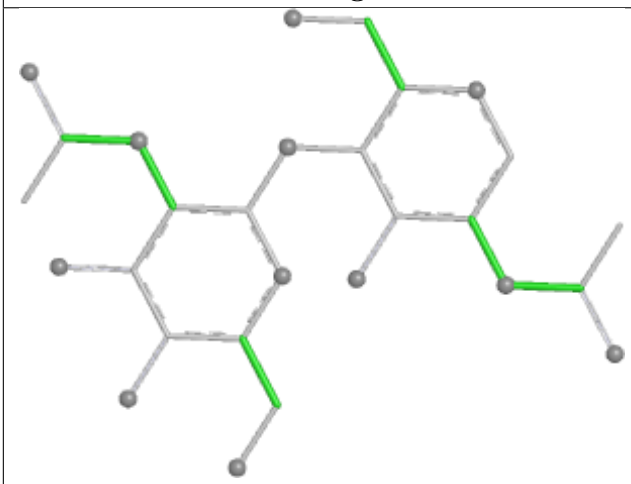
Oligosaccharide Chain S



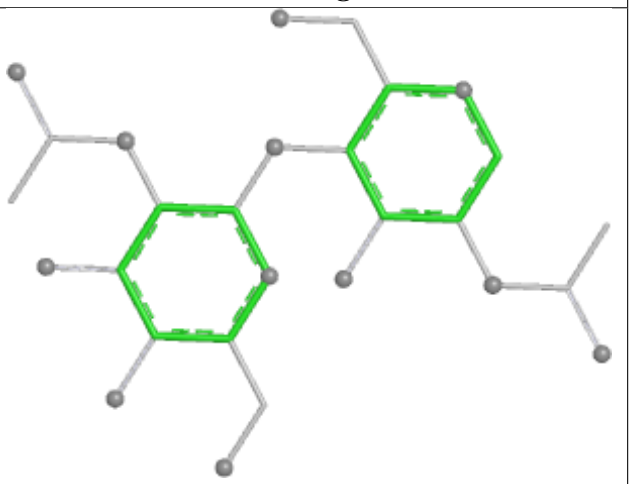
Bond lengths



Bond angles

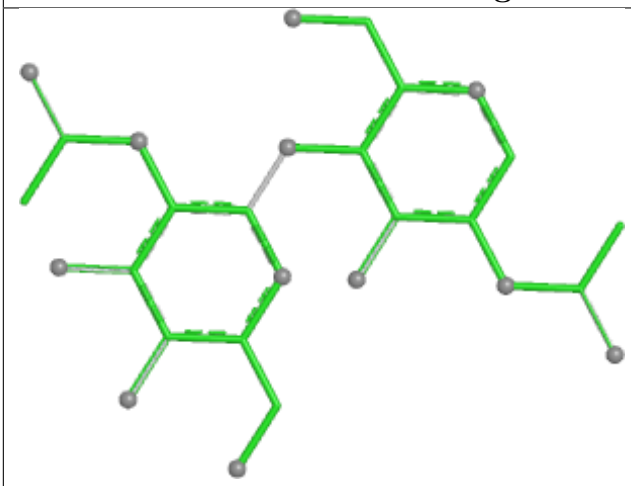


Torsions

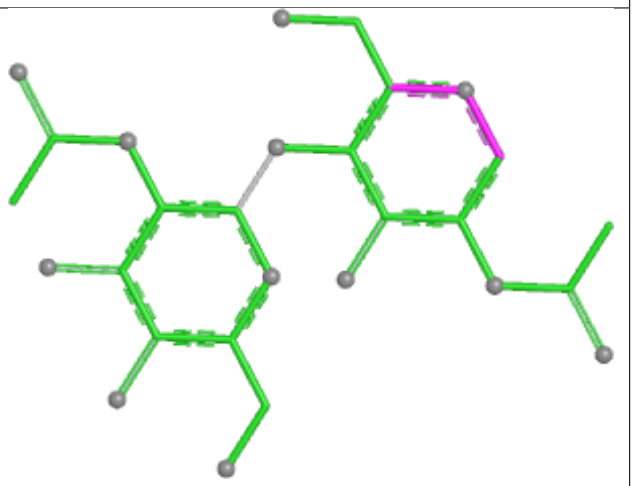


Rings

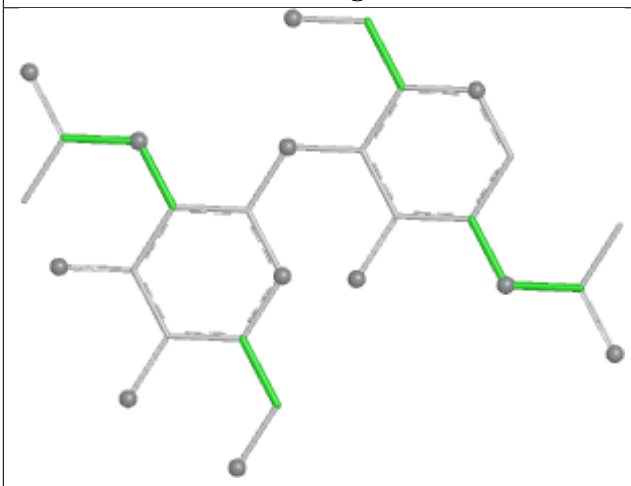
Oligosaccharide Chain U



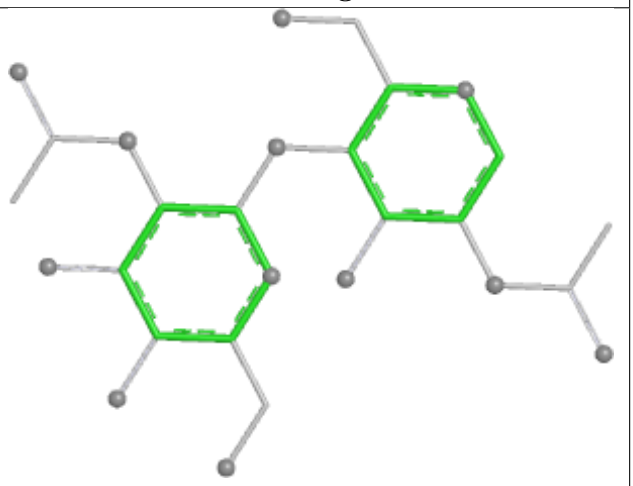
Bond lengths



Bond angles

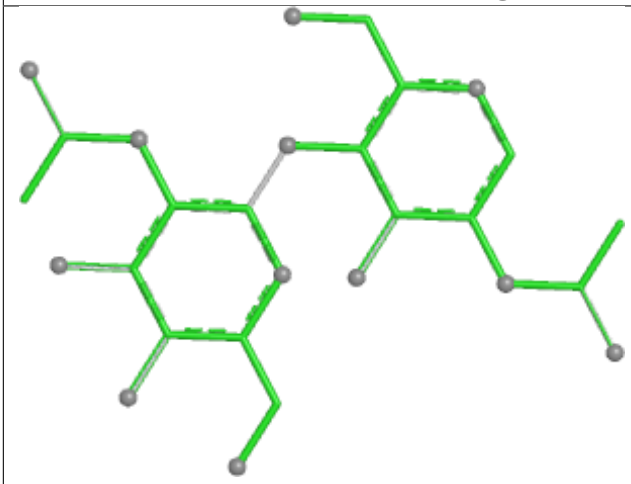


Torsions

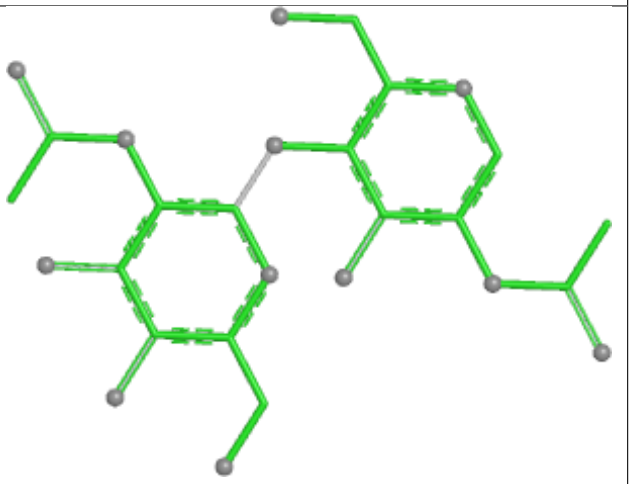


Rings

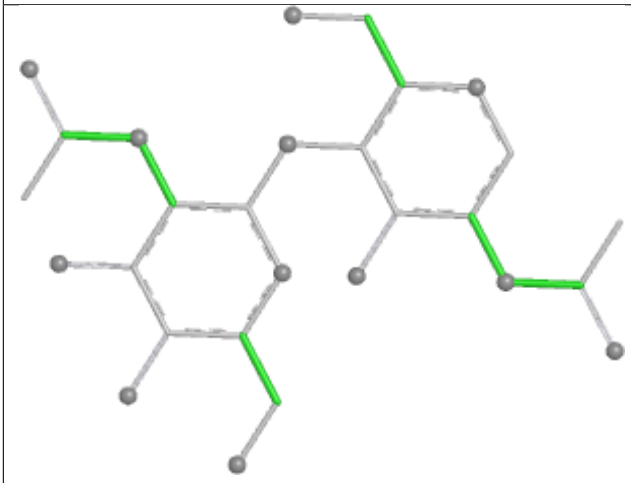
Oligosaccharide Chain V



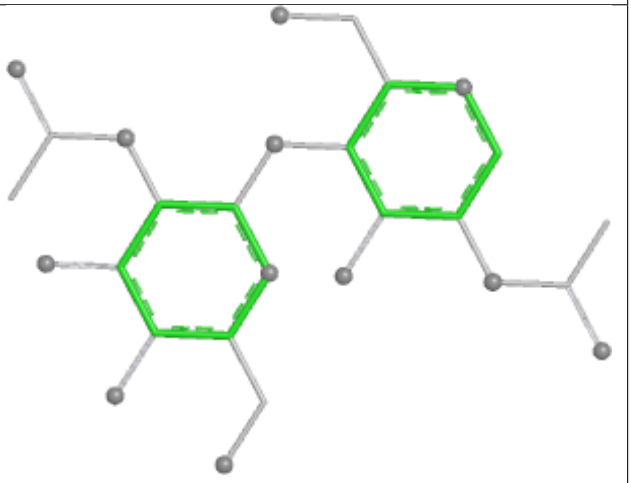
Bond lengths



Bond angles

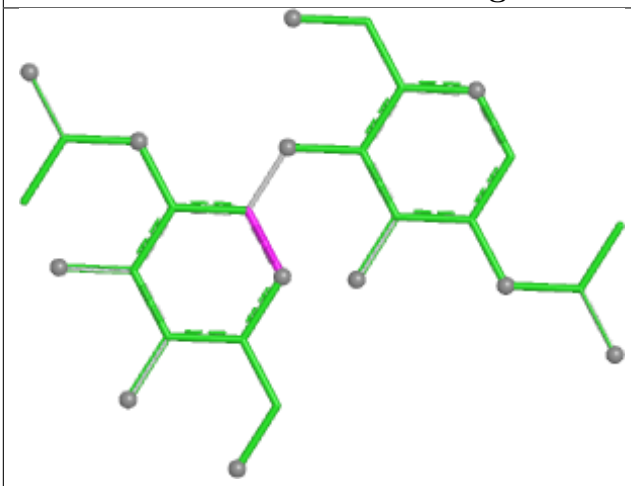


Torsions

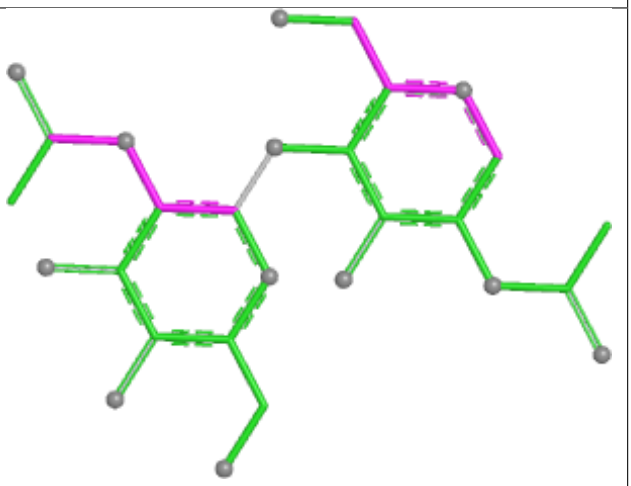


Rings

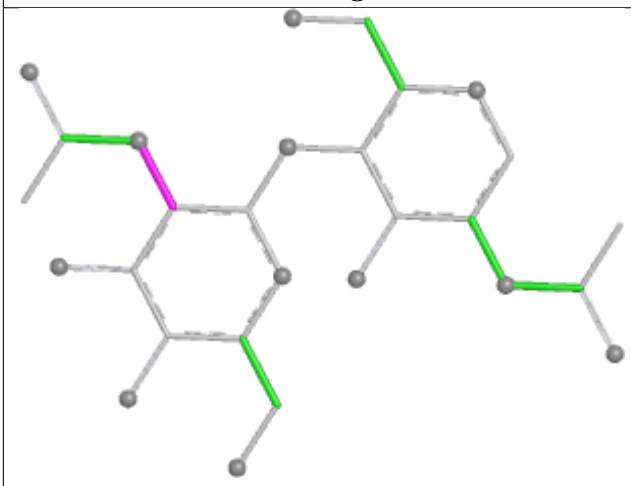
Oligosaccharide Chain W



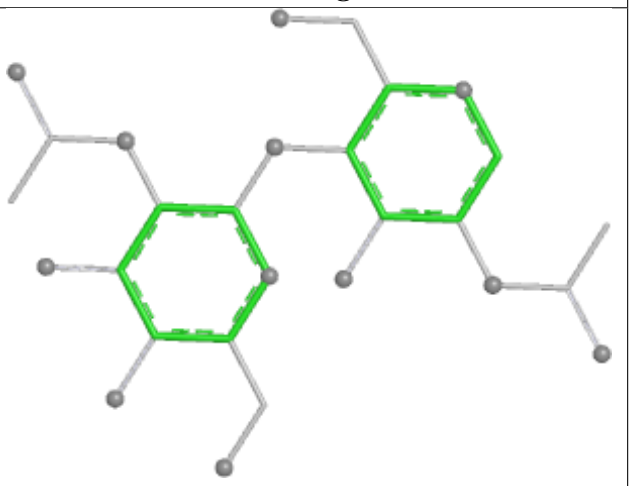
Bond lengths



Bond angles

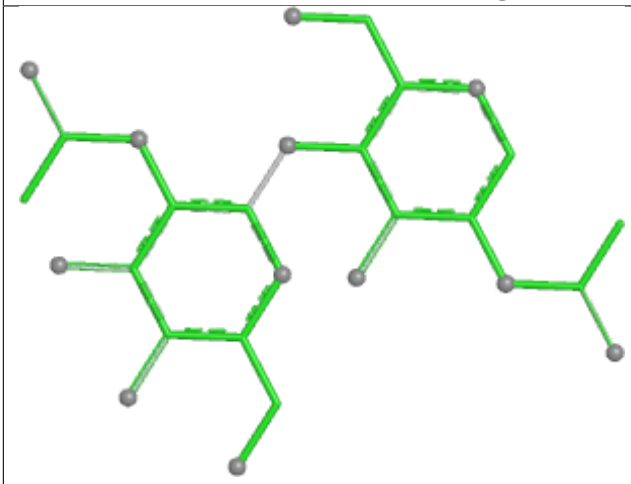


Torsions

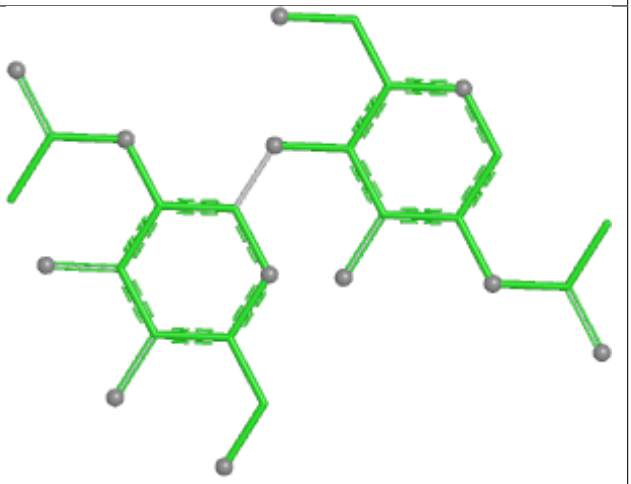


Rings

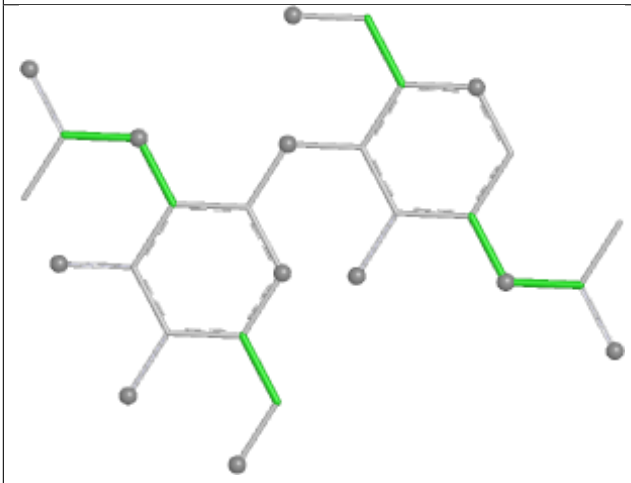
Oligosaccharide Chain Y



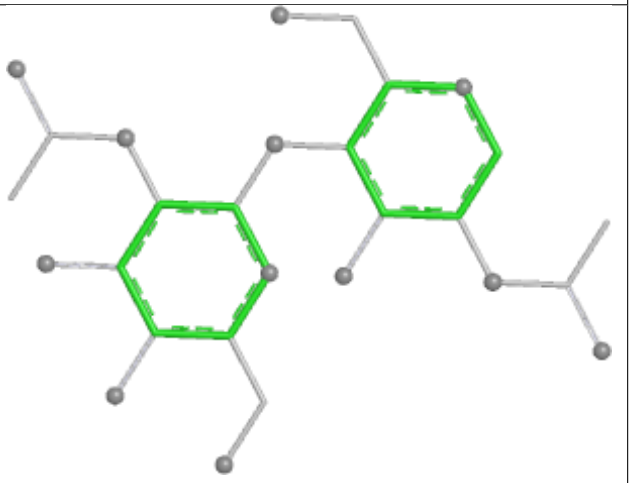
Bond lengths



Bond angles

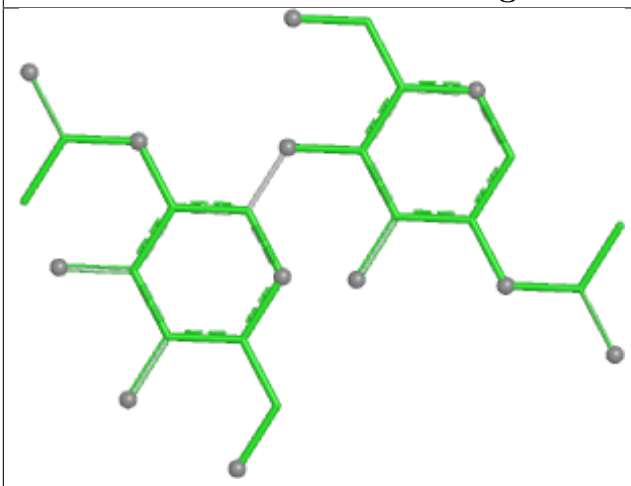


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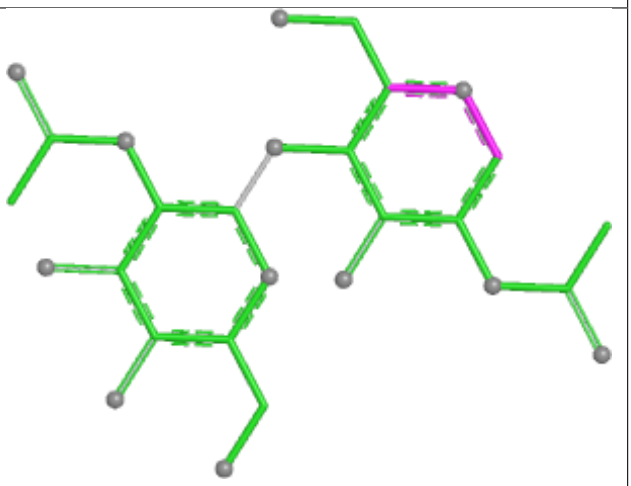


Rings

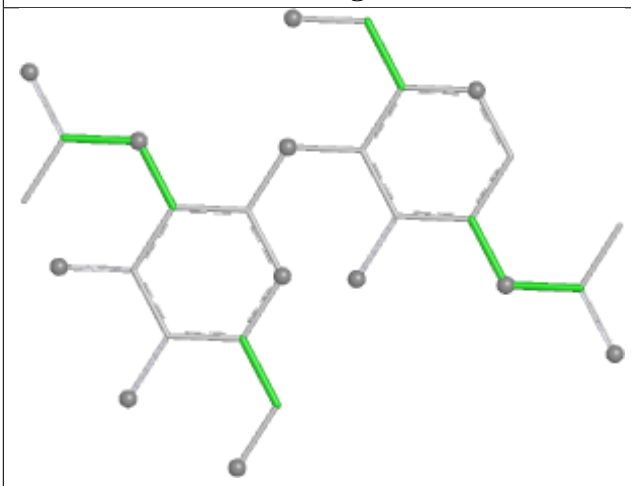
Oligosaccharide Chain a



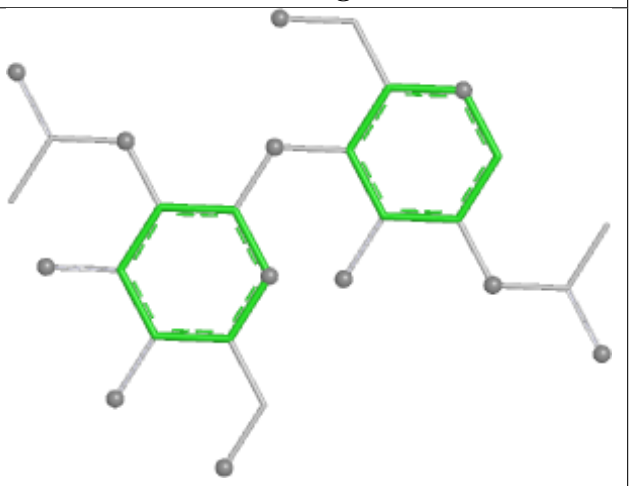
Bond lengths



Bond angles

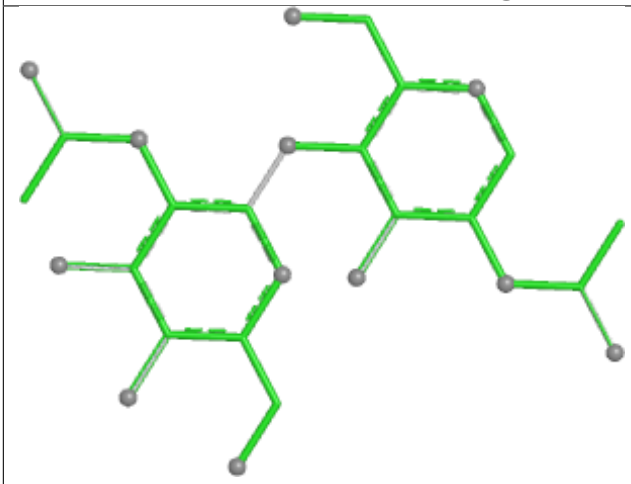


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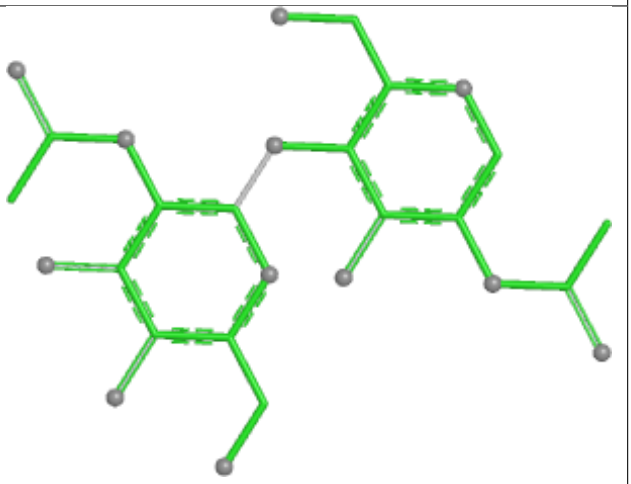


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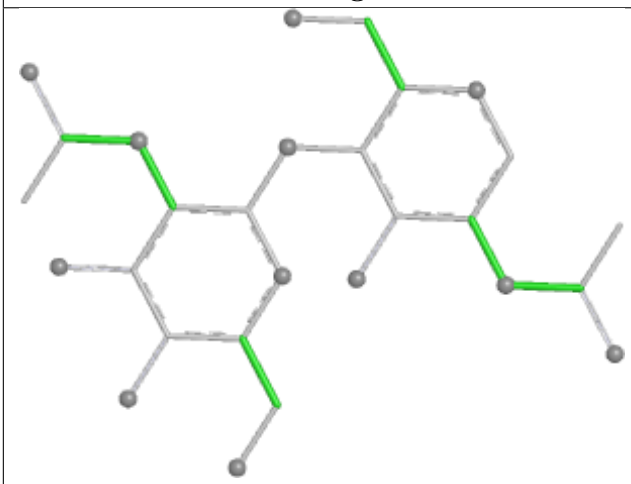
Oligosaccharide Chain b



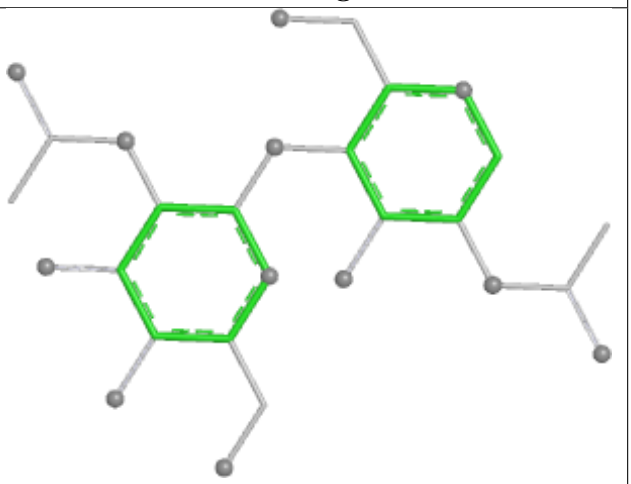
Bond lengths



Bond angles

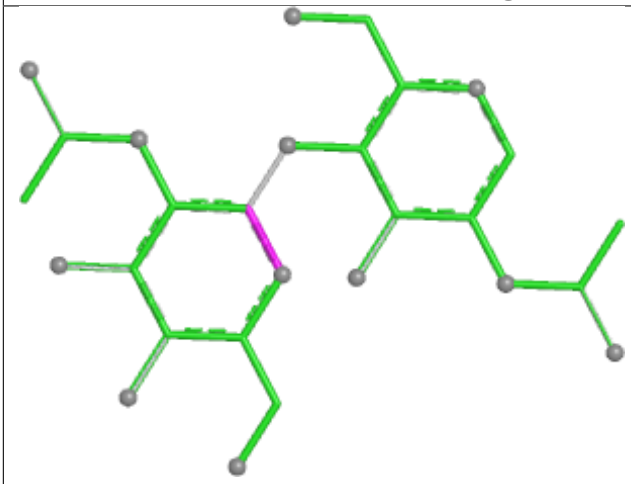


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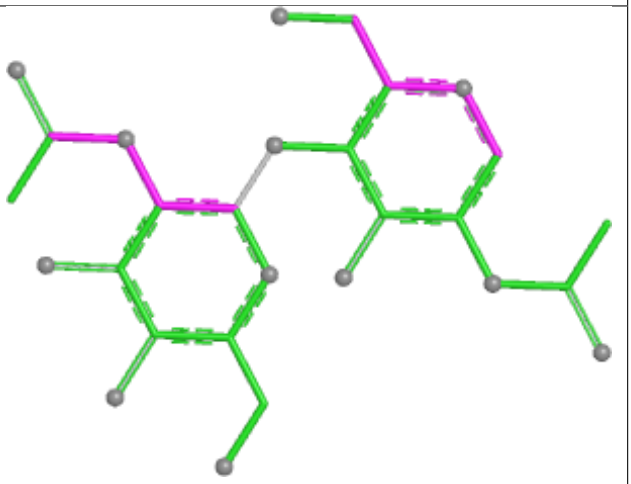


Rings

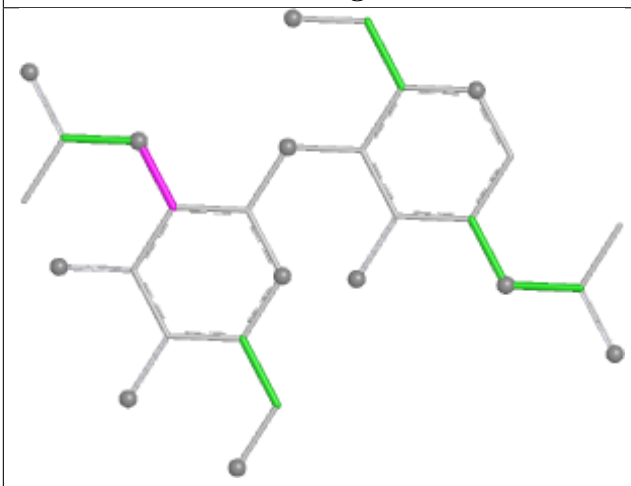
Oligosaccharide Chain c



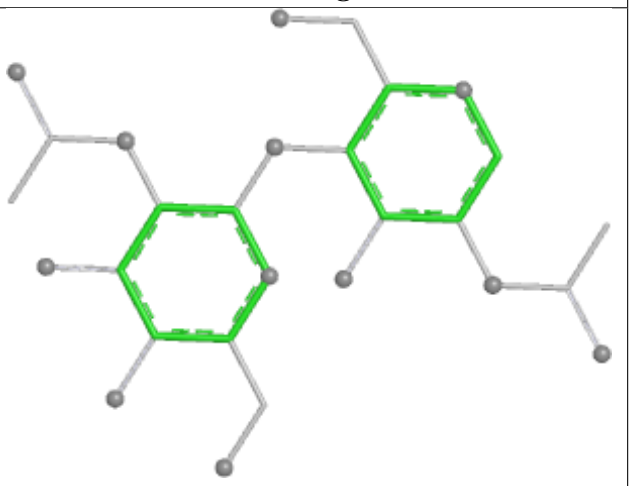
Bond lengths



Bond angles

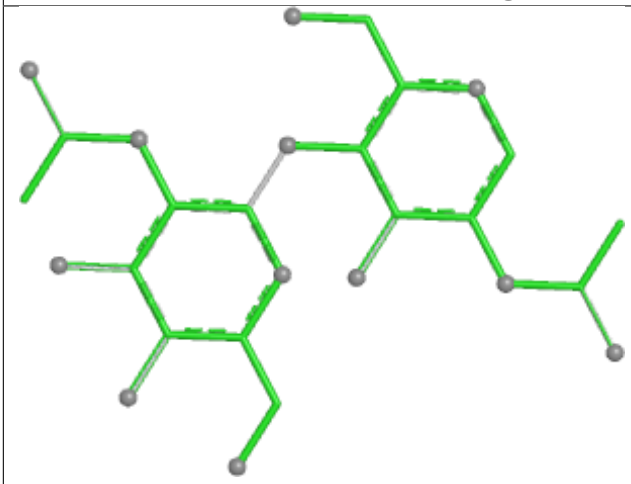


Torsions

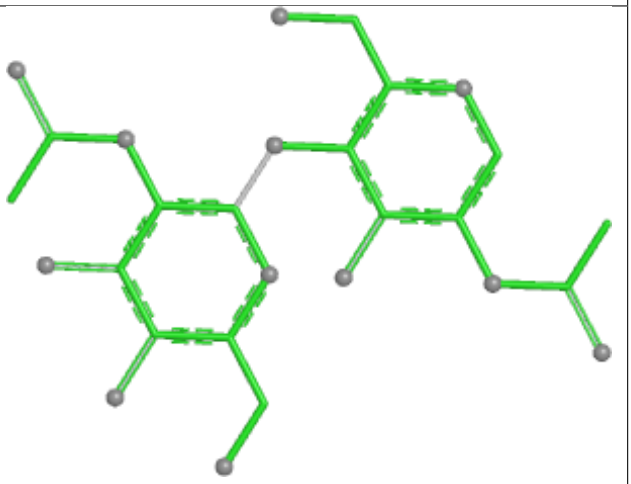


Rings

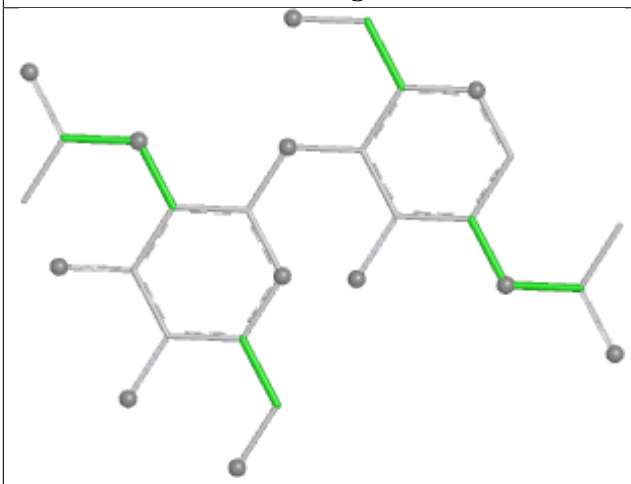
Oligosaccharide Chain e



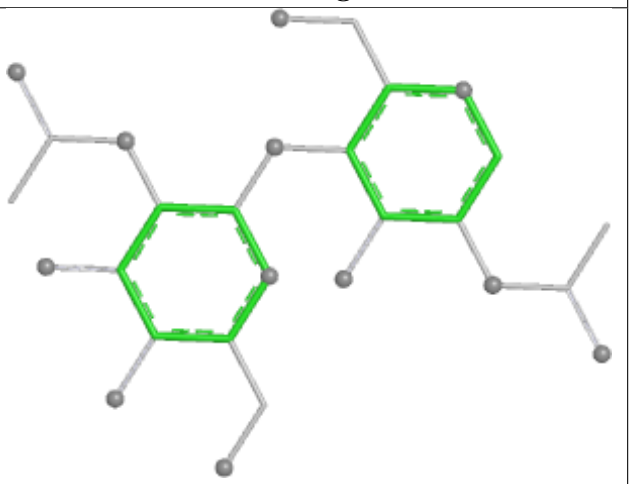
Bond lengths



Bond angles

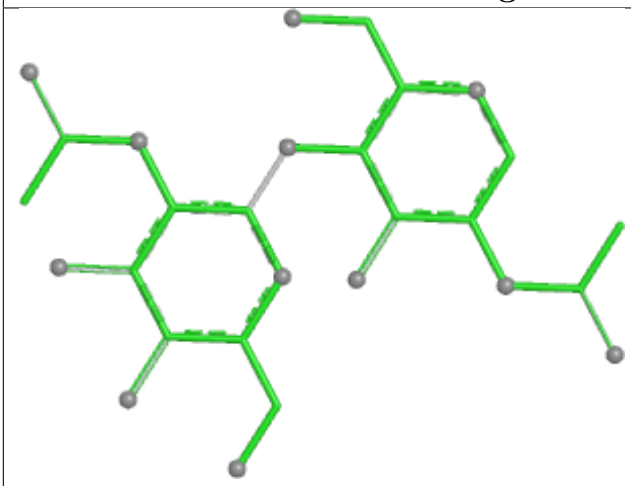


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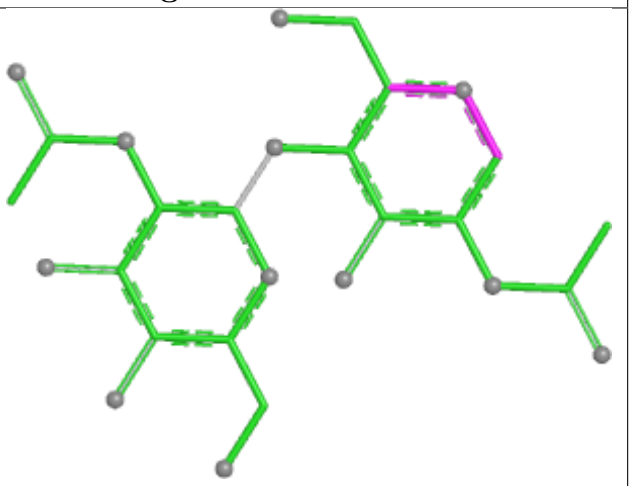


Rings

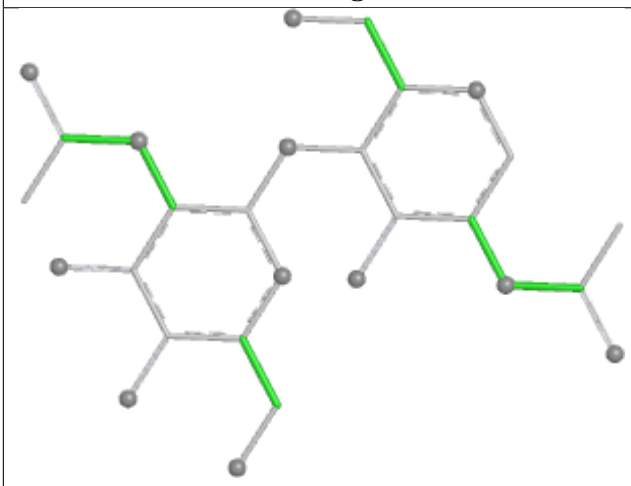
Oligosaccharide Chain g



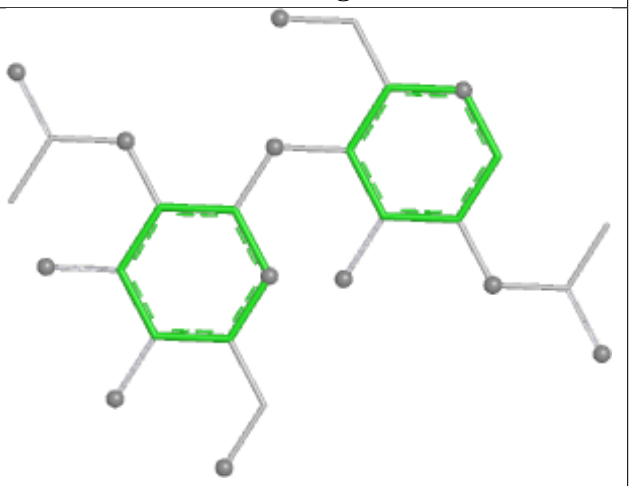
Bond lengths



Bond angles

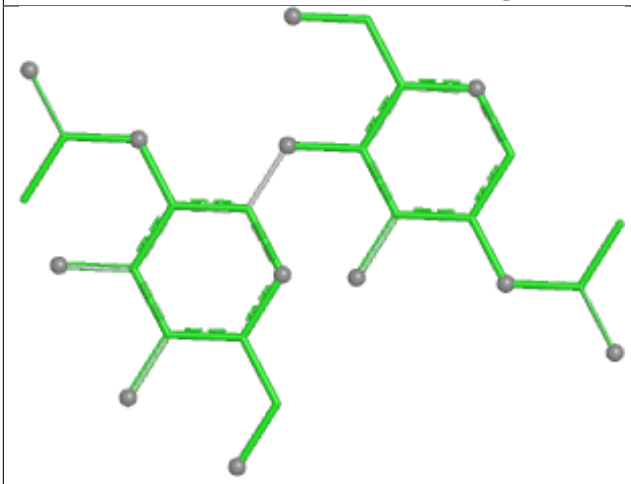


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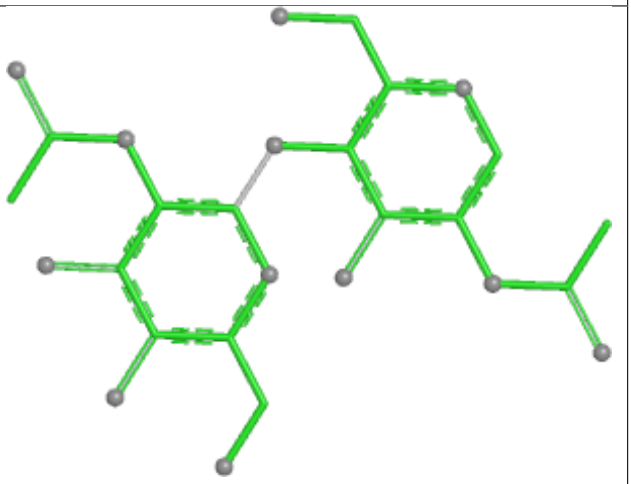


Rings

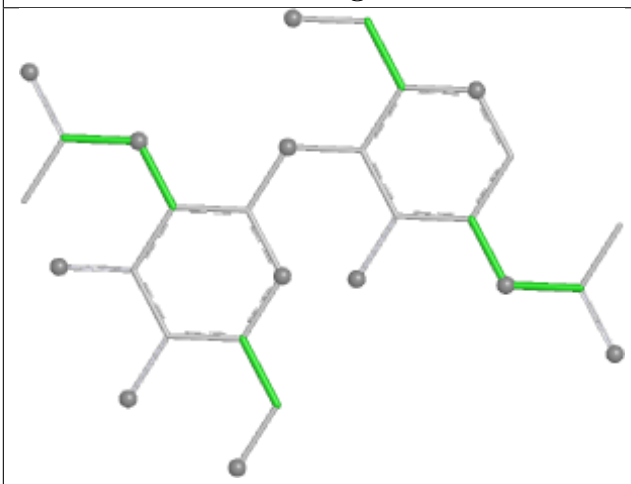
Oligosaccharide Chain h



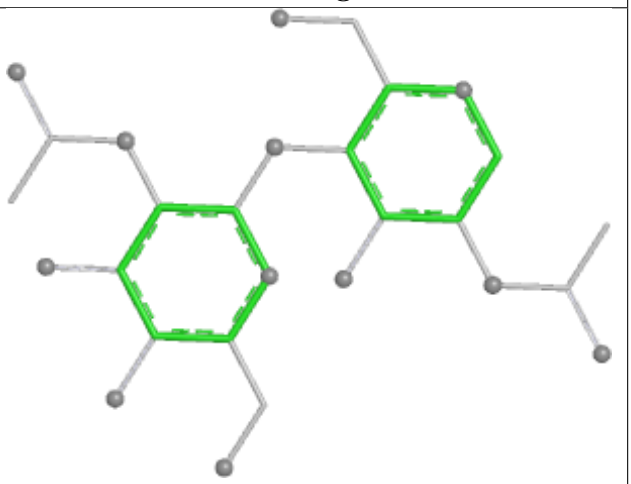
Bond lengths



Bond angles

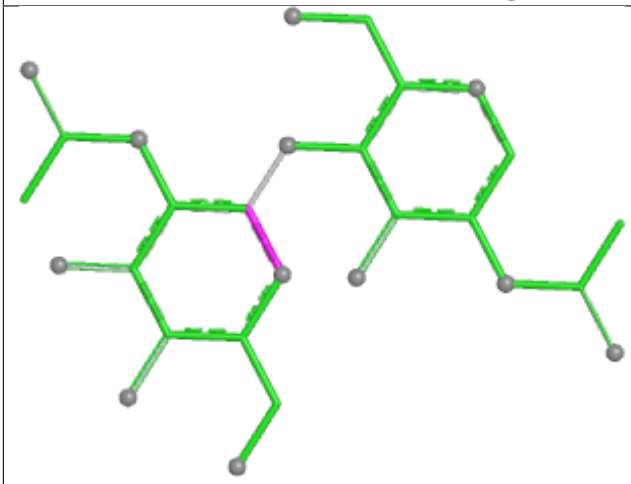


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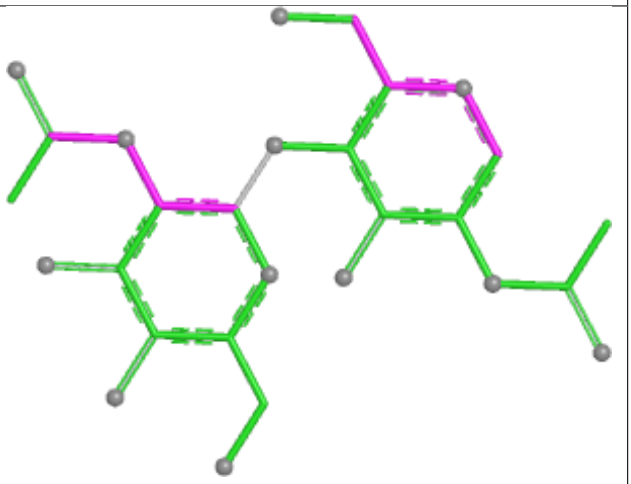


Rings

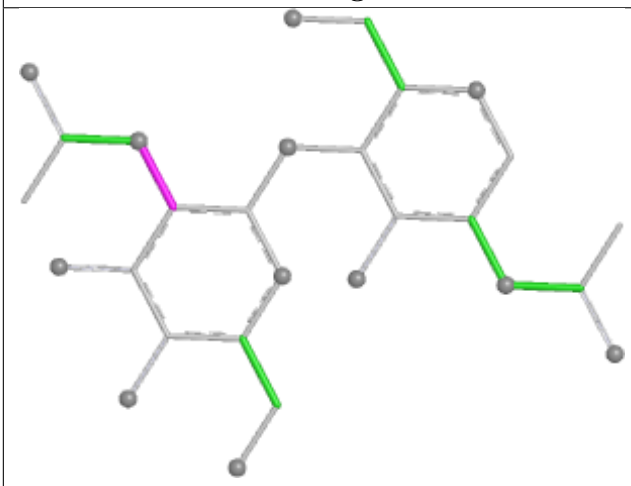
Oligosaccharide Chain i



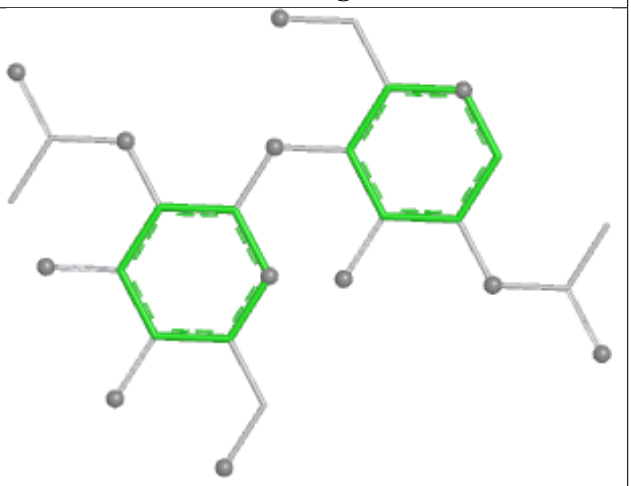
Bond lengths



Bond angles

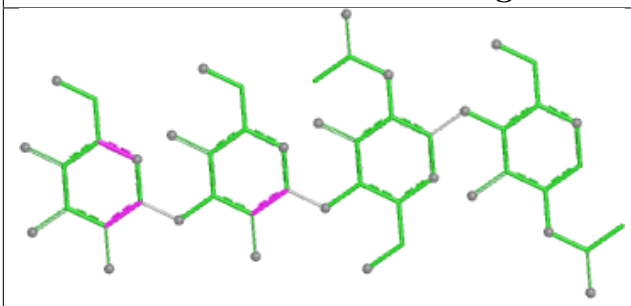


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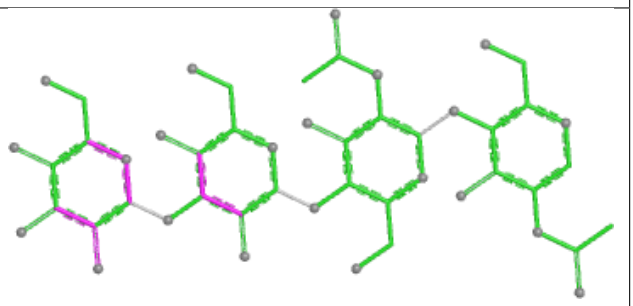


Rings

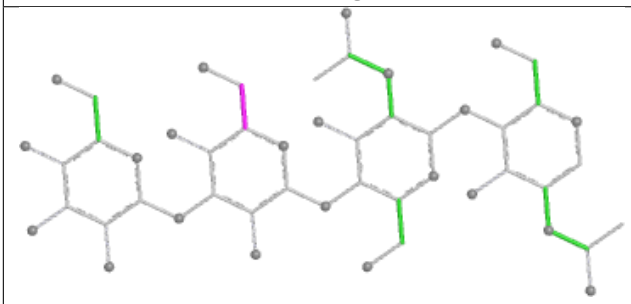
Oligosaccharide Chain T



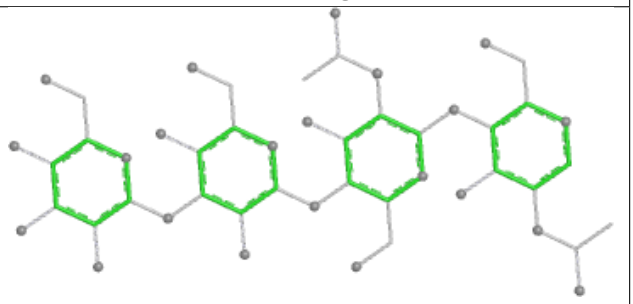
Bond lengths



Bond angles

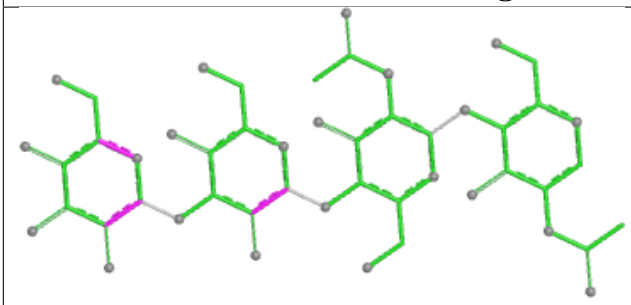


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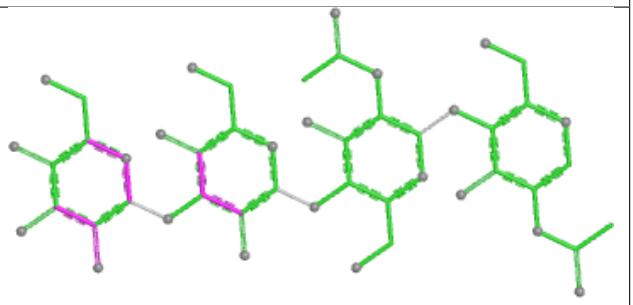


Rings

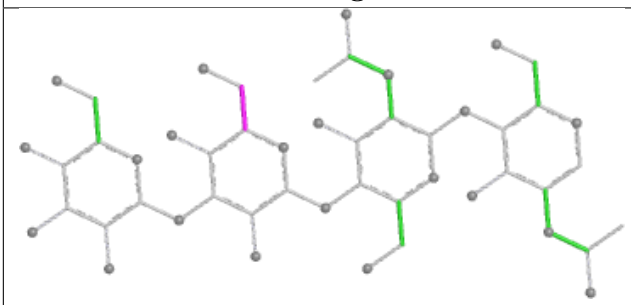
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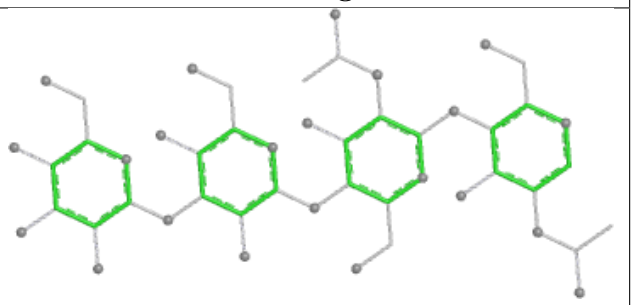
Bond lengths



Bond angles

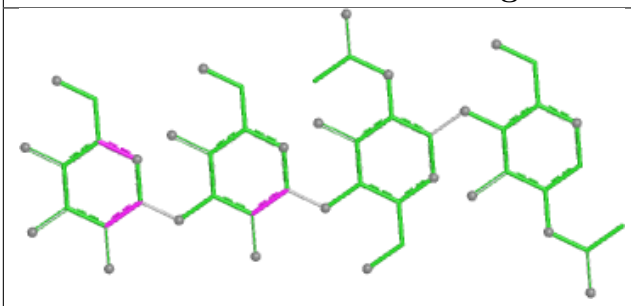


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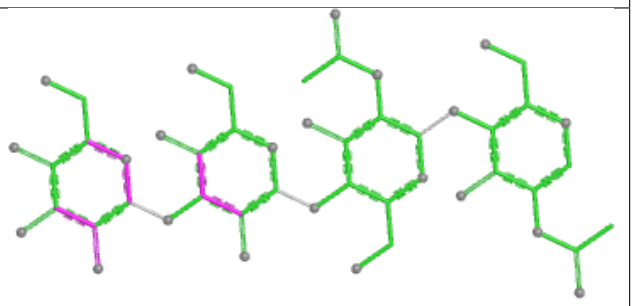


Rings

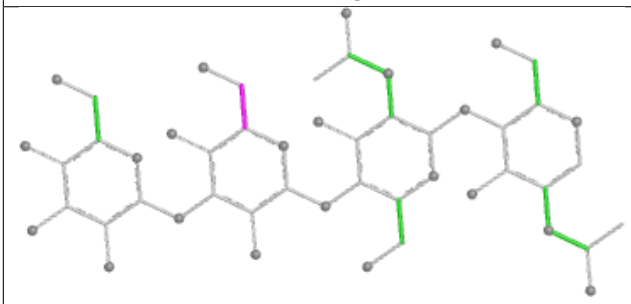
Oligosaccharide Chain f



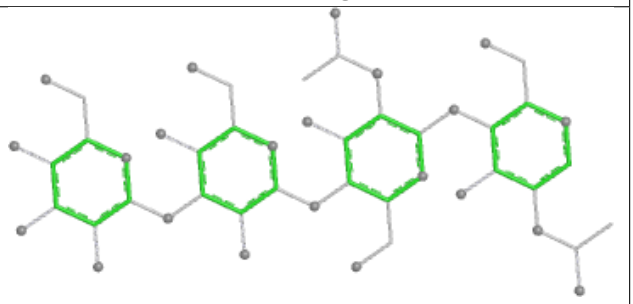
Bond lengths



Bond angles

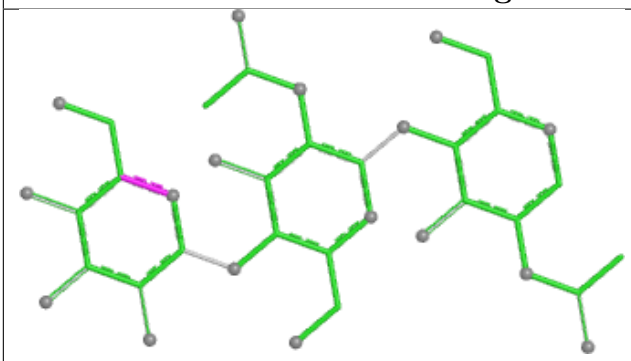


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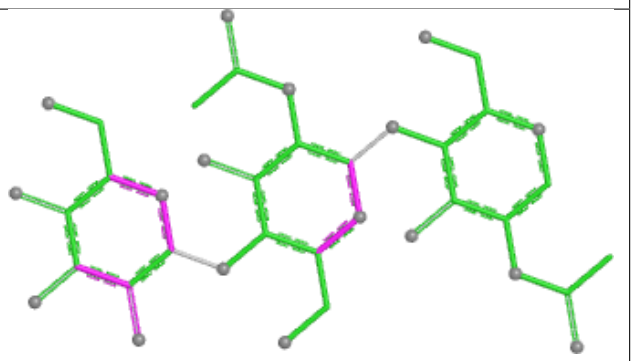


Rings

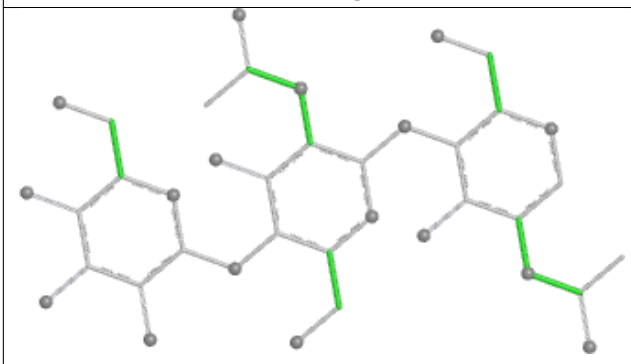
Oligosaccharide Chain X



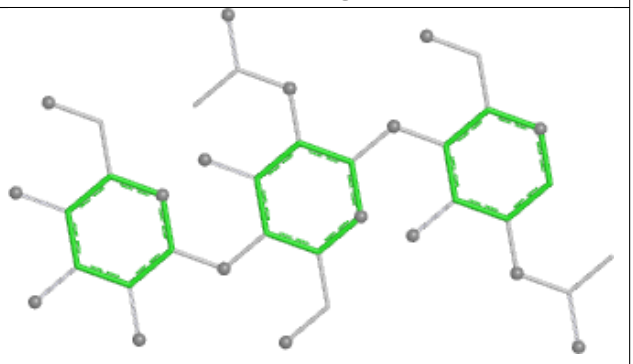
Bond lengths



Bond angles

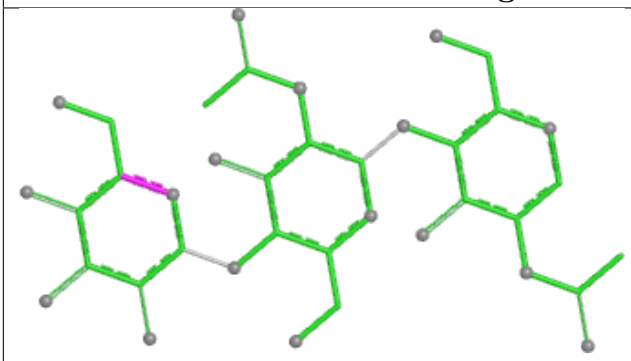


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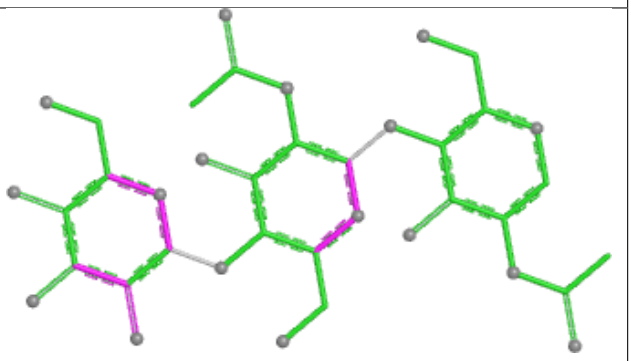


Rings

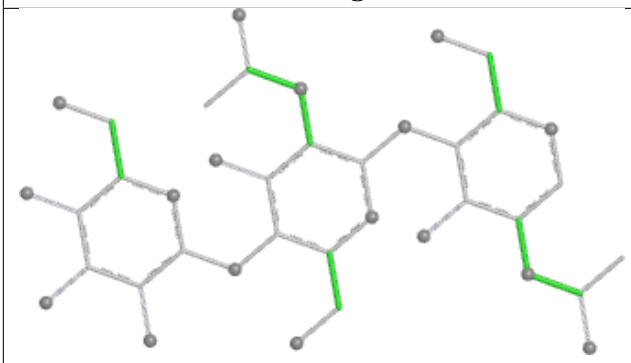
Oligosaccharide Chain d



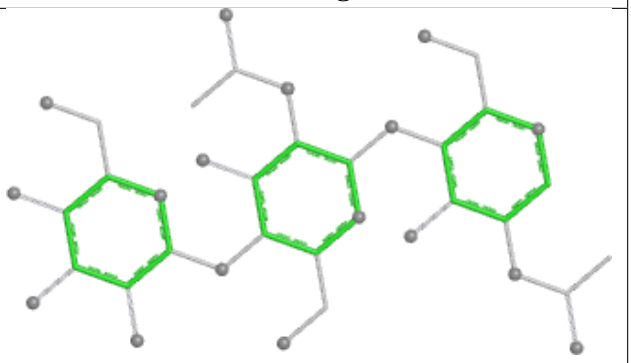
Bond lengths



Bond angles

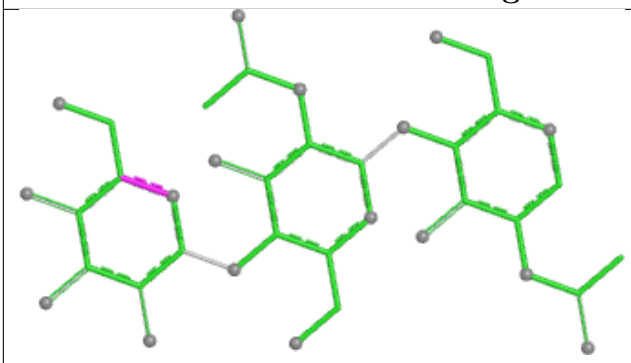


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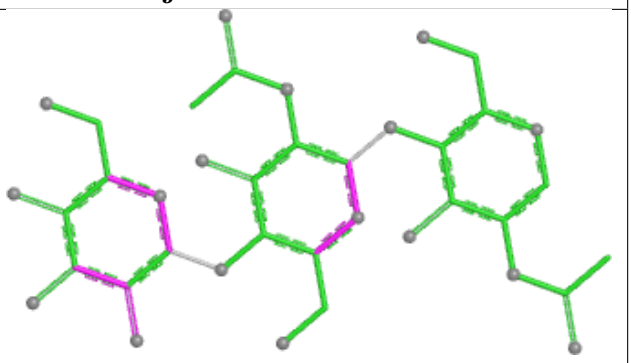


Rings

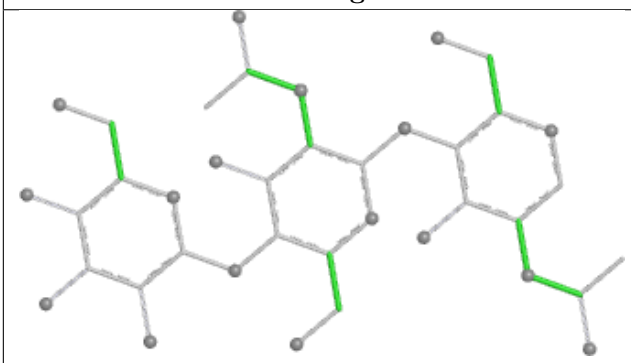
Oligosaccharide Chain j



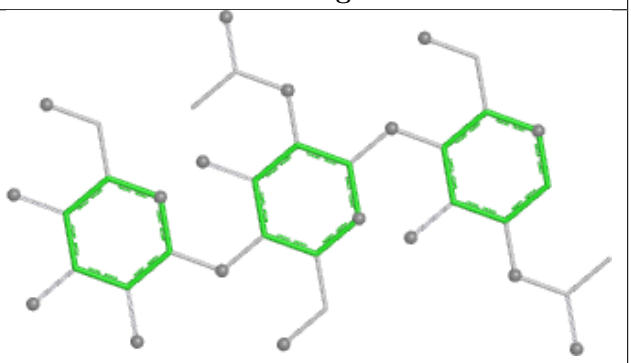
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

42 ligands 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	$\#\|Z\| > 2$
10	NAG	A	605	1	14,14,15	0.48	0	17,19,21	0.57	0
10	NAG	C	611	1	14,14,15	0.41	0	17,19,21	0.56	0
10	NAG	C	606	1	14,14,15	0.47	0	17,19,21	0.61	0
10	NAG	A	604	1	14,14,15	0.44	0	17,19,21	0.59	0
10	NAG	A	601	1	14,14,15	0.48	0	17,19,21	0.54	0
10	NAG	C	607	1	14,14,15	0.55	0	17,19,21	0.82	1 (5%)
10	NAG	D	605	1	14,14,15	0.48	0	17,19,21	0.57	0
10	NAG	A	607	1	14,14,15	0.56	0	17,19,21	0.82	1 (5%)
10	NAG	D	606	1	14,14,15	0.47	0	17,19,21	0.61	0
10	NAG	F	701	2	14,14,15	0.69	1 (7%)	17,19,21	0.54	0
10	NAG	F	702	2	14,14,15	0.46	0	17,19,21	0.56	0
10	NAG	C	605	1	14,14,15	0.48	0	17,19,21	0.57	0
10	NAG	C	610	1	14,14,15	0.49	0	17,19,21	0.53	0
10	NAG	A	606	1	14,14,15	0.47	0	17,19,21	0.61	0
10	NAG	D	610	1	14,14,15	0.48	0	17,19,21	0.53	0
10	NAG	D	603	1	14,14,15	0.57	0	17,19,21	0.50	0
10	NAG	D	604	1	14,14,15	0.43	0	17,19,21	0.59	0
10	NAG	E	702	2	14,14,15	0.46	0	17,19,21	0.56	0
10	NAG	C	602	1	14,14,15	0.52	0	17,19,21	0.56	0
10	NAG	D	602	1	14,14,15	0.52	0	17,19,21	0.56	0
10	NAG	C	601	1	14,14,15	0.47	0	17,19,21	0.54	0
10	NAG	A	603	1	14,14,15	0.57	0	17,19,21	0.50	0
10	NAG	A	609	1	14,14,15	0.33	0	17,19,21	0.63	0
10	NAG	E	701	2	14,14,15	0.68	1 (7%)	17,19,21	0.53	0
10	NAG	D	608	1	14,14,15	0.40	0	17,19,21	0.58	0
10	NAG	E	703	2	14,14,15	0.43	0	17,19,21	0.58	0
10	NAG	D	611	1	14,14,15	0.41	0	17,19,21	0.56	0
10	NAG	A	608	1	14,14,15	0.40	0	17,19,21	0.58	0
10	NAG	A	602	1	14,14,15	0.52	0	17,19,21	0.56	0
10	NAG	C	603	1	14,14,15	0.57	0	17,19,21	0.50	0
10	NAG	D	601	1	14,14,15	0.48	0	17,19,21	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
10	NAG	B	702	2	14,14,15	0.45	0	17,19,21	0.56	0
10	NAG	C	608	1	14,14,15	0.40	0	17,19,21	0.58	0
10	NAG	B	703	2	14,14,15	0.42	0	17,19,21	0.58	0
10	NAG	A	611	1	14,14,15	0.41	0	17,19,21	0.56	0
10	NAG	C	604	1	14,14,15	0.44	0	17,19,21	0.59	0
10	NAG	F	703	2	14,14,15	0.43	0	17,19,21	0.58	0
10	NAG	A	610	1	14,14,15	0.48	0	17,19,21	0.53	0
10	NAG	C	609	1	14,14,15	0.32	0	17,19,21	0.64	0
10	NAG	D	609	1	14,14,15	0.33	0	17,19,21	0.64	0
10	NAG	B	701	2	14,14,15	0.68	1 (7%)	17,19,21	0.54	0
10	NAG	D	607	1	14,14,15	0.56	0	17,19,21	0.81	1 (5%)

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
10	NAG	A	605	1	-	1/6/23/26	0/1/1/1
10	NAG	C	611	1	-	0/6/23/26	0/1/1/1
10	NAG	C	606	1	-	1/6/23/26	0/1/1/1
10	NAG	A	604	1	-	0/6/23/26	0/1/1/1
10	NAG	A	601	1	-	0/6/23/26	0/1/1/1
10	NAG	C	607	1	-	1/6/23/26	0/1/1/1
10	NAG	D	605	1	-	1/6/23/26	0/1/1/1
10	NAG	A	607	1	-	1/6/23/26	0/1/1/1
10	NAG	D	606	1	-	1/6/23/26	0/1/1/1
10	NAG	F	701	2	-	0/6/23/26	0/1/1/1
10	NAG	F	702	2	-	0/6/23/26	0/1/1/1
10	NAG	C	605	1	-	1/6/23/26	0/1/1/1
10	NAG	C	610	1	-	3/6/23/26	0/1/1/1
10	NAG	A	606	1	-	1/6/23/26	0/1/1/1
10	NAG	D	610	1	-	3/6/23/26	0/1/1/1
10	NAG	D	603	1	-	1/6/23/26	0/1/1/1
10	NAG	D	604	1	-	0/6/23/26	0/1/1/1
10	NAG	E	702	2	-	0/6/23/26	0/1/1/1
10	NAG	C	602	1	-	0/6/23/26	0/1/1/1
10	NAG	D	602	1	-	0/6/23/26	0/1/1/1
10	NAG	C	601	1	-	0/6/23/26	0/1/1/1
10	NAG	A	603	1	-	1/6/23/26	0/1/1/1
10	NAG	A	609	1	-	0/6/23/26	0/1/1/1
10	NAG	E	701	2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	NAG	D	608	1	-	0/6/23/26	0/1/1/1
10	NAG	E	703	2	-	0/6/23/26	0/1/1/1
10	NAG	D	611	1	-	0/6/23/26	0/1/1/1
10	NAG	A	608	1	-	0/6/23/26	0/1/1/1
10	NAG	A	602	1	-	0/6/23/26	0/1/1/1
10	NAG	C	603	1	-	1/6/23/26	0/1/1/1
10	NAG	D	601	1	-	0/6/23/26	0/1/1/1
10	NAG	B	702	2	-	0/6/23/26	0/1/1/1
10	NAG	C	608	1	-	0/6/23/26	0/1/1/1
10	NAG	B	703	2	-	0/6/23/26	0/1/1/1
10	NAG	A	611	1	-	0/6/23/26	0/1/1/1
10	NAG	C	604	1	-	0/6/23/26	0/1/1/1
10	NAG	F	703	2	-	0/6/23/26	0/1/1/1
10	NAG	A	610	1	-	3/6/23/26	0/1/1/1
10	NAG	C	609	1	-	0/6/23/26	0/1/1/1
10	NAG	D	609	1	-	0/6/23/26	0/1/1/1
10	NAG	B	701	2	-	0/6/23/26	0/1/1/1
10	NAG	D	607	1	-	1/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	F	701	NAG	O5-C1	2.41	1.47	1.43
10	B	701	NAG	O5-C1	2.38	1.47	1.43
10	E	701	NAG	O5-C1	2.36	1.47	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	A	607	NAG	C1-O5-C5	2.27	115.22	112.19
10	D	607	NAG	C1-O5-C5	2.27	115.22	112.19
10	C	607	NAG	C1-O5-C5	2.26	115.22	112.19

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	610	NAG	O5-C5-C6-O6
10	C	610	NAG	O5-C5-C6-O6
10	D	610	NAG	O5-C5-C6-O6
10	A	603	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
10	C	603	NAG	O5-C5-C6-O6

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.

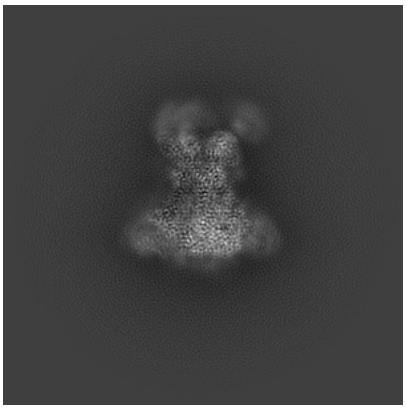
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-70319. These allow visual inspection of the internal detail of the map and identification of artifacts.

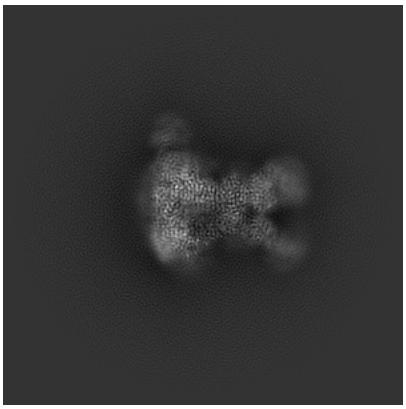
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

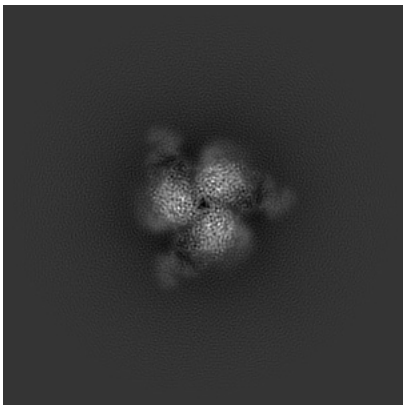
6.1.1 Primary map



X

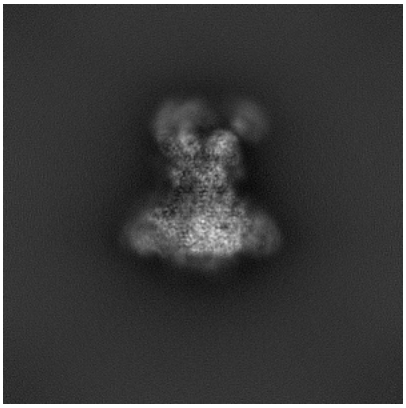


Y

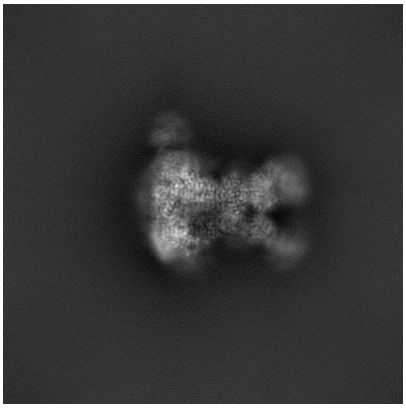


Z

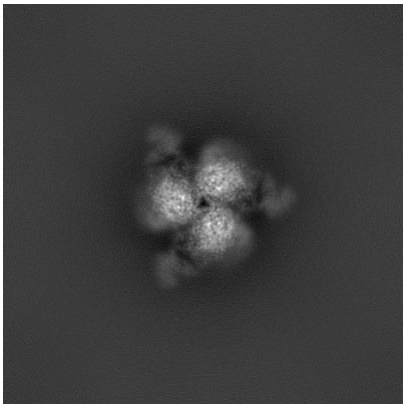
6.1.2 Raw map



X



Y

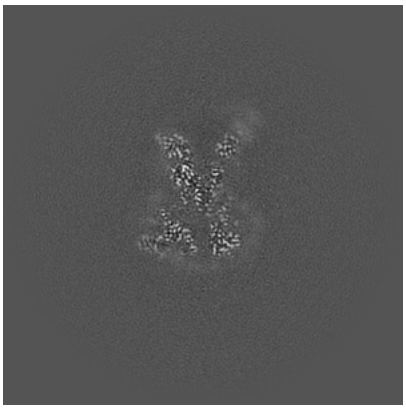


Z

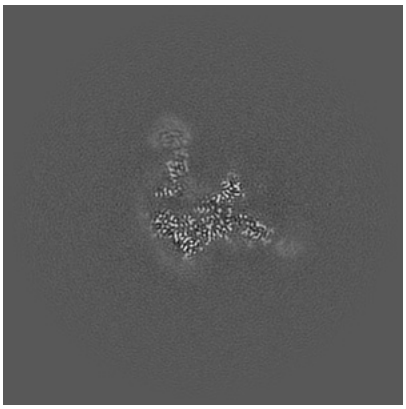
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

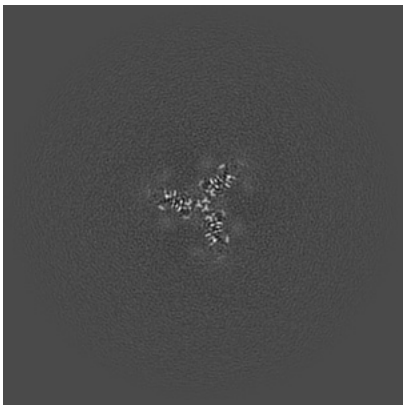
6.2.1 Primary map



X Index: 200

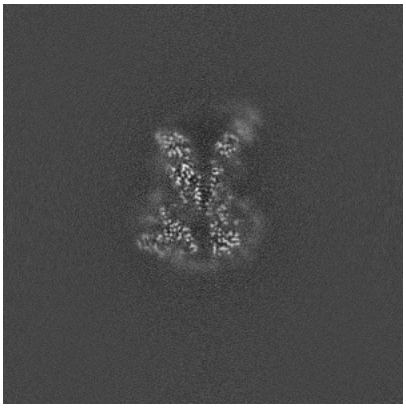


Y Index: 200

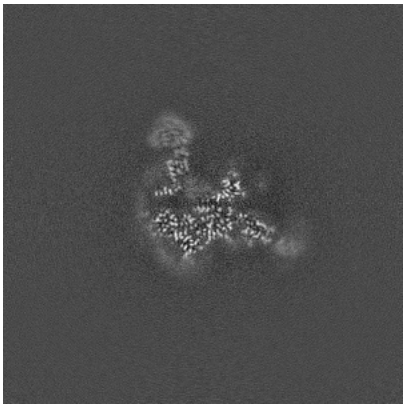


Z Index: 200

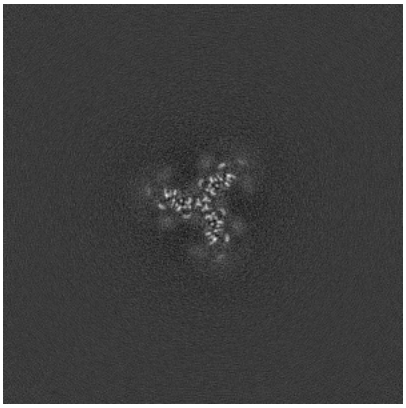
6.2.2 Raw map



X Index: 200



Y Index: 200

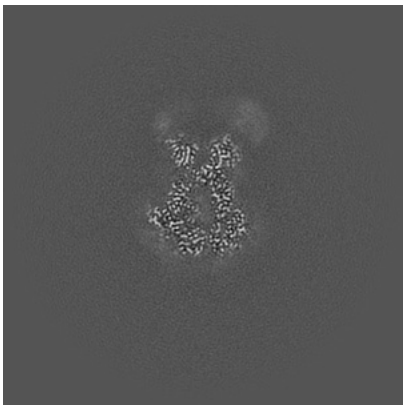


Z Index: 200

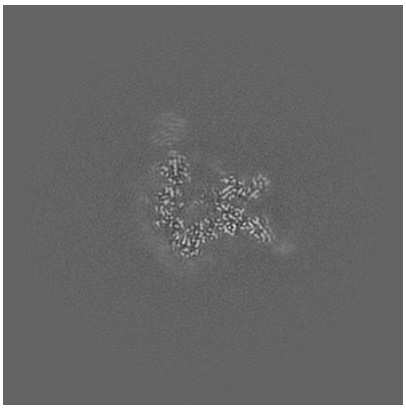
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

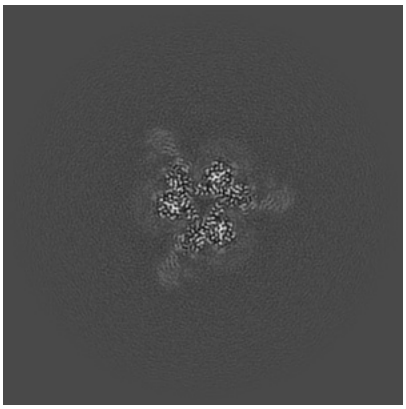
6.3.1 Primary map



X Index: 214

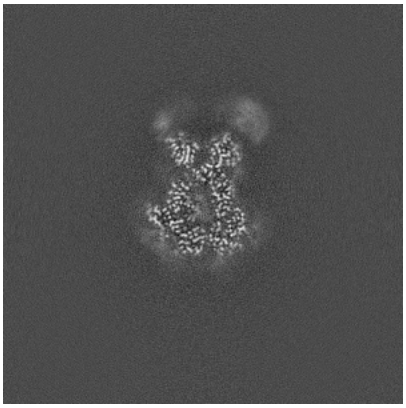


Y Index: 208

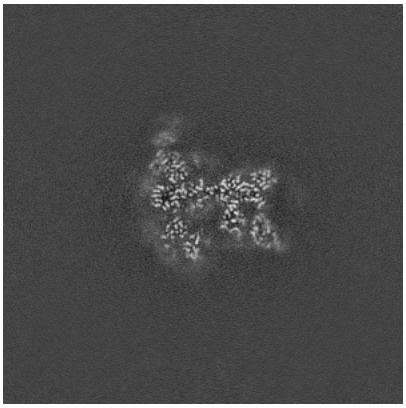


Z Index: 173

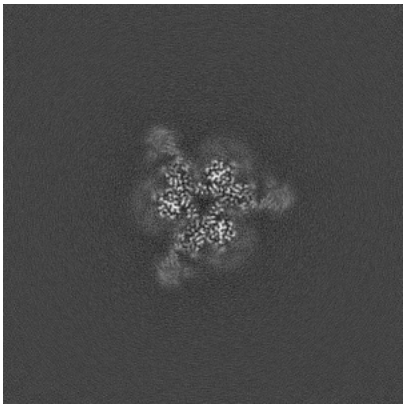
6.3.2 Raw map



X Index: 214



Y Index: 216

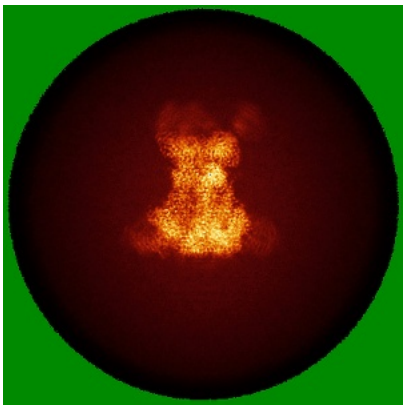


Z Index: 173

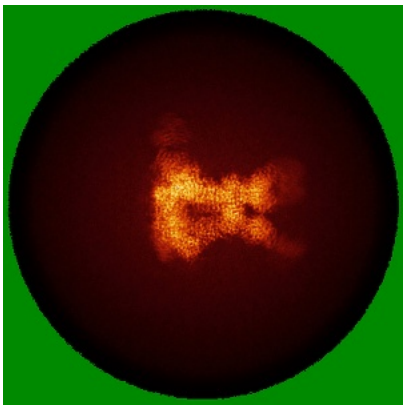
The images above show the largest variance slices of the map in three orthogonal directions.

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

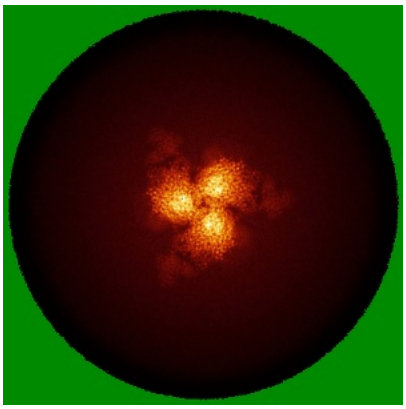
6.4.1 Primary map



X

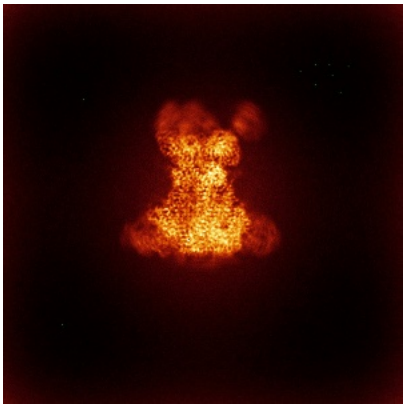


Y

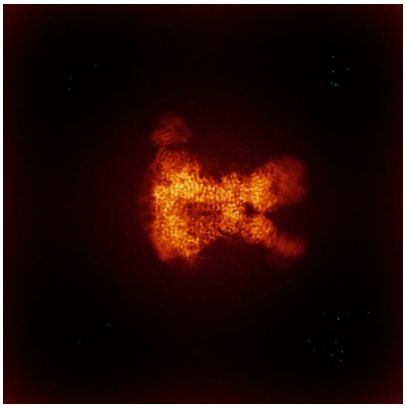


Z

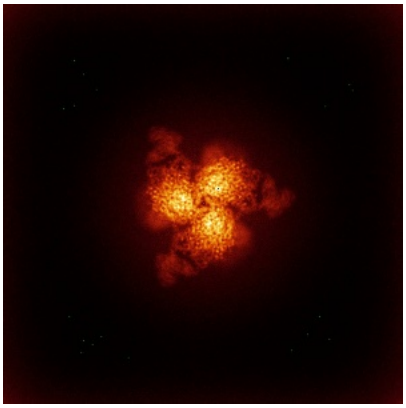
6.4.2 Raw map



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

6.5.2 Raw map



X Y Z

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

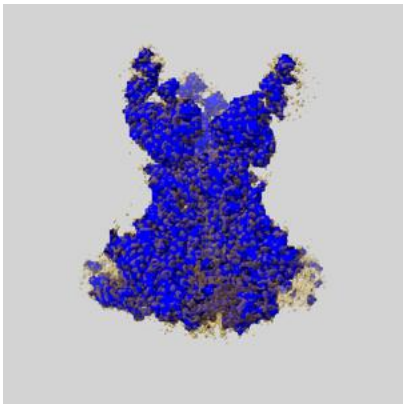
6.6 Mask visualisation

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

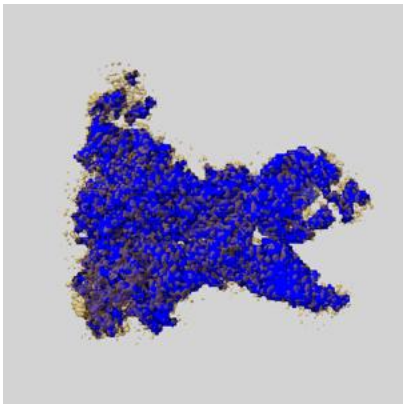
A mask typically either:

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

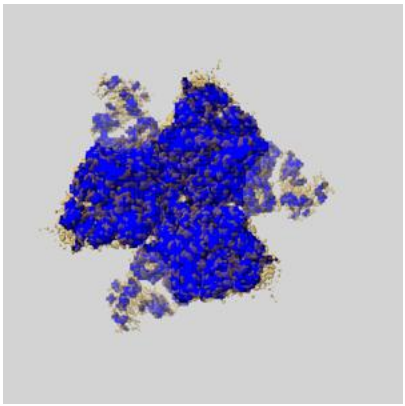
6.6.1 emd_70319_msk_1.map



X



Y

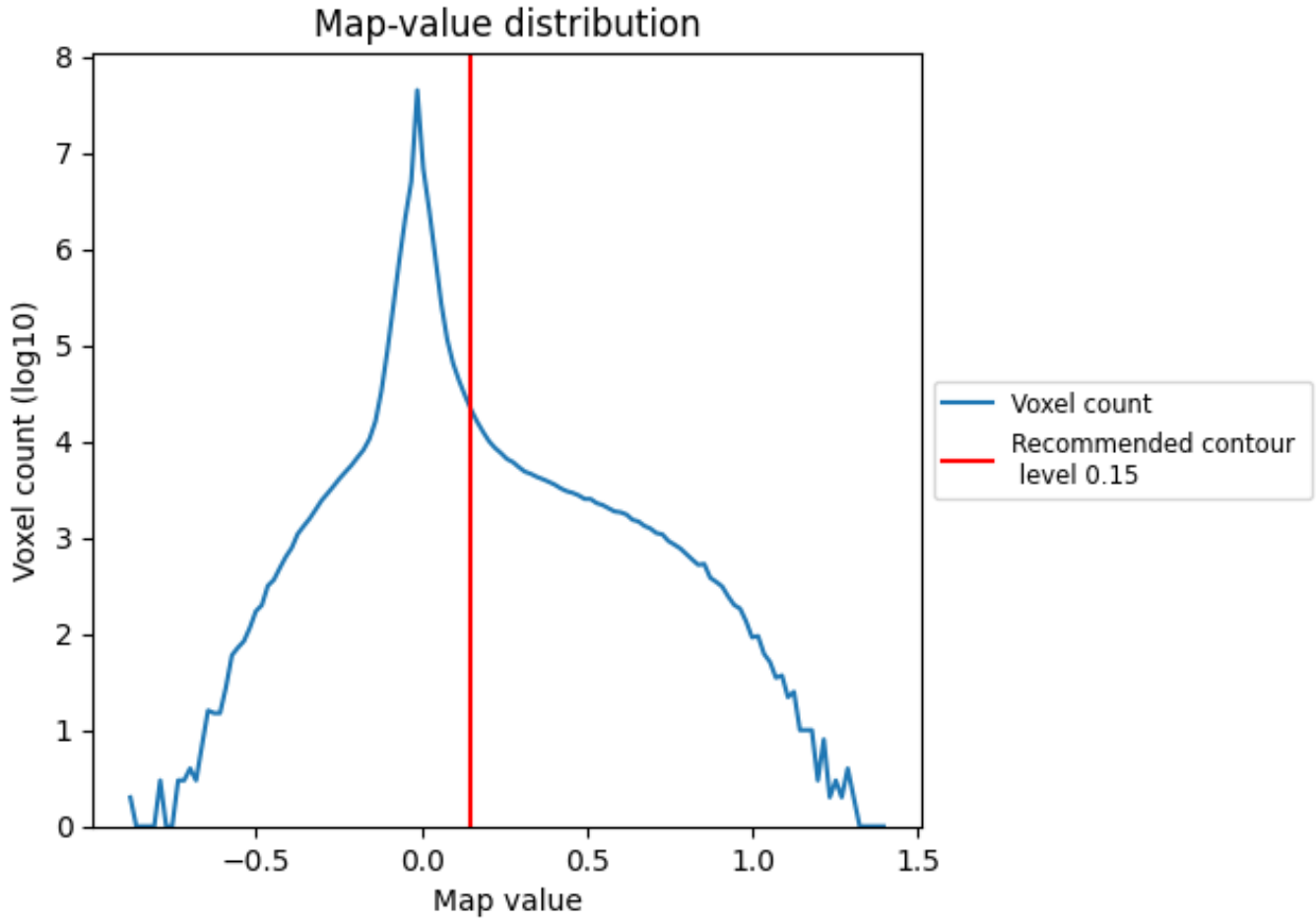


Z

7 Map analysis

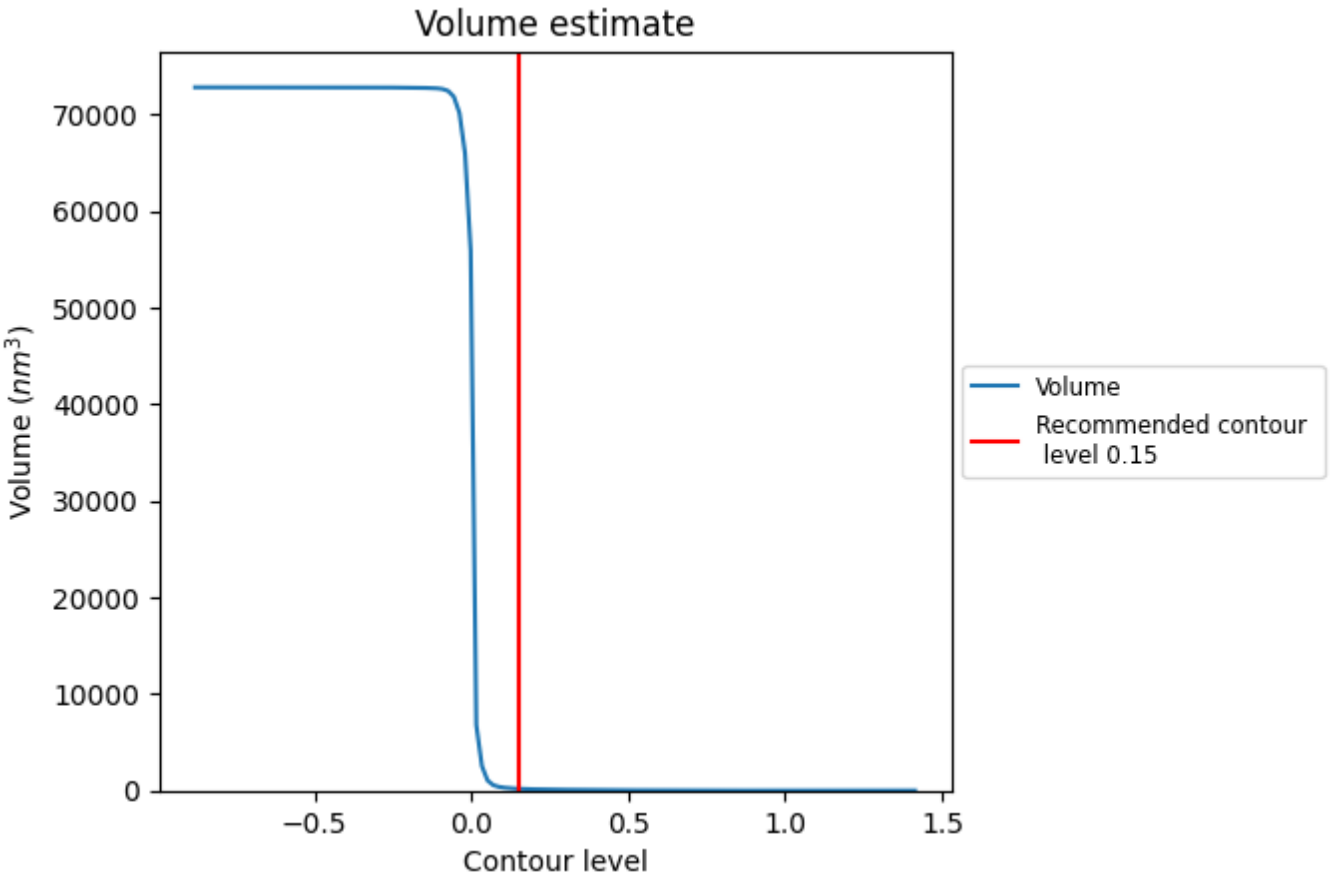
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

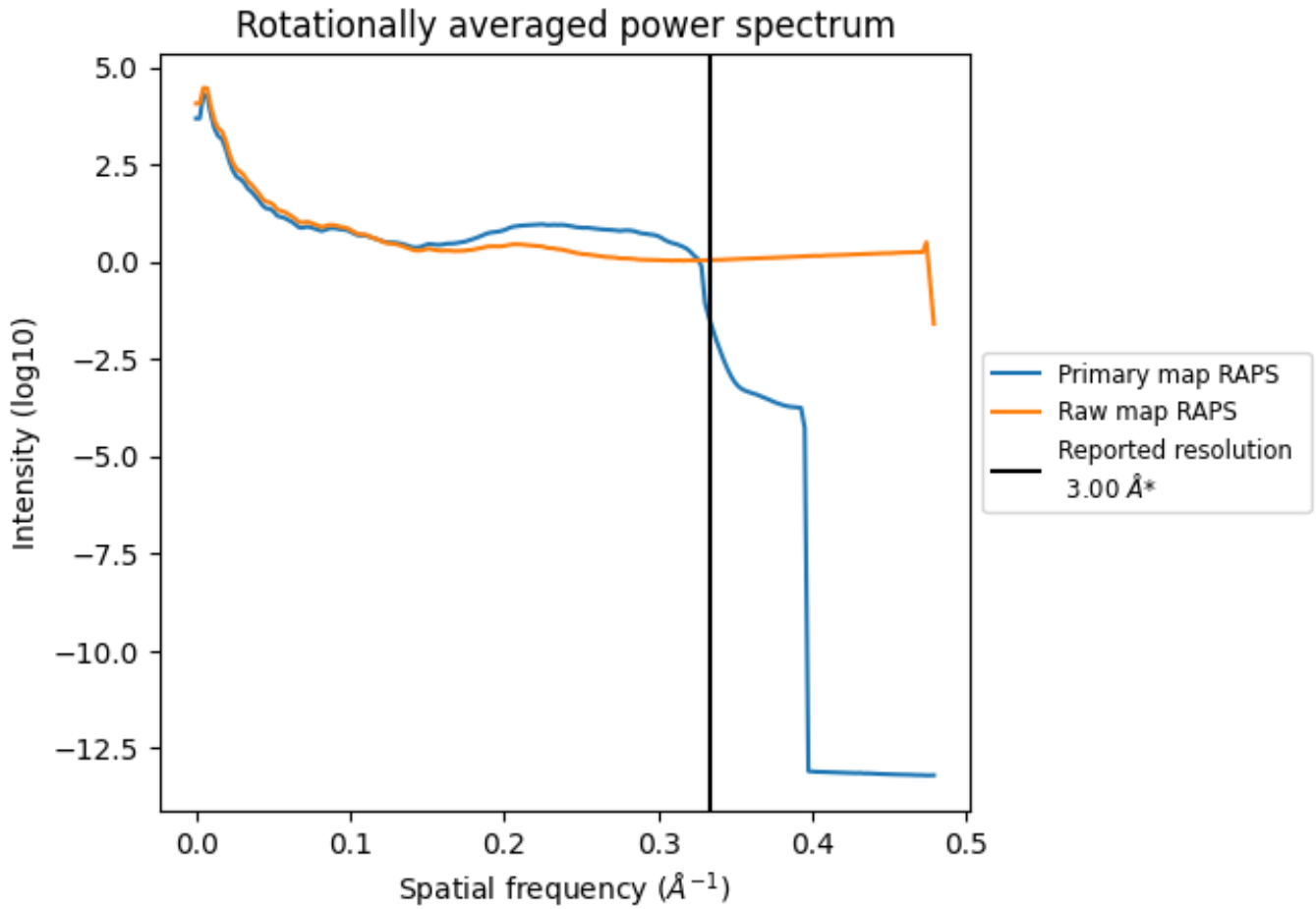
7.2 Volume estimate (i)



The volume at the recommended contour level is 186 nm^3; this corresponds to an approximate mass of 168 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)

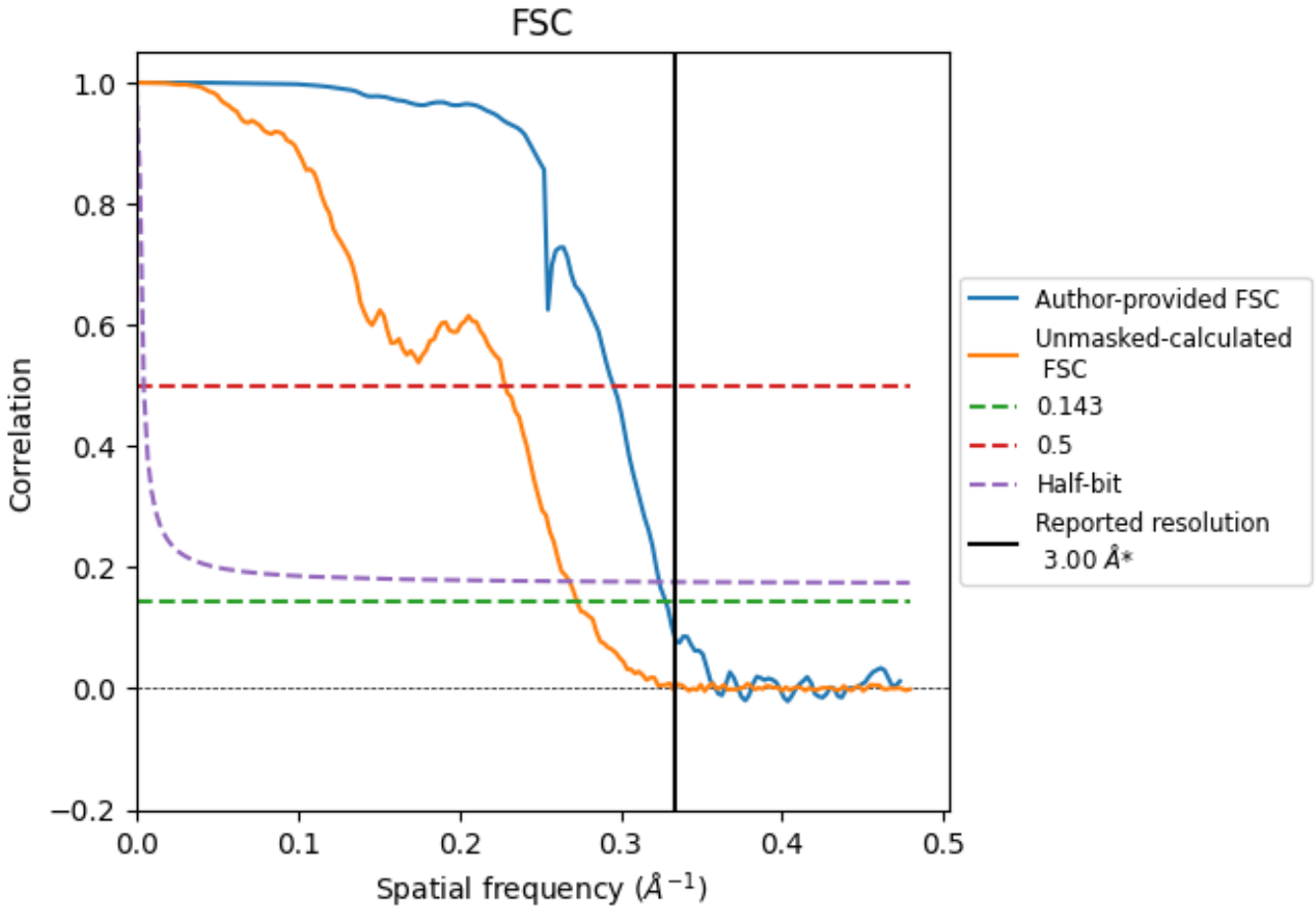


*Reported resolution corresponds to spatial frequency of 0.333 $Å^{-1}$

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 0.333 Å^{-1}

8.2 Resolution estimates (i)

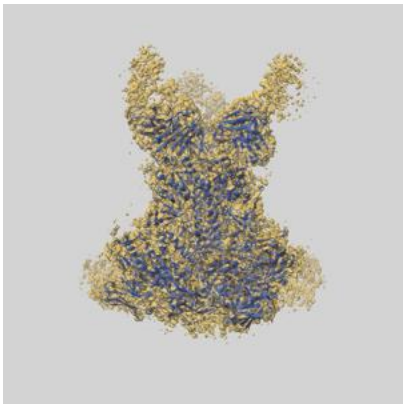
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.05	3.38	3.09
Unmasked-calculated*	3.66	4.38	3.73

*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 3.66 differs from the reported value 3.0 by more than 10 %

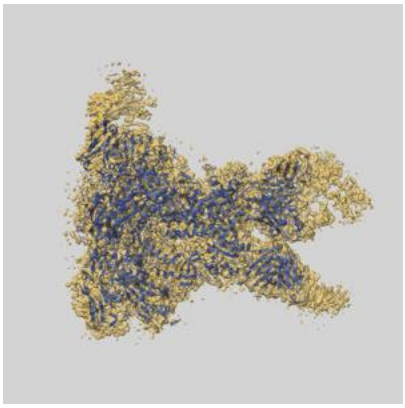
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-70319 and PDB model 9OCN. Per-residue inclusion information can be found in section 3 on page 14.

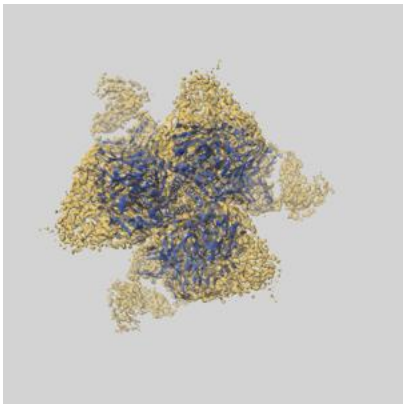
9.1 Map-model overlay



X



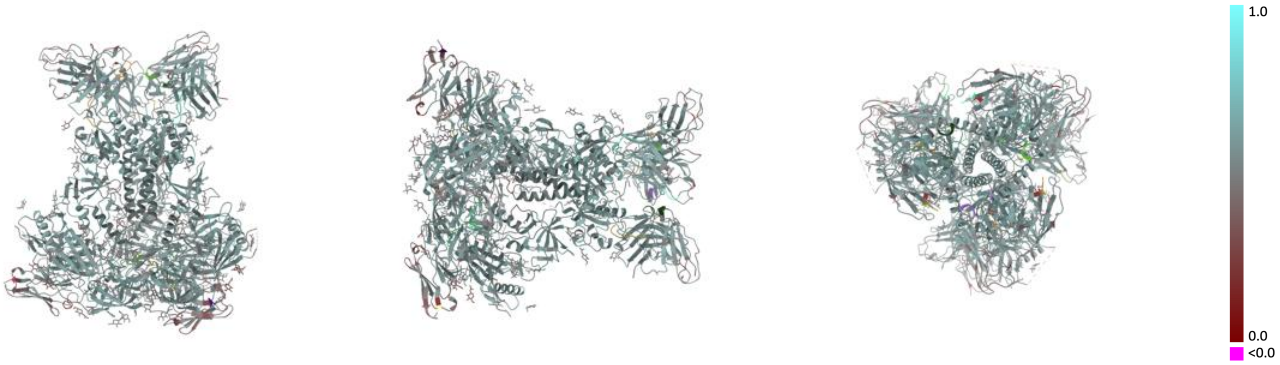
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15 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.

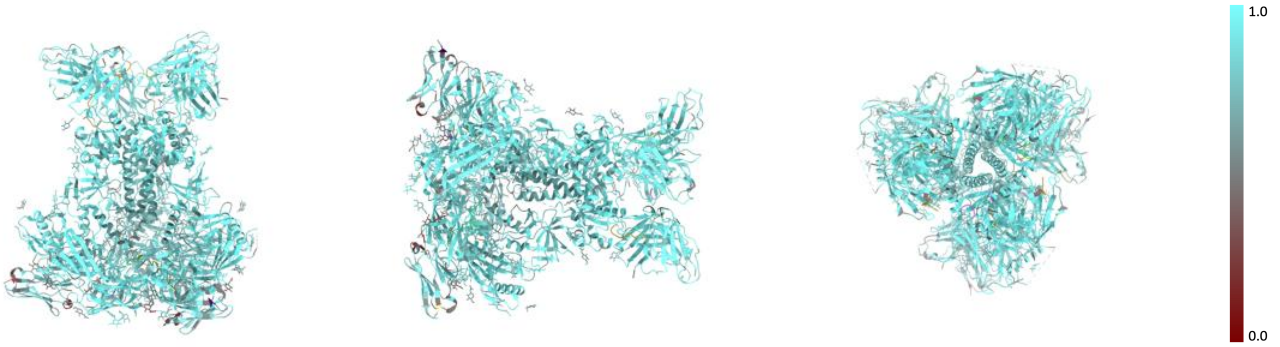
9.2 Q-score mapped to coordinate model (i)



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.

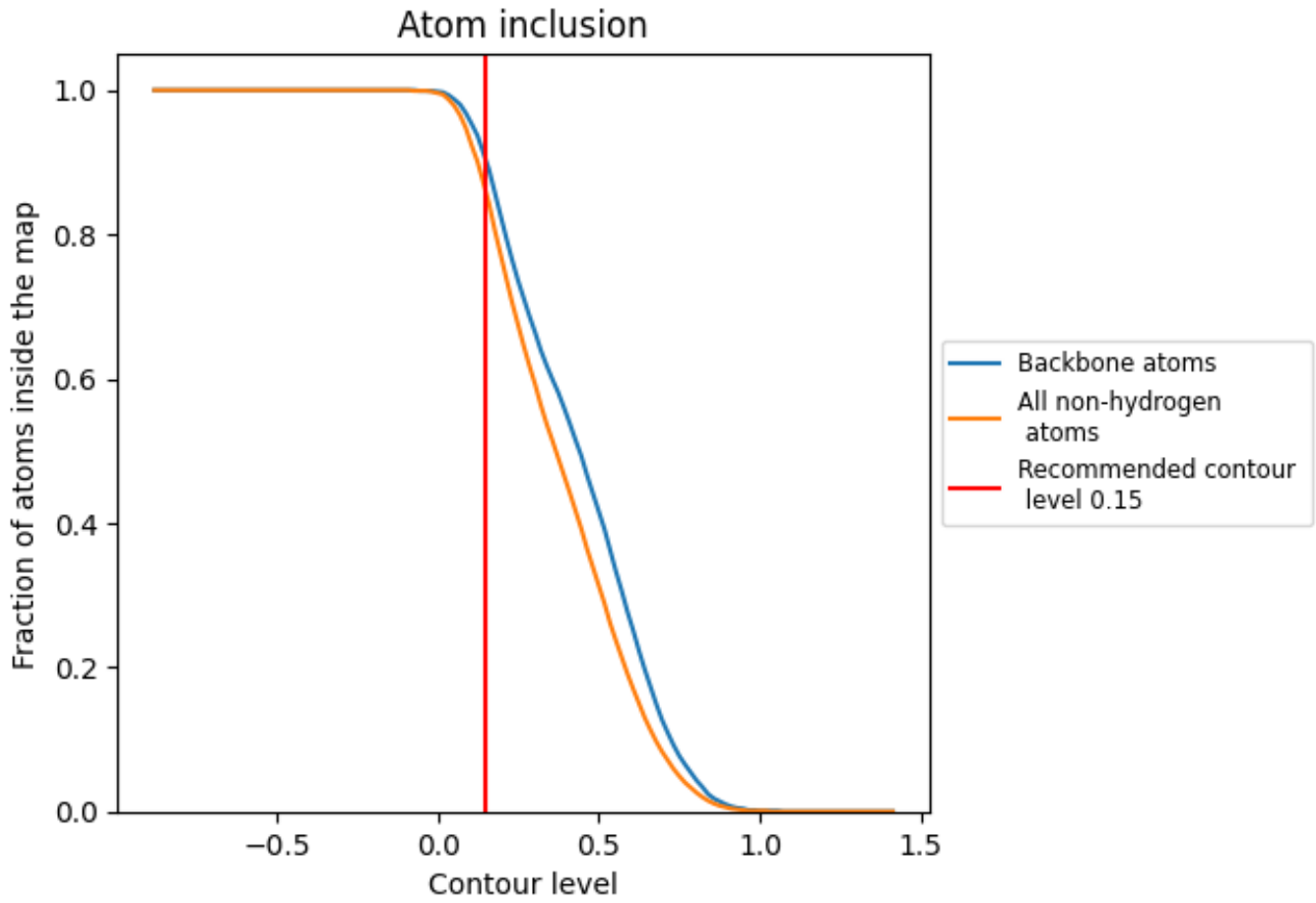
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.15).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 86% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8590	0.5450
A	0.8830	0.5610
B	0.8900	0.5680
C	0.8860	0.5590
D	0.8810	0.5600
E	0.8870	0.5710
F	0.8880	0.5720
G	0.8200	0.5430
H	0.8210	0.5420
I	0.8210	0.5430
J	0.7320	0.4780
K	0.7330	0.4810
L	0.7310	0.4820
M	0.8960	0.5530
N	0.8670	0.5210
O	0.8940	0.5520
P	0.8970	0.5510
Q	0.8700	0.5240
R	0.8730	0.5230
S	0.8210	0.5180
T	0.8600	0.5170
U	0.6790	0.4760
V	0.7140	0.4850
W	0.6790	0.4480
X	0.4100	0.4570
Y	0.8210	0.4990
Z	0.8800	0.5130
a	0.6790	0.4730
b	0.7500	0.4790
c	0.7140	0.4450
d	0.4100	0.4560
e	0.8210	0.5180
f	0.8600	0.4980
g	0.7140	0.4650
h	0.6790	0.4780



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Chain	Atom inclusion	Q-score
i	0.6790	0.4170
j	0.4100	0.4520