Full wwPDB EM Validation Report

Oct 6, 2024 – 09:28 AM JST

PDB ID	:	7WC2
EMDB ID	:	EMD-32412
Title	:	Cryo-EM structure of alphavirus, Getah virus
Authors	:	Wang, M.; Sun, Z.Z.; Wang, J.F.
Deposited on	:	2021-12-18
Resolution	:	3.50 Å(reported)

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

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

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

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

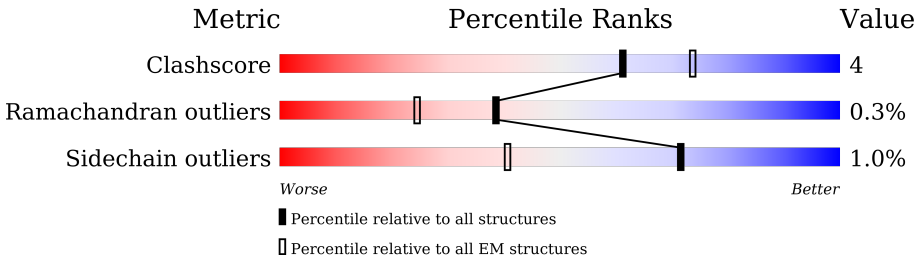
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 3.50 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	438	19% 87% 12%
1	D	438	27% 85% 14%
1	G	438	24% 90% 10%
1	J	438	13% 87% 12%
2	B	422	26% 86% 14%
2	E	422	24% 91% 8%
2	H	422	29% 84% 16%
2	K	422	20% 86% 14%

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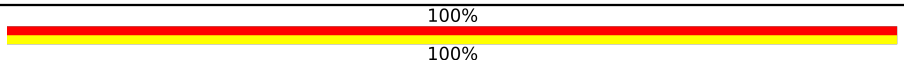
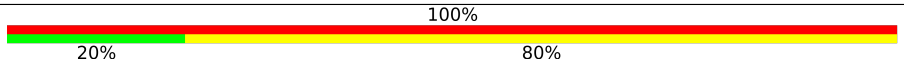
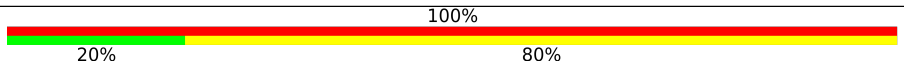
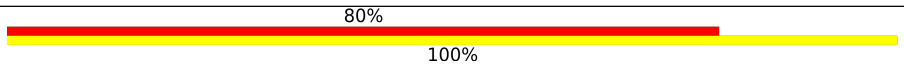
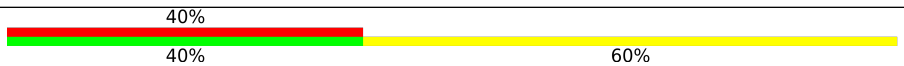
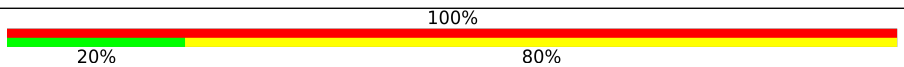
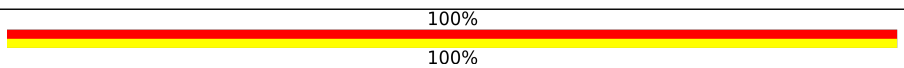
Mol	Chain	Length	Quality of chain
3	a	5	
3	b	5	
3	c	5	
3	d	5	
3	e	5	
3	f	5	
3	g	5	
3	h	5	
3	i	5	
3	j	5	
3	k	5	
3	l	5	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 27108 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 Spike glycoprotein E1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	438	Total	C	N	O	S	0	0
			3336	2103	567	640	26		
1	D	438	Total	C	N	O	S	0	0
			3336	2103	567	640	26		
1	G	438	Total	C	N	O	S	0	0
			3336	2103	567	640	26		
1	J	438	Total	C	N	O	S	0	0
			3336	2103	567	640	26		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	239	SER	GLY	conflict	UNP Q5Y388
D	239	SER	GLY	conflict	UNP Q5Y388
G	239	SER	GLY	conflict	UNP Q5Y388
J	239	SER	GLY	conflict	UNP Q5Y388

- Molecule 2 is a protein called Spike glycoprotein E2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	422	Total	C	N	O	S	0	0
			3258	2059	575	603	21		
2	E	422	Total	C	N	O	S	0	0
			3258	2059	575	603	21		
2	H	422	Total	C	N	O	S	0	0
			3258	2059	575	603	21		
2	K	422	Total	C	N	O	S	0	0
			3258	2059	575	603	21		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	4	GLU	LYS	variant	UNP Q5Y388

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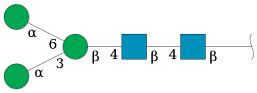
Chain	Residue	Modelled	Actual	Comment	Reference
B	323	GLU	ASP	variant	UNP Q5Y388
E	4	GLU	LYS	variant	UNP Q5Y388
E	323	GLU	ASP	variant	UNP Q5Y388
H	4	GLU	LYS	variant	UNP Q5Y388
H	323	GLU	ASP	variant	UNP Q5Y388
K	4	GLU	LYS	variant	UNP Q5Y388
K	323	GLU	ASP	variant	UNP Q5Y388

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[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.



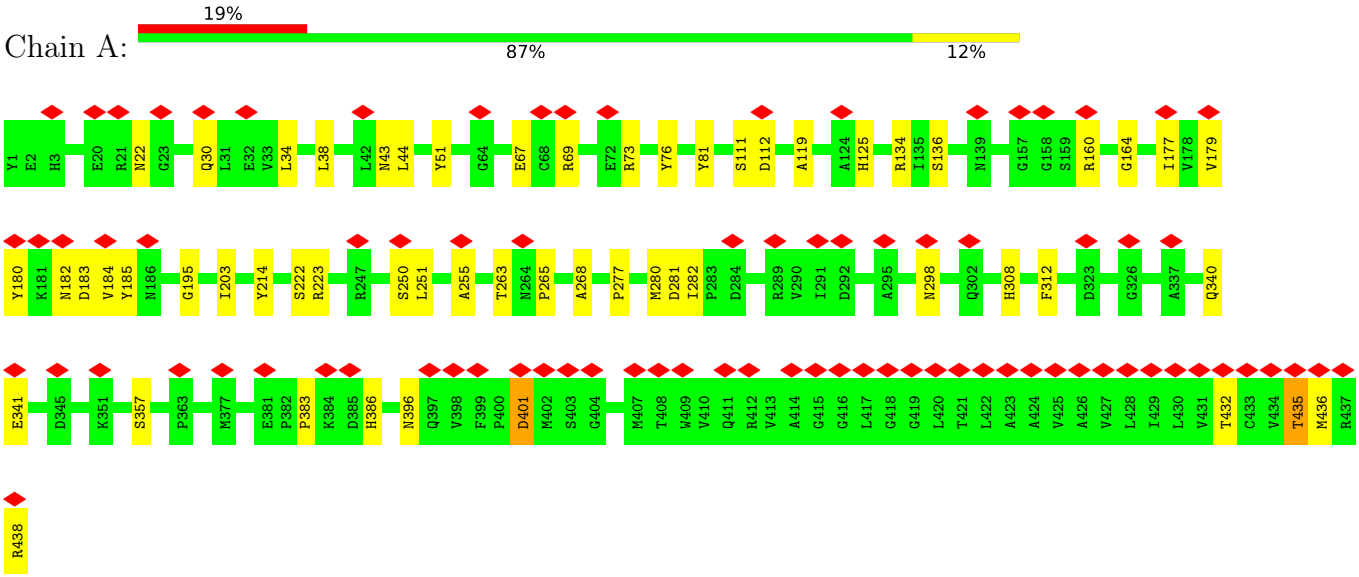
Mol	Chain	Residues	Atoms				AltConf	Trace
3	a	5	Total	C	N	O	0	0
			61	34	2	25		
3	b	5	Total	C	N	O	0	0
			61	34	2	25		
3	c	5	Total	C	N	O	0	0
			61	34	2	25		
3	d	5	Total	C	N	O	0	0
			61	34	2	25		
3	e	5	Total	C	N	O	0	0
			61	34	2	25		
3	f	5	Total	C	N	O	0	0
			61	34	2	25		
3	g	5	Total	C	N	O	0	0
			61	34	2	25		
3	h	5	Total	C	N	O	0	0
			61	34	2	25		
3	i	5	Total	C	N	O	0	0
			61	34	2	25		
3	j	5	Total	C	N	O	0	0
			61	34	2	25		
3	k	5	Total	C	N	O	0	0
			61	34	2	25		
3	l	5	Total	C	N	O	0	0
			61	34	2	25		

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.

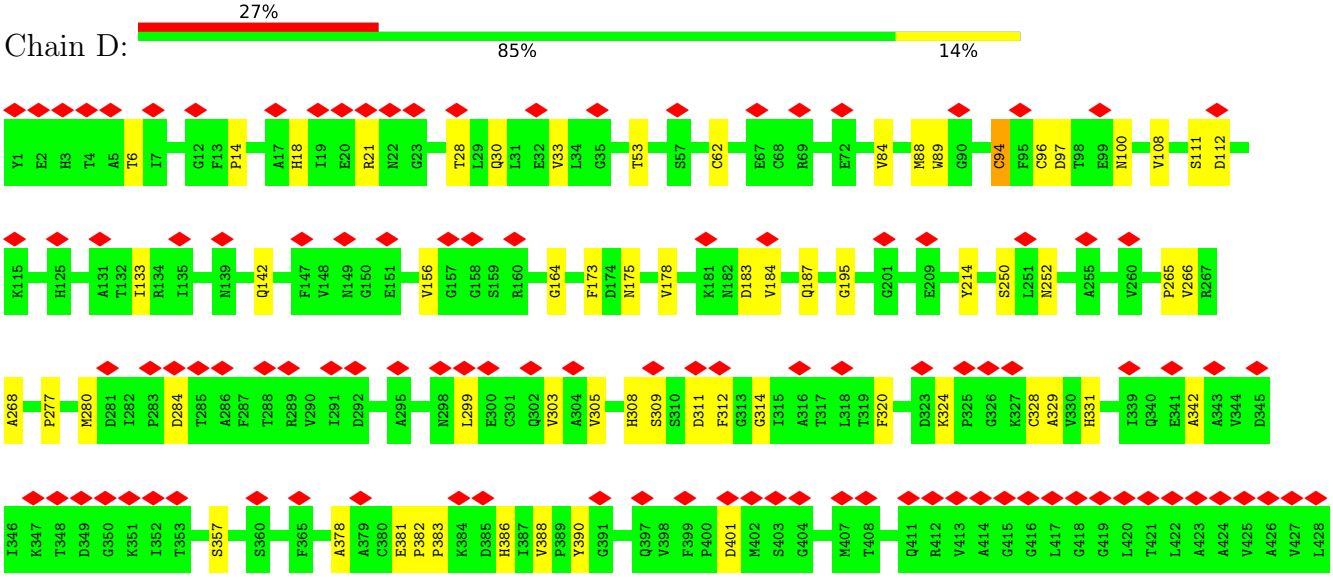
• Molecule 1: Spike glycoprotein E1

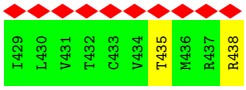
Chain A:



• Molecule 1: Spike glycoprotein E1

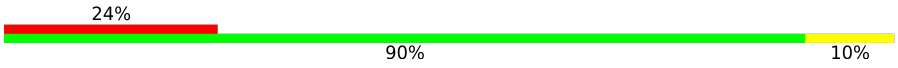
Chain D:

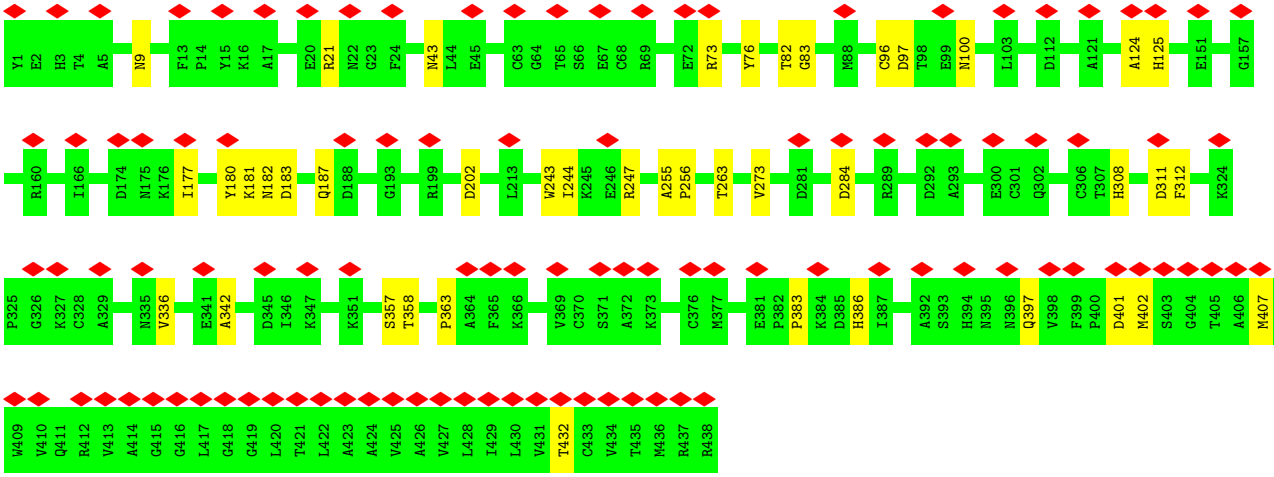




• Molecule 1: Spike glycoprotein E1

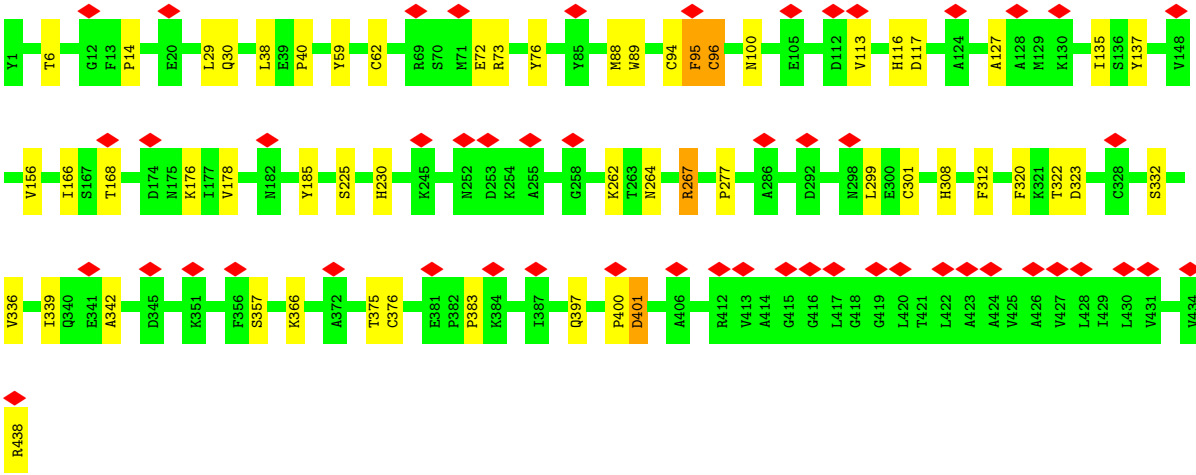
Chain G:





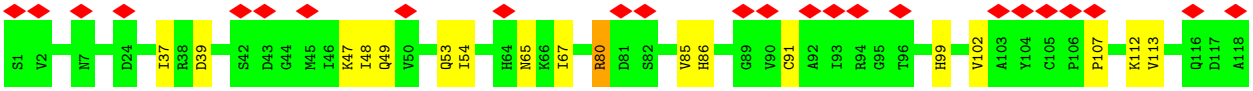
• Molecule 1: Spike glycoprotein E1

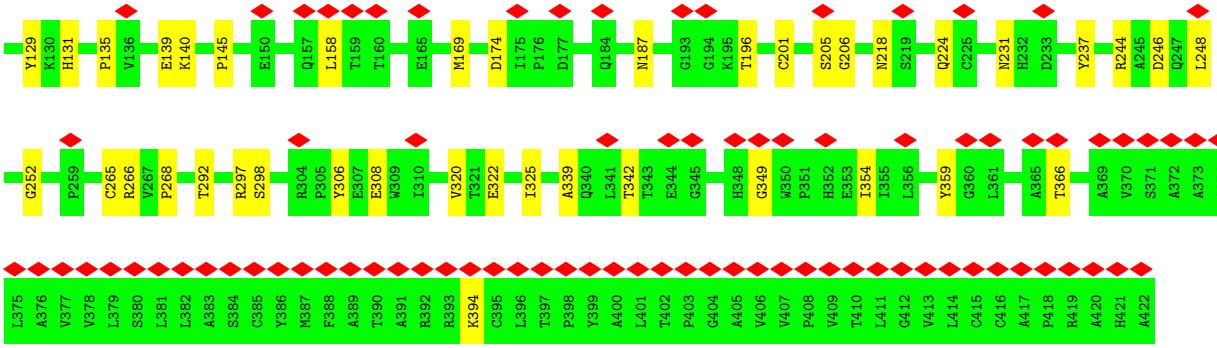
Chain J:



• Molecule 2: Spike glycoprotein E2

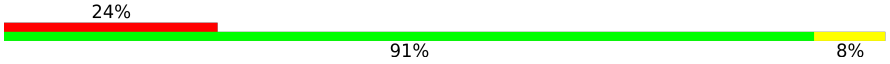
Chain B:

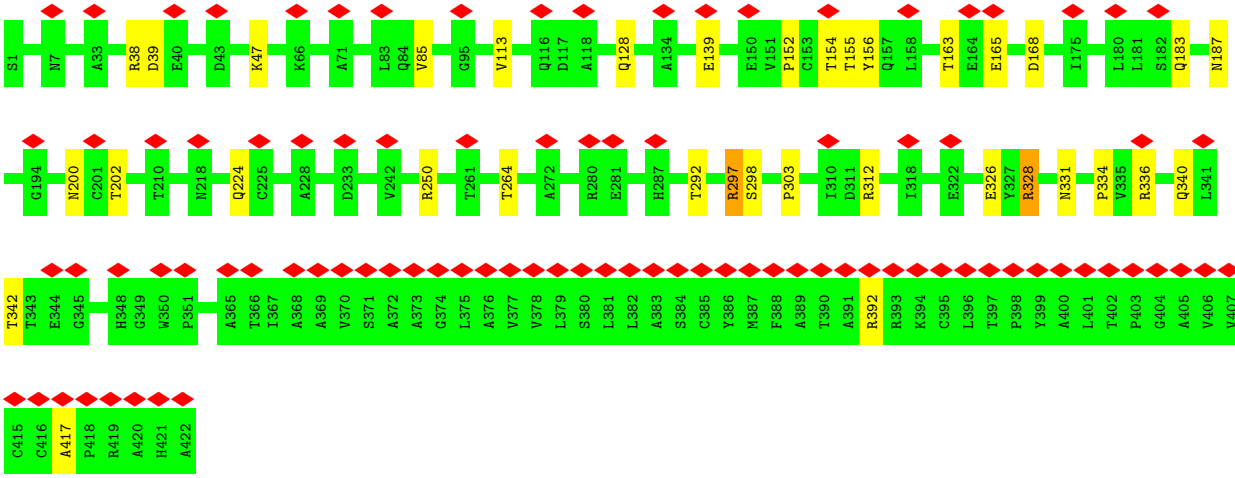




• Molecule 2: Spike glycoprotein E2

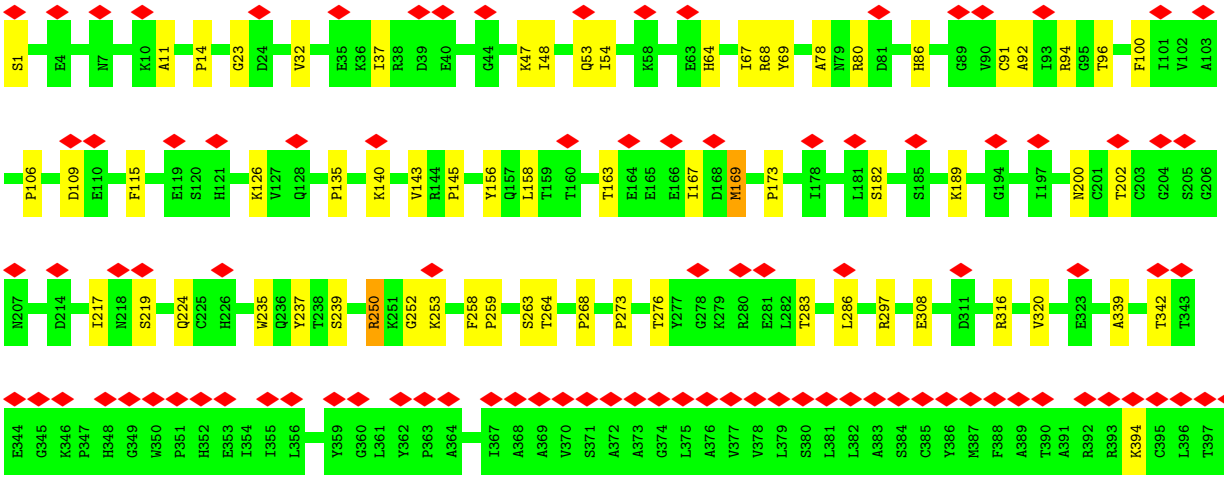
Chain E:

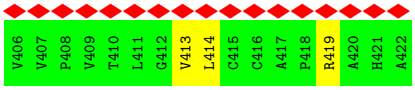




• Molecule 2: Spike glycoprotein E2

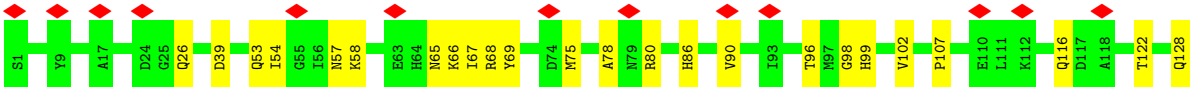
Chain H:

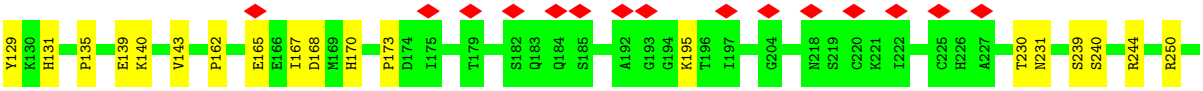


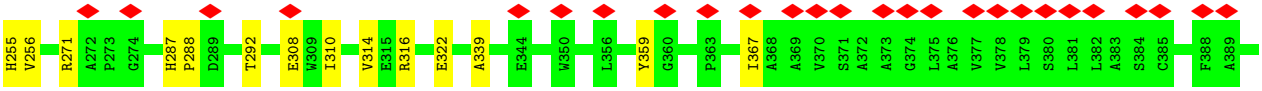


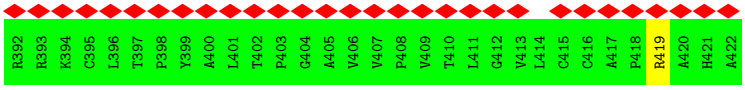
• Molecule 2: Spike glycoprotein E2

Chain K:



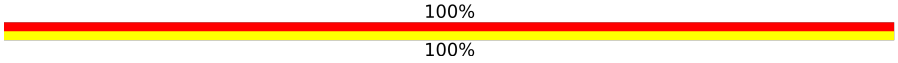






• Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a:



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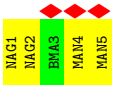
Chain b:



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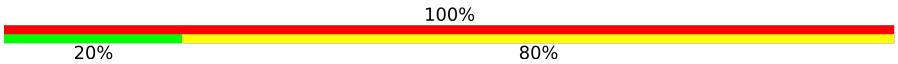
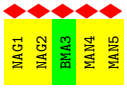
Chain c:





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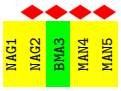
Chain d:



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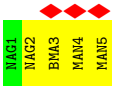
Chain e:



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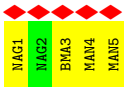
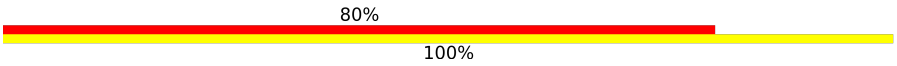
Chain f:



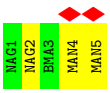
• Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain g:



• Molecule 3: alpha-D-mannopyranose-(1-3)-[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

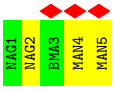
Chain h:



• Molecule 3: alpha-D-mannopyranose-(1-3)-[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-glucopyra

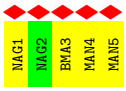
nose

Chain i:



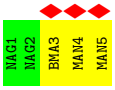
• Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain j:



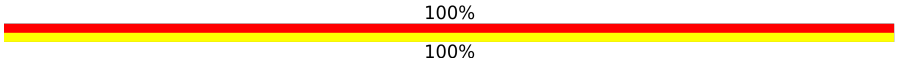
• Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain k:



• Molecule 3: alpha-D-mannopyranose-(1-3)-[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	30996	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	35	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.107	Depositor
Minimum map value	-0.071	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	816.0, 816.0, 816.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.37	0/3420	0.59	1/4666 (0.0%)
1	D	0.35	0/3420	0.60	0/4666
1	G	0.36	0/3420	0.61	0/4666
1	J	0.38	0/3420	0.62	1/4666 (0.0%)
2	B	0.37	0/3346	0.61	0/4565
2	E	0.35	0/3346	0.58	0/4565
2	H	0.34	0/3346	0.60	0/4565
2	K	0.36	0/3346	0.60	1/4565 (0.0%)
All	All	0.36	0/27064	0.60	3/36924 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	D	0	2
1	J	0	6
2	E	0	1
2	H	0	1
2	K	0	1
All	All	0	14

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	J	38	LEU	CA-CB-CG	5.96	129.00	115.30
1	A	44	LEU	CA-CB-CG	5.85	128.76	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	K	170	HIS	C-N-CA	5.28	134.91	121.70

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	265	PRO	Peptide
1	A	435	THR	Mainchain,Peptide
1	D	265	PRO	Peptide
1	D	435	THR	Mainchain
2	E	163	THR	Peptide
2	H	419	ARG	Mainchain
1	J	264	ASN	Peptide
1	J	400	PRO	Peptide
1	J	435	THR	Mainchain,Peptide
1	J	95	PHE	Peptide
1	J	96	CYS	Peptide
2	K	419	ARG	Peptide

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	3336	0	3244	28	0
1	D	3336	0	3244	36	0
1	G	3336	0	3242	25	0
1	J	3336	0	3244	27	0
2	B	3258	0	3204	33	0
2	E	3258	0	3202	20	0
2	H	3258	0	3206	39	0
2	K	3258	0	3204	30	0
3	a	61	0	52	0	0
3	b	61	0	52	0	0
3	c	61	0	52	0	0
3	d	61	0	52	0	0
3	e	61	0	52	0	0
3	f	61	0	52	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	g	61	0	52	0	0
3	h	61	0	52	0	0
3	i	61	0	52	0	0
3	j	61	0	52	0	0
3	k	61	0	52	0	0
3	l	61	0	52	0	0
All	All	27108	0	26414	223	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.

All (223) 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:73:ARG:HB3	1:A:76:TYR:HB2	1.71	0.73
2:H:86:HIS:HA	2:H:91:CYS:HB3	1.72	0.71
1:G:308:HIS:HB2	1:G:383:PRO:HD3	1.72	0.71
1:J:73:ARG:HB2	1:J:76:TYR:HB2	1.74	0.69
1:D:62:CYS:SG	1:D:100:ASN:ND2	2.69	0.65
2:B:244:ARG:NH2	2:B:248:LEU:O	2.31	0.63
1:J:308:HIS:HB2	1:J:383:PRO:HD3	1.81	0.63
1:A:30:GLN:HB3	1:A:136:SER:HB3	1.81	0.62
1:A:179:VAL:HG22	1:A:184:VAL:HG22	1.82	0.61
1:A:308:HIS:HB2	1:A:383:PRO:HD3	1.81	0.61
1:D:388:VAL:HG12	1:D:390:TYR:H	1.66	0.61
1:J:312:PHE:HA	1:J:357:SER:HB2	1.83	0.60
2:H:202:THR:OG1	2:H:224:GLN:NE2	2.35	0.60
2:B:349:GLY:H	2:B:354:ILE:HD11	1.67	0.59
1:A:312:PHE:HA	1:A:357:SER:HB2	1.85	0.58
1:G:124:ALA:HB2	1:G:177:ILE:HD11	1.85	0.58
1:J:262:LYS:HB2	1:J:267:ARG:HE	1.68	0.58
2:E:298:SER:HB3	2:E:303:PRO:HA	1.85	0.58
1:G:312:PHE:HA	1:G:357:SER:HB2	1.85	0.58
2:B:47:LYS:HG2	2:B:102:VAL:HG22	1.86	0.58
1:J:62:CYS:SG	1:J:100:ASN:ND2	2.74	0.57
2:B:85:VAL:HG12	2:B:113:VAL:HG12	1.85	0.57
1:G:21:ARG:NH1	1:G:284:ASP:OD1	2.39	0.56
1:G:255:ALA:O	2:H:297:ARG:NH2	2.38	0.56
2:E:168:ASP:HB3	2:E:250:ARG:HE	1.70	0.55
1:D:308:HIS:HB2	1:D:383:PRO:HD3	1.88	0.55
1:J:299:LEU:HD23	1:J:320:PHE:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:39:ASP:OD2	2:K:129:TYR:OH	2.25	0.55
2:H:37:ILE:HG22	2:H:48:ILE:HA	1.88	0.54
2:E:328:ARG:HB3	2:E:334:PRO:HB3	1.89	0.54
2:H:94:ARG:NH1	2:K:26:GLN:OE1	2.41	0.54
1:D:6:THR:HA	1:D:277:PRO:HA	1.90	0.54
2:B:135:PRO:HG3	2:B:140:LYS:HG2	1.90	0.53
1:A:401:ASP:OD1	1:A:401:ASP:N	2.40	0.53
2:E:85:VAL:HG12	2:E:113:VAL:HG12	1.89	0.53
1:G:73:ARG:HB2	1:G:76:TYR:HB2	1.89	0.53
2:B:196:THR:OG1	2:B:231:ASN:OD1	2.26	0.53
1:D:250:SER:OG	1:D:252:ASN:OD1	2.26	0.53
1:A:340:GLN:HG2	1:A:341:GLU:HG3	1.91	0.53
1:D:164:GLY:HA3	1:D:277:PRO:HG2	1.91	0.53
2:H:1:SER:OG	2:H:64:HIS:NE2	2.40	0.53
1:J:178:VAL:HG13	1:J:185:TYR:HB2	1.92	0.52
2:K:135:PRO:HG3	2:K:140:LYS:HG2	1.91	0.52
1:D:252:ASN:O	2:E:297:ARG:NH2	2.42	0.52
2:B:265:CYS:SG	2:B:266:ARG:N	2.80	0.52
1:D:173:PHE:HE2	1:D:268:ALA:HB2	1.75	0.52
2:H:169:MET:HB3	2:H:235:TRP:HB3	1.91	0.52
2:H:91:CYS:SG	2:H:92:ALA:N	2.83	0.52
2:H:263:SER:OG	2:H:264:THR:N	2.42	0.51
2:K:288:PRO:HG3	2:K:310:ILE:HG22	1.92	0.51
1:D:299:LEU:HD23	1:D:320:PHE:HB3	1.90	0.51
1:A:432:THR:HG22	2:B:394:LYS:HE2	1.92	0.51
1:G:187:GLN:HE22	1:G:243:TRP:HE1	1.59	0.51
1:J:113:VAL:HB	1:J:116:HIS:HB2	1.92	0.51
2:H:308:GLU:OE1	2:H:316:ARG:NH2	2.43	0.51
1:D:328:CYS:SG	1:D:329:ALA:N	2.84	0.51
1:D:401:ASP:N	1:D:401:ASP:OD1	2.43	0.51
1:A:34:LEU:HD11	1:A:134:ARG:HD2	1.93	0.51
2:E:392:ARG:HE	2:E:414:LEU:HD13	1.76	0.51
1:J:14:PRO:HB3	1:J:30:GLN:HE21	1.76	0.51
2:K:139:GLU:HG2	2:K:292:THR:HG22	1.93	0.51
2:H:135:PRO:HG3	2:H:140:LYS:HG2	1.93	0.51
2:H:320:VAL:HG12	2:H:339:ALA:HB2	1.93	0.51
2:B:320:VAL:HG22	2:B:325:ILE:HG12	1.93	0.50
1:D:84:VAL:H	1:D:100:ASN:HB2	1.76	0.50
1:A:119:ALA:HA	1:A:180:TYR:HA	1.93	0.50
1:D:303:VAL:HG21	1:D:378:ALA:HA	1.93	0.50
2:H:14:PRO:HB3	2:H:53:GLN:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:298:SER:HA	2:B:325:ILE:HG22	1.94	0.50
2:K:167:ILE:HG13	2:K:168:ASP:H	1.76	0.50
1:D:28:THR:HG21	1:D:342:ALA:HB1	1.94	0.50
2:K:39:ASP:OD1	2:K:39:ASP:N	2.44	0.50
1:D:33:VAL:HG12	1:D:133:ILE:HG12	1.92	0.50
1:D:96:CYS:SG	1:D:97:ASP:N	2.85	0.49
2:K:165:GLU:HB3	2:K:256:VAL:HG22	1.94	0.49
2:E:139:GLU:OE1	2:E:331:ASN:ND2	2.45	0.49
2:B:37:ILE:HG22	2:B:48:ILE:HA	1.94	0.49
2:H:169:MET:HB2	2:H:252:GLY:HA3	1.95	0.49
1:J:135:ILE:HG13	1:J:156:VAL:HG21	1.94	0.49
2:H:91:CYS:HB2	2:H:106:PRO:HD2	1.95	0.49
2:H:69:TYR:HE1	2:H:78:ALA:HB2	1.78	0.49
2:B:39:ASP:OD2	2:B:129:TYR:OH	2.31	0.48
1:A:81:TYR:OH	1:A:222:SER:O	2.30	0.48
1:D:112:ASP:HB3	2:E:165:GLU:HG2	1.95	0.48
1:D:305:VAL:HG23	1:D:314:GLY:HA2	1.95	0.48
1:G:432:THR:HG22	2:H:394:LYS:HD3	1.95	0.48
1:A:255:ALA:O	2:B:297:ARG:NH2	2.47	0.48
2:B:85:VAL:HG23	2:B:91:CYS:HB2	1.95	0.48
1:G:183:ASP:N	1:G:183:ASP:OD1	2.45	0.48
2:K:57:ASN:O	2:K:68:ARG:NE	2.47	0.48
2:K:54:ILE:HG22	2:K:67:ILE:HG23	1.94	0.48
2:B:53:GLN:HB3	2:B:99:HIS:CD2	2.49	0.48
1:G:358:THR:HG21	1:G:363:PRO:HG3	1.95	0.48
1:J:401:ASP:OD1	1:J:401:ASP:N	2.45	0.48
2:B:174:ASP:OD1	2:B:174:ASP:N	2.46	0.48
2:E:183:GLN:OE1	2:E:187:ASN:N	2.39	0.48
1:D:21:ARG:NH1	1:D:284:ASP:OD1	2.47	0.47
2:K:65:ASN:HA	2:K:80:ARG:HD2	1.96	0.47
1:A:182:ASN:HA	1:A:263:THR:HG21	1.96	0.47
2:B:49:GLN:NE2	2:B:237:TYR:OH	2.47	0.47
2:B:169:MET:HB2	2:B:252:GLY:HA3	1.96	0.47
1:D:195:GLY:H	1:D:214:TYR:HE2	1.63	0.47
1:D:312:PHE:HA	1:D:357:SER:HB2	1.95	0.47
2:H:96:THR:OG1	2:H:100:PHE:O	2.27	0.47
2:H:143:VAL:HG22	2:K:128:GLN:HB2	1.95	0.47
2:H:308:GLU:OE2	2:H:316:ARG:NH1	2.43	0.47
2:H:11:ALA:O	2:H:235:TRP:N	2.41	0.47
1:D:178:VAL:HG21	1:D:187:GLN:HE21	1.79	0.47
1:D:183:ASP:N	1:D:183:ASP:OD1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:301:CYS:HB3	1:J:376:CYS:HB3	1.54	0.47
1:D:184:VAL:HG21	1:D:266:VAL:HG13	1.97	0.47
1:J:59:TYR:HA	2:K:244:ARG:HB3	1.96	0.47
1:A:183:ASP:OD1	1:A:183:ASP:N	2.47	0.47
2:K:239:SER:OG	2:K:240:SER:N	2.48	0.46
1:G:311:ASP:OD1	1:G:311:ASP:N	2.47	0.46
2:H:23:GLY:HA2	2:H:126:LYS:HE3	1.96	0.46
1:J:62:CYS:HB3	1:J:94:CYS:HB2	1.67	0.46
1:A:43:ASN:OD1	1:A:43:ASN:N	2.48	0.46
2:K:58:LYS:NZ	2:K:75:MET:O	2.48	0.46
2:K:310:ILE:HD12	2:K:314:VAL:HG21	1.98	0.46
1:A:111:SER:OG	1:A:112:ASP:N	2.49	0.46
2:B:139:GLU:HG2	2:B:292:THR:HG22	1.97	0.46
2:K:57:ASN:HA	2:K:66:LYS:HG2	1.96	0.46
2:H:217:ILE:HG23	2:H:219:SER:H	1.81	0.46
2:H:158:LEU:HA	2:H:258:PHE:HD1	1.81	0.46
2:K:322:GLU:HA	2:K:339:ALA:HB3	1.97	0.45
1:D:309:SER:HA	2:E:340:GLN:HE21	1.80	0.45
2:K:54:ILE:O	2:K:98:GLY:N	2.40	0.45
2:B:322:GLU:HA	2:B:339:ALA:HB3	1.97	0.45
2:H:276:THR:HB	2:H:283:THR:HB	1.98	0.45
2:K:107:PRO:HA	2:K:131:HIS:HD2	1.81	0.45
1:A:67:GLU:O	1:A:69:ARG:NH1	2.50	0.45
1:A:280:MET:HB3	1:A:282:ILE:HD12	1.99	0.45
2:E:392:ARG:HH22	2:E:417:ALA:H	1.65	0.45
1:A:51:TYR:HB3	1:A:203:ILE:HD13	1.97	0.45
2:B:54:ILE:HG22	2:B:67:ILE:HB	1.99	0.45
2:K:359:TYR:HE1	2:K:367:ILE:HD11	1.82	0.45
2:E:154:THR:OG1	2:E:155:THR:N	2.49	0.44
2:B:86:HIS:HB2	2:B:112:LYS:HG2	1.99	0.44
2:K:271:ARG:HH11	2:K:287:HIS:HB3	1.82	0.44
1:A:164:GLY:HA3	1:A:277:PRO:HG2	1.99	0.44
1:J:336:VAL:HG22	1:J:397:GLN:HG2	1.99	0.44
1:D:111:SER:OG	1:D:112:ASP:N	2.50	0.44
2:B:145:PRO:HG3	2:B:268:PRO:HB3	2.00	0.44
1:J:322:THR:OG1	1:J:323:ASP:N	2.51	0.44
2:E:326:GLU:HB3	2:E:336:ARG:HG2	1.99	0.44
2:B:187:ASN:HB3	2:B:218:ASN:HA	1.99	0.44
1:D:311:ASP:N	1:D:311:ASP:OD1	2.51	0.44
2:H:163:THR:HG21	2:H:259:PRO:HG3	2.00	0.44
1:A:185:TYR:CE1	1:A:250:SER:HA	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:96:CYS:SG	1:G:97:ASP:N	2.87	0.43
1:G:180:TYR:CZ	1:G:181:LYS:HE2	2.54	0.43
2:H:145:PRO:HG3	2:H:268:PRO:HB3	1.99	0.43
2:H:250:ARG:HH21	2:H:253:LYS:HA	1.82	0.43
1:J:366:LYS:HB3	1:J:375:THR:HG22	2.00	0.43
2:E:139:GLU:HG3	2:E:292:THR:HG22	2.00	0.43
1:D:88:MET:HG2	1:D:89:TRP:H	1.83	0.43
2:H:32:VAL:HB	2:H:115:PHE:HE1	1.84	0.43
1:D:386:HIS:HD2	2:E:342:THR:HG21	1.84	0.43
2:H:202:THR:H	2:H:224:GLN:HE22	1.67	0.43
1:J:6:THR:HA	1:J:277:PRO:HA	2.00	0.43
2:E:47:LYS:HB2	2:E:156:TYR:HE2	1.83	0.43
2:H:47:LYS:HG3	2:H:156:TYR:CD2	2.54	0.43
2:B:158:LEU:HD13	2:B:158:LEU:HA	1.81	0.43
1:G:336:VAL:HG22	1:G:397:GLN:HG2	2.01	0.43
1:A:38:LEU:HB3	1:A:268:ALA:HB3	2.00	0.42
1:A:125:HIS:CE1	1:G:125:HIS:HE1	2.37	0.42
1:G:386:HIS:HD2	2:H:342:THR:HG21	1.83	0.42
1:A:195:GLY:H	1:A:214:TYR:HE2	1.66	0.42
1:D:381:GLU:HA	1:D:382:PRO:HD3	1.92	0.42
2:E:202:THR:OG1	2:E:224:GLN:OE1	2.36	0.42
2:B:205:SER:OG	2:B:206:GLY:N	2.49	0.42
2:E:152:PRO:HA	2:E:264:THR:HA	2.00	0.42
1:G:402:MET:HA	1:G:407:MET:HG2	2.01	0.42
1:J:225:SER:H	1:J:230:HIS:CE1	2.38	0.42
1:A:177:ILE:HG23	1:A:184:VAL:HG13	2.01	0.42
1:G:82:THR:OG1	1:G:83:GLY:N	2.52	0.42
1:G:202:ASP:OD1	1:G:202:ASP:N	2.51	0.42
2:H:109:ASP:N	2:H:109:ASP:OD1	2.53	0.42
1:J:40:PRO:HA	1:J:127:ALA:HA	2.02	0.42
2:K:162:PRO:HA	2:K:255:HIS:CD2	2.55	0.42
1:A:435:THR:HA	1:A:438:ARG:HG3	2.02	0.42
2:B:65:ASN:O	2:B:80:ARG:HB2	2.19	0.42
2:B:246:ASP:N	2:B:246:ASP:OD1	2.53	0.42
1:D:62:CYS:HB2	1:D:94:CYS:HB2	1.36	0.42
1:J:72:GLU:O	1:J:73:ARG:NE	2.49	0.42
2:H:14:PRO:HG3	2:H:68:ARG:HG3	2.02	0.42
1:G:182:ASN:HA	1:G:263:THR:HG21	2.02	0.42
2:K:69:TYR:HE1	2:K:78:ALA:HB2	1.85	0.42
2:B:201:CYS:HA	2:B:224:GLN:HG3	2.02	0.42
2:K:230:THR:OG1	2:K:231:ASN:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:359:TYR:HA	2:B:366:THR:HG21	2.02	0.41
1:J:225:SER:H	1:J:230:HIS:HE1	1.69	0.41
2:B:107:PRO:HA	2:B:131:HIS:HD2	1.86	0.41
1:G:43:ASN:OD1	1:G:43:ASN:N	2.52	0.41
1:J:29:LEU:HG	1:J:137:TYR:HB3	2.01	0.41
2:K:308:GLU:OE2	2:K:316:ARG:NH1	2.54	0.41
1:J:332:SER:HB3	1:J:339:ILE:HG12	2.02	0.41
2:H:413:VAL:HG12	2:H:414:LEU:HD12	2.02	0.41
1:J:117:ASP:OD1	1:J:117:ASP:N	2.53	0.41
1:D:53:THR:HG22	1:D:108:VAL:HB	2.01	0.41
1:D:142:GLN:HG3	1:D:156:VAL:HG13	2.01	0.41
2:H:237:TYR:HD2	2:H:239:SER:HB2	1.85	0.41
2:K:86:HIS:HB3	2:K:90:VAL:HA	2.03	0.41
1:A:386:HIS:CD2	2:B:342:THR:HG21	2.55	0.41
2:B:306:TYR:OH	2:B:308:GLU:OE1	2.29	0.41
1:J:166:ILE:HG22	1:J:168:THR:H	1.85	0.41
1:D:6:THR:HG22	1:D:277:PRO:HB3	2.03	0.41
1:G:100:ASN:OD1	1:G:100:ASN:N	2.54	0.41
2:K:53:GLN:HB3	2:K:99:HIS:CD2	2.55	0.41
1:A:160:ARG:NH1	1:A:281:ASP:OD2	2.54	0.40
2:H:182:SER:HB3	2:H:189:LYS:HB3	2.03	0.40
2:K:116:GLN:HE22	2:K:122:THR:HG22	1.86	0.40
2:E:128:GLN:HB2	2:K:143:VAL:HG22	2.02	0.40
1:G:9:ASN:ND2	1:G:273:VAL:O	2.43	0.40
1:G:401:ASP:OD1	1:G:401:ASP:N	2.53	0.40
1:J:88:MET:HG2	1:J:89:TRP:H	1.86	0.40
1:D:18:HIS:HB2	1:D:331:HIS:CD2	2.56	0.40
2:H:273:PRO:HB3	2:H:286:LEU:HD13	2.03	0.40
1:G:244:ILE:O	1:G:247:ARG:NE	2.55	0.40
1:D:14:PRO:HB3	1:D:30:GLN:HE21	1.86	0.40
2:E:39:ASP:N	2:E:39:ASP:OD1	2.55	0.40
2:H:54:ILE:HG22	2:H:67:ILE:HG23	2.03	0.40

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	436/438 (100%)	367 (84%)	68 (16%)	1 (0%)	44 75
1	D	436/438 (100%)	372 (85%)	64 (15%)	0	100 100
1	G	436/438 (100%)	368 (84%)	66 (15%)	2 (0%)	25 59
1	J	436/438 (100%)	371 (85%)	61 (14%)	4 (1%)	14 49
2	B	420/422 (100%)	367 (87%)	53 (13%)	0	100 100
2	E	420/422 (100%)	373 (89%)	47 (11%)	0	100 100
2	H	420/422 (100%)	376 (90%)	43 (10%)	1 (0%)	44 75
2	K	420/422 (100%)	363 (86%)	56 (13%)	1 (0%)	44 75
All	All	3424/3440 (100%)	2957 (86%)	458 (13%)	9 (0%)	38 68

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	96	CYS
1	A	401	ASP
1	J	342	ALA
1	J	95	PHE
1	J	401	ASP
1	G	342	ALA
1	G	256	PRO
2	K	173	PRO
2	H	173	PRO

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	369/369 (100%)	363 (98%)	6 (2%)	58 76
1	D	369/369 (100%)	364 (99%)	5 (1%)	62 79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	G	369/369 (100%)	369 (100%)	0	100 100
1	J	369/369 (100%)	366 (99%)	3 (1%)	79 88
2	B	351/351 (100%)	350 (100%)	1 (0%)	91 96
2	E	351/351 (100%)	346 (99%)	5 (1%)	62 79
2	H	351/351 (100%)	346 (99%)	5 (1%)	62 79
2	K	351/351 (100%)	347 (99%)	4 (1%)	70 83
All	All	2880/2880 (100%)	2851 (99%)	29 (1%)	71 84

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	223	ARG
1	A	251	LEU
1	A	298	ASN
1	A	396	ASN
1	A	436	MET
2	B	80	ARG
1	D	94	CYS
1	D	175	ASN
1	D	280	MET
1	D	324	LYS
1	D	438	ARG
2	E	38	ARG
2	E	200	ASN
2	E	297	ARG
2	E	312	ARG
2	E	328	ARG
2	H	80	ARG
2	H	167	ILE
2	H	169	MET
2	H	200	ASN
2	H	250	ARG
1	J	176	LYS
1	J	267	ARG
1	J	438	ARG
2	K	96	THR
2	K	102	VAL
2	K	195	LYS
2	K	250	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	116	HIS
1	A	125	HIS
1	A	298	ASN
1	A	396	ASN
2	B	49	GLN
2	B	64	HIS
2	B	99	HIS
2	B	131	HIS
2	B	232	HIS
1	D	3	HIS
1	D	116	HIS
1	D	175	ASN
1	D	308	HIS
1	D	331	HIS
1	D	386	HIS
1	D	396	ASN
2	E	62	HIS
2	E	64	HIS
1	G	386	HIS
2	H	131	HIS
2	H	218	ASN
2	H	224	GLN
2	H	255	HIS
1	J	30	GLN
1	J	331	HIS
1	J	386	HIS
2	K	86	HIS
2	K	99	HIS
2	K	116	GLN
2	K	131	HIS
2	K	146	HIS
2	K	170	HIS
2	K	226	HIS
2	K	232	HIS
2	K	255	HIS

5.3.3 RNA

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)

60 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	$\#\|Z\| > 2$
3	NAG	a	1	1,3	14,14,15	1.24	1 (7%)	17,19,21	1.37	1 (5%)
3	NAG	a	2	3	14,14,15	0.34	0	17,19,21	0.80	1 (5%)
3	BMA	a	3	3	11,11,12	1.10	1 (9%)	15,15,17	0.90	0
3	MAN	a	4	3	11,11,12	0.95	1 (9%)	15,15,17	0.98	1 (6%)
3	MAN	a	5	3	11,11,12	0.86	0	15,15,17	1.08	2 (13%)
3	NAG	b	1	2,3	14,14,15	0.73	1 (7%)	17,19,21	0.68	0
3	NAG	b	2	3	14,14,15	0.32	0	17,19,21	1.12	2 (11%)
3	BMA	b	3	3	11,11,12	0.84	0	15,15,17	0.84	0
3	MAN	b	4	3	11,11,12	0.80	0	15,15,17	1.08	1 (6%)
3	MAN	b	5	3	11,11,12	0.79	0	15,15,17	1.00	2 (13%)
3	NAG	c	1	2,3	14,14,15	0.27	0	17,19,21	0.64	1 (5%)
3	NAG	c	2	3	14,14,15	0.50	0	17,19,21	0.69	1 (5%)
3	BMA	c	3	3	11,11,12	0.93	0	15,15,17	1.03	0
3	MAN	c	4	3	11,11,12	0.89	0	15,15,17	0.99	2 (13%)
3	MAN	c	5	3	11,11,12	0.85	0	15,15,17	0.91	1 (6%)
3	NAG	d	1	1,3	14,14,15	0.88	1 (7%)	17,19,21	2.43	4 (23%)
3	NAG	d	2	3	14,14,15	0.34	0	17,19,21	1.08	2 (11%)
3	BMA	d	3	3	11,11,12	0.75	0	15,15,17	0.85	0
3	MAN	d	4	3	11,11,12	0.74	0	15,15,17	1.02	2 (13%)
3	MAN	d	5	3	11,11,12	0.73	0	15,15,17	1.04	2 (13%)
3	NAG	e	1	2,3	14,14,15	0.66	0	17,19,21	0.61	0
3	NAG	e	2	3	14,14,15	0.30	0	17,19,21	0.72	1 (5%)
3	BMA	e	3	3	11,11,12	0.97	1 (9%)	15,15,17	0.97	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	MAN	e	4	3	11,11,12	0.77	0	15,15,17	1.08	2 (13%)
3	MAN	e	5	3	11,11,12	0.81	0	15,15,17	0.98	2 (13%)
3	NAG	f	1	2,3	14,14,15	0.63	0	17,19,21	1.12	3 (17%)
3	NAG	f	2	3	14,14,15	0.52	0	17,19,21	0.59	0
3	BMA	f	3	3	11,11,12	0.77	0	15,15,17	0.87	1 (6%)
3	MAN	f	4	3	11,11,12	0.81	0	15,15,17	1.04	2 (13%)
3	MAN	f	5	3	11,11,12	0.85	0	15,15,17	1.28	2 (13%)
3	NAG	g	1	1,3	14,14,15	1.58	1 (7%)	17,19,21	2.71	5 (29%)
3	NAG	g	2	3	14,14,15	0.50	0	17,19,21	0.83	1 (5%)
3	BMA	g	3	3	11,11,12	0.94	1 (9%)	15,15,17	0.89	0
3	MAN	g	4	3	11,11,12	0.82	0	15,15,17	1.11	2 (13%)
3	MAN	g	5	3	11,11,12	0.97	1 (9%)	15,15,17	1.24	2 (13%)
3	NAG	h	1	2,3	14,14,15	0.54	0	17,19,21	0.64	0
3	NAG	h	2	3	14,14,15	0.36	0	17,19,21	1.00	1 (5%)
3	BMA	h	3	3	11,11,12	0.74	0	15,15,17	0.94	0
3	MAN	h	4	3	11,11,12	1.14	2 (18%)	15,15,17	1.10	0
3	MAN	h	5	3	11,11,12	0.95	0	15,15,17	0.94	2 (13%)
3	NAG	i	1	2,3	14,14,15	0.30	0	17,19,21	0.55	0
3	NAG	i	2	3	14,14,15	0.36	0	17,19,21	0.96	1 (5%)
3	BMA	i	3	3	11,11,12	0.96	0	15,15,17	1.15	0
3	MAN	i	4	3	11,11,12	1.01	1 (9%)	15,15,17	0.92	1 (6%)
3	MAN	i	5	3	11,11,12	0.80	0	15,15,17	1.02	2 (13%)
3	NAG	j	1	1,3	14,14,15	0.60	0	17,19,21	1.75	4 (23%)
3	NAG	j	2	3	14,14,15	0.48	0	17,19,21	0.68	0
3	BMA	j	3	3	11,11,12	1.09	0	15,15,17	1.04	1 (6%)
3	MAN	j	4	3	11,11,12	0.84	0	15,15,17	0.96	1 (6%)
3	MAN	j	5	3	11,11,12	0.85	0	15,15,17	0.99	2 (13%)
3	NAG	k	1	2,3	14,14,15	0.31	0	17,19,21	0.57	0
3	NAG	k	2	3	14,14,15	0.43	0	17,19,21	0.69	0
3	BMA	k	3	3	11,11,12	1.02	1 (9%)	15,15,17	1.16	2 (13%)
3	MAN	k	4	3	11,11,12	0.77	0	15,15,17	1.09	2 (13%)
3	MAN	k	5	3	11,11,12	0.82	0	15,15,17	1.14	2 (13%)
3	NAG	l	1	2,3	14,14,15	0.78	1 (7%)	17,19,21	1.14	2 (11%)
3	NAG	l	2	3	14,14,15	0.80	1 (7%)	17,19,21	2.24	3 (17%)
3	BMA	l	3	3	11,11,12	0.74	0	15,15,17	1.06	1 (6%)
3	MAN	l	4	3	11,11,12	0.96	0	15,15,17	0.91	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	MAN	l	5	3	11,11,12	0.72	0	15,15,17	1.08	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
3	NAG	a	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	a	2	3	-	3/6/23/26	0/1/1/1
3	BMA	a	3	3	-	0/2/19/22	0/1/1/1
3	MAN	a	4	3	-	0/2/19/22	0/1/1/1
3	MAN	a	5	3	-	2/2/19/22	0/1/1/1
3	NAG	b	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	b	2	3	-	2/6/23/26	0/1/1/1
3	BMA	b	3	3	-	2/2/19/22	0/1/1/1
3	MAN	b	4	3	-	1/2/19/22	0/1/1/1
3	MAN	b	5	3	-	2/2/19/22	0/1/1/1
3	NAG	c	1	2,3	-	1/6/23/26	0/1/1/1
3	NAG	c	2	3	-	3/6/23/26	0/1/1/1
3	BMA	c	3	3	-	2/2/19/22	0/1/1/1
3	MAN	c	4	3	-	0/2/19/22	0/1/1/1
3	MAN	c	5	3	-	2/2/19/22	0/1/1/1
3	NAG	d	1	1,3	-	5/6/23/26	0/1/1/1
3	NAG	d	2	3	-	3/6/23/26	0/1/1/1
3	BMA	d	3	3	-	2/2/19/22	0/1/1/1
3	MAN	d	4	3	-	2/2/19/22	0/1/1/1
3	MAN	d	5	3	-	0/2/19/22	0/1/1/1
3	NAG	e	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	e	2	3	-	3/6/23/26	0/1/1/1
3	BMA	e	3	3	-	2/2/19/22	0/1/1/1
3	MAN	e	4	3	-	1/2/19/22	0/1/1/1
3	MAN	e	5	3	-	2/2/19/22	0/1/1/1
3	NAG	f	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	f	2	3	-	3/6/23/26	0/1/1/1
3	BMA	f	3	3	-	2/2/19/22	0/1/1/1
3	MAN	f	4	3	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	f	5	3	-	0/2/19/22	0/1/1/1
3	NAG	g	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	g	2	3	-	3/6/23/26	0/1/1/1
3	BMA	g	3	3	-	2/2/19/22	0/1/1/1
3	MAN	g	4	3	-	2/2/19/22	0/1/1/1
3	MAN	g	5	3	-	2/2/19/22	0/1/1/1
3	NAG	h	1	2,3	-	4/6/23/26	0/1/1/1
3	NAG	h	2	3	-	3/6/23/26	0/1/1/1
3	BMA	h	3	3	-	2/2/19/22	0/1/1/1
3	MAN	h	4	3	-	0/2/19/22	0/1/1/1
3	MAN	h	5	3	-	0/2/19/22	0/1/1/1
3	NAG	i	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	i	2	3	-	2/6/23/26	0/1/1/1
3	BMA	i	3	3	-	2/2/19/22	0/1/1/1
3	MAN	i	4	3	-	0/2/19/22	0/1/1/1
3	MAN	i	5	3	-	0/2/19/22	0/1/1/1
3	NAG	j	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	j	2	3	-	2/6/23/26	0/1/1/1
3	BMA	j	3	3	-	2/2/19/22	0/1/1/1
3	MAN	j	4	3	-	0/2/19/22	0/1/1/1
3	MAN	j	5	3	-	0/2/19/22	0/1/1/1
3	NAG	k	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	k	2	3	-	4/6/23/26	0/1/1/1
3	BMA	k	3	3	-	2/2/19/22	0/1/1/1
3	MAN	k	4	3	-	0/2/19/22	0/1/1/1
3	MAN	k	5	3	-	2/2/19/22	0/1/1/1
3	NAG	l	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	l	2	3	-	5/6/23/26	0/1/1/1
3	BMA	l	3	3	-	2/2/19/22	0/1/1/1
3	MAN	l	4	3	-	0/2/19/22	0/1/1/1
3	MAN	l	5	3	-	2/2/19/22	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	g	1	NAG	C1-C2	5.28	1.60	1.52
3	a	1	NAG	O5-C1	4.27	1.50	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	d	1	NAG	O5-C1	-2.53	1.39	1.43
3	b	1	NAG	O5-C1	-2.52	1.39	1.43
3	a	3	BMA	C4-C5	2.51	1.58	1.53
3	g	5	MAN	C1-C2	2.37	1.57	1.52
3	k	3	BMA	C4-C5	2.32	1.57	1.53
3	l	2	NAG	C1-C2	2.31	1.55	1.52
3	l	1	NAG	O5-C1	-2.27	1.40	1.43
3	h	4	MAN	C2-C3	2.19	1.55	1.52
3	a	4	MAN	C2-C3	2.13	1.55	1.52
3	e	3	BMA	C4-C5	2.12	1.57	1.53
3	i	4	MAN	O5-C1	-2.09	1.40	1.43
3	h	4	MAN	C1-C2	2.06	1.56	1.52
3	g	3	BMA	C4-C5	2.00	1.57	1.53

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	d	1	NAG	C2-N2-C7	8.04	134.35	122.90
3	l	2	NAG	C2-N2-C7	7.81	134.03	122.90
3	g	1	NAG	C2-N2-C7	7.12	133.04	122.90
3	g	1	NAG	C1-O5-C5	5.41	119.52	112.19
3	a	1	NAG	C1-O5-C5	5.20	119.24	112.19
3	j	1	NAG	C1-O5-C5	4.72	118.58	112.19
3	j	1	NAG	C3-C4-C5	4.17	117.68	110.24
3	g	1	NAG	C1-C2-N2	4.12	117.53	110.49
3	d	1	NAG	C1-C2-N2	4.01	117.33	110.49
3	g	1	NAG	C4-C3-C2	3.90	116.73	111.02
3	l	2	NAG	C1-C2-N2	3.59	116.62	110.49
3	f	5	MAN	C1-O5-C5	3.43	116.84	112.19
3	d	2	NAG	C2-N2-C7	3.13	127.36	122.90
3	b	2	NAG	C2-N2-C7	3.07	127.27	122.90
3	h	2	NAG	C2-N2-C7	3.04	127.23	122.90
3	k	5	MAN	C1-O5-C5	2.99	116.24	112.19
3	i	2	NAG	C2-N2-C7	2.94	127.09	122.90
3	l	1	NAG	C3-C4-C5	2.86	115.35	110.24
3	g	5	MAN	C1-O5-C5	2.84	116.04	112.19
3	g	4	MAN	C1-O5-C5	2.81	116.00	112.19
3	l	3	BMA	C1-O5-C5	2.79	115.97	112.19
3	l	5	MAN	C1-O5-C5	2.79	115.97	112.19
3	e	4	MAN	C1-O5-C5	2.78	115.97	112.19
3	f	4	MAN	C1-O5-C5	2.72	115.88	112.19
3	i	5	MAN	C1-O5-C5	2.70	115.85	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	d	4	MAN	C1-O5-C5	2.69	115.84	112.19
3	a	2	NAG	C1-O5-C5	2.67	115.81	112.19
3	k	4	MAN	C1-O5-C5	2.65	115.78	112.19
3	f	1	NAG	C4-C3-C2	2.57	114.78	111.02
3	b	5	MAN	C1-O5-C5	2.55	115.65	112.19
3	g	2	NAG	C1-O5-C5	2.55	115.64	112.19
3	f	1	NAG	C3-C4-C5	2.53	114.76	110.24
3	l	1	NAG	C4-C3-C2	2.50	114.69	111.02
3	l	5	MAN	O2-C2-C3	-2.49	105.15	110.14
3	d	5	MAN	C1-O5-C5	2.48	115.55	112.19
3	a	5	MAN	C1-O5-C5	2.43	115.48	112.19
3	b	4	MAN	O2-C2-C3	-2.37	105.39	110.14
3	k	4	MAN	O2-C2-C3	-2.36	105.41	110.14
3	j	1	NAG	C4-C3-C2	2.34	114.44	111.02
3	k	5	MAN	O2-C2-C3	-2.33	105.46	110.14
3	k	3	BMA	O5-C1-C2	-2.32	107.19	110.77
3	e	5	MAN	O2-C2-C3	-2.30	105.53	110.14
3	l	4	MAN	O2-C2-C3	-2.30	105.53	110.14
3	c	5	MAN	O2-C2-C3	-2.26	105.61	110.14
3	j	5	MAN	C1-O5-C5	2.26	115.26	112.19
3	i	4	MAN	O2-C2-C3	-2.26	105.61	110.14
3	j	4	MAN	O2-C2-C3	-2.24	105.66	110.14
3	c	4	MAN	O2-C2-C3	-2.23	105.66	110.14
3	d	5	MAN	O2-C2-C3	-2.23	105.66	110.14
3	f	4	MAN	O2-C2-C3	-2.23	105.66	110.14
3	e	2	NAG	C1-O5-C5	2.22	115.20	112.19
3	d	4	MAN	O2-C2-C3	-2.22	105.70	110.14
3	g	4	MAN	O2-C2-C3	-2.21	105.70	110.14
3	c	4	MAN	C1-O5-C5	2.21	115.19	112.19
3	h	5	MAN	C1-O5-C5	2.21	115.19	112.19
3	c	1	NAG	C1-O5-C5	2.20	115.17	112.19
3	b	5	MAN	O2-C2-C3	-2.20	105.73	110.14
3	b	2	NAG	C1-O5-C5	2.19	115.16	112.19
3	k	3	BMA	C1-C2-C3	-2.18	106.99	109.67
3	e	4	MAN	O2-C2-C3	-2.18	105.78	110.14
3	a	5	MAN	O2-C2-C3	-2.18	105.78	110.14
3	e	5	MAN	C1-O5-C5	2.14	115.09	112.19
3	l	2	NAG	C8-C7-N2	2.14	119.72	116.10
3	g	5	MAN	O2-C2-C3	-2.13	105.87	110.14
3	i	5	MAN	O2-C2-C3	-2.13	105.87	110.14
3	g	1	NAG	C3-C4-C5	2.13	114.04	110.24
3	d	1	NAG	C8-C7-N2	2.13	119.70	116.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	j	3	BMA	C1-C2-C3	-2.13	107.05	109.67
3	j	5	MAN	O2-C2-C3	-2.12	105.89	110.14
3	c	2	NAG	C1-O5-C5	2.08	115.01	112.19
3	j	1	NAG	O5-C5-C4	2.08	115.89	110.83
3	d	1	NAG	C3-C4-C5	2.07	113.94	110.24
3	d	2	NAG	C1-O5-C5	2.07	115.00	112.19
3	h	5	MAN	O2-C2-C3	-2.06	106.00	110.14
3	a	4	MAN	O2-C2-C3	-2.03	106.06	110.14
3	f	5	MAN	O2-C2-C3	-2.02	106.09	110.14
3	f	1	NAG	C1-O5-C5	2.02	114.93	112.19
3	f	3	BMA	O2-C2-C3	-2.02	106.09	110.14

There are no chirality outliers.

All (108) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	k	1	NAG	O5-C5-C6-O6
3	h	3	BMA	O5-C5-C6-O6
3	g	4	MAN	O5-C5-C6-O6
3	l	2	NAG	C4-C5-C6-O6
3	d	1	NAG	O5-C5-C6-O6
3	g	1	NAG	O5-C5-C6-O6
3	h	2	NAG	O5-C5-C6-O6
3	k	5	MAN	O5-C5-C6-O6
3	k	5	MAN	C4-C5-C6-O6
3	f	1	NAG	C4-C5-C6-O6
3	g	1	NAG	C4-C5-C6-O6
3	a	1	NAG	O5-C5-C6-O6
3	j	1	NAG	O5-C5-C6-O6
3	h	1	NAG	C4-C5-C6-O6
3	k	1	NAG	C4-C5-C6-O6
3	f	1	NAG	O5-C5-C6-O6
3	g	4	MAN	C4-C5-C6-O6
3	h	1	NAG	O5-C5-C6-O6
3	i	1	NAG	O5-C5-C6-O6
3	k	2	NAG	O5-C5-C6-O6
3	g	3	BMA	O5-C5-C6-O6
3	d	1	NAG	C4-C5-C6-O6
3	g	3	BMA	C4-C5-C6-O6
3	h	3	BMA	C4-C5-C6-O6
3	i	1	NAG	C4-C5-C6-O6
3	k	2	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
3	h	2	NAG	C4-C5-C6-O6
3	a	2	NAG	C8-C7-N2-C2
3	a	2	NAG	O7-C7-N2-C2
3	c	2	NAG	C8-C7-N2-C2
3	c	2	NAG	O7-C7-N2-C2
3	d	1	NAG	C8-C7-N2-C2
3	d	1	NAG	O7-C7-N2-C2
3	e	2	NAG	C8-C7-N2-C2
3	e	2	NAG	O7-C7-N2-C2
3	f	2	NAG	C8-C7-N2-C2
3	f	2	NAG	O7-C7-N2-C2
3	g	1	NAG	C8-C7-N2-C2
3	g	1	NAG	O7-C7-N2-C2
3	g	2	NAG	C8-C7-N2-C2
3	g	2	NAG	O7-C7-N2-C2
3	h	1	NAG	C8-C7-N2-C2
3	h	1	NAG	O7-C7-N2-C2
3	j	2	NAG	C8-C7-N2-C2
3	j	2	NAG	O7-C7-N2-C2
3	k	2	NAG	C8-C7-N2-C2
3	k	2	NAG	O7-C7-N2-C2
3	l	2	NAG	C8-C7-N2-C2
3	l	2	NAG	O7-C7-N2-C2
3	l	2	NAG	O5-C5-C6-O6
3	b	3	BMA	O5-C5-C6-O6
3	e	5	MAN	O5-C5-C6-O6
3	l	3	BMA	O5-C5-C6-O6
3	a	1	NAG	C4-C5-C6-O6
3	d	4	MAN	O5-C5-C6-O6
3	l	1	NAG	O5-C5-C6-O6
3	b	5	MAN	O5-C5-C6-O6
3	b	3	BMA	C4-C5-C6-O6
3	j	3	BMA	C4-C5-C6-O6
3	i	3	BMA	O5-C5-C6-O6
3	l	3	BMA	C4-C5-C6-O6
3	e	5	MAN	C4-C5-C6-O6
3	i	3	BMA	C4-C5-C6-O6
3	c	3	BMA	O5-C5-C6-O6
3	l	5	MAN	O5-C5-C6-O6
3	c	3	BMA	C4-C5-C6-O6
3	c	5	MAN	O5-C5-C6-O6
3	f	3	BMA	O5-C5-C6-O6

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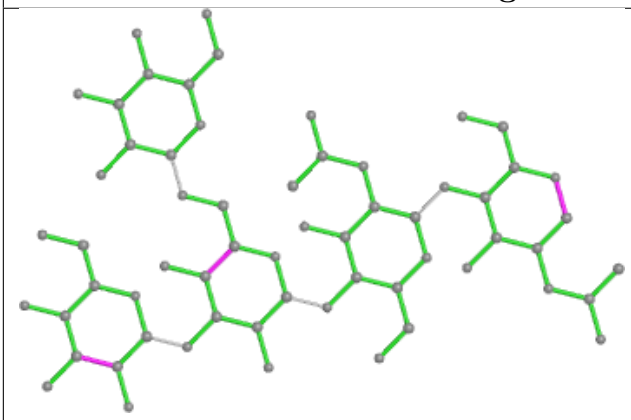
Mol	Chain	Res	Type	Atoms
3	k	3	BMA	C4-C5-C6-O6
3	j	3	BMA	O5-C5-C6-O6
3	b	1	NAG	C4-C5-C6-O6
3	c	5	MAN	C4-C5-C6-O6
3	a	2	NAG	O5-C5-C6-O6
3	f	3	BMA	C4-C5-C6-O6
3	l	5	MAN	C4-C5-C6-O6
3	k	3	BMA	O5-C5-C6-O6
3	d	2	NAG	C4-C5-C6-O6
3	d	3	BMA	O5-C5-C6-O6
3	b	2	NAG	O5-C5-C6-O6
3	a	5	MAN	O5-C5-C6-O6
3	c	1	NAG	O5-C5-C6-O6
3	d	4	MAN	C4-C5-C6-O6
3	d	2	NAG	O5-C5-C6-O6
3	f	2	NAG	O5-C5-C6-O6
3	i	2	NAG	O5-C5-C6-O6
3	d	3	BMA	C4-C5-C6-O6
3	c	2	NAG	O5-C5-C6-O6
3	e	2	NAG	O5-C5-C6-O6
3	b	1	NAG	O5-C5-C6-O6
3	b	5	MAN	C4-C5-C6-O6
3	g	5	MAN	O5-C5-C6-O6
3	e	3	BMA	C4-C5-C6-O6
3	g	5	MAN	C4-C5-C6-O6
3	j	1	NAG	C4-C5-C6-O6
3	e	1	NAG	C4-C5-C6-O6
3	e	4	MAN	C4-C5-C6-O6
3	b	2	NAG	C3-C2-N2-C7
3	d	1	NAG	C3-C2-N2-C7
3	i	2	NAG	C3-C2-N2-C7
3	e	3	BMA	O5-C5-C6-O6
3	l	1	NAG	C4-C5-C6-O6
3	g	2	NAG	C4-C5-C6-O6
3	a	5	MAN	C4-C5-C6-O6
3	b	4	MAN	C4-C5-C6-O6
3	e	1	NAG	O5-C5-C6-O6
3	d	2	NAG	C3-C2-N2-C7
3	h	2	NAG	C3-C2-N2-C7
3	l	2	NAG	C3-C2-N2-C7

There are no ring outliers.

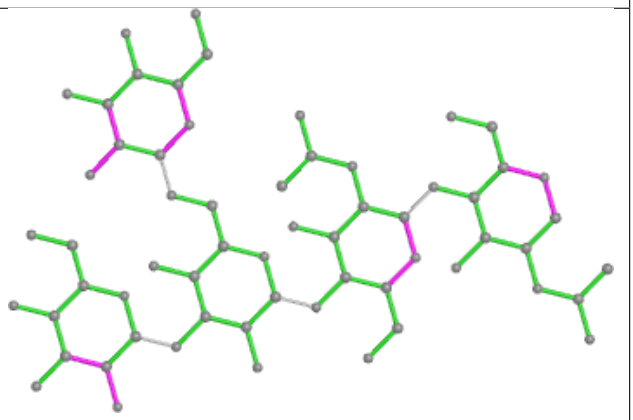
No monomer is involved in short contacts.

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

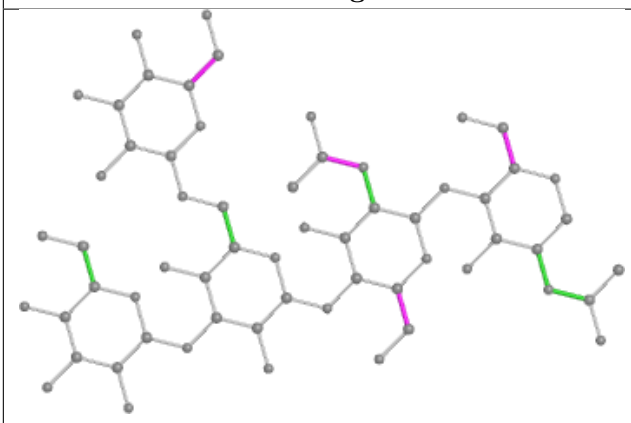
Oligosaccharide Chain a



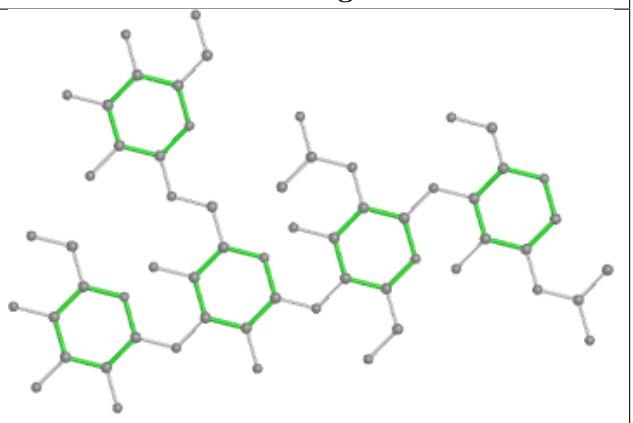
Bond lengths



Bond angles

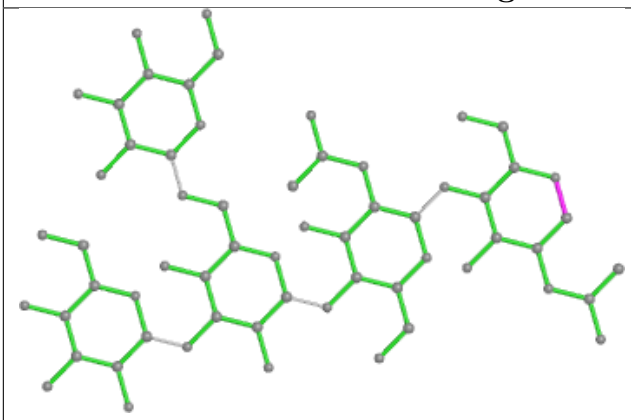


Torsions

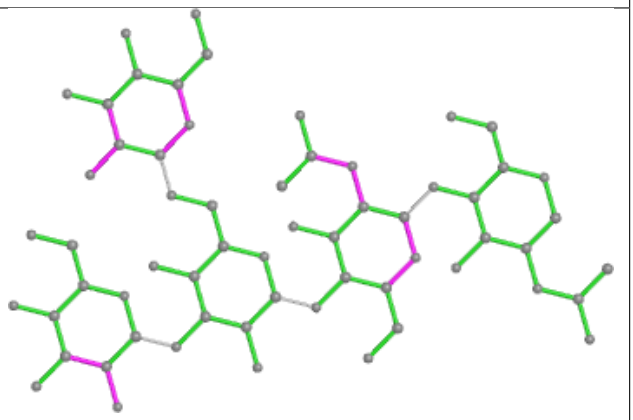


Rings

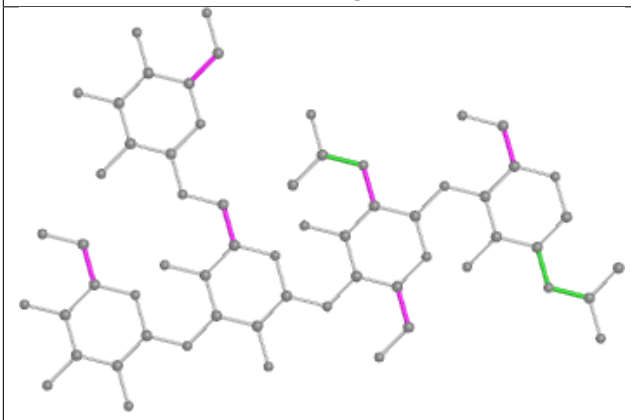
Oligosaccharide Chain b



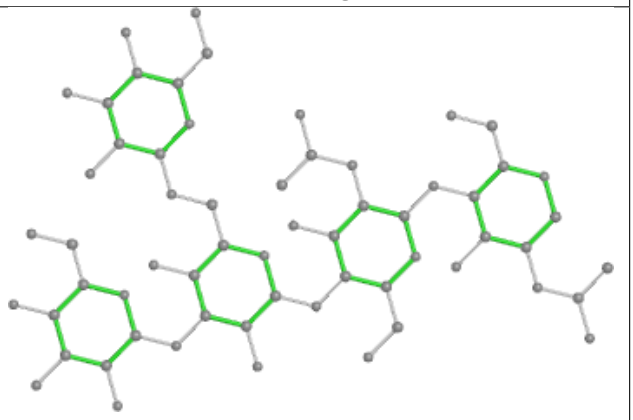
Bond lengths



Bond angles

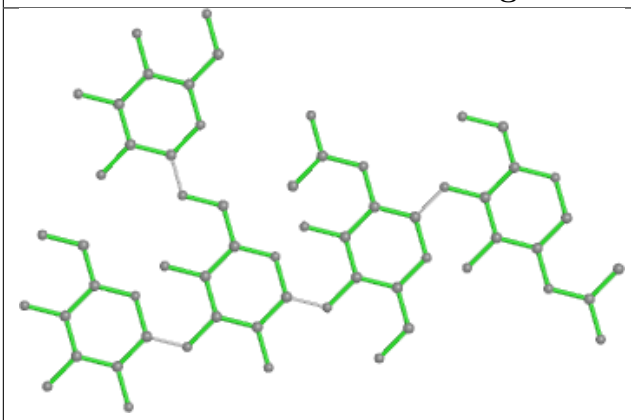


Torsions

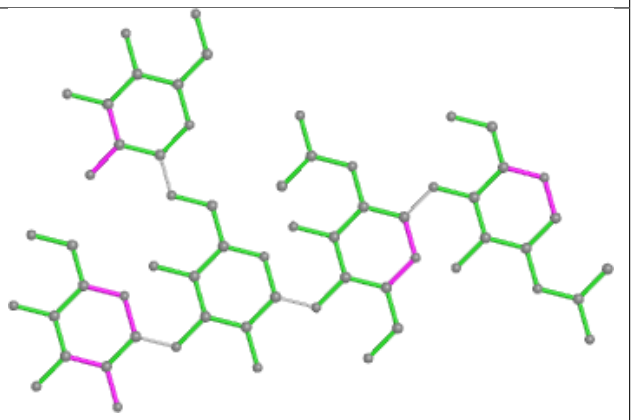


Rings

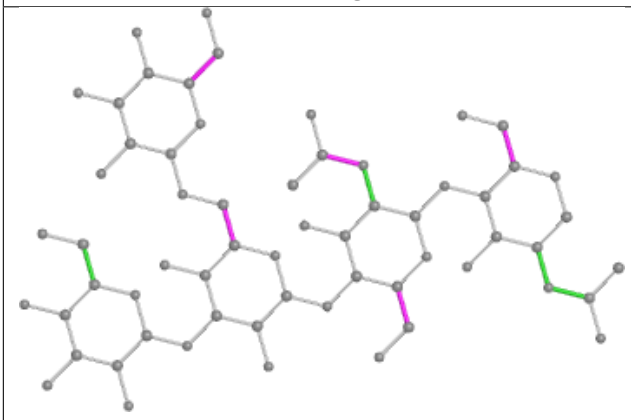
Oligosaccharide Chain c



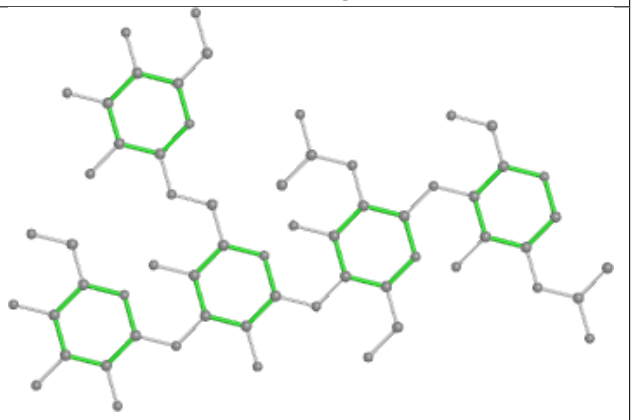
Bond lengths



Bond angles

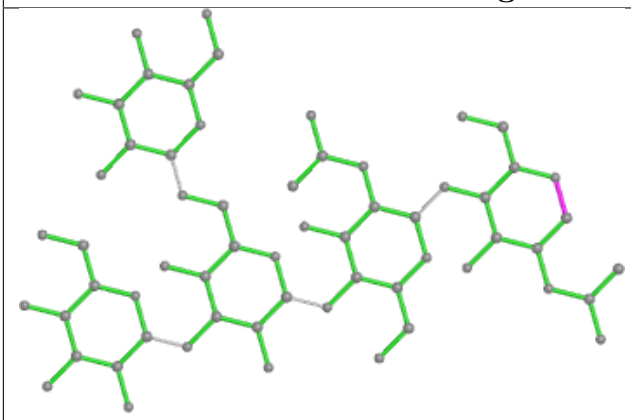


Torsions

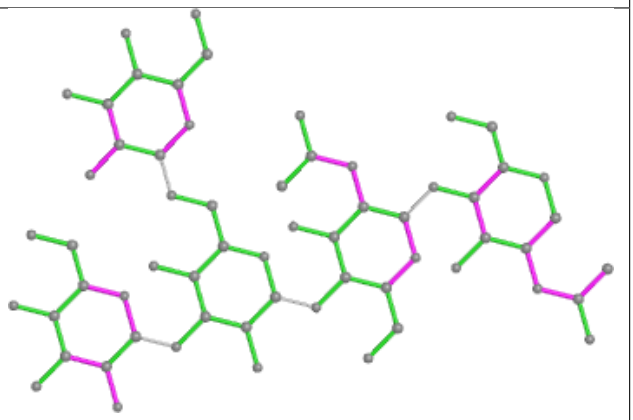


Rings

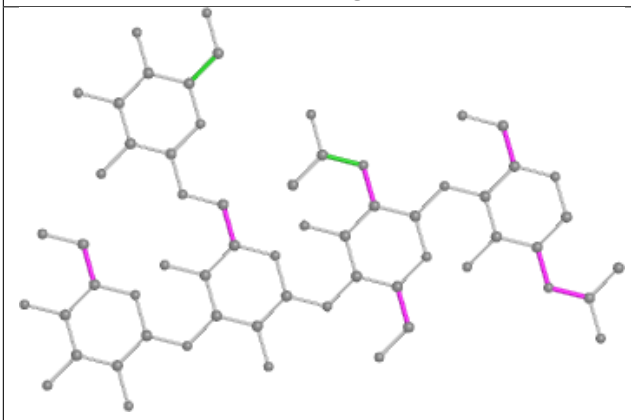
Oligosaccharide Chain d



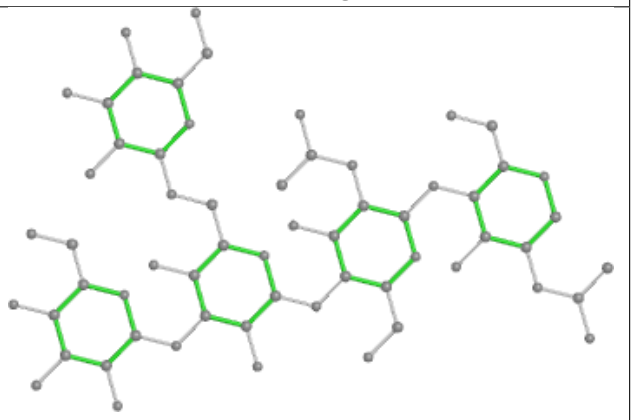
Bond lengths



Bond angles

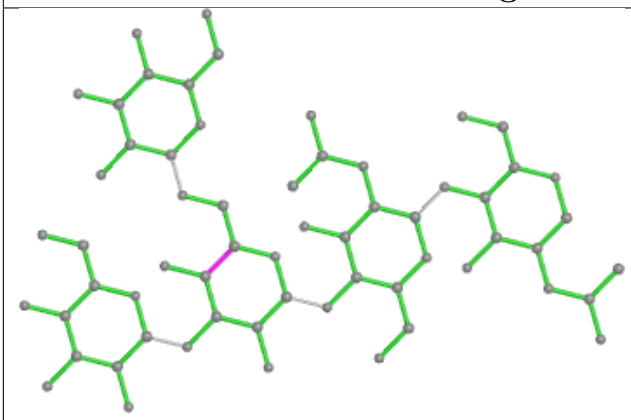


Torsions

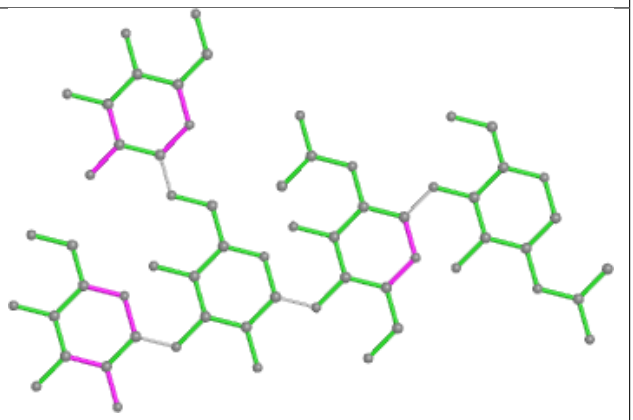


Rings

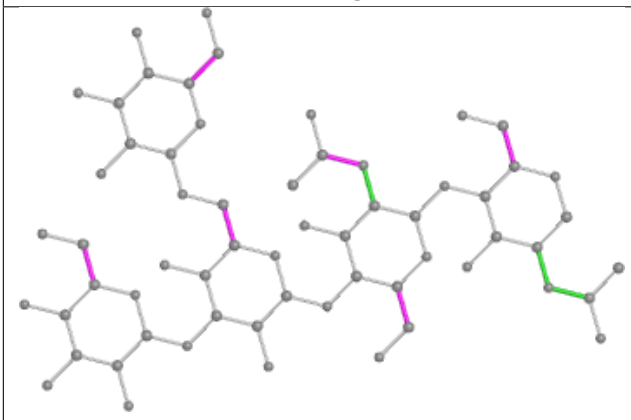
Oligosaccharide Chain e



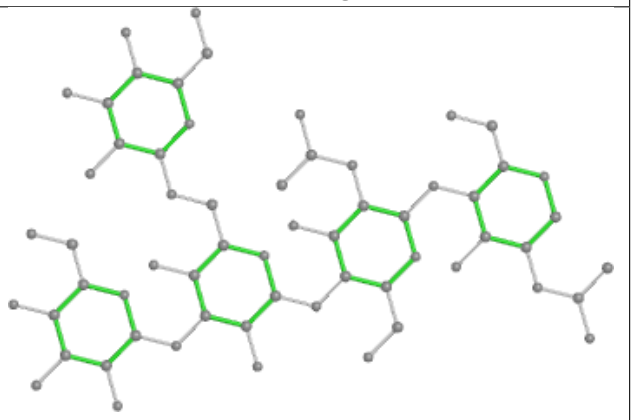
Bond lengths



Bond angles

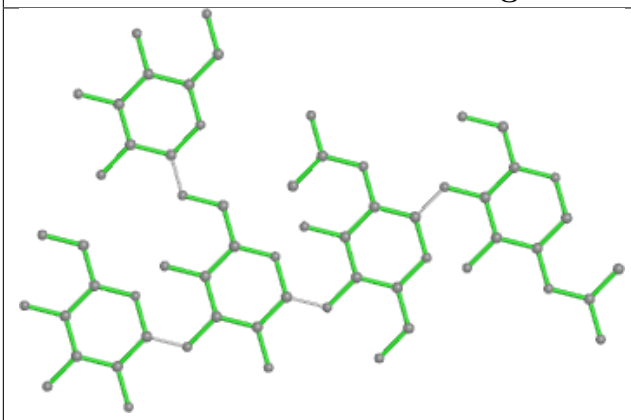


Torsions

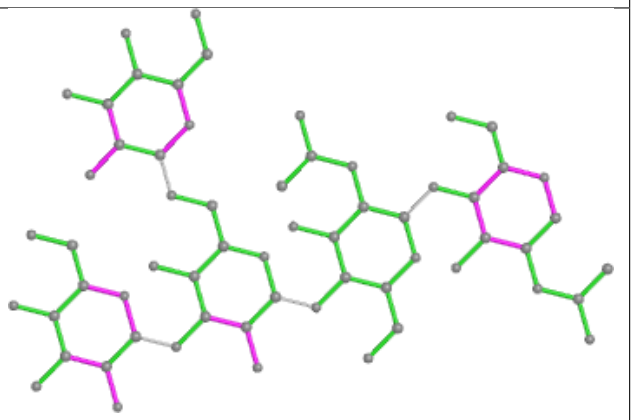


Rings

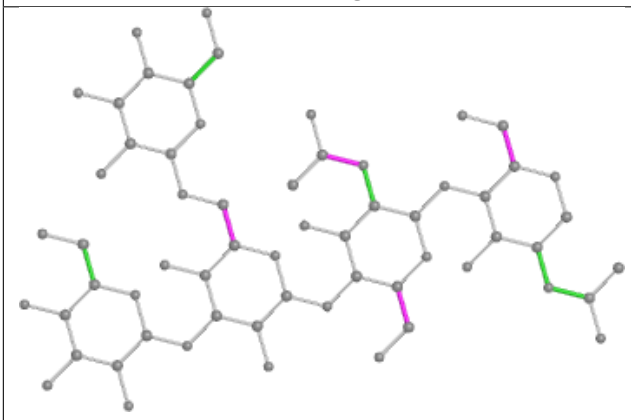
Oligosaccharide Chain f



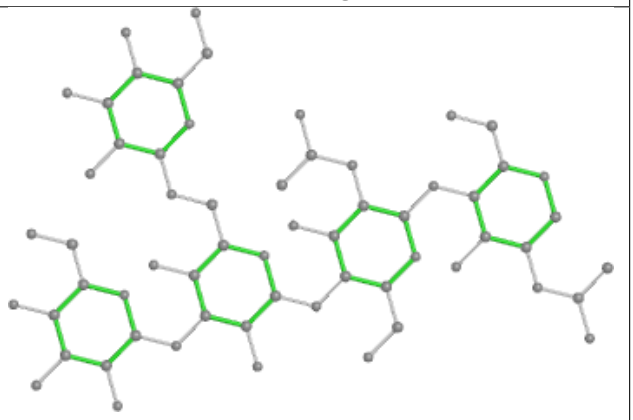
Bond lengths



Bond angles

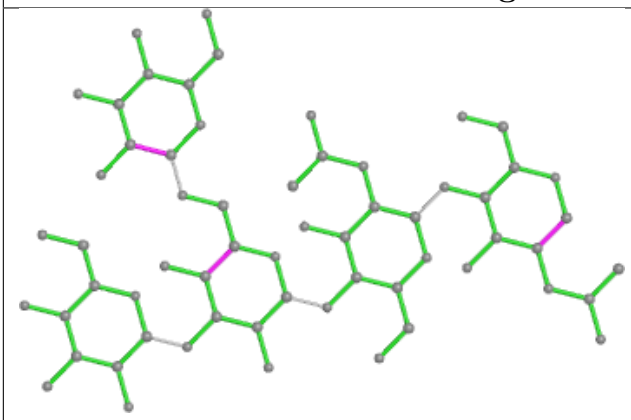


Torsions

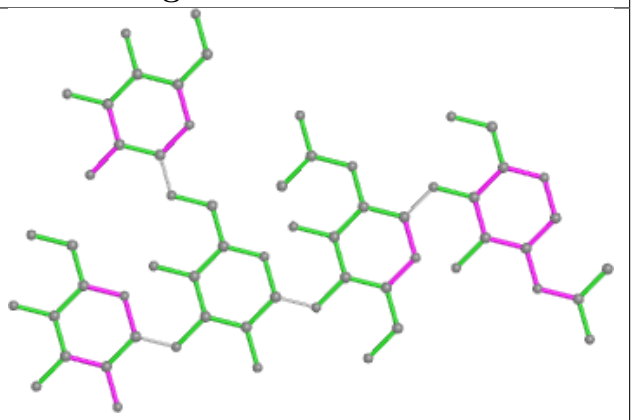


Rings

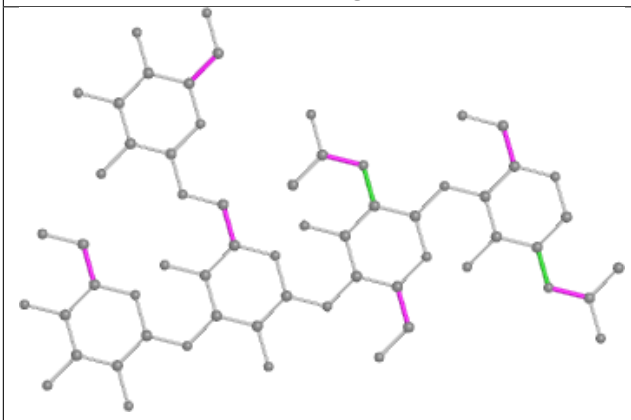
Oligosaccharide Chain g



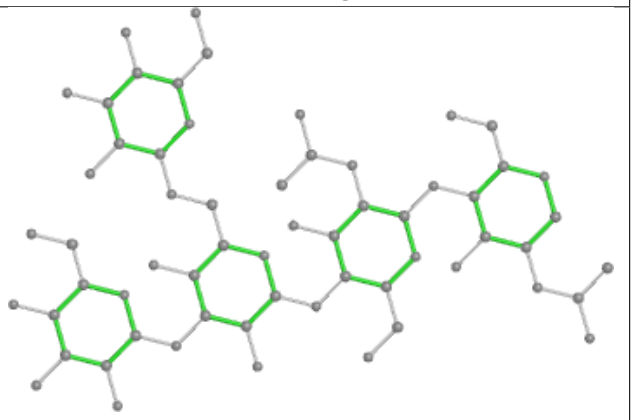
Bond lengths



Bond angles

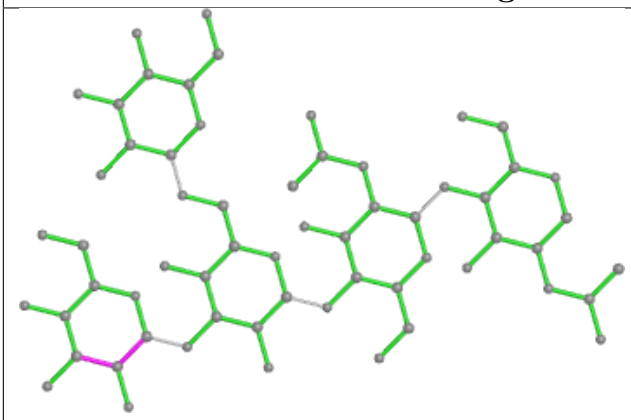


Torsions

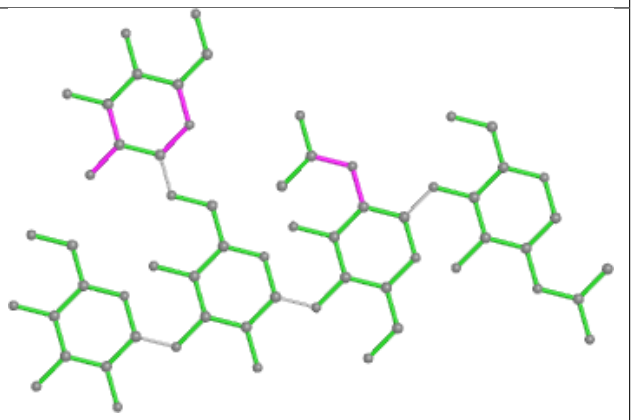


Rings

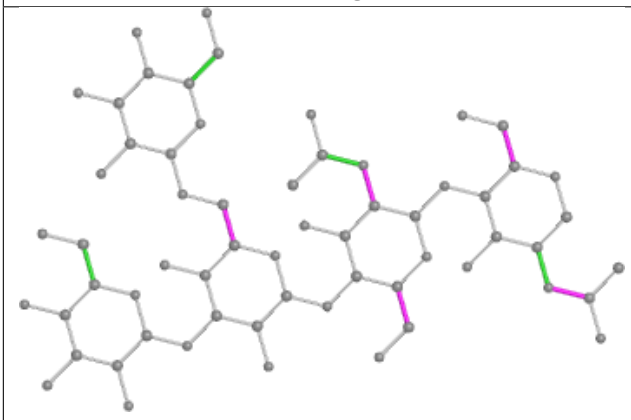
Oligosaccharide Chain h



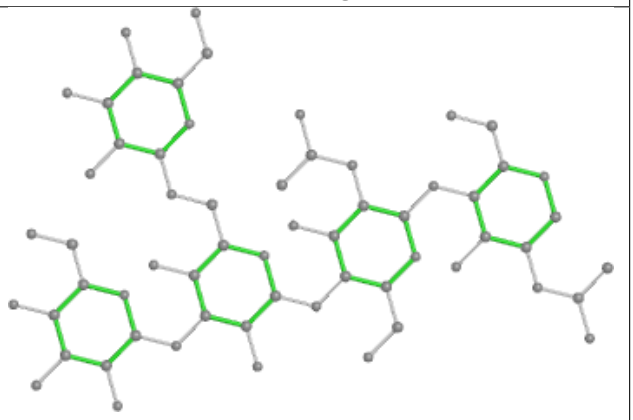
Bond lengths



Bond angles

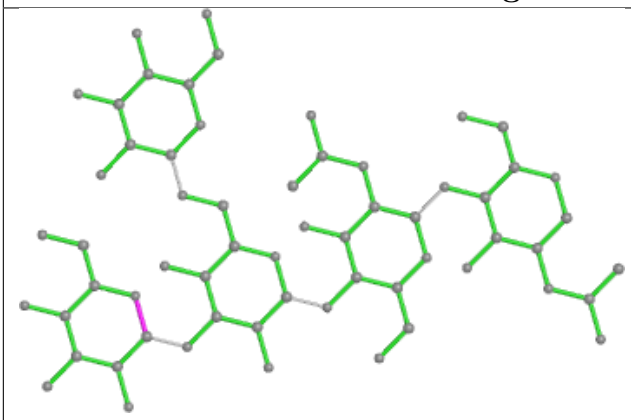


Torsions

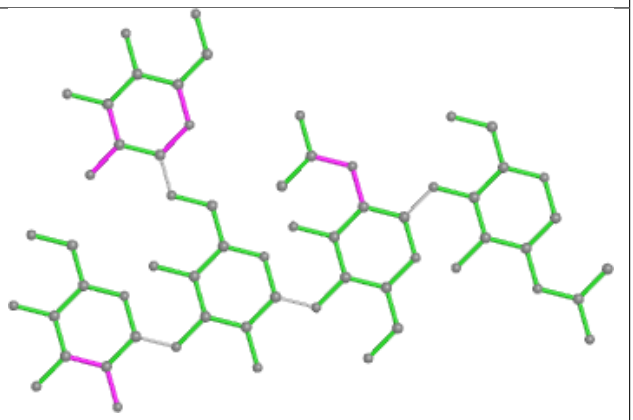


Rings

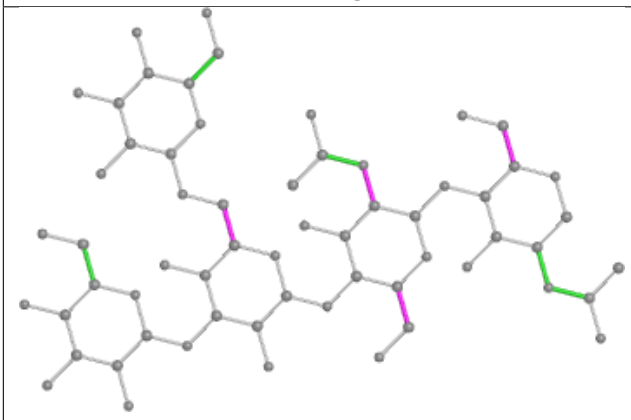
Oligosaccharide Chain i



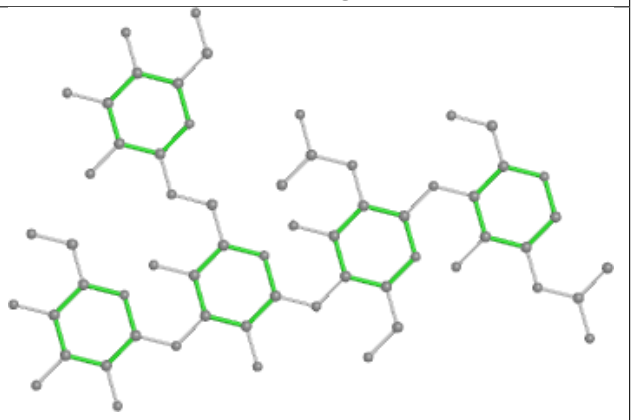
Bond lengths



Bond angles

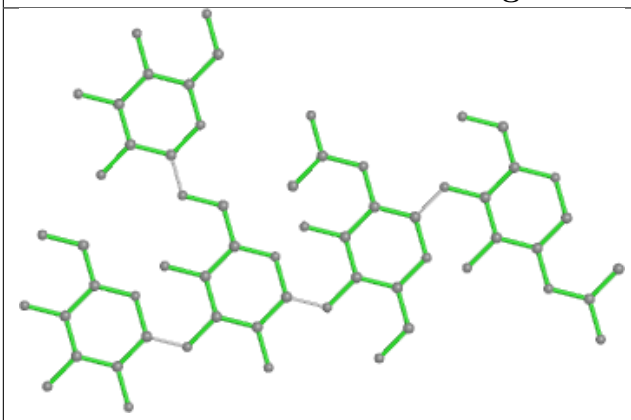


Torsions

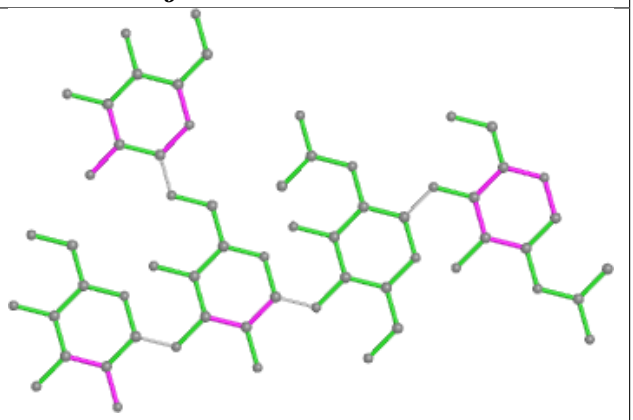


Rings

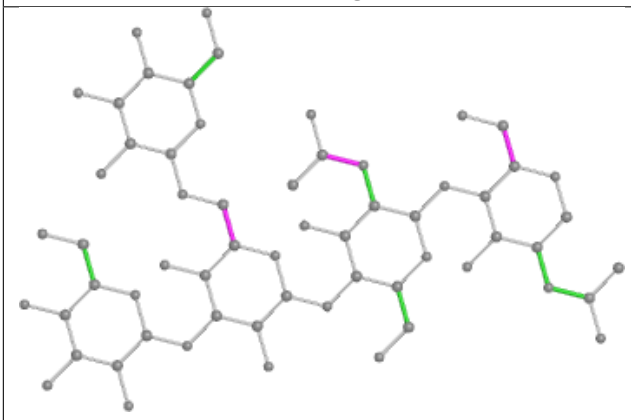
Oligosaccharide Chain j



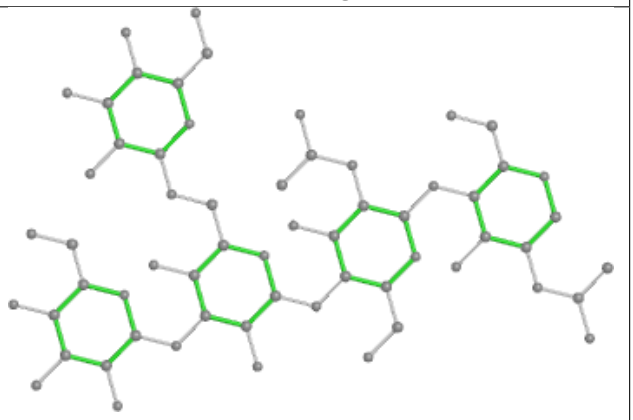
Bond lengths



Bond angles

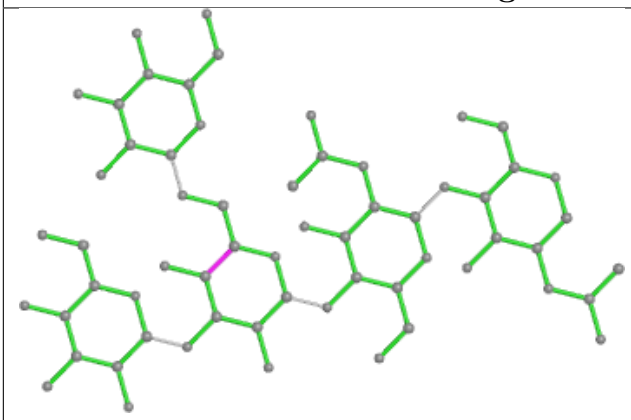


Torsions

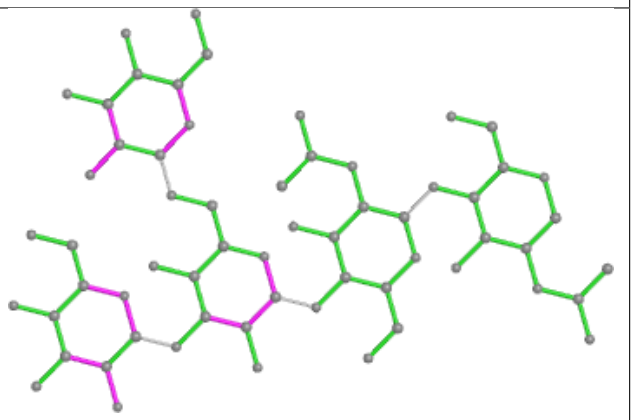


Rings

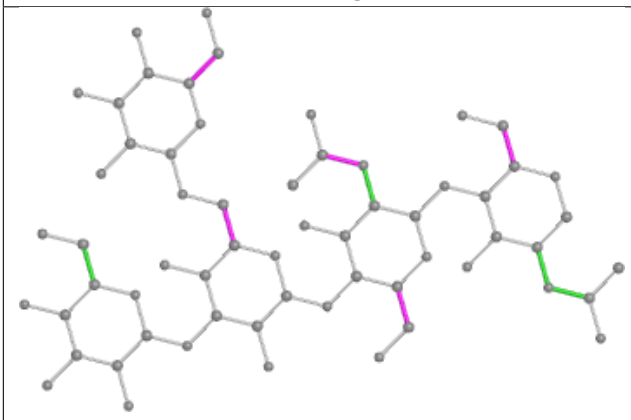
Oligosaccharide Chain k



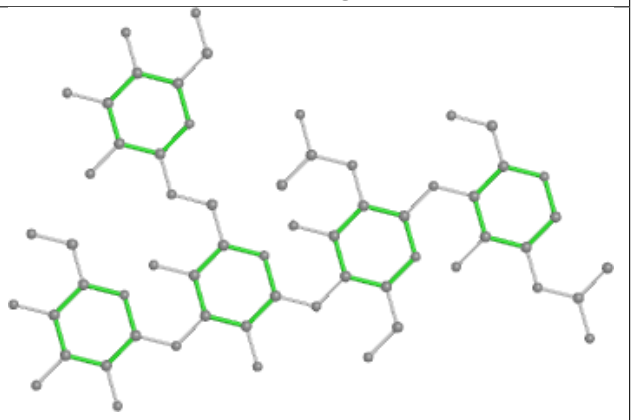
Bond lengths



Bond angles

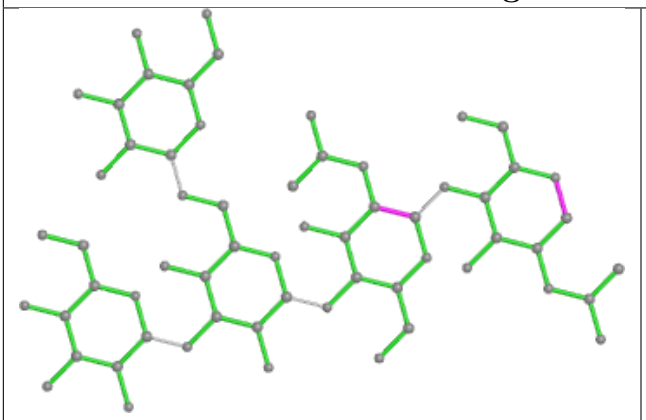


Torsions

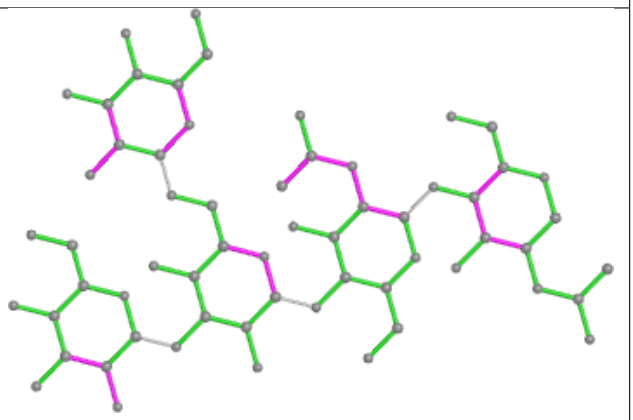


Rings

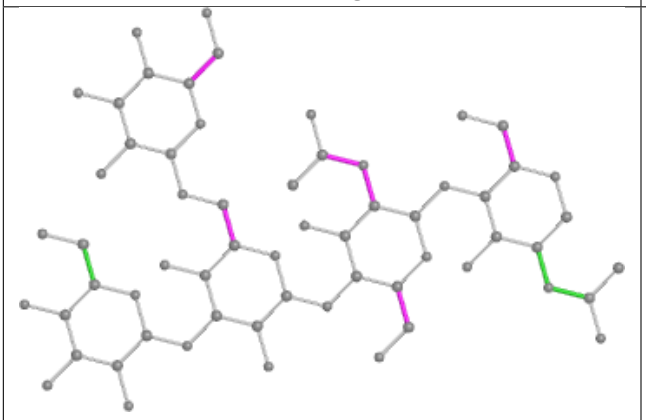
Oligosaccharide Chain l



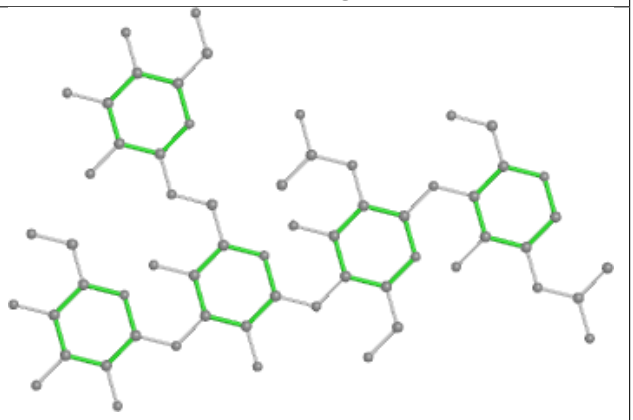
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

There are no ligands in this entry.

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.

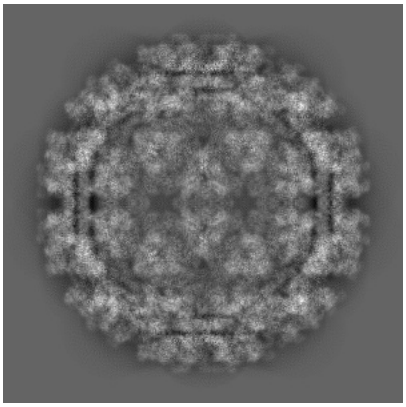
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-32412. These allow visual inspection of the internal detail of the map and identification of artifacts.

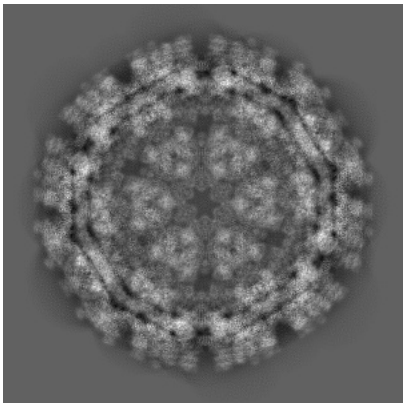
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

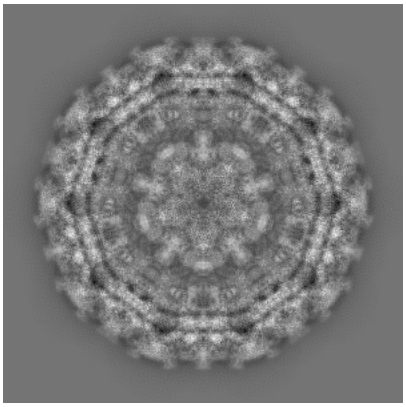
6.1.1 Primary map



X



Y

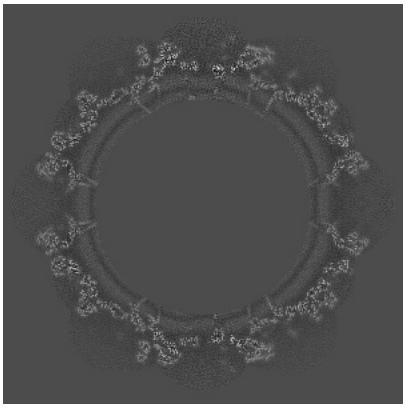


Z

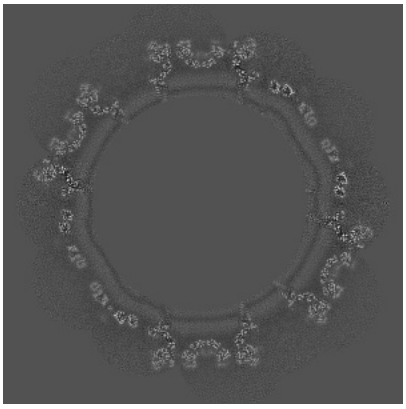
The images above show the map projected in three orthogonal directions.

6.2 Central slices

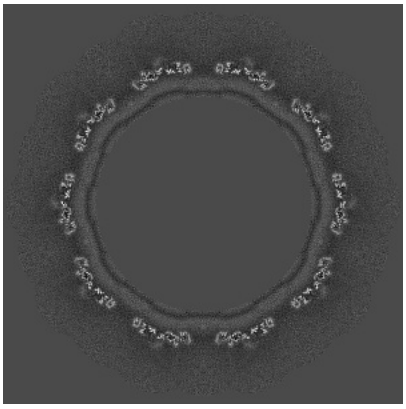
6.2.1 Primary map



X Index: 300



Y Index: 300

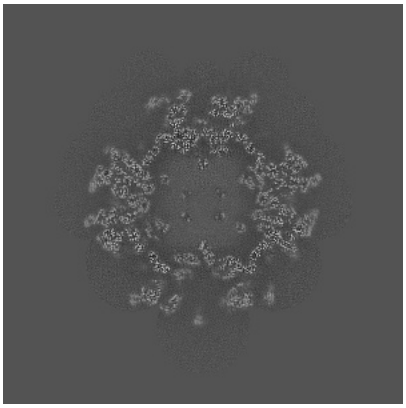


Z Index: 300

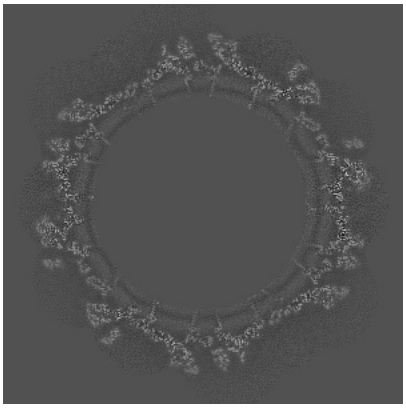
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

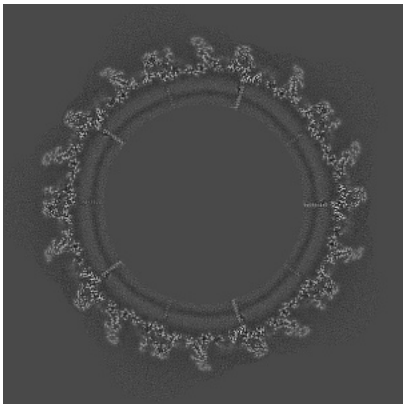
6.3.1 Primary map



X Index: 480



Y Index: 279

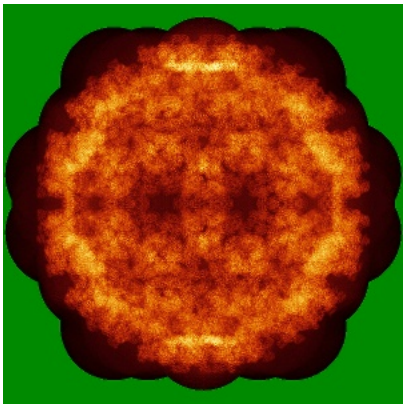


Z Index: 355

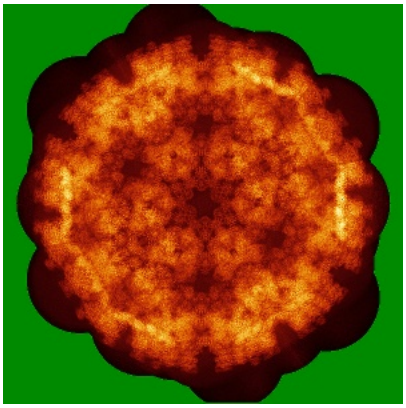
The images above show the largest variance slices of the map in three orthogonal directions.

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

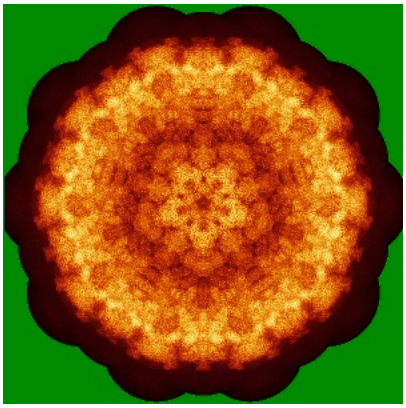
6.4.1 Primary map



X



Y

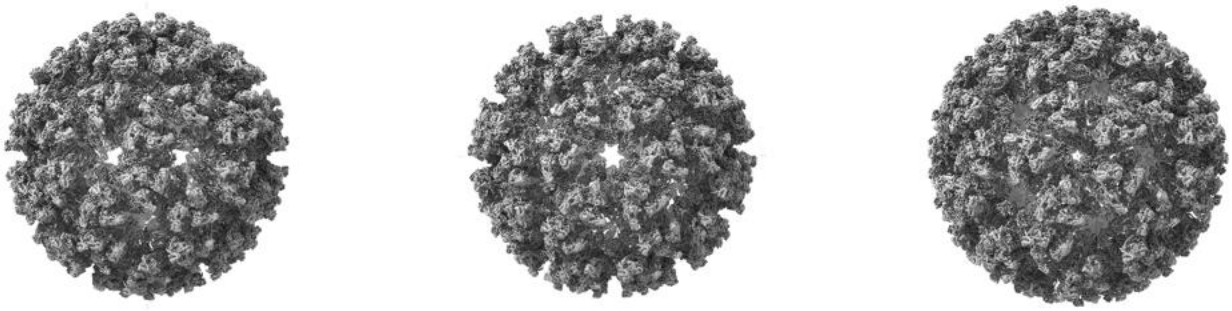


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

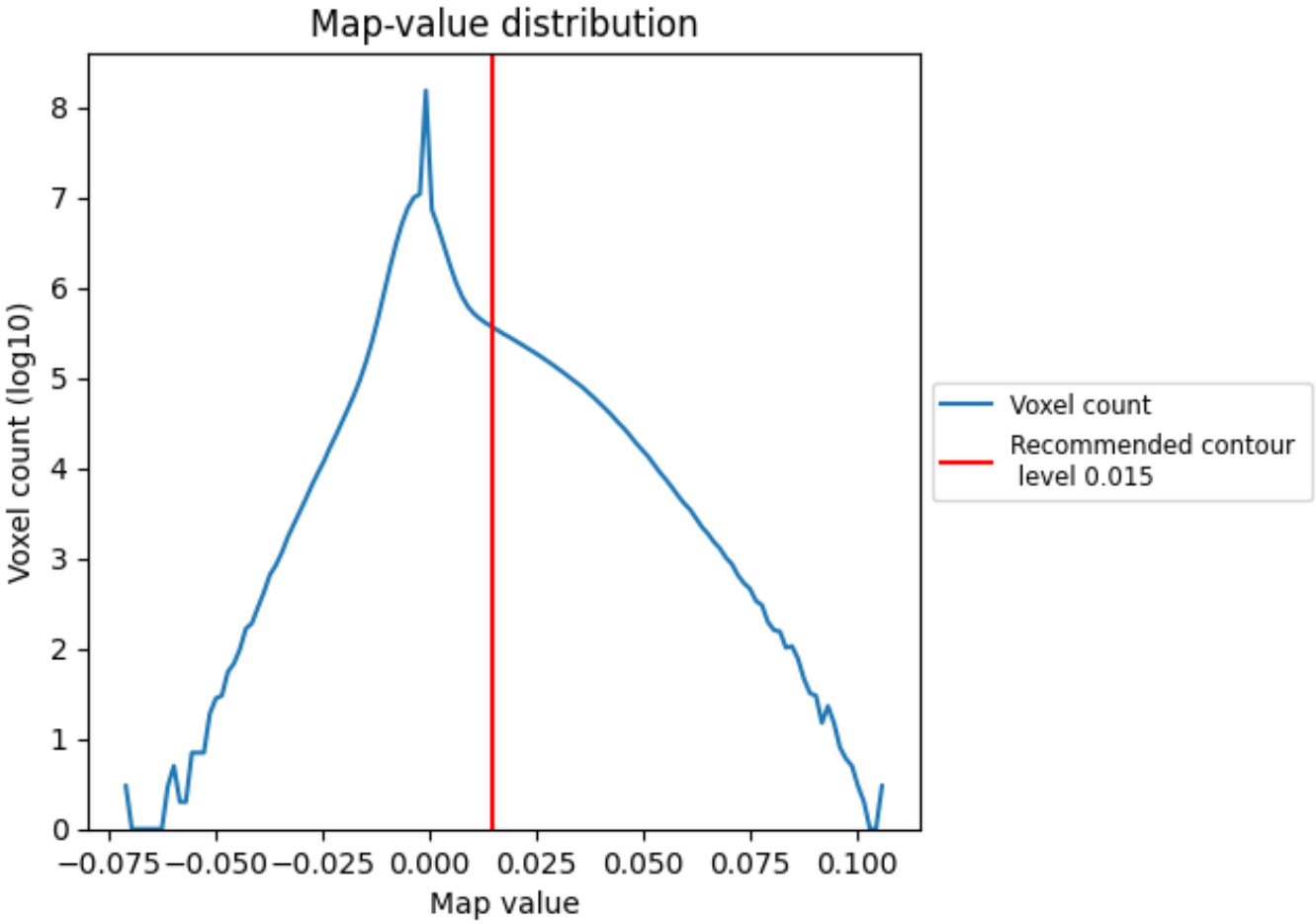
6.6 Mask visualisation (i)

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

7 Map analysis

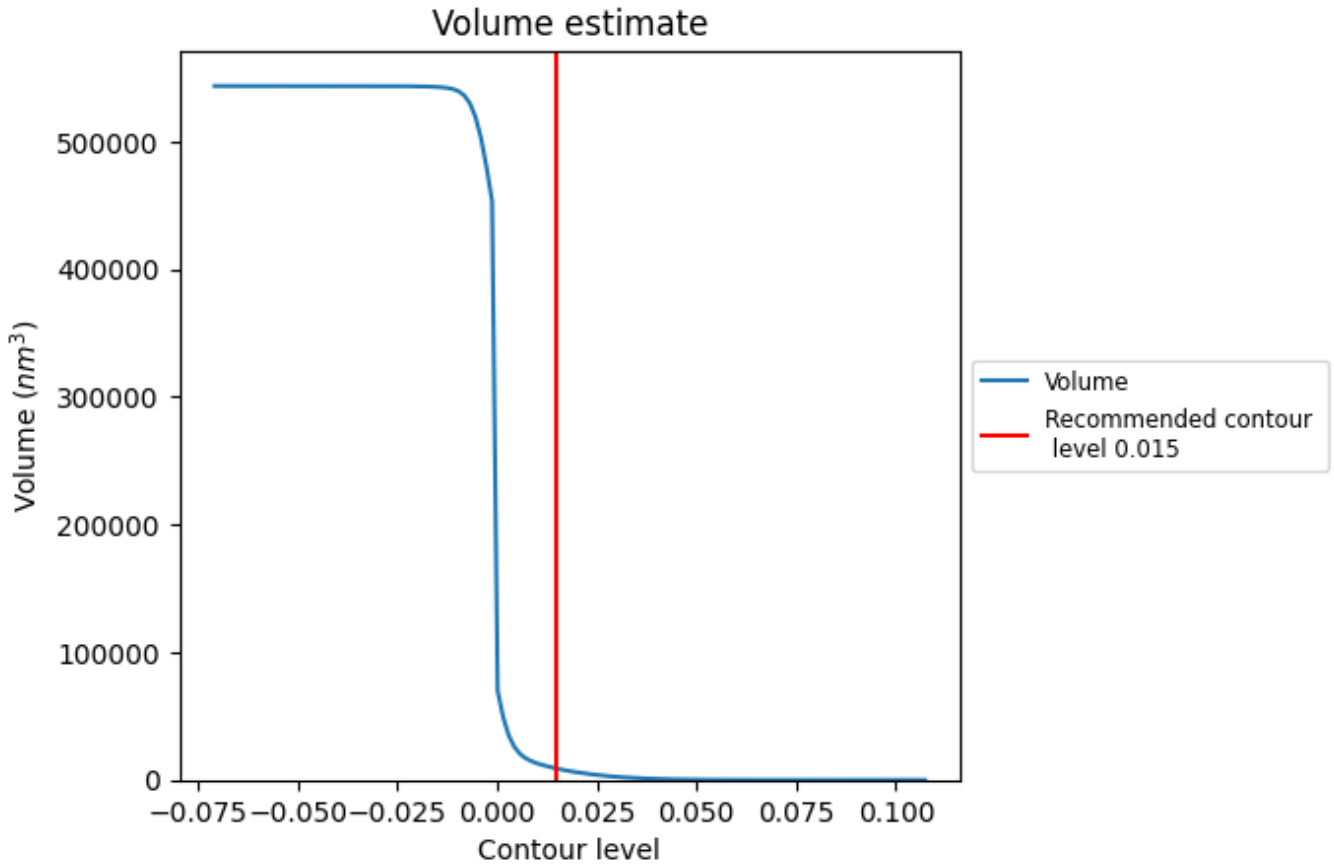
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

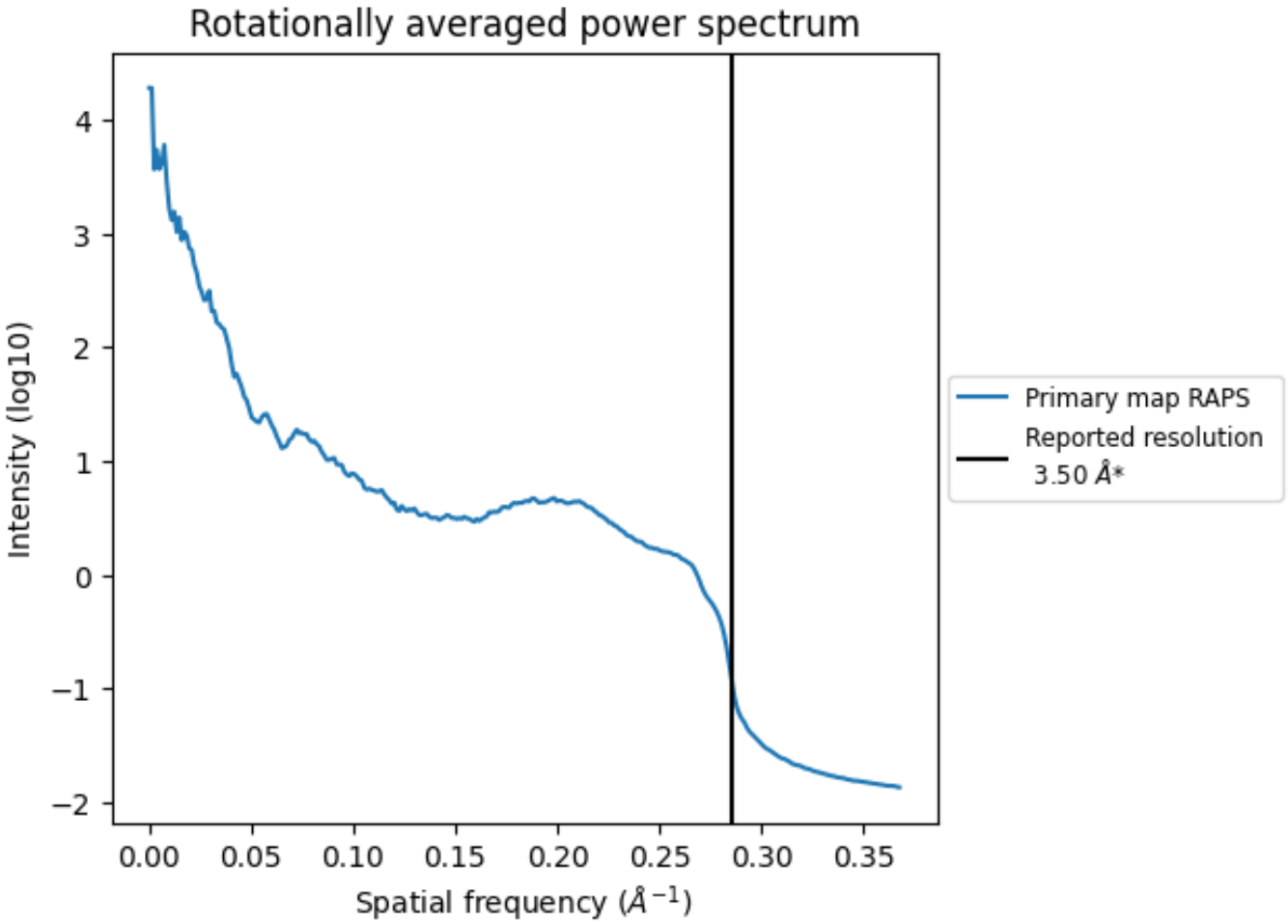
7.2 Volume estimate



The volume at the recommended contour level is 8892 nm^3; this corresponds to an approximate mass of 8032 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 0.286 Å^{-1}

8 Fourier-Shell correlation

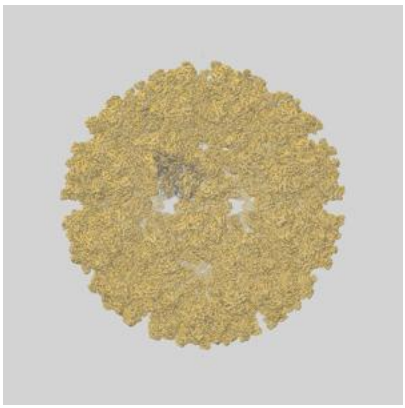
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

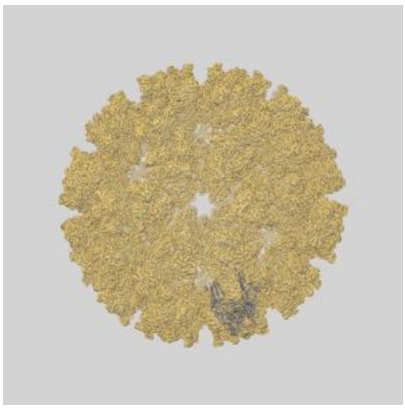
This section contains information regarding the fit between EMDB map EMD-32412 and PDB model 7WC2. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

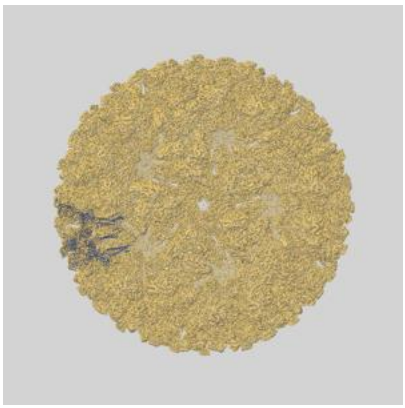
9.1.1 Map-model overlay



X

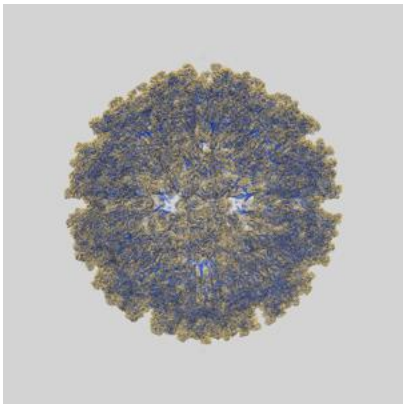


Y

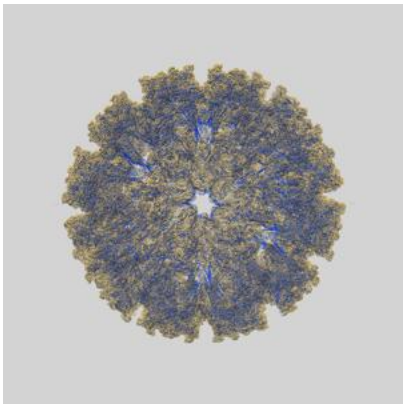


Z

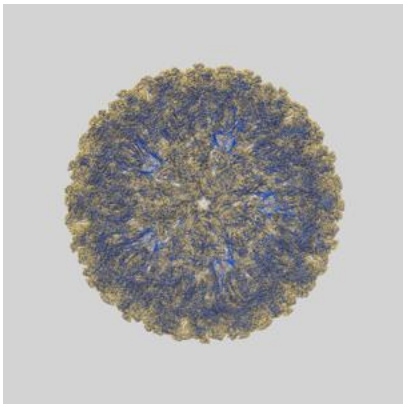
9.1.2 Map-model assembly overlay



X



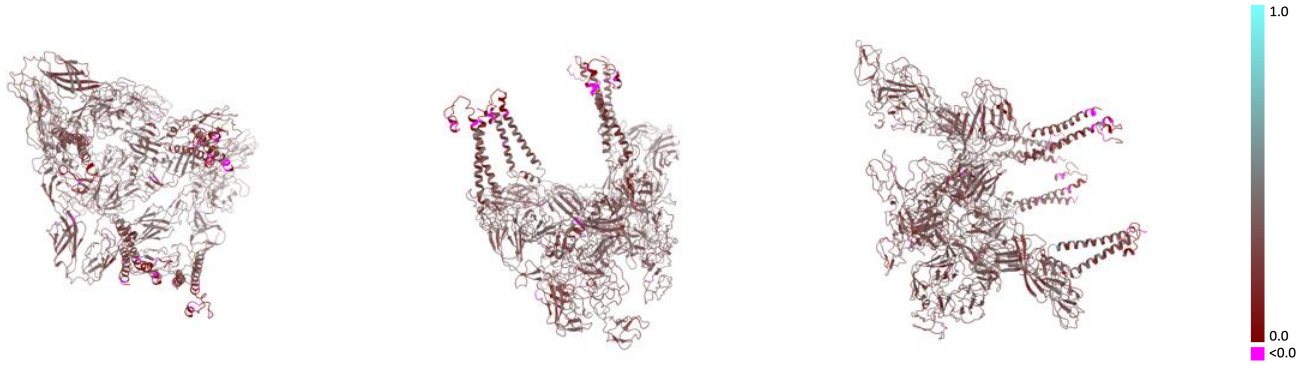
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015 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.

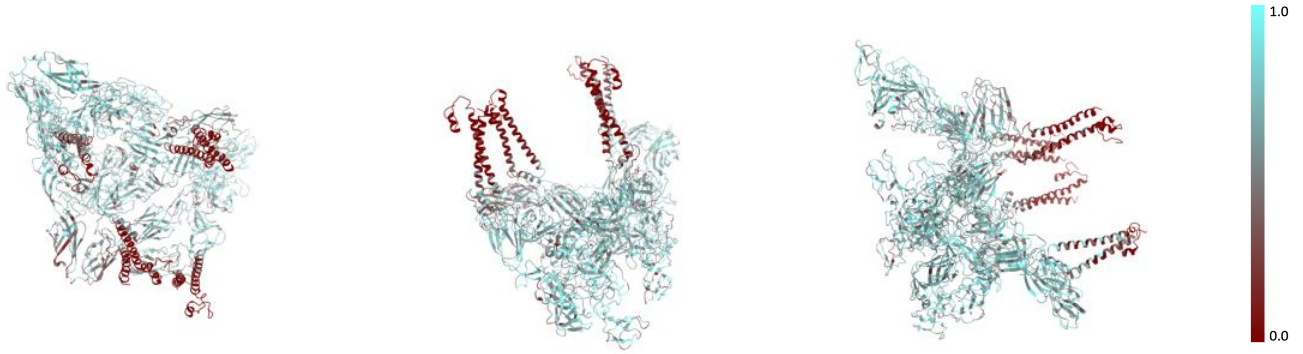
9.2 Q-score mapped to coordinate model (i)



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.

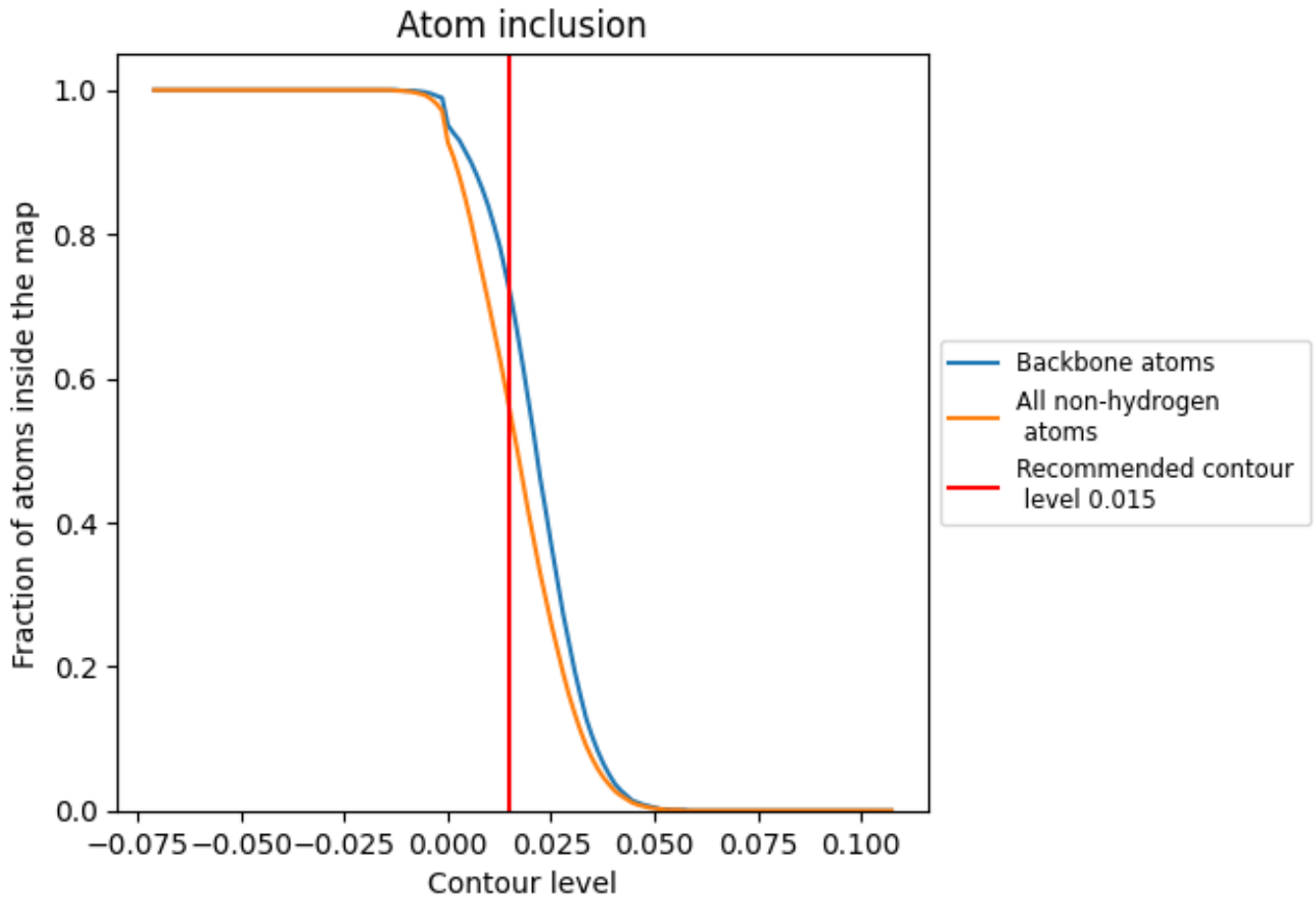
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.015).

9.4 Atom inclusion (i)



At the recommended contour level, 72% of all backbone atoms, 56% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5580	0.3010
A	0.5800	0.3250
B	0.5530	0.2900
D	0.5380	0.3110
E	0.5590	0.2900
G	0.5540	0.2940
H	0.5430	0.2810
J	0.6210	0.3160
K	0.5960	0.3180
a	0.0490	0.1640
b	0.3770	0.2650
c	0.0820	0.1460
d	0.1800	0.2540
e	0.2460	0.1790
f	0.0820	0.2080
g	0.1470	0.2970
h	0.4590	0.2950
i	0.2460	0.2780
j	0.0660	0.1400
k	0.4100	0.3040
l	0.0330	0.1860