wwPDB EM Validation Summary Report (i)

Dec 7, 2022 – 09:04 AM JST

PDB ID	:	5JNX
EMDB ID	:	EMD-8169
Title	:	The 6.6 A cryo-EM structure of the full-length human NPC1 in complex with the cleaved glycoprotein of Ebola virus
Authors	:	Gong, X.; Qian, H.W.; Zhou, X.H.; Wu, J.P.; Wan, T.; Shi, Y.; Gao, F.; Zhou, Q.; Yan, N.
Deposited on	:	2016-05-01
Resolution	:	6.56 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:

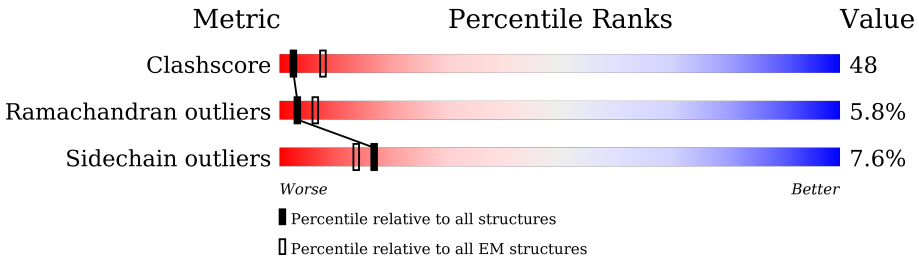
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 6.56 Å.

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



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

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	1278	10% 47% 30% 10% • 11%
2	C	158	14% 86% 12% •
2	E	158	14% 80% 18% •
2	G	158	18% 86% 12% •
3	D	130	8% 52% 14% • 33%
3	F	130	5% 52% 14% • 33%
3	H	130	6% 52% 14% • 33%
4	B	2	100%

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Mol	Chain	Length	Quality of chain
4	I	2	50% 50% 50%
4	K	2	50% 50%
4	M	2	100% 50% 50%
4	N	2	50% 50% 50%
4	O	2	100% 50% 50%
4	P	2	50% 50%
5	J	3	100%
6	L	4	100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	J	1	-	-	X	-
5	NAG	J	2	-	-	X	-
6	NAG	L	1	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 13749 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 Niemann-Pick C1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1133	Total	C	N	O	S	1	0
			7695	4862	1315	1476	42		

- Molecule 2 is a protein called Envelope glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	158	Total	C	N	O	S	0	0
			1194	757	209	223	5		
2	E	158	Total	C	N	O	S	0	0
			1194	757	209	223	5		
2	G	158	Total	C	N	O	S	0	0
			1194	757	209	223	5		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	31	ARG	-	expression tag	UNP P87666
C	42	VAL	THR	engineered mutation	UNP P87666
E	31	ARG	-	expression tag	UNP P87666
E	42	VAL	THR	engineered mutation	UNP P87666
G	31	ARG	-	expression tag	UNP P87666
G	42	VAL	THR	engineered mutation	UNP P87666

- Molecule 3 is a protein called Envelope glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	87	Total	C	N	O	S	0	0
			687	441	121	122	3		
3	F	87	Total	C	N	O	S	0	0
			687	441	121	122	3		
3	H	87	Total	C	N	O	S	0	0
			687	441	121	122	3		

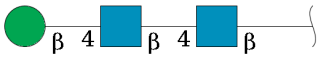
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	633	HIS	-	expression tag	UNP P87666
D	634	HIS	-	expression tag	UNP P87666
D	635	HIS	-	expression tag	UNP P87666
D	636	HIS	-	expression tag	UNP P87666
D	637	HIS	-	expression tag	UNP P87666
D	638	HIS	-	expression tag	UNP P87666
F	633	HIS	-	expression tag	UNP P87666
F	634	HIS	-	expression tag	UNP P87666
F	635	HIS	-	expression tag	UNP P87666
F	636	HIS	-	expression tag	UNP P87666
F	637	HIS	-	expression tag	UNP P87666
F	638	HIS	-	expression tag	UNP P87666
H	633	HIS	-	expression tag	UNP P87666
H	634	HIS	-	expression tag	UNP P87666
H	635	HIS	-	expression tag	UNP P87666
H	636	HIS	-	expression tag	UNP P87666
H	637	HIS	-	expression tag	UNP P87666
H	638	HIS	-	expression tag	UNP P87666

- Molecule 4 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
4	B	2	Total	C	N	O	0	0
			28	16	2	10		
4	I	2	Total	C	N	O	0	0
			28	16	2	10		
4	K	2	Total	C	N	O	0	0
			28	16	2	10		
4	M	2	Total	C	N	O	0	0
			28	16	2	10		
4	N	2	Total	C	N	O	0	0
			28	16	2	10		
4	O	2	Total	C	N	O	0	0
			28	16	2	10		
4	P	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 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.

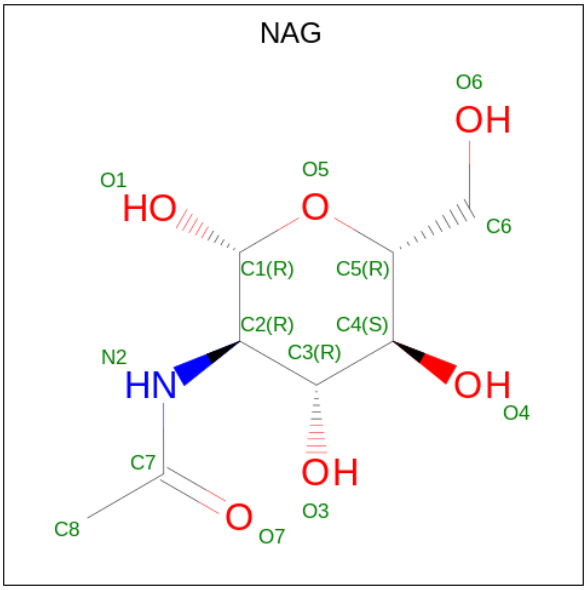


Mol	Chain	Residues	Atoms				AltConf	Trace
5	J	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-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
6	L	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



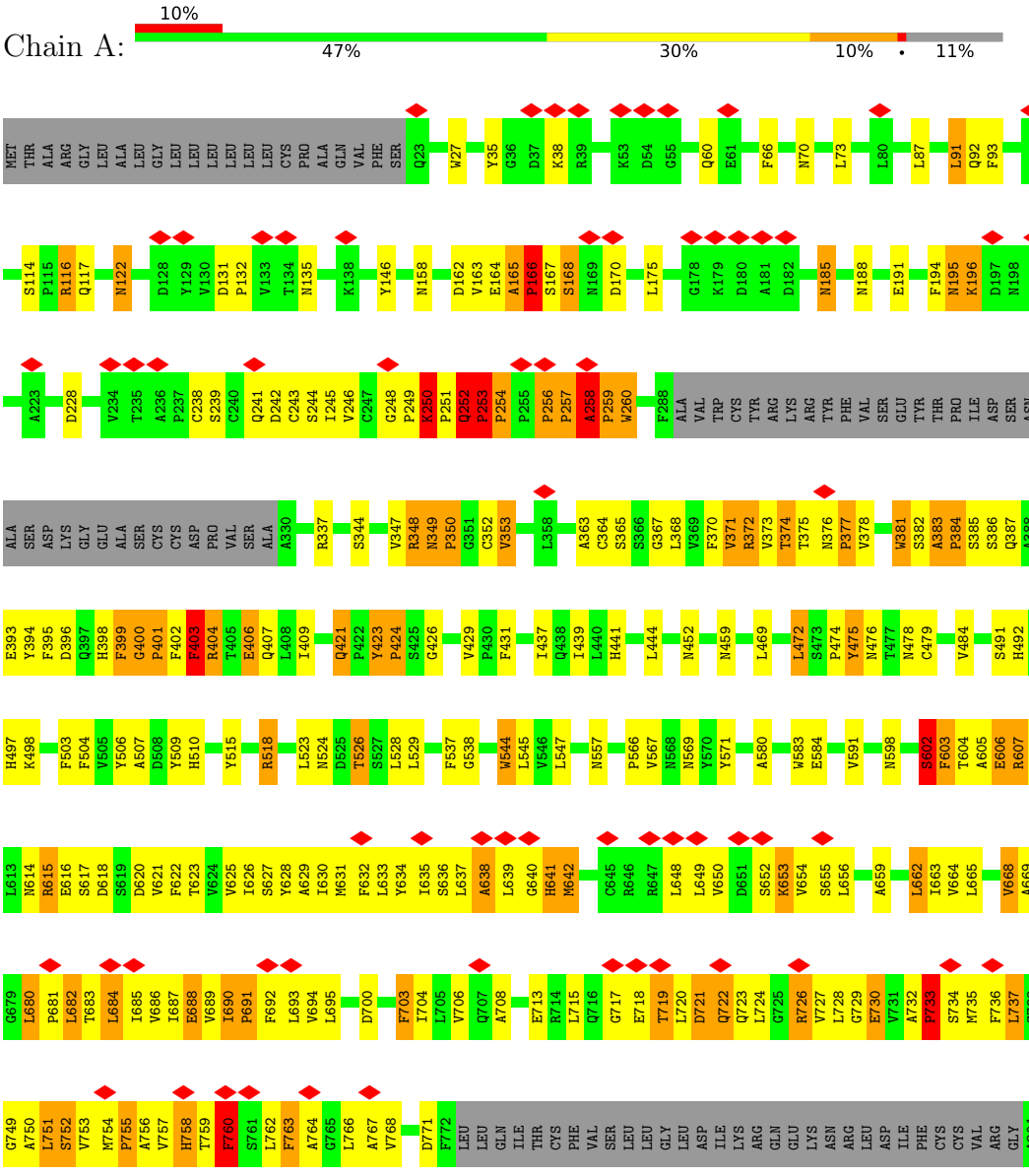
Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total 126	C 72	N 9	O 45	0
7	A	1	Total 126	C 72	N 9	O 45	0
7	A	1	Total 126	C 72	N 9	O 45	0
7	A	1	Total 126	C 72	N 9	O 45	0
7	A	1	Total 126	C 72	N 9	O 45	0
7	A	1	Total 126	C 72	N 9	O 45	0
7	A	1	Total 126	C 72	N 9	O 45	0
7	A	1	Total 126	C 72	N 9	O 45	0
7	A	1	Total 126	C 72	N 9	O 45	0

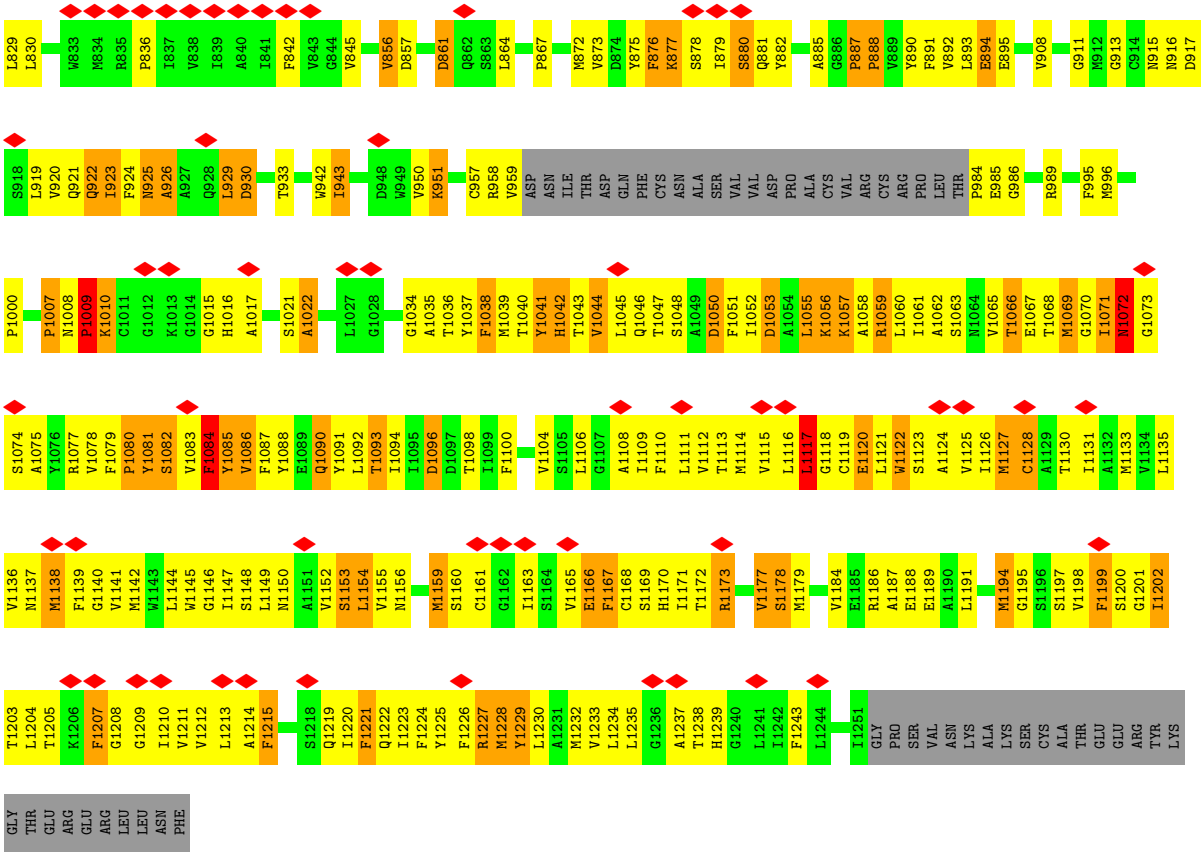
3 Residue-property plots (i)

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: Niemann-Pick C1 protein

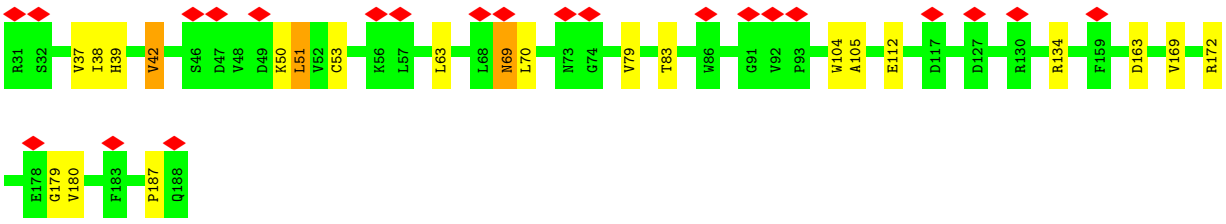
Chain A:





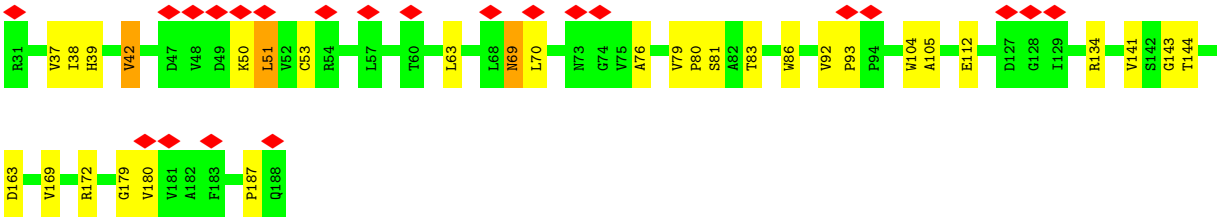
• Molecule 2: Envelope glycoprotein

Chain C:



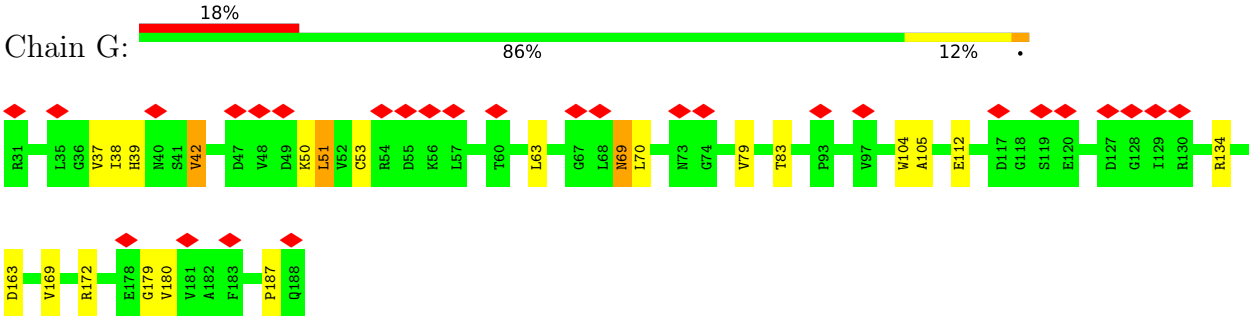
• Molecule 2: Envelope glycoprotein

Chain E:



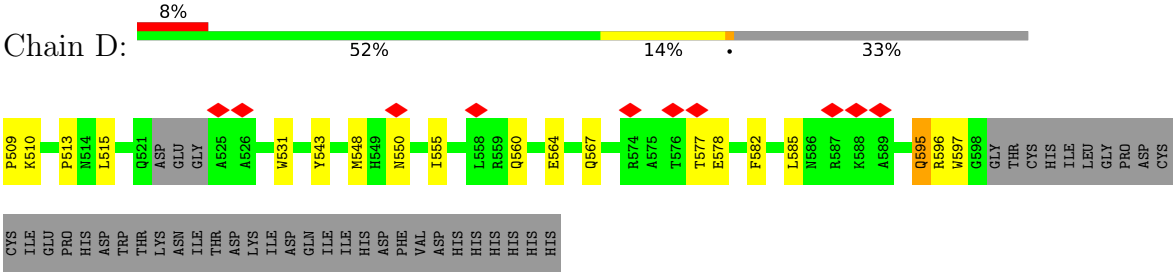
• Molecule 2: Envelope glycoprotein

Chain G:



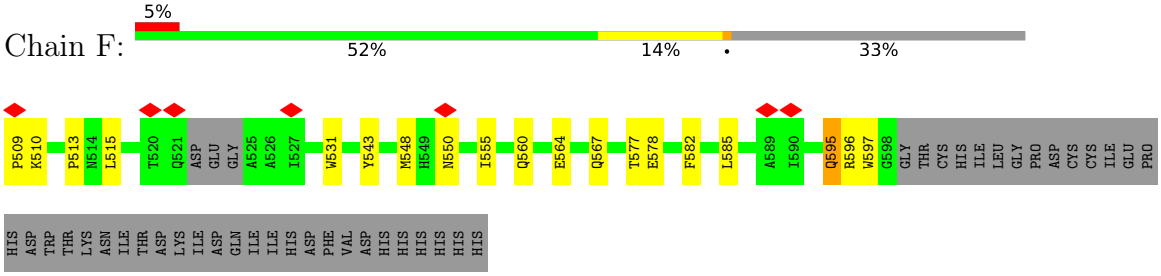
• Molecule 3: Envelope glycoprotein

Chain D:



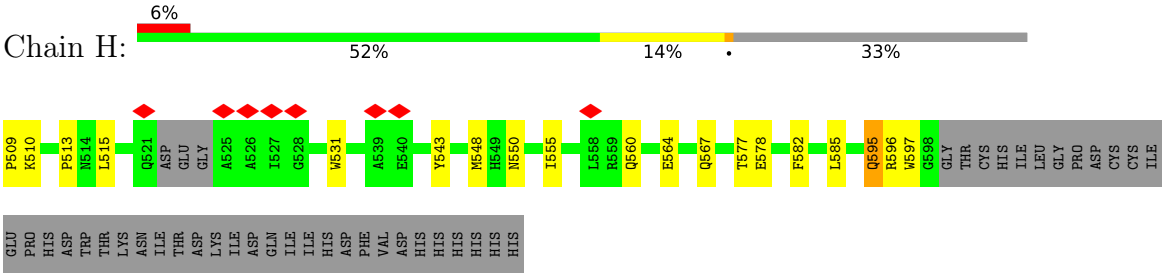
• Molecule 3: Envelope glycoprotein

Chain F:



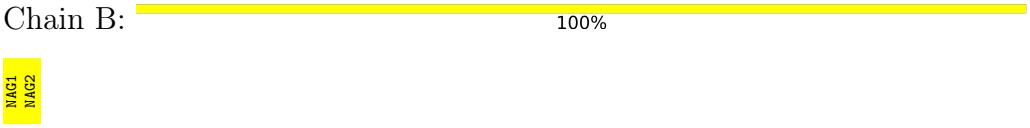
• Molecule 3: Envelope glycoprotein

Chain H:



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

Chain B:



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

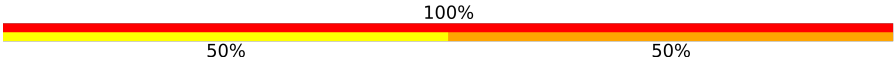
Chain I:

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

Chain K:

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

Chain M:

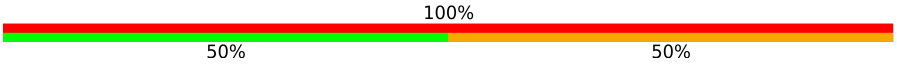


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:

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

Chain O:

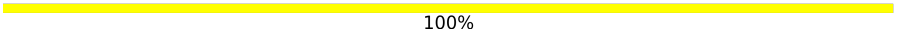


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:

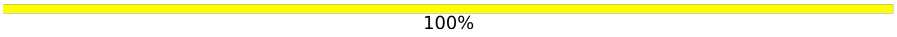
• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:



• Molecule 6: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	50223	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1700	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	38270	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.090	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	334.47424, 334.47424, 334.47424	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.30654, 1.30654, 1.30654	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	0.49	6/7843 (0.1%)	0.67	29/10748 (0.3%)
2	C	0.42	0/1223	0.59	1/1664 (0.1%)
2	E	0.44	0/1223	0.59	1/1664 (0.1%)
2	G	0.43	0/1223	0.59	1/1664 (0.1%)
3	D	0.42	0/702	0.62	0/952
3	F	0.42	0/702	0.62	0/952
3	H	0.42	0/702	0.62	0/952
All	All	0.47	6/13618 (0.0%)	0.64	32/18596 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
2	C	0	1
2	E	0	1
2	G	0	1
All	All	0	5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	429	VAL	C-N	-5.49	1.23	1.34
1	A	166	PRO	N-CD	5.22	1.55	1.47
1	A	469	LEU	C-N	-5.20	1.22	1.34
1	A	424	PRO	N-CD	5.08	1.54	1.47
1	A	249	PRO	N-CD	5.07	1.54	1.47

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	602	SER	CB-CA-C	-9.99	91.12	110.10
1	A	755	PRO	CA-N-CD	-8.22	99.99	111.50
1	A	996	MET	C-N-CA	-6.63	105.12	121.70
1	A	887	PRO	N-CA-CB	6.58	111.20	103.30
1	A	836	PRO	N-CA-CB	6.46	111.06	103.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	602	SER	Peptide
1	A	603	PHE	Peptide
2	C	69	ASN	Sidechain
2	E	69	ASN	Sidechain
2	G	69	ASN	Sidechain

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	7695	0	6476	1133	0
2	C	1194	0	1153	17	0
2	E	1194	0	1153	69	0
2	G	1194	0	1153	17	0
3	D	687	0	679	19	0
3	F	687	0	679	20	0
3	H	687	0	679	18	0
4	B	28	0	25	0	0
4	I	28	0	25	2	0
4	K	28	0	25	3	0
4	M	28	0	25	3	0
4	N	28	0	25	1	0
4	O	28	0	25	2	0
4	P	28	0	25	1	0
5	J	39	0	34	17	0
6	L	50	0	43	9	0
7	A	126	0	117	8	0
All	All	13749	0	12341	1252	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 48.

The worst 5 of 1252 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:724:LEU:HD22	1:A:1170:HIS:CE1	1.29	1.62
1:A:656:LEU:CD1	1:A:685:ILE:HG13	1.17	1.60
1:A:656:LEU:HD11	1:A:685:ILE:CG1	1.31	1.58
1:A:598:ASN:HD21	4:K:1:NAG:C1	0.99	1.57
1:A:693:LEU:HD11	1:A:763:PHE:CE2	1.41	1.53

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	1126/1278 (88%)	897 (80%)	135 (12%)	94 (8%)	1	12
2	C	156/158 (99%)	142 (91%)	12 (8%)	2 (1%)	12	48
2	E	156/158 (99%)	141 (90%)	13 (8%)	2 (1%)	12	48
2	G	156/158 (99%)	142 (91%)	12 (8%)	2 (1%)	12	48
3	D	83/130 (64%)	77 (93%)	4 (5%)	2 (2%)	6	33
3	F	83/130 (64%)	77 (93%)	4 (5%)	2 (2%)	6	33
3	H	83/130 (64%)	77 (93%)	4 (5%)	2 (2%)	6	33
All	All	1843/2142 (86%)	1553 (84%)	184 (10%)	106 (6%)	3	18

5 of 106 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	250	LYS
1	A	256	PRO

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Mol	Chain	Res	Type
1	A	350	PRO
1	A	372	ARG
1	A	374	THR

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	643/1109 (58%)	558 (87%)	85 (13%)	4 18
2	C	126/130 (97%)	124 (98%)	2 (2%)	62 79
2	E	126/130 (97%)	124 (98%)	2 (2%)	62 79
2	G	126/130 (97%)	124 (98%)	2 (2%)	62 79
3	D	70/111 (63%)	69 (99%)	1 (1%)	67 80
3	F	70/111 (63%)	69 (99%)	1 (1%)	67 80
3	H	70/111 (63%)	69 (99%)	1 (1%)	67 80
All	All	1231/1832 (67%)	1137 (92%)	94 (8%)	17 37

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1057	LYS
1	A	1138	MET
1	A	1066	THR
1	A	1082	SER
1	A	1166	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	554	ASN
2	G	69	ASN
1	A	1046	GLN
2	E	69	ASN

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Mol	Chain	Res	Type
1	A	722	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)

21 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	$\#\|Z\| > 2$
4	NAG	B	1	4,1	14,14,15	0.66	0	17,19,21	1.09	1 (5%)
4	NAG	B	2	4	14,14,15	0.57	0	17,19,21	0.73	1 (5%)
4	NAG	I	1	4,1	14,14,15	0.48	0	17,19,21	1.45	3 (17%)
4	NAG	I	2	4	14,14,15	0.29	0	17,19,21	0.62	0
5	NAG	J	1	5,1	14,14,15	0.31	0	17,19,21	0.56	0
5	NAG	J	2	5	14,14,15	0.30	0	17,19,21	0.61	0
5	BMA	J	3	5	11,11,12	0.27	0	15,15,17	0.63	0
4	NAG	K	1	4,1	14,14,15	0.35	0	17,19,21	1.55	3 (17%)
4	NAG	K	2	4	14,14,15	0.64	0	17,19,21	1.10	1 (5%)
6	NAG	L	1	1,6	14,14,15	0.29	0	17,19,21	0.61	0
6	NAG	L	2	6	14,14,15	0.27	0	17,19,21	0.81	0
6	BMA	L	3	6	11,11,12	0.29	0	15,15,17	0.72	0
6	MAN	L	4	6	11,11,12	0.36	0	15,15,17	1.15	1 (6%)
4	NAG	M	1	4,1	14,14,15	0.40	0	17,19,21	1.16	2 (11%)
4	NAG	M	2	4	14,14,15	0.40	0	17,19,21	1.16	2 (11%)
4	NAG	N	1	4,3	14,14,15	0.70	0	17,19,21	0.99	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	NAG	N	2	4	14,14,15	0.29	0	17,19,21	0.55	0
4	NAG	O	1	4,3	14,14,15	0.71	0	17,19,21	0.99	1 (5%)
4	NAG	O	2	4	14,14,15	0.29	0	17,19,21	0.56	0
4	NAG	P	1	4,3	14,14,15	0.69	0	17,19,21	0.98	1 (5%)
4	NAG	P	2	4	14,14,15	0.29	0	17,19,21	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
4	NAG	B	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	B	2	4	-	0/6/23/26	0/1/1/1
4	NAG	I	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	I	2	4	-	4/6/23/26	0/1/1/1
5	NAG	J	1	5,1	-	5/6/23/26	0/1/1/1
5	NAG	J	2	5	-	2/6/23/26	0/1/1/1
5	BMA	J	3	5	-	2/2/19/22	0/1/1/1
4	NAG	K	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
6	NAG	L	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	L	2	6	-	0/6/23/26	0/1/1/1
6	BMA	L	3	6	-	0/2/19/22	0/1/1/1
6	MAN	L	4	6	-	2/2/19/22	0/1/1/1
4	NAG	M	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	0/6/23/26	0/1/1/1
4	NAG	N	1	4,3	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	4/6/23/26	0/1/1/1
4	NAG	O	1	4,3	-	0/6/23/26	0/1/1/1
4	NAG	O	2	4	-	4/6/23/26	0/1/1/1
4	NAG	P	1	4,3	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	I	1	NAG	O5-C1-C2	-4.28	104.53	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	L	4	MAN	C1-C2-C3	3.47	113.93	109.67
4	K	1	NAG	C1-O5-C5	3.42	116.83	112.19
4	K	1	NAG	O4-C4-C3	-3.29	102.75	110.35
4	N	1	NAG	O5-C1-C2	-3.03	106.50	111.29

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	J	1	NAG	C8-C7-N2-C2
5	J	1	NAG	O7-C7-N2-C2
5	J	2	NAG	C8-C7-N2-C2
5	J	2	NAG	O7-C7-N2-C2
4	I	2	NAG	O5-C5-C6-O6

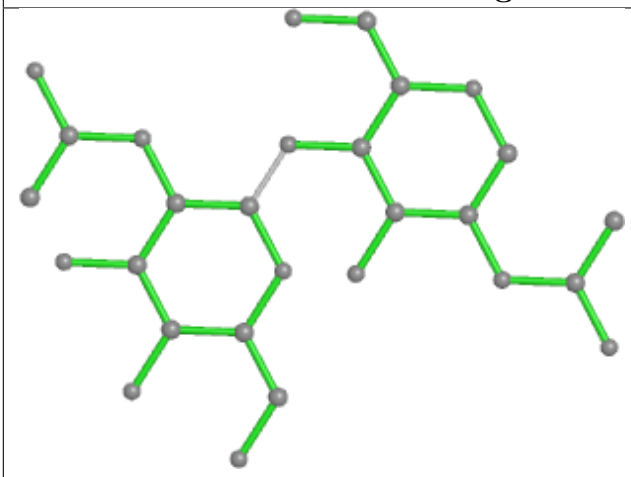
There are no ring outliers.

13 monomers are involved in 38 short contacts:

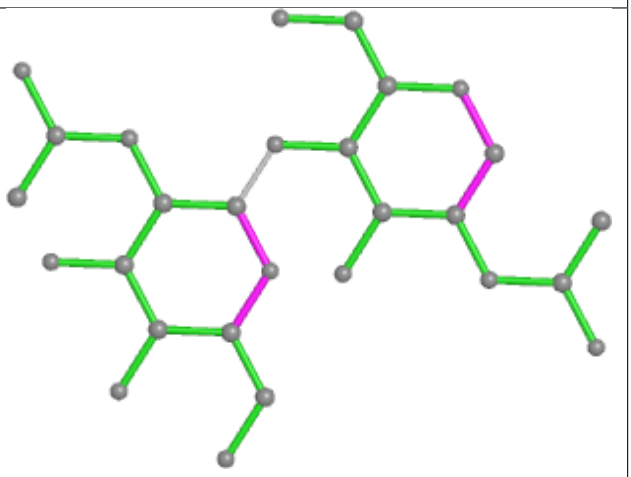
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	N	1	NAG	1	0
6	L	3	BMA	2	0
4	I	1	NAG	1	0
4	P	1	NAG	1	0
5	J	1	NAG	14	0
5	J	3	BMA	3	0
4	I	2	NAG	1	0
6	L	2	NAG	6	0
5	J	2	NAG	12	0
4	M	1	NAG	3	0
4	O	1	NAG	2	0
6	L	1	NAG	7	0
4	K	1	NAG	3	0

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

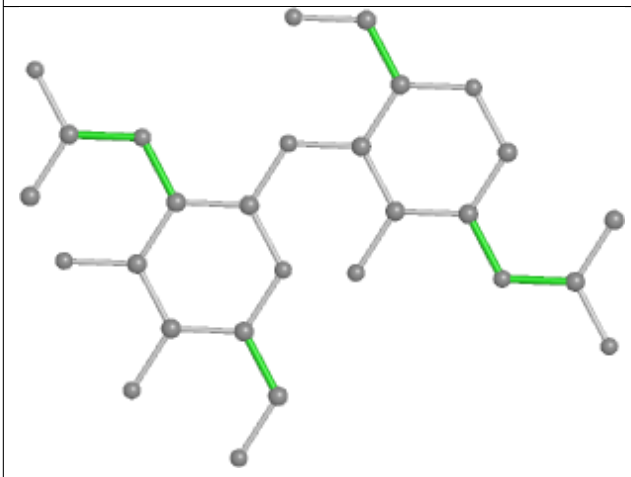
Oligosaccharide Chain B



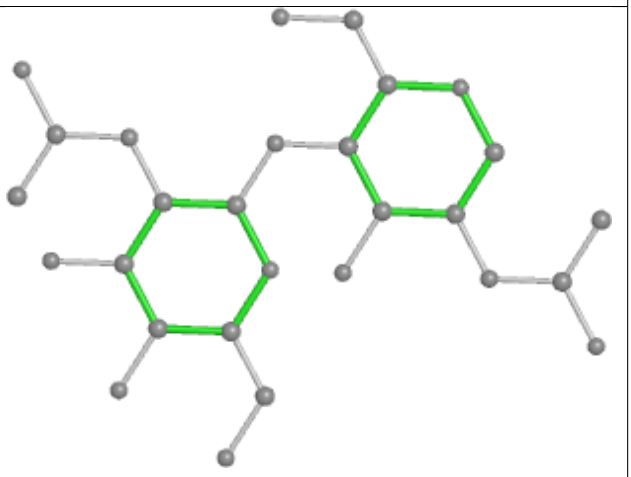
Bond lengths



Bond angles

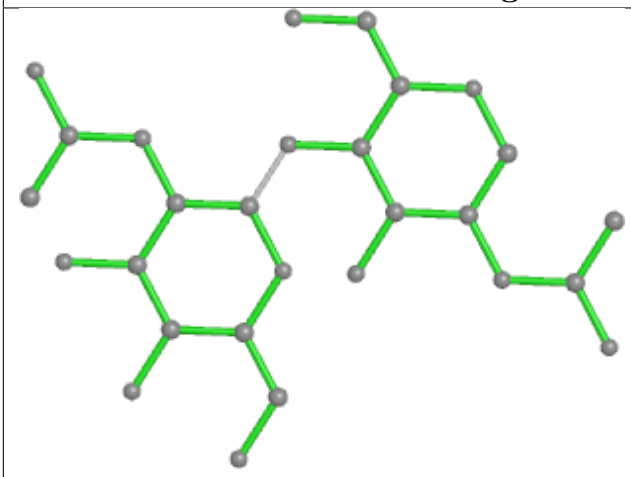


Torsions

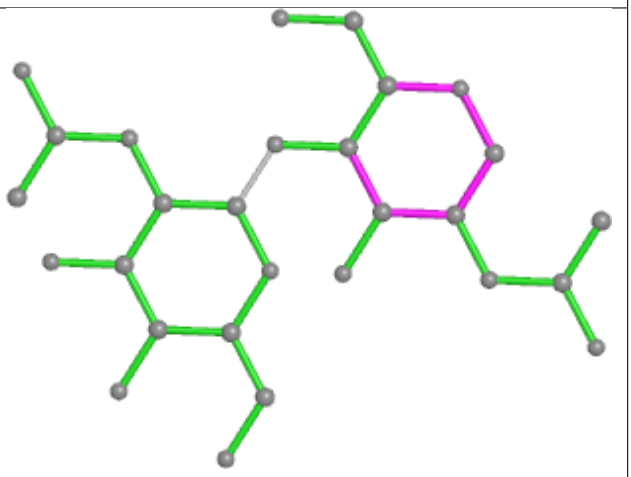


Rings

Oligosaccharide Chain I



Bond lengths



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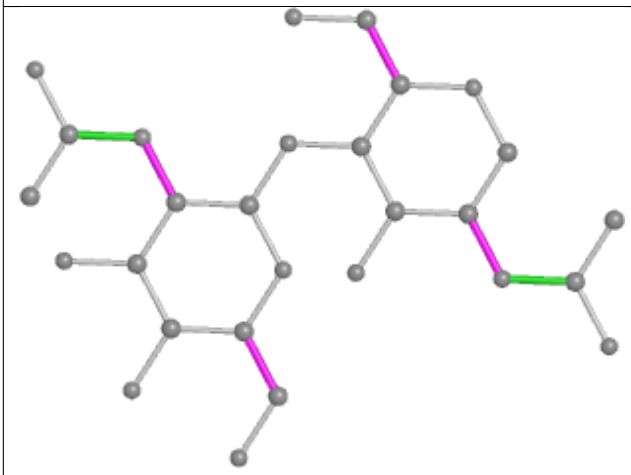

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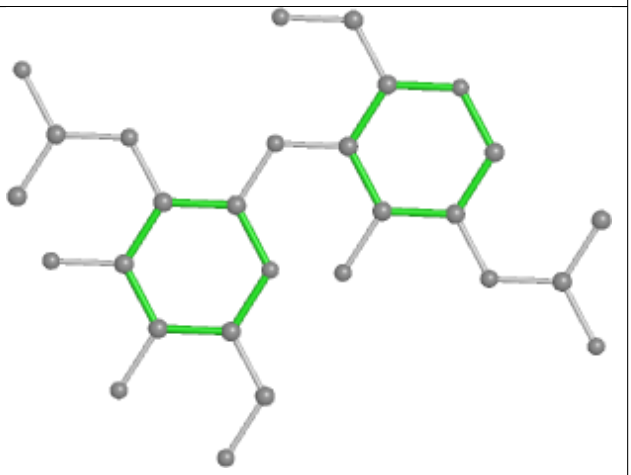
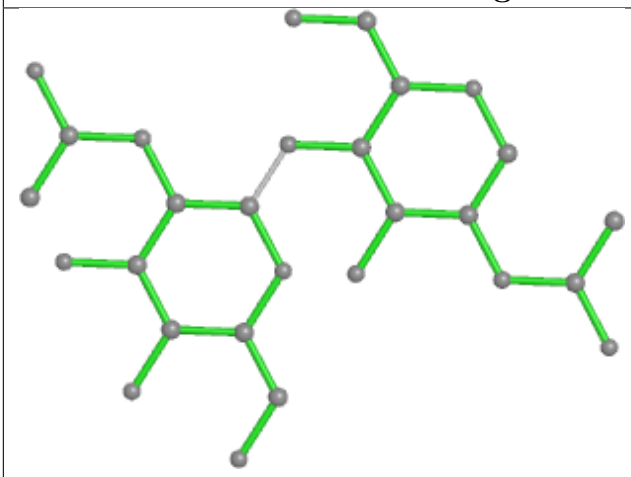
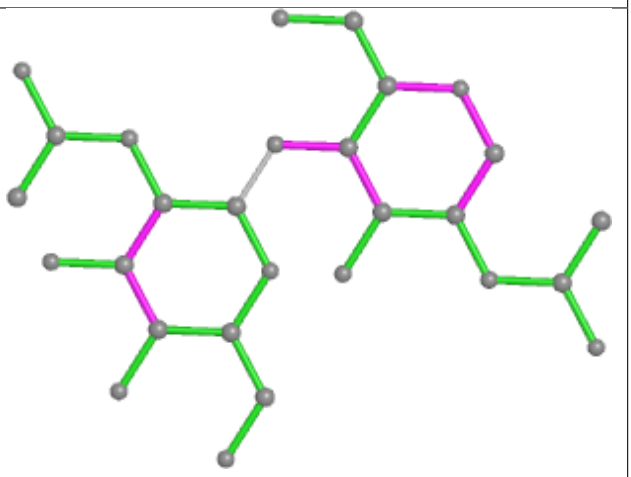


Rings

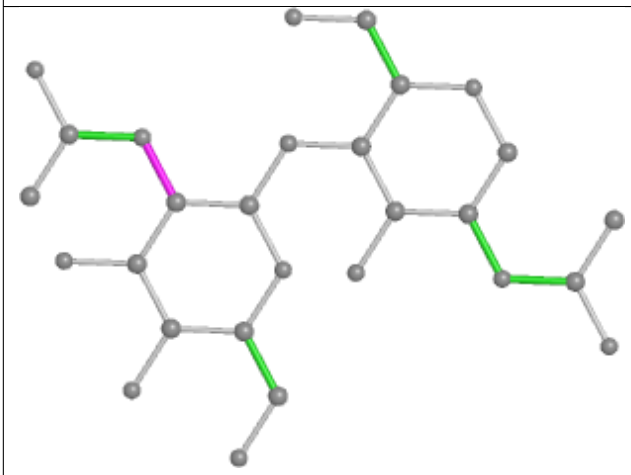
Oligosaccharide Chain K



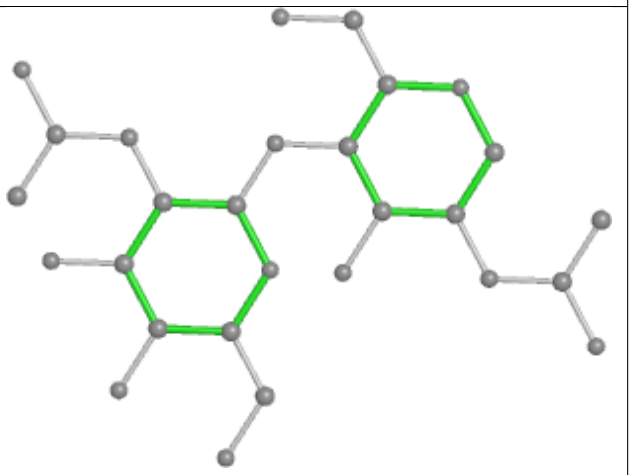
Bond lengths



Bond angles

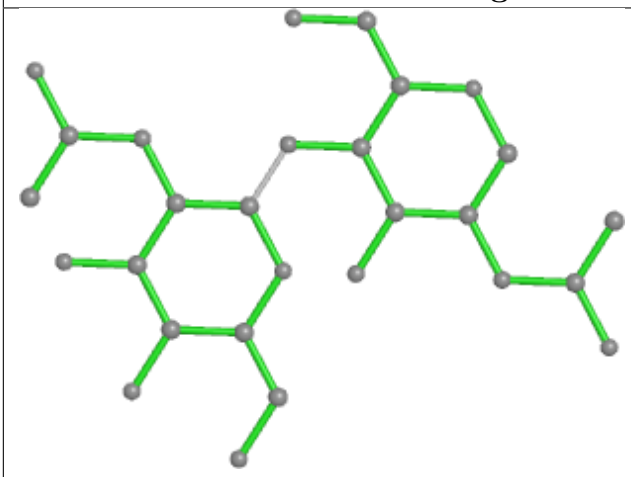


Torsions

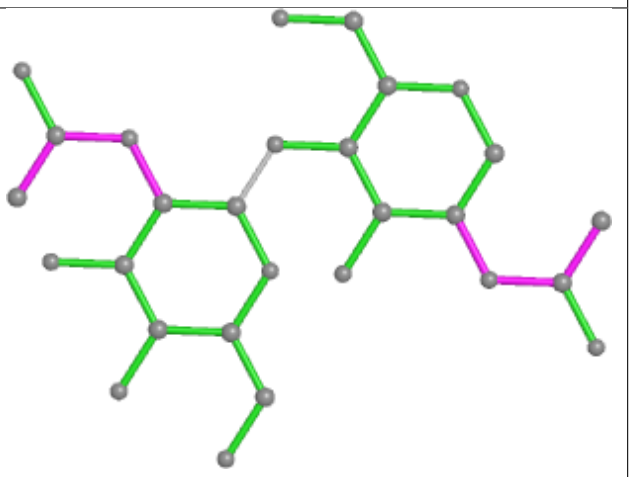


Rings

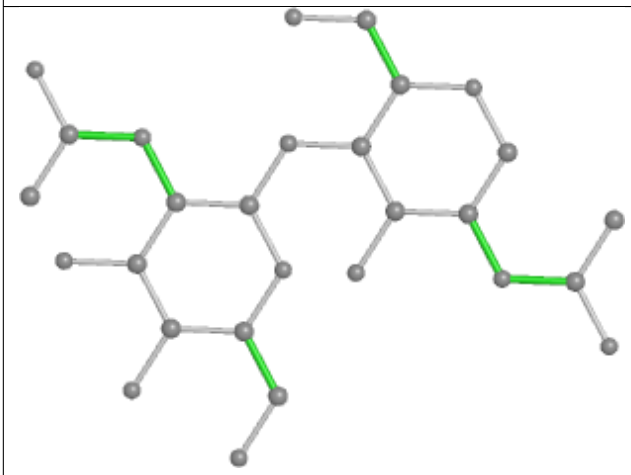
Oligosaccharide Chain M



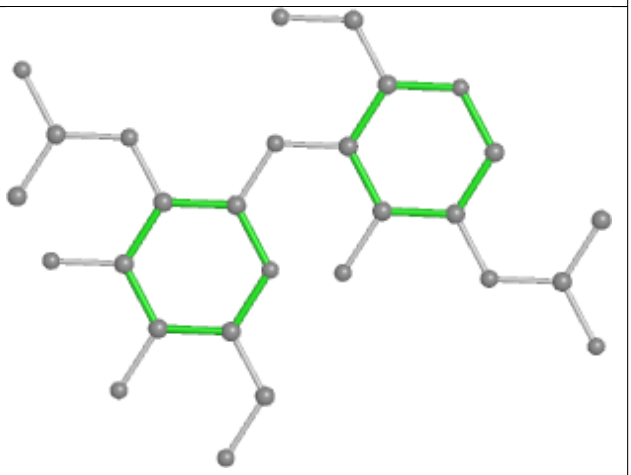
Bond lengths



Bond angles

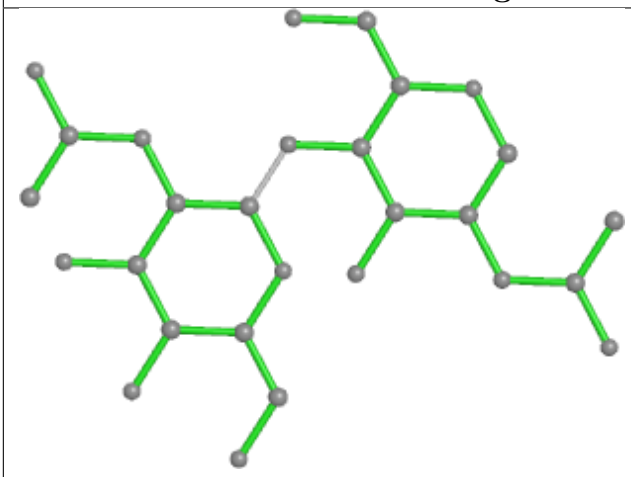


Torsions

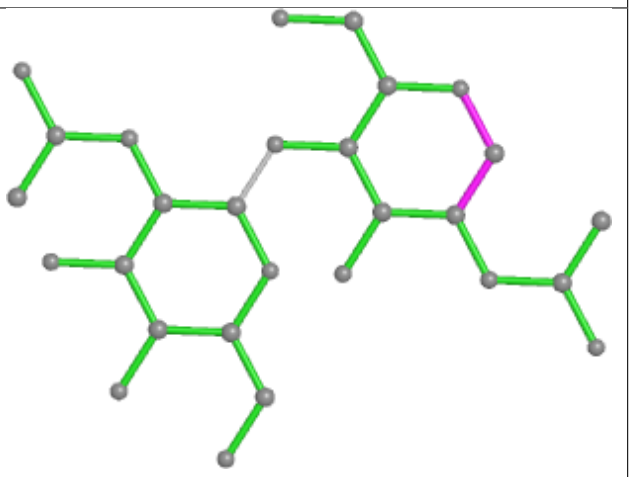


Rings

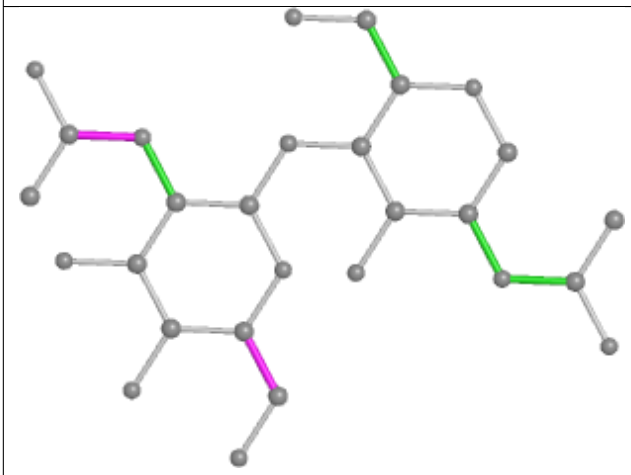
Oligosaccharide Chain N



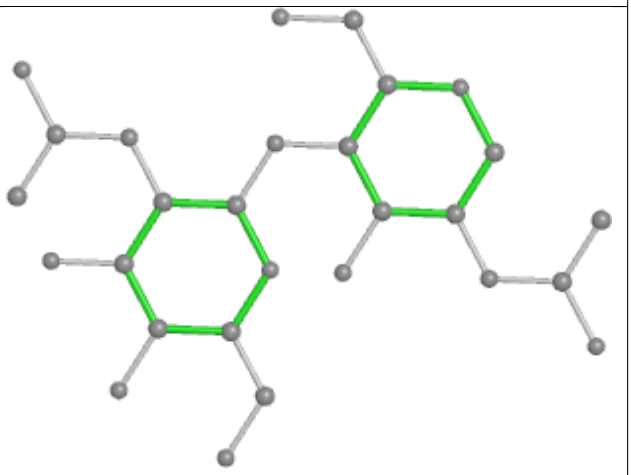
Bond lengths



Bond angles

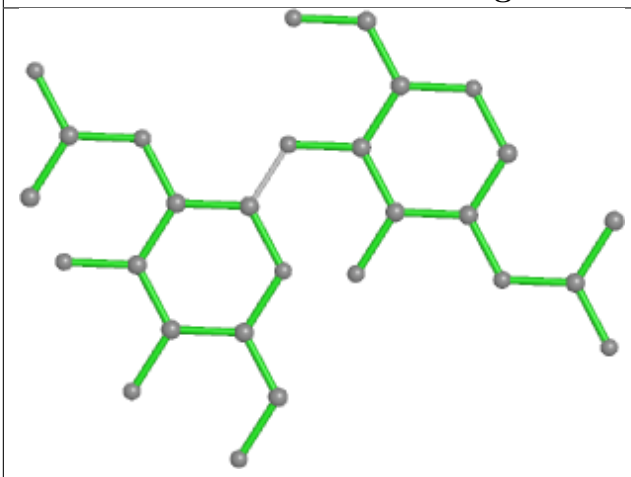


Torsions

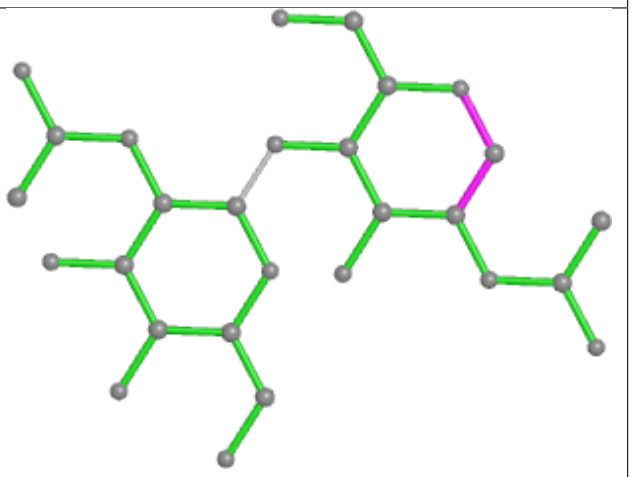


Rings

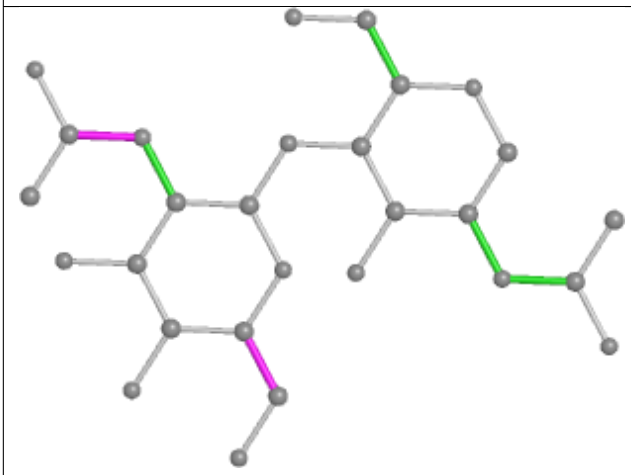
Oligosaccharide Chain O



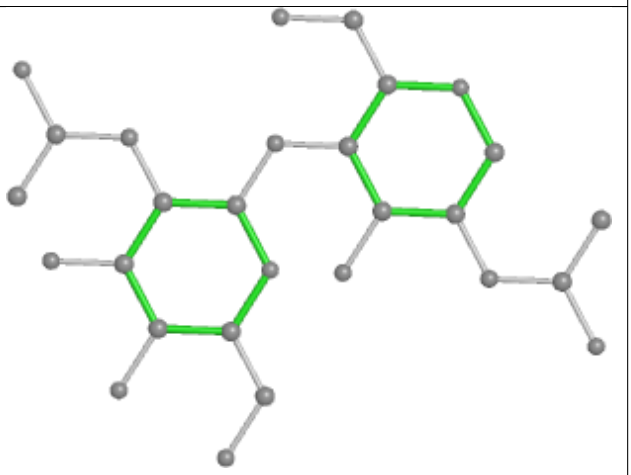
Bond lengths



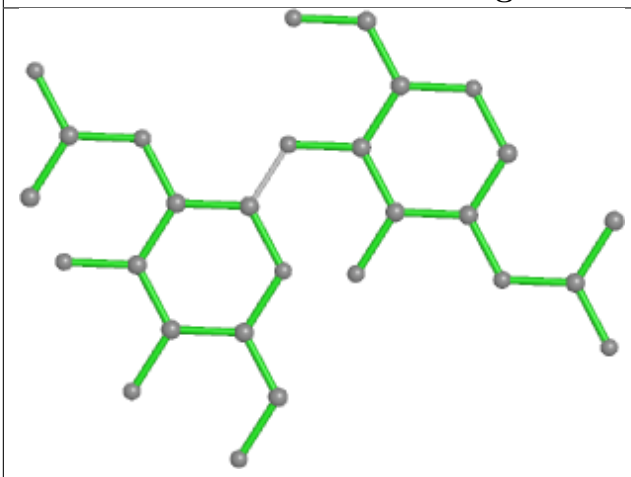
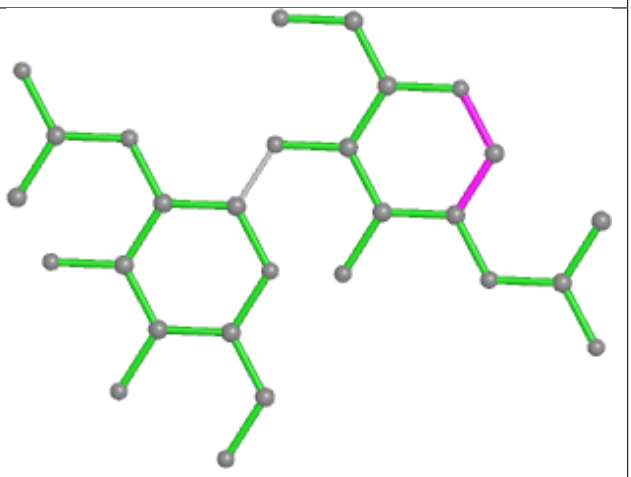
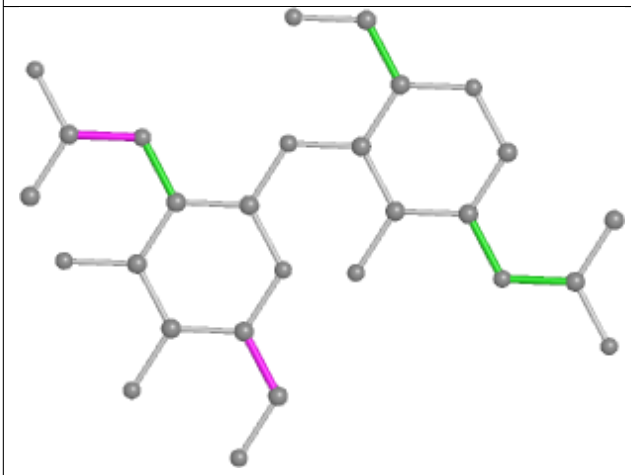
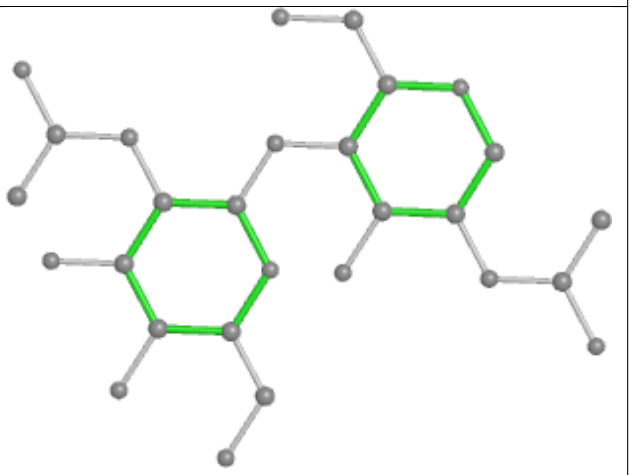
Bond angles



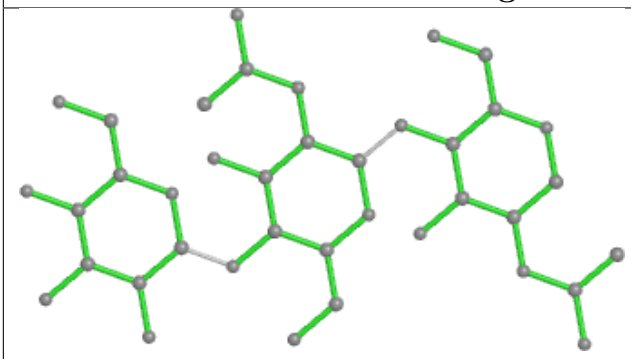
Torsions



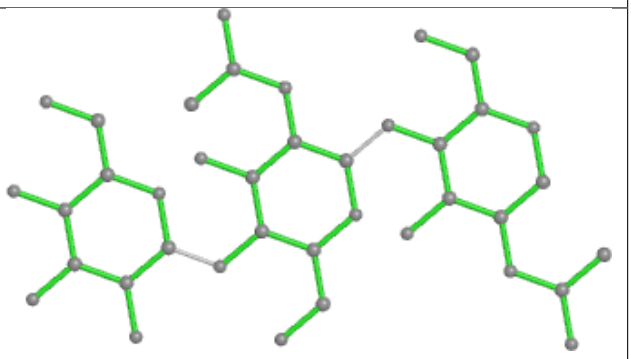
Rings

Oligosaccharide Chain P	
 Bond lengths	 Bond angles
 Torsions	 Rings

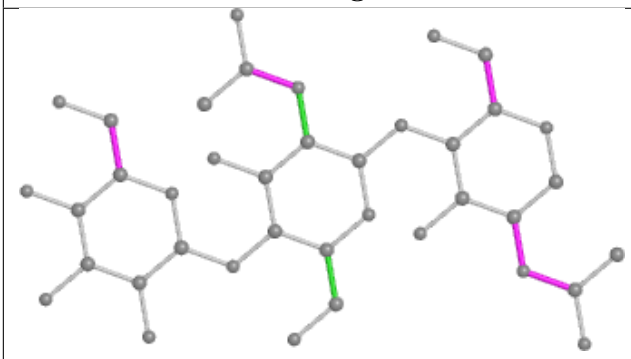
Oligosaccharide Chain J



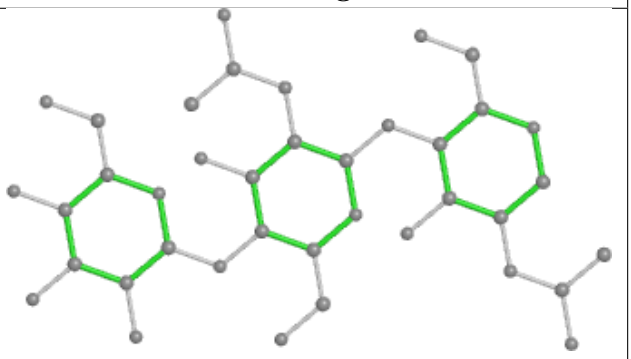
Bond lengths



Bond angles

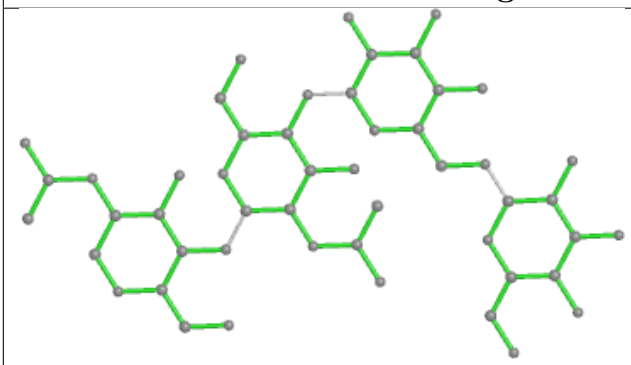


Torsions

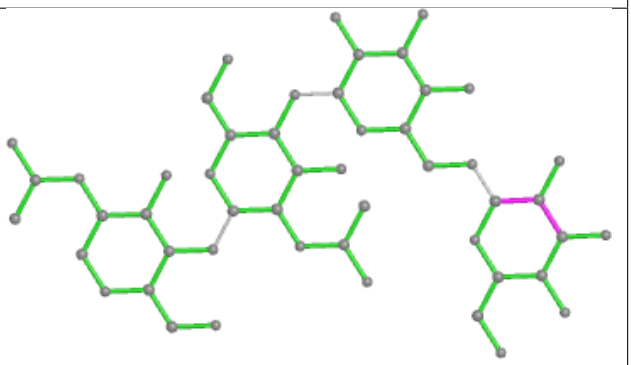


Rings

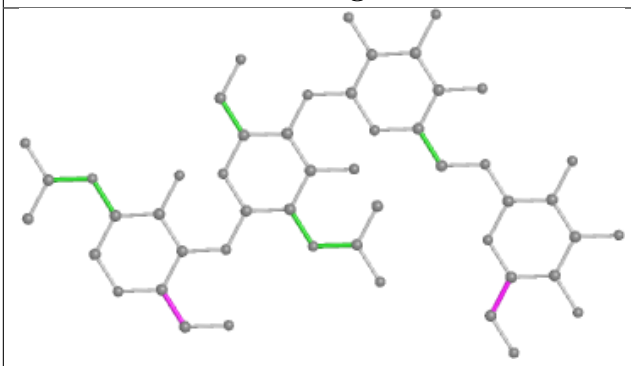
Oligosaccharide Chain L



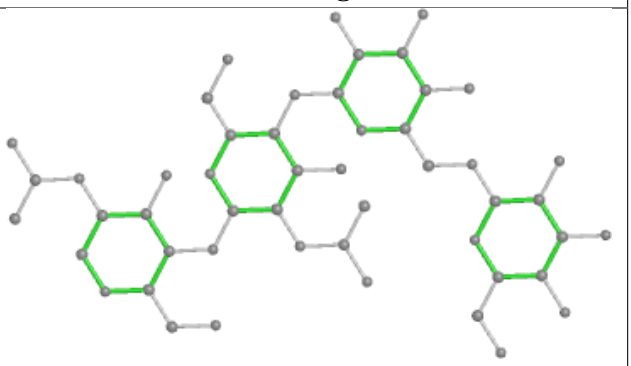
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

9 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	$\#\|Z\| > 2$
7	NAG	A	1316	1	14,14,15	0.42	0	17,19,21	1.16	2 (11%)
7	NAG	A	1309	1	14,14,15	0.50	0	17,19,21	1.17	0
7	NAG	A	1323	1	14,14,15	0.29	0	17,19,21	0.61	0
7	NAG	A	1324	1	14,14,15	0.43	0	17,19,21	1.18	2 (11%)
7	NAG	A	1322	1	14,14,15	0.30	0	17,19,21	0.62	0
7	NAG	A	1317	1	14,14,15	0.29	0	17,19,21	0.61	0
7	NAG	A	1303	1	14,14,15	0.30	0	17,19,21	0.60	0
7	NAG	A	1320	1	14,14,15	0.30	0	17,19,21	0.62	0
7	NAG	A	1321	-	14,14,15	0.30	0	17,19,21	0.62	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
7	NAG	A	1316	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1309	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1323	1	-	4/6/23/26	0/1/1/1
7	NAG	A	1324	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1322	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1317	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1303	1	-	6/6/23/26	0/1/1/1
7	NAG	A	1320	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1321	-	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	A	1324	NAG	C8-C7-N2	2.29	119.97	116.10
7	A	1316	NAG	C8-C7-N2	2.27	119.94	116.10
7	A	1324	NAG	C2-N2-C7	-2.08	119.94	122.90
7	A	1316	NAG	C2-N2-C7	-2.04	120.00	122.90

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1303	NAG	C8-C7-N2-C2
7	A	1303	NAG	O7-C7-N2-C2
7	A	1322	NAG	C8-C7-N2-C2
7	A	1322	NAG	O7-C7-N2-C2
7	A	1323	NAG	C8-C7-N2-C2

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1323	NAG	1	0
7	A	1324	NAG	2	0
7	A	1322	NAG	3	0
7	A	1317	NAG	1	0
7	A	1303	NAG	1	0

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.

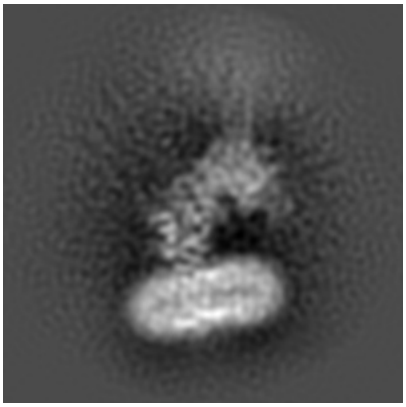
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-8169. These allow visual inspection of the internal detail of the map and identification of artifacts.

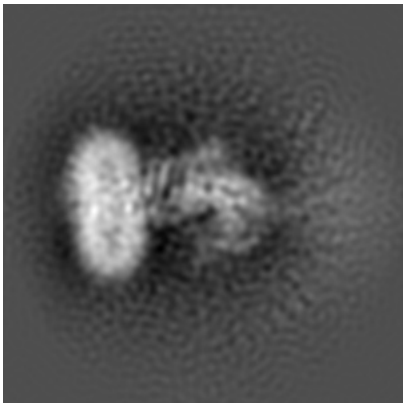
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

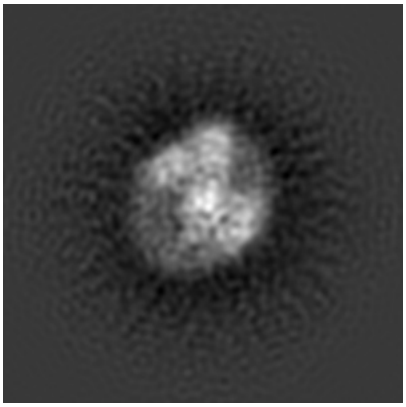
6.1.1 Primary map



X



Y

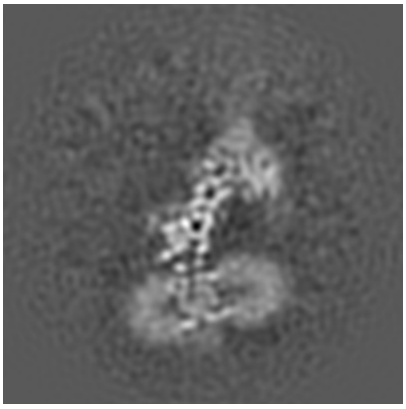


Z

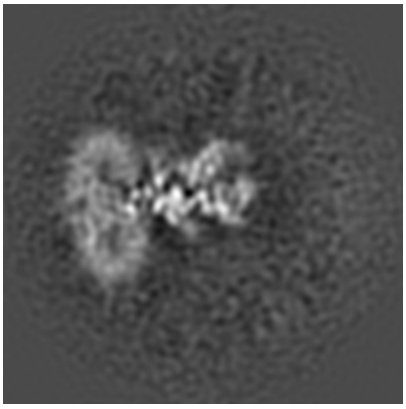
The images above show the map projected in three orthogonal directions.

6.2 Central slices

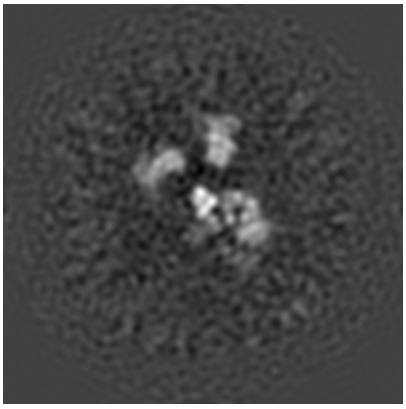
6.2.1 Primary map



X Index: 128



Y Index: 128

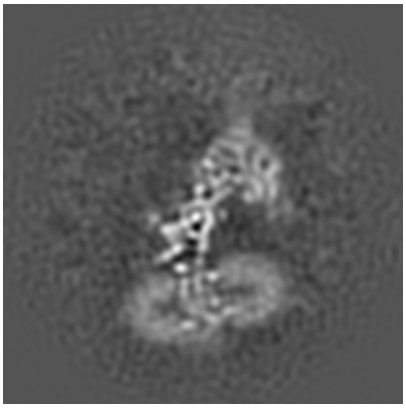


Z Index: 128

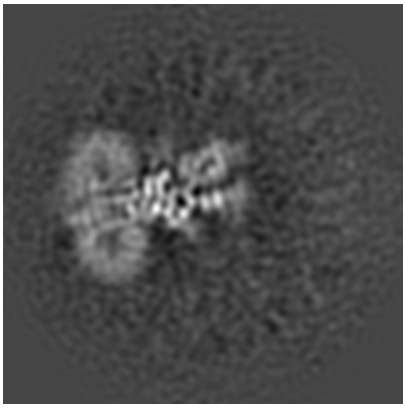
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

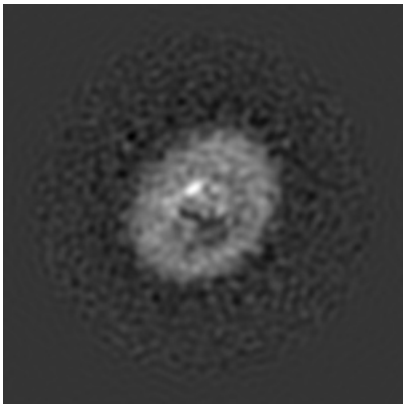
6.3.1 Primary map



X Index: 130



Y Index: 125

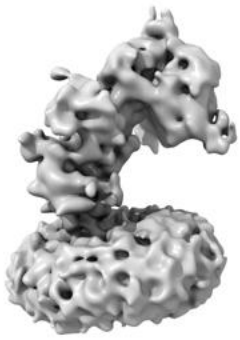


Z Index: 57

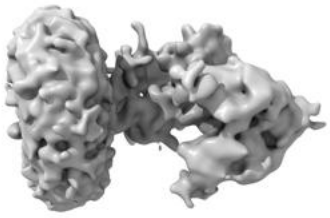
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

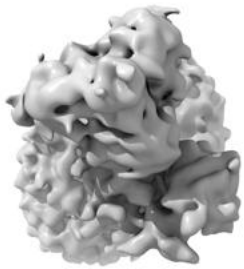
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

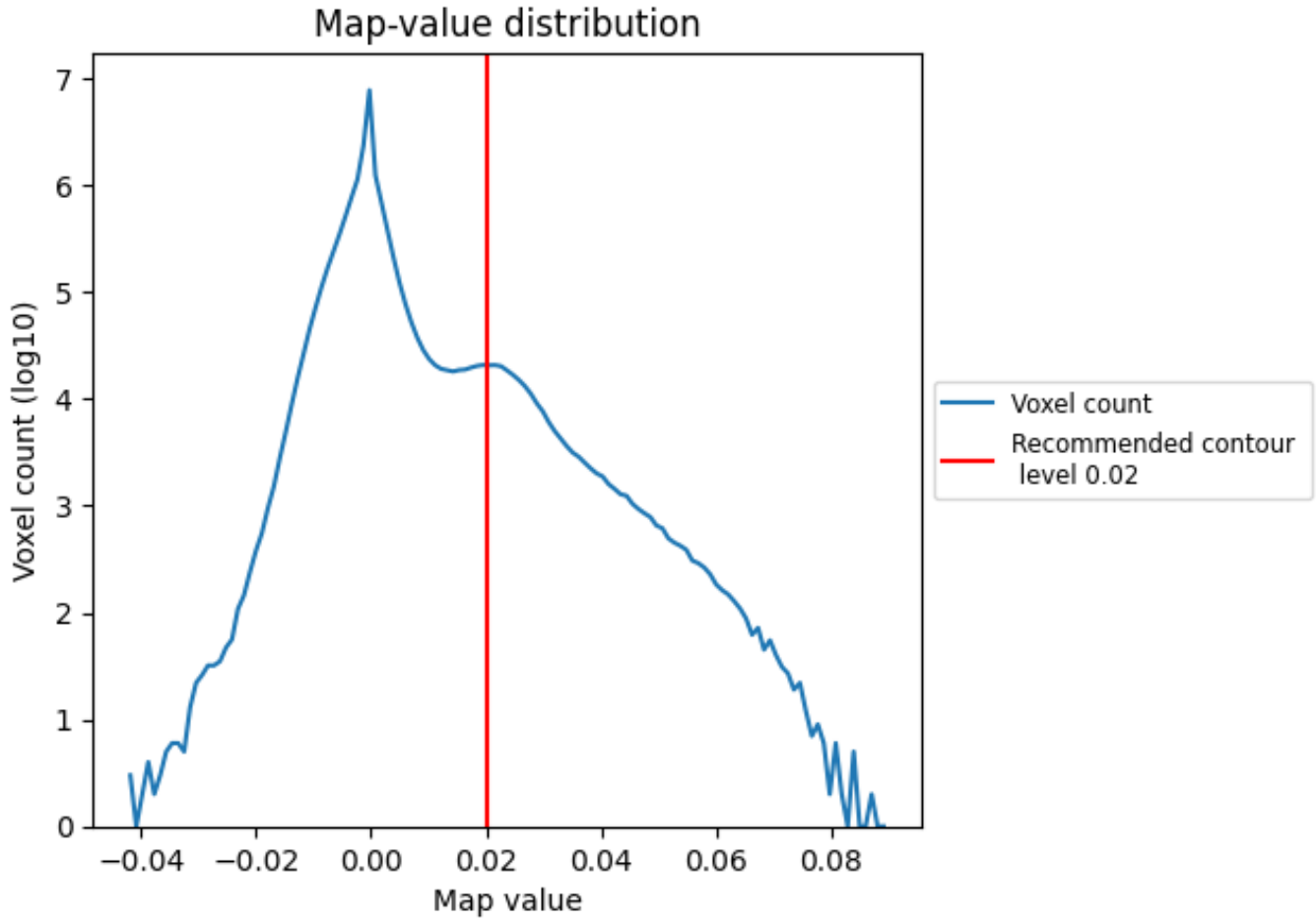
6.5 Mask visualisation (i)

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

7 Map analysis

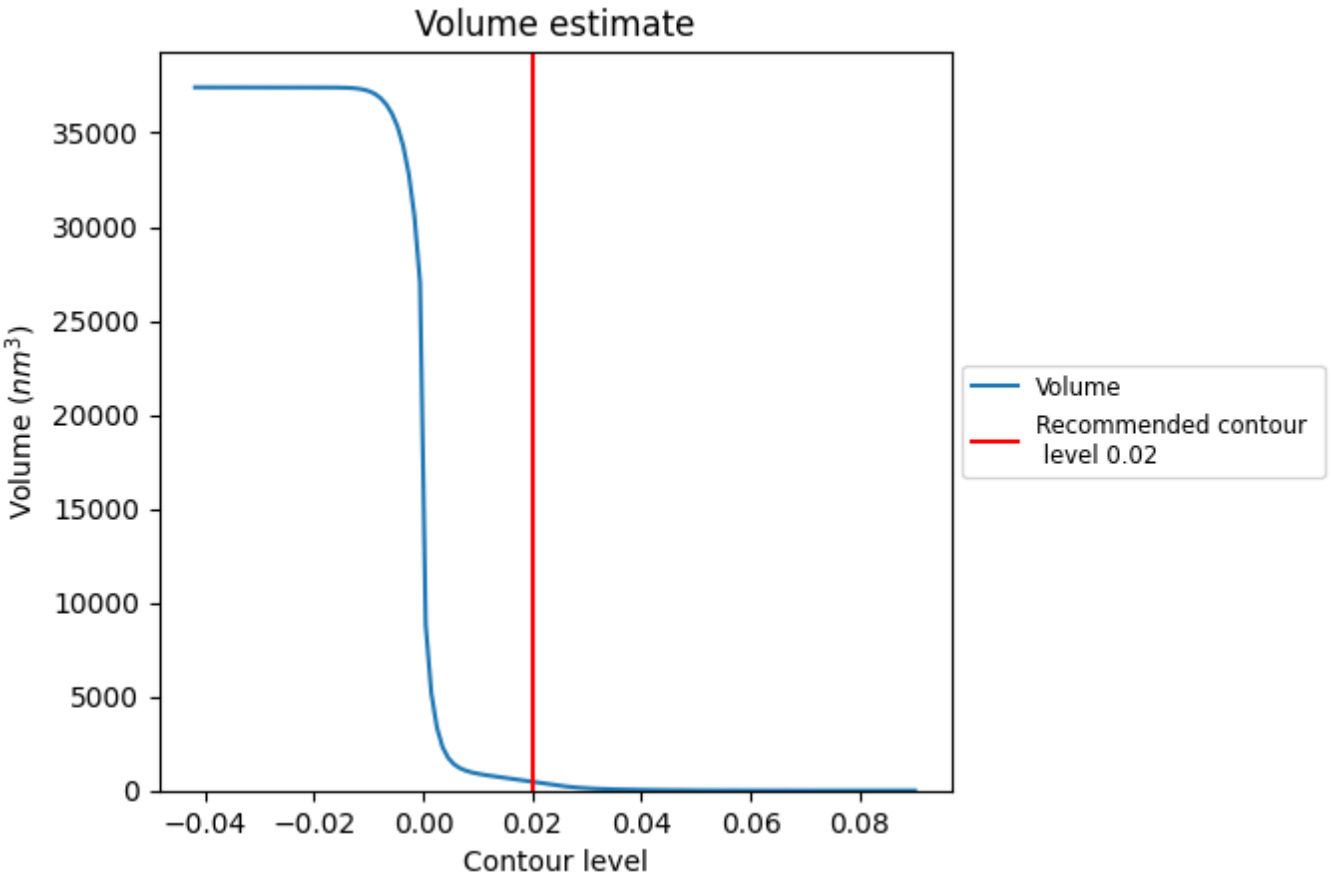
This section contains the results of statistical analysis of the map.

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.

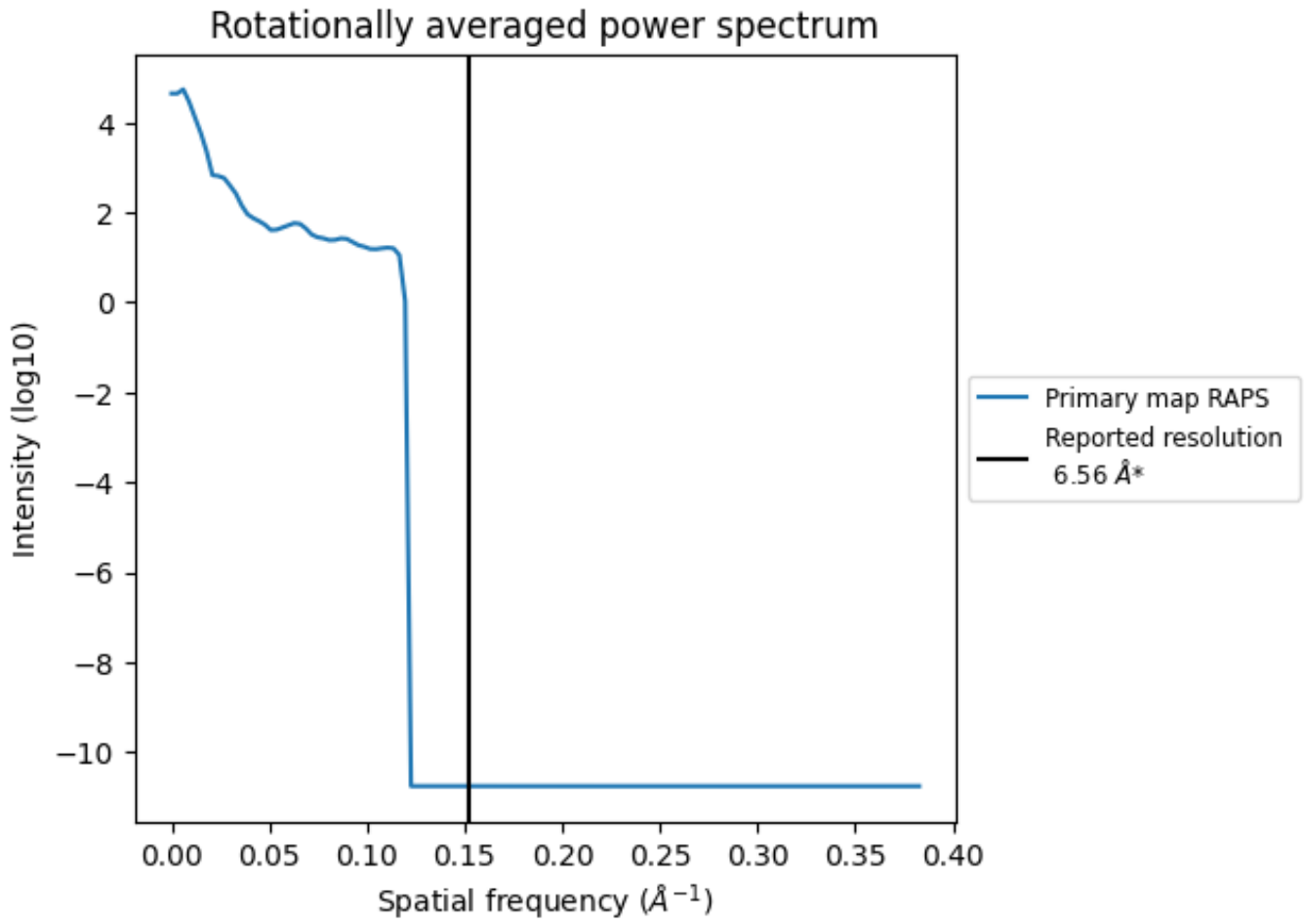
7.2 Volume estimate (i)



The volume at the recommended contour level is 471 nm^3; this corresponds to an approximate mass of 425 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 0.152 Å^{-1}

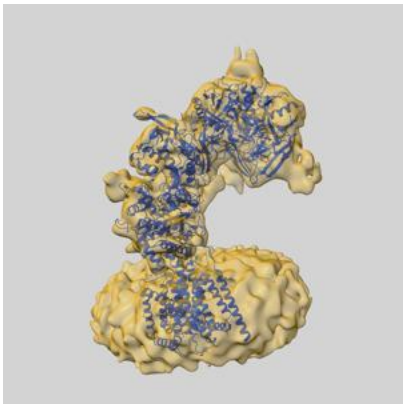
8 Fourier-Shell correlation (i)

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

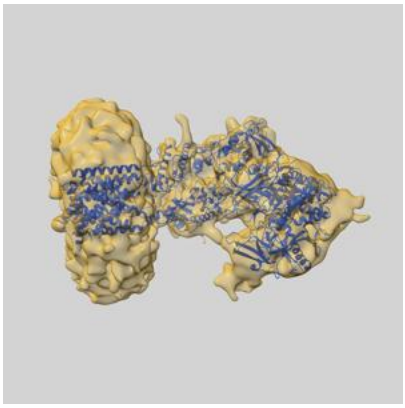
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-8169 and PDB model 5JNX. Per-residue inclusion information can be found in section 3 on page 8.

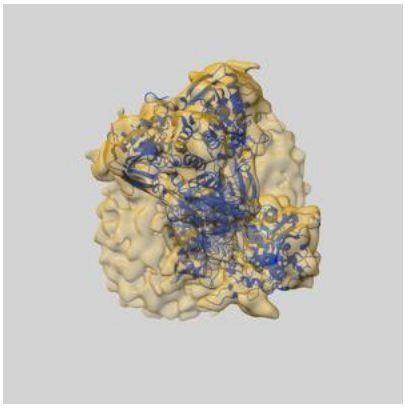
9.1 Map-model overlay



X



Y



Z

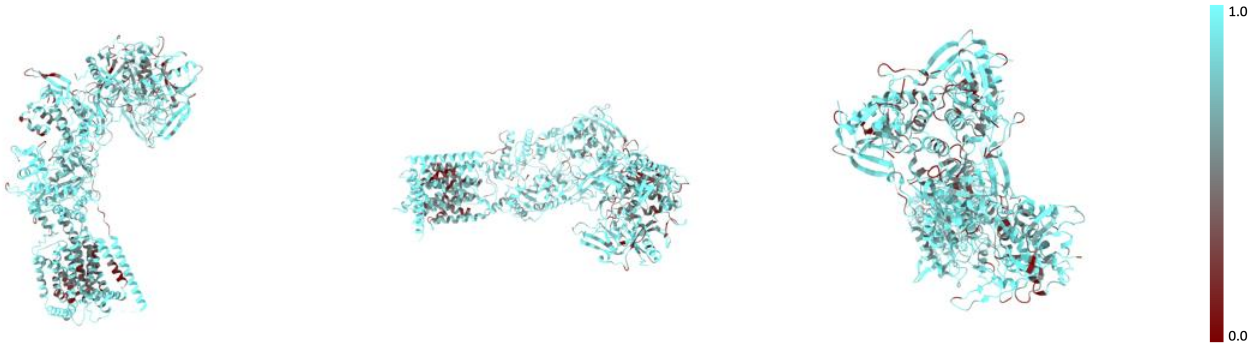
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model

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.

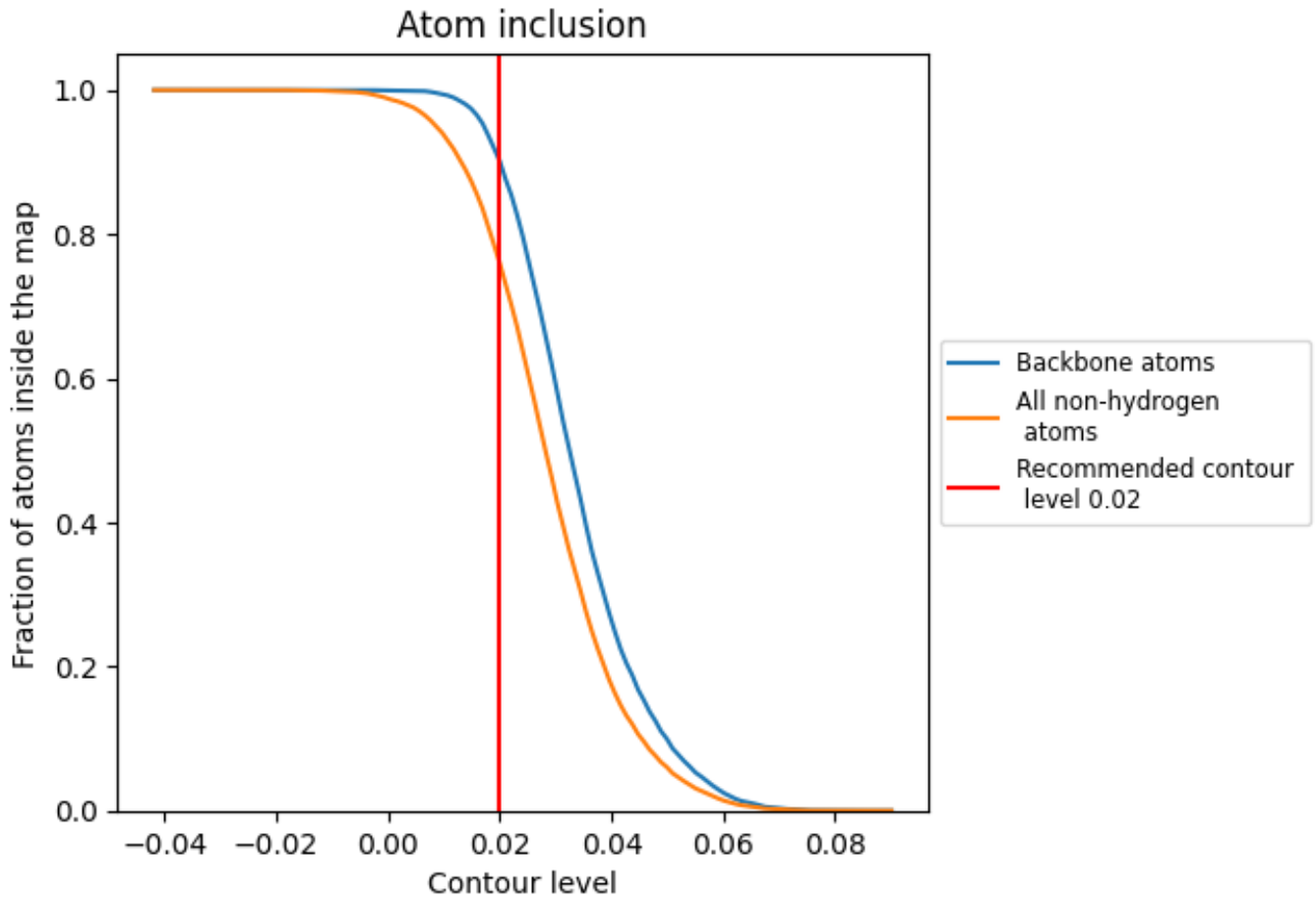
9.3 Atom inclusion mapped to coordinate model



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 (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 76% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7602	0.1400
A	0.7693	0.1550
B	0.8214	0.1610
C	0.7494	0.1050
D	0.7887	0.1200
E	0.7246	0.1120
F	0.7783	0.1470
G	0.7528	0.1110
H	0.7902	0.1460
I	0.3214	0.0630
J	0.8462	0.1830
K	0.8214	0.2580
L	0.7800	0.2320
M	0.0714	0.1200
N	0.2143	0.0730
O	0.1071	0.0200
P	0.7143	0.1440